

>1510259A metalloprotease [Protobothrops flavoviridis]  
ERFPQRYIELAIVVDHGMYYKYNQNSDKIKVRVHQMVNHINEMYRPLNIAISLNRLQIWS  
KKDLITVKSASNVLTESFGNWRETVLLKQQNNDCAHLLTATNLNDNTIGLAYKKGMCNPK  
LSVGLVQDYSPNVFMVAVTMTHELGHNLGMEHDDKDKCKCEACIMSDVISDKPSKLFSDC  
SKNDYQTFLLTKYNPQCILNAP

>3S18\_B lectin [Cicer arietinum]  
TKTGYINAAFRSSRNNEAYLFINDKYVLLDYAPGTSNDKVLYGSPFVRDGYKSLAKTIFG  
TYGIDCSFDTEYNEAFIFYENFCARIDYAPHSDKDKIISGPKKIADMFPFFKGTVFENGI  
DAAFRSTKGKEVYLFKGDYARIDYLTNRLVQNKISISDTGFPCLRGTIFEAGMDSAFASH  
KTNEAYLTKGEYARINFTPGSTNDIMGGVKKTLDYWPSLRGIIPLE

>4ZCE\_A Der p 23; peritrophin [Dermatophagoides pteronyssinus]  
SFTKFECPSRFGYFADPKDPHKFYICSNWEAVHKDCPGNTRWNEDEETCT

>5E1R\_A Car i 2; 7S globulin, vicilin-like [Carya illinoensis]  
MSREEEQQRHNPYYFHSQGLRSRHESGEVYLERFTELLRGIENYRVVILEANPN  
TFVLPYHKDAESVIVVTRGRATLTFVSQERRESFNLEYGDVIRVPAGATEYVINQDSNER  
LEMVLLQPVNPNPQGFREYYAAGAQRSTESYLRVFSNDILVAALNTPRDRLERFFDQQEQR  
EGVIIRASQEKLRALSQHAMSAGQRPWGRSSGGPISLKSQRSSYSNQFGQFFACPEEH  
RQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVVVEGTGRFEMACPHDVSSQSYEYKGR  
REEEEEESSTGQFQKVARTARLARGDIFVIPAGHPAITASQENLRLVGFINGKNNQRNF  
LAGQNNIINQLEREAKELSFNMPREEIEEIFERQVESYFVPMERQSRRGQGRDHPLASIL  
DFAGFF

>5EM0\_A Art v 4; profilin [Artemisia vulgaris]  
GSGSWQTYVDDHLMXDIEGTGQHLTSAAIIFGTDGTVWAKSASFPEFKPNEIDAIKEFNE  
AGQLAPTGLFLGGAKYMIQGEAGAVIRGKKGAGGICIKKTGQAMVFGIYDEPVAPGQCN  
MVVERLGDYLLDQGM

>5EM1\_A Amb a 8; profilin [Ambrosia artemisiifolia]  
GSGSWQTYVDEHLMXDIEGTGQHLSAAIIFGTDGNVWAXSSSFPEFXPDEINAIKEFSE  
PGALAPTGLFLAGAXYMIQGEPAVIRGXXGAGGICIXXTGQAMVFGIYEPPVNPQCN  
MVVERLGDYLVLDQGM

>5EV0\_A Amb a 8; profilin [Ambrosia artemisiifolia]  
SGSWQTYVDEHLMXDIEGTGQHLASAAIIFGTDGNVWAKSSSFPEFKPDEINAIKEFSEP  
GALAPTGLFLAGAKYMIQGEPAVIRGKKGAGGICIKKTGQAMVFGIYEPPVNPQCNM  
VVERLGDYLVLDQGM

>A0A161AT60.1 Pis s 3; lipid transfer protein [Pisum sativum]  
MARSMKLACVALVICMVVIAPMAEAAALSCGTVSADMAPCVTYLQAPNNASPPPPCCAGVK  
KLLAAATTPDRQAACNCLKSAAGSIPKLNNTNAAAALPGKCGVSIPYKISTSTNCNTVRF

>AAU43733 Citr l 2; profilin [Citruillus lanatus]  
MSWQAYVDDHLMCEIEGNHLTSAAIIGQDGSVWAKSENFQPKPEEITGILNDFNEPGTL  
APTGLYIGGSKYMIQGEPAVIRGKKGPGGVTVKKTALALVIGIYDEPMTPGQCNMIVE  
RLGDYLIEQGL

>ADV71357.1 metalloprotease [Protobothrops mucrosquamatus]  
MIEVLLVTICLAVFPYQGSSIILESQNVNDYEVVYPRKVSALPKGAVQPKYEDTMQYELK  
ENGEVVLHLEKKNGLFSEDYSETHYSPDGREITTYPSVEDHCYHGRIHNDADSTASIS  
ACDGLKGYFKLQGQTYLIEPLKLPDSEAHAVFKYENIEKEDEAPKMGVTVQNWESDESIK  
KASQLYLTPEQQRFPQRYVKLAIIVVDYRMYIKYNRDSNKITVRVHEMNVHVNEMYKPLNV  
AITLSLLRIWSTRDLITVQSDSKVTLSFGDWRKTVLLKQQSHDCAHLLTDITFTKNVIG  
VAYKKGMCDPKLSVGLVQDYSSNVFVAAIMTHELGHNLGMEHDEDENGKKCKCDTCIMS  
PAISDPPAQLFSDCSKNDYHTFLTNSKPQCILNAPLRTDTVSTPVSQNEPL

>AEB54655.1 Pro c 8; triosephosphate isomerase [Procamburus clarkii]  
MANQRKFFVGGNWKMNDRAGIDSIIISFMKGPLSADTEVVVVGCPQCYLMTREHLPSNIG

VAAQNCYKVAKGAFTEISPSMIKDCGCEWVILGHSERRNVFNEPDTLISEKVGHALEAG  
LKVIPICIGEKLEERESNRTEEVVFAQMKALVPNISDWSRVVIAAYEPVWAIGTGKTATPEQ  
AQEVHAKLRQWLRDNVNAEVADSTRIIYGGSVTPGNCKELAKTGDIDGFLVGGASLKPDF  
VQIINARD

>AFJ80778.1 Scy p 4; calcium-binding protein, sarcoplasmic calcium-binding protein  
[Scylla paramamosain]

MAYSWDNRVKYVVRYMYDIDNNGYLDKNDFECLALRNTLIEGRGEFNSDAYANNQKIMSN  
LWNEIAELADFNKDGQVTVDEFKQAVQNLCCGKSFDFGPPCFKTVIGRLFKTIDINGDGL  
AGVDEYRLDCISRSAFSSVKEIDDAYAKLCTDDDKKAGGISLNRYQELYAQFISNPDEKC  
NAVYLFGLPLKEVQ

>AHZ10957.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]

MGVFTYETEFTSVIPPPRLFKAFILDADNLIPKIAPQAVKCAEIVEGDGGVGTIKKITFG  
EGSQFGSVTHKIDGIDKENFVYSYSLVEGDALSDKIEKISYETKLVASSDGGSVIKSTSN  
YHTKGDVEIKEEHVKAGKEKASHLFLKLVEDYLLANPNEYC

>AHZ10958.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]

MGVFTYETEFTSVIPPPRLYKAFVLDTDNLIPKIAPQAVKSTELVQGDGGVGTIKKIHLG  
EGSEYSYVKHQIDGLDKDNFVYNYSIIEGDAIGDKVEKISYEIKLVASPSGGSIKSTSH  
YHCKGEVEIKEEHVKAGKERAAGLFKIIENYLLGNPDAYN

>AHZ10959.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]

MGVFTYETEFTSVIPPPRLYKAFVLADNLIPKIAPQAVKSAEIVQGDGGVGTIKKIHLG  
EGSEYSYVKHQIDGLDKDNFVYNYSIIEGDAIGDKVEKISYEIKLVASPSGGSIKSTSH  
YHCKGEVEIKEEHVKAGKEKAAGLFKIIENHLLANPEAYN

>AHZ97469.1 Alt a 15; serine protease [Alternaria alternata]

PQRQMSAKEVPNSYVVFKKHVVDASKHHDWVQSVHSKNNEERMELRKRSSQFPVTTEV  
FDGLKHVYEMAGMKGYSGHFDDETIEAIRNHPDVDYIERDSEVHTLGHDEPEIEKNSPWG  
LARISHRDSLSFGTWNKYLYAADGGEGVDVYVIDTGTNTKHVDFEGRAKWGKTIPNGDAD  
EDGNHGHTHCSGTVAGKKYVAKKAHVYAVKVLRSNGSGTMSDVVKGVEYAAKAHSDTVQ  
AAKDGKKKGFKGSANMSLGGGKSTTLDLAVNAAVDAGIHFAVAAGNDNADSCNYSPPAA  
ENAVTVGASTLLDERAYFSNYGKCNDIFAPGLNILSTWIGSEHATNTISGTSMASPHIAG  
LLAYMLSLQPAKDSAYAVADITPKKLLKANLISVATVGALSDVPRNTKNILAWNGGGSSNY  
TEIVEKGGYTVKKAEEKNEESEFRITIPSLSEIEDDFEKAKESAGRNAHRVGGKQLQHLE  
AEIEDFIAEEMESMFVKERVASQKL

>AJA79001.1 Fus p 9; serine protease [Fusarium proliferatum]

DKCDGETERQAPWGLARISHRNTLNFGTFNKYLYSSDGGEGVDAYIVDTGTNVHDVDFEG  
RAHWGKTIPSGDADEDGNHGHTHCSGTVAGKKYVAKKANVYAVKVLRSNGSGSMSDVVK  
GVEFAATSHLEQKKKAKDGKRKGFKGSVANMSLGGGKTQALDAAVNAAVRTGIHFAVAAG  
NDNADACNYSPPAAASEPVTVGASALDDSRAYFSNYGKCTDIFAPGLNIQSTWIGSKYAVN  
TISGTSMASPHIAGLLAYLQPAEDSEYALASITPKKLLKENLISVATEDALSDIPSDT  
PNLLAWNGGGCSDYKKIVEAGSYKVAAPSSRVVEIKHAVEQEVNLLVSGKLTGAKELGS  
KAEKFSKKIHELVDDEELEEFLKELNL

>COMPARE0350 unknown function, translation from AK068307.1 [Oryza sativa]

MKLVSIIYLLVLCVVGANELLVVAASGNDGGGGRFVYSGFAGANLTLDTATVTPAGLIEL  
TNGTLQLKGHAFHPTPLRFGFGSGGGGGGDGWWVRSFSASFVFGILSAYPDMSAHGIVFL  
VSPTTDFSAALASQYLGLVNVTSNGDARNRIFAVELDTLQQDEFRDINDNHVGVINDINGLV  
SLQSTSAGYYAADINGGGFRNLTLISHEAMRVWVDYDAGDARIDVTLAPLAVAKPVRPLI  
SAAYNLSSVITDTAYVGFSSATGSFNSRHVYLGWSFAVDGGPAPAIDVAKLPKLPREGPK  
ARSKFLEIFLPIASAAVVLAMGILVILLVRRRKRYTELREDWEVEFGPHRFYKDLHHT  
QGFESKCLLVGGGFRVYKGVLPNSNVEIAVKRVSHDSSQGVKEFVAEVVSLGRLQHCNL  
VRLLGYCRRKGELMLVYEYMSNGSLDKYHLHGQDNKPTLSWAQRFQIHKDIASGLLYLHEE  
CDKVVIIHRDIKASNVLLDNEMNARLGDGFLARLYDHGEDPQSTHVVTIGYLAPELGRTS

KATPLTDVFAFGTFILEVTCGRRPIYHDSHGTVMLVDWVLDHWHKQSLVDTVDLKLHGE  
FDVGEACLVLKGLLCSHPFINARPDMMRVMQYLKREVALPELMPTSMSFHMLALMQNDG  
FDSYVQSYSSNSKGNISTATSSLLEEG

>COMPARE0351 unknown function, translation from AK119653.1 [*Oryza sativa*]

MDRVRGCAFLGLVLLAGSLFAFSVAKEETKLLGTVIGIDLGTTYSCVGVYKNGHVEIIAN  
DQGNRITPSWVAFTDSERLIGEAAKNQAAVNPRTIFDVKRLIGRKFEDKEVQRDMKLV  
YKIVNKDGGKPYIQVKIKDGENKVFSPPEVSAMILGKMKETAAYLGGKINDAVVTVPAYF  
NDAQRQATKDAGVIAGLNVARIIINEPTAAAIAYGLDKKGGKKNILVFDLGGGTFDVSILT  
IDNGVFEVLATNGDTHLGGEDFDQRIMEYFIKLIKKKYSKDISKDNRALGKLRREAERAK  
RALSNQHQVRVEIESLFDGTDSEPLTRARFEELNNDLFRKTMGPVKAMDDAGLEKSQI  
HEIVLVGGSTRIPKAQQLLRDYFEGKEPNKGVNPDEAVAYGAAVQGSILSGEGGDETKDI  
LLLDVAPLTLGIETVGGVMTKLIPRNTVIPTKKSQVFTTYQDQQTTSIQVFEGERSMTK  
DCRLLGKFDLSGIPAAPRGTPQIEVTFEVDANGILNVKAEDKGTGKSEKITITNEKGRSL  
PEEIDRMVREAEFEAEEDKKVKERIDARNQLETVVYNNMKNVTGDKDKLADKLESEEKEKV  
EEALKEALEWLDENQTAEKEEYEEKLKEVEAVCNPIISAVYQRTGGAPGGGADGEGGVDD  
EHDEL

>COMPARE0352 unknown function, translation from AK242260.1 [*Oryza sativa*]

MKIIFV FALLAIAACSASAQFDVLGQSYRQYQLQSPVLLQQQVLSPLYNEFVRQQYGI  
AASPFLQSAAFQLRNNQVWQQLALVAQQSHYQDINIVQAIQQLQLQQFGDLYFDRNLAQAQA  
LLAFNVPSRYGIYPRYYGAPSTITTLGGVL

>AKF12278.1 Par h 1; defensin [*Parthenium hysterophorus*]

MAKSSTSYLVFLLLVLVVAISEIASVNGKVCEKPSKTWFGNCKDTEKCDKRCMEWEGAKH  
GACHQRESKYMCFYFDCDPKKNPGPPGAPGTPGTPAPPGGGEGDAPPGGGAPPAGG  
EGGGGGGEGGGGAPPAGGEGGGGGGGGGGAPPAA

>AKV72166.1 Aca f 1; Ole e 1-like [*Acacia farnesiana* (*Vachellia farnesiana*)]

DDVPKPPVSQFHVQGLVYCDTCRYPFITEASPIMEGATVKLECRNITAGTQTFKAEAVTD  
KVGQYSIPVDGDHEDDICEIELVKSPDNQCSEIPHVDVYAKQSAKVSLTSNNGEASDV  
RSANALGFMRKEPLPECPEVLKEKLDMYDVKAN

>AKV72167.1 Pro j 1; Ole e 1-like [*Prosopis juliflora*]

DDVAKPPVSQFHIQGLVYCDTCRIQFMTRVSTIMEGATVKLECRNITAGTQTFKAEAVTD  
KVGQYSIPVNGDFEDDICEIELVKSPNSDCSEIPHVDVYAKQSAKVSLTSNNGEASDIR  
SANALGFMRKEPLKECEVSKEPLDMYDVKAN

>ALM30773.1 triosephosphate isomerase [*Amphioctopus fangsiao*]

MGRKFFVGGNWKLNKKSIDGIIEFMAGPLNADTEVVVGGPPSCYLEYVRSKLGKGNIGV  
AAQNCYKVPSTGFTGDISPAMIKDIGLRYVILGHSERRNVFGETDELIGEKEIEHAVSEGL  
IVIACIGEKLEEREAGKTEEVVFSQTKTIKHTKDWKSVVIAYEPIWAIIGTGKTATPEQA  
QSVHASLRKFIENASKEIADNVRILYGGSVSAANCKELGQKPDIDGFLVGGASLKP  
DFVKIVNARA

>ANQ43386.1 glyceraldehyde-3-phosphate-dehydrogenase [*Mangifera indica*]

MAGGKKIKIGINGFGRIGRLVARVALQRNDVELVAVNDPFITTDYMTYMFKYDTVHGQWK  
HHEVKIKDQKTLLEFDEKPVTVFGIRNPEEIPWAETGAEFVVESTGVFTDKEKAAAHLKGG  
AEKVVISAPSKDAPMFVVGNEKEYKPELNIVSNASCTTNCLAPLAKVINDRFGIVEGLM  
TTVHSITATQKTVDGPSMKDWRGGRAASFNIIPSSGAAKAVGKVLPSLNGKLTGMSFRV  
PTVDVSVVDLTVRLEKEATYEEIKAAIKEESEGLKLGILGYTEEDVSTDFVGDSSR  
SIFDAKAGIALNKKFVKLVSWYDNEWGYSSRVIDLIVHMASTA

>ANZ22900.1 Amb a 12; enolase [*Ambrosia artemisiifolia*]

MATIKAVKARQIFDSRGNPTVEVDITLSDGTLARAAPVSGASTGIYEALERDGGSDYLG  
KGVSKAVANVNTIIGPALVGKDPTDQTGIDNFMVQQLDGTQNEWGWCKQKLGANAILAVS  
LAVCKAGASVLKTPLYKHIANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPIGA  
SSFKEAMKMGVEVYHNLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKAG

YTDKVVIGMDVAASEFYGEKDKTYDLNFKEENNDGKEKISGEQLKDLYKSFVSEYPIVSI  
EDPFDQDDWEHYAKMTAECGEQVQIVGDDLLVTNPTRVKKKAIDEKTCNALLLKVNQIGSV  
TESIEAVRMSKHAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL  
LRIEEELGSEAVYAGANFRKPVEPY

>ANZ22901.1 Amb a 12; enolase [*Ambrosia artemisiifolia*]  
MLFVDEIKVDITLSDGTLARAAVPSGASTGIYEALERDGGSDYLKGVSKAVANVNTII  
GPALVGKDPTDQTGIDNFMVQQLDGTQNEWGWCKQKLGANAILAVPLAVCKAGASVLKTP  
LYKHIANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPIGASSFKEAMKMGVEVY  
HNLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKAGYTDKVVIGMDVAAS  
EFYGEKDKTYDLNFKEENNDGKEKISGEQLKDLYKSFVSEYPIVSI  
EDPFDQDDWEHYAKMTAECGEQVQIVGDDLLVTNPTRVKKKAIDEKTCNALLLKVNQIGSV  
TESIEAVRMSKHAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL  
LRIEEELGSEAVYAGANFRKPVEPY

>XP\_005598291.1 uteroglobin [*Equus caballus*]  
MRLFLPVLLVTLALCCCEATNAATCPAVATDIASFFLLPDSLFLKQLIKYQAPPEAKDATM  
QVKQCINEISAGDRYIITETLGKIVLQCGA

>XP\_003362701.1 uteroglobin [*Equus caballus*]  
MKLVTVLMLVAFPLYCYAGSGCQLLEDVVEKTITAELSPAIEYVEAVQEFIPDEATEKAAI  
QLKQCYLKQSNETLNDFRMTMMNSMYNSAYCALF

>APD76154.1 Jug r 5; pathogenesis related protein, PR-10, Bet v 1-like [*Juglans regia*]

MGVFTYETESTSVIPPARLFKAFVLDADNLIKVPVQAVKSSEIEGNGGPGTIKKINFG  
EGSQYKYVKHRTDAIDEANFTYAYSVEGDALADKIEKISYETKIVASHEGGSILKSISH  
YHSKGDHEIKEEDVKDGKEKASGLFKAVEGYLLAHPDAYN

>APR62629.1 Jug n 4; 11S globulin, cupin [*Juglans nigra*]  
MAKPILLSISLCLVALVNGCLAQSGGRQQPRFGECKLKRVALEPSNRIEAEAGVIESWD  
PNNQQFQCAGVAVRRTIEPNGLLLPQYSNAPQLLYIVKGRGITGVLFPGCPETFEESSQQ  
GQSRIRPSLRASAFQRDRHQKIRHFREGDVIAFPAGVAHWCYNDGDPVVAVALMDTTNN  
ANQLDQNPFRNYLAGNPDEFPRPQQEYEQHRRQQHQQRHGEPGQQQRGSGNNVFSGF  
DADFLADAFNVDTETARRLQSENDHRRSIVRVEGRQLQVIRPRWSREEQEREERKERERE  
RESEERRQSRGRDDNGLEETICTLRLRENIGDPSRADIYTEEAGRISTANSHTLPVL  
RWLQLSAERGAALYSDALVPHWNLNAHSVYALRGRAEVQVVDNFGQTVFDDELREGQLL  
TIPQNFVAVKRARNEGFEWVSFKTNENAMVSPLAGRTSAIRALPEEVLANALQIPREDAR  
RLKFNRQESTLVRSRPSRSSRSERRAEV

>ARG42047.1 lipocalin [*Mesocricetus auratus*]  
MKLLLLLLVGLLELTVCVHAEKTSLTGKNFNPEKIVGKWHILLSKDKREMIEEYGS  
RMFMEYIRLFKNSSLAVKFHTIANEECTELYLVCCKTEKGGVYDAKYDGYNRFTILDY  
NDYIITHLRNIKNGETFQMLKLCGRKPKLSSNIKKKFGDLCQKHGIVKENIIDL  
TEADHC LKTQVEIVA

>ARS33724.1 Sal k 6; polygalacturonase [*Salsola kali*]  
MKTFNLPLLVALFYLFVSVARSQGPIDITKFGAKPNADATSALLAAWKEACAAAAPAKIV  
VPAGEFLLNAVKLQGPCKAPLTIEIAGNFKAPADVAQMKGEDTWVKIENVQGLTITCLPT  
GGTDFDQGGQAAWKQNKCAQSGMCNSLPYNFRFNTLTNAQISGIKSLNSKLYHMGVMGCKN  
ITLTGLTIDAPKDSLNTDGMHIGRSNGVHATNSKIGTGDDCISMGDGAVDVHVEGITCGP  
GHGISIGSMGKFAEAPNTGIFVKNCSFTDNDNGVRIKSWMNSFEASASDLHFEDITVTN  
VLNPVIIDQEYCPYNHCKEKTSPKVKLSKISFKNVHGAAKSAEVVKLLCSSAVPCDGV  
ELADIDLTFPGGAAVSQCKNVKPIVTGKQNPVACGAPATPAAP

>B8AL97.1 cupincin [*Oryza sativa*]  
MAKKKTSSSMARSQLAALLISLCLSLASNAVGWSRRGEREEEDERRRHGGEGGRPYHFG  
EESFRHWTRTRHGRFSVLERFPDEQVVGAAVGGYRVAVLEAAPRAFLQPSHYDADEVFVY

KEGEGVIVLLREGRKESFCVREGDAMVIPAGAIVVSANTHSSKWFRVVMLLNPVSTPGHF  
EEYFPVGGDRPESFFSAFSDDVLQAAFNTRREELEKVFERQREGGEITTAPEEQIRELSK  
SCSRGGGGGSGSEWEIKPSSLTGKSPYFSNMHGKLFELTGDECRHLKKLDLQIGLANITR  
GSMIAPNYNTRATKLAVVLQSGSYFEMACPHVSGGSSERREREREHGRRREREEQEEEEH  
GERGEKARRYHKVRAQVREGSVIVIPASHPATIVASEGESLAVVCFVVGANHDEKVF LAG  
RNSPLRQLDDPAKKL VFGGSAAREADRVLAAQPEQILLRGP HGRGSVSDM  
>BAG86826.1 unknown function [*Oryza sativa*]  
MKMKALLPVAAMLLLVSGQLAAPVTADGYVQQLAVFWGRHKEEGSLREACDTGRYNIVVI  
TFYNVFGYQRGRYGLDFSGHPVAAVGADIKHCQSKGVQVLLSIGGQGGEYSLPSSQSASD  
VADNLWNAV LGGRRAGVPRPFGDAVVDGIDFFIDQGGADHYEQ LARQLHGRGVLLTATVR  
CAYPDSRMEAAATGVFARIHVRIFGDDQCTMFPKDAWEKWAAAYPRCTVFLTVVASPEQ  
DEGYMFQKDL YGVQQFIDKEPNYGGIAIWD RRYDKKANYSGEG  
>BAG88472.1 unknown function [*Oryza sativa*]  
MASSSFSLVAALLGLASWKAIASDPSP LQDFCVADLNSPVRVNGFVCKNPMNASADDF  
FKAAMLDKPRDTNNKVGSNVTLVNVLQLPGLNTLGIS IARLDFAPLGLNPPHHPRATEI  
FTVLEGLTYVGFVTSNPDNRLLSKVLNKG DVFVFEGLIHFQFNPNPHKPAVAIAALSSQ  
NPGVITIANAVFGSNPPISDDILMKAFQVDK KIIDLQAQF  
>BAG93480.1 unknown function [*Oryza sativa*]  
MPPDVEVIRHEHIDHPSSTRDRSVVSSNSL SNTVSAYTDMKNTSSLCLLLLVLCSLTC  
NSGQAQVLFQGFNWE SWKQGGWYNMLKGQVDDIAKAGVTHVWLP PPSHVSAPQGYMPGR  
LYDL DASKYGTAAELKSLIAAFHGKGVQCVADV VINHRCAEKKDARGVYCVFEGGTPDDR  
LDWGP GMICSDDTQYSDGTGHRDTGEGFGA APDIDHLNPRVQREL TDWLNWLKSDVGF DG  
WRLDFAKGYSTDI AKMYVESCKPGFVVAE IWNLSYNGDGKPAANQDQGRQELVNWVNAV  
GGPAMTFDFTTKGLLQAGVQGELWRLRDGNGKAAGMIGWLPEKAVTFVDNHDTGSTQKLW  
PFP SDKVMQGYAYILTHPGVPCIFYDHMF DWNLKQEITALAAIRERNGINAGSKLRIVVA  
DADAYVAVVDEKVMVKIGTRYDVGN AVPSDFHQTVHGKDYSVWEKGS LRV PAGRHL  
>BAG95020.1 unknown function [*Oryza sativa*]  
MEQYEKVEKIGEGTYGVVYK GKHRHTNETIALKKIRLEQEDEGVPSTAI REISLLKEMQH  
RNIVRLQDVVHKEKCIYLVFEYLDL DLKHKHMDSSPDFKNHRIVKSFLYQILRGIAYCHSH  
RVLHRDLK PQNLLIDRRTNSLKLAD FGLARAFGIPVRTFTHEVVT LWYRAPEILLGARHY  
STPVDMMWSVGCIFAEMVNQKPLFPGDSEIDELFKIFSIMGTPNEETWPGVASLPDYISTF  
PKWPSVDLATV VPTLDSSGLDLLSKMLRLDPSKRINARA ALEHEYFKDLEVA  
>BAH01262.1 unknown function [*Oryza sativa*]  
MKIIFFFALLAIAACSASAQFDAVTQVYRQYQLQPHLMLQQQMLSPCGEFVRQQCSTVAT  
PFFQSPVFQLRNCQVMQQCCQQLRMIAAQQSHCQAIS SVQAIVQQLRLQQFASVYFDQSQ  
AQAQAMLALNMP SICCIGIYPSYNTAPCSIPTVGGI WY  
>BAV90601.1 Der f 34; enamine/imine deaminase [*Dermatophagoides farinae*]  
MSPKRIISTPLAPQPIGPYSQAVQVGN TVYLSGQIGMNVRTNEMVTGP IRDEAQQAF TNM  
KAVVEASGAKMSDVVKVNI FIRNFND FPAINDVMKEFFQSPFPARSTVGVAELPKNARVE  
IESIVVIE  
>BAW03242.1 Lip b 1; unknown function [*Liposcelis bostrychophila*]  
MAAIKFILIAFLAFSVSQTTEANVVAQPKAFDIIAIVKQVIDIVRIVVKAVNDAVPDIDK  
ILQQLVALLPSDVAATVTTVLDAIKQAITDENARIDHIIQVLEKAMDDL LAIDPCYQPQA  
DAIKAVL DKALSGIDGVLHGSIDAHKADIDNVIAGFSQDLEDLRNLYDTQLPAAVCLTP  
GNAESCGCLDGVKETV VNGVVS LAANFVLHLTAASDV LKVVVPEVINGSTPIVNDGLAAA  
GPLIDNVCTCVAAM  
>BAW03243.1 Lip b 1; unknown function [*Liposcelis bostrychophila*]  
MAAFKFILLAF LAFSVSQTTEANVVAQPRAFDIIDIVKKVIQIVEIVVEAVNGAVEPIDK  
ILQELIALLPADVAKTVTAVVDALRQAIADENVRIDHIEVLNKALDDL LAIDPCYQPQA  
DAIKAVLDTALSGIDKVLHGSIDAHKADIDNVIAGFSQDLEDLRNLYDTQLPAAVCLTP

GNADSCTCLDGVKETVWNGVWSLAANFVLHLTAASDVLKVVVPEVIDGATPVVNDGLAAA  
GPLIDNVCACVQGM  
>BAX34757.1 Der f 35; NPC2-like [Dermatophagoides farinae]  
MIKFLCIFALTFAVASAGMKMFVDCGHKEVISLDVSGCEGDYCVLHKGKTIDLDMKCKSN  
QDSEHLKLIISADVNGIEIEVPGFDQDGCHYVQCPIHKGQDYDIKYSYNVPAVLPNIKGT  
LTAKVIGDNGLVGCLKLNGEIAAD  
>C0HJX6.1 Pla l 2; profilin, partial [Plantago lanceolata]  
AILGQDGSVWAQGLHLGGAKYVIAGEPGAVIRLGDYLLDQGL  
>C0HKB1.1 Cup s 2; polygalacturonase [Cupressus sempervirens]  
DVAIVFNVEHTLSAVFLVPANKKVDGIIAAYPDPVKIWMHFARTVCNDKGRPTAIKIDFS  
KSELTLMNSPEFHLVFGEDGVKIQGKIKRFEIEKDLTCGPGHGMSIGSLGKGNRSRSEV  
SFVHLDGAKFIDTQNGLSAVKIEDVTFKNANGYYTNPLNPPCK  
>C0HKC0.1 Pun g 7; gibberellin-regulated protein [Punica granatum]  
GSSFCDKCAVRCSKAGVQD  
>CAA58223.1 fibrinogenolytic protease [Protobothrops mucrosquamatus]  
MVLIRVLANLLILQLSYAQKSELVIGDECNINEHPFLVLYVYDDYQCGGTLNNEEWL  
TAAHCNGKDMEIYLGVHSHKVPNKDVQRRVPKEKFFCDSSKTYTKWVKDIMLIRLDRPVR  
KSAHIAPLSLPSSPPSVGSVCRVMGWTITSPQETYPDVPHCANINLLDYEVCRAAYAGL  
PATSRITL CAGILEGGKDCVGDGSGGPLICNGQFQGI VSWGGDPCAQPREPGVYTNVFDHL  
DWIKGIIAGNTDVTCP  
>CEE03318.1 unknown function [Thaumetopoea solitaria]  
VPQLSEKAEKAVDLTYQEKNL FELGSVVDIISKNGCHVSFGCHKGYCWAGCGNPTNPW  
SWGEMWCYTTKTYQSYSYVQCTQDSECDGCWKCGGPCSA  
>L7UZ85.1 alpha-actinin [Dermatophagoides farinae]  
MTQDGYMQEEEEWEREGLLDPAWEKQQRKFTTAWCNSHLRKAGTQIDNIEEDFRNGLKL  
MLLLEVISGETLGKPDGRGMRFKIANVVKALDFIESKGVKLVSIGAEEIVDGNKMTLG  
LIWTIILRFQIDISVEEMTAKEGLLLWCQRKTAPYKNNVQNFHLSWKDGLAFCALIHR  
HRPDLIDYGLRKNPMDNFNLAFDVAEKHLNIPRMLDAEDVYVYAKPDERAIMTYVSWY  
YHAFHGAQQAETAANRICKVLKVNQDNERLMEEYERLASDLEWIRRTTPWLENRTDNT  
LPGTQKKLEEFRSYRRQHKPPRVEQKANLETNFNTLQTKLRLSKRPAYMPSEGKMSDIT  
GAWKGLESAEKGFEEWLLSEMMRLERLDHLAQKFKHKADIHEEWTQGEEMLVSHDFRQC  
KLNEIKALKKKHEAFESDLAAHQDRVEQIAAIAQELNALGYHDIASINARCQRICDQWDR  
LGLTTRRRRQALDEAEQILEKVDL FHLFEAKRAAPFNWLDRETREDLVDMFIVHSIEEIQ  
QLIDAHESFKNTLGEADKEYKTIVGLAQEVQPMATQYQIPGGLENPYTTLTPEVITTKWR  
DVKQLVPQRDHTLQTELIRQQCNENLRQFAEKANVVGPIERQMDAVTAIGMGMQGTLE  
DQLQRLHEYDQAVVQYRPHVDDLEKIHQEVQEAMIFENRYTQYTMETLRVGEQLLTSIH  
RNINEVENQILTRDSKGITQEQLNEFRTSFNHFDKRTGRLAPEEFKSCLVSLGYNIRND  
DRPEFRIRLAIIVDPNKTGYVHFAFLDFMTREYTDTDTAEQMIDSFIRLAGDKPYITADE  
LRRELPPDQAEYCIRRMTPYNGQCAVPGALDYRSFSTALYGESDL  
>NP\_001003242.2 Can f 7; NPC2-like [Canis familiaris]  
MRLLVAAFLLLALGASALAEVHFVKDCGSAVGVIKELNVNCPAQPCPKLHKGQSYSVNVT  
FTSNIPSQSSKAVVHGIVLGVAVPFPIPEADGCKSGINCP IQKDKTYSYLNKLPVKNEY  
SIKLVVQWMLLDGNNQHLCWEIPVQIEG  
>NP\_001005208 Sus s 1; serum albumin [Sus scrofa]  
MKWVTFISLLFLFSSAYSRGVFRRTYKSEIAHRFKDLGEQYFKGLVLIAFSQHLQQCPY  
EEHVKL VREVTEFAKTCVADESAENCDSIHTLFGDKLCAIPSLREHYGDLADCCKEEP  
ERNECF LQHKNDPDIPKLPDPVALCADFQEDEQKFWGKLYEYIARRHPYFYAPELLYY  
AIIYKDV FSECCQAADKAACL LPKIEHLREKVL TSAAQRLKCAISIQKFGERAFKAWSLA  
RLSQRFPKADFTEISKIVTDLAKVHKECCHGDLLECADDRADLAKYICENQDTISTKLKE  
CCDKPLLEKSHCIAEAKRDEL PADLNPLEHDFVEDKEVCKNYKEAKHVFLGTFLYEYSRR

HPDYSVSLLLRIAKIYEATLEDCCAKEDPPACYATVFDKFQPLVDEPKNLKQNCLEFEK  
LGEYGFQNALIVRYTKKVPQVSTPTLVEVARKLGLVGSRCCKRPEEERLSCAEDYLSLVL  
NRLCVLHEKTPVSEKVKCTESLVNRRPCFSALTPDETYKPKFVEGTFTFHADLCTLP  
EDEKQIKKQTALVELLKHKPHATEEQLRTVLGNFAAFVQKCCAAPDHEACFAVEGPKFVI  
EIRGILA

>NP\_001036878.1 glycoprotein [Bombyx mori]  
MMWKTVLITIFAAGVLADDFSQITAVVTSQCTKNNAEDKVPEVEAALRTFGNCLKGLVDL  
NVLKTEIEEAKPNGALDEVFKKYCDKSAQLKGCISSVLQGVPCVGNAYANHINDAQNST  
NQLIDFVCYKGDRIALFIAEGGPECFQKQKTENLKTCLNKLKQSFPTVESANNLSLVEKC  
AKVDEMTSCIVKSLEECSTPTPANMAESLIKFMKDSPCHTALPKTD

>NP\_001037083 thiol peroxidase [Bombyx mori]  
MPLQMTKPAPQFKATAVVNGEFKDISLSDYKGYVVLFFYPLDFTFVCPTEIIAFSEKAD  
EFRKIGCEVLGASTDSHFTHLAWINTPRKQGGGLPMNIPLISDKSHRISRDIYGLDEETG  
IPFRGLFIIDDKQNLRQITINDLPVGRSVEETLRLVQAFQFTDKHGVECPANWRPGAKTI  
KPDTKAAQYFGDAN

>NP\_001316123 Sola 1 7; lipid transfer protein [Solanum lycopersicum]  
MKAIAILVVLAVFQLAMVARGAITCGQVDANLAPCVPLTQGGEPGAACCSGVRTLNG  
NTQSSDDRRACNCVKAANRYPNLKDDAAQSLPSKCGISLTVPISTRVNCDTIS

>P13080.1 Aed a 4; alpha-glucosidase [Aedes aegypti]  
MKIFVPLLSFLLAGLTTGLDWEHGNFYQVYPRSFKDSGDGIGDLGDVTEKLYLKDIDG  
MDGVWLSPIFSSPMADFGYDISNFREIQTEYGDLDADFQRLSDKCKQLGLHLILDFVPNHT  
SDQHEFYFKKSVQKDETYKDFYVWHPGVHGNNTKVPPSNWISVFRGSSWEWNEERQEFYL  
HQFLKEQPDNLNRPVAVVEEMKNVLRVWLDGVSFRIDAVPYLFESDIIDGRYRNEPES  
RTTDDPENPAYLVHTQTMDQPETYDMIYQWRAVLDEYSKTDNRTRIMTEGYTSLPKIIE  
FFGNATANGAQIPNFVVISNVKKNSTGADFATYVVRWLDKAPANRRSNWVLGNHNNRL  
GSRLGENKIDLYNIALQTLPDIAVTTYGEEIGMLDQWIPWNETVDPAAACRSDEASYSAYS  
RDPARTPMQWDSGKNAGFSKAAKTWLPVADNYKTLNVKIQDRARKSHLKFKLTKYRKR  
QILTEGDIDIKVSGENLLVYKRKVDKVGYYVVALNFGTEPVALGLSSLFDRADQRMQVWV  
SSNRVSTPDNVWVDVNYVLIGESGIVLQYLWGKNPIVS

>P29022 Zea m 8; chitinase [Zea mays]  
MANAPRILALGLLALLCAAAGPAAAQNCGCPNFCCSKFGYCGTTDAYCGDGCQSGPCRS  
GGGGGGGGGGGGGGGGANVANVVTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVNAYPG  
FAHGGTEVEGKREIAAFFAHVTHETGHFCYISEINKSNAYCDASNRQWPCAAGQKYGRG  
PLQISWNYNYGPAGRDIGFNGLADPNRVAQDAVIAFKTALWFWMNNVHGVMPPQGFATIR  
AINGALECNGNPAQMNAARVGYKQYCCQLRVDPGPNLIC

>Q75GX9.1 7S globulin, vicilin-like [Oryza sativa]  
MATRARATILLLLAAVLFAAAAAASGEDRRRETSRRLRCLQRCEQDRPPYERARCVQECKD  
QQQQQQERRREHGGHDDRRDRRRGEGSSEEEDEGRERGRRRPYVFGRRSFRQVVRSD  
QGSVRLPPPFHQASSLLRGIKNYRVAVLEANPRSFVMPHTHTDAHCICYVAQGEVVAIIE  
NGEKWSYAIRQGDVVFAPAGTINYLANTDGRRKLVTKILHTISVPGQIQFFAPGGRNP  
ESFLSSFSKGVQRAAFKISEEKLEKLLGKQDKGVIIRASEEQVRELRRHASEGGHGPHWP  
LPPFGESSRGPFNILEQRPRFANRHGRLYEADARSFHDLAEHDIRVAVVNI TAGSMNAPF  
YNTRSVKVAVVLDGEGEAEIVCPHL SRGGRGGESEERRRERGGKWKWEEEEEEEEQQKGQ  
EEEEEEQVGGQYETIRARLSRGTVFVWPSGHPVVTSSRDSTLQIVCFDVHANNNERMYL  
AGMNSVLKLLDPQAKELAFASAREVDELLNAQQESAF LAGPEKSGRRGEESEDEDRRRR  
RSHRGRGDEAVETLLRMAAAAV

>Q7X7E6.1 alpha-amylase/trypsin inhibitor [Oryza sativa]  
MASASDKLVLSAIVLAVLAAVVAASGYGDVGEYCRVGKAVSRNPVPSCRNYIARWCAA  
GGRMDSRKQPPREFLEPCRELAAVPMQCRCDALSVLVRGVVTEEGDRVSGMISQHAAPG  
CDAATIAGMASALTDYGRCLNQH TAGSFACLMFGGGMD

>Q7X8H9.1 alpha-amylase/trypsin inhibitor [*Oryza sativa*]  
MALASDKFVLSAIVLAVLTVAAAAAGYGGYGDVGEYCRVGVKAVSRNPVPSCRNYIARWCA  
VAGGRLDGKQPPRQLLEPCCRELAAVPMQCRCDALSVLVRGVVTEEGDRVAGMISQHAA  
PGCDAATIAGMASALTDYGRCNLQHTGFFGCPMFGGGMD

>Q852L2.2 cupincin [*Oryza sativa*]  
MAKKKTSSSMARSQLAALLISLCLSLASNAVGSRRGEREEEDERRRHGGEGGRPYHLG  
EESFRHWTRTRHGRFSVLERFPDEQVVGAAVGGYRVAVLEAAPRAFLQPSHYDADEVFVY  
KEGEGVIVLLREGRRESFCVREGDAMVIPAGAIVYSANTHSSKWFRVVMLLNPVSTPGHF  
EEYFPVGGDRPESFFSAFSDDVLQAAFNTRREELEKVFERQREGGEITTAPEEQIRELSK  
SCSRGGGGGSGSEWEIKPSSLTGKSPYFSNMHGKLFELTGDECRHLKLDLQIGLANITR  
GSMIAPNYNTRATKLAVVLQSGGYFEMACPHVSGGGSSERREREREHGRRRREEEQEEEEH  
GERGEKARRYHKVRAQVREESVIVIPASHPATIVASEGESLAVVCFVFGANHDEKVF LAG  
RNSPLRQLDDPAKKL VFGGSAAREADRVLAAQPEQILLRGP HGRGSVSDM

>Q9DG84.1 serine protease [*Protobothrops mucrosquamatus*]  
MVLIRVLANLLILQLSYAQKSSSELVIGDECNINEHPFLVLVYDDYQCGGTLINEEWVL  
TAAHCNGENMEIYLGMSKKVPNKDRRRRVPKEKFFCDSSKNYTKWNKDIMLIRLNRPVR  
KSAHIAPLSLPSSPPSVGSVCRIMGWGTISP TKVTL PDVPRCANINLLDYEVCRAVYPEL  
PATSR TL CAGILEGGK DSCGGD SGGPLICNGQFQGIVSWGGDPCAQPHEPGLYTNVFDHL  
DWIKGIIAGNTDVTCP L

>Q9YGJ8.2 plasminogen activator [*Gloydius brevicaudus*]  
MALIRVLANLLILQLSYAQKSSSELVVGDECNINEHRSLVWLFNSSGLICSGTLINQEWV  
LTAHCDSKNFQMLFGVHSKKILNEDEQTRDPKEKFCIPNKKKDDKDKDIMLIRLDSPV  
SNSEHIAPLSLPSSSPTVDSVCRIMGWGTIKPADETYPDVPHCANINILDHTVCRAAYPV  
LLAGSSTLCAGTQQGGKDTCVGDSGGPLICNGQIQGIVSWGAHPCGGQSKPGVYTKVFDH  
LDWIKSIIAGNTAVTCP P

>SHD75397.1 apolipoprotein, partial [*Sarcoptes scabiei*]  
MSARSAKFMYSRGNAGASGDL SVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK  
AELQIQVMSLSERLEEAEGSSSESVEMNKKRDESELAKLRKLLLEDVHLESEETAHHLRQKH  
QAAIQEMQDQLDQVQKAKNKSDEKQKQFAEVFELLAQLETANKEKLTAMKTVEKLEYTV  
HELNIKIEEINRTVIELTSQKTRLSQENTELIKEVHEHKMQLDNANHLKQQLAQQL EDTK  
HRLEEEERKRASLENHAHTLEVELES LKVQLDEESEARLELERQLTKANGDAASWKS KYE  
AELQAHADVEEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAT  
THAQQLEKRV AQLEKLNLDLKNKLEEV TMLMEQAQKEARAKAAELQKLQHEYEKLRDQRD  
ALARENKKL TDDLAECKVFRHHDARRSTNRRSKSNDWRTREKSYLLPTKKRKP YANKRR  
LRINDLP SWLKYDTITRNVWHRKRKSKHLENNIKSRNSLICDLK LKLNKPRSHDRRNI  
KLKSLNWNCHWMLPIKPI LIYRKQSKNKPYKLSRFKHTMMRRQSNHCTGSSIGSHPKTMP  
SVTSRAGRAKNRFGTSESCQTTSRTIAGSCRKSTYHHQCSCFSKQIGIGIRCSTKRLRSP  
QRTQNFTSTETYHAQIYQGLISGGTGTISENGDRKEIFGARSSYPTCPYRRGRSQCFGWR  
TCHCTGEQNSCDRSGRGTKTRDGNKAKRSSTQGIVGAKRGGPQTNP IASRN GRQNERK  
GQSLTTNARTGGNEPTKSDSCSTLPTIGSCRSSGSSIKSIVHPCQTPF

>XP\_015646887.1 casein kinase [*Oryza sativa*]  
MSKARVYTDVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNEKC  
IIKILKPVKKKKIKREIKILQNL CGGNIVKLLDIVRDQHSKTPSLIFEYVNN TDFKVL Y  
PTLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNMIDHELRLRLIDWGLAEFYHPG  
KEYNVRVASRYFKGPELLVDLQDYDYS LDMWSL GCMFAGMIFRKEPFFYGHNDHDQLVKI  
AKVLGTDLSNSYLNKYRIELDPQLEALVGRHSRKPWSKFINADNQH LVSPEAIDFLDKLL  
RYDHDRLTAREAMAHPYFLQVRAAENS RPRAQ

>COMPARE247 Blo t 1; cysteine protease [*Blomia tropicalis*]  
MKFLLVAALCALVAIGSCKPTREEIKTFEQFKKVF GKVYRNAEEEEARREHHFKEQLKWE  
EHNGIDGVEYAIN EYSDMSEQEF SFHLSGGGLNFTYMKMEAAKEPLINTYGSLPQNFDWR

QKARLTRIRQQGACGSCWAFAAAGVAESLYSIQKQSIGLSEQELVDCTYNRYDPSYQCN  
GCGSGYSTAEFKYMIRTGLVEERNYPYNMRTQWCDPDVEGQRYHVSGYQQLRYHSSDEDV  
MYTIQQHGPVVIYMHGSNNYFRNLGNGVLRGVAYNDAYTDHAVILVGGTVQGVYWIIR  
NSWGTGWNGGYYVERGHNSLGINNYVYATL

>COMPARE248 Gal d 6; vitellogenin, partial [Gallus gallus]  
PEIASQIAQEDQSTCEVSKGDFKTFDRMSFTCSFNKSCNVVVAQDCTEHPKFIITTRKVD  
HQSLSREHVHINTSSANITICPAADSSLLVTCNKESVLSDSGVSEYEKDNIKIYKNGKTVI  
VEAPIHGLKNVNFDFGEILKVTVASWMRGKTCGVCGNNDREKHNELLMPNHKLAHSCSAFV  
HSWVLLLEETCSGGCKLQRRYVKLNRNPTIDGEEESTCYSVDPVLKCMKDCPTIEKTSVKVG  
FHCFPKATAVSLLEWQRSSDKKASSEDVVESVDADIDCTCTGDCS

>FG438715.1 Act d 9; profilin [Actinidia deliciosa]  
MSWQTYVDDHLMCEIEGNYLTSAAIIGQDGSIAQASAFPQFKPEEITAIMNDFSEPGTL  
APTGLYLGGTKYMIQGEAGAVIRGKKKGGVTVKKTNQALIIGIYDEP

>CAA32835.1 Bos d 5; beta-lactoglobulin [Bos taurus]  
MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVE  
ELKPTPEGDLEILLQKWENDECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLL  
VCMENSAEPEQSLVCQLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHI

>CAA68720.1 Can f 5; arginine esterase [Canis familiaris]  
MWFALCLAMSLGWTGAEPHFQPRIIGRECLKNSQPWQVAVYHNGEFACGGVLVNPEWV  
LTAAHCANSNCEVWLGRHNLSESEDEGQLVQVRKSFHPLYKTKVPRAVIRPGEDRSHDL  
MLLHLEEPAKITKAVRVMDLPKKEPPLGSTCYVSWGSDPETIFHPGSLQCVDLKLKLSN  
NQCAKVVYTKVTKFMLCAGVLEGGKDTCKGDSGGPLICDGELVGITSWGATPCGKPMPS  
LYTRVMPHLMWIKDTMKANT

>CAA26038.1 Api m 4; melittin [Apis mellifera]  
MKFLVNVALVMVYISYIYAPEPEPEAEADAEADPEAGIGAVLKVLTTGLPALI  
SWIKRKRQQG

>CAA35692.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]  
LFLENKDPKPLKKISIMKFIIAFFVATLAVMTVSGEDKKHDYQNEFDFLLMERIHEQIKK  
GELALFYLQEQINHFEKPTKEMKDKIVAEMDTIIMIDGVRGVLDRMLQKDLDFEQY  
NLEMAKSGDILERDLKKEEARVKKIEV

>CAA34486.1 Act d 1; actinidin [Actinidia deliciosa]  
MGLPKSFVMSLLFFSTLLILSLAFNAKNTQRTNDEVKAMYESWLIKYGKSYNSLGEWE  
RRFEIFKETLRFIDEHNADTNRSYKVLNQFADLTDEEFRSTYLGFTSGSNKTKVSNRYE  
PRFGQVLPYSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKIVTGVLSLSEQELI  
DCGRTQNTTRGCNGGYITDGFQFIINNGGINTENYPYTAQDGCNLDLQNEKYVTIDTYE  
NVPYNNEWALQTAVTYQPVSVALDAAGDAFKHYSSGIFTGPCGTAIDHAVTIVGYGTEGG  
IDYWIWVKNWDTTWGEEGYMRILRNVGAGTCGIATMPSYPVKYNNQNHKPYSSLINPP  
AFSMKDGVPVGGVDDGQRYSA

>CAA46782.1 Bra r 1; 2S albumin, conglutin [Brassica rapa]  
MANKLFLVSATLALFFLLTNASVYRTGSEFDEHDATNPAGPFRIPKCRKEFQQAQHLKAC  
QQWLHKQAMQSGSGPSWTLDFEFDMENTQGPQQEPPLLQCCNELHQEEPLCVCPT  
LKGASKAVKQVVRQQGQQQQMQQVISRIYQTSHTLPRVCNIRQVSICPFQKTMGPSY

>CAA33887.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAA35691.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]

MMRARFPLLLLGLVFLASVSVSFGIAYWEKENPKHNKCLQSCNSERDSYRNQACHARNL  
LKVEKEECEEGEIPRRPRPQHPEREPQQPGEKEEDEDEQPRPIPFRPQPRQEEHEQR

EEQEWPKEEKRGKEGSEEEDEDEEEDERQFPFPRPPHQKEERNEEEDEEEQQRESE  
ESEDSELRHKNKPNFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNS  
KPNLLLLPNHADADYLIVILNGTAILSLVNMDDRSYRLQSGDALRVPSGTTYVVNPDN  
NENLRLITLAIKPNKGRFESFFLSSTEAQQSYLQGF SRNILEASYDTKFEEINKVLF SR  
EEGQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTISSEDKPFLRSRDIYSNKL  
KFFEITPEKPNQLRDLIFLSIVDMNEGALLLPHFNSKAIVILVINEGDANIELVGLKEQ  
QQEQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVNATSNLNFFAIGINAENNQRNFLA  
GSQDNVISQIPVQVQLAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKGPLSSI  
LRAFY

>CAA26575.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MAKLVLSLCFLFFSGCFALREQAQQNECQIQKLNALKPGNRIESEGGFIETWNPNNKPFQ  
CAGVALSRCTLRNALRRPSYTNQPQEIYIQQGNGIFGMIFPGCPSTYQEPQESQQRGRS  
QRPQDRHQKVRHFREGDLIAVPTGVAVWWMYNNEDTPVAVSIIIDTNSLENQLDQMPRRFY  
LAGNQEQEF LKYQQQQGGSSQSQKQKQEEENEENEGSNILSGFAPEFLKEAFGVNMQIVRNL  
QGENEEEDSGAIVTVKGGRLVTAAPAMRKPPQEEEDDDDEEQPQCVETDKGCQRQSKRSRN  
GIDETICTMRLRQNIQNSSPDIYNPQAGSITTATSLDFPALWLLKLSAQYGLRKNAMF  
VPHYTLNANSIIYALNGRALVQVNCNGERVFDGELQEGGVLI VPQNFVAVAKSQSDNFE  
YVSFKTNDRPSIGNLAGANSLLNALPEEVIQHTFNLKSQQARQVKNNNPFSLVPPQESQ  
RRAVA

>CAA26723.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MAKLVFSLCFLFFSGCCFAFSSREQPQQNECQIQKLNALKPGNRIESEGGFIETWNPNNK  
PFQCAGVALSRCTLRNALRRPSYTNQPQEIYIQQGKGFMIYPGCSSTFEEPQQPQQR  
GQSSRPQDRHQKIYNSREGDLIAVPTGVAVWWMYNNEDTPVAVSIIIDTNSLENQLDQMPR  
RFYLAGNQEQEF LKYQQEQGGHSQKQKQEEENEENEGGSILSGFTLEFLEHAFVVDKQIA  
KNLQGENEGEDKGAIVTVKGGSLVVKPPTDEQQQRQEEEEEEDEKQCKGDKHQCQR  
RGSQSKSRNGIDETICTMRLRHNIQTSSPDIYNPQAGSVTTATSLDFPALSWLRLSAG  
FGSLRKNAMFVPHYNLNANSIIYALNGRALI QVVNCNGERVFDGELQEGRVLI VPQNFV  
AARSQSDNF EYVSFKTNDTPMIGTLAGANSLLNALPEEVIQHTFNLKSQQARQIKNNNPF  
KFLVPPQESQKRAVA

>CAA33217.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MAKLVLSLCFLFFSGCCFAFQREFPQQNECQIQRLNALKPDNRIESEGGFIETWNPNNK  
PFQCAGVALSRCTLRNALRRPSYTNAPQEIYIQQGSGIFGMIFPGCPSTFEEPQQKGQS  
SRPQDRHQKIYHFRREGDLIAVPTGFAYWWMYNNEDTPVAVSLIDTNSFQNLQDQMPRRFY  
LAGNQEQEF LQYQPQKQGGTQSQKGRQEEENEENEGGSILSGFAPEFLEHAFVVDRIVR  
KLQGENEEEEEKGAIVTVKGGLSVISPPTTEEQQRPEEEEEKPCDEKDKHCQSQSRNGIDE  
TICTMRLRHNIQTSSPDIYNPQAGSITTATSLDFPALSWLKLSAQFGSLRKNAMFVPHY  
NLNANSIIYALNGRALVQVNCNGERVFDGELQEGQVLI VPQNFVAVAARSQSDNF EYVSF  
KTNDRPSIGNLAGANSLLNALPEEVIQHTFNLRRQQARQVKNNNPFSLVPPKESQRRVV  
A

>CAA37044.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MGKPF TSLSSCLLLLSSACFAISSSKLNECQLNNLNALEPDHRVEFEGGLIQTWNSQH  
PELKCAGVTVSKLTLNRNGLHLPSPYPRMIIIAQKGGALQCKPGCPETFEEPQEQSNR  
RGRSRSQKQLQDSHQKIRHFNQGDVLI VPPGVYWTYNTGDEPVVAISLLDTSNFNQLD  
QTPRVFYLAGNPDIEY PETMQQQQQKSHGGRKQGHQEQEEEEEGGSVLSGFSKHF LAQS  
FNTNEDIAEKLQSPDDERKQIVTVEGGLSVISPKWQEQQDEDEDEDEDEDEDEEQIPSHPPR  
RPSHGKREQDEDEDEDEDKPRPSRSQKREQDQDQDEDEDEDEDEDEDEDEDEDEDEDEDE  
RRPRQEEPRERCETRNGVEENICTLKLHENIARPSRADFY NPKAGRISTLNSLTLPALR  
QFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQGVKRVVNCQGNVFDGELRRGQLLV  
VPQNFVVAEQAGEQGF EYIVFKTHHNAVTSY LKDVFR AIPSEVLAHSYNLRQSQVSELKY  
EGNWGPLVNPESQQGSPRVKVA

>CAA42646.1 Gly m 4; pathogenesis related protein, PR-10, Bet v 1-like [Glycine max]

MGVFTFEDEINSPVAPATLYKALVTDADNVIPKALDSFKSVENVEGNGGPGTIKKITFLE  
DGETKFLVHKIESIDEANLGYSSVVGGAALPDTAEKITFDSKLVAGPNGGSAGKLVKY  
ETKGAEPNQDELKTGKAKADALFKAIEAYLLAHPDYN

>CAA45777.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLFCAFTTSYLPSAIADFLVDNEGNPLENGGTYIILSDITAFGGIRAAPTG  
NERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTESV  
VEDLPEGPAVKIGENKDAMDGWFRLEERSDDEFNMYKLVFCPQQAEDDKCGDIGISIDHD  
DGTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

>CAA45778.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLFCAFTTSYLPSAIADFLVDNEGNPLDSGGTYIILSDITAFGGIRAAPTG  
NERCPLTVVQSRNELDKGIGTIISSPFRIIRFIAEGNPLRLKFDSFAVIMLCVGIPTESV  
VEDLPEGPAVKIGENKDAVDGWFRLEERSDDEFNMYKLVFCTQQAEDDKCGDIGISIDHD  
DGTRRLVVSKNKPLVVQFQKVDKESLAKKNHGLSRSE

>CAA39880.1 Hev b 1; rubber elongation factor [Hevea brasiliensis]

MAEDEDNQGGQGEGLKYLGFVQDAATYAVTTFSNVYLFKDKSGPLQPGVDIIEGPVKNV  
AVPLYNRFSYIPNGALKFVDSTVVASVTIIDRSLPPIVKDASIQVVSIRAAPAAARSLA  
SSLPGQTKILAKVYFGEN

>CAA41956.1 alpha-amylase inhibitor [Hordeum vulgare]

MASKSSITPLLLAAVLASVFAAAAATGOYCYAGMGLPSNPLEGCREYVAQQTCGVTIAGS  
PVSSEPGDTPKDRCCQELDEAPQHCRRCRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFAK  
VLVTPGQCNVLTVHNAPYCLGLDI

>CAA45085.1 Hor v 15; alpha-amylase inhibitor, partial [Hordeum vulgare]

PTSAVDQGSMSVNSPGEWCWPGMGYPVYFPRCRALVKSQCAGGQVVESIQKDCCRQIA  
AIGDEWCICGALGSMRGSYKELGVALADDKATVAEVFPGCRTEVMDRAVASLPAVCNQY  
IPNTNGTDGVCYWLSYYQPPRQMSR

>CAA46705.1 alpha-amylase inhibitor [Hordeum vulgare]

MAFKYQLLLSAAVMLAILVATATSGDSCAPGDALPHNPLRACRTYVVSQICHQGPRLLT  
SDMKRRCCDELSAIPAYCRCEALRIIMQGVVWQGAFFEGAYFKDSPNCPREERQTSYAANL  
VTPQECNLGTIHGSAYCPELQPGYGVVL

>CAA42832.1 lipid transfer protein [Hordeum vulgare]

MARAQVLLMAAALVLMMLTAAPRAAVALNCGQVDSKMKPCLTYVQGGPGPSGECNGVRDL  
HNQAQSSGDRQTVCNCLKGIARGIHNLNLNNAASIPSKCNVNPYTIISPDIIDCSRFTERR  
SVKLVLSSSIHVLEL

>CAA38097.1 Ric c 1; 2S albumin, conglutin [Ricinus communis]

MAKLIPTIALVSVLLFIIANASFAYRTTITTTIEIDESKGEREGSSSQQRQEVQRKDLSS  
CERYLRQSSSRSPGEEVLRMPGDENQQQESQQLQCCNQVKQVRDECQCEAIKYIAEDQ  
IQQGQLHGEESERVAQRAGEIVSSCGVRCMRQTRTNPSQQGCRGQIQEQQLNRQCQEYIK  
QQVSGQGPRRSDNQERSLRGCCDHLKQMOSQCRCEGLRQAIEQQQSQQQLQGQDVFEAFR  
TAANLPSMCGVSPTECRF

>CAA31575.1 Sola t 1; patatin [Solanum tuberosum]

MATTKSFLILFFMILATTSSTCAKLEEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN  
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPFAAAADIVPFYFEHGPPIFNYSGSI  
LGPMYDGKYLQLVLEKLGQTRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM  
YDICYSTAAPIYFPPHVFVTHTSNGARYEFNLVDGAVATVGDPAALLSLSVATRLAQEDP  
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAEAAKWGPLRWMLAIQQMTNAASSYMTD  
YYISTVVFQARHSQNNYLRVQENALNGTTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE  
TYEEALKRFAKLLSDRKKLRANKASH

>CAA27571.1 Sola t 1; patatin [Solanum tuberosum]

MATTNSFTILIFMILATTSSTFATLGEMVTVLSIDGGGIKGIIPATILEFLEGQLQEVDN  
NTDARLADYFDVIGGTSTGGLLTAMITTPNETNRPFAAAKDIVPFYFEHGPKIFQSSGSI  
FGPKYDGYLMQVLQEKLGTRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM  
YDICYSTAAAPTFFPPHYFATNTSNGDKYEFNLVDGAVATVDDPALLSISVATKLAQVDP  
KFASIKSLNYKQMLLLSLGTGTTSEFDKTYTAEETAKWGTARWMLVIQKMTSAASSYMTD  
YYLSTAFQALDSQNNYL RVQENALTGTTTELDDASEANMQLLVQVGEDLLKKS VSKDNPE  
TYEEALKRFAKLLSDRKKLRANKASY

>CAA27588.1 Sola t 1; patatin [Solanum tuberosum]  
MATTKSFLILFFMILATTSSTCATLGEMVTVLSIDGGGIKGIIPAILEFLEGQLQEVDN  
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAKDIVPFYFEHGP HIFNYSGSI  
FGPRYDGYLLQVLQEKLGTRVHQALTEVAISSFDIKTNKPVIFTKSNLAESPQLDAKM  
YDICYSTAAAPIYFPPHVFTHTSNGATYEFNLVDGAVATVGD PALLSLSVATRLAQDDP  
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMTNAASSYMTD  
YYISTV FQARHSQNNYL RVQENALTGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE  
TYEEALKRFAKLLSDRKKLRANKASH

>CAA35238.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALLAIVATTARIAVRVPVPLQVQNPSSQQQPQEQVPLVQQQQQFPGQQQPFPPQ  
QPYPQPQPFPSQQPYLQLQPFQPLPYPQPLPYPQPLPYPQPFPRPQQPYPQSQPQ  
YSQPQPISQQQQQQQQQQQQKQQQQQQQILQQILQQQLIPCRDVVLQQHSIAYGSSQV  
LQQSTYQLVQQLCCQQLWQIPEQSRCQAIHNVWHAIILHQQQQQQQQQQPLSQVSFQQ  
PQQQYPSGQGSFQPSQQNPQAQGSVQPPQLPQFEEIRNLALETLPAMCNVYIPPYCTIAP  
VGIFGTN

>CAA35598.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]  
MASKSSISPLLLATVLSVFAAATATGPYCYAGMGLPINPLEGCREYVAQQTCGISISGS  
AVSTEPGNTPRDRCKELYDASQHCRC EAVRYFIGRRSDPNSSVLKDLPGCPREPQRDFA  
KVLVTSGHCNVMTVHNAPYCLGLDI

>CAA42453.1 Tri a 40; alpha-amylase inhibitor [Triticum aestivum]  
MASKSNYNLLFTALLVFIFA AVAAVGNEDCTPWTSTLITPLPSCRNYVEEQACRIEMPGP  
PYLAKQECCEQLANIPQQCRQCALRYFMGPKSRPDQSGLMELPGCPREVQMNFPILVTP  
GYCNLTTVHNTPYCLGMEESQWS

>CAA35597.1 Tri a 30; alpha-amylase inhibitor [Triticum aestivum]  
MACKSSCSLLLLAAVLLSVLAAASASGSCVPGVAFRTNLLPHCRDYVLQQTCGTFTPGSK  
LPEWMTSASIYSPGKPYLAKLYCCQELAEISQQCRCEALRYFIALPVPSQPVDPRSGNVG  
ESGLIDLPGCPREMQWDFVRLLVAPGQC NLATIHNVRYP AVEQPLWI

>CAA43331.1 Tri a 26; HMW glutenin [Triticum aestivum]  
MTKRLVLF AAVVALVALTAAEGEASGQLQCERELQEHS LKACRQVVDQQLRDVSPECQP  
VGGGPVARQYEQVVVPPKGGSFYPGETTPPQQLQQSILWGIPALLRRYYLSVTSPQQVS  
YYPGQASSQRPGQGQPQGGQGEYLLTSPQQSGWQQPGQGQAGYYPTSPQQSGQE QPGY  
YPTSPWQPEQLQPTQGGQRQPQGGQQLRQGQQGQQSGQGQPRYYPTSSQQPGQLQQLA  
QGQQGQQPERGQQGQQSGGQQLGQGQQGQQPGQKQQSGQGQQGYYPISPQQLGQGQQSG  
QGQLGYYP TSPQQSGQGQSGYYPTSAQQPGQLQQTSTEQQLGQEQQDQQSGQGRQGQQSG  
QRQQDQQSGQGQQPGQRQPGYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQ  
QGQQPEQGQQGQQPGQGEQGQQPGQGQQGQQPGQGQPGYYPTSPQQSGQGQPGYYPTSPQ  
QSGQLQQPAQGQQPGQEQQGQQPGQGQQGQQPGQGQPGYYPTSPQQSGQEQQLE  
QWQQSGQGQPGHYPTSPLQPGQGQPGYYPTSPQQIGQGQQPGQLQPTQGGQQQPGQGQ  
QGQQPGQGQQGQQPGQGQQPGQGQPGYYPTSLQQSGQGQQPGWQQPGQLPGYYPTSSL  
QPEQGQQGYYP TSPQQPGQPQGWQQSGQGQQGYYP TSPQQSGQGQQPGQWLQPGQWL  
QSGYYLTSPQQLGQGQQPRQWLQPRQGQQGYYP TSPQQSGQGQQLGQGQQGYYP TSPQQS  
GGQGGYD SPYHVSAEHQAASLKVAKAQQLAAQLPAMCRLEGGDALLASQ

>CAA31396.1 Tri a 26; HMW glutenin [Triticum aestivum]

MAKRLVLF AAVVIALVALTTAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG  
LQMRCCQQLRDVSAKCRSVAVSQVARQYEQTVVPPKGGSFYPGETTPLQQLQQGIFWGTS  
SQTVMGYYPGVTSRQGSYYPGQASPPQGQGGQPGKQWQEPGQGGQWYYPTSLQPPGQGG  
QIGKGGQGGYYPTSLQPPGQGGQGGYYPTSLQHTGQRQQPVQGGQPEQGGQPGQWQQGYYPT  
SPQQLGQGGQPRQWQQSGQGGQGGHYPTSLQPPGQGGQGGHYLASQQQPGQGGQGGHYPASQQ  
QPGQGGQGGHYPASQQQPGQGGQGGHYPASQQEPGQGGQGGIPASQQQPGQGGQGGHYPASLQ  
QPGQGGQGGHYPTSLQQLGQGGQGTGQPGQKQPPGQGGQGTGQGGQPEQEQQPGQGGQGGYYPT  
SLQPPGQGGQGGQGGQGGYYPTSLQPPGQGGQGGHYPASLQPPGQGGQPGQRQQPGQGGHPEQ  
GKQPGQGGQGGYYPTSPQQPGQGGQQLGQGGQGGYYPTSPQQPGQGGQPGQGGQGGHPTSPQQ  
SGQAQQPGQGGQIGQVQQPGQGGQGGYYPTSVQQPGQGGQSGQGGQSGQGHQPGQGGQSGQ  
EQQGYDSPYHVS AEQAASPMVAKAQQPATQLPTVCRMEGGDALSASQ

>CAA25593.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILVLLAIVATTATTAVRFPVPLQPPQNPSSQQPQEQVPLVQQQQFLGQQQPFPPQ  
QPYPQPQPFPSQLPYLQLQPFQPPQLPYSQPQPFPPQPPYPQPQPPQYSQPQQPISQQQQQ  
QQQQQQQQQQQQQILQQILQQQLIPCMDVVLQQHNI AHGRSQV LQQSTYQLLQELCCQHL  
WQIPEQSQCQAILKVVHAIILHQQQKQQQPSSQV SFQQPLQQYPLGQGSFRPSQQNPQA  
QGSVQPQQLPQFEEIRNLALQTL PAMCNVYIPPYCTIAPFGIFGTN

>CAA26383.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALLAIVATTATTAVRVPVPPQPPQNPSSQQPQEQVPLVQQQQFPGQQQQFPPQ  
QPYPQPQPFPSQPYLQLQPFQPPQLPYPQPPPFSPQQPYPQPQPPQYSQPQQPISQQQQQ  
QQQAQQQQQQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVLQQHNI AHARSQV LQQSTYQP  
LQQLCCQQLWQIPEQSRCQAIHNVVHAIILHQQQRQQQPSSQVSLQQPQQQYPSGQGFQ  
PSQQNPQAQGSVQPQQLPQFEEIRNLALQTLPRMCNVYIPPYCSTTIAPFGIFGTN

>CAA26384.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILVLLAIVATTATTAVRFPVPLQPPQNPSSQQPQEQVPLVQQQQFLGQQQPFPPQ  
QPYPQPQPFPSQLPYLQLQPFQPPQLPYSQPQQFRPQQPYPQPQPPQYSQPQQPISQQQQQ  
QQQQQQQQQQQQQQQILQQILQQQLIPCMDVVLQQHNI AHGRSQV LQQSTYQLLQELCCQHL  
WQIPEQSQCQAIHNVVHAIILHQQQKQQQPSSQV SFQQPLQQYPLGQGSFRPSQQNPQA  
QGSVQPQQLPQFEEIRNLALQTL PAMCNVYIPPYCTIAPFGIFGTN

>CAA26385.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALVATTATTAVRVPVPLQPKNPSSQQPQEQVPLVQQQQFPGQQQQFPPQQPY  
PQPQPFPSQPYLQLQPFQPPQLPYPQPPQSFPPQQPYPQQRPMYLQPPQISQQQ  
AQQQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVLQQHNI AHASSQV LQQSTYQLLQQL  
CCQQLLQIPEQSRCQAIHNVVHAIIMHQEQQQQLQQQQQQQLQQQQQQQQQQQPSSQV  
SFQQPQQQYPSQGSFQPSQQNPQAQGSVQPQQLPQFAEIRNLALQTL PAMCNVYIPPHC  
STTIAPFGIFGTN

>CAA31685.1 Tri a 36; LMW glutenin [Triticum aestivum]  
MKTFLV FALLAVAATSAIAQMETRCIPGLERPWQQQLPQQPQTFPQQPLFSQQQQQQLFP  
QQPSFSQQQPPFWQQQPPFSQQQPILPQQPPFSQQQQLVLPQQPPFSQQQQPVLPPQQSP  
FPQQQQHQQLVQQIPVWQPSILQQLNPKVFLQQQCSPVAMPQRLARSQMLQQSSCHV  
MQQQCCQQLPQIPQSSRYEAIRAIYSIILQEQQQVQGSIQSQQQQPQQLGQCVSQPQQQ  
SQQQLGQQPQQQQLAQGTFLQPHQIAQLEVMTSIALRILPTMCSVNVPLYRTTTSVPFGV  
GTGVGAY

>CAA26847.1 Tri a 26; HMW glutenin [Triticum aestivum]  
MAKRLVLF AAVVIALVALTTAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG  
LQMRCCQQLRDVSAKCRSVAVSQVARQYEQTVVPPKGGSFYPGETTPLQQLQQGIFWGTS  
SQTVMGYYPSVTSRQGSYYPGQASPPQGQGGQPGKQWQEPGQGGQWYYPTSLQPPGQGG  
QIGKGGKGGYYPTSLQPPGQGGQIGQGGQGGYYPTSPQHTGQRQQPVQGGQIGQGGQPEQGG  
QPGQWQQGYYPTSPQQLGQGGQPGWQQSGQGGQGGHYPTSLQPPGQGGQGGHYLASQQQPA  
QGGQGGHYPASQQQPGQGGQGGHYPASQQQPGQGGQGGHYPASQQEPGQGGQGGIPASQQQPG

GGQQGHYPASLQQPGQQGHYPTSLQQLGQQQIGQPGQKQQPGQQQTGGQQQPEQEQQP  
GGQQQGYPTSLQQPGQQQQGGQQQGYPTSLQQPGQQGHYPASLQQPGQQGGQPGQ  
RQQPGQQHPEQQQQPGQQQGYPTSPQQPGQQQLGGQQQGYPTSPQQPGQQQPGQ  
GQQGHCPMSQQQTGAQQQLGGQQQIGQVQQPGQQQGYPTSLQQPGQQQSGQQQSGQ  
GHQPGQQQSGQEKQGYDSYHVSAEQQAASPMVAKAQQPATQLPTVCRMEGGDALSASQ  
>CAA30570.1 Tri a 36; LMW glutenin [Triticum aestivum]  
MKTFLV FALLALAAASAVAQISQQQQAPPFSQQQQPPFSQQQQPPFSQQQQSPFSQQQQ  
PPFAQQQQPPFSQQPPISQQQQPPFSQQQQPQFSQQQQPPYSQQQQPPYSQQQQPPFSQQ  
QQPPFSQQQQPPFTQQQQQQQQPPFTQQQQPPFSQQPPISQQQQPPFLQQQRPPFSRQ  
QQIPVIHPSVLQQLNPKVFLQQQCIPVAMQRCLARSQMLQQSICHVMQQQCCQQLRQIP  
EQSRHESIRAIISIIILQQQQQQQQQQQQQQGQSIIQYQQQQPQQLGQCVSQPLQQLQQQ  
LGQQPQQQLAHQIAQLEVMTSIALRTLPTMCNVNPLYETTTTSVPLGVGIGVGVY  
>CAA24934.1 Tri a 26; HMW glutenin, partial [Triticum aestivum]  
LVSVEHQAARLKVAKAQQQLAAQLPAMCRLEGGDALSASQ  
>CAA34709.1 alpha-amylase inhibitor [Triticum turgidum]  
MASKSNCVLLLLAAVLVSIFAFAVAAGNEDCTPWMTLITPLPSCRDYVEQQACRIETPGS  
PYLAKQQCCGELANIPQQCRCQALRYFMGPKSRPDQSGLMELPGCPREVQMDVFVIRILVTP  
GYCNLTTVHNTPYCLAMEESQWS  
>CAA39099.1 alpha-amylase inhibitor [Triticum turgidum]  
MASKSSITHLLLAAVLVSVFAAAAATGPYCYPGMGLPSNPLEGCREYVAQQTCGVGIVGS  
PVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRTSDPNVSGVLKDLPGCPREPQRDFA  
KVLVTPGHCVNMTVHNTPYCLGLDI  
>CAA36063.1 glutenin [Triticum turgidum]  
MKTFLV FALLAVVATSTIAQMETSCIPGLERPWQEQLPPQHTLFPQQQPFPPQQQPPFS  
QQQPSFLQQQPILPQLPFSQQQQPVLPQQSPFSQQQLVLPQQQQYQQVLQQQIPIVQPSV  
LQQLNPKVFLQQQCNPVAMPQRLARSQMLQQSSCHVMQQQCCQQLPQIPEQSRVDVIRA  
ITYSIIILQEQQQGFVQAQQQQPQQLGQGVVSQSQQQSQQQLGQCSFQQPQQQLGQQPQQQQ  
VLQGTFLQPHQIAHLEVMTSIALRTLPTMCSVNVPLYSSTTTSVPFVSVGTGVGAYL  
>CAA44473.1 LMW glutenin [Triticum turgidum]  
MKTFLV FALLAVVATSAIAQMDTSCIPGLERPWQQQLPPQQTFPQQPPFSQQQQQQPFP  
QQPSFSQQQPILPQGPFPQQTQPVLPQQSPFSQQQLILPPQQQQQLPQQQISIVQPSV  
LQQLNPKVFLQQQCSPVAIPQRLARSQMWQQSSCHVMQQQCCQQLSQIPEQSRYDAIRA  
ITYSIIILQEQQQGSQQQQPQQSGQGVVSQSQQQSQQQLGQCSFQQPQQQLGQQPQQQQVQ  
QGTFLQPHQIAHLEVMTSIALRTLPTMCSVNVPLYSSTTTSVPFGV  
>CAA43361.1 Tri a 26; HMW glutenin [Triticum aestivum]  
MAKRLVLFATVVITLVALTAAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG  
LQMRCCQQLRDVSAKCRPVAVSQVVRQYEQTVVPPKGGSFYPGETTPLLQQVIFWGTS  
SQTVQGYYPVSSPQQGPPYYPGQASPQQPGQQPGKQWELGGQQQGYPTSLHQSGQQGQ  
QGYYPSSLQQPGQQQIGQGGQQGYPTSLQQPGQQQIGQGGQQGYPTSPQHPGQRQQPG  
QQQQIGQGGQLGQGRQIGQGGQSGQQQGYPTSPQQLGQQQPGQWQQSGQQQGYPT  
SQQQPGQQQQYPASQQQPGQQQQGYPASQQQPGQQQYYPASQQQPGQQQGHYLA  
SQQQPGQQQRHYPASLQQPGQQGHYASLQQPGQQGHYPASLQQVGGQQQIGQLG  
QRQQPGQQQTRQGGQLEQGGQPGQQQTRQGGQLEQGGQPGQQQGYPTSPQQSGQQGQ  
QPGQSQQPGQQQGYSSSLQQPGQGLQGHYPASLQQPGQGHQGRQQPGQQQPEQQQ  
PGQQQGYPTSPQQPGQKQLGQGGQGYPTSPQQPGQQQPGQQGHCPSTPQQTGQ  
AQPPGQQQIGQVQQPGQQQGYYPISLQQSGQQQSGQQQSGQGHQLGQQQSGQEQQ  
GYDNPYHVNTEQQTASPKVAKVQQPATQLPIMCRMEGGDALSASQ  
>CAA50325.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNYEAEETTSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG

EGSRYKYVKERVDEVDNTNFTYSYTVIEGDVLGDKLEKVCHELKIVAAPGGGSILKISSK  
FHAKGDHEINAEIEIKGAKEMAELLRVAVETYLLAHSAEYN  
>CAA50326.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNVEVETPSVISAARLFKSYVLDGDKLIPKVAPQAITSVENVGGNGGPGTIKNITFG  
EGSRYKYVKERVDEVDNTNFKYSYTVIEGDVLGDKLEKVCSELKIVAAPGGGSTLKISSK  
FHAKGDHEINAEEMKGAKEMAELLRVAVETYLLAHSAEYN  
>CAA50327.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNVEVETPSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG  
EGSRYKYVKERVDEVDNTNFTYSYTVIEGDVLGDKLEKVCHELKIVAAPGGGSILKISSK  
FHAKGDHEINAEEMKGAKEMAELLRVAVETYLLAHSAEYN  
>CAA50328.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNVEVETPSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG  
EGSRYKYVKERVDEVDNTNFKYSYTVIEGDVLGDKLEKVCSELKIVAAPGGGSILKISSK  
FHAKGDHEINAEEMKGAKEMAELLRVAVETYLLAHSAEYN  
>CAA23681.1 Gal d 2; ovalbumin [Gallus gallus]  
MGSIAAASMEFCFDVFKELKVHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF  
DKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNVYVSFSLASRLYAEERYPILPEYFQ  
CVKELYRGGLEPINFQTAADQARELINSWVESQTN  
>CAA23711.1 Gal d 4; lysozyme [Gallus gallus]  
MRSLILVLCLFLPLAALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCVAKFESNFNTQA  
TNRNTDGDSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDG  
NGMSAWVAWRNRCKGTDVQAWIRGRL  
>CAA43098.1 Gal d 5; serum albumin [Gallus gallus]  
MKWVTLISFIFLFSSATSRNLQRFARDAEHKSEIAHRYNDLKEETFKAVAMITFAQYLQR  
CSYEGLSKLVKDVVLAQKCVANEDAPECSKPLPSIILDEICQVEKL RDSYGAMADCCSK  
ADPERNECFLSFKVSPDFVQPYQRPASDVICQEYQDNRVSLGHFIYSVARRHPFLYAP  
AILSFAVDFEHALQSCCKESDVGACLDTKEIVMREKAKGVSVKQQYFCGILKQFGDRVFQ  
ARQLIYLSQKYPKAPFSEVSKFVHDSIGVHKECCEGDMVECMDDMARMMSNLCSQQDVSF  
GKIKDCCEKPIVERSQCIMEAEFDEKPADLPSLVEKYIEDKEVCKSF EAGHD AFMAEFVY  
EYSRRHPEFSIQLIMRIAKGYESLLEKCKTDNPAECYANAQEQLNQHIKETQDVVKTNC  
DLLHDHGEADFLKSILIRYTKKMPQVPTDLLLETGKKMTTIGTKCCQLGEDRRMACSEGY  
LSIVIHDTCRKQETTPINDNVSQCCS QLYANRRPCFTAMGVDTKYVPPFPNPFMFDFEK  
LCSAPAEEREVGMKLLINLIKRPQMTEEQIKTIADGFTAMVDKCKQSDINTCFGEEG  
ANLIVQSRATLGIGA  
>P23110.1 2S albumin, conglutin [Helianthus annuus]  
MARFSIVFAAGVLLLVAMAPVSEASTTTIITIIIEENPYGRGRTESGCYQQMEEAEMLN  
HCGMYLMKNL GERSQVSPRMREEDHKQLCCMQLKNLDEKCMCPAIMMMLNEPMWIRMRDQ  
VMSMAHNLPIECNLMSQPCQM  
>P04403.2 Ber e 1; 2S albumin, conglutin [Bertholletia excelsa]  
MAKISVAAAALLVLMALGHATAFRATVTTTVEEENQEECREQMQRQQMLSHCRMVYMRQQ  
MEESPYQTMPPRRGMPEHMS ECEQLEGMDESCRCEGLRMMMMRMQQEEMQPRGEQMRRMM  
RLAENIPSRCNLSPMRCPMGGSIAGF  
>P27759.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKHCYIYFTLALVTL LQPVRS AEDLQEILPVNETRRLTTS GAYNIIDGCWRGKADW  
AENRKALADCAQGF GKGTVGGKDGDIYTVTSELDDDVANPKEGTLRF GAAQNRPLWIIFE  
RDMVIRLDKEMVNSDKTIDGRGAKVEIINAGFTLNGVKNV IHNINMHDVKVNPGLIK  
SNDGPAAPRAGSDGDAISISGSSQIWIHDHCSLSKSV DGLVDAKLGTTRLTVSNSLFTQHQ

FVLLFGAGDENIEDRGMLATVAFNTFTDNVDQRMPCRHRGFFQVVNNNYDKWGSYAIGGS  
ASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPV  
LTPEQSAGMIPAEPGESALSLTSSAGVLSQPGAPC

>P27760.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTL LQPVRSAEDVEEFLPSANETRRSLKACEAHNIIDKCWRCKA  
DWANNRQALADCAQGFAGKTYGGKHGDVYTVTSDKDDDVANPKEGTLRF AAAQNRPLWII  
FKRNMVIHLNQELVVNSDKTIDGRGVKVNIVNAGL TLMNVKNI IHNINI HDIKVCPGGM  
IKSNDGPPILRQQSDGDAINVAGSSQIWI DHCSLSKASDGLLDITLGSSHVTVS NCKFTQ  
HQFVLLL GADDTHYQDKGMLATVAFNMFTDHVDQRMPCRFRGFFQVVNNNYDRWGTYAIG  
GSSAPTILSQGNRFAPDDIIKKNVLARTGTGNAESMSWNWRTDRDLLENGAIFLPSGSD  
PVLTPSEQAGMIPAEPGEAVLRLTSSAGVLSCHQGAPC

>P27761.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKQCCYILYFTLALVALLQPVRSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGKWDVYTVT SNLDDDVANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINI HDVKVLPGGMI  
KSNDGPPILRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTIS NCKFTQQ  
SKAILLGADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRF LAPDDQIKKNVLARTGTGAAESMAWNWRS DKDLLENGAIFVTS GSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVFSCHPGAPC

>P28744.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTL LQPVRSAEDLQQILPSANETRSLTTCGTYNIIIDGCWRGKAD  
WAENRKALADCAQGFAGKTI GGKGDGIYTVTSELDDDVANPKEGTLRF GAAQNRPLWII F  
ARDMVIRLDRELAINNDKTIDGRGAKVEIINAGFAIYNVKNIIHNIMHDIVVNPGLI  
KSHDGGPPVPRKGS DGAIGISGGSQIWI DHCSLSKAVDGLIDAKHGSTHFTVSNCLFTQH  
QYLLL FWFDFDERGMLCTVAFNKFTDNVDQRMPLNRHGFVQVVNNNYERWGSYALGGSAGP  
TILSQGNRF LASDIKKEVVGRYGESAMSESINWNWRSYMDVFENGAI FVPSGVDPVLTPE  
QNAGMIPAEPGEAVLRLTSSAGVLSQPGAPC

>P27762.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD  
WAENRQALGNCAQGF GKATHGGKWDIYMVTS DQDDDVNPKEGTLRF GATQDRPLWII F  
QRDMIYIY LQQEMVVTSDKTIDGRGAKVELVYGGITLMNVKNV IHNIDIHDVRLP GGRI  
KSNGGPAIPRHQSDGDAIHVTGSSDIWIDHCTLSKSF DGLVDVNWGSTGVTIS NCKFTHH  
EKAVLLGASDTHFQDLKMHVTLAYNIFTNTVHERMPPCRFRGFFQIVNNFYDRWDKYAIGG  
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEPEWMTWNWRTQNDVLENGAIFVASGSDP  
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLT CSPGAPC

>P22284.1 unknown function [*Poa pratensis*]  
MDKANGAYKTALKAASAVAPAEKFPVFQATFDK NLKEGLSGPD AVGF AKKLDAFIQTSYL  
STKAAEPKEKFDL FVLSL TEVLR FMAGAVKAPPASKFPAKPAPKVAAYTPAAPAGAAPKA  
TTDEQK LIEKINVGFKAAVAAAAGVPAASKYKTFVATFGAASNKAF AEALSTEPKGAAVA  
SSKAVLTSKLDAA YKLAYKSAEGATPEAKYDAYVATLSEALRIIAGTLEVHGVKPAEEV  
KAIPAGELQVIDKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYQSYKFI  
ALEAAVKQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAKPAAAVTGTATSAVGAA  
TGAATAAAGGYKV

>P22285.1 unknown function [*Poa pratensis*]  
MAVHQYTVALFLAVALVAGPAASYAADVGYGAPATLATPATPAAPAAGYTPAAPAGAAPK  
ATTDEQK LIEKINAGFKAAVAAAAGVPAVDKYKTFVATFGTASNKAF AEALSTEPKGA  
ASSNAVLTSKLDAA YKLAYKSAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKPAGEE  
VKAI PAGELQVIDKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYQSYKFI  
PALEAAVKQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAKPAAAVTATATGAVGA  
ATGAVGAATGAATAAAGGYKTGAATPTAGGYKV

>P22286.1 unknown function [*Poa pratensis*]  
MAVQKYTVALFLVALVVGPAASYAADLSYGAPATPAAPAAGYTPAAPAGAAPKATTDEQK  
MIEKINVGFKA AVAAAGGVPAANKYKTFVATFGAASNKAF AEALSTEPKGA AVDSSKAAL  
TSKLDAA YK LAYKSAEGATPEAKYDDYVATLSEALRIIAGTLEVHGVKPA AEEVKATPAG  
ELQVIDKVDAAFKVAATAANAAPANDKFTVF EAAFND AIKASTGGAYQSYKFIPALEAAV  
KQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAPAAAATGTATAAVGAATGAATA  
AAGGYKV

>P02878.1 Amb a 5; unknown function [*Ambrosia artemisiifolia*]  
LVPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESS EICSKKCGK

>P10414.2 Amb t 5; unknown function [*Ambrosia trifida*]  
MKNIFMLTLFILIIITSTIKAIGSTNEVDEIKQEDDGLCYEGTNCGKVGKYCCSPIGKYCV  
CYDSKAICNKNCT

>P20723.1 enterotoxin [*Staphylococcus aureus*]  
MKKFNILIALLLFFTSLVISPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP  
IIGENKSTGDQFLENTLLYKFFFTDLINFEDLLINFNSKEMAQHFKSKNVDVYPIRYSIN  
CYGGEIDRTACTYGGVTPHEGNLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL  
DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSD  
NKTLSTEHLHIDIYLYEK

>P02229.2 Chi t 1; hemoglobin [*Chironomus thummi thummi*]  
MKFLILALCFAAASALSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKD  
LESIKGTAPFEIHANRIVGFFFSKIIGELPNI EADVNTFVASHKPRGVTHDQLNNFRAGFV  
SYMKAHTDFAGAEAAWGATLD TFFGMIFSKM

>P02230.1 Chi t 1; hemoglobin [*Chironomus thummi thummi*]  
MKLLILALCFAAASALTADQISTVQSSFAGVKGDAVGILYAVFKADPSIQAKFTQFAGKD  
LDSIKGSADFSAHANKIVGFFFSKIIGDLPNIDGDVTTFVASHTPRGVTHDQLNNFRAGFV  
SYMKAHTDFAGAEAAWGATLDAFFGMVFAKM

>P02227.1 Chi t 3; hemoglobin [*Chironomus thummi thummi*]  
AVTPMSADQLALFKSSWNTVKHNEVDILYAVFKANPDIQAKFPQFAGKDLDSIKDSADFA  
VHSGRIVGFFSEVIGLIGNPENRPAKTLIDGLASSHKARGIEKAQFEFRASLVDYLSH  
HLDWNDTMKSTWDLALNNMFFYILHALEVAQ

>P12548.1 Chi t 3; hemoglobin [*Chironomus thummi thummi*]  
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVDILAAVFAAYPDIQAKFPQFA  
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNESNASAVNSLVSKLGDDHKARGVSAAQ  
FGFERTALVAYLSNHVSWGDNVAAA WNKALDNTYAI VVPR L

>P12549.1 Chi t 3; hemoglobin [*Chironomus thummi thummi*]  
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVEILAAVFAAYPDIQNKFSQFA  
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNDSNAAAVNSLVSKLGDDHKARGVSAAQ  
FGFERTALVAYLQANVSWGDNVAAA WNKALDNTFAI VVPR L

>P12550.1 Chi t 3; hemoglobin [*Chironomus thummi thummi*]  
MKFFAVLALCVVGAIASPLSADEAAIVKSSWDQVKHNEVDILAAVFAAYPDIQAKFPQFA  
GKDLASIKDTAAAFATHATRIVSFFTEVISLSGNQANLSAVYALVSKLGV DHKARGISAAQ  
FGFERTALVSYLQAHVSWGDNVAAA WNHALDNTYAVALKSLE

>P02231.1 Chi t 4; hemoglobin [*Chironomus thummi thummi*]  
VATPAMPSTDAQVA AVKGDWEKIKGSGVEILYFFLNKFPGNFPMFKKLGNDLAAAKGTA  
EFKDQADKIIAFLQGVI EKLGSMDGGAKALLNQLGTSHKAMGITKDQFDQFRQALTELLG  
NLGFGGNIGAWNATVDLMFHVIFNALDGPV

>P02228.1 Chi t 9; hemoglobin [*Chironomus thummi thummi*]  
DPEWHTLDAHEVEVQVQATWKAVSHDEVEILYTVFKAHDPIMAKFPKFAGKDLEAIKDTAD  
FAVHASRIIGFFGEYV TLLGSSGNQAAIR TLLHDLGVFHKTRGITKAQFGEFRETMAYL  
KGNKNWNADISHSWDDAFDKAFSVIFEVLES

>P25974.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]  
MMRVRFP LLVLLGTVFLASVCSLKVRE DENNPFYFRSSNSFQTLFENQNV RIRLLQRFN  
KRSPQLENLRDYRIVQFQSKPNTILLPHHADADFLFVLSGRAILTLVNNDDRDSYNLHP  
GDAQRIPAGTTYLVNPHDQNLKIIKLAIPVKNKPGRYDDFFLSSTQAQQSYLQGF SHNI  
LET SFHSEFEEINRVLFGE EEEQRQQEGVIVELSKEQIRQLSRRAKSSSRKTI SSEDEPF  
NLR SRNPIYSNNFGKFFEITPEKNPQLRDL DIFLSSVDINEGALLLPHFNSKAI VILVIN  
EGDANIELVGIKEQQQKQKQEEEP LEVQRYRAELSEDDV FVIPAAYPFV V NATS NLNFLA  
FGINAENNRN FLAGEKDNVVRQIERQVQELAFPGSAQDVERLLKKQRESYFVDAQPQQK  
EEGSKGRKGPFP SILGALY

>P24337.1 Gly m 1; lipid transfer protein [Glycine max]  
ALITRPSCPDLSICLNILGGS LGTVDDCCALIGGLGDIEAIVCLCIQLRALGILNLNRNL  
QLILNSCGRSYPSNATCPRT

>P16348.1 Sola t 2; aspartic protease inhibitor [Solanum tuberosum]  
ESPLPKPVLDTNGKELNPSSYRIISIGRGALGGDVYLGKSPNSDAPCPDGVFRYNSDVG  
PSGTPVRFIPLSGGIFEDQLLNIQFNIATVKLCVSYTIWKVGNLNAYFR TMLLETGGTIG  
QADSSYFKIVKLSNFGYNLLYCPITPPFLCPFCRDDNFCAKVGVIQNGKRRRLALV NENP  
LDVLFQEV

>P01005.1 Gal d 1; ovomucoid [Gallus gallus]  
MAMAGV FVLF SFVLCGFLPDAAFGAEVDCSRFPNATDKEGKDVLCNKDLR PICGTDGVT  
YTNDCLLCAYSIEFGTNISKEHDGECKETVPMNCSSYANTTSEDGKVMVLCNRAFNPVCG  
TDGVTYDNECLLCAHKVEQ GASVDKRHDGGCRKELAAVSVDCEY PKPDCTAEDRPLCGS  
DNKTYGNKCNFCNAVVESNGTLT LSHFGKC

>P02754.3 Bos d 5; beta-lactoglobulin [Bos taurus]  
MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVE  
ELKPTPEGDLEILLQKWENGECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYK KYLL  
FCMENS AEPEQSLACQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEE QCHI

>P14946.2 Lol p 1; beta-expansin [Lolium perenne]  
MASSSSVLLVVALFAVFLGSAHGI AKVPPGNITAEYGDKWLD AKSTWYGKPTGAGPKDN  
GGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVTITDDNE  
EPIAPYHFDLSGHAFGSM AKKGEEQNVRSAGELELQFRRVKCKYPDDTKPTFHVEKASNP  
NYLAILVKYVDGDGDVVAVDIKEGKDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEG  
GTKSEFEDVIPEGWKADTSYSAK

>P14947.1 Lol p 2; expansin [Lolium perenne]  
AAPVEFTVEKGSDEKNLALS IKYNKEGDSMAEVELKEHGSNEWLALKKNGDGVWEIKSDK  
PLKGFNFRFVSEKGM RN VFDDVVPADFKVGT TYKPE

>P14948.1 Lol p 3; expansin [Lolium perenne]  
TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQH GSEEWEPMTKKGNLWEVKS AKPL  
TGPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPEYN

>P00698.1 Gal d 4; lysozyme [Gallus gallus]  
MRSL LILVLCFLPLAALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQA  
TNRNTDGSTDY GILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASV NCAKKIVSDG  
NGMNAWVAWRNRCKGTDVQAWIRGCR L

>P01502.1 melittin [Apis dorsata]  
GIGAILKVLSTGLPALISWIKRKRQE

>P16312.1 Der m 1; cysteine protease, partial [Dermatophagoides microceras]  
TQACRINSGNVPSELDRSLRTVTPIRMQG

>P02761.1 Rat n 1; lipocalin, urinary globulin [Rattus norvegicus]  
MKLLLLLLCLGLTLVCGHAE EASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVF  
MQHIDVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYV  
MFHLINFKNGETFQLMVLYGR TKDLSSDIKEKFAKLCEAHGITRDNIIIDLTKTDRCLQAR

G

>P12547.2 Asp o 13; alkaline serine protease [*Aspergillus oryzae*]

MQSIKRTLLLLGAILPAVLGAPVQETRRAAEKLPQKYIVTFKPGIDEAKIQEHTTWATNI  
HQRSLERRGATGGDLPVGIERNYKINKFAAYAGSFDDATIEEIRKNEDVAYVEEDQIYYL  
DGLTTQKSAPWGLGSISHKGGQSTDYIYDTSAGEGTYAYVVDSGVNVDHEEFEGRASKAY  
NAAGGQHVDSIGHGTHVSGTIAGKTYGIACKASILSVKVFQGESSTSVILDGFNWAAND  
IVSKKRTSKAAINMSLGGGYSKAFNDAVENAFEQVLSVVAAGNENS DAGQTSPASAPDA  
ITVAAIQKSNRASFSNFGKVVDFAPGQDILSAWIGSSSATNTISGTSMATPHIVGLSL  
YLAALENLDGPAAVTKRIKELATKDVVKDVKGSPNLLAYNGNA

>P01012.2 Gal d 2; ovalbumin [*Gallus gallus*]

MGSIGAASMEFCFDVFKELKVHANENIFYCPIAIMSALAMVYLGAKDSTRQINKVVRF  
DKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNVYVSFSLASRLYAEERYPILPEYLQ  
CVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIV  
FKGLWEKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTM  
SMLVLLPDEVSGLEQLESIINFEKLTWTSSNVMEERKIKVYLPRMKMEEKYNLTSVLMA  
MGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAGVDAASVSEEFR  
ADHPFLFCIKHIATNAVLFFGRCVSP

>P22895.1 thiol protease [*Glycine max*]

MGLFVLLLFSLGLSSSSSISTHRSIDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE  
EAKRLEIFKNNSNYIRDMNANRKS PSHRGLGNKFADITPQEF SKKYLQAPKDV SQQIKM  
ANKMKKEQYSCDHPASWDWRKKG VITQVKYQGGCGRGWAFSATGAI EAAHAIATGDLV  
SLSEQELVDCVEESEGSYNGWQYQSF EWLEHGGIATDDDY PYRAKEGRCKANKIQDKVT  
IDGYETLIMSDESTESETEQAFLSAILEQPISVSIDAKDFHLYTGGIYDGENCTSPYGIN  
HFVLLVGYSADGVYWI AKNSWGF DWGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES  
ETLVSARVKGHRRVDHSPL

>P00784.1 cysteine protease, papain [*Carica papaya*]

MAMIPSISKLLFVAICLFVYMGLSFGDFSIVGYSQNDLTSTERLIQLFESWMLKHNKIYK  
NIDEKIYRFEIFKDNLKYIDETNKKNNSYWLGLNVFADMSNDEFKEKYTGSIAGNYTTTE  
LSYEEVLNDGDVNIPEYVDWRQKGA VTPVKNQGSCGSCWAFSAVVTIEGIIKIRTGNLNE  
YSEQELLDCCRYSYGCNGGYPWSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKT  
DGVRQVQPYNEGALLYSIANQPVS VLEAAGKDFQLYRGGIFVGP CGNKVDHAVA AVGYG  
PNYILIKNSWGTGWGENGYIRIKRGTGNSYGVCGLYTSSFPVKV

>P02622.1 Gad c 1; calcium-binding protein, parvalbumin [*Gadus callarias*]

AFKGLSNADIKAAEAACFKEGSFDEDGFYAKVGLDAFSADELKFLFKIADEDKEGFIEE  
DELKFLIAFAADLRAL TDAETKAF LKAGSDGDGKIGVDEFGALVDKWKAGK

>P02620.1 calcium-binding protein, parvalbumin [*Merluccius merluccius*]

AFAGILADADITAALAAACKAEGSFKHGEFFTKIGLKGKSAADIKKVFGIIDQDKSDFVEE  
DELKFLQNF SAGARAL TDAETATFLKAGSDGDGKIGVEEFAAMVKG

>P05946.1 Pon 1 4; calcium-binding protein, sarcoplasmic calcium-binding protein [*Pontastacus leptodactylus*]

AYSWDNRVKYVVRYMYDIDNNGFLDKNDFECLALRNTLIEGRGEFNEAAYANNQKIMSNL  
WNEIAELADFNKDGEVTIDEFKKAVQNV CVGKAFATFPAAFKVF IANQFKTVDVNGDGLV  
GVDEYRLDCISRSAFANIKEIDDAYNKLATDADKKAGGISLARYQELYAQFISNPDESAN  
AVYLFGLKEVQ

>P00780.1 alkaline serine protease [*Bacillus licheniformis*]

MMRKSFWLGLMTAFMLVFTMAFSDSASAAQPAKNVEKDYIVGFKSGVKTASVKKDIIKE  
SGGKVDKQFRIINA AKAKLDKEALKEVKNDP DVAYVEEDHVAHALAQTPYGIPLIKADK  
VQAQGFKGANVKVAVLDTGIQASHPDLN VVGAS FVAGEAYNTDGNHGTHVAGTVAALD  
NTTGVLGVAPSVSLYAVKVLNSSSGSTYS GIVSGIEWATTNGMDVINMSLGGPSGSTAMK  
QAVDNAYARGVVVVAAAGNSGSSGNTNTIGYPAKYDSVIAVGA VDSNSNRASFSSVGAE L

EVMAPGAGVYSTYPTSTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATY  
LGSSFYGKGLINVEAAAQ  
>P27357.1 thaumatin-like [*Triticum aestivum*]  
MATSPVFLLLLAVFAAGASAATFNIKNNCGFTIWPAGIPVGGGFALGSGQTSSINVPAGT  
QAGRIWARTGCSFNNGSGSCQTGDCGGQLSCSLSGRPPATLAEYTIIGGGSTQDFYDISVI  
DGFNLAMDFSCSTGDALQCRDPSCPPPQAYQHPNDVATHACSGNNNYQITFCP  
>P06886.1 toxic shock syndrome toxin [*Staphylococcus aureus*]  
MNKLLMNFIVSPLLLATTATDFTPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTF  
TNSEVLDNSLGSMRIKNTDGSISLIIFSPYYPFAFTKGEKVDLNTKRTKKSQHTSEGTY  
IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYGPKFDDKQLAISTLDFEIRHQLTQI  
HGLYRSSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN  
>AAA28301.1 DoI m 5; unknown function, antigen 5 [*Dolichovespula maculata*]  
MEIGGLVYLILIIITIINLSFGETNNYCKIKCRKGIHTLCKFGTSMKPNCGRNVVKAYGLT  
NDEKNEILKRHNDFRQNVAKGLETRGKPGQPPOPPAKNMMNLVWVWDELAQIAQWANQCFN  
HDDCRNTAKYQVGQNIASSTTATQFDRPSKLIKQWEDEVTEFNKYVGLQNSNFRKVGHY  
TQMVGKTKEIGCGSIKYIEDNWYTHYLVCNYGPGGNDNFNQPIYERK  
>AAA28303.1 DoI a 5; unknown function, antigen 5 [*Dolichovespula arenaria*]  
NNYCKICPKGHTLTKYGTSMKPNCGGKIVKSYGVTNDEKNEIVKRHNEFRQKVAQGLT  
RGNGPQPPOPPAKNMMNLVWVWDELAQIAQWANQCFNHQDQCRNTAKYPVGQNVVAIASTTGN  
SYQTM SYLIKWEDEVKDYNPDKMLMHNNSKVGHYTQMVGKTKEIGCGSVKYIENKWH  
THYLVCNYGPAGNYMNPVYERK  
>AAA29793.1 Pol a 5; unknown function, antigen 5 [*Polistes annularis*]  
SSQGVVYCKIKCPSGIHTVCQYGESTKPSKNCAGKVIKSVGPTHEEKKLIVSEHNFRQK  
VAQGLETRGNGPQPPOPPAKNMMNLVWVWDELAHIAQVWASQCQFLVHDKCRNTAKYPVGQNI  
AYAGGSNLPDVVSLIKLWENEVKDFNYNTGITKQNFQKIGHYTMVGKTKEIGCGSLKY  
MENNMQNHYLICNYGPAGNYLGLPYTKK  
>AAA30333.1 Ves v 5; unknown function, antigen 5 [*Vespula vulgaris*]  
MEISGLVYLIIIVTIIIDLPYGKANNYCKIKCLKGGVHTACKYGSCLKPNCGNKVVVSYGLT  
KQEKQDILKEHNDFRQKIARGLETRGNGPQPPOPPAKNMMNLVWVWDELAQVAVANQCYG  
HDTCDRVAKYQVGQNVALTGSTAAKYDDPVKLVKWEDEVKDYNPKKKFSGNDFLKTGHY  
TQMVAWNTKEVGCOSIKYIQEKWHKHVLCNYGPSGNFMNEELYQTK  
>AAA51411.1 Bos d 6; serum albumin [*Bos taurus*]  
MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHRFKDLGEEHFGLVLIAFSQYLQQCPF  
DEHVKLVELTEFAKTCVADESHAGCEKSLHTLFGDELCKVASLRETYGDMADCCQEP  
ERNECFLSHKDDSPDLPKLPDPNTLCDEFKADEKKFWGKYLYEIARRHPYFYAPELLYY  
ANKYNGVVFQEQCAEDKGACLKPKIETMREKVLASSARQRLRCASIQKFGERALKAWSVA  
RLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLECADRADLAKYICDNQDTISSKLKE  
CCDKPLLEKSHCIAEVEKDAIPENLPLTADFAEDKDVCKNYQEAQDAFLGSLFLEYYSRR  
HPEYAVSVLLRLAKEYEATLEECCAKDDPHACYSTVFDKLLKHLVDEPQNLIKQNCQDFEK  
LGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESEMPCTEDYLSLIL  
NRLCVLHEKTPVSEKVTKCTESLVNRRPCFSALTPDETYVPKAFDEKLFTHADICTLP  
DTEKQIKQTALVELLKHKPKATEEQKLTVMENFVAFVVKCAADDKEACFAVEGPKLVV  
STQ TALA  
>AAA62707.1 Bos d 9; alphaS1-casein, partial [*Bos taurus*]  
PQLEIVPNSAEERLHSMKEGIHAQQKPEMIGVNPQELAYFYPELFRQFYQLDAYPSGAWY  
VPLGTQYTDAPSFSDIPNPIGLENSKTTMPLW  
>AAA30413.1 Bos d 5; beta-lactoglobulin, partial [*Bos taurus*]  
NSAEPXQSLVCECL  
>AAA30429.1 Bos d 9; alphaS1-casein [*Bos taurus*]  
MKLLILTCLVAVALARPKHPIKHQGLPQEVLNENLLRFFVALFPEVFGKEKVNELSKDIG

SESTEDQAMEDIKQMEAESISSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLLRLLKYYK  
VPQLEIVPNSAEERLHSMKEGIDAQQKEPMIGVNVQELAYFYPELFRQFYQLDAYPSGAWY  
YVPLGTQYTDAPSFSDIPNPIGSENSEKTTISLW

>AAA30430.1 Bos d 11; beta-casein [Bos taurus]

MKVLILACLVALALARELEELNVPGEIVESLSSEESITRINKKIEKFQSEEQQQTEDEL  
QDKIHPFAQTQSLVYPPFGPIPNLQNIPLTQTPVVVPPFLQPEVLGVSKVKEAMAPK  
HKEMPFKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSL  
SQSKVLPVPQKAVPYPQRDMPIQAFLLYQQPVLGPVVRGPFPIIV

>AAA30431.1 Bos d 11; beta-casein [Bos taurus]

MKVLILACLVALALARELEELNVPGEIVESLSSEESITRINKKIEKFQSEEQQQTEDEL  
QDKIHPFAQTQSLVYPPFGPIHNSLPQNIPLTQTPVVVPPFLQPEVMGVSKVKEAMAPK  
HKEMPFKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSL  
SQSKVLPVPQKAVPYPQRDMPIQAFLLYQEPVLGPVVRGPFPIIV

>AAA30433.1 Bos d 12; kappa-casein [Bos taurus]

MMKSFVFLVVTILALTLPLFLGAQEONQEQPIRCEKDERFFSDKIAKYIPIQYVLSRYPSYG  
LNYYQQKPVALLINQFLPYPPYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTTARHP  
HPHLSFMAIPPKKNQDKTEIPTINTIASGPTSTPTIEAVESTVATLEASPEVTESPEI  
NTVQVTSTAV

>AAA30478.1 Bos d 9; alphaS1-casein, partial [Bos taurus]

LSKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLL  
RLKYYKVPQLEIVPNS

>AAA30615.1 Bos d 4; alpha-lactalbumin [Bos taurus]

MMSFVSLLLVGLFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAI  
VQNNDSLEYGLFQINNKIWKDQDQNPSSNICNISCDKFLDDDLTDDIMCVKKILDKVGI  
NYWLAHKALCSEKLDQWLCEKL

>AAC41616.1 Fel d 1; uteroglobin [Felis catus]

MRGALLVLLALLVTQALGVKMAETCPIFYDVFFAVANGNELLLDLSLTKVNATEPERTAMK  
KIQDCYVENGLISRVLQGLVMTTISSSKDCMGEAVQNTVEDLKLNTLGR

>AAC37318.1 Fel d 1; uteroglobin [Felis catus]

MKGARVLLVLAALLIWWGNCEICPAVKRDVDFLTGTPDEYVEQVAQYKALPVVLENA  
RILKNCVDAKMTEEDKENALSLLDKIYTSPLC

>AAA32629.1 Act d 1; actinidin [Actinidia deliciosa]

MGLPKSFVMSLLFFSTLLILSLAFNAKNTQRTNDEVKAMYESWLIKYGKSYNSLGEWE  
RRFEIFKETLRFIDEHNADTNRSYKVLNQFADLTDEEFRSTYLGFTSGSNKTKVSNRYE  
PRVGQVLPYVVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGVLISLSEQELI  
DCGRTQNRTRGCGNGGYITDGFQFIINNGGINTENYPYTAQDGEKNVELQNEKYVTIDTYE  
NVPYNNEWALQTAVTYQPVSVLDAAGDAFKQYSSGIFTGPCGTAIDHAVTIVGYGTEGG  
IDYWIVKNSWDTTWGEEGYMRILRNVGAGTCGIATMPSYPVKYNNQNYPEPYSSLINPP  
AFSMSKDGVPVGEDGQRYSA

>AAA32669.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKQCCYILYFTLALVALLQPVRSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGKWGDVYVTSNLDLDDVANPKEGTLRFAAAQNRPLWIIF  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGLTLMNVKNIHNIHNDVKVLPGGMI  
KSNDGPPILRQASDGDITVAGSSQIWIHCSLSKSFGLVDVTLGSTHVTISNCKFTQQ  
SKAILLGADDTHVQDKGMLATVAFNMFTDNDVQRMPCRFRGFFQVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQIKKNVLARTGTGAAESMAWNWRSDKDLLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVFSCRPGAPC

>AAA32708.1 Asp o 21; taka-amylase, alpha-amylase [Aspergillus oryzae]

MMVAWWSLFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKYCG  
GTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQQDIYSLNENYGTADD

LKALSSALHERGMYLMVDVVANHMGYDAGSSVDYSVFKPFSSQDYFHPFCLIQNYEDQT  
QVEDCWLGDNTVSLPDLDTTKDVVKNEWYDVGSLVSNYSIDGLRIDTVKHVQKDFWPGY  
NKAAGVYCI GEVL DGDPA YTC PYQNVMDGVLNYPIYYPLLNAFKSTSGSMHDLNMIN TV  
KSDCPDSTLLGTFVENHDNPRFAS YTN DIALAKNVA AF IILNDGIPIIYAGQE QHYAGGN  
DPANREATWASGYPTDSELYKLIASANAIRNYAISKDTGFV TYKNWPIYKDDTTIAMRKG  
TDGSQIVTILSNKGASGDSYTL SLSGAGYTAGQQLTEVIGCTTVTVGSDGNV PVP MAGGL  
PRVLYPTEKLAGSKICSSS

>AAA16522.1 Bet v 2; profilin [*Betula pendula*]  
MSWQTYVDEHLMCDIDGQASNSLASAIVGHDG SVWAQSSSFPQFKPQEITGIMKDFEEPG  
HLAPTGLHLGGIKYMIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEEPVTPGQCNMV  
VERLGDYLIDQGL

>AAA32970.1 lipid transfer protein [*Hordeum vulgare*]  
MARAQVLLMAAALVLM LTAAPRAAVALNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDL  
HNQAQSSGDRQTV CNCLKGIARGIHNLNNAASIPSKCNVNPYTI SPDIDCSRIY

>AAA63278.1 Lol p 1; beta-expansin [*Lolium perenne*]  
ALFAVFLGSAHGI AKVPPGNITAEYGD KWLDAKSTWYGKPTGAGPKDNGGACGYKD VDK  
APFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVITDDNEEPIAPYHFDLS  
GHAFGSM AKKGEEQNVR SAGELELQFRRVKCKYPDDTKPTFHVEKGSNP NYLAILVKYVD  
GDGDVVAVDIKEKGKDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEGGTKSEVEDVIP  
EGWKADTSYSAK

>AAA63279.1 Lol p 1; beta-expansin [*Lolium perenne*]  
MASSSSVLLVVALFAVFLGSAHGI AKVPPGNITAEYGD KWLDAKSTWYGKPTGAGPKDN  
GGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVITDDNE  
EPIAPYHFDLSGHAFGSM AKKGEEQNVR SAGELELQFRRVKCKYPDDTKPTFHVEKASNP  
NYLAILVKYVDGDGDVVAVDIKEKGKDKWTELKESWGAVWRIDTPDKLTGPFTVRYTTEG  
GTKSEFEDVIPEGWKADTSYSAK

>AAA33493.1 Zea m 14; lipid transfer protein [*Zea mays*]  
MARTQQLAVVATAVVALVLLAAATSEAAISCGQVASAIAPCISYARGQSGGPSAGCCSGV  
RSLNNAARTTADRRAACNCLKNAAGV SGLNAGNAASIPSKCGVSIPYTI STSTDCSRVN

>AAA33494.1 Zea m 14; lipid transfer protein [*Zea mays*]  
SCGQVASAIAPCISYARGQSGGPSAGCCSGV RSLNNAARTTADRRAACNCLKNAAGVSG  
LNAGNAASIPSKCGVSIPYTI STSTDCSRYSRRMHASAD

>AAA33819.1 Sola t 1; patatin [*Solanum tuberosum*]  
MATTKSFLILFFMILATTSSTCAKLEEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN  
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAKDIVPFYFEHGPHIFNYSGSI  
IGPMYDGKYLQLVLEKLG ETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM  
YDICYSTAAPIYFP PHYFITHTSNGDIYEFNLVDGGVATVGD PALLSLSVATRLAQEDP  
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAQEAAKWGPLRWMLAIQQMTNAASSYMTD  
YYISTVFQARHSQNNYLRVQENALTGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE  
TYEEALKRFAKLLSDRKKLRANKASY

>AAA33947.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [*Glycine max*]  
SKRAKSSSRKTISSEDKPFNLGSRDPIYSKLLGKFFEITPEKNPQLRDL DIFLSIVDMNE  
GALLLPHFN SKAIVILVINEGDANIELVGLKEQQEQQEEQPLEVRKYRAELSEQDIFV  
IPAGYPVVVNATSNLNF FAIGINAENNRNFLAGSQDNVISQIP SQVQELAFPGSAQAVE  
KLLKNQRESYFVDAQPNEKEEGNKGRKGPLSSILRAFY

>AAB01374.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [*Glycine max*]  
MMRARFPLLLLGVVFLASVSVSFGIAYWEKQNP SHNKCLRSCNSEKDSYRNQACHARC NL  
LKVEEEEEEEEGQIPRPRPQHPERERQQHGEKEE DEGEQPRPFPRPRPQPHQEEEEHEQK  
EEHEWHRKEEKHGKGSEEEQDEREHPRPHQPHQKEEEKHEWQHKQEKHQGKESEEEEEED  
QDEDEEQDKESQESGESQREPRRHKNKNPFHFNSKRFQTLFKNQYGHVRVLQRFNKRS

QQQLQNLRDYRILEFNPKPNTLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDALRVPAGTTFYVVPDNDENLRMIAGTTFYVVPDNDENLRMITLAIPVKNKGRFESFFLSTQAQQSYLQGFSKNILEASYDTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQIR  
ELSKHAKSSSRKTISSEDKPFNLGSRDPIYSNKLGLKFEITQRNPQLRDLDFLSVDMN  
EGALFLPHFNSKAIIVLVINEGEANIELVGIKEQQQRQQEEQPLEVRKYRAELSEQDIF  
VIPAGYPVMVNATSDLNFFAFGINAENNRNFLAGSKDNVISQIPVQVQELAFPRSAKDI  
ENLIKQSESYFVDAQPQQKEEGNKGRKGPLSSILRAFY  
>AAA33964.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MGKPFFTLSLSSLCLLLLSSACFAITSSKFNECQLNMLNALEPDHRVESEGGLIETWNSQ  
HPELQCAGVTVSKRTLNRNGSHLPSYLPYPQMIIVVQGGKAIGFAFPGCPETFEPKQQQS  
SRRGSRSQQLQDSHQKIRHFNEGDVLPVPLGVPYWTYNTGDEPVVAISPLDTSNFNQL  
DQNPRVLYLAGNPDI EHPETMQQQQQKSHGGRKQGQHRQQEEEGSVLSGFSKHFLAQS  
FNTNEDTAEKLRSPDDERKQIVTVEGGLSVISPKWQEQEDEDDEDEEYGRTPSYPPRRP  
SHGKHEDDEDEEEDQPRPDHPPQRPSPRPEQQEPRGRGCQTRNGVEENICTMKLHENIA  
RPSRADFYNPKAGRISTLNSLTLPALRQFGLSAQYVLYRNGIYSPDWNLNANSVTMTRG  
KGRVRRVNCQGNVFDGELRRGQLLVVPQNPAAVEQGGEGLEVVFKTHHNAVSSYIKD  
VFRVIPSEVLSNSYNLQSQVRQLKYQGNVSGPLVNP  
>AAA33965.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
QEDEDDEDEEYEQTPSYPPRRPSHGKHEDDEDEEHEHQRPRPDHPPQRPSPRPEQQEPRG  
RGCQTRNGVEENICTMKLHENIARPSRADFYNPKAGRISTLNSLTLPALRQFGLSAQYLV  
LYRNGIYSPHWNLNANSVIYVTRGKGRVRRVNCQGNVFDGDLTRGQLLVVPQNFVADQ  
GGKQGLEVVFKTQHNAVSSYIKDLFRAIPSEVLSNSYNLQSQVRQLKYQGNVSGPLVNP  
>AAA33966.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MAKLVFSLCFLFSGCCFAFSSREQPQQNECQIQKLNALKPDNRIESEGGLIETWNPNNK  
PFQCAGVALSRCTLNRNALRRPSYTNQPQEIYIQGGKIFGMIYPGCPSTFEFPQQPQQR  
GQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDTPVVAVSIIDTNSLENQLDQMPR  
RFYLAGNQEQEFLKYQQEQGGHQSQKGGKQQEENEGGSILSGFTLEFLEHAFSVDKQIA  
KNLQGENEGEDKGAIVTVKGLSVIKPPTDEQQQRPEEEEEEEDEKPKCKGDKHCQRP  
RGSQSKSRRNGIDETICTMRLRHNIQTSSPDIYNPQAGSVTTATSLDFPALSRLSAE  
FGSLRKNAMFVPHYNLNANSIIYALNGRALIQVNCNGERVFDGELQEGRVLIVPQNFVV  
AARSQSDNFYVSFKTNDTPMIGTLAGANSLNALPEEVIQHTFNLKSQQARQIKNNNPF  
KFLVPPQESQKRAVA  
>AAA34272.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
MKTLLILTILAMATTIATANMQVDPVSGVQVWPQQPFPQPQQPFCQQPQRTIPQPHQTFH  
HQPQQTFPQPQQTYPHQPQQFPQTQQPQQPFPQPQQTFPQQPQLPFPQQPQQPFPQPQQ  
PQQPFPQSQQPQQPFPQPQQFPQPQQPQQSFPQQQPAIQSFLQQQMNPKNFLLQQCN  
HVSLVSSLVSIILPRSDCQVMQQCCQQLAQIPQQLQCAAIHVAHSIIMQQEQQQGVPI  
LRPLFQLAQGLGIIQPQQAQLEGIRSLVLKTLPTMCNVVYPPDCSTINVPYANIDAGIG  
GQ  
>AAA34274.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
MKTLLILTILAMAITIATANMQADPSGQVQVWPQQPFLQPHQPFSSQQPQQIFPQPQQTFP  
HQPQQQFPQPQQPQQQLQPRQFPQPQQPQQPYPQQPQQPFPQTQQPQQPFPQSKQPQQPF  
PQPQQPQQSFPQQPSLIQQSLQQQLNPKCNFLLQQCKPVSLVSSLVSIILPPSDCQVMR  
QQCCQQLAQIPQQLQCAAIHVVHSIIMQQEQEQQLQGVQILVPLSQQQVGGQILVQQG  
GIIQPQQPAQLEVIRSLVLQTLPTMCNVVYPPYPCSTIRAPFASIVASIGGQ  
>AAA34275.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALLAIVATTATTAVRVPVPLQLPQNPSSQQPQEQVPLVQQQQFPGQQQQFPPQ  
QPYPQPQPFPSQQPYLQLQPFQPQPFPLPYQPQSFPPQQPYPQQQPQYLQPPQPIISQ  
QQAQQQQQQQQQQQQQQQILQQILQQQLIPCRDVLQQHNIHASSQVLQQSTYQLLQQQL  
CCQQLLQIPEQSQCQAIHNVAAHAIIMHQQQQQQQEQKQQLQQQQQQQQQLQQQQQQQQQQ

PSSQVSFQQPQQQYPSQVSFQPSQLNPQAQGSVQPQQLPQFAEIRNLALQTLPAMCNVY  
IPPHCSTTIAPFGISGTN

>AAA34276.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFFILALLAIVATTATTAVRVPVPLQLQNPSSQQQPQEQVPLVQEQQFQGGQQPFPPQ  
QPYPQPQPFPSQQPYLQLQPFQPLYPQPFQFRPQQPYPQPQYSQPQQPISQQQQQ  
QQQQQQQQQQILQQILQQQLIPCRDVVLQQHNIHAGSSQVLQESTYQLVQQLCCQQLWQI  
PEQSRCQAIHNVVHAIILHQQHHHHQQQQQQQQQPLSQVSFQQPQQQYPSGGQFFQPSQ  
QNPQAQGSFQPPQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN

>AAA34279.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALVATTATTAVRVPVPLQPKNPSQQQPQEQVPLVQQQQFPGQQQFPPQQPY  
PQPQPFPSQQPYLQLQPFQPLPQLPYPQPFQFPQQPYPQQRPKYLQPPQISQQQ  
AQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHNIHAGSSQVLQQSTYQLLQQL  
CCQQLLQIPEQSRCQAIHNVVHAIIMHQEQQQQLQQQQQQQLQQQQQQQQQQPSSQV  
SFQQPQQQYPSQGSFQPSQQNPQAQGSVQPQQLPQFAEIRNLALQTLPAMCNVYIPPHC  
STTIAPFGIFGTN

>AAA34280.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILVLLAIVATTATTAVRFPVPLQPNPSQQQPQEQVPLVQQQQFLGQQQPFPPQ  
QPYPQPQPFPSQLPYLQLQPFQPLPYSQPQFRPQQPYPQPQYSQPQQPISQQQQQ  
QQQQQQQQQQQQQQILQQILQQQLIPCMDVVLQQHNIHAGRSQVLQQSTYQLLQELCCQHL  
WQIPEQSQCQAIHNVVHAIILHQQKQQQQPSSQVSFQQPLQQYPLGQGSFRPSQQNPQA  
QGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN

>AAA34281.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALLAIVATTATTAVRVPVPLQPNPSQQQPQEQVPLVQQQQFLGQQQPFPPQ  
QPYPQPQPFPSQQPYLQLQPFQPLPYSQPQFRPQQPYPQPQYSQPQQPISQQQQQ  
QQQQQQQQQQQQQQQQIIQQILQQQLIPCMDVVLQQHNIHAGSSQVLQQSTYQLLQELCCQH  
LWQIPEQSQCQAIHNVVHAIILHQQKQQQQPSSQVSFQQPLQQYPLGQGSFRPSQQNPQ  
AQGSVQPQQLPQFEEIRNLARK

>AAA34282.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALRAIVATTATI AVRVPVPLQPNPSQQQPQKQVPLVQQQQFPGQQQPFPPQ  
QPYPQQQPFPSQQPYMLQPFQPLPYPQPLPYPQPFQFRPQQSYQPQPQYSQPQQP  
ISQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHSHIAGSSQVLQQSTYQLVQQFC  
CQQLWQIPEQSRCQAIHNVVHAIILHQQQQQQQQQQQQQQQPLSQVCFQQSQQQYPSGG  
SFQPSQQNPQAQGSVQPQQLPQFEEIRNLAETLPAMCNVYIPPYCTIAPVGIFGTN

>AAA34283.1 Tri a 21; gliadin [Triticum aestivum]  
MKTFLILALLAIVATTATS AVRVPVPLQPNPSQQQPQEQVPLMQQQQQFPGQQEQFPP  
QQPYPHQQPFPSQQPYQPQFPFPQLPYPQTQFPFPQQPYPQPQYPQPQQPISQQQAQ  
QQQQQQQTLQQILQQQLIPCRDVVLQQHNIHAGSSQVLQQSSYQQLQQLCCQQLFQIPEQ  
SRCQAIHNVVHAIILHHHQQQQQQPSSQVSQYQPQEQYPSGQVSFQSSQQNPQAQGSVQP  
QQLPQFQEIRNLALQTLPAMCNVYIPPYCSTTIAPFGIFGTN

>AAA34284.1 Tri a 21; gliadin, partial [Triticum aestivum]  
PQPQPQYSQPQQPISQQQQQQQQQQQQQQEQQILQQILQQQLIPCMDVVLQQHNIHAGR  
SQVLQQSTYQLLQELCCQHLWQIPEQSQCQAIHNVVHAIILHQQKQQQQPSSQFSFQQ  
PLQQYPLGQGSFRPSQQNPQAQGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPF  
GIFGTN

>AAA34285.1 gamma-gliadin [Triticum aestivum]  
MKTFLVFALIAVWATSIAI AQMETSCISGLERPWQQQLPQQSFSQQPPFSQQQQQPLPQ  
QPSFSQQQPPFSQQQPILSQQPPFSQQQPVLVQQSPFSQQQLVLPQQQQQQQLVQQQI  
PIVQPSVLQQLNPKVFLQQQCSVPAMPQRLARSQMWQQSSCHVMQQQCCQQLQQIPEQS  
RYEAIRAIIYSIILQEQQQGFVQPQQQQPQQSGQVVSQSQSQQLGQCSFQQPQQQLG  
QQPQQQQQQQLVQGTFLQPHQIAHLEAVTSIALRTLPTMCSVNVP LYSATTSVPFGVGTG

VGAY

>AAA34286.1 gamma-gliadin [Triticum aestivum]  
TITRTFPIPTISSNNHHFRSNSNHFFHSNMQFYRNNSPQHNNPLNNSPNNNSPSN  
HHNNSPNNNFQYHTHPSNHKNLPHNTNIQQQQPPFSQQQQPPFSQQQQPVLPPQSPFSQQ  
QQLVLPQQQQQQLVQQQIPIVQPSVLQQLNPKVFLQQQCSPVAMPQRLARSQMWQSS  
CHVMQQCCQQLQOIQEQRYSYAIRAIYSIILQEQQQGFVQPPQQQPQQSGQVVSQSQ  
QSQQQLGQCSFQQPQQQLGQQPQQQQQQVLOGTFLQPHQIAHLEAVTSIALRTLPTMCS  
VNVPLYSATTSVPFGVGTGVGAY

>AAA34287.1 gamma-gliadin [Triticum aestivum]  
PQQPFPLQPQSFQSQPPFLQQPQQPSPQPPQVQIISPATPTTIPSAGKPTSAPFPQ  
QQQQHQQLAQQQIPVVQPSILQQLNPKVFLQQQCSPVAMPQRLARSQMLQQSSCHVMQQ  
QCCQQLPQIPQQSRYQAIRAIYSIILQEQQQVQGSIQSQQQPQQQLGQCVSQPQQSQ  
QLGQQPQQQLAQGTFLQPHQIAQLEVMTSIALRILPTMCSVNVPLYRTTTSVPFGVGTG  
VGAY

>AAA34288.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
MKTLILLITILAMAITIGTANMQVDPSSQVQWPQQPVPQPHQPFSSQQPQTFPQPQTFP  
HQPQQQFPQPQQPQQFLQPQQPFPQQPQQPYPQQPQQPFPQTQQPQLFPQSQQPQQQF  
SQPQQQFPQPQQPQQSFPQQPPFIQPSLQQQVNPCKNFLLQCKPVSLVSSLWSMIWPQ  
SDCQVMRQQCCQLAQIPQQQLCAAHTIHSIIMQQEQQEQQQGMHILLPLYQQQQVGG  
GTLVQGGGIIQ

>AAA34289.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
MKTLILLITILAMAITIGTANIQVDPSSQVQWLQQQLVPLQQLPSSQQPQTFPQPQTFP  
HQPQQQVPPQPQQPQQPFLQPQQPFPQQPQQPFPQTQQPQQPFPQQPQQPFPQTQQPQQP  
PQQPQQPFPQTQQPQQPFPQLQQPQQPFPQPQQQLPQPQQPQQSFPQQQRPFIQPSLQQ  
LNPKNILLQQSKPASLSSLWSIWPQSDCQVMRQQCCQLAQIPQQQLCAAHSVVS  
IIMQQQQQQQQGIDIFLPLSQHEQVGGSLVQGGIIPQPPAQLEAIRSLVLQTLPS  
MCNVYVPPECSIMRAPFASIVAGIGGQ

>AAA34290.1 gliadin [Triticum urartu]  
MKTFLLILALLAIVATTATTAVRVPVPPQPQNPSPQPQRQVPLVQQQQFPGQQQFPPQ  
QPYPQPQPFPSQQPYLQLQPFPPQPPFPQLPYPQPPFSPQQPYPQPQPYPQPQQPIS  
QQQAQQQQQQQQQQQQQQQQQILPQILQQQLIPCRDVVLQQHNIHARSQVLQQSTYQP  
LQQLCCQQLWQIQEQRCAIHNVVHAIILHQQQQQQPSSQVSLQQPQQQYPSGQGGFFQ  
PSQONPQAQGSVPPQQLPQFEEIRNLALQTLPRMCNVYIPPYCSTTTAPFGIFGTN

>AAB02788.1 Tri a 26; HMW glutenin [Triticum aestivum]  
MTKRLVLF AAVVALVALTAAEGEASGQLQCERELQEHSKACRQVVDQQLRDVSPECQP  
VGGGPVARQYEQQVVVPPKGGSFYPGETTPPQQLQQSILWGIPALLRRYYLSVTSPQQVS  
YYPGQASSQRPGQGQQEYLLTSPQQSGQWQQPGQGQSGYYPTSPQQSGQKQPGYYPTSPW  
QPEQLQQPTQGQRQPPGQQLRQGQQGQSGQGQPRYYPTSSQQPGQLQQLAQGGQGG  
QPERGQQGQSGGQQLGQGQQGQPPGQKQSGQGQGGYYPISPQQLGQGQSGGQGLGY  
YPTSPQQSGGQSGYYPTSAQQPGQLQQSTQEQLGQEQDQSGQGRGQSGQRQDDQ  
QSGGQPPGQRQPGYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQQGQQPE  
QGQQGQQQRQGEQGGQPPGQGGQPPGQGGQPGYYPTSPQQSGGQPGYYPTSPQQSGQLQ  
QPAQGGQPPGQEQQGQPPGQGGQPPGQGGQPGYYPTSPQQSGQEQLQWQQSGGQPPGHYPT  
SPLPQGQPPGYYPTSPQQIGQGQPPGQLQQPTQGQQGQPPGQGGQPPGEGQQGQPPG  
QGQQPPGQPPGYYPTSLQQSGGQPPGQWQQPGQGGQPPGYYPTSSLQPEQGQQGYYPTSQ  
QPPGQPPGQWQQSGGQGGYYPSTPQQSGGQPPGQWQQPGQWQQSGYYLTSPQQLGQG  
QQPRQWLQPRQGQQGYYPTSPQQSGGQQLGQGQQGYYPTSPQQSGGQGGYDPSYHVSA  
EHQAASLKVAKAQLAAQLPAMCRLEGGDALLASQ

>AAA39768.1 Mus m 1; lipocalin, urinary globulin [Mus musculus]  
MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRFL

EQIHVLEKSLVLKFHTVRDEECELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM  
AHLINKEKDGETFQLMGLYGREPDLSSDIKERFAKLCEEHGILRENIIDLSNANRCLQARE  
>AAA41198.1 Rat n 1; lipocalin, urinary globulin [Rattus norvegicus]  
LLLLLCLGLTLVCGHAEASSTSGNLDVAKLNGDWFISIVVASNKREKIEENGSMRVFMQHI  
DVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYVMFHL  
INFKNGETFQLMVLYGRTKDLSSDIKEKFAKLCEAHGITRDNIIDLTKTDRCLQARG  
>AAA48944.1 Gal d 4; lysozyme [Gallus gallus]  
MNAWVAWRNSCKGTDVQAWIRGCR  
>BAA01239.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
SLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAK  
IEIKASLDGLEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKLI  
GDNGVLACAIATHGKIRD  
>BAA01240.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA  
NQNKTAKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDIKYTWNVPKIAPKSEN  
VVTVKLIIGDNGVLACAIATHGKIRD  
>BAA01241.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
SLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAK  
IEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSENVVTVKLV  
GDNGVLACAIATHAKIRD  
>BAA01998.1 unknown function [Oryza sativa]  
MASNKVVFSAALLLIIVSVLAATTRMADHHKDQVVYSLGERCQPGMGYPMYSLPRCRAVVK  
RQCVGTRSPGAVDEQLAQDCCRELAAVDDSWCRCSALNHMVGGIYRELGATDVGHMAEV  
FPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGPRTPTGH  
>BAA01996.1 unknown function [Oryza sativa]  
MASNKVVFVLLAVVSVLAATATMAEYHHQDQVVYTRARCQPGMGYPMYSLPRCRAVVK  
RQCRGSAAAAEQVRRDCCRQLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEVFRG  
CRRGDLERAAASLPAFCNVDIPNGGGGVCYWLARSY  
>BAA00154.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]  
MAKLVLVSLCFLLFSGCFALREQAQQNECQIQKLNALKPDNRIESEGGFIETWPNPKPFQ  
CAGVALSRCTLNRNALRRPSYTNQPQEIYIQQNGIFGMIFPGCPSTYQEPQESQQRGRS  
QRPQDRHQKVRHFREGDLIAVPTGVAWWMYNNEDTPVVAVSIIDTNSLENQLDQMPRRFY  
LAGNQEQEF LKYQQQQQGSQSQKQKQEEENEENEGSNILSGFAPEFLKEAFGVNMQIVRNL  
QGENEEEDSGAIVTVKGLRVTAPAMRKPQEEEDDDDEEQPQCVETDKGCQRQSKRSRN  
GIDETICTMRLRQNIQNSSPDIYNPQAGSITTATSLDFPALWLLKLSAQYGLRKNAMF  
VPHYTLNANSIIYALNGRALVQVNCNGERVFDEGELQEGGVLIVPQNFVAVAASQSDNFE  
YVSFKTNDRPSIGNLAGANSLNALPEEVIQHTFNLKSQQARQVKNNNPFSLVPPQESQ  
RRAVA  
>P30575.1 enolase [Candida albicans]  
MSYATKIHARYVYDSRGNPTVEVDFTTDDKGLFRSIVPSGASTGVHEALELRDGDKSKWLG  
KGVLKAVANVNDIIAPALIKAKIDVVDQAKIDEFLSLDGTDPNKSCLGANAILGVSLAAA  
NAAAAAQGIPLYKHIANISNAKKGFVLPVPFQNVLNGGSHAGGALAFQEFMIAPTGVST  
FSEALRIGSEVYHNLKSLTKKKYQGSAGNVGDEGGVAPDIKTPKEALDLIMDAIDKAGYK  
GKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLSPQLADLYEQLISEYPIVSIEDPF  
AEDDWDVAWHFFERVGDKIQIVGDDLTVTNPTRIKTAIEKKAANALLLVNQIGTLTESI  
QAANDSYAAGWGMVSHRSGETEDTFIADLSVGLRSGQIKTGAPARSERLAKLNQILRIE  
EELGSEAIYAGKDFQKASQL  
>AAB22817.1 agglutinin [Arachis hypogaea]  
MKPFCVFLTFLLLAASSKKVDSAETVSFNFNSFSEGNPAINFQGDVTVLSNGNIQLTNL  
NKVNSVGRVLYAMPVRIWSSATGNVASFLTSFSFEMKDIKDYDPADGIIFFIAPEDTQIP

AGSIGGGTLGVSDTKGAGHFVGVFEDTYSNSEYNDPPTDHSVGDVNSVDSVKTVPWNSVS  
GAVVKVTVIYDSSTKTLVAVTNDNGDITTTIAQVVDLAKALPERVKFGFSASGSLGGRQI  
HLIRWSFTSTLITTTTRRSIDNNEKKIMMASA  
>AAB23464.1 trypsin-inhibitor [Glycine max]  
MKSTIFFLFLCAFTTSYLPSAIADFLVDNEGNPLENGGTYIYILSDITAFGGIRAAPTGN  
ERCPLTVVQSRNELDKIGIGTISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTESV  
EDLPEGPAVKIGENKDAMDGWFRLEERSVSDDEFNRYKLVFCPQQAEDDKCGDIGISIDHDD  
GTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE  
>AAB23482.1 trypsin-inhibitor [Glycine max]  
MKSTIFFALFLVCAFTISYLPSATAQFVLDTDDDPQNGGTYIYMLPVMRGKGGGIEVDST  
GKEICPLTVVQSPNELDKIGLVFTSPLHALFIAERYPLSIKFGSFAVITLCAGMPTWEA  
IVEREGLQAVKLAARDTVDGFNIERSVREYNDYKLVFCPQQAEDNKCEDIGIQIDDDGI  
RRLVLSKNKPLVVQFQKFRSSTA  
>AAB23483.1 trypsin-inhibitor [Glycine max]  
MKSTIFFALFLVCAFTISYLPSATAQFVLDTDDDPQNGGTYIYMLPVMRGKSGGIEGNST  
GKEICPLTVVQSPNKHNGIGLVFKSPLHALFIAERYPLSIKFGSFAVIPLCGVMPTKWA  
IVEREGLQAVTLAARDTVDGFNIERSVREYNDYYKLVFCPQQAEDNKCEDIGIQIDNDG  
IRRLVLSKNKPLVVEFQKFRSSTA  
>AAB24432.1 Aln g 1; pathogenesis related protein, PR-10, Bet v 1-like [Alnus  
glutinosa]  
MGVFNYEAETPSVIPAARLFKAFILDGDKLLPKVAPEAVSSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDVNFVFKYSFVIEGGAVGDALEKVCNEIKIVAAPDGGGILKISNK  
FHTKGDHEINAEQIKIEKEKAVGLLKAVERSYLLAHSDAYN  
>P29600.1 alkaline serine protease [Bacillus lentus]  
AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPSTQDGN  
GHGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVA  
NLSLGSPPSATLEQAVNSATSRGVLVVAASGNSGAGSISYPARYANAMAVGATDQNNNR  
ASFSQYGAGLDIVAPGVNVQSTYPGSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQI  
RNHLKNTATSLGSTNLYGSGLVNAEAATR  
>CAA47341.1 Do1 m 1; phospholipase A1 [Dolichovespula maculata]  
RLIMFVGDPPSSNELDRFSVCPFSNDTVKMIFLTRENKHFYTLDTMNRHNEFKKSIK  
RPVVFITHGFTSSATEKNFVAMSEALMHTGDFLIIMVDWRMAACTDEYPGLKYMFKAAV  
GNTRLVGNFIAMIAKKLEQYKVPMTNIRLVGHSGLGAHISGFAGKRVQELKLGKFSEIIG  
LDPAGPSFKKNDCSERICETDAHVVQILHTSSNLGTERTLGTVDYFYNNGSNQPGCRYII  
GETCSHTRAVKYFTECIRRECLIGVPQSKNPQPVSKCTRNECVGLNAKKYPKRGFSFY  
VPVEAEAPYCNNGKII  
>AAA32702.1 serine protease [Aspergillus niger]  
MKGILGLSLLPLLLTAASPVFVDSIHNEAAPILSATNAKEVPDSYIVVFKKHVTSELASAH  
HSWVDIHDQSERTELKRSFLGGLDEVYLGKNTFDIAGSLIGYSGHFHEDVIEQVRR  
HPDVDYIERDSEVHTMEGATEKNAPWGLARISHRDSLTFGNFNKYLYASEGGEGVDAYTI  
DTGINVDHVDVEGRATWGKTIPTNDEDLDGNGHGHGTHCSGTMAGKKYGVAKKANLYAVKVL  
RSSGSGTMSDVVSGVEYAVQAHIKKAKDAKNGKVKGFKGSVANMSLGGGKSKTLEDAVNA  
GVEAGLHFAVAAGNDNADACNYSAAAEEKAITVGASTLADERAYFSNYGECTDIFAPGLN  
ILSTWIGSNYATNIISGTSMASPHIAGLLAYFVSLQPSSDSFAVEELTPAKLKKDIIAI  
ATEGALTDIPSNTPNVSHAAVGIYKRNELTQKFSSLPGTVVVPRTTPTSLLAAVATRSPLP  
RTASRTVLRVSFTRPKSCSPRSLVPSTARSRMPSSHRSELVLSRRRSEDLVFF  
>CAA29664.1 Bos d 4; alpha-lactalbumin [Bos taurus]  
MMSFVSLLLVGLFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTAFHTSGYDTQAI  
VQNNDSTEYGLFQINNKIWCKDDQNPSSNICNISCDKFLDDDLTDDIMCVKKILDKVGI  
NYWLAHKALCSEKLDQWLCEKL

>CAA26953.1 Mus m 1; lipocalin, urinary globulin [Mus musculus]  
MKMLLLLCLGLTLVCHAAEEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRFL  
EQIHVLENSLVLFHTVRDEECELSMVDKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM  
AHLINKEKDGTFQLMGLYGREPDLMSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE  
>AAB25850.1 unknown function, partial [Betula sp.]  
GVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAITSVENIYERYGXG  
>AAB25851.1 unknown function, partial [Betula sp.]  
SVFNYETETTSVIPAAFLFKAFILDGDKLFPKVAPQXQSIVXNXRVVYXPK  
>CAA49760.1 Myr p 1; pilosulin [Myrmecia pilosula]  
MKLSCLLLTLTIIFVLTIVHAPNVEAKDLADPESEAVGFADAFGEADAVGEADPNAGLGS  
VFGRLARILGRVIPKVAKKLGPVKVAVLPKVMKEAIPMAVEMAKSQEEQQPQ  
>CAA51718.1 Zea m 12; profilin [Zea mays]  
MSWQTYVDEHLMCEIEGHHLTSAIVGHDGATWAQSTAFPEFKPEEMAAIMKDFDEPGHL  
APTGLILGGTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQSLIIGIYDEPMTPGQCNLVE  
RLGDYLLEQGM  
>CAA51719.1 Zea m 12; profilin [Zea mays]  
MSDRAKMSWQAYVDEHLMCEIEGHHLAAAAIVGHDGAAWAQSTAFPEFKTEDMANIMKDF  
DEPGHLAPTGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVVGIYDEPMTPGQ  
CNMVVERLGDYLLEQGM  
>CAA51720.1 Zea m 12; profilin [Zea mays]  
MSWQTYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQPKPEEMTNIIMKDFDEPGFL  
APIGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVIGIYDEPMTPGQCNMVE  
RLGDYLVEQGL  
>A45786 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial [Betula  
pendula]  
GVFNYEAETTSVIPAAWLKXFILDGDNLFKVPAPQAXTSVENIYERGGWG  
>B45786 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial [Betula  
pendula]  
SVFNYETETTSVIPAAMLFKAFILDGDKLFPKVAPQXQSIVXNXRVVYXPK  
>E37396 beta-expansin [Agrostis alba]  
YTTEGGTKAEAEDVIPEGWKADTSYE  
>G37396 expansin, partial [Anthoxanthum odoratum]  
YTTEGGKKVEAEDVIPEGWKADTSYE  
>C37396 beta-expansin, partial [Schedonorus arundinaceus]  
YTTEGGTKSEAEDVIPE  
>D37396 beta-expansin, partial [Schedonorus arundinaceus]  
YTTEGGTKSEVEDVIPEGWK  
>F37396 beta-expansin, partial [Poa pratensis]  
YTTEGGTKAEAEDVIPEGWKVDTSYE  
>AAA16792.1 Hev b 10; superoxide dismutase [Hevea brasiliensis]  
MALRSLVTRKNLPSAFKAATGLGQLRGLQTFSLPDLPHYDYGALPAISGEIMQLHHQKHH  
QTYITNYNKALEQLNDAIEKGDAAVVKLQSAIKFNGGGHVNHSIFWKNLAPVREGGGEL  
PHGSLGWAIDADFGSLEKLIQLMNAEGAALQSGWVWLALDKELKKLVVETTANQDPLVT  
KGPTLVPLLIGIDVWEHAYYLQYKNVRPDYLNKNIWKVMNWKYASEVYAKECPSS  
>AAA28296.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
MSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAA  
TESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPR  
>CAA44345.1 Fel d 1; uteroglobin [Felis catus]  
MRGALLVLLALLVTQALGVKMAETCPIFYDVFFAVANGNELLLDLSLTKVNATEPERTAMK  
KIQDCYVENGLISRVL DGLVMIAINEYCMGEAVQNTVEDLKLNTLGR

>CAA52753.1 Phl p 5; unknown function [Phleum pratense]  
MAVHQYTVALFLAVALVAGPAASYAADLGYGPATPAAPAAGYTPATPAAPAEAAPAGKAT  
TEEQKLIKINAGFKAALAAAAGVQPADKYRTFVATFGAASNKAFKAEGLSGEPKGAAESS  
SKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKPAEEVK  
VIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYESYKFI  
LEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAKPAAAAATATATAAVGAAT  
GAATAATGGYKV

>CAA52194.1 Equ c 3; serum albumin [Equus caballus]  
MKWVTFVSLFLFSSAYSRGLRRDTHKSEIAHRFNDLGEKHFGLVAVFSQYLQQCPF  
EDHVKLKLVNEVTEFAKKCAADESAENCDKSLHTLFGDKLCTVATLRATYGEADCCQEP  
ERNECFLTHKDDHPNLPLKLPKPEPDAQCAAFQEDPKFLGKLYLEVARRHPYFYGPPELLFH  
AEEYKADFTCCPADDKLAACLIPKLDALKERILLSSAKERLKCSSFQNFGERAVKAW  
SVARLSQKFPKADFAEVSKIIVTDLTKVHKECCHGDLLECADDRADLAKYICEHQDSISGK  
LKACCCKPLQKSHCIAEVKEDDLPSDLPALAADFAEDKEICKHYKDAKDVFLGTFLYEYS  
RRHPDYSVSLLLRIAKTYEATLEKCCAEADPPACYRTVFDQFTPLVEEPKSLVKKNCDF  
EEVGEYDFQNALIVRYTKKAPQVSTPTLVEIGRTLKGVGSRCKLPESERLPCSENHLAL  
LALNRLCVLHEKTPVSEKITKCTDLSAERRPCFSALELDEGYVPKEFKAETFTFHADICT  
LPDEKQIKKQSALAEVLVHKPKATKEQLKTVLGNFSAFVAKCCGREDKEACFAEEGPKL  
VASSQLALA

>CAA47366.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

GVFNYEAEETPSVIPAARLFKSYVLDGDKLIPKVAPQVISSVENVGGNGGPGTIKNITFAE  
GIPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF  
HAKGYHEVNAAEKMGAKEMAELLLRAVESYLLAHTAEYN

>CAA47357.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

GVFNYEAEETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFAE  
GSPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF  
HAKGYHEVNAAEEMKGAEMAELLLRAVESYLLAHTAEYN

>CAA47367.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

GVFNYEAEETTSVIPAARLFKAFILDGNKLIPKVSPQAVSSVENVEGNGGPGTIKKITFSE  
GSPVKYVKERVEEIDHTNFYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF  
HAKGYHEVNAAEEMKGAEMAELLLRAVESYLLAHTAEYN

>AAB27594.1 Der f 6; chymotrypsin, serine protease [Dermatophagoides farinae]  
AVGGQDADLAEAPFQISLLK

>AAB27445.1 beta-expansin, partial [Phalaris aquatica]  
IAKVPPGGXITAIEYGDKWL

>CAA81610.1 Hol 1 1; beta-expansin [Holcus lanatus]  
MASSRSVLLLVAAALFAVFLGSAHGIKAVPPGNITATYGDWLDKSTWYGKPTGAGPK  
DNGGACGYKDVDPKPPFSGMTGCGNTPIFKDRGRCGSCFEIKCTKPESCSGEPVTVHITDD  
NEEPIAPYHFDLSGHAFGSMKKGEEQKLSAGELELKFRRVKCKYDPDGKPTFHVEKGS  
NPNYLALLVKYIDGDGDVVAVDIKEKGDKWIELKESWGAWRVDTDPDKLTGPFTVRYTT  
EGGKGEAEDVIPEGWKADTAYEAK

>CAA53529.1 Phl p 2; expansin [Phleum pratense]  
MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFVTEKGSNEKHLAVLVKYEAGDTMAEVELR  
EHGSDEWVAMTKGEGGVWTFDSEELQGPFRFLTEKGMKNVFDVPEKYTIGATYAP  
EE

>P00304.2 Amb a 3; plastocyanin [Ambrosia artemisiifolia]  
GKVYLVGGPELGGWKLQSDPRAYALWSARQQFKTTDVLWVFNFTTGEDSVAEWWREEAYHA

CDIKDPIRLEPGGPDRFTLLTPGSHFICTKDQKFVACVPGR  
>P24296.2 lipid transfer protein [Triticum aestivum]  
AQVMLMAVALVLMMLAAVPRAAVAIDCGHVDSLVRPCLSYVQGGPGPSGQCCDGVKNLHNQ  
ARSQSDRQSACNCLKGIARGIHNLNEDNARSIPPKCGVNLPTYISLNIDCSR  
>S32101 Phl p 5; unknown function [Phleum pratense]  
EAPAGKATTEEQKLIKINAGFKAALARRLQPADKYRTFVATFGPASNKAFAEGLSGEPK  
GAAESSKAALTSKLDAAVKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKP  
AAEEVKVIPAAELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFNDEIKASTGGAYES  
YKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAKPPPLPPPPQPP  
PLAATGAATAATGGYKV  
>CAA49555.1 alpha-amylase inhibitor [Hordeum vulgare]  
MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLPSNPLEGCREYVAQQTCGVTIAGS  
PVSSEPGDTPKDRCCQELDEAPQHRCCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDFA  
KVLVTPGQCNVLTVHNAPYCLGLDI  
>CAA54421.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDHEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN  
>AAB28566.1 Cyn d 1; beta-expansin, partial [Cynodon dactylon]  
AMGDDPGPKITATYGSKWLDKATF  
>AAB28567.1 Cyn d 1; beta-expansin, partial [Cynodon dactylon]  
GAAPDDHGGAXGYKDVDPKPPFDGMTAXGNEPIFKDDL  
>CAA54481.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYESETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDQEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN  
>CAA54482.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEIETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA54483.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYTEATSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGIPFKYVKGRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK  
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN  
>CAA54484.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEIETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK  
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN  
>CAA54487.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYTEATSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK  
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN  
>CAA54488.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]

MGVFNYESSETTSVIPAAARLFKAFILEGDTLIPKVPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN

>CAA54489.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

MGVFNYESSETTSVIPAAARMFKAFILDGDKLVKVPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAA54686.1 Phl p 12; profilin [Phleum pratense]

MSWQTYVDEHLMCEIEGHHLASAAIILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAGAKYMIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNM VVE  
RLGDYLVEQGM

>AAA33405.1 Lol p 5; unknown function [Lolium perenne]

MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPATPAAVP  
SGKATTEEQKLEIKINAGFKAAVAAA VPPADKYKTFVETFGTATNKAFVEGLASGYAD  
QSKNQLTSKLDAAKLAYEAAQGATPEAKYDAYVATL TEALRVIAGTLEHVAVKPAEEV  
KVGAI PAEVQLIDKVDAA YRTAATAANAAPANDKFTVFENTFNNAIKVSLGAA YDSYKF  
IPTLVA AVKQAYAAKQATAPEVKYTVSETALKKAVTAMSEAEKEATPAAAATATPTPAAA  
TATATPAAAYATATPAAATATATPAAATATPAAAGGYKV

>AAB29137.1 Bos d 11; beta-casein [Bos taurus]

MKVLILACLVALALARELEELNVPGEIVESLSSEESITRINKKIEKFQSEEQQQTEDEL  
QDKIHPFAQTQSLVYPPFGPIPNLQNIPLTQTPVVVPPFLQPEVMGVSKVKEAMAPK  
QKEMPFKYPVEPFTESQSLTLTDVENLHLPLPLLQSWMHQPHQPLPPTVMFPPQSVLSL  
SQSKVLPVVPQAVPYPQRDMPIQAFLLYQEPVLGPVVRGPFPIIV

>P34071.1 enterotoxin [Staphylococcus aureus]

MNKSRLFISCVILIFALILVLF TPNVLAESQPDPTDELHKSSEFTGTMGNMKYLYDDHYV  
SATKVMSVDKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYVNC  
YFSSKDNVGVKVTGGKTCMYGGITKHEGNHFDNGLQNVLIRVYENKRNTISFEVQTDKKS  
VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKY  
LMMYNDNKTVDKSVKIEVHLTTKNG

>P33556.1 lipid transfer protein, partial [Vitis vinifera]

AITCGQVSSALSSCLGYLKNNGAVPPGSSCGIKNLNSA

>P80274.1 lipid transfer protein, partial [Vitis vinifera]

TVTTCGQVASALSPCIDYLQKDGAVPAGSCCXKXLSA

>CAA55068.1 Cla h 7; unknown function [Cladosporium herbarum]

MAPKIAIIFYSTWGHVQTLAEAEAKGIREAGGSVDLYRVPETLTQEVLTKMHAPPKDDSI  
PEITDPFILEQYDRFPHGHPTRYGNFPAQWRTFWDRTGGQWQTGAFWGKYAGLFISTGTQ  
GGGQESTALAAMSTLSHHGIIYVPLGYKTTFHLLGDNSEVRGAAVWGAGTFSGGDGSRQP  
SQKELELTAQKAFYEAVAKVNFQ

>CAA55070.1 Cla h 6; enolase [Cladosporium herbarum]

MPISKIHSRYVYDSRGNPTVEVDIVTETGLHRAIVPSVASTGSHEACELRDGDKSKWAGK  
GVTKAVANVNEIIPALIKENLDVKDQAAVDAFLNKLDGTTNKTIGANAILGVSMVAK  
AAAAEKRVPL YAHISDLSGTKKPFVLPVPMNVVNGGSHAGGR LAFQEFMIVPSGAPSFT  
EAMRQGAEVYQKLSLTKKRYQSAGNVGDEGGVAPDIQTAEALDLITDAIEEAGYTGQ  
IKIAMDVASSEFYKADEKKYDLDFKNPDSKSKWITYEQLADQYNELAAKYPIVSIEDPF  
AEDDWEAWSYFYKTS GDFQIVGDDLTVTNPEFIKKA IETKACNALLLVNQIGTITEAI  
NAAKDSFAAGWGMVSHRSGETEDVTIADIVVGLRAGQIKTGAPARSERLAKLNQILRIE  
EELGDKRLYAGDNFRTAINL

>CAA55390.1 Phl p 1; beta-expansin [Phleum pratense]

MASSSSVLLVVFLFAVFLGSAYGIPKVPVPPGNITATYGDKWLDKSTWYGKPTGAGPKDN

GGACGYKDVDKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNE  
EPIAPYHFDLSGHAFGAMAKKGDQKLSAGELELQFRRVKCKYPEGTKVTFHVEKGSNP  
NYLALLVKYVNGDGDVVAVDIKEKGDKWIELKESWGAIWRIDTPDKLTGPFTVRYTTEG  
GTKTEAEDVIPEGWKADTSYESK

>S38584 Phl p 5; unknown function [Phleum pratense]

MAVPRRGPRGGPGRSYTADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKAAVAARQ  
RPAADKFKTFEASPRHRPLRQAGLVPKLDAAYSVAYKAAVGATPEAKFDSFVASLTE  
ALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFVAATAAATAPADDKFTVF  
EAAFNKAIKESTGGAYDXYKIPSLEAAVKQAYAAVAAAAEVKYAVFEAALTKAITAMS  
EVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>CAA5584.1 Bet v 3; calcium-binding protein, polcalcin [Betula pendula]

MPCSTEAMEKAGHGHASTPRKRSLSNSSFRRLRSESLNLRRLRRIFDLFDKNSDGIITVDE  
LSRALNLLGLETDLSELESTVKSFTREGNIGLQFEDFISLHQSLNDSYFAYGGEDEDDNE  
EDMRKSILSQEEADSFGGFKVFEDEGDGYISARELQMVLGKLGFESEIDRVEKMIVSV  
DSNRDGRVDFEFKDMMRSLVLRSS

>BAA05542.1 Cry j 1; pectate lyase [Cryptomeria japonica]

MDSPCLVALLVLSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD  
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLMKPMYIAGYKTFDGRGAQV  
YIGNGGPCVFIKRVSNVHIIHGLHLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT  
NIWIDHNSFSNSSDGLVDVTLSTGVTISNNLFFNHHKVMMLGHDDAYSDDKSMKVTVAF  
NQFGPNCGQRMPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSTAPNESYKKQV  
TIRIGCKTSSSSCSNWWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPQLT  
KNAGVLTCSLSKRC

>BAA05543.1 Cry j 1; pectate lyase [Cryptomeria japonica]

MDSPCLVALLVFSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD  
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLMKPMYIAGYKTFDGRGAQV  
YIGNGGPCVFIKRVSNVHIIHGLYLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT  
NIWIDHNSFSNSSDGLVDVTLTSTGVTISNNLFFNHHKVMMLGHDDAYSDDKSMKVTVAF  
NQFGPNCGQRMPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSTAPNESYKKQV  
TIRIGCKTSSSSCSNWWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPHLT  
QNAGVLTCSLSKRC

>BAA06172.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRNIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNVIEDLICGPGHGIGSLGRENSRAEVSYVHVN  
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVYKNIIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGIASCLNDNANGYFS  
GHVIPACKNLSAPAKRKEKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>CAA56343.1 trypsin-inhibitor [Glycine max]

MKSTTSLALFLLCALTSSYQPSATADIVFDTEGNPIRNGGTYVLPVIRGKGGGIEFAKT  
ETETCPLTVVQSPFEGLQRGLPLIISSPFKILDITEGLILSLKFHLCTPLSLNSFSVDRY  
SQGSARRTPCQTHWLQKHNRWFRIQRASSESNYKLVFCTSNDDSSCGDIVAPIDREGN  
RPLIVTHDQNHPLLVQFQKVEAYESSTA

>AAA19973.1 Der p 3; trypsin [Dermatophagoides pteronyssinus]

MIIYNILIVLLLAINTLANPILPASP NATIVGGEKALAGECPYQISLQSSSHFCGGTILD  
EYWILTAACHVAGQTASKLSIRYNSLKHSLGGEKISVAKIFAHEKYDSYQIDNDIALIKL  
KSPMKLNQKNAKAVGLPAKGS DVKVGQVRVSGWGYLEEGSYSLPSELRRVDIAVVS RKE

CNELYSKANA EVDNMICGGDVANGGKDSCQGDSSGGPVVDVKNQVVGIVSWGYGCARKG  
YPGVYTRVGNFIDWIESKRSQ  
>AAA68279.1 DoI m 2; hyaluronidase [Dolichovespula maculata]  
SERPKRVFNIIYWNVPTFMCHQYGLYFDEVTFNFIKHNSKDDFQGDKISIFYDPGEFPALL  
PLKEGNYKIRNGGVPQEGNITIIHLQRFIENLDKTYPNRNFNGIGVIDFERWRPIFRQNWG  
NMMIHKKFSIDLVRNEHPFWDKKMIELEASKRFEKYARLFMEETLKLAKKTRKQADWGY  
GYPYCFNMSPNNLVPDCDATAMLENDKMSWLFNNQNVLLPSVYIRHELTPDQRVGLVQGR  
VKEAVRISNNLKHSPKVLSYWWVYVYQDDTNTFLTETDVKKTFQEIAINGGDGIIIWSSS  
DVNSLSKCKRLREYLLTVLGPITVNVVTETVN  
>AAB60215.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
MKIVLAIASLLALSAVYARPSSIKTFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSN  
GGAINHLSLSDLEDFKNRFLMSAEAFEHLKTQFDLNAETNACSSINGNAPAEIDL RQMRTV  
TPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEY  
IQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNVNKIREALQTHSAIAVII  
GIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNAQGVYWI VRNSWDTNWGDNGYG  
YFAANIDLMMIEEYPYVVIL  
>AAA20065.1 Amb p 5; unknown function [Ambrosia psilostachya]  
MNNEKNVSFEFIGSTDEVEIKLLPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESSEI  
CSQKCGKMRMNVTNKNTI  
>AAA20067.1 Amb p 5; unknown function [Ambrosia psilostachya]  
MNNEKNVSFEFIGSTDEVEIKLLPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESSKI  
CSQKCGKMRMNVTNKNTI  
>AAA20064.1 Amb p 5; unknown function [Ambrosia psilostachya]  
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYCSSDPGRYCPWQVVCYESRKI  
CAKNAAKMRMNVTNKNTI  
>AAA20066.1 Amb p 5; unknown function [Ambrosia psilostachya]  
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYSSSDPGRYCPWQVVCYESRKI  
CAKNAAKMRMNVTNKNTI  
>AAA20068.1 Amb p 5; unknown function [Ambrosia psilostachya]  
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYCTNPGRYCPWQVVCYESRKI  
CAKNAAKMRMNVTNKNTI  
>BAA07020.1 Cry j 1; pectate lyase [Cryptomeria japonica]  
MDSPCLVALLVFSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD  
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLKMPMYIAGYKTFDGRGAQV  
YIGNGGPCVFIKRVSNVHIIHGLYLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT  
NIWIDHNSFSNSSDGLVDVTLTSTGVTISNNLFFNHHKVMMLLGHDDAYSDDKSMKVTVAF  
NQFGPNCGQRMPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSTAPNESYKKQV  
TIRIGCKTSSSSCSNWVWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPQLT  
KNAGVLTCSLSKRC  
>CAA54696.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEDEATSVIAPARLFKSFVLDADNLIPKVAPENVSSAENIEGNGGPGTIKKITFP  
EGSHFKYMKHRVDEIDHANFKYCYSIIEGGPLGDTLEKISYEIKIVAAPGGGSILKITSK  
YHTKGDISLNEEEIKAGKEKGAGLFAVENYLV AHPNAYN  
>CAA54695.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
GVFDYEGETTSVIPAARLFKAFILDGDNLIPKVAPQAVSCVENIEGNGGPGTIKKITFPE  
GSPFKYVKERVDEVD RVNFKYSYSVIEGGAVGDTLEKICNEIKIVPAPGGGSILKISNKY  
HTKGNHEMKAEQIKASKEKAEALFRAVESYLLAHS DAYN  
>CAA54694.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula

pendula]

MGVFDYEGETTSVIPAAARLFKAFILDGDNLIPKVAPQTVSCVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHVNFKYSYSVIEGGAVGDTLEKICNEIKIVPAPGGGSILKISNK  
YHTKGNHEMKAQIKASKEKAEALFRAVESYLLAHSDAYN

>A60373 unknown function [Poa pratensis]

EFPGELQVIDKVDAAFKVAATAANAAPANDKFTVFEEAFNDAIKASTGGAYQSYKFIPAL  
EAAVKQSYAATVATAPAVKYTVFETALKKAITAMAQAQKAAPAAAVTGIATSAVGAATG  
AATAAAGGYKA

>AAB29344.1 unknown function, partial [Blattella germanica]

APPGCSNHFNLETVFGNFVK

>AAB29345.1 unknown function, partial [Blattella germanica]

GLNICQIDCNKIQSLPXLVFTIGGD

>P35775.1 Sol i 2; unknown function [Solenopsis invicta]

MKSFVLATCLLGFAQIIYADNKEIKIIRKDVAECLRTLPKCGNQPDPLARVDVWHCAMA  
KRGVYDNPDPVAVIKERSMKMCTKIITDPANVENCKKVASRCVDRETQGPKNRQKAVNII  
GCALRAGVAETTVLARKK

>P35781.1 Vesp c 5; unknown function, antigen 5 [Vespa crabro]

NNYCKIKCRSGIHTLCKYGTSTKPNCGKNVVKASGLTKQENLEILKQHNEFRQKVARGLE  
TRGNPGPQPPAKSMNTLVWNEDELAQIAQVWANQCNYGHDNCRNSAKYSVGQNI AEGSTTA  
DNFGSVSNMVKMWEDEVKDYQYGSPKNLKNKVGHYTQMVWAKTKEIGCGSIKYIENGWHR  
HYLVCNYGPAGNVGNEPIYERK

>P35782.1 Vesp c 5; unknown function, antigen 5 [Vespa crabro]

NNYCKIKCRSGIHTLCKYGTSTKPNCGKNVVKASGLTKQENLEILKQHNEFRQKVARGLE  
TRGNPGPQPPAKSMNTLVWNEDELAQIAQVWANQCNYGHDNCRNSAKYSVGQNI AEGSTSA  
DNFVNVSNMVKMWEDEVKDYQYGSPKNLKNKVGHYTQMVWAKTKEIGCGSEDIYEDGWHR  
HYLVCNYGPAGNVGNEPIYERK

>P35780.1 Pol f 5; unknown function, antigen 5 [Polistes fuscatus]

VDYCKIKCSSGIHTVCQYGESTKPSKNCADKVIKSVGPTEEEKLLIVNEHNFRQKVAQG  
LETRGNPGPQPAASDMNNLVWNEDELAHIAQVWASQCQILVHDKCRNTAKYQVGQNIAYAG  
GSKLPDVVSLIKLWENEVKDFNYNKGITKQNFQKVGHYTQMIWAKTKEIGCGSLKYMKN  
MQHHYLICNYGPAGNYLGQLPYTKK

>P35783.1 Ves f 5; unknown function, antigen 5 [Vespula flavopilosa]

NNYCKIKCLKGGVHTACKYGLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLVWNEDELAQVVAQVWANQCQYGHDTCRDIAKYQVGQNVALTGSTA  
AKYDDPVKLVKMWEDEVKDYNPKKKFSGNFLKGTGHYTMVWANTKEVGCSSIKFIQEKW  
HKHYLVCNYGPSGNFQNEELYQTK

>P35784.1 Ves g 5; unknown function, antigen 5 [Vespula germanica]

NNYCKIKCLKGGVHTACKYESLKPNCANKKVAYGLTKQEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLVWSEDELAQVVAQVWANQCQYGHDTCRDVAKYPVGQNVALTGSTA  
AKYDNPVKLVKMWEDEVKDYNPKKKFSENNFLKIGHYTMVWANTKEVGCSSIKYIQDKW  
HKHYLVCNYGPSGNFQNEELYQTK

>P35760.1 Ves m 5; unknown function, antigen 5 [Vespula maculifrons]

NNYCKIKCLKGGVHTACKYGLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLVWSEDELAQVVAQVWANQCQYGHDTCRDVAKYPVGQNVALTGSTA  
AVYNDPVKLVKMWEDEVKDYNPKKKFSENNFLKIGHYTMVWANTKEVGCSSIKYIQENW  
HKHYLVCNYGPSGNFQNEELYQTK

>P35785.1 Ves p 5; unknown function, antigen 5 [Vespula pensylvanica]

NNYCKIKCLKGGVHTACKYGLKPNCGNKIVVSYGLTKEEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLVWNEDELAQVVAQVWANQCQYGHDTCRDVAKYPVGQNVALTGSTA  
DKYDNPVKLVKMWEDEVKDYNPKKKFSENNFKIGHYTMVWANTKEIGCGSIKYIQNEW

HKHYLVCNYGPSGNFGNEELYQTK  
>P35786.1 Ves s 5; unknown function, antigen 5 [Vespa squamosa]  
VDYCKIKCLKGGVHTACKYGTSTKPNCGMMVVKSYGVTQAEKQEILKIHNDFRNKVARGL  
ETRGNPGPQPPAKNMNLLVWNNELANIAQIWASQCKYGHDTCKDITTKYVNGQNIIVSSST  
AAVYENVGNLVKAWENEVKDFNPTISWEQNEFKKIGHYTMVWAKTKEIGCGSIKYVDNN  
WYTHYLVCNYGPAGNFGNQEVYERK  
>P35787.1 Ves vi 5; unknown function, antigen 5 [Vespa vidua]  
KVNYCKIKCLKGGVHTACKYGTSTKPNCGMMVVKAYGLTEAEKQEILKVHNDFRQKVAKG  
LETRGNPGPQPPAKNMNLLVWNNELANIAQVWASQCNVYGHDTCKDTEKYPVNGQNIIVKRS  
TAALFDSPGKLVKMWENEVKDFNPNIEWSKNLKKTGHYTMVWAKTKEIGCGSVKYVKD  
EWYTHYLVCNYGPSGNFRNEKLYEKK  
>AAA28302.1 DoI m 5; unknown function, antigen 5 [Dolichovespula maculata]  
PIINLSFGEANNYCKIKCSRGIHTLCKFGTSMKPNCGSKLVKVHGVSNDEKNEIVNRHNQ  
FRQKVAKGLETRGNPGPQPPAKNMNLLVWNNELAKIAQTWANQCSFGHDQCRNTEKYQVG  
QNVIASTTGNYSATMSKLIEMWENEVKDFNPKKGTMGDNNFSKVGHYTMVWGTKEIG  
CGSVKYIENNWHTHYLVCNYGPAGNYMDQPIY  
>AAC37218.1 Aed a 1; apyrase [Aedes aegypti]  
MAGRPGYSAVIFLYVVSVAVIARATDNMPNPKDVSCLFPLTLIHINDLHARFEETNMKSN  
ACTQKDQCIAGIARVYQKIKDLLKEYESKNPIYLNAGDNFQGTWYNLLRWNVTADFIKK  
LKPAAMTLGNHEFDHTPKGLAPYLAELNKEGIPTIVANLVMNNDPDLKSSKIPKSIKLV  
GKRKIGIIGVLYDKTHEIAQTGKVTLSNAVEAVRREAAALKKDKIDIIIVVLSHCSYEEDK  
KIAAEAGDDIDVIVGAHSHSFLYSPDSKQPHDPKDKVEGYPYPTIVESKNKRKIPVQAKS  
FGKYVGRLLTYFDDTGEVQHWEGYPVFDHVKVQDPQILKDLVPWREKVEAIGSTVVG  
KIELDRDSCRDQECTLGVLADGFADQYTNDFRPAIIQAGNFRNPIKVGKITNGDIE  
AAPFGSTADLIRLKGADIWDVAEHSFALDDEGRNCLQVSGLRIVIDISKPIRSRVKIE  
VMDYTNPKSDELKPLDKQAEYYIVVPSYLADGKDGFSAMKRATARRTGPLDSDVFKNYVE  
KIKKVDNLKLRVIVCKGSKCT  
>Q08169.1 Api m 2; hyaluronidase [Apis mellifera]  
MSRPLVITEGMMIGVLLMLAPINALLLGFVQSTPDNNKTVREFNVYWNVPTFMCHKYGLR  
FEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALLKDPNGNVVARNGGVPLGNLTKHL  
QVFRDHLINQIPDKSFPVGVVIDFESWRPIFRQNWASLQPYKLSVEVVRREHPFWDQQR  
VEQEAKRRFEKYGQLFMEETLKAARMRPAANWGYAYPYCYNLTPNQPSAQCEATTMQE  
NDKMSWLFESEVLLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKKVLPYYWY  
KYQDRRDTDLRADLEATLRKITDLGADGFIWGSDDINTKAKCLQFREYLNNELGPAV  
KRIALNNNANDRLTVDVSDQV  
>P32936.2 alpha-amylase/trypsin inhibitor [Hordeum vulgare]  
MASKSSCDLLAAVLVSIFAAVAAGSEDCPTWATPITPLPSCRDYVEQQACRIETPGP  
PYLAKQQCCGELANIPQQCRQALRFFMGRKSRPDQSGLMELPGCPREVQMDVFRILVTP  
GFCNLTTVHNTPYCLAMDEWQWNRQFCSS  
>CAA57160.1 Lep d 2; NPC2-like, partial [Lepidoglyphus destructor]  
IHRGKMTLEAKFAANQDTAKVTIKVLAKVAGTTIQVPGLETDGCKFIKCPVKKGEALDF  
IYSGTIPAITPKVKADVTAELIGDHGVMACGTVHGQVE  
>AAA60330.1 Met e 1; tropomyosin [Metapenaeus ensis]  
MKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQVQESLLKANNQ  
LVEKDKALSNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAADSERMRKVL  
ENRSLSDERMDALENLKEARFLAEEADRKYDEVARKLAMVEADLERAEERAETGESKI  
VELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNLKAEEARAEFAERSVQKLQ  
KEVDRLEDELVNEKEYKSITDELDTFSELSGY  
>CAA57342.1 Cand a 1; alcohol dehydrogenase [Candida albicans]  
MSEQIPKTQKAVVFDTNGGQLVYKDYVPVTPKPNELLIHVKYSGVCHTDLHARKGDWPLA

TKLPLVGGHEGAGVVVGMGENVKGWKIGDFAGIKWLNGLSCMSCEFCQQGAEPNCGEADLS  
GYTHDGSFEQYATADAVQAAKIPAGTDLANVAPILCAGVTVYKALKTADLAAGQWVAISG  
AGGGLGSLAVQYARAMGLRVVAIDGGDEKGEFVKSLGAEAYVDFTKDKDIVEAVKATDG  
GPHGAINVSVSEKAIDQSVEYVRPLGKVVVLVGLPAHAKVTAPVFDVAVKSIEIKGSYVGN  
RKDTAEAIIDFFSRGLIKPIKIVGLSDLPEVFKLMEEGKILGRYVLDTSK  
>S43242 Syr v 1; Ole e 1-like [*Syringa vulgaris*]  
EDVPQPPIPQFHIQGVYCDTCRARFITESEFIPGASIRLQCKDRENGKITFTEIGYTR  
AEGLYSMLVEGDHKNFCEITLISSGREDCDEIPVEGWAKPSLKFKLNTVNGTTRTINPI  
GFFKKEALPKCTQVYNKLGMYPPNM  
>S43243 Syr v 1; Ole e 1-like [*Syringa vulgaris*]  
EDVPQPPVPPQFHIQGVYCDTCRARFITESEFIPGAGIRLQCKDGEHGKITFTEIGYTR  
AEGLYSMLVEGDHKNFCEITLLSSSRKDCCEEIPIEGWVKPSLKFKLNTVNGTTRTINPL  
GFFKKEVLPKCPQVFNKLGMYPPNM  
>S43244 Syr v 1; Ole e 1-like [*Syringa vulgaris*]  
EDVPQPPVPPQFHIQGVYCDTCRARFITESEFIPGASIRLQCKDGENGKITFTEIGYTR  
AEGLYSMLVEGDHKNFCEITLISSGRKDCDEIPVEGWVKPSLKFKLNTVNGTTRTINPI  
GFFKKEALPKCTQVYNKLGMYPPNM  
>AAB30434.1 Can f 3; serum albumin [*Canis familiaris*]  
LSSAKERFKCASLQKFGDRAFKAWSVARLSQRFPKADFAEISKVVTDLTKVHKECCHGDL  
LECADDRADLAKYMCENQDSISTKLKECCDKPVLEKSQCLAEVERDELPGDLPSLAADFV  
EDKEVCKNYQEAQDVFLGTFLYEYSRRHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCY  
AKVLDEFKPLVDEPQNLVKTNCELFEKLGEGYGFQNALLVRYTKKAPQVSTPTLVVEVSRK  
LGKVGTKCCKKPESEMSCADDFLS  
>AAB07620.1 Asp f 2; unknown function, partial [*Aspergillus fumigatus*]  
SARDEAGLNEAVELARHAKAHILRWGNESIEYRKYFGNRPTMEAVGAYDVIIVNGDKANVL  
FRCDNPDGNCALEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSETNTFW  
ASDLMHRLYHVPVAVGQGVVDHFDADGYDEVIALAKSNGTESTHDSEAFEFYFALEAYAFDIA  
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGGATTTPTDSPSATIDVPSNCH  
THEGGQLHCT  
>AAB32317.1 Cyn d 1; beta-expansin, partial [*Cynodon dactylon*]  
AIGDKPGPKITATYXXKWLKATFYGSNPRGAA  
>CAA59370.1 Par j 1; lipid transfer protein [*Parietaria judaica*]  
MRTVSARSSVALVVIVA AVLVTSSASVAPAPAGSEETCGTVV GALMPCLPFVQGKEKE  
PSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGKLVSEVPKHCGIIVDSKLPP  
IDVNMDCCTLGVLHYKGN  
>P40918.1 heat shock protein 70 [*Cladosporium herbarum*]  
MAPAIGIDLGTYSVCGIYRDDRIEIIANDQGNRTTPSFVAFDTERLIGDSAQNQVAIN  
PHNTVFDARLIGRKFQDAEVQADMKHFVFKVIEKAGKPVTVQVEFKGETKDFTPPEISSM  
ILTKMRETAESYLGTVNNAVITVPAYFNDSQRQATKDAGLIAGLNVLRIINEPTAAIA  
YGLDKKQEGEKNVLI FDLGGGTFDVSFLTIEEGIFEVKSTAGDTHLGGEDFDNRLVNHFS  
NEFKRKHKKDLSDNARALRRLRTACERAKRTLSSSAQTSIEIDSLFEGIDFFTSNTRARF  
EEVGQDLFRGNMEPGERTLRDDKIDKSSVHEIVLGGGSTRIPKVQKLVSDFFNGKEPCKS  
INPDEAVAYGAAVQAAILSGDTSSKSTKEILLLDVAPLSLGIETAGGVM TALIKRNTTIP  
TKKSETFSTFSDNQPGVLIQVFEGERARTKDINLMGKFELSGIRPAPRGVQPQIEVTFDLD  
ANGIMNVSALFKGTGKTNKIVITNDKGRLSKEEIERMLADAKEYKEEDEAEAGRIQAKNG  
LESYAYSLKNTVSDPKVEEKLSAEDKETLTGAIDKTVAWIDENQTATKEEYEAQKQLES  
VANPVMKIIYGAEGGAPGGMPGQGAGAPPPGAGDDGPTVEEVD  
>P16311.2 Der f 1; cysteine protease [*Dermatophagoides farinae*]  
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSELDRLSLRT

VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQRCRRPNSQHYGISNYCQIYPPDVKQIREALTQTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGDDYIWRNSWDTTWGDSGY  
GYFQAGNNLMMIEQYPYVWIM

>CAA26478.1 Gly m 6; 11S globulin, glycinin, cupin [*Glycine max*]  
MGKPFTLSLSSCLLLLSSACFAISSSKLNECQLNNLNALPDHRVESEGGLIQTWNSQH  
PELKCAGVTVSKLTLNRNGLHSPSYSPYPRMIIAQGKGALGVAIPGCPETFEEPQEQSN  
RRGSRSQKQQLQDSHQKIRHFNEGDVLVIPPSVPYWTYNTGDEPVVAISLLDTSNFNNQL  
DQTPRVFYLGNPDIEYPETMQQQQQKSHGGRKQGQHQEEEEEGGSVLSGFSKHF LAQ  
SFNTNEDIAEKLESPDDEKQIVTVEGGLSVISPKWQEQDEDEDEDEDEDEQIPSHPP  
RRPSHGKREQDEDEDEDEKPRPSRPSQGKRNKTGQDEDEDEDEDEQPRKSREWRSKKTQP  
RRRQEEPRERGCETRNGVEENICTLKLHENIARPSRADFYNPKAGRISTLNSLTLPALR  
QFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQKVRVWNCQGNVAVFDGELRRGQLLV  
VPQNFVVAEQAGEQGFYIVFKTHHNAVTSYLKDVFRAPSEVLAHSYNLRQSQVSELKY  
EGNWGPLVNPESQGGSPRVKVA

>CAA27052.1 Tri a 26; HMW glutenin [*Triticum aestivum*]  
MAKRLVLFVAVVVALVALTVAEGEASEQLQCERELQELQERELKACQQVMDQQLRDISPE  
CHPVVVPVAGQYEQIIVPKGGSFYPPGETTPPQQQQRIFWGIPALLKRYPSVTSPQQ  
VSYYPGQASPQRPGQGGQPGGQGGQGGQGGYPTSPQQPGWQQPEQGGQPGYPTSPQQ  
PGQLQQAQGGQPGGQGGQPGGQGGYPTSSQLQPGQLQQAQGGQGGQGGQGGQGGQ  
QPGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQ  
QLGGQGGQGGYPTSPQQPGGQGGQGGQLQQAQGGQPEQGGQGGQGGQGGQGGQGGQGG  
QGGQPGYPTSPQQSGGQGGYPTSSQQPTQSQQPGGQGGQGGQGGQGGQGGQGGQGGQ  
QGGQPGYPTSPQLSGGQGGYPTSPQQSGGQGGQGGQLQQAQGGQGGQGGQGGQGGQGGQ  
QGGQPGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQ  
PGYDPTSPQQPGGQGGQGGQLQQAQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG  
QGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG  
QWQQPGQWQQPGGQGGYPTSPQLQGGQGGYPTSPQQPGGQGGQGGQGGQGGQGGQGGQ  
YPTSPQLSGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG  
QTGGQGGQGGQGGYSSYHVSVEHQAAASLKVAKAQLAAQLPAMCRLEGGDALASASQ

>2008179A Par j 1; lipid transfer protein [*Parietaria judaica*]  
MVRALMPCLPFVQGEKEPSKGCSSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK  
LVSEVPKHCIGIVDSKLPIDVNMCKTVGVVPRQPQLPVSLRHGPVTGPSRSRPPTKHGW  
RDRLEFRPPHRKKNPAFSTLG

>CAA58646.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVYTFENEFTSEIPPSRLFKAFVLDADNLIPKIAQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVKKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKVGEKAHGLFKLIESYKDHDPDAYN

>CAA26040.1 Gal d 3; ovotransferrin [*Gallus gallus*]  
MKLILCTVLSLGLIAAVCFAPPKSVIRWCTISSPEEKKCNLRDLTQQERISLTCVQKAT  
YLDCIKAIANNEADAISLDGGQVFEAGLAPYKLPKPIAAEIEYEHTEGSTTSYYAVAVVKKG  
TEFTVNDLQGKNSCHTGLGRSAGWNIPIGTLHGWAIWEGIESGSVEQAVAKFFSASCV  
PGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAVFKHTTVNENAPDLN  
DEYELLCLDGRSQPVDNYKTCNWARVAHAVVARDNKVEDIWSFLSKAQSDFGVDTKSD  
FHLFGPPGKDPVLFKDFLFDKSAIMLKRVPKSLMDSQLYLGFEYYSQSMRQDQLTPSPR  
ENRIQWCAVGKDEKSKDRWSVSNVDVECTVDETKDCIIMKGEADAVLDGGLVYT  
AGVCGLVPVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWNLNKGGKKSCHTAVGRT  
AGWVIPMGLIHNRTGTCNFDEYFSEGCAPGSPNSRLCQLCQGGGIPPEKCVASSHEKY  
FGYTGALRCLVEKGDVAFIQHSTVEENTGGKNKADWAKNLQMDDFELLC TDGRRANVMDY

RECNLAEVPTHAVVVRPEKANKIRDLLERQEKFRGVNGSEKSKFMMFESQNKDLLFKDLT  
KCLFKVREGTTYKEFLGDKFYTVISNLKTCNPSDILQMCSFLEGK

>CAA60533.1 unknown function [Glycine soja]

MGKPFITLSLSSCLLLLSSACFAISSSKLNECQLNNLNALEPDHRVESEGGLIQTWNSQH  
PELKCAGVTVSKLTLNRNGLHLPSYSPYPRMIIIAQKGALGVAIPGCPETFEEPQEQSN  
RRGSRSQKQLQDSHQKIRHFNEGDVLVIPPVGYWYTYNTGDEPVVAISLLDTSNFNQL  
DQTPRVFYLAGNPDI EYPETMQQQQQKSHGGRKQGHHQEEEEEGGSVLSGFSKHF LAQ  
SFNTNEDIAEKLPSPDDERKQIVTVEGGLSVISPKWQEQDEDEDEDEDEDEDEQIPSHPP  
RRPSHGKREQDEDEDEDEDEKPRPSRPSHGKREQDQDQDEDEDEDEDEQPRKSREWRSKKTQ  
PRRPRQEPRERGCE TRNGVEENICTLKLHENIARPSRADFYNP KAGRISTLNSLTLPAL  
RQFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQGVKRVVNCQGNVDFGELRRGQLL  
VVPQNFVVAEQAGEQGF EYIVFKTHHNAVTSYLKDFVRAIPSEVL AHSYNLRQSQVSELK  
YEGNWGPLVNPESQOGSPRVKVA

>AAB32224.1 Der p 8; glutathione S-transferase [Dermatophagoides pteronyssinus]

MSQPILGYWDIRGYAQPIRLLLLTYSGVDFVDKRYQIGPAPDFDRSEWLNEKFNGLDFPN  
LPYYIDGDMKMTQTFAILRYLGRKYKLNDSNDHEEIRISMAEQQTEDMMAAMIRVCYDAN  
CDKLPDYKSLPDLKLMKSFVGEHAFIAGANISYVDFNL EYELCHVKVMVPEVFGQFE  
NLKRYVERMESLPRVSDYIKKQPKTFNAPTSKWNASYA

>BAA06905.1 Cuc m 1; serine protease, cucumisin [Cucumis melo]

MSSSLIFKLFSSLFFSNRLASRLSDDDGKNIYIVYMGKLEDPDSAHLHHRAMLEQVV  
GSTFAPESVLHTYKRSFNGFAVKL TEEEAEKIASMEGVSVFLNEMNELHTTRSWDFLGF  
PLTVPRRSQVESNIIVGVLDTGIWPESPSFDDEGFSPPPKWKGTCE TSNNFRCNRKIIG  
ARSYHIGRPISPGDVNGPRDTNGHGHTASTAAGGLVSQANLYGLGLGTARGGVPLARIA  
AYKVCWNDGCSDTDILAAAYDDAIADGVDIISLSVGGANPRHYFVDAIAIGSFHAVERGIL  
TSNSAGNGGNFFTTASLSPWLLSVAASTMDRKFVTQVQIGNGQSFQGV SINTFDNQYYP  
LVSGRDIPNTGFDKSTSRFCTDKSVNPNLLKGIIVVCEASFGPHEFFKSLDGAAGVLMTS  
NTRDYADSYPLPSSVLDPNLLATLRYIYSIRSPGATIFKSTTILNASAPVVVFSRGP  
NRATKDVIKPDISGPGVEILAAWPSVAPVGGIRRNTLFNIISGTSMSCPHITGIATYVKT  
YNPTWSPAAIKSALMTTASPMNARFNPAEFAYGSGHVNPLKAVRPLVYDANESDYVKF  
LCGQGYNTQAVRRITGDYSACTSGNTGRVWDLNYP SFGLSVSPSQT FNQYFNRTLTSVAP  
QASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFTLTVRGSIKGFVVSASLVWSDGVHY  
VRSPITITSLV

>CAA23682.1 Gal d 2; ovalbumin [Gallus gallus]

MGSIGAASMEFCFDVFKELKVH HANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF  
DKLPFGGDSIEAQCGT SVNVHSSLRDILNQITKPN DVYSFSLASRLYAEERYPILPEYLQ  
CVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIV  
FKGLWEKTFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILEL PFASGTM  
SMLVLLPDEVSGLEQLESIIINFEKLT EWTSSNVMEERKIKVYLPRMKMEEKYNLTSVLMA  
MGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGS AEAAGVDAASVSEEFR  
ADHPFLFCIKHIATNAVLFFGRCVSP

>CAA60628.1 Bet v 4; calcium-binding protein, polcalcin [Betula pendula]

MADDHPQDKAERERIFKRFDANGDGKISAAELGEALKTLGSITPDEVKHMMAEIDTDGDG  
FISFQEFTDFGRANRGLLKDVAKIF

>AAB01362.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]

MGVYTFENEY TSEIPPPRLFKAFLVDADNLPK IAPQAIKHAEILEGDGGPGTIKKITFG  
EGSQYGYVKKHKIDSVD EANYSYAYTLIEGDALTD TIEKVSYETKLVASGSGSIIKSISHY  
HTKGDVEIKEEHVKAGKEKAHGLFKLIESY LKGHPDAYN

>CAA59279.1 Fel d 2; serum albumin [Felis catus]

MKWVTFISLLLLFSSAYS RGVTRREAHQSEIAHRFN DLGEEHFRGLVLVAFS QYLQQCPF

EDHVKLVNEVTEFAKGCVADQSAANCEKSLHELLGDKLCTVASLRDKYGENADCCCEKKEP  
ERNECFLQHKDDNPGFGQLVTPEADAMCTAFHENEQRFLGKYLYEIARRHPYFYAPELLY  
YAEYKGVFTECEAADKAACLTPKVDALREKVLASSAKERLKCASLQKFGERAFKAWSV  
ARLSQKFPKAEFAEISKLVTDLAKIHKECCHGDLLECADDRADLAKYICENQDSISTKLLK  
ECCGKPVLEKSHCISEVERDELPAIDLPLAVDFVEDKEVCKNYQEAKDVFLGTFLYEYSR  
RHPEYSVSLLLRLAKEYEATLEKCCATDDPPACYAHVDFEFKPLVEEPHNLVKTNCELFE  
KLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRSLGKVGSKCCTHPEAERLSAEDYLSVV  
LNRLCVLHEKTPVSEKCTESLVNRRPCFSALQVDETYVPKEFSAETFTFHADLCTL  
PEAEKQIKKQSALVELLKHKPKATEEQKTKVMGDFGSFVDKCCAAEDKEACFAEEGPKLV  
AAAQAALA

>CAA88833.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]

MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPOAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALTDITIEKISYETKLVACGSGATIKSISHY  
HPKGNIEIKEEHVKVGEKKGHGLFKLIESYLGHPDAYN

>CAA59338.1 Tri a 36; LMW glutenin [Triticum aestivum]

FALIAVATSTIAQMETSCIPGLERPWQQQLPQQQLTFPQQQPFPPQQPPFSQQQPSFS  
QQQPPFSQQQPILPEPPFSLQQQVLPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL  
QQLNPCVKVFLQQQCSVPAMPQRLARSQMWQQSRCHVMQQCCQQLSQIPEQSRDAICAI  
TYSIILQEQQQGFVQAQQQQPQQSGQVVSQSQQQSQQQLGQCSFQQPQQ

>CAA59339.1 Tri a 36; LMW glutenin [Triticum aestivum]

HIPSLEKPLQQQLPLLQQILWYQQQPIQQQPQPFPPQQPPCSQQQQPPLSQQQQPPFSQQ  
QPPFSQQQPILPQQPPFSQQQQQPFQQQQPLLQQPPFSQQQPPFSQQQQQPPFSQQQQ  
QPILLQQPPFSQHQPVLPPQQIPSVQPSILQQLNPCVKVFLQQQCSVPAMPQSLARSQML  
WQSSCHVMQQCCCRQLPQIPEQSRDAIRAIISIVLQEQQHGQGLNQPQQQQPQQSVQG  
VSQPQQQQKQLGQCSFQQPQQ

>CAA59340.1 Tri a 36; LMW glutenin [Triticum aestivum]

HIPSLEKPSQQQLPLLQQILWYHQQPIQQQPQPFPPQQPPCSQQQQPPLSQQQQPPFSQQ  
QPPFSQQQLPILPQQPPFSQQQQQPFQQQQPLLQQPPFSQQRPPFSQQQQQ  
PVLPPQQPPFSQQQQQPILPQQPPFSLHQQPVLPPQQIPYVQPSILQQLNPCVKVFLQQC  
SPVAMPQSLARSQMLWQSSCHVMQQCCQQLPRIPEQSRDAIRAIISIVLQEQQHGQG  
FNQPQQQQPQQSVQVQVQPQQQQKQLGQCSFQQPQQ

>AAB48072.1 Ves v 1; phospholipase A1 [Vespula vulgaris]

MEENMNLKYL L LFVYFVQVLNCCYGHGDLPSYELDRGPKCFNSDTVSIIEETRENRRD  
LYTLQTLQNHPEFKKKTITRPVVFITHGFTSSASETNFINLAKALVDKDNMVISIDWQT  
AACTNEAAGLKYLYPTAARNTRLVQYIATITQKLVKHYKISMANIRLIGHSLGAHASG  
FAGKKVQELKLGKYEIIGLDPARPSFDSNHCSERLCETDAEYVQIIHTSNYLGTEKTLG  
TVDFYMNNGKNQPGCRFFSEVCSHRAVIYMAECIKHECCLIGIPKSKSSQPISSTKQ  
ECVCVGLNKKYPSRGSFYVPVESTAPFCNNKGKII

>CAA24933.1 Tri a 26; HMW glutenin, partial [Triticum aestivum]

EKLGQGGQPRQWLQPRQGGQGYPTSPQQSGGQQLGQGGQGYPTSPQQSGGQGGYDS  
PYHVSAEHQAASLKVAKAQQQLAAQLPAMCRLEGGDALLASQ

>AAA78904.1 Blo t 12; chitin-binding protein [Blomia tropicalis]

MKSVLIFLVAIALFSANIVSADEQTTRGRHTEPDDHHEKPTTQCTHEETTSTQHHEEVV  
TTQTPHHEEKTTEETHSDDLIVHEGGKTYHVVCHEEGPIHIQEMCNKYIICSKSGSLW  
YITVMPCSIGTKFDPISRNCVLDN

>AAB32842.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]

MKFIIAFVATLAVMTVSGEDKKHDYQNEFDLLMERIHEQIKKGELALFYLQEQINHFE  
AKPTKEMKDKIVAEMDTIAMIIDGVRGVLDRMLQQRKDLDFEQYNLEMAKSGDILERDL  
KKEEARVKKIEV

>CAA51775.1 Lol p 2; expansin [*Lolium perenne*]  
EFTVEKGSDEKNLALSIKYSKEGDAMAEVELKEHGSNEWLALKKNGDGVWEIKSDKPLKG  
PFNFRFVSEKGMWNVFDDVVPADFKVGT

>CAA59419.1 Asp f 10; aspartate protease [*Aspergillus fumigatus*]  
MVVFSKVTAVVVGLSTIVSAVPVQPRKGFTINQVARPVTNKKTVNLPVAVYANALTKYGG  
TVPDSVKAASSSGSAVTTPEQYDSEYLTVPVKVGGTTLNLDFDTGSADLWVFSSELSASQS  
SGHAIYKPSANAQKLNQYTWKIYQYDGGSSASGDVYKDTVTVGGVTAQSQAVEAASHISSQ  
FVQDKDNDGLLGLAFSSINTVSPRPQTTFDFTVKSQLDSPFAVTLKYHAPGTDFGYID  
NSKFQGELTYTDVDSQGFWMFTADGYGVNGAPNSNSISGIADTGTLLLLLDDSVVADY  
YRQVSGAKNSNQYGGYVFPSTKLPSTTVIGGYNAVVPGEYINYAPVTDGSSSTCYGGIQ  
SNSGLGFSIFGDIFLKSQYVWFDSQGPRLGFAPQA

>CAA54587.1 Par j 1; lipid transfer protein [*Parietaria judaica*]  
MVRALMPCLPFVQGEKEPSKGCSSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK  
LVSEVPKHCIGIVDSKLPPIIDVNMDCKTGVVPRQPQLPVSLRHGPVTGSPDPAHKARLER  
PQIRVPPPAPEKA

>BAA04149.1 Sola t 4; serine protease inhibitor [*Solanum tuberosum*]  
MKCLFLLCLCLVPIVVSSTFTSKNPINLPSDATPVLVDVAGKELDSRLSYRIISTFWGAL  
GGDVYLGKSPNSDAPCANGIFRYNSDVGPSGTPVRFIGSSSHFGQGFENELLNIQFAIS  
TSKLCVSYTIWVKVDYDASLGTMLLETGGTIGQADSSWFKIVKSSQFGYNLLYCPVTSTM  
SCPFSDDQFCLKVGVVHQNGKRRLLALVKDNPLDVSFQVQ

>AAB34365.1 Sec c 38; alpha-amylase inhibitor [*Secale cereale*]  
EQCYGESCRVKGKSISSNPVPACREYV

>AAB34785.1 Pen ch 20; N-acetylglucosaminidase, N-acetylhexosaminidase [*Penicillium chrysogenum*]  
GPYKTWQRIYDYDFLTNLTSSEANDIIGAEAPLWSEQVDDVTVSSVFWPRAAALGELVWS  
GNRDAAGRKRRTTSFTQRILNFREYLVANGVMAAALVPKYCLQHPHACDLYKNQTVMS

>CAA58755.1 Lep d 2; NPC2-like [*Lepidoglyphus destructor*]  
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDISGCSGDTCVIHRGQKMTLDAKFAANQ  
DTNKVTIKVLAKVAGTTIQVPLETDGCKVLKCPKIKKGEALDFNYGMTIPAITPKIKADV  
TAEVGDHGVMACGTIHGQVE

>CAA50008.1 Vig r 4; 2S albumin, conglutin [*Vigna radiata*]  
MSNLPYINAAFRFSSRDYEVYFFAKNKYVRLQYTPGKTEDKILTNLRLISSGFPSLAGTP  
FAEPGIDSAFHTEASEAYVFSANNRAYIDYAPGTTNDKILAGPTTIAEMFPVLRNTVADF  
SIDSAFRSTKGKEYVLFKGNKYVRIDYDSKQLVGSIRNISDGFVPLNGTGFESGIDASFA  
SHKEPEAYLFGDKYVRIHFTPGKTDDTLVGDVVRPILDGWPVLKAFCLCELNKPSSLSCIN  
HLSLVTINKAFISNVCLFFFNVTLGLEACFLS

>AAB34907.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[*Carpinus betulus*]  
GVFNVEAETPSVMPAARLFKSYVLDLDFDKLIPKVAPQVISSVENVGGNGGPGTIKNITFAE  
GIPFKFVKERVDEVDNANFK

>AAB34908.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[*Carpinus betulus*]  
GVFNVEAETPSVIPAARLFKSYVLDLDFDKLIPKVAPQVISSVENVGGNGGPGTIKNITFAE  
GIPFKFVKERVDEVDNANFK

>AAB34909.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[*Carpinus betulus*]  
GVFNVEAETTSVIPAARLFKAFILDGNKLIPKVSPQVSSVENVEGNGGPGTIKKITFSE  
GIPVKYVKERVVEIDHTNFK

>CAA62909.1 Sin a 1; 2S albumin, conglutin [*Sinapis alba*]  
PAGPFGIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDFEFDFEDDMENPQGPQQ

RPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLLEQQGQQGPHLQHVISRIYQTA  
THLPRVCNIRQVSVC PFKKTMPGPS  
>CAA62910.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]  
PAGPFRIPKCRKEFQQAQHLRACQQWLHKQAMQSGSGPSWTLEGEFDFEDDMENPQGPQQ  
RPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLLEQQGQQGPHLQHVISRIYQTA  
THLPKVCNIPQVSVC PFKKTMPGPS  
>CAA62911.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]  
PAGPFGIPKCRKEFQQAQHLRACQQWLHKQAMQSGSGPSWTLDDFDFEDDMENPQGPQQ  
RPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLGQQGQQGPVQHVVISRIYQTA  
THLPKVCNIPQVSVC PFKKTMPGPS  
>CAA62912.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]  
PAGPFRIPKCRKEFQQAQHLRACQQWLHKQAMQSGSGPSWTLDDFDFEDDMENPQGPQQ  
RPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLLEQQGQQGPHLQHVISRIYQTA  
THLPKVCNIPQVSVC PFKKTMPGPS  
>CAA62908.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]  
PAGPFGIPKCRKEFQQAQHLRACQQWLHKQAMQSGSGPSWTLDDFDFEDDMENPQGPQQ  
KPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLGQQGQQGPVQHVVISRIYQTA  
THLPKVCNIPQVSVC PFKKTMPGPS  
>AAA80264.1 Der p 7; bactericidal permeability-increasing like [Dermatophagoides  
pteronysinus]  
MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSKFER  
HIGIIDLKGELDMRNIQVRGLKQMKRVGDANVKSSEDGVVKAHLLVGVHDDVVSMEYDLAY  
KLGDLHPNTHVISDIQDFVVELSLEVSEEGNMTLTSFEVRQFANVVNHIGGLSILDPIFA  
VLSDVLTAIQDTVRAEMTKVLAPAFKKELEARNQ  
>BAA11251.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
NIQVDPGSGVQWPQQQPFQPHQPFSSQQPQQTFPQPQQTFPHQPPQQFSQPQQPQQQFIQ  
PQQPFPQQPQQTYPQRPPQFPQTQQPQQPFQSQQPQQPFQPPQQQFPQPQQPQQSFPQ  
QQPSLIQQSLQQQLNPKCNFLQOQCKPVSLVSSLSMILPRSDCQVMRQQCCQQLAQIPQ  
QLQCAAIHSIVHSIIMQQEQEQRQGVQILVPLSQQQVVGQGLVQGGQIIQPQQPAQLE  
VIRSSVLQTLATMCNVYVPPYCSTIRAPFASIVAGIGGQ  
>2023228A Phl p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGADAAGKATTEEQKLEIKINAGFKAALAGAGVQP  
ADKYRTFVATFGPASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATPE  
AKYDAYVATLSEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAANA  
APANDKFTVFEAAFNDEIKASTGGAYESYKFIPALEAAVKQAYAAATVATAPEVKYTVFET  
ALKKAITAMSEAQAAPPPPLPPPPQPPPLAATGAATAATGGYKV  
>2103117A expansin-like [Dactylis glomerata]  
EAPVTFTVEKGSDEKNLALSIKYNKEGDSMAEVELKEHGSNEWLALKKNGDGVWEIKSDK  
PLKGFNFRFVSEKMRNVFVDVVPADFKVGTTYKPEEAAAASARRRSSEVFQFLILSCQ  
GRIVNCEVLICVMRRGNAMCLIASISMHILTLDRFFFFDGLIYYKIFKMMFQKPRTRT  
CIEKDFRRSSSSSIPT  
>AAB38064.1 Pru av 2; thaumatin-like [Prunus avium]  
MMKTLVVVLSLSLTILSFGGAHAATISFKNNCPYMWVPGTLTSDQKQQLSTTGFE LASQA  
SFQLDTPVPWNGRFWARTGCSTDASGKFCATADCASGQVMCNGNGAIPPATLAEFNIPA  
GGGQDFYDVSLVDGFNLPM SVTPQGGTGDCKTASCPANVNAVCPSELQKKGSDGSVVACL  
SACVKFGTPQYCTPPQNTPETCPPTNYSEIFHNACPDAYSAYDDKRGTFTCNGGPNYA  
ITFCP  
>AAA87851.1 Bla g 4; lipocalin [Blattella germanica]  
AVLALCATDTLANEDCFRHESLVPNLDYERFRGSWIIAAGTSEAL TQYKCWIDRFSYDDA  
LVSKYTDSQGKNRTTIRGRTKFEGNKFTIDYNDK GKAFSAPYSVLATDYENYAIVEGCPA

AANGHVIYVQIRFSVRRFHPKLGDKEMIQHYTLDQVNQHKKAEEDLKHFNLKYEDLHST  
CH

>CAA93121.1 Hol l 1; beta-expansin [*Holcus lanatus*]  
VFLGSAHGIKVPPGNITATYGDWLDKSTWYGKPTGAGPKDNGGACGYKDVKPPFS  
GMTGCGNTPIFKDGRGCGSCFEIKCSKPESCSGEPVTVHITDDNEEPIAPYHFDLSGHAF  
GSMAKKGEEQKLSAGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYIDGDGD  
VVAVDIKEKGGKDWIELKESWGAWVRVDTDPDKLTGPFVRYTTEGGTKGEAEDVIPEGWK  
ADTAYEAK

>P43237.1 Ara h 1; 7S globulin, vicilin [*Arachis hypogaea*]  
MRGRVSPLMLLLGILVLASVSATQAKSPYRK TENPCAQRCLQSCQQEPDDLKQKACESRC  
TKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDRRQPRREEGGRWGPAPRERERE  
EDWRQPREDRRPSHQPRKIRPEGREGEQEWGTPGSEVREETSRRNPFYFPSRRFSTRY  
GNQNGRIRVLQRFQDQSKQFQNLQNHRIVQIEARPNTLVLPKHADADNILLVIQQQATVT  
VANGNNRKSFNLDDEGHALRIPSGFISYILNRHDNQNLRVAKISMPVNTPGQFEDFFPASS  
RDQSSYLQGF SRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGRRRSTRSSDNEGVIVK  
VSKEHVQELTKHAKSVSKKSEEEEDITNPNL RDGEPDLSNNFGRLFVVKPKKPNQLQD  
LDMMLTCVEIKEGALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREQEWEWEE  
EDEEEEGSNREVRRYTARLKEGDFIMPAAHPVAINASSELHLLGFGINAENNRIFLAG  
DKDNVIDQIEKQAKDLAFPGSGEQVEKLIKQRESHFVSARPQSQS SPSSPEKEDQEEENQ  
GGKGPLLSILKAFN

>P43238.1 Ara h 1; 7S globulin, vicilin [*Arachis hypogaea*]  
MRGRVSPLMLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACES  
RCTKLEYDPRCVYDPRGHTGTTNQRSPGERTRGRQPGDYDDRRQPRREEGGRWGPAGP  
REREREEDWRQPREDRRPSHQPRKIRPEGREGEQEWGTPGSHVREETSRRNPFYFPSR  
RFSTRYGNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILLVIQQ  
GQATVTVANGNNRKSFNLDDEGHALRIPSGFISYILNRHDNQNLRVAKISMPVNTPGQFED  
FFPASSRDQSSYLQGF SRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGRRWSTRSEN  
NEGVIVKVSKEHVEELTKHAKSVSKKSEEEEDITNPNLREGEPLDLSNNFGKLFVVKPD  
KKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRR  
EEEEDEDEEEEGSNREVRRYTARLKEGDFIMPAAHPVAINASSELHLLGFGINAENNR  
IFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIKQKESHFVSARPQSQS SPSSPEKE  
SPEKEDQEEENQGGKGPLLSILKAFN

>P42058.1 Alt a 7; unknown function [*Alternaria alternata*]  
MAPKIAIVYYSMYGHIKKADAELKGIQEAGGDAKLFQVAETLPQEVLDKMYAPPKDVSSV  
PVLEDPVLEEFDGILFGIPTRYGNFPAQFKTFWDKTGKQWQQGAFWKGKYAGVVFVSTGTL  
GGGQETTAITSMSTLVDHGFIYVPLGYKTAFSMLANLDEVHGGSPWGAGTFSAGDGRQP  
SELELNIAQAQGGKAFYEAVAKAHQ

>P43180.2 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYESSETTSVIPAAARLFKAFILEGDNLIPKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAQVKASKEMGETLLRAVESYLLAHS DAYN

>P43186.2 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYESSETTSVIPAAARLFKAFILDGDNLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDHEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN

>P30438.2 Fel d 1; uteroglobin [*Felis catus*]

MKGACVLVLLWAALLISGGNCEICPAVKRDVDLFLTGTDPDEYVEQVAQYKALPVVLENA  
RILKNCVDAKMTEEDKENALSVDLKIYTSPLC

>P46436.3 Asc s 13 glutathione S-transferase [Ascaris suum]  
MPQYKLT YFDIRGLGEGARLIFHQAGVKFEDNRLKREDWPALKPKTPFGQLPLLEVDGEV  
LAQSAAIYRYLGRQFGLAGKTPMEEAQVDSIFDQFKDFMAELRPCFRVLAGFEEGDKEKV  
LKEVAVPARDKHLPLLEKFLAKSGSEYMGKSVTWADLVITDSLASWESLIPDFLSGHLQ  
LKKYIEHVRELPNIKKWIAERP KTPY

>P43212.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKFIAPMAFVAMQLIIMAAAEDQSAQIMLDS DIEQYLR SNRSLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNNRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFD FSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDS PNTD GIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGSISL GRENSRAEVS YVHVN  
GAKFIDTQNGLR IKTWQGGSGMASHIYENVEMINSENPI LINQFYCTSASACQNQRSAV  
QIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTS GKIASC LNDNANGYFS  
GHVIPACKNLS PAKRKESKSHKHPKTMVKNMGAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMC SRHGKIYHP

>P42037.1 Alt a 5; ribosomal protein P2 [Alternaria alternata]  
MKHLAAYLLLGLGNTSPSAADV KAVLESV GIEADSDRLDKLISELEGKDINELIASGSE  
KLASVPSGGAGGAAA SGGAAAAGGSAQAEAAPEAAKEEEKEESDEDMGFGLFD

>AAA86533.1 Ory s 1; beta-expansin [Oryza sativa]  
MASSSLLLACVVAAMVSPSPAGHPKVPPGNITTSYGDKWLEARPPGMVRPRVLAPKDN  
GGACGYKDV DKAPFLGMNSCGNDPIFKDGKGC GSCFEIKCSKPEACSDK PALIHV TDMND  
EPIAAYHFDLSGLAMAKDGKDEELRKAGI IDTQFRRVKCKYPADTKITFHIEKASNP NYL  
ALLVKYVAGDGDVVEVEIKEK GSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEGARR  
SSAEDAIPDPGRRQRVQVNVQAK

>AAA86744.1 Bla g 2; inactive aspartic protease [Blattella germanica]  
MIGLKLVTVLF AVATITHAAELQRVPLYKLVHVFINTQYAGITKIGNQNF LTVFDSTSCN  
VVVASQECVGGACVCPNLQKYEKLPKYISDGNVQVKFFDTGSAVGRGIEDSLTISNLTT  
SQQDIVLADEL SQEVCILSADVVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHHAR  
FQDGEHFGEIIFGGSDWKYVDGEFTYVPLVGDDSWKFRLDG VKIGD TT VAPAGTQAIIDT  
SKAIIIVGPKAYVNPINEAIGCVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNISSQY  
YIQQNGNLCYSGFQPCGSHDFFIGDFFVDHYHSEFNWENKTMGFGRSVESV

>AAA87456.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAISSSTSGTSSSFPSRTTVMLLLFFFAASVGITDAQVGV CYGMQGNLPPVSEVIALYK  
KSNITRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWVQKNVRGFWSSV  
LFRYIAVGNEISPVNRTAWLAQFVLPAMRN IHDAIRSAGLQDQIKVST AIDLTLVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLL ANIYPYFTYAYNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGGSLEV VVSESGWPSAGAF AATFDNGR TYLSNLI  
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHFGLFFPDKRPKYNLNF GA EKNWDIS  
TEHNATILFLKSDM

>AAB09252.1 thiol protease [Glycine max]  
MGFLVLLLFSLLGLSSSSSISTHR SILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE  
EAKRLEIFKNNSNYIRDMNANR KSPHSHRLGLNKFADITPQEF SKKYLQAPKDVSQQIKM  
ANKKMKKEQYSCDHPPASWDWRKKG VITQVKYQGGCGRGWAFSATG AIEAAHAIATGDLV  
SLSEQELVDCVEESEGSYNGWQYQSFEWVLEHGGIATDDDPYRAKEGRCKANKIQDKVT  
IDGYETLIMSDESTESETEQAFLSAILEQPISV SIDA KDFHLYTGGIYDGENCTSPYGIN  
HFVLLVGYGSADGVYWI AKNSWGEDWGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES  
ETLVSARVKGHRRVDHSPL

>BAA05540.1 unknown function [Bacillus sp.]  
MRQSLKVMVLSTVALLFMANPAAASEEKKEYLIVVEPEEVS AQSV EESYDVDVIHEFE EI  
PVIHAELTKKELK LKKDPNVKAI EENA EVTISQTVPWGISFINTQQAHNRGIFGNGARV

AVLDTGIASHPDLRIAGGASFISSEPSYHDNNGHGHVAGTIAALNNSIGVLGVAPSADL  
YAVKVLDRNGSGSLASVAQGI EWAINNNMHIINMSLGSTSGSSTLELAVNRANNAGILLV  
GAAGNTGRQGVNYPARYSGVMAVAVDQNGQRASFSTYGPEIEISAPGVNVNSTYTGNRY  
VLSLGTSMATPHVAGVAALVKSRYPSYTNQIRQRINQATATYLGSPSLYGNGLVHAGRAT  
Q

>CAA01909.1 Cyn d 7; calcium-binding protein, polcalcin [Cynodon dactylon]  
GTRRFDTNGDGKISLAELTDALRTL GSTSADEVQRMMAEIDTDGDGFIDFDEFISFCNAN  
PGLMKDVAKVF

>CAA01910.1 Cyn d 7; calcium-binding protein, polcalcin [Cynodon dactylon]  
GTSFKRFDTNGDGKISLAELTDALRTL GSTSADEVQRMMAEIDTDGDGFIDFDEFISFCN  
ANPGLMKDVAKVF

>BAA09634.1 Bra r 5; calcium-binding protein, polcalcin [Brassica rapa]  
MADAEHERIFKKFDTDGDGKISAAELEEALKKLGSVTPDDVTRMMAKIDTDGDGNISFQE  
FTEFASANPGLMKDVAKVF

>CAA65341.1 Mala s 1; unknown function [Malassezia sympodialis]  
MRYSTVLAALALLGTSAVSVLAALPDQIDVKVKNLTPEDTIYDRTRQVIFYQSNLYKGRIE  
VYNPKTQSHFNVIDGASSNGDGEQQMSGLSLLTHDNSKRLFAVMKNAKSFNFADQSSHG  
ASSFHSFNLPLSENSKPVSVNF EKVQDEF EKKAGKRPFGVVQSAQDRDGN SYVAFALGM  
PAIARVSADGKTVSTFAWESGNGGQRP GYSGITFDPHSNKLI AFGGPRAL TAFDVSKPYA  
WPEPVKINGDFGTL SGTEKIVTVPVGNESVLVGARAPY AISFRSWDNWKSANIKKTRSE  
LQNSGFTAVADYYQGEQGLYAVSAFFDNGAHGGRSDYPLYKLDNSILNF

>BAA07772.1 unknown function [Oryza sativa]  
RHEVKRQCVATTHPAAPGTEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVG  
HPMAEVFPGCRRGDLERRRSLPAFCNVDIPNGTGGVCYWLGPRTPTRTGH

>BAA07773.1 unknown function [Oryza sativa]  
RVVKRQCVATRRTGGADEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHP  
MAEVFPGCRRGDLERARATLPAFCNVDIPNGTGGVCYWLGPRTPTRTGH

>BAA07774.1 unknown function [Oryza sativa]  
FGTRFRQRQCVGPRRTRRRWTQQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATD  
VGHPMAEVFPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGPRTPTRTGH

>BAA12318.1 Tri a 21; gliadin [Triticum aestivum]  
VRVPVPLQLPQNPSQQQPQEQVPLVQQQQFLGQQQPFPPQPYPQPQPFPSQQPYLQLQP  
FPQPQLPYSQPQPFPRPQQPYPQPQPYQSQPQEPISQQQQQQQQQQQILQQILQQQLIPCM  
DVVLQQHNI AHGRSQVLQQSTYQLLQELCCQHLWQIPEQSQCQAIQNVVHAILHQQQKQ  
QQQPSSQVSFQQPLQQYPLGQGSFRPSQQNPQDQGSVQPQQLPQFEEIRNLALQTL PAMC  
NVYIPPYCTIAPFGIFGTN

>BAA09920.1 Der f 3; trypsin [Dermatophagoides farinae]  
MMILTIVVLLAANILATPILPSSPNATIVGGVKAQAGDCPYQISLQSSSHFCGGSILDEY  
WILTAHCVNGQS AKKLSIRYNTLKHASGGEKIQVAE IYQHENYDSMTIDNDVALIKLKT  
PMTLDQTN AKPVPLPAQGS DVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD  
QLYSKAGADVSENMICGGDVANGGV DSCQGDSSGPPVVDVATKQIVGIVSWGYGCARKGYP  
GVYTRVGNFVDWIESKRSQ

>AAB36008.1 unknown function, partial [Parietaria officinalis]  
APAGGVVPIIMPPXXFF

>AAB36009.1 unknown function, partial [Parietaria officinalis]  
APAGGVVVAAMPPLL

>AAB36010.1 unknown function, partial [Parietaria officinalis]  
GPVGGVVHAHMPLL

>AAB36011.1 unknown function, partial [Parietaria officinalis]  
EEXGGVVGALMPPLL

>AAB36012.1 unknown function, partial [*Parietaria officinalis*]  
GTTGTVVGALMPPLFVQGKEKEXPPSXXKG

>CAA96534.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFNJETEFTSVIPARL FNAFVL DADNLI PKIAPQAVKSAEILEG DGGVGTI K KINFG  
EGSTYSYVVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSHY  
HTKSDVEIKEEHVKAGKEKASHLFKLIENYLLAHS DAYN

>CAA96535.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFNJETETTSVIPAPRLF KAFILDG DNLIPK IAPQAIKSTEIIEG DGGVGTI K KVTFG  
EGSQYGYVVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTTS  
YHAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN

>CAA96536.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFNJETEFTSVIPAPRLF KAFILDG DNLIPK IAPQAIKSTKIIEG DGGVGTI K KVTFG  
EGSQYGYVVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTNSH  
YHAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN

>CAA96537.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFNJETEFTSVIPAPRLF KAFILDG DNLIPK IAPQAIKSTEIIEG DGGVGTI K KVTFG  
EGSQYGYVVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTTS  
YRAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN

>AAA99805.1 Der f 3; trypsin [*Dermatophagoides farinae*]  
IVGGVKAKAGDCPYQISLQSSSHFCGGSILDEYWIL TAAHC VNGQS AKKLSIRYNTLKHA  
SGGEKIQVAEIQHENYDSMTIDNDVALIKLKT PMLDQ TNAKPVPLPPQGS DVKVGDKI  
RVSWG YLQEGSYSLPSELQRVDIDVVSREQDQLYSKAGADVSENMICGGDVANGGVDS  
CQGD SGGPVVDIATKQIVGIVSWGYGCARKGYPGVYTRVGNFVDWIESKRSQ

>CAA96546.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNJETETPSVIPAARLF KAFILDG DKL LPKVAPEAVSSVENIEGNGGPGTI K KITFP  
EGSPFKYVKERVDEVD RNFYKYSFVIEGGAVGDALEKVCNEIKIVAAPDGG SILKISNK  
FHTKGDHEINAEQIKIEKEKAEGLLKAVESYH LAHS DAYN

>CAA96539.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNJETEATSVIPAARLF KAFILDG DNLFPKVAPQAISSVENIEGNGGPGTI K KISFP  
EGIPFKYVKDRVDEVDHANFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKA EQIKASKEMGETLLRAVERYLLAHS DAYN

>CAA96540.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNJETETTSVIPAARLF KAFILDG DNLIPKVAPQAISSVENIEGNGGPGTI K KITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNK  
YHTKGDHEMKA EHMKAIKEKAEALLRAVESYLLAHS DAYN

>CAA96541.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNJETEATSVIPAARLF KAFILDG DNLFPKVAPQAISSVENIEGNGGPGTI K KISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKA EQVKASKEMGETLLRAVESYLLAHS DAYN

>CAA96542.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNJETETTSVIPAARLF KAFILDG DNLIPKVAPQAISSVENIEGNGGPGTI K KITFP

EGSPFKYVKERVDEVDHANFKYAYSMEIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN  
>CAA96543.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMEIEGGALGDTLEKICNEIKIVATPDGGSILKISNK  
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN  
>CAA96544.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETEATSVIPAAARLFKASILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGSPFKYVKERVDEVDVRFNKYSFSVIEGGAVGDALEKVCNEIKIVAAPDGG SILKISNK  
FHTKGDHEINAEQIKIEKEKAVGLLKAVESYLLAHS DAYN  
>CAA96547.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVAHKNFKYSYSVIEGGPIGDTLEKISNEIKIVATPDGRSILKISNK  
YHTKGDHEVKAQIKASKEMGETLLRAVESYLLAHS DAYN  
>CAA96548.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNYETESTSVIPAAARLFKAFILDGNNLIPKVAPQAVSSVENIEGNGGPGTIKKITFS  
EGSPFKYVKERVEVDHTNFKYSYTVIEGGPVGDKVEKICNEIKIVAAPDGG SILKISNK  
YHTKGDHEVDAEHKGGKKEVEGLFRAVEAYLLAHS DAYN  
>CAA96549.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus  
avellana]  
MGVFNYETETTSVIPPARLFKRFVLDSDNLI PKVAPKAIKSIEIEGNGGPGTIKKICFD  
EGSPFNYIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGSILKSISK  
YHTIGDHELKDEQIKAGKEKASGLFKAVEGYLLAHS DAYN  
>CAA66403.1 Sal s 1; calcium-binding protein, parvalbumin [Salmo salar]  
MACAHLCKEADIKTALEACKAADTFSFKTFFHTIGFASKSADDVKKAFKVIDQDASGFIE  
VEELKLFQNFCKARELDTAETKAFKAGDADGDMIGIDEFAVLVKQ  
>AAB01092.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus  
carota]  
LIFLLILSNLILNIMGAQSHSLEITSSVSAEKIFXXIVLDVDTVIPKAAPGAYKSVDVKG  
DGGAGTVRIITLPEGSPITSMTVRTDAVNKEALTYDSTVIDGDILLEFIESIETHMVVVP  
TADGGSITKTTAIFHTKGDVAVPEENIKFADAQNTALFKAIEAYLIAN  
>P49370.1 Ves v 2; hyaluronidase [Vespula vulgaris]  
SERPKRVFNIIYWNVPTFMCHQYDLYFDEVTNFNIRNSKDDFQGDKIAIFYDPGEFPALL  
SLKDGKYYKRNNGVPEQGNITIHQKFIENLDKIYPNRNFSGIGVIDFERWRPIFRQNWG  
NMKIHKNFSIDLVRNEHPTWNKKMIELEASKRFEKYARFFMEETLKLAKKTRKQADWGYY  
GYPYCFNMSPNNLVPECDVTAMHENDKMSWLFNNQNVLLPSVYVRQELTPDQRIGLVQGR  
VKEAVRISNNLKHSPKVL SYWVYVYQDETNTFLTETDVKKTFQEIVINGGDGIIIWSSS  
DVNSLSKCKRLQDYLLTVLGP IAINVTEAVN  
>P49372.1 Api g 1; pathogenesis related protein, PR-10, Bet v 1-like [Apium  
graveolens]  
MGVQTHVLELTSSVSAEKIFQGFVIDVTVLPKAAPGAYKSVEIKGDGGPGTLKIITLPD  
GGPITMTLRIDGVNKEALTFDYSVIDGDILLGFIESIENHVVLVPTADGGSICKTTAIF  
HTKGDVAVPEENIKYANEQNTALFKALEAYLIAN  
>P49148.1 Alt a 12; acidic ribosomal protein P1 [Alternaria alternata]  
MSTSELATSYAALILADDGVDITADKQLQSLIKAAKIEEVEPIWTTLFAKALEGKDVKDLL  
LNVGSGGGAAPLPEALLLRWRAADAAPAAEKKKEEKEEESDEDMGFGLFD

>P02789.2 Gal d 3; ovotransferrin [*Gallus gallus*]  
MKLILCTVLSLGLIAAVCF AAPPKSVIRWCTISSPEEKKCNLRDLTQQERISLTCVQKAT  
YLDCIKAIANNEADAISLDGGQAFEAGLAPYKLPKPIAAEVYEHTEGSTTSYYAVAVVKKG  
TEFTVNDLQGKTSCHTGLGRSAGWNIPIGTL LHRGAI EWEGIESGSVEQAVAKFFSASCV  
PGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAFVKHTTVNENAPDQK  
DEYELLCLDGSRQPVVDNYKTCNWARVA AHAVVARD DNKVEDIWSFLSKAQSDFGVDTKSD  
FHLFGPPGKKDPVLKDLLFKDSAIMLKRVP SLMDSQLYLGF EYYS AIQSMRKDQLTPSPR  
ENRIQWCAVGKDEKSKCDRWSVVSNGDV ECTVVD ETKDCI IKIMKGEADAVALDGGGLVYT  
AGVCGLVPVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWN NLKGKKSCHTAVGRT  
AGWVIPMGLIHNRTGTCNFDEYFSEGCAPGSPNSRLCQLCQSGGIPPEKCVASSHEKY  
FGYTGALRCLVEKGDVAFIQHSTVEENTGGKNKADWAKNLQMDDFELLCTDGRRANVMDY  
RECNLAEVPTHAVVVRPEKANKIRDLLERQEKRFVNGSEKSKFMMFESQNKDLLFKDLT  
KCLFKVREGTTYKEFLGDKFYTVISSLKTCNPSDILQMC SFLE GK  
>P49277.1 Der p 6; chymotrypsin, serine protease [*Dermatophagoides pteronyssinus*]  
AIGXQPAAEAEAPFQISLMK  
>BAA04557.1 Der f 10; tropomyosin [*Dermatophagoides farinae*]  
FFFVAAKQQQPSTKMEAIKKM QAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRA  
LQKKIQIENELDQVQEQLSAANTKLEEKALQTAEGDVAALNRRIQLIEEDLERSEER  
LKIATAKLEEASQSADESERMRKMLEHRSITDEERMDGLENQLKEARMAEDADRKYDEV  
ARKLAMVEADLERAEERAETGESKIVELEEE LRVVGNLKSLEVSEEKAQQREEAYEQQI  
RIMTAKLKEAEARAEFAERSVQKLQKEVDRL EDELVHEKEKYKISDEL DQTF AELTGY  
>CAA64868.1 Cas s 5; chitinase [*Castanea sativa*]  
MKLFLSLLLFLAFL LGTSAEQCGRQAGGAACANLCCSQFGWCGNTAEYCGAGCQSQCSSP  
TTTTSSPTASSGGGVDGSLISASLFDQMLKYRNDPRCKSNGFYTYNAFIAAARSFNGFG  
TTGDVTTTRKRELA AFLAQTSHETTGGWATAPDGPYAWGYCFVMENNKQTYCTSKSWPCVF  
GKQYYGRGPIQLTHNYNYGQAGKAIGADLINNPDLVATNPTISFKTAIWFWMTPQANKPS  
SHDVIIGNWRPSAADTSAGRVPSYGVITNIINGGLECGHGSDDR VANRIGFYKRYCDTLG  
VSYGNLDCYNQK PFA  
>I53806 Ole e 1; Ole e 1-like [*Olea europaea*]  
SQFHIQGQVYCDTCRARFITELSEFIPGAGVRLQCREKNGDITFTEVGYTRAEGLYSML  
IERDHKNEFCEITLASSSRKDCDEIPVEGWKPSLKFILNTVNGTTRTINPLGFFKKEVL  
PKCPQVFNKLGMYPNNM  
>E53806 Ole e 1; Ole e 1-like [*Olea europaea*]  
QFHIQGQVYCDTCHARFITELSEFIPGASVRLQCREKNGDITFTEVGYTRAEGLYSMLV  
ERDHKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTINPLGFFKKEALP  
KCAQVYNKLGMYPPNM  
>F53806 Ole e 1; Ole e 1-like [*Olea europaea*]  
QFHIQGQVYCDTCRAGFINELSEFIPGASVRLQCREKNGDITFTEVGYTRAEGLYSMLV  
ERDHKNEFCEITLISSGRKDCNEIPIEGWAKPSLKFILNTVNGTTRTINPLGFYKKEALP  
KCAQVYNKLGMYPPNM  
>C53806 Ole e 1; Ole e 1-like [*Olea europaea*]  
EDVPQPPISQFYVQGVYCDTCRTRFITEFSEFIPGAGVRLQCKDGENGKITFTEVGYTR  
AEGLYSMLIERDHKNEFCEITLSSSRKDCDEIPTEGWVKPSVKFILNTVNGTTRTINPL  
GFFKKEALPKCPQVFNKLGMYPNNM  
>A38968 Ole e 1; Ole e 1-like [*Olea europaea*]  
QFHIQGQVYCDTCRARFITELSEFIPGAGVRLQCREKNGDITFTEVGYTRAEGLYSMLI  
ERDHKNEFCEITLASSSRKDCDEIPVEGWKPSLKFILNTVNGTTRTINPLGFFKKEVLP  
KCAPQVFNKLGMYPNNM  
>G53806 Ole e 1; Ole e 1-like [*Olea europaea*]  
QFHIQGQVYCDTCRAGFINELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLV

ERDHKNEFCEITLISSGSKDCNEIPTEGWGKPSLKFILNTVNGTTRTVNPLGFYKKEALP  
KCAQVYNKLGMYPPNM  
>B53806 Ole e 1; Ole e 1-like [Olea europaea]  
EDVPQPPVSQFHIQGGVYCDTCRARFITELSEFIPGASVRLQCKDGENGSITFTEVGYTR  
AEGLYSMLIERDHKDEFCEITLISSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPL  
GFFKKEALPKCPQVFNKLGMYPPNM  
>H53806 Ole e 1; Ole e 1-like [Olea europaea]  
QFHIQGGVYCDTCRARFITELSEFIPGAGVRLECKDGGKGSITFTEVGYTRAEGLYSMLI  
ERDHKNEFCEITLASSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEVLP  
KCPQVFNKLGMYPPNM  
>CAA44343.1 Fel d 1; uteroglobin [Felis catus]  
VRRSPSTLPYCCGHSRDCEICPAVKRDVDFLTGTDPDEYVEQVAQYNALPVVLENARILK  
NCVDAKMTEEDKENALSVDKIYTSPLC  
>CAA44344.1 Fel d 1; uteroglobin [Felis catus]  
EGGLCSRASLGCLALDLGWKDCEICPAVKRDVDFLTGTDPDEYVEQVAQYNALPVVLENA  
RILKNCVDAKMTEEDKENALSVDKIYTSPLC  
>AAC80579.1 Blo t 13; fatty acid-binding protein [Blomia tropicalis]  
MPIEGKYKLEKSDNFDKFLDELGVGFMVKTAAKTLKPTLEVDVQGDYVFRSLSTFKNTE  
IKFKLGEEFEEDRADGKRVKTVVNKEGDNKFIQTQYGDKEVKIVRDFQGDDVVVTASVGD  
VTSVRTYKRI  
>BAA07710.1 unknown function [Oryza sativa]  
MASNKVVFSAALLIIVSVLAATGPMADHHKDQVVYSLGERCQPGMGYPMYSLPRCRAVVK  
RQCVATAHPAARGNEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAE  
VFPGCRRGDLERAAASLPAFCNVDIPNGTGGVVCYWLGPRTPTRGH  
>BAA07711.1 unknown function [Oryza sativa]  
GTRLLLIIVSVLAATRRMADHHKDQVVYSLGERCQPGMGYPMYSLPRCRAVVKRQCVGHG  
APGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAEVFPGCRR  
GDLERAAASLPAFCNVDIPNGTGGVVCYWLGYTPRTPTRGH  
>BAA07712.1 unknown function [Oryza sativa]  
MASNKVVIPALLVVVSVLAATTTMADHHQEQQVYTPGQLCQPGIGYPTYPLPRCRAFVK  
RQCVAPGTLDEQVRRGCCRQLAGIDSSWCRCDALNHMLRIIYREERAADAGHPMAEVFRG  
CRRGDIERAAASLPAFCNVDIPNGVGGVVCYWLPGTGY  
>BAA07713.1 unknown function [Oryza sativa]  
MASNKVVFVSVLLAVVSVLAATATMAEYHHQDQVVYTPAPLCQPGMGYPMYPLPRCRALV  
KRQCVGRGTAATAAEQVRRDCCRQLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEV  
FRGCRRGDLERAAASLPAFCNVDIPNGGGVVCYWLARSGY  
>CAA35188.1 alpha-amylase/trypsin inhibitor [Hordeum vulgare]  
MAFKYQLLLSAVMLAILVATATSFQDSCAPGDALPHNPLRACRTYVVSQICHQGPRLLT  
SDMKRRCCDELSAIPAYCRCEALRIIMQGVVWQGAFFGAYFKDSPNCPRERQTSYAANL  
VTPQECNLGTIHGSAYCPELQPAY  
>AAB36316.1 Myr p 2; pilosulin [Myrmecia pilosula]  
MKLSCLLLTLAIIFVLTIVHAPNVEAKALADPESDAVGFADAVGEADPIDWKKVDWKKVS  
KKTCKVMLKACKFLG  
>AAB35897.1 Mal d 2; thaumatin-like [Malus domestica]  
AKITFTNNXPNTVWPGILTGFQKPKQ  
>AAC49447.1 Hev b 5; unknown function [Hevea brasiliensis]  
MASVEVESAAATLPKNETPEVTKAEETKTEEPAAPPASEQETADATPEKEEPTAAPAEPE  
APAPETEKAEEVEKIEKTEEPAPEADQTTPEEKPAEPEPVAEEEEPKHETKETETEAPAAP  
AEGEKPAEEEEKPIEAAETATTEVPVEKTEE  
>AAC02632.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus

avium]

MGVFTYESEFTSEIPPPRLFKAFLVDADNLVPKIAPQAIKHSEILEGGPGTIKKITFG  
EGSQYGYVKKHIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIKSTSH  
YHTKGNVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN

>BAA08246.1 Cha o 1; pectate lyase [*Chamaecyparis obtusa*]  
MASCTLLAVLVFLCAIVSCFSDNPIDSCWRGDANWDQNRMKLADCAVFGSSAMGGKGA  
FYTVTSSDDDPVNPAPGTLRYGATRERSLWIIIFSKNLNIKLNMPYIAGNKIDGRGAEV  
HIGNGGPCLFMRTVSHVILHGLNIHGCNTSVSGNVLISEASGVVPVHAQDGDITMRNVT  
DVWIDHNSLSDSSDGLVDVTLASTGVTISNNHFFNHHKVMMLLGHSDIYSDDKSMKVTVAF  
NQFGPNAGQRMPRARYGLIHVANNNYDPWSIYAIGSSNPTILSEGNSFTAPNDSKKEV  
TRRVGCEPSTCANWVWRSTQDSFNNGAYFVSSGKNEGTNIYNNNEAFKVENGSAAPQLT  
KNAGVLTCILSKPCS

>AAB09632.1 Per a 3; hemocyanin, arylphorin [*Periplaneta americana*]  
DIGDHYDIEANIGHYKYPHVKNFISYKKGLLPRGEPFSVYVEKHREQAIKLFELFFAA  
NDYDTFYKTACWARDRVNEGFMFYALTVAAFHREDTKDLVLPPEVNPYLFVEDDVIQQ  
AYKYWTKESGTDKHVEHVIPVNFARSQEDLVAYFREDVDLNAFNMYFRYIYPSWFNTTL  
YGKSFDRRGEQFYTYHQIYARYFLERLSNSLPDVKPFQYSKPLKTGYNPHLRYHNGEEM  
PARPSNMYPTNFDLFYVSDIKNYERRVEKAIDFGYAFDEHRTPYSLYHDQHGM DYLGQMI  
EGTRNSPHQYFYGSVFHFYRLLVGHVVDVPHKNGLAPSALEHPQTALRDPAFYQLWKRID  
HIVQYKYNRLPRYTYDELSFPGVKIENVVDVGKLYTYFEHFEHSLGNAMYLGKLEDYMKAS  
IRARHYRLNHKPFYTYNIEVSSDKAQDVYVRIFLGPKYDSLGHCELDERRHYFVEMDRFV  
HKVEAGKTVIERKSHDSSIISSDHSYRNLFKKVS DALQEKDQYYIDKSHKYCGYPENLL  
LPKGGKGGQTFTFYVIVTPYVKQDEHDFEPYHYKAFSYCGVGHGRKYPDDKPLGFPPDRK  
IHDYDFYTPNMYFKDVVIFHKKYDEVHVDVTH

>CAA65122.1 Par j 2; lipid transfer protein [*Parietaria judaica*]  
MRTVSMALVVAALAWTSSAELASAPAPGEGPCGKVVHIMPCLKFVKGEEKEPSKSC  
CSGTKKLSSEVKTTEQKREACKCIVAATKGISGIKNELVAEVPKCKGITTTLPITADFD  
CSKIESTIFRGYY

>CAA65123.1 Par j 1; lipid transfer protein [*Parietaria judaica*]  
MRTVSAPSAVALVVAAGLAWTSLASVAPPAPAGSEETCGTVVRALMPCLPFVQGKEK  
EPSKGGCCSGAKRLDGETKTGLQRVHACECIQTAMKTYSDIDGKLVSEVPKHCGIVDSKLP  
PIDVNMDCKTLGVVPRQPQLPVSLRHGPVTGSPDPAHKARLERPQIRVPPPAPEKA

>CAB02155.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAB02156.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAB02157.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDILEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAB02158.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP

GGLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAB02159.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAB02160.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEETETTSVIPAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAB02161.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYEETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMRETLRAVESYLLAHS DAYN  
>CAB02206.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAAEKMGAKEMA EKLLRAVESYLLAHTDEYN  
>CAB02207.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKYNYTVIEGDVLGDNLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAAEEMKGAKEMA EKLLRAVESYLLAHTDEYN  
>CAB02208.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAAEKMGAKEMA EKLLRAVESYLLAHTDEYN  
>CAB02209.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAAEEMKGAKEMA EKLLRAVESYLLAHTAEYN  
>CAB02213.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKFSYTVIEGDVLGDKLEKVSLELKIVAAPGGGSILKISGK  
FHAKGDHEVNAAEEMKGAKEMA EKLLRAVESYLLAHTAEYN  
>CAB02215.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETPSVMPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFKERVDEVDNANFKFSYTVIEGDVLGDKLEKVSLELTIVAAPGGGSILKISGK  
FHAKGDHEVNAAEEMKGAKEMA EKLLRAVESYLLAHTAEYN  
>CAB02216.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAETTSVIPAARLFKAFILDGNKLIPKVSPQAVSSVENVEGNGGPGTIKKITFS

EGSPVKYVKERVEEVDHTNFKYSYTVIEGGFVGDKVEKICNEIKIVAAPDGG SILKITSK  
YHTKGDHEVPAEHIKGGKERVEGLLKPVEAYLLAHTAEYNN  
>CAB02217.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNYEAEETTSVIPAARLFKAFILDGNNLIPKVAPQAVSSVENVEGNGGPGTIKKITFS  
EGSPVKYVKERVEEVDHTNFKYSYTVIEGGFVGDKVEKICNEIKIVAAPDGG SILKITSK  
YHTKGDHEVPAEHIKGGKERVEGLLKPVEAYLLAHTAEYNN  
>AAB63099.1 Sola t 3; cysteine protease inhibitor [Solanum tuberosum]  
TCHDDDLVLPVEYDQDGNPLRIGERYIKNPLL GAGAVYLDNIGNLQCPNAVLQHMSIP  
QFLGKGT PVV FIRKSESDYGDVRLMTAVYIKFFVKTTLKCVDET VWKVNNEQLVVTGGN  
VGNENDIFKIKKTDLVRIGMKNVYKLLHCPHLECKNIGSNFKNGYPRLVTVNDEKDFIP  
FVFIKA  
>AAC48691.1 Equ c 1; lipocalin [Equus caballus]  
MKLLLLLCLGLILVCAQQEENSVAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFV  
DVIRALDNSSLYAEYQTKVNGECTEFPMVFDKTEEDGVYSLNYDGYNVFRISEFENDEHI  
ILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCFQLR  
GNGVAQA  
>AAB62731.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]  
LNAFNMYFRYIYPTWFNTTLYGKTFDRRGEQFYTYHQIYARYFLERLSNSLPDVKPFQY  
SKPLKTGYNPHLR YQNGEEMPARPSNMYPTNIDLFYVSDIKNYESRVEKAIDFADFDEHR  
TPYSLYHDQHGM DYLGQMI EGTSNSPYQYFYGSIFHFYRLLVGHVVDVPHKNGLAPSALE  
HHQTALRDP AFYQLWKRIDHIVQKYKNR LPRYTYDELSFPGVKIENVDVGKLYTYFEHFE  
HSLGNAMYLGKLEDVLKANIRARHYRLNHKPFTYNI EVSSDKAQDVYVRIFLGPKYDSL G  
HECELDERRHYFVEMDRFVHKVEAGKTVIERKSHDSSII SDSHDSYRNLFKKVSDALEGK  
DQYYIDNSHKYCGYPENLLL PKGKGGQTFTFYVIVTPYVKQDEHDLESYHYKAFTYCGV  
GHGRKYPDDKPLGFPFDRKIHDYDFYTPNMYFKDVVIFHKKYDEVHNETN  
>AAB63595.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]  
EMPARPSNMYPTNIDLFYVSDIKNYESRVEKAIDFGYAFDEHRTPYSLYHDQHGM DYLGQ  
MIEGTSNSPYQYFYGSIFHFYRLLVGHVVDVPHKNGLAPSALEHHQTALRDP AFYQLWKR  
IDHIVQKYKNR LPRYTYDELSFPGVKIENVDVGKLYTYFEHFEHSLGNAMYIGKLEDLLK  
ANIRASHYRLNHKPFTYNI EVSSDKAQDVYVRIFLGPKYDSL GHECELDERRHYFVEMDR  
FVHKVEAGKTVIERKSHDSSII SDSHDSYRNLYKKVADALEEKDQYYIDKSHKYCNYPEN  
LLL PKGKGGQTFTFYVIVTPYVKQEQHDFEPYHYKAFSYCGVGHGRKYPDDKPLGFPFD  
RKIHDYDFYTPNMYFKDVVIFHKKYDEVHEVTH  
>2118249A Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDITGCSGDTCVIHRGEKMTLEAKFAANQ  
DTAKVTIKVLAKVAGTTIQVPGLET DGCKFIKCPVKKGEALDFIYSGTIPAITPKVKADV  
TAEI GDHGMACGT VHGVQE  
>2118249B Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDISGCSGDTCVIHRGQKMTLDAKFAANQ  
DTNKVTIKVLAKVAGTTIQVPGLET DGCKVLKCPIKKGEALDFNYGMTIPAITPKIKADV  
TAE LVGDHGMACGTI HGVQE  
>2118271A Phl p 1; beta-expansin [Phleum pratense]  
MASSSSVLLVVALFAVFLGSAHGIPKVP PGNITATYGDKWLD AKSTWYGKPTAAGPKDN  
GGACGYKD VDKPPFSGMTGCGNTPIFKSGRGC GSCFEIKCTKPEACSGEPVVVHITDDNE  
EPIAAYHFDLSGIAFGSMAKKGDEQKLR SAGEVEIQFRRVKCKYPEGTKVTFHVEKGSNP  
NYLALLVKFSGDGDVAVDIKEKGKDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEGG  
TKARAKDVIPEGWKADTAYESK  
>2206305A Myr p 2; pilosulin [Myrmecia pilosula]  
MKLSCLLLTLAIIFVLTIVHAPNVEAKALADPESDAVGFADAVGGADPIDWKKVDWKKVS

KKTCKVMLKACKFLG

>2209273A unknown function [*Zea mays*]

MASVPAPATTTAAVILCLCVLSCAAADPNLPDYVIQGRVYCDTCRAGFVTNVTEYIAG  
AKVRLECKHFGTGKLERAIIDGVTDATGTYTIELKDSHEEDICQVVLVASPRKDCDEVQAL  
RDRAGVLLTRNVGISDSLRPANPLGYFKDVPLPVCAALLKQLDSDDDDDDQ

>1ESF\_B enterotoxin [*Staphylococcus aureus*]

SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHQFLQHTILFKGFFTD  
HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT  
EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVVQ  
RGLIVFHTSTEPSVNYDLFGAQQQYSNTLLRIYRDNKTINSEMHIDIYLYTS

>AAB60779.1 Asp f 6; superoxide dismutase [*Aspergillus fumigatus*]

GTSP IQTPINTMSQQYTL PPLPYPYDALQPYISQQIMELHHKHHQTYVNGLNAALEAQK  
KAAEATDVPKLVSVQQAIFKNGGGHINHS LFWNLAPEKSGGGKIDQAPVLKAAIEQRWG  
SFDKFKDAFN TLLGIQGSWGWLVTDGPKGKLDITTTTHDQDPVTGAAPVFGVDMWEHAY  
YLQYLNDKASYAKGIWNVINWAEENRYIAGDKGGHPFMKL

>BAA13604.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVDVKDGGAGTVRIITLPE  
GSPITSMTVRTDAVNKEALTYDSTVIDGDILLEFIESIETHMVVPTADGGSITKTTAIF  
HTKGD AVVPEENIKFADAQNTALFKAIEAYLIAN

>CAB05371.1 Phl p 5; unknown function [*Phleum pratense*]

AVPRRGPRGGPGRSYAADAGYAPATPAAAGAEAGKATTEEQKLI EDINVGFKAAVAAAAS  
VPAGDKFKTFEAAFTSSSKAATAKAPGLV PKLDAAYSVA YKAAV GATPEAKFDSFVASLT  
EALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAATAPADDKFTV  
FEAAFNKAIKESTGGAYD TYKCIPSLEAAVKQAYAATVAAAAPQVKYAVFEAALTKAITAM  
SEVQKVSQPATGAATVAAGAATTATGAASGAATVAAGGYKV

>CAB05372.1 Phl p 5; unknown function [*Phleum pratense*]

ADLGYGGPATPAAPAEAAPAGKATTEEQK LIEKINDGFKAALAAAAGVPPADKYKTFVAT  
FGAASNKAF AEGLSAEPKGAEESSSKGALTSKLEAAYKLAYKTSEGATPEAKYDAYVATL  
SEALRIIAGTLEVHAVKPAEEVKVIPAGELQFIEKVDSALKVAATAANAAAANDKFTVF  
EAAFNHAIKASTGGAYESYKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMS  
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>AAB37403.1 Sec c 20; gamma secalin, partial [*Secale cereale*]  
NMQVNP SGVQVWPQQQPPFPQPQQ

>P02222.2 Chi t 3; hemoglobin [*Chironomus thummi thummi*]

MKFLVLALCIAAAVAAPLSADEASLV RGSWAQVKHSEVDILYYIFKANPDIMAKFPQFAG  
KDLET LKGTGQFATHAGRIVGFVSEIVALMGNSANMPAMETLIKDMAANHKARGIPKAQF  
NEFRASLVSYLQSKVSWNDSLGAAWTQGLDNVFNMMFSYL

>P02223.2 Chi t 3; hemoglobin [*Chironomus thummi thummi*]

MKFFIVLALCIVGAIADPVSSDQANAIRASWAGVKHNEVDILAAVFS DHPDIQARFPQFA  
GKDLASIKDTGAFATHAGRIVGFISEIVALVGNESNAPAMATLINELSTSHHNRGITKGQ  
FNEFRSSLVSYLSSHASWNDATADAWTHGLDNIFGMIFAHL

>P80198.1 Hor v 20; gamma-hordein-3 [*Hordeum vulgare*]

ITTTT MQFNPSGLELERPQQ LFPQWQPLPQQPPFLQQEPEQYPYQQQPLPQQQPPFPQQPQ  
LPHQHQPQQPLPQQQFPQQMPLQPQQQFPQQMPLQPQQQFPQQKPFQYQQPLTQQPY  
PQQQPLAQQQPSIEEQHQLNLCKEFL LQQCTLDEKVPLLQSVISFLRPHISQQNSCQLKR  
QQCCQQLANINEQSRCPAIQTIVHAIVMQQQVQQQVGHGFVQS QLQQLGQGMP IQLQQQP  
GQAFVLPQQQAQFKVVGSLVIQTL PMLCNVHVPPYCS PFGSMATGSGGQ

>P53357.1 Do1 m 1; phospholipase A1 [*Dolichovespula maculata*]

GILPECKLVPEEISFVLSTREN RDGVYLT LQKLKNGKMFKNSDLSSKKVPFLIHGFISSA

TNKNYADMTRALLDKDDIMVISIDWRDGACSNFALLKFIGYPKAVENTRAVGKYIADFS  
KILIQKYKVLLENIRLIGHSLGAQIAGFAGKEFQRFKLGKYPEIIGLDPAGPSFKKKDCP  
ERICETAHVYQILHTSSNLGTERTLGTVDFYINDGSNPQPGCTYIIGETCSHTRAVKYLT  
ECIRRECCLIGVPQSKNPQPVSKCTRNECVGLNAKEYPKKGSFYVPVEAKAPFCNNNG  
KII  
>P51528.1 Ves m 1; phospholipase A1 [*Vespula maculifrons*]  
GPKCFNSDTVSIIEETRENRRDLYTLQTLQNHPEFKKKTITRPVVFITHGFTSSASEK  
NFINLAKALVDKDNMVISIDWQTAECTNEYPGLKYAYYPTAASNTRLVGGQYIATITQKL  
VKDYKISMANIRLIGHSLGAHVSGFAGKRVQELKLGKYEIIGLDPARPSFDSNHCSERL  
CETDAEYVQIIHTSNYLGTTEKILGTVDYFMMNGKNMPGCRFFSEVCSHTRAVIYMAECI  
KHECCLIGIPRSKSSQPISRCTKQECVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII  
>AAB41308.1 Jug r 1; 2S albumin, conglutin [*Juglans regia*]  
AALLVALLFVANAAAFRTTITTEMEIDEDIDNPRRRGEGCREQIQRQQNLNHCQYYLRQQS  
RSGGYDEDNQRQHFRQCCQQLSQMDEQCQCEGLRQVRRRQQQQGLRGEEMEEMVQSARD  
LPNECGISSQRCEIRRSWF  
>AAB42069.1 Sola l 3; lipid transfer protein [*Solanum lycopersicum*]  
MEMFGKIACFVVFVCMVVVAPHAESLSCGEVTSGLAPCLPYLEGRGPLGGCCGGVKGLLGA  
AKTPEDRKTACTCLKSAANSIKGIDTGKAAGLPGVCGVNIPYKISPSTDCSTVQ  
>AAB42200.1 Dac g 3; expansin [*Dactylis glomerata*]  
VKVTFKVEKGS DPKKLVLDIKYTRPGDTLAEVELRQHGESEWEPLTKKGNLWEVKSSKPL  
TGPFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE  
>AAB46819.1 Par o 1; lipid transfer protein [*Parietaria officinalis*]  
ATGKVVQDIMPPLLFVVQGKEKPSS  
>AAB46820.1 Par o 1; lipid transfer protein [*Parietaria officinalis*]  
GPXGKVVHIIMPPLKFVKGESEEP  
>AAB47552.1 Alt a 1; unknown function [*Alternaria alternata*]  
MQFTTIASLFAAAGLAAAAPLESRQDTASCPVTTEGDYVWKISEFYGRKPEGTYYNLSLF  
NIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDFSFSDSDRSGLLLKQKVSDDITYVA  
TATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS  
>AAB48041.1 Alt a 5; ribosomal protein P2 [*Alternaria alternata*]  
MKHLAAYLLLGLGNTSPSAADVKALESVGEADSDRLDKLISELEGKDINELIASGPE  
KLASVPSGGAGGAAASGGAAAAGGSAAEAAPEAAKEEEEKEESDEDMGFGLFD  
>CAA62634.1 Cyn d 7; calcium-binding protein, polcalcin [*Cynodon dactylon*]  
KTMADTGDMEHIFKRFDTNGDGKISLAELTDALRTL GSTSADEVQRMMAEIDTDGDGFID  
FDEFISFCNANPGLMKDVAKVF  
>CAA72273.1 Tri a 33; serpin [*Triticum aestivum*]  
MATTLATDVRLSIAHQTRFALRLASTISSNPKSAASNAAFSPVSLHSALSLLAAGAGSAT  
RDQLVATLGTGEVEGGHALAEQVVQFVLADASSAGGPRVAFANGVFVDASLLLKPSFQEL  
AVCKYKAETQSVDFQTKAAEVTTQVNSWVEKVTSGRIKNILPSGSVDNNTTKLVLANALYF  
KGAWTDQFDSYGTKNDFYLLDGGSSVQTPFMSSMDDDQYISSSDGLKVLKLPYKQGGDNR  
QFSMYILLPEAPGGLSSLAEKLSAEPDFLERHIPRQRVAIRQFKLPKFKISFGMEASDLL  
KCLGLQLPFSDEADFSEMVDSPMPQGLRVSSVFHQAFVEVNEQGTEAAASTAIKMVPQQA  
RPPSVMDFIADHPFLFLLREDISGVVLFMGHVVNPLLSS  
>AAB50883.1 Myr p 1; pilosulin [*Myrmecia pilosula*]  
MKLSCLLLTLAIIIFVLTIVHAPNVEAKDLADPESEAVGFADAFGEADAVGEADPNAGLGS  
VFGRLARILGRVIPKVAKKLGPVAKVLPKVMKEAIPMAVEMAKSQEEQQPQ  
>AAC27724.1 Hev b 7; patatin [*Hevea brasiliensis*]  
MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDLDPDARIADYFDIIAGT  
STGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIHSIGPIYDGEY  
LRELCNNLLKDLTVKDTSTDVVIPTFDIKLLLPVIFPSDDAKCNALKNARLADVCISTSA

APVLLPAHSFTTEDDKNIHTFELIDGGVAATNP TLLAL THIRNEIIRQNPRFIGANL TES  
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDSHLSAL  
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES  
IPGAPTNEAAIAKFAKLLSEERKLRQLK

>AAB58417.1 Aed a 3; unknown function [Aedes aegypti]  
MKPLVKLFLFCLVGI VLSRPMPEDEEPVAEGGDEETTDDAGGDGGEENE GEEHAGDED  
AGGEDTGKEENTGHEDAGEEDAGEEDAGEEDA EKEEGEKEDAGDDAGSDDGEEDSTGGDE  
GEANAEDSKGSEKNDPADTYRQVVALLDKDTKVDHIQSEYLR SALNNDLQSEVRVPVVEA  
IGRIGDYSKIQGC FKS MGKDVKKVISEEEKFKSCMSKKKSEYQCS EDSFAAAKSKLSPI  
TSKIKSCVSSKGR

>S65144 calcium-binding protein [Brassica napus]  
MADATEKTEHDRFFKKFDANGDGTISSTELGDALKNLGSVTHDDIKRMMAEIDTDGDGFI  
SYQEFSDFAKANRGLMKDVAKIF

>S65145 calcium-binding protein [Brassica napus]  
MADATEKAEHDRFFKKFDANGDGTISSTELGDALKNLGSVTHDDIKRMMAEIDTDGDGFI  
SYQEFSDFAKANRGLMKDVAKIF

>S65143 Bra r 5; calcium-binding protein, polcalcin [Brassica rapa]  
ETERAEHDRIFKKFDANGDGKISASELGDALKNLGSVTHDDIKRMMAEIDTDGDGYISYQ  
EFSDFASANRGLMKDVAKIF

>CAA73782.1 Asp f 18; vacuolar serine protease [Aspergillus fumigatus]  
MKGYSLSLILPLLVAASPVVVDSIHNGAAPILSSMNAKEVPDSYIVVFKKHVNAESAAA  
HSWVQDIHSAQNERVELRKRS LFGFGEEAYLGLKNTFDIAGSLVGYSGHFHEDVIEQVRK  
HPDVEYIEKDSEVHTMEDPTVEKSAPWGLARISHRDSLSFGTFNKYL YASEGGEV DAYT  
IDTGINVDHVDFEGRAQWGKTIPTDDEDADGNHGTHCSGTIAGRKYGVAKKANLYAVKV  
LRSSSGTMSD VVAGVEWAVKSHLKKVKDAKD GKIKGFKGSVANMSLGGGKSRTLEAAVN  
AGVEAGLHFAVAAGNDNADACNYSPAAAENPITVGASTLQDERAYFSNYGKCTDIFAPGL  
NILSTWIGSKHAVNTISGTSMASPHIAGLLAYFVSLQPSKDSAFVDELTPKLLKDDIA  
IATQGALTDIPSDTPNLLAWNGGSSNYTDIIASGGYKVNASVKDRFEGLVHKA EKLLTE  
ELGAIYSEIHDAAVA

>CAA69670.1 Cyn d 12; profilin [Cynodon dactylon]  
MSWQAYVDDHLMCEIEGHHLTSAAIIGHDGTVWAQSAAFPAFKPEEMANIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPAVIRGKKGSGGVTVKKTGQALVIGIYDEPMPGQCNM VIE  
KLG DYLIEQGM

>CAB03715.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAATGAYKSVEVKGDGGAGTVRIITLPE  
GSPITTM TVRTDAVNKEALS YDSTVIDGDILLGFIESIETHM VVVPTADGGSITKTTAIF  
HTKGD AVVPEENIKFADAQNTALFKAIEAYLIAN

>CAB03716.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVDVKGDGGAGTVRIITLPE  
GSPITSM TVRTDAVNKEALTYDSTVIDGDILLGFIESIETHLVVVPTADGGSITKTTAIF  
HTKGD AVVPEENIKFADEQNTALFKAIEAYLIAN

>CAB06416.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVEVKGDGGAGTVRIITLPE  
GSPITSM TVRTDAVNKEALTYDSTVIDGDILLGFIESIETHLVVVPTADGGSITKTTAIF  
HTKGD AVVPEENIKFADAQNTALFKAIEAYLIAN

>CAB06417.1 Asp n 14; beta-xylosidase [Aspergillus niger]  
MAHMSRPVAATAAALLALALPQALAQANTS YVDYNI EANPDLYPLCIETIPLSFPDCQN

GPLRSHLICDETATPYDRAASLISLFTLDEL IANTGNTGLGVSRLGLPAYQVWSEALHGL  
DRANFSDSGAYNWATSFPQPILTTAALNRTL I HQIASIISTQGRAFNNAGRYGLD VYAPN  
INTFRHPVWGRGQETPGEDVSLAAVYAYEYITGIQGPDPESNLKLAATAKH YAGYDIENW  
HNHSRLGNDMNITQQDLSEYYTPQFHVAARDAKVQSVMCAYNAVNGVPACADSYFLQTL  
RDTFGFVDHGYVSSDCDAAYNIYNPHGYASSQAAAAAEAILAGTDIDCGTTYQWHLNESI  
AAGDL SRDDIEQGVIRLYTTLVQAGYFDSNTTKANNPYRDL SWSDVLETDAWNISYQAAT  
QGIVLLKNSNNVLPLETEKAYPPSNTTVALIGPWANATTQLLGNYYGNAPY MIS PRAAFEE  
AGYKVNFAEGTGISSTSTSGFAAALSAAQSADV IYAGGIDNTLEAEALDRESIAWPGNQ  
LDLIQKLASAAGKKPLIVLQMGQQVDSSSLKNNTNVSALLWGGYPGQSGGFALRDIITG  
KKNPAGRLVTTQYPASYAEFPATDMNLRPEGDNPQTYKWTGEAVYEFHGHLFYTTFA  
ESSNNTTKEVKLNIQDILSQTHEDLASITQLPVLNFTANIRNTGKLES DY TAMVFANTS  
DAGPAPYPKKWL VGWDRLGEVKVGETREL RVPVEVGSFARVNEDGDWVVPFGTFELALNL  
ERKVRVKVWLEGE EEWLKWPGKE

>CAA73221.1 Tyr p 2; NPC2-like [Tyrphagus putrescentiae]  
MKFLILFALVAVAAAGQVKFTDCGKKEIASVAVDGCEGLCVIHKSKPVHVIAEFTANQD  
TCKIEVKVTGQLNGLEVPIPIGIETDGCKVLKCP LKKGT KYTMNYSVNVPSVVPNIKT VVK  
LLATGEHGV LACGAVNTDVKP

>AAC34736.1 Per a 1; nitrile-specifier protein [Periplaneta americana]  
INEIHSIIGLPPFVPPSRRHARRGVINGLI DDVIAILPVDELKALFQEKLETS PDFKAL  
YDAIRSPEFQSIISTLNAMQRSEHHQNL RDKGVDVDHF IQLIRALFGLSRAARNLQDDL N  
DFLHSL EPI SPRHRHGLPRQRRRSARVSAYLHADD FHKIIT TIEALPEFANFYNFLKEHG  
LDVVYDINEIHSIIGLPPFVPPSRRHARRGVINGLI DDVIAILPVDELKALFQEKLETS  
PDFKALYDAIRSPEFQSIISTLNAMPEYQELLQNL RDKGVDVDHFIRVDQGT LRTLSSGQ  
RNLQDDL NDFLAL IPTDQILAIAMDYLANDAEVQELVAYLQSDDFHKIIT TIEALPEFAN  
FYNFLKEHGLD VVDYINEIHSIIGLPPFVPPSQRHARRGVINGLI DDVIAILPVDELKA  
LFQEKLETS PDFKALYDAIDL RSSRA

>AAC34737.1 Per a 1; nitrile-specifier protein [Periplaneta americana]  
VGVDGLIDDIIAILPIDDLKALFQEKLETS LDFKAFYDAVRSPEFQSI VQTLNAMPEYQD  
LLQKL RDKGVDVDHYIELIRALFGLTREARNLQDDL NDFLAL IPTDQILAIAMDYLANDA  
EVQELVAYLQSDDFHKIINTIEALPEFANFYNFLKGHGLDVANYINEIHSIIGLPPFVPP  
SRRHARRGVINGLI DDVIAILPVDELKTLFQEKLETS PDFKALYDAIRSPEFQSIISTL  
NAMPEYQELLQNL RDKGVDVDHFIELIRSWFGLP

>CAB10766.1 Hol 1 5; ribonuclease [Holcus lanatus]  
QKLL EDVNASFKA AVAAA KVPADKYKTF LRAFTVLDRGSTEQSKAEETKMP ELSSKLV  
DAYMAAFKASTGGTQEAKYDAFVTTL TEALRVIAGALEVH AVK PATEEVPAAKIPAGDLQ  
VVDKIDASF KIAATAANAAPANDKFTVFETAFNKALKESTGGAYESYKFIPSLEAAVKQA  
YASTVAAAPEVKYAVFEAALTKAITAMSQAQKVAQPAAAATGAATVAAGAATTAAGGYKV

>CAB10765.1 Hol 1 5; ribonuclease [Holcus lanatus]  
ADAGYTPAAPAAAGAGGKATTDEQKLL EDVNAGFKTAVAAAAANVPPADKYKTFEAAFTAS  
SKASIAAAATKAPGLIPQLNAATNTAYAAAQGATPEAKYDAFVTTL TEALRVIAGALEVH  
AVK PATEEVGA AKIPAGELQIVDKIDAAFRIAATAANAAPVNDKFTVFEGAFNKAIKEST  
GGAYEAYKFIPSLETA VKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKEAKPVAAA  
TGAATAAAGVAAGAATAAAGGYKV

>AAB66909.1 Ole e 6; unknown function [Olea europaea]  
DEAQFKECYDTCHKECSDKNGFTFC EMKCDTDCSVKDVKEKLENYKPKN

>AAB65434.1 Sol i 3; unknown function [Solenopsis invicta]  
MELIVSILWLAITAENLANTLATNYCNLQ SCKRNNAIHTMCQYTSPTPGPMC LEYSNVGF  
TDAEKDAIVNKHNELRQRVASGKEMRGTNGPQPPAVKMPNL TWDP ELATIAQRWANQCTF  
EHDACRNVERFAVGQNI AATSSSGKNKSTPNEMILLWYNEVKDFDNRWISSFP SDDNILM  
KVGHYTTQIVWAKTTKIGCGRIMFKEPDNWT KHYLVCNYGPAGNVLGAPIYEIKK

>AAB72147.1 Bla g 5; glutathione S-transferase [*Blattella germanica*]  
YKLTYPVKALGEPPIRFLLSYGEKDFEDYRFQEGDWPNLKPSMPFGKTPVLEIDGKQTHQ  
SVAISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDADENSKQKKWDPLKK  
ETIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQP NLKALRE  
KVLGLPAIKAWVAKRPPTDL

>AAB69424.1 Der p 10; tropomyosin [*Dermatophagoides pteronyssinus*]  
MEAIKKKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV  
QEQLSAANTKLEEKEKALQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA  
DESERMRKMLEHRSITDEERMEGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEKYKSISDELDQTF AELTGY

>CAA50281.1 Phl p 5; unknown function [*Phleum pratense*]  
ADLGYGPATPAAPAAGYTPATPAAPAGADAAGKATTEEQK LIEKINAGFKAALAGAGVQP  
ADKYRTFVATFGPASNKAF AEGLSGEPKGAAESSKAALTSKLDAAVKLAYKTAEGATPE  
AKYDAYVATLSEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAANA  
APANDKFTVFEEAFNDEIKASTGGAYESYKFI PALEAAVKQAYAATVATAPEVKYTVFET  
ALKKAITAMSEAQKAAK PAAAATATATAAVGAATGAATAATGGYKV

>CAA81609.1 Phl p 5; unknown function [*Phleum pratense*]  
AAAAVPRRGPRGGPGRSYTADAGYAPATPAAAGAAAGKATTEEQK LIEDINVGFKAAVAA  
AASVPAADKFKTFEAAFTSSSKAAAAPGLV PKLDAAYSVAYKAAVGATPEAKFDSFVA  
SLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAATAPADDK  
FTVFEEAFNKAIKESTGGAYD TYKCIPSLEAAVKQAYAATVAAAAPQVKYAVFEAALTKAI  
TAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>CAA96545.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFNYETETTSVIPAARLFKAFFLDGDNLF PKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFRYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKEEQIKASKEMGETLLRAVESYLLAHS DAYN

>CAA70608.1 Phl p 12; profilin [*Phleum pratense*]  
MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAGAKY MVIQGEPEGAVIRGKKGAGGITIKKTGQALVVG IYDEPMTPGQCNM VVE  
RLGDYLVEQGM

>CAA70609.1 Phl p 12; profilin [*Phleum pratense*]  
MSWQTYVDEHLMCEIEGHHLASAAIFGHDGTVWAQSADFPQFKPEEITGIMKDLDEPGHL  
APTGMFVAAA KY MVIQGEPEGAVIRGKKGAGGITIKKTGQALVVG IYDEPMTPGQCNM VVE  
RLGDYLVEQGM

>CAA75141.1 Der p 10; tropomyosin [*Dermatophagoides pteronyssinus*]  
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV  
QEQLSAANTKLEEKEKALQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA  
DESERMRKMLEHRSITDEERMEGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE  
FAERSVQKLQKEVGRLEDELVHEKEKYKSISDELDQTF AELTGY

>AAD13683.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVYTFENEY TSEIPPPRLF KGFVL DADNLI PKIAPQA I KHAEI LEGDGGPGTIKKITFG  
EGSQYGYVKKHIDSVD EANYSYAYTLIEGDALDTIEKVS YETKLVASGSGSIIKSISHY  
HTKGDVEIKEEHVKAGKEKAHGLFKLIESY LKHPDAYN

>CAA73038.1 Ole e 1; Ole e 1-like [*Olea europaea*]  
MEDVPQPPVSQFHIQGVYCDTCRAGFITELSEFIPGASVRLQCKDKENG DVTFT EIGYT  
RAEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNP

LRFYKKEALPKCAQVYNKLGMYPPNM

>CAA73037.1 Ole e 1; Ole e 1-like [Olea europaea]  
MEDVPQPPVSQFHIQGVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDVTFTEIGYT  
RAEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILSTVNGTTRTVNP  
LGFYKKEALPKCAQVYNKLGMYPPNM

>CAA73036.1 Ole e 1; Ole e 1-like [Olea europaea]  
MEDVPQPPVSQFHIQGVYCDTCRSRIFITELSEFIPGASVRLQCREKENGDITFTEIGYT  
RAEGLYSMLVERDHKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTVNP  
LGFFKKEALPKCAQVYNKLGMYPPNM

>CAA73035.1 Ole e 2; profilin [Olea europaea]  
MSWQAYVDDHLMCDIEGHEDHRLTAAAIVGHGDSVWAQSATFPQFKPEEMNGIMTDFNEP  
GHLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEPPVTPGQCNM  
VVERLGDYLVEQGM

>Q28050.1 Bos d 3; calcium-binding protein [Bos taurus]  
MSSSQLEQAITDLINLFHKYSGSDDTIEKEDLLRLMKDNFPNFLGACEKRGRDYLNSNIFE  
KQDKNKDRKIDFSEFLSLLADIATDYHNHSHGAQLCSGGNQ

>Q28133.1 Bos d 2; lipocalin [Bos taurus]  
MKAVFLTLLFGLVCTAQETPAEIDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIEC  
INDCESLSITFYLDKQGTCLLLTEVAKRQEGYVYVLEFYGTNTLEVIHVSENMLVTYVEN  
YDGERITKMTEGLAKGTSFTPEELEKYQQLNSERGVNENIENLIKTDNCPP

>P55958.1 Par j 2; lipid transfer protein [Parietaria judaica]  
MRTVSMALVIAALAWTSSAEPAPAPAGEEACGKVVQDIMPCLHFVKGEEKEPSKEC  
CSGTKKLSEEVKTTEQKREACKCIVRATKGISGINKELVAEVPKCDIKTTLPPITADFD  
CSKIQSTIFRGYY

>Q41260.1 Pha a 1; beta-expansin [Phalaris aquatica]  
MMKMVCSSSSSLLVVAALLAVFVGSQAQGIKAVPPGNITAEYGDKWLDKSTWYGKPTG  
AGPKDNGGACGYKDVDPKAPFNGMTGCGNTPIFKDGRGCGSFCFELKCSKPESCSGEPITVH  
ITDDNEEPIAPYHFDLSGHAFGSMKKGEEENVRGAGELELQFRRVKCKYDPDGTKPTFHV  
EKGSNPNYLALLVKYVDGDGDVAVDIKEKGDKWIELKESWGAIWRIDTPDKLTGPFTV  
RYTTEGGTKAEFEDVIPEGWKADTHDASK

>P56164.1 Pha a 5; unknown function [Phalaris aquatica]  
MAVQKYTMALFLAVALVAGPAAPTPTPTPLPPPRARDKATLTSRVEDINAASRRP  
WWASVPPADKFKTFADHVLCPNADVTSAAKAPQLKAKLDAAYRVAYEAAEGSTPEAKY  
DAFIAALTEALRVIAGAFEVHAVKPATEEVDVADPVGELQIVDKIDAAFKAATAANSAPA  
NDKFTVFEFAGFNKAIKESTAGAYETYKFIPLSLEAAVKQAYGATVARAPEVKYAVFEAGLT  
KAITAMSEAQKVAKPPLSPQPPQVPLAAGGAATVAAAASDVRVCRSHGTLQDACLLRG  
GCQPVVWRGGSHRARGGYKV

>P56165.1 unknown function [Phalaris aquatica]  
MAVQKYTVALFLAVALVAGPAALYAGDGYAPATPAASATLATPATPAASPOHAGTTEYHI  
VRKAGLNEEKNAARQTDDEQKRSDEINCPDFNKSVCRADRLPVCSSSTAHSKQDVAVM  
LGYGSIQGFSDMDDASVGSVSSEFHVIESAIEVITYIGEEVKVIPAGEVEVINKVKAFAST  
AATAADEAPANDKFTVVFSSFNKAIKETTGGAYAGYKFIPTLEAAVKQAYAASSATAPEV  
KYAVFETALKKAISAMSEAQKEAKPAAISAATTTISASTATPAAPPPPQLGTATPAAVA  
GGYKV

>P56166.1 unknown function [Phalaris aquatica]  
MAVQKYTVALFLAMALVAGPAASYAADAGTPTPATPAVPGAAAGKATTHEQKLIEDINA  
AFKWWPASAPPADKYKTFETAFSKANIAGASTKGLDAAYSVVYNTAAGATPEAKYDSFVT  
ALTEALRIMAGTLEHVAVKPATEEEVPSAKILRANSRSTRSSRFKIAATVATPLSHSTA  
ANSAPANDKFTVFEFAGFNKAIKERHGGPTETYKFIPLSLEAAVKQAYGATVARAPEVKYAV  
FEAGLTAKAITAMSEAQKVAKPVRLLSPQPPQVPLAAGGAATVAAAASDSRGGYKV

>P56167.1 unknown function [*Phalaris aquatica*]  
AKYDAFIAALTEALRVIAGAFEVHAVKPATEEVPAAKIPAGELQIVDKIDA AFKIAATAA  
NSAPANDKFTVFEFAGFNKAIKERHGGAYETYKFIPSLEASRSKQAYGATVARAPEVKYAV  
FEAGLTKAITAMSEAQKVAKPVRSVTAAAAGAATAAGGAATVAASRPTSAGGYKV  
>P02221.2 Chi t 2; hemoglobin [*Chironomus thummi thummi*]  
MKFLILALCVAAAMAGPSGDQIAAAKASWNTVKNNQVDILYAVFKANPDIQTAFS QFAGK  
DLDSIKGTPDFSKHAGR VVGLFSEVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDN  
FRKSLVVYLK GATKWDSAVESSWAPVLDVFVSTLKNEL  
>P02224.2 Chi t 3; hemoglobin [*Chironomus thummi thummi*]  
MKFLVLALCIAAASAAVLTTEQADLVKKTWSTVKFNEVDILYAVFKAYPDIMAKFPQFAG  
KDLSIKDSAAFATHATRIVSFLSEVISLAGSDANIPAIQNLAKELATSHKPRGVSKDQF  
TEFRTALFTYLKAHINF DGPTETA WTLALDTTYAMLFSAMDS  
>CAA05186.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFN YETETTSVIP AARLFKAFILDGDNLV PKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA05187.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFN YETETTSVIP AARLFKAFILDGDNLV PKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA05188.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFN YETETTSVIP AARLFKAFILDGDNLV PKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA05190.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
MGVFN YETETTSVIP AARLFKAFILDGDNLV PKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>AAB82404.1 Per a 1; nitrile-specifier protein [*Periplaneta americana*]  
MKLPIMILAVLGVAFGKSLPNRNLQDDLNDFLALLPVDEITAI VMDYLANDAEVQEAVAY  
LQGE EFHKIVFTVEGLQEFGNFVQFLEDHGLDAVG YINRLHSVFGWDPYVPSSKRKHTRR  
GVGVDGLIDDIIAILPIDDLKALFQEKLETSPDFKAFYDAVRSPEFQSIVQTLNAMPEYQ  
DLLQKLRDKGVDVDHYIELIRALFGLTRAARNLQDDLNDFLAL IPTDQILAIAMDYLAND  
AEVQELVAYLQSDDFHKIINTIEALPEFANFYNFLKGHGLDVADYINEIHSIIGLPPFVP  
PSRRHARRGVGINGLIDDVIAILPVDELKALFQEKLETSPDFKALYDAIRSPEFQSIIST  
LNAMPEYQELLQNL RDKAVD VDHFIELIRSLFGLP  
>AAC48794.1 Can f 1; lipocalin [*Canis familiaris*]  
MKTL LLLTIGFSLIAILQAQDTPALGKDTVAVSGKWY LKAMTADQEVPEKPD SVTPMILKA  
QKGGNLEAKITMLTNGQCQ NITVVLHKTSEPGKYTAYEGQRV VFIQPSPVRDHYILYCEG  
ELHGRQIRMAKLLGRDPEQSQEAL EDFREFSRAKGLNQEILELAQSETCSPGGQ  
>AAC48795.1 Can f 2; lipocalin [*Canis familiaris*]  
MQL LLLTVGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLIKPWGHFRVFI  
HSMSAKDGNLHGDILIPQDGQCEKVSLTAFKTATS NKFDLEYWGHNDLYLAEVDPKSYLI  
LYMINQYND DTSLV AHLMVRDL SRQQDFLPAFESVCE D IGLHKDQIVVLSDDDR CQGSRD  
>AAB86960.1 Zea m 12; profilin [*Zea mays*]  
MSWQAYVDEHLMCEIEGQHL SAAAI VGH DGSVWAQSESFPELKPEEVAGI IKDFDEPGTL

APTGLFVGGTKYMVIQGEPIVIRGKKGTTGGITIKKTGMSLIIGVYDEPMTPGQCNMVVE  
RLGDYLIEQGF

>AAC48287.1 Hom a 1; tropomyosin [Homarus americanus]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKTEEEIRITHKKMQQVENELDQV  
QEQLSLANTKLEEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLEDELVNEKEKYKSITDELDTFSELSGY

>AAC48288.1 Hom a 1; tropomyosin [Homarus americanus]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANTQLEEKDALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLEDELVNEKEKYKSITDELDTFSELSGY

>AAB97141.1 Pru ar 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus  
armeniaca]

MGVFTYETEFTSVIPPEKLFKAFILDADNLIPKVAPTAVKGTETILEGDDGGVGTIKKVTFG  
EGSQYAYVKHRVDGIDKDNLSYSYTLIEGDALSDVIENIAYDIKLVASPDGGSIVKTTSH  
YHTKGDVEIKEEQVKAGKEKAAGLFLVEAYLLANPDAYN

>AAD13644.1 unknown function [Ascaris lumbricoides]  
HHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKDLQAKILYYYDELEGDAKKEATEHL  
KDGCREILKHVVGEEKEAELKCLKDSGASKEEVKAKVEEALHAVTDEEKKQYIADFGPAC  
KKIFAAAHTSRRRR

>AAD13645.1 unknown function [Ascaris lumbricoides]  
HHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKDLQAKILHYYDELEGDAKKEATEHL  
KDGCREILKHVVGEEKEAELKCLKDSGASKEEVKTKVEEALHAVTDEEKKQYIADFGPAC  
KKIFGAAHTSRRRR

>AAD13646.1 unknown function [Ascaris lumbricoides]  
HHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKDLQAKILHYYDELEGDAKKEATEHL  
KDGCREILKHVVGEEKEAELKCLKDSGASKEEVKAKVEEALHAVTDEEKKQYIADFGPAC  
KKIFGAAHTSRRRR

>AAD13647.1 unknown function [Ascaris lumbricoides]  
HHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKELEAKILHYYDELEGDAKKEATEHL  
KGGCREILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTDEEKKQYIADFGPAC  
KKIYGVHTSRRRR

>AAD13649.1 unknown function [Ascaris lumbricoides]  
HHFTLESSLDTHLKWLSQEQKDES LKMKKGGKAKKELEAKILHYYDEPEGDAKKEATEHL  
KGGCREILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVIDE EKKQYIADFGPAC  
KKIFGVHTSRRRR

>AAD13650.1 unknown function [Ascaris lumbricoides]  
HTMEHYLKTYLSWL TEEQEKLEKEMKEAGQTKAEIQHEVMHYDQLHGEEKQQATEKLV  
GCKMLLKGIIIGEEKVVELRNVKEAGADIQELQKQVEKMLSEVTDEKQKEKVHEYGPACKK  
IFGATTLQHRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYYD  
ELEGDAKKEATEHLKGGCPEILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTD  
EKKQYIADFGPACKKIYGVHTSRRRR

>AAD13651.1 unknown function [Ascaris lumbricoides]  
HTMEHYLKTYLSWL TEEQEKLEKEMKEAGKTKAEIQHEVMRYDQLHGEEKQQATEKLV  
GCKMLLKGIIIGEEKVVELRNMKEAGADIQELQKQVEKMLSEVTDEKQKEKVHEYGPACKK  
IFGATTLQHRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYYD  
ELEGDAKKEATEHLKGGCREILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTD

EEKKQYIADFGPACKKIYGVHTSRRRR

>AAD13652.1 unknown function [*Ascaris lumbricoides*]  
HTMEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHYDQLHGEEKQQATEKLV  
GCKMLLKGIIIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK  
IFGATTLQHRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKELEAKILHYD  
ELEGDADKEATEQLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTD  
EEKKQYIADFGPACKKIYGVHTSRRRR

>AAB93837.1 unknown function [*Ascaris lumbricoides*]  
HTMEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMRYDQLHGEEKQQATEKLV  
GCKMLLKGIIIGEEKVVELRNMKEAGADIQELRQKVEKMLSEVTDEKQKEKVHEYGPACKK  
IFGATTLQHRRRR

>AAB93839.1 unknown function [*Ascaris lumbricoides*]  
HTMEHYLKTYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLV  
GCKMLLKGVIIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK  
IFGATTLQHRRRR

>AAC67308.1 unknown function [*Schistosoma japonicum*]  
MATTEYRLSLMEQFIRAFIEIDKDNELIDKQELTKYCQQNQMDMKQIDPWIARFDTDKD  
GKVSLEEFRCRFGFLKVVWRREKEELKKDKEGKVESTLPLDIQIIAATMSKAKQYNICCKF  
KELLDKTSRTGDEVRAVANDLKAFLDSEYGRVWQVIILTGSYWMNFSHEPFLSMQFKYSN  
YVCLLWRTPSS

>AAB95638.1 Asp f 3; peroxisomal protein [*Aspergillus fumigatus*]  
MSGLKAGDSFSPDVVFSYIPWSEDKGEITACGIPINYNASKEWADKKVILFALPGAFTPV  
CSARHVPEYIEKLEPEIRAKGVDVAVLAYNDAYVMSAWGANQVTGDDILFLSDPDARFS  
KSIWADEEGRTKRYALVIDHGKITYAALEPAKNHLEFSSAETVLKHL

>AAB99797.1 unknown function [*Oryza sativa*]  
MASNKVVFVLLAVVSVLAATATMAEYHHQDQVYVTPGPLCQPGMGYPMYPLRVAGVGE  
APLLGRARPRRRRAVPDCCRQFPVDYSWCRCEAISHMLGGIYRELGAPDVGHMSEVFR  
GCRRGTWSARRRAPGVLQVDIPNGGGGVCYWLARSGY

>CAA05978.1 Hev b 6; hevein [*Hevea brasiliensis*]  
EQCGRQAGGKLCNNLCCSQWGWCGSTDEYCSPDHNCQSCKDSGEGVGGGSASNVLATY  
HLYNSQDHGWDLNAASAYCSTWDANKPYSWRSKYGWTAFCGPVGAHGQPSCGKCLSVTNT  
GTGAKATVRIVDQCSNGGLDLVNVFRQLDTDGKGYERGHLLTVNYQFVDCGDSFNPLFSV  
MKSSVIN

>Q25641.1 Per a 3; hemocyanin, arylphorin [*Periplaneta americana*]  
MKTALVFAAVFAARFPDHDYKQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVGI  
PMTSKQTSATTVPSPGEAVHGVLEQGHARPRGEPFSVNYEKHREQAIMLYDLLYFANDYD  
TFYKTACWARDRVNEGFMYSFSIAVFHRDDMQGVMLPPPYEVYYPYLFVDHVDVIHMAQKY  
WMKNAGSGEHHSHVIPVNFTRLRTQDHLLAYFTSDVNLNAFNYYRYYPSWYNTTLYGHN  
IDRRGEQFYTYKQIYARYFLERLSNDLPDVYFPYYSKPVKSAYNPNLRYHNGEEMPVRP  
SNMYVTNFDLYYIADIKNYEKRVEDAIDFGYAFDEHMKPHSLYHDVHGMEYLADMIEGNM  
DSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPSLEHPETVLRDPVFYQLWKRVDHLFQK  
YKNRLLPRYTHDELAFEGVKVENVDVGLTYTYFEQYDMSLDMAVVYNNVDQISNVDVQLAV  
RLNHKPFYTYNIEVSSDKAQDVYVAVFLGPKYDYLGREYDLNDRRHYFVEMDRFPYHVGAG  
KTVIERNSHDSNIIAPERDSYRTFYKKVQEAIEGKSQYVVDKGHNKCGYPENLLIPKGGK  
GGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVGSERKYPDNKPLGYPFDRKIYSNDF  
YTPNMYFKDVIIFHKKYDEVGQGH

>CAA11266.1 Asp f 9; unknown function [*Aspergillus fumigatus*]  
KRSFILRSADMYFKYTAALAAVPLPLCSAQTSKCNPLEKTCPPNKGLAASTYTADFTSA  
SALDQWEVTAGKVPVGPQGAFTVAKQGDAPTIDTDFYFFFGKAEVVMKAAPGTGVVSSI  
VLESDDLDEVDWEVLGGDTTQVQNTNYFGKGDTTTTYDRGTYVPVATPQETFHTYIDWTKD

AVTWSIDGAVVRTLTYNDAKGGTRFPQTPMRLRLGWSWAGGDPSPKGTIEWAGGLTDYSA  
GPYTMVYKSVRIENANPAESYTYSDNSGWSQSIKFDGSVDISSSSSVTSSTTSTASSASS  
TS

>CAA75803.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [*Solanum lycopersicum*]

MGVNTYTYESTTTISPTLRFKALVLDLDFDNLVPKLLSQHVKNNETIEGDGGVGSIKQMNFB  
EGGPIKYLKHKIHHVIDDKNLETKYSLIEGDILGEKLESITYDIKFEANDNGGCVYKTTE  
YHTKGDHVVSEEEHNVGRRENHEYFQGCRSIPSRESFCLRLNIDEKESGLHVRNYACT

>AAC34312.1 Per a 1; nitrile-specifier protein [*Periplaneta americana*]

SIISTLNAMPEYQDLLQNLRDKGVDVDHYIELIRALFGLTRAARNLQDDLNDLFLALIPTD  
QILAIAMDYLANDAEVQELVAYLQSDDFHKIITTTIEGLPEFANFYNFLKEHGLDVADFLN  
EIHIIIGLPPFVPPSRRHARRGVINGLIDDVIAILPVDELKALFDEKLETSPDFKALYD  
AIRSPEFQSIISTLNAMPEYQDLLQNLRDKGVDVDHFIELIRSLFGLP

>CAA73720.1 Mer a 1; profilin [*Mercurialis annua*]

MSWQTYVDDHLMCDIDGQGQHLAAASIVGHDGSIWAQSASFQPKPEEITGIMKDFDEPG  
HLAPTGLYIAGTKYMIQGESGAVIRGKKGSGGITIKKTGQALVFGIYEEPVTPGQCNMV  
VERLGDYLIEQGM

>CAA76556.1 Phl p 6; unknown function [*Phleum pratense*]

MAAHKFMVAMFLAVAVVLGLATSPTAEGGKATTEEQKLIEDINASFRAAMATTANVPPAD  
KYKTFEAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSE  
ALHIIAGTPEVHAVKPGA

>CAA76557.1 Phl p 6; unknown function [*Phleum pratense*]

MAAHKFMVAMFLAVAVVLGLATSPTAEGGKATTEEQKLIEDVNASFRAAMATTANVPPAD  
KYKTFEAAFTVSSKRNLADAVSKAPQLVPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSE  
ALRIIAGTPEVHAVKPGA

>CAA76558.1 Phl p 6; unknown function [*Phleum pratense*]

TEEQKLIEDVNASFRAAMATTANVPPADKYKTLAAFTVSSKRNLADAVSKAPQLVPKL  
EVYNAAYNAADHAAPEDKYEAFVLHFSEALRIIAGTPEVHAVKPGA

>CAA04959.1 Asp f 4; unknown function [*Aspergillus fumigatus*]

GEVGDVTYATINGVLVSWINEWSGEAKTSDAPVSQATPVSNAAAAAASTPEPSSSHSD  
SSSSSGVSADWTNTPAEGEYCTDGFGRTEPSGSGIFYKGNVGPWGSNIIEVSPENAKK  
YKHVAQFVGSDDPWTVWFNKGIPDGGLTGWYGNSALTLHLEAGETKYVAFDENSQGAW  
GAAKGDELPKDQFGGYSCTWGEFDFDSKINHGWSGWDVSAIQAENAHHEVQGMKICNHAG  
ELCSIISHGLSKVIDAYTADLAGVDGIGKVVPGPTRLVVNLDYKE

>CAA06305.1 Asp f 1; ribonuclease mitogillin, partial [*Aspergillus fumigatus*]

RLVYNQAKAESNSHHAPLSDGKTGSSYPHFWTNGYDGDGKLIKGRMPIKFGKADCDRPPK  
HGKDGMGKDDHYLLEFPTFPDGHDKFDSKPKEDPGPARVIYTPNKVFCGIVAHGERGN  
QGDLR

>CAA11755.1 Gly m 3; profilin [*Glycine max*]

MSWQAYVDDHLLCGIEGNHLTHAAIIGQDGSVWLQSTDFPQFKPEEITAIMNDFNEPGSL  
APTGLYLGGTKYMIQGEPAVIRGKKGPGGVTVKKTGAALIIGIYDEPMTPGQCNMVVE  
RLGDYLIDQGY

>CAA11756.1 Gly m 3; profilin [*Glycine max*]

MSWQAYVDDHLLCDIEGNHLTHAAIIGQDGSVWAQSTDFPQFKPEEITAIMNDFNEPGSL  
APTGLYLGGTKYMIQGEPAVIRGKKGPGGVTVKKTGAALIIGIYDEPMTPGQCNMVVE  
RPGDYLDQGY

>AAC38996.1 Pan s 1; tropomyosin [*Panulirus stimpsoni*]

MKLEKDNAMDRADTLEQQNKEANIRAEEKAEVEVHNLQKRMQQLENDLDQVQESLLKANTQ  
LEEKDKALSNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAADSERMRKVL  
ENRSLSDAERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAEERAETGESKF

VELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAFAERSVQKLQ  
KEVDRLEDELVNEKEYKSITDELDQTFSELSGY

>CAA11041.1 Hev b 7 patatin [*Hevea brasiliensis*]

MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDLDPDARIADYFDIIAGT  
STGGLITMTLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIHSIGPIYDGEY  
LRELCNNLLKDLTVKDTLTDVVIPTFDIKLLLPVIFSSDDAKCNALKNARLADVCISTSA  
APVLLPAHSFTTEDDKNIHTFELIDGGAAATNPTLLALHIRNEIIRQNPRFIGANLTES  
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL  
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTRLLEKQESRINLDTGRLES  
IPGASTNEAAITKFAKLLSEERKLRQLK

>BAA25899.1 thiol protease [*Glycine max*]

MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE  
EAKRLEIFKNNLNIRDMNANRKSPPHSHRGLGNKFADITPQEFSSKKYLQAPKDVSQQIKM  
ANKKMKKEQYSCDHPASWDWRKKGVITQVKYQGGCGSGWAFSATGAIEAAHAIATGDLV  
SLSEQELVDCVEESEGCYNGWHYQSFVWLEHGGIATDDDPYRAKEGRCKANKIQDKVT  
IDGYETLIMSDESTESETEQAFLSAILEQPISVSIKADDFHLYTGGIYDGENCTSPYGIN  
HFVLLVGYGSADGVYWIAKNSWGEDWGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES  
ETLVSARVKGHRRVDHSPL

>P81216.1 Equ c 2; lipocalin [*Equus caballus*]

SQXPQSETDYSQLSGEWNTIYGAASNIXK

>P81217.1 Equ c 2; lipocalin [*Equus caballus*]

QDPQSETDYSQLSGEWNT

>AAC16525.1 Phl p 5; unknown function [*Phleum pratense*]

ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT  
FGAASNKAFAEGLSAEPKGAEESSKAALTSKLDAAAYKLAYKTAEGATPEAEYDAYVATL  
SEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDSALKVAATAANAAPANDKFTVF  
EAAFNNAIKASTGGAYESYKFIPALEAAVKQAYAAATVATAPEVKYTVFETALKKAITATS  
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>AAC16526.1 Phl p 5; unknown function [*Phleum pratense*]

ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT  
FGAASNKAFAEGLSAEPKGAEESSKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATL  
SEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF  
EAAFNNAIKASTGGAYESYKFIPALEAAVKQAYAAATVATAPEVKYTVFETALKKAITAMS  
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>AAC16527.1 Phl p 5; unknown function [*Phleum pratense*]

ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT  
FGAASNKAFAEGLSAEPKGAEESSKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATL  
SEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF  
EAAFNNAIKASTGGAYESYKFIPALEAAVKQAYAAATVATAPEVKYTVFETALKKAITAMS  
EAQKAAPAAAATATATS AVGAATGATTAAGGYKV

>AAC16528.1 Phl p 5; unknown function [*Phleum pratense*]

ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT  
FGAASNKAFAEGLSAEPKGAEESSKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATL  
SEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF  
EAAFNNAIKASTGGAYESYKFIPALEAAVKQAYAAATVATAPEVKYTVFETALKKAFTAMS  
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>CAA75312.1 Hev b 8; profilin [*Hevea brasiliensis*]

MSWQTYVDERLMCEIEGNHLTAAAIIGQDGSVWAQSSNFPQFKSEEITAIMSDFDEPGTL  
APTGLHLGGTKYMIQGEAGAVIRGKKGPGGVTVRKTNQALIIIGIYDEPMTPGQCNMIVE  
RLGDYLLEQGM

>CAB01591.1 Pers a 1; chitinase [*Persea americana*]  
MVYCTASLPLLLLLLVGLLAGEAFAEQCGRQAGGALCPGGLCCSQFGWCGSTSDYCGPTC  
QSQCQGVTPSPGGVASLISQSVFNQMLKHRNDAACQAKGFYTYNAFIAAANSFNGFASV  
GDTATRKREIAAFLAQTSHETTGGWATAPDGPYAWGYCFLKEQGNPPDYCVPTAQWPCAP  
GKKYYGRGPIQISYNYNYGPAGRAIGYDLINNPDAVATDPVISFKTALWFWMTQSPKPS  
CHNVITGRWTPSAADRAAGRLPGYGVITNIINGGIECGKGFNDKVADRIGFYKRYCDLLG  
VSYGSNLDCYNQRSFGVSTNPLAASS

>AAC24001.1 Pyr c 5; isoflavon reductase-like protein, phenylcoumaran benzylic  
ether reductase [*Pyrus communis*]  
MASKSQILFIGGTGYIGKFIVEASAKAGYPTYVLLVREASLSDPAKSKVIENFKALGVNFV  
LGDLYDHESLVKAIKQVDVWISTVGHGQLADQGKIIAAIKEAGNVKRRFFPSEFGNDVDRS  
HAVEPAKSAFETKAKIRRAVEAEGIPYTYVSSNFFAGYFLPTLNQPGASSAPRDKVWILG  
DGNPKAIFNKEDDIGTYTIRAVDDPRTLNVLYIRPPANTISFNELVSLWEKKIGKTLER  
IYVPEEQLLKNIQEAAPLVNLSISHAVFVKGDHTNFEIEPSFGVEATALYPDVKYTTV  
DEYLNQFV

>CAA54818.1 Lig v 1; Ole e 1-like [*Ligustrum vulgare*]  
EDVPQPPVSQFYIQGQVYCDTCRARFITELSEFIPGAGVRLQCKDGENGKVTFTTEVGYTK  
AEGLYNMLIERDHKNEFCEITLISSSRKDCDEIPIEGWVKPSLKFVLTNTVNGTTRTINPL  
GFLKKEVLPKCPQVFNKLGMYPPNM

>CAA54819.1 Lig v 1; Ole e 1-like [*Ligustrum vulgare*]  
EDVPQPPVSQFYIQGQVYCDTCRARFITELSEFIPGAGVRLQCKDGENGKITFTEVGYTR  
AEGLYSMLIERDHKNEFCEITLISSSRKDCDEIPIEGWVKPSLKFMLNTVNGTTRTINPL  
GFFKKEALPKCPQVFNKLGMYPPNM

>P81402.1 Pru p 3; lipid transfer protein [*Prunus persica*]  
ITCGQVSSALAPCIPYVRGGGAVPPACCNGIRNVNMLARTTPDRQAACNCLKQLSASVPG  
VNPNNAAALPGKCGVHIPYKISASTNCATVK

>CAA11042.1 Hev b 7; patatin [*Hevea brasiliensis*]  
MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDLDPDARIADYFDIIAGT  
STGGLITTMLTAPNEDKKPIYQAKDIKDFYLENCPKIFPKESRDYDPIHSIGPIYDGEY  
LRELCNNLLKDLTVKDTLTDVVIIPAFDIKLLLPVIFSSDDAKCNALKNARLADVCISTSA  
APVLLPAHSFTTEDDKNIHTFELIDGGVAAAANPTLLALHTRNEIIRQNPRFIGANL TES  
KSRLVLSLGTGKSEYKEKNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL  
FKSLDCEDYYLRIQDDTLTGEESSGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES  
IPGAPTNEAAIAKFAKLLSEERKLRQLK

>AAC25994.1 Phl p 5; unknown function [*Phleum pratense*]  
MAVHQYTVALFLAVALVAGPAGSYAADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKAT  
TEEQKLIIEKINAGFKAALAAAAGVPPADKYRTFVATFGAASNKAFAEGLSGEPKGAAESS  
SKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATVSEALRIIAGTLEVHAVKPAEEVK  
VIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYESYKFIPA  
LEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQAQKAAKAAAATATATAAVGAAT  
GAATAATGGYKV

>AAC25995.1 Phl p 5; unknown function [*Phleum pratense*]  
SVKRSNGSAEVHRGAVPRRGRGGPGRSYAADAGYAPATPAAAGAEAGKATTEEQKLIED  
INVGFKAAVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVPKLDAAYSVAAYKAAVGA  
TPEAKFDSFVASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFVAA  
TAAATAPADDKFTVFEAAFNKAIKESTGGAYDYTKCIPSLEAAVKQAYAATVAAAAPQVKY  
AVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>AAC25997.1 Phl p 5; unknown function [*Phleum pratense*]  
MAVQKYTVALFLAVALVAGPAASYAADAGYAPATPAAAGAEAGKATTEEQKLIEDINVG  
KAAVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVPKLDAAYSVAAYKAAVGAATPEAK

FDSFVASLTEALRVIAGALEVHAVKPVTEPAWPKIPAGELQIIDKIDAAFVAATAAAT  
APADDKFTVFEAAFNKAIKESTGGAYDXYKCIPSL EAAVKQAYAATVAAAPQVKYAVFEA  
ALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATVAAGGYKV  
>AAC25998.1 Phl p 5; unknown function [Phleum pratense]  
MAVQKYTVALFLAVALVAGPAASYAADAGYAPATPAAAGAEAGKATTEEQKLIEDINVG  
KAAVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVPKLDAAYSVSYKAAVGATPEAK  
FDSFVASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFVAATAAAT  
APADTVFEAAFNKAIKESTGGAYDXYKCIPSL EAAVKQAYAATVAAAPQVKYAVFEAAL  
KAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV  
>CAA76831.1 Aln g 4; calcium-binding protein, polcalcin [Alnus glutinosa]  
MADDHPQDQAEHERIFKCFDANGDGKISASELGDALKTLGVSVPDEVKHMMAEIDTDGDG  
FISFQEFTNFARANRGLVKDVAKIF  
>CAA76841.1 Can f 3; serum albumin [Canis familiaris]  
MDTYKSEIAHRYNDLGEEHFRGLVLFVAFSQYLQCPDFEDHVKLAKVTEFAKACAAEESG  
ANCDKSLHTLFGDKLCTVASLRDKYGDMDACCQEPDRNECF LAHKDDNPGFPPLVAPE  
PDRLCAAFQDNEQLFLGKLYEYIARRHPYFYAPELLYYAQQYKGVFAECCQAADKAACLG  
PKTEALREKVL LSSAKERFKCASLQKFGDRAFKAWSVARLSQRFPKADFAEISKVVDLT  
KVHKECCHGDLLECADDRADLAKYMCENQDSISTKLKECCDKPVLEKSQCLAEVERDEL  
GDLPSLAADFVEDKEVCKNYQEAKDAFLGTFLEYSRRHPEYSVSLLLRLAKEYEATLEK  
CCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCELFEKLGEGFQNALLVRYTKKAPQVS  
TPTLVEVSRKLGKVGTKCKKPESERMSCADDFLSVVLNRLCVLHEKTPVSEVTKCCSE  
SLVNRPCFSGLEVDETYVPKEFNAETFTFHADLCTLPEAEKQVKKQTALVELLKHKPKA  
TDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLVAAAQAAALV  
>CAA76847.1 Bos d 6; serum albumin [Bos taurus]  
MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHRFKDLGEEHFKGLVLIAFSQYLQCPDF  
DEHVKL VNELTEFAKTCVADESHAGCEKSLHTLFGDELCKVASLRETYGDMACCQEP  
ERNECF LSHKDDSPDL PKLKPDPNTLCDEFKADEKKFWGKLYEYIARRHPYFYAPELLYY  
ANKYNGVFQEQCAEDKGACLLPKIETMREKVL TSSARQRLRCASIQKFGERALKAW  
SVARLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLECADDRADLAKYICDNQDTISS  
KLKECCDKPLLEKSHCIAEVEKDAIPENLPLTADFAEDKDVCKNYQEAKDAFLGSLY  
EYSRRHPEYAVSVLLRLAKEYEATLECCAKDDPHACYSTVFDK LKHLVDEPQNLIKQ  
NCDQFEKLGEGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESE  
RMPCTEDYLSLILNRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDETYVPKAF  
DEKLFTHADICTLPDTEKQIKKQTALVELLKHKPKATEEQKLTVMENFVAFVDKCCA  
ADDKEACFAVEGPKLVVSTQ TALA  
>AAD05375.1 Ole e 3; calcium-binding protein, polcalcin [Olea europaea]  
MADDPQEVAEHERIFKRFDANGDGKISSSELGETLKTGVSVPTEEIQRMMAEIDTDGDG  
FISFEEFTVFARANRGLVKDVAKIF  
>CAA08836.1 alpha-amylase inhibitor [Hordeum vulgare]  
MGAMWMSMLLVLLLCLMVTPMTGARS DNSGPMWCDPEM GHKVSPLTRCRALVKLECV  
GNRVPEDVLRDCCQEVANISNEWCRCGDLGSM LRSVYAALGVGGGPEEVFPGCQKDV  
MKLVAGVPALCNVPIPNAAAGTRGVCYWSASTDT  
>CAA76887.1 Phl p 7; calcium-binding protein, polcalcin [Phleum pratense]  
MADDMERIFKRFDTNGDGKISLSELTALRTL GSTSADEVQRMMMAEIDTDGDGFIDFNE  
FISFCNANPGLMKDVAKVF  
>BAA32435.1 Mala f 2; peroxisomal protein [Malassezia furfur]  
MPGDPTATAKNEIPDTLMGYIPWTPELD SGVCGIPTTFKTRDEWKGKKVIVSIPGAY  
TPICHQHQHIPPLVKRVDLAKAGVDAVYVIA SNDFVMAAWGNFNNAKDKVVFATDIDL  
A FSKALGATIDLSAKHFGERTARYALIIDDNKIVDFASDEGDTGKLQNASIDTILTKV  
>BAA32436.1 Mala f 3; peroxisomal protein [Malassezia furfur]

EIGSTIPNATFAYVPYSPELEDHKVCGMPTSFQSHERWKGKKVIVAVPGAFTPTCTANH  
VPPYVEKIQELKSKGVDEVVVISANDPFVLSAWGITEHAKDNLTFAQDVNCEFSKHFNAT  
LDLSSKGMGLRTARYALIANDLKVEYFGIDEGEPKQSSAATVLSKL  
>CAA75506.1 He1 a 2; profilin [*Helianthus annuus*]  
MSWQAYVDEHLMCDIEGTGQHLTSAAILGLDGTVWAQSAKFPQFKPEEMKGIKEFDEAG  
TLAPTGMFIAGAKYMLVQGEPAVIRGKKGAGGICIKKTGQAMIMGIYDEPVAPGQCNMV  
VERLGDYLLEQGM  
>AAC36740.1 Mal d 2; thaumatin-like [*Malus domestica*]  
MMKSQVAPRPTLAILFFFSGAHAAKITFTNCPNTVWPGTLTGDKPQLSLTGFELASKA  
SRSVDAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSQVACNGAGAVPPATLVEITIAA  
NGGQDYDVSVDGFNLPMVAPQGGTGECKPSSCPANVNKVCAPLQVKAADGSVISCK  
SACLAFGDSKYCCTPPNTPETCPPTSEIFEKQCPQAYSAYDDKNSTFTCSGGPDYV  
ITFCP  
>AAC61869.1 tropomyosin [*Crassostrea virginica*]  
RNRKVLNENLNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAITEVDLERAEARLE  
AAEAKVLELEEEELKVVGNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRATEAER  
TVSKLQKEVDRLEDELLAEKERYKAISDELDQTFAELAGY  
>AAC63045.1 Ara h 3; 11S globulin, cupin [*Arachis hypogaea*]  
RQQPEENACQFQRLNAQRPNRIESEGGYIETWNPNNQEFECAGVALSRLVLRNALRRP  
FYSNAPQEIFIQQGRGYFGLIFPGCPRHYEEPHTQGRRSQSQRPPRRLQGEDQSQQQRDS  
HQKVHRFDEGLIAVPTGVAFWLYNDHDTDVAVSLTDTNNDNQLDQFPRRFNLAGNTE  
QEFRLRYQQSRQSRRLSLPYSYSPQSQPRQEEREFSRPGQHSRRERAGQEEENEENGNIF  
SGFTPEFLEQAFQVDDRQIVQNLRGETESEEEGAIIVTVRGGRLILSPDRKRRADEEEEEYD  
EDEYEDDEDRRRGRGRGRNGIEETICTASAKKNIGRNRSPDIYNPQAGSLKTANDLN  
LLILRWLGPSEAEGNLYRNALFVAHYNTNAHSIIYRLRGRAHVQVDSNGNRVYDEELQE  
GHVLLVVPQNFVAVAGKSQSENFYVAFKTDSPSIANLAGENSVIDNLPEEVVANSYGLQR  
EQARQLKNNNPFKFFVPPSQSPRAVA  
>CAA83015.1 Asp f 5; metalloprotease [*Aspergillus fumigatus*]  
MRGLLL LAGALALPASVFAHPAHQSYGLNRRTVDLNAFRLKSLAKYVNATETVIEAPSSFA  
PFPKQSYVEVATQHVKMIAPDATFRVDDHYVGDNGVAHVHFRQTANGLDIDNADFVNV  
GKDGKVSFSGNSFYTGQIPSSAALTKRDFSDPVTALKGTTNTLQLPITVDSASSESTEEK  
ESYVFKGVSQVSDPKAKLVYFVKDDGTLALAWRVETDIDSNWLLTYIDAKSGEEIHGVV  
DYVAEADYQVYAWGINDPTEGERTVIKDPWDSVASEFTWISDGSSTNYTTSRGNNGIAQSN  
PSGGPSYLNRYRPSSSSLSFKYPYSVSSSPSSYIDASIIQLFYTANIYHDLLYTLGFTE  
KAGNFYNTNGQGGLGNDYVILNAQDGGSTNNANFATPPDGQPGRMRMYVWTESTPYRDG  
SFEAGIVIHEYTHGLSNRLTGGPANSNCLNALESGGMGEGWSDFMATAIRLKPDKRSTD  
YTMGEWASNRRAGGIRQYPYSTSLSTNPLTYTSVNSLNAVHAIGTVWASMLYEVLLWNLIDK  
HGKNDAPKPTLRDGVPTDGKYLAMKLVMDGMALQPCNPNFVQARDAILDADTALTGGENQ  
CEIWTAFKRGLGAGAKYSSRNRVVGSTEVPSGVC  
>AAC82355.1 Hev b 3; small rubber particle protein [*Hevea brasiliensis*]  
MAEEVEEERLKYLDVRAAGVYAVDSFSTLYLYAKDISGPLKPGVDTIENVVKTVPVTPVY  
YIPLEAVKFVDKTVDSVTSLDGVVPPVIKQVSAQTYVAQDAPRIVLDVASSVFNTGVQ  
EGAKALYANLEPKAEQYAVITWRALNKLLVPQVANVVVPTAVYFSEKYNDVVRGTTEQG  
YRVSSYLPLLPTEKITKVFGEAS  
>CAA10140.1 Ho1 l 1; beta-expansin [*Holcus lanatus*]  
MASSSLVLLVVALFAVFLGTAHGIKAVPPGNITATYGDKWLDAKSTWYGKPTGAGPKDN  
GGACGYKDVDPKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPESCSGEPVWHITDDNE  
EPIAAHYHLDLSGKAFGAMAKKGEQKLRSALELELKFRRVKCEYKGTGKVTFFHVEKGSNP  
NYLALLVKYVDGDGDVAVDIKEKGDKWIELKESWGAVWRVDTDPDKLTGPFTVRYTTEG  
GTKVEADVIEGWKADTAYESK

>CAA81613.1 Phl p 1; beta-expansin [Phleum pratense]  
MASSSSVLLVVALFAVFLGSAHGIPKVPVPPGNITATYGDKWLDKSTWYGKPTAAGPKDN  
GGACGYKDVDPKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNE  
EPIAAYHFDLSGIAFGSMAKKGDQKLRSAQEVEIQFRRVKCKYPEGTKVTFHVEKGSNP  
NYLALLVKFVAGDGDVVAVDIKEKGDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEG  
GTKGEAKDVIPEGWKADTAYESK  
>P81496.1 unknown function, partial [Triticum aestivum]  
SFREQCVPGREITYECLNACAEYAVRQ  
>O24170.1 Ole e 2; profilin [Olea europaea]  
MSWQAYVDDHLMCDIEGHEGHRLTAAAIIVGHDGGSVWAQSATFPQFKPEEMNGIMTDFNEP  
GHLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEPPVTPGQCNM  
VVERLGDYLLLEQGL  
>O24171.1 Ole e 2; profilin [Olea europaea]  
MSWQAYVDDHLMCDIEGHEGHRLTAAAIIVGHDGGSVWAQSATFPQFKPEEMNGIMTDFNEP  
GHLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEPPVTPGQCNM  
VAERLGDYLLLEQGL  
>AAC82349.1 Eur m 2; NPC2-like [Euroglyphus maynei]  
MYKILCLSLVAVAADQVDIKDCANHEIKKVMVPGCKGSEPCVIHRGTAFQLEAVFDAN  
QNSNAKIEIKATIDGVEIDVPGIDNNLCHFMCPLVKGQEYDIKYTWNVPRIAPKSENV  
VVTVKLLGDNGVLACAIATHAKIRD  
>AAC82350.1 Eur m 2; NPC2-like [Euroglyphus maynei]  
VAVAADQVDVVKDCANHEIKKVMVPGCKGSEPCVIHRGTAFQLEAVFDANQNSNAKIEI  
KATIDGVEIDVPGIDNNLCHFMCPLVKGQEYDIKYTWNVPRIAPKSENVVVTVKLLGDN  
GVLACAIATHAKIRD  
>AAC82351.1 Eur m 1; cysteine protease [Euroglyphus maynei]  
MKIILAIASLLVLSAVYARPASIKTFFEEFKAFNKTYATPEKEEVARKNFLES�KYVESN  
KGAINHLSLSDLSDEFKNQFLMNANAFEQLKTQFDLNAETYACINSVSLPSELDLRLSLRT  
VTPIRMQGGCGSCWAFSGVASTESAYLAYRNMSLDLAEQELVDCASQNGCHGDTIPRGIE  
YIQQNGVVQEHYPPYVAREQSCHRPNAQRYGLKNYCQISPPDSNKIRQALTQHTAVAVI  
IGIKDLNAFRHYDGRITIMQHDNGYQPNYHAVNIVGYGNTQGVDYWIVRNSWDTTWGDNGY  
GYFAANINLMMIEQYPYVVML  
>AAC82352.1 Eur m 1; cysteine protease [Euroglyphus maynei]  
KHLSTIMKIIILAIASLLVLSAVYARPASIKTFFEEFKAFNKSYATPEKEEVARKNFLES  
KYVESNKGAINHLSLSDLSDEFKNQFLMNANAFEQLKTQFDLNAETYACINSVSLPSELD  
LRLSLRTVTPIRNQGGCGSCWAFSGVASTESAYLAYRNMSLDLAEQELVDCASQNGCHGDT  
IPRGIEYIQQNGVVQEHYPPYVAREQSCHRPNAQRYGLKNYCQISPPDSNKIRQALTQHT  
TAVAVIIGIKDLNAFRHYDGRITIMQHDNGYQPNYHAVNIVGYGNTQGVDYWIVRNSWDTT  
WGDNGYGYFAANINLMMIEQYPYVWIL  
>CAA07318.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVTTPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA07319.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNJETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVEGYLLAHS DAYN  
>CAA07320.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Betula pendula]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNN  
>CAA07323.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA07324.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKLVATPDGGSILKISNK  
YHTKGDHEMKAEHMKAIKEKGETLLRAVESYLLAHS DAYN  
>CAA07325.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA07326.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA07327.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA07328.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Betula pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNN  
>CAA07329.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILDGDNLIPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKLVATPDGGSILEISNK  
YHTKGDHEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN  
>CAA07330.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula  
pendula]  
MGVFNYETETTSVIPAAARLFKAFILEGDNLIPKVAPQAISSVENIEGNGGPGTIKKITFP  
EGSPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAA10345.1 unknown function [Dactylis glomerata]  
MSMASSSSSSGLLAMAVLAALFAGAWCVPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELR  
EHGSDEWVAMTKGEGGVWTFDSEEP LQGFNFRFLTEKGMKNVFDVVPKYTIGATYAP  
EE  
>CAA65313.1 Tri a 37; alpha-purothionin [Triticum aestivum]  
MGSKGFKGVIVCLLILGLVLEQLQVEGKSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKI  
SSGLSCP KGF PKLALESNSDEPDTIEYCNLGRSSVCDYMVNAAAADDEEMKLYVENCADA  
CVSFCNGDAGLPSLDAY  
>AAC97369.1 Sol i 4; unknown function [Solenopsis invicta]

MKTFVLVSCLLVFTQIIYALDIKEISIMNRILEKCIKRTVVPKRENDPINPLRNVNVWYCAF  
TKRGIFTPKGVNTKQYINYCEKTAISPADIKLCKKIASKCVKKVYDRPGPIIERSKNLLS  
CVLKKGLELTVYGKKK

>AAC97370.1 Sol i 4; unknown function [Solenopsis invicta]  
MKTFVLVSCLLVFTQIIYALDIKEISIMNRILEKCIKRTVVPKRENDPINPLKNNVLYCAF  
TKRGIFTPKGVNTKQYINYCEKTIISPADIKLCKKIASKCVKKVYDRPGPIIERSKNLLS  
CVLKKGLELTVYGKKK

>CAA10520.1 Poa p 1; beta-expansin [Poa pratensis]  
MASSSSVLLVVALFAVFLGTAHGIKAVPPGNITATYGDKWLDKSTWYGKPTGAGPKDN  
GGACGYKDVDPKAPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPESCSGEPVLVHITDDNE  
EPIAAYHFDLSGKAFGAMAKKGEQKLSAGELELKFRRVKCEYPEGTKVTFHVEKGSNP  
NYLALLVKYVTDGDVAVDIKEKGDKWIELKESWGSIWVDTDPDKLTGPFTVRYTTEG  
GTKGEAEDVIPEGWKADTAYASK

>AAD09630.1 Gly m 8; 2S albumin, conglutin [Glycine max]  
MTKLTILLIALLFIAHTCCASKWQQHQEQESCRLKGINLNPCHEIMEKIQAGRRGEDGS  
DEDHILIRTMPGRINRYIRKKEGKEEEEEEGHMQKCCSEMSELKSPICQCKALQKIMDNQSE  
QLEGKEKKQMERELMNLAIKRLGPMIGCDLSSDD

>CAA09883.1 Mala s 5; unknown function [Malassezia sympodialis]  
MSATTGSQAPNTTFTYIPWAPELDSDGKVCVGPQTFKAHDRWKGGKVVVAIPGAFTPACH  
QNHIPGFVEKINELKAKGVDEVVIAVNDADFVMSGWGVTVGGKDQIVYACDNDLAFSKAL  
GGTDLTSGGMVVRTARYAVVLDLKITVFGMDEGNMGAPEKSSVDAVLAQL

>CAA09884.1 Mala s 6; cyclophilin/peptidyl-prolyl isomerase [Malassezia  
sympodialis]

MSNVFFDITKNGAPLGTIKFKLFDDVVPKTAANFRALCTGEKGFYAGSHFHRVIPDFML  
QGGDFTAGNGTGGKSIYAKFADENFQLKHNKPGLLSMANAGPNTNGSQFFITTVVTSWL  
DGKHVVFGVIDGMNVVKAIEAEGSGSGKPRSRIEIAKCGVC

>CAA09885.1 Mala s 7; unknown function [Malassezia sympodialis]  
AVSASPTPSKHNLGYAQQKDLFEFHINDTVTKDVCKSLNSGKYHNMNNEKYCSVADYDV  
KWFKERCQSHPTDVKTKWIAGTDLKIEMDPKPEYELYCFNYTTFGNLPDAGAKELDDD  
ATKKACSAKSGKYQSDPKKSCRMDKKDIDQFKEQCSQYQPSDRPPYGDWSAGTSLNVV  
LNLKNA

>AAD03608.1 Jun a 1; pectate lyase [Juniperus ashei]  
MASPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVFGSSTMGGKGGD  
FYTVTSTDDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV  
HLGNGGPCLFMRKVSHVILHSLHIHCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMMLLGHDDTYDDDMSKVTVAF  
NQFGPNAGQRMPRARYGLVHVANNYDPWNIYAIGSSNPTILSEGNSTAPSESYKKEV  
TKRIGCESPSACANWVWRSTRDAFINGAYFVSSGKTEETNIYNSNEAFKVENGNAAAPQLT  
KNAGVVT

>BAA74451.1 Vig r 6; pathogenesis related protein, PR-10, Bet v 1-like [Vigna  
radiata]

MVKEFNTQTELSVRLEALWAVLSKDFITVVPKVLPHIVKDVQLIEGDGGVGTILIFNFLP  
EVSPSYQREEITEFDESSHEIGLQVIEGGYLNQGLSYYKTTFKLSEIEEDKTLVNVKISY  
DHSDIEEKVTPKTSQSTLMYLRRLERYLSNGSA

>AAD10850.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]  
MKFAIVLIACFAASVLAQEHPKPKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDL  
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKD  
LKETEQKVKDIQTQ

>AAD13106.1 Asp n 14; beta-xylosidase [Aspergillus niger]  
MAHMSRPVAATAAALLALALPQALAQANTSYYVDYNVEANPDLYPLCIETIPLSFPDCQN

GPLRSHLICDESATPYDRAASLISLFTLDEL IANTGNTGLGVSRLGLPAYQVWSEALHGL  
DRANFSDSGSYNWATSFPQPILTAAALNRTL I HQIASIISTQGRAFNNAGRYGLDVYAPN  
INTFRHPVWGRGQETPGEDVSLAAVYAYEYITGIQGPDPDSNLKLAATAKHAYAGYDIENW  
HNHSRLGNDMNITQQDLSEYYTPQFHVAARDAKVHSMCAYNVAVDGV PACADSYFLQTLL  
RDTFGFVDHGYVSSDCDAAYNIYNPHGYASSQAAAAAEAILAGTDIDCGTTYQWHLNESI  
TAGDLSRDDIEKGVIRLYTTLVQAGYFDSNTTKANNPYRDLTWSVLETDAWNISYQAAT  
QGIVLLKNSNNVLPLETEKAYPPSNTTVALIGPWANATTQLLGNYYGNAPY MISPRAAFEE  
AGYKVNFAEGTGISSTSTSGFAAALSAARSADV IYAGGIDNTLEAEALDRESIAWPGNQ  
LDLIQKLASSAGSKPLIVLQMGQQVDSSSLKNNTNVTALLWGGYPGQSGGFALRDIITG  
KKNPAGRLVTTQYPASYAEFPATDMNLRPEGDNPQTYKWTGEAVYEFHGHLFYTTFA  
ESSNNTTKEVKLNIQDILSQTHEELASITQLPVLNFTANIKNTGKLES DY TAMVFANTS  
DAGPAPYPVKWLVGWDR LGDVKVGRETREL RVPVEVGSFARVNEDGDWVLPFGTFELALNL  
ERKVRVKVWLEGE EEWLKWPGKE

>AAD13531.1 Bla g 1; microvilli-like protein with unknown function [Blattella germanica]

NAIEFLNNIHDLLGIPHIPVTARKHRRRGVITGLIDDI IAILPVDDL YALFQEKLETSP  
EFKALYDAIRSPEFQSIVGTLEAMPEYQNLIQK LKDKGVDVDHIEEL I HQIFNIVRDRG  
LPEDLQDFLALIP TDQVLAIAADYLANDAEVKA AVEYLK SDEFETIVVTVD SLPEFKNFL  
NFLQTNGLNAIEFLNNIHDLLGIPHIPVTGRKHLRRRGVITGLIDDI IAILPVDDL YALF  
QEKLETSPFEKALYDAIRSPEFQSIVETL KAMPEYQSLIQK LKDKGVDVDHIEEL I HQIF  
NIVRDRGLPEDLQDFLALIPIDQILAI AADYLANDAEVQA AVEYLK SDEFETIVVTVD S  
LPEFKNFLNFLQTNGLNAIEFLNNIHDLLGIPHIPATGRKHVRRRGVINGL IDDVIAILP  
VDELYALFQEKLESSPEF KALYDAIRSPEFQSIVQTLKAMPEYQDLIQRLKDKGVDVDHF  
IELIKKLFGLSH

>AAD13533.1 Per a 1; nitrile-specifier protein [Periplaneta americana]

EFQSIISTLNAMPEYQELLQNL RDKGVDVDHYIELIRALFGLTRAARNLQDDL NDFLALI  
PTDQILAIAMDYLANDAEVQELVAYLQSDDFHKIITTI EGLPEFANFYNFLKEHGLDVAD  
FLNEIHSIIIGLPPFVPPSRRHARRRGVINGL IDDVIAILPVDELKALFQEKLETSPDFKA  
LYDAIRSPEFQSIIISTLNAMPEYQDLLQNL RDKGVDVDHFIELIRSLFGLP

>BAA74953.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]

MGKPF TSLSSLLCLLLLSSACFAISSSKLNECQLNMLNALEPDHRVESEGGLIQTWNSQH  
PELKCAGVTVSKLTLNRNGLHLPSYSPYPRMIIIAQGGKALGVAIPGCPETFEEPQE QSN  
RRGSRSQKQQLQDSHQKIRHFNEGDV LVI PP GPVYWTYNTGDEPVVAISLLDTSNFNNQL  
DQTPRVFYLAGNPDI EYPETMQQQQQKSHGGRKQGQHQQEEEEEGGSVLSGFSKHF LAQ  
SFNTNEDIAEKLQSPDDERKQIVTVEGGLSVISPKWQEQQDEDEDEDEDEDEDEQIPSHPP  
RRPSHGKREQDEDEDEDEDEKPRPSRPSQKREQDQDQDEDEDEDEDEQPRKSREWRSKKTQ  
PRRPRQE EPRERG CETRNGVEENICTLKLHENIARPSRADFY NPKAGRISTLNSL TLPAL  
RQFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQGKVRV VNCQGNVDFGELRRGQLL  
VVPQNFVVAEQAGEQGF EYIVFKTHHNAVTSYLKDFRAIPSEVL AHSYNLRQSQVSELK  
YEGNWGPLVNPESQQGSPRVKVA

>CAA04823.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNYEIETT SVIPAARLFKAFILDGDNLVKVPAPQAIS SVENIEGNGGPGTIKKINFPE  
GFPFKYVKDRVDEVDHTNFKNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISHKY  
HTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAA04826.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNYESETT SVIPAARLFKAFILDGDNLIPKVPAPQAIS SVENIEGNGGPGTIKKITFPE  
GSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNKY  
HTKGDHEMKA EHMKAIEKGETLLKAVESYLLAHS DAYN

>CAA04827.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNYETEATSVIPAARLFKAFILDGDNLFPKVAPQAISVENIEGNGGPGTIKKISFPE  
GIPFKYVKDRVDEVDHANFKYSYSLIEGGPVGDTLEKISNEIKIVATPDGGSILKISNKY  
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN

>CAA04828.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNYESSETTSVIPAARLFKAFILDGDNLIIPKVAPQAISVENIEGNGGPGTIKKITFPE  
GSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNKY  
HTKGDHEMKAEHMKAIKEKGETLLRAVESYLLAHS DAYN

>CAA04829.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNYEIGATSVIPAARLFKAFILVGDNLFPKVAPQAISVENIEGNGGPGTIKKISFPE  
GFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNKY  
HTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN

>AAD19606.1 Per a 7; tropomyosin [Periplaneta americana]

MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARS LQKKIQQIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAA  
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLDEDELVHEKEKYKFCDDLDMTFTELIGN

>AAD20386.1 Lol p 5; unknown function [Lolium perenne]

MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL  
EDVNAGFKA AVAAAANAPPADKFKIFEAAFSSESKGLLATSAAKAPGLIPKLDTAYDVAY  
KAAEGATPEAKYDAFVTALTEALRVIAGALEVHAVKPATEEVPAAKIPTGELQIVDKIDA  
AFKIAATAANAAPTNDKFTVFESAFNKALNECTGGAYETYKFIPLSLEAAVKQAYAATVAA  
APEVKYAVFEAALTKAITAMTQAQKAGKPAAAAATGAATVATGAATAAAGAATAAAGGYK  
A

>CAB38044.1 Hel as 1; tropomyosin [Helix aspersa]

MDAIKKKMLAMKMEKENALDRAEQVEQKL RDCECNKNKVEEDLNNLQKKFAILENDFDSI  
NEQLLDANTKLEASEKKNAEIESETAGLQRRIQLEEDLERSEERLQSATEKLEEASKAA  
DESERGRKVLERSLADDERLDGLEAQLKEAKYIAEDAERKFDEAARKLAITEVDLERAE  
ARLEAAEAKILELEEEELKVVGNNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRAS  
EAERTVSKLQKEVDRLDEELLAEKERYKATSDEL DSTFAELAGY

>CAB38086.1 Per a 7; tropomyosin [Periplaneta americana]

MDAIKKKMQAMKLEKDNAMDCALLCEQQARDANLRAEKAEFEARS LQKKIQQIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAV  
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLDEDELVHEKEKYKFCDDLDMTFTELAGY

>CAB39376.1 Cop c 1; leucine zipper protein [Coprinus comatus]

RFLPSSSHLNPQHLPWL VHPAPVLLL PVL PQLKPV AHP LLLL PLDTTTLHMP LLLL QLQL  
PPLLSQGNPACSPKWLQLLVP

>AAD13530.2 Bla g 1; microvilli-like protein with unknown function [Blattella germanica]

NLLEKLRKGV D VDKIIE LIRALFGLTLNAKASRN LQDDLQDFLALIPVDQIIAIATDYL  
ANDA EVQA AVAYLQSDEFETIVVALDALPELQNFLNFLEANGLNAIDFLNGIHDLLGIPH  
IPVSGRKYHIRRGV GITGLID DVLA I LPIEDLKALFNEKLETSPDFLALYNAIRSPEFQS  
IVQTLNAMPEYQNL LQKLREKGV D VDKIIE LIRALFGLTLNGKASRN LQDDLQDFLALIP  
VDQIIAIATDYLANDAEVQA AVAYLQSDEFETIVVTLDALPELQNFLNFLEANGLNAIDF

LNGIHDLLGIPHIPVSGRKYHIRRGVITGLIDDLVLAAILPLDDLKALFNEKLETSPDFLA  
LYNAIKSPEFQSIVQTLNAMPEYQNLLEKLREKGVVDVKIIEILIRALFGLTH

>AAD25926.1 serine protease [*Penicillium citrinum*]

MGFLKVLATSLATLAWVDAGTLLTASNTDAVIPSSYIVVMNDDVSTAEFNTHREWATNVH  
ARLSRRKNGETGPGKHFEINGLKGYTASFDESTAKDIANDPAVKYIEPDMIVNATANVVQ  
SNVPSWGLARISSKRTGTTSYTYDSTAGEGVVFGVDTGIDISHSDFGGRAKWGTNVVDN  
DNTDGNHGHGHTASTAAGSKYGVAKKATLVAVKVLGADGSGTNSGVISGMDWAVKDAKSR  
GANGKYVMNMSLGGEFSKAVNDAAANVVKSGIFLSVAAGNEAENASNSSPASAAEVCTIA  
ASTSTDGSASFNTFGSVVDLYAPGQSITAAYPGGSKTLSGTSMAPHVAGVAAAYLMALE  
GVSAGNACARIVQLATSSISRAPSGTTSKLLYNGINV

>AAD25927.1 Mala f 4; mitochondrial malate dehydrogenase [*Malassezia furfur*]

MFARAALRNSVRAPASARYFSQTAANRNVAVLGASGGIGQPLSLLMKLNPKVTELRLYD  
IRLAPGVAADLSHINTPAVTSGYAQDDLEGAVDGAEIVLIPAGMPRKPGMTRDDLFSNA  
SIVRDLAKVVAKVAPKAYIGVISNPVNSTVPIVAEVFKKAGVYDPKRLFGVTTLDTTRAA  
TFLSGIAGSDPQTTNVPVIGGHSVTVIPLISQAAQGDVQAGEQYDKLVHRIQFGGDEV  
VKAKDGAGSATLSMAYAAAVFTEGLLKGLDGEAVTQCTFVESPLFKDQVDFASPVEFGP  
EGVKNIPALPKLTAEQKLLDACLPDLAKNIKKGVAAWAENP

>AAD25995.1 serine protease [*Penicillium citrinum*]

MKGFLGLALLPLLTAASPVSVESIHNGAAPIISSMNSQEIPDSYIVVFKKHVDTSAAAA  
HSWVQDIHSAVNGRMELKKRGLFGFDTAFLGVKHSFHVAGSLMGYAGHFHEDVIEQVRR  
HPDVVDYIEKDSEVHHFSDPSVEKNAPWGLARISHRDSL SFGTFNKYLYAEDGGEGVDAYV  
IDTGTNTDHDVDFEGRASWGKTIPQGDDEDVDGNHGHGTHCSGTIAGKKYGVAKKANVYAVKV  
LRSNGSGTMSDVVKGVWAAEAHIKKSKAAKDGKAKGFKGSVANMSLGGGSSRTLDAVN  
AAVDAGMHFAVAAGNDNADACNYSAAA EKAVTVGASTLADERAYFSNYGKCTDIFAPGL  
NILSTWIGSKYAVNTISGTSMASPHIAGLLAYVSLQPSDDSAFAVEKITPKKLEALIT  
VATSGALTDIPSDTPNLLAWNGGGSSNYTDIVAQGGY

>AAD26546.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]

MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPIKQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALTDTIEKISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKHPDAYN

>AAD26547.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]

MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPIKQAIKHAEILEGDGGPGTIKKITFG  
EGSQYGYVVKHKIDSVDANYSYAYTLIEGDALTDTIEKVSYETKLVASGSGSIIKSISHY  
HTKGDVEIKEEHVKAGKEKAHGLFKLIESHLKHPDAYN

>AAD26548.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]

MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPIKQAIKHAEILEGDGGPGTIKKITFG  
EGSQYGYVVKHKIDSVDANYSYAYTLIEGDALTDTIEKVSYETKLMASGSGSIIKSISHY  
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYLKHPDAYN

>AAD26552.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]

MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPIKQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALTDTIEKISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKHPDAYN

>AAD26553.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]

MGVCTFENEFTSEIPPSRLFKAFLVDADNLIPIKQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALTDTIEKISYETKLVACGSGSTIKSISHY

HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKDHPDAYN  
>AAD26554.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]  
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIENISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKDHPDAYN  
>AAD26555.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]  
MGVYTFENEYTSSEIPPSRLFKAFLVDADNLIPIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKAGKAKAHGLFKLIESYLKGHDPDAYN  
>AAD26558.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]  
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPIKQAEILEGDGGPGTIKKITFG  
EGSQYGYVVKHRIDSVDEANYSYAYTLIEGDALDTIEKISYETKLVASGSGSIIKSISHY  
HTKGDVEIKEEHVMAGKEKAHGLFKLIESYLKGHDPDAYN  
>AAD26560.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]  
MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLKAVESYLLAHS DAYN  
>AAD26561.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]  
MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGPILKISNK  
YHTKGDHEVKAEQVKASKEMGETLLRAVESYPLAHS DAYN  
>AAD26562.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]  
MGVFNJETEATSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGIPFKYVVKDRVDEVDHANFKYSYSLIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK  
YHTKGNHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN  
>AAD29409.1 Api g 4; profilin [Apium graveolens]  
MSWQAYVDDHLMCEVEGNPQQLTAAAIIGHDGSVWAQSSTFPQIKPEEIIAGIMKDFDEP  
GHLAPTGLYLGGAKYMIQGEPPNAVIRGKKKSGGVTIKKTGQALVFGVYDEPVTGQCNCV  
IVERLGDYLLIDQGL  
>AAD29410.1 Pyr c 4; profilin [Pyrus communis]  
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAQSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMIQGEAGAVIRGKKKSGGVTVKKTSQALVFGIYEEPLTPGQCNMIVE  
RLGDYLLIDQGL  
>AAD29411.1 Pru av 4; profilin [Prunus avium]  
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPKFKPEEIAAILKDLDQPGTL  
APTGLFLGGTKYMIQGEAGAVIRGKKKSGGIVVKKTNQALIIIGIYDEPLTPGQCNMIVE  
RLGDYLLIEQGL  
>AAD29412.1 Mal d 4; profilin [Malus domestica]  
MSWQAYVDDRLMCDIDGHHLTAAAILGHDGSVWAHSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMIQGEAGAVIRGKKKSGGVTVKKTGQALVFGIYEEPLTPGQCNMIVE  
RLGDYLLIDQGL  
>AAD29413.1 Mal d 4; profilin [Malus domestica]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHNGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL  
APTGLYLGGTKYMIQGEPPVIRGKKKGGVTVKKSTMALLIGIYDEPMTGQCNMVVE

RLGDYLIEQGL  
>AAD29414.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL  
APTGLFLGGTKYMVIQGEPAVIRGKKKSGGITIKKTSQALLIGIYDEPVTGQCNIIVVE  
RLGDYLIEQGL  
>AAD29671.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVYTFENEFTSEIPPSRLFKAFVLDADNLIPIKIAQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY  
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKDHDPDAYN  
>CAB42886.1 Phl p 13; polygalacturonase [*Phleum pratense*]  
GKKEEKKEEKESGDAASGADGYDITKLGAKPDGKTDCCTKEVEEAWASACGGTGKNTIV  
IPKGDFLTGPLNFTGPKGDSVTIKLDGNLLSSNDLAKYKANWIEIMRIKKLTITGKGT  
DGQGKAVWGNKNSCAKNYNCKILPNTLVLDLFCDDALIEGITLLNAKFFHMNIYECKGVTVK  
DVTITAPGDSPTDGIHIGDSSKVTITDITIGTDDCISIGPGSTGLNITGVTGCPGHGI  
SVGSLGRYKDEKDVTDITVKNKCVLKKSTNGLRIKSYEDAKSPLTASKLTYENVKMEDVGY  
PIIIDQKYCPNKICTSKGDSARVTVKDVTFRNITGTSSTPEAVSLLCSDKQPCNGVTMND  
VKIEYSGTNNKTMVCTNAKVTAAGVSEANTCAA  
>CAB42887.1 Ves v 5; unknown function, antigen 5 [*Vespa vulgaris*]  
NNYCKIKCLKGGVHTACKYGLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLWVNDLAYIAQVWANQCEYGHDTCRDVAKYQVQGNVALTGSTA  
AKYDDPVKLVKMWEDEVKDYNPKKKFSGNFLKTGHYTMVWANTKEVGCOSIKYIQEKW  
HKHYLVCNYGPSGNFKNEELYQTK  
>CAB44442.1 Asp f 11; cyclophilin/peptidyl-prolyl isomerase [*Aspergillus fumigatus*]  
FHQTPSAMSQVFFDVEYAPVGTAEKTVGRIVNLFDDKDVPKTAKNFRELCKRPAGEGYRE  
STFHRIIPNFMIIQGGDFTRNGTGGRSIYGDKFADENFSRKHDKKGIKLSMANAGPNTNGS  
QFFITTAVTWSWLDGKHVVFGVEVADEKSYSVWKEIEALGSSSGSVRSNTRPKIVNCGEL  
>AAD38942.1 Der p 4; alpha-amylase [*Dermatophagoides pteronyssinus*]  
KYHNPFIHNRSVITHLMEWKYDDIGDECERFLGPYGYGGVQVSPVNEHAILDRRPWYER  
YQPVSYDIRTRSGDEQQFRMVKRCNKAGVRIYVDIVLNHMTGAQSGKGTNGHHYDGNTL  
QYPGVFPFPNDFHGHESCPTQDLEIHDTNPKEARNCRSLGLRDLKQQSEYVRQKQVDFL  
NHLIDIGVAGFRSDASTHQWPDDLRSIYSRLHNLNKEFFPENSQPFYHETIYYGGNGIN  
SNEYTSLGRIIEFRFYKEITNVFRGNPLHLKNGFTEWGLVPSGDALVMIDSHDLRVGH  
TGKLGFNINCFEGRLLKAATAFMLAWNYGVPRVMSSYFWNQI IKDGKDVNDWVGPPSDKN  
GNILSVHPNPDMTCNHEWICEHRWREIYNMVKFRMIAGQEPVHNWWDNGDYQIAFSRGNR  
AFIAINLQKNQQLQKLTGLPAGTYCDIISGNLIDNKCTGKSIHVDKNGQADVYVGH  
EFDVAVYHIGARIVS  
>AAD42074.1 Pen c 3; peroxisomal protein [*Penicillium citrinum*]  
MSLKAGDSFPEGVTFYSIPWAEDASEITSCGIPINYNASKEFANKKVLFALPGAFTPVC  
SANHVPEYIQLPELRAKGVQVAVLAYNDAYVMSAWGKANGVTGDDILFLSDPEAKFSK  
SIGWADEEGRTYRYVLVIDNGKIIYAAKEAAKNSLELSRADHVLKQL  
>AAD42942.1 Ses i 5; oleosin [*Sesamum indicum*]  
MAEHYQQQQTRAPHLQLQPRARVVAATAVTTAGGSLLVLSGLTLAGTVIALTIATPLL  
VIFSPVLVPAVITIFLLGAGFLASGGFGVAALSLSWIYRYLTGKHPPGADQLESATKL  
ASKAREMKDRAEQFSQQPVAGSQT  
>AAD42943.1 Ses i 2; 2S albumin, conglutin [*Sesamum indicum*]  
MARFTIVLAVLFAAALVSASAHKTVVTTVAEEGEEENQRGCEWESRQCQMRHCMQWMRS  
MRGQYEEFLRSAAEQGFQEHFRECCNELRDVKSHCRCEALRCMMRQMQQEYGMQEMQ  
QMQQMMQYLPRMCGMSYPTECRMRPIFA  
>AAD42944.1 Ses i 6; 11S globulin, cupin [*Sesamum indicum*]

MVAFKFL LALS LLLVSA AIAQTREPRLTQGQCRFQRISGAQPSLRIQSEGGTTELWDE  
RQEQFCAGIVAMRSTIRPNGLSLPNYHPSRLVYIERGQGLISIMVPGCAETYQVHRSQ  
RTMERTEASEQQDRGSVRDLHQKVHRLRQGDIVAIPSGAAHWCYNDGSEDLVAVSINDVN  
HLSNQLDQKFRAFYLGGVPRSGEQEQARQTFHNIFFRAFDAELLSEAFNVPQETIRRMQ  
SEEEERGLIVMARERMTFVRPDEEEGEQEHRGRQLDNGLEETFCTMKFRTNVESRREADI  
FSRQAGRHHVDRNKLPILKYMDLSAEKGNLYSNALVSPDWSMTGHTIVVYVTRGDAQVQV  
VDHNGQALMNDRVNQGEMFVVPQYYTSTARAGNNGFEWVAFKTTGSPMRSPLAGYTSVIR  
AMPLQVITNSYQISPNQAQALKMNRGSQSFLSPGGRRS  
>AAC15474.2 Jun o 4; calcium-binding protein, polcalcin [*Juniperus oxycedrus*]  
MDEVPSDDGSKSACSSEVMEQSVHELEEVFKKFDANGDGKISGSELADILRSLGSDVGE  
AEVKAMMEEADADGDGYVSLQEFVDLNNKGASVKDLKNAFKVDFDRDCNGSISAAELCHTL  
ESVGEPCTIEESKNIIHNVDKNGDGLISVEEFQTMMTSEMTDKSK  
>AAD46493.1 unknown function [*Strongyloides stercoralis*]  
NSARDENGLIYTYNGNDYDTKEAMEDAIQRDYPDKIFTFGGDNNGKRRKIDISKWKGN  
NTFSNKIFDEIWEGYNYDNDKAKNFVMMKTKLFNEQNKYRIAHGAKKLIKSKDLEKKAQA  
YAEVIARLGRLEHDPKNRIEGTGENLAYGTTFFIHLAVKGWYDEIALYNFKKPGFSPATG  
HFTQLVWKGTTAGFGVVEKGRVYVVKYSPPGNYPRQFXANVLQRKQ  
>CAB51914.1 Hev b 8; profilin [*Hevea brasiliensis*]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGQDGSVWAQSANFPQFKSEEITGIMSDFHEPGTL  
APTGLYIGGTMYMVIQGEPAVIRGKKKGGVTVKKTNQALIIIGIYDEPMTPGQCNMIVE  
RLGDYLIDQGY  
>AAD47382.1 Ara h 3; 11S globulin, cupin [*Arachis hypogaea*]  
MAKLELSFCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWPNPN  
QEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYEEPAQQGR  
RYQSQRPPRRLQEEDQSQQQDQSHQKVHRFNEGDLIAVPTGVAFWLYNDHDTDVAVSLT  
DTNNNDNQLDQFPRRNLNAGNHEQEFLRYQQSRQSRRRSLPYSPPSPHSRPRREERFR  
PRGQHSRRERAGQEEDEEGNIFSGFTPEFLEQAFQVDDRQIVQNLWGENESEEEGAIVT  
VRGGLRILSPDGTGDADEEEYDEDEQYEHQDGRRRGRSGGGNGIEETICTACVKKNI  
GGNRSPHIYDPQRWFTQCHDLNLLILRWLGLSAEYGNLYRNALFVPHYNTNAHSIIYAL  
RGRAHVQVVDNSNGNRVYDEELQEGHVLVVPQNFVAVAGKSQSENFEYVAFKTDSPRSIANF  
AGENSFIDNLPEEVVANSYGLPREQARQLKNNMPKFFVPPFQQSPRAVA  
>AAD48405.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [*Corylus  
avellana*]  
MGVFCYEDEATSVIPPARLFKSFVLADNLIIPKVAPQHFTSAENLEGNGGPGTIKKITFA  
EGNEFKYMKHKVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS  
KYHTKGNASINEEIKAGKEKAAGLFAVEAYLLAHPDAYC  
>CAB52710.1 Tri a 33; serpin [*Triticum aestivum*]  
MATTLATDVRLSIAHQTRFGFRLASTISSNPESTANNVAFSPVSLHVALSLITAGAGGAT  
RDQLVATLGEGEAERLHALAEQVVQFVLADASYADSPRVTFANGVFVDASLPLKPSFQEL  
AVCKYKAEAQSVDFQTKAAEVTAQVNSWVEKVTGLIKDILPAGSISNTTRLVLGNALYF  
KGAWTDQFDSRVTKSDYFYLLDGSSIQTPFMYSSSEEQYISSSDGLKVLKLPYKQGGDKRQ  
FSMYILLPEAPSGIWSLAEKLSAEPELLERHPRQKVALRQFKLPKFKISFGIEASDLLK  
HLGLQLPFSDEADLSEMVDSPMPQGLRISSVFHKTFVEVNETGTEAAAAATIAKAVLLSAS  
PPSDMDFIADHPFLFLIREDTSGVVLFIGHVNPLRSL  
>CAB53458.1 Hev b 10; superoxide dismutase [*Hevea brasiliensis*]  
QTFSLPDLPYDGALEPAISGEIMQLHHQKHQTYITNYNKALEQLNDAIEKGDSAAVVK  
LQSAIKFNGGGHVNSIFWKNLAPVREGGGELPHGSLGWAIADDFGSLEKLIQLMNAEGV  
ALQSGSWVWLALDKELKLVVETTANQDPLVTKGPTLVPLLIDVWEHAYYLQYKNVRPD  
YLNKIWKVMNWKYASEVYAKECPSS  
>CAA55067.2 Cla h 5 acidic ribosomal protein P2 [*Cladosporium herbarum*]

MKYLA AFL L L L G L A G N S S P S A E D I K T V L S S V G I D A D E E R L S S L L K E L E G K D I N E L I S S G S E  
K L A S V P S G G A G A A S A G G A A A A G G A A E A P E A E R A E E E E K E E S D D D M G F G L F D

>AAD52012.1 Tri r 4; serine protease [Trichophyton rubrum]  
M A A A K W L I A S L A F A S S G L A F T P E D F I S A P R R G E A I P D P K G E L A V F H V S K Y N F D K K D R P S G  
W N L L N L K N G D I N V L T T D S D V S E I T W L G D G T K V V Y I N G T D S V K G G V G I W I S D A K N F G N A Y K  
A G S V N G A F S G L K L A K S G D K I N F V G Y G Q S T T K G D L Y N E A A A K E A V S S A R I Y D S L F V R H W D T  
Y V G T Q F N A V F S G T L T K S G D K Y S F D G K L K N L V Q P V K Y A E S P Y P P F G G S G D Y D L S S D G K T V A  
F M S K A P E L P K A N L T T S Y I F L V P H D G S R V A E P I N K R N G P R T P Q G I E G A S S S P V F S P D G K R I  
A Y L Q M A A K N Y E S D R R V I H I A E V G T N K P V Q R I A S N W D R S P E A V K W S S D G R T L Y V T A E D H A T  
G K L F T L P A D A R D N H K P A V V K H D G S V S S F Y F I G S S K S V L I S G N S L W S N A L Y Q V A T P D R P N R  
K L F Y A N E H D P E L K G L G P N D I E P L W V D G A R T K I H S W I V K P T G F D K N K V Y P L A F L I H G G P Q G  
S W G D N W S T R W N P R V W A D Q G Y V V V A P N P T G S T G F G Q K L T D D I T N D W G G A P Y K D L V K I W E H V  
H D H I K Y I D T D N G I A A G A S F G G F M V N W I Q G Q D L G R K F K A L V S H D G T F V G S S K I G T D E L F F I  
E H D F N G T F F E A R Q N Y D R W D C S K P E L V A K W S T P Q L V V H N D F D F R L S V A E G V G L F N V L Q E K G  
V P S R F L N F P D E T H W T K P E N S L V W H Q Q V L G W V N K W S G I N K S N P K S I K L S D C P I E V V D H E A  
H S Y F D Y

>AAD52013.1 Tri r 2; secreted alkaline protease [Trichophyton rubrum]  
M G F I T K A I P I V L A A L S T V N G A R I L E A G P H A E A I P N K Y I V M K R E V S D E A F N A H T T W L S Q S  
L N S R I M R R A G S S K P M A G M Q D K Y S L G G I F R A Y S G E F D D A M I K D I S S H D D V D F I E P D F V V R T  
T T N G T N L T H Q D N V P S W G L A R V G S K K P G G T T Y Y Y D P S A G K G V T A Y I I D T G I D I D H E D F Q G R  
A K W G E N F V D Q Q N T D C N G H G T H V A G T V G G T K Y G L A K G V S L V A V K V L D C D G S G S N S G V I K G M  
E W A M R Q A S G G G N T A K A A G K S V M N M S L G G P R S E A S N Q A A K A I S D A G I F M A V A A G N E N M D A  
Q H S S P A S E P S V C T V A A S T K D D G K A D F S N Y G A V D V Y A P G K D I T S L K P G G S T D T L S G T S M A  
S P H V C G L G A Y L I G L G K Q G G P L C D T I K K M A N D V I Q S P G E G T T G K L I Y N G S G K

>AAD52615.1 Pol a 1; phospholipase A1 [Polistes annularis]  
M S P D C T F N E K D I V F Y V Y S R D K R D G I I L K K E T L T N Y D L F T K S T I S K Q V V F L I H G F L S T G N N  
E N F V A M S K A L I E K D D F L V I S V D W K K G A C N A F A S T K D A L G Y S K A V G N T R H V G K F V A D F T K L  
L V E K Y K V L I S N I R L I G H S L G A H T S G F A G K E V Q K L K L G K Y K E I I G L D P A G P Y F H R S D C P D R  
L C V T D A E Y V Q V I H T S I I L G V Y Y N V G S V D F Y V N Y G K N Q P G C N E P S C S H T K A V K Y L T E C I K H  
E C C L I G T P W K K Y F S T P K P I S Q C R G D T C V C V L N A K S Y P A R G A F Y A P V E A N A P Y C H N E G I K  
L

>AAD52616.1 Pol a 2; hyaluronidase [Polistes annularis]  
Y V S L S P D S V F N I I T D D I S H Q I L S R S N C E R S K R P K R V F S I Y W N V P T F M C H Q Y G M N F D E V T D  
F N I K H N S K D N F R G E T I S I Y Y D P G K F P A L M P L K N G N Y E E R N G G V P Q R G N I T I H L Q Q F N E D L  
D K M T P D K N F G G I G V I D F E R W K P I F R Q N W G N T E I H K K Y S I E L V R K E H P K W S E S M I E A E A T K  
K F E K Y A R Y F M E E T L K L A K K T R K R A K W G Y Y G F P Y C Y N V T P N N P G P D C D A K A T I E N D R L S W M  
Y N N Q E I L F P S V Y V R H E Q K P E E R V Y L V Q G R I K E A V R I S N N L E H S P S V L A Y W W Y V Y Q D K M D I  
Y L S E T D V E K T F Q E I V T N G G D G I I I W G S S S D V N S L S K C K R L R E Y L L N T L G P F A V N V T E T V N  
G R S S L N F

>AAD52672.1 Der f 15; chitinase [Dermatophagoides farinae]  
M K T I Y A I L S I M A C I G L M N A S I K R D H N D Y S K N P M R I V C Y V G T W S V Y H K V D P Y T I E D I D P F K  
C T H L M Y G F A K I D E Y K Y T I Q V F D P Y Q D D N H N S W E K R G Y E R F N N L R L K N P E L T T M I S L G G W Y  
E G S E K Y S D M A A N P T Y R Q Q F I Q S V L D F L Q E Y K F D G L D L D W E Y P G S R L G N P K I D K Q N Y L A L V  
R E L K D A F E P H G Y L L T A A V S P G K D I D R A Y D I K E L N K L F D W M N V M T Y D Y H G G W E N F Y G H N A  
P L Y K R P D E T D E L H T Y F N V N Y T M H Y L N N G A T R D K L V M G V P F Y G R A W S I E D R S K L K L G D P A  
K G M S P P G F I S G E E G V L S Y I E L C Q L F Q K E E W H I Q Y D E Y N A P Y G Y N D K I W G Y D D L A S I S C  
K L A F L K E L G V S G V M W S L E N D D F K G H C G P K N P L L N K V H N M I N G D E K N S F E C I L G P S T T T P  
T P T T T P T T T T P T T P S P T T P T T T P S P T T P T T T P S P T T P T T T P S P T T P T T T P T P A P T T S  
T P S P T T T E H T S E T P K Y T T Y V D G H L I K Y K E G D I P H P T N I H K Y L V C E F V N G G W W H I M P C P  
P G T I W C Q E K L T C I G E

>AAD55587.1 Ara h 5; profilin [Arachis hypogaea]  
MSWQTYVDNHLLEIEGDHLLSSAAILGQDGGVWAQSSHFQFKPEEITAIMNDFAEPSL  
APTGLYLGGTKYMIQGEPAIIPGKKGGVTIEKTNQALIIGIYDKPMTPGQCNMIVE  
RLGDYLIDTGL

>AAD56337.1 Ara h 6; 2S albumin, conglutin [Arachis hypogaea]  
AHASAMRRERGRQGDSSSCERQVDGVNLKPCEQHIMQRIMGEQEYDSYNGSTRSSDQQ  
QRCCDELNEMENTQRCMCEALQQIMENQCDGLQDRQMVQHFKRELMNLPQQCNFGAPQRC  
DLDVSGGRC

>AAD56719.1 Ara h 7; 2S albumin, conglutin [Arachis hypogaea]  
MMVKSILVALLGALLVVASATRWDPDRGSRGRWDAPSRGDDQCQRQLQRANLRPCEEH  
MRRRVEQEQQEQDEYPYSRRGRGRQPGESDENQEQRCCNELNRFQNNQRMCQALQQI  
LQNQSFVWPAGQEPVASDGEQAQELAPELRVQVTKPLRPL

>P42040.2 Cla h 6; enolase [Cladosporium herbarum]  
MPISKIHSRYVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKSWAGK  
GVTKAVANVNEIIPALIKENLDVKDQAAVDAFLNKLDGTTNKTIGANAILGVSMVAVK  
AAAAEKRVPLYAHISDLGTTKPFVLPVPMNVVNGGSHAGRLAFQEFMIVPSGAPSFT  
EAMRQGAEVYQKLKSLTKKRYQGSAGNVGDEGGVAPDIQTAEALDLITDAIEEAGYTGO  
IKIAMDVASSEFYKADEKDYDLDFKNPDSKSKWITYEQLADQYKQLAAKYPIVSIEDPF  
AEDDWEAWSYFYKTSQSDQFQVGGDLTVTNPEFIKKAIETKACNALLLKVNIQGTITEAI  
NAAKDSFAAGWGMVSHRSGETEDVTIADIVVGLRAGQIKTGAPARSERLAKLNQILRIE  
EELGDKAVYAGDNFRTAINL

>CAB58171.1 troponin C [Anisakis simplex]  
MAEDIEEILAEIDGSQIEEYHKFFDMFDRGKQGYIMATQIGQIMHAMEQDFDEKQLRKL  
RKFDADGSGKLEFDEFKALVYTVANTVDKETLQKELREAFRLFDKEGNGYISRPTLKALL  
KEIADDLSDDQLEAAVDEIDEDGSGKIEFEFEWELMAGEAD

>AAB82772.2 Mus a 5; beta-1,3-glucanase [Musa acuminata]  
MATKASLSIKGFALLVSVLVAVPTRVQSIGVCYGLGNNLPPPSEVVSLYKSNNIARMRL  
YDPNQAALQALRNSNIQVLLDVPKSDVQSLASNPAAAGDWIRRNVVAYWPSVSVFRYI  
AVG NELIPGSDLAQYILPAMRNINYLSSAGLQNKQIKVSTAVDTGVLGTSYPPSAGAFSSAAQ  
AYLSPIVQFLASNGAPLLVNVYPYFSYTGNGQISLPYALFTASGVVVDGGRFSYQNLFD  
AIVDAVFAALERVGGANVAVVSESGWPSAGGGAEASTSNARTYNQNLIRHVGGGT  
PRRP GKEIEAYIFEMFNENQKAGGIEQNFGLFYPNKQPVYQISF

>P35776.2 Sol r 2; unknown function [Solenopsis richteri]  
DIEAQRVLRKDIAECARTLPKCVNQPDPLARVDVWHCAMS KRGVYDNPDPVAVKEKNSK  
MCPKIITDPADVENCKKVVSRVDRQPRSNRQKAINITGCILRAGVVEATVLAREK

>P35779.2 Sol r 3; unknown function [Solenopsis richteri]  
TNYCNLQSCKRNNAIHTMCQYTSPTPGPMCLEYSNVGFTDAEKDAIVNKHNELRQRVASG  
KEMRGTNGPQPAPVKMPLNLTWDELATIAQRWANQCTFEHDACRNVERFAVGQNI  
AATSS SGKNKSTLSDMILLWYNEVKDFDNRWISSFPSDGNILMHVGHYQI  
VWAKTKKIGCGRIM FKEDNWNKHVLCNYGPAGNVLGAQIYEIKK

>P81657.1 Vesp m 5; unknown function, antigen 5 [Vespa mandarinia]  
NNYCKIKCRSGIHTLCKFGISTKPCGKNVVKASGLTKAEKLEILKQHNEFRQK  
VARGLE TRGKPGPQPPAKSMNTLVWNEDELAQIAQVWAGQCDYGHVCRNTAKYS  
VGVQNIENGSTA ASFASVSNMVQMWAVEVKNYQYGSTKNKLEI  
VGHYQMVWAKTKEIGCGSIKYIENGWHR HYLVCNYGPAGNIGNEPIYERK

>CAB59976.1 Gly d 2; NPC2-like [Glycyphagus domesticus]  
GKMNFDTDCGHNEIKELSVSNTGNYCVIHRGKPLTLDAKFDANQDTASVGLVLT  
AIDGD IAIDIPGLETNACKLMKCPKIRKGEHQELIYNIGEIPDATPEIKAKVKAQL  
IGEHLVGLACG WVDGEVQE

>CAB62212.1 Lep d 5; unknown function, partial [Lepidoglyphus destructor]

DDFRNEFDRLLIHMTEEQFAKLEQALAHLSHQVTELEKSKSKELKAQILREISIGLDFID  
SAKGHFERELKRADLNLAEKFNFESALSTGAVLHKDLTALATKVKAIETK  
>CAB62213.1 Lep d 13; fatty acid-binding protein [Lepidoglyphus destructor]  
MANIAGQYKLDKSENFQFLDKLGVGFLVKTAAKTVKPTLEVAVDGDYIFRSLSTFKNT  
EIKFKLGEEFEEDRADGKRKTVIVKDGDNKQVQYGDKEVKVREFKGDVEVEVTASVD  
GVTSVRPYKRA  
>CAB62551.1 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]  
DNPIDSCWRGDSNWDQNRMKLADCVVGFSGSSTMGGKGGIYTVTSSDNPVNPTPGTLRY  
GATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGAVVHLGNNGPCLFMRKASHVILHG  
LHIHGNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVNTNAWIDHNSLSDCSIDLVT  
GSTGITISNNHFFNHKVMLLGHDDTYDDKSMKVTVAFNQFGPNAGQRMPRARYGLVHV  
ANNNDQWNIYAIGGSSNPTILSEGNSFTAPNESYKKEVTKRIGCETTSACANWVWRSTR  
DAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQNAAGVVA  
>AAF18269.1 Jug r 2; 7S globulin, vicilin-like [Juglans regia]  
RGRDDDEENPRDPREYRQCQEYCRROGQOQQCQIRCEERLEEDQRSQEERERRR  
GRDVEDQNPDPPEQRYEQCQQCERQRRGQEQTLRRRCEQRRQEEERERQRGRDRQDPQ  
QQYHRCQRRQIQEQSPERQRCQRCERQYKEQQGRERGPESPRRESRGREEEQQRHN  
PYYFHSQSIRSRHESEEVEVKYLERFTELLRGIENYRVVILDANPNTSMLPHHKDAE  
SVAVVTRGRATLTLVSQETRESFNLCEGDVIRVPAGATVYVINQDSNERLEMVKLLQPVN  
NPGQFREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREGVIRASQE  
KLRALSQHAMSAGQRPWGRSSGGPISLKSESPSYSNQFGQFFEACPEEHRQLQEMDVLV  
NYAEIKRGAMMVPHYNSKATVVVVVVEGTGRYEMACPHVSSQSYEGQRRREQEEEEESTGR  
FQKV TARLARGDIFVIPAGHPAITASQENLRLGFDINGENNRDFLAGQNNIINQLE  
REAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPASILDFAFF  
>CAB63699.1 Lol p 1; beta-expansin [Lolium perenne]  
MASSSSVLLVVALFAVFLGSAHGIKAVPPGNITAEYGDKWLDKSTWYKPTGAGPKDN  
GGACGYKDVDPKAPFNMGMTGCGNTPIFKDGRCGSCFEIKCTKPESCSGEAVTVITDDNE  
EPIAPYHFDLSGHAFGSMKKGEEQKLRSAGELELQFRRVKCKYDPDGTPTFHVEKASNP  
NYLAILVKYVDGDGDVAVDIKEKGDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEG  
GTKSEVEDVIPEGWKADTSYSAK  
>CAB64344.1 Lol p 5; unknown function [Lolium perenne]  
MAVQKYTVALFLAVALVAGPADSYAADAGYTPAAAATPATPAATPAAGGGKATTDEQKLL  
EDVNAGFKAABAADANAPPADKFKIFEAAFSSECKGLLATSADAKAPGLILKLDTDYDVAY  
KAGEGATPEAKYDAFVTALTEALRVIAGALEVHAVKPATEEVPAAKIPTGELQIVDKIDA  
AFKIAATAANAAPTNDKFTVFESAFNKALKECTGGAYETYKFIPLSLEAAVKQAYATTVAA  
APEVKYAVFEAALTKAITAMSQAQKVAKPAAAAATGAATVATGAATAAAGGATAAAGGYK  
A  
>AAF23726.1 Pen ch 13; alkaline serine protease [Penicillium chrysogenum]  
MGFLKVLATSLATLAVVDAGTLLTASNTDAVIPSSYIVVMNDDVSTAEFSTHREWATNVH  
ARLSRRKNGETGPGKHFEINGLKGYTASFDENTAKDIANDPAVKYIEPDMIVNATANVVQ  
SNVPSWGLARISSKRTGTTSTYTYDSTAGEGVVYFGVDTGIDISHSDFGGRAKWTNVVDN  
DNTDGNHGHGHTASTAAGSKYVAKKATLVAVKVLGADGSGTNSGVISGMDWAVKDAKSR  
GANGKYVMNTSLGGFEFSKAVNDAAANVVKSGIFLSVAAGNEAENASNSSPASAAEACTIA  
ASTSTDGSASFNTFGSVVDLYAPGQSITAAYPGGSKTLSGTSMAAPHVAGVAAAYLMALE  
GVSAGNACARIVQLATSSISRAPSGTTSKLLYNGINV  
>CAB64688.1 Asp f 8; acidic ribosomal protein P2 [Aspergillus fumigatus]  
MKYLAAFLLLALAGNTSPSSEDVKAVLSSVGIDAEERLNKLI AELEGKDLQELIAEGST  
KLASVPSGGAAAAAPAAAGAAAGGAAAPAAKEKNEEEKEESDEDMGFGLFD  
>CAB65963.1 Lep d 7; bactericidal permeability-increasing like [Lepidoglyphus  
destructor]

MQYLAIIVIVALAGLSAAAHKPAYYDDNMANQMVDQIVKSLTTKKELDPFKIEQTKVPID  
KKIGLIHIKGSATIKNAVITGLSHISRREGDAKIDTDGGFAAATLKLGDKNIRIKTDLHLD  
LGKIIHPNLKFEHGIDIMKLLKLDLDAEGKPSLDQFEIDFEQVELFIHGLGPLDPLVD  
VIADSFVKYFNPQARKLVTDMLKPILVEEIKKLLKN  
>AAF25553.1 Hev b 7; patatin [Hevea brasiliensis]  
MATGSTPLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDLGDGPDARIADYFDIIAGT  
STGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIHSIGPIYDGEY  
LRELCNNLLKDLTVKDTLTDVVIPTFDIKLLLPIVIFSSDDAKCNALKNARLADVCISTSA  
APVLLPAHSFTTEDDKNIHTFELIDGGVAATNPPLLALHTRNEIIRQNPRFIGANL TES  
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL  
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES  
IPGAPTNEAAIAKFAKLLSEERKLRQLK  
>AAF26449.1 Pru av 3; lipid transfer protein [Prunus avium]  
MACSAMTKLALVVALCMVSVPIAQUALTCGVSSNLAPCIAYVRGGGAVPPACNGIRNI  
NNLAKTTADRQTACNCLKQLSASVPGVNNANAAALPGKCGVNVYPYKISPSTNCATVK  
>AAF26451.1 Pyr c 3; lipid transfer protein [Pyrus communis]  
MASSAVIKLALVVALCMAVSVAHAITCSQVSANLAPCINIVRSRGGAVPPACNGIKTING  
LAKTTPDRQAACNCLKNLAGSVSGVNPNAESLPGKCGVNVYPYKISTSTNCATVK  
>AAF28423.1 Der f 6; chymotrypsin, serine protease [Dermatophagoides farinae]  
MIKIFLVITILIVITVTVDARFPRSLQPKWAYLDSNEFPRSKIGDSP IAGVVGGQDADLAE  
APFQISLLKDYLLIMKRHMCGGSLISESTVVTAACHTYGQKASSLSVRYGTNQR TSSSYGD  
LKVKPIIQHESYEQDQTQDKTIIILPNPVVPTSNVQMNEIETEDIVDGDKVTIYGWGLT  
DGNGKDLDPKQLKQGSMTIVGNDRCNKWSINAIHPGMICALDKTQSGCNGDSGGPLVSA  
NRKLTGIVSWGPSKCPPGEYMSVFTRPKYYLDWITKNIV  
>CAB71342.1 Lep d 10; tropomyosin [Lepidoglyphus destructor]  
MEAIKNKMQAMKLEKDNAIDRAEIAEQSRDANLRAEKSEEEVRGLQKKIQQIENELDQV  
QESLTQANTKLEEKESLQTAEGDVAALNRRRIQLIEEDLERSEGR LKIATSKLEEASQSA  
DESERMKMLEHRSITDEERMEGLESQKLEARMMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQIRIMTTKLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEKYKSISDELDTFAELTGY  
>AAF31151.1 Ole e 8; calcium-binding protein, polcalcin [Olea europaea]  
MAANTDRNSKPSVYLQEPNEVQGVFNRFDANGDGKISGDELAVL KALGSNTSKEEIGRI  
MEEIDTDKDGFINVQEF AAFVKAETDPYPSSGGENELKEAFELYDQDHNGLISSVELHKI  
LTRLGERYA EHDCEMIKSVSDSDGDGYVSFEF FKKMMTNKSGNNSQAEPK  
>AAF31152.1 Ole e 8; calcium-binding protein, polcalcin [Olea europaea]  
MAANTDRNSKPSVYLQEPNEVQGVFNRFDANGDGKISGDELACAL KALGSNTSKEEIARM  
MEEIDTDKDGFINVQEF AAFVKAETDPYPSSGGENELKEAFELYDQDHNGLISSVELHKI  
LTRLGERYA EHDCEMIKSVSDSDGDGYVSFEF FKKMMTNKSGNNSQAEPK  
>AAF34341.1 Hev b 8; profilin [Hevea brasiliensis]  
MSWQTYVDEHLMCDIDGHHLTAAAIIGHDGSVWAQSSSFQFKPEEVA AIMKDFDEPGSL  
APTGLHLGGTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALIIGIYDEPLTPGQCNMIVE  
RLGDYLLEQGM  
>AAF34342.1 Hev b 8; profilin [Hevea brasiliensis]  
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFQFKSDEVA AIMKDFDEPGSL  
APTGLHLGSTKYMVIQGEPEGAVIRGKKGSGGITVKKTSQALIIGIYDEPLTPGQCNMIVE  
RLGDYLLEQGM  
>AAF34343.1 Hev b 8; profilin [Hevea brasiliensis]  
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSGFQFKSDEVA AIMKDFDEPGSL  
APTGLHLGGTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALIIGIYDEPLTPGQCNMIVE  
RLGDYLLEQGM

>AAF35431.1 Cha f 1; tropomyosin [*Charybdis feriata*]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLPEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEK

>CAB76459.1 Gly d 2; NPC2-like [*Glycyphagus domesticus*]  
GKMKFKDCGKGEVTELDITDCSGDFCVIHRGKPLTLEAKFAANQDTTKATIKVLAKVAGT  
PIQVPGLETGCKFVKCPIKKGDPIDFKYTTTVPAILPKVKAEVTAELVGDHGV LACGRF  
GRQVE

>CAA09886.2 Mala s 8; unknown function [*Malassezia sympodialis*]  
MVALKFAAVLSVVAAMAAAPSSMDRRASPDNQVWVTSASDYCLILPRHRESIGDSESPG  
RMRSFCSKPYDSSQGQINPGFWKEVHFKKTKNYVQLTGCINPRVQSTLLSHDDGGQYDSN  
GNGGVGNPEGSVCLGYSSYVELVPSDGKACIRCCVNDKYCDVGHDEGCEAVIPGQYC

>CAA09938.2 Chi k 10; tropomyosin [*Chironomus kiiensis*]  
MDAIKKKMQAMKLEKDNALDRALLCENQARDANLRAEKAEEEARTLQKKIQTIENDLDQT  
QGQETLVNGKLEGKEKALQNAESEVAALNRRIQLLGEDLDRSEERLASATAKLSEASAAA  
DESERARKILENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE  
ERAEGEAKIVELEEEELRVVGNLKSLEVSEEKANQREEEYKNQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLDEDELVSEKEKYREIGDDLDTAFVELILKE

>CAB82855.1 Pis s 2; 11S globulin, cupin [*Pisum sativum*]  
MATTIKSRPLLLLLGIIFLASVVCVYANYDEGSEPRVPAQRERGRQEGEKEEKRHGEW  
RPSYEKEEDEEEGQRERGRQEGEKEEKRHGEWRPSYEKQEDDEEEKQKYRYQREKEDEEEK  
QKYQYQREKKEQKEVQPGRRERWEREEDEEQVDEEWRGSQRREDPEERARLRHREERTKRD  
RRHQREGEEERSSESQERRNPFLFKSNKFLTLFENENGHIRLLQRFDKRSDFENLQNY  
RLVEYRAKPHTIFLPQHIDADLILVVLVSGKAILTVLSPNDRNSYNLERGDTIKLPAGTTS  
YLVNQDDEEDLRLVLDVIPVNGPGKFEAFDLAKNKNQYLRGFSKNILEASYNTRYETIEK  
VLLLEEQEKDRRRRQGEETDAIVKVSREQIEELKKLAKSSSKSLPSEFEPINLRSHKPE  
YSNKFGLFEITPEKKYPQLQDLDFVSCVEINEGALMLPHYNSRAIVVLLVNEGKGNLE  
LLGLKNEQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAITASSNLNLLGFGINAE  
NNERNFLSGSDDNVISQIENPVKELTFPGSVQEIINRLIKNQKQSHFANAEPQKEQGSQG  
KRSPLSSILGTFY

>A59055 Api c 1; phospholipase A2 [*Apis cerana*]  
IIYPGTLWCGHGNVSSGPNELGRFKHTDACCRTDHMCPCDMSAGESKHGLTNTASHTRLS  
CDCDDTFYDCLKNSGEEKISSYFVGKMYFNLIDTKCYKLEHPVTGCGERTEGRCLRYTVDK  
SKPKVYQWFDLRKY

>AAF65312.1 Sol g 4; unknown function [*Solenopsis geminata*]  
MKTFVLVSCLLVFTQIIYAVDIKELKIMNRILEKCIRTVPKGENDPINPLKNVNVLYCAF  
SKRGIFTP KGVNTKQYIN YCEKTIINPADIKQCKKLISKCIKKVYDRPGPIIERSKNLLS  
CVLKKGVLELTVYGKKK

>AAF65313.1 Sol g 4; unknown function [*Solenopsis geminata*]  
MKTFVLVSCLLVFTQIIYAVDIKELKIVNRILKCKIRTVPKGENDPINPLKNVNVLYCAF  
SKRGIFTP KGVNTKQYIN YCEKTIINPADIKQCKKLISKCIKKVYDRPGPIIERSKNLLS  
CVRKKGVLELTVYGKKK

>AAB50734.2 Cyn d 1; beta-expansin [*Cynodon dactylon*]  
AIGDKPGPNITATYGSKWLEARATFYGSNPRGAAPDDHGGACGYKDVDKPPFDGMTACGN  
EPIFKDGLGCRACYEIKCKEPEVCSGEPVLVKITDKNYEHIAAYHFDLSGKAFGAMAKKG  
QEDKLRKAGELTLQFRRVKCKYPSGTKITFHIEKGSNDHYLALLVKYAAGDGNIVAVDIK  
PRDSDEFIPMKSSWGAIWRIDPKKPLKGPFSIRLTSEGGHALVQDDVIPANWKPDTVYTS  
KLQFGA

>AAF71379.1 Pen ch 18; serine protease [*Penicillium chrysogenum*]  
MKGFLSLTLLPLLVAASPVAVNSIHNDAAPI LSSM TSKDIPDSYIVVFKKHVDPSSASAH  
QSWLQEVHTAHTGRMELKKRSLFGDFEAFMGLKHTFHIAGSLLGYAGHFHEDVIEQIRR  
HPDVDYIEKDSEVRTMSEGSVEKNAPWGLARISHRESLSFGNFNKYLYAEEGGEGVDAYV  
IDTGANVKHVDFEGRANWGKTIPQGDAD EDGNHGHTCSGTIAGKKFGVAKKANVYAVKV  
LRSNGSGTMSDVVKGVEWAAEAHIKKS KKGDKKFKG SVANMSLGGGSSRTL DLAVNAAVD  
AGIHFAVAAGNDNADACNYS PAAAEKAITVGASTLADERAYFSNYGKCTDIFAPGLNILS  
TWVGS DHATNTISGTS MASPHIAGLLAYVVS LAPAKDSAYAVADVTPKQLKAALISVATE  
GTLTDIPSDTPNLLAWNGGGSANYTKILADGGYKAHNAETTVEDRIGI IIDS AEKAFHKE  
LGAIYSEIKDAVSV

>AAF72534.1 Bla g 7; tropomyosin [*Blattella germanica*]  
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANIRA EKAEFEARS LQKKIQQIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRRIQLLEEDLERSEERLATATAKLAESQAA  
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEE LR VVGNNLSLEVSEEKANLREEEYKQ QIKTLNTRLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEKYKYICDDLDMTFTELIGN

>AAF72625.1 Cup s 1; pectate lyase [*Cupressus sempervirens*]  
MDSPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD  
IYTATSAEDNPVNPTPGTLRYGATREKALWII F SQNMNIK LKMP LYVAGHK TIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHCNTSVLGDV LVSE SIGVEPVHAQDGD AITMRNVT  
NAWIDHNSLSDCSDGLIDVTL SSTGITISNNHFNH HKVML LGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRM PRARYGLVHVANNYDQWNIYAIGGSSNPTILSEGN SFAAPNENYKKEV  
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT  
KNAGVVA

>AAF72626.1 Cup s 1; pectate lyase [*Cupressus sempervirens*]  
MDSPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD  
IYTVTSAEDNPVNPTPGTLRYGATREKALWII F SQNMNIK LEMPLYVAGHK TIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHCNTSVLGDV LVSE SIGVEPVHAQDGD AITMRNVT  
NAWIDHNSLSDCSDGLIDVTL SSTGITISNNHFNH HKVML LGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRM PRARYGLVHVANNYDQWNIYAIGGSSNPTILSEGN SFTAPNENYKKEV  
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT  
KNAGVVA

>AAF72627.1 Cup s 1; pectate lyase [*Cupressus sempervirens*]  
MDSPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD  
IYTVTSAEDNPVNPTPGTLRYGATREKALWII F SQNMNIK LKMP LYVAGHK TIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHCNTSVLGDV LVSE SIGVEPVHAQDGD AITMRNVT  
NAWIDHNSLPDCSDGLIDVTL SSTGITISNNHFNH HKVML LGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRM PRARYGLVHVANNYDQWNIYAIGGSSNPTILSEGN SFTAPNENYKKEV  
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT  
KNAGVVA

>AAF72628.1 Cup s 1; pectate lyase [*Cupressus sempervirens*]  
MDSPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD  
IYTVTSAEDNPVNPTPGTLRYGATREKALWII F SQNMNIK LKMP LYVAGHK TIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHCNTSVLGNV LVSE SIGVEPVHAQDGD AITMRNVT  
NAWIDHNSLSDCSDGLIDVTL SSTGITISNNHFNH HKVML LGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRM PRARYGLVHVANNYDQWNIYAIGGSSNPTILSEGN SFAAPNENYKKEV  
TKRIGCVSTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT  
KNAGVVA

>AAF72629.1 Cup s 1; pectate lyase [*Cupressus sempervirens*]  
MDSPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD

IYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLKMPLYVAGHKTIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGNVLVSESIGVEPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLSTGTITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFAAPNENYKKEV  
TKRIGCVSTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYTSNEAFKVENGLAPQLT  
KNAGVVA

>AAF72991.1 *Oryza sativa*; beta-expansin [*Oryza sativa*]  
MASSCLLLACVVAAMVSAVSCGPPKVPVPPGNITAAAYGKQWLEARGTWYGKPKGAGPDDN  
GGACGYKDIDKAPFLGMNSCGNDPIFKDGKGCSCFEVKCSKPEACSDKPVIIHITDMNT  
EPIAAYHFDLSGHAFGAMAKEGKDEELRKAGIIDMQFRRVRCKYPGETKVTFFHVEKGSNP  
NYFAVLVKYVGGDGDVVKVELKEKGSEEWKPLNESWGAIWRIDTPKPLKGPFSLRVTES  
DQKLVANDVIPDNWKANALYKSEIQVD

>AAF75225.1 *Anisakis simplex*; paramyosin, partial [*Anisakis simplex*]  
PRAAGELQMKMSLYEKAQEALARENKKLQDELHEAKEALADANRKLHELDLENARLA  
GEIRDLQTALKESDAARREANRAQRLAADLQQLRIEMERRLQEKKEEEMEALRKNMQFEI  
DRLTAALADAEARMKAEISRLKKKYQAEIAELEMTVDNLNRANIEAQTIKKQSEQMKIL  
QASLEDTQRHLQQLDQYALAQRKISALSAELEECKVALDNAIRARKQAEVDLEEANVRI  
AELVSLTNNLTTIKNKLETELSTVRADLDETTKELHAADERANRALADAARAIEQLHEEQ  
EHSMKIDALRRSLEEQVKQLQVQIQEAEAAALLGGKRVIKLETRIRDLETALDEETRRH  
KETQNALRKKDRRIKEVQMQVDEEHKQFVMAQDTADRLLEKMNIQKRQLGEAESFTMANI  
QRVRRYQRELEDAEGRADQAESSLHLIRAKHRSSVVTGRSASASKVYVLEDEQ

>AAF80164.1 *Juniperus virginiana*; pectate lyase [*Juniperus virginiana*]  
MASPCLIAFLVFLCAIVSCCSDNPIDSCWRGDSNWGQNRMKLADCAVGFSGSSTMGGKGGD  
FYTVTSADDNPVNPTPGTLRYGATREKTLWIIIFSQNMNIKLKMPLYVAGHKTIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVVPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLGSTGTITIFNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRMPRARYGLVHVANNYDPWNIYAIGSSNPTILSEGNSFTAPNENYKKEV  
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT  
KNAGVVA

>AAF80166.1 *Juniperus virginiana*; pectate lyase [*Juniperus virginiana*]  
MASPCLIAFLVFLCAIVSCCSDNPIDSCWRGDSNWGQNRMKLADCAVGFSGSSTMGGKGGD  
FYTVTSADDNPVNPTPGTLRYGATREKTLWIIIFSQNMNIKLKMPLYVAGHKTIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVVPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLGSTGTITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF  
NQFGPNAGQRMPRARYGLVHVANNYDPWNIYAIGSSNPTILSEGNSFTAPNENYKKEV  
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT  
KNAGVVA

>CAB96215.1 *Hevea brasiliensis*; profilin [*Hevea brasiliensis*]  
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFQFKSDEVAAMKDFDEPGSL  
APTGLHLGGTKYMIQGEPAVIRGKKGSGGITVKKTGQALIIGIYDEPLTPGQCNMIVE  
RLGDYLLDQGL

>AAF82096.1 *Glossina morsitans*; unknown function, antigen 5 [*Glossina morsitans*]  
MNFVLATLSLLILGSAAVGGDYCGLCDNHDACVMQNVFQSGCPSGAKMIDLNKYQSALLD  
AHNKKRNHVAGGGESKLKRACQMATMKWDSELAKLAEYNVKQCQMNHDCRNTVKFKYAG  
QNLAELGRSGGPPPDYRKLIEKAVDKWYEEVKDCNQGYIDSYPMNRYRGAIGHFTVMVAE  
RNTHVGAASEYTKSNGFQYFLMACNYATTNMMEFPIYKSCGSSAQDCKSGKNSKYPNLC  
SPNEKYEVENKWIKNNGVEYH

>CAB96931.1 *Triticum aestivum*; thioredoxin [*Triticum aestivum*]  
MAASAATATAAAVGAGEVISVHSLEQWTMQIEEANAACKLVVIDFTASWCGPCRIMAPIF  
ADLAKKFPAAVFLKVDVDELKSIAEQFSVEAMPTFLFMKEGDVKDRVVGAIKEELTNKVG

LHAAQ

>P81295.1 Jun a 3; thaumatin-like [Juniperus ashei]

MARVSELAFLLAATLAISLHMQEAGVVKFDIKNQCGYTVWAAGLPGGGKRLDQGQTWTVN  
LAAGTASARFWGRTGCTFDASGKGSCQTGDCGGQLSCTVSGAVPATLAEYTSQSDQDYDDV  
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVDGGCNSACNVFKTDQYCCRNAY  
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>AAF86369.1 Asp f 1; ribonuclease mitogillin [Aspergillus fumigatus]

MTWTCINQQLNPKTNKWEDKRLLYNQAKAESNSHHAPLSDGKTGSSYAHWFTNGYDGNK  
LIKGRTPIKFGKADCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDKFDSKNKPKEDPGPA  
RVIYTYPNKVFVCGIVAHQRGNEGLRLCSH

>AAF86462.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]

MYKILCLSLVAAVARDQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEAN  
QNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVVKIAPKSENV  
VTVKVMGDDGVLACAIATHAKIRD

>P82534.1 Pru d 3; lipid transfer protein [Prunus domestica]

ITCGQVSSNLAPCINIVKGGGAVPPACCNGIRNVNMLARTTADRRAACNCLKQLSGSIPG  
VNPNNAAALPGKCGVNVYPKISASTNCATVK

>CAC0532.1 Hev b 9; enolase [Hevea brasiliensis]

MAITIVSVRARQIFDSRGNPTVEADVKLSDGYLARAAPVSGASTGIYEALERDGGSDYL  
GKGVSKAVENVNIIIGPALVGKPTDQVGDIDNFMVQQLDGTVNEWGWCKQKLGANAILAV  
SLAVCKAGAHVKGIPLYEHIANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPVG  
ASSFKEAMKMGAEVYHHLKSVIKKYGQDATNVGDEGGFAPNIQENKEGLELLKTAIAKA  
GYTGKVVIGMDVAASEFYGSDQTYDLNFKENNGSQKISGEALKDLYKSFVAEYPIVSI  
EDPFDQDDWAHYAKLTSEIGEKVQIVGDDLLVTNPKRVEKAIKEKACNALLLVNQIGSV  
TESIEAVKMSKRAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL  
LRIIEELGSEAVYAGANFRKPVEPY

>CAC05258.1 thaumatin-like [Cupressus arizonica (Hesperocyparis arizonica)]

VKFDIKNQCGYTVWAAGLPGGGKEFDQGTWTVNLAAGTASARFWGRTGCTFDASGKGSC  
RSGDCGGQLSCTVSGAVPATLAEYTSQSDQDYDDVSLVDGFNIPLAINPTNTKCTAPACKA  
DINAVCPSELKVDGGCNSACNVLQTDQYCCRNAYVNNCPATNYSKIFKNQCPQAYSYAKD  
DTATFACASGTDYSIVFCP

>AAG08987.1 tropomyosin [Haliothis diversicolor]

MDAIIKKMLAMKMEKENAVDRAEQNEQKLRDTEEQKAKIEEDLNNLQKKCANLENDFDNV  
NEQLQEAMAKLETSEKRVTEMEQEVSGTTRKITLLEEDLERNEERLQTATERLEEASKAA  
DESERGARVLESRLADDERIDQLEAQLKEAKYIAEDAERKYDEAARKLAITEVDLERAE  
ARLEAAEAKILEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT  
EAERTVSKLQKEVDRLDELLAEKEKYKAISDELDQTFAEELAGY

>AAG08988.1 tropomyosin [Perna viridis]

MDAIIKKMVAMKMEKKNALDRAEQLEQKLRTEEAKAKIEDDYNSLVKKNIQTENDYDNC  
NTQLQDVQAKYERAQKIQEHEQEIQSLTRKISLLEEGIMKAEERFTTASGKLEEASKAA  
DESERNRNVLENLNSGNDERIDQLEKQLTEAKWIAEEADKKYEEAARKLAITEVDLERAE  
ARLEAAEAKVIDLEEQLTVVGANIKTLQVQNDQASQREDSYEETIRDLTNRKDAENRAT  
EAERTVSKLQKEVDRLDELLTEKEKYKAISDELDATFAELAGY

>AAG08989.1 tropomyosin [Mimachlamys nobilis]

MDAIIKKMQAMKVDRENAQDLAEQMEQKLDKETAKAKLEEEFNELQKKLTATENNYDTV  
NEQLQEANTKLENSKQITQLESDVGGQLRRRLTLEEDYERSEEKLNSTTEKLEEASKAA  
DESERNRNVLEGRNSYEERIDELEKQLETAKNVATDADHKFDEAARKLAITEVDLERAE  
TRLEAADAKVLEEEELTVVGANIKTLQVQNDQASQREDSYEETIRDLTSLKDAENRAT  
EAERQVVKLQKEVDRLDELLAEKERYKAISDDLDQTFAEIAGY

>CAC05582.1 Jun a 2; polygalacturonase [Juniperus ashei]

MSMKFMAALAF LALQLIVMAAGEDQSAQIMLSDTKQYHRSSRNLRKRVHHRHDVAIVF  
NVEHYGAVGDGKHDSTDAFEKTNAAACNKL SAVFLVPANKKFVNNLVFYGPCQPHFSFK  
VDGTIAAYPDPKWKNSKIWMHFARL TDFNLMGTGVIDGQGNRWSDQCKTINGRTVCND  
KGRPTAIKIDFSKSVTVKELT LNSPEFHLVFGECDGVKIQGIKIKAPRDSPTNDGIDIF  
ASKRFEIEKCTIGTGDDCVAVGTGSSNITIKDLTCGPGHGMSIGSLGKGNRSRSEVSFVHL  
DGAKFIDTQNGLRITWQGGSLASHITYENVEMINAENPILINQFYCTSAACKNQRSA  
VKIQDVTFKNIHGTSATTAIQLMCSDSVPCSNIKLSNVFLKLTSGKVATCVNKNANGYY  
TNPLNPSCKSLHPGRTPKELELHQKPTLLMDEKMGASLNSSPPNCKNKCKGCQPCPKL  
IIVHPNPEDYYPQRWVCSCHNKIYNP

>BAA23360.2 Gly m 5; 7S globulin, vicilin, beta-conglycinin, partial [Glycine max]

VEKEECEEIIPRPRRQHPEREPQQPGEKEEDEDEQPRPIPFRPQPRQEEHEQREE  
QEWPRKEEKRGEKGSSEEEDEDEEEDERQFPFPRPPHQKEERKQEEDEDEEQRESEES  
EDSELRRHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNSKP  
NTLLLPHADADYLIVILNGTAILSLVNDDDRSYRLQSGDALRVPSGTTYVVNPDNNE  
NLRLITLAIPVKNPGRFESFFLSSTEAQQSYLQGF SRNILEASYDTKFEEINKVLFSREE  
GQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTISSEDKPFNLSRDPISNKLKGF  
FEITPEKNPQLRDLDFLSIVDMNEGALLPHFNSKAIIVILVINEGDANIELVGLKEQQQ  
EQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVNATSNLNFFAIGINAENNRNFLAG  
QDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKGPLSSILR  
AFY

>BAA74452.2 Gly m 5; 7S globulin, vicilin, beta-conglycinin, partial [Glycine max]

VEEEEECEEQIPRPRRQHPERERQQHGEKEEDEGEQPRPFPRRQPHQEEHEQKEE  
HEWHRKEEKHGKGSSEEEQDEREHRPHQPHQKEEKEHEWQHKQEKHQGKESEEEEEEDQD  
EDEEQDKESQESGESQREPRRHKNKNPFFHNSKRFQTLFKNQYGHVRVLQRFNKRSSQ  
LQNLRDYRILEFNSKPNTLLLPHADADYLIVILNGTAILTLVNDDDRSYNLQSGDALR  
VPAGTTYVVNPDNDENLRMITLAIPVKNPGRFESFFLSSTQAQQSYLQGF SKNILEASY  
DTKFEEINKVLFGREEGQQQGEERLQESVIVEISKKQIRELSKHAKSSSRKTISSEDKPF  
NLSRDPISNKLKGLFEITPEKNPQLRDLDFLSVDMNEGALFLPHFNSKAIIVLVIN  
EGEANIELVGIKEQQQRQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVNATSDLNFFA  
FGINAENNRNFLAGSKDNVISQIPSQVQELAFPGSAKDIENLIKSSQSESYFVDAQPQK  
EEGNKGRKGPLSSILRAFY

>CAC09234.1 Der p 7; bactericidal permeability-increasing like [Dermatophagoides pteronyssinus]

MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSKFER  
HIGIIDLKGQLDMRNIQVRGLKQMKRVGDANVKSEGDVKAHLLVGVHDDVVSMEYDLAY  
KLGDLHPNTHVISDIQDFVVELSLEVSEEGNMTLTSFEVRQFANVVNHIGGLSILDPIFA  
VLSDVLTAIQDTVRAEMTKVLAPAFKKELEARNQ

>AAF80379.2 Cyn d 1; beta-expansin [Cynodon dactylon]

AMGDKPGPNITATYGDKWLDAKATFYGSDPRGAAPDDHGGACGYKDVDKAPFDGMTGCGN  
EPIFKDGLACGSCYEIKCKEPAECSGEPVLIKITDKNYEHIAAYHFDLSGKAFGAMAKKG  
EEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSPPNYLALLVKYAAGDGNIVGVDIK  
PKGSDEF LPMKQSWGAIWRMDPPKPLKGPFTIRLTSESGHVEQDDVIPEDWKPDTVYKS  
KIQF

>BAB15802.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]

MGKPFFTLSLSSLCLLLLSSACFAITSSKFNECQLNMLNALEPDHRVESEGGLIETWNSQ  
HPELQCAVTVSKRTLNRNGLHLPSSYPYQMIIVVQKGGAIGFAFPGCPETFEPKQQQS  
SRRGSRSSQQQLQDSHQKIRHFNEGDVLVIPPVGYWYNTGDEPVVAISLLDTSNFNQQL  
DQNPRVLYLAGNPDIEHPETMQQQQQKSHGGRKQGQHQQQEEEGSVLSGFSKHFLAQS  
FNTNEDTAEKLRSPDDERKQIVTVEGGLSVISPKWQEQEDEDDEDEEYEQTPSYPPRRP  
SHGKHEDDEDEEEDQPRPDHPPQRPSRPEQQEPRGRGCQTRNGVEENICTMKLHENIA

RPSRADFYNPKAGRISTLNSLTLPALRQFGLSAQYVWLYRNGIYSPHWNLNANSVIYVTR  
GKGRVRVVCQGNVDFGELRRGQLLVVPQNFVVAEQGGEQGLEVVFKTHHNAVSSYIK  
DVFRAIPSEVLSNSYNLQSQVRQLKYQGNLPLVNP

>AAG22740.1 Bet v 6; phenylcoumaran benzylic ether reductase [Betula pendula]

MAHKSILIIIGGTGYIGKFIVEASAKSGHPTFALVRESTVSDPVKGLVEKFKGLGVTL  
HGDLYDHESLVKAFKQVDVVISTVGHQLADQVKIIAAIKEAGNIKRFFPSEFGNDVDRV  
HAVEPAKTAFAKAEIRRKTEAEGIPYTYVSSNFFAGYFLPTLAQPGLTSPPREKVVIFG  
DGNARAVFNKEDDIGTYTIRAVDDPRTLKNIYIKPAKNIYSFNEIVALWEKKIGKTLEK  
IYVPEEKLLKDIQESPIPINVILAINHSVFKGDHTNFEIEASFGVEASELYPDVKYTTV  
EEYLQQFV

>AAG23840.1 Ses i 4; oleosin [Sesamum indicum]

MADRDRPHPHQIQVHPQHPRHYEGGVKSLLPQKGPSTTQILAIITLLPISGTLCLAGIT  
LVGTILGLAVATPVFVIFSPVLVPAAILIAGAVTAFLTSGAFGLTGLSSLSWLNLSFRRA  
TGQGPLEYAKRGVQEGTLVYVGEKTKQAGEAIKSTAKEGGREGTART

>CAC13961.1 Hev b 10; superoxide dismutase [Hevea brasiliensis]

QTFSLPDLPHYDGALEPAISGEIMQLHHQKHQTYITNYNKALEQLNDAIEKGDAAVVK  
LQSAIKFNGGGHVNSIFWKNLAPVREGGELPHGSLGWADADFGSLEKLIQLMNAEGA  
ALRSGSWWVWALDKELKLVWETTANQDPLVTKGPTLVPLLGIDVWEHAYYLQYKNVRPD  
YLNKIWKVMNWKYASEVYAKECPSS

>CAC14917.1 Tri a 31; triosephosphate isomerase [Triticum aestivum]

MGRKFFVGGNWKCNVTVEQVESIVNTLNAGQIASTDVVEVWVSPPYVFLPTVKGLRPEI  
QVAAQNCWVKKGGAFTEVSAEMLVNLGVPWVILGHSERRSLMGESSEFVGEKVAYALAQ  
GLKVIACVGETLEQREAGSTMAVVAEQTKAIADKIKDWTNVVWVAYEPVWAIPTGKVASPA  
QAQEVHANLRDWLKTNVSPEVAESTRIIYGGSVTGASCKELAAQPDVDGFLVGGASLKPE  
FIDIINAAAVKSA

>AAG31026.1 alkaline serine protease [Bacillus licheniformis]

MMRKKSFWLGLTAFMLVFTMAFSDSASAAQPAKNVEKDYIVGFKSGVKTASVKKDIIKE  
SGGKVDKQFRIINAAKAKLDKEALKEVKNDPDVAYVEEDHVAHALAQTPYGIPLIKADK  
VQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNHGHGTHVAGTVAALD  
NTTGVLGVAPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNGMDVINMSLGGASGSTAMK  
QAVDNAYAKGVVVVAAAGNSGSSGNTNTIGYPAKYDSVIAVGAVDSNSNRASFSSVGAEL  
EVMAPGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATY  
LGSSFYYGKGLINV

>AAG35601.1 Zea m 12; profilin [Zea mays]

MSWQAYVDDHLLCDIEGQHLASAAIVGHDGSVWAQSENFPELKPEEVAGMIKDFDEPGTL  
APTGLFVGGTKYMIQGEQGVVIRGKKGTGGITIKKTGMSLIIGIYDEPMPGQCNMVE  
RLGDYLLIEQGF

>1G5U\_A Hev b 8; profilin [Hevea brasiliensis]

MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFQFKSDEVAAVMKDFDEPGSL  
APTGLHLGGTKYMIQGEQGVVIRGKKGSGGITVKRTGQALIIGIYDEPLTPGQCNMIVE  
RLGDYLLDQGL

>1QNX\_A Ves v 5; unknown function, antigen 5 [Vespula vulgaris]

AEAEFNKYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQEKQDILKEHNDFRQKI  
ARGLETRGNPGPPAKNMKNLVWDELAYVAQVWANQCQYGHDTCRDVAKYQVGGQNVAL  
TGSTAACYDDPVKLVKMWEDVVDYNPKKKFSGNDFLKTGHYTMVWANTKEVGCISIKY  
IQEKWHKHLYLVCNYGPSGNFKNEELYQTK

>1QMR\_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]

GVFNJETETTSVIPAARLFKAFILDGDTLFPQVAPQAISVENISGNGGPGTIKKISFPE  
GLPFKYVKDRVDEVDHTNFKNYSVIEGGPIGDTLEKISNEIKIVATGDGGSILKISNKY  
HTKGDHEVKAQVKASKEMGETLLRAVESYLLAHSDAYN

>AAG40329.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus avellana]

MGVFSYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTGAENLEGNGGPGTIKKITFA  
EGSEFKYMKHKVVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS  
KYHTKGNASISEEEIKAGKEKAAGLFKAVEAYLLAHPDTC

>AAG40330.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus avellana]

MGVFCYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTGAENLEGNGGPGTIKKITFA  
EGSEFKYMKHKVVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS  
KYHTKGNASISEEEIKAGKEKAAGLFKAVEAYLLAHPDTC

>AAG40331.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus avellana]

MGVFSYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTSAENLEGNGGPGTIKKITFA  
EGNEFKYMKHKVVEEIDHANFKYCYSIIEGGPLGHTLEKIPYEIKMAAAPHGGGSILKITS  
KYHTKGNASINEEEIKAGKEKAAGLFKAVEAYLLAHPDAYC

>AAG42254.1 Poa p 5; unknown function [Poa pratensis]

MAVQKYTVALFLTVALVAGPAASYAADAGYAPATPAAAGAAAGKITPTQEQLMEDINVG  
FKA AVAAAAGAPPADKFKTFQA AFSASVEASA AKLNAAQAPGFVSHVAATSDATYKAAVG  
ATPEAKFDSFVA AFTEALRIIAGVLKVHAVKPI TEETGAAKIPAGEQQIIDKIDAAFKVA  
ATAANAAPANDKFTVFEAAFNNAIKESTGGAYD TYKSIPSL EAAVKQAYAATIAAAPEVK  
FAVFKAALTKAITAMA EVQKVS KPVAGAATAATGAATGAAGAATGAATVSAGG  
YKV

>AAG42255.1 Hol l 5; ribonuclease [Holcus lanatus]

MAVQKYTVALFLTVALVAGPAASYAADAGYAP TTPAAAGAAAGKITPTQEQLMEDINVG  
FKA AVAAAAGAPPADKFKTFQA AFSASVEASA AKLNAAQAPGFVSHVAATSDATYKAAVG  
ATPEAKFDSFVA AFTEALRVIAGVLKVHAVKPI TE EIGAAKIPAGELQIIDKIDAAFKVA  
ATAANAAPANDKFTVFEAAFNNAIKESTGGAYD TYKSIPSL EAAVKQAYAATIAAAPEVK  
FAVFKAALTKAITAMA EVQKVS KPVAGAATAATGAATGAAGAATGAATVSAGGYKV

>AAG42802.1 Ory c 3; lipophilin [Oryctolagus cuniculus]

MKLLVPLLLLVALALGCYEADAAACPAFVLDSVGF LFDPKPVYRQKLAKYDAPPEAVEAKL  
QVKECTDEIDKGRVLI AAVLTKIVKECAL

>AAG42806.1 Ory c 3; lipophilin [Oryctolagus cuniculus]

MKVVMVLLLLAALPLYCYAGSGCVLLESVVEKTIDPSVSV E EYKADLQRFIDTEQTEAAVE  
EFKECFLSQSNETLANFRVMVHTIYDSLYCAAY

>AAG44478.1 Pen o 18; serine protease [Penicillium oxalicum]

MKGLLSLTLPLLAASPTWSETIHNGAAP LISSTSAKEIPDSYIVVFKKHVGASAASAH  
HSWVQDIHSDNVRMELKKRSLFGFESEPYLGVKHTFHVAGSLMGYAGHFHEDVIEQVRRH  
PDVEYIEKDSEVHHFEDPAIEKNAPWGLARISHRDSLSFGS FNKYLYAEDGGEGV DAYVI  
DTGTNV DHDVDFEGRASWGKTIPQGDQDVGNGHGT HCSGTIAGKKYGVAKKANVYAVKVL  
RSNGSGTMSDVVKGV EWA AEAHIKKSKAAKD GKAKGFKGSVANMSLGGGSSRTL DLAVNA  
AVDAGMHFAVAAGNDNADACNYS PAAA EKAVTVGASTLADERAYFSNYGKCTDIFAPGLN  
ILSTWIGSKYAVNTISGTS MASPHIAGLLAYYVSLQPASDSAYAVEEITPKKLDALITI  
ATSGALSDIPSDTPNLLAWNGGSSNYTEIVSKGGYKAGASESMKKHLDELVGKVEEVIA  
KEQKVL SHELGAIYSEIKDAVSA

>AAG44480.1 serine protease [Penicillium citrinum]

DSPSVEKNAPWGLARISHRDSLSFGTFNKYLYAEDGGEGV DAYVIDTGTNTDHDVDFEGR  
NWGKTIP EGDEVDGNGHGT HCSGTIAGKKYGVAKKANVYAVKVLRSNGSGTMSDVVKGV  
EWA AEAHIKKAGKKGFKGSVANMSLGGGSSRTL DLAVNAAVDAGIHFVAAGNDNADA  
CNYS PAAA ENAVTVGASTLADERAYFSNYGKCTDIFAPGLNILSTWIGSKYAVNTISGTS  
MASPHIAGLLAYYVSLQPSDDSAFAVEKITPKKLEALITVATSGALTDIPSDTPNLLAW

NGGGSSNYTDIVAQGGYKAGSTVEDFEEHIIHKLNVHAAEEVMHKELGAIYSEIKDAVAV  
>BAB21489.1 unknown function [Betula platyphylla]  
MGVFNJETEATSVIPAARLFKAFILDGDKLVPKVAPQAISSVENIEGNGGPGTIKKINFP  
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN  
>BAB21490.1 unknown function [Betula platyphylla]  
MGVFNJETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFKYVKDGVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN  
>BAB21491.1 unknown function [Betula platyphylla]  
MGVFNJETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP  
EGFPFEYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK  
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN  
>AAK01235.1 Cor a 2; profilin [Corylus avellana]  
MSWQTYGDEHLMCEIEGNRLAAAAIIGHDGSVWAQSSTFPQLKPEEITGMNDFNEPGSL  
APTGLYLGGTKYMVIQGEPEGAVIRRRKKGGVTVKKTSQLIIGIYDEPMTPGQCNMIVE  
RLGDYLIDQGL  
>AAK01236.1 Cor a 2; profilin [Corylus avellana]  
MSWQAYGDEHLMCEIEGNRLAAAAIIGHDGSVWAQSSTFPQLKPEEITGMNDFNEPGSL  
APTGLYLGGTKYMVIQGEPEGAVIRGKKGGVTVKKTSQLIIGIYDEPMTPGQCNMIVE  
RLGDYLIDQGL  
>AAK09361.1 Api c 1; phospholipase A2 [Apis cerana]  
IIYPGTLWCCHGNVSSGPNELGRFKHTDACCRTDHMCPPVMSAGESKHGLTNTASHTRLS  
CDCDDTFYDCLKNSGDKISSYFVGKMYFNLIIDTKCYKLEHPVTGCGERTEGRCLRYTVDK  
SKPKAYQWFDLRKY  
>AAD55792.2 Mes a 1; lipocalin [Mesocricetus auratus]  
MVKFLLLALALGVSCAQHQNLVSPSEVDGKWHSLYIAADNKSXVSEGGPLRVVVKHLEC  
SDECQFTTIKFYTKVENVCQEHVVRGKKGDKGYITDFSGQNYFHVVEKADDTMTFHNVN  
VDDSGKTNVILVVGKGESSSIEQKQRFKTAEKYDIPKENIEHLVTTDTCNQ  
>AAK15087.1 Ses i 7; 11S globulin, cupin [Sesamum indicum]  
MALTSLLSFFIVVTLIRGLSAQLAGEQDFYWDLQSQQHKLQARTDCRVERLTAQEPT  
IRFESEAGLTFWDRNNQQFECAGVAAVRNVIQPRGLLLPHYNNAPQLLYVVRGRGIQGT  
VIPGCAETFERDTPRQDRRRRFRMDRHQKVRQFRQGDILALPAGLTLWFYNNNGEPLITV  
ALLDGTGNAANQLDQTFRHFFLAGNPQGGQSYFGRPQTEKQQGETKNIFNGFDDEILADA  
FGVDVQTARRLKGQDDLGRIVRAERLDIVLPGEERWERDPYSGANGLEETLCTAKL  
RENLEPARADVYNPHGGRISSLSLTLPLVLSWLRLSAEKGVLVYRNLVAPHWNLNAHSI  
IYITRGSGRFQVVGHTGRSVFDGVVREGQLIIVPQNYVAKRASQDEGLEWISFKTNDNA  
MTSQLAGRLSAIRAMPEEVMTAYQVSRDEARRLKYNREESRVFSSTSRYSWPRSSRPM  
YMPKPFYVLDVIKSM  
>AAK15088.1 Ses i 1; 2S albumin, conglutin [Sesamum indicum]  
MAKKLALAAVLLVAMVALASATYTTTTVTTTAIDDEANQQSQCRQQLQGRQFRSCQRYL  
SQGRSPYGGEEDEVLEMSTGNQQSEQLRDCCQQLRVNVDRCRCEAIRQAVRQQQEGGY  
QEGSQQVYQRARDLPRRCNMRPQQCFRVIFV  
>AAK15089.1 Ses i 3; 7S globulin, vicilin-like [Sesamum indicum]  
MSCGGRLCLVLFALLASAVVASESKDPELKQCKHQCKAQQQISKEQKEACIQACKKEYIR  
QKHQGEHGRGGDILEEEVWNRKSPIERLRECSRGCEQQHGEQREELRRCQEEYQREKG  
RQDDNDPTDPEKQYQQCRLQCRRQEGGGFSREHCERRREEKYREQQGREGGRGEMYEGR  
EREEEQEEQGRGRIPYVFDQHFITGFRTQHGRMRVLQKFTDRSELLRGIENYRVAILEA  
EPQTFIVPNHWAESVVFVAKGRGTISLVRQDRRESLNIKQGDILKINAGTTAYLINRDN  
NERLVLAKLLQPVSTPGEFELFFGAGGENPESFFKSFSDILEAAFNTRRDLRQIFGQQ

RQGVIVKASEEQVRAMSRHEEGGIWPFGGESKGTINIYQQRPTHSNQYQQLHEVDASQYR  
QLRDLTLVSLANITQGAMTAPHYNSKATKIALVVDGEGYFEMACPHMSRSRGSYQGETR  
GRPSYQRVASRLTRGTVVIIPAGHPFVAVASSNQNLQVLCFEVNANNNEKFPLAGRNNVM  
NQLEREAKELAFGMPAREVEEVSRSQQEFFFFKGRPQQQGRADA

>AAB32652.2 Ole e 1; Ole e 1-like [Olea europaea]

QVYCDTCRAGFITELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLVERDHKN  
EFCEITLISSGSKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQVY  
NKLGMYPNNM

>AAK25823.1 Phl p 5; unknown function [Phleum pratense]

PISVTAPPPQLPRPPATPPPPPPQLGASPYKLGSPKARSERPAIVPPADKYRTFVATF  
GAASNKAFAEGLSGEPKGAESSKAALTSKLDAAVKLAYKTAEGATPEAKYDAYVATLS  
EALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFE  
AAFNNAIKAGTGGAYESYKFPALAAVKQAYAATVATAPEVKYTVFETALKKAITAMSE  
AQKAAKPAATAATATATSAVGAPTGATTAAGGYKV

>AAK28533.1 Cor a 8; lipid transfer protein [Corylus avellana]

MGSLKLVCAVLLCMMVAAPVARASLTCPQIKGNLTPCVLYLKNGGVLPSCCKGVRVND  
ASRTTSDRQSACNCLKDTAKGIAGLNPNLAAGLPGKCGVNIPYKISPSTNCNNVK

>AAK39511.1 Der f 11; paramyosin [Dermatophagoides farinae]

MNKKRDELAKLRKLLLEDVHIESEETAHHLRQKHQAATQEMQDQLDQLQKAKNKSDKEKQ  
KFQAEVFELLAQLETANKEKLTALKNVEKLEYTVHELNIKIEEINRTVIELTSHKQRLSQ  
ENTELIKEVHEVKLQLDNANHLKTQIAQQLDTRHRLEEEERKRASLENHAHTLEVELES  
LKVQLDEESEARLELERQLTKANGDAASWKSKEYAELQAHADVEEELRRKMAQKISEYEE  
QLEALLNKCSSLEKQKSRQLQSEVEVLIMDLEKATRHAQQLKRVQLEKINLDLKNKLEE  
VTMLMEQAQKELRVKIAELQKLQHEYEKLRDQRDLARENKKLTDDLAEAKSQLNDAHRR  
IHEQEIEIKRLENERDELSAAYKEAETLRKQEEAKNQRLIAELAQVRHDYEKRLAQKDEE  
IEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLKKKYQAQITELELSLDAANKANIDLQK  
TIKKQALQITELQAHYDEVHRQLQQAVDQLGVTQRRQALQAELEEMRIALEQANRAKRQ  
AEQLHEEAVVRVNELTTINVNLASAKSKLESEFSALQADYDEVHKELRISDERVQKLTIE  
LKSTKDLLIEEQERLVKLETVKKSLQEVRTLHVRIEEVEANALAGGKRVIKLESIRID  
VEIEVEEERRRHAETDKMLRKKDHRVKELLLQ

>AAK49451.1 Asp f 22; enolase [Aspergillus fumigatus]

MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGK  
GVLKAVKNVNETIGPALIKENIDVKDQSKVDEF LNKL DGTANKSNL GANAILGVSLAVAK  
AGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVNLGGSHAGGR LAFQEFMIVPDSAPSFS  
EALRQGAEVYQKLKALAKKKYQGSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTGK  
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPF  
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPGRIKKAIELEKSCNALLLVNQIGTLTESIQA  
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPCRSERLAKLNQILRIEEE  
LGENTVYAGSKFR TAVNL

>AAK51201.1 Pen c 22; enolase [Penicillium citrinum]

MPIAKVHARSVYVSRGNPTVEVDVVTETGLHRAIVPSGASTGQHEAVEL RDGDKAKWGGK  
GVLKAVKNVNETIGPALIKENIDVKDQAKVDEF LNKL DGTANKGNL GANAILGVSLAIAK  
AAAAEKGVPLYVHISDLAGTKKPYVLPVPFQNVNLGGSHAGGR LAFQEFMIVPDTAESFS  
EGLRQGAEVYQKLKALAKKKYQGSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTGK  
ISIAMDVASSEFYKTDKAKYDLDFKNPDSPTKWLTYEQLADLYKSLAAKYPIVSIEDPF  
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPLRIKKAIELEKSCNALLLVNQIGTLTESIQA  
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPARSERLAKLNQILRIEEE  
LGENAIYAGKNFR TSVNL

>AAK54834.1 Mus a 1; profilin [Musa acuminata]

MSWQAYVDDHLLCDIDGQCLTAAAI VGHGDSVWAQSDAF PQCKPEEIAAIMKDFDEPGSL

APTGLYLGGTKYMVIQGEPEGAVIRGKKKSGGVTIKKNLALIIGIYNEMTPGQCNMVVE  
RLGDYLFDDQGF  
>AAK56124.1 Zea m 1; beta-expansin [*Zea mays*]  
MGSLVNNIMVVGAVLAALVAGGSCGPPKVPVPPGNITTTNYNGKWL TARATWYGQPNGAGAP  
DNGGACGIKVNLPYSGMTACGNVPIFKDGKGCSCYEVRCCKEPECSGNPVTVYITDM  
NYEPIAPYHFDLSGKAFGLAKPGLNDKIRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGC  
NPNYLAVLVKYVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPF SIRLTS  
ESGKKVIAKDVIPANWRPDAVYTSNVQFY  
>AAG44693.2 Pen ch 18; serine protease [*Penicillium chrysogenum*]  
MKGFLSLTLLPLLVAASPVAVNSIHNDAAPISSMSTK DIPDSYIVVFKKHVDPSSASAH  
QSWLQEVHTAHTGRMELKKRSLFGDFEAFMGLKHTFHIAGSLLGYAGHFHEDVIEQIRR  
HPDVVDYIEKDSEVRTMSEGSVEKNAPWGLARISHRESLSFGNFNKYLYAEEGGEGV DAYV  
IDTGANVKHVDFEGRANWGKTIPQGDADDEGNGHGTHCSGTIAGKKFGVAKKANVYAVKV  
LRSNGSGTMSDVVKGVEWAAEAHIKSKKGDKKFKGVSANMSLGGGSSRTL DLAVNAAVD  
AGIHFAVAAGNDNADACNYSAAA EKAITVGASTLADERAYFSNYGKCTDIFAPGLNLS  
TWVGS DHATNTISGTSMASPHIAGLLAYVVS LAPAKDSAYAVADVTPKQLKAALISVATE  
GTLTDIPSDTPNLLAWNGGGSANYTKILADGGYKAHNAETTVEDRIGGIIDSAEKAFHKE  
LGAIYSEIKDAVSA  
>AAK58415.1 Blo t 1; cysteine protease [*Blomia tropicalis*]  
IPANFDWRQKTHVNP I RNQGGCGSCWAF AASSVAETLYAIHRHQNIILSEQELLDCTYHL  
YDPTYKCHGCQSGMSPEAFKYMKQKGLLEESHYPYKMKLNQCQANARGTRYHVSSYNSLR  
YRAGDQEIQAAIMNHGPVVIYIHGTEAHRNLRKGILRGAGYNDAQIDHAVVLVGGWTQN  
GIDYWIVRTSWGTQWGDAGYGFVERHHNSLGINNYPIYASL  
>AAK58515.1 Ole e 9; beta-1,3-glucanase [*Olea europaea*]  
MAANVQTSSLLFLVFLLLQNFYSANSQSFLGVNYGQLSDNLPSLQATVNLLKSTTIQKVR  
LFGAEPAVIKAFANTGVEIVIGFDNGDIPTLASNPNVASQFVKSNVMSFYPASNIIAITV  
GNEVLTSGDQKLISQLLPAMQNVQNALNAASLGKVKVSTVHAMAVLSQSYPPSSGVFNP  
GLGDTMKALLQFQSANDAPFMISPYFAYKNQPTPDTLAFCLFQPNAGQVDSGNHGKYT  
NMFDAQVDAVHSALNAMGFKDIEIVVAETGWPHGGDSNEVGPSLDNAKAYVGNLINHLKS  
KVGTPMPGKSIDTYLFSLYDEDKKTGASSEKYFGLFKPDGSTTYDVGLLKNTQNPTTPA  
TPTPTPKAAGSWCVPKPGVSDDQLTGNINYACGQIDCGPIQPGGACFEPNTVKAHAAYV  
MNLYYQSAGRNSWNCDFSQTATLTNTNPSYGACNFPSGSN  
>O04004.1 Amb a 6; lipid transfer protein [*Ambrosia artemisiifolia*]  
MDCIRILWSVAVGLLLVSWRPTMFAASPTCDTVQNILAPCAGFLTQEPSKACCTGVNNL  
NNSRKTADRVAVCNCIKELTKSIAYPDKRMP L LSTKCGVKPDFPAVDKNLDCSKLPV  
>CAC41633.1 Pla l 1; Ole e 1-like [*Plantago lanceolata*]  
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETDQD  
GVYRPLPVVGYHEDCEIKLVKSSRPDCSEIPKLAKGTIQT SKVDLSKNTTITEKTRHVKPL  
SFRAKTDAPGC  
>CAC41634.1 Pla l 1; Ole e 1-like [*Plantago lanceolata*]  
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETGQD  
GVYRPLPVVGYHEDCEIKLVKSSRPDCSEIPKLAKGTIQT SKVDLSKNTTITEKTRHVKPL  
SFRAKTDAPGC  
>CAC41635.1 Pla l 1; Ole e 1-like [*Plantago lanceolata*]  
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETGQD  
GVYRPLPVVGYHEDCEIKLVKSGRPDCSEIPKLAKGTIQT SKVDLSKNTTITEKTRHVKPL  
SFRAKTDAPGC  
>AAK62278.1 unknown function [*Dactylis glomerata*]  
MAVQKYTVALFLAVVLVAGPVASYAADAGYTPAAAATPATAGGKAMTEEQTLIEDVNAGF  
KAAVAAAASSAPPADKFKTFEATFTAACKANIAAAAATKVPLFVAKLDAAYAVAYKTATGPT

PEAKYDAFVAALTEALRVIAGALEVHAVKPAEEVPAAKIPAGELQIVDKIDAAYKIAAT  
AANAAPANDKFTVFEFAGFNKAIKESTGGAYESYKFIPTLEAAVKQAYAATVAAAPEVKYA  
VFEEALTKAITAMSEAQKVATPAAVATGAATAAASAATGAATAAAGGYKV  
>P92918.1 Api g 1; pathogenesis related protein, PR-10, Bet v 1-like [Apium  
graveolens]

MGVQKTVVEAPSTVSAEKMYQGFLLDMDTVFPKVLPQLIKSVEILEGDGGVGTVKLVHLG  
EATEYTTMKQKVDVIDKAGLAYTYTTIGGDILVDVLESVNEFVVVPTDGGCIVKNTTIY  
NTKGDVLPEDKIKEATEKSALAFKAVEAYLLANLQFLA

>Q9HDT3.2 Alt a 6; enolase [Alternaria alternata]

MTITKIHARSVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKSKWGGK  
GVTKAVANVNDTIAPALIKEKLDVKDQSAVDAFLNKLDTTNTNLGANAILGVSMIAIK  
AAAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVNLGGSHAGRLAFQEFMIVPCEAPTFS  
EAMRQGAEVYQKLKALAKKTYGQSAGNVGDEGGVAPDIQTAEALDLITKAIEEAGYTGK  
IKIAMDVASSEFYKADEKKYDLDFKNPDSKSKWLTYEQLAEMYKSLAEKYPIVSIEDPF  
AEDDWEAWSYFFKTYDQGQIVGDDLTVTNPEFIKKAIELKSCNALLLVNQGIGTITEAIQA  
AKDAFGAGWGMVSHRSGETEDVTIADIVVGLRSGQIKTGAPARSERLAKLNQILRIEEE  
LGDNAVYAGNNFRNAVNL

>Q9LEI9.1 Hev b 9; enolase [Hevea brasiliensis]

MAITIVSVRARQIFDSRGNPTVEADVKLSDGYLARAAPVPRGASTGIYEALERDGGSDYL  
GKGVSKAVENVNIIIGPALVGKPTDQVGDIDNFMVQQLDGTVNEWGWCKQKLGANAILAV  
SLAVCKAGAHVKGIPLYKHVANLAGNKNLVLVVPFNFVINGGSHAGNKLAMQEFMILPVG  
ASSFKEAMKMGAEVYHHLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKA  
GYTGKVVIGMDVAASEFYGSDKTYDLNFKEENNGSQKISGDVLDLYKSFVTEYPIVSI  
EDPFDQDDWEHYAKLTSEIGVKVQIVGDDLLVTNPKRVEKAIKEKACNALLLVNQIGSV  
TESIEAVKMSKRAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL  
LRIEEELGAEAVYAGANFRTPVEPY

>P78983.2 Alt a 3; heat shock protein 70 [Alternaria alternata]

KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS  
KVDEKLDAGDKQLTAEIDKTQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE  
GGMPGGMPGGGMPGGAPGGAAGDDGPTVEEVD

>Q92260.1 Pen c 19; heat shock protein 70 [Penicillium citrinum]

AYLGGTVNNAVITVPAYFNDSQRQATKDAGLIAGLNVLRIINEPTAAAIAYGLDKKTEGE  
RNVLIFFDLGGGTFDVSLLTIEEGIFEVKSTAGDTHLGGEDFDNRLVNHVNEFKRKHKKD  
LTTNARALRRLRTACERAKRTLSSAAQTSIEIDSLFEGIDFYTSITRARFEELCQDLFRG  
TMPEPVERVLDAKIDKSSVHEIVLVGGSTRIPKIQKLVSDFFNKDANKSINPDEAVAYGA  
AVQAAILSGDTSSKSTNEILLDVAPLSLGIETAGGVMTPLIKRNTPITTKSETFSTYS  
DNQPGVLIQVFEGERARTKDNLLGKFELTGIPPAPRGVPIEVTFDLDANGIMNVSASE  
KGTGKSNKITITNDKGRLSKEEIERMLAEAEKYKAEDEAEASRIQAKNGLESYAYSLKNT  
ITEGKLQMSDDDKKIEDKISEIISWLDNNQTAEKDEYESQQKELEAIANPIMQAAYGAA  
GGAPPQQRADGETEKKDEEELD

>Q9M5X7.1 Mal d 3; lipid transfer protein [Malus domestica]

MASSAVTKLALVVALCMAVSVAHAITCGQVTSSLAPCIGYVRSAGVPPACNGIRTING  
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLPGKCGVNPYKISTSTNCATVK

>P82971.1 Bom t 1; phospholipase A2 [Bombus terrestris]

IIFPGTLWCGNGLANGTNQLGSWKETDSCCRTHDMCPDLIEAHGSKHGLTNAADYTRLS  
CECDEEFRRCLHNSGDTVSAGFVGRYFTVLHTQCFRLDYPIVKCKVKSTILHRSKCYDF  
ETFAPKKYQWFDVLQY

>P58171.1 Syr v 3; polcalcin [Syringa vulgaris]

MAEEVAELERIFKRFDANGDGKISSSELGETLKTLSVTPPEEIQRMMAEIDTDGDFISF  
EEFKDFARANSGLIKDVAKIF

>Q9T0M8.1 Par j 3; profilin [*Parietaria judaica*]  
MSWQAYVDDHLMCDVGDGNTLASAAIIGHDGSVWAQSANFPQLKPEEVTGIMNDFNEGGF  
LAPTGLFLGGTKYMVIQGESGAVIGKKKSGGATLKKTGQAIVIGIYDEPMTPGQCNLVVE  
RLGDYLLEQGM

>Q9XG85.1 Par j 3; profilin [*Parietaria judaica*]  
MSWQAYVDDHLMCDVGDGNTPASAAIIGHDGSVWAQSANFPQLKPEEVTGIMNDFNEAGF  
LAPTGLFLGGTKYMVIQGESGAVIRGKKKSGGATLKKTGQAIVIGIYDEPMTPGQCNLVV  
ERLGDYLLEQGL

>O65200.1 Pyr c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Pyrus communis*]  
MGLYTFENEFTSEIPPPRLFKAFLVLDADNLIPKIAQAIKHAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRVDSIDEASYSYAYTLIEGDALDTIEKISYEAKLVASGSGSTIKSISHY  
HTKGDIEIKEEHVKAGKEKAHGLFKLIESYLKDHPDAYN

>Q9NAS5.1 Ani s 3; tropomyosin [*Anisakis simplex*]  
MDAIKKKMQAMKIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKKMMQTENDLDKA  
QEDLSTANSNLEEKEKKVQEAEEVAALNRRMTLLEEELERAEEERLKLATAKLEEATHA  
DESERVRKVMENRSFQDEERANTVESQLKEAQMLAEADRKYDEVARKLTMVEADLERAE  
ERAETGENKIVELEEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE  
FAERSVQKLQKEVDRLDEDELVHEKERYKSISEELDQTFQELSGY

>P19963.2 Ole e 1; Ole e 1-like [*Olea europaea*]  
EDIPQPPVSQFHIQGVYCDTCRAGFITELSEFIPGASLRLQCKDKENGDVTFTEVGYTR  
AEGLYSMLVERDHKNFECEITLISSGRKDCNEIPTEGWAKPSLKFKLNTVNGTTRTVNPL  
GFFKKEALPKCAQVYNKLGMYPPNM

>AAK63086.1 Gad m 1; calcium-binding protein, parvalbumin [*Gadus morhua*]  
MAFAGILADADCAA AVKACEAAESFSYKAFFAKCGLSGKSADDIKKAFFVIDQDKSGFIE  
EDELKLFQVFKAGARALDAETKAFKAGDSGDGGAIGVDEWAVLVKA

>AAK63087.1 Gad m 1; calcium-binding protein, parvalbumin [*Gadus morhua*]  
MAFAGILNDADITAALAACKAEGSFDHKAFFTKVGLAAKSPADIKKVFEIIDQDKSDFVE  
EDELKLFQNFASAGARALSDAETKVFLKAGDSGDGKIGVDEFAMGIKA

>AAK63088.1 calcium-binding protein, parvalbumin [*Theragra chalcogramma*]  
MSFAGVLADADVKAALAGCAAADSFNYKTFKACGLAAKSHEEVKKAFFVIDQDQSGFIE  
EDELKLFQTFGAGARELTAAETKAFLAAGDEDGDMIGVDEFVTLVKA

>AAK63089.1 calcium-binding protein, parvalbumin [*Theragra chalcogramma*]  
MAFAGILKDAEVAALAEACKSAGSFDHTKFFKSCGLAGKSSDDVKKAFGIIDQDQDFIE  
EEELKLFQNFASASARALSDAETKAFKAGDSGDGKIGVDEFAMVKA

>CAC42881.1 Hev b 11; chitinase [*Hevea brasiliensis*]  
EQCGRQAGGALCPGGLCCSQYGCANTPEYCGSGCQSCDGGGGGEGGIDLGSIISRST  
FEEMLKHRNDAACPAKGFYTYDAFISAAKAFPAFGTTGDVDTCKREIAAFFGQTSHTTG  
GWPTAPDGPYAWGYCYKEELNQASSYCSPPAYPCAPGKKYYGRGPIQLSWNYNYGQCGQ  
ALGLDLLNPNLDVATDRVISFKAAIWFWMTPQFPKPSCHDVITGQWSPTGHDISAGRAPG  
YGVITNIINGGLECGRGDARVEDRIGFYKRYCDMFAVGYGSNLDCYNQTPFGLG

>AAK67491.1 Cur l 2; enolase [*Curvularia lunata*]  
MAITKIHARSVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKTKWGGK  
GVTKAVANVNDIIPALIKEKLDVKDQSAVDAFLNKLDTENKTKLGANAILGVSMIAIAK  
AAAAEKGVPLYAHISDLAGTKKPYVFRFLSKNVLNGGSHAGGFLLFQEFMIAPAKTFAEA  
LRIRQGAEVYQKLKALTKKTYGQSAGNYGDEGGVAPDIQTAEALDLIVDAIEAAGHTGQ  
IKIAMDVASSEFFKDDEKKYDLDFKNPDSKSKWLTYPQLAEMYKSLAEKYPIVSIEDPF  
AEDDWEAWSHFYKDGDFQIVGDDLTVTNPEFIKTAIELKSCNALLLKVNQIGTISEAINA  
AKDAFGAGWGMVSHRSGETEDVTIADIVVGLRSGQIKTNAPARSERLAKYNQILRIEEE  
LGDKRLFAGNKFHNTAINLYL

>AAK67492.1 Cur l 3; cytochrome c [*Curvularia lunata*]  
MGFEQGDAAKGANLFKTRCAQCHTLKAGEGNKIGPELHGLFGRKTGSVAGYSYTDANKQK  
GIEWNHDTLFEYLENPKKYIPGTKMAFGGLKKPKDRNDLITFLEQETK  
>AAG02250.1 ferritin [*Dermatophagoides pteronyssinus*]  
MAANPESTTKTSRVRMNFHKECEAGINKQINLELYASYVYQQMAFHFNRREDVALPGFEKF  
FHESSEEEEREHAEKLMKLNQRGGRIVLQDIPKPVQQDWSSGLEALKASLELEKTVNQSL  
LDLHDLATKHNDAQFADFIESNYLHEQVEAIKKLADYITNLERCOSVGLGEYLFDRHTLQ  
>CAC48400.1 Jun o 1; pectate lyase [*Juniperus oxycedrus*]  
MASPCLRAVLVFLCAIVSCYSDNPIDSCWRGDSNWGQNRMKLADCVVGFSGSSTMGGKGG  
FYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKKMPLYVAGHKIDGRGADV  
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMMLLGHDDTYDNDKSMKVTVAF  
NQFGPNAGQRMPPRARYGLVHVANNYDPWNIYAIGSSNPTILSEGNSFTAPSESYKKEV  
TKRIGCESTSACANWVWRSTRDAFTNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT  
KNAGVVT  
>AAK96255.1 Cyn d 1; beta-expansin [*Cynodon dactylon*]  
AMGDKPGPNITATYGDKWLDAKATFYGSDPRGAAPDDHGGACGYKDVKAPFDGMTGCGN  
EPIFKDGLACGSCYEIKCKEPAECSGEPVLIKITDKNYEHIAAYHFDLSGKAFGAMAKKG  
EEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSPPNYLALLVKYAAGDGNIVGVDIK  
PKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGHVEQDDVIPEDWKPDTVYKS  
KIQF  
>AAK96887.1 Ara h 2; 2S albumin, conglutin [*Arachis hypogaea*]  
MAKLTILVALALFLAAHASARQQWELQGDRCQSQLERANLRPCEQHLMQKIQRDEDSY  
ERDPYSPSQDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRMCCEALQQIMENQSDRL  
QGRQQEQQFKRELRLNPQQGLRAPQRCDLDVESGG  
>AAK13027.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFTYESEFTSVIPPARLFNAFVLADNLIPIKQAVKSAEILEGDDGGVGTIKKINFG  
EGSTYSYVVKHRIDGVKDNFVYKYSVIEGDAISETIEKISYETKLVAAGSGSVIKSTSHY  
HTKGDVEIKEEHVKAGKEKASHLFLKIENYLLEHQDAYN  
>AAK13029.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVCTFENEFTSEIPPSRLFKAFVLADNLIPIKQAIKQAEILEGNGGPGTIKKITFG  
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVAAGSGSTIKSISHY  
HTKGNIEIKEEHVKVKGKEKAHGLFKLIESYLKDHDPDAYN  
>AAK13030.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVYTFENEYTSIPPPRLFKAFVLADNLIPIKQAIKHAIEILEGDDGGPGTTKKITFG  
EGSQYGYVVKHKIDSVDANYSAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY  
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYLKGHDPDAYN  
>AAK96889.1 Cra g 1; tropomyosin [*Crassostrea gigas*]  
NSARGFDTVNEKYQECQTKMEEAEKTASEAEQEIQSLNRRRIQLLEEDMERSEERLQTATE  
KLEEASKAADESERNRNVLENLNNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAI  
TEVDLERAEARLEAAEAKVLELEELKVVGNMKSLEISEQEASQREDSYEETIRDLTQR  
LKDAENRATEAERTVSKLQKEVDRLLEDELLAEKERYKAISDELDTFAELAGY  
>BAB64303.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [*Glycine max*]  
MMRARFPLLLLGVVFLASVSVSFGIAYWEKQNP SHNKCLRSCNSEKDSYRNQACHARCNL  
LKVEEEEECEEGQIPRPRPQHPERERQQHGEKEEDEGEQPRPFPPRPRQPRQEGEHEQK  
EEHEWHRKEEKHGKGSEEEQDGREHPRPHQPHQKEEEKHEWQHKQEKHQKESEEEEED  
QDEDEEQDKESQESGESQREPRRHKNKNPFFHNSKRFQTLFKNQYGHVRVLQRFNKR

QQQLQNLRDYRILEFNPKPNTLLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDALRVPAGTTYVVPNDNDENLRMITLAIPVKNKGRFESFFLSSTQAQQSYLQGFSGKNILEASDYDTKFEINKVLFREEGQQQGEERLQESVIVEISKKQIRELSKRAKSSSRKTISSEDKPFNLRSRDIYSNKLGLKFEITPEKNPQLRDLDFLSVDMNEGALFLPHFNSKAIIVLVINEGEANIELVGIKEQQQRQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVVNATSDLNFAFGINAENNQRNFLAGSKDNVISQIPVQVQELAFVLSAKDIENLIKSSQSESYFVDAQPQKKEEGNKGRKGPLSSILRAFY

>BAB64306.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]

MMRVRFPLLVLGTVFLASVCSLKVREDDENPFYFRSSNSFQTLFENQNGRIRLLQRFNKRSPQLENLRDYRIVQFQSKPNTILLPHHADADFLFVLSGRAILTLVNNDDRDSYNLHPGDAQRIPAGTTYLVNPHDQNLKIIKLAIPVKNKPSRYDDFFLSSTQAQQSYLQGFSHNILETSFHSEFEIINRVLFGEEEEQRQQEGVIVELSKEQIRQLSRRAKSSSRKTISSEDEPFNLRSRNPIYSNNFGKFFEITPEKNPQPRDLDFLSSVDINEGALLLPHFNSKAIIVILVINEGDANIELVGIKEQQQKQKQEEEPLEVRKYRAELSEDDVVFVIPAAYPFVVNATSNLNLFAFGINAENNQRNFLAGKDNVVRQIERQVQELAFVLSAQDVERLLKKQRESYFVDAQPQQKEEGSKGRKGPFPSSILGALY

>AAF07903.2 Tria p 1; procalin [Triatoma protracta]

MKTFFIVITFIGILSYAYADECENPEPMQGFSAQFYQGXWYVTHETSAXTLSECNILTTSDNDNGKFTVKHKYTKDGXVGECEGQASANNKFTYDCKFXGZTMEQVTRTAMDTDYNDYALYYLCTTYKXGPNAGKKEGHYILSRRQPNTIIPDALKTKTKDLNLKLCG

>AAL07320.1 Lit c 1; profilin [Litchi chinensis]

MSWQTYVDDHLMCETDGOHLTAATAIIGHDGSVWAQSANFPQFKPAEIAAIMKDFDEPGSLAPTGLHLGGTKYMIQGEPEGAVIRGKKKGGGITVKKTTQALIIGIYDEPMTPGQCNMVERLGDYLVQGL

>1JTI\_A Gal d 2; ovalbumin [Gallus gallus]

GSIGAASMEFCDFVKELKVHANNENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPFGDGSIEAQCGTSVNVHSSLRDILNQITKPNVVSFSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIVFKGLWEKTFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIIINFELTEWTSSNVMEERKIKVYLPKMKMEEKYNLTSVLMAMGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGTEVVGSAEAGVDAASVSEEFRA DHPFLFCIKHIATNAVLFFGRCVSP

>CAC85911.1 Plo i 1; arginine kinase [Plodia interpunctella]

MVDAATLEKLEAGFSKLAASDSKSLKYLTRVDFDALKNKKTSFGSTLLDSIQSGVENLHSGVGIYAPDAEAYVVFADLFDPIIEDYHNGFKKTDKHPKKNWGDVETLGNLDPAGEFVVSTRVRCGRSMEGYPFNCLTEAQYKEMEEKVSSLSGLEGELKGTFFPLTGMSKETQQQLIDDHFLFKEGDRFLQAANACRFWPSGRGIYHNENKTFVWCNEEDHLRLISMQMGDLKQVYKRLVRGVNDIAKRIPFSHNERLGFLLFCPTNLGTTVRASVHIKLPKLAADKAKLEEVA SKYHLQVRGTRGEHTEAEGGVYDISNKRMRGLTEYEAVKEMYDGAELIKIEKSL

>AAL14077.1 Cyn d 1; beta-expansin [Cynodon dactylon]

MLAVVAVVLASMVGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGACGYKDVKAPFDGMTGCGNEPIFKDGLACGSCYEIKCKEPAECSGEPVLIKITDKNYEHIAAYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLALLVKYAAGDGNIVSVDIKSKGSDEFVLPKQSWGAIWRIDPPKPLKGPFTIRLTSESAGGHVEQEDVIPEDWKPDTVYKSKIQF

>AAL14078.1 Cyn d 1; beta-expansin [Cynodon dactylon]

MLAAVAVVLASMVGGAWCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGACGYKDVKAPFDGMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIAAYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKITFHVEKGSNPNYLALLVKYAAGDGNIVGVDIKPKGSDVFLPMKLSWGAIWRMDPPKPLKGPFTIRLTSESAGGHV

EQEDVIPEDWKPDTVYKSKIQF

>AAL14079.1 Cyn d 1; beta-expansin [*Cynodon dactylon*]  
MLAVVAVVLASVMGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC  
GYKDVKAPFDSMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA  
AYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLA  
LLVKYAAGDGNIVSVDIKSKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGGHV  
EQEDVIPEDWKPDTVYKSKIQF

>CAD10374.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]

MGVFTHENEITSAIPPGRLFKAFVLDADNLIPKLAPHAIKSAEIIEGNGGPGTIKKITFG  
EGSQFKYVXHRIDEIDQANFTYCYSVIEGDVNNELLEKISYEIKIVASPDGGSILKNTSK  
YHTKGEQEIKEEKVMAGKEKAAGLFKAVEAYLLAHS DAYN

>CAD10376.1 Cap a 2; profilin [*Capsicum annuum*]

MSWQTYVDDHLMCEIEGNRLTSAAIIGQDGSVWAQSATFPQFKPEEITAIMNDFAEPTL  
APTGLYLGGTKYMVIQGEAGAVIRGKKKGGGITVKKTNQALIIGIYDEPMTPGQCNMIVE  
RLGDYLI EQSL

>CAD10377.1 Sola l 1; profilin [*Solanum lycopersicum*]

MSWQTYVDEHLLCENEGNHLTSAAIIGQDGTVWAQSANFPQFKPEEITGIMNDFAVPGTL  
APTGLYLGGTKYMVIQGEPEAVIRGKKKGGGITIKKTNQALIIGIYDEPMTPGQCNMIVE  
RLGDYLI EQSL

>BAB71741.1 glyoxalase [*Oryza sativa*]

MASGSEAEKSPEVVLEWPKKDKKRVLHAVYRVGDLDRITKCYTECFGMKLLRKRDPVEEK  
YTNAFLGFGPEDTNFALELTNYNGVDKYDIGAGFGHFAIATEDVYKLAEKIKSSCCCKIT  
REPGPVKGGSTVIAFAQDPDGYMFE LIQRGPTPEPLCQVMLRVGDLDRSIKFYEKALGMK  
LLRKKDVPDYKYTIAMLYADEDKTTVIELTYNYGVTEYTKGNAYAQVAIGTEDVYKSAE  
AVELVTKELGGKILRQPGPLPGLNTKIASFLDPDGWKVVLVDNADFLKELQ

>CAC34055.2 Cap a 1; thaumatin-like [*Capsicum annuum*]

MGYLRSSFVLFLLAFVITYYAATFEVRNNCPTYVWAASTPVGGRRDRGQWTINAPPG  
TAMARIWGRNTCNFDGSGRSCQTGDCGGVLQCTGWGKPPNTLAEYALNQFNLD FWDIS  
LVDGFNIPMTFAPTNPSGGKCHAIQCTANINGECPGSLRVPGGCNPCTTFGGQQYCCTQ  
GPCGPTLSKFFKRCRCPDAYSYPQDDATSTFTCPSGSTNYRVVFCPNGVTGPNFLEMPG  
SDGVAK

>AAL29690.1 profilin [*Solanum lycopersicum*]

MSWQTYVDDHLMCDIEGNHLTSAAIIGQDGSVWAQSANFPQFKPEEITAIMNDFAEPTL  
APTGLHLGGTKYMVIQGEAGAVIRGKKGAGGITVKKTNQALIIGIYDEPMTPGQCNMIVE  
RLGDYIIEQGL

>AAL37561.1 Ara h 6; 2S albumin, conglutin [*Arachis hypogaea*]

AKSTILVALLALVLVAHASAMRRERGRQGDSSSCERQVDRVNLKPCEQHIMQRIMGEQE  
YDSYDIRSTRSSDQQQRCCDELQMENTERCMCEALQQIMENQCDRLQDRQMVQQFKREL  
MNL PQCNFRAPQRCDL DVSGGRC

>BAB79444.1 2S albumin, conglutin [*Fagopyrum esculentum*]

MKLFLILAAASLLIVASHADSQMRSKCRKQMRMMEPQLEQCEGYMTMDMMDDSMRGREC  
RSEESCMRGCLAMKEMDDECMCEWMMMMVQQQRGEMGEEDMRMVMRKMQLPNKCGMGH  
MRCHMGIGTRDYE

>CAC81811.1 Mus a 2; chitinase [*Musa acuminata*]

MKALLLVI FT LASSLGAFAEQCRQAGGALCPGG LCCS QY GWCNTDPYCGQGCQSQCGG  
SGGSGGGSVASIISSSLFEQMLKHRNDAACPGKGFYTYNAFIAAANSFSGFGTTGDDAKK  
KREIAAFLAQTSHETTGGWATAPDGPYAWGYCFVQE QNPSSDYCVASSQWPCAAGKKYYG  
RGPIQISFNINYGPAGRAIGS DLLNNDLVATDATISFKTALWFWMTPQSPKPSCHDVIT  
GSWTPSNADQAAGRLPGYGVTTNIINGGLECGKGYDARVADRIGFYKRYCDLLGVS YGDN

LDCYNQRPFFASTAATATF

>AAL49391.1 Fel d 3; cystatin A [*Felis catus*]

MIPGGLSEAKPATPEIQEIANEVKPKLEEKTNETYQKFEAIEYKTQVVAGINYYIKVQVD  
DNRYIHIKVKFKGLPVQDSSLTLTGYQTGKSEDELDTGF

>CAC83658.1 Cyp c 1; calcium-binding protein, parvalbumin [*Cyprinus carpio*]

MAFAGILNDADITAALQGCQAADSFYKSFFAKVGLSAKTPDDIKKAFVIDQDKSGFIE  
EDELKLFQNFSAGARALDAETKAFLKAGDSDGDGKIGVDEFAALVKA

>CAC83659.1 Cyp c 1; calcium-binding protein, parvalbumin [*Cyprinus carpio*]

MAFAGVLNDADITAALAEACKAADSFNHKTFFAKVGLTSKSAADDVKKAFVIDQDKSGFIE  
EDELKLFQNFSAGARALDGETKTFKAGDSDGDGKIGVDEFTALVKA

>AAL47677.1 Der f 2; NPC2-like [*Dermatophagoides farinae*]

DQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAKIEIKASLDG  
LEIDVPGIDTNACHFMKCLPVKGGQYDAKYTWNVPKIAPESENVVTVKLVGDNGVLACA  
IATHAKIRD

>CAD20405.1 unknown function [*Dactylis glomerata*]

ADAGYTPAAAATPAAAGGKAMTEEQKLIEDVNAGFKAAVAAAASSAPPADKFKTFEATFTA  
ACKANIAAAAATKVPLFVAKLDAAYAVAYKTAAGPTPEAKYDAFVAALTEALRVIAGALEV  
HAVKPAEEVPAAKIPAGELQIVDKIDAAYKIAATAANAAPANDKFTVFEGAFNKAIKES  
TGGAYESYKFIPTLEAAVKQAYAATVAAAPEVKYAVFEAALTKAITAMSEAQKVATPAAA  
ATGAATAAASAATGAATAAAGGYKV

>CAD20406.1 beta-expansin [*Dactylis glomerata*]

MASSSSSVLLVVALFAVFLGSAHGIPKVPVPGPNITATYGDKWLDKSTWYGKPTGAGPKD  
NGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVHITDDN  
EEPIAPYHFDLGSAFGSMACKGEEQKLRSGELELQFRRVKCKYPEGTVTFHVEKGSN  
PNYLALLVKYVDGDDVAVDIKEKKGDKWIALKESWGAIWRVDPDKLTGPFTVRYTTE  
GGTKSEVEDVIPEGWKADTSYEAK

>Q91483.3 Sal s 1; calcium-binding protein, parvalbumin [*Salmo salar*]

MSFAGLNDADVAAALAACTAADSFNHKAFFAKVGLASKSSDDVKKAFYVIDQDKSGFIEE  
DELKLFQNFSAARALDAETKAFLADGDKDGMIGVDEFAAMIKG

>CAC86258.1 Fra a 3; lipid transfer protein [*Fragaria x ananassa*]

MASSTAMKLSLVALLCIVVALPIAQAITCGQVASNISPLTYVKSGGAVPAACCSGIRNL  
NGMAKTTADRQAACNCLKQAAGGIKGLNPNLAAGLPGKCGVSVPYKISTTTNCAAVK

>AAL73404.1 Cor a 9; 11S globulin, cupin [*Corylus avellana*]

MAKLILVSFSLCLLVLFNGCLGINVGLRRQQRYFGECNLDRLNALEPTNRIEAEACQIE  
SWDHNDQQFQCAGVAVIRRTIEPNGLLLPQYSNAPELIYIERGRGITGVLPFGCPETFED  
PQQSQQQGQRQGGQSQRSEQRHQRHFRFREGDIALPAGVAHWYNDGSDSPVVTVSL  
HTNNYANQLDENPRHFYLAGNPDDHEQRQGGQQFGQRRRQQQHSHEGQEQEQEGENNV  
FSGFDAEFLADAFNVDVDTARRLQSNQDKRRNIVKVEGRLQVVRPERSRQEWERQERQER  
ESEQERERQRRQGGGRDVGFEETICSLRLRENICTRSRADIYTEQVGRINTVNSNTLP  
VLRWLQLSAERGLDQREGLYVPHWNLNAHSVYAIRGRARVQVDDNGNTVFDDELRRQGG  
VLTIPQNFVAVAKRAESEGFVAFKTNDNAQISPLAGRTSAIRALPDDVLANAFQISREE  
ARRLKYNRQETTLVRSRSSSERKRRSESEGRAEA

>AAL75449.1 Sola l 2; beta-fructofuranosidase [*Solanum lycopersicum*]

MATQCYDPENSASRYTLDPDQPSGHRKSLKIISGIFLSVFLLLSVAFFPILNNQSPDLQ  
IDSRSPAPPSRGVSVQGVSDKTRFDVAGASHVSYAWSNAMLSWQRTAYHFQPPQKNMNDPN  
GPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLFPFAMVPDQWYDINGVWTGS  
ATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWWKFKGNPVLVPPPGIGVKDF  
RDPTTAWTGPQNGQWLLTIGSKIGKTGVALVYETSNTSFKLLDGLHAVPGTGMWECVD  
FYPVSTKKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLGKNKWTDPNPELDCGI  
GLRLDYGKYYASKTFYDPKKERRVLWGWIGETDSEADLQKGWASVQSIPTVLYDKKTG

THLLQWPVEEIESLRVGDPTVKQVDLQPGSIELLRVDSAAELDIEASFEVDKVALQGIIE  
ADHVGFSCTSGGAASRGILGPFVIVIAEQTLSELTPVYFYISKGADGRAETHFCADQT  
RFAFLSGTINLSL

>AAL75450.1 Sola l 2; beta-fructofuranosidase [*Solanum lycopersicum*]

MATQCYDPENSASRYTLLPDQPDGHRKSLKIISGIFLSVFLLSVAFFPILNNQSPDLQ  
IDSRSPAPPSRGVVSQGVSDKTFRDVAGASHVSYAWSNAMLSWQRTAYHFQPKQKNWMDPN  
GPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGS  
ATILPDGQIIMLYTGDYVQVQNLAYPANLSDPLLLDWWKFKANPVLVPPPVGIVKDF  
RDPITAWTGPQNGQWLLTIGSKIGKTGVALVCETSNTSFKLLDGVLHAVPGTGMWECVD  
FYPVSTKKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLGKNKWTDPNPELDCGI  
GLRLDYGKYASKTFYDPKRERRVLWGWIGETDSEADLQKGWASVQSIPTVLYDKKTG  
THLLQWPVEEIESLRVGDPTVKQVDLQPGSIELLRVDSAAELDIEASFEVDKVALQGIIE  
ADHVGFSCTSGGAASRGILGPFVIVIAEQTLSELTPVYFYISKGADGRAETHFCADQT  
RSSEAPGVGKQVYGVSSVPLDGEKHSRLLVDHSIVESFAQGGRTVITSRIYPTKAVNGA  
ARLFFVFNATGASVTASVKIWSLESANIQSFPLQDL

>AAL76932.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKTEVEAPSTVSAEKMYQGFLLDMDTVFVKVLPQLIKSVEILEGGVGTVRLVHLG  
EATEYTTMKQKVDVIDKAGLGTYTTTIGGDILVEGLESVVNQFVVVPTDGGCIVKNTTIY  
NTKGDVLPEDKVKEATEKSALAFKAVEAYLLAN

>AAL76933.1 Dau c 4; profilin [*Daucus carota*]

MSWQTYVDDHLMCEVDGNPQQLSAAAIIGHDGSVWAQSSTFPKFKPEEITGIMKNFDEP  
GHLAPTGLYLGGTKYMIQGEPIAVIRGKKGSGGVTIKKTGQALVFGVYDEPVTGQCNL  
IVERLGDYLIQGL

>CAC37790.2 Cup a 1; pectate lyase [*Cupressus arizonica* (*Hesperocyparis arizonica*)]

MASPCLVAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCVVGFGLTMGGKGGE  
IYTVTSSDDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGADV  
HLGNGGPCLFMRTASHVILHGLHIHCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVT  
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMMLLGHDDTYDDDISMKVTVAF  
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFTAPSESYKKEV  
TKRIGCESTSACANWVWRFTRDAFTNGAYFVSSGKAEETNIYNSNEAFKVENGNAAPQLT  
QNAGVVT

>CAA09887.4 Mala s 9; unknown function [*Malassezia sympodialis*]

MSNVIKKVFNTDKAEAEESKVADAPQEAGHKGEGLHDAKDRLQGFAGHGHNAQNAASG  
VAGSAGAGGAPSVPSANVDVTPVNDASVQGGVEAPRSWSTQLPQSQSVADTTGATSAGR  
NNLTQTTSTGSGVNVAAGNVDDQVQHLAPVTRHVHHRHEIEELLREREHHIHQHHIQHHV  
QPVVDEHLEAEQIHSRVVPQTTVREHANTDKDAALMRAVAGNPKDTFTQAAIDRSVIDK  
GETVREIVHHHHIHNIVQPIIEKETHEYHRIRTTIPTTHITHEAPIVHESTAHQPIRKEDF  
LKGGGVLTSTTRSIEEVGLLNLGNNQRTVEGETYTGGLPLSQ

>AAL86701.1 tropomyosin [*Periplaneta fuliginosa*]

MDAIIKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARSQKKIQQIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATAKLAEASQAA  
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVLEEEELRVVGNLKSLEVSEEKANLREEAYKQQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMFTTELIGN

>AAL86739.1 Cor a 11; 7S globulin, vicilin-like [*Corylus avellana*]

MLPKDEPELKKCKHKCRDERQFDEQRRDGKQICEEKARERQQEEGNSSEESYGKEQEEN  
PYVFQDEHFEESRVKTEEGRVQVLENFTKRSRLLSGIENFRLAILEANPHTFISPAHFDAE  
LVLVAKGRATITMVREEKRESFNVEHGDIIIRIPAGTPVYMINRDENEKLFIVKILQPVS  
APGHFEAFYGGAGEDPESFYRAFSWEVLEAALKVRRREQLKVFGEQSKGSIVKASREKIR

ALSQHEEGPPRIWPFGGESSGPINLLHKHPSQSNQFGRLYEHPDDHKQLQDLDLMVSFA  
NITKGS MAGPYNSRATKISVVVEGEGFFEMACPHLSSSSGSYQKISARLRRGVVVFVAPA  
GHPVAVIASQNNNLQVLCFEVNAHGNSRFPLAGKGNIVNEFERDAKELAFNLPSREVERI  
FKNQDQAFFPQPNKQQEEGRRGRAFE

>AAK27264.1 isoflavon reductase-like protein, phenylcoumaran benzylic ether reductase [*Cryptomeria japonica*]

MGGSRVLIIGGTGYIGRHVTNASLAQGHPTFLLVREITPSNPEKAQLLESFTSKGATLVQ  
GSIDDHASLVAALKKVDVISTLGAPQIADQFNLIKAIKEVGTIKRFFPSEFGNDVDKHH  
AVEPMKSMFDLKIKLRRTIEAEGIPHTYVVPFCFAGYFLTNLAQLGLAAPPDKIVYIGD  
GTTKAVYMKEEDIGTFTIKAVDDPRTLNTLYLKPPANTISTNDLVALWEAKIGKTLEKV  
YLSEEQVLKLLQDTPFPQFMVSI FHTIYVKGDQTNFQIGPDGVEASALYDPVKYTTVEE  
YISAFV

>AAL79930.1 Fus c 1; ribosomal protein P2 [*Fusarium culmorum*]  
MKHLAAYLLLGLGGNTSPSAADV KAVLTSVGDADEDRLNKLISELEGKDIQQLIAEGSE  
KLASVPSGGAGGASGGAAAAGGAAEEAKEEEEEKEESEDEDMGFGLFD

>AAL79931.1 Fus c 2; thioredoxin [*Fusarium culmorum*]  
MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQ LSTKHSVPDVLAFKVVN  
DHVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAAAELGGLAQKRVAG  
A

>BAB88129.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTMTLRTDGLDKKNCTIDYSYIDGDILMGFIEKIENHLSVVPNADGGSTTKTTAIF  
HTKGDVAVPEENIKYAEEQNTMLFKAVEAYLIAN

>AAL25839.1 Hev b 12; lipid transfer protein [*Hevea brasiliensis*]  
MAALKMVSFLVLCMLVAAPMTAQAITCGQVQSALVPCLSYLKTTGPTPPATCCNGVRTIN  
NAAKTTADRRTACQCLKSAAGSVKGLNPTTVAGLPGKCGVNIPYKISLSTNCATVK

>P20347.3 Sola t 3; cysteine protease inhibitor [*Solanum tuberosum*]  
MKSINILSFLLLSSTLSLVAFARSFTSENPIVLPTTCHDDDNLVLPEVYDQDGNPLRIGE  
RYIINNPLL GAGAVLYNIGNLQCPNAV LQHMSIPQFLGEGTPVVFVRKSESDYGDVVRV  
MTVVYIKFFVKTKLKVDTQTVWKNDEQLVVTGGKVG NENDIFKIMKTDLVTPGGSKYVY  
KLLHCPSHLGCKNIGGNFKNGYPRLVTVDDDKDFIPVFVFIKA

>P02762.2 Mus m 1; lipocalin, urinary globulin [*Mus musculus*]  
MKMLLLLCLGLTLVCHVAAEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFL  
EQIHVLENSLVLFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM  
AHLIN EKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

>AAM21322.1 Der p 14; apolipoprotein [*Dermatophagoides pteronyssinus*]

LLTACLLGLGQAQHCEVACPRSIPQLINPKAQSTYVYSLDAKTVLTPRDSQKVTIKGDAE  
VAFVSDCEAVLRLQNVAIDGVPNGAELAAELAAKPFAGYFNGRILGVC PADDQDWSLN  
VKAIVSSQLALSDGNVEKAE EIDFSGRCPTEYRKIRSQDDNTVVIEKRKDLNLCDDRI  
DLRQTPDQALGQLKELMRHYMHPMDSLS CRM TLKDKVVTEVDCEERHVLVHRSNKPVHM  
SYVKMMLKQNKDGVAA DLGPTNAQPKRPYLSFDHKHKNPTETDVVEVLKLCSEITEPQA  
SIETSFTFQKLVDKLRYSAEETASVDES VKTSVCPAHARLRELFLDASAF AASDGSIR  
TLVKAHENQELSITRSTALFTVAAIKAAPNKETVQVLLPVIASEKTIRPMLLGFSVLVRR  
YCEKTNDCATNSGVKDARDAYLARLAVARDASERMTIVRALENLNVNTDGVNDMVMNAMDE  
I IKSTDAEPAMRAAAVNALPN DASHMDRYKSLVMDESMPNEARIAAFQKMMKNGGMSHIK  
DLFAVKGECKMKNYVLT YVDNLKSKNDLRRQTVGEDVELPEKPKREIGITRNIAREYGPY  
TFEYDVIYPETHENVTR SINGRLIRSKNDQLKELVEFQVTQSGFDRELN NAMS LLEKKS F  
QSVMQFLRDMLKMLSQIRKNADDNHMKITVQINGKNVYFTDLFQDTKKMKELLMKRVEK  
IINDKKVDRSIGVLLD SKLVLP TITGLPLMYKFGDNLVVR YDGEFSGEKGD RNIRMNGG

VVAGLYGKMKLMVKDHKMGYEYDAKASYTPMIDMNVQKQEHSLLVRFNMKMDQHTVMRF  
KQSLREKRATGEEKDYENEITPDARSDRCFSFFLLDYCRKASHIKGLMLPNVEYYVVKPE  
KEVTALEMLKSETQDKTRRYIAEMTAVGSPSNKQAKAELEVTKGEQYRVSVKLPEHEFN  
TEFTINADKNNLKMMDLPNVLQADLTGSFEHDKENNVNRKNRLNLQYKFAGDEKPHTVDY  
ENEFLFNLKRSSKEKNSAVEYRAKYMSSHFPILNHKVNQFKYRPFKVNELNLEGEFGRE  
LQHKFRLMRNSQMEVEEVRPFKMHGNSDIKLMANDLDIDYDLKSEFKYESNKGTPIELQY  
KVSGKDRSKRAAEMNAEDVEGVIDYKNSGSPIDSKMHAHLKVKGNNYGYDSELKQTEPQQ  
YEGKMTLSKNDKKIFITHKTEMTKPTSTFLLKTDADVSYSESDMKKHMHMEFKKENDIYT  
LRSTVERDQGLFYENYLVHKGKLNLYRRNDRKILLDLNALSREGTMKLNKIDREY  
NFVLKRDPMRYRDITVEGNENAYVKNGLHLSLIDPSTLSLVTKADGQIDMTVDLISPIT  
KRASLKVDSKYNLFHEGELSASLVNPRLSWHQYTKRDSREYKTDVDLSLRSSDIAVKIT  
MPDYNSKIHYSRQNDQISMDIDGTLIEGHAKGTIKEGKIHIKGRQSDFEIESNYRYEDGK  
MLIEPVKSENGKLEGLSRKVPSTLETETPRVKMMNQYDRHSPVKMFKLDYDGIHLEKHT  
DLLYEPGVQYKIIIGNKIKDDGSHYSIDIQKPRKAFKLDADMMNFKLVNPKPEDSNKAQ  
FSYTFNDYTETEEYFDPHAYYINWISSIRKYIQNFIVEDH

>CAC84590.2 Lep s 1; tropomyosin [*Lepisma saccharina*]  
MEAIKKKMQAMKLEKDNAMDKADALEAQARDANRKADKILEEVQDLKKKPSQVETDFTTT  
KENLATANKNLEDKEKTLTNTSEVASLNRKVQMIEENLERSEERLGTALTKLGEASHAA  
DEASRMCKVLENRSQQDEERMDQLTNQLKEARMLAEDADGKSDEVSARKMAQVEDDLEVAE  
DRVKSGDSKIMELEEEELKVVGNLSKLEVSEEKANQRVEEYKRQIKTLTVKLEAEARAE  
YAEKYVKKLQKEVDRLDEDELGINKDRYRALADEMDQTFEAELSGY

>CAC84593.2 tropomyosin [*Lepisma saccharina*]  
MEAIKKKMQAMKLEKDNVDRARQNEQEAKDANLRAEKAEFEARSQKKIQTIENELDQT  
QEQLMQVNAKLEEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATQKLAEASQAA  
DESERMKVLENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREEEYKQIKTLTTRLKEAEARAC  
WLL

>CAC83046.1 Ran e 1; calcium-binding protein, parvalbumin [*Rana esculenta*]  
MPMTDLLAAGDISKAVSAFAAPESFNHKKFFELCGLKSKSKEIMQKVFHVLDQDQSGFIE  
KEELCLILKGFTEPGRSLSDKETTALLAAGDKDGDGKIGVDEFVTLVSES

>CAC83047.1 calcium-binding protein, parvalbumin [*Rana sp.*]  
MPMTDVLAAACDISKAMAAPFAEPFNHKKFFELCGLKGSQDDMKKVFHMLDKDQSGFIE  
KDELALILKGFTEPGRDLSDKETTALLAAGDKDGDGKIGVDEFVKLVSEC

>CAC95152.1 Ran e 2; calcium-binding protein, parvalbumin [*Rana esculenta*]  
MSITDIVSEKDIDAALLESVKAAGSFNYKIFFQKVLGAGKSAADAKKVFEILDRDKSGFIE  
QDELGLFLQNFRA SARVLSAETS AFLKAGDSGDGKIGVEEFQALVKA

>CAC95153.1 calcium-binding protein, parvalbumin [*Rana sp.*]  
MSITDIVSEKNIEAALLESVKAAGSFNYKIFFQKVLGAGKSAADAKKVFEILDRDKSGYIE  
KDELCLFLQNFKSSARALNDAETS AFLKAGDSGDGKIGVEEFQALVKA

>AAM33821.1 Pen ch 13; alkaline serine protease [*Penicillium chrysogenum*]  
MGFLKLLSTSLATLAVVNAAGKLLTANDGDEVVPSYIVVMNDGVSTAQFETHRNWAANVH  
ARTRSLKGGESGPGKHFDINGMKGYSASFDDRTVKDIASDPTVKYVEPDMVNVNATANVVQ  
RNAPSWGLSRISKKSGATDYVVDSTAGEGIVYGVDTGIDIGHADFGGRAEWGTNTADN  
DDTDGNGHGHTASTAAGSKFGVAKKASVVAVKVLGADGSGTNSQVIAGMDWAVKDSKSR  
GATGKSVMMNSLGGAYSRAMNDAAANVVRSGVFLSVAAGNEAQDASNSSPASAPNVCTIA  
ASTNSDGSASFNFGSVVDLYAPGKDITAAYPGGGSKTSLSGTSMAPHVAGAAAYLMALE  
GVTSKACARIVELAISSISSAPSGTTSKLLYNGINAQ

>CAD32313.1 Lep d 2; NPC2-like [*Lepidoglyphus destructor*]  
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDITGCSGDTCVIHRGEKMTLEAKFAANQ  
DTAKVTIKVLTKVAGTTIQVPLETDGCKFIKCPVKKGEALDFIYSGTIPAITPKVKADV

TAELIGDHGVMACGTVHGQVE

>CAD32314.1 Lep d 2; NPC2-like [*Lepidoglyphus destructor*]  
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDISGCSGDTCVIHRGQKMTLDAKFAANQ  
DTNKVTIKVLAKVAGTTIQVPGLETGCKVLKCPKIKKGEALDFNYGMTIPAITPKIKVDV  
TAELVGDHGVMACGTIHGQVE

>AAM43909.1 Asp f 23; L3 ribosomal protein [*Aspergillus fumigatus*]  
MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSFPKYDPKPKVHLTASMGYKAGMTTVVRDL  
DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK  
NWKYKSKKAFTKYAKKHAEEENGASITRELERIKKYCTVVRVLAHTQIRKTPKQKKAHLM  
EIQVNGGSVADKVDFAFNLFKPIEIDSIFEKDEMIDVIAVTKGHGFQGVTSRWGTTKLP  
RKTHKGLRKVACIGAWHPSHVQWTVARAGQMGYHHRTSCNHKVFRIKGSDEGNASTDFD  
ISKKQITPMGGFVRYGEVKNDYIMVKGSVPGVKKRVMTRLRKTLYPQTSRRATEKVELKWI  
DTSSKFGHGAFQTPEEKRAFMTLKKDLVTS

>AAM46958.1 Ara h 3; 11S globulin, cupin [*Arachis hypogaea*]  
MGKLLALSVCFCFLVLGASSISFRQQPEENACQFQRLNAQRPNRIESEGGYIETWNPNN  
QEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYEEPAQQGR  
RHQSQRPPRRFQGGDQSQQQDQSHQKVHRFDEGDLIAVPTGVAFWYNDHDTDVAVSLT  
DTNNNDNQLDQFRRFNLAGNHEQEFRLRYQQSRRRSLPYSYSPQTQPKQEDREFSPRG  
QHRRERAGQEENEGGNI FSGFTPEFLAQAFQVDDRQILQNL RGENESDEQGAI VTVRG  
GLRILSPDRKRRQYERPEDEEEYDEDEYDEEERQQDRRRRGRSGRSGNGIEETICTA  
SFKKNIGRNRSPDIYNPQAGSLKTANELQLNLLILRWLGLSAEYGNLYRNALFVPHYNTN  
AHSIIYALRGRAHVQVVDSDNGDRVDFEELQEGHVLVVPQNFVAVAGKSQSENFEYVAFKTD  
SRPSIANLAGENSFIDNLPEEVVANSYGLPREQARQLKNMNPFFVPPSEQLRAVA

>CAD10390.1 Pho d 2; profilin [*Phoenix dactylifera*]  
MSWQAYVDEHLMCEIDGHHLTAAAILGHDGSVWAQSSSFQFKSEEITNIMNDFNEPGSL  
APTGLYL GSTKYMVIQGEPAVIRGKKKSGGVTVKKTNQALIFGIYEEPMTPGQCNMVVE  
RLGDYLIEQGM

>1KTJ\_A Der p 2; NPC2-like [*Dermatophagoides pteronyssinus*]  
SEVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDDGVLACA  
IATHAKIRD

>AAM55492.1 Man e 5; glutamic acid rich protein, Hev b 5-like [*Manihot esculenta*]  
MATAEVVTAQTALPEEKPAEEVKVSEIVTEEAAPAVEPVAEPEKAEPPVAVSEEPKEADD  
APAEVAVETKEVEVEEAKTVTEEPTVEKTEEEETPKEETPEPVVVKETPKEEPAETV  
VVEAPKETTEAATEAEAPAPESAPASASETPAEEVPEKEEGDEKKSEAEVEAEKTE

>AAM64112.1 Der f 16; gelsolin-like [*Dermatophagoides farinae*]  
MAAHDKNFDVIPIGHTFFFIWRIKQFELVPVPKEDYGKFKYKGCYIVACCTENPTGGHSHK  
MESKPILNGHGCHIHFHWIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREIEEFESRQF  
SSYFKNGIYILKGGYESGFTKMIDELKPSLLHVKGKKRPIVYECAEISWKVMNNGDVFIL  
LVPNFVFWVTGKHSNRMERTTAIRVANDLKSELNRFKLSSVILEDGKEVEQTSGAEYDAF  
NKALS LDKKIDILKQMPKGYDYAASDKSFESHRSFVTLTKCFEGTETIDISFVKNGLS  
RADLDTNDTFIVENGSEGLWVWVGKATQKERQSAIKYAMELINKKKYPNNTPVTKVLEG  
DESVEFKSLFESWQMSEQEKITSARLFRVSRNGIFKQVANYEPDDLEEDNIMILDVMDKI  
YVWIGNQFAERIADEAHVDKVAQRFIQEDKSGRKFQPNQIILKQGSDEGAFKSYFPKWN

>AAM73729.1 Ana o 1; 7S globulin, vicilin-like [*Anacardium occidentale*]  
PPTKFSFSLFLVSVLVLCLGFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVECEKYYK  
EKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQER  
YKKERGQHNYKREDEDEDEDEAEEDENPYVFEDEDFTTKVKTEQGKVVLLPKFTQKSK  
LLHALEKYRLAVLVANPQAFVVP SHMDADSIFFVSWGRGTITKILENKRESINVRQGDIV  
SISSGTPFYIANNDENEKLYLVQFLRPVNLPGHFEV FHGPGGENPESFYRAFSWEILEAA

LKTSKDTLEKLF EKQDQGTIMKASKEQVRAMSRREGPKIWPFTTEESTGSFKLFKKDPSQ  
SNKYGQLFEAERIDYPPLEKLDMMVSYANITKGGMSVPFYNSRATKIAIIVVSGEGCVEIA  
CPHLSSSKSSHPSYKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNIRY  
TLAGKKNIIKVMKEAKEKELAFKMEGEEVDKVFVGKQDEEFFFGPEWRKEKEGRADE  
>CAD32318.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]  
GVYTYENEYTS EIPPPRLF KAFVLDADNLIPKIA PQAIKHAEILEGDGGPGTIKKITFGE  
GSQYGYVKKHIDSVD EANYSYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHYH  
TKGDVEIMEEHVKAGKEKAHGLFKLIESYLKDHPDAYN  
>CAD38361.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMRTVTTIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38362.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMRTVTTIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38363.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMETVTPIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38364.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMQTVPIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQQDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38365.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMRTVTTIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYRYVAEEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQQDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38366.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMETVTPIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYRYVAEEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38367.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPAEIDL RQMQTVPIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYRYVAEQSCRRPNAQRFGISNYCQIY  
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQEDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38368.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPASIDL RQMRTVTTIRM QGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEQSCRRPNADRFGISNYCQIY  
PPNVNKIEEALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQTNHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38369.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]

TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPQGI EYIQHNGVVQESYRYVAEEQSCRRPNADRFGISNYCQIY  
PPNVNKIQEALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQTN YHAVNIVGYSNA  
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38370.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYRYVAEQSCRRPNADRFGISNYCQIY  
PPNVNKIEEALAQTHSAIAVIIGIKDLDAFRHYDGTIIQEDNGYQTN YHAVNIVGYSNA  
QGV DYWIVRNSFDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38371.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ  
ELVDCASQHGCHGDTIPQGI EYIQHNGVVQESYRYVAEEQSCRRPNADRFGISNYCQIY  
PPNVNKIQEALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQTN YHAVNIVGYSNA  
QGV DYWIVRNSFDTNWGDNGYGYFAANIDLMMIEEYPYVVIL  
>CAD38372.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIRD  
>CAD38373.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPKSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38374.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG  
LEVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38375.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSKTAKIEIKASIDG  
LSVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38376.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38377.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KKVLPVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACHYMNCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38378.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCI IHS GKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACNYMKCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIRD  
>CAD38379.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCI IHS GKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACNYMKCLVNGQQYDIKYTWNVPKIAPKSEN VVVTVKVLGDNGVLACA  
IATHAKIQD  
>CAD38381.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEI KEVLVPGCHGNEPCI IHS GKPFQLEALFEANQNSATAKIEIKASIDG  
LEVDVPGIDPNACNYMKCLVNGQQYDIKYTWNVPKIAPNSEN VVVTVKVLGDNGVLACA  
IATHAKIQD

>CAD38382.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEIKEVLPVPGCHGSEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACNYMKCLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA  
IATHAKIQD

>CAD38383.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEIKKVLVPGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG  
LSVDVPGIDPNACNYMKCLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA  
IATHAKIQD

>CAD38384.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38385.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVP  
PADKYNTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38386.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSEALSIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38387.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSEALRKIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38388.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANHKFTVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38389.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKFTVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKAYAATVATAGEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38390.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAEESSKAALTSKLDAAVKLAYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDAIKASTGGAYESYKFIPALEAAVKKQAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38391.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDIAIKASTGGAYESYNFIPALEAAVKQAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38392.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVP  
PADKYNTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSEALSIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDIAIKASTGGAYESYKFIIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38393.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVP  
PADKYNTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSEALRKIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKITVFEAAFNDIAIKASTGGAYESYKFIIPALEAAVKKAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38394.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANHKFTVFEAAFNDIAIKASTGGAYESYKFIGALEAAVKQAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38395.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANHKFTVFEAAFNDIAIKASTGGAYESYNFIPALEAAVKQAYAATVATAPEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38396.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKFTVFEAAFNDIAIKASTGGAYESYKFIGALEAAVKQAYAATVATAGEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38397.1 Ph1 p 5; unknown function [Phleum pratense]  
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP  
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP  
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN  
AAPANDKFTVFEAAFNDIAIKASTGGAYESYNFIPALEAAVKQAYAATVATAGEVKYTVFE  
TAEKKAITAMSEAKKAAKPAAAAATATATAAVGAATGAATAATGGYKV

>CAD38166.1 nuclear transport factor 2 [Cladosporium herbarum]  
MSDFNAIAQQFTEFYKTFDTRDRAQLAPLYRENSMLTFEQSPFLGTANIVGKLQELPFQR  
IEHQVATVDAQPSNESGGILVVVSGALLVEEERRPMSYQTQFQLLPADGAYVFNDFVRL  
VYPAA

>CAD38167.1 nuclear transport factor 2-like [Alternaria alternata]  
MSDFNAIAQQFVEFYKTFDGNRAGLGALYKEHSMLTFEAQGTQGSAAIVEKLQNLPFQE  
IQHRTDTVDAQPSADDGILVLTGALLLGESKPMSTQAFQLKNAEGNWFVLDVDFRLV  
YPAA

>CAC84116.1 Bet v 7; cyclophilin/peptidyl-prolyl isomerase [Betula pendula]  
MASNPKVFFDMEVGGQPVGRIVMELYADTTTPRTAENFRALCTGEKGNRSGKPLHYKKSS  
FHRVIPGFMCGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPGTNGSQF  
FICTAKTEWLDGKHVVFGQVVEGLDIVKAIEKVGSSSGRTSKPVVVADCGQLS

>AAM77471.1 Alt a 1; unknown function, partial [Alternaria alternata]  
MQFTTIASLFAAAGLAAAAPLESRQDNASCPVTTKGDYVWKISEFYGRKPEGTYYNLSLGF  
NIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMDFSFSDSDRSGLLLLKQKVSDE

>AAM73730.2 Ana o 1; 7S globulin, vicilin-like [Anacardium occidentale]  
MGPPTKFSFSLFVLVCLCLGFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVKECEKY  
YKEKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQ  
ERYKKERGQHNYKREDEDEDEDEAEEDENPYVFEDEDFTTKVKTEQGKVVLLPKFTQK  
SKLLHALEKYRLAVLVANPQAFVVP SHMDADSIFFVSWGRGTITKILENKRESINVRQGD  
IVSISSTGTPFYIANNDENEKLYLVQFLRPVNLPGHFEVVFHGGENPESFYRAFSWEILE  
AALKTSKDTLEKLFKQDQGTIMKASKEQIRAMSRRGEGPKIWPFTTEESTGSFKLFKKDP  
SQSNKYGQLFEAERIDYPPLEKLDMVSYANITKGGMSVPFYNSRATKIAIIVSGEGCVE  
IACPHLSSSKSSHPSYKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNI  
RYTLAGKKNIIKMEKEAKELAFKMEGEEVDKVFQKQDEEFFFGPEWRKEKEGRADE

>AAM83103.1 Blo t 11; paramyosin [Blomia tropicalis]  
MAARSAKYMYQSSRAGHGGDISIEYGTDLGALTRLEDKIRLLSEDLERELRQRVEREK  
SDITVQLMNLTERLEETEGSSESVTEMNKKRDESELAKLRKLLLEDVHMESEETAHHLRQKH  
QAAIQEMQDQLDQVQKAKNKSDKEKQKQFAEVFELLAQVETANKDKLVAQKTVEKLEYTV  
HELNIKIEEINRTVVEVTAHRQLSQENSELIKEVHEYKISLDNANHLKGQIAQQLEDTR  
HRLDEERKRSSLENHAHTLEVELESLKVQLEEESEARLELERQLTKANGDAASWKSKEYE  
AELQAHVDEVEELRRKMAQKISEYGEQLEALLNKCSALEKQKARLQSEVEVLIMDLEKAT  
AHAQALEKRVSQLEKINLDLKSLEEVSMLEEQTKDLRVKIADLQKLQHEYEKLRDQKE  
ALARENKKLADDLAEAKSQLNDAHRRHEQEIEIKRENEREEAAAAYKEAETLRKQEEA  
KNQRLTAELAQTRHDYKRLAQKEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEVARLK  
KKYQAQITELLSLDAANKANIDLQKTIKKQALQITGLQAHYDEVHRQLQQAQVQLGVTQ  
RRCQALTAELEEMRVNLEQALRAKRAAEQMHEEAVVRVNLTTINVNLASAKSKLETEFS  
ALQNDYDEVHKLRISSDERVQKLTIEVKSTKDLLESETERVTKLETIKKSLETEVRNLQI  
RIEEVEANALAGGKRVIKLESIRIDVEIEVEEERRRHAETEKMLRKKDHRVKELLLQNE  
EDHKQIQLLQEMSDKLNKVKVYKQMQEQEGMSQQNLTRVRRFQRELEAAEDRADQAES  
NLSFIRAKHRSWVTTSQVPGGTRQVFVTEQESSNF

>P81430.2 Ole e 7; lipid transfer protein, partial [Olea europaea]  
APSQSTVTALLTSCVSYIDDQ

>AAL07319.1 Che a 1; Ole e 1-like [Chenopodium album]  
MAKQAVFLLVGCALCVLSLAGVANAAENHFVKVQGMVYCDTCRIQFMTRISTIMEGATVKL  
ECRNITAGTQTFKAEAVTDKVGQYSIPVNGDFEDDICEIELVKSPNSECSEVSHDVYAKQ  
SAKVSLTSSNNGEASDIRSANALGFMRKEPLKECPEVLKELDLYDVKAN

>AAM93157.1 Ara h 3; 11S globulin, cupin, partial [Arachis hypogaea]  
NYLHMLLALSVCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNP  
NNQEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYEPAQQ  
GRRHQSQRP RRFFQGDQSQQQQDSHQKVHRFDEGDLIAVPTGVAFWYNDHDTDVVAVS  
LTDNNDNDQLDQFRRFNLAGNHEQEFLRYQQSRRRS

>BAC10663.1 Can f 3; serum albumin [Canis familiaris]  
MKWVTFISLFFLFSSAYSRLVRRREAYKSEIAHRYNDLGEEHFRGLVLLVAFSQYLQQCPF  
EDHVKLAKEVTEFAKACAAEESGANCDKSLHTLFGDKLCTVASLRDKYGMADCCCEKQEP  
DRNECF LAHKDDNPGFPPLVAPEPDALCAAFQDNEQLFLGKYLYEIAARRHPYFYAPELLY  
YAQQYKGVFAECCQAADKAACLGPKIEALREKVLSSAKERFKCASLQKFGDRAFKAWSV  
ARLSQRFPKADFAEISKVVTDLTKVHKECCHGDLLCADDRADLAKYMCENQDSISTKLLK

ECCDKPVLEKSQCLAEVERDELPGDLPSLAADFVEDKEVCKNYQEAKDVFLGTFLYEYAR  
RHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCELFE  
KLGEGYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCAEDFLSVV  
LNRLCVLHEKTPVSEKTKCCSESLVNRPCFSGLEVEDETYVPKEFNAETFTFHADLCTL  
PEAEKQVKKQTALVELLKHKPKATDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLV  
AAAQAALV

>CAD42710.1 hydrophobin [Cladosporium herbarum]  
MAFIKSLLIASVAAVAFAAPQGGASDNKKVEIDGQDSAPVCGNGQKVACCNSGEDLIGL  
NCLSIPIIAIPIQKACGSNIAACCQTGDSEGNLLNLEANCLAIPL

>AAN32987.1 Ph1 p 11; Ole e 1-like [Phleum pratense]  
DKGPGFVVTGRVYCDPCRAFETNVSHNVQGATVAVDCRPFNGGESKLLKAEATTDGLGWY  
KIEIDQDHQEEICEVVLAKSPDTCSEIEEFRDRARVPLTSNNGIKQQGIRYANPIAFFR  
KEPLKECGGILQAYDLRDAPETP

>BAC19997.1 unknown function [Oryza sativa]  
MASNKVVFVSVLLLAVVSVLAATATMAEYHHQDQVWYTPGPLCQPGMGYPMYPLPRCRAV  
KRQCVGRGTAATAAEQVRRDCCRQLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEV  
FRGCRRGDLERAAASLPAFCNVDIPNGGGVVCYWLARSGY

>BAC20650.1 unknown function [Oryza sativa]  
MAFIKVVFSVLLPVVVSMLVATTTMADHRGQVWYTPGQLCAAGRGYPMYPLPRCRAV  
QCAGGAVDEQVRQDCCRQLAAIDDSFCRCPALSHMLVGMKELGAPAKGQPMDEVFPGCR  
RGDMKRVAASLPAFCNVDIPIGIGGVVCYWLSYPMNPATGH

>BAC20657.1 unknown function [Oryza sativa]  
MASNKVVISALLVVVSVLAATTTMADHHQEQQVWYTPGQLCQPGIGYPTYPLPRCRAV  
RQCVAPGTVDEQVRRGCCRQLAAIDSSWCRCDALNHMLRIIYRESGAADAGHPMAEVFRG  
CRRGDIERAAASLPAFCNVDIPNGVGGVVCYWLPGTGY

>CAD23374.1 unknown function [Trichophyton schoenleinii]  
MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKDRPSG  
WNLNLKNGDISVLTDDSDVSEITWLDGDKVWVYVNGTDSVEGGVGIWISDAKNFGNAYK  
AGSVNGAFSGLKLAAGDKINFGYQSTTKGDLYNEAAAKEAVSSARIYDGLFVRHWDT  
YVGTQFNAVFSGLTKNGDKYSFDGKLNKLVQPVKYAESPPYPPFGGSDYDLSSDGKTVA  
FMSKAPELPKANLTTSYIFLVPHDGSRAEPINKRNGPRTPQGIEGASSSPVFPDGGKRI  
AYLQMATKNYESDRRVIHIAEVSNGKPVQRIASSWDRSPEAVKWSDDGRTLYVTAEDHAT  
GKLFTLPADARDNHKPSVVKHDGVSFVYFYGSSKSVLISGNSLWSNLYQVATPGRPNR  
KLFYANEHDPKGLGPKDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG  
SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFGQKLTDITNDWGGAPYKDLVKIWEHV  
RDHIKYIDTDNGIAAGASFGGFMVNWIQGQDLGRKFKALVSHDGT FVGSSKIGTDELFFI  
EHDFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHNDSDFRLSVAEGVGLFNVLQKEG  
IPSRFLNFPDETHWVTKPENSLVWHQQVLGWINKWSGINKSNPKSIKLSDCPIEVIDHEA  
HSYFDY

>CAD23611.1 unknown function [Trichophyton benhamiae (Arthroderma benhamiae)]

MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKDRPSG  
WNLNLKNGDISVLTDDSDVSEITWLDGDKVWVYVNGTDSVEGGVGIWISDAKNFGNAYK  
AGSVNGAFSGLKLAAGDKINFGYQSTTKGDLYNEAAAKEAVSSARIYDGLFVRHWDT  
YVGTQFNAVFSGLTKNGDKYSFDGKLNKLVQPVKYAESPPYPPFGGSDYDLSSDGKTVA  
FMSKAPELPKANLTTSYIFLVPHDGSRAEPINKRNGPRTPQGIEGASSSPVFPDGGKRI  
AYLQMATKNYESDRRVIHIAEVSNGKPVQRIASSWDRSPEAVKWSDDGRTLYVTAEDHAT  
GKLFTLPADARDNHKPSVVKHDGVSFVYFYGSSKSVLISGNSLWSNLYQVATPGRPNR  
KLFYANEHDPKGLGPKDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG  
SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFGQKLTDITNDWGGAPYKDLVKIWEHV  
RDHIKYIDTDNGIAAGASFGGFMVNWIQGQDLGRKFKALVSHDGT FVGSSKIGTDELFFI

EHDFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHNDDFRLSVAEGVGLFNVLQEKG  
IPSRFLNFPDETHWVTKPENSLVWHQQVLGWINKWSGINKSNPKSIKLSDCPIEVIDHEA  
HSYFDY

>CAD23613.1 unknown function [Trichophyton benhamiae (Arthroderma benhamiae)]  
NHDDVDYIEPDFVVRTSTNGTNLTRQENVPSWGLARVGSKKAGGTTYYYDSSAGKGV  
IITDGIDINHEDFGGRAKWKGNFVDKMEDEDCNGHGHVAGTVGGTKYGLAKGVTLVAVKV  
LDCDGSNSGVIIEGMEWAMREASGGNGTAKAAGKAVMMSLGGPRSQASNDAAKAISD  
AGIFMAVAAGNENMDAQHSSPASEPSVCTVAASTEDDGKAEFSNYGAVVDVYAPGKDITS  
LKPGGSTDTLSGTSMASPHVCGLGAYLIGLGKQGGPGLCDTIKEMANEAIQR

>CAD23614.1 unknown function [Trichophyton benhamiae (Arthroderma benhamiae)]  
FITKAIPVLAALSAVNGAKILEAGPHAETIPNKYIVVMKKDVSDAEFSTHTTWLSQNLN  
RRLMRRSGSSKAMAGMQNKYSLGGIFRAYSGEFDDAMIKDISNHDDVDYIEPDFVVRTST  
NGTNLTRQENVPSWGLARVGSQAGGTTYYYDSSAGKGVTAVIDTGIDIEHEDFGGRAK  
WGNFVDQRDEDCNGHGHVAGTVGGTKYGLAKSVSLVAVKVLDCDGSNSGVIIRGMEW  
AMREASGGNGTAKAAGKSVMMMSLGGPRSQASNDAARAISEAGIFMAVAAGNENMDAQHS  
SPASEPSVCTVAASTEDDGKAEFSNYGAVVDVYAPGKDITSLKPGGSTDTLSGTSMASPH  
VCGLGAYLIGLGKQGGPGLCDTIKQMANEAIQRPGEGETTGKLIY

>P00630.3 Api m 1; phospholipase A2 [Apis mellifera]  
MQVVLGSLFLLLLSTSHGWQIRDRIGDNELEERIIYPGLWCGHGNKSSGPNELGRFKHT  
DACCRTHDMCPDVMSAGESKHGLTNTASHTRLSCDCDDKFYDCLKNSADTISSYFVGKMY  
FNLIDTKCYKLEHPVTGCGERTEGRCLHYTVDKSKPKVYQWFDLRKY

>AAL91662.1 Pru du 4; profilin [Prunus dulcis]  
MSWQQYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFKPEEIAAILKDFDQPGTL  
APTGLFLGGTKYMIQGEAGAVIRGKKGSGGITVKKTNQALIIIGIYDEPLTPGQCNMIVE  
RLGDYLIEQGL

>AAL91665.1 Ana o 3; 2S albumin, conglutin [Anacardium occidentale]  
MAKFLLLLSAFVLLLVANASIYRAIVEVEEDSGREQSCQRQFEEQQRFRNCQRYVKQEV  
QRGGRYNQREQESLRECCQELQEVDRRCRCQNLEQMVRQLQQQEIQKGEVRELYETASEL  
PRICISISPSQGCQFQSSY

>P83340.1 Epi p 1; serine protease [Epicoccum nigrum]  
ADGIVAVELDTYRGSFXK

>BAC23082.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKFIAPMAFVAMQLIIMAAEDQSAQIMLDSIEQYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDPNTDGIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISIGSLGRENSRAEVSYVHV  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKNINLSDISLKLTSGKIASCLNDNANGYFS  
GHVIPACKNLSAPAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCHGKIYHP

>BAC23083.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKLIAPMAFLAMQLIIMAAVEDQSAQIMLDSVVEKYLRSNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDPNTDGIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISIGSLGRENSRAEVSYVHV  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSLKLTSGKIASCLNDNANGYFS  
GHVIPACKNLSAPAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC

SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP  
>BAC23084.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRNIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLRLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGISIGSLGRENSRAEVSVHVHN  
GAKFIDTQNGLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRS  
QIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRKEKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP  
>P83181.1 Sal k 1; pectin methylesterase [Salsola kali]  
PTITIGGPEYRTIFFDAYLGTSYVIVIKEPAEEFTTISDAVK  
>P83332.1 Pru p 2; thaumatin-like [Prunus persica]  
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKQLSLTGFELATG  
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGGAAPPATLVEITIA  
SNGGQDFYDVS LVDGFNL PMSVAPQGGTGKCKASTCPADINKVCPAPLQVKGSDGSVIAC  
KSACLAFNQPKYCCTPPNDKPETCPPPDYSKLFKTQCPQAYSAYDDKSSTFTCSGRPAY  
LITFCP  
>P83335.1 Pru p 2; thaumatin-like [Prunus persica]  
MMKTLGAVLSLSLTLSSFGGAHAATMSFKNNCPYTVWPASFGNPQLSTTGFE LASQAS  
LDTPVPWSGRFWARTRCSTDASGKFCETADCDSGQLMCNGKTGIPPATLAEFTIAAGGG  
QDFYDVS LVDGFNL PMSVTPQGGTGCKMGSAAANVNLVCPSELQKIGSDGSSVACL  
VKFGE PQYCCTPPQETKEKCPPTNYSQIFHEQCPDAYSAYFDDNKGLFTCSGGPNYLIT  
CP  
>P83377.1 Pol g 5; unknown function, antigen 5 [Polistes gallicus]  
NDYCKIKCSSGVHTVCQYGESTKPSKNCAGKVIKSVGPTEEEKKLIVEEHNRFQKVAQ  
LETRGNPGPQPAASNMMNLVWVNDQAKIAQVWASQCQILVHDKCRNTEKYQVGNIA  
YAGSSNHFPSVTKLIQLWENEVKDFNYNTGITNKNFGKVGHYTQMVWGNTKEVGC  
GSLKYVEKMMKIHLYLICNYGPAGNYLQPIYTKK  
>AAN73248.1 unknown function [Fusarium culmorum]  
MAGDHAGDQSFYDFLIEEPEMIAPTTPGQFPHQQPISSPNRTSRNTPLRPESTEIETH  
HHANHPALPVLGMQLPVPPTVPESSRAQSRASLNLDIDLHAPSHPSHLSHGAPHEQ  
EHAHEIQRHRAHSAQSSAGLPPTGFASHLPPASSGPVSLGWNMYHVPPNLHLNANQ  
FNFEVPGHMNVSGHPTLHESSNPNNSFHYEHNIVSPSSIHPSAHFDGEVPSQWDD  
SLGHGASTPKVRTPSHHVSSNPWAEINEPTGGDNDNLAPVTRPRKPARARRQKKE  
PRKLSDASQGARSS TGGTAHSVSDAASPSSTSHQSASLTSKSASMTSAASTASSR  
KSKLRSASRTSKNTLDKPNDTAEDRRTRASHNLVEKQYRNRLNAQFESLLHALPE  
QIRHGDNGGGNGNVDNESEQANDLDRRVSKGEVLEMARRHIEALERERNQLGT  
>CAD12861.1 Art v 4; profilin [Artemisia vulgaris]  
MSWQTYVDDHLMCDIEGTGQHLTSAAIIFGTDGTWAKSASFPEFKPNEIDAIKEF  
NEAGQLAPTGLFLGGAKYMIQGEAGAVIRGKKGAGGICIKKTGQAMVFGIYDEP  
VAPGQCNMVERLGDYLLDQGM  
>CAD12862.1 Art v 4; profilin [Artemisia vulgaris]  
MSWQTYVDDHLMCDIEGTGQHLTAAAILGLDGTWAKSDFPEFKPEEMKGIINEF  
NEVGTLPAPTGLFLGGAKYMLQGEAGAVIRGKKGAGGICIKKTGQAMVMGIYDEP  
VAPGQCNMVERLGDYLVQNM  
>AAM10779.1 Blo t 3; trypsin [Blomia tropicalis]  
MKVLVLFCLVSLAAAGPLKDALNKAQVDAFYAEGYIVGGSNAADGDAPYQVSLQ  
RTSHFCGGSIADNYILTAAHCIQGLSASSLTTRYNTLRHNSGGLTVKASRIIGHE  
KYDSNTIDND

IALIQTASKMSTGTTNAQAIKLPEQGSDPKASSEVLITGWGTLSSGASSLPTKLQKVTVP  
IVDRKTCNANYGAVGAEITDNMFCAGILNVGGKDACQGDSGGPVAANGVLVGAVSWGYG  
AQAKYPGVYTRVGNYSWIKGKGVVPV

>AAN76862.1 Ana o 2; 11S globulin, glycinin, cupin [Anacardium occidentale]

LSVCFLLIFHGCLASRQEWQQDECQIDRLDALEPDNRVEYEAGTVEAWDPNHEQFRCAG  
VALVRHTIQPNGLLLPQYSNAPQLIYVVQEGEGMTGISYPGCPETYQAPQQGRQQGQSGRF  
QDRHQKIRRFRRGDIIAIPAGVAHWCYNEGNPVTVTLLDVSNSQNQLDRTPRKFHLAG  
NPKDVFQQQQHQSRGRNLFSGFDTELLAEAFQVDERLIKQLKSEDNRRGGIVKVKDDEL  
VIRPSRSQSERGSESEEESEDEKRRWQQRDNIEETICTMRLKENINDPARADIYTPVVG  
RLTTLNSLNLPIKWLQLSVEKGVLYKNALVLPWNLSHSIIYGCKGKGQVQVVDNFGN  
RVFDGEVREGQMLVVPQNFVVKRAREERFEWISFKTNDRAMTSPLAGRTSVLGGMPEEV  
LANAFQISREDARKIKFNNQTTLTSGESSHMRDDA

>CAD20556.1 Pla a 1; invertase inhibitor [Platanus acerifolia]

MKLSFSLCIIFFNLLLLLQAVISADIVQGTCKKVAQRSPNVNYDFCVKSLGADPKSHTAD  
LQGLGVISANLAIQHGSKIQTFFIGRILKSKVDPALKKYLNDVGLYADAKSSVQEAIADF  
KSKDYASANVKMSAALDDSVTCEDGFKEKKGIVSPVTKENKDYVQLTAISLAITKLLGA

>AAN77576.1 Ara h 2; 2S albumin, conglutin [Arachis hypogaea]

MAKLTILVALALFLAAHASARQQWELQGDRRCCQSLERANLRPCEQHLMQKIQRDEDSY  
GRDPYSPSQDPYSPSQDPDRRDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRMCCEA  
LQQIMENQSDRLQGRQQEQQFKRELRLNPQQCGLRAPQRCDLEVESGGRDRY

>AAN86249.1 Bra n 1; 2S albumin, conglutin [Brassica napus]

QPQKCQREFQQEQHLRACQQWIRQQLAGSPFSENQWGPQQGPSLREQCCNELYQEDQVCV  
CPTLKQAASVVRVQGHGPFQSTRIYQIAKNLPNVCNMKQIGTCPFIAI

>AA015607.1 glutathione S-transferase [Sarcoptes scabiei]

MSSKPTLGYWDLRGLGQSIRILLTYAGVDFVDKRYKIGSAPDFDRGEWLNDKFNGLDFFP  
NLPYYIEGDVKLQTSIAILRYLGRKHKLGDQNEQEWRRITLCEQQIMDLLMALARICYDP  
NFEKLLDLVAKLPDDLKLFKFLGDHGFVAGTNISYIDFLVYEYLIRVKIFAPEIFTKF  
PNLNSYITRIESMPKISAYIKQQEPQLFNGPMAKWNTKY

>AA015613.1 unknown function [Sarcoptes scabiei]

FVELKKDKDLYSMKSNVKNRNEIFYENNMDEKNGKMNWYYKRNDRWTWNMDLDNAFNPRD  
GTMKLVQKDRIYDIKLRKREPFYRGLHIEGNENALIKKGDHMSLVDPPLTNVLTKNDDGI  
VDMTLDLVSPNTKKAALKINSKDYLDHDGEITVSIIFNPRMTWKHHTRKGDMELNIDADI  
TRKGLSITYSRKEPDDSTKVRYSRQGNQVSMVDSKLIIEGHANGTLTDGKIHVKGRESDF  
EIESTYKVEDGKLMIEPTKTQNGKLEGLLSRKVPSHLVLETPRVKMNMKYDRFAPVKILK  
LDYDGLNIEKHIDAIEYPSNHYYFTDGKS

>AA015713.1 Pen m 2; arginine kinase [Penaeus monodon]

MADAAVIEKLEAGFKLEAATDCKSLLKKYLSKAVFDQLKEKKTSLGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYTLFSPLFDPIIEDYHVGFKQTDKHPNKDFGDVNTFVNVDPEGKYV  
ISTRVRCGRSMGYFPNPLTEAQYKEMEAKVSSTLSSLEGELKGTYYPLTGMSKEVQQK  
LIDDHFLFKEGDRFLQAANACRYWPAGRGIYHNDNKTFLVWVNEEDHLRIISMQMGDLG  
QVFRRLTSAVNEIEKRIPFSHHDRLGFLTFCPTNLGTTARASVHIKLPKLAANREKLEEV  
AGKYNLQVRGTRGEHTEAEGGIYDISNKRMMGLTEFQAVKEMQDGILELIKMEKEM

>CAD24068.1 Hev b 11; chitinase [Hevea brasiliensis]

EQCGRQAGGALCPGGLCCSQYGCANTPEYCGSGCQSQCDGGVGGEGGCVDLGSIIIRST  
FEEMLKHRNNAACPAKGFYTYDAFISAAKAFPAFGTTGDVDTCKREIAAFFGQTSHTTG  
GWPTAPDGPYAWGYCHKEELNQASSYCSPPAYPCAPGKKYYGRGPIQLSWNYNYGQCGQ  
ALGLDLLNPNLDVATDRVISFKAAIWFMTQPFKPSCHDVITGQWSPTGHDISAGRAPG  
YGVITNIINGGLECGSGWDARVEDRIGFYKRYCDMFGVGYGSNLDYCNQTPFGLG

>CAD37201.1 Pru p 4; profilin [Prunus persica]

MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAFKPEEIAAILKDFDQPGTL

APTGLFLGGTKYMVIQGEAGAVIRGKKKSGGITVKKTNQALIIGIYDEPLTPGQCNMIVE  
RLGDYLIEQGL

>CAD37202.1 Pru p 4; profilin [*Prunus persica*]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGILNDFNEPGSL  
APTGLYLGGTKYMVIQGEPAVIRGKKKPGGVTVKKSTLALLIGIYDEPMTGQCNMIVE  
RLGDYLVEQGL

>BAC53948.1 Der f 1; cysteine protease [*Dermatophagoides farinae*]  
MKFVLAIASLLVLSTVYARPASIKTFEEFKKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRSRRT  
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVYWIWRNSWDTTWGDSGY  
GYFQAGNNLMMIEQYYPYVIM

>AAM19082.1 Der f 18; chitin-binding protein [*Dermatophagoides farinae*]  
MTRFSLTVLAVLAACFGSNIRPNVATLEPKTVCYYESWVHWRQGEKMDPEDIDTSLCTH  
IVYSYFGIDAATHEIKLLDEYLMKDLHDMEHFTQHKGNAMIAVGGSTMSDQFSKTA  
EHYRETFVSTVDLMTRYGFDGVMIDWSGMQAKSDNFIKLLDKFDEKFAHTSFVMGVT  
PATIASYDNYNIPASISNYVDFMNVLSLDYTGSAHTVGHASPFPEQLKLEAYHKRGAPR  
HKMVMVAVPFYARTWILEKMNKQDIGDKASGPGPRGQFTQTDGFLSYNELCVQIQAE  
TNAFTITRDHDNTAIYAVYVHSNHAEWISFEDRHTLGEKAKNITQQGYAGMSVY  
TNSNEDVHGVCGDKNPLLHAIQSNYYHGVVTEPTVVTLPPVTHTEHVTDIPGVFHC  
HEEGFFRDKTYCATYYECKKGFLEKTVHHCANHLQAFDEVSRTCIDHTKIPGC

>NP\_776945.1 collagen [*Bos taurus*]  
MLSFVDTRTLLLLAVTSCLATCQSLQEATARKGPSGDRGPRGERGPPGPPGRDGD  
DGIPIPGPPPPGPPGLGGNFAAQFDAQGGGPGMGLMGPGRPPGASGAPGPGQGFQ  
GPPGEPGEPGQTGPAGARGPPGPPGKAGEDGHPGKPGRPGERGVVGPQGARGFP  
GTPGLPGFKGIRGHNGLDGLKGQPGAPGVKGEPPGAPGENGTPGQTGARGLPGER  
GRVGPAGPAGARGSDGSVGPVGPAGPIGSAGPPGFPAGPGKGLGPVGNP  
GAPGAPRGEVGLPGLSGPVGPPGNPGA  
NGLPGAKGAAGLPGVAGAPLPGPRGIPGPVGAAGATGARGLVGEPG  
PAGSKGESGKGE PGAVGQPPGPPSGE  
EGKRGSTGEIGPAGPPGPPGLRGNP  
GSRGLPGADGRAGVMGPAGS  
RGATGPAGVRGPNGDSGRPGEP  
GLMGPGRGFPGSPGNI  
GPAGKEGPVGLPGIDGRPGPI  
GAGARGEPGNIGFP  
GPKGPSGDPGKAGEK  
GHAGLAGARGAPDP  
GNNGAQGPPGLQGVQGG  
KGEQGPAGPPGFQGL  
PGPAGTAGEAGK  
PGERGIPGEFGL  
PGPAGARGER  
GPPGESGAAGP  
TGPIGSRGSP  
GPPGPDGNGEP  
GVVGPAGT  
AGPSG  
PSGLPGERGAAG  
IPGGKGEK  
GETGLRGD  
IGSPGRD  
GARGAPGAI  
GAPGAPAG  
ANGDRGEAG  
PAGPAGPR  
GSPGERGE  
VGPAGP  
NGFAGP  
AAGQPGAK  
GERGKGP  
KGENGP  
VGPVGAAG  
PSGPN  
GPPGAGS  
RGDGGP  
PGATG  
FPGAAGRT  
GPPG  
PSGISG  
PPGPPG  
PAGKEGL  
RGP  
RGDQGP  
VGRS  
GETGAS  
GPPGF  
VGEK  
GPSGEP  
GTAGPP  
GTPG  
PQGLL  
GAPG  
FLGL  
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AGSV  
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AGP  
PGAR  
GPPGN  
VGNP  
GVNGAP  
GEAG  
RDGN  
PNDG  
PPGRD  
GQPG  
HKG  
GERG  
YPGN  
AGPV  
GAAGA  
PGP  
QGP  
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>NP\_776953.1 Bos d 10; alphaS2-casein [*Bos taurus*]  
MKFFIFTCLLAVALAKNTMEHVSSEESIISQETYKQEKNNMAINPSKENLCSTFCKEVVR  
NANEEEYSIGSSSEESAEVATEEVKITVDDKHQKALNEINQFYQKFPQYLQYLYQGP  
IVLNPWDQVKNRAVPITPTLNREQLSTSEENSKKTVDMESTEVEFTKTKLTEEEKNRLN  
FLK

KISQRYQKFALPQYLKTVYQHQAAMKPWIQPKTKVIPYVRYL  
>AA024900.1 Art v 1; defensin [*Artemisia vulgaris*]  
MAKCSYVFCVALLIFIVAIGEMEAAGSKLCEKTSKTYSGKCDNKKCDKCKIEWEKAQHGA  
CHKREAGKESCFCYFDCSKSPPGATPAPPGAAPPPAAGGSPSPADGGSPPPPADGGSP  
VDGGSPPPPSTH  
>NP\_776719.1 Bos d 12; kappa-casein [*Bos taurus*]  
MMKSFFLVVITLALTLPLFLGAQEQNQEQPIRCEKDERFFSDKIAKYIPIQVLSRYPSYG  
LNYYQQKPVALLINQFLPYPPYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTTMAPHP  
HPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTVATLEDSPEVIESPPEI  
NTVQVTSTAV  
>AA025113.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [*Malus domestica*]  
MGVFTYESEFTSVIPPARLFNAFVLADNLIPIKIAVQAVKSAEILEGGVGTIKKINFG  
EGSTYSYVVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSHY  
HTKGDVEIKEEHVKAGKEKASHLFKLIENYLLEHPDAYN  
>AA032314.1 Car i 1; 2S albumin, conglutin [*Carya illinoensis*]  
MARVAALLVALLFVANAAAFRTTITTEIDEDEDIDNPRRRGESCREQIQRQQYLNRCDYL  
RQQCRSGGYDEDNRQHFRCQCCQLSQMEEQCQCEGLRQAVRQQQEEGIRGEEMEEMVQ  
CASDLPKECGISSRSCEIRRSWF  
>1NLX\_N Phl p 6; unknown function [*Phleum pratense*]  
MGKATTEEQKLIEDVNASFRAAMATTANVPPADKYKTFEAAFTVSSKRNLADAVSKAPQL  
VPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALRIIAGTPEVHAVKPGA  
>CAD20981.3 Mala s 10; heat shock protein 70 [*Malassezia sympodialis*]  
MSSVVGLDIGNSSKIGVARARGVDIVSNEVSNRSTPSLVSGQKARLLGEGAATAQTSN  
FKNTVGLSKRLIGRTFQDESIQTYEKPFVNAELVDAKGEVGVKVRQNEEHIFSATQLLA  
MYLGKLLDTTQNELGGSGVSDVLSVPIWFTDAQRRAHLHAAEIANLNPLRVMNEPTATA  
LGYITKTDLPEPDSRNVIFVDIGHSSYQVSVVAFCKGQLTVLGAWADPNFGGRNFDRV  
LMEHFAEEFKGKYKIDVFFNPKATFRLAAGCERLKKVLSANTLAQLNVESLMNDIDAASQ  
LKRDEFESLIAPYLERVNGPLDAALSQSLTKDEIHSVELVGGSSRVPALKERIAAWYGK  
PLSYTLNQDEAIVRGCTLACATLSPVFRVREFSVHDISSYPIKVSWEPAVDVPDEENELV  
VFNTNPNVPSTKILTFYRKEPFSLDATYADASTLPKGTNPWLGRVTIKNVAPNEKGEHSI  
VKVKARLNLHGVLNVEASAYTVDEIEKEEEVPPVDPNAAEDAEPKTEKKIVKKLQRKDDL  
IVSGIGLLDPTLLAELKEREGQMYAADKLVADETRKNALEEYIYDTRSKLDERYATFVQ  
SEEKEKLLAMLAESDLYTEEGEDATKSAYVSRLTLQKVGAPIHFRWKEHEERPKAAA  
QLREVVNKYMSVFEENEPEKYDHLSDDDKTKVIEKAATVGKWLDDYMYKQSELPKNVDPKL  
TSEEILKKKDDVIYVCTPILTKPKPRVPVDTSKPEENAQTSNENEKQGDMDVD  
>CAD68071.1 Mala s 11; superoxide dismutase [*Malassezia sympodialis*]  
PFYPIPSALPFPLPIHSLFSRRTRLFRFSRTAARAGTEHTLPPLPYEYNALEPFISADIM  
MVHGHKHHQTYVNNLNASTKAYNDAVQAQDVLKQMEELLTAVKFNGGGHVNHALFWKTMAP  
QSQQGGQLNDGPLKQAIKDFEKFKAFTAKALGIQSGGWCWLGSLTGSLLDLVVAK  
DQDTLTTTHPIIGWDGWEHAWYLQYKNDKASYLKQWNNVNVNWEAESRYSEGLKASL  
>AA045607.1 Zea m 1; beta-expansin [*Zea mays*]  
MGSLANNIMVVGAVLAALVVGSCGPPKVPVPPGNITTTNYNGKWL TARATWYGQPNGAGAP  
DNGGACGIKVNLPYSGMTACGNVPIFKDGKGCSCYEVRCKEKPECSGNPVTVFITDM  
NYEPIAPYHFDLSGKAFGLAKPGLNDKLRHCGIMDVEFRVRCKYPAGQKIVFHIEKGC  
NPNYVAVLVKFAVDDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPFISIRLTS  
ESGKKVIAKDIIPANWRPDAVYTSNVQFY  
>AA045608.1 Zea m 1; beta-expansin [*Zea mays*]  
MGSLANNIMVVGAVLAALVAGGSCGPPKVPVPPGNITTTNYNGKWL TARATWYGQPNGAGAP  
DNGGACGIKVNLPYSGMTACGNVPIFKDGKGCSCYEVRCKEKPECSGNPVTVYITDM

NYEPIAPYHFDLSGKAFGLAKPGLNDKIRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGC  
NPNYLAVLVKYVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPFSIRLTS  
ESGKKVIAKDVIPANWRPDAVYTSNVQFY  
>CAD69036.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]  
MKFIIAFFVATLAVMTVSGEDKKHDYQNEFDLLMERIHEQIKKGELALFYLQEQINHFE  
EKPTKEMKDKIVAEMDTIIAMIDGVRGVLDRMLQQRKDLDFEQYNLEMLKKS GDILERDL  
KKEEARVKNIEV  
>CAD46559.1 Mal d 4; profilin [Malus domestica]  
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAHSSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQALVFGIYEEPLTPGQCNMIVE  
RLGDYLIDQGL  
>CAD46560.1 Mal d 4; profilin [Malus domestica]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL  
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGVTVKKSTMASLIGIYDEPMPGQCNMVVE  
RLGDYLIEQGL  
>CAD46561.1 Mal d 4; profilin [Malus domestica]  
MSWQAYVDDHLMCDIDGYRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL  
APTGLFLGGTKYMVIQEGPGAVIRGKKKSGGITIKKTSQALLIGIYDEPVTGQCNIVVE  
RLGDYLIEQGL  
>1L3P\_A Phl p 5; unknown function, partial [Phleum pratense]  
IPAGELQIIDKIDAAFKVAATAAATAPADDKFTVFEEAFNKAIKETTGGAYDITYKCIPSL  
EAAVKQAYAATAVAAPQVKYAVFEAALTKAITAMSEVQKVSQ  
>CAD80019.1 Pla l 1; Ole e 1-like [Plantago lanceolata]  
MVKLTQVAAILLIGAFFLIASSTSIATQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAG  
AQVQL  
>AA065960.1 Cor a 13; oleosin [Corylus avellana]  
MAEHRQLQDPAHQPRSHQVKAATAATAGGSLLVPSGLILAGTVIALTLATPLFVIFSP  
VLVPAVITVSLIIMGFLASGGFGVAAVTVLSWIYRYVTGRHPPGADQLDHARMKLASKAR  
EMKDRAEQFGQQHVTGSQGS  
>CAD82911.1 Can f 2; lipocalin [Canis familiaris]  
STFCLGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLIKPWGHRVFIHSM  
SAKDGNLHGDILIPQDQCEKVS LTAFKTATSNKFDLEYWGHNDLYLAEVDPKSYLILYM  
INQYNDTSLVAHLMVRDL SRQQDFLPAFESVCEDIGLHKDQIVVLSDDDRCCQGSRD  
>CAD82912.1 Can f 2; lipocalin [Canis familiaris]  
QLLLLTVGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLT KPWGHRVFIH  
SMSAKDVNLHGDILIPQDQCEKVS LTAFKTATSNKFDLEYWGHNDLYLAEVDPKSYLIL  
YMINQYNDTSLVAHLMVRDL SRQQDFLPAFESVCEDIGLHKDQIVVLSDDDRCCQGSRD  
>CAD56944.1 Api m 12; vitellogenin [Apis mellifera]  
MLLLLTLFFFAGTVAADFQHNWQVGN EYTYLVR SRTL TSLGDLSDVHTGILIKALLTVQA  
KDSNVLAAKVWNGQYARVQQSMPDGWETEISDQMLELRDLPI SGKPFQIRMKHGLIRDLI  
VDRDVPTWEVNILKSIVGQLQVDTQGENAVKVN SVQVPTDDEPYASF KAMEDSVGGKCEV  
LYDIAPLSDFVIHRSP ELPMPPTLKG DGRHMEVIKIKNFDCDQRINYHFGMTD NSRLEP  
GTNKNKGFFSRSSSTRIVISESLKHFTIQSSVTTSKMMVSPRLYDRQNGLVLSRMNLT LA  
KMEKTSKPLPMVDNPESTGNLVYIYNPFS DVEERRVSKTAMNSNQIVSDNSLS SSEEKL  
KQDILNLRDTDISSSSSSISSEENDFWQPKPTLEDAPQNSLLPNFVGYKKGKHIGKSGKVD  
VINAAKELIFQIANELE DASNIPVHATLEKFMILCNLMRTMNRKQISELESNMQISP NEL  
KPNDKSQVIKQNTWTVFRDAITQTGTGPAFLTIKEWIERGTTKSMEANIMSKLPKTVRT  
PTDSYIRSF FELLQNPKVSNEQFLNTAATLSFCEMIHN AQVNKRSIHNNYPVHTFGRLTS  
KHDNSLYDEYIPFLERELRKAHQEKDSPRIQTYIMALGMIGEPKILSVFEPYLEGKQQMT  
VFQRTL M V G S L G K L T E T N P K L A R S V L Y K I Y L N T M E S H E V R C T A V F L L M K T N P P L S M L Q R M

AEFTKLDTNRQVNSAVKSTIQSLMKLKSPWEKDLAKKARSVNHLLTHHEYDYELSRGYID  
EKILENQNIITHMILNYVGSSESVIPRILYL TWYSSNGDIKVPSTKVLAMISSVKSFMEL  
SLRSVKDRETIISAEEKIAEELKIVPEELVPLEGNLMINNKYALKFFPFDKHILDKLP  
ISNYIEAVKEGKFMNVNMLDYESVHSFPTETGLPFVYTFNVIKLTKTSGTVQAQINPDF  
AFIVNSNLRLLTFKSNVQGRVGFVTPFEHRHFISGIDSNLHVYAPLKLISLDVNTPKGNMQW  
KIWPMKGEEKSRLFHYSVVPFVSNHDILNLRPLSMEKGRPMIPDDNTSLALPKNEGPF  
LNVETAKTNEEMWELIDTEKLTDRLPYPWTMDNERYVKVDMYMNLEGEQKDPVIFSTSF  
SKVMTRPDTSENWTPKMMAVEPTDKQANSKTRRQEMMREAGRGIESAKSYVVDVRVHVP  
GESESETVLT LAWSESNVESKGRLLGFWRVEMPRSNADYEVCIQSQIMVSPETLLSYDEK  
MDQPKMDFNVDIRYGNKCGKERIDMNGKLRQSPRLKELVGATSIKDCVEDMKRGNKI  
LRTCQKAVVLSMLLDEVDISMEVPSDALIALYSQGLFSLSEIDNLDVSLDVSNPKNAGKK  
KIDVRAKLNEYLDKADVIVNTPIMDAHFKDVKLSDFGFSTEDILDTADEDLLINNVFYED  
ETSCMLDKTRAQTFDGDYPLRLGPCWHAVMTTYPRINPDNHNEKLHHPKDKSVSVLSRE  
NEAGQKEVKVLLGSDKIKFVPGTTSQPEVFNVEKIVSRNKAYQKVEENEIIFEIYKMG  
DRFIGLTSDFKFDVSLALDGERVMLKASEDYRYSVRGLCGNFDHDS TNDVFGPKNCLFRKP  
EHFVASYALISNQCEGDSLNVAKSLQDHDCIRQERTQQRNVISDESSEGRLDTEMSTWGYH  
HNVNKHCTIHRQVKETDDKICFTMRPVVSCASGCTAVETKSKPYKFHCMEKNEAAMKLL  
KRIEGANPDLSQKPVSTTEELTVPFVCKA

>BAC66618.1 calcium-binding protein, parvalbumin [*Scomber japonicus*]  
MAFASVLKDAEVTAAALDGCKAAGSFDHKKFFKACGLSGKSTDEVKKAFAIIDQDKSGFIE  
EEELKFLQNFKAGARALSDAETKAFKAGDSGDGKIGIDEFAAMIKG

>AAL92578.1 Ole e 10; beta-1,3-glucanase [*Olea europaea*]  
MRGTAGVPDQPVPTPTPSVPTSSSPVPKPPTQGNKKWCVPKAEATDAQLQSNIDYVCSQS  
GMDCGPIQANGACFNPTVRAHASYAMNSWYQSKGRNDFDCDFSGTGAITSSDPSNGSCS  
FLS

>AAL92870.1 Che a 2; profilin [*Chenopodium album*]  
MSWQTYVDDHLMCDIEGNHLSAAAILGHDGTVWAQSPSFPQLKPEEVSAIMKDFNEPGSL  
APTGLHLGGTKYMIQGEVIRGKGGVGIKKTNQALIIIGIYGEPMTPGQCNMVVE  
RIGDYLVEQGM

>AAL92871.1 Che a 3; calcium-binding protein, polcalcin [*Chenopodium album*]  
MAAEDTPQDIADRERIFKRFDTNGDGKISSSELGDALKTLGVSVPDEVRRMMAEIDTDGD  
GFISFDEFTDFARANRGLVKDVKIF

>CAD87529.1 Phl p 5; unknown function [*Phleum pratense*]  
ADLGYGPATPAAPAAGYTPAAPAGAEPAGKATTEEQKLIKINAGFKAALAAAAGVPPAD  
KYRTFVATFGAASNKAFAEGLSGEPKGAEESSSKAALTSKLDAAAYKLAYKTAEGATPEAK  
YDAYVATLSEALRIIAGTLEVHAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAANAAP  
ANDKFTVFEAAFNNAIKASTGGAYESYKFI PALEAAVKQAYAAATVATAPEVKYTVFETAL  
KKAITAMSEAQAAKPAAAATATATSAVGAATGAATAATGGYKV

>CAD87730.1 Len c 1; 7S globulin, vicilin [*Lens culinaris*]  
SRSDQENPFIFKSNRFQTIYENENGHIRLLQRFDKRSKIFENLQNYRLLLEYKSKPHTIFL  
PQFTDADFILVVLGKAILTVLNSNDRNSFNLERGDTIKLPAGTIAYLANRDDNEDLRVL  
DLAIPVNRPGQLQSFLLSGTQNPQSFLSGFSKNILEAAFNTEYEEIEKVLLLEEQEQKSQH  
RRSLRDKRQEITNEDVIVKVSREQIEELSKNAKSSSKSVSSESEPFNLSRNPIYSNKF  
GKFFEITPEKNPQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVNEGKGFELVGQRN  
ENQQEQREENDEEEGQEEETTKQVQRYRARLSPGDVLPVAGHPVAINASSDLNLIGFGI  
NAKNNQRNFLAGEDNVISQIQRPVKELAFPSSREVDRLLTNQKQSHFANAQPLQIE

>CAD87731.1 Len c 1; 7S globulin, vicilin [*Lens culinaris*]  
SRSDQENPFIFKSNRFQTIYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPHTLFL  
PQYTDADFILVVLGKAVLTVLNSNDRNSFNLERGDTIKLPAGTIAYLANRDDNEDLRVL  
DLAIPVNNPGQLESFLLSGTQNPQSFLSGFNKSILEAAFNTEYEEIEKVLLLEDQEQEPQH

RRSLRDRRQEINKENVIVKVSREQIKELSKNAKSSSSKKSVSSESEPFNLRSRNPIYSNKF  
GKFFEITPEKNPQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVNEGKGYFELVQQRN  
ENQREENDDEEEQEEETSTQVQRYRAKLSPGDVFPVAPAGHPVAINASSDLNLIGFGINAK  
NNQRNFLAGEEDNVISQIQRPVKELAFPGSSREVDRLLTNQKQSHFANAQPLQIE

>O23878.1 13S globulin [Fagopyrum esculentum]

MSTKLILSFSLCLMVLSCSAQLLPWRKQQRSRPHRGHQFHHQCDVQRLTASEPSRRVRS  
EAGVTEIWDNDTPEFRCAFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVPGC  
PETFQSESEFEYEQSRDQSRQSESEESSRGDQRTRQSESEEFSSRGDQRTRQSESEEFSS  
RGDQRTRQSESEEFSSRGDQRTRQSESEEFSSRGDQHQKIFRIRDGDVIPSPAGVVQWTHND  
GDNDLISITLYDANSFQNLQDGNVRNFFLAGQSKQSREDRRSQRQTRREEGSDRQSRESDD  
DEALLEANILTGFQDEILQEIFRNVDQETISKLRGNDQRGFIVQARDLKLVPPEEYEEE  
LQREGRDRKRGGSGRSNGLEQAFCNLKFQNVNRP SRADVFNP RAGRINTVNSNLP ILE  
FIQLSAQHVVLYKNAIILGPRWNLNAHSALYVTRGEGRVQVVGDEGRSVFDDNVQRGQILV  
VPQGFVAVL KAGREGL EWELKNDDNAITSPIAGKTSVLR AIPVEVLANSYDISTKEAFR  
LKNRQEVVFLPFQSRDEKERERF

>O23880.1 13S globulin [Fagopyrum esculentum]

MSTKLILSFSLCLMVLSCSAQLWPWQKQGSRPHHGRQQHQFQHQCDIQRLTASEPSRRV  
RSEAGVTEIWDHDTPEFRCTGFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVIP  
GCPETFQSDSEFEYEQSRGRHSRQSESEESSRGDQHQKIFRIREGDVIPSPAGVVQWT  
HNDGNDLLISVTLLDANSYHKQLDENVRSFFLAGQSQRETRREEGSDRQSRESDDDEALLG  
ANILSGFQDEILHELFRDVDRETISKLRGENDQRGFIVQAQDLKLVPQDFEEYERERG  
DRRRGQGGSGRSNGVEQGF CNLKFRRNFNTPTNTYVFNPRAGRINTVNSNLP ILEFLQL  
SAQHVVLYKNAIIGPRWNLNAHSALYVTRGEGRVQVVGDEGKSVFDDKVQRGQILVVPQG  
FAVVLKAGREGL EWELKNSGNAITSPIGGRTSVLR AIPVEVLANSYDISTKEAYKLKNG  
RQEVVFRPFQSRDEKERERFSIV

>Q9XFM4.1 13S globulin [Fagopyrum esculentum]

MSTKLILSFSLCLMVLSCSAQLLPWQKQQRSRPHHGHQFQHQCDIQRLTASEPSRRVRS  
EAGVTEIWDHDTPEFRCAFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVPGC  
PETFQSGSEFEYPRSQRDQSRQSESEESSRGDQSRQSESEESSRGDQSRQSESEEFSS  
RGDQHQKIFRIRDGDVIPSPAGVVQWTHNMGNDLISITLYDANSFQNLQDENVRNFFLA  
GQSKQSREDRRSQRQTRREEGSDRQSRESQDDEALLEANILSGFEDEILQEIFRNVDQETI  
SKLRGENDQRGFIVQARDLKLVPPEEYEEELQREGRDRKRGGSGRSNGLEQAFCNLKFQ  
NVNRP SRADVFNP RAGRINTVDSNLP ILEFIQLSAQHVVLYKNAIILGPRWNLNAHSALY  
VTRGEGRVQVVGDEGRSVFDDNVQRGQILVVPQGFVAVL KAGREGL EWELKNDDNAITS  
PIAGKTSVLR AIPVEVLANSYDISTKEAFRLKNRQEVVFRPFQSRDEKERERFSIV

>AAP06493.1 unknown function [Schistosoma japonicum]

MSADSWDNHCVTYVANCKLKNLCMTAIDGSHLGTSPDFRIPPELILQLKSILDGGLDT  
SIFFMGEKYIVLQHDSSCLVSRGKKSIFYATGKICLVGQTVDDDQNNCTQGNFAISRM  
RDHYERMGY

>AAP13554.1 Per a 1; nitrile-specifier protein, partial [Periplaneta americana]

NSARGEHGLDVADFLNEIHSIIGLPPFVPPSRRRHARRGVINGLIDDVIAILPVDELKAL  
FQEKLETSPDFKALYDAIRSPEFQSIISTLNAMPEYQDLLQNL RDKGVDVDHFIELIRSL  
FGLP

>AA038859.1 Ber e 2; 11S globulin, cupin [Bertholletia excelsa]

MAKLFLLSLGIFLLFHCCIAIEYEQEELYECRIQRLTAQEPQYRLEAEAGVSEVWDYTDQ  
QFRCAFVAALRNTIRPQGLLLPVYTNAPKLYVVTQGRGILGVLMPGCPETFQSMSQFQGS  
REQEEERGRFQDQHQKVHLLKKGDIIPAAGVALWCYNDGDEDLVTVLVQHTASDLNQLD  
QNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALADVLGFGMDTETARK  
VRGEDDQRGHIVRVEQGLKVIRPPRIREELEQQEGGGYNGLEETICSATFIQNIIDNPAEA  
DFYNPRAGRLTTVNSLKVPIILTFQLSAMKGVLYENAMMAPLWRLNANSVVYAVRGEARV

QIVDHRGETVFDDNLREGQMVVVPQNFVVKQAGSRGFVWFNTNDNALFSTAAGRTSP  
LRGIPVGLANAYRLSQEEARRIKLNRDEAVLFQPGSRSRGRASA

>AAP30720.1 Rho m 1; enolase [*Rhodotorula mucilaginosa*]  
MAISKIHSRYVYDSRGNPTVEVELTTEKGTFRSIVPSGASTGVHEALELRDGDKSKWLK  
GVLKAVANVNDTIAPALIEANIDVADQAKIDEFLLKLDGTPNKAKLGANAILGVSLAAAK  
AGAAQKDVPLYKHIADISKAKEGKFLVPPFQNVLNGGSHAGGDLAFQEFMIVPSGAPSF  
SEGLRIGSEVYHHLKSLTKKKYQVSAGNVGDEGGVAPDIKTAEALDLIVSAIEAAGYTG  
QVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWITGPQLAELYEQLLNEYPIVSIEDPFA  
EDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKKAIEETKAADALLLVNQIGTLTESIQ  
AANDSYAAGWGMVSHRSGETEDTFIADLSVGIRSGQTKTGAPARSERLAKLNQILRIEE  
ELGDKAIYAGKDFHKAHSL

>BAC76688.1 Tri a 27; thiol reductase [*Triticum aestivum*]  
GDVATGRGSEKVVHVAIYYESLCPYSVRFVANHLFKAYRDGLLDAANLTLVPYGNVAVRND  
GTISCQHGPPEECLLNTVEACAIDAWPDVKVHLGFIYCVSDLVVKKXREWESCFQKQGLD  
PKPVTCEYKGERGHNLSLEYGRQTAELVPPHQFVPPVWVVDGKPLYNDYGNFKAYICKAYK  
GYPLLEACRSLGLEAHDVYGR

>NP\_851341.1 lactotransferrin [*Bos taurus*]  
MKLFVPALLSLGALGLCLAAPRKNVRWCTISQPEWFKCRRWQWRMCKLGAPSITCVRRAF  
ALECIRAIKADAVTLDGGMVFEAGRPYKLRPVAAEYGTKEPQTHYYAVAVVKKG  
SNFQLDQLQGRKSCHTGLGRSAGWIIPMGILRPYLSWTESLEPLQGAVAKFFSASCVPCI  
DRQAYPNLCQLCKGEGENQCACSSREPYFGYSGAFKCLQDGAGDVAFVKETTTFENLPEK  
ADRDQYELLCLNNSRAPVDAFKECHLAQVPSHAVVARSVDGKEDLIWLLSKAQEKFGKN  
KRSRQFLFGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLTTLKNLRETAEEVKAR  
YTRVWCAVGPEEQKCKQWSQSGQNVTCATASTTDDCIVLVKGEADALNLDGGYIYT  
AGKCGLVVLAENRKSXSSLDVLRPTEGYLAVAVVKKANEGLTWNLSLKDCKSHTAV  
DRTAGWNIPMGLIVNQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKE  
KYYGYTGAFRCCLAEDVGDVAFVKNNTVWENTNGESTADWAKNLNREDFRLLCLDGTRKPV  
TEAQSCHLAVAPNHAVVSRSDRAAHVKQVLLHQQALFGKNGKNCVDFCLFKSETKNLLF  
NDNTECLAKLGGRPTEYEEYLGTEYVTAIANLKKCSTSPLEACAFLTR

>NP\_851372.1 Bos d 9; alphaS1-casein [*Bos taurus*]  
MKLLILTCLVAVALARPKHPKIKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNELSKDIG  
SESTEDQAMEDIKQMEAESSSEEIVPNSVEQKHIQKEDVPSERYLGYLEQLRLKYYK  
VPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNQELAYFYPELFRQFYQLDAYPSGAWY  
YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW

>AAP37482.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[*Betula pendula*]

MRVFNKGETTSLIPLARLFK  
>AAP37470.1 Hev b 13; esterase [*Hevea brasiliensis*]  
MEFPETNNPIITLSFLLCMLSLAYASETCDFAIFNFGDSNSDTGGKAAAFYPLNPPYG  
ETFFHRSTGRYSDGRLLIIDFIAESFNLPYLSPYLSSLSNFKHGADFATAGSTIKLPTTI  
IPAHGGFSPFYLDVQYSQRFQFIPRSQFIRETGGIFAELVPEEYFYEKALYTFDIGQNDL  
TEGFLNLTVEEVNATVPDLVNSFSANVKKIYDLGARTFWIHNTGPIGCLSFILTYFPWAE  
KDSAGCAKAYNEVAQHFNHKLKEIVAQLRKDLPLATFVHVDIYSVKYSLFSEPEKHGFEF  
PLITCCGYGGKYNFSVTAPCGDVTADDGTKIVVGSACPSVRVNWGDGAHYTEAANEYFF  
DQISTGAFSDPPVPLNMACHKTESLRTLASV

>AAP37412.1 Pol d 4; serine protease [*Polistes dominula*]  
MNCCKIILLFITIIGVAKSREENCKCGWDNPSRIVNGVETEINEFPMVARLIYPSGMYC  
GGTIITPQHIVTAAHCLQKYKRTNYTGIHVWVGEHDYTTDTETNVTKRYTIAEVTIHPNY  
NSHNNDIAIVKTNERFEYSMKVGPVCLPFNYMTRNLNETVTALGWGKLRVNGQNSKVLK  
KVDLHVITREQCETHYGAAIANANLLCTFDVGRDACQNDSSGGPILWRSPTTDNLILVGVV

NFGRTCADDAPGGNARVTSFMEFIHNATIGETYCKAD

>AAM54365.1 Jug n 1; 2S albumin, conglutin [*Juglans nigra*]  
RHEARKCIFHTFSLTMARLATLAALLVALLFVANAAAFRTTITTTMEIDEDIDNPRRRGEG  
CQEIQRQQNLNHCQYYLRQQSRSGGYDEDNQRQHFRQCCQQLSQIEEQCQCEGLRQAVR  
RQQQQQLRGEEMEEMVQSARDLPKECGISSQRCEIRRSWF

>AAM54366.1 Jug n 2; 7S globulin, vicilin-like [*Juglans nigra*]  
GRDRQDPQQYHRCQRRCCIQEQSPERQRCQQRCEQYKEQQGRERGPESPRRESKGR  
EEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFAERTELLRGIENYRVVILDANPNTFM  
LPHHKDAESVIVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATEYVINQDSNERLEM  
VKLLQPVNPNPGQVREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREG  
VIIRASQEKLRALSQHAMSAGQRPWGRSSGGPISLKSERPSYSNQFGQFFEACPEEHRQ  
LQEMDVLVNYAEIKRGAMMVPHYNSKATVVVVVVEGTGRYEMACPHVSSQSFEDQGRREQ  
EEEESTGRFQKVTARLARGDIFVIPAGHPAITASQENLRLLGFGINGENNRNFLAGQ  
NSIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPLASILGFAF  
F

>AAM78596.1 Ara h 2; 2S albumin, conglutin [*Arachis hypogaea*]  
LTILVAPALFLAAHASARQQWELQGDRCQSCLERANLRPCEQHLMQIKRDEDSYGRD  
PYSQSPYSPSQDPDRDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRMCCEALQQ  
IMENQSDRLQGRQQEQQFKRELNRNLPQQCGLRAPQRCDLEVESGGRRDRY

>AAP47226.1 Hel a 3; lipid transfer protein [*Helianthus annuus*]  
MKGTSMGVAILAMIVMAQLMVHPSVAITCNDVTGNLTPLPYLRSGGKPTACCAGAKKL  
LGATRTQADRRTACKCAKTAAPQLKVRPDMASSLPKCGISTSIPIPNVNCNTIP

>CAD92666.1 profilin [*Cucumis melo*]  
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFRLEEIAAILKDFDQPGTL  
APTGLFLGGTKYMIQGEAGAVIRGKKGSGGITVKKTNQALIIGIYDEPLTPGQCNMIVE  
RLGDYLIEQGL

>P80207.1 Bra j 1; 2S albumin, conglutin [*Brassica juncea*]  
AGPFRFRPCRKEFQQAQHLRACQQWLHKQAMQSGSGPQPQPQQRPLLQCCNELHQEE  
PLCVCPTLKGASKAVKQQIRQQGQQGQQGQQQLQHEISRIYQTATHLPRVCNIPRVSICP  
FQKTMPGPS

>P81729.1 Bra r 2; chitin-binding protein [*Brassica rapa*]  
QAGGQTCAGNICCSQYGYCGTTADYCSPDNMCQATYHYYNPAQNNWDLRAVSAYCSTWDA  
DKPYSWRYGWTAFCGPAGPRCLRTNAAVTVR

>P82946.1 Dac g 4; FAD-containing oxidase [*Dactylis glomerata*]  
DIYNYMEPYVSKVDPTDYFGNEQARTAWVDSGAQLGELS YGVLFN IQV VNYWFAP

>P83507.1 Cav p 1; lipocalin [*Cavia porcellus*]  
SEINGDWNTIALSAD

>AAP87281.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]  
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYGMQGNLPPVSEVIALYK  
QSNIKRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
LFRYIAVGNIEISPVNGGTAWLAQFVLPAMRNHDAIRSAGLQDQIKVSTAILDLTLVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYYPYFTYAGNPRDISLPYALFTSPSVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFATFDNGRTYLSNLI  
QHVKGGTPKRPNRAIETYLFAMFDENKKQPEVEKHFGLFFPDKRPKYNLNFGAEKNDIS  
TEHNATILFLKSDM

>AAP94213.1 Hum j 1; unknown function [*Humulus japonicus*]  
MKNLQHHNKIITFKTPDDSTTLELNHISLPYHWEQCLDLKTGEIYYINWRNGMKAKEDP  
RTTITEYNSNGSNGDYYYSEEDSSYDSEESSSESSPPATTRESQYRGAEKDHVLLVGG  
CKSCFMVMPKQVQECPKCCGQPLHFDRSQSGSQ

>AAP96759.1 beta-expansin [*Dactylis glomerata*]

IPKVPPGNITATYGDKWLDKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNT  
PIFKDGRGCGSCFEIKCTKPESCSGEAVTVHITDDNEEPIAPYHFDLSGHAFGSMKKG  
EQKLR SAGELELQFRRVKCKYPEGKLTTFHVEKGSNPYLALLVKYVDGDGDVVAVDIKE  
KGKDKWIALKESWGAIWRVDPDKLTGPFVRYTTEGGTKSEVEDVIPEGWKADTSYEAK  
>P81943.3 *Api g 5*; FAD-containing oxidase [*Apium graveolens*]  
LPNPSGFVTCLSSISKSVMYTPAINLKAVIADPVAKTAVVQAGATLGEVYXIIYARVLW  
GNTTQKLEWIRSLHDYQSSFFPFFSA  
>AAQ08190.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
IRTVYCDTCRAGFITELSEFIPGASVRLQCKDKENG DITFTEVGYTRAEGLYSMLVERDH  
KNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ  
VYNKLGMYPPNM  
>AAQ08947.1 *Fra e 1*; *Ole e 1-like, partial* [*Fraxinus excelsior*]  
EDVPQPPVSLFYVQGVYCDTCRAGFITELSEFIQAGVRLQCKDKENGKVTFTTEVGYTR  
AEGLYSMVIERDHKNEFCEIVLLSSSRKDCDEIPTEGWVKPSLKFILNTVNGTTRTINPL  
GFFKKEVLPKCPQVYNKLGMYPPNM  
>AAQ10268.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
ILTVYCDTCRAGFITELSEFIPGASVRLQCKDKENG DITFTEVGYTRAEGLYSMLVERDH  
KNEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ  
VYNKLGMYPPNM  
>AAQ10271.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
IWTVYCDTCRAGFITELSEFIPGASVRLQCKDKENG DITFTEVGYTRAEGLYSMLVERDH  
KNEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ  
VYNKLGMYPPNM  
>AAQ10274.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
WTVSCDTCRAGFITELSEFIPGASVRLQCKDKENG DITFTEVGYTRAEGLYSMLVERDHK  
NEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV  
YNKLGMYPPNM  
>AAQ10276.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
SYCDTCRAGFITELSEFIPGAGVRLQCKDGENG NITFTEVGYTRAEGLYSMLVERDHKNE  
FCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTINPLGFFKKEALPKCAQVYN  
KLGMYPPNM  
>AAQ10277.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
QAVYCDTCRAGFITELSEFIPGASVRLQCKDRENG DITFTEVGYTRAEGLYSMLVERDHK  
NEFCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV  
YNKLGMYPPNM  
>AAQ10278.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
QDSYRDTCRAGFITELSEFIPGASVRLQCKDRENG DITFTEVGYTRAEGLYSMLVERDHK  
NEFCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV  
YNKLGMYPPNM  
>AAQ10279.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
IRTVSQDTCCARFITELSEFIPGAGVRLQCKDGENG NVTFTTEVGYTRAEGLYSMLIERDH  
KNEFCEITLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQ  
VFNKLGMYPPDM  
>AAQ10280.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
IRTVFRVTCRARFITELSEFIPGAGVRLQCKDGENG NVTFTTEVGYTRAEGLYSMLIERDH  
KNEFCEITLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQ  
VFNKLGMYPPDM  
>AAQ10281.1 *Ole e 1*; *Ole e 1-like* [*Olea europaea*]  
QDSYSGHCRARFITELSEFIPGAGVRLQCKDGENG NVTFTTEVGYTRAEGLYSMLIERDHK  
NEFCEITLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQV

FNKLGMYPPDM

>AAQ24541.1 Blo t 1; cysteine protease [Blomia tropicalis]  
MKFLLVAALCALVAIGSCKPTREEIKTFEQFKKVFVKVYRNAEEEEARREHHFKEQLKWVE  
EHNGIDGVEYAINESDMSSEQEFSFHLSSGGLNFTYMKMEAAKEPLINTYGSLLPQNFQDWR  
QKARLTRIRQQGSCGSCWAFAAAGVAESLYSIQKQQSIELSEQELVDCTYNRYDSSYQCN  
GCGSGYSTAEFKYMIRTGLVEEENYPYNMRTQWCNPDVEGQRYHVSGYQQLRYQSSDEDV  
MYTIQQHGPPVVIYMHGSNNYFRNLGNGVLRGVAYNDAYTDHAVILVGGTVQGVQVYIIR  
NSWGTGWGNGGYGYVERGHNSLGINNFVYATL

>AAQ24542.1 Blo t 3; trypsin [Blomia tropicalis]  
MKVLVLFCLVSLAAAGPLKDALNKAQVDAFYAEGYIVDGSNAADGDAPYQVSLQRTSHFC  
GGSIADNYILTAAHCIQGLSASSLTIRYNTLRHNSGGLTVKASRIIGHEKYDSNTIDND  
IALIQTASKMSTGTTNAQAIKLPEQGSDPKASSEVLITGWGTLSSGASSLPTKLQKVTVP  
IVDRKTCNANYGAVGADITDNMFCAGILNVGGKDACQGDSSGPPVAANGVLVGAWSWGYGC  
AQAKYPGVYTRVGNYSWIKGKGPV

>AAQ24543.1 Blo t 4; alpha-amylase [Blomia tropicalis]  
MIVELIVFSLALTIPYQTLASSPYSDFHFNHRKVITHLMQWKFVDIADECERFLGPYGY  
GGVQVSPVNEHASLDRHPWYELYQPVSRYRIVSRGTEQFRDMVHRCNKAGVRIYVDVVL  
NHMTGPQSGVGDGTHYDGNMSPYGPFGPNDFFHGHECPTSNDIQNYDDPTQARNCR  
LSGLRDLKQSADYVRTKQADFLNHLIDIGVAGFRFDASKHMWPGDLQAIYSKLHHLNEKY  
FPSNSNPFYIYHEVIYSNNNAISISDYTKLGRSIEFHYYHEL CNVIRGNKLLKWLHNFQGP  
WGMVPNDALIMVDSHDLQRGHTGQLGLNINIFYESRLLKVAATFMLAWPYGIPRVMSYR  
WNQKIVNGKDENDWIGPPADGSGSILSVKPNSDLTCNQEWICEHRWKQIYNMVQFRNTAG  
DEPVKNWWDNGDYQIAFSRGAKTFAINLQNGQHLKQNLHTGLPSGNYCNLVTGNVHNGK  
CSGQMVHVDGSGHAMISIGANADDHL

>AAQ24545.1 Blo t 7; bactericidal permeability-increasing like [Blomia tropicalis]  
MKSTIVLLACFVGIASFSDAANQLVDQVVDALKTQKGFDSMHVKGKHTTELDQKIGLVTFK  
GKLIKDATVTGLSRAAGSDVKIHSNIELIVGLIQSHLTLDVDIGKLQIMFSAGLAAEG  
PSVKDFHIDEFEAVRIHVHGLGPLDPFIDIIGDAIIXLAXSQVREMISXMMRPIIESEVK  
KFLQNTTPAPAF

>AAQ54603.1 unknown function [Glycyphagus domesticus]  
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE

>AAQ55550.1 unknown function [Lepidoglyphus destructor]  
MKSVLIFLVAIALFSANIVSADEQTTRGRHTEPDDHHEKPTTHATHEETTSTQHHHEEVT  
TQTPHHEEKTTEETHSDDLIVHEGGKTYHVWCHEEGPIPHPGNVHKEYIICKSKSGSLWY  
ITVMPCSIGTKFDPISRNCVLDN

>AAQ73484.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE

>AAQ73486.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE

>AAQ73487.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGQSVTLDAKFVANQD  
SAKATIKVLAKVAGTQIQVPGFDTDGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEVT  
AELIGDHGILACGTVNGQVE

>AAQ73488.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]

MMKFIVLFALVAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIIKCPICPKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE  
>AAQ73489.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALVAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIIKCPICPKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE  
>AAQ73490.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALNAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIIKCPICPKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE  
>AAQ73491.1 NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALVAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIIKCPICPKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGQVE  
>AAQ73492.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]  
MMKFIVLFALVAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ  
DSAKATIKVLAKVAGTQIQVPGFDTDGCKIIKCPICPKKGDPIDFKYSGTIPAITPKIKAEV  
TAEIIGDHGILACGTVNGTVE  
>AAQ73493.1 Lep d 5; unknown function [Lepidoglyphus destructor]  
MTGVKTHLEHELKRTDLNLFLEKFNLDITATLNVLTKELTEVQKHVKAVESDEVDVAIPN  
PDEFRNEFDRLLIHMTEEQFAKLEQALAHLSHQVTELEKSKSKELKAQILREISIGLDFI  
DSAKGHFERELKRADLNLAEKFNFEFESALSTGAVLHKDLTALATKVKAIETK  
>AAQ73494.1 Lep d 5; unknown function [Lepidoglyphus destructor]  
MTGVKTHLQHELKRTDLNLFLEKFNLDITAPLNVLTKELTEVQKHVKAVESDEVAIPND  
EFRNEFDRLLIHMTEEQFAKLEQALAHLSHQVTELEKSKSKELKAQILREISIGLDFIDS  
AKGHFERELKRADLNLAEKFNFEFESALSTGAVLHKDLTALATKVKAIETK  
>AAP15199.1 profilin [Humulus scandens]  
MSWQAYVDDHLMCEIDGQHLTAAAIIGHDGSVWAQSSTFPQFKPEEIAAIMKDFEEPGSL  
APTGLHLGGIKYVMVIMGEQGA VIRGKKGAGGITVKKTGAAAMIIGIYDEPLTPGQCNMIVE  
RLGDYLIDQNL  
>AAP15200.1 profilin [Humulus scandens]  
MSWQAYVDDHLMCEIDGNHLSAAAIIGHDGSVWAQSAAFPQLKPEEVTGIMNDFNEPGTL  
APTGLYLGGTKYMIQGEPEGAVIRGKKGAGGVTIKKTSQLIIGVYDEPMTPGQCNMIVE  
RLGDYLIDQGL  
>AAP15201.1 Amb a 8; profilin [Ambrosia artemisiifolia]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGVVWAQSATFPQVKPEEITGIMNDFNEPGSL  
APTGLYLGGTKYMIQGEPEGAVIRGKKGPGGVTIKKTSMALIIGIYDEPMPAGQCNMIVE  
RLGDYLLEQGF  
>AAP15202.1 Amb a 8; profilin [Ambrosia artemisiifolia]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGVVWAQSATFPQVKPEEITGIMNDFNEPGSL  
APTGLYLGGTKYMIQGEPEGAVIRGKKGPGGVTIKKTMSLIIGIYDEPMTPGQCNMLVE  
RPGDYLLLEQGF  
>AAP15203.1 Amb a 8; profilin [Ambrosia artemisiifolia]  
MSWQAYVDEHLMCDIEGTGHHLSAAILGHDGTVWAQSSNFPQFKPEEMKGIITEFDQAG  
TLAPTGMFIAGAKYMLVQGEQGA VIRGKKGAGGICIKKTGQALVMGIYDEPVAPGQCNMV  
VERLGDYLIDQGM  
>AAQ83588.1 Fra e 1; Ole e 1-like [Fraxinus excelsior]  
MEDVPQPPVSQFHIQGVYCDTCRARFITKLSEFITGASVRLQCRDKENGDVTFTEIGYT  
RGEGLYSMFVERDHKNEFCEITLLSSGRKDCNEIPIEGWVKPSLKFILNTVNGTTRTINP

LGFFKKEALPQCAQVYNKLGMYPPNM

>AAQ91847.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis hypogaea]

MGVFTFEDEITSTVPPAKLYNAMKDADSITPKIIDDVKSVEIVEGNGGPGTIKKLTIVED  
GETKFILHKVESIDEANYAYNYSVVGVALPPTAEKITFETKLVEGPNGGSIGKLTLYH  
TKGDAKPDEEELKKGKAKGEGLFRAIEGYVLANPTQY

>AAN11300.1 Cand a 3; peroxisomal protein [Candida albicans]

MVKVLLALTSYNETFYSDGKKTGVFVVEALHPFEVFRKKGYEIQLASETGTFGWDDHSVV  
PDFLNGEDKEIFDNVNSEFNVALKNLKKASDLDPNDYDIFFGSAGHGTLDYDYPHAKDLQK  
IATTVYNKGGVSAVCHGPAIFENLNDPKTGEPLIKGKKITGFTDIGEDILGVTDIMKKG  
NLLTIKQVAEKEGATYIEPEGPWDNFTVTDGRIVTGVNQPQSAVKAEDVIAAFECN

>AAN18044.1 Ole e 1; Ole e 1-like [Olea europaea]

IGQVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDTFTEVGYTRAEGLYSMLVERDH  
KNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ  
VYNKLGMYPPNM

>AA022132.1 Ole e 1; Ole e 1-like [Olea europaea]

SDSYCDTCRAGFITELSEFIPGASLRLQCKDKENGDTVTFTEVGYTRAEGLYSMLVERDHK  
NEFCEITLISSGRKDCNEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV  
YNKLGMYPPNTWNVTI

>AA022133.1 Ole e 1; Ole e 1-like [Olea europaea]

RTVTGYCRAGFITELSEFIPGASLRLQCKDKENGDTVTFTEVGYTRAEGLYSMLVERDHKN  
EFCEITLISSGRKDCNEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQVY  
NKLGMYPNHNHMSR

>AA033897.1 Ole e 3; calcium-binding protein, polcalcin, partial [Olea europaea]

EHERIFKRFDKAGDGKISSSELGETLKLPLGSVTLEEIQRMMAEIDTDGDGFL

>AA073464.1 Der p 11; paramyosin [Dermatophagoides pteronyssinus]

MSARTAKYMYRSSGAGASGDISVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK  
AELQIQVMSLSERLEEAEGSSSVTEMNKKRDESELAKLRKLLLEDVHMESEETAHHLRQKH  
QAAVHEMQDQLDQLQKAKNKSDEKQKQFAEVFELLSQLETANKEKLTALKSVEKLEYTV  
HELNIKIEEINRTVIELTSHKQRLTQENTELIKEVHEVKLQLDNANHLKQQIAQQLEDTR  
HRLEEEERKRSSLENHAHTLEVELESKLVQLDDESEARLELERQLTKANGDAASWKSKEYE  
AELQAHADVEEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAA  
AHAQQLEKRVAQLEKINLDLKDLEEVMTLMEQAQKELRIKIGELQKLQHEYEKVRDQRD  
QLARENKKLTDDLAEAKSQLNDAHRRRIHEQEIEIKRENERDELSAAYKEAETLRKQEEA  
KNQRLIAELAQVRHDYEKRLAQKDEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLK  
KKYQAQITELSLDAANKANIDLQKTIKKQALQITELQAHYDEVHRQLQQAVDQLGVTQ  
RRCQALQAELEEMRIALEQASRAKRQAEQLHEEAVVRVNELTTINVNLSAKSKLESEFS  
ALQADYDEVHKLRIISDERVQKLTIELKSTKDLLIEEQERLVKLETVKKSLQEVRTLHV  
RIEEVEANALAGGKRVIAKLESIRRDVEIEVEEERRRHAETEKMLRKKDHRVKELLLQNE  
EDHKQIQLLQEMTDKLNKVKVYKQMQEQEGMSQQNLTRVRRFQRELEAAEDRADQAES  
NLSFIRAKHRSWVTTSSQVPGGTRQVFTTQEETNY

>AA091800.1 Alt a 8; mannitol dehydrogenase [Alternaria alternata]

MPITVPQATELKDLSLKGKVVIVTGASGPTGIGTEAARGCAEYGADLAITYNSRAEGAE  
KNAKEMSEKYGVKVKAYKQVNEYAQCEKLVQDVIKDFGKVDVFIANAGKTADNGILDAT  
VEQWNEVIQTDLTGTFNCARAVGLHFRERKTGSLVITSSMSGHIANFPQEASYNVAKAG  
CIHLAKSLANEWRDFARVNSISPGYIDTGLSDFVPQDIQKLWHSMPMGRDAKATELKGA  
YVYFASDASSYCTGSDLLIDGGYCVR

>AA091801.1 Cla h 8; NADP-dependent mannitol dehydrogenase [Cladosporium herbarum]

MPGQQATKHESLLDQLSLKGVVVVTGASGPKGMGIEAARGCAEMGAAVAITYASRAQGA  
EENVKELEKTYGIKAKAYKQVDSYESCEKLVKDVVADFQIDAFIANAGATADSGILDG

SVEAWNHHVQVDLNGTFHCAKAVGHHFKERGTGSLVITASMSGHIANFPQEQTSYNVAKA  
GCIHMARSLANEWRDFARVNSISPGYIDTGLSDFVPKETQQLWHSMPMGRDGLAKELKG  
AYVYFASDASTYTTGADLLIDGGYTTR  
>AAP57094.1 Der f 20; arginine kinase [Dermatophagoides farinae]  
MVDQAVIDKLEAGFQKLQSSAECHSLLKKYLTRNVLDACKGRKTGMGATLVDVVQSGFEN  
LDSGVGLYAPDAESYTLFKELFDPVIEDYHKGFKPTDKHPQTDGVDVNTLCNVDPNNEFV  
ISTRVRCGRSLQGYPFNCLTEAQYKEMEEKVKGQLNSFEGELKGTYYPLLGMKATQQQ  
LIDDHFLFKEGDRFLQAANACRFWPVGRGIFHNDNKTFLIWVNEEEHLRIISMQKGGDLK  
QVFSRLINGVNHIEKKLPFSRDDRLGFLTFPCPTNLGTTIRASVHIKLPKLAADRKXLEEV  
AGKYNLQVRGTAGEHTESVGGVYDISNKRMRGLTEYQAVKEMQDGILELIKIEKSM  
>AAP35065.1 Der f 29; cyclophilin/peptidyl-prolyl isomerase [Dermatophagoides  
farinae]  
MALPRVFFDIAADNQPLGRIVIELRSDVWPKTAENFRALCTGEKGFQKSSSFHRIIPNF  
MIQGGDFTNHNGTGGKSIYGNKFADENFTLQHTGPGIMSMANAGPNTNGSQFFITTVKTT  
WLDGKHVVFGSVVEGMDIVKKVESYGSQSGKPSKVTIANCGQL  
>AAP35069.1 Blo t 8; glutathione S-transferase [Blomia tropicalis]  
MAPLKIGYWDIRGFAEPIRMLLKHNLNIEFEETRYGFGNDSEESFPNRDEWLAEKFTLGFE  
FPNLPYLFDGDFKMTESVAILKRLARANGMIATTEPALSYSSEMIEAMVIDIRNRLVYVIY  
AENSGTPEEFEQKLABLRLERLETSLGQLEAFFQKHGSQWVAGDKLTYVDFLAYEYLDWYR  
VFKSTPIFEKFAKVS DYMKRFEELPSLKEYIASDEHRSASCLSPFARIGHRWAKE  
>AAP35073.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
MVSLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKT  
AKIEIKASLDGLEIDVPGIDTNACHFMCPLVKGQQYDAKYTWNVPKIAPKSENVVTVK  
LVGDNGVLACAIATHGKIRD  
>AAP35075.1 Der f 1; cysteine protease, partial [Dermatophagoides farinae]  
MKFVLAIASLLVLSTVYARPASIKTFFEEFKAFNKNYATVEEEVARKNFLES�KYVEAN  
KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRT  
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDLS  
>AAP35077.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides  
farinae]  
MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEQSETIDPMKVPDHADKFER  
HVGILDFKGE LAMRNI EARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY  
KLGDLHPTTHVISDIQDFVVALSLEIPDEGNITMTSFVVRQFANVNVNHIGGLSILDPIFG  
VLSDVLT AIFQD TVRKEMTKVLAPAFKRELEKN  
>AAP35078.1 Der f 13; fatty acid-binding protein [Dermatophagoides farinae]  
MASIEGKYKLEKSEKFEFLDKLGVGMVKTAAKTLKPTFEVAIENDQYIFRSLSTFKNT  
EAKFKLGEFEEDRADGKRVKTVIQKEGDNKFVQTQFGDKEVKIIREFNGDEVVVTASCD  
GVTSVRTYKRI  
>AAP35082.1 Der f 27; serpin [Dermatophagoides farinae]  
MKFFLLSFVLMVVAATATYAAHVSGSRDNNNNKPVPAEGFAKASNEFGFHLLKEVIQHR  
SSSGSRGSSENVLFSPYSVAVALSMVHQGTQGSTAEQFKRVLYYDRVQQNLNGGEYQTVAN  
SVKQIQNQINQSDQSNQFDWGNMLMVDQOMPVKDQYKKIIEQYYDGQVMSVDFRKEKSNV  
MERINQFVSNKTHGLIDRMLQPPSADTGLALINAVYFKGEWLKPFDSMRTEQSVFYGGH  
GQEYKNVQYINGQGPYGYVEVPQWNSDLIQLPYKGEDIAFYGVLPREERNYDLDKIRQ SIN  
STFVDEIVGQITGSQSSTVYFPKIELSTSYQLPEILKSMGLQDVFTEADLSGITDKKPM  
KIDDAIHAKLILNEQGTEAGAGTYIQMAVLSALETSHFRFDHPFMYFIRHLPTGQILF  
LGEIHDF  
>AAR17475.1 Pen c 24; elongation factor [Penicillium citrinum]

MGFTDFVSDAGLSLANNYLATRSYIVGHAPSQADVVTYKAFTASPD AEKYPHVARWYKHI  
ASYESEFPTLPGDASKAFTAYGPEGSEASANPKDKPAEEEEEDLFASDSEDEDPAVVAE  
RNKNLEEKKKKAAGKPKAAKSLVTLVTKPWWDETNLEELANVRAIEMDGLVWGASKF  
VAVGFGIKKLQINLVEDEKVVSTDELQAQIEEDEDHVQSTDVAAMQKL  
>AAR21071.1 thaumatin-like [Juniperus rigida]  
MARVSELALLLVATLAISLHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGQTWTLN  
LAAGTASARFWGRTGCTFDASGKGSCKTGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDDV  
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVEGGCNSACNVFQTDQYCCRNAY  
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP  
>AAR21072.1 thaumatin-like [Juniperus rigida]  
MARVSELALLLVATLAISLHMQEAGAVKFDIRNQCQGYTVWAAGLPGGGKRLDQGQTWTLN  
LAAGTASARFWGRTGCTFDASGKGSCKTGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDDV  
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVEGGCNSACNVFQTDQYCCRNAY  
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP  
>AAR21073.1 Cup s 3; thaumatin-like [Cupressus sempervirens]  
MARVSELALLLVATS AISLHMQEAGAVKFDIKNQCRYTVWAAGLPGGGKRLDQGQTWTVN  
LAAGTASARFWGRTGCTFDASGKGSCRS GDCGGQLSCTVSGAVPATLAEYTDQSDQDYDDV  
SLVDGFNIPLAINPTNTKCTAPACKADINAVCPSELKVDGGCNSACNVLQTDQYCCRNAY  
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP  
>AAR21074.1 Cup s 3; thaumatin-like [Cupressus sempervirens]  
MARVSELALLLVATLAISLHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGQTWTVN  
LAAGTASARFWGRTGCTFDASGKGSCRS GDCGGQLSCTVSGAVPATLAEYTDQSDQDYDDV  
SLVDGFNIPLAINPTNTKCTAPACKADINAVCPSELKVDGGCNSACNVLQTDQYCCRNAY  
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP  
>AAR22488.1 Mal d 3; lipid transfer protein [Malus domestica]  
MACSAVIKLALVVALCMAVSVAHAITCGQVTSS LAPCIGYVRS GGAVPPACNGIRTING  
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLP GKCGVNVYPYKISTSTNCATVK  
>1LLT\_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]  
GVFN YETETTSVIP AARLFKAFILDGDNLF PKVAPQAIS SVENISGNGGPGTIKKISFPE  
GLPFKYVKDRVDEVDHTNFKNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY  
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>CAD21706.2 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTT VTGNLSGLK PGLHGFHVHALGDTTNGCMSTG  
PHFNVPV GKEHGAPGDENRHAGDLGNITVGEDGTA AINIVDKQIPLTGPHSIIGRAVVHS  
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG  
>AAR92223.1 Act d 4; phytocystatin [Actinidia deliciosa]  
MVPKPLSLLLFLLLALSAAVVGG RKLVAAGGWRPIESLNSAEVQDVAQFAVSEHNKQAND  
ELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGN YEAVVWDKPMHFRNLTSFRKV  
>P83542.1 Pol g 1; phospholipase A1 [Polistes gallicus]  
GITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFKES  
>AAS02108.1 FAD-linked oxidoreductase [Cynodon dactylon]  
MARSRAFALLICAVAASCHVALSAPPPYAKQVERDFLTCLTKDIPPRQLYAKSSPAYA  
SVWSSTVRNIKFLSDKTVKPLYIITPTNASHIQAAVVCGRRHGMRI RVRSGGHDEGLSY  
RSEKPEPFAVDMNKMRAVSIDGKAATAWVDSGAQLGDLYYGI AKASPKLGFPAGVCTTI  
GVGGHFGSGGGFGLLRKYGTAADNVIDAKVVD AQGRLLDRKAMGEDHFWAIRGGGGESFG  
IVASWQVKLLPVPPKVTVFQVHKG IKEGAIDLVTWKQTVAPALPDDL MIRIMAMGQGAMF  
EALYLGTCCKDLVLLMTARFPELGMNATHCKEMTWIESVPYIPMGPKGTVRDLLNRTSNIK  
AFGKYKSDYVLEPIPKSDWEKIFTWLVKPGAGVMIMDPYGGGIASVPESATPFPRRSGVL  
FNIQYVVYWFGEAAAALPTQWTRDIYDFMTPYVSKNPRQAYVNYRDLDLGVNQVGVNST  
YASGKVVGEKYFKGNFERLARTK GKIDPEYFRNEQSIPPLL

>CAE85467.1 Hev b 7; patatin [*Hevea brasiliensis*]  
ATGSTTLTQGKKITVLSIDGGGIRGIIPGIILASLESKLDQDLDGPDARIADYFDIIAGTS  
TGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIHSIGPIYDGEYL  
RELCNNLLKDLTVKDTLTDVVIPTFDIKLLLLPVIFSSDDAKCNALKNARLADVCISSAA  
PVLLPAHSFTTEDDKNIHTFELIDGGVAATNPTLLALTHRNEIIRQNPRFIGANLTESK  
SRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSALF  
KSLDCEDYYLRIQDDTLTGEESSGHIAATEENLQRLVEIGTRLLEKQESRINLDTGRLESI  
PGASTNEAAITKFAKLLSEERKLRQLK

>CAF25232.1 Pis s 1; 7S globulin, vicilin-like [*Pisum sativum*]  
SRSDQENPFIFKSNRFQTYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPHTLFL  
PQYTDADFILVVLGSKATLTVLKSNDNRNSFNLERGDAIKLPAGTIAYLANRDDNEDLRVL  
DLAIPVKNKPGQLQSFLLSGTQNQPSLLSGFSKNILEAAFNNTNYEEIEKVLLLEQQEQEPQH  
RRSLKDRRQEINEENVIVKVSREQIEELSKNAKSSSKKSVSSESSESGPFNLSRNPIYSNKF  
GKFFEITPEKNQQLQDLDFVNSVDIKEGSLLLPNYNSRAIVIVTVTEGKGFELVGQRN  
ENQKENDKEEEQEEETSKQVQLYRAKLSPGDVFPVAGHPVAINASSDLNLIGFGINAE  
NNERNFLAGEEDNVISQVERPVKELAFPGSSHEVDRLLNQKQSYFANAQPLQRE

>CAF25233.1 Pis s 1; 7S globulin, vicilin-like [*Pisum sativum*]  
SRSDQENPFIFKSNRFQTYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPRTLFL  
PQCTDADFILVVLGSKATLTVLKSNDNRNSFNLERGDTIKLPAGTIAYLANRDDNEDLRVL  
DLTIPVKNKPGQLQSFLLSGTQNQPSLLSGFSKNILEAAFNNTNYEEIEKVLLLEQQEQEPQH  
RRSLKDRRQEINEENVIVKVSREQIEELSKNAKSSSKKSVSSESSESGPFNLSRNPIYSNKF  
GKFFEITPEKNQQLQDLDFVNSVDIKEGSLLLPNYNSRAIVIVTVTEGKGFELVGQRN  
ENQKENDKEEEQEEETSKQVQLYRAKLSPGDVFPVAGHPVAINASSDLNLIGFGINAE  
NNERNFLAGEEDNVISQVERPVKELAFPGSSHEVDRLLNQKQSYFANAQPLQRE

>Q9NJA9.1 Ani s 2; paramyosin [*Anisakis simplex*]  
MSDTLYRSPMAIRSSTADMGALTSMSVADLGLSTRLEDKIRLLQDDFESERELRNRIER  
ERADLSVQLIALTDRLQDAECATDSQIESNRKREVELSKLRKLLLEESQLENEEDAMNVLRK  
KHQDVCLDYTEQIEQLQKKNKSIDRERQRLQHEVIELTATIDQLQKDKHVAEKMAQKFEQ  
QTIELSNKVEDLNKHVNDLAQQRQRLQAENSDDLAEIHDQKVQLDNLQHVKYQLAQQLEE  
SRRRLEDAERERSQMQAQLHQVQLELDSVRVALDEESAARVEAEHKLSLANTEITQWKS  
FDAEVALHHEEVEDLRKKMMQKQAEYEEQIEIMLQKVSQLEKAKARLQSEVEVLIVDLEK  
AQNTIAILERAKEQLEKQVLEMKSRIDELLVELEAAQREARAALAEELQKMKQLYEKAVEQ  
KEALARENKKLQDDLHEANEALADANRKLHELDLENARLAGEIRDQLVALKESEAARRDA  
EARAQRALAEELQVRIEMERRLQEKKEEEMEALRKSMQFEIDRLTAALADAEARMKAEIAR  
LRKKYQAEIAELEMTVDNLNRANLEAQTIKKQSEQIIQLQANLEDTQRQLQQTLDQYAL  
AQRKISALSALAELECKTALDNAIRARKQAEADLEEAHVRIISDLTSINSNLTAIKNKLETE  
LSTAQADLDEVTKELHAADERANRALADAARAVQELHEEQEHSMKIDALRKSLEEQVKQL  
QVQIQEAEEAALLGGKRVIAKLETRIRDLEVALDEETRRHKETQSALRKKDRRIKEVQMQ  
IDEEHKMFVMAQDTADMLEKLNQKQRLGEAEAMTMQNLQRVRRYQRELEDAEGRADQA  
ESSLNLIRAKHRGTVAVGKATDVVVVEED

>Q25632.1 tropomyosin [*Onchocerca volvulus*]  
MDAIIKKMQAMKIEKDNALDRADAAEEKVRQMTEKLERIEEELRDTQKKMMQTENDLVKA  
QEDLSVANTNLEDKEKKVQEAEEVAALNRRMTLLEEEELERAEEERLKIATDKLEEATHA  
DESERVKVMENRSFQDEERANTVESQEKQAQLLAEADRKYDEVARKLAMVEADLERAE  
ERAEAGENEIVELEEEELRVVGNLKSLEVSEEKALQREDSYQEQIRTVSVRLKEAETRAE  
FAERSVQKLQKKVDRLEDELVHEKERYKNISEELDQTFQELSGY

>AAS47035.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [*Prunus avium*]  
MGVFTYSDESTSVIPPPRLFKALVLEADTLIPKIAQSVKTAIEIVEGDGGVGTIKKISFG  
EGSHYSYVKKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTSN

YHTTGDEIKEEDVKAGKEKATGLFKLIENYLAANPDACN

>AAS47036.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus avium]

MGVFTYADESTSVIPPRLLFKALVLEADTLIPKIPQSVKSAEIVEGDGGVGTIKKISFG  
EGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTSN  
YHTTGDEIKEEDVKAGKEKATGLFKLIENYLVANPDAYN

>AAS47037.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus avium]

MGVFTYADESTSVITPPRLLFKALVLEADTLIPKIPQSVKGAEIVEGDGGVGTIKKISFG  
EGSHYSYVKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTSN  
YHTTGDEIKEEDVRAGKEKATGLFKLIENYLVANPDAYN

>CAF32566.2 Phl p 4; berberine bridge enzyme [Phleum pratense]

YFPPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT  
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRVWVDGKART  
AWVDSGAQLGELYYAIHKASTVLAFFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVKVRLLPVPPTVTVFKIPKKASE  
GAVDIINRWQVVAPQLPDDLMIRVIAQGPATFEAMYLGTQCQTLTPMMSSKFPELGMNAS  
HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFVKRWEQIFSTW  
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAAPLSWSKEI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK  
VDPTDYFRNEQSIPPLIKKY

>CAF32567.2 Phl p 4; berberine bridge enzyme [Phleum pratense]

YFPPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT  
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRVWVDGKART  
AWVDSGAQLGELYYAIHKASPVLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVKVRLLPVPPTVTVFKIPKKASE  
GAVDIINRWQVVAPQLPDDLMIRVIAQGPATFEAMYLGTQCQTLTPMMSSKFPELGMNAS  
HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFVKRWEQIFSTW  
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAAPLSWSKEI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK  
VDPTDYFRNEQSIPPLIKKY

>AAS67041.1 Pol d 1; phospholipase A1 [Polistes dominula]

MNFKYSILFICFVKVLDNDCYAADDLTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNG  
IILKKEILKNYDLFQKSQISHQIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWK  
KGACNAFASTNDVLGYSQAVGNTRHVGVYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTS  
GFAGKEVQRLKLGKYKEIIGLDPAGPSFLTNTKCPNRLCETDAEYVQAIHTSAILGVYYNV  
GSVDFYVNYGKSQPGCSEPCSHTKAVKYLTECIKRECCIGTPWKSYPSTPKPISQCKR  
DTCVCVGLNAQSYPAKGSFYVPVVDKAPYCHNEGIKL

>AAS67042.1 Pol d 1; phospholipase A1 [Polistes dominula]

ADDLTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFQKSQISH  
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG  
NTRHVGVYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL  
DPAGPSFLTNTKCPNRLCETDAEYVQAIHTSAILGVYYNVGSVDFYVNYGKSQPGCSEPC  
SHTKAVKYLTECIKRECCIGTPWKSYPSTPKPISQCKRDTVCVGLNAQSYPAKGSFYV  
PVEKDAPYCHNEGIKL

>AAS67043.1 Pol d 1; phospholipase A1 [Polistes dominula]

ADDLTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFQKSQISH  
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG  
NTRHVGVYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL  
DPAGPSFLTNTKCPDRLCETDAEYVQAIHTSAILGVYYNVGSVDFYVNYGKSQPGCSEPC

SHTKAVKYLTECIKRECCLIGTPWKSYPSTPKPISQCKRDTCCVGLNAQSYPAKGSFYV  
PVDKDAPYCHNEGIKL

>AAS67044.1 Pol d 1; phospholipase A1 [*Polistes dominula*]  
ADDLTTLRNGTLDRGITPDCTFNEKDIELHVSRDKRNGIILKKEILKNYDLFQKSQISH  
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG  
NTRHVGVYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL  
DPAGPSFLTSTKCPDRLCETDAEYVQAIHTSAILGVYYNVGSVDFVYVNYGKSQPGCSEPC  
SHTKAVKYLTECIKRECCLIGTPWKSYPSTPKSISQCKRDTCCVGLNAQSYPAKGSFYV  
PVEKDAPYCHNEGIKL

>AAS75297.1 Alt a 1; unknown function [*Alternaria alternata*]  
MQFTTIASLFAAAGLAAAAPLESRQDTASCPVTTEGDYVWKISEFYGRKPEGTYNSLGF  
NIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMNFSFGSDRSGLLLKQKVSDDITYVA  
TATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

>BAD13150.1 calcium-binding protein, polcalcin [*Oryza sativa*]  
MAAASSADMERIFKRFDTNGDGKISLSELTALRTLGSTSADEVQRMMAEIDTDGDGFID  
FNEFISFCNANPGLMKDVAKFV

>AAS75831.1 NPC2-like [*Suidasia medanensis*]  
MKFIILAMFVAVAAAGEMKFQDCGHGEVKKLLVSDCSGDYCIHKGKKSMEADDFVANQD  
SPTAVIKISAKVNGVELQVPGIETNGCHHMCKPLVKGQSYQFKYDLVIPQILPNVKADVT  
ASLTGAHGLLACGTVHGEVQN

>AAS77253.1 Fel d 4; lipocalin [*Felis catus*]  
MKLLLLLCLGLILVCAHEEENVRSNIDISKISGEWYSILLASDVKEKIEENGSMRVFVEH  
IKALDNSSLSFVHTKENGKCTEIFLVADKTKDGVYTVVYDGYNVFSIVETVYDEYILLH  
LLNFDKTRPFQLVEFYAREPDVSQKLKEKFKYQCQEHGIVNILDLTEVDRCLQARGSEVA  
QDSSVE

>CAG24374.1 Phl p 1; beta-expansin [*Phleum pratense*]  
IPKVPPGNITATYGGKWLDAKSTWYGKPTAAGPKDNGGACGYKDVKPPFSGMTGCGNT  
PIFKSGRGCSCFEIKCTKPEACSGEPVWHITDDNEEPIAAYHFDLSGIAFGSMAKKGD  
EQKLSRAGEVEIQFRRVKCKYPEGKTVTFHVEKGSNPYLALLVKFVAGDGDVVAVDIKE  
KKGDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEGGTKGEAKDVIPEGWKADTCYESK

>P83834.1 Cuc m 3; pathogenesis related protein, PR-1 [*Cucumis melo*]  
DFVDAHNAARAQVGVGPVHWTVDAYARQYANDRNLVHSATR

>AAS93669.1 cysteine protease [*Sarcoptes scabiei*]  
MSFIRFFSIFLLCFVSFLVARIIECDEFEIKTFEQFKARFNKTYSNYFIETYRRRVFYRTL  
KYVEENKHRGVSINAHADLTVNEFSAYLSKAPKTEDLLDEYKLFSCDKFEGVKLGELDL  
RKEGRVTKIREQLACGSCWAFSVTANVESLLLGSNCTRWSNDWLSPPQLVDCASDHGCN  
GEKTSTGLEYYVQHKGIVKEGVYPYKARVGVCKHPCGPYYHIKSFCGISPPDPDQVKIALS  
KTRSALSASIIIVYDVEHLKNYNGKPLADDGKLIGEQLSHAINIVGYTQRNGVEVWIVRN  
SWGETWGDHGYGYFKILPKRGVMGITRMVIVADLGKETVA

>AAS93674.1 unknown function [*Sarcoptes scabiei*]  
MERKQFNLLYLQILLSVAIITRGYYFETTPSIDDENVRLSDLDWIGEPDDSDFKLPDSFI  
RKFKQDLMRDLNKKCRNHFSIIKLIHPGLQFCKVPKVVYQALPTWFDLRNLELVTPTRDNS  
TEKQCKASWAFGPIASLESAWLESHDRIASDAFSLSAQNLDICAGYQGCNGGVDVIEAFN  
YLQEKGVVKEENYKYKGGKHACRWRLFYRRYKIKSYCAICPATVETIKKFLFKHKTALTT  
VISVRNLTAFKNIDDEILYEDEGPSVQRRLLVNIIGGWRHDDATDRDYWVVKNSWGRKWGM  
GGYGFVDAEENLFGILDQNYLLSVKDEVIPFEAEPDDS

>AAS93675.1 cysteine protease [*Sarcoptes scabiei*]  
MESKKFKSFLFQLIISAAIITRGYYFETTPSDAEENARLSDVRYTGEPDDPDFKLPDSFI  
QKFKKDLRELTRKCRKGRQARLEHPELQFCKIPKVFQKLPKWFDLRNLEFVTPTRDNS  
TESKCKASWAFGPVASMESAWLESHDRIASDSFFLSPQNLIDCAGYQGCDDGGVDVIEAFN

YMKHKGIVKEEFYKYRAKKHRCRKRRLRARRYKIRSYCAICPATIFTIKKFLFKHKTALTT  
VISVRNLTAFKHIDDEILYEDEGTRVQRRLVNVIVGWRHDDATDRDYWVVKNSWGKKWGM  
GGYGFVDAENNPLHILDHNYLVRVKEDVIPFENEPEDFE

>AAS93676.1 cysteine protease [*Sarcoptes scabiei*]

LMRELTRKCRKGFRRARLEHPELQFCEIPKVFQKLPKWFDLRNLELVTPTRDNSTEKKCK  
ASWAFGPVASMESAWLESHDRIASDSFFLSPQNLIDCAGYQCGDGGVDVIEAFNYMKHKG  
IVKEEFYKYKAKKHHRCRKRRLRARRYKIRSYCAICPATIFTIKKFLFKLKTALTTVISVRN  
LTAFKNIDDEILYEDEGPRVQRRLVNVIVGWRHDDATDRDYWVVKNSWGKKWGMGGYGFV  
DAENPPFHILDHNYLVRVKEDVIPFENEPEDFE

>AAR98518.1 Hev b 4; lecithinase-like [*Hevea brasiliensis*]

MASLAYSILSLFTFTLLNPVCTELDEYLFSGDGLYDAGNAKFIYDPKYLPSYHHPYG  
TTFDYPTGRFSDGRTVVDFVAENVSLPRIPPFKNKEANFTYGANFASEGATASDSNPLI  
DFRSQIRDFGELKLEWAVQLVNVTELARRLKKAVYLISFGADDYLNIEIPSEASREQLES  
IVDVVLGNISDRIKELYDFGARKFVVENVAPLGLIPFIKQTSNDSTLFYELASLHAMKLP  
QILEKIQDGYLFPEFNVTVFNYFGIIEIIDAPGEHGFYKYGDIACCGNSTYRGQACGFLD  
YEFCVCGNKTEYLFFDGTHTDAANLLAELMWDKESGFISPYGVKDFFPSPPTTIQTLT  
EATALG

>AAS98889.1 arginine kinase, partial [*Penaeus chinensis* (*Fenneropenaeus chinensis*)]  
YNLQVRGTRGEHTEAEGGIYDISNKRRMGLTEFQAVKEMQDGILELIKMEKEM

>AAS98890.1 arginine kinase, partial [*Penaeus chinensis* (*Fenneropenaeus chinensis*)]  
YNLQARGTRGEHTEAEGGIYDISNKRRMGLTEFQAVKEMLDGILELIKMEKEM

>AAT00594.1 Ara h 1; 7S globulin, vicilin, partial [*Arachis hypogaea*]

GNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRRSTRSSDNEGVIKVSKEHVQELTK  
HAKSVSKKGSEEDITNPNINLRDGEPLDSNMFGRLEFVKPDKKNPQLQDLDMMLTCVEIK  
EGALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREQEWEDEDEDEDEEGSNRE  
VRRYTARLKEGDVFImpAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEK  
QAKDLAFPGSGEQVEKLIKQKESHFVSARPOSSPSPEKEDQEEENQGGKGPLLSILK  
AFN

>AAT00595.1 Ara h 1; 7S globulin, vicilin, partial [*Arachis hypogaea*]

LEAAFNAAFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEGVIKVSKEHVEELTKHA  
KSVSKKGSEEGDITNPNINLREGEPDLSNMFGLFVKPDKKNPQLQDLDMMLTCVEIKE  
GALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREDEDEDEDEEGSNREVRRY  
TARLKEGDVFImpAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKD  
LAFPGSGEQVEKLIKQKESHFVSARPOSSPSPEKEDQEEENQGGKGPLLSILKAFN

>AAT00596.1 Ara h 1; 7S globulin, vicilin, partial [*Arachis hypogaea*]

GFDQRSRQFQNLQNHRIQIEAKPNTLVLPKHADADNILVIQQQATVTVANGNRRKSFN  
LDEGHALRIPSGFISYILNRHDNQLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGF  
RNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEGVIKVSKEHVEELT  
KHAKSVSKKGSEEGDITNPNINLREGEPDLSNMFGLFVKPDKKNPQLQDLDMMLTCVEI  
KEGALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREDEDEDEDEEGSNREVR  
RYTARLKEGDVFImpAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQA  
KDLAFPGSGEQVEKLIKQKESHFVSARPOSSPSPEKESPEKEDQEEENQGGKGPL  
LSILKAFN

>Q7M4I5.1 Api d 1; phospholipase A2 [*Apis dorsata*]

IIYPGTLWCGHNVSSSPDELGRFKHTDSCCRSHDMCPDMSAGESKHGLTNTASHTRLS  
CDCDDKFYDCLKNSSDTISSYFVGEMYFNILDTKCYKLEHPVTGCGKRTEGRCLNYTVDK  
SKPKVYQWFDLRKY

>Q7M4I6.1 Bom p 1; phospholipase A2 [*Bombus pennsylvanicus*]

IIYPGTLWCGNNGNIANGTNELGLWKETDACCRTTHDMCPDIEAHGSKHGLTNPADYTRLN  
CECDEEFRHCLHNSGDAVSAFVGRTYFTILGTQCFRLDYPIVKCKVKSTILRECKEYEF

DTNAPQKYQWFDVLSY

>Q7Z1K3.1 Ani s 1; serine protease inhibitor [*Anisakis simplex*]  
MASMQHFSLAALLLAASICLGADARTECQLPLDKGTPCTQEGGVKPSVAWWHDDKSGICL  
SFKYTGCGGNANRFTTIKNCEQHCKMPDRGACALGKKPAEDSNGEQLVCAGMREDKCPNG  
YQCKMMAFMGLCCPTKEEELFAREYEGVCKSGKPVKMDRGSWMMTILGKSCDDQFCPED  
AKCERGLFANCK

>Q7M1X5.1 Lol p 11; Ole e 1-like [*Lolium perenne*]  
DKGPGFVVTGRVYCDPCRAGFETNVSHNVEGATVAVDCRPFDDGGESKLLKAEATTDKDGWY  
KIEIDQDHQEEICEVVLAKSPDKSCSEIEEFRRARVPLTSNXGIKQQGIRYANPIAFFR  
KEPLKECGGILQAY

>Q7M1E7.1 Cha o 2; polygalacturonase [*Chamaecyparis obtusa*]  
MGMKFMAAVAF LALQLIVMAAAEDQSAQIMLDSIEQYLRNRSLLKLVHSRHDAATVFN  
VEQYGAVGDGKHDSTEAFATTWNAACKKASAVLLVPANKKFFVNNLVFRGPCQPHLSFKV  
DGTIVAQPDPARWKNKSIWLQFAQLTDFNLMGTGVIDGQGGQWAGQCKVNGRTVCNDR  
NRPTAIKIDYSKSVTKELTLMNSPEFHLVFGCEGVKIQGLKIKAPRDPNTDGDIDIFA  
SKRFHIEKCVIGTGDDCIAIGTGSSNITIKDLICGPGHGIGSLGRDNSRAEVSHVHVN  
RAKFIDTQNGLRIKTWQGGSGLASIYIYENVEMINSENPI LINQFYCTSASACQNQRS  
QIQGVTYKNIHGTSATAAAIQLMCSDSVPCTGIQLSNVSLKLTSGKPASCVDKNARGFYS  
GRLIPTCKNLRPGSPKEFELQQPTTVMDENKGCACAKGDSTCISLSSSPPNCKNKCKGC  
QPCPKLIIVHPNKPQDYYPQKWVCSCHNKIYNP

>AAT40866.1 Tyr p 10; tropomyosin [*Tyrophagus putrescentiae*]  
MDAIKNKMQAMKLEEDNAIDRAEIAEQKARDANLKSEKTEEEVVALQKKIQIENELDQV  
QENLTQATTKLEEKEKALQTAADVAALNRRIQLIEEDLERSEERLKVATAKLEEASHSA  
DESERMKMLEHRSITDEERMDGLESQLEEARLMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQIRIMTSKLKEAERAE  
FAERSVQKLQKEVDRLDEDELVHEKEKEYESISDELDTFAELTGY

>AAT45383.1 Lat c 1; calcium-binding protein, parvalbumin [*Lates calcarifer*]  
MAFSNVLSDSDVAAAALDGGCKDAGTFDHKKFFSACGLSNKTSDDVKKAFIDQDKSGFIE  
EEELKFLFQNFKADARVLT DVETSTFLKAGDTDGDGKIGADEFTALVKP

>AAT66566.1 Alt a 1-like [*Stemphylium vesicarium*]  
ALFAAAGLAAAAPFEARQADASCPVSTQGDYVWKISEFSGRKPEGTYYNLSFNKATNK  
GTLDFTCQAQADKLEDDKFYSCGENSFMSFAFQSDRNGLLFRQDVSEITYVATATLPNY  
CHAGGNGPKDFVCQGV

>AAT66567.1 Alt a 1-like [*Stemphylium callistephi*]  
TLFAAAGLAAAAPLEAPQANTTTPVSTQGDYVWKISEFSGRKPEGTYYNLSFNKATNG  
GTLDFTCQAQADKLEDEFYSCGENSFISFAFQSDRSGLLLRQDVSEITYLATATLPNY  
CRAGGNGPNDFICQGV

>CAE52833.1 Pla a 2; polygalacturonase [*Platanus acerifolia*]  
RGVQSSGSVFNVDYGAAGDISQAVMKAWKAACASQGPSTVLIPKGNYNMGEVAMQGP  
CKGSKIGFQIDGVKAPADPSKFKSDGWSFYRIDGLTVSGTGLDGGQTAWAKNNCDK  
NPNCXHAAMNLRDFDLKHAMVRDITSLNSKMFHINVLECEDITFQHVTVTAPGTSINTDG  
IHVGISKVITINTKIATGDDCISIGPGSQNVITITQVNCGPGHGIGSLGRYNNKEEVR  
GITVKGCTFSGMTMNGVRVKTWPNSPPGAATDLTFQDLTMNNVQNPVILDQEYCPYGCQR  
QAPSRIKLSNINFNNIRGTSTGKVAVVIACSHGMPCSNMKIGEINLSYRGAGPATSTCS  
NVKPTFSGKQVPAIKCA

>AA067349.2 Cor a 12; oleosin [*Corylus avellana*]  
MADRPQQLQVHPQRGHGHYEGGIKNQRGGPSAVKVMVAALPVGGTLLALAGLTLGAS  
VIGLLVTSPLFIIFSPVLVPAAIWVGLAVASFLSSGALGLTGLSSLSWVNLNLRASQSL  
PREMDQAKRRMQDMAAFVQKTREVGQEIQSRAQEGRR

>CAH03799.1 Cit s 3; lipid transfer protein [*Citrus sinensis*]

ITCGQVTGSLAPCIVYLRSGGPIVPCNGVRSLNAAARTTPDRQTACNCLKQAAGSIPN  
LNPNAVGLPRACGVSIPIKISISTDCSKVR  
>AAT77152.1 Per a 9; arginine kinase [Periplaneta americana]  
MVDAAVLEKLEAGFAKLAASDSKSLKKYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN  
HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI  
ISTRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEAELKGQFYPLTGMTKEVQQK  
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDKTFVLWCNEEDHLRIISMQMGGDLG  
QVYRRLVTAVNDIEKRIPFSHDDRLGFLTFCPTNLGTTVRASVHIKVPKLAADKAKLEEV  
AGKYNLQVRGTRGEHTEAEGGVYDISNKRMMGLTEYDAVKEMNDGIAELIKLESSL  
>AAT80649.1 Mal d 3; lipid transfer protein [Malus domestica]  
MASSAVTKLALVVALCMAVSVAHAITCGQVTSSLAPCIGYVRNGGAVPPACCNGIRTINS  
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLPGKCGVNVYPYKISTSTNCATVK  
>AAT80659.1 Mal d 3; lipid transfer protein [Malus domestica]  
MASSAVIKLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRSGGVPPACCNGIRTING  
LAKTTPDRQAACNCLKSLAGSVSGVNPNGAESLPGKCGVNVYPYKISTSTNCATVK  
>AAT80662.1 Mal d 3; lipid transfer protein [Malus domestica]  
MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRSGGVPPACCNGIRTING  
LAKTTPDRQAACNCLKSLAGSVSGVNPNGAESLPGKCGVNVYPYKISTSTNCATVK  
>AAT80664.1 Mal d 3; lipid transfer protein [Malus domestica]  
MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRSVSDGPVPPACCNGIRTING  
LAKTTPDRQAACNCLKSLAGSVSGVNPNGAESLPGKCGVNVYPYKISTSTNCATVK  
>AAT80665.1 Mal d 3; lipid transfer protein [Malus domestica]  
MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRSGGVPPACCNGIRTING  
LAKTTPDRQAACNCLKSLAGSVSGVNPNGVESLPGKCGVNVYPYKISTSTNCATVK  
>AAT95008.1 Sol i 1; phospholipase A1 [Solenopsis invicta]  
MRKFAAIFVVFVQCTHLYSLAQARAEPDPGVEYLKQSCVYGNSSYINVYLYNSRFQ GK  
NLGNQQSCQDINASLPVVFITHGFTSSAQVSTFKDLANAFVQKGHTAFIVDWSEAACTDG  
LPGVQFAEYNAAASNTYDIGQLMAKYTVDLMNKCKIPLNNIQYVGHSLGSHVCGFAAKHV  
KKLINKTMPYILALDPADPSFGSNKCGERICKSDAKRIVVFKTSILGIGENIIGHLLIVF  
DGGKSQPACSWYDVPCHSESIYATGMVSGRCQH LAVPWTAAQRINPIQWKFWRVFTSN  
IPAYPTSDDTTNCVVLNTNVFKNDNTFEGEYHAFPCARNLFKCRQQ  
>AAT95009.1 Pol e 5; unknown function, antigen 5 [Polistes exclamans]  
MEIGGLVYLIVVVAIIHSSQGVYDCKIRCPSGIHTVCQYGESTKPSKNCAGKVIKSVGPT  
EEEKLLIVSEHNRFRQKVAQGLETRGNPGPQPAASDMNDLVWDELAKIAQVWASQCQFL  
VHDKCRNTAKYPVQGNIAAYAGGSKLPDVVSLIKLWENEVKDFNYNTGITKQNF AKIGHYT  
QMVGKTKKEIGCGSLKYMENKMQNHYLICNYGPAGNYLGQLPNTKK  
>AAT95010.1 Pol d 5; unknown function, antigen 5 [Polistes dominula]  
MKISCLICLVIVLTIIHLSQANDYCKIKCSSGVHTVCQYGESTKPSKNCAGKLIKSVGPT  
EEEKLLIVEEHNRFRQKVAQGLETRGNPGPQPAASNMMNLVWDELAKIAQVWASQCQIL  
VHDKCRNTEKYQVQGNIAAYAGSSNHFPVTKLIQLWENEVKDFNYNTGITNKNFGKVGHY  
TQMVGNTKEVGCGLKYVEKNMQIHYLICNYGPAGNYLGQPIYTKK  
>BAD36780.1 Myr p 3; pilosulin [Myrmecia banksi]  
MKLSCLLLTLAIIIFVLTIVHAPNVKAKALADPESDAVGFADAVGEADPFDITKLNKIKLT  
KATCKVISKGASMCKVLFDKKKQE  
>AAT99258.1 Sal k 1; pectin methylesterase [Salsola kali]  
MEEHVSMLLVGFVLINIAFTSIAQLIPPNPAELESWFQGAVKPVSEQKLEPSVVQTESG  
GVETIEVRQDGSQKFKTISDAVKHVKGNTKRVIITIGPGEYREKVKIERLHPYITLYGI  
DPKNRPTITFAGTAAEFVTSATVIVESDYSVGAHLIVTNSAPRPDGKRKGAQAGALRI  
SGDRAAFYNCKFTGFQDTVCDKGNHFFDCYTEGTVDFIFGEARSLYLNTELHVVPDGP  
MAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFDAARVVF SYCNLSDAAKPEGW

SDNNKPEAQKTILFGEYKNTGPGAAPDKRAPYTKQLTEADAKTFTSLEYIEAAKWLLPPP  
KV  
>Q9LD79.2 Jun v 3; thaumatin-like [Juniperus virginiana]  
AFLLAATLTISSHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGQWTWVNLAAGTAS  
ARFWGRTGCTFDASGKGCQTDGDCGRQLSCTVSGAVPATLAEYTSQSDQDY  
>P15322.2 Sin a 1; 2S albumin, conglutin [Sinapis alba]  
PAGPFRIPKCRKEFQQAQHLRACQOWLHKQAMQSGSGPSWTLDDDEFDFEDDMENPQGPQQ  
RPPLLQCCNELHQEELCVCPTLKGASKAVKQQVRQQLGQQGQQGPHLQHVISRIYQTA  
THLPKVCNIRQVSVCPFKKTMGPS  
>AAU11502.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]  
MVQLNGSYKLEKSDNFDAFLKELGVNFVTRNLAKSASPTVEIVDGDSDYTIKTSSTLKNS  
EIKFKLGEFEEDRADGKVKQTSVTKEGDNKLVQVQKGDKPVITIVREFSEEGTLVTATVN  
GVTSVRFYKRQ  
>AAU21500.1 Ara h 10; oleosin [Arachis hypogaea]  
MTDRTQPHAVQVHTTAGRFGDTAAGTNRYADRGPTSKVIAVITGLPIGGTLLLFAGLAL  
AGTLLGLAVTTPLFILFSPVIVPATIVVGLSVAGFLTSGACGLTGLSSFSWMMNYIRQTH  
GSVPEQLEMAMHRMADVAGYVQKTKDVGQ  
>P84159.1 Cit s 1; germin-like, partial [Citrus sinensis]  
TDPGHLQDVXVAINDPKXGVFVNRK  
>P84160.1 Cit l 3; lipid transfer protein [Citrus limon]  
ITCGQVTGSLAPXIPFLRTG  
>P84161.1 Cit s 3; lipid transfer protein [Citrus sinensis]  
ITXGQVTGSLAPXIAFLRTK  
>P67875.1 Asp f 1; ribonuclease mitogillin [Aspergillus fumigatus]  
MVAIKNLFLLAATAVSVLAAPSPLDARATWTCINQQLNPKTNKWEDKRLLYSQAKAESNS  
HHAPLSDGKTGSSYPHWFTNGYDGNGLIKGRTPIKFGKADCDRPPKHSQNGMGKDDHYL  
LEFPTFPDGHYDFDSKKPKEDPGPARVIYTYPNKVFVCGIVAHQRGNQGDRLRCSH  
>CAD54670.2 Phl p 4; berberine bridge enzyme [Phleum pratense]  
SSCEVALSYPTPLAKEDFLRCLVKEIPRLLYAKSSPAYPSVLGQTIIRNSRWSSPDNVK  
PIYIVTPTNASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFVVDLSKMRAV  
WVDGKARTAWVDSGAQLGELYAIHKASPVLAFPAGVCPTIGVGGNFAGGGFGMLLRKYG  
IAAENVIDVKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVKVRLLPVPPTVTVF  
KIPKASEGAVDIINRWQVVPAPQLPDDLIRVIAQGPATFEAMYLGTCQTLTPMMSSKF  
PELGMNASHCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPKEV  
WEQIFSTWLLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAA  
PLSWSKEIYNMPEYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQ  
RLAITKGKVDPTDYFRNEQSIPPLIQKY  
>CAD54671.2 Phl p 4; berberine bridge enzyme [Phleum pratense]  
SSCQVAFSYFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIIRNSRWSSPDNVK  
PLYIITPTNVSHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPETFAVVDLNMRAV  
WVDGKARTAWVDSGAQLGELYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYG  
IAAENVIDVKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVQVKLLPVPPTVTIF  
KISKTVSEGAVDIINKWQVVPAPQLPADLMIRIIAQGPKATFEAMYLGTCQTLTPLMSSKF  
PELGMNPSHCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTV  
WEQILNTWLVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAA  
PLSWSKDIYNMPEYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKLVWGQKYFKGNFE  
RLAITKGKVDPTDYFRNEQSIPPLIKKY  
>AAV33670.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus bombycis]  
MGVFTFDDEFTSTVAPARFFKAAVLADADNLFKVPAPQAASAEVTEGNGGPGTVKKITLP  
DGKYVVKQRLDSIDHDNFTYGHSHIEGDVLSADIEKISHVTKFVASPSGGSIKVTTFHT

VGDA PVDEAKAKEGKEKA EGLFKLVEGYLEANPSAYN

>AAV33672.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus bombycis]  
MGVSTHNDEFTSTVAPARLFKAAVLDADNLFPKIAPDAAKSAENIEGNGGPGTIKKITFP  
DGKYVKQKLD AIDL DNYSSHSII EGDILSAE LEKISHETKFVAAPGGGGSVIKVT TTT FHT  
VGNATVDEAKAKEGKEKAAGL FKLVEGYLEANPSAYN

>AAT37679.1 Rho m 2; serine protease [Rhodotorula mucilaginosa]  
TMELLEDLIEQVRQLPMVNFIEKNSLVHANEFTVAKGAPWGLARISHRDPLSLGSFDQYL  
YDSNGGTGVTSYVIDTGVNVHHEQFEGRAKWGKTIPQGEDEDEDGNGHGTHCAGTIGSNAY  
GVAKNAEIVAVKVLRSNGSGSMSDVIKGVEFAVKSHQDSVKKGKNSFSTANMSLGGGKSP  
ALDLAVNAAVKAGLHFAVAAGNENQDACNTSPAENAITVGASTISDARAYFSNYGKCV  
DIFAPGLNILSTYIGSDAATAYLSGTSMASPHIAGLLTYYSLSLQPSDSEFFIGAEGITP  
AQLKKNLIAFGTPDVLADIPADTPNILAFNGAGQNLTKFWGH

>AAV40850.1 lipid transfer protein [Prunus persica]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQASSSLAPCIPYVRGGGAVPPACNGIRNV  
NNLARTTPDRQAACNCLKQLSASVPGVNPNNAAALPGKCGVSIPYKISASTNCATVK

>P02604.3 Gal d 7; myosin light chain [Gallus gallus]  
MAPKKDVKKPAAAAAPAPAPAPAPAPAKPKPAIDLKSIKIEFSKEQQDDFKEAFLLF  
DRTGDAKITLSQVGDIVRALGQNPTNAEINKILGNPSKEEMNAKKITFEELPMLQAAAN  
NKDQGT FEDFVEGLRVFDKEGNGTVMGAELRHVLA TLG EKMT EEEVEELMKGQEDSNGCI  
NYEAFVKHIMSV

>CAH92627.1 berberine bridge enzyme [Secale cereale]  
NYRAFALALLFCALSCQAAAAAYAPVPAKADFLGCLMKEIPARLLYAKSSPDYPTVLAQT  
IRNSRWSSPQNVKPIYIITPTNASHIQSAVVCGRRHGIRLRVRSGGHDYEGLSYRSEKPE  
TFAVVDLNMRAVSVVDGYARTAWVESGAQLGELYAIKNSPVLAFAPAGVCPSIGVGGNF  
AGGGFGMLLRKYGIAAENVIDVKVVDPNGKLLDKSSMSADHFWAVRGGGGESFGI VVSWQ  
VKLLPVPPTVTVLKIPKTVQEG AIDL VNKWQLVGPALPGDLMIRIILAGNSATFEAMYLG  
TCSTLTPLMSSKFPELGMNPSHCNEMSWIKSIPFIHLGKQNLDDLNRNNTFKPFAEYKS  
DYVYQPFKPVWEQIFGWLVKPGAGIMIMDPYGATISATPEAATPFPHRQGVLFNIQYVN  
YWFAESAGAAPLQWSKDIYKFMEPYVSKNPRQAYANYRDIDLGRNEVVNDISTYSSGKVV  
GEKYFKGNFQRLAITKGKVDPPQDYFRNEQSIPPLVEKY

>CAH92630.1 berberine bridge enzyme [Secale cereale]  
NSRAFALVPLLICVLSCHAAVSYAAAPVPAKEDFFGCLVKEIPARLLYAKSSPAFPTVLA  
QTIRNSRWSSPQSVKPLYIITPTNASHIQSAVVCGRRHGVIRVRSGGHDYEGLSYRSER  
PEAFVVDLNMRAVVVDGKARTAWVDSGAQLGELYAIKNSPVLAFAPAGVCPTIGVGG  
NFAGGGFGMLLRKYGIAAENVIDVKVVDANGTLLDKSSMSADHFWAVRGGGGESFGI VVS  
WQVKLLPVPPTVTVFKIPKTVQEGAVELINKWQLVAPALPDDLIRIIFGGTAKFEAMY  
LGTCKALTPLMSSRFPELGMNASHCNEMPWIKSVPFIHLGKQATLSDLLNRNNTFKPFAE  
YKSDYVYQVPKPVWAQIFVWLVKPGAGIMVMDPYGAAISATPEAATPFPHRKDVL FNIQ  
YVNYWFDEAGGAAPLQWSKDMYRFMEPYVSKNPRQAYANYRDIDLGRNEVVNDISTYASG  
KVWGEKYFKGNFQRLAITKGKVDPPQDYFRNEQSIPPLLGK

>CAH92637.1 Lol p 4; FAD-containing oxidase [Lolium perenne]  
AVVCGRRYDVRIRVRSGGHDYEGLSYRSLOPENFAVVDLNMRAVLDGKARTAWVDSGA  
QLGELYAIKYSRTLAFAPAGVCPTIGVGGNLAGGGFGMLLRKYGIAAENVIDVKLVDAN  
GKLDHKKSMGDDHFWAVRGGGGESFGI VVSWQVKLLPVPPTVTIFKIPKSVSEGAVDIIN  
KWQLVAPQLPADLMIRI IAMGPKATFEAMYLGTCKLTPMMQSKFPELGMNASHCNEMSW  
IESIPFVHLGHRDSLEGDLLNRNNTFKPFAEYKSDYVYEPFKSVWEQIFGTWLVKPGAG  
IMIFDPYGATISATPEAATPFPHRKGVL FNIQYVNYWFAPGAGAAPLSWSKEIYNYMEPY  
VSKNPRQAYANYRDIDLGRNEVVNGVSTYSSGKVVWGQKYFKGNFERLAITKGKVDPTDYF  
RNE

>CAI05848.1 Der f 2; NPC2-like [Dermatophagoides farinae]

MISKILCLSLVAAVVADQVDVKDCANHEIKKVMVDGCHGSDPCIHRGKPFNLEAIFDA  
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN  
VVVTVKLVGDNGVLACAIATHAKIRD  
>CAI05849.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFNLEAIFDA  
NQNTKTAKIEIKANINGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN  
VVVTVKLVGDNGVLACAIATHAKIRD  
>CAI05850.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFNLEAIFDA  
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN  
VVVTVKLVGDNGVLACAIATHAKIRD  
>CAI23765.1 Cit s 2; profilin [Citrus sinensis]  
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFRLEEIAAILKDFDQPGTL  
APTGLFLGGTKYMIQGEAGAVIRGKKKSGGIIVKKTNQALIIIGIYDEPLTPGQCNMIVE  
RLGDYLIEQGL  
>AAV74343.1 Fra e 1; Ole e 1-like, partial [Fraxinus excelsior]  
EDVPQPPVSLFYVQGGVYCDTCRAGFITELSEFIQAGVRLQCKEKENGKVTFTTEVGYTR  
AEGLYSMVIERDHKNEFCEIVLLSSSRKDCHEIPTEGWVKPSLKFILNTVNGTTRTINPL  
GFFKKEALPKCPQVYVYKLGMYPPNM  
>P84296.1 Chi t 3; hemoglobin [Chironomus thummi thummi]  
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVDILAAVFAAYPDIQAKFPQFA  
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNASNAAAVEGLLNKLGSDHKARGVSAQA  
FGFERTALVSYLSNHVSWGDNVAAAWNKALDNTMAVAVAH  
>P84298.1 Chi t 3; hemoglobin [Chironomus thummi thummi]  
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVEILAAVFAAYPDIQNKFSQFA  
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNTSNAAVNSLVSKLGDDHKARGVSAQA  
FGFERTALVAYLQANVSWGDNVAAAWNKALDNTFAIVVPR  
>P02226.2 Chi t 3; hemoglobin [Chironomus thummi thummi]  
MKFFAVLALCIVGAIASPLSADQAALVKSTWAQVRNSEVEILAAVFTAYPDIQARFPQFA  
GKDVASIKDTGAFATHAGRIVGFVSEIIALIGNESNAPAVQTLVGQLAASHKARGISQAQ  
FNEFRAGLVSYVSSNVAAWNAAAESAWTAGLDNIFGLLFAAL  
>BAD77932.1 chitinase [Cryptomeria japonica]  
MQIMATQNSKSNIFWSSASVVLVLLLLVDVGVQCQNCGCNGLCCSQYGYCGSGEAYCGAG  
CKEGPCSSSSPSTGTGVSIVSSDVFNIVGGAASGCAGNGFYTYDSFISAANAFNGFG  
TSGSSDVNKREIAAFFANAHAHETGGFCYIEEQNPTSICYDASNTQYPCASGKTYHGRGPL  
QLSWNYNYGAAGSYIQFDGLNNPEIVGTDSTISFKTAVWFWMVNSNCHTAITSGQFGAT  
IRAINSMEDCGGNAATVASRVNYQKFCQQLNVDTGSNLQC  
>AAV97933.1 Lat c 1; calcium-binding protein, parvalbumin [Lates calcarifer]  
MAFAGILNEADITAALAACAADSFKHKDFVVKVGLAGKSDDDVKKAFVIDQDKSGFIE  
EDELKFLQNFASARALDAETKEFLKAGSDGDGKIGVDEFAALVKV  
>AAW29810.1 Jug r 4; 11S globulin, cupin [Juglans regia]  
MAKPILLSIYFLIVALFNGCLAQSGGRQQQFGQCQLNRLDALEPTNRIEAEAGVIESW  
DPNNQQFQCAGVAVVRRTEPNGLLLPQYSNAPQLVYIARGRGITGVLPFGCPETFEESSQ  
RQSQQQSREFQQRHQRIRHFRREGDIIAFPAGVAHWSYNDGSNPVVAISLLDTNNANQ  
LDQNPRNFYLAGNPDDEFRQGGQEQEYEQHRRQQQRQRPGEHGQQQRGLGNNVFSGFAD  
FLADAFNVDTETARRLQSENDHRRSIVRVEGRQLQVIRPRWSREEQEREERKERERERES  
ESERRQSRRGRDDNGLEETICTLRLRENIGDPSRADIYTEEAGRISTVNSHTLPVLRWL  
QLSAER GALYSDALYVPHWNLNAHSVVYALRGRAEVQVVDNFGQTVFDELREGQLLTIP  
QNFVAVKRARNEGFEWVSFKTNENAMVSPLAGRTSAIRALPEEVLATAFQIPREDARRLK  
FNRQESTLVRSRPSRSRSSRSERRAEV

>AAP13533.2 Cuc m 2; profilin [Cucumis melo]  
MSWQVYVDEHLMCEIEGNHLTSAAIIGQDGSVWAQSQNFQPKPEEVAGIVGDFADPGTL  
APTGLYIGGTYMVIQGEPAVIRGKKKGGVTVKKTGMALVIGIYDEPMTPGQCNMIVE  
RLGDYLDIDQGL

>CAE17316.1 villin [Nicotiana tabacum]  
EGGGKIEVWRINGSAKTPVPGDDIGKFYSGDCYIVLYTYHCNDRKEDYYLCWWIGKDSVE  
EDQNMAAKLASTMCNSLKARPVLGRVYQGEPPQFVAIFQPMLVLKGGGLSSGYKSYIADK  
GLNDETYTADSVALIRLSGTSVHNNKAVQVDAVATSLNSNECFLLQSGSSVFSWHGNQST  
YEQQQLAAKVAEFLKPGVTVKHAKEGESSTFWFALGGKQSYTSKKIASEVARDPHLFAY  
SFNKGKFEIEEYIYNSQDDLLTEDVLLLDTHAEVFWVWGQSSDPKEKQSSFEVGGQKYIEM  
AASLEGLSPHVPLYKVMNEPCFFTTFFSWDPAKAIAGNSFQKKVMLLFGVGHASENQ  
QRFNGTNQGGATQRASALAALNSAFSSSSPAKSSSAPRSAGKSPGSQRAAAIAALSSALS  
AEKKQPEEGSPLRLSRTSSVDAIAPGNEVSTAEIEDSKEVPERKEIETVEPAETDGEDV  
GPKPEPEQDETGNSSQTTFSYERLKAIXENPVGTGIDLRREAYLSDEEFESVLEMTKEA  
FYKLPKWKQDIHKKKVDLF

>CAE17317.1 villin [Nicotiana tabacum]  
REDYYLCWWIGKDSIEEDQSMARLASTMCNSFKGRPVLGRVFQGEPPQFVAIFQPMLV  
LKGGLSSGYKNIADKGLNDETYAADSVALIRLSGTSVHNNKAVQVDAVPASLNSNECFLL  
LQSGSSIFSWHGNQSTYEQQQLAAKVAEFLKPGATVKHTKEGTESSAFWFAVGGKQSYTS  
KKVATEVSRDPLHFAYSFNKGKFEVEEYIYNSQDDLLTEDILLLDTHAEVFWVWGQSSADS  
KEKQSAFDVGGQKYVEMAASLEGLSPNVPLYKVTEGNEPCFFTTFFSWDPAKRSAGNSFQ  
KKVMLLFGVGHASENQQRNSNGSGGPTQRASALAALNSAFSSPSPPKSSSAPRPAGTSSAS  
QRAAAIAALSGVLTAEKKQSSEGGSPVRSNRSSPVRSSRSPVRSADSGPTENDLSTAEV  
QDSEKASEPKEIVEPAESNGSEPKPEAEQDEGGNESGQAIYSYEQLKAKSDNPVTGIDFK  
RREAYLSDEEFESVLGMKKEAFYKLPKWKQDMHKKRVDLF

>AAW69549.1 Cuc m 2; profilin [Cucumis melo]  
MSWQVYVDEHLMCEIEGNHLTSAAIIGQDGSVWAQSQNFQPKPEEVAGIVGDFADPGTL  
APTGLYIGGTYMVIQGEPAVIRGKKKGGATVKKKTGMALVIGIYDEPMTPGQCNMIVE  
RLGDYLDIDQGL

>CAG26895.1 Arg r 1; lipocalin [Argas reflexus]  
MALIILLVACLVSVDSCGKTDAWTSIKGPKTGGYWLKQTTKTGENECTYVKGTDKFKE  
NTKTATYTYGYKSDASGLTKTTGTATAKGSDIVVGSSTSTVIYTDGKTCDVVKHGGHTEL  
VHSSKTSGGYNNCCDKKFTETRGSTPANEVYKCCPGMP

>NP\_001011564.1 Api m 11; major royal jelly protein [Apis mellifera]  
MIRWLLMYLGITCQGVTDIHSRNLNLSLKVYIYEWKYIDYDFGSDEKRQAAIQSGDYNNT  
MNYLLDTDQWGDKTFVIIMKFNVPSSLNVITNKTGNGGPLLAPYPDWTWAKNENCSGIT  
SAYKIEIDMCDRLWVLDLGLINNVRSVCPQLLVFDLNTSLLKQVKIPHDIAVNTTTEK  
GALVTLVSVQLLSCEVNGSTLVYIGDNEGFALIIYNNSDMSFQRLTSSTFASDPRTTFTI  
NGESFTLQSGIFGMALSPLTQNLVYSSALSSHNLNRYNTEQFVKSQYQANNVHYQGKENIL  
WTQASAKGISDNGVLFGLVGDTSLACWNNRLLDRRNIEVVAKNKETLQAITGLKVKRR  
ISFILVHGFPLEYEVVLAVSNRIQKVIYGFDFNDVNFRIANVNDLIKNTRCISP

>AAW81034.1 Cro s 2; profilin [Crocus sativus]  
MSWQTYVDEHLMCDMDGHVLTSAAILGHDGSVWAQSAAGFPELKPAEITAILNDFNEPGSL  
APTGMINGAKYMVIQGEPAVIRGKKKGGVTVKKTGMALVIGIYDEPMTPGQCNLVE  
RLGDYLDIEQGY

>P69199.1 Bra r 5; calcium-binding protein, polcalcin [Brassica rapa]  
MADATEKAEHDIRFKFDANGDGKISASELGDALKNLGSVTHDDIKRMMAEIDTDGDGYI  
SYQEFSDFASANRGLMKDVAKIF

>AAX11194.1 Pen b 26; acidic ribosomal protein P1 [Penicillium brevicompactum]  
MSTAEALVSYAALILADDGIEVSADKIQTILGAAKVQEVETWATIFAKALEGKDIKEIL

TNVSAGPATAGAPAAAGAAAPAEKKEEKEEKEEESDEDMGFGLFD  
>AAX11261.1 Sal k 1; pectin methylesterase [*Salsola kali*]  
QIIPPNAELESWFQGAVKPVSEQKGLEPSVQAESGGVETIEVRQDGSQKFKTISDAVK  
HVKVGNTKRVIITIGPEYREKVKIEGLHPYITLYGIDPKNRPTITFAGTAAEFQTVDSA  
TLIVESDYFVGANLIVSNSAPRPAGKRKGAQASALRISGDRAAFYNCKFTGFQDTVCDK  
GNHLFKDCYIEGTVDLIFGEARSLYLNTELVVPGDPMAMITAHARKNADGVGGYSFVHC  
KVTGTGGTALLGRAWFEARVVSFCNLSDAVKPEGWSDNNKPAQKTIFFGEYKNTGPG  
AAADKRVPTYTKQLTEADAKTFTSLEYIEAAKWLPKPKV  
>AAX11262.1 Sal k 1; pectin methylesterase [*Salsola kali*]  
QIIPPNAELESWFQGAVKPVSEQKGLEPSVQAESGGVETIEVRQDGSQKFKTISDAVK  
HVKVGNTKRVIITIGPEYREKVKIERLHPYITLYGIDPKNRPTITFAGTAAEFQTVDSA  
TLIVESDYFVGANLIVSNSAPRPDGRKRGARASALRISGDRAAFYNCKFTGFQDTVCDK  
GNHLFKDCYIEGTVDLIFGEARSLYLNTELVVPGDPMAMITAHARKNADGVGGYSFVHC  
KVTGTGGTALLGRAWFEARVVSFCNLSDAVKPEGWSDNNKPAQKTIFFGEYKNTGPG  
AAADKRVPTYTKQLTEADAKTFTSLEYIEAAKWLPKPKV  
>AAX14379.1 Cla h 9; serine protease [*Cladosporium herbarum*]  
MRGALAGLSLATLATASPLVNSIHNDAAPIISASNAKEIADNYMIKFKDHVTQNLAAEH  
HGWVQDLHEKTQVAKTELKRKRSQSPMVDDIFNGLKHTYNIAGGLMGYAGHFDEVDIEQIR  
RHPDVELVERDQEVHVLGSESEVEKNAPWGLARISHRDSLSFGTFNKLYTEDGGEGVDV  
YVVDGTGTVNDHVDVEGRASWGTIPQGDADGNGHGHGTHCSGTVAGKKYGVAKKAHVAV  
KVLRSNGSGSMSDVVKGVEYAAESHLEQVSITKKGKRGFKGSTANMSLGGKSPILDKA  
VNAAVDAGIHFAVAAGNDNADSCNYSAAAENAVTVGASTLADERAYFSNYGKCNDIFAP  
GLNIQSTWIGSKYAVNTISGTSMASPHVAGLLAYLLSLQPAKDSAFVADISPKKLKANL  
ISIAVTGALTDVPSNTANILAWNGGGESNYSATIVEKGGYKATHRPTMLEEIESEAKVASK  
KVYSEGDELAKVAELTEKVEDLIAGELKDMFRELKRE  
>AAX19848.1 Mal d 2; thaumatin-like [*Malus domestica*]  
MMKSQVASLLGLTLAILFFSGAHAAKITFTNNCPNTVWPGTLTGDQKPKQLSLTGFELASK  
ASQSVDPSPWSGRFWGRTRCSTDAAGKFTCETADCGSQVACNGAGAVPPATLVEITIA  
ANGGQDYDVSLLVDGFNLPMVAPQGGTGECKPSSCPANVNMCPAQLQVKAADGSVISC  
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGPDY  
VITFCP  
>AAX19851.1 Mal d 2; thaumatin-like [*Malus domestica*]  
MMKSQAASLLGLTLAILFFSGAHAAKITFTNNCPNTVWPGTLTGDQKPKQLSLTGFELASK  
ASQSVDPSPWSGRFWGRTRCSTDAAGKFTCETADCGSQVACNGAGAVPPATLVEITIA  
ANGGQDYDVSLLVDGFNLPMVAPQGGTGECKPSSCPANVNMCPAQLQVKAADGSVISC  
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGPDY  
VITFCP  
>AAX19854.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGVSVAHSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQALVFGIYEETLTPGQCNMIVE  
RLGDYLIDQGL  
>AAX19856.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGVSVAQSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQDLVFGIYEEPLTPGQCNMIVE  
RLGDYLIDQGL  
>AAX19858.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGVSVAQSATFPQLKPEEVTGIMNDFNEPGSL  
APTGLYLGGTKYMVIQEGPGVVIRGKKKSGGVTVKKSTMALLIGIYDEPMTGQCNMVVE  
RLGDYLIEQGL  
>AAX19860.1 Mal d 4; profilin [*Malus domestica*]

MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGVMNDFNEPGSL  
APTGLYLGGTKYMVIQGEQGVVIRGKKKGGVTVKKSTMALLIGIYDEPMPGQCNMVVE  
RLGDYLIEQGL  
>AAX19889.1 Vig r 1; pathogenesis related protein, PR-10, Bet v 1-like [Vigna radiata]  
MAVFTFDDQATSPVAPATLYNALAKDADNIIPKAVGSFQSVEIVEGNGGPGTIKKISFVE  
DGETKFVLHKIESVDEANLGYSSIVGGVALPDTAEKITIDTKISDGADGGSLIKLTISY  
HGKGDAPPNEDELKAGKAKSDALFKAVEAYLLANP  
>AAX33727.1 Per a 2; aspartic protease [Periplaneta americana]  
MTFLIQSAFVALAAISAVLCDPVVPLQKRAPVEEYINTQYVGPVQLGNQYFLCVFDTSS  
YTTVIPASASCVSGGCNCANVHKYYSNKPVSNNVASVPILGSGYANGSEAHDYIAVSTLNA  
TNQGFLLADDISNDICSLGADCVIGLGRPKSGRAAFNLPTVMENFVNQDNIANSFSFHGG  
RYPDQGHRGVLVLGGPIPAYYRGDFTYVPLVDQDTWNFKVDSISVGNEVIATDQLAFVDS  
SKYVITGPAEEIKKINDRLGCTNKVIGSRTL CVFDCDKLDNVPSTFTIGGVAFNISSTY  
QIQQNGDLCYSGFQYSAGKCFHFDFMDNYYGEFDGQNKRMGFAKSVEEL  
>AAX33728.1 Per a 4; lipocalin [Periplaneta americana]  
MLSILVVCLLAGFQLAAGDDSCQIGTSFTGLDMTKYVGTWYELFRTPNSDEEDFTNCEYD  
KYTLDENGVIQVTSVAYTNSTRGFITSTGTVPSWTENTFDIAYGDNETWSSTYFMIGTDY  
QTYISIVAGCLDNDYSRHLYWIASHGTSFDDATKAKVNEVLAPYNLSLDDMEPVDQSYCVQ  
YKS  
>AAX33729.1 Per a 5; glutathione S-transferase [Periplaneta americana]  
MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQPHTIPTLNDK  
GFCLWESRAILSYLADQYGGKDDSLYRRDAKKRALVDQRLYFDIGTLYHRFGEYYPYIFA  
KQAADPEKMKKLEEAFFLNKFLFESQEFVAGNKLTIADLAIVSSVSTADIMGFDVSKYSN  
VAKWFEKCKKIVPGYEELNHSGLCKFKEMCDNLAKK  
>AAX33730.1 Per a 6; troponin C [Periplaneta americana]  
MDELPDEQIQLLKKAFDAFDREKNGFISTDMVGTILEMLGHPLDDDMLEEIIAEVDADGS  
GELEFQEFVTLAARFLVEEDAAMQQLKEAFRLYDKEGNGYITTTVLREILKELDDKLT  
NEDLDAMIEEIDSDGSGTVDFDEFMEVMTGE  
>AAX33734.1 Per a 10; serine protease [Periplaneta americana]  
MLRYLVLASLIACSLSAVPKAKRPRLDGRIVGGRPADYADYPYQLSFYEGSHMCGASII  
SPNWWVTAHCVDGVSASSATFRAGGSIRESGGSVHQATQLIANPNYDYITIDFDVAVAR  
VSPAFSYGTGVQPIPLASSEPSAGQIATVSGWGTTEGGSTLPSQLQVVSVPVSRSECN  
QAYS DYGGITDDMICAAEQQGGKDACQGDSSGGLVVNGQLAGIVSWGVCAGQYGPVYS  
NVASLKGFFITEQTGVN  
>AAX34047.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]  
MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLHITHEVDDLEKT  
GNKDEKARLLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLKDLKA  
LQKRVQDSE  
>AAX35807.1 Len c 3; lipid transfer protein [Lens culinaris]  
MARGMKLACVVLVICMVVIAPMAEGAISCGAVTSDLSPCLTYLTGGPGPSPQCCGGVKKL  
LAAANTTPDRQAACNCLKSAAGSITKLNNTNAAALPGKCGVNIPYKISTTTNCNTVKF  
>AAX37288.1 Pen m 1; tropomyosin [Penaeus monodon]  
MDAIIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY  
>AAX37321.1 glutathione S-transferase [Sarcoptes scabiei]

MSSKPTLGYWNIRGLAQPIRMMLSYAGVDFVDKRYNYGPAPDFDRSEWLNEKFNLGLDFP  
NLPPYIDGDVKLTQSLAILRYLARKHKLDGHNEQEWLRIALCEQQIVDLYMAMGRISYDP  
NFEKLPDYLEKLPDNLKLFSEFLGDHPFVAGTNLSYVDFVVEYLIRLKAMTPEVFAKF  
QNLGNYVNRFESEMPKISAYLKQQQPQFFNGLMAKWNMKY

>AAX37326.1 Der p 8; glutathione S-transferase [Dermatophagoides pteronyssinus]

MSQPILGYWDIRGYAQPIRLLLLTYSVDFVDKRYQIGPAPDFDRSQWLNEKFNLGLDFPN  
LPYYIDGDMKMTQTFAILRYLGRKYKLNDSNDHEEIRISMAEQTKDMAAMIRVCYDAN  
CDKLPDYKSLPDCLKLMKSFVGEHPFVAGANISYVDFLYEYLCRVKVMVPEVFGQFE  
NLKRYVERMESLPRVSDYIKKQPKTFNAPTSKWNASYA

>AAX40948.1 Ziz m 1; chitinase [Ziziphus mauritiana]

MVPQAKLVVASLILTSALIQTSEAVGGIATYWGQYTETEESLAEACASNLYSYINIAYL  
NIFGEGRYLSLNI SGHSDCTFLGEEIKACQSQGVKIFLSLGGPYGDYHLTTDGDADRA  
EQLWSSFLGGSKSTGVYQPLLGDVELDGDIDLDIQIPPEEYDVLARNLKDLDKDRTRPFY  
LSAAPKCSAYNDSDAYLWTAVETGLDFVWVKFYNDTSCQYNNDTAAGLDAFYRSWYDWT  
VSLAEGNKLLIGIPASNETDNSPLGGYIPSDVLDNDQIVSVIMTSSKFGGVNWNRYDLK  
TNYSSSIILEYVNSGTKYLPLRTRKFMYQNA

>AAX47076.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]

NEIAXAKIDLRQMRTVTPIXMQGGCGSCWALSQVAATESAYLAYGNXSLDLAEQELVDC  
SQHGCHGDTIPRGIEYIQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPNVNK  
IREALAQTHSAIAVIIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNAQGV  
DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>AAX57578.1 Fag e 2; 2S albumin, conglutin [Fagopyrum esculentum]

RDEGFDLGETQMSSKCMRQVKMNEPHLKKCNRYIAMDILDDKYAEALSRVEGEGCKSEES  
CMRGCCVAMKEMDDECVCEWMMVENQKGRIGERLIKEGVRDLKELPSKCGLSEMECGS  
RGNRYFV

>CAI77218.1 Ves v 2; hyaluronidase [Vespula vulgaris]

DRTIWPKKGFSIYWNIPTHFCHNFGVYFKELKQFNKYNMNNFRGETISLFYDPGNFPS  
MVLKNGTYEIRNEGVPQKGNLTIHLEQFTKELDEIYPKKIAGGIGVIHFHNWRPIFRN  
VDNLKINKDISIDLVRKEHPKWDKSMIEKEASNRFETSAKIFMEKTLKLAKEIRKKT  
EWG YHGYPHCLSGSTDKPSFDCDALSMSSENDKMSWLFNNQNVLLPSIYLKNVLP  
DEKIHVLQ ERLKEAIRISKNFKHLPKVLPYWWYTYQDKESIFLTEADVKNTFKEIL  
TNGADGIIWGV SYELTDRKRCEKLKEYLMKILGPIAFKVTKAVKENTPLNF

>AAX77383.1 Sin a 2; 11S globulin, cupin [Sinapis alba]

MVKLAHLVAVTVGVLLVLNGCLARQSLGVPPQVKDACNLNDLVLQPTTEVIKSEAGQVEY  
WDHNNPQIRCAGVSIARLVIQKGLYLPTFFSSPFI SYVVQGMGISGRVIPGCAETFMDS  
QPMQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGG  
VEHVRHGDIAIAMPQSAQWIYNTGDQPLIIVSLIDIANYNQLDRNPRTFRLAGNNQGS  
SQQQQQQQNLSGFDPQVLAQALKIDVRLAQELQNNQDKRGNIVRVKGPQVVRPPLRQ  
AYESEQWRHPRGPPQSPQDNGLEETICSMRTHENIDDPARADIYKPNLGRVTSVNSY  
TLP ILQYIRLSATRGI LQGSAMVLPKYNMNEI LYCTQGQARIQVVNDNGQNVLDQVQK  
GQLVVIPQGFAYVVQSQNNFEWISFKTNANAMISTLAGRTSALRALPLEVITNAYQIS  
LEEAR KIKFNTLETTLTRARGGQQPQLIEEIVEV

>AAX77384.1 Sin a 2; 11S globulin, cupin [Sinapis alba]

MVKLAHLVAVTVGVLLVLNGCLARQSLGVPPQVKDACNLNDLVLQPTTEVIKSEAGR  
LEYWDHNNPQIRCAGVSIARLVIEQGGFYLPTFFSSPKISYVVQGMGISGRVIPGCA  
ETFMDS QPMQGGQQGHQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGG  
QQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGG  
FRLAGNPNQGGFGPPQQQPQNILNGFDPQVIAQALKIDVRLAQELQNKQDSRGNIVRV  
KGPQVVRPPLRQAYESEQWRHPRGPPQSPQDNGLEETICSMRTHENIDDPARADIYK  
PNLGRVTSVNSYTIPI LQYIRLSATRGI LQGSAMVLPKYNMNEI LYCTQGQARIQV  
VNDN

GQNVLDQQVQKQQLVVIPOGFAYVVQSQNNFEWISFKTNANAMISTLAGRTSALRALPLE  
VITNAFQISLEEARKIKFNTLETTLTRARGGQQQLIEEIVEV  
>AAX77684.1 Amb a 9; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]  
MAEEDKAERDRIFGAFDANKDGKISSSTELGESLKNLGSVSPEEVQTMMEELDTDGDGFI  
SYEFTDFYNANRGLMKDVGKIF  
>AAX77685.1 Amb a 9; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]  
MAEDEDKAERDRIFGAFDANKDGKISSNELGEALKNLGSVSPEEVQTMMEELDTDGDGFI  
SYEFTDFYNANRGLMKDVGKIF  
>AAX77686.1 Amb a 10; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]  
MAPENNKHSIFPTDKEEVTKIFNRFDTNGDGQISEDELFAILKSLGSDTSPDEVKRVMAE  
IDADGDGFISLDEFILFCKGIESEGDEINDLKEAFKFYDQNNNGVISANELHQILGRLGE  
NYSVESCADIKSVSDSDGDGFVDFEEFRKMMSRKGGDGAM  
>AAX77687.1 Amb a 8; profilin [Ambrosia artemisiifolia]  
MSWQTYVDEHLMCDIEGTGQHLASAAIFGTDGNVWAKSSSFPEFKPDEINAIKEFSEPG  
ALAPTGLFLAGAKYMIQGEPAVIRGKKGAGGICIKKTGQAMVFGIYEPPVNPQCNMV  
VERLDYLVQGM  
>AAX77688.1 Amb a 8; profilin [Ambrosia artemisiifolia]  
MSWQTYVDEHLMCDIDGSGHLLSAAIFGTDGAVWAKSGSFPEFKPDEINAIKEFDAAG  
TLAPTGLFLAGAKYMIQGEPAVIRGKKGAGGICIKKTGQAMVFGIYEPPVAPGQCNMV  
VERLDYLVQGM  
>CAI78902.1 gamma-gliadin [Triticum aestivum]  
MQVNPSVQVQPTQQQYPESQQPFISQSQQQFPQPQQPFPQPPQPPQSQQQCLQQPQH  
QFPQPTQQFPQRPLLPTFHPFLTFPDQLLPQPPHQSFPQPQSYPQPPLQFPQPQQKY  
PEQPQQPFPWQQPTIQLYLQQQLNPCKEFLQQCRPVSLLSYLWSKIVQQSSCRMQQQC  
CLQLAQIPEQYKCTAIDSIVHAIIFMQQQRQGVQIVQQQPQPQQVGGCVLVQGGVVPQ  
QLAQMEAIRTLVLQSVSPMCNFNVPNCSTIKAPFVGVVTVGGGQ  
>AAX85388.1 Art v 6; pectate lyase [Artemisia vulgaris]  
MEKHVFVILFTAAFVFGAAARADIGDELEAAQFNSTRRLHECAAHNIIDKCWRCKADW  
EKNRQALAKCAQGFAGKTTGGLGGEIYVVTDCSDDNAANPKPGTLRCGVTQDKPLWIIFK  
KDMVIKIKHELKINKDKTIDGRGANVEITCGGLTIHNVCNVVIHNIHDIKIVTEGGI  
ATDAKPGHRHKSDDGDCVAGSSKIWDHCTLSHGPDGLIDVTLGSTAVTISNCKFHHQ  
KILLGADNSHVDDKMHVTVAFNRFAEACDQRMPCRFRGFFQVNNDYTSWGTYAIGGS  
ANPTILSQGNRFHAPNDPMKKNVLRADAPHTESMKWNWRSEKDLLENGAIFVASGCDPH  
LTPEQKSHLIPAEPGSAVLQLTSCAGTLKCVPGKPC  
>AAX85389.1 Art v 5; calcium-binding protein, polcalcin [Artemisia vulgaris]  
MADEDKAECDRIFGAFDKNKGKISAAELGESLTKLGSVSPEEVQTMMEELDTDGDGYIS  
YDEFAEFFNANRGLMKDVGKIF  
>CAI79052.1 Tri a 36; LMW glutenin [Triticum aestivum]  
MSHIPGLERPSQQQLRPQQTLSSHQQPIQQQPQQFPQQQPCSQQQQPPLSQQQQPP  
FSQQQQPPFSQQQQPVLPQQPSFSQQQLPPFSQQQQPPFSQQQQPVLPQQPSFSQQQLPP  
FSQQLPFSQQQQPVLLQQQIPFVHPSILQQLNPKVFLQQQCSPVAMPQSLARSQMLQQ  
SSCHVMQQQCCQQLPQIPQQSRYEAIRAIVYSIILQEQQVQGSIQTQQQQPQQLGQCVS  
QPQQQSQQQLGQCSFQQPQQLQQLGQQPQQQIPQGIQFLQPHQISQLEVMTSIALRTLPT  
MCGVNVPLYSSTTIMPFSIGTVGGY  
>1YG9\_A Bla g 2; inactive aspartic protease [Blattella germanica]  
GASIVPLYKLVHVFINTQYAGITKIGNQNFLLTVFDSTSCNVVVASQECVGGACVCPNLQK  
YEKLPKYISDGNVQVKFFDTGSAVGRGIEDSLTISQLTTSQQDIVLADELSQEVCI  
LSADVVVGIAPGCPNALKGTVLENFVEENLIAPVFSIHARFQDGEHFGEIIFGGSDWKYV  
DGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDTSKAIIVGPKAYVNPINEAIG  
CVVEKTTTRICKLDCSKIPSLPDVTFVINGRNFNISSQYYIQQNGNLCYSGFQXPXGHS

HFFIGDFFVDHYYSEFNWENKTMGFGRSVE

>AAY21180.1 Api m 11; major royal jelly protein [*Apis mellifera*]  
MSFNIWWLILYFSIVCQAKAHYSLRDFKANIFQVKYQWKYFDYNFGSDEKRQAAIQSGEY  
NYKNNVPIDVDRWNGKTFVTILRNDGVPSSLNVISNKIGNGGPILLEPYPNWSWAKNQNC  
GITSVYRIAIDEWDRLLWLDNGISGETSVCPSSQIVVFDLKNKLLKQVKIPHDIAINSTT  
GKRNVVTPIVQSFQDYNNWVYIADVEGYALIIYNNADDSFQRLTSSTFVYDPRYTKYTIN  
DESFLQDGLGMALSHKTQNLYYSSAMSSHNLYVNTKQFTQGKFQANDIQYQGASDILW  
TQASAKAISETGALFFGLVSDTALGCWNNRPLKRRNIEIVAKNNDTLQFISGIKIIKQI  
SSNIYERQNEEYIIVSNKYQKIANGDLNFNEVNFRLNAPVNQLIRYTRCENPKTNFFS  
IFL

>CAI64396.1 serine carboxypeptidase [*Triticum aestivum*]  
GNGLIDDYHDYVGTFFFWNHGLVSDDTYQRLREACLHDSFIHPSACDAATDVATAEQG  
NIDMYSLYTPVCNITSSSSSSSSSSLSQRRSRGRYPWLTGSYDPCTERYSTAYNRRDVQ  
TALHANVTGAMNYTWSTCSDTINTHWHADAPRSMPLIYRELIAAGLRIWVFSGDTDAVPL  
TATRYSIGALGLPTTTSWYPWYDDQEVGGSQVYKGLTLVSVRGAGHEVPLHRPRQALVL  
FQYFLQGKPMGPQATNATVA

>CAI64397.1 unknown function [*Triticum aestivum*]  
KPVAANQDVALSALRRGLQDPNGELKNWDANLVDACTWSHITCDRDNNRVTRIDLNKMN  
LSGPLAPELGKLDRLQYLEIDHNRLTGPIPRELAGLSNLKHADFSNNNLGPIPTTGAFQ  
RIPRSSFANNPRLGRKC

>CAI64398.1 Tri a 44; lipid transfer protein [*Triticum aestivum*]  
IAVAVSADECEGDRRAMIKECAKYQWPANPKLDPSDACCVAWQKANIPCLCAGVTKEKE  
KIYCMKVAVVANFCKKPFPHGYKCGSYTFPPLA

>CAI64400.1 Zea m 25; thioredoxin [*Zea mays*]  
MAASEAAAAAATPVAPTEGTVIAIHSLEEWSIQIEEANSACKLVVIDFTATWCPPCRAMA  
PIFADMAKKSPNVVFLKVDVDEMKTIAEQFSVEAMPTFLFMREGDVKDRVVGAAKEELAR  
KLELHMAS

>EAL89830.1 Asp f 2; unknown function [*Aspergillus fumigatus*]  
MAALLRLAVLLPLAAPLVATLPTSPVPIAARATPHEPVFFSWDAGAVTSFPIHSSCNATQ  
RRQIEAGLNEAVELARHAKAHILRWGNESEIYRKYFGNRPTMEAVGAYDIVNGDKANVL  
FRCDNPDGNCALLEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSETNTFW  
ASDLMHRLYHVPVAVGQGWVDHFADGYDEVIALAKSNGTESTHDSEALQYFALEAYAFDIA  
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGSGATTTPTDPSATIDVPPVRT  
VRIS

>AAY83341.1 Fra a 3; lipid transfer protein [*Fragaria x ananassa*]  
MASSTAMKLSLVALLCIVVALPIAQAITCGQVASSISPCVNVYKSGGAVPAACCGIRSL  
NSAAKTTADRQATCNCLKQASGAIKGLNPSLAAGLPGKCGVSVPYKISTSTNCAAVK

>AAY83342.1 Fra a 3; lipid transfer protein [*Fragaria x ananassa*]  
MASSTAMKLSLVALLCIVVALPIAQAITCGQVASNISPCVTYVYKSGGAVPAPCCSGIRNL  
NGMAKTTADRQATCNCLKQAAGGIKGLNPNLAAGLPGKCGVSVPYKISTTTNCAAVK

>AAY83345.1 Fra a 3; lipid transfer protein [*Fragaria x ananassa*]  
MAISTAMKLSLVALLCIVVALPIAQAITCGQVASSISPCVNVYKSGGAVPAACCGIRSL  
NSAAKTTADRQATCNCLKQASGAIKGLNPNLAAGLPGKCGVNVYKISTSTNCAAVK

>AAY84563.1 Der p 18; chitin-binding protein [*Dermatophagoides pteronyssinus*]  
MTRLSFTVLIFLAAYFGSNIRPNVATLDPKTVCCYYESWVHWRQGDGKMDPEDIDTSLCSH  
IVYSYFGIDASSHEIKLLDQYLMITLHDMHFTHKKGNAKAMIAVGGASMSDQFSKTA  
EHYRETFVSTIDLMTKYGFDGVMIDWSGMQAKDSDFVKLLDKFDEKFAQTSFVMGVTL  
PATIASYDNYNIPAIISNYVDFMNVLTLDYDGPWAYTVGHASALPEQLKTLAAYNKRGA  
PRHKMVMVAVPFFARTWILEKMDKQDVGDKASGPGPKGQFTQTPGFLSYNELCVQIQAE  
TNAF  
SITRDHDNTAIYAVVYVHDNHAEWISFEDRHTLGDKARNITEQGYGGMSVYTLNEDVHGV

CGDKNPLLHAINSNYFRGIVTEPTVVTVPVTHTEHVTDIPGVFHCHQEGFFRDKYCA  
KYYECKKGDFGLEQTVHHCPNHSQAFDEVSRTCVDHAKIPGC  
>AAY84565.1 Der p 15; chitinase [Dermatophagoides pteronyssinus]  
MKTSCAILILMACFGLMNAAVKRDNHNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK  
CTHLMYGFAKIDEYKYTIQVFDQDDNHNTWEKHGYERFNLRRLKNPELTTMISLGGWY  
EGSEKYSDMVANPTYRKQFVQSVLDFLQYKFDGLDLDEYPGSRLGNPKIDKQNYLTLV  
RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNMVMTYDYHGGWENVFGHNA  
PLYKRPDETDELHTYFNVNYTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGPA  
KGMSPPGFITGEEVLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC  
KLAFKELGVSGVMIWSLENDDFKGCCKPKYPLLNKVHNMINGDEKNSYECLLGPSTTTT  
TPTTPSTPTTTPTPTPTSTPTTTPTPTTSTPTTTTPTTTTPTTTTPTTTDSTSETPKYT  
TYVDGH  
LIKCYKEGDLPHPTNIIHKYLVEYVNGGWVWHIMPCPPGTIWCQEKLTTCITE  
>P83958.1 thaumatin-like, partial [Actinidia chinensis]  
ATFNFINNCPFTVWAAAVPG  
>AAY88919.1 Ole e 11; pectin methylsterase [Olea europaea]  
MSCIAVEAVLLGILLYIPIVLSDRAPIPANSACLNSWFDGIIQPVAVRKATMDPALVTA  
EGQAKVIKLSKDSGDFKSINEAISKIPDDNTRVILSFSPGNSEKVKIGMYKHYITFY  
GEDPNMPILVFGGTAAEYGTVDSATLIVESNYFSAVNLKIVNSAPRPDGKRGAQAAAL  
RISGDKASFYVVKIYGFQDTLCDKDKHFKYKDCYIEGTVDIFGSGKSIFLNTLHAPV  
G  
DQPAIITAQARKTESEDYGVVNCRVTVGGVAFGRSWMPPAAKVVFAYTEMGDAIHPEGW  
ILVKEPEHESTVRFPEYNNKGPANMEKRAKFKVRLSDAEAKQSISLGSEASKWLLPPRV  
VGLP  
>AAZ20276.1 Ara h 11; oleosin [Arachis hypogaea]  
MAEALYYGGRQRQEQPRSTQLVKATTAVVAGGSLLILAGLVLVGLTIGLTTITPLFVIFS  
PVLVPAVITVALLGLGLASGGFVAAITVLTWIIYRYVTGKHPGANQLDARHKLMGKA  
REIKDFGQQQTSGAQAS  
>CAI38795.2 Act d 2; thaumatin-like [Actinidia deliciosa]  
MSTFKSLSLSALLFIAFLFTCARGATFNIINNCPFTVWAAAVPGGGKRLDRGQNWIIINPG  
AGTKGARVWPRTGCNFDGAGRKCGTGCNGLLQCGQAFGQPPNTLAEYALNQFNLDFFD  
ISLVDGFNVAMEFSPSSGGCTRGKCTADINGQCPNELRAPGGCNPCTVFKTDQYCCNS  
GNCGLTNFSKFFKDRCPDAYSYPKDDQTSTFTCPAGTNYKVVFPC  
>AAZ23584.1 Tri a 26; HMW glutenin [Triticum aestivum]  
MAKRLVLFVAVVVVALVALTAEEGEASGQLQCEHELEACQQVVDQQLRDVSPGCRPITVSP  
GTRQYEQQPVPVPSKAGSFYPSSETTSSQQLQMMIFWGIAPALLRRYYPSVTSSQQGSYYPGQ  
ASPQQSGQGQQPGQEQQPGQGGQQDQQPGQRQQGYYPTSPQQPGQGGQLGGQPGYPTSPQ  
QPGQKQQAGQGQQSGQGQQGYYPTSPQQSGQGQQPGQGQPGYPTSPQQSGQWQPGQGQ  
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QWQQPGQGQQPGQGQQGQQPGQGQQSGQGQQGYYPTSLQQPGQGQQLGQGQPGYPTSPQ  
SEQGQQPGQGKQPGQGQQGYYPTSPQQSGQGQQLGQGQPGYPTSPQQSGQGQQSGQGQQ  
GYYPTSPQQSGQGQQPGQGQQSGYFPTSQQSGQGQQPGQGQQSGQGQQGQQPGQGQQAYY  
PTSSQQSRQRQQAGQWQRPGQGQPGYPTSPQQPGQEQQSGQAQQSGQWQLVYYPTSPQQ  
PGQLQQPAQQGQQPAQGQQSAQEQQPGQAQQSGQWQLVYYPTSPQQPGQLQQPAQQGQQGYY  
PTSPQQSGQGQQGYYPTSPQQSGQGQQGYYPTSPQQSGQGQQPGQGQQPRQGQQGYYPTIS  
PQQSGQGQQPGQGQQGYYPTSPQQSGQGQQPGHEQQPGQWLQPGQGQQGYYPTSSQSGQ  
GHQSGQGQQGYYPTSLWQPGQGQQPGQGQQGYASPHYVSAEYQAARLKVAKAQQLLAAQLP  
AMCRLEGSDALSTRQ  
>CAJ19705.1 Solo l 3; lipid transfer protein [Solanum lycopersicum]  
MEMVNKIACFVLLCMVVVAPHAEALTCGQVTSTLAPCLPYLMNRGPLRNCCDGVKGLLGQ  
AKTTVDRQAACCTCLKSAASSFTGLNLGKAAALPNTCSVNIPIYKISPSTDCSKVQ  
>AAZ76743.1 tropomyosin [Penaeus aztecus]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQTFSELSGY  
>1WKX\_A Hev b 6; hevein, partial [Hevea brasiliensis]  
EQCGRQAGGKLCPDNLCCSQWGWCGSTDEYCSPDHNCQSNCKD  
>P0C088.1 Art v 3; lipid transfer protein [Artemisia vulgaris]  
ALTCSDVSNKISPCLSYLKQGGVEPADCCAGVKGLND  
>BAE20328.1 Tri a 19; omega-5 gliadin [Triticum aestivum]  
MKTFIIFVLLAMAMNIASASRLLSPRGKELHTPQEQQFQQQQFPQPQQFPQQQIPQQHQI  
PQQPQQFPQQQQFLQQQQIPQQQIPQQHQIPQQPQQFPQQQQFPQQHQSPQQQFPQQQFP  
QQKLPQQEFPQQQISQQPQQLPQQQQIPQQPQQFLQQQQFPQQQPPQQHQFPQQQLPQQQ  
QIPQQQQIPQQPQQIPQQQQIPQQPQQFPQQQFPQQQFPQQQFPQQEFPQQQQFPQQQIA  
RQPQQLPQQQQIPQQPQQFPQQQQFPQQQSPQQQFPQQQFPQQQLPQKQFPQPQQIPQ  
QQQIPQQPQQFPQQQFPQQQFPQQQFPQQQFPQQQFHQQQLPQQQFPQQQFPQQQFPQ  
QQQFPQQQLTQQQFPRPQQSPEQQQFPQQQFPQQPPQQFPQQQFPYPPQQSEEPSY  
QQYPQQQPSGSDVISISGL  
>AAZ91659.1 polygalacturonase [Lilium longiflorum]  
MASISSARLLLLSSVLLIVKLTAGLVPETKVNKVSFGAVGDGKTDSTQAILRAWDQACNG  
FGKQRVIVPEGVYLTGPMAFRGPCCNGFISMQVRGELRAYGDVGYKYPNAKWVSYEDLNGLL  
VTGGGRFNAQGSQAWTQNDCTKKNCALLTTSVKFDHCTNATIRRINSIDSKFFHIAIDQ  
CTDITVHHINITAPGTSPTNDGIHIGRSTNVNISNAIIGTGDDCISLPGSSHITISKVQ  
CGPGHGISVGLGRYMNEENVWDVKVKNCTLTGTTNGVRIKTKWKGSSPSEASQFIFQDIE  
MREVQNPIIIDQEYCSYDYCANPPAPSKVKLSDIQFMNIKGTSTSKVAINLICSSAVPC  
EGIQLSDISLKYIRAGKPTMANCASHVSGTTSGLVSPSPSCIKGADVSLFTTQML  
>CAJ28930.1 Ves g 5; unknown function, antigen 5 [Vespa germanica]  
NNYCKIKCLKGGVHTACKYESLKPNCANKKVVAYGLTKQEKQDILKEHNDFRQKIARGLE  
TRGNPGPQPPAKNMKNLWVNDLAYIAQVWANQCQYGHDTCRDVAKYPVGQNVALTGSTA  
AKYDNPVKLVKMWEDVVDKYNPKKFKSENFLKIGHYTMVWANTKEVGCYSIKYIQDKW  
HKHYLVLCNYGPSGNFGNEELYQTK  
>CAJ28931.1 unknown function [Vespa germanica]  
GPKCFNTDTVSMIETRENRRDLTYLQTLQNHPEFKEKTITRPVVFITHGFTSSASET  
NFINLSKALVDKDNMVISIDWQTAACNEAAGLKYLYPTAASNTRLVGQYIATITQKL  
VKQYKISMANIRLIGHSLGAHVSGFAGKKVQELKLGKYSEIIGLDPAGPSFSSNKCSDRL  
CETDAEYVQILHTSNHLGTERILGTVDYFMMNGKNQPGCGRFFTEVCSHSRAVIYMAECI  
KHECCLIGIPKSKSSQPISSCTKQECVCVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII  
>Q6R4B4.1 Alt a 13; glutathione S-transferase [Alternaria alternata]  
MSDKPSELAVQKLVLFAVKGTATSTHNTVRPLILLDELGVPHEIYVDRVSAPWFTEINP  
HRMVPVILEKSPDGRDTRLAWESTSTLMIYADAYDKDGTFFGGRNVQESSDINNWLTLHTA  
ALGPTAKYWLYFYKLHPEKLPKTIEKLRNITVQYDILERRLNEPGQQLAWLNEKFKRS  
SYNRRHCYASLCYEKYRRVVRAGVKVAQTARVVCPYGGDTRRGVWPARKST  
>Q875I9.1 chitosanase [Aspergillus fumigatus]  
MRLSEILTVALVTGATAYNLPNNLKQIYDKHKGKCSKVLAKGFTNGDASQKSFSYCGDI  
PGAIFISSSKGYTNMIDCDGANNSAGKCANDPSGQGETAFKSDVKKFGISDLNANIHPY  
VVFNGEDHSPKFKPQSHGMQPLSVMVAVCNGQLHYGIWGDNTGGVSTGEASISLADLCFP  
NEHLDGNHGHDPNDVLFIGFTSKDAVPGATAKWKAKNAKEFEDSIKSIGDKLVAGLKA  
>Q8J077.1 dipeptidyl peptidase [Trichophyton schoenleinii]  
FITKAIPVLAALSAVNGAKILEAGPHAETIPNKYIVVMKKDVSDEAFSTHTTWLSQNLN  
RRLMRRSGSSKAMAGMKNKYSLGGIFRAYSGEFDDAMIKDISNHDDVDYIEPDFVVRTST

NGTNLTRQENVPSWGLARVGSKQAGGTTYYYDSSAGKGVTAVIDTGIDIEHEDFGGRAK  
WGKNFVDQRDEDCNGHGTHVAGTVGGTKYGLAKSVSLVAVKVLDCDGSNSGSGVIRGMEW  
AMREASGGGNGTAKAAGKSMNMSLGGPRSQASNDAARAISEAGIFMAVAAGNENMDAQH  
SSPASEPSVCTVAASTEDDGKAEFSNYGAVVDVYAPGKDITSLKPGGSTDTLSGTSMASP  
HVCGLGAYLIGLGKQGGPGLCDTIKQMANEAIQRPGEGETTGKLIY

>Q9UVU3 serine protease [*Aspergillus flavus*]  
MQSIKRTLLLLGAILPAVLGAPVQETRRAAEKLPKGYIVTFKPGIDEAKIQEHTTWATNI  
HQRSLERRGATGGDLPVGIERNYKINKFAAYAGSFDDATIEEIRKNEDVAYVEEDQIYYL  
DGLTTQKSAPWGLGSIHKGQSTDYIYDTSAGEGYAYVVDSGVNVVDHEEFEGRASKAY  
NAAGGQHVDSIGHGTHVSGTIAGKTYGIAKKASILSVKVFQGESSTSVILDGFNWAAND  
IVSKKRTSKAAINMSLGGGYSKAFNDAVENAFEQVLSVVAAGNENS DAGQTS PASAPDA  
ITVAAIQKSNRASFSNFGKVVDVFAPGQDILSAWIGSSSATNTISGTSMATPHIVGLSL  
YLAALENLDGPAAVTKRIEELATKDVVKDVKGSPNLLAYNGNA

>Q4WB37.1 chitosanase [*Aspergillus fumigatus*]  
MHFLATAAVLAGVGLASAYTPANLQQIYNKHKGTGCQNKLQDGFSDGISGSRSFAYCGD  
IEGAI FLHSSANGGQYVNMIDCDGANNSAGDCANDPSGQSMATFMDTVKQYGISDL DAN  
IHPYVVFNGSGSSPTFDPQQYGMELSVMAVVCNNQLFYGIWGD TNGGTSTGEASISLAK  
LCFPNDGITGDNGHGEEDVLYIGFMQDAVPGASAAWTARDTKTFEESIKALGDRLVAKL  
SA

>Q5BLY5.1 Api m 3; acid phosphatase [*Apis mellifera*]  
MSVIAILAMVVGVAELKQINVIFRHGDRIPDEKNEMYPKDPYLYDFYPLER GELTNSG  
KMREYQLGQFLRERYGDFLGDYIYTESVSALSSFYDRTKMSLQLVLAALYPPNKLQQWNE  
DLNWQPIATKYLRRYEDNIFLPEDCLLFTIELDRVLESPRGKYEF SKYDKLKKKLEEW TG  
KNITTPWDYIYHTLVAEQSYGLTLPSWTNNIFPRGELFDATVFTYNITNSTPL LKKLY  
GGPLLRIFTKHM LDVVSQTQKKRKYLFSGHESNIASVLHALQLYYPHVP EYSSSIIME  
LHNIEGTHYVKIVYYL GIPSEARELQLPGCEVLCPLYKYLQLIENVIPSNEELICDKRFV  
DESANNLSIEELDFV KLNLRIRIAGTENK

>Q7M4I3.1 Bom p 4; protease [*Bombus pennsylvanicus*]  
VVGKPAKLGAWPMMVALGFHNYRQPKKSPKCGGSLRISRHLV TAAHCAIHRSLYVVR  
IADLNLKRDDDGAHP IQMGIESKLIHPDYVYSEHHDDIAILKLEKDV SFSEYIRPICLPI  
EESLRNNNFIGYNPFVAGWGR LRYKGPLSDALMEVQVPVVRNKVCKRAYSDVSDTVICAG  
YPKGRKDSCQGD SGGPLMIPQESTYIEIGVVSYGHECALPKYPGVYTRVTSY LDSFILPA  
LKK

>P80208.1 Bra n 1; 2S albumin, conglutin [*Brassica napus*]  
SAGPFRI PKCRKEFQQAQHLRACQQLHKKQAMQSGSGPQGPQQR PPLLQCCNELHQEEP  
LCVCPTLKGASRAVKQVVRQQGQQGQQQLQQVISRIYQTATHLPKVCNIPQVS VCPFQKT  
MPGPS

>P82952.1 2S albumin, conglutin, partial [*Prunus dulcis*]  
TKSQTHVPIRPNKLV LKVKQKDRATN

>Q647G9.1 Ara h 6; 2S albumin, conglutin [*Arachis hypogaea*]  
MAKSTILVALLALV LVAHASAMRRERGRQGDSSSCERQVDRVNLK PCEQHIMQRIMGEQE  
QYDSYDIRSTRSSDQQQRCCDELNEMENTQRCEALQQIMENQCDRLQDRQMVQQFKRE  
LMNLPQQCNFRAPQRCDLDVSGGRC

>Q6EBC1.1 7S globulin, vicilin, beta-conglutin [*Lupinus albus*]  
MGKMRVRFPTLV LVLGIVFLMAVSIGIAYGEKDV LKSHERPEEREQE EWQPRRQRPQSRR  
EEREQE QE QGSPYPRRQSGYERRQYHERSEQREEREQEQQGSPYSRRQRNPHYFSSQ  
RFQTLYKNRNGKIRVLERFDQRTNRLENLQNYRIVEFQSKPNTLILPKHSDADYV LVLV LN  
GRATITIVNPD RRQAYNLEYGDALRIPAGSTSYILNPDDNQKLRVVKLAIPINNPGYFYD  
FYPSSTKDQQSYFSGFSRNTLEATFNTRYEEIQRIILGNEDEQEYEEQRRGQE QSDQDEG  
VIVIVSKKQIQKLTKHAQSSSGKDKPSDSGPFNLRSNEPIYSNKYGNFYEITPDRNPQVQ

DLNISLTYIKINEGALLLPHYNSKAIYVVVVDEGEGNYELVGIRDQQRQQDEQEKEEEEEV  
IRYSARLSEGDIFVIPAGYPISINASSNLRLLGFGINADENQRNFLAGSKDNVIRQLDRA  
VNELTFPGSAEDIERLIKNQQSYFANGQPQQQQQQSEKEGRRRGRSSLPF  
>Q7M1E8 Par o 1; lipid transfer protein [Parietaria officinalis]  
ATGKVVQGAMPP  
>Q7M1L8 Phl p 5; unknown function, partial [Phleum pratense]  
DLGYAPATPAAPGAGYTPATPAAP  
>Q7M1X6 Ant o 1; beta-expansin, partial [Anthoxanthum odoratum]  
IAKVPPGPNITATYGDKWLDAKSTWYGKPTGA  
>Q7M1X7 beta-expansin [Agrostis alba]  
IAKVPPGPNITADYGDKWLDAKSTWYGKPTGAGPK  
>Q7M1X9 beta-expansin [Agrostis alba]  
IAKVPPGPNITATYGDKWLDAKSTWYGKPTGAGPK  
>Q7M1Y0 Ant o 1; beta-expansin, partial [Anthoxanthum odoratum]  
IAKVPPGPNITADYGDKWLDAKSTWYGKPTGA  
>Q7M1Y1 beta-expansin, partial [Schedonorus arundinaceus]  
IAKVPPGPNITAEYGDKWLDAKSTFYGKPTGAGPK  
>Q7M262 Hol l 5; ribonuclease [Holcus lanatus]  
ADAGYTPAAPAATGAGGDAT  
>Q7M263 Sec c 5; unknown function, partial [Secale cereale]  
ADAGYAPAAPGTQPKA  
>O22108 Tri a 36; LMW glutenin [Triticum aestivum]  
RCIPGLERPWQQQLPQQTFPQQPLFSQQQQQQQLFPQQPSFSQQQPPFWQQQPPFSQQQ  
PILPQQPPFSQQQLVLPQQSPFSQQQQQLLPPQQQQQLPQQQISIVQPSVLQQLNPCKV  
FLQQQCSPVAMPQRLARSQMWWQQSSCHVMQQCCQQLSQIPEQSRYDAIRAITYSIILQE  
QQQGFVQAQQQQPQQSGQGVSSQQQSQQQLGQCSFQQPQQQLGQQPQQQQVQQGTFLQP  
HQIAHLEVMTSIALRTLPMCSVNVPLYSSSTTSVPFGVGTGVGAY  
>O23791.1 Ana c 2; bromelain, sulfhydryl protease [Ananas comosus]  
MASKVQLVFLFLFLCAMWASPSAASRDEPNPMMKRFEEMAEYGRVYKDDDEKMRRFQI  
FKNNVKHIETFNSRNENSYTLGINQFTDMTKSEFVAQYTGVSLLPLNIEREPVVSFDDVNI  
SAVPQSIDWRDYGAVNEVKQNPQCGSCWSFAAIATVEGIYKIKTGYLVSLSQEVLDCAV  
SYGCKGGVWVKAYDFIISNNGVTTEENYPYLAYQGTGNANSFPNSAYITGYSYVRRNDER  
SMMYAVSNQPIAALIDASENFQYNGGVFSGPCGTSLNHAIITIIIGYQDSSGTYWIVRN  
SWGSSWEGGYVRMARGVSSSSGVCGIAMAPLFPPTLQSGANAIEVIMVSET  
>Q94JN2.1 Ana c 1; profilin [Ananas comosus]  
MSWQAYVDDHLMCEIDGQHLSSAAILGHDSTVWAQSPNFPQFKPEEISAILNDFENPGSL  
APTGLYLGGTKYMIQGEQGVVIRGKKGTTGGITVKKTNLALIIGVYDEPMTPGQCNMVE  
RLGDYLLEQGF  
>O22116 Tri a 36; LMW glutenin [Triticum aestivum]  
ASAVAQISQQQPPPPFSQQQQPPFSQQQQPPFSQQQQSPFSQQQQPPFSQQQQPPFSQQ  
PLISQQQLPFSQQQQPQFSQQQQPPYSQQQQPPYSQQQQPPFSQQQQPPFSQQQQPSFS  
QQQQPPFTQQQQPPFSQQSPISQQQQQQQQQQQPFQQQQPPFSQQPPISQQQQPPFS  
QQQQPPFSQQQQIPVIHPSVLQQLNPCMVFLQQQCIPVAMQRCLARSQMLQQSICHVMQR  
QCCQQLRQIPEQSRHESIRAIYSIILQQQQQQQQQQQQGQSIIQYQQQPPQQLGQCV  
SQPQQQLQQQLGQQPQQQLAHGTFLQPHKIAQLEVMTSIALRTLPRMCSVNVPLYETTT  
SVPLGVGIGVGVY  
>Q6W8Q2.1 Tri a 32; peroxiredoxin [Triticum aestivum]  
MPGLTIGDTPNLELDSTHGKIRIHDIYVNGYVILFSHPGDFTPVCTTELAAMANYAKEF  
EKRGVKLLGISCDVQSHKEWTKDIEAYKPGSKVTYPIMADPDRSAIKQLNMVDPDEKDA  
EQGLPSRTLHIVGPDKKVLSFLYPSCTGRNMDEVVRAVDSLLTAAKHKVATPANWNPGE

CVVIAPGVSDDEAKKMFQGFETADLPSKKGYLRF TKV

>ABA39435.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
RPSSIKPFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSNGGAINHLSDSLDEFKNR  
FLMSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGV  
AATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYVARE  
QSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGR TIIQ  
RDNGYQPNYHAVNIVGYSNAQGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVV  
IL

>ABA39436.1 Der f 1; cysteine protease [Dermatophagoides farinae]  
RPASIKTFEEFKAFNKNYATVEEEVARKNFLES LKYVEANKGAINHLSDSLDEFKNR  
YLMSAEAFEQLKTQFDLNAETSACRINSVNPSEL DLRLRRTVTPIRMQGGCGSCWAFSG  
VAATESAYLAYRN TSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVAR  
EQQCRRPNSQHYGISNYCQIYPPDVKQIREAL TQHTAIAVIIGIKDLRAFQHYDGR TII  
QRDNGYQPNYHAVNIVGYGSTQGV DYWIVRNSWDTT

>ABA39437.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCLPVKGQYDIKYTWNVPKIAPKSENVVTVKVLGDNGVLACA  
IATHAKIRD

>ABA39438.1 Der f 2; NPC2-like [Dermatophagoides farinae]  
DQVDVKDCANNEIKKVMVDGRHGSDPCIHRGKPF TLEALFDANQNTKTAKIEIKANING  
LEVDVPGIDTNACHFVKCLPVKGQYDIKYTWNVPKIAPKSENVVTVKVLIGDNGVLACA  
IATHAKIRD

>ABA42918.1 hydrolase [Cladosporium herbarum]  
MPAGLQYVTTDGGRLAVEITGKETDPLVICSPGMG DTRDAYKPLAKVLVSNGYRVAAMDA  
RAHGESSAKFARYGDEATADDFLTVANELSPGSPVVL AGASFSAAAATIAAAKQPERVSK  
IILLGPF LRNGMGVVLWLMVPMFAWPWGPAAWEM YAATLWPGLEGDGAKKRAATTRASL  
TRPGRWAGFQALISSLDHRVWAPYISSVRAPALVVMGDKDPDWSDPKVEAEWVASFQV  
DTLMVPEAGHAPMYERPQVVAERVLSFLGDQTNV

>CAA55071.2 Alt a 10; aldehyde dehydrogenase [Alternaria alternata]  
MTSVKLSTPQTGEFEQPTGLFINNEFVKAVD GKTDFVINPSTEEVICSVQEATEKDVDIA  
VAAARKAFNGPWRKETPENRGKLLNKLADLFEKNADL IAAVEALDNGKAFSMAKNVDVPA  
AAGCLRYGGWADKIEGKVVDTAPDSFN YIRKEPIGVCGQIIPWNFPILMWSWKIGPAIA  
TGNTVVLKTAEQTPLSAYIACKLIQEAGFP PGVINVITGFGKIAGAAMSAHMDIDKIAFT  
GSTVVG RQIMKSAAGSNLKKVTLELGGKSPNIVFADADLDEAIHWVNF GIYFNHGQACCA  
GSRIYVQEEIYDKFIQRFKERAAQNAVGD PFAADTFQGPQVSQLQFDRIMGYIEEGKKSG  
ATIETGGNRKGDKGYFIEPTIFSNVTE DMKIQQEEIFGPVCTISKFKTKADVIKIGNNTT  
YGLAAAVHTSNLTTAIEVANALRAGTVWVNSYNTLHWQLPFGGYKESGIGRELGEAALDN  
YIQTKTVSIRLGDVLF G

>CAA55072.2 Cla h 10; aldehyde dehydrogenase [Cladosporium herbarum]  
MTSVQLETPHSGKYEQPTGLFINNEFVKGQEGK TDFVINPSDES VITQVHEATEKDVDIA  
VAAARKAFEGSWRQETPENRGKLLNNLANLFEKNIDLLAAVESLDNGKAISMAKGDISM C  
VGCLRYGGWADKITGKVIDTTPDTFN YVKKEPIGVCGQIIPWNFP LLMWAWKIGPAIAC  
GNTVVLKTAEQTPLGGLVAASLVKEAGFP PGVINVISGFGKVAGAALSSHMDVDKVAFTG  
STVVGRTILKAAASSNLKKVTLELGGKSPNIVF EDADIDNAISWVNF GIFFNHGQCCCAG  
SRVYVQESIYDKFVQKFKERAAQKNVVD PFAADTFQGPQVSKVQFDRIMEYIQAGKDAGA  
TVETGGKRKGDKGYFIEPTIFSNVTE DMKIVKEEIFGPVCSIAKFKTKEDA IKLGNASTY  
GLAAAVHTKNLNTAIEVSNALKAGTVWVNTYNTLHHQMPFGGYKESGIGRELGEDALANY  
TQTKTVSIRLGDALFG

>Q06811.2 Asc s 1; unknown function [Ascaris suum]  
TMEHYLKYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHYDQLHGEEKQQATEKLVG

CKMLLKGIIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKI  
FGATTLQHRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKELEAKILHYDE  
LEGDAKKEATEHLKGGCGEILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDE  
EKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAK  
KELEAKILHYDELEGDAKKEATEHLKGGCAEILKHVVGEEKAAELKNLKDSGASKEELK  
AKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQK  
DELLKMKKDGKTKKDLQAKILHYDELEGDAKKEATEHLKDGCREILKHVVGEEKAAELK  
KLKDSGASKEEVKAKVEEALHAVTDEEKKQYIADFGPACKKIFGAAHTSRRRRRHFTLES  
SLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDAKKEATEHLKGGCREI  
LKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVH  
TSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDAK  
EATEHLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIA  
DFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKI  
LHYDELEGDAKKEATEHLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEAL  
HAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMK  
KDGKAKKELEAKILHYDELEGDAKKEATEHLKGGCREILKHVVGEEKAAELKNLKDSGA  
SKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKW  
LSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDAKKEATEHLKGGCREILKHVVGEE  
KAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRH  
FTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDAKKEATEHLK  
GCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKK  
IYGVHTSRRRRYHAEDGTDDIDGLAQSRRSGFFEKLIDVFAFF

>ABA81885.1 profilin-like [Solanum tuberosum]

MSWQTYVDEHLLCEIEGNHLTSAAIIGQDGTVWAQSANFPQFKPEEITGVMNDFAEPTGL  
APTGLYLGGTKYMIQGEPAVIRGKKGPGGITIKKTNQALIIGIYDEPMTPGQCNMIVE  
RLGDYLVEQGL

>BAE46763.1 calcium-binding protein, parvalbumin [Trachurus japonicus]

MAFKGVLNDADVTAALDGCASFHDHKAFFKACGLAAKSADDIKKAFIIDDQKSGFIEED  
ELKLFQNFCAGARALSDAETKAFKAGDSGDGKIGVDEFAAMVKH

>ABB16985.1 profilin [Solanum tuberosum]

MSWQTYVDEHLLCEIEGNHLTSAAIIGQDGTVWAQSANFPQFKPEEISGIMNDFAEPTGL  
APTGLYLGGTKYMIQGEPAVIRGKKGPGGITIKKTNQALIIGIYDEPMTPGQCNMIVE  
RLGDYLVEQGL

>CAI43283.4 Mala s 12; glucose-methanol-choline oxidoreductase [Malassezia  
sympodialis]

MKGIVSWAVVSAALVLSATESLAFANVSSF EKRTTTGNGWDL DGKSYDYVIVGGGTAGLV  
LANRLSANQGTTVAVIEAGNSGYDDNDKFVVPDANLYNSAVNTQYDWQFHTSSQKHMNNR  
RASWPRGKVLGGSSAVNGLYYVRPSETEVNVWSKLAGGSGRWSWNSLLSGMKKSEHFRGP  
VKSQVQNLQIQYNAGSHGSNGPIGTTWPAVTYDPVERFIKTADSMGAINNDPYNNGNNG  
TYVALSSIDKTNWQRSFSRNGYLDPISKRSNLHVL TGHTVTGIIFDRSGKNAQATGVHYA  
ASSNEASHTVHANKEVIISSGAINSPQILQLSGIGDKNLLNGLGIDVVVDLPGVGENLQD  
HVSAGMSFKPKNKDAGPTSVTGDADKADSYVNSAVSYTSLGKLFNNKDSILGKIARAKQ  
IADSHNVSPAVKQGQSKAYNALADTIFPSKVSPVEILGNVMFGSISIQAAALQHPLSRGSI  
KITSKDPFAYPKINPNYFAENLDLVLREGFKLIREMSQQSPLKDVIDFETVPGDKVQTN  
EDWENWIRSAAGTEYHPSSTCAMLPRGDGGVVDENLKVYGTSNLRVVDASVTPIAMSCHL  
ESVYVGLAEVAADIILGN

>AAY84564.2 Der p 15; chitinase [Dermatophagoides pteronyssinus]

MKTSCAILILMACFGLMNAAVKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK  
CTHLMYGF AKIDEYKYTIQVFDPYQDDNHNTWEKHGYERFNNLR LKNPELTTMISLGGWY  
EGSEKYS DMVANPTYRQQVFQSVLDFLQ EYKFDGLDL DWEYPGSRLGNPKIDKQNYLTLV

RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA  
PLYKRPEDETDELHTYFNVNYTMHYLLNNGATRDKLVMGVPFYGRAWSIEDRSKVKLGDP  
KGMSPPGFITGEEGLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYYDDLASIS  
KLAFLKELGVSVMISLENDDFKGCCKPKYPLLNKVNMMINGDEKNSYECLLGPSTTTP  
TPTTPSTPSTTTPPTTTPSTPSTTTPPTTTPSTPSTTTPPTTTPSTPSTTTPPTTTPST  
STTTPPTTTPDSTSETPKYTTYVDGHLIKCYKEGDLPHPTNIHKYLVCEYVNGGWVWHIM  
PCPPGTIWCQEKLTCITE

>ABB52642.1 Der p 10; tropomyosin [*Dermatophagoides pteronyssinus*]  
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRLQKKIQQIENELDQV  
QEQLSAANTKLEEKEKALQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA  
DESERMKMLEHRSITDEERMEGLENQSKARMMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAERAE  
FAERSVQKLQKEVGRLEDELVHEKEKYKSISDELDTFAEL

>Q63213 Rat n 1; lipocalin, urinary globulin [*Rattus norvegicus*]  
MKLLLLLLCLGLTLVCGHAAEEASFERGNLDVDKLNWDWFSIVVASKREKIEENGSMRVF  
VQHIDVLENSLGFTRIKENGVCTEFSLVADKTAKDGEYFVEYDGENFTILKTDYDNYV  
MFHLVNVNNGETFQLMELYGRTKDLSSDIKEKFAKLCVAHGITRDNIIDLTKTDRCLQAR  
G

>ABB78006.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [*Prunus persica*]  
MGVFTYESEFTSEIPPPRLFKAFLVLDADNLVPKIAPQAIKHSEILEGDGGPGTIKKITFG  
EGSQYGYVKKHIDSIDKENHSYSYTLIEGDALGDNLEKISYETKLVASPSGGSIKSTSH  
YHTKGDVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN

>ABB88514.1 Bomb m 1; arginine kinase [*Bombyx mori*]  
MVDAATLEKLEAGFSKLQGSDSKSLKYLTVREVFDSLKNKKSFGSTLLDCIQSGVENL  
DSGVGIYAPDAESYSVFAELFDPIIEDYHNGFKKTDKHPKNWGDVDTLGNLDPAGEFVV  
STRVRCGRSLEGYFPNCLTESQYKEMEDKVSGLSSLEGEKGTFFYPLTGMSKETQQQL  
IDDHFLFKEGDRFLQANACRFWPTGRGIYHNENKTFVWCNEEDHLRIISMQMGDLQQ  
VYKRLVSAVNEIEKKIPFSHHDRLGFLTFCPTNLGTTVRASVHIKLPKLAADKKKLEEVA  
SKYHLQVRGTRGEHTEAEGGVYDISNKRMRGLTEYDAVKEMYDGAELIKIEKSL

>ABB89296.1 Bla g 6; troponin C [*Blattella germanica*]  
MDELPPEQIQLLKKAFDAFDREKKGCISTEMVGTILEMLGHRLDDMLQEIIAEVDADGS  
GELEFEFVSLASRFLVEEDAAMQQLREAFRLYDKEGNGYITTNVLRILKELDDKIT  
AEDLMMIEEIDSDGSGTVDFDEFMEVMTGE

>ABB89297.1 Bla g 6; troponin C [*Blattella germanica*]  
MDEIPAEQVLLKKAFDAFDREKKGCISTEMVGTILEMLGTRLDQDMLDEIIAEVDADGS  
GELEFEFCTLASRFLVEEDAAMQHELREAFRLYDKEGNGYITTAVLRILKELDDKIT  
AEDLMMIEEIDSDGSGTVDFDEFMEVMTGE

>ABB89298.1 Bla g 6; troponin C [*Blattella germanica*]  
MADEQLQLPPEQISVLRKAFDAFDREKSGSISTNMVEEILRLMGQPFNRRTLEELIDEVD  
ADKSGRLEFDEFVTLAAKFIIEEDSEAMEKELREAFRLYDKEGNGYIPTSCLEILRELD  
EQLTSDDELMMIEEIDADGSGTVDFDEFMEMMTG

>ABB89950.1 Pen c 30; catalase [*Penicillium citrinum*]  
MHLLAFATDLVGIANAACPYMTGEVPGDYSPHELHRRADGAADNTEEFLSQFYLNKDA  
YLTSVGGPIEDQNSLSAGERGPTLLEDFIFRQKIQHFDHERVPERAVHARGAGAHGVFT  
SYADWSNITAASFSLKDKETPMFVRFSTVAGSRGSADTARDVHGFATRFYTDEGNFDIV  
GNNIPVFFIQDAIQFPLDIHAVKPSGDNEIPQAATAHDSAWDFFSQQPSSLHTLLWAMAG  
HGIPRSFRNVDFGVHTFRFVTDGSKSLVKFHWKGLQKASLVWEEAQQISGKNPDFLR  
QDLWDAIEAGRFPWELGVQIMDEEDQLRFGFDLLDPTKIVPEEIPVTKLGKMTLNRNP  
RNYFAETEQVMFQPGHIVRGVDFDTPDLLQGRVLSYLDLQNRHGGPNFEQLPINRPTP

IHNNNRDGAGQMFIPLNKDAYSPNTLNNASPKQANQTTGKGFFTTPSRKNGKLRQTVSS  
TFEDVWSQPRLFWNSLVEAEKQFVVDATRFENSNVSDIVRNNVIIQLNRISNDLAKRVA  
EAIGIEAPKPDPSFYHDNTTAHIGAFGQKLLKLEGLKVGVLASVQNASSVSSAASLQSQL  
KDAGVDVVVVAERLGDGVNQTYSGSDAIQFDVVVADGAEGLFSSRSFTEKPVKNKASSL  
FPAGRPLDILVDAFRFGKPVGAIGKGAALRAAQISSDREGVYAAKSIGNEFVKGLKEGL  
RIFKFLDRFALDA

>Q96X30.3 Asp f 22; enolase [Aspergillus fumigatus]  
MPISKIHARSVYDSRGNPTVEVDVVTETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGK  
GVLKAVKNVNETIGPALIKENIDVKDQSKVDEF LNKL DGTANKSNL GANAILGVS LAVAK  
AGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVLN GGS HAGGR LAFQEFMIVPDSAPSFS  
EALRQGAEVYQKLKALAKK KYQSAGNVGDEGGVAPDIQTAE EALDLITEAIEQAGYT GK  
IKIAMDVASSEFYKADVKKYDLDFKNPESDP SKWLT YEQ LADLYKSLAAKYPIVSIEDPF  
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPGRIKKAIELKSCNALLLKV NQIGTLTESIQ A  
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPCRSERLAKLNQILRIEE E  
LGENAVYAGSKFR TAVNL

>P79017.2 Asp f 2; unknown function [Aspergillus fumigatus]  
MAALLRLAVLLPLAAPLVATLPTSPVPIAARATPHEPVFFSWDAGAVTSFPIHSSCNATQ  
RRQIEAGLNEAVELARHAKAHILRWGNES EIRKYFGNRPTMEAVGAYDVI VNGDKANVL  
FRCDNPDGNCAL EGGHWRGANATSETVICDRSYTTRR WLVSMCSQGYTVAGSETNTFW  
ASDLMHRLYHVPVAVGQGWVDHFADGYDEVIALAKSNGTESTHDSEALQYFALEAYAFDIA  
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGSGATTTPTDSPSATIDVPSNCH  
THEGGQLHCT

>O60024.2 Asp f 4; unknown function [Aspergillus fumigatus]  
MQLKNSMLLLTALAAGSSVARLHGHERHLHHAGEKREVGD TVYATINGV LVS WINESG  
EAKTSDAPVSQATPVSNAAAAA AASTPEPSSSHSDSSSSSGVSADWTNTPAEGEYCTDG  
FGGRTEPSGSGIFYKGNV GKPWGSNIIEVSPENAKKYKHVAQFVGS DTD PWT VVFWNKIG  
PDGGLTGWYNSAL TLHLEAGETKYVAFDENSQGA WGAAGDELPKDQFGGYSCTWGEFD  
FDSKINQGWSGWDVSAIQ AENAHHEVQGMKICNHAGELCSIISHGLSKVIDAYTADLAGV  
DGIGGKVVPGPTRLV VNL DYKE

>O42799.2 Asp f 7; unknown function [Aspergillus fumigatus]  
MAPIFKSLALVSALFAA ISSAAPVNL DKREVDVWTTVTTVWTTIDVTTTIYPTPQAPT  
PPVVESTPTPTPSAAPEQA EPIETSTQPETTKSQPTQPSVATFIPVAAAAAADS AAPIP  
EEPAPQPATTAAPSTSTTTQAAPSAPPAANS GSTEKAASSGYSGPCSKGSPCVGQLTYD  
TATSASAPSSCGLTNDGFSENVVALPVGIMTDADC GKTVTITYNGITKTATVVDKCMGCK  
PTDLDASRH LFGELADFSAGRIDGMSWYFN

>Q8NKF4.2 Asp f 23; L3 ribosomal protein [Aspergillus fumigatus]  
MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSF PKDDPKKPVHLTASMGYKAGMTTVRDL  
DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK  
NWKYKSKKAFTKYAKKHAEEENGASITRELERIKKYCTVVRVLAHTQIRKTPLKQKKAHLM  
EIQVNGG SVADK VDFARNLFEKPIEIDSIFEKDEMIDVIAVTKGHGFQGVTSRWGTKKLP  
RKTHKGLRKVACIGAWHPSHVQWTVARAGQMGYHHRTSCNHKVFRIGKGSDEGNASTDFD  
ISKKQITPMGGFVRYGEVKNDYIMVKG SVPGVKKRVM TLRKTLYPQTSRRATEKVELKWI  
DTSSKFGHGAFQTPEEKRAFMGTLKKDLV TSA

>Q9UUZ6.2 Asp f 8; acidic ribosomal protein P2 [Aspergillus fumigatus]  
MKHLAAYLLLALAGNTSPSSEDVKAVLSSV GIDADEERLNK LIAELEGKDLQELIAEGST  
KLASVPSGGA AAAA PAAAGAAAGAAAPAAEEKKEEKEE SDEDMGFGLFD

>Q92450.3 Asp f 6; superoxide dismutase [Aspergillus fumigatus]  
MSQYTLPLPYPYDALQPYISQQIMELHKKKHHQTYV NGLNAALEAQKAAEANDVPKL  
VSVQQAIFNGGGHINHSLFWKNLAPEKSGGGKIDQAPV LKAAIEQRWGSFDKFKDAFNT  
TL LIGIQSGSGWGLVTDGPKGLDITTT HDQDPV TGAAPVFGVDMWEHAYYLQYLNDKASY

AKGIWNVINWAEAENRYIAGDKGGHPFMKL  
>CAJ43561.1 enterotoxin [Staphylococcus aureus]  
IFVLILVISTPNVLAESQDPKPDELHKASKFTGLMENMKVLYDDNHVSAINVKSIDQFL  
YFDLIYSIKDTKLGNVDNVRVEFKNDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSH  
QTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDEGKNLLSFDVQTNKKKVTQAQELDYLTR  
HYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDS  
KDVKIEVYLTTKKK  
>ABC02750.1 Lit c 1; profilin [Litchi chinensis]  
MSWQAYVDDHLMCETDGQHLTAAAIIGHDGSVWAQSANFPQFKPVEITAIMKDFDEPGSL  
APTGLHLGGTKYMIQGEPAVIRGKKKGGGITVKKTTQALIIGIYDEPMTPGQCNMVE  
RLGDYLVQGL  
>ABC18306.1 Fag e 2; 2S albumin, conglutin [Fagopyrum esculentum]  
MKLFIIILATATLLIAATQATYPRDEGFDLGETQMSSKCMRQVKMNEPHLKKCNRYIAMDI  
LDDKYAEALS RVEGEGCKSEESCMRGCCVAMKEMDDECVCEWMKMMVENQKGRIGERLIK  
EGVRDLKELPSKCGLSELECGSRGNRYFV  
>BAE54429.1 tropomyosin [Sepia esculenta]  
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKTEEDLSTLQKKYSNLENDFDNA  
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLEEDLERSEERL TSAQSKLEDASKAA  
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE  
ARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA  
EAERTVSKLQKEVDRLDELLAEKERYKSISDELDTFAELAGY  
>BAE54430.1 tropomyosin [Sepioteuthis lessoniana]  
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKTEEDLSTLQKKYANLENDFDNA  
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLEEDLERSEERFSSAQSKLEDASKAA  
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE  
ARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA  
EAERTVSKLQKEVDRLDELLAEKERYKTISDELDTFAELAGY  
>BAE54431.1 tropomyosin [Todarodes pacificus]  
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEAAKNTIEEDLSTLQKKYSNLENDFDNA  
KENLTVANTNLEASEKRVNECESEIQGLNRRIQLEEDLERSEERL TSAQSKLEDASKAA  
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE  
ARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA  
EAERTVSKLQKEVDRLDELLAEKERYKSISDELDTFAELAGY  
>BAE54432.1 tropomyosin [Ommastrephes bartramii]  
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKTEEDLSTLQKKYANLENDFDNA  
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLEEDLERSEERFSSAQSKLEDASKAA  
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE  
ARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA  
EAERTVSKLQKEVDRLDELLAEKERYKTISDELDTFAELAGY  
>BAE54433.1 tropomyosin [Octopus vulgaris]  
MDAIKKKMLAMKMERELATDKAEQTDQKL RDTEDNKNKLEEDLTTLQKKFSNLENDFDNA  
KEQLAEANQKLETSEKRVGECSEIAGLNRRIQLEEDLERSEERLSTAQTKLDEASKAA  
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE  
ARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA  
EAERTVSKLQKEVDRLDELLAEKERYKAISDELDTFAELAGY  
>2AS8\_B Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNACSIGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRQQSLDLAEQ  
ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYRYRYVAREQSCRPNQAQRFGISNYCQIY  
PPNANKIREALAQTHSAIAVIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNA  
QGVVYIWRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>2CYG\_A Mus a 5; beta-1,3-glucanase [*Musa acuminata*]  
IGVCYGM LGNNLPPPSEVVSLYKSNNIARMRLYDPNQ AALQALRNSNIQVLLDVPRSDVQ  
SLASNPSAAGDWIRRN VVAYWPSV SFRYI AVGNELIPGSDL AQYILPAMRNIYNALSSAG  
LQNQIKVSTAVDVTGVLGTSYPPSAGAFSSAAQAYLSPIVQFLASNGAPLLVNVYPYFSYT  
GNPGQISLPYALFTASGVVVQDGRFSYQNLFDAIVDAVFAALERVGGANVAVVSESGWP  
SAGGGAEASTSNAQTYNQNLIRHVGGGT PRRPGKEIEAYIFEMFNENQKAGGIEQNFGLF  
YPNKQP VYQISF

>Q948T6.2 lactoylglutathione lyase [*Oryza sativa*]  
MASGSEAEKSPEVVLEWPKKDKRLLHAVYRVGDLDRITKCYTECFGMKLLRKRDPVEEK  
YTNAFLGFGPEDTNFALELTNYGV D KYDIGAGFGHFAIATEDVYKLAEKIKSSCCCKIT  
REPGPVKGGSTVIAFAQDPDGYM FELIQRGPTPEPLCQVMLRVGDLDRSIFYEKALGMK  
LLRKKDVPDYKYTIAM LGYADEDKTTVIELTYNYGVTEYTKGNAYAQVAIGTEDVYKSAE  
AVELVTKELGGKILRQPGPLPGLNTKIASFLDPDGWKVVLVDNADFLKELQ

>ABC68516.1 Bla g 11; alpha-amylase [*Blattella germanica*]  
MKLFPLVALLVLLVVGVL SQKDPHVWDGRSAIVHLFEWK FADIAD ECERFLGPKGFAGVQV  
SPVHENVI ISSPFRPW WERYQLVSYKLVSRSGDENAFRDMVRR CNV GIRIYVDVVLNQM  
SGSWPDAHGQGGSTADTYNLQYPAVPYGP GDFHSTCTVSNYQDPSNVRNCELVGLHDLNQ  
GSDYVRGKMI EYLNHLVDCGVAGFRVDAAKHMWPADLQYIYSKVN LNTD HGFP SGARPF  
FYQEVIDLGG EAIHSTEYTGFRVTEFKYSRDIGDAFRGNNAIKWLVNFGVWG YIPDGD  
ALVFVDNHDNQRGHGAGGASILT YKTSKLYKMAVAFMLAYPYGYPRVMSSFSFDNSDQGP  
PQDGN GNII SP SINADGTCGNGWVCEHRWRQIFNMVGF RNAVAGTAVSNWWDNGDKQISF  
CRGNKGFVAFNDEFNNDLKQTLQ TCLPAGDYCDVISGSYENG SCTGKTVTVGSDGKAYIE  
ILSSADDGVLAIHVNSKVGSKSQ TTTTQSSHCTCS

>P46075.3 Asp f 5; metalloprotease [*Aspergillus fumigatus*]  
MRGLLLAGALALPASVFAHPAHQSYGLNRRTVDLNAFRLKSLAKYVNATETVIEAPSSFA  
PFPKQSYVEVATQHVKMIAPDATFRVDDHYVGDNGVAHVHFRQTANGLDIDNADFNVNV  
GKDGVKFSYGN SFYTGQIPSSAALTKRDFSDPVTALKGTTNTLQLPITVDSASSESTEEK  
ESYVFKGVS GTVSDPKAKLVYFVKDDGTLALAWRVETDIDSNWLLTYIDAKSGEEIHGVV  
DYVAEADYQVYAWGINDPTEGERTVIKDPWDSVASEFTWISDGSTNYTTSRGNNGIAQSN  
PSGGSSYLNNYRPS SSSLSFKYPYSVSSSPSSYIDASIIQLFYTANIYHDL LYL T LGFTE  
KAGNF EYNTNGQGG LGNDYVILNAQDGS GTNANFATPPDGQPGRMRMYVWTESTPYRDG  
SFEAGIVIHEYTHGLSNRLTGGPANSNCLNALES GGMGEGWSDFMATAIRLKP GDKRSTD  
YTMGEWASN RAGGIRQYPYSTSLSTNPLTYTSVNSLNAVHAIGTVWASMLYEVLWNLIDK  
HGKNDAPKPTLRDGVPTDGKYLAMKLVMDGMALQPCNPNFVQARDAILDADTALTGGENQ  
CEIWTAFAKRGLGAGAKYSSRN RVGSTEVP SGVC

>P82947.1 unknown function, partial [*Glycine max*]  
ANPTFGFTPLGLSSDAN

>ABC73068.1 unknown function, antigen 5 [*Vespula maculifrons*]  
MEISGLVYLIIIVTIIDL PYGKANNYCKIKCLKGGVHTACKYGS LKPNCGNKVVVSYGLT  
KQEKQDILKEHNDFRQKVARGLETRGNPGPQPPAKNMKNLWVND E LAYVAQVWANQCQYG  
HDTCRDVAKYQVGVQNVALTGSTAAKYENPVNLVKM WENEVKDYNP KKKFSENNFIKIGHY  
TQM V WANTKEIGCGSMKYTENKWHYHYLV CNYGPSGNFGNEELYQTK

>ABC73706.1 Der p 21; unknown function [*Dermatophagoides pteronyssinus*]  
MKFIITLFAAIVMAAAVSGFIVGDKKEDEWRMAFDRLMMEELETKIDQVEKGLLHLSEYQ  
KELEKTKSKELKEQILREL TIGENFMKGALKFFEMEAKRTDLNMFERYNYEFALESIKLL  
IKKLDELAKKVKAVNPDEYY

>Q00002.2 Alt a 4; disulfide isomerase [*Alternaria alternata*]  
ARDMTKQALPAVSEVTKDTLEEFKTADKVVLVAYFAADDKASNETFTSVANGLRDNFLFG  
ATNDAALAKAEGVKQPGLVCTSPSTTARTSSPRPSMRTYPRLRKVASTPLIGEVGPETYA  
GYMAAGIPLAYIFAETPEERE EFAKELKPLALKHKGEINFATIDAKSFGQHAGNLNLKVG

TWPAFAIQRTEKNEKFPTNQEAKITEKEIGKFVDDFLAGKIDPSIKSEPIPESNDGPVTV  
VVAHNYKDVVIDNDKDVLFVEFYAPWCGHCKALAPKYEELGQLYASDELSKLVIAKVDAT  
LNDVPDEIQGFLPSSLFPLARRMPQSTTLVPHCRGSRPVHRRERLTQASASVGEAVEDAT  
ESAKASASSATDSAASAVSEGTE TVKSGASVASDSASSAASEATKSVKSAASEVTNSASS  
AASEASASASSVKDEL

>ABC96702.1 NPC2-like [Dermatophagoides siboney]  
MISKILCLSLLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA  
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHFIKCPLVKGGQYDAKYTWNVPKIAPKSEN  
VVVTVKLIQDNGVLACAIATHAKIRD

>ABD39049.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x  
ananassa]

MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPIKIAPQAVKCAEILEGDDGGPGTIKKITFG  
EGSHYGYVKKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVSAPHGGTVIKTTSK  
YHTKGDVEIKEEHVKAGKEKASHLFKLIIEGYLKDHPSEYN

>1Z3Q\_A Mus a 4; thaumatin-like [Musa acuminata]  
ATFEIVNRCSTVWAAAVPGGGRQLNQGQSWTINVNAGTTGGRIWGRGTGCSFDGSGRGRG  
QTGDCGGVLSCTAYGNPNTLAEFALNQFNNLDFDISLVDGFNVPMDFSPTSGGCRGIR  
CAADINGQCPGALKAPGGCNPCTVFKTDQYCCNSGACSPDYQFFKRNCPCDAYSYPKD  
DQTTTFTCPGGTNYRVVFCP

>ABD51779.1 Api m 6; unknown function [Apis mellifera]  
MSRLVLASFLLAVFSMLVGGFGGFGGGLGGRGKCPSEIFSRCDGRCQRFPCNVVVK  
PLCIKICAPGCVCRLGYLRNKKKVCVPRSKCLPG

>ABD79094.1 Zea m 1; beta-expansin [Zea mays]  
MWSLMQAQVAMVVALSFLVSGAWCGPPKVPKGNITATYKDWLDAKATWYGKPTGAGPD  
DNGGGCGYKDVNKPFFNSMGACGNIPIFKDGLGCGSCFEIKCDKPVCEGSKPVVHITDM  
NYEPIAAYHFDLAGTAFGAMAKKGEELRKGAIIDMQFRRVKCKFGSKVSFHLEKGCGR  
NYLALLVKYVDGDGDIVPVDIIEKGSPTYEPLKHSWGAIWRKDSKPLKGPLTVRLTTEG  
GTKTVYDDVIPANWKANTAYTAK

>ABD79095.1 Zea m 1; beta-expansin [Zea mays]  
ARALVFLVSGAWCGPPKVPKGNITATYKDWLDAKATWYGKPTGAGPDDNGGGCGYKDV  
NKPPFNSMGACGNIPIFKDGLGCGSCFEIKCDKPVCEGSKPVVHITDMNYEPIAAYHFD  
LAGTAFGAMAKKGEELRKGAIIDMQFRRVKCKYDSKVTFHLEKGCGRNYLALLVKYVD  
GDGDIVAVDVKEKGSPTYEPLKHSWGAIWRKDSKPLKGPLTVRLTTEGGTKSVYDDVIP  
ANWKANTAYTAK

>ABD79096.1 polygalacturonase [Zea mays]  
MACIDNAMRALFLLALFCVVHGEKAKSKDNDKASGPGGSFDITKLGASNGKTDSTKAV  
QEAWASACGGTGKQTIIPKGDFLVGPLNFTGPCKGDVTIQVNGNLLATDLSQYKDHGN  
WIEILRVDNLVITGKGKLDGQPAVWSKNSCVKDYCKILPNSLVMDFVNNGEVSGITLL  
NSKFFHMNYKCKDMLIKDVNVTAPGDSPTDGIHMGDSSGVTITNTVIGVGDCCISIGP  
GTSKVNITGVTGPGHGIGISIGSLGRYKDEKDVTDINVKDCTLKKTANGVRIKAYEDAASV  
LTASKIHYENIKMEDSGYPIIIDMKYCPNKLCTANGASKVTVKDVTFKNITGTSSTPEAV  
NLLCSAKIPCTGVTMDDVNIKYSGTNNKTMVCKNAKGSAGCKELACF

>ABD79097.1 polygalacturonase [Zea mays]  
ARGALFLLALFCVVHGEKAKSKDNDKASGPGGSFDITKLGASNGKTDSTKAVQEAWAS  
ACGGTGKQTIIPKGDFLVGPLNFTGPCKGDVTIQVNGNLLATDLSQYKDHGNWIEILR  
VDNLVITGKGKLDGQPAVWSKNSCVKDYCKILPNSLVMDFVNNGEVSGITLLNSKFFH  
MNYKCKDMLIKDVNVTAPGDSPTDGIHMGDSSGVTITNTVIGVGDCCISIGPGTFKVN  
ITGVTGPGHGIGISIGSLGRYKDEKDVTDINVKDCTLKKTANGVRIKAYEDAASVLTASKI  
HYENIKMEDSGYPIIIDMKYCPNKLCTANGASKVTVKDVTFKNIPGTSSSTPEAVNLLCSA  
KIPCTGVTMDDVNIKYSGTNNKTMVCKNAKGSAGCKELACF

>ABD79098.1 polygalacturonase [Zea mays]  
ARACTDNAMRALFLLVLFIVHGEKEESKIDAKASGPGGFFDITKLGASGNGKTDSTKA  
VQEAWASACGGTQKQILIPKGDFLVGLNFTGPKGDVTIQVDGNLLATDLSQYKEHG  
NWIEILRVDNLVITGKGNLDGQGPVAVSKNFCTKKYDCKILPNSLVMDFVNNGEVSGITL  
LNSKFFHMNMYQCKNMLIKDVTVTAPGDSPTNDGIHMGDSSGITITNTVIGVGDCCISIG  
PGTSKVNITGVTCGPGHGISIGSLGRYKDEKDVDRDINVKDCTLKKTMTFVRIKAYEDAAS  
VLTVSKIHYENIKMEDSANPIFIDMKYCPNKLCTANGASKVTVKDITFKNITGTSSTPEA  
ISLLCTAKVPCTGVTMDDVNVEYSGTNNKTMAICTNAKGSTKGCLKELACF

>CAI84850.2 7S globulin, vicilin, beta-conglutin, partial [Lupinus albus]  
MGKMRVRFPTLVLVLGIVFLMAVSIGIAYGEKDVLSHERPEEREQEWEQPRRQRPQSRR  
EEREQEQQGSPSYPRRQSGYERRQYHERSEQREEREQEQQGSPSYRRQRNPYHFNSQ  
RFQTLTKNRNGKIRVLERFDQRTNRLNQLNYRIVEFQSKPNTLILPKHSDADYVLLVVLN  
GRATITIVNPDRRQAYNLEYGDALRIPAGSTSYILNPDDNQKLRVVKLAIPINNPYFYD  
FYPSSTKDQQSYFSGFSRNTLEATFNTRYEEIQRIILLGNEDEQEYEEQRRGQEQSHQDEG  
VIVRVSREQIQELTKYAQSSSGKDKPSQSGPFNLSNEPIYSNKYGNFYEITPDRNPQVQ  
DLDISLTFTEINEGALLPHYNSKAIFIVVVGEGNGKYELVGIRDQQRQQDEQEPEEV  
RRYSARLSEGDIFVIPAGYPISVNASSNLRLLGFGINAYENQRNFLAGSEDNVIRQLDRE  
VKELTFPGSAEDIERLIKNQQSYFANALPQQQQQSEKEGRRRRRGPISII

>CAJ85641.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x  
ananassa]  
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAIKCAEILEGDGGPGTIKKITFG  
EGSHYGYVKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVSAHPHGTTIITTSK  
YHTKGDVEIKEEHVKAGKEKASHLFKLIIEGYLKDHPSEYN

>CAJ85642.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x  
ananassa]  
MGGYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAIKCAEILEGDGGPGTIKKITFG  
EGSHYGYVKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVSAHPHGTTIITTSK  
YHTKGDVEIKEEHVKAGKEKASHLFKLIIEGYLKDHPSEYN

>CAJ85644.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x  
ananassa]  
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKITFG  
EGSHYGYVKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVSAHPHGTTIITTSKY  
HTKGDVEIKEEHVKAGKEKASHLFKLIIEGYLKDHPSEYN

>CAJ85646.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x  
ananassa]  
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKITFG  
EGSHYGYVKHKIHSIDKVNHTYSYSLIEGDALSDNIEKIDYETKLVSAHPHGTTIITTSK  
YHTKGDVEIKEEHVKAGKEKAAHLFKLIIEGYLKDHPSEYN

>CAI78448.1 Asp f 27; cyclophilin/peptidyl-prolyl isomerase [Aspergillus fumigatus]  
MVVKTFFDITIDGQPAGRITFKLFDEVVPKTVENFRALCTGEKGFYKGSFHRIPQFM  
LQGGDFTKGNVTGGKSIYGRFPDENFQLKHDKPGLLSMANAGKNTNGSQFFITTVVTSW  
LDGAHVVFGEVEDGMDLVKKIESYGSASGTPKKKITIADCGQL

>CAI78449.1 Asp f 28; thioredoxin [Aspergillus fumigatus]  
MSHGKVIADVNPPIIYKALTSSGPVVVDFATWCGPCRAVAPKVGELSEKYSNVRFIQVDV  
DKVRSVAHEMNIRAMPTFVLYKDGQPLEKRVVGGNVRELEEMIKSISA

>CAI78450.1 Asp f 29; thioredoxin [Aspergillus fumigatus]  
MSHNVEKITDAKVFEKQVQEGSGPVIVDCSATWCGPCKAISPVFQRLSTSEEFKNAKFYE  
IDVDELSEVAAELGVRAMPTFMFFKDGQKVNVEVGGANPPALEAAIKAHVA

>NP\_001035360.1 Api m 6; unknown function [Apis mellifera]  
MSRLVLASFLLLAIFSMVLVGGFGGFGGGLGGRGKCPNSNEIFSRCDGRCQRFPCNVVVK

PLCIKICAPGCVCRLGYLRNKKKVCVPRSKCG  
>ABF18122.1 Aed a 3; unknown function [*Aedes aegypti*]  
MKPLVKLFLFLFCLVGLVLSRPMPEDEEPVAEGGDDASGESEGEETDDAGGDGEEEN  
EGEEHAGDKDAGGEDTGKEENTGHDDAGEEDAGEEDAGEEDAGEEDAEKEEKEKE  
DAGDDAGSDDGEEDSTGGDEGEDNAEDSKGSEKNDPADTYRQVVALLDKDTKVDHIQSEY  
LRSALNNDLQSEVRVPVVEAIGRIGDYSKIQGCFCFSMGKDVKKVISEEEKFKSCMSKKK  
SEYQCSSEDSFAAAKSKLSPITSKIKSCVSSKGR  
>ABF21077.1 Api m 10; icarapin [*Apis mellifera*]  
MKTGLVLFIAAWFIACHTSFPGAHDEDSKEERKNVDTVLVLPSTIERDQMMMAATFDFPSSL  
FEDSDEGSNWNWNTLLRPNFLDGYQLQSAISAHMKKVREQMAGILSRIPREQGVVNWK  
IPEGANTTSTTKIIDGHVVTINETYTDGSDDYSTLIRVRVIDVRPQNETILTTSSEAD  
SDVTTLPTLIGKNETSTQSSRSVESVEDFDNEIPKNQGDVLT  
>P0C1B3.1 Asp o 21; taka-amylase, alpha-amylase [*Aspergillus oryzae*]  
MMVAWWSLFLYGLQVAAPALAAPADWRSQSIYFLLTDRFARTDGGSTTATCNTADQKYCG  
GTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTAYGDAYHGYWQQDIYSLNENYGTADD  
LKALSSALHERGMYLMVDVVAHMGYDAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQT  
QVEDCWLGDNTVSLPDLDTTKDVVNEWYDWVGSLSVSNYSIDGLRIDTVKHVQKDFWPGY  
NKAAGVYCIGEVLGDPAITCPYQNVMDGVLNYPYIYPLNNAFKSTSGSMDDLNMINTV  
KSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEYHYAGGN  
DPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVYKNWPIYKDDTTIAMRKG  
TDGSQIVTILSNKGASGDSYTLSSGAGYTAGQQLTEVIGCTTVTVGSDGNVPMAGGL  
PRVLYPTEKLAGSKICSSS  
>CAI94601.1 Par j 1; lipid transfer protein [*Parietaria judaica*]  
QETCGTMVRALMPCLPFVQGEKEEPSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTY  
SDIDGKLVSEVPKHCIGIVDSKLPIDVNMDCCTLGVVPRQPQLPVSLRHGPVTGSPDPAH  
KARLERPQIRVPPPAPEKA  
>CAK22338.1 Der p 2; NPC2-like [*Dermatophagoides pteronyssinus*]  
MMYKILCLSLVAVAADQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEALFEA  
NQNTKNAKIEIKASIDGLEVDVPGIDPNACHYVKCPLVKGQYDIKYTWNVPKIAPKSEN  
VVVTVKVLGDNGVLACAIATHAKIRD  
>ABF81661.1 Zea m 1; beta-expansin [*Zea mays*]  
CKYGSKVTFHLEKGCNPNYLALLVKYVDGDGDIVAVDIKEKGSPTYEPLKHSWGAIWRKD  
SDKPIKGPITVRLTTEGGTKTVYDDVIPAEWKPNTAYTT  
>ABF81662.1 Zea m 1; beta-expansin [*Zea mays*]  
MTVVSIMWSLVQVQLVAVALSFLVGGAWCGPPKVPKGNITANYGSDWLDKATWYKGP  
TGAGPDDNGGGCGYKDVNKAPFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSGKPVV  
VYITDMNYEPIAAHYFDLAGTAFGAMAKKGEELRKAGIIDMQFRRVKCKYGSKVTFHL  
EKGCNPNYLALLVKYVDGDGDIVAVDIKEKGSPTYEPLKHSWGAIWRKDSKPIKGPITV  
RLTTEGGTKTVYDDVIPTDWPNTAYTTK  
>ABG02262.1 Vig r 2; 8S globulin, vicilin [*Vigna radiata*]  
MVRARVQLLLGILFLASLSVSGIVHREHQESQEESSDRGQNNPFYFNDRRFHTLFKNQ  
YGHRLVIHRFDQRSKQIQNLENYRVVEFKSKPNTLLLPHHADADFLVVLNGRAILTLVN  
PDGRDSYILEQGHAKIPAGTTFFLVNPNNDNLRRIKLAIPVNNPHRFQNFLLSSTEAQ  
QSYLRGFSKNILEASFDSDFKIDRVLFGEEERQQQHGEESQEEGVIVELKREQUIRELIK  
AKSSSRKELSSQDEPNLRNSNPIYSNKFGRWYEITPEKNPQLKDLDFISSVDMKEGGL  
LLPHYNSKAIIVILVINEGEAKIELVGPSSDQQQDESLEVQRYRAELSEDDVVFVIPAAYPV  
AINATSNLNFFAFGINAENQRNFLAGEKDNMSEIPTEVLDVSPASGNKVEKLIKQKS  
ESHFVDAQPEQQQREEGHKGRKGLSSILGSLY  
>Q40638.2 Ory s 1; beta-expansin [*Oryza sativa*]  
MASSSLLLACVVVAAMVSAVSCGPPKVPKGNITTSYGDKWLEAKATWYGAPKGAGPKDN

GGACGYKDVDPKAPFLGMNSCGNDPIFKDGKGCSCFEIKCSKPEACSDKPALIHVTDMMND  
EPIAAYHFDLSGLAFGAMAKDGKDEELRKAGIIDTQFRRVKCKYPADTKITFHIEKASNP  
NYLALLLVKYVAGDGDVVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEG  
GEKIIAEDAIPDGWKADSVYKSNVQAK  
>ABG54494.1 Rub i 3; lipid transfer protein [Rubus idaeus]  
MACSAVMKLALVALLCIVVAVPVAQAITCGQVTQNVAPCFNYVKNNGGAVPAACCNGVRNL  
NSQAKTTADRQQTNCCLKNAAGSIPGLNPSLAAGLPGKCGVSVPYKISTSTNCATVK  
>ABG54495.1 Rub i 1; pathogenesis related protein, PR-10, Bet v 1-like [Rubus  
idaeus]  
YTSVIPPPKLFKAFVLDADNLIPKIAQAVKSVEIIEGDGGVGTVKKIHLGEGTEHSYVK  
HKIDGLDKVNFVYSYSITEGDALGDKIEKISYEIKLVASGRGSIKTTSHYHCKGGAEIK  
EEQVKDGGKERAAGLFKI  
>CAL07989.1 Pla a 3; lipid transfer protein [Platanus acerifolia]  
MAFSRVAKLACLLLACMVATAPHAEEAITCGTVVTRLTPCLTFLRSGGAVAPACCNGVKA  
LNNDAKTTPDRQAACGLKTAISTSISGIQLGNAASLAGKCGVNLPHYKISPTIDCSKVK  
>CAK50389.1 Ani s 4; cysteine protease inhibitor [Anisakis simplex]  
MQSRIVVAVVVFCIIILMQTEAGMLGGSSDQVNDPEIKELAGKSIKISAMINDGKPH  
LVKVVSAKKQVVAGDKYTLLEILVKDGDHQLDCTVTIWKQKVENFEEVKVLKCDHQ  
>ABG73108.1 Pis v 1; 2S albumin, conglutin [Pistacia vera]  
MAKLVLLLSAFAFLILAANASIYRATVEVEGENLSSGQSCQKQFEEQQKFKHCQMYVQQE  
VQKSQDGHSLTARINQRQQCFKQCCQELQEVDKKCRQNLEQMVKRQQQQGQFRGEKLQE  
LYETASELPRMCNISPSQGCQFSSPYWSY  
>ABG73109.1 Pis v 2; 11S globulin, cupin [Pistacia vera]  
MGYSSLLSFSLGFLLLFHCSFAQIEQVWNSQQRQQQRFQTQCQIQNLNALEPKRRIESE  
AGVTEFWDQNEEQQLQCANVAVFRHTIQSRGLLVPSYDPAPELVYVVQGSIGAVFPGCP  
ETFQEESSQSRRSERSQQSGEQHQKVRPIQEGDVIALPAGVAHWIYNNQSKLVLVALAD  
VGNSENQLDQYLKRFVLGGSPQQEIQGSGQSRRSRSQSQRSGGQQQSNILSAFDEEI  
LAQSFNIDTQLARRLQKEKRQRGIIVRVQEDLEVLSPHRQEQEQEYEEERERRQRNGLEE  
TFCTMTLKYININDPSRADVYNPRGGRVSSVNALNLPILRFLQLSAKKGVLHRDAILAPHW  
NVNAHSIVYITRGNRIQIVSENGESVFDEEIREGQLVVVPQNFVAVKRASSDKFEWVSF  
KTNGLSQTSQLAGRVSVFRALPLDVIKNSFDISREDARRLKESSRSETTIFAPGSSSQRKS  
QSERERQREREEREIH  
>ABG73110.1 Pis v 2; 11S globulin, cupin [Pistacia vera]  
MGYSSLLSFSLGFLLLFHCSFAQIEQVWNSQQRQQQRFQTQCQIQNLNALEPKRRIESE  
AGVTEFWDQNEEQQLQCANVAVFRHTIQSRGLLVPSYNNAPPELVYVVQGSIGAVFPGCP  
ETFQEESSQSRRSQHSRSERSQQSGEQHQKVRHIREGDIALPAGVAHWIYNNQSKLVL  
VALADVGNSENQLDQYLKRFVLGGSPQQEIQGGGQSWQSRSRSGGQQSNILSAFDEEI  
LAQSFNIDTQLVKKLQREEKQRGIIVRVKEDLQVLSQRQEQEYSDNGLEETFCTMTLKL  
NINDPSRADVYNPRGGRVTSINALNLPILRFLQLSVEKGVLYQNAIMAPHWNMNAHSIVY  
ITRGNRMQIVSENGESVFDEEIREGQLVVVPQNFVAVKRASSDGFVWVSFKTNGLAKIS  
QLAGRISVMRGLPLDVIQNSFDISREDAWNLKESRSEMTIFAPGSRSQQRN  
>ABG76196.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
RDQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASID  
GLEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDNGVLAC  
AIATHAKIRD  
>ABG81289.1 Phl p 12; profilin [Phleum pratense]  
MSWQAYVDEHLMCEIEGHHLASAAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAAAKYMIQGEPAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLVKQGL  
>ABG81290.1 Phl p 12; profilin [Phleum pratense]

MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAAAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81291.1 Phl p 12; profilin [Phleum pratense]

MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVATAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81292.1 Phl p 12; profilin [Phleum pratense]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVATAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81293.1 Phl p 12; profilin [Phleum pratense]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAAAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81294.1 Phl p 12; profilin [Phleum pratense]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVAAAKYMVIQGEPEGAVTRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLVKQGL

>ABG81295.1 Phl p 12; profilin [Phleum pratense]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL  
APTGMFVATAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCSMVVE  
RLGDYLVKQGL

>ABG81312.1 Zea m 12; profilin [Zea mays]

MSWQTYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQFKPEEMTNIKDFDEPGFL  
APIGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE  
RLGDYLVKQGL

>ABG81313.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQFKTEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQAMVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81314.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAAWAQSTAFPEFKTEDMANIMKDFDEPGHL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81315.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQFKTEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE  
RLGDYLLKQGM

>ABG81316.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQFKTEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81317.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQSKTEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQAMVVGIIYDEPMTPGQCNMVVE  
RLGDYLLKQGL

>ABG81318.1 Zea m 12; profilin [Zea mays]

MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFQFKTEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQAMVVGIIYDEPMTPGQCNMVVE

RLGDYLLNRA

>ABG85155.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis hypogaea]

MGVFTFEDEITSTLPPAKLYNAMKDADSLTPKIIDDVKSVEIVEGSGGPGTIKKLTIVED  
GETRFILHKVEAIDEANYAYNYSVVGVALPPTAEKITFETKLVEGHNGGSTGKLSVKFH  
SKGDAKPEEEDMKKGKAKGEALFKAIEGYVLNPTQY

>ABH06346.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLHITHEVDDLEKT  
GNKDEKARPLRELVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLKDLKA  
LQKRVQDSE

>ABH06348.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFIIALAALIAVACALPVSNDNFRHEFDHMIINTATQRFHEIEKFLHITHEVDDLEKT  
GNKDEKARLLRELVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLKDLKA  
LQKRVQDSE

>ABH06350.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLHITHEVDDLEET  
GNKDEKARLLRELVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLKDLKA  
LQKRVQDSE

>ABH06352.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDEL  
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNVEEAQTLKILLKD  
LKETEQQVKDIQTQ

>ABH06359.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDEL  
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNVEEAQTLKILLKD  
LKETEQQVKDIQTQ

>ABH06347.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]

MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNAATQRFHEIEKFLHITHEVDDLEKT  
GNKDEKARLLRELVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLKDLKA  
LQKRVQDSE

>ABI17154.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]

MAKLLALSCLFCVVLVGASSVTFRQGGREENECQFQRLNAQRPNRIESEGGYIETWPNPN  
QEFQCAGVALSRTVLRNALRRPFYSNAPLEIYVQQGSGYFGLIFPGCPSTYEEPAQEGR  
RYQSQKPSRRFQVQDDPSQQQDSHQKVHRFDEGDLIAVPTGVAFWVYNDVVT  
LSDTSSIHNQLDQFRRFYLAGNQEQEFLRYQQQGSRPHYRQISPRVRGDEQENEGSNI  
FSGFAQEFQLQAFQVDRQTVENLRGENEREQGAIVTVKGLRILSPDEEDESRSPPSR  
REEFDEDRSRPQQRGKYDENRRGYKNGIEETICSASVKKNLGRSSNPDIYNPQAGSLRSV  
NELDLPILGWLGLSAQHGTIYRNAMFVPHYTLNAHTIIVVALNGRAHVQVDSNGNRVYDE  
ELQEGHVLVVPQNFVAQAQSENIEYLAFKTDSPSIANLAGENSIIDNLPEEVVANSY  
RLPREQARQLKNNNPFKFFVPPFDHQSREVA

>ABI26088.1 translationally controlled tumor protein [Alternaria alternata]

MLIYKDILTGEIISDSYNLKEIDGVVYEADCTKITVGGESFDTGANASAEQEEGAEDS  
AETKIDVVYSFRLNETGFDKKGYLTYLKGVMKAVKDGLKKKGADKATIKDFETKASGYAK  
KIISNFKDYEFFTGESMNPDMIVLLNYREDGVTPYVTVWKHGLEEMKV

>ABI32184.1 unknown function [Fagopyrum tataricum]

MSTKLILSFLCLMVLSCSAQAQLWPWRKGGQDSRPHHGHQQFQQQCDIQRILTASEPSRR

VRSEAGVTEIWDHNTPEFRCTGFVAVRYVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVI  
PGCPETFQSDSEYPPQSQRGQHSRESESQESSRGDQHQKIFRVREGDVIPSPAGVVQWTHN  
DGDQDLISVTLLDANSFHNQLDENVRSFFLAGQSQQGREERRSQQQTREEGGDRQSRES  
DVEALIGANILSGFQDEILHELFRDVEDRETISKLRGENDQRFIVQAQDLKLRVPEDSEE  
GYERQGRDRKRDERGSGRSNGLEQAFCNLKRQNVNRP SHADVFNPRAGRINTVNSNNLP  
ILEFLQLSAQHVVLYKNAIIGPRWNLNAHSALYVTRGEGRVQVVGDEGKSVFDDNVQRGQ  
ILVVPQGFVAVVVKAGRQGLEWVELKNNDNAITSPIAGRTSVLRAIPVEVLANSYDISTEE  
AYKLNKRQEVEVFRPFQSRYEKEEEEKERERFSIV  
>AAU21499.2 Ara h 10; oleosin [Arachis hypogaea]  
MTDRTQPHTVQVHTTAGRFGDAAAGTNRYPDRGPSTSKVIAVITGLPIGGTLLLFAGLAL  
AGTLLGLAVTTPLFILFSPVIVPAIIVVGLSVAGFLTSGACGLTGLSSFSWVMNYIRQTH  
GSVPEQLEMAMHRMADVAGYVVGQKTKDVGQKTKEVGQEIQTKAQDSKRT  
>Q01883.2 unknown function [Oryza sativa]  
MASNKVVFVSVLLLVLVSLVLAAMATMADHHQVYSPGEQCRPGISYPTYSLPQCRTLVRRO  
CVGRGAASAADQVWQDCCRQLAAVDDGWCRCGALDHMLSGIYRELGATEAGHPMAEVFP  
GCRRGDLERAAASLPAFCNVDIPNGPGGVCYWLGYPRTPRTGH  
>Q01882.2 unknown function [Oryza sativa]  
MASNKVVFVSVLLLIIIVSVLAATATMADHHKQVYVYSLGERCQPGMGYPMYSLPRCRAVVK  
RQCVGHGAPGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHVMAE  
VFPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH  
>NP\_001041618.1 Fel d 1; uteroglobin [Felis catus]  
MLDAALPPCPTVAATADCEICPAVKRDVDFLTGTPDEYVEQVAQYKALPVVLENARILK  
NCVDAKMTEEDKENALSLLDKIYTSPLC  
>2HCZ\_X Zea m 1; beta-expansin [Zea mays]  
GPPKVPPGXNITTTNYNGKWL TARATWYGPNGAGAPDNGGACGIKNVNLPYSGMTACGN  
VPIFKDGGKCGSCYEVRCKEPECSGNPVTVYITDMNYEPIAPYHFDLSGKAFGLAKPG  
LNDKIRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYLAVLVKYVADDGDIVLMEIQ  
DKLSAEWKPMKLSWGAIWRMDTAKALKGPF SIRLTSESGKKVIAKDVIPANWRPDAVYTS  
NVQFY  
>BAF32105.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN  
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPI LINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRKEKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP  
>BAF32110.1 Cry j 2; polygalacturonase [Cryptomeria japonica]  
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPQFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN  
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPI LINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRKEKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP  
>BAF32116.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVS YVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32119.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKFIAPMAFVAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVS YVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDINLSDISLKLTSKGKIASCLNDNANGYFS  
GNVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32122.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVS YVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GNVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32128.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGTENSRAEVS YVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>BAF32130.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDFFSTGLIIQGLRLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVS YVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32133.1 Cry j 2; polygalacturonase [Cryptomeria japonica]

MAMKLIAPMAFLAMQLIIMAAAEQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVSVHVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRS  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSGKIASCLNDNANGYFS  
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWMCSCHGKIYHP

>BAF32134.1 Cry j 2; polygalacturonase [*Cryptomeria japonica*]

MAMKLIAPMAFLAMQLIIMAAAEQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN  
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV  
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR  
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA  
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLIGRENSRAEVSVHVHVN  
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRS  
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSGKIASCLNDNANGYFS  
GHVIPACKNLSNAPAKRRESKSHKHPKTMVENMAYDKGNRTRILLGSRPPNCTNKCHGC  
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>BAF32143.1 Cha o 2; polygalacturonase, partial [*Chamaecyparis obtusa*]

LDSDIEQYLRNRSRLKLVHSRDAATVFNVEQYGAUGDVGKHDSTEAFETAWNAACKKAS  
AVLVVPANKKFFVNNLVFRGPCPHLSFKVDGTIVAQPDPARWKNKSIWLQFAQLTDFNL  
MGTGVIDGQGGQWAGQCKWVNGRVCNDRNRPTAIKIDYSKSVTVKELTLMNSPEFHLV  
FGECEGVKIQGLKIKAPRDSPTDGDIDIFASKRFHIEKCVIGTGDDCIAIGTGSSNITIK  
DLICGPGHGIGISLGRDNSRAEVSHVHVNRRAKFIDTQNGRLRIKTWQGGSGLASIYIYEN  
VEMINSENPIILINQFYCTSASACQNQRSQIQGVITYKNIHGTSAATAAAIQLMCSDSVPC  
TGIQLSNVSLKLTSGKPASCVDKNARGFYSGRLIPTCKNLRPGSPKEFELQQQPTTVM

>ABI98020.1 Lit v 2; arginine kinase [*Litopenaeus vannamei* (*Penaeus vannamei*)]

MADAAVIEKLEAGFKLEAATDCKSLLKKYLTKVFDKLDKRTSLGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFQTDKHPNKDFGDVNSFVNVDPGKFKV  
ISTRVRCGRSLQGYFPNCLTESQYKEMEAKVSSTLSSLEGELKGTYYPLTGMSKEVQQK  
LIDDHFLFKEGDRFLQAANACRYWPAGRGYHNDNKTFLVWVNEEDHLRIISMQMGDLG  
QVFRRLTSAVNEIEKRIPFSSHDRGLFTFCPTNLGTTVRASVHIKLPKLAANREKLEEV  
AGKYNLQVRGTRGEHTEAEGGIYDISNKRRLMGLTEFQAVKEMQDGIKELIKIEKEM

>Q1ZYQ8.2 Zea m 1; beta-expansin [*Zea mays*]

MAVNVRTMWSMRAQVAMVVALVFLVRGAWCGPPKVPVPGKNITATYKGDWLDKATWYGK  
PTGAGPDDNNGGGCGYKDVNKPPFNSMGACGNPIFKDGLGCGSCFEIKCDKPAECSGKPV  
VVHITDMNYEPIAAYHFDLAGTAFGAMAKKGEEELRKAGIIDMQFRRVKCKYDSKVTFH  
LEKGCNPYLALLVKYVDGDGDIVAVDVIKEKGSPTYEPLKHSWGAIWRKDSKPLKGPLT  
VRLTTEGGTKSVYDDVIPANWKANTAYTAK

>P0C1Y5.1 Zea m 1; beta-expansin [*Zea mays*]

MTVVSIMWSLVQVQVLVAVALAFLVGGAWCGPPKVPVPGKNITAKYGSWLDKATWYGK  
TGAGPDDNNGGGCGYKDVNKAPFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSGKPV  
VYITDMNYEPIAAYHFDLAGTAFGAMAKKGEEELRKAGIIDMQFRRVKCKYGSKVTFH  
EKGCNPYLALLVKYVDGDGDIVAVDVIKEKGSPTYEPLKHSWGAIWRKDSKPIKGPITV  
QLTTEGGTKTVYDDVIPAGWKPNAYTAK

>CAL59818.1 hyaluronidase [*Vespa germanica*]

SERPKRVFNIIYWNVPTFMCHQYDLYFDEVTFNFIKRNKDDFQGDKIAIFYDPGEFPALL  
SLKDGKYYKRNNGVVPQEGNITIIHLQKFIENLDKTYPNRNFSGIGVIDFERWRPFRQNWG  
NMKIHKNFSIDLVRNEHPTWNKKMIELEASKRFEKYARFFMEETLKLAKKTRKQADWGY

GYPYCFNMSPNNLVPECDVTAMHENDKMSWL FNNQNVLLPSVYVRQELTPDQRIGLVQGR  
VKEAVRISNNLKHSPKVL SYWVYVYQDETNTYL TETDVKKTFQEIVINGGGIIIWGSSS  
DVNSLSKCKRLQDYLLTVLGP IAVNVTEAVN

>CAL59819.1 phospholipase A1 [*Vespa germanica*]

VITIWPKKGF SIYWNIP THFCHNFGVYFKELKQFN IYKYNMNNFRGETISL FYPGNFPS  
MVL LKNGTYEIRNEGVPQKGNL TIHLEQFTKELDEIYPKKIAGGIGVIHFHNWRPIFRRN  
VDNLKINKDISIDLVRKEHPKWDKSMIEKEASNR FETS AKIFMEKTLKLAKEIRKKTEWG  
YHGYPHCLSGSTDKPSFDCDALSMS ENDKMSWL FNNQNVLLPSIYLKNVLPDEKIHVQ  
ERLKEAIRISKNLKHLPKVLPYWVYTYQDKESIFL TEADVKNTFKEILTNGADGIIIWGV  
SYELTDRKRCEKLKEYLMKILGP

>ABK78766.1 Cup a 1; pectate lyase [*Cupressus arizonica* (*Hesperocyparis arizonica*)]

SDNPIDSCWRGDSNWDQNRMKLADCVVGFSGSSTMGKGGEIYTVTSS EDNPVNPTPGTLR  
YGATREKALWII F SQNMNIKLQMPLYVNGYKTIDGRGADVHLGNGGPCLFMRKASHVILH  
GLHIHGCNTSVLGDVLVSESIGVEPVHAQDGAITMRNVTNAWIDHNSLSDCSDGLIDVT  
LGSTGITISNNHFFNHHKVML LGHDDTYDDD KSMKVTVAFNQFGPNAGQRMPRARYGLVH  
VANNNYDQWNIYAIGSSNPTILSEGN SFTAPNESYKKEVTKRIGCETTSACANWVWRST  
RDAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQNAGVVA

>P00791.3 pepsin [*Sus scrofa*]

MKWL LLSLVVLESECLVKVPLVRKKSRLQNL IKNGLKDFL KTHKHPASKYFPEAAALI  
GDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDS  
STFEATSQELSITYGTGSMTGILGYD TVQVGGISDTNQIFGLSETEPGSFLYYAPFDGIL  
GLAYPSISASGATPVFDNLWDQGLV SQDLFSVYLSSNDDSGSVLLGGIDSSYYTGS LNW  
VPVSVEGYWQITLDSITMDGETIACSGGCQAI VDTGTSLLTGPTSAIANIQSDIGASENS  
DGEMVISCSSIDSLPDI VFTINGVQYPLSPSAYILQDDSDCTS GFEGMDVPTSSGELWIL  
GDVFIRQYYTVFDRANKVGLAPVA

>P0C0Y4.2 Alt a 8; mannitol dehydrogenase [*Alternaria alternata*]

MPISVPQATELKD L FSLKGVVIVTGASGPTGIGTEAARGCAEYGADLAITYNSRAEGAE  
KNAKEMSEKYGVKVKAYKQVNEYAQCEKLVQDVIKDFGKVDFIANAGKTADNGILDAT  
VEQWNEVIQTDLTGTFNCARAVGLHFRERKTGSLVITSSMSGHIANFPQE QASYNVAKAG  
CIHLAKSLANEWRDFARVNSISPGYIDTGLSDFVPQDIQKLW HSMIPMGRDAKATEL KGA  
YVYFASDASSYCTGSDLLIDGGYCVR

>ABL09307.1 Aca s 13; fatty acid-binding protein [*Acarus siro*]

MVQINGSYKLEKSDNFDAFLKELGLNFVTRNLAKSATPTVEVSVNGDSYTIKTASTLKNT  
EISFKLGEFEFEARADGKT VTKVWNKESDTK FVQVQGDKEVTIVREFSDEGLTVTATVN  
GVTSVRFYKRQ

>ABL09312.1 amylase-like [*Acarus siro*]

MAHLL LAVVAITLALSQSVF GSPYSNPHFTGSR SVITHLMQWK FDDIAAECERFLGPKG  
YGGIQLSPVNEHAVLGNRPWYELYQPVGYKI QSRSGNEEQFKGMVQRCNKVGVRIYVDIV  
MNHMSGAQEGHGNCWFKLQWHHDVSRCSLLVPNDFHG RESCHTDNMDIKNYDNPEEARNC  
RLSGLRDLKQSSEYVRQKQADFLNHLIDLGVAGSRSDASKHMWPGDLEAIYGLHNLNTA  
YFPANSRPF IYHEVIYYGGDIKSSDYTKLGRAIEFH FYRDIANVRRHNQLKTVKNFGQ  
PWGMVPSDDALVMVDS HDLQRFHGTQVGVNIN YFESRLLKVATAFMLAWPYGVPRVMSSY  
HWDQKIEDGKDKNDWIGPPSDGSGNILSVTPQ PDDTCNKEWICEHRWRQIYNMVHFRNVA  
GNEAVSHWWDNGDYQIAFGRGSKAFIAINLQDQGGLNRKLATGLPQGT YCDLVTGNLAGG  
KCTGGT VTVDGSGNADINI AKTAEDPFVAIHVEAKLH

>ABL77410.1 Ani s 7; unknown function [*Anisakis simplex*]

AKYGSQFCKNLLANCL SSGATLPMQSPWQIP PVSSCITSGMAKGDH NKKDV MATCIQ  
RYGADFCNMVGS CAALTDVTLTSYIGSVLPQVIVDCMTSEMSSPSIMWQC VQKYGTEF  
CKKLLQDCSASTGASLSPQAPWLIPSVIAECMAKGMVNGGRQADDTMAICIQKYGIKFCN  
IIGAACSVLTQVPFFPQLPGTVQQLPSEL RACVRSETQKPNVMTKCV EKYGTEFCSSLLQ

SCSASTGAILPLREPWKIPHPADIADCMYAGMNPESKEDRGGIMSKCIRRYGDFDFCKKML  
CSALTSVQHDSRNTNYASLPQVLKDCMASEMDSVPMFECVQRYGTFCKGLLETCTEKT  
RASLSPQAPWLIPTAIAQCMRQGMNQDEKKTLMSLCVRRYGADYCNLAAACSVLTNLP  
FFPQTPPSEQNLPPMMHKCLKSEMENPGIMSTCVQRYGTQFCKNLLNSCTASTGMHLPYD  
APWKIPEPIAACMAQGMNGGDHKKPKEDAMARCIRKYGVTYCNMLASCSVLTNVNYDPSG  
GQMPGILSECVTAETDEPSAMCQCVQYKGFTEFCKKRLASCIASCTGMNLPATTPWKLPPPV  
ARCMQHGSPNDNRGQGSNDVMSQCIARYGAEFCQRLARFCYAMNSLQYPGETFDPQQQ  
TPTQVARCMKSEMDSPSVMWHCVQKYGQEFCKNLAATCSTETNTPLPQQDPWRLPQPIIA  
CMLGKMNNPNPTSKPQSVMSQCTARYGDDFCLSLGKACAELNVPSSMISLSAQQLPQPV  
SSCMKAEMNNPSALWQCIQYQYGFIEFCKKLRDACSAMTGASLSTTTPWILPQPVSNMRNE  
MNNPSAMWLCIQKYGIEFCNRLASACAMIKKVTMPTVTINLPEIIASCVASENSQAMCYA  
RKGPEQCKTEENICRNPNNPPGSPLTIPETECMKSQVAMATCQKKFGSECVLQQECVAG  
TGAPPVTIGARGAFMLATALRSCIFNGGVIGSCVLYHPPSQCDQWVQQCATALQTSAGVT  
VAGGYRQLSPPMAVCVASQDLMTRCMTRLGQGTCCQAVKNCKRRFNTSSRLPGRLWLSL  
SELINCLYRPVNRASN

>ABL84749.1 Der f 1; cysteine protease [Dermatophagoides farinae]  
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPELDLRLSLRT  
ATPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY  
GYFQAGNNLMMIEQYPYVVM

>ABL84750.1 Der f 1; cysteine protease [Dermatophagoides farinae]  
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPELDLRLSLRT  
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY  
GYFQAGNNLMMIEQYPYVVM

>ABL84751.1 Der f 1; cysteine protease [Dermatophagoides farinae]  
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPELDLRLSLRT  
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY  
GYFQAGNNLMMIEQYPYVVM

>ABL89183.1 tropomyosin [Portunus sanguinolentus]  
MDAIKKKMQAMKLEKDNAMDRAADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEYKSITDELQDTFSELSGY

>ABM53030.1 profilin [Caryota mitis]  
MSWQAYVDHHLMCEIDGQRLAAAAILGHDGSVWAQSETFPQVKPEEISGIMNDFAEPNL  
APTGLYLGN TKYMIQGEPEGAVIRGKKGSGGVTIKKTNMALIIGIYDEPMPGQCNIIE  
RLGDYLIDQGF

>ABM53751.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]  
MTIEGKYKLEKSENFDAFLDKLGVGFMVKTAAKTLKPTLEVEVAGDTYTLRSLSTFKNTE  
IKFKLGEEFEEDRADGKKVKTVVNKEGDNKLVQTFQGDKEVKIIREFNGDDVVVTASVDG  
VTSVRSYKRI

>BAF43534.1 Ani s 5; SXP/RAL-2 family protein [Anisakis simplex]  
MKTLLIVAALFCTIGMALADDTPPPPFLAGAPQDVVKAFFELLKKDETKTDPEIEKDLDA  
WVDTLGGDYKAKFETFKKEMKAKEAELAKAHEEAVAKMTPEAKKADAELSKIAEDDSLNG  
IQKAQKIQAIYKTLQPQSVKDELEKGIGPAVPQ

>ABM60783.1 Pen c 32; pectate lyase [Penicillium citrinum]  
VGDVATGYASENGGTTGGSGGTTTTVSSYAAFTEAVSGDDAKVVFVSGKISKADQARVG  
SNTSIIIGKDSNAILSGFGVLVKEASNVIIRNLGVEKVLADNGDAIGIQKSNVWVDHCDV  
SSDRDHDKDYDGLIDITHAADYVTVSNTSIHDHWKACLIGHSDSNGDEDKGHLHVTLNN  
NYWYNINSRGPFSFRFGTGHVYNSYLLDMSDGINTRQGAQHLVESNTFSGSKKPLYSTDDG  
YAVANDNDFGDGENNAEKGLTSPVSYDLVGSVKVDAVVGTAGQTLTF

>P80740.2 Ole e 5; superoxide dismutase, partial [Olea europaea]  
MVKAVTVLNSSEGGPHGIVYFAQEGDGPTTV

>P82977.2 Tri a 39; serine protease inhibitor [Triticum aestivum]  
MSSVVKPLGGNTDTGDHNNQKTEWPELVGKSVVEAKKVLQDKSEAQIVVLPVGTIVTM  
EYRIDRVRLFVDSLKIAQVPRVG

>Q45W86 Ara h 11; oleosin [Arachis hypogaea]  
MAEALYYGGRQRQDQPRSTQLVKATTAVVAGGSLILLAGLVLAATVIGLTTITPLFVIFS  
PVLVPAVITVALLGLGLASGGFGVAAITVLTWIIYRYVTGKHPPGANQLDTARHKLMSKA  
REIKDYGQQQTSGAQAS

>BAF45320.1 Cry j 2; polygalacturonase, partial [Cryptomeria japonica]  
MAMKLIAPMAFLAMQLIIMAAEDQSAQIMLDSVVEKYLRSNRSLRRVEHSRHDAINIFN  
VEKYG

>ABN03965.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYGMQGNLPSVSEVIALYK  
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
RFRYIAVGNIEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILDLTVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYADNPRDISLPYALFTSPSVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFAAATFDNGRTYLSNLI  
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHFGLFFPDKRPKYNLNFGAEKNWDIS  
TEHDATILFLKSDM

>ABN03966.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAISSSTSGTSSSLPSRTTVMLLLIFFTASVGITDAQVGVGYGMQGNLPPVSEVIALYK  
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWWQKNVRGFWSSV  
RFRYIAVGNIEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILDLTVRNSY  
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFAAATFDNGRTYLSNLI  
QHVKRGTPKRPKRAIETYL FAMFDENKKQPEVEKHFGLFFPNKWQKYNLNFGAEKNWDIS  
TEHNATILFLKSDM

>ABN09653.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAISSSTSGTSSSLPSRTTVMLLLIFFTASIGITDAQVGVGYGMQGNLPSVSEVIALYK  
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
RFRYIAVGNIEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILDLTVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLTNIYPYFTYAYNPRDISLPYALFTSPSVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFAAATFDNGRTYLSNLI  
QHVKGGTPKRPNRAIETYL FATFDENKKQPEVEKHFGLFFPDKRPKYNLNFGAEKNWDIS  
TEHNATILFLKSDM

>ABN09654.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYGMQGNLPSVSEVIALYK  
KSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
RFRYIAVGNIEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILDLTVGNSY

PPSAGAFRDDVRSYLDPIIGFLSSSXSPLLANIYPYFTYAYNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFATFDNGRITYLSNLI  
QHVKGGTPKRPNRAIETYLFAMFDENKKQPEVEKHFGLFFPDKRPKYNLNFSAEKNWDIS  
TEHNATILFLKSDM

>ABN09655.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]  
MAISSSTSGTSSSLPSRTTVMLLLFFFTASVGITDAQVGVGYMGGNNLPPVSEVIALYK  
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWVQKNVRGFWSV  
RFRYIAVGNIEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILTLVGNSY  
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAFATFDNGRITYLSNLI  
QHVKRGTTPKRPKRAIETYLFAMFDENKKQPEVEKHFGLFFPNKWQKYNLNFSAEKNWDIS  
TEHNATILFLKSDM

>ABN14313.1 Der f 2; NPC2-like [*Dermatophagoides farinae*]  
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA  
NQNTKTAKIEIKANINGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTNVVKIAPKSEN  
VVVTVKLIGDNGVLACAIATHGKIRD

>BAF46896.1 tropomyosin [*Balanus rostratus*]  
MDAIKKKMQAMKLEKENALDKAEQLEQKLRDVEETKAKAEEDLTLLQKKYTNLENEFDQV  
NEQYNEGVTKLEVSEKRVTEAEDEIKGYTRRIQLLEDDLERTPVKLEATFKLEDATKTA  
DESERGRKVLERSIADDDRIDALEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERSE  
TRLEAAEAKITELSEELAVVGNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA  
EAERVVNLKQKEVDRLDEDELLAEKEKYKASDELDTFAELAGM

>P08819.2 serine carboxypeptidase [*Triticum aestivum*]  
VEPSGHAADRIARLPQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLN  
GGPGCSSVAYGASEELGAFRVKPRGAGLVLENYRWKVANVLF LDSPAGVGF SYTNTSSD  
IYTSNGNRTAHD SYAFLAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVIN  
LKGFMVGNGLIDDYHDYVGTFFFWWNHGVSDDTYRRLKEACLHDSFIHPSACDAATDV  
ATAEQGNIDMYSLYTPVCNITSSSSSSSSSSLSQRRSRGRYPWLTGSYDPCTERYSTAYY  
NRRDVQMALHANVTGAMNYTWCSDTINTHWHADAPRSMPLIYRELIAAGLRIWVFSGDT  
DAVVPLTATRYSIGALGLPTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRP  
RQALVLFQYFLQGKMPGQTKNAT

>BAF47263.1 tropomyosin [*Marsupenaeus japonicus*]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANIQLVEKDKALSNAEGEVAALNRRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKLTLNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY

>BAF47265.1 tropomyosin [*Paralithodes camtschaticus*]  
MDAIKKKMQAMKLEKDNAMDKADTLEQQNKEANNRAEKAEVHGLQKRMQQLENDLDQV  
QESLLKANTQLEDKDKALSNAEGEVAALNRRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKLTLNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY

>BAF47266.1 tropomyosin [*Paralithodes camtschaticus*]  
MDAIKKKMQAMKLEKDNAMDKADTLEQQNKEANNRAEKTEEEIRLTQKKMQQVENELDVA  
QEQLSLANTKLEEKALQNAEGEVAALNRRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKLTLNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKNIADMDQAFSELSGF

>BAF47268.1 tropomyosin [*Erimacrus isenbeckii*]

MDAIKKKMQAMKLEKDNAMDRAHTLEQQNKEANLRAEKTEEEIRATQKKMQQIENELDHA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLLEDELVNEKEKYKSITDELDTFSELSGY  
>BAF47269.1 tropomyosin [Erimacrus isenbeckii]  
MDAIKKKMQAMKLEKDNAMDRAHTLEQQNKEANLRAEKTEEEIRATQKKMQQIENELDHA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLLEDELVNEKEKYKNIADMDQAFSELSGF  
>AAM09530.3 Equ c 4; latherin [Equus caballus]  
MLKVSCLFVLLCGLLVPSSAQIPPEVSSQITDALTQGLLDGNFLSLLNAINLEGLLNTI  
LDQVTGLLNILVGPLLGPSDAEIKLQDTRLLQLSLEFSPDSKGIDIWIPLELSVYLKLLI  
LEPLTLVVRTDIRVQLRLESDDEDGKYRLAFGHCSLLPRAIELQSGNPLSLPVNAVLTGIE  
NALGNFITEDLGAGLCPTLNSLVSNDLQLVNNLNLILDRANVDLSV  
>AB036677.1 Pis v 3; 7S globulin, vicilin-like [Pistacia vera]  
KTDPELKQCKHQCKVQRQYDEEQKEQCAKGCYKKEKKGREQEEEEEEWGSGRGRGDE  
FSTHEPGEKRLSQCMKQCEQDGGQQQLCRFRQCQEKYKKERREHSYSRDEEEEEEGDEE  
QEEEDENPYVFEDEHFTTRVKTEQGGVVLPKFTKRSKLLRGLKRYRLAFLVANPQAFV  
PNHMDADSIFFVSWGRGTITKIRENKRESMNVKQGDIIIRIRAGTPFYIVNTDENEKLYIV  
KLLQPVNLPGHYEVFHGPGGENPESFYRAFSREVLAAALKTPRDKLEKLFQDEGAIVK  
ASKEQIRAMSRRGEGPSIWPFTGKSTGTFLFKKDPQSNNYQQLFESEFKDYPPQLQELD  
IMVSYVNITKGGMSGPFYNSRATKIAIIVVSGEGRLEIACPHLSSSKNSGQEKSGPSYKLL  
SSSIRTDSVFVVPAGHPFVTVASGNQNLIELCFEVNAEGNIRYTLAGKKNIIIEVMEKEAK  
ELAFKTKGEEVDKVFQKQDEEFFQGPKWRQHQQGRADE  
>CAM54066.1 Asp f 34; PhiA cell wall protein [Aspergillus fumigatus]  
MQIKSFVLAASAAATASAAACQAPTNYKYGIVAIHSGSAVQYQPFSAKSSIFAGLNSQN  
ASCDRPDEKSATFYIQDGSLYLYAASATPQEIFVDRSGMGQKIGYTTGAQPAPRNSERQ  
GWAIDSQNLHQFGKDLIACPNSIDGAWSIWADAGVANPAGNTDCVGIARVEDVTNPNS  
CVYTQ  
>AB071783.1 tropomyosin [Eriocheir sinensis]  
MDAIKKKMQAMKLEKDNAMDRAHTLEQQNKEANNRAEKTEEEIRATQKKMQQVENELDQA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLLEDELVNEKEKYKSITDELDTFSELSGY  
>BAF51970.1 thaumatin-like [Cryptomeria japonica]  
MAKVSDLALLLVAGMAISLYIQTGAVKFDIKNQCGYTVWAAGLPGGGQQLTQGQWTWVN  
LAAGTQSARFWGRTGCSFDASGKGTCTGDCGGQLSCTVSGAVPATLAEYTSQSDQDYVDV  
SLVDGFNIPLSINPTNAQCTAPACKADVNAVCPAELKVDGGCKSACAAFTDQYCCTGT  
ANSCPATNYSMIFKNQCPQAYSYPKDDTATFACPSGTDYSIVFCP  
>AB084963.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIFCAIVMAVSVSGFIVDVTEDKWRNAFDRMLMEEFGEKIDQIEHGLLMLSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK  
DLAELAKKVKAVKSDD  
>AB084964.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIFCAIVMAVSVSGFIVDVTEDKWRNAFDRMLMEEFEEKMDQIEHGLLMLSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK  
DLAELAKKVKAVKSDD

>AB084966.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIIFCAIVMAVSVSGFIVDVDTEDKWRNAFDRMLMEEFEEKIDQIEHGLMLSEQYKE  
SEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK  
DLAELAKKVKAVKSDD

>AB084967.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIIFCAIVMAVSVSGFIVDVDTEDKWRNAFDRMLMEEFEEKIDQIEHGLMLSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK  
DLAELAKKVKAVKSDD

>AB084968.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIIFCAIVMAVSVSGFIVDVDTEDKWRNAFDRMLMEEFEEKMDQIEHGLMLSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VPTIEILVK  
DLAELAKKVKAVKSDD

>AB084969.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIIFCAIVMAVSVSGFIVDVDTEDKWRGAFDRMLMEEFEEKMDQIEHGLMLSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK  
DLAELAKKVKAVKSDD

>AB093594.1 2S albumin, conglutin [Fagopyrum tataricum]  
MKLFLILAAASLLIVASHADSQMRSKCRKQMRMMEPQLEQCEGYMTDMMDADSMRGQEC  
RSEESCMRGCCMAMKEMDDECMCEWMKMMVQQQRGEMGEEDMRMVMRKMQLPNKCGMGH  
MRCHMGMGTRVYE

>ABP04043.1 Bla g 4; lipocalin [Blattella germanica]  
AVLALCASDTLAMEDCFRHESLVPNLDYERFRGSWIIAAGTSEALTQYKCWIDRFSYDDA  
LYSLYTD SKGNKTAIRGR TKFEGNKFTIDYNDKGKAFSAPYSVLATDYDNYAIVEGCPA  
AANGHVIYVQLRLTWRRFHPKLGDKEMI QHYTLDQVNQHKAIEEDLKHFNLYEDLHST  
CH

>ABP04044.1 Bla g 5; glutathione S-transferase [Blattella germanica]  
YKLTYPVKALGEPPIRFLLSYGEKDFEDYRFQEGDWPCLKPSMPFGKTPVLEIDGKQTHQ  
SVAISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDADENSKQKKWDPLKK  
ETIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALRE  
KVLGLPAIKAWVAKRPPTDL

>ABP35603.1 Bla g 2; inactive aspartic protease [Blattella germanica]  
MIGLKIVTVLFAVATITHAAELQRVPLYKLVHVFINTQYAGITKIGNQNFLT VFDSTSCN  
VVVASQECVGGACVCPNLQKYEKLPYRISDGNVQVKFFDTGSAVGRGIEDSLTIFNLTT  
SQQDIVLADELSQEV CILSADGVVGI AAPGCPNALKGKTVLENFVEENLIAPVFSIHAR  
FQDGEHFGEIIFGGSDWKYVDGEFTYVPLVGDDSWKFRLDGVKIGDTTVAPAGTQAIIDT  
SKAIIVGPKAYVNPINEAIGCVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNFISSQY  
YIQQNGNLCYSGFQPCGHS DHFFIGDFFVDHYHYSEFNWENKAMGFGRSVESV

>ABP58627.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGT VYFTQEGDGPTTVTGNLSGLK PGLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGTPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABP58632.1 Ole e 1; Ole e 1-like [Olea europaea]  
PPVSQFHIQGGIYCDTCRSR FITELSEFIPGASVRLQCREKENG DITFTEIGYTRAEGLY  
SMLVERD HKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTVNPLGFFKK  
EALPKCAQVYNKLGMYPPNM

>ABP58633.1 Ole e 1; Ole e 1-like [Olea europaea]  
PPVSQFHIQGGVYCDTCRAGFITELSEFIPGASVRLQCREKKNGDITFTEVGYTRAEGLY  
SMLVERD HKNEFCEITLISSGRKDCNEIPIEGWAKPSLKFILNTVNGTTRTINPLGFYKK  
EALPKCAQVYNKLDMYPPNM

>ABP58635.1 Ole e 1; Ole e 1-like [Olea europaea]

PPVSQFHIQGQVYCDTCRARFITELSEFIPGASVRLQCRDGENGSITFTEVGSTRAEGLY  
SMLIERDHKDEFCEITLISSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTVNPLGFFKK  
EALPKCPQVFNKLGMYPPDM  
>ABP58636.1 Ole e 1; Ole e 1-like [Olea europaea]  
PPVSQFHIQGQVYCDTCRAGFITELSEFIPGASVRLQCREKKNGDITFTEVGYTRAEGLY  
SMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTINPLGFYKK  
EALPKCAQVYNKLGMYPPNM  
>ABP58637.1 Ole e 1; Ole e 1-like [Olea europaea]  
PPVSQFHVQGGIYCDTCRAGFIAELSEFILGAGVRLQCRDSKKNITFTEVGYTRAEGLY  
SMLIERDHKNEFCEVNSLSSSRKDCDEIPIEGWVRPSLRFLNNTVNGTTCTIKPLGFFKN  
KALPKCPQVFNKLGMYPPDL  
>P80273.2 lipid transfer protein, partial [Vitis vinifera]  
LSCGDVATQMASCINYLRGAGPLPAACCVGNLKNLSATTTQDRRTACKCLISASKTISG  
VNFGLAAGLPAKCGVSIPYKISPSTNCDQVN  
>ABP97433.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis  
hypogaea]  
MGVHTFEEESTSPVPPAKLFKATVVDGDELTPKLIPAIQSIEIVEGNGGPGTVKKVTAVE  
DGKTSYVLHKIDAIDEATYTYDYTISGGTGFQEILEKVSFKTKLEAADGGGSIKVSVTFH  
TKGDAPLPDEVHQDVQKKSQGFKAIEGYVLSN  
>ABQ10638.1 Fag e 3; 7S globulin, vicilin-like, partial [Fagopyrum esculentum]  
GDYPFEPRRQIEHCRQRCQDRSQGFRETRELETCEKRAFDDDEPSKEVDSYTTDTRSRD  
PQQEFRQCRHRCQTQEEGGRQQRKCEQRCEKQLERQQGYDDEEFGQGRSNIGAPVRNYDD  
CTEMCGGSPLCALFCE  
>ABQ42566.1 Act d 2; thaumatin-like [Actinidia deliciosa]  
ATFNIINNCPTVWAAAVPGGGKRLDRGQNWIIINPSAGTKGARVWPRTGCNFDGAGRGKC  
QTGDCNGLLQCAFGQPNTLAEYALNQFNLDFFDISLVDGFNVAMEFSPTSGGCTRGI  
KCTADINGQCPNELRAPGGCNPCTVFKTDQFCCNSGNCGLTNFSKFFKDRCPDAYSYPK  
DDQTSTFTCPAGTNYKVVFCP  
>CAM56785.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]  
MAFAGILADADCAA AVKACEAAESFSYKAFFAKGLSGKSADDIKKAFFVIDQDKSGFIE  
EDELKFLQVFKAGARALDAETKAFKAGDSGDGAIGVEEWA VLVKA  
>CAM56786.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]  
MAFAGILNDADITAALAACKAEGSFDHKAFFTKVGLAAKSSADIKKVFEEIDQDKSDFVE  
EDELKFLQNF SAGARALSDAETKVFLKAGDSGDGKIGVDEFGAMIKA  
>ABQ59329.1 Cla c 9; vacuolar serine protease [Cladosporium cladosporioides]  
DQEVHVLKSESEVEKNAPWGLARISHRDSLSFGTFNKLYTEDGGEGVDVYVVDGTGTVND  
HVD FEGRASWGKTIPQGDAD EDGNGHGTHCSGT VAGKKYGVAKKAHV KAVKVLRSNGSGS  
MSDVVKGVEYAAESHLEQVSI AKKGKRKGFKGSTANMSLGGGKSPILDKAVNA AVDAGIH  
FAVAAGNDNADSCNYS PAAAENAVTVGASTLS DERAYFSNYGKCNDIFAPGLNIQSTWIG  
SKYAVNTISGTS MASPHVAGLLAYLLSLQPAKDSAF AVADISP KKLKANLISIATV GALT  
DVPSNTANILAWNGGGESNYS AIVEKGGYKAAVRPTMLEEIESEAKVASKKVYSEGDELA  
KKVAELTEKIEDLISGDLKDMFRDLKRE  
>ABQ96644.1 Tyr p 10; tropomyosin [Tyrophagus putrescentiae]  
MEAIKKKMQAMKLEKDNAIDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLGNDLDQV  
QESLLKANIQLVEKDRALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERM RKVLENRSL SDEKRM DALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE  
FAERSVQKLQKEVDRL EDELVNEKEYKSITDEL DQTFSELTGY  
>CAK50834.1 Art v 2; pathogenesis related protein, PR-1 [Artemisia vulgaris]  
MGHLGNFWLVLAISFAILHLSHAHETYGEPGNT PDDYVHAHNCIRRV LGMKPLCWDEIGK

VAQAWAETRTPCSLIHSDRCGENMAQGAINGSMVQLWLDERLDYDYNENKCIKMGHY  
TQIVWANSERVGCGRALCSNGWAYIIVCNYPGPNVVGQKPY  
>ABR21771.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
EERQEERERRREPCREREQEQQPHGRREEEEEEEEWQPRRLRPQSRKEEREQEQQSSS  
SSRKQSGYERRQYHERREQRDEKEKEQDSRSDSRRQRNPYHFSSERFQTRYRNRNGQIRV  
LERFDQRTNRLLENLQNYRIVEFQSNPNTLILPKHSDADYILVVLNGRATITIVNPKRQA  
YNLEYGDALRLPAGTTSYILNPDDNQNLRVVLAIPINNPNSNFYDFYPSSTKDQQSYFSG  
FSKNTLEATFNTRYEEIQRILLGNEDEQEDEEQRRGQEQSYQDEGVIVRVSKEIQELRK  
HAQSSSRKGPSESGPFNLSNESIYSNKFGNFYEITPERNPQVQDLDISLTFTEINEGA  
LLLPHYNSKAIFIVVDEGEGNYELVGIRDQQRQQDEQEEEEEEVRRYSARLSEGDFVI  
PAGYPISVNASSNLRLLGFGINANENQRNFLAGSEDNVISQLDREVKELTFPGSAQDVER  
LIKNQQQSYFANAQPQQKQREKEGRRRSLISSILSTLY  
>ABR21772.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MAKMRVRLPMLILLGGVFLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQEE  
QEREHRREEKHGEPGRSRSQSEESQEEHERRREHREEREQEQQPRPQRRQEEEEEE  
WQPRRQRPSRREEREEREQEQQSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDSR  
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNQRTNRLLENLQNYRIIEFQSKPNTLILPKH  
SDADFILVVLNGRATITIVNPKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA  
IPINNPGLKYDFYPSTTKDQQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENEKQR  
RGQEQSHQDEGVIVRVSQKQIQELRKHAQSSSGEGKPSSESGPFNLSNKPIYSNKFGNFY  
EITPDINPQFQDLNISLTFTEINELWLTKEKEIMN  
>ABR29644.1 Pis v 4; superoxide dismutase [Pistacia vera]  
MALLSYVTRKTLTESLRLGLKSHVRGLQFTFLPDLPEYEGALEPAISSEIMQLHHQHHQ  
TYITNYNKALEQLDQAINKGDAVVKLQSAIKFNGGGHINHSIFWKNLTPVSEGGGEP  
HGSLGWAIDTNFGSMEALIQRMNAGAALQGGVWVWGLDKESKLLVVETTANQDPLVTK  
GPSLVPLLGIDVWEHAYYLQYKNVRPDYLNKIWKVINWKYAGELYQKECP  
>ABS12233.1 Scy p 1; tropomyosin [Scylla serrata]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY  
>ABS12234.1 tropomyosin [Portunus trituberculatus]  
MDAIKKKMQAMKLEKDNAMDRANTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA  
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY  
>ABS29033.1 Alt a 1-like [Stemphylium sp.]  
LAAAAPFEARQADASCPVSTQGDYVWKISEFSGRKPEGTYYNLSLFSNIKATNKGTLDFTC  
SAQADKLEDDKFYSCGENSFMSFAFQSDRNGLLFRQDVSDEITYVATATLPNYCHAGNG  
PKDFVCQGVSDAYFTLV  
>ABS58503.1 Tri a 39; serine protease inhibitor [Triticum aestivum]  
MSPVVKKPEGGNTDTGDHNNQKTEWPELVGKSVVEAKKVIMQDKSEAQIVVLPVGTIVTM  
EYRIDRVRLFVDSLKDIAQVPRVG  
>BAF75681.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAVVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAEEEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNQGGQS  
>BAF75704.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]

MRVLFFVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75705.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVADSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQATEEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75706.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVPLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75707.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAYAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75708.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFRDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75709.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FANDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTATADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75710.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNNHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75711.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAESTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS  
>BAF75712.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]  
MKVLFVVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ  
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA  
AKHDKIVQTFESLPPAVKEELDKLNNQQGQS  
>ABU42022.1 Pis v 2; 11S globulin, cupin [Pistacia vera]  
MGYSSLLSFLGFLLLFHCSFAQIEQVNSQQRQQQRFQTQCQIQNLNALEPKRRIESE  
AGVTEFWQNEEQQLQCANVAVFRHTIQSRGLLVPSYNNAPELVYVVQGSIGHAVFPGCP  
ETFQEESQSQRSRSRSRSRSRSQSGEQHQKVRHIREGDIIALPAGVAHWIYNNQSKLVL  
VALADVGENSEQLDQYLKRFVLGGSPQQEIQGGGQSWQSRSRSGQQSNNILSAFDEEI  
LAQSLNIDTQLVKKLQREEKQRGIIVRVKEDLQVLSPQRQEKEYSDNGLEETFCTMTLKL  
NINDPSRADVYNPRGGRVTSINALNLPILRFLQLSVEKGVLYQNAIMAPHWNMNAHSIVY  
ITRGNRMQIVSENGESVFDEEIREGQLVVVPQNFVAVKRASSDGFVWVSKTNGLAKIS  
QLAGRISVMRGLPLDVIQNSFDISREDAWNLKESRSEMTIFAPGSRQRQRN  
>ABU49605.1 Der f 1; cysteine protease [Dermatophagoides farinae]  
MKFVLAIVSLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN  
KGAINHLSLSDLEDFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRSRT  
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE  
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHTAIAVI  
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY

GYFQAGNNLMMIEQYPYVWIM

>ABU53681.1 tropomyosin [*Sinonovacula constricta*]  
MDAIKKKMQAMKIEKENALDKSEQLNKLKEIEDVKVKEEDLTSLQKKYTNQENEYDKV  
NEQFNSTVKLEASEKRVTECEDEIKGFTRRIQLLEDELERTQQKAEAVLKLEEASKAA  
DESERGRKVLERSIADDDRIDKLEKDVKDSKYLAEEADRKYDEAARKLAITEVDLERAE  
TRLEAAESKITELSEELQVVGNNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA  
EAERVVKNLQKEVDRLDELELLQEKEKYKQISDELDQTFAELAGM

>BAF76430.1 tropomyosin [*Euphausia superba*]  
MDAIKKKMQAMKMEKDSAMDRSDALEAQNKETNAKADKADDEVHNLQKRLQTLLENDLDQV  
SEALLKANTQLVEKDKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSMLEERMDALESQKLEARLLAEADRKYDEVARKLAMVEADLERAE  
ERAEGENKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKHLTHKLTAEARAE  
FAERSVQKLQKEVDRLDELELVNEKEKYKGITDELDTFNFELSGY

>BAF76431.1 tropomyosin [*Euphausia pacifica*]  
MDAIKKKMQAMKMEKDSAMDRADALEAQNKETNARAEKADDEVHNLQKRLQTLLENDLDQV  
SEALLKANTQLVEKDKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLLEERMDALENQLKLEARLLAEADRKYDEVARKLAMVEADLERAE  
ERAEGENKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKHLTHKLTAEARAE  
FAERSVQKLQKEVDRLDELELVNEKEKYKGITDELDTFNFELSGY

>ABU95411.1 Sin a 3; lipid transfer protein [*Sinapis alba*]  
ALSCGTVNSNLAACIGYLTQNAPLPKGCCTGVTNLNMARTTPDRQQACRCLVGAANSFP  
SLNAARAAALPKACGVNIPYKISKSTNCNSVR

>ABU95412.1 Sin a 4; profilin [*Sinapis alba*]  
MSWQTYVDDHLMCDVEGNRLTAAAILGQDGSVWAQSANFPQLKPEEIKGINNDFAEPTGL  
APTGLFIGGTYMVIQGEPAVIRGKKGAGGVTIKKTQAFVFGIYEEMTPGQCNMVVE  
RLGDYLIEQGL

>ABU97466.1 Blo t 10; tropomyosin [*Blomia tropicalis*]  
MEAIKKKMQAMKLEKDNAIDRAEIAEQSRDANLRAEKSEEEVRALQKKIQQIENELDQV  
QESLTQANTKLEEKESLQTAEGDVAALNRRIQLIEEDLERSEERLKVATAKLEEASHSA  
DESERMKMLEHRSITDEERMDGLESQKLEARMMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGETKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQIRMMTGKLEAEARAE  
FAERSVRKLQKEVDRLDELELVHEKEKYKSISDELDQTFAEELTGY

>ABU97470.1 Der f 20; arginine kinase [*Dermatophagoides farinae*]  
MVDQATLSKLEAGFQKLQNAQDCHSLLKKYLTRDVLQKTKKTDMGATLLDVIQSGVEN  
LDSGVGIYAPDAQSYKTFEALFDPIIDDYHKGFKPTDKHPQDFGNIEHFVNVDPKNEYV  
ISTRVRCGRSLKGYFPNPLTEAQYKEMETKVKGQLATFEGELKGTYYPLLGMKATQQK  
LIDDHFLFKEGDRFLQAANACRYWPVGRGIFHNDKKTFLMWNNEEDHLRIISMQKGGDLK  
EVFGRLLVAVKHIEQKIPFSRDDRLGYLTFCTNLGTTIRASVHIKLPKLAADRKKLEEV  
AARYNLQVRGTAGEHTESVGGIYDISNKRMMGLTEYQAVKEMQDGIIELIKMEKSL

>ABU97472.1 Gly m 3; profilin [*Glycine max*]  
MSWQAYVDDHLLCEIEGNHLTHAAIIGQDGSVWAQSTNFPQFKPEEITAINNDFNEPGSL  
APTGLYIGGTYMVIQGEPAVIRGKKKGGVTVKKTGAALIIGIYDEPMPGQCNMVVE  
RLGDYLIDQGL

>ABU97479.1 Tyr p 10; tropomyosin [*Tyrophagus putrescentiae*]  
MEAIKKKMQAMKLEKDNAIDRAEIAEQKARDANLKSEKTEEEVRALQKKIQQIENELDQV  
QENLTQATTKLEEKEKALQTAADVAALNRRIQLIEEDLERSEERLKVATAKLEEASHSA  
DESERMKMLEHRSIPDEERMDGLESQKLEARLMAEDADRKYDEVARKLGMVEAHLERAE  
ERAQLGIXIAKLERTARLRHT

>ABU97480.1 Tyr p 13; fatty acid-binding protein [*Tyrophagus putrescentiae*]  
MVQLNGSYKLEKSDNFDAFLKELGVNFVTRNLAKSASPTVEIVDGDSTYIKTSSTLKNS

EIKFKLGEEFEEDRADGKKVQTSVTKEGDNKLVQVQKGDKPVTIVREFSEGLTVTATVN  
GATSVRFYKRQ  
>ABV55106.1 Ani s 9; unknown function [Anisakis simplex]  
MKLCILAVAVFVAVSAQGGPPPLPPFVANAPPVQAEFRQLANGAPDKTEAEIEAQIEQW  
VASKGGAVQAEFNKFKQMLEQGGKARAEAAHQASLTRLSPAAKAADARLSAIASNRALKVG  
EKQRQLAAAFQALDPAVKAELQKEMQG  
>ABV66255.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
TNACSSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQ  
ELVDCASQHNCHGDTIPRGI EYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQI  
YPQNVNKIREALAQTHSAIAV IIGIKDLDAFRHYDGR TIIQRDNGYQPNYHAVNIVGYSN  
AQGVYDWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVIL  
>1A9V\_A Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
SQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA  
IATHAKIRD  
>1CQA\_A Bet v 2; profilin [Betula pendula]  
MSWQTYVDEHLMCDIDGQGEELAASAVGHGDSVWAQSSSFQFKPQEITGIMKDFEEPG  
HLAPTGLHLGGIKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEPPVTPGQCNMV  
VERLGDYLIDQGL  
>ABW17159.1 Ara h 7; 2S albumin, conglutin [Arachis hypogaea]  
MVKLSILVALLGALLVVASATRWDPDRGSRGSRWDAPSRGDDQCQRQLQRANLRPCEEHI  
RQRVEKEQEQEYQYIQRGSRGQRPGESEDEDQEQRCCNELNRFQNNQRCMCQALQQIL  
QNQSFRFQQDRSQLHQMERE LRNL PQNCGFRSPSRCDLSSRTPY  
>ABW23574.1 Vig r 2; 8S globulin, vicilin [Vigna radiata]  
MVRARIPLLLLLGILFLASLSVSGIVHRENIDGAEVSVSRGKNNPFYFNSDRWFHTLFR  
NQFGHLRVLQRFDQRSKQMQLNENYRVVELMSKPNTLLLPHHADADFLVVLNGRAVLT  
VNPDRGDSNILEQGHAAQIPAGTTFFLVNPPDNENLRIIKLAVPVNPHRFQDFFLSSTE  
AQQSYLQGF SKNILEASFDSDIKEISRVLFGEEGQQQQQEQESQQEGVIVELKREQIREL  
TKHAKSSSKSLSSDQPFNLRNQKPIYSNKLGRWFEITPEKNPQLRDLDMFIRSVDMKE  
GSLLLPHYNSKAIVILVINEGKANIELVGQREQKQEQEEQESWEVQRYRAELSEDDVFI  
IPATYPVAINATSNLNFFAFGINAENNRNFLAGEDKNVISEIPTEVLDVTFPASGEKVK  
KLIKQSESQFVDAQPEQQERE EARKGGKGPVY  
>ABW34946.1 Hev b 6; hevein [Hevea brasiliensis]  
MNI FIVVLLCLTGVAIAEQCGRQAGGKLCPNLCCSQWGWCGSTDEYCS PDHNCQSNCKD  
SGEGVGGGSASNVLATYHLYNSQDHGWDLNAASAYCSTWDANKPYSWR SKYGTAF CGPV  
GAHGQPSCGKCLSVTNTGTGAKTTVRIVDQCSNGGLDLVDNVFRQLD TDGKGYERGH LTV  
NYQFVDCGDSFNPLFSVMKSSVIN  
>P15476.2 Sola t 1; patatin [Solanum tuberosum]  
MATTKSFLILFFMILATTSSTCAKLEEMTVLSIDGGGKGIIPAIILEFLEGQLQEVDN  
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAAKDIVPFYFEHGPHIFNYSGSI  
FGPRYDGKYLQLVLEKLG ETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM  
YDICYSIAAAPIYFPPHHFVTHTSNGATYEFNLVDGGVATVGD PALLSLSVATRLAQEDP  
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQLTNAASSYMTD  
YYISTVVFQARHSQNNYLRVQENAL TGTTEMDDASEANMELLVQVGETLLKKPVSKDSPE  
TYEEALKRFAKLLSNRKKLRANKASY  
>ABW86978.1 Car i 4; 11S globulin, cupin [Carya illinoensis]  
MAKPILLSIYLCLIIVALFNGCLAQSGGRQQHKFGQCQLNRLDALEPTNRIEAEAGVIES  
WDPNHQQLQCAGVAVRRTIEPNGLLLPHYSNAPQLVYIARGRGITGVLFPGCPETFEES  
QRQSQQGQRREFQQDRHQKIRHFREGDIIAFPAGVAHWCYNDGSSPVVAIFLLDTHNNAN  
QLDQNP RN FYLAGNP DDEF RPQGGQEQYEQHRRQQHQQR RGEHGEQQRDLGNNVFSGFDA

EFLADAFNVDTEARRLQSENDHRGSIVRVEGRQLQVIRPRWSREEQEHEERKERERERE  
SESERRQSRRGRRDDNGLEETICTLSLRENIGDPSRADIYTEEAGRISTVNSHNLPILRW  
LQLSAERGALYSDALYVPHWNLNAHSVYALRGRAEVQVVDNFGQTVFDDELREGQLLTI  
PQNFAVVKRARDEGFVVSFKTNENAMVSPLAGRTSAIRALPEEVLVNAFQIPREDARRL  
KFNRQESTLVRSSRSRSERRAEV

>ABW86979.1 Car i 4; 11S globulin, cupin [*Carya illinoensis*]  
MAKPILLSIYLCLIIIVALFNGCLAQSGGRQOHKFGQCQLNRLDALEPTNRIEAEAGVIES  
WDPNHQQLQCAGVAVVRRRTIEPNGLLLPHYSNAPQLVYIARGRGITGVLFPGPCPETFEES  
QRQSQQGQRREFQQRHQRIRHFREGDIIAFPAHVAVHCYNDGSSPVVAIFLLDTHNNAN  
QLDQNPFRNFYLAGNPDEFQRPQGGQEQYEQHRRQQHQQRGEHGEQQRDLGNNVFSGFDA  
EFLADAFNVDTEARRLQSENDHRGSIVRVEGRQLQVIRPRWSREEQEHEERKERERERE  
SGSERRQSRRGRRDDNGLEETICTLSLRENIGDPSRADIYTEEAGRISTVNSHNLPILRW  
LQLSAERGALYSDALYVPHWNLNAHSVYALRGRAEVQVVDNFGQTVFDDELREGQLLTI  
PQNFAVVKRARNEGFVVSFKTNENAMVSPLAGRTSAIRALPEEVLVNAFQIPREDARRL  
KFNRQESTLVRSSRSRSERRAEV

>1B6F\_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]  
GVFNYETETTSVIPAARLFKAFILDGDNLFKVPAPQAISVENIEGNGGPGTIKKISFPE  
GFPFKYVKDRVDEVDHTNFKNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY  
HTKGDHEVKAQVQKASKELGETLLRAVESYLLAHSDAYN

>1H20\_A Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [*Prunus avium*]  
GVFTYESEFTSEIPPPRLFKAFVLDADNLVPKIAPQAIKHSEILWGDGGPGTIKKITFGE  
GSQYGYVKKHIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIKSTSHY  
HTKGNVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN

>1W2Q\_A Ara h 6; 2S albumin, conglutin [*Arachis hypogaea*]  
GPMRRERGRQGDSSSCERQVDRVNLKPCEQHIMQRMGEQEQYDSYDIRSTRSSDQQQRC  
CDELNEMENTQGCMEALQQIMENQCDRLQDRQMVQQFKRELMQLPQQCNFRAPQRCDLD  
VSGGRCS

>ABW98943.1 Bos d 9; alphaS1-casein [*Bos taurus*]  
VSAALARPKHPKHQGLPQEVNLNLLRFFVAPFPEVFGKEKVNELSKDIGSESTEDQAM  
EDIKQMEAESISSSEEIVPNSVEQKHQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPN  
SAEERLHSMKEGIHAQQKEPMIGVNQELAYFYPELFRQFYQLDAYPSGAWYYVPLGTQYT  
DAPSFSDIPNPIGSENSEKTTMPLW

>ABW98945.1 Bos d 9; alphaS1-casein, partial [*Bos taurus*]  
FSEVFGKEKVNELSKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQKHQKEDVP  
SERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNQELAYFYP  
ELFRQFYQLDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW

>ABW98953.1 Bos d 9; alphaS1-casein, partial [*Bos taurus*]  
IVPNSVEQKHQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQ  
QKEPMIGVNQELAYFYPELFXQFYQPDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSEN  
SEKTTMPLW

>2JMH\_A Blo t 5; unknown function, group 5/21 mite allergen [*Blomia tropicalis*]  
GSQEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDLENENKSKELQEKIIRE  
LDVVCAMIEGAQGALERELKRTDLNILERFNYYEAQTLKILLKDLKETEQVKVDIQTQ

>ABX26131.1 Ole e 5; superoxide dismutase [*Olea europaea*]  
MVKAVTVLNSSEGVTGTVYFTQEGDPTTGTGNLSGLKPLGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNIAVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26132.1 Ole e 5; superoxide dismutase [*Olea europaea*]  
MVKAVTVLNSSEGVTGTVYFTQEGDGLTTVTGNLSGLKPLGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGTAAINIVDKQIPLTGPHSIIGRAVVVHSDPDDLGRG

CHELSKSTGNAGGRVACGIIGLQG

>ABX26134.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHEQSKSTGNAGGRVACGIIGLQG

>ABX26138.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFDPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26139.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVFNSSEGVTGTVYFTQEGDGLTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGDAGGRVACGIIGLQG

>ABX26140.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTITGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVTCGIIGLQG

>ABX26141.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26143.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDRQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26145.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26147.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX54842.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTITGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX54844.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDATNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX54849.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDITNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX54855.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTGTGNLSGLKPGHGFHVALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAASIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRSGHELSKSTGNAGGRVACGIIGLQG

>ABX54859.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG  
>ABX54862.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDFGRGGHELKSTGNAGGRVACGIIGLQG  
>ABX54864.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVINSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGTAAINIVDKQIPLTGPHSIIGRAVVVHSDPDDLGRG  
GHELKSTGNAGGRVACGIIGLQG  
>ABX54866.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG  
>ABX54869.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHVLSKSTGNAGGRVACGIIGLQG  
>ABX54876.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVLNSSEGVAGTVYFTQKGDGPTTITGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFLPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG  
>ABX54877.1 Ole e 5; superoxide dismutase [Olea europaea]  
MVKAVTVFNSSEGVAGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG  
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS  
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG  
>ABX56711.1 Ara h 9; lipid transfer protein [Arachis hypogaea]  
MASLKFAFVMLVCMAMVGMVNAISCGVNSALAPCIPFLTKGGAPPPACCSGVRGLLG  
ALRTTADRQAACNCLKAAAGSLRGLNQGNAAALPGRGCVSIPYKISTSTNCATIKF  
>ABX57814.1 glutathione S-transferase [Blattella germanica]  
MTIDFYLLPGSAPCRSVLLAAKAFGVNLLKVTNLMAGEHLTPEFLKMPQHTIPTLNDN  
GFCLWESRAILSYLADQYKDDSLYPKDPKRALVDQRLYFDLGTLYQRFQDYYPIMFA  
KASPDAEKMKKLEEAYQFLDKFLEGQKQFVAGNSLTIADIATIASVSTAAILGFDITRYPN  
VNKWFENAKKVIPGYDELNHSGLCFRKMWDNLTKQ  
>ABX75045.1 Ara h 9; lipid transfer protein [Arachis hypogaea]  
LSCGQVNSALAPCITFLTKGGVPSGPPCSGVRGLLGAAKTTADRQAACNCLKAAAGSLHG  
LNQGNAAALPGRGCVSIPYKISTSTNCATIKF  
>BAF95206.1 tropomyosin [Oratosquilla oratoria]  
MDAIAKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKAEVHNLQKRMQQLENDLDQV  
QEQLLKANTQLEEKDKALQNAEVEAALNRRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKQLTNLKAEEARAE  
FAERSVQKLQKEVDRLEDELVNEKEKYKSITDELDTFSELSGY  
>ABY21305.1 Pla or 1; invertase inhibitor [Platanus orientalis]  
MKLSFSLCIIFFLISADIVQGTCKKVAQRSPNVNYDFCVKSLGADPKSHSADLQGLGVISA  
NLAIQQGSKIQTFIGRILKSKVDPALKKYLNDKCVGLYADAKSSVQEAIAIDFKSKDYASAN  
VKMSAALDDSVTCEDGFKEKKGIAKSPVTKENKDYVQLTAISLAIKLLGA  
>ABY21306.1 Pla or 2; polygalacturonase [Platanus orientalis]  
MRGVQSSGGTFNVNDYGAKGSGDISQAVMKAWAACAASPGPSTVLIPTGNYIMGEVLLLEG

PCKGSKIGFQLDGVVKAPADVSAFKSEGWVFNHVDGLTVSGKGTFDGQGGQKAWAANNCD  
KDENCNRPPMNIRFNFLKNAVVRDITSMNSKMFHINVLECDNISFQHVTISAPGTSINTD  
GIHIGLSRGVTITDTNIATGDDCVSIGPGSQNVTVTKVNCGPGHGISVGSGLGKYKDEKDV  
RGITVTGCTFTGTNSGVRVKTWPDSPPGVATDMAFEDLTMKNVQNPVILDQEYCPYQCS  
LKAPSRVKLSNIKFNNIRGTSSGPDIAIVACSHGFPCSNLEIGEINLALHAAGAPANSTC  
TNAKPIFSGKQVPAIKCA

>ABY28115.1 Der f 3; trypsin [*Dermatophagoides farinae*]  
MMILTIVVLLAANILATPILPSSPNATIVGGVKAQAGDCPYQISLQSSSHFCGGSILDEY  
WILTAACHCVNGQSACKLSIRNNTLKHASGGEKIQVAEIQHENYDSMTIDNDVALIKLKT  
PTTLDQTNAPVPLPAQGSQVGVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD  
QLYSKAGADVSENMICGGDVANGGVDSCQGDSGGPVVDIATKQIVGIVSWGYGCARKGYP  
GVYTRVGNFVDWIESKRSQ

>ABY53034.1 Der p 2; NPC2-like [*Dermatophagoides pteronyssinus*]  
MYKILCLSLVAAVARDQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEADFEAN  
QNRKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVPKIAPKSENV  
VVTVKVMGDDGVLACAIATHAKIRD

>CAK93713.1 Mal d 4; profilin [*Malus domestica*]  
MSWQTYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL  
APTGLYLGGTKYMVIQGEPPVIRGKKKGGVTVKKSTMALLIGIYDEPMPGQCNMVE  
RLGDYLIEQGL

>CAK93753.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCDIDGNSLTAAAILGQDGSVWAQSATFPAPFKPEEIAAILKDFDQPGTL  
APTGLFLGGTKYMVIQGEPPAVIRGKKKGGGITIKKTSQALLIGIYDEPVTGQCNIVVE  
RLGDYLIEQGL

>CAK93757.1 Mal d 4; profilin [*Malus domestica*]  
MSWQAYVDDHLMCDIDGNSLTAAAILGQGGSVWAQSATFPAPFKPEEIAAILKDFDQPGTL  
APTGLFLGGTKYMVIQGEPPAVIRGKKKGGGITIKKTSQALLIGIYDEPVTGQCNIVVE  
RLGDYLIEQGL

>A2VBC4.1 Poly p 1; phospholipase A1 [*Polybia paulista*]  
MNFKYSILFICFGTLDRGLIPECPFNEYDILFFVYTRQQRDQIVLTEETLQNYDLFKKST  
ISRQVVFIDHGFLSNGNENFIAMAKALIEKDNFLVISVDWKKGACNAFASTLDYLGYST  
AVGNTRHVGKYVADFTKLLVEQYKVSMSNIRLIGHSLGAHTSGFAGKEVQELKLNKYSNI  
DGLDPAGPSFDSNDCPERLCETDAEYVQIIHTSNILGVYSKIGTVDFYMNNGSHQPGCGR  
FFSPSCSHTKAVKYLTECIKHECCLIGTPWKYFSTPKPISQCTKDTCCVGLNAKSYPA  
RGSFYVPVEATAPYCHNEGIL

>2JON\_A Ole e 9; beta-1,3-glucanase, partial [*Olea europaea*]  
ATPTPTPKAAGSWCVPKPGVSDQLTGNINYACSQGIDCGPIQPGGACFEPNTVKAHAAY  
VMNLYYQHAGRNSWNCDFSQTATLTNTNPSYGACNFPSGSM

>ABZ81040.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [*Carpinus betulus*]

MGVFNIEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSILKISSK  
FHAKGDHEVNAAEMKGAKEMAELLRAVESYLLAHTAEYN

>ABZ81041.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [*Carpinus betulus*]

MGVFNIEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSVVKISSK  
FHAKGDHEVNAAEMKGAKEMAELLRAVESYLLAHTAEYN

>ABZ81042.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [*Carpinus betulus*]

MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAEKMKGAKEMA EKLLRAVESYLLAHTAEYN  
>ABZ81043.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAEEMKGAKEMA EKLLRAVESYLLAHTAEYN  
>ABZ81044.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus  
betulus]  
MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFA  
EGIPFKFVKERVDEVDNANFKYSYTVIEGDVLGDKLEKVSHELKIVAAPGGGSIVKISSK  
FHAKGDHEVNAEEMKGAKEMA EKLLRAVESYLLAHTAEYN  
>ABZ81045.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus  
alba]  
MGVFTHESQETSVIAPARLFKALFLDSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG  
EASKFKYAKHRIDALDPENCTYSFSVIEGDALVMESVSTEIKCVASPDGGSIMKSTTKY  
QTKGDFQLKEEQIAAIEKAAGLLKAVEAYLVAHPDLYK  
>ABZ81046.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Quercus alba]  
MGVFTYESEDASVIPPARLFKAFVLDSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG  
EGSHLKHAKHRIDVIDPENFTYSFSVIEGDALFDKLENVSTETKIVASPDGGSIVKSTSK  
YQTKGDFQLTDELIRGGKEKASEVFKAVEAYLVAHPDLYK  
>ABZ81047.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus  
alba]  
MGVFTHESQETSVIAPARLFKALFLDSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG  
EGSHLKHAKHRIDVIDPENFTYSFSVIEGDALFDKLENVSTETKIVASPDGGSIAKSTSK  
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDLYK  
>ABZ81991.1 Tyr p 3; trypsin [Tyrophagus putrescentiae]  
MKILLFLCFLVSVAFAPPTIQLKSNTKSQNGFIVGGTEAVDGDAPHQVSLQHTSHFCGG  
SIISERWILTAACIDADDLSNPGGMSVRYNTLNLKSGTLVKVKSIVHEQYSNVTSDND  
IALLETVASMNLNQTNAVAALPAKGNPDQDGLFLSGWGLHSGDTTIPTNLQKVTVPL  
TNRSVCAEAYTGIVNITENMFCAGKMGIGGVDSQCQDSSGGGAMLNKELVGVVSVFVGGCGD  
PKYPGVYTRVSQYLDWIELSAKSSATTLVAVNITLFLTLFIGAIW  
>ACA00159.1 Ves v 3; dipeptidyl peptidase [Vespula vulgaris]  
MVPLRSFVLLNSLFLVLLAARTVVTRVIDKDNSDRIVKTQNDQNLKVPFNLEETYTADF  
LAYVFNGTWTSDTTIVYTRRTGDILQFDVIKQRSTLIVDSSVMDAYIVSNYVLSPKGRY  
LLIGYDLKKGYRYSTFMRYVIYDIEHRAVYHKIGNDMHIALAKWAPLTDDLIIYILDNDIYY  
MRFSNNGFNDVQRVTYDGISGIVYNGVPDWVYEEVLDQSSAIWFSPDGNHLAYASFDDR  
NVQEILYLHYGEPGNLDDQYPTVEKIKYKPVGTLNPPVSLTLVDLHDPTLNKIDLKAPHY  
AVGTDNLLYNVQWKDFDHVVVWTSNRVQNKTEIVWYNMYGEIVKTLHVVEHKGWLDIKHL  
FFYKGSVYIRKLQPSGKAGRFHHVTRYDETFKQSPTQMDLTPDAIEVQNICTIDQSNR  
IYYLASGLGKPSQKNLYSVPADGSEKPTCISCNVLTPEGNVCTYADAI FSP LGQYVYVLC  
HGPDPAFVSI FNNAHQKVYSWENNL SLRKKLAKRHLPLVKDLDRANGYESKVRFLPHN  
FDESKSYPM LVNVYAGPNTLKIIDAASYGHQVYMTTNRSVIYAYIDGRGSSNKGSKMLFS  
IYRKLGTVEVEDQITVTRQLQEMFPWIDSKRTGVWGSYGGFSTAMILAKDTSFVFKCGI  
AIAPVSSWIYYDSIYTERFMGFPTPEDNL SGNETDVSRRVEDIRGKKFMLIHGSGDDNV  
HYQQSLALAKALEKADVMFEQITYTDEAHALFGVLP HLYHTMDRFWSDCFSL SHAH  
>ACA00204.1 Per a 9; arginine kinase [Periplaneta americana]  
MVDAAVLEKLEAGFAKLAASDSKSLKKYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN

HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPPKDWGDVDTLGNLDPAGEYI  
ISTRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEAEPKGQFYLLTGMTKEVQQK  
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDKTFLLVWCNEEDHLRIISMQMGDLG  
QVYRRLVTAVNDIEKRIPFSHDDRLGLFTFCPTNLGTTVRASVHIKVPKLAADKAKLEEV  
AGKYNLQVRGTRGEHTEAEGGVYDISNKRRMGLTEYDAVKEMNDGIAELIKLESSL  
>ACA23876.1 Pas n 1; beta-expansin [*Paspalum notatum*]  
MGSLAKIVAVAAVLAALVAGGSCGPPKVPPGNITTNYNKWLPAKATWYGQPNGAGPDD  
NGGACGIKNVNLPPYNGFTACGNPPIFKDGKGCSCYEIRCNKPECSGQPVTVFITDMNY  
EPIAPYHFDLSGKAFGAMAKPGLNDKLRHYGIFDLEFRRVRCKYQGGQKIVFHVEKGSNP  
NYLAMLVKFVADDGDIVLMELKEKSSDWKPKLSWGAIWRMDTPKALVPPFSIRLTSESG  
KKVIAQDVIPVNWKPDTVYNSNVQF  
>ACA79908.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [*Arachis hypogaea*]  
MGVFTFEDEITSTLPPAKLYNAMKDADSITPKIIDDVKSVEIVEGNGGPGTIKKTIVED  
GETKFILHKVEAIDEANYAYNYSVVGVALPPTAEKITFETKLVGEPNGGSIGKLSVKFH  
SKGEAKPEEEDMKKGKAKGEALFKAIEGYVLNPTQY  
>ACA96507.1 Pac c 3; unknown function, antigen 5 [*Pachycondyla chinensis*]  
TEGGAVHTMCQYTSPQSPNCGTYSNAHITAADKETILKVHNDERQVKAGQETRGNPGP  
QPAASNMPDLTWDNELAAIAQRWVNQCKIGHDGCNRVERYQVGQNIAMSGSTAKGPCNMN  
NLVQMWINEVNALNAADVSSMPSDGNVFMKIGHYTQLVWGKTTKVGCIIQFLDGKFYKC  
YLACNYGPAGNMFAPYQ  
>ACB05815.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [*Lupinus angustifolius*]  
MAKMRVRLPMLILLGLVFLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQQEE  
QEREHRREEKHDEGPESRGRSQSEESQEEHERRREHREEREQQPRPQRRQEEEEEEEE  
WQPRRQRPQSRREEREEREQEQSSSGSQRGGGDERRQHRERRVHREEREQEQDSRSDSR  
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNQRTNRLNLQNYRIIEFQSKPNTLILPKH  
SDADFILVVLNGRATITIVNPDQRQVYNLEQGDALRLPAGTTSYILNPDDNQLRVAKLA  
IPINNPGLYDFYPSTTKDQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENKQR  
RGQEQSHQDEGVIVRVSKKQIQELRKHAQSSSGEGKPSSESGPFNLRNPKIYSNKFNGFY  
EITPDINPQFDLNLISLTFTEINEGALLLPHYNSKAIFFVVDDEGEGNYELVGIRDQQRQ  
QDEQEEYEQGEVEVRRYSKLSKGDVFIIPAGHPLSINASSNLRLLGFGINANENQRNF  
LAGSEDNVIKQLDREVKELTFPGSIEDVERLIKNQQQSYFANAQPQQQQREKEGRRGRR  
GPISSILNALY  
>ACB38288.1 Lit v 1; tropomyosin [*Litopenaeus vannamei* (*Penaeus vannamei*)]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANIQLVEKDKALSNAEAGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLLKAAEARAE  
FAERSVQKLQKEVDREDELVNEKEKYKSITDELDTFSELSGY  
>ACB45874.1 pathogenesis related protein, PR-1 [*Cucumis melo*]  
MLPFSFAQDSIKDFVDAHNAARAQVGVGVHWNKTVADYAHQYANKRIKDCNLVHSGPY  
GENIAWGSRLAGTVAVRMWVSEKQFYNYDTNSCVRGKMGHYTQVWVRNSVRIGCAKVR  
CKSGGTFITCNYDPRGNIRGQRPYGGTLQL  
>ACB46292.1 Der p 23; peritrophin [*Dermatophagoides pteronyssinus*]  
MKFNIIIVFISLAILVHSSYAANDNDDDPTTTVHPTTTEQPDDKFECPSRFGYFADPKDP  
HKFYICSNWEAVHKDCPGNTRWNEDEETCT  
>ACB55491.1 aldehyde dehydrogenase [*Sesamum indicum*]  
MQFFSSRLLGSSRVLATTLSHFHYNPCTNKAHFTKAQLLPAAPYSNKLIVIRSMASGQQF  
PPQKQEGQPGEHIMDPTPQATTPEYKPAKLVGKVALVTGGDSGIGRAVGHCFALEGAT  
VAFTYVKGQEDKDANDTLGMLMKAKHADAKDPIAIPDLDGYDENCRRVVEEVNNYGRID

ILVNAAEQYEASTVEEIDEPRLERVFRITNIFSFFTSRHALKHMKEGSSIINTTSVNAV  
KGNAKLLDYATKGAIVAFTRGLALQMVEKIRVNGVAPGPIWTPILIPASFTEDENAKFG  
SQTPMKRAGQPHEVAPSYVFLASNIDSSYITGQVLHPNGGTIVNG  
>ACC76803.1 Lit v 3; myosin light chain [Litopenaeus vannamei (Penaeus vannamei)]  
MSRKSGSRSSSKRSKKS GGGSNVDFMFTQRQVAEFKEGFQLMDRDKDGVIGKTDLRGTFD  
EIGRIATDQELDEMLADAPAPINF TMLLNMF AERQTGESDDDDVAKAF LAF ADEEGNID  
CDTFRHALMTWGD K FSSQEADDALDQMDIDDGGKIDVQGV IQMLTAGGGDDAAAEAA  
>NP\_001119715.1 Api m 5; dipeptidyl peptidase [Apis mellifera]  
MEVLVQLALLLVVHGLVVLVAGKSVPRVIDQDLERYEPLEEDHRGARVPFNLEETYDQ  
SFRANSFNGTWKT DREILYSDNYVGD IRLFDVTTGSGTVLLDSSVTADFDKASVMF SFDN  
SHVAIGHDYVNGFRYSIHQKCTVYNIKSRTFTDIANGDRIP LFKWSPTRNALIYVHKNDI  
YYQVF FEGGSDTRRITNTGVPDIVFNIGIPDWVYEEV LGSPVAFWISPDGRHLAFATFND  
TNVRDIVISKY GSPGNSRDQYPNEIRIKYPKAGTTNPFVSLVIDLHDPSSKLIDLPPP  
DVVGADNVLYTANWRRDGEIVATWTNRVQNK AQLVLYDTKGNANNIYEEETEGWLRIQP  
PLYHDRVIVAKLQDSGTKAGRFLHATRLEYRNGALVDETDLTPGTCEVISLLLVDHARA  
RLYYLGT ELGKPSHKNLYSVQLSGNEPPVCLSCDVLTPEGNRCTYAYAYFSTNGSHYALY  
CAGPDPVFI AIVNANHRQIS IWEENRSLRRKLAARTQPIVKNFVNANGYTNKVKLYLPP  
DFDETKKYPLLITVYAGPNTIRITEEATYGFESYIVTNRSVIYGRIDGRGSAYKGSKMLF  
EIYRRLGTVEIEDQIIITRTLQEKYSWIDSNRTGIWGSYGGFSAAMVLATDAESVFKCG  
ISVAPVTSWIYYDSLYTERFMGLPTPEDNQSGYNDTDVSRRVEGMRGKKYMLIHGTADDN  
VHYQQTMMLNKALVNSDIMFQQQTYTDEAHALGNVFP HLYHTTDRFWANCLGYSH  
>ACD36974.1 7S globulin, vicilin, partial [Glycine max]  
LDSNLIIFIRRG EAKLGF IYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSI  
DPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTVVEEIFSKELDGPIMFV  
DDSHVPSLWTKFLQLKKDDKEQQLKMMQDQE EDEEEKQTSRSWRKLLLETVFGKVNEKIE  
NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEY PPLSEPDIGVLLVKLSAGSMLAPH  
VNPISDEYTI VLSGYGELHIGYPNGSKAMKTKIKQGDV FVVP RYFPFCQVASRDGPLEFF  
GFST SARKNKPQFLAGAASLLR TLMGP ELSAAFVSEDTLRRAVDAQHEAVILPSAWAAP  
PENAGKLMEEEP  
>ACD36975.1 7S globulin, vicilin, partial [Glycine max]  
LDSNLIIFIRRG EAKLGF IYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSI  
DPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTVVEEIFSKELDGPIMFV  
DDSHAPS L WTKFLQLKKDDKEQQLKMMQDQE EDEEEKQTSRSWRKLLLETVFGKVNEKIE  
NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEY PPLSEPDIGVLLVKLSAGSMLAPH  
VNPISDEYTI VLSGYGELHIGYPNGSKAMKTKIKQGDV FVVP RYFPFCQVASRDGPLEFF  
GFST SARKNKPQFLAGAASLLR TLMGP ELSAAFVSEDTLRRAVDAQHEAVILPSAWAAP  
PENAGKLMEEEP  
>ACD36976.1 7S globulin, vicilin, partial [Glycine max]  
LDSNLIIFIRRG EAKLGF IYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICSI  
DPSTSLGLETFQSFNIGGGANSHSVLSGFEP AILETAFNESRTVVEETFSKELDGPIMFV  
DDSHAPS L WTKFLQLKKDDKEQQLKMMQDQE EDEEEKQTSRSWRKLLLETVFGKVNEKIE  
NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEY PPLSEPDIGVLLVKLSAGSMLAPH  
VNPISDEYTI VLSGYGELHIGYPNGSKAMKTKIKQGDV FVVP RYFPFCQVASRDGPLEFF  
GFST SARKNKPQFLAGAASLLR TLMGP ELSAAFVSEDTLRRAVDAQHA AVILPSAWAAP  
PENAGKLMEEEP  
>ACD36978.1 7S globulin, vicilin, partial [Glycine max]  
VLCHGVATTTMAFHDEGGDKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYRHHM  
IGFISMEPKSLFVPQYLD SNLIIFIRRG EAKLGF IYDDELAERRLKTGDLYMIPSGSAFY  
LVNIGEGQRLHVICSIDPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTV  
VEEIFSKELDGPIMFVDDSHAPS L WTKFLQLKKDDKEQQLKMMQDQE EDEEEKQTSRSW

RKLLLETVFGKVNEKIENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLEPDI  
GVLLVKSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFFVPRY  
FPFCQVASRDGPLEFFGFSTARKNKPFQFLAGAASLLRRLMGPELSAAFVSEDTLRRAV  
DAQHEAVILPSAWAAPRKMQEAEEMESQMLLKLKQ

>ACD50950.1 Der p 20; arginine kinase [Dermatophagoides pteronyssinus]

MVDPATLSKLEAGFQKLQNAQDCHSLLKKYLTRDVFQDLKNNKTDMGATLLDVIQSGVEN  
LDSGVGIYAPDAQSYKTFEALFDPIIDDYHKGFKPTDKHPKTDGNIENFVNVDPKNEYV  
LSTRVRCGRSLNGYFPNPLTEAQYKEMETKVKGQLATFEGELKGTYYPLLGMKATQQQ  
LIDDHFLFKEGDRFLQAANACRYWPVGRGIFHNDKKTFLMWVNEEDHLRIISMQKGGDLK  
EYVGRVLKAVKHIEQKIPFSRDDRLGLFTFCPTNLGTTIRASVHIKLPKLAADRKKLEEV  
AGRYNLQVRGTAGEHTESVGGIYDISNKRRLMGLTEYQAVKEMQDGIKELIKMEKSM

>ACD65080.1 For t 1; serine/threonine protein kinase [Forcipomyia taiwana]

GTRVDEIKGHPFFREIDWTKELRNQKAPYEPKIKYPTDTSNFDPIDPKLHDSNADDYM  
IEEFFGSGPKCHHGFEEFTFRFFDADCKISLNHGNSGDRNDNNSNDNQSGAIYV

>ACD65081.1 For t 2; eukaryotic translation initiation factor [Forcipomyia taiwana]

MKPLMMQGHRAITQIKYNREGDLLFSCAKDHPNVWFSLNGERLGTFFNGHAGAVWCVDV  
DWTTKLITGSGDMSVRLWDVETGTSVACIPCKSSARTVGFSGNQAAYSTDRAMGHIC  
ELFVIDSREPDSSLNDGDAIKIPIISQSKITAMIWGTLDIITGHENGQITLWDLRIGR  
EINSVNDHMGAINDLQLSKDGTMFVSSSRDITAKLFDSDSLMCLKTYKTERPVNSAAISP  
LLEHVVLGGQDAMEVTTTSARQKGFDSRFFHLYEEEEFARVKGHFGPINSLAFHPDGRS  
YATGGEDGFVRLQTFDSSYYEYIFD

>CAQ55938.1 Ph1 p 4; berberine bridge enzyme [Phleum pratense]

YYPTPLAKEDFLRCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT  
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRAVWVDGKART  
AWVDSGAQLGELYAIHKASTVLAFFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGIIVVAVKVRLLPVPPTVTVFKIPKASE  
GAVDIINRWQVVAPQLPDDLMIRVIAQGPATFEAMYLGTCQTLTPMMGSKFPELGMNAS  
HCNEMSWIQSIPFVHLGHRDNIEDLLNRNNTFKPFAEYKSDYVYEPFPRVWEQIFSTW  
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAAPLSWSKEI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK  
VDPTDYFRNEQSIPPLIQY

>CAQ55939.1 Ph1 p 4; berberine bridge enzyme [Phleum pratense]

YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT  
NVSHIQSAVVCGRRHVIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART  
AWVDSGAQLGELYAIYKASPTLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDANGKLHDKKSMGDDHFWAVRGGGGESFGIIVVAVQVKLLPVPPTVTIFKISKTVE  
GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCCKTLTPLMSSKFPELGMNPS  
HCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTVWEQILNTW  
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAAPLSWSKDI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQKYFKGNFERLAITKGK  
VDPTDYFRNEQSIPPLIKY

>CAQ55940.1 Ph1 p 4; berberine bridge enzyme [Phleum pratense]

YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT  
NVSHIQSAVVCGRRHVIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART  
AWVDSGAQLGELYAIYKASPTLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDPNGKLHDKKSMGDDHFWAVRGGGGESFGIIVVAVQVKLLPVPLTVTIFKISKTVE  
GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCCKTLTPLMSSKFPELGMNPS  
HCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTVWEQILNTW  
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAAPLSWSKDI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQKYFKGNFERLAITKGK

VDPTDYFRNEQSIPPLIKKY

>CAQ55941.1 Phl p 4; berberine bridge enzyme [Phleum pratense]  
YFPPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT  
NVSHIQSAVVCGRRTVIRIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART  
AWVDSGAQLGELYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID  
VKLVDPNGKLHDKKSMGDDHFWAVRGGGGESFGIWWAQVKLLPVPLTVTIFKISKTVSE  
GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCKLTPLMSSKFPELGMNPS  
HCNEMSWIQSIPFVHLGHRDALEDDLNRNNSFKPFAEYKSDYVYQFPFKTVWEQILNTW  
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQVNYWFAPGAAAAPLSWSKDI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQYFKGNFERLAITKGGK  
VDPTDYFRNEQSIPPLIKKY

>ACE07186.1 Art v 3; lipid transfer protein [Artemisia vulgaris]  
MKMMKFFCAMVVMVSSSYAEALKCSDVSNKISACLSYLKQGGEVPADCCTGVKGLNDA  
AKTTPDRQTACNCLKTTFKSNKDFKSDFAASLPSKCGVNIPYKISLETDCNKVK

>ACE07187.1 Art v 3; lipid transfer protein [Artemisia vulgaris]  
MAMKMMKFFCAMVVMVSSSYAEALTCSDVSNKITPCLNYLKQGGEVPADCCTGVKGLN  
DAAKTTPDRQTACNCLKTSFKSNKDLKSDFAASLPSKCGVNIPYKISLETDCNKVK

>ACE07188.1 Art v 3; lipid transfer protein [Artemisia vulgaris]  
MAIKMMKVFCIMVVMVSTSYAESALTCSDVSTKISPCLSYLKKGGEVPADCCTGVKGL  
NDATKTTTPDRQTACNCLKASFKNKDLKSDFAVPLPSKCGLNLPYKLSLETDCNKVK

>ACE07189.1 Art v 3; lipid transfer protein [Artemisia vulgaris]  
MAIKMMKVFCMVVMVSSSYAEALTCSDVSTKISPCLNYLKKGGEVPADCCTGVKGL  
NDATKTTTPDRQTACNCLKASFKNKDLKSDFAVPLPSKCGLNLPYKLSLETDCNKVK

>P00785.4 Act d 1; actinidin [Actinidia chinensis]  
MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGEWE  
RRFEIFKETLRFIDEHNADTNRSYKVLNQFADLTDEEFRSTYLRFTSGSNKTKVSNRYE  
PRVGQVLPSYVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGVLI SLSEQELI  
DCGRTQNTGRCNGGYITDGFQFIINNGGINTENYPYTAQDGE CNVDLQNEKYVTIDTYE  
NVPYNNEWALQTAVTYQPVSVLDAAGDAFKQYSSGIFTGPCGTAVDHAVTIVGYGTEGG  
IDYWIWVKNWDTTWGEEGYMRILRNVGAGTCGIATMPSYPVKYNNQNHPKPYSSLINPP  
AFMSKDGPPVGDGQRYSA

>ACE80939.1 pathogenesis related protein, PR-10, Bet v 1-like [Prunus dulcis x Prunus persica]

MGVFTYESEFTSEIPPPRLFKAFLVLDADNLVPKIAPOAIKHSEILEGDGGPGTIKKITFG  
EGSQYGYVKKHIDSIDKENHSYSYTLTEGDALGDNLEKISYETKLVASPSGGSIKSTSH  
YHTKGDVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN

>ACE80955.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]  
MMKTLVAVLSLSLTLFSFGAHAATMSFKNCPYTVWPASFGNPQLSTTGFE LASQASFQ  
LDTPVPWSGRFWARTRCSTDASGKFCETADCDGQMLCNGKTGIPPATLAEFTIAAGGG  
QDFYDVSLVDGFNLPMVTPQGGTGCKMGSCAANVNLVCPSELQKIGSDGSSVACL SAC  
VKFGEPQYCCTPPQETKEKCPPTNYSQIFHEQCPDAYSYAFDDNKGLFTCSGGPNYLITF  
CP

>ACE80956.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]  
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTG DQKPQLSLTG FELATG  
ISRSVDAPSPWSGRFFGRTRCSTDASGKFCATADCGSGQVSCNGNGAAPPATLVEITIA  
SNGGQDFYDVSLVDGFNLPMVAVPQGGTGECKASTCPADVNKVCPAQLQVKGSDGSSVIAC  
KSACLAFNQPQYCCTPPNDKPETCPPTDYSKIFKTQCPQAYSAYDDKSSTFTCSASPDY  
LITFCP

>ACE80957.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]  
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTG DQKPQLSLTG FELATG

ISNSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAVPPATLVEITIA  
ENGGQDFYDVS LVDGFNL PMSVAPQGGTGECKASTCPADINKVCPAELQVKGSDGSVIAC  
KSACLALNQPQYCCTPPNDKPETCPPTDYSKLFKTQCPQAYSAYDDKSSTFTCSGRPDY  
LITFCP

>ACE80958.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]  
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFKLATG  
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA  
SNGGQDFYDVS LVDGFNL PMSVAPQGGTGKCKASTCPANVNAACPAQLQVKGSDGKVIAC  
KSACLAFNQPKYCCTPPNDKPATCPPTDYSRFFKTQCPQAYSAYDDKSSTFTCNGRPDY  
LITFCP

>ACE80959.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]  
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFKLATG  
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA  
SNGGQDFYDVS LVDGFNL PMSVAPQGGTGKCKASTCPADINKVCPAPLQVKGSDGSVIAC  
KSACLAFNQPKYCCTPPNDKPETCPPTDYSKLFKTQCPQAYSAYDDKSSTFTCSGRPDY  
LITFCP

>ACE80972.1 profilin [Prunus dulcis x Prunus persica]  
MSWQTYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGILNDFNEPGSL  
APTGLYLGGTKYMVIQGEPEGAVIRGKKKPGGVTVKKSTLALLIGIYDEPMTPGQCNMIVE  
RLGDYLVEQGL

>ACE80974.1 thaumatin-like [Prunus dulcis]  
MMKTLVVVLSLSLTLSSFGGAHAATISFKNCPYTVWPASFGNPQLSTTGFEPSQASFP  
LDTPAPWSGRFWARTGCTDASGKFCETADCDGQLMCNGKTGIPPATLAEFTIAAGGGQ  
DYYDVSLVDGFNL RMSVTPQGGTGTCTGSCAANVNAVCPSELQKIGSDGSVVACL SACY  
KFNQPQYCCTPPQETKEKCPPTNYSQIFHDQCPDAYSAYDDNKGLFTCSGGPNYLITFC  
P

>ACE82289.1 glutathione S-transferase [Triticum aestivum]  
MAGEKGLVLLDFWVSPFGQVRVIALAEKGLPYEYAEEDLMAGKSDRLLRANPVHKKIPVL  
LHDGRPVNESLIILQYLEDAFPDAPALLSPDPYARAQARFWADYVDKVVYDCGSRLLWKLK  
GEPQAQARAEMLDILKTLDGALGDKPF FGGDKFGFVDAAFAPFTAWFHSYERYGEFSLPE  
VAPKIAAWAKRCGERESVAKSLYSPDKVYDFIGLLKKKYIE

>ACE82290.1 Tri a 32; peroxiredoxin [Triticum aestivum]  
MPGLTIGDTPVNL ELDSTHGKIRIHDIYVNGYVILF SHPGDFTPVCTTELAAMANYAKEF  
EKRGVKLLGISCDVQSHKEWTKDIEAYKPGSRVTYPIMADPDRSAIKQLNMVDPDEKDG  
QGQLPSRTLHIVGPDKVVKLSFLYPSCTGRNMDEVVRAVDSLLTAAKHKVATPANWKPGE  
CVVIAPGVSDEEAKMFPQGFETADLPSKKGYLRF TKV

>ACE82291.1 Tri a 12; profilin [Triticum aestivum]  
MSWQTYVDDHLCCEIDGQHLTSAAILGHDGSVWAESPFPKFKPEEIAGIVKDFEEPGHL  
APTGLFLGGTKYMVIQGEPEGVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE  
RLGDYPVEQGF

>CAQ68366.1 Sar sa 1; calcium-binding protein, parvalbumin [Sardinops sagax]  
MALAGLVKEADITAAL EACKAADSFDHKAFFHKVGMMSGKSADELKKAFAIIDQDKSGFIE  
EEELKFLFNFCFKARALTDGETKKFLKAGDNVGDGKIGIDEFNHLVKH

>ACF19589.1 Cur l 4; serine protease [Curvularia lunata]  
MKYSLIAALPALAAASPTFSTETIHKQSAPVLSSTSAKEVPNSYMWVFKKHVKDASKHHD  
WVQSVHSKNTQERMELRKRSSDL PVSNEVFAGLKHTYELSGLKGYSGHFDEETLEAIRNH  
PDVDYIERDSEVRILGGDEPETENNSPWGLARISHRDSLSFGTWNKYLYAADGGEGVDVY  
VIDTGTNVDHVDFEGRAKWGKTIPNGDAEEDGNGHGT HCSGTVAGKKYGVAKKAHVYAVK  
VLRNSGSGTMSDVVKGVFAAKSHSEAVSAAKNGKKKGFKGSTANMSLGGGKSTLDMAV  
NAAVDAGLHFAVAAGNDNADSCNYSAAAENAVTVGASTLLDERAYFSNYGKCNDIFAPG

LNILSTWIGSKHATNTISGTSMASPHIAGLLAYMLSLQPAKDSAYAVADITPKKLLKANLI  
AIGTVGALSDVPSNTANVLAWNGGSSNYTDIIEKGGYTVKKAASKEEEESEFRITIPS  
LSELEDDFEKAKESAGRKAHHVGGKL

>P50635.2 Aed a 1; apyrase [*Aedes aegypti*]

MAGRPGYSEVIFLYVVSVAVIARATDNMPVNDVSKLFPLTLIHINDLHARFEETNMKSN  
VCTQKDQCIAGIARVYQKIKDLLKEYESKNPIYLNAGDNFQGLWYNLLRWNVTADF  
LKPAAAMLGNHEFDHTPKGLAPYLAELNKEGIPTIVANLVMNNDPDLKSSKIPKSIKLT  
V GKRKIGIIGVLYDKTHEIAQTGKVTLSNAVEAVRREAAALKKDNIDIIVVLSHCSYEEDK  
KIAAEAGDDIDVIVGAHSHSFLYSPDSKQPHDPKDKVEGYPYPTLVESKNKRKIPVQAKS  
FGKYVGRLLTYFDEEGEVKNWEGYPVFDHKVQQDPQILKDLVPWRAKVEAIGSTVVG  
ET MIELDRDSCRDQECTLGVLADGFADQYTNDTFRPFAIIQAGNFRNPIKVGKITNGDIE  
AAPFGSTADLIRLKGADIWDVAEHSFALDDEGRNCLQVSGLRIVIDISKPVRSRVK  
KIE VMDYTNPKSDKLLKPLDKEAEYYIVVPSYLADGKDGFSAMKRATARRTG  
PLDSDVFKNYVE KIKKVDNLKLRVIVCKGSKCT

>A5HII1.1 Act d 1; actinidin [*Actinidia deliciosa*]

MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGE  
WE RRFEIFKETLRFIDEHNADTNRSYKVLNQFADLTDEEFRSTYLGFTSGSNKTKV  
SNRYE PRVQVQLPSYVDWRSAGAVDIKSQGECGGCWAFAIATVEGINKIVTGV  
LISLSEQELI DCGRTQNTRGCNGGYITDGFQFIINNGGINTENYPPYTAQDGE  
CNLDLQNEKYVTIDTYE NVPYNNEWALQTAVTYQPVSVLDAAGDAFKHYSSGIF  
TGPCGTAIDHAVTIVGYGTEGG IDYWIVKNSWDTTWGEEGYMRILRN  
VGGAGTCGIATMPSPVYKYNQNHKPKPYSSLINPP AFSMSKDG  
PVGDDGQRYSA

>ACF53836.1 Bla g 4; lipocalin [*Blattella germanica*]

MCITGVILFAVLAVCATDTLANEDCFRHESLVPLNDYKFKFIGTWIAAGTSEAL  
TQYKCN DLFFFNNALVSKYTDSKGNRTTIRGRTKFEGNKFTIDYDDEGKA  
FSAPYSVLATDYDN YAIVEGCPAAANGHVIVQLRLTLRSFHPEQGDKEAL  
QHHTVHQVQNHKKAIEEDLKHFNL KYEDLHSTCH

>ACF53837.1 Bla g 4; lipocalin [*Blattella germanica*]

MCITGVILFAVLALCATDTLADEDCFRHESLVPLNDYERFRGMWVIVAGTSEAL  
TQYKCN IDWFSYDDALVSKYTDSKQGNKILIGKIKFEGNKFTIDYDDEGKA  
FSAPYSVLATDYDNY AIVEGCPAAANGHVIVQLRLTWRRFHPKLGDKEM  
IQHYTLQVQNHKKAIEEDLKHFNL KYEDLHSTCH

>ACG58378.1 Der p 1; cysteine protease [*Dermatophagoides pteronyssinus*]

MKITLAIASLLALSAVYARPSSIKTFEYKAFNKSYATFEDEEAARKNFLESV  
KYVQSN GGAINHLSLSDLEFKNRFLMSAEAFEHLKTQSDLNAETNACNING  
NAPAEIDLRQMRV TPIRMQGGCSCWAFSGVAATESAYLAYRNQSLDLAEQEL  
VDCASQHGCHGDTIPRGIEY IQHNGVVQESYYRYVAREQSCRRPNAQR  
FGISNYCQIYPPNVNKIREALQTHSAIAVII GIKDLDAFRHYDGR  
TIIQRDNGYQPNYHAVNIVGYSNAQGVYWI  
VRNSWDTNWGDNGY YFAANIDLMMIEEYPYVVIL

>ACG59280.1 Bos d 5; beta-lactoglobulin [*Bos taurus*]

MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQ  
SAPLRVYVE ELKPTPEGDLEILLQKWEDECAQKKIIAEKTKIPAVFKIDAL  
NENKVLVLDTDYKKYLL FCMENSAEPEQSLVCQLV  
RTPVEDDEALEKFDKALKALPMHIRLSFNPTQLEE  
QCHI

>ACG59281.1 Tri a 40; alpha-amylase inhibitor [*Triticum aestivum*]

MASESNCVLLLLAAVLVSIFAFAVAAGNEDCTP  
WMSTLITPLPSCRDYVEQQACRIETPGS  
PYLAKQCCGELANIPQQCRCQALRYFMGPKSR  
PDQSGLMELPGCPREVQMDFVRILVTP  
GYCNLTTVHNTPYCLAMEESQWS

>ACH70931.1 Sal s 2; enolase [*Salmo salar*]

MSITKIHAREILDSRGNPTVEVDLYTAKGRFRAAV  
PSGASTGVHEALELRDGDKSRYLGK  
GTVKAVDHNKDIAAKLEKFFSVVDQEKIDHFM  
LELDGTENKSKFGANAILGVSLAVCK

AGAAEKGVPLYRHIADLAGHKDVILPCPAFNVIINGGSHAGNKLAMQEFMILPIGASNFHE  
AMRIGAEVYHNLKNVIKAKYKDATNVGDEGGFAPNILENNEALELLKTAIEKAGYDPDKI  
IIGMDVAASEFYKAGKYDLDFKSPDDPARYITGDQLGDLYKSFYKGYPVQSIEDPFDQDD  
WAAWTKFTAAVDIQVVGDDLTVTNPKRIQQAVEKKACNCLLLKVNQIGSVTESIKACKLA  
QSNWGVVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEELGAK  
AKFAGKDYRHPKIN

>ACH85188.1 Ses i 5; oleosin [*Sesamum indicum*]  
MAEHYQQQQTRAPHPQLQPRAQRVKAATAVTAGGSLLVLSGLTLAGTVIALTIATPLL  
VIFSPVLVPAVITIFLLGAGFLASGGFGVAALSVLWYRYLTGKHPPGADQLESATKL  
ASKAREMKDRAEQFSQQPVAGSQT

>ACH91862.1 Ara h 3; 11S globulin, cupin [*Arachis hypogaea*]  
MAKLELSFCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNPNN  
QEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYEPAQQGR  
RYQSQRPPRRLLQEEDQSQQQDQSHQKVHRFNEGDLIAVPTGVAFWLYNDHDTDVAVSLT  
DTNNNDNQLDQFPRRNLNLAGNHEQEFRLRYQQSRQSRRRSLPSPYSPQSQRQEEREF  
PRGQHSRRERAGQEEENEGGNIFSGFTPEFLAQAFQVDDRQIVQNLRGENESEEQGAIVT  
VRGGLRILSPDRKRGADDEEYDEDEYDEEDRRRGRGSRGSGNGIEETICTATVKKNI  
GRNRSPDIYNPQAGSLKTANELNLLILRWLGLSAEYGNLYRNALFVPHYNTNAHSIIYAL  
RGRAHVQVVDNSNGNRVYDEELQEGHVLVVPQNFVAVAGKSQSDNFEYVAFKTDSPSIANL  
AGENSVIDNLP EEVVANSYGLPREQARQLKNNNPFKFFVPPSQSPRAVA

>CAP05019.1 Par j 4; calcium-binding protein, polcalcin [*Parietaria judaica*]  
MADKQIDRAEQERIFKRFDNSGDGKISSSELGEALKALGSVTADEVHRMMAEIDTDGDGA  
ISLEEFSSFADANRGLIKDIKIF

>P18153.2 Aed a 2; unknown function [*Aedes aegypti*]  
MKLPLLLAIVTTFSVASTGPFDPPEMLFTFTRCMEDNLEDGPNRLPMLAKWKEWINEPV  
DSPATQCFGKCVLVRTGLYDPVAQKFDASVIQEQFKAYPSLGEKSKVEAYANAVQQLPST  
NNDCAAVFKAYDPVHKAHKDTSKNL FHGNKELTKGLYEKLGKDIRQKKQSYFEFCENKYY  
PAGSDKRQQLCKIRQYTVLDDALFKEHTDCVMKGIRYITKNNELDAEEVKRDFMQVNKDT  
KALEKVLNDCKSKEPSNAGEKSWHYKCLVLESSVKDDFKEAFDYREVRVRSQIYAFNLPKKQ  
VYSKPAVQSQVMEIDGKQCPQ

>P85984.1 Beta v 2; profilin [*Beta vulgaris*]  
YMQIQGEPGAVIRLGDYLIDQGL

>CAQ57979.1 Tri a 12; profilin [*Triticum aestivum*]  
MSWKAYVDDHLCEIDGQHLTSAAILGHDGSVWAQSPNFPQFKPEEIAGIVKDFEEPGHL  
APTGLFLGGTKYMQIQGEPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE  
RLGDYLIDQGY

>ACI25605.1 Api m 3; acid phosphatase [*Apis mellifera*]  
MSVIAILAMVGVQAELKQINVIFRHGDRIPDEKNEMYPKDPYLYYDFYPLERGETNSG  
KMREYQLGQFLRERYGDFLGDIIYTESVSALSSFYDRTKMSLQLVLAALYPPNKLQQWNE  
DLNWQPIATKYLRRYEDNIFLPEDCLLFTIEFDRVLES PRGKYEF SKYDKLKKKLEEWG  
KNITTPWDYIIYHTLVAEQSYGLTLPSWTNNIFPRGELFDATVFTYNI TNSTPLLKLY  
GGPLLRIFTKHM LDVSGTQKKRKYLFSGHESNIAAVLHALQLYYPHVPEYSSSIIME  
LHNIIEGTHYVKIVYLLGIPSEAGELQLPGCEVLCPLYKYLQLIENVIPSNEELICDKRFA  
DESANNLSIEELDFVKNLIRIAGTENK

>CAR82265.1 LMW glutenin [*Triticum aestivum*]  
MARQLNPSNKEQSPQQSFHQQQPFPQQPYPQQPYPQQPYPQQPFPPTPQQPFPQQSQ  
QPFTQPQQPTLPQQPFPQQPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFP  
QQPQQPFPQQPQLQFPQQPEQIIPQQPQQPFLLESQQPFPQQPQQPFPQQPFPQQP  
FPQQSQSQPFPQGFQQLFPELQQPQPQQPQQPFPQQPFPQQPFPQQPFPQQPFPQQP  
FPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFP  
FPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFPQQPFP

SILQPQQPFLQPQQQLSQLEQTISQQPQQPFPQQPHQPQQPYPQQQPYGSSLTSIDGQ  
>CAR82266.1 LMW glutenin [*Triticum aestivum*]  
MGRLLSPRGKELHTPQEQQPQQQFPQPQQFPQQQILQQHQIPQQPQQFPQQQFLQQQQ  
IPQQQIPQQHQIPQQPQQFPQQQFPQQQFPQQHQSPQQFPQQFPQQQLPQQEFSQQQ  
ISQQPQLPQQQQIPQQPQQFLQQQFPQQQPPQQHQFPQQQLPQQQQIPQQQQIPQQPQ  
QIPQQQQIPQQPKQFPQQQFPQQQFPQQQFPQQEFQQQQFPQQQIAQQPQQLPQQQFPI  
PYPPQQSQEPSYQQYPQQQPSGSDVISICGL  
>CAR82267.1 LMW glutenin [*Triticum aestivum*]  
MGRLLSPRGKELHTPQEQQPQQQFPQPQQFPQQQILQQHQIPQQPQQFPQQQFLQQQQ  
IPQQQIPQQHQIPQQPQQFPQQQFPQQQFPQQHQSPQQFPQQFPQQQLPQQEFSQQQ  
ISQQPQLPQQQQIPQQPQQFLQQQFPQQQPPQQHQFPQQQLPQQQQIPQQQQIPQQPQ  
QIPQQQQIPQQPKQFPQQQFPQQQFPQQQFPQQEFQQQQFPQQQIAQQPQQLPQQQQIP  
QQPQLFPQQQFPQQQSPQQQFPQQQFPQQQLPQQQFPQPQQIPQQQQIPQQPQQFPQ  
QQFPQQQFPQQQFPQQQFPQQQFHQQQLPQQQPSGSDVISICGL  
>CAP17694.1 Lep w 1; calcium-binding protein, parvalbumin [*Lepidorhombus whiffiagonis*]  
MTFAGLDAAEIKAAALDGCAADSFDYKFFGACGLAKKSAEEVKA AFNKIDQDESGFIEE  
DELKLFQNFASARALTDKETANFLKAGVDGDGKIGIEEFTDLVRSK  
>ACI32128.1 Der p 10; tropomyosin [*Dermatophagoides pteronyssinus*]  
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV  
QEQLSAANTKLEEKAPQTAEGDVAALNRRIQLEEDLERSEERLKIATAKLEEASQSA  
DESERMKMLEHRSITDEERMEGLENQLKEARMMMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEYKSISDELDTFAELTGY  
>ACI41244.1 Ses i 1; 2S albumin, conglutin [*Sesamum indicum*]  
MAKKLALAAVLLVAMVALASATYTTTTVTTTAIDDEANQQSQCRQQLQGRQFRSCQRYL  
SQGRSPYGGEEDEVLEMSTGNQQSEQSLRDCCQQLGNVDERCRCEAIRQAVRQQQEGGY  
QEGQSQQVYQRARDLPRRCNMRPQQCQFRVIFV  
>ACI47547.1 Jug r 3; lipid transfer protein [*Juglans regia*]  
MTGSLVLKLSGMVLLCMVVAAPVAEAVITCGQVASSVGSIGYLRGTVPTVPPSCCNGVK  
SLNKAATTADRQAACECLKKTSIPSGLNPLAAGLPGKCGVSVPYKISTSTNCKAVK  
>ACI68103.1 Sal s 1; calcium-binding protein, parvalbumin [*Salmo salar*]  
MACAHLCKEADIKTALEACKAADTFNFKTFHTIGFASKSADDVKKAFKVIDQDASGFIE  
VEELKLFQNFQCPKARELTAETKAFKAGDADGDMIGIDEFAVLVKQ  
>ACJ04729.1 Gal d 1; ovomucoid [*Gallus gallus*]  
MAMAGVFLVFSFVLCGLPDAVFGAEVDCSRFPNATDMEGKDVLCNKDLRPICTDGV  
YTNDCLLCAYSVEFGTNIKEHDGCKETVPMNCSSYANTTSEDGKVMVLCNRAFNPVCG  
TDGVTYDNECLLCAHKVEQGASVDKRHDGGCRKELAAVSVDCEYPKPDCTAEDRPLCGS  
DNKTYGNKCNFCNAVVESNGTLTSLSHFGKC  
>ACJ23861.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]  
MGVFTHESETSVIPPARLFKAFVLDSNLIIPKVLPAQAIKSTEIEGNGGPGTIKKITFG  
EASKYKYSKHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY  
QTKGDFQLKEEQVQAAIEKATGLFKA VEAYLLANPDLYK  
>ACJ23862.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]  
MGVFTHESETSVIPPARLFKAFVLDSNLIIPKVLPAQAIKSTEIEGDGPGTIKKITFG  
EASKYKYSKHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY  
QTKGDFQLKEEQVQAAIEKATGLFKA VEAYLLANPDLYK  
>ACJ23863.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea*

sativa]

MGVFTHESQETSVIPPARLFKAFVLDSDNLI PKVLPQAIKSTEIEGNGGPGTIKKITFG  
EASKYKYSRHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY  
QTKGDFQLKEEQVQAAIEKATGLFKAVEAYLLANPDLYK

>ACJ23864.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG  
EGSQFN YVKHRIDEIDNANFTYACTLIEGDAISETLEKIAYEIKLVASPDGG SILKSTSK  
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAYH

>ACJ23865.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG  
EGSQFN YMKHRIDEIDNANFTYAYTLIEGDAISETLEKIAYEIKLVASPDGG SILKSTSK  
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAYH

>ACJ23866.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG  
EGSQFN YVKHRIDEIDNTNFTYACTLIEGDAISETLEKIAYEIKLVASPDGG SILKSTSK  
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAYH

>ACJ37389.1 Bla g 4; lipocalin [Blattella germanica]

VLALCATDTLANEDCFRHESLVPNLDYERFRGSWIIAAGTSEAL TQYKCWIDRFSYDDAL  
VSKYTD SQGKNRTTIRGR TKFEGNKFTIDYNDK GKAFSAPYSVLATDYENYAIVEGCPAA  
ANGHVIIYVQLRMTLRRFHPKLGDKEMLQHYTLDQVNQNKKAIEEDLKHFNLKYEDLHSTC  
H

>ACJ37391.1 Per a 4; lipocalin [Periplaneta americana]

AGDSDSCQIGTSFTGLDMTKYVGTWYELFRTPNSDEEDFTNCEYDKYTL DENGVIQVTSVA  
YTNSIRGFITSTGTVPSWTEDTFDIAYGDDETSSTYFMVGTDYQTY SIVAGCLDNDYSR  
HLYWIASHETSFDATKAKVNEVLAPYNLSLDDMEPVDQSYCVQYKS

>NP\_001133181.1 Sal s 3; aldolase [Salmo salar]

MPHAFPF LTPDQKKELSDI ALKIVAKGKGILAADESTG SVAKRFQSINTENTEENRRLYR  
QLLFTADDRAGPCIGGVIFFHETLYQKTDAGKTFPEHVKS RGVVGIKVDKGVVPLAGTN  
GETTTQGLDGLYERCAQYKKGDCDFAKWRCVLKITSTTPSRLAIMENCNVLARYASICQM  
HGIVPIVEPEILPDGDHDLKRTQYVTEKVLAAAMYKALSDHHVYLEGTL LKPNMVTAGHSC  
SHKYTHQEIAMATVTALRRTVPPAVPGVTF LSGGQSEEEASINLNMNQ CPLHRPWALTF  
SYGRALQASALKAWGGKPGNGKAAQEEFIKRALANSLACQGYVASGDSAAAGDSL FVAN  
HAY

>CAT99611.1 Mal d 2; thaumatin-like [Malus domestica]

ASRSVDAPSPWSGRLWGRTRCSTDAAGKFT CETADCGSGQVACNGAGAVPPATLVEITIA  
ANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNMCPAQLQVKAADG SVISC  
KSACLAFGDSKYCCTPPNDTPETCPPT EYSEIFEKQCP

>CAT99612.1 Mal d 2; thaumatin-like [Malus domestica]

ASRSVDAPSPWSGRFGWGRTRCSTDAAGKFT CETADCGSGQVACNGAGAVPPATLVEITIA  
ANGGQDYDVS LVDGFNL PMYVAPQGGTGECKPSSCPANVNMCPAQLQVKAADG SVISC  
KSACLAFGDSKYCCTPPNDTPETCPPT EYSEIFEKQCP

>CAT99617.1 Mal d 4; profilin [Malus domestica]

MSWQAYVDDHLMCDIDGHHLTAAAILGHDG SVWAHSSTFPKFKPEEITAIMKDFDEPGSL  
APTGLHLGGTKYMIQEGGAVIRGKKGSGGVTVKKTGQALVFGIYEETLTPGQCNMIVE  
RLGDYLIDQGV

>CAT99618.1 Mal d 4; profilin [Malus domestica]

AQSATFPQLKPEEVTGVMNEFNEPGSLAPTGLYFGGTYKVMIPGEPGVVIRGKKGPGGV

VKKSTMALLIGIYDEPM

>CAT99619.1 Mal d 4; profilin [*Malus domestica*]  
GNSLTAAAILGQDGSVWAQSATFPAPFKPEEIAAILKDFDQPGTLAPTGLFLGGTKYMVIIQ  
GEPGAVIRGKKKSGGITIKKTSQALLIGIYDEPLTPGQCNIIVVERLGDYLIEQGL

>ACK76291.1 Der f 3; trypsin [*Dermatophagoides farinae*]  
MMILTIVVLLAANTWATPILPSSPNATIVGGVKAKAGDCPYQISLQSSSHFCGGSILDEY  
RILTAAHCVNGQSACKLSIRYNTLKHASGGKEIQVAEIQHENYDSMTIDNDVALIKLKT  
PMTLDQTNAPVPLPPQGS DVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD  
QLYSKAGADVSENMICGGDVANGGVDSQCQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYP  
GVYTRVGNFVDWIESKRSQ

>ACK76292.1 Der f 3; trypsin [*Dermatophagoides farinae*]  
MMILTIVVLLAANTWATPILPSSPNATIVGGVKAKAGDCPYQISLQSSSHFCGGSILDEY  
WILTAAHCVNGQSACKLSIRYNTLKHASGGKEIQVAEIQHENYDSMTIDSDVALIKLKT  
PMTLDQTNAPVPLPPQGS DVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD  
QLYSKAGADVSENMICGGDVANGGVDSQCQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYP  
GVYTRVGNFVDWIESKRSQ

>ACK76296.1 Der f 6; chymotrypsin, serine protease [*Dermatophagoides farinae*]  
MIKIFLVTILIVITVTVDARFPRSLQPKWAYLDSNEFSRSKIGDSPIACVGGQDADLAE  
APFQISLLKDYLIKMSHMCGLISESTVVTAAHCTYQKASSLSVRYGTNQRRTSSSYGD  
LKVKTI IQHESYDPDTIQNDISLLILSKPVVSTNVRMIEIETDDIVDGDKVTIYGWGLT  
DGNGKDL PDKLQKGSMTIVGNDRCNKWSINAIHPGMICALDKTQSGCNGDSGGPLVSA  
NRKLTGIVSWGSPKCPPGEYMSVFTRPKYYLDWITKNIV

>ACK76297.1 Der f 6; chymotrypsin, serine protease [*Dermatophagoides farinae*]  
MIKIFLVTILIVITVTVDARFPRSLQPKWAYLDSNEFSRSKIGDSPIAGVGGQDADLAE  
APFQISLLKDYLIKMSHMCGLISESTVVTAAHCTYQKASSLSVRYGTNQRRTSSSYGD  
LKVKTI IQHESYDPDTIQNDISLLILSKPVVSTNVQMIETDDIVDGDKVTIYGWGLT  
DGNGKDL PDKLQKGSMTIVGNDRCNKWSIDAIHPGMICALDKTQSGCNGDSGGPLVSA  
NRKLTGIVSWGSPKCPPGEYMSVFTRPKYYLDWITKNIV

>ACK76299.1 Der f 7; bactericidal permeability-increasing like [*Dermatophagoides farinae*]  
MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEQSETIDPMKVPDHADKFER  
HVGILDFKGE LAMRNI EARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY  
KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFG  
VLSDVLT AIFQD TVRKEMTKVLAPAFKRELEKN

>BAH09387.1 dipeptidyl peptidase [*Trichophyton mentagrophytes*]  
MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKDRPSG  
WNLNLKNGDISVLT TDSVSEITWLG DGT KIVVNGTDSVKGGVGIWISDAKNFGNAYK  
AGSVNGAFSGLKLAKSGDKINFGVYQSTTKGDLYNEAAAKEAVSSARIYDSL FVRHWD T  
YVGTQFNAVFSGALTKSGDKYSFDGKLNKLVHPVKYAESPYPPFGGSGDYDLSSDGKTVA  
FMSKAPELPKANL TTTYIFVPHDGSRVAEPINKRNGPRTPQGIEGASSSPVFS PDGKRI  
AYLQMATKNYESDRRVIYIAEVGSNKPVQRIASNWD RSPEVVKWSSDGR TLYVTAEDHAT  
GKLFTLPADARD SHKPAVVKHDG SVSSFYFVGS SKSVLISGNSLWSNALFQVATPGRPNR  
KLFYANEHDP ELKGLPNDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG  
SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFQKLTDDITNDWGGAPYKDLVKIWEHV  
RDHIKYIDTDNGIAAGASFGGF MVNWIQGHDLGRKFKALVSHDGT FVGS SKIGTDELFFI  
EHDFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHND FDFRLSVAEGVGLFNVLQKEG  
IPSRFLNFPDETHWVTKPENSLVWHQQVLGWINKWSGINKSNPKSIKLSDCPIE VVDHEA  
HSYFDY

>BAH10157.1 tropomyosin [*Ruditapes philippinarum* (*Venerupis philippinarum*)]  
MDAIIKKMQAMKLEKENALDKAEQLEQLRDVEETKAKAEEDL TLLQKKYTNLENEFDQV

NEKYNEGVNKLQEVSEKRVTEAEDEIKGYTRRIQLLEDDLERTQVKLDEATSKLEDATKTA  
DESERGRKLVLESRSIADDDRIDALEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERSE  
TRLEAAEAKITELSEELAVVGNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA  
EAERVVNLQKEVDRLDELLAEKEKYKAISDELDQTF AELAGM

>BAH10148.1 tropomyosin [*Haliotis discus*]  
MDAIKKKMLAMKMEKENAVDRAEQNEQKLRDTEEQKAKIEEDLNNLQKKCANLENDFDNV  
NEQLQEAMAKLETSEKRVTEMEQEVSGTTRKITLLEEDLERNEERLQTATERLEEASKAA  
DESERGRKLVLESRSIADDDRIDQLEAQLKEAKYIAEDAERKYDEAARKLAITEVDLERAE  
ARLEAAEAKILELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT  
EAERTVSKLQKEVDRLDELLAEKEKYKAISDELDQTF AELAGY

>BAH10149.1 tropomyosin [*Turbo cornutus*]  
MDAIKKKMLAMKMEKENALDRAEQLEQKLRDTEEQKAKIEEDLNNLQKKCANLENDFDNV  
NEQLQDALSKLENSEKRVTEMEQEVSGTTRKITLLEEDLERNEEGLQTATERLEEASKAA  
NESERGLADDERIDQLEAQLKEAKYIAEDAKYIAEDAERKYDEAARKLAITEVDLERAE  
ARLEAAEAKILELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT  
EAERTVSKLQKEVDRLDELLAEKEKYKAISDELDQTF AELAGY

>BAH10150.1 tropomyosin [*Neptunea polycostata*]  
MDLIKKKMLSMKMDKENALDRADVMEQKFRDAEDQKSKLEDDLNNLQKKYSQLENEFDNV  
NEGLLDANAKLETQDKRVNEMEQEISGLNRRRIQLLEEDLERSEERLQTATEKLEEATKAA  
DESERARKVLESKNQTAESADSLEAQLKESKYIAEDAERKYDEAARKLAITEIDLERA  
TRLEAAEAKCYELDEQLHVVGNNIKTLSIQNDQASQREDSYEETIRDLTQRLKDAENRAQ  
EAERTVTKLQKEVDRLDELLAEKERYKNISDELDQTF AELAGY

>BAH10151.1 tropomyosin [*Scapharca broughtonii*]  
MDSIKKKMIAMKMEKENALDRSEQLEQKLRDTEEQKAKVEEELGAYQKKFSILENDFDTV  
NTKWEDASVKLEEA EKLT ESEQEIASLTRKTTLLEDDIAKNEEKLSATQKLEEASHAA  
DESERGRKLVLESRSFADDERIDALEAQLKEAKYIAEDADRKYDEAARKLAITEVDLERAE  
ARLEAAEAKIIELEEEELTVVGANIKTLQVQNDQASQREDSYEETIRDLTANLKDAENRAT  
EAERTVSKLQKEVDRLDELLAEKERYKAISDELDQTF AELAGY

>BAH10152.1 Cra g 1; tropomyosin [*Crassostrea gigas*]  
MDSIKKKMIAMKMEKENAQDRAEQLEQQLRDTEEQKAKIEEDLTSLQKKHSNLENEFDTV  
NEKYQECQTKLEEA EKTA SEAEQEIQSLNRRRIQLLEEDMERSEERLQTATEKLEEASKAA  
DESERNRKVLENLNNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAITEVDLERAE  
ARLEAAEAKVYLEEQLSVVANNIKTLQVQNDQASQREDSYEETIRDLTQRLKDAENRAT  
EAERTVSKLQKEVDRLDELLAEKERYKAISDELDQTF AELAGY

>BAH10153.1 tropomyosin [*Fulvia mutica*]  
MEAIKKKMQSMKNEKENAIDKAEQLEIKLKDTEDESKAKIEEDLTSLQKKYTNLENEFDQV  
NEKHADSVAKLEAAEKRLTETEDEIKGYTRKIQLLEDDLERTQVKLDEATGKLEEATKSA  
DESERGRKLVLESRSIADDDRIDGLEKQVKDAKYVAEESDRKYDEAARKLAITEVDLERAE  
TRLEAAEAKIVELTEELSVVGNLKGALQNAVDQASQREDSYEETIRDLTQRLKDAENRAS  
EAERVVIKLQKEVDRLDELLQEKEKYKQISDELDQTF AELAGM

>BAH10154.1 tropomyosin [*Pseudocardium sachalinense*]  
MDSIKKKMQAMKIEKENALDKSEQLDQKLDVEETKAKVEEDLSSLQKKYTNLENEFDKV  
NEQYNESVVKLEASEKRVTECEDEIKGYTRRIQLLEDDLERTQVKLDEALLKLEDATKTA  
DESERGRKLVLESRSIADDDRIDGLEKQVKDAKYVAEADRKYDEAARKLAITEVDLERAE  
TRLEAAEAKITELSEELSVVANNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA  
EAERVVNLQKEVDRLDELLAEKEKYKTISDELDQTF AELAGM

>BAH10155.1 tropomyosin [*Tresus keenae*]  
MDSIKKKMQAMKIEKENALDKAEQLDQKLDTEDESKAKIEEDLSSLQKKYTNLENEFDQV  
NEKYNDGVVKLESSEKRVTECEDEIKGYTRRIQLLEDDLERTQVKLEEATLKLEDATKTA  
DESERGRKLVLESRSIADDDRIDQLEKQVKDAKYVAEADRKYDEAARKLAITEVDLERAE

TRLEAAEAKITELSEELSVVANCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAS  
EAERVVKNLQKEVDRLDELLAEKEKYKQISDELDTFAELAGM  
>BAH10156.1 tropomyosin [*Solen strictus*]  
MDSIKKKMQAMKLEKENALDKSEQLKQKLEKEDSKARAEEDLSSLQKKFTNLENEFDKV  
NEQYQEGVIKLEASEKRVTECEDEIKGFTRRIQLLEDDLERTQAKLDEALLKLEDASKTA  
DESERGRKVLERSIADDDRIDQLEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERAE  
TRLEAAEAKITELSEELQVVGNNKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA  
EAERVVKNLQKEVDRLDELLAEKEKYKQISDELDTFAELAGM  
>ACL36923.1 Tyr p 34; troponin C [*Tyrophagus putrescentiae*]  
MSVEELSKEQVQMLRKAQDFDRDKGYIHTNMVSTILRTLQGTFFENDLQQLIIEIDAD  
GSGELEFDEFLLTARFLVEEDTEAMQEELEAFRMYDKEGNGYIPTSALREILRALDDK  
LTEDELDEMIAEIDTDGSGTVDFDEFMEMMTGD  
>ACM24358.1 Bla g 9; arginine kinase [*Blattella germanica*]  
MVDAAVLEKLEAGFAKLAASDSKSLKLYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN  
HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI  
ISTRVRCGRSMQGYFPNPLTEAQYKEMEDKVSSTLSGLEAELKGFYPLTGMTKEVQQK  
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGDLG  
QVYRRLVTAVNDIEKRIPFSDHDDLGLTFCPTNLGTTVRASVHIKVPKLAADKAKLEEV  
AGKYNLQVRGTRGEHTEAEGGVYDISNKRMMGLTEYDAVKEMNDGIAELIKLESSL  
>CAR48256.1 Xip g 1; calcium-binding protein, parvalbumin [*Xiphias gladius*]  
MAFAGVLSADADVAALAEACKDAGTFDYKFFKSCGLAAKSTDDVKKAFAIIDQDKSGFIE  
EDELKFLQNFKAAARPLTDAETEAFLKAGSDGDGKIGAEFFAALVTA  
>ACM89179.1 Lit v 4; calcium-binding protein, sarcoplasmic calcium-binding protein  
[*Litopenaeus vannamei* (*Penaeus vannamei*)]  
MAYSWDNRVKYVVRMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN  
LWNEIAELADFNKDGVEVTVDEFKQAVQKHCQGGKYGDFPGAFKVFIANQFKAIDVNGDGK  
VGLDEYRLDCITRSFAAEVKEIDDAYNKLTTEDDRKAGGLTLERYQDLYAQFISNPDESC  
SACYLFGPLKVVQ  
>ACN32322.1 Asc l 3; tropomyosin [*Ascaris lumbricoides*]  
MDAIIKKKMQAMKIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKKMMQTENDLDKA  
QEDLSVANSNLEEKEKKVQEAEEVAALNRRMTLLEEELERAEEERLKLATEKLEEATHA  
DESERVRKVMENRSFQDEERANTVESQLKEAQMLAEADRKYDEVARKLAMVEADLERAE  
ERAEEGENKIVELEEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE  
FAERSVQKLQKEVDRLDEDELVHEKERYKSISEELDTQFQELSGYRSD  
>3C3V\_A Ara h 3; 11S globulin, cupin [*Arachis hypogaea*]  
ISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNPNNQEFECAGVALSRLVLRNAL  
RRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYEEPAQQGRRYQSQRPPRRLQEEDQSQQQ  
QDSHQKVHRFNEGDLIAVPTGVAFWLYNDHDTDVAVSLTDTNNDNQLDQFPRRFNLAG  
NHEQEFLRYQQSRQRSRRRSLPSPYSPQSQPRQEEREFSPRGQHSRRERAGQEEHEGG  
NIFSGFTPEFLAQAFQVDDRQIVQNLGENESEEQGAIIVTVRGGLRILSPDRKRGADEEE  
EYDEDEYDEYDEEDRRRGRGSRGSGNGIEETICTATVKKNIGRNRSPDIYNPQAGSLKTAN  
ELNLLILRWLGLSAEYGNLYRNALFVPHYNTNAHSIIYALRGRAHVQVVDNNGNRVYDEE  
LQEGHVLVVPQNFVAVAGKSQSDNFYVAFKTDSPRSIANLAGENSVIDNLPPEEVVANSYG  
LPREQARQLKNNNPFKFFVPPSQQSRAVA  
>ACN62248.1 Ara h 2; 2S albumin, conglutin [*Arachis hypogaea*]  
MLTILVALALFLAAHASARQQWELQGDRRQCQSLERANLRPCEQHLMQKIQRDEDSYER  
DPYSPSQDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRMCCEALQQIMENQSDRLQG  
RQQEQQFKRELRLNPQQCGLRAPQRCDLDVESGGDRDY  
>ACN87223.1 Pro c 1; tropomyosin [*Procambarus clarkii*]  
MDAIIKKKMQATKLEKDNAMDRADTLEQQNKEANIRAEKAEEEVHNLQKRMQHLENDLDQV

QESLLKANTQLEEKDKAISNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQDTFSELTGY

>AC034813.1 Sal k 1; pectin methyltransferase [Salsola kali]  
QLIPPNPAAELESWFQGAVKPVSEQKLEPSVWQAESGGVETIEVRQDGSQKFKTISDAVK  
HVKVGNTKRVIITIGPGEYREKVKIERLHPYITLYGIDPKNRPTITFAGTAAEFQTVDSA  
TLIVESDYFVGANLIVSNSAPRPDQKRGKAQASALRISGDRAAFYNCKFTGFQDTVCDK  
GNHLFKDCYIEGTVDIFGEARSYLNLTELHVVPDPMAMITAHARKNADGVGGYSFVHC  
KVTGTGGTALLGRAWFEARVVSFCNLSDAVKPEGWSDNNKPAQKTIFFGEYKNTGPG  
AAADKRVPTKQLTEADAKTFTSLEYIEAAKWLPKPPKPV

>AC034814.1 Sal k 3; cobalamin independent methionine synthase [Salsola kali]  
MASHVVGYPKMPKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQADAGIKYIPSN  
TFAYYDQVLDTTAMLGAVPARYGFNGGEIGFDLYFSMARGNASLPAMEMTKWFDTNYHYI  
VPELGPEVKFAYSSHKAVDEYKEAKALGVDTVPVLVGPVSYLLLSKAAKGVESFPLLSL  
LPKILPVYKEVIAELKAAGASTIQFDEPTLVMDLESHQLKAFTDAYADLESTLSGLNVLV  
ETYFADLTPEAYKTLVSLNGVTAFGFDLVRGKTLDLIKSGFSPGKYLFAGVVDGRNIWA  
NDLAASLTLQSLIVGKDKLVVSTSCSLLHTAVDLVNETKLDDEIKSWLAFAAQKQVLE  
VNALAKALAGQKDEAFFSANAAALASRKS SPRVTNEAVQKAAAGLKGSDHRRATTVSARL  
DAQQKLNLPVLPPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAIKEEISKVVKLQEE  
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTVNGWVQSYGSRVCPPIIYGDVSRPKAMTV  
FWSSLAQSMTSRPMKGLTGPVTILNWSFVRNDQPRHETCYQIALAIEDEAEDLEKAGIN  
VIQIDEAALREGLPLRKS GHGFYLVAVHSFRITNVGIQDQTTQIHTHMCYSNFNDIHSI  
IDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRIPPTTEELADRIRKMLA  
VLESNVLWVNPDCGLKTRKYNEVNPALSNMYYAAKPI

>CAX32963.1 Gal d 8; calcium-binding protein, parvalbumin [Gallus gallus]  
MAMTDVLSAEDIKAVGAFSAAESFNKFFEMVGLKKKSPEDVKKVFHILDKDRSGFIE  
EEELKFVLKGFPTDGRDLSKDKETKALLAAGDKDGDGKIGADEFATMVAES

>AC056333.1 Cor a 14; 2S albumin, conglutin [Corylus avellana]  
MARLATLAALFAALLLVAAAAFRTTITTTVDVEDIVNQQRGREGSCREQAQRQQLNQ  
QRYMRQSQYGSYDGSNQQQQQEQLEQCCQQLRQMDERCRCEGLRQAVMQQQGEMRGEEMR  
EVMETARDLPNQRLSPQRCEIRSARF

>ACP43298.1 Ama r 2; profilin [Amaranthus retroflexus]  
MSWQAYVDDHLMCEIEGTTNHLTGAAILGLDGSVWQAQSAFQPKPDEIAAIVEDFDEPG  
TLAPTGLHLGGTKYMIQGEPAVIRGKKGAGGICVKKTGQALVMGIYDEPVTGQCENMI  
VERLGDYLIEQGY

>BAH59276.1 abhydrolase [Protortonia cacti]  
MPVRMLFSILISLILSVVVGNEHYPKVSPAQFSAAFHGYELPQKEGRADEVDSNEVKFY  
LYTRQNLHKYELHTGYNCSNSYESLRNSTYNVRKETKFLIHAWTQSPKDINDIYIYLYA  
ENVNVIMVDWMSYQTCNYNSTSYVVIPKVAKALSDLMKLLTGYGAVPQKNFHVIGFLHG  
AHIAGIAGKYISPLRISRISGLDPVGYNIDGTALPVLQNGDADFIDVIYTSIEYYGTQRQ  
IGDLSFYPPDRGTHPQKQCPPDPNEWVCSALASIKYWRESITSPTAFSAIRCDNVVQYHES  
RCPGPNTTMGEYASRNAPFGKYLLNTNPEPPYSQS

>ACR43473.1 Cra c 1; tropomyosin [Crangon crangon]  
MDAIKKKMQAMKLEKDNAMDRAADTLEQQNKEANNRAEKSEEEVFSLQKRMQQLENDLDSV  
QEALLKANAHLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQDTFSELSGY

>ACR43474.1 Cra c 2; arginine kinase [Crangon crangon]

MVDAEVLKLEAGYKLEAATDCKSLKKYLTKEVFDELKTKKTALGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFKQSDKHPGKDFGDLEKFNVDPEGTFV  
VSTRVRCGRSMGYFPNPLTEAQYKEMESKVSSTLSSLEGELKGTYYPLTGMSKDVQQK  
LIDDHFLFKEGDRFLQAANACRYWPAGRGIYHNDNKTFLVWVNEEDHLRIISMQMGDLG  
QVFRRLTSAVNEIEKRIPFSHHDRLGFLTFPCPTNLGTTVRASVHIKLPKLAANRDKLESV  
AGKYNLQVRGTRGEHTEAEGGIYDISNKRRLMGLTEFQAVKEMQDGIKMEKEM  
>ACR43475.1 Cra c 4; calcium-binding protein, sarcoplasmic calcium-binding protein  
[Crangon crangon]  
MAYTWDNRVYVRYMYDIDNNGFLDKNDFECLAVKNTLIECRGEWSAEKYAANQKIMSN  
LWNEIAELADFNKDG EVTVEEFKQAVQKHCNGKPF GDFPSAFKTFIANQFKTIDVNGDGL  
VGVDEYRLDCISRSAFSCIKEIDDAYNLLCTEEDKKAGGINIARYQELYAQFISNPDEKC  
NAVYLFGLKEVV  
>ACR43476.1 Cra c 8; triosephosphate isomerase [Crangon crangon]  
MSGSRKFFVGGNWKMNKDAAIDGIVDFMKGKPLNPNTTEVWVGCPQCYLSYTREKLP AEI  
GVAAQNCYKVAKGAFTEISPAMVKDCGCEWVILGHSERRNVFNEPDQLISEKVGHALEA  
GLKVIPCIGEKLDERESNRTEEVVFAQMKALVPNISDWSRVVIAYEPVWAIGTGKTASPE  
QAQDVHAKLRQWL TENVSAEVAESCRIIYGGSVSPSNCAELAKMGDIDGFLVGGASLKPD  
FVTIINARG  
>ACR43477.1 Cra c 5; myosin light chain [Crangon crangon]  
MAADLSARDVERVKFAFSIYDFEFGNQIDAFYIGDCLRALNLTALIAKLGTEKRKE  
KMIKLDLDFMPLFAQVKKDKDAGSYEDFIEVLKLYDKAENGTMMYAELEHILLSLGERLDK  
AELEPILRECCPPEDDEGLIPFEPFVKKLTQLL  
>ACR43478.1 Cra c 6; troponin C [Crangon crangon]  
MDSLEPDQIDALKKAFDSFDTENQGFITADTVATILRMMGVKISDKNLAEVIAETDEDGS  
GQLEFEFVLDLSSKFLIEEDEEALKAELREAFRIYDKEGQGFITTDVLKEILTEIDNKLT  
PEDLDGIIIEVDEDEGSGTLDLDFDEFMEMMSG  
>ACR77509.1 Che a 2; profilin [Chenopodium album]  
MSWQTYVDDHLMFPIEETGNHLTAAAIIVGLDGSVWAQSSTFPQLKQE EVKAICNEFDV PN  
TLAPTGLFLGG EKYMVIQGE PGAVIRGKKKPGGVCIKKTNQALVFGIYNPVT PGQCNMV  
VEKLG DYLV EQGM  
>ACS14052.1 Per a 7; tropomyosin [Periplaneta americana]  
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAE EEARSLQKKTQ QIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAD  
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANLREEEYKQIKLTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMTFTEL VGY  
>ACS34771.1 Sal k 4; profilin [Salsola kali]  
MSWQTYVDDHLMCEIEGTNNHLTAAAILGVDGSVWAQSANFPQFKPDEISAVVKEFDEAG  
TLAPTGLHLGGTKYMVIQGEAGQVIRGKKKPGGICVKKTGQALIFGIYDEPVT PGQCNMI  
VERLGDYLV EQGM  
>CAQ72968.1 Seb m 1; calcium-binding protein, parvalbumin [Sebastes marinus]  
MALAASLNAADITAALAACSGVDTFKHKDFFGKVGLSAKSADDIKNAFKVIDQDKSGFIE  
EEELKFLQNF SATARALTEAET AFLKAGDSGDGMIGMDEFAAMVKG  
>CAQ72969.1 Seb m 1; calcium-binding protein, parvalbumin [Sebastes marinus]  
MAFASVGLKDADIAAALDGCKDAGKFNHKTFFKTCGLSGKSSDEVKKAFAIIDQDISGFI  
EEEELKLFLQTFKAGARALSDAETKEFLKAGDSGDGKIGADEWAAMVQ  
>CAQ72970.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]  
MALASLLKGADIDAALKACEAKDSFKHKDFFAKIGLATKSAADLKKAFEIIDQDKSGFIE  
EEELKFLQNFKAGARALDAETKAFKAGDADGDGMIGVDEFVAVMIKP  
>CAQ72971.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]

MAFAGLLSDADIAAALGACTAADTFDHKSFFKKVGLSGKSADDVKKPFYIIDQDKSGFIE  
EEELKFLQNFKAGARALSDKETKAFLAAGDADGDMIGVDEFAMVKAR  
>CAQ72972.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]  
MAFAAFLKEADITAALGACKGADSFDHKAFFAKVGLKKGSGDELKKAFFEIIDQDKSGFIE  
EEELKFLQNFCKGARALTDGETKKFLKAGSDNDGKIGIDEFAALINH  
>CAZ76054.1 Tri a 34; glyceraldehyde-3-phosphate-dehydrogenase [Triticum aestivum]  
MGKIKIGINGFGRIGRLVARVALQSDDELVAVNDPFITTEYMTYMFKYDTHVGHWHKHS  
IKLKDDKTLFGEKPVTVFGVRNPEEIPWGEAGADYVVESTGVFTDKDKAAAHLKGGAKK  
VVISAPSKDAPMFVGVNEDKYTSVDNIVSNASCTTNCLAPLAKIINDNFGIIEGLMTTV  
HAITATQKTVDGPSSKDWRRGGAASFNIIPSSTGAACKAVGKVLPELNGKLTGMSFRVPTV  
DVSVDLTVRTEKAASYDDIKKAIAKAASEGKLGKIMGYVEEDLVSTDFVGDSSIFDAK  
AGIALNDHFVKLVSWYDNEWGYSNRVVDLIRHMAKTQ  
>CAZ76052.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]  
TGPYCYAGMGLPINPLEGREYVAQQTGCGISISGSAVSTEPGNTPRDRCKELYDASQHC  
RCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDFAKVLVTPGHCVMTVHNAPYCLGLDI  
>ACT37324.1 Sta c 3; exodesoxyribonuclease [Stachybotrys chartarum]  
ASVTFWTLDNVDRTLVTFTGNPGSAAIETITVGAENTTVEFPGSWVGNWYAYPTDAEDVP  
GMLGEVQFGWNGLTDFVSAIVNPTDHDNVKQMPAESRKPMSGCEVFPCDNAYWLPDD  
IQTKVTHEVDLWTTLLGAGSTGLTF  
>CAQ68249.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]  
DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVPKIAPKSENVVTVKVMGDNGVLACA  
IATHAKIRD  
>CAQ68250.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]  
RPSSIKTFEEYKKAFFNKSATFEDEEAARKNFLESVKYVQSNNGGAINHLSLDEFKNR  
FLMSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGV  
AATESAYLAYRNQSLDLAEQELVDCASQHGCGNGDTIPRGIEYIQHNGVVQESYRYVARE  
QSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQ  
RDNGYQPNYHAVNIVGYSNAQGVYWIWRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVV  
IL  
>ACV04796.1 Api g 2; lipid transfer protein [Apium graveolens]  
MGVSKVAIAVAVMLMVVINHPAVVEGLTCGQVTGKLGGLGKGGYPSACC GGKVG  
LNSLAKTPADRKQACACLKTLGASVKGINYGAAALPGKCGIRIPYPISTDCSRVN  
>BAD74060.2 Der f 2; NPC2-like [Dermatophagoides farinae]  
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFLEALFDA  
NQNTKTAKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQYDAKYTWNVPKIAPKSEN  
VVVTVKLVGDNGVLACAIATHGKIRD  
>ACV04860.1 Blo t 8; glutathione S-transferase [Blomia tropicalis]  
MAPLKIGYWDVRGFAEPIRMLLKHNLIEFEETRYGFGNDSEESLPNRDEWLAEKFTLGL  
FPNLPYLFDGDFKMTESVAIILKRLARANGMIATTEPALSYSSEMIEAMIIDIRNRLINVVY  
AENSGTPEEFQKLDLRLERLETSLGQLEAFFQKHGSQWVAGDKLTYVDFLAYEYLDWYR  
VFKSTPIFEKFAKVS DYMKRFEELPSLKEYIARDEHRSASCLSPFARIGHRWAKE  
>ACY01951.1 unknown function [Cupressus arizonica (Hesperocyparis arizonica)]  
MDEVPSDESASGKRVLQSVHELEEVFKKFDANGDGKISGSELADILRSMGSEVDE  
AEVKAMMEEADTDGDGYVSLQEFVDLNIKATVKDLKNAFKVDFDRDCNGTISPALCETL  
KSVGEPCTIEESKNIIHNVKNGDGLINVEEFQTMMTSEM TDKSK  
>ACY38525.1 Can f 4; lipocalin [Canis familiaris]  
MKILLLCLALVLASDAQPLPNVLTQVSGPWKTLYISSNLDKIGDNGPFRIYMRGINVD  
IPRLKMSFNFYVKVDGECVENS VGASIGRDNLKGEYNGGNYFRIIDMTPNALIGYDVNV  
DSK GKITKVALLMGRGAHVNEEDIAKFKKLSREKGIPEENIYLGDTDNCPNHE

>ACY40650.1 Bla g 3; hemocyanin, arylphorin [Blattella germanica]  
IPADKVF LRKQWDVLR LRVHRIHQHSI IPEQVTVGDSYDIEANINNYKNPRVVKNFMALYK  
KDPVKRGEFSTYYIKHREQAIMLFELFYANDYDTFYKTACWARDRVNEG MFLYSFNIA  
IMHREDMQDIVIPAFYEIYPFLFVENDVIQKAYDYKMKESGHLNPHTHVIPVNFTLRNQ  
EQLLSYFTEDVFLNAFNNTYFRMYPTWFNKYEYDVPRHGEQFYYFYQQIYARYMLERY  
SNDMPDIKPFYTNKAFKTPYNPQLRYPNGQEV PARPAYMVPQDFDLYVSDIKNYERRVA  
DAIDFGYVFCDKMISHSLYNDKKGFEMLAIEIEGNSMHPDYGHIFHMYRSL LGHVTDPF  
HKNGEAPSALEHPETALRDPAFYQIWKRVQHYFYKFMKLPYYTREELTFDGVKIDNVDV  
GKLYTYFEPYEMSLGYSVKVENIQDAANVDIRARNYRLNHKPFYTNIEVTSEKETPVYVR  
VFLGPKYNYGHEYDLNERRNKFEIDRFYQLHAGKNAIERN SHESTVVAKEQDTPKVL  
YKKVNEAYEGKATYNYDKQTKFCGLPEHLLIPKGGKGGQAF TVYVIVTPYDKAVEKEEHH  
FKAYSYCGVGPHTY PDDKPLGFPFDRPIHSYDFVTPNMF MKDVFIFHKKYEEVEQH

>ACY40651.1 Bla g 3; hemocyanin, arylphorin [Blattella germanica]  
IPADKVF LRKQWDVLR LRVHRIHQHSI IPEQVTVGDSYDIEANINNYKNPRVVKNFMALYK  
KDPVKRGEFSTYYIKHREQAIMLFELFYANDYDTFYKTACWARDRVNEG MFLYSFNIA  
IMHREDMQDIVVPAFYEIYPFLFVENDVIQKAYDYKMKESGHLNPHTHVIPVNFTLRNQ  
EQLLSYFTEDVFLNAFNNTYFRMYPTWFNKYEYDVPRHGEQFYYFNQQMFARYMLERY  
SNDMPEIQPFYTKPFKTPYNPQLRYPNGQEV PARPAYMMPQDFDLMYVSDIKNYEK RVA  
DAVDFGYVFCDKMISHSLYNNKGL EWLGGQIVEGNSMHPDFYGHIFHMYRSL LGHITDPF  
HKHGVAPSALEHPETSLRDPAFYQIWKRVQHYFNKFMKQPYYTREELAFDGVKIDNVDV  
GKLYTYFEPYEMGLSNAVKVGKLEDV PNVDIRARNYRLNHKPFYTNVEVTSEK DTPVYVR  
VFLGPKYNYGHEYDLNERRNYFVEIDRFYQLHTGKNTIQRNSHDSSVVAQE QD TYKVL  
YKKVNEAYEGKTTYTYEKQDKYCGLPEHLLIPKGGKGGQAF TVYVIVTPYDKAVEKEEHH  
FKAYSYCGVGP HDSVYDKKPLGFPFDRPIHSYDFVTPNMF MKDVFIFHKKYEEVEQH

>ACY91851.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAICSSTSGTSSSLP SRTTVMLLLFFFTASVGITDAQVGV CYGMQGNLPPVSEVIALYK  
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWVQKNVRGFWSSV  
RFRYIAVGNEISPVNRTAWLAQFVLPAMRN IHDAIRSAGLQDQIKVST AIDLTLVGNSY  
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGG SLEVVVSESGWPSAGAF AATFDNGRTYLSNLI  
QHVKRGT PKRPKRAIETYL FAMFDENKKQPEVEKHFGLFFPNKQKYNLNFSAEKNWDIS  
TEHNATILFLKSDM

>ACZ57582.1 Ole e 11; pectin methylesterase [Olea europaea]  
MSCIAVEAVLLGILLYIPIVLSDDRAPIPSNSAQLNSWFDGIIQPVA VRKATMDPALVTA  
EGQTKVIK LKSDGSGDFKSINEAIKSIPDDNTKRVILSLAPGN YSEKVKIGMYKH YITFY  
GEDPNNM P ILVFGGTA AEYGTVD SATLIVESNYFSAVNLKIVNSAPRPD GKR VGAQAAAL  
RISGDKASFYNVKIYGFQDTL CDDK GKHFYKDCYIEGTVDFIFGSGKSIFLNTELH AVPG  
DQPAIITAQARKT DSED TGYFVNCRV TGGGAF LGRSWMPAAK VVFAYTEMVDAIHPEGW  
ILVKPEHESTVRFSEYNNKGPANMEKRAK FVKRLSDAEAKQSISLGSIEASKWLLPPRV  
VGLP

>ACZ74626.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]  
MAMLSSTSR TTGSLLSRTPVMLLLILYIASLGITDAQVGV CYGKLGNNLPPASEVIALYK  
QSNIKRMRIYDPNQEVLQALRGSNIELILGVPNSDLQSLTNPSNANSWVQKNVRDFWSSV  
RLRYIAVGNEISPVNGGTAWLAQFVLPAMRN IHDAIRSAGLQDQIKVST AIDLTLMGNTY  
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGG SLEVVVSESGWPSAGAF AATFDNGRTYLSNLI  
QHVKGGTPKRPDRAIETYL FAMFDENQKQPEVEKHFGLFFPDKR PKYNLNFSAKKNWDIS  
TEHNATVFLKSDM

>ACZ95445.1 Ani s 10; unknown function [Anisakis simplex]  
MHLITALVLLLQLIHFITSSPIPQE VVGGPGPVVGGSGIGNVWEKANEQAAEQQNI GGPG

PVISGSGIGDVWVKANEPAEQQENIGGPGPVVSGSGIGNVWEKANEQAAHQQSIEGPGPV  
VSGSGIGNVWEKANEQAAHQQSIEGPGPVVSGSGIGDVWVKANEAQAAEQQNIIGGPGPVIS  
GSGIGNVWEKANEQAAEQQNIIGVGGPGPVKSGSGIGNVWEETNEEAASMQA  
>CAM31908.1 Act c 8; pathogenesis related protein, PR-10, Bet v 1-like [Actinidia  
chinensis]  
MGVVTYDMEIPSKVPPVKLYKAFILDGDTLVPKVLPHAIKCVKILEGDGCAGTIKEVTFG  
EGSHHKCVKQRVDAIDKDNLTYSYTIIEGDVLAEKFESISYHIKIVACPDGGSICKNRSI  
YTTKGDCKVSEEEIKLGKEKAAEIFKALEAYLLANPDYC  
>CAM31909.1 Act d 8; pathogenesis related protein, PR-10, Bet v 1-like [Actinidia  
deliciosa]  
MGAITYDMEIPSSISAEMFKAFVLDGDTIIPKALPHAITGVQTLLEGDGGVGTIKLTTFG  
EGSVHKSVKHRIDGLDENFTYSYSIIIEGALDVFESISYHIKIVATPDGGCICKNRSIY  
TPKCDAAQVSEEEIKAGKERASGIFKKVEAYLLANPDC  
>CBA13559.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]  
TGPYCYPGMGLPSNPLEGREYVAQQTGCVGIVGSPVSTEPGNTPRDRCKELYDASQHC  
WCEAVRYFIGRTSDPNSGVKLDLPGCPREPQRDSAKVLVTPGHCVMTVHNTPYCLGLDI  
>CBA13560.1 Tri a 15; alpha-amylase inhibitor [Triticum aestivum]  
SGPWSWCDPATGYKVSALTGCRAMVKLQCVGSQVPEAVLRDCCQQLADVNNNEWCRCELDL  
SMLRSVYQELGAREGKEVLPGRKVMKLTAAASVPEVRKVPINPSGDRAGVCYWAAYPD  
V  
>CAY54134.1 Tri a 21; gliadin [Triticum aestivum]  
VRVPVPQLQPQNPSQQQPQEQVPLVQQQQFLGQQQHFPGQQPFPPQQPYPQPQFLPQ  
LPYPQPQFPQQSYQPQPQPQPQPIISQQQAQLQQQQQQQQQILQQILQQQLIPCR  
DVVLQQPNIAHASSQVSQQSYQLLQQQLCCQLWQTPEQSRCQAIHNVIAIILHHQQQQQ  
QQQQQQQQQQQQQQQQQQQQQQSSQVSQYQQPQQQYPSGQGSFQPSQQNPQAQGFVQPQ  
QLPQFEEIRNLALQTLPAMCNVYIPPYCSTTIAPFGIFSTN  
>3FT1\_A Phl p 3; expansin [Phleum pratense]  
AVQVTFVTQKGSPPKLVLDIKYTRPGDSLAEVELRQHGSEWEPLTKKGNVWEVKSSKP  
LVGPFNFRFMSKGGMRNVFDEVIPTAFSIGKTYKPEEQEF  
>ADB92492.1 Per a 1; nitrile-specifier protein [Periplaneta americana]  
MKLPIMILAVLGVAFGKSLPTRNLQDDLNDLFALVPTDEIVAVIMDYLANDAEVQEAVAY  
LQGDEFHKIVSTVEGLQEFNFVQFLEDHGLDAVGYNQLHSLVGLWDPYVPPSQRKHARR  
GVGVDGLIDDIIAILPIDDLKALFQEKLETSPDFKAFYDAIRSPEFQSIQVQTLNAMPEYQ  
ELLQKLRDKGVDVDHYIELIRALFGLSRATRNLQDDLNDLFALIPTDQILAIAMDYLAND  
AEVQELVAYLQSDDFHKIITTVGLDAFNMFYFMKEHGLDWDYINEIHSIIGLPPFVP  
PTRRHARRGVINGLIDDVIAILPVDELKALFQEKLETSPDFKALYDAIRSPEFQSIIST  
LNAMPEYQELLQNLKRDGVDVDHFIELIRSLFGLP  
>ADB92493.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]  
MKTALVFAAVVALVACAAPAHKDYKQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVG  
NTYDIEANIGNYKYPRVVKQFMAYFKKGMPLRGEFVSVEKHFREQAIMLYNLFYFANDY  
DTFYKTACWARDRVNEGFMYSFSIAVFRDDMQGVMLPPPVEVYPYLFVDHVDIHMAQK  
YWMKNAGSNEHHSYVIPVNFLLKNQDQLLAYFTSDVNLNAFNNTYYRYYPYPSWYNTTLYGH  
TIDRRGEQFYTYKQIYARYFLERLSNDLPDVPYFYYSKPVKSAYNPRLRYHNGEEMPVR  
PSNLYVTNFDLYYIADIKNYEKREDAIDFGYVFEHVKPHSLYHDVHGMEYVADMIEGN  
MDSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPSALEHPETVLRDPAFYQLWKRVDHLF  
QKYKNRLLPRYTHDELAFEGVKVENVDVGKLYTYFEQYDVS LDMSVYVNVKVDQIPNVVDVHA  
RQYRLNHKPFYTYNIEVSSDKAQDVYVRVFLGPKYDYLGREYDLNDRRHVYFVEMDRFPHHV  
EAGKTVIERNSHDSNIVAPERDSYRTFYKKVQEAAYEGKSQYVVDKGHNYCGYPENLLIPK  
GKKGGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVGSNRKYPDNMPLGYPFDRKIYS  
NDFYTPNMYFKDVIIIFHKKYDEVGVQGH





>CBK62693.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
MAAGLLVFLVLAISEIASVKGLCEKPSLTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR  
DSKATCFYFDCDPTKNPGPPGAPKGKAPAPSPSSGGGAPPPSGGEGGER

>CBK62694.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
KLCEKPSLTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKRDSKATCFYFDCDPTKNPGP  
PPGAPKGKAPAPSPSSGGGAPPPSGGEGGDGPPPEGGEGGGDGGGEGGGDGGGEGGGEG  
GGDGGGDGGGEGGGEGGGER

>CBK62695.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
KLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKRDSKASCFCYFDCDPTKNPGP  
PPGAPKGKAPAPSPSSGGGAPPPSGGEGGGDGGGEGGGEGGGGGEGGGEGGGGGEGGGEG  
GGGGEGGGEGGGER

>CBK62697.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
KLCEKPSVTWSGNKVKQTDKCDKRCIEWEGAKHGACHKRDSKASCFCYFDCDPTKNPGPP  
PGAPKGKAPAPSPSSGGGAPPPSGGEGGGDGGGGRR

>CBK62698.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
MAAGLLVFLVLAISEIASVKGLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR  
DSKASCFCYFDCDPTKNPGPPGAPKGKAPAPSPSSGGGGEGGGEGGGER

>CBK62699.1 Amb a 4; defensin [*Ambrosia artemisiifolia*]  
MAAGLLVFLVLAISEIASVKGLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR  
DSKASCFCYFDCDPTKNPGPPGAPKGKVVKEVVVEGGGEGGGGGEGGGEGGGER

>BAI94503.1 lipid transfer protein [*Cryptomeria japonica*]  
MAMRMKSSSSMSSYRFSYQMMMLVLMVMTLVQIGAAQSDTNSCVNSLVPCASYLNATTKPP  
DSCCVPLLNVIQTQQQLCNLLNSSIVKQSSINITQALNIPRLCGDTNVSTDACSTNATA  
NAPSASTTSPVADTGDSSGIGATSLQIFLPLLAVFFLGVFKSFP

>BAJ04354.1 unknown function [*Cryptomeria japonica*]  
MARRLCSFLLSFLIIVSVWAENSKFARLNLASFTWKDAEDNKNC SAGELETSSLSVMHIQ  
GKCSFPRLLNSSWWTAVSESIKGD TARYRAMVKGWSAGKTMVNPQEDADIPLASGQAIS  
SSNYIIKLGFGTTPQSFYTVLDTGSNIAWIPCNPSCSGCSSKQPFEPKSSSTYNYLTCAS  
QQCQLLRVCTKSDNSVNC SLTQRYGDQSEVDEILSSETLSVGSQQVENFVFGCSNAARGL  
IQRTPSLVGFGRNPLSFVSQTATLYDSTFSYCLPSLFSSAFTGSLLLGKEALSAQGLKFT  
PLLSNSRYP SFYYVGLNGISVGEELVSI PAGTLSLDESTGRGTIIDS GTVITR LVEPAYN  
AMRDSFRS QLSNL TMASPTDLFDTCYNRPSGDVEFPLITLHFDDNLDLTLPLDNILYPGN  
DDGSVLC LAFLPPGGGDDV LSTFGNYQQQLRIVHDVAESRLG IASENC DG

>ADE74975.1 Asp v 13; alkaline serine protease [*Aspergillus versicolor*]  
MYSIKRTILLGALLPAVFGAPILEARRQTEKVPKYIVTFKSGLQAEQIDAHTTWASNV  
HKRNLERRDLTRDLYPGIEKNFKIHKFAAYVGSFDDATIEEIRNHKDV AHVEEDQVWYL  
DALTTQSDAPWGLGAISHQGDASSDYIYDTSAGADTYAYVVDTGINVDHSEFDGRASLAY  
NAAGGQHVDSVGHGTHVAGTIGGKTFGVSKKANLLSVKVFEGESSSTSIILDGYNWAAND  
IVSKSRTGKSAINLSLGGGYSYAFSNAVESAFDEGVLSVVAAGNENVDASNTSPASAPNA  
LTVAASTERNARASFSNYGEVVDIFAPGEDILSAWIGGNSATNTISGTSMATPHIVGLSL  
YLIALEGLSSPGDVT SRIKELATQ GALSGVSGSPNALAYNGAE

>BAJ07603.1 Onc k 5; vitellogenin, partial [*Oncorhynchus keta*]  
SMTDLSPFDDNIVNKIHYLFSEVNAVKCSMVGD TLTTFN NRKYPVNMPLSCYQVLAQDCT  
IELKFMVLLKKDHASEQNHINVKISDIDVDLYTEDHGVMVKV NEMEISKDNL PYTDPSGS  
IMIKQKGEVSLYAKSHGLQEVYFDSNSWKIKVVDWMKGQTCGLCGKADGEHRQEYRTPS  
GRLTKSSVSFAHS

>ADH10372.1 Cof a 1; chitinase [*Coffea arabica*]  
AGIVRYWGRGHDEPSSLAEFGRQEFATDVNIAFL EDFGGGRMPELNISHPLPSASDIEYC  
QKHQTKVFI SIAGQPSLSSVEDAE EVAAYVWNTYLGGKSSDRPFGKAVLDGVELHIHSGN  
TTYLDL LARAL KGYSNVISAVAAECPIPDALD TTIRTGVVDQVRVEFFDNPSCQFTPPK

DTSLLFPSWDNWSYDYPGVHKLKYLGIPISTIAPEGGYIPPNELVYHVLPLYLKKSPVYGGI  
MVFPYLHHEVNFQSMLRSYARAA  
>ADK22841.1 Sal k 4; profilin [*Salsola kali*]  
MSWQAYVDEHLMCNIEDTGNHILTSSAIVGVDGSIWAQSSNFPQVKPQEIEAINKEFDGPN  
TLAPTGLFLGGKYMVIQGEPAVIRGKKKPGGVCICKTTQALIFGIYDEPVAPGQCNMV  
VERLGDYLIEQGL  
>ADK22842.1 Sal k 5; Ole e 1-like [*Salsola kali*]  
KGGKGGHNLHVHVKGMVYCDTCRIQFITRVSTMMEGATVSLQCRNLTAGTETFKAQAVTDKL  
GMYTIKVDGDHEDDQCIVLVKSPGQECSEIPNDVYSEQAAKVTLTSNNGEASDVRNANA  
LGFLKKAPLPECPEVLKELDMYDVPGSVTQN  
>ADK27483.1 Pen ch 35; aldolase [*Penicillium chrysogenum*]  
MSSSLEQLKASGTTVVCDSGDFATIGKYKPDATTNPSLILAASKKPEYAAALIDTAVAYG  
KQNGKTLDEQVEATLDRLLVEFGKEILKIIPGKVSTEVDAKLSFDTQGSVNKALEIIKLY  
ADNGISKDRVLIKIASTYEGIKAAHILQTHGINCNTLMFSLVQAIAAAEEAGAYLISPF  
VGRILDWYKAAHKRDYTPQEDPGVKSVDIYNYKKFGYNTIVMGASFRNVGEITELAGC  
DYLTISPNNLEDLFNSTDAVPQKLNPAAGAASLEIKKREYLNNEADFRFDNFEEAMGVEKL  
REGISKFAADAVTLKQLLAQKIQA  
>ADK39021.1 Ost c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Ostrya  
carpinifolia*]  
MGVFNYEAEPSVIPAARLFKSYVLDGDKLIPKVAPQAISKVENVGGNGGPGTIKNITFA  
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSILKISSK  
FHAKGDHEVNAEEMKGAKEMAEKLLRAVESYLLAHTAEYN  
>ADK47394.1 Cla c 14; aldolase [*Cladosporium cladosporioides*]  
MSSSLDQLKASGTTVVCDSGDFATIGKYKPDATTNPSLILAASKKPEYAKLIDDAVAYG  
MKHGKTTEEKIDATFDNLLVQFGSEILKIVPGKVSTEVDAKLSFDTQGSVNKALEIIKLY  
KEAGIDKERVLIKLASTWEGIQAAHELQTKHGINCNTLMFSLVQAIAAAEEAGAYLISPF  
VGRILDWYKANTKQEYNASNDPGVKSVDIYNYKKYDYKTIVMGASFRNIGEITELAGC  
DYLTIPALLEQLYNSTDAVPQKKAEDVAKLDIEKKSULKDEALFRFDNFEDPMAVNKL  
SEGISKFAADAVTLKDILREKIEKA  
>ADK47876.1 Tha p 1; unknown function [*Thaumatococcus panyocampa*]  
MKLLILALTCAAAVWARPGETYSKYDTIDVNEVLQSERLLKGYVECLLDKGRCTPDGKE  
LKDTLPDALEHECSKCTEKQKSGADTVIRHLVKNRPELWKE LAVKYDPENIYQERYKDRL  
ESVKEH  
>ADK56160.1 Fel d 7; lipocalin [*Felis catus*]  
MKALLLAVGLSLITVLQAQDPPASGEDTMAMSGKWYLKAMITDRETSWKKPELVTPMTLT  
VLEGGNLKAETLLTNGQCKEVELILEKTSEPKKYTTYGGKRVVYIEPTEVKDHYIFYCE  
GEMQGEQARMAKLVGRDPESNEEALNFREFLRKAGFNQEIFSPKQSDTCPPGTDQEPEV  
>ADK92390.1 Der p 13; fatty acid-binding protein [*Dermatophagoides pteronyssinus*]  
MASIEGKYKLEKSEKFEFLDKLGVGFMVKTAAKTLKPTFEVAKENDQYVFRSLSTFKNT  
EIKFKLGEFEEDRADGKRVKTVINKDGNKVFVQTFQGDKEVKIVREFNGDEVVVTASCD  
GVTSVRTYKRI  
>CBW30986.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTLQPVSAEDLQEILPVNETRRLTTSYGAYNIIDGCWRGKADW  
AENRKALADCAQGFQKGTGGKDGDIYTVTSDLDDVDANPKETLRFGAAQNRPLWIIFE  
RDMVIRLDKEMVNSDKTIDGRGAKVEIINAGFTLNGVKNVVIHINMHDKVNPGLLIK  
SNDGPAAPRAGSDGDAISISGSSQIWIWDHCSLSKSVLDGLVDAKLGTTTLTVSNSLFTQHQ  
FVLLFGADENIEDRGMATVAFNTFTDNVDQRMPCRHRGFFQVNNNYDKWGSYAIGGS  
ASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPV  
LTPEQSAGMIPAEPGESALSLTSSAGVLSCQPGAPC  
>CBW30987.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]

MGIKHCCYILYFTLALVTLQPVRS AEDVEEFLPSANETRRLKACEAHNIIDKCWRCKA  
DWANNRQALADCAQGFAGKTYGGKHGDVYTVTSDKDDVANPKEGTLRF AAAQNRPLWII  
FKRNMVIHLNQELVVNSDKTIDGRGVKVNIVNAGL TLMNVKNI IHNINIHDIKVC PGGM  
IKSNDGPPILRQSDGDAINVAGSSQIWI DHCSLSKASDGLLDITLGSSHVTVSNCKFTQ  
HQFVLLL GADDTHYQDKGMLATVAFNMFTD HVDQRMPCRFRGFFQVVNNNYDRWGTYAIG  
GSSAPTILSQGNRFFAPDDI IKNVLARTGTGNAESMSWNWR TDKD LLENGAIFLPSGSD  
PVLTP EQKAGMIPAEPGEAVLRLTSSAGVLSCHQGAPC

>CBW30988.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKQCCYILYFTLALVALLQPVRS AEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGK WGDVYTVT SNLDDD VANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINIHDKVLP GGMI  
KSNDGPPILRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ  
SKAILL GADDTHVQDKGMLATVAFNMFTD NV DQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQ IKNVLARTGTGAAESMAWNWRSDK D LLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLS CRPGAPC

>CBW30989.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKQCCYILYFTLALVALLQPVRS AEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGK WGDVYTVT SNLDDD VANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINIHDKVLP GGMI  
KSNDGPPILRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ  
SKAILL GADDTHVQDKGMLATVAFNMFTD NV DQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQ IKNVLARTGTGAAESMAWNWRSDK D LLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLS CRPGAPC

>CBW30990.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKQCCYILYFTLALVALLQPVRS AEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGK WGDVYTVT SNLDDD VANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINIHDKVLP GGMI  
KSNDGPPIFRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ  
SKAILL GADDTHVQDKGMLATVAFNMFTD NV DQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQ MKNVLARTGTGVAESMAWNWRSDK D LLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLS CRPGAPC

>CBW30991.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKQCCYILYFTLALVALLQPVRS AEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGK WGDVYTVT SNLDDD VANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINIHDKVLP GGMI  
KSNDGPPILRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ  
SKAILL GADDTHVQDKGMLATVAFNMFTD NV DQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQ MKNVLARTGTGVAESMAWNWRSDK D LLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLS CRPGAPC

>CBW30992.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
MGIKQCCYILYFTLALVALLQPVRS AEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD  
WENNRQALADCAQGFAGKTYGGK WGDVYTVT SNLDDD VANPKEGTLRF AAAQNRPLWII F  
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNI IHNINIHDKVLP GGMI  
KSNDGPPILRQASDGD TINVAGSSQIWI DHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ  
SKAILL GADDTHVQDKGMLATVAFNMFTD NV DQRMPCRFRGFFQVVNNNYDRWGTYAIGG  
SSAPTILCQGNRFLAPDDQ MKNVLARTGTGVAESMAWNWRSDK D LLENGAIFVTSGSDP  
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLS CRPGAPC

>CBW30993.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]  
CCYILYFTLALVILLQPVRS AEDLQQILPSVNETRSLTTCGTYNIIDGCWRGKADWAENR  
KALADCAQGFAGKTIGGKGD IYTVTSELDDD VANPKEGTLRF GAAQNRPLWII FARDMV

IRLDRELAINNDKTIDGRGAKVEIINAGFAIYNVKNIIHNIIMHDIWVNPGLIKCNDG  
PPAPRKGSDGDAIGISGGSQIWIHDHCSLSKAVDGLIDAKHGSTHFTVSNCLFTQHQYLLL  
FWDFDERGMLCTVAFNKFTDNVDQRMPNLRHGFVQVNNNYERWGSYALGGSAGPTILSQ  
GNRFLASDIKKEVGRYGESAMESINWNWRSYMDVFENGAI FVPSGVDVLTPEQNAGM  
IPAEPGEAVLRLTSSAGVLSQPCTPC

>CBW30994.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD  
WAENRQALGDCAQGF GKATHGGKWDIYMVTSDDDDVNPKEGTLRFGATQDRPLWIIF  
QRDMIIYLQEMVVTSDKTIDGRGAKVELVYGGITLMNVKNVIIHNIIDHDIHVRVLPGGRI  
KSNGGPAIPRHQSDGDAIHVTGSSDIWIDHCTLSKSF DGLVDVNWGSTGVTISNCKFTHH  
EKAVLLGASDTHFQDLKMHVTLAYNIFTNTVHERMPRCRFGFFQIVNNFYDRWDKYAIGG  
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEPEWMTWNNWRTQNDVLENGAIFVASGSDP  
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLTCS PGAPC

>CBW30995.1 Amb a 1; pectate lyase [*Ambrosia artemisiifolia*]  
MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD  
WAENRQALGDCAQGF GKATHGGKWDIYMVTSDDDDVNPKEGTLRFGATQDRPLWIIF  
QRDMIIYLQEMVVTSDTTIDGRGAKVELVYGGITLMNVKNVIIHNIIDHDIHVRVLPGGRI  
KSNGGPAIPRHQSDGDAIHVTGSSDVWIDHCTLSKSF DGLVDVNWGSTGVTISNCKFTHH  
EKAVLLGASDTHFQDLKMHVTLAYNIFTNTVHERMPRCRFGFFQIVNNFYDRWDKYAIGG  
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEPEWMTWNNWRTQNDVLENGAIFVASGSDP  
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLTCS PGAPC

>ADL09135.1 hyaluronidase [*Polybia paulista*]  
SWVEFALSERPKRVFNIIYWNVPTFMCHQYGINFDEVTDFNIKHNSKDNFRGETLAIYYDP  
GNFPALIPVNNNGKYKERNNGVPQRGNITIHLLQGFNEDLDKMPDKSFGGIGVIDFERWRP  
VFRQNWGNTEIHKESIELVRKEHPKWSKSMIEAEATKKFEKYARYFMEETLKLAKKTRK  
RAKWGYYGFYCYNASPNPSPSCDAKAIENDRMSWMMYNNQEILLPSVYVRHKQDPEER  
IYLVQGRVKEAVRVSNNLEHSPSVLPYWWVYVQDEMEIFLSETDVKKTFQEIVTNGGDGI  
IIWSSSDVNSLSKCKRLREYLLNLTGPIAVNVTVNRRSSLNF

>ADL32660.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAA PGAYKNVEIKGDGGVGTIKHITLPD  
GGPVTTMTLRTDGLDKKGFIDYSVIDGDVLMGFIDKIENHLSVVPADGGSTTKTTAIF  
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32661.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAA PGAYKNVEIKGDGGVGTIKHITLPD  
GGPVTTMTLRTDGLDKKGFIDYSVIDGDVLMGFIDKIENHLSVVPADGGSTTKTTAIF  
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32662.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAA PGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTTMTLRTDGLDKKNTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF  
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32663.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAA PGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTTMTLRTDGLDKKNTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF  
HTKGDVVPEENIKFAEAQNTMLFKAVEAYLIAN

>ADL32664.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Daucus carota*]

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTTMTQRTDGLDKKCTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF  
HTKGDVAVPEENIKYAEQNTMLFKAVEAYLIAN

>ADL32665.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAAPGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTTMTLRTDGLDKKGFIDYSVIDGDVLLGFIDKIENHLSVVPADGGSTTKTTAIF  
HTKGDVAVPEENIKYAEQNTMLFKAVEAYLIAN

>ADL32666.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNLPKAAPGAYKNVEIKGDGGVGTIKHITLPE  
GGPVTTMTLRTDGLDKKGFIDYSVIDGDVLMGFIDKIENHLSVVPADGGSTTKTTAIF  
HTKGDVAVPEENIKYAEQNTMLFKAVEAYLIAN

>P86687.1 Poly p 2; hyaluronidase [Polybia paulista]

GETISIIYDPGKFPALMPLKNGNYEERNGGVPQQRGNITIHLLQFQFNEEDLDMTPDKNFGGI  
GVIDFERWKPPIFRQNWGNTIEIHKKYSIELVRYEHPKWESESMIEAEATKKFEKYARLFMEE  
TLKLAKKTRKRAKWGYGFPYCYNYTPNPGPDCDAKAMIENDRLSWMYNNQEILFPSVY  
VRHELTPDQRVYLQGRRIKEAVRISNNLKHSPKVLVSYWVYVYQDKMDIFLSETDVKKTFQ  
EIVTNGGDGIIWGSSSDVNSLSKCKRLREYLLNLTLPFAVNVTTETVN

>P86686.1 Poly p 5; unknown function, antigen 5 [Polybia paulista]

NKYCNKCSKVAHTVCQTGESTKPKSSKNCAKVSITSVGVTEEEKLLIVDEHNFRFRQKVAQ  
GLETRGNPGPQPAASDMNVLWVNDLAYIAQVWASQCQFFVHDKCRNTAQYQVGGQNIAYS  
ASTAAYPGVVKLIVLWENEVKDFNYNTGITKENFAKVGHYTVVWAKTKEVGCSSIKYIE  
KGMKSHYLVLCNYGPAGNVLGAQIYEIK

>XP\_003030591.1 Sch c 1; glucoamylase [Schizophyllum commune]

MGLASTVSLALLGLCSLARAQTSAADAYVSAESPIAQAGILANIGPSGSKSHGAASGVII  
ASPSTSNPDYLYTWTRDAALVSRALVDEFIEGESSLQSVIDSYVSSQQKLQRVDNPSGSY  
TSGGLGEPKFNIDLTAFGTAWGRPQRDGPALRAITLITYGNHLLSSGNTSYVTDTIWPVV  
KADLDYVVSYWNQTFGDLWEEVSSSSFFTTAEQHTALRLGATFATAVGASASTYLTQADN  
VLCFLQSYWNSNGGYATANTGGGRSGIDANTVLTSHITFDIEAGCDSVTFQPCSDRALSN  
LKVVYVDSFRGLYSINPTGATDPILTGRYKEDVYNGNPWYLTTFAVAEQLYDALNTWDKL  
GSLDVTSTSLAFFKQFDSSITAGTYASSTSEYATLTSAIRNWADGFLEVLADFTPADGGL  
TEQIDKSSGNPTSAADLTWSYASAITAFKARGGAIPASWGAAGLTPATCSTGGGGGSGG  
DTVAVTLNVQATTVYGENIYVTGSVNQLANWSPDNAIALNADNYPTWSVTVNLPANTQIE  
YKYIRKNNQVQVWESDPNRSITTSASGSFTQNDTWR

>ADM15668.1 Fel d 8; latherin [Felis catus]

MLKVSSLFILLCGLLASSSTQEVLSRVSSHITDALTQGLLGMNPLPTLQTFIDFQGPLKDI  
FSLVVLGHQLTNGEANFMVQMKDLRLFQVFIETSPDFKIDLRMPLAFSIQIKFPALNPYI  
FHVRTDMKVQLYLEKDVNRYQLTFGHCRIVPETVWIQSGNFITPMKNFIVENIERALGN  
VIIHNFQAKMCPFINSWLYNLPQVTNQLISLLLQHGTYQATVEIPAK

>ADM18345.1 Tab y 5; unknown function, antigen 5 [Tabanus yao]

MAPIIVPCLLLLVLVQLQCSVINSLDYCSLCRGGGEHVGCGSPGFSSDCGQKARTRKFTK  
EHKKVILDKINDVRDHVAKGSWGLPVASRMKVIVWDEELAALAKRHTQGCVPEAYKCRHT  
LRFWSPGQLNFEFYADKMPSTMSLISTAIKRHTQKHNITRDIIEKYQPAGPKGNVKELA  
LAISDRVTAVGCGLTTWKLGGKARALLTCNFSSENDYNRPVYKGTNSPGEKCIKKDETFK  
NLCSAQEPINPNEHNF

>ADM18346.1 Tab y 2; hyaluronidase [Tabanus yao]

MKLHQGLVCLSVLILLPTCILGDRKFEVYWNIPTFMCPDQNKTIMDLNKKHGVIQNTEDL  
FRGDKISLLYHPGAFPAITRNKTTNTLIYENGGVPPQAGNLSLHLKLEKDINEQITDKNF  
SGLAVIDFELWRPIFRQNGGSLSDYQNLSLKLEKDLHPEFNEDQLRKEAERRIEKFGRSF

IKQTLIKAKKLRPKAQWGYAFPYCFNGRRRYVDTCPISAKIDNDRILYMFENSVDIYPA  
VYLQTDLAQKNQTGLVKGRVDEAVRMAKMVKKPAKPPVLVYHRYVFTDTLEYISKENTTA  
VFKAMKDNGADGVIIWSSFDLNSKEKCAKFLDYLRVLPVIDEVKRS

>ADM52184.1 Der f 1; cysteine protease [Dermatophagoides farinae]

RPASIKTFEEFKAFNKNYATVEEEVARKNFLESKYVEANKGAINHLSLDEFKNR  
YLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLRVTPTIRMQGGCGSCWAFSG  
VAATESAYLAYRQTSLDLSEQELVDCASQHGCHGDTIPRGI EYIQNGVVEERSYPYVAR  
EQRCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAI AVIIGIKDLRAFQHYDGR TII  
QHDNGYQPNYHAVNIVGYGSTQGVYWI VRNSWDTTWGDSGYGYFQAGNNLMMIEQYPYV  
VIM

>ADN39439.1 Cas s 5; chitinase [Castanea sativa]

EQCGRQAGGAACANNLCCSQFGWCGNTAEYCGAGCQSQCSSPTTTTSSPTASGGGGGDVG  
SLISASLFDQMLKYRNDPRCKSNGFYTYNAFIAAARSFNGFGTTGDVTRKRELAFLAQ  
TSHETTGGWATAPDGPYAWGYCFIMENNKQTYCTSKSWPCVFGKQYYGRGPIQLTHNYNY  
GQAGKAI GADLINNPDLVATNPTISFKTAIWFWMTPQANKPSSHDVIIGNWRPSAADTSA  
GRVPSYGVITNIINGGLECGHGSDDRVANRIGFYKRYCDTLGVSYGNNLDCYNQK PFA

>ADN39440.1 Pru du 6; 11S globulin, cupin [Prunus dulcis]

MAKAFVFLCLLLVFNGLAARQSLSQPQCQLNQLQAREPDNRIQAEAGQIETWVFNQ  
EDFQCAGVAASRITIQRNLHLPSYSNAPQLIYIVQGRGVLGAVFSGCPETFEESQSSQ  
QGRQQEQEQERQQQQQGEQGRQQGQQEQQQERQGRQQGQQQEEGRQQEQQQGQQGRPQQ  
QQQFRQFDRHQKTRRIREGDVVAIPAGVAYWSYNDGDQELVAVNLFHVSSDHNQLDQNP  
KFYLAGNPENEFNQGGQSPPRQQGEQGRPGQHQQPFGRPRQQEQQGSNNVFSGFNTQLL  
AQALNVNEETARNLQGNDRNQIIRVRGNLDFVQPPRGRQEREHEERQQEQQLQERQQQ  
GGQLMANGLEETFCSLRLKENIGNPERADIFSPRAGRISTLNSHNLPIILRFLRLSAERGF  
FYRNGIYSPHWNVAHSVYVIRGNARVQVNVNENGDAILDQEVQQGQLFIVPQNHGVIQQ  
AGNQGF EYFAFKTEENAFINTLAGRTSFLRALPDEVLANAYQISREQARQLKYNRQETIA  
LSSSQRRRAVV

>ADN39441.1 Pru du 6; 11S globulin, cupin [Prunus dulcis]

CLLLL FNGCLASRQHIFGQNK EWQLNQL EAREPDNHIQSEAGVTESWNPSDPQFQLAGVA  
VVRRTIEPNGLHLPSYVNA PQLIYIVRGRGVLGAVFPGCAETFEDSQPQQFQQQQQQQQF  
RPSRQEGGQQQQFQGEDQQDRHQKIRHIREGDIIPAGVAYWSYNNGEQPLVAVSLLD  
LNNDQNQLDQVPRRFLAGNPQDEFNPQQGQQQQQQQQGQNGNIFSGFDTQLLAQA  
LNVNPE TARNLQGDNRNEIVRVQGQLDFVSPFSRSAGGRGDQERQQEEQQSQREREK  
QREQEQQGGGQDNGVEETFC SARLSQNI GDP SRADFYNPQGGRISVVRNHLPIILRYLR  
LSAEKGVLYNNAIYTPHWHTNANALVYAIRGNARVQVNVNENGDPILDDEVREGQLFLIPQ  
NHA VITQASNEGF EYISFR TDENFTNTLAGRTSVLRALPDEVLQNAFRISRQEARNLKY  
NRQESRLLSATSPRGR LMSILGY

>C7E3T4.1 Pen m 2; arginine kinase [Penaeus monodon]

MADAAVIEKLEAGFKLEAATDCKSLLKKYLSKAVFDQLKEKKTSLGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYTLFSPLFDPIIEDYHVGFKQTDKHPNKDFGDVNTFVNVDPGKYV  
ISTRVRCGRSMEGYPFNPLTEAQYKEMEAKVSSTLSSLEGELKGTYYPLTGMSKEVQQK  
LIDDHFLFKEGDRFLQAANACRYWPAGRGIYHNDNKTFVWVNEEDHLRIISMQMGDLG  
QVFRRLTSAVNEIEKRIPF SHHDRLGFLTFCPTNLGTTVRASVHIKLPKLAANREKLEEV  
AGKYNLQVRGTRGEHTEAEGGIYDISNKR RMGLTEFQAVKEMQDGILELIKMEKEM

>P86739.1 calcium-binding protein, parvalbumin [Macrurus magellanicus]

SFAGILDDADITAALAACKAEGSFKHVEFFAKIGLAGKKVFAIIDQDKSDFVEEDELKLF  
LQVFSAGARALTDAETKAGSDGDGKIGVDEFAQMIKG

>P86745.1 calcium-binding protein, parvalbumin [Merluccius australis]

AFAGILADADITAALAACKAEGTFTHG VFFTKIGLKGKSAADIKKVFGIIDQDKSDFVEE  
DELKLF LQNF SAGARALTDAETATFLKAGSDGDGKIGVDEFAAMVKG

>P86749.1 calcium-binding protein, parvalbumin [Merluccius australis]  
AFAGILADADITAALAACKAEGTFTHGEEFFTKIGLKGKSAADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFAAMVKG

>P86761.1 calcium-binding protein, parvalbumin [Merluccius gayi]  
AFAGILADADITAALAACKAEGTFKHGEEFFTKIGLKGKSAADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFAAMVKG

>P86768.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]  
AFAGILADADITAALAACKAEGTFKHGEEFFTKIGLKGKSPADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFAAMVKG

>P86774.1 calcium-binding protein, parvalbumin [Merluccius productus]  
AFAGILADADITAALAACKAEGTFKHGEEFFTKIGLKGKSAADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFTAMIKG

>P86741.1 calcium-binding protein, parvalbumin [Macruronus magellanicus]  
AFAGILADADCAAALKACEAADSFNKAFKAVGLASKSAEEIKKAFVVIDQDKSGFIEE  
DELKLFQNFVAGARALDAETKAFKAGDSDGDGAIGVDEFAALVKA

>P86750.1 calcium-binding protein, parvalbumin [Merluccius australis]  
AFSGILAEADIAAALKACEAADSFNKAFKAVGLSAKSADDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDAETKAFKAGDSDGDGAIGVDEFAVLVKA

>P86752.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]  
AFAGILADADIAAALKACEAEGSFKHGEYFAKIGLKGKSAADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFAAMVKG

>P86757.1 calcium-binding protein, parvalbumin [Merluccius capensis]  
AFSGILAEADIAAALKACEAAGTFNKAFFKAVGLTGKSADDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDDETKAFKAGDSDGDGAIGVEEWAALVKA

>P86765.1 calcium-binding protein, parvalbumin [Merluccius merluccius]  
AFAGILADADITAALAACKAEGSFKHGEYFAKIGLKGKSAADIKKVFGLIIDQDKSDFVEE  
DELKLFQNFSAAGARALDAETATFLKAGDSDGDGKIGVDEFAAMVKG

>P86769.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]  
AFSGILAEADIAAALKACEAAGTFNKAFFKAVGLTGKSADDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDDETKAFKAGDSDGDGAIGVDEWAALVKA

>P86771.1 calcium-binding protein, parvalbumin [Merluccius polli]  
AFSGILAEADIAAALKACEAAGTFNKAFFKAVGLTGKSADDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDAETKAFKAGDSDGDGAIGVDEWAVLVKA

>P86775.1 calcium-binding protein, parvalbumin [Merluccius productus]  
AFSGILAEADIAAALKACAAADTFNKAFFKAVGLSAKSADDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDAETKAFKAGDSDGDGAIGVDEFAVLVKA

>P86740.1 calcium-binding protein, parvalbumin [Macruronus magellanicus]  
TFFKSNDVKKAFVVIDQDKSGFIEEDELKLFQNFSAAGARALTAGETKTFLAAGDSDGD  
GMIGVDEFQALVKA

>P86742.1 calcium-binding protein, parvalbumin [Macruronus novaezelandiae]  
SFNYKTFKLAASNDVKKAFVVIDQDKSGFIEEDELKLFQNFSAAGARALTAGETKTF  
LAAGDSDGDGMIGVDEFQALVKA

>P86753.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]  
AFSGILADADIAAALKACEAADSFNKAFKAVGLSAKSAEDIKKAFVVIDQDKSGFIEE  
DELKLFQVFSAGARALDAETKAFKAGDSDGDGAIGVDEFAVLVKA

>P86770.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]  
AFAGVLADADIKAAALAGCAAESFNKTFKACGLAGKFFAIIDQDHSGFIEEDELKLF  
QTFSAAGARALSDAETKDVGDGMIGVDEFVALVKA

>P86772.1 calcium-binding protein, parvalbumin [Merluccius polli]  
AFAGVLADADIKAAALAGCAAESFNKTFKFFAIIDQDHSGFIEEELKLFQTFSAAG

RALSDAETK

>P86754.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]  
AFAGVLADADIKAAALAGCAAADSFNYKTFKACGLFFAIIDQDHSGFIEEEEELKFLQTF  
SAGARALSDAETKTFLAAGDVGDMIGVDEFAA

>P86760.1 calcium-binding protein, parvalbumin [Merluccius gayi]  
AFAGVLADADIKAAALAGCAAADSFNYKTFKFFAIIDQDHSGFIEEEEELKFLQTF  
RALSDAETKAFLAAGDSDGDGKIGFVALVKA

>A2V735.1 tropomyosin [Chionoecetes opilio]  
MDAIKKKMQAMKLEKDNAMDKADTLEQQNKEANLRAEKTEEEIRANQKKSQLVENELDHA  
QEQLSAATHKLVEKEKAFANAEGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKNIADEMDQAFSELSGF

>CBW45298.1 Plo i 2; thioredoxin [Plodia interpunctella]  
MSIHIKDVEDLTARL TEAGDKLVVIDFMATWCGPCKIIGPKLDEIAAEMADSI VVKVDV  
DECEDIATEYSINTMPTFV FVKNKGPVEQFSGANVEKLRSTILK LK

>ADQ53858.1 Ara h 1; 7S globulin, vicilin [Arachis hypogaea]  
MRGRVSPLMLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACES  
RCKLEYDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDDRRQPRREEGGRWGPAGP  
REREREEDWRQPREDWRRPSHQPRKIRPEGREGEQEWGTPGSHVREETS RNPFYFPSR  
RFSTRYGNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQ  
GQATVTVANGNNRRALILTRAMHSESHPFHFLHLDMPPEL RVAKSHAVNTPGQFEDFFP  
ASSRDQSSYLQGF SRNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSENNEG  
VIVEVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPDLSDNFGRLFVVKPDKKN  
PQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVINKGTGNLELVAVRKEQQQRGRREQE  
WEEEEEEDEEEEGSNREVRRTARLKEGDVFI MPAAHPVAINASSELHLLGFGINAENNR  
IFLAGDKDNVVDQIEKQAKDLAFPGSGEQVEKLIKQRESHFVSAR PQSQSPSSPEKEDQ  
EEENQGGKGPLLSILKAFN

>ADQ53859.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]  
MAKLLALS LCFVVLV GASSVTFRQGGREENECQFQRLNAQRPNRIESEGGYIETWPNPN  
QEFQCAGVALSRTVLRNALRRPFYSNAPLEIYVQQGSGYFGLIFPGCPSTYEEPAQEGR  
RYQSQKPSRRFVQVQDDPSQQQQDSHQKVHRFDEGDLIAVPTGVAFWYND ETDVVTVT  
LSDTSSIHNQLDQFRRFYLAGNQEQEFLRYQQQGSRPHYRQISPRVRGDEQENEGSNI  
FSGFAQEF LQHAFVDRQTVENLRGENERE EQAIVTVKGLRILSPDEEDES SRSPNR  
REEFDEDRSRPQQRGKYDENRRGYKNGIEETICSASVKKNLGRSSNPDIYNPQAGLSRV  
NELDLPILGWLGLSAQHGTIYRNAMFVPHYTLNAHTIIVALNGRAHVQVDSNGNRVYDE  
ELQEGHVLVVPQNFVA AKAQSENYEYLAFKTD SRPSIANQAGENS IIDNLPEEVVANSY  
RLPREQARQLKNNNPFKFFVPPFDHQSMREVA

>CBY17558.1 Pan b 1; tropomyosin [Pandalus borealis (Pandalus eous)]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVFLGQKQLQLENDLDSV  
QEALLKANQHLEEKDKALSNAEGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA  
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNLKLAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELG Y

>P0CH89.1 Ves m 2; hyaluronidase [Vespula maculifrons]  
DRCIWPKEGFSIYWNIPTHFCHNFGVYFKEL

>P0CH87.1 Vesp c 1; phospholipase A1 [Vespa crabro]  
FNPCPYSDDTVKMIVLTRENKKYDFYTLDTIKNHNEFKDTITLKP HVFITHGFTSSATAE  
NFVVMAKALLDKGNLVILTDWRMAACTNEIAGLKLAYYPYAASNTRLVGN YIATVTKML  
VQKYNVPMANIRLIGHSLGAHISGFAGKKVQELGLGKYPEIIGLDPAGPSFKSND CSQRI

CETDANYVQIIHTSNRLGTERTLGTVDFYMNNGYNQPGCLPIIGETCSHTRAVKYFTEC  
IKHECCLIGVPSKSNPQVSKCTRNECVGLNAKTYPKTGSFYVPVESKAPYCNNKGKI  
I

>P0CH86.1 Ves s 1; phospholipase A1 [*Vespula squamosa*]  
GSKCPFSDDTVAMVIVTRENRRDFYTLQTLRNHDEFKKAITRPVVFITHGFTSSATVE  
SFVDLQTAILEXXXXKVTVSDWRVAACNRRTGLLYVVTAVSNTRLVGRYIATVTKKLVD  
YNVSMADIRLIGHSLGAHVSGFAGKEVQKLEKYSEIIGLDPAGPSFESNDCAERLCKT  
DAHVVQIIHTSKKFGIEKSIGHVDFYVNVQGNQPGCGIPLKDVCSHSRAITYMTECIKR  
ECCLIGIPQSKSSKSISSCTRQECVGLKAKSYPNTGSFYVPVESTAPFCNNKGKII

>P0CH88.1 Bom t 4; protease, partial [*Bombus terrestris*]  
VVGKPAKLGAWPMMVALGF

>ADR66939.1 lipid transfer protein [*Prunus persica*]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIPYVRGGGAVPPACNGIRNV  
NNLARTTPDRQAACNCLKQLSASVPGVNPNNAAAALPGKCGVSIPYKISASTNCATVK

>ADR66943.1 Pru av 3; lipid transfer protein [*Prunus avium*]  
MACSAMTKLALVVALCMVSVPIAQALTCGQVSSNLAPCIPYVRGGGAVPPACNGIRNI  
NNLAKTTADRQTACNCLKQLSASVPGVNANAAAALPGKCGVNPYKISPSTNCATVK

>ADR66944.1 Pru av 3; lipid transfer protein [*Prunus avium*]  
MACSSMTKLALVVALCMVSVPIAQALTCGQVSSNLAPCIAVVRGGGAVPPACNGIRNI  
NNLAKTTADRQTACNCLKQLSASVPGVNANAAAALPGKCGVNPYKISPSTNCATVK

>ADR66945.1 lipid transfer protein [*Prunus armeniaca*]  
MAYSAMTKLALVVALCMVSVPIAQQAQAITCGQVVSTLAPCINVYKSGGAVPPACNGIR  
TLNGLAKTTADRQAACNRLKQLSGSIPGVNPNNAAAALPGKCGVNPYKISISTNCAAVK

>ADR66946.1 lipid transfer protein [*Prunus armeniaca*]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSNVAPCIPYVIGGGAVPPACNGIRNV  
ENLAKTTADRQAACNCLKQLSGSIPGVNPNNAAAALPGKCGVNPYKISISTNCAAVK

>ADR66947.1 Pru ar 3; lipid transfer protein [*Prunus armeniaca*]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIGYVRGGGAVPPACNGIRNV  
NNLARTTPDRRTACNCLKQLSGSISGVNPNNAAAALPGKCGVNIPYKISASTNCATVK

>ADR66948.1 lipid transfer protein [*Prunus armeniaca*]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIGYVRGGGAVPPACNGIRNV  
NNLARTTPDRRTACNCLKQLSGSISGVNPNNAAAALPGKCGVNIPYKISISTNCAAVK

>ADR82196.1 Hev b 14; hevamine [*Hevea brasiliensis*]  
GGIVIIYWGQNGNEGTLTQTCSTRKYSYVNIAFLNKFNGQTPQINLAGHCNPAAGGCTIV  
SNGIRSCQIQGIKVMLSLGGGIGSYTLASQADAKNVADYLWSNFLGGKSSSRPLGDAVLD  
GIDFDIEHGSTLYWDDLARYLSAYSQKQKVVYLTAAAPQCPFPDRYLGTALNTGLLTMYGF  
NSITIIHHASIAQVTLTTSLTRGIDGPHL

>ADR82198.1 Per a 2; aspartic protease [*Periplaneta americana*]  
MTFLIQSAFVALAAISAVLCDPVVPLQKRAPVEEYINTQYVGPVQLGNQYFLCVFDTSS  
YTTVIPASASCVSGGCNCANVHKYYSNKPVSNNVASVRILGSGYANGSEAHDYIAVSTLNA  
TNQGFLLADDISNDICSLGADCVIGLGRPKSGRAAFNLPTVMENFVNQDNIANSFSFHGG  
RYPDGQHRGVLVLGGTIPAYYRGDFTYVPLVDKDTWNFKVDSISVGNEVVATDQLAFVDS  
SKYVITGPAEEIKKINDRLGCTNKVIGSRTL CVFDCDKLDNVPSTFTIGGVAFNISSTY  
HIQQNGDLCYSGFQYSAGKCFHGFDFMDNYYAKFDGQNKRMGFAKSVEEL

>3LIZ\_A Bla g 2; inactive aspartic protease [*Blattella germanica*]  
EAEASIVPLYKLVHVFINTQYAGITKIGNQNFLTVFDSTSCNWWWASQECVGGACVCPNL  
QKYEKLKPKYISDGNVQVKFFDTGSAVGRGIEDSLTISQLTTSQQDIVLADELSQEVCIL  
SADVVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHHARFQDGEHFGEIIFGGSDWK  
YVDGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDTSKAIIVGPKAYVNPINEA  
IGCVVEKTTTRICKLDCSKIPSLPDVTFVINGRNFNISSQYYIQQNGNLCYSGFQPCGH

SDHFFIGDFFVDHYYSEFNWENKTMGFGRSVESV

>CBY83816.1 Vesp ma 2; hyaluronidase [*Vespa magnifica*]  
MLLVTLFLFFLQALVNGDSCGSNCEKSERPKRVFNIIYWNVPTFMCHQYGLYFDEVTFNFI  
KHNSKDNFQGDKIAIFYDPGEFPALLPLNYGKYKIRNGGVPQEGNITIIHLQRFIEYLDKT  
YPNRNFSGIGVIDFERWRPIFRQNWGNMKIYKNFSIDLVRKEHPFVNKKMIELEASKRFE  
KYARLFMEETLKLAKKTRKQADWGYGYPCFNMSPTNFVPCDVTARDENNEMSWLFNN  
QNVLLPSVYIRRELTDPQRIGLVQGRVKEAVRISNKLKHSPKVFYSYWWVYQDETNTFLT  
ETDVKKTFFQEIIVGGDIIIWGSSSDVNSLSKCTRLREYLLTVLGPiAVNVTEAVN

>ADT89774.1 Poly p 1; phospholipase A1 [*Polybia paulista*]  
GLIPECPFNEYDILFFVYTRDKQDGIILKKNMLTSYNLFQQPQISHRVVFLIHGFISTGN  
NGNFDAMAKALIAKDNFLVMSVDWRRACDASVFNVAGYSKAVANTRRVGKYVADFTKIL  
VDKYKVPMSNIRLIGHSLGAHTSGFAGKQVQKLLGKYSEIIGLDPAGPSFRSTNCPDRL  
CETDAQYVQVLHTSSKLGTYDQIGSVDFYVNYGGSQPGCLVRTCSHTKAVLYMTECIKRE  
CCLIGTPWSSTGSSPKPKPISACKRDICVGLNAKSYPAGGSFYVPVEKNSPYCHNEGI  
KL

>ADV17342.1 Pen m 3; myosin light chain [*Penaeus monodon*]  
MSRKSGSRSSSKRSKSGGGSNVDFMFTQRQVAEFKEGFQLMDRDKDGVIGKTDLRGTFD  
EIGRIATDQELDEMLADAPAPINFMTLLNMFAERQTGESDDDDVAKAFLAFADEGGNID  
CDTFRHALMTWGDKFSSQEADDALDQMDIDDAGKIDVQSVIQMLTAGGGDDAAAEAA

>ADV17343.1 Pen m 4; calcium-binding protein, sarcoplasmic calcium-binding protein [*Penaeus monodon*]  
MAYSWDNRVKVVRYMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN  
LWNEIAELADFNKDG EVTVEFKQAVQKHCQGGKYGFPGAFKVFIANQFKAIDVNGDGK  
VGLDEYRLDCITRSFAAEVKEIDDAYNKLTTEDDRKAGGLTLERYQDLYAQFISNPDESC  
SACYLFGPLKVVQ

>BAJ61596.1 paramyosin [*Haliotis discus*]  
MDYGDVSSKVVRTVSHRSYNVYRGSSPATQNRLEARIRELEDALDTERDCRVRAEKNLAE  
ITFYQDQVADRLEEQQGVTVQQIEINKKRESELNKVRKDLELAVISHESAEASLRKRNQE  
TINDLTDQLEYMTKQKNRVEKEKHQLIIEIDTLQGMTDSLAKAKSSAESRADGLQGSVDR  
LKLQVDDL SRQLTDANS AKARLTQENFDLQHQQVQELDSANAALAKAKSQLQASNDLKRQ  
LDDESQRQNLQVQFSQLQSGYDNLNARYEESESASTLRTQLSKVNAEFAALKARFEKE  
LMAKSEALEELRRRLNTRIAQLEDECETLRARNNLEKTKAKLTAEIKEITIELENTQII  
VQDLTKRNRTELENGILQRRCELGAEVSALRAEKASLEAEVHRLRVANAELTERNDNL  
QRENKNLSDQLREAQLALKDANRELNELRQIRAQLEMERDSLASQLRDTEEALRDAEGKL  
AAAQAALNQLRIDMENRLREKDEEIDNIRRSSARAIEELQRTLIEVETRYKTEISRISIKK  
YETDIRELEGALDNANKANAELYKQIRSLQLRVKELEVLLLEEERRLADDLRGQLSISERK  
RIALQQEVEDVRSLL EAAERARKNAENELNDANARLSELQIQVTALSNDKRRMEADISAM  
QSDLEDAINAQRAAEERADRLFNENVRLADELQEQENYKNAESLRKQLEIEIREITVRL  
EEAEAFATREGKRMVAKLQARIRDLEAELEAEQRRVREAFATSRLKLERQYKEIQMQTEDD  
RRILAETMSINDQLSMKVKAYKRQIEESEDVANLTMNKYRKAQQLEIEADHRADMAEKNL  
VAVRRSRMSVTRDVKIVRI

>CBY93636.1 Vesp ma 5; unknown function, antigen 5 [*Vespa magnifica*]  
MKISGFVYLILITTIINLSFSEANNYCKIKCRSGIHTLCKFGISTKPNCCKNNVKGSGLT  
KAEKLEILKQHNEFRQKVARGLETRGKPGPPAKSMNTLVWNLDELAQIAQVWASQCKYG  
HDDCRNTAKHSVGNIAQQSTTAASFGSVSNMVQMWAVEVKNYQYGSTKNKLEIEVGHYTQ  
MVWAKTKEIGCGSIKYIENGWHRHLYVCNYGPAGNIGNEPIYEKK

>ADW27428.1 Fag t 2; 2S albumin, conglutin [*Fagopyrum tataricum*]  
MKLFIILATATLLIAATQAKYLRDEGFDLGETQMSSKCTRQVKMMEPELVKCNRYIAMDI  
MDDKYEEALSRIQEGECSEEFKLRGCCVAMKEMEDECVCEWMMKMMVENQKGRIGETLMR  
KGIRDLKELPNKCGISEMECHSRGNWYVV

>2X45\_A Arg r 1; lipocalin [Argas reflexus]  
MDDCSGKTDAWTSIKGPKTGGYWLKQTTKTGENECTYVKGTDKFKENTKTATYTYGYKDAS  
GKLTKTGTATAKGSDIVVGSSTSTVIYTDGKTCDVVKHGGHTELWVHSSKTSGGYNNCC  
DKKFTETRGSTPANEVYKCKCPGMP

>ADX78255.1 Tab y 1; apyrase [Tabanus yao]  
MFKITVFIYVLQLILPSKVHSSPVPDSNGLREFPLSIVHINDFHARFEQTDELGGQCKP  
TAKCVGGYARLVTTVKKLKEEGQNTIFLNAADNYQGLWYNLKGWNVTAIFMNLTPADAM  
TLGNHEFDDKIEGIVPFLLEVIKTPIVVANIDDSLEPTFKGKYTKSVVLERGGKRKIGIVGV  
IAQNTDNISSPGKLRFLDEIQSVKNESKRLREEEKVDIVIVLSHIGLDHDYDLAEQAGDY  
IDAIIGGHSFSLWTGDNPPGKEKVVDAYPVEIVQTSKKVLIQASAFARYVGNITLYF  
GENNLIYAGAPVYLDSDVPEVPQIVEEMKAWEEFVHEKNEIIAESRVVLSRENCRV  
DCNIGNFFTDAYVHEVYVTSHTGPYWTPVSVGLMNVGGIRASVDRGNITFSQLITMAPFEN  
TVDTFDLSGKHLLEAFEHAVTVPNRLGFNGQNMQLQVSGVKLVYDVTKCEGQRVVSARKIRC  
QKCDIPKYEPLDPEETYRIVTASFLANGGDGFTMIRDNKKNYKVGRKDYDVLINYAKYSS  
PITIGEEGRIRIIQ

>BAJ78220.1 Ani s 11; unknown function [Anisakis simplex]  
MHSTAILLLLVLQLSCYFAASFILPGGANPPRFPVGGPGPIISGDGVNVWQKANSIPKDKD  
NAGQRQVNIPIPPFIRGPGPVVSGSGIGEVQIPIGGPGPVVSGSGIGQVFPQPQSGQLPIG  
GPGPVVSGSGIGGANPPRFPVGGPGPIISGDGVNVWQKANSIPKDKDNAGQRQVNIPIPP  
FIRGPGPVVSGSGIGEVQIPIGGPGPVVSGSGIGQVFPQPQSGQLPIGGPGPVVSGSGIG  
GGANPPRFPVGGPGPIISGDGVNVLQKANSIPKDKGNANPPQLPVGGPGPVISVDGESVL  
QKEENSL

>BAJ78221.1 Ani s 11; unknown function, partial [Anisakis simplex]  
MHSTAILLLLVLQLSCYFAASFILPGDHGLPVGGPGPVISVDGKNVWEDANGMSELHGPGP  
VSGSGIGRVFPFRSQQLPIGGPGPVVSGSGIGGANPPRFPVGGPGPIISGDGVNVWQK  
ANSIPKDKGNANPPQLPVGGPGPVISVDGESVLQKEENSL

>BAJ78222.1 Ani s 11; unknown function [Anisakis simplex]  
VGGPGPVISVDGKNVWEDANGMSELHGPGPVVSGSGIGRVFPFRSQQLPIGGPGPVVSGS  
GIGGANPPRFPVGGPGPIISGDGVNVWQKANSIPKDKDNAGQRQVNIPIPPPFIRGPGPV  
VSGSGIGEVQVPIGGPGPVVSGSGIGRVFPFRSQQLPIGGPGPVVSGSGIGRVFPFRSQQL  
PIGGPGPVVSGSGIGQVFPQPQSGQLPIGGPGPVVSGSGIGGANPPRFPVGGPGPIISGD  
GVNVWQKANSIPKDKGNANPPQLPVGGPGPVISVDGESVLQKEENSL

>BAJ78223.1 Ani s 12; unknown function [Anisakis simplex]  
MLSHLWLIQLCIVAVLSNSEREEFAFLCPVWKNLPPSVREQCIESQIVIRDCKEKKYGEN  
CAELIKQCVTITGAPPVTIGGSGQYRVASSLRDCIKKGGYMGYCSNFTTHENCIKWKDEC  
APSEAAEKKDENSELVFPETFSQCFKSQVVMQCMNEGEEECCKIEKECVDALGTPPVTT  
AANGAYQMAAPLHRCIENGWMMCMSTWINATICERWKQECSDKDAEPPTNFSQCIQTQ  
TVMLQCKLEFGDKCKALQEECAATYAPTAYVDANPPIFTSETIRCVQRKMAKGL

>CAX62129.1 Cav p 2; lipocalin [Cavia porcellus]  
MMQILLLALAVSLACADSIDYSKVPGNWRTIAIAADHVEKIEVNGELRAYFRQVDCTEGC  
DKISITFYTNTDGVCTEHTVVGARGENDVYTVDYAGENTFQILCNSDDAFVIGSVNTDQ  
NGQTTKEVAIAAKRNFLTPEEQEQKFQKAVQVQAGIPLNIRYVIETDTCPD

>CAX62130.1 Cav p 3; lipocalin [Cavia porcellus]  
MQILLLALTIGLAYAHQTLDPSEINGQWHTISIAADNVEKIGEGGPLRGYFHNHLCYDGC  
KNIGLTFYVKLDGNCQRFQVLDGAKQEDSDVYVAQYSGTNHFEVIGKKEDAIAYFNHNTDE  
TGKETKMIVVVARRDSLTEEEQKLQEVAGEKGIKDNIRYFRERDTCQAQ

>BAK09232.1 calcium-binding protein, parvalbumin [Evynnis japonica]  
MPFKGLQDADVAKALEGCKDAGTFDHHKFFHACGLSGKSGADVKAFFVIDQDKSGFIEE  
EELKLFQNFKAGARALTDEETKKFLKAGSDGDGKIGADEFAEMVKV

>BAK09233.1 calcium-binding protein, parvalbumin [Evynnis japonica]

MAFSGVLSADADMKAAALDGCSAADSFYKFFKACGLSGKSADEVKKAFAIIDQDKSGFIE  
EEELKFLQNFGKSARALTDKETKAFLAAGSDGDGKIGVDEFAALVKA

>CBG76811.1 Sec c 5; unknown function [*Secale cereale*]

MAVQQYTVALLFLAVALVAGPAVSYGTYAPAAPGTQPKATTPEQKLMENINNGFKAAVEEA  
AAVAPADKYKTFQTTFFIKGSNKAFADVLTAASGQIPAQSDSMARLSTSLSSYKLAYDS  
AEGATPETKYDYVASLTESLRVISGAFEVHAVKPAEVEVKVPAPQLKVVDQIDAAYRT  
AATAANAAPTNDKFNVFESSFNKAIKENTGGAYASYTFVPALESVAVKQAYAATVASAPEV  
KYAVFQAALSKAINAMVEAEKDAKPAAAAAATATATATVAAAAGAAAGGYKA

>Q40240.2 Lol p 5; unknown function [*Lolium perenne*]

MAVQKYTVALLFLAVALVAGPAASAAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL  
EDVNAGFKAASAAAANAPPADKFKIFEAAFESSKGLLATSAAKAPGLIPKLDAYDVAY  
KAAEATPEAKYDAFVTALTEALRVIAGALEVHAVKPATEEVLAAKIPTGELQIVDKIDAA  
FKIAATAANAAPTNDKFTVFESAFNKALNECTGGAYETYKFIPLSLEAAVKQAYAATVAAA  
PEVKYAVFEAALTKAITAMTQAQKAGKPAAAAAATAATVATAAATAAAVLPPLLVVQSL  
ISLLIYY

>P85524.1 Act d 11; pathogenesis related protein, PR-10, Bet v 1-like [*Actinidia  
deliciosa*]

MDLSGKMKVQVEILSDGIVFYEIFRYRLYLISEMSPVNIQGVLDLLEGNWGTVGSVIFFKY  
TIDGKEKTAKDIVEAIDEETKSVTFKIVEGLMELYKTFIIIVQVDTKGEHNSVTWTFHY  
EKLKEDVEEPNTLMNFCIEITKDIETYHLK

>AEE98392.1 Man e 5; glutamic acid rich protein, Hev b 5-like [*Manihot esculenta*]

MATAEVVTAQTALPEEKPAEEVKVSEIVTEEAAPAVEPVAEEPKEAEPVAVSEEPKGGDD  
APAEVAVETKEVEVEEAKTVTEEPTVEKTEEEEEETPKEETPEPVVVKETPKEEPTAETV  
VEEAPKETTEAATEAEAPAPESAPASAPETPAEEEEVPKEEEGDEKKSEAEVEAEKTE

>AEH31546.1 Tri a 36; LMW glutenin [*Triticum aestivum*]

MKTFLIFALLAIVATSAIAQMENSHIPGLERPSQQQPLPPQQTLSSHQQQQPIQQQPQPF  
SQQQPCSQQQQPLSQQQQPPFSQQQPPFSQQQQQPLSQQQQPPFSQQQPPFSQQQQPPF  
SQQQPPFSQQQQPVLQQQPSFSQQQLPPFSQQQSPFSQQQIVLQQQPPFLQQQPSLPQ  
QPPFSQQQQQLVLPQQQIPFVHPSILQQLNPCVKVFLQQQCSPVAMPQSLARSQMLQQSSC  
HVMQQQCCQQLPQIPQSRYEAIRAIIYSIILQEQQQVQGSIQTPQQQPQQLGQCVSQPQ  
QQSQQQLGQQPQQQQLAQGTFLQPHQIAQLEVMTSIALRTLPTMCRVNVPLYRTTTTSVPF  
GVGTGVGSY

>CBM42660.1 polygalacturonase [*Paspalum notatum*]

MAWRKEEGAMTMLRALLVVALAVCGAHAAGDKKKAEEESKKGDSAAAAASGPGGSFDITK  
LGASGDGKTDSTKALEEAWASACGGKQKQTLIPKGDYLTGALNFTGPCTGDVTFQLDGN  
LLASTDLSQFKANWIEILRVDNLVITGKGLDGGQSAVWSKNNSCAKKYDCKILPNSLVLD  
FCNKAEVSGISIIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIIDT  
TIGVGDDCISIGPGSTKVNITGVTCGPHGISIGSLGRYKDEKDVTDINVKDCTLKKSSN  
GLRIKAYEDAKSVLTCNSIHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTF  
KDITGTSSTPEAVSLLCSDSTPCSGITMNNVKVEY

>CBM42661.1 polygalacturonase [*Paspalum notatum*]

MAWGAMTMLRALLVVALAVCGAHAAGDKKKAEEESKKGDSAAAAASGPGGSFDITKLGAS  
GDGKTDSTKALEEAWASACGGKQKQTLIPKGDYLTGALNFTGPCTGDVTFQLDGNLLAS  
TDLSQFKANWIEILRVDNLVITGKGLDGGQSAVWSKNNSCAKKYDCKILPNSLVLDFCNK  
AEVSGISIIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIIDTTIGV  
GDDCISIGPGSTKVNITGVTCGPHGISIGSLGRYKDEKDVTDINVKDCTLKKSSNGLRI  
KAYEDAKSVLTCNSIHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKDIT  
GTSSTPEAVSLLCSDSTPCSGITMNNVKVEY

>CBM42662.1 polygalacturonase [*Paspalum notatum*]

MAWRKEEGAMTMLRALLVVALAVCGAHAGAKKAEESKKGDSAAAAASGPGGSFDITKLG

ASGDGKTDSTKALEEAWASACGGKQKQITILIPKGDYLTGALNFTGPCTGDVTFQLDGNLL  
ASTDLSQFKANWIEILRVDNLVITGKGLDGGQAVWSKNSCAKKYDCKILPNSLVLDLFC  
NKAEVSGISIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIDTTI  
GVGDDCISIGPGSTKVNITGVTCGPGHGHSIGSLGRYKDEKDVTDINVKDCTLKKSTNGL  
RIKAYEDAKSVLTCSNIHYENVKMEDAGYPPIIDMKYCPNKICSASAGSKVTVKDVTFKD  
ITGTSSTPEAVSLLCSDSTPCSGITMNNVKVEY

>CBM42663.1 polygalacturonase [*Paspalum notatum*]  
MAWRKEEGAMTMLRALLVLAALVCGAHAGAKKVEESKKGDSAAAAASGPGGSFDITKLG  
ASGDGKTDSTKALEEAWASACGGKQKQITILIPKGDYLTGALNFTGPCTGDVTFQLDGNLL  
ASTDLSQFKANWIEILRVDNLVITGKGLDGGQAVWSKNSCAKKYDCKILPNSLVLDLFC  
NKAEVSGISIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIDTTI  
GVGDDCISIGPGSTKVNITGVTCGPGHGHSIGSLGRYKDEKDVTDINVKDCTLKKSTNGL  
RIKAYEDAKSVLTCSNIHYENVKMEDAGYPPIIDMKYCPNKICSASAGSKVTVKDVTFKD  
ITGTSSTPEAVSLLCSDSTPCSGITMNNVKVEY

>CBM42664.1 polygalacturonase [*Paspalum notatum*]  
ITGINITGVTCGPGHGHSVGLGRYKDEKDVTDINVKGCTLKKTSTNGVRIKSYEDAASVL  
SASNLHYENIAMEDVANPIIIDMKYCPNKICTKNGASKVTIKDVTFKNITGTSSTPEAVS  
LLCSEKLPCTGVTLDNVKEVYKGTNNKTMAVCNNAKGSSTGCLKELACL

>CBM42665.1 polygalacturonase [*Paspalum notatum*]  
STGINITGVTCGPGHGHSVGLGRYKDEKDVTDINVKGCTLKKTSTNGVRIKSYEDAASVL  
SASNLHYENIAMEDVANPIIIDMKYCPNKICTKNGASKVTIKDVTFKNITGTSSTPEAVS  
LLCSEKLPCTGVTLDNVKEVYKGTNNKTMAVCNNAKGSSTGCLKELACL

>CBM42666.1 polygalacturonase [*Paspalum notatum*]  
STKVNITGVTCGPGHGHSIGSLGRYKDEKDVTDINVKDCTLKKSTNGLRIKAYEDAKSVL  
TCSNIHYENVKMEDAGYPPIIDMKYCPNKICSASAGSKVTVKDVTFKDITGTSSTPEAVS  
LLCSDSTPCSGITMNNVKVEYSGSNKTMAVCKNAKGSATGGLKELACF

>CBM42667.1 polygalacturonase [*Paspalum notatum*]  
STKVNITGVTCGPGHGHSIGSLGRYKDEKDVTDINVKDCTLKKSSNGLRIKAYEDAKSVL  
TCSNIHYENVKMEDAGYPPIIDMKYCPNKICSASAGSKVTVKDVTFKDITGTSSTPEAVS  
LLCSDSTPCSGITMNNVKVEYSGSNKTMAVCKNAKGSATGGLKELACF

>AEK65120.1 arginine kinase [*Amphioctopus fangsiao*]  
MAEELFKTLQNAKECHSLLKKHLTKERFDKLGKTKFGGTLADCIRSGCKNPDSGVGIY  
ASDPDAYTVFAEVLDAVIMDYHKIDKVHHPIDPFGDVNNLNIGDLDPGSGNMIVSTRVRVG  
RSHDSFGFPVLLKDDRIKMEQVSVEALKSLDGEAGSYFPLANMSADVQKQLTEDHFLF  
NDSDFRLKAASGYDDWPIGRGIYFSENKTFLCWVNEEDHLRLISMQKGGNLGEVYKRLVS  
AINKMEKKNLFAKKNMGYLTFPCPSNLGTTMRASVHIKIPKLSQRSDFKSIDKYNLQAR  
GIHGEHTESVCGVYDISNKRMRGLTEYEAVTEMMRGVNEIIREETNST

>2XV9\_A Asc s 1; unknown function, partial [*Ascaris suum*]  
GSPEFHHTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYYDELEGDAKKE  
ATEHLKGGCREILKHVVGEKAAELKNLKDGSASKEELKAKVEEALHAVTDEEKKQYIAD  
FGPACKKIYGVHTS

>AEM89226.1 enolase, partial [*Penaeus merguensis* (Fenneropenaeus merguensis)]  
FTEAMRMGSEVYHHLKAVIKGRFGLDATAVGDEGGFAPNILNNDKDALTLIQESIEKAGYT  
GKIEIGMDVAASEFYKGENIYDLDFKTANNDGSQKITGDQLRDMYMEFCNEFPVSI

>CCD28287.1 Ph1 p 5; unknown function [*Phleum pratense*]  
MAVHQYTVALFLAVALVAGPAASYAADLGYGPATPAAPAAGYTPAAPAGAEPAGKATTEE  
QKLIIEKINAGFKAALAAAAGVPPADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKA  
ALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKPAEEVKVIP  
AGELQVIEKVDAAFKVAATAANAAPANDKFTVFEEAFNNAIKASTGGAYESYKFI PALEA  
AVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQAAPAAAAATATATSAVGAATGAA

TAAAGGYKV

>3S7E\_A Ara h 1; 7S globulin, vicilin, partial [*Arachis hypogaea*]

MSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIEAKPNTLVLPK  
HADADNILLVIQQGQATVTVANGNNRKSFNLDDEGHALRIPSGFISYILNRHDNQNLRVAKI  
SMPVNTPGQFEDFFPASSRDQSSYLQGFSRNTLEAAFNAEFNEIRRVLLEENAGGEQEER  
GQRRWSTRSSENEGVIKVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPDLS  
NNFGKLFVVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVKGTGNLELV  
AVRKEQQQRGRREEEEDDEEEEGSNREVRRYTARLKEGDVFIMPAAHPVAINASSELHL  
LGFGINAENHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIKQKESHFVSAR

>AEQ28167.1 tropomyosin [*Anisakis simplex*]

MDAIKKKMQAMKIEKDNALDRADAAEGKVRQMTDKLERIEEELRDTQKKMMQTENDLDKA  
QEDLSTANSNLEEKVKQEAEEVAALNRRMTLLEEEELERAEEERLKLATXKLEEATHA  
DESERVKVMENRSFQDEERANTVESQLKEXQMLAEFADRKYDEVARKLAMVEADLERAE  
ERAEAGENKIVLEEEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE  
FAERSVQKLQKEVDRLEDELVHEKERYKSISEELDQTFQELSGY

>NP\_001238443.1 Gly m 8; 2S albumin, conglutin [*Glycine max*]

MTKFTILLISLLFCIAHTCSASKWQHQQDSCRKQLQGVNLTPEKHIMEKIQGRGDDDDDD  
DDDDNHILRTMRGRINYIRRNKDEDEEEEGHMQKCCTEMSELRSPKCQCKALQKIMEN  
QSEEELEEKQKKMEKELINLATMCRFGPMIQCDLSSDD

>AET05730.1 Pyr c 3; lipid transfer protein [*Pyrus communis*]

AHAITCSQVSSNLAPCINIVRSGGAVPPACCNIGIKTINGLANATTPDRQAACNCLKNLAGS  
VSGVNPNAESLPGKCGVNPYKISTSTNCATVK

>AET05732.1 Pyr c 3; lipid transfer protein [*Pyrus communis*]

AHAITCSQVSSNLAPCINIVRSGGAVPPACCNIGIKTINGLANATTPDRQAACNCLKNLAGS  
VSGVNPNAESLPGKCGVNPCKISTPTNCATVK

>AET05733.1 lipid transfer protein, partial [*Pyrus communis*]

AHAITCSQVTSNLGACIGYVKNNGVPPACCNIGIRTVNGLARTTADRQTTCNCLKSLAGS  
IKGVNPNNAATLPGKCGVNPFKISTSTNCATVK

>AEV23867.1 Per a 5; glutathione S-transferase [*Periplaneta americana*]

MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQHTIPTLNDN  
GFCLWESRAILSYLADQYGKDDSLYPKDAKKRALVDQRLYFDIGTLYHRFGEYYPYIYFA  
KQAADPEKMKKLEEAFFLNKFLSQEFVAGNKLTIADLAIVSSVSTADIMGFDVSKYSN  
VAKWFEKCKKIVPGYEELNHSGLKFKEMCDNLAKK

>AEV41413.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]

MAIFSSNSATSSSLPSRTTSILLVLFIASLSITDAQVGVVGYMLGNNLPPASQVISLYKQ  
ANIKRMRIYDPNQAALQALRGSNIQLMLGVPNSDLQSLTNPNSNANSWIQRNVRAFVPSVR  
FRYIAVGNIEISPVNGGTASLAKFVLPAMRNIYNAIRSAGLQDQIKVSTAIMDMLIGNSYP  
PSAGAFRGDVRSYLDPIIGFLSSIRSPLLANIYPYFSYAGNPRDISLPYALFTSPSIVVW  
DGQRGYKNLFDAMLDALYSALERAGGGSLEVVSSESGWPSAGAFATFDNGRTYLSNLIQ  
HVKGGTPKRPGRFIETYLFAMFDENQKQPEFEKHFGLFFPNKQKYNLNFAGAKKNWDISA  
DYNATVLLLLKSDI

>AEV57471.1 Pru p 2; thaumatin-like [*Prunus persica*]

MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKQQLSLTGFELATG  
ISNSVDAPSPWSGRFFGRTRCSTDASGKFCATADCGSGQVSCNNGAVPPATLVEITIA  
ENGGQDFYDVSLVDGFNLPMVAVPQGGTGECKASTCPADVNAVCPAELQVKGSDGSVIAC  
KSACLALNQPQYCCTPPNDKPETCPPTTEYSKIFKDQCPQAYSAYDDKSSTFTCSARPDY  
LITFCP

>B3A0N2.1 lipid transfer protein, partial [*Lycium barbarum*]

GPLGGCCGGIKKSAAGISGINYGIAAGLPGKCGVNIPYKISPSTDCSKVQ

>AEX34122.1 Pen cr 26; ribosomal phosphoprotein P1 [*Penicillium crustosum*]

MSTAELACSYAALILADDGIEISADKIQTLISAANVQEVPIWASIFARALEGKDIKELL  
TNVGSAGPASAAPAGAAGAAAPAEKAEKEEKEEESDEDMGFGLFD  
>AEY79726.1 cyclophilin/peptidyl-prolyl isomerase [*Daucus carota*]  
MANPKVFFDMTIGGTPAGKIVMELYADTTPKTAENFRALCTGEKGTGKSGKPLHYKSSFF  
HRVIPGFMCQGGDFTAGNGTGGESIYGAKFADENFERKHTGPGILSMANAGPGTNGSQFF  
ICTAKTEWLDGKHVVFGKVVVEGMDVVKAIKVGSGSGKTSKPVAIADCGQC  
>AEY79727.1 Dau c 5; isoflavon reductase-like protein, phenylcoumaran benzylic  
ether reductase [*Daucus carota*]  
MATKILIVGGTGYIGKFIVEASAKAGHPTFVLVREATLTSPDKSQLIDSFKSLGVTFVHG  
DLYDHGSLVKAIKQVDVVISALGHGQLADQDKLLAAIVEAGNVKRRFFPSEFGQDVDRVNA  
VEPAKSAFAAKALFRRTVEAAGVPFTYVACNFFAGYFLPTLAQAGAAAPPRDKAVILGDG  
IPKVAFNKEEDIATYTIKAVDDPRTLNKILYVRPPHNTLSFNELLSVWEKKIGKTLEKIY  
VPPEQVLKNIQESVPIINVLLSISHSAFVKGQDQTSFEIEPSYGVEASALYPDVKYTTVDV  
YLSQFV  
>AEY79728.1 Dau c 5; isoflavon reductase-like protein, phenylcoumaran benzylic  
ether reductase [*Daucus carota*]  
MATKILIVGGTGYIGKFIVEASAKAGHPTFVLVREATLTSPDKSQLIDSFKSLGVTFVHG  
DLYDHGSLVKAIKQVDVVISTLGHGQLADQDKLLAAIVEAGNVKRRFFPSEFGQDVDRVNA  
VEPAKSAFAAKAQFRRTVEAAGVPFTYVACDFFAGYFLPTLAQAGAAAPPRDKAVILGDG  
IPKVAFNKEEDIATYTIKAVDDPRTLNKILYVRPPHNTLSFNELLSVWEKKIGKTLEKIY  
VPPEQVLKSIQESVPIINVLLSISHSAFVKGQDQTSFEVEPSFGVEASALYPDVKYTTVDE  
YLSQFV  
>CCF72371.1 Can f 6; lipocalin [*Canis familiaris*]  
MKLLLLLCLGLILVHAHEEENDVVKGNFDISKISGDWYSILLASDIKEKIEENGSMRVFVK  
DIEVLSNSSLIFTMHTKVNKCTKISLICNKTEKDGEYDVVHDGYNLFRIIETAYEDYII  
FHLNNVNQEQEFQLMELYGRKPDVSPKVKEKRVRYCQGMIPKENILDLTQVDRCLQARQ  
SEAAQVSSAE  
>AFA45339.1 Pro c 2; arginine kinase [*Procambarus clarkii*]  
MADAATIAKLEEGFKLEAATDCKSLLKKYLSKSIKSLKAKKTGLGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYSFLAPLFDPIIEDYHKGFQTDKHPNKDFGDVNQFVNVDPDGKFV  
ISTRVRCGRSLEGYPFNPLTEAQYKEMEEKVSSTLSGLEGELKGTYYPLAGMTKEVQQK  
LIDDHFLFKEGDRFLQAANACRYWPVGRGIYHNDNKTFVWCNEEDHLRIISMQMGDLG  
QVYRRLVSAVNIEKRVPFSSHDLGLFTFCPTNLGTTIRASVHIKLPKLAANREKLEEV  
AARYSLQVRGTRGEHTEAEGGVYDISNKRRMGLTEFQAVKEMQDGILELIKIEKEMA  
>AFA45340.1 Scy p 2; arginine kinase [*Scylla paramamosain*]  
MADA AVIEKLEEGFKLEAATDCKSLLKKYLT KSVFDQLKGGKTS LGATLLDVIQSGVEN  
LDSGVGVYAPDAEAYTLFAPLFDPIIEDYHKGFQTDKHPNKDFGDVNQFVNVDPDGKFV  
ISTRVRCGRSMEGYPFNPLTEAQYKEMESKVSSTLSNLEGELKGTYYPLTGMTKDVQQK  
LIDDHFLFKEGDRFLQAANACRYWPTGRGIYHNDNKTFVWCNEEDHLRIISMQMGDLG  
QVYRRLVSAVNEIEKRVPFSSHDLGLFTFCPTNLGTTVRASVHIKLPKLAANREKLEEV  
AGKYSLQVRGTRGEHTEAEGGVYDISNKRRMGLTEFQAVKEMQDGILELIKIEKEMQ  
>P86137.2 Act d 10; lipid transfer protein [*Actinidia deliciosa*]  
AVSCGQVDTALTPCLTYLT KGGTPSTQCCSGVRSLSMTGTKVPDRQAACNCLKQAAARY  
QGIKDAAAALSQKCGVQLSVPIRSTDCSKIS  
>P85204.1 Act c 10; lipid transfer protein, partial [*Actinidia chinensis*]  
AVSCGQVDTALTPCL  
>P85206.1 Act d 10; lipid transfer protein [*Actinidia deliciosa*]  
TVSCGQVDTALTPCLTYLT KGGTPSTQCCSGVRSLSMTGTKVPDRQAACNCLKQAAARY  
QGIKDAAAALSQKCGVQLSVPIRSTDCSKIS  
>CBL79147.1 Sal s 3; aldolase [*Salmo salar*]

MPHAFPFLLTPDQKKELSDIAHKIVAQGGKILAADESTGSAKRFQSINTENTEENRRLYR  
QLLFTADERAGPCIGGVIFFHETLYQKTDAGKTFPQHVKSRGWLVGKVDKGVVPLAGTN  
GETTTQGLDGLYERCAQYKKGDCDFAKWRCVLKITSTTPSRLTIMENCNVLARYASICQM  
HGIVPIVEPEILPDGDHDLKRTQYVTEKVLAAAMYKALSDHHVYLEGTLKPNMVTAGHSC  
SHKYTHQDIAMATITALRRTVPPAVPGITFLSGGQSEEEASINLNMNQCP LHRPWAITF  
SYGRALQASALKAWGGKPKNGKAAQEEFIKRALANSLACQGYVSSGDSAAAGDSL FVAN  
HAY

>CBL79145.1 enolase [*Thunnus albacares*]

MSILKIHAREIFDSRGNPTVEVDLYTKKGLFRAAVPSGASTGIYEALERDNDKTRYMGK  
GVKRAVKYINEFLAPALCNQDVTVIEQEKIDKMLDMDGTENKYKFGANAILGVSLAVCK  
AGAAEKGVPLRYHIADLAGNPEVILPVPFNVINGGSHAGNKLAMQEFMILPVGASSFKD  
AMRIGAEVYHNLKNVIKEKYGDATNVGDEGGFAPNILENKEALKLLKNAIGKAGYTDKI  
VIGMDVAASEFYKGGKYDLDFKSPDDPSRYIPSDKLADLYKGFVKDYPVVSIEDPFDQDD  
WEAWSKFTASTSIQVVGDDLTVTNPKRIAKGVAEKSCNCLLLKVNQIGSVTESLQACKMA  
QSSGWGVMVSHRSGETEDTLISDLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEEELGAK  
AKFAGKNFRHPI

>CBL79146.1 Sal s 2; enolase [*Salmo salar*]

MSILKIHAREIFDSRGNPTVEVDLYTKKGLFRAAVPSGASTGIYEALERDNDKTRYLGK  
GVKRSVKYINEFLAPALCNQDVSVLEQEKVQDQLMLDMDGTENKSKFGANAILGVSLAVCK  
AGAAEKGVPLRYHIADLAGNPNVILPVPFNVINGGSHAGNKLAMQEFMTLPVGASTFKE  
AMRIGAEVYHNLKNVIKKNYQDATNVGDEGGFAPNILENKEALELLKEAIGKAGYTDKI  
VIGMDVAASEFYKDGKYDLDFKSPDDPSRYITPDQLGDLYKSFVKDYPVVSIEDPFDQDD  
WAAWSKFTAETSIQVVGDDLTVTNPKRIAKGVADKACNCLLLKVNQIGSVTESLQACKMA  
QTNGWGVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEEELGDK  
AVFAGKNFRHPI

>AFJ68065.1 Der p 1; cysteine protease [*Dermatophagoides pteronyssinus*]

EARPSSIKTFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSNNGGAINHLSLDEFK  
NRFLMSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRVTVP IRMQGGCGSCWAFS  
GVAATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVA  
REQSCRRPNAQRFGISNYCQIYPPNVNKIREALQTHSAIAVIIGIKDLDAFRHYDGRTI  
IQRDNGYQPNYHAVNIVGYNSAQSVDYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPY  
VVIL

>AFJ68066.1 Der f 1; cysteine protease [*Dermatophagoides farinae*]

EARPASIKIFEEFKAFNKNYATVEEEEVARKNFLESVKYVEANKGAINHLSLDEFK  
NRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRSRRTVTP IRMQGGCGSCWAF  
SGVAATESAYLAYRNQSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYV  
AREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHSAIAVIIGIKDLRAFQHYDGRT  
IIQHDNGYQPNYHAVNIVGYGSGTQGVYDVIWRNSWDTNWGDSGYGYFQAGNNLMMIEQYP  
YVIM

>AFJ68067.1 Der p 2; NPC2-like [*Dermatophagoides pteronyssinus*]

DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA  
IATHAKIRD

>AFJ68070.1 Der p 2; NPC2-like [*Dermatophagoides pteronyssinus*]

DQVDVKDCANHEIKKVLVPGCHGSETCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG  
LEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA  
IATHAKIRD

>AFJ68072.1 Der f 2; NPC2-like [*Dermatophagoides farinae*]

DQVDVKDCANHEIKKVMVDGCHGSDPCIIHRGKPFQLEALFEANQNTKTAKIEIKASLDG  
LEIDVPGIDTNACHFVKCPLVKGQYDIKYTWNVPKIAPKSENVVVTVKVLIGDNGVLACA

IATHGKIRD

>AFJ97274.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]  
MAISSSTSGTSSSLPSRTTVMLLLIFFFTASLGITDAQVGVGYMGMQNNLPSVSEVIALYK  
QSNIKRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
RFRYIAVGNIEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDKIKVSTAIIDLTLVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSSRSPLLANIYPYFTYAYNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGGSEVWVSESGWPSAGAFAAATFDNGRTYLSNLI  
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHFGLFFPDKRPKYNLNFGAEKNWDIS  
TEHNATILFLKSDM

>AFJ97275.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]  
MAISSSTSGTSSSLPSRTTVMLLLIFFFTASLGITDAQVGVGYMGMQNNLPSVSEVIALYK  
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV  
RIRYIAVATKLVVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY  
PPSAGAFRDDVRSYLDPIIGFLSSSRSPLLANIYPYFTYADNPRDISLPYALFTSPSVVV  
WDGQRGYKNLFDATLDALYSALERASGGSEVWVSESGWPSAGAFAAATFDNGRTYLSNLI  
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHSGLFFPDKRPKYNLNFGAEKNWDIS  
TEHDATILFLKSDM

>3V0R\_A Alt a 1; unknown function [*Alternaria alternata*]  
MDTASCPVTTEGDYVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDH  
KWYSCGENSFMDFSFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVA  
DAYITLVTLPKSS

>AFM77001.1 Mal d 2; thaumatin-like [*Malus domestica*]  
LTGFELASKASRSVDASSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPP  
ATLVEITIAANGGQDYDVSLVDGFNLPMVAPQGGTGECKPSSCPANVNAACPAQLQVK  
AADGSVISCKSACLAFGDSKYCCTPPNNTPETCPPTEYSEIFEKQCPQAYSAYDDKNST  
FTCSGGPDYVITF

>CCK33471.1 Tri a 39; serine protease inhibitor [*Triticum aestivum*]  
MSPVVKKPEGRNTDTSDDHNNQKTEWPELVGKSVVEAKKILQDKSEAQIVVLPVGTIVTM  
EYRIDRVRLFVDSLKDIAQVPRVG

>3TSH\_A Phl p 4; berberine bridge enzyme [*Phleum pratense*]  
YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT  
QVSHIQSAVVCGRHSVRIRVRSGGHDYEGLSYRSLQPETFVVDLNMRAVWVDGKART  
AWVDSGAQLGELYAIYKASPTLAFPAVGCPTIGVGNFAGGGFGMLLRKYGIAAENVID  
VKLVDANGKLHDKKSMGDDHFWAVRGGGGESFGIWWAWQVLLPVPPTVTIFKISKTVSE  
GAVDIINKWQVVPQLPADLMIRIIAQGPKATFEAMYLGTCKTLTPLMSSKFPELGMNPS  
HCNEMSWIQSIPFVHLGHRDALEDDLNRQNSFKPFAEYKSDYVYQFPKTVWEQILNTW  
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAAPLSWSKDI  
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQYFKGNFERLAITKGK  
VDPTDYFRNEQSIPLIKKY

>P86360.1 Tha p 2; unknown function [*Thaumatococcus panyocampa*]  
MKLLIFAILIALSSSVPQLSEKAEAEAVDLAYQEKNLFDLGSVAGDILSRSGCHVSFGCH  
KGYCWAGCGDPTNPWSWGENWCYTTKSYSQSYSVYQCTQDSECDGCWKCGGPCSA

>P86888.1 Pru p 7; gibberellin-regulated protein [*Prunus persica*]  
GSSFCDSKCGVRCSKAGYQERCLKYCGICCEKCHCVPSGTYGNKDECPCYRDLKNSKGNP  
KCP

>AFV53352.1 Ore m 4; tropomyosin [*Oreochromis mossambicus*]  
MDAIIKKMQMLKLDKENALDRAEQAESDKAAEDRSKQLEDDLVALQKLLKGTEDLDKY  
SEALKDAQEKLELAEKIATDAEGEVASLNRRIQLVVEEELDRAQERLATALTKLEEAEKAA  
DESERGMKVIENRAMKDEEKMELQEIQKKEAKHIAEEADRKYEEVARKLVIIEGDLERTE  
ERAELSEGKCELEEEELKTVTNLKSLEAQAEKYSQKEDKYEIEIKALTDKLEAETRAE

FAERSVAKLEKTIDDLEDELYAQKLYKAISEELDHALNDMTSI  
>BAB21619.2 7S globulin, vicilin, partial [Glycine max]  
MGNKTTLLLLLFLVCHGVATTTMAFHDDDEGGDKSPKSLFLMSNSTRVFKTDAGEMRVLK  
SHGGRIFYRHMHIGFISMEPKSLFVPQYLDNLIIFIRRGAEALGFIYDDELAERRLKTG  
DLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLETFQSFYIGGGANSHSVLSGFEP  
ILETAFNESRTVVEEIFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKMMQDQE  
EDEEEKQTSRSWRKLLLETVFGKVNKIEKNTAGSPASYNLYDDKKADFKNAYGWSKALH  
GGEYPLSEPDIGVLLVKLKLSAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSRAMTK  
IKQGDVVFVPRYFPFCQVSRDGPLEFFGFSTARKNKPFQFLAGAASLLRRLMGPELSAA  
FGVSEDTLRRRAVDAQHEAVILPSAWAAPPENAGKLMEEEPNAIRSFANDVVMDF  
>AGA84056.1 Ara h 5; profilin [Arachis hypogaea]  
MSWQTYVDDHLLCEIEGNHLSSAAILGQDGSVWAQSSNFQFKPEEITAIMNDFAEPSL  
APTGLYLGGTKYMIQGEPTVIRGKKKGGVTIKKTNQALIIIGIYDEPMPGQCNMIVE  
KLG DYLI DTGL  
>AGC39164.1 Act d 5; kiwellin [Actinidia deliciosa]  
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGLICIKGKCNDDPQVGTHIC  
RGTTSPSPQPGGCKPSGTLTCRGSHPYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39165.1 Act d 5; kiwellin [Actinidia deliciosa]  
MAQLALLLSLFLTLISLAPPGTSISSCNGPCRDLNDCDGLICIKGKCNDPEVGTHIC  
RGTTSPSPQPGGCKPSGTLTCRGSHPYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39166.1 Act d 5; kiwellin [Actinidia deliciosa]  
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGLICIKGKCNDDPQVGTHIC  
RGTTSPSPQPGGCKPSGTLTCRGSYPTYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39167.1 Act d 5; kiwellin [Actinidia deliciosa]  
MAQLSLLVLSLFLTLISLPPPASISSCNGPCRDLNDCDGLICIEGKCNDPEVGTHIC  
RGTTSPSPQPGGCKPSGTLTCRGSHPYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39168.1 Act c 5; kiwellin [Actinidia chinensis]  
MAQLSLLLSLFLTLISLPPPASISSCNGPCRDLNDCDGLICIKGKCNDPEVGTHIC  
RGTTSPSPQPGGCKPSGTLTCQGKSHPTYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLNKNVGVVDITWSMA  
>AGC39169.1 kiwellin [Actinidia eriantha]  
MAQLSLLLSLFLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDPEVGTHIC  
RGTTSPSPQPGGCNPSGTLTCRGSYPTYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ERYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39170.1 kiwellin [Actinidia eriantha]  
MAQLSLLLSLFLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDDPQVGTHIC  
RGTTSPSPQPGGCNPSGTLTCRGSYPTYDYDCSPPVTSSTPAKLTNNDFSEGGDGGGPSECD  
ERYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECD SRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>AGC39171.1 kiwellin [Actinidia eriantha]

MAQLSLLFSLFSLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC  
RGTTTSPQPGGCNPSGTLTCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD  
ERYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVECDSDRHRGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA

>AGC39172.1 kiwellin [Actinidia arguta]

MAQLTLLLLSLFSLTLISLPPPAGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC  
GGTTTSPQPGSCNPSGTLTCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVECDSDRHRGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA

>AGC39173.1 kiwellin [Actinidia arguta]

MAQLTLLLLSLFSLTLISLPPPAGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC  
GGTTTSPQPGSCKPSGTLTCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVECDSDRHRGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA

>AGC39174.1 kiwellin [Actinidia arguta]

MAQLTLLLLSLFSLTLISLPPPAGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC  
GGTTTSPQPGGCNPSGTLTCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD  
ESYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVECDSDRHRGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA

>AGC39176.1 thaumatin-like [Actinidia chinensis]

MSTFKSLSLALLFIAFLFTCARGATFNIINNCPFTVWAAAVPGGGKRLDRGQNWIIINPG  
AGTKGARVWARTGCNFDGAGRKQGTGDCNGLLQCQAFGQPPNTLAEYALNQFNLDFFD  
ISLVDGFNVAMEFSPTSGGCTRGIKCTANINEQCPNELRAPGGCNPCTVFKTDQYCCNS  
GNCGPTDYSRFFKTRCPDAYSYPKDDQTSTFTCPGGTNYKVVFVCP

>AGC56216.1 Der f 25; triosephosphate isomerase [Dermatophagoides farinae]

MGRKFFVGGNWKMNNGKTAIKEIVDFLKNGPLDSNVEVVVGVPAIYLMCKNILPDNIRV  
AAQNCYKVDKGAFTGEISPAMIKDVGAEWVILGHSERRNVFGEVDQLIGEKVEHALQEGL  
HVIACIGELLEEREAGKTTEVVRQQTQVISKHVKDWFKVVLAYEPVWAIWGTGKTASPQQA  
QEVHQKLRQCFSENVSPQIAETIRIYGGSVTANNAKELASQADVDGFLVGGASLKPEFV  
QIVNARQ

>AGC56218.1 Der f 28; heat shock protein 70 [Dermatophagoides farinae]

MSKTPAIGIDLGTYSVGVFQHGKVEIANDQGNRTTSPYVGFDTTERLIGDAAKNQVA  
MNPSNTVFDKRLIGRKFDETTVQADMKHWPFKVIEKGNKPAIEVEFKGETKQFIPEEIS  
SMVLVKMRETAAYLGGTVNNAVITVPAYFNDSQRQATKDSGLIAGLNVLRIINEPTAAA  
IAYGLDKKGGAGERNVLIIFDLGGGTFDVSLLTIEEGIFEVKSTAGDTHLGGEDFDNRLVN  
HFVKEFKRKHKKDLTTNARALRRLTSCERAKRTLSSAAQTSIEIDSLFEGIDFYTSITR  
ARFEELCADLFRSTMEPVERVLRDAKTDKSSVNEIVLVGGSTRIPKIQRVADFFNKDPN  
KSINPDEAIAYGAAVQASILSGDTSSKSTNEIILLDVALPLSLGIETAGGVM TALIKRDTT  
IPTRSPRLSLPTPTTSLVSRFRSTRVSLAPRTTSLVSSSSPVSPCSSWCSSDRGHFDV  
DANGIMNVGAVEKGTGKTNKITITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARIHAKN  
GPESYAYSLRNTVNEGKLSISDSDEKLRARLRLSTGSTTTRPPARRSTLNRRSSRVL  
PTPSFWLPTVVLAVVVPPLVWTPVLVALVWLTRLRSALRSLTKKVFNQVFLFPVLFVDS

>AGC56219.1 Der f 30; ferritin [Dermatophagoides farinae]

MAANPESTTKTSRVRMNIQINLEFYASYVYQQMAYHFNRDDVALPGFEKFFDVSSKEERE  
HAERFMKLQNRGGRIVLDDIHKPQQQDWSSGLEAMRAALELEKTVNQALLDLHAVATKH  
NDAQFADFIETHYLTEQVEAIKKLADYITNLERCQGLGEYLFDRHTLHSS

>AGC60020.1 paramyosin [Anisakis pegreffii]

MSDTLYRSPMAIRSSTADMGALTSMSVADLGLSLRLEDKIRLLQDDFESERELRNRIER  
ERADLSVQLIALTDRLQDAECATDSQIESNRKREVELSKLRKLLLEESQLENE DAMNVLRK  
KHQDVCLDYTEQIEQLQKKNSKIDRERQRLQHEVIELTATIDQLQKDKHVAEKMAQKFEQ

QTIELSNKVEDLNKHVNDLAQQRQRLQAENSDLLAEIHDQKVQLDNLQHVKYQLAQQLEE  
SRRRLEDAERERSQMQAQLHQVQLELDSVRVALDEESAARVEAEHKLSLANTEITQWKS  
FDAEVALHHEEVEDLRKKMMQKQAEYEEQIEIMLQKVSQLEKAKARLQSEVEVLIVDLEK  
AQNTIAILERAKEQLEKQVLEMKSRIDELLEVEEAAQREARAALAEELQKMKQLYEKAVEQ  
KEALARENKKLQDDLHEANEALADANRKLHELDLENARLAGEIRDLQVALKESEAARRDA  
EARAQRALAELOQVRIEMERRLOKEEEMEALRKSMQFEIDRLTAALADAEARMKAEIAR  
LRKKYQAEIAELEMTVDNLNRANLEAQKTIKKQSEQIIQLQANLEDTQRQLQQTLDQYAL  
AQRKISALSAELEECKTALDNAIRARKQVEADLEEAHVRISDLTSINSNLTAIKNKLETE  
LSTAQADLDEVTKELHAADERANRALADAARAVQELHEEQEHSMKIDALRKSLEEQVKQL  
QVQIQEAEAAALLGGKRVIKLETRIRDLEVALDEETRRHKETQSALRKKDRRIKEVQMQ  
IDEEHKMFVMAQDTADRMLEKLNQKRQLGEAEAMTMQNLQRVRRYQRELEDAEGRADQA  
ESSLNLIRAKHRGTVAVGKATDVYVVEED

>AGC60026.1 unknown function [Anisakis pegreffii]  
MVKNLPPSVREQCIESQIVIRNCKEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS  
SLRDCIKKGGYMGYCKTFTTEENCIWKDECAPSEAAEKKDENSLEVPETFSQCFKSQV  
VMQQCMSKGEEECSKIQKECVDAFGTPPVTYAANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT  
VDANPPIFTSKMNTCVKRKMAKGL

>AGC60027.1 unknown function [Anisakis pegreffii]  
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS  
SLRDCIKKGGYMGYCSNFTTHENCIWKDECAPSEAAEKKDENSLEVPETFSQCFKSQV  
VMQQCMSKGEEECLKIQKECVDAFGTPPVTSANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT  
VDANPPIFTSKMIRCVKRKMAKGL

>AGC60028.1 unknown function [Anisakis pegreffii]  
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS  
SLRDCIKKGGYMGYCSNFTTPENCIWKDECAPSEAAEKTDENSLEVPETFSQCFKSQV  
VMQQCMSKGEEECLKIQKECVDAFGTPPVTSANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT  
VDANPPIFTSKMNTCVKRKMAKGL

>AGC60029.1 Ani s 12; unknown function [Anisakis simplex]  
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS  
SLRDCIKKGGYMGYCSNFTTHENCIWKDECAPSEAAEKKDENSLEVPETFSQCFKSQV  
VMQQCMSKGEEECSKIQKECVDAFGTPPVTYAANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT  
VDANPPIFTSKMNTCVKRKMAKGL

>AGC60030.1 Ani s 12; unknown function [Anisakis simplex]  
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAT  
SLRDCIKKGGYMGYCKTFTTEENCIWKDECAPSEAAEKTDENSLEVPETFSQCFKSQV  
VMQQCMNEGEECSKIQKECVDAFGTPPVTYAANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQEECVAAATDAPT  
VDANPPIFTSKMIRCVKRKMAKGL

>AGC60031.1 Ani s 12; unknown function [Anisakis simplex]  
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS  
SLRDCIKKGGYMGYCSNFTTHENCIWKDECAPSEAAEKTDENSLEVPETFSQCFKSQV  
VMQQCMNKGEEECSKIQKECVDAFGTPPVTYAANGAYQMAAPLHRCIENGGWMKMCSTWI  
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT  
VDANPPIFTSKMITCVKRKMAKGL

>AGC60035.1 Ani s 1; serine protease inhibitor [Anisakis simplex]  
MDKGTPTQEGGVKPSVAWWHDDKTGICLSFKYTGCGGNANRFTTIKNCEQHCKMPDRGA

CALGKKPAEDSNGEQLVCAGMREDKCPNGYQCKMMAFMGLCCPTKEEELFAREYEGVCKS  
GKPVKMDRGSWMMTILGKSCDDQFCPEDAKCEQGKLFANCCCK  
>AGC60036.1 Ani s 1; serine protease inhibitor [Anisakis simplex]  
MDKGTPTQEGGVKPSVAWWHDDKSGICLSFKYTGCGGNANRFTTIKNCEQHCKMPDRGA  
CALGKKPAEDSNGEQLVCAGMREDKCPNGYQCKMMAFMGLCCPTKEEELFAREYEGVCKS  
GKPVKMDRGSWMMTILGKSCDDQFCPEDAKCEQGKLFANCCCK  
>B3EWS0.1 thaumatin-like, partial [Manilkara zapota]  
ATFDIVNQCTFT  
>CCP19647.1 Par j 3; profilin [Parietaria judaica]  
MSWQTYVDDHLMCEIEGNHLTAAAILGQDGSVWAQSASFQFKPEEIAAIVKDFEETPGTL  
APTGLFLGGAKYMIQGEAGVIRGKKGSGGVTVKKTGQALVIGIYDEPMPAGQCNMIVE  
RLGDYLIETGL  
>AGE44125.1 Por p 1; tropomyosin [Portunus pelagicus]  
MDAIIKKKMQAMKLEKDDAMDRAADLEQQNKEANIRAEKAEVHNLQKRMQQLENDLDQV  
QESLLKANTQLEEKDKALSNAEAGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE  
FAERSVQKLQKEVDRLEDELVNEKEYKSTTDELQDQAFSELSGY  
>E1U332.1 Ole e 12; isoflavon reductase-like protein, phenylcoumaran benzylic ether  
reductase [Olea europaea]  
MADKTKILIIIGGTGYIGKFIVEASAKSEHPTFALARESTISDPVKGKIIQGFKNQSGVTIL  
TGDLYDHESLVKAIKQVDVVISTVGLQLADQVKIIAAIKEAGNVKRRFFPSDFGTDVDR  
HAVEPAKSSFEIKSQIRRAIEAEGIPYTFVSANYFAGYSLPTLVQPEVTAPPRDKVIILG  
DGNKAVFNEENDIGTYTIKAVDDARTLNKILYIKPPKNIYSFNELVALWEKKIGKTLEK  
IYVPEEQVLKQIQESPFPIVMAINHSFVKGDLTNFKIEPSFGVEASELYPDVKYTTV  
EYLDQFV  
>E3SU11.1 Ole e 13; thaumatin-like [Olea europaea]  
MNFSKNLPLLVSLWAIFFAYTHAATFDIVNQCTYTVWAAAASPGGGRRLDQGSWNINVA  
PGTTQARIWGRNTCNFDANGRGQETGDCNGLLECGYGRPPNTLAEFALNQPNNLDFVD  
ISNVDGFNIPLFSPPTTNCRRLLVCNAPIVQCPSELRTPGGCNNPCTVFNTNEYCCTNG  
PGSCGPTPLSRFFKERCPDAYSYPQDDPTSLFTCPAGTNYRVVFCP  
>AGG10560.1 Tyr p 8; glutathione S-transferase [Tyrophagus putrescentiae]  
MSSKPVLYWDIRGLAQPIRLLLAYLDVDYEDKRYQLGANFDRSAWLTEKFNGLDFPNL  
PYYIDGNVSKLSQTLAILRYIGRKYKLTGANPEELRVSLVEQQVVDGNQSLSRVAYDPNA  
DKLKPDFLKTLPDSVKQLSHFLGNSPFVAGTSITYVDFWLYEYLVKLSVLVPEVFGQFDN  
LKKFVERIESLPRVSVYIKAQQPKLFNGPMAKWNGQYA  
>NP\_001306883 Sola l 6; lipid transfer protein [Solanum lycopersicum]  
MKMTKVCFSFVAVMLVMILVCDQFGANEAATCSASQLSPCLGAIQGGTAPSQDCCARLKNQ  
QPCICGFMKDPNLRQYVNSPNARKVAGQCGVSIKSC  
>CCU98198.1 Mala s 13; thioredoxin [Malassezia sympodialis]  
MGVQVISSYDQFKQVTGGDKVWIDFWATWCGPCKMIGPVFEKISDTPAGDKVGFYKVDV  
DEQSQIAQEVGIRAMPTFVFFKNGQKIDTVVGADPSKLAQAAITQHS  
>CCU99206.1 Mala s 9; unknown function [Malassezia sympodialis]  
MSNVIKKVFNTDKAEAGSKVADAPQEAHGKGEFLHDAKDRLQGFAGHGHNAQNAASG  
VAGSAGAGGAPSVPSANVDVNTNPVNDASVQGGVEAPRSWSTQLPQSQSVADTTGATSAGR  
NNLTQTTSTGSGVNVAAGNVQDQVHLAPVTRHVHHRHEIEELLREREHHIHQHHIQHVV  
QPVVSEHLAEQIHSRVVPQTTVREHANTDKDAALMRAVAGNPKDFTTQAAIDRSVIDK  
GETVREIVHHHHIHNIQPIIEKETHEYHRIRTTIPTTHITHEAPIVHESTAHQPIRKEDF  
LKGGGVLSTTRSIEEAGLLNLGNNQRTVEGETYTGGLPLSQ  
>CCU99457.1 Mala s 5; unknown function [Malassezia sympodialis]

MSATTGSQAPNTTFTYIPWAPELD SGKVCVGPQTFKAHDRWKGKKVWVAIPGAFTPVCH  
QNHIPGFVEKINELKAKGVDEVVVI AVNDAFVMSGWGVTVGGKDQIVYACDNDLAFSKAL  
GGTLDLTSGMGVRTARYAVVLDLKIT YFGMDEGNMGAPEKSSVDAVLAQL  
>CCV00099.1 Mala s 11; superoxide dismutase [Malassezia sympodialis]  
MTEHTLPPLPYEYNALEPFISADIMMVHGHGKHQTYVNNLNASTKAYNDAVQAQDVLKQM  
ELLTAVKFNGGGHVNHALFWKTMAPQS QGGGQLNDGPLKQAIDKEFGDFEKFAAFTAKA  
LGIQGSWCWLGLSKTGLDLVVAKDQDTLTTTHPIIGWDGWEHAWYLQYKNDKASYLKQ  
WNNVVNWSEAESRYSEGLKASL  
>CCU97864.1 Mala s 10; heat shock protein 70 [Malassezia sympodialis]  
MSSVVGLDIGNSSSKIGVARARGVDIVSNEVSNRSTPSLVSFGQKARLLGEGAATAQTSN  
FKNTVGLSLKRLIGRTFQDESIQTYE KPFVNAELVDAKGEVGVKVRFQNEEHIFSATQLLA  
MYLGKLRDTTQNELGGSGVSDVWLSVPIWFTDAQRRAHLHAAEIANLNPLRVMNEPTATA  
LGYGITKTDLPEPDSPRNVIFVDIGHSSYQVSVVAFCKGQLTVLGAWADPNFGGRNFDRV  
LMEHFAEEFKGKYKIDVFFNPKATFRLAAGCERLKKVLSANTLAQLNVEESLMNDIDAASQ  
LKRDEFESLIAPYLERVNGPLDAALSQ SGLTKDEIHSVELVGGSSRVPALKERIAAWYGK  
PLSYTLNQDEAIVRGCTLACATLSPVFRVREFSVHDISSYPIKVSWEPA PDVPDEENELV  
VFNTNPNPVPSTKILTFYRKEPFSLDATYADASTLPKGTNPWLGRVTIKNVAPNEKGEHSI  
VKVKARLNLHGVLNVESAYTVDEIEKEE EEPVVDPNAAEDAEPKTEKKIVKKLQRKDDL P  
IVSGIGLLDPTLLAELKEREGQMYAADKLVADTEDRKNAL E EYIYDTRSKLDERYATFVQ  
SEEKEKLLAMLAESEDWLYTEEGEDATKSAYVSRL ETLQKVGAPIHFRWKEHEERPKAAA  
QLREVVNKYMSVFENEPEKYDHLSDDDKTKVIEKAATVGKWLDDYMYKQSEL PKNVDPKL  
TSEEILKKKDDVIYVCTPILTKPKPRVPVDTSKPEENAQTSNEKQGDMDVD  
>AGI78542.1 Der f 24; ubiquinol-cytochrome c reductase binding protein  
[Dermatophagoides farinae]  
MVHLTKTLRFINNPGFRKFYGLQGYNKYGLYD DFYDYTDAAHLEAVRRLPPDL YDQHT  
YRLVRASQLEITKQFLPKEQWPSYEEDMDKGRFLTPYLDEVMKEKKEKEEWINFLSKD  
>AGL34967.1 Cof a 2; metallothionein [Coffea arabica]  
MSCCGNCGCGAGCKCSGGCGGCKMYPELSY TENTAETLILGVAPPKTAYLEGAGEEAA  
AENGGCKCGPDCKCNPCK  
>AGL34968.1 Cof a 3; metallothionein [Coffea arabica]  
MSDKCGNCDCADRSQCCKGSSYAADIVETENTFVETFVMMEGGAQNGKCKCGPSCACVN  
CTCDN  
>AGM48615.1 unknown function, partial [Sarcoptes scabiei]  
DLDNAFNPRDGTMLKQVKDRIYDIK LKREPFYRGLHIEGNENALIKKGD LHMSLVDPLT  
LNVLTKN DGIVDMTLDLVS PNTKKAALKINSK KYDLHDHGEITVSIFNPRMTWKHHTRKG  
DMELNIDADITRKGSLITYSRKEPDDSTKVRYSRQGNQVSM EVDSK LIEGHANGTLTDGK  
IHVKGRESDFEIESTYKVEDGKLMIEPTKTQNGKLEGLLSRKVPSHLVLETPRVKMMNKY  
DRFAPVKILKLDYDGLN YEKHIDA EYEPSNH YKYFTDGKSKRS GKGYSIKIDGKPKKALK  
VDVDMPDFKF  
>BAN29066.1 Tri a 20; gamma-gliadin [Triticum aestivum]  
NMQVDPSSQVQWPQQQPVPQPHQPF SQQPQQTFPQPQQTFPHQPPQQFPQPQQPQQQLQ  
PQQPFQPPQQPYPPQQPFPQTQQPQQLFPQSQQPQQQFSQPQQQFPQPQQPQQSFPQ  
QQPPFIQPSLQQQVNPKCNFL LQCKPVS LVSSLWSMIWPQSDCQVMRQQCCQQLAIPQ  
QLQCAAIHTIIHSIIMQQEQEQEQGMHILLPLYQQQVVGQGLVQGGGIIQPQQPAQLE  
AIRSLVLQTLPTMCNVYVPPECSI I KAPFSSV VAGIGGQ  
>BAN29067.1 omega-5 gliadin, partial [Triticum aestivum]  
ARELNPSNKE LQSPQQSF SHQQPFPQQPYPPQQPYPSQQPYPSQQPFPTPQQQFPQQSQQ  
PFTQPQQPTPLQPQQPFPQQPQQPQQPFPQPQQPFPWQPQQPFPQTQQSFPLQPQQPFPQ  
QPQQPFPQPQLPFPQQSEQIIPQQPQQPFPPLQPQQPFPQQPQQPFPQPQQPFPVQPQQSF  
PQQSQQSQQPFAQPQQLFPELQQPIPQQPQQPFPPLQPQQPFPQQPQQPFPQQPQQSFPQQ

PQQPFPQQPQQPFPQQPQQPFPQQPFPPLRPQQPFPQQPQQSQQSFPQPQQPQQPS  
ILQPQQPLPQQPQQPFPQQPQQLSQQPEQTISQQPQQPFPQQPHQPQQPYPQQQPYGSSS  
TSIGGQ

>BAN29068.1 Tri a 26; HMW glutenin [Triticum aestivum]  
EGEASEQLQCERELQEHSLKACRQVVDQQLRDVSPQCQPVGGGPVARQYEQQVVVPPKGG  
SFYPGETTPPQQQLQQSILWGIPALLRRYYLSVTSPQQVSYYPGQASSQRPGQGQQEYLLT  
SPQQSGQWQQPGQGQSGYYPTSPQQSGQKQPGYYPTSPWQPEQLQQPTQGGQRQQPGQGQ  
QLRQGQQGQSGQGQPRYYPTSSQQPGQLQQLAQGGQGGQPERGQQGQSGQGQQLGQGQ  
QGQQPGQKQSGQGQGGYYPTSPQQLGQGQSGQGQLGYYPTSPQQSGQGQSGYYPTSAQ  
QPGQLQQSTQEQLGQEQQDQSGQGRQGQSGQRQQDQSGQGQPGQRQPGYYSTSPQ  
QLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQQGQQPEQGQQGQQQRQGEQGQQPGQGQ  
QGQQPGQGQPGYYPTSPQQSGQGQPGYYPTSPQQSGQLQQPAQGQQPGQEQQGQQPGQGQ  
QPGQGQPGYYPTSPQQSGQEQQLEQWQQSGQGQPGHYPTSPLPQGQGPYYPTSPQQIG  
QGQQPGQLQQPTQGGQQGQPGQGQQGQPGEGQQGQPGQGQPGQGQPGYYPTSLQQSG  
QGQQPGQWQQPGQGQPGYYPTSSLPQEQQGQGGYYPTSPQQPGQGPQPGQWQQSGQGQGY  
YPTSPQQSGQGQPGQWLQPGQWLSGYYLTSPQQLGQGQPRQWLQPRQGQGGYYPTSP  
QQSGQGQQLGQGQGGYYPTSPQQSGQGQGGYDSPYHVSAEHAASLKVAKAQQQLAAQLPA  
MCRLEGGDALSASQ

>BAN29069.1 Tri a 36; LMW glutenin [Triticum aestivum]  
ENSHIPGLERPWQQQLPQQTFPQQPLFSQQQQLFPQQPSFSQQQPPFWQQQPPFSQQQ  
PILPQQPPFSQQQQLVLPQQPPFSQQQOPVLPPQQSPFPQQQHQQLVQQQIPVVQPSIL  
QQLNPCKLFLQQQCSVPAMPQRLARSQMLQQSSCHVMQQCCQQLPQIPQQSRYEAIRAI  
IYSIILQEQQQVQGSIQSQQQPPQLGQCVSQPQQSQQQLGQQPQQQQLAQGTFLQPHQ  
IAQLEVMTSIALRTLPTMCRVNVPLYRTTTSVPFGVGTGVGGY

>AGR27935.1 Pru du 6; 11S globulin, cupin, partial [Prunus dulcis]  
DNHIQSEAGVTESWNPSPDQFQLAGVAVVRRTEPNGLHLPVSYVNAPQFIYIVRGRGVLG  
AVFPGCAETFEDESQPPQFQQQQQQQQFRPSRQEGGQGGQFQGEDQLDRHQKIRHIREG  
DIIALPAGVAYWSYNNGEQPLVAVSLDLSDNDQNLQDQVPRRFYLAGNPQDEFNPQQQ

>AGS80276.1 Alt a 14; superoxide dismutase [Alternaria alternata]  
MELHHSKHHQTYITNLNGLLKTQAEAVSTSDITSQVSIQQGIKFNAGGHINHSLFWQNL  
PASSNEAKISAAPLVKQIQATWGEDKFKFAFSAALLGIQGSWGWLIKTDMGKEQRLS  
IVTTKQDPVVGKGEVPIFGVDMWEHAYYLQYQNGKAAYVKNIWNVINWKTAEERYLGS  
ADAFSVLKASI

>AGT20779.1 hemocyanin, arylphorin [Penaeus merguensis (Fenneropenaeus  
merguensis)]

MRVLVVLGLIAAAAFQVVSADVQKQKDVLYLLHRIYGDIDADLLATANSFDPAGGSYSD  
GGAAVQRLKGLNDGRLLEQKHWFSLFNTRHRNEALLLFDVLIHSSDWATFVGNAAFFRQ  
KINEGEFVYALYVAVIHSPLTEDVWLPPLYEITPHLFTNSEVIEAAYRAKQKQTPGKFES  
TFTGTTKKNPEQRVAYFGEDIGLNTHHTVHMEFPFWWDEYGHHLDRKGENFFVHHQLT  
VRFDAERLSNYLDPVGEHLHWYKPIVDGFAPHTTYKYGGQFPARPDNVKFEDVDDVARIRD  
MVIVESRIRDIAIHGYIIDSHGKQIDISNEKGIDILGDVIESSLYSPNVQYYGALHNTAH  
IVLGRQGDPHGKFDLPPGVLEHFETATRDPSFFRLHKYMDNIFKEHKDSLPPYTKADLEF  
SGVSISEVNVVGELETYFEDFEYNLINAVDDAEGIPDVIDISTYVPRLNHKEFTFKIDIEN  
GGSPRLATVRIFAWPHKDNNGIEFTFDEGRWNAIELDKFWVSLAGGKNSIERKSTESSVT  
VPDVPISIDTLFAKTAAGGDGLSEFASATGLPNRFLLPKGNDKGLEFDLVVAVTDGDADAA  
VPDLHLNNTKYNHYGANGVYDPKRPBGYPLDRRVPDERVFEELPNFKHIQVKVFNHGEH  
S

>AGT28425.1 Phod s 1; general odorant-binding protein [Phodopus sungorus]  
NDYAELEGKWDTIAIAADNDAKIKEEGLRLYVRELYCNEDCSEMEVTFYVNANNQCSKT  
TVIGYKQADGTYRTQFEGDNRFPVYATPENIVFTSKNVDRAGQETNLIFVVGKSQPLTP

EQHEKLVFAHENNIPEENIHNVLATDTCPK  
>AGW21344.1 lipid transfer protein [*Prunus persica*]  
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIPYVRGGGAVPPACCCNGIRNV  
NNLARTTPDRQAACNCLKQLSASVPGVNPNAAVLPGKCGVSIPYKISASTNCATVK  
>CAA61943.2 Tri a 12; profilin, partial [*Triticum aestivum*]  
MSWQTYVDDHLCCEIDGQHLTSAAILGHDGSVWTESPNFPKFKPEEIAGIVKDFEEPGHL  
APTGLFLGGTKYMVIQGEPPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVE  
RLGDYLIDQGY  
>CAA61944.2 Tri a 12; profilin, partial [*Triticum aestivum*]  
MSWQAYVDDHLCCEIDGQHLTSAAILGHDGSVWAESPFPKFKPEEIAGIVKDFEEPGHL  
APTGLFLGGTKYMVIQGEPPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVE  
RLGDYLIDQGY  
>CAA61945.2 Tri a 12; profilin, partial [*Triticum aestivum*]  
MSWKAYVDDHLCCEIDGQNLTSAAAILGHDGSVWAQSPNFPQFKPEENAGIVKDFEEPGHL  
APTGLFLGGTKYMVIQGEPPGVVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVVE  
RLGDYLIDQGY  
>P86809.1 Api g 6; lipid transfer protein [*Apium graveolens*]  
ATCSAVQLSPCLAAITKNTPPSAACCNKLKEQKPCCLCGYLKDPNLKNYVNSPGARKTASS  
CGVALKC  
>4C9C\_B Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [*Fragaria x  
ananassa*]  
AMAGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAQAVKCAEILEGDGGPGTIKKIT  
FGEGSHYGYVKKHKIHSIDKVNHTYSYSLIEGDALSENIEKIDYETKLVSAHPHGGTIIKTT  
SKYHTKGDVEIKEEHVKAGKEKAAHLFKLIEGYLKDHPSEYN  
>AHA36627.1 Cor a 9; 11S globulin, cupin [*Corylus avellana*]  
MAKLILVFSFLCLLVLFNGCLGIDVGLRRQQQRHFGEENLDRLNALEPTNRIEAEAGQIE  
SWDHNDQQFQCAGVAVIRRTIEPNGLLLPQYSNAPELIYIERGRGITGVLFPGCPETFED  
PQQQSQQGQGSQRSEQDRHQKIRYFQEGDIIALPAGVAHWCYNDGDSPPVAVSLLHT  
NNYANQLDENPRHFYLAGNPDDEHQRQGGQQFGQRRRQQQHSRGKEGEQEQQGEGNNVFS  
GFDAEFLADAFNVDVDTARRLQSNQDKRRNIVKVEGRLQMV RPERSRQEWERQERQERES  
EQERERQRRQGGRRDVGFEETICSLRLMENIGRSRADIYTEQVGRINTVNSNTLPVL  
RWLQLSAERGLDQREGLYVPHWNLNAHSVYAIRGRARVQVDDNGNTVFDDELRRQGVV  
TIPQNFVAVAKRAESEGEFVAFKTDNAQISPLAGRTSAIRALPDDVLANAFQISREEAR  
RLKYNRQETTLARSSRSSSERMRRRSESEGRAEA  
>AHA85706.1 tropomyosin [*Macrobrachium rosenbergii*]  
MDAIIKKKMQAMKLEKDNAMDRAADTLEQQNKEANNRAEKSEEEVFSLQKRMQQLENDLDSV  
QEALLKANQHLEEKDKALSNAEAGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY  
>AHB19225.1 Pun g 1; lipid transfer protein [*Punica granatum*]  
MASSGFLRLAGFVLVCMVAVASTVAEAGITCGQVSSSLAGCIQYARGNGAGPVPQACCNGI  
RSLNSAAKTTTPDRQAACRCLKSLASSISGINYGLVAGAPGKCGVSIPYKIAPSTNCDNVK  
>AHB19226.1 Pun g 1; lipid transfer protein [*Punica granatum*]  
MASKRFLNNLVPALFLCMVVAASVAVTCGQVTSSTLPCIPYARGVVAAPSAACCSGV  
RSLNNAKTTTPDRQTACNCLKVIARSITGINYGRVGLALPGKCGVSIPYKISPSTDCSRVK  
>AHB19227.1 Pun g 1; lipid transfer protein [*Punica granatum*]  
MTGSGLFKLACAVFAVALVAAPIATEAAVTCGQVASSLAPCIPYARSAGGAVPPACCSGI  
KTLDGMARTTPDRQATCKCLKSASTSISGINYGLVASLPAKCGVNIPYKISPSTDCARVK  
>4BK6\_B Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [*Betula pendula*]

GVFNCETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE  
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY  
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>4BK7\_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]  
GVFNFETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE  
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY  
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN  
>AHC08073.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [Solanum  
lycopersicum]  
MGVNTYTYESTTTTISPTRLFKALVLDLDFDNLVPKLLSQHVKNNETIEGDGGVGSIKQMN FV  
EGGPIKYLKHKIHHVIDDKNLETKYS LIEGDILGEKLESITYDIKFEANDNGGC VYKTTTE  
YHTKGDHVVSEEEHNVGRERIMNISKAVEAYLLANPSVYA  
>AHC08074.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [Solanum  
lycopersicum]  
MGVNTFTHESTTTTIAPTRLFKGLVLDLDFDSLVPKLLSHDVKSIEIVEGDGGAGSIKQMN FV  
EGGPIKYLKHKIHHVIDDKNLVTKYSLIEGDVLGDKLESIAVDVKFEAAGDGGCVCKTTTE  
YHTKGDHVVSEEEHNVGKGAIDL FKAIEAYLLANPSVYA  
>AHC94806.1 Der f 21; unknown function [Dermatophagoides farinae]  
MKFIIFCAIVMAVSVSGFIVDVEDTKWRNAFDHMLMEEFEEKMDQIEHG LLM LSEQYKE  
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK  
DLAELAKKVKAVKSDD  
>CCK33472.1 Can s 3; lipid transfer protein [Cannabis sativa]  
ITCGQVASSLAPCLSYLKVGGAVPDGCCNDIKSLSGAAKTPADRQAACKCLKSAASSIKG  
VNFNLASGLPGKCGVSIPYKISPSTDCSSVK  
>CCW27997.1 Hev b 15; serine protease inhibitor [Hevea brasiliensis]  
MASQCPVKDAWPELIGTNGDIAAGIIETENANVKAIVLKKGSPMTMEYNLCRVLV FVDDN  
RVVTQAPAIG  
>AHF71027.1 Bet v 8; glutathione S-transferase [Betula pendula]  
MADASVKEHLPTPLDATSNPPPIFDGTTTRYTCYTCPFAQRVWITRNYKGLQE KIKLVPI  
NLQNRPAWYKEKVYPENKVPAL EHNKVGIGESLDLIKVVDINFEGPSLLPNDPAKKAF AE  
ELVAYSDTFNKTVFTSFKGDPVKEAGPAFDHLEKALHKFDDGPFPLGQFSAVDIVYIPFV  
ERFQIFLLDALKYDITAGRPKLAKWIEELNKIDAYKPTKTDPKELVEFYKARFAAQQ  
>P86980.1 Gad m 3; aldolase [Gadus morhua]  
PHAYPFLSPEQKKE L  
>P86979.1 Thu a 3; aldolase [Thunnus albacares]  
PHAFPFLTPEQKKE LSDIAHKIVAPGKGILAADESTG  
>B3A0L6.1 Gad m 2; enolase [Gadus morhua]  
SITKIKAREIL  
>P86978.1 Thu a 2; enolase [Thunnus albacares]  
SITKIKAREILD  
>P0DMB4.1 phospholipase A1 [Vespa affinis]  
MMNLKYLLFFCLVQALHYCYAYGDP SLSNELDRFNPCPYSDDTVKMIILTRENKKHDFYT  
LNTIKNHNEFKKSTIKHQVVFITHGFTSTATAENFLAMAEALLDKGN YLVILIDWRVAAC  
TNEMAGVKLAYYSYAASNTRLVGN YIATVTKMLVQYQNVPMANIRLIGHSLGAHTSGFAG  
KKVQELRLGKYSEIIGLDPAGPSFKSQECSQRICETDANYVQI IHTSNHLGTLVTLGTVD  
FYMNNGYNQPGCGLPIIGETCSHTRAVKYFTECIRHECCLIGVPQSKNPQPVSKCTRNEC  
VCVGLNAKTYPKTGSFYVPVESKAPYCNNGKII  
>P0DMB5.1 phospholipase A1 [Vespa affinis]  
MMNLKYLLFFCLVQALHYCYAYGDP SLSNELDRFNPCPYSDDTVKMIILTRENKKHDFYT  
LNTIKNHNEFKKSTIKHQVVFITHGFTSTATAENFLAMAEALLDKGN YLVILIDWRVAAC

TNEMAGVKLAYYSYAASNTRLVGNVIATVTKMLVQQYNVPMANIRLVGHSLGAHTSGFAG  
KKVQELRLGKYSEIIGLDPAGPSFKSQECSQRICETDANYVQIIHTSNHLGTLVTLGTVD  
FYMNNQYNQPGCLPIIGETCSHTRAVKYFTECIRHECCLIGVPQSKNPQPVSKCTRNC  
VCVGLNAKTYPKTGSFYVPVESKAPYCNKKGKII

>A4GFC3.1 Ole e 2; profilin [*Olea europaea*]  
MSWQAYVVEHLMCEIESHHLSAAAILGHDGTVWAQSTAFQPKPEEITGIMKDFDEPGHL  
APTGMFVAGAKYMIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLEQGG

>A4KA39.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQAYVDEHLMCDIDGQGGQQLAASAIIVGHDGVSVAQSSSFPQLKPEEITGIMKDFDEPG  
HLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMV  
VERLGDYLLEQGL

>A4KA45.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQTYVDEHLMCDIDGQGGQQLAASAIIVGHDGVSVAQSSSFPQLKPEEITGIMKDFDEPG  
HLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMV  
VERLGDYLIDQGL

>A4KA43.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQAYVDEHLMCEIEGHHLSAAAILGHDGTVWAQSADFQPKPEEITGIMKDFDEPGHL  
APTGMFVAAAKYMIQGEPEGVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCDMVVG  
RLGDYLLEQGL

>A4KA44.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQAYVDEHLMCDIDGQGGQQLAASAIIVGHDGVSVAQSSSFPQLKPEEITGIMKDFDEPG  
HLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMV  
VERLGDYLVEQGL

>A4GFC0.1 Ole e 2; profilin [*Olea europaea*]  
MSWQTYVDEHLMCEIEGLHLASTAIIGHAGTVWAQSTAFQPKPEEITGIMKDFDEPGHL  
APTGMFVAGAKYMIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE  
RLGDYLLEQGL

>A4KA40.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQAYVDEHLMCDIDGQGGQQLAASAIIVGHDGVSVAQSSSFPQLKPEEITGIMKDFDEPG  
HLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMV  
VERLGDYLAEQGL

>A4KA41.1 Cor a 2; profilin [*Corylus avellana*]  
MSWQAYVDEHLMCEIDGHHLSSAAIIGHGHDGVSVAQSSSFPQPKPEEIAAIKDFDEPGSL  
APTGLHLGGIKYMIQGESGAVIRGKKGAGGITVKKTSQALIFGIYDEPLTPGQCNMIVE  
RLGDYLLKQGL

>A4K9Z8.1 Bet v 2; profilin [*Betula pendula*]  
MSWQTYVDEHLMCDIDGQGGQQLAASAIIVGHDGVSVAQSSSFPQPKPEEITGIMKDFEETPG  
HLAPTGLHLGGIKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMV  
VERLGDYLIDQGL

>BA050870.1 13S globulin [*Fagopyrum esculentum*]  
MLLGVLICIMVSLAASETRSRGSSTMRARQCRLDQLTSSQPNQKIQSEGGTIEVWDEEED  
QFQCAGVAAMRVTVQPDLSLPSYSSPRLVYVEQGEVFGLSLPGCPETYQSRGMMERG  
DEEEEGFESGRRMTDAHQPTRRVRKGDVVALPQGTVHWCNFNDGQEDLVVAVHNLNTDA  
NQLDQSLKTFFLAGGVQGGSKGKSQKLNFNILSAFETKLLAEALGTEETVRKMQESD  
ERGPIVKARKNMRQMVTPPRFGREQDEDETNGLEESFCNMRFRHNLGPRTEADIASRQAG  
RIHSVDQNKLPILFIDMSAEKGHLLPNAMLAPAWPLSGHRVYVLRGEAQMQIVDDNGQ  
TVLDDRVSEGSMMVPIQFYISTCRAGRDLGLEYVSFETTANPMSSPLNGHASVFKGMPIPV  
LSNSYQISPRAAAYELKQTRSHEHGLFSPFGGRS

>BA050872.1 13S globulin [*Fagopyrum esculentum*]

MLLGVLLCIMVSLAASETTRTRGSSTMRARQCRLDQLTSSQPQKIRSEGGTIEVWDEEED  
QFQCAGVAAMRVTVQPSLSLPSYYSSPRLVYVEQGEVFGLSLPGCPETYQSRGMEMRG  
DEEEEGFESGRRMTDAHQPTRRVRKGDVVALPQGTVHWC FNDGQEDLVVVAVHNLNTDA  
NQLDQSLKTFFLAGGVQGGSKGKSQKLNFNILSAFETKLLAEALGTEEEETVRKMQESD  
ERGPIVKARKNMQRMTVPPRFGRQDEDETNGLSEFCNMRFHNLGPRTEADIASRQAG  
RIHSVDQNKLPILFIDMSAEKGHLLPNAMLAPAWPLSGHRVFYVLRGEAQMQUIVDDNGQ  
TVLDDRVSSEGSMMVIPQFYISTCRAGRDGLEVVSFETTANPMSSPLNGHASVFKGMPIPV  
LSNSYQISPRAAAYELKQTRSHEHGLFSPFGGRS  
>AHL24658.1 Sal k 4; profilin [Salsola kali]  
MSWQAYVDDHLMCEIEGTNNHLTAAAILGVDGSVWAQSANFPQFKPDEISAVVKEFDEAG  
TLAPTGLHLGGTKYMIQSEAGQVIRGKKKGGPGICVKKTGQALIFGIYDEPVTGQCNCMI  
VERLGDYLVIEQGL  
>AHL24660.1 profilin [Fraxinus excelsior]  
MSWQAYVDDHLMCDIEGHEGHRLTAAAIIVGHGDSVWAQSATFPQFKPEEINGITDFNEP  
GHLAPTGLHLGGTKYMIQGEAGAVIRGKKKGGGITIKKTGQALVFGIYEPIPTGQCNCM  
VVERLGDYLVIEQGL  
>AHL24661.1 calcium-binding protein, polcalcin [Fraxinus excelsior]  
MADDPQEVQLERIFKRLDANGDGKISSSELGETLKTLSITPDEIQRMMAEIDTDGDGF  
ISYEEFTDFARANRGLVKDVAKIF  
>AHM25035.1 Api m 10; icarapin, partial [Apis mellifera]  
FPGAHDSDSKEERMPPAPNLQGVWKASRISTTRYRRTKEMY  
>AHM25036.1 Api m 10; icarapin, partial [Apis mellifera]  
FPGAHDSDSKERTLPLPPRSSMDTW  
>AHM25037.1 Api m 10; icarapin, partial [Apis mellifera]  
FPGAHDSDSKEERKNVDTW  
>AHM25038.1 Api m 10; icarapin, partial [Apis mellifera]  
FPGAHDSDSKVL  
>AHW81906.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus alba]  
MGVFTFDDEFPSTVAPARFFKAAVLDADNLFPKVAPQAAKSAETVEGNGGPGTVKKITLP  
DGKYVKQRLDSIDHDNFTYGHSHIEGDVLSADIEKISHVTKFVASSSSGSIKVTTFHT  
VGNAPVDEAKAKEGKEKAEGFLKLVEGYLEANPSAYN  
>AHY02994.1 Fus p 4; aldolase [Fusarium proliferatum]  
MSSSLEQLKATGTTVSDSGDFVVISGKYKPDATTNPSLILAASKKAEYAKLIDVAIDYA  
KQKGGSIDQVDDALDRLLVEFGKEILKIIPGKVSTEV DARYSFDTEASVNKALHLIELY  
GEQGISKDRILIKIAATWEGIKAAEILQRDHGINTNLTMFSLVQAIGAAEAGAYLISPF  
VGRILDWFKASTKKEYSKEEDPGVQSVKTIFFNYKKGYNITVMGASFRNTGEITELAGC  
DYLTISPNNLEDLLNSNEPVPKLLDASQAASLDIEKKSINDEALFRFDNFEDQMAVEKL  
REGISKFAADAVTLKSILKEKLA  
>AHY24177.1 Pro j 2; profilin, partial [Prosopis juliflora]  
MSWQTYVDDHLMCEIEGTNNHLSAAAILGVDGSVWAQSASFPQFKPDEISAVVKDFDGGP  
TLAPTGLHLGGTKYMIQGEQVIRGKKKGGPGICVKKTGQALIIGIYDEPVTGQCNCMI  
VERLGDYLVIEQGM  
>XP\_008286259.1 calcium-binding protein, parvalbumin [Stegastes partitus]  
KAFAIIDQDKSGFIEDELKLFQNFSAAGARA  
>2MC9\_A Cat r 1; cyclophilin/peptidyl-prolyl isomerase [Catharanthus roseus]  
GSFTGSMNPRVFFDMSVGGQPAGRIVMELFADTTPTAENFRALCTGEKGTGRSGKPLH  
YKDSSFHRVIPGFMCGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPNT  
NGSQFFICTAKTEWLDGKHVVFGQVVEGMDVVKAIKVGSSSGRTAKKVVVEDCGQLS  
>G5DC91.2 thaumatin-like [Manilkara zapota]  
ATFDVVNQCTFTVWAGASPGGGKQLDQGTWTITVAPGSTKARIWGRGTCNFDANGQGKC

QTGDCNGLLQCQGYGSPNNTLAEFSLNQPNNLDYVDISLVDGFNIPMDFSPAAAGVCKDI  
RCATDITAQCPAELQAPGGCNPCTVYKTNEYCCTNGQGTGPTALSKFFKDRCPDAYS  
PQDDPTSLFTCPAGTNYKVVFPCNLDA

>KEY78748.1 Asp f 7; unknown function [*Aspergillus fumigatus*]  
MAPIFKSLALVSALFAAIISSAAPVNLDKREVDVWTTVTTVVWTTIDVTTTTIYPTPQAPT  
PPVVESTPTPTPSAAPEQAETSTQPETTKSQPTQPSVATFIPVAAAAAADSAAVP  
EEPAPQPATTAAPSTSTTTQAAPSAPPAANSGSTEKAASSGYSGPCSKGSPCVGQLTYD  
TATSASAPSSCGLTNDGFSENVVALPVGIMTDADCCKTVTITYNGITKTATVVDKCMGCK  
PTDLDASRHLFGELADFSAGRIDGMSWYFN

>KEY81716.1 Asp f 4; unknown function [*Aspergillus fumigatus*]  
MQLKNSMLLLTALAAGSSVARLHGHERRHLHHAGEKREVGDTVYATINGVLVSWINEWSG  
EAKTSDAPVSQATPVSNAAAAAASTPEPSSSHSDSSSSSGVSADWTNTPAEGEYCTDG  
FGGRTEPSGSGIFYKGNVKGKPGWSNIIEVSPENAKKYKHVAQFVGSDDPWTVFWNKIG  
PDGGLTGWYGNALTLHLEAGETKYVAFDENSQGAWGAAGDELPKDQFGGYSCTWGEFD  
FDSKINHGWSGWDVSAIQAENAHHEVQGMKICNHAGELCSIISHGLSKVIDAYTADLAGV  
DGIGGKVVPGPTRLVVNLDYKE

>AIL01316.1 Sor h 1; beta-expansin [*Sorghum halepense*]  
MGVNMMSWSMQVALVVALAFLVGGAWCGPPKVPAGKNITATYGSWLEAKATWYGKPTGA  
GPDDNGGACGYKDVNKAPFNSMGACGNLPIFKDGLGCGSCFEIKCDKPAECSGEAVVHI  
TDMNYEQIAAYHFDLAGTAFGAMAKKGEELKRLKAGIIDMKFRRVKCKYGEKVTFHVEKG  
SNPNYLALLVKYVDGDDVVGVDIKEKGGDAYQPLKHSWGAIWRKDSDKPIKFPVTVQIT  
TEGGTKTAYEDVIPEGWKADTTYTAK

>AIL01317.1 Sor h 1; beta-expansin [*Sorghum halepense*]  
MGSLANKIVAMAALVLAALVTGGSCAPKKFPPGPNITTYNGQWLSARATWYGQPNGAGPD  
DNGGACGIKNVNLPPYNGFTACGNVPIFKDGGKCGSCYEVRCCKEMPECSGNPITVFITDM  
NYEPIAPYHFDGSGKAFGLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNP  
NYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKPVKGPFSIRLTSES  
GKKLVAPNVIPATWKPDTLYNSNIQF

>AIL01320.1 Sor h 13; polygalacturonase [*Sorghum halepense*]  
MALGSNAMRVFFLLAMVCAHAAGKAAPKEKEKGDGSGGAPAEAPSGSAGGSDISKL  
GAKGDGKTDSTKALNEAWAAACGKEGPQTLMIKGDYLTGPLNFSGPCKGSVTIQLDGNL  
LGTDLDSAYKTNWIEIEHVDNLVISGKGLDGGQKQVWDNNKCAQKYDCKILPNSLVLDY  
VNNGEVSGITLLNAKFFHMNVFQCKGVTIKDVTVTAPGDSPTDGIHIGDSSKVTITGTT  
IGVGDDCISIGPGSTGINVTGVTCPGPHGISVGS LGRYKDEKDVTDINVKDCTLKKTNSG  
VRIKSYEDAACVITASKLHYENIAMDDVANPIIIDMKYCPNKICTAKGDSKVTVKDVTFK  
NITGTSSTPEAVSLLCSDKIPCSGVTMDNIKVEYKGTNNKTMAVCQNAKGSATGCLKELACF

>AIL01321.1 Sor h 13; polygalacturonase [*Sorghum halepense*]  
MACTGNAMRAFFLLAFVCAAHAGKDAPAKDGA KAASGPGGSFDISKLGASGDGKKDSTK  
AVQEAWTSACGGTGKQITILIPKGDYLVGPLNFTGPCKGDVTIQVDGNLLATDLSQYKGN  
WIEILRVDNLVITGKGLDGGQPAVWSKNSCAKKYDCKILPNSLVLDYVNNGEVSGITLL  
NAKFFHMNVFQCKGVTIKDVTVTAPGDSPTDGIHIGDSSKVTITGTTIGVGDDCISIGP  
GSTGINVTGVTCPGPHGISVGS LGRYKDEKDVTDINVKDCTLKKTNSGVRIKSYEDAACV  
ITASKLHYENIAMDDVANPIIIDMKYCPNKICTAKGDSKVTVKDVTFKNITGTSSTPEAV  
SLLCSDKIPCSGVTMDNIKVEYKGTNNKTMAVCQNAKGSATGCLKELACF

>AI008848.1 Der f 28; heat shock protein 70 [*Dermatophagoides farinae*]  
MPSKTLKAPAIIGIDLTTYSCVGVFQNGSVEIANDQGNRTTPSYVAFNDTERLIGDAAK  
NQVSMNPTNTIFDAKRLIGRRFDESSVKSDMKHWPFKVSVSESGPKLEVEFKGERKRFWP  
EEISAMVLTKMKETAAYLGQKVTDVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEP  
TAAAIAYGLDKKGGGEKNVLI FDLGGGTFDVSVLTIDNGIFEVKSTAGDTHLGGEDFDNR

LVNHVFQEFKRKFGKDIMS NKRALRRLRTSCERAKRTLSSSTQTSIEIDSLHEGIDFYST  
ITRARFEELCSDLFRSTLEPVEKALRDAKLDKSKIDEIVLVGGSTRIPKIQKLLSDFFN  
KELNKSINPDEAVAYGA AVQAAILTGDNSNMVKDLLLLDVAPLSLGIETAGGVM TTIKR  
NTTIPTKQTQFTTYADNP AVTIQVYEGERAMTKDNRLGTFDLTGIPPAPRGV PQIEV  
TFD VDANGILNVS AVDKSTGRQNKITITNDKGRLSKADIEK MVQEA EQYREDDERQRERI  
AAKNQLEAYAFQLKSTMEEEAVKSKLSEEDRKT VLNKVD ETLRWLDSNQLADKEEF EHRQ  
KEIENACRPIMMKIYQQQQQHHPGANGSCGSNAYPGYNGFKSNNDGPVVEEVN

>AI008850.1 Der f 20; arginine kinase [Dermatophagoides farinae]  
MVDQAVIDKLEAGFQKLQSSAECHSLLKKYLTRNVLDACKGRKTGMGATLVDVVQSGFEN  
LDSGVGLYAPDAESYTLFKELFDPVIEDYHKGFKPTDKHPQTD FGDVNTLCNVDPNNEFV  
ISTRVRCGRSLQGYFPNCLTEAQYKEMEEKVKGQLNSFEGELKGTYYPLLGMKATQQQ  
LIDDHFLFKEGDRFLQAANACRFWPVCGGIFHNDNKTFLIWVNEEDHLRIISMQKGGDLK  
QVFSRLINGVNHIEKKLPFSRDDRLGFLTFCPTNLGTTIRASVHIKLPKLAADRKKLEEV  
AGKYNLQVRGTAGEHTESVGGVYDISNKRRMGLTEYQAVKEMQDGILELIKIEKSM

>AI008851.1 Der f 27; serpin [Dermatophagoides farinae]  
MKFFLLSFVLMIVAATATYAAHVGSGRDNMNNKPVPAEGFAKASNEFGFHLLKEVIQHR  
SSSGSRGSSENVLFSPYSVAVALSMVHQGTQGSTAEQFKRVLYYDRVQQLNGGEYQTVAN  
SVKQIQNQIKQSDQSNQFDWGNMLMVDQQIPVKDQYKKIIEQYDQVMSVDFR KESKNV  
MERINQFVSNKTHGLIDRMLEQPPSADTGLALINAVYFKGEWLKPFDSMRTEQSVFYGHH  
GQYKQVQYINGQGPYGYVEVPQWNSDLIQLPYKGEDIAFYGVLP RERNYDLDKIRQSIN  
STFVDEIVGQITGGQSSTVYFPKIELSTSYQLPEILKSMGLQDVFTEADLSGITDKKPM  
KIDDAIHKAKLILNEQGTEAGAGTYIQMAVLSALETSHTFRFDHPFMYFIRHLPTGQILF  
LGEIHF

>AI008853.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides  
farinae]  
MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEKSETIDPMKVPDHTDKFER  
HVGILDFK GELAMRNI EARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY  
KLGDLHPNTHVISDIQDFVVALSLEISDEGNITM TSFEVRQFANVVNHIGGLSILDPIFG  
VLSDVLT AIFQDTVRKEMTKVLAPAFKRELEKN

>AI008860.1 Der f 25; triosephosphate isomerase [Dermatophagoides farinae]  
MVRKFFVGGNWKMNRSRATNEDLIKTL SNGPLDPNTD VVVGVPSIYMAEVRQKLPKTIGV  
AAQNCYKVPKGAFTGEISPAMIKDVGAEWVILGHSERRNVFGESDQLIGEKVEHALQEGL  
HVIACIGELLEEREAGKTTEVVRQQTQVISKHV KDWSKVVLAYEPVWAIGTGKTASPQQA  
QEVHQKL RQWFSENVSPQIAETIRIYGGSVTANNAKELASQADVDGFLVGGASLKPEFV  
QIVNARQ

>AI008864.1 Der f 11; paramyosin [Dermatophagoides farinae]  
MSARTAKYMYRSSGAGASGDISVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK  
AELQIQVMSLGERLEEAEGSSESVTEMNKKR DSELAKLRKLL EDVHIESEETAHHLRQKH  
QAAIQEMQDQLDQLQKAKNKS DKEKQKQFAEVFELLAQLETANKEKL TALKNVEKLEYTV  
HELNIKIEEINRTVIELTSHKQRLSQENTELIKEVHEVKLQLDNANHLKTQIAQQLEDTR  
HRLEEEERKRASLENHAHTLEVELES LKVQLDEESEARLELERQLTKANGDAASWKS KYE  
AELQAHADVEVEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAT  
AHAQQL EK RVAQLEKINLDLKNKLEEV TMLMEQAQKELRVKIAELQK LQHEYEKLRDQRD  
QLARENKKL TDDLAEAKSQLNDAHRR IHEQEIEIKRLENERDEL SAAYKEAETLRKQEEA  
KNQRLIAELAQRH DY EKRLAQKDEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLK  
KKYQAQITELESLDAANKANIDLQKTIKKQALQITAE LQAHYDEVHRQLQQAVDQLGVT  
QRRCALQAELEEMRIALEQANRAKRAEQLHEEAVVRVNELTTINVN LASAKS KLESEF  
SALQADYDEVHKELRISDERVQKLTIELKSTKDLLIEEQERLVKLETVKKSLQEVRTLH  
VRIEEVEANALAGGKRVI AKLESRIRDVEIEVEEERRRHAETDKMLRKKDHRVKELLLQN  
EEDHKIQILLQEMTDKLNKVKVYKQRMQEQEGMSQQNL TRVRRFQRELEAAEDRADQAE

SNLSFIRAKHRSWVTTTSQVPGGTRQVFTTQEETNY  
>AI008866.1 profilin [Dermatophagoides farinae]  
MSWQSYVDNQICQHV DCTLAAIANIQDGSVWAKFEKDDKINPKELKTIADTIRQNPSGF  
LETGIHIGGEKYICIQADNQLVRGRRGSSALCIVATNTCLLAAATVDGFPFGQLNNVIEK  
LGDYLRSNYY  
>AIS82657.1 Rhi o 1; aspartyl endopeptidase [Rhizopus oryzae]  
MKFFALSLVVSAAFSVFTDAAITKIPIKKVHETATEKLSRYSHTGEYLTQKYFNSQRNNQ  
PMETFKLNPDGGSANHGVP LSNYLNAQYYGEIEIGTPPQPFTVVFDTGSSNLWVPSHCTS  
IACFLHKRYDSASSRTYSENGTEFAIQYGTGSLEGFISQDTLSVGGIQVEDQGFAESTKE  
PGLTFFAKFDGIFGLGYDTISVKHTIPPFYHVMNRDLVDEPLFSFWLNDANKDQDNGGE  
LIFGGVDEDFEGDIHWSVRRKGYWEITMENIKFGDDYVDIDPVGAAIDTGSSLLVAPT  
TVAALINKELGAEKNWAGQYVVD CNKVPSPLEFCFVFNGKDFCLEGKDYVLEVQGCISG  
FMGMDIPEPAGPLWIVGDVFLRKFYSVYDLGNNRVGLAPSK  
>2MFK\_A Blo t 12; chitin-binding protein, partial [Blomia tropicalis]  
GPLGSDLIVHEGGKTYHVVCHEEGPIPHPGNVHKYIICS KSGSLWYITVMPCSIGTKFDP  
ISRNCVLDN  
>AJE61290.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus  
persica]  
MGVFTYSDESTSVIPPPRLFKALVLEADTLIPKIA PQSVKSAEIVEGDGGVGTIKKISFG  
EGSHYSYVKHRIDGLDKDNFVYNYTLVEGDALSDKVEKITYEIKLVASADGGSIKSTSN  
YHTKGDVEIKEEDVKAGKEKATGLFKLIENYLVANPDAYN  
>AJE61291.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus  
persica]  
MGVFTYETEFTSVIPPEKLFKAFILDADNLIPKIAPTAVKDTEILEGDGGVGTIKKVTFG  
EGSQYGYVKHRIDGIDKDNLTYSYTLIEGDALSDVIEKIVYDIKLVASPNNGGSIVKTISH  
YHTKGDVEIKEEQVKAGKEKAAGL FKLVEGYLLANPDAYN  
>CEJ95862.1 2S albumin, conglutin, partial [Pinus pinea]  
CRDYLQRRREQPSERRCEELERMSPQCRCAIQQLDQSQSYDSITDDL FMDSEAAPNQR  
RRRRESRGREEEEEAEERAAALPETCNVRQPPRRCDVQRRSRYFTSGTDF  
>AJ053282.1 chymotrypsin, serine protease [Blattella germanica]  
MQYCAVLFFAAAVACAYGAELAALDPSTRVVGGTNAATGEFPFIVSLRSTSN SHFCGGSI  
ISNYVITAACHCVSGSSASSVVVAGTNTLNSGGTSYRVSRIVVHSGYNSNTIVNDIALL  
RLSSAISYNSYVQPIALPAQGETSGAGVA AVASGWGYTSYPGWSLPNNLQKVLSVISNT  
QCSSYMNNIYSSSICASGGNGKVCNGDSGGPLTAGGKLIGLVSWGRPCAVGYPDVYTRV  
SSYVSWINQNAV  
>AKH04310.1 Per a 11; alpha-amylase [Periplaneta americana]  
MKLFALLALVLLAGVQSQKDPKLVPESTLLRLFEWKFD DIADECERFLAPKGYAGVQV  
SPVHKNL LYTATAPGLWERYQPMSYKLVSRSGDETAFRDMVRRNAVGVRIYVDVVLNHM  
SGNWDNAVGTGGSTADTYNYSYPGPYDHSDFHPYCILNDYQDPEIVRNCELVGLHDL DQ  
SQDYVREKLIDFLNHLVDAGVAGFRVDAAKHMWPADLEYIYGKVNRRNSDAGYCGDSSPS  
RYQEVIDLGG EAVSKFEYNGFGRVTEFKHSEQIGYAFRGNRLEWYTYKPNWGLLPSGD  
ALVFVDNHDNQRGGGNAILTYKTPKNYKMAIAFILAHPYGYPRVMSSFDFAHDQGPPQD  
SDKNILSP SINADGTCGNGWVCEHRWRQHANMVGF RNAVRGTEITNWWDNGNHQIGFCRG  
DRGFVAFNVEDNDLKQTLQ TCLPAGTYCDVISGSKNNRAHLGAELV VAPNGEAFSVRLIS  
DDDGVLAIHLEEKL  
>AKH04311.1 Per a 12; chitinase [Periplaneta americana]  
MKLTSLVAVGVGVFLAAALQTCKGFIRDFKTHRQLQEKGDDRAVFCY YGSWATYRWGIAT  
FEVDNIDTRLCTHIVYAFTGLRDGVIVSLDEYNDY EENWGKGLMKKFTTLAKNNGIKALV  
GLGGWNEGSVKYSEMAATQAGRETFADSAVAFLQKQGF DGLDL DWEYPARRGGVPEDKDN  
FTLLLKTLSEK LHARGLILTVAVSADPKTAANAYDFPNVAKYADYITLMSFDYHTPSSDT

VTGLNSPLDSLQDGTGYNKKNVYKSVNQWLKGGVPPNKLVLGVPLYGRTRYRLADPDQHG  
LGAPILGPGTAGLYTQEAGFLAYYEICSNPDWNVWVWVNDTSSYLAYKDYQWLSYDDPNTI  
TIKAQWVLEKNLGGVMVWSLESDDFHGNCGKAYPLLAVNKALGRL  
>AKJ77985.1 Tri a 45; elongation factor [*Triticum aestivum*]  
MGKRKAAAKPPPRKGMKLDLTVFSCPFCNHGSSVECRIDLKNLIGEANCQICQESFSTTA  
NALTEAIDVYSEWIDECERVNTVEGDDGA  
>AKJ77986.1 Tri a 42; unknown function [*Triticum aestivum*]  
EFTNTCMECLVCDVHVACGDFASNDVIDPAKFRRLGINDCLVNDGKSIEPSFPVVSFQYGN  
SFPYPMTVASASDCDN  
>AKJ77987.1 Tri a 43; unknown function [*Triticum aestivum*]  
MTLVASSSLDPVWVEVLGDPLLRLLRFIFCRATLSLFKASNDKAECLPSCVPPLPESV  
GGESMLSQCCVMRVASFLGAADQFSFAEVTTWPDIDEPTSSGGVDKEL  
>AKJ77988.1 Tri a 41; mitochondrial ubiquitin ligase activator of NFKB 1 [*Triticum  
aestivum*]  
EMGDGQLCVICLRKRRRAAFVPCGHLVCCCNCAKRVELMDEPLCPVCRQDIQYMLRVYDS  
>AKJ77990.1 Tri a 44; endosperm transfer cell specific PR60 [*Triticum aestivum*]  
MAKLMCLCFIILTIADVVSADCEGDRQEMIKQCAKYQWPANPKVNPSPDACCVAWQKAN  
IPCLCAGVTKEKEKIWCMEKVAYVANFCKKPFPHGYKCGSYTFPPLA  
>4X9U\_A Act d 5; kiwellin, partial [*Actinidia deliciosa*]  
ISSCNGPCRDLNDCDQGLICIKGKCNDPQVGTHTICRGTTSXQPGGCKPSGTLTCRGKS  
HPTYDCSPVTSSTPAKLTNDFSEGGDDGGPSECDESYHNNNERIVALSTGWYNGGSRC  
GKMIRITASNGKSVSAKVVDECDSRHGCDKEHAGQPPCRNNIVDGSNAVWSALGLDKNVG  
VVDITWSMA  
>AKV72168.1 Ama r 1; Ole e 1-like [*Amaranthus retroflexus*]  
MAKQAVFLLVGCALCVLSLDDVAKAPVSQFHIQGLVYCDTCRIQFMTRISTIMEGATVKL  
ECRNITAGTQTFKAEAVTDKVGQYSIPVNGDFEDDICEIELVKSPNSECSEVSHDVYAKQ  
SAKVSLSNNGEASDIRSANALGFMRKEPLEECPEVLKELDLYDVKAN  
>AKV72169.1 Koc s 1; Ole e 1-like [*Bassia scoparia*]  
MAKQAVFLLVGCALCVLSLDDVAKAPVSQFHIQGLVYCDTCPYPSSYVLPMLLEGATVKLE  
CRNITAGTQTFKAEAVTDKVGQYSIPVDGDFEDDICEIELLKSPDNQCSEVSHDVYAKQS  
AKVSLTSNNGEASDVRSANALGFMRKEPLEECPEVLKELDLYDVKAN  
>XP\_013623213.1 lipid transfer protein [*Brassica oleracea*]  
MASALSFFTCLVLTVCIVASVDAAISCGVTSTNLAPCAVYLMKGGPVPAPCCAGVSKLNS  
MAKTTDPDRQQACKCLKTAAKNVNPSLASSLPKCGVSIPYPISMSTNCDTVK  
>ALA65345.1 Der p 24; ubiquinol-cytochrome c reductase binding protein  
[*Dermatophagoides pteronyssinus*]  
MVHLTKTLRFINNPGRKFFYYGLQGYNKYGLYYDDFYDYDPAHLEAVRRLPPDLYDQHT  
YRVIRASQLEITKQFLPKEQWPSYEEDMDKGRFLTPYLDEVMKEKKEKEEWVNFSLKD  
>ALF39466.1 Pla a 3; lipid transfer protein [*Platanus acerifolia*]  
AAITCGQVSKLTNCLSYLRSGGTVSTACCNGVTSLNKMANSTSDRQAACNCLKSAYKSI  
SGIKLQYSQSLAGKCGVNLPHYKISPDIIDCSKVK  
>XP\_005902099.2 Bos d 11; beta-casein [*Bos taurus*]  
MPLNTIYKQPQNQIIHSAPPSLLVLYFGKELRAMKVLILACLVALALARELEELNVP  
EIVESLSSESSEITRINKKIEKFQSEEQQTEDELQDKIHPFAQTQSLVYPPFGPIPNSL  
PQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFKYPVEPFTEQSLSLTLTDV  
ENLHLPLPLLQSWMHQPHQPLPPTVMFPQSVLSLSQSKVLPVPQKAVPYPQRDMPIQAF  
LLYQEPVLPVVRGPFPIIV  
>BAT62430.1 Ani s 14; unknown function [*Anisakis simplex*]  
MQVKCIAKYGEQFCSSMLSVCSMLSIPWKNDSVQRLPPGIVGCAQTTPVQVQCRAYSE  
SFCNRLGAACSKVTGTDIPAFSRGGGEYRLPEAISQCIAQENIVAMCYASKCSQQCDGWR

VTCNINGGMAQLTPEQVTCFEKQSGLVALKTSCRTNPLNAQCRQIREPFETPKCTTAIPY  
LKISQTVINGQIHVQQLVSGGMTGVQVSKTVETVIKT

>F5B8V9.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MAKMRVRLPMLILLLGVVFLLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQEE  
QEREHRREEKHGEPSSRGRSQSEESQEEHERRREHREEREQQPRPQRRQEEEEEEEE  
WQPRRQRPQSRREEREEREQEQGSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDSR  
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNRQRTNRLNLQNYRIIEFQSKPNTLILPKH  
SDADFILVVLNGRATITIVNPKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA  
IPINNPGLKYDFYPSSTTKDQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENKQR  
RGQEQSHQDEGVIVRVSKEQIQELRKHAQSSSGEGKPSSESGPFNLSNKPIYSNKFNGFY  
EITPDINPQFQDLNISLTFTEINEGALLLPHYNSKAIFVWVDEGEGNYELVGIRDQQRQ  
QDEQEEYEQGEVRRYSKLSKGDVFIIPAGHPLSINASSNLRLLLGFGINANENQRNF  
LAGSEDNVIKQLDREVKELTFPGSIEDVERLIKNQQQSYFANAQPQQQQQREKEGRRGR  
GPISSILNALY

>F5B8W0.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MANMRVKFPTLVLLLGVVFLMAVSIGIAYGEKNAIKNHERPQEREQEERDPRQQPRPHQ  
EEQEREHGREERNREPSRGRSESEESREEEREQRREPSRGREEQQPQHGRREEEEWQ  
PRRQRPQSRREEREQEQGSSSSSGRQSGYERREEREEREQQEQDSRSESRRQRNPYYFS  
YERFQTLYKNRNGQIRVLERFDQRTNRLNLQNYRIVEFQSKPNTLILPKHSDADYILVV  
LNGRATITIVNPKRQAYNLEHGDALRLPAGTTSYILNPDDNQNLRVVLAIPINNPNGF  
YDFYPSSTTKDQSYFNGFSRNTLEATFNTRYEEIQRIILGNEDEQDEEQSRGQEQSHQD  
QGVIVRVSKEQIQELRKHAQSSSGKPKPSSESGPFNLSDEPIYSNKFNGFYEITPDRNPQ  
AQDLDISLTFIEINEGGLLLPHYNSKAIFVWVDEGEGNYELVGIRDQERQQDEQEEV  
RRYNAKLSEGDIFVIPAGHPISINASSNLRLLLGFGINADENQRNFLAGSEDNVIRQLDKE  
VKQLTFPGSVEDVERLIKNQQQSYFANAQPQQQQQREKEGRRGRRGLSFPFRSLFTKLLS  
TIM

>F5B8W1.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MAKMRVRFPTLVLLLGVVFLMAVSIGIAYGEKNVKNHERPQEREQEERDPRQQPRPHQ  
EEQEREHRRESEESQEEEREQRREPRREREQEQQPQHGRREEEEWQPRRQRPQSRREER  
EQEQGSSSSSRQSGYERREEREEREQEQEQGSRSDSRQRNPYYFSSERFQTLYRNRNG  
QIRVLERFDQRTNRLNLQNYRIVEFQSKPNTLILPKHSDADYILVVLNGSATITIVNPD  
KRQSYNLENGDALRLPAGTTSYILNPDDNQNLRVVLAIPINNPNGFYDFYPSSSKDQQS  
YFSGFSKNTLEATFNTRYEEIQSILLGNEDEQEDDEQWHGQEQSHQDEGVIVRVSKEQVQ  
ELRKYAQSSSRKGPYSESGPFNLSNKPIYSNKFNGFYEITPDRNPQAQDLDISLTFIEI  
NEGALLLPHYNSKAIFVWVDEGEGNYELVGIRDQQRQQDEQEVRRYSARLSEGDIFVIP  
AGHPISINASSNLRLLLGFGINADENQRNFLAGSEDNVIRQLDREVKGLIFPGSAEDVERL  
IKNQQQSYFANAQPQQQQQREEREGRHGRGHISILSTLY

>F5B8W2.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MIKMRVRFPTLVLLLGVVFLMAVSIGIAYGEKNVKNHERPQEREQEERDPRQQPRPHQ  
EEQEREHRREEERDREPSRGRSESEESREEEREQRREPRREREQEQQPQHGRREEEEWQ  
PRRQRPQSRREEREQEQGSSSSSRQSGYERREEREQEQEQGSRSDSRQRNPYYFSSER  
FQTLYRNRNGQIRVLERFDQRTDRLNLQNYRIVEFQSKPNTLILPKHSDADYILVVLNG  
SATITIVNPKRQSYNLENGDALRLPAGTTSYILNPDDNQNLRVVLAIPINNPNGFYDF  
YPSSSKDQQSYFSGFSRNTLEATFNTRYEEIQRIILGNEDEQEDDEQRHGQEQSHQDEGV  
IVRVSKEQVQELRKYAQSSSRKGPYSESGPFNLSNKPIYSNKFNGFYEITPNRNPQAQD  
LDISLTFIEINEGALLLPHYNSKAIFVVLVDEGEGNYELVGIRDQQRQQDEQEVRRYSAR  
LSEGDIFVIPAGHPISINASSNLRLLLGFGINADENQRNFLAGSEDNVIRQLDTEVKGLTF  
PGSTEDVERLIKNQQQSYFANAQPQQQQQREEREGRHGRGHISILSTLY

>F5B8W3.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]  
MAKMRVRFPLVLLLGVVFLLAVSIGIAYGEKDVKNPERPEERQEERDPRQQPRSRQQ

EEQEREHRREKERDREPSRGRSESKQSQEEERERRKEHDREREQEQQPQYGRRHHEEEK  
EEEEEGQARRQRPQRREEREQEQQSSSESRRQSGDERRHRHEKREQREEREQEQQSSSG  
RQSDYGRQRHEGREQREEREQEQQSSSESHRLRNPYYFSSERFQTRYKNKNGQIRVL  
FDQRTNRLLENLQNYRIVEFQSRPNTLILPKHSDADYILVVLNGRATITIVNPKRQAYNL  
EYGDALRLPAGTTSYILNPDNDQDLRVVLAIPINNPGKFYDFYPSRTKDQQSYFSGFSK  
NTLEATFNTHYEEIQRILLGYEDEQEDEEQRREQEQSHQDEGVIVRVSKEQIQELRKHAQ  
SSSRKKGKPSSESGPFNLRNSNEPIYSNKFNGFYEITPDRNPQVQDLDISLIFTEISEGALL  
PHYNSKAI FVIVVDEGEGNYELVGIRNQQRQQDEQEVEEVRSYNARLSEGDILVIPAGHP  
LSINASSNLRLLGFGINADENQRNFLAGSEDNIRQLDREVKELIFPGSAEDVERLIRNQ  
QQSYFANAQPQQQQQREKEGRRRGRPISSILSALY

>F5B8W5.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [*Lupinus angustifolius*]

MARMRVRFPTLVLLLGLFLMAVSI GIAYGEKDV IKNHERPGEREHEERDPRQQPRPRKQ  
EEQEREHRREEEHDRDPSRGRRESEERQEERERRRREPCREEREQEQQPQHGRREEEEE  
EWQPRRLRPQSRKEEREQEQQSSSSSRKQSGYERRQYHERREQRDEKEKEQDSRSDSRRQ  
RNPYHFSSERFQTRYRNRNGQIRVLERFDQRTNRLLENLQNYRIVEFQSNPNTLILPKHSD  
ADYILVVLNGRATITIVNPKRQAYNLEYGDALRVPA GTTSYILNPDNDQNLRVVLAIP  
INNPSNFYDFYPSSTKDQQSYFSGFSKNTLEATFNTRYEEIQRILLGNEDEQEDEEQRG  
QEQSYQDEGVIVRVSKEQIQELRKHAQSSSRKKGKPSSESGPFNLRNSNEIYSNKFNGFYE  
TPERNPQVQDLDISLTFTEINEGALLPHYNSKAI FVIVVDEGEGNYELVGIRDQQRQQD  
EQEEEEEEVRRYSARLSEGDIFVIPAGYPISVNASSNLRLLGFGINANENQRNFLAGSED  
NVISQLDREVKELTFPGSAQDVERLIKNOQQSYFANAQPQQKQREKEGRRRGRSLISSI  
LSTLY

>B3EWP3.1 Ara h 12; defensin [*Arachis hypogaea*]

KTVAGFCIFFLVFLAQEGVVKTEAKLCNHLADTYRGP CFTNASCDHCKNKEHFVSGTC  
MKMACWCAHNC

>B3EWP4.1 Ara h 13; defensin [*Arachis hypogaea*]

VQKRTIIMEKKMAGFCIFFLILFLAQEYGVGKECLNLSDKFKGPCLGSKNCDHHC RDIE  
HLLSGVCRDDFRCWCNRKC

>C0HJZ1.1 Ara h 13; defensin [*Arachis hypogaea*]

MEKKMAGFCIFFLVFLAQEYGVGKVCNLSDKFKGPCLGTKNCDHHC RDIEHLLSGVC  
RDDFRCWCNRNC

>ACX47057.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [*Fragaria x ananassa*]

MGVFTYETEFTSVIPPPRLFKA FILDADNLI PKIAPQAVKCAEIIEGDGGVGTIKKITFG  
EGSQFGSVTHKIDGIDKENFVYSYSLIEGDALSDKIEKISYETKLVSSSDGGSIIKSTSN  
YHTKGDVEIKEEHVKAGKEKASHL FKLVEGYLLANPNEYC

>ACX47058.1 pathogenesis related protein, PR-10, Bet v 1-like [*Fragaria x ananassa*]

MGVFTYSEFTSVIPPPKLFKA FVLDADNLI PKIAPQAVKSAEIIEGDGGVGTIKKIHLG  
EGSEYSYVKKHIDGIDKDNFVYSYIIEGDAIGDKIEKISYEIKLVASGGGSIKSTSHY  
HTKGEVEIKEEHVKAGKERAAGL FKIIEHLLAHPEEYN

>AHA56102.1 Amb a 11; cysteine protease [*Ambrosia artemisiifolia*]

MEINKLVCF SFLV LILGLVESFHYHERELESEEGFMGYDRWREQHNIEMRSPERFNVF  
KYNVRRIHESNKMDKPYKLVNEFADMTNLEFVNTYANSKISHFQALRGSAPGSIDTDPN  
KDFIYANVTKIPDKVDWREKNAVTDVKGGCGSCWAF AAVVALEGINAIRTGKLVKFSE  
QQLVDCDMT NAGCDGGLMEPAFTYVIKHGGIAPEASYPYVGKRETCDAKIKDVLKIDGR  
QNVPLDEEALRKAVAHQPVATGIQLSGHGLQFYSEG VYTGDCGTEPNHGVGIVGYGENE  
KGIKFWTVKNSWGPTWGEKGYIHLQRGARKEGLCGVAMHSSFPIMNDPNPPKDDPNGP KD  
DPDAPKDPKFKTTQRLQGIRTKLLEL

>5X7Y\_A Can f 6; lipocalin [*Canis familiaris*]

GSHEEENDVVKGNFDISKISGDWYSILLASDIKEKIEENGSMRVFVKDIEVLSNSSLIFT

MHTKVNGKCTKISLICNTEKDGEDVVDHGYNLFRIIETAYEDYIIFHLNNVNQEQEFQ  
LMELYGRKPDVSPKVKKEKFRVRYCQGMEIPKENILDLTQVDRCLQARQSEAAQVSSAE

>AAV83993.1 arginine kinase [*Penaeus chinensis*]  
MADA AVIEKLEAGFKKLEAATDCKSLLKKYLTKAVFDQLKDKKTSLGATLLDVIQSGVEN  
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFKQTDKHPNKDFGDVTSFVNVDPEGKYV  
ISTRVRCGRSMEGYPFNPCLTEDQYKEMESKVSSTLSSLEGELKGTYYPLTGMGKEVQQK  
LIDHFLFKEGDRFLQAANACRYWPSGRGIYHNDNKTFVWVNEEDHLRIISMQMGDLG  
QVFRRLTSAVNEIEKRIPFSSHDRGLGFLTFCPTNLGTTVRASVHIKLPKLAANRDKLEEV  
AGKYNLQVRGTRGEHTEAEGGIYDISNKRMRGLTEFQAVKEMQDGIKELIKMEKEM

>COMPARE001 Bla g 9; arginine kinase [*Blattella germanica*]  
VDAAVLEKLEAGFAKLAASDSKSLKKYLTKEVFDNLKTKKTPFGSTLLDVIQSGLENH  
DSGVGIYAPDAEAYTVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYII  
STRVRCGRSMQGYFPNPCLTEAQYKEMEDKVSSTLSGLEGELKGFYPLTGMTKEVQQKL  
IDHFLFKEGDRFLQHANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGDLGQ  
VYRRLVTAVNDIEKRVFSSHDRGLGFLTFCPTNLGTTVRASVHIKVPKLAADKKKLEEVA  
GKYNLQVRGTRGEHTEAEGGVYDISNKRMRGLTEYDAVKEMNDGIAELIKIESSL

>ABV55108.1 catalase [*Musa acuminata*]  
MDPYKFRPSSSFDNFTTTNAGAPVWDDQALTVGSRGPILLEDYHLVEKIAHFARERIP  
ERVVHARGASAKGFFECTHDVTHLTCADFLRAPGVQTPPIILRFSTVIHERGSPETIRDPR  
GFAVKFYTREGNWDLLGNNFPVFFIRDGIKFPDVIHAFKPNPKSHVQEYWRVDFLSHHP  
ESLHTFFFLLFDDVGVPSDYRHMEGFGVNTYTFVSKGKVNYYVFKHWKPTCGVKCLLEDEA  
IVVGGKNHSHATQDLYDSIAAGNYPEWKL FVQVMDPDTEDRYDFDPLDDTKTWPEDLLPL  
QPVGRLVLRNIDNFFSENEQLAFGPGLVVPGIYYSDDKMLQCRVFAYGDTQRYRLGPNY  
LTLPVNAPKCAHHNNHYDGLMNMVHRDEEVDYFPSRHASLRHAERFPINRVVTGKREKN  
VIPKQNDFKQPGERYRSWAPDRQERFVRRWAEQLAHPKVSVELRSIWISFLSKCDTSLGQ  
KVANRLNMRANI

>ACV85695.1 Cari p 1; polygalacturonase [*Carica papaya*]  
MAVLYYDNYNRTHLLILSFSILFFSFSSRLVNSGFHGERRRERVHGYYHDELNNFSEDQE  
GGTLTLLSGAGYDPEAHSFLSSINGDRDEEFTEAEPVLSFKGIEDLRSAPRSVIFNVD  
DFGAEGDGIHDDTQQVFEEAWEKACSYKGPALFLVPERRTYLIGPIRFLGPCKSNLVIQV  
QISGTLASDNRSYRKDPRHWIVIDSVDNLLVEGGGTIHGNGQIWRNSCKAPCKEAPT  
VTFYKCKNLMVRNVKQDAQQMQVSFEKCEVTASDLTVTAPEKSPNTDGIHVTNTQNIL  
ITNTFIGGDDCISIESGSHNVQIEELTCGPGHGINVDSLGDNNSKAFVSFVTVNGAKLSG  
TTNGVRIKTYQGGSGSASNIKFNQVDMENVKNPIIIDQNYCDQKPKCKQKSAVQVKDV  
LYQNIQGNSASDVAIDFDCSENYPCLVKLVQNVRLQRADRVDEEAKAICNHVELTETGVV  
FPRCPDYHLKHDEL

>AHY24648.2 Can f 4; lipocalin [*Canis familiaris*]  
MKILLLCLALVLASDAQPLPNVLTQVSGPWKTLVSSNMLDKIGENGFRIYLRGINVD  
IPRLKMLFNFYVKVDGECVENS VGASIGRDNLIKGEYNGGNYFRIIDMTPNALIGYDVNV  
DSKGITKVALLMGRGAHVNEEDIAKFKKLSREKGIPEENIYLGDTDNCPNHE

>COMPARE013 Der f 31; cofilin [*Dermatophagoides farinae*]  
MASGVIVATEAKTLYEVEVKDKKYRYIYHIKDERVIEVETTGPRDATYSDFVARLQDYK  
NECRYCVDFPANIPVEGGGEKSNMSVDRLVMTWCPESAKIKQKMLYSSSYDALKKALV  
GVYRYVQACDYEEASEEAI AEA FRKGG

>AIV43661.1 Koc s 2; profilin [*Bassia scoparia*]  
MSWQTYVDDHLMCDIEGTTNHLTGAAILGVDGVSVAQSANFPQFKPDEIAAIVKEFDEPG  
TLAPTGLHLGGTKYMIQGEAGQVIRGKKGPGGICVKKTGQALIFGIYDEPVTGQCENMI  
VERLGDYLVEQGM

>AIV43662.1 Aca f 2; profilin [*Acacia farnesiana* (*Vachellia farnesiana*)]  
MCWQTYVDDHLMCEIEGTNNHLSGAAILGVDGVSVAQSAFQFKPDEIAAVVKDFDGP

TLAPTGLHLGGTKYMVIQGEPRFIRGKKGGGICVKKTGQALVFGIYDEPVTGQCENMI  
VERLGDYLVEQGM  
>COMPARE009 Der p 23; peritrophin [Dermatophagoides pteronyssinus]  
MKFNIIIVFISLAILVHSSYAANDNDDPTTTVHPTTTEQPDDKFECPSRFGYFADPKDP  
HKRYICSNWEAVHKDCPGNTRWNEDEETCT  
>ANW82807.1 Poly p 5; unknown function, antigen 5 [Polybia paulista]  
NKYCNICKSKVAHTVCQYGESTKPSSKCNKVSITSVGVTEEEKKLIVDEHNRFQKVAQG  
LETRGNPGPQPAASDMNLLVWNEDELAYIAQVWASQCQFFVHDKCRNTAQYQVGQNIAYSA  
STAAYPGIVSLIVLWENEVKDFNYSQGITKENFSKVGHYTQVWAKTKEVCGSIIKYIEK  
GMKSHYLVLCNYGPAGNYMGQPIYTKK  
>AAP35068.1 Der f 5; unknown function [Dermatophagoides farinae]  
MKFIIAIAVCTLAVVCVSGEPKKHDYQNEFDLLMQRIHQMRKGEEALLHLHQINTFEE  
NPTKEMKEQILASEMDTIIALIDGVRGVLNRLMKRTDLDFERYNVEIALKSNEILERDL  
KKEEQRVKKIEV  
>AAX34057.1 unknown function [Tyrophagus putrescentiae]  
MKFAILALAFGLGAVMAQGGPKVPAKGDFRNEFDHLLVSTLMEGMYKGEQHLLRLSEEIAH  
LESTKTKVEQDRIVREIEVTVAFIEGGVRVVEQELKRTDLNILERFNFEVQALSLLVK  
DLKEAEVKVAVKTR  
>AAX34059.1 unknown function [Tyrophagus putrescentiae]  
MKFVIALAALLAVACAAPTTPKPARPTPAKGDFRNEFDHLIVAAVQRFHDLEEFLLKLSE  
QVADLEKTKNREEKAKILREITIADGLVVGGRTYFEKELKRTDLDLVEKFNFEAVLATIG  
ILDRDLKALATRVNAIKV  
>AAV39514.1 Tri a 28; alpha-amylase inhibitor [Triticum aestivum]  
SGPWMCYPGQAFQVPALPACRPLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSM  
LDSMYKEHGAQEQAGTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAA  
YPDA  
>Q4W1F6 Zea m 25; thioredoxin [Zea mays]  
MASEQGVVIACHSKAEFDAHMTKAQEAGKLVVIDFTAACGPCRAIAPLVEHAKKFTQV  
VFLKVDVDEVEKVTAAAYEVEAMPTFHFVKNGKTVATIVGAKKDELLALIEKHAAPAPASA  
SA  
>Q4W1F8 expansin [Triticum aestivum]  
MASSSIAVAAALILCILVAHAHGCYAKHHAAPSATNSSWLDAKATWYPPHGAGPDDNGG  
ACGFKNVNLPFFSSMTSCGNQPLFKDGGKCGSCYQIRCLKSDHPACSGVPKTVIITDMNY  
YPVSRYHFDLSGTAFGAMAKDGRNDEL RHAGMINMQFKRVPCQYPGLTVTFHVEEGSNPF  
YMAILVEYENGDDVNQLDIMESRPNGGKMAPTGQWVPMKESWGS IWRMDAHHPMKAPFS  
LRITNESGKTLVAEQVIPIDWKPNKTYSSLVQFH  
>Q4W1G2 unknown function [Triticum aestivum]  
ANGDTAFKASGKNKTATGGVAKPKRAPTPFFAF LAEFRPQYMEKHPEAKGVAAVTKAAGE  
KWRMSDEEKAKYGGKADAPASKAVNKKESTSSKAKTGS DVEDDGEEDDEE  
>ARQ16437.1 Art an 7; galactose oxidase [Artemisia annua]  
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPEIDDGGGDKPVPGNNDGASDYAKP  
AFEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPINPDAN  
NQPDICYAHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPKGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYEVPPQMEFKPKRFDLPFM  
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNRI  
QPMAADAAWIPEQNMSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELTPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTEL RVEKFSF  
PYLDPALLETERTQIDPANTDAVLKYGKPFKITAALMEKQPLVLGEVKVTL LYPPFTTHGF  
SQNQRMI VPAITSVQNGVITAVAPPSGQIAPP GYYIMFVSHLGIPGAGIWHID

>ARQ16438.1 galactose oxidase [*Artemisia argyi*]  
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPVDDGGGDKPVPGNNDGASDYAKP  
AFEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPNNPDAN  
NQPDYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPNGDFTTKIGALADTRWYSSNQVLPDGSVVLGGRDSYSYEIVPPQMEFKPRRFDLPFM  
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNKPAYELVDARHVTEKQFLPALQDCNRI  
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELSPPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFTELVEKFS  
PYLDPALPERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF  
SQNQRMI VPAITSVENGVITAIAPPSGEIAPPGYYIMFVSHLGIPGAGIWHID

>ARQ16439.1 galactose oxidase [*Artemisia capillaris*]  
MASSIKTAILFLLPLLLAYSVLAAPDITDGGDKPGPLIDDGGGDKPVPGNNDGASDYAKP  
AIEPEFMGEWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPINPDAN  
NQPDYAHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPNGDFTTKIGALADTRWYSSNQVLPDGSVVLGGRDSYSYEIVPPQMEFKPKRFDLPLF  
QQTTEPPLGPRPVENNLYPFQFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPPSGSAALFPLKLTADNAPVPEIVICGGNQPNAYELVDARHVTEKKFLPALQDCNRI  
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELSPPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFTELVEKFS  
PYLDPALPERTLIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF  
SQNQRMI VPAITGVENGVITAVAPPSGEIAPPGYYIMFVSHLGIPGAGIWHID

>ARQ16440.1 galactose oxidase [*Artemisia gmelinii*]  
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPEIDDGGGDKPVPGNNDGASDYAKP  
AIEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGPSGYKLPEGTPCPINPDAN  
NQPDYAHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPKGDFTTKIGALADTRWYSSNQVLPDGSVVLGGRDSYSYEIVPPQMEFKPKRFDLPFM  
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNRI  
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELTPPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFTELVEKFS  
PYLDPALERTERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF  
SQNQRMI VPAITSVENGVITAVAPPSGQIAPPGYYIMFVSHLGIPGAGIWHID

>ARQ16441.1 galactose oxidase [*Artemisia lavandulifolia*]  
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPVDDGGGDKPVPGNNDGASDYAKP  
AFEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPNNPDAN  
NQPDYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPNGDFTTKIGALADTRWYSSNQVLPDGSVVLGGRDSYSYEIVPPQMEFKPRRFDLPFM  
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNKPAYELVDARHVTEKQFLPALQDCNRI  
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELSPPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFTELVEKFS  
PYLDPALPERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF  
SQNQRMI VPAITSVENGVITAIAPPSGEIAPPGYYILFVSHLGIPGAGIWHID

>ARQ16442.1 galactose oxidase [*Artemisia sieversiana*]  
MASSIKTVILFLLPLLLAYSILAAPDITDAGDKPGPVDDGGGDKPVPGNNDGASDYAK  
PAIESEFMGQWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPINPDA  
NNQPDYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIPN  
DDPNGDFTTKIGALADTRWYSSNQVLPDGSVVLGGRDSYSYEIVPPQMEFKPKRFDLPLF  
MQQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGG

RNYPPSGSAALFPLKLTADNAPVVEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNR  
IKPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEPNLTPVLYT  
PYKPMGQRFKELRPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTEL RVEKFS  
PPYLDPALELERSQIDPANTDVVLKYGKPFKITAGLMEKQPLVLGEVKVTLLYPPFTTHG  
FSQNQRMIVPAITSVENGVITAIAPPSGEIAPPGYYIMFVSHLGIPGAGIWWHID  
>ARQ16443.1 galactose oxidase [*Artemisia vulgaris*]  
MASSIKTVVLFLLPLLLAYSVLAAPDITDGGDKPGPQVDDGGGDKPVPGNNDGASDYAKP  
AFEPEFMGAVIDNPAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPNNPDAN  
NQPDYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND  
DPNGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYEIVPPQMEFKPRRFDL PFM  
QQTTEPPLGPRPVENNLPPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR  
NYPSSGSAALFPLKLTADNAPVIPEIVICGGNKPNAYELVDARHVTEKQFLPALQDCNRI  
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP  
YKPMGQRFKELSPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTEL RVEKFS  
PYLDPALEPERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLLYPPFTTHGF  
SQNQRMIVPAITSVENGVITAIAPPSGEIAPPGYYIMFVSHLGIPGAGIWWHID  
>ATI08931.1 Der f 36; unknown function [*Dermatophagoides farinae*]  
MKFYNILTVATIVILVAFFDNVHADSQAQEQCRQLHHVDIDPSGKFLNNNCRNLNCNIHG  
QIYGHNINEGRTCMIGQTNVYCQNGECVGHNRQHVGHIDIELISASLYEKANAYATVCIM  
NNSLPISLPIQDRRNCISCSTHVKENTNYPVWNEVCVGSNNYLFVSDSRVTTEVWDHHS  
NNNVFLGGVTLTIDQLVNHGDNRQINLAMAGGHNPGQLSTRITWTQRT  
>ATI08932.1 Der p 36; unknown function [*Dermatophagoides pteronyssinus*]  
MKFYNVLTITIGVILLSVFDNVQADTVAQEQCRQLHHVDVDPSTGQFLNNNCLLDCNIHG  
KIYSHNMNEGRTCMVGRNTNYVCRNGQCVGNQHVGHVDIELISASLYEKANAYASVCIKN  
NSMPISLPIQDRRDCITCSTQVRSNTNPIWNEVCTGSGNYLLVSDSRVAIEVWNHLGTS  
NNIFLGGVSLTIDQLVNHGDNRHRAINLAMAGNKPGQLTTRITWTQRN  
>AUH28179.1 Que m 1; pathogenesis related protein, PR-10, Bet v 1-like [*Quercus  
mongolica*]  
MGVVAYESEDASVIPPARLFKAFVLDSNLIKVPVQALKSTEIEGNGGPGTIKKITFG  
EGSHLKHAKHRIDVIDPENFTFSFSVIEGDALFDKLENVSTETKIVASPDGGSIVKSTCK  
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDGY  
>AUW37958.1 Per a 5; glutathione S-transferase [*Periplaneta americana*]  
MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQHTIPTLNDN  
GFCLWESRAILSYLADQYKDDSLYPKDAKKRALVDQRLYFDIRTYHRFGEYYYPIYFA  
KQAADPEKMKKLEEFELNKFLESQEFVAGNKLTADLAIVSSVSTADIMGFVSKYSN  
VAKWFEKCKKIVPGYEELNHSGLKFKEMCDNLAKK  
>BBD75204.1 Der f 14; apolipoprotein [*Dermatophagoides farinae*]  
MRLFALLFTAALLGLGQAQHTVACPNISIPQLINPKAQSTYVYTLDAKTVLTPRDSQKVT  
IKADA EVAIVSACEAVLRLQNVAIDGVPNGAELASELASKSFAFGYFNGRILGVC PANDD  
QDWSLNIKKAIVSALQVQFDENKDKVEESDFSGRCPT EYRKIRNEDNMVMEKRKDLNLC  
DDRRIDL RQTPDQALGQLKEMIRHYMHPMGSDLSCRMTLKDQVVSEVDCEERHVLVHRSH  
KPVHLSYVKMMLKESKDGVAADLGQTDSEPKRYPYLSFDHKKHKNPTETDVVEVLKLCSEI  
SEPQASIETSFTFQKLVDKLRYLSAEETASVDES VKTSVCPAHAYRIRELF LDASAF AAS  
DGSIRTLVKAHENQELSITRSTALFTVVAMKAAPNKETVQVLLPVIASEKTIRPMLLGFS  
VLVRRYCEKSADCASNSGVKDARDAYLARLATAKDANERITIVRALENLNVNTEGVDNMI  
NAMDEIIKSDAEPALRAAVNALSN DASHMDRYKSLVMDESMPEARIAAFQKMMKNGGM  
SHIKDLFTVKGECKMNYVLT YVDNLKSKNDLRRQTVSGDVELPEQPKREIGITRNIARE  
YGPYTFEYDVIYPETHENVTR SINGRLIRAKNDQLKEIVEIQITQNGFERELTNAMALME  
KKSFSQSIMQFVRDTL KMLAQIRKNADDNHHMKITVQINGKDVYYTDVFDLKKMKELI IK  
RAEKIINEKKVDRSIGVLLD SKLVLP TITGLPLMYKFGDNFLIRYDGEFSGEKGRHIK

LNGGFVAGVYGQMKLLVKDQKMGYEYDGLAYTPILDMDIQKKEHSLLLRFNTKDVERRT  
IMRFKQSLREKRATGEEKDYENEITPESRSDQCFSFFLLDYCRKASHIKGLIFPNVEYYV  
VKPEKEVTALELLKGETEDKTRRYVAELTAVGSPSNKQAKAQIEVTKGEEYKITLKSPE  
HEFNTEFTIHADKNNLKMHMDFPNVFQADLTGTFQHDKENNVRKNQLNLQYKFAGDEKPH  
TVDYENEFNFNLKRSSKDKNSGVDRAKYSSSHFPILNHKVNIQFKYRPFKVNELNLEGE  
FGRELQHKFQLMRNSQIEVEEVRPFKMHGNSDIKLMANDLDIDYDLKSEFKYESNKGTP  
ELQYKISGKDRSKRAADLGAEDVEGVIDYKNNGSPIDSKMHAHLKMKGNNGYDSELKQT  
QPQQYEGKITLSKNDKKIFINHKSEMTKPTNTFHLKTDADVSYSDSMDKHKHYQMEFKKEN  
DIYTMSTVERNGQMFYENHLTIHKGGKLNLYRRNDRKILLDLDNALSPREGTMKLNK  
DREYNFVMKREPLRFRDITVEGNENAYIKNGKLHLSLMDPSTLSLVTKADGKIDMTVDLI  
SPVTKRASLKIDSKKYNLFHEGELSASIVNPRLSWHQYTKRDSREYKSDVELSLRSSDIA  
LKITMPDYNKSIHYSRQGDQINMDIDGTLIEGHAQGTIREGKIHIKGRQTD FEIESNYRY  
EDGKLIIEPVKS ENKLEGLVSRKVP SHLTLET PRVKMMNKYDRYAPVKVFKLDYDGIHF  
EKHTDIEYEPGVRYKIIIGNGLKDDGRHYSIDVQGI PRKAFNL DADLMDFKLVSKPEDS  
NKAQFSYTFNEYTETEYEFDPHRAYYVNWLSIRKYIQNFIVEDN

>BBE74942.1 unknown function [*Cryptomeria japonica*]  
MTATAMTTAALRLLIALLLLVAAPAECLPLRARGRWIVDEATGLRVKLACVNWPGLHLEPGL  
PEGLNRLPVTTIAHTISSLGFNCVRLTYSIQMVTEKSYTEATVGQTFQAQLNLTEPASGIE  
GNNPGFLQLGHVAAYDSIVAALAEAGVMVILDNHVSKPKWCCA VDDGNGFFGDSYFDPRL  
WQRGLGLMATHFNNTPNVAMSLRNELRGNRSTSARWSKYMQRGAATVHEANPNVLVLS  
GLHFDTILSFLPVLPVTLPFKEKIVYEGHWYSFGVPWHDGLPNDICLNETSRFKDNIGFL  
TSSINGTAAPL FVSEFGIDQRYVNDNDNRYLNCILAF LAEEDVDWALWTMGGSYNYRSDK  
EPVQDFEETYGFFNRDWSRIRNPDFISRLKEIQQPIQDPYLSGPPYYQIIYHPASGLC  
VESSIGNTIHLGSCQSVRSRWNYDASVEGPIGLMGSSSCISTQGNGLPAIMTEKCSAPNNTL  
WSTVSSGQLQLGTRVFEDEGKEKWMCLDGSRSPLITTTTECICITD SHCYPNQNP EKQWFK  
VITTNKQLLHQL

>COMPARE010 Cha o 3; glycosyl hydrolase 5 family [*Chamaecyparis obtusa*]  
MTSAGVAPTALRLLTALLLLLVAAPSHSLPLLTRGRWIVDEATGLRVKLACVNWVGHLEP  
GLPEGLNRLPVATVAHTISSLGFNCVRLTYSIHMLTRTSYTNATVAQTFARLNLTEAASG  
IEHNNPELDDLGHVAAYHHVVAALSEAGVMVILDNHYSKPKWCCA VDDGNGFFGDRYFNP  
NTWVEGLGLMATYFNNTPNVAMSLRNELRGNRSTPISWSRHMQWGAATVHKANPKVLVI  
LSGLQFDTDLSFLPVLPVTLPFKEKIVYEGHWYSFGVPWRTGLPNDVCKNETGRFLSNVG  
FVTSSANATAAPL FMSEFGIDQRYVNDNDNRYLNCILAYLARRDLWALWTMGGSYYYRS  
DKQPVKDFEETYGFFNHDSRIRNPFISRLKEIQQPIQDPYLAPGPYYQIIYHPASGLC  
VESGIGNTVHLGSCQSVRSRWNYDASVKGPIGLMGSSSCISTQGNGLPAIMTENC SAPNN  
TLWSTVSSAQLQLGTRVLGKDGKEKWMCLDGSKSPLISTNECICITD SHCYPKLNPEKQW  
FKVITTNKQLLHQLQL

>SHD75396.1 tropomyosin [*Sarcoptes scabiei*]  
MYEAIKKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRLQKKIQQIENELDQV  
QEQLSAANTKLEEKALQTAEGDVAALNRRIQLI EEDLERSEERLKIATAKLEEASQSA  
DESERMKMLEHRSITDEERMDGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVLEEEELRVVGNLKSLEVSEEKAQQREEAYEQQIRISTAKLKDAEARAE  
FAERSVQKLQKEVDRL EDELVHEKEKYKSISDELDTFAELLAI

>COMPARE002 unknown function, partial from KAF8044512.1 [*Sinapis alba*]  
SPDSDLEAFSHNPAHGSFAPLAFQPSAMTNCANQRFLSY

>COMPARE003 unknown function, partial [*Sinapis alba*]  
ITLKVVVHFLRRSSHLYFYSQVISQSRTRVKLNRVFFPR

>COMPARE004 unknown function, partial [*Sinapis alba*]  
IKARLRNRSRRCRKTVA

>COMPARE005 unknown function, partial [*Sinapis alba*]

GKETNKDSLNSGERTGKSPA  
>P02845 vitellogenin [Gallus gallus]  
AEAPSAVLENLKARCSVSYNKIKTFNEVKFNYSMPANCYHILVQDCSSELKFLVMMKSAG  
EATNLKAINIKIGSHEIDMHPVNGQVKLLVDGAESPTANISLISAGASLWIHNENQGFAL  
AAPGHGIDKLYFDGKTTITIQVPLWMAGKTCGICGKYDAECEQEYRMPNGYLAKNAVSFGH  
SWILEEAPCRGACKLHRSFVKLEKTVQLAGVDSKCYSTEPVLRCAKGC SATK TTPVTVGF  
HCLPADSANS�TDKQMKYDQKSEDMQDTVDAHTTCSCENEEST  
>Q647G8 Ara h 7; 2S albumin, conglutin [Arachis hypogaea]  
MVKLSILVALLGALLVVASATRWDPDRGSRGLRWDAPSRGDDQCQRQLQRANLRPCEEHI  
RQRVEQEQQEQDEYPYSQRGSRGRRPGESDEDQEQRCCNELNRFQNNQRMCQALQQIL  
QNQSFRFQQDRSQLHQNGEGAQELAPELRVQVTKPLRP  
>COMPARE014 Mes a 1; lipocalin [Mesocricetus auratus]  
HYQNLEVSPSEVDGKWYSLYIAADNKEKVSEGGPLRAYIKNVECIDEQTLKITFYTKVE  
GVCQEHTIVGRKGEDGKYITDFSGQNYFHIVEKSDDTMTFHNVNVDSDGKTNVILVVGRG  
ESSSIEQKQRFEKTAEEYDIPKENIEDLVPTDNCDQ  
>COMPARE006 Que m 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus  
mongolica]  
MGVVAYESEDASVIPPARLFKAFVLDSNLIPIKVVQALKSTEIEGNGGPGTIKKITFG  
EGSHLKHAKHRIDVIDPENFTFSFVFGDALFDKLENVSTETKIVASPDGGSIVKSTCK  
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDGY  
>ANW10058.1 Ras k 1; calcium-binding protein, parvalbumin [Rastrelliger kanagurta]  
MAFASVLKDAEITAALDGCKADGSFDHKKFFKACGLAGKSGDDVKKAFAIIDQDKSGFIE  
EEELKFLQNFKAGARTLSDAETKAFKAGDTDGDGKIGVDEFAAMIKG  
>COMPARE011 unknown function [Malassezia furfur]  
MNNEKYCSVADYDVKWFKERCQSHPTDVKTTKWIAGTDLKIEMDPKPEYELYCFNYTTF  
GNLPDAGAKELDDDATKKACSAKSGKYQSDPKKKSCRMDKKDIDQFKEQCSQYQPSDRP  
PYGDWSAGTSLNVVLNLKNA  
>COMPARE012 tropomyosin [Anisakis pegreffii]  
MDAIIKKMRKAMEIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKMMQTENDLDK  
AQEDLSTANSNLEEKVKQEAEEVAALNRRMTLLEEELERAEERLKLATDKLEEATHT  
ADESERVRKVMENRSFQDEERANTVESQLKEAQM LAEEADRKYDEVARKLAMVEADLERA  
EERAEAGENKIVELEELRVDGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRA  
EFAERSVQKLQKEVDRLEDELVHEKERYKSISELDLLQELSGY  
>XP\_001732036 unknown function [Malassezia globosa]  
MVSLNIFSAAFVASLASAVFAAPSALERRAAPDNTVWVTSVADHCLILPRHKMSVGDSSES  
PGNMRSFCTKPYSSKQQLASDFWTKAHFKKTDKYVQITGCINPNVQSTLLSNDEGGQYD  
SNGGEGGRGNPAGSVCLGYSSYVELVEPAGNRACIRCCYDPSDCDVSQDEAGCETVIPGK  
YDC  
>XP\_015174445.1 Pol d 3; dipeptidyl peptidase [Polistes dominula]  
MISLRSFVFLNGFIFVLLTGRTVSYVLDKDNLDRVVFRVQDDSNFPKRPFQLEETYTADY  
LPRNFNGTWTSDTTLIYISETVGEILQFDVVKQSTVIIDVSIFFDYLVESYLLSPTGRF  
LLIGYDLQKGFYRSTFMRYVIYDTELGQYDKIGNGMHIALVRWAPLTDDLIIYILDNNIYY  
KRFKNGFNDVQRVTDDGIAGIINYGVADWVYEEVLEHGSSAIWFSPDGKRLAYATFDDR  
KVHEILYLHYGEPGLDQYPTVEVKIKYPKAGTPNPVSLTLVDLHDPTLNKINLEAPVD  
IVGIDNVL TNVQWKDFNTIIATWSNRVQNETEIVWYNVYGETVETLHIEEPEGWVDIKNL  
FFYNGSTYMRKLQQSGTKAGRHHVTRYEKVGSTLIQKDLTPGAIEVQDIRAIDHFNRI  
YYLASGPGEPSQRNLYSVPADGSKEPTCISCNVITPEGNQCKYADVSFSPFRSYALVCQ  
GPDPTFIDIFDSNHRKIFSWEHNLMRLRLTKRELPIVKDLYVHANGYDSKVRLLLPHNF  
DESKSYPM LVN VYAGPNTAKINDAASYSYQSYM TTNRSVIYAYIDGRGSSNKGSNMLFEI  
YRNLGTVEVEDQITVTRKQLQEMYSWIDSKRTAIWGSYGGFCTAMVLAKDVDSVFKCGIS

VAPVSSWIYYDSIYTERFMGLPTPEDNLKGYDGTVDVSRRVEGIRGKKFMLIHGTGDDNVH  
YQQLALAKSLEESDILFEQITYTDEAHALYGVLPPLYHSMDFWSECFWSNTH  
>XP\_016648029.1 Pru m 7; gibberellin-regulated protein [Prunus mume]  
MKLGFATFLLVCLLLSSSVFEVTMAGSSFCDSKCGVRCCKAGYQERCLKYCGICCEKCHC  
VPSGTYGNKDEPCYRDLKNSKGNPKCP  
>COMPARE172 Fag e 4; antimicrobial peptide, partial from P0DKH7.1 [Fagopyrum  
esculentum]  
AQCGAQGGGATC  
>AEG47274.1 Tri tu 14; lipid transfer protein [Triticum turgidum]  
MARSVAQVVLVAVVAAMLLAVTEAAVSCGQVSSALSPCISYARGNGASPSAACCSGVRS  
LASSARSTADKQAACKCIKSAAAGLNAGKAAGIPTKCGVSVPYAISSSVDCSKIR  
>COMPARE059 Ole e 7; lipid transfer protein, partial [Olea europaea]  
APSQGTVTAKLTSCVSYKDXQ  
>COMPARE138 Tri t 1; beta-glucosidase, partial [Trichophyton tonsurans]  
NNMAFSLGVKGPDGSVKQLVDFEQDFVAL  
>BAA23361.2 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]  
LKVREDENNPFFYFRSSNSFQTLFENQNGRIRLLQRFNKRSPQLENLRDYRIVQFQSKPNT  
ILLPHHADADFLFVLSGRAILTLVNNDDRSYNLHPGDAQRIIPAGTTYLVNPHDHQNL  
KIIKLAIPVKNPKGRYDDFFLSSTQAQQSYLQGFSHNILETSFHSEFEEINRVLFGEEEEQ  
RQQEGVIVELSKEQIRQLSRRAKSSSRKTISSEDEPFNLRSRNPPIYSNNGKFFFEITPEK  
NPQLRDLDFLSSVDINEGALLLPHFNKAIVILVINEGDANIELVGIKEQQQKQKQEEE  
PLEVQRYRAELSEDDVVFIPAAYPFVFNATSNLNLAFGINAENNRNFLAGEKDNVVRQ  
IERVQVELAFPGSAQDVERLLKKQRESYFVDAQPQQKEEGSKGRKGFPPSILGALY  
>COMPARE103 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Corylus avellana]  
GVFNYEAEETTSVIPAAAXLFKSYVLDGDKLLPKVAPQALTSVENVGGNXXP  
>CBA35339.1 calcium-binding protein, parvalbumin [Oncorhynchus mykiss]  
MACAHLCKEADIKTALEACKAADSFNFKTFHTIGFASKSADDVKKAFKVIDQDASGFIE  
VEELKFLQNFPCARVLTDAETKAFLKAGDADGDMIGIDEFAVWVKQ  
>CBA35340.1 calcium-binding protein, parvalbumin [Oncorhynchus mykiss]  
MAFAGLNDADVAALAATAADSFNHKAFFAKVGLAGKSNDVKKAFYVIDQDKSGFIEE  
DELKFLQNFASARALDAETKAFADGDKDGDGMIGVDEFAAMIKG  
>BAB55663.1 collagen [Oncorhynchus mykiss]  
MLSFVDNRILLLLAVTSLLASCSGGLKGPGRGAKGPRGDRGPQGPNGRDGKAGLPGIAGP  
PGPPGLGGNFAAQFDGKGSDDPGPMGLMGSRGPNPPGAPGPQGF TGHAGEPGEPGQT  
GSI GARGPTGSAGKPGEDGNNGRPGKPGDRGGPGTQGARGFPGTPGLPGMKGHRGYNGLD  
GRKGESGTAGAKGETGAHGANSPGPAGSRGLNGERGRAGPAGPAGARGADGSTGPAGPA  
GPLGAAGPPGFPAGPGPKGEIGGAGSNGPSGPQGGRRGEPGINGAVGPVGPVGNPNNGIN  
GAKGAAGLPGVAGAPGFPGRGGPGPQGPQGSTGARGLGGDPGSPGQKGDGSAKGEPPGHS  
GVQGAAGPAGEEGKRSTGEVGTATGAGLRGARGGAGTRGLPGLEGRGGPIGMPGARGAT  
GPGGIRGAPGDAGRAGESGLTGARGLPNGSQQGPPGKEGPPGAAGLDGRTGPPGPTGPR  
GQPGNIGFPGPKPGGGEAGKGGDKGPTGATGLRGGPGADGNNGAPGPAGVVGNTGEKGEQ  
GPAGAPGFQGLPGPAGPAGEAGKAGNQMPGDQGLPGPAGVKGERGNSGPAGSAGSQAIGAI  
GARGPAGTPGPDGGKGEPSVGI VGAAGHQGPGGMPGERGAGGTPGPKGEKGEGGHRGLE  
GNMGRDARGGPGSPGPPGSPGANKEKGESGSGFPAGPAGLRGPSGERGEGGPAGLPGFA  
GPPGSDGQSGPRGEKGPAGGKGDVGPAGPAGPSGQSGPSGASGPAGPPGGRGDAGPSGLT  
GFPGAAGRVGGPGPAGIAGPPGSAGPAGKDGPRGLRGDPGPGGPQGEQGVVGPAGISGDK  
GPSGESGPPGAPGTAGPQGVLPSSGFVGLPGSRGDKGLPGGPGAVGEPGRLGPAGASGPR  
GPAGNIGMPGMTGTQGEAGREGNSGNDGPPGRPGAAGFKGDRGEPGSPGALGSSGQPGPN  
GPAGSAGRPGNRGESGPTGNGGPPGAVGARGAPGPAGPRGEKGGAGEKGDGMKGLRGHG

GLQMPGPNGPSGETGSAGITGPAGPRGPAGPHGPPGKDGRAGGHGAIGPVGHRGSPGHL  
GPAGPPGSPGLPGPAGPAGGGYDQSGGYDEYRADQPSFRAKDYEVDATIKSLNSQIENLL  
TPEGSKKNPARTCRDIRLSHPDWSSGFYWDPNQGCIAADAIKAYCDFSTGHTCIHPHPES  
IARKNWYRSSENKKHVWFGETINGGTEFAYNDETLSPQSMATQLAFMRLLANQATQNTITY  
HCKNSVAYMDGENGLKKAVLLQGSNDVELRAEGNSRFTFNVLEDGCTRHTGQWSKTVIE  
YRTNKPSRLPILDIAPLDIGEADQEFGLDIGPVCFK  
>BAG93005.1 Ole e 1-like [Oryza sativa]  
MARPRFATTAPLLALAVLAAVVSVAVATAPAGKDPGGFVVTGRVYCDPCRAGFETNVSKS  
IPGATVSVVECRHYGAGRESLKA EATTDEKGWYKVEIDQDHQEEICEVVLKSSDPACSET  
EKTRDRSRVPLTSNGLKQNGIRYANPIAFFRKEPLADCGSILQKYDLKDAPEP  
>BAG94438.1 Ory s 12; profilin [Oryza sativa]  
MSWQTYVDEHLMCEIEGHHLTSA AIVGHDGTVWAQSAAFPQFKPEEMTNIMKDFDEPGFL  
APTGLFLGPTKYMVIQGEPAVIRGKKKSGGITVKKTGQALVVGIIYDEPMTPGQCNMVE  
RLGDYLVEQGL  
>BAG93129.1 polygalacturonase [Oryza sativa]  
MGFVRALFLLAMVCVAHAHAKDYPKEEGAKAEGPAAASGGGGGSTHDVVKLGGKGDGKTDS  
TKAVNEAWTAACAGTGKQTIVVPKGF LTGPLNFTGPCKGDIVIQLDGNLLGSTD LALFK  
SNWIEIMRLESLEISGKGLDQGA AVWSKNSCAKKYDCKILPNTLVLD FVNGLISGIS  
LVNPKFFHMNVFKSKNITIKDVTITAPG DSPNTDGIHMGDSSKISIIDTVIGTGDDCISI  
GPGTEGVNISGVTCPGPHGISVGS LGRYKDEKDVTDVTVKNCVLKSTNGVRIKSYEDAA  
SVLTASKFTYENIKMEDVANPIIIDMKYCPNKICTANGNSKVTIKDITFKNITGTSSTPE  
AVSLLCSDKLPCTGVTLNDIKVEYSGTNMKTMAVCKNAKGTATGCLKELSCF  
>COMPARE073 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]  
RLIFHQAGVKFEDNRLKREDWPALKPKTPFGQPLLEVDGEVLAQSAAIYR  
>COMPARE074 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]  
FGLAGKTPMEEAQVDSIFDQFKDFMAELRPCFRVLAGFEEGDKEKVLKEVAVPARDKHL  
LLEK  
>COMPARE075 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]  
WIAERP KTPY  
>AFP95338.1 Pro c 5; myosin light chain [Procambarus clarkii]  
MAADLSARDVERVKFAFSIYDFEGNGTMDAFYIGDCLRALN LNPTLAIIEKVGKKEKRKE  
KIIKLEEFIPIFAQVKKDKDAGSYEDFMEVLKLYDKSENGTMMYAELEHILLSLGERLEK  
SELEPVLKECCNEEDEDGFIPYEPFLKMTQLL  
>AI008861.1 Der f 33; alpha-tubulin [Dermatophagoides farinae]  
MRECISLHVQGAGVQIGNACWELYCLEHEIQPDGQLSPVKSTTTLSSETISNDSFSTFF  
NETGNRFRVPRSIYVDLEPTVVDEVRTGEYRRLFHPEQLITGKEDAANNYARGHYTEGKT  
LIEPVMRRIAKLAEQCSGLQGFLIFHSFGGGTGSGFSSLLMERLSVEYGKSKLEFAIYP  
APAISTAVVEPYNSILTTHTTLEHSDCSFMVDNEAIYDICRRNLNIERPSYMNLRNLIGQ  
IVSSITASLRFDGALNVDL TEFQTNLVPYPRIHFLVSYAPIVSSEKAYHEQFTVPEITG  
TCFEP SNQMVKCNTRNGKYMACCLLYRGDVVPKDVNA AIAAIKAKSTIQFVQWCPTGFKI  
GINYRPPTVVP SGDLAKVQRAVCLLSNTT AISEAWSRLNHKFDLMYSKRAFVHWYVGE  
EEGEFSEAREDLAAL EKDYEEVA AEYNADDDDDYDRDGE EF  
>QAT18644.1 Der p 33; alpha-tubulin [Dermatophagoides pteronyssinus]  
MRECISVHVQGAGVQIGNACWELYCLEHGIQPDGQMP SDKTIGTGDDSFNTFFSETGSGK  
HVPRAVYVDLEPTVVDEVRTGT YRQLFHPEQLITGKEDAANNYARGHYTIGKEIVDLVLD  
RIRKLS DQCTGLQGFLIFHSFGGGTGSGFTSLLMERLSVDY GKKSKLEFAVYPAPQVSTA  
VVEPYNSILTTHTTLEHSDCAF MVDNEAIYDICRRNLDIERPTYTNLNRNLIGQIVSSITA  
SLRFDGALNVDL TEFQTNLVPYPRIHFLV TYAPVISA EKAYHEQLTVSEITNTCFEPAN  
QMVKCDPRHGKYMACCLLYRGDVVPKDVNA AIASIKTKRSIQFVDWCPTGFKVGINYQPP  
TVVQVVIWLKYNVLFVCCPTLLPSLKLGLDWIINLI

>QAT18643.1 Der p 32; inorganic pyrophosphatase [Dermatophagoides pteronyssinus]  
MSIRSINLLTRQTIPGSLISIIIGINNNFHNRYIYFSFKHPHQSFKYHHLSSASLSINFSI  
SKNVHYKQOPYNIGNKVHFVQNHQLRKFFATKTNNKMSTNYSVDNRGALNSLDYRIYFKN  
DSNGKIISPWHDIPLFADKSAKQYNMVVEIPRWTNEKMEIATAEPMTPIKQDVKKGALRY  
VKNVFPKGYIWNYGAFPQTWENPNHIDQGTAKAGDNDPIDVIEIGSRIAKRGDVIPVKI  
LGTIALIDEGETDWKIITIDTRDELQGMNNVDDVEKLLPGLLRATVEWFRIYKIPDGKP  
ANKFAFNGEAKDREFAEKVVEETHQYWREMMENKAGEHQLDLKNITLGNSTINDEQAKQ  
FLETRPASNTVEPNPIADQVAIDKWHHVKLI

>QAT18639.1 Der p 28; heat shock protein 70 [Dermatophagoides pteronyssinus]  
MPSKTSKAPAIGIDLGTYSVGVFQNGSVEIIANQGNRTTPSYVAFTDTERLIGDAAK  
NQVAMNPANTIFDAKRLIGRRFDEPSVKSDMKHWPFKVSESGPKIEVEFKGEQKRFWP  
EEVSAMVLTMKMETAEAYLGQKVTDVAVITVPAYFNDSQRQATKDGVIAGLNVLRINEP  
TAAAIAYGLDKKGGGKENVLIFDLGGGTFDVSVLTIDNGIFEVKSTAGDTHLGGEDFDNR  
LVNHVFQEFKRKFGKDIMSNKRALRRLRTACERAKRTLSSSTQTTIEIDSLHEGTDYFST  
ITRARFEELCSDLFRSTLEPVEKALRDAKLDKSKIDEIVLVGGSTRIPKIQKLLSDFNG  
KELNKSINPDEAVAYGAQAAIILTGDTSNMVKDLLLLDVAPLSLGIETAGGVMTTLIKR  
NTTIPTKQTQFTTYADNPQAVTIQVYEGERAMTKDNRLGTFDLTGIPPAPRGVQPQIEV  
TFDVDANGILNVSADVSTGRQNKITITNDKGRLSKADIEKMNVEAEQYREEDERQRERI  
SAKNQLEAYAFQLKSTMEEEAIKSKLSEEDRKTVLNKVEETLRWLDNSQLADKEEYEHQ  
KELESACRPIMTKIYQQQQHPGAPGANGSCGSNAYPGYGGFNSNNDGPVVEEVN

>QAT18638.1 Der p 26; myosin light chain [Dermatophagoides pteronyssinus]  
MADLRPPEVEKARLHFDIYDFEGQGVVYHLLGDLLRSLDLRPTQEMVAKNGWEKKKGQK  
YMTFEEFLPIYSQVKKDKDCGAYEDLVEGLKVYDKAENGTMMEAELAHLVLLSLGENWMIR  
K

>QAT18637.1 Der p 25; triosephosphate isomerase [Dermatophagoides pteronyssinus]  
MGRKFFVGGNWKMNRSRATNDLIKILTNTPLDPNTEVVVGVPSIYLADVRHKLSKLSIGV  
AAQNCYKVAKGAFTEISPAMIKDVGAEWVILGHSERRNVFGENDQLIGEKVEHALNEGL  
NVIACIGELFEEREAGKTTEVFRQTVQVSKHVVDWSKVVLAYEPVWAIGTGKTASPQQA  
QEVHQQLRQWFSTNISQIAETIRIYGGSVTASNAKELASQADVDGFLVGGASLKPEFV  
QIVNARQ

>AGM32377.1 Copt f 7; tropomyosin [Coptotermes formosanus]  
MDAIKKKMQAMKLEKDNMMDRALLCEQQARDANLRAEKAEFEARSQKKIQQIENDLDQT  
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAA  
DESERARKILESKGLADEERMDALENLKEARFMAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVLEEEELRVVGNLKSLEVSEEKANLREEEYKQIKLTLTTLKEAEARAE  
FAERSVQKLQKGSRQA

>NP\_001138311.1 unknown function [Apis mellifera]  
MVVWLVLIIATSSSVYLAEEAIPDPPNSKISTVNP SKLSTAVDCTGIIAFSATHASVDHAK  
AVFAETLVDKGVGYVPQTGIFITNCPGLYQFSFAGYGSTDLRLTLKKKQNNSDSWRPVVG  
TGAGGGANLILLEVDVGDQLAVFVDSGKISDGVTFSGYRIAKI

>XP\_392204.2 platelet-derived growth factor/vascular endothelial growth factor,  
PVF1-like [Apis mellifera]  
MPYSKCRFTLRFFAICSFSTCGLVMAQLEDTRYPDQRIVFPDRGRETANPALEGGPSGGG  
IGELAKSIQLAKKISSINSRDDFLKLVKDVPKDISFFSSSSRMGETERSNAERPQALCM  
PELQTVPLLENESVIYYPTCTRIKRCGGCCTHSLSCOPTATEIRNFEILVTILESSGK  
LKYQGRIVPIEHTQCTCDCKIKETDCNKKQSYVPEECTCACNNVDEQKKNESNIKMW  
HPDLCSFCRETQECSTGFYFDQNSCRCLQVPLSRTWFTSTKGSYRFGQTQRPDNPVPPV  
IIALDSDPRRKPDPPE

>COMPARE147 calcium-binding protein, parvalbumin, partial from 5ZGM\_A, 5ZGM\_B  
[Mustelus griseus]

EVFEILDKDQSGFIEEEELK

>COMPARE148 calcium-binding protein, parvalbumin, partial from 5ZGM\_A, 5ZGM\_B [Mustelus griseus]

ALLAAGDSDHDGKIGADEFAK

>COMPARE149 calcium-binding protein, parvalbumin, partial [Mustelus griseus]  
LFLKNFSATAR

>COMPARE028 7S globulin, vicilin [Lathyrus sativus]

YRLLEYKSKPHTLFLPQYTDADFILVVLGSKAILTVLNSNDRNSFSLERGDITIKIPAGTI  
AYLANRDDNEDLRVLDLAIIPVKNKPGQLQPFLLSGTQNPQPSLLSGFSKKVLEAAFNTNYEE  
IEKVLLEQQEQHRRSLKDRRQEINEENVIVKVSREQIEELSKNAKSSSKSVSSESEPF  
NLRSRNPIYSNKFGEFTEITPEKNQQQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVN  
EGKGFELLGIRNENQREESDEEEEQEEETSKQVQRYRAKLSPGDVFVIPAGHPVAINAS  
SNLNLIGFGINAENNQRNFLAGEEDNVISQIQRPVKELVFPGSSREVDKLLKNQRQSYFA  
NAQPLQRE

>ABG35122.1 Der f 22; unknown function [Dermatophagoides farinae]

MNRFLIVCMALFCLAAAVQADETNAVQYKDCGHNEIKSFFVTGGNPQKSCVVIHKHKNQL  
RISFVANENTGNKINTRFICNLGGIELGWPGIDGTACQGHGLSCPLTKGQTYNYHLDFN  
LGDDVPTANVTATVRLENGHGGDLLCGRMHISLQN

>COMPARE170 Cit s 7; gibberellin-regulated protein, partial [Citrus sinensis]  
GSDFCDSKCAVRCSKAGR

>AVD29823.1 Art ar 2; pathogenesis related protein, PR-1 [Artemisia argyi]

MGHLRNISLVLAISFAILHLSHAHEHYGEPGNTDDYVHAHNCIRRVLMKPLCWDELA  
KVAQAWAETRTPDCLSIHSDRCGENMAQGAINGSMVQLWLDERLDYDYNENKCIKMCGRH  
YTQIVWANSERVGCGRALCSNGWAYIIVCNYPGNNVVGQKPY

>ABC86902.1 Bla g 9; arginine kinase [Blattella germanica]

MVDAAVLEKLEAGFAKLAASDSKSLLRKYLTKEVFDNLKTKKTPTFGSTLLDVIQSGLEN  
HDSGVGIYAPDAEAYTVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI  
ISTRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEGELKGQFYPLTGMTKEVQQK  
LIDDHFLFKEGDRFLQHANACRFWPTGRGIYHNDAKTFLVWCNEEDHLRIISMQMGDLG  
QVYRRLVTAVNDIEKRVPFSHDDRLGFLTFCTNLGTTVRASVRIKVPKLAADKKKLEEV  
AGKYNLQVRGTRGEHTEAEGGVYDISNKRMRGLTEYDAVKGMNDGIAELIKIESSL

>AHL24656.1 Ole e 14; polygalacturonase [Olea europaea]

IPHNGVRRGLVGETIFDVMKYGAKADGRFDNAQAFIKAWKAACESTGPAKVVIPKGFVA  
GEVVFQGPCTAPKPITIEIQGNVLASTDVSAYTSGSWIMLEEIDGLVINGGGTINGRGKS  
SWQFAGANNEGPLLVPVSLTFKKVKNSEMHDVNFVDSMGFHSKVADSENKISKLKISAPG  
DSPNTDGMHISCSTNVNVTDSIIGTGDDCVSIGHGTTDILVSGITCGPGHGISVGLGKR  
PDETVDKGISVINCTLTGTTNGARIKTYHASPSIQASDILYKDIIVTDVKNPILIDQHYD  
SKKKPEQSKVKISGVHFVNIKTTVSEIPVALNCSEAVPCEDVELADIDLAPSGAAGSLK  
SVCANAKFVLKKGKPIPPGC

>COMPARE128 Pun g 14; chitinase, partial from G1UH28.1 [Punica granatum]  
GDIAIYWQNG

>QFG58557.1 7S globulin, vicilin, beta-conglutin [Prunus dulcis]

MAIKITIKASYKLPFFFFFFLSTLFLASSSVTPLINALSDYHNQKCCQSIKRGVGGRRHLL  
RSKDHPQDAREEYFYCSQSCGTSEDPEQCETECRERFDEQLKKEAEEQQKGQEEEEEGP  
TFNPNPYYPFKFLRPRFLAEEGAYFVLGSFARLSHLLRGRIQNYRAALLQTTPTGTFVLP  
YHLDAESIFVWNGRGLTLVLMKDKQSFKIENGVDVIRVPAGATTYLINNHTTENLSLVQ  
LFQPVNTPDLFEFFFPAGYKDPPEGSDYSFLHGTESYYSVFSNDLLEAAFDVPREQLEKA  
FGQQKREGMIIRASKEQLDALSKQAYPWWRKLVPSMGSDLNFNLLSQRPLHSNNYKGFY  
EASPQEFKQLQDMNVSAMLDINPEAMMVPHYNSKATYLMVVVDGMGYFEMACPKFTIPA  
SEEMEYQEEQADQQSGVFSKVSGLSLGDFVIPAGHPVSIQAQNNNNNNNNNGNQNK

LRIVGFGINAGNNIRNFLAGQEGNIMKQMEREATQLTFGQEMEQLTSQKQSYFVPASRR  
GSSTEKA

>CAA67128.1 Tri a 17; beta-amylase [*Triticum aestivum*]  
MAGNMLANYVQVYVMLPLDVSVDNKFEGDEIRAQLKLLTEAGVDGVMIDVWVWGLVEGK  
GPKAYDWSAYKQVFDLVHEAGLKLQAIMSFHQCGGNVGDVVNIPIQWVRDVGATDPDIF  
YTNRGGTRNIEYLTGLVDDQPLFHGRTAVQMYADYMASFRENMKKFLDAGTIVDIEVGLG  
PAGEMRYPSPYQSQGWVFPGIGEFICYDKYLEADFKA AAAKAGHPWELPDDAGEYNDTP  
EKTQFFKDNNGTYLTEKGFFLSWYSNKLKHKGDKILDEANKVFLGCRVQLAIKISGIHWW  
YRVPNHAAELTAGYYNLDLDRDGYRTIARMLTRHHASMNFTCAEMRDSEQSEEAKSAPEEL  
VQQVLSAGWREGLHVACENALGRYDATAYNTILRNARPKGINKNGPPEHKLFGFTYLRLS  
NELLEGQNYATFQTFVEKMHANLGHDPVDPVAPLERSKPEMPIEMILKAAQPKLEPPFF  
DKNTDLPVKDHTDVGDEVLVAPV

>COMPARE153 calcium-binding protein, polcalcin, partial [*Amaranthus retroflexus*]  
MAAEDTPQDIADRERIFKRKETNGDGKISSSELGDALKTLGSVTPDEVRRMMAEIDTDGD  
GFISFDEFTDFARANRGLVKDVKIF

>QCB92083.1 beta-expansin [*Urochloa mutica*]  
MLAVVAVVLASVMGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC  
GYKDVKAPFDSMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA  
AYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLA  
LLVKYAAGDGNIVSVDIKSKGSEDFLPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGGHV  
EQEDVIPEDWKPDTVYKSKIQF

>QCB92082.1 Uro m 1; beta-expansin [*Urochloa mutica*]  
DGKWLDKATWYGKPTGAGPDDNGGACGYKDVNKAPFNSMGACGNPPIFKDGLGCGSCYE  
IKCDKPAECSGEPVIVHITDQNYEPIAAYHFDLAGTAFGAMAKKGEEEKLRKAGIIDMQF  
RRVKCKYPANTKIAFHVEKGCNPNYFALLIKYAAGDGDIVAVDIKEKGSEEFIPLKHSWG  
AIWRIDSPKPIKGPPIAVRLTSEGTTLVQDDAIPEGWKADTVYTSKQLQF

>QCB92084.1 beta-expansin [*Urochloa mutica*]  
MGLANIVAVAAVLAALVGGGSCGPPKVPVPPGNITANYNGKWLPARATWYGKPTGAGPDD  
NGGACGKIDVNLPPYSGMTACGNIPFKDGGKCGSCYEIRCKAPVECSNNPVTVFITDMN  
YEPIAPYHFDSLGAFGALAKPGLNDKLRHAGIMDIEFRRVRCKYTGGQKIVFHVEKACN  
PNYLAVLVKVFVADDGDIVNMELEKASA EWKPMKLSWGAIWRVDTPKALKGPF SIRTSE  
SGKKLVANDVIPANWKANTAYPSNIQF

>COMPARE060 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
APSCSTVTAK

>COMPARE061 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
APSQSTVTAKLTSCVSYLDDQ

>COMPARE063 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
LTSCVSYLDDKSAKPTSDCCAGVK

>COMPARE064 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
TVLAQATSKPDK

>COMPARE065 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
SALALVGNKVD TGR

>COMPARE066 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
SALANVGNKVD TGR

>COMPARE067 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
VDTGRVSSLPK

>COMPARE068 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
KCGMSVDLPPLDK

>COMPARE069 Ole e 7; lipid transfer protein, partial [*Olea europaea*]  
PPIDKNYDCSKVP

>COMPARE058 gibberellin-regulated protein, partial from Q948Z4.1 [Solanum tuberosum]  
VPSGTYGNKHECPCYRDKKNSKGSKCP

>COMPARE107 phospholipase A2, partial [Myrmecia pilosula]  
MVELNADAPFCALYNDR

>COMPARE108 phospholipase A2, partial [Myrmecia pilosula]  
IGASVLVADTTMSR

>COMPARE109 phospholipase A2, partial [Myrmecia pilosula]  
GVIQRMVLGADPR

>COMPARE110 phosphoglycerate mutase, partial [Myrmecia pilosula]  
DAGYTFDVAHTSVLTR

>COMPARE111 phosphoglycerate mutase, partial [Myrmecia pilosula]  
YGEEQVQIWR

>COMPARE112 phosphoglycerate mutase, partial [Myrmecia pilosula]  
TLPYWNETIIPQLK

>COMPARE113 phosphoglycerate mutase, partial [Myrmecia pilosula]  
AAMA AVAAQ GK

>COMPARE114 phosphoglycerate mutase, partial [Myrmecia pilosula]  
IIIAAHGNSLR

>COMPARE115 phosphoglycerate mutase, partial [Myrmecia pilosula]  
YADGPKPEEFKPFESLK

>COMPARE116 unknown function, partial [Myrmecia pilosula]  
WDNELETIAQR

>COMPARE117 hyaluronidase, partial [Myrmecia pilosula]  
NGGVPQEGDLKK

>COMPARE118 arginine kinase, partial [Myrmecia pilosula]  
VSSTLSGLTGELK

>COMPARE119 arginine kinase, partial [Myrmecia pilosula]  
LGLTEYQAVK

>COMPARE120 arginine kinase, partial [Myrmecia pilosula]  
GEHTEAEGGIYDISNK

>COMPARE121 arginine kinase, partial [Myrmecia pilosula]  
LVTAVNEIEK

>COMPARE122 esterase, partial [Myrmecia pilosula]  
DEFGGVVAVEK

>COMPARE123 esterase, partial [Myrmecia pilosula]  
YAEPTGQQR

>COMPARE124 esterase, partial [Myrmecia pilosula]  
APGNLGLKDQVVALR

>COMPARE125 dipeptidyl peptidase, partial [Myrmecia pilosula]  
VYYLATAPGEPSQR

>COMPARE126 dipeptidyl peptidase, partial [Myrmecia pilosula]  
NLYSVPLDASQKPT

>COMPARE127 dipeptidyl peptidase, partial [Myrmecia pilosula]  
EYDHYITTNR

>COMPARE129 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]  
AGDWVQTNVLAYSADVK

>COMPARE131 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]  
GSNIELILDVPKDKLQDLTDSAK

>COMPARE132 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]

IYDPDQATLQALR

>COMPARE133 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]  
NGNNLPPQAEVVTLYK

>COMPARE134 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]  
NVYNAIAAANLQGQIK

>COMPARE136 beta-1,3-glucanase, partial from ABD16200.1 [Mangifera indica]  
YIAVGNEIRPGDAEAQYVLPAMR

>COMPARE070 glyceraldehyde-3-phosphate-dehydrogenase, partial [Fusarium lateritium]  
RVPTANVSVDLTVRI

>COMPARE071 glyceraldehyde-3-phosphate-dehydrogenase, partial [Fusarium lateritium]  
RTTYFGPTGNDSTVLKY

>COMPARE072 elongation factor [Echinococcus granulosus]  
FDAHSYHQFPNYHEMESAYMRFLSKDIGKTSATEQKGD SYLVKEIQKVRDNIKSSLESNG  
SWNERMEKLEAIVKEMSLRVNELEVQIQRLGQILPSESLKGAKPIRPVVVKAPPAEGGDD  
DDIDLFGSEDEGEADKCKQMMAEQNKAAASKKEKPVAKSMIVLDVKPWDDTTNMAEMEK  
VRAITADGLLWGTSKLVPLVHGINKLQIACVVEDDKVGTDFLEESIMELEDYVQSVDDVAS  
FNKL

>P81531.2 Bet v 7; cyclophilin/peptidyl-prolyl isomerase [Betula pendula]  
DFTAGNGTGGESIYGA KDXXXXXXXXXTGP GILSMANAGPGTNG

>COMPARE145 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]  
DNPIDSCWRGDSNWDQNRMKLADCVVGFSGSTMGGKGGIYTVTSS EDNPVNPTPGTLRY  
GATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGAVVHLGN GGPCLFMRKASHVILHG  
LHIHGNTSVLGDV LVS ESIGVEPVHAQDGAITMRNV TNAWIDHNSLSDCSDGLIDVTL  
GSTGITISNNHFFNHKVM L LGHDDTYDDKSMKVTVAFNQFGPNAGQRM PRARYGLVHV  
ANNNYDQWNIYAIGGSSNPTILSEGNSFTAPNESYKKEVTKRIGCETTSACSNWWRSTR  
DAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQ NAGVVA

>AAC61261.1 Asp f 16; unknown function [Aspergillus fumigatus]  
MYFKYTAALAAVLPLCSAQ TWSKCNPLAETCPPNKGLAASTCTADFTSASALDQWEVTA  
GKVPVGPQGA EFTVAKQGDAPTIDTDFYFFF GKA EVMKAAPGTGVVSSIVLESDDLDEV  
DLVRLGGD TTQVQTNYFGKGD TTT YDRGTYVPVATPQETFH TYTIDWTKDAVTWSIDGAV  
VRTLTYNDAKGGTRFPQTPMRLRLAAGPAATPATPGHHRVGRWLDRLQRGT VHHVRQVRP  
YRERQPRRVLHLLGQLWLLAEHQVRRRLRRYSSSSSVTSS TTSTASSASSTSSKTPSTSTL  
ATSTKATPTPSGTSSGSSNSSSAEPTTTGGSGSSNTG SWLRRLRLWLWLYSSTGSSTSAGA  
SATPELSQGAAGSIKGSVTPALWCSAPSLPCWHSKQNDDFGLMHDTHHEGDVRTIHF GIG  
VSPSFGV

>COMPARE023 2S albumin, conglutin, partial [Prunus dulcis]  
VTXEEGXYSISDQSKVGE

>C0HJM6 Trip s 1; chitinase [Triplochiton scleroxylon]  
EQGGSQAGGSL

>COMPARE021 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Malus domestica]

GVYTFENEY TSEIPPGR LFKA FVLDADNLIPK IAPQA

>COMPARE137 Par j 1; lipid transfer protein [Parietaria judaica]  
MVRALMPCLPFVQGEKEPSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK  
LVSEVPKHC GIVDSKLPPI DVNM DCKTLGVVPRQPQLPVSLRHGPVTG PSRSRPPTKHGW  
RDPRLFRPPHRKKNPAFSTLG

>AAB35977.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides  
farinae]

MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER  
HVGIVDFK GELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY

KLGDLPHTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFG  
VLSVDLTAIFQDTRKEMTKVLAPAFKRELEKN  
>P14292.3 Cand b 2; peroxisomal protein [Candida boidinii]  
MAPIKRGDRFPTTDDVYYIPPEGGEPGLELSKFVKTKKFVVSVPGAFTPPCTEQHLPG  
YIKNLPRIKSGVDFVLVISQNDPFVLKGWKKEGAADAKKLVFVSDPNLKLTKKLGSTI  
DLSAIGLGRSRLALIVNRSGIVEYAAIENGGEVDVSTAQKIIAKL  
>COMPARE018 lipid transfer protein [Brassica rapa]  
MKIMVLTLMVFVILLTLFPAPNEAADTNVEAACDPKQLQPCLAAITGGGQPSGDCCAKLK  
EQQPCLCGFSKNPAFAQYISSPNSRKVLTACGIPYPSC  
>C0HJF9.1 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]  
NRQPSKYGLEETI  
>COMPARE020 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial  
[Fragaria x ananassa]  
KITFGEGSQYGYVK  
>COMPARE176 phytocystatin, partial [Actinidia chinensis]  
VAAGGWRPIEE  
>AAX84656.1 alpha-tubulin [Tyrophagus putrescentiae]  
MRECISVHVQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGTGDDSFNTFFSETGSGK  
HVPRAVYVDLEPTVWDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIVDVVLD  
RIRKLSDQCTGLQGFLIFHSFGGGTSGSFTSLLMERLSVDYGKKSLEFAVYPAPQVSTA  
VVEPYNSILTTHTTLEHSDCAFMDNEAIYDICRRNLDIERPTYTNLNLRLIGQIVSSITA  
SLRFDGALNVELTEFQTNLVPYPRIFPLVTYSPVISA EKAYHEQLTVAEITNTCFEPQN  
QMVKCDPRHGKYMACL LLYRGDVVPKDVNAAIAGIKTKRSIQFVDWCPTGFKVGINYQPP  
TVVPGDLAKVQRAVCM LSNTTAAIEAWARLDHKFDL MYAKRAVHWVYVGEEMEEGEFSE  
AREDLAALEKDYEEVGLDSTEAEGGDGEEF  
>Q5QKR2 Eri s 2; ovary development-related protein [Eriocheir sinensis]  
MWCSILLAAMVAVAGGQSRFSYDGTPLADDVWVWVSGQRQQFFASRQPRPQQQLFVQERPQ  
QVFVQQQPQPVPVQPEPQQVFVQPPRPMFQMLPSFSQQA AVIQSVQPQVSSACPATYS  
LVHTTYQGRVYHSSWCNLPGHRFSQSAARDYCRGLGEVTVMNRRGSFDLYSVDRTTDFDY  
FFELLQHQIPSVWTRDLASTAPYEIRGSITRSGDSTAGQDCLSLEASTDGLFLLQDSCS  
DRKAAVCVAHWQ  
>BAF43535.1 Ani s 6; serine protease inhibitor [Anisakis simplex]  
MFQSTFFLVLMVCVATARFANKDHCPPNEEYNECGNPCQEKCNDGEPVICTYQCEHRCFC  
KQGYVRLTEDGECVPEEFCKPIHY  
>AAR08428.1 translationally controlled tumor protein [Cladosporium herbarum]  
MLIYNDIISGDELISDSYDLVEVDGVAYEADCRKITIGGETFDTGANASAEGGDEEADDQ  
KETKIDVVHAFQLQETNFDKKAYLGHLKSYMKKIKESMAASGASEDEVKEFEKGAQTFAK  
RVVGSFKDYEFLLIGPSMDPDAMVLLNYREDGVTPYVTLWKHGLKSTKV  
>COMPARE162 arabinase, partial from EAL84189.1 [Aspergillus fumigatus]  
EDYQFGWNQL  
>COMPARE163 Asp f 15; cerato-platanin, partial from O60022.1 [Aspergillus  
fumigatus]  
WPTFGSVPGFAR  
>COMPARE164 Asp f 15; cerato-platanin, partial [Aspergillus fumigatus]  
PTLPGWNSPNCG  
>COMPARE139 Blo t 12; chitin-binding protein [Blomia tropicalis]  
MKSVLIFLVAIALFSANIVSADEQTTRGRHTEPDDHHEKPTTHATHEETTSTQHHHEEVT  
TQTPHHEEKTTEETHHSDDLIVHEGGKTYHVWCHEEGPIPHPGNVHKYIICSKSGSLWY  
ITVMPCSIGTKFDPISRNCVLDN  
>P86699 arginine kinase [Chionoecetes opilio]

MADAATISKLEEGFKKLQGATDCKDVFQDLKQTDKHPNKDFGDVNQFVNVDPDGKVFVIST  
RVRLIDDHFLFKEGDRFLQAANACRYWPSGRGIFHNDKKIISMQMGGDLGQVYRRLVSAV  
NEIEKRVPFSSHDLGLFTFCPTNLGTTVRASVHIKLPKXEKLEEVAGKYSLQVRGTRGE  
HTEAEGGVYDISNKRRMGLTEFQAVKEMQDGILELIKIEKEMQ  
>ACT37323.1 unknown function, partial [Stachybotrys chartarum]  
AGPIASRQIVPNYPASSTSKGFHLVNVTDPSADFTPSINNFYVNSIHVGAALNYVGVTA  
VPGRIFYQNGTAEIIRYAQSTVISDGATPPVPFGLSLRPDEGSDVVSTARLDAGPGTTGV  
RVSRFPEPYRFLQPETFLACNESLAYYQGDYFTVIKQADVTVGDDGSIDYNVPDNCISVR  
LIPECTELNELPEDAYASHEFAADTQCYDDVSALNWSEYGP  
>ACV96855.1 arginine kinase [Scylla serrata]  
MADAIVIEKLEEGFKKLEAATDCKSLLKKYLTKSVFDQLKGKKTSLGATLLDVIQSGVEN  
LDSGVGVYAPDAEAYTLFAPLFDPIIEDYHKGFKQTDKHPNKDFGDVNQFVNVDPDGKVF  
ISTRVRCGRSMEGYFPNCLTEAQYKEMESKVSSTLSNLEGELKGTYYPLTGMTKDVQQK  
LIDDHFLFKEGDRFLQAANACRYWPTGRGIYHNDNKTFVWCNEEDHLRIISMQMGGDLG  
QVYRRLVSAVNEIEKRVPFSSHDLGLFTFCPTNLGTTVRASVHIKLPKLAANREKLEEV  
AGKYSLQVRGTRGEHTEAEGGVYDISNKRRMGLTEFQAVKEMQDGILELIKMEKEM  
>ADM53099.1 fibronectin-binding protein [Staphylococcus aureus]  
MAYDGLFTKKMVESLQFLTTRGVHKINQPDNDTILMVVRQNRQNHQLLSIHPNFSRLQL  
TTKKYDNPFPNPFARVFRKHLEGGIIESIKQIGNDRRIEIDIKSKDEIGDTIYRTVILE  
IMGKHSNLILVDENRKIIIEGFKHLTPNTNHYRTVMPGFNYEAPPTQHKINLYDITGAEVL  
KYIDFNAGNIAKQLLNQFEGFSPLITNEIVSRRQFMTSSTLPEAFDEVMAETKLPPTPIF  
HKNHETGKEDFYFIKLNQFNDDTVTYDSLNDLLDRFYDARGERERVKQRANDLVRVQVQ  
LHKYQNKLAKLIEEYEQSKNKDTEQLYGELITANIYRIKQGDKEVTALNYTNEEVVIPL  
NPTKSPSANAQYYYKQYNRMKTRERELQHQIQLTKDNIDYFSTIEQQLHHISVHDIDEIR  
DELAEQGFMKQRKNQTKKKKAQIQLQHVVSTDGDDIYVGKNNKQNDYLTNKKAKKHTHWL  
HTKDIPGSHVVFNDAPSDTTIKEAAMLGAGYFSKAGNSGQIPVDYTLIKNVHKPSGAKPG  
FVTYDNQKTLYATPDYELIQMKQS  
>CAY85463.1 Tri a 35; dehydrin [Triticum aestivum]  
MEHQGHGAGEKKGVSITEKLPGGHGDHQQATGGTYGQQGHAGVTGENIKEKLPGGHGD  
HQQTGTGMTGSETHATTATTDGNYGKSGHTGTDGTGENKSIMDKIKDKLPGQH  
>COMPARE057 unknown function, partial [Phaseolus mungo]  
GRREDDYDNLQL  
>BAL72725.1 Pen m 4; calcium-binding protein, sarcoplasmic calcium-binding protein  
[Penaeus monodon]  
MAYSWDNRVKYYVRYMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN  
LWNEIAELADFNKDG EVT VDEFKQAVQKHCQGGKKGFEFPGAFKVFIANQFKAIDVNGDGK  
VGLDEYRLDCITRSFAFAEVKEIDEAYNKLTTEDDRKAGGLTLERYQDLYAQFISNPEESC  
SACYLFGPLKVVQ  
>COMPARE140 pathogenesis related protein, PR-10, Bet v 1-like, partial [Foeniculum  
vulgare]  
GVQKSEVVITSA  
>COMPARE141 lipid transfer protein, partial [Foeniculum vulgare]  
AITXGQVTSKLG  
>COMPARE142 lipid transfer protein, partial [Foeniculum vulgare]  
GGDPTPACCGVK  
>COMPARE143 lipid transfer protein, partial [Foeniculum vulgare]  
GINYGAASALPGK  
>COMPARE144 lipid transfer protein, partial [Foeniculum vulgare]  
CGISIPYPISTNCSR  
>AER70365.1 Ves v 6; vitellogenin [Vespa vulgaris]

MRSRFILLLLGVAVSNLDNNIEHGKVGEEYQYLVRSTLTGLQTLSDQYAGILMKATLR  
IQCNTPDLRAQLLKPQYAIHKKLPDGDWSRISDQMLEHKHPLSNPFVIKLGKGVIR  
DLIVSKNVPTWEVNIKSIISQFQADTQGENLKGKNTQIPEDDNPFFATFRVMEDCVSGK  
CEVLYDVVPLTEDVLQHRPHILPKPELRNGEHIYITKTRNYDKCEQRMDYFYGISGNAN  
WESDIRNNDKIMKKSSTSNMVISGNLKNFVIQTAVTTTEIIMKPRLVDDQESIVISKMN  
TLVSVNKVSSPIPAPNNPESTGNLVYTYNDPFSKTVQRRGRPSVSPNSMSNELDSSADS  
DEDLRLMREKYGKSDKMNVSDEDEKAFRQMKPTLHEAPKNPMLPLFIGNNGKAVVMSDKI  
NSGKMVMTLVQEIASEMEDPNVMPDRETLEKFTIVSRLISSMSLEQINKAEGSLHSVWNE  
IGSDETNRMKKENARAVFRDAIANAGTGPALMTIKRWIEKKEIEGCEAADVLASIPKTAR  
TPTAEYVDAFFSLASNEVQKQTCNLSSAVLSFAELVHRAQVSNSSIYNHYPVNVFGRLS  
SRRNDAVLRKYIPFFAEELKKAIKDGDSPRIQVYILALGLTGHPKILNVLEPYLEGKERV  
STYQRFMLVMSLRKLCVVKPSLARSVLYKIYLNWVHQIRCAAVNLIMRTNPPLDMLTR  
MAQFTNTDFSGQVNSAVKSAIESAANLNYPEWEELTRNARKVLHLMNTESDKYYYSESHF  
TEMEENDQLSYRMMLNYIGSVDNVIPLSTHFALQPSYNGFLSPVYELDMSISSVKSLLEM  
YWHKSEKGDTEESFAEKTAKMLHIESDNVEQVEGNVFFKTPYLNRYFSFDNHTIERILHD  
MVSPRHSHHVNMNKLSDYDITLSFPTETGLPFVYSLHVPTIKKFSVISKPDMKSKFDVRL  
LTSTKHQGRVGFITPFDHQAFLSGIDNMQVFLPCKLDFHLNNEKSRLDAALQPLKHNSK  
TRLGHFSVIPYTSQYEIMSLRPLLEKNTHRIQEKKTTTHIRIPQNPNSIFSVEVEADNLA  
EKIQQLRSENKWEMLSPSSALGTYEKIDLFVKPDLQENEAVKFTATLDTKEIRSNNL  
DTNDESWKSGNKVLKTMHQALDSPARRKEFLQEVVKGINSKAYVIDAGLEVPGLWKS  
ACTLCLASSNDENKFRSIFYWYTNIPSQDITYQMCVNGQTRSSPTTTPFDYKKILDSNPTN  
EFSINIQSGRTCTDNSLVTIKGQIKQSEDYKYVQESRIVKRCDENVRNSVKDCQKAAEM  
AKNLNEIDMTITKHNSAEESDTELEKIFHGTTKMLTGLNVRVSEIQEHSVDNDNDIRVQ  
IKLSPNMTSAEGMASKSGQILTFSDIHIDMGIDNDEMNEIEKILHGATCTLRNNEAET  
FDGKVYPLKLGKCAHVLFTTYPRNAPNEPNKRMSIPENMKVTVIAEETENKKEQLILLG  
NDEILFKSSGTEVSAWVNGQVKKCSQKESYQHINKNDETLFEIFELPGPAIKLISDKYDIK  
LAYDTHVQIEVPHTYQQSVRGLCGDFDGRSENFVTPKNCMLQKPEEFAATYILKERCE  
GPALNNAKKAERSKCIRKVLRFSDVISDGEAGRPYVNWQWGYHKKENKKQCNTYRTQII  
TKDDNICFTIRPVPTCSSGCKSVVTKLKEYQLYCLPKNDSSLGMKKRIEQGANPDL  
SRTPTDNAMISVPLECVAT

>COMPARE079 glutathione S-transferase [*Dermatophagoides farinae*]  
MELGTLEGSMSETKPILGYWDARGLGQAIRLLLLTYAGVDFIDKRYTVGPPPNYDRSQWLN  
DKYNLGLDFPNCPPYIDGNVKSLSQSLAIRIYIARKQKLGQNEHEEIRASLAEQQIIDMN  
MAIARIAYNFNCEKLPKPEFLKSLPEQVELLSKFLGDQPF TAGANISYADFLLYEYLTKLK  
ILVPEVYDKFENLKKFHGNVLEALPRVSEYIKKQPKAFHGPTSLWNGTYA

>AGF86397.1 Mel 1 1; tropomyosin [*Penaeus latisulcatus*]  
MDAIIKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKAEDDVNKLQKLLQQLLENDFDQV  
QEALLLANTNAVEKDKALSNAEAGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA  
DESERMKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTQTFSELSTGY

>BAG92398.1 lipid transfer protein [*Oryza sativa*]  
MARAQLVLVAVVAALLAAPHAAVAITCGQVNSAVGPCLTYARGGGAGPSAACCNGVRS  
KSAARTTADRRTACNCLKNAARGIKGLNAGNAASIPSKCGVSVPYTISASIDCSRVR

>Q28895 Can f 7; NPC2-like [*Canis familiaris*]  
MRLVAAFLLLALGLDLPGGAVHFKDCGSVGVKELNVNCPAQPCCKLHKGQSYSVNVT  
FTSNIPSQSSKAVVHGIVLGVAVPFPIPEADGCKSGINCPIQKDKTYSYLNKLPVKNEY  
SIKLVVQWMLLDGNNQHLCWEIPVQIEG

>COMPARE029 11S globulin, cupin, partial [*Lupinus albus*]  
PAEVLANAFGLR

>BA050858.1 13S globulin [Fagopyrum esculentum]  
MSTKLILSFLCLMLVLSCSAQLLPWQKGQRSRPHHGHQQFQHQCQDVQRLTASEPSRRVRS  
EAGVTEIWDNDTPEFRCAQFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVVPGC  
PETFQSESEFEYFQSQDRQRSESEESSRGDQRTRQSESEEFSSRGDQHSRQSESEESS  
HGDQHQKIFRIRDGDVIPSPAGVVQWTHNDGDNDLISITLYDANSFQNQLDGNVRNFFLA  
GQSKQSREDRRSQRQTREEGGDRQSRESDDDEALLEANILSGFQDEILQEIFRNVDQETI  
SKLRGETDQRGFIVQARDLKLVRPEEYEEELQREERGDRKRGGSGRSNGLEQAFCNLKFQKQ  
NVNRP SRADVFNPRAGRINTVNSNLP ILEFIQLSAQHVVLYKNAILGPRWNLNAHSALY  
VTRGEGRVQVVGDEGRSVFDDNVQRGQILVVPQGFVAVL KAGNEGLEWVELKNDDNAITS  
PIAGKTSVLRAIPVEVLANSYDISTKEAFRLKNGRQEVEVFRFPQSRDEKERERY SIV  
>AAS48514.1 Fag e 5; 8S globulin, vicilin [Fagopyrum esculentum]  
IAVVTNGKGFQMACPHISAEGKQSKRQREGKSIVHYETVNGDLSSGTVFVVPAGHPFVT  
AASLEDNLELICFEVNADDNERIPLAGKNSL FKQFEREAKELAFEEKADVVDKLLLEKQQQ  
EFFFEQPRRRKEQEAGRSDA  
>COMPARE101 Phod s 1; lipocalin, partial [Phodopus sungorus]  
AGQETNEMYVVGK  
>COMPARE102 Phod s 1; lipocalin, partial [Phodopus sungorus]  
FKPVYATPENIVFTNK  
>COMPARE168 Coc n 1; 7S globulin, vicilin-like, partial [Cocos nucifera]  
VSEGDVFWLPR  
>COMPARE169 Coc n 1; 7S globulin, vicilin-like, partial [Cocos nucifera]  
LSPHVNP SATEYGLLLL  
>ACS49840.1 Gly m 7; seed biotinylated protein [Glycine max]  
MASEQLARRENTTTEKEIHVEKHRVPKMATHEHLAEQAKESDITAGKDT PQGSIEALQA  
GERVKDHAGKAMGDI GGRGKARETHELGAHFESLADKVTDHAAANVVGNKESQREARGGV  
RDVGK FEMRTEGGEKGNKDRPELKT RTREVIGRTEKERGRESGGQVVAEKRETETARGR  
VGAENEGARTTAVITCTLEKGGGTQKPIREEERESERSAWEQISNYSDQATQGVKEY  
ERAKQAASET LNTTTTQTAQEKSQAQKNLAAQAKDATLEKGGQGYAVTKDTISSAAKTASE  
KTAPVAEKAKDYTLQAAEKAKSAGGTTASYVGEKAVQAKDVAVESGKSAAGYAAKVAADL  
RDKATAVGWAAAHFSAEKTVEGTKAAAHVVEGAAGYAGHKA AELASMSAGAVKGLAASAG  
ETAKEYTAKKKEEAQRELEAKKPSQPQEAERPSEGIGETVRQYAQKPKPSERNPQKEGT  
GSIVFTAIGETVSSAGEKVKKPFKNTTGGESEGGGGKEEGKSVIGKSLTSIGEKLGDAKQ  
REELLDNVTGNITEGGGEVLGAVGETVAEIGQNMMPAEIVQERAHVRQAGGVLD AIGET  
IAEIAETTRVMVSGEDERVLRQSVVLETRVTGRAKHEEGSHGA  
>CTQ87571.1 Pin p 1; 2S albumin, conglutin [Pinus pinea]  
MGVFSSPMSTLRWVTLFAALLSLLLEWGT AHEDIVMDGDQV VQQQGRSCDPQRLSACRDYL  
QRRREQP SERCCEELQRMSPHCR CRAIERALDQS QSYDSSTDSQDGAPLNQRRRRRGE  
GRGEEEEEAVERAEELPNRCNLRESPRRCDIRRHRSRYSIIGGSD  
>XP\_014705584.1 Equ a 6; lysozyme [Equus asinus]  
MRSTLIISLLSCFFAVYEAKVFSKCELAHKLKAQEMDGF GGYS LANWVCMAEYESNFNTR  
AFNGKNANGSSDYGLFQLNNKWWCKDNKRSSSNACNIMCSKLLDDNIDDDISCAKRVRD  
PKGMSAWKAWVKHCKDKDLSEYLASCNL  
>P11376 Equ c 6; lysozyme [Equus caballus]  
KVFSKCELAHKLKAQEMDGF GGYS LANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLN  
NKWWCKDNKRSSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDL  
SEYLASCNL  
>XP\_018814692.1 Jug r 6; 7S globulin, vicilin [Juglans regia]  
MAFKPKIPIALLLLTSLLAICAGLALAMQDPELKQCKHQCRHQRFDEQEKEHCQRSCDE  
YHIEKKARERAERRRSEEGSSREEGYEEELGGEREENPYVFEDEFETRVRTDEGRIQ  
VLEKFTKRSKLLRGIENFRVAILEANPQTFISP AHFDAELVVFVAKGRATITTVREEKRE

NFNVEQGDIMRIPAGTPVYLINRDENEKLYIVKILRPVSVPGHFHFEAFHGSGGEDPESFYR  
AFSWEVLEAALKTRRDQLEKLFQKQVGIKASKEQIRSMKHEETTPRIWPFGGDSTH  
PFNLFHKRPSQSNQFGRLEFETDPKECKQLQDLMLVFSANITKGS MAGPYNSRATKISV  
VIEGEGYFEMACPHLSSSGSRGQREGSGSSRRRSRSGPSYQQIRGRLRPGMVVAPAGHP  
VAVIASRNKNLQVLCFDVNAQGNIRFPLAGKNNIVNEFEKEAKEAFNFPAREVEKIFRN  
QDQEFFFPGPSRQPEEGGRAFE  
>COMPARE165 unknown function, partial [Aspergillus fumigatus]  
RLQSEVEVAIMD  
>COMPARE166 unknown function, partial [Aspergillus fumigatus]  
QALIAELAQVH  
>COMPARE178 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]  
GEAVFNDRIR  
>COMPARE180 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]  
LVENIDNPSRADIFNPR  
>COMPARE015 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]  
LTSVNSFNLPIILNYLRLSAEKGVLRY  
>COMPARE080 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
DVDEIVLVGGSTR  
>COMPARE081 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
AKFEELNMDLFR  
>COMPARE082 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
ITPSYVAFTADGER  
>COMPARE083 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
NQLTTNPENTVFDAGR  
>COMPARE084 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
DNHLLGKFDLTGIPPAPR  
>COMPARE085 Aed a 8; heat shock protein 70, partial from Q1HR69 [Aedes aegypti]  
KVTHAVVTVPAYFNDAQR  
>COMPARE086 Aed a 8; heat shock protein 70, partial [Aedes aegypti]  
IEIESFYEGDDFSETLTR  
>COMPARE150 Alt a 1-like [Ulocladium botrytis]  
MQFTTIASLFAAAGLAAAAPLESRQDNASCPVTTKGDYVWKISEFYGRKPEGTYYNLSLGF  
NIKATNGGTLDFTCQAQADKLEGHKWYSCGENSFMDFSFSDRSGLLLKQKVSDE  
>COMPARE158 Tha p 2; unknown function, partial [Thaumatococcus panyocampa]  
SYSQSYSYVQCIQDSECNGCWK  
>COMPARE159 Tha p 2; unknown function, partial [Thaumatococcus panyocampa]  
KAEEAIDLTYQEK  
>COMPARE160 Tha p 2; unknown function, partial [Thaumatococcus panyocampa]  
NNLFNLGSAVDILSR  
>COMPARE044 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus  
angustifolius]  
AGIALGAHHLEENLVVFDLERSR  
>COMPARE030 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus  
albus]  
AGIALGTHQLEENLVVFDLAR  
>COMPARE054 7S globulin, vicilin, beta-conglutin, partial [Lupinus luteus]  
AIFIVVDEGEGNYELVGIR  
>COMPARE055 putative TAG factor protein, partial [Lupinus luteus]  
AVCNLFALEGATVIFTYVK  
>COMPARE034 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus

albus]  
HSIFEVFTQVFANNVPK  
>COMPARE046 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus angustifolius]  
ISGGAPSVDLILDKNDVWR  
>COMPARE048 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus angustifolius]  
KISGGAPSVDLILDK  
>COMPARE036 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]  
KISGGVPSVDLIMDK  
>COMPARE056 unknown function, partial [Lupinus luteus]  
RPFYTNAPQEIIYIQGR  
>COMPARE051 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus angustifolius]  
SRVGFNSNSLK  
>COMPARE041 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]  
SRVGFNTNSLK  
>COMPARE052 7S globulin, vicilin, beta-conglutin, partial [Lupinus angustifolius]  
SVPAEATEVGLLVFST  
>COMPARE053 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus angustifolius]  
VGFNSNSLKSYGK  
>COMPARE043 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]  
VGFNTNSLKSHGK  
>COMPARE146 dioscorin, partial [Dioscorea opposita]  
VEDEFSYIEGNPH  
>COMPARE087 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein, partial from Q16XK7 [Aedes aegypti]  
AFIDAHYQMMDINNDGLVSIEEYR  
>COMPARE088 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein, partial from Q16XK7 [Aedes aegypti]  
YQELYAQFMGNESDK  
>COMPARE089 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein, partial from Q16XK7 [Aedes aegypti]  
KVDDSYNQLVSDENK  
>COMPARE090 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein, partial from Q16XK7 [Aedes aegypti]  
ALWDEISALADLDHDGK  
>COMPARE091 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein, partial from Q16XK7 [Aedes aegypti]  
VDDSYNQLVSDENKR  
>COMPARE181 Aed a 6; porin, partial from Q1HR57 [Aedes aegypti]  
VTANNFALGYSTGDFVLHTNVNDGR  
>COMPARE092 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
DPSAAEGGEIIFGGSDSNK  
>COMPARE093 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes

aegypti]  
QTFAEAINEPGLVFVAAK  
>COMPARE094 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
SFDLEGADYVLR  
>COMPARE095 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
YTGDFTYLSVDRK  
>COMPARE096 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
ECSFTNIACLMHMK  
>COMPARE097 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
VVFDTGSSNLWVPSK  
>COMPARE098 Aed a 11; lysosomal aspartic protease, partial from Q03168.2 [Aedes aegypti]  
YYTEFDMGNDR  
>COMPARE154 Beta v 1; Ole e 1-like, partial [Beta vulgaris]  
VQGMVYCDTCR  
>COMPARE155 Beta v 1; Ole e 1-like, partial [Beta vulgaris]  
AEGLYNMLIERD  
>COMPARE156 Beta v 1; Ole e 1-like, partial [Beta vulgaris]  
DCNEIPTEGWAKPSLKVSLTSMNGEASDIRSANALGFMR  
>ABC88428.1 alcohol dehydrogenase [Curvularia lunata]  
MSNIPQEQAQVIEKTGGPVEYKIPVQKPGPDEVLVNIKFSGVCHTDLHAVNGDWPLPT  
KLPLVGGHEGAGVVVARGELVNDVELGDHVGKWLNGSCLSCDYCQTADEPLCPKPLLSG  
YTVDTGTFQQYCIAKAAHVARIPEKCDLAAIAPVLCAGITVYKGLKESGVKPGQFAAIVGA  
GGGLGSLACQYAKAMGVRTIAIDAGEEKKKMCVNDLGAETFVDFSTSKNLVADVQKATPD  
GLGPHVVILVAVNEKPFQAAEYVVRPRGTVICIGLPAGAYLKAPVFETVIKMIRIQGSYV  
GNRKDSSEAIIEFFRRGLIKAPFKIVGLSELQMVYDKMHQGAVVGRYVLDTSK  
>COMPARE152 Alt a 1-like, partial [Stemphylium botryosum]  
KISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCSAQADKLEDHKWYSCGENSFMSFSFD  
SDRS  
>COMPARE174 7S globulin, vicilin-like, partial [Fagopyrum esculentum]  
GDYPLEXCRQKIEH  
>COMPARE175 trypsin-inhibitor, partial [Fagopyrum esculentum]  
SDKPQQLLEECRYLXRI  
>COMPARE100 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]  
SIQKIHAREI  
>QE43417 Sola m 1; profilin [Solanum melongena]  
MSWQTYVDDHLMCDLEGHHLASAAILGFDGSVWAQSPAFPKQHTMCDRCSRSGVNCYIM  
RPLYLYQAKFKPEEITNIMKDFDEPGFLAPTGLFLGGTKYMVIQEGPAVIRGKKGSSGI  
TIKKTQALIFGIYEVPVTPGQCNMVVEKIGDYLVDDQGY  
>QCI56568.1 tropomyosin [Acheta domesticus]  
MDAIKKKMQAMKLEKDNAMDKADTCEGQAKDANNKADKINEDVQELTKKLAQVENDLITT  
KANLEQANKDLEDKEKALQAAESEMAALNRKVQLVEEDLERSEERAATAATKLQEASEAA  
DEAQRMCVKLENRSQQDEERMDQLTNQLKEARLLAEDADGKSDEVSRLAFVEDELEVAE  
DRVKSGDSKIMELEEELKVVGNLSK  
>QCI56569.1 tropomyosin [Acheta domesticus]  
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARGLQKKIQTIENELDQT

QEQLMQVNAKLEEKDKALQTAEGEIAALNRRIQLLEEDLERSEERLATATAKLAEASQAA  
DESERARKILENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE  
ERAEGESKIVELEEELRVVGN

>QCI56570.1 tropomyosin [*Gromphadorhina portentosa*]  
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANIRAEKAEFEARSQKKIQQIENDLDQT  
LEQLMQVNAKLEEKDKAFQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAA  
DESERARKILESKGLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEELRVVGNLKSLEVSEEKANLREEEYKQIQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDRLDEDELVHEKEKYKYICDDLDMFTFELIGN

>QCI56571.1 tropomyosin [*Galleria mellonella*]  
MDAIKKKMQAMKLEKDNALDRAAMCEQQAKDANLRAEKAEFEARQLQKKIQTIENTLDQT  
QESLMQVNGKLEEKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLSEASQAA  
DESERARKVLENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEEELRVVGNLKSLEVSEEKANQREEEYKNQIKTLTTRLKEAEARAE  
FAERSVQKLQKEV

>QCI56572.1 tropomyosin [*Galleria mellonella*]  
MDAIKKKMQAMKLEKDNAMDKADTCEQQARDANLRAEKVNEEVRELQKKLAQVEEDLTLN  
KNKLDQANKDLEEREKQLAATEAEVASLNRKVQQIEEDLEKSEERSGTAQQKLLEAQQSA  
DENNRMKVLENRAQQDEERMDQLTNQLKEARLLAEDADGKSDEVSRLAFVEDELEVAE  
DRVKSGDAKISELEEELKVVGN

>QCI56573.1 tropomyosin [*Litopenaeus setiferus*]  
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV  
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKVLENRSLDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLLKAAEARAE  
FAERSVQKLQKEVDRLDEELVN

>QCI56574.1 tropomyosin [*Tenebrio molitor*]  
AKLIAEEADKKYEEVARKLVLMEQDLERAEEAEQSESKIVELEEELRVVGNLKSLEVS  
EEKATLKEEYSVTLKQVDQRLQEAARAEFAERSVQKLQKEVDRLDEDDLLA

>QCI56575.1 tropomyosin [*Tenebrio molitor*]  
RKLAMVEADLERAEERAEAGESKIVELEEELRVVGNLKSLEVSEEKANQREEEYKNQIK  
NLTTRLKEAEARAEFAERSVQKLQKEVDRLDEELVAEKERYKEIGDDLDTAFVELIL

>QCI56576.1 tropomyosin [*Zophobas atratus*]  
EARFLAEEADKKYDEVARKLAMVEADLERAEERAEAGESKIVELEEELRVVGNLKSLEV  
SEEKANQREEEYKNQIKNLTTRLKEAEARAEFAERSVQKLQKEVDRLDEELVAEKERYKE  
IGDDLDTAFVELIL

>COMPARE209 Aed al 2; D7 like salivary odorant-binding protein, partial from  
P18153.2 [*Aedes albopictus*]  
QSYFEFCENK

>COMPARE211 Aed al 2; D7 like salivary odorant-binding protein, partial [*Aedes*  
*albopictus*]  
KSYFEFCENK

>COMPARE214 Aed al 2; D7 like salivary odorant-binding protein, partial from  
P18153.2 [*Aedes albopictus*]  
CMEDNLEDGPNR

>COMPARE216 Aed al 3; unknown function, partial from AAV90693.1 [*Aedes albopictus*]  
VVAILDKDTK

>COMPARE217 Aed al 3; unknown function, partial from AAV90693.1 [*Aedes albopictus*]  
VDNIQSEYLR

>COMPARE219 Aed al 3; unknown function, partial from AAV90693.1 [*Aedes albopictus*]

SALNNDLQSEVR  
>COMPARE221 Ano d 2; general odorant-binding protein, partial from Q7YT43  
[Anopheles cracens]  
NAVDYNELLK  
>COMPARE223 Ano d 2; general odorant-binding protein, partial from Q7YT43  
[Anopheles cracens]  
ANTFYTCFLGTSSSPAFK  
>COMPARE224 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
FQQAVQALGTIDSADCLK  
>COMPARE228 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
YGPVHAQFTDVQR  
>COMPARE229 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
EITDKIYNSDSTVK  
>COMPARE230 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
SNFKDGSEELCTLR  
>COMPARE231 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
TGITTNNHLDCLFR  
>COMPARE232 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
NGNINPDEIK  
>COMPARE233 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
DKDAAVDNALNCK  
>COMPARE234 Cul q 2; salivary odorant-binding protein, partial from Q95V92 [Culex  
quinquefasciatus]  
YFIENTDPYDVAK  
>COMPARE235 Cul q 3; salivary odorant-binding protein, partial from Q95V93 [Culex  
quinquefasciatus]  
GFIQVNNANKGVLEK  
>COMPARE236 Cul q 3; salivary odorant-binding protein, partial from Q95V93 [Culex  
quinquefasciatus]  
NGEMDESAILR  
>COMPARE237 Pru p 9; pathogenesis related protein, PR-1, partial from  
XP\_007199020.1 [Prunus persica]  
MAFNTKLLLAICCVLVFTLVSANISK  
>COMPARE238 Pru p 9; pathogenesis related protein, PR-1, partial from  
XP\_007199020.1 [Prunus persica]  
VGDCAMEHSMGR  
>COMPARE239 Pru p 9; pathogenesis related protein, PR-1, partial from  
XP\_007199020.1 [Prunus persica]  
TTEVCGISKCNNGQNYVVCSYDPMYQPEDERP  
>QFI57017.1 Scy p 9; filamin C [Scylla paramamosain]  
MPSGKSDVPVIEDNRDGTVSVRYSPREEGLHELHVKYNAEHVQGSPPFKFHVDSIASGYVT  
AYGPGLVHGITGEPANFTISTKDAGAGSSTLRGGLSLAVEGSSKAEISCHDNKDGTVSVS  
YLPTAPGEYKVSVKFAEKHIRGSPYSVKITGEGRKRNQISVGSQSEVSLPGKVTDSDIKS

LNASIQAPSGLEEPCFLKKLPNGHLGISFTPREVGEHLVSVKRMGNHIANSPFKINVGEK  
EVDGASKVKISGKCLSEGQTHKENQFTIDTRDAGYGGLSLSIEGPSKADIQCKDNEDGTL  
TIGYTPTEPGYYIINLKFADNHVPGSPFTVKVTGEGTNRQTERIKRQREAVPLTEVGSQC  
RLTFKLPGISPFDLGATVTSPGGVTEAAEIGEVEDGLYGVNFVPKELGVHTVSVKYQEMH  
IPGSPFQFTVGPLKDGGAHRVHAGGPGLERGEQMPNEFNWWTREAGAGSLAISVEGSPK  
AEIDFKDRKDGSCYVSYVAEPGEYRVGIKFNDKHIPDSPYKVYITPSLGEARKVELAQL  
PEQGSMPNKAQSLLVCKNGAKGTLDCFKVAPSGAEEDCFDLLDGDLYSVRFVPKEMGIH  
YVHIKFNGIHIPGSPFRLRIGKDEADPAAVSVSGKGLESCVSGQKTDFFIVDTCNAGAGTL  
AVTIDGPSKVSMDCTEVEEGYKVRYPVLPVPGDYIYAVKYNAYHVVGSPWKVKCTGEAHAE  
KGTIQESSVWVETVEKTKSGDKGHGTIIPKFHSDANKVTSKGLGLKKAHINRQNNFTV  
NASGAGNNILYVGVYGPSPCEEVYIKHVGHNNYQVSYKVKERGNHILMVMWGEHPIGS  
PFKLDMF

>QIJ32297.1 Cra a 4; calcium-binding protein, sarcoplasmic calcium-binding protein  
[Crassostrea angulata]

MDYLNKKWKIWNLSLDVNHGDKISIEDVEESRNKFTNLHELVDKAKGVQVNFEDWWNKY  
IFRTGAGKEISESEFVQQLTEAYKKDKVGFIEKEMQACFDCIFDVIDTNKDRIDEDEFVY  
AFKAFGHENEALVRKAFSLYNKENKHVPLKDIVSEWVKFVTEEDTGKKDIIMEAFKEGF

>COMPARE240 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus  
domestica]

MGVFTYESEFTSVIPPARLYNAFVLADADNLIPKIAPQAVKSTEILEGDGGVGTIKKINFG  
EGSTYSYVVKHRIDGLDKDNFVYKYSVIEGDAISETIEKISYETKLVASDSGSIKSTSHY  
HTKGDVEIKEEHVKAGKEKASHLFKLIENYLLEHHDAYN

>COMPARE241 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus  
domestica]

MGVLTYTEYASIIIPPARLYNALVLDADNLIPKIAPQAVKTVEILEGDGGVGTIKKVSFG  
EGSEYNYVKKHVEGIDKDNFVYSYSLIEGDAISDKIEKISYEIKLVASGSGSIKKNISHY  
HTKGDVEIKEEHVKAGKERAHGLFKLIENYLVANPDAYN

>COMPARE242 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus  
domestica]

MGVFTYESEFTSVVPPARLFNAFVLADADNLIPKIAPQAVKSTEILEGDGGVGTIKKINFG  
EGSTYSYVVKHRIDGVDKDNFVYQYSVIEGDAISETIEKISYETKLVASGSGSVIKSISHY  
HTKGDVEIKEEHVKAGKEKASHLFKLIENYLLEHHDAYN

>COMPARE243 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus  
domestica]

MGVTKISQKFVTVQVTPQRMFNALILDHANNICPKLMFSSIKSIEFLSGSGEVGTIKQINFT  
EASPMKYAKHRIDALDKEALSCTYTFIESDATDHLKLEYITYDVKFEGYGRGGCICHL  
TSTYKAKDDIQIKEEDIELGKDRAIGMYEVLEAYLMAHPRAYV

>COMPARE244 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus  
domestica]

MGVFTYETEFAVSCAPARLYNALVLDADNLIPKIAPQAVKTAEILEGDGGVGTIKKISFG  
EGSEYSYVKKHVDGIDKDNFVYNYSLIEGDVISDKIEKISYETKLVASGSGSVIKSTSHY  
HTKGDVEIKEEHVKAGKERAHGLFKLIENYLVANPDAI

>COMPARE245 Mal d 2; thaumatin-like [Malus domestica]

MTMMKSQVASLLGLTLAILFFSGAHAAKITFTNNCPNTVWPGTLTGDQKPQLSLTGFELA  
SKASRSVDAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEIT  
IAANGGQDYDVS�VDGFNLPMSPVAPQGGTGECKPSSCPANVNKVCAPLQVKAADGSVI  
SCKSACLAFGDSKYCCTPPNNTPETCPPTSEYSEIFEKQCPQAYSAYDDKNSTFTCSGGP  
DYVITFCP

>COMPARE246 Mal d 4; profilin [Malus domestica]

MSWQQYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL

APTGLFLGGTKYMVIQGEPEGAVIRGKKKSGGITIKKTSQALLIGIYDEPVTGQCNIIVVE  
RLGDYLIEQGL  
>ALU66112.1 Der f 23; peritrophin [Dermatophagoides farinae]  
MKFNITIAFVSLAILVHSSYADIDHFDNDQNSSTSRPDDPTTMIDVQTTTVQPSSMPT  
TSESESTVKPTTTTTPKSPPTTVKPTTTTTLKLTSTTVKPSPTTVKPTTTTTPKSPPTTTT  
TTEQPEDEFECPTRFGYFADPKDPCKFYICSNWEAIHKSCPGNTRWNEKELTCT  
>AVV30163.1 Ole e 15; cyclophilin/peptidyl-prolyl isomerase [Olea europaea]  
MANPKVFFDMTIGGQPVGRIVMELFADVVPRTSENFALCTGEKGVGKSGKPLHYKGSFAF  
HRVIPNFMCGGDFTAGNGTGGESIYSGKFADENFVKKHTGPGILSMANAGPGTNGSQFF  
ICTAKTEWLDGKHVVFQVVEGFYVVKAIIEQVSGSGKTAKEPVVADCGQLS  
>COMPARE188 enolase, partial [Penaeus monodon]  
AGAAELGIPLYR  
>COMPARE189 enolase, partial [Penaeus monodon]  
AAVPSGASTGVHEALEMR  
>AAD32205.1 Pru ar 5; glutamic acid rich protein, Hev b 5-like [Prunus armeniaca]  
MATVEVAPAATLQENEAKTVEVIKTEEKTPEEPVAAAAPAAVPESEAAATEEPKETTPVEA  
EAEAEAEAPAAPEAETPVPAEVEETKEVAEEPKAAEAEAEPAATETEKTEKTEAEEPKEV  
TAAEPVAAVAEETKEETTESAETPAAPPAEEEAEEATTDVPVEKTEE  
>QD073345.1 Pru du 8; cysteine-rich anti-microbial protein [Prunus dulcis]  
MATMTKAELPLLVFLSTLLLATSVPVRAQVTCEEQCYISDQSKVGECLQMCSSHGQS  
CEDRCMREARWPQQEQCLRMCRQQEQGHHLPCREQCIRSPDREMCERACQQQQGQGGGR  
QCLQRCKMITRDPRERLKCVRTCTQGQQQGVFQGGQQQQVEQQCRQHQCQSERDPMRQQE  
CQEYCVGQMMQQEYEQCRSRQCWERPRREQQEQCECTEKIRQLEQCQEGCKIQGQYG  
PQQQEQRMCREQFEQGGIRMVA  
>AI008849.1 Der f 32; secreted inorganic pyrophosphatase [Dermatophagoides farinae]  
MSTTNYSVDHRGSFNSLDYRIYFKDNSNGKIISPWHDIPFVDKSAKHYNMVEIPRWTN  
EKMEIATAEPMSPKQDIKKGALRYVKNVFPKGYIWNYGAFQPTWENPNHIDQDTKTKG  
DNDPIDVIEIGSRVAKRGDVPVKILGTIALIDEGETDWKIIAIDTRDELASQMNNDVDDV  
EKLLPGLLRATVEWFKIYKIPDGKPAKFAFNGEAKDREFAEKIVEETHQYWQEMMENKS  
GEHKLKLVNLTGNSFSINDEQAKQFLETRPSSDAVEPTPIADQVAIDKWHHVKLI  
>COMPARE0339 Art ab 1; defensin, partial from AHF71021.1 [Artemisia absinthium]  
AGSKLCEKTSKTSWKGKCDNKKCDKCKIEWEKAQHGACHKREAGKESCFCYFDCSK  
>COMPARE0340 Art an 1; defensin, partial from AHF71022.1 [Artemisia annua]  
TWSGKCDNKKCDKCKIEWEKAQHGACHKREAGKESCFCYFDCSK  
>COMPARE0341 Art c 1; defensin, partial from AHF71023.1 [Artemisia californica]  
CDNKKCDKCKIEWEKAQHGACHKREAGKESCFCYFDCSK  
>COMPARE0342 Art f 1; defensin, partial from AHF71024.1 [Artemisia frigida]  
SGKCDNKKCDKCKIEWEK  
>COMPARE0343 Art f 1; defensin, partial from AHF71024.1 [Artemisia frigida]  
EAGKESCFCYFDCSK  
>COMPARE0344 Art t 1; defensin, partial from AHF71026.1 [Artemisia tridentata]  
CDNKKCDKCKIEWEK  
>COMPARE0345 Art t 1; defensin, partial from AHF71026.1 [Artemisia tridentata]  
EAGKESCFCYFDCSK  
>COMPARE0348 Art l 1; defensin, partial from AHF71025.1 [Artemisia ludoviciana]  
SGKCDNKKCDKCKIEWEK  
>COMPARE0349 Art l 1; defensin, partial from AHF71025.1 [Artemisia ludoviciana]  
EAGKESCFCYFDCSK  
>ABG76185.1 Blo t 2; NPC2-like [Blomia tropicalis]  
MFKFICLALLVSYAAAGDVKFTDCAHGEVTSLDLSGCSGDHCTIHKGKSFTLKTFFIANQ

DSEKLEIKISATMNGIEVPVPGVDKDGCKHTTCPLKKGQKYELDYSLIIPTILPNLKTVT  
TASLVGDHGVVACGKVNTEVVD  
>QDH76468.1 Scy p 3; myosin light chain [Scylla paramamosain]  
MAADLSARDVERAKFAFSIYDFEGKGTMDAFYVGDCLRALNLNPTLAVIEKVGKTKKKE  
KMLKVDDFLPIFAQVKKDKDAGSFEDFMEVLKLYDKTENGTMLYAELEHILLSLGERLEK  
SELEPVLKDCCDEEDEDGFIPYEPFLKKLTLQLL  
>COMPARE210 defensin, partial [Buchanania lanzan]  
MAGFCIFFLILFLAQEYGVGEGK  
>COMPARE212 defensin, partial [Buchanania lanzan]  
ECLNLSDKFK  
>COMPARE213 defensin, partial [Buchanania lanzan]  
DIEHLLSGVCR  
>COMPARE182 Tri a 19; omega-5 gliadin, partial from AAT01617.1 [Triticum aestivum]  
HLNPSDQELQSPQQQFLEK  
>COMPARE183 Tri a 19; omega-5 gliadin, partial from AAT01617.1 [Triticum aestivum]  
TNNLATPTTIPPATATTIPPATR  
>COMPARE184 Tri a 19; omega-5 gliadin, partial from AAT01617.1 [Triticum aestivum]  
TNNPATATTIPPAPQQR  
>COMPARE185 Tri a 19; omega-5 gliadin, partial from AAT01617.1 [Triticum aestivum]  
SSQQPQQPFSLQPQQPFS  
>APP94292.1 Scy p 8; triosephosphate isomerase [Scylla paramamosain]  
MANQRKFFVGGNWKMNKDAAIDGIISFMKGPLNADTEVVVGCPCYLYMTREHMPANIG  
VAAQNCYKTAKGAFTGEISPAMIKDCGCEWVILGHSERRNVFGEQDLISEKVGHALEAG  
LKVIPCIGEKLEERESNRTEEVVFAQMKALVPNISDWSRVVIAIYEPVWAIGTGKTATPEQ  
AQDVHAKLRQWLRDNVSPQVAESTRIIYGGSVSAGNCKELAKTGDIDGFLVGGASLKPDP  
VTIINARA  
>QBP14757.1 elongation factor [Dermatophagoides farinae]  
MVNFTVDEIRVLMNKKRNIRNMSVIAHVDHGKSTLTDSLVSAGIIAAAKAGEMRFTDR  
KDEQERCITIKSTAISMYFEMREQDMVFITSADQKESDEKGFILNIDSPGHVDFSSSEVT  
AALRVTDGALVVVDCVSGVCVQTETVLRQAIAERIKPVLFMNKMDLAMLTLQLEQEDLYQ  
KFTRIVENVNVIIISTYADENGPMDIRVDPKSGSVGFGSGLHGWAFLKQFAELYSEKFK  
IDVDKLMNRLWGENFYNPTAKKWSKRFDEGYKRAFCMFVLDPIFKVFDAIMNFKKEETAK  
LLEKLNIVLKGEDKEKDGKNNLLKVMRTWLPAGDSLLQMIATHLPSPITAQKYRMELLYE  
GPHDDEAAVAIKSCNPEGPLMMYISKMVPTSDKGRFYAFGRVFSGIVASGQKVRIMGPNY  
VHGKKEDLVEKAIQRTVLMGGRYVESIENVPCGNICGLVGVQDFLVKGTISTFKDAHNM  
KVMKFSVSPVVRVAVEPKNPADLPKLVEGLKRLAKSDPMVQCIIEESGEHIVAGAGELHL  
EICLKDLEEDHAQIPIKTSDPVVSRETSESEIMCLSKSPNKHNRLEFMKACPLQDGLA  
EDIDKGDINPRDDFKVRARFLADKYNWDATDARKIWAFFGPEGTGPNLLVDVTKGVQYLNE  
IKDSVVAGFQWATKESVLCEENMRGVRFNHDTVTLHADAIHRGGGQIIPARRCLYACLL  
TAQPRLLPEVYLVIEIQCPQAVGGIYGVLNRRRRGHVFEESSQVVGTPMFTVKAYLPVNESF  
GFTADLRNNTGGQAFPCVFDHWQILPGDPLDGKSRPYQIVMDTRKRKGLKDSLPELDNY  
FDKL  
>COMPARE215 Exo m 1; tropomyosin [Exopalaemon modestus]  
MDAIIKKMQAMKLEKDNAMDRALTCEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDSV  
QEALLKANAHLEEKDKALSNAEAGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA  
DESERMKRVLENRSLSEERMDALENLKEARFLAEEADRKYDEVARKLAMVEADLERAE  
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE  
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQTFSELSGY  
>COMPARE0346 vitellogenin, partial from BAM22586.1 [Gadus chalcogrammus]  
KKILNPSVKRSSSSSSSSSSSSAKLFSSSSSSSSSSSSRSSSSSSRSSLNSKSSSSSS

SSSSSSSSRSARSRLSNTVVYP

>COMPARE0347 vitellogenin, partial from BAM22586.1 [Gadus chalcogrammus]  
QVYEAQCSYAKNTLTTFNRRYKNEMLSCNQVLAQDCSKELKFMVLLKKDNIEQNWINV  
KLADIDIDLYPEENDNMIVKVMGMQIPISNLPHYQHTGTIQTIKSNGEGISVYAASHGLHEV  
YFDRSSWKVKLADWMKGTQCGICGKADGEVRQEFRTPNGQLAKDAVSYAHSWVIPAENCQ  
DASECRMREQESVKLEKQIMVHGOESNCHSVETVLRCLPGCIPVKTPVTVGFHCLPISAE  
QQRSGDLSSVLEQSVDLRESVMAHLACNCANLCA

>ALM24136.1 Rhi o 2; cyclophilin/peptidyl-prolyl isomerase [Rhizopus oryzae]  
MSNPKVFFDVSANSKPLGRIVMELRADVVPQTAENFRALCTGEKGFYKGCSEFHRVIPEF  
MLQGGDFTNHNGTGGKSIYGNKFRDENFTLKHGTGPGDLSMANAGPNTNGSQFFITTIKCS  
WLDGKHVVFGFRVTEGMDVWQNIESLGPNGTPRAKIIIDNCGQL

>CAA55009.1 Pru du 6; 11S globulin, cupin [Prunus dulcis]  
MAKAFVFSLCLLLVFNGLAARQSQLSPQNQCQLNQLQAREPDNRIOAEAGQIETWNFNQ  
GDFQCAGVAASRITIQRNLHLPSYSNAPQLIYIVQGRGVLGAVFSGCPETFEESSQSSQ  
QGRQQEQEQERQQQQQGEQGRQQGQQEQQQERQGRQQGRQQQEEGRQQEQQQGQQGRPQQ  
QQQFRQLDRHQKTRRIRREGDVVAIPAGVAYWSYNDGDQELVAVNLFHVSSDHNQLDQNP  
KFYLAGNPENEFNQQQSQPRQQGEQGRPGHQHQPFRGRPRQQEQQGNGNNVFSGFNTQLL  
AQALNVNEETARNLQGQNDNRNQIIQVRGNLDFVQPPRGRQEREHEERQQEQQLQERQQQ  
GEQLMANGLEETFCSLRLKENIGNPERADIFSPRAGRISTLNHNLPIILRFLRLSAERGF  
FYRNGIYSPHWNVAHSVVYVIRGNARVQVWNENGDAILDQEVQQQLFIVPQNHGVIQQ  
AGNQGFYFAFKTEENAFINTLAGRTSFLRALPDEVLANAYQISREQARQLKYNRQETIA  
LSSSQRRRAVV

>COMPARE218 glutelin, partial [Oryza sativa]  
GLLLPHYTNGASLVYIIQGR

>ADG36438.1 Mus a 5; beta-1,3-glucanase [Musa acuminata]  
IGVCYGMGLGNNLPPPSEVVSLSYKSNDIARMRLYDPNQAAALQALRNSNIQVLLDVPRSDVQ  
SLASNPSAAGDWIRRVVAYWPSVSVFRYIAVGNELIPGSDLAQYILPAMRNIYNALSSAG  
LQNQIKVSTAVDTGVLGTSYPPSAGAFSSAAQAYLSPIVQFLASNGAPLLVNVYPYFSYT  
GNPGQISLPYALFTASGVVVQDGRFSYQNLFDIVDAVFAALERVGGANVAVVVSSESWP  
SAGGGAEASTSNAQTYNQNLIRHVGGGTPRRPGKEIEAYIFEMFNENQKAGGIEQNFGLF  
YPNKQPVYQMSF

>AAX93750.1 Cro s 1; Ole e 1-like [Crocus sativus]  
MGKCQAVFLLVGALCVLSLAGVANAENHFVKVQGMVYCDTCRIQFMTRVSTIMEGATVKL  
ECRNITAGTQTFKAEAVTDKVGQYSIPVHGFQDDICEIELVKSPNSECEVSHDVYAKQ  
SAKVSLTSNNGEASDIRSANALGFMRKEPLKECPEVLKELDLYDVKAN

>COMPARE220 Tri a 28; alpha-amylase inhibitor, partial [Triticum aestivum]  
EHGVSEGGAGTGAFPSR

>COMPARE222 alpha-amylase inhibitor, partial from P16347.1 [Triticum aestivum]  
STEWHSIDSELVSGR

>X76395 Ole e 1; Ole e 1-like [Olea europaea]  
EDVPQPPVSQFHIQGGVYCDTCRAGFITELSEFIPGASLRLQCKDKENGDTVTFTEVGYTR  
AEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWVKPSLKFILNTVNGTTRTVNPL  
GFFKKEALPKCAQVYNKLGMYPPNM

>COMPARE225 malate dehydrogenase, partial [Cynodon dactylon]  
TPASGQPERKVAILG

>COMPARE226 Ole e 1-like, partial [Cynodon dactylon]  
FTVTGEVYXDPXRA

>BAA09632.1 calcium-binding protein, polcalcin [Brassica napus]  
MADAEHERIFKKFDTDGDGKISAAELEEALKKLGSVTPDDVTRMMAKIDTDGDGNISFQE  
FTEFASANPGLMKDVAKVF

>BAA09633.1 calcium-binding protein, polcalcin [Brassica napus]  
ADATEKAEHDRIFKKFDANGDGKISASELGDALKNLGSVTHDDIKRMMAEIDTDGDGYIS  
YQEFSDFASANRGLMKDVAKIF

>COMPARE190 7S globulin, vicilin-like, partial [Phoenix sylvestris]  
EAVILPTSPHR

>COMPARE191 7S globulin, vicilin-like, partial [Phoenix sylvestris]  
GPELAAAFGVSEEQLER

>COMPARE192 7S globulin, vicilin-like, partial [Phoenix sylvestris]  
NRPQFLVGASSLLHSMR

>COMPARE193 7S globulin, vicilin-like, partial [Phoenix sylvestris]  
YFPFCQIASNGAPLEFFGFTTTSAR

>COMPARE194 carbonic anhydrase, partial [Phoenix sylvestris]  
TYPFVEEALEK

>COMPARE195 carbonic anhydrase, partial [Phoenix sylvestris]  
YAGVGSATIEYAVHHLK

>COMPARE196 carbonic anhydrase, partial [Phoenix sylvestris]  
VVFDFQPGEAFTVR

>COMPARE197 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]  
MAGASVKPTPLLKDELDIVIPTIR

>COMPARE198 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]  
YDDMWAGWCTK

>COMPARE199 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]  
YFGLMGDGGQPIGR

>COMPARE200 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]  
VPEGFDYELYNR

>COMPARE201 glycerol kinase, partial [Phoenix sylvestris]  
GSLDKGTTSTR

>COMPARE202 isoflavon reductase-like protein, phenylcoumaran benzylic ether  
reductase, partial [Phoenix sylvestris]  
PSEFGNDVDR

>COMPARE203 isoflavon reductase-like protein, phenylcoumaran benzylic ether  
reductase, partial [Phoenix sylvestris]  
YTTVDEYLNLR

>COMPARE204 S-adenosylmethionine synthase 1-like, partial [Phoenix sylvestris]  
FVIGGPHGDAGLTGR

>COMPARE205 S-adenosylmethionine synthase 1-like, partial [Phoenix sylvestris]  
TLFHLNPSGR

>COMPARE206 S-adenosylmethionine synthase 1-like, partial [Phoenix sylvestris]  
YKNEGGAMVPLR

>COMPARE207 beta-galactosidase, partial [Phoenix sylvestris]  
EIQNAGLYAILR

>COMPARE208 beta-galactosidase, partial [Phoenix sylvestris]  
WLLLFEEAKTRR

>COMPARE186 Sec c 20; gamma secalin, partial [Secale cereale]  
NMQVGPSGQVEWPQQQPLPQQQ

>COMPARE187 Hor v 20; gamma-hordein-3, partial [Hordeum vulgare]  
ITTTTTFNPSGLELERPQQQLFPQW

>COMPARE00247 NPC2-like, partial from XP\_003987882.1 [Felis catus]  
EPVIFKDCGSGFGVIKELNVSPCPTQPCKLHKGQSYSVNVTFSTNVSSQGSKALVYGILM  
GVAVPFPIPEADGCKSGINCPIQQGKTYSYLNKLPVKNEYPSIKVMVKWQLLDGKEQNLF

CWEIPVQIEG

>A0A484HRI4 Cav p 1; lipocalin [*Cavia porcellus*]  
MVQILLLALAVGLSCVESSQISGDWDTIALSADNKEKIEEGPLRVYFRQIDCNADCSEI  
TFRLYVKLNGECKESTVVASQSLGGLYTVQFAGQNTFVIVDKQEDTITFFNTNVDEGLV  
TRGYVVVVGKRDSLTPREETLSFEEANEVKGIPQENIEYLAGTDDCPE

>ABU97467.1 apolipoprotein [Blomia tropicalis]  
MSAVGTANSHEHLAQLEVTPKDPAPKEVKLLKSPENSFETKFALNLDASRNLDIKLNLP  
HLIDIHLKNQFEKDKETNLMKNDMVLEYKFPNDET VHTLKTTHHELGYNLKRNGKDKVANF  
DFKSKFESSRRPFLNHRSLVQFKYRKYKLQELVLEFGYGEKMDNVYKFSRISKIDVQEFK  
PFKMNSETDLNIVATDFDVYIEKADNRVLNDRGNALFDMNLKGGKDRSKRAAENGNQEI  
EGKIKYRNKGSVDSKLEASLKGVGHDFAWNSELKQVEPQKYEGKITIQTEDKKIFITH  
KEEISKPTKEIHFKSEADISYSYKPKKTYVMEAKKQGTAYILKGEAKKDGTVIFSNIN  
FESSNGNLKALIKRDRSYDLNVDNVFRPREATLLFKIKDREYNIKMDREPFKYINLKVD  
GNENALIKNGKAHLSIMDPTTLNLVTKANSNVDFSMDLFAIRHQIALKIDSPKYNFFHD  
GDIDLSIVNRRLLWKSLTKKDDREYKFNADIARKGSMISLTKVTPDRTSSVQYSRNGEKI  
EVNIDTEYLEGKVEGDRFSGKIVLKNKQNDYELESTYKRENGRLVIESVNGKNAKMEAVF  
SRKEPSKFVLETPNTKAKIDMDLTAPVKTFKLDNPRYQKKIDASMEPESKFYSSYSN  
QKNEKKERKIEIDGVHMKELNVDIDFPDFKFKVKQPESSKKVEFSYTFNNYTETEEYDFD  
PHKAYLVNWNALRQYVQTFVVQN

>AAQ24549.1 chitinase [Blomia tropicalis]  
MTKLCLVALATLATIAALVPVNHATKDPKTVCYYESWVHWRHGDGKMEPNEIDTSLCTHI  
VYTYFGIDAITHLKWLDPYLMKDLHDIEKFVQAKGKAKAMIAIGGASMSDQFSITAGNE  
QYRDIFARSVVNFLAQYHFDGIMIDWYGVQERDSENLIHLLDKFDEKFASTTYSMGITLP  
ATVATLDHYNVPKITVYVDFINVLTLDYAGPWGKVVNDASPLPEQLKTMEEYHHRGAPRS  
KLVMAVPMYARTWRLASPLHQDLGDAAISGGTKGPTYDTEGILSYNELCVRIKGSNSFN  
IVRDVANTAVHAVYHLHGNEAEFYSFEDTKTLAAKAHVTTMGYGGLSIFTLNEDSHGTC  
GKKYPLLHSIVENYNHDPIDEVPITTIPTTPHPTVVDIPGVFKCHSVGKFRDHEYCF  
KYYDCVMGDFGLESTVMYCERHQAFDEKTYKVEASQIPGC

>D2T2K2 Tri a 14; lipid transfer protein [*Triticum aestivum*]  
ISCSQVDSTLMPCLQYVQGGSPARGCCTGIQNLLEANNSPDRRTICGCLKNVANGASG  
GPYITRAAALPSKCNVALPYKISPSVDCNTVH

>AHX03180 Der f 4; alpha-amylase [*Dermatophagoides farinae*]  
MLPKFFFILITVLTLLVSLFVNGDSKFSNPHFIGNRSVITHLMEWKYDDIGDECERFLGP  
YGYGGVQVSPVNEHAIMDGRPWYERYQPVSYDIHTRSGDEQQFRRMVQRCNKAGVRIYVD  
IVLNHMTGGQSGLGTNGHHYDGVAMQYPGVFPFNDFHGHECTPTNDLEIHNYSNRIEAR  
NCRLVGLRDLKQSEYVKQKQVDFLNHLIDIGVAGFRSDASTHQWPDLLRSIYSRLHNLN  
NEFFTENSHPFYHETIYYGGNGINSNEYTSLGRIIEFRFYKEITNVFRNNQLRWLRF  
GTEWGLVPSGDALVMIDSHDLRVGHTGQLGFNINCFEARLLKAATAFMLAWNYGIPRVM  
SYFWDQIIRDGKVDNDWVGPPTDQHGNILSVHPNPDMTCNHEWICEHRWREIYNMVKFKL  
IAGQEPVNNWWDNGDNQIAFSRGNRAFIAINLQKNGNDHDKNLQKRLQTGLPPGIYCDII  
SGNLINNRRCMGKSIQVDKNGLSDIYVGHDEFDAFVAYHIDARVES

>NP\_001103782.1 Bomb m 3; tropomyosin [*Bombyx mori*]  
MDAIIKKKMQAMKLEKDNALDRAAMCEQQAKDANLRAEKAEFEARQLQKKIQTIENELDQT  
QESLMQVNGKLEEKALQNAESEVAALNRRIQLLLEEDLERSEERLATATAKLSEASQAA  
DESERARKVLENRSLADEERMDALENQLKEARFLAEAEADKKYDEVARKLAMVEADLERAE  
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREEEYKNQIKTLTTRLKEAEARAE  
FAERSVQKLQKEVDREDELVAEKEKYKDIGDDLDTAFVELILKE

>AAU21501.1 Ara h 15; oleosin [*Arachis hypogaea*]  
MSDQTRTGYGGGSSYSSYGGGGTYGSSYGTSDPSTNQPIRQAIKFMFASTIGVSFLIL  
SGLILTGTVIIGLIIATPLLIVFSPILVPAAITLALAAGGFLFSGGCGVAAIAALSWLYSY

VTGKHPAGSDRLDYAKGVIADKARDVKDRAKDYAGAGRAQEGTPGY  
>QCY53440.1 Cten i 1; calcium-binding protein, parvalbumin [Ctenopharyngodon idella]  
MAFAGILNDADIAAALEACKAADSFNHKAFFAKVGLSAKSGDDVKKAFAIIDQDKSGFIE  
EDELKLFQNFKADARALTAETKIFLKGSDSDGDGKIGVDEFAALVKA  
>XP\_019446786.1 Lup an 3; lipid transfer protein [Lupinus angustifolius]  
MAGIVKLACAVLICMVVVSAPLTKAITCGQVTANLAQCLNYLRSGGAVPAPCCNGIKNIL  
NLAKTTPDRRTACNCLKAAAANTPGLNPSNAGSLPGKCGVNIPYKISTSTNCASIK  
>COMPARE00280 Lup a 5; profilin [Lupinus albus]  
SWQTYVDEHLLCDIEGNQLTSAAIIGQDGSVWAQSSSFPQFKPEEITAIVNDFAEPGSLA  
PTGLYLGGTKYMVIIQGEPEGAVIRGKKGPGGVTVKKTNQALIIGIYDEPMTPGQCNVVVER  
LGDYLIDTGL  
>AFN42528.1 Can s 5; pathogenesis related protein, PR-10, Bet v 1-like [Cannabis sativa]  
MGVFTYESEFTSSIIAPARLFKAFVLDGDNLVPKIAPQAVEKVEILEGNGGVGTIKKITFG  
QGVVPFKYVKHKIEAIDKESLTYSYSIIEGDALEGNQLEKITHESKLVASGDGGNVIKTVS  
KYYSAGDAQVNEEKVKEGEKQATQMLKTVEAYLKDHPPEAYN  
>P84527.2 Act d 5; kiwellin [Actinidia deliciosa]  
MAQLALLLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGLICIKGKCNDPQVGTHTIC  
RGTTTSPQPGGCKPSGTLTCRGSYPTYDCSPPVTSSTPAKLTNNDFSEGGDDGGPSECD  
ESYHNNNERIVALSTGWYNGGSRGKMIRITASNGKSVSAKVVDECDSRHGCDKEHAGQP  
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA  
>P62927 2S albumin, conglutin [Pisum sativum]  
MASVKLASLMVLFATLGMFLTKNVGAASCNGVCSPFEMPPCGSSACRCIPVGLVVGYCRH  
PSGVFLRTNDEHPNLCESDADCRKKGSGNFCGHYPNPDIIEYGCWCFASKSEAEDFFSKITQ  
KDLLKSVSTA  
>GFG40850.1 arginine kinase [Coptotermes formosanus]  
MVDQAVLKDLEAGYAKLAASDSKSLKFLTKFVDFNLKTKKTPSFGSSLLDVIQSGLEN  
HDSGVGIYAPDAEAYSVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI  
ISTRVRCGRSLEGYPFNPLTEAQYKEMEEKVSSTLSGLEGELKGFYPLTGMTKEVQQK  
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDAKTFLVWCNEEDHLRIISMQMGDLG  
QVYRRLVTAVNDIEKRIPFSDHDDLGLFTFCPTNLGTTVRASVHIKVPKLAADRALLEEV  
AGKYNLQVRGRTRGEHTEAEGGVYDISNKRMMGLTEYEAVKEMHDGIAELIKLESSL  
>QOL11118.1 pectin methylesterase [Humulus japonicus]  
SVTAAKDGTDGDFRTINDALAAIPTKYEGRYVIYVKEGLYEETVTVTKKMANVTMYGDGSQ  
KSIITGSKNFVDGVRTFQTATFVVLGGGFMGKAMGFGNTAGPEKHQVAARVQADRAIFA  
NCRFEGYQDTLYTQTHRQFYRSCVWAGTIDFIFGDAAVVFQNCMLVVRLPMANQKNIVTA  
RGRVDKQQTGIVIHNCRIMADKLEPEKARVKSFLGRPWKEYSRTIIMESTIEDLIHPD  
GWLPEGEFALKTLTYAAYNNKGPAGKVTTRVNWPGYSVINKKEAEKFTVENFLQNDWL  
NIKGIPVRYTLILRANRSEVQ  
>ABM53752.1 fatty acid-binding protein [Tyrophagus putrescentiae]  
MANKLLLALALVLAATTSVLAEDIDFSGRYKMTVADTSNYKDLLYELGIGYFKRLAAGA  
SGSEYVITRNKEAGTYTLQTVTTFSTAATVFKSGEEFDEPRADGQTVKSTIVIAGNKWTH  
VQKGSPTVTIERTFQGGNPPTYIDVITKCAVVPVTRKYERQ  
>A0A161X1M2 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]  
MGVQKTEAEVTSSVSAEKLKALCLDIDTLLPQVLPGAIKSSETLEGDGGVGTVKLVHLG  
DASPFKTMKQKQVDAIDKESFTYAYSIIIDGILLGFIESINNHFAYVNPADGGCTVKSTIT  
FNTKGDVAVPEENIKFANDQNRAIFQAVEAYLIAN  
>COMPARE00248 peroxidase-1, partial from ADJ67792.1 [Triticum aestivum]

GAVVSCADILALAAR  
>COMPARE00249 peroxidase-1, partial from ADJ67792.1 [Triticum aestivum]  
LFPRPDPTINPPFLAR  
>COMPARE00250 peroxidase-1, partial from ADJ67792.1 [Triticum aestivum]  
DIGLAAGLLR  
>COMPARE00251 peroxidase-1, partial from ADJ67792.1 [Triticum aestivum]  
TPNVFDNQYYVDLVNR  
>COMPARE00252 peroxidase-1, partial from ADJ67792.1 [Triticum aestivum]  
DFFEQFGVSMGK  
>COMPARE00253 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
IVGAFADYAEFCFK  
>COMPARE00254 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
TEPYIVTHNIILSHAAVQR  
>COMPARE00255 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
VVGYFAWSLLDNFEWR  
>COMPARE00256 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
DFHIGWFLDPITNGR  
>COMPARE00257 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
IGILLDFVWYEPHSNSNADQGAAQR  
>COMPARE00258 beta-glucosidase 4, partial from AEV76986.1 [Triticum aestivum]  
FGIAYVDFNTLK  
>COMPARE00259 luminal-binding protein 5, partial [Delonix regia]  
RVEIESLFDGIDFSEPLTRA  
>COMPARE00260 luminal-binding protein 5, partial [Delonix regia]  
KFDLSGIPPAPRG  
>COMPARE00261 ATP synthase beta subunit, partial [Delonix regia]  
KVVDLLAPYQRG  
>COMPARE00262 ATP synthase beta subunit, partial [Delonix regia]  
RVLNTGSPITVPVGRA  
>COMPARE00263 ATP synthase beta subunit, partial [Delonix regia]  
RIPSAVGYQPTLATDLGGLQERI  
>COMPARE00264 ATP synthase beta subunit, partial [Delonix regia]  
RVGLTGLTVAEHFRD  
>COMPARE00265 actin, partial [Delonix regia]  
RAVFPSIVGRPRH  
>COMPARE00266 actin, partial [Delonix regia]  
KSYELPDGQVITIGAERF  
>COMPARE00267 actin, partial [Delonix regia]  
KDLYGNIVLSGGSTMFGIADRM  
>COMPARE00268 actin, partial [Delonix regia]  
RTTGIVLDSGDGVSHTVPIYEGYALPHAILRL  
>COMPARE00269 actin, partial [Delonix regia]  
KAEYDESGPSIVHRK  
>COMPARE00271 ADP, ATP carrier protein 1, partial [Delonix regia]  
RLADDDEFMVPSVFNSRF  
>COMPARE00272 ADP, ATP carrier protein 1, partial [Delonix regia]  
KGNFLIDFLMGGVSAAVSKT  
>COMPARE00273 S-adenosylmethionine synthase 1-like, partial [Delonix regia]  
RFVIGGPHGDAGLTGRK  
>COMPARE00274 S-adenosylmethionine synthase 1-like, partial [Delonix regia]

KTAAYGHFGRDDPDFTWETVKL  
 >COMPARE00275 S-adenosylmethionine synthase 1-like, partial [Delonix regia]  
 KTCPWLRPDGKT  
 >COMPARE00276 unknown function, partial [Delonix regia]  
 REGEGEGVAAAGVGVRR  
 >COMPARE00277 UDP-arabinopyranose mutase, partial [Delonix regia]  
 KTINVPDGFYELYNRN  
 >COMPARE00278 UDP-arabinopyranose mutase, partial [Delonix regia]  
 MSKPATPVAPPLKDELDIVIPTIRN  
 >COMPARE00279 UDP-arabinopyranose mutase, partial [Delonix regia]  
 KASNPFVNLRK  
 >S0BDX9 Cav p 6; lipocalin [Cavia porcellus]  
 MKLQLLCLGLILLCTQGEGDEVVRGNFDAEKISGNWYTVKEASDKRETIIEGGSMRVFVE  
 SIEPVKDSALSFKFWAHENGECKQISLICNRVAEGVYAVEYDGYNVFRVAETDYKNYAIF  
 QLRNFKAEGSFQLELYGREPDVSGEIKTRFEDFCHKNGIGEGNIIDMTTVDRCLQARGE  
 K  
 >C0HLQ1 Cry j 7; gibberellin-regulated protein [Cryptomeria japonica]  
 AHIDCDKECNRRCSKASAHDRCLKYCGICCEKCNCVPPGTYGNEDSCPCYANLKNKSKGGH  
 KCP  
 >C0HLQ0 Jun a 7; gibberellin-regulated protein [Juniperus ashei]  
 AQIDCDKECNRRCSKASAHDRCLKYCGICCKKCHCVPPGTAGNEDVCPCYANLKNKSKGGH  
 KCP  
 >QID21357.1 Pop n 2; profilin [Populus nigra]  
 MSWQVYVDDHLMCDIEGNTLTSAAIIGHDGSVWALSASFQFTQEVSAIMKDFEEPGSL  
 APTGLFLGGTKYMIQGEPAVIRGKKKSGGVTVKKTNQALIIGVYDEPLTPGQCNMIVE  
 RLG DY LIDQGL  
 >QGS84240.1 Que i 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus  
 ilex]  
 MGVSTHESQETSVIPPARLFKAFVLDSNLI PKVLPQAIKSIERIEGNGGPGTIKKITFG  
 EASKFKYSKHRIDALDPENCTYSFSVIEGDALDMVSVSTEIKFVASPDGGSIKKSTTKY  
 QTKGDFQLKEEQIQTIEKITGLSKAVEAYLLAHPDLTY  
 >ABM53753 Tyr p 1; cysteine protease [Tyrophagus putrescentiae]  
 MALLFYILFLFFTFIQRHLEKVPWEQYKVKFGKNYLTINEENFRKNNYFNSLTKIVKN  
 NGKNGVTLGLNDMSDWSDEEFFSLNSKSPSSVFVSARPTSTVNTSPFPKSWDWRNIIAFN  
 SIEQQGRCSWCWAAATTVEAAYAHQKNKHNHLHSRQELVDCTNRTFDQHLYLNYGCKGG  
 WPTEAYKYIMDHGVYEDKLYHYTETFNEVCYADKVAHDKGHPVKYIISNYGRLAYNDTDE  
 AIMAMLVTYGPVTDIHGTSDFRFYKGGIMRNVMPSAYTNHIVVVVGYGTDSSSGVDYW  
 IIRNSWGKTWGEHGYRLEHHPNLLGFNKNYNYPII  
 >ABM53750 Tyr p 7; bactericidal permeability-increasing like [Tyrophagus  
 putrescentiae]  
 MKSAVLVLVACFAGIADVADNGNANQFVDQIVTALKTQKNFDPLVIPPHEMNIDRKIGAIH  
 LKGTADLKETKITGLSHVRRVGDALLKNENGSTAKLHLGDDNVKLFSDISLHFLHNIIH  
 PNLKVEIDIGNIGVGFVTIGADGPKALKDFDIEEFKHVKIHVHGLGPLDHLVDLIGEAY  
 ISLANTQARHMITGIVRPILDQELKNFKMGGF  
 >QOI58528.1 Tyr p 20; arginine kinase [Tyrophagus putrescentiae]  
 MVDQATLDKLEAGFKKLQSSGDACHSLLKLYLTEDVFNKLDKKTGMGATLLDVIQSGVE  
 NLD SGVGLYAPDAEAYTLFADLFNPVIEGYHGGFKSTDKHPPSDFGDINQLVNVDPNNEF  
 VISTRVRCGRSLQGYFPNCLTEAQYKEME EKVKAQLESFEGELKGTYYPLTGMDKATQQ  
 QLIDDHFLFKEGDRFLQAANACRFWPTGRGIFHNASKTFMWWNEEDHLRIISMQKGGDL  
 KEVFGRLVKAHQHIEKKIPFSRDDRLGFLTFCPTNLGTTIRASVHIKLPKLAADRKKLEE

VAAKYNLQVRGTAGEHTESVGGVYDISNKRRMGLTEYQAVKEMQDGILELIKIEKSL  
>AII81930 Bla g 12; chitinase [Blattella germanica]  
MKTSQILFLCGVWFLSVLVSTSGDKPSRVVCYFSNWA VYRPGLSYKIEDIPTDLCTHLI  
YSFIGVSNVTWGPLILDQENDVDLRGFLNFTDLKAKGVKTSVAMGGWEGGRKYSHLVSD  
KKLRDTFIPALVEFLHKYNFDGLDIDWEYPGASDRGGSYGDRQNFYFVEELRRAFDKEG  
KGWEITMAVPLANFRLNEGYPDLCELIDAVHVMAYDLRGNWAGFADVHSPLYQRPNEG  
YGYQALNDNDGMQLWVDKGCSPDKLVLGTPFYGRFTLSQGNTNKDIGTYINKDAGGGDA  
GPYTGAKGMLAYYEICNMLQVNASKWTQKFDDIGKCPYAYDDGNQWVGYDNEISLQYKMD  
FIKEKGYLGAMTWAIDMDDFHGTGCGKQNLINVLAKNMKDYVPTLQISTTPRPEWDRPK  
STTFEGGSVTTSTTTTTTMMKTTIPETTTTGTSTIDPTITTPSFPPSETTTDATTGGPT  
VTPSCANANFYPAANCNQYYMCNQGTPIMLTCSPTVWVQEGIRCDWPAASTRAECSA  
>C0HLQ2 Cup s 7; gibberellin-regulated protein, cypmaclein [Cupressus sempervirens]  
AQIDCDKECNRRCSKASAHDRCLKYCGICCEKCHCVPPGTAGNEDVCPCYANLKNKSGGH  
KCP  
>COMPARE00338 Ara h 14; oleosin, partial from Q9AXI1.1, Q9AXI0.1, Q6J1J8.1 [Arachis hypogaea]  
ATATDRAPHQVQVHTPTTQR  
>COMPARE00281 Ara h 14; oleosin, partial from Q9AXI1.1, Q9AXI0.1, Q6J1J8.1 [Arachis hypogaea]  
MADMADYVVGK  
>COMPARE00282 Cuc ma 5; 2S albumin, conglutin, partial from Q39649.1 [Cucurbita maxima]  
PWRREGGSFD  
>XP\_030492464 Can s 2; profilin [Cannabis sativa]  
MSWQTYVDEHLMCDIDGQGHATAAAIIGHDGSIWAQSSSFPQLKAQEITDITKDFEEPG  
HLAPTGLHLSGTYKMYIQGEPGAVIRGKKGSGGVTIKKTGQALIFGIYEEPVTPGQCNMV  
VERLGDYLVQGL  
>COMPARE00283 Act d 3; unknown function, partial from P85063.3 [Actinidia deliciosa]  
FTDGLMKNGNFELAP  
>COMPARE00284 Ara h 14; oleosin, partial from Q9AXI1.1, Q6J1J8.1 [Arachis hypogaea]  
RGYDVSGGGIKTLLPER  
>COMPARE00285 Ara h 14; oleosin, partial from Q9AXI0.1 [Arachis hypogaea]  
RGYDVSGGGVKTFLPDR  
>COMPARE00286 Ara h 14; oleosin, partial from Q9AXI1.1, Q6J1J8.1 [Arachis hypogaea]  
QVHGTTVPDQLDSVK  
>COMPARE00287 Ara h 14; oleosin, partial from Q9AXI0.1 [Arachis hypogaea]  
QVHGTTVPDQLDSAK  
>COMPARE00288 Gal d 9; beta-enolase, partial [Gallus gallus]  
REILDSRGNPTVEVDLHTAKGHFRAAVPSGASTGIHEALELRDGDKKRF  
>COMPARE00289 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]  
KAVEHINKTIGPALIEKKISVVEQEKIDKVMIEMDGTENKSKFGANAILGVSLAVCKA  
>COMPARE00290 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]  
KAGAAEKGVPLYRHIADLAGNTEILIPVPAFNVINGGSHAGNKLAMQEFMVLVPGAASFH  
DAMRVGAEVYHSLKGVKA  
>COMPARE00291 Gal d 9; beta-enolase, partial [Gallus gallus]  
KAAIAQAGYTDKVVIGMDVAASEFCRDGRYDLDFKS  
>COMPARE00292 Gal d 9; beta-enolase, partial [Gallus gallus]  
KRIITGEQLGEIYRGIKDYVVSIEDPFDQDDWEAWKRF  
>COMPARE00293 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]

KVNQIGSVTESIQACKLAQSHGWGMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSE  
RL  
>COMPARE00294 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]  
RIEEALGDKAKF  
>COMPARE00295 Gal d 10; aldolase, partial [Gallus gallus]  
PHQYPALTPEQKKELHDIAKRIVAPGKGILAADESTGSIKRLSSVGAENTEENRRW  
>COMPARE00296 Gal d 10; aldolase, partial [Gallus gallus]  
RVDPCIGGVILFHETLYQKADDGRPFQVIKS  
>COMPARE00297 Gal d 10; aldolase, partial [Gallus gallus]  
KVDKGVVPLAGTNGETTTQGLDGLMERC  
>COMPARE00298 Gal d 10; aldolase, partial [Gallus gallus]  
KKDGADFAKWRVCLKISEHTPTRLAIMENANVLARYASICQONGIVPIVEPEILPDGDHD  
LKH  
>COMPARE00299 Gal d 10; aldolase, partial [Gallus gallus]  
KKYSPEEIAMATVTALRRT  
>COMPARE00300 Gal d 10; aldolase, partial [Gallus gallus]  
RALQASALRAWAGKK  
>COMPARE00301 Gal d 10; aldolase, partial [Gallus gallus]  
KAAQEYVKRA  
>COMPARE00302 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
LVPEQISFILSTR  
>COMPARE00303 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
NGVFLTLDSLKKGILNK  
>COMPARE00304 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
ALLEKNDCMVISIDWRNGACTNEFQILKFIGYPKAVENTR  
>COMPARE00305 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
YIADFSKLLMQK  
>COMPARE00306 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
LIGHSLGAQIAGFAGK  
>COMPARE00307 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
LGKYPEIIGLDPAGPLFK  
>COMPARE00308 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
ICETDAHVVQIIHTSNLGTERR  
>COMPARE00309 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
AVQYFTECIRHECCLIGVPQSK  
>COMPARE00310 Vesp v 1; phospholipase A1, partial from C0HLL3.1 [Vespa velutina]  
CTRNECVCVGLNAKRYPKTGSFYVPVESKAPYCNK  
>COMPARE00311 Vesp v 5; unknown function, antigen 5, partial from P0DMB9.2 [Vespa  
velutina]  
SGIHTLCKYGTSTKPNCGR  
>COMPARE00312 Vesp v 5; unknown function, antigen 5, partial from P0DMB9.2 [Vespa  
velutina]  
AEKLEILKQHNEFR  
>COMPARE00313 Vesp v 5; unknown function, antigen 5, partial from P0DMB9.2 [Vespa  
velutina]  
GLETRGNPQPAPAKSMNTLVWDELAQIAQVWASQCK  
>COMPARE00314 Vesp v 5; unknown function, antigen 5, partial from P0DMB9.2 [Vespa  
velutina]  
NTAKYLVGQNIAEQSTTAASFEPVSNMVKMWSDEVKDYQYGSSKNKLNDVGHYTMVWAK  
TKEIGCGNIKYIENGWHHHYLVCNYGPAGNIGNEPIYEKK

>COMPARE00315 Rap v 2; paramyosin, partial [Rapana venosa]  
ITELEDSCEQLR

>COMPARE00316 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]  
QLENENAGLQR

>COMPARE00317 Rap v 2; paramyosin, partial [Rapana venosa]  
VANAELTERNDNLQR

>COMPARE00318 Rap v 2; paramyosin, partial [Rapana venosa]  
DTEDALRDAAEAKLANAQAALNQLR

>COMPARE00319 Rap v 2; paramyosin, partial [Rapana venosa]  
LREKDEEIEIENIRR

>COMPARE00320 Rap v 2; paramyosin, partial [Rapana venosa]  
ELEGALDNANRANAELYLKQIK

>COMPARE00321 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]  
LADELRLQEQENYK

>COMPARE00322 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]  
VRDLEAELENEAR

>COMPARE00323 Pru du 10; mandelonitrile lyase 2, partial from Q945K2.1 [Prunus dulcis]  
GSLPTAYPNVLTADGFVYNLQQEDDGKTPVERFVSEDGIDNVRGRVLGGTSIINAGVYAR

>COMPARE00324 Pru du 10; mandelonitrile lyase 2, partial from Q945K2.1 [Prunus dulcis]  
KTAFLEAGVHPNHGFSLDHEEGTRITGSTFDNKGTRHAADELLNKGNSNLRVGVHASVE  
KIIIFSNA PGLTATGVIYRDSNGTPHQAFVR

>COMPARE00325 Pru du 10; mandelonitrile lyase 2, partial [Prunus dulcis]  
DFYQCSFSSLPFTTPPFQFFSASYPNPFSTFAHFASKVAGPLSYGSLTLKSSSNVRSVSP  
NVKFNYYSNLTDLSHCVSGMKKIGELSTDALKPYKVEDLPGVEGFNIIIGIPLPKDQTDDA  
AFETFCRESVASYWHYHGGCLVGKVLGDGFRVTGINALRVVDGSTFPYTPASHPQGFYLM  
LGRYVGIKILQER

>COMPARE00326 Pru du 8; cysteine-rich anti-microbial protein, partial from PQQ11123.1 [Prunus dulcis]  
AQVTCEEGCYSLSDQSKVGECLQMCSSHGQSCEDR

>COMPARE00328 Pru du 8; cysteine-rich anti-microbial protein, partial from PQQ11123.1 [Prunus dulcis]  
RCMQVEQQGVFQGGQQQQQQQVEQQCRQHCQSERDPMRQQEQEDCVGQMMQQEYEQQCR

>COMPARE00329 Pru du 8; cysteine-rich anti-microbial protein, partial from PQQ11123.1 [Prunus dulcis]  
REQQEQCQEECTEKIRQLEQCQEGCKMQGQYGPQQQECQR

>COMPARE00330 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1 [Cucurbita maxima]  
GLLLPGFSNAPK

>COMPARE00331 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1 [Cucurbita maxima]  
GIAIPGCAETYQTDLR

>COMPARE00332 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1 [Cucurbita maxima]  
EGDLLVVPAGVSHWMYNRGQSDLVLIVFADTRNVANQIDPYLRKFYLAGRPEQVER

>COMPARE00333 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1 [Cucurbita maxima]  
SGNIFSGFADEFLEEAQIDGGLVR

>COMPARE00334 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1

[Cucurbita maxima]  
IVQVDEDFEVLLPEKDEEER  
>COMPARE00335 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1  
[Cucurbita maxima]  
GRYIESESESENGLEETICTLR  
>COMPARE00336 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1  
[Cucurbita maxima]  
GVLYSNAMVAPHYTVNSHSVMYATRGNARVQVVDNFGQSVFDGEVR  
>COMPARE00337 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1  
[Cucurbita maxima]  
MLPLGVLSNMYR  
>COMPARE00426 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
APGKMLVVLPAAGVAHWCLNDGK  
>COMPARE00427 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
EDLVAVSVNNLNNQANQLNQK  
>COMPARE00429 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
LCHGSWSNTYQNLSPFNQNLADALNVDVETVR  
>COMPARE00430 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
LDGGPQLHAGPHWLMNAHSLFYLTR  
>COMPARE00431 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
LKDANVFVPR  
>COMPARE00432 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]  
MGPAQVLAQSYKSFAGEAQNLIK  
>ADK66280.1 Lit v 13; fatty acid-binding protein [Litopanaeus vanna (Penaeus vanna)]  
MAKIEGKFKMESSENFDEFMKALGVGLVLRKMGNAATPTVEITKDGDTYTMKTTTTFKTT  
EIKFKLGEFEETTADGRVVKSTITLDGNKLVHKQVGDKEKKEKDSSELLREFTDCKMLME  
CKVDDVCKRVYSRLE  
>NP\_001037486.1 Bomb m 4; unknown function [Bombyx mori]  
MRLTLFAFVLAVCALASNATLAPRTDDVLAELQLYMSVVIGEYETAIKACSEYLKEKKGEV  
IKEAVKRLIENGKRNTMDFAYQLWTKDGKEIVKSYFPIQFRVIFTEQTVKLINKRDHHL  
KLIDQQNHNKIAFGDSKDKTSKVKSWKFTPVLENNRVYFKIMSTEDKQYLKLDNTKGSSD  
DRIIYGDSTADTFKHHWYLEPSMYESDVMFFVYNREYNSVMTLDEDMANEDREALGHSG  
EVSGYPQLFAWYIVPY  
>AVQ67919.1 Per a 13; glyceraldehyde-3-phosphate-dehydrogenase [Periplaneta americana]  
MSKIGINGFGRIGRLVLAALAEKGAQVVAINDPFIGLDYVMVMFKYDSTHGRFKGEVSAE  
GDQLVVNGQKISVFAERDPKAIIPWGKAGADYVVESTGVFTTIDKASAHLEGGAKKVIISA  
PSADAPMFVVGVNLEAYDPSLKIVSNASCTTNCLAPLAKVIHDNFEIVEGLMTTVHAVTA  
TQKTVDGSPGKLRDGRGADQNIIPASTGAAKAVGKVIPALNGKLTGMAFRVPPVNSVV  
DLTVRLGKPASYDDIKAKVKEAATGPLKGILDYTEDDVVSSDFISDTHSSIFDAKAGIPL  
NNNFVKLISWYDNEFGYSNRVIDLIKYMOSKD  
>COMPARE00503 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
LLYHVQQPTLVKEEQEIAK  
>COMPARE00504 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
VELFWKYYVDVGFPLK  
>COMPARE00505 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
DFETFYKTAVWAR  
>COMPARE00506 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
DVTLPAPYEVYPQLFVNAEVIQQAYDAYLR

>COMPARE00507 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
AVDYNHPVVLVGYYPELR

>COMPARE00508 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
EAPARPEGIFARNVDILYVEEIR

>COMPARE00509 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
DGIDYGYLAGYNYEK

>COMPARE00510 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
NLISLFGHIVDPVHRYGVPASVLEQPETQLRDPLFYR

>COMPARE00511 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
SSNDFPFYAKEAPSWYDLYK

>COMPARE00512 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
SGLPLSVFTIVTQASPDANKPILEHGDHLHAAGFPFDR

>COMPARE00513 hexamerin, partial from ACU78069.1 [Locusta migratoria]  
VVEFEFDVPAHFDETFVHRRVEDLNATA

>AWS00995.1 Cyp c 2; beta-enolase [Cyprinus carpio]  
MSISKIHAREILDSRGNPTVEVDLYTAKGRFRAAVPSGASTGVHEALELRDGDKTRYLGK  
GTQKAVDHVNIKIAPKLEKFKSVVEQEKIDKFMLELDGTENKSKFGANAILGVSLAVCK  
AGAAEKGVPLRYHIADLAGNKDVLVPAFNVINGGSHAGNKLAMQEFMILPVGAKNFHE  
AMRIGAEVYHNLKNVIKAKYKDATNVGDEGGFAPNILENNEALELLKSAIEKAGYDPKI  
IIGMDVAASEFFKNGKYDLDFKSPDDPKRHITGDQLGDLYKSFIGNYPVQSIEDPFDQDD  
WENWSKFTGSDVIQVVGDDLTVTNPKRIQQACEKKACNCLLLKVNQIGSVTESIQACKLA  
QSNWGWVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEEELGDK  
AKFAGKDFRHPKL

>COMPARE00414 Fag t 6; oleosin, partial from QZM06934.1 [Fagopyrum tataricum]  
MADQHYHQAKDHTNQAQQHGQQALSMMAGYLQEK

>COMPARE00415 Fag t 6; oleosin, partial from QZM06934.1 [Fagopyrum tataricum]  
AYDARAHEVGRTTA

>QEA69430.1 Sco m 5; unknown function, antigen 5 [Scolopendra mutilans]  
MTIFLTSTLFLVLLVFQILGKGMGCDMKVRGLDANMKKMILDLHNKKRQTVANGQQSGQPS  
AANMKELHWDDQIAANAQRSAETCVFQHTAKNLRKTSKYSYLGENIYMGSYPDPIPRSVN  
AWYDEVKDVTPAVVKSFRSGGPMIGHYTQMVWANTEALGCGLVTASDKNTYIFCQYGPSG  
NYPGEPIYKQGSPASDCKKKGSSKYPGLCN

>ALQ56981.1 Coc n 1; 7S globulin, vicilin-like [Cocos nucifera]  
MVSAMGDRTASAILALLLSSWSLMVVMAYQGRGMEGREKRVEEKAPRSPEDRGLFILRR  
SKEVLKTDAGEVRLMMGYRYRGNHSPMHIGFITMEPNTLYIPQYIDASLILFVRRGEAKV  
GYIYKNKLVEKRLKSGYVDAIPAGSSFYIVNSDKSERLHIICSIDTLESMEYYGAYPQSF  
YVGGGVLPRSVLSGFDASTLSAAFNVSSDQLEMILNSQRGGPIIRLNGEAAEQRDYLSSI  
MQLKERMVQEKEMSDDDDEAEQEEDDVWTRCLLKSLGKDCRVQRKHKLAHSPGSYN  
LYDTEPSYQNDYGYSIAIDGHDYSALKHSNLGVYLVNLKAGAMLSPHVNPTATEYGIILR  
GSGTIQVVPNGTAAMNAKVSEGDVFWIPRYFPFCQIASDGALEFFGFTSARKNRPQF  
LVGKSSLLHSMRGPPELAAAFVGVSEEQLERIVKAQREAVILPTSPHREMEEINGKKWKGEE  
VLVMKRGLFA

>COMPARE00488 glycerol dehydrogenase, partial [Aspergillus ochraceus]  
NGIMPEAYSPLGSQNQVPTTGER

>COMPARE00489 glycerol dehydrogenase, partial [Aspergillus ochraceus]  
GTFASEGASGETYR

>COMPARE00490 oxidoreductase, partial [Aspergillus ochraceus]  
NTGKEFVFEDPR

>COMPARE00491 oxidoreductase, partial [Aspergillus ochraceus]  
FIHLDLSDQDSV

>COMPARE00492 unknown function, partial [Aspergillus ochraceus]  
ATPPTAPCSQR

>COMPARE00493 malate dehydrogenase, partial [Aspergillus ochraceus]  
GSEIVLIPAGVPR

>COMPARE00494 malate dehydrogenase, partial [Aspergillus ochraceus]  
GGPGVAADLSHINTNSTV

>COMPARE00495 malate dehydrogenase, partial [Aspergillus ochraceus]  
SGYEATPSGLR

>COMPARE00496 serine protease, partial [Aspergillus ochraceus]  
YLYASEGGEGVDAYTIDTGINVDHVDVEGR

>COMPARE00497 cyanide hydratase, partial [Aspergillus ochraceus]  
AAAVNAEPGWFDLQESVR

>COMPARE00498 cyanide hydratase, partial [Aspergillus ochraceus]  
LVFGDGTGDTTESVMDTEIGR

>COMPARE00499 unknown function, partial [Aspergillus ochraceus]  
IAENGSRVWAENVR

>COMPARE00500 unknown function, partial [Aspergillus ochraceus]  
ASSLGMFPGSR

>Q0L10866.1 Que ac 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus acutissima]  
MGVYNYESQETSVIPPARLFKAFVLDSNLIKVLPHAVKSTEIEGNGGPGTIKKFTFG  
EASKVKYAKHRIDTLDPENCSYSFSVIEGEALTDIASISTEVKFFVASPDGGSIMKSTTKY  
QTKGGFQLKEEQIQAAVEKGTGLFKAVEAYLLAHPDLYN

>QVU02258.1 Que ac 2; profilin [Quercus acutissima]  
MSWQTYVDEHLMCDIDGQGHAAAAIIGHDGSVWAQSSNFPQFKAEIISDIMKDFEEPG  
HLAPTGLHLGGTKYMIQGEAGAVIRGKKKSGGVTIKKTSQALVFGIYEETVTPGQCNMV  
VERLGDYLVLDQGL

>QVU02259.1 calcium-binding protein, polcalcin [Quercus acutissima]  
MATNSAPLNNSSTQNKSSPSLSNQSTEEVEKVFNRFDNNGDGKISVTELGAVFSSLGSS  
FSDEEELRRIMDELSDHDGFISLTFEAAFCRSSSAEDGGASELRDAFKLYDQDQNLIS  
ASELHLVLNRLGMNCSVEDCHRMIRSVSDGDGNNVFEEFQKMMNTANTSNSNASPL

>QEM21451.1 Cor a 15; oleosin [Corylus avellana]  
MADYQHQQHQRPADAFKGMFPEKQQAQVQGPSASKVIAVVTLLPLGGFLLLLLAGLTFAG  
TLIGLALSTPLFVLCSPVLVPAIIVIGLAVTGFLTSGAFGITGISSLSWILKYLRGTSVP  
EQMEHAKRRAQDTAGHLGQKARETGQTVTGKGQEQEAGKTLEGGRGEEKKT

>COMPARE00353 7S globulin, vicilin, partial [Prosopis juliflora]  
REQEQGSSSESRRQ

>COMPARE00354 7S globulin, vicilin, partial [Prosopis juliflora]  
RRQSGDERRH

>QCX36431.1 Zoy m 1; beta-expansin [Zoysia matrella]  
MASSSARRQAQLAAVAVLLSAMVGSALCEIGDKPGPNITATYNEEWQDAKATFYGSNPRG  
AAPDDDDGGACGYKNVDKAPFFGMTGCGNEPIFKDGLGCGSCFEIKCKEPAECSKPVLR  
ITDKNYEHIAAYHFDLSGKAFGSMKQGEDNLRKAGELTLQFRRVKCEYPSKTKITFHV  
EKGCNDNYLALLVEYAAGDGDIVAVDIKPKGSDEF LPMKPSWGAIWRIDPKKPLKGPFTV  
RLTSESGAKLVQEDVIPADWKPNTAYTSNLQY

>COMPARE00466 tropomyosin, partial from QX082627.1 [Macrobrachium lanchesteri]  
LAMVEADLER

>COMPARE00467 tropomyosin, partial from QX082627.1 [Macrobrachium lanchesteri]  
IQLLEEDLER

>COMPARE00468 tropomyosin, partial from QX082627.1 [Macrobrachium lanchesteri]

LAEASQAADER  
>COMPARE00469 tropomyosin, partial from QX082628.1 [Cherax quadricarinatus]  
LAMVEADLER  
>COMPARE00472 tropomyosin, partial from QX082628.1 [Cherax quadricarinatus]  
ALSNAEGEVAALNR  
>COMPARE00473 tropomyosin, partial from QX082628.1 [Cherax quadricarinatus]  
LAEASQAADERMR  
>COMPARE00474 tropomyosin, partial from QX082628.1 [Cherax quadricarinatus]  
IQLLEEDLERSEER  
>COMPARE00475 tropomyosin, partial from QX082628.1 [Cherax quadricarinatus]  
SLSDEERMDALENQLK  
>AEN62318.1 unknown function [Polistes dominula]  
LVTVLATIFFDTSSEAVCNERQDKPRFYTCQGVNLAQLDLSLPDSVVGLRLEKSTISRIP  
ADAFSRFAASLIELRITGCSLESIEAHAFRRDKLETLDLSNNRIQAEASWVRGLFNLK  
ELIVLRNRIARIEPEFYELLPKLETLDVAYNELVECITKDNFKKLKLNKLVLIASNPWSY  
RCRSDMTYAFKTNHVNFIKDWISIGDLLIEECLAHEQGADSDVILKHCVDKRSFESITPI  
LPDLEKKVLELSNKVEELRNEVNNIKKR  
>XP\_015185303.1 endothelial growth factor [Polistes dominula]  
MSYFEMKLAFLVLCGIVFSQSDNRKIDNSERIVFPEHTDQDAIGNVKRSTVPSELDDNL  
LMTSLEIAQKINSMSTYEEFLKFINVPPEKKVLIASRIGGGGEKSNAERPYPAGCIPENQ  
TVSLRPNKFFSTFYPPSCTRVRKRCGGCCGHYLLSCQPIETETRNFEVIVSELNADSTVSY  
KNKEIPIEIEHTKCKCDCKIKAQHCKKQAYRRNECSCVCMNIDEENCKKANKAVKIWDS  
ETCTACRENEICSTGFYFDNNTCRCRQVPILSRFGDISRKSgyrFDQTERPESVPPVIV  
HLDASDPRRQHKDDPEYK  
>XP\_015183815.1 phospholipase A2 [Polistes dominula]  
MLTASLCILSVLWAQKTMAVSVLVADTTMSRMVELNAGEPICSLYNDRGVIQRMILGADPK  
KVRQMPNSLVADLEETCLASKNRTPAGGLIYPGKWCWGPVNVASSYDDLQGHAAEDACCR  
EHDHCPIAMSSQCCIHGICNNSPFTRSHCDCAKFRRCLOLNTEVANTIGALFFNVIQV  
TCFKERRPCSQWQRNGYDEAVSNRLCSQYKFRPSEKYVPLMPLNMNI  
>QZP44316.1 Cra a 2; arginine kinase [Crassostrea angulata]  
MSDLPELWKKLSEGESKSLKKHCTKEVYEKLDKKTLLGGTLADCIRSGALNLNSGAGV  
YACDPEGYEVFKELLDPVIMDYHKVDKVEHPPCDFGPQDKLGFDPDATGEFIVSTRVRV  
GRSHEGYFPFPVSTDEQRKEMENKTIAALNTLEGELKGYYSLETMTPEENQQLIDDFM  
FKNDKMLGDAGGYNGWPKARGIFFNDNKTFWCWINEEDHLRFISMQKGGDVGEVYKRLV  
SAIKQLEKCLTFAYSKRHGYLTFCTNLGTTLRASVHIKVPKLAKEEVLNKCADNKLQ  
LRGIHGEHTESVGGVYDISNKRRLGLTEYQAMQEMYNGIKEIQAENAK  
>COMPARE00502 gibberellin-regulated protein, partial from RXH72835.1 [Malus  
domestica]  
GSPFCDSKCGVRCCKAG  
>AGS43084.1 tropomyosin [Schistosoma mansoni]  
MKLQIDQLKQELSSKQAILRKEEENKIKAEAEVASLQKRIRQLEDELESTETRLQEATVK  
LEEASKAADESRRARRVLEARQTAEDERILHLESVVQETAKSVRDAETKYEEAARKLAIT  
EVELERAESRLEAAESRLKELQSIHGTMGQLKSLHQSRLNQRSLHQSRLASLSKQL  
IEAERRVKEASHQEEMKQIELCKLEETLAEQLNHTNLRREMETMFTEVENI  
>AGS43085.1 tropomyosin [Schistosoma mansoni]  
MEHIKKMLAMKLDKENAVDEADQLEAKLREKELEMQTKDEEVAEVLKQVDTDKETA  
QTQLAETNTKLEETDKRATEAEAEVASLQKRIRQLEDELESTETRLQEATVKLEEASKAA  
DESDRGRKVLNRTFADEERINQLEEQLKESTFMAEDADRKYDEAARKLAITEVELERA  
SRLEAAESKITELLEEELRIVGNVKSLEISEQEAQAQREEAYEENIRDLTERLKAEDRAQ  
ESERLVNTLQADADRLDEDELVTEKEKYKALSEELDSTFAELTGN

>AGS43086.1 tropomyosin [*Schistosoma mansoni*]  
MEEALSAVYLNSTGLIKMAIIGVELQNVIKVSLRKAEEVASLQKRIRQLEDELESTETR  
LQEATVKLEEASKAADESDRGRKVLNRTFADEERINQLEEQLKESTFMAEDADRKYDEA  
ARKLAITEVELERAESRLEAAESKITELEEEELRIVGNVKSLEISEQEAAQREEAYEENI  
RDLTERLKAAEDRAQESERLVNTLQADADRLEDELVTEKEKYKALSEELDSTFAELTGN  
>AGS43087.1 tropomyosin [*Schistosoma mansoni*]  
MEHIKKKMLAMKLDKENAVDEADQLEAKLREKELEMQTKDEEVAEVLKIKQVDTDKETA  
QTQLAETNTKLEETDKRATEAAEAVASLQKRIRQLEDELESTETRLQEATVKLEEASKAA  
DESDRGRKVLNRTFADEERINQLEEQLKESTFMAEDADRKYDEVHF  
>CAA77666.1 Asp f 13; alkaline serine protease [*Aspergillus fumigatus*]  
ALTTQKGAPWGLGSISHKGQASTDYIYDTSAGAGTYAYVVDSGINVNHFESRASLAYN  
AAGGSHVDSIGHGTHVAGTIGGKTYGVAKKTNLLSVKVFQGESSSTSIIIDGFNWAVNDI  
VSKGRTKKAAINMSLGGGYSYAFNNAVENAFDEGLSVVAAGNENSASNTSPASAPNAL  
TVAAINKSNARASFSNYGSVVDIFAPGQDILSAWIGSTTATNTISGTSMATPHIVGLSVY  
LMGLENLSGPAAVTARIKELATNGVVTNVKGSNKLAYNGNA  
>QUJ17885.1 Api g 7; defensin [*Apium graveolens*]  
MAPKASSLTLIAIFLLFLVASYSVGAQGARAAATEGEVWYPEALCEKPSQWTWGKCGNTK  
NCDNQCQWETARHGACHKRGGKWMCFYFDRC  
>XP\_025675300.1 Ara h 18; cyclophilin/peptidyl-prolyl isomerase [*Arachis hypogaea*]  
MANPRVFFDMTIGGQPAGRIIMELFADTTTPRTAENFRALCTGEKGVGRSGKPLHYKGSFF  
HRVIPNFMCGGDFTAGNGTGGESIYGSKFADENFIKKHTGPGILSMANAGQNTNGSQFF  
ICTAKTEWLDGKHVVFQVVEGLDVVREIEKVGSSSGRTSKPVVWADCGQLS  
>COMPARE00363 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
RDAEQDVLLFIDNIFRF  
>COMPARE00364 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
REMMESGVIKL  
>COMPARE00365 ATP synthase beta subunit, partial from XP\_042978511.1 [*Carya  
illinoensis*]  
RFQEGLPPILTALVLDNSIRL  
>COMPARE00366 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
RFTQANSEVSALLGRI  
>COMPARE00367 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
KIGLFGGAGVGKT  
>COMPARE00368 ATP synthase beta subunit, partial from XP\_042985737.1 [*Carya  
illinoensis*]  
RIMNVIGEPIDERG  
>COMPARE00369 ATP synthase beta subunit, partial from XP\_042978511.1 [*Carya  
illinoensis*]  
KITDEFTGAGSIGQVCQVIGAVVDVRF  
>COMPARE00370 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
KNLQDIIAILGMDELSEDDKLTVARA  
>COMPARE00371 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [*Carya illinoensis*]  
RQISELGIYPAVDPLDSTSRM  
>COMPARE00372 ATP synthase beta subunit, partial from XP\_042978511.1,

XP\_042985737.1 [Carya illinoensis]  
RTIAMDGTEGLVRG  
>COMPARE00373 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [Carya illinoensis]  
KTVLIMELINNVAKA  
>COMPARE00374 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [Carya illinoensis]  
RVLNTGSPITVPVGRA  
>COMPARE00375 ATP synthase beta subunit, partial from XP\_042978511.1,  
XP\_042985737.1 [Carya illinoensis]  
KVVDLLAPYQRG  
>COMPARE00376 malate dehydrogenase, partial from KAG6732567.1, KAG7996745.1 [Carya  
illinoensis]  
KEFAPSIPQKN  
>COMPARE00377 malate dehydrogenase, partial from KAG6732567.1, KAG7996745.1 [Carya  
illinoensis]  
KLDLTAEELTEEKA  
>COMPARE00378 malate dehydrogenase, partial from KAG6732567.1, KAG7996745.1 [Carya  
illinoensis]  
RLNVQVSDVKN  
>COMPARE00379 malate dehydrogenase, partial from KAG6732567.1, KAG7996745.1 [Carya  
illinoensis]  
KMELVDAAFPLKKG  
>COMPARE00380 malate dehydrogenase, partial from KAG6732567.1, KAG7996745.1 [Carya  
illinoensis]  
KVLVVANPANTNALILKE  
>COMPARE00381 glyceraldehyde-3-phosphate-dehydrogenase, partial from XP\_042984133.1  
[Carya illinoensis]  
KAGIALNDNFVKL  
>COMPARE00382 glyceraldehyde-3-phosphate-dehydrogenase, partial from XP\_042984133.1  
[Carya illinoensis]  
KDAPMFVVGVNEKE  
>COMPARE00384 glyceraldehyde-3-phosphate-dehydrogenase, partial from XP\_042984133.1  
[Carya illinoensis]  
KVIISAPSKD  
>COMPARE00385 glyceraldehyde-3-phosphate-dehydrogenase, partial from XP\_042984133.1  
[Carya illinoensis]  
KVLPALNGKL  
>COMPARE00386 glyceraldehyde-3-phosphate-dehydrogenase, partial from XP\_042984133.1  
[Carya illinoensis]  
RVPTVNVSVVDLTVRL  
>COMPARE00387 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
KGAIPALPTETEVLLKGG  
>COMPARE00388 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
RGITFDQGART  
>COMPARE00389 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
KIVDDQSILGDEPRL  
>COMPARE00390 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
KLGDEFGRM  
>COMPARE00391 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]

KLLLVTLGEKG  
>COMPARE00392 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
KVSDVELDFLTGSDKC  
>COMPARE00393 fructokinase, partial from XP\_042966566.1 [Carya illinoensis]  
KDAGVLLSYDPNLRRL  
>COMPARE00399 acyltransferase, transacylase, partial from XP\_042956292.1 [Carya illinoensis]  
KLDSTVISQPAIYVTSLAAVELLRA  
>COMPARE00400 acyltransferase, transacylase, partial from XP\_042956292.1 [Carya illinoensis]  
RLEAALAATEIRT  
>COMPARE00401 malate dehydrogenase, partial from XP\_042949260.1 [Carya illinoensis]  
KGANVVVIPAGVPRK  
>COMPARE00402 malate dehydrogenase, partial from XP\_042949260.1 [Carya illinoensis]  
KLIDVDVPVVGGHAGITILPLLSKT  
>COMPARE00403 malate dehydrogenase, partial from XP\_042949260.1 [Carya illinoensis]  
KVAVLGAAGGIGQPLALLIKM  
>COMPARE00404 malate dehydrogenase, partial from XP\_042949260.1 [Carya illinoensis]  
RIQNAGTEVVEAKA  
>COMPARE00405 carbonic anhydrase-like, partial from XP\_042969845.1 [Carya illinoensis]  
KEAVNVSLGNLLTYPFVRD  
>COMPARE00406 carbonic anhydrase-like, partial from XP\_042969845.1 [Carya illinoensis]  
KGGYYDFVKG  
>COMPARE00407 carbonic anhydrase-like, partial [Carya illinoensis]  
KYSVGAAVEYAVLHLKV  
>COMPARE00408 carbonic anhydrase-like, partial from XP\_042969845.1 [Carya illinoensis]  
RNVANLVPPFDKT  
>COMPARE00409 carbonic anhydrase-like, partial from XP\_042969845.1 [Carya illinoensis]  
RYSVGAAVEYAVLHLKV  
>COMPARE00410 profilin, partial from XP\_042972635.1 [Carya illinoensis]  
KYMVIQGEAGAVIRG  
>COMPARE00411 profilin, partial from XP\_042972635.1 [Carya illinoensis]  
RLGDYLADQGL  
>COMPARE00412 nucleoside diphosphate kinase, partial from XP\_042954926.1, XP\_042958473.1 [Carya illinoensis]  
KIIGATNPSDSAPGTIRG  
>COMPARE00413 nucleoside diphosphate kinase, partial from XP\_042954926.1, XP\_042958473.1 [Carya illinoensis]  
RGDFAVEIGRN  
>XP\_018654157.1 unknown function [Schistosoma mansoni]  
MATETKLSQMEEFIRAFLEIDADSNEMIDKQELIKYCQKYRLDMKLIDPWIAFDTKDN  
KISIEEFCRGGFLKVSEIRREKDELKKERDGGKFKLPPNIEIIAATMSKTKQEICCCQFK

EYVDNTSRTGNDMREVANKMKSLLDNTYGRVWQVLLTGSYWMNFSHEPFLSIQFKYNNY  
VCLAWRTPSQ  
>XP\_018649273.1 unknown function [Schistosoma mansoni]  
MDSPEKFIQTYLTLLRDGDETVETSKLSESCRKEKLDKQVNEWIALFDVDKQKITFE  
EFCRGLGLKQEMRIERNHIKTVQSGREQSLPEGVSIISTMPKPKQVEVTQLFKDIYNE  
VKKDPMNKVVKTFKSELERRYGRVWQVNAVTHSYWASFHEPFSIQFQYDNKIILAWR  
TPSN  
>XP\_018649275.1 unknown function [Schistosoma mansoni]  
MEPFVQVFFAIDRDGTETITVEELKKYVAENKLDMMVTKWKSLEFDPKGTGRITFKTFCD  
VLGLSPAQAVAMKTQHQQASSLKLHPDVVVIYEQLPLDRQVAISNKAIELLTSSKKFDEK  
DQAVQLKQWLDITYGKAHVIVKGSFSSSYSHSANKCFIFRVRDVSYLWVWRTPEEITS  
A  
>XP\_018649276.1 unknown function [Schistosoma mansoni]  
MEPFITTFGAIDKRGVNVITINELRNYVAENHLDKEMIPKWQALFDPEGTGKITFRRFCE  
VLGVQPERHQAIINRPLYGIPTTGLRPEIFVIMQELPLQDQIKISEEAYRLTQPQDKFIE  
KEASEKLRWLDTTYGRHWHTIVRGSYWTTYTHIPNCSFHFKINQHSFIIYRTNA  
>CCE94314.1 unknown function [Schistosoma mansoni]  
MEPFVNIFFAIDEQQNETITRDELRRYVKHNHLDEGMITRWQSLFDPTNSGIITFQKFCF  
VLGVKPEQARTLRKSVINNRPLPKDLQIISQNMSSDQFQIFEFVRSLLDKNLSVQDMTQ  
MIKQWLDKTFDPSRHVVIIDGSYWISYSHLPEQSLQFRLKEKCYLVWVWRTPKH  
>CCE94321.1 unknown function [Schistosoma mansoni]  
MQTIHKLDGFTEIYFMVDRKKGWITMPELRKMEENDVDEKMFERWKTLDPESTGRIT  
LEKFCFVGLQDEVINVQTAIQGNEMQDVHVIQTMNTKMKLTICGLIDEGILYQDDSK  
LAEFLKNELDKYFGKLWNVVIIGRYWSRYCHETGYNFCFKDDRIFLVYKIPDLE  
>COMPARE00476 calcium-binding protein, parvalbumin, partial [Thunnus tonggol]  
SGFIEEDELK  
>COMPARE00477 creatine kinase, partial [Thunnus tonggol]  
GGDDLDPNYVLSSR  
>COMPARE00478 creatine kinase, partial [Thunnus tonggol]  
GFTLPPHNSR  
>COMPARE00479 creatine kinase, partial [Thunnus tonggol]  
DLLDPVISDR  
>COMPARE00480 creatine kinase, partial [Thunnus tonggol]  
GTGGVDTASVGGVFDISNADR  
>COMPARE00481 creatine kinase, partial [Thunnus tonggol]  
GEAIDSMIPAQK  
>COMPARE00482 enolase, partial [Thunnus tonggol]  
IGAENVYHNLK  
>COMPARE00483 enolase, partial [Thunnus tonggol]  
VNQIGSVTESIQACK  
>COMPARE00484 enolase, partial [Thunnus tonggol]  
AAVPSGASTGVHEALELR  
>COMPARE00485 enolase, partial [Thunnus tonggol]  
FMLELDGTENK  
>COMPARE00486 enolase, partial [Thunnus tonggol]  
DATNVGDEGGFAPNILENNEALELLK  
>COMPARE00487 enolase, partial [Thunnus tonggol]  
EVILPVPAFNVINGGSHAGNK  
>COMPARE00416 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]

RFGFFQVVNNNYDRWGTYAIGGSSAPTILSQGNRFLAPDDAAKK  
>COMPARE00355 7S globulin, vicilin, partial [Prosopis juliflora]  
RDPRQPPRSRQ  
>COMPARE00356 7S globulin, vicilin, partial [Prosopis juliflora]  
RSESKQSQEEERE  
>COMPARE00357 7S globulin, vicilin, partial [Prosopis juliflora]  
KGEEEEEGQARRQ  
>COMPARE00358 7S globulin, vicilin, partial [Prosopis juliflora]  
RFQTRYKNKN  
>COMPARE00359 7S globulin, vicilin, partial [Prosopis juliflora]  
RVVKLAIPINNPCKF  
>COMPARE00361 7S globulin, vicilin, partial [Prosopis juliflora]  
KFYDFYPSRTKD  
>COMPARE00362 7S globulin, vicilin, partial [Prosopis juliflora]  
RSNEPIYSNKF  
>COMPARE00417 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]  
RQAMADCAQGFAKG  
>COMPARE00418 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]  
KQIWIDHCSFSKA  
>COMPARE00419 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]  
KVEITNGGLTMDVKN  
>COMPARE00420 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]  
KVMLLGADDGHHQDKN  
>COMPARE00421 Hel a 6; pectate lyase, partial from XP\_022025296.1 [Helianthus  
annuus]  
RADAPESESMTWNWRT  
>COMPARE00501 glycerol dehydrogenase, partial [Aspergillus ochraceus]  
GGNTLAQVLIAWGLR  
>CAD1459612.1 lipid transfer protein [Macadamia integrifolia]  
MANSQVMKLVCLVLACMVVAAPLAEEAITCGQVSKLAPCLTYLRSGGAVPGTCCNAVKN  
LNNSAKTTPDRQTACGCLKNAYNSISGINAAYAGGLPAKCGVNLPHYKISPSINCATYTLS  
LYNF  
>AHM25029.1 Api m 10; icarapin, partial [Apis mellifera]  
FPGAHDEDSKEERKNVDTVLVLPSEIERDQMAATFDFPSSLSFEDSDEGSNWNWNTLLRPN  
FLDGWYQTLQTHMKKVREQMAGILSRIPEQGVNWNKIPEGANTTSTTKIIDGHVVTINE  
TTYTDGSDDYSTLIRVRVIDVRPQNETILTTVSSEADSDVTTLPTLIGKNETSTQSSRSV  
ESVEDFDNEIPKNQGDVLT  
>COMPARE00541 11S globulin, cupin, partial [Linum usitatissimum]  
FTETQEQQPQR  
>COMPARE00542 11S globulin, cupin, partial [Linum usitatissimum]  
ALPADVLANAXR  
>COMPARE00543 11S globulin, cupin, partial [Linum usitatissimum]  
QSSERFEWVAFK  
>COMPARE00544 11S globulin, cupin, partial [Linum usitatissimum]  
EVSIFSPGNQSQR  
>XP\_042518524.1 Mac i 2; 11S globulin, cupin [Macadamia integrifolia]

MANKHLILLSFLSLLL VANHGLATNKAEGTIELVTNKPEAIGYEGRQSHTRLREARQCRL  
QQISVSQPRQRIQSEGGVTEFWDENEDQFQCTGVAAMRNIIQPNSLSLPNYSPPRLVYI  
ERGRGLLGVTFFPGCPETYQSSRDEQSYRGSSRRGDEQSYRGSSRRGDEQSYGGSSRRGGE  
QSYGGPSRRGDEQSYRGSEGRGEQEELRSGEDQHQKIHRVRGGDLVVLPAGVAHWCLND  
GKEDLVAVSVNDLNNQANQLDQKLRSYLAGSQNQESQRGQSYESQRGSQKGPQQGSGES  
DTYQNILNPFDENLMADALNVDVETVRTMRKEDGRGYIVKVREDM SVIRPDEDYEEDDER  
ERERERERERYIKRREGSRGTGERRYIKRREGSRRTNGLEETICTARIHHYLDNPREADV  
YSRDAGRLNIVNMLKLPILSYLDLSAEKGDLLPNAIHAPHWLMNAHSIFYITRGEAQVQV  
VGNNGQRLDDRVNEGDI FTVPQYFAATFRAGSEGVEWVAFRTSALPISNPVAGSTSVFR  
GMPAQVIAESYGIGLQEAQNIKYGRQQHTLLLPPGRRSSN  
>COMPARE00604 actin, partial [Pila polita]  
VAPEEHPVLLTEAPXNPK  
>COMPARE00605 actin, partial [Pila polita]  
AVFP SLVGRPR  
>COMPARE00606 actin, partial [Pila polita]  
SYELPDGQVITIGNER  
>UZC36340 Per a 17; alpha-tubulin [Periplaneta americana]  
MRECISVHIGQAGVQIGNACWELYCLEHGIQPDGQMP SDKTIGGGDDSFNTFFSETGAGK  
HVPRAVFVDLEPTVVDEVRTGT YRQLFHPEQLITGKEDAANNYARGHYTIGKELVDLVLD  
RVRKLADQCTGLQGFLIFHSFGGGTGS GFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTA  
VVEPYNSILTTHTTLEHSDCAF MVDNEAIYDICRRNLDIERPTYTNLNR LIGQIVSSITA  
SLRFDGALNVDL TEFQTNLVPYPR IHFPLATYAPVISA EKAYHEQLTVAEITNACFEPAN  
QMVKCDPRHGKYM ACCMLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYQPP  
TVVPGGDLAKVQRAVCM LSNTT AIAEAWARLDHKFDL MYAKRA FVHWVYV GEGMEEGEFSE  
AREDLAALEKDYEEVGVDSADGEVDEGDDEY  
>COMPARE00526 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
MWTENWTGWFK  
>COMPARE00527 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
TAEDLSYSVAR  
>COMPARE00528 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
KGDETIKDLSSHK  
>COMPARE00529 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
TFKAPLGTD AVVV DLQGLGK  
>COMPARE00530 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
RVLQSGSIHYPRSTPEMWPDLIR  
>COMPARE00531 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
EYDFSGNLDLIRFIQTIQAEGLYAVLR  
>COMPARE00532 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
VAGGPYITTSYDYDAPLDEF GNLNQP K  
>COMPARE00533 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
LFASQGGPIIIAQIENEYGNIMAPYGDAGK  
>COMPARE00534 beta-galactosidase, partial from D7TCB5 [Vitis vinifera]  
VNAQTSVMVKNKNEAEDQPASL KWSWRPEMIDDTAVLGK  
>COMPARE00627 chitinase, partial from XP\_007137307.1 [Phaseolus vulgaris]  
EQCGRQAGGALCPG  
>CAA66378 Cari p 2; cysteine protease, papain [Carica papaya]  
MATMSSISKIIFLATCLIIHMGLSSADFYTVGYSQDDLTSIERLIQLFDSWMLKHNKIYE  
SIDEKIYRFEIFRDNLMYIDETNKKNNSYWLGLNGFADLSNDEFK KKYVGFVAEDFTGLE  
HFDNEDFTYKHVTNYPQSIDWRAKGAVTPVKNQGACGSCWAFSTIATVEGINKIVTGNLL  
ELSEQELVDCDKHSYGCKGGYQTTSLQYVANNGVHTSKVYPYQAKQYKCRATDKPGPKVK

ITGYKRVPSNCETSFLGALANQPLSVLVEAGGKPFQLYKSGVFDGPGTKLDHAVTAVGY  
GTSDBGNYIIIKNSWGPNWGEKGYMRLKRQSGNSQGTGCVYKSSYYPFKGFA  
>UY079699.1 Man i 1; chitinase [Mangifera indica]  
MAFNMRKNLLTFALLGLFSLAIVPKNVMSQNCDCAPNLCCSQFGYCGTGEAYCGLGCKGG  
PCTSTPSTPSPTPTGGGVSIVTVDFFDGIKNQAAASCAGKSFYTRDGLNAANSFPQF  
GSGSADESKREIAAFFAHVTHETGHLCTEEDKSNAYCDQSNQYPCVPGKKYYGRGPM  
QLTWNYNYGACGKAVGFDGLNAPETVSNPDAVSFKAALWFWMTNVHSMNQFGGATIQKI  
NGALECGGKQDPKVNARIGYYTDYCQKFGVDPGQNLSC  
>UZC36339 Per a 16; cofilin [Periplaneta americana]  
MASGVTVSDVCKTTYEEIKKDKKHRYVVFIRDEKQIDVEVIGERNAAYDQFLEDLQKGG  
TGECRYGLDFEYTHQCQGTSEASKKQKFLMSWCPDTAKVKKKMLYSSSFDALKKSLVG  
VQKYIQATDLSEASQEAVEEKLDRTRQ  
>COMPARE00523 Lin u 1; 2S albumin, conlinin, partial from CAC94011.1 [Linum  
usitatissimum]  
DLPGQCGTQPSR  
>COMPARE00524 Lin u 1; 2S albumin, conlinin, partial from CAC94011.1 [Linum  
usitatissimum]  
QIQEQDYLRSCQQFLWEKVQK  
>COMPARE00525 Lin u 1; 2S albumin, conlinin, partial from CAC94011.1 [Linum  
usitatissimum]  
SYYYNQGRGGGQSQHFDSCCDDLKQLRSECTCRGLERAIGQMRQDIQQQQQQQEVERWV  
QQAQ  
>UTE00285.1 Cor a 11; 7S globulin, vicilin [Corylus avellana]  
LPKEDPELKKCKHKCRDERQFDEQRRDCKQICEEKARERQQEEGNSSEESYGEEQEENP  
YVFQDEHFESRVKTEEGRVQVLENFTKRSRLLSGIENFRLAILEANPHTFISPAPHDAEL  
VLFVAKGRATITMVREEKRESFNVEHGDIIIRIPAGTPVYMINRDENEKLFIVKILQPVSA  
PGHFEEAFYGAGGEDPESFYRAFSWEVLEAALKVRREQLEKVFGEQSKGSIVKASREQIRA  
LSQHEEGPPRIWPFGGESSGPINLLHKHPSQSNQFGRLYEAHPDDHKQLQDLDMVSFAN  
ITKGS MAGPYNSRATKISVVVEGEGFFEMACPHLSSSSGSYQKISARLRRGVVVFVAPAG  
HPVAVIASQNNNLQVLCFEVNAHGNSRFLAGKGNIVNEFEREAKELAFNLPSREVERIF  
KNQDQAFFFPGNKQQEEGGRGGRAFE  
>UTE00286.1 Cor a 16; 7S globulin, vicilin [Corylus avellana]  
HETLEEPRYELRQKDDRDPEPRREFQQCQERCRREREERGQRQQQQCQQRCQEEQLRERERQ  
REREIDAVNQDPRRQYEECQRRRCERQEPQQQQCQRRRCERQFEEQREGEGRGRRGGSRD  
DDEENTREPREFQFQQCLQRQREAOQGRQQQQCQRRCEERYEEEQRRERGRQGGRDNIEE  
YTRDPQQYQQCQQRCEQEQQHRRQQQCQRRCDERYEEEQRRREQEQGERGRQGGRDNIEE  
YTRDPQQYQQCQQRCEQEQQGRQQQQCQRRCEERYEEEQRRREQEQGGRDNIEEYTRDP  
RQQYQQCQQRCEQEQQGRQQQQCQRRCEERYEEEQRRREQEQEGGRDNIEEYTRDPQQQ  
YQQCQQRCEQEQQGRQQQQCQRRCEERYEEEQRRREQEQEGGRQERDIDQEHIRDPPQQQ  
YQQCQQRCEQEQQGRHQQQCQRRCAERYEEEQRRREQEREGRDTEEDTRDPQQYQQCQQ  
RCQRQEQQHRRQQQQCQRRCEERYEEEQRRREQEEREGGRQRRDTEEDTRDPQQYQQCQQ  
QQRCLSRQGRQERCQRRCEERYEEDQRKKGGGKRGQKYSYTRDPQQRYEQCQQQC  
QRYQGDQEKQLCRRRCEQQRQQEEREHQRRDQDPQQYQQCQRRCTREQRPERQRQC  
QQRCEEQYREQQTREWGEGNPSKQGRRSEEHNPYYFHSQRFQLVHRSEEGYVRSLEFRT  
ERSELLSGIDNYRLVILEANPNSFMLPHHKDADAIVVVMGKATINFVRQDKRNERESFN  
LECGDVLMPAGTTTTMVAVNQDSNEKLQIVVLVVPVNNPGQFREYFAAGAQNRRESYLRAF  
SEDILEASLNTPIEKLERAFQQEQQRQGVIIIRASQEQLRALSQRAMSAGRQSSRGPISLR  
SLSPSYSNQFGQFFEASPEDHRQLQDMDVFNVAEIKQGAVMVPHYNSRATVVVFVVEGT  
GRFEMACPHLSSQSQESRGRREQEESGKQFQVRSARLSPGDAFVIPAGHP IAVVASER  
ENLRMVGFGINGQNNQRNFLAGQDNIINQLEREAKEKELAFNLPQEEIEQIFGRQRESYFVP

KERQSQRGQGRDHPLASILNLAGFF  
>COMPARE00628 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
HGHFVKLERFDHELLR  
>COMPARE00629 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
SKGEGEIYEASEEQIR  
>COMPARE00630 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
SGGSGRPYHFGQESYREWAK  
>COMPARE00631 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
FHQITGDQCHHLRKLDMVTLVNITR  
>COMPARE00632 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
RESFCIREGDVIVIPAGSIVYSANTHR  
>COMPARE00633 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
VAYLDAAPRAFLQPSHHDAEIAFVREGGVLVLLR  
>COMPARE00634 cupincin, partial from XP\_044383364.1 [Triticum aestivum]  
VVMFINPVSTPGRFQEFFLIGSGDERPQSFLSVFSDEVIQAALNTR  
>UZC36338 Per a 15; cytochrome c [Periplaneta americana]  
MGVPDGADEKGGKVFVQRCAQCHTVEASGKHKTGPNLHGLFGRKTGQAPGFVYTDANKAK  
GITWNKDTLFFVYLENPKKYIPGTKMVFAGIKKPQERADLIAYLEQSTK  
>UZC36337 Per a 14; enolase [Periplaneta americana]  
MPIQKCLARRIFDSRGNPTVEVDLVTDLGLFRAAVPSGASTGVHEALELRDNDKNNYHAK  
DVSKAIDNVNKKIIVPELLKQNFQTEIDEFMLKLDGTPNKSCLGANAILGVSLAVCK  
AGAAKKGVPYRHIADLAGVLDLVPVPAFNVINGGSHAGNKLAMQEFMVLPTGAASFTE  
AMKMGSEVYHHLKVKIKDKFGLDATAVGDGEGFAPNILDNKAGLLLIKEAIEKAGYTGKV  
EIGMDVAASEFYREGKYDLDFKNPQSDKSKWIDAKELTNLYMEFIKEFPVVSIEDPFDQD  
HWDWAEMTANTPIQIVGDDLTVTNPTRIQTAVDKKACNCLLLKVNQIGSVTESIKAHNL  
AKSNGWGTVMVSHRSGETEDTFIADLVVGLSTGQIKTGAPCRSERLAKYNQILRIEEELGA  
NAKYAGKNFRKPV  
>UYQ90943.1 Pla a 6; enolase [Platanus acerifolia]  
MATIKAVKARQIFDSRGNPTVEVDVTISDGLLARAAPVSGASTGIYEALERDGGSDYLG  
KGVLKAVENVNAIIGPALIGKDPTEQTKIDNFMVQELDGTVNEWGWCKQKLGANAILAVS  
LAICKAGASVKKIPLYKHIANLSGNKTLVLPVPAFNVINGGSHAGNKLAMQEFMILPVGA  
TSFKEAMKMGVEVYHHLKAVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKAG  
YTGKVVIGMDVAASEFYDNKDKTYDLNFKENNDGSQKISGDSLKNVYKSFVTDYPIVSI  
EDPFDQDDWEHYAKLTAEIGQQVQIVGDDLVTNPKRVDKAIKEKTCNALLKVNQIGSV  
TESIEAVKMSKRAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL  
LRIEEELGSAAVYAGANFRAPVEPY  
>COMPARE00514 glyceraldehyde-3-phosphate-dehydrogenase, partial from A0A438H737  
[Vitis vinifera]  
AASFNIIPSSTGAACKAVGK  
>COMPARE00515 glyceraldehyde-3-phosphate-dehydrogenase, partial from A0A438H737  
[Vitis vinifera]  
VKDSKTLFLGDKAVTVFGAKNPEEIPWGEAGAEYVVESTGVFTDKDK  
>COMPARE00516 glyceraldehyde-3-phosphate-dehydrogenase, partial from A0A438H737  
[Vitis vinifera]  
VIISAPSSNAPMFVGVNEKEYKSNIDIVSNASCTTNCLAPLAKVIHDKFGIVEGLMTTV  
HSITATQKTVDGSPMKDWR  
>COMPARE00517 glyceraldehyde-3-phosphate-dehydrogenase, partial from A0A438H737  
[Vitis vinifera]  
LTGMAFRVPTADVSVVDLTVRTEKKASYDDIKAAIKAESEGNLKGILGYTEDEVSSDFL  
GDSRSSIFDAKAGIALNENFIKLVSWYDNEWGYSSR

>URW11955.1 Pen m 14; glycogen phosphorylase [Penaeus monodon]  
MAAPQTDLEKRKQISVRGIAQVENVGNVKKTFNRHLHYTLVKDRNVSTPRDYFALAHTV  
RDHLTSRWIRTQQHYEKDPKRVYLSLEYMGRSLTNTMINLGIQSACDEALYQLGLDI  
EELESLEEDAGLNGGLGRLAACFLDSMATLGMMAAYGYGIRYEYGIFAQKIRNGEQVEEP  
DDWLRFGNPWEKARPEYMIPVNFYGRVEDTPQGKKWVDTQIVFAMPYDNPIPGYKNNVVN  
TMRLWSAKSPNNFNLKFFNDGDYIQAVLDRNFAENISRVLYPNDNFFEGKELRLKHEYFM  
VAATLQDIIRRFKASKFGSKDQVRTDFDTPDKVALQLNDTHPSLAIPELMRILVDIEGL  
PWAKAWDICVRTCAYTNHTVLPEALERWPTSMLEHILPRHLQIIYEINHFHLQEVSCKWP  
GMDRVRMSLVEEHGEKRINMAHL CIVGAHAVNGVAAIHSEIIKRDIFKFAEMNPEKF  
QNKTNGITPRRWLLLCNPALADVIAEKIGEEVWVHLDQLTKLKPLAKDAGFIRAVQTAKQ  
ENKLR LAKQLEQDYGVKVPSSMFDIQVKRIHEYKRQLLNCLHIITMYNRIKANPGAPFV  
PRTVMIGGKAAPGYHTAKQIIRL ICAVGRVWVNDPIVGDKLKVYLENYRVTLAEQIIPA  
ADLSEQISTAGTEASGTGNMFKMLNGALTIGTLDGANIEMMEEMGKENIFIFGMTVEEVE  
ELKRRGYNAHDYYNRIPELRQCIDQISSGFFSPSNPDQFKDLVNILMYHDFYLFADFES  
YIKCQDSVSMLYQKPNEWTSKAIMNIIASSGKFSSDRTIAQYGREIWGVEPSWEKLPAPHE  
PRDTDITREEAK

>NP\_001069969.2 Bos d 13; myosin light chain [Bos taurus]  
MAPKKPDPKDEAKAGAKAAAAAPAPAPAPPPAPEPSKEPEFDPSKIKIEFTPEQIEEFKE  
AFTLFDRTPKCEMKITYGQCGDVLRALGQNPQAEVLRVLGKPKQEELNSKMMDFDTFLP  
MLQHISKNKDTGTIEDFVEGLRVFDKEGNGTVMGAELRHVLATLGEKLTETEVEKLMAGQ  
EDSNGCINYEAFVKHIMAG

>AAI26717.1 Bos d 13; myosin light chain [Bos taurus]  
MAPKKDVKKPAAAAAPAPAPAPAPAPAPAPPKEEKIDLSAIKIEFSKQQQDEFKEAFLLF  
DRTGECKITLSQVGDVLRALGTNPTNAEVKVKVLGNPSNEEMNAKKIEFEQFLPMLQAISN  
NKDQGTIEDFVEGLRVFDKEGNGTVMGAELRHVLATLGEKMKEEEEVEALMAGQEDSNGCI  
NYEAFVKHIMSN

>COMPARE00518 NADPH dehydrogenase, partial from A5AS18 [Vitis vinifera]  
LAEI IKGAASVEGVEAKLWQVPETLPEEVLGK

>COMPARE00519 NADPH dehydrogenase, partial from A5AS18 [Vitis vinifera]  
VKGGSPPYAGTFAGDGSRQPSELELEQAFHQGKYIAGITKK

>COMPARE00520 NADPH dehydrogenase, partial from A5AS18 [Vitis vinifera]  
SDTPIITPTDLAEADGFVFGFPTRFGMMAAQFKAFLDATGGLWR

>XP\_035472139.1 calcium-binding protein, parvalbumin [Scophthalmus maximus]  
MAFKGVLDDAKITAAL ECKKPE SFCHKKFFGT CGLSAKSPADVKAAFDIIDQDKSGFIE  
EDELKFLQTFKAGARSLDTETKNLLKAGD TDNDGKIGADEFASMVKV

>XP\_035472137.1 calcium-binding protein, parvalbumin [Scophthalmus maximus]  
MSFAGLNAAEIKTALDGCAAADTFNYKKFFGACGLAKKSADDVKAAFQIIDQDNSGFIEE  
EELKFLQNFSAGARALTDKETAFLKAGDADGDGKIGIEEFANLVKE

>UY079702.1 Man i 2; pathogenesis related protein, PR-10, Bet v 1-like [Mangifera indica]  
MGVLHHSNETTTAVAPSRMFQAFILD SHNLLPKLAPQSFKNIELIEGDGGVGSIKLINFP  
DGSYYKMKHRIDVLDKENFVCKYTLIEGDSLGEKLESVVYEVKFEPSGNGGSICKVASE  
YHTKGDHEIKEEVFKASQEKAELYKVVEAHLLANPDLYA

>XP\_017220806.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]  
MGVQKSEVVIASPVPAAKLFGKICLDIDTLLPQVLPGAIKGAEILEGDGGAGTVKLVTLG  
DASPYKTMKQKTEAIDKEAFTFSYSIIDGDILLGYIDSITTEFTFTPTADGGCTAKSVST  
FNTKGDVAVPEENINFANEQNGIIFKAIEAYLIAN

>XP\_017215843 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKSEVEATSSVSAEKLFKALCLDIDTLLPQVVPGAIKSAEILEGDGGVGTVKLIHLG  
DASPFKTMKQKVDVIDKDSFTYSYTIIDGDILLDFVESINNHFTYVPTADGGCTVKSTIT  
FTTKGDAVVPEENIKFANDQNLAIFKAIEAHLIAN  
>XP\_016553101.1 Cap a 7; gibberellin-regulated protein [Capsicum annuum]  
MKLSFATLVLTILLTSFFIQPTIAGSAFCDSKCNFRCSKAGRKDRCLKYCGICCADCNC  
VPSGTFGNKDECPCYRDKKNSKGGPKCP  
>UZC36341 Per a 18; cyclophilin/peptidyl-prolyl isomerase [Periplaneta americana]  
MAHAALGLYRQSWSRCSFQRIGIASGLQSGLCVAVLRNLSSKMGLPRVFFDMSADGQPVG  
RIVMELRNDVVPKTAENFRALCTGEKGFYKGSTFHRVIPNFMCCQGGDFTNHNGTGGKSI  
YGTKFEDENFQLKHTGPGILSMANAGPNTNGSQFFITTAKTSWLDNRHVVFSGSVVEGMDV  
VKKLESLGSQSGKTSKKINVVDCGQI  
>UZC36342 Per a 19; porin [Periplaneta americana]  
MSPPPYNDLGNARDVFSKGYHFGLLKLDCKTKTKSGVEFSSGGVSNLDSGNVFGSLETK  
YRVSDYGM  
>COMPARE00609 profilin, partial [Citrullus lanatus]  
LGDYLVEQGL  
>COMPARE00521 profilin, partial from A5BLM8 [Vitis vinifera]  
TPEITGIMNDFAEPLGHLAPTGLYLGGTKYMIQGEPEGAVIRGKKGSGGITIKKTGQALVF  
GIYEPPVTPGQCNMVERLGDYLVQGL  
>UYQ90947.1 Pla a 4; profilin [Platanus acerifolia]  
MSWQTYVDDHLMCDLEGNHLSHAAIIGHDGSVWAQSAAFPQFKPEEMTGIMNDFAEPLGSL  
APTGLYLGGTKYMIQGEPEGAVIRGKKGSGGVTIKKTSLALIIGIYEELTPGQCNMIVE  
RLGDYLIDQGL  
>UY079700.1 Man i 4; profilin [Mangifera indica]  
MSWQTYVDDHLMCEIDGLHLTAAAIIGQDGTVWAQSANFPQLKPEEITGIMNDFAEPLGTL  
APTGLFLGGVKYMIQGEPEGAVIRGKKGSGGVTVKKTNQALIIGIYDEPLTPGQCNMIVE  
RLGDYLIDQGL  
>UY079701.1 Man i 4; profilin [Mangifera indica]  
MSWQAYVDDHLMCDIEGNHLAAAAILGQDGSVWAQSANFPQLKPEEVTGINNDFNEPGL  
APTGLYLGGTKYMIQGEPEGAVIRGKKGPGGVTVKKTSMFVIGIYDEPMTGQCNMIVE  
RLGDYLVEQGL  
>ACE80951.1 Pru du 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus  
dulcis x Prunus persica]  
MGIFTYTDDESTSVIPPPRLFKALVLEADTLIPKIAQSVKSAEIVEGDGGVGTIKKISFG  
EGSHYSYVKHQIDGLDKDNFVYNYSLVEGDALSDKVEKISYEIKLVASADGGSVIKSTSN  
YHTKGDVEIKEEDVKAGKEKATGLFKLIENYLVANPDAYN  
>COMPARE00539 ribosomal protein S15a, partial from KAF9498209.1 [Pleurotus eryngii]  
HGYIGEFEIIDDHR  
>COMPARE00540 ribosomal protein S15a, partial from KAF9498209.1 [Pleurotus eryngii]  
YNIQANQIESWVNLPLPAR  
>COMPARE00538 ribosomal protein S8, partial from GAW05875.1 [Lentinula edodes]  
GFGIILTTSSGILDHEEAR  
>COMPARE00610 triosephosphate isomerase, partial [Citrullus lanatus]  
VIACVGETLEQR  
>COMPARE00535 triosephosphate isomerase, partial from D7TLU7 [Vitis vinifera]  
IIYGGSVSGANCKELAAKPDVDGFLVGGASLKPEFIDIK  
>COMPARE00536 triosephosphate isomerase, partial from D7TLU7 [Vitis vinifera]  
IVSTLNAGEVPSGDVVEVVVSPPFVFLPLVKSTLRPDFHVAQNCWVK  
>COMPARE00537 triosephosphate isomerase, partial from D7TLU7 [Vitis vinifera]  
RLLLNESNEFVGEKVAYALSKGLKVIACVGETLEQRESGSTMEVVAQTKAIADKVSNWA

NVVLAYEPVWAIGTGKVATPAQAQEVHSELR  
>COMPARE00607 tropomyosin, partial [Pila polita]  
SLADDERLDGLEAQLK  
>COMPARE00608 tropomyosin, partial [Pila polita]  
IQLLEEDLERSEER  
>ADV17344.1 Pen m 6; troponin C [Penaeus monodon]  
MDSLDEEQIETLRKAFNSFDTEGAGSINAETVGVILRMMGVKISEKNLQEVIAETDEDGS  
GMLEFEFFAELAALKFLIEEDEEALKAELREAFRIYDKDCQGYITTDILKEILVELDPKLT  
PTDLEGIIEEVEDGSGTLDLDFDEFMEMMSG  
>QXY82447.1 Der p 39; troponin C [Dermatophagoides pteronyssinus]  
MSVEELTKEQVQMLRKAFDMFDREKKGHIHTNMVSTILRTLGGQTFEEKDLQTLITEIDAD  
GSGELEFDEFLLTLARFLVEEDAAMQEELREAFRMYDKEGNGYIPTSALREILRALDDK  
LTNDELDEMIAEIDTDGSGTVDFDEFMEMMTGD  
>UXW65969.1 Tyr p 11; paramyosin [Tyrophagus putrescentiae]  
MSARSAKMYQSSSGNRGGDISIEYGTDLGALTRLEDKIRLLSEDLERELRQRVEREK  
SDVMVQLMNLTERLEEAEGSSESVTEMNKKRDELAKLRKLLLEDVHMESEETAHHLRQKH  
QAAITEMQDQLDQVQKAKNKSDEKQKQFAEVFELLAQVETANKEKLI AQKTVEKLEYTV  
HELNIKIEEVNRTVTEVTAHRQRLSVENSELIKEVHEYKISLDNANHLKGQIAQQLEDTR  
HRLDEERLENHAHTLEVELESKLVQLEEESEARLELERQLTKANGDAASWKSKEYAELQ  
AHADEVEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKATAHAQ  
ALEKKVVQLEKINLDLKSKEEVSILLEQTQKDLRVKIADLQKQLQHEYEKLRDQKEALAR  
ENKKTEDLAEAKSQLNDAHRRRIHEQEIEIKRLENEREELAAAYKENQRLTAE LAQVRHD  
YEKRLAQKEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEVARLKKKYQAQITELELSLD  
AANKANIDLQKTIKKQALQITELQAHYDEVHRQLQQAQVDQLGVTQRRCCQLQAELEEMRV  
NLEQAQRAKRAEQLYEEAVRVNELTTINVNLASAKSKLETEFSALQNDYDEVHKEKRL  
TIELKSTKDVLIIEEQERVTKLETIKKSLEVEVEANALAGGKRVI AKLESRI RDVEIEVEE  
ERRRHAETEKMLRKKDHRVKELLLQTEEDHKQLHLLQEMADKLNKVKVYKRQMQEQEGV  
SQQNL SRVRRFQRELEAAEDRADQAESNLSFIRAKHRSWTTSQVPGGTRQVFVTEQETS  
NF  
>UXW65972.1 Tyr p 20; arginine kinase [Tyrophagus putrescentiae]  
MGDVPKETLEKLEAGFAKLQGAADCKSLLKKHLTKEIFEELKGKKTQMGATLLDVVQSGM  
ENLDSGVGMYPADAEAYTVFENLFPVIEEYHFGFKATDKHPASDFGNAESLCNLDPNSE  
FVISTRVRCGRSLKGFQFNPCMTEENYKDLETQVKGALLEGASGELKGIYYPLVGM DTKQ  
QKLIDLHYLFKEGDRFLQAANASRFWPTGRGIFINLTKTFTWINEEDHIRIISLQEGGN  
LKTVYSRMLKGLNYLSGKLEFNRS DRLGFLTFCPTNLGTTIRASVHIMLPKLAANKAKLD  
EVAEKYKMQVRGETGEHSDSSSGIFDISNKRRLGLTEFQALKEMQEGILELIKIEKSL  
>Q9SPL5.1 Mac i 1; 7S globulin, vicilin-like [Macadamia integrifolia]  
QCMQLETSGQMRRCVSVQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRRCRQQESGPRQQY  
CQRRCKEICEEEEEYNRQRDPQQYEQCQKHCQRRETEPRHMQTCQQRCERRY EKEKRKQ  
QKRYEEQQREDEEKEYEERMKEEDNKRPQQREYEDCRRRCEQQEPRQQHQQLRCREQQR  
QHGRGGDMMNPQRGGSGRYEEGEEEQSDNPYYFDEERSLSTRFRTEEGHISVLENFYGRSK  
LLRALKNYRLVLLLEANPNAFVLP THLDADAILLVIGGRGALKMIHHDNRESYNLECGDVI  
RIPAGTTFFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPPEYLS TFSKEILEAA  
LNTQTEKLRGVFGQQREGVIIRASQEQIRELTRDSESRHWHIRRGGESSRGPYNLFNKR  
PLYSNKYQAYEVKPEDYRQLQDMDLSVFIANVTQGSMMGPF FNTTRSTKVVVVASGEADV  
EMACPHLSGRHGRRGGGRHEEEEDVHYEQVRARLSKREAI VVLAGHPVVFVSSGNENLL  
LFAFGINAQNNHENFLAGRERNVLQQIEPQAMELAFAPRKEVEESFNSQDQSIFFPGPR  
QHQQQSPRSTKQQQLVSI LDFVGF  
>Q9SPL3.1 Mac i 1; 7S globulin, vicilin-like [Macadamia integrifolia]  
QCMQLETSGQMRRCVSVQCDKRFEEDIDWSKYDNQEDPQTECQQCQRRRCRQQESDPRQQY

CQRRCKEICEEEEEYNRQRDPQQQYEQCQKRCQRRETEPRHMQICQQRCEERRYKEKRKQ  
QKRYEEQQREDEEKEYEERMKEGDNRDPQQREYEDCRRHCEQQEPRLQYQCQRRCEQQR  
QHGRGGDLMNPPQRGGSGRYEEGEEKQSDNPYYFDEDSLSTRFRTEEGHISVLENFYGRSK  
LLRALKNYRLVLLLEANPNAFVLPHTLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI  
RIPAGTTFFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAA  
LNTQTERLRGVLGQQREGVIIRASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKR  
PLYSNKYQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFNTRSTKVVVVASGEADV  
EMACPHLSGRHGGRRGGKRHEEEEEVHYEQVRARLSKREAIWLAGHPVVFVSSGNENLL  
LFAFGINAQNNHENFLAGRERNVQQIEPQAMELAFASRKEVEELFNSQDESIFFPGPR  
QHQQQSPRSTKQQQPLVSIILDFVGF

>Q9SPL4.1 Mac i 1; 7S globulin, vicilin-like [*Macadamia integrifolia*]

QCMQLETSGQMRRCVSQCDKRFEEIDWSKYDNQDDPQTDCCQQRRCRQQESGPRQQQY  
CQRRCKEICEEEEEYNRQRDPQQQYEQCQERCQRHETEPHRMQTCQQRCEERRYKEKRKQ  
QKRYEEQQREDEEKEYEERMKEEDNRDPQQREYEDCRRRCEQQEPQQYQCQRRCREQQR  
QHGRGGDLINPPQRGGSGRYEEGEEKQSDNPYYFDEDSLSTRFRTEEGHISVLENFYGRSK  
LLRALKNYRLVLLLEANPNAFVLPHTLDADAILLVIGGRGALKMIHRDNRESYNLECGDVI  
RIPAGTTFFYLINRDNNERLHIAKFLQTISTPGQYKEFFPAGGQNPEPYLSTFSKEILEAA  
LNTQAERLRGVLGQQREGVIISASQEQIRELTRDDSESRRWHIRRGGESSRGPYNLFNKR  
PLYSNKYQAYEVKPEDYRQLQDMDVSVFIANITQGSMMGPFNTRSTKVVVVASGEADV  
EMACPHLSGRHGGRRGGKRHEEEEEVHYEQVKARLSKREAIWVPGHPVVFVSSGNENLL  
LFAFGINAQNNHENFLAGRERNVQQIEPQAMELAFAPRKEVEELFNSQDESIFFPGPR  
QHQQQSSRSTKQQQPLVSIILDFVGF

>COMPARE00611 calcium binding protein, calmodulin, partial [*Artemisia lavandulifolia*]

ADQLTDDQISEFKEAFSLFDKDGDCITTKELGTMVMSLQGNPTEAELQDMINEVDADGN  
GTIDFPEFLNLMARKMKDTSSEELKEAFRVFDKQNGFISAAELRHVMTNLGEKLTDEE  
VDEMIREADVDDGQINYEFEVKVMMAK

>COMPARE00612 calcium binding protein, calmodulin, partial [*Artemisia sieversiana*]

ADQLTDDQISEFKEAFSLFDKDGDCITTKELGTMVMSLQGNPTEAELQDMINEVDADGN  
GTIDFPEFLNLMARKMKDTSSEELKEAFRVFDKQNGFISAAELRHVMTNLGEKLTDEE  
VDEMIREADVDDGQINYEFEVKVMMAK

>COMPARE00587 superoxide dismutase, partial [*Prosopis velutina*]  
KYASEVYEKE

>COMPARE00588 superoxide dismutase, partial [*Prosopis velutina*]  
RLVVETTANQDPLVTKG

>COMPARE00589 superoxide dismutase, partial [*Prosopis velutina*]  
KHHQTYITNYNKA

>COMPARE00590 superoxide dismutase, partial [*Prosopis velutina*]  
KALEQLHDAMEKG

>COMPARE00593 triosephosphate isomerase, partial [*Prosopis velutina*]  
KWIHSNVSAEVASSVRI

>COMPARE00594 triosephosphate isomerase, partial [*Prosopis velutina*]  
KVIACVGETLEQRE

>COMPARE00595 triosephosphate isomerase, partial [*Prosopis velutina*]  
KVAYALSQGLKV

>COMPARE00597 triosephosphate isomerase, partial [*Prosopis velutina*]  
RQLFNEANEFVADKV

>COMPARE00598 triosephosphate isomerase, partial [*Prosopis velutina*]  
KIVTTLNEAQVPGEDVVEVVVSPPFVFLSLVKS

>COMPARE00599 triosephosphate isomerase, partial [*Prosopis velutina*]

RIIYGGSVNGANCKE  
>COMPARE00600 triosephosphate isomerase, partial [Prosopis velutina]  
KFFVGGNWKC  
>COMPARE00601 triosephosphate isomerase, partial [Prosopis velutina]  
REAGSTMAVVAEQTKA  
>COMPARE00562 glutelin, partial [Prosopis velutina]  
KLALEKNGFALPRY  
>COMPARE00563 glutelin, partial [Prosopis velutina]  
RAQVVGPDGKRV  
>COMPARE00564 glutelin, partial [Prosopis velutina]  
RTSDAIFPPPK  
>COMPARE00565 glutelin, partial [Prosopis velutina]  
KTLVGSQSGKG  
>COMPARE00566 glutelin, partial [Prosopis velutina]  
KALSPTVLQAGFNVDKSL  
>COMPARE00567 glutelin, partial [Prosopis velutina]  
KAGNLFIVPRF  
>COMPARE00555 glucan endo-1,3-beta-glucosidase, partial [Prosopis velutina]  
KYIAVGNVNPVGRN  
>COMPARE00556 glucan endo-1,3-beta-glucosidase, partial [Prosopis velutina]  
RTYLDNLIRH  
>COMPARE00557 glucan endo-1,3-beta-glucosidase, partial [Prosopis velutina]  
RLYDPNQAALALRN  
>COMPARE00558 glucan endo-1,3-beta-glucosidase, partial [Prosopis velutina]  
RGYQNLFDALLDSVHAALDSTKI  
>COMPARE00559 glucan endo-1,3-beta-glucosidase, partial [Prosopis velutina]  
RAVQNVYQAIRA  
>COMPARE00568 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
RVPTVDVSVVDLTVRL  
>COMPARE00569 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KVLPSLNGKL  
>COMPARE00570 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KVIISAPSKD  
>COMPARE00571 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KTLVFGDKPVSVFGTKN  
>COMPARE00572 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KSDINIVSNASCTTNCLAPLAKV  
>COMPARE00573 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KIGINGFGRI  
>COMPARE00574 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KGVLGYTEDDVSTDFVGDGRS  
>COMPARE00575 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KEASEGSLKGGKASYDEIKA  
>COMPARE00576 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KDAPMFVVGVNEKE  
>COMPARE00577 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
KAGISLSNNFVKL  
>COMPARE00578 glyceraldehyde-3-phosphate-dehydrogenase, partial [Prosopis velutina]  
RAASFNIIPSSTGAACA  
>COMPARE00545 fructose-bisphosphate aldolase, partial [Prosopis velutina]

KYQDELIANAAYIGTPGKG  
>COMPARE00546 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
RVAPEVIAEHTVRA  
>COMPARE00547 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
KTASGKPFVDVLKE  
>COMPARE00548 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
RLASINVENVESNRR  
>COMPARE00549 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
KIGPNEPSPLAIHENAYGLARY  
>COMPARE00550 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
KGILAADESTGTIGKRL  
>COMPARE00552 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
KEGGVLPGIKV  
>COMPARE00553 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
KANSEATLGTYKG  
>COMPARE00554 fructose-bisphosphate aldolase, partial [Prosopis velutina]  
RALQQSTIKA  
>COMPARE00583 S-adenosylmethionine synthase 1-like, partial [Prosopis velutina]  
KVACETCTKT  
>COMPARE00584 S-adenosylmethionine synthase 1-like, partial [Prosopis velutina]  
KSVVASGLARR  
>COMPARE00585 S-adenosylmethionine synthase 1-like, partial [Prosopis velutina]  
RGIGFVSADVGLDADNCKV  
>COMPARE00586 S-adenosylmethionine synthase 1-like, partial [Prosopis velutina]  
RFVIGGPHGDAGLTGRK  
>COMPARE00602 triosephosphate isomerase, partial [Prosopis velutina]  
KVATPAQAQEVHAELRKW  
>COMPARE00579 polygalacturonase, partial [Prosopis velutina]  
RYDNEAPVSNVNVKN  
>COMPARE00580 polygalacturonase, partial [Prosopis velutina]  
RYNNEQPVSNVNVKN  
>COMPARE00581 polygalacturonase, partial [Prosopis velutina]  
KVLVGAGTYNMNAVDLKG  
>COMPARE00582 polygalacturonase, partial [Prosopis velutina]  
KAWTDACAATEASKV  
>COMPARE00591 thaumatin-like, partial [Prosopis velutina]  
KVTGSDGNVIACKS  
>COMPARE00592 thaumatin-like, partial [Prosopis velutina]  
KANINAACPNDLKV  
>COMPARE00613 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula  
(Crassostrea plicatula)]  
MDSIKKKMIAMK  
>COMPARE00620 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes  
bellicosus]  
AATIAKLEEGFKKLEAATDCK  
>COMPARE00522 27kD gamma zein, partial from AAL16977.1 [Zea mays]  
THTSGGCGCQPPPPVH  
>COMPARE00614 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula  
(Crassostrea plicatula)]  
AEQLEQLRDTEEQKAKIEEDLTSLQKKHSNLENEFDTVNEKYQECQTK

>COMPARE00615 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula (Crassostrea plicatula)]  
TASEAEQEIQSLNRRIQLLEEDMERSEERLQTATEKLEEASK

>COMPARE00616 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula (Crassostrea plicatula)]  
KVLLENLNNASEERTDVLEKQLTEAKLIAEEADKK

>COMPARE00617 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula (Crassostrea plicatula)]  
KLAITEVDLERAEARLEAAEAKVYELEEQLSVVANNIKTLQVQNDQASQREDSYEETIRD  
LTQR

>COMPARE00618 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula (Crassostrea plicatula)]  
EVDRLLEDELLAEKER

>COMPARE00619 tropomyosin, partial from UTA91547.1 [Alectryonella plicatula (Crassostrea plicatula)]  
AISDELDQTFEELAGY

>Q1KS35 Pen m 13; fatty acid-binding protein [Penaeus monodon]  
MAKIEGKFKMESSENFDEFMKALGVGLVMRKMGNAAATPTVEITKDGDTYAMKTTTTFTKT  
EIKFKLGEFEFEETTADGRVVKSTITLDGNKLVHKQVGDKEKKEKDSSELLREFTDDKMLME  
CKVDDIVCKRVYSRLE

>G1AP69 Pen m 7; hemocyanin [Penaeus monodon]  
MGTVMNKVLLLLFALVAAAAWPNFGFQSDAGGAADAQKQHDVNFLLHKKIYGDIRDNSNLKG  
KADSFDPKANLSHYSDDGGKAVQKLMRDLKDNRLQQRHWFSLFNPRQREELMLFDVLIH  
CKDWDTFVSNAAAYFRQIMNEGEFVYALYVAVIHSPLSEHVLPPLYEVTPLHFTNSEVIE  
AAYRAKQTQKPGKFKSSFTGTKKNPEQRVAYFGEDIGMNTHHVTWHMEFPFWDDKYSHH  
LDRKGENFFVWHHQLTVRFDAERLSNYLDPVDELHWEKPIVQGFAPHTTYKYGGQFPSPR  
DNVDFEDVDGVARIRDLLIVESRIRDAIAHGIVDRAGNHIDIMNERGIDVLGDVIESSL  
YSPNVQYYGALHNTAHIVLGRQSDPHGKYDLPPGVLEHFETATRDPSFFRLHKYMDNIFK  
EHKDSLPPYTVEELTFAGVSVDNVAIEGELETFEEDFEYNLINAVDDETEQIPDVEISTYV  
PRLNHKDFKIKIDVSNKNGQEVLATVRIFAWPHLDNNGIEFTFDEGRWNAIELDKFWVKL  
PAGTHHFERKSSSEAVTVPDVPSFATLFEKTKEALAGADSGLTDFESATGIPNRFLLPKG  
NEQGLEFDLVAVTDGAADAADVGLHENTEFNHYGSHGKYPDNRPHGYPLDRKVPDERVF  
EDLPNFGHIQVKVFNHGEYIQHD

>F8QN77 Pen m 8; triosephosphate isomerase [Penaeus monodon]  
MSSPRKFFVIGNWKMNVDKNRINGIVKMMNNAALDANTEAVVGCPSCYLSYAREHLTHNI  
GIAAQNCYKVARGNFSGEISPEMIKDCGCDWVILGHPERRTVFNEPDSFIAEKVAHAQEA  
GMKIIACLCEETDDRQKGRTEEVLFKQLTSLAAAITDWSRVVLAFAEALWASNTGVFATNQ  
QVQDALGLVRNWLRRNVSDKVADTTRLIYAGSVSSDNCREMASLENLDGFLVGGASLKPD  
IVDIINSRRSHVSELLTSLRIEEQQG

>COMPARE00621 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]  
QTDKHPNKDFGDVNQFVNVDPDGKFFVISTR

>COMPARE00622 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]  
SMEGYPFNPCLTEAQYKEMESKVSSTLSNLEGELEKGTYPPLTGMTK

>COMPARE00623 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]  
LIDDHFLFKEGDRFLQAANACR

>COMPARE00624 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]

TFLVWCNEEDHLRIISMQMGGDLGQVYRRLVSAVNEIEKR

>COMPARE00625 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]

LGFLTFCPTNLGTTVR

>COMPARE00626 Cal b 2; arginine kinase, partial from UVH30529.1 [Callinectes bellicosus]

MGLTEYQAVKEMQDGILELIKIEKEMQ