

>COMPARE0339 Art ab 1; defensin, partial from AHF71021.1 [*Artemisia absinthium*]
AGSKLCEKTSKTSWGGKCDNKKCDKKCIEWEKAQHGACHKREAGKESCFCYFDCSK

>COMPARE0340 Art an 1; defensin, partial from AHF71022.1 [*Artemisia annua*]
TWSGKCDNKKCDKKCIEWEKAQHGACHKREAGKESCFCYFDCSK

>COMPARE0341 Art c 1; defensin, partial from AHF71023.1 [*Artemisia californica*]
CDNKKCDKKCIEWEKAQHGACHKREAGKESCFCYFDCSK

>COMPARE0342 Art f 1; defensin, partial from AHF71024.1 [*Artemisia frigida*]
SGKCDNKKCDKKCIEWEK

>COMPARE0343 Art f 1; defensin, partial from AHF71024.1 [*Artemisia frigida*]
EAGKESCFCYFDCSK

>COMPARE0344 Art t 1; defensin, partial from AHF71026.1 [*Artemisia tridentata*]
CDNKKCDKKCIEWEK

>COMPARE0345 Art t 1; defensin, partial from AHF71026.1 [*Artemisia tridentata*]
EAGKESCFCYFDCSK

>COMPARE0346 vitellogenin, partial from BAM22586.1 [*Gadus chalcogrammus*]
KKILNPSVSRSSSSSSSSSSAKLFSSSSSSSSSSSRSSSSSSSRSSSKLNSKSSSSSS
SSSSSSSSRSARSRLSNTVVYP

>COMPARE0347 vitellogenin, partial from BAM22586.1 [*Gadus chalcogrammus*]
QVYEAQCSYAKNTLTTFNRRYKNEMLSCNQVLAQDCSKELKFMVLLKKNIEQNWINV
KLADIDIDLYPENDNMIVKVNMGQIPIISNLPYQHPTGTIQIKSNGEGISVYAASHGLHEV
YFDRSSWKVVLADWMKQTCGICGKADGEVRQEFRTPNGQLAKDAVSYAHSWVIPAENCQ
DASECRMREQESVKLEKQIMVHGQESNCHSVETVLRCLPGCIPVKTPVTVGFHCLPISAE
QQRSGDLSSVLEQSVDLRESVMAHLACNCANLCA

>COMPARE0348 Art l 1; defensin, partial from AHF71025.1 [*Artemisia ludoviciana*]
SGKCDNKKCDKKCIEWEK

>COMPARE0349 Art l 1; defensin, partial from AHF71025.1 [*Artemisia ludoviciana*]
EAGKESCFCYFDCSK

>P13080.1 Aed a 4; alpha-glucosidase [*Aedes aegypti*]
MKIFVPLLSFLLAGLTTGLDWEHGNFYQVYPRSFKSDGDGIGDLDGVTTEKLYLKDIG
MDGVWLSPIFSSPMADFGYDISNFREIQTEYGDLDQFRLSDKCKQLGLHLILDFVPNHT
SDQHEYFKKSVQKDETYKDFYVWHPGVHGPNTKVPPSNWISVFRGSSWEWNEERQEFYL
HQFLKEQPDLYRNPVVEEMKNVLRVWLDRGVSGFRIDAVPYLFESDIIDGRYRNEPES
RTTDDPENPAYLVHTQTMDQPETYDMIYQWRAVLDEYSKTDNRTRIMMTEGYTSLPKIIE
FFGNATANGAQIPNFVEVISNVKKNSTGADFATYVVKRWLDAKPANRRSNWVLGNHDNNRL
GSRLGENKIDLYNIALQTLPIAVTYGEEIGMLDQWIPWNETVDPAAACRSDEASYSAYS
RDPARTPMQWDSGKNAGFSKAAKTWLPVADNYKTLNVKIQDRARKSHLKFKKLTKYRKR
QILTEGDIDIKVSGENLLVYKRKVDKVGYYVVALNFGTEPVALGLSSLFDRADQRMQVVV
SSNRVSTPDNVWVDVNYVLIGESGIVLQYLWGKNPIVS

>COMPARE0350 unknown function, translation from AK068307.1 [*Oryza sativa*]
MKLVSIYLLVLCVVGANELLVVAASGNDGGGGRFVYSGFAGANLTLTGTATVTPAGLIEL
TNGTLQLKGHAFHPTPLRFGFGSGGGGGGDGVVRSFSASFVFGILSAYPDMSAHGIVFL
VSPTTDFSAALASQYLGLVNVTSNGDARNRIFAVELDTLQQDEFRDINDNHVGV DINGLV
SLQSTSAGYYAADINGGGFRNLTLISHEAMRVWVDYDAGDARIDVTLAPLAVAKPVRPLI
SAAYNLSSVITDTAYVGFSSATGSFNSRHVYLGWSFAVDGGPAPAIDVAKLPKLPREGPK
ARSKFLEIFLPIASAAVVLAMGILVILLVRRRKRYTELREDWEVEFGPHRFYPYKDLHHT
QGFESKCLLVGGGFRVYKGVLPNSNVEIAVKRVS HDSSQGVKEFVAEVVSLGRLQHCNL
VRLGVCRRKGEMLVYEYMSNGSLDKYLHGQDNKPTLSWAQRFQI IKDIASGLLYLHEE
CDKVVIHRDIKASNVLLDNEMNARLGD FGLARLYDHGEDPQSTHVVTIGYLAPELGRTS
KATPLTDVFAFGTFILEVTCGRRPIYHDSHGTVMLVDWVLDHWHKQSLVDTVDLKLHGE
FDVGEACLVLKLLCSHPFINARPDMMRRVMQYLKREVALPELMPTSMSFHMLALMQNDG

FDSYVQSYSSNSKGNISTATSSLLEEG

>COMPARE0351 unknown function, translation from AK119653.1 [*Oryza sativa*]
MDRVRGCAFLGLVLLAGSLFAFSVAKEETKLLGTVIGIDLGTTYSCVGVYKNGHVEIIAN
DQGNRITPSWVAFTDSERLIGEAANKQAAVNPERTIFDVKRLIGRKFEDKEVQRDMKLV
YKIVNKDGPYIQVKIKDGENKVFSPPEVSAMILGKMKETAAYLGGKINDAVVTVPAYF
NDAQRQATKDAGVIAGLNVARIINEPTAAAIAYGLDKKGGKKNILVFDLGGGTFDVSILT
IDNGVFEVLATNGDTHLGGEDFDQRIMEYFIKLIKKKYSKDISKDNRALGKLRREAERAK
RALSNQHQRVEIESLFDGTDSEPLTRARFEELNNDLFRKTMGPVKKAMDDAGLEKSQI
HEIVLVGGSTRIPKAQQLLRDYFEGKEPNKGVNPDEAVAYGAAVQGSILSGEGGDETKDI
LLLDVAPLTLGIETVGGVMTKLIPRNTVIPTKKSQVFTTYQDQQTTSIQVFEGERSMTK
DCRLLGKFDLSGIPAAPRGTPQIEVTFEVDANGILNVKAEDKGTGKSEKITITNEKGRLS
PEEIDRMVREAEFEAEEDKVKKERIDARNQLETYVYNMKNVTGDKDKLADKLESEEKEKV
EEALKEALEWLDENQTAEEYEEKLEVEAVCNPIISAVYQRTGGAPGGGADGEGGVDD
EHDEL

>COMPARE0352 unknown function, translation from AK242260.1 [*Oryza sativa*]
MKIIFV FALLAIAACSASAQFDVLGQSYRQYQLQSPVLLQQQVLSPLYNEFVRQQYGI
AASPFLQSAAFQLRNNQVWQQLALVAQQSHYQDINIVQAIQQLQLQQFGDLYFDRNLAQA
AQLLAFNVPSRYGIYPRYYGAPSTITTLGGVL

>AKV72166.1 Aca f 1; Ole e 1-like [*Acacia farnesiana*]
DDVPKPPVSQFHVQGLVYCDTCRYPFITEASPIMEGATVKLECRNITAGTQTFKAEAVTD
KVGQYSIPVDGDHEDDICEIELVKSPDNQCSEIPHDVYAKQSAKVSLTSNNGEASDVRS
ANALGFMRKEPLPECPEVLKEKLDMYDVKAN

>ABL09312.1 amylase-like [*Acarus siro*]
MAHLLAVVAITLALSQSVFVGGSPYSNPHFTGSRSVITHLMQWKFDIAAECERFLGPKG
YGGIQLSPVNEHAVLGNRPWYELYQPVGYKIQSRSGNEEQFKGMVQRNCNKVGVRIYVDIV
MNHMSGAQEGHNCWFKLQWHHDVSRCSLLVPNDFHGRECHTDNMDIKNYDNPEEARN
RLSGLRDLKQSSEYVRQKQADFLNHLIDLGVAGSRSDASKHMPGDLEAIYGLHNLNTA
YFPANSRPFYHEVIYYGGDIKSSDYTKLGRAIEFHFYRDIANVRRHNQLKTVKNFGQ
PWGMVPSDDALVMVDSHDLQRFTGQVGVNINIFYESRLLKVATAFMLAWPYGVPRVMSSY
HWDQKIEDGKDKNDWIGPPSDGSGNLSVTPQDDTCNKIEWICEHRWRQIYNMVHFRNVA
GNEAVSHWWDNGDYQIAFGRGSKAFIAINLQDQGGLNRKLATGLPQGTCDLVTGNLAGG
KCTGGTVDGSGNADINIAKTAEDPFVAIHVEAKLH

>ABL09307.1 Aca s 13; fatty acid-binding protein [*Acarus siro*]
MVQINGSYKLEKSDNFDALFKELGLNFVTRNLAKSATPTVEVSVNGDSYTIKTASTLKNT
EISFKLGEFEEARADGKTVKTVVNKESDTKFFVQVQQGDKEVTIVREFSDEGLTVTATVN
GVTSVRFYKRQ

>QCI56568.1 tropomyosin [*Acheta domesticus*]
MDAIKKKMQAMKLEKDNAMDKADTCEGQAKDANNKADKINEDVQELTKKLAQVENDLITT
KANLEQANKDLEDKEKALQAAESEMAALNRKVQLVEEDLERSEERAATAATKLQEASEAA
DEAQRMCVKLENRSQQDEERMDQLTNQLKEARLLAEDADGKSDEVSRLAFVEDELEVAE
DRVKSGDSKIMELEEEELKVVGNLSK

>QCI56569.1 tropomyosin [*Acheta domesticus*]
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARGLQKKIQTIENELDQT
QEQLMQVNAKLEEKDKALQTAEGEIAALNRRIQLLEEDLERSEERLATATAKLAEASQAA
DESERARKILENRS LADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE
ERAEAGESKIVELEEEELRVVGN

>AGC39172.1 kiwellin [*Actinidia arguta*]
MAQLTLLLLSLFLTLISLPPPGASISSCNGPCRDLNDCDGLICIKGKCNDDPEVGT
HICGGTTPSPQPGSCNPSGTLTCQGKSYPTYDCSPPVTSSTPAKLTNNDFSEGGDGGGP
SECD ESYHSNNERIVALSTGWYNGGSRGKMIRITASNGKSVSAKVVDECDSRHGCDKEHAGQP

PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA
>AGC39173.1 kiwellin [Actinidia arguta]
MAQLTLLLLLSLFFTLISLPPPASISSCNGPCRDLNDCNGQLICIKGKCNDDEVEGTHIC
GGTTPSPQPGSCKPSGLTLCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAGQP
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA
>AGC39174.1 kiwellin [Actinidia arguta]
MAQLTLLLLLSLFLTLISLPPPASISSCNGPCRDLNDCDQQLICIKGKCNDDEVEGTHIC
GGTTPSPQPGGCNPSGLTLCQGKSYPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAGQP
PCRNNIVDGSNAVWSALGLDKNVGVVDITWSMA
>P00785.4 Act d 1; actinidin [Actinidia chinensis]
MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGEWE
RRFEIFKETLRFIDEHNADTNRSYKVLNQFADLTDEEFRSTYLRFSTSGSNKTKVSNRYE
PRVQVLPSPYVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGLISLSEQELI
DCGRTQNRGCGGYITDGFQFIINNGGINTENYPYTAQDGEKNVDLQNEKYVTIDTYE
NVPYNNEWALQTAVTYQPVSVDAAGDAFKQYSSGIFTGPCGTAVDHAVTIVGYGTEGG
IDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKYNNQNHKPKPYSSLINPP
AFSMSKDGVPVDDGQRYSA
>AGC39168.1 Act c 5; kiwellin [Actinidia chinensis]
MAQLSLLLLLSLFLTLISLPPPASISSCNGPCRDLNDCDQQLICIKGKCNDDEVEGTHIC
RGTTPSPQPGGCKPSGLTLCQGKSHPTYDCSPPVTSSTPAKLTNNDSEGGDGGGPSECD
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAGQP
PCRNNIVDGSNAVWSALGLNKNVGVVDITWSMA
>P85204.1 Act c 10; lipid transfer protein, partial [Actinidia chinensis]
AVSCGQVDTALTPCL
>CAM31908.1 Act c 8; pathogenesis related protein, PR-10, Bet v 1-like [Actinidia
chinensis]
MGVVTYDMEIPSKVPPVKLYKAFILDGDTLVPKVLPHAIKCVKILEGDGCAGTIKEVTFG
EGSHHKCVKQRVDAIDKDNLTYSYTIIEGDVLAEKFESISYHIKIVACPDGGSICKNRSI
YTTKGDKVSEEEIKLGKEKAAEIFKALEAYLLANPDYC
>COMPARE176 phytocystatin, partial [Actinidia chinensis]
VAAGGWRPIEE
>AGC39176.1 thaumatin-like [Actinidia chinensis]
MSTFKSLSLALLFIAFLFTCARGATFNIINNCPTVWAAAVPGGGKRLDRGQNWIIINPG
AGTKGARVWARTGCNFDGAGRGKQGTGDCNGLLQCQAFGQPPNTLAEYALNQFNLDFFD
ISLVDGFNVAMEFSPTS GGGCTRGIKCTANINEQCPNELRAPGGCNPCTVFKTDQYCCNS
GNCGPTDYSRFFKTRCPDAYSYPKDDQTSTFTCPGGTNYKVVFCP
>P83958.1 thaumatin-like, partial [Actinidia chinensis]
ATFNFINNCPFTVWAAAVPG
>COMPARE178 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]
GEAVFNDRIR
>COMPARE015 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]
LTSVNSFNLPILNYLRLSAEKVLYR
>C0HJF9.1 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]
NRQPSKYGLEETI
>COMPARE180 Act d 12; 11S globulin, cupin, partial [Actinidia deliciosa]
LVENIDNPSRADIFNPR
>CAA34486.1 Act d 1; actinidin [Actinidia deliciosa]
MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGEWE

RRFEIFKETLRFIDEHNADTNRSYKVGLNQFADLTDEEFRSTYLGFTSGSNKTKVSNRYE
PRFGQVLPSYVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGVLISLSEQELI
DCGRTQNTRGCNGGYITDGFQFIINNGGINTENYPYTAQDGEENLDLQNEKYVTIDTYE
NVPYNNEWALQTAVTYQPVSVDAAGDAFKHYSSGIFTGPCGTAIDHAVTIVGYGTEGG
IDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKYNNQNHHPKPYSSLINPP
AFSMSKDGPVGVDDGQRYSA

>AAA32629.1 Act d 1; actinidin [Actinidia deliciosa]
MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGWE
RRFEIFKETLRFIDEHNADTNRSYKVGLNQFADLTDEEFRSTYLGFTSGSNKTKVSNRYE
PRVGQVLPSYVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGVLISLSEQELI
DCGRTQNTRGCNGGYITDGFQFIINNGGINTENYPYTAQDGEENVELQNEKYVTIDTYE
NVPYNNEWALQTAVTYQPVSVDAAGDAFKQYSSGIFTGPCGTAIDHAVTIVGYGTEGG
IDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKYNNQNYPEPYSSLINPP
AFSMSKDGPVGVDDGQRYSA

>A5HII1.1 Act d 1; actinidin [Actinidia deliciosa]
MGLPKSFVMSLLFFSTLLILSLAFNAKNLTQRTNDEVKAMYESWLIKYGKSYNSLGWE
RRFEIFKETLRFIDEHNADTNRSYKVGLNQFADLTDEEFRSTYLGFTSGSNKTKVSNRYE
PRVGQVLPSYVDWRSAGAVVDIKSQGECGGCWAFAIATVEGINKIVTGVLISLSEQELI
DCGRTQNTRGCNGGYITDGFQFIINNGGINTENYPYTAQDGEENLDLQNEKYVTIDTYE
NVPYNNEWALQTAVTYQPVSVDAAGDAFKHYSSGIFTGPCGTAIDHAVTIVGYGTEGG
IDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKYNNQNHHPKPYSSLINPP
AFSMSKDGPVGVDDGQRYSA

>AGC39164.1 Act d 5; kiwellin [Actinidia deliciosa]
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGQLICIKGKCNDPQVGT
RGTTPSPQPGGCKPSGTLTCRGKSHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGG
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAG
PCRNNIVDGSNAVWSALGLDKNVGVDDITWSMA

>AGC39165.1 Act d 5; kiwellin [Actinidia deliciosa]
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGQLICIKGKCNDPVEVGT
RGTTPSPQPGGCKPSGTLTCRGKSHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGG
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAG
PCRNNIVDGSNAVWSALGLDKNVGVDDITWSMA

>AGC39166.1 Act d 5; kiwellin [Actinidia deliciosa]
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGQLICIKGKCNDPQVGT
RGTTPSPQPGGCKPSGTLTCRGKSHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGG
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAG
PCRNNIVDGSNAVWSALGLDKNVGVDDITWSMA

>AGC39167.1 Act d 5; kiwellin [Actinidia deliciosa]
MAQLSLLVLSLFLTLISLPPPASISSCNGPCRDLNDCDGQLICIEGKCNDPVEVGT
RGTTPSPQPGGCKPSGTLTCRGKSHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGG
ESYHSNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAG
PCRNNIVDGSNAVWSALGLDKNVGVDDITWSMA

>P84527.2 Act d 5; kiwellin [Actinidia deliciosa]
MAQLALLLSLFLTLISLAPPGASISSCNGPCRDLNDCDGQLICIKGKCNDPQVGT
RGTTPSPQPGGCKPSGTLTCRGKSHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGG
ESYHNNERIVALSTGWYNGGSRGCMIRITASNGKSVSAKVVDECDRHRGCDKEHAG
PCRNNIVDGSNAVWSALGLDKNVGVDDITWSMA

>4X9U_A Act d 5; kiwellin, partial [Actinidia deliciosa]
ISSCNGPCRDLNDCDGQLICIKGKCNDPQVGTICRGTTSXQPGGCKPSGTLTCRGK
SHPTYDCSPPVTSSTPAKLTNNDPSEGGDGGGSECDSESYHNNERIVALSTGWYNGGSR

GKMIRITASNGKSVSAKVVDECDRHRGCDKEHAGQPPCRNNIVDGSNAVWSALGLDKNVG
VVDITWSMA
>P86137.2 Act d 10; lipid transfer protein [Actinidia deliciosa]
AVSCGQVDTALTPCLTYLTKGGTPSTQCCSGVRSLSMTGKVPDRQAACNCLKQAAARY
QGIKDAAAALSQKCGVQLSVPIRSTDCSKIS
>P85206.1 Act d 10; lipid transfer protein [Actinidia deliciosa]
TVSCGQVDTALTPCLTYLTKGGTPSTQCCSGVRSLSMTGKVPDRQAACNCLKQAAARY
QGIKDAAAALSQKCGVQLSVPIRSTDCSKIS
>CAM31909.1 Act d 8; pathogenesis related protein, PR-10, Bet v 1-like [Actinidia
deliciosa]
MGAITYDMEIPSSISAEMFKAFVLDGDTIIPKALPHAITGVQTLLEGDGGVGTIKLTTFG
EGSVHKSVKHRIDGLKENFTYSYSIIEGGALDVFESISYHIKIVATPDGGCICKNRSIY
TPKCDQVSEEEIKAGKERASGIFKKVEAYLLANPDC
>P85524.1 Act d 11; pathogenesis related protein, PR-10, Bet v 1-like [Actinidia
deliciosa]
MDLSGKMKVQVEILSDGIVFYEIFRYRLYLISEMSPVNIQGVLDLLEGNWGTVGSVIFFKY
TIDGKEKTAKDIVEAIDEETKSVTFKIVEGLMELYKTFIIIVQVDTKGEHNSVTWTFHY
EKLKEDVEEPNTLMNFCIEITKDIETYHLK
>AAR92223.1 Act d 4; phytocystatin [Actinidia deliciosa]
MVPKPLSLLLFLLLALSAAVVGGRKLVAAAGWRPIESLNSAEVQDVAQFAVSEHNKQAND
ELQYQSVVRGYTQVVAGTNYRLVIAAKDGAVVGNYEAVVWDKPMHFRNLTSFRKV
>FG438715.1 Act d 9; profilin [Actinidia deliciosa]
MSWQTYVDDHLMCEIEGNYLTSAAIIGQDGSIIWAQSASFQFKPEEITAIMNDFSEPGTL
APTGLYLGGTKYMIQGEAGAVIRGKKGGVTVKKTNQALIIGIYDEP
>CAI38795.2 Act d 2; thaumatin-like [Actinidia deliciosa]
MSTFKSLSLALLFIAFLFTCARGATFNIINNCPTVWAAAVPGGGKRLDRGQNWIIINPG
AGTKGARVWPRTGCNFDGAGRKCTQGDENGLLQCQAFGQPPNTLAEYALNQFNLDFFD
ISLVDGFNVAMEFSPTS GGCTRGIKCTADINGQCPNELRAPGGCNPCTVFKTDQYCCNS
GNCGLTNFSKFFKDRCPDAYSYPKDDQSTFTCPAGTNYKVVFCEP
>ABQ42566.1 Act d 2; thaumatin-like [Actinidia deliciosa]
ATFNIINNCPTVWAAAVPGGGKRLDRGQNWIIINPSAGTKGARVWPRTGCNFDGAGRKCT
QGDENGLLQCQAFGQPPNTLAEYALNQFNLDFFDISLVDGFNVAMEFSPTS GGCTRGI
KCTADINGQCPNELRAPGGCNPCTVFKTDQFCCNSGNCGLTNFSKFFKDRCPDAYSYPK
DDQSTFTCPAGTNYKVVFCEP
>COMPARE00283 Act d 3; unknown function, partial from P85063.3 [Actinidia
deliciosa]
FTDGLMKNGNFELAP
>AGC39169.1 kiwellin [Actinidia eriantha]
MAQLSLLLLSLFLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC
RGTTSPSPQPGGCNPSGTLTCRGSYPTYDCSPPVTSSTPAKLTNNDPSEGGDGGGPSECD
ERYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECDRHRGCDKEHAGQP
PCRNNIVDGSNAVWSALGLDKNVGVDITWSMA
>AGC39170.1 kiwellin [Actinidia eriantha]
MAQLSLLLLSLFLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDDPQVGTHIC
RGTTSPSPQPGGCNPSGTLTCRGSYPTYDCSPPVTSSTPAKLTNNDPSEGGDGGGPSECD
ERYHSNNERIVALSTGWYNGGSRGKMRITASNGKSVSAKVVDECDRHRGCDKEHAGQP
PCRNNIVDGSNAVWSALGLDKNVGVDITWSMA
>AGC39171.1 kiwellin [Actinidia eriantha]
MAQLSLLFLSLFLTLISLAPSGASISSCNGPCRDLNDCDGLICIKGKCNDDEVEGTHIC
RGTTSPSPQPGGCNPSGTLTCRGSYPTYDCSPPVTSSTPAKLTNNDPSEGGDGGGPSECD

ERYHSNNERIVALSTGWYNGGSRGKMIRITASNGKSVSAKVVDECDRHHGCDKEHAGQP
PCRNINVDGSAVWSALGLDKNVGVVDITWSMA

>AAC37218.1 Aed a 1; apyrase [Aedes aegypti]

MAGRPGYSAVIFLYVVSVAVIARATDNMPPNKDVSCLFPLTLIHINDLHARFEETNMKSN
ACTQKDQCIAGIARVYQKIKDLLKEYESKNPIYLNAGDNFQGLWYNLLRWNVTADFIKK
LKPAAMTLGNHEFDHTPKGLAPYLAELNKEGIPTIVANLVMNNDPDLKSSKIPKSIKLT
GKRKIGIIGVLYDKTHEIAQTGKVTLSNAVEAVRREAAALKKDKIDIIIVVLSHCSYEEDK
KIAAEAGDDIDVIVGAHSHSFLYSPDSKQPHDPKDKVEGYPYPTIVESKNKRKIPIVQAKS
FGKYVGRLLTYFDDETGEVQHWEGYPVFDHVKVQDQPQILKDLVPWREKVEAIGSTVVGET
KIELDRDSCRDQECTLGVLVYADGFADQYTNDTFRPFAIIQAGNFRNPIKVGKITNGDIE
AAPFGSTADLIRLKGADIWDVAEHSFALDDEGRTNCLQVSGLRIVIDISKPIRSRVKKIE
VMDYTNPKSDELKPLDKQAEYYIVVPSYLADGKDGFSAMKRATARRTGPLDSDVFKNYVE
KIKKVDNLKLRVIVCKGSKCT

>P50635.2 Aed a 1; apyrase [Aedes aegypti]

MAGRPGYSEVIFLYVVSVAVIARATDNMPVNDVSKLFLPLTLIHINDLHARFEETNMKSN
VCTQKDQCIAGIARVYQKIKDLLKEYESKNPIYLNAGDNFQGLWYNLLRWNVTADFIKK
LKPAAMTLGNHEFDHTPKGLAPYLAELNKEGIPTIVANLVMNNDPDLKSSKIPKSIKLT
GKRKIGIIGVLYDKTHEIAQTGKVTLSNAVEAVRREAAALKKDNIDIIIVVLSHCSYEEDK
KIAAEAGDDIDVIVGAHSHSFLYSPDSKQPHDPKDKVEGYPYPTLVESKNKRKIPIVQAKS
FGKYVGRLLTYFDEEGEVKNWEGYPVFDHVKVQDQPQILKDLVPWRAKVEAIGSTVVGET
MIELDRDSCRDQECTLGVLVYADGFADQYTNDTFRPFAIIQAGNFRNPIKVGKITNGDIE
AAPFGSTADLIRLKGADIWDVAEHSFALDDEGRTNCLQVSGLRIVIDISKPVRSRVKKIE
VMDYTNPKSDKLLKPLDKEAEEYYIVVPSYLADGKDGFSAMKRATARRTGPLDSDVFKNYVE
KIKKVDNLKLRVIVCKGSKCT

>COMPARE087 Aed a 5; calcium-binding protein, sarcoplasmic calcium-binding protein,
partial from Q16XK7 [Aedes aegypti]

AFIDAHYQMMDINNDGLVSIIEEYR

>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

>COMPARE086 Aed a 8; heat shock protein 70, partial [Aedes aegypti]

IEIESFYEGDOFSETLTR

>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]

NQLTTNPENTVFDKR

>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
>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]
QTFAEAINPGLVFVAAK
>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]
ECSFTNIACLMHNK
>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
>COMPARE181 Aed a 6; porin, partial from Q1HR57 [Aedes aegypti]
VTANNFALGYSTGDFVLHTNVNDGR
>AAB58417.1 Aed a 3; unknown function [Aedes aegypti]
MKPLVKLFLFLFCLVGIVLSRPMPEDEEPVAEGGDEETDDAGGDGEEENEHAGDED
AGGEDTGKEENTGHEDAGEEDAGEEDAGEEDAEKEEGEKEDAGDDAGSDDGEEDSTGGDE
GEANAEDSKGSEKNDPADTYRQVVALLDKDTKVDHIQSEYLRSALENDLQSEVRVPVVEA
IGRIGDYSKIQGCFCMSGKDVKKVISEEEKFKSCMSKKKSEYQCSSEDSFAAAKSKLSPI
TSKIKSCVSSKGR
>ABF18122.1 Aed a 3; unknown function [Aedes aegypti]
MKPLVKLFLFLFCLVGIVLSRPMPEDEEPVAEGGDDASGESEGEETDDAGGDGEEENE
EGEEHAGDKDAGGEDTGKEENTGHDDAGEEDAGEEDAGEEDAGEEDAEKEEGEKE
DAGDDAGSDDGEEDSTGGDEGEDNAEDSKGSEKNDPADTYRQVVALLDKDTKVDHIQSEY
LRSALENDLQSEVRVPVVEAIGRIGDYSKIQGCFCMSGKDVKKVISEEEKFKSCMSKKK
SEYQCSSEDSFAAAKSKLSPITSKIKSCVSSKGR
>P18153.2 Aed a 2; unknown function [Aedes aegypti]
MKLPLLLAIIVTTFVASTGPFDPPEMLFTFTRCMEDNLEDGPNRPLMLAKWKEWINEPV
DSPATQCFGKCVLVRTGLYDPVAQKFDASVIQEQFKAYPSLGEKSKVEAYANAVQQLPST
NNDCAAVFKAYDPVHKAHKDTSKNTL FHNKELTKGLYEKLGKDIRQKKQSYFEFCENKYY
PAGSDKRQQLCKIRQYTVLDDALFKEHTDCVMKIRYITKNNELDAEEVKRDFMQVNKDT
KALEKVLNDCKSKEPSNAGEKSWHYKCLVSESSVKDDFKEAFDYREVRSQIYAFNLPKKQ
VYSKPAVQSQVMEIDGKQCPQ
>COMPARE211 Aed a 1 2; D7 like salivary odorant-binding protein, partial [Aedes albopictus]
KSYFEFCENK
>COMPARE209 Aed a 1 2; D7 like salivary odorant-binding protein, partial from
P18153.2 [Aedes albopictus]

QSYFEFCENK

>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

>E37396 beta-expansin [*Agrostis alba*]

YTTEGGTKAEAEDVIPEGWKADTSYE

>Q7M1X7 beta-expansin [*Agrostis alba*]

IAKVPPGPNITADYGDKWLDKSTWYGKPTGAGPK

>Q7M1X9 beta-expansin [*Agrostis alba*]

IAKVPPGPNITATYGDWLDKSTWYGKPTGAGPK

>CAA76831.1 Aln g 4; calcium-binding protein, polcalcin [*Alnus glutinosa*]

MADDHPQDQAEHERIFKCFDANGDGKISASELGDALKTLGVSVPDEVKHMMAEIDTDGDG

FISFQEFTNFARANRGLVKDVAKIF

>AAB24432.1 Aln g 1; pathogenesis related protein, PR-10, Bet v 1-like [*Alnus glutinosa*]

MGVFNVEAETPSVIPAARLFKAFILDGDKLLPKVAPEAVSSVENIEGNGGPGTIKKITFP

EGSPFKYVKERVDEVDVRFKYSFSVIEGGAVGDALEKVCNEIKIVAAPDGGSSILKISNK

FHTKGDHEINAEQIKIEKEKAVGLLKAVERSYLLAHSDAYN

>P49148.1 Alt a 12; acidic ribosomal protein P1 [*Alternaria alternata*]

MSTSELATSYAALILADDGVDITADKLQSLIKAKEEVEPIWTTLFAKALEGKDVKDLL

LNVGSGGGAAPLPEALLLRWRAADAAPAAEKEKEEESDEDMGFGLFD

>CAA55071.2 Alt a 10; aldehyde dehydrogenase [*Alternaria alternata*]

MTSVKLSTPQTGEFEQPTGLFINNEFVKAVDGKTFDVINPSTEEVICSVQEATEKDVDIA

VAAARKAFNGPWRKETPENRGKLLNKLADLFKADLIAAVEALDNGKAFSMAKNVDVPA

AAGCLRRYGGWADKIEGKVVDTPDSFNIRKEPIGVCGQIIPWNFPILMWSWKIGPAIA

TGNTVVLKTAEQTPLSAYIACKLIQEAGFPPGVINVTGFGKIAGAAMSAHMDIDKIAFT

GSTVVGRQIMKSAAGSNLKKVTELEGGKSPNIVFADADLDEATHWVNFNGIYFNHGQACCA

GSRIYVQEEIYDKFIQRFKERRAAQNAVDPFAADTFQGPQVSQLQFDRIMGYIEEGKKSG

ATIETGGNRKGDGKYFIEPTIFSNVTEDMKIQQEIEFGPVCTISKFKTKADVIGKGNNTT

YGLAAAVHTSNLTTAIEVANALRAGTVWVNSYNTLHWQLPFGGYKESGIGRELGEAALDN

YIQTKTVSIRLGDVFLFG

>Q00002.2 Alt a 4; disulfide isomerase [*Alternaria alternata*]

ARDMTKQALPAVSEVTKDTLEEFKTADKVVLVAYFAADDKASNETFTSVANGLRDNFLFG

ATNDAALAKAEGVKQPGLVCTSPSTTARTSSPRPSMRTYPRLRKVASTPLIGEVGPETYA

GYMAAGIPLAYIFAETPEEREFAKELKPLALKHKGEINFATIDAKSFGQHAGNLNLKVG

TWPAFAIQRTEKNEKFTNQEAKITEKEIGKFVDDFLAGKIDPSIKSEPIPESNDGPVTV

VVAHNYKDVVIDNDKDVLFVYFAPWCGHCKALAPKYEELGQLYASDELSKLVTIKVDAT

LNDVPDEIQGFLPSSLFPLARRMPQSTTLVPHCRGSRPVHRRERLTQASASVGEAVEDAT

ESAKASASSATDSAASAVSEGTETVKSGASVASDSASSAASEATKSVKSAASEVTNSASS

AASEASASASSVKDEL

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

MTITKIHARSVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKSKWGGK

GVTKAVANVNDTIAPALIKEKLDVKDQSAVDAFLNKLDGTTNKNLGNAILGVSMIAIAK

AAAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVNLNGGSHAGGRALAFQEFMIVPCEAPTFS

EAMRQGAEVYQKLKALAKKTYGQSAGNVGDEGGVAPDIQTAEALDLITKAIEEAGYTGK
IKIAMDVASSEFYKADEKKYDLDFKNPDSKSKWLTYEQLAEMYKSLAEKYPIVSIEDPF
AEDDWEAWSYFFKTYDQGIVGDDLTVTNPEFIKKAIELKSCNALLLKVNQIGTITEAIQA
AKDAFGAGWGMVSHRSGETEDVTIADIVVGLRSGQIKTGAPARSERLAKLNQILRIEE
LGDNAVYAGNNFRTAVNL
>Q6R4B4.1 Alt a 13; glutathione S-transferase [Alternaria alternata]
MSDKPSELAVQKLVLFAVKGTATSTHNTVRPLILLDELGVPHEIYVDRVSAPWFTEINP
HRMVPVILEKSPDGRDTRLAWESTSTLMYIADAYDKDGTFGGRNVQESSDINNWLTLHTA
ALGPTAKYWLYFYKHLPEKLPKTIKLRNITVQYDILERRLNEPGQQYLAWLNEKFKRS
SYNRRHCYASLCYEKYRRVVRAGVKVAQTARVVCYGGDTRRGVWPARKST
>P78983.2 Alt a 3; heat shock protein 70 [Alternaria alternata]
KTNKIVITNDKGRLSKEEIERMLAEAEKYKAEDEAEAAARISAKNALESYAYSLRNTLSDS
KVDEKLDAGDKQKLTAEIDKTVQWLDDNQATKDEYESQQKELEGVANPIMMKFYGAGGE
GGMPGGMPGGGMPGGAPGGAAGDDGPTVEEVD
>AA091800.1 Alt a 8; mannitol dehydrogenase [Alternaria alternata]
MPITVPQATELKDLSLKGKVVIVTGASGPTGIGTEAARGCAEYGADLAITYNSRAEGAE
KNAKEMSEKYGVKVKAYKQVNEYAQCEKLVQDVIKDFGKVDVFIANAGKTADNGILDAT
VEQWNEVIQTDLTGTFNCARAVGLHFRERKTGSLVITSSMSGHIANFPQEASYNVAKAG
CIHLAKSLANEWRDFARVNSISPGYIDTGLSDFVPQDIQKLWHSMPMGRDAKATELKGA
YVYFASDASSYCTGSDLLIDGGYCVR
>P0C0Y4.2 Alt a 8; mannitol dehydrogenase [Alternaria alternata]
MPISVPQATELKDLSLKGKVVIVTGASGPTGIGTEAARGCAEYGADLAITYNSRAEGAE
KNAKEMSEKYGVKVKAYKQVNEYAQCEKLVQDVIKDFGKVDVFIANAGKTADNGILDAT
VEQWNEVIQTDLTGTFNCARAVGLHFRERKTGSLVITSSMSGHIANFPQEASYNVAKAG
CIHLAKSLANEWRDFARVNSISPGYIDTGLSDFVPQDIQKLWHSMPMGRDAKATELKGA
YVYFASDASSYCTGSDLLIDGGYCVR
>CAD38167.1 nuclear transport factor 2-like [Alternaria alternata]
MSDFNAIAQQFVEFYKTFDGNRAGLGALYKEHSMLTFFAQGTQGSAAIVEKLQNLFPQE
IQHRTDTVDAQPSADDGILVLTGALLLGGESKPMSTQAFQLKNAEGNWFVLDVFRVLV
YPAA
>P42037.1 Alt a 5; ribosomal protein P2 [Alternaria alternata]
MKHLAAYLLLGLGGNTSPSAADVKALESVGIADSDRLDKLISELEGKDINELIASGSE
KLASVPSGGAGGAAASGGAAAAGGSAQAEEAAPEAAKEEEEKEESDEDMGFGLFD
>AAB48041.1 Alt a 5; ribosomal protein P2 [Alternaria alternata]
MKHLAAYLLLGLGGNTSPSAADVKALESVGIADSDRLDKLISELEGKDINELIASGPE
KLASVPSGGAGGAAASGGAAAAGGSAEAAPEAAKEEEEKEESDEDMGFGLFD
>AHZ97469.1 Alt a 15; serine protease [Alternaria alternata]
PQRQMDSAKEVPNSYVVFKKHVKDASKHHDWVQSVHSKNNEERMELRKRSSQFPVTTEV
FDGLKHVYEMAGMKGYSGHFDDEIEAIRNHPDVDYIERDSEVHTLGHDEPEIEKNSPWG
LARISHRDSLSFGTWNKYLYAADGGEGVDVYVIDTGTNTKHVDFEGRAKWGKTIPNGDAD
EDGNHGHTHCSGTVAGKKYVAKKAHVYAVKVLRSNGSGTMSDVVKGVEYAAKAHSDTVQ
AAKDGGKKKGFKGSANMSLGGGKSTTLDLAVNAAVDAGIHFVAAGNDNADSCNYSPPAA
ENAVTVGASTLLDERAYFSNYGKCNDIFAPGLNILSTWIGSEHATNTISGTSMASPHIAG
LLAYMLS LQPAKDSAYAVADITPKKLANLISVATVGALSDVPRNTKNILAWNGGGSSNY
TEIVEKGGYTVKKAEEKNEESEFRITIPSLSEIEDDFEKAKESAGRNAHRVGGKQLQHLE
AEIEDFIAEEMESMFVKERVASQKL
>AGS80276.1 Alt a 14; superoxide dismutase [Alternaria alternata]
MELHHSKHHQTYITNLNGLLKTQAEAVSTSDITSQVSIQGIKFNAGGHINHSLFWQNL
PASSNEAKISAAPLVKQIQATWGEDKFKFAFSAALLGIQGSWGWLIKTDMGKEQRLS
IVTTKQDPVVGKGEVPIFGVDMWEHAYYLQYQNGKAAAYVKNIWNVINWKTAEERYLGS

ADAFSVLKASI

>ABI26088.1 translationally controlled tumor protein [Alternaria alternata]
MLIYKDILTGEIISDSYNLKEIDGVVYEADCTKITVGGESFDGTANASAEQEEGAEDS
AETKIDVVYSFRLNETGFDKKGYLTYLKGVMKAVKDGLKKGGADEATIKDFETKASGYAK
KIISNFKDYEFFTGESMNPDMIVLLNYREDGVTPYVTVWKHGLEEMKV

>P42058.1 Alt a 7; unknown function [Alternaria alternata]
MAPKIAIVVYSSMYGHIKKMADAELKGIQEAGGDAKLFQVAETLPQEVLDKMYAPPKDSSV
PVLEDPAVLEEFDFGILFGIPTRYGNFPAQFKTFWDKTGKQWQQGAFWGWKYAGVVFVSTGTL
GGGQETTAITSMSTLVDHGFIIYVPLGYKTAFSMLANLDEVHGGSPWGAGTFSAGDGSRQP
SELELNIAQAQGFYEAVALAHQ

>AAS75297.1 Alt a 1; unknown function [Alternaria alternata]
MQFTTIASLFAAAGLAAAAPLESRQDTASCPVTTEGDYVWKISEFYGRKPEGTYYNLSLGF
NIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMMNFSFGSDRSGLLLKQKVSDDITYVA
TATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

>3V0R_A Alt a 1; unknown function [Alternaria alternata]
MDTASCPVTTEGDYVWKISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDH
KWYSCGENSFMDFSFSDRSGLLLKQKVSDDITYVATATLPNYCRAGGNGPKDFVCQGVA
DAYITLVTLPKSS

>AAB47552.1 Alt a 1; unknown function [Alternaria alternata]
MQFTTIASLFAAAGLAAAAPLESRQDTASCPVTTEGDYVWKISEFYGRKPEGTYYNLSLGF
NIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMDFSFSDRSGLLLKQKVSDDITYVA
TATLPNYCRAGGNGPKDFVCQGVADAYITLVTLPKSS

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

>COMPARE153 calcium-binding protein, polcalcin, partial [Amaranthus retroflexus]
MAAEDTPQDIADRERIFKRKETNGDGKISSSELGDALKTLGVSVPDEVRRMMAEIDTDGD
GFISFDEFTDFARANRGLVKDVKIF

>AKV72168.1 Ama r 1; Ole e 1-like [Amaranthus retroflexus]
MAKQAVFLLVGLCVLSLDDVAKAPVSQFHQGLVYCDTCRIQFMTRISTIMEGATVKL
ECRNITAGTQTFKAEAVTDKVGQYSIPVNGDFEDDICEIELVKSPNSECSEVSHDVYAKQ
SAKVSLSNNGEASDIRSANALGMRKEPLEECPEVLKELDLYDVKAN

>ACP43298.1 Ama r 2; profilin [Amaranthus retroflexus]
MSWQAYVDDHLMCEIEGTTNHLTGAAILGLDGSVWAQSADFPQFKPDEIAAIVEDFDEPG
TLAPTGLHLGGTKYMVIQGEPAVIRGKKGAGGICVKKTGQALVMGIYDEPVTGQCENMI
VERLGDYLIEQGY

>AAX77684.1 Amb a 9; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]
MAEEDKAERDRIFGAFDANKDGKISSTELGESLKNLGSVSPEEVQTMMEELDTDGDGFI
SYEFTDFYNANRGLMKDVGKIF

>AAX77685.1 Amb a 9; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]
MAEEDKAERDRIFGAFDANKDGKISSNELGEALKNLGSVSPEEVQTMMEELDTDGDGFI
SYEFTDFYNANRGLMKDVGKIF

>AAX77686.1 Amb a 10; calcium-binding protein, polcalcin [Ambrosia artemisiifolia]
MAPENNKHSIFPTDKEEVTKIFNRFDTNGDGQISEDELFAILKSLGSDTSPDEVKRVMAE
IDADGDGFISLDEFILFCKGIESEGDEINDLKEAFKFYDQNNNGVISANELHQILGRLGE
NYSVESCADIKSVSDGDGFVDFEERKMMSRKGGDGAM

>AHA56102.1 Amb a 11; cysteine protease [Ambrosia artemisiifolia]
MEINKLVCFSLVILGLVESFHYHERELESEEGFMGYDRWREQHNIEMRSPERFNVF
KYNVRRIHESNKMDKPYKLVNEFADMTNLEFVNTYANSKISHFQALRGSAPGSIDTDPN
KDFIYANVTKIPDKVDWREKNAVTDVKGGCGSCWAAAVVALEGINAIRTGKLVKFSE

QQLVDCDMTNAGCDGGLMEPAFTYVIKHGGIAPEASYPYVGKRETCDAKIKDVLKIDGR
QNVPLDEEALRKAVAHQPVATGIQLSGHGLQFYSEGYYTGDCGTEPNHGVGIVGYGENE
KGIKFVTVKNWSGPTWGEKGYIHLQRGARKEGLCGVAMHSSFPIMNDPNPPKDDPNGPKD
DPDAPKDPKFKTTQRLQGIRTKLLEL

>CBJ24286.1 Amb a 4; defensin [Ambrosia artemisiifolia]
MAAGLLVFVLAISEIASVKGLCEKPSLTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR
DSKATCFYFDCDPTKNPGPPPAPKPKAPAPSPPSGGGAPPPSGGEGGDGPPPEGGEG
GGDGGGEGGGEGGGDGGGEGGGEGGGDGGGDGGGEGGGEGGGGER

>CBK52317.1 Amb a 4; defensin [Ambrosia artemisiifolia]
MAAGLLVFVLAISEIASVKGLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR
DSKATCFYFDCDPTKNPGPPPAPKPKAPAPSPPSGGGAPPPSGGEGGDGPPPEGGEG
GGDGGGEGGGEGGGDGGGEGGGEGGGDGGGDGGGEGGGEGGGGER

>CBK62693.1 Amb a 4; defensin [Ambrosia artemisiifolia]
MAAGLLVFVLAISEIASVKGLCEKPSLTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR
DSKATCFYFDCDPTKNPGPPPAPKPKAPAPSPPSGGGAPPPSGGEGGER

>CBK62694.1 Amb a 4; defensin [Ambrosia artemisiifolia]
KLCEKPSLTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKRDSKATCFYFDCDPTKNPGP
PPGAPKPKAPAPSPPSGGGAPPPSGGEGGDGPPPEGGEGGGDGGGEGGGDGGGEGGGEG
GGDGGGDGGGEGGGEGGGGER

>CBK62695.1 Amb a 4; defensin [Ambrosia artemisiifolia]
KLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKRDSKASCFCYFDCDPTKNPGP
PPGAPKPKAPAPSPPSGGGAPPPSGGEGGGDGGGEGGGEGGGGGEGGGGGEGGGEG
GGGEGGGEGGGGER

>CBK62697.1 Amb a 4; defensin [Ambrosia artemisiifolia]
KLCEKPSVTWSGNKVKQTDKCDKRCIEWEGAKHGACHKRDSKASCFCYFDCDPTKNPGPP
PGAPKPKAPAPSPPSGGGAPPPSGGEGGGDGGGGRR

>CBK62698.1 Amb a 4; defensin [Ambrosia artemisiifolia]
MAAGLLVFVLAISEIASVKGLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR
DSKASCFCYFDCDPTKNPGPPPAPKPKAPAPSPPSGGGEGGGEGGGGER

>CBK62699.1 Amb a 4; defensin [Ambrosia artemisiifolia]
MAAGLLVFVLAISEIASVKGLCEKPSVTWSGKCKVKQTDKCDKRCIEWEGAKHGACHKR
DSKASCFCYFDCDPTKNPGPPPAPKPKVVEVVVEGGGEGGGGGEGGGEGGGGER

>ANZ22900.1 Amb a 12; enolase [Ambrosia artemisiifolia]
MATIKAVKARQIFDSRGNPTVEVDITLSDGTLARAAPVSGASTGIYEALERDGGSDYLG
KGVSKAVANVNTIIGPALVGKDPTDQTGIDNFMVQQLDGTQNEWGWCKQKLGANAILAVS
LAVCKAGASVLKTPLYKHIANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPIGA
SSFKEAMKMGVEVYHNLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKAG
YTDKVVIGMDVAASEFYGEKDKTYDLNFKENNDGKEKISGEQLKDLYKSFVSEYPIVSI
EDPFDQDDWEHYAKMTAECGEQVQIVGDDLLVTNPTRVKKKAIDEKTCNALLLKVNOIGSV
TESIEAVRMSKHAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL
LRIEEELGSEAVYAGANFRKPVEPY

>ANZ22901.1 Amb a 12; enolase [Ambrosia artemisiifolia]
MLFVDEIKVDITLSDGTLARAAPVSGASTGIYEALERDGGSDYLGKGVSKAVANVNTII
GPALVGKDPTDQTGIDNFMVQQLDGTQNEWGWCKQKLGANAILAVPLAVCKAGASVLKTP
LYKHIANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPIGASSFKEAMKMGVEVY
HNLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKAGYTDKVVIGMDVAAS
EFYGEKDKTYDLNFKENNDGKEKISGEQLKDLYKSFVSEYPIVSIEDPFDQDDWEHYAK
MTAECGEQVQIVGDDLLVTNPTRVKKKAIDEKTCNALLLKVNOIGSVTESIEAVRMSKHAG
WGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQLLRIEEELGSEAVYA
GANFRKPVEPY

>004004.1 Amb a 6; lipid transfer protein [Ambrosia artemisiifolia]

MDCIRILWSVAVGLLLVSWRPTMFAASPTCDTVQNILAPCAGFLTGGQEPSKACCTGVNNL
NNSRKTADRVAVCNCIKELTKSIAYDPKRMPLLLSTKCGVKPDFPAVDKNDLDCSKLPV

>P27759.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKHCCYILYFTLALVTLQPVSAEDLQEILPVNETRRLTTSYGAYNIIDGCWRGKADW
AENRKALADCAQGFQKGTGKGDGDIYVTVSELDVDDVANPKEGTLRFQAAQNRPLWIIFE
RDMVIRLDKEMVVNSDKTIDGRGAKVEIINAGFTLNGVKNVNIHNINMHDVKVNPGGLIK
SNDGPAAPRAGSDGDAISISGSSQIWIHDHCSLSKSDGLVDAKLGTTTLTVSNLFTQH
FVLLFGAGDENIEDRGMATVAFNTFTDNVDQRMPCRHRGFFQVNNNYDKWGSYAIGGS
ASPTILSQGNRFCAPDERSKKNVLGRHGEAAAESMKWNWRTNKDVLENGAI FVASGVDPV
LTPEQSAGMIPAEPGESALS LTSSAGVLSQPGAPC

>P27760.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKHCCYILYFTLALVTLQPVSAEDVEEFLPSANETRRSLKACEAHNIIDKCWRCKA
DWANNRQALADCAQGFQKGTGKGDVYVTSDKDDVANPKEGTLRFQAAAQNRPLWII
FKRNMVIHLNQELVVNSDKTIDGRGVKNIVNAGL TLMNVKNIIHNINIHDIKVCPPGM
IKSNDGPPILRQSDGDAINVAGSSQIWIHDHCSLSKASDGLDITLGSSHVTVSNCKFTQ
HQFVLLL GADDTHVQDKGMLATVAFNMFTDHVDQRMPCRFRGFFQVNNNYDRWGTYAIG
GSSAPTILSQGNRF FAPDDI KKNVLARTGTGNAESMSWNWRTDRDLLENGAI FLPSGSD
PVLTPSEQAGMIPAEPGEAVLRLTSSAGVLSCHQGAPC

>P27761.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD
WENNRQALADCAQGFQKGTGKGDVYVTSNLDDVANPKEGTLRFQAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNIIHNINIHDKVLPGGMI
KSNDGPPILRQASDGD TINVAGSSQIWIHDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILL GADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVNNNYDRWGTYAIGG
SSAPTILCQGNRF LAPDDQIKKNVLARTGTGAAESMAWNWRS DKDLLENGAI FVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVFSCHPGAPC

>P28744.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKHCCYILYFTLALVTLQPVSAEDLQQLPSANETRSLTTCGTYNIIIDGCWRGKAD
WAENRKALADCAQGFQKGTIGKGDGDIYVTVSELDVDDVANPKEGTLRFQAAQNRPLWIIF
ARDMVIRLDRELAINNDKTIDGRGAKVEIINAGFAIYNVKNIIHNINIMHDIVVNPGGLI
KSHDGPVPRKGS DGAIGISGSSQIWIHDHCSLSKAVDGLIDAKHGSTHFTVSNCLFTQH
QYLLL FWFDFERGM LCTVAFNKFTDNVDQRM PNLRHGFVQVNNNYERWGSYALGGSAGP
TILSQGNRF LASDIKKEVVGRYGESAMSE SINWNWRSYMDVFENGAI FVPSGVDPVLTPE
QNAGMIPAEPGEAVLRLTSSAGVLSQPGAPC

>P27762.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD
WAENRQALGNCAQGFQKATHGGKWDIYMVTS DQDDVNPKEGTLRFQATQDRPLWIIF
QRDMIYLLQ QEMVVTSDKTIDGRGAKVELVYGGITLMNVKNVNIHNIDIHDVRLPGGRI
KSNGGPAIPRHQSDGDAIHVTGSSDIWIDHCTLSKSF DGLVDVNWGSTGVTISNCKFTHH
EKAVLL GASDTHFQDLKMHVTLAYNIFTNTVHERMPPCRFRGFFQIVNNFYDRWDKYAIGG
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEP EWM TWNWR TQNDVLENGAI FVASGSDP
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLTCS PGAPC

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

MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD
WENNRQALADCAQGFQKGTGKGDVYVTSNLDDVANPKEGTLRFQAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGL TLMNVKNIIHNINIHDKVLPGGMI
KSNDGPPILRQASDGD TINVAGSSQIWIHDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILL GADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVNNNYDRWGTYAIGG
SSAPTILCQGNRF LAPDDQIKKNVLARTGTGAAESMAWNWRS DKDLLENGAI FVTSGSDP

VLTPVQSAGMIPAEPGEAAIKLTSSAGVFSCRPGAPC
>CBW30986.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKHCCYILYFTLALVTLQPVSAEDLQEILPVNETRRLTTSYGAYNIIDGCWRGKADW
AENRKALADCAQGFQKGTGGKGDGIYTVTSDLDDDVANPKEGTLRFGAAQNRPLWIIFE
RDMVIRLDKEMVNSDKTIDGRGAKVEIINAGFTLNGVKNVIIHNINMHVDKVNPGGLIK
SNDGPAAPRAGSDGDAISISGSSQIWIIDHCSLSKSDGLVDAKLGTTTLTVSNLFTQHQ
FVLLFGAGDENIEDRGMLATVAFNFTFDNVDQRMPCRHRGFFQVVNNNYDKWGSYAIGGS
ASPTILSQGNRFCAPDERSKKNVLGRHGEEAAESMKWNWRTNKDVLENGAI FVASGVDPV
LTPEQSAGMIPAEPGESALSLTSSAGVLSQPGAPC
>CBW30987.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKHCCYILYFTLALVTLQPVSAEDVEEFLPSANETRRSLKACEAHNIIDKCWRCKA
DWANNRQALADCAQGFAGKTYGGKHGDVYTVTSDKDDDVANPKEGTLRFAAAQNRPLWII
FKRNMVIHLNQELVVNSDKTIDGRGVKNIVNAGLTLMNVKNI IHNINIHDIKVCPPGM
IKSNDGPPILRQSDGDAINVAGSSQIWIIDHCSLSKASDGLLDITLGSSHVTVSNCKFTQ
HQFVLLL GADDTHVQDKGMLATVAFNMFTDHVDQRMPCRFRGFFQVVNNNYDRWGTYAIG
GSSAPTILSQGNRFFAPDDI IKKNVLARTGTGNAESMSWNWRTDKD LLENGAIFLPSGSD
PVLTPQKAGMIPAEPGEAVLRLTSSAGVLSCHQGAPC
>CBW30988.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD
WENNRQALADCAQGFAGKTYGGKWDVYTVTSLNDDDVANPKEGTLRFAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGLTLMNVKNI IHNINIHDKVLPGGMI
KSNDGPPILRQASDGD TINVAGSSQIWIIDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILLGADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVVNNNYDRWGTYAIGG
SSAPTILCQGNRFLAPDDQIKKNVLARTGTGAAESMAWNWRSKDLLENGAIFVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLSRPGAPC
>CBW30989.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD
WENNRQALADCAQGFAGKTYGGKWDVYTVTSLNDDDVANPKEGTLRFAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGLTLMNVKNI IHNINIHDKVLPGGMI
KSNDGPPILRQASDGD TINVAGSSQIWIIDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILLGADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVVNNNYDRWGTYAIGG
SSAPTILCQGNRFLAPDDQIKKNVLARTGTGAAESMAWNWRSKDLLENGAIFVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLSRPGAPC
>CBW30990.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD
WENNRQALADCAQGFAGKTYGGKWDVYTVTSLNDDDVANPKEGTLRFAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGLTLMNVKNI IHNINIHDKVLPGGMI
KSNDGPPIFRQASDGD TINVAGSSQIWIIDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILLGADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVVNNNYDRWGTYAIGG
SSAPTILCQGNRFLAPDDQMKNVLARTGTGVAESMAWNWRSKDLLENGAIFVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLSRPGAPC
>CBW30991.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKQCCYILYFTLALVALLQPVSAEGVGEILPSVNETRSLQACEALNIIDKCWRGKAD
WENNRQALADCAQGFAGKTYGGKWDVYTVTSLNDDDVANPKEGTLRFAAAQNRPLWIIF
KNDMVINLNQELVVNSDKTIDGRGVKVEIINGGLTLMNVKNI IHNINIHDKVLPGGMI
KSNDGPPILRQASDGD TINVAGSSQIWIIDHCSLSKSF DGLVDVTLGSTHVTISNCKFTQQ
SKAILLGADDTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVVNNNYDRWGTYAIGG
SSAPTILCQGNRFLAPDDQMKNVLARTGTGVAESMAWNWRSKDLLENGAIFVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLSRPGAPC
>CBW30992.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]

MGIKQCCYILYFTLALVALLQPVRSAEGVGEILPSVNETRSLQACEAYNIIDKCWRGKAD
WENNRQALADCAQGFAGKTYGGKWDVYTVTSNLDDDVANPKEGTLRFAAAQNRPLWIIIF
KNDMVINLNQELVNSDKTIDGRGVKVEIINGGLTLMNVKNIIIHNIHIDVKVLPGGMI
KNSDGPPIRLRQASDGDITINVAGSSQIWIHDHCSLSKSFGLVDVTLGTHVTISNCKFTQQ
SKAILLGGADTHVQDKGMLATVAFNMFTDNVDQRMPCRFRGFFQVNNNYDRWGTYAIGG
SSAPTILCQGNRFLAPDDQMKNVLRARTGTGVAESMAWNRSDKDLENGAIFVTSGSDP
VLTPVQSAGMIPAEPGEAAIKLTSSAGVLSRPGAPC

>CBW30993.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
CCYILYFTLALVILLQPVRSAEDLQQILPSVNETRSLTTCGTYNIIIDGCWRGKADWAENR
KALADCAQGFAGKTYGGKWDIYTVTSELDDDVANPKEGTLRFGAAQNRPLWIIIFARDMV
IRLDRELAINNDKTIDGRGAKVEIINAGFAIYNVKNIIIHNIIMHDI VVNPGLIKCNDG
PPAPRKGSDGDAIGISGGSQIWIHDHCSLSKAVDGLIDAKHGSTHFTVSNCLFTQHQLLL
FWDFDERGLCTVAFNKFTDNVDQRMPLRHGFVQVNNNYERWGSYALGGSAGPTILSQ
GNRFLASDIKKEVVGRYGESAMESINWNRSYMDVFENGAI FVPSGVDVLTPEQNAGM
IPAEPGEAVLRLTSSAGVLSQPPTPC

>CBW30994.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD
WAENRQALGDCAQGFAGKATHGGKWDIYMTSDQDDDVANPKEGTLRFGATQDRPLWIIIF
QRDMIIYLQQEMVVTSDKTIDGRGAKVELVYGGITLMNVKNVIIHNIHIDVRLVLPGGRI
KSNGGPAIPRHQSDGDAIHVTGSSDIWIDHCTLKSKSFGLVDVNWGSTGVTISNCKFTHH
EKAVLLGASDTHFQDLKMHVTLAYNIFTNTVHERMPPCRFRGFFQIVNNFYDRWDKYAIGG
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEPEWMTWNRWRTQNDVLENGAIFVASGSDP
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLTCSPGAPC

>CBW30995.1 Amb a 1; pectate lyase [Ambrosia artemisiifolia]
MGIKHCCYILYFTLALVTLVQAGRLGEEVDILPSPNDTRRSLQGCEAHNIIDKCWRCKPD
WAENRQALGDCAQGFAGKATHGGKWDIYMTSDQDDDVANPKEGTLRFGATQDRPLWIIIF
QRDMIIYLQQEMVVTSDTTIDGRGAKVELVYGGITLMNVKNVIIHNIHIDVRLVLPGGRI
KSNGGPAIPRHQSDGDAIHVTGSSDVWIDHCTLKSKSFGLVDVNWGSTGVTISNCKFTHH
EKAVLLGASDTHFQDLKMHVTLAYNIFTNTVHERMPPCRFRGFFQIVNNFYDRWDKYAIGG
SSNPTILSQGNKFVAPDFIYKKNVCLRTGAQEPEWMTWNRWRTQNDVLENGAIFVASGSDP
VLTAEQNAGMMQAEPGDMVPQLTMNAGVLTCSPGAPC

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

>5EM1_A Amb a 8; profilin [Ambrosia artemisiifolia]
GSGSWQTYVDEHLMXDI EGTGQHLASAAIFGTDGNVWAXSSSFPEFXPDEINAIKEFSE
PGALAPTGLFLAGAXYMIQGEPEGAVIRGXXGAGGICIXXTGQAMVFGIYEEPVNPGQCN
MVVERLGDYLVLDQGM

>5EV0_A Amb a 8; profilin [Ambrosia artemisiifolia]
SGSWQTYVDEHLMXDI EGTGQHLASAAIFGTDGNVWAKSSSFPEFKPDEINAIKEFSEP
GALAPTGLFLAGAKYMIQGEPEGAVIRGKKGAGGICIKKTGQAMVFGIYEEPVNPGQCNM
VVERLGDYLVLDQGM

>AAP15201.1 Amb a 8; profilin [Ambrosia artemisiifolia]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGVVWAQSATFPQVKPEEITGIMNDFNEPGSL
APTGLYLGGTKYMIQGEPEGAVIRGKKGPGGVTIKKTMMALIIGIYDEPMAPGQCNMIVE
RLGDYLLEQGF

>AAP15202.1 Amb a 8; profilin [Ambrosia artemisiifolia]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGVVWAQSATFPQVKPEEITGIMNDFNEPGSL
APTGLYLGGTKYMIQGEPEGAVIRGKKGPGGVTIKKTMSLIIGIYDEPMTPGQCNMLVE
RPGDYLVLEQGF

>AAP15203.1 Amb a 8; profilin [*Ambrosia artemisiifolia*]
MSWQAYVDEHLMCDIEGTGHHLTSAAILGHDGTVWAQSSNFPQFKPEEMKGIITEFDQAG
TLAPTGMFIAGAKYMLVQGEQGA VIRGKKGAGGICIKKTGQALVMGIYDEPVAPGQCNMV
VERLGDYLDIDQGM

>AAX77687.1 Amb a 8; profilin [*Ambrosia artemisiifolia*]
MSWQTYVDEHLMCDIEGTGQHLASAAIFGTDGNVWAKSSSFPEFKPDEINAI I KEFSEPG
ALAPTGLFLAGAKYMIQGEPEGAVIRGKKGAGGICIKKTGQAMVFGIYE E P V N P G Q C N M V
VERLGDYLDVDQGM

>AAX77688.1 Amb a 8; profilin [*Ambrosia artemisiifolia*]
MSWQTYVDEHLMCDIDGSGHLLSSAAIFGTDGAVWAKSGSFPEFKPDEINAI I KEFDAAG
TLAPTGLFLAGAKYMIQGEPEGAVIRGKKGAGGICIKKTGQAMVFGIYE E P V N P G Q C N M V
VERLGDYLDVDQGM

>P02878.1 Amb a 5; unknown function [*Ambrosia artemisiifolia*]
LVPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESS E I C S K K C G K

>AAA20065.1 Amb p 5; unknown function [*Ambrosia psilostachya*]
MNNEKNVSFEFIGSTDEVEIKLLPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESS E I
CSQKCGKMRMNVTKN TI

>AAA20067.1 Amb p 5; unknown function [*Ambrosia psilostachya*]
MNNEKNVSFEFIGSTDEVEIKLLPCAWAGNVCGEKRAYCCSDPGRYCPWQVVCYESSKI
CSQKCGKMRMNVTKN TI

>AAA20064.1 Amb p 5; unknown function [*Ambrosia psilostachya*]
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYCSSDPGRYCPWQVVCYESRKI
CAKNAAKMRMNVTKN TI

>AAA20066.1 Amb p 5; unknown function [*Ambrosia psilostachya*]
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYSSSDPGRYCPWQVVCYESRKI
CAKNAAKMRMNVTKN TI

>AAA20068.1 Amb p 5; unknown function [*Ambrosia psilostachya*]
MNNEKNVSFEFIGSTNEVEIKVMACYAAGSICGEKRGYCTNPGRYCPWQVVCYESRKI
CAKNAAKMRMNVTKN TI

>P10414.2 Amb t 5; unknown function [*Ambrosia trifida*]
MKNI F M L T L F I L I I T S T I K A I G S T N E V D E I K Q E D D G L C Y E G T N C G K V G K Y C C S P I G K Y C V
CYDSKAICNKNCT

>AEK65120.1 arginine kinase [*Amphioctopus fangsiao*]
MAEELFKTLQNAKECHSLLKKHLTKERFDKLGKLTGKFGGTLADCI R S G C K N P D S G V G I Y
ASDPDAYTVFAEVLDAVIMDYHKIDKVHHPIPDFGDVNNLNIGDLDP S G N M I V S T R V R V G
RSHDSFGFPPVLKKDDRIKMEQVSVEALKSLDGELAGSYFPLANMSADVQKQLTEDHFLF
NDSDRFLKAASGYDDWPIGRGIYFSENKTFLCWVNEEDHLRLISMQKGGNLGEVYKRLVS
AINKMEKKNLNAFKKDNMGYLTFPCPSNLGTTMRASVHIKIPKLSQRSDFKSIDKYNLQAR
GIHGEHTESVCGVYDISNKRMRGLTEYEAVTEMMRGVNEI I REETNST

>ALM30773.1 triosephosphate isomerase [*Amphioctopus fangsiao*]
MGRKFVGGNWKLN GNKKSIDGII E F M N A G P L N A D T E V V G P P S C Y L E Y V R S K L K G N I G V
AAQNCYKVP S G A F T G D I S P A M I K D I G L R Y V I L G H S E R R N V F G E T D E L I G E K I E H A V S E G L
I V I A C I G E K L E E R E A G K T E E V V F S Q T K T I I K H T K D W S K V V I A Y E P I W A I G T G K T A T P E Q A
Q S V H A S L R K F I S E N A S K E I A D N V R I L Y G G S V S A A N C K E L G Q K P D I D G F L V G G A S L K P D F V
K I V N A R A

>AAN76862.1 Ana o 2; 11S globulin, glycinin, cupin [*Anacardium occidentale*]
LSVCF L I L F H G C L A S R Q E W Q Q Q D E C Q I D R L D A L E P D N R V E Y E A G T V E A W D P N H E Q F R C A G
V A L V R H T I Q P N G L L L P Q Y S N A P Q L I Y V V Q G E G M T G I S Y P G C P E T Y Q A P Q Q G R Q Q G Q S G R F
Q D R H Q K I R R F R R G D I I A I P A G V A H W C Y N E G N S P V V T V T L L D V S N S Q N Q L D R T P R K F H L A G
N P K D V F Q Q Q Q H Q S R G R N L F S G F D E L L A E A F Q V D E R L I K Q L K S E D N R G G I V K V K D D E L R

VIRPSRSQSERGSESEEESEDEKRRWGQRDNIEETICTMRLKENINDPARADIYTPEVG
RLTTLNSLNLPIKWLQLSVEKGVLYKNALVLPWHNLNSHSIIYGCKGKGQVQVVDNFGN
RVFDGEVREGQMLVVPQNFVAVKRAREERFEWISFKTNDRAMTSPLAGRTSVLGGMPEEV
LANAFQISREDARKIKFNNQQTTLTSGESSHMRDDA

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

>AAM73729.1 Ana o 1; 7S globulin, vicilin-like [Anacardium occidentale]
PPTKFSFSLFLVSVLVLCGLFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVKECEKYYK
EKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQER
YKKERGQHNYKREDEDEDEDEAEEDENPYVFEDEDFTTKVKTEQKGVVLLPKFTQKSK
LLHALEKYRLAVLVANPQAFVVP SHMDADSIFFVSWGRGTITKILENKRESINVRQGDIV
SISSGTPFYIANNDENEKLYLVQFLRPVNLPGHFEVVFHGGGGENPESFYRAFSWEILEAA
LKTSKDTLEKLFKQDQGTIMKASKEQVRAMSRRGEGPKIWPFTTEESTGSFKLFKKDPSQ
SNKYGQLFEAERIDYPPLEKLDMVSYANITKGGMSVFPYNSRATKIAIIVS GEGCVEIA
CPHLSSSKSSHPSYKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNIRY
TLAGKKNIIKMEKEAKELAFKMEGEEVDKVFQKQDEEFFQGPWEWRKEKEGRADE

>AAM73730.2 Ana o 1; 7S globulin, vicilin-like [Anacardium occidentale]
MGPPTKFSFSLFLVSVLVLCGLFALAKIDPELKQCKHQCKVQRQYDEQQKEQCVKECEKY
YKEKKGREREHEEEEEEWGTGGVDEPSTHEPAEKHLSQCMRQCERQEGGQQKQLCRFRCQ
ERYKKERGQHNYKREDEDEDEDEAEEDENPYVFEDEDFTTKVKTEQKGVVLLPKFTQK
SKLLHALEKYRLAVLVANPQAFVVP SHMDADSIFFVSWGRGTITKILENKRESINVRQGD
IVSISSGTPFYIANNDENEKLYLVQFLRPVNLPGHFEVVFHGGGGENPESFYRAFSWEILE
AALKTSKDTLEKLFKQDQGTIMKASKEQIRAMSRRGEGPKIWPFTTEESTGSFKLFKKDP
SQSNKYGQLFEAERIDYPPLEKLDMVSYANITKGGMSVFPYNSRATKIAIIVS GEGCVE
IACPHLSSSKSSHPSYKLRARIRKDTVFIVPAGHPFATVASGNENLEIVCFEVNAEGNI
RYTLAGKKNIIKMEKEAKELAFKMEGEEVDKVFQKQDEEFFQGPWEWRKEKEGRADE

>O23791.1 Ana c 2; bromelain, sulfhydryl protease [Ananas comosus]
MASKVQLVFLFLFCAMWASPSAASRDEPNPMMKRFEEMAEGRYVYKDDDEKMRRFQI
FKNNVKHIETFNRSNENSYTLGINQFTDMTKSEFVAQYTGVSPLPLNIEREPVVSFDDVNI
SAVPQSIDWRDYGAVNEVKQNPCGSCWSFAAIATVEGIYKIKTGYLVSLSQEVLDCAV
SYGCKGGVWVKAYDFIISNNGVTTEENYPYLAYQGTNCNANSFPNSAYITGYSYVRRNDER
SMMYAVSNQPIAALIDASENFQYNGGVFSGPCGTSLNHAITIIIGYQDSSGTYWIVRN
SWGSSWEGGGYVRMARGVSSSSGVCIAMAPLFPPTLQSGANAIEVIMVSET

>Q94JN2.1 Ana c 1; profilin [Ananas comosus]
MSWQAYVDDHLMCEIDGQHLSSAAILGHDSTVWAQSPNFPQFKPEEISAILNDFENPGSL
APTGLYLGGTKYMIQGEQGVVIRGKKGTTGGITVKKTNLALIIGVYDEPMTPGQCNMVE
RLGDYLLEQGF

>AGC60020.1 paramyosin [Anisakis pegreffii]
MSDTLYRSPMAIRSSTADMGALTSMSVADLGLSTRLEDKIRLLQDDFESERELRNRIER
ERADLSVQLIALTDRLQDAECATDSQIESNRKREVELSKLRKLLLEESQLENEEDAMNVLRK
KHQDVCLDYTEQIEQLQKKNKSIDRERQRLQHEVIELTATIDQLQKDKHVAEKMAQKFEQ
QTIELSNKVEDLNKHVNDLAQQRQRLQAENSDDLAEIHDQKQVLDNLQHVKYQLAQQLEE
SRRRLEDAERERSQMQAQLHQVQLELDSVRVALDEESAARVEAEHKLSLANTEITQWKS
FDAEVALHHEEVEDLRKMMQKQAEYEEQIEIMLQKVSQLEKAKARLQSEVEVLIVDLEK
AQNTIAILERAKEQLEKQVLEMKSRIDELLVELEAAQREARAALAE LQKMKQLYEKAVEQ
KEALARENKKLQDDLHEANEALADANRKLHELDLENARLAGEIRDLQVALKESEAARRDA
EARAQRALAE LQQVRIEMERRLQEKKEEMEALRKSMQFEIDRLTAALADAEARMKAEIAR
LRKKYQAEIAELEMTVDNLNRANLEAQKTIKKQSEQIIQLQANLEDTQRQLQQTLDQYAL

AQRKISALSAELECKTALDNAIRARKQVEADLEEAHVRISDLTSINSLTAIKNKLETE
LSTAQADLDEVTKELHAADERANRALADAARAVQELHEEQEHSMKIDALRKSLEEQVKQL
QVQIQEAEEAALLGGKRVIKLETRIRDLEVALDEETRRHKETQSALRKKDRRIKEVQMQ
IDEEHKMFVMAQDTADRMLEKLNQKRQLGEAEAMTMQNLQRVRRYQRELEDAEGRADQA
ESSLNLIRAKHRGTVAVGKATDVYVVEED

>COMPARE012 tropomyosin [Anisakis pegreffii]
MDAIKKKMRKAMEIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKKMMQTENDLDK
AQEDLSTANSNLEEKQVQEAEEVAALNRRMTLLEEEELERAEERLKLATDKLEEATH
ADESERVRKVMENRSFQDEERANTVESQLKEAQMALAEADRKYDEVARKLAMVEADLERA
EERAEAGENKIVELEELRVDGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRA
EFAERSVQKLQKEVDRLLELVHEKERYKSISELDLLQELSGY

>AGC60026.1 unknown function [Anisakis pegreffii]
MVKNLPPSVREQCIESQIVIRNCKEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS
SLRDCIKKGGYMGYCKTFTTEENCIWQKDECAPSEAAEKKDENSLEVPETFSQCFKSQV
VMQQCMSKGEEECSKIQKECVDAFGTPPVTYAANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDGKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT
VDANPPIFTSKMNTCVKRKMAKGL

>AGC60027.1 unknown function [Anisakis pegreffii]
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS
SLRDCIKKGGYMGYCSNFTTHENCIWQKDECAPSEAAEKKDENSLEVPETFSQCFKSQV
VMQQCMSKGEEECLKIQKECVDAFGTPPVTSANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDGKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT
VDANPPIFTSKMIRCVKRKMAKGL

>AGC60028.1 unknown function [Anisakis pegreffii]
MVKNLPPSVREQCIESQIVIRDCEEKKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS
SLRDCIKKGGYMGYCSNFTTPENCIKWQKDECAPSEAAEKTDENSLEVPETFSQCFKSQV
VMQQCMSKGEEECLKIQKECVDAFGTPPVTSANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDGKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT
VDANPPIFTSKMNTCVKRKMAKGL

>CAK50389.1 Ani s 4; cysteine protease inhibitor [Anisakis simplex]
MQSRIVVAVVVFCCIILMQTEAGMLGGSSDVNDPEIKELAGKSIKISAMINDGKPH
LVKVVSAKKQVAVGDKYTLLEILVKDGDHQLCTVTIWQKKWENFEVVKVLCDHQ

>Q9NJA9.1 Ani s 2; paramyosin [Anisakis simplex]
MSDTLYRSPMAIRSSTADMGALTSMSVADLGSLTRLEDKIRLLQDDFESERELRNRIER
ERADLSVQLIALTDRLQDAECATDSQIESNRKREVELSKLRKLLLEESQLENEEDAMNVLK
KHQDVCLDYTEQIEQLQKKNKIDRERQRLQHEVIELTATIDQLQDKHVAEKMAQKFEQ
QTIELSNKVEDLNKHVNDLAQQRQRLQAENSDDLAEIHDQKVQLDNLQHVYQLAQQLEE
SRRRLEDAERERSQMQAQLHQVQLELDSVRVALDEESAARVEAEHKLSLANTEITQWKS
FDAEVALHHEEVEDLRKKMMQKQAEYEEQIEIMLQKVSQLEKAKARLQSEVEVLIVDLEK
AQNTIAILERAKEQLEKQVLEMKSRIDELLVELEAAQREARAALAEQKMKQLYEKAVEQ
KEALARENKKLQDDLHEANEALADANRKLHELDLENARLAGEIRDQLQVALKESEAARRDA
EARAQRALAEQVRIEMERRLOKEEEMEALRKSMQFEIDRLTAALADAEARMKAEIAR
LRKKYQAEIAELEMTVDNLNANLEAQTIKKQSEQIIQLQANLEDTQRQLQQTLDQYAL
AQRKISALSAELECKTALDNAIRARKQAEADLEEAHVRISDLTSINSLTAIKNKLETE
LSTAQADLDEVTKELHAADERANRALADAARAVQELHEEQEHSMKIDALRKSLEEQVKQL
QVQIQEAEEAALLGGKRVIKLETRIRDLEVALDEETRRHKETQSALRKKDRRIKEVQMQ
IDEEHKMFVMAQDTADRMLEKLNQKRQLGEAEAMTMQNLQRVRRYQRELEDAEGRADQA
ESSLNLIRAKHRGTVAVGKATDVYVVEED

>AAF75225.1 Ani s 2; paramyosin, partial [Anisakis simplex]
PRAAGELQKMKSLYEKAVEQKEALARENKKLQDELHEAKEALADANRKLHELDLENARLA

GEIRDLQTALKESDAARREAENRAQRLAADLQQLRIEMERRLQEKEEEMEALRKNMQFEI
DRLTAALADAEARMKAEISRLKKKYQAEIAELEMTVDNLNRANIEAQKTIKKQSEQMKIL
QASLEDTQRHLQQTLDQYALAQRKISALSAELEECKVALDNAIRARKQAEVDLEEANVRI
AELVSLTNNLTTIKNKLETELSTVRADLDETTKELHAADERANRALADAARAIEQLHEEQ
EHSMKIDALRRSLEEQVKQLVQVIQEAEEAALLGGKRVIKLETRIRDLETALDEETRRH
KETQNALRKKDRRIKEVQMQVDEEHKQFVMAQDTADRILLEKMNIQKRQLGEAESFTMANI
QRVRRYQRELEDAEGRADQAESSLHLIRAKHRSSVVTGRSASASKVYVLEDEQ
>AGC60035.1 Ani s 1; serine protease inhibitor [Anisakis simplex]
MDKGTPTQEGGVKPSVAWWHDDKTGICLSFKYTGCGGNANRFTTIKNCEQHCKMPDRGA
CALGKKPAEDSNGEQLVCAGMREDKCPNGYQCKMMAFMGLCCPTKEEELFAREYEGVCKS
GKPVKMDRGSWMMTILGKSCDDQFCPEDAKCEQGKLFANCK
>AGC60036.1 Ani s 1; serine protease inhibitor [Anisakis simplex]
MDKGTPTQEGGVKPSVAWWHDDKSGICLSFKYTGCGGNANRFTTIKNCEQHCKMPDRGA
CALGKKPAEDSNGEQLVCAGMREDKCPNGYQCKMMAFMGLCCPTKEEELFAREYEGVCKS
GKPVKMDRGSWMMTILGKSCDDQFCPEDAKCEQGKLFANCK
>BAF43535.1 Ani s 6; serine protease inhibitor [Anisakis simplex]
MFQSTFFLVLMVCVATARFANKDHCPPNEEYNECGNPCQEKCDNGEPVICTYQCEHRCFC
KQGYVRLTEDGECVPEEFCKPIHY
>BAF43534.1 Ani s 5; SXP/RAL-2 family protein [Anisakis simplex]
MKTILIVAALFCTIGMALADDTPPPPFLAGAPQDVVKAFFELLKKDETKTDPEIEKDLDA
WVDTLGGDYKAKFETFKKEMKAKEAELAKAHEEAVAKMTPEAKKADAELSKIAEDDSLNG
IQKAQKIQAIIYKTLQPQSVKDELEKIGPAVPQ
>BAF75681.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75704.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MRVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75705.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75706.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVPLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75707.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAYAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75708.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFRDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS
>BAF75709.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFVAAVAVSLAQDQGPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FANDHPAIKDAYEAEKKEVLAAQQAAEEHKKLVAALPPDAQKADAELTATADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNNQQGQS

>BAF75710.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFFVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNNHPAIKDAYEAEKKEVLAAQQAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNQGGQS

>BAF75711.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFFVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAEEHKKLVAALPPDAQKADAESTAIAIADDASLTLA
AKHDKIVQTFESLPPAVKEELNKLNQGGQS

>BAF75712.1 Ani s 8; SXP/RAL-2 family protein [Anisakis simplex]
MKVLFFVAAVVAVSLAQDQGPPPLPKFLDGADQATKDAFAALAQTFKDDTDKQVEDAVQQ
FVNDHPAIKDAYEAEKKEVLAAQQAEEHKKLVAALPPDAQKADAELTAIADDASLTLA
AKHDKIVQTFESLPPAVKEELDKLNQGGQS

>Q9NAS5.1 Ani s 3; tropomyosin [Anisakis simplex]
MDAIKKKMQAMKIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKKMMQTENDLDKA
QEDLSTANSNLEEKEKKVQEAEEVAALNRRMTLLEEELERAEEERLKLATAKLEEATHA
DESERVKVMENRSFQDEERANTVESQLKEAQMIAEEADRKYDEVARKLTMVEADLERAE
ERAETGENKIVELEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE
FAERSVQKLQKEVDRLEDELVHEKERYKSISEELDQTFQELSGY

>AEQ28167.1 tropomyosin [Anisakis simplex]
MDAIKKKMQAMKIEKDNALDRADAAEGKVRQMTDKLERIEEELRDTQKKMMQTENDLDKA
QEDLSTANSNLEEKEKKVQEAEEVAALNRRMTLLEEELERAEEERLKLATXKLEEATHA
DESERVKVMENRSFQDEERANTVESQLKEXQMLAEEADRKYDEVARKLAMVEADLERAE
ERAEAGENKIVELEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE
FAERSVQKLQKEVDRLEDELVHEKERYKSISEELDQTFQELSGY

>CAB58171.1 troponin C [Anisakis simplex]
MAEDIEEILAEIDGSQIEEYHKFFDMFDRGKQGYIMATQIGQIMHAMEQDFDEKQLRKLII
RKFDADGSGKLEFDEFICALVYTVANTVDKETLQKELREAFRLFDKEGNGYISRPTLKALL
KEIADDLSDDQLEAAVDEIDEDGSGKIEFEFFWELMAGEAD

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

>ABL77410.1 Ani s 7; unknown function [Anisakis simplex]
AKYGSQFCKNLLANCLSSGATLPMQSPWQIPPVVSSCITSGMAKGTDHNKKDVMTACIQ
RYGADFCKNMVGSAAALTDVLTLSYGIGSVLPQVIVDCMTSEMSSPSIMWQCVQKYGTEF
CKKLLQDCSASTGASLSPQAPWLIPSVIAECMAKGMVNGGRQADDTMAICIQKYGIKFCN
IIGAACSVLTQVPFFPQLPGTVQQLPSELRACVRSRSETQKPNVMTKCVKYEKGFTEFCSSLLQ
SCSASTGAILPLREPWKIPHPHIAADCMYAGMNPESKEDRGGIMSKCIRRYGDFDFCKKML
CSALTSVQHDSRNTNYASLPQVLKDCMASEMDSPSVMFECVQRYPGTFPCKGLLETCTEKT
RASLSPQAPWLIPTAIAQCMRQGMNQGDEKKTLMSLCVRRYGADYCNLAAACSVLTNLP
FFPQTPPSEQNLPPMMHKCLKSEMENPGIMSTCVQRYGTQFCKNLLNSCTASTGMHLPYD
APWKIPEPIAACMAQGMNGGDHKKEDAMARCIRKYGVTYCNMMLASCSVLTNVNYDPSG
GQMPGILSECVAETDEPSAMCQCQVQKYGTEFCKKRLASCIASGMNLPATTPWKLPPP
ARCMQHGSPNDNRGQGGQGSNDVMSQCIARYGAFCQRLARFCYAMNSLQYPGETFDPQQQ
TPTQVARCMKSEMDSPSVMWHCVQKYGQEFCKNLAATCSTETNTPLPQQDPWRLPQPIIA
CMLGKMNNPNPTSKPQSVMSQCTARYGDDFCLSLGKACAELNVPSSMISLSAQQLPQPV
SSCMKAEMNNPSALWQCIQYQYIEFCKKLRDACSAMTGASLSTTPWILPQPVSNMCRNE
MNNPSAMWLCIQKYGIEFCNRLASACAMIKKVTMPTVTINLPEIIASCVASENSQAMCYA
RKGPEQCKTEENICRNPNNPPGSPLTIPETECKMSQVAMATCQKKFGSECVLQQECVAG

TGAPPVTIGARGAFMLATALRSCIFNNGVIGSCVLYHPPSQCDQWVQQCATALQTSAGVT
VAGGYRQLSPPMAVCVASQDLMTRCMTLRLGQGTCCQAVKNCKRRFNTSSRLPGRLWSLS
SELINCLYRPVNRASN

>ABV55106.1 Ani s 9; unknown function [Anisakis simplex]
MKLCILAVAVFVAVSAQGGPPLPPFVANAPPAVQAEFRQLANGAPDKTEAEIEAQIEQW
VASKGGAVQAEFNKFKQMLEQGKARAEAAHQASLTRLSPAACAADARLSAIASNRALKVG
EKQRQLAAAFQALDPAVKAELQKEMQG

>BAJ78222.1 Ani s 11; unknown function [Anisakis simplex]
VGGPGPVISVDGKNVWEDANGMSELHGGPGPVVSGSGIGRVFPFRSGQLPIGGPGPVVSGS
GIGGGANPPRFVGGPGPIISGDGVNVWQKANSIPKLDNAGQRQVNIPPPFIRGPGPV
VSGSGIGEVGVQVPIGGPGPVVSSASGRVFPPLRGLPIGGPGPVVSGSGIGRVFPFRSGQL
PIGGPGPVVSGSGIGQVFPQSGQLPIGGPGPVVSGSGIGGANPPRFVGGPGPIISGD
GVNVWQKANSIPKLDGNANPPQLPVGGPGPVISVDGESVLQKEENSL

>AGC60029.1 Ani s 12; unknown function [Anisakis simplex]
MVKNLPPSVREQCIESQIVIRDCEKCKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS
SLRDCIKKGGYMGYCSNFTTHENCIKWKDECAPSEAAEKDENSLEVPETFSQCFKSQV
VMQQCMSKGEEECSKIQKECVDAFGTTPVYAANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT
VDANPPIFTSKMNTCVKRMKAKGL

>AGC60030.1 Ani s 12; unknown function [Anisakis simplex]
MVKNLPPSVREQCIESQIVIRDCEEKCKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAT
SLRDCIKKGGYMGYCKTFTTEENCIKWKDECAPSEAAEKTDENSLEVPETFSQCFKSQV
VMQQCMNEGEECSKIQKECVDAFGTTPVYAANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQEECVAATDAPT
VDANPPIFTSKMIRCVKRMKAKGL

>AGC60031.1 Ani s 12; unknown function [Anisakis simplex]
MVKNLPPSVREQCIESQIVIRDCEEKCKYGENCAELIKQCVTITGAPPVTIGGSGQYRVAS
SLRDCIKKGGYMGYCSNFTTHENCIKWKDECAPSEAAEKTDENSLEVPETFSQCFKSQV
VMQQCMNKGEEECSKIQKECVDAFGTTPVYAANGAYQMAAPLHRCIENGGWMKMCSTWI
NATICERWKQECSDKDAELPPNFSQCIQTQMVMLQC�LKFQDKCKALQDECVAATDAPT
VDANPPIFTSKMITCVKRMKAKGL

>BAT62430.1 Ani s 14; unknown function [Anisakis simplex]
MQVKCIAKYGEQFCSSMLSVCSMLSIPWKNDSVQRLPPGIVGCAQTTPVQCRKAYSE
SFCNRLGAACSKVTGTDIPAFSRGGGEYRLPEAISQCIAQENIVAMCYASKCSQQCDGWR
VTCNINGGMAQLTPEQVTCFEKQSGLVALKTSCRTPNLAQCRQIREPFETPKCTTAIPY
LKISQTVINGQIHVQQLVSGGMTGVQVSKTVETVIKT

>ACZ95445.1 Ani s 10; unknown function [Anisakis simplex]
MHLITALVLLLQLIHFITSSPIPQEVVGGPGPVVGGSGIGNVWEKANEQAAEQQNIIGGPG
PVISGSGIGDVWKNANEPAEQQENIGGPGPVVSGSGIGNVWEKANEQAAHQQSIEGPGPV
VSGSGIGNVWEKANEQAAHQQSIEGPGPVVSGSGIGDVWKNANEQAAEQQNIIGGPGPVIS
GSGIGNVWEKANEQAAEQQNIIGVGGPGPVKSGSGIGNVWEETNEEAASMQA

>BAJ78220.1 Ani s 11; unknown function [Anisakis simplex]
MHSTAILLLLVLQLSCYFAASFILPGGANPPRFVGGPGPIISGDGVNVWQKANSIPKLD
NAGQRQVNIPPPFIRGPGPVVSGSGIGEVGVQIPIGGPGPVVSGSGIGQVFPQSGQLPIG
GPGPVVSGSGIGGANPPRFVGGPGPIISGDGVNVWQKANSIPKLDNAGQRQVNIPPP
FIRGPGPVVSGSGIGEVGVQIPIGGPGPVVSGSGIGQVFPQSGQLPIGGPGPVVSGSGIG
GGANPPRFVGGPGPIISGDGVNVLQKANSIPKLDGNANPPQLPVGGPGPVISVDGESVL
QKEENSL

>BAJ78223.1 Ani s 12; unknown function [Anisakis simplex]
MLSHLWLIQLCIVAVLSNSEREEFAFLCPVKNLPPSVREQCIESQIVIRDCEEKCKYGEN

CAELIKQCVTITGAPPVTIGGSGQYRVASSLRDCIKKGGYMGYCSNFTTHENCIKWKDEC
APSEAAEKKDENSLEVPETFSSQCFKSQVVMQCMNEGEECSKIEKECVDALGTPPVTT
AANGAYQMAAPLHRCIENGWMMCMSTWINATICERWKQECSRDKDAEPPTNFSQCIQTQ
TVMLQCKLEFGDKCKALQEECAATYAPTAYVDANPPIFTSETIRCVQRKMAKGL
>BAJ78221.1 Ani s 11; unknown function, partial [Anisakis simplex]
MHSTAILLLLVLQLSCYFAASFILPGDHGLPVGGPGPVISVDGKNVWEDANGMSELHGPGP
VVS GSGIGRVPFRSGQLPIGGPGPVVSGSGIGGANPPRFPVGGPGPIISGDGVNVWQK
ANSIPKLGANPPQLPVGGPGPVISVDGESVLQKEENSL
>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
>Q7M1X6 Ant o 1; beta-expansin, partial [Anthoxanthum odoratum]
IAKVPPGNITATYGDKWLDAKSTWYGKPTGA
>Q7M1Y0 Ant o 1; beta-expansin, partial [Anthoxanthum odoratum]
IAKVPPGNITADYGDKWLDAKSTWYGKPTGA
>G37396 expansin, partial [Anthoxanthum odoratum]
YTTEGGKKVEAEDVIPEGWKADTSYE
>A59055 Api c 1; phospholipase A2 [Apis cerana]
IIYPGTLWCGHGNVSSGPNELGRFKHTDACCRTDMPDMSAGESKHGLTNTASHTRLS
CDCDDTFYDCLKNSGKISSYFVGKMYFNLDTKCYKLEHPVTGCGERTEGRCLRYTVDK
SKPKVYQWFDLRKY
>AAK09361.1 Api c 1; phospholipase A2 [Apis cerana]
IIYPGTLWCGHGNVSSGPNELGRFKHTDACCRTDMPDMSAGESKHGLTNTASHTRLS
CDCDDTFYDCLKNSGDKISSYFVGKMYFNLDTKCYKLEHPVTGCGERTEGRCLRYTVDK
SKPKAYQWFDLRKY
>P01502.1 melittin [Apis dorsata]
GIGAILKVLSTGLPALISWIKRKRQE
>Q7M4I5.1 Api d 1; phospholipase A2 [Apis dorsata]
IIYPGTLWCGHGNVSSSPDELGRFKHTDSCCRSHDMPDMSAGESKHGLTNTASHTRLS
CDCDDKFYDCLKNSSDTISSYFVGEMYFNILDTKCYKLEHPVTGCGKRTEGRCLNYTVDK
SKPKVYQWFDLRKY
>Q5BLY5.1 Api m 3; acid phosphatase [Apis mellifera]
MSVIAILAMVVGVAELKQINVIFRHGDRIPDEKNEMYPKDPYLYDFYPLERGETNSG
KMREYQLGQFLRERYGDFLGDYIYTESVSALSSFYDRTKMSLQLVLAALYPPNKLQQWNE
DLNWQPIATKYLRRYEDNIFLPEDCLLFTIELDRVLES PRGKYEF SKYDKLKKKLEEWG
KNITTPWDYIIYHTLVAEQSYGLTLPSTWNNIFPRGELFDATVFTYNITNSTPLKLY
GGPLLRIFTKHLMDVVSQTQKKRRIYLFSGHESNIASVLHALQLYYPHVPEYSSSIIME
LHNIIEGTHYVKIVYYLGPSEARELQLPGCEVLCPLYKYLQLIENVIPSNEELICDKRFV
DESANNLSIEELDFVKNLIRIAGTENK
>ACI25605.1 Api m 3; acid phosphatase [Apis mellifera]
MSVIAILAMVVGVAELKQINVIFRHGDRIPDEKNEMYPKDPYLYDFYPLERGETNSG
KMREYQLGQFLRERYGDFLGDYIYTESVSALSSFYDRTKMSLQLVLAALYPPNKLQQWNE
DLNWQPIATKYLRRYEDNIFLPEDCLLFTIEFDRVLES PRGKYEF SKYDKLKKKLEEWG
KNITTPWDYIIYHTLVAEQSYGLTLPSTWNNIFPRGELFDATVFTYNITNSTPLKLY
GGPLLRIFTKHLMDVVSQTQKKRRIYLFSGHESNIAAVLHALQLYYPHVPEYSSSIIME
LHNIIEGTHYVKIVYYLGPSEAGELQLPGCEVLCPLYKYLQLIENVIPSNEELICDKRFA
DESANNLSIEELDFVKNLIRIAGTENK

>ABD51779.1 Api m 6; unknown function [*Apis mellifera*]
MSRLVLASFLLLAVFMSLVGGFGGFGGFGLGGRGKPCSNEIFSRCDGRCQRFPCNVVVK
PLCIKICAPGCVCRLGLYLRNKKKVCVPRSKCLPG

>NP_001119715.1 Api m 5; dipeptidyl peptidase [*Apis mellifera*]
MEVLVQLALLLVHGLVWLVAGKSVPRVIDQDLERYEPLLEEDHRGARVPFNLEETYDQ
SFRANSFNGTWKTREILYSDNYVGDIRLFDVTTGSGTVLLDSSVTADFDKASVMFSFDN
SHVAIGHDYVNGFRYSIHQKCTVYNIKSRTFTDIANGDRIPLFKWSPTRNALIYVHKNDI
YYQVFFEGGSDTRRITNTGVPDIVFNGIPDWVYEEVLGSPVAFWISPDGRHLAFATFND
TNVRDIVISKYSGPGNSRDQYPNEIRIKYPKAGTTNPFVSLVIDLHDPSSKLIDLPPP
DVVGADNVLYTANWRRDGEIVATWTNRVQNAQLVLYDTKGNANNIYEEEEEGWLRIQP
PLYHDRVIVAKLQDSGTKAGRFLHATRLEYRNGALVDETDLTPGTCEVISLLLVDHARA
RLYYLGTTELGKPSHKNLYSVQLSGNEPPVCLSCDVLTPEGNRCTYAYAYFSTNGSHYALY
CAGPDPVFIIVNANHRQISIWENRSLRRKLAARTQPIVKNFNVNANGYTNKVKLYLPP
DFDETKKYPLLITVYAGPNTIRITEEATYGFESYIVTNRSVIYGRIDGRGSAYKGSKMLF
EIYRRLGTVEIEDQIIITRTLQEKYSWIDSNRTGIWGSYGGFSAAMVLATDAESVFKCG
ISVAVPTSWIYYDSLYTERFMGLPTPEDNQSGYNDTDSRRVEGMRGKKYMLIHGTADDN
VHYQQTMMMLNKALVNSDIMFQQQTYTDEAHALGNVFPPLYHTTDRFWANCLGYSH

>Q08169.1 Api m 2; hyaluronidase [*Apis mellifera*]
MSRPLVITEGMMIGVLLMLAPINALLLGFVQSTPDNNKTVREFNVYWNVPTFMCHKYGLR
FEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALLKDPNGNVVARNGGVPQLGNLTKHL
QVFRDHLINQIPDKSFPVGVVIDFESWRPIFRQNWASLQPYKKLSVEVVRREHPFWDQR
VEQEAKRRFEKYGQLFMEETLKAARMRPAANWGYAYPYCYNLTPNQPSAQCEATTMQE
NDKMSWLFESVDVLLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKKVLPYYWY
KYQDRRDTLSDRADLEATLRKITDLGADGFIIWGSDDINTKAKCLQFREYLNNELGPAV
KRIALNNANDRLTVDVSDQV

>ABF21077.1 Api m 10; icarapin [*Apis mellifera*]
MKTGLGVLFIAAWFIACHTSFPGAHDEDSKEERKNVDTVLVLPISIERDQMMMAATFDFP
SLSFEDSDEGSNWNWNTLLRPNFLDGWYQTLQSAISAHMKKVREQMAGILSRIP
EQGVVNWNIPEGANTTSTTKIIDGHVVTINETTYTDGSDDYSTLIRVRVIDVRPQ
NETILTTSSEADSDVTTLPTLIGKNETSTQSSRSVESVEDFDNEIPKNQGDVLT
A

>ABF21078.1 Api m 10; icarapin [*Apis mellifera*]
ERDQMMMAATFDFP
SLSFEDSDEGSNWNWNTLLRPNFLDGWYQTLQTHMKKVREQMAGILSRIP
EQGVVNWNIPEGANTTSTTKIIDGHVVTINETTYTDGSDDYSTLIRVRVIDVRPQ
NETILTTSSEADSDVTTLPTLIGKNETSTQSSRSVESVEDFDNEIPKNQGDVLT
A

>AHM25035.1 Api m 10; icarapin, partial [*Apis mellifera*]
FPGAHDEDSKEERMRPAPNLQGVWKASRISTTRYRRTKEMY

>AHM25036.1 Api m 10; icarapin, partial [*Apis mellifera*]
FPGAHDEDSKERTLPLPPRSSMDTW

>AHM25037.1 Api m 10; icarapin, partial [*Apis mellifera*]
FPGAHDEDSKEERKNVDTW

>AHM25038.1 Api m 10; icarapin, partial [*Apis mellifera*]
FPGAHDEDSKVL

>NP_001011564.1 Api m 11; major royal jelly protein [*Apis mellifera*]
MIRWLLLMYLGITCQGVTDIHSRNLNLSLKVIYEWKYIDYDFGSDEKRQAAIQSGDYNYT
MNYLLDTDQWGDKTFVIIMKFNGVPSSLNVITNKTGNGGPLLAPYDPWTWAKNENCSGIT
SAYKIEIDMCDRLWLDSGLINNVRVSVCPQQLLVFDLNTSQLLKQVKIPHDIAVNTTTEK
GALVTLVSQLLSCEVNGSTLVYIGDNEGFALIIYNNSDNSFQRLTSSSTFASDP
RYTTFTI
NGESFTLQSGIFGMALSPLTQNLYYALS
SSHNLNYYNTEQFVKSQYQANNVHYQ
GKENIL
WTQASAKGISDNGVLFGLVGD
TSLACWENRLLDRRNIEVVAKNK
ETLQAITGLKVKRR
ISFILVHGFPLEYEV
LAVSNRIQKVIYGFDFNDV
NFRILIANVNDLIK
NTRCISP

>AAY21180.1 Api m 11; major royal jelly protein [*Apis mellifera*]

MSFNIWWLILYFSIVCQAKAHYSLRDFKANIFQVKYQWKYFDYNFGSDEKRQAAIQSGEY
NYKNNVPIDVDRWNGKTFVTILRNDGVPSSLNVISNKIGNGGPILLEPYPNWSWAKNQNC
GITSVYRIAIDEWDRLLWLDNGISGETSVCPQSIVVFDLKNKSKLLKQVKIPHDIAINST
GKRNVVTPIVQSFQDYNNWVYIADVEGYALIIYNNADDSFQRLTSSTFVYDPRYTKYTIN
DEFSLQDGLGMALSHKTQNLVYSSAMSSHNLYVNTKQFTQGKFQANDIQYQGASDILW
TQASAKAISETGALFFGLVSDTALGCWENRPLKRRNIEIVAKNNDTLQFISGIKIKQI
SSNIYERQNEEYIWIWVSNKYQKIANGDLNFNEVNFRLNAPVNLIRYTRCENPKTNFFS
IFL

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

MKFLVNVALVMVYISYIYAPEPEPEPEAEADAEADPEAGIGAVLKVLTTGLPALI
SWIKRKRQQG

>P00630.3 Api m 1; phospholipase A2 [*Apis mellifera*]

MQVVLGSLFLLLLSTSHGWQIRDRIQDNELEERIIYPGTLWCGHGNKSSGPNELGRFKHT
DACCRTHDMCPDVMSAGESKHGLTNTASHTRLSCDCDDKFYDCLKNSADTISSYFVGKMY
FNLIDTKCYKLEHPVTGCGERTEGRCLHYTVDKSKPKVYQWFDLRKY

>XP_392204.2 platelet-derived growth factor/vascular endothelial growth factor,
PVF1-like [*Apis mellifera*]

MPYSKCRTRFLRFFAICSFSTCGLVMAQLEDTRYPDQRIVFPDRGRETANPALEGGPSGGG
IGELAKSIQLAKKISSINSRDDFLKLVKDVPKDISFFSSSRMGETERSNAERPNOALCM
PELQTVPLLENEPSVIYYPTCTRIKRCGGCCTHSLLSQOPTATEIRNFEILVTILESSGK
LKYQGKRIVPIEEHTQCTCDCKIKETDCNKKQSYVPEECTCACNNVDEQKCCNESNIKMW
HPDLCSCFCRETQECSTGFYFDQNSCRCLQVPLSRTWFTSTKGSYRFGQTQRPDNPVPV
IIALDSDDPRRKPKPDPE

>NP_001138311.1 unknown function [*Apis mellifera*]

MVVWLVLIIATSSSVYLAEEAIPDPPNSKISTVNP SKLSTAVDCTGIIAFSATHASVDHAK
AVFAETLVDKGVGYVPQTGIFITNCPGLYQFSFAGYGSTDLRLTLKKKQNNSDSWRPVVG
TGAGGGANLILLEVDVGDQLAVFVDSGKISDGVTFSGYRIAKI

>NP_001035360.1 Api m 6; unknown function [*Apis mellifera*]

MSRLVLASFLLLAIFSMVGGFGGFGGFGLGGRGKCPSEIFSRCDGRCQRFPCNVVVK
PLCIKICAPGCVCRLGYLNRNKKKVCVPRSKCG

>CAD56944.1 Api m 12; vitellogenin [*Apis mellifera*]

MLLLLTLFFFAGTVAADFQHNWQVQNEEYTYLVRSRRTLSTLGDLSDVHTGILIKALLTVQA
KDSNVLAAKVWNGQYARVQQSMPDGWETEISDQMLELRDLPISGKPFQIRMKHGLIRDLI
VDRDVPTWEVNILKSIVGQLQVDTQGENAVKVNVSQVPTDDEPYASFKAMEDSVGGKCEV
LYDIAPLSDFVIHRPELVPMPTLKGDRHMEVIKIKNFDCDQRINYHFGMTDNSRLEP
GTNKGKFFSRSSSTRIVISESLKHFTIQSSVTTSKMMVSPRLYDRQNGLVLSRMNLTLA
KMEKTSKPLPMVDNPESTGNLVYIYNNPFSVDEERRVSKTAMNSNQIVSDNSLSSSEEK
KQDILNLRDIISSSSSSISSEENDFWQPKPTLEDAPQNSLLPNFVGYKKGKHHIGKSGKVD
VINAAKELIFQIANELEASNIPVHATLEKFMILCNLMRTMNRKQISELESNMQISPNE
KPNDSQVIKQNTWTVFRDAITQTGTGPAFLTIKEWIERGTTKSMEANIMSKLPKTVRT
PTDSYIRSFELLQNPKVSNEQFLNTAATLSFCEMIHNAAQVNRKSIHNNYPVHTFGRLLTS
KHDNSLYDEYIPFLERELRKAHQEKDSPRIQTYIMALGMIGEPKILSVFEPYLEGKQMT
VFQRTLMVGSGLKLTETNPKLARSVLYKIYLNTEMESHEVRCTAVFLLMKTNPPLSMLQRM
AEFTKLDNTRQVNSAVKSTIQSLMKLKSPEWKDLAKKARSVNHLLTHHEYDYELSRGYID
EKILENQNIITHMILNYVGSSEDSVIPRILYL TWYSSNGDIKVPSTKVLAMISSVKSFMEL
SLRSVKDRETIISAAEKIAEELKIVPEELVPLEGNLMINNKYALKFFPFDKHILDKLP
ISNYIEAVKEGKFMNVNMLDYESVHSFPTETGLPFVYTFNVIKLTKTSGTVQAQINPDF
AFIVNSNLRLTFSKNVQGRVGFVTPFEHRHFISGIDSNLHVYAPLKLISLDVNTPKGNMQW
KIWPMKGEEKSRLFHYSVVPFVSNHDI LNLRLPLSMEKGRPMIPDDNTSLALPKNEGPF

LNVETAKTNEEMWELIDTEKLTDRLPYPWTMDNERYVKVDMYMNLEGEQKDPVIFSTSFDSKVMTRPDTDSENWTPKMMAVEPTDKQANSKTRRQEMMREAGRGIESAKSYVVDVRVHVPGESESETVLTAWSESNVESKGRLLGFWRVEMPRSNADYEVCIQSQIMVSPETLLSYDEKMDQPKPMDFNVDIRYGKNCCKGERIDMNGKLRQSPRLKELVGATSIIKDCVEDMKRGNKI LRTCQKAVVLSMLLDEVDISMEVPSDALIALYSQGLFSLSEIDNLDVSLDVSNPKNAGKK KIDVRAKLNEYLDKADVIVNTPIMDAHFKDVKLSDFGFSTEDILDTADEDLLINNVFYED ETSCMLDKTRAQTFDQKDYPLRLGPCWHAVMTTYPRINPDNHNEKLHHPKDKSVSVLSRE NEAGQKEVKVLLGSDKIKFVPGTTSQPEVFNVEKIVVSRNKAYQKVEENEIIFEIYKMG DRFIGLTSDFKFDVSLALDGERVMLKASEDYRYSVRGLCGNFDHDSNDVFGPKNCLFRKP EHFVASYALISNQCEGDSLNVAKSLQDHDCIRQERTQQRNVISDESSEGRLDTEMSTWGYH HNVNKHCTIHRQVKETDDKICFTMRPVVSCASGCTAVETKSKPYKFHCMEKNEAAMKLL KRIEKGANPDLSQKPVSTTEELTPFVCKA

>P81943.3 Api g 5; FAD-containing oxidase [Apium graveolens]
LPNPSGFVTCLSSISKSVYTPAINLKAVIADPVAKTAVVQAGATLGEVYYXIIYARVLWV
GNTTQKLEWIRSLHDYQSSFFPFSSA

>ACV04796.1 Api g 2; lipid transfer protein [Apium graveolens]
MGVSKVAIAVAVMLMVVINHPAVVEGLTCGQVTGKLGGLGKGGYPSACC GGKGL
LNSLAKTPADRKQACACLKTLGASVKGINYGAAALPGKCGIRIPYIPSPSTDCSRVN

>P86809.1 Api g 6; lipid transfer protein [Apium graveolens]
ATCSAVQLSPCLAAITKNTPPSAACCNKLKEQKPCLCGYLKDPNLKNVYVNSPGARKTASS
CGVALKC

>P49372.1 Api g 1; pathogenesis related protein, PR-10, Bet v 1-like [Apium graveolens]

MGVQTHVLELTSSVSAEKIFQGFVIDVDTVLPKAAFGAYKSVEIKGDGGPGTLKIITLPD
GGPITMTLRIDGVNKEALTFDYSVIDGDILLGFIESIENHVVLVPTADGG SICKTTAIF
HTKGDVAVPEENIKYANEQNTALFKALEAYLIAN

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

MGVQKTVVEAPSTVSAEKMYQGFLLDMDTVFPKVLQQLIKSVEILEGDGGVGTVKLVHLG
EATEYTTMKQKVDVIDKAGLAYTYTTIGGDILVDVLESVVNEFVVVPTDGGCIVKNTTIY
NTKGDVAVLPEDKIKEATEKSALAFKAVEAYLLANLQFLA

>AAD29409.1 Api g 4; profilin [Apium graveolens]

MSWQAYVDDHLMCEVEGNPGQTLTAAAIIGHDGSVWAQSSTFPQIKPEEIAGIMKDFDEP
GHLAPTGLYLGGAKYMIQGEPAVIRGKKGSGGVTIKKTGQALVFGVYDEPVTGQC NV
IVERLGDYLIDQGL

>AAC63045.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]

RQQPEENACQFQRLNAQRPNRIESEGGYIETWNPNNQEFECAGVALSRLVLR RNALRRP
FYSNAPQEIFIQQGRGYFGLIFPGCPRHYE EPHQTGRRSQSQRP RRLLQGEDQSQQQRDS
HQKVHRFDEGLIAVPTGVAFWLYNDHDTDVAVSLTDTNNDNQLDQFPRRFNLAGNTE
QEFRLRYQQRSRQRSLPSPYSPQSQPRQEEREFSPRGQHSRRERAGQEEENE GGNIF
SGFTPEFLEQAFQVDDRQIVQNLRGETESEEEGAIIVTVRGGLRILSPDRKRRAD EEEEEYD
EDEYEYDEEDRRRGRGRGRNGIEETICTASAKKNIGRNRSPDIYNPQAGSLKTANDLN
LLILRWLGPSAEYGNLYRNALFVAHYNTNAHSIIYRLRGRAHVQVVD SNGNRVYDEELQE
GHVLLVVPQNFVAVAGKSQSENFYVAFKTDSPSIANLAGENSVIDNLP EEVVANSYGLQR
EQARQLKNNNPFKFFVPPSQSPRAVA

>AAD47382.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]

MAKLELSFCFCFLVLGASSISFRQQPEENACQFQRLNAQRPNRIESEGGYIETWNPNN
QEFECAGVALSRLVLR RNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYE EPAQQGR
RYQSQRPPRRLLQEEDQSQQQDSDHQKVHRFNEGLIAVPTGVAFWLYNDHDTDVAVSLT
DTNNDNQLDQFPRRFNLAGNHEQEFRLRYQQRSRQRSLPSPYSPHSRPRREER EFR

PRGQHSRRERAGQEEDEEGNIFSGFTPEFLEQAFQVDDRQIVQNLWGENESEEEGAIVT
VRGGLRILSPDGRGADEEEYDEDEQYEHYEQDGRRRGRSGGGNGIEETICTACVKKNI
GGNRSPHIYDPQRWFTQNC HDLNLILRLWLGLSAEYGNLYRNALFVPHYNTNAHSIIYAL
RGRAHVQVVD SNGNRVYDEELQEGHVLVVPQNF AVAGKSQSENFEYVAFKTD SRPSIANF
AGENSFIDNLP EEVANSYGLPREQARQLKNNNPFKFFVPPFQQSPRAVA
>AAM46958.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]
MGKLLALSVCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNPNN
QEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYE EPAQQGR
RHQSQRPPRRFQGDQSQQQD SHQKVHRFDEGDLIAVPTGVAFWYNDHDTDVAVSLT
DTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQSRRRSLPYSYSPQTPKQEDREFSPRG
QHRRERAGQE QENEGNIFSGFTPEFLAQAFQVDDRQILQNL RGENESDEQGAIVTVRG
GLRILSPDRKRRQYERPDEEEYDEDEYDEEERQQDRRRRGRSGSGNGIEETICTA
SFKKNIGRNRSPDIYNPQAGSLKTANELQNLNLILRLWLGLSAEYGNLYRNALFVPHYNTN
AHSIIYALRGRAHVQVVD SNGDRVFDEELQEGHVLVVPQNF AVAGKSQSENFEYVAFKTD
SRPSIANLAGENSFIDNLP EEVANSYGLPREQARQLKNNNPFKFFVPPSEQSLRAVA
>3C3V_A Ara h 3; 11S globulin, cupin [Arachis hypogaea]
ISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNPNNQEFECAGVALSRLVLRNAL
RRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYE EPAQQGRRYQSQRPPRRLQEEDQSQQQ
QD SHQKVHRFNEGDLIAVPTGVAFWLYNDHDTDVAVSLTDTNNNDNQLDQFPRRFNLAG
NHEQEFLRYQQSRQSRRRSLPYSYSPQSQRQEEREFSPRGQHSRRERAGQEEHEGG
NIFSGFTPEFLAQAFQVDDRQIVQNL RGENESEEQGAIVTVRGGLRILSPDRKRGAD EEE
EYDEDEYDEEEDRRRGRSGSGNGIEETICTATVKKNIGRNRSPDIYNPQAGSLKTAN
ELNLILRLWLGLSAEYGNLYRNALFVPHYNTNAHSIIYALRGRAHVQVVD SNGNRVYDEE
LQEGHVLVVPQNF AVAGKSQSDNFEYVAFKTD SRPSIANLAGENSVIDNLP EEVANSY
LPREQARQLKNNNPFKFFVPPSQQSPRAVA
>AAM93157.1 Ara h 3; 11S globulin, cupin, partial [Arachis hypogaea]
NYLHMLLALSVCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNP
NNQEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYE EPAQQ
GRRRHQSQRPPRRFQGDQSQQQD SHQKVHRFDEGDLIAVPTGVAFWYNDHDTDVAVS
LTDTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQSRRRS
>ABI17154.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]
MAKLLALSFCFLVLGASSVTRQGG ENECQFQRLNAQRPDNRIESEGGYIETWNPNN
QEFQCAGVALSRTVLRNALRRPFYSNAPLEIYVQQGSGYFGLIFPGCPSTYE EPAQEGR
RYQSQKPSRRFVQGD DPSQQQQD SHQKVHRFDEGDLIAVPTGVAFWYND EDDTDVVTVT
LSDTSSIHNQLDQFPRRFYLAGNHEQEFLRYQQQGSRPHYRQISPRVRGDEQENEGSNI
FSGFAQEFLQHAFQVDRQTVENLRGENERE EQGAIVTVKGLRILSPDEE DESSRPPSR
REEFDEDRSRPQQRGKYDENRRGYKNGIEETICSASVKKNLGRSSNPDIYNPQAGLSRV
NELDLPI LGWLGLSAQHGTIYRNAMFVPHYTLNAHTIVVALN GRAHVQVVD SNGNRVYDE
ELQEGHVLVVPQNF AVAAKAQSENYEYLA FKTD SRPSIANLAGENS IIDNLP EEVANSY
RLPREQARQLKNNNPFKFFVPPFDHQSMREVA
>ACH91862.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]
MAKLELSFCFCFLVLGASSISFRQQPEENACQFQRLNAQRPDNRIESEGGYIETWNPNN
QEFECAGVALSRLVLRNALRRPFYSNAPQEIFIQQGRGYFGLIFPGCPSTYE EPAQQGR
RYQSQRPPRRLQEEDQSQQQQD SHQKVHRFNEGDLIAVPTGVAFWLYNDHDTDVAVSLT
DTNNNDNQLDQFPRRFNLAGNHEQEFLRYQQSRQSRRRSLPYSYSPQSQRQEEREF S
PRGQHSRRERAGQEEENEGNIFSGFTPEFLAQAFQVDDRQIVQNL RGENESEEQGAIVT
VRGGLRILSPDRKRGAD EEEYDEDEYDEEEDRRRGRSGSGNGIEETICTATVKKNI
GRNRSPDIYNPQAGSLKTANELNLILRLWLGLSAEYGNLYRNALFVPHYNTNAHSIIYAL
RGRAHVQVVD SNGNRVYDEELQEGHVLVVPQNF AVAGKSQSDNFEYVAFKTD SRPSIANL
AGENSVIDNLP EEVANSYGLPREQARQLKNNNPFKFFVPPSQQSPRAVA

>ADQ53859.1 Ara h 3; 11S globulin, cupin [Arachis hypogaea]
MAKLLALSCLFCVLVLGASSVTRQGGREENECQFQRLNAQRPDNRIESEGGYIETWNPNN
QEFQCAGVALSRTLRRNALRRPFYSNAPLEIYVQQGSGYFGLIFPGCPSTYEIPAQEGR
RYQSQKPSRRFVQVQDDPSQQQQDQSHQKVHRFDEGLIAVPTGVAFWYNDDETDVVTVT
LSDTSSIHNLQDQFPRRFYLAGNQEQEFLRYQQQGSRPHYRQISPRVRGDEQENEGSNI
FSGFAQEFLQHAFQVDRQTVENLRGENEREQGAIVTVKGLRILSPDEEDESRRSPNR
REEFDEDRSRPQQRGKYDENRRGYKNGIEETICSASVKKNLGRSSNPDIYNPQAGLSRV
NELDLPILGWLGLSAQHGTIYRNAMFVPHYTLNAHTIVVALNGRAHVQVVDNSGNRVYDE
ELQEGHVLVVPQNFVAQAQSENIEYLAFAKTDSPSIANQAGENSIIIDNLPEEVVANSY
RLPREQARQLKNNNPFKFFVPPFDHQSMREVA

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

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

>AAK96887.1 Ara h 2; 2S albumin, conglutin [Arachis hypogaea]
MAKLTILVALALFLLAAHASARQQWELQDRRCCQSQLERANLRPCEQHLMQKIQRDEDSY
ERDPYSPSQDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRCMCEALQQIMENQSDRL
QGRQEQQFKRELRLNPQQCGLRAPQRCDLDVESGG

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

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

>AAM78596.1 Ara h 2; 2S albumin, conglutin [Arachis hypogaea]
LTILVAPALFLLAAHASARQQWELQDRRCCQSQLERANLRPCEQHLMQKIQRDEDSYGRD
PYSPSQDPYSPSQDPDRRDYSPSPYDRRGAGSSQHQRCCNELNEFENNQRCMCEALQQ
IMENQSDRLQGRQEQQFKRELRLNPQQCGLRAPQRCDLEVESGGDRDY

>Q647G9.1 Ara h 6; 2S albumin, conglutin [Arachis hypogaea]
MAKSTILVALLALVLAHASAMRRERGRQGDSSSCERQVDRVNLKPCEQHIMQRIMGEQE
QYDSYDIRSTRSSDQQQRCCDELNEMENTQRCMCEALQQIMENQCDRLQDRQMVQQFKRE
LMNLPQQCNFRAPQRCDLDVSGGRC

>ABW17159.1 Ara h 7; 2S albumin, conglutin [Arachis hypogaea]
MVKLSILVALLGALLVVASATRWDPDRGSRGSRWDAPSRGDDQCQRQLQRANLRPCEEHI
RQRVEKEQEQQEQDEYPYIQRGSRGRQPGESDEDQEQRCCNELNRFQNNQRCMCQALQQIL
QNQSFQFQDRSQLHQMERELRLNPQNCGFRSPSRCDLSSRTPY

>1W2Q_A Ara h 6; 2S albumin, conglutin [Arachis hypogaea]
GPMRRERGRQGDSSSCERQVDRVNLKPCEQHIMQRIMGEQEYDSYDIRSTRSSDQQQR
CDELNEMENTQRCMCEALQQIMENQCDRLQDRQMVQQFKRELMNLPQQCNFRAPQRCDLD
VSGGRCS

>ACN62248.1 Ara h 2; 2S albumin, conglutin [Arachis hypogaea]
MLTILVALALFLLAAHASARQQWELQDRRCCQSQLERANLRPCEQHLMQKIQRDEDSYER
DPYSPSQDPYSPSPYDRRGAGSSQHQRCCNELNEFENNQRCMCEALQQIMENQSDRLQ
RQEQEQQFKRELRLNPQQCGLRAPQRCDLDVESGGDRDY

>Q647G8 Ara h 7; 2S albumin, conglutin [Arachis hypogaea]
MVKLSILVALLGALLVVASATRWDPDRGSRGLRWDAPSRGDDQCQRQLQRANLRPCEEHI
RQRVEQEQQEQDEYPYSQRGSRGRRPGESDEDQEQRCCNELNRFQNNQRCMCQALQQIL
QNQSFRFQQDRSQLHQNGEGAQELAPELRVQVTKPLRP

>P43237.1 Ara h 1; 7S globulin, vicilin [Arachis hypogaea]
MRGRVSPLMLLLGILVLASVSATQAKSPYRK TENPCAQRCLQSCQQEPDDLKQKACESRC
TKLEYDPRCVYDTGATNQRHPPGERTRGRQPGDYDDDRRQPRREEGGRWGPAPRERERE
EDWRQPREDWRRPSHQPRKIRPEGREGEQEWGTPGSEVREETS RNPNPFYFPSRRFSTRY
GNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEARPNTLVLPKHADADNILVIQQGQATVT
VANGNNRKSFNLDDEGHALRIPSGFISYILNRHDNQLRVAKISMPVNTPGQFEDFFPASS
RDQSSYLQGF SRNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRRSTRSSDNEGVIVK
VSKEHVQELTKHAKSVSKKGSEEEEDITNPINLRDGE PDL SNNFGRLFEVKPDKKNPQLQD
LDMMLTCVEIKEGALMLPHFNSKAMVIVVWNKGTGNLELVAVRKEQQQRGRREQEWEEEE
EDEEEEGSNREVRRYTARLKEGDFVIMPA AHPVAINASSELHLLGFGINAENNHRIFLAG
DKDNVIDQIEKQAKDLAFPGSGEQVEKLIK NQRESHFVSAR PQSQSPSSPEKEDQEEENQ
GGKGPLLSILKAFN

>P43238.1 Ara h 1; 7S globulin, vicilin [Arachis hypogaea]
MRGRVSPLMLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACES
RCKLEYDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDDDRRQPRREEGGRWGPAGP
REREREEDWRQPREDWRRPSHQPRKIRPEGREGEQEWGTPGSHVREETS RNPNPFYFPSR
RFSTRYGNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQ
GQATVTVANGNNRKSFNLDDEGHALRIPSGFISYILNRHDNQLRVAKISMPVNTPGQFED
FFPASSRDQSSYLQGF SRNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRWSTRSSEN
NEGVIVKVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPDLSNFGKLFVVKPD
KKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVWNKGTGNLELVAVRKEQQQRGRR
EEEEDEDEEEEGSNREVRRYTARLKEGDFVIMPA AHPVAINASSELHLLGFGINAENNHRI
FLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIK NQKESHFVSAR PQSQSQSPSSPEKE
SPEKEDQEEENQGGKGPLLSILKAFN

>ADQ53858.1 Ara h 1; 7S globulin, vicilin [Arachis hypogaea]
MRGRVSPLMLLLGILVLASVSATHAKSSPYQKKTENPCAQRCLQSCQQEPDDLKQKACES
RCKLEYDPRCVYDPRGHTGTTNQRSPPGERTRGRQPGDYDDDRRQPRREEGGRWGPAGP
REREREEDWRQPREDWRRPSHQPRKIRPEGREGEQEWGTPGSHVREETS RNPNPFYFPSR
RFSTRYGNQNGRIRVLQRFQDQSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQ
GQATVTVANGNNRRALILTRAMHSESHPFHFLHDDMTPEL RVAKSHAVNTPGQFEDFFP
ASSRDQSSYLQGF SRNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRWSTRSSENNEG
VIVEVSKEHVEELTKHAKSVSKKGSEEEGDITNPINLREGEPDLSNFGKLFVVKPDKKN
PQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVINKGTGNLELVAVRKEQQQRGRREQE
WEEEEDEDEEEEGSNREVRRYTARLKEGDFVIMPA AHPVAINASSELHLLGFGINAENNHRI
FLAGDKDNVVDQIEKQAKDLAFPGSGEQVEKLIK NQRESHFVSAR PQSQSQSPSSPEKEDQ
EEENQGGKGPLLSILKAFN

>AAT00594.1 Ara h 1; 7S globulin, vicilin, partial [Arachis hypogaea]
GNTLEAAFNAAFNEIRRVLLEENAGGEQEERGQRRRSTRSSDNEGVIVKVSKEHVQELTK
HAKSVSKKGSEEEEDITNPINLRDGE PDL SNNFGRLFEVKPDKKNPQLQDLDMMLTCVEIK
EGALMLPHFNSKAMVIVVWNKGTGNLELVAVRKEQQQRGRREQEWEEEEDEEEEGSNRE
VRRYTARLKEGDFVIMPA AHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEK
QAKDLAFPGSGEQVEKLIK NQRESHFVSAR PQSQSQSPSSPEKEDQEEENQGGKGPLLSILK
AFN

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

GALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREEEEDQEEEGSNREVERRY
TARLKEGDVFIIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQAKD
LAFPGSGEQVEKLIKNQRESHFVSARPQSQSPSSPEKEDQEEENQGGKGPLLSILKAFN
>AAT00596.1 Ara h 1; 7S globulin, vicilin, partial [Arachis hypogaea]
GFDQRSRQFQNLQNHRIVQIEAKPNTLVLPKHADADNILVIQQGQATVTVANGNNRKSFN
LDEGHALRIPSGFISYILNRHDNQNLRVAKISMPVNTPGQFEDFFPASSRDQSSYLQGF
RNTLEAAFNAEFNEIRRVLLEENAGGEQEERGQRRWSTRSENNEGVIVKVSKEHVEELT
KHAKSVSKKGSEEGDITNPINLREGEPDLSNMFGLFEVKPDKKNPQLQDLDMMLTCVEI
KEGALMLPHFNSKAMVIVVVKGTGNLELVAVRKEQQQRGRREEEEDQEEEGSNREVR
RYTARLKEGDVFIIMPAAHPVAINASSELHLLGFGINAENNHRIFLAGDKDNVIDQIEKQA
KD LAFPGSGEQVEKLIKNQKESHFVSARPQSQSPSSPEKESPEKEDQEEENQGGKGPL
LSILKAFN
>3S7E_A Ara h 1; 7S globulin, vicilin, partial [Arachis hypogaea]
MSRNNPFYFPSRRFSTRYGNQNGRIRVLQRFDQRSRQFQNLQNHRIVQIEAKPNTLVLPK
HADADNILVIQQGQATVTVANGNNRKSFNLDEGHALRIPSGFISYILNRHDNQNLRVAKI
SMPVNTPGQFEDFFPASSRDQSSYLQGF SRNTLEAAFNAEFNEIRRVLLEENAGGEQEER
GQRRWSTRSENNEGVIVKVSKEHVEELTKHAKSVSKKGSEEGDITNPINLREGEPDLS
NNFGLFEVKPDKKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVVKGTGNLELV
AVRKEQQQRGRREEEEDQEEEGSNREVERRYTARLKEGDVFIIMPAAHPVAINASSELHL
LFGGINAENNHRIFLAGDKDNVIDQIEKQAKDLAFPGSGEQVEKLIKNQKESHFVSAR
>AAB22817.1 agglutinin [Arachis hypogaea]
MKPFCVFLTFLLLAASSKKVDSAETVSFNFNSFSEGNPAINFQGDVTVLSNGNIQLTNL
NKVNSVGRVLYAMPVRIWSSATGNVASFLTSFSFEMKDIKDYDPADGIIFFIAPEDTQIP
AGSIGGGTLGVSDTKGAGHFVGVFDTYSNSEYNDPPTDHVGDVNSVDSVKTVPWNSVS
GAVVKVTVIYDSSTKTLVAVTNDNGDITIAQVVDLAKALPERVKFGFSASGSLGGRQI
HLIRSWSFTSTLITTTTTRRSIDNNEKKIMMASA
>B3EWP3.1 Ara h 12; defensin [Arachis hypogaea]
KTVAGFCIFFLVFLAQEGVVKTEAKLCNHLADTYRGPCTNASCDHCKNKEHFVSGTC
MKMACWCAHNC
>B3EWP4.1 Ara h 13; defensin [Arachis hypogaea]
VQKRTIIMEKKMAGFCIFFLILFLAQEYGVGKECLNLSDKFKGPCLGSKNCDHHCARDIE
HLLSGVCRDDFRCWCNRKC
>C0HJZ1.1 Ara h 13; defensin [Arachis hypogaea]
MEKKMAGFCIFFLVFLAQEYGVGKVCNLSDKFKGPCLGTKNCDHHCARDIEHLLSGVC
RDDFRCWCNRNC
>ABX56711.1 Ara h 9; lipid transfer protein [Arachis hypogaea]
MASLKFAFVMLVCMAMVGMVNAISCGQVNSALAPCIPFLTKGGAPPPACCSGVRGLLG
ALRTTADRQAACNCLKAAAGSLRGLNQGNAALPGRCGVSIPYKISTSTNCATIKF
>ABX75045.1 Ara h 9; lipid transfer protein [Arachis hypogaea]
LSCGQVNSALAPCITFLTKGGVPSGPPCSGVRGLLGAAKTTADRQAACNCLKAAAGSLHG
LNQGNAALPGRCGVSIPYKISTSTNCATIKF
>AAU21500.1 Ara h 10; oleosin [Arachis hypogaea]
MTDRTQPHAVQVHTTAGRFGDTAAGTNRVYADRGPTSKVIAVITGLPIGGTLLLFAGLAL
AGTLLGLAVTTPLFILFSPVIVPATIVVGLSVAGFLTSGACGLTGLSSFSWMMNYIRQTH
GSVPEQLEMAKHRMADVAGYVQKTKDVGQ
>AAZ20276.1 Ara h 11; oleosin [Arachis hypogaea]
MAEALYGGRRQRQEQRSTQLVKATTAVVAGGSLILLAGLVLAGTVIGLTTITPLFVIFS
PVLVPAVITVALLGLGLASGGFVAAITVLTWYRYVTGKHPPGANQLDTARHKLMGKA
REIKDFGQQQTSGAQS
>AAU21499.2 Ara h 10; oleosin [Arachis hypogaea]

MTDRTQPHTVQVHTTAGRFGDTAAGTNRYPDGRGPSTSKVIAVITGLPIGGTLLLFAGLAL
AGTLLGLAVTTPLFILFSPVIVPAIIVVGLSVAGFLTSGACGLTGLSSFSWVMNYIRQTH
GSVPEQLEMAMHRMADVAGYVQKTKDVGQKTKEVGQEIQTKAQDSKRT
>Q45W86 Ara h 11; oleosin [Arachis hypogaea]
MAEALYYGGRQRQDQPRSTQLVKATTAVVAGGSLILAGLVLAATVIGLTTITPLFVIFS
PVLVPAVITVALLGLGLASGGFGVAAITVLTWYRYVTGKHPPGANQLDTARHKLMSKA
REIKDYGQQQTSGAQAS
>AAU21501.1 Ara h 15; oleosin [Arachis hypogaea]
MSDQTRTGYGGGSSYGGGTYGSSYGTSDPSTNQPIRQAIKFMTASTIGVSFLIL
SGLILTGTVIGLIIATPLLVI FSPILVPAAITLALAAGGFLFSGGCGVAAIAALS WLYSY
VTGKHPAGSDRLDYAKGVIADKARDVKDRAKDYAGAGRAQEGTPGY
>COMPARE00285 Ara h 14; oleosin, partial from Q9AXI0.1 [Arachis hypogaea]
RGYDVSGGGVKTFLPDR
>COMPARE00287 Ara h 14; oleosin, partial from Q9AXI0.1 [Arachis hypogaea]
QVHGTTVPDQLDSAK
>COMPARE00284 Ara h 14; oleosin, partial from Q9AXI1.1, Q6J1J8.1 [Arachis hypogaea]
RGYDVSGGGIKTLLPER
>COMPARE00286 Ara h 14; oleosin, partial from Q9AXI1.1, Q6J1J8.1 [Arachis hypogaea]
QVHGTTVPDQLDSVK
>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]
MADMADYVGQK
>AAQ91847.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis
hypogaea]
MGVFTFEDEITSTVPPAKLYNAMKDADSITPKIIDDVKSVEIVEGNGGPGTIKKLTIVED
GETKFILHKVESIDEANYAYNYSVVGVALPPTAEKITFETKLVEGPNGGSIGKLTLYH
TKGDAKPDEEELKKGKAKGEGLFRAIEGYVLANPTQY
>ABG85155.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis
hypogaea]
MGVFTFEDEITSTLPPAKLYNAMKDADSLTPKIIDDVKSVEIVEGSGGPGTIKKLTIVED
GETRFILHKVEAIDEANYAYNYSVVGVALPPTAEKITFETKLVEGHNGGSTGKLSVKFH
SKGDAKPEEEDMKKKGKAKGEALFKAIEGYVLANPTQY
>ABP97433.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis
hypogaea]
MGVHTFEEESTSPVPPAKL FKATVVDGDELTPKLIPAIQSIEIVEGNGGPGTVKKVTAVE
DGKTSYVLHKIDAIDEATYTYDYTISGGTGFQEILEKVSFKTKLEAADGGSKIKVSVTFH
TKGDAPLPDEVHQDVQKKSQGFKAIEGYVLSN
>ACA79908.1 Ara h 8; pathogenesis related protein, PR-10, Bet v 1-like [Arachis
hypogaea]
MGVFTFEDEITSTLPPAKLYNAMKDADSITPKIIDDVKSVEIVEGNGGPGTIKKLTIVED
GETKFILHKVEAIDEANYAYNYSVVGVALPPTAEKITFETKLVEGPNGGSIGKLSVKFH
SKGEAKPEEEDMKKKGKAKGEALFKAIEGYVLANPTQY
>AAD55587.1 Ara h 5; profilin [Arachis hypogaea]
MSWQTYVDNHL LCEIEGDHLSSAAILGQDGGVWAQSSHFQFKPEEITAIMNDFAEPSL
APTGLYLGGTKYMIQGEPGAII PGKKGGVTIEKTNQALIIGIYDKPMTPGQCNMIVE
RLGDYLIDTGL
>ADB96066.1 Ara h 5; profilin [Arachis hypogaea]

MSWQTYVDNHLCEIEGNHLSSAAILGQDGSVWAQSSNFPQFKPEEITAIMNDFAEPSGL
APTGLYLGGTKYMVIQGEPEGAVIRGKKKGGVTIKKTNQALIIGIYDEPMTPGQCNMIVE
RLGDYLIDTGL

>AGA84056.1 Ara h 5; profilin [*Arachis hypogaea*]

MSWQTYVDDHLLCEIEGNHLSSAAILGQDGSVWAQSSNFPQFKPEEITAIMNDFAEPSGL
APTGLYLGGTKYMVIQGEPTVIRGKKKGGVTIKKTNQALIIGIYDEPMTPGQCNMIVE
KLG DYLI DTGL

>CAG26895.1 Arg r 1; lipocalin [*Argas reflexus*]

MALIILLVACL SVVSADDCSGKTD A WTSIKGPKTGGYWLKQTTKTGENECTYVKG TDFKE
NTKTATYTYGYK DASGLTKTTGTATAKGS DIVVGS DTSTVIYTDGKTC DVVKHGGHTEL
WVHSSKTSGGYNNCCDKKFTETR GSTPANEVYKKCPGMP

>2X45_A Arg r 1; lipocalin [*Argas reflexus*]

MDDCSGKTD A WTSIKGPKTGGYWLKQTTKTGENECTYVKG TDFKENTKTATYTYGYK DAS
GKLT KTTGTATAKGS DIVVGS DTSTVIYTDGKTC DVVKHGGHTEL WVHSSKTSGGYNNCC
DKKFTETR GSTPANEVYKKCPGMP

>ARQ16437.1 Art an 7; galactose oxidase [*Artemisia annua*]

MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPEIDDGGGDKPVPGNNDGASDYAKP
AFEPEFMGAWVIDNPAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPINPDAN
NQPD CYAHGIA YDWKTSKYRPLTLQGD AWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPKGFDTTKIGALADTRWYSSNQVLPDGS SVVLGGRDSYSYEIVPPQMEFKPKRFDLPFM
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNRI
QPMAADA AWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP
YKPMGQRFKELTPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELRVEKFSP
PYLDPALLETERTQIDPANTDAVLKYGKPFKITAALMEKQPLVLGEVKVTL LYPPFTTHGF
SQNQRMIVPAITSVQNGVITAVAPPSGQIAPPGYYIMFVSHLGIPGAGIWWHID

>ARQ16438.1 galactose oxidase [*Artemisia argyi*]

MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPQVDDGGGDKPVPGNNDGASDYAKP
AFEPEFMGAWVIDNPAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPNNPDAN
NQPD CYVHGIAYDWKTSKYRPLTLQGD AWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPNGDFTTKIGALADTRWYSSNQVLPDGS SVVLGGRDSYSYEIVPPQMEFKPRRFDLPFM
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNKPAYELVDARHVTEKQFLPALQDCNRI
QPMAADA AWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP
YKPMGQRFKELSPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELRVEKFSP
PYLDPAL EPERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTL LYPPFTTHGF
SQNQRMIVPAITSVENG VITAIAPPSGEIAPPGYYIMFVSHLGIPGAGIWWHID

>AVD29823.1 Art ar 2; pathogenesis related protein, PR-1 [*Artemisia argyi*]

MGLHRNISLVLAISFAILHLSHAHETYGEPGNTDDYVHAHNCIRRVLGMPKPLCWDELA
KVAQAWAETRTPDCLIHSDRCGENMAQGAINGSM AVQLWLDERLDYDYNENKCIKMC GH
YTQIVWANSERVGCGRALCSNGWAYIIVCNYDPPGNVVGQKPY

>ARQ16439.1 galactose oxidase [*Artemisia capillaris*]

MASSIKTAILFLLPLLLAYSVLAAPDITDGGDKPGPLIDDGGGDKPVPGNNDGASDYAKP
AIEPEFMGEWVIDNPAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPEGTPCPINPDAN
NQPD CYAHGIA YDWKTSKYRPLTLQGD AWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPNGDFTTKIGALADTRWYSSNQVLPDGS AVVLGGRDSYSYEIVPPQMEFKPKRFDLPFL
QQTTEPPLGPRPVENNLYPFQFLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPV VPEIVICGGNQPNAYELVDARHVTEKKFLPALQDCNRI
QPMAADA AWIPEQNMPSPRTMGDLHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP
YKPMGQRFKELSPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELRVEKFSP

PYLDPALEPERTLIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF
SQNQRMIWPAITGVENGIVTAVAPPSGEIAPPGYYIMFVSHLGIPGAGIWWHID

>ARQ16440.1 galactose oxidase [*Artemisia gmelinii*]
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPEIDDGGGDKPVPGNNDGASDYAKP
AIEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGPGSYKLPFGTGPCINPDAN
NQPDICYAHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPKGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYIEVPPQMEFKPKRFDLPFM
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNRI
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP
YKPMGQRFKELTPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELVEKFS
PYLDPALETERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF
SQNQRMIWPAITSVENGIVTAVAPPSGQIAPPGYYIMFVSHLGIPGAGIWWHID

>ARQ16441.1 galactose oxidase [*Artemisia lavandulifolia*]
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPQVDDGGGDKPVPGNNDGASDYAKP
AFEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPFGTGPCNNPDAN
NQPDICYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPNGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYIEVPPQMEFKPRRFDLPFM
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNKNAYELVDARHVTEKQFLPALQDCNRI
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP
YKPMGQRFKELSPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELVEKFS
PYLDPALEPERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF
SQNQRMIWPAITSVENGIVTAVAPPSGEIAPPGYYILFVSHLGIPGAGIWWHID

>ARQ16442.1 galactose oxidase [*Artemisia sieversiana*]
MASSIKTVILFLLPLLLAYSILAAPDITDAGADKPGPQVDDGGGDKPVPGNNDGASDYAK
PAIESEFMGQWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPFGTGPCINPDA
NNQPDICYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIPN
DDPNGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYIEVPPQMEFKPKRFDLPF
MQQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
RNYPPSGSAALFPLKLTADNAPVPEIVICGGNQPNAYELVDARHVTEKQFLPALQDCNR
IKPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEPNLTPVLYT
PYKPMGQRFKELRPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELVEKFS
PPYLDPALELERSQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHG
FSQNQRMIWPAITSVENGIVTAVAPPSGEIAPPGYYIMFVSHLGIPGAGIWWHID

>AAX85389.1 Art v 5; calcium-binding protein, polcalcin [*Artemisia vulgaris*]
MADEDKAECDRIFGAFDKNKGDKISAAELGESLTKLGSVSPEEVQTMDELDTDGDGYIS
YDEFAEFFNANRGLMKDVGKIF

>AA024900.1 Art v 1; defensin [*Artemisia vulgaris*]
MAKCSYVFCVLLIFIVAIGEMEAAGSKLCEKTSKTYSGKCDNKKCDKCKIEWEKAQHGA
CHKREAGKESCFCYFDCSKSPPGATPAPPGAAPPPAAGGSPSPPADGGSPPPADGGSP
VDGGSPPPSTH

>ARQ16443.1 galactose oxidase [*Artemisia vulgaris*]
MASSIKTVILFLLPLLLAYSVLAAPDITDGGDKPGPQVDDGGGDKPVPGNNDGASDYAKP
AFEPEFMGAWVIDNPNAGVAAMQLQLMPNDQIVWFDTTSLGASGYKLPFGTGPCNNPDAN
NQPDICYVHGIAYDWKTSKYRPLTLQGDWCSSGNLWPNGNLMATGGTFSGDKAIRVIAND
DPNGDFTTKIGALADTRWYSSNQVLPDGSSVVLGGRDSYSYIEVPPQMEFKPKRFDLPFM
QQTTEPPLGPRPVENNLYPFLFLLPDGNIFLFANNRAITFEPATGKTVKEFPVLPGGSR
NYPPSGSAALFPLKLTADNAPVIPEIVICGGNKNAYELVDARHVTEKQFLPALQDCNRI
QPMAADAAWIPEQNMPSPRTMGDLIHLANGDMLMLNGAKKGTSGWEDATEANLTPVLYTP

YKPMGQRFKELSPTTIARMYHSCSALLPDTRVLVAGSNMHQFYTFDTEFPTELVEKFSF
PYLDPALERTQIDPANTDVVLKYGKPFKITAALMEKQPLVLGEVKVTLTYPPFTTHGF
SQNQRMIVPAITSVENGVITAIAPPSGEIAPPGYYIMFLSHLGIPGAGIWWHID
>P0C088.1 Art v 3; lipid transfer protein [Artemisia vulgaris]
ALTCDVSNKISPCLSYLKQGGEVPADCCAGVKGLND
>ACE07186.1 Art v 3; lipid transfer protein [Artemisia vulgaris]
MKMMKFFCAMVVMVSSSYAEALKCDVSNKISACLSYLKQGGEVPADCCTGVKGLNDA
AKTTPDRQTACNCLKTTFKSNKDFKSDFAASLPSKCGVNIPYKISLETDCNKVK
>ACE07187.1 Art v 3; lipid transfer protein [Artemisia vulgaris]
MAMKMMKFFCAMVVMVLSSSYAEALTCSDVSNKITPCLNYLKQGGEVPADCCTGVKGLN
DAAKTTPDRQTACNCLKTSFKSNKDLKSDFAASLPSKCGVNIPYKISLETDCNKVK
>ACE07188.1 Art v 3; lipid transfer protein [Artemisia vulgaris]
MAIKMMKVFCIMVVMVSTSYAESALTCSDVSTKISPCLSYLKKGGEVPADCCTGVKGL
NDATKTTTPDRQTACNCLKASFKNKDLKSDFAVPLPSKCGLNLPYKLSLETDCNKVK
>ACE07189.1 Art v 3; lipid transfer protein [Artemisia vulgaris]
MAIKMMKVFCVMVVMVSSSYAEALTCSDVSTKISPCLNYLKKGGEVPADCCTGVKGL
NDATKTTTPDRQTACNCLKASFKNKDLKSDFAVPLPSKCGLNLPYKLSLETDCNKVK
>CAK50834.1 Art v 2; pathogenesis related protein, PR-1 [Artemisia vulgaris]
MGHLGNFWLVLAISFAILHLSHAHEITYGEPGNTPPDDYVHAHNCIRRVLGMKPLCWDEIGK
VAQAWAETRTPDCSLIHSRDCGENMAQGAINGSMVAQLWLDERLDYDYNENKCIKMGHY
TQIVWANSERVGCGRALCSNGWAYIIVCNYPGPNVVGQKPY
>AAX85388.1 Art v 6; pectate lyase [Artemisia vulgaris]
MEKHVFVILFTAQVAVGAAARADIGDELEAAQFNSTRRLHECAAHNIIDKCWRCKADW
EKNRQALAKCAQGFAGKTTGGLGGEIYVVTDCSDDNAANPKPGTLRCGVTQDKPLWIIFK
KDMVIKHLKHELVINKDKTIDGRGANVEITCGGLTIHNVNVIHNIHDIKIVTEGGI
ATDAKPGHRHKSDDGDCVAGSSKIWDHCTLSHGPDGLIDVTLGSTAVTISNCKFSSHQ
KILLGADNSHVDDKMMHVTVAFNRFACDQRMPCRFRGFFQVNNNDYTSWGTYAIGGS
ANPTILSQGNRFHAPNDPMKKNVLRADAPHTESMKWNWRSEKDLLENGAIFVASGCDPH
LTPEQKSHLIPAEPGSAVLQLTSCAGTLKCVPGKPC
>5EM0_A Art v 4; profilin [Artemisia vulgaris]
GSGSWQTYVDDHLMCDIEGTGQHLTSAIFGTDGTWAKSASFPEFKPNEIDAIKEFNE
AGQLAPTGLFLGGAKYMIQGEAGAVIRGKKGAGGICIKKTGQAMVFGIYDEPVAPGQCN
MVVERLDYLLDQGM
>CAD12861.1 Art v 4; profilin [Artemisia vulgaris]
MSWQTYVDDHLMCDIEGTGQHLTSAIFGTDGTWAKSASFPEFKPNEIDAIKEFNEAG
QLAPTGLFLGGAKYMIQGEAGAVIRGKKGAGGICIKKTGQAMVFGIYDEPVAPGQCNMV
VERLDYLLDQGM
>CAD12862.1 Art v 4; profilin [Artemisia vulgaris]
MSWQTYVDDHLMCDIEGTGQHLTAAAILGLDGTWAKSDFPEFKPEEMKGIINEFNEVG
TLAPTGLFLGGAKYMLQGEAGAVIRGKKGAGGICIKKTGQAMVMIYDEPVAPGQCNMI
VERLDYLVQNM
>COMPARE073 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]
RLIFHQAGVKFEDNRLKREDWPALKPKTPFGQPLLEVDGEVLAQSAAIYR
>COMPARE074 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]
FGLAGKTPMEEAQVDSIFDQFKDFMAELRPCFRVLAGFEEGDKKVLKEVAVPARDKHLPL
LLEK
>COMPARE075 Asc l 13; glutathione S-transferase, partial [Ascaris lumbricoides]
WIAERPPTY
>ACN32322.1 Asc l 3; tropomyosin [Ascaris lumbricoides]
MDAIKKKMQAMKIEKDNALDRADAAEEKVRQMTDKLERIEEELRDTQKKMMQTENDLKA

QEDLSVANSNLEEKKEKKVQEAEEVAALNRRMTLLEEELERAEEERLKLATEKLEEATHTA
DESERVKVMENRSFQDEERANTVESQLKEAQM LAEEADRKYDEVARKLAMVEADLERAE
ERA EAGENKIVELEEELRVVGNLKSLEVSEEKALQREDSYEEQIRTVSARLKEAETRAE
FAERSVQKLQKEVDRLDEDELVHEKERYKSISEELDQTFQELSGYRSD

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

>AAD13645.1 unknown function [Ascaris lumbricoides]
HHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKDLQAKILHYYDELEGDAKKEATEHL
KDGCREILKHVVGEEKEAELKPKDSGASKEEVKTKVEEALHAVTDEEKKQYIADFGPAC
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 SGASKEELKAKVEEALHAVIDEKKQYIADFGPAC
KKIFGVHTSRRRR

>AAD13650.1 unknown function [Ascaris lumbricoides]
HTMEHYLKTYLSWL TEEQKEK LKEMKEAGQTKAEIQHEVMHYDQLHGEEKQQATEKLV
GCKMLLKGIIIGEEKVV ELRNVKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK
IFGATTLQHRRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYYD
ELEGDAKKEATEHLKGGCP EILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTD
EKKQYIADFGPACKKIYGVHTSRRRR

>AAD13651.1 unknown function [Ascaris lumbricoides]
HTMEHYLKTYLSWL TEEQKEK LKEMKEAGKTKAEIQHEVMRYDQLHGEEKQQATEKLV
GCKMLLKGIIIGEEKVV ELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK
IFGATTLQHRRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYYD
ELEGDAKKEATEHLKGGCREILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTD
EKKQYIADFGPACKKIYGVHTSRRRR

>AAD13652.1 unknown function [Ascaris lumbricoides]
HTMEHYLKTYLSWL TEEQKEK LKEMKEAGKTKAEIQHEVMHYDQLHGEEKQQATEKLV
GCKMLLKGIIIGEEKVV ELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK
IFGATTLQHRRRRRHHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKELEAKILHYYD
ELEGDAKKEATEQLKGGCREILKHVVGEEKAAELKNLKD SGASKEELKAKVEEALHAVTD
EKKQYIADFGPACKKIYGVHTSRRRR

>AAB93837.1 unknown function [Ascaris lumbricoides]
HTMEHYLKTYLSWL TEEQKEK LKEMKEAGKTKAEIQHEVMRYDQLHGEEKQQATEKLV
GCKMLLKGIIIGEEKVV ELRNMKEAGADIQELRQKVEKMLSEVTDEKQKEKVHEYGPACKK
IFGATTLQHRRRRR

>AAB93839.1 unknown function [Ascaris lumbricoides]
HTMEHYLKTYLSWL TEEQKEK LKEMKEAGKTKAEIQHEVMHFYDQLHGEEKQQATEKLV
GCKMLLKGVIIGEEKVV ELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKK
IFGATTLQHRRRRR

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

>Q06811.2 Asc s 1; unknown function [Ascaris suum]
TMEHYLKYLSWLTEEQKEKLEKEMKEAGKTKAEIQHEVMHYDQLHGEEKQQATEKLVG
CKMLLKGIIGEEKVVELRNMKEAGADIQELQQKVEKMLSEVTDEKQKEKVHEYGPACKKI
FGATTLQHRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKTKKELEAKILHYDE
LEGDAKKEATEHLKGGCGEILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDE
EKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAK
KELEAKILHYDELEGDACKEATEHLKGGCAEILKHVVGEEKAAELKNLKDSGASKEELK
AKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQK
DELLKMKKDGKTKKDLQAKILHYDELEGDACKEATEHLKDGCREILKHVVGEEKAAELK
KLDKDSGASKEEVKAKVEEALHAVTDEEKKQYIADFGPACKKIFGAAHTSRRRRRHFTLES
SLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDACKEATEHLKGGCREI
LKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVH
TSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDACK
EATEHLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIA
DFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKI
LHYDELEGDACKEATEHLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEAL
HAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKWLSQEQKDELLKMK
KDGKAKKELEAKILHYDELEGDACKEATEHLKGGCREILKHVVGEEKAAELKNLKDSGA
SKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRHFTLESSLDTHLKW
LSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDACKEATEHLKGGCREILKHVVGEE
KAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKKIYGVHTSRRRRRH
FTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDACKEATEHLKGG
CREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIADFGPACKK
IYGVHTSRRRRYHAEDGTDDIDGLAQSRRRSGFFEKLDVFAFF

>2XV9_A Asc s 1; unknown function, partial [Ascaris suum]
GSPEFHHTLESSLDTHLKWLSQEQKDELLKMKKDGKAKKELEAKILHYDELEGDACKE
ATEHLKGGCREILKHVVGEEKAAELKNLKDSGASKEELKAKVEEALHAVTDEEKKQYIAD
FGPACKKIYGVHTS

>Q9UVU3 serine protease [Aspergillus flavus]
MQSIKRTLLLLGAILPAVLGAPVQETRRAAEKLPKGYIVTFKPGIDEAKIQEHTTWATNI
HQRSLERRGATGGDLPVGIERNYKINKFAAYAGSFDDATIEEIRKNEDVAYVEEDQIYYL
DGLTTQKSAPWGLGSIHKGQSTDYIYDTSAGEGTYAYVDSGVNVDHEEFEGRASKAY
NAAGGQHVDSIGHGTHVSGTIAGKTYGIKASILSVKVFQGESSTSVILDGFNWAAND
IVSKKRTSKAAINMSLGGGYSKAFNDAVENAFEQGVLSVVAAGNENS DAGQTS PASAPDA
ITVAAIQKSNNRASFSNFGKVVDVFAPGQDILSAWIGSSSATNTISGTSMATPHIVGLSL
YLAALENLDGPAAVTKRIEELATKDVVKDVKGSPNLLAYNGNA

>CAB64688.1 Asp f 8; acidic ribosomal protein P2 [Aspergillus fumigatus]
MKYLAAFLLLLAGNTSPSSEDVKAVLSSVGIDAEERLNKLI AELEGKDLQELIAEGST
KLASVPSGGAAAAAPAAAGAAAGAAAPAAKEKNEEKEEESDEDMGFGLFD

>Q9UUZ6.2 Asp f 8; acidic ribosomal protein P2 [Aspergillus fumigatus]
MKHLAAYLLLAGNTSPSSEDVKAVLSSVGIDAEERLNKLI AELEGKDLQELIAEGST
KLASVPSGGAAAAAPAAAGAAAGAAAPAAEKKKEEKEEESDEDMGFGLFD

>COMPARE162 arabinase, partial from EAL84189.1 [Aspergillus fumigatus]
EDYQFGWNQL

>CAA59419.1 Asp f 10; aspartate protease [Aspergillus fumigatus]

MVVFskvtAVVVGLSTIVSAVPVVQPRKGFTINQVARPVtnkktVnLPAVYANALTKYGG
TVPDSVKAASSGSAVTTPEQYDSEYLTPVKVGGTTLNLDFTGSADLWVFSSELSASQS
SGHAIYKPSANAQKLNQYTKIQYGDGSSASGDVYKDTVTVGGVTAQSQAVEAASHISSQ
FVQDKDNDGLLGLAFSSINTVSPRPQTTFDFTVKSQLDSPLFAVTLKYHAPGTYDFGYID
NSKFQGELTYTDVSSQGFWMFTADGYGVNGAPNSNSISGIADTGTLLLLLDDSVVADY
YRQVSGAKNSNQYGGYVFPCKLPSFTTVIGGYNAVVPGEYINYAPVTDGSSTCYGGIQ
SNSGLGFSIFGDIFLKSQYVVFDSQGPRLGFAPQA
>COMPARE164 Asp f 15; cerato-platanin, partial [Aspergillus fumigatus]
PTLPGWNSPNCG
>COMPARE163 Asp f 15; cerato-platanin, partial from 060022.1 [Aspergillus
fumigatus]
WPTFGSVPGFAR
>Q875I9.1 chitosanase [Aspergillus fumigatus]
MRLSEILTVALVTGATAYNLPNNLKQIYDKHKGKCSKVLAKGFTNGDASQKSFSYCGDI
PGAIFISSSKGYTNMDIDCDGANNSAGKCANDPSGQGETAFKSDVKKFGISDLANIHPY
VVFgnEDHSPKFKPQSHGMQPLSMAVVCNQLHYGIWGDtNGGVSTGEASISLADLCFP
NEHLdGNHGHDPNDVLFIGFTSKDAVPGATAKWKAKNAKEFEDSIKSIgDKLVAGLKA
>Q4WB37.1 chitosanase [Aspergillus fumigatus]
MHFLATAAVLAGVGLASAYTPANLQQIYNKHKtGTCQNKLQDGFSDGISGSRSFAYCGD
IEGAIFLHSSANGGQYVNMIDCDGANNSAGDCANDPSGQSMtAFMDTVKQYGISDLAN
IHPYVVFgnSGSSPTFDPPQYGMELPSMAVVCNNQLFYGIWGDtNGGTSTGEASISLAK
LCFPNDGITGDNGHGEEDVLYIGFMGDVAVPGASAAWTARDTKTFEESIKALGDRLVAKL
SA
>CAI78448.1 Asp f 27; cyclophilin [Aspergillus fumigatus]
MVVKTFDFDITIDGQPAGRITFKLFDEVVPKTVENFRALCTGEKGFYKGS SFHRIIPQFM
LQGGDFTKGNGTGGKSIYGRFPDENFQLKHDKPGLLSMANAGKNTNGSQFFITTVVTSW
LDGAHVVFGEVEDGMDLVKKIESYGSASGTPKKKITIADCGQL
>AAK49451.1 Asp f 22; enolase [Aspergillus fumigatus]
MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGK
GVLKAVKNVNETIGPALIKENIDVKDQSKVDEF LNKL DGTANKSNL GANAILGVSLAVAK
AGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVLN GGS HAGGR LAFQEFMIVPDSAPSFS
EALRQGAEVYQKLKALAKKQYQSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTgK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQ LADLYKSLAAKYPIVSIEDPF
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPGRIKKAIElKSCNALLLKV NQIGTLTESIQa
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPCRSERLAKLNQILRIIEE
LGENTVYAGSKFRTAVNL
>Q96X30.3 Asp f 22; enolase [Aspergillus fumigatus]
MPISKIHARSVYDSRGNPTVEVDVVTETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGK
GVLKAVKNVNETIGPALIKENIDVKDQSKVDEF LNKL DGTANKSNL GANAILGVSLAVAK
AGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVLN GGS HAGGR LAFQEFMIVPDSAPSFS
EALRQGAEVYQKLKALAKKQYQSAGNVGDEGGVAPDIQTAEALDLITEAIEQAGYTgK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQ LADLYKSLAAKYPIVSIEDPF
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPGRIKKAIElKSCNALLLKV NQIGTLTESIQa
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPCRSERLAKLNQILRIIEE
LGENAVYAGSKFRTAVNL
>AAM43909.1 Asp f 23; L3 ribosomal protein [Aspergillus fumigatus]
MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSF PKYDPKPKPVHLTASMGYKAGMTTVVRDL
DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHL SDEVKRRFYK
NWKSKKKAFTKYAKKHAEEENGASITRELERIKKYCTVVRVLAHTQIRK TPLKQKKAHLM
EIQVNGGsvADKvDFARNLFEKPIEIDSI FEKDEMIDVIAVTKGHGFQGVTSRWGTKKLP

RKTHKGLRKVACIGAWHPSHVQWTVARAGQMGYHHRTSCNHKVFRIKGSDEGNASTDFD
ISKKQITPMGGFVRYGEVKNNDYIMVKGSVPGVKKRVMTRLRKTLYPQTSRRATEKVELKWI
DTSSKFGHGAFTPEEKRAFMGTLKKDLVTS

>Q8NKF4.2 Asp f 23; L3 ribosomal protein [Aspergillus fumigatus]

MSHRKYEAPRHGSLAFLPRKRAARHRGKVKSFPKDDPKKPVHLTASMGYKAGMTTVVRDL
DRPGAKMHKKEIVEAVTIIETPPLVAVGVVGYIETPRGLRSLTTVWAEHLSDEVKRRFYK
NWKSKKKKAFTKYAKKHAEEENGASITRELERIKKYCTVVRVLAHTQIRKTPKQKKAHLM
EIQVNGGSVADKVDFAFARNLFEKPIEIDSIKDEKIDVIAVTKGHGFQGVTSRWGTKKLP
RKTHKGLRKVACIGAWHPSHVQWTVARAGQMGYHHRTSCNHKVFRIKGSDEGNASTDFD
ISKKQITPMGGFVRYGEVKNNDYIMVKGSVPGVKKRVMTRLRKTLYPQTSRRATEKVELKWI
DTSSKFGHGAFTPEEKRAFMGTLKKDLVTS

>CAA83015.1 Asp f 5; metalloprotease [Aspergillus fumigatus]

MRGLLLAGALALPASVFAHPAHQSYGLNRRRTVDLNAFRLKSLAKYVNATETVIEAPSSFA
PFPKQSYVEVATQHVKMIAPDATFRVDDHYVGDNGVAHVHFRQTANGLDIDNADFNVV
GKDGKVSFYGNSFYTGQIPSSAALTKRDFSDPVTALKGTTNTLQLPITVDSASSESTEEK
ESYVFKGVSQVSDPKAKLVYFVKDDGTLALAWRVETDIDSNWLLTYIDAKSGEEIHGVV
DYVAEADYQVYAWGINDPTEGERTVIKDPWDSVASEFTWISDGSTNYTTSRGNGIAQSN
PSGGPSYLNRYRPSSSSSLSFKYPYSVSSSPSSYIDASIIQLFYTANIYHDLTYLGFTE
KAGNFYNTNGQGGLGNDYVILNAQDQSGTNNANFATPPDGQPGRMRMYVWTESTPYRDG
SFEAGIVIHEYTHGLSNRLTGGPANSNCLNALESGMGEGWSDFMATAIRLKPDKRSTD
YTMGEWASNRRAGGIRQYPYSTSLSTNPLTYTSVNSLNAVHAIGTVWASMLYEVWNLIDK
HGKNDAPKPTLRDGVPTDGKYLAMKLVMDGMALQPCNPNFVQARDAILDADTALTGGENQ
CEIWTAFKRGLGAGAKYSSRNRYGSTEVPSSGVC

>P46075.3 Asp f 5; metalloprotease [Aspergillus fumigatus]

MRGLLLAGALALPASVFAHPAHQSYGLNRRRTVDLNAFRLKSLAKYVNATETVIEAPSSFA
PFPKQSYVEVATQHVKMIAPDATFRVDDHYVGDNGVAHVHFRQTANGLDIDNADFNVV
GKDGKVSFYGNSFYTGQIPSSAALTKRDFSDPVTALKGTTNTLQLPITVDSASSESTEEK
ESYVFKGVSQVSDPKAKLVYFVKDDGTLALAWRVETDIDSNWLLTYIDAKSGEEIHGVV
DYVAEADYQVYAWGINDPTEGERTVIKDPWDSVASEFTWISDGSTNYTTSRGNGIAQSN
PSGGSSYLNRYRPSSSSSLSFKYPYSVSSSPSSYIDASIIQLFYTANIYHDLTYLGFTE
KAGNFYNTNGQGGLGNDYVILNAQDQSGTNNANFATPPDGQPGRMRMYVWTESTPYRDG
SFEAGIVIHEYTHGLSNRLTGGPANSNCLNALESGMGEGWSDFMATAIRLKPDKRSTD
YTMGEWASNRRAGGIRQYPYSTSLSTNPLTYTSVNSLNAVHAIGTVWASMLYEVWNLIDK
HGKNDAPKPTLRDGVPTDGKYLAMKLVMDGMALQPCNPNFVQARDAILDADTALTGGENQ
CEIWTAFKRGLGAGAKYSSRNRYGSTEVPSSGVC

>AAB07620.1 Asp f 2; unknown function, partial [Aspergillus fumigatus]

SARDEAGLNEAVELARHAKAHILRWGNESEIYRKYFGNRPTMEAVGAYDVIWNGDKANVL
FRCDNPDGNCALEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSETNTFW
ASDLMHRLYHVPVAVGQGWDFADGYDEVIALAKSNGTESTHDSEAFYFALEAYAFDIA
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGSGATTTPTDPSATIDVPSNCH
THEGGQLHCT

>EAL89830.1 Asp f 2; unknown function [Aspergillus fumigatus]

MAALLRLAVLLPLAAPLVATLPTSPVPIAARATPHEPVFFSWDAGAVTSFPIHSSCNATQ
RRQIEAGLNEAVELARHAKAHILRWGNESEIYRKYFGNRPTMEAVGAYDVIWNGDKANVL
FRCDNPDGNCALEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSETNTFW
ASDLMHRLYHVPVAVGQGWDFADGYDEVIALAKSNGTESTHDSEALQYFALEAYAFDIA
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGSGATTTPTDPSATIDVPPVRT
VRIS

>CAB44442.1 Asp f 11; peptidyl-prolyl isomerase [Aspergillus fumigatus]

FHQTPSAMSQVFFDVEYAPVGTAEKTVGRIVFNLFDKDVPKTAKNFRELCKRPAGEGYRE

STFHRIIPNFMIIQGGDFTRNGTGGRSIYGDKFADENFSRKHDKKGILSMANAGPNTNGS
QFFITTAVTSWLDGKHVVFGEVADEKSYSVVEIEALGSSSGSVRSNTRPKIVNCGEL
>AAB95638.1 Asp f 3; peroxisomal protein [Aspergillus fumigatus]
MSGLKAGDSFPSDVVFSYIPWSEDKGEITACGIPINYNASKIEWADKKVILFALPGAFTPV
CSARHVPYIEKLEPEIRAKGVVVAVLAYNDAYVMSAWGKANQVTGDDILFLSDPDARFS
KSIQWADEEGRTKRYALVIDHGKITYAALEPAKNHLEFSSAETVLKHL
>CAM54066.1 Asp f 34; PhiA cell wall protein [Aspergillus fumigatus]
MQIKSFVLAASAAATASAAACQAPTNNKYFGIVAIHSGSAVQYQPFSAKSSIFAGLNSQN
ASCDRPDEKSATFYIQDGLYLYAASATPQEIFVDRSGMGQKIGYTTGAQPAPRNSERQ
GWAIDSQNHLLQFQGKDLIACPN SIDGAWSIWADAGVANPAGNTDCVGIARVEDVTNPNS
CVYTQ
>AAF86369.1 Asp f 1; ribonuclease mitogillin [Aspergillus fumigatus]
MTWTCINQQLNPKTNKWEDKRLLYNQAKAESNSHHAPLSDGKTGSSYAHWFTNGYDGNKG
LIKGRTPIKFGKADCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDKFDSKNKPKEDPGPA
RVIYTYPNKVFVCGIVAHQRGNEGDLRLCSH
>P67875.1 Asp f 1; ribonuclease mitogillin [Aspergillus fumigatus]
MVAIKNLFLLAATAVSVLAAPSLDARATWTCINQQLNPKTNKWEDKRLLYSQAKAESNS
HHAPLSDGKTGSSYPHWFTNGYDGNGLIKGRTPIKFGKADCDRPPKHSQNGMGKDDHYL
LEFPTFPDGHDKFDSKPKEDPGPARVIYTYPNKVFVCGIVAHQRGNQGDRLRLCSH
>CAA06305.1 Asp f 1; ribonuclease mitogillin, partial [Aspergillus fumigatus]
RLVYNQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLIKGRMPIKFGKADCDRPPK
HGKDGMGKDDHYLLEFPTFPDGHDKFDSKPKEDPGPARVIYTYPNKVFVCGIVAHHERGN
QGDLR
>AAB60779.1 Asp f 6; superoxide dismutase [Aspergillus fumigatus]
GTSPITPINTMSQQYTLPLPYDALQPYISQQIMELHHKHHQTYVNGLNAALEAQK
KAAEATDVPKLVSVQQAIFNGGGHINHSLFWKNLAPEKSGGGKIDQAPVLKAAIEQRWG
SFDKFKDAFNTLLGIQSGSGWLVTDGPKGKLDITTTTHDQDPVTGAAPVFGVDMWEHAY
YLQYLNDKASYAKGIWNVINWAEAEENRYIAGDKGGHPFMKL
>Q92450.3 Asp f 6; superoxide dismutase [Aspergillus fumigatus]
MSQQYTLPLPYDALQPYISQQIMELHHKHHQTYVNGLNAALEAQKAAEANDVPKL
VSVQQAIFNGGGHINHSLFWKNLAPEKSGGGKIDQAPVLKAAIEQRWGSFDKFKDAFNT
LLGIQSGSGWLVTDGPKGKLDITTTTHDQDPVTGAAPVFGVDMWEHAYYLQYLNDKASY
AKGIWNVINWAEAEENRYIAGDKGGHPFMKL
>CAI78449.1 Asp f 28; thioredoxin [Aspergillus fumigatus]
MSHGKVIADVNPPIYKALTSSGPVVVDFATWCGPCRAVAPKVGELSEKYSNVRFIQVDV
DKVRSVAHEMNIRAMPTFVLYKDGQPLEKRVVGGNVRELEEMIKSISA
>CAI78450.1 Asp f 29; thioredoxin [Aspergillus fumigatus]
MSHNVEKITDAKVFEKQVQEGSGPVIVDCSATWCGPCKAISPVFQRLSTSEEFKNAKFYE
IDVDELSEVAAELGVRAMPTFMFFKDGQKVNEVVGANPPALEAAIKAHVA
>CAA11266.1 Asp f 9; unknown function [Aspergillus fumigatus]
KRSFILRSADMYFKYTAALAAVLPLCSAQTWSKCNPLEKTCPPNKGLAASTYTADFTSA
SALDQWEVTAGKVPVGPQGAFTVAKQGDAPTIDTDFYFFFGKAEVVMKAAAPGTGVVSSI
VLESDDLDEVDWEVLGGDTTQVQTNFYFGKDTTTYDRGTYVPVATPQETFHTYTIDWTKD
AVTWSIDGAVVRTLTYNDAKGGTRFPQTPMRLRLGSWAGGDPSPKGTIEWAGGLTDYSA
GPYTMVYKSVRIENANPAESYTYSDNSGSWQSIKFDGSVDISSSSSVTSSTTSTASSASS
TS
>CAA04959.1 Asp f 4; unknown function [Aspergillus fumigatus]
GEVGDVYATINGVLVSWINEWSGEAKTSDAPVSQATPVSNVAAAAAASTPEPSSSHSD
SSSSSGVSADWTNTPAEGEYCTDGFGRTEPSGSGIFYKGNVKGKWPWSNIIIEVSPENAKK
YKHVAQFVGSDDTPWTVVFWNKIGPDGGLTGWYGNSALTLHLEAGETKYVAFDENSQGAW

GAAKGDELPKDQFGGYSCTWGEFDFDSKINHGWSGWDVSAIQAENAHHEVQGMKICNHAG
ELCSIISHGLSKVIDAYTADLAGVDGIGGKVVPGPTRLVVNLDYKE
>P79017.2 Asp f 2; unknown function [Aspergillus fumigatus]
MAALLRLAVLLPLAAPLVATLPTSPVPIAARATPHEPVFFSWDAGAVTSFPIHSSCNATQ
RRQIEAGLNEAVELARHAKAHILRWGNESIYRKYFGNRPTMEAVGAYDVIIVNGDKANVL
FRCDNPDGNCALLEGWGGHWRGANATSETVICDRSYTTRRWLVSMCSQGYTVAGSETNTFW
ASDLMHRLYHVPVAVGQGWVDHFADGYDEVIALAKSNGTESTHDSEALQYFALEAYAFDIA
APGVGCAGESHGPDQGHDTGSASAPASTSTSSSSSSGSGSGATTTPTDPSATIDVPSNCH
THEGGQLHCT
>060024.2 Asp f 4; unknown function [Aspergillus fumigatus]
MQLKNSMLLLTALAAGSSVARLHGHERHLHHAGEKREVGDTVYATINGVLVSWINEWSG
EAKTSDAPVSQATPVSNAAAAAASTPEPSSSHSDSSSSSSGVSADWTNTPAEGEYCTDG
FGGRTEPSGSGIFYKGNVKGKWPWSNIIEVSPENAKKYKHVAQFVGSDDPWTVVFWNKIG
PDGGLTGWYGNALTLHLEAGETKYVAFDENSQGAWGAAGDELPKDQFGGYSCTWGEFD
FDSKINQGWSGWDVSAIQAENAHHEVQGMKICNHAGELCSIISHGLSKVIDAYTADLAGV
DGIGGKVVPGPTRLVVNLDYKE
>042799.2 Asp f 7; unknown function [Aspergillus fumigatus]
MAPIFKSLALVSALFAAIISSAAPVNLDKREVDVWTTVTTVVWTTIDVTTTIYPTPQAPT
PPVVESTPTPTPSAAPEQAETSTQPETTKSQPTQPSVATFIPVAAAAAADSAAPIP
EEPAPQPATTAAPSTSTTTQAAPSAPPAANSNGSTEKAASSGYSGPCSKGSPCVGQLTYD
TATSASAPSSCGLTNDGFSENVVALPVGIMTDADCGKTVTITYNGITKTATVVDKCMGCK
PTDLASRHLFGELADFSAGRIDGMSWYFN
>KEY78748.1 Asp f 7; unknown function [Aspergillus fumigatus]
MAPIFKSLALVSALFAAIISSAAPVNLDKREVDVWTTVTTVVWTTIDVTTTIYPTPQAPT
PPVVESTPTPTPSAAPEQAETSTQPETTKSQPTQPSVATFIPVAAAAAADSAAPIP
EEPAPQPATTAAPSTSTTTQAAPSAPPAANSNGSTEKAASSGYSGPCSKGSPCVGQLTYD
TATSASAPSSCGLTNDGFSENVVALPVGIMTDADCGKTVTITYNGITKTATVVDKCMGCK
PTDLASRHLFGELADFSAGRIDGMSWYFN
>KEY81716.1 Asp f 4; unknown function [Aspergillus fumigatus]
MQLKNSMLLLTALAAGSSVARLHGHERHLHHAGEKREVGDTVYATINGVLVSWINEWSG
EAKTSDAPVSQATPVSNAAAAAASTPEPSSSHSDSSSSSSGVSADWTNTPAEGEYCTDG
FGGRTEPSGSGIFYKGNVKGKWPWSNIIEVSPENAKKYKHVAQFVGSDDPWTVVFWNKIG
PDGGLTGWYGNALTLHLEAGETKYVAFDENSQGAWGAAGDELPKDQFGGYSCTWGEFD
FDSKINHGWSGWDVSAIQAENAHHEVQGMKICNHAGELCSIISHGLSKVIDAYTADLAGV
DGIGGKVVPGPTRLVVNLDYKE
>AAC61261.1 Asp f 16; unknown function [Aspergillus fumigatus]
MYFKYTAALAAVLPLCSAQTSKCNLAETCPPNKGLAASTCTADFTSASALDQWEVTA
GKVPVGPQGAFTVAKQGDAPTIDTDFYFFFKAEVVMKAAPGTGVVSSIVLESDDLDEV
DLVRLGGDTTQVQNTNYFGKGDTTTTYDRGTYVPVATPQETFHTYIDWTKDAVTWSIDGAV
VRTLTYNDAKGGTRFPQTPMRLRLAAGPAATPATPGHHRVGRWLDRLQRGTVHHVRQVRP
YRERQPRRVLHLLGQLWLLAEHQVRRRLRRYSSSSSVTSSSTTSTASSASSTSSKTPSTSTL
ATSTKATPTPSGTSNSSSSAEPSTTTGGSGSSNTGSLRLRLWLYSSTGSSTSAGA
SATPELSQGAAGSIKGSVTPALWCSAPSLPCWHSKQNDDFGLMHDTHHEGDVRTIHFHIG
VSPSFGV
>COMPARE165 unknown function, partial [Aspergillus fumigatus]
RLQSEVEVAIMD
>COMPARE166 unknown function, partial [Aspergillus fumigatus]
QALIAELAQVH
>CAA73782.1 Asp f 18; vacuolar serine protease [Aspergillus fumigatus]
MKGYLSLSILPLLVAASPVVDSIHNGAAPILSSMNAKEVPDSYIVVFKKHVNAESAAA

HSWVQDIHSAQNERVELRKRS LFGFGEEAYLGLKNTFDIAGSLVGYSGHFHEDVIEQVRK
HPDVEYIEKDSEVHTMEDPTVEKSAPWGLARISHRDSL SFGTFNKYLYASEGGEGVDAYT
IDTGINVDHVD FEGRAGWGKTIPTDDEDADGNHGHTHCSGTIAGRKYVAKKANLYAVKV
LRSSGSGTMSDVVAGVEWAVKSHLKKVKDAKDGKIKGFKGSVANMSLGGGKSRTLEAAVN
AGVEAGLHFAVAAGNDNADACNYS PAAAENPITVGASTLQDERAYFSNYGKCTDIFAPGL
NILSTWIGSKHAVNTISGTSMASPHIAGLLAYFVSLQPSKDSAFVDELTPKKLKKDIIA
IATQGALTDIPSDTPNLLAWNGGGSSNYTDIIASGGYKVNASVKDRFEGLVHKAEKLLTE
ELGAIYSEIHDAAVA

>CAB06417.1 Asp n 14; beta-xylosidase [*Aspergillus niger*]
MAHMSRPVAATAAALLALALPQALAQANTS YVDYNI EANPDLYPLCIETIPLSFPDCQN
GPLRSHLICDETATPYDRAASLISLFTLDEL IANTGNTGLGVSRLGLPAYQVWSEALHGL
DRANFSDSGAYNWATSFPQPILTTAALNRTL IHQIASIISTQGRAFNNAGRYGLDVYAPN
INTFRHPVWGRGQETPGEDVSLAAVYAYEYITGIQGPDPESNLKLAATAKHYAGYDIENW
HNHSRLGNDMNITQQDLSEYYTPQFHVAARDAKVQSVMCAYNAVNGVPACADSYFLQTL
RDTFGFVDHGYVSSDCDAAYNIYNPHGYASSQAAAAEA ILAGTDIDCGTTYQWHLNESI
AAGDL SRDDIEQGVIRLYTTLVQAGYFDSNTTKANNPYRDL SWSVLETDAWNISYQAAT
QGIVLLKNSNNVLP L TEKAYPPSNTTVALIGPWANATTQL LGNYGNAPY MISPRAAFEE
AGYKVNFAEGTGISSTSTSGFAAALSAAQSADV IYAGGIDNTLEAEALDRESIAWPGNQ
LDLIQKLASAAGKKPLIVLQMGGGQVDSSSLKNNTNVSALLWGGYPGQSGGFALRDIITG
KKNPAGRLVTTQYPASYAEFPATDMNLRPEGDNPGQTYKWYTG EAVYEFHGHLFYTTFA
ESSSNTTTKEVKLNIQDILSQTHEDLASITQLPVLNFTANIRNTGKLESDYTAMVFANTS
DAGPAPYPKKWLVGWDR LGVEVKVGETREL RVPVEVGSFARVNEDGDWVFPGTFFELALNL
ERKVRVKVVLEGE EEEVLLKWPGE

>AAD13106.1 Asp n 14; beta-xylosidase [*Aspergillus niger*]
MAHMSRPVAATAAALLALALPQALAQANTS YVDYNI EANPDLYPLCIETIPLSFPDCQN
GPLRSHLICDESATPYDRAASLISLFTLDEL IANTGNTGLGVSRLGLPAYQVWSEALHGL
DRANFSDSGSYNWATSFPQPILTTAALNRTL IHQIASIISTQGRAFNNAGRYGLDVYAPN
INTFRHPVWGRGQETPGEDVSLAAVYAYEYITGIQGPDPDSNLKLAATAKHYAGYDIENW
HNHSRLGNDMNITQQDLSEYYTPQFHVAARDAKVH SVMCAYNAV DGV PACADSYFLQTL
RDTFGFVDHGYVSSDCDAAYNIYNPHGYASSQAAAAEA ILAGTDIDCGTTYQWHLNESI
TAGDLSRDDIEKGVIRLYTTLVQAGYFDSNTTKANNPYRDL TWSVLETDAWNISYQAAT
QGIVLLKNSNNVLP L TEKAYPPSNTTVALIGPWANATTQL LGNYGNAPY MISPRAAFEE
AGYKVNFAEGTGISSTSTSGFAAALSAAARSADV IYAGGIDNTLEAEALDRESIAWPGNQ
LDLIQKLASSAGSKPLIVLQMGGGQVDSSSLKNNTNVTALLWGGYPGQSGGFALRDIITG
KKNPAGRLVTTQYPASYAEFPATDMNLRPEGDNPGQTYKWYTG EAVYEFHGHLFYTTFA
ESSSNTTTKEVKLNIQDILSQTHEELASITQLPVLNFTANIKNTGKLESDYTAMVFANTS
DAGPAPYPVKWLVGWDR LGDVKVGETREL RVPVEVGSFARVNEDGDWVLPGTFFELALNL
ERKVRVKVVLEGE EEEVLLKWPGE

>AAA32702.1 serine protease [*Aspergillus niger*]
MKGILGLSLLPLLLTAASPVFVDSIHN EAAPI LSATNAKEVPDSYIVVFKKHVTSELASAH
HSWVQDIHDSQSERTELKRS LFGLGDEVY LGLKNTFDIAGSLIGYSGHFHEDVIEQVRR
HPDVYIERDSEVHTMEGATEKNAPWGLARISHRDSL TFGNFNKYLYASEGGEGVDAYTI
DTGINVDHVD FEGRATWGKTIPTNDEDLDGNHGHTHCSGT MAGKKYVAKKANLYAVKVL
RSSGSGTMSDVVSGVEYAVQAHIKKAKDAKNGKVKGFKGSVANMSLGGGKSKTLEDAVNA
GVEAGLHFAVAAGNDNADACNYS PAAAEKAITVGASTLADERAYFSNYGECTDIFAPGLN
ILSTWIGSNYATNIISGTSMASPHIAGLLAYFVSLQPSSDSAFAVEELTPAKLKKDIIAI
ATEGALTDIPSNTPNVSHAAGVIYKRNELTQKFSSLP GTVVVPRTTPTS LAAVATRSPLP
RTASRTVLRV SFTRPKSCSPRSLVPSTARSRMPSSHRSELVLSRRRSEDLVFF

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

HQRSLERRGATGGDLPVGIERNYKINKFAAYAGSFDDATIEEIRKNEDVAYVEEDQIYYL
DGLTTQKSAPWGLGSIHKGQSTDYIYDTSAGEGYAYVVD SGVNVVDHEEFEGRASKAY
NAAGGQHVD SIGHGTHVSGTIAGKTYGIAKKASILSVKVFQGESSTSVILDGFNWAAND
IVSKKRTSKAAINMSLGGGYSKAFNDAVENAFEQGLSVVAAGNENS DAGQTS PASAPDA
ITVAAIQKSNRRASF SNFGKVVDFAPGQDILSAWIGSSSATNTISGTS MATPHIVGLSL
YLAAL ENLDGPAAVTKRIKELATKD VVKDVKGSPNLLAYNGNA

>AAA32708.1 Asp o 21; taka-amylase, alpha-amylase [*Aspergillus oryzae*]
MMVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCG
GTWQGIIDKLDYIQGMGFTAIWITPVT AQLPQT TAYGDAYHGYWQQDIYSLNENYGTADD
LKALSSALHERGMYLMVDV VANHMGYDGAGSSVDY SVFKPFSSQDYFHPFCLIQNYEDQT
QVEDCWLGDNTVSLPDLDTTKDVV KNEWYDWV GSLVSNYSIDGLRIDTVKHVQKDFWPGY
NKAAGVYCI GEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLN AFKSTSGSMHDLYNMINTV
KSDCPDSTLLGTFVENHDNPRFAS YTNDIALAKNVAAFIILNDGIP IYAGQE QHYAGGN
DPANREATWASGYPTDSELYKLIASANAIRNYAISKDTGFV TYKNWPIYKDDTTIAMRKG
TDGSQIVTILSNKGASGDSYTL SLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGL
PRVLYPTEKLAGSKICSSS

>P0C1B3.1 Asp o 21; taka-amylase, alpha-amylase [*Aspergillus oryzae*]
MMVAWWSLFLYGLQVAAPALAATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCG
GTWQGIIDKLDYIQGMGFTAIWITPVT AQLPQT TAYGDAYHGYWQQDIYSLNENYGTADD
LKALSSALHERGMYLMVDV VANHMGYDGAGSSVDY SVFKPFSSQDYFHPFCFIQNYEDQT
QVEDCWLGDNTVSLPDLDTTKDVV KNEWYDWV GSLVSNYSIDGLRIDTVKHVQKDFWPGY
NKAAGVYCI GEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLN AFKSTSGSMDDL YNMINTV
KSDCPDSTLLGTFVENHDNPRFAS YTNDIALAKNVAAFIILNDGIP IYAGQE QHYAGGN
DPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFV TYKNWPIYKDDTTIAMRKG
TDGSQIVTILSNKGASGDSYTL SLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGL
PRVLYPTEKLAGSKICSSS

>ADE74975.1 Asp v 13; alkaline serine protease [*Aspergillus versicolor*]
MYSIKRTILLGALLPAVFGAPILEARRQTEKVP GKYIVTFKSGLQAEQIDAHTTWASNV
HKRNLERRDLTDRDLYPGIEKNFKIHKFAAYVGSFDDATIEEIRNHKDV AHVEEDQVWYL
DALTTQSDAPWGLGAISHQGDASSDYIYDTSAGADTYAYVVD TGINVDHSEFDGRASL AY
NAAGGQHVD SVGHGTHVAGTIGGKTFGVSKKANLLSVKVFEGESSTSIILDGYNWAAND
IVSKSRTGKSAINLSLGGGYSYAFSNAVESAFDEGLSVVAAGNENVDASNTSPASAPNA
LTVAASTERNARASF SNYGEVVDIFAPGEDILSAWIGGNSATNTISGTS MATPHIVGLSL
YLIALEGLSSPGDVT SRIKELATQ GALSGVSGSPNALAYNGAE

>P29600.1 alkaline serine protease [*Bacillus lentus*]
AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGE PSTQDGN
GHGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVA
NLSLGSPPSATLEQAVNSATSRGVLVVAASGNSGAGSISYPARYANAMAVGATDQNNNR
ASFSQYGAGLDIVAPGVNVQSTYPGSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQI
RNHLKNTATSLGSTNLYGSGLVNAEATR

>P00780.1 alkaline serine protease [*Bacillus licheniformis*]
MMRKKSFWLGM LTAFLVFTMAFSDSASAAQPAKNVEKDYIVGFKSGVKTASVKKDIIKE
SGGKVDKQFRIINA AKALDKEALKEVKNDPDVAYVEEDHVAHALAQTVPYGIPLIKADK
VQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNHGHTHVAGTVAALD
NTTGVLGVAPSVSLYAVKVLNSSGSGTYSGIVSGIEWATTNGMDVINMSLGGPSGSTAMK
QAVDNAYARGVVVVAAAGNSGSSGNTNTIGYPAKYDSVIAVGAVDSNSNRASFSSVGAEL
EVMAPGAGVYSTYPTSTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATY
LGSSFYYGKGLINVEAAAQ

>AAG31026.1 alkaline serine protease [*Bacillus licheniformis*]
MMRKKSFWLGM LTAFLVFTMAFSDSASAAQPAKNVEKDYIVGFKSGVKTASVKKDIIKE

SGGKVDKQFRIINAAKAKLDKEALKEVKNDPDVAYVEEDHVAHALAQTVPYGIPLIKADK
VQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNHGHGTHVAGTVAALD
NTTGVLGVAPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNGMDVINMSLGASGSTAMK
QAVDNAYAKGVVVVAAAGNSGSSGNTNTIGYPAKYDSVIAVGAVDSNSNRASFSSVGAE
EVMAPGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATY
LGSSFYGKGLINV

>BAA05540.1 unknown function [Bacillus sp.]

MRQSLKVMVLSTVALLFMANPAAASEEKKEYLIVVEPEEVSQAQSVESYDVDVIHEFEEI
PVIHAELTKKELKKLKKDPNVKAI EENA EVTISQTPWGISFINTQQAHNRGIFGNGARV
AVLDTGIASHPDLRIAGGASFISSEPSYHDNNGHGHGTHVAGTIAALNNSIGVLGVAPSADL
YAVKVLDRNGSGSLASVAQGI EWAINNMHIINMSLGSTSGSSTLELAVNRANNAGILLV
GAAGNTGRQGVNYPARYSGVMAVA AVDQNGQRASFSTYGPEIEISAPGVNVNSTYTGNRY
VLSLGTSMATPHVAGVAALVKSRYPSYTNQIRQRINQTATYLGSPSLYGNGLVHAGRAT
Q

>BAF46896.1 tropomyosin [Balanus rostratus]

MDAIIKKKMQAMKLEKENALDKAEQLEQKLRDVEETKAKAEEDLTLQKKYTNLENEFDQV
NEQYNEGVTKEVSEKRVTEAEDEIKGYTRRIQLLEDDLERTPVKLEATFKLE DATKTA
DESERGRKVLERSIADDDRIDALEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERSE
TRLEAAEAKITELSEELAVVGNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA
EAERVVNKLQKEVDRL EDELLAEKEKYKAISDELDQTF AELAGM

>AKV72169.1 Koc s 1; Ole e 1-like [Bassia scoparia]

MAKQAVFLLV GALCVLSLDDVAKAPVSQFH I QGLVYCDTCPYPSSYVLP MLEGATVKLE
CRNITAGTQTFKAEAVTDKVGQYSIPVDGDFEDDICEIE LLKSPDNQCSEVSHD VYAKQS
AKVSLTSNNGEASDVRSANALGFMRKEPLEECPEVLKELDLYDVKAN

>AIV43661.1 Koc s 2; profilin [Bassia scoparia]

MSWQTYVDDHLMCDIEGTTNHLTGAA I LGVDGSVWAQSANFPQFKPDEIAAIVKEFDEPG
TLAPTGLHLGGTKYMIQGEAGQVIRGKKGPGGICVKKTGQALIFGIYDEPVTGQC NMI
VERLGDYLVEQGM

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

MAKFLLSLGI FLLFHCC LAIEYEQEELYECRIQRLTAQEPQYRLEAEAGVSEVWDYTDQ
QFRCAGVAALRNTIRPQGLLLPVYTNAPKLYYVTQGRGILGVLMPGCPETFQSMSQFQGS
REQEEERGRFQDQH QKVHLLKKGDI IAIPAGVALWCYNDGDEDLVTVLVQHTASDLNQLD
QNPRHFFLAGNIQRSQKQRGERYGLRGGQQILADNVFKGFNMEALADVLGFGMDTETARK
VRGEDDQRGHIVRVEQGLK VIRPPRIREELEQQEGGGYNGLEETICSATFIQNIDNPAEA
DFYNPRAGRLTTVNSLKVPI LTFLLQLSAMKGVLYENAMMAPLWRLNANSVVYAVRGEARV
QIVDHRGETVFDDNLREGQMVVVPQNFVVKQAGSRGF EWVFNNDNALFSTAAGRTSP
LRGIPVGVLANAYRLSQEEARRIKLNRDEAVLFQPGSRSRGRASA

>P04403.2 Ber e 1; 2S albumin, conglutin [Bertholletia excelsa]

MAKISVAAAALLVLMALGHATAFRATVTTTVVEEENQE ECREQMQRQQMLSHCRM YMRQQ
MEESPYQTMPRRGM EPHMSECCEQLEGMDESCRCEGLRMMMMRMQQEEMQPRGEQMRRMM
RLAENIPSRCNLSPMRCPMGGSIAGF

>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]

DCNEIPTEGWAKPSLKVSLTSNNGEASDIRSANALGFMR

>P85984.1 Beta v 2; profilin [Beta vulgaris]

YMVIQGE PGAVIRLGDYLIDQGL

>CAA55854.1 Bet v 3; calcium-binding protein, polcalcin [Betula pendula]

MPCSTEAMEKAGHGHASTPRKRSLSNSSFRLRSESLNTRLRLRRIFDLFDKNSDGIITVDE
LSRALNLLGLETDLSELESTVKSFTREGNIGLQFEDFISLHQSLNDSYFAYGGEDEDDNE
EDMRKSILSQEEADSFQGFKVFDEDDGDGYISARELQMVGLGKLGSEIDRVEKMIVSV
DSNRDGRVDFEFKDMMRSVLVRSS
>CAA60628.1 Bet v 4; calcium-binding protein, polcalcin [Betula pendula]
MADDHPQDKAERERIFKRFDANGDGKISAAELGEALKTLGSITPDEVKHMMAEIDTDGDG
FISFQEFTDFGRANRGLLKDVAKIF
>CAC84116.1 Bet v 7; cyclophilin [Betula pendula]
MASNPKVFFDMEVGGQPVGRIVMELYADTTTPRTAENFRALCTGEKGNRSGKPLHYKKSS
FHRVIPGFMCGGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPGTNGSQF
FICTAKTEWLDGKHVVFQWVEGLDIVKAIKVGSSSGRTSKPVVADCGQLS
>P81531.2 Bet v 7; cyclophilin [Betula pendula]
DFTAGNGTGGESIYGAKDXXXXXXXXTGPILSMANAGPGTNG
>AHF71027.1 Bet v 8; glutathione S-transferase [Betula pendula]
MADASVKEHLPTPLDATSNPPPIFDGTTTRYTCYTCPFAQRVWITRNYKGLQEIKLVP
NLQNRPAWYKEKVYPENKVPALHNGKVIKESLDLIKVVDINFEGPSLLPNDPAKKAF
ELVAYSDTFNKTVFTSFKGDVPEAGPAFDHLEKALHKFDDGPFPLGQFSAVDIVYIPFV
ERFQIFLLDALKYDITAGRPKLAKWIEELNKIDAYKPTKTDPKELVEFYKARFAAQ
>CAA33887.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETETTSVIPAAARLFKAFILDGDNLFKVPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA54421.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA54481.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYESETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDQEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA54482.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYEIETTSVIPAAARLFKAFILDGDNLVKVPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA54483.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETEATSVIPAAARLFKAFILDGDNLFKVPQAISSVENIEGNGGPGTIKKISFP
EGIPFKYVKGRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>CAA54484.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYEIETTSVIPAAARLFKAFILDGDNLFKVPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>CAA54487.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]

MGVFNYTEATSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPNGGSILKINNK
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>CAA54488.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYESETTSVIPAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA54489.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYTEATSVIPAARMFKAFILDGDKLVPKVAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA54696.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYEDEATSVIAPARLFKSFVLDADNLI PKVAPENVSSAENIEGNGGPGTIKKITFP
EGSHFKYMKHRVDEIDHANFKYCSIIIEGGPLGDTLEKISYEIKIVAAPGGGSILKITSK
YHTKGDISLNEEEIKAGKEKGAGL FKA VENYLVAHPNAYN
>CAA54695.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
GVFDYEGETTSVIPAARLFKAFILDGDNLI PKVAPQAVSCVENIEGNGGPGTIKKITFPE
GSPFKYVKERVDEVD RVNFKYSYSVIEGGAVGDTLEKICNEIKIVPAPGGGSILKISNKY
HTKGNHEMKAEQIKASKEKAEALFRAVESYLLAHS DAYN
>CAA54694.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFDYEGETTSVIPAARLFKAFILDGDNLI PKVAPQTVSCVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHVNFKYSYSVIEGGAVGDTLEKICNEIKIVPAPGGGSILKISNK
YHTKGNHEMKAEQIKASKEKAEALFRAVESYLLAHS DAYN
>P43180.2 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYESETTSVIPAARLFKAFILEGDNLI PKVAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>P43186.2 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYESETTSVIPAARLFKAFILDGDNLI PKVAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDHEMKAHEMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA96546.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYTEETPSVIPAARLFKAFILDGDKLLPKVAPEAVSSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVD RVNFKYSFSVIEGGAVGDALEKVCNEIKIVAAPDGGGSILKISNK
FHTKGDHEINAEQIKIEKEKAEGLLKAVESYHLAHS DAYN
>CAA96539.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYTEATSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGIPFKYVKDRVDEVDHANFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQIKASKEMGETLLRAVERYLLAHS DAYN
>CAA96540.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNK
YHTKGDHEMKAEHMKAIKEKAEALLRAVESYLLAHS DAYN
>CAA96541.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETEATSVIPAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA96542.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYAYS MIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDHEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA96543.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGSILKISNK
YHTKGDHEMKAEHMKAIKEKGEALLRAVESYLLAHS DAYN
>CAA96544.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETEATSVIPAARLFKASILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGSPFKYVKERVDEVDVNFKYSFSVIEGGAVGDALEKVCNEIKIVAAPDGG SILKISNK
FHTKGDHEINAEQIKIEKEKAVGLLKA VESYLLAHS DAYN
>CAA96547.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVAHKNFKYSYSVIEGGPIGDTLEKISNEIKIVATPDGRSILKISNK
YHTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>CAB02155.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02156.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02157.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDILEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02158.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFKVPAPQAISSVENIEGNGGPGTIKKISFP
GGLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02159.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]

MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02160.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAB02161.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMRETLRAVESYLLAHS DAYN
>CAA96545.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFFLDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFRYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKEEQIKASKEMGETLLRAVESYLLAHS DAYN
>CAA05186.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA05187.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA05188.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA05190.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA07318.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVTTPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA07319.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVEGYLLAHS DAYN
>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]
MGVFNYETETTSVIPAAARLFRAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA07327.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNYETETTSVIPAAARLFKAFILEGDTLIPKVAPQAISSVENIEGNGGPGTIKKITFP
EGSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>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
>CAA04823.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
GVFNYEIETT SVIPAAARLFKAFILDGDNLVPKVAPQAISSVENIEGNGGPGTIKKINFPE
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISHKY
HTKGNHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA04826.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
GVFNYESETTSVIPAAARLFKAFILDGDNLIPKVAPQAISSVENIEGNGGPGTIKKITFPE
GSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNKY
HTKGDHEMKAEHMKAIKEKGETLLKAVESYLLAHS DAYN
>CAA04827.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
GVFNYE TEATSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE
GIPFKYVKDRVDEVDHANFKYSYSLIEGGPVGDTLEKISNEIKIVATPDGGSILKISNKY
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>CAA04828.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]

GVFNYESSETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKITFPE
GSPFKYVKERVDEVDHANFKYSYSMIEGGALGDTLEKICNEIKLVATPDGGSILKISNKY
HTKGDHEMKAHEMKAIKEKGETLLRAVESYLLAHS DAYN
>CAA04829.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
GVFNYEIGATSVIPAARLFKAFILVGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE
GFPFKYVKDRVDEVDHTNFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKINNKY
HTKGDHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>AAD26560.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLKAVESYLLAHS DAYN
>AAD26561.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGPILKISNK
YHTKGDHEVKAEQVKASKEMGETLLRAVESYPLAHS DAYN
>AAD26562.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula
pendula]
MGVFNJETEATSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGIPFKYVKDRVDEVDHANFKYSYSVIEGGPVGDTLEKISNEIKIVATPDGGSILKISNK
YHTKGNHEVKAEQIKASKEMGETLLRAVESYLLAHS DAYN
>1QMR_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]
GVFNJETETTSVIPAAARLFKAFILDGDTLFPQVAPQAISSVENISGNGGPGTIKKISFPE
GLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATGDGGSILKISNKY
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>1LLT_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]
GVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENISGNGGPGTIKKISFPE
GLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>1B6F_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]
GVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY
HTKGDHEVKAEQVKASKELGETLLRAVESYLLAHS DAYN
>4BK6_B Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]
GVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>4BK7_A Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like [Betula pendula]
GVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPE
GFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKY
HTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHS DAYN
>A45786 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial [Betula
pendula]
GVFNIEAETTSVIPAAMLWKXFILDGDNLFPKVAPQAXTSVENIYERGGWG
>B45786 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial [Betula
pendula]
SVFNJETETTSVIPAAMLKAFILDGDKLFPKVAPQXQSI VNXNXYRVYXPK
>CAA07320.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial

[Betula pendula]

MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNN

>CAA07328.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial

[Betula pendula]

MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPMGDTLEKISNEIKIVATPDGGSILKISNN

>AAP37482.1 Bet v 1; pathogenesis related protein, PR-10, Bet v 1-like, partial

[Betula pendula]

MRVFNYKGETTSLIPLARLFK

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

MAHKSILIIIGGTGYIGKFIVEASAKSGHPTFALVRESTVSDPVKGLVEKFKGLGVTL
HGDLYDHESLVKAFKQVDVVISTVGHQLADQVKIIAAIKEAGNIKRFFPSEFGNDVDRV
HAVEPAKTAFATKAEIRRKTEAEGIPYTYVSSNFFAGYFLPTLAQPGLTSPPREKVVIFG
DGNARAVFNKEDDIGTYTIRAVDDPRTLKIVYIKPAKNIYSFNEIVALWEKKIGKTLEK
IYVPEEKLLKDIQESPIPINVILAINHSVFKGDHTNFEIEASFGVEASELYPDVKYTTV
EEYLQQFV

>AAA16522.1 Bet v 2; profilin [Betula pendula]

MSWQTYVDEHLMCDIDGQASNSLASAIVGHDGVSVAQSSSFQFKPQEITGIMKDFEEPG
HLAPTGLHLGGIKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLIDQGL

>1CQA_A Bet v 2; profilin [Betula pendula]

MSWQTYVDEHLMCDIDGQGEELAASAIVGHDGVSVAQSSSFQFKPQEITGIMKDFEEPG
HLAPTGLHLGGIKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLIDQGL

>A4K9Z8.1 Bet v 2; profilin [Betula pendula]

MSWQTYVDEHLMCDIDGQGGQOLAASAIVGHDGVSVAQSSSFQFKPQEITGIMKDFEEPG
HLAPTGLHLGGIKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLIDQGL

>BAB21489.1 unknown function [Betula platyphylla]

MGVFNJETEATSVIPAARLFKAFILDGDKLVKAPQAISSVENIEGNGGPGTIKKINFP
EGFPFKYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN

>BAB21490.1 unknown function [Betula platyphylla]

MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFKYVKDGVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN

>BAB21491.1 unknown function [Betula platyphylla]

MGVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFP
EGFPFEYVKDRVDEVDHTNFKYNYSVIEGGPVGDTLEKISNEIKIVATPDGGCVLKISNK
YHTKGNHEVKAEQVKASKEMGETLLRAVESYLLSHSDAYN

>AAB25850.1 unknown function, partial [Betula sp.]

GVFNJETETTSVIPAAARLFKAFILDGDNLFPKVAPQAITSVENIYERYGXG

>AAB25851.1 unknown function, partial [Betula sp.]

SVFNJETETTSVIPAAFLKAFILDGDKLVKAPQXQSIVXNXYRVYXPK

>ABC68516.1 Bla g 11; alpha-amylase [Blattella germanica]

MKLFPLVALLLVVGLVLSQKDPHVWDGRSAIVHLFEWKFADIADCECERFLGPKGFAGVQV
SPVHENVISSPFRPWERYQLVSYKLVSRGDENAFRDMVRRCNVGIIRIYVDVVLNQM
SGSWPDAHGQGGSTADTYNLQYPAVPYGPDFHSTCTVSNYQDPSNVRNCELVGLHDLNQ
GSDYVRGKMIIEYLNHLVDCGVAGFRVDAAKHMWPADLQYIYSKVNNLNTDHGFPSGARPF

FYQEVIDLGGEAIHSTEYTGFRVTEFKYSRDIGDAFRGNNAIKWLVNFGVGGYIPDGD
ALVFDVNDHNDQRGHGAGGASILTYSKLYKMAVAFMLAYPYGYPRVMSSFSFDNSDQGP
PQDGNNGNIISPSINADGTCNGWVCEHRWRQIFNMVGFNAVAGTAVSNWWDNGDKQISF
CRGNKGFVAFNDEFNNDLKQTLQTCPLPAGDYCDVISGSYENGSCGTGKTVTVGSDGKAYIE
ILSSADDGVLAIHVNSKVGSKSQTTTTQSSHCTCS

>ACM24358.1 Bla g 9; arginine kinase [Blattella germanica]
MVDAAVLEKLEAGFAKLAASDSKSLKLYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN
HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPPKDWGDVDTLGNLDPAGEYI
ISTRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEAELKGQFYPLTGMTKEVQQK
LIDDFLFKEGDRFLQANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGGDLG
QVYRRLVTAVNDIEKRIPFSDHDLGFLTFPCPTNLGTTVRASVHIKVPKLAADKAKLEEV
AGKYNLQVRGTRGEHTEAEGGVYDISNKRRMGLTEYDAVKEMNDGIAELIKLESSL

>COMPARE001 Bla g 9; arginine kinase [Blattella germanica]
VDAAVLEKLEAGFAKLAASDSKSLKLYLTKEVFDNLKTKKTPFGSTLLDVIQSGLENH
DSGVGIYAPDAEAYTVFADLFDPIIEDYHGGFKKTDKHPPKDWGDVDTLGNLDPAGEYII
STRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEGELKGQFYPLTGMTKEVQQKL
IDDFLFKEGDRFLQHANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGGDLGQ
VYRRLVTAVNDIEKRVFSDHDLGFLTFPCPTNLGTTVRASVHIKVPKLAADKKKLEEVA
GKYNLQVRGTRGEHTEAEGGVYDISNKRRMGLTEYDAVKEMNDGIAELIKIESSL

>ABC86902.1 Bla g 9; arginine kinase [Blattella germanica]
MVDAAVLEKLEAGFAKLAASDSKSLRKYLTKEVFDNLKTKKTPFGSTLLDVIQSGLEN
HDSGVGIYAPDAEAYTVFADLFDPIIEDYHGGFKKTDKHPPKDWGDVDTLGNLDPAGEYI
ISTRVRCGRSMQGYFPNCLTEAQYKEMEDKVSSTLSGLEGELKGQFYPLTGMTKEVQQK
LIDDFLFKEGDRFLQHANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGGDLG
QVYRRLVTAVNDIEKRVFSDHDLGFLTFPCPTNLGTTVRASVRIKVPKLAADKKKLEEV
AGKYNLQVRGTRGEHTEAEGGVYDISNKRRMGLTEYDAVKGMNDGIAELIKIESSL

>AII81930 Bla g 12; chitinase [Blattella germanica]
MKTSQILFLCGVFLSVLVSTSGDKPSRVVVCYFSNWAVYRPGLSYKIEDIPTDLCTHLI
YSFIGVSNVTWGPLILDQENDVDLRGFLNFTDLKAKGVKTSVAMGGWEGGRKYSHLVSD
KKLRDTFIPALVEFLHKYNFDGLDIDWEYPGASDRGGSYGDRQNFYFVEELRRAFDFKEG
KGWEITMAVPLANFRLNEGYPDLCELDIVHVMAYDLRGNWAGFADVHSPLYQRPNEG
YGYQALNDNDGMQLWVDKGCSPDKLVLTGTPFYGRFTLSQGNNTKDIGTYINKDAGGGDA
GPYTGAKGMLAYYEICNMLQVNASKWTQKFDIGKCPYAYDDGNQWVGYDNEISLQYKMD
FIKEKGYLGAMTWAIDMDDFHGTGCGQKNPLINVLAKNMKDYVPTLQISTTPRPEWDRPK
STTFEGGSVTTSTTTTTTMMKTTIPETTTTGTSTIDPTITTPSFPPSETTTDATTGGPT
VTPSCANANFYPAANCNQYMCNQGTPIMLMTCPSGTWVWQEGIRCDWPAASTRAECRSA

>AJ053282.1 chymotrypsin, serine protease [Blattella germanica]
MQYCAVLFFAAAVACAYGAELAALDPSTRVVGGTNAATGEFPFIVSLRSTSNSHFCGGSI
ISNYVVITAAHCVSGSSASSVVVVAGTNTLNSGGTSYRVSRIVVHSGYNSNTIVNDIAL
RLSSAISYNSYVQPIALPAQGETSGAGVAASGWSLPPNNLQKVSLSVISNT
QCSSYMNNIYSSSICASGGNGKVCNGDSGGPLTAGGKLIGLVSWGRPCAVGYPDVYTRV
SSYVSWINQNAV

>AAB72147.1 Bla g 5; glutathione S-transferase [Blattella germanica]
YKLTYPVKALGEPFIRFLLSYGEKDFEDYRFQEGDWPNLKPSMPFGKTPVLEIDGKQTHQ
SVAISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDADENSKQKKWDPLKK
ETIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPPLKALRE
KVLGLPAIKAWVAKRPPTDL

>ABP04044.1 Bla g 5; glutathione S-transferase [Blattella germanica]
YKLTYPVKALGEPFIRFLLSYGEKDFEDYRFQEGDWPPLKPSMPFGKTPVLEIDGKQTHQ
SVAISRYLGKQFGLSGKDDWENLEIDMIVDTISDFRAAIANYHYDADENSKQKKWDPLKK

ETIPYYTKKFDEVVKANGGYLAAGKLTWADFYFVAILDYLNHMAKEDLVANQPNLKALRE
KVLGLPAIKAWVAKRPPTDL

>ABX57814.1 glutathione S-transferase [Blattella germanica]
MTIDFYLLPGSAPCRSVLLAAKAFGVNLLKVTNLMAGEHLTPEFLKMNQHTIPTLNDN
GFCLWESRAILSYLADQYKDDSLYPKDPKRALVDQRLYFDLGTLYQRFGDYYPIMFA
KASPDAEKMKKLEEAYQFLDKFLEGQKRVAGNSLTIADIATIASVSTAAILGFDITRYPN
VNKWFENAKKVIPGYDELNHSGLCFRKMWDNLTKQ

>ACY40650.1 Bla g 3; hemocyanin, arylphorin [Blattella germanica]
IPADKVF L R K Q W D V L R L V H R I H Q H S I I P E Q V T V G D S Y D I E A N I N N Y K N P R V V K N F M A L Y K
K D P V K R G E P F S T Y Y I K H R E Q A I M L F E L F Y Y A N D Y D T F Y K T A C W A R D R V N E G M F L Y S F N I A
I M H R E D M Q D I V I P A F Y E I Y P F L F V E N D V I Q K A Y D Y K M K E S G H L N E P H T H V I P V N F T L R N Q
E Q L L S Y F T E D V F L N A F N T Y F R Y M Y P T W F N Y T K Y E Y D V P R H G E Q F Y Y F Y Q Q I Y A R Y M L E R Y
S N D M P D I K P F T Y N K A F K T P Y N P Q L R Y P N G Q E V P A R P A Y M V P Q D F D L Y Y V S D I K N Y E R R V A
D A I D F G Y V F C D K M I S H S L Y N D K K G F E M L A E I I E G N S M H P D Y Y G H I F H M Y R S L L G H V T D P F
H K N G E A P S A L E H P E T A L R D P A F Y Q I W K R V Q H Y F Y K F Q M K L P Y Y T R E E L T F D G V K I D N V D V
G K L Y T Y F E P Y E M S L G Y S V K V E N I Q D A A N V D I R A R N Y R L N H K P F T Y N I E V T S E K E T P V Y V R
V F L G P K Y N Y Y G H E Y D L N E R R N K F V E I D R F P Y Q L H A G K N A I E R N S H E S T V V A K E Q D T P K V L
Y K K V N E A Y E G K A T Y N Y D K Q T K F C G L P E H L L I P K G K K G G Q A F T V Y V I V T P Y D K A V E K E E H H
F K A Y S Y C G V G P H D T Y P D D K P L G F P F D R P I H S Y D F V T P N M F M K D V F I F H K K Y E E V E Q H

>ACY40651.1 Bla g 3; hemocyanin, arylphorin [Blattella germanica]
IPADKVF L R K Q W D V L R L V H R I H Q H S I I P E Q V T V G D S Y D I E A N I N N Y K N P R V V K N F M A L Y K
K D P V K R G E P F S T Y Y I K H R E Q A I M L F E L F Y Y A N D Y D T F Y K T A C W A R D R V N E G M F L Y S F N I A
I M H R E D M Q D I V V P A F Y E I Y P F L F V E N D V I Q K A Y D Y K M K E S G H L N E P H T H V I P V N F T L R N Q
E Q L L S Y F T E D V F L N A F N T Y F R Y M Y P T W F N Y T K Y E Y D V P R H G E Q F Y Y F N Q Q M F A R Y M L E R Y
S N D M P E I Q P F T Y T K P F K T P Y N P Q L R Y P N G Q E V P A R P A Y M M P Q D F D L M Y V S D I K N Y E K R V A
D A V D F G Y V F C D K M I S H S L Y N N E K G L E W L G Q I V E G N S M H P D F Y G H I F H M Y R S L L G H I T D P F
H K H G V A P S A L E H P E T S L R D P A F Y Q I W K R V Q H Y F N K F Q M K Q P Y Y T R E E L A F D G V K I D N V D V
G K L Y T Y F E P Y E M G L S N A V K V G K L E D V P N V D I R A R N Y R L N H K P F T Y N V E V T S E K D T P V Y V R
V F L G P K Y N Y Y G H E Y D L N E R R N Y F V E I D R F P Y Q L H T G K N T I Q R N S H D S S V V A Q E Q D T Y K V L
Y K K V N E A Y E G K T T Y T Y E K Q D K Y C G L P E H L L I P K G K K G G Q A F T V Y V I V T P Y D K A V E K E E H H
F K A Y S Y C G V G P H D S V Y D K K P L G F P F D R P I H S Y D F V T P N M F M K D V F I F H K K Y E E V E Q H

>AAA86744.1 Bla g 2; inactive aspartic protease [Blattella germanica]
MIGLKLVTVLFAVATITHAAELQRVPLYKLVHVFINTQYAGITKIGNQNFLTVDSTSCN
VVVASQECVGGACVCPNLQKYEKLPKYISDGNVQVKFFDTGSAVGRGIEDSLTISNLTT
SQQDIVLADELSQEVCSILSADVVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHAR
FQDGEHFGEIIFGGSDWKYVDGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDT
SKAIIIVGPKAYVNPINEAIGCVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNISSQY
YIQQNGNLCYSGFQPCGSHDFFIGDFFVDHYHSEFNWENKTMGFGRSVESV

>1YG9_A Bla g 2; inactive aspartic protease [Blattella germanica]
GASIVPLYKLVHVFINTQYAGITKIGNQNFLTVDSTSCN VVASQECVGGACVCPNLQK
YEKLPKYISDGNVQVKFFDTGSAVGRGIEDSLTISQLTTSQQDIVLADELSQEVCSILS
DVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHARFQDGEHFGEIIFGGSDWKYV
DGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDTSKAIIIVGPKAYVNPINEAIG
CVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNISSQY YIQQNGNLCYSGFQXPXGHS
HFFIGDFFVDHYHSEFNWENKTMGFGRSVE

>ABP35603.1 Bla g 2; inactive aspartic protease [Blattella germanica]
MIGLKIIVTVLFAVATITHAAELQRVPLYKLVHVFINTQYAGITKIGNQNFLTVDSTSCN
VVVASQECVGGACVCPNLQKYEKLPKYISDGNVQVKFFDTGSAVGRGIEDSLTIFNLTT
SQQDIVLADELSQEVCSILSADVVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHAR
FQDGEHFGEIIFGGSDWKYVDGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDT

SKAIIVGPKAYVNPINEAIGCVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNISSQY
YIQQNGNLCYSGFQPCGSHDFFIGDFFVDHYYSEFNWENKAMGFGRSVESV
>3LIZ_A Bla g 2; inactive aspartic protease [Blattella germanica]
EAEASIVPLYKLVHVFINTQYAGITKIGNQNFLTVDSTSCNVVVASQECVGGACVCPNL
QKYEKLPKYISDGNVQVKFFDGTSAVGRGIEDSLTISQLTTSQQDIVLADELSQEVCIL
SADVVVGIAAPGCPNALKGKTVLENFVEENLIAPVFSIHHARFQDGEHFGEIIFGGSDWK
YVDGEFTYVPLVGDDSWKFRLDGKIGDTTVAPAGTQAIIDTSKAIIVGPKAYVNPINEA
IGCVVEKTTTRRICKLDCSKIPSLPDVTFVINGRNFNISSQYIQQNGNLCYSGFQPCGH
SDHFFIGDFFVDHYYSEFNWENKTMGFGRSVESV
>AAA87851.1 Bla g 4; lipocalin [Blattella germanica]
AVLALCATDTLANEDCFRHESLVPNLDYERFRGSWIIAAGTSEALTQYKCWIDRFSYDDA
LVSKYTDSQGNRTTIRGRTKFEGNKFTIDYNDKGKAFSAPYSVLATDYENYAIVEGCPA
AANGHVIYVQIRFSVRRFHPKLGDKEMIQHYTLDQVNQHKKAI EEDLKHFNLKYEDLHST
CH
>ABP04043.1 Bla g 4; lipocalin [Blattella germanica]
AVLALCASDTLAMEDCFRHESLVPNLDYERFRGSWIIAAGTSEALTQYKCWIDRFSYDDA
LYSLYTDSKGNKTAIRGRTKFEGNKFTIDYNDKGKAFSAPYSVLATDYDNYAIVEGCPA
AANGHVIYVQLRLTWRRFHPKLGDKEMIQHYTLDQVNQHKKAI EEDLKHFNLKYEDLHST
CH
>ACF53836.1 Bla g 4; lipocalin [Blattella germanica]
MCITGVILFAVLAVCATDTLANEDCFRHESLVPNLDYKKFIGTWVIAAGTSEALTQYKCW
NDLFFFNNALVSKYTDSKGNRTTIRGRTKFEGNKFTIDYDDEGKAFSAPYSVLATDYDN
YAIVEGCPAAANGHVIYVQLRLTLRSFHPEQGDKEALQHYTVHQVNQHKKAI EEDLKHFNL
LKYEDLHSTCH
>ACF53837.1 Bla g 4; lipocalin [Blattella germanica]
MCITGVILFAVLALCATDTLADDECFRHESLVPNLDYERFRGMWVIVAGTSEALTQYKCW
IDWFSYDDALVSKYTDSKQGNKILIGKIKFEGNKFTIDYDDEGKAFSAPYSVLATDYDNY
AIVEGCPAAANGHVIYVQLRLTWRRFHPKLGDKEMIQHYTLDQVNQHKKAI EEDLKHFNL
KYEDLHSTCH
>ACJ37389.1 Bla g 4; lipocalin [Blattella germanica]
VLALCATDTLANEDCFRHESLVPNLDYERFRGSWIIAAGTSEALTQYKCWIDRFSYDDAL
VSKYTDSQGNRTTIRGRTKFEGNKFTIDYNDKGKAFSAPYSVLATDYENYAIVEGCPAA
ANGHVIYVQLRMTLRRFHPKLGDKEMLQHYTLDQVNQNKKAIEEDLKHFNLKYEDLHSTC
H
>AAD13531.1 Bla g 1; microvilli-like protein with unknown function [Blattella
germanica]
NAIEFLNNIHDLLGIPHIPVTARKHRRGVGITGLIDDIAILPVDDLYALFQEKLETSP
EFKALYDAIRSPEFQSIVGTLEAMPEYQNLIQKLDKGDVDVDHIEELIHQIFNIVRDTRG
LPEDLQDFLALIPDQVLAIAADYLANDAEVKA AVEYLK SDEFETIVVTVDSLPEFKNFL
NFLQTNGLNIAIEFLNNIHDLLGIPHIPVTGRKHLRRGVGITGLIDDIAILPVDDLYALF
QEKLETSPFEKALYDAIRSPEFQSIVETLKAMPEYQSLIQKLDKGDVDVDHIEELIHQIF
NIVRDTRGLPEDLQDFLALIPIDQILAI AADYLANDAEVQA AVEYLK SDEFETIVVTVDS
LPEFKNFLNFLQTNGLNIAIEFINNIHDLLGIPHIPATGRKHVRRGVGINGLIDDVIAILP
VDELYALFQEKLESSPEFKALYDAIRSPEFQSIVQTLKAMPEYQDLIQRLKDKGDVDVDF
IELIKKLFGLSH
>AAD13530.2 Bla g 1; microvilli-like protein with unknown function [Blattella
germanica]
NLLEKLRKGVDDVKIIEELIRALFGLTLNAKASRNLDQDLQDFLALIPVDQIIAIATDYL
ANDA EVQA AAVAYLQSDEFETIVVALDALPELQNFLEANGLNAIDFLNGIHDLLGIPH
IPVSGRKYHIRRGVITGLIDDVLA ILPIEDLKALFNEKLETSPDFLALYNAI RSPEFQS

IVQTLNAMPEYQNLQLKREKGVVDVKIIEELIRALFGLTLNGKASRNLDLQDFLALIP
VDQIIAIATDYLANDAEVQAAVAYLQSDEFETIVVTLDALPELQNFNFLEANGLNAIDF
LNGIHDLLGIPHIPVSGRKYHIRRGVITGLIDDLVLAAILPLDDLKALFNEKLETSDFLA
LYNAIKSPEFQSIVQTLNAMPEYQNLLEKREKGVVDVKIIEELIRALFGLTH
>AAF72534.1 Bla g 7; troponin C [Blattella germanica]
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANIRAEKAEFEARSLOKKIQIENDLDQT
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAA
DESERARKILESGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQIKTLNTRLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKICDDLDMTFTELIGN
>ABB89296.1 Bla g 6; troponin C [Blattella germanica]
MDELPPEIQILKKAFAFDREKKGCISTEMVGTILEMLGHRLLDDMLQEIIAEVDADGS
GELEFEFVSLASRFLVEEDAEMQQLREAFRLYDKEGNGYITTNVLRILKELDDKIT
AEDLDMMIEEIDSDGSGTVDFDEFMEVMTGE
>ABB89297.1 Bla g 6; troponin C [Blattella germanica]
MDEIPAEQVVLKKAFAFDREKKGCISTEMVGTILEMLGTRLDQDMLDEIIAEVDADGS
GELEFEFCTLASRFLVEEDAEMQHELREAFRLYDKEGNGYITTAVLRILKELDDKIT
AEDLDMMIEEIDSDGSGTVDFDEFMEVMTGE
>ABB89298.1 Bla g 6; troponin C [Blattella germanica]
MADEQLQLPPEQISVLRKAFDAFDREKSGSISTNMVEEILRLMGQPFNRRTLEELIDEVD
ADKSGRLEFDEFVTLAAKFIIEDSEAMEKELREAFRLYDKEGNGYIPTSLREILRELD
EQLTSDDELDMMIEEIDADGSGTVDFDEFMEMMTG
>AAB29344.1 unknown function, partial [Blattella germanica]
APPGCSNHFNLETVFGNFVK
>AAB29345.1 unknown function, partial [Blattella germanica]
GLNICQIDCNKIQSLPXLVFTIGGD
>AAQ24543.1 Blo t 4; alpha-amylase [Blomia tropicalis]
MIVELIVFSLALTIPYQTLASSPYSDFPHQHNKRVITHLMQWKVVDIADECERFLGPYGY
GGVQVSPVNEHASLDRHPWYELYQPVSYRIVSRGTESQFRDMVHRCNKAGVRIYVDVVL
NHMTGPGSGVGIDGTHYDGNMQYPGIPFGPNDFHGHESCPTSNDIQNYDDPTQARNCR
LSGLRDLKQSADYVRTKQADFLNHLIDIGVAGFRFDASKHMWPGDLQAIYSKLHHLNEKY
FPSNSNPFYIHEVIYSNNAISISDYTKLGRSIEFHYYHEL CNVIRGNNKLKWLHNFQGP
WGMVPNDALIMVDSHDLQRGHTGQLGLNINIFYESRLLKVATAFMLAWPYGIPRVMSSYR
WNQKIVNGKDENDWIGPPADGSGSILSVKPNSDLTCNQEWICEHRWKQIYNMVQFRNTAG
DEPVKNWWDNGDYQIAFSRGAKTFFIAINLQNGQHLKQNLHTGLPSGNYCNLVTGNVHNGK
CSGQMVHVDGSGHAMISIGANADDHL
>ABU97467.1 apolipophorin [Blomia tropicalis]
MSAVGTANSHEHLAQLVETYPKDAPKEVKLLKSPENSFETKFALNLDASRNLDIKLNLP
HLIDIHLKNQFEKDKETNLMKNDMVLEYKFPNDETVHTLKTTHHELGYNLKRNGKDKVANF
DFKSKFESSRRPFLNHRSLVQFKYRYPYKLQELVLEFGYGEKMDNVYKFSRISKIDVQEFK
PFKMNSETDLNIVATDFVDYEIKADNRVLDNRGNALFDMNLKGGKDRSKRAAENGNQEI
EGKIKYRNKGSVDSKLEASLKGVDHFAWNSLQVPEPQKYEGKITIQTEDKKIFITH
KEEISKPTKEIHFKEADISYSYKPKKTYVMEAKKQGTAYILKGEAKKDGTVIFSNIN
FESSNGNLKALIKRDRSYDLNVDNVFRPREATLLFKIKDREYNIKMDREPFKYINLKVD
GNENALIKNGKAHLSIMDPTTLNLVTKANSNVDFSMDFASIRHQIALKIDSPKYNFFHD
GDIDLSIVNRRLLWKSLLTKKDDREYKFNADIARKGSMISLTKVTPDRTSVQYSRNGEKI
EVNIDTEYLEGKVEGDRFSGKIVLKNKQNDYELESTYKRENGRLVIESVNGKNAKMEAVF
SRKEPSKFVLETPNTKAKIDMDLTAPVKTFKLDNPRYQKKIDASMEPESEKFKYSSYSN
QKNEKKERKIEIDGVHMKELNVDIDFPDFKFKVKQPESSKKVEFSYTFNNYTETEEYDFD
PHKAYLVNWNALRQYVQTFVVQN

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

>AAQ24549.1 chitinase [Blomia tropicalis]
MTKLCLVALATLATIAALVPVNHATKDPKTVCCYYESWVHWRHGDGKMEPNEIDTSLCTHI
VYTYFGIDAITHELKWLDPYLMKDLHDIEKFVQAKGKAKAMIAIGGASMSDQFSITAGNE
QYRDIFARSVVNFLAQYHFDGIMIDWYGVQERDSENLIHLLDKFDEKFASTTYSMGITLP
ATVATLDHYNVPKITVYVDFINVLTLDYAGPWGKVVDNASPLPEQLKTMEEYHKRGAPRS
KLVMAVPMYARTWRLASPLHQDLGDAAISGGTKGPYDTEGILSYNELCVRIKGSNSFN
IVRDVANTAVHAVYHLHGNEAEFYSFEDTKTLAAKAHVTTMGYGGLSIFTLNEDSHGTC
GKKYPLLHSIVENYNHDPIDEVPITTIPTTPHPTTEVVDIPGVFKCHSVGKFRDHEYCF
KYYDCVMGDFGLESTVMYCERHQAFDEKTYKVEASQIPGC

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

>COMPARE139 Blo t 12; chitin-binding protein [Blomia tropicalis]
MKSVLIFLVAIALFSANIVSADEQTTRGRHTEPDDHHEKPTTHATHEETTSTQHHHEEVT
TQTPHHEEKTTEETHSDDLIVHEGGKTYHVVCHEEGPIPHPGNVHVKYIICKSKSGSLWY
ITVMPCSIGTKFDPISRNCVLDN

>2MFK_A Blo t 12; chitin-binding protein, partial [Blomia tropicalis]
GPLGSDLIVHEGGKTYHVVCHEEGPIPHPGNVHVKYIICKSKSGSLWYITVMPCSIGTKFDP
ISRNCVLDN

>MANUAL2 Blo t 1; cysteine protease [Blomia tropicalis]
MKFLLVAALCALVAIGSCKPTREEIKTFEQFKKVFVKVYRNAEEEEARREHHFKEQLKWVE
EHNGIDGVEYAINSEYSDMSEQEFSFHLSSGGLNFTYMKMEAAKEPLINTYGSLLPQNFQNR
QKARLTRIRQQGACGSCWAFAAAGVAESLYSIQKQSSIGLSEQLVDCTYNRYDPSYQCN
GCGSGYSTAEFKYMIRTGLVEERNYPYNNMRTQWCPDVEGQRYHVSGYQQLRYHSSDEDV
MYTIQQHGPPVVIYMHGSNNYFRNLGNGVLRGVAYNDAYTDHAVILVGGTVQGVQVYWIIR
NSWGTGWNGGYYGYVERGHNSLGINNYVYATL

>AAK58415.1 Blo t 1; cysteine protease [Blomia tropicalis]
IPANFDWRQKTHVNPPIRNOGCGSCWAFAAASSVAETLYAIHRHQNIILSEQELLDCTYHL
YDPTYKCHGCGSGMSPEAFKYMKQKGLLEESHYPYKMKLNQCQANARGTRYHVSSYNSLR
YRAGDQEIQAAIMNHGPPVVIYIHGTEAHRNLRKGIILRGAGYNDAQIDHAVVVLVGGTQN
GIDYWIVRTSWGTQWGDAGYGFVERHHNSLGINNYPIYASL

>AAQ24541.1 Blo t 1; cysteine protease [Blomia tropicalis]
MKFLLVAALCALVAIGSCKPTREEIKTFEQFKKVFVKVYRNAEEEEARREHHFKEQLKWVE
EHNGIDGVEYAINSEYSDMSEQEFSFHLSSGGLNFTYMKMEAAKEPLINTYGSLLPQNFQNR
QKARLTRIRQQGSCGSCWAFAAAGVAESLYSIQKQSSIELSEQELVDCTYNRYDSSYQCN
GCGSGYSTAEFKYMIRTGLVEEENYPYNNMRTQWCNPDVEGQRYHVSGYQQLRYQSSDEDV
MYTIQQHGPPVVIYMHGSNNYFRNLGNGVLRGVAYNDAYTDHAVILVGGTVQGVQVYWIIR
NSWGTGWNGGYYGYVERGHNSLGINNFVYATL

>AAC80579.1 Blo t 13; fatty acid-binding protein [Blomia tropicalis]
MPIEGKYKLEKSDNFDKFLDELGVGFMVKTAAKTLKPTLEVDVQGDYVFRSLSTFKNTE
IKFKLGEEFEEDRADGKRVKTVVNKEGDNKFIQTQYGDKEVKIVRDFQGDDVVVTASVGD
VTSVRTYKRI

>AAP35069.1 Blo t 8; glutathione S-transferase [Blomia tropicalis]
MAPLKIGYWDIRGFAEPIRMLLKHLNIEFEETRYGFGNDSEESFPNRDEWLAEKFTLGFE

FPNLPYFLDGDGFKMTESVAILKRLARANGMIATTEPALSYSSEMIAMVIDIRNRLVYVIY
AENSGTPEEFEQKLADLRERLETSLGQLEAFFQKHGSQWVAGDKLTYVDFLAYEYLDWYR
VFKVSTPIFEKFAKVS DYMKRFEELPSLKEYIASDEHRSASCLSPFARIGHRWAKE
>ACV04860.1 Blo t 8; glutathione S-transferase [Blomia tropicalis]
MAPLKIGYWDVRGFAEPIRMLLKHLNIEFEETRYGFGNDSEESLPNRDEWLAEKFTLGL
FPNLPYFLDGDGFKMTESVAILKRLARANGMIATTEPALSYSSEMIAMVIDIRNRLINVVY
AENSGTPEEFEQKLADLRERLETSLGQLEAFFQKHGSQWVAGDKLTYVDFLAYEYLDWYR
VFKVSTPIFEKFAKVS DYMKRFEELPSLKEYIARDEHRSASCLSPFARIGHRWAKE
>ABG76185.1 Blo t 2; NPC2-like [Blomia tropicalis]
MFKFICLALLVSYAAAGDVKFTDCAHGEVTSLDLSDGSGDHCTIHKGKSFTLTKTFFIANQ
DSEKLEIKISATMNGIEVPVPGVDKDGCKHTTCLPKKQKYELDYSLIIPTILPNLKTVT
TASLVGDHGVVACGKVNTEVVD
>AAM83103.1 Blo t 11; paramyosin [Blomia tropicalis]
MAARS AKYMYQSSRAGHGGDISIEYGTDLGALTRLEDKIRLLSEDLERELRQRVEREK
SDITVQLMNLTERLEETEGSSESVTMKNKRDELAKLRKLLLEDVHMESEETAHHLRQKH
QAAIQEMQDQLDQVQKAKNKSDEKQKQFAEVFELLAQVETANKDKLVAQKTEKLEYTV
HELNIKIEEINRTVVEVTAHRQRLSQENSELIKEVHEYKISLDNANHLKGQIAQQLEDTR
HRLDEERKRSSLENHAHTLEVELESKLVQLEEESEARLELERQLTKANGDAASWKSKEYE
AELQAHVDEVEELRRKMAQKISEYGEQLEALLNKCSALEKQKARLQSEVEVLIMDLEKAT
AHAQALEKRVSQLKINLDLKSKEEVSMLEEQTKDLRVKIADLQKLQHEYEKLRDQKE
ALARENKKLADDLAEAKSQLNDAHRRHEQEIEIKRENEREEAAAAYKEAETLRKQEEA
KNQRLTAELAQTRHDYKRLAQKEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEVARLK
KKYQAQITELSLDAANKANIDLQKTIKKQALQITGLQAHYDEVHRQLQQAVDQLGVTQ
RRCQALTAELEEMRVNLEQALRAKRAAEQMHEEAVVRVNELTTINVNLASAKSKLETEFS
ALQNDYDEVHKLRISSDERVQKLTIEVKSTKDLLESETERVTKLETIKKSLETEVRNLQI
RIEEVEANALAGGKRVIAKLESIRIDVEIEVEEERRRHAETEKMLRKKDHRVKELLLQNE
EDHKQIQLLQEMSDKLNKVKVYKQMQEQEGMSQQNLTRVRRFQRELEAAEDRADQAES
NLSFIRAKHRSWVTTSQVPGGTRQVVFVTEQESSNF
>ABU97466.1 Blo t 10; tropomyosin [Blomia tropicalis]
MEAIKKKMQAMKLEKDNAIDRAEIAEQKSRDANLRAEKSEEEVRALQKKIQQIENELDQV
QESLTQANTKLEEKESLQTAEGDVAALNRRIQLEEDLERSEERLKVATAKLEEAASHSA
DESERMKMLEHRSITDEERMDGLESQLEKARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGETKIVELEEEELRVVGNLKSLEVSEEKAQQREEAYEQQIRMMTGKLEAEARAE
FAERSVRKLQKEVDRLDEDELVHEKEKYKSISDELDTFAELTGY
>AAM10779.1 Blo t 3; trypsin [Blomia tropicalis]
MKVLVLFCLVSLAAAGPLKDALNKAQVDAFYAEGYIVGGSNAADGDAPYQVSLQRTSHFC
GGSIADNYILTAHCIQGLSASSLTTRYNLRHNSGGLTVKASRIIGHEKYDSNTIDND
IALIQTASKMSTGTTNAQAIKLPEQGS DPKASSEVLITGWGTLSSGASSLPTKLQKVTVP
IVDRKTCNANYGAVGAEITDNMFCAGILNVGGKDACQGDSSGGPVAANGVLLGAVSWGYGC
AQAKYPGVYTRVGNYSWIKGKGPV
>AAQ24542.1 Blo t 3; trypsin [Blomia tropicalis]
MKVLVLFCLVSLAAAGPLKDALNKAQVDAFYAEGYIVDGSNAADGDAPYQVSLQRTSHFC
GGSIADNYILTAHCIQGLSASSLTIRYNLRHNSGGLTVKASRIIGHEKYDSNTIDND
IALIQTASKMSTGTTNAQAIKLPEQGS DPKASSEVLITGWGTLSSGASSLPTKLQKVTVP
IVDRKTCNANYGAVGADITDNMFCAGILNVGGKDACQGDSSGGPVAANGVLLGAVSWGYGC
AQAKYPGVYTRVGNYSWIKGKGPV
>AAD10850.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFAIVLIACFAASVLAQEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQLDEL
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYEEAQTLSKILLKD
LKETE QVKVDIQTQ

>AAX34047.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLFHITHEVDDLEKT
GNKDEKARLLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLLLKDLKA
LQKRVQDSE

>ABH06346.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLFHITHEVDDLEKT
GNKDEKARPLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLLLKDLKA
LQKRVQDSE

>ABH06348.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFIIALAALIAVACALPVSNDNFRHEFDHMIINTATQRFHEIEKFLFHITHEVDDLEKT
GNKDEKARLLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLLLKDLKA
LQKRVQDSE

>ABH06350.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNTATQRFHEIEKFLFHITHEVDDLEET
GNKDEKARLLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLLLKDLKA
LQKRVQDSE

>ABH06352.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFAIVLIACFAASVLAQGHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDEL
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKD
LKETEQQVKDIQTQ

>ABH06359.1 Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFAIVLIACFAASVLAQEHKPEKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDEL
NENKSKELQEKIIRELDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKD
LKETEQQVKDIQTQ

>ABH06347.1 Blo t 21; unknown function, group 5/21 mite allergen [Blomia tropicalis]
MKFIIALAALIAVACALPVSNDNFRHEFDHMIVNAATQRFHEIEKFLFHITHEVDDLEKT
GNKDEKARLLRELTVSEAFIEGSRGYFQRELKRTDLDLLEKFNFEAALATGDLLLKDLKA
LQKRVQDSE

>2JMH_A Blo t 5; unknown function, group 5/21 mite allergen [Blomia tropicalis]
GSQEHKPKKDDFRNEFDHLLIEQANHAIEKGEHQLLYLQHQDELNENKSKELQEKIIRE
LDVVCAMIEGAQGALERELKRTDLNILERFNYYEEAQTLSKILLKDLKETEQQVKDIQTQ

>Q7M4I6.1 Bom p 1; phospholipase A2 [Bombus pennsylvanicus]
IIYPGTLWCGNGNIANGTNELGLWKETDACCRTDHMCPLIEAHGSKHGLTNPADYTRLN
CECDEEFRHCLHNSGDAVSAAFVGRTYFTILGTQCFRLDYPVCKVKSTILRECKEYEF
DTNAPQKYQWFDVLSY

>Q7M4I3.1 Bom p 4; protease [Bombus pennsylvanicus]
VVGKPAKLGAWPVMVALGFHNYRQPKKSPEWKCGGSLRISRHVLTAAHCAIHRSLYVVR
IADLNLKRDDDGAHPIQMGIESKLIHPDYVYSEHHDDIAILKLEKDVFSFYIRPICLPI
EESLRNNNFIGNPFFVAGWGRRLRYKGPLSDALMEVQVPVVRNKVCKRAYSDVSDTVICAG
YPKGRKSDSCQGDSGGPLMIPQESTYYEIGVVSYGHECALPKYPGVYTRVTSYLDSEILPA
LKK

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

>P0CH88.1 Bom t 4; protease, partial [Bombus terrestris]
VVGKPAKLGAWPMMVALGF

>ABB88514.1 Bomb m 1; arginine kinase [Bombyx mori]
MVDAATLEKLEAGFSKLGSDSKSLLKYLTVREVFDSLKNKKSFGSTLLDCIQSGVENL
DSGVGIYAPDAESYSVFAELFDPIIEDYHNGFKKTDKHPKNWGDVDTLGNLDPAGEFVV
STRVRCGRSLEGYPFNPCLTESQYKEMEDKVSGLTSSLEGELKGTFFYPLTGMSKETQQQL
IDDHFLFKEGDRFLQAANACRFWPTGRGIYHNENKTFVLWCNEEDHLRIISMQMGDLQQ
VYKRLVSAVNEIEKKIPFSHHDRLGFLTFCPTNLGTTVRASVHIKLPKLAADKKKLEEVA
SKYHLQVRGTRGEHTEAEGGVYDISNKRMMGLTEYDAVKEMYDGAELIKIEKSL

>NP_001036878.1 glycoprotein [Bombyx mori]
MMWKTVLITIFAAGVLADDFSQITAVVTSQCTKNNAEDKVPEVEAALRTFGNCLKGLVDL
NVLKTEIEEAKPNGALDEVFKKYCDKSAQLKGCISVVLQGVPCVGNAYANHINDAQNST
NQLIDFVCYKDGDRIALFIAEGGPECFQKQKTENLKTCLNLKQSFPTVESANNLSLVEKC
AKVDEMTSCIVKSLEECSTPTPANMAESLIKFMKRDSPCHTALPKTD

>NP_001037083 thiol peroxidase [Bombyx mori]
MPLQMTKPAQFKATAVVNGEFKDISLSYKGYVVLFFYPLDFTFVCPTEIIAFSEKAD
EFRKIGCEVLGASTDSHFTHLAWINTPRKQGGGLPMNIPLISDKSHRISRDIYGLDEETG
IPFRGLFIIDDKQNLRQITINDLPVGRSVEETLRLVQAFQFTDKHGEVCPANWRPGAKTI
KPDTKAAQEYFGDAN

>NP_001103782.1 Bomb m 3; tropomyosin [Bombyx mori]
MDAIIKKKMQAMKLEKDNALDRAAMCEQQAKDANLRAEKAEFEARQLQKKIQTIENELDQT
QESLMQVNGKLEEKALQNAESEVAALNRRIQLEEDLERSEERLATATAKLSEASQAA
DESERARKVLENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREEEYKNQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLDELVAEKEYKDIGDDLDTAFVELILKE

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

>CAA29664.1 Bos d 4; alpha-lactalbumin [Bos taurus]
MMSFVSLLLVGLFHATQAEQLTKCEVFRELKDLKGYGGVSLPEWVCTAFHTSGYDTQAI
VQNNDSLEYGLFQINNKIWCKDDQNPSSNICNISCDKFLDDDLTDDIMCVKKILDKVGI
NYWLAHKALCSEKLDQWLCEKL

>AAA30429.1 Bos d 9; alphaS1-casein [Bos taurus]
MKLLILTCLVAVALARPKHPKHQGLPQEVLNENLLRFFVALFPEVFGKEKVNELSKDIG
SESTEDQAMEDIKQMEAEISSSEEIVPNSVEQKHQKEDVPSERYLGYLEQLLRLKYYK
VPQLEIVPNSAEERLHSMKEGIDAQQKEPMIGVNVQELAYFYPELFRQFYQLDAYPSGAWY
YVPLGTQYTDAPSFSDIPNPIGSENSEKTTISLW

>NP_851372.1 Bos d 9; alphaS1-casein [Bos taurus]
MKLLILTCLVAVALARPKHPKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNELSKDIG
SESTEDQAMEDIKQMEAEISSSEEIVPNSVEQKHQKEDVPSERYLGYLEQLLRLKYYK
VPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNVQELAYFYPELFRQFYQLDAYPSGAWY
YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW

>ABW98943.1 Bos d 9; alphaS1-casein [Bos taurus]
VSAALARPKHPKHQGLPQEVLNENLLRFFVAPFPEVFGKEKVNELSKDIGSESTEDQAM
EDIKQMEAEISSSEEIVPNSVEQKHQKEDVPSERYLGYLEQLLRLKYYKVPQLEIVPN
SAEERLHSMKEGIHAQQKEPMIGVNVQELAYFYPELFRQFYQLDAYPSGAWYYVPLGTQY
DAPSFSDIPNPIGSENSEKTTMPLW

>AAA62707.1 Bos d 9; alphaS1-casein, partial [Bos taurus]
PQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNVQELAYFYPELFRQFYQLDAYPSGAWYY

VPLGTQYTDAPSFSDIPNPIGLENSEKTTMPLW
>AAA30478.1 Bos d 9; alphaS1-casein, partial [Bos taurus]
LSKDIGSESTEDQAMEDIKQMEAESISSSEEEIVPNSVEQKQIQKEDVPSERYLGYLEQLL
RLKKYKVPQLEIVPNS
>ABW98945.1 Bos d 9; alphaS1-casein, partial [Bos taurus]
FSEVFGKEKVNELSKDIGSESTEDQAMEDIKQMEAESISSSEEEIVPNSVEQKHIQKEDVP
SERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQQKEPMIGVNQELAYFYF
ELFRQFYQLDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW
>ABW98953.1 Bos d 9; alphaS1-casein, partial [Bos taurus]
IVPNSVEQKHIQKEDVPSERYLGYLEQLLRLKKYKVPQLEIVPNSAEERLHSMKEGIHAQ
QKEPMIGVNQELAYFYFPELFXQFYQPDAYPSGAWYYVPLGTQYTDAPSFSDIPNPIGSEN
SEKTTMPLW
>NP_776953.1 Bos d 10; alphaS2-casein [Bos taurus]
MKFFIFTCLLAVALAKNTMEHVSSSEESIISQETYKQEKMAINPSKENLCSTFCKEVVR
NANEEEYSIGSSSEESAEVATEEVKITVDDKHQKALNEINQFYQKFPQYLQYLYQGPIV
LNPWDQVKNRAVPITPTLNREQLSTSEENSKKTVDMESTEVFTKTKLTEEEKNRLNFK
KISQRYQKFALPQYLKTVYQHQAAMKPIQPKTKVIPYVRYL
>AAA30430.1 Bos d 11; beta-casein [Bos taurus]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDEL
QDKIHFAQTQSLVYFPGPIPNSLPQNIPPLTQTPVVVPPFLQPEVLGVSKVKEAMAPK
HKEMPFKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSL
SQSKVLPVVPQKAVPYPQRDMPIQAFLLYQQPVLGPVVRGPFPIIV
>AAA30431.1 Bos d 11; beta-casein [Bos taurus]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDEL
QDKIHFAQTQSLVYFPGPIHNSLPQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPK
HKEMPFKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSL
SQSKVLPVVPQKAVPYPQRDMPIQAFLLYQEPVLGPVVRGPFPIIV
>AAB29137.1 Bos d 11; beta-casein [Bos taurus]
MKVLILACLVALALARELEELNVPGEIVESLSSSEESITRINKKIEKFQSEEQQQTEDEL
QDKIHFAQTQSLVYFPGPIPNSLPQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPK
QKEMPFKYPVEPFTESQSLTLTDVENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSL
SQSKVLPVVPQKAVPYPQRDMPIQAFLLYQEPVLGPVVRGPFPIIV
>XP_005902099.2 Bos d 11; beta-casein [Bos taurus]
MPLNTIYKQPQNQIIHSAPPSLLVLYFGKELRAMKVLILACLVALALARELEELNVP
GIVESLSSSEESITRINKKIEKFQSEEQQQTEDELQDKIHFAQTQSLVYFPGPIPNSL
PQNIPPLTQTPVVVPPFLQPEVMGVSKVKEAMAPKHKEMPFKYPVEPFTESQSLTLTDV
ENLHLPPLLLQSWMHQPHQPLPPTVMFPPQSVLSLSQSKVLPVVPQKAVPYPQRDMPIQAF
LLYQEPVLGPVVRGPFPIIV
>CAA32835.1 Bos d 5; beta-lactoglobulin [Bos taurus]
MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVE
ELKPTPEGDLEILLQKWENDECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLL
VCMENSAEPEQSLVCQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHI
>P02754.3 Bos d 5; beta-lactoglobulin [Bos taurus]
MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVE
ELKPTPEGDLEILLQKWENGECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLL
FCMENSAEPEQSLACQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHI
>ACG59280.1 Bos d 5; beta-lactoglobulin [Bos taurus]
MKCLLLALALTCGAQALIVTQTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVE
ELKPTPEGDLEILLQKWENDECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLL
FCMENSAEPEQSLVCQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQCHI

>AAA30413.1 Bos d 5; beta-lactoglobulin, partial [Bos taurus]
NSAEPXQSLVCECL

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

>NP_776945.1 collagen [Bos taurus]
MLSFVDTRTL LLLAVTSCLATCQSLQEATARKGPSGDRGPRGERGPPGPPGRDGDGIPG
PPGPPGPPGPPGLGGNFAAQFDAKGGGPGMGLMGPRGPPGASGAPGPQGFQPPGEPGE
PGQTGPAGARGPPGPKAGEDGHPGKPRPGERGVVGPQGARGFPGTPGLPGFKGIRGH
NGLDGLKGQPGAPGVKGEPPGAPGENGTPGQTGARGLPGERGRVGPAGPARGSDGSVGP
VGPAGPIGSAGPPGFPAGPCKGELGPVGNPAGPAGPRGEVGLPGLSGPVGPPGNPGA
NGLPGAKGAAGLPVAGAPGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGE
PGAVGQPPGPPSGE EGKRSTGEIGPAGPPGPPGLRGNPGRGLPGADGRAGVMGPAGS
RGATGPAGVRPNGDSGRPGEPGLMGRGFPGPSGNIGPAGKEGPVGLPGIDGRPGPIGP
AGARGEPPNIGFPGPKGPSGDPGKAGEKGHAGLAGARGAPPDGNGAQPPGLQGVQGG
KGEQGPAGPPGFQGLPGPAGTAGEAGKPGERGIPGEFGLPGPAGARGERGPPGESGAAGP
TGPIGSRGPSGPPGPDGNGKEPVGVPAGTAPSGPSGLPGERGAAGIPGGKGEKGETGL
RGDIGSPGRDARGAPGAIAPGPAGANGDRGEAGPAGPAGPRGSPGERGEVGPAGP
NGFAGPAGAAGQPAGKGERGKPKGENGPVGPVGAAGPSGPNPAGSAGSDGGP
PGATGFPGAAGRTGPPGPSGISGPPGPPGAGKEGLRGRDQGPVGRSGETGASGPPGF
VGEKGPSGEPGTAGPPGTPGPQGLL GAPGFLGLPGSRGERGLPGVAGSVGEPGLGIAGP
PGARGPPGNVGNPVGNGAPGEAGRDGNPNDGPPGRDQPGHKGERGYPGNAGPVGAAGA
PGPQGPVGPVKGHNREGEPPAGAVGPAGVGRGSPGQIRGDKGEPGDKGPRGLPGL
KGHNGLQGLPGLAGHHGDQGAPGAVGPAGPRGPAGPSGPAGKDGRIGQPGAVGPAGIRGS
QGSQGPAGPPGPPGPPGPPGSSGGYEFDFDGFYRADQPRSP TSLRPKDYEV DATL KSL
NNQIETLLTPEGRKNPARTCRDLRLSHPEWSSGYWIDPNQGCTMDAIKVYCDFSTGET
CIRAQPEDIPVKNWYRNSKAKKHVWVGETINGGTQFEYNVEGVTTKEMATQLAFMRLLAN
HASQNITYHCKNSIAYMDEETGNLKKAVILQGSNDVELVAEGNSRFTYTVLVDGCSKKTN
EWQKTIIIEYKTNKPSRLPILDIAPLDIGGADQEIRLNIGPVCFK

>AAA30433.1 Bos d 12; kappa-casein [Bos taurus]
MMKSFFLVVITLALTL PFLGAQEQNQEPIRCEKDERFFSDKIAKYIPIQYVLSRYPSYG
LNYYQQKPVALINNQFLPYPPYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTT MARHP
HPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTIEAVESTVATLEASPEVTESPEI
NTVQVTSTAV

>NP_776719.1 Bos d 12; kappa-casein [Bos taurus]
MMKSFFLVVITLALTL PFLGAQEQNQEPIRCEKDERFFSDKIAKYIPIQYVLSRYPSYG
LNYYQQKPVALINNQFLPYPPYAKPAAVRSPAQILQWQVLSNTVPAKSCQAQPTT MARHP
HPHLSFMAIPPKKNQDKTEIPTINTIASGEPTSTPTIEAVESTVATLEASPEVTESPEI
NTVQVTSTAV

>NP_851341.1 lactotransferrin [Bos taurus]
MKLFVPALLSLGALGLCLAAPRKNVRWCTISQPEWFKCRRWQWRMKKLGAPSITCVRRAF
ALECIRAI AEKKADAVTLDGGMVFEAGRDPYKLRPVAAE IYGTKE SPQTHYYAVAVVKKG
SNFQLDQLQGRKSCHTGLGRSAGWIIPMGI LRPYLSWTESLEPLQGAVAKFFSASCVPCI
DRQAYPNLCQLCKGEGENQCACSSREPYFGYSGAFKCLQDGAGDVA FVKETT V FENLPEK
ADRDQYELLCLNNSRAPVDAFKECHLAQVPSHVVARSVDGKEDL IWKLLSKAQEKFGKN
KSRSFQLFGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYL T T LKNLRETAEEVKAR
YTRVVWCAVGPEEQKCKQWSQSGQNVTCATASTTDDCIVLVLKGEADALNLDGGYIYT
AGKCGLVVLAENRKSSKHSSLDVLRPTEGYLAVAVVKKANEGLTWNLSLKD KKSCHTAV
DRTAGWNIPMGLIVNQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKE
YYYGYTGAFRCLAEDVDVAFVKN DTVWENTNGESTADWAKNLNREDFRLLCLDGTRKPV

TEAQSCHLAVAPNHAVVSRSDRAAHVKQVLLHQALFGKNGKNCPDKFCLFKSETKNLLF
NDNTECLAKLGGPRTYEEYLGTEYVTAIANLKKCSTSPILLEACAFLTR
>Q28133.1 Bos d 2; lipocalin [Bos taurus]
MKAVFLTLLFGLVCTAQETPAEIDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIEC
INDCESLSITFYLDQGTCLLLTEVAKRQEGYVYVLEFYGTNTLEVIHVSENMLVTYVEN
YDGERITKMTEGLAKGTSFTPEELEKYQQLNSERGVNENIENLIKTDNCP
>AAA51411.1 Bos d 6; serum albumin [Bos taurus]
MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHRFKDLGEEHFKGLVLIASFQYLQQCPF
DEHVKLVELTEFAKTCVADESHAGCEKSLHTLFGDELCKVASLRETYGDMADCCCKQEP
ERNECFLSHKDDSPDLPKLPDPNTLCDEFKADEKKFWGKLYEIAARRHPYFYAPELLYY
ANKYNGVFQEQCAEDKGACLLPKIETMREKVLASSARQRLRCASIQKFGERALKAWSVA
RLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLCADDRADLAKYICDNQDTISSKLKE
CCDKPLLEKSHCIAEVEKDAIPENLPPLTADFAEDKDVCKNYQEAKDAFLGSLYEYSRR
HPEYAVSVLLRLAKEYEATLEECCAADDPHACYSTVFDKLLKHLVDEPQNLKQNCQDFEK
LGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLIL
NRLCVLHEKTPVSEKVKCTESLVNRRPCFSALTPDETYVPKAFDEKLFTHADICTLP
DTEKQIKKQALVELLKHKPKATEEQKKTVMENFVAFVDKCCAADDKEACFAVEGPKLVV
STQATALA
>CAA76847.1 Bos d 6; serum albumin [Bos taurus]
MKWVTFISLLLLFSSAYSRGVFRDTHKSEIAHRFKDLGEEHFKGLVLIASFQYLQQCPF
DEHVKLVELTEFAKTCVADESHAGCEKSLHTLFGDELCKVASLRETYGDMADCCCKQEP
ERNECFLSHKDDSPDLPKLPDPNTLCDEFKADEKKFWGKLYEIAARRHPYFYAPELLYY
ANKYNGVFQEQCAEDKGACLLPKIETMREKVLSSARQRLRCASIQKFGERALKAWSVA
RLSQKFPKAEFVEVTKLVTDLTKVHKECCHGDLLCADDRADLAKYICDNQDTISSKLKE
CCDKPLLEKSHCIAEVEKDAIPENLPPLTADFAEDKDVCKNYQEAKDAFLGSLYEYSRR
HPEYAVSVLLRLAKEYEATLEECCAADDPHACYSTVFDKLLKHLVDEPQNLKQNCQDFEK
LGEYGFQNALIVRYTRKVPQVSTPTLVEVSRSLGKVGTRCCTKPESERMPCTEDYLSLIL
NRLCVLHEKTPVSEKVKCTESLVNRRPCFSALTPDETYVPKAFDEKLFTHADICTLP
DTEKQIKKQALVELLKHKPKATEEQKKTVMENFVAFVDKCCAADDKEACFAVEGPKLVV
STQATALA
>P80207.1 Bra j 1; 2S albumin, conglutin [Brassica juncea]
AGPFRFPRCRKEFQQAQHLRACQQWLHKQAMQSGSGPQPQGPQQRPPLLQQCCNELHQEE
PLCVCPTLKGASKAVKQQIRQQGQQGQQGQQQLQHEISRIYQTATHLPRVCNIPRVSICP
FQKTMGPS
>AAN86249.1 Bra n 1; 2S albumin, conglutin [Brassica napus]
QPQKQREFQEQHLRACQQWIRQQLAGSPFSENQWGPQQGPSLREQCCNELYQEDQVCV
CPTLKQAAKSVRVQGHGPFQSTRIYQIAKNLPNVCNMKQIGTCPFIAI
>P80208.1 Bra n 1; 2S albumin, conglutin [Brassica napus]
SAGPFRIPKCRKEFQQAQHLRACQQWLHKQAMQSGSGPQPQGPQQRPPLLQQCCNELHQEEP
LCVCPTLKGASRAVKQQVRQQGQQGQQQLQQVISRIYQTATHLPKVCNIPQVSVCPPFKT
MPGPS
>S65144 calcium-binding protein [Brassica napus]
MADATEKTEHDRFFKKFDANGDGTISSTELGDALKNLGSVTHDDIKRMMAEIDTDGDGFI
SYQEFSDFAKANRGLMKDVAKIF
>S65145 calcium-binding protein [Brassica napus]
MADATEKAEHDRFFKKFDANGDGTISSTELGDALKNLGSVTHDDIKRMMAEIDTDGDGFI
SYQEFSDFAKANRGLMKDVAKIF
>BAA09632.1 calcium-binding protein, polcalcin [Brassica napus]
MADAEHERIFKKFDTGDGKISAAELEEALKKLGSVTPDDVTRMMAKIDTDGDGNISFQE
FTEFASANPGLMKDVAKVF

>BAA09633.1 calcium-binding protein, polcalcin [Brassica napus]
ADATEKAEHDRIFKKFDANGDGKISASELGDALKNLGSVTHDDIKRMMAEIDTDGDGYIS
YQEFSDFASANRGLMKDVAKIF

>XP_013623213.1 lipid transfer protein [Brassica oleracea]
MASALSFFTCLVLTVCIVASVDAAISCGTVTSNLAPCAVYLMKGGPVPAPCCAGVSKLNS
MAKTTTPDRQQACKCLKTAAKNVNPSLASSLPGKCGVSIPYPISMSTNCDTVK

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

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

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

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

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

>COMPARE018 lipid transfer protein [Brassica rapa]
MKIMVLTLMVFVILLTLFPAPNEAADTNVEAACDPKQLQPCLAAITGGGQPSGDCCAKLK
EQQPCLCGFSKNPAFAQYISSPNSRKVLTACGIPYPSC

>COMPARE210 defensin, partial [Buchanania lanzan]
MAGFCIFFLILFLAQEYGVGK

>COMPARE212 defensin, partial [Buchanania lanzan]
ECLNLSDKFK

>COMPARE213 defensin, partial [Buchanania lanzan]
DIEHLLSGVCR

>CAA57342.1 Cand a 1; alcohol dehydrogenase [Candida albicans]
MSEQIPKTQKAVVFDNTGGQLVYKDYPVPTPKPNELLIHVKYSGVCHTDLHARKGDWPLA
TKLPLVGGHEGAGVVVGMGENVKGWKIGDFAGIKWLNCSCEFCQQGAEPNCGEADLS
GYTHDGSFEQYATADAVQAQIPAGTDLANVAPILCAGVTVYKALKTADLAAGQWVAISG
AGGGLGSLAVQYARAMGLRVVAIDGGDEKGEFVKSLGAEAYVDFTKDKDIVEAVKKATDG
GPHGAINVSVSEKAIDQSVEYVRPLGKVVVLVGLPAHAKVTAPVFDVAVKSIKGSYVGN
RKDTAEAIIDFFSRGLIKPIKIVGLSDLPEVFKLMEEGKILGRYVLDTSK

>P30575.1 enolase [Candida albicans]
MSYATKIHARYVYDSRGNPTVEVDFTTDKGLFRSIVPSGASTGVHEALELRDGDKSKWLG
KGVLKAVANVNDIIAPALIKAKIDVVDQAKIDEFLSLDGTTPNKSCLGANAILGVSLAAA
NAAAAAQGIPLYKHIANISNAKKGFVLPVPFQNVNLNGGSHAGGALAFQEFMIAPTGVST
FSEALRIGSEVYHNLKSLTKKKYQGSAGNVGDEGGVAPDIKTPKEALDLIMDAIDKAGYK
GKVGIAMDVASSEFYKDGKYDLDFKNPESDPKWLSPQLADLYEQLISEYPIVSIEDPF
AEDDWDVAVVHFFERVGDKIQIVGDDLTVTNPTRIKTAIEKKAANALLLVNQIGTLTESI
QAANDSYAAGWGMVSHRSGETEDTFIADLSVGLRSGQIKTGAPARSERLAKLNQILRIE
EELGSEAIYAGKDFQKASQL

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

IATTVYNKGGVVS AVCHGPAIFENLNDPKTGEPLIKGKKITGFTDIGEDILGVTDIMKKG
NLLTIKQVAEKEGATYIEPEGPWNFTVTDGRIVTGVNPPQSAVKTAEDVIAAFECN
>P14292.3 Cand b 2; peroxisomal protein [Candida boidinii]
MAPIKRGDRFPTTDDVYYPPEGGEPGLELSKFVKTKKFVVVSVPGAFTPPCTEQHLP
YIKNLPRIKSGVDFVLVISQNDPFVLKGWKELGAADAKKLVFVSDPNLKLTKKLGSTI
DLSAIGLGRSRLALIVNRS GIVEYAAIENGGEVDVSTAQKIIAKL
>CAA68720.1 Can f 5; arginine esterase [Canis familiaris]
MWFLALCLAMSLGWTGAEPHFQPRIIGGRECLKNSQPWQVAVYHNGEFACGGVLVNP
EWLTAAHCANSNCEVWLGRHNLSESEDEGQLVQVRKSFHPLYKTKVPRVIRPGEDRSHDL
MLLHLEEPAKITKAVRVMIDLKKEPPLGSTCYVSGWGSTDPEIFHPGSLQCVDLKLLSN
NQCAKVYTKVTKFMLCAGVLEGGKDTCKGDSGGPLICDGEVGVITSWGATPCGKQMP
S LYTRVMPHLMWIKDTMKANT
>AAC48794.1 Can f 1; lipocalin [Canis familiaris]
MKTLTLLTIGFSLIAILQAQDTPALGKDTVAVSGKWYLKAMTADQEVPEKPD
SVTPMILKAQKGGNLEAKITMLTNGQCQNTVVLHKTSEPGKYTAYEGQVRFIQ
PSPVRDHYILYCEGELHGRQIRMAKLLGRDPEQSQALEDFREFSRAKGLNQEILELAQ
SETCSPGGQ
>AAC48795.1 Can f 2; lipocalin [Canis familiaris]
MQLLLLTVGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLIK
PWGHFRVFIHMSAKDGNLHGDILIPQDQCEKVSLTAFKTATSNKFDLEYWGHND
LYLAEVDPKSYLILYMINQYNDTSLVAHLMVRDLRQQDFLPAFESVCE
DIGLHKDQIVVLSDDDRCCQGSRD
>CAD82911.1 Can f 2; lipocalin [Canis familiaris]
STFCLGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLIK
PWGHFRVFIHMSAKDGNLHGDILIPQDQCEKVSLTAFKTATSNKFDLEYWGHND
LYLAEVDPKSYLILYMINQYNDTSLVAHLMVRDLRQQDFLPAFESVCE
DIGLHKDQIVVLSDDDRCCQGSRD
>CAD82912.1 Can f 2; lipocalin [Canis familiaris]
QLLLLTVGLALICGLQAQEGNHEEPQGGLEELSGRWHSVALASNKSDLT
KPWGHFRVFIHMSAKDGNLHGDILIPQDQCEKVSLTAFKTATSNKFDLEYWGHND
LYLAEVDPKSYLILYMINQYNDTSLVAHLMVRDLRQQDFLPAFESVCE
DIGLHKDQIVVLSDDDRCCQGSRD
>ACY38525.1 Can f 4; lipocalin [Canis familiaris]
MKILLLCLALV LASDAQPLPNVLTQVSGPWKTLYISSNLDKIGDNGPFRIYMR
GINVDIPRLKMSFNFYVKVDGECVENS VGASIGRDNLIKGEYNGGNYFRIID
MTPNALIGYDVNVDSK GKITKVALLMGRGAHVNEEDIAKFKKLSREKGIPEENI
IYLGDTDNCPNHE
>CCF72371.1 Can f 6; lipocalin [Canis familiaris]
MKLLLLLCLGLILVHAHEEENDVVKGNFDISKISGDWYSILLASDIKEKIEENG
SMRVFVKDIEVLSNSSLIFTMHTKVNGKCTKISLICNKTEKDGEYDVVHDGYNL
FRIIETAYEDYIIFHLNNVNQE QEFQLMELYGRKPDVSPKVKEK FVRYCQMEI
PKENILDLTQVDRCLQARQSEAAQVSSAE
>5X7Y_A Can f 6; lipocalin [Canis familiaris]
GSHEEENDVVKGNFDISKISGDWYSILLASDIKEKIEENGSMRVFVKDIEVLS
NSSLIFTMHTKVNGKCTKISLICNKTEKDGEYDVVHDGYNL FRIIETAYEDYI
IFHLNNVNQE QEFQLMELYGRKPDVSPKVKEK FVRYCQMEIPKENILDLTQV
DRCLQARQSEAAQVSSAE
>AHY24648.2 Can f 4; lipocalin [Canis familiaris]
MKILLLCLALV LASDAQPLPNVLTQVSGPWKTLYVSSNLDKIGENGPFR IYLR
GINVDIPRLKMLFNFYVKVDGECVENS VGASIGRDNLIKGEYNGGNYFRIID
MTPNALIGYDVNVDSK GKITKVALLMGRGAHVNEEDIAKFKKLSREKGIPEENI
IYLGDTDNCPNHE
>NP_001003242.2 Can f 7; NPC2-like [Canis familiaris]
MRLLVAAFLLLALGASALAEVHFKDCGSAVGVIKELNVNCPAQPC K LHKGQSY
SVNVTFTSNIPSQSSKAVVHGIVLGVAVPFPIPEADGCKSGINCPIQKDKTYSY
LNKLPVKNEYPSIKLVVQWMLLDGNNQHLCWEIPVQIEG
>Q28895 Can f 7; NPC2-like [Canis familiaris]

MRLVAAFLLLALGDLGPGGAVHFKDCGSAVGVIKELNVNCPAQPCCKLHKGQSYSVNVV
FTSNIPSQSSKAVVHGIVLGVAVPFPIPEADGCKSGINCPIQKDKTYSYLNKLPVKNEY
SIKLVVQWMLLDGNNQHLCWEIPVQIEG

>BAC10663.1 Can f 3; serum albumin [Canis familiaris]
MKWVTFISLFFLFSSAYSRLVRRREAYKSEIAHRYNDLGEEHFRGLVAVAFSQYLQQCP
EDHVKLAKEVTEFAKACAAEESGANCDKSLHTLFGDKLCTVASLRDKYGMADCCCEKQEP
DRNECF LAHKDDNPGFPPLVAPEPDALCAAFQDNEQLFLGKYLIEIARRHPYFYAPELLY
YAQQYKGVFAECCQAADKAACLGPKEALREKVLSSAKERFKCASLQKFGDRAFKAWSV
ARLSQRFKADFAEISKVVTDLTKVHKECCHGDLLECADDRADLAKYMCENQDSISTKLL
ECCDKPVLEKSQCLAEVERDELPGDLPSLAADFVEDKEVCKNYQEAKDVFLGTFLYEYAR
RHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCLE
KLGEYGFQNALLVRYTKKAPQVSTPTLVEVSRKLGKVGTKCCKKPESERMSCAEDFLSV
LNRLCVLHEKTPVSRVTKCCSESLVNRRCFSGLEVDETYVPKEFNAETTFHADLCTL
PEAEKQVKKQTALVELLKHKPKATDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLV
AAAQAALV

>AAB30434.1 Can f 3; serum albumin [Canis familiaris]
LSSAKERFKCASLQKFGDRAFKAWSVARLSQRFKADFAEISKVVTDLTKVHKECCHGDL
LECADDRADLAKYMCENQDSISTKLLKECCDKPVLEKSQCLAEVERDELPGDLPSLAADFV
EDKEVCKNYQEAKDVFLGTFLYEYSRRHPEYSVSLLLRLAKEYEATLEKCCATDDPPTCY
AKVLDEFKPLVDEPQNLVKTNCLEFEKLGEYGFQNALLVRYTKKAPQVSTPTLVVEVSRK
LGKVGTKCCKKPESERMSCADDFLS

>CAA76841.1 Can f 3; serum albumin [Canis familiaris]
MDTYKSEIAHRYNDLGEEHFRGLVAVAFSQYLQQCPEDHVKLAKEVTEFAKACAAEESG
ANCDKSLHTLFGDKLCTVASLRDKYGMADCCCEKQEPDRNECF LAHKDDNPGFPPLVAPE
PDRLCAAFQDNEQLFLGKYLIEIARRHPYFYAPELLYYAQQYKGVFAECCQAADKAACL
PKTEALREKVLSSAKERFKCASLQKFGDRAFKAWSVARLSQRFKADFAEISKVVTDLT
KVHKECCHGDLLECADDRADLAKYMCENQDSISTKLLKECCDKPVLEKSQCLAEVERDEL
GDLPSLAADFVEDKEVCKNYQEAKDAFLGTFLYEYSRRHPEYSVSLLLRLAKEYEATLEK
CCATDDPPTCYAKVLDEFKPLVDEPQNLVKTNCLEFEKLGEYGFQNALLVRYTKKAPQVS
TPTLVEVSRKLGKVGTKCCKKPESERMSCADDFLSVVLNRLCVLHEKTPVSRVTKCCSE
SLVNRRCFSGLEVDETYVPKEFNAETTFHADLCTLPEAEKQVKKQTALVELLKHKPKA
TDEQLKTVMGDFGAFVEKCCAAENKEGCFSEEGPKLVAAAQAALV

>CCK33472.1 Can s 3; lipid transfer protein [Cannabis sativa]
ITCGQVASSLAPCLSYLKVGGAVPDGCCNDIKSLSGAAKTPADRQAACKCLKSAASSIKG
VNFNLASGLPGKCGVSIPYKISPSTDCSSVK

>AFN42528.1 Can s 5; pathogenesis related protein, PR-10, Bet v 1-like [Cannabis sativa]

MGVFTYESEFTSSIPARLFKAFVLDGDNLVPKIAPQAVEKVEILEGNGGVGTIKKITFG
QGVPFKYVKHKIEAIDKESLTYSYSIIEGDALEGNQLEKITHESKLVASGDGGNVIKTVS
KYYSAGDAQVNEEKVKEGEKQATQMLKTVEAYLKDHPPEAYN

>XP_030492464 Can s 2; profilin [Cannabis sativa]
MSWQTYVDEHLMCDIDGQGHATAAIIIGHDGSIAWQSSSFPQLKAQEITDITKDFEEPG
HLAPTGLHLSGTYMVIQGEPAVIRGKKKSGGVTIKKTGQALIFGIYEETVTPGQCNMV
VERLDYLVLDQGL

>CAD10376.1 Cap a 2; profilin [Capsicum annuum]
MSWQTYVDDHLMCEIEGNRLTSAIIIGQDGSVWAQSATFPQFKPEEITAIMNDFAEPTL
APTGLYLGGTYMVIQGEAGAVIRGKKKGGGITVKKTNQALIIGIYDEPMTGQCNMIVE
RLGDYLIQSL

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

TAMARIWGRNTCNFDGSGRGSCQTGDCGGVLQCTGWGKPPNTLAEYALNQFNNLDFWDIS
LVDGFNIPMTFAPTNPSGGKCHAIQCTANINGECPGSLRVPGGCNPCTTFGGQQYCCTQ
GPCPTELSKFFKRCPDAYSYPQDDATSTFTCPSGSTNYRVVFCPNGVTGPNFPLEMPG
SDGVAK

>P00784.1 cysteine protease, papain [Carica papaya]
MAMIPSISKLLFVAICLVYMGSLFGDFSIVGYSQNDLTSTERLIQLFESWMLKHNKIYK
NIDEKIYRFEIFKDNLKYIDETNKKNSYWLGLNVFADMSNDEFKEKYTGSIAGNYTTTE
LSYEEVLNDGDVNIPEYVDWRQKGAIVTPVKNQSGSCSWAFSAVVTIEGIIKIRTGNLNE
YSEQELLDCCRYSYGCNGGYPWSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKT
DGVRQVQPYNEGALLYSIANQPVSVVLEAAGKDFQLYRGGIFVGP CGNKVDHAVAAGVYG
PNYILIKNSWGTGWGENGYIRIKRGTGNSYGVCGLYTSSFPVKV

>ACV85695.1 Cari p 1; polygalacturonase [Carica papaya]
MAVLYYDNYNRTHLLILSFSILFFSFSSRLVNSGFHGERRRERVHGYYHYDELNNFSEDQE
GGTLTLLSGAGYDPEAHPFLSSINGDRDEEFTEAEPVLSFKGIEDLRSAPRSVIFNVD
DFGAEGDGIHDDTQQVFEEAWEKACSYKGPALFLVPERRTYLIGPIRFLGPCKSNLVIQV
QISGTILASDNRSYRKDPRHWIVIDSVDNLLVEGGGTIHGNGQIWWRNCKAPCKEAPT
VTFYKCKNLMVRNVKQDAQQMQVSFEKCEVTASDLTVTAPEKSPNTDGIHVTNTQNIL
ITNTFIGGDDCISIESGSHNVQIEELTCGPGHGINVDSLGDNNSKAFVSFVTVNGAKLSG
TTNGVRIKTYQGGSGSASNIKFNQVDMENVKNPIIIDQNYCDQKKPCKKQKSAVQVKDV
LYQNIQGNSASDVAIDFDCSENYPCLGVKLQNVRLQRADRVDEEAKAICNHVELTETGVV
FPRCPDYHLKHDEL

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

GVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQVISSVENVGGNGGPGTIKNITFAE
GIPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF
HAKGYHEVNAAEMKGAEMAEKLLRAVESYLLAHTAEYN

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

GVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFAE
GSPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF
HAKGYHEVNAAEMKGAEMAEKLLRAVESYLLAHTAEYN

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

GVFNVEAETPSVIPAARLFKAFILDGNKLIIPKVSPQAVSSVENVEGNGGPGTIKKITFSE
GSPVKYVKERVEEIDHTNFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF
HAKGYHEVNAAEMKGAEMAEKLLRAVESYLLAHTAEYN

>CAB02206.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFAE
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF
FHAKGDHEVNAAEMKGAEMAEKLLRAVESYLLAHTAEYN

>CAB02207.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFAE
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLDGNLEKVSHELKIVAAPGGGSIVKISSKF
FHAKGDHEVNAAEMKGAEMAEKLLRAVESYLLAHTAEYN

>CAB02208.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]

MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISSVENVGGNGGPGTIKNITFAE
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLDGKLEKVSHELKIVAAPGGGSIVKISSKF

FHAKGDHEVNAAEKMKGAKEMA EKLLRAVESYLLAHTDEYN
>CAB02209.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D F D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K Y N Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S I V K I S S K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>CAB02213.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D F D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K F S Y T V I E G D V L G D K L E K V S L E L K I V A A P G G G S I L K I S G K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>CAB02215.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V M P A A R L F K S Y V L D F D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K F S Y T V I E G D V L G D K L E K V S L E L T I V A A P G G G S I L K I S G K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>CAB02216.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T T S V I P A A R L F K A F I L D G N K L I P K V S P Q A V S S V E N V E G N G G P G T I K K I T F S
E G S P V K Y V K E R V E E V D H T N F K Y S Y T V I E G G F V G D K V E K I C N E I K I V A A P D G G S I L K I T S K
Y H T K G D H E V P A E H I K G G K E R V E G L L K P V E A Y L L A H T A E Y N N
>CAB02217.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T T S V I P A A R L F K A F I L D G N N L I P K V A P Q A V S S V E N V E G N G G P G T I K K I T F S
E G S P V K Y V K E R V E E V D H T N F K Y S Y T V I E G G P V G D K V E K I C N E I K I V A A P D G G S I L K I T S K
Y H T K G D H E V P A E H I K G G K E R V E G L L K P V E A Y L L A H T A E Y N N
>ABZ81040.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D G D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K Y N Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S I L K I S S K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>ABZ81041.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D G D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K Y N Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S V K I S S K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>ABZ81042.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D G D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K Y N Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S I V K I S S K
F H A K G D H E V N A E K M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>ABZ81043.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D G D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G S P F K F V K E R V D E V D N A N F K Y N Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S I V K I S S K
F H A K G D H E V N A E E M K G A K E M A E K L L R A V E S Y L L A H T A E Y N
>ABZ81044.1 Car b 1; pathogenesis related protein, PR-10, Bet v 1-like [Carpinus betulus]
MGVFN YEAE T P S V I P A A R L F K S Y V L D G D K L I P K V A P Q A I S S V E N V G G N G G P G T I K N I T F A
E G I P F K F V K E R V D E V D N A N F K Y S Y T V I E G D V L G D K L E K V S H E L K I V A A P G G G S I V K I S S K

FHAKGDHEVNAEEMKGAKEMAELLLRAVESYLLAHTAEYN
>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
GIPVKYVKERVEEIDHTNFK
>ABW86978.1 Car i 4; 11S globulin, cupin [Carya illinoensis]
MAKPILLSIYLCLIIIVALFNGCLAQSGGRQQHKFGQCQLNRLDALEPTNRIEAEAGVIES
WDPNHQQLQCAGVAVVRRRTIEPNGLLLPHYSNAPQLVYIARGRGITGVLFPGPCPETFEES
QRQSQQGQRREFQQDRHQKIRHFREGDIIAFPAHVAVHCYNDGSSPVVAIFLLDTHNNAN
QLDQNPVNFYLAGNPDEFQPGQEQEYEQHRRQQQHQRRGEHGEQQRDLGNNVFSGFDA
EFLADAFNVDTEARRLQSENDHRGSIVRVEGRQLQVIRPRWSREEQEHEERKERERERE
SESERRQSRGGRRDDNGLEETICTLSLRENIGDPSRADIYTEEAGRISTVNSHNLPIILRW
LQLSAERGALYSDALYVPHWNLNAHSVYALRGRAEVQVVDNFGQTVFDDELREGQLLTI
PQNFAVVKRARDEGFVWSFKTNENAMVSPLAGRTSAIRALPEEVLVNAFQIPREDARRL
KFNRQESTLVRSRSRSSRSERRAEV
>ABW86979.1 Car i 4; 11S globulin, cupin [Carya illinoensis]
MAKPILLSIYLCLIIIVALFNGCLAQSGGRQQHKFGQCQLNRLDALEPTNRIEAEAGVIES
WDPNHQQLQCAGVAVVRRRTIEPNGLLLPHYSNAPQLVYIARGRGITGVLFPGPCPETFEES
QRQSQQGQRREFQQDRHQKIRHFREGDIIAFPAHVAVHCYNDGSSPVVAIFLLDTHNNAN
QLDQNPVNFYLAGNPDEFQPGQEQEYEQHRRQQQHQRRGEHGEQQRDLGNNVFSGFDA
EFLADAFNVDTEARRLQSENDHRGSIVRVEGRQLQVIRPRWSREEQEHEERKERERERE
SGSERRQSRGGRRDDNGLEETICTLSLRENIGDPSRADIYTEEAGRISTVNSHNLPIILRW
LQLSAERGALYSDALYVPHWNLNAHSVYALRGRAEVQVVDNFGQTVFDDELREGQLLTI
PQNFAVVKRARNEGFVWSFKTNENAMVSPLAGRTSAIRALPEEVLVNAFQIPREDARRL
KFNRQESTLVRSRSRSSRSERRAEV
>AA032314.1 Car i 1; 2S albumin, conglutin [Carya illinoensis]
MARVAALLVALLFVANAAAFRTTITTTMEIDEDIDNPRRRGESCREQIQRQQYLNRCQDYL
RQQCRSGGYDEDNQRQHFRQCCQQLSQMEEQCQCEGLRQAVRQQQEEGIRGEEMEEMVQ
CASDLPKECGISSRSCEIRRSWF
>5E1R_A Car i 2; 7S globulin, vicilin-like [Carya illinoensis]
MSREEEQQRHNPYYFHSQGLRSRHESGEGEVKYLERFTELLRGIENYRVVILEANPN
TFVLPYHKDAESVIVVTRGRATLTFVSQERRESFNLEYGDVIRVPAGATEYVINQDSNER
LEMVKLLQPVNPNPQGFREYYAAGAQRSTESYLRVFSNDILVAALNTPRDRLERFFDQQEQR
EGVIIRASQEKLRALSQHAMSAGQRPWGRSSGGPISLKSQRSSYSNQFGQFFEACPEEH
RQLQEMDVLVNYAEIKRGAMMVPHYNSKATVVVVVVEGTGRFEMACPHDVSSQSSEYKGR
REQEESSTGQFQKVTARLARGDIFVIPAGHPAITASQENLRLVGFINGKNNQRNF
LAGQNNIINQLEREAKELSFNMPREEIEEIFERQVESYFVPMERQSRRGQGRDHPLASIL
DFAGFF
>ABM53030.1 profilin [Caryota mitis]
MSWQAYVDHHLMCEIDGQRLAAAAILGHDGSVWAQSETFPQVKPEEISGIMNDFAEPGNL
APTGLYLGNTKYMIQGEPAVIRGKKKSGGVTIKKTNMALIIIGIYDEPMTPGQCNMIIIE
RLGDYLDIDQGF

>ADN39439.1 Cas s 5; chitinase [*Castanea sativa*]
EQCGRQAGGAACANNLCCSQFGWCGNTAEYCGAGCQSQCSSPTTTTSSPTASGGGGGDVG
SLISASLFDQMLKYRNDPRCKSNNGFYTYNAFIAAARSFNGFGTTGDVTRKRELAFLAQ
TSHETTGGWATAPDGPYAWGYCFIMENNKQTYCTSKSWPCVFGKQYYGRGPIQLTHNYY
GQAGKAIAGDLINPDLVATNPTISFKTAIWFWMTPQANKPSSHDVIIGNWRPSAADTSA
GRVPSYGVITNIINGGLECGHGSDDRVANRIGFYKRYCDTLGVSYGNNLDCYNQKPPFA
>CAA64868.1 Cas s 5; chitinase [*Castanea sativa*]
MKLFSLLLFLAFLLLGTSAEQCGRQAGGAACANNLCCSQFGWCGNTAEYCGAGCQSQCSSP
TTTTSSPTASSGGGGDVGSLISASLFDQMLKYRNDPRCKSNNGFYTYNAFIAAARSFNGFG
TTGDVTRKRELAFLAQTSHETTGGWATAPDGPYAWGYCFVMENNKQTYCTSKSWPCVF
GKQYYGRGPIQLTHNYYGQAGKAIAGDLINPDLVATNPTISFKTAIWFWMTPQANKPS
SHDVIIGNWRPSAADTSAGRVPSYGVITNIINGGLECGHGSDDRVANRIGFYKRYCDTLG
VSYGNNLDCYNQKPPFA
>CAD10374.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]
MGVFTHENEITSAIPPGRLFKAFVLADNLIPLKAPHAIKSAEIEGNGGPGTIKKITFG
EGSQFKYVKHRIDEIDQANFTYCYSVIEGDVVMELLEKISYEIKIVASPDGGSILKNTSK
YHTKGEQEIKEEKVMAGKEKAAGLFKAVEAYLLAHS DAYN
>ACJ23861.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]
MGVFTHESEQETSVIPPARLFKAFVLDSNLIPLKVLQAIKSTEIEGNGGPGTIKKITFG
EASKYKYSKHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY
QTKGDFQLKEEQVQAAIEKATGLFKAVEAYLLANPDLYK
>ACJ23862.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]
MGVFTHESEQETSVIPPARLFKAFVLDSNLIPLKVLQAIKSTEIEGDGGPGTIKKITFG
EASKYKYSKHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY
QTKGDFQLKEEQVQAAIEKATGLFKAVEAYLLANPDLYK
>ACJ23863.1 Cas s 1; pathogenesis related protein, PR-10, Bet v 1-like [*Castanea sativa*]
MGVFTHESEQETSVIPPARLFKAFVLDSNLIPLKVLQAIKSTEIEGNGGPGTIKKITFG
EASKYKYSRHRIDALDPENCTYSFSVIEGDVLTDIENVSTETK FVASPDGGTIMKSTTKY
QTKGDFQLKEEQVQAAIEKATGLFKAVEAYLLANPDLYK
>2MC9_A Cat r 1; peptidyl-prolyl isomerase [*Catharanthus roseus*]
GSFTGSMNPRVFFDMSVGGQPAGRIVMELFADTTPTAENFRALCTGEKGTGRSGKPLH
YKSSFFHRVIPGFMCGQGGDFTAGNGTGGESIYGAKFADENFIKKHTGPGILSMANAGPNT
NGSQFFICTAKTEWLDGKHVVFQVVEGMDVVKAIKVGSSSGRTAKKVVVEDCGQLS
>A0A484HRI4 Cav p 1; lipocalin [*Cavia porcellus*]
MVQILLLALAVGLSCVSSQISGDWDTIALSADNKEKIEEGGPLRVYFRQIDCNADCSEI
TFRLYVKLNGECKESTVVASQSLGGLYTVQFAGQNTFVIVDKQEDTITFFNTNVDENGLV
TRGYVVVVKRDSLTPPEETLSFEEANEVKGIPQENIEYLAGTDDCPE
>S0BDX9 Cav p 6; lipocalin [*Cavia porcellus*]
MKLQLLCLGLILLCTQGEGDEVVRGNFDAEKISGNWYTVKEASDKRETIEEGGSMRVFVE
SIEPVKDSALSFKFWAHENGECKQISLICNRVAEGVYAVEYDGYNVFRVAETDYKNYAIF
QLRNFKAEGSFQLLELYGREPDVSGEIKTRFEDFCHKNGIGEGNIIDMTTVDRCLQARGE
K
>P83507.1 Cav p 1; lipocalin [*Cavia porcellus*]
SEINGDWNTIALSAD
>CAX62129.1 Cav p 2; lipocalin [*Cavia porcellus*]
MMQILLLALAVSLACADSIDYSKVPGNWRTIAIAADHVEKIEVNGELRAYFRQVDCTEGC

DKISITFYTNTDGVCTEHTVVGARNGENDVYTVDYAGENTFQILCNSDDAFVIGSVNTDQ
NGQTTKEVAIAAKRNFLTPEQEKFQKAVQNAIGIPLNIRYVIETDTCPD
>CAX62130.1 Cav p 3; lipocalin [*Cavia porcellus*]
MQILLLALTIGLAYAHQTLDPSEINGQWHTISIAADNVEKIGEGGPLRGYFHNHLCYDGC
KNIGLTFYVKLDGNCQRFVDVLGAKQEDSDVYVAQYSGTNHFEVIGKKEDAI AFYNHNTDE
TGKETKMIVVVARRDSLTEEEQKQLQEVAGEKGI PKDNIRYFRERDTCAQ
>COMPARE010 Cha o 3; glycosyl hydrolase 5 family [*Chamaecyparis obtusa*]
MTSAGVAPTALRLLTALLLLLLVAAPSHSLPLLTRGRWIVDEATGLRVKLACVNWVGHLEP
GLPEGLNRLPVATVAHTISSLGFNCVRLTYSIHMLTRTSYTNATVAQTFARLNLTEAASG
IEHNNPELLDLGHVAAYHHVVAALSEAGVMVILDNHYSKPKWCCA VDDGNGFFGDRYFNP
NTWVEGLGLMATYFNNTPNVWAMSLRNELRGNRSTPISWSRHMQGAATVHKANPKVLVI
LSGLQFDTDLSFLPVLVPTLPFKEKIVYEGHWYSFGVPWRTGLPNDVCKNETGRFLSNVG
FVTSSANATAAPLFMSEFGIDQRYVNDNDNRYLNCILAYLARRDLWALWTMGGSYYYRS
DKQPVKDFEETYGFFNHDSRIRNPF FISR LKEIQQPIQDPYLAPGPYYQIIYHPASGLC
VESGIGNTVHLGSCQSVRSRWNYDASVKGP IGLMGSSSCISTQGNGLPAIMTENC SAPNN
TLWSTVSSAQLQLGTRVLGKDGKEKWMCLDGSKSPLISTNECICITDSHCYPKLNPEKQW
FKVITTNKQLLHQLQL
>BAA08246.1 Cha o 1; pectate lyase [*Chamaecyparis obtusa*]
MASCTLLAVLVFLCAIVSCFSDNPIDSCWRGDANWDQNRMKLADCAVGF GSSAMGGKGGGA
FYTVTSSDDDPVNPAPGTLRYGATRERSLWII FSKNLNIKLNMP LYIAGNKTIDGRGAEV
HIGNGGPCLFMRTVSHVILHGLNIHGCNTSVSGNVLISEASGVVPVHAQDGD AITMRNVT
DVWIDHNSLSDSSDGLVDVTLASTGVTISNNHFFNHHKVM L LGHSDIYSDDKSMKVT VAF
NQFGPNAGQRMPRARYGLIHVANMNYDPWSIYAIGSSNPTILSEGN SF TAPNDSKKEV
TRRVGCEPSTCANWVWRSTQDSFNNGAYFVSSGKNEG T NIYNNEAFKVENGSAAPQLT
KNAGVLT CILSKPCS
>Q7M1E7.1 Cha o 2; polygalacturonase [*Chamaecyparis obtusa*]
MGMKFMAAVAF LALQLIVMAAAEDQSAQIMLDS D IEQYLR SNRSLK KLVHSRHD AATVFN
VEQYGAVGDGKHDSTEAFATTWNAACKKASAVLLVPANKKFFVNNLVFRGPCQPHLSFKV
DGTIVAQPDPARWKN SKIWLQFAQLTDFNL MGTGVIDGQGGQW WAGQCKV VNGRTVCNDR
NRPTAIKIDYSKSVTVKEL TLMNSPEFHLV FGECEGVKI QGLKIKAPRDS PNTDGIDIFA
SKRFHIEKCVIGTGDDCIAIGTGSSNITIKDLICGPGHG ISIGSLGRDNSRAEVSHVHV N
RAKFIDTQNGLR IKTWQGGSGLAS YITYEN VEMINSENPI LINQFYCTSASACQ NQRS AV
QIQGVTYKNIHGTSATAAAIQLMCSDSVPCTGIQLSNVSLKLTSGKPASCVDKNARGFYS
GRLIPTCKNLRPGSPKEFELQQQPTTVMDENKGACAKGDSTCISLSSSPPNCKNKCKGC
QPCKPKLIIVHPNKPQDYYPQKWVCSCHNKIYNP
>BAF32143.1 Cha o 2; polygalacturonase, partial [*Chamaecyparis obtusa*]
LDS D IEQYLR SNRSLK KLVHSRHD AATVFNVEQYGAVGDGKHDSTEAFETA WNAACKKAS
AVLVVPANKKFFVNNLVFRGPCQPHLSFKVDGTIVAQPDPARWKN SKIWLQFAQLTDFNL
MGTGVIDGQGGQW WAGQCKV VNGRTVCNDRNRPTAIKIDYSKSVTVKEL TLMNSPEFHLV
FGECEGVKI QGLKIKAPRDS PNTDGIDIFASKRFHIEKCVIGTGDDCIAIGTGSSNITIK
DLICGPGHG ISIGSLGRDNSRAEVSHVHV NRAKFIDTQNGLR IKTWQGGSGLAS YITYEN
VEMINSENPI LINQFYCTSASACQ NQRS AVQIQGVTYKNIHGTSATAAAIQLMCSDSVP C
TGIQLSNVSLKLTSGKPASCVDKNARGFYS GRLIPTCKNLRPGSPKEFELQQQPTTV M
>AAF35431.1 Cha f 1; tropomyosin [*Charybdis feriata*]
MDAIKKKMQAMKLEKDNAMD RADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLPEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSL SDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRL EDELVNEK
>AAL92871.1 Che a 3; calcium-binding protein, polcalcin [*Chenopodium album*]

MAAEDTPQDIADRERIFKRFDNNGDGKISSSELGDALKTLGSVTPDEVRRMMAEIDTDGD
GFISFDEFTDFARANRGLVKDVKIF

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

>ACR77509.1 Che a 2; profilin [Chenopodium album]
MSWQTYVDDHLMFPIEETGNHLTAAAIIVGLDGSVWAQSSTFPQLKQEEVKAICNEFDVPN
TLAPTGLFLGGKYMVIQGEPEGAVIRGKKKGGVCIKKTNQALVFGIYNPVTGQCNMV
VEKLG DYLV EQGM

>AAL92870.1 Che a 2; profilin [Chenopodium album]
MSWQTYVDDHLMCDIEGNHLSSAAILGHDGTVWAQSPSPFQLKPEEVSAIMKDFNEPGSL
APTGLHLGGTKYMVIQGEPEGD VIRGKKKGGVTIKKTNQAL IIGIYGEPMTPGQCNMVE
RIGDYLV EQGM

>P86699 arginine kinase [Chionoecetes opilio]
MADAATISKLEEGFKKLQGATDCKDVFQKQTDKHPNKDFGDVNFVNVDPDGK FVIST
RVRLIDDHFLFKEGDRFLQAANACRYWPSGRGIFHNDKKIISMQMGDLGQVYRRLVSAV
NEIEKRVPFSHDRLGLFTFCPTNLGTTVRASVHIKLPKXEKLEEVAGKYSLQVRGTRGE
HTEAEGGVYDISNKRRLMGLTEFQAVKEMQDGILELIKIEKEMQ

>A2V735.1 tropomyosin [Chionoecetes opilio]
MDAIKKKMQAMKLEKDNAMDKADTLEQQNKEANLRAEKTEEEIRANQKKSQLVENELDHA
QEQLSAATHKLVEKEKAFANAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEYKNIADMDQAFSELSGF

>CAA09938.2 Chi k 10; tropomyosin [Chironomus kiiensis]
MDAIKKKMQAMKLEKDNALDRALLCENQARDANLRAEKAE EEARLQKKIQTIENDLDQT
QGQETLVNGKLEGGKALQNAESEVAALNRRIQLLGEDLDRSEERLASATAKLSEASAAA
DESERARKILENRSLADEERMDALENQLKEARFLAEEADK KYDEVARKLAMVEADLERAE
ERA EAGEAKIVELEEEELRVVGNLKSLEVSEEKANQRE EYKNQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLDEDELVSEKEYREIGDDLDTAFVELILKE

>P02229.2 Chi t 1; hemoglobin [Chironomus thummi thummi]
MKFLILALCF AAASALSADQISTVQASFDKVKGDPV GILYAVFKADPSIMAKFTQFAGKD
LESIKGTAPFEIHANRIVGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFV
SYMKAHTDFAGAEAAWGATLD TFFGMIFSKM

>P02230.1 Chi t 1; hemoglobin [Chironomus thummi thummi]
MKLLILALCF AAASALTADQISTVQSSFAGVKGDAVGILYAVFKADPSIQAKFTQFAGKD
LDSIKGSADFSAHANKIVGFFSKIIGDLPNIDGDV TTFVASHTPRGVTHDQLNNFRAGFV
SYMKAHTDFAGAEAAWGATLD AFFGMVFAKM

>P02227.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
AVTPMSADQLALFKSSWNTVKHNEVDILYAVFKANPDIQAKFPQFAGKDLDSIKDSADFA
VHSGRIVGFFSEVIGLIGNPENRPAKTLIDGLASSHKARGIEKAQFEFRASLV DYL SH
HLDWNDTMKSTWDLALNNMFFYILHALEVAQ

>P12548.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVDILAAVFAAYPDIQAKFPQFA
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNESNASAVNSLVSKLGDDHKARGV SAAQ
FGFERTALVAYLSNHVSWGDNVAAAANKALDNTYAIIVPRL

>P12549.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVEILAAVFAAYPDIQNKFSQFA
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNDSNAAA VNSLVSKLGDDHKARGV SAAQ

FGFERTALVAYLQANVSWGDNVAAAANKALDNTFAIVVPRL
>P12550.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCVVGAIASPLSADEAAIVKSSWDQVKHNEVDILAAVFAAYPDIQAKFPQFA
GKDLASIKDTAAFATHATRIVSFFTEVISLSGNQANLSAVYALVSKLGVDPHKARGISAAQ
FGFERTALVSYLQAHVSWGDNVAAAANKALDNTYAVALKSLE
>P02231.1 Chi t 4; hemoglobin [Chironomus thummi thummi]
VATPAMPSTDAQVAAVKGDWEKIKGSGVEILYFFLNKFPGNFPMFKKLGNDLAAAKGTA
EFKDQADKIIAFLQGVIEKLGSDMGAKALLNQLGTSHKAMGITKDQFDQFRQALTELLG
NLGFGGNIGAWNATVDLMFHVIFNALDGPV
>P02228.1 Chi t 9; hemoglobin [Chironomus thummi thummi]
DPEWHTLDAHEVEVQATWKAIVSHDEVEILYTVFKAHPDIMAKFPKFAGKDLEAIKDTAD
FAVHASRIIGFFGEYVTLTGSSGNQAAIRTLHLDLGVFHKTRGITKAQFGEFRETMTAYL
KGNHKNADISHSWDDAFDKAFSVIFEVLES
>P02222.2 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFLVLALCIAAAVAAPLSADEASLVRGSAQVKHSEVDILYYIFKANPDIMAKFPQFAG
KDLETLKGTGQFATHAGRIVGFVSEIVALMGNSANMPAMETLIKDMAANHKARGIPKAQF
NEFRASLVSYLQSKVSWNDSLGAAWTQGLDNVFNMMFSYL
>P02223.2 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFIVLALCIVGAIADPVSSDQANAIRASWAGVKHNEVDILAAVFSHPDIQARFPQFA
GKDLASIKDTGAFATHAGRIVGFISEIVALVGNESNAPAMATLINELSTSHHNRGITKGQ
FNEFRSSLVSYLSSHASWNDATADAWTHGLDNIFGMIFAHL
>P02221.2 Chi t 2; hemoglobin [Chironomus thummi thummi]
MKFLILALCVAAMAGPSGDQIAAAKASWNTVKNNQVDILYAVFKANPDIQTAFSQFAGK
DLDSIKGTPDFSKHAGRIVVGLFSEVMDLLGNDANTPTILAKAKDFGKSHKSRASPAQLDN
FRKSLVVYLKGTKWDSAVESSWAPVLDFVSTLKNEL
>P02224.2 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFLVLALCIAAASAALVTEQADLVKKTWSTVKFNEVDILYAVFKAYPDIMAKFPQFAG
KDLDSIKDSAAFATHATRIVSFLSEVISLAGSDANIPAIQNLAKELATSHKPRGVSKDQF
TEFRTALFTYLKAHINFDPGTETAWTLALDTTYAMLFSAMDS
>P84296.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVDILAAVFAAYPDIQAKFPQFA
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNASAAAVEGLLNKLGSDHKARGVSAQA
FGFERTALVSYLSNHVSWGDNVAAAANKALDNTMAVAV AHL
>P84298.1 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCIVGAIASPLTADEASLVQSSWKAVSHNEVEILAAVFAAYPDIQNKFSQFA
GKDLASIKDTGAFATHATRIVSFLSEVIALSGNTSAAAANVSLVSKLGDDHKARGVSAQA
FGFERTALVAYLQANVSWGDNVAAAANKALDNTFAIVVPRL
>P02226.2 Chi t 3; hemoglobin [Chironomus thummi thummi]
MKFFAVLALCIVGAIASPLSADQAALVKSTWAQVRNSEVEILAAVFTAYPDIQARFPQFA
GKDVASIKDTGAFATHAGRIVGFVSEIIALIGNESNAPAVQTLVGQLAASHKARGISQAQ
FNEFRAGLVSYVSSNVAAWNAAAESAWTAGLDNIFGLLFAAL
>3S18_B lectin [Cicer arietinum]
TKTGYINAAFRSSRNNEAYLFINDKYVLLDYAPGTSNDKVLYGSPFVRDGYKSLAKTIFG
TYGIDCSFDTEYNEAFIFYENFCARIDYAPHSKDKIISGPKKIADMFPFFKGTVFENGI
DAAFRSTKGKEVYLFKGDYARIDYLTNRLVQNKISDGTGFPLRGTIFEAGMDSAFASH
KTNEAYLFGGEYARINFTPGSTNDIMGGVKKTLDYWPSLRGIIPLE
>AAU43733 Citr I 2; profilin [Citruillus lanatus]
MSWQAYVDDHLMCEIEGNHLTSAAIIGQDGSVWAKSENFPQLKPEEITGILNDFNEPGTL
APTGLYIGGSKYMIQGEPAVIRGKKKGGVTVKKTALALVIGIYDEPMTPGQCNMIVE
RLGDYLIIEQGL

>P84160.1 Cit 1 3; lipid transfer protein [Citrus limon]
ITCGQVTGSLAPXIPFLRTG

>P84159.1 Cit s 1; germin-like, partial [Citrus sinensis]
TDPGHLQDVXVAINDPKXGVFVNRK

>COMPARE170 Cit s 7; gibberellin-regulated protein, partial [Citrus sinensis]
GSDFCDSKCAVRCCKAGR

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

>P84161.1 Cit s 3; lipid transfer protein [Citrus sinensis]
ITXGQVTGSLAPXIAFLRTK

>CAI23765.1 Cit s 2; profilin [Citrus sinensis]
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFRLEEIAAILKDFDQPGTL
APTGLFLGGTKYMIQGEAGAVIRGKKKSGGIIVKKTNQALIIGIYDEPLTPGQCNMIVE
RLGDYLIEQGL

>ADK47394.1 Cla c 14; aldolase [Cladosporium cladosporioides]
MSSSLDQLKASGTTVVCDSDGFATIGKYKPDATTNPSLILAASKKPEYAKLIDDAVAYG
MKHGKTTEEKIDATFDNLLVQFGSEILKIVPGKVSTEV DARFSFDKDVSIQKALRIIDLY
KEAGIDKERVLIKLASTWEGIQAAHELQTKHGINCNLTMFSLPQAIAAAEEAGAYLISPF
VGRILDWYKANTKQEYNASNDPGVKSVDIFNYKKYDYKTIVMGASFRNIGEITELAGC
DYLT IAPALLEQLYNSTDAVPQKKAEDVAKLDIEKKSULKDEALFRFDNFEDPMAVNKL
SEGISKFAADAVTLKDILREKIEKA

>ABQ59329.1 Cla c 9; vacuolar serine protease [Cladosporium cladosporioides]
DQEVHVLKSESEVEKNAPWGLARISHRDSLSFGTFNKLYTEDGGEGVDVYVVDGTGTVND
HVDFEGRASWGKTIPQGDADGDNGHGTHCSGTVAGKKYGVAKKAHVAVKVLRSNGSGS
MSDVVKGVEYAAESHLEQVSIAKKGRKGFKGSTANMSLGGGKSPILDKAVNAAVDAGIH
FAVAAGNDNADSCNYSAAAENAVTVGASTLSDERAYFSNYGKCNDIFAPGLNIQSTWIG
SKYAVNTISGTSMAVPHVAGLLAYLLSLQPAKDSAFVADISPKKLANLISIATVGALT
DVPSNTANILAWNGGGSNYSATVEKGGYKAAVRPTMLEEIESEAKVASKKVYSEGDELA
KKVAELTEKIEDLISGDLKDMFRDLKRE

>CAA55067.2 Cla h 5 acidic ribosomal protein P2 [Cladosporium herbarum]
MKYLAAFLLLGLAGNSSPSAEDIKTVLSSVGIDADEERLSSLLKELEGKDINELISSGSE
KLASVPSGGAGAASAGGAAAAGGAAEAPEAERAEKEEESDDDMGFGLFD

>CAA55072.2 Cla h 10; aldehyde dehydrogenase [Cladosporium herbarum]
MTSVQLETPHSGKYEQPTGLFINNEFVKGOEGKTFDVINPSDESIVITQVHEATEKDVDIA
VAAARKAFEGSWRQETPENRGKLLNNLANLFEKNIDLLAAVESLDNGKAISMAKGDISM
VGCLRYGGWADKITGKVIDTTPDTFNYVKKKEPIGVCQIIPWNFPLLMWAWKIGPAIAC
GNTVVLKTAEQTPGLGLVAASLVKEAGFPVGINVISGFGKVGAAALSSHMDVDKVAFTG
STVVGRTILKAAASSNLKVTLELGGKSPNIVFEDADIDNAISWVNFIFFNHGQCCCAG
SRVYVQESIYDKFVQKFKERAQKNVVGDPFAADTFQGPQVSKVQFDRIMEYIQAGKDAGA
TVETGGKRKGDGKYFIEPTIFSNVTEDMKIVKEEIFGPVCSIAKFKTKEDA I KLG NASTY
GLAAAVHTKNLNTAIEVSNALKAGTVWVNTYNTLHHQMPFPGGYKESGIGRELGEDALANY
TQTKTVSIRLGDALFG

>CAA55070.1 Cla h 6; enolase [Cladosporium herbarum]
MPISKIHSRYVYDSRGNPTVEVDIVTETGLHRAIVPSVASTGSHEACELRDGDKSKWAGK
GVTKAVANVNEIIPALIKENLDVKDQAAVDAFLNKLDTTNTKIGANAILGVSMVAVAK
AAAAEKRVPLIAHISDLSGTTKPFVLPVPMNVVNGGSHAGGR LAFQEFMIVPSGAPSFT
EAMRQGAEVYQKLSLTKKRYGQSAGNVGDEGGVAPDIQTAEALDLITDAIEEAGYTGQ
IKIAMDVASSEFYKADEKKYDLDFKNPDSKSKWITYEQLADQYNELAAKYP IVSIEDPF
AEDDWEAWSYFYKTSGSDFQIVGDDLTVTNPEFIKKA IETKACNALLLKV NQIGTITEAI

NAAKDSFAAGWGMVSHRSGETEDVTIADIVVGLRAGQIKTGAPARSERLAKLNQILRIE
EELGDKRLYAGDNFRTAINL

>P42040.2 Cla h 6; enolase [Cladosporium herbarum]

MPISKIHSRYVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKSKWAGK
GVTKAVANVNEIIPALIKENLDVVKDQAAVDAFLNKLDGTTNKTIGANAILGVSMATAK
AAAAEKRVPLYAHISDLSTGKKPFVLPVPMNVVNGGSHAGGRALFQEFMIVPSGAPSFT
EAMRQGAEVYQKLKSLTKKRYGQSAGNVGDEGGVAPDIQTAEALDLITDAIEEAGYTGQ
IKIAMDVASSEFYKADEKKYDLDFKNPDSKSKWITYEQLADQYKQLAAKYPIVSIEDPF
AEDDWEAWSYFYKTSGSDFQIVGDDLTVTNPEFIKKAIEKACNALLKVNQIGTITEAI
NAAKDSFAAGWGMVSHRSGETEDVTIADIVVGLRAGQIKTGAPARSERLAKLNQILRIE
EELGDKAVYAGDNFRTAINL

>P40918.1 heat shock protein 70 [Cladosporium herbarum]

MAPAIGIDLGTYSVGIYRDDRIEIIANDQGNRTTPSFVAFTDTERLIGDSAKNQVAIN
PHNTVFDKRLIGRKFQDAEVQADMKHFVFKVIEKAGKPVTVQVEFKGETKDFTPPEISSM
ILTKMRETAESYLGTVNNAVITVPAYFNDSQRQATKDAGLIAGLNVLRIINEPTAAAIA
YGLDKKQEGEKNVLIQVFEGERARTKDINLMGKFEISGIRPAPRGVPQIEVTFDL
ANGIMNVSALFKGTGKTNKIVITNDKGRLSKEEIERMLADAKEYKEEDEAEAGRIQAKNG
LESYAYSLKNTVSDPKVEEKLKSAEDKELTGAIKTVAWIDENQTATKEEYEAQKQLES
VANPVMKIYGAEGGAPGGMPGQAGAPPPGAGDDGPTVEEVD

>ABA42918.1 hydrolase [Cladosporium herbarum]

MPAGLQYVTTDGGRLAVEITGKETDPLVICSPGMGDRDAYKPLAKVLVSNNGYRVAAMDA
RAHGESSAKFARYGDEATADDFLTVANELSPGSPVVLGASFSAAAATIAAAKQPERVSK
IILLGPFRLNMGVGLWLMVPMFAWPWGPAAWEMYAATLWPGLEGDGAKKRAATTRASL
TRPGRWAGFQALISSLDHRVVAPYISSVRAPALVVMGDKDPDWSDPKVEAEWVSNFSQV
DTLMVPEAGHAPMYERPQVVAERVLVSLGQDQTNV

>CAD42710.1 hydrophobin [Cladosporium herbarum]

MAFIKSLIASVAVAFAAPQGGASDNKKVEIDGQDSAPVCGNGQKVACCNSGEDLIGL
NCLSIPIAIPQKACGSNIAACCQTGDSEGNLLNLEANCLAIPL

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

MPGQQATKHESLLDQLSLKGVVVVTGASGPKMGIEAARGCAEMGAAVAITYASRAQGA
EENVKELEKTYGIKAKAYKQVDSYESCEKLVKDVVADFQIDAFIANAGATADSGILDG
SVEAWNHHVQVDLNGTFHCAKAVGHFKERGTGSLVITASMSGHIANFPQEQTSYNVAKA
GCIHMARSLANEWRDFARVNSISPGYIDTGLSDFVPKETQQLWHSMPMGRDGLAKELKG
AYVYFASDASTYTTGADLLIDGGYTTR

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

MSDFNAIAQQTFEFYKTFDTRAQPLAPLYRENSMLTFEQSPFLGTANIVGKLQELPFQR
IEHQVATVDAQPSNESGGILVWVSGALLVEEERRPMSYQTQFQLLPADGAYVVFNDVFR
LYPAA

>AAX14379.1 Cla h 9; serine protease [Cladosporium herbarum]

MARGALAGLSLATLATASPVLVNSIHNDAAPIISASNAKEIADNYMIKFKDHVTQNLAAEH
HGWVQDLHEKTQVAKTELKRSQSPMVDDIFNGLKHTYNIAGGLMGYAGHFDEEDVIEQIR
RHPDVELVERDQEVHVLGSESEVEKNAPWGLARISHRDSLSFGTFNKYLYTEDGGEGVDV
YVVDGTGTVNDHVDVEGRASWGTIPQGDADDEGNGHGTHCSGTVAGKKYGVAKKAHVAV
KVLRSNGSGSMSDVVKGVEYAAESHLEQVSITKKGKRGFKGSTANMSLGGGKSPILDKA
VNAAVDAGIHFVAAGNDNADSCNYSAAAENAVTVGASTLADERAYFSNYGKCNDIFAP
GLNIQSTWIGSKYAVNTISGTSMASPHVAGLLAYLLSLQPAKDSFAFAVADISPKKLLKANL

ISIATV GALT D V P S N T A N I L A W N G G G E S N Y S A I V E K G G Y K A T H R P T M L E E I E S E A K V A S K
K V Y S E G D E L A H K V A E L T E K V E D L I A G E L K D M F R E L K R E
>AAR08428.1 translationally controlled tumor protein [Cladosporium herbarum]
M L I Y N D I I S G D E L I S D S Y D L V E D G V A Y E A D C R K I T I G G E T F D T G A N A S A E G G D E E A D D Q
K E T K I D V V H A F Q L Q E T N F D K K A Y L G H L K S Y M K K I K E S M A A S G A S E D E V K E F E K G A Q T F A K
R V V G S F K D Y E F L I G P S M D P D A M V V L L N Y R E D G V T P Y V T L W K H G L K S T K V
>CAA55068.1 Cla h 7; unknown function [Cladosporium herbarum]
M A P K I A I I F Y S T W G H V Q T L A E A E A K G I R E A G G S V D L Y R V P E T L T Q E V L T K M H A P P K D D S I
P E I T D P F I L E Q Y D R F P H G H P T R Y G N F P A Q W R T F W D R T G G Q W Q T G A F W G K Y A G L F I S T G T Q
G G G Q E S T A L A A M S T L S H H G I I Y V P L G Y K T T F H L L G D N S E V R G A A V W G A G T F S G G D G S R Q P
S Q K E L E L T A Q G K A F Y E A V A K V N F Q
>CAQ72970.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]
M A L A S L L K G A D I D A A L K A C E A K D S F K H K D F F A K I G L A T K S A A D L K K A F E I I D Q D K S G F I E
E E E L K L F L Q N F K A G A R A L T D A E T K A F L K A G D A D G D G M I G V D E F A V M I K P
>CAQ72971.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]
M A F A G L L S D A D I A A A L G A C T A A D T F D H K S F F K K V G L S G K S A D D V K K P F Y I I D Q D K S G F I E
E E E L K L F L Q N F K A G A R A L S D K E T K A F L A A G D A D G D G M I G V D E F A V M V K A R
>CAQ72972.1 Clu h 1; calcium-binding protein, parvalbumin [Clupea harengus]
M A F A A F L K E A D I T A A L G A C K G A D S F D H K A F F A K V G L K G K S G D E L K K A F E I I D Q D K S G F I E
E E E L K L F L Q N F C K G A R A L T D G E T K K F L K A G D S D N D G K I G I D E F A A L I N H
>COMPARE168 Coc n 1; 7S globulin, vicilin-like, partial [Cocos nucifera]
V S E G D V F W L P R
>COMPARE169 Coc n 1; 7S globulin, vicilin-like, partial [Cocos nucifera]
L S P H V N P S A T E Y G L L L R
>COMPARE167 Coc n 1; 7S globulin, vicilin-like, partial from A0A0S3B0K0 [Cocos
nucifera]
E L A A A F G V S E E Q L E R
>ADH10372.1 Cof a 1; chitinase [Coffea arabica]
A G I V R Y W G R G H D E P S S L A E F G R Q E F A T D V N I A F L E D F G G G R M P E L N I S H P L P S A S D I E Y C
Q K H Q T K V F I S I A G Q P S L S S V E D A E E V A A Y V W N T Y L G G K S S D R P F G K A V L D G V E L H I H S G N
T T Y L D D L A R A L K G Y S N V I S A V A A E C P I P D P A L D T T I R T G V V D Q V R V E F F D N P S C Q F T P P K
D T S L L F P S W D N W S D Y P G V H K L Y L G I P I S P T I A P E G G Y I P P N E L V Y H V L P Y L K K S P V Y G G I
M V F P Y L H H E V N F Q S M L R S Y A R A A
>AGL34967.1 Cof a 2; metallothionein [Coffea arabica]
M S C C G N C G C G A G C K C S G G C G G C K M Y P E L S Y T E N T A A E T L I L G V A P P K T A Y L E G A G E E A A
A E N G G C K C G P D C K C N P C N C K
>AGL34968.1 Cof a 3; metallothionein [Coffea arabica]
M S D K C G N C D C A D R S Q C V K K G S S Y A A D I V E T E N T F V E T F V M M E G G A Q N G K C K C G P S C A C V N
C T C D N
>CAB39376.1 Cop c 1; leucine zipper protein [Coprinus comatus]
R F L P S S S H L N P Q H L P W L V H P A P V L L L P V L P Q L K P V A H P L L L L P L D T T L H M P P L L L Q L Q L
P P L L S Q G N P A C S P K W L Q L L V P
>GFG40850.1 arginine kinase [Coptotermes formosanus]
M V D Q A V L D K L E A G Y A K L A A S D S K S L L K K F L T K E V F D N L K T K K T P S F G S S L L D V I Q S G L E N
H D S G V G I Y A P D A E A Y S V F A D L F D P I I E D Y H G G F K K T D K H P P K D W G D V D T L G N L D P A G E Y I
I S T R V R C G R S L E G Y P N P C L T E A Q Y K E M E E K V S S T L S G L E G E L K G Q F Y P L T G M T K E V Q Q K
L I D D H F L F K E G D R F L Q A A N A C R F W P T G R G I Y H N D A K T F L V M C N E E D H L R I I S M Q M G G D L G
Q V Y R R L V T A V N D I E K R I P F S H D D R L G F L T F C P T N L G T T V R A S V H I K V P K L A A D R A K L E E V
A G K Y N L Q V R G T R G E H T E A E G G V Y D I S N K R R M G L T E Y E A V K E M H D G I A E L I K L E S S L
>AGM32377.1 Copt f 7; tropomyosin [Coptotermes formosanus]

MDAIKKKMQAMKLEKDNTMDRALLCEQQARDANLRAEKAEFEARSQKKIQIENDLDQT
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLLEEDLERSEERLATATAKLAEASQAA
DESERARKILESKGLADEERMDALENLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE
FAERSVQKLQKGSRQA

>AAL73404.1 Cor a 9; 11S globulin, cupin [*Corylus avellana*]
MAKLILVSFSLCLLVLFNGCLGINVGLRRQQQRYFGECNLDRLNALEPTNRIEAEACQIE
SWDHNDQQFQCAGVAVIRRTIEPNGLLLPQYSNAPELIYIERGRGITGVLFPGCPETFED
PQQQSQQGQSQRSRSEQRDRHQKIRHFREGDIIALPAGVAHWCYNDGDSPPVTVSLL
HTNNYANQLDENPRHFYLAGNPDDDEHQRQGGQQFGQRRRQQQSHHGEGEQEQGEGNNV
FSGFDAEFLADAFNVDVDTARRLQSNQDKRRNIVKVEGRLQVVRPERSRQEWERQERQER
ESEQERERQRRQGGGRDVGFEETICSLRLRENICTRSRADIYTEQVGRINTVNSNTLP
VLRWLQLSAERGLDQREGLYVPHWNLNAHSVYAIRGRARVQVDDNGNTVFDDELRRQGG
VLTIPQNFVAVAKRAESEGFVAVFKTNDNAQISPLAGRTSAIRALPDDVLANAFQISREE
ARRLKYNRQETTLVRSRSSSERKRRSESEGRAEA

>AHA36627.1 Cor a 9; 11S globulin, cupin [*Corylus avellana*]
MAKLILVSFSLCLLVLFNGCLGIDVGLRRQQQRHFGEENLDRLNALEPTNRIEAEAGQIE
SWDHNDQQFQCAGVAVIRRTIEPNGLLLPQYSNAPELIYIERGRGITGVLFPGCPETFED
PQQQSQQGQSQRSRSEQRDRHQKIRYFQEGDIIALPAGVAHWCYNDGDSPPVAVSLLHT
NNYANQLDENPRHFYLAGNPDDDEHQRQGGQQFGQRRRQQQHSRGKEGEQEQQGEGNNVFS
GFDAEFLADAFNVDVDTARRLQSNQDKRRNIVKVEGRLQMVVRPERSRQEWERQERQERES
EQERERQRRQGGGRDVGFEETICSLRLMENIGSRSRADIYTEQVGRINTVNSNTLPVL
RWLQLSAERGLDQREGLYVPHWNLNAHSVYAIRGRARVQVDDNGNTVFDDELRRQGGVL
TIPQNFVAVAKRAESEGFVAVFKTNDNAQISPLAGRTSAIRALPDDVLANAFQISREEAR
RLKYNRQETTLARSSRSSSERMRRRSESEGRAEA

>AC056333.1 Cor a 14; 2S albumin, conglutin [*Corylus avellana*]
MARLATLAALFAALLLVAAHAAAFRTTITTVDDVEDIVNQQGRRGESCRESQAQRQNLNQC
QRYMRQSSQYGSYDGSNQQQQQEQLEQCCQQLRQMDERCRCEGLRQAVMQQQGEMRGEEMR
EVMETARDLPNQCRLSPQRCEIRSARF

>AAL86739.1 Cor a 11; 7S globulin, vicilin-like [*Corylus avellana*]
MLPKEDPELKKCKHKCRDERQFDEQRRDQKQICEEKARERQQEEGNSSEESYGKEQEEN
PYVFQDEHFESRVKTEEGRVQVLENFTKRSRLLSGIENFRLAILEANPHTFISPAHFDAE
LVLFVAKGRATITMVREEKRESFNVEHGDIIIRIPAGTPVYMINRDENEKLFIVKILQPVS
APGHFEAFYAGGEDPESFYRAFSEVLEAALKVRREQLEKVFGEQSKGSIVKASREKIR
ALSQHEEGPPRIWPFGGESSGPINLLHKHPSQSNQFGRLYEAHPDDHKQLQDLDMVSFA
NITKGS MAGPYNSRATKISVVVEGEGFFEMACPHLSSSSGSYQKISARLRRGVVAVAPA
GHPVAVIASQNNNLQVLCFEVNAHGNSRFPLAGKGNIVNEFERDAKELAFNLPSREVERI
FKNQDQAFFFPGNKQQEEGGRGGRAFE

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

>AA065960.1 Cor a 13; oleosin [*Corylus avellana*]
MAEHRQLQDPAHQPRSHQVKAATAATAGGSLLVPSGLILAGTVIALTLATPLFVIFSP
VLVPAVITVSLIIMGFLASGGFGVAAVTVLSWIYRYVTGRHPPGADQLDHARMKLASKAR
EMKDRAEQFGQQHVTGSQGS

>AA067349.2 Cor a 12; oleosin [*Corylus avellana*]
MADRPQQLQVHPQRGHGHYEGGIKNQRGGGSPAVKVMVAALPVGGTLLALAGLTLAGS
VIGLLVTSPLFIIFSPVLVPAAIWVGLAVASFLSSGALGLTGLSSLSWVNLNYLRASQSL
PREMDQAKRRMQDMAAFVQKTREVGQEIQSRAQEGRRRT

>CAA50325.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [*Corylus*

avellana]

MGVFNYEAEETTSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG
EGSRYKYVKERVDEVDNTNFTYSYTVIEGDVLGDKLEKVCHELKIVAAPGGGSILKISSK
FHAKGDHEINAEIEIKGAKEMAELLRVETVYLLAHSAEYN

>CAA50326.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFNYEVEETPSVISAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG
EGSRYKYVKERVDEVDNTNFKYSYTVIEGDVLGDKLEKVCSELKIVAAPGGGSTLKISSK
FHAKGDHEINAEEMKGAKEMAELLRVETVYLLAHSAEYN

>CAA50327.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFNYEVEETPSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG
EGSRYKYVKERVDEVDNTNFTYSYTVIEGDVLGDKLEKVCHELKIVAAPGGGSILKISSK
FHAKGDHEINAEEMKGAKEMAELLRVETVYLLAHSAEYN

>CAA50328.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFNYEVEETPSVIPAARLFKSYVLDGDKLIPKVAPQAITSVENVEGNGGPGTIKNITFG
EGSRYKYVKERVDEVDNTNFKYSYTVIEGDVLGDKLEKVCSELKIVAAPGGGSILKISSK
FHAKGDHEINAEEMKGAKEMAELLRVETVYLLAHSAEYN

>CAA96548.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFNYETESTSVIPAARLFKAFILDGNLIPKVAPQAVSSVENVEGNGGPGTIKKITFS
EGSPFKYVKERVEVDHTNFKYSYTVIEGGPVGDKVEKICNEIKIVAAPDGGGSILKISNK
YHTKGDHEVDAEHKGGKEKVEGLFRAVEAYLLAHSADAYN

>CAA96549.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFNYETETTSVIPPARLFKRFVLDSDNLIPKVAPKAIKSIEIEGNGGPGTIKKICFD
EGSPFNKIKQKVEEIDQANFSYRYSVIEGDALSDKLEKINYEIKIVASPHGGGSILKSISK
YHTIGDHELKDEQIKAGKEKASGLFKAVEGYLLAHSADAYN

>AAD48405.1 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like [Corylus
avellana]

MGVFCYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTSAENLEGNGGPGTIKKITFA
EGNEFKYMKHKVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS
KYHTKGNASINEEEIKAGKEKAAGLFKAVEAYLLAHPDAYC

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

MGVFSYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTGAENLEGNGGPGTIKKITFA
EGSEFKYMKHKVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS
KYHTKGNASISEEEIKAGKEKAAGLFKAVEAYLLAHPDTC

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

MGVFCYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTGAENLEGNGGPGTIKKITFA
EGSEFKYMKHKVEEIDHANFKYCYSIIEGGPLGHTLEKISYEIKMAAAPHGGGSILKITS
KYHTKGNASISEEEIKAGKEKAAGLFKAVEAYLLAHPDTC

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

MGVFSYEDEATSVIPPARLFKSFVLDADNLIPKVAPQHFTSAENLEGNGGPGTIKKITFA
EGNEFKYMKHKVEEIDHANFKYCYSIIEGGPLGHTLEKIPYEIKMAAAPHGGGSILKITS
KYHTKGNASINEEEIKAGKEKAAGLFKAVEAYLLAHPDAYC

>COMPARE103 Cor a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial

[Corylus avellana]

GVFNIEAETTSVIPAAAXLFKSYVLDGDKLLPKVAPQALTSVENVGGNXXP

>AAK01235.1 Cor a 2; profilin [Corylus avellana]

MSWQTYGDEHLMCEIEGNRLAAAAIIGHDGSVWAQSSTFPQLKPEEITGVMNDFNEPGSL
APTGLYLGGTKYMVIQGEPEGAVIRRRKKKGGVTVKKTSQLIIGIYDEPMPGQCNMIVE
RLGDYLIDQGL

>AAK01236.1 Cor a 2; profilin [Corylus avellana]

MSWQAYGDEHLMCEIEGNRLAAAAIIGHDGSVWAQSSTFPQLKPEEITGVMNDFNEPGSL
APTGLYLGGTKYMVIQGEPEGAVIRGKKKGGVTVKKTSQLIIGIYDEPMPGQCNMIVE
RLGDYLIDQGL

>A4KA39.1 Cor a 2; profilin [Corylus avellana]

MSWQAYVDEHLMCDIDGQGGQLAASAIIVGHDGSVWAQSSSFQQLKPEEITGIMKDFDEPG
HLAPTGLHLGGTKYMVIQGEAGAVIRGKKKGGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLLEQGL

>A4KA45.1 Cor a 2; profilin [Corylus avellana]

MSWQTYVDEHLMCDIDGQGGQLAASAIIVGHDGSVWAQSSSFQQLKPEEITGIMKDFDEPG
HLAPTGLHLGGTKYMVIQGEAGAVIRGKKKGGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLIDQGL

>A4KA43.1 Cor a 2; profilin [Corylus avellana]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAAAKYMVIQGEPEGVIRGKKKGGGITIKKTGQALVFGIYDEPMPGQCDMVG
RLGDYLLEQGL

>A4KA44.1 Cor a 2; profilin [Corylus avellana]

MSWQAYVDEHLMCDIDGQGGQLAASAIIVGHDGSVWAQSSSFQQLKPEEITGIMKDFDEPG
HLAPTGLHLGGTKYMVIQGEAGAVIRGKKKGGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLVEQGL

>A4KA40.1 Cor a 2; profilin [Corylus avellana]

MSWQAYVDEHLMCDIDGQGGQLAASAIIVGHDGSVWAQSSSFQQLKPEEITGIMKDFDEPG
HLAPTGLHLGGTKYMVIQGEAGAVIRGKKKGGGITIKKTGQALVFGIYEETVTPGQCNMV
VERLGDYLAEQGL

>A4KA41.1 Cor a 2; profilin [Corylus avellana]

MSWQAYVDEHLMCEIDGHHLSAAAIIGHDGSVWAQSSTFPQFKPEEIAAIIKDFDEPGSL
APTGLHLGGIKYMVIQGESGAVIRGKKKGGGITVKKTSQALIFGIYDEPLTPGQCNMIVE
RLGDYLLKQGL

>ACR43474.1 Cra c 2; arginine kinase [Crangon crangon]

MVDAEVLEKLEAGYKLEAATDCKSLLKKYLTKEVFDELKTKKTALGATLLDVIQSGVEN
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFKQSDKHPGKDFGDLEKFNVDPEGTFV
VSTRVRCGRSMEGYPFNPLTEAQYKEMESKVSSTLSSLEGELKGTYYPLTGMSKDVQQK
LIDHFLFKEGDRFLQAANACRYWPAGRGYHNDNKTFVWVNEEDHLRIISMQMGDLG
QVFRRLTSAVNEIEKRIPFSSHDRGLGFLTCPTNLGTTVRASVHIKLPKLAANRDKLESV
AGKYNLQVRGRGEHTEAEGGIYDISNKRRMGLTEFQAVKEMQDGILEPIKMEKEM

>ACR43475.1 Cra c 4; calcium-binding protein, sarcoplasmic calcium-binding protein [Crangon crangon]

MAYTWDNRVKYVVRYMYDIDNNGFLDKNDFECLAVKNTLIECRGEWSAEKYAANQKIMSN
LWNEIAELADFNKDG EVTVEEFKQAVQKHCNGKPF GDFPSAFKTFIANQFKTIDVNGDGL
VGVDEYRLDCISRSAFSCIKEIDDAYNLLCTEEDKKAGGINIARYQELYAQFISNPDEKC
NAVYLFGLKEVV

>ACR43477.1 Cra c 5; myosin light chain [Crangon crangon]

MAADLSARDVERVKFAFSIYDFEENGQIDAFYIGDCLRALNLNPTLALIAKLGTEKRKE
MKIKLDDFMPLFAQVKKDKDAGSYEDFIEVLKLYDKAENGTMMYAELEHILLSLGERLDK

ALEPILRECCPPEDDEGLIPFEPFVKKLTQLL

>ACR43476.1 Cra c 8; triosephosphate isomerase [Crangon crangon]
MSGSRKFFVGGNWKMNKDAAIDGIVDFMCKGPLNPTEVVVGCPQCYSYTREKLPAEI
GVAAQNCYKVAKGAFTEISPAMVKDCGCEWVILGHSERRNVFNEPDQLISEKVGHALEA
GLKVIPCIGEKLERESNRTEEVVFAQMKALVPNISDWSRVVIAYEPVWAIWIGTGKTASPE
QAQDVHAKLRQWL TENVSAEVAESCRIIYGGSVSPSNCAELAKMGDIDGFLVGGASLKP
D FVTIINARG

>ACR43473.1 Cra c 1; tropomyosin [Crangon crangon]
MDAIKKKMQAMKLEKDNAMDRAADTLEQQNKEANNRAEKSEEEVFSLQKRMQQLENDLDSV
QEALLKANAHLEEKDKALSNAEAGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSLDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE
FAERSVQKLQKEVDREDELVNEKEKYKSITDELDTFSELSGY

>ACR43478.1 Cra c 6; troponin C [Crangon crangon]
MDSLEPDQIDALKKAFDSFDTENQGFITADTVATILRMMGVKISDKNLAEVIAETDEDGS
GQLEFEFVLDLSSKFLIEEDEEALKAELREAFRIYDKEGQGFITTDVLKEILTEIDNKLT
PEDLDGIIIEVDEDESGTLDLDFDEFMEMMSG

>QIJ32297.1 Cra a 4; calcium-binding protein, sarcoplasmic calcium-binding protein
[Crassostrea angulata]

MDYLNKKWKIWNLSLDVNHGDKISIEDVEESRNKFTNLHELVGDKAKGVQVNFEDWWNKY
IFRTGAGKEISESEFVQQLTEAYKKDKVGFIKEMQACFDCIFDVIDTNKDRIDEDEFVY
AFKAFGHENEALVRKAFSLYNKENKHVPLKDIVSEWVKFVTEEDTGKKDIIMEAFKEGF

>AAK96889.1 Cra g 1; tropomyosin [Crassostrea gigas]
NSARGFDTVNEKYQECQTKMEEAEKTASEAEQEIQSLNRRIQLLEEDMERSEERLQTATE
KLEEASKAADESERNRVLENLNNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAI
TEVDLERAEARLEAAEAKVLELEEEELKVVGNMKSLEISEQEASQREDSYEETIRDLTQR
LKDAENRATEAERTVSKLQKEVDREDELLAEKERYKAISDELDTFAELAGY

>BAH10152.1 Cra g 1; tropomyosin [Crassostrea gigas]
MDSIKKKMIAMKMEKENAQDRAEQLEQQLRDTEEQKAKIEEDLTSLQKKHNSLENEFDTV
NEKYQECQTKLEEAETASEAEQEIQSLNRRIQLLEEDMERSEERLQTATEKLEEASKAA
DESERNRVLENLNNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAI TEVDLERAE
ARLEAAEAKVYLEEQLSVANNIKTLQVQNDQASQREDSYEETIRDLTQRLKDAENRAT
EAERTVSKLQKEVDREDELLAEKERYKAISDELDTFAELAGY

>AAC61869.1 tropomyosin [Crassostrea virginica]
RNRKVLENLNNASEERTDVLEKQLTEAKLIAEEADKKYDEAARKLAI TEVDLERAEARLE
AAEAKVLELEEEELKVVGNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRATEAER
TVSKLQKEVDREDELLAEKERYKAISDELDTFAELAGY

>AAX93750.1 Cro s 1; Ole e 1-like [Crocus sativus]
MGKCQAVFLLVGCALCVLSLAGVANAAENHFVKVQGMVYCDTCRIQFMTRVSTIMEGATVKL
ECRNITAGTQTFKAEAVTDKVGQYSIPVHGDFQDDICEIELVKSPNSECSEVSHDVYAKQ
SAKVSLSNNGEASDIRSANALGFMKREPLKECPEVLKELDLYDVKAN

>AAW81034.1 Cro s 2; profilin [Crocus sativus]
MSWQTYVDEHLMCDMDGHVLTSAAILGHDGVSVAQSAGFPELKPAEITAILNDFNEPGSL
APTGMINGAKYMIQGEQGVVIRGKKGSGGVTIKKSNMALIFGLYDEPMPGQC�LVVE
RLGDYLIEQGY

>BAD77932.1 chitinase [Cryptomeria japonica]
MQIMATQNSKSNIFWSSASVVLVLLLLVDVGVQCQNCGCNGLCCSQYGYCGSGEAYCGAG
CKEGPCSSSSPPSTGTGVSIVSSDVFNISIVGGAASGCAGNGFYTYDSFISAANAFNGFG
TSGSSDVNKREIAAFFANAHAHETGGFCYIEEQNPTSIYCDASNTQYPCASGKTYHGRGPL
QLSWNYNYGAAGSYIQFDGLNNPEIVGTDSTISFKTAVWFWMVNSNCHTAITSQQFGAT

IRAINSMCEDGGNAATVASRVNYYQKFCQQLNVDGTSNLQC

>C0HLQ1 Cry j 7; gibberellin-regulated protein [Cryptomeria japonica]
AHIDCDKECNRRCSKASAHDRCLKYCGICCEKCNVPPGTYGNEDSCPCYANLKNSKGGH
KCP

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

MGGSRVLIIGGTGYIGRHVTNASLAQGHPTFLLVREITPSNPEKAQLLESFTSKGATLVQ
GSIDDHASLVAALKKVDVISTLGAPQIADQFNLIKAIKEVGTIKRFFPSEFGNDVDKHH
AVEPMKSMFDLKIKLRRTIEAEGIPHTYVPHCFAGYFLTNLAQLGLAAPPRDKIVIIYGD
GTTKAVYMKEEDIGTFTIKAVDDPRTLNKTLYLKPPANTISTNDLVALWEAKIGKTLEKV
YLSEEQVLKLLQDTPFPGFMTVSIFHTIYVKGDQTNFQIGPDGVEASALYPDVKYTTVEE
YISAFV

>BAI94503.1 lipid transfer protein [Cryptomeria japonica]

MAMRMKSSSSSYRFSYQMMMLVLMVMTLVQIGAAQSDTNSCVNSLVPCASYLNATTKPP
DSCCVPLLNVIQTQQQLCNLLNSSIVKQSSINITQALNIPRLCGDTNVSTDACSTNATA
NAPSASTTSPVADTGDSSGIGATSLQIFLPLLAVFFLGVFKSFP

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

MDSPCLVALLVLSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLMKPMYIAGYKTFDGRGAQV
YIGNGGPCVFIKRVSNVHGLHLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT
NIWIDHNSFSNSSDGLVDVTLTSTGVTISNNLFFNHHKVMMLGHDDAYSDDKSMKVTVAF
NQFGPNCGQRMPPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSFTAPNESYKKQV
TIRIGCKTSSSSCSNWWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPQLT
KNAGVLTCSLSKRC

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

MDSPCLVALLVFSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLMKPMYIAGYKTFDGRGAQV
YIGNGGPCVFIKRVSNVHGLYLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT
NIWIDHNSFSNSSDGLVDVTLTSTGVTISNNLFFNHHKVMMLGHDDAYSDDKSMKVTVAF
NQFGPNCGQRMPPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSFTAPNESYKKQV
TIRIGCKTSSSSCSNWWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPHLT
QNAGVLTCSLSKRC

>BAA07020.1 Cry j 1; pectate lyase [Cryptomeria japonica]

MDSPCLVALLVFSFVIGSCFSDNPIDSCWRGDSNWAQNRMKLADCAVGFSGSSTMGGKGGD
LYTVTNSDDDPVNPAPGTLRYGATRDRPLWIIIFSGNMNIKLMKPMYIAGYKTFDGRGAQV
YIGNGGPCVFIKRVSNVHGLYLYGCSTSVLGNVLINESFGVEPVHPQDGDALTLRTAT
NIWIDHNSFSNSSDGLVDVTLTSTGVTISNNLFFNHHKVMMLGHDDAYSDDKSMKVTVAF
NQFGPNCGQRMPPRARYGLVHVANNYDPWTIYAIGGSSNPTILSEGNSFTAPNESYKKQV
TIRIGCKTSSSSCSNWWQSTQDVFYNGAYFVSSGKYEGGNIYTKKEAFNVENGNATPQLT
KNAGVLTCSLSKRC

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

MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSRKRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDGFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRSPNTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGSISLGRENSRAEVSYVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV
QIQDVTYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS
GHVIPACKNLSPSAKRKEKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>P43212.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKFIAPMAFVAMQLIIMAAAEDQSAQIMLDSIEQYLRNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVMKMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMC SRHGKIYHP

>BAC23082.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKFIAPMAFVAMQLIIMAAAEDQSAQIMLDSIEQYLRNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKNINLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVMENMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMC SCHGKIYHP

>BAC23083.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAVEDQSAQIMLDSVVEKYLRSNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVMENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICS CHGKIYHP

>BAC23084.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAVEDQSAQIMLDSVVEKYLRSNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLRLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVMENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICS CHGKIYHP

>BAF32105.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAVEDQSAQIMLDSVVEKYLRSNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVMENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICS CHGKIYHP

>BAF32110.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPQFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>BAF32116.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32119.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKFIAPMAFVAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDINLSDISLKLTSKG IASCLNDNANGYFS
GNVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32122.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVS YVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GNVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMCSCCHGKIYHP

>BAF32128.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRSNRSLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKQWAGQCKWNGREICNDR
DRPTAIKFDFFSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGTENSRAEVS YVHVN
GAKFIDTQNGRLRIKTWQGGSGMASHIYEN VEMINSENPI LINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKG IASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>BAF32130.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKGQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLRLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVSVHVH
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMCSCHGKIYHP

>BAF32133.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKKPSAMLLVPGNKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKGQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVSVHVH
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS
GHVIPACKNLSPSAKRRESKSHKHPKTMVENMGAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWMCSCHGKIYHP

>BAF32134.1 Cry j 2; polygalacturonase [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRKVEHSRHDAINIFN
VEKYGAVGDGKHDCTEAFSTAWQAACKNPSAMLLVPGSKKFVNNLFFNGPCQPHFTFKV
DGIIAAYQNPASWKNRRIWLQFAKLTGFTLMGKGVIDGQKGQWAGQCKWVNGREICNDR
DRPTAIKFDSTGLIIQGLKLMNSPEFHLVFGNCEGVKIIIGISITAPRDSPTDGDIDIFA
SKNFHLQKNTIGTGDDCVAIGTGSSNIVIEDLICGPGHGIGISLGRENSRAEVSVHVH
GAKFIDTQNGRLIKTWQGGSGMASHIYENVEMINSENPIILINQFYCTSASACQNQRSAV
QIQDVITYKNIRGTSATAAAIQLKCSDSMPCKDIKLSDISLKLTSKGKIASCLNDNANGYFS
GHVIPACKNLSNAPKRRESKSHKHPKTMVENMRAYDKGNRTRILLGSRPPNCTNKCHGC
SPCKAKLVIVHRIMPQEYYPQRWICSCHGKIYHP

>BAF45320.1 Cry j 2; polygalacturonase, partial [Cryptomeria japonica]
MAMKLIAPMAFLAMQLIIMAAAEDQSAQIMLDSVVEKYLRNRSRLRRVEHSRHDAINIFN
VEKYG

>BAF51970.1 thaumatin-like [Cryptomeria japonica]
MAKVSDLALLLVAGMAISLYIQETGAVKFDIKNQCGYTVWAAGLPGGGQQLTQGQTWTVN
LAAGTQSARFWGRTGCSFDASGKGTCTGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDV
SLVDGFNIPLSINPTNAQCTAPACKADVNAVCPAELKVDGGCKSACAAAFQTDQYCCTGT
ANSCPATNYSMIFKNQCPQAYSYPKDDTATFACPSGTDYSIVFCP

>BAJ04354.1 unknown function [Cryptomeria japonica]
MARRLCSFLLSFLIIVSVAENSKFARLNLASFTWKDAEDNKNCSAGELETSSLSVMHIQ
GKCSPFRLNSSSWTAVSESIKGDRTARYRAMVKGWSAGKTMVNPQEDADIPLASGQAIS
SSNYIIKLGFGTTPQSFYTVLDTGSNIAWIPCNPSCSGCSSKQPFEPSSSTYNLTCAS
QQCQLLRVCTKSDNSVNCSTLQRYGDQSEVDEILSSETLSVGSQQVENFVFGCSNAARGL
IQRTPSLVGFGRNPLSFVSQTATLYDSTFSYCLPSLFSSAFTGSLLLGKEALSAQGLKFT
PLLSNSRYPFSFYVGLNGISVGEELVSIPAGTSLDESTGRGTIIDS GTVITRIVEPAYN
AMRDSFRSQLSNLTMASPTDLFDTCYNRPSGDVEFPLITLHFDDNLDLTLPLDNILYPGN
DDGSVLCLAFGLPPGGGDDVLSTFGNYQQQLRIVHDVAESRLGIASENC DG

>BBE74942.1 unknown function [Cryptomeria japonica]
MTATAMTTAALRLLIALLLVAAPAECLPLRARGRWIVDEATGLRVKLACVNWPGLHLEPGL
PEGLNRLPVTTIAHTISSLGFNCVRLTYSIQMVTEKSYTEATVGQTFQAQLNLTEPASGIE

GNNPGFLQLGHVAAYDSIVAALAEAGVMVILDNHVSKPKWCCAADDGNGFFGDSYFDPRL
 WQRGLGLMATHFNNTPNVAMSLRNELRGNRSTSARWSKYMQRGAATVHEANPNVLLVLS
 GLHFDTILSFLPVLVPTLPFKEKIVYEGHWYSFGVPWHDGLPNDICLNETSFRKDNIGFL
 TSSINGTAAPL FVSEFGIDQRYVNDNDNRYLNCILAF LAEEDVDWALWMTMGGSYNYSRDK
 EPVQDFEETYGFFNRDWSRIRNPDFISRLKEIQQPIQDPYLSGPPYQIYHPASGLCVE
 SSIIGNTIHLGSCQSVRSRWNYDASVEGPIGLMGSSSCISTQGNGLPAIMTEKCSAPNNTL
 WSTVSSGQLQLGTRVFEDEGKEKWMCLDGSRSPLITTECICITDSHCYPNQNPKEKQWFK
 VITTNKQLLHQL
 >QCY53440.1 Cten i 1; calcium-binding protein, parvalbumin [Ctenopharyngodon
 idella]
 MAFAGILNDADIAAALEACKAADSFNHKAFFAKVGLSAKSGDDVKKAFIAIDQDKSGFIE
 EDELKFLFLQNFKADARALTAETKIFLKAGSDSDGDKIGVDEFAALVKA
 >P83834.1 Cuc m 3; pathogenesis related protein, PR-1 [Cucumis melo]
 DFVDAHNAARAQVGVGPVHWTVDAYARQYANDRNLVHSATR
 >ACB45874.1 pathogenesis related protein, PR-1 [Cucumis melo]
 MLPFSFAQDSIKDFVDAHNAARAQVGVGPVHWNKTVDYAHQYANKRIKDCNLVHSGKPY
 GENIAWGSRLAGTVAVRMWVSEKQFYNYDTNSCVRGKMGHHTQVVRNSVRIGCAKVR
 CKSGGTFITCNYDPRGNIRQRPHYGEGTLQL
 >CAD92666.1 profilin [Cucumis melo]
 MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFRLEEIAAILKDFDQPGTL
 APTGLFLGGTKYMVIQGEAGAVIRGKKKGGGITVKKTNQALIIIGIYDEPLTPGQCNMIVE
 RLGDYLIEQGL
 >AAP13533.2 Cuc m 2; profilin [Cucumis melo]
 MSWQVYVDEHLMCEIEGNHLTSAAIIGQDGSVWAQSQNFQPKPEEVAGIVGDFADPGTL
 APTGLYIGGTYMVIQGEPAVIRGKKKGGGVTVKKTGMLVIGIYDEPMTPGQCNMIVE
 RLGDYLIDQGL
 >AAW69549.1 Cuc m 2; profilin [Cucumis melo]
 MSWQVYVDEHLMCEIEGNHLTSAAIIGQDGSVWAQSQNFQPKPEEVAGIVGDFADPGTL
 APTGLYIGGTYMVIQGEPAVIRGKKKGGGATVKKTGMLVIGIYDEPMTPGQCNMIVE
 RLGDYLIDQGL
 >BAA06905.1 Cuc m 1; serine protease, cucumisin [Cucumis melo]
 MSSSLIFKLFSSFLFNRLASRLDSDDDGKNIYIVYMGRKLEDPDSAHLHHRAMLEQVV
 GSTFAPESVLHTYKRSFNGFAVKLTEEEAEKIASMEGVVSVFLNEMNELHTTRSWDFLGF
 PLTVPRRSQVESNIIVVGLDTGIWPESPSFDDEGFSPPPPKWKGTCETSNNFRCNRKIIG
 ARSYHIGRPISPGDVNGPRDTNGHGHTHTASTAAGGLVLSQANLYGLGLGTARGGVPLARIA
 AYKVCWNDGCSDTDILAAAYDDAIADGVDIISLSVGGANPRHYFVDAIAIGSFHAVERGIL
 TSNSAGNGGPNFFTTASLSPWLLSVAASTMDRKFVTQVQIGNGQSFQGVINTFDNQYYP
 LVSGRDIPNTGFDKSTSRFCTDKSVNPNLLKGGKIVVCEASFPHFEFFKSLDGAAGVLMTS
 NTRDYADSYPLSSVLDPNLLATLRYIYSIRSPGATIFKSTTILNASAPVVVFSRSGP
 NRATKDVIKPDISGPGVEILAAWPSVAPVGGIRRNTLFNIISGTSMSCPHITGIATYVKT
 YNPTWSPAAIKSALMTTASPMNARFNPAEFAYGSGHVNPLKAVRPGLVYDANESDYVKF
 LCGQGYNTQAVRRITGDYSACTSGNTGRVWDLNYPSPFGLSVSPSQTFNQYFNRTLTSVAP
 QASTYRAMISAPQGLTISVNPVLSFNGLGDRKSFTLTVRGSIKGFVVSASLVWSDGVHY
 VRSPITITSLV
 >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]
SGNIFSGFADEFLEEEAFQIDGGLVR

>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]
GVLYSNAMVAPHYTVNSHSMYATRGNARVQVVDNFGQSVFDGEVR

>COMPARE00337 Cuc ma 4; 11S globulin, glycinin, cupin, partial from P13744.1
[Cucurbita maxima]
MLPLGVLSNMYR

>COMPARE00282 Cuc ma 5; 2S albumin, conglutin, partial from Q39649.1 [Cucurbita
maxima]
PWRREGGSFD

>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]
TGITTNNNHLDCLEFR

>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]
DKDAAVDNALNNCK

>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

>CAB62551.1 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]
DNPIDSCWRGDSNWDQNRMKLADCVVGFSGSSTMGGKGGEIYVTSSDNPVNPTPGTLRY
GATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGAVVHLGNGGPCLFMRKASHVILHG
LHIHGCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVTNAWIDHNSLSDCSDGLIDVTL
GSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAFNQFGPNAGQRMPPRARYGLVHV
ANNNYDQWNIYAIGGSSNPTILSEGENSFTAPNESYKKEVTKRIGCETTSACANWVWRSTR
DAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQNAGVVA

>CAC37790.2 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]
MASPCLVAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCVVGFSGSLTMGGKGG
IYVTSSDDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGADV
HLGNGGPCLFMRTASHVILHGLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVT
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPPRARYGLVHVANNNYDQWNIYAIGGSSNPTILSEGENSFTAPSESYKKEV
TKRIGCESTSACANWVWRSTRDAFTNGAYFVSSGKAEEETNIYNSNEAFKVENGNAAPQLT
QNAGVVT

>ABK78766.1 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]
SDNPIDSCWRGDSNWDQNRMKLADCVVGFSGSSTMGGKGGEIYVTSSDNPVNPTPGTLR
YGATREKALWIIIFSQNMNIKLQMPLYVNGYKTIDGRGADVHLGNGGPCLFMRKASHVILH
GLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVTNAWIDHNSLSDCSDGLIDVT
LGSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAFNQFGPNAGQRMPPRARYGLVH
VANNNYDQWNIYAIGGSSNPTILSEGENSFTAPNESYKKEVTKRIGCETTSACANWVWRST
RDAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQNAGVVA

>COMPARE145 Cup a 1; pectate lyase [Cupressus arizonica (Hesperocyparis arizonica)]
DNPIDSCWRGDSNWDQNRMKLADCVVGFSGSSTMGGKGGEIYVTSSDNPVNPTPGTLRY
GATREKALWIIIFSQNMNIKLQMPLYVAGYKTIDGRGAVVHLGNGGPCLFMRKASHVILHG
LHIHGCNTSVLGDVLVSESIGVEPVHAQDGDAITMRNVTNAWIDHNSLSDCSDGLIDVTL
GSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAFNQFGPNAGQRMPPRARYGLVHV
ANNNYDQWNIYAIGGSSNPTILSEGENSFTAPNESYKKEVTKRIGCETTSACSNWVWRSTR
DAFTNGAYFVSSGKAEDTNIYNSNEAFKVENGNAAPQLTQNAGVVA

>CAC05258.1 thaumatin-like [Cupressus arizonica (Hesperocyparis arizonica)]
VKFDIKNQCGYTVWAAGLPGGGKEFDQGTWTVNLAAGTASARFWGRTGCTFDASGKGGSC
RSGDCGGQLSCTVSGAVPATLAEYTSQSDQDYDVSLVDGFNIPLAINPTNTKCTAPACKA
DINAVCPSELKVDGGCNSACNVLQTDQYCCRNAYVNNCPATNYSKIFKNQCPQAYSYAKD
DTATFACASGTDYSIVFCP

>ACY01951.1 unknown function [Cupressus arizonica (Hesperocyparis arizonica)]
MDEVPSDESSEKSSASSGKRVLEQSVHELEEVFKKFDANGDGKISGSELADILRSMGSEVDE
AEVKAMMEEADTDGDGYVSLQEFVDLNIKGATVKDLKNAFKVDFRDCNGTISPAELCETL
KSVGEPCTIEESKNIIHNVDKNGDGLINVEEFQMTTSEMTDKSK

>C0HLQ2 Cup s 7; gibberellin-regulated protein, cypmaclein [Cupressus sempervirens]
AQIDCDKECNRRCSKASAHDRCLKYCGICCEKCHCVPPGTAGNEDVCPCYANLKNKSGGH
KCP

>COMPARE105 Cup s 7; gibberellin-regulated protein, cypmaclein, partial from
BBP47166.1 [Cupressus sempervirens]
AQIDCDKECNRRCSKA

>COMPARE106 Cup s 7; gibberellin-regulated protein, cypmaclein, partial from
BBP47166.1 [Cupressus sempervirens]
YCGICCEKCHCVPPGT

>AAF72625.1 Cup s 1; pectate lyase [Cupressus sempervirens]
MDSPLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD

IYTATSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLSSSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFAAPNENYKKEV
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT
KNAGVVA

>AAF72626.1 Cup s 1; pectate lyase [Cupressus sempervirens]
MDSPLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD
IYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLEMPYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLSSSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFTAPNENYKKEV
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT
KNAGVVA

>AAF72627.1 Cup s 1; pectate lyase [Cupressus sempervirens]
MDSPLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD
IYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVLVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLPDCSDGLIDVTLSSSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFTAPNENYKKEV
TKRIGCESTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT
KNAGVVA

>AAF72628.1 Cup s 1; pectate lyase [Cupressus sempervirens]
MDSPLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD
IYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGNVLVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLSSSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFAAPNENYKKEV
TKRIGCVSTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT
KNAGVVA

>AAF72629.1 Cup s 1; pectate lyase [Cupressus sempervirens]
MDSPLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSGSSTMGGKGGD
IYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGNVLVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLSSSTGITISNNHFFNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDQWNIYAIGSSNPTILSEGNSFAAPNENYKKEV
TKRIGCVSTSACANWVWRSTRDAFSNGAYFVSSGKTEETNIYNSNEAFKVENGNLAPQLT
KNAGVVA

>C0HKB1.1 Cup s 2; polygalacturonase [Cupressus sempervirens]
DVAIVFNVEHTLSAVFLVPANKKVDGIIAAYPDPVKIWMHFARTVCNDKGRPTAIKIDFS
KSELTLMNSPEFHLVFGEDGVKIQGKIKRFEIEKDLTCGPGHGMSIGSLGKGNRSEV
SFVHLDGAKFIDTQNGLRSAVKIEDVTFKNANGYYTNPLNPPCK

>AAR21073.1 Cup s 3; thaumatin-like [Cupressus sempervirens]
MARVSELALLLVATSAISLHMQEAGAVKFDIKNQCRYTVWAAGLPGGGKRLDQGQTWTVN
LAAGTASARFWGRTGCTFDASGKGCRCRSGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDV
SLVDGFNIPLAINPTNTKCTAPACKADINAVCPSELKVDGGCNSACNVLQTDQYCCRNAY
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>AAR21074.1 Cup s 3; thaumatin-like [Cupressus sempervirens]
MARVSELALLLVATLAIISLHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGQTWTVN
LAAGTASARFWGRTGCTFDASGKGCRCRSGDCGGQLSCTVSGAVPATLAEYTDQSDKDYDV

SLVDGFNIPLAINPTNTKCTAPACKADINAVCPSELKVDGGCNSACNVLQTDQYCCRNAY
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>ABC88428.1 alcohol dehydrogenase [Curvularia lunata]
MSNIPQEQAQVIEKTGGPVEYKIPVQKPGPDEVLVNIKFSGVCHTDLHAVNGDWPLPT
KLPLVGGHEGAGVVVARGELVNDVELGDHVGKWLNGSCLSCDYCQTADEPLCPKPLLSG
YTVDTGTFQQYCIAKAAHVARIPECDLAAIAPVLCAGITVYKGLKESGVKPGQFAAIVGA
GGGLGSLACQYAKAMGVRTIAIDAGEEKKKMCVNDLGAETFVDFSTSKNLVADVQKATPD
GLGPHVVILVAVNEKPFQAAEYVRPRGTVICIGLPAGAYLKAPVFETVIKMIRIQGSYV
GNRKDSSEAEIEFFRRGLIKAPFKIVGLSELQMVYDKMHQGAVVGRYVLDTSK

>AAK67492.1 Cur 1 3; cytochrome c [Curvularia lunata]
MGFEQGDAAKGANLFKTRCAQCHTLKAGEGNKIGPELHGLFGRKTGSVAGYSYTDANKQK
GIEWNHDTLFEYLENPKKYIPGTKMAFGGLKKPKDRNDLITFLEQETK

>AAK67491.1 Cur 1 2; enolase [Curvularia lunata]
MAITKIHARSVYDSRGNPTVEVDIVTETGLHRAIVPSGASTGSHEACELRDGDKTKWGGK
GVTKAVANVNDIIPALIKEKLDVKDQSAVDAFLNKLDTENKTKLGANAILGVSMIAIAK
AAAAEKGVPLYAHISDLAGTKKPYVFRFLSKNVLNGGSHAGGFLLFQEFMIAPAKTFAEA
LRIRQGAEVYQKLKALTKKTYGQSAGNYGDEGGVAPDIQTAEALDLIVDAIEAAGHTGQ
IKIAMDVASSEFFKDEKDYDLDFKNPDSKSKWLTYPQLAEMYKSLAEKYPVIVSIEDPF
AEDDWEAWSHFYKDGDFQIVGDDLTVTNPEFIKTAIELKSCNALLLKVNQIGTISEAINA
AKDAFGAGWGMVSHRSGETEDVTIADIVVGLRSGQIKTNAPARSERLAKYNQILRIEEE
LGDKRLFAGNKFHTAINLYL

>ACF19589.1 Cur 1 4; serine protease [Curvularia lunata]
MKYSLIAALPALAAASPTFSTETIHKQSAPVLSSTSAKEVPNSYMWVFKKHVKDASKHHD
WVQSVHSKNTQERMELRKRSSDLVPSNEVFAGLKHTYELSGLKGYSGHFDEETLEAIRNH
PDVDYIERDSEVRILGGDEPETENNSPWGLARISHRDSLSFGTWNKYLYAADGGEGVDVY
VIDTGTNVHDVDFEGRAKWGKTIPNGDADEDGNGHGHCSGTVAGKKYGVAKKAHVYAVK
VLRNSGSGTMSDVVKGEFAAKSHSEAVSAAKNGKKKGFKGSTANMSLGGGKSTLDMAV
NAAVDAGLHFAVAAGNDNADSCNYSAAAENAVTVGASTLLDERAYFSNYGKCNDIFAPG
LNILSTWIGSKHATNTISGTSMASPHIAGLLAYMLSLQPAKDSAYAVADITPKKLLKANLI
AIGTVGALS DVPSNTANVLAWNGGSSNYTDIIEKGGYTVKKAASKEEEEKESFRITIPS
LSELEDDFEKAKESAGRKAHHVGGKL

>AAB50734.2 Cyn d 1; beta-expansin [Cynodon dactylon]
AIGDKPGPNITATYGSKWLEARATFYGSNPRGAAPDDHGGACGYKDVDKPPFDGMTACGN
EPIFKDGLGCRACYEIKCKEPEVCSGEPVLVKITDKNYEHIAAYHFDLSGKAFGAMAKKG
QEDKLRKAGELTLQFRRVKCKYPSGKTFHIEKGSNDHYLALLVKYAAGDGNIVAVDIK
PRDSDEFIPMKSSWGAIWRIDPKKPLKGPFSIRLTSEGG AHLVQDDVIPANWKPDTVYTS
KLQFGA

>AAF80379.2 Cyn d 1; beta-expansin [Cynodon dactylon]
AMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGACGYKDVDKAPFDGMTGCGN
EPIFKDGLACGSCYEIKCKEPAECSGEPVLKIKITDKNYEHIAAYHFDLSGKAFGAMAKKG
EEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSPPNYLALLVKYAAGDGNIVGVDIK
PKGSDEF LPMKQSWGAIWRMDPPKPLKGPFTIRLTSESGHVEQDDVIPEDWKPDTVYKS
KIQF

>AAK96255.1 Cyn d 1; beta-expansin [Cynodon dactylon]
AMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGACGYKDVDKAPFDGMTGCGN
EPIFKDGLACGSCYEIKCKEPAECSGEPVLKIKITDKNYEHIAAYHFDLSGKAFGAMAKKG
EEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSPPNYLALLVKYAAGDGNIVGVDIK
PKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGHVEQDDVIPEDWKPDTVYKS
KIQF

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

MLAVVAVVLASVMGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC
GYKDVDKAPFDGMTGCGNEPIFKDGLACGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA
AYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLA
LLVKYAAGDGNIVSVDIKSKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGGHV
EQEDVIPEDWKPDTVYKSKIQF
>AAL14078.1 Cyn d 1; beta-expansin [Cynodon dactylon]
MLAAVAVVLASVMGGAWCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC
GYKDVDKAPFDGMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA
AYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKITFHVEKGSNPNYLA
LLVKYAAGDGNIVGVDIKPKGSDVFLPMKLSWGAIWRMDPPKPLKGPFTIRLTSESGGHV
EQEDVIPEDWKPDTVYKSKIQF
>AAL14079.1 Cyn d 1; beta-expansin [Cynodon dactylon]
MLAVVAVVLASVMGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC
GYKDVDKAPFDSMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA
AYHFDLSGKAFGAMAKKGEEDKLRKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLA
LLVKYAAGDGNIVSVDIKSKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGGHV
EQEDVIPEDWKPDTVYKSKIQF
>AAB28566.1 Cyn d 1; beta-expansin, partial [Cynodon dactylon]
AMGDDPGPKITATYGSKWLDKATF
>AAB28567.1 Cyn d 1; beta-expansin, partial [Cynodon dactylon]
GAAPDDHGGAXGYKDVDKPPFDGMTAXGNEPIFKDDL
>AAB32317.1 Cyn d 1; beta-expansin, partial [Cynodon dactylon]
AIGDKPGPKITATYXXKWLEAKATFYGSNPRGAA
>CAA01909.1 Cyn d 7; calcium-binding protein, polcalcin [Cynodon dactylon]
GTRRFDTNGDGKISLAELTDALRTLSTSADEVQRMMAEIDTDGDGFIDFDEFISFCNAN
PGLMKDVAKVF
>CAA01910.1 Cyn d 7; calcium-binding protein, polcalcin [Cynodon dactylon]
GTSFKRFDTNGDGKISLAELTDALRTLSTSADEVQRMMAEIDTDGDGFIDFDEFISFCN
ANPGLMKDVAKVF
>CAA62634.1 Cyn d 7; calcium-binding protein, polcalcin [Cynodon dactylon]
KTMADTGDMEHIFKRFDTNGDGKISLAELTDALRTLGSTSADEVQRMMAEIDTDGDGFID
FDEFISFCNANPGLMKDVAKVF
>AAS02108.1 FAD-linked oxidoreductase [Cynodon dactylon]
MARSRAFALLICAVAASCHVALSAPPPYAKQVERDFLTCLTKDIPPRQLYAKSSPAYA
SVWSSTVRNIKFLSDKTVKPLYIITPTNASHIQAAVVCGRRHGMRI RVRSGGHHDYEGLSY
RSEKPEPFAVDMNKMRAVSIDGKAATAWVDSGAQLGDLYYGIKASPKLGFAPAGVCTTI
GVGGHFSGGGFGMLLRKYGTAADNVIDAKVVDAQGRLLDRKAMGEDHFWAIRGGGGESFG
IVASWQVKLLPVPPKVTVFQVHKGIKEGAIDLVTWKQTVAPALPDDLIRIMAMGQGAMF
EALYLGTCCKDLVLLMTARFPELGMNATHCKEMTWIESVPYIPMGPKGTVRDLLNRTSNIK
AFGKYKSDYVLEPIPKSDWEKIFTWLVKPGAGVMIMDPYGGGIIASVPESATPFPRRSGVL
FNIQYVVYWFGEAAALPTQWTRDIYDFMTPYVSKNPRQAYVNYRDLDLGVNQVVGNVST
YASGKVVGEKYFKGNFERLARTKKGIDPEYFRNEQSIPPLL
>COMPARE225 malate dehydrogenase, partial [Cynodon dactylon]
TPASGQPERKVAILG
>COMPARE226 Ole e 1-like [Cynodon dactylon]
FTVTGEVYXDPXRA
>CAA69670.1 Cyn d 12; profilin [Cynodon dactylon]
MSWQAYVDDHLMCEIEGHHLTSAAIIGHDGTVWAQSAAFPAPFKPEEMANIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPAVIRGKKKSGGVTVKKTGQALVIGIYDEPMTPGQCNMVE
KLGDYLIEQGM

>CAC83658.1 Cyp c 1; calcium-binding protein, parvalbumin [Cyprinus carpio]
MAFAGILNDADITAALQGCQAADSFYKSFYAKVGLSAKTPDDIKKAFVIDQDKSGFIE
EDELKLFQNFSAARALDAETKAFKAGDSDGDGKIGVDEFAALVKA
>CAC83659.1 Cyp c 1; calcium-binding protein, parvalbumin [Cyprinus carpio]
MAFAGVLNDADITAALAEACKAADSFNHKTFFAKVGLTSKSADDVKKAFVIDQDKSGFIE
EDELKLFQNFSAARALDGETKTFLKAGDSDGDGKIGVDEFTALVKA
>CAD20406.1 beta-expansin [Dactylis glomerata]
MASSSSSVLLVVALFAVFLGSAHGIPKVPVPPGNITATYGDKWLDKSTWYGKPTGAGPKD
NGGACGYKDVKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVHITDDN
EPIIAPYHFDLSGHAFGSMACKGEEQKLRSAAGELELQFRRVKCKYPEGTVTFHVEKGSN
PNYLALLVKYVDGDGDVAVDIKEKKGDKWIALKESWGAIWRVDPDKLTGPFTVRYTTE
GGTKSEVEDVIPEGWKADTSYEAK
>AAP96759.1 beta-expansin [Dactylis glomerata]
IPKVPVPPGNITATYGDKWLDKSTWYGKPTGAGPKDNGGACGYKDVKAPFNGMTGCGNT
PIFKDGRGCGSCFEIKCTKPESCSGEAVTVHITDDNEPIIAPYHFDLSGHAFGSMACKGE
EQKLRSAAGELELQFRRVKCKYPEGTVTFHVEKGSNPNYLALLVKYVDGDGDVAVDIKE
KKGDKWIALKESWGAIWRVDPDKLTGPFTVRYTTEGGTKSEVEDVIPEGWKADTSYEAK
>AAB42200.1 Dac g 3; expansin [Dactylis glomerata]
VKVTFKVEKGSDPKLLVDIKYTRPGDTLAEVELRQHGSEEWELTKKGNLWEVKSSKPL
TGFNFRFMSKGGMRNVFDEVIPTAFKIGTTYTPEE
>2103117A expansin-like [Dactylis glomerata]
EAPVTFVVEKGSDEKLNLSIKYNKEGDSMAEVELKEHGSNEWLALKKNGDGVWEIKSDK
PLKGFNFRFVSEKGMNRNVFVDPADFKVGTTYKPEEAAAASARRRSSEVFQFLILSCQ
GRIVNCEVLICVMRRGNAMCLIASISMHHILTLDRFFFDGLEIIYKIFKMMFQKPRTRT
CIEKDFPRRSSSIPT
>P82946.1 Dac g 4; FAD-containing oxidase [Dactylis glomerata]
DIYNYMEPYVSKVDPTDYFGNEQARTAWVDSGAQLGELSYGVLFNIQVNYWFAP
>CAA10345.1 unknown function [Dactylis glomerata]
MSMASSSSSGLLAMAVLAALFAGAWCVPKVTFVVEKGSNEKHLAVLVKYEGDTMAEVELR
EHGSDEWVAMTKGEGGVWTFDSEEPLQGFNFRFLTEKGMKNVFDVVPPEKYTIGATYAP
EE
>AAK62278.1 unknown function [Dactylis glomerata]
MAVQKYTVALFLAVVLVAGPVASYAADAGYTPAAAATPATAGGKAMTEEQTLIEDVNAGF
KAAVAAAASSAPPADKFKTFEATFTAACKANIAAAAATKVPLFVAKLDAAYAVAYKTATGPT
PEAKYDAFVAALTEALRVIAGALEVHAVKPAEEVPAKIPAGELQIVDKIDAAYKIAAT
AANAAPANDKFTVFEGAFNKAIKESTGGAYESYKFIPTLEAAVKQAYAATVAAAPEVKYA
VFEEALTKAITAMSEAQKVATPAAVATGAATAAASAATGAATAAAGGYKV
>CAD20405.1 unknown function [Dactylis glomerata]
ADAGYTPAAAATPAAAGGKAMTEEQKLIEDVNAGFKAAVAAAASSAPPADKFKTFEATFTA
ACKANIAAAAATKVPLFVAKLDAAYAVAYKTAAGPTPEAKYDAFVAALTEALRVIAGALEV
HAVKPAEEVPAKIPAGELQIVDKIDAAYKIAATAANAAPANDKFTVFEGAFNKAIKES
TGGAYESYKFIPTLEAAVKQAYAATVAAAPEVKYAVFEAALTKAITAMSEAQKVATPAAA
ATGAATAAASAATGAATAAAGGYKV
>AEY79726.1 cyclophilin [Daucus carota]
MANPKVFFDMTIGGTPAGKIVMELYADTTPKTAENFRALCTGEKGTGKSGKPLHYKGSFF
HRVIPGFMCGGDFTAGNGTGGESIYGAKFADENFERKHTGPGILSMANAGPGTNGSQFF
ICTAKTEWLDGKHVVFVKVVEGMDVVKAIKGVSGSGKTSKPVAIADCGQC
>AEY79727.1 Dau c 5; isoflavon reductase-like protein, phenylcoumaran benzylic
ether reductase [Daucus carota]
MATKILIVGGTGYIGKFIVEASAKAGHPTFVLVREATLTSPDKSQLIDSFKSLGVTFVHG

DLYDHGSLVKAIKQVDVVISALGHGQLADQDKLLAAIVEAGNVKRFFPSEFGQDVDRVNA
VEPAKSAFAAKALFRRTVEAAGVPFTYVACNFFAGYFLPTLAQAGAAAPPRDKAVILGDG
IPKVAFNKEEDIATYTIKAVDDPRTLNKILYVRPPHNTLSFNELLSVWEKKIGKTLEKIY
VPEEQVLKNIQESVPIINVLLSISHSAFVKGDQTSFEIEPSYGVEASALYPDVKYTTVDV
YLSQFV

>AEY79728.1 Dau c 5; isoflavon reductase-like protein, phenylcoumaran benzylic ether reductase [Daucus carota]

MATKILIVGGTGYIGKFIVEASAKAGHPTFVLVREATLTSPDKSQLIDSFKSLGVTFVHG
DLYDHGSLVKAIKQVDVVISTLGHGQLADQDKLLAAIVEAGNVKRFFPSEFGQDVDRVNA
VEPAKSAFAAKAQFRRTVEAAGVPFTYVACDFFAGYFLPTLAQAGAAAPPRDKAVILGDG
IPKVAFNKEEDIATYTIKAVDDPRTLNKILYVRPPHNTLSFNELLSVWEKKIGKTLEKIY
VPEEQVLKSIQESVPIINVLLSISHSAFVKGDQTSFEVEPSFGVEASALYPDVKYTTVDE
YLSQFV

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

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKGDGGVGTIKHITLPE
GGPVTMTLRTDGLDKKNCTIDYSYIDGDILMGFIEKIENHLSVVPNADGGSTTKTTAIF
HTKGDVVPEENIKYAEQNTMLFKAIEAYLIAN

>AAB01092.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

LIFLLILSNNILNIMGAQSHSLEITSSVSAEKIFXXIVLDVDTVIPKAAPGAYKSVDVKG
DGGAGTVRIITLPEGSPITSMTVRTDAVNKEALTYDSTVIDGDILLEFIESIETHMVVVP
TADGGSITKTTAIFHTKGDVVPEENIKFADAQNTALFKAIEAYLIAN

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

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVDVKGDDGAGTVRIITLPE
GSPITSMTVRTDAVNKEALTYDSTVIDGDILLEFIESIETHMVVVPTADGGSITKTTAIF
HTKGDVVPEENIKFADAQNTALFKAIEAYLIAN

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

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAATGAYKSVEVKGDGGAGTVRIITLPE
GSPITMTVRTDAVNKEALSVDSTVIDGDILLGFIESIETHMVVVPTADGGSITKTTAIF
HTKGDVVPEENIKFADAQNTALFKAIEAYLIAN

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

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVDVKGDDGAGTVRIITLPE
GSPITSMTVRTDAVNKEALTYDSTVIDGDILLGFIESIETHLVVPTADGGSITKTTAIF
HTKGDVVPEENIKFADEQNTALFKAIEAYLIAN

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

MGAQSHSLEITSSVSAEKIFSGIVLDVDTVIPKAAPGAYKSVEVKGDGGAGTVRIITLPE
GSPITSMTVRTDAVNKEALTYDSTVIDGDILLGFIESIETHLVVPTADGGSITKTTAIF
HTKGDVVPEENIKFADAQNTALFKAIEAYLIAN

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

MGVQKTEVEAPSTVSAEKMYQGFLLDMDTVFVKVLPQLIKSVEILEGGGVGTVRLVHLG
EATEYTTMKQKVDVIDKAGLGTYTTIGGDILVEGLESVNVQFVVVPTDGGCIVKNTTIY
NTKGDVLPEDKVKEATEKSALAFKAIEAYLLAN

>ADL32660.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNILPKAAPGAYKNVEIKDGGVGTIKHITLPD
GGPVTTMTLRTDGLDKKGFTIDYSVIDGDVLMGFIDKIENHLSVPTADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32661.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNILPKAAPGAYKNVEIKDGGVGTIKHITLPD
GGPVTTMTLRTDGLDKKGFTIDYSVIDGDVLMGFIDKIENHLSVPTADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTLLFKAVEAYLIAN

>ADL32662.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKDGGVGTIKHITLPE
GGPVTTMTLRTDGLDKKNCTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32663.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKDGGVGTIKHITLPE
GGPVTTMTLRTDGLDKKNCTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF
HTKGDVVPEENIKFAEAQNTMLFKAVEAYLIAN

>ADL32664.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNVLPKAAPGAYKNVEIKDGGVGTIKHITLPE
GGPVTTMTQRTDGLDKKNCTIDYSYIDGDILMGFIDKIENHLSVVPNADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32665.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNILPKAAPGAYKNVEIKDGGVGTIKHITLPE
GGPVTTMTLRTDGLDKKGFTIDYSVIDGDVLLGFIDKIENHLSVPTADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>ADL32666.1 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKHEQEITSSVPAEKMFHGLILDIDNILPKAAPGAYKNVEIKDGGVGTIKHITLPE
GGPVTTMTLRTDGLDKKGFTIDYSVIDGDVLMGFIDKIENHLSVPTADGGSTTKTTAIF
HTKGDVVPEENIKYAEAQNTMLFKAVEAYLIAN

>A0A161X1M2 Dau c 1; pathogenesis related protein, PR-10, Bet v 1-like [Daucus carota]

MGVQKTEAEVTSSVSAEKLFKALCLDIDTLLPQVLPGAIKSSETLEGDGGVGTVKLVHLG
DASPFKTMKQKVDAIDKESFTYYSIIDGDILLGFIESINNHFAVVPNADGGCTVKSTIT
FNTKGDVVPEENIKFANDQNRAIFQAVEAYLIAN

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

MSWQTYVDDHLMCEVDGNPQQLSAAAIIIGHDGSVWAQSSTFPKFKPEEITGIMKNFDEP
GHLAPTGLYLGGTKYMIQGEPIAVIRGKKGSGGVTIKKTGQALVFGVYDEPVTGQCNL
IVERLGDYLIIEQGL

>COMPARE00265 actin, partial [Delonix regia]
RAVFPISIVGRPRH

>COMPARE00266 actin, partial [Delonix regia]
KSYELPDGQVITIGAERF

>COMPARE00267 actin, partial [Delonix regia]
KDLYGNIVLSGGSTMFPGIADRM

>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

>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]
RIPSAVGYPQLATDLGGLQERI

>COMPARE00264 ATP synthase beta subunit, partial [Delonix regia]
RVGLTGLTVAEHFRD

>COMPARE00259 luminal-binding protein 5, partial [Delonix regia]
RVEIESLFDGIDFSEPLTRA

>COMPARE00260 luminal-binding protein 5, partial [Delonix regia]
KFDLSGIPPAPRG

>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

>COMPARE00277 UDP-arabinopyranose mutase, partial [Delonix regia]
KTINVPDGFYELYNRN

>COMPARE00278 UDP-arabinopyranose mutase, partial [Delonix regia]
MSKPATPVAPPLKDELDIVIPTIRN

>COMPARE00279 UDP-arabinopyranose mutase, partial [Delonix regia]
KASNPFVNLRK

>COMPARE00276 unknown function, partial [Delonix regia]
REGEGEGVAAAGVGVR

>L7UZ85.1 alpha-actinin [Dermatophagoides farinae]
MTQDGYMQEEEEWEREGLLDPAAWEKQQRKFTAWCNSHLRKAGTQIDNIEEDFRNGLKL
MLLLEVISGETLGGKPDGRGKMRFHKIANVNKALDFIESKGVKLVSIGAEEIVDGNKMTLG
LIWTIILRFQIDISVEEMTAKEGLLLWCQRKTAPYKNVNVQNFHLSWKDGLAFCAL IHR
HRPDLIDYGKLRKDNPMDFNLAFDVAEKHLNIPRMLDAEDVVYAKPDERAIMTYVSWY
YHAFHGAQQAETAANRICKVLKVNQDNERLMEEYERLASDLEWIRRTTPWLENRTDNT
LPGTQKKLEEFRSRRQHKPPRVEQKANLETNFNTLQTKLRLSKRPAYMPSEGKMSDIT
GAWKGLESAEKGFEEWLLSEMMRLERLDHLAQKFKHKADIHEEWTQGKEEMLVSHDFRQC
KLNEIKALKKKHEAFESDLAAHQDRVEQIAAIAQELNALGYHDIASINARCQRICDQWDR
LGTLTTRRRQALDEAEQILEKVDLFHLEFAKRAAPFNNWLDRETREDLVDMFIVHSIEEIQ
QLIDAHESFKNTLGEADKEYKTIVGLAQEQPMATQYQIPGGLENPYTTLTPEVITTKWR
DVKQLVPRDHTLQTELIRQQCNENLRQFAEKANVVGPIERQMDAVTAIGMGMQGTLE
DQLQRLHEYDQAVVQYRPHVDDLEKIHQEQEAMIFENRYTQYTMETLRVGWEQLLTSIH
RNINEVENQILTRDSKGITQEQLNEFRTSFNHFDKRTGRLAPEEFKSCLVSLGYNIRND
DRPEFRRI LAIVDPNKTGYVHFDALDFMTREYTDTDTAEQMIDSFRI LAGDKPYITADE
LRRELPPDQAEYCIRRMTPYNGQCAVP GALDYRSFSTALYGESDL

>AHX03180 Der f 4; alpha-amylase [Dermatophagoides farinae]
MLPKFFFILITVLTLLVSLFVNGDSKFSNPHFIGNRSVITHLMEWKYDDIGDECERFLGP

YGYGGVQVSPVNEHAIMDGRPWYERYQPVSYDIHTRSGDEQQFRRMVQRCNKAGVRIYVD
IVLNHMTGGQSGGLGTNGHHYDGVAMQYPGVFPGNDFHGHETCPTNDLEIHNYSNRIEAR
NCRLVGLRDLKQQSEYVKQKQVDFLNHLIDIGVAGFRSDASTHQWPDLLRSIYSRLHNLN
NEFFTENSHPFYIYHETIYYGGNGINSNEYTSLGRIIEFRFYKEITNVFRNNNQLRWLRF
GTEWGLVPSGDALVMIDSHDLRVGHTGQLGFNINCFEARLLKAATAFMLAWNYGIPRVMS
SYFWDQIIRDGKDVNDWVGPPDQHGNIILSVHPNPDMTCNHEWICEHRWREIYNMVKFKL
IAGQEPVNNWWDNGDNQIAFSRGNRAFIAINLQKNGNDHDKNLQKRLQTGLPPGIYCDII
SGNLIINRCMGKSIQVDKNGLSDIYVGHDEFDAFVAYHIDARVES

>AI008861.1 Der f 33; alpha-tubulin [Dermatophagoides farinae]
MRECISLHVQAGVQIGNACWELYCLEHEIQPDGQLSPVKSTTTLSSETISNDSFSTFF
NETGNRFVPRSIYVDLEPTVVDEVRTGEYRRLFHPEQLITGKEDAANNYARGHYTEGKT
LIEPVMRRIAKLAEQCSGLQGFLIFHSFGGGTSGSFSLLMERLSVEYGKSKLEFAIYP
APAISTAVVEPYNSILTTHTLEHSDCSFMVDNEAIYDICRRNLNIERPSYMNLRNLIGQ
IVSSITASLRFDGALNVDLTFEQTNLVPYPRIFPLVSYAPIVSSEKAYHEQFTVPEITG
TCFEPNQMVKCNTRNGKYMACECLLYRGDVPKDVNAIAAIAKAKSTIQFVQWCPTGFKI
GINYRPPTVPSGDLAKVQRAVCLLSNTTASEAWSRLNHKFDLMYSKRAFVHWYVGEEM
EEGEFSEAREDLAALEKDYEEVAEYNADDDYDDRGEFF

>BBD75204.1 Der f 14; apolipoprotein [Dermatophagoides farinae]
MRLFALLFTACLLGLGQAQHTVACPNISIPQLINPKAQSTYVYTLDAKTVLTPRDSQKVT
IKADA EVAIVSACEAVLRLQNVADGVPNGAELASELASKSFAFGYFNGRILGVC PANDD
QDWSLNIKKAIVSALQVQFDENKDKVEESDFSGRCPT EYRKIRNEDNMVMEKRKDLNLC
DDRRIDL RQTPDQALGQLKEMIRHYMHPMGSDLS CRMTLKDQVSEVDCEERHVLVHRSH
KPVHLSYVKMMLKESKDGVAADLGTQDSEPKRYPYLSFDHKHKNPTE TDVVEVLKLCSEI
SEPQASIETSFTFQKLVDKLRYLSAEETASVDES VKTSVCPAHAYRIRELF LDASAF AAS
DGSIRTLVKAHENQELSITRSTALFTV VAMKAAPNKETVQVLLPVIASEKTIRPMLL GFS
VLVRRYCEKSADCASNSGVKDARDAYLARLATAKDANERITIVRALENLNVNTEGVDNMI
NAMDEI IKS DAEPALRAAAVNAL S NDASHMDRYKSLVMDESMPNEARIAAFQKMMKNGGM
SHIKDLFTVKGECMKNYVLT YVDNLKSKNDLRRQTVSGDVELPEQPKREIGITRNIARE
YGPYTFEYDVIYPETHENVTR SINGRLIRAKNDQLKEIVEIQITQNGFERELTNAMALME
KKS FQSIMQFVRDTLKM LAQIRKNADDNHMKITVQINGKDVYYTDVFQDLKMKEL IIK
RAEKIINEKKVDRSIGGVL LSKLVLPITITGLPLMYKFGDNFLIRYDGEFSGEKGDRHIK
LNGGFVAGVYGQMKLLVKDQKMGYEYDGKLAYTPI LDMDIQKKEHSLLLRFNTKDVERT
IMRFKQSLREKRATGEEKDYENEITPESRSDQCFSFFLLDYCRKASHIKGLIFPNVEYYV
VKPEKEVTALELLKGETEDKTRRYVAELTAVGSPSNKQAKAQIEVTKGEEYKITLKSPE
HEFNTEFTIHADKNNLKM HMDFPNVFQADLTGTFQHDKENNVRKNQLNLQYKFAGDEKPH
TVDYENEF SFNLKRSSKDKNSGVDR AKYMSSHFPILNHKVNIQFKYRPFKVNELNLEGE
FGRELQHKFQLMRNSQIEVEEVRPFKMHGNSDIKLMANDLIDYDLKSEFKYESNKGTP I
ELQYKISGKDRSKRAADLGAEDVEGVIDYKNNGSPIDSKMHAHLKMKGNNGYDSELKQT
QPQQYEGKITLSKNDKKIFINH KSEMTKPTNTFHLKTDADVSYSDSDMKKHYQMEFKKEN
DIYTMSTVERNGQMFYENHLTIHKGGKLNLYRRNDRKILLDLDNALSPREGTMKLN I K
DREYNFVMKREPLRFRDITVEGNENAYIKNGKHLHSLMDPSTLSLVTKADGKIDMTVDLI
SPVTKRASLKIDS KKYNL FHEGELSASIVNPRLSWHQYTKRDSREYKSDVELSLRSSDIA
LKITMPDYNSKIHYSRQGDQINMDIDGTLIEGHAQGTIREGKIHIKGRQTD FEIESNYRY
EDGKLIIEPVKSENGKLEGLSRKVP SHLTLET PRVKMNMKYDRYAPVKVFKLDYDGIHF
EKHTDIEYEPGVRYKII GNGLKDDGRHYSIDVQGI PRKAFNL DADLMDFKLVSKPEDS
NKAQFSYTFNEYTETEEYFDPHRAYYVNW LSSIRKYIQNFIVEDN

>AAP57094.1 Der f 20; arginine kinase [Dermatophagoides farinae]
MVDQAVIDKLEAGFQKLQSSAECHSLLKKYLTRNVL DACKGRKTGMGATLVDVVQSGFEN
LDSGVGLYAPDAESYTLFKEL FDPVIEDYHKGFKPTDKHPQTD FGDVNTLCNVDPNNEFV
ISTRVRCGRSLQGYFPNCLTEAQYKEMEEKVKGQLNSFEGELKGTYYPLLGM DKATQQQ

LIDDHFLFKEGDRFLQAANACRFWPVGRGIFHNDNKTFLIWVNEEEHLRIISMQKGGDLK
QVFSRLINGVNHIEKKLPFSRDDRLGLFTFCPTNLGTTIRASVHIKLPKLAADRKXLEEV
AGKYNLQVRGTAGEHTESVGGVYDISNKRRMGLTEYQAVKEMQDGILELIKIEKSM
>ABU97470.1 Der f 20; arginine kinase [Dermatophagoides farinae]
MVDQATLSKLEAGFQKLQNAQDCHSLLKKYLTRDVLQKTKKTDMGATLLDVIQSGVEN
LDSGVGIYAPDAQSYKTF AALFDPIIDDYHKGFKPTDKHPQTDFGNIEHFVNVPKNEYV
ISTRVRCGRSLKGYPFNPLTEAQYKEMETKVKGQLATFEGELKGTYYPLLGMKDQKQK
LIDDHFLFKEGDRFLQAANACRYWPVGRGIFHNDKKTFLMWVNEEDHLRIISMQKGGDLK
EVFGRLLVKAVKHIEQKIPFSRDDRLGLFTFCPTNLGTTIRASVHIKLPKLAADRKKLEEV
AARYNLQVRGTAGEHTESVGGIYDISNKRRMGLTEYQAVKEMQDGIIELIKMEKSL
>AI008850.1 Der f 20; arginine kinase [Dermatophagoides farinae]
MVDQAVIDKLEAGFQKLQSSAECHELLKKYLTRNVLDACKGRKTMGATLVDDVQSGFEN
LDSGVGLYAPDAESYTLF KELFDPVIEDYHKGFKPTDKHPQTDFGDVNTLCNVDPNNEFV
ISTRVRCGRSLQGYFPNCLTEAQYKEMEEKVKGQLNSFEGELKGTYYPLLGMKDQKQK
LIDDHFLFKEGDRFLQAANACRFWPVCGIFHNDNKTFLIWVNEEDHLRIISMQKGGDLK
QVFSRLINGVNHIEKKLPFSRDDRLGLFTFCPTNLGTTIRASVHIKLPKLAADRKKLEEV
AGKYNLQVRGTAGEHTESVGGVYDISNKRRMGLTEYQAVKEMQDGILELIKIEKSM
>AAP35077.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides
farinae]
MMKFLIIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEQSETIDPMKVPDHADKFER
HVGILDFKGE LAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
KLGDLHPTTHVISDIQDFVVALSLEIPDEGNITMSTFEVRQFANVVNHIGGLSILDPIFG
VLSDVLT AIFQDTRKEMTKVLAPAFKRELEKN
>ACK76299.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides
farinae]
MMKFLIIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEQSETIDPMKVPDHADKFER
HVGILDFKGE LAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMSTFEVRQFANVVNHIGGLSILDPIFG
VLSDVLT AIFQDTRKEMTKVLAPAFKRELEKN
>AI008853.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides
farinae]
MMKFLIIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEKSETIDPMKVPDHTDKFER
HVGILDFKGE LAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
KLGDLHPNTHVISDIQDFVVALSLEISDEGNITMSTFEVRQFANVVNHIGGLSILDPIFG
VLSDVLT AIFQDTRKEMTKVLAPAFKRELEKN
>AAB35977.1 Der f 7; bactericidal permeability-increasing like [Dermatophagoides
farinae]
MMKFLIIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAAIEQSETIDPMKVPDHADKFER
HVGIVDFKGE LAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY
KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMSTFEVRQFANVVNHIGGLSILDPIFG
VLSDVLT AIFQDTRKEMTKVLAPAFKRELEKN
>AAD52672.1 Der f 15; chitinase [Dermatophagoides farinae]
MKTIYAILSIMACIGLMNASIKRDHNDYSKNP MRIVCYVGTWSVYHKVDPYTIEDIDPFK
CTHLMYGF A KIDEYKYTIQVFDPYQDDNHNSWEKRGYERFNLR LKNPELTTMISLGGWY
EGSEKYS DMAANPT YRQQFIQSVLDFLQEYKFDGLDLDWEYPGSRLGNPKIDKQNYLALV
RELKDAFEPHG YLLTAAVSPGKDKIDRAYDIKELNKLFDW MNVMTYDYHGGWENFYGHNA
PLYKRPEDETDELHTYFNVNMTMHYYL NNGATRDKLV MGVPFYGRAW SIEDRSK LKLGDP A
KGMSPPGFISGEEGLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYDDLASISC
KLAFLKELGVSGVMVWSLENDDFKGHCGPKNPLLNKVHNMINGDEKNSFECILGPSTTTP
TPTTTPTT

TPSPTTTEHTSETPKYTTYVDGHLIKCYKEGDIPHPTNIHKYLVCEFVNGGWWVHIMPCP
PGTIWCQEKLTCIGE

>AAM19082.1 Der f 18; chitin-binding protein [Dermatophagoides farinae]

MTRFSLTVLAVLAACFGSNIRPNVATLEPKTVCYYESVHWRQEGEKMDPEDIDTSLCTH
IVYSYFGIDAATHEIKLLDEYLMKDLHDMEHFTQHKGNAKAMIAVGGSTMSDQFSKTA
AV EHYRETFVSTVDLMTRYGFDGVMIDWSGMQAKSDNFILKLLDKFDEKFAHTSFVMG
VTL PATIASYDNYNIPAISNYVDFMNVLSLDYTGSAHTVGHASPFPEQLKTLEAYH
KRGAPR HKMVMVAVPFYARTWILEKMNKQDIGDKASGPGPRGQFTQTDGFLSYNEL
CVQIQAE
TNAF TITRDHDNTAIYAVVHSNHAEWISFEDRHTLGEKAKNITQQGYAGMSVY
TLSNEDVHGV CGDKNPLLHAIQSNYYHGVVTEPTVVTLPPVTHTEHVTDIPGVF
HCHEEGFFRDKTYCA TYYECKKGFLEKTVHHCANHLQAFDEVSRTCIDHTKIPGC

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

>AAF28423.1 Der f 6; chymotrypsin, serine protease [Dermatophagoides farinae]

MIKIFLVTILIVITVTVDARFPRSLQPKWAYLDSNEFPRSKIGDSPIAGVGGQDADLAE
APFQISLLKDYLMKRMHCGGSLISESTVVTAACHTYGQKASSLSVRYGTNQR
TSSSYGD LKVKPIIQHESYEQDQTQDKTIIILPNPVVSTNVQMNEIETEDIVD
GDKVTIYGWGLT DGNGKDL PDKLQKGSMTIVGNDRCNKWSINAIHPGMICALDKTQSGC
NGDSGGPLVSA NRKLTGIVSWGPSKCPPGEYMSVFRPKYYLDWITKNIV

>ACK76296.1 Der f 6; chymotrypsin, serine protease [Dermatophagoides farinae]

MIKIFLVTILIVITVTVDARFPRSLQPKWAYLDSNEFSRSKIGDSPIACVGGQDADLAE
APFQISLLKDYLMKSHMCGGSLISESTVVTAACHTYGQKASSLSVRYGTNQR
TSSSYGD LKVKTIIQHESYDPDTIQNDISLLILSKPVVSTNVRMIEIETDDIVD
GDKVTIYGWGLT DGNGKDL PDKLQKGSMTIVGNDRCNKWSINAIHPGMICALDKTQSGC
NGDSGGPLVSA NRKLTGIVSWGPSKCPPGEYMSVFRPKYYLDWITKNIV

>ACK76297.1 Der f 6; chymotrypsin, serine protease [Dermatophagoides farinae]

MIKIFLVTILIVITVTVDARFPRSLQPKWAYLDSNEFSRSKIGDSPIAGVGGQDADLAE
APFQISLLKDYLMKSHMCGGSLISESTVVTAACHTYGQKASSLSVRYGTNQR
TSSSYGD LKVKTIIQHESYDPDTIQNDISLLILSKPVVSTNVQMIEIETDDIVD
GDKVTIYGWGLT DGNGKDL PDKLQKGSMTIVGNDRCNKWSIDAIHPGMICALDKTQSGC
NGDSGGPLVSA NRKLTGIVSWGPSKCPPGEYMSVFRPKYYLDWITKNIV

>COMPARE013 Der f 31; cofilin [Dermatophagoides farinae]

MASGVIVATEAKTLYEEVKDKKYRYIIYHIKDERVIEVETTGRDATYSDFVARLQDYK
NECRYCVDFPANIPVEGGGEKSNMSVDRLLMTWCPESAKIKQKMLYSSSYDALKKALV
GVYRYVQACDYEEASEEAIAEAFRKG

>AAP35065.1 Der f 29; cyclophilin [Dermatophagoides farinae]

MALPRVFFDIAADNQLGRIVIELRSDVVPKTAENFRALCTGEKGFVKSSSFHRIIPNF
MIQGGDFTNHNGTGGKSIYGNKFADENFTLQHTGPGIMSMANAGPNTNGSQFFITTVKTT
WLDGKHVVFGSVVEGMDIVKKVESYGSQSGKPSKKVTIANCGQL

>P16311.2 Der f 1; cysteine protease [Dermatophagoides farinae]

MKFVLAIASLLVLSTVYARPASIKTFFEEFKAFNKNYATVEEEEVARKNFLES
LKYVEAN KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSV
NVPSELRLSLRT VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQ
HGCHGDTIPRGIE YIQQNGVVEERSYPYVAREQRCRRPNSQHYGISNYCQIYPPDV
KQIREALTQHTHTAIAVI IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYG
STQGDDYWIVRNSWDTTWGDSGY GYFQAGNNLMMIEQYPYVWIM

>BAC53948.1 Der f 1; cysteine protease [Dermatophagoides farinae]

MKFVLAIASLLVLSTVYARPASIKTFFEEFKAFNKNYATVEEEEVARKNFLES
LKYVEAN KGAINHLSLSDLSDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSV
NVPSELRLSLRT VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQ
HGCHGDTIPRGIE

YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY
GYFQAGNNLMMIEQYPYVIM

>ABA39436.1 Der f 1; cysteine protease [Dermatophagoides farinae]
RPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEANKGAINHLSDSLDEFKNR
YLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRTVTPIRMQGGCGSCWAFSG
VAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVAR
EQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVIIGIKDLRAFQHYDGRITII
QRDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTT

>ABL84749.1 Der f 1; cysteine protease [Dermatophagoides farinae]
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRT
ATPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY
GYFQAGNNLMMIEQYPYVIM

>ABL84750.1 Der f 1; cysteine protease [Dermatophagoides farinae]
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRT
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY
GYFQAGNNLMMIEQYPYVIM

>ABL84751.1 Der f 1; cysteine protease [Dermatophagoides farinae]
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRT
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY
GYFQAGNNLMMIEQYPYVIM

>ABU49605.1 Der f 1; cysteine protease [Dermatophagoides farinae]
MKFVLAIVSLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEAN
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRT
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVI
IGIKDLRAFQHYDGRITIIQHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGY
GYFQAGNNLMMIEQYPYVIM

>ADM52184.1 Der f 1; cysteine protease [Dermatophagoides farinae]
RPASIKTFEEFKAFNKNYATVEEEEVARKNFLES�KYVEANKGAINHLSDSLDEFKNR
YLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRTVTPIRMQGGCGSCWAFSG
VAATESAYLAYRQTSDDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYVAR
EQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVIIGIKDLRAFQHYDGRITII
QHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGYGYFQAGNNLMMIEQYPY
VIM

>AFJ68066.1 Der f 1; cysteine protease [Dermatophagoides farinae]
EARPASIKIFEEFKAFNKNYATVEEEEVARKNFLES�KYVEANKGAINHLSDSLDEFK
NRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRLSLRTVTPIRMQGGCGSCWAF
SGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIEYIQQNGVVEERSYPYV
AREQQCRRPNSQHYGISNYCQIYPPDVKQIREALTQHTAIAVIIGIKDLRAFQHYDGRITII
QHDNGYQPNYHAVNIVGYGSTQGVDYWIVRNSWDTTWGDSGYGYFQAGNNLMMIEQYP

YVVIM

>AAP35075.1 Der f 1; cysteine protease, partial [Dermatophagoides farinae]
MKFVLAIASLLVLSTVYARPASIKTFEEFKAFNKNYATVEEEVARKNFLES�KYVEAN
KGAINHLSDSLDEFKNRYLMSAEAFEQLKTQFDLNAETSACRINSVNVPSSELDLRS�RT
VTPIRMQGGCGSCWAFSGVAATESAYLAYRNTSLDLSEQELVDCASQHGCHGDTIPRGIE
YIQQNGVVEERSYPYVAREQQCRRPNSQHYGISNYCQIYPPDVKQIREALQTHTAIAVI
IGIKDLRAFQHYDGRITIIQHDL

>QBP14757.1 elongation factor [Dermatophagoides farinae]
MVNFTVDEIRVLMNKKRNIRNMSVIAHVDHGKSTLTDSLVS KAGIIAAAKAGEMRFTDTR
KDEQERCITIKSTAISMYFEMREQDMVFITSADQKESDEKGFLLINLIDSPGHVDFSSSEVT
AALRVTDGALVVVDCVSGVCVQTETVLRQAI AERIKPVLFMNKMDLAMLTLQLEQEDLYQ
KFTRIVENVNVIISTYADENGPMDIRVDP SKGSGVFGSGLHGWFSLKQFAELYSEKFK
IDVDKLMNRLWGENFYNPTAKKWSKRFDEGYKRAF CMFVLDPIFKVFDAIMNFKKEETAK
LLEKLNIVLKGEDKEKDGNL LKVV MRTWL PAGD SLLQMI AIHL P SPIT AQ KYRMELLYE
GPHDDEAAVAIKSCNPEGPLMMYISKMVPTSDKGRFYAFGRVFSGIVASGQKVRIMGP NY
VHGKKE DLVEKAIQRTVLMGRYVESIENVPCGNICGLVGV DQFLVKTGTISTFKDAHNM
KVMKFSVSPVVRVAVEPKNPADLPKLV EGLKRLAKSDPMVQCIIEESGEHIVAGAGELHL
EICLKDLEEDHAQIPIKTS DPVVS YRET VSE ESEIMCLSKSPNKHNR LFMKACPLQD G IA
EDIDKGDINPRDDFKVRARFLADKYNWDATDARKI WAFGPEGTGP NLLVDVT KG VQYLNE
IKDSVVAGFQWATKESVLC EENMRGVR FN IHDVTLHADAIHRGGGQI IPTARRCLYACL L
TAQPR LLEPVYLVEIQCEQAVGGIYGV LNR RRGHVFEESQVVGTPMFTVKAYLPVNESF
GFTADLR SNTGGQAF PQCVFDHWQILPGDPLDGKSRPYQIVMDTRKRKGLKDSLPELDNY
FDKL

>BAV90601.1 Der f 34; enamine/imine deaminase [Dermatophagoides farinae]
MSPKRIISTPLAPQPIGYPYSQAVQVGN TVYLSGQIGMNVRTNEMVTGPIRDEAQQAFNM
KAVVEASGAKMSDVVKVNI FIRNFND FPAINDVMKEFFQSPF PARSTVGV AELPKNARVE
IESIVVIE

>AAP35078.1 Der f 13; fatty acid-binding protein [Dermatophagoides farinae]
MASIEGKYKLEKSEKDFEFLDKLGVGFMVKTAAKTLKPTFEVAIENDQYIFRSLSTFKNT
EAKFKLGEEFEEDRADGKRKVTIQKEGDNKFVQTQFGDKEVKIIREFNGDEVVWTASCD
GVTSVRTYKRI

>AGC56219.1 Der f 30; ferritin [Dermatophagoides farinae]
MAANPESTTKTSRVRMNIQINLEFYASYVYQQMAYHFNRDDVALPGFEKFFDVSSKEERE
HAERFMKLQNRGGRIVLDDIHKPQQD WSSGLEAMRAALELEKTVNQALLDLHAVATKH
NDAQFADFIETHYLTEQVEAIKKLADYITNLERC GPGLGEYLFDRHTLHSS

>AAM64112.1 Der f 16; gelsolin-like [Dermatophagoides farinae]
MAAHDKNFDVIPIGHTFFFIWRIKQFELVPVPKEDYGKFYKGCYIVACCTENPTGGHSHK
MESKPILNGHG YCHIHF WIGSESTKDEAGVAAIKSVELDDFLGGYPVQHREIEEFESRQF
SSYFKNGI IYLKGGYESGFTKMI DELKPSLLHVKGKKRPIVYEC AEISWKVMNNGDVFIL
LVPNFVFWVTGKHSNRMERTTAIRVANDL KSELNRFKLSSVILEDGKEVEQTS GA EYDAF
NKALS LDKKID LKQMPKGYDYAASDKSFESHRSFVTL YKCFEGTETIDISFVKNGLS
RADLDTNDTFIVENGSEGLWVWVGKATQKERQSAIKYAMEL INKKKYPNNTPVTKVLEG
DESVEFKSLFESWQMSEQE KITSARLFRVSRNGIFKQVANYEPDDLEEDNIMILDVMDKI
YVWIGNQFAERIADEAHVDKVAQRFIQEDKSGRKFQPNQI IKLKQGS EDGAFKSYFPKWN

>COMPARE079 glutathione S-transferase [Dermatophagoides farinae]
MELGTLEGSMSETKPILGYWDARGLGQAIRLLLTYAGVDFIDKRYTVGPPPNYDRSQWLN
DKYNLGLDFPNC PYYIDGNV KLSQS LAIRYIARKQK LIGQNEHEEIRASLAEQQIIDMN
MAIARIAYNFNCEK LKPEFLKSLPEQVELLSKFLGDQPFTAGANISYADFLLYEYLTKLK
ILVPEVYDKFENLKKFHGNVLEALPRVSEYIKKQPKAFHGPTSLWNGTYA

>AGC56218.1 Der f 28; heat shock protein 70 [Dermatophagoides farinae]

MSKTPAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVGFDTTERLIGDAAKNQVA
MNPSNTVFDKRLIGRKFDETTVQADMKHWPFKVIEKGNKPAIEVEFKGETKQFIPEEIS
SMVLVKMRETAAYLGGTVNNAVITVPAYFNDSQRQATKDSGLIAGLNVLRINEPTAAA
IAYGLDKKGGAGERNVLIIFDLGGGTFDVSLLTIEEGIFEVKSTAGDTHLGGEDFDNRLVN
HFVKEFKRKHKKDLTTNARALRRLRTSCERAKRTLSSAAQTSIEIDSLFEGIDFYTSITR
ARFEELCADLFRSTMEPVERVLRDAKTDKSSVNEIVLVGGSTRIPKIQRLVADFFNKDPN
KSINPDEAIAYGAAVQASILSGDTSSKSTNEILLLDVAPLSLGIETAGGVM TALIKRDTT
IPTRSPRLSLPTPTTSLVSRFRSTRVSVLAPRTTSLVSSSSPVSPCSSWCSSDRGHFDV
DANGIMNVGAVEKGTGKTNKITITNDKGRLSKEEIERMLAEAEKYKAEDEAEAARIHAKN
GPESYAYSLRNTVNEGKLSISDSDEKLRARLRLSTGSTTRPPARRSTTLNRRSSRVL
PTPSFWLPTVVLAVVWVPLVWTPVLVALVVLTRLRSALRSLTKKVFNGVFLFPVLFVDS
>AI008848.1 Der f 28; heat shock protein 70 [Dermatophagoides farinae]
MPSKTLKAPAIGIDLGTTYSCVGVFQNGSVEIANDQGNRTTPSYVAFNDTERLIGDAAK
NQVSMNPTNTIFDAKRLIGRRFDESSVKSDMKHWPFKVSESGKPKLEVEFKGERKRFWP
EEISAMVLTMKMETAEAYLGQKVTDVITVPAYFNDSQRQATKDAGVIAGLNVLRINEP
TAAAIAYGLDKKGGGKENVLIIFDLGGGTFDVSVLTIDNGIFEVKSTAGDTHLGGEDFDNR
LVNHVFQEFKRKFGKDIMSNKRALRRLRTSCERAKRTLSSSTQTSIEIDSLHEGIDFYST
ITRARFEELCSDLFRSTLEPEKALRDAKLDKSKIDEIVLVGGSTRIPKIQKLLSDFFNK
KELNKSINPDEAVAYGAAVQAAILTGDNSNVKDLLLDDVAPLSLGIETAGGVM TLLIKR
NTTIPTKQTQFTTYADNPQAVTIQVYEGERAMTKDNNRLGTFDLTGIPPAPRGVQPQIEV
TFDVDANGILNVSADKSTGRQNKITITNDKGRLSKADIEKMOVQAEQYREDDERQRERI
AAKNQLEAYAFQLKSTMEEEAVKSKLSEEDRKTVLNKVDETLRWLDSNQLADKEEFEHRQ
KEIENACRPIMMKIYQQQQQHHPGANGSCGSNAYPGYNGFKSNNDGPVVEEVN
>BAX34757.1 Der f 35; NPC2-like [Dermatophagoides farinae]
MIKFLCIFALTFAVASAGMKFVDCGHKEVISLDVSGCEGDYCVLHKGKTIDLDMKCKSN
QDSEHLKLIISADVNGIEIEVPGFDQDGHYVQCPHKGQDYDIKYSYNVPAVLPNIKGT
LTAKVIGDNLVGLKLNGEIAD
>BAA01239.1 Der f 2; NPC2-like [Dermatophagoides farinae]
SLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAK
IEIKASLDGLEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKLI
GDNGVLACAIATHGKIRD
>BAA01240.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA
NQNTKTAKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDIKYTWNVPKIAPKSEN
VVTVKLIIGDNGVLACAIATHGKIRD
>BAA01241.1 Der f 2; NPC2-like [Dermatophagoides farinae]
SLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAK
IEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSENVVTVKLV
GDNGVLACAIATHAKIRD
>AAL47677.1 Der f 2; NPC2-like [Dermatophagoides farinae]
DQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKTAKIEIKASLDG
LEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPSENVVTVKLVGDNGVLACA
IATHAKIRD
>AAP35073.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MVSLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDANQNTKT
AKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSENVVTVK
LVGDNGVLACAIATHGKIRD
>CAI05848.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLVAAVVADQVDVKDCANHEIKKVMVDGCHGSDPCIHRGKPFNLEAIFDA
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN

VVTVKLVGDNGVLACAIATHAKIRD
>CAI05849.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA
NQNTKTAKIEIKANINGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN
VVTVKLVGDNGVLACAIATHAKIRD
>CAI05850.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN
VVTVKLVGDNGVLACAIATHAKIRD
>ABA39438.1 Der f 2; NPC2-like [Dermatophagoides farinae]
DQVDVKDCANNEIKKVMVDGRHGSDPCIHRGKPFLEALFDANQNTKTAKIEIKANING
LEVDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKLVGDNGVLACA
IATHAKIRD
>ABN14313.1 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA
NQNTKTAKIEIKANINGLEVDVPGIDTNACHYIKCPLVKGQQYDAKYTWNVPKIAPKSEN
VVTVKLVGDNGVLACAIATHGKIRD
>BAD74060.2 Der f 2; NPC2-like [Dermatophagoides farinae]
MISKILCLSLLLVAAVVADQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFDA
NQNTKTAKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSEN
VVTVKLVGDNGVLACAIATHGKIRD
>AFJ68072.1 Der f 2; NPC2-like [Dermatophagoides farinae]
DQVDVKDCANNEIKKVMVDGCHGSDPCIHRGKPFLEALFGANQNTKTAKIEIKASLDG
LEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKLVGDNGVLACA
IATHGKIRD
>AAK39511.1 Der f 11; paramyosin [Dermatophagoides farinae]
MNKKRDELAKLRKLLLEDVHIESEETAHHLRQKHQAQAIQEMQDQLDQLQKAKNKSDKEKQ
KFQAEVFEELLAQLETANKEKLTALKNVEKLEYTVHELNIKIEEINRTVIELTSHKQRLSQ
ENTELIKEVHEVKLQLDNANHLKTQIAQQLEDTRHRLEEEERKRASLENHAHTLEVELES
LKVQLDEESEARLELERQLTKANGDAASWKSKEYAELQAHADVEVEELRRKMAQKISEYEE
QLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKATRHAQQLEKRVAQLEKINLDLKNKLEE
VTMLMEQAQKELRVKIAELQKLQHEYEKLRDQRDQLARENKKLTDDLAEAKSQLNDAHRR
IHEQEIEIKRLENERDELSAAYKEAETLRKQEEAKNQRLIAELAQVRHDYEKRLAQKDEE
IEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLKKKYQAQITELELSLDAANKANIDLQK
TIKKQALQITELQAHYDEVHRQLQQAVDQLGVTQRRQALQAELEEMRIALEQANRAKRQ
AEQLHEEAVVRVNELTTINVNLASAKSKLESEFSALQADYDEVHKELRISDERVQKLTIE
LKSTKDLLIEEQERLVKLETVKKSLQEVRTLHVRIEEVEANALAGGKRVIKLESIRID
VEIEVEEERRRHAETDKMLRKKDHRVKELLLQ
>AI008864.1 Der f 11; paramyosin [Dermatophagoides farinae]
MSARTAKYMYRSSGAGASGDISVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK
AELQIQVMSLGERLEEAEGSSESVTEMNKKRDELAKLRKLLLEDVHIESEETAHHLRQKH
QAQAIQEMQDQLDQLQKAKNKSDKEKQKFQAEVFEELLAQLETANKEKLTALKNVEKLEYTV
HELNIKIEEINRTVIELTSHKQRLSQENTELIKEVHEVKLQLDNANHLKTQIAQQLEDTR
HRLEEEERKRASLENHAHTLEVELES LKVQLDEESEARLELERQLTKANGDAASWKSKEY
AELQAHADVEVEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAT
AHAQQLEKRVAQLEKINLDLKNKLEEVMTMLMEQAQKELRVKIAELQKLQHEYEKLRDQRD
QLARENKKLTDDLAEAKSQLNDAHRRRIHEQEIEIKRLENERDELSAAYKEAETLRKQEEA
KNQRLIAELAQVRHDYEKRLAQKDEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLK
KKYQAQITELELSLDAANKANIDLQKTIKKQALQITAEQAHYDEVHRQLQQAVDQLGVT
QRRQALQAELEEMRIALEQANRAKRQAEQLHEEAVVRVNELTTINVNLASAKSKLESEF

SALQADYDEVHKELRISDERVQKLTIELKSTKDLLIEEQERLVKLETVKKSLEQEVRTLH
VRIEEVEANALAGGKRVIAKLESRIRDVEIEVEEERRRHAETDKMLRKKDHRVKELLQ
EEDHKQIQLLQEMTDKLNKVKVYKRQMQEQEGMSQQNLTRVRRFQRELEAAEDRADQAE
SNLSFIRAKHRSWVTTSQVPGGTRQVFTTQEETNY

>ALU66112.1 Der f 23; peritrophin [Dermatophagoides farinae]
MKFNITIAFVSLAILVHSSYADIDHFDNDDQNSSTRPDDPTMIDVQTTTVQPSSMPT
TSESESTVKPTTTTVKPSPTTVKPTTTTVKLTSTTVKPSPTTVKPTTTTVKPSPTTTT
TTEQPEDEFECPTRFGYFADPKDPCKFYICSNWEAIHKSCPGNTRWNEKELTCT

>AI008866.1 profilin [Dermatophagoides farinae]
MSWQSYVDNQCQHVDTLAAIANIQDGSVWAKFEKDDKINPKELKTIADTIRQNPSGF
LETGIHIGGEKYICIQADNQLVRGRRGSSALCIVATNTCLLAAATVDGFPFGQLNNVIEK
LGDYLRSNYY

>AI008849.1 Der f 32; secreted inorganic pyrophosphatase [Dermatophagoides farinae]
MSTTNYSDHRGSFNSLDYRIYFKDNSNGKIISPWHDIPLFVDKSAKHYNMVEIPRWTN
EKMEIATAEPMSPKQDIKKGALRYVKNVFPKGYIWNYGAFQPTWENPNHIDQDTKTKG
DNDPIDVIEIGSRVAKRGDVPVKILGTIALIDEGETDWKIIAIDTRDELASQMNNVDDV
EKLLPGLLRATVEWFKIYKIPDGKPAKFAFNGEAKDREFAEKIVEETHQYWQEMMENKS
GEHKLDLKNVTLGNSFSINDEQAKQFLETRPSSDAVEPTPIADQVAIDKWHHVKLI

>AAP35082.1 Der f 27; serpin [Dermatophagoides farinae]
MKFFLLSFVLMVVAATATYAAHVGSGRDNNNNKPVPAEGFAKASNEFGFHLLKEVIQHR
SSSGSRGSSENVLFSPYSVAVALSMVHQGTQGSTAEQFKRVLYYDRVQQLNGGEYQTVAN
SVKQIQNQINQSDQSNQFDWGNMLMVDQQMPVKDQYKKIIEQYYDGQVMSVDFRKESKNV
MERINQFVSNKTHGLIDRMLEQPPSADTGLALINAVYFKGEWLKPFDSMRTEQSVFYGHH
GQEYKNVQYINGQGPYGYVEVPQWNSDLIQLPYKGEDIAFYGVLPREERNYDLDKIRQSIN
STFVDEIVGQITGSQSSTVYFPKIELSTSYQLPEILKSMGLQDVFTEADLSGITDKKPM
KIDDAIHKAKLILNEQGTEAGAGTYIQMAVLSALETSHTRFDHPFMYFIRHLPTGQILF
LGEIHDF

>AI008851.1 Der f 27; serpin [Dermatophagoides farinae]
MKFFLLSFVLMIVAATATYAAHVGSGRDNNNNKPVPAEGFAKASNEFGFHLLKEVIQHR
SSSGSRGSSENVLFSPYSVAVALSMVHQGTQGSTAEQFKRVLYYDRVQQLNGGEYQTVAN
SVKQIQNQIQSDQSNQFDWGNMLMVDQQIPVKDQYKKIIEQYYDGQVMSVDFRKESKNV
MERINQFVSNKTHGLIDRMLEQPPSADTGLALINAVYFKGEWLKPFDSMRTEQSVFYGHH
GQEYKNVQYINGQGPYGYVEVPQWNSDLIQLPYKGEDIAFYGVLPREERNYDLDKIRQSIN
STFVDEIVGQITGGQSSTVYFPKIELSTSYQLPEILKSMGLQDVFTEADLSGITDKKPM
KIDDAIHKAKLILNEQGTEAGAGTYIQMAVLSALETSHTRFDHPFMYFIRHLPTGQILF
LGEIHDF

>AGC56216.1 Der f 25; triosephosphate isomerase [Dermatophagoides farinae]
MGRKFFVGGNWKMNNGKTAIKEIVDFLKNGLPDSNVEVVVGVPAIYMLCKNILPDNIRV
AAQNCYKVKGAFTGEISPAMIKDVGAEWVILGHSERRNVFGESDQLIGEKEVEHALQEGL
HVIACIGELLEEREAGKTTEVFRQTQVISKHVKDWFKVVLAYEPVWAIGTGKTASPQQA
QEVHQKLRCFSENVSPQIAETIRIYGGSVTANNAKELASQADVDGFLVGGASLKPEFV
QIVNARQ

>AI008860.1 Der f 25; triosephosphate isomerase [Dermatophagoides farinae]
MVRKFFVGGNWKMNNGSRATNEDLIKTLNGLPNDVDDVVGVPSIYMAEVRQKLPKTIGV
AAQNCYKVPKGAFTGEISPAMIKDVGAEWVILGHSERRNVFGESDQLIGEKEVEHALQEGL
HVIACIGELLEEREAGKTTEVFRQTQVISKHVKDWKSVVLAYEPVWAIGTGKTASPQQA
QEVHQKLRCWFSENVSPQIAETIRIYGGSVTANNAKELASQADVDGFLVGGASLKPEFV
QIVNARQ

>BAA04557.1 Der f 10; tropomyosin [Dermatophagoides farinae]
FFFVAAKQQQPSTKMEAIKKKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRA

LQKKIQIENELDQVQEQLSAANTKLEEKALQTAEGDVAALNRRIQLIEEDLERSEER
LKIATAKLEEASQSADESERMRKMLEHRSITDEERMDGLENQLKEARMAEDADRKYDEV
ARKLAMVEADLERAEERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQI
RIMTAKLKEAEARAFAERSVQKLQKEVDRLEDELVHEKEKYKSISDELQDTFAELTGY
>BAA09920.1 Der f 3; trypsin [Dermatophagoides farinae]
MMILTIVVLLAANILATPILPSSPNATIVGGVKAQAGDCPYQISLQSSSHFCGGSILDEY
WILTAHCVNGQSACKLSIRYNTLKHASGGEKIQVAEIQHENYDSMTIDNDVALIKLKT
PMTLDQTNAPVPLPAQGSQDVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD
QLYSKAGADVSENMICGGDVANGGVDSCQGDSGGPVVDVATKQIVGIVSWGYGCAKRGYP
GVYTRVGNFVDWIESKRSQ
>AAA99805.1 Der f 3; trypsin [Dermatophagoides farinae]
IVGGVKAKAGDCPYQISLQSSSHFCGGSILDEYWILTAHCVNGQSACKLSIRYNTLKHA
SGGEKIQVAEIQHENYDSMTIDNDVALIKLKTTPMTLDQTNAPVPLPPQGSQDVKVGDKI
RVSGWGYLQEGSYSLPSELQRVDIDVVSREQCDQLYSKAGADVSENMICGGDVANGGVD
CQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYPGVYTRVGNFVDWIESKRSQ
>ABY28115.1 Der f 3; trypsin [Dermatophagoides farinae]
MMILTIVVLLAANILATPILPSSPNATIVGGVKAQAGDCPYQISLQSSSHFCGGSILDEY
WILTAHCVNGQSACKLSIRNNTLKHASGGEKIQVAEIQHENYDSMTIDNDVALIKLKT
PTTLDQTNAPVPLPAQGSQDVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD
QLYSKAGADVSENMICGGDVANGGVDSCQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYP
GVYTRVGNFVDWIESKRSQ
>ACK76291.1 Der f 3; trypsin [Dermatophagoides farinae]
MMILTIVVLLAANTWATPILPSSPNATIVGGVKAKAGDCPYQISLQSSSHFCGGSILDEY
RILTAHCVNGQSACKLSIRYNTLKHASGGEKIQVAEIQHENYDSMTIDNDVALIKLKT
PMTLDQTNAPVPLPPQGSQDVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD
QLYSKAGADVSENMICGGDVANGGVDSCQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYP
GVYTRVGNFVDWIESKRSQ
>ACK76292.1 Der f 3; trypsin [Dermatophagoides farinae]
MMILTIVVLLAANTWATPILPSSPNATIVGGVKAKAGDCPYQISLQSSSHFCGGSILDEY
WILTAHCVNGQSACKLSIRYNTLKHASGGEKIQVAEIQHENYDSMTIDSDVALIKLKT
PMTLDQTNAPVPLPPQGSQDVKVGDKIRVSGWGYLQEGSYSLPSELQRVDIDVVSREQCD
QLYSKAGADVSENMICGGDVANGGVDSCQGDSGGPVVDIATKQIVGIVSWGYGCAKRGYP
GVYTRVGNFVDWIESKRSQ
>AGI78542.1 Der f 24; ubiquinol-cytochrome c reductase binding protein
[Dermatophagoides farinae]
MVHLTKTLRFINNPGRKFFYYGLQGYNKYGLYYDDFYDYDAAHLEAVRRLPPDLYDQHT
YRLVRSQLEITKQFLPKEQWPSYEEDMDKGRFLTPYLDEVMKEKKEKEEWINFLSKD
>AB084963.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIFCAIVMAVSVSGFIVDVEDTKWRNAFDRMLMEEFGEKIDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK
DLAELAKKVKAVKSDD
>AB084964.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIFCAIVMAVSVSGFIVDVEDTKWRNAFDRMLMEEFEEKMDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK
DLAELAKKVKAVKSDD
>AB084966.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIFCAIVMAVSVSGFIVDVEDTKWRNAFDRMLMEEFEEKIDQIEHGLMLSEQYKE
SEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETA VSTIEILVK
DLAELAKKVKAVKSDD
>AB084967.1 Der f 21; unknown function [Dermatophagoides farinae]

MKFIIIFCAIVMAVSVSGFIVDVEDKWRNAFDRMLMEEFEEKIDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK
DLAELAKKVKAVKSDD
>AB084968.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIIFCAIVMAVSVSGFIVDVEDKWRNAFDRMLMEEFEEKMDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVPTIEILVK
DLAELAKKVKAVKSDD
>AB084969.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIIFCAIVMAVSVSGFIVDVEDKWRGAFDRMLMEEFEEKMDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK
DLAELAKKVKAVKSDD
>AHC94806.1 Der f 21; unknown function [Dermatophagoides farinae]
MKFIIIFCAIVMAVSVSGFIVDVEDKWRNAFDHMLMEEFEEKMDQIEHGLMLSEQYKE
LEKTKSKELKEQILRELTIAENYLRGALKFMQQEAKRTDLNMFERYNFETAVSTIEILVK
DLAELAKKVKAVKSDD
>AAP35068.1 Der f 5; unknown function [Dermatophagoides farinae]
MKFIIAIAVCTLAVVCVSGEPKKHDYQNEFDFLLMQRIHQMRKGEEALLHLHQINTFEE
NPTKEMKEQILASEMDTIIALIDGVRGVLNRLMKRTDLIDIFERYNVEIALKSNEILERDL
KKEEQRVKKIEV
>ATI08931.1 Der f 36; unknown function [Dermatophagoides farinae]
MKFYNILTVATIVILVAFFDNVHADSQAQEQCRQLHHVDIDPSGTFKLNNNCRNLNCNIHG
QIYGHNINEGRTCMIGQTNVVCQNGECVGHNRQHVGHIDIELISASLYEKANAYATVCIM
NNSLPISLPIQDRRNCISCSTHVKENTNYPVWNEVCVGSNYL FVSDSRVTTEVWDHHS
NNNVFLGGVTLTIDQLVNHGDNHRQINLAMAGGHNPGLSTRITWTQRT
>ABG35122.1 Der f 22; unknown function [Dermatophagoides farinae]
MNRFLIVCMALFCLAAAVQADETENVQYKDCGHNEIKSFFVTGGNPNQKSCVIHKHKNQL
RISFVANENTGNKINTRFICNLGGIELGWPGIDGTACQGHGLSCPLTKGQTYNYHLDFN
LGDDVPTANVTATVRLENGHGGDLLCGRMHISLQN
>P16312.1 Der m 1; cysteine protease, partial [Dermatophagoides microceras]
TQACRINSGNVPSELDLRSLRTVTPIRMQG
>AAD38942.1 Der p 4; alpha-amylase [Dermatophagoides pteronyssinus]
KYHNPFIGNRSVITHLMEWKYDDIGDECERFLGPYGYGGVQVSPVNEHAILDRRPWYER
YQPVSYDIRTRSGDEQQFRMVKRCNKAGVRIYVDIVLNHMTGAQSGKGTNGHHYDGNTL
QYPGVVPGPNDFHGHESCPTQDLEIHDTNPKEARNCRSLGLRDLKQQSEYVRQKQVDFL
NHLIDIGVAGFRSDASTHQWPDDLRSIYSRLHNLNKEFFPENSQPFYHETIYYGGNGIN
SNEYTSLGRIIEFRFYKEITNVFRGNPLHLWLNKFGTEWGLVPSGDALVMIDSHDLRVGH
TGKLGFNINCFEGRLLKAATAFMLAWNYGVPRVMSSYFWNQI IKDGKDVNDWVGPPSDKN
GNILSVHPNPDMTCNHEWICEHRWREIYNMVKFRMIAGQEPVHNWWDNGDYQIAFSRGNR
AFIAINLQKNQNLQQLLHTGLPAGTYCDIISGNLIDNKCTGKSIHV DKNQADVYVGH
EFDAFVAYHIGARIVS
>QAT18644.1 Der p 33; alpha-tubulin [Dermatophagoides pteronyssinus]
MRECISVHVQAGVQIGNACWELYCLEHGIQPDGQMP SDKTIGTGDDSFNTFFSETGSGK
HVPRAVYVDLEPTVVDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIVDLVLD
RIRKLSQDCTGLQGFLIFHSFGGGTSGSFTSLLMERLSVDYGGKSKLEFAVYPAPQVSTA
VVEPYNSILTTHTLEHSDCAFMDNEAIYDICRRNLDIERPTYTNLNLIGQIVSSITA
SLRFDGALNVDLTFQTNLVPYPRIHPLVTYAPVISA EKAYHEQLTVSEITNTCFEPAN
QMVKCDPRHGKYMACL LLYRGDVVPKDVNAAIASIKTKRSIQFVDWCPTGFKVGINYQPP
TVVQVVIWLKYNVLFVCCPTLLPSLKLGLDWIINLI
>AAM21322.1 Der p 14; apolipophorin [Dermatophagoides pteronyssinus]
LLTACLLGLGQAQHCEVACPR SIPQLINPKA QSTYVYSLDAKT VLTTPRDSQKVTIKGDAE

VAFVSDCEAVLRLQNVAIDGVPNGAELAAELAAKPFAFGYFNIGRILGVCPADDDQDWSLN
VKKAIVSSLQALSDGNEKAEEDFSGRCPTFYRKIRSQDDNTVVEIKRKDLNLCDDRRRI
DLRQTPDQALGQLKELMRHYMHPMDSLSRMTLKDKVTEVDCEERHVLVHRSNKPVHM
SYVKMMLKQNKDGVAAADLGPNAQPKRPLYSLFDHKHKNPTETDVVEVLKCLCSEITEPQA
SIETSFTFQKLVKDLRYLSAEETASVDESVKTSVCPAHAHRLRELFLDASAFASDGSIR
TLVKAHENQELSITRSTALFTVAAIKAAPNKETVQVLLPVIASEKTIRPMLLGFVSVLVR
YCEKTNDCATNSGVKDARDAYLARLAVARDASERMTIVRALENLNVNTDGDVNMVNAME
IIKSTDAEPAMRAAAVNALPNDASHMDRYKSLVMDESMPEARIAAFQKMMKNGGMSHIK
DLFAVKGECMKNYVLYVDNLKSKNDLRRQTVGEDVELPEKPKREIGITRNIAREYGPY
TFEYDVIYPETHENVTRSINGRLIRSKNDQLKELVEFQVTQSGFDRELNAMSLEKKSF
QSVMQFLRDMLKMLSQIRKNADDNHMKITVQINGKNVYFTDLFQDTKKMKELLMKRVEK
IINDKKVDRSIGGVL LSKLVLPITITGLPLMYKFGDNLVVRDGEFSGEKGDRNIRMNGG
VVAGLYGKMKMLMVKDHKMGYEDAKASYTPMIDMNVQKQEHSLVRFNMKMDMDQHTVMRF
KQSLREKRATGEEKDYENEITPDARSDRCFSFFLLDYCRKASHIKGLMLPNVEYYVVKPE
KEVTALEMLKSETQDKTRRYIAEMTAVGSPSNKQAKAELEVTKGEQYRVSVKLPEHEFN
TEFTINADKNNLKMMDLPNVLQADLTGSFEHDKENNVKRNRLNLQYKFAGDEKPHTVDY
ENEFLFNLKRSSKEKNSAVEYRAKYMSSHFPILNHKVNQFKYRPFKVNELNLEGEFGRE
LQHKFRLMRNSQMEVEEVRPFKMHGNSDIKLMANDLDIDYDLKSEFKYESNKGTPIELQY
KVS GKDRSKRAAEMNAEDVEGVIDYKNSGSPIDSKMHAHLKVKGNNGYDSELKQTEPQQ
YEGKMTLSKNDKKIFITHKTEMKPTSTFLLKTDADVSYSESDMKKHMHMEFKKENDIYT
LRSTVERDQGLFYENYLVHKGKLNLYRRNDRKILLDLDNALSPREGTMKLNKIDREY
NFVLKRDPMRYRDITVEGNENAYVKNGLHLSLIDPSTLSLVTKADGQIDMTVDLISPIT
KRASLKVDSKKNLNFHEGELSASLVNPRLSWHQYTKRDSREYKTDVDLSLRSSDIKAVKIT
MPDYNYSKIHYSRQNDQISMDIDGTLIEGHAKGTIKEGKIHIKGRQSDFEIESNYRYEDGK
MLIEPVKSENGKLEGLSRKVPSTLLETPRVKMMQYDRHSPVKMFKLDYDGIHLEKHT
DLLYEPGVQYKIIIGNKIKDDGSHYSIDIQKPRKAFKLDADMMNFKLNVNKPEDSNKAQ
FSYTFNDYTETEEYFDPHRAYYINWISSIRKYIQNFIVEDH

>ACD50950.1 Der p 20; arginine kinase [Dermatophagoides pteronyssinus]

MVDPATLSKLEAGFQKLQNAQDCHSLLKKYLTRDVFQDLKNKKTDMGATLLDVIQSGVEN
LD SGVGIYAPDAQSYKTF AALFDPIIDDYHKGFKPTDKHPKTD FGN IENFVNVDPKNEYV
LSTRVRCGRSLNGYFPNPLMTEAQYKEMETKVKGLATFEGELKGTYYPLLGMKATQQQ
LIDDHFLFKEGDRFLQAANACRYWPVGRGIFHNDKKTFLMWVNEEDHLRIISMQKGGDLK
EYVGRLVKAVKHIEQKIPFSRDDRLGLFTFCPTNLGTTIRASVHIKLPKLAADRKKLEEV
AGRYNLQVRGTAGEHTESVGGIYDISNKRMMGLTEYQAVKEMQDGI LELIKMEKSM

>AAA80264.1 Der p 7; bactericidal permeability-increasing like [Dermatophagoides pteronyssinus]

MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSDKFER
HIGIIDLKGELDMRNIQVRGLKQMKRVGDANVKSE DG VVKAHLLVGVHDDVVSMEYDLAY
KLGDLHPNTHVISDIQDFVVELSLEVSEEGNMTLTSFEVRQFANVVNHIGGLSILDPIFA
VLSDVLT AIFQDTVRAEMTKVLAPAFKKE LERNQ

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

MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSDKFER
HIGIIDLKGQLDMRNIQVRGLKQMKRVGDANVKSE DG VVKAHLLVGVHDDVVSMEYDLAY
KLGDLHPNTHVISDIQDFVVELSLEVSEEGNMTLTSFEVRQFANVVNHIGGLSILDPIFA
VLSDVLT AIFQDTVRAEMTKVLAPAFKKE LERNQ

>AAY84565.1 Der p 15; chitinase [Dermatophagoides pteronyssinus]

MKTSCAILILMACFGLMNAAVKRDNHNSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
CTHLMYGF AKIDEYKYTIQVFDPYQDDNHNTWEKHGYERFNNLRLKNPELTTMISLGGWY
EGSEKYS DMVANPTYRKQFVQSVLDFLQ EYKFDGLDL DWEYPGSRLGNPKIDKQNYLTLV

RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA
PLYKRPDETDELHTYFNVNYTMHYLLNNGATRDKLVMGVVPFYGRAWSIEDRSKVKLGDP
KGMSPPGFITGEEGLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYYDDLASIS
KLAFLKELGVSVMISLENDDFKGGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP
TPTTPSTPSTTTPTPTTPSTPSTTTPTPTTPSTPSTTTPTPTTDDSTSETPKYTTYVDGH
LIKCYKEGDLPHPTNIHKYLVCEYVNGGWVHIMPCPPGTIWCQEKLTCITE

>AAY84564.2 Der p 15; chitinase [Dermatophagoides pteronyssinus]
MKTSCAILILMACFGLMNAAVKRDHNNYSKNPMRIVCYVGTWSVYHKVDPYTIEDIDPFK
CTHLMYGFIDEYKYTIQVDFPYQDDNHNTWEKHGYSERFNNLRLKNPELTTMISLGGWY
EGSEKYSMDVANPTYRQQFVQSVLDFLQYKFDGLDLWEYPGSRLGNPKIDKQNYLTLV
RELKEAFEPFGYLLTAAVSPGKDKIDVAYELKELNQLFDWMNVMTYDYHGGWENVFGHNA
PLYKRPDETDELHTYFNVNYTMHYLLNNGATRDKLVMGVVPFYGRAWSIEDRSKVKLGDP
KGMSPPGFITGEEGLSYIELCQLFQKEEWHIQYDEYYNAPYGYNDKIWVGYYDDLASIS
KLAFLKELGVSVMISLENDDFKGGHCGPKYPLLNKVHNMINGDEKNSYECLLGPSTTTP
TPTTPSTPSTTTPTPTTPSTPSTTTPTPTTPSTPSTTTPTPTTPSTPSTTTPTPTTPST
STTTPTPTTDDSTSETPKYTTYVDGHLIKCYKEGDLPHPTNIHKYLVCEYVNGGWVHIM
PCPPGTIWCQEKLTCITE

>AAY84563.1 Der p 18; chitin-binding protein [Dermatophagoides pteronyssinus]
MTRLSFTVLIFLAAYFGSNIRPNVATLDPKTVCCYYESWVHWRQGDGKMDPEDIDTSLCSH
IVYSYFGIDASSHEIKLLDQYLMITLHDMEHFTKHKGNAMIAVGGASMSDQFSKTA
EHYRETFVSTIDLMTKYGFDGVMIDWSGMQAKSDNFVKLLDKFDEKFAQTSFVMGVT
PATIASYDNYNIPASISNYVDFMNVLTLDYDGPWAYTVGHASALPEQLKTLEAYNKRGA
PRHKMVMVAVPFARTWILEKMDKQDVGDKASGPGPKGQFTQTPGFLSYNELCVQIQAE
TNAFSITRDHDNTAIYAVYVHDNHAEWISFEDRHTLGDKARNITEQGYGMSVYTL
SNEDVHGVCGDKNPLHAINSNYFRGIVTEPTVVTVPVTHTEHVTDIPGVFHCHQEGFFRDKTYCA
KYECKKGFDFGLEQTVHHCNHSQAFDEVSRTCVDHAKIPGC

>P49277.1 Der p 6; chymotrypsin, serine protease [Dermatophagoides pteronyssinus]
AIGXQPAEAEAPFQISLMK

>AAA28296.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
MSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAA
TESAYLAHRNQSLDLAEQELVDCASQHGCHGDTIPR

>AAB60215.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
MKIVLAIASLLALSAVYARPSSIKTFEYKAFNKSYATFEDEEAARKNFLESVKYVQSN
GGAINHLSLDEFKRNFLMSAEAFEHLKTQFDLNAETNACSINGNAPAEIDLRQMRTV
TPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEY
IQHNGVVQESYYRYVAREQSCRPNARQFGISNYCQIYPPNVNKIREALQTHSAIAVII
GIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNAQGVYWIIVRNSWDTNWGDNGY
YFAANIDLMMIEEYPYVVIL

>CAD38361.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNACSINGNAPAEIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYYRYVAEQSCRPNARQFGISNYCQIY
PPNVNKIREALQTHSAIAVIIIGIKDLDAFRHYDGTIIQEDNGYQTNHAVNIVGYSNA
QGVYWIIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>CAD38362.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNACSINGNAPAEIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPQIEYIQHNGVVQESYYRYVAEEQSCRPNARQFGISNYCQIY
PPNVNKIREALQTHSAIAVIIIGIKDLDAFRHYDGETIIQQDNGYQTNHAVNIVGYSNA
QGVYWIIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>CAD38363.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNACSINGNAPAEIDLRQMETVTPIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ

ELVDCASQHGCHGDTIPQIEYIQHNGVVQESYYRYVAQEQSCRRPNAQRFGISNYCQIY
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38364.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQM QTVTPIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYYRYVAEEQSCRRPNAQRFGISNYCQIY
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQQDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38365.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAEEQSCRRPNAQRFGISNYCQIY
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQQDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38366.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQMETVTPIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAEEQSCRRPNAQRFGISNYCQIY
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38367.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQM QTVTPIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCANQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAQEQSCRRPNAQRFGISNYCQIY
PPNVNKIREALAQTHSAIAVIIGIKDLDAFRHYDGETIIQEDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38368.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYYRYVAQEQSCRRPNADRFGISNYCQIY
PPNVNKIEEALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38369.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPQIEYIQHNGVVQESYYRYVAEEQSCRRPNADRFGISNYCQIY
PPNVNKIQEALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38370.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPEGIEYIQHNGVVQESYYRYVAQEQSCRRPNADRFGISNYCQIY
PPNVNKIEEALAQTHSAIAVIIGIKDLDAFRHYDGQTIIQEDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>CAD38371.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPASIDLRQMRTVTTIRMQGGCGSCWAFSGVAATESAYLAVRNQSLDLAEQ
ELVDCASQHGCHGDTIPQIEYIQHNGVVQESYYRYVAEEQSCRRPNADRFGISNYCQIY
PPNVNKIQEALAQTHSAIAVIIGIKDLDAFRHYDGETIIQQDNGYQNTNYHAVNIVGYSNA
QGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>AAX47076.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
NEIAXAKIDLRQMRTVTPIXMQGGCGSCWALSGVAATESAYLAYGNXSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNVNK
IREALAQTHSAIAVIIGIKDLDAFRHYDGRITIIQRDNGYQPNYHAVNIVGYSNAQGVYDIWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL
>ABA39435.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
RPSSIKPFEYKKA FNKSYATFEDEEAARKNFLESVKYVQSNNGGAINHLSLDEFKNR

FLMSAEAFEHLKTQFDLNAETNAC SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGV
AATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVARE
QSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRTIIQ
RDNGYQPNYHAVNIVGYSNAQGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVV
IL

>2AS8_B Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQ
ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIY
PPNANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNA
QGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>ABV66255.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
TNAC SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQ
ELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQI
YPQNVNKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSN
AQGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVVIL

>ACG58378.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
MKITLAIASLLALS AVYARPSSIKTFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSN
GGAINHLS DLSLDEFK N RFLMSAEAFEHLKTQSDLNAETNAC NINGNAPAEIDLRQMRTV
TPIRMQGGCGSCWAFSGVAATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEY
IQHNGVVQESYYRYVAREQSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVII
GIKDLDAFRHYDGRTIIQRDNGYQPNYHAVNIVGYSNAQGV DYWIVRNSWDTNWGDNGY
GYFAANIDLMMIEEYPYVVIL

>CAQ68250.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
RPSSIKTFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSNGGAINHLS DLSLDEFK N R
FLMSAEAFEHLKTQFDLNAETNAC SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFSGV
AATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVARE
QSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRTIIQ
RDNGYQPNYHAVNIVGYSNAQGV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPYVV
IL

>AFJ68065.1 Der p 1; cysteine protease [Dermatophagoides pteronyssinus]
EARPSSIKTFEEYKKA FNKSYATFEDEEAARKNFLESVKYVQSNGGAINHLS DLSLDEFK
NRFLMSAEAFEHLKTQFDLNAETNAC SINGNAPAEIDLRQMRTVTPIRMQGGCGSCWAFS
GVAATESAYLAYRNQSLDLAEQELVDCASQHGCHGDTIPRGIEYIQHNGVVQESYYRYVA
REQSCRRPNAQRFGISNYCQIYPPNANKIREALAQTHSAIAVIIIGIKDLDAFRHYDGRTI
IQRDNGYQPNYHAVNIVGYSNAQSV DYWIVRNSWDTNWGDNGYGYFAANIDLMMIEEYPY
VVIL

>ADK92390.1 Der p 13; fatty acid-binding protein [Dermatophagoides pteronyssinus]
MASIEGKYKLEKSEKFDEF LDKLGVGF MVKTA AKTLKPTFEVAKENDQYVFRSLSTFKNT
EIKFKLGEFEEDRADGKR VKTVINKDGNK FVQTQFGDKEVKIVREFNGDEVVVTASCD
GVTSVRTYKRI

>AAG02250.1 ferritin [Dermatophagoides pteronyssinus]
MAANPESTTKTSRVRMNFHKECEAGINKQINLELYASYVYQQMAFHFNREDVALPGFEKF
FHESSEEEEREHA EKLMKLQNRGGRIVLQDIPKPVQQDWSSGLEALKASLELEKTVNQSL
LDLHDLATKHND AQFADFIESNYLHEQVEAIKKLADYITNLERCGSVGLGEYLFDRHTLQ

>AAB32224.1 Der p 8; glutathione S-transferase [Dermatophagoides pteronyssinus]
MSQPILGYWDIRGYAQPIRLLLTYSGVDFVDKRYQIGPAPDFDRSEWLNEKFNGLDFPN
LPYYIDGDMKMTQTFAILRYLGRKYKLNGSNDHEEIRISMAEQQTEDMMAAMIRVCYDAN
CDKLPDY LKSLPDCLKLMSK FVGEHAFIAGANISYVDFNLYEYLCHVKVMVPEVFGQFE
NLKRYVERMESLPRVSDYIKKQPKTFNAPTSKWNASYA

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

MSQPILGYWDIRGYAQPIRLLLLTYSGVDFVDKRYQIGPAPDFDRSQWLNEKFNGLDFPN
LPYYIDGDMKMTQTFAILRYLGRKYKLNGSNDHEEIRISMAEQQTKDMAAMIRVCYDAN
CDKLPDYKSLPDLKLMKSFVGEHPFVAGANISYVDFLYLEYLCRVKVMVPEVFGQFE
NLKRYVERMESLPRVSDYIKKQPKTFNAPTSKWNASYA

>QAT18639.1 Der p 28; heat shock protein 70 [Dermatophagoides pteronyssinus]

MPSKTSKAPAIGIDLGTYSVGVFQNGSVEIANDQGNRTTPSYVAFDTERLIGDAAK
NQVAMNPANTIFDAKRLIGRRFDEPSVKSDMKHWPFKVSESGKPKIEVEFKGEQKRFWP
EEVSAMVLTMMKETAEAYLGQKVTDAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEP
TAAAIAYGLDKKGGGKENVLIFDLGGGTFDVSFLTIDNGIFEVKSTAGDTHLGGEDFDNR
LVNHVFQEFKRKFGKDIMSNKRALRRLTACERAKRTLSSSTQTTIEIDSLHEGTDYFST
ITRARFEELCSDLFRSTLEPEKALRDAKLDKSKIDEIVLVGGSTRIPKIQKLLSDFENG
KELNKSINPDEAVAYGAQAAILTGDTSNVVDLDDVAPLSLGIETAGGVMTTLIK
NTTIPTKQTQFTTYADNQPAVTIQVYEGERAMTKDNRLGTFDLTGIPPAPRGVQPQIEV
TFDVDANGILNVSVDKSTGRQNKITITNDKGRLSKADIEKMNVAEQYREEDERQRERI
SAKNQLEAYAFQLKSTMEEEAIKSKLSEEDRKTVLNKVEETLRWLDNQLADKEEYHRQ
KELESACRPIMTKIYQQQQHPGAPGANGSCGSNAYPGYGGFNSNNDGPVVEEVN

>QAT18643.1 Der p 32; inorganic pyrophosphatase [Dermatophagoides pteronyssinus]

MSIRSINLLTRQTIPLSLISIIGINNNFHRYIYFSFKHPHQSFKYHHLSSASLSINFSI
SKNVHYKQPPYINIGNKVHFVQNHQLRKFATKTNNKSTNYSVDNRGALNSLDYRIYFKN
DSNGKIIISPWHDIPLFADKSAKQYNMVEIPRWTNEKMEIATAEPMTPKQDVKKGALRY
VKNVFPKGGYIWNYGAFPTWENPNHIDQGTAKAGDNDPIDVIEIGSRIAKRGDVIPVKI
LGTIALIDEGETDWKIITIDTRDELQGMNVDDEKLLPGLLRATVEWFRIYKIPDGKP
ANKFAFNGEAKDREFAEKVVEETHQYWREMMENKAGEHQLDLKNITLGNSTINDEQAKQ
FLETRPASNTVEPNPIADQVAIDKWHHVKLI

>QAT18638.1 Der p 26; myosin light chain [Dermatophagoides pteronyssinus]

MADLRPEVEKARLHFDIYDFEGQGKVDYHLLGDLLRSLDLRPTQEMVAKNGWEKKKGQK
YMTFEEFLPIYSQVKKDKDCGAYEDLVEGLKVYDKAENGTMMEAELAHVLLSLGENWMIR
K

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

MYKILCLSLVAAVARDQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEAN
QNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVVKIAPKSENV
VVTVKVMGDDGVLACAIATHAKIRD

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

SEVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPLVKGQYDIKYTWNVVKIAPKSENVVVTVKVMGDDGVLACA
IATHAKIRD

>CAD38372.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]

DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACHYMNCPVNGQYDIKYTWNVVKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIRD

>CAD38373.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]

DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACHYMNCPVNGQYDIKYTWNVVKIAPKSENVVVTVKVLGDNGVLACA
IATHAKIQD

>CAD38374.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]

DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG
LEVDVPGIDPNACHYMNCPVNGQYDIKYTWNVVKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD

>CAD38375.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]

DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG

LSVDVPGIDPNACHYMNCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38376.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKEVLVPGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACHYMNCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38377.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACHYMNCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38378.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKEVLVPGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACNYMKCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIRD
>CAD38379.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKEVLVPGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACNYMKCPVNGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38381.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKEVLVPGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG
LEVDVPGIDPNACNYMKCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38382.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKEVLVPGCHGSEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACNYMKCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>CAD38383.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGNEPCIHSGKPFQLEALFEANQNSATAKIEIKASIDG
LSVDVPGIDPNACNYMKCPVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA
IATHAKIQD
>ABA39437.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPVKGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA
IATHAKIRD
>CAK22338.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
MMYKILCLSLLLVAAVAADQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEALFEA
NQNTKNAKIEIKASIDGLEVDVPGIDPNACHYVKCPVKGQQYDIKYTWNVPKIAPKSEN
VVVTVKVLGDNGVLACAIATHAKIRD
>ABG76196.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
RDQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEALFEANQNSKTAKIEIKASID
GLEVDVPGIDPNACHYMKCPVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDNGVLAC
AIATHAKIRD
>1A9V_A Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
SQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA
IATHAKIRD
>ABY53034.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
MYKILCLSLLLVAAVARDQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEADFEAN
QNRKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPVKGQQYDIKYTWNVPKIAPKSEN
VVVTVKVMGDDGVLACAIATHAKIRD

>CAQ68249.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDNGVLACA
IATHAKIRD

>AFJ68067.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGSEPCIHRGKPFQLEALFEANQNSKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVLGDNGVLACA
IATHAKIRD

>AFJ68070.1 Der p 2; NPC2-like [Dermatophagoides pteronyssinus]
DQVDVKDCANHEIKKVLVPGCHGSETCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG
LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKVMGDDGVLACA
IATHAKIRD

>AA073464.1 Der p 11; paramyosin [Dermatophagoides pteronyssinus]
MSARTAKYMYRSSGAGASGDISVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK
AELQIQVMSLSERLEEAEGSSESVTENMKKRDSSELAKLRKLLLEDVHMESEETAHHLRQKH
QAAVHEMQDQLDQLQKAKNKSDEKQKQFAEVFELLSQLETANKEKLTALKSVEKLEYTV
HELNIKIEEINRTVIELTSHKQRLTQENTELIKEVHEVKLQLDNANHLKQQIAQQLEDTR
HRLEEEERKRSSLENHAHTLEVELESKLVQLDDESEARLELERQLTKANGDAASWKSKEYE
AELQAHADEVEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAA
AHAQQLEKRVAQLEKINLDLKDKEEVTMLMEQAQKELRIKIGELQKLQHEYEKVRDQRD
QLARENKKTDDLAEAKSQLNDAHRRHEQEIEIKRLENERDELSAAYKEAETLRKQEEA
KNQRLIAELAQVRHDYKRLAQKDEEIEALRKQYQIEIEQLNMRLAEAEAKLKTEIARLK
KKYQAQITELELSLDAANKANIDLQKTIKKQALQITELQAHYDEVHRQLQQAVDQLGVTQ
RRCQALQAELEEMRIALEQASRAKRQAEQLHEEAVVRVNELTTINVNLASAKSKLESEFS
ALQADYDEVHVELRISDERVQKLTIELKSTKDLLIEEQERLVKLETVKKSLEQEVRTLHV
RIEEVEANALAGGKRVIAKLESRIRDVEIEVEEERRRHAETEKMLRKKDHRVKELLLQNE
EDHKQIQLLQEMTDKLNKVKVYKRQMQEQEGMSQQNLTRVRRFQRELEAAEDRADQAES
NLSFIRAKHRSWVTTTSQVPGGTRQVFTTQEETTNY

>4ZCE_A Der p 23; peritrophin [Dermatophagoides pteronyssinus]
SFTKFECPSRFGYFADPKDPHKFYICSNWEAVHKDCPGNTRWNEDEETCT

>ACB46292.1 Der p 23; peritrophin [Dermatophagoides pteronyssinus]
MKFNIIIVFISLAILVHSSYAANDNDDPTTTVHPTTTEQPDDKFECPSRFGYFADPKDP
HKFYICSNWEAVHKDCPGNTRWNEDEETCT

>COMPARE009 Der p 23; peritrophin [Dermatophagoides pteronyssinus]
MKFNIIIVFISLAILVHSSYAANDNDDPTTTVHPTTTEQPDDKFECPSRFGYFADPKDP
HKRYICSNWEAVHKDCPGNTRWNEDEETCT

>QAT18637.1 Der p 25; triosephosphate isomerase [Dermatophagoides pteronyssinus]
MGRKFFVGGNWKMNRSRATNDDLKILTNTPLDPNTEVVVGVPSIYLADVRHKLSKLSIGV
AAQNCYKVAKGAFTEGESPAMIKDVGAEWVILGHSERRNVFGENDQLIGEKVEHALNEGL
NVIACIGELFEEREAGKTTEVVRFTQVQVISHKVKDWSKVVLAYEPVWAIGTGKTASPQQA
QEVHQQLRQWFSTNISQIAETIRIYGGSVTASNAKELASQADVDFLVGGASLKPEFV
QIVNARQ

>AAB69424.1 Der p 10; tropomyosin [Dermatophagoides pteronyssinus]
MEAIKKKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV
QEQLSAANTKLEEKALQTAEGDVAALNRRIQLEEDLERSEERLKIATAKLEEASQSA
DESERMKMLEHRSITDEERMEGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVLEEEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE
FAERSVQKLQKEVDRLDEDELVHEKEKYKSISDELDTFAELTGY

>CAA75141.1 Der p 10; tropomyosin [Dermatophagoides pteronyssinus]
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV

QEQLSAANTKLEEKEKALQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA
DESERMRKMLEHRSITDEERMEGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE
FAERSVQKLQKEVGRLEDELVHEKEKYKSISDELDTFAELTGY
>ABB52642.1 Der p 10; tropomyosin [Dermatophagoides pteronyssinus]
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV
QEQLSAANTKLEEKEKALQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA
DESERMRKMLEHRSITDEERMEGLENQSKARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE
FAERSVQKLQKEVGRLEDELVHEKEKYKSISDELDTFAEL
>ACI32128.1 Der p 10; tropomyosin [Dermatophagoides pteronyssinus]
MEAIKNKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRALQKKIQQIENELDQV
QEQLSAANTKLEEKEKAPQTAEGDVAALNRRIQLIEEDLERSEERLKIATAKLEEASQSA
DESERMRKMLEHRSITDEERMEGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAHEQQIRIMTTKLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKSISDELDTFAELTGY
>AAA19973.1 Der p 3; trypsin [Dermatophagoides pteronyssinus]
MIIYNILIVLLLAINTLANPILPASP NATIVGG EKALAGECPYQISLQSSSHFCGGTILD
EYWILTAACHVAGQ TASKLSIRYNSLKHSLGGEKISVAKIFAHEKYDSYQIDNDIALIKL
KSPMKLNQKNAKAVGLPAKGS DVKVG DQVRVSGWGYLEEGSYSLPSELRRVDIAVSRKE
CNELYSKANA EVDNMICGGDVANGGK DSCQGDSSGGPVVDVKNQVVGIVSWGYG CARKG
YPGVYTRVGNFIDWIESKRSQ
>ALA65345.1 Der p 24; ubiquinol-cytochrome c reductase binding protein
[Dermatophagoides pteronyssinus]
MVHLTKTLRFINNPGRKFFYGLQGYNKYGLYYDDFYDYTPAHLEAVRRLPPDLYDQHT
YRVIRASQLEITKQFLPKEQWPSYEEDMDKGRFLTPYLDEVMEKKEKEEWNFLSKD
>CAA35692.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]
LFLENKDPKPLKKISIMKFIIAFFVATLAVMTVSGEDKKHDYQNEFDL LMERIHEQIKK
GELALFYLQEQINHFEEKPTKEMKDKIVAEMDTI IAMIDGVRGVLDRMLMQRKDL DIFEQY
NLEMAKKS GDILERDLKKEEARVKKIEV
>AAB32842.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]
MKFIIAFFVATLAVMTVSGEDKKHDYQNEFDL LMERIHEQIKK GELALFYLQEQINHF
AKPTKEMKDKIVAEMDTI IAMIDGVRGVLDRMLMQRKDL DIFEQYNLEMAKKS GDILERDL
KKEEARVKKIEV
>CAD69036.1 Der p 5; unknown function [Dermatophagoides pteronyssinus]
MKFIIAFFVATLAVMTVSGEDKKHDYQNEFDL LMERIHEQIKK GELALFYLQEQINHF
EKPTKEMKDKIVAEMDTI IAMIDGVRGVLDRMLMQRKDL DIFEQYNLEMLKKS GDILERDL
KKEEARVKNIEV
>ABC73706.1 Der p 21; unknown function [Dermatophagoides pteronyssinus]
MKFIITLFAAIVMAAAVSGFIVGDKKEDEWRMAFDRLMMEELET KIDQVEKGLLHLSEQY
KELEKTKSKELKEQILRELTIGENFMKGALKFFEMEAKRTDLNMFERYNYEFALESIKLL
IKKLDELAKKVKAVNPDEYY
>ATI08932.1 Der p 36; unknown function [Dermatophagoides pteronyssinus]
MKFYNVLTITIGVILLSVFDNVQADTVAQEQRQLHHVDVDPSTQFLNNNCLLD CNIHG
KIYSHNMNEGRTCMVGRNTNYVCRNGQCVGNQHVGHVDIELISASLYEKANAYASVCIKN
NSMPISLPIQDRRDCITCSTQVRSNTNPIWNEVCTGSGNYLLVSDSRVAIEVWNHLGTS
NNIFLGGVSLTIDQLVNHGDNHRAINLAMAGNKP GQLTTRITWTQRN
>ABC96702.1 NPC2-like [Dermatophagoides siboney]
MISKILCLSL LVA AVVADQVDVKDCANNEIKKVMVDGCHGSDPCI IHRGKPF TLEALFDA
NQNTKTAKIEIKANIDGLEVDVPGIDTNACHFIKCP LVKGQYDAKYTWNVPKIAPKSEN

VWTVKLIQDNGVLACAIATHAKIRD
>COMPARE146 dioscorin, partial [Dioscorea opposita]
VEDEFSYIEGNPH
>AAA28303.1 DoI a 5; unknown function, antigen 5 [Dolichovespula arenaria]
NNYCKICPKGHTLCKYGTSMKPNCGGKIVKSYGVTNDEKNEIVKRHNEFRQKVAQGLET
RGNPGPQPPAKNMNLLVWDELAKIAQTWANQCNFGHDQCRNTAKYPVGQNVIASTTGN
SYQTMSYLIKMWEEVKDYNPHKDLMHNNFNSKVGHYTQMVGKTKKEIGCGSVKYIENKWH
THYLVLCNYGPAGNYMNPVYERK
>AAA68279.1 DoI m 2; hyaluronidase [Dolichovespula maculata]
SERPKRVFNIIYWNVPTFMCHQYGLYFDEVTFNFIKHNKDDFQGDKISIFYDPGEFPALL
PLKEGNYKIRNGGVPQEGNITIHQRFIENLDKTYPNRNFNGIGVIDFERWRPFRQNWG
NMMIHKKFSIDLVRNEHPFWDKKMIELEASKRFEKYARLFMEETLKLAKKTRKQADWGY
GYPYCFNMSPNLVPDCDATAMLENDKMSWL FNNQNVLLPSVYIRHELTPDQRVGLVQGR
VKEAVRISNNLKHSPKVSLSYWWYVYQDDTNTFLTETDVKKTFQEIAINGGDGIIIWSS
DVNSLSKCKRLREYLLTVLGPITVNVTTETVN
>CAA47341.1 DoI m 1; phospholipase A1 [Dolichovespula maculata]
RLIMFVGDPSSENELDRFSVCPFSNDTVKMIFLTRENKHFYTLDTMNRHNEFKKSIK
RPVVFITHGFTSSATEKNFVAMSEALMHTGDFLIIMVDWRMAACTDEYPGLKYMFKAAV
GNTRLVGNFIAMI AKKLEQYKVPMTNIRLVGHS LGAHISGFAGKRVQELKLGKFSEIIG
LDPAGPSFKKNDCSERICETDAHVVQILHTSSNLGTERTLGTVDYFYNNGSNQPGCRYII
GETCSHTRAVKYFTECIRRECCLIGVPQSKNPQPVSKCTRNECVGLNAKKYPKRGsfy
VPVEAEAPYCNNGKII
>P53357.1 DoI m 1; phospholipase A1 [Dolichovespula maculata]
GILPECKLVPEEISFVLSTRENDRGVYLT LQKLKNGKMFKNSDLSSKKVPFLIHGFSSA
TNKNYADMTRALLDKDDIMVISIDWRDGACSNFALLKFIGYPKAVENTRAVGKYIADFS
KILIQKYKVLLENIRLIGHSLGAQIAGFAGKEFQRFKLGKYPEIIGLDPAGPSFKKDCP
ERICETDAHVVQILHTSSNLGTERTLGTVDYFINDGSNPGCTYIIGETCSHTRAVKYLT
ECIRRECCLIGVPQSKNPQPVSKCTRNECVGLNAKEYPKKGSFYVPVEAKAPFCNNG
KII
>AAA28301.1 DoI m 5; unknown function, antigen 5 [Dolichovespula maculata]
MEIGGLVYLILIIITIINLSFGETNMYCKIKCRKGIHTLCKFGTSMKPNCGRNVVKAYGLT
NDEKNEILKRHNDFRQNVAKGLETRGKPGPQPPAKNMNVLVWDELAKIAQTWANQCFN
HDDCRNTAKYQVGQNI AISSTTATQFDRPSKLIKQWEDEVTEFNKYVGLQNSNFRKVGHY
TQMVGKTKKEIGCGSIKYEIDNWyTHYLVLCNYGPGGNDFNQPIYERK
>AAA28302.1 DoI m 5; unknown function, antigen 5 [Dolichovespula maculata]
PIINLSFGEANNYCKIKCSRGIHTLCKFGTSMKPNCGSKLVKHVGVSNDEKNEIVNRHNQ
FRQKVAKGLETRGNPGPQPPAKNMNVLVWDELAKIAQTWANQCSFGHDQCRNTEKYQVG
QNVIASTTGN SYATMSKLIEMWENEVKDFNPKKGTMGDNNFNSKVGHYTQMVGKTKKEIG
CGSVKYIENNWHTHYLVLCNYGPAGNYMDQPIY
>COMPARE072 elongation factor [Echinococcus granulosus]
FDAHSYHQFPNYHEMESAYMRFLSKDIGKTSATEQKGD SYLVKEIQKVRDNIKSSLESNG
SWNERMEKLEAIVKEMSLRVNELEVQIQRLGQILPSESLKGAKPIRPVVVKAPPAEGGDD
DDIDLFGSEDEGEADKCKQMMAEQNKAAASKKEKPVAKSMIVLDVKPDDTTNMAEMEG
VRAITADGLLWGTSKLVPLVHGINKLQIACVVEDDKVGTDFLEESIMELEDYVQSVDVAS
FNKL
>P83340.1 Epi p 1; serine protease [Epicoccum nigrum]
ADGIVAVELDTYRGSFXK
>XP_014705584.1 Equ a 6; lysozyme [Equus asinus]
MRSTLIISLLSCFFAVYEAKVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTR
AFNGKNANGSSDYGLFQLNNKWWCKDNKRSSSNACNIMCSKLLDDNIDDDISCAKRVVRD

PKGMSAWKAWVKHCKDKDLSEYLASCNL
>AAM09530.3 Equ c 4; latherin [Equus caballus]
MLKVSCLFVLLCGLLVPSSAQQIPPEVSSQITDALTQGLLDGNFLLNAINLEGLLNTI
LDQVTGLLNILVGPLLGPSDAEIKLQDTRLLQLSLEFSPDSKGIDIWIPLELSVYLKLLI
LEPLTLYVRTDIRVQLRLESEDEGKYRLAFGHCSLLPRAIEIQSGNPLSLPVNAVLTIE
NALGNFITEDLGAGLCPTLNSLVSNDLQLVNNLINLILDRANVDLSV
>AAC48691.1 Equ c 1; lipocalin [Equus caballus]
MKLLLLLCLGLILVCAQQEENSVAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFV
DVIRALDNSSLYAEYQTKVNGECTEFPMVFDKTEEDGVYSLNYDGYNVFRISEFENDEHI
ILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCFQLR
GNGVAQA
>P81216.1 Equ c 2; lipocalin [Equus caballus]
SQXPQSETDYSQLSGEWNTIYGAASNIXK
>P81217.1 Equ c 2; lipocalin [Equus caballus]
XQDPQSETDYSQLSGEWNT
>P11376 Equ c 6; lysozyme [Equus caballus]
KVFSKCELAHKLKAQEMDGGYSLANWVCMAYESNFNTRAFNGKNANGSSDYGLFQLN
NKWWCKDNKRSSSNACNIMCSKLLDENIDDDISCAKRVRDPKGMSAWKAWVKHCKDKDL
SEYLASCNL
>CAA52194.1 Equ c 3; serum albumin [Equus caballus]
MKWVTFVSLFLFSSAYSRGVLRRDTHKSEIAHRFNDLGEKHFKGLVLVAFSQYLQQCPF
EDHVKLNVNEVTEFAKKCAADESAENCDSKSLHTLFGDKLCTVATLRATYGEADCCCEKQEP
ERNECFLTHKDDHPNLPKPKPEPDAQCAAFQEDPKFLGKLYEVARRHPYFYGPPELLFH
AEEYKADFTCCPADDKLAACLIPKLDALKERILLSSAKERLKCSSFQNFGERAVKAWSWA
RLSQKFPKADFAEVSKIIVDTLTKVHKECCHGDLLCADDRADLAKYICEHQDSISGKKA
CCDKPLLQKSHCIAEVKEDDLPSDLPALAADFAEDKEICKHYKDAKDVLGTFLYEYSRR
HPDYSVSLLLRIAKTYEATLEKCCAEADPPACYRTVFDQFTPLVEEPKSLVKKNCDFEE
VGEYDFQNALIVRYTKKAPQVSTPTLVEIGRTLKGVGSRCKLPESERLPCSENHLALAL
NRLCVLHEKTPVSEKITKCTDLSAERRPCFSALELDEGYVPKEFKAETFTFHADICTLP
EDEKQIKKQSALAEVLKHKPKATKEQLKTVLGNFSAFVAKCCGREDKEACFAEEGPKLVA
SSQLALA
>XP_005598291.1 uteroglobin [Equus caballus]
MRLFLPVLLVTLALCCCETNAATCPAVATDIASFFLLPDSLFLKQLIKYQAPPEAKDATM
QVKQCINEISAGDRYIITETLGKIVLQCGA
>XP_003362701.1 uteroglobin [Equus caballus]
MKLVTVLMVAFPLYCYAGSGCQLLEDVVEKTITAEELSPAAYVEAVQEFIPDEATEKAAI
QLKQCYLKQSNETLNDFRMTMMNSMYNSAYCALF
>BAF47268.1 tropomyosin [Erimacrus isenbeckii]
MDAIIKKMQAMKLEKDNAMDRAHTLEQQNKEANLRAEKTEEEIRATQKKMQQIENELDHA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVLEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY
>BAF47269.1 tropomyosin [Erimacrus isenbeckii]
MDAIIKKMQAMKLEKDNAMDRAHTLEQQNKEANLRAEKTEEEIRATQKKMQQIENELDHA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVLEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKNIADEMDOAFSELSGF
>Q5QKR2 Eri s 2; ovary development-related protein [Eriocheir sinensis]

MWC S I L L A A V M V A V A G G Q S R F S Y D G T P L A D D V V V G S G Q R Q Q F F A S R Q P R P Q Q L F V Q E R P Q
Q V F V Q Q Q P P P V F V Q P E P Q V F V Q P Q P R P M F Q M L P S F S Q Q A A V I Q S V Q P Q V S S A C P A T Y S
L V H T T Y Q G R V Y H S S W C N L P G H R F S Q S A A R D Y C R G L G E V T V M N R R G S F D L Y S V D R T T D F D Y
F F E L L L Q H Q I P S V W T R D L A S T A P Y E I R G S I T R S G D S T A G Q D C L S L E A S T D G L F L L Q D S C S
D R K A A V C V A H W Q

>AB071783.1 tropomyosin [*Eriocheir sinensis*]
M D A I K K K M Q A M K L E K D N A M D R A D T L E Q Q N K E A N N R A E K T E E E I R A T Q K K M Q Q V E N E L D Q A
Q E Q L S A A N T K L D E K E K A L Q N A E G E V A A L N R R I Q L L E E D L E R S E E R L N T A T T K L A E A S Q A A
D E S E R M R K V L E N R S L S D E E R M D A L E N Q L K E A R F L A E E A D R K Y D E V A R K L A M V E A D L E R A E
E R A E S G E S K I V E L E E E L R V V G N N L K S L E V S E E K A N Q R E E T Y K E I K T L A N K L K A A E A R A E
F A E R S V Q K L Q K E V D R L E D E L V N E K E K Y K S I T D E L D Q T F S E L S G Y

>BAF76431.1 tropomyosin [*Euphausia pacifica*]
M D A I K K K M Q A M K M E K D S A M D R A D A L E A Q N K E T N A R A E K A D D E V H N L Q K R L Q T L E N D L D Q V
S E A L L K A N T Q L V E K D K A L Q N A E G E V A A L N R R I Q L L E E D L E R S E E R L N T A T T K L A E A S Q A A
D E S E R M R K V L E N R S L L D E E R M D A L E N Q L K E A R L L A E E A D R K Y D E V A R K L A M V E A D L E R A E
E R A E A G E N K I V E L E E E L R V V G N N L K S L E V S E E K A N Q R E E A Y K E I K H L T H K L K T A E A R A E
F A E R S V Q K L Q K E V D R L E D E L V N E K E K Y K G I T D E L D Q T F N E L S G Y

>BAF76430.1 tropomyosin [*Euphausia superba*]
M D A I K K K M Q A M K M E K D S A M D R S D A L E A Q N K E T N A K A D K A D D E V H N L Q K R L Q T L E N D L D Q V
S E A L L K A N T Q L V E K D K A L Q N A E G E V A A L N R R I Q L L E E D L E R S E E R L N T A T T K L A E A S Q A A
D E S E R M R K V L E N R S M L D E E R M D A L E S Q L K E A R L L A E E A D R K Y D E V A R K L A M V E A D L E R A E
E R A E A G E N K I V E L E E E L R V V G N N L K S L E V S E E K A N Q R E E A Y K E I K H L T H K L K T A E A R A E
F A E R S V Q K L Q K E V D R L E D E L V N E K E K Y K G I T D E L D Q T F N E L S G Y

>AAC82351.1 Eur m 1; cysteine protease [*Euroglyphus maynei*]
M K I I L A I A S L L V L S A V Y A R P A S I K T F E E F K K A F N K Y A T P E K E E V A R K N F L E S L K Y V E S N
K G A I N H L S D L S L D E F K N Q F L M N A N A F E Q L K T Q F D L N A E T Y A C S I N S V S L P S E L D L R S L R T
V T P I R M Q G G C G S C W A F S G V A S T E S A Y L A Y R N M S L D L A E Q E L V D C A S Q N G C H G D T I P R G I E
Y I Q Q N G V V Q E H Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H T A V A V I
I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T W G D N G Y
G Y F A A N I N L M M I E Q Y P Y V V M L

>AAC82352.1 Eur m 1; cysteine protease [*Euroglyphus maynei*]
K H L S T I M K I I L A I A S L L V L S A V Y A R P A S I K T F E E F K K A F N K S Y A T P E K E E V A R K N F L E S L
K Y V E S N K G A I N H L S D L S L D E F K N Q F L M N A N A F E Q L K T Q F D L N A E T Y A C S I N S V S L P S E L D
L R S L R T V T P I R N Q G G C G S C W A F S G V A S T E S A Y L A Y R N M S L D L A E Q E L V D C A S Q N G C H G D T
I P R G I E Y I Q Q N G V V Q E H Y P Y V A R E Q S C H R P N A Q R Y G L K N Y C Q I S P P D S N K I R Q A L T Q T H
T A V A V I I G I K D L N A F R H Y D G R T I M Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T
W G D N G Y G Y F A A N I N L M M I E Q Y P Y V V I L

>AAC82349.1 Eur m 2; NPC2-like [*Euroglyphus maynei*]
M Y K I L C L S L L V A A V A A D Q V D I K D C A N H E I K K V M P G C K G S E P C V I H R G T A F Q L E A V F D A N
Q N S N A A K I E I K A T I D G V E I D V P G I D N N L C H F M K C P L V K G Q E Y D I K Y T W N V P R I A P K S E N V
V V T V K L L G D N G V L A C A I A T H A K I R D

>AAC82350.1 Eur m 2; NPC2-like [*Euroglyphus maynei*]
V A A V A A D Q V D V K D C A N H E I K K V M P G C K G S E P C V I H R G T A F Q L E A V F D A N Q N S N A A K I E I
K A T I D G V E I D V P G I D N N L C H F M K C P L V K G Q E Y D I K Y T W N V P R I A P K S E N V V V T V K L L G D N
G V L A C A I A T H A K I R D

>BAK09232.1 calcium-binding protein, parvalbumin [*Evynnis japonica*]
M P F K G L Q D A D V A K A L E G C K D A G T F D H K K F F A C G L S G K S G A D V K D A F F V I D Q D K S G F I E E
E E L K L F L Q N F K A G A R A L T D E E T K K F L K A G D S D G D G K I G A D E F A E M V K V

>BAK09233.1 calcium-binding protein, parvalbumin [*Evynnis japonica*]
M A F S G V L S D A D M K A A L D G C S A A D S F D Y K K F F K A C G L S G K S A D E V K K A F A I D Q D K S G F I E

EEELKLFQNFGKSARALTDKETKAFLAAGSDGDGKIGVDEFAALVKA
>COMPARE215 Exo m 1; tropomyosin [Exopalaemon modestus]
MDAIKKKMQAMKLEKDNAMDRALTCEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDSV
QEALLKANAHLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVLEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY

>O23878.1 13S globulin [Fagopyrum esculentum]
MSTKLILSFLCMLVLSCSAQLLPWRKQGRSRPHRGHQFHQCDVQRLTASEPSRRVRS
EAGVTEIWDNDTPEFRCAQFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVPGC
PETFQSESEFEYQSQRDQRSRQSESEESSRGDQRTRQSESEEFSSRGDQRTRQSESEEFSS
RGDQRTRQSESEEFSSRGDQRTRQSESEEFSSRGDQHQKIFRIRDGDVIPSPAGVVQWTHND
GDNDLISITLYDANSFQNLQDGNVRNFFLAGQSKQSREDRRSQRQRTREEGSDRQSRRESDD
DEALLEANILTGFDQEIILQEIFRNVDQETISKLRGDNDRGFIVQARDLKLVPPEEYEEE
LQRRERDRKRGGSGRSNGLEQAFCNLKFQNVNRPVSRADVFNPAGRINTVNSNLPPILE
FIQLSAQHVVLYKNAIILGPRWNLNAHSALYVTRGEGRVQVVGDEGRSVFDDNVQRGQILV
VPQGFVAVLKAGREGLWELKNDDNAITSPIAGKTSVLRRAIPVEVLANSYDISTKEAFR
LKNRQEVFVLPFQSRDEKERERF

>O23880.1 13S globulin [Fagopyrum esculentum]
MSTKLILSFLCMLVLSCSAQLWPWQKQGSRPHHGRQHQFHQCDIQRLTASEPSRRV
RSEAGVTEIWDHDTPEFRCTGFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVIP
GCPETFQSDSEFEYQSQRGRHSRQSESEESSRGDQHQKIFRIREGDVIPSPAGVVQWT
HNDGNDDLISVTLLDANSYHKQLDENVRFFLAGQSQRETREEGSDRQSRRESDDDEALLG
ANILSGFDQEIILHELFRDQVRETISKLRGENDQRGFIVQAQDLKLVPQDFEEYERERER
DRRRGQGGSGRSNGVEQGFENLKFRRNFNTPTNTYVFNPRAGRINTVNSNLPPILEFLQL
SAQHVVLYKNAIIGPRWNLNAHSALYVTRGEGRVQVVGDEGKSVFDDKVQRGQILVVPQG
FAVVLKAGREGLWELKNSGNAITSPIGGRTSVLRRAIPVEVLANSYDISTKEAYKLKNG
RQEVFVFRPFQSRDEKERERFSIV

>Q9XFM4.1 13S globulin [Fagopyrum esculentum]
MSTKLILSFLCMLVLSCSAQLLPWQKQGRSRPHHGHQFHQCDIQRLTASEPSRRVRS
EAGVTEIWDHDTPEFRCAQFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVPGC
PETFQSGSEFEYPRSQRDQRSRQSESEESSRGDQRSRQSESEESSRGDQRSRQSESEEFSS
RGDQHQKIFRIRDGDVIPSPAGVVQWTHNNGDNDLISITLYDANSFQNLQDENVRNFFLA
GQSKQSREDRRSQRQRTREEGSDRQSRRESQDDEALLEANILSGFEDEILQEIFRNVDQETI
SKLRGENDQRGFIVQARDLKLVPPEEYEEELQRRERDRKRGGSGRSNGLEQAFCNLKFQ
NVNRPVSRADVFNPAGRINTVDSNLPPILEFIQLSAQHVVLYKNAIILGPRWNLNAHSALY
VTRGEGRVQVVGDEGRSVFDDNVQRGQILVVPQGFVAVLKAGREGLWELKNDDNAITS
PIAGKTSVLRRAIPVEVLANSYDISTKEAFRLKNRQEVFVFRPFQSRDEKERERFSIV

>BA050870.1 13S globulin [Fagopyrum esculentum]
MLLGVLLCIMVSLAASETRSRGSSTMRARQCRLDQLTSSQPNQKIQSEGGTIEVWDEEED
QFQCAGVAAMRVTVQPDLSLPSYYSSPRLVYVEQGEVFGLSLPGCPETYQSRGMMEMRG
DEEEEGFESGRRMTDAHQPTRRVRKGDVVALPQGTVHWCNFDGQEDLVVVAVHNLNTDA
NQLDQSLKTFFLAGGVQGGKSKGKSLNFNILSAFETKLLAEALGTEETVRKMQESD
ERGPVIVKARKNMRQMVTPPRFGREQDEDETNGLSEFCNMRFRHNLGPRTEADIASRQAG
RIHSVDQNKLPILFIDMSAEKGHLLPNAMLAPAWPLSGHRVFYVLRGEAQMIVDDNGQ
TVLDDRVSEGSMMVVPQFYISTCRAGRDGLEVVSFETTANPMSSPLNGHASVFKGMPIPV
LSNSYQISPRAYELKQTRSHEHGLFSPFGGRS

>BA050872.1 13S globulin [Fagopyrum esculentum]
MLLGVLLCIMVSLAASETRTRGSSTMRARQCRLDQLTSSQPNQKIRSEGGTIEVWDEEED
QFQCAGVAAMRVTVQPDLSLPSYYSSPRLVYVEQGEVFGLSLPGCPETYQSRGMMEMRG

DEEEEGFESGRRMTDAHQPTRRRVRKGDVVALPQGTVHWCFNDDGQEDLVVVAVHNLNTDA
NQLDQSLKTFFLAGGVQGGKSKGKSLNFNILSAFETKLLAEALGTEETVRKMQESD
ERGPIVKARKNMRQMVTPPRFGREQDEDETNGLSEFCNMRFRHNLGPRTEADIASRQAG
RIHSVDQNKLPILFIDMSAEKGHLLPNAMLAPAWPLSGHRVYVLRGEAQMQUIVDDNGQ
TVLDDRVSEGSVMVPIQFYISTCRAGRDGLEYVSFETTANPMSSPLNGHASVFKGMPIPV
LSNSYQISPRAAAYELKQTRSHEHGLFSPFGGRS
>BA050858.1 13S globulin [Fagopyrum esculentum]
MSTKLILSFLCLMLVLSCSAQLLPWQKQGRSRPHHGHQFQHQCDVQRLTASEPSRRVRS
EAGVTEIWDNDTPEFRCAQFVAVRVVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVPGC
PETFQSESEFEYQSQDRQSRQSESEESSRGDQRTRQSESEEFSSRGDQHSRQSESEESS
HGDQHQKIFRIRDGDIVPSPAGVVQWTHNDGNDLISITLYDANSFQNQLDGNVRNFFLA
GQSKQSREDRRSQRQTRREEGGDRQSRESDDDEALLEANILSGFQDEILQEIFRNVDQETI
SKLRGETDQRGFIVQARDLKLRVPEEYEEELQRERGRDRKGGSGRSNGLEQAFCNLKFQ
NVNRP SRADVFNPRAGRINTVNSNLPILFIIQLSAQHVVLYKNAILGPRWNLNAHSALY
VTRGEGRVQVVGDEGRSVFDDNVQRGQILVVPQGFVAVLKAGNEGLEWELKNDDNAITS
PIAGKTSVLRAIPVEVLANSYDISTKEAFRLKNGRQEVVFRPFQSRDEKERERYSIV
>BAB79444.1 2S albumin, conglutin [Fagopyrum esculentum]
MKLFLILAAASLLIVASHADSQMRSKCRKQMRMMEPQLEQCEGYMTDMMDDDSMRGREG
RSEESCMRGCCLAMKEMDDECMCEWMKMMVQQQRGEMGEEDMRMVMRKMQLPNKCGMGH
MRCHMGIGTRDYE
>AAX57578.1 Fag e 2; 2S albumin, conglutin [Fagopyrum esculentum]
RDEGFDLGETQMSSKCMRQVKMNEPHLKKCNRYIAMDILDDKYAEALSRVEGEGCKSEES
CMRGCCVAMKEMDDECVCEWMKMMVENQKGRIGERLIKEGVRDLKELPSKCGLSEMECGS
RGNRYFV
>ABC18306.1 Fag e 2; 2S albumin, conglutin [Fagopyrum esculentum]
MKLFIILATATLLIAATQATYPRDEGFDLGETQMSSKCMRQVKMNEPHLKKCNRYIAMDI
LDDKYAEALSRVEGEGCKSEESCMRGCCVAMKEMDDECVCEWMKMMVENQKGRIGERLIK
EGVRDLKELPSKCGLSELECGSRGNRYFV
>ABQ10638.1 Fag e 3; 7S globulin, vicilin-like, partial [Fagopyrum esculentum]
GDYPFEPRRQIEHCRQRCQDRSQGFRETRELETCEKRAFDEPSKEVDSYTTDTRSRD
PQQEFRQCRHRCQTQEEGRQQRKCEQRCEKQLERQQGYDDEEFGQGRSNIGAPVRNYDD
CTEMCGGSPLCALFCE
>COMPARE174 7S globulin, vicilin-like, partial [Fagopyrum esculentum]
GDYPLEXCRQKIEH
>AAS48514.1 Fag e 5; 8S globulin, vicilin [Fagopyrum esculentum]
IAVVTNGKGFQMACPHISAEGKQSKRQREGKSIVHYETVNGDLSSGTVFVVPAGHPFVT
AASLEDNLELICFEVNADDNERIPLAGKNSLQFEREAKELAFEEKADVVDKLLLEKQQQ
EFFFEGPRRRKEQEAGRSDA
>COMPARE172 Fag e 4; antimicrobial peptide, partial from P0DKH7.1 [Fagopyrum
esculentum]
AQCGAQGGGATC
>COMPARE175 trypsin-inhibitor [Fagopyrum esculentum]
SDKPQQLLEECRYLXRI
>AB093594.1 2S albumin, conglutin [Fagopyrum tataricum]
MKLFLILAAASLLIVASHADSQMRSKCRKQMRMMEPQLEQCEGYMTDMMDDDSMRGQEC
RSEESCMRGCCMAMKEMDDECMCEWMKMMVQQQRGEMGEEDMRMVMRKMQLPNKCGMGH
MRCHMGMGTRVYE
>ADW27428.1 Fag t 2; 2S albumin, conglutin [Fagopyrum tataricum]
MKLFIILATATLLIAATQAKYLRDEGFDLGETQMSSKCTRQVKMMEPELVKCNRYIAMDI
MDDKYEEALSRIQEGCESEEKFLRGCCVAMKEMEDECVCEWMKMMVENQKGRIGETLMR

KGIRDLKELPNKCGISEMECHSRGNWYVV

>ABI32184.1 unknown function [Fagopyrum tataricum]

MSTKLILSFSLCLMVLSCSAQAAQLWPWRKGQDSRPHHGQQFQQQCDIQRLTASEPSRR
VRSEAGVTEIWDHNTPEFRCTGFVAVRYVIQPGGLLLPSYSNAPYITFVEQGRGVQGVVI
PGCPETFQSDSEYPQSQRGQHSRESESQESSRGDQHQKIFRVREGDVIPSPAGVVQWTHN
DGDQDLISVTLLDANSFHNQLDENVRSFFLAGQSQQGREERRSQQQTREEGGDRQSRES
DVEALIGANILSGFQDEILHELFRDVEDRETISKLRGENDQRGFIVQAQDLKLRVPEDSEE
GYERQRGDRKRDERGSGRSNGLEQAFCNLKFRQNVNRP SHADVFNPRAGRINTVNSNNLP
ILEFLQLSAQHVVLYKNAIIGPRWNLNAHSALYVTRGEGRVQVVGDEGKSVFDDNVQRGQ
ILVVPQGFVAVVKAGRQGLEWVELKNNDNAITSPIAGRTSVLRAIPVEVLANSYDISTEE
AYKLKNGRQEVEVFRPFQSRYEKEEERERFSIV

>ACJ23864.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG
EGSQFNVMKHRIDEIDNANFTYACTLIEGDAISETLEKIAYEIKLVASPDGGSILKSTSK
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAHY

>ACJ23865.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG
EGSQFNVMKHRIDEIDNANFTYAYTLIEGDAISETLEKIAYEIKLVASPDGGSILKSTSK
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAHY

>ACJ23866.1 Fag s 1; pathogenesis related protein, PR-10, Bet v 1-like [Fagus sylvatica]

MGVFTYESETTTVITPARLFKAFVLDADNLI PKVAPQAIKSSEIEGSGGPGTIKKITFG
EGSQFNVMKHRIDEIDNTNFTYACTLIEGDAISETLEKIAYEIKLVASPDGGSILKSTSK
YHTKGDHEIKEDQIKAGKEEASGIFKAVEAYLLANPAAHY

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

MIPGGLSEAKPATPEIQEIANEVKPKQLEEKTNETYQKFEAIEYKTQVVAGINYYIKVQVD
DNRYIHIKVFVKGLPVQDSSLTLTGYQTGKSEDELTF

>ADM15668.1 Fel d 8; latherin [Felis catus]

MLKVSSLFILLCGLLASSSTQEVLSRVSSHITDAL TQGLLGMNFLTPTLQTIDFQGPLKDI
FSLVLGHQLTNGEANFMVMKDLRFLQVFIETSPDFKGD LRMPLAFSIQIKFPALNPYI
FHVRTDMKVQLYLEKDV DNRYQLTFGHCRIVPETVWIQSGNFITPMKNFIVENIERALGN
VIIHNF GAKMCPFINSWLYNLNPQVTNQLISLLLQHGTYQATVEIPAK

>AAS77253.1 Fel d 4; lipocalin [Felis catus]

MKLLLLLCLGLILVCAHEEENVVRSNIDISKISGEWYSILLASDVKEKIEENGSMRVFVEH
IKALDNSSLSFV FHTKENGKCTEIFLVADKTKDGVYTVVYDGYNVFSIVETVYDEYILLH
LLNFDKTRPFQLVEFYAREPDVSQKLKEKFKVYKQCEHGIVNILD LTEVDRCLQARGSEVA
QDSSVE

>ADK56160.1 Fel d 7; lipocalin [Felis catus]

MKALLLAVGLSLITVLQAQDPPASGEDTMAMSGKWYLKAMITDRETSWKKPELVTPMTLT
VLEGGNLKAETLLTNGQCKEVELILEKTSEPKKYTTYGGKRVVYIEPTEVKDHYIFYCE
GEMQGEQARMAKLVGRDPESNEEALENFREFLRAKGFNQEIFSPKQSDTCPGTDQEPEV

>COMPARE00247 NPC2-like, partial from XP_003987882.1 [Felis catus]

EPVIFKDCGSGFGVIKELNVSPCPTQPCKLHKGQSYVNVTF TSNVSSQGSKALVYGILM
GVAVFPPIPEADGCKSGINCPIQQGKTYSYLNKLPVKNEYPSIKVMVKWQLLGDKEQNLF
CWEIPVQIEG

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

MKWVTFISLLLLFSSAYSRGVTRREAHQSEIAHRFNDLGEEHFRGLVLVAFS QYLQQCPF
EDHVKLVNEVTEFAKGCVADQSAANCEKSLHELLGDKLCTVASLRDKY GEMADCCCKEKEP

ERNECFLQHKDDNPGFGQLVTPHADAMCTAFHENEQRFLGKYLVEIARRHPYFYAPELLY
YAEYKGVFTECEAADKAACTPKVDALREKVLASSAKERLKCASLQKFGERAFKAWSV
ARLSQKFPKAEFAEISKLVTDLAKIHKECCHGDLLECADDRADLAKYICENQDSISTKLK
ECCGKPVLEKSHCISEVERDELPAIDLPLAVDFVEDKEVCKNYQEAKDVFLGTFLYEYSR
RHPEYSVSLLLRLAKEYEATLEKCCATDDPPACYAHVFDEFKPLVEEPHNLVKTNCELFE
KLGEYGFQNALLVRYTKKVPQVSTPTLVEVSRS LGKVGSKCCTHPEAERLSCAEDYLSVV
LNRLCVLHEKTPVSRVTKCTESLVNRRPCFSALQVDETYVPKEFSAETFTFHADLCTL
PEAEKQIKKQSALVELLKHKPKATEEQKLTVMGDFGSFVDKCCAAEDKEACFAEEGPKLV
AAAQAALA

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

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

>CAA44345.1 Fel d 1; uteroglobin [Felis catus]
MRGALLVLALLVTQALGVKMAETCPIFYDVF FAVANGNELLLDLSLTKVNATEPERTAMK
KIQDCYVENGLISRVLDGLVMIAINEYCMGEAVQNTVEDLKLNTLGR

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

>CAA44343.1 Fel d 1; uteroglobin [Felis catus]
VRRSPSTLPYCCGHSRDCEICPAVKRDVDLFLTGTDPDEYVEQVAQYNALPVVLENARILK
NCVDAKMTEEDKENALSVDLKIYTSPLC

>CAA44344.1 Fel d 1; uteroglobin [Felis catus]
EGGLCSRASLGCLALDLGWKDCEICPAVKRDVDLFLTGTDPDEYVEQVAQYNALPVVLENA
RILKNCVDAKMTEEDKENALSVDLKIYTSPLC

>NP_001041618.1 Fel d 1; uteroglobin [Felis catus]
MLDAALPPCPTVAATADCEICPAVKRDVDLFLTGTDPDEYVEQVAQYKALPVVLENARILK
NCVDAKMTEEDKENALSLLDKIYTSPLC

>COMPARE141 lipid transfer protein, partial [Foeniculum vulgare]
AITXGQVTSKLG

>COMPARE142 lipid transfer protein, partial [Foeniculum vulgare]
GGGDPTPACCGVK

>COMPARE143 lipid transfer protein, partial [Foeniculum vulgare]
GINYGAASALPGK

>COMPARE144 lipid transfer protein, partial [Foeniculum vulgare]
CGISIPYPISPSTNCSR

>COMPARE140 pathogenesis related protein, PR-10, Bet v 1-like, partial [Foeniculum
vulgare]
GVQKSEVVITSA

>ACD65081.1 For t 2; eukaryotic translation initiation factor [Forcipomyia taiwana]
MKPLMMQGHRAITQIKYNREGDLLFSCAKDHPNVWFSLNGERLGTFNHAGAVWCVDV
DWTTKLITGSGDMSVRLWDVETGTSVACIPCKSSARTVGFSGNQAAYSTDRAMGHIC
ELFVIDSREPDSSLNDGDAILKIPISQSKITAMIWGTLDIITGHENGQITLWDLRIGR
EINSVNDHMGAINDLQLSKDGMTFVSSSRDITAKLFSDSLMCLKTYKTERPVNSAAISP
LLEHVVLGGGQDAMEVTTTSARQGGKFDSEFFHLYEEEEFARVKGHFGPINSLAFHPDGRS
YATGGEDGFVRLQTFDSSYYEYIFD

>ACD65080.1 For t 1; serine/threonine protein kinase [Forcipomyia taiwana]
GTRVDEIKGHPFFREIDWTKELRNQKAPYEPKIKYPTDTSNFDPIDPKLHDSSNADDYM

IEEFFGSGKPCHHGFFEFTFRFFDADDADCKISLNHGNSGDRNDNNSNDNQSGAIYV
>CAC86258.1 Fra a 3; lipid transfer protein [Fragaria x ananassa]
MASSTAMKLSLVALLCIVVALPIAQAITCGQVASNISPCCLTYVKSGGAVPAACCSGIRNL
NGMAKTTADRQAACNCLKQAAGGIKGLNPNLAAGLPGKCGVSVPYKISTTTNCAAVK
>AAY83341.1 Fra a 3; lipid transfer protein [Fragaria x ananassa]
MASSTAMKLSLVALLCIVVALPIAQAITCGQVASSISPCVNVYKSGGAVPAACCSGIRSL
NSAAKTTADRQATCNCLKQASGAIKGLNPSLAAGLPGKCGVSVPYKISTSTNCAAVK
>AAY83342.1 Fra a 3; lipid transfer protein [Fragaria x ananassa]
MASSTAMKLSLVALLCIVVALPIAQAITCGQVASNISPCVTYVKSGGAVPAPCCSGIRNL
NGMAKTTADRQATCNCLKQAAGGIKGLNPNLAAGLPGKCGVSVPYKISTTTNCAAVK
>AAY83345.1 Fra a 3; lipid transfer protein [Fragaria x ananassa]
MAISTAMKLSLVALLCIVVALPIAQAITCGQVASSISPCVNVYKSGGAVPAACCSGIRSL
NSAAKTTADRQTTCNCLKQASGAIKGLNPNLAAGLPGKCGVNVYKISTSTNCAAVK
>AHZ10957.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
MGVFTYETEFTSVIPPPRLFKAFILDADNLIPKIAPQAVKCAEIVEGDGGVGTIKKITFG
EGSQFGSVTHKIDGIDKENFVYSYSLVEGDALSDKIEKISYETKLVASSDGGSVIKSTSN
YHTKGDVEIKEEHVKAGKEKASHLFLKVEDYLLANPNEYC
>AHZ10958.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
MGVFTYETEFTSVIPPPRLYKAFVLDADNLIPKIAPQAVKSTELVQGDGGVGTIKKIHLG
EGSEYSYVKKHQIDGLDKDNFVYNYSIIIEGDAIGDKVEKISYEIKLVASPSGGSIKSTSH
YHCKGEVEIKEEHVKAGKERAAGLFKIIENYLLGNPDAYN
>AHZ10959.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
MGVFTYETEFTSVIPPPRLYKAFVLDADNLIPKIAPQAVKSAEIVQGDGGVGTIKKIHLG
EGSEYSYVKKHQIDGLDKDNFVYNYSIIIEGDAIGDKVEKISYEIKLVASPSGGSIKSTSH
YHCKGEVEIKEEHVKAGKEKAAGLFKIIENHLLANPEAYN
>ABD39049.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x
ananassa]
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKITFG
EGSHYGYVKKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVASPHGGTVIKTTSK
YHTKGDVEIKEEHVKAGKEKASHLFLKIEGYLKDHPSEYN
>CAJ85641.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x
ananassa]
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAIKCAEILEGDGGPGTIKKITFG
EGSHYGYVKKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVASPHGGTIIKTTSK
YHTKGDVEIKEEHVKAGKEKASHLFLKIEGYLKDHPSEYN
>CAJ85642.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x
ananassa]
MGGYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAIKCAEILEGDGGPGTIKKITFG
EGSHYGYVKKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVASPHGGTIIKTTSK
YHTKGDVEIKEEHVKAGKEKASHLFLKIEGYLKDHPSEYN
>CAJ85644.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x
ananassa]
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKITFG
EGSHYGYVKKHKIHSIDKENHTYSYSLIEGDALSDNIEKIDYETKLVASPHGGTIIKTTSKY
HTKGDVEIKEEHVKAGKEKASHLFLKIEGYLKDHPSEYN
>CAJ85646.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x
ananassa]
MGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKITFG
EGSHYGYVKKHKIHSIDKVNHTYSYSLIEGDALSENIEKIDYETKLVASPHGGTIIKTTSK
YHTKGDVEIKEEHVKAGKEKAHLFLKIEGYLKDHPSEYN

>4C9C_B Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
AMAGVYTYENEFTSDIPAPKLFKAFVLDADNLIPKIAPQAVKCAEILEGDGGPGTIKKIT
FGEESHYGYVVKHKIHSIDKVNHTYSYSLIEGDALSENIEKIDYETKLVSAHPHGTTIIKT
SKYHTKGDVEIKEEHVKAGKEKAAHLFKLIEGYLKDHPSEYN

>ACX47057.1 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
MGVFTYETEFTSVIPPPRLFKAFILDADNLIPKIAPQAVKCAEIEGDGGVGTIKKITFG
EGSQFGSVTHKIDGIDKENFVYSYSLIEGDALSDKIEKISYETKLVSSSDGGSIIKSTSN
YHTKGDVEIKEEHVKAGKEKASHLFLKVEGYLLANPNEYC

>ACX47058.1 pathogenesis related protein, PR-10, Bet v 1-like [Fragaria x ananassa]
MGVFTYEEFTSVIPPPKLFKAFVLDADNLIPKIAPQAVKSAEIEGDGGVGTIKKIHLG
EGSEYSYVVKHKIDGIDKDNFVYSYSLIEGDAIGDKIEKISYEIKLVASGGGSIIKSTSHY
HTKGEVEIKEEHVKAGKERAAGLFKIENHLLAHPEEYN

>COMPARE020 Fra a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial [Fragaria x ananassa]
KITFGEQSQYGYVK

>AHL24661.1 calcium-binding protein, polcalcin [Fraxinus excelsior]
MADDPQEVAQLERIFKRLDANGDGKISSSELGETLKTLSITPDEIQRMMAEIDTDGDGF
ISYEFTDFARANRGLVKDVAKIF

>AAQ83588.1 Fra e 1; Ole e 1-like [Fraxinus excelsior]
MEDVPQPPVSVFHIQGGVYCDTCRARFITKLSEFITGASVRLQCRDKENGDVTFTEIGYT
RGEGLYSMFVERDHKNEFCEITLLSSGRKDCNEIPIEGWVKPSLKFILNTVNGTTRTINP
LGFFKKEALPQCAQVYNKLGMYPPNM

>AAQ08947.1 Fra e 1; Ole e 1-like, partial [Fraxinus excelsior]
EDVPQPPVSLFYVQGGVYCDTCRAGFITELSEFIQAGVRLQCKDKENGKVTFTTEVGYTR
AEGLYSMVIERDHKNEFCEIVLLSSSRKDCDEIPTEGWVKPSLKFILNTVNGTTRTINPL
GFFKKEVLPKCPQVYNKLGMYPPNM

>AAV74343.1 Fra e 1; Ole e 1-like, partial [Fraxinus excelsior]
EDVPQPPVSLFYVQGGVYCDTCRAGFITELSEFIQAGVRLQCKEKENGKVTFTTEVGYTR
AEGLYSMVIERDHKNEFCEIVLLSSSRKDCHEIPTEGWVKPSLKFILNTVNGTTRTINPL
GFFKKEALPKCPQVYNKLGMYPPNM

>AHL24660.1 profilin [Fraxinus excelsior]
MSWQAYVDDHLMCDIEGHEGHRLTAAAIIVGHDGVSVAQSATFPQFKPEEINGITDFNEP
GHLAPTGLHLGGTKYMIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETITPGQCNM
VVERLGDYLIDQGL

>BAH10153.1 tropomyosin [Fulvia mutica]
MEAIKKKMQSMKNEKENAIDKAEQLEIKLKDTEDSKAKIEEDLTSLQKKYTNLENEFDQV
NEKHADSVAKLEAAEKRLTETEDEIKGYTRKIQLLEDDLERTQTKLDEATGKLEEATKSA
DESERGRKVLESRLADDDRIDGLEKQVKDAKYVAEESDRKYDEAARKLAITEVDLERAE
TRLEAAEAKIVELTEELSVVGNLKGQNAVDQASQREDSYEETIRDLTQRLKDAENRAS
EAERVVIKLQKEVDRELELLQEKEYKQISDELDTFAELAGM

>AAL79930.1 Fus c 1; ribosomal protein P2 [Fusarium culmorum]
MKHLAAYLLLGLGGNTSPSAADVAVLTSVGIDADEDRNLKLISELEGKDIQQLIAEGSE
KLASVPSGGAGGASGGAAAAGGAAEEAKEEEEEKEEESDEDMGFGLFD

>AAL79931.1 Fus c 2; thioredoxin [Fusarium culmorum]
MVHHITSNDELQKLLSSTTYVVVDFADWCPPCKAIAPVYEQLSTKHSVPDVLAFKVVN
DHSVQDAAQQYGITAMPTFMFFKEGKQVAVNGQAVIKGADPRTLGAEEKLGGLAQKRVAG
A

>AAN73248.1 unknown function [Fusarium culmorum]

MAGDHAGDQSFYDFLIEEPEMIAPTPPGQFPHQPISSPNRTSRNTPLRPESTEIETHHH
ANHPPALPVLGMQLPVPGTVPESRAQSRASLNLDIDLHLHAPSHPSHLSHGAPHEQEHA
HEIQRHRAHSAQSSAGLPPTGFASHLPASSGPVSLGWNMYHVPPNLHLNANQFNFEVPG
HMNVSGHPHLEHSSNPNSFHYEHNIVSPSSIHPSTAHDGVEVPSQWDDSLGHGASTPK
VRTPSHHVSSNPWAEINEPTGGDNDNLAPVTRPRKPARARRQKKEPRKLSDASQGARSSS
TGGTAHSVSDAASPSSTSHQSRASLTSKSASMTSAASTASSRKSCLRSASRTSKNTLDKP
NDAEDRRRTRASHNLVEKQYRNRLNAQFESLLHALPEQIRHGDNGGGNGNVDNESEQAND
LDRRVSKGEVLEMARRHIEALERERNQLGT
>COMPARE070 glyceraldehyde-3-phosphate-dehydrogenase, partial [Fusarium lateritium]
RVPTANVSVVDLTVRI
>COMPARE071 glyceraldehyde-3-phosphate-dehydrogenase, partial [Fusarium lateritium]
RTTYFGPTGNDSSSTVLKY
>AHY02994.1 Fus p 4; aldolase [Fusarium proliferatum]
MSSSLEQLKATGTTVVSDSGDFVSIKGYKQDATTNPSLILAASKKAEYAKLIDVAIDYA
KQKGGSIDQVDDALDRLLVEFGKEILKIIPGKVSTEVDARYSFDTEASVNKALHLIELY
GEQGISKDRILIKIAATWEGIKAAEILQRDHGINTNLTMFSLVQAIGAAEAGAYLISPF
VGRILDWFKASTKKEYSKEEDPGVQSVKTIFFNYKKGYNITVMGASFRNTGEITELAGC
DYLTISPNNLEDLLNSNEPVPKLDASQAASLDIEKKSINDEALFRFDNFEDQMAVEKL
REGISKFAADAVTLKLSILKEKLA
>AJA79001.1 Fus p 9; serine protease [Fusarium proliferatum]
DKCDGETERQAPWGLARISHRNTLNFGTFNKYLYSSDGGEGVDAYIVDTGTNVDHVDVFE
RAHWGKTIPSGDADEGNGHGTHCSGTVAGKKYGVAKKANVYAVKVLRSNGSGSMSDVVK
GVEFAATSHLEQKKKAKDGKRKGFKGSVANMSLGGGKTQALDAAVNAAVRTGIHFAVAAG
NDNADACNYSAAAASEPVTVGASALDDSRAYFSNYGKCTDIFAPGLNIQSTWIGSKYAVN
TISGTSMASPHIAGLLAYYLSLQPAEDSEYALASITPKKLNENLISVATEDALSDIPS
PNLLAWNGGGCSDYKKIVEAGSYKVAAPSSRVVEIKHAVEQEVLNLSGKLTGAKELGS
KAEKFSKKIHELVDDEELEEFLKELNL
>P02622.1 Gad c 1; calcium-binding protein, parvalbumin [Gadus callarias]
AFKGIILSNADIKAAEAACFKEGSFDEDFYAKVGLDAFSADELKLLFKIADEDKEGFIEE
DELKFLIAFAADLRALTAETKAFLKAGDSGDGKIGVDEFGALVDKWKAGK
>P86980.1 Gad m 3; aldolase [Gadus morhua]
PHAYPFLSPEQKEL
>AAK63086.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]
MAFAGILADADCAA AVKACEAAESFSYKAFFAKCGLSGKSADDIKKAFFVIDQDKSGFIE
EDELKFLQVFKAGARALTAETKAFLKAGDSGDGGAIGVDEWAVLVKA
>AAK63087.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]
MAFAGILNDADITAALAACKAEGSFDHKAFFTKVGLAAKSPADIKKVFEEIDQDKSDFVE
EDELKFLQNFSAGARALSDAETKVFLKAGDSGDGKIGVDEFGAMIKA
>CAM56785.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]
MAFAGILADADCAA AVKACEAAESFSYKAFFAKCGLSGKSADDIKKAFFVIDQDKSGFIE
EDELKFLQVFKAGARALTAETKAFLKAGDSGDGGAIGVEEWAVLVKA
>CAM56786.1 Gad m 1; calcium-binding protein, parvalbumin [Gadus morhua]
MAFAGILNDADITAALAACKAEGSFDHKAFFTKVGLAAKSSADIKKVFEEIDQDKSDFVE
EDELKFLQNFSAGARALSDAETKVFLKAGDSGDGKIGVDEFGAMIKA
>B3A0L6.1 Gad m 2; enolase [Gadus morhua]
SITKIKAREIL
>QCI56571.1 tropomyosin [Galleria mellonella]
MDAIKKKMQAMKLEKDNALDRAAMCEQQAQKANDLRAEKAEFEARQLQKKIQTIENTLDQT
QESLMQVNGKLEEKALQNAESEVAALNRRIQLL EEDLERSEERLATATAKLSEASQAA
DESERARKVLENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE

ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREEEYKNQIKTLTTRLKEAEARAE
FAERSVQKLQKEV
>QCI56572.1 tropomyosin [Galleria mellonella]
MDAIKKKMQAMKLEKDNAMDKADTCEQQARDANLRAEKVNEEVRELQKKLAQVEEDLTLN
KNKLDQANKDLEEREKQLAATEAEVASLNRKVQQIEEDLEKSEERSGTAQQKLLLEAQQSA
DENNRMCVKLENRAQQDEERMDQLTNQLKEARLLAEDADGKSDEVSRKLAFVEDELEVAE
DRVKSGDAKISELEEEELKVVGN
>COMPARE00295 Gal d 10; aldolase, partial [Gallus gallus]
PHQYPALTPEQKELHDIKRIVAPGKGILAADESTGSIKRLSSVGAENTEENRRW
>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]
KKDGADFAKWRVCVKISEHTPTRLAIMENANVLARYASICQQNGIVPIVEPEILPDGDHD
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
>COMPARE00288 Gal d 9; beta-enolase, partial [Gallus gallus]
REILDSRGNPTVEVDLHTAKGHFRAAVPSGASTGIHEALELRDGDKKRF
>COMPARE00291 Gal d 9; beta-enolase, partial [Gallus gallus]
KAAIAQAGYTDKVVIGMDVAASEFCRDGRYDLDFKS
>COMPARE00292 Gal d 9; beta-enolase, partial [Gallus gallus]
KRIITGEQLGEIYRGFIKDYPVVSIEDPFDDWEAWKRF
>COMPARE100 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]
SIQKIHAREI
>COMPARE00289 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]
KAVEHINKTIGPALIEKKISVVEQEIKDKVMIEMDGTENKSKFGANAILGVSLAVCKA
>COMPARE00290 Gal d 9; beta-enolase, partial from P07322.3 [Gallus gallus]
KAGAAEKGVPLYRHIADLAGNTEILIPVPAFNVINGGSHAGNKLAMQEFMVLPVGAASFH
DAMRVGAEVYHSLKGVKA
>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
>CAX32963.1 Gal d 8; calcium-binding protein, parvalbumin [Gallus gallus]
MAMTDVLSAEDIKKAVGAFSAAESFNYKKFFEMVGLKKKSPEDVKKVFHILDKDRSGFIE
EEELKFVLKGFPTDGRDLSKDKETKALLAAGDKDGDGKIGADEFATMVAES
>CAA23711.1 Gal d 4; lysozyme [Gallus gallus]
MRSLILVLVLCFLPLAALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCVAKFESNFNTQA
TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDG
NGMSAWVAWRNRCKGTDVQAWIRGRL
>P00698.1 Gal d 4; lysozyme [Gallus gallus]
MRSLILVLVLCFLPLAALGKVFGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQA
TNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCACKIVSDG

NGMNAWVAWRNRCKGTDVQAWIRGCRL
>AAA48944.1 Gal d 4; lysozyme [Gallus gallus]
MNAWVAWRNSCKGTDVQAWIRGCR
>P02604.3 Gal d 7; myosin light chain [Gallus gallus]
MAPKKDVKKPAAAAAPAPAPAPAPAPAPAKPKEPAIDLKSIKIEFSKEQQDDFKEAFLLF
DRTGDAKITLSQVGDIVRALGQNPTNAEINKILGNPSKEEMNAKKITFEFELPMLQAAAN
NKDQGTFFEDFVEGLRVFDKEGNGTVMGAELRHVLATLGEKMTEEEVEELMKGQEDSNGCI
NYEAFVKHIMSV
>CAA23681.1 Gal d 2; ovalbumin [Gallus gallus]
MGSIAAASMEFCFDVFKELKVHGANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF
DKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNVYSFSLASRLYAEERYPILPEYFQ
CVKELYRGGLEPINFQTAADQARELINSWVESQTN
>P01012.2 Gal d 2; ovalbumin [Gallus gallus]
MGSIGAASMEFCFDVFKELKVHGANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF
DKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNVYSFSLASRLYAEERYPILPEYLQ
CVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIV
FKGLWEKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPEFASGTM
SMLVLLPDEVSGLEQLESIINFEKLTWETSSNVMEERKIKVYLPRMKMEEKYNLTSVLMA
MGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFR
ADHPFLFCIKHIATNAVLFFGRCVSP
>CAA23682.1 Gal d 2; ovalbumin [Gallus gallus]
MGSIGAASMEFCFDVFKELKVHGANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF
DKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNVYSFSLASRLYAEERYPILPEYLQ
CVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIV
FKGLWEKTFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPEFASGTM
SMLVLLPDEVSGLEQLESIINFEKLTWETSSNVMEERKIKVYLPRMKMEEKYNLTSVLMA
MGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFR
ADHPFLFCIKHIATNAVLFFGRCVSP
>1JTI_A Gal d 2; ovalbumin [Gallus gallus]
GSIGAASMEFCFDVFKELKVHGANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRF
KLPFGGDSIEAQCGTSVNVHSSLRDILNQITKPNVYSFSLASRLYAEERYPILPEYLQC
VKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSVDSQTAMVLVNAIVF
KGLWEKTFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPEFASGTM
MLVLLPDEVSGLEQLESIINFEKLTWETSSNVMEERKIKVYLPRMKMEEKYNLTSVLMAM
GITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGTEVVGSAEAGVDAASVSEEFRA
DHPFLFCIKHIATNAVLFFGRCVSP
>P01005.1 Gal d 1; ovomucoid [Gallus gallus]
MAMAGVFVLFVLCGFLPDAAFGAEVDCSRFPNATDKEGKDVLCNKDLRPICGTDGVT
YTNDCLLCAYSIEFGTNISKEHDGECKETVPMNCSSYANTTSEDGKVMVLCNRAFNPVCG
TDGVTYDNECLLCAHKVEQASVDKRHDGGCRKELAAVSVDCEYKPDCTAEDRPLCGS
DNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
>ACJ04729.1 Gal d 1; ovomucoid [Gallus gallus]
MAMAGVFVLFVLCGFLPDAVFGAEVDCSRFPNATDMEGKDVLCNKDLRPICGTDGVT
YTNDCLLCAYSVEFGTNISKEHDGECKETVPMNCSSYANTTSEDGKVMVLCNRAFNPVCG
TDGVTYDNECLLCAHKVEQASVDKRHDGGCRKELAAVSVDCEYKPDCTAEDRPLCGS
DNKTYGNKCNFCNAVVESNGTLTSLSHFGKC
>CAA26040.1 Gal d 3; ovotransferrin [Gallus gallus]
MKLILCTVLSLGLIAAVCF AAPPKSVIRWCTISSPEEKCNLRDLTQQERISLTCVQKAT
YLDICAIANNEADAISLDGGQVFEAGLAPYKLPKPIAAEIEYEHTEGSTTSYYAVAVVKKG
TEFTVNDLQGGNSCHTGLGRSAGWNIPIGTLHGWGAEWEGIESGSVEQAVAKFFSASCV

PGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAFVKHTTVNENAPDLN
DEYELLCLDGSRQPVVDNYKTCNWARVAHAHVARDNDNKVEDIWSFLSKAQSDFGVDTKSD
FHLFGPPGKDPVLKDFLFKDSAIMLKRVPVSLMDSQLYLGFEYYSIAIQSMRKDQLTPSPR
ENRIQWCAVGKDEKSKCDRWSVVSNGDVECTVDETKDCIIMKGEADAVALDGGLVYT
AGVCGLVPVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWNNLKGGKSCHTAVGRT
AGWVIPMGLIHNRTGTCNFDEYFSEGCAPGSPNSRLCQLCQSGGIPPEKCVASSHEKY
FGYTGALRCLVEKGDVAFIQHSTVEENTGGKNKADWAKNLQMDDFELLCTDGRANVMDY
RECNAEVPHTAVVVRPEKANKIRDLLERQEKRFVNGSEKSKFMMFESQNKDLLFKDLT
KCLFKVREGTTYKEFLGDKFYTVISNLKTCNPSDILQMCSFLEGK

>P02789.2 Gal d 3; ovotransferrin [Gallus gallus]

MKLILCTVLSLGLIAAVCFAPPKSVIRWCTISSPEEKCNLRDLTQQERISLTCVQKAT
YLDCIKAIANNEADAISLDGGQAFEAGLAPYKLPKPIAAEVYEHTEGSTTSYYAVAVVKKG
TEFTVNDLQGKTSCHTGLGRSAGWNIPIGTLHARGAIEWEGIESGSVEQAVAKFFSASCV
PGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAFVKHTTVNENAPDQK
DEYELLCLDGSRQPVVDNYKTCNWARVAHAHVARDNDNKVEDIWSFLSKAQSDFGVDTKSD
FHLFGPPGKDPVLKDLFLKDSAIMLKRVPVSLMDSQLYLGFEYYSIAIQSMRKDQLTPSPR
ENRIQWCAVGKDEKSKCDRWSVVSNGDVECTVDETKDCIIMKGEADAVALDGGLVYT
AGVCGLVPVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWNNLKGGKSCHTAVGRT
AGWVIPMGLIHNRTGTCNFDEYFSEGCAPGSPNSRLCQLCQSGGIPPEKCVASSHEKY
FGYTGALRCLVEKGDVAFIQHSTVEENTGGKNKADWAKNLQMDDFELLCTDGRANVMDY
RECNAEVPHTAVVVRPEKANKIRDLLERQEKRFVNGSEKSKFMMFESQNKDLLFKDLT
KCLFKVREGTTYKEFLGDKFYTVISSLKTCNPSDILQMCSFLEGK

>CAA43098.1 Gal d 5; serum albumin [Gallus gallus]

MKWVTLISFIFLSSATSRNLQRFARDAEHKSEIAHRYNDLKEETFKAVAMITFAQYLQR
CSYEGLSKLVKDVVLAQKCVANEDAPECSKPLPSIILDEICQVEKL RDSYGAMADCCSK
ADPERNECFLSFKVSPDFVQPYQRPASDVICQEQYQDNRVSF LGHFYISVARRHPFLYAP
AILSFAVDFEHALQSCCKESDVGACLDTKEIVMREKAKGVSVKQQYFCGILKQFGDRVFQ
ARQLIYLSQKYPKAPFSEVSKFVHDSIGVHKECCEGDMVECMDDMARMMSNLCSQQDVFS
GKIKDCCEKPIVERSQCIMEAEFDEKPADLPSLVEKYIEDKEVCKSF EAGHDAFMAEFVY
EYSRRHPEFSIQLIMRIAKGYESLLEKCKTDNPAECYANAQEQLNQHIKETQDVVKTNC
DLLHDHGEADFLKSILIRYTKMPQVPTDLLLETGKKMTTIGTKCCQLGEDRRMACSEGY
LSIVIHTDCRKQETTPINDVNSQCCS QLYANRRPCFTAMGVDTKYVPPFPNPMFSFDEK
LCSAPAEEREVGMKLLINLIKRPQMTEEQIKTIADGFTAMVDKCKQSDINTCFGEEG
ANLIVSRATLGIGA

>P02845 vitellogenin [Gallus gallus]

AEAPSAVLENL KARCSVSYNKIKTFNEVKFNYSMPANCYHILVQDCSSELKFLVMMKSAG
EATNLKAINIKIGSHEIDMHPVNGQVKLLVDGAESPTANISLISAGASLWIHNENQGFAL
AAPGHGIDKLYFDGKTITIQVPLWMAGKTCGICGKYDAECEQEYRMPNGYLAKNAVSFGH
SWILEEAPCRGACKLHRSFVKLEKTVQLAGVDSKCYSTEPVLRCAKGC SATKTPVTVGF
HCLPADSANS LTKQMKYDQKSEDMQD TVDAHTTCSCENE ECST

>MANUAL3 Gal d 6; vitellogenin, partial [Gallus gallus]

PEIASQIAQEDQSTCEVSKGDFKTFDRMSFTCSFNKSCNVVVAQDCTEHPKFIITTRKVD
HQLSREHVHINTSSANITICPAADSSLLVTCNKESVLSDSGVSEYEKDN IKIYKNGKTVI
VEAPIHGLKNVNF DGEILKVTVASWMRGKTCGVCGNNDREKH NELLMPNHKLAHSCSAFV
HSWVLEETCSGGCKLQRRYVKLNRNPTIDGEESTCYSVDPVLKCMKDCTPIEKTSVKVG
FHC FPKATAVSLLEWQRSSDKKSASEDVVESVDADIDCTCTGDCS

>AAF82096.1 Glo m 5; unknown function, antigen 5 [Glossina morsitans]

MNFVLATLSLLILGSAAVGGDYCGLCDNH DACVMQNVFQSGCPSGAKMIDLNKYQSALLD
AHNKKRNHVAGGESKLRACQMATMKW DSELAKLAEYNVKQCQMNHDCRNTVKFKYAG
QNLAELGRSGGPPPDYRKLIEKAVDKWYEEVKDCNQGYIDSYPMN YRGAIGHFTVMVAE

RNTHVGCASEYTKSNGFQYFLMACNYATTNMMEFPIYKSCGSSAQDCKSGKNSKYPNLC
SPNEKEYEVNKWIKNGVEYH

>ADD18879.1 Glo m 5; unknown function, antigen 5 [Glossina morsitans]
MKFVLATLNLVLSAGSVDYCNLCEKHVACVSQNVFQSGCSDAKMIDLKKYQTLLDA
HNKKRDNVAGGGESKLRACRMATMKWNSLAKLAEYNVRQCEMNHDKCRNTNTFKYAGQ
NLAELGRSGAGTPDYGQLIQKAVDSWYEEVNDNCNQYIDSYPKDYKGPAGHFTVMVAER
NTHMGCAASQYTRSNGFTYFLLACNYATTNMMEFPIYKSCSASAQDCKTGKNSKYQNLCS
ANEKEYEVNRWFKDQVEYQ

>ADD19985.1 Glo m 5; unknown function, antigen 5 [Glossina morsitans]
MNFVLATLSLLILLSAAVSADYCGLCDNHVACVMQNVFQSGCPSGAKMIDLNKYQSTLLD
AHNKKRNHVAGGGESKLRACQMATMKWDPELAKLAEYNVKQCQMNHDKCRNTVKFKYAG
QNLAEGRSGGPDYDYGQLIQKAVDKWYEEVKDCNQYIDAYPMNYRGPAGHFTVLVAE
RNTHMGCAASEYTKSNGFKYFLMACNYATTNMMDFPIYKSCGSSAQDCKSGKNSKYPNLC
SPNEKEYEVNKWIKNGMEYH

>ADD19989.1 Glo m 5; unknown function, antigen 5 [Glossina morsitans]
MNFVLATLSLLILGSAAVGGDYCGLCDNHVACVMQNVFQSGCPSGAKMIDLNKYQSALLD
AHNKKRNHVAGGGESKLRACQMATMKWSELAKLAEYNVKLIEKAVDKWYEEVKDCNQG
YIDSYPMNYRGPAGHFTVMVAERNTHVGCASEYTKSNGFQYFLMACNYATTNMMEFPI
YKSCGSSAQDCKSGKNSKYPNLCSPNEKEYEVNKWIKNGVEYH

>Q9YJ8.2 plasminogen activator [Gloydius brevicaudus]
MALIRVLANLLILQLSYAQKSSSELVVGDECNINEHRSLVLFNSSGLICSGTLINQEWV
LTAAHCDKSNFQMLFGVHSHKILNEDEQTRDPKEKFCPNKKKDDKDKDIMLIRLDSPV
SNSEHIAPLSLSSSPTVDSVCRIMGWGTIKPADEYTPDVPHCANINILDHTVCRAAYPV
LLAGSSTLCAGTQQGGKDTCVGDSGGPLICNGQIQGIVSWGAPCGQGSKPGVYTKVFDH
LDWIKSIIAGNTAVTCP

>CAA26575.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MAKLVLSLCFLLFSGCFALREQAQQNECQIQKLNALKPGNRIESEGGFIETWPNPNNKPFQ
CAGVALSRCTLNARNALRRPSYTNQPQEIYIQQNGIFGMIFPGCPSTYQEPQESQQRGRS
QRPQDRHQVHRFREGDLIAVPTGVAVWMMYNNEDTPVAVSIIIDTNSLENQLDQMPRRFY
LAGNQEQEFLKYQQQQQGGQSQKQKQEEENEENEGSNILSGFAPEFLKEAFGVNMQIVRNL
QGENEEEDSGAIVTVKGGRLVTAPAMRKPQEEEDDDDEEQPQCVETDKGCQRQSKRSRN
GIDETICTMRLRQNIQNSSPDIYNPQAGSITTATSLDFPALWLLKLSAQYGSRLKRNAMF
VPHYTLNANSIIYALNGRALVQVNCNGERVFQDQEGGVLIQVQNFVAVAKSQSDNFE
YVSFKTNDRPSIGNLAGANSLNALPEEVIQHTFNLKSQQARQVKNNNPFSLVPPQESQ
RRAVA

>CAA26723.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MAKLVFSLCFLLFSGCCFAFSSREQPQQNECQIQKLNALKPGNRIESEGGFIETWPNPNNK
PFQCAGVALSRCTLNARNALRRPSYTNQPQEIYIQQGGKIFGMIFPGCPSTFEPPQQPQR
GQSSRPQDRHQKIYNSREGDLIAVPTGVAVWMMYNNEDTPVAVSIIIDTNSLENQLDQMPR
RFYLAGNQEQEFLKYQQEQGGHQSQKQKHQEEENEENEGGSILSGFTLEFLEHAFVVDKQIA
KNLQGENEGEDKGAIVTVKGGLSVIKPPPTDEQQQRQEEEEEEDEKPKQCKGDKHCQRP
RGSQSKSRRNGIDETICTMRLRHNIQGTSSPDIYNPQAGSVTTATSLDFPALSRLSAG
FGSLRKNAMFVPHYNLANSIIYALNGRALIQVNCNGERVFQDQEGRVLIVPQNFV
AARSQSDNFEYVSFKTNDTPMIGTLAGANSLNALPEEVIQHTFNLKSQQARQIKNNNPF
KFLVPPQESQKRAVA

>CAA33217.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MAKLVLSLCFLLFSGCCFAFSSREQPQQNECQIQRLNALKPDNRIESEGGFIETWPNPNNK
PFQCAGVALSRCTLNARNALRRPSYTNAPQEIYIQQGGSGIFGMIFPGCPSTFEPPQQKQGS
SRPQDRHQKIYHFREGDLIAVPTGFAYWMMYNNEDTPVAVSLIDTNSFNQQLDQMPRRFY
LAGNQEQEFLQYQPKQGGTQSQKQKQEEENEENEGGSILSGFAPEFLHAFVVDKQIVR

KLQGENEEEEKGAIVTVKGGLSVISPPTEEQQRPEEEEEKPCDEKDKHCQSQRNGIDE
TICTMRLRHNIQTSSPDIENPQAGSITTATSLDFPALS WLKLSAQFGSLRKNAMFVPHY
NLNANSIIYALNGRALVQVNCNGERVF DGE LQEGQV L IVPQNFAVAARSQSDNF EYVSF
KTNDRPSIGNLAGANS LLNALPEEVIQQT FNLR RQQRARQVKNNNPF SFLVPPKESQRRVV
A

>CAA37044.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MGKPF T L S L S L C L L L L S S A C F A I S S S K L N E C Q L N N L N A L E P D H R V E F E G G L I Q T W N S Q H
P E L K C A G V T V S K L T L N R N G L H L P S Y S P Y P R M I I A Q G K G A L Q C K P G C P E T F E E P Q E Q S N R
R G S R S Q K Q Q L Q D S H Q K I R H F N E G D V L V I P P G V P Y W T Y N T G D E P V V A I S L L D T S N F N N Q L D
Q T P R V F Y L A G N P D I E Y P E T M Q Q Q Q Q K S H G G R K Q G Q H Q Q E E E E E G G S V L S G F S K H F L A Q S
F N T N E D I A E K L Q S P D D E R K Q I V T V E G G L S V I S P K W Q E Q Q D E D E D E D E D E D E Q I P S H P P R
R P S H G K R E Q D E D E D E D E D K P R P S R P S Q G K R E Q D Q D Q D E D E D E D E D Q P R K S R E W R S K K T Q P
R R R P R Q E E P R E R G C E T R N G V E E N I C T L K L H E N I A R P S R A D F Y N P K A G R I S T L N S L T L P A L R
Q F Q L S A Q Y V V L Y K N G I Y S P H W N L N A N S V I Y V T R G Q G K V R V V N C Q G N A V F D G E L R R G Q L L V
V P Q N F V V A E Q A G E Q G F E Y I V F K T H H N A V T S Y L K D V F R A I P S E V L A H S Y N L R Q S Q V S E L K Y
E G N W G P L V N P E S Q Q G S P R V K V A

>AAA33964.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MGKPF T L S L S L C L L L L S S A C F A I T S S K F N E C Q L N N L N A L E P D H R V E S E G G L I E T W N S Q
H P E L Q C A G V T V S K R T L N R N G S H L P S Y L P Y P Q M I I V V Q G K G A I G F A F P G C P E T F E K P Q Q Q S
S R R G S R S Q Q L Q D S H Q K I R H F N E G D V L V I P L G V P Y W T Y N T G D E P V V A I S P L D T S N F N N Q L
D Q N P R V F Y L A G N P D I E H P E T M Q Q Q Q Q K S H G G R K Q G H R Q Q E E E G G S V L S G F S K H F L A Q S
F N T N E D T A E K L R S P D D E R K Q I V T V E G G L S V I S P K W Q E Q E D E D E D E D E E Y G R T P S Y P P R R P
S H G K H E D D E D E D E E D Q P R P D H P P Q R P S R P E Q Q E P R G R G C Q T R N G V E E N I C T M K L H E N I A
R P S R A D F Y N P K A G R I S T L N S L T L P A L R Q F G L S A Q Y V V L Y R N G I Y S P D W N L N A N S V T M T R G
K G R V R V V N C Q G N A V F D G E L R R G Q L L V P Q N P A V A E Q G G E Q G L E Y V V F K T H H N A V S S Y I K D
V F R V I P S E V L S N S Y N L G Q S Q V R Q L K Y Q G N S G P L V N P

>AAA33965.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
Q E D E D E D E D E E Y E Q T P S Y P P R R P S H G K H E D D E D E D E E H Q P R P D H P P Q R P S R P E Q Q E P R G
R G C Q T R N G V E E N I C T M K L H E N I A R P S R A D F Y N P K A G R I S T L N S L T L P A L R Q F G L S A Q Y L V
L Y R N G I Y S P H W N L N A N S V I Y V T R G K G R V R V V N C Q G N P V F D G D L T R G Q L L L V P Q N F V V A D Q
G G K Q G L E Y V V F K T Q H N A V S S Y I K D L F R A I P S E V L S N S Y N L G Q S Q V R Q L K Y Q G N S G P L L N P

>AAA33966.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
M A K L V F S L C F L L F S G C C F A F S S R E Q P Q Q N E C Q I Q K L N A L K P D N R I E S E G G L I E T W N P N N K
P F Q C A G V A L S R C T L N R N A L R R P S Y T N G P Q E I Y I Q Q G K I F G M I Y P G C P S T F E E P Q Q P Q Q R
G Q S S R P Q D R H Q K I Y N F R E G D L I A V P T G V A W W M Y N N E D T P V V A V S I I D T N S L E N Q L D Q M P R
R F Y L A G N Q E Q E F L K Y Q Q E Q G G H Q S Q K G K H Q Q E E E N E G G S I L S G F T L E F L E H A F S V D K Q I A
K N L Q G E N E G E D K G A I V T V K G G L S V I K P P T D E Q Q Q R P Q E E E E E E D E K P Q C K G K D K H C Q R P
R G S Q S K S R R N G I D E T I C T M R L R H N I G Q T S S P D I Y N P Q A G S V T T A T S L D F P A L S W L R L S A E
F G S L R K N A M F V P H Y N L N A N S I I Y A L N G R A L I Q V V N C N G E R V F D G E L Q E G R V L I V P Q N F V V
A A R S Q S D N F E Y V S F K T N D T P M I G T L A G A N S L L N A L P E E V I Q H T F N L K S Q Q A R Q I K N N N P F
K F L V P P Q E S Q K R A V A

>BAA00154.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
M A K L V L S L C F L L F S G C F A L R E Q A Q Q N E C Q I Q K L N A L K P D N R I E S E G G F I E T W N P N N K P F Q
C A G V A L S R C T L N R N A L R R P S Y T N G P Q E I Y I Q Q G N G I F G M I F P G C P S T Y Q E P Q E S Q Q R G R S
Q R P Q D R H Q K V H R F R E G D L I A V P T G V A W W M Y N N E D T P V V A V S I I D T N S L E N Q L D Q M P R R F Y
L A G N Q E Q E F L K Y Q Q Q Q G G S Q S Q K G K Q Q E E E N E G S N I L S G F A P E F L K E A F G V N M Q I V R N L
Q G E N E E E D S G A I V T V K G G L R V T A P A M R K P Q Q E E D D D E E E Q P Q C V E T D K G C Q R Q S K R S R N
G I D E T I C T M R L R Q N I G Q N S S P D I Y N P Q A G S I T T A T S L D F P A L W L L K L S A Q Y G S L R K N A M F
V P H Y T L N A N S I I Y A L N G R A L V Q V V N C N G E R V F D G E L Q E G G V L I V P Q N F A V A A K S Q S D N F E
Y V S F K T N D R P S I G N L A G A N S L L N A L P E E V I Q H T F N L K S Q Q A R Q V K N N N P F S F L V P P Q E S Q

RRAVA

>CAA26478.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MGKPF T L S L S L C L L L L S S A C F A I S S S K L N E C Q L N N L N A L E P D H R V E S E G G L I Q T W N S Q H
P E L K C A G V T V S K L T L N R N G L H S P S Y P Y P R M I I A Q G K G A L G V A I P G C P E T F E E P Q E Q S N
R R G S R S Q K Q Q L Q D S H Q K I R H F N E G D V L V I P P S V P Y W T Y N T G D E P V V A I S L L D T S N F N N Q L
D Q T P R V F Y L A G N P D I E Y P E T M Q Q Q Q Q K S H G G R K Q G H Q Q E E E E E G G S V L S G F S K H F L A Q
S F N T N E D I A E K L E S P D D E R K Q I V T V E G G L S V I S P K W Q E Q Q D E D E D E D E D E D E Q I P S H P P
R R P S H G K R E Q D E D E D E D E D E D K P R P S R P S Q G K R N K T G Q D E D E D E D E D Q P R K S R E W R S K K T Q P
R R P R Q E E P R E R G C E T R N G V E E N I C T L K L H E N I A R P S R A D F Y N P K A G R I S T L N S L T L P A L R
Q F Q L S A Q Y V V L Y K N G I Y S P H W N L N A N S V I Y V T R G Q G K V R V V N C Q G N A V F D G E L R R G Q L L V
V P Q N F V V A E Q A G E Q G F E Y I V F K T H H N A V T S Y L K D V F R A I P S E V L A H S Y N L R Q S Q V S E L K Y
E G N W G P L V N P E S Q Q G S P R V K V A

>BAA74953.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MGKPF T L S L S L C L L L L S S A C F A I S S S K L N E C Q L N N L N A L E P D H R V E S E G G L I Q T W N S Q H
P E L K C A G V T V S K L T L N R N G L H L P S Y S P Y P R M I I A Q G K G A L G V A I P G C P E T F E E P Q E Q S N
R R G S R S Q K Q Q L Q D S H Q K I R H F N E G D V L V I P P G V P Y W T Y N T G D E P V V A I S L L D T S N F N N Q L
D Q T P R V F Y L A G N P D I E Y P E T M Q Q Q Q Q K S H G G R K Q G H Q Q E E E E E G G S V L S G F S K H F L A Q
S F N T N E D I A E K L Q S P D D E R K Q I V T V E G G L S V I S P K W Q E Q Q D E D E D E D E D E D E Q I P S H P P
R R P S H G K R E Q D E D E D E D E D K P R P S R P S Q G K R E Q D Q D Q D E D E D E D E D Q P R K S R E W R S K K T Q
P R R P R Q E E P R E R G C E T R N G V E E N I C T L K L H E N I A R P S R A D F Y N P K A G R I S T L N S L T L P A L R
R Q F Q L S A Q Y V V L Y K N G I Y S P H W N L N A N S V I Y V T R G Q G K V R V V N C Q G N A V F D G E L R R G Q L L
V V P Q N F V V A E Q A G E Q G F E Y I V F K T H H N A V T S Y L K D V F R A I P S E V L A H S Y N L R Q S Q V S E L K
Y E G N W G P L V N P E S Q Q G S P R V K V A

>BAB15802.1 Gly m 6; 11S globulin, glycinin, cupin [Glycine max]
MGKPF T L S L S L C L L L L S S A C F A I T S S K F N E C Q L N N L N A L E P D H R V E S E G G L I E T W N S Q
H P E L Q C A G V T V S K R T L N R N G L H L P S Y S P Y P Q M I I V V Q G K G A I G F A F P G C P E T F E K P Q Q Q S
S R R G S R S Q Q Q L Q D S H Q K I R H F N E G D V L V I P P G V P Y W T Y N T G D E P V V A I S L L D T S N F N N Q L
D Q N P R V F Y L A G N P D I E H P E T M Q Q Q Q Q K S H G G R K Q G H Q Q E E E G G S V L S G F S K H F L A Q S
F N T N E D T A E K L R S P D D E R K Q I V T V E G G L S V I S P K W Q E Q E D E D E D E D E E Y E Q T P S Y P P R R P
S H G K H E D D E D E D E E D Q P R P D H P P Q R P S R P E Q Q E P R G R G C Q T R N G V E E N I C T M K L H E N I A
R P S R A D F Y N P K A G R I S T L N S L T L P A L R Q F G L S A Q Y V V L Y R N G I Y S P H W N L N A N S V I Y V T R
G K G R V R V V N C Q G N A V F D G E L R R G Q L L V P Q N F V V A E Q G G E Q G L E Y V V F K T H H N A V S S Y I K
D V F R A I P S E V L S N S Y N L G Q S Q V R Q L K Y Q G N S G P L V N P

>AAD09630.1 Gly m 8; 2S albumin, conglutin [Glycine max]
M T K L T I L L I A L L F I A H T C C A S K W Q H Q Q E S C R E Q L K G I N L N P C E H I M E K I Q A G R R G E D G S
D E D H I L I R T M P G R I N Y I R K K E G K E E E E E G H M Q K C C S E M S E L K S P I C Q C K A L Q K I M D N Q S E
Q L E G K E K K Q M E R E L M N L A I R C R L G P M I G C D L S S D D

>NP_001238443.1 Gly m 8; 2S albumin, conglutin [Glycine max]
M T K F T I L L I S L L F C I A H T C S A S K W Q H Q Q D S C R K Q L Q G V N L T P C E K H I M E K I Q G R G D D D D D
D D D D N H I L R T M R G R I N Y I R R N E G K D E D E E E E G H M Q K C C T E M S E L R S P K C Q C K A L Q K I M E N
Q S E E L E E K Q K K K M E K E L I N L A T M C R F G P M I Q C D L S S D D

>CAA35691.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
M M R A R F P L L L L G L V F L A S V S V S F G I A Y W E K E N P K H N K C L Q S C N S E R D S Y R N Q A C H A R C N L
L K V E K E E C E E G E I P R P R P R P Q H P E R E P Q Q P G E K E E D E D E Q P R P I P F P R P Q P R Q E E E H E Q R
E E Q E W P R K E E K R G E K G S E E E D E D E E E Q D E R Q F P F P R P P H Q K E E R N E E E D E D E E Q Q R E S E
E S E D S E L R R H K N K N P F L F G S N R F E T L F K N Q Y G R I R V L Q R F N Q R S P Q L Q N L R D Y R I L E F N S
K P N T L L L P N H A D A D Y L I V I L N G T A I L S L V N N D D R D S Y R L Q S G D A L R V P S G T T Y Y V V N P D N
N E N L R L I T L A I P V N K P G R F E S F F L S S T E A Q Q S Y L Q G F S R N I L E A S Y D T K F E E I N K V L F S R
E E G Q Q Q G E Q R L Q E S V I V E I S K E Q I R A L S K R A K S S S R K T I S S E D K P F N L R S R D P I Y S N K L G
K F F E I T P E K N P Q L R D L D I F L S I V D M N E G A L L L P H F N S K A I V I L V I N E G D A N I E L V G L K E Q

QQEQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVVNATSNLNFFAIGINAENNQRNFLA
GSQDNVISQIPVQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKGPLSSI
LRAFY

>P25974.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
MMRVRFPLLVLVLLGTVFLASVCSLKVREDENNPFFYFRSSNSFQTLFENQNVIRILLQRFN
KRSPQLENLRDYRIVQFQSKPNTILLPHHADADFLFVLSGRAILTLVNNDDRDSYNLHP
GDAQRIPAGTTYLVNPHDQNLKIIKLAIPVKNKPGRYDDFFLSSTQAQQSYLQGFSHNI
LETSFHSEFEEINRVLFGEERQEQEGVIVELSKEQIRQLSRRAKSSSRKTISSEDEPF
NLRSRNPIYSNNGFKFFEITPEKNPQLRDLDFLSSVDINEGALLLPHFNKAIIVILVIN
EGDANIELVGIKEQQQKQKQEEPLEVQRYRAELSEDDVFVIPAAYPFVVVNATSNLNFLA
FGINAENNQRNFLAGEKDNVVRQIERQVQELAFPGSAQDVERLLKKQRESYFVDAQPQK
EEGSKGRKGFPSILGALY

>AAA33947.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
SKRAKSSSRKTISSEDKPFNLGSRDPIYSKLGKFFEITPEKNPQLRDLDFLSIVDMNE
GALLLPHFNKAIIVILVINEGDANIELVGLKEQQEQQEEQPLEVRKYRAELSEQDIFV
IPAGYPVVVNATSNLNFFAIGINAENNQRNFLAGSQDNVISQIPVQVQELAFPGSAQAVE
KLLKNQRESYFVDAQPNEKEEGNKGRKGPLSSILRAFY

>AAB01374.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
MMRARFPLLLLGVVFLASVSVSFGIAYWEKQNP SHNKCLRSCNSEKDSYRNQACHARCNL
LKVEEEEECEEGQIPRPRPQHPERERQQHGEKEEDEGEQPRPFPRPRQPHQEEEEHEQK
EEHEWHRKEEKHGKGSSEEQDEREHPRHQPHQKEEEKHEWQHKQEKHQKESEEEEED
QDEDEEQDKESQESGESQREPRRHKNKNPFFHNSKRFQTLFKNQYGHVRLQRFNKRS
QQQLNLRDYRILEFNKSPNTLLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDA
LRVPAGTTYVVPNDNENLRMIAGTTYVVPNDNENLRMITLAIPVKNKGRFESFFLS
STQAQQSYLQGFKNILEASYDTKFEEINKVLFGREEGQQGEERLQESVIVEISKKQIR
ELSKHAKSSSRKTISSEDKPFNLGSRDPIYSNKLGLKFEITQRNPQLRDLDFLSVDMN
EGALFLPHFNKAIIVLVINEGEANIELVGIKEQQQRQQEEQPLEVRKYRAELSEQDIF
VIPAGYPVMVNATSDLNFFAFGINAENNQRNFLAGSKDNVISQIPVQVQELAFPRSAKDI
ENLIKSSQSESYFVDAQPQQKEEGNKGRKGPLSSILRAFY

>BAB64303.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
MMRARFPLLLLGVVFLASVSVSFGIAYWEKQNP SHNKCLRSCNSEKDSYRNQACHARCNL
LKVEEEEECEEGQIPRPRPQHPERERQQHGEKEEDEGEQPRPFPRPRQPRQEGEHEQK
EEHEWHRKEEKHGKGSSEEQDGREHPRHQPHQKEEEKHEWQHKQEKHQKESEEEEED
QDEDEEQDKESQESGESQREPRRHKNKNPFFHNSKRFQTLFKNQYGHVRLQRFNKRS
QQQLNLRDYRILEFNKSPNTLLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDA
LRVPAGTTYVVPNDNENLRMITLAIPVKNKGRFESFFLSSTQAQQSYLQGFKNILEA
SYDTKFEEINKVLFGREEGQQGEERLQESVIVEISKKQIRELSKRAKSSSRKTISSEDK
PFNLRSDPIYSNKLGLKFEITPEKNPQLRDLDFLSVDMNEGALFLPHFNKAIIVLV
INEGEANIELVGIKEQQQRQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVVNATSDLN
FAFGINAENNQRNFLAGSKDNVISQIPVQVQELAFVLSAKDIENLIKSSQSESYFVDAQPQ
QKEEGNKGRKGPLSSILRAFY

>BAB64306.1 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]
MMRVRFPLLVLVLLGTVFLASVCSLKVREDENNPFFYFRSSNSFQTLFENQNGRIRILLQRFN
KRSPQLENLRDYRIVQFQSKPNTILLPHHADADFLFVLSGRAILTLVNNDDRDSYNLHP
GDAQRIPAGTTYLVNPHDQNLKIIKLAIPVKNKPSRYDDFFLSSTQAQQSYLQGFSHNI
LETSFHSEFEEINRVLFGEERQEQEGVIVELSKEQIRQLSRRAKSSSRKTISSEDEPF
NLRSRNPIYSNNGFKFFEITPEKNPQPRDLDFLSSVDINEGALLLPHFNKAIIVILVIN
EGDANIELVGIKEQQQKQKQEEPLEVQRYRAELSEDDVFVIPAAYPFVVVNATSNLNFLA
FGINAENNQRNFLAGEKDNVVRQIERQVQELAFPGSAQDVERLLKKQRESYFVDAQPQK
EEGSKGRKGFPSILGALY

>BAA23361.2 Gly m 5; 7S globulin, vicilin, beta-conglycinin [Glycine max]

LKVREDENNPFYFRSSNSFQTLFENQNGRIRLLQRFNKRSPQLENLRDYRIVQFQSKPNT
ILLPHHADADFLFVLSGRAILTLVNNDDRDSYNLHPGDAQRIPAGTTYLVNPHDHQNL
KIIKLAIPVKNKPGRYDDFFLSSTQAQQSYLQGFSHNILETSFHSEFEEINRVLFGEEEEQ
RQQEGVIVELSKEQIRQLSRRRAKSSSRKTISSEDEPFNLSRNPIYSNNFGKFFEITPEK
NPQLRDLDFLSSVDINEGALLLPHFNKAIVILVINEGDANIELVGIKEQQQKQKQEEE
PLEVQRYRAELSEDDVVFIPAAYPFVFNATSNLNF LAFGINAENNRNFLAGEKDNVVRQ
IERVQVQELAFPGSAQDVERLLKKQRESYFVDAQPQQKEEGSKGRKGPFPSPILGALY

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

VEKEECEEGEIPRPRRQHPEREPQQPGEKEEDEDEQPRPIPFRPQPRQEEHEQREE
QEWPRKEEKRGEKGSSEDEDEDEEEDERQFPFRPPHQKEERKQEEDEDEEQRESEES
EDSELRRHKNKNPFLFGSNRFETLFKNQYGRIRVLQRFNQRSPQLQNLRDYRILEFNPKP
NTLLLPHHADADYLIVILNGTAILSLVNNDDRDSYRLQSGDALRVPSGTTYVVNPDNNE
NLRLITLAIPVKNKPGRFESFFLSSTEAQQSYLQGF SRNILEASYDTKFEEINKVLF SREE
GQQQGEQRLQESVIVEISKEQIRALSKRAKSSSRKTISSEDKPFNLSRDPIYSNKLKGF
FEITPEKNPQLRDLDFLSIVDMNEGALLLPHFNKAIVILVINEGDANIELVGLKEQQQ
EQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVFNATSNLNF FAIGINAENNRNFLAG S
QDNVISQIPSQVQELAFPGSAQAVEKLLKNQRESYFVDAQPKKKEEGNKGRKGPLSSILR
AFY

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

VEEEEECEEGQIPRPRRQHPERERQQHGEKEEDEGEQPRPFPRRPRQPHQEEHEQKEE
HEWHRKEEKHGGKGSSEEQDEREHPRHQPHQKEEEKHEWQHKQEKHQKESSEEEEDQD
EDEEQDKESQESGESQREPRRHKNKNPFFHNSKRFQTLFKNQYGHVRVLQRFNKR SQQ
LQNLRDYRILEFNPKPNTLLLPHHADADYLIVILNGTAILTLVNNDDRDSYNLQSGDALR
VPAGTTYVVNPDNDENLRMITLAIPVKNKPGRFESFFLSSTQAQQSYLQGF SKNILEASY
DTKFEEINKVLF GREEGQQQGEERLQESVIVEISKKQIRELSKHAKSSSRKTISSEDKPF
NLSRDPIYSNKLKGLFEITPEKNPQLRDLDFLSVDMNEGALFLPHFNKAIVVLVIN
EGEANIELVGIKEQQQRQQQEEQPLEVRKYRAELSEQDIFVIPAGYPVVFNATSDLNFFA
FGINAENNRNFLAGSKDNVISQIPSQVQELAFPGSAKD IENLIKSESYFVDAQPQQK
EEGNKGRKGPLSSILRAFY

>ACD36974.1 7S globulin, vicilin, partial [Glycine max]

LDSNLIIFIRRGAEAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICS I
DPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTVVVEIFSKELDGPIMFV
DDSHVPSLWTKFLQLKKDDKEQQLKMMQDQEED EEEKQTSRSWRKLLLETVFGKVNEKIE
NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLEPDIGVLLVKLSAGSMLAPH
VNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDV FVPRYFPFCQVASRDGPLEFF
GFSTSARKNKPQFLAGAASLLR TLMGP ELSAAFVSEDTLRRAVDAQHEAVILPSAWAAP
PENAGKLMEEEP

>ACD36975.1 7S globulin, vicilin, partial [Glycine max]

LDSNLIIFIRRGAEAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICS I
DPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTVVVEIFSKELDGPIMFV
DDSHAPSLWTKFLQLKKDDKEQQLKMMQDQEED EEEKQTSRSWRKLLLETVFGKVNEKIE
NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLEPDIGVLLVKLSAGSMLAPH
VNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDV FVPRYFPFCQVASRDGPLEFF
GFSTSARKNKPQFLAGAASLLR TLMGP ELSAAFVSEDTLRRAVDAQHEAVILPSAWAAP
PENAGKLMEEEP

>ACD36976.1 7S globulin, vicilin, partial [Glycine max]

LDSNLIIFIRRGAEAKLGFYDDELAERRLKTGDLYMIPSGSAFYLVNIGEGQRLHVICS I
DPSTSLGLETFQSFNIGGGANSHSVLSGFEP AILETAFNESRTVVVEETFSKELDGPIMFV
DDSHAPSLWTKFLQLKKDDKEQQLKMMQDQEED EEEKQTSRSWRKLLLETVFGKVNEKIE

NKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLEPDIGVLLVKL SAGSMLAPH
VNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPYFPFCQVASRDGPLEFF
GFST SARKNK PQFLAGAASLLR TLMGPELSAAFVSEDTL RRAVDAQHA AVILPSAWAAP
PENAGKLMEEEP

>ACD36978.1 7S globulin, vicilin, partial [Glycine max]
VLCHGVATTTMAFH DDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLKSHGGRIFYRHM
HIGFISMEPKSLFVPQYLD SNLIIFIRRG EAKLGFYDDELAERRLKTGDLYMIPSGSAFY
LVNIGEGQRLHVICSIDPSTSLGLETFQSFYIGGGANSHSVLSGFEP AILETAFNESRTV
VEEIFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKMMQDQE EDEEEKQTSRSW
RKLLETVFGKVNEKIENKDTAGSPASYNLYDDKKADFKNAYGWSKALHGGEYPPLEPDI
GVLLVKL SAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSKAMKTKIKQGDVFVVPY
FPFCQVASRDGPLEFFGFST SARKNK PQFLAGAASLLR TLMGPELSAAFVSEDTL RRAV
DAQHEAVILPSAWAAPRKMQEAEEMESQMLLKL CQ

>BAB21619.2 7S globulin, vicilin, partial [Glycine max]
MGNKTTLLLLL FVLCHGVATTTMAFH DDEGGDKKSPKSLFLMSNSTRVFKTDAGEMRVLK
SHGGRIFYRHM HIGFISMEPKSLFVPQYLD SNLIIFIRRG EAKLGFYDDELAERRLKTG
DLYMIPSGSAFYLVNIGEGQRLHVICSIDPSTSLGLETFQSFYIGGGANSHSVLSGFEP A
ILETAFNESRTVVEEIFSKELDGPIMFVDDSHAPSLWTKFLQLKKDDKEQQLKMMQDQE
EDEEEKQTSRSWRK LLETVFGKVNEKIENKDTAGSPASYNLYDDKKADFKNAYGWSKALH
GGEYPPLEPDIGVLLVKL SAGSMLAPHVNPISDEYTIIVLSGYGELHIGYPNGSRAMKTK
IKQGDVFVVPYFPFCQVASRDGPLEFFGFST SARKNK PQFLAGAASLLR TLMGPELSAA
FGVSEDTL RRAVDAQHEAVILPSAWAAPPENAGKLMEEEPNAIRSFANDVVMDF

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

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

MGVFTFEDEINSPVAPATLYKALVTDADNVIPKALDSFKSVENVEGNGGPGTIKKITFLE
DGETK FVLHKIESIDEANL GYSYSVVGGAALPD TAEKITFDSKLVAGPNGGSAGKLT VKY
ETKGDAEPNQDELKTGKAKADALFKAIEAYLLAHPDYN

>CAA11755.1 Gly m 3; profilin [Glycine max]
MSWQAYVDDHLLCGIEGNHLTHAAIIGQDGSVWLQSTDFPQFKPEEITAIMNDFNEPGSL
APTGLYLGGTKYMVIQGE PGAVIRGKKKPGGVT VKKTGAALIIGIYDEPMT PGQCNM VVE
RLGDYLIDQGY

>CAA11756.1 Gly m 3; profilin [Glycine max]
MSWQAYVDDHLLCDIEGNHLTHAAIIGQDGSVWAQSTDFPQFKPEEITAIMNDFNEPGSL
APTGLYLGGTKYMVIQGE PGAVIRGKKKPGGVT VKKTGAALIIGIYDEPMT PGQCNM VVE
RPGDYLIDQGY

>ABU97472.1 Gly m 3; profilin [Glycine max]
MSWQAYVDDHLLCEIEGNHLTHAAIIGQDGSVWAQSTNFPQFKPEEITAINNDFNEPGSL
APTGLYIGGTYMVIQGE PGAVIRGKKKPGGVT VKKTGAALIIGIYDEPMT PGQCNM VVE
RLGDYLIDQGL

>ACS49840.1 Gly m 7; seed biotinylated protein [Glycine max]
MASEQLARRENTTTEKEIHVEKHRVPK MATHFEHLAEQAKESDITAGKDTPQGSIEALQA
GERVKDHAGKAMGDI GGRGKARETHELG AHFESLADKVTDHAAANVVG NKESQREARGGV
RDVGK FEMRTEGGEKGNKDRPEL KTRTREVIGRTEKERGRESGGQVVAEKGRE TETARGR
VGAENEGARTTAVITCTLEKGGGTQKPIREEEERESERSAWEQISNYSDQATQGVKEY
ERAKQAASETLN TTTTQAQEKSAQAKNLAQA KDATLEKGQQGYAVTKDTISSAAKTASE
KTAPVAEKAKDYTLQAAEKAKSAGGTTASYVGEKAVQAKDVAVESGKSAAGYAAKVAADL
RDKATAVGWAAAHFSAEKTVEGT KAAAHVVEGAAGYAGHKAAELASMSAGAVKGLAASAG

ETAKEYTAKKKEEAQRELEAKKPSQPQEAERPSEGIGETVRQYAQKPKPSERNPQKEGT
GSIVFTAIGETVSSAGEKVKKPKFNTTGGESEGGGKKEEGKSVIGKSLTSIGEKLGDAKQ
REELLDNVTGNITEGGGEVLGAVGETVAEIGQNMMPAEIVQERAHVRQAGGVLDIAIGET
IAEIAETTRVMVSGEDERVLRQSVVLETRVTGRAKHEEGSHGA

>P22895.1 thiol protease [Glycine max]

MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE
EAKRLEIFKNNSNYIRDMNANRKSPHSHRLGLNKFADITPQEFSSKYLQAPKDVSQQIKM
ANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFSATGAIEAAHAIATGDLV
SLSEQELVDCVEESEGSYNGWQYQSFVWLEHGGIATDDDPYRAKEGRCKANKIQDKVT
IDGYETLIMSDESTESETEQAFLSAILEQPISVSIKAKDFHLYTGGIYDGENCTSPYGIN
HFVLLVGYSADGVYWIAKNSWGFWDGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES
ETLVSARVKGHRRVDHSPL

>AAB09252.1 thiol protease [Glycine max]

MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE
EAKRLEIFKNNSNYIRDMNANRKSPHSHRLGLNKFADITPQEFSSKYLQAPKDVSQQIKM
ANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFSATGAIEAAHAIATGDLV
SLSEQELVDCVEESEGSYNGWQYQSFVWLEHGGIATDDDPYRAKEGRCKANKIQDKVT
IDGYETLIMSDESTESETEQAFLSAILEQPISVSIKAKDFHLYTGGIYDGENCTSPYGIN
HFVLLVGYSADGVYWIAKNSWGFWDGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES
ETLVSARVKGHRRVDHSPL

>BAA25899.1 thiol protease [Glycine max]

MGFLVLLLFSLGLSSSSSISTHRSILDLDLTKFTTQKQVSSLFQLWKSEHGRVYHNHEE
EAKRLEIFKNNSNYIRDMNANRKSPHSHRLGLNKFADITPQEFSSKYLQAPKDVSQQIKM
ANKMKKEQYSCDHPPASWDWRKKGVITQVKYQGGCGRGWAFSATGAIEAAHAIATGDLV
SLSEQELVDCVEESEGCYNGWHYQSFVWLEHGGIATDDDPYRAKEGRCKANKIQDKVT
IDGYETLIMSDESTESETEQAFLSAILEQPISVSIKAKDFHLYTGGIYDGENCTSPYGIN
HFVLLVGYSADGVYWIAKNSWGFWDGEDGYIWIQRNTGNLLGVCGMNYFASYPTKEES
ETLVSARVKGHRRVDHSPL

>CAA45777.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLCAFTTSYLPSAIADFLVDNEGNPLENGGTYIILSDITAFGGIRAAPTG
NERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTESV
VEDLPEGPAVKIGENKAMDGWFRLEVSDEFNMYKLVFCPQQAEDDKCGDIGISIDHD
DGTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

>CAA45778.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLCAFTTSYLPSAIADFLVDNEGNPLDSGGTYIILSDITAFGGIRAAPTG
NERCPLTVVQSRNELDKGIGTIISSPFIRFIAEGNPLRLKFDSFAVIMLCVGIPTESV
VEDLPEGPAVKIGENKDAVDGWFRLEVSDEFNMYKLVFCTQQAEDDKCGDIGISIDHD
DGTRRLVVSKNKPLVVQFQKVDKESLAKKNHGLSRSE

>AAB23464.1 trypsin-inhibitor [Glycine max]

MKSTIFFLFLCAFTTSYLPSAIADFLVDNEGNPLENGGTYIILSDITAFGGIRAAPTGN
ERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTESVV
EDLPEGPAVKIGENKAMDGWFRLEVSDEFNMYKLVFCPQQAEDDKCGDIGISIDHDD
GTRRLVVSKNKPLVVQFQKLDKESLAKKNHGLSRSE

>AAB23482.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLVCAFTTISYLPASATAQFVLDTDDDPQNGGTYIIMLPVMRGKGGGIEVDST
GKEICPLTVVQSPNELDKGIGLVFTSPLHALFIAERYPLSIKFGSFAVITLCAGMPTEWA
IVEREGLQAVKLAARDTVDGFNIERSREYNDYKLVFCPQQAEDNKCEDIGIQIDDDGI
RRLVLSKNKPLVVQFQKFRSSTA

>AAB23483.1 trypsin-inhibitor [Glycine max]

MKSTIFFALFLVCAFTTISYLPASATAQFVLDTDDDPQNGGTYIIMLPVMRGKSGGIEGNST

GKEICPLTVVQSPNKHNGIGLVFKSPLHALFIAERYPLSIKFDSFAVIPLCGVMPTKWA
IVEREGLQAVTLAARDTVDGFNFIERSREYNDYYKLVFCPQEAEDNKCEDIGIQIDNDG
IRRLVLSKNKPLVVEFQKFRSSTA

>CAA56343.1 trypsin-inhibitor [Glycine max]

MKSTTSLALFLLCALTSYQPSATADIVFDTEGNPIRNGGTYYVLPVIRGKGGGIEFAKT
ETETCPLTVVQSPFEGLRGLPLIISSPFKILDITEGLILSLKFHLCTPLSLNSFSVDRY
SQGSARRTPCQTHWLQKHNRCWFRIQRASSESNYYKLVFCTSNDSSCGDIVAPIDREGN
RPLIVTHDQNHPLLQVQKVEAYESSTA

>P82947.1 unknown function, partial [Glycine max]

ANPTFGFTPLGLSSDAN

>CAA60533.1 unknown function [Glycine soja]

MGKPFITLSLSSCLLLLSSACFAISSSKLNECQLNNLNALEPDHRVESEGGLIQTWNSQH
PELKCAGVTVSKLTLNRNGLHLPSPYPRMIIAQKGGALGVAIPGCPETFEEPQEQS
RRGSRSQKQQLQDSHQKIRHFNEGDVLPVPPGVPYWTYNTGDEPVVAISLLDTSNFNNQL
DQTPRVFYLAGNPDIIEYPETMQQQQQKSHGGRKQGHHQEEEEEGGSVLSGFSKHF
LAQSFNTNEDIAEKLPSPDDERKQIVTVEGGLSVISPKWQEQDEDEDEDEDEDEDE
QIPSHPPRRPSHGKREDEDEDEDEKPRPSRPSHGKREQDQDEDEDEDEDEDEDE
QPRKSREWRSKKTQPRRPRQEERERGCESTRNGVEENICTLKLHENIARPSRADFY
NPKAGRISTLNSLTLPALRQFQLSAQYVVLYKNGIYSPHWNLNANSVIYVTRGQK
VRVNCQGNVAVFDGELRRGQLLVVPQNFVVAEQAGEQGFYIVFKTHHNAVTSY
LKDVFRAPSEVLAHSYNLRQSQVSELKYEGNWGPLVNPESQQGSPRVKVA

>CAB59976.1 Gly d 2; NPC2-like [Glycyphagus domesticus]

GKMNFTDCGHNEIKELSVSNCTGNYCVIHRGKPLTLDAKFDANQDASVGLVLT
AIDGDIAIDIPGLETNACKLMKCPIRKGEHQELIYNIGEIPDATPEIKAKVKAQL
IGEHEGVLACGWVDGEVQE

>CAB76459.1 Gly d 2; NPC2-like [Glycyphagus domesticus]

GKMKFKDCGKGEVTELDITDCSGDFCVIHRGKPLTLEAKFAANQDTTKATIKV
LAKVAGTPIQVPGLETGCKFVKCPIKKGDPIDFKYTTTVPAILPKVKAEVTAEL
VGDHGV LACGRFGRQVE

>AAQ54603.1 unknown function [Glycyphagus domesticus]

MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTL
DAKFVANQDSAKATIKVLAKVAGTQIQVPGFDTDGCKIICKPIKKGDPIDFKY
SGTIPAITPKIKAEVTAELIGDHGILACGTVNGQVE

>QCI56570.1 tropomyosin [Gromphadorhina portentosa]

MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANIRAEKAEFEARSQKKIQQI
ENDLDQTLLEQLMQVNAKLDEKDKAFQNAESEVAALNRRIQLLLEEDLERSEER
LATATAKLAEASQAADESERARKILESKGLADEERMDALENQLKEARFMAEEAD
KKYDEVARKLAMVEADLERAEERAESGESKIVELEELRVVGNLKSLEVSEEKAN
LREEEYKQIQIKTLTTRLKEAEARAEFAERSVQKLQKEVDRLDEDELVHEKE
KYKICDDLDMFTTELIGN

>BAJ61596.1 paramyosin [Haliotis discus]

MDYGDVSSKVVRTVSHRSYNVYRGSSPATQNRLEARIERELEDALDTERDCR
VRAEKNLAEITFYDQVADRLEEQQGVTVQQIEINKKRESELNKVRKDLELAVI
SHESAEASLRKRNQETINDLTDQLEYMTKQKNRVEKEKHQLIIEIDTLQGMTD
SLAKAKSSAESRADGLQGSVDR LKLQVDDL SRQLTDANS AKARLTQENFDLQ
HQVQELDSANAALAKAKSQLQASNDDLKRQLDDESRQRQNLQVQFSQLQSGY
DNLNARYEESESASTLRTQLSKVNAEFAALKARFEKELMAKSEALEELRRRL
NTRIAQLEDECETLRARNNLEKTKAKLTAEIKEITIELENTQII VQDLTKR
NRTLENGILQRRCEDELGAEVSALRAEKASLEAEVHRLRVANAELTERNDNL
QRENKNSDQLREAQLALKDANRELNELRQIRAQLEMERDSLASQLRDTEEAL
RDAEGKLAQAALNQLRIDMENRLREKDEEIDNIRRSSARAIEELQRTLIEVET
RYKTEISRISRIKKK YETDIRELEGALDNANKANAELYKQIRSLQLRVKELE
VLLLEEERRLADDLRGQLSISERK

RIALQQEVEDVRSLL EAAERARKNAENELNDANARLSELQIQVTALSNDKRRMEADISAM
QSDLEDAINAQRAAEERADRLFNENVRLADELKQEQENYKNAESLRKQLEIEIREITVRL
EEAEAFATREGKRMVAKLQARIRDLEAELEAEQRRVREAFATSRLKLERQYKEIQMQTEDD
RRILAETMSINDQLSMKVKAYKRQIEESEDVANLTMNKYRKAQQLIEEADHRADMAEKNL
VAVRRSRMSVTRDVKIVRI

>BAH10148.1 tropomyosin [*Haliotis discus*]
MDAIKKKMLAMKMEKENAVDRAEQNEQKLRDTEEQKAKIEEDLNNLQKKCANLENDFDNV
NEQLQEAMAKLETSEKRVTEMEQEVSGTTRKITLEEDLERNEERLQTATERLEEASKAA
DESERGRKVLESRLADDERIDQLEAQLKEAKYIAEDAERKYDEAARKLAITEVDLERAE
ARLEAAEAKILELEEEELKVVGNNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT
EAERTVSKLQKEVDRLDELLAEKEKYKAISDELDQTF AELAGY

>AAG08987.1 tropomyosin [*Haliotis diversicolor*]
MDAIKKKMLAMKMEKENAVDRAEQNEQKLRDTEEQKAKIEEDLNNLQKKCANLENDFDNV
NEQLQEAMAKLETSEKRVTEMEQEVSGTTRKITLEEDLERNEERLQTATERLEEASKAA
DESERGARVLESRLADDERIDQLEAQLKEAKYIAEDAERKYDEAARKLAITEVDLERAE
ARLEAAEAKILELEEEELKVVGNNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT
EAERTVSKLQKEVDRLDELLAEKEKYKAISDELDQTF AELAGY

>P23110.1 2S albumin, conglutin [*Helianthus annuus*]
MARFSIVFAAGVLLLVAMAPVSEASTTTTITTTIIEENPYGRGRTESGCYQQMEEAEMLN
HCGMYLMKNL GERSQVSPRMREEDHKQLCCMQLKNLDEKCMCPAIMMMLNEPMWIRMRDQ
VMSMAHNLPIECNLMSQPCQM

>AAP47226.1 Hel a 3; lipid transfer protein [*Helianthus annuus*]
MKGTSMGVAAILAMIVMAQLMVHPSVAITCNDVTGNLTPCLPYLRSGGKPTACCAGAKKL
LGATRTQADRRACKCAKTAAPQLKVRPDMASSLP GKCGISTSIPINPNVNCNTIP

>CAA75506.1 Hel a 2; profilin [*Helianthus annuus*]
MSWQAYVDEHLMCDIEGTGQHLTSAAILGLDGTVWAQSAKFPQFKPEEMKGIKEFDEAG
TLAPTGMFIAGAKYMLVQGEPAVIRGKKGAGGICIKKTGQAMIMGIYDEPVAPGQCNMV
VERLGDYLLEQGM

>CAB38044.1 Hel as 1; tropomyosin [*Helix aspersa*]
MDAIKKKMLAMKMEKENALDRAEQVEQKLRDCECNKNKVEEDLNNLQKKFAILENDFDSI
NEQLLDANTKLEASEKKNAEIESETAGLQRRIQLLLEEDLERSEERLQSATEKLEEASKAA
DESERGRKVLESRLADDERLDGLEAQLKEAKYIAEDAERKFDEAARKLAITEVDLERAE
ARLEAAEAKILELEEEELKVVGNNMKSLEISEQEASQREDSYEETIRDLTQRLKDAENRAS
EAERTVSKLQKEVDRLDELLAEKERYKATSDELDSTFAELAGY

>AAA87456.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]
MAISSSTSGTSSSFPSRTTVMLLLFFFAASVGITDAQVGV CYGMQGNLPPVSEVIALYK
KSNITRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWVQKNVRGFWSSV
LFRYIAVGNEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYAYNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAF AATFDNGR TYLSNLI
QHVKGGT PKRPNRAIETYLFAMFDENKKQPEVEKHFGLFFPDKRPKYNLNF GA EKNWDIS
TEHNATILFLKSDM

>AAP87281.1 Hev b 2; beta-1,3-glucanase [*Hevea brasiliensis*]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGV CYGMQGNLPPVSEVIALYK
QSNIKRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWVQKNVRGFWSSV
LFRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAILTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSLVWVSESGWPSAGAF AATFDNGR TYLSNLI
QHVKGGT PKRPNRAIETYLFAMFDENKKQPEVEKHFGLFFPDKRPKYNLNF GA EKNWDIS
TEHNATILFLKSDM

>ABN03965.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYGMQGNLPSVSEVIALYK
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV
RFRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYADNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHFGFLFFPDKRPKYNLNFGAEKNWDIS
TEHDATILFLKSDM

>ABN03966.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLFFFTASVGITDAQVGVGYGMQGNLPPVSEVIALYK
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWWQKNVRGFWSSV
RFRYIAVGNEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVRNSY
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKRGTPKRPKRAIETYL FAMFDENKKQPEVEKHFGFLFFPNKWQKYNLNFSAEKNWDIS
TEHNATILFLKSDM

>ABN09653.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASIGITDAQVGVGYGMQGNLPSVSEVIALYK
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV
RFRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLTNIYPYFTYAYNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPNRAIETYL FATFDENKKQPEVEKHFGFLFFPDKRPKYNLNFGAEKNWDIS
TEHNATILFLKSDM

>ABN09654.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYGMQGNLPSVSEVIALYK
KSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWWQKNVRGFWSSV
RFRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSSXSPLLANIYPYFTYAYNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPNRAIETYL FAMFDENKKQPEVEKHFGFLFFPDKRPKYNLNFGAEKNWDIS
TEHNATILFLKSDM

>ABN09655.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLFFFTASVGITDAQVGVGYGMQGNLPPVSEVIALYK
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWWQKNVRGFWSSV
RFRYIAVGNEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKRGTPKRPKRAIETYL FAMFDENKKQPEVEKHFGFLFFPNKWQKYNLNFSAEKNWDIS
TEHNATILFLKSDM

>ACY91851.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAICSSTSGTSSSLPSRTTVMLLLFFFTASVGITDAQVGVGYGMQGNLPPVSEVIALYK
KSNITRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNAKSWWQKNVRGFWSSV
RFRYIAVGNEISPVNRTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLNPIIRFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKRGTPKRPKRAIETYL FAMFDENKKQPEVEKHFGFLFFPNKWQKYNLNFSAEKNWDIS
TEHNATILFLKSDM

>ACZ74626.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAMLSSTRTTGSLLSRTPVMLLLILYIASLGITDAQVGVGYGKLGNNLPPASEVIALYK

QSNIKRMRIYDPNQEVQLQALRGSNIELILGVPNSDLQSLTNPSNANSWQKNVRDFWSSV
RLRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLMGNTY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYAGNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSELEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPDRAIETYLFAMFDENQKQPEVEKHFGLFFPDKRPKYNLNFSAKKNWDIS
TEHNATVLFKSDM

>AEV41413.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAIFSSNSATSSSLPSRTTILLSLFIASLSITDAQVGVGYMLGNNLPPASQVISLYKQ
ANIKRMRIYDPNQAAALQALRGSNIQLMLGVPNSDLQSLTNPSNANSWIQRNVRAFWPSVR
FRYIAVGNEISPVNGGTASLAKFVLPAMRNIYNAIRSAGLQDQIKVSTAIIDMTLIGNSY
PSAGAFRGRDVSYLDPIIGFLSSIRSPLLANIYPYFSYAGNPRDISLPYALFTSPSIVVW
DGQRGYKNLFDAMLDALYSALERAGGGSELEVVVSESGWPSAGAFAAATFDNGRTYLSNLIQ
HVKGGTPKRPGRFIETYLFAMFDENQKQPEFEKHFGLFFPNKQKYNLNFAGAKKNWDISA
DYNATVLLLKSDI

>AFJ97274.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYMQGNNLPSVSEVIALYK
QSNIKRMRIYDPNRAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWQKNVRGFWSSV
RFRYIAVGNEISPVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDKIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSRSPLLANIYPYFTYAYNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSELEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPNRAIETYLFAMFDENKQKQPEVEKHFGLFFPDKRPKYNLNFGAEKNWDIS
TEHNATILFLKSDM

>AFJ97275.1 Hev b 2; beta-1,3-glucanase [Hevea brasiliensis]
MAISSSTSGTSSSLPSRTTVMLLLIFFTASLGITDAQVGVGYMQGNNLPSVSEVIALYK
QSNIKRMRIYDPNQAVLEALRGSNIELILGVPNSDLQSLTNPSNANSWQKNVRGFWSSV
RIRYIAVATKLVVNGGTAWLAQFVLPAMRNIHDAIRSAGLQDQIKVSTAIIDLTLVGNSY
PPSAGAFRDDVRSYLDPIIGFLSSIRSPLLANIYPYFTYADNPRDISLPYALFTSPSVVV
WDGQRGYKNLFDATLDALYSALERASGGSELEVVVSESGWPSAGAFAAATFDNGRTYLSNLI
QHVKGGTPKRPNRAIETYLFAMFDENKQKQPEVEKHSGLFFPDKRPKYNLNFGAEKNWDIS
TEHDATILFLKSDM

>CAC42881.1 Hev b 11; chitinase [Hevea brasiliensis]
EQCGRQAGGALCPGGLCCSQYGCANTPEYCGSGCQSQCDGGGGGGEDGGIDLGSIIISRST
FEEMLKHRNDAACPAKGFYTYDAFISAACAFAFGTTGDVDTCKREIAAFFGQTSHTTG
GWPTAPDGPYAWGYCYKEELNQASSYCSPPAYPCAPGKYYGRGPIQLSWNYNYGQCGQ
ALGLDLLNPNLDVATDRVISFKAAIWFWMTPQFPKPSCHDVITGQWSPTGHDISAGRAPG
YGVITNIINGGLECGRGWDARVEDRIGFYKRYCDMFAVGYGSNLDVCYNQTPFGLG

>CAD24068.1 Hev b 11; chitinase [Hevea brasiliensis]
EQCGRQAGGALCPGGLCCSQYGCANTPEYCGSGCQSQCDGGVGGEGGCVDLGSIIISRST
FEEMLKHRNNAACPAKGFYTYDAFISAACAFAFGTTGDVDTCKREIAAFFGQTSHTTG
GWPTAPDGPYAWGYCHKEELNQASSYCSPPAYPCAPGKYYGRGPIQLSWNYNYGQCGQ
ALGLDLLNPNLDVATDRVISFKAAIWFWMTPQFPKPSCHDVITGQWSPTGHDISAGRAPG
YGVITNIINGGLECGSGWDARVEDRIGFYKRYCDMFGVGYGSNLDVCYNQTPFGLG

>CAC00532.1 Hev b 9; enolase [Hevea brasiliensis]
MAITIVSVRARQIFDSRGNPTVEADVKLSDGYLARAAPVSGASTGIYEALERDGGSDYL
GKGVSKAVENVNIIIGPALVGKDPDQVGDIDNFMVQQLDGTVNEWGWCKQKLGANAILAV
SLAVCKAGAHVKGIPLYEHIANLAGNKNLVPVPAFNVINGGSHAGNKLAMQEFMILPVG
ASSFKEAMKMGAEVYHHLKSVIKKKYQDATNVGDEGGFAPNIQENKEGLELLKTAIAKA
GYTGKVVIGMDVAASEFYGSDQTYDLNFKENNNNGSQKISGEALKDLYKSFVAEYPIVSI
EDPFDQDDWAHYAKLTSEIGEKVQIVGDDLLVTNPKRVEKAIKEKACNALLLVNQIGSV
TESIEAVKMSKRAWGVMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL

LRIEEELGSEAVYAGANFRKPVEPY

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

MAITIVSVRARQIFDSRGNPTVEADVKLSDGYLARAAPVPRGASTGIYEALERDGGSDYL
GKGVSKAVENVNIIIGPALVKGDPDQVQIDNFMVQQLDGTVNEWGWCKQKLGANAILAV
SLAVCKAGAHVKGIPLYKHVANLAGNKNLVLVPAFNVINGGSHAGNKLAMQEFMILPVG
ASSFKEAMKMGAEVYHHLKSVIKKKYGQDATNVGDEGGFAPNIQENKEGLELLKTAIAKA
GYTGKVVIGMDVAASEFYGSDKTYDLNFKEENNGSQKISGDVLDKLYKSFVTEYPIVSI
EDPFDQDDWEHYAKLTSEIGVKVQIVGDDLLVTNPKRVEKAIKEKACNALLKVNQIGSV
TESIEAVKMSKRAGWGMASHRSGETEDTFIADLSVGLATGQIKTGAPCRSERLAKYNQL
LRIEEELGAEAVYAGANFRTPVEPY

>AAP37470.1 Hev b 13; esterase [Hevea brasiliensis]

MEFPETNNNPIITLSFLLCMLSLAYASETCDFPALFNFVFGDSNSDTGGKAAAFYPLNPPYG
ETFFHRSTGRYSDGRLIIDFIAESFNLPLYLSPYLSSLGNSFKHGADFATAGSTIKLPTTI
IPAHGGFSPFYLDVQYSQFRQFIPRSQFIRETGGIFAELVPEEYFYEKALYTFDIGQNDL
TEGFLNLTVEEVNATVPDLVNSFSANVKKIYDLGARTFWIHNTGPIGCLSFILTYFPWAE
KDSAGCAKAYNEVAQHFNHKLKEIVAQLRKDLPLATFVHVDIYSVKYSLFSEPEKHGFEF
PLITCCGYGGKYNFSVTAPCGDVTADDGTKIVVGSACPSVRVNWGDGAHYTEAANEYFF
DQISTGAFSDPPVPLNMACHKTESLRTLASV

>ADR82196.1 Hev b 14; hevamine [Hevea brasiliensis]

GGIVIIYWGQNGNEGTLTQTCSTRKYSYVNIAFLNKFNGGQTPQINLAGHCNPAAGGCTIV
SNGIRSCQIQGIKVMLSLGGGIGSYTLASQADAKNVADYLWSNFLGGKSSSRPLGDAVLD
GIDFDIEHGSTLYWDDLARYLSAYSQKQKVVYLAAPQCPFPDRYLGALNTGLLTMYGF
NSITIIHHASIAQVTLTSLTRGIDGPHL

>CAA05978.1 Hev b 6; hevein [Hevea brasiliensis]

EQCGRQAGGKLCNNLCCSQWGWCGSTDEYCSPDHNCQSNCKDSGEGVGGGSASNVLATY
HLYNSQDHGDLNAASAYCSTWDANKPYSWRSKYGTAFVCGPVGAHQPPSCGKCLSVTNT
GTGAKATVRIVDQCSNGGLDLVNVFRQLDLDGKGYERGHLLTVNYQFVDCGDSFNPLFSV
MKSSVIN

>ABW34946.1 Hev b 6; hevein [Hevea brasiliensis]

MNIFIVVLLCLTGVAIAEQCGRQAGGKLCNNLCCSQWGWCGSTDEYCSPDHNCQSNCKD
SGEGVGGGSASNVLATYHLYNSQDHGDLNAASAYCSTWDANKPYSWRSKYGTAFVCGPV
GAHQPPSCGKCLSVTNTGTGAKTTVRIVDQCSNGGLDLVNVFRQLDLDGKGYERGHLLTV
NYQFVDCGDSFNPLFSVMKSSVIN

>1WKX_A Hev b 6; hevein, partial [Hevea brasiliensis]

EQCGRQAGGKLCNDLCCSQWGWCGSTDEYCSPDHNCQSNCKD

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

MASLAYSFLFSLFTFTLLNPVCTELDEYLFSGDGLYDAGNAKFIYDPKYLPSYHHPYG
TTFDFYPTGRFSDGRTVVDFVAENVSLPRIPPFKNKEANFTYGANFASEGATASDSNPLI
DFRSQIRDFGELKLEWAVQLVNVTELARRLKKAAYLISFGADDYLNIEIPSEASREQLS
IVDVVLGNISDRIKELYDFGARKFVENVAPLGLIPFIKQTSNDSTLIFYELASLHAMKLP
QILEKIQDGYLFPEFNFTVFNFYGIIKEIIDAPGEHGFYKGDIAACGNSTYRQACGFLD
YEFVCGNKTEYLFDFGTHNTDAANLLAELMWDKESGFISPYGVKDFFPSPPTTIQTLT
EATALG

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

MAALKMVSFLVLCMLVAAPMTAQAITCGQVQSALVPCLSYLKTGTGPTPPATCCNGVRTIN
NAAKTADRRTACQCLKSAAGSVKGLNPTTVAGLPKCGVNIPIYKISLSTNCATVK

>AAC27724.1 Hev b 7; patatin [Hevea brasiliensis]

MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDLDPDARIADYFDIIAGT
STGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIHSIGPIYDGEY
LRELCNNLLKDLTVKDTSTDVVIPTFDIKLLLPVIFPSDDAKCNALKNARLADVCISTSA

APVLLPAHSFTTEDDKNIHTFELIDGGVAATNP TLLAL THIRNEIIRQNPRFIGANL TES
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDSHLSAL
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES
IPGAPTNEAAIAKFAKLLSEERKLRQLK

>CAA11041.1 Hev b 7 patatin [Hevea brasiliensis]
MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDL DGP DARIADYFDIIAGT
STGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIH SIGPIYDGEY
LRELCNNLLKDLTVKDTLTDVVIPTFDIKLLL PVIFSSDDAKCNALKNARLADVCISTSA
APVLLPAHSFTTEDDKNIHTFELIDGGAAATNP TLLAL THIRNEIIRQNPRFIGANL TES
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTRLLEKQESRINLDTGRLES
IPGASTNEAAITKFAKLLSEERKLRQLK

>CAA11042.1 Hev b 7; patatin [Hevea brasiliensis]
MATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDL DGP DARIADYFDIIAGT
STGGLITTMLTAPNEDKKPIYQAKDIKDFYLENCPKIFPKESRDYDPIH SIGPIYDGEY
LRELCNNLLKDLTVKDTLTDVVIIPAFDIKLLL PVIFSSDDAKCNALKNARLADVCISTSA
APVLLPAHSFTTEDDKNIHTFELIDGGVAAAATNP TLLAL THIRNEIIRQNPRFIGANL TES
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES
IPGAPTNEAAIAKFAKLLSEERKLRQLK

>AAF25553.1 Hev b 7; patatin [Hevea brasiliensis]
MATGSTPLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDL DGP DARIADYFDIIAGT
STGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIH SIGPIYDGEY
LRELCNNLLKDLTVKDTLTDVVIPTFDIKLLL PVIFSSDDAKCNALKNARLADVCISTSA
APVLLPAHSFTTEDDKNIHTFELIDGGVAATNP TLLAL THIRNEIIRQNPRFIGANL TES
KSRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSAL
FKSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTELLEKQESRINLDTGRLES
IPGAPTNEAAIAKFAKLLSEERKLRQLK

>CAE85467.1 Hev b 7; patatin [Hevea brasiliensis]
ATGSTTLTQGGKITVLSIDGGGIRGIIPGIILASLESKLQDL DGP DARIADYFDIIAGTS
TGGLITTMLTAPNEDKKPMYQAKDIKDFYLENCPKIFPKESRDNYDPIH SIGPIYDGEYL
RELCNNLLKDLTVKDTLTDVVIPTFDIKLLL PVIFSSDDAKCNALKNARLADVCISTSA
PVLLPAHSFTTEDDKNIHTFELIDGGVAATNP TLLAL THIRNEIIRQNPRFIGANL TESK
SRLVLSLGTGKSEYKEKYNADMTSKWRLYNWALYNGNSPAVDIFSNASSDMVDFHLSALF
KSLDCEDYYLRIQDDTLTGEESGHIATEENLQRLVEIGTRLLEKQESRINLDTGRLESI
PGASTNEAAITKFAKLLSEERKLRQLK

>CAA75312.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDERLMCEIEGNHLTAAAIIGQDGSVWAQSSNFPQFKSEEITAIMSDFDEPGTL
APTGLHLGGTKYMVIQGEAGAVIRGKKGGPGGVTVRKTNQALIIGIYDEPMTPGQCNMIVE
RLGDYLLEQGM

>CAB51914.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQAYVDDHLMCEIEGNHLSAAAIIGQDGSVWAQSANFPQFKSEEITGIMSDFHEPGTL
APTGLYIGGTYKMVIQGEPAVIRGKKGGPGGVTVKKTNQALIIGIYDEPMTPGQCNMIVE
RLGDYLIDQGY

>AAF34341.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDEHLMCDIDGHHLTAAAIIGHDGSVWAQSSSFPQFKPEEVAAIMKDFDEPGSL
APTGLHLGGTKYMVIQGEPAVIRGKKGGGITVKKTGQALIIGIYDEPLTPGQCNMIVE
RLGDYLLEQGM

>AAF34342.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFPQFKSDEVAAIMKDFDEPGSL

APTGLHLGSTKYMVIQGEPEGAVIRGKKKSGGITVKKTSQALIIGIYDEPLTPGQCNMIVE
RLGDYLLEQGM
>AAF34343.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSGFQFKSDEVAAVMKDFDEPGSL
APTGLHLGGTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALIIGIYDEPLTPGQCNMIVE
RLGDYLLEQGM
>CAB96215.1 Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFQFKSDEVAAVMKDFDEPGSL
APTGLHLGGTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALIIGIYDEPLTPGQCNMIVE
RLGDYLLDQGL
>1G5U_A Hev b 8; profilin [Hevea brasiliensis]
MSWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFQFKSDEVAAVMKDFDEPGSL
APTGLHLGGTKYMVIQGEPEGAVIRGKKKSGGITVKKRTGQALIIGIYDEPLTPGQCNMIVE
RLGDYLLDQGL
>CAA39880.1 Hev b 1; rubber elongation factor [Hevea brasiliensis]
MAEDEDNQGGQGEGLKYLGFVQDAATYAVTTFSNVYLFKDKSGPLQPGVDIIEGPVKNV
AVPLYNRFSYIPNGALKFVDSTVVASVTIIDRSLPPIVKDASIQVVSIRAAPAAARSLA
SSLPGQTKILAKVYGEN
>CCW27997.1 Hev b 15; serine protease inhibitor [Hevea brasiliensis]
MASQCPVKDAWPELIGTNGDIAAGIETENANVKAIVLKKGSPMTMEYNLCRVLVFDND
RVVTQAPAIG
>AAC82355.1 Hev b 3; small rubber particle protein [Hevea brasiliensis]
MAEEVEEERLKYLDVRAAGVYAVDSFSTLYLYAKDISGPLKPGVDTIENVKTVVTPVY
YIPLEAVKFVDKTVDSVSLDGVVPPVIKQVSAQTYSVAQDAPRIVLDVASSVFNTGVQ
EGAKALYANLEPKAEQYAVITWRALNKLPLVPQVANVVVPTAVYFSEKYNDVVRGTTEQG
YRVSSYLPLLPTEKITKVFGEAS
>AAA16792.1 Hev b 10; superoxide dismutase [Hevea brasiliensis]
MALRSLVTRKNLPSAFKAATGLGQLRGLQTFSLPDLPHYDYGALPAISGEIMQLHHQKHH
QTYITNYNKALEQLNDAIEKGDSAAVVKLQSAIKFNGGGHVNHSIFWKNLAPVREGGEL
PHGSLGWAIDADFGSLEKLIQLMNAEGAALQSGGWVWALDKELKLLVETTANQDPLVT
KGPTLVPLLGIDVWEHAYYLQYKNVRPDYLNKNIWKVMNWKYASEVYAKECPSS
>CAB53458.1 Hev b 10; superoxide dismutase [Hevea brasiliensis]
QTFSLPDLPHYDYGALPAISGEIMQLHHQKHHQTYITNYNKALEQLNDAIEKGDSAAVVK
LQSAIKFNGGGHVNHSIFWKNLAPVREGGELPHGSLGWAIDADFGSLEKLIQLMNAEGV
ALQSGGWVWALDKELKLLVETTANQDPLVTKGPTLVPLLGIDVWEHAYYLQYKNVRPD
YLNKNIWKVMNWKYASEVYAKECPSS
>CAC13961.1 Hev b 10; superoxide dismutase [Hevea brasiliensis]
QTFSLPDLPHYDYGALPAISGEIMQLHHQKHHQTYITNYNKALEQLNDAIEKGDSAAVVK
LQSAIKFNGGGHVNHSIFWKNLAPVREGGELPHGSLGWAIDADFGSLEKLIQLMNAEGA
ALRSGGWVWALDKELKLLVETTANQDPLVTKGPTLVPLLGIDVWEHAYYLQYKNVRPD
YLNKNIWKVMNWKYASEVYAKECPSS
>AAC49447.1 Hev b 5; unknown function [Hevea brasiliensis]
MASVEVESAAATLPKNETPEVTKAEETKTEEPAAPPASEQETADATPEKEEPTAAPAEPE
APAPETEKAEVEKIEKTEEPAPEADQTTPEEKPAEPEPVAEEEPKHETKETETEAPAAP
AEGEKPAEEEPITEAAETATTEVPVEKTEE
>CAA81610.1 Hol 1 1; beta-expansin [Holcus lanatus]
MASSRSVLLLVAALFAVFLGSAHGIKAVPPGNITATYGDEWLDKSTWYGKPTGAGPK
DNGGACGYKDVDPKPPFSMTGCGNTPIFKDRGRCGSCFEIKCTKPESCSGEPVTVHITDD
NEEPIAPYHFDLSGHAFGSMAKKGEQKLSAGELELKFRRVKCKYPDGTKPTFHVEKGS
NPNYLALLVKYIDGDGDVAVDIKEKGDKWIELKESWGAVWRVDTDPDKLTGPFTVRYTT

EGGTKGEAEDVIPEGWKADTAYEAK

>CAA93121.1 Hol 1 1; beta-expansin [Holcus lanatus]
VFLGSAHGIKAVPPGNITATYGDWLDKSTWYGKPTGAGPKDNGGACGYKDVKPPFS
GMTGCGNTPIFKDGRGCGSCFEIKCSKPESCSGEPVTVHITDDNEEPIAPYHFDLSGHAF
GSMAKKGEEQKLSAGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYIDGDGD
VVAVDIKEKGDWIELKESWGAVWRVDTDPDKLTGPFTVRYTTEGGTKGEAEDVIPEGWK
ADTAYEAK

>CAA10140.1 Hol 1 1; beta-expansin [Holcus lanatus]
MASSSLVLLVVALFAVFLGTAHGIKAVPPGNITATYGDWLDKSTWYGKPTGAGPKDN
GGACGYKDVKPPFSGMTGCGNTPIFKSGRGCGSCFEIKCTKPESCSGEPVTVHITDDNE
EPIAAYHLDLSGKAFGAMAKKGEEQKLSAGELELKFRRVKCEYPKGTVTFHVEKGSNP
NYLALLVKYVDGDGDVVAVDIKEKGDWIELKESWGAVWRVDTDPDKLTGPFTVRYTTEG
GTKVEAEDVIPEGWKADTAYESK

>CAB10766.1 Hol 1 5; ribonuclease [Holcus lanatus]
QKLLLEDVNASFKA AVAAA KVPADKYKTF LRAFTVLDRGSTEQSKAEETKMP ELSSKLV
DAYMAAFKASTGGTQEAKYDAFVTTL TEALRVIAGALEVHAVKPATEEVPAAKIPAGDLQ
VVDKIDASFKIAATAANAAPANDKFTVFETAFNKALKESTGGAYESYKFIPSLEAAVKQA
YASTVAAPEVKYAVFEAALTKAITAMSQAQKVAQPA AAAATGAATVAAGAATTAAGGYKV

>CAB10765.1 Hol 1 5; ribonuclease [Holcus lanatus]
ADAGYTPAAPAAAGAGGKATTDEQKLL EDVNAGFKTAVAAAA NVPPADKYKTFEAAFTAS
SKASIAAAATKAPGLIPQLNAATNTAYAAAQ GATPEAKYDAFVTTL TEALRVIAGALEVH
AVKPATEEVGA AKIPAGELQIVDKIDAAFRIAATAANAAPVNDKFTVFEGAFNKAIKEST
GGAYEAYKFIPSLETAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKEAKPVA AA
TGAATAAAGVAAGAATAAAGGYKV

>AAG42255.1 Hol 1 5; ribonuclease [Holcus lanatus]
MAVQKYTVALFLTVALVAGPAASYAADAGYAPTT PAAAGAAAGKITPTQE QKLMEDINVG
FKA AVAAAAGAPPADKFKTFQA AFSASVEASA AKLNAAQAPGFVSHVAATSDATYKAAVG
ATPEAKFDSFVA AFTEALRVIAGVLKVHAVKPITEE IGA AKIPAGELQIIDKIDAAFKVA
ATAANAAPANDKFTVF EAAFNNAIKESTGGAYD TYKSIPSLEAAVKQAYAATIAAAPEVK
FAVFKAAALTKAITAMA EVQKVS KPVAGAATAATGAATGAAGAATGAATVSAGGYKV

>Q7M262 Hol 1 5; ribonuclease [Holcus lanatus]
ADAGYTPAAPAATGAGGDAT

>AAC48287.1 Hom a 1; tropomyosin [Homarus americanus]
MDAIIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRA EKTEEEIRITHKKMQQVENELDQV
QEQLSLANTKLEEK EKALQNAEGEVAALNRRIQ LLEEDLERSEERLNTATTKLAEASQAA
DESERM RKVLENRSL SDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRL EDELVNEKEKYKSITDEL DQTFSELSGY

>AAC48288.1 Hom a 1; tropomyosin [Homarus americanus]
MDAIIKKKMQAMKLEKDNAMDRADTLEQQNKEANIRA EKSEEEVHNLQKRMQQLENDLDQV
QESLLKANTQLEEKDKALSNAEGEVAALNRRIQ LLEEDLERSEERLNTATTKLAEASQAA
DESERM RKVLENRSL SDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRL EDELVNEKEKYKSITDEL DQTFSELSGY

>CAA41956.1 alpha-amylase inhibitor [Hordeum vulgare]
MASKSSITPLLLAAVLASVFAAAAATGQYCYAGMGLPSNPLEGCREYVAQQTCGVTIAGS
PVSSEPGDTPKDRCCQELDEAPQHCR CRVRYFIGRRSHPDWRVLKDLPGCPKEPQRDFAK
VLVTPGQC NVLTVHNAPYCLGLDI

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

SDMKRRCDELTAIPAYCRCEALRIIMQGVVWQGAFFEGAYFKDSPNCPRERQTSYAANL
VTPQECNLGTIHGSAYCELPQGYGVVL
>CAA49555.1 alpha-amylase inhibitor [Hordeum vulgare]
MASKSSITPLLLAAVLASVFAAATATGQYCYAGMGLSPNPLEGCREYVAQQTCGVTIAGS
PVSSEPGDTPKDRCCQELDEAPQHCRCEAVRYFIGRRSHPDWSVLKDLPGCPKEPQRDFA
KVLVTPGQCNVLTVHNAPYCLGLDI
>CAA08836.1 alpha-amylase inhibitor [Hordeum vulgare]
MGAMWMSMLLVLLLCLMVTMTGARSDNSGPMMWCDEMGHKVSPLTRCRALVKLECV
GNRVPEDVLRDCCQEVANISNEWCRCDLGSMLRSVYAALGVGGGPEEVFPGCQKDVMLK
LVAGVPALCNVPIPNAAAGTRGVCYWSASTDT
>CAA45085.1 Hor v 15; alpha-amylase, partial [Hordeum vulgare]
PTSAVDQGSMSVNSPGEWCWPGMGYPVYFPRCRALVKSQCAGGQVVEIQKDCCRQIA
AIGDEWCICGALGSMRGSYKELGVALADDKATVAEVFPGCRTEVMDRAVASLPAVCNQY
IPNTNGTDGVCYWLSYYQPPRQMSSR
>P32936.2 alpha-amylase/trypsin inhibitor [Hordeum vulgare]
MASKSSCDLLLAAVLVSIFAAVAAGVSEDCTPWTATPITPLPSCRDYVEQQACRIETPGP
PYLAKQQCCGELANIPQQCRQCALRFFMGRKSRPDQSGLMELPGCPREVQMDVFVILVTP
GFCNLTTVHNTPYCLAMDEWQWNRQFCSS
>CAA35188.1 alpha-amylase/trypsin inhibitor [Hordeum vulgare]
MAFKYQLLLSAAVMLAILVATATSFQDSCAPGDALPHNPLRACRTYVVSQICHQGPRLLT
SDMKRRCDELTAIPAYCRCEALRIIMQGVVWQGAFFEGAYFKDSPNCPRERQTSYAANL
VTPQECNLGTIHGSAYCELPQPAY
>P80198.1 Hor v 20; gamma-hordein-3 [Hordeum vulgare]
ITTTTQMFPNSGLELERPQQFLFPQWQLPQQPPFLQQEPEQPYPQQQLPQQQPFPPQQPQ
LPHQHQPQQPLPQQQFPQQMPLPQQQFPQQMPLPQQQFPQQKPFQYQQPLTQQPY
PQQQPLAQQQPSIEEQHQLNLCKEFLQLQCTLDKVPQLLQSVISFLRPHISQQNSCQLKR
QQCCQQLANINEQSRCPAIQTIVHAIVMQQQVQQQVGHGFVQSLLQQLGQGMPIQLQQQP
GQAFVLPQQQAQFKVVGSLVIQTLPLMNCNVHVPYCPFGSMATGSGGQ
>COMPARE187 Hor v 20; gamma-hordein-3, partial [Hordeum vulgare]
ITTTTTFNPSGLELERPQQFLFPQW
>CAA42832.1 lipid transfer protein [Hordeum vulgare]
MARAQVLLMAAALVLMMLTAAPRAAVALNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDL
HNQAQSSGDRQTVCNCLKGIARGIHNLNNAASIPSKCNVNPYITISPDIDCSRFTERR
SVKLVLSSEIHVEL
>AAA32970.1 lipid transfer protein [Hordeum vulgare]
MARAQVLLMAAALVLMMLTAAPRAAVALNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDL
HNQAQSSGDRQTVCNCLKGIARGIHNLNNAASIPSKCNVNPYITISPDIDCSRIY
>Q0L11118.1 pectin methylesterase [Humulus japonicus]
SVTAAKDGTDGDFRTINDALAAIPTKYEGRYVIYVKEGLYEETVTVTKKMANVTMYGDGSQ
KSIITGSKNFVDGVRTFQTATFVVLGGGFMGKAMFGNTAGPEKHQAVAAARVQADRAIFA
NCRFEGYQDTLYTQTHRQFYRSCVWAGTIDFIFGDAAVVFQNCMLVVRLPMANQKNIVTA
RGRVDKQQTGIVIHNCRIMADKLEPEKARVKSFLGRPWKEYSRTIIMESTIEDLIHPD
GWLPEWEGEFALKTLYYAEYNNKGPQAKVTTRVNWPGYSVINKKEAEKFTVENFLQGNLWL
NIKGIPVRYTLILRANRSEVQ
>AAP94213.1 Hum j 1; unknown function [Humulus japonicus]
MKNLQHNNKIITFKTPDDSTTLELNHISLPYHWEQCLDLKTGEIYYINWRNGMKAKEDP
RTTITEYNSNGSNGDYYSSEEDSSYDSESSSESSPPATTRESQYRGAEKDHVLLVGG
CKSCFMVYFVMPKQVQECPKCCGQPLHFDRSQSGSQ
>AAP15199.1 profilin [Humulus scandens]
MSWQAYVDDHLMCEIDGQHLTAAAIIGHDGSVWAQSSTFPQFKPEEIAAIMKDFEEPGSL

APTGLHLGGIKYVMIMGEQGA VIRGKKGAGGITVKKTGAAMIIGIYDEPLTPGQCNMIVE
RLGDYLIDQNL

>AAP15200.1 profilin [*Humulus scandens*]

MSWQAYVDDHLMCEIDGNHLSAAAIIGHDGSVWAQSAAFPQLKPEEVTGIMNDFNEPGTL
APTGLYLGGTKYMIQGEPAVIRGKKGAGGVTIKKTSQLIIGVYDEPMTGQCNMIVE
RLGDYLIDQGL

>APR62629.1 Jug n 4; 11S globulin, cupin [*Juglans nigra*]

MAKPILLSISLCLVALVNGCLAQSGGRQQPRFGECKLKRLVALEPSNRIEAEAGVIESWD
PNNQQFQCAGVAVVRRRTIEPNGLLLPQYSNAPQLLYIVKGRGITGVLFPGCPETFEESSQQ
GQSRI RPSLRASAFQRDRHQKIRHFREGDVIAFPAGVAHWYNDGDTPVVAVALMDTTNN
ANQLDQNP RN FYLAGNP DDEF RPQGGQEQYEQHRRQQHQQRHGEPGQQQ RGS GNNVFSGF
DADFLADAFNVD TETARRLQSENDHRRSIVRVEGRQLQVIRPRWSREEQEREERKERERE
RESE SERRQSRRGGRDDNGLEETICTLRLRENIGDPSRADIYTEEAGRISTANSHTLPVL
RWLQLSAER GALYS DALYVPHWNLNAHSVVYALRGRAEVQVVDNFGQTVFDDELREGQLL
TIPQNF AVVKRARNEGFEWVSFKTNENAMVSPLAGRTSAIRALPEEVLANALQIPREDAR
RLKFNRQESTLVRSRPSSSRSSRSERRAEV

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

RHEARKCIFHTFSLTMARLATLAALLVALLFVANAAAFRTTITIMEIDEDIDNPRRRGEG
CQEIQRQQNLNHCQYYLRQQSRSGGYDEDNQRQHFRQCCQQLSQIEEQCQCEGLRQAVR
RQQQQQLRGEEMEEMVQSARDLPKECGISSQRCEIRRSWF

>AAM54366.1 Jug n 2; 7S globulin, vicilin-like [*Juglans nigra*]

GRDRQDPQQYHRCQRRCIQEQSPERQRQCQR CERQYKEQQGRERGPESPRRESKGR
EEEQQRHNPYYFHSQSIRSRHESEEGEVKYLERFAERTELLRGIENYRVVILDANPNTFM
LPHHKDAESVIVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATEYVINQDSNERLEM
VKLLQPVNPNPGQVREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREG
VIIRASQEKLRALSQHAMSAGQRPWGRSSGGPISLKSERPSYSNQFGQFFEACPEEHRQ
LQEMDVLVNYAEIKRGAMMVPHYNSKATVVVVVVEGTGRYEMACPHVSSQS FEDQGRREQ
EEEESTGRFQKV TARLARGDIFVIPAGHP IAITASQENLRLLGFGINGENNRNFLAGQ
NSIINQLEREAKELSFNMPREEIEEIFESQMESYFVPTERQSRRGQGRDHPLASILGF AF
F

>AAW29810.1 Jug r 4; 11S globulin, cupin [*Juglans regia*]

MAKPILLSIYFLIIVALFNGCLAQSGGRQQQQFGQCQLNRLDALEPTNRIEAEAGVIESW
DPNNQQFQCAGVAVVRRRTIEPNGLLLPQYSNAPQLVYIARGRGITGVLFPGCPETFEESSQ
RQSQQGQSREFQDRHQKIRHFREGDIIAFPAGVAHWSYNDGSNPVVAISLLDTNNANQ
LDQNP RN FYLAGNP DDEF RPQGGQEQYEQHRRQQQRQRPGEHGQQQRGLGNNVFSGF DAD
FLADAFNVD TETARRLQSENDHRRSIVRVEGRQLQVIRPRWSREEQEREERKERERERES
ESERRQSRRGGRDDNGLEETICTLRLRENIGDPSRADIYTEEAGRISTVNSHTLPVLRWL
QLSAER GALYS DALYVPHWNLNAHSVVYALRGRAEVQVVDNFGQTVFDDELREGQLL TIP
QNF AVVKRARNEGFEWVSFKTNENAMVSPLAGRTSAIRALPEEVLATAFQIPREDARRLK
FNRQESTLVRSRPSSSRSSRSERRAEV

>AAB41308.1 Jug r 1; 2S albumin, conglutin [*Juglans regia*]

AALLVALLFVANAAAFRTTITIMEIDEDIDNPRRRGEGCREQIQRQQNLNHCQYYLRQQS
RSGGYDEDNQRQHFRQCCQQLSQMDEQCQCEGLRQVRRRQQQQQLRGEEMEEMVQSARD
LPNECGISSQRCEIRRSWF

>XP_018814692.1 Jug r 6; 7S globulin, vicilin [*Juglans regia*]

MAFKPKIPIALLLLTSLLAICAGLALAMQDPELKQCKHQCRHQRFDEQEKEHCQRSCDE
YHIEKKARERAERRRSEEGSSREEGYEEEEELGGEREEENPYVFEDEDFETRVRTDEGRIQ
VLEKFTKRSKLLRGIENFRVAILEANPQTFISP AHFDAELVVVFAKGRATITTVREEKRE
NFNVEQGDIMRIPAGTPVYLINRDENEKLYIVKILRPVSVPGHF EAFHGSGGEDPESFYR
AFSWEVLEAALKTRRDQLEKLF GKQTQGVIIKASKEQIRSMKHEETTPRIWPFGGDSTH

PFNLFHKRPSQSNQFGRLFETDPKECKQLQDLMLVMSFANITKGS MAGPYNSRATKISV
VIEGEGYFEMACPHLSSSGSRGQREGSGSSRRRSRSGPSYQQIRGRLRPGMVFVAPAGHP
VAVIASRNKNLQVLCFDVNAQGNIRFPLAGKNNIVNEFEKEAKELAFNFPAREVEKIFRN
QDQEFFFPGPSRQPEEGGRAFE

>AAF18269.1 Jug r 2; 7S globulin, vicilin-like [Juglans regia]
RGRDDDEENPRDPREQYRQCQEYCRRRQGQGRQQQQCQIRCEERLEEDQRSQEERERRR
GRDVDDQNPRDPEQRYEQCQQQCERQRRGQEQTLRRCRRCEQRRQEEERERQGRDRQDPQ
QQYHRCQRRCCIQQEQSPERQRCQQRRCERQYKEQQGRERGPESPRRESRGREEEQQRHN
PYYFHSQSIRSRHESEEGEVKYLERTERTELLRGIENYRVVILDANPNTSMLPHHKDAE
SVAVVTRGRATLTLVSQETRESFNLECGDVIRVPAGATVYVINQDSNERLEMVLLQPVN
NPGQFREYYAAGAKSPDQSYLRVFSNDILVAALNTPRDRLERFFDQQEQREGVIIRASQE
KLRALSQHAMSAGQRPWGRRSSGGPISLKSESPSYSNQFGQFFEACPEEHRQLQEMDVLV
NYAEIKRGAMMVPHYNSKATVVVVVEGTGRYEMACPHVSSQSYEGQRRREEEEEESTGR
FQKVTARLARGDIFVIPAGHPAITASQENLRLLGFDINGENNRDFLAGQNNIINQLE
REAKELSFNMPREEIEEIEFESQMESYFVPTERQSRRGQGRDHPLASILDFAFF

>ACI47547.1 Jug r 3; lipid transfer protein [Juglans regia]
MTGSLVLKLSGMVLLCMVVAAPVAEAVITCGQVASSVGSIGYLRGTVPVPPSCCGVK
SLNKAATTADRQAACECLKKTSIPSGLNPLAAGLPGKCGVSVPYKISTSTNCKAVK

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

MGVFTYETESTSVIPPARLFKAFVLDADNLIPKVVPAVKSSSEIEGNGGPGTIKKINFG
EGSQYKYVKHRTDAIDEANFTYAYSVIEGDALADKIEKISYETKIVASHEGGSILKSISH
YHSKGDHEIKEEDVKDGKEKASGLFKAVEGYLLAHPDAYN

>C0HLQ0 Jun a 7; gibberellin-regulated protein [Juniperus ashei]
AQIDCDKECNRRCSKASAHDRCLKYCGICCKKCHCVPPGTAGNEDVCPCYANLKNKSGGH
KCP

>AAD03608.1 Jun a 1; pectate lyase [Juniperus ashei]
MASPCLIAVLVFLCAIVSCYSDNPIDSCWRGDSNWDQNRMKLADCAVGFSS TMGGKGD
FYTVTSTDDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLMPLYVAGHKTIDGRGADV
HLGNGGPCLFMRKVS HVILHSLHIHGNTSVLGDVLVSESIGVEPVHAQDGD AITMRNVT
NAWIDHNSLSDCSDGLIDVTLGSTGITISNHF FNHHKVMLLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPRARYGLVHVANNYDPWNIYAIGGSSNPTILSEGNSFTAPSESYKKEV
TKRIGCESPSACANWWRSTRDAFINGAYFVSSGKTEETNIYNSNEAFKVENGNAAPQLT
KNAGVVT

>CAC05582.1 Jun a 2; polygalacturonase [Juniperus ashei]
MSMKFMAALAF LALQLIVMAAGEDQSAQIMLSDTKQYHRSSRNL RKR VH HARHDVAIVF
NVEHYGAVGDGKHDSTDAFEKTWNAACNKLSAVFLVPANKKFVNNLVFYGPCQPHFSFK
VDGTIAAYPDPKWKNSKIWMHFARL TDFNLMTGVIDGQGNRWSDQCKTINGRTVCND
KGRPTAIKIDFSKSVTVKELTLTNSPEFHLVFGEDGVKIQGIIKAPRDS PNTDGIDIF
ASKRFEIEKCTIGTGDDCVAVGTGSSNITIKDLTCGPGHGMSIGSLGKGNRSRSEVSFVHL
DGAKFIDTQNGLRITWQGGSGLASHITYENVEMINAENPILINQFYCTSA AACKNQRSA
VKIQDVTFFKNIHGTSATTAIQLMCSDSVPCSNIKLSNVFLKLTSGKVATCVNKNANGYY
TNPLNPSCSKSLHPGRTPKELELHQKPTTLLMDEKMGASLNSSPPNCKNKCKGCQPCPKL
IIVHPNQPEDYYPQRWVCSCHNKIYNP

>P81295.1 Jun a 3; thaumatin-like [Juniperus ashei]
MARVSELAFLAATLAISLHMQEAGVVKFDIKNQCGYTVWAAGLPGGGKRLDQGTWTVN
LAAGTASARFWGRTGCTFDASGKGCQTGDCGGQLSCTVSGAVPATLAEYTQSDQDYD
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVDGGCNSACNVFKTDQYCCRNAY
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>AAC15474.2 Jun o 4; calcium-binding protein, polcalcin [Juniperus oxycedrus]

MDEVPSDGSKSACSGEVVMEQSVHELEEVFKKFDANGDGKISGSELADILRSLGSDVGE
AEVKAMMEEADADGDGYVSLQEFVDLNNKGASVKDLKNAFKVFDRDCNGSISAAELCHTL
ESVGEPTIEESKNIHNVDKNGDGLISVEEFQTMMTSEMTDKSK

>CAC48400.1 Jun o 1; pectate lyase [*Juniperus oxycedrus*]
MASPCLRAVLVFLCAIVSCYSDNPIDSCWRGDSNWGQNRMKLADCVVGFSGSSTMGGKGGE
FYTVTSAEDNPVNPTPGTLRYGATREKALWIIIFSQNMNIKLKMPYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVSVSESIGVEPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMMLGHDDTYDNDKSMKVTVAF
NQFGPNAGQRMPPRARYGLVHVANNYDPWNIYAIGGSSNPTILSEGNSFTAPSESYKKEV
TKRIGCESTSACANWVWRSTRDAFTNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT
KNAGVVT

>AAR21071.1 thaumatin-like [*Juniperus rigida*]
MARVSELALLLVATLAISLHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGGQTWTLN
LAAGTASARFWGRTGCTFDASGKGSCGTGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDV
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVEGGCNSACNVFQTDQYCCRNAY
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>AAR21072.1 thaumatin-like [*Juniperus rigida*]
MARVSELALLLVATLAISLHMQEAGAVKFDIRNQCGYTVWAAGLPGGGKRLDQGGQTWTLN
LAAGTASARFWGRTGCTFDASGKGSCGTGDCGGQLSCTVSGAVPATLAEYTDQSDQDYDV
SLVDGFNIPLAINPTNAQCTAPACKADINAVCPSELKVEGGCNSACNVFQTDQYCCRNAY
VDNCPATNYSKIFKNQCPQAYSYAKDDTATFACASGTDYSIVFCP

>AAF80164.1 Jun v 1; pectate lyase [*Juniperus virginiana*]
MASPCLIAFLVFLCAIVSCCSDNPIDSCWRGDSNWGQNRMKLADCAVGFSGSSTMGGKGGD
FYTVTSAEDNPVNPTPGTLRYGATREKTLWIIIFSQNMNIKLKMPYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVSVSESIGVVPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLGSTGITIFNHHKVMMLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPPRARYGLVHVANNYDPWNIYAIGGSSNPTILSEGNSFTAPNENYKKEV
TKRIGCESTSACANWVWRSTRDAFVNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT
KNAGVVA

>AAF80166.1 Jun v 1; pectate lyase [*Juniperus virginiana*]
MASPCLIAFLVFLCAIVSCCSDNPIDSCWRGDSNWGQNRMKLADCAVGFSGSSTMGGKGGD
FYTVTSAEDNPVNPTPGTLRYGATREKTLWIIIFSQNMNIKLKMPYVAGHKTIDGRGADV
HLGNGGPCLFMRKVSHVILHGLHIHGCNTSVLGDVSVSESIGVVPVHAQDGDITMRNVT
NAWIDHNSLSDCSDGLIDVTLGSTGITISNNHFFNHHKVMMLGHDDTYDDDKSMKVTVAF
NQFGPNAGQRMPPRARYGLVHVANNYDPWNIYAIGGSSNPTILSEGNSFTAPNENYKKEV
TKRIGCESTSACANWVWRSTRDAFVNGAYFVSSGKIEETNIYNSNEAFKVENGNAAPQLT
KNAGVVA

>Q9LD79.2 Jun v 3; thaumatin-like [*Juniperus virginiana*]
AFLAATLTISSHMQEAGAVKFDIKNQCGYTVWAAGLPGGGKRLDQGGQTWTVNLAAGTAS
ARFWGRTGCTFDASGKGSCGTGDCGRQLSCTVSGAVPATLAEYTDQSDQDY

>COMPARE227 Lac s 1; lipid transfer protein, partial from XP_023731522.1 [*Lactuca sativa*]
AISXGQVTANLA

>AAT45383.1 Lat c 1; calcium-binding protein, parvalbumin [*Lates calcarifer*]
MAFSNVLSDSVAAALDGGKDGTFDHKKFFSACGLSNKTSDDVKKAFIDQDKSGFIE
EEELKFLQNFKADARVLTDVETSTFLKAGD TDGDGKIGADEFTALVKP

>AAV97933.1 Lat c 1; calcium-binding protein, parvalbumin [*Lates calcarifer*]
MAFAGILNEADITAALAACAADSFKHKDFVVKVGLAGKSDDDVKKAFIDQDKSGFIE
EDELKFLQNFASARALTAETKEFLKAGDSGDGKIGVDEFAALVKV

>COMPARE028 7S globulin, vicilin [*Lathyrus sativus*]

YRLLEYKSKPHTLFLPQYTDADFILVVLVSGKAILTVLNSNDRNSFSLERGDITIKIPAGTI
AYLANRDDNEDLRVLDLAIPVKNPGQLQPFLLSGTQNPQPSLLSGFSKKVLEAAFNTNYEE
IEKVLLEQQEQHRRSLKDRRQEINEENVIVKVSREQIEELSKNAKSSSKSVSSESEPF
NLRSRNPIYSNKF GKFFFEITPEKNQQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVN
EGKGFDELLGIRNENQREESDEEEEQEETSQVQRYRAKLSPGDVFVIPAGHPVAINAS
SNLNLIGFGINAENNQRNFLAGEEDNVISQIQRPVKELVFPGSSREVDKLLKNQRQSYFA
NAQPLQRE

>CAD87730.1 Len c 1; 7S globulin, vicilin [*Lens culinaris*]
SRSDQENPFIFKSNRFQTIYENENGHIRLLQRFDKRSKIFENLQNYRLLLEYKSKPHTIFL
PQFTDADFILVVLVSGKAILTVLNSNDRNSFNLERGDITIKLPAGTIAYLANRDDNEDLRVL
DLAIPVNRPGQLQSFLLSGTQNPQPSFLSGFSKNILEAAFNTYEEIEKVLLEEQEQSQH
RRSLRDKRQEITNEDVIVKVSREQIEELSKNAKSSSKSVSSESEPFNLRSRNPIYSNKF
GKFFFEITPEKNPQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVNEGKGFELVGQRN
ENQQEQREENDEEEGQEEETTKQVQRYRARLSPGDVLPVIPAGHPVAINASSDLNLIGFGI
NAKNNQRNFLAGEEDNVISQIQRPVKELAFPGSSREVDRLLTNQKQSHFANAQPLQIE

>CAD87731.1 Len c 1; 7S globulin, vicilin [*Lens culinaris*]
SRSDQENPFIFKSNRFQTIYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPHTLFL
PQYTDADFILVVLVSGKAVLTVLNSNDRNSFNLERGDITIKLPAGTIAYLANRDDNEDLRVL
DLAIPVNNPGQLESFLLSGTQNPQPSFLSGFNKSILEAAFNTDYEEIEKVLLEDQEQEPQH
RRSLRDRRQEINKENVIVKVSREQIKELSKNAKSSSKSVSSESEPFNLRSRNPIYSNKF
GKFFFEITPEKNPQLQDLDFVNSVEIKEGSLLLPNYNSRAIVIVTVNEGKGYFELVGQRN
ENQREENDDEEEQEEETSTQVQRYRAKLSPGDVFVVPAGHPVAINASSDLNLIGFGINAK
NNQRNFLAGEEDNVISQIQRPVKELAFPGSSREVDRLLTNQKQSHFANAQPLQIE

>AAX35807.1 Len c 3; lipid transfer protein [*Lens culinaris*]
MARGMKLACVVLVICMVVIAPMAEGAISCGAVTSDLSPLCLTYLTGGPGPSPQCCGGVKKL
LAAANTTPDRQAACNCLKSAAGSITKLNNTNAAALPGKCGVNIPYKISTTTNCNTVKF

>CAB65963.1 Lep d 7; bactericidal permeability-increasing like [*Lepidoglyphus destructor*]

MQYLAIATIVAVALAGLSAAAHKPAYYDDNMANQMVDQIVKSLTTKKELDPFKIEQTKVPID
KKIGLIHIKGSATIKNAVITGLSHISRREGDAKIDTDGGFAAATLKLGDKNIRIKTDLHLD
LGKIIHPNLKFEHGIGDIDMKLKLKLD AEGKPSLDQFEIDFEQVELFIHGLGPLDPLVD
VIADSFVKYFNPQARKLVTDMLKPILVEEIKKLLKN

>CAB62213.1 Lep d 13; fatty acid-binding protein [*Lepidoglyphus destructor*]
MANIAGQYKLDKSENFQFLDKLGVGFLVKTAAKTVKPTLEVAVDGDTYIFRSLSTFKNT
EIKFKLGEFEEDRADGKRKVTIVKVDGNKVFVQTYGDKEVKVREFKGDVEVETASVD
GVTSVRPYKRA

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

>2118249A Lep d 2; NPC2-like [*Lepidoglyphus destructor*]
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDITGCSGDTCVIHRGEKMTLEAKFAANQ
DTAKVTIKVLAKVAGTTIQVPGLETDGCKFIKCPVKKGEALDFIYSGTIPAITPKVKADV
TAEIIGDHGVMACGTVHGVQE

>2118249B Lep d 2; NPC2-like [*Lepidoglyphus destructor*]
MMKFIALFALVAVASAGKMTFKDCGHGEVTELDISGCSGDTCVIHRGQKMTLDAKFAANQ
DTNKVTIKVLAKVAGTTIQVPGLETDGCKVLKCPICPKKGEALDFNYGMTIPAITPKIKADV
TAEVLGDHGVMACGTIHGQVE

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

DTAKVTIKVLTKVAGTTIQVPGLETGCKFIKCPVKKGEALDFIYSGTIPAITPKVKADV
TAEIIGDHGVMACGTVHGQVE
>CAD32314.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIALFALVAVASAGKMTFKDCGKGEVTELDISGCSGDFCVIHRGQKMTLDAKFAANQ
DTNKVTIKVLAKVAGTTIQVPGLETGCKVLKCPICKGEALDFNYGMTIPAITPKIKVDV
TAEIVGDHGMACGTVHGQVE
>AAQ73484.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALIAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73486.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALDAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73487.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGQSVTLDAKFVANQD
SAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
AELIGDHGILACGTVNGQVE
>AAQ73488.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALVAVASAGNMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73489.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73490.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALNAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73491.1 NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGQVE
>AAQ73492.1 Lep d 2; NPC2-like [Lepidoglyphus destructor]
MMKFIVLFALVAVASAGKMKFKDCGKGEVTELDITDCSGDFCVLHRGKSVTLDAKFVANQ
DSAKATIKVLAKVAGTQIQVPGFDTGCKIICKPIKKGDPIDFKYSGTIPAITPKIKAEV
TAEIIGDHGILACGTVNGTVE
>CAA57160.1 Lep d 2; NPC2-like, partial [Lepidoglyphus destructor]
IHRGEKMTLEAKFAANQDTAKVTIKVLAKVAGTTIQVPGLETGCKFIKCPVKKGEALDF
IYSGTIPAITPKVKADVTAELIGDHGVMACGTVHGQVE
>CAB71342.1 Lep d 10; tropomyosin [Lepidoglyphus destructor]
MEAIKNKMQAMKLEKDNAIDRAEIAEQKSRDANLRAEKSEEEVRLQKKIQQIENELDQV
QESLTQANTKLEEKESLQTAEGDVAALNRRIQLIEEDLERSEGRKLIATSKLEEASQSA
DESERMKMLEHRSITDEERMEGLESQLEARMMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEELRVVGNLKSLEVSEEKAQQREEAYEQQIRIMTTKLKEAEARAE
FAERSVQKLQKEVDRLLEDELVHEKEKYKSISDELDTFAELTGY
>AAQ55550.1 unknown function [Lepidoglyphus destructor]
MKSVLIFLVAIALFSANIVSADEQTTTRGRHTEPDDHHEKPTTHATHEETTSTQHHHEEVT
TQTPHHEEKTTEETHHSDDLIVHEGGKTYHVWCHEEGPIPHPGNVHKEYIICKSKSGSLWY

ITVMPCSIGTKFDPISRNCVLDN

>AAQ73493.1 Lep d 5; unknown function [Lepidoglyphus destructor]
MTGVKTHLEHELKRTDLNFLEKFNLDITATLNVLTKELTEVQKHVKAVESDEVDAIPN
PDEFRNEFDRLLIHMTEEQFAKLEQALAHLSHQVTELEKSKSKELKAQILREISIGLDFI
DSAKGHFERELKRADLNLAEKFNFESALSTGAVLHKDLTALATKVKAIETK

>AAQ73494.1 Lep d 5; unknown function [Lepidoglyphus destructor]
MTGVKTHLQHELEKRTDLNFLEKFNLDITAPLNVLTKELTEVQKHVKAVESDEVAIPNP
EFRNEFDRLLIHMTEEQFAKLEQALAHLSHQVTELEKSKSKELKAQILREISIGLDFIDS
AKGHFERELKRADLNLAEKFNFESALSTGAVLHKDLTALATKVKAIETK

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

>CAP17694.1 Lep w 1; calcium-binding protein, parvalbumin [Lepidorhombus whiffiagonis]

MTFAGLDAAEIKAAALDGCAAADSFYKFFGACGLAKKSAAEVKAAFNKIDQDESGFIEE
DELKLFQNFASARALTDKETANFLKAGVDVGDGKIGIEEFTDLVRSK

>CAC84590.2 Lep s 1; tropomyosin [Lepisma saccharina]
MEAIKKKMQAMKLEKDNAMDKADALEAQARDANRKADKILEEVQDLKKKPSQVETDFTTT
KENLATANKNLEDKEKTLTNTSEVASLNKRVQMIEENLERSEERLGTALTKLGEASHAA
DEASRMCKVLENRSQQDEERMDQLTNQLKEARMLAEDADGKSDEVSRKMAQVEDDLEVAE
DRVKSGDSKIMELEEEELKVVGNLSKLEVSEEKANQRVEEYKQIKTLTVKLKEAEARAE
YAEKYVKKLQKEVDRLDEDELGINKDRYRALADEMDQTFAELSGY

>CAC84593.2 tropomyosin [Lepisma saccharina]
MEAIKKKMQAMKLEKDNVDRARQNEQEAKDANLRAEKAEFEARSQKKIQTIEENELDQT
QEQLMQVNAKLEEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATQKLAEASQAA
DESERMCKVLENRSLADEERMDALENQLKEARFLAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANQREEEYKQIKTLTTRLKEAEARAC
WLL

>CAA54818.1 Lig v 1; Ole e 1-like [Ligustrum vulgare]
EDVPQPPVVSQFYIQGQVYCDTCRARFITELSEFIPGAGVRLQCKDGENGKVTFTVEVGYTK
AEGLYNMLIERDHKNEFCEITLISSSRKDCDEIPTGWWKPSLKFVLNTVNGTTRTINPL
GFLKKEVLPKCPQVFNKLGMYPNNM

>CAA54819.1 Lig v 1; Ole e 1-like [Ligustrum vulgare]
EDVPQPPVVSQFYIQGQVYCDTCRARFITELSEFIPGAGVRLQCKDGENGKITFTVEVGYTR
AEGLYSMLIERDHKNEFCEITLLSSSRKDCDEIPIEGWWKPSLKFMLNTVNGTTRTINPL
GFFKKEALPKCPQVFNKLGMYPNNM

>AAZ91659.1 polygalacturonase [Lilium longiflorum]
MASISSARLLLLSSVLLIVKLTAGLVPETKVNKSFVAVGDKTDSTQAILRAWDQACNG
FGKQRVIVPEGVYLTGPMAFRGPNGFISMQVRGELRAYGDVGVKYPNAKWWSYEDLNGLL
VTGGGRFNAQGSQAWTQNDSTCKKNCALLTTSVKFDHCTNATIRRINSIDSKFFHIAIDQ
CTDITVHHINITAPGTSPNTDGIHIGRSTNVNISNAIIGTGDDCISLPGSSHITISKVQ
CGPGHGISVGLGRYMNEENVWVVKVKNCTLTGTTNGVRIKTWKGSPPSEASQFIFQDIE
MREVQNPIIIDQEYCSYDYCANNPPAPSKVKLSDIQFMNIKGTSTSKVAINLICSSAVPC
EGIQLSDISLKYIRAGKPTMANCSHVSGETTSGLVSPSPSCIKGADVSLFTTQML

>BAW03242.1 Lip b 1; unknown function [Liposcelis bostrychophila]
MAAIKFILIAFLAFSVSQTTEANVVAQPKAFDIIAIVKQVIDIVRIVVKAVNDAVPDIDK
ILQQLVALLPSDVAATVTVLDAIKQAIDENARIDHIIQVLEKAMDDLLAIDPCYQPQA
DAIKAVLDAKALSGIDGVLHGSIDAHKADIDNVIAGFSQDLEDLRNLYDTQLPAAVVCLTP
GNAESCGCLDGVKETVWVNGVVSAAANFVHLTAASDVLKVVVPEVINGSTPIVNDGLAAA
GPLIDNVCTCVAAM

>BAW03243.1 Lip b 1; unknown function [*Liposcelis bostrychophila*]
MAAFK FILLAF LAFSVSQTTEANVVAQPRAFDIIDIVKKVIQIVEIVVEAVNGAVEPIDK
ILQELIALLPADVAKTVAVVDALRQAIADENVRIDHIEVLNKA LDDLLAIDPCYQPQA
DAIKAVLDTALSGIDKVLHGSIDAHKADIDNVIAGFSQDLEDLRNLYDTQLPAAVVCLTP
GNADSCTCLDGVKETVWNGVWSLAANFVLHLTAASDVLKVVVPEVIDGATPVVNDGLAAA
GPLIDNVCACVQGM

>AAL07320.1 Lit c 1; profilin [*Litchi chinensis*]
MSWQTYVDDHLMCETDGQHLTAAAIIGHDGSVWAQSANFPQFKPAEIAAIMKDFDEPGSL
APTGLHLGGTKYMIQGEPEGAVIRGKKKPGGITVKKTTQALIIGIYDEPMTPGQCNMVVE
RLGDYLV DQGL

>ABC02750.1 Lit c 1; profilin [*Litchi chinensis*]
MSWQAYVDDHLMCETDGQHLTAAAIIGHDGSVWAQSANFPQFKPVEITAIMKDFDEPGSL
APTGLHLGGTKYMIQGEPEGAVIRGKKKPGGITVKKTTQALIIGIYDEPMTPGQCNMVVE
RLGDYLV DQGL

>QCI56573.1 tropomyosin [*Litopenaeus setiferus*]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERM RKVLENRSL SDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRL EDELVN

>ABI98020.1 Lit v 2; arginine kinase [*Litopenaeus vannamei* (*Penaeus vannamei*)]
MADA AVIEKLEAGFKKLEAATDCKSLLKKYLTKEVFDKLDKRTSLGATLLDVIQSGVEN
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFQTKDHPNKDFGDVNSFVNVDPEGKFV
ISTRVRCGRSLQGYFPNCLTESQYKEMEAKVSSTLSSLEGELKGTYYPLTGMSKEVQQK
LIDDHFLFKEGDRFLQAANACRYWPAGRGYHNDNKTFLVWVNEEDHLRIISMQMGDLG
QVFRRLTSAVNEIEKRIPFSSHDR LGFLTFCPTNLGTTVRASVHIKLPKLAANREKLEEV
AGKYNLQVRGTRGEHTEAEGGIYDISNKR RMGLTEFQAVKEMQD GILELIKIEKEM

>ACM89179.1 Lit v 4; calcium-binding protein, sarcoplasmic calcium-binding protein
[*Litopenaeus vannamei* (*Penaeus vannamei*)]
MAYSWDNRVKVVRYMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN
LWNEIAELADFNKDG ETVDFEKQAVQKHCQGGKYGDFPGAFKVFIANQFKAIDVNGDGK
VGLDEYRLDCITRS AFAEVKEIDDAYNKLT TEDDRKAGGLTLERYQDLYAQFISNPDESC
SACYLFGPLKVVQ

>ACC76803.1 Lit v 3; myosin light chain [*Litopenaeus vannamei* (*Penaeus vannamei*)]
MSRKSGSRSSSKRSKKS GGGSNVDFMFTQRQVAEFKEGFQLMDRDKDGVIGKTDLRGTFD
EIGRIATDQELDEMLADAPAPINF TMLLNMF AERQTGESDDDDVAKAF LAFADEEGNID
CDTFRHALMTWGDKFSSQEADDALDQMDIDDGGKIDVQGV IQMLTAGGGDDAAAEAA

>ACB38288.1 Lit v 1; tropomyosin [*Litopenaeus vannamei* (*Penaeus vannamei*)]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERM RKVLENRSL SDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRL EDELVNEKEYKSITDEL DQTFSEL SGY

>P14946.2 Lol p 1; beta-expansin [*Lolium perenne*]
MASSSSVLLVVALFAVFLGSAHGI AKVPPGNITAEYGDKWLD AKSTWYGKPTGAGPKDN
GGACGYKNVDKAPFN GMTGCGNTP IFKDGRGCGS CFEIKCTKPESCSGEAVTVITDDNE
EPIAPYHFDLSGHAFGSM AKKGEEQNVRSAGELELQFRRVKCKYPDDTKPTFHVEKASNP
NYLAILVKYVDGDGDVVAVDI KEKGDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEG
GTKSEFEDVIPEGWKADTSYSAK

>AAA63278.1 Lol p 1; beta-expansin [*Lolium perenne*]

ALFAVFLGSAHGIKVPVPPGNITAEYGDKWLDKSTWYGKPTGAGPKDNGGACGYKDVDK
APFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVITDDNEEPIAPYHFDLS
GHAFGSMKKGEEQNVR SAGELELQFRRVKCKYPDDTKPTFHVEKGSNP NYLAILVKYVD
GDGDVVAVDIKEKGKDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEGGTKSEVEDVIP
EGWKADTSYSAK

>AAA63279.1 Lol p 1; beta-expansin [Lolium perenne]
MASSSSVLLVVALFAVFLGSAHGIKVPVPPGNITAEYGDKWLDKSTWYGKPTGAGPKDN
GGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVITDDNE
EPIAPYHFDLSGHAFGSMKKGEEQNVR SAGELELQFRRVKCKYPDDTKPTFHVEKASNP
NYLAILVKYVDGDGDVVAVDIKEKGKDKWTELKESWGAVWRIDTPDKLTGPFTVRYTTEG
GTKSEFEDVIPEGWKADTSYSAK

>CAB63699.1 Lol p 1; beta-expansin [Lolium perenne]
MASSSSVLLVVALFAVFLGSAHGIKVPVPPGNITAEYGDKWLDKSTWYGKPTGAGPKDN
GGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKCTKPESCSGEAVTVITDDNE
EPIAPYHFDLSGHAFGSMKKGEEQKLSAGELELQFRRVKCKYPDGTKPTFHVEKASNP
NYLAILVKYVDGDGDVVAVDIKEKGKDKWIELKESWGAVWRIDTPDKLTGPFTVRYTTEG
GTKSEVEDVIPEGWKADTSYSAK

>P14947.1 Lol p 2; expansin [Lolium perenne]
AAPVEFTVEKGSDEKNLALS IKYKNEGDSMAEVELKEHGSNEWLALKKNGDGVWEIKSDK
PLKGFNFRFVSEKGMNVFDDVVPADFKVGT TYKPE

>P14948.1 Lol p 3; expansin [Lolium perenne]
TKVDLTVEKGSDAKTLVLNIKYTRPGDTLAEVELRQHGESEWEPMTKKGNLWEVKSAPL
TGPMNFRFLSKGGMKNVFDEVIPTAFTVGTKYTYTPEYN

>CAA51775.1 Lol p 2; expansin [Lolium perenne]
EFTVEKGSDEKNLALS IKYSKEGDAMA EVELKEHGSNEWLALKKNGDGVWEIKSDKPLKG
PFNFRFVSEKGMWNVFDDVVPADFKVGT

>CAH92637.1 Lol p 4; FAD-containing oxidase [Lolium perenne]
AVVCGRRYDVRIRVRS GGHDYEGLSYRSLQPENFAVVDL NQMR AVLVDGKARTAWVDSGA
QLGELYAISKYSRTLAFPAGVCPTIGVGGNLAGGGFGMLLRKYGIAAENVIDVKLVDAN
GKLHDKKSMGDDHFWAVRGGGGESFGI VVSWQVKLLPVPPTVTIFKIPKSVSEGAVDIIN
KWQLVAPQLPADLMIRI IAMGPKATFEAMYLGTCKLTPMMQSKFPELGMNASHCNEMSW
IESIPFVHLGHRDSLEGDLLNRNNTFKPFAEYKSDYVYEPFKSVWEQIFGTWLVKPGAG
IMIFDPYGATISATPEAATPFPHRKGVL FNIQYVNYWFAPGAGAAPLSWSKEIYNMEPY
VSKNPRQAYANYRDIDLGRNEVWNGVSTYSSGK VWGQKYFKGNFERLAITK GKVDPTDYF
RNE

>Q7M1X5.1 Lol p 11; Ole e 1-like [Lolium perenne]
DKGPGFVVTGRVYCDPCRAGFETNVSHNVEGATVAVDCRPFDDGGESK LKAEATTDKDGWY
KIEIDQDHQEEICEVVLAKSPDKSCSEIEEFRDRARVPLTSNXGIKQQGIRYANPIAFFR
KEPLKECGGILQAY

>AAA33405.1 Lol p 5; unknown function [Lolium perenne]
MAVQKHTVALFLAVALVAGPAASYAADAGYAPATPATPAAPATAATPATPATPATPAAVP
SGKATTEEQKLI EKINAGFKA AVAAA VPPADKYKTFVETFGTATNKAFVEGLASGYAD
QSKNQLTSKLDAAKLAYEAAQGATPEAKYDAYVATL TEALRVIAGTLEVHAVKPAEEV
KVGAI PAAEVQLIDKVDAA YRTAATAANAAPANDKFTVFENTFNNAIKVSLGAAYDSYKF
IPTLVA AVKQAYAAKQATAPEVKYTVSETALKKAVTAMSEAEKEATPAAAATATPTPAAA
TATATPAAAYATATPAAATATATPAAATATPAAAGGYKV

>AAD20386.1 Lol p 5; unknown function [Lolium perenne]
MAVQKYTVALFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
EDVNAGFKA AVAAAANAPPADKFKIFEAAFSESSKGLLATSAAKAPGLIPKLD TAYDVAY
KAAEGATPEAKYDAFVTAL TEALRVIAGALEVHAVKPAATEEV PAAKIPTGELQIVDKIDA

AFKIAATAANAAPTNDKFTVFESAFNKALNECTGGAYETYKFIPLSLEAAVKQAYAATVAA
APEVKYAVFEAALTKAITAMTQAQKAGKPAAAAATGAATVATGAATAAAGAATAAAGGYK
A

>CAB64344.1 Lol p 5; unknown function [Lolium perenne]
MAVQKYTVLFLAVALVAGPADSYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
EDVNAGFKAAVAADANAPPADKFKIFEAFSECKGLLATSADAKAPGLILKLDTDYDVAY
KAGEGATPEAKYDAFVTALTEALRVIAGALEVHAVKPATEEVPAAKIPTGELQIVDKIDA
AFKIAATAANAAPTNDKFTVFESAFNKALKECTGGAYETYKFIPLSLEAAVKQAYATTVAA
APEVKYAVFEAALTKAITAMSQAQKVAKPAAAAATGAATVATGAATAAAGGATAAAGGYK
A

>Q40240.2 Lol p 5; unknown function [Lolium perenne]
MAVQKYTVLFLAVALVAGPAASYAADAGYTPAAAATPATPAATPAAAGGKATTDEQKLL
EDVNAGFKAAVAAAANAPPADKFKIFEAFSESSKGLLATSAAKAPGLIPKLDTAYDVAY
KAAEATPEAKYDAFVTALTEALRVIAGALEVHAVKPATEEVVLAAKIPTGELQIVDKIDAA
FKIAATAANAAPTNDKFTVFESAFNKALNECTGGAYETYKFIPLSLEAAVKQAYAATVAAA
PEVKYAVFEAALTKAITAMTQAQKAGKPAAAAATAAATVATAAATAAAVLPPPLLVVQSL
ISLLIYY

>COMPARE029 11S globulin, cupin, partial [Lupinus albus]
PAEVLANAFGLR

>Q6EBC1.1 7S globulin, vicilin, beta-conglutin [Lupinus albus]
MGKMRVRFPTLVVLGIVFLMAVSIGIAYGEKDVLSHERPEEREQE EWQPRRQRPQSRR
EEREQE QEQGSPSYPRRQSGYERRQYHERSEQREEREQEQQGSPSYRRQRNPYHFSSQ
RFQTLTKNRNGKIRVLERFDQRTNRLNENLQNYRIVEFQSKPNTLILPKHSDADYVLLVNL
GRATITIVNPD RRQAYNLEYGDALRIPAGSTSYILNPDDNQKLRVVKLAIPINNP GYFYD
FYPSSTKDQ QSYFSGFSRNTLEATFNTRYEEIQRIILGNEDEQEYEEQRRGQE QSDQDEG
VIVIVSKKQIQKLT KHAQSSSGKDKPSDSGPFNLSNEPIYSNKYGNFYEITPDRNPQVQ
DLNISLTYIKINEGALLLPHYNSKAIYVVVDEGEGNYELVGIRDQQRQ QDEQE EEEEEV
IRYSARLSEGDIFVIPAGYPISINASSNLRLLGFGINADENQRNFLAGSKDNVIRQLDRA
VNELTFPGSAEDIERLIKNQQQSYFANGQPQQQQQSEKEGRRRRRGS SLPF

>CAI84850.2 7S globulin, vicilin, beta-conglutin, partial [Lupinus albus]

MGKMRVRFPTLVVLGIVFLMAVSIGIAYGEKDVLSHERPEEREQE EWQPRRQRPQSRR
EEREQE QEQGSPSYPRRQSGYERRQYHERSEQREEREQEQQGSPSYRRQRNPYHFNSQ
RFQTLTKNRNGKIRVLERFDQRTNRLNENLQNYRIVEFQSKPNTLILPKHSDADYVLLVNL
GRATITIVNPD RRQAYNLEYGDALRIPAGSTSYILNPDDNQKLRVVKLAIPINNP GYFYD
FYPSSTKDQ QSYFSGFSRNTLEATFNTRYEEIQRIILLGNEDEQEYEEQRRGQE QSHQDEG
VIVRVSREQIQELTKYAQSSSGKDKPSQSGPFNLSNEPIYSNKYGNFYEITPDRNPQVQ
DLDISLTFTEINEGALLLPHYNSKAI FIVVVGEGNGKYELVGIRDQQRQ QDEQE EEEEEV
RRYSARLSEGDIFVIPAGYPISV NASSNLRLLGFGINAYENQRNFLAGSEDNVIRQLDRE
VKELTFPGSAEDIERLIKNQQQSYFANALPQQQQQSEKEGRRRRRGPIS SI

>COMPARE030 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]

AGIALGTHQLEENLVVFDLAR

>COMPARE034 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]

HSIFEVFTQVFANNVPK

>COMPARE036 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]

KISGGVPSVDLIMDK

>COMPARE041 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]

SRVGFNTNSLK

>COMPARE043 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus]

VGFNNTSLKSHGK

>COMPARE00280 Lup a 5; profilin [Lupinus albus]

SWQTYVDEHLLCDIEGNQLTSAAIIGQDGSVWAQSSSFQPKPEEITAIVNDFAEPGSLA
PTGLYLGGTKYMVIQGEPAVIRGKKKGGVTVKKTNQALIIGIYDEPMTPGQCNVVVER
LGDYLI DTGL

>ABR21771.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]

EERQEEERERRREPCREREQEQQPHGRREEEEEEEWQPRRLRQSRKEEREQEQQSSS
SSRKQSGYERRQYHERREQRDEKEKEQDSRSDSRRQRNPYHFSSERFQTRYRNRNGQIRV
LERFDQRTNRENLQNYRIVEFQSNPNTLILPKHSDADYILVVLNGRATITIVNPKRQA
YNLEYGDALRLPAGTTSYILNPDDNQNLRVVLAIPINNPNSNFYDFYPSSTKDQQSYFSG
FSKNTLEATFNTRYEEIQRILLGNEDEQEDEEQRRGQEQSYQDEGVIVRVSKEIQELRK
HAQSSSRKGGKPSSESGPFNLSNESIYSNKFGNFYEITPERNPQVQDLDISLTFTEINEGA
LLLPHYNSKAIFIVVDEGEGNYELVGIRDQQRQDEQEEEEEEVRRYSARLSEGDIFVI
PAGYPISVNASSNLRLLGFGINANENQRNFLAGSEDNVISQLDREVKELTFPGSAQDVER
LIKNQQSYFANAQPQQKQREKEGRRGRRLISSILSTLY

>ABR21772.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]

MAKMRVRLPMLILLLGVVFLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQEE
QEREHRREEKHDGEPSSRGRSQSEESQEEHERRREHREEREQEQQPRPQRRQEEEEEE
WQPRRQRQPSRREEREEREQEQQSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDS
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNQRTNRENLQNYRIIEFQSKPNTLILPKH
SDADFILVVLNGRATITIVNPKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA
IPINNPGLKYDFYFSTTKDQQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENKQR
RGQEQSHQDEGVIVRVSQKQIQELRKHAQSSSGEGKPSSESGPFNLSNKPIYSNKFGNFY
EITPDINPQFQDLNISLTFTEINELWLTKEKEIMN

>ACB05815.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]

MAKMRVRLPMLILLLGVVFLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQEE
QEREHRREEKHDGEPSSRGRSQSEESQEEHERRREHREEREQEQQPRPQRRQEEEEEE
WQPRRQRQPSRREEREEREQEQQSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDS
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNQRTNRENLQNYRIIEFQSKPNTLILPKH
SDADFILVVLNGRATITIVNPKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA
IPINNPGLKYDFYFSTTKDQQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENKQR
RGQEQSHQDEGVIVRVSQKQIQELRKHAQSSSGEGKPSSESGPFNLSNKPIYSNKFGNFY
EITPDINPQFQDLNISLTFTEINEGALLLPHYNSKAIFIVVDEGEGNYELVGIRDQQRQ
QDEQEEYEQGEVRRYSKLSKGDVFIIPAGHPLSINASSNLRLLGFGINANENQRNF
LAGSEDNVIKQLDREVKELTFPGSIEDVERLIKNQQSYFANAQPQQQQREKEGRRGR
GPISSILNALY

>F5B8V9.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]

MAKMRVRLPMLILLLGVVFLAASIGIAYGEKDFTKNPPKEREHEPRQQPRPRQEE
QEREHRREEKHDGEPSSRGRSQSEESQEEHERRREHREEREQEQQPRPQRRQEEEEEE
WQPRRQRQPSRREEREEREQEQQSSSGSQRGSGDERRQHRERRVHREEREQEQDSRSDS
RQRNPYHFSSNRFQTYRNRNGQIRVLERFNQRTNRENLQNYRIIEFQSKPNTLILPKH
SDADFILVVLNGRATITIVNPKRQVYNLEQGDALRLPAGTTSYILNPDDNQNLRVAKLA
IPINNPGLKYDFYFSTTKDQQSYFSGFSKNTLEATFNTRYEEIERVLLGDDELQENKQR
RGQEQSHQDEGVIVRVSQKQIQELRKHAQSSSGEGKPSSESGPFNLSNKPIYSNKFGNFY
EITPDINPQFQDLNISLTFTEINEGALLLPHYNSKAIFIVVDEGEGNYELVGIRDQQRQ
QDEQEEYEQGEVRRYSKLSKGDVFIIPAGHPLSINASSNLRLLGFGINANENQRNF
LAGSEDNVIKQLDREVKELTFPGSIEDVERLIKNQQSYFANAQPQQQQREKEGRRGR

GPISSILNALY

>F5B8W0.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]
MANMRVKFPTLVLLLGVFLMAVSIYGEKNAIKNHERPQEREQEERDPRQQPRPRHQ
EEQEREHGREERNREPSRGRSESEESREEEREQRREPSRGREQEQPQHGRREEEEEWQ
PRRQRPQSRREEREQEQQSSSSSSGRQSGYERREEREQEQQEQDSRSESRRQRNPYYFS
YERFQTLYKNRNGQIRVLERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVV
LNGRATITIVNPKRQAYNLEHGDLRLPAGTTSYILNPDDNQNLRVVKLAIPINNPNGNF
YDFYPSSTKDQQSYFNGFSRNTLEATFNTRYEEIQRILLGNEDGQEDDEEQSRGQEQSHQD
QGVIVRVSKEQIQELRKHAQSSSGKGPSESGPFNLRSDEPIYSNKFGNFYEITPDRNPQ
AQDLDISLTFIEINEGGLLLPHYNSKAIFVVVVDEGEGNYELVGIRDQERQQDEQEQUEEV
RRYNAKLSEGDIFVIPAGHPISINASSNLRLLGFGINADENQRNFLAGSEDNVIRQLDKE
VKQLTFPGSVEDVERLIKNQQQSYFANAQPQQQQQREKEGRRGRRGLSFPFRSLFTKLLS
TIM

>F5B8W1.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]
MAKMRVRFPTLVLLLGVFLMAVSIYGEKVLKNHERPQEREQEERDPRQQPRPHHQ
EEQEREHRRESEESQEEEREQRREPRREREQEQQPQHGRREEEEEWQPRRQRPQSRREER
EQEQGSSSSSRQSGYERREEREQEQQEQGSRSDSRRQRNPYYFSSERFQTLYRNRNG
QIRVLERFDQRTNRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVVLNGSATITIVNPD
KRQSYNLENGDALRLPAGTTSYILNPDDNQNLRVVKLAIPINNPNGNFYDFYPSSSKDQQS
YFSGFSKNTLEATFNTRYEEIQSILLGNEDEQEDDEQWHGQEQSHQDEGVIVRVSKEQVQ
ELRKYAQSSSRKGPYESGPFNLRSNKPIYSNKFGNFYEITPDRNPQAQDLDISLTFIEI
NEGALLPHYNSKAIFVVVVDEGEGNYELVGIRDQQRQQDEQEVRRYSARLSEGDIFVIP
AGHPISINASSNLRLLGFGINADENQRNFLAGSEDNVIRQLDREVKGLIFPGSAEDVERL
IKNQQQSYFANAQPQQQQQREEREGRRGHISILSTLY

>F5B8W2.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]
MIKMRVRFPTLVLLLGVFLMAVSIYGEKVIKNHERPQEREQEERDPRQQPRPHHQ
EEQEREHRREEREERDREPSRGRSESEESREEEREQRREPRREREQEQQPQHGRREEEEEWQ
PRRQRPQSRREEREQEQQSSSSSSRRQSGYERREEREQEQQEQGSRSDSRRQRNPYYFSSER
FQTLYRNRNGQIRVLERFDQRTDRLLENLQNYRIVEFQSKPNTLILPKHSDADYILVVLNG
SATITIVNPKRQSYNLENGDALRLPAGTTSYILNPDDNQNLRVVKLAIPINNPNGNFYDF
YPSSSKDQQSYFSGFSRNTLEATFNTRYEEIQRILLGNEDEQEDDEQRHGQEQSHQDEGV
IVRVSKEQVQELRKYAQSSSRKGPSPKSGPFNLRSNKPIYSNKFGNFYEITPNRNPQAQD
LDISLTFIEINEGALLPHYNSKAIFVVLVDEGEGNYELVGIRDQQRQQDEQEVRRYSAR
LSEGDIFVIPAGHPISINASSNLRLLGFGINADENQRNFLAGSEDNVIRQLDTEVKGLTF
PGSTEDVERLIKNQQQSYFANAQPQQQQQREEREGRRGRRGHISILSTLY

>F5B8W3.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]
MAKMRVRFPMPLVLLLGVVFLAVSIYGEKDVKNPERPEERQEEERDPRQQPPRSRQQ
EEQEREHRREKERDREPSRGRSESKQSQEEERERRKEHDREEREQEQQPQYGRRHHEEEK
EEEEEGQARRQRPQRREEREQEQQSSSESRRQSGDERRHRHEKREEREQEQQSSSG
RQSDYGRQRHEGREEREQEQQSSSESHRLRNPYYFSSERFQTRYKNKNGQIRVLER
FDQRTNRLLENLQNYRIVEFQSRPNTLILPKHSDADYILVVLNGRATITIVNPKRQAYNL
EYGDALRLPAGTTSYILNPDDNQDLRVVKLAIPINNPNGFYDFYPSRTKDQQSYFSGFSK
NTLEATFNTHYEEIQRILLGYEDEQEDEEQREQEQQSHQDEGVIVRVSKEQIQELRKHAQ
SSSRKGPSESGPFNLRSNEPIYSNKFGNFYEITPDRNPQVQDLDISLIFTEISEGALL
PHYNSKAIFVIVVDEGEGNYELVGIRNQQRQQDEQEVEEVRSYNARLSEGDILVIPAGHP
LSINASSNLRLLGFGINADENQRNFLAGSEDNVIRQLDREVKELIFPGSAEDVERLIRNQ
QQSYFANAQPQQQQQREKEGRRGRRGPISSILSALY

>F5B8W5.1 Lup an 1; 7S globulin, vicilin, beta-conglutin [Lupinus angustifolius]
MARMRVRFPTLVLLLGVFLMAVSIYGEKDVKNHERPGEREHEERDPRQQPRPRKQ
EEQEREHRREEEHHRDPSRGRRESEERQEEERERRREPCREEREQEQQPQHGRREEEEE

EWQPRRLRPQSRKEEREQEQGSSSSSRKQSGYERRQYHERREQRDEKEKEQDSRSDSRRQ
RNPYHFSSERFQTRYRNRNGQIRVLERFDQRTNRLLENLQNYRIVEFQSNPNTLILPKHSD
ADYILVVLNCRATITIVNPKRQAYNLEYGDALRVPAGTTSYILNPDDNQNLRVVLAIP
INNPSNFYDFYPSSTKDQQSYFSGFSKNTLEATFNTRYEEIQRILLGNEDEQEDEEQRRG
QEQSYQDEGVIVRVSKEQIQELRKHAQSSSRKGPSESGPFNLRNLSNESIYSNKFGNFYEI
TPERNPQVQDLDISLTFTEINEGALLPHYNSKAIFIVVDEGEGNYELVGIRDQQRQD
EQEEEEEEVRRYSARLSEGDIFVIPAGYPISVNASSNLRLLGFGINANENQRNFLAGSED
NVISQLDREVKELTFPGSAQDVERLIKNQQSYFANAQPQKQKQREKEGRRGRRSLISSI
LSTLY
>COMPARE052 7S globulin, vicilin, beta-conglutin, partial [Lupinus angustifolius]
SVPAEATEVGLLVFST
>COMPARE044 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus
angustifolius]
AGIALGAHHLEENLVVFDLERSR
>COMPARE046 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus
angustifolius]
ISGGAPSVDLILDKNDAVWR
>COMPARE048 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus
angustifolius]
KISGGAPSVDLILDK
>COMPARE051 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus
angustifolius]
SRVGFNSNSLK
>COMPARE053 7S globulin, vicilin, gamma-conglutin, partial from Q42369.1 [Lupinus
angustifolius]
VGFNSNSLKSYGK
>XP_019446786.1 Lup an 3; lipid transfer protein [Lupinus angustifolius]
MAGIVKLACAVLICMVVVSAPLTKAITCGQVTANLAQCLNYLRSGGAVPAPCCNGIKNIL
NLAKTTPDRRTACNCLKAAAANTPGLNPSNAGSLPGKCGVNIPYKISTSTNCASIK
>COMPARE054 7S globulin, vicilin, beta-conglutin, partial [Lupinus luteus]
AIFIVVDEGEGNYELVGIR
>COMPARE055 putative TAG factor protein, partial [Lupinus luteus]
AVCNLFALEGATVIFTYVK
>COMPARE056 unknown function, partial [Lupinus luteus]
RPFYTNAPQEIIYIQGR
>B3A0N2.1 lipid transfer protein, partial [Lycium barbarum]
GPLGGCCGGIKKSAAAGISGINYGIAAGLPGKCGVNIPYKISPSTDCSKVQ
>ADC55380.1 Mac r 1; tropomyosin [Macrobrachium rosenbergii]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDSV
QEALLKANQHLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLDEERMDALENLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY
>AHA85706.1 tropomyosin [Macrobrachium rosenbergii]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVFSLQKRMQQLENDLDSV
QEALLKANQHLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLDEERMDALENLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY
>P86739.1 calcium-binding protein, parvalbumin [Macruronus magellanicus]

SFAGILDDADITAALAACKAEGSFKHVEFFAKIGLAGKKVFAIIDQDKSDFVEEDELKLF
LQVFSAGARALTAETKAGSDGDGKIGVDEFAQMIKG
>P86741.1 calcium-binding protein, parvalbumin [Macruronus magellanicus]
AFAGILADADCAAALKACEAADSFNKYAFFAKVGLASKSAEEIKKAFFVIDQDKSGFIEE
DELKFLQNFVAGARALTAETKAFKAGSDGDGAGVDEFAALVKA
>P86740.1 calcium-binding protein, parvalbumin [Macruronus magellanicus]
TFFKSNDVKKAFFVIDQDKSGFIEEDELKFLQNFVAGARALTAGETKTFLAAGSDSDG
GMIGVDEFQALVKA
>P86742.1 calcium-binding protein, parvalbumin [Macruronus novaezelandiae]
SFNYKTFKLAASNDVKKAFFVIDQDKSGFIEEDELKFLQNFVAGARALTAGETKT
LAAGSDSDGGMIGVDEFQALVKA
>AAD25927.1 Mala f 4; mitochondrial malate dehydrogenase [Malassezia furfur]
MFARAALRNSVRAPASARYFSQTAAANRQVAVLGASGGIGQPLSLLMKLNPKVTELRLYD
IRLAPGVAADLSHINTPAVTSQYQDDLEGAVDGAEIVLIPAGMPRKPGMTRDDLNSNA
SIVRDLAKVVAKVAPKAYIGVISNPVNSTVPIVAEVFKKAGVYDPKRLFGVTTLDTTRAA
TFLSGIAGSDPQTTNVPVIGGHSVTVIPLISQAAQGDQVQAGEQYDKLVHRIQFGGDEV
VKAKDGAGSATLSMAYAAAVFTEGLLKGLDGEAVTQCTFVESPLFKDQVDFASPVEFGP
EGVKNIPALPKLTAEQKLLDACLPDLAKNIKKGVAAWAENP
>BAA32435.1 Mala f 2; peroxisomal protein [Malassezia furfur]
MPGDPTATAKNEIPDTLMGYIPWTPELDSEVCGIPTTFKTRDEWKGKKVIVSIPGAY
TPICHQQHIPPLVKRVDLAKAGVDAVVYIASNDPFVMAAWGNFNNAKDKVVFATDIDLA
FSKALGATIDLSAKHFGERTARYALIIDDNKIVDFASDEGDTGKLNASIDTILTKV
>BAA32436.1 Mala f 3; peroxisomal protein [Malassezia furfur]
EIGSTIPNATFAYVPYSPELEDHKVCGMPTSFQSHERWKGKKVIVAVPGAFTPTCTANH
VPPYVEKIQELKSKGVDEVVVISANDPFVLSAWGITEHAKDNLTFAQDVNCEFSKHFNAT
LDLSSKGMGLRTARYALIANDLKVEYFGIDEGEPKQSSAATVLSKL
>COMPARE011 unknown function [Malassezia furfur]
MNNEKYCSVADYDVKWFKERQSHPTDVKTTKWIAGTDLKIEMDPKPEYELYCFNYTTF
GNLPDAGAKELDDDATKKACSALKSGKYQSDPKKKSCRMDKKDIDQFKEQCSQYQPSDRP
PYGDWSAGTSLNVVNLNKKNA
>XP_001732036 unknown function [Malassezia globosa]
MVSLNIFSAAFVASLASAVFAAPSALERRAAPDNTVWVTSVADHCLILPRHKMSVGDSES
PGNMRSFCTKPYSSKQGLASDFWTKAHFKKTDKYVQITGCINPNVQSTLLSNDEGGQYD
SNGGEGGRGNPAGSVCLGYSSYVELVEPAGNRACIRCCYDPSDCDVSQDEAGCETVIPGK
YDC
>CAA09884.1 Mala s 6; cyclophilin [Malassezia sympodialis]
MSNVFFDITKNGAPLGTIKFKLFDDVVPKTAANFRALCTGEKGFYAGSHFHRVIPDFML
QGGDFTAGNGTGGKSIYAKFADENFQLKHNKPGLLSMANAGPNTNGSQFFITTVVTSWL
DGKHVVFGVIDGMNVVKAIEAEGSGSGKPRSRIEIAKCGVC
>CAI43283.4 Mala s 12; glucose-methanol-choline oxidoreductase [Malassezia
sympodialis]
MKGIVSWAVVSAALVLSATESLAFANVSSFEKRTTTGNGWDLGKSYDYVIVGGGTAGLV
LANRLSANQGTTVAVIEAGNSGYDDNDKFVVPDANLYNSAVNTQYDWQFHTSSQKHMNNR
RASWPRGKVLGGSSAVNGLYYVRPSETEVNVWSKLAGGSGRWSWNSLLSGMKKSEHFRGP
VKSQVQNLQIQYNAGSHGNSNGPIGTTWPAVYDPPVERFIKTADSMGAINNDPYNNGNHG
TYVALSSIDKTNWQSRFSRNGYLDPISKRSNLHVLTGHTVTGIIFDRSGKNAQATGVHYA
ASSNEASHTVHANKEVIISGGAINSPQILQLSGIGDKNLLNGLGIDVVVDLPVGENLQD
HVSAGMSFKPKNKDAGPTSVTGDAAKADSYVNSAVSYTSLGKLFNNKDSILGKIQARAKQ
IADSHNVSPAVKQGSKAYNALADTIFPSKVSPVEILGNVMFGSISIQAAALQHPLSRGSI
KITSKDPFAYPKINPNYFAENLDLVLLREGFKLIREMSQQSPLKDVDFETVPGDKVQTN

EDWENWIRSAAGTEYHPSSTCAMLPRGDGGVVDENLKVYGTSNLRVVDASVTPIAMSCHL
ESVYVYGLAEVAADIILGN

>CAD20981.3 Mala s 10; heat shock protein 70 [Malassezia sympodialis]

MSSVVGLDIGNSSKIGVARARGVDIVSNEVSNRSTPSLVSFGQKARLLGEGAATAQTSN
FKNTVGLKRLIGRTFQDESIQTYEKPFFVNAELVDAKGEVGVKVRFQNEEHIFSATQLLA
MYLGKLLDTTQNELGGSGVSDVVLVSPWIWFTDAQRRAMLHAAEIANLNPLRMNEPTATA
LGYGITKTDLPEPDSPRNVIFVDIGHSSYQVSVVAFCKGQLTVLGAWADPNFGGRNFDRV
LMEHFAEEFKGKYKIDVFFNPKATFRLAAGCERLKKVLSANTLAQLNVESLMNDIDAASQ
LKRDEFESLIAPYLERVNGPLDAALSQSGLTKDEIHSVELVGGSSRVPALKERIAAWYGK
PLSYTLNQDEAIVRGCTLACATLSPVFRVREFSVHDISSYPKIVSWEPAPDVPDEENELV
VFNTNPNVPSTKILTFYRKEPFLDATYADASTLPKGTPWLGRVTIKNVAPNEKGEHSI
VKVKARLNLHGVLNVESAYTVDEIEKEEEVPPVDPNAAEDAEPKTEKKIVKKLQKDDLP
IVSGIGLLDPTLLAELKEREGQMYAADKLVADETRKNAL E EYIYDTRSKLDERYATFVQ
SEEKEKLLAMLAESEDWLYTEEGEDATKSAYVSRL ET LQKVGAPIHFRWKEHEERPKAAA
QLREVVNKYMSVFENEPEKYDHLSDDDKTKVIEKAATVGKWLDDYMYKQSEL PKNVDPKL
TSEEILKKKDDVIYVCTPILT KPKPRVPVDTSKPEENAQTSNENEKQGDMDVD

>CCU97864.1 Mala s 10; heat shock protein 70 [Malassezia sympodialis]

MSSVVGLDIGNSSKIGVARARGVDIVSNEVSNRSTPSLVSFGQKARLLGEGAATAQTSN
FKNTVGLKRLIGRTFQDESIQTYEKPFFVNAELVDAKGEVGVKVRFQNEEHIFSATQLLA
MYLGKLRDTTQNELGGSGVSDVVLVSPWIWFTDAQRRAMLHAAEIANLNPLRMNEPTATA
LGYGITKTDLPEPDSPRNVIFVDIGHSSYQVSVVAFCKGQLTVLGAWADPNFGGRNFDRV
LMEHFAEEFKGKYKIDVFFNPKATFRLAAGCERLKKVLSANTLAQLNVESLMNDIDAASQ
LKRDEFESLIAPYLERVNGPLDAALSQSGLTKDEIHSVELVGGSSRVPALKERIAAWYGK
PLSYTLNQDEAIVRGCTLACATLSPVFRVREFSVHDISSYPKIVSWEPAPDVPDEENELV
VFNTNPNVPSTKILTFYRKEPFLDATYADASTLPKGTPWLGRVTIKNVAPNEKGEHSI
VKVKARLNLHGVLNVESAYTVDEIEKEEEVPPVDPNAAEDAEPKTEKKIVKKLQKDDLP
IVSGIGLLDPTLLAELKEREGQMYAADKLVADETRKNAL E EYIYDTRSKLDERYATFVQ
SEEKEKLLAMLAESEDWLYTEEGEDATKSAYVSRL ET LQKVGAPIHFRWKEHEERPKAAA
QLREVVNKYMSVFENEPEKYDHLSDDDKTKVIEKAATVGKWLDDYMYKQSEL PKNVDPKL
TSEEILKKKDDVIYVCTPILT KPKPRVPVDTSKPEENAQTSNENEKQGDMDVD

>CAD68071.1 Mala s 11; superoxide dismutase [Malassezia sympodialis]

PFYPIPSALPFPLPIHSLFSRRTRLFRFSRTAARAGTEHTLPPLPYEYNALEPFISADIM
MVHHGKHHQTYVNNLNASTKAYNDAVQAQDVLKQME LLTAVKFNGGGHVNHALFWKTMAP
QSQGGGQLNDGPLKQAIDKEFGDFEKFAAFTAKALGIQSGWCWLGLSKTGSLDLVVAK
DQDTLTTHHP IIGWDGWEHAWYLQYKNDKASYLKQWNNVNWSEAESRYSEGLKASL

>CCV00099.1 Mala s 11; superoxide dismutase [Malassezia sympodialis]

MTEHTLPPLPYEYNALEPFISADIMMVHHGKHHQTYVNNLNASTKAYNDAVQAQDVLKQM
ELLTAVKFNGGGHVNHALFWKTMAPQSQGGGQLNDGPLKQAIDKEFGDFEKFAAFTAKA
LGIQSGWCWLGLSKTGSLDLVVAKDQDTLTTHHP IIGWDGWEHAWYLQYKNDKASYLKQ
WNNVNWSEAESRYSEGLKASL

>CCU98198.1 Mala s 13; thioredoxin [Malassezia sympodialis]

MGVQVISSYDQFKQVTGGDKVWVIDFWATWCGPCKMIGPVFEKISDTPAGDKVGFYKVDV
DEQSQIAQEVGIRAMPTFVFFKNGQKIDTVVGADPSKLQAAITQHSA

>CCU99457.1 Mala s 5; unknown function [Malassezia sympodialis]

MSATTGSQAPNTTFTYIPWAPELDSGKVCVGPQTFKAHDRWKGKKVVVAIPGAFTPVCH
QNHIPGFVEKINELKAKGVDEVVIAVNDAFVMSGWGVTVGGKDQIVYACDNDLAFSKAL
GGTDLTSSGGMVVRTARYAVWLDDLKITYFGMDEGNMGAPEKSSVDAVLAQL

>CAA65341.1 Mala s 1; unknown function [Malassezia sympodialis]

MRYSTVLAALALLGTSAVSVLAALPDQIDVKVKNLTPEDTIYDRTRQVFYQSNLYKGRIE
VYNPKTQSHFNVIDGASSNGDGEQQMSGLSLLTHDNSKRLFAVMKNAKSFNFADQSSHG

ASSFHSFNLPLSENSKPVWSVNF EKVQDEF EKKAGKRPF GVVQSAQDRD GNSYVAFALGM
PAIARVSADGKTVSTFAWESGNGGQRP GYSGITFDPHSNKLI AFGGPRAL TAFDVSKPYA
WPEPVKINGDFGLTSGTEKIVTVPGNESVLV GARAPYAI SFRSWDNWKSANIKKTKRSE
LQNSGFTAVADYYQ GSEQGLYAVSAFFDNGAHGGRSDYPLYKLDNSILNF
>CAA09883.1 Mala s 5; unknown function [Malassezia sympodialis]
MSATTGSQAPNTTFTYIPWAP ELD SGKVC GVPQTFKAHDRWK GKKVVVVAIPGAFTPACH
QNHIPGFVEKINELKAKGVDEVVVIAVND AFVMSGWGVTVGGKDQIVYACDNDLAFSKAL
GGTLDLTSGGMGVRTARYAVVLD DLKITYFGMDEGNMGAPEKSSVDAVLAQL
>CAA09885.1 Mala s 7; unknown function [Malassezia sympodialis]
AVSASPTPSKHNL CYAQGKDLFEFHINDTVTKDVCKSLNSGKYHNMNNEKYCSVADYDV
KWFKERCSHPTDVKTTKWIAGTDLK IEMDPKEPYELYCFNYTTFGNLPDAGAKELDDD
ATKACALSALSGKYQSDPKK KSCRMDDKIDQFKEQCSQYQPSDRPPYGDWSAGTSLNVV
LNLKKNA
>CAA09886.2 Mala s 8; unknown function [Malassezia sympodialis]
MVALKFAAVLSVVA AAVMAAPSSMDRRASPDNQVWVTSASDYCLILPRHRESIGDSESPG
RMRSFCSKPYDSSQGQINPGFWKEVHF KTKNYVQLTGCINPRVQSTLLSHDDGGQYDSN
GNGGVGNPEGSVCLGYSSYVELV EPSDGKACIRCCVNDKYCDVGHDEGCEAVIPGQYC
>CAA09887.4 Mala s 9; unknown function [Malassezia sympodialis]
MSNVIKKVFNTDKAE AEGSKVADAPQEAGHKGEGFLHDAKDRLQGFAGHGHHNAQNAASG
VAGSAGAGGAPSVPSANVDVTNPVNDASVQGGVEAPRSWSTQLPQSQSVADTTGATSAGR
NNLTQTTSTGSGVNVAAGNVDQDVQHLAPVTRHVHHRHEIEELLREREHHIHQHIIQHVV
QPVV DSEHLAEQIHSRVVPQTTVRE V HANTDKDAALMRAVAGNPKDTFTQAAIDRSVIDK
GETVREIVHHHHIHNI VQPIIEKETHEYHRIRTTIPTTHITHEAPIVHESTAHQPIRKEDF
LKGGGVLTSTTRSIEEVGLLNLGN NQRTVEGETYTGGLPLSQ
>CCU99206.1 Mala s 9; unknown function [Malassezia sympodialis]
MSNVIKKVFNTDKAE AEGSKVADAPQEAGHKGEGFLHDAKDRLQGFAGHGHHNAQNAASG
VAGSAGAGGAPSVPSANVDVTNPVNDASVQGGVEAPRSWSTQLPQSQSVADTTGATSAGR
NNLTQTTSTGSGVNVAAGNVDQDVQHLAPVTRHVHHRHEIEELLREREHHIHQHIIQHVV
QPVV DSEHLAEQIHSRVVPQTTVRE V HANTDKDAALMRAVAGNPKDTFTQAAIDRSVIDK
GETVREIVHHHHIHNI VQPIIEKETHEYHRIRTTIPTTHITHEAPIVHESTAHQPIRKEDF
LKGGGVLTSTTRSIEEAGLLNLGN NQRTVEGETYTGGLPLSQ
>Q9M5X7.1 Mal d 3; lipid transfer protein [Malus domestica]
MASSAVTKLALVVALCMAVSVAHAITCGQVTSS LAPCIGYVRS GGAVPPACNGIRTING
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLPGKCGVNPYKISTSTNCA TVK
>AAR22488.1 Mal d 3; lipid transfer protein [Malus domestica]
MACSAVIKLALVVALCMAVSVAHAITCGQVTSS LAPCIGYVRS GGAVPPACNGIRTING
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLPGKCGVNPYKISTSTNCA TVK
>AAT80649.1 Mal d 3; lipid transfer protein [Malus domestica]
MASSAVTKLALVVALCMAVSVAHAITCGQVTSS LAPCIGYVRNGGAVPPACNGIRTINGS
LARTTADRQTACNCLKNLAGSISGVNPNNAAGLPGKCGVNPYKISTSTNCA TVK
>AAT80659.1 Mal d 3; lipid transfer protein [Malus domestica]
MASSAVIKLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRS GGVPVPPACNGIRTING
LAKTTPDRQAACNCLKSLAGSVSGVNPGNAESLPGKCGVNPYKISTSTNCA TVK
>AAT80662.1 Mal d 3; lipid transfer protein [Malus domestica]
MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRS GGVPVPPACNGIRTING
LAKTTPDRQAACNCLKSLAGSVSGVNPGNAESLPGKCGVNPYKISTSTNCA TVK
>AAT80664.1 Mal d 3; lipid transfer protein [Malus domestica]
MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRS DGPVPPACNGIRTING
LAKTTPDRQAACNCLKSLAGSVSGVNPGNAESLPGKCGVNPYKISTSTNCA TVK
>AAT80665.1 Mal d 3; lipid transfer protein [Malus domestica]

MASSAVINLALVVALCMAVSVAHAITCGQVSSNLVPCFDYVRSGGPVPPACNGIRTING
LAKTTPDRQAACNCLKSLAGSVSGVNPNGNVEESLPGKCGVNVYPYKISTSTNCATVK
>CAA58646.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEILEGNGGPGTIKKITFG
EGSQYGYVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKVKGKEKAHGLFKLIESYLKDHDPDAYN
>AAB01362.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAEILEGDGGPGTIKKITFG
EGSQYGYVKKHIDSVDANYSYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYLKGHPDAYN
>CAA88833.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEILEGNGGPGTIKKITFG
EGSQYGYVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGATIKSISHY
HPKGNIEIKEEHVKVKGKEKGHGLFKLIESYLKGHPDAYN
>CAA96534.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFNYETEFTSVIPPAPRLFNAFLVDADNLIPKIAPQAVKSAEILEGDGGVGTIKKINFG
EGSTYSYVVKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSHY
HTKSDVEIKEEHVKAGKEKASHLFLKIENYLLAHS DAYN
>CAA96535.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFNYETETTSVIPAPRLFKAFLVDADNLIPKIAPQAIKSTEIEGDGGVGTIKKVTFG
EGSQYGYVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTTS
YHAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN
>CAA96536.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFNYETEFTSVIPPAPRLFKAFLVDADNLIPKIAPQAIKSTKIEGDGGVGTIKKVTFG
EGSQYGYVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTNSH
YHAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN
>CAA96537.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFNYETEFTSVIPPAPRLFKAFLVDADNLIPKIAPQAIKSTEIEGDGGVGTIKKVTFG
EGSQYGYVKQRVNGIDKDNFTYSYSMIEGDTLSDKLEKITYETKLIASPDGGSIIKTTS
YRAKGDVEIKEEHVKAGKEKASGLFKLLEAYLLAHS DAYN
>AAD13683.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKGFVLDADNLIPKIAPQAIKHAEILEGDGGPGTIKKITFG
EGSQYGYVKKHIDSVDANYSYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYLKGHPDAYN
>AAD26546.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEILEGNGGPGTIKKITFG
EGSQYGYVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYLKGHPDAYN
>AAD26547.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAEILEGDGGPGTIKKITFG

EGSQYGYVVKHKIDSVDANYSYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY
HTKGDVEIKEEHVKAGKEKAHGLFKLIESHLKGHPDAYN
>AAD26548.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAIELEGDGGPGTIKKITFG
EGSQYGYVVKHKIDSVDANYSYAYTLIEGDALDTIEKVSYETKLMASGSGSIIKSISHY
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYKLGHPDAYN
>AAD26552.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYKLDHPDAYN
>AAD26553.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVCTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYKLDHPDAYN
>AAD26554.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIENISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYKLDHPDAYN
>AAD26555.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKAKAHGLFKLIESYKLGHPDAYN
>AAD26558.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAIELEGDGGPGTIKKITFG
EGSQYGYVVKHKIDSVDANYSYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY
HTKGDVEIKEEHVMAGKEKAHGLFKLIESYKLGHPDAYN
>AAD29671.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKAGKEKAHGLFKLIESYKLDHPDAYN
>AAK13027.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFTYESEFTSVIPPARLFNAFLVDADNLIPKIAPQAVKSAEIELEGDGGVGTIKKINFG
EGSTYSYVVKHRIDGVDKDNFVYKYSVIEGDAISETIEKISYETKLVAAAGSGSVIKSTSHY
HTKGDVEIKEEHVKAGKEKASHLFLKIENYLLEHQDAYN
>AAK13029.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVCTFENEFTSEIPPSRLFKAFLVDADNLIPKIAPQAIKQAEIELEGNGGPGTIKKITFG
EGSQYGYVVKHRIDSIDEASYSYSYTLIEGDALDTIEKISYETKLVACGSGSTIKSISHY
HTKGNIEIKEEHVKVGEKAHGLFKLIESYKLDHPDAYN
>AAK13030.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVYTFENEYTSSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAIELEGDGGPGTTKKITFG

EGSQYGYVKKHKIDSVDENYASYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHY
HTKGDVEIKEEHVKAGKEKAHGLFKLIESYLKHPDAYN
>CAD32318.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
GVYTYENEYTSSEIPPRFLKAFVLDADNLIPKIAPQAIKHAEILEGDGGPGTIKKITFGE
GSQYGYVKKHKIDSVDENYASYAYTLIEGDALDTIEKVSYETKLVASGSGSIIKSISHYH
TKGDVEIMEEHVKAGKEKAHGLFKLIESYLKHPDAYN
>AA025113.1 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFTYESEFTSVIPPARLFNAFVLDADNLIPKIAPQAVKSAEILEGDGGVGTIKKINFG
EGSTYSYVKKHRIDGVDKENFVYKYSVIEGDAISETIEKISYETKLVASGSGSVIKSTSHY
HTKGDVEIKEEHVKAGKEKASHLFLKIENYLLEHPDAYN
>COMPARE021 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
GVYTFENEYTSSEIPPRFLKAFVLDADNLIPKIAPQA
>COMPARE240 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFTYESEFTSVIPPARLYNAFVLDADNLIPKIAPQAVKSTEILEGDGGVGTIKKINFG
EGSTYSYVKKHRIDGLDKDNFVYKYSVIEGDAISETIEKISYETKLVASDSGSGSIKSTSHY
HTKGDVEIKEEHVKAGKEKASHLFLKIENYLLEHHDAYN
>COMPARE241 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVLTYYETEYASIIIPPARLYNALVLDADNLIPKIAPQAVKTVEILEGDGGVGTIKKVSFG
EGSEYNYVKKHVEGIDKDNFVYSYSLIEGDAISDKIEKISYEIKLVASGSGSIIKNISHY
HTKGDVEIKEEHVKAGKERAHGLFKLIENYLVANPDAYN
>COMPARE242 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFTYESEFTSVVPPARLFNAFVLDADNLIPKIAPQAVKSTEILEGDGGVGTIKKINFG
EGSTYSYVKKHRIDGVDKDNFVYQYSVIEGDAISETIEKISYETKLVASGSGSVIKSISHY
HTKGDVEIKEEHVKAGKEKASHLFLKIENYLLEHHDAYN
>COMPARE243 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVTKISQKFVTQVTPQRMFNALILDHAHNICPKLMFSSIKSIEFLSGSGEVGTIKQINF
EASPMKYAKHRIDALDKEALSCTYTFIESDATDHLDDKLEYITYDVKFEGYGRGGCICHL
TSTYKAKDDIQIKEEDIELGKDRAIGMYEVLEAYLMAHPRAYV
>COMPARE244 Mal d 1; pathogenesis related protein, PR-10, Bet v 1-like [Malus domestica]
MGVFTYETEFAVCAPARLYNALVLDADNLIPKIAPQAVKTAEILEGDGGVGTIKKISFG
EGSEYSYVKKHKVDGIDKDNFVYNYSVIEGDVISDKIEKISYETKLVASGSGSVIKSTSHY
HTKGDVEIKEEHVKAGKERAHGLFKLIENYLVANPDAI
>AAD29412.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDRLMCDIDGHHLTAAAILGHDGSVWAHSSTFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMVIQEGGAVIRGKKKGGVTVKKTGQALVFGIYEEPLTPGQCNMIVE
RLGDYLIDQGL
>AAD29413.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHNGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGVTVKKTSTMALLIGIYDEPMTGQCNMVVE
RLGDYLIEQGL
>AAD29414.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL

APTGLFLGGTKYMVIQEGP GAVIRGKKKSGGITIKKTSQALLIGIYDEP VTPGQCNIIVVE
RLGDY LIEQGL
>CAD46559.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAHSS TFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQALVFGIYEEPLTPGQCNMIVE
RLGDYLIDQGL
>CAD46560.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGGVTVKKSTMASLIGIYDEPMTPGQCNMVVE
RLGDY LIEQGL
>CAD46561.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGYRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMVIQEGP GAVIRGKKKSGGITIKKTSQALLIGIYDEP VTPGQCNIIVVE
RLGDY LIEQGL
>AAX19854.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAHSS TFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQALVFGIYEE TLTPGQCNMIVE
RLGDYLIDQGL
>AAX19856.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAQSSTFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQDLVFGIYEEPLTPGQCNMIVE
RLGDYLIDQGL
>AAX19858.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGGVTVKKSTMALLIGIYDEPMTPGQCNMVVE
RLGDY LIEQGL
>AAX19860.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGVMNDFNEPGSL
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGGVTVKKSTMALLIGIYDEPMTPGQCNMVVE
RLGDY LIEQGL
>CAK93713.1 Mal d 4; profilin [Malus domestica]
MSWQTYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGIMNDFNEPGSL
APTGLYLGGTKYMVIQEGPGVVIRGKKKGGGVTVKKSTMALLIGIYDEPMTPGQCNMVVE
RLGDY LIEQGL
>CAK93753.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGNSLTAAAILGQDGSVWAQSATFPAFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMVIQEGP GAVIRGKKKSGGITIKKTSQALLIGIYDEP VTPGQCNIIVVE
RLGDY LIEQGL
>CAK93757.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGNSLTAAAILGQGGSVWAQSATFPAFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMVIQEGP GAVIRGKKKSGGITIKKTSQALLIGIYDEP VTPGQCNIIVVE
RLGDY LIEQGL
>CAT99617.1 Mal d 4; profilin [Malus domestica]
MSWQAYVDDHLMCDIDGHHLTAAAILGHDGSVWAHSS TFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMVIQEGGAVIRGKKKSGGVTVKKTGQALVFGIYEE TLTPGQCNMIVE
RLGDYLIDQGV
>CAT99618.1 Mal d 4; profilin [Malus domestica]
AQSATFPQLKPEEVTGVMNEFNEPGSLAPTGLYFGGTYKYMVIPGEPGVVIRGKKKGGGVT
VKKSTMALLIGIYDEPM
>CAT99619.1 Mal d 4; profilin [Malus domestica]

GNSLTAAILGQDGSVWAQSATFFPAFKPEEIAAILKDFDQPGTLAPTGLFLGGTKYMVIQ
GEPGAVIRGKKKSGGITIKKTSQALLIGIYDEPLTPGQCNIWVERLGDYLIEQGL
>COMPARE246 Mal d 4; profilin [Malus domestica]
MSWQQYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSASFPAFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMVIQGEPGAVIRGKKKSGGITIKKTSQALLIGIYDEPVTGQCNIWVE
RLGDYLIEQGL
>AAB35897.1 Mal d 2; thaumatin-like [Malus domestica]
AKITFTNXPNTVWPGILTGFQKPKQ
>AAC36740.1 Mal d 2; thaumatin-like [Malus domestica]
MMKSQVAPRPTLAILFFSGAHAAKITFTNCPNTVWPGTLTGDQKQQLSLTGFELASKA
SRSVDAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITIAA
NGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNKVCAPLQVKAADGSVISCK
SACLAFGDSKYCCTPPNTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGPDYV
ITFCP
>AAX19848.1 Mal d 2; thaumatin-like [Malus domestica]
MMKSQVASLLGLTLAILFFSGAHAAKITFTNCPNTVWPGTLTGDQKQQLSLTGFELASK
ASQSV DAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITIA
ANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNMACPAQLQVKAADGSVISCK
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGPDY
VITFCP
>AAX19851.1 Mal d 2; thaumatin-like [Malus domestica]
MMKSQAASLLGLTLAILFFSGAHAAKITFTNCPNTVWPGTLTGDQKQQLSLTGFELASK
ASQSV DAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITIA
ANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNMACPAQLQVKAADGSVISCK
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGPDY
VITFCP
>CAT99611.1 Mal d 2; thaumatin-like [Malus domestica]
ASRSVDAPSPWSGRLWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITIA
ANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNMACPAQLQVKAADGSVISCK
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCP
>CAT99612.1 Mal d 2; thaumatin-like [Malus domestica]
ASRSVDAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEITIA
ANGGQDYDVS LVDGFNL PMYVAPQGGTGECKPSSCPANVNMACPAQLQVKAADGSVISCK
KSACLAFGDSKYCCTPPNDTPETCPPEYSEIFEKQCP
>AFM77001.1 Mal d 2; thaumatin-like [Malus domestica]
LTGFELASKASRSVDASSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPP
ATLVEITIAANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNAACPAQLQVK
AADGSVISCKSACLAFGDSKYCCTPPNTPETCPPEYSEIFEKQCPQAYSAYDDKNST
FTCSGGPDYVITF
>COMPARE245 Mal d 2; thaumatin-like [Malus domestica]
MTMMKSQVASLLGLTLAILFFSGAHAAKITFTNCPNTVWPGTLTGDQKQQLSLTGFELA
SKASRSVDAPSPWSGRFWGRTRCSTDAAGKFTCETADCGSGQVACNGAGAVPPATLVEIT
IAANGGQDYDVS LVDGFNL PMSVAPQGGTGECKPSSCPANVNKVCAPLQVKAADGSVI
SCKSACLAFGDSKYCCTPPNTPETCPPEYSEIFEKQCPQAYSAYDDKNSTFTCSGGP
DYVITFCP
>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

>ANQ43386.1 chitinase [Mangifera indica]

MAGGKKIKIGINGFGRIGRLVARVALQRNDVELVAVNDPFITTDYMTYMFKYDTHVHGQWK
HHEVKIKDQKTLFLFDEKPVTVFGIRNPEEIPWAETGAEFVVESTGVFTDKEKAAAHLKGG
AEKVVISAPSKDAPMFVVGNEKEYKPELNIVSNASCTTNCLAPLAKVINDRFGIVEGLM
TTVHSITATQKTVDGSPMKDWRGGRAASFNIIPSSTGAAKAVGKVLPSLNGKLTGMSFRV
PTVDVSVVDLTVRLEKEATYEEIKAAIKEESEGLKLGILGYTEEDVVSTDFVGDSSRSIF
DAKAGIALNKKFVKLVSWYDNEWGYSSRVIDLIVHMASTA

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

MATAEVVTAQTALPEEKPAEEVKVSEIVTEEAAPAVEPVAEEPKEAEPVAVSEEPKEADD
APAEVAVETKEVEVEEAKTVTEEPTVEKTEEEEEETPKEETPEPVVVKETPKEEPAETV
VVEAPKETTEAATEAEAPAPESAPASASETPAEEVVPKEEEGDEKKSEAEVEAEKTE

>AEE98392.1 Man e 5; glutamic acid rich protein, Hev b 5-like [Manihot esculenta]

MATAEVVTAQTALPEEKPAEEVKVSEIVTEEAAPAVEPVAEEPKEAEPVAVSEEPKGGDD
APAEVAVETKEVEVEEAKTVTEEPTVEKTEEEEEETPKEETPEPVVVKETPKEEPTAETV
VEEAPKETTEAATEAEAPAPESAPASAPETPAEEVVPKEEEGDEKKSEAEVEAEKTE

>G5DC91.2 thaumatin-like [Manilkara zapota]

ATFDVVNQCTFTVWAGASPGGGKQLDQGQWTITVAPGSTKARIWGRGTCNFDANGQGKC
QTGDCNGLLQCQGYGSPNTLAEFSLNQPNLDYVDISLVDGFNIPMDFSPAAAGVCKDI
RCATDITAQCPAELQAPGGCNPCTVYKTNEYCCTNGQGTGCPITALSKFFKDRCPDAYS
PQDDPSTLFTCPAGTNYKVVFCPNLDA

>B3EWS0.1 thaumatin-like, partial [Manilkara zapota]

ATFDIVNQCTFT

>BAF47263.1 tropomyosin [Marsupenaeus japonicus]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVLEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLEDELVNEKEYKSITDELDTQTFSELVSGY

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

MSWQTYVDDHLMCDIDGQGQLAAASIVGHDGSIWAQSASFPQLKPEEITGIMKDFDEPG
HLAPTGLYIAGTKYMIQGESGAVIRGKKGSGGITIKKTGQALVFGIYEEPVTPGQCNMV
VERLGDYLIEQGM

>P86745.1 calcium-binding protein, parvalbumin [Merluccius australis]

AFAGILADADITAALAACKAEGTFTHGVEFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKLFQNFSAAGARALTAETATFLKAGSDGDGKIGVDEFAAMVKG

>P86749.1 calcium-binding protein, parvalbumin [Merluccius australis]

AFAGILADADITAALAACKAEGTFTHGEFFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKLFQNFSAAGARALTAETATFLKAGSDGDGKIGVDEFAAMVKG

>P86750.1 calcium-binding protein, parvalbumin [Merluccius australis]

AFSGILAEADIAAALKACEAADSFNKAFKAVGLSAKSADDIKKAFVIDQDKSGFIEE
DELKLFQVFSAGARALTAETKAFKAGSDGDGAIGVDEFAVLVKA

>P86752.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]

AFAGILADADIAAALAACKAEGSFKHGEYFAKIGLKGKSAADIKKVFIIIDQDKSDFVEE

DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVDEFAAMVKG
>P86753.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]
AFSGILADADIAAALKACEAADSFNKYAFFAKVGLSAKSAEDIKKAFFVIDQDKSGFIEE
DELKFLQVFSAGARALDAETKAFKAGSDGDGAIGVDEFAVLVKA
>P86754.1 calcium-binding protein, parvalbumin [Merluccius bilinearis]
AFAGVLADADIKAAALAGCAAADSFNKYKTFKACGLFFAIIDQDHSGFIEEEELKFLQTF
SAGARALSDAETKTFLAAGDVGDMIGVDEFAA
>P86757.1 calcium-binding protein, parvalbumin [Merluccius capensis]
AFSGILAEADIAAALKACEAAGTFNKYAFFAKVGLTGKSADDIKKAFFVIDQDKSGFIEE
DELKFLQVFSAGARALDDETKAFKAGSDGDGAIGVEEWAALVKA
>P86761.1 calcium-binding protein, parvalbumin [Merluccius gayi]
AFAGILADADITAALAACKAEGTFKHGEFFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVDEFAAMVKG
>P86760.1 calcium-binding protein, parvalbumin [Merluccius gayi]
AFAGVLADADIKAAALAGCAAADSFNKYKTFKFAIIDQDHSGFIEEEELKFLQTF SAGA
RALSDAETKAF LAAGSDGDGKIGFVALVKA
>P02620.1 calcium-binding protein, parvalbumin [Merluccius merluccius]
AFAGILADADITAALAACKAEGSFKHGEFFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVEEFAAMVKG
>P86765.1 calcium-binding protein, parvalbumin [Merluccius merluccius]
AFAGILADADITAALAACKAEGSFKHGEFFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVDEFAAMVKG
>P86768.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]
AFAGILADADITAALAACKAEGTFKHGEFFTKIGLKGKSPADIKKVFIIIDQDKSDFVEE
DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVDEFAAMVKG
>P86769.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]
AFSGILAEADIAAALKACEAAGTFNKYAFFAKVGLTGKSADDIKKAFFVIDQDKSGFIEE
DELKFLQVFSAGARALDDETKAFKAGSDGDGAIGVDEWAALVKA
>P86770.1 calcium-binding protein, parvalbumin [Merluccius paradoxus]
AFAGVLADADIKAAALAGCAAESFNKYKTFKACGLAGKFFAIIDQDHSGFIEEDELKFL
QTF SAGARALSDAETKDVDGDMIGVDEFVALVKA
>P86771.1 calcium-binding protein, parvalbumin [Merluccius polli]
AFSGILAEADIAAALKACEAAGTFNKYAFFAKVGLTGKSADDIKKAFFVIDQDKSGFIEE
DELKFLQVFSAGARALDAETKAFKAGSDGDGAIGVDEWAVLVKA
>P86772.1 calcium-binding protein, parvalbumin [Merluccius polli]
AFAGVLADADIKAAALAGCAAESFNKYKTFKFAIIDQDHSGFIEEEELKFLQTF SAGA
RALSDAETK
>P86774.1 calcium-binding protein, parvalbumin [Merluccius productus]
AFAGILADADITAALAACKAEGTFKHGEFFTKIGLKGKSAADIKKVFIIIDQDKSDFVEE
DELKFLQNFSAAGARALDAETATFLKAGSDGDGKIGVDEFTAMIKG
>P86775.1 calcium-binding protein, parvalbumin [Merluccius productus]
AFSGILAEADIAAALKACAAADTFNKYAFFAKVGLSAKSADDIKKAFFVIDQDKSGFIEE
DELKFLQVFSAGARALDAETKAFKAGSDGDGAIGVDEFAVLVKA
>ARG42047.1 lipocalin [Mesocricetus auratus]
MKLLLLLLVGLLELTLVLCVHAEKTSLTGKNFNPEKIVGKWH SILLASDKREMIIEYGSM
RMFMEYIRLFKNSSLAVKFHTIANEECTELYLVCDKTEKGGVYDAKYDGYNRFTILD TDY
NDYIITHLRNLIKNGETFQLMKLCGRKPKLSSNIKKKFGDLCQKHGIVKENIIDLTEADHC
LKTQVEIVA
>AAD55792.2 Mes a 1; lipocalin [Mesocricetus auratus]
MVKFLLLALALGVSCAQHQNLVSPSEVDGKWHSLYIAADNKS K VSEGGPLRVVYKHLEC

SDECQFTTIKFYTKVENVCQEHRVVGRKKGDKGYITDFSGQNYFHVVEKADDTMTFHNVN
VDDSGKTNVILVVGKGESSIEQKQRFEKTAEKYDIPKENIEHLVTTDTCNQ
>COMPARE014 Mes a 1; lipocalin [Mesocricetus auratus]
HYQNLEVPSEVDGKWYSLYIAADNKEKVSEGGPLRAYIKNVECIDECQTLKITFYTKVE
GVCQEHTIVGRKGEDGKYITDFSGQNYFHIVEKSDDTMTFHNVNVDDSGKTNVILVVGRG
ESSSIEQKQRFEKTAEEYDIPKENIEDLVPTDNCQDQ
>AAA60330.1 Met e 1; tropomyosin [Metapenaeus ensis]
MKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQVQESLLKANNQ
LVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAADSERMRKVL
ENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAEERAETGESKI
VELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAEFAERSVQKLQ
KEVDRLDEDELVNEKEYKSITDELQTFSELSGY
>AAG08989.1 tropomyosin [Mimachlamys nobilis]
MDAIKKKMQAMKVDRENAQDLAEQMEQKLKDTETAKAKLEEEFNELQKKLTATENNYDTV
NEQLQEANTKLENSKQITQLESVDVGGVLRRLTLLLEEDYERSEEKLNSTTEKLEEASKAA
DESERNRKVLEGRSNSYEERIDELEKQLETAKNVATDADHKFDEAARKLAITEVDLERAE
TRLEAADAKVLELEEELTVVGANIKTLQVQNDQASQREDSYEETIRDLTKSLKDAENRAT
EAERQVVKLQKEVDRLDELLAEKERYKAISDDLQTFAEIAGY
>AHW81906.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus alba]
MGVFTFDDEFSTVAPARFFKAAVLDADNLFPKVAPQAAKSAETVEGNGGPGTVKKITLP
DGKYVVKQRLDSIDHDNFTYGHSSIIIEGDVLSADIEKISHVTKFVASSSGGSIKVTTFHT
VGNAPVDEAKAKEGKEKAEGFLKLVEGYLEANPSAYN
>AAV33670.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus bombycis]
MGVFTFDDEFSTVAPARFFKAAVLDADNLFPKVAPQAAKSAETVEGNGGPGTVKKITLP
DGKYVVKQRLDSIDHDNFTYGHSSIIIEGDVLSADIEKISHVTKFVASPSGGSIKVTTFHT
VGDAPVDEAKAKEGKEKAEGFLKLVEGYLEANPSAYN
>AAV33672.1 pathogenesis related protein, PR-10, Bet v 1-like [Morus bombycis]
MGVSTHNDEFSTVAPARLFKAAVLDADNLFPKIAPDAAKSAENIEGNGGPGTIKKITFP
DGKYVVKQKLDAIDLNDNYSYSHSIIIEGDILSAELEKISHETKFVAAPGGGSIKVTTFHT
VGNATVDEAKAKEGKEKAAGFLKLVEGYLEANPSAYN
>P85894.1 Mor n 3; lipid transfer protein [Morus nigra]
ITCGQVSSSLAPCINYL RAGGVVPANCCNGVRS LNNAAKTTADRQAACNCLKSAFNSIKG
LNLNLAAGLPGKCGVSVYPYKISPSTDCSKVK
>AAA39768.1 Mus m 1; lipocalin, urinary globulin [Mus musculus]
MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFL
EQIHVLEKSLVLFHTVVRDEECELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM
AHLIN EKDGETFQLMGLYGREPDLSSDIKERFAKLCEEHGILRENIIDLSNANRCLQARE
>CAA26953.1 Mus m 1; lipocalin, urinary globulin [Mus musculus]
MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFL
EQIHVLENSLVLFHTVVRDEECELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM
AHLIN EKDGETFQLMGLYGREPDLMSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE
>P02762.2 Mus m 1; lipocalin, urinary globulin [Mus musculus]
MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFL
EQIHVLENSLVLFHTVVRDEECELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLM
AHLIN EKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE
>AAB82772.2 Mus a 5; beta-1,3-glucanase [Musa acuminata]
MATKASLSIKGFALLVSVLVAVPTRVQSIGVCYGM LGNNLPPPSEVVSLYKSNNIARMRL
YDPNQAALQALRNSNIQVLLDVP RSDVQSLASNPSAAGDWIRRNVVAYWPSVSFRYIAVG
NELIPGSDLAQYILPAMRNIYNALSSAGLQIQVSTAVDTGVLGTSYPPSAGAFSSAAQ
AYLSPIVQFLASNGAPLLVNVYPYFSYTGNGPQISLPYALFTASGVVVQDGRFSYQNLFD

AIVDAVFAALERVGGANVAVVSESGWPSAGGGAEASTSNARTYNQNLIRHVGGGTPRRP
GKEIEAYIFEMFNENQKAGGIEQNFGLFYPNKQPVYQISF

>2CYG_A Mus a 5; beta-1,3-glucanase [Musa acuminata]
IGVCYGMGLGNNLPPPSEVVSLEYKSNNIARMRLYDPNQAALQALRNSNIQVLLDVPRSDVQ
SLASNPSAAGDWIRRNVVAYWPSVSVFRYIAVGNELIPGSDLAQYILPAMRNIYNALSSAG
LQNQIKVSTAVDTGVLGTSYPPSAGAFSSAAQAYLSPIVQFLASNGAPLLVNVYPYFSYT
GNPGQISLPYALFTASGVVVQDGRFSYQNLFDAIVDAVFAALERVGGANVAVVSESGWP
SAGGGAEASTSNAQTYNQNLIRHVGGGTPRRPGKEIEAYIFEMFNENQKAGGIEQNFGLF
YPNKQPVYQISF

>ADG36438.1 Mus a 5; beta-1,3-glucanase [Musa acuminata]
IGVCYGMGLGNNLPPPSEVVSLEYKSNNDIARMRLYDPNQAALQALRNSNIQVLLDVPRSDVQ
SLASNPSAAGDWIRRNVVAYWPSVSVFRYIAVGNELIPGSDLAQYILPAMRNIYNALSSAG
LQNQIKVSTAVDTGVLGTSYPPSAGAFSSAAQAYLSPIVQFLASNGAPLLVNVYPYFSYT
GNPGQISLPYALFTASGVVVQDGRFSYQNLFDAIVDAVFAALERVGGANVAVVSESGWP
SAGGGAEASTSNAQTYNQNLIRHVGGGTPRRPGKEIEAYIFEMFNENQKAGGIEQNFGLF
YPNKQPVYQMSF

>ABV55108.1 catalase [Musa acuminata]
MDPYKFRPSSSFDNFTTTNAGAPVWDDQALTVGSRGPILLEDYHLVEKIAHFARERIP
ERVVHARGASAKGFFECTHDVTHLTCADFLRAPGVQTPPIILRFSTVIHERGSPETIRDPR
GFAVKFYTREGNWDLLGNNFPVFFIRDGIKFPDVIHAFKPNPKSHVQEYWRVDFLSHHP
ESLHTFFFLFDDVGVPSDYRHMEGFGVNTYTFVSKEGKVNYYVFKHWPCTCGVKCLLEDEA
IVVGGKNHSHATQDLYDSIAAGNYPEWKL FVQVMDPDTEDRYDFDPLDDTKTWPEDLLPL
QPVGRLVLRNIDNFFSENEQLAFGPGLVVPGIYYSDDKMLQCRVFAYGDTQRYRLGPNY
LTLPVNAPKCAHHNNHYDGLMNMHRDEEVDYFPSRHASLRHAERFPINRVVTGKREKN
VIPKQNDFKQPGERYRSWAPDRQERFVRRWAEQLAHPKVSYELRSIWISFLSKCDTSLGQ
KVANRLNMRANI

>CAC81811.1 Mus a 2; chitinase [Musa acuminata]
MKALLLVIFTLASSLGAFAEQCGRQAGGALCPGGLCCSQYGCNGNTDPYCGQGCQSQC
SGGSGGGSVASIISSSLFEQMLKHRNDAACPGKGFYTYNAFIAAANSFSGFGTTGDDAKK
KREIAAFLAQTSHETTGGWATAPDGPYAWGYCFVQEQNPSSDYCVASSQWPCAAGKKYYG
RGPIQISFNINYGPAGRAIGSDLLNPNLDVATDATISFKTALWFWMTQSPKPSCHDVIT
GSWTPSNADQAAGRLPGYGVTTNIINGGLECGKGYDARVADRIGFYKRYCDLLGVSYGDN
LDCYNQRPFASTAATATF

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

>1Z3Q_A Mus a 4; thaumatin-like [Musa acuminata]
ATFEIVNRCSTVWAAAVPGGGRQLNQGSWTINVNAGTTGGRIWGRGTGCSFDGSGRGRC
QTGDCGGVLSCTAYGNPNTLAEFALNQFNLDFFDISLVDGFNVPMDFSPSSGGCRGIR
CAADINGQCPGALKAPGGCNPCTVFKTDQYCCNSGACSPDYQFFKRNCPCDAYSYPKD
DQTTTTFTCPGGTNYRVVFCP

>COMPARE149 calcium-binding protein, parvalbumin, partial [Mustelus griseus]
LFLKNFSATAR

>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]
ALLAAGSDHDGKIGADEFAK

>BAD36780.1 Myr p 3; pilosulin [Myrmecia banksi]
MKLSCLLLTLAIIFVLTIVHAPNVKAKALADPESDAVGFADAVGEADPFIDITKLNKIKKLT
KATCKVISKGASMCKVLFDKKKQE
>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
>COMPARE125 dipeptidyl peptidase, partial [Myrmecia pilosula]
VYYLATAPGEPSSQR
>COMPARE126 dipeptidyl peptidase, partial [Myrmecia pilosula]
NLYSVPLDASQKPT
>COMPARE127 dipeptidyl peptidase, partial [Myrmecia pilosula]
EYDHYITTNR
>COMPARE122 esterase, partial [Myrmecia pilosula]
DEFGGVVVAVEK
>COMPARE123 esterase, partial [Myrmecia pilosula]
YAEPTGQQR
>COMPARE124 esterase, partial [Myrmecia pilosula]
APGNLGLKDQVVALR
>COMPARE117 hyaluronidase, partial [Myrmecia pilosula]
NGGVPQEGDLKK
>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]
YADGPKPEEFPKFESLK
>COMPARE107 phospholipase A2, partial [Myrmecia pilosula]
MVELNADAPFCALYNDR
>COMPARE108 phospholipase A2, partial [Myrmecia pilosula]
IGASVLVADTTMSR
>COMPARE109 phospholipase A2, partial [Myrmecia pilosula]
GVIQRMVLGADPR
>CAA49760.1 Myr p 1; pilosulin [Myrmecia pilosula]
MKLSCLLLTLTIIFVLTIVHAPNVEAKDLADPESEAVGFADAFGEADAVGEADPNAGLGS
VFGRLARILGRVIPKVAKKLGPKVAKVLPKVMKEAIPMAVEMAKSQEEQQPQ
>AAB36316.1 Myr p 2; pilosulin [Myrmecia pilosula]
MKLSCLLLTLAIIFVLTIVHAPNVEAKALADPESDAVGFADAVGEADPIDWKKVDWKKVS
KKTCKVMLKACKFLG
>2206305A Myr p 2; pilosulin [Myrmecia pilosula]

MKLSCLLLTLAIIFVLTIVHAPNVEAKALADPESDAVGFADAVGGADPIDWKKVDWKKVS
KKTCKVMLKACKFLG

>AAB50883.1 Myr p 1; pilosulin [*Myrmecia pilosula*]
MKLSCLLLTLAIIFVLTIVHAPNVEAKDLADPESEAVGFADAFGEADAVGEADPNAGLGS
VFGRLARILGRVIPKVAKKLGPVAKVLPKVMKEAIPMAVEMAKSQEEQQPQ

>COMPARE116 unknown function, partial [*Myrmecia pilosula*]
WDNELETIAQR

>BAH10150.1 tropomyosin [*Neptunea polycostata*]
MDLIKKKMLSMKMDKENALDRADVMEQKFRDAEDQKSKLEDDLNLQKKYSQLENEFDRV
NEGLLDANAKLETQDKRVNEMEQEISGLNRRIQLEEDLERSEERLQTATEKLEEATKAA
DESERARKVLESKNQTAESADSLEAQLKESKYIAEDAERKYDEAARKLAITEIDLERAE
TRLEAAEAKCYELDEQLHVVGNNIKTLSIQNDQASQREDSYEETIRDLTQRLKDAENRAQ
EAERTVTKLQKEVDREDELLAEKERYKNISDELDQTFFAELAGY

>CAE17316.1 villin [*Nicotiana tabacum*]
EGGGKIEVWRINGSAKTPVPGDDIGKFYSGDCYIVLYTYHCNDRKEDYYLCWWIGKDSVE
EDQNMAAKLASTMCNSLKARPVLGRVYQGKEPPQFVAIFQPMLVLKGGSSGYKSYIADK
GLNDETYTADSVALIRLSGTSVHNNKAVQVDAVATSLNSNECFLLQSGSSVFSWHGNQST
YEQQQLAAKVAEFLKPGVTVKHAKEGTESSTFWFALGGKQSYTSKKIASEVARDPHLFAY
SFNKGKFEIEEYIYNSQDDLLTEDVLLLDTHAEVFWVWGQSSDPKEKQSSFEVGGQKYIEM
AASLEGLSPHVPLYKVMENPCFFTTFFSWDPAKAIAGNSFQKKVMLLFGVGHASENQ
QRFNGTNQGGATQRASALAALNSAFSSSSPAKSSSAPRSAGKSPGSQRAAAIAALSSALS
AEKKQPPEGGSPRLSRTSSVDAIAPGNEVSTAEIEDSKEVPERKEIETVEPAETDGEDV
GPKPEPEQDETGNSSQTTFSYERLKAIXENPVTGIDLKREAYLSDEEFESVLEMTKEA
FYKLPKWKQDIHKKKVDLF

>CAE17317.1 villin [*Nicotiana tabacum*]
REDYYLCWWIGKDSIEEDQSMAARLASTMCNSFKGRPVLGRVFQKKEPPQFVAIFQPMLV
LKGGLSSGYKNIYADKGLNDETYAADSVALIRLSGTSVHNNKAVQVDAVPASLNSNECF
LQSGSSIFSWHGNQSTYEQQQLAAKVAEFLKPGATVKHTKEGTESSAFWFAVGGKQSYTS
KKVATEVSRDPLHFAYSFNKGKFEVEEYIYNSQDDLLTEDILLDTHAEVFWVWGQSSADS
KEKQSAFDVGGQKYVEMAASLEGLSPNVPLYKVTEGNEPCFFTTFFSWDPAKRSAGNSFQ
KKVMLLFGVGHASENQRSNGSGGPTQRASALAALNSAFSSPSPKSSSAPRPAGTSSAS
QRAAAIAALSGVLTAEEKQSSEGGSPVRSNRSSPVRSSRSPVRSADSGPTENDLSTAEV
QDSEKASEPKEIPEAESNGSEPKPEAEQDEGGNESGQAIYSYEQLKAKSDNPVTGIDFK
RREAYLSDEEFESVLGMKKEAFYKLPKWKQDMHKKKVDLF

>BAE54433.1 tropomyosin [*Octopus vulgaris*]
MDAIKKKMLAMKMERELATDKAEQTDQKLRDTEENKKNLEEDLTTLQKKFSNLENDFDNA
KEQLAEANQKLETSEKRVGECESEIAGLNRRIQLEEDLERSEERLSTAQTKLDEASKAA
DESERGRKVLNRSQGEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE
ARLEAAEAKIVELEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA
EAERTVSKLQKEVDREDELLAEKERYKAISDELDQTFFAELAGY

>AAK58515.1 Ole e 9; beta-1,3-glucanase [*Olea europaea*]
MAANVQTSSLLFLVFLLLQNFYSANSQSFLGVNYGQLSDNLPSLQATVNLLKSTTIQKVR
LFGAEPAVIKAFANTGVEIVIGFDNGDIPTLASNPVNASQFVKSVMMSFYFASNIIAITV
GNEVLTSGDQKLISQLLPAMQNVQNALNAASLGKVKVSTVHAMAVLSQSYPPSSGVFNP
GLGDTMKALLQFQSANDAPFMISPYFYFAYKNQPTPDTLAFCLFQPNAGQVDSGNHGYT
NMFDAQVDAVHSALNAMGFKDIEIVVAETGWPHGGDSNEVGPSLDNAKAYVGNLINHLKS
KVGTPMPGKSIDTYLFSLYDEDKKTGASSEKYFGLFKPDGSTTYDVGLLKNTQNPPTPA
TPTPTPKAAGSWCVKPGVSDDQLTGNINYACGQIDCGPIQPGGACFEPNTVKAHAAYV
MNLYYQSAGRNSWNCDFSQATLTNTNPSYGACNFPSSGSN

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

MRGTAGVPDQPVPTPTPSVPTSSSPVPKPPTQGNKKWCVPKAEATDAQLQSNIDYVCSQS
GMDCGPIQANGACFNPTVRAHASYAMNSWYQSKGRNDFDCDFSGTGAITSSDPSNGSCS
FLS
>2JON_A Ole e 9; beta-1,3-glucanase, partial [Olea europaea]
ATPTPTPKAAGSWCVPKPGVSDQLTGNINYACSQGIDCGPIQPGGACFEPNTVKAHAAY
VMNLYYQHAGRNSWNCDFSQTATLTNTNPSYGACNFPSPGSN
>AAD05375.1 Ole e 3; calcium-binding protein, polcalcin [Olea europaea]
MADDPQEVAEHERIFKRFDANGDGKISSSELGETLKLGSVTPPEEIQRMMAEIDTDGDGF
ISFEEFTVFARANRGLVKDVAKIF
>AAF31151.1 Ole e 8; calcium-binding protein, polcalcin [Olea europaea]
MAANTDRNSKPSVYLQEPNEVQGVFNRFDANGDGKISGDELAVLKLALGSNTSKEEIGRI
MEEIDTDKDGFINVQEFAAFVKAETDPYPSSGGENELKEAFELYDQDHNLISSVELHKI
LTRLGERIAEHDCVEMIKSVSDSDGDGYVSFEFFKMMTNKSGNNSQAEPK
>AAF31152.1 Ole e 8; calcium-binding protein, polcalcin [Olea europaea]
MAANTDRNSKPSVYLQEPNEVQGVFNRFDANGDGKISGDELACALKALGSNTSKEEIARM
MEEIDTDKDGFINVQEFAAFVKAETDPYPSSGGENELKEAFELYDQDHNLISSVELHKI
LTRLGERIAEHDCVEMIKSVSDSDGDGYVSFEFFKMMTNKSGNNSQAEPK
>AA033897.1 Ole e 3; calcium-binding protein, polcalcin, partial [Olea europaea]
EHERIFKRFDKAGDGKISSSELGETLKLPLGSVTLEEIQRMMAEIDTDGDGFL
>AVV30163.1 Ole e 15; cyclophilin [Olea europaea]
MANPKVFFDMTIGGQPVGRIVMELFADVVPRTSENFALCTGEKGVGKSGKPLHYKGSFAF
HRVIPNFMCGGDFTAGNGTGGESIYGSKFADENFVKKHTGPGILSMANAGPGTNGSQFF
ICTAKTEWLDGKHVVFQVVEGFYVKAIEQVGSVSGKTAKPVVADCGQLS
>E1U332.1 Ole e 12; isoflavon reductase-like protein, phenylcoumaran benzylic ether
reductase [Olea europaea]
MADKTKILIIIGGTGYIGKFIVEASAKSEHPTFALARESTISDPVKGKIIQGFKNSGVTL
TGDLYDHESLVKAIKQVDVISTVGLQLADQVKIIAAIKEAGNVKRFFPSDFGTDVDR
HAVEPAKSSFEIKSQIRRAIEAEGIPYTFVSANYFAGYSLPTLVQPEVTAPPRDKVILG
DGNKAVFNEENDIGTYTIKAVDDARTLNKILYIKPPKNIYSFNELVALWEKKIGKTLEK
IYVPEEQVLKQIQESPFPINIVMAINHSFAVKGDLTNFKIEPSFGVEASELYPDVKYTTV
EEYLDQFV
>P81430.2 Ole e 7; lipid transfer protein, partial [Olea europaea]
APSQSTVTALLTSCVSYIDDQ
>COMPARE059 Ole e 7; lipid transfer protein, partial [Olea europaea]
APSQGTVTAKLTSCVSYKDXQ
>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]
SALALVGNKVDGTGR
>COMPARE066 Ole e 7; lipid transfer protein, partial [Olea europaea]
SALANVGNKVDGTGR
>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

>I53806 Ole e 1; Ole e 1-like [Olea europaea]

SQFHIQGQVYCDTCRARFITELSEFIPGAGVRLQCRDGEKGSITFTEVGYTRAEGLYSML
IERDHKNEFCEITLASSSRKDCDEIPVEGWVKPSLKFILNTVNGTTRTINPLGFFKKEVL
PKCPQVFNKLGMYPPNM

>E53806 Ole e 1; Ole e 1-like [Olea europaea]

QFHIQGQVYCDTCHARFITELSEFIPGASVRLQCREKENGDITFTEIGYTRAEGLYSMLV
ERDHKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALP
KCAQVYNKLGMYPPNM

>F53806 Ole e 1; Ole e 1-like [Olea europaea]

QFHIQGQVYCDTCRAGFINELSEFIPGASVRLQCREKNGDITFTEVGYTRAEGLYSMLV
ERDHKNEFCEITLISSGRKDCNEIPIEGWAKPSLKFILNTVNGTTRTINPLGFYKKEALP
KCAQVYNKLGMYPPNM

>C53806 Ole e 1; Ole e 1-like [Olea europaea]

EDVPQPPISQFVYQGVYCDTCRTRFITEFSEFIPGAGVRLQCKDGENGKITFTEVGYTR
AEGLYSMLIERDHKNEFCEITLSSSRKDCDEIPTEGWVKPSVKFILNTVNGTTRTINPL
GFFKKEALPKCPQVFNKLGMYPPNM

>A38968 Ole e 1; Ole e 1-like [Olea europaea]

QFHIQGQVYCDTCRARFITELSEFIPGAGVRLQCRDGEKGSITFTEVGYTRAEGLYSMLI
ERDHKNEFCEITLASSSRKDCDEIPVEGWVKPSLKFILNTVNGTTRTINPLGFFKKEVLP
KCAPQVFNKLGMYPPNM

>G53806 Ole e 1; Ole e 1-like [Olea europaea]

QFHIQGQVYCDTCRAGFITELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLV
ERDHKNEFCEITLISSGSKDCNEIPTEGWGKPSLKFILNTVNGTTRTVNPLGFYKKEALP
KCAQVYNKLGMYPPNM

>B53806 Ole e 1; Ole e 1-like [Olea europaea]

EDVPQPPVVSQFHIQGQVYCDTCRARFITELSEFIPGASVRLQCKDGENGSITFTEVGYTR
AEGLYSMLIERDHKDEFCEITLISSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPL
GFFKKEALPKCPQVFNKLGMYPPNM

>H53806 Ole e 1; Ole e 1-like [Olea europaea]

QFHIQGQVYCDTCRARFITELSEFIPGAGVRLQCRDGEKGSITFTEVGYTRAEGLYSMLI
ERDHKNEFCEITLASSSRKDCDEIPVEGWVKPSLKFILNTVNGTTRTINPLGFFKKEVLP
KCPQVFNKLGMYPPNM

>CAA73038.1 Ole e 1; Ole e 1-like [Olea europaea]

MEDVPQPPVVSQFHIQGQVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDTVTFTEIGYT
RAEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNP
LRFYKKEALPKCAQVYNKLGMYPPNM

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

MEDVPQPPVVSQFHIQGQVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDTVTFTEIGYT
RAEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILSTVNGTTRTVNP
LGFYKKEALPKCAQVYNKLGMYPPNM

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

MEDVPQPPVVSQFHIQGQVYCDTCRSRITELSEFIPGASVRLQCREKENGDITFTEIGYT
RAEGLYSMLVERDHKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTVNP
LGFYKKEALPKCAQVYNKLGMYPPNM

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

QVYCDTCRAGFITELSEFIPGASVRLQCKEKKNGDITFTEVGYTRAEGLYSMLVERDHKN
EFCEITLISSGSKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQVY

NKLGMYPPNM

>P19963.2 Ole e 1; Ole e 1-like [Olea europaea]
EDIPQPPVSQFHIQGGVYCDTCRAGFITELSEFIPGASLRLQCKDKENGDTVTFTEVGYTR
AEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPL
GFFKKEALPKCAQVYNKLGMYPPNM

>AAQ08190.1 Ole e 1; Ole e 1-like [Olea europaea]
IRTVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDITFTEVGYTRAEGLYSMLVERDH
KNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ
VYNKLGMYPPNM

>AAQ10268.1 Ole e 1; Ole e 1-like [Olea europaea]
ILTVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDITFTEVGYTRAEGLYSMLVERDH
KNEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ
VYNKLGMYPPNM

>AAQ10271.1 Ole e 1; Ole e 1-like [Olea europaea]
IWTVYCDTCRAGFITELSEFIPGASVRLQCKDKENGDITFTEVGYTRAEGLYSMLVERDH
KNEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQ
VYNKLGMYPPNM

>AAQ10274.1 Ole e 1; Ole e 1-like [Olea europaea]
WTVSCDTCRAGFITELSEFIPGASVRLQCKDKENGDITFTEVGYTRAEGLYSMLVERDHK
NEFCEITLISSGRKDCDEIPTEGWAKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV
YNKLGMYPPNM

>AAQ10276.1 Ole e 1; Ole e 1-like [Olea europaea]
SYCDTCRAGFITELSEFIPGAGVRLQCKDGENGNITFTEVGYTRAEGLYSMLVERDHKNE
FCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTINPLGFFKKEALPKCAQVYN
KLGMYPPNM

>AAQ10277.1 Ole e 1; Ole e 1-like [Olea europaea]
QAVYCDTCRAGFITELSEFIPGASVRLQCKDRENGDITFTEVGYTRAEGLYSMLVERDHK
NEFCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV
YNKLGMYPPNM

>AAQ10278.1 Ole e 1; Ole e 1-like [Olea europaea]
QDSYRDTCRAGFITELSEFIPGASVRLQCKDRENGDITFTEVGYTRAEGLYSMLVERDHK
NEFCEITLISSGRKDCDEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV
YNKLGMYPPNM

>AAQ10279.1 Ole e 1; Ole e 1-like [Olea europaea]
IRTVSQDTCCARFITELSEFIPGAGVRLQCKDGENGNVTFTEVGYTRAEGLYSMLIERDH
KNEFCEITLLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQ
VFNKLGMYPPDM

>AAQ10280.1 Ole e 1; Ole e 1-like [Olea europaea]
IRTVFRVTCRARFITELSEFIPGAGVRLQCKDGENGNVTFTEVGYTRAEGLYSMLIERDH
KNEFCEITLLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQ
VFNKLGMYPPDM

>AAQ10281.1 Ole e 1; Ole e 1-like [Olea europaea]
QDSYSGHCRARFITELSEFIPGAGVRLQCKDGENGNVTFTEVGYTRAEGLYSMLIERDHK
NEFCEITLLSSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTINPLGFFKKEALPKCPQV
FNKLGMYPPDM

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

>AAO22132.1 Ole e 1; Ole e 1-like [Olea europaea]

SDSYCDTCRAGFITELSEFIPGASLRLQCKDKENGDVTFTEVGYTRAEGLYSMLVERDHK
NEFCEITLISSGRKDCNEIPTEGWVKPSLKFILNTVNGTTRTVNPLGFFKKEALPKCAQV
YNKLGMYPPPTWNVTI

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

>ABP58632.1 Ole e 1; Ole e 1-like [Olea europaea]
PPVSQFHIQGGIYCDTCRSRIFITELSEFIPGASVRLQCREKENGDIPTFEIGYTRAEGLY
SMLVERDHKNEFCEITLISSGRKDCDEIPIEGWAKPSLKFILNTVNGTTRTVNPLGFFKK
EALPKCAQVYNKLGMYPPNM

>ABP58633.1 Ole e 1; Ole e 1-like [Olea europaea]
PPVSQFHIQGGVYCDTCRAGFITELSEFIPGASVRLQCREKNGDITFTEVGYTRAEGLY
SMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTINPLGFYKK
EALPKCAQVYNKLDMYPPNM

>ABP58635.1 Ole e 1; Ole e 1-like [Olea europaea]
PPVSQFHIQGGVYCDTCRARFITELSEFIPGASVRLQCRDGENGSITFTEVGSTRAEGLY
SMLIERDHKDEFCEITLISSSRKDCDEIPVEGWVKPSLKFMLNTVNGTTRTVNPLGFFKK
EALPKCPQVFNKLGMYPPDM

>ABP58636.1 Ole e 1; Ole e 1-like [Olea europaea]
PPVSQFHIQGGVYCDTCRAGFITELSEFIPGASVRLQCREKNGDITFTEVGYTRAEGLY
SMLVERDHKNEFCEITLISSGRKDCNEIPTEGWAKPSLKFILNTVNGTTRTINPLGFYKK
EALPKCAQVYNKLGMYPPNM

>ABP58637.1 Ole e 1; Ole e 1-like [Olea europaea]
PPVSQFHVQGGIYCDTCRAGFIAELSEFILGAGVRLQCRDSKKNITFTEVGYTRAEGLY
SMLIERDHKNEFCEVNSLSSSRKDCDEIPIEGWVRPSLRFLLNTVNGTCTIKPLGFFKN
KALPKCPQVFNKLGMYPPDL

>X76395 Ole e 1; Ole e 1-like [Olea europaea]
EDVPPVVSQFHIQGGVYCDTCRAGFITELSEFIPGASLRLQCKDKENGDVTFTEVGYTR
AEGLYSMLVERDHKNEFCEITLISSGRKDCNEIPTEGWVKPSLKFILNTVNGTTRTVNPL
GFFKKEALPKCAQVYNKLGMYPPNM

>AAY88919.1 Ole e 11; pectin methylesterase [Olea europaea]
MSCIAVEAVLLGILLYIPIVLSDDRAPIPANSAQLNSWFDGIIQPVAVRKATMDPALVTA
EGQAKVIKLSKDSGSGDFKSINEAIKSIPDDNTKRVILSFSPGNYSKVKIGMYKHYITFY
GEDPNNMPILVFGGTAAEYGTVDSATLIVESNYFSAVNLKIVNSAPRPDGKRVGAQAAAL
RISGDKASFYNVKIYGFQDTLCDDKKGKHFYKDCYIEGTVDFIFGSGKSIFLNTELHAVPG
DQPAIITAQARKTESEDYGYFVNCRVTTGGGAF LGRSWMPAAKVV FAYTEMGDAIHPEGW
ILVKPEHESTVRFPEYNNKGPANMEKRAKFKRLSDAEAKQSISLGSIEASKWLLPPRV
VGLP

>ACZ57582.1 Ole e 11; pectin methylesterase [Olea europaea]
MSCIAVEAVLLGILLYIPIVLSDDRAPIPNSAQLNSWFDGIIQPVAVRKATMDPALVTA
EGQTKVIKLSKDSGSGDFKSINEAIKSIPDDNTKRVILSLAPGNYSKVKIGMYKHYITFY
GEDPNNMPILVFGGTAAEYGTVDSATLIVESNYFSAVNLKIVNSAPRPDGKRVGAQAAAL
RISGDKASFYNVKIYGFQDTLCDDKKGKHFYKDCYIEGTVDFIFGSGKSIFLNTELHAVPG
DQPAIITAQARKTDESDYGYFVNCRVTTGGGAF LGRSWMPAAKVV FAYTEMVDAIHPEGW
ILVKPEHESTVRFSEYNNKGPANMEKRAKFKRLSDAEAKQSISLGSIEASKWLLPPRV
VGLP

>AHL24656.1 Ole e 14; polygalacturonase [Olea europaea]
IPHNGVRRGLVGETIFDVMKYGAKADGRFDNAQAFIKAWKAACESTGPAKVVIPKGFVA
GEVVFQGPCTAPKPITIEIQGNVLASTDVSAYTSGSWIMLEEIDGLVINGGGTINGRGKS

SWQFAGANNEGPLL PVSLTFKKVKNSEMHVNFVDSMGFHSKVADSENKISKLKLISAPG
DSPNTDGMHISCSTNVNVTDSIIGTGDDCVSIGHGTTDILVSGITCGPGHGISVGS LGKR
PDETDVKGISVINCTLTGTTNGARIKTYHASPSIQASDILYKDIIVTDVKNPILIDQHYD
SKKKPEQSKVKISGVHFVNIKTTVSEIPVALNCSEAVPCEDVELADIDLAPSGAAGSLK
SVCANAKFVLKGPPIPPGC

>CAA73035.1 Ole e 2; profilin [Olea europaea]
MSWQAYVDDHLMCDIEGHEDHRLTAAAIVGHDGSVWAQSATFPQFKPEEMNGIMTDFNEP
GHLAPTGLHLGGTKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNM
VVERLGDYLV EQGM

>O24170.1 Ole e 2; profilin [Olea europaea]
MSWQAYVDDHLMCDIEGHGHRHTAAAIVGHDGSVWAQSATFPQFKPEEMNGIMTDFNEP
GHLAPTGLHLGGTKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNM
VVERLGDYLV EQGL

>O24171.1 Ole e 2; profilin [Olea europaea]
MSWQAYVDDHLMCDIEGHGHRHTAAAIVGHDGSVWAQSATFPQFKPEEMNGIMTDFNEP
GHLAPTGLHLGGTKYMVIQGEAGAVIRGKKKSGGITIKKTGQALVFGIYEETVTPGQCNM
VAERLGDYLV EQGL

>A4GFC3.1 Ole e 2; profilin [Olea europaea]
MSWQAYVYEHLMCEIESHLLSSAAILGHDGTVWAQSTAFPQFKPEEITGIMKDFDEPGHL
APTGMFVAGAKYMVIQGEPAVIRGKKKSGGITIKKTGQALVFGIYDEPMTPGQCNMVVE
RLGDYLV EQGQ

>A4GFC0.1 Ole e 2; profilin [Olea europaea]
MSWQTYVDEHLMCEIEGLHLASTAIIGHAGTVWAQSTAFPQFKPEEITGIMKDFDEPGHL
APTGMFVAGAKYMVIQGEPAVIRGKKKSGGITIKKTGQALVFGIYDEPMTPGQCNMVVE
RLGDYLV EQGL

>CAD21706.2 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPLGHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABP58627.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPLGHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGTPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26131.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPLGHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNIAVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26132.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGLTTVTGNLSGLKPLGHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGTAAINIVDKQIPLTGPHSIIGRAVVVHSDPDDLGRG
CHELSKSTGNAGGRVACGIIGLQG

>ABX26134.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPLGHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHEQSKSTGNAGGRVACGIIGLQG

>ABX26138.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPLGHGFHVNALGATTNGCMSTG
PHFDPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELSKSTGNAGGRVACGIIGLQG

>ABX26139.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVFNSSEGVTGTVYFTQEGDGLTTVTGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGDAGGRVACGIIGLQG

>ABX26140.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVTCGIIGLQG

>ABX26141.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHHAHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX26143.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDRQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX26145.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX26147.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54842.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54844.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDATNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54849.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54855.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAISIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRSGHELKSTGNAGGRVACGIIGLQG

>ABX54859.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54862.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVLNSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDFGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54864.1 Ole e 5; superoxide dismutase [Olea europaea]

MVKAVTVINSSEGVTGTVYFTQEGDPTTITGNLSGLKPGLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGTAANIVDKQIPLTGPHSIIGRAVVVHSDPDDLGRG

GHELKSTGNAGGRVACGIIGLQG

>ABX54866.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG
PHFNPVGKEQGAPGDENRHAGVLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54869.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHVLSKSTGNAGGRVACGIIGLQG

>ABX54876.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVLNSSEGVTGTVYFTQKGDGPTTITGNLSGLKPGHLHGFHVHALGDTTNGCMSTG
PHFLPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>ABX54877.1 Ole e 5; superoxide dismutase [Olea europaea]
MVKAVTVFNSSEGVTGTVYFTQEGDGPTTVTGNLSGLKPGHLHGFHVHALGDTTNGCMSTG
PHFNPVGKEHGAPGDENRHAGDLGNITVGEDGTAAINIVDKQIPLTGPHSIIGRAVVVHS
DPDDLGRGGHELKSTGNAGGRVACGIIGLQG

>P80740.2 Ole e 5; superoxide dismutase, partial [Olea europaea]
MVKAVTVLNSSEGPHGIVYFAQEGDGPTTV

>E3SU11.1 Ole e 13; thaumatin-like [Olea europaea]
MNFSKNLPLLVSLWAITFFAYTHAATFDIVNQCTYTVWAAASPGGGRRLDQGQSWNINVA
PGTTQARIWGRNTCNFDANGRGQCETGDCNGLLECGYGRPPNTLAEFALNQPNLDFVD
ISNVDFGNIPLEFSPTTNVCRRLVCNAPIVQQCPSELRTPGGCNNPCTVFNTNEYCCTNG
PGSCGPTPLSRFFKERCPDAYSYPQDDPTSLFTCPAGTNYRVVFCP

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

>BAE54432.1 tropomyosin [Ommastrephes bartramii]
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKTEEDLSTLQKKYANLENDFDNA
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLLLEEDLERSEERFSSAQSKLEDASKAA
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE
ARLEAAEAKIVELEELKVVGNMKSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA
EAERTVSKLQKEVDRLLEDELLAEKERYKTISDELDQTFQELAGY

>Q25632.1 tropomyosin [Onchocerca volvulus]
MDAIKKKMQAMKIEKDNALDRADAAEKKVRQMTEKLERIEEELRDTQKKMMQTENDLVKA
QEDLSVANTNLEDKEKKVQEAEEVAALNRRMTLLEELERAEERLKIATDKLEEATHTA
DESERVKVMENRSFQDEERANTVESQEKEAQLLAEADRKYDEVARKLAMVEADLERAE
ERAEAGENEIVELEELRVVGNMKSLEVSEEKALQREDSYQEQIRTVSVRLKEAETRAE
FAERSVQKLQKKVDRLEDELVHEKERYKNISEELDQTFQELSGY

>BAJ07603.1 Onc k 5; vitellogenin, partial [Oncorhynchus keta]
SMTDLSPFDDNIVNKIHYLFSEVNAVKCSMVGDTLTTFNNRKYPVNMPLSCYQVLAQDCT
IELKFMVLLKKDHASEQNHINVKISDIDVDLYTEDHGMVKNEMEISKDNLPYTDPSGS
IMIKQKGEVSLYAKSHGLQEVYFDSNSWKIKVVDWMKGQTCGLCGKADGEHRQEYRTPS
GRLTKSSVSFAHS

>P86431.1 Onc m 1; calcium-binding protein, parvalbumin [Oncorhynchus mykiss]
ACAHLCKEADLKTALAEACKAADSFNFKTFHTLGFASKXXDDVKKXXXVLDQDASGFLEV
EELKFLQNFQPKXXXLTDAETKAFKAGDADGDGMLGLDEFVAVLVKQ

>P86432.1 Onc m 1; calcium-binding protein, parvalbumin [Oncorhynchus mykiss]
SFAGLNDADVAAAALAAACAADSFNHKAFFAKXXXXXXSPDDLKXXXXLDQDKSGFLEED
ELKFLQNFASARALTAETKXXXXAGDADGDGMLGLDEFVAVLVKQ

>CBA35339.1 calcium-binding protein, parvalbumin [Oncorhynchus mykiss]

MACAHLCKEADIKTALEACKAADSFNFKTFFHTIGFASKSADDVKKAFKVIDQDASGFIE
VEELKLFQNFCKARVLTDAETKAFLKAGDADGDMIGIDEFAVWKQ
>CBA35340.1 calcium-binding protein, parvalbumin [Oncorhynchus mykiss]
MAFAGLNDADVAALAATAADSFNHKAFFAKVGLAGKSNDVKKAFYVIDQDKSGFIEE
DELKLFQNFASARALTDAETKAFLADGDKDGMIGVDEFAAMIKG
>BAB55663.1 collagen [Oncorhynchus mykiss]
MLSFVDNRILLLLAVTSLASCQSGGLKGPRAKGPGRDGPQGNRDKAGLPGIAGP
PGPPGLGGNFAAQFDGGKGSDDPGPMGLMGSRGPNGPPGAPGPQGFTHAGEPGEPGQT
GSIARGPTGSAGKPEDGNNRPGKPGDRGGPGTQGARGFPGTPGLPGMKGHRGYNGLD
GRKGESGTAGAKGETGAHGANGSPGPAGSRGLNGERGRAGPAGPAGARGADGSTGPAGPA
GPLGAAGPPGFPAGPCKEIGGAGSNGPSGPQGGRGEPINGAVGPVGNPNNGIN
GAKGAAGLPGVAGAPGFPGRGGPGPQGPQGSTGARGLGGDPGPSGQKGDGSAKGEPEGHS
GVQGAAGPAGEEGKRSTGEVGTGPAGLRGARGGAGTRGLPGLRGGPIGMPGARGAT
GPGGIRGAPGDAGRAGESGLTGARGLPGNSGQGGPPGKEGPPGAAGLDGRTGPPGPTGPR
GQPGNIGFPGKPGGGEAGKGGDKGPTGATGLRGGPGADGNNGAPGPAGVVGNTGEKGEQ
GPAGAPGFQGLPGPAGPAGEAGKAGNQMPGDQGLPGPAGVKGERGNSGPAGSAGSQGAI
GARGPAGTPGPDGGKGEPSVGI VGAAGHQGPGMPGERGAGGTPGPKGEKGEGGHRGLE
GNMGRDARGGPGSPGPPGSGANGEKGESGSGFPAGPAGLRGPSGERGEGGPAGLPGFA
GPPGSDGQSGPRGEKGPAGGKGDVGPAGPAGPSGQSGPSGASGPAGPPGGRGDAGPSGLT
GFPGAAGRVGGPGPAGIAGPPGSAGPAGKDGPRGLRGDPGPGGPQGEQGVVGPAGISGDK
GPSGESGPPGAPGTAGPQVLPVSGFVGLPGSRGDKLPGGPGAVGEPGRLGPAGASGPR
GPAGNIGMPGMTGTQGEAGREGNSGNDGPPGRPGAAGFKGDRGEPGSPGALGSSGQPGPN
GPAGSAGRPGNRGESGPTGNGGPGVAVGARGAPGPAGPRGEKGGAGEKGDGMKGLRGHG
GLQGMPPNGPSGETGSAGITGPAGPRGPAGPHGPPGKDGRAGGHGAIGPVGHRGSPGHL
GPAGPPGSPGLPGPAGPAGGGYDQSGGYDEYRADQPSFRAKDYEVDATIKSLNSQIENLL
TPEGSKKNPARTCRDIRLSHPDWSSGFYWDPNQGCIAADAIKAYCDFSTGHTCIHPHPES
IARKNWYRSSENKKHVWFGETINGGTEFAYNDETLSPQSMATQLAFMRLLANQATQNTITY
HCKNSVAYMDGENGLKKAVALLQGSNDVELRAEGNSRFTFNVLEDGCTRHTGQWSKTVIE
YRTNKPSRLPILDIAPLDIGEADQEFGLDIGPVCFK
>BAF95206.1 tropomyosin [Oratosquilla oratoria]
MDAIKKKMQAMKLEKDNAMDRA DTLEQQNKEANNRAEKAE EEVHNLQKRMQQLENDLDQV
QEQLLKANTQLEEKDKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKVLENRSLSDERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVLEEEELRVVGNLKSLEVSEEKANQREEAYKEQIKQLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY
>AFV53352.1 Ore m 4; tropomyosin [Oreochromis mossambicus]
MDAIKKKMQMLKLDKENALDRAEQAESDKAAEDRSKQLEDDLVALQKLLKGTEDLDKY
SEALKDAQEKLELAEKIATDAEGEVASLNRRIQLVEEELDRAQERLATALKLEEAEKAA
DESERGMKVIENRAMKDEEKMELQEIQLEAKHIAEEADRKYEEVARKLVIIEGDLERTE
ERAELSEGKCELEEEELKTVTNNLKSLEAQAEKYSQKEDKYEEEIKALTDKLEAETRAE
FAERSVAKLEKTIDDELELYAQKLKYKAISEELDHALNDMTSI
>AAG42802.1 Ory c 3; lipophilin [Oryctolagus cuniculus]
MKLLVPLLLVALALGCYEADAAACPAFLVDSVGF LFDPKPVYRQKLAKYDAPPEAVEAKL
QVKECTDEIDKGRVLI AAVLTKIVKECAL
>AAG42806.1 Ory c 3; lipophilin [Oryctolagus cuniculus]
MKVVMVLLLAALPLYCYAGSGCVLLESVVEKTIDPSVSVVEEKADLQRFIDTEQTEAAVE
EFKECFLSQSNETLANFRVMVHTIYDSLYCAAY
>Q75GX9.1 7S globulin, vicilin-like [Oryza sativa]
MATRARATILLLLAAVLFAAAAAASGEDRRRRETS LRRCLQRCEQDRPPYERARCVQECKD
QQQQQQERRREHGHHDDRRDRRRREGESSEEEDEGRERGSRRRPYVFGRRSFRQVVRSD

QGSVRLLPFFHQASSLLRGIKNYRVAVLEANPRSFVMPHTHTDAHICICYVAQEGGVVAIIE
NGEKWSYAIRQGDVVFAPAGTINYLANTDGRRKLVTKILHTISVPGQIQFFFAPGGRNP
ESFLSSFSKGVQRAAFKISEEKLEKLLGKQDKGVIIRASEEQVRELRRHASEGGHGPHWP
LPPFGESSRGPFNILEQRPRFANRHGRLYEADARSFHDLAEHDIRVAVVNITAGSMNAPF
YNTRSVKVAVYVLDGEGEAEIVCPHLSRGGRGGESEERRRERGGKGWREEEEEEEQQKGGQ
EEEEEEQVGGQYETIRARLSRGTVFVWPSGHPVVTSSRDSTLQIVCFDVHANNNERMYL
AGMNSVLKLLDPQAKELAFAASAREVDELLNAQQESAFLAGPEKSGRRGEESEDEDRRRR
RSHRGRGDEAVETLLRMAAAAV

>Q7X7E6.1 alpha-amylase/trypsin inhibitor [Oryza sativa]
MASASDKLVLSAIVLAVLAAVVAASGYGDVGEYCRVGKAVSRNPVPSCRNYIARWCAA
GGRMDSRKQPPREFLEPCCRELAAVPMQCRCDALSVLVRGVVTEEGDRVSGMISQHAAPG
CDAATIAGMASALTDYGRCNLQHTAGSFACLMFGGGMD

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

>AAA86533.1 Ory s 1; beta-expansin [Oryza sativa]
MASSSLLLACVVAAMVSPSPAGHPKVPPGNITTSYGDKWLEARPPGMVRPRVLAPKDN
GGACGYKDVKAPFLGMNSCGNDPIFKDGKGCSCFEIKCSKPEACSDKPALIHVTDMND
EPIAAYHFDLSGLAMAKDGKDEELRKAGIIDTQFRRVKCKYPADTKITFHIEKASNPYL
ALLVKYVAGDGDVVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEGARR
SSAEDAIPDPGRRQRVQVNVQAK

>AAF72991.1 Ory s 1; beta-expansin [Oryza sativa]
MASSCLLLACVVAAMVSAVSCGPPKVPPGNITTAAYGKQWLEARGTWYGKPKGAGPDDN
GGACGYKDIDKAPFLGMNSCGNDPIFKDGKGCSCFEVKCSKPEACSDKPVIIHITDMNT
EPIAAYHFDLSGHAFGAMAKEGKDEELRKAGIIDMQFRRVRCKYPGETKVTFFHVEKGSNP
NYFAVLVKYVGGDGDVVKVELKEKGSEEWKPLNESWGAIWRIDTPKPLKGPFSLRVTTES
DQKLVANDVIPDNWKANALYKSEIQVD

>Q40638.2 Ory s 1; beta-expansin [Oryza sativa]
MASSSLLLACVVAAMVSAVSCGPPKVPPGNITTSYGDKWLEAKATWYGAPKGAGPKDN
GGACGYKDVKAPFLGMNSCGNDPIFKDGKGCSCFEIKCSKPEACSDKPALIHVTDMND
EPIAAYHFDLSGLAFGAMAKDGKDEELRKAGIIDTQFRRVKCKYPADTKITFHIEKASNP
NYLALLVKYVAGDGDVVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKGPFSVRVTTEG
GEKIIAEDAIPDGWKADSVYKSNVQAK

>BAD13150.1 calcium-binding protein, polcalcin [Oryza sativa]
MAAASSADMERIFKRFDNTGDGKISLSELTALRTLGSTSADEVQRMMAEIDTDGDGFID
FNEFISFCNANPGLMKDVAKVF

>XP_015646887.1 casein kinase [Oryza sativa]
MSKARVYTDVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNEKC
IIKILKPVKKKKIKREIKILQNLCGGNIVKLLDIVRDQHSKTPSLIFEYVNNNTDFKVLVY
PTLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNVMIDHELRLRLIDWGLAEFYHPG
KEYNVRVASRYFKGPELLVDLQDYDYSLDMWSLGCMAFAGMIFRKEPFFYGHNDHDQLVKI
AKVLGTDLSNSYLNKYRIELDPQLEALVGRHSRKPWSKFINADNQHLVSPEAIDFLDKLL
RYDHQDRLTAREAMAHPYFLQVRAAENSRRPRAQ

>B8AL97.1 cupincin [Oryza sativa]
MAKKKTSSSMARSQLAALLISLCLSLASNAVGSRRGEREEEDERRRHGGEGGRPYHFG
EESFRHWTRTRHGRFSVLERFPDEQVVGAAVGGYRVAVLEAAPRAFLQPSHYDADEVFYV
KEGEGVIVLLREGRKESFCVREGDAMVIPAGAIVYSANTHSSKWFRVVMMLNPNVSTPGHF
EEYFPVGGDRPESFFSAFSDDVLQAAFNTRREELEKVFERQREGGEITTAPEEQIRELSK
SCSRGGGGGSGSEWEIKPSSLTGKSPYFSNNHGKLFELTGDECRHLKLLDLQIGLANITR

GSMIAPNYNTRATKLAVVLQSGGYFEMACPHVSGGGSSERREREREHGRRRREEEQGEEEH
GERGEKARRYHKVRAQVREGSVIVIPASHPATIVASEGESLAVVCFVFGANHDEKVF LAG
RNSPLRQLDDPAKKL VFGGSAAREADRVLAAQPEQILLRGP HGRGSVSDM

>Q852L2.2 cupincin [*Oryza sativa*]

MAKKKTSSSMARSQLAALLISLCFLSLASNAVGWSRRGEREEEDERRRHGGEGGRPYHLG
EESFRHWTRTRHGRFSVLERFPDEQVVGAAVGGYRVAVLEAAPRAFLQPSHYDADEVFVY
KEGEGVIVLLREGRRESFCVREGDAMVIPAGAIVYSANTHSSKWFRVVMLLNPVSTPGHF
EEYFPVGGDRPESFFSAFSDDVLQAAFNTRREELEKVFERQREGGEITTAPEEQIRELSK
SCSRGGGGGSGSEWEIKPSSLTGKSPYFSNMHGKLFELTGDECRHLKLDLQIGLANITR
GSMIAPNYNTRATKLAVVLQSGGYFEMACPHVSGGGSSERREREREHGRRRREEEQGEEEH
GERGEKARRYHKVRAQVREESVIVIPASHPATIVASEGESLAVVCFVFGANHDEKVF LAG
RNSPLRQLDDPAKKL VFGGSAAREADRVLAAQPEQILLRGP HGRGSVSDM

>COMPARE218 glutelin, partial [*Oryza sativa*]

GLLLPHYTNGASLVYIIQGR

>BAB71741.1 glyoxalase [*Oryza sativa*]

MASGSEAEKSPEVVLEWPKKDKKRVLHAVYRVGDLDRTIKCYTECFGMKLLRKRDPPEEK
YTNAFLGFGPEDTNFALELTNYNGVDKYDIGAGFGHFAIATEDVYKLAEKIKSSCCCKIT
REPGPVKGGSTVIAFAQDPDGYMFELIQRGPTPEPLCQVMLRVGDLDRSIK FYEKALGMK
LLRKKDVPDYKYTIAMLYADEDKTTVIELTYNYGVTEYTKGNAYAQVAIGTEDVYKSAE
AVELVTKELGGKILRQPGPLPGLNTKIASFLDPDGWKVVLVDNADFLKELQ

>Q948T6.2 lactoylglutathione lyase [*Oryza sativa*]

MASGSEAEKSPEVVLEWPKKDKKRLHAVYRVGDLDRTIKCYTECFGMKLLRKRDPPEEK
YTNAFLGFGPEDTNFALELTNYNGVDKYDIGAGFGHFAIATEDVYKLAEKIKSSCCCKIT
REPGPVKGGSTVIAFAQDPDGYMFELIQRGPTPEPLCQVMLRVGDLDRSIK FYEKALGMK
LLRKKDVPDYKYTIAMLYADEDKTTVIELTYNYGVTEYTKGNAYAQVAIGTEDVYKSAE
AVELVTKELGGKILRQPGPLPGLNTKIASFLDPDGWKVVLVDNADFLKELQ

>BAG92398.1 lipid transfer protein [*Oryza sativa*]

MARAQLVLVAVVAALLAAPHAAVAITCGQVNSAVGPCLTYARGGGAGPSAACCVRSRSL
KSAARTTADRRTACNCLKNAARGIKGLNAGNAASIPSKCGVSVPYTISASIDCSRVR

>BAG93005.1 Ole e 1-like [*Oryza sativa*]

MARPRFATTAPLLALAVLAAVSVAVATAPAGKDPGGFVVTGRVYCDPCRAGFETNVSKS
IPGATVSVECRHYGAGRESLKA EATTDEKGWYKVEIDQDHQEEICEVVLDKSSDPACSET
EKTRDRSRVPLTSNGLKQNGIRYANPIAFFRKEPLADCGSILQKYDLKDAPETP

>BAG93129.1 polygalacturonase [*Oryza sativa*]

MGFVRALFLAMVCVAHAHAKDYPKEEAKAEGPAAASGGGGGSTHDVVKLGKGDGKTDS
TKAVNEAWTAACAGTGKQTIIVVPKGDFLTGPLNFTGPCKGDIVIQLDGNLLGSTDALFK
SNWIEIMRLESLEISGKGKLDGQGA AVWSKNSCAKKYDCKILPNTLVLD FVNNGLISGIS
LVNPKFFHMNVFKSKNITIKDVTITAPGDS PNTDGIHMGDSSKISIIDTVIGTGDDCISI
GPGTEGVNISGVTCPGPHGISVGLGRYKDEKDVTDVTVKNCVLLKSTNGVRIKSYEDAA
SVL TASKFTYENIKMEDVANPIIIDMKYCPNKICTANGNSKVTIKDITFKNITGTSSTPE
AVSLLCSDKLPCTGVTLNDIKVEYSGTNNKTMVACKNAKGTATGCLKELSCF

>BAG94438.1 Ory s 12; profilin [*Oryza sativa*]

MSWQTYVDEHLMCEIEGHHLTSA AIVGHDGTVAQSAAFPQFKPEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPEGAVIRGKKGSGGITVKKTGQALVVG IYDEPMPGQCNM VVE
RLGDYLVEQGL

>BAG86826.1 unknown function [*Oryza sativa*]

MKMKALLPVAAMLLLVSGQLAAPVTADGYVGLAVFWGRHKEEGSLREACDTGRYNIIVVI
TFYNVFGYQRGRYGLDFSGHPVA AVGADIKHCQSKGVQVLLSIGGQGG EYSLPSSQSASD
VADNLWNAYLGGRRAGVPRPFGDAVVDGIDFFIDQGGADHYEQ LARQLHGRGVLLTATVR
CAYPDSRME AALATGVFARIHVRIFGDDQCTMFPKDAWEK WAAA YPRCTVFLTVVASPEQ

DEGYMFQKDLYYGVQQFIDKEPNYGGIAIWDRIYDKKANYSGEG
>BAG88472.1 unknown function [Oryza sativa]
MASSFSFLLVAALLGLASWKAIASDPSPLQDFCVADLNSPVRVNGFVCKNPMNASADDF
FKAAMLDKPRDNTNKKVGSNVTLVNVLQLPGLNLTGISIARLDFAPLGLNPPHPTHPRATEI
FTVLEGLTYVGFVTSNPDNRLLSKVLNKGDFVVFPEGLIHFQFNPNPHKPAVAIAALSSQ
NPGVITIANAVFGSNPPISDDILMKAFQVDKKIIDLLQAQF
>BAG93480.1 unknown function [Oryza sativa]
MPPDVEVIRHEHIDHPSSTRDRSVVSSNSLSNTVSAYTDMKNTSSLCLLLLVVLCSLTC
NSGQAQVLFQGFNWESWKQGGWYNMLKGQVDDIAKAGVTHVWLPSPSHSVAPQGYMPGR
LYDL DASKYGTAAELKSLIAAFHGKGVQCVADVINHRCAEKKDARGVYCVFEGGTPDDR
LDWGPGMICSDDTQYSDGTGHRDTGEGFGAAPDIDHLNPRVQRELTDWLNWLKSDVGFDFG
WRLDFAKGYSTDIKMYVESCKPGFVVAEIWNSLSYNGDGKPAANQDQGRQELVNWVNAV
GGPAMTFDFTTKGLLQAGVQGELWRLRDGNGKAAGMIGWLPEKAVTFVDNHDTGSTQKLLW
PFPSDKVMQGYAYILTHPGVPCIFYDHMFdwNLKQEITALAAIRERNGINAGSKLRIVVA
DADAYVAVVDEKVMVKIGTRYDVGNVPSDFHQTVHGKDYSVWEKGLRVPAGRHL
>BAG95020.1 unknown function [Oryza sativa]
MEQYEKVEKIGEGTYGVVYKGRHRTNETIALKKIRLEQEDEGVPSTAIRESLLKEMQH
RNIVRLQDVVHKEKCIYLVFEYLDLCLKHMDSSPDFKNHRIVKSFLYQILRGIAYCHSH
RVLHRDLKPNLLIDRRNTSLKLADFLARAFGIPVRTFTHEVVTWYRAPEILLGARHY
STPVDMMWSVGCIFAEMVNQKPLFPGDSEIDELFKIFSIMGTPNEETWPGVASLPDYISTF
PKWPSVDLATVVPTLDSSGLDLLSKMLRLDPSKRINARAAL EHEYFKDLEVA
>BAH01262.1 unknown function [Oryza sativa]
MKIIFFFALLAIAACSASAQFDAVTQVYRQYQLQPHMLQQQMLSPCGEFVRQQCSTVAT
PFFQSPVFQLRNCQVMQQCCQLRMIAQQSHCQAISVQAIVQQLRLQQFASVYFDQSQ
AQAQAMLALNMPASICGIYPSYNTAPCSIPTVGGIYW
>BAA01998.1 unknown function [Oryza sativa]
MASNKVVSALLLIIVSVLAATTRMADHKKDQVVYSLGERCQPGMGYPMYSLPRCRAVVK
RQCVRTRSPGAVDEQLAQDCCRELAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAEV
FPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH
>BAA01996.1 unknown function [Oryza sativa]
MASNKVVSVLLLLAVSVLAATATMAEYHQDQVVYTRARCQPGMGYPMYSLPRCRALVK
RQCRGSAAAQVRRDCCRQLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEVFRG
CRRGDLERAAASLPAFCNVDIPNGGGGVCYWLARSGY
>BAA07772.1 unknown function [Oryza sativa]
RHEVKRQCVATTHPAAPGTEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVG
HPMAEVFPGCRRGDLERRRSLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH
>BAA07773.1 unknown function [Oryza sativa]
RVVKRQCVATRRTGGADEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHM
MAEVFPGCRRGDLERARATLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH
>BAA07774.1 unknown function [Oryza sativa]
FGTRFRQRQCVGPRRTRRRWTQQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATD
VGHMMAEVFPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH
>BAA07710.1 unknown function [Oryza sativa]
MASNKVVSALLLIIVSVLAATGPMADHKKDQVVYSLGERCQPGMGYPMYSLPRCRAVVK
RQCVRATAHPAARGNEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAE
VFPGCRRGDLERAAASLPAFCNVDIPNGTGGVCYWLGYPRTPRTGH
>BAA07711.1 unknown function [Oryza sativa]
GTRLLLIIVSVLAATRRMADHKKDQVVYSLGERCQPGMGYPMYSLPRCRAVVKRQCVRHG
APGGAVDEQLRQDCCRQLAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAEVFPGCRR
GDLERAAASLPAFCNVDIPNGTGGVCYWLGYTPRTPTGH

>BAA07712.1 unknown function [*Oryza sativa*]
MASNKVVIPALLVVVSVLAATTTMADHHQEQQVYTPGQLCQPGIGYPTYPLPRCRAFK
RQCVPAGTLDEQVRRGCCRLAGIDSSWCRCDALNHMLRIIYREERAADAGHPMAEVFRG
CRRGDIERAAASLPAFCNVDIPNGVGGVVCYWLPGTGY

>BAA07713.1 unknown function [*Oryza sativa*]
MASNKVVFVSVLLAVVSVLAATATMAEYHHQDQVYTPAPLCQPGMGYPMYPLPRCRAFK
KRQCVGRGTAATAEQVRRDCCRLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEV
FRGCRRGDLERAAASLPAFCNVDIPNGGGGVVCYWLARSGY

>AAB99797.1 unknown function [*Oryza sativa*]
MASNKVVFVSVLLAVVSVLAATATMAEYHHQDQVYTPGPLCQPGMGYPMYPLRVAGVGE
APLLGRARPRRRVAVPGDCCRFPPVDYSWCRCEAISHMLGGIYRELGAPDVGHMSEVFR
GCRRGTWSARRRAPGVLQVDIPNGGGGVVCYWLARSGY

>BAC19997.1 unknown function [*Oryza sativa*]
MASNKVVFVSVLLAVVSVLAATATMAEYHHQDQVYTPGPLCQPGMGYPMYPLPRCRAFK
KRQCVGRGTAATAEQVRRDCCRLAAVDDSWCRCEAISHMLGGIYRELGAPDVGHMSEV
FRGCRRGDLERAAASLPAFCNVDIPNGGGGVVCYWLARSGY

>BAC20650.1 unknown function [*Oryza sativa*]
MAFIKVVFSVLLPVVVSMLVATTTMADHRGQVYTPGQLCAAGRGYPMYPLPRCRAFK
QCAGGAVDEQVRQDCCRLAAIDDSFCRCPALSHMLVGMKELGAPAKGQPMDEVFPGCR
RGDMKRVAASLPAFCNVDIPIGIGGVVCYWLSYPMNPATGH

>BAC20657.1 unknown function [*Oryza sativa*]
MASNKVVISALLVVVSVLAATTTMADHHQEQQVYTPGQLCQPGIGYPTYPLPRCRAFK
RQCVPAGTVDEQVRRGCCRLAAIDSSWCRCDALNHMLRIIYRESGAADAGHPMAEVFRG
CRRGDIERAAASLPAFCNVDIPNGVGGVVCYWLPGTGY

>Q01883.2 unknown function [*Oryza sativa*]
MASNKVVFVSVLLLVLSVLAAMATMADHHQVYSPGEQCRPGISYPTYSLPQCRTLVRQ
CVGRGAASAADQVWQDCCRLAAVDDGWCRCGALDHMLSGIYRELGATEAGHPMAEVFP
GCRRGDLERAAASLPAFCNVDIPNGPGGVVCYWLGPRTPTRGH

>Q01882.2 unknown function [*Oryza sativa*]
MASNKVVFVSVLLIIVSVLAATATMADHHKQVYVSLGERCQPGMGYPMYSLPRCRAVK
RQCVGHGAPGGAVDEQLRQDCCRLAAVDDSWCRCSALNHMVGGIYRELGATDVGHMMAE
VFPGCRRGDLERAAASLPAFCNVDIPNGTGGVVCYWLGPRTPTRGH

>ADK39021.1 Ost c 1; pathogenesis related protein, PR-10, Bet v 1-like [*Ostrya carpinifolia*]
MGVFNVEAETPSVIPAARLFKSYVLDGDKLIPKVAPQAISKVENVGGNGGPGTIKNITFA
EGSPFKFVKERVDEVDNANFKYNYTVIEGDVLGDKLEKVSHELKIVAAPGGGSILKISSK
FHAKGDHEVNAEEMKGAKEAELLRAVESYLLAHTAEYN

>ACA96507.1 Pac c 3; unknown function, antigen 5 [*Pachycondyla chinensis*]
TEGGAVHTMCQYTSPQSPNCGTYSNAHITAADKETILKVHNDERQVKAGQETRGNPGP
QPAASNMPDLTWDNELAAIAQRWVNQCKIGHDGCNRVERYQVQNIAMSGSTAKGPCNMN
NLVQMWINEVNALNAADVSSMPSDGNVFMKIGHYTLVWGTKTKVGCIIQFLDGKFYKC
YLACNYGPAGNMFAPYIYQ

>CBY17558.1 Pan b 1; tropomyosin [*Pandalus borealis* (*Pandalus eous*)]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVFLQKKLQQLENDLDSV
QEALLKANQHLEEKDALSNAEAGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKVLNRSLSDEERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEYKSITDELDTFSELSGY

>BAF47264.1 Pan b 1; tropomyosin [*Pandalus borealis* (*Pandalus eous*)]
MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVFLQKKLQQLENDLDSV

QEALLKANQHLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLEDELVNEKEYKSITDELQDTFSELSGY
>AAC38996.1 Pan s 1; tropomyosin [Panulirus stimpsoni]
MKLEKDNAMDRADTLEQQNKEANIRAEEKAEVHNLQKRMQQLENDLDQVQESLLKANTQ
LEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAADESERMVKV
ENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAEERAETGESKF
VELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAEFAERSVQKLQ
KEVDRLEDELVNEKEYKSITDELQDTFSELSGY
>BAF47265.1 tropomyosin [Paralithodes camtschaticus]
MDAIIKKKMQAMKLEKDNAMDKADTLEQQNKEANNRAEKAEVHGLQKRMQQLENDLDQV
QESLLKANTQLEDKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRLEDELVNEKEYKSITDELQDTFSELSGY
>BAF47266.1 tropomyosin [Paralithodes camtschaticus]
MDAIIKKKMQAMKLEKDNAMDKADTLEQQNKEANNRAEKTEEEIRLTQKKMQQVENELDVA
QEQLSLANTKLEEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRLEDELVNEKEYKNIADMDQAFSELSGF
>CAP05019.1 Par j 4; calcium-binding protein, polcalcin [Parietaria judaica]
MADKQIDRAEQERIFKRFDNSGDGKISSSELGEALKALGSVTAEVHRMMAEIDTDGDGA
ISLEEFSSFADANRGLIKDIAKIF
>CAA59370.1 Par j 1; lipid transfer protein [Parietaria judaica]
MRTVSARSSVALVIVA AVLWVTSSASVAPAPAGSEETCGTVVVGALMPCLPFVQGEKE
PSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGKLVSEVPKHCGIVDSKLPP
IDVNMDCCTLGVLHYKGN
>2008179A Par j 1; lipid transfer protein [Parietaria judaica]
MVRALMPCLPFVQGEKEPSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK
LVSEVPKHCGIVDSKLPPIDVNMDCCTVGVVPRQPQLPVSLRHGPVTGSPSRPPTKHGW
RDRPLEFRPPHRKKNPAFSTLG
>CAA54587.1 Par j 1; lipid transfer protein [Parietaria judaica]
MVRALMPCLPFVQGEKEPSKGCCSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK
LVSEVPKHCGIVDSKLPPIDVNMDCCTVGVVPRQPQLPVSLRHGPVTGSPDPAHKARLER
PQIRVPPPAPEKA
>CAA65122.1 Par j 2; lipid transfer protein [Parietaria judaica]
MRTVSMAALVIAAALAWTSSAELASAPAPGEGPCGKVVHHIMPCLKFVKGEEKEPSKSC
CSGTKKLSEEVKTTEQKREACKCIVAATKGISGIKNELVAEVPKCGITTTLPPITADFD
CSKIESTIFRGYY
>CAA65123.1 Par j 1; lipid transfer protein [Parietaria judaica]
MRTVSAPSAVALVIVAAGLAWTSLASVAPPAPAGSEETCGTVVRALMPCLPFVQGEKE
EPSKGCCSGAKRLDGETKTGLQRVHACECIQTAMKTYSDIDGKLVSEVPKHCGIVDSKLP
PIDVNMDCCTLGVVPRQPQLPVSLRHGPVTGSPDPAHKARLERPQIRVPPPAPEKA
>P55958.1 Par j 2; lipid transfer protein [Parietaria judaica]
MRTVSMAALVIAAALAWTSSAEPAPAPAGGEEACGKVVQDIMPCLHFVKGEEKEPSKEC
CSGTKKLSEEVKTTEQKREACKCIVRATKGISGIKNELVAEVPKCDIKTTLPPITADFD
CSKIQSTIFRGYY
>CAI94601.1 Par j 1; lipid transfer protein [Parietaria judaica]

QETCGTMVRALMPCLPFVQGEKEPSKGCSSGAKRLDGETKTGPQRVHACECIQTAMKTY
SDIDGKLVSEVPKHCIGIVDSKLPIDVNMDCCKTLGVVPRQPQLPVSLRHGPVTGPSDBPAH
KARLERPQIRVPPPAPEKA
>COMPARE137 Par j 1; lipid transfer protein [Parietaria judaica]
MVRALMPCLPFVQGEKEPSKGCSSGAKRLDGETKTGPQRVHACECIQTAMKTYSDIDGK
LVSEVPKHCIGIVDSKLPIDVNMDCCKTLGVVPRQPQLPVSLRHGPVTGPSRSRPPTKHGW
RDPRLFRPPHRKKPNPAFSTLG
>Q9T0M8.1 Par j 3; profilin [Parietaria judaica]
MSWQAYVDDHLMCDVGDGNTLASAAIIGHDGSVWAQSANFPQLKPEEVTGIMNDFNEGGF
LAPTGLFLGGTKYMIQGESGAVIGKKGSGGATLKKTGQAIVIGIYDEPMTPGQCNLVE
RLGDYLLEQGM
>Q9XG85.1 Par j 3; profilin [Parietaria judaica]
MSWQAYVDDHLMCDVGDGNTPASAAIIGHDGSVWAQSANFPQLKPEEVTGIMNDFNEAGF
LAPTGLFLGGTKYMIQGESGAVIRGKKGSGGATLKKTGQAIVIGIYDEPMTPGQCNLVV
ERLGDYLLEQGL
>CCP19647.1 Par j 3; profilin [Parietaria judaica]
MSWQTYVDDHLMCEIEGNHLTAAAILGQDGSVWAQSASFQPKPEEIAAIVKDFEETPGTL
APTGLFLGGAKYMIQGEAGVVIRGKKGSGGVTVKKTGQALVIGIYDEPMAPGQCNMIVE
RLGDYLIETGL
>AAB46819.1 Par o 1; lipid transfer protein [Parietaria officinalis]
ATGKVVQDIMPPLLFVQGEKEPSS
>AAB46820.1 Par o 1; lipid transfer protein [Parietaria officinalis]
GPXGKVVHIIMPPLKFVKGESESE
>Q7M1E8 Par o 1; lipid transfer protein [Parietaria officinalis]
ATGKVVQGAMPP
>AAB36008.1 unknown function, partial [Parietaria officinalis]
APAGGVVPIIMPXXFF
>AAB36009.1 unknown function, partial [Parietaria officinalis]
APAGGVVVAAMPPPL
>AAB36010.1 unknown function, partial [Parietaria officinalis]
GPVGGVVHAHMPLL
>AAB36011.1 unknown function, partial [Parietaria officinalis]
EEXGGVVGALMPPLL
>AAB36012.1 unknown function, partial [Parietaria officinalis]
GTTGTVVGALMPPLFVQGEKEEXPPSXXKG
>AKF12278.1 Par h 1; defensin [Parthenium hysterophorus]
MAKSSTSylvfllllvvaaiseiasvngkvcekskpwfgnckdtekcdkrcmevegakh
GACHQRESKYMCFYFDCDPKKNPpppgapgtppappggggedappgggapppagg
EGGGGGEGGGGAPPAGGEGGGGGGGDGGGGAPPAA
>ACA23876.1 Pas n 1; beta-expansin [Paspalum notatum]
MGLAKIVAVAAVLAALVAGGSCGPPKVPppgnittnyngkwlpakatwygqpngagpdd
NGGACGIKVNLPpyngftacgnppifkdgkcgscyeircnkpecsqpvtfvitdmny
EPIAPYHFDLSGKAFGAMAKPGLNDKLRHYGIFDLEFRRVRCKYQGGQKIVFHVEKGSNP
NYLAMLVKFVADDGDIVLMELKEKSSDWKPMKLSWGAIWRMDTPKALVPPFSIRLTSESG
KKVIAQDVIPVNWKPDTVYNSNVQF
>CBM42660.1 polygalacturonase [Paspalum notatum]
MAWRKEEGAMTMLRALLVVALAVCGAHAAGDKKKAEESSKKGDSAAAAASGPGGSFDITK
LGASGDGKTSTKALEEAWASACGGKQKQITILIPKGDYLTGALNFTGPCTGDVTFQLDGN
LLASTDLSQFKANWIEILRVDNLVITGKGLDGOGSVWVSKNSCAKKYDCKILPNSLVLD
FCNKAEVSGISIIINSKFFHMMNVFQCKDVKIKDVTVSAPGDSPTDGIHMGDSSGVSIIIDT

TIGVGDDCISIGPGSTKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSSN
GLRIKAYEDAKSVLTCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTF
KDITGTSSTPEAVSLLCSDSTPCSGITMNNVKEY

>CBM42661.1 polygalacturonase [Paspalum notatum]

MAWGAMTMLRALLVVALAVCGAHAAGDKKKAEEESKKGDSAAAAASGPGGSFDITKLGAS
GDGKTDSTKALEEAWASACGGKQKQILIPKGDYLTGALNFTGPCTGDVTFQLDGNLLAS
TDLSQFKANWIEILRVDNLVITGKGLDGOQSAVWSKNNSCAKKYDCKILPNSLVLDFCNK
AEVSGISIIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIIDTTIGV
GDDCISIGPGSTKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSSNGLRI
KAYEDAKSVLTCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKDIT
GTSSTPEAVSLLCSDSTPCSGITMNNVKEY

>CBM42662.1 polygalacturonase [Paspalum notatum]

MAWRKEEGAMTMLRALLVVALAVCGAHAGAKKAEESKKGDSAAAAASGPGGSFDITKLG
ASGDGKTDSTKALEEAWASACGGKQKQILIPKGDYLTGALNFTGPCTGDVTFQLDGNLL
ASTDLSQFKANWIEILRVDNLVITGKGLDGOQAVWSKNNSCAKKYDCKILPNSLVLDFC
NKAEVSGISIIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIIDTTI
GVGDDCISIGPGSTKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSTNGL
RIKAYEDAKSVLTCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKD
ITGTSSTPEAVSLLCSDSTPCSGITMNNVKEY

>CBM42663.1 polygalacturonase [Paspalum notatum]

MAWRKEEGAMTMLRALLVVALAVCGAHAGAKKAEESKKGDSAAAAASGPGGSFDITKLG
ASGDGKTDSTKALEEAWASACGGKQKQILIPKGDYLTGALNFTGPCTGDVTFQLDGNLL
ASTDLSQFKANWIEILRVDNLVITGKGLDGOQAVWSKNNSCAKKYDCKILPNSLVLDFC
NKAEVSGISIIINSKFFHMNVFQCKDVVVKDVTVSAPGDSPTDGIHMGDSSGVSIIIDTTI
GVGDDCISIGPGSTKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSTNGL
RIKAYEDAKSVLTCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKD
ITGTSSTPEAVSLLCSDSTPCSGITMNNVKEY

>CBM42664.1 polygalacturonase [Paspalum notatum]

ITGINITGVTCGPGHGISVGLGRYKDEKDVTDINVKGCTLKKTSNGVRIKSYEDAASVL
SASNLHYENIAMEDVANPIIIDMKYCPNKICTKNGASKVTIKDVTFKNITGTSSTPEAVS
LLCSEKLPCTGVTLDNVKEYKGTNNKTMAVCNNAKGSSTGCLKELACL

>CBM42665.1 polygalacturonase [Paspalum notatum]

STGINITGVTCGPGHGISVGLGRYKDEKDVTDINVKGCTLKKTSNGVRIKSYEDAASVL
SASNLHYENIAMEDVANPIIIDMKYCPNKICTKNGASKVTIKDVTFKNITGTSSTPEAVS
LLCSEKLPCTGVTLDNVKEYKGTNNKTMAVCNNAKGSSTGCLKELACL

>CBM42666.1 polygalacturonase [Paspalum notatum]

STKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSTNGLRIKAYEDAKSVL
TCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKDITGTSSTPEAVS
LLCSDSTPCSGITMNNVKEYSGSNKTMAVCKNAKGSATGGLKELACF

>CBM42667.1 polygalacturonase [Paspalum notatum]

STKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKSSNGLRIKAYEDAKSVL
TCSNHYENVKMEDAGYPIIIDMKYCPNKICSASAGSKVTVKDVTFKDITGTSSTPEAVS
LLCSDSTPCSGITMNNVKEYSGSNKTMAVCKNAKGSATGGLKELACF

>AAZ76743.1 tropomyosin [Penaeus aztecus]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKVLENRSLDEERMDALENQLKEARFLAEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEYKSITDELDTFSELSGY

>AAV83993.1 arginine kinase [Penaeus chinensis]

MADAAVIEKLEAGFKKLEAATDCKSLKKYLTKAVFDQLKDKKTSLGATLLDVIQSGVEN
LDSGVGIYAPDAEAYTLFAPLFDPIIEDYHVGFQTKHPNKDFGDVTSFVNVDPGKYV
ISTRVRCGRSMGYFPNCLTEDQYKEMESKVSSTLSSLEGELKGTYYPLTGMGKEVQQK
LIDDHFLFKEGDRFLQAANACRYWPSGRGIYHNDNKTFLVWVNEEDHLRIISMQMGDLG
QVFRRLTSAVNEIEKRIPFSHHDRLGFLTFPCPTNLGTTVRASVHIKLPKLAANRDKLEEV
AGKYNLQVRGTRGEHTEAEGGIYDISNKRMMGLTEFQAVKEMQDGILELIKMEKEM
>AGF86397.1 Mel 1 1; tropomyosin [Penaeus latisulcatus]
MDAIIKKMQAMKLEKDNAMDRADTLEQQNKEANIRAEKAEDDVNKLQKKLQQLLENDFDQV
QEALLLANTNAVEKDKALSNAEGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA
DESERMKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE
FAERSVQKLQKEVDRLDELELVNEKEYKSITDELDTFSELSGY
>AEM89226.1 enolase, partial [Penaeus merguensis (Fenneropenaeus merguensis)]
FTEAMRMGSEVYHHLKAVIKGRFGLDATAVGDGEGFAPNILNNDKDALTLIQESIEKAGYT
GKIEIGMDVAASEFYKGENIYDLDFKTANNDGSQKITGDQLRDMYMEFCNEFPVSI
>AGT20779.1 hemocyanin, arylphorin [Penaeus merguensis (Fenneropenaeus
merguensis)]
MRVLVVLGLIAAAAFQVVSADVQKQKDVLYLLHRIYGDIIQDADLLATANSFDPAGGSYSD
GGAAVQRLKGLNDGRLLEQKHWFSLFNTRHRNEALLLFDVLIHSSDWATFVGNAAFRRQ
KINEGEFVYALYVAVIHSPLTEDVWLPPLYEITPHLFTNSEVIEAAYRAKQKQTPGKFES
TFTGTTKKNPEQRVAYFGEDIGLNTHHVTWHMEFPFWWDEYGHHLDRKGENFFWVHHQLT
VRFDAERLSNYLDPVGEHLHWYKPIVDGFAPHTTYKYGGQFPARPDNVKFEDVDDVARIRD
MVIVESRIRDIAHGYIIDSHGKQIDISNEKGIDILGDVIESSLYSPNVQYYGALHNTAH
IVLGRQGDPHGKFDLPPGVLEHFETATRDPSFFRLHKYMDNIFKEHKDSLPPYTKADLEF
SGVSISEVNVVGELETYFEDFEYNLINAVDDAEGIPDVIDISTYVPRLNHKEFTFKIDIEN
GGSPRLATVRIFAWPHKDNNGIEFTFDEGRWNAIELDKFWVSLAGGKNSIERKSTESSVT
VPDVPISIDTLFAKTAAGGDGLSEFASATGLPNRFLLPKGNDKGLEFDLVVAVTDGDADAA
VPDLHLNTKYNHYGANGVYPDKRPHGYPLDRRVPDERVFEELPNFKHIQVKVFNHGEHIH
S
>AA015713.1 Pen m 2; arginine kinase [Penaeus monodon]
MADAAVIEKLEAGFKKLEAATDCKSLKKYLSKAVFDQLKEKTSLGATLLDVIQSGVEN
LDSGVGIYAPDAEAYTLFSPLFDPIIEDYHVGFQTKHPNKDFGDVNTFVNVDPGKYV
ISTRVRCGRSMGYFPNCLTEAQYKEMEAKVSSTLSSLEGELKGTYYPLTGMGKEVQQK
LIDDHFLFKEGDRFLQAANACRYWPAGRGIYHNDNKTFLVWVNEEDHLRIISMQMGDLG
QVFRRLTSAVNEIEKRIPFSHHDRLGFLTFPCPTNLGTTARASVHIKLPKLAANREKLEEV
AGKYNLQVRGTRGEHTEAEGGIYDISNKRMMGLTEFQAVKEMQDGILELIKMEKEM
>C7E3T4.1 Pen m 2; arginine kinase [Penaeus monodon]
MADAAVIEKLEAGFKKLEAATDCKSLKKYLSKAVFDQLKEKTSLGATLLDVIQSGVEN
LDSGVGIYAPDAEAYTLFSPLFDPIIEDYHVGFQTKHPNKDFGDVNTFVNVDPGKYV
ISTRVRCGRSMGYFPNCLTEAQYKEMEAKVSSTLSSLEGELKGTYYPLTGMGKEVQQK
LIDDHFLFKEGDRFLQAANACRYWPAGRGIYHNDNKTFLVWVNEEDHLRIISMQMGDLG
QVFRRLTSAVNEIEKRIPFSHHDRLGFLTFPCPTNLGTTVRASVHIKLPKLAANREKLEEV
AGKYNLQVRGTRGEHTEAEGGIYDISNKRMMGLTEFQAVKEMQDGILELIKMEKEM
>ADV17343.1 Pen m 4; calcium-binding protein, sarcoplasmic calcium-binding protein
[Penaeus monodon]
MAYSWDNRVKYVVRYMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN
LWNEIAELADFNKDG EVT VDFEKQAVQKHCQGGKYGDFPGAFKVFIANQFKAIDVNGDGK
VGLDEYRLDCITRSFAFAEVKEIDDAYNKLTTEDDRKAGGLTLERYQDLYAQFISNPDESC
SACYLFGPLKVVQ
>BAL72725.1 Pen m 4; calcium-binding protein, sarcoplasmic calcium-binding protein

[*Penaeus monodon*]

MAYSWDNRVKYVVRYMYDIDNNGFLDKNDFECLAVRNTLIEGRGEFSADAYANNQKIMRN
LWNEIAELADFNKDG EVT VDFEKQAVQKHCQGGKKG YGFPGAFKVF IANQFKAIDVNGDGK
VGLDEYRLDCITRSAFEVKEIDEAYNKLTTEDDRKAGGLTLERYQDL YAQFISNPEESC
SACYLFGPLKVVQ

>COMPARE188 enolase, partial [*Penaeus monodon*]

AGAAELGIPLYR

>COMPARE189 enolase, partial [*Penaeus monodon*]

AAVPSGASTGVHEALEMR

>ADV17342.1 Pen m 3; myosin light chain [*Penaeus monodon*]

MSRKSGSRSSSKRSKSGGGSNVFDMFTQRQVAEFKEGFQLMDRDKDGVIGKTDLRGTFD
EIGRIATDQELDEMLADAPAPINF TMLLNMF AERQTGESDDDDV VAKAFLAFADEGGNID
CDTFRHALMTWGDKFSSQEADDALDQMDIDDAGKIDVQSVIQMLTAGGGDDAAAEAA

>AAX37288.1 Pen m 1; tropomyosin [*Penaeus monodon*]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLENDLDQV
QESLLKANIQLVEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEYKSITDELQDTFSELSGY

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

YNLQVRGTRGEHTEAEGGIYDISNKRMRGLTEFQAVKEMQDGIILELIKMEKEM

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

YNLQARGTRGEHTEAEGGIYDISNKRMRGLTEFQAVKEMLDGIILELIKMEKEM

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

MSTAE LAVSYAALILADDGIEVSADKIQTILGAAKVQVEPIWATIFAKALEGKDIKEIL
TNVGSAGPATAGAPAAAGAAAPAEKKEEKEEKEEEDMGMGFLFD

>ADK27483.1 Pen ch 35; aldolase [*Penicillium chrysogenum*]

MSSSLEQLKASGTTVVCDSDGFATIGKYKPDATTNPSLILAASKKPEYAAALIDTAVAYG
KQNGKTLDEQVEATLDRLLVEFGKEILKIIPGKVSTEVDKLSFDTQGSVNKALEIIKLY
ADNGISKDRVLIKIASTYEGIKAAHILQTHGINCNLTMFSLVQAIAAAEAGAYLISPF
VGRILDWYKAAHKRDYTPQEDPGVKSVDIYNYKKFGYNTIVMGASFRNVGEITELAGC
DYLTISPNNLEDLFNSTDAVPQKLNPAAGAASLEIKKREYLNNEADFRDFNNEAMGVEKL
REGISKFAADA VTLKQLLAQKIQA

>AAF23726.1 Pen ch 13; alkaline serine protease [*Penicillium chrysogenum*]

MGFLKVLATSLATLAVVDAGTLLTASNTDAVIPSSYIVVMNDDVSTAEFSTHREWATNVH
ARLSRRKNGETGPGKHFEINGLKGYTASFDENTAKDIANDPAVKYIEPDMIVNATANVVQ
SNVPSWGLARISSKRTGTTSYTYDSTAGEGVVFGVDTGIDISHSDFGGRAKWGTNVVDN
DNTDGNHGHTHTASTAAGSKYGVAKKATLVAVKVLGADGSGTNSGVISGMDWAVKDAKSR
GANGKYVMNTSLGGFEFSKAVNDAAAANVVKSGIFLSVAAGNEAENASNSPPASAAEACTIA
ASTSTDGSASF T NFGSVVDLYAPGQSITAAYPGGGSKT LSGTSM AAPHVAGVAAYLMALE
GVSAGNACARIVQLATSSISRAPSGTTSKLLYNGINV

>AAG44693.2 Pen ch 18; serine protease [*Penicillium chrysogenum*]

MKGFLSLTLLPLLVAASPVAVNSIHNDAAPI LSSMTSKDIPDSYIVVFKKHVDPSSASAH
QSWLQEVHTAHTGRMELKKRSLFGFDFAFMGLKHTFH IAGSLLGYAGHFHEDVIEQIRR
HPDVDYIEKDSEVRTMSEGSVEKNAPWGLARISHRESLSFGNFNKYLYAEEGGEGVDAYV
IDTGANVKHVDFEGRANWGKTIPQGDADDEGNGHGTHCSGTIAGKKFGVAKKANVYAVKV
LRNSGSGTMSDVVKGVEWAAEAHIKKSKKGDKKFKGVSANMSLGGGSSRTL DLAVNAAVD
AGIHFAVAAGNDNADACNYSPAAA EKAITVGASTLADERAYFSNYGKCTDIFAPGLNILS
TWVGS DHATNTISGTS MASPHIAGLLAYYVSLAPAKDSAYAVADVTPKQLKAALISVATE
GTLTDIPSDTPNLLAWNGGGSANYTKILADGGYKAHNAETTVEDRIGGIIDSAEKAFHKE

LGAIYSEIKDAVSA

>AAM33821.1 Pen ch 13; alkaline serine protease [Penicillium chrysogenum]

MGFLKLLSTSLATLAVVNAGKLLTANDGDEVVPSYIVVMNDGVSTAQFETHRNWAANVH
ARTRSLKGGESGPGKHFDFINGMKGYSASFDDRTVKDIASDPTVKYVEPDMVFNATANVVQ
RNAPSWGLSRISKKSGATDYVYDSTAGEGIVYGVDTGIDIGHADFGGRAEWGTNTADN
DDTDGNGHGTHTASTAAGSKFGVAKKASVVAVKVLGADGSGTNSQVIAGMDWAVKDSKSR
GATGKSVNMMSLGGAYSRAMNDAANVVRSGVFLSVAAGNEAQDASNSSPASAPNVCTIA
ASTNSDGSASFNTFGSVVDLYAPGKDITAAYPPGGGSKTLSGTSMAPHVAGAAAYLMALE
GVTSDKACARIVELAISSISSAPSGTTSKLLYNGINAQ

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

GPYKTWQRIYDYDFLTNLTSSSEANDIIGAEAPLWSEQVDDVTVSSVFWPRAAALGELVWS
GNRDAAGRKRRTTSFTQRILNFREYLVANGVMAAALVPKYCLQHPHACDLYKNQTVMS

>AAF71379.1 Pen ch 18; serine protease [Penicillium chrysogenum]

MKGFLSLTLLPLLVAASPVAVNSIHNDAAPISSMTSKDIPDSYIVVFKKHVDPSSASAH
QSWLQEVHTAHTGRMELKKRSLFGDFEAFMGLKHTFHIAGSLLGYAGHFHEDVIEQIRR
HPDVDYIEKDSEVRTMSEGSVEKNAPWGLARISHRESLSFGNFKYLYAEEGGEGVDAYV
IDTGANVKHVDFEGRAWGKTIPQGDADDEGNGHGTSCSGTIAGKKFGVAKKANVYAVKV
LRSNGSGTMSDVVKGVEWAAEAHIKKSKKGDKKFKGSVANMSLGGGSSRTLDELAVNAVD
AGIHFAVAAGNDNADACNYSPAAAEKAITVGASTLADERAYFSNYGKCTDIFAPGLNILS
TWVGS DHATNTISGTSMASPHIAGLLAYYVSLAPAKDSAYAVADVTPKQLKAALISVATE
GTLTDIPSDTPNLLAWNGGGSANYTKILADGGYKAHNAETTVEDRIGIIDS AEKAFHKE
LGAIYSEIKDAVSV

>ABB89950.1 Pen c 30; catalase [Penicillium citrinum]

MHLAFATDLVGIANAACP YMTGEVPGDYSPHELHRRAD EGAADNTEEFLSQFYLN DKDA
YLTS DVGPIEDQNSLSAGERGPTLLED FIFRQKIQHFDHERVPERAVHARGAGAHGVFT
SYADWSNITAASF LSKKDKETPMFVRFSTVAGSRGSADTARDVHGFATRFYTDEGNFDIV
GNNIPVFFIQDAIQF PDLIHAVKPSGDNEIPQAATAHDSAWDFFSQQPSSLHTLLWAMAG
HGIPRSFRNVDGFGVHTFRFVTD S GSKLVKFHWKGLQGKASLVWEEAQQISGKNPDFLR
QDLWDAIEAGRFP EWELGVQIMDEEDQLRFGFDLLDPTKIVPEEIPVTKLGKMTLNRNP
RNYFAETE QVMFQPGHIVRGVDF TDDPLLQGR LFSYLD TQLNRHGGPNFEQLPINRPRTP
IHNNNRD GAGQMF IPLNKDAYSPNTLNNASPKQANQTTGKGFF TTPSRKNGK LQRTVSS
TFEDVWSQPRLFWNSLVEAEKQFVVDATRFENS NVVSDIVRNNV IQLNRISNDLAKRVA
EAIGIEAPKPDPSFYHDNTTAHIGAFGQKLLKLEGLKVGVLASVQNASSVSSAASLQSQL
KDAGVDVVVAERLGDGVNQTYSGSDAIQFD AVVVADGA EGLFSSRSFTEKPVKNKASSL
FPAGRPLDILVDAFRFGKPVGAIGKGAALRAAQISSDREGVYAAK SIGNEFVKGLKEGL
RIFKFLDRFALDA

>AAR17475.1 Pen c 24; elongation factor [Penicillium citrinum]

MGFTDFVSDAGLSLANNYLATRSYIVGHAPSQADVVTYKAF TASPDAEKYPHVARWYKHI
ASYESEFPTLP GDASKAFTAYGPEGSEASANPKDKPAEEEEEEEDLFASDSEDEDPAVVAE
RNKNLE EYK KKA AKGPKPAAKSLVTL EVKPWDETNLE ELEANVRAIEMDGLVWGASKF
VAVGFGIKKLQINLVVEDEK VSTDELQAQIEEDEDHVQSTDVAA MQKL

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

MPIAKVHARSVYVSRGNPTVEVDVVTETGLHRAIVPSGASTGQHEAVELRDGDKAKWGGK
GVLKAVKNVNETIGPALIKENIDVKDQAKVDEF LNKL DGTANKGNL GANAILGVSLAIK
AAAAEKGVPLYVHISDLAGTKKPYVLPVPFQNVNLNGGSHAGGR LAFQEFMIVPDTAESFS
EGLRQGA EYVQKLKALAKK KYQSAGNVGDEGGVAPDIQTAE EALDLITEAIEQAGYTGK
ISIAMDVASSEFYKTD AKKYDLDFKNPDS DPTKWLTYEQ LADLYKSLAAKYPIVSIEDPF
AEDDWEAWSYFYKTSDFQIVGDDLTVTNPLRIKKAIELKSCNALLLKV NQIGTLTESIQA
AKDSYADNWGMVSHRSGETEDVTIADIAVGLRSGQIKTGAPARSERLAKLNQILRIEE

LGENAIYAGKNFRTSVNL

>Q92260.1 Pen c 19; heat shock protein 70 [Penicillium citrinum]
AYLGGTVNNAVITVPAYFNDSQRQATKDAGLIAGLNLVRIINEPTAAAIAYGLDKKTEGE
RNVLIFDLGGGTFDVSLLTIEEGIFEVKSTAGDTHLGGEDFDNRLVNHVNEFKRKHKKD
LTTNARALRRLRTACERAKRTLSSAAQTSIEIDSLFEGIDFYTSITRARFEELCQDLFRG
TMPEVERVLRLDAKIDKSSVHEIVLVGGSTRIPKIQKLVSDFFNKDANKSINPDEAVAYGA
AVQAAILSGDTSSKSTNEILLLDVAPLSLGIETAGGVMTPLIKRNNTTIPTKKSETFSTYS
DNQPGVLIQVFEGERARTKDNLLGKFELTGIPPAPRGVPQIEVTFDL DANGIMNVSASE
KGTGKSNKITITNDKGRLSKEEIERMLAEAEKYKAEDEAEASRIQAKNGLESYAYS LKNT
ITEGKLQMSDDDKKIEDKISEIISWLDNMQTAEKDEYESQQKELEAIANPIMQAAYGAA
GGAPPQQRADGETEEKKDEEELD

>ABM60783.1 Pen c 32; pectate lyase [Penicillium citrinum]
VGDVATGYASENGGTTGGSGGTTTTVSSYAAFTEAVSGDDAKVVFVSGKISK TADQARVG
SNTSIIIGKDSNAILSGFGVLVKEASNVIIRNLGVEKVLADNGDAIGIQKSNVWVDHCDV
SSDRDHDKDYDGLIDITHAADYVTVSNTSIHDHWKACLIGHSDSNGDEDKGHLHVT LNN
NYWYNINSRGPSPFRFGTGHVYNSYLLDMSDGINTRQGAQHLVESNTFSGSKKPLYSTDDG
YAVANDNDFGDGENNAEKGLTSPYSYDLVSGSKVKDAVVG TAGQTLTF

>AAD42074.1 Pen c 3; peroxisomal protein [Penicillium citrinum]
MSLKAGDSFPEGVTFSYIPWAEDASEITSCGIPINYNASKEFANKKVVL FALPGAFTPVC
SANHVPEYIQKLP LRAKGV DQVAVLAYNDAYVMSAWGKANGVTGDDILFLSDPEAKFSK
SIGWADEEGRTYRYV LVIDNGKIIYAAKEAAKNSLELSRADHVLKQL

>AAD25926.1 serine protease [Penicillium citrinum]
MGFLKVLATSLATLAVVDAGTLLTASNTDAVIPSSYIVVMNDDVSTAEFNTHREWATNVH
ARLSRRKNGETGPGKHFEINGLKGYTASFDESTAKDIANDPAVKYIEPDMIVNATANVVQ
SNVPSWGLARISSKRTGTTSYTYDSTAGEGVVFGVDTGIDISHSDFGGRAKWGTNVVDN
DNTDGNHGHTHTASTAAGSKYGVAKKATLVAVKVLGADGSGTNSGVISGMDWAVKDAKSR
GANGKYVMNMSLGGFEFSKAVNDAAANVVKSGIFLSVAAGNEAENASNSSPASAAEVCTIA
ASTSTDGSASF TNGSVVDLYAPGQSITAAYPGGSKT LSGTSM AAPHVAGVAAYLMALE
GVSAGNACARIVQLATSSISRAPSGTTSKLLYNGINV

>AAD25995.1 serine protease [Penicillium citrinum]
MKGFLGLALLPLLTAASPVSVESIHNGAAPIISSMNSQEIPDSYIVVFKKHVDTSAAAAH
HSWVDIHSAVNGRMELKKRGLFGFD TDAFLGVKHSFHVAGSLMGYAGHFHEDVIEQVRR
HPDVDYIEKDSEVHHFDSPSVEKNAPWGLARISHRDSLSFGTFNKYLYAEDGGEGVDAYV
IDTGTNTDHVDFEGRASWGKTIPQGD EDVDGNGHGTHCSGTIAGKKYGVAKKANVYAVKV
LRSNGSGTMSDVVKGV EAAEAHIKKSKAAKDGKAKGFKGSVANMSLGGSSRTL DLAVN
AAVDAGMHFAVAAGNDNADACNYSPAAA EKAVTVGASTLADERAYFSNYGKCTDIFAPGL
NILSTWIGSKYAVNTISGTSMASPHIAGLLAYVVS LQPSDDSAFAVEKITPKKLKEALIT
VATSGALTDIPSDTPNLLAWNGGGSSNYTDIVAQQGY

>AAG44480.1 serine protease [Penicillium citrinum]
DSPSVEKNAPWGLARISHRDSLSFGTFNKYLYAEDGGEGVDAYVIDTGTNTDHVDFEGRA
NWGKTIP EGDEVDGNGHGTHCSGTIAGKKYGVAKKANVYAVKVLRSNGSGTMSDVVKGV
EWAAEAHIKKAKAGKKGFKGSVANMSLGGSSRTL DLAVNAAVDAGIHFAVAAGNDNADA
CNYSPAAAENAVTVGASTLADERAYFSNYGKCTDIFAPGLNILSTWIGSKYAVNTISGTS
MASPHIAGLLAYVVS LQPSDDSAFAVEKITPKKLKEALITVATSGALTDIPSDTPNLLAW
NGGGSSNYTDIVAQQGYKAGSTVEDFEEH IHKLVNHAEEVMHKELGAIYSEIKDAVAV

>AEX34122.1 Pen cr 26; ribosomal phosphoprotein P1 [Penicillium crustosum]
MSTAELACSYAALILADDGIEISADKIQT LISAAANVQVEPEIWASIFARALEGKDIKELL
TNVGSAGPASAAPAGAAGAAAPAEKEAEEKEEKEEESDEDMGFGLFD

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

HSWVQDIHSDNVRMELKKRSLFGFESEPYLGVKHTFHVAGSLMGYAGHFHEDVIEQVRRH
PDVEYIEKDSEVHHFEDPAIEKNAPWGLARISHRDSLSFGSFKYLYAEDGGEGVDAYVI
DTGTNVHDVDFEGRASWGKTIPQGDQDVGNGHGTCSGTIAGKKYGVAKKANVYAVKVL
RSNGSGTMSDVVKGEVAAEAHIKKSKAAKDGKAKGFKGSVANMSLGGGSSRTLDELAVNA
AVDAGMHFAVAAGNDNADACNYSAAAAEKAVTVGASTLADERAYFSNYGKCTDIFAPGLN
ILSTWIGSKYAVNTISGTSMASPHIAGLLAYVSLQPASDSAYAVEEITPKKLDALITI
ATSGALSDIPSDTPNLLAWNGGGSSNYTEIVSKGGYKAGASESMKKHLDELVGKVEEVIA
KEQKVLSELGAIYSEIKDAVSA

>AKH04310.1 Per a 11; alpha-amylase [Periplaneta americana]
MKLFALLALVLLAGVQSQKDPKLPDESTLLRLF EWKFDDIADECERFLAPKGYAGVQV
SPVHKNNLLYTATAPGLWERYQPMSYKLVSRSGDETAFRDMVRRCNAGVRIYVDVVLNHM
SGNWDNAVGTGGSTADTYNYSYPGVYPYDHSDFHPYCILNDYQDPEIVRNCELVGLHLDLQ
SQDYVREKLIDFLNHLVDAGVAGFRVDAAKHMMWADLEYIYGKVNRRNSDAGYCGDSSPS
RYQEVIDLGGEAVSKFEYNGFGRVTEFKHSEQIGYAFRGNRLEWYTYKPNWGLLPSGD
ALVFVDNHDNQRGGGNAILTYKTPKNYKMAIAFILAHYPGYPRVMSSFDFEAHDQGGPPQD
SDKNILSPSINADGTCGNGWVCEHRWRQHANNMVGFRNAVRGTEITNWDNGNHQIGFCRG
DRGFVAFNVEDNDLKQTLQTCLPAGTYCDVISGSKNNRAHLGAELVVAPNGEAFSVRLIS
DDDGLVAIHLEEKL

>AAT77152.1 Per a 9; arginine kinase [Periplaneta americana]
MVDAAVLEKLEAGFAKLAASDSKSLKLYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN
HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI
ISTRVRCGRSMQGYFPNPLTEAQYKEMEDKVSSTLSGLEAELKGQFYPLTGMTKEVQQK
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGDLG
QVYRRLVTAVNDIEKRIPFSDHDDLGLFTFCPTNLGTTVRASVHIKVPKLAADKAKLEEV
AGKYNLQVRGTRGEHTEAEGGVYDISNKRMMGLTEYDAVKEMNDGIAELIKLESSL

>ACA00204.1 Per a 9; arginine kinase [Periplaneta americana]
MVDAAVLEKLEAGFAKLAASDSKSLKLYLTKEVFDNLKTKKTPSFGSTLLDVIQSGLEN
HDSGVGIYAPDAEAYAVFADLFDPIIEDYHGGFKKTDKHPKDWGDVDTLGNLDPAGEYI
ISTRVRCGRSMQGYFPNPLTEAQYKEMEDKVSSTLSGLEAEPKGQFYLLTGMTKEVQQK
LIDDHFLFKEGDRFLQAANACRFWPTGRGIYHNDKTFVWCNEEDHLRIISMQMGDLG
QVYRRLVTAVNDIEKRIPFSDHDDLGLFTFCPTNLGTTVRASVHIKVPKLAADKAKLEEV
AGKYNLQVRGTRGEHTEAEGGVYDISNKRMMGLTEYDAVKEMNDGIAELIKLESSL

>AAX33727.1 Per a 2; aspartic protease [Periplaneta americana]
MTFLIQSAFVALAAISAVLCDPVVWPLQKRAPVEEYINTQYVGPVQLGNQYFLCVFDTSS
YTTVIPSASCVSGGCNCANVHKYYSNKPVSNVAVSVPILGSGYANGSEAHDYIAVSTLNA
TNQGFLLADDISNDICSLGADCVIGLGRPKSGRAAFNLPTVMENFVNQDNIANFSFHGG
RYPDQGHRGVLVLLGGPIPAYRGRDFTYVPLVDQDTWNFKVDSISVGNEVIATDQLAFVDS
SKYVITGPAEEIKKINDRLGCTNKVIGSRTL CVFDCDKLDNVPSVTFTIGGVAFNISSTY
QIQQNGDLCYSGFQYSAGKCFHGFDFMDNYYGEFDGQNKRMGFAKSVEEL

>ADR82198.1 Per a 2; aspartic protease [Periplaneta americana]
MTFLIQSAFVALAAISAVLCDPVVWPLQKRAPVEEYINTQYVGPVQLGNQYFLCVFDTSS
YTTVIPSASCVSGGCNCANVHKYYSNKPVSNVAVSVPILGSGYANGSEAHDYIAVSTLNA
TNQGFLLADDISNDICSLGADCVIGLGRPKSGRAAFNLPTVMENFVNQDNIANFSFHGG
RYPDQGHRGVLVLLGGTIPAYRGRDFTYVPLVDKDTWNFKVDSISVGNEVVATDQLAFVDS
SKYVITGPAEEIKKINDRLGCTNKVIGSRTL CVFDCDKLDNVPSVTFTIGGVAFNISSTY
HIQQNGDLCYSGFQYSAGKCFHGFDFMDNYYAKFDGQNKRMGFAKSVEEL

>AKH04311.1 Per a 12; chitinase [Periplaneta americana]
MKLTSLVAVGVGVFLAAALQTCKGFIRDFTKTHRQLQEKGDRAVFCYYGSWATYRWGIAT
FEVDNIDTRLCTHIVYAFTGLRDGVIVSLDEYNDYEEENWGKGLMKKFTTLAKNNGIKALV
GLGGWNEGSVKYSEMAATQAGRETFADSAVAF LQKQGF DGLDL DWEYPARRGGVPEDKDN

FTLLLKTLSEKLGARGLILTVAVSADPKTAANAYDFPNVAKYADYITLMSFDYHTPSSDT
VTGLNSPLDSLQDGTGYNKKNLVKYSVNVQWLKGGVPPNKLVLGVPLYGRYRLADPDQHG
LGAPILGPGTAGLYTQEAGFLAYYEICSNPDWVWVWVNDTSSYLYAYKDYQWLSYDDPNTI
TIKAQWVLEKNLGGVMVWSLESDDFHGNCCKGAYPLLTAVNKALGRL
>AAX33729.1 Per a 5; glutathione S-transferase [Periplaneta americana]
MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQHTIPTLNDK
GFCLWESRAILSYLADQYGGKDDSLYRRDAKKRALVDQRLYFDIGTLYHRFGEYYYPIYFA
KQAADPEKMKKLEEAFAEFLNKFLESQEFVAGNKLTIADLAIVSSVSTADIMGFDVSKYSN
VAKWFEKCKKIVPGYEELNHSGLCKFKEMCDNLAKK
>AEV23867.1 Per a 5; glutathione S-transferase [Periplaneta americana]
MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQHTIPTLNDN
GFCLWESRAILSYLADQYGGKDDSLYPKDAKKRALVDQRLYFDIGTLYHRFGEYYYPIYFA
KQAADPEKMKKLEEAFAEFLNKFLESQEFVAGNKLTIADLAIVSSVSTADIMGFDVSKYSN
VAKWFEKCKKIVPGYEELNHSGLCKFKEMCDNLAKK
>AUW37958.1 Per a 5; glutathione S-transferase [Periplaneta americana]
MTIDFYLLPGSAPCRSVLLAAKAIGVDLNLKVTNLMAGEHLTPEFLKMNQHTIPTLNDN
GFCLWESRAILSYLADQYGGKDDSLYPKDAKKRALVDQRLYFDIRTYHRFGEYYYPIYFA
KQAADPEKMKKLEEAFAEFLNKFLESQEFVAGNKLTIADLAIVSSVSTADIMGFDVSKYSN
VAKWFEKCKKIVPGYEELNHSGLCKFKEMCDNLAKK
>AAB09632.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]
DIGDHYDIEANIGHYKYPHVKNFISYYKGLLPRGEPFSVYVEKHKREQAIFELFFAA
NDYDTFYKTACWARDRVNEGFMFYALTVAAFHREDTKDLVLPYEVNPNYLFVEDDVIQQ
AYKYWTKESGTDKHEVHVPVNFARSQEDLVAYFREDVDLNAFNMYFRYIYPSWFNTTL
YGKSFDRRGEQFYTYHQIYARYFLERLSNSLPDVKPFQYSKPLKTGYNPHLRHNGEEM
PARPSNMYPTNFDLFYVSDIKNYERRVEKAIDFGYAFDEHRTPYSLYHDQHGMMDYLGQMI
EGTRNSPHQYFYGSVHFYRLLVGHVVDVPHKNGLAPSALEHPQTALRDPAFYQLWKRID
HIVQYKYNRLPRYTYDELSFPGVKIENVVDVGKLYTYFEHFEHSLGNAMYLGKLEDYMKAS
IRARHYRLNHPFTYNIENVSSDKAQDVVVRIFLGPKYDSLGHCELDERRHYFVEMDRFV
HKVEAGKTVIERKSHDSSIISSDSDSYRNLFKKVS DALQEKDQYYIDKSHKYCGYPENLL
LPKGKGGQTFTFYVIVTPYVKQDEHDFEPYHYKAFSYCGVGHGRKYPDDKPLGFPFDRK
IHDYDFYTPNMYFKDVVIFHKKYDEVHVDVTH
>AAB62731.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]
LNAFNMYFRYIYPTWFNTTLYGKTFDRRGEQFYTYHQIYARYFLERLSNSLPDVKPFQY
SKPLKTGYNPHLRQNGEEMPAPRPSNMYPTNIDLFYVSDIKNYESRVEKAIDFADFDEHR
TPYSLYHDQHGMMDYLGQMIEGTSNSPYQYFYGSIFHFYRLLVGHVVDVPHKNGLAPSALE
HHQTALRDPAFYQLWKRIDHIVQYKYNRLPRYTYDELSFPGVKIENVVDVGKLYTYFEHFE
HSLGNAMYLGKLEDVVKANIRARHYRLNHPFTYNIENVSSDKAQDVVVRIFLGPKYDSLGH
HECELDERRHYFVEMDRFVHKVEAGKTVIERKSHDSSIISSDSDSYRNLFKKVS DALEGGK
DQYYIDNSHKYCGYPENLLLPKGKGGQTFTFYVIVTPYVKQDEHDLSEYHYKAFYTCGV
GHGRKYPDDKPLGFPFDRKIHDYDFYTPNMYFKDVVIFHKKYDEVHNETN
>AAB63595.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]
EMPAPRPSNMYPTNIDLFYVSDIKNYESRVEKAIDFGYAFDEHRTPYSLYHDQHGMMDYLGQ
MIEGTSNSPYQYFYGSIFHFYRLLVGHVVDVPHKNGLAPSALEHHQTALRDPAFYQLWKR
IDHIVQYKYNRLPRYTYDELSFPGVKIENVVDVGKLYTYFEHFEHSLGNAMYIGKLEDLLK
ANIRASHYRLNHPFTYNIENVSSDKAQDVVVRIFLGPKYDSLGHCELDERRHYFVEMDR
FVHKVEAGKTVIERKSHDSSIISSDSDSYRNLKVVADALEEKDQYYIDKSHKYCNYPEN
LLLPGKGKGGQTFTFYVIVTPYVKQEQHDFEPYHYKAFSYCGVGHGRKYPDDKPLGFPFD
RKIHDYDFYTPNMYFKDVVIFHKKYDEVHEVTH
>Q25641.1 Per a 3; hemocyanin, arylphorin [Periplaneta americana]
MKTALVFAAVFAVFAARFPDHKDYKQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVGI

PMTSKQTSATTVPSPGEAVHGV LQEGHARPRGEPFSVNYEKHREQAIMLYDLLYFANDYD
TFYKTACWARDRVNEGFMYSFSIAVFHRDDMQGVMLPPPYEVYPYLFVDHVDIHMAQKY
WMKNAGSGEHHSHVIPVNFTLRTQDHL LAYFTSDVNLNAFNTYYRYYYPSWYNTTLYGHN
IDRRGEQFYTYKQIYARYFLERLSNDLPDVYPFYYSKPVKSAYNPNLRYHNGEEMPVRP
SNMYVTNFDLYYIADIKNYEKREDAIDFGYAFDEHMKPHSLYHDVHGMEYLADMIEGNM
DSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPSLEHPETVLRDPVFYQLWKRVDHLFQK
YKNR LPRYTHDELAFEGVKVENVDVGKLYTYFEQYDMSLDMAVVNNVDQISNVDVQLAV
RLNHKPFYTYNIEVSSDKAQDVYVAVFLGPKYDYL GREYDLNDRRH YFVEMDRFPYHVGAG
KTVIERNSHDSNIIAPERDSYRTFYKKVQEAYEGKSQYYVDKGHNYCGYPENLLIPKGKK
GGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVGSERKYPDNKPLGYPFDRKIYSNDF
YTPNMYFKDVIIIFHKKYDEVG VQGH

>ADB92493.1 Per a 3; hemocyanin, arylphorin [*Periplaneta americana*]

MKTALVFAAVVALVACAAPAHKDYKQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVG
NTYDIEANIGNYKYPRVVKQFMAYFKKGLM PRGEPFSVYFEKHREQAIMLYNLYFANDY
DTFYKTACWARDRVNEGFMYSFSIAVFHRDDMQGVMLPPPYEVYPYLFVDHVDIHMAQK
YWMKNAGSNEHSHVIPVNFTLKNQDQL LAYFTSDVNLNAFNTYYRYYYPSWYNTTLYGH
TIDRRGEQFYTYKQIYARYFLERLSNDLPDVYPFYYSKPVKSAYNPNLRYHNGEEMPVR
PSNLYVTNFDLYYIADIKNYEKREDAIDFGYVFEHVKPHSLYHDVHGMEYVADMIEGN
MDSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPSALEHPETVLRDPAFYQLWKRVDHLF
QKYKNR LPRYTHDELAFEGVKVENVDVGKLYTYFEQYDVS LDM SVVYVNVKVDQIPNV DVHA
RQYRLNHKPFYTYNIEVSSDKAQDVYVAVFLGPKYDYL GREYDLNDRRH YFVEMDRFP HHV
EAGKTVIERNSHDSNIVAPERDSYRTFYKKVQEAYEGKSQYYVDKGHNYCGYPENLLIPK
GKKGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVGSNRKYPDNMPLGYPFDRKIYS
NDFYTPNMYFKDVIIIFHKKYDEVG VQGH

>ADD17628.1 Per a 3; hemocyanin, arylphorin [*Periplaneta americana*]

MKTALVFAAVVAFVAARFPDHKDYKQLADKQFLAKQRDVLRLFHRVHQHNILNDQVEVGI
PMTSKQTSATTVPSPGEAVHGV LQEGHARPRGEPFSVNYEKHREQAIMLYDLLYFANDYD
TFYKTACWARDRVNEGFMYSFSIAVFHRDDMQGVMLPPPYEVYPYLFVDHVDIHMAQKY
WMKNAGSGEHHSHVIPVNFTLRTQDHL LAYFTSDVNLNAFNTYYRYYYPSWYNTTLYGYF
LERLSNDLPDVYPFYYSKHNIIDRRGEQFYTYKQIYARPVKSAYNPNLRYHNGEEMPVRP
SNMYVTNFDLYYIADIKNYEKREDAIDFGYAFDEHMKPHSLYHDVHGMEYLADMIEGNM
DSPNFYFYGSIYHMYHSMIGHIVDPYHKMGLAPSLEHPETVLRDPVFYQLWKRVDHLFQK
YKNR LPRYTHDELAFEGVKVENVDVGKLYTYFEQYDMSLDMAVVNNVDQISNVDVQLAV
RLNHKPFYTYNIEVSSDKAQDVYVAVFLGPKYDYL GREYDLNDRRH YFVEMDRFPYHVGAG
KTVIERNSHDSNIIAPERDSYRTFYKKVQEAYEGKSQYYVDKGHNYCGYPENLLIPKGKK
GGQAYTFYVIVTPYVKQDEHDFEPYNYKAFSYCGVGSERKYPDNKPLGYPFDRKIYSNDF
YTPNMYFKDVIIIFHKKYDEVG VQGH

>AAX33728.1 Per a 4; lipocalin [*Periplaneta americana*]

MLSILVVCLLAGFQLAAGDDSCQIGTSFTGLDMTKYVGTWYELFRTPNSDEEDFTNCEYD
KYTLDENGVIQVTSVAYTNSTRGFITSTGTVPSWTENTFDIAYGDNETWSSTYFMIGTDY
QTYSIVAGCLDNDYSRHL YWIASHGTSFDDATKAKVNEVLAPYNLSLDDMEPVDQSYCVQ
YKS

>ACJ37391.1 Per a 4; lipocalin [*Periplaneta americana*]

AGDDSCQIGTSFTGLDMTKYVGTWYELFRTPNSDEEDFTNCEYDKYTLDENGVIQVTSVA
YTNSIRGFITSTGTVPSWTE DTFDIAYGDETWSSSTYFMVGTDYQTYSIVAGCLDNDYSR
HLYWIASHETSFDDATKAKVNEVLAPYNLSLDDMEPVDQSYCVQYKS

>AAC34736.1 Per a 1; nitrile-specifier protein [*Periplaneta americana*]

INEIHSIIIGLPPFVPPSRRHARRGVINGLI DDVIAILPVDELKALFQEKLETSPDFKAL
YDAIRSPEFQSIISTLNAMQRSEHHQNL RDKGV D VDHFIQLIRALFGLSRAARNLQDDLN
DFLHSL EPI SPRHRHGLPRQRRRSARVSAYLHADD FHKIIT TIEALPEFANFYNFLKEHG

LDVVYINEIHSIIGLPPFVPPSRRHARRGVINGLIDDVIAILPVDELKALFQEKLETS
PDFKALYDAIRSPEFQSIISTLNAMPEYQELLQNLRDKGVDVDFIRVDQGTLRLLSSGQ
RNLQDDLNDLFLALIPDQILAIAMDYLANDAEVQELVAYLQSDDFHKIITTTIEALPEFAN
FYNFLKEHGLDVVYINEIHSIIGLPPFVPPSQRHARRGVINGLIDDVIAILPVDELKA
LFQEKLETSPDFKALYDAIDLRSSRA

>AAC34737.1 Per a 1; nitrile-specifier protein [Periplaneta americana]
VGVVDGLIDDIIAILPIDDLKALFQEKLETSDFKAFYDAVRSPEFQSIIVQTLNAMPEYQD
LLQKLRDKGVDVDHYIELIRALFGLTREARNLQDDLNDLFLALIPDQILAIAMDYLANDA
EVQELVAYLQSDDFHKIINTIEALPEFANFYNFLKGGHGLDVANYINEIHSIIGLPPFVPP
SRRHARRGVINGLIDDVIAILPVDELKTLFQEKLETSDFKALYDAIRSPEFQSIISTL
NAMPEYQELLQNLRDKGVDVDFIELIRSWFGLP

>AAB82404.1 Per a 1; nitrile-specifier protein [Periplaneta americana]
MKLPIMILAVLGVAFGKSLPNRNLQDDLNDLFLALLPVDEITAIIVMDYLANDAEVQEAVAY
LQGEFHKIVFTVEGLQEFGNFVQFLEDHGLDAVGYINRLHSVFGWDPYVPSSKRKHTRR
GVGVVDGLIDDIIAILPIDDLKALFQEKLETSDFKAFYDAVRSPEFQSIIVQTLNAMPEYQ
DLLQKLRDKGVDVDHYIELIRALFGLTRAARNLQDDLNDLFLALIPDQILAIAMDYLAND
AEVQELVAYLQSDDFHKIINTIEALPEFANFYNFLKGGHGLDVADYINEIHSIIGLPPFVPP
PSRRHARRGVINGLIDDVIAILPVDELKALFQEKLETSDFKALYDAIRSPEFQSIIST
LNAMPEYQELLQNLRDKAVDVDFIELIRSLFGLP

>AAC34312.1 Per a 1; nitrile-specifier protein [Periplaneta americana]
SIISTLNAMPEYQDLLQNLRDKGVDVDHYIELIRALFGLTRAARNLQDDLNDLFLALIPD
QILAIAMDYLANDAEVQELVAYLQSDDFHKIITTTIEGLPEFANFYNFLKEHGLDVADFLN
EHSIIGLPPFVPPSRRHARRGVINGLIDDVIAILPVDELKALFDEKLETSDFKALYD
AIRSPEFQSIISTLNAMPEYQDLLQNLRDKGVDVDFIELIRSLFGLP

>AAD13533.1 Per a 1; nitrile-specifier protein [Periplaneta americana]
EFQSIISTLNAMPEYQELLQNLRDKGVDVDHYIELIRALFGLTRAARNLQDDLNDLFLALI
PTDQILAIAMDYLANDAEVQELVAYLQSDDFHKIITTTIEGLPEFANFYNFLKEHGLDVAD
FLNEIHSIIGLPPFVPPSRRHARRGVINGLIDDVIAILPVDELKALFQEKLETSDFKA
LYDAIRSPEFQSIISTLNAMPEYQDLLQNLRDKGVDVDFIELIRSLFGLP

>ADB92492.1 Per a 1; nitrile-specifier protein [Periplaneta americana]
MKLPIMILAVLGVAFGKSLPTRNLQDDLNDLFLALVPTDEIVAIIVMDYLANDAEVQEAVAY
LQGDEFHKIVSTVEGLQEFNFVQFLEDHGLDAVGYINQLHSVLGWDYVPSPSQRKHARR
GVGVVDGLIDDIIAILPIDDLKALFQEKLETSDFKAFYDAIRSPEFQSIIVQTLNAMPEYQ
ELLQKLRDKGVDVDHYIELIRALFGLSRATRNLQDDLNDLFLALIPDQILAIAMDYLAND
AEVQELVAYLQSDDFHKIITTTVEGLDAFNFNFMKEHGLDVVYINEIHSIIGLPPFVPP
PTRRHARRGVINGLIDDVIAILPVDELKALFQEKLETSDFKALYDAIRSPEFQSIIST
LNAMPEYQELLQNLRDKGVDVDFIELIRSLFGLP

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

>AAX33734.1 Per a 10; serine protease [Periplaneta americana]
MLRYLVLASLIACSLSAVPKAKRPRLDGRIVGGRPADYADYPYQLSFEYGGSHMCGASII
SPNWWVTAACVGVASSATFRAGGSIRESGSVHQATQLIANPNYDYTTIDFDVAVAR
VSPAFSYGTGVQPIPLASSEPSAGQIATVSGWGTSEGGSTLPSQLQVSVPIVSRSECN
QAYSIDYGGITDDMICAEEQGGKDACQGDSSGGLVNVNGQLAGIVSWGVCAGQYGPVYS
NVASLKGFFITEQTGVN

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

DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMTFTELIGN

>CAB38086.1 Per a 7; tropomyosin [*Periplaneta americana*]
MDAIKKKMQAMKLEKDNAMDCALLCEQQARDANLRAEKAEFEARSQKKIQIENDLDQT
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATAKLAEASQAV
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMTFTELAGY

>ACS14052.1 Per a 7; tropomyosin [*Periplaneta americana*]
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARSQKKIQIENDLDQT
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATAKLAEASQAD
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEEYKQQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMTFTELVGY

>AAX33730.1 Per a 6; troponin C [*Periplaneta americana*]
MDELPDEQIQLLKKAFAFDREKNGFISTDMVGITILEMLGHPLDDDMLEEIIAEVDADGS
GELEFQEFVTLAARFLVEEDAEMQQELKEAFRLYDKEGNGYITTTVLREILKELDDKLT
NEDLDAMIEEIDSDGSGTVDFDEFMEVMTGE

>AAL86701.1 tropomyosin [*Periplaneta fuliginosa*]
MDAIKKKMQAMKLEKDNAMDRALLCEQQARDANLRAEKAEFEARSQKKIQIENDLDQT
MEQLMQVNAKLDEKDKALQNAESEVAALNRRIQLEEDLERSEERLATATAKLAEASQAA
DESERARKILESKGLADEERMDALENQLKEARFMAEEADKKYDEVARKLAMVEADLERAE
ERAESGESKIVELEEEELRVVGNLKSLEVSEEKANLREEAYKQQIKTLTTRLKEAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKFCDDLDMTFTELIGN

>AAG08988.1 tropomyosin [*Perna viridis*]
MDAIKKKVMAMKMEKKNALDRAEQLEQKLRETEEAKAKIEDDYNLSLVKKNIQTENDYDNC
NTQLQDVQAKYERAQKIQEHEQEIQSLTRKISLLEEGIMKAEERFTTASGKLEEASKAA
DESERNRNVLENLNSGNDERIDQLEKQLTEAKWIAEEADKKYEEAARKLAITEVDLERAE
ARLEAAEAKVIDLEEQLTVVGANIKTLQVQNDQASQREDSYEETIRDLTNRLKDAENRAT
EAERTVSKLQKEVDRLEDELLTEKEKYKAISDELDTFAELAGY

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

>Q41260.1 Pha a 1; beta-expansin [*Phalaris aquatica*]
MMKMVCSSSSSLLVVAALLAVFVGSAQGIKAVPPGNITAEYGDKWLDKSTWYGKPTG
AGPKDNGGACGYKDVDPKAPFNMGTCGNTPIFKDGRGCGSFCFLKCSKPESCSGEPITVH
ITDDNEEPIAPYHFDLSGHAFGSMKKGEEENVRGAGELELQFRRVKCKYDPDGKPTFHV
EKGSNPNYLALLVKYVDGDGDVVAVDIKEKGDKWIELKESWGAIWRIDTPDKLTGPFTV
RYTTEGGTKAEFEDVIPEGWKADTHDASK

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

>P56164.1 Pha a 5; unknown function [*Phalaris aquatica*]
MAVQKYTMALFLAVALVAGPAAPTPTPTPLPPPRARDKATLTSRSVEDINAASRRP
WWASVPPADKFKTFADHVLCPNADVTSAAATKAPQLKAKLDAAYRVAYEAAEGSTPEAKY
DAFIAALTEALRVIAGAFEVHAVKPATEEVVADPVGELQIVDKIDAAFKAATAANSAPA

NDKFTVFEGAFNKAIKESTAGAYETYKFIPLSLEAAVKQAYGATVARAPEVKYAVFEAGLT
KAITAMSEAQKVAKPPLSPQPPQVLPLAAGGAATVAAAASDVRVCRSHGTLQDACLLRCRG
GCQPVVWRGGSHRARGGYKV

>P56165.1 unknown function [Phalaris aquatica]

MAVQKYTVLFLAVALVAGPAALYAGDGYAPATPAASATLATPATPAASPOHAGTTEYHI
VRKAGLNEEKNAARQTDDEQKRSDEINCPDFNKSVMCRADRLPVCSS TSAHSSKQDVAWM
LGYGSIQGF SMDDASVGSVSSEFHVIESAIEVITYIGEEVKVIPAGEVEVINKVKAASF
AATAADEAPANDKFTVFVSSFNKAIKETTGGAYAGYKFIPTLEAAVKQAYAASSATAPEV
KYAVFETALKKAISAMSEAQKEAKPAAAI SAATTTISASTATPAAPPPPQLGTATPAAVA
GGYKV

>P56166.1 unknown function [Phalaris aquatica]

MAVQKYTVLFLAMALVAGPAASYAADAGTPPTPATPAVPGAAAGKATTHEQKLIEDINA
AFKWWPASAPPADKYKTFETAFSKANIAGASTKGLDAAYSVVYNTAAGATPEAKYDSFVT
ALTEALRIMAGTLEVHAVKPATEEEVPSAKILRANSRSSTRSSRFKIAATVATPLSHSTA
ANSAPANDKFTVFEGAFNKAIKERHGGPTETYKFIPLSLEAAVKQAYGATVARAPEVKYAV
FEAGLT KAITAMSEAQKVAKPVR LSPQPPQVLPLAAGGAATVAAAASDSRGGYKV

>P56167.1 unknown function [Phalaris aquatica]

AKYDAFIAALTEALRVIAGAFEVHAVKPATEEVPAKIPAGELQIVDKIDA AFKIAATAA
NSAPANDKFTVFEGAFNKAIKERHGGAYETYKFIPLSLEASRSKQAYGATVARAPEVKYAV
FEAGLT KAITAMSEAQKVAKPVR SVTAAAAGAATAAGGAATVAASRPTSAGGYKV

>COMPARE057 unknown function, partial [Phaseolus mungo]

GRREDDYDNLQL

>ADC80502.1 Pha v 3; lipid transfer protein [Phaseolus vulgaris]

MASVKFACVVVLCMVVGAHTAQGMTCGQVQSNLVPVTF LQNGGFVPAGCCNGVRNIMN
SARSTADRRGICNCLKTAAGAVRGLNPNNAQALPGKCGVNIPYKISTSTNCASIN

>ADC80503.1 Pha v 3; lipid transfer protein [Phaseolus vulgaris]

MATLNSACVVAVLCLVLTAPTAAHAASCGQVTSS LASCIPFLTKGGPVPASCCSGVRSL
NAAAKTTPDRQAVCNCLKSAAGAIPGFNANNAGILPGKCGVSIKYKISTSTNCATIKF

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

YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFVVDLSKMRAVWVDGKART
AWVDSGAQLGELLYAIIHKASTVLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGI VVAVKVRLLPVPPTVTVFKIPKKASE
GAVDIINRWQVVAPQLPDDL MIRVIAQGPTATFEAMYLGT CQTLTPMMSSKFPELGMNAS
HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPF PKRVWEQIFSTW
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVL FNIQYVNYWFAPGAGAAPLSWSKEI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQYFKGNFQRLAITKKG
VDPTDYFRNEQSIPPLIKKY

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

YFPPPAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFVVDLSKMRAVWVDGKART
AWVDSGAQLGELLYAIIKASPVLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGI VVAVKVRLLPVPPTVTVFKIPKKASE
GAVDIINRWQVVAPQLPDDL MIRVIAQGPTATFEAMYLGT CQTLTPMMSSKFPELGMNAS
HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPF PKRVWEQIFSTW
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVL FNIQYVNYWFAPGAGAAPLSWSKEI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQYFKGNFQRLAITKKG
VDPTDYFRNEQSIPPLIKKY

>CAD54670.2 Phl p 4; berberine bridge enzyme [Phleum pratense]

SSCEVALSYYP TPLAKEDFLRCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVK

PIYIVTPTNASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPPEFAVVDLSKMRAV
WVDGKARTAWVDSGAQLGELYYAIHKASPVLAFFPAGVCPTIGVGGNFAGGGFGMLLRKYG
IAAENVIDVKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVKVRLLPVPPTVTVF
KIPPKASEGAVDIINRWQVVAPQLPDDLIRVIAQGPATFEAMYLGTCQTLTPMMSSKF
PELGMNASHCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPKEV
WEQIFSTWLLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAA
PLSWSKEIYNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQ
RLAITKGKVDPTDYFRNEQSIPPLIQKY

>CAD54671.2 Phl p 4; berberine bridge enzyme [Phleum pratense]
SSCQVAFSYFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVK
PLYIITPTNVSHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPETFVAVVDLNKMRAV
WVDGKARTAWVDSGAQLGELYYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYG
IAAENVIDVKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVQVKLLPVPPTVTIF
KISKTVSEGAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCCKTLTPLMSSKF
PELGMNPSHCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTV
WEQILNTWLVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAA
PLSWSKDIYNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVVWGQKYFKGNFE
RLAITKGKVDPTDYFRNEQSIPPLIKKY

>CAQ55938.1 Phl p 4; berberine bridge enzyme [Phleum pratense]
YYPTPLAKEDFLRCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT
NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPPEFAVVDLSKMRAVWVDGKART
AWVDSGAQLGELYYAIHKASTVLAFFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVKVRLLPVPPTVTVFKIPPKASE
GAVDIINRWQVVAPQLPDDLIRVIAQGPATFEAMYLGTCQTLTPMMGSKFPELGMNAS
HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPKRVWEQIFSTW
LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAAAPLSWSKEI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK
VDPTDYFRNEQSIPPLIQKY

>CAQ55939.1 Phl p 4; berberine bridge enzyme [Phleum pratense]
YFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT
NVSHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPETFVAVVDLNKMRAVWVDGKART
AWVDSGAQLGELYYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVLDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAVQVKLLPVPPTVTIFKISKTVSE
GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCCKTLTPLMSSKFPELGMNPS
HCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTVWEQILNTW
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAAAPLSWSKDI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVVWGQKYFKGNFERLAITKGK
VDPTDYFRNEQSIPPLIKKY

>CAQ55940.1 Phl p 4; berberine bridge enzyme [Phleum pratense]
YFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT
NVSHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPETFVAVVDLNKMRAVWVDGKART
AWVDSGAQLGELYYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVDPNGKLHDKKSMGDDHFWAVRGGGGESFGIVVAVQVKLLPVPLTVTIFKISKTVSE
GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCCKTLTPLMSSKFPELGMNPS
HCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQFPKTVWEQILNTW
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQYVNYWFAPGAAAAAPLSWSKDI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVVWGQKYFKGNFERLAITKGK
VDPTDYFRNEQSIPPLIKKY

>CAQ55941.1 Phl p 4; berberine bridge enzyme [Phleum pratense]
YFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT

NVSHIQSAVVCGRRHTRVIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART
AWVDSGAQLGELLYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVDPNGKLDHKKSMGDDHFWAVRGGGGESFGIVVAWQVKLLPVPLTVTIFKISKTVSE
GAVDIINKWQVVPAPQLPADLMIRIIAQGPKATFEAMYLGTCCKLTPLMSSKFPELGMNPS
HCNEMSWIQSIPFVHLGHRDALEDDLNRNNSFKPFAEYKSDYVYQFPFKTVWEQILNTW
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQVYNYWFAPGAAAAPLSWSKDI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQKYFKGNFERLAITKKG
VDPTDYFRNEQSIPPLIKKY

>3TSH_A Ph1 p 4; berberine bridge enzyme [Phleum pratense]
YFPPAAKEDFLGCLVKEIPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT
QVSHIQSAVVCGRRHTRVIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART
AWVDSGAQLGELLYAIYKASPTLAFAPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID
VKLVDPNGKLDHKKSMGDDHFWAVRGGGGESFGIVVAWQVKLLPVPPPTVTIFKISKTVSE
GAVDIINKWQVVPAPQLPADLMIRIIAQGPKATFEAMYLGTCCKLTPLMSSKFPELGMNPS
HCNEMSWIQSIPFVHLGHRDALEDDLNRQNSFKPFAEYKSDYVYQFPFKTVWEQILNTW
LVKPGAGIMIFDPYGATISATPESATPFPHRKGVLFNIQVYNYWFAPGAAAAPLSWSKDI
YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVGQKYFKGNFERLAITKKG
VDPTDYFRNEQSIPPLIKKY

>CAA55390.1 Ph1 p 1; beta-expansin [Phleum pratense]
MASSSSVLLVWVLFVAVFLGSAYGIPKVPVPPGNITATYGDKWLDKSTWYGKPTGAGPKDN
GGACGYKDVKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNE
EPIAPYHFDLSGHAFGAMAKKGDQKLSAGELELQFRRVKCKYPEGTKVTFHVEKGSNP
NYLALLVKYVNGDGDVAVDIKEKGDKWIELKESWGAIWRIDTPDKLTGPFTVRYTTEG
GTKTEAEDVIPEGWKADTSYESK

>2118271A Ph1 p 1; beta-expansin [Phleum pratense]
MASSSSVLLVVALFAVFLGSAHGIPKVPVPPGNITATYGDKWLDKSTWYGKPTAAGPKDN
GGACGYKDVKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNE
EPIAAYHFDLSGIAFGSMAKKGDQKLSAGEVEIQFRRVKCKYPEGTKVTFHVEKGSNP
NYLALLVKFVAGDGDVAVDIKEKGDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEG
TKARAKDVIPEGWKADTAYESK

>CAA81613.1 Ph1 p 1; beta-expansin [Phleum pratense]
MASSSSVLLVVALFAVFLGSAHGIPKVPVPPGNITATYGDKWLDKSTWYGKPTAAGPKDN
GGACGYKDVKPPFSGMTGCGNTPIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNE
EPIAAYHFDLSGIAFGSMAKKGDQKLSAGEVEIQFRRVKCKYPEGTKVTFHVEKGSNP
NYLALLVKFVAGDGDVAVDIKEKGDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEG
GTKGEAKDVIPEGWKADTAYESK

>CAG24374.1 Ph1 p 1; beta-expansin [Phleum pratense]
IPKVPVPPGNITATYGGKWLDKSTWYGKPTAAGPKDNGGACGYKDVKPPFSGMTGCGNT
PIFKSGRGCSCFEIKCTKPEACSGEPVVVHITDDNEEPIAAYHFDLSGIAFGSMAKKGD
EQKLSAGEVEIQFRRVKCKYPEGTKVTFHVEKGSNPYLALLVKFVAGDGDVAVDIKE
KGDKWIALKESWGAIWRIDTPEVLKGPFTVRYTTEGGTKGEAKDVIPEGWKADTCYESK

>CAA76887.1 Ph1 p 7; calcium-binding protein, polcalcin [Phleum pratense]
MADDMERIFKRFDNTGDGKISLSELTALRTLGS TSADEVQRMMAEIDTDGDGFIDFNEF
ISFCNANPGLMKDVAKVF

>CAA53529.1 Ph1 p 2; expansin [Phleum pratense]
MSMASSSSSSLLAMAVLAALFAGAWCVPKVTFVVEKGSNEKHLAVLVKYEGDTMAEVELR
EHGSDEWVAMTKGEGGVWTFDSEELQGPFRFLTEKGMKNVFDVPEKYTIGATYAP
EE

>3FT1_A Ph1 p 3; expansin [Phleum pratense]
AVQVTFVQKGSPPKLVLDIKYTRPGDSLAEVELRQHGSEWEPLTKKGNVWEVKSSKP

LVGPFNFRFMSKGGMRNVFDEVIPTAFSIGKTYKPEEQEF
>AAN32987.1 Phl p 11; Ole e 1-like [Phleum pratense]
DKGPGFVVTGRVYCDPCRAGFETNVSHNVQGATVAVDCRPFNGGESKLLKAEATTDGLGWY
KIEIDQDHQEEICEVVLAKSPDTCSEIEEFRDRARVPLTSNNGIKQQGIRYANPIAFFR
KEPLKECGGILQAYDLRDAPEPTP
>CAB42886.1 Phl p 13; polygalacturonase [Phleum pratense]
GKKEEKKEEKESGDAASGADGTYDITKLGAKPDGKTDCTKEVEEAWASACGGTGKNTIV
IPKGDFLTGPLNFTGPCKGDSVTIKLDGNLLSSNDLAKYKANWIEIMRIKLLTITGKGTL
DGQGKAVWGNKNSCAKNYNCKILPNTLVLDFCDDALIEGITLLNAKFFHMNIYECKGVTVK
DVTITAPGDSPTDGIHIGDSSKVTITDITIGTGDDCISIGPGSTGLNITGVTCGPGHGI
SVGSLGRYKDEKDVTDITVKNVLLKSTNGLRIKSYEDAKSPLTASKLTYENVKMEDVGY
PIIIDQKYCPNKICTSKGDSARVTVKDVTFRNITGTSSTPEAVSLLCSDKQPCNGVTMND
VKIEYSGTNNKTMVCTNAKVTAAGVSEANTCAA
>CAA54686.1 Phl p 12; profilin [Phleum pratense]
MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAGAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLVEQGM
>CAA70608.1 Phl p 12; profilin [Phleum pratense]
MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAGAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLVEQGM
>CAA70609.1 Phl p 12; profilin [Phleum pratense]
MSWQTYVDEHLMCEIEGHHLASAAIFGHDGTVWAQSADFPQFKPEEITGIMKDLDEPGHL
APTGMFVAAAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLVEQGM
>ABG81289.1 Phl p 12; profilin [Phleum pratense]
MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAAAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLVKQGL
>ABG81290.1 Phl p 12; profilin [Phleum pratense]
MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAAAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLLKQGL
>ABG81291.1 Phl p 12; profilin [Phleum pratense]
MSWQTYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVATAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLLKQGL
>ABG81292.1 Phl p 12; profilin [Phleum pratense]
MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVATAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLLKQGL
>ABG81293.1 Phl p 12; profilin [Phleum pratense]
MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAAAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLLKQGL
>ABG81294.1 Phl p 12; profilin [Phleum pratense]
MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVAAAKYMVIQGEPRVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCNMVVE
RLGDYLVKQGL
>ABG81295.1 Phl p 12; profilin [Phleum pratense]

MSWQAYVDEHLMCEIEGHHLASAAILGHDGTVWAQSADFPQFKPEEITGIMKDFDEPGHL
APTGMFVATAKYMVIQGEPEGAVIRGKKGAGGITIKKTGQALVVGIIYDEPMTPGQCSMVVE
RLGDYLVKQGL

>AAC25994.1 Ph1 p 5; unknown function [Phleum pratense]
MAVHQYTVALFLAVALVAGPAGSYAADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKAT
TEEQKLIKINAGFKAALAAAAGVPPADKYRTFVATFGAASNKAFAEGLSGEPKGAAESS
SKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATVSEALRIIAGTLEVHAVKPAAEEVK
VIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYESYKFIPA
LEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAKAAAAATATATAAVGAAT
GAATAATGGYKV

>AAC25995.1 Ph1 p 5; unknown function [Phleum pratense]
SVKRSNGSAEVHRGAVPRRGRGGPGRSYAADAGYAPATPAAAGAEAGKATTEEQKLIED
INVGFKA AVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVLPKLDAAYSVAYKAAVGA
TPEAKFDSFVASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAA
TAAATAPADDKFTVFEAFNKAIKESTGGAYDITYKCIPSL EAAVKQAYAATVAAAAPQVKY
AVFEAALTKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>AAC25997.1 Ph1 p 5; unknown function [Phleum pratense]
MAVQKYTVALFLAVALVAGPAASYAADAGYAPATPAAAGAEAGKATTEEQKLIEDINVGF
KAAVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVLPKLDAAYSVAYKAAVAVGATPEAK
FDSFVASLTEALRVIAGALEVHAVKPVTEDEPAWPKIPAGELQIIDKIDAAFKVAATAAAT
APADDKFTVFEAFNKAIKESTGGAYDITYKCIPSL EAAVKQAYAATVAAAAPQVKYAVFEA
ALTKAITAMSEVQKVSQPATGAATVAAGAATTATGAASGAATVAAGGYKV

>AAC25998.1 Ph1 p 5; unknown function [Phleum pratense]
MAVQKYTVALFLAVALVAGPAASYAADAGYAPATPAAAGAEAGKATTEEQKLIEDINVGF
KAAVAAAASVPAADKFKTFEAAFTSSSKAATAKAPGLVLPKLDAAYSVSYKAAVAVGATPEAK
FDSFVASLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAAT
APADTVFEAFNKAIKESTGGAYDITYKCIPSL EAAVKQAYAATVAAAAPQVKYAVFEAAL
TKAITAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>1L3P_A Ph1 p 5; unknown function, partial [Phleum pratense]
IPAGELQIIDKIDAAFKVAATAAATAPADDKFTVFEAFNKAIKETTGGAYDITYKCIPSL
EAAVKQAYAATVAAAAPQVKYAVFEAALTKAITAMSEVQKVSQ

>CAA52753.1 Ph1 p 5; unknown function [Phleum pratense]
MAVHQYTVALFLAVALVAGPAASYAADLGYGPATPAAPAAGYTPATPAAPAEAAPAGKAT
TEEQKLIKINAGFKAALAAAAGVQPADKYRTFVATFGAASNKAFAEGLSGEPKGAAESS
SKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKPAAEEVK
VIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFNDAIKASTGGAYESYKFIPA
LEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAKAAAAATATATAAVGAAT
GAATAATGGYKV

>S32101 Ph1 p 5; unknown function [Phleum pratense]
EAPAGKATTEEQKLIKINAGFKAALARRLQPADKYRTFVATFGPASNKAF EGLSGEPK
GAAESSKAALTSKLDAAAYKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKP
AAEEVKVIPAAELQVIEKVDAAFKVAATAANAAPANDKFTVFEAAFND EIKASTGGAYES
YKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAKPPPLPPPQPP
PLAATGAATAATGGYKV

>S38584 Ph1 p 5; unknown function [Phleum pratense]
MAVPRRGRGGPGRSYTADAGYAPATPAAAGAAAGKATTEEQKLIEDINVGFKA AVAARQ
RPAADKFKTFEASPRHRPLRQGAGLVLPKLDAAYSVAYKAAVAVGATPEAKFDSFVASL
TEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAATAPADDKFTV
FEAFNKAIKESTGGAYDITYKCIPSL EAAVKQAYAATVAAAAEVKYAVFEAALTKAITAMS
EVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>2023228A Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGADAAGKATTEEQKLI EKINAGFKAALAGAGVQP
ADKYRTFVATFGPASNKAF AEGLSGEPKGA AESSKAALTSKLD AAYKLAYKTAEGATPE
AKYDAYVATLSEALRIIAGTLEVHAVKPA AEEVKVIPAGELQVIEKVDA AFKVAATAANA
APANDKFTVFEA AFNDEIKASTGGAYESYKFIPALEAAVKQAY AATVATAPEVKYTVFET
ALKKAITAMSEAQKAAKPPPLPPPPQPPPLAATGAATAATGGYKV

>CAB05371.1 Phl p 5; unknown function [Phleum pratense]
AVPRRGPRGGPGRSYAADAGYAPATPAAAGAEAGKATTEEQKLI EDINVGFKAAVAAAAS
VPAGDKFKTFEAAFTSSSKAATAKAPGLV PKLDAAYS VAYKAAVGATPEAKFDSFVASLT
EALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAATAPADDKFTV
FEAAFNKAIKESTGGAYD TYKCIPSLEAAVKQAY AATVAAAAPQVKYAVFEAALTKAITAM
SEVQKVSQPATGAATVAAGAATTATGAASGAATVAAGGYKV

>CAB05372.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGGPATPAAPAEAAPAGKATTEEQKLI EKINDGFKAALAAAAGVPPADKYKTFVAT
FGAASNKAF AEGLSAEPKGA AESSK GALTSKLEAAYKLAYKTSEGATPEAKYDAYVATL
SEALRIIAGTLEVHAVKPA AEEVKVIPAGELQFIEKVDSAL KVAATAANAAAANDKFTVF
EAAFNHAIKASTGGAYESYKFIPALEAAVKQAY AATVATAPEVKYTVFETALKKAITAMS
EAQKAAKPATEATATATAAVGAATGAATAATGGYKV

>CAA50281.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGADAAGKATTEEQKLI EKINAGFKAALAGAGVQP
ADKYRTFVATFGPASNKAF AEGLSGEPKGA AESSKAALTSKLD AAYKLAYKTAEGATPE
AKYDAYVATLSEALRIIAGTLEVHAVKPA AEEVKVIPAGELQVIEKVDA AFKVAATAANA
APANDKFTVFEA AFNDEIKASTGGAYESYKFIPALEAAVKQAY AATVATAPEVKYTVFET
ALKKAITAMSEAQKAAKPA AATATATAAVGAATGAATAATGGYKV

>CAA81609.1 Phl p 5; unknown function [Phleum pratense]
AAA AVPRRGPRGGPGRSYTADAGYAPATPAAAGAAAGKATTEEQKLI EDINVGFKAAVAA
AASVPAADKFKTFEAAFTSSSKAAA AKAPGLV PKLDAAYS VAYKAAVGATPEAKFDSFVA
SLTEALRVIAGALEVHAVKPVTEEPGMAKIPAGELQIIDKIDAAFKVAATAAATAPADDK
FTVFEA AFNKAIKESTGGAYD TYKCIPSLEAAVKQAY AATVAAAAPQVKYAVFEAALTKAI
TAMSEVQKVSQPATGAATVAAGAATTAAGAASGAATVAAGGYKV

>CAA76556.1 Phl p 6; unknown function [Phleum pratense]
MAAHKFMVAMFLAVAVLGLATSPTAEGGKATTEEQKLI EDINASFRAMATTANVPPAD
KYKTFEAAFTVSSKRNLADAVSKAPQLV PKLDEVYNAAYNAADHAAPEDKY EAFVLHFSE
ALHIIAGTPEVHAVKPGA

>CAA76557.1 Phl p 6; unknown function [Phleum pratense]
MAAHKFMVAMFLAVAVLGLATSPTAEGGKATTEEQKLI EDVNASFRAMATTANVPPAD
KYKTFEAAFTVSSKRNLADAVSKAPQLV PKLDEVYNAAYNAADHAAPEDKY EAFVLHFSE
ALRIIAGTPEVHAVKPGA

>CAA76558.1 Phl p 6; unknown function [Phleum pratense]
TEEQKLI EDVNASFRAMATTANVPPADKYK TLEAAFTVSSKRNLADAVSKAPQLV PKLD
EVYNAAYNAADHAAPEDKY EAFVLHFSEALRIIAGTPEVHAVKPGA

>AAC16525.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGGPATPAAPAEAAPAGKATTEEQKLI EKINDGFKAALAAAAGVPPADKYKTFVAT
FGAASNKAF AEGLSAEPKGA AESSKAALTSKLD AAYKLAYKTAEGATPEAEYDAYVATL
SEALRIIAGTLEVHAVKPA AEEVKVIPAGELQVIEKVDSAL KVAATAANAAPANDKFTVF
EAAFNNAIKASTGGAYESYKFIPALEAAVKQAY AATVATAPEVKYTVFETALKKAITATS
EAQKAAKPATEATATATAAVGAATGAATAATGGYKV

>AAC16526.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGGPATPAAPAEAAPAGKATTEEQKLI EKINDGFKAALAAAAGVPPADKYKTFVAT
FGAASNKAF AEGLSAEPKGA AESSKAALTSKLD AAYKLAYKTAEGATPEAKYDAYVATL

SEALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF
EAAFNNIAKASTGGAYESYKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMS
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>AAC16527.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT
FGAASNKAF AEGLSAEPKGAAESSKAALTSKLDAAKLYKTAEGATPEAKYDAYVATL
SEALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF
EAAFNNIAKASTGGAYESYKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMS
EAQKAAPAAAATATATS AVGAATGATTAAGGYKV

>AAC16528.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGGPATPAAPAEAAPAGKATTEEQKLIIEKINDGFKAALAAAAGVPPADKYKTFVAT
FGAASNKAF AEGLSAEPKGAAESSKAALTSKLDAAKLYKTAEGATPEAKYDAYVATL
SEALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDSAFKVAATAANAAPANDKFTVF
EAAFNNIAKASTGGAYESYKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAFTAMS
EAQKAAPATEATATATAAVGAATGAATAATGGYKV

>AAK25823.1 Phl p 5; unknown function [Phleum pratense]
PISVTAPPPQLPRPPATPPPPPPQLGASPYKLGSPKARSERPAIVPPADKYRTFVATF
GAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATPEAKYDAYVATLS
EALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAANAAPANDKFTVFE
AAFNNIAKAGTGGAYESYKFIPALEAAVKQAYAATVATAPEVKYTVFETALKKAITAMSE
AQKAAPAAAATATATS AVGAPTGATTAAGGYKV

>CAD38384.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAPAAAATATATAAVGAATGAATAATGGYKV

>CAD38385.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKNAGFKAALAAAAGVP
PADKYNTFVATFGAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAPAAAATATATAAVGAATGAATAATGGYKV

>CAD38386.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSEALSIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAPAAAATATATAAVGAATGAATAATGGYKV

>CAD38387.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSEALRKIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAPAAAATATATAAVGAATGAATAATGGYKV

>CAD38388.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAF AEGLSGEPKGAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANHKFTVFEAAFNDIAKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE

TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38389.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKFTVFEAAFNDIAIKASTGGAYESYKFIPALEAAVKKAYAATVATAGEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38390.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAIKASTGGAYESYKFIGALEAAVKQAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38391.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAIKASTGGAYESYNFIPALEAAVKQAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38392.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVP
PADKYNTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSEALSIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38393.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVP
PADKYNTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSEALRKIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKITVFEAAFNDIAIKASTGGAYESYKFIPALEAAVKKAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38394.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANHKFTVFEAAFNDIAIKASTGGAYESYKFIGALEAAVKQAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38395.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANHKFTVFEAAFNDIAIKASTGGAYESYNFIPALEAAVKQAYAATVATAPEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38396.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAKLYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEHVAVKPAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKFTVFEAAFNDIAIKASTGGAYESYKFIGALEAAVKQAYAATVATAGEVKYTVFE
TAEKKAITAMSEAKKAAKPAAAATATATAAVGAATGAATAATGGYKV
>CAD38397.1 Phl p 5; unknown function [Phleum pratense]

ADLGYGPATPAAPAAGYTPATPAAPAGAEPAGKATTEEQKLIIEKKNAGFKAALAAAAGVP
PADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAVKLAYKTAEGATP
EAKYDAYVATVSSALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAAN
AAPANDKFTVFEEAFNDAIKASTGGAYESYNFIPALEAAVKQAYAATVATAGEVKYTVFE
TAEKKAITAMSEAKKAAPAAAATATATAAVGAATGAATAATGGYKV
>1NLX_N Phl p 6; unknown function [Phleum pratense]
MGKATTEEQKLIEDVNASFRAAMATTANVPPADKYKTFEAAFTVSSKRNLADAVSKAPQL
VPKLDEVYNAAYNAADHAAPEDKYEAFVLHFSEALRIIAGTPEVHAVKPGA
>CAD87529.1 Phl p 5; unknown function [Phleum pratense]
ADLGYGPATPAAPAAGYTPAAPAGAEPAGKATTEEQKLIIEKINAGFKAALAAAAGVPPAD
KYRTFVATFGAASNKAFAEGLSGEPKGAAESSKAALTSKLDAAVKLAYKTAEGATPEAK
YDAYVATLSEALRIIAGTLEVHAVKPAAEEVKVIPAGELQVIEKVDAAFKVAATAANAAP
ANDKFTVFEEAFNNAIKASTGGAYESYKFIIPALEAAVKQAYAATVATAPEVKYTVFETAL
KKAITAMSEAQKAAPAAAATATATS AVGAATGAATAATGGYKV
>CCD28287.1 Phl p 5; unknown function [Phleum pratense]
MAVHQYTVALFLAVALVAGPAASYAADLGYGPATPAAPAAGYTPAAPAGAEPAGKATTEE
QKLIIEKINAGFKAALAAAAGVPPADKYRTFVATFGAASNKAFAEGLSGEPKGAAESSKA
ALTSKLDAAVKLAYKTAEGATPEAKYDAYVATLSEALRIIAGTLEVHAVKPAAEEVKVIP
AGELQVIEKVDAAFKVAATAANAAPANDKFTVFEEAFNNAIKASTGGAYESYKFIIPALEA
AVKQAYAATVATAPEVKYTVFETALKKAITAMSEAQKAAPAAAATATATS AVGAATGAA
TAAAGGYKV
>Q7M1L8 Phl p 5; unknown function, partial [Phleum pratense]
DLGYAPATPAAPGAGYTPATPAAP
>AGT28425.1 Phod s 1; general odorant-binding protein [Phodopus sungorus]
NDYAELEGKWDTIAIAADNDAKIKEEGLRLYVRELYCNEDCSEMEVTFYVNANNQCSKT
TVIGYKQADGTYRTQFEGDNRFQPVYATPENIVFTSKNVDRAGQETNLIFVVGKSQPLTP
EQHEKLVFAHENNIPEENIHNVLATDTCPK
>COMPARE101 Phod s 1; lipocalin, partial [Phodopus sungorus]
AGQETNEMYVVGK
>COMPARE102 Phod s 1; lipocalin, partial [Phodopus sungorus]
FKPVYATPENIVFTNK
>CAD10390.1 Pho d 2; profilin [Phoenix dactylifera]
MSWQAYVDEHLMCEIDGHHLTAAAILGHDGSVWAQSSSFPQFKSEEITNIMNDFNEPGSL
APTGLYL GSTKYMVIQGE PGAVIRGKKGSGGVTVKKTNQALIFGIYEPMTPGQCNMVVE
RLGDYLI EQGM
>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]
YFPFCQIASNGAPLEFFGF TTSAR
>COMPARE197 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]
MAGASVKPTPLKDEL DIVIPTIR
>COMPARE198 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]
YDDMWAGWCTK
>COMPARE199 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]
YFGLMGDGP IGR
>COMPARE200 alpha 1, 4 glucan synthase, partial [Phoenix sylvestris]

VPEGFYELYNR
>COMPARE207 beta-galactosidase, partial [Phoenix sylvestris]
EIQNAGLYAILR
>COMPARE208 beta-galactosidase, partial [Phoenix sylvestris]
WLLLFEEAKTRR
>COMPARE194 carbonic anhydrase, partial [Phoenix sylvestris]
TYPFVEEALEK
>COMPARE195 carbonic anhydrase, partial [Phoenix sylvestris]
YAGVGSATIEYAVHHLK
>COMPARE196 carbonic anhydrase, partial [Phoenix sylvestris]
VVFDFQGEAFTVR
>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
>CTQ87571.1 Pin p 1; 2S albumin, conglutin [Pinus pinea]
MGVFSSPMSTLRWVTLFAALLSLEWGTAHEDIVMDGDQVQQQGRSCDPQRLSACRDYL
QRRREQPSERCCEELQRMSPHCRCAIERALDQSQSYDSSTDSQDGAPLNQRRRRRGE
GRGEEEEEAVERAEELPNRCNLRESPRRCDIRRHRSRYSIIGGSD
>CEJ95862.1 2S albumin, conglutin, partial [Pinus pinea]
CRDYLQRRREQPSERRCEELERMSPQCRCRAIQVLDQSQSYDSITDDL FMDSEAAPNQR
RRRRESRGEEEEEAERAAALPETCNVRQPPRRCDVQRRSRYFTSGTDF
>ABG73109.1 Pis v 2; 11S globulin, cupin [Pistacia vera]
MGYSSLLSFLGFLLLFHCSFAQIEQVWNSQQRQQQRFQTQCQIQNLNALEPKRRIESE
AGVTEFWDQNEEQQLQCANVAVFRHTIQSRGLLVPSYDPAPELVVVVQSGSIHGAVFPGCP
ETFQEEQSRSRSERSQQSGEQHQKVRPIQEGDVIALPAGVAHWIYNNGQSKLVLVALAD
VGNSENQLDQYLKRFVLGGSPQEQIQGSGQSRSSRSQSSRRGQQGQQSNNILSAFDEEI
LAQSFNIDTQLARRLQKEKRQRGIIVRVQEDLEVLSPHRQEQEQEYEEERERRQRNGLEE
TFCTMTLKYININDPSRADVYNPRGGRVSSVNALNLPILRFLQLSAKKGVLHRDAILAPHW
NVNAHSIVYITRGNRIQIVSENGESVFDEEIREGQLVVVPQNFVAVKRASSDKFEWVSF
KTNGLSQTSQLAGRVSVFRALPLDVIKNSFDISREDARRLKESSRSETTIFAPGSSSQRKS
QSERERQREEREIEH
>ABG73110.1 Pis v 2; 11S globulin, cupin [Pistacia vera]
MGYSSLLSFLGFLLLFHCSFAQIEQVWNSQQRQQQRFQTQCQIQNLNALEPKRRIESE
AGVTEFWDQNEEQQLQCANVAVFRHTIQSRGLLVPSYNNAPPELVVVVQSGSIHGAVFPGCP
ETFQEEQSRSRSQHSRSERSQQSGEQHQKVRHIREGDIIALPAGVAHWIYNNGQSKLVL
VALADVGNSENQLDQYLKRFVLGGSPQEQIQGGQSWQSRSRSGQQSNNILSAFDEEI
LAQSFNIDTQLVKKLQREEKQRGIIVRVKEDLQVLSPQRQEQEYSDNGLEETFCMTLKL
NINDPSRADVYNPRGGRVTSINALNLPILRFLQLSVEKGVLYQNAIMAPHWNMNAHSIVY
ITRGNRMIQIVSENGESVFDEEIREGQLVVVPQNFVAVKRASSDGFVWVSFKTNGLAKIS

QLAGRISVMRGLPLDVIQNSFDISREDAWNLKESRSEMTIFAPGSRQRN
>ABU42022.1 Pis v 2; 11S globulin, cupin [*Pistacia vera*]
MGYSSLLSFLGLLLFHCSFAQIEQVNSQQRQQQRFQTCQIQNLNALEPKRRIESE
AGVTEFDWQNEEQLCANVAVFRHTIQSRGLLVPSYNNAPELVYVVQGSIGHAVFPGCP
ETFQEESSQSRSQHSRSERSQQSGEQHQKVRHIREGDIIALPAGVAHWIYNNQSKLVL
VALADVGENSEQLDQYLRFVLLGGSPQQEIQGGQSWQSRSRKGQQSNNILSAFDEEI
LAQSLNIDTQLVKKLQREEKQRGIIVRVKEDLQVLSPQRQEKEYSDNGLEETFCTMTLKL
NINDPSRADVYNPRGGRVTSINALNLPILRFLQLSVEKGVLYQNAIMAPHWNMNAHSIVY
ITRGNRMQIVSENGESVFDEEIREGQLVVVPQNFVVKRASSDGFVWVSKTNGLAKIS
QLAGRISVMRGLPLDVIQNSFDISREDAWNLKESRSEMTIFAPGSRQRN
>ABG73108.1 Pis v 1; 2S albumin, conglutin [*Pistacia vera*]
MAKLVLLLSAFALILAANASIYRATVEVEGENLSSGQSCQKQFEEQQKFKHCQMYVQQE
VQKSQDGHSLTARINQRQQCFKQCCQELQEVDKKCRQNLEQMVKRQQQQQFRGEKLE
LYETASELPRMCNISPSQGCQFSSPYWSY
>AB036677.1 Pis v 3; 7S globulin, vicilin-like [*Pistacia vera*]
KTDPELKQCKHQKQVQRQYDEEQKEQCAKGCEKYYKEKKGREQEEEEEEWGSGRGRGDE
FSTHEPGEKRLSQCМКQСERQDGGQKQLCRFRQCEKYKKERREHSYSRDEEEEEEGDEE
QEEEDENPYVFEDEHFTTRVKTEQGGVVVLPKFTKRSKLLRGLKRYRLAFLVANPQAFVV
PNHMDADSIFFVSWGRGTITKIRENKRESMNVKQGDIIIRIRAGTPFYIVNTDENEKLYIV
KLLQPVNLPGHYEVFHGPGGENPESFYRAFSREVLEAALKTPRDKLEKLFKQDEGAIVK
ASKEQIRAMSRRGEGPSIWPFTGKSTGTFNLFKKDPQSNNYQQLFESEFKDYPLQELD
IMVSYVNITKGGMSGPFYNSRATKIAIIVVSGEGRLEIACPHLSSSKNSGQEKSGPSYKLL
SSSIRTDSVFVVPAGHPFVTVASGNQNLILCFEVNAEGNIRYTLAGKKNIIEVMEKEAK
ELAFKTKGEEVDKVFQKQDEEFFQGPKWQRHQQGRADE
>ABR29644.1 Pis v 4; superoxide dismutase [*Pistacia vera*]
MALLSYVTRKTLTESLRLGLKSHVRGLQFTFLPDLPEYEGALEPAISSEIMQLHHQKHHQ
TYITNYNKALEQLDQAINKGDASAVVKLQSAIKFNGGGHINHSIFWKNLTPVSEGGGEP
HGSLGWAIDTNFGSMEALIQRMNAGAALQSGGWVWGLDKESKLLVVETTANQDPLVTK
GPSLVPLLGIDVWEHAYYLQYKNVRPDYLNKIWKVINWKYAGELYQKECP
>CAB82855.1 Pis s 2; 11S globulin, cupin [*Pisum sativum*]
MATTIKSRFPLLLLLGIIFLASVVCVYANYDEGSEPRVPAQRERGRQEGEKEEKRHGEW
RPSYEKEEDEEGQRERGRQEGEKEEKRHGEWRPSYEKQEDEEEKQKYRYQREKEDEEEK
QKYQYQREKKEQKEVQPGRRERWEREEDEEQVDEEWRGSQRREDPEERARLRHREERTKRD
RRHQREGEERSSSESQERRNPFLFKSNKFLTLFENENGHIRLLQRFDKRSDLFENLQNY
RLVEYRAKPHTIFLPQHIDADLILVVLGKAILTVLSPNDRNSYNLERGDTIKLPAGTTS
YLVNQDDEEDLRLVDLVIPVNGPGKFEAFDLAKNKNQYLRGFSKNILEASYNTRYETIEK
VLLLEEQEKDRRRQQGEETDAIVKVSREQIEELKKLAKSSSKSLPSEFEPINLRSHKPE
YSNKFGKLFETPEKKYPQLQDLDFVSCVEINEGALMLPHYNSRAIVVLLVNEGKGNLE
LLGLKNEQEREDRKERNNEVQRYEARLSPGDVVIIPAGHPVAITASSNLLLGFGINAE
NNERNFLSGDDNVISQIENPVKELTFPGSVQEIINRLIKNQKQSHFANAEPQKEQGSQG
KRSPLSSILGTFY
>P62927 2S albumin, conglutin [*Pisum sativum*]
MASVKLASLMVLFATLGMFLTKNVGAASCNGVCSPFEMPPCGSSACRCIPVGLVVGYCRH
PSGVFLRTNDEHPNLCESDADCRKKKSGNFCGHYPNPDIIEYGCWCFASKSEAEDFFSKITQ
KDLLKSVSTA
>CAF25232.1 Pis s 1; 7S globulin, vicilin-like [*Pisum sativum*]
SRSDQENPFIFKSNRFQTYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPHTLFL
PQYTDADFILVVLGKATLTVLKSNDNRNSFNLERGDAIKLPAGTIAYLANRDDNEDLRVL
DLAIPVNKPGQLQSFLLSGTQNPQLLSGFSKNILEAAFNTNYEEIEKVLLEQQEQEPQH
RRSLKDRRQEIENEVIVKVSREQIEELSKNAKSSSKSVSSESQPFNLSRNPIYSNKF

GKFFEITPEKNQQLQDLDFVNSVDIKEGSLLLPNYNSRAIVIVTVTEGKGFELVGQRN
ENQ GKENDKEEEQEEETSKQVQLYRAKLSPGDV FVIPAGHPVAINASSDLNLIGFGINAE
NNERNFLAGEEDNVISQVERPVKELAFPGSSHEVDRL LKNQKQSYFANAQPLQRE
>CAF25233.1 Pis s 1; 7S globulin, vicilin-like [Pisum sativum]
SRSDQENPFIFKSNRFQTLYENENGHIRLLQKFDKRSKIFENLQNYRLLLEYKSKPRTLFL
PQCTDADFILVVLGKATLTVLKSNDRNSFNLERGDTIKLPAGTIAYLANRDDNEDLRVL
DLTIPVKNKPGQLQSFLLSGTQNP SLLSGFSKNILEAAFNTNYEEIEKV LLEQQEQEPQH
RRSLKDRRQEINEENVIVKVSREQIEELSKNAKSSSKSVSSESGPFNLSRNPIYSNKF
GKFFEITPEKNQQLQDLDFVNSVDIKEGSLLLPNYNSRAIVIVTVTEGKGFELVGQRN
ENQ GKENDKEEEQEEETSKQVQLYRAKLSPGDV FVIPAGHPVAINASSDLNLIGFGINAE
NNERNFLAGEEDNVISQVERPVKELAFPGSSHEVDRL LKNQKQSYFANAQPLQRE
>A0A161AT60.1 Pis s 3; lipid transfer protein [Pisum sativum]
MARSMKLACVALVICMVVIAPMAEAAALSCGTVSADMAPCVTYLQAPNNASPPPPCCAGVK
KLLAAATTTTPDRQAACNCLKSAAGSIPKLN TNNAALPGKCGVSI PYKISTSTNCNTVRF
>CAC41633.1 Pla l 1; Ole e 1-like [Plantago lanceolata]
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETDQD
GVYR LPPVGYHEDCEIKLVKSSRPDCSEIPKLAKGTIQT SKVDLSKN TTITEKTRHVKPL
SFRAKTDAPGC
>CAC41634.1 Pla l 1; Ole e 1-like [Plantago lanceolata]
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETGQD
GVYR LPPVGYHEDCEIKLVKSSRPDCSEIPKLAKGTIQT SKVDLSKN TTITEKTRHVKPL
SFRAKTDAPGC
>CAC41635.1 Pla l 1; Ole e 1-like [Plantago lanceolata]
TQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAGAQQVQLDCKDSSKKVIYSIGGETGQD
GVYR LPPVGYHEDCEIKLVKSSRPDCSEIPKLAKGTIQT SKVDLSKN TTITEKTRHVKPL
SFRAKTDAPGC
>CAD80019.1 Pla l 1; Ole e 1-like [Plantago lanceolata]
MVKLTQVAAILLIGAFFLIAS TSIATQTSHPAKFHVEGEVYCNVCHSRNLINELSERMAG
AQVQL
>C0HJX6.1 Pla l 2; profilin, partial [Plantago lanceolata]
AILGQDGSVWAQGLHLGGAKYVIAGEPGAVIRLGDYLLDQGL
>ABY21305.1 Pla or 1; invertase inhibitor [Platanus orientalis]
MKLSFSLC IFFLISADIVQGTCKKVAQRSPNVNYDFCVKSLGADPKSHSADLQGLGVISA
NLAIQQGSKIQTFIGRILKSKVDPALKKYLND CVGLYADAKSSVQEAIADF KSKDYASAN
VKMSAALDDSVTCE DGFKEKKGIASPVTKENKDYVQLTAISLAITKLLGA
>ABY21306.1 Pla or 2; polygalacturonase [Platanus orientalis]
MRGVQSSGGTFNVNDYGAKGSGDISQAVMKAWEAACASPGPSTVLIPTGNYIMGEVLLLEG
PCKGSKIGFQLDGVVKAPADVSAFKSEGWVFNHVDGLTVSGKGTFDGQGQKAWAANNCD
KDENCNRPPMNIRFNFLKNAVVRDITSMNSKMFHINVLECDNISFQHVTISAPGTSINTD
GIHIGLSRGVTITDTNIATGD DCVSIGPGSQNVTVTKVNCGPGHGISVGS LGKYKDEKDV
RGITVTGCTFTGT SNGVRVKTWPDSPPGVATDMAFEDLT MKNVQNPVILDQEYCPYGQCS
LKAPSRVKLSNIKFNNIRGTSSGPDAIIV IACSHGFPCSNLEIGEINLALHAAGAPANSTC
TNAKPIFSGKQVPAIKCA
>CAD20556.1 Pla a 1; invertase inhibitor [Platanus x acerifolia]
MKLSFSLC IFFFNLLLLLQAVISADIVQGTCKKVAQRSPNVNYDFCVKSLGADPKSHTAD
LQGLGVISANLAIQHGSKIQTFIGRILKSKVDPALKKYLND CVGLYADAKSSVQEAIADF
KSKDYASANVKMSAALDDSVTCE DGFKEKKGIVSPVTKENKDYVQLTAISLAITKLLGA
>CAL07989.1 Pla a 3; lipid transfer protein [Platanus x acerifolia]
MAFSRVAKLACLLLACMVATAPHAEEAITCGTVVTRLTPCLTFLRSGGAVAPACCNGVKA
LNNDAKTTPDRQAACGLKTASTSISGIQLGNAASLAGKCGVNL PYKISPTIDCSKVK

>ALF39466.1 Pla a 3; lipid transfer protein [Platanus x acerifolia]
AAITCGQVSKLTNCLSYLRSGGTVSTACCNGVTSLNKMANSTSDRQAACNCLKSAYKSI
SGIKLQYSQSLAGKCGVNLPHYKISPDIIDCSKVK

>CAE52833.1 Pla a 2; polygalacturonase [Platanus x acerifolia]
RGVQSSGSVFNVDYGAAGAGDISQAVMKAWKAACASQGPSTVLIPKGNYNMGEVAMQGP
CKGSKIGFQIDGVVKAPADPSKFKSDGWVSFYRIDGLTVSGTGLDGGQQTAWAKNCDK
NPNCKHAAMNLRFDLFLKHAMVRDITSLNSKMFHINVLECEDITFQHVTVTAPGTSINTDG
IHVGISKGVITINTKIATGDDCISIGPGSQNVITITQVNCGPGHGISIGSLGRYNNEKEVR
GITVKGCTFSGMTNGVRVKTWPNSPPGAATDLTFQDLTMNNVQNPVILDQEYCPYGGCSR
QAPSRIKLSNINFNNIRGTSTGKVAVVIACSHGMPCSNMKIGEINLSYRGAGGPATSTCS
NVKPTFSGKQVPAIKCA

>CAC85911.1 Plo i 1; arginine kinase [Plodia interpunctella]
MVDAATLEKLEAGFSKLAASDSKSLKLYLTREVFDAKLNKKTSGSTLLDSIQSGVENL
HSGVGIYAPDAEAYVVFADLFDPIIEDYHNGFKKTDKHPKNWGDVETLGNLDPAGEFVV
STRVRCGRSMEGYPFNPCLTEAQYKEMEEKVSSLSGLEGELKGTFFPLTGMSKETQQQL
IDDFHFLKEGDRFLQAANACRFWPSGRGIYHNENKTFVWCNEEDHLRLISMQMGDLKQ
VYKRLVRGVNDIAKRIPFSHNERLGFLLFCPTNLGTTVRASVHIKLPKLAADKAKLEEVA
SKYHLQVRGTRGEHTEAEGGYDISNKRMRGLTEYEAVKEMYDGIKIEKIEKSL

>CBW45298.1 Plo i 2; thioredoxin [Plodia interpunctella]
MSIHIKDVEDLTARL TEAGDKLVVIDFMATWCGPCKIIGPKLDEIAAEMADSIWVKVDV
DECEDIATEYSINTMPTFVVFVKNKGPVEQFSGANVEKLRSTILKLLK

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

>F37396 beta-expansin, partial [Poa pratensis]
YTTEGGTKAEAEDVIPEGWKVDTSYE

>P22284.1 unknown function [Poa pratensis]
MDKANGAYKTALKAASAVAPAEKFPVFQATFDKLNKEGLSGPDAVGFACKLDAFIQTSYL
STKAAEPKEKFDLFLVLSLTEVLRFMAGAVKAPPASKFPAKPAPKVAAYTPAAPAGAAPKA
TTDEQKLIKINVGFKA AVAAAAGVPAASKYKTFVATFGAASNKAF AEALSTEPKGAAVA
SSKAVLTSKLDAAAYKLAYKSAEGATPEAKYDAYVATLSEALRIIAGTLEVHGVKPAEEV
KAIPAGELQVIDKVDAAFKVAATAANAAPANDKFTVF EAAFNDAIKASTGGAYQSYKFIP
ALEAAVKQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAKAAAATGTATSAVGAA
TGAATAAAGGYKV

>P22285.1 unknown function [Poa pratensis]
MAVHQYTVALFLAVALVAGPAASYAADVGYGAPATLATPATPAAPAAGYTPAAPAGAAPK
ATTDEQKLIKINAGFKA AVAAAAGVPAVDKYKTFVATFGTASNKAF AEALSTEPKGA
ASSNAVLTSKLDAAAYKLAYKSAEGATPEAKYDAYVATLSEALRIIAGTLEVHGVKPAGEE
VKAIPAGELQVIDKVDAAFKVAATAANAAPANDKFTVF EAAFNDAIKASTGGAYQSYKFI
PALEAAVKQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAKAAAATGTATGAVGA
ATGAVGAATGAATAAAGGYKTGAATPTAGGYKV

>P22286.1 unknown function [Poa pratensis]
MAVQKYTVALFLVALVVGPAASYAADLSYGAPATPAAPAAGYTPAAPAGAAPKATTDEQK
MIEKINVGFKA AVAAAAGVPAANKYKTFVATFGAASNKAF AEALSTEPKGA AVDSSKAAL
TSKLDAAAYKLAYKSAEGATPEAKYDDYVATLSEALRIIAGTLEVHGVKPAEEVKATPAG
ELQVIDKVDAAFKVAATAANAAPANDKFTVF EAAFNDAIKASTGGAYQSYKFI PALEAAV
KQSYAATVATAPAVKYTVFETALKKAITAMSQAQKAAKAAAATGTATAAVGAATGAATA

AAGGYKV

>A60373 unknown function [Poa pratensis]

EFPGELQVIDKVDAAFKVAATAANAAPANDKFTVFEEAFNDAIKASTGGAYQSYKFIPAL
EAAVKQSYAATVATAPAVKYTVFETALKKAITAMAQAQKAAKPAAAVTGIATSAVGAATG
AATAAAGGYKA

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

MAVQKYTVALFLTVALVAGPAASYAADAGYAPATPAAAGAAAGKITPTQEQKLMEDINVG
FKA AVAAAAGAPPADKFKTFQAAFSASVEASAAKLNAAQAPGFVSHVAATSDATYKAAVG
ATPEAKFDSFVAAFTALRIIAGVLKVHAVKPIETEETGAAKIPAGEQQIIDKIDAAFKVA
ATAANAAPANDKFTVFEEAFNNAIKESTGGAYDTYKSIPSLEAAVKQAYAATIAAAPEVK
FAVFKAAALKAITAMAQKQVSKPVAGAATVAAGAATAATGAATGAAGAATGAATVSAGG
YKV

>AAD52616.1 Pol a 2; hyaluronidase [Polistes annularis]

YVSLSPDSVFNIITDDISHQILSRNCERSKRPKRVFSIYWNVPTFMCHQYGMNFDEVTD
FNIKHNKDNFRGETISIIYDPGKFPALMPLKNGNYEERNGGVPPQRGNITIHLLQQFNEDL
DKMTPDKNFGGIGVIDFERWKPFRQNWGNTIEHKKYSIELVRKEHPKWSESMIEAEATK
KFEKYARYFMEETLKLAKKTRKRAKWGYGFPYCYNVTPNPPGDCDAKATIENTRSLWM
YNNQEILFPSVYVRHEQKPEERVYLVQGRIKEAVRISNNLEHSPSVLAYWWVYVYQDKMDI
YLSETDVEKTFQEIVTNGGDGIIWSSSDVNSLSKCKRLREYLLNTLGPFAVNVTTETVN
GRSSLNF

>AAD52615.1 Pol a 1; phospholipase A1 [Polistes annularis]

MSPDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNN
ENFVAMSKALIEKDDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGKFAVDFTKL
LVEKYKVLISNIRLIGHSLGAHTSGFAGKEVQKLLKLGKYKEIIGLDPAGPYFHRSDCPDR
LCVTD AEYVQVIHTSIILGVYYNVGSDVDFVYVNYGKNQPGCNEPSCSHTKAVKYLTECIKH
ECCLIGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAPVEANAPYCHNEGIK
L

>AAA29793.1 Pol a 5; unknown function, antigen 5 [Polistes annularis]

SSQGV DYCKIKCPSGIHTVCQYGESTKPSKNCAGKVIKSVGPTEEEKKLIVSEHNFRQK
VAQGLETRGNPGPQPAASDMNDLVWNEDELAHIAQVWASQCQFLVHDKCRNTAKYPVGQNI
AYAGGSNLPDVVSLIKLWENEVDFNYNTGITKQNFAGIKGHYTMVWVKTEIGCGSLKY
MENNMQNHYLICNYGPAGNYLGLQLPYTKK

>XP_015174445.1 Pol d 3; dipeptidyl peptidase [Polistes dominula]

MISLRSFVFLNGFIFVLLTGRTVSYVLDKDNLDREVFRVQDDSNFPKRPFQLEETYTADY
LPRNFNGTWTSDTTLIYISETVGEILQFDVVKQOSTVIIDVSIFFDDYLVESYLLSPTGRF
LLIGYDLQKGFYRSTFMRYVIYDTELGQYDKIGNGMHIALVRWAPLTDLLIYILDNNIYY
KRFSKNGFNDVQRVTDDGIAGIYNGVADWVYEEVHLHGSSAIWFSPDGKRLAYATFDDR
KVHEILYLHYGEPGSLGDQYPTVEVKKIKYPKAGTPNPVSLTLVDLHDPTLNKINLEAPVD
IVGIDNVL TNVQWKDFNTIIATWSNRVQNETEIVWYNVYGETVETLHIEEPEGWVDIKNL
FFYNGSTYMRKLQQSGETKAGRFHHVTRYEKVGSTLIQKDLTPGAIEVQDIRAIDHFNGRI
YYLASGPGEPSQRNLYSVPADGSKEPTCISCNVITPEGNQCKYADVSFSPFRSYALVCQ
GPDPTFIDIFDSNHRKIFSWEHNLMLRLRLTKRELPIVKDLYVHANGYDSKVRLLLPNHF
DESKSYPM LVN VYAGPNTAKINDAASYSYQSYM TTNRSVIYAYIDGRGSSNKGSNMLFEI
YRNLGTVEVEDQITVTRKQLQEMYSWIDSKRTAIWGSYGGFCTAMVLAKDVDSVFKCGIS
VAPVSSWIYYDSIYTERFMGLPTPEDNLKGYDGTDSRRVEGIRGKKFMLIHGTGDDNVH
YQQLALAKSLEESDILFEQITYTDEAHALYGVLP HLYHSMDFWSECFWSNTH

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

MNFKYSILFICFVKVLDNDCYAADDLTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNG
IILKKEILKNYDLFQKSQISHQIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWK
KGACNAFASTNDVLGYSQAVGNTRHVGKYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTS

GFAGKEVQRLKLGKYKEIIGLDPAGPSFLTNNKCPNRLCETDAEYVQAIHTSAILGVYYNV
GSVDFYVNYGKSQPGCSEPCSHTKAVKYLTECIKRECLIGTPWKSYPSTPKPISQCKR
DTCVGLNAQSYPAKGSFYVPVVDKAPYCHNEGIKL

>AAS67042.1 Pol d 1; phospholipase A1 [Polistes dominula]
ADDLTTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFQKSQISH
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG
NTRHVKGKYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL
DPAGPSFLTNNKCPNRLCETDAEYVQAIHTSAILGVYYNVGSVDFYVNYGKSQPGCSEPC
SHTKAVKYLTECIKRECLIGTPWKSYPSTPKPISQCKRDTCCVGLNAQSYPAKGSFYV
PVEKDAPYCHNEGIKL

>AAS67043.1 Pol d 1; phospholipase A1 [Polistes dominula]
ADDLTTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFQKSQISH
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG
NTRHVKGKYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL
DPAGPSFLTNNKCPDRLCETDAEYVQAIHTSAILGVYYNVGSVDFYVNYGKSQPGCSEPC
SHTKAVKYLTECIKRECLIGTPWKSYPSTPKPISQCKRDTCCVGLNAQSYPAKGSFYV
PVDKAPYCHNEGIKL

>AAS67044.1 Pol d 1; phospholipase A1 [Polistes dominula]
ADDLTTLRNGTLDRGITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFQKSQISH
QIAILIHGFLSTGNNENFDAMAKALIEIDNFLVISVDWKKGACNAFASTNDVLGYSQAVG
NTRHVKGKYVADFTKLLVEQYKVPMSNIRLIGHSLGAHTSGFAGKEVQRLKLGKYKEIIGL
DPAGPSFLTNNKCPDRLCETDAEYVQAIHTSAILGVYYNVGSVDFYVNYGKSQPGCSEPC
SHTKAVKYLTECIKRECLIGTPWKSYPSTPKSISQCKRDTCCVGLNAQSYPAKGSFYV
PVEKDAPYCHNEGIKL

>AAP37412.1 Pol d 4; serine protease [Polistes dominula]
MNCGKIILLFITIIGVAKSREENCKCGWDNPSRIVNGVETEINEFPMVARLIYPSPGMYC
GGTIITPQHIVTAAHCLQKYKRTNYTGIHVWVGEHDYTTDTETNVTKRYTIAEVTIHPNY
NSHNNDIAIVKTNERFEYSMKVGPVCLPFNYMTRNLNETVTALGWGKLRVNGQNSKVL
KVDLHVITREQCETHYGAAIANANLLCTFDVGRDACQNDSSGGPILWRSPTDNLILVGVV
NFGRTCADDAPGGNARVTSFMFEIHNATIGETYCKAD

>AAT95010.1 Pol d 5; unknown function, antigen 5 [Polistes dominula]
MKISCLICLVIVLTIHLSQANDYCKIKCSSGVHTVCQYGESTKPSKNCAGKLIKSVGPT
EEEKKLIVEEHNFRFRQKVAQGLETRGNPGPQPAASNMMNLVWNLDELAKIAQVWASQCQIL
VHDKCRNTEKYQVGQNIAYAGSSNHFPVTKLIQLWENEVKDFNYNTGITNKNFGKVGHY
TQMVGNTKEVGCGLKYVEKNMQIHLYLICNYGPAGNYLGQPIYTKK

>AAT95009.1 Pol e 5; unknown function, antigen 5 [Polistes exclamans]
MEIGGLVYLVIIVVAIIHSSQGVYDYCKIRCPSGIHTVCQYGESTKPSKNCAGKVIKSVGPT
EEEKKLIVSEHNFRFRQKVAQGLETRGNPGPQPAASDMNDLVWNLDELAHIAQVWASQCQFL
VHDKCRNTAKYPVQNIAYAGGSKLPDVVSLIKLWENEVKDFNYNTGITKQNFAGHYT
QMVWGKTEIGCGSLKYMENKMQNHLYLICNYGPAGNYLGQLPNTTK

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

>P83542.1 Pol g 1; phospholipase A1 [Polistes gallicus]
GITPDCTFNEKDIELHVYSRDKRNGIILKKEILKNYDLFKES

>P83377.1 Pol g 5; unknown function, antigen 5 [Polistes gallicus]
NDYCKIKCSSGVHTVCQYGESTKPSKNCAGKVIKSVGPTEEEKKLIVEEHNFRFRQKVAQG
LETRGNPGPQPAASNMMNLVWNLDEQAKIAQVWASQCQILVHDKCRNTEKYQVGQNIAYAG

SSNHFPSVTKLIQLWENEVKDFNYNTGITNKNFGKVGHYTQMVWGNTKEVCGGSLKYVEK
NMKIHLYLICNYGPAGNYLGQPIYTKK

>ADL09135.1 hyaluronidase [Polybia paulista]

SWVEFALSERPkrvfNIYwNvPTFMCHQYGINFDEVTDFNIKHNSKDNFRGETLAIYYDP
GNFPALIPVNNgkyKERNggVPQRGNITihLQQFNEDLDKMTpDKSFGGIGVIDFERWRP
VFRQNWGNTeIhKEYSIElVRKEHPKWSKSMIEAEATKKFEKYARYFMEETLKLAKKTRK
RAKWgYyGfPYCYNASpNnPGPSCDAKAIENDRMSWMyNNQeILLPSVYVRHKQDPEER
IYLVQGRVKEAVRVSNNLEHSPSVLPYwWVYyQDEMEIFLSETDVKKTFQEIVTNGGDGI
IIWGSsSDVNSLSKCKRLREYLLNTLGPiAVNVtETVNRrSSLNF

>P86687.1 Poly p 2; hyaluronidase [Polybia paulista]

GETISIYYDPGKFPALMPLKNGYEERNggVPQRGNITihLQQFNEDLDKMTpDKNFGGI
GVIDFERWkPIFRQNWGNTeIhKkYSIElVRYEHPKwSESMIEAEATKKFEKYARLFMEE
TLKLAKKTRKRAKWgYyGfPYCYNYTPNnPGPDCDAKAMIENDRLSWMyNNQeILFpSVY
VRHElTPDQRVYLVQGRiKEAVRISNNLKHSPKVLsYwWVYyQDKMDIFLSETDVKKTFQ
EIVTNGGDGIiIWGSsSDVNSLSKCKRLREYLLNTLGPFAVNVtETVN

>A2VBC4.1 Poly p 1; phospholipase A1 [Polybia paulista]

MNFKYSILFICFGTLDRGLIPECPFNEYDILFFVYTRQQRDGIVLTEETLQNYDLFKKST
ISRQVVFIDHGFLSNGNENFIAMAKALIEKDNFLVISVDWKKGACNAFASTLDYLYGST
AVGNTRHVgKYVADFTKLLVEQYKVSMSNIRLIGHSLGAHTSGFAGKEVQELKLNKYSNI
DGLDPAGPSFDsNDcPERLCETDAEYVQIiHTSNILGVYSKIGTVDFYmNYGSHQPGCGR
FFSPSCSHTKAVKYLTECIKHECCLIGTPWKKYFSTPKPISQCTKDTcVCVGLNAKSYP
RGSFYVPVEATAPYCHNEGIKL

>ADT89774.1 Poly p 1; phospholipase A1 [Polybia paulista]

GLIPECPFNEYDILFFVYTRDQDGIILKKNLTSYNLFQQPQISHRVVFLIHGFISTGN
NGNFDAMAKALIAKDNFLVMSVDWRRACDASVFNVAGYSKAVANTRRVGKYVADFTKIL
VDKYKVPMSNIRLIGHSLGAHTSGFAGKQVQKLKLGKYSEIIGLDPAGPSFRSTNCPDR
CETDAQYVQVLHTSSKLGTyDQIGSVDFYVNYGGSQPGCLVRTCSHTKAVLYMTECIKRE
CCLIGTPWSSTGSSPKPKPISACKRDICVCVGLNAKSYPAGKSFYVPVEKNSPYCHNEGI
KL

>P86686.1 Poly p 5; unknown function, antigen 5 [Polybia paulista]

NKYCNiKCSKVAHTVCQTGESTKPSKNCaKVSITSVGVTEEEKklivDEHNrFRQKVAQ
GLETRGNPGPQPAASDMNnLVWnDELAyIAQVWASQCQFFVHDKCRNTAQYQVGQNIAYS
ASTAAYPGVVKLIVLWENEVKDFNYNTGITKENFAKVGHYtQVvWAKTKEVCGGSiKYIE
KGMKSHYLVCNYGPAGNVLGAQIYEIK

>ANW82807.1 Poly p 5; unknown function, antigen 5 [Polybia paulista]

NKYCNiKCSKVAHTVCQYGESTKPSKCNKVSITSVGVTEEEKklivDEHNrFRQKVAQG
LETRGNPGPQPAASDMNnLVWnDELAyIAQVWASQCQFFVHDKCRNTAQYQVGQNIAYS
STAAYPGIVSLIVLWENEVKDFNYSQGITKENFSKVGHYtQVvWAKTKEVCGGSiKYIEK
GMKSHYLVCNYGPAGNYMGQPIYTKK

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

AYSWdNRVkyVVRYMYDIDNNGFLDKNDfECLALRNTLIEGRGEFNAAAYANNQKIMSNL
WNEIAELADFNKDGEVTIDeFKKAVQNVcVgKAFATFPAAFKVFIANQFKTVdVNGDGLV
GVDEYRLDCISRSAFANIKEIDDAyNKLATDADKKAGGISLARYQELyAQFISNPDESAN
AVYLFGLKEVQ

>QID21357.1 Pop n 2; profilin [Populus nigra]

MSWQVYVDDHLMCDIEGNTLTSAAIIGHDGSVWALSASFpQFTQEEVSAIMKDFEEPGSL
APTGLFLGGTKYmVIQGEpGAVIRGKKGSGGVTVKKTnQALiIGVYDEPLTPGQCNMIVE
RLGDYLIDQGL

>AGE44125.1 Por p 1; tropomyosin [Portunus pelagicus]

MDAIKKKMQAMKLEKDDAMDRADTLEQQNKEANIRAEKAEVHNLQKRMQQLENDLDQV
QESLLKANTQLEEKDKALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSTTDELQDQAFSELSGY

>ABL89183.1 tropomyosin [Portunus sanguinolentus]

MDAIKKKMQAMKLEKDNAMDRADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQDQTFSELSGY

>ABS12234.1 tropomyosin [Portunus trituberculatus]

MDAIKKKMQAMKLEKDNAMDRANTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVELEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQDQTFSELSGY

>AFA45339.1 Pro c 2; arginine kinase [Procamburus clarkii]

MADAATIAKLEEGFKLEAATDCKSLLKKYLSKSIKSLKAKKTGLGATLLDVIQSGVEN
LDSGVGIYAPDAEAYSFLAPLFDPIIEDYHKGFKQTDKHPNKDFGDVNQFVNVDPDGKQV
ISTRVRCGRSLEGYFPNCLTEAQYKEMEEKVSSTLSGLEGELKGTYYPLAGMTKEVQQK
LIDDHFLFKEGDRFLQAANACRYWPVGRGIYHNDNKTFVWCNEEDHLRIISMQMGDLG
QVYRRLVSAVNDIEKRVPFSSHDRGLFTFCPTNLGTTIRASVHIKLPKLAANREKLEEV
AARYSLQVRGTRGEHTEAEGGVYDISNKRMLTEFQAVKEMQDGIKIEKEMA

>AFP95338.1 Pro c 5; myosin light chain [Procamburus clarkii]

MAADLSARDVERVKFAFSIYDFEGNGTMDAFYIGDCLRALNLPNTLAIIEKVGKKEKRKE
KIIKLEEFIPIFAQVKKDKDAGSYEDFMEVLKLYDKSENGTMMYAELEHILLSLGERLEK
SELEPVLKECCNEEDEDGFIPYEPFLKKMTQLL

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

MANQRKFFVGGNWKMNDRAGIDSIIISFMKGPLSADTEVVVGCPCYLYMTREHLPSNIG
VAAQNCYKVAKGAFTEISPSMIKDCGCEWVILGHSERRNVFNPDTLISEKVGHALEAG
LKVIPCIGEKLEERESNRTEEVVFAQMKALVPNISDWSRVVIAIYEPVWAIWGTATPEQ
AQEVHAKLRQWLRDNVNAEVADSTRIIYGGSVTPGNCKELAKTGDIDGLVGGASLKPDP
VQIINARD

>ACN87223.1 Pro c 1; tropomyosin [Procamburus clarkii]

MDAIKKKMQATKLEKDNAMDRADTLEQQNKEANIRAEKAEVHNLQKRMQHLENDLDQV
QESLLKANTQLEEKDKAISNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMVKVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLANKLKAAEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELQDQTFSELTGY

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

DDVAKPPVSQFHIQGLVYCDTCRIQFMTRVSTIMEGATVKLECRNITAGTQTFKAEAVTD
KVGQYSIPVNGDFEDDICEIELVKSPNSDCSEIPHVDVYAKQSAKVSLTSNNGEASDIRSA
NALGFMKREPLKECPEVSKEPLDMYDVKAN

>AHY24177.1 Pro j 2; profilin, partial [Prosopis juliflora]

MSWQTYVDDHLMCEIEGTNNHLSAAAILGVDGVSVAQSASFQPKPDEISAVVKDFDGGP
TLAPTGLHLGGTKYMIQGEQVIRGKKGPGGICVKKTGQALIIGIYDEPVTGQCENMI
VERLGDYLVEQGM

>1510259A metalloprotease [Protobothrops flavoviridis]

ERFPQRYIELAIVVDHGMYYKYNQNSDKIKVRVHQMVNHINEMYRPLNIAISLNLQIWS

KKDLITVKSASNVTLSEFGNWRETVLLKQQNNDCAHLLTATNLNDNTIGLAYKKGMCNPK
LSVGLVQDYSPNVFMAVTMTHELGHNLGMEHDDKDKCKCEACIMSDVISDKPSKLFSDC
SKNDYQTFLLTKYNPQCILNAP

>CAA58223.1 fibrinogenolytic protease [Protobothrops mucrosquamatus]
MVLIRVLANLLILQLSYAQKSELVIGGDECNINEHPFLVLVYYDDYQCGGTLNNEEWL
TAAHCNGKDMEIYLGVHKKVPNKDVQRRVPKEKFFCDSSKTYTKWNKDIMLIRLDRPVR
KSAHIAPLSLPSSPPSVGSVCRVMGWTITSPQETYPDVPHCANINLLDYEVCRAAYAGL
PATSRITL CAGILEGGKDCVSGDGGPLICNGQFQGI VSWGGDPCAQPREGVYTNVFDHL
DWIKGIIAGNTDVTCP

>ADV71357.1 metalloprotease [Protobothrops mucrosquamatus]
MIEVLLVTICLAVFPYQGSIIILESGNVNDYEVVYPRKVSALPKGAVQPKYEDTMQYELK
ENGEVVLHLEKKNGLFSEDYSETHYSPDGREITTYPSVEDHCYYHGRIHNDADSTASIS
ACDGLKGYFKLQGGTYLIEPLKLPDSEAHAVFKYENIEKEDEAPKMGVTQNWESDESIS
KASQLYLTPEQQRFPQRYVVKLAIWVDYRMYIKYNRDSNKITVRVHEMVNHNEMYKPLNV
AITLSLLRIWSTRDLITVQSDSKVTLGSFGDWRKTVLLKQQSHDCAHLLTDITFTKNVIG
VAYKKGMCDPKLSVGLVQDYSSNVFVAAIMTHELGHNLGMEHDEDENGKKCKCDTCIMS
PAISDPPAQLFSDCSKNDYHTFLTNSKPQCILNAPLRTDTVSTPVSUNEPL

>Q9DG84.1 serine protease [Protobothrops mucrosquamatus]
MVLIRVLANLLILQLSYAQKSELVIGGDECNINEHPFLVLVYYDDYQCGGTLNNEEWL
TAAHCNGENMEIYLGMSKVPNKDRRRRVPKEKFFCDSSKNYTKWNKDIMLIRLNRPVR
KSAHIAPLSLPSSPPSVGSVCRIMGWTISPTKVTLPDVPRCANINLLDYEVCRAVPEL
PATSRITL CAGILEGGKDCVSGDGGPLICNGQFQGI VSWGGDPCAQPHEPGLYTNVFDHL
DWIKGIIAGNTDVTCP

>BAH59276.1 abhydrolase [Protortonia cacti]
MPVRMLFSILISLILSVVVGNEHYPKVSPAQFSAAFHGYELPQKEGRADEVDSNEVKFY
LYTRQNLHKEYELHTGYNCSNSYESLRNSTYNVRKETKFLIHAWTQSPKDINDIYIYLYA
ENVNVIMVDWMSYQTCNYNSTSYVWIPKVAKALSDLMKLLTGYGAVPQKNFHVIGFLHG
AHIAGIAGKYISPLRISRISGLDPVGYNIDGTALPVLQNGDADFIDVIYTSIEYYGTQRQ
IGDLSFYPRDRGTHPQKQCPPDPNEWVCSALASIKYWRESITSPTAFSAIRCDNVYQYHES
RCPGPNTTMEYASRNAPFGKYLLNTNPEPPYSQS

>AAD32205.1 Pru ar 5; glutamic acid rich protein, Hev b 5-like [Prunus armeniaca]
MATVEVAPAATLQENEAKTVEVIKTEEKTPEEPVAAAAPAAVPESEAAATTEPKETTPVEA
EAEAEAEAPAPEAETPVPAEVEETKEVAEPEKAAEAEAEPEAATETEKTEKTEAEEPKEV
TAAEPVAAVAEETKEETTESAETPAAPPAEEEEKAEATTDVPVEKTEE

>ADR66945.1 lipid transfer protein [Prunus armeniaca]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSTLAPCINVKSGGAVPPACCNGIR
TLNGLAKTTADRQAACNRLKQLSGSIPGVNPNNAALPGKCGVNPYKISISTNCAAVK

>ADR66946.1 lipid transfer protein [Prunus armeniaca]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSNVAPCIPYVIGGGAVPPACCNGIRNV
ENLAKTTADRQAACNCLKQLSGSIPGVNPNNAALPGKCGVNPYKISISTNCAAVK

>ADR66947.1 Pru ar 3; lipid transfer protein [Prunus armeniaca]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIGYVRGGGAVPPACCNGIRNV
NNLARTTPDRRTACNCLKQLSGSISGVNPNNAALPGKCGVNIPYKISASTNCATVK

>ADR66948.1 lipid transfer protein [Prunus armeniaca]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIGYVRGGGAVPPACCNGIRNV
NNLARTTPDRRTACNCLKQLSGSISGVNPNNAALPGKCGVNIPYKISISTNCAAVK

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

MGVFTYETEFTSVIPPEKLFKAFILDADNLIIPKVAPTAVKGTEILEGDGGVGTIKKVTFG
EGSQYAYVKKHRVDGIDKDNLSYSYTLIEGDALSDVIENIAYDIKLVASPDGGSIKVTTS

YHTKGDVEIKEEQVKAGKEKAAGLFLKVEAYLLANPDAYN
>AAF26449.1 Pru av 3; lipid transfer protein [Prunus avium]
MACSAMTKLALVVALCMVSVPIAQALTCGQVSSNLAPCIAYVRGGGAVPPACCNGIRNI
NNLAKTTADRQTACNCLKQLSASVPGVNANNAALPGKCGVNPYKISPSTNCATVK
>ADR66943.1 Pru av 3; lipid transfer protein [Prunus avium]
MACSAMTKLALVVALCMVSVPIAQALTCGQVSSNLAPCIPYVRGGGAVPPACCNGIRNI
NNLAKTTADRQTACNCLKQLSASVPGVNANNAALPGKCGVNPYKISPSTNCATVK
>ADR66944.1 Pru av 3; lipid transfer protein [Prunus avium]
MACSSMTKLALVVALCMVSVPIAQALTCGQVSSNLAPCIAYVRGGGAVPPACCNGIRNI
NNLAKTTADRQTACNCLKQLSASVPGVNANNAALPGKCGVNPYKISPSTNCATVK
>AAC02632.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
avium]
MGVFTYESEFTSEIPPPRLFKAFLVLDADNLVPKIAPQAIKHSEILEGDGGPGTIKKITFG
EGSQYGYVKKHIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIKSTSH
YHTKGNVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN
>AAS47035.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
avium]
MGVFTYSDESTSVIPPPRLFKALVLEADTLIPKIAPQSVKTAIEIVEGDGGVGTIKKISFG
EGSHYSYVKKHRIDGLDKDNFVYNYTLVEGDALSDKIEKITYEIKLVASADGGSIKSTSN
YHTTGDEVIKEEDVKAGKEKATGLFKLIENYLAANPDACN
>AAS47036.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
avium]
MGVFTYADESTSVIPPPRLFKALVLEADTLIPKIAPQSVKSAEIVEGDGGVGTIKKISFG
EGSHYSYVKKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTSN
YHTTGDEVIKEEDVKAGKEKATGLFKLIENYLVANPDAYN
>AAS47037.1 Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
avium]
MGVFTYADESTSVITPPRLFKALVLEADTLIPKIAPQSVKGAEIVEGDGGVGTIKKISFG
EGSHYSYVKKHRIDGLDKDNFVYSYSLVEGDALSDKVEKISYEIKLVASADGGSIKSTSN
YHTTGDEVIKEEDVRAGKEKATGLFKLIENYLVANPDAYN
>1H20_A Pru av 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus avium]
GVFTYESEFTSEIPPPRLFKAFLVLDADNLVPKIAPQAIKHSEILWGDGGPGTIKKITFGE
GSQYGYVKKHIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIKSTSHY
HTKGNVEIKEEHVKAGKEKASNLFKLIETYLKGHDPDAYN
>AAD29411.1 Pru av 4; profilin [Prunus avium]
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAFKPEEIAAILKDLDQPGTL
APTGLFLGGTKYMIQGEAGAVIRGKKGSGGITVKKTNQALIIGIYDEPLTPGQCNMIVE
RLGDYLIEQGL
>AAB38064.1 Pru av 2; thaumatin-like [Prunus avium]
MMKTLVVVLSLSLTILSFGGAHAATISFKNNCPYMWVPGTLTSDQKPQLSTTGFELASQA
SFQLDTPVPWNGRFWARTGCSTDASGFVFCATADCASGQVMCNGNGAIPPATLAEFNIPA
GGGQDFYDVSLVDGFNLPMSVTPQGGTGDCKTASCPANVNAVCPSELQKKGSDGSVVACL
SACVKFGTPQYCTPPQNTPETCPPTNYSEIFHNACPDAYSAYDDKRGTFCTCNGGPNYA
ITFCP
>P82534.1 Pru d 3; lipid transfer protein [Prunus domestica]
ITCGQVSSNLAPCINIVKGGGAVPPACCNGIRNVNLLARTTADRRACNCLKQLSGSIPG
VNPNNAAALPGKCGVNPYKISASTNCATVK
>ADN39440.1 Pru du 6; 11S globulin, cupin [Prunus dulcis]
MAKAFVFSLCLLLVFNGLAARQSQLSPQNCQLNQLQAREPDNRIQAEAGQIETWVFNQ
EDFQCAGVAASRITIQRNLHLPYSNAPQLIYIVQGRGVLGAVFSGCPETFEESQQSSQ

QGRQQEQEQERQQQQQGEQGRQQGQQEQQQERQGRQQGRQQQEEGRQQEQQQGQQGRPQQ
QQQFRQFDRHQKTRRIREGDVVAIPAGVAYWSYNDGDQELVAVNLFHVSSDHNQLDQNP
KFYLAGNPENEFNQQGSQPRQQGEQGRPGQHQQPFGRPRQQEQQSGNNVFSGFNTQLL
AQALNVNEETARNLQGQNDNRNQIIRVRGNLDFVQPPRGRQEREHEERQQEQQLQQERQQQ
GGQLMANGLEETFCSLRLKENIGNPERADIFSPRAGRISTLNHNLPIILRFLRLSAERGF
FYRNGIYSPHWNVNAHSVVYVIRGNARVQVWVWENGDAILDQEVQQGQLFIVPQNHGVIQQ
AGNQGFYFAFKTEENAFINTLAGRTSFLRALPDEVLANAYQISREQARQLKYNRQETIA
LSSSQRRRAVV

>ADN39441.1 Pru du 6; 11S globulin, cupin [*Prunus dulcis*]
CLLLLNGCLASRQHIFGQNKELNQLLEAREPDNHIQSEAGVTESWNPSPDPQFQLAGVA
VVRRTIEPNGLHLPSYVNAPQLIYIVRGRGVLGAVFPGCAETFEDSQPQQFQQQQQQQF
RPSRQEGGQGGQQFQGEDQQRHQRKIRHIREGDIIPAGVAYWSYNNGEQPLVAVSLLD
LNNDQNLQDQVPRRFYLAGNPQDEFNPQQQGRQQQQQQGQQGNGNIFSGFDTQLLAQA
LNVNPETARNLQGQDDNRNEIVRVQGLDFVSPFSRSAGGRGDQERQQEQQSQREREK
QREQEQQGGGGQDNGVEETFC SARLSQNIQDPSRADFYNPQGGRISVVRNHLPIILRYLR
LSAEKGVLYNNAIYTPHWHTNANALVYAIRGNARVQVWVWENGDPIIDDEVREGQLFLIPQ
NHAVITQASNEGFYISFRDENGFTNTLAGRTSVLRALPDEVLQNAFRISRQEARNLKY
NRQESRLLSATSPRGRRLMSILGY

>AGR27935.1 Pru du 6; 11S globulin, cupin, partial [*Prunus dulcis*]
DNHIQSEAGVTESWNPSPDPQFQLAGVAVVRRTIEPNGLHLPSYVNAPQFIYIVRGRGVLG
AVFPGCAETFEDSQPQQFQQQQQQQQQFRPSRQEGGQGGQQFQGEDQLDRHQRKIRHIREG
DIIPAGVAYWSYNNGEQPLVAVSLLDLSNDQNLQDQVPRRFYLAGNPQDEFNPQQQ

>CAA55009.1 Pru du 6; 11S globulin, cupin [*Prunus dulcis*]
MAKAFVFSLCLLLVFNGLAARQSQLSPQNQCQLNQLQAREPDNRIQAEAGQIETWVFNQ
GDFQCAGVAASRITIQRNLHLPSYSNAPQLIYIVQGRGVLGAVFSGCPETFEESQQSSQ
QGRQQEQEQERQQQQQGEQGRQQGQQEQQQERQGRQQGRQQQEEGRQQEQQQGQQGRPQQ
QQQFRQLDRHQKTRRIREGDVVAIPAGVAYWSYNDGDQELVAVNLFHVSSDHNQLDQNP
KFYLAGNPENEFNQQGSQPRQQGEQGRPGQHQQPFGRPRQQEQQNGNNVFSGFNTQLL
AQALNVNEETARNLQGQNDNRNQIIQVRGNLDFVQPPRGRQEREHEERQQEQQLQQERQQQ
GEQLMANGLEETFCSLRLKENIGNPERADIFSPRAGRISTLNHNLPIILRFLRLSAERGF
FYRNGIYSPHWNVNAHSVVYVIRGNARVQVWVWENGDAILDQEVQQGQLFIVPQNHGVIQQ
AGNQGFYFAFKTEENAFINTLAGRTSFLRALPDEVLANAYQISREQARQLKYNRQETIA
LSSSQRRRAVV

>P82952.1 2S albumin, conglutin, partial [*Prunus dulcis*]
TKSQTHVPIRPNKLVKQKDRATN

>COMPARE023 2S albumin, conglutin, partial [*Prunus dulcis*]
VTXEEGXYSISDQSKVGE

>COMPARE022 7S globulin, vicilin, beta-conglutin, partial from QFG58557.1 [*Prunus dulcis*]

MAIKITIKASYKLPFFFFFFLSTLFLASSSVTPLINALSDYHNQKCCQQSICRGVGGRHSL
RSKDHPQDAREEYFYCSQSCGTSEDPEQCETECRERFDEQLKKEAEEQQKQEEEEEEGP
TFNPNPYFPKFLRPRFLAEEGAYFVLGSEFARLSHLLRGRIQNYRAALLQTTPTGTFVLP
YHLDAESIFVWVWNGRGTLLVMKDTKQSFKIENGDVIRVPAGATTYLINNHTTENLSLVQ
LFQPVNTPDLFEFFPAGYKDPEPGSDYSFLHGTESYYSVFSNDLLEAAFDVPREQLEKA
FGQQKREGMIIRASKEQLDALSKQAYPWWRKLVPSMGSDLNFNLLSQRPLHSNNYKGFY
EASPQEFKQLQDMNVSAMLDINPEAMMVPHYNSKATYLMVVDGMGYFEMACPKFTIPA
SEEMEYQEEQADQQSGVFSKVSGLSLGDFVIVIPAGHPVSIVAQNNNNNNNNNNGNQNK
LRIVGFGINAGNIRNFLAGQEGNIMKQMEREAQTFTFGQEMEQLTSQKQSYFVPASRR
GSSTEKA

>QD073345.1 Pru du 8; cysteine-rich anti-microbial protein [*Prunus dulcis*]

MATMTKAELPLLVLFLSTLLLATSVPVRAQVTCEEGCYSISDQSKVGECLQMCSHGQS
CEDRCMREARWPQQEQCLRMCRQQEQGHHLPCREQCIRSPDREMCERACQQQQGGGR
QCLQRCKMITRDPRERLKCVRTCTQGQQQGVFQGGQQQQVEQQCRQHCQSERDPMRQQE
CQEYCVGQMMQQEYEQQCRSRCQWERPRREQQEQEQEECTEKIRQLEQCQEGCKIQGGY
PQQEQCRMCREQFEQGGGIRMVA
>COMPARE00326 Pru du 8; cysteine-rich anti-microbial protein, partial from
A0A314YX39 [Prunus dulcis]
AQVTCEEGCYSLSQSKVGECLQMCSHGQSCEDR
>COMPARE00327 Pru du 8; cysteine-rich anti-microbial protein, partial from
A0A314YX39 [Prunus dulcis]
WPQQEQCLR
>COMPARE00328 Pru du 8; cysteine-rich anti-microbial protein, partial from
A0A314YX39 [Prunus dulcis]
RCMQVEQQGVFQGGQQQQQQVEQQCRQHCQSERDPMRQQEQEDCVGQMMQQEYEQQCR
>COMPARE00329 Pru du 8; cysteine-rich anti-microbial protein, partial from
A0A314YX39 [Prunus dulcis]
REQQEQEQEECTEKIRQLEQCQEGCKMQGQYGPQQEQCR
>COMPARE00325 Pru du 10; mandelonitrile lyase 2, partial [Prunus dulcis]
DFYQCSFSSLPFTTTPFFGFFPSASYPLPNSTFAHFASKVAGPLSYGSLTLKSSSNVRVSP
NVKFNYYSNLTDLSHCVSGMKKIGELSTDALKPYKVEDLPGVEGFNILGIPLPKDQTD
AFETFCRESVASYWHYHGGCLVGKVLGDGFRVTGINALRVVDGSTFPYTPASHPQGFYLM
LGRYVGIKILQER
>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
KIIFSNAPGLTATGVIYRDSNGTPHQAFVR
>AAL91662.1 Pru du 4; profilin [Prunus dulcis]
MSWQYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMVIQGEAGAVIRGKKGSGGITVKKTNQALIIGIYDEPLTPGQCNMIVE
RLGDYLIEQGL
>ACE80974.1 thaumatin-like [Prunus dulcis]
MMKTLVVVLSLSLTLSSFGGAHAATISFKNNCPYTVWPASFGNPQLSTTGFEPLSQASFP
LDTPAPWSGRFWARTGCTDASGKFVCETADCDGSLMCMNGKTGIPPATLAEFTIAAGGGQ
DYVDVSLVDGFNLMSVTPQGGTGTCTGSCAANVNAVCPSELQKIGSDGSVVACLSACV
KFNQPYCCTPPQETKEKCPPTNYSQIFHDQCPDAYSAYDDNKGLFTCSGGPNYLITFC
P
>ACE80939.1 pathogenesis related protein, PR-10, Bet v 1-like [Prunus dulcis x
Prunus persica]
MGVFTYESEFTSEIPPPRLFKAFLVDADNLVPKIAPQAIKHSEILEGDDGGPGTIKKITFG
EGSQYGYVKKHIDSIDKENHSYSYTLTEGDALGDNLEKISYETKLVASPSGGSIKSTSH
YHTKGDVEIKEEHVKAGKEKASNLFKLIETYLKGHPDAYN
>ACE80972.1 profilin [Prunus dulcis x Prunus persica]
MSWQTYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGILNDFNEPGSL
APTGLYLGGTKYMVIQGEPAVIRGKKGPGGVTVKKSTLALLIGIYDEPMTGQCNMIVE
RLGDYLVEQGL
>ACE80955.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]
MMKTLVAVLSLSLTLSSFGGAHAATMSFKNNCPYTVWPASFGNPQLSTTGFEPLSQASQ

LDPVPWSGRFRWARTRCSTDASGKFCVETADCDGQMLCNGKTGIPPATLAEFTIAAGGG
QDFYDVS�VDGFNLPM SVTPQGGTGTCKMGSCAANVNLVCPSELQKIGSDGSVVACL SAC
VKFGEPQYCCTPPQETKEKCPPTNYSQIFHEQCPDAYSYAFDDNKGLFTCSGGPNYLITF
CP

>ACE80956.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFELATG
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA
SNGGQDFYDVS�VDGFNLPM AVAPQGGTGECKASTCPADV NKVCPAQLQVKGSDGSVIAC
KSACLAFNQPYCCTPPNDKPETCPPTDYSKIFKTQCPQAYSYAYDDKSSTFTCSASPDY
LITFCP

>ACE80957.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFELATG
ISNSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAVPPATLVEITIA
ENGGQDFYDVS�VDGFNLPM SVAPQGGTGECKASTCPADINKVCPAELQVKGSDGSVIAC
KSACLALNQPYCCTPPNDKPETCPPTDYSKLFKTQCPQAYSYAYDDKSSTFTCSGRPDY
LITFCP

>ACE80958.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFKLATG
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA
SNGGQDFYDVS�VDGFNLPM SVAPQGGTGTCKKASTCPANVNAACPAQLQVKGSDGKVIAC
KSACLAFNQPKYCCTPPNDKPATCPPTDYSRFFKTQCPQAYSYAYDDKSSTFTCNGRPDY
LITFCP

>ACE80959.1 Pru p 2; thaumatin-like [Prunus dulcis x Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKPQLSLTGFKLATG
ISRSVDAPSPWSGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA
SNGGQDFYDVS�VDGFNLPM SVAPQGGTGTCKKASTCPADINKVCPAPLQVKGSDGSVIAC
KSACLAFNQPKYCCTPPNDKPETCPPTDYSKLFKTQCPQAYSYAYDDKSSTFTCSGRPDY
LITFCP

>XP_016648029.1 Pru m 7; gibberellin-regulated protein [Prunus mume]
MKLGFATFLLVCLLLSSSVFEVTMAGSSFCDSKCGVRCSKAGYQERCLKYCGICCEKCHC
VPSGTYGNKDECPCYRDLKNSKGNPKCP

>P86888.1 Pru p 7; gibberellin-regulated protein [Prunus persica]
GSSFCDSKCGVRCSKAGYQERCLKYCGICCEKCHCVPSGTYGNKDECPCYRDLKNSKGNP
KCP

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

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

>ADR66939.1 lipid transfer protein [Prunus persica]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIPYVRGGGAVPPACCNGIRNV
NNLARTTPDRQAACNCLKQLSASVPGVNPNNAAALPGKCGVSIPYKISASTNCATVK

>AGW21344.1 lipid transfer protein [Prunus persica]
MAYSAMTKLALVVALCMVSVPIAQAITCGQVSSSLAPCIPYVRGGGAVPPACCNGIRNV
NNLARTTPDRQAACNCLKQLSASVPGVNPNNAAALPGKCGVSIPYKISASTNCATVK

>COMPARE237 Pru p 9; pathogenesis related protein, PR-1, partial from
XP_007199020.1 [Prunus persica]
MAFNTKLLLAICCVALVFTLV SANISK

>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
>ABB78006.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
persica]
MGVFTYESEFTSEIPPPRLFKAFLVLDADNLVPKIAPQAIKHSEILEGDGGPGTIKKITFG
EGSQYGYVVKHKIDSIDKENHSYSYTLIEGDALGDNLEKISYETKLVASPSGGSIKSTSH
YHTKGDVEIKEEHVKAGKEKASNLFKLIETYLKGHPDAYN
>AJE61290.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
persica]
MGVFTYSDESTSVIPPPRLFALVLEADTLIPKIAPQSVKSAEIVEGDGGVGTIKKISFG
EGSHYSYVVKHRIDGLDKDNFVYNYTLVEGDALSDKVEKITYEIKLVASADGGSIKSTSN
YHTKGDVEIKEEDVKAGKEKATGLFKLIENYLVANPDAYN
>AJE61291.1 Pru p 1; pathogenesis related protein, PR-10, Bet v 1-like [Prunus
persica]
MGVFTYETEFTSVIPPEKLFKAFILDADNLIPKIAPTAVKDTEILEGDGGVGTIKKVTFG
EGSQYGYVVKHRIDGIDKDNLTYSYTLIEGDALSDVIEKIVYDIKLVASPNGGSIVKTISH
YHTKGDVEIKEEQVKAGKEKAAGLFLVEGYLLANPDAYN
>CAD37201.1 Pru p 4; profilin [Prunus persica]
MSWQAYVDDHLMCDIDGNRLTAAAILGQDGSVWSQSATFPAPFKPEEIAAILKDFDQPGTL
APTGLFLGGTKYMIQGEAGAVIRGKKKGGGITVKKTNQALIIGIYDEPLTPGQCNMIVE
RLGDYLIEQGL
>CAD37202.1 Pru p 4; profilin [Prunus persica]
MSWQAYVDDHLMCEIEGNHLSAAAIIGHDGSVWAQSATFPQLKPEEVTGILNDFNEPGSL
APTGLYLGGTKYMIQGEPAVIRGKKKGGGVTVKKSTLALLIGIYDEPMTGQCNMIVE
RLGDYLVEQGL
>P83332.1 Pru p 2; thaumatin-like [Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKQQLSLTGFELATG
ISRSVDAPSPWGRFFGRTRCSTDASGKFTCATADCGSGQVSCNGNGAAPPATLVEITIA
SNGGQDFYDVS LVDGFNL PMSVAPQGGTGKCKASTCPADINKVCPAPLQVKGSDGSVIAC
KSACLAFNQPKYCCTPPNDKPETCPPPDYSKLFKTQCPQAYSAYDDKSSTFTCSGRPAY
LITFCP
>P83335.1 Pru p 2; thaumatin-like [Prunus persica]
MMKTLGAVLSLSLTL LLSFGGAHAATMSFKNNCPYTVWPASFGNPQLSTTGFELASQASFQ
LDTPVPWGRFFWARTRCSTDASGKFCETADCDGQLMCNGKTGIPPATLAEFTIAAGGG
QDFYDVS LVDGFNL PMSVTPQGGTGCKMGSCAANVNLVCPSELQKIGSDGSSVACL SAC
VKFGEPQYCCTPPQETKEKCPPTNYSQIFHEQCPDAYSAYFDDNKGLFTCSGGPNYLITF
CP
>AEV57471.1 Pru p 2; thaumatin-like [Prunus persica]
MMKSQAALLGLTTLAILFFSGAHAAKITFTNKCSYTVWPGTLTGDQKQQLSLTGFELATG
ISNSVDAPSPWGRFFGRTRCSTDASGKFCATADCGSGQVSCNGNGAVPPATLVEITIA
ENGGQDFYDVS LVDGFNL PMAVAPQGGTGECKASTCPADVNAVCPAELQVKGSDGSVIAC
KSACLALNPQYCCTPPNDKPETCPPEYSKIFKDQCPQAYSAYDDKSSTFTCSARPDY
LITFCP
>BAH10154.1 tropomyosin [Pseudocardium sachalinense]
MDSIKKKMQAMKIEKENALDKSEQLDQKLDVEETKAKVEEDLSSLQKKYTNLENEFDKV
NEQYNESVVKLEASEKRVTECEDEIKGYTRRIQLLEDDLERTQVKLDEALLKLEDATKTA
DESERGRKVLERSIADDDRIDGLEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERA

TRLEAAEAKITELSEELSVVANCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA
EAERVVNLQKEVDRLEDELLAEKEKYKTISDELDQTFAELAGM
>COMPARE128 Pun g 14; chitinase, partial from G1uh28.1 [Punica granatum]
GDIAIYWQNG
>C0HKC0.1 Pun g 7; gibberellin-regulated protein [Punica granatum]
GSSFCDSKCAVRCSKAGVQD
>AHB19225.1 Pun g 1; lipid transfer protein [Punica granatum]
MASSGFLRLAGFVLVCMVAFASTVAEAGITCGQVSSSLAGCIQYARGNGAGPVPQACNGI
RSLNSAAKTTTPDRQAACRCLKSLASSISGINYGLVAGAPGKCGVSIPYKIAPSTNCDNVK
>AHB19226.1 Pun g 1; lipid transfer protein [Punica granatum]
MASKRFLNLLVPALFLCMVVAASVAVTCGQVTSSLTPCIPYARGVVAAPSAACCSGV
RSLNNAKTTTPDRQTACNCLKVIARSITGINYGRVGALPGKCGVSIPYKISPSTDCSRVK
>AHB19227.1 Pun g 1; lipid transfer protein [Punica granatum]
MTGSGLFKLACAVFAVALVAAPIATEAAVTTCGQVASSLAPCIPYARSAGGAVPPACCSGI
KTLDMARTTPDRQATCKCLKSASTSISGINYGLVASLPAKCGVNIPYKISPSTDCARVK
>AAC24001.1 Pyr c 5; isoflavon reductase-like protein, phenylcoumaran benzylic
ether reductase [Pyrus communis]
MASKSQILFIGGTGYIGKFIVEASAKAGYPTYVLLVREASLSDPAKSKVIENFKALGVNFV
LGDLYDHESLVKAIKQVDVISTVGHGQLADQGKIIAAIKEAGNVKRFPPSEFGNDVDRS
HAVEPAKSAFETKAKIRRAVEAEGIPYTYVSSNFFAGYFLPTLNQPGASSAPRDKVVILG
DGNPKAIFNKEDDIGTYTIRAVDDPRTLNVLYIRPPANTISFNELVSLWEKKIGKTLER
IYVPEEQLLKNIQEAAPLVNLSISHAVFVKGDHTNFEIEPSFGVEATALYPDVKYTTV
DEYLNQFV
>AAF26451.1 Pyr c 3; lipid transfer protein [Pyrus communis]
MASSAVIKLALVVALCMAVSVAHAITCSQVSANLAPCINIVRSGGAVPPACCNIGIKTING
LAKTTTPDRQAACNCLKNLAGSVSGVNPNGNAESLPGKCGVNPYKISTSTNCATVK
>AET05730.1 Pyr c 3; lipid transfer protein [Pyrus communis]
AHAITCSQVSSNLAPCINIVRSGGAVPPACCNIGIKTINGLANTTPDRQAACNCLKNLAGS
VSGVNPNGNAESLPGKCGVNPYKISTSTNCATVK
>AET05732.1 Pyr c 3; lipid transfer protein [Pyrus communis]
AHAITCSQVSSNLAPCINIVRSGGAVPPACCNIGIKTINGLANTTPDRQAACNCLKNLAGS
VSGVNPNGNAESLPGKCGVNPCKISTPTNCATVK
>AET05733.1 lipid transfer protein, partial [Pyrus communis]
AHAITCSQVTSNLGACIGYVKNGGVPPACCNIGIRTVNGLARTTADRQTTNCLKSLAGS
IKGVNPNNAATLPGKCGVNPFKISTSTNCATVK
>065200.1 Pyr c 1; pathogenesis related protein, PR-10, Bet v 1-like [Pyrus
communis]
MGLYTFENEFTSEIPPPRLFKAFLVDADNLIPKIAPQAIKHAEILEGNGGPGTIKKITFG
EGSQYGYVVKHRVDSIDEASYSAYTLIEGDALDTIEKISYEAKLVASGSGSTIKSISHY
HTKGDIEIKEEHVKAGKEKAHGLFKLIESYLKDHDPDAYN
>AAD29410.1 Pyr c 4; profilin [Pyrus communis]
MSWQAYVDDHLMCDIDGHHLTAAILGHDGSVWAQSSTFPKFKPEEITAIMKDFDEPGSL
APTGLHLGGTKYMIQEGGAVIRGKKGSGGVTVKKTSQALVFGIYEEPLTPGQCNMIVE
RLGDYLIDQGL
>ABZ81045.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus
alba]
MGVFTHESEQETSVIAPARLFKALFLDSNLIQKVLQAIKSTEIEGNGGPGTIKKITFG
EASKFKYAKHRIDALDPENCTYSFSVIEGDALTMESVSTEIKCVASPDGGSIMKSTTKY
QTKGDFQLKEEQIQAIEKAAGLLKAVEAYLVAHPDLYK
>ABZ81047.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus

alba]

MGVFTHESQETSVIAPARLFKALFLSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG
EGSHLKHAKHRIDVIDPENFTYSFSVIEGDALFDKLENVSTETKIVASPDGGSIAKSTSK
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDLYK

>ABZ81046.1 Que a 1; pathogenesis related protein, PR-10, Bet v 1-like, partial
[Quercus alba]

MGVFTYESEDASVIPPARLFKAFVLSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG
EGSHLKHAKHRIDVIDPENFTYSFSVIEGDALFDKLENVSTETKIVASPDGGSIVKSTSK
YQTKGDFQLTDELIRGGKEKASEVFKAVEAYLVAHPDLYK

>QGS84240.1 Que i 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus
ilex]

MGVSTHESQETSVIPARLFKAFVLSDNLIQKVLQAIKSIERIEGNGGPGTIKKITFG
EASKFKYSKHRIDALDPENCTYSFSVIEGDALDMVSVSTEIKFVASPDGGSIKKSTTKY
QTKGDFQLKEEQIQATIEKITGLSKAVEAYLLAHPDLYT

>AUH28179.1 Que m 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus
mongolica]

MGVVAYESEDASVIPPARLFKAFVLSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG
EGSHLKHAKHRIDVIDPENFTFSFSVIEGDALFDKLENVSTETKIVASPDGGSIVKSTCK
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDGY

>COMPARE006 Que m 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus
mongolica]

MGVVAYESEDASVIPPARLFKAFVLSDNLIQKVLQAIKSTEIEGNGGPGTIKKITFG
EGSHLKHAKHRIDVIDPENFTFSFSVIEGDALFDKLENVSTETKIVASPDGGSIVKSTCK
YQTKGDFQLTDELIRGGKEKASGVFKAVEAYLVAHPDGY

>CAC83046.1 Ran e 1; calcium-binding protein, parvalbumin [Rana esculenta]
MPMTDLLAAGDISKAVSAFAAPESFNHKKFFELCGLKSKSKEIMQKVFHVLDDQDQSGFIE
KEELCLILKGFTPEGRSLSDKETTALLAAGDKDGDGKIGVDEFVTLVSES

>CAC95152.1 Ran e 2; calcium-binding protein, parvalbumin [Rana esculenta]
MSITDIVSEKDIDAALLESVKAAGSFNYKIFFQKVLGKSAADAKKVFIEILDRDKSGFIE
QDELGLFLQNFARASARVLSAETSFLKAGDSGDGKIGVEEFQALVKA

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

>CAC95153.1 calcium-binding protein, parvalbumin [Rana sp.]
MSITDIVSEKNIEAALLESVKAAGSFNYKIFFQKVLGKSAADAKKVFIEILDRDKSGYIE
KDELCLFLQNFARASARVLSAETSFLKAGDSGDGKIGVEEFQALVKA

>COMPARE00315 Rap v 2; paramyosin, partial [Rapana venosa]
ITELEDSCEQLR

>COMPARE00317 Rap v 2; paramyosin, partial [Rapana venosa]
VANAELTERNDNLQR

>COMPARE00318 Rap v 2; paramyosin, partial [Rapana venosa]
DTEDALRDAEAKLANAQAALNQLR

>COMPARE00319 Rap v 2; paramyosin, partial [Rapana venosa]
LREKDEEIEENIRR

>COMPARE00320 Rap v 2; paramyosin, partial [Rapana venosa]
ELEGALDNANRANAAYLQKQIK

>COMPARE00316 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]
QLEENENAGLQR

>COMPARE00321 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]
LADELRLQEQENYK

>COMPARE00322 Rap v 2; paramyosin, partial from QPB41107.1 [Rapana venosa]
VRDLEAELENEAR

>ANW10058.1 Ras k 1; calcium-binding protein, parvalbumin [Rastrelliger kanagurta]
MAFASVLKDAEITAALDGGKADGSDHKKFFKACGLAGKSGDDVKKAFIAIDQDKSGFIE
EEELKFLQNFKAGARTLSAETKAFKAGD TDGDGKIGVDEFAAMIKG

>P02761.1 Rat n 1; lipocalin, urinary globulin [Rattus norvegicus]
MKLLLLLLCLGLTLVCGHAE EASSTRGNLDVAKLNGDWF SIVVASNKREKIEENGSMRVF
MQHIDVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYV
MFHLINFKNGETFQMLMVLGRTKDLSSDIKEKFAKLCEAHGITRDNIIIDLTKTDRCLQAR
G

>AAA41198.1 Rat n 1; lipocalin, urinary globulin [Rattus norvegicus]
LLLLLCLGLTLVCGHAE EASSTSGNLDVAKLNGDWF SIVVASNKREKIEENGSMRVFMQHI
DVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYVMFHL
INFKNGETFQMLMVLGRTKDLSSDIKEKFAKLCEAHGITRDNIIIDLTKTDRCLQARG

>Q63213 Rat n 1; lipocalin, urinary globulin [Rattus norvegicus]
MKLLLLLLCLGLTLVCGHAE EASFERGNLDVDKLN DWF SIVVASDKREKIEENGSMRVF
VQHIDVLENSLGFTFRIKENG VCTEFSLVADKTAKDGEYFVEYDGGNTFTILKTDYDNYV
MFHLVNVNNGETFQMLMVLGRTKDLSSDIKEKFAKLCEAHGITRDNIIIDLTKTDRCLQAR
G

>AIS82657.1 Rhi o 1; aspartyl endopeptidase [Rhizopus oryzae]
MKFFALS LVVSAAFSVFTDAAITKIPIKKVHETATEKLSRYSHTGEYLTQKYFNSQRNNQ
PMETFKNLNP DGSANHG VPLSNYLNAYQYGEIEIGTPPQPFTVVFDTGSSNLWVPSHCTS
IACFLHKRYDSASSRTYSENGTEFAIQYGTGSLEGFISQDTLSVGGIQVEDQGFAESTKE
PGLTFAFAKFDGIFGLGYDTISVKHTIPPFYHVMNRDLVDEPLFSFWLNDANKDQDNGGE
LIFGGVDEDFEGDIHWSVRRKGYWEITMENIKFGDDYVDIDPVGAAIDTGSSLLVAPT
TVAALINKELGAEKNWAGQYVVD CNKVPSPLEFCFVFNGKDFCLEGKDYVLEVQGCISG
FMGMDIPEPAGPLWIVGDVFLRKFYSVYDLGNNRVGLAPSK

>ALM24136.1 Rhi o 2; cyclophilin [Rhizopus oryzae]
MSNPKVFFDVSANSKPLGRIVMELRADVVPQTAENFRALCTGEKGFYKGC SFHRVIPEF
MLQGGDFTNHNGTGGKSIYGNKFRDENFTLKHTGPGDLSMANAGPNTNGSQFFITTIKCS
WLDGKHVVFGRVTEGMDVVQNIESLSPNGTPRAKIIIDNCGQL

>AAP30720.1 Rho m 1; enolase [Rhodotorula mucilaginosa]
MAISKIHSRYVYDSRGNPTVEVELTTEKGTFRSIVPSGASTGVHEALELRDGDKSKWLK
GVLKAVANVNDTIAPALIEANIDVADQAKIDEFLKLDGTPNKAKLGANAILGVSLAAAK
AGAAQKDVPLYKHIADISKAKEGKFVLPVPFQNVLNGGSHAGGDLAFQEFMIVPSGAPSF
SEGLRIGSEVYHHLKSLTKKKYQGSAGNVGDEGGVAPDIKTAKEALDLIVSAIEAAGYTG
QVDIAMDVASSEFYKDGLYDLDFKNPNSDKSKWITGPQLAELYEQLLNEYPIVSIEDPFA
EDDWEAWSHFFSKVEGKTQIVGDDLTVTNPIRIKKA IETKAADALLLVNQIGTLTESIQ
AANDSYAAGWGMVSHRSGETEDTFIADLSVGIRSGQTKTGAPARSERLAKLNQILRIE
ELGDKAIYAGKDFHKAHSL

>AAT37679.1 Rho m 2; serine protease [Rhodotorula mucilaginosa]
TMELLEDLIEQVRQLPMVNFIEKNSLVHANEFTVAKGAPWGLARISHRDPLSLG SFDQYL
YDSNGGTGVTSYVIDTG VNVHHEQFEGRAKWKGTIPQGEDEDEDGNGHGTHCAGTIGSNAY
GVAKNAEIVAVKVLRSNGSGSMSDVIKGVEFAVKSHQDSVKKGKNSFSTANMSLGGGKSP
ALDLAVNAAVKAGLHFAVAAGNENQDACNTSPASAENAITVGASTISDARAYFSNYGKCV
DIFAPGLNILSTYIGSAAATAYLSGTSMASPHIAGLLTYYSLSLQPSSEFFIGAEGITP
AQLKKNLIAFGTPDVLADIPADTPNILAFNGAGQNLTKFWGH

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

IQQGQLHGEESERVAQRAGEIVSSCGVRCMRQTRTNPSQQGCRGQIQEQQLNRQCQEYIK
QQVSGQPPRRSDNQERSLRGCCDHLKQMQSQRCEGLRQAIEQQQSQGQLQGQDVFEAFR
TAANLPSMCGVSPTECRF
>ABG54494.1 Rub i 3; lipid transfer protein [Rubus idaeus]
MACSAVMKLALVALLCIVVAVPVAQAITCGQVTQNVAPCFNYVKNGGAVPAACCNGVRNL
NSQAKTTADRQOTCNCLKNAAGSIPGLNPSLAAGLPGKCGVSVPYKISTSTNCATVK
>ABG54495.1 Rub i 1; pathogenesis related protein, PR-10, Bet v 1-like [Rubus
idaeus]
YTSVIPPPKLFKAFVLDADNLIPKIAQAVKSVEIIEGDGGVGTVKKIHLGEGTEHSYVK
HKIDGLDKVNFVYSYSITEGDALGDKIEKISYEIKLVASGRGSIKTTSHYHCKGGAEIK
EEQVKD GKERAAGL FKI
>NP_001133181.1 Sal s 3; aldolase [Salmo salar]
MPHAFPFLLTPDQKKELSDIALKIVAKGKILAADESTGSVAKRFQSINTENTEENRRLYR
QLLFTADDRAGPCIGGVIFFHETLYQKTDAGKTFPEHVKS RGVVVG I KVDKGVVPLAGTN
GETTTQGLDGLYERCAQYKKDGCDFAKWRCVLKITSTTPSRLAIMENCNVLARYASICQM
HGIVPIVEPEILPDGDHDLKRTQYVTEKVLAAAMYKALSDHHVYLEGTL LKPNMVTAGHSC
SHKYTHQEIAMATVTALRRTVPPAVPGVTF LSGGQSEEEASINLNMNQCP LHRPWALTF
SYGRALQASALKAWGGKPGNGKAAQE E FIKRALANSLACQGYVASGDSAAAGDSL FVAN
HAY
>CBL79147.1 Sal s 3; aldolase [Salmo salar]
MPHAFPFLLTPDQKKELSDIAHKIVAQKGI LAADESTGSVAKRFQSINTENTEENRRLYR
QLLFTADERAGPCIGGVIFFHETLYQKTDAGKTFPQHVKSRGWL VG I KVDKGVVPLAGTN
GETTTQGLDGLYERCAQYKKDGCDFAKWRCVLKITSTTPSRLTIMENCNVLARYASICQM
HGIVPIVEPEILPDGDHDLKRTQYVTEKVLAAAMYKALSDHHVYLEGTL LKPNMVTAGHSC
SHKYTHQDIAMATITALRRTVPPAVPGITFLSGGQSEEEASINLNMNQCP LHRPWAIF
SYGRALQASALKAWGGKPKNGKAAQE E FIKRALANSLACQGYVSSGDSAAAGDSL FVAN
HAY
>CAA66403.1 Sal s 1; calcium-binding protein, parvalbumin [Salmo salar]
MACAHLCKEADIKTAL EACKAADTF SFKTF FHTIGFASKSADDVKKAFKVIDQDASGFIE
VEELKLF LQNF C PKAREL TDAETKAF LKAGDADGDGMIGIDEFAVLVKQ
>Q91483.3 Sal s 1; calcium-binding protein, parvalbumin [Salmo salar]
MSFAGLNDADVA AALAACTAADS FNHKAFFAKVGLASKSSDDVKKAFYVIDQDKSGFIEE
DELKLF LQNF SASARAL TDAETKAF LADGDKDGDGMIGVDEFAAMIKG
>ACI68103.1 Sal s 1; calcium-binding protein, parvalbumin [Salmo salar]
MACAHLCKEADIKTAL EACKAADTF NFKTF FHTIGFASKSADDVKKAFKVIDQDASGFIE
VEELKLF LQNF C PKAREL TDAETKAF LKAGDADGDGMIGIDEFAVLVKQ
>ACH70931.1 Sal s 2; enolase [Salmo salar]
MSITKIHAREILDSRGNPTVEVDLYTAKGRFRAAVPSGASTGVHEALELRDGDKSRYLGK
GTVKAVDHVNKDIAAKLIEKKFSVVDQEKIDHFMLELDGTENKSKFGANAILGVSLAVCK
AGAAEKGVPLRYRHIADLAGHKD VILPCPAFNVINGGSHAGNKLAMQEFMILPIGASNFHE
AMRIGAEVYHNLKNVIKAKYKDATNVGDEGGFAPNILENNEALELLKTAIEKAGY PDKI
IIGMDVAASEFYKAGKYDLDFKSPDDPARYITGDQLGDLYKSF IKGYPVQSIEDPFDQDD
WAAWTKFTA AVDIQVVGDDLTVTNPKRIQQAVEKKACNCLLLKVNQIGSVTESIKACKLA
QSNGWGVMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEEELGAK
AKFAGKDYRHPKIN
>CBL79146.1 Sal s 2; enolase [Salmo salar]
MSILKIHAREIFDSRGNPTVEVDLYTKKGLFRAAVPSGASTGIYEALELRDNDKTRYLGK
GVKRSVKYINEFLAPALCNQDVSVLEQEKVDQLMLDMDGTENKSKFGANAILGVSLAVCK
AGAAEKGVPLRYRHIADLAGNPNVILPVPAFNVINGGSHAGNKLAMQEFMTLPVGASTFKE
AMRIGAEVYHNLKNVIKKNYGQDATNVGDEGGFAPNILENKEALELLKEAIGKAGYTDKI

VIGMDVAASEFYKDGKYDLDFKSPDDPSRYITPDQLGDLYKSFVKDYPVVSIEDPFDQDD
WAAWSKFTAETSIQVVGDDLTVTNPKRIAKGVADKACNCLLLKVNQIGSVTESLQACKMA
QTNGWGMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLLRIEEEELGDK
AVFAGKNFRHPI

>AC034814.1 Sal k 3; cobalamin independent methionine synthase [Salsola kali]

MASHVVGYPYPRMGPKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQADAGIKYIPSN
TFAYYDQVLDTTAMLGAVPARYGFNGGEIGFDLYFSMARGNASLPAMEMTKWFDNYHYI
VPELGPEVKFAYSSHKAVDEYKEAKALGVDTVPVVLVGPVSYLLLSKAAKGVEKSFPLLSL
LPKILPVYKEVIAELKAAGASTIQFDEPTLVMDLESHQLKAFTDAYADLESTLSGLNVLV
ETYFADLTPEAYKTLVSLNGVTAFGFDLVRGKTKLDLIKSGFSPGKYLFAGVVDGRNIWA
NDLAASLTLQSLIVGKDKLVVSTSCSLLHTAVDLVNETKLDDEIKSWLAFAAQKQVLE
VNALAKALAGQKDEAFFSANAAALASRKSSPRVTNEAVQKAAAGLKGSDHRRATTVSARL
DAQQKKNLNPVLPPTTTIGSFPQTVELRRVRREYKAKKISEEEYVKAIKEEISKVVKLQEE
LDIDVLVHGEPERNDMVEYFGEQLSGFAFTVNGWVQSYGSRVCPPIIYGDVSRPKAMTV
FWSSLAQSMTSRPMKGMTGPVTILNWSFVRNDQPRHETCYQIALAIEDEAEDLEKAGIN
VIQIDEAALREGLPLRKS GHGFYLQWAVHSFRITNVGIQDTTQIHTHMCYSNFNDIIHSI
IDMDADVITIENSRSDEKLLSVFREGVKYAGIGPGVYDIHSPRIPPTTEELADRIRKMLA
VLESNVLWVNPDCGLKTRKYNEVNPALSNMVYAAKPI

>ADK22842.1 Sal k 5; Ole e 1-like [Salsola kali]

KGKGGHNLVHVKGMVYCDTCRIQFITRVSTMMEGATVSLQCRNLTAGTETFKAEAVIDKL
GMYTIKVDGDHEDDICQIVLVKSPGQECSEIPNDVYSEQAQKVTLSNNGEASDVRNANA
LGFLKKAPLPECPEVLKELDMYDVPGSVTQN

>P83181.1 Sal k 1; pectin methylesterase [Salsola kali]

PTITIGGPEYRTIFFDAYLGTSYVIVIKEPAEEFTTISDAVK

>AAT99258.1 Sal k 1; pectin methylesterase [Salsola kali]

MEEHVSMMLLVGFVLINIAFTSIAQLIPPNPAAELSWFQGAVKPVSEQKGLEPSVVQTESG
GVETIEVRQDGSQKFKTISDAVKHVKVGNTKRVIITIGPGEYREKVKIERLHPYITLYGI
DPKNRPTITFAGTAAEFVTVDSATVIVESDYSVGAHLIVTNSAPRPDGKRKGAQAGALRI
SGDRAAFYNCKFTGFQDTCDDKGNHFFDCYTEGTVDFIFGEARSLYLNTELVVPGDP
MAMITAHARKNADGVGGYSFVHCKVTGTGGTALLGRAWFDAARVVSFVSYCNLSDAKPEGW
SDNNKPEAQKTIIFGEYKNTGPGAAPDKRAPYTKQLTEADAKTFTSLEYIEAAKWLLPPP
KV

>AAX11261.1 Sal k 1; pectin methylesterase [Salsola kali]

QIIPPNPAAELSWFQGAVKPVSEQKGLEPSVVQAESGGVETIEVRQDGSQKFKTISDAVK
HVKVGNTKRVIITIGPGEYREKVKIERLHPYITLYGIDPKNRPTITFAGTAAEFVTVDSA
TLIVESDYFVGANLIVSNSAPRPAGKRKGAQASALRISGDRAAFYNCKFTGFQDTCDDK
GNHLFKDCYIEGTVDLIFGEARSLYLNTELVVPGDPMAMITAHARKNADGVGGYSFVHC
KVTGTGGTALLGRAWFEARVVSFVSYCNLSDAVKPEGWSDNNKPAQKTIFFGEYKNTGPG
AAADKRVPTYTKQLTEADAKTFTSLEYIEAAKWLLPPPKV

>AAX11262.1 Sal k 1; pectin methylesterase [Salsola kali]

QIIPPNPAAELSWFQGAVKPVSEQKGLEPSVVQAESGGVETIEVRQDGSQKFKTISDAVK
HVKVGNTKRVIITIGPGEYREKVKIERLHPYITLYGIDPKNRPTITFAGTAAEFVTVDSA
TLIVESDYFVGANLIVSNSAPRPDGKRK GARASALRISGDRAAFYNCKFTGFQDTCDDK
GNHLFKDCYIEGTVDLIFGEARSLYLNTELVVPGDPMAMITAHARKNADGVGGYSFVHC
KVTGTGGTALLGRAWFEARVVSFVSYCNLSDAVKPEGWSDNNKPAQKTIFFGEYKNTGPG
AAADKRVPTYTKQLTEADAKTFTSLEYIEAAKWLLPPPKV

>AC034813.1 Sal k 1; pectin methylesterase [Salsola kali]

QLIPPNPAAELSWFQGAVKPVSEQKGLEPSVVQAESGGVETIEVRQDGSQKFKTISDAVK
HVKVGNTKRVIITIGPGEYREKVKIERLHPYITLYGIDPKNRPTITFAGTAAEFVTVDSA
TLIVESDYFVGANLIVSNSAPRPDGKRKGAQASALRISGDRAAFYNCKFTGFQDTCDDK

GNHLFKDCYIEGTVDFFIFGEARSLYLNTELHVVPGDPMAMITAHARKNADGVGGYSFVHC
KVTGTGGTALLGRAWFEEARVVSFCNLSDAVKPEGWSDNNKPAAQKTIFFGEYKNTGPG
AAADKRVPTYKQLTEADAKTFTSLEYIEAAKWLP PPPKV

>ARS33724.1 Sal k 6; polygalacturonase [*Salsola kali*]
MKTFNLPLLVALFYLFVSVARSQGPIDITKFGAKPNADATSALLAAWKEACAAAAPAKIV
VPAGEFLLNAVKLQGPCKAPLTIEIAGNFKAPADVAQMKGEDTWVKIENVQGLTITCLPT
GGTFDGGQQAAWKQNKCAQSGMCSL PYNFRFNTLTNAQISGIKSLNSKLYHMGVMGCKN
ITLTGLTIDAPKDSLNTDGMHIGRSNGVHATNSKIGTGDDCISMGDGAVDVHVEGITCGP
GHGISIGSMGKFA NEAPNTGIFVKNCSTDTDNVRIKSWMNSFEASASDLHFEDITVTN
VLNPVIIDQEYCPYNHCKEKTPSKVKLSKISFKNVHGAAKSAE VVKLLCSSAVPCDGVEL
ADIDLTFPGGA AVSQCKNVKPIVTGKQNPVACGAPATPAAP

>ACS34771.1 Sal k 4; profilin [*Salsola kali*]
MSWQTYVDDHLMCEIEGTNNHLTAAAILGVDG SVWAQSANFPQFKPDEISAVVKEFDEAG
TLAPTGLHLGGTKYMIQGEAGQVIRGKKGPGGICVKKTGQALIFGIYDEP VTPGQC NMI
VERLGDYLV EQGM

>ADK22841.1 Sal k 4; profilin [*Salsola kali*]
MSWQAYVDEHLMCNIEDTGNHLTSSAIVGVDGSIWAQSSNFPQVKPQEIEAINKEFDGPN
TLAPTGLFLGG EKYMVIQGEPEGAVIRGKKGPGGVCIKKTTQALIFGIYDEP VAPGQC NMI
VERLGDYLV IEQGL

>AHL24658.1 Sal k 4; profilin [*Salsola kali*]
MSWQAYVDDHLMCEIEGTNNHLTAAAILGVDG SVWAQSANFPQFKPDEISAVVKEFDEAG
TLAPTGLHLGGTKYMIQSEAGQVIRGKKGPGGICVKKTGQALIFGIYDEP VTPGQC NMI
VERLGDYLV IEQGL

>CAX32966.1 calcium-binding protein, parvalbumin [*Salvelinus fontinalis*]
MACAHLCKEADIKTAL EACKAADS FNFKTFHTIGFASKSADDVKKAFKVIDQDASGFIE
VEELKLF LQNF CPKARVLTDAETKAF LKAGDADGDMIGIDEFAVWVKQ

>CAX32967.1 calcium-binding protein, parvalbumin [*Salvelinus fontinalis*]
MAFAGLNDADVA AALACTAADS FNHKAFFAKVGLAGKSND DVKKAFYVIDQDKSGFIEE
DELKLF LQNF SASARAL TDAETKAF LADGDKDGDGMIGVDEFAAMIKG

>SHD75397.1 apolipoporphin, partial [*Sarcoptes scabiei*]
MSARSAKFMYSRGNAGASGDL SVEYGTDLGALTRLEDKIRLLSDDLESEREMRQRIEREK
AELQIQVMSLSERLEEAEGSSESVEMNKKRDELAKLRKLL EDVHLESEETAHHLRQKH
QAAIQEMQDQLDQVQKAKNKS DKEKQKFQAEVFELLAQLETANKEKLTAMKTVEKLEYTV
HELNIKIEEINRTVIELTSQKTRLSQENTELIKEVHEHKMQLDNANHLKQQLAQQLEDTK
HRL EEEERKRASLENHAHTLEVELES LKVQLDEESEARLELERQLTKANGDAASWKS KYE
AELQAHADVEEELRRKMAQKISEYEEQLEALLNKCSSLEKQKSRLQSEVEVLIMDLEKAT
THAQQLEKRVAQLEKLNLDLKNKLEEV TMLMEQAQKEARAKAAELQKLQHEYEKLRDQRD
ALARENKKL TDDLAECKVFRHHD AHRSTNRRSKSNDWRTREKSYLLPTKKRKP YANKRR
LRINDLP SWLKYDTITRN VWHRRKRSKHLENNIKSRSNSLICDLK LKLNKPRSHDRRNI
KLKSLNWNCHWMLPIKPIL IYRKQSKNKPYKLR SFKHTMMRRQSNHCTGSSIGSHPKTMP
SVTSRAGRAKNRFGTSESCQTTSRTIAGSCRKSTYHHQCSCFSKQIGIGIRCSTKRLRSP
QRTQNFTSTETYHAQIYQGLISGGTGTISENGDRKEIFGARSSYPTCPYRRGRSQCFGWR
TCHCTGEQNSCDRSGRGTKTRDGN AKKRSTQGIVGAKRGGPQTNPIASRNGRQNERK
GQSLTTNARTGGNEPTKSDSCSTLPTIGSCRSSGSSIKSIVHPCQTPF

>AAS93669.1 cysteine protease [*Sarcoptes scabiei*]
MSFIRFFSIFLLCFV SFLVARI ECDEF EIKTFEQFKARFNKTYSNYFIETYRRRVFYRTL
KYVEENKHRGVSINAHADLTVNEFS AKYLSKAPKTEDLLDEYKLFSCDKFEGVKLGELDL
RKEGRVTKIREQLACGSCWAF SVTANVESLLLGSNCTRWSTNDWLS PQQLVDCASDHGCN
GEKTSTGLE YVQHKGIVKEGVYPYKARVGVCKHPCGPYYHIKSF CGISPPDPDQVKIALS
KTRSALSASII VYDVEHLKNYNGKLP LADDGKLIGEQLSHAINIVGYTQRNGVEVWIVRN

SWGETWGDHGYGYFKILPKRGVMGITRMVIVADLGKETVA
>AAS93675.1 cysteine protease [Sarcoptes scabiei]
MESKKFKSFLFQLIISAAIITRGYYFETTPSDAEENARLSDVRYTGEPDDPDFKLPDSFI
QKFKKDLRELTRKCRKGFRQARLEHPELQFCKIPKVFQKLPKWFDLRNLEFVTPTRDNS
TESKCKASWAFGPVASMESAWLESHDRIASDSFFLSPQNLIDCAGYQGCDDGGVDVIEAFN
YMKHKGIVKEEFYKYRAKKHRCRKRRLRARRYKIRSYCAICPATIFTIKKFLFKHTALT
VISVRNLTAFAKHIDDEILYEDEGTRVQRRLLVNVIVGWRHDDATDRDYWVVKNSWGKKWGM
GGYGFVDAENNPLHILDHNYLVVRKEDVIPFENEPEDFE
>AAS93676.1 cysteine protease [Sarcoptes scabiei]
LMRELTRKCRKGFRRARLEHPELQFCEIPKVFQKLPKWFDLRNLELVTPTRDNSTEKKCK
ASWAFGPVASMESAWLESHDRIASDSFFLSPQNLIDCAGYQGCDDGGVDVIEAFNYMKHKG
IVKEEFYKYKAKKHRCRKRRLRARRYKIRSYCAICPATIFTIKKFLFKHTALT
LTAFAKNIDDEILYEDEGPRVQRRLLVNVIVGWRHDDATDRDYWVVKNSWGKKWGMGGYGFV
DAENPFHILDHNYLVVRKEDVIPFENEPEDFE
>AA015607.1 glutathione S-transferase [Sarcoptes scabiei]
MSSKPTLGYWDLRGLGQSIRILLTYAGVDFVDKRYKIGSAPDFDRGEWLNDKFNGLDFP
NLPPYYIEGDVCLTQSIAILRYLGRKHKLDGQNEQEWRRITLCEQQIMDLLMALARICYDP
NFEKLLDLVAKLPDDLKLFKFLGDHGFVAGTNSYIDFLVYEYLIRVKIFAPEIFTKF
PNLNSYITRIESMPKISAYIKQQEPQLFNGPMAKWNTKY
>AAX37321.1 glutathione S-transferase [Sarcoptes scabiei]
MSSKPTLGYWNIRGLAQPIRMMLSYAGVDFVDKRYNYGPAPDFDRSEWLNEKFNGLDFP
NLPPYYIDGDVCLTQSLAILRYLARKHKLDGHNEQEWLRIALCEQQIVDLYMAMGRISYDP
NFEKLLKPDYLEKLPDNLKLFSEFLGDHPFVAGTNSYVDFVVEYLIRLKAAMPVEVFAKF
QNLGNVYVNRFEEMPKISAYLKQQQPQFFNGLMAKWNMKY
>SHD75396.1 tropomyosin [Sarcoptes scabiei]
MYEAIKKMQAMKLEKDNAIDRAEIAEQKARDANLRAEKSEEEVRGLQKKIQQIENELDQV
QEQLSAANTKLEEKALQTAEGDVAALNRRRIQLIEEDLERSEERLKIATAKLEEASQSA
DESERMKMLEHRSITDEERMDGLENQLKEARMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQIRISTAKLKDAEARAE
FAERSVQKLQKEVDRLEDELVHEKEKYKSISDELDTFAELLAI
>AA015613.1 unknown function [Sarcoptes scabiei]
FVELKKDKDLYSMKSNVKNRNEIFYENMDLEKNGKMNWYYKRNDRTWMDLDNAFNPRD
GTMKLVKVDRIYDIKLRKREPFYRGLHIEGNENALIKKGDHMSLVDPPLTNVLTKNLGI
VDMTLDLVSPNTKKAALKINSKDYLDHDGEITVSIFNPRMTWKHHTRKGMELNIDADI
TRKGLSITYSRKEPDDSTKVRYSRQGNQVSMEDVSKLIEGHANGTLTDGKIHVKGRESDF
EIESTYKVEDGKLMIEPTKTQNGKLEGLLSRKVPSHLVLETPRVKMNMKYDRFAPVKILK
LDYDGLNVEKHIDAIEYEPSNHYKYFTDGKS
>AAS93674.1 unknown function [Sarcoptes scabiei]
MERKQFNLLYQLILSVAIITRGYYFETTPSIDDENVRLSDLDWIGEPDDSDFKLPDSFI
RKFKQDLMRDLNKKCRNHFSSIIKLIHPGLQFCKVPKVVYQALPTWFDLRNLELVTPTRDNS
TEKQCKASWAFGPIASLESAWLESHDRIASDAFSLSAQNLIDCAGYQGCNGGVDVIEAFN
YLQEKGVVKEENYKYKGGKHACRWRLFYRRYKIKSYCAICPATVETIKKFLFKHTALT
VISVRNLTAFAKNIDDEILYEDEGPSVQRRLLVNVIGWRHDDATDRDYWVVKNSWGRKWGM
GGYGFVDAEENLFGILDQNYLLSVKDEVIPFEAEPDSDS
>AGM48615.1 unknown function, partial [Sarcoptes scabiei]
DLDNAFNPRDGTMLKLVKVDRIYDIKLRKREPFYRGLHIEGNENALIKKGDHMSLVDPPL
LNVLTKNLGI
VDMTLDLVSPNTKKAALKINSKDYLDHDGEITVSIFNPRMTWKHHTRKGMELNIDADI
TRKGLSITYSRKEPDDSTKVRYSRQGNQVSMEDVSKLIEGHANGTLTDGKIHVKGRESDF
EIESTYKVEDGKLMIEPTKTQNGKLEGLLSRKVPSHLVLETPRVKMNMKYDRFAPVKILK
LDYDGLNVEKHIDAIEYEPSNHYKYFTDGKSKRSGKGYSIKIDGKPKKALK

VDVDMPDFKF

>CAQ68366.1 Sar sa 1; calcium-binding protein, parvalbumin [Sardinops sagax]
MALAGLVKEADITAALEACKAADSFDHKAFFHKVGMMSGKSADELKKAFAIIDQDKSGFIE
EEELKLFQNFCKKARALTDGETKKFLKAGDNVGDGKIGIDEFNHLVKH

>BAH10151.1 tropomyosin [Scapharca broughtonii]
MDSIKKKMIAMKMEKENALDRSEQLEQKLRDTEEQKAKVEEELGAYQKKFSILENDFDTV
NTKWEDASVKLEEAEEKL TESEQEIASLTRKTTLLEDDIAKNEEKLSATQKLEEASHAA
DESERGRKVLERSFADDERIDALEAQLKEAKYIAEDADRKYDEAARKLAITEVDLERAE
ARLEAAEAKIIELEELTVVGANIKTLQVQNDQASQREDSYEETIRDLTANLKDAENRAT
EAERTVSKLQKEVDRLEDELLAEKERYKAISDELDTFAELAGY

>C37396 beta-expansin, partial [Schedonorus arundinaceus]
YTTEGGTKSEAEDVIPE

>D37396 beta-expansin, partial [Schedonorus arundinaceus]
YTTEGGTKSEVEDVIPEGWK

>Q7M1Y1 beta-expansin, partial [Schedonorus arundinaceus]
IAKVPPGNITAEYGDKWLDKSTFYGKPTGAGPK

>AAC67308.1 unknown function [Schistosoma japonicum]
MATTEYRLSLMEQFIRAFIEIDKDNNELIDKQELTKYCQQNQMDMKQIDPWIARFDTDKD
GKVSLEEFRCRGFLKVVWEVRREKEELKKDKEGKVVSTLPLDIQIIAATMSKAKQYNICCKF
KELLDKTSRTGDEVRAVANDLKAFLDSEYGRVWQVIILTGSYWMNFSHEPFLSMQFKYSN
YVCLLWRT PSS

>AAP06493.1 unknown function [Schistosoma japonicum]
MSADSWDNHCVTYVANCKLNLKMTAIDGSHLGTSPDFRIPPELILQLKSILDGGLDT
SIFFMGEKYIVLQHDSCLVSRGKSLIFYATGKICLVGQTVDDDQNNCTQGNFAISRM
RDHYERMGY

>XP_003030591.1 Sch c 1; glucoamylase [Schizophyllum commune]
MGLASTVSLALLGLCSLARAQTSAADAYVSAESPIAQAGILANIGPSGSKSHGAASGVII
ASPSTSNPDYLYTWRDAALVSRALVDEFIEGESSLQSVIDSYVSSQQKLQRVDNPSGSY
TSGGLGEPKFNIDLTAF TGAWGRPQRDGPALRAITLITYGNHLLSSGNTSYVTDTIWPVV
KADLDYVVSYWNQTGFDLWEEVSSSSFFTTAEQHTALRLGATFATAVGASASTYL TQADN
VLCFLQSYWNSNGGYATANTGGGRSGIDANTVLT SIHTFDIEAGCDSVTFQPCSDRALSN
LKVVYVDSFRGLYSINPTGATDPILTGRYKEDVYNGNPWYL TTFVAEQLYDALNTWDKL
GSLDVTSTSLAFFKQFDSSITAGTYASSTSEYATL TSAIRNWADGFLEVLADFTPADGGL
TEQIDKSSGNPTSAADLTWSYASAITAFKARGGAIPASWGAAGLTVPATCSTGGGGGSGG
DTVAVTLNVQATTVYGENIYVTGSVNQLANWSPDNAIALNADNYPTWSVTVNLPANTQIE
YKYIRKNNGQVTWESDPNRSITTSASGSFTQNDTWR

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

>CAX32965.1 Sco s 1; calcium-binding protein, parvalbumin [Scomber scombrus]
MAFASVLKDAEITAALDGCKAAGSFDHKKFFKACGLSGKSADEVKKAFAIIDQDKSGYIE
EEELKLFQNFKAGARALSDAETKAFLKAGDSGDGKIGVDEFAAMIKG

>AFA45340.1 Scy p 2; arginine kinase [Scylla paramamosain]
MADA AVIEKLEEGFKLEAATDCKSLLKKYLTKSVFDQLKGKKTSLGATLLDVIQSGVEN
LD SGVGVYAPDAEAYTLFAPLFDPIIEDYHKGFQTDKHPNKDFGDVNQFVNVDPDGKFV
ISTRVRCGRSMGYFPNCLTEAQYKEMESKVSSTLSNLEGELKGTYYPLTGMTKDVQQK
LIDDHFLFKEGDRFLQAANACRYWPTGRGIYHNDNKTFLVWCNEEDHLRIISMQMGDLG
QVYRRLVS AVNIEKRVPF SHHDRLGFLTFCPTNLGTTVRASVHIKLPKLAANREKLEEV
AGKYSLQVRGTRGEHTEAEGGVYDISNKRRLMGLTEFQAVKEMQDGILELIKIEKEMQ

>AFJ80778.1 Scy p 4; calcium-binding protein, sarcoplasmic calcium-binding protein

[Scylla paramamosain]

MAYSWDNRVKVVRYMYDIDNNGYLDKNDFECLALRNTLIEGRGEFNSDAYANNQKIMSN
LWNEIAELADFNKDGQVTVDEFKQAVQNLCCGKSFDFPPCFKTVIGRLFKTIDINGDGL
AGVDEYRLDCISRSAFSSVKEIDDAYAKLCTDDDKKAGGISLNRYQELYAQFISNPDEKC
NAVYLFGLKEVQ

>QFI57017.1 Scy p 9; filamin C [Scylla paramamosain]

MPSGKSDVPVIEDNRDGTVSVRYSPREEGLHELHVKYNAEHVQGSPPFKFHVDSIASGYVT
AYGPGLVHGITGEPANFTISTKDAGAGSSTLRGGLSLAVEGSSKAEISCHDNKDGTVSVS
YLPTAPGEYKVSVKFAEKHIRGSPYSVKITGEGRKRNQISVGSQSEVSLPGKVTDSDIKS
LNASIQAPSGLEEPCFLKKLPNGHLGISFTPREVGEHLVSVKRMGNHIANSPFKINVGEK
EVDGASKVKISGKCLSEGQTHKENQFTIDTRDAGYGGLSLSIEGPSKADIQCKDNEDGTL
TIGYTPTEPGYYIINLKFADNHVPGSPFTVKVTGEGTNRQTERIKRQREAVPLTEVGSQC
RLTFKLPGISPFDLGATVTSPPGVTEAAEIGEVEDGLYGVNFVPKELGVHTVSVKYQEMH
IPGSPFQFTVGPLKDGGHRVHAGGPGLERGEQMPNEFNVWTREAGAGSLAISVEGPSK
AEIDFKDRKDGSCYVSYVAEPGEYRVGIKFNDKHIPDSPYKVYITPSLGEARKVELAQL
PEQGSMPNKAQSLLVCKNGAKGTLDCFKVAPSGAEEDCFDLDLGDLYSVRFVPKEMGIH
YVHIKFNGIHIPGSPFRLRIGKDEADPAAVSVSGKGLESCVSGQKTDIFVDTCNAGAGTL
AVTIDGPSKVSMDCTEVEEGYKVRYPVLPVPGDYIYAVKYNAYHVVGSPWKVKCTGEAHAE
KGTIQESSVVVETVEKTKSGDKGHGHTIIPKFHSDANKVTSKGLGLKKAHINRQNNFTV
NASGAGNNILYVGVYGPKSPCEEVYIKHVGHNNYQVSYKVKERGNHILMVMWGEEHIPGS
PFKLDMF

>QDH76468.1 Scy p 3; myosin light chain [Scylla paramamosain]

MAADLSARDVERAKFAFSIYDFEGKGTMDAFYVGDCLRALNLNPTLAVIEKVGKTKKKE
KMLKVDDFLPIFAQVKKDKDAGSFEDFMEVLKLYDKTENGTMLYAELEHILLSLGERLEK
SELEPVLKDCCEDEDEDGFIPYEPFLKLTQLL

>APP94292.1 Scy p 8; triosephosphate isomerase [Scylla paramamosain]

MANQRKFVGGNWKMNMGDKAAIDGIISFMKGPLNADTEVVVGCPCQCYLMTREHMPANIG
VAAQNCYKTAKGAFTGEISPAMIKDCGCEWVILGHSERRNVFGEPDQLISEKVGHALEAG
LKVIPICIGEKLEERESNRTEEVVFAQMKALVPNISDWSRVVIAEPVWAIGTGKTATPEQ
AQDVHAKLRQWLRDNVSPQVAESTRIIYGGSVSAGNCKELAKTGDIDGFLVGGASLKPDF
VTIINARA

>ACV96855.1 arginine kinase [Scylla serrata]

MADAAVIEKLEEGFKKLEAATDCKSLLKKYLTKSVFDQLKGGKTSLGATLLDVIQSGVEN
LDSGVGVYAPDAEAYTLFAPLFDPIIEDYHKGFKQTDKHPNKDFGDVNQFVNVDPDGKVF
ISTRVRCGRSMEGYPFNPLTEAQYKEMESKVSSTLSNLEGEKGTYYPLTGMTKDQVQK
LIDDHFLFKEGDRFLQAANACRYWPTGRGIYHNDNKTFLVWCNEEDHLRIISMQMGDLG
QVYRRLVSAVNEIEKRVPFSSHDRGLGFLTFCTNLGTTVRASVHIKLPKLAANREKLEEV
AGKYSLQVRGTRGEHTEAEGGVYDISNKRMRGLTEFQAVKEMQDGILELIKMEKEM

>ABS12233.1 Scy p 1; tropomyosin [Scylla serrata]

MDAIAKKMQAMKLEKDNAMDRADTLEQQNKEANLRAEKTEEEIRATQKKMQQVENELDQA
QEQLSAANTKLDEKEKALQNAEGEVAALNRRIQLEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSLSDERMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAESGESKIVLEEEELRVVGNLKSLEVSEEKANQREETYKEQIKTLANKLKAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKYKSITDELDTFSELSGY

>CAQ72968.1 Seb m 1; calcium-binding protein, parvalbumin [Sebastes marinus]

MALAASLNAADITAALAACSGVDTFKHKDFFGKVGLSAKSADDIKNAFKVIDQDKSGFIE
EEELKFLQNFSATARALTEAETTAFLKAGSDGDGMIGMDEFAAMVKG

>CAQ72969.1 Seb m 1; calcium-binding protein, parvalbumin [Sebastes marinus]

MAFASVGLKDADIAAALDGCKDAGKFNHKTFFKTCGLSGKSSDEVKKAFAIIDQDISGFI
EEEELKLFLQTFKAGARALSDAETKEFLKAGSDGDGKIGADEWAAMVKQ

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

>CAH92627.1 berberine bridge enzyme [Secale cereale]
NYRAFALALLFCALSCQAAAAAYAPVPAKADFLGCLMKEIPARLLYAKSSPDYPTVLAQT
IRNSRWSSPQNVKPIYIITPTNASHIQSAVVCGRRHGIRLRVRSGGHDYEGLSYRSEKPE
TFAVVDLNMRAVSDGYARTAWVESGAQLGELYAIKNSPVLAFAPAGVCPSIGVGGNF
AGGGFGMLLRKYGIAAENVIDVKVDPNGKLLDKSSMSADHFWAVRGGGGESFGIVVSWQ
VKLLPVPPTVTVLKIPKTVQEGAILVKNWQLVGPALPGDLMIRIILAGNSATFEAMYLG
TCSTLTPLMSSKFPELGMNPSHCNEMSWIKSIPFIHLGKQNLDDLLNRNNTFKPFAEYKS
DYVYQPFKPVWEQIFGWLVKPGAGIMIMDPYGATISATPEAATPFPHRQGVLFNIQYVN
YWFAESAGAAPLQWSKDIYKFMPEYVSKNPRQAYANYRDIDLGRNEVVNDISTYSSGKVV
GEKYFKGNFQRLAITKGVDPQDYFRNEQSIPPLVEKY

>CAH92630.1 berberine bridge enzyme [Secale cereale]
NSRAFALVPLLICVLSCHAAVSYAAAPVPAKEDFFGCLVKEIPARLLYAKSSPAFPTVLA
QTIRNSRWSSPQSVKPLYIITPTNASHIQSAVVCGRRHGVIRVRSGGHDYEGLSYRSER
PEAFVVDLNMRAVVVDGKARTAWVDSGAQLGELYAIKNSPVLAFAPAGVCPTIGVGG
NFAGGGFGMLLRKYGIAAENVIDVKVVDANGTLLDKSSMSADHFWAVRGGGGESFGIVVS
WQVKLLPVPPTVTVFKIPKTVQEGAVELINKWQLVAPALPDDLIRIIFGGTAKFEAMY
LGTCKALTPLMSSRFPELGMNASHCNEMPWIKSVPFHILGKQATLSDLLNRNNTFKPFAE
YKSDYVYQVPKPVWAQIFVWLKPGAGIMVMDPYGAAISATPEAATPFPHRKDVLFNIQ
YVNYWFDEAGGAAPLQWSKDMYRFMEPYVSKNPRQAYANYRDIDLGRNEVVNDISTYASG
KVWGEKYFKGNFQRLAITKGVDPQDYFRNEQSIPPLLGK

>COMPARE186 Sec c 20; gamma secalin, partial [Secale cereale]
NMQVGPSGQVEWPQQQLPQPQQ

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

>CBG76811.1 Sec c 5; unknown function [Secale cereale]
MAVQQYTVALLFAVALVAGPAVSYGTYAPAAPGTQPKATTPEQKLMENINNGFKAAVEAA
AAVAPADKYKTFQTTFIKGSNKAADVLTAAASGQIPAQSDSMARLSTSLESSYKLAYDS
AEGATPETKYDITYVASLTESLRVISGAFEVHAVKPAVEEVKGVPAQQLKVVQIDAAAYRT
AATAANAAPTNDKFNVESSFNKAIKENTGGAYASYTFVPALESVAVKQAYAATVASAPEV
KYAVFQAALSKAINAMVEAEKDAKPAAAAAATATATATVGAAGAAAGGYKA

>Q7M263 Sec c 5; unknown function, partial [Secale cereale]
ADAGYAPAAPGTQPKA

>BAE54429.1 tropomyosin [Sepia esculenta]
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKTEEDLSTLQKKYSNLENDFDNA
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLEEDLERSEERL TSAQSKLEDASKAA
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE
ARLEAAEAKIVELEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA
EAERTVSKLQKEVDRELEDELLAEKERYKSISDELDTFAELAGY

>BAE54430.1 tropomyosin [Sepioteuthis lessoniana]
MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEDAKNKIEEDLSTLQKKYANLENDFDNA
NEQLTAANTNLEASEKRVAECESEIQGLNRRIQLEEDLERSEERFSSAQSKLEDASKAA
DESERGRKVLNRSQGDEERIDLLEKQLEEAKWIAEDADRKFDEAARKLAITEVDLERAE
ARLEAAEAKIVELEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAA
EAERTVSKLQKEVDRELEDELLAEKERYKTISDELDTFAELAGY

>AAD42944.1 Ses i 6; 11S globulin, cupin [Sesamum indicum]
MVAFKFLALLSLSLLVSAIAAQTREPRLTQGGQCRFQRISGAQPSLRIQSEGGTTELWDE
RQEQFQCAGIVAMRSTIRPNGLSLPNYHPSRLVYIERGQGLISIMVPGCAETYQVHRSQ
RTMERTEASEQQDRGSVRDLHQKVHRLRQGDIVAIPSGAAHWYNDGSEDLVAVSINDVN

HLSNQLDQKFRAYLAGGVPRSGEQEQARQTFHNIFFRAFDAELLSEAFNVPQETIRRMQ
SEEEERGLIVMARERMTFVRPDEEEGEQEHRGRQLDNGLLETFCTMKFRTNVESRREADI
FSRQAGRHHVDRNKLPIILKYMDLSAEKGNLYSNALVSPDWSMTGHTIVYVTRGDAQVQV
VDHNGQALMNDRVNQGMFVVPQYYTSTARAGNNGFEWVAFKTTGSPMRSPLAGYTSVIR
AMPLQVITNSYQISPNQAQALKMNRGSQSFLLSPGGRRS

>AAK15087.1 Ses i 7; 11S globulin, cupin [Sesamum indicum]
MALTSLLSFFIIVVTLIRGLSAQLAGEQDFYWDLQSQQHKLQARTDCRVERLTAQEPT
IRFESEAGLTFWDRNNQQFECAGVAAVRNVIQPRGLLLPHYNNAPQLLYVVRGRGIQGT
VIPGCAETFERDTQPRQDRRRRFRMDRHQKVRQFRQGDILALPAGLTLWFYNNNGGEPLITV
ALLDTGNAANQLDQTFRHFFLAGNPQGGRSYFGRPQTEKQQGETKNIFNGFDDEILADA
FGVDVQTARRLKGQDDLGRIVRAERLDIVLPGEERWERDPYSGANGLEETLCTAKL
RENLEPARADVYNPHGGRISLNSLTLVLSWLRLSAEKGVLYRNGLVAPHWNLNAHSI
IYITRGSGRFQVVGHTGRSVFDGVDVREGQLIIVPQNYVVAKRASQDEGLEWISFKTNDNA
MTSQLAGRLSAIRAMPEEVMTAYQVSRDEARRLKYNREESRVFSSTSRYSWPRSSRPMS
YMPKPFYVLDVIKSM

>AAD42943.1 Ses i 2; 2S albumin, conglutin [Sesamum indicum]
MARFTIVLAVLFAAALVSASAHKTVVTTVAEEGEEENQRGCEWESRQCQMRHCMQWMRS
MRGQYEEFSLRSEANQQQFEHFRECCNELRDVKSHCRCEALRCMMRQMQQEYGMQEQEQ
QMQMMQYLPRMCGMSYPTECRMPIFA

>AAK15088.1 Ses i 1; 2S albumin, conglutin [Sesamum indicum]
MAKKLALAAVLLVAMVALASATYTTTVTTTAIDDEANQQSQCRQLQGRQFRSCQRYL
SQGRSPYGGEEDEVLEMSTGNQQSEQLRDCCQQLRNVDERCRCCEAIRQAVRQQQEGGY
QEGSQQVYQRARDLPRRCNMRPQQCQFRVIFV

>ACI41244.1 Ses i 1; 2S albumin, conglutin [Sesamum indicum]
MAKKLALAAVLLVAMVALASATYTTTVTTTAIDDEANQQSQCRQLQGRQFRSCQRYL
SQGRSPYGGEEDEVLEMSTGNQQSEQLRDCCQQLGNVDERCRCCEAIRQAVRQQQEGGY
QEGSQQVYQRARDLPRRCNMRPQQCQFRVIFV

>AAK15089.1 Ses i 3; 7S globulin, vicilin-like [Sesamum indicum]
MSCGGRLCLVLFALLLASAVVASESKDPELKQCKHQCKAQQQISKEQKEACIQACKEYIR
QKHQGEHGRGGDILEEEVWNRKSPIERLRECSRGCEQQHGEQREELRRCQEEYQREKG
RQDDNDPTDPEKQYQQCRLQCRQEGGGFSREHCERRREEKYREQQGREGGRGEMYEGR
EREEEQEQGRGRIPYVFDQHFITGFRTQHGRMRVLQKFTDRSELLRGIENYRVAILEA
EPQTFIVPNHWAESVVFVAKGRGTISLVRQDRRESLNIKQGDILKINAGTTAYLINRDN
NERLVLAKLLQPVSTPGEFELFFGAGGENPESFFKFSFDEILEAAFNTRRDLRQIFGQQ
RQGVIVKASEEQVRAMSRHEEGGIWPFGGESKGTINIYQQRPTHSNQYQGLHEVDASQYR
QLRDLTLVSLANITQGAMTAPHYNSKATKIALVVDGEGYFEMACPHMSRSRGSYQGETR
GRPSYQVRASRLTRGTVIIIPAGHPFVAVASSNQNQLVLCFEVNANNNEKFPLAGRRNVM
NQLEREAKELAFGMPAREVEEVSRSQQEFFFKGRPQQQGRADA

>ACB55491.1 aldehyde dehydrogenase [Sesamum indicum]
MQFFSSRLLGSSRVLATTLSHFHYNPCTNKAHFTKAQLLPAAPYSNKLIVIRSMASGQQF
PPQKQEGQPKEHIMDPTPQATTPEYKPAKLVGKVALVTGGDSGIGRAVGHCFALLEGAT
VAFTYVKGQEDKDANDTLGMLMKAKHADAKDPIAIPDLGYDENCRRVVEEVNNYGRID
ILVNNAAEQYEASTVEEIDEPRLERVFRNTNIFSYFFTSRHALKHMKEGSSIINTTSVNAY
KGNAKLLDYATKGAIVAFTRGLALQMVEKGRVNGVAPGPIWTPILIPASFTEENAKFG
SQTPMKRAGQPHEVAPSYVFLASNIDSSYITGQVLHPNGGTIVNG

>AAD42942.1 Ses i 5; oleosin [Sesamum indicum]
MAEHYQQQQTRAPHLQLQPRARVKAATAVTAGGSLLVLSGLTLAGTVIALTIATPLL
VIFSPVLVPAVITIFLLGAGFLASGGFGVAALSVLSWIYRYLTGKHPPGADQLESATKL
ASKAREMKDRAEQFSQQPVAGSQT

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

MADRRPHPHQIQVHPQHPRHYEGGVKSLLPQKGPSTTQILAIITLLPISGTLCLLAGIT
LVGTLLIGLAVATPVFVIFSPVLVPAAILIAGAVTAFLLTSGAFGLTGLSSLSWVLSFRRA
TGQGPLEYAKRGVQEGTLYVGEKTKQAGEAIKSTAKEGGREGTART
>ACH85188.1 Ses i 5; oleosin [Sesamum indicum]
MAEHYQQQQTRAPHPQLQPRARVVKAAATAVTAGGSLLVLSGLTLAGTVIALTIATPLL
VIFSPVLVPAVITIFLLGAGFLASGGFGVAALSVLSWIYRYLTGKHPPGADQLESATKL
ASKAREMKDRAEQFSQQPVAGSQT
>AAX77383.1 Sin a 2; 11S globulin, cupin [Sinapis alba]
MVKLAHLLVATVGVLLVNLGCLARQSLGVPVQKDACNLNDLVLQPTTEVIKSEAGQVEY
WDHNNPQIRCAGVSIARLVIQKGLYLPTFFSSPFISYVVQGMGISGRVIPGCAETFMD
QPMQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQFRDMHQK
VEHVRHGDIAIAMPQSAQWIYNTGDQPLIIVSLIDIANYQNQLDRNPRTFRLAGNNQGS
SQQQQQQQNLSGFDQVLAQALKIDVRLAQELQNNQDKRGNIVRVKGPQVVRPPLRQ
AYESEQRHPRGPPQSPQDNGLEETICSMRTHENIDDPARADIYKPNLGRVTSVNSYTL
ILQYIRLSATRIGLQGSAMVLPKYNMNEILYCTQGQARIQVNDNGQNVLDQQVQKGG
LVVIPQGFAYVVQSQNNFEWISFKTNANAMISTLAGRTSALRALPLEVITNAYQISLEEA
RKIKFNTLETTLTRARGGQQPQLIEEIVEV
>AAX77384.1 Sin a 2; 11S globulin, cupin [Sinapis alba]
MVKLAHLLVATVGVLLVNLGCLARQSLGVPVQKDACNLNDLVLQPTTEVIKSEAGRLEY
WDHNNPQIRCAGVSIARLVIEQGGFYLPPTFFSSPKISYVVQGMGISGRVIPGCAETFMD
QPMQGGQQGHQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGGQQGG
GQQGFRDMYQKVEHVRHGDVIANTPGSAHWIYNTGDKPLVIISLLDIANYQNQLDRNPRV
FRLAGNNPQGGFGGPPQQPQNIILNGFDQVIAQALKIDVRLAQELQNKQDSRGNIVRV
KGPQVVRPPLRQAYESEQRHPRGPPQSPQDNGLEETICSMRTHENIDDPARADIYKPN
LGRVTSVNSYTIPIILQYIRLSATRIGLQGSAMVLPKYNMNEILYCTQGQARIQVNDN
GQNVLDQQVQKGGQLLVVIPQGFAYVVQSQNNFEWISFKTNANAMISTLAGRTSALRALPLE
VITNAFQISLEEARIKIKFNTLETTLTRARGGQQPQLIEEIVEV
>CAA62909.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFGIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDDFDFEDDMENPQGPQQ
RPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA
THLPRVCNIRQVSVCPFKTTPGGS
>CAA62910.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFRIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLGEGDFDFEDDMENPQGPQQ
RPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA
THLPKVCNIPQVSVCPFKKTPGGS
>CAA62911.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFGIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDDFDFEDDMENPQGPQQ
RPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA
THLPKVCNIPQVSVCPFKKTPGGS
>CAA62912.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFRIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDDFDFEDDMENPQGPQQ
RPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA
THLPKVCNIPQVSVCPFKKTPGGS
>CAA62908.1 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFGIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDDFDFEDDMENPQGPQQ
KPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA
THLPKVCNIPQVSVCPFKKTPGGS
>P15322.2 Sin a 1; 2S albumin, conglutin [Sinapis alba]
PAGPFRIPKCRKEFQQAQHLRACQQLHKKQAMQSGSGPSWTLDDDFDFEDDMENPQGPQQ
RPPLLQCCNELHQEELCVCPTLKGASKAVKQVVRQQLGQQGQQGPHLQHVISRIYQTA

THLPKVCNIRQVSVC PFKKTMPGPS
>ABU95411.1 Sin a 3; lipid transfer protein [Sinapis alba]
ALSCGTVNSNLAACIGYLTQNAPLPKGCCTGVTNLNMARTTPDRQQACRCLVGAANSFP
SLNAARAAALPKACGVNIPYKISKSTNCNSVR
>ABU95412.1 Sin a 4; profilin [Sinapis alba]
MSWQTYVDDHLMCDVEGNRLTAAAILGQDGSVWAQSANFPQLKPEEIKGINNDFAEPTGL
APTGLFIGGTYMVIQGEPCNAVIRGKKGAGGVTIKKTQAFVFGIYEEPMPGQCNMVVE
RLGDYLIEQGL
>COMPARE003 unknown function, partial [Sinapis alba]
ITLKVVVHFLRRSSHLYTSQVISQSRTRVKLN RVFFPR
>COMPARE004 unknown function, partial [Sinapis alba]
IKARLRNRSRRCRKTVA
>COMPARE005 unknown function, partial [Sinapis alba]
GKETNKDSLNGERTGKSPA
>COMPARE002 unknown function, partial from KAF8044512.1 [Sinapis alba]
SPDSDLEAFSHNPAHGSFAPLAFQPSAMTNCANQRFLSY
>ABU53681.1 tropomyosin [Sinonovacula constricta]
MDAIIKKMQAMKIEKENALDKSELENLKEIEDVKVKEEDLTSLQKKYTNQENEYDKV
NEQFNSTVKLEASEKRVTECEDEIKGFTRRIQLLEDELERTQQKAEAVLKLEEASKAA
DESERGRKVLERSIADDDRIDKLEKDVKDSKYLAEEADRKYDEAARKLAITEVDLERAE
TRLEAAESKITELSEELQVVGNNCKALQNAVDQASQREDSYEETIRDLTQRLLKDAENRAA
EAERVVKNLQKEVDRLEDELLQEKEYKQISDELDQTFAELAGM
>AAL75449.1 Sola l 2; beta-fructofuranosidase [Solanum lycopersicum]
MATQCYDPENSASRYTLLPDQPD SGHRKSLKIISGIFLSVFLLLSVAFFPILNNQSPDLQ
IDSRSPAPPSRGVSVQGVSDKTRFDVAGASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPN
GPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGS
ATILPDGQIMMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKFKGNPVLVPPP GIGVKDF
RDPPTAWTGPQNGQWLLTIGSKIGKTGVALVYETS NFTSFKLLDGV LHAVPGTGMWECVD
FYPVSTKKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLGKNKWTPDNPELDCGI
GLRLDYGKYASKTFYDPKERRVWLWGWIGETDSEADLQKGWASVQSIPRTVLYDKKTG
THLLQWPVEEIESLRVGDPTVKQVDLQPGSIELLRVDSAAELDIEASFEVDKVALQGIIE
ADHVGFCSTSGGAASRGILGPFVIVIA DQTLSELTPVYFYISKGADGRAETHFCADQT
RFAFLSGTINLSL
>AAL75450.1 Sola l 2; beta-fructofuranosidase [Solanum lycopersicum]
MATQCYDPENSASRYTLLPDQPD SGHRKSLKIISGIFLSVFLLLSVAFFPILNNQSPDLQ
IDSRSPAPPSRGVSVQGVSDKTRFDVAGASHVSYAWSNAMLSWQRTAYHFQPQKNWMNDPN
GPLYHKGWYHLFYQYNPDSAIWGNITWGHAVSKDLIHWLYLPFAMVPDQWYDINGVWTGS
ATILPDGQIIMLYTGDTDDYVQVQNLAYPANLSDPLLLDWVKFKANPVLVPPP GIGVKDF
RDPITAWTGPQNGQWLLTIGSKIGKTGVALVCETS NFTSFKLLDGV LHAVPGTGMWECVD
FYPVSTKKTNGLDTSYNGPGVKHVLKASLDDNKQDHYAIGTYDLGKNKWTPDNPELDCGI
GLRLDYGKYASKTFYDPKRERRVWLWGWIGETDSEADLQKGWASVQSIPRTVLYDKKTG
THLLQWPVEEIESLRVGDPTVKQVDLQPGSIELLRVDSAAELDIEASFEVDKVALQGIIE
ADHVGFCSTSGGAASRGILGPFVIVIA DQTLSELTPVYFYISKGADGRAETHFCADQT
RSSEAPGVGKQVYGVSSVPVLDGEEKSMRLLDVHSIVESFAQGGRVITSRIYPTKAVNGA
ARLFVFNATGASVTASVKIWSLESANIQS FPLQDL
>NP_001316123 Sola l 7; lipid transfer protein [Solanum lycopersicum]
MKAIAILVVLAVFQLAMVARGAITCGVDANLAPCVPLTQGGEPGAACCSGVRTLNG
NTQSSDDRRTACNCVKAANRYPNLKDDAAQSLPSKCGISLTVPISRVNC DTIS
>AAB42069.1 Sola l 3; lipid transfer protein [Solanum lycopersicum]
MEMFGKIACFVVF CMVVVAPHAESLSCGEVTSGLAPCLPYLEGRGPLGGCCGGVKGLLGA

AKTPEDRKTACTCLKSAANSIKGIDTGKAAGLPGVCGVNIPYKISPSTDCSTVQ
>CAJ19705.1 Sola l 3; lipid transfer protein [Solanum lycopersicum]
MEMVNKIACFVLLCMVVVAPHAERALTCGQVTSTLAPCLPYLMNRGPLRNCCDGVKGLLGQ
AKTTVDRQAACTCLKSAASSFTGLNLGKAAALPNTCSVNIPYKISPSTDCSKVQ
>NP_001306883 Sola l 6; lipid transfer protein [Solanum lycopersicum]
MKMTKVCFSVAVMLVMILVCDQFGANEAATCSASQLSPCLGAIQGGTAPSQDCCARLKNQ
QPCICGFMKDPNLRQYVNSPNARKVAGQCQGVSIIPSC
>CAA75803.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [Solanum lycopersicum]
MGVNTYTYESTTTISPTRLFALVLDLDFDNLVLPKLLSQHVKNNETIEGDGGVGSIKQMNFB
EGGPIKYLKHKIHVIDDKNLETKYSLIEGDILGEKLESITYDIKFEANDNGGCVYKTTTE
YHTKGDHVVSEEEHNVGRRENHEYFQGCRSIPSRESFCLRLNIDEKESGLHVRNYACT
>AHC08073.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [Solanum lycopersicum]
MGVNTYTYESTTTISPTRLFALVLDLDFDNLVLPKLLSQHVKNNETIEGDGGVGSIKQMNFB
EGGPIKYLKHKIHVIDDKNLETKYSLIEGDILGEKLESITYDIKFEANDNGGCVYKTTTE
YHTKGDHVVSEEEHNVGRERIMNISKAVEAYLLANPSVYA
>AHC08074.1 Sola l 4; pathogenesis related protein, PR-10, Bet v 1-like [Solanum lycopersicum]
MGVNTFTHESTTTIAPTRLFKGLVLDLDFDSLVPKLLSHDVKSIEIVEGDGGAGSIKQMNFB
EGGPIKYLKHKIHVIDDKNLVTKYSLIEGDVLGDKLESIAVDVKFEAAGDGGCVCKTTTE
YHTKGDHVVSEEEHNVGKGAIDLKFAIEAYLLANPSVYA
>CAD10377.1 Sola l 1; profilin [Solanum lycopersicum]
MSWQTYVDEHLLCENEGNHLTSAAIIGQDGTVAQSANFPQFKPEEITGIMNDFAVPGTL
APTGLYLGGTKYMVIQGEPEAVIRGKKKGGGITIKKTNQALIIGIYDEPMTPGQCNMIVE
RLGDYLIIEQSL
>AAL29690.1 profilin [Solanum lycopersicum]
MSWQTYVDDHLMCDIEGNHLTSAAIIGQDGSVWAQSANFPQFKPEEITAIMNDFAEPTGL
APTGLHLGGTKYMVIQGEAGAVIRGKKKAGGITVKKTNQALIIGIYDEPMTPGQCNMIVE
RLGDYIIEQGL
>QE43417 Sola m 1; profilin [Solanum melongena]
MSWQTYVDDHLMCDLEGHHLASAAIIGFDGSVWAQSPAFKPEEQHTMCDRCRSRSGVNCYIM
RPLYLYQAKFKPEEITNIMKDFDEPGFLAPTGLFLGGTKYMVIQGEPEAVIRGKKKSSGI
TIKKTGQALIFGIYEPPVTPGQCNMVEKIGDYLVQGY
>P16348.1 Sola t 2; aspartic protease inhibitor [Solanum tuberosum]
ESPLPKPVLDTNGKELNPNSSYRIISIGRGALGGDVYLGKSPNSDAPCPDGVFRYNSDVG
PSGTPVRFIPLSGGIFEDQLLNIQFNIATVKLCVSYTIWKVGNLNAYFRMTLLETGGTIG
QADSSYFKIVKLSNFGYNLLYCPITPPFLCPFCRDDNFCAKVGVIQNGKRRRLALVNEP
LDVLFQEV
>AAB63099.1 Sola t 3; cysteine protease inhibitor [Solanum tuberosum]
TCHDDDLVLPVEYDQDGNPLRIGERYIKNPLLGGAGAVYLDNIGNLQCPNAVQLQHMSIP
QFLGKGTVPVVFIRKSESDYGDVVRMLTAVYIKFFVKTTLKCVDETVMKVNNEQLVVTGGN
VGNENDIFKIKKTDLVIRGMKNVYKLLHCPHLECKNIGSNFKNGYPRLVTVNDEKDFIP
FVFIKA
>P20347.3 Sola t 3; cysteine protease inhibitor [Solanum tuberosum]
MKSINILSFLLSSTLSLVAFARSFTSENPIVLPPTCHDDDLVLPVEYDQDGNPLRIGE
RYIINNPLLGGAVYLYNIGNLQCPNAVQLQHMSIPQFLGEGTPVVFVRKSESDYGDVVRV
MTVVYIKFFVKTTLKCVDTVMKVNDEQLVVTGGKVGNEENDIFKIMKTDLVTPGGSKYVY
KLLHCPHSLGCKNIGGNFKNGYPRLVTVDDDKDFIPVFIKA
>COMPARE058 gibberellin-regulated protein, partial from Q948Z4.1 [Solanum

tuberosum]

VPSGTYGNKHECPCYRDKKNSKGKSKCP

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

MATTKSFLILFFMILATTSSTCAKLEEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAAKDIVPFYFEHGPHIFNYSGSI
LGP MYDGKYL LQVLQEKLGETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM
YDICYSTAAPIYFPPHFFVTHTSNGARYEFNLVDGAVATVGD PALLSLSVATRLAQEDP
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMTNAASSYMTD
YYISTVFQARHSQNNYL RVQENALNGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE
TYEEALKRFAKLLSDRKKLRANKASH

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

MATTNSFTILIFMILATTSSTFATLGEMVTVLSIDGGGIKGIIPATILEFLEGQLQEVDN
NTDARLADYFDVIGGTSTGGLLTAMITTPNETNRPF AAAKDIVPFYFEHGPKIFQSSGSI
FGPKYDGKYL MQVLQEKLGETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM
YDICYSTAAAPTFFPPHYFATNTSNGDKYEFNLVDGAVATVDD PALLSISVATKLAQVDP
KFASIKSLNYKQMLLLSLGTGTTSEFDKTYTAEETAKWGTARWMLVIQKMTSAASSYMTD
YYLSTAFQALDSQNNYL RVQENALTGTTTELDDASEANMQLLVQVGEDLLKKS VSKDNPE
TYEEALKRFAKLLSDRKKLRANKASY

>CAA27588.1 Sola t 1; patatin [Solanum tuberosum]

MATTKSFLILFFMILATTSSTCATLGEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAAKDIVPFYFEHGPHIFNYSGSI
FGPRYDGKYL LQVLQEKLGETRVHQALTEVAISSFDIKTNKPVIFTKSNLAESPQLDAKM
YDICYSTAAPIYFPPHFFVTHTSNGATYEFNLVDGAVATVGD PALLSLSVATRLAQDDP
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQMTNAASSYMTD
YYISTVFQARHSQNNYL RVQENALTGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE
TYEEALKRFAKLLSDRKKLRANKASH

>AAA33819.1 Sola t 1; patatin [Solanum tuberosum]

MATTKSFLILFFMILATTSSTCAKLEEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAAKDIVPFYFEHGPHIFNYSGSI
IGP MYDGKYL LQVLQEKLGETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM
YDICYSTAAPIYFPPHYFITHTSNGDIYEFNLVDGGVATVGD PALLSLSVATRLAQEDP
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAQE EAAKWGPLRWMLAIQQMTNAASSYMTD
YYISTVFQARHSQNNYL RVQENALTGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE
TYEEALKRFAKLLSDRKKLRANKASY

>P15476.2 Sola t 1; patatin [Solanum tuberosum]

MATTKSFLILFFMILATTSSTCAKLEEMVTVLSIDGGGIKGIIPAIILEFLEGQLQEVDN
NKDARLADYFDVIGGTSTGGLLTAMITTPNENNRPF AAAKDIVPFYFEHGPHIFNYSGSI
FGPRYDGKYL LQVLQEKLGETRVHQALTEVAISSFDIKTNKPVIFTKSNLAKSPELDAKM
YDICYSIAA APIYFPPHFFVTHTSNGATYEFNLVDGGVATVGD PALLSLSVATRLAQEDP
AFSSIKSLDYKQMLLLSLGTGTNSEFDKTYTAE EAAKWGPLRWMLAIQQLTNAASSYMTD
YYISTVFQARHSQNNYL RVQENALTGTTTEMDDASEANMELLVQVGETLLKKPVSKDSPE
TYEEALKRFAKLLSNRKKLRANKASY

>ABB16985.1 profilin [Solanum tuberosum]

MSWQTYVDEHLLCEIEGNHLTSA AIVGQDGTVWAQSANFPQFKPEEISGIMNDF AEPGTL
APTGLYLGGTKY MVIQGE PGAVIRGKKGPGGITIKKTNQAL IIGIYDEPMPGQCNMIVE
RLGDYLVEQGL

>ABA81885.1 profilin-like [Solanum tuberosum]

MSWQTYVDEHLLCEIEGNHLTSA AIIIGQDGTVWAQSANFPQFKPEEITGVMNDF AEPGTL
APTGLYLGGTKY MVIQGE PGAVIRGKKGPGGITIKKTNQAL IIGIYDEPMPGQCNMIVE
RLGDYLVEQGL

>BAA04149.1 Sola t 4; serine protease inhibitor [Solanum tuberosum]
MKCLFLLCLCLVPIVVSSTFTSKNPINLPSDATPVLVDVAGKELDSRLSYRIISTFWGAL
GGDVYLGKSPNSDAPCANGIFRYNSDVGPSGTPVRFIGSSSHFGQGIFENELLNIQFAIS
TSKLCVSYTIWKVGDYDASLGTMLLETGGTIGQADSSWFKIVKSSQFGYNLLYCPVTSTM
SCPFSSDDQFCLKVGVVHQNGKRRLLALVKDNPLDVSFKQVQ
>BAH10156.1 tropomyosin [Solen strictus]
MDSIKKKMQAMKLEKENALDKSEQLEQKLEKEDSKARAEEDLSSLQKKFTNLENEFDKV
NEQYQEGVIKLEASEKRVTECEDEIKGFTRRIQLLEDDLERTQAKLDEALLKLEDASKTA
DESERGRKVLESRSIADDDRIDQLEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERAE
TRLEAAEAKITELSEELQVVGNSKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA
EAERVVNLQKEVDRLDELLAEKEKYKQISDELDTFAELAGM
>AAF65313.1 Sol g 4; unknown function [Solenopsis geminata]
MKTFVLVSCLLVFTQIIYAVDIKELKIVNRILKCKCIRTVPKGENDPINPLKNVNVLYCAF
SKRGIFTPKGVNTKQYINYCEKTIINPADIKQCKKLISKCIKKVYDRPGPIIERSKNLLS
CVRKKGVLELTVYGKKK
>AAF65312.1 Sol g 4; unknown function [Solenopsis geminata]
MKTFVLVSCLLVFTQIIYAVDIKELKIMNRILEKCIKRTVPKGENDPINPLKNVNVLYCAF
SKRGIFTPKGVNTKQYINYCEKTIINPADIKQCKKLISKCIKKVYDRPGPIIERSKNLLS
CVLKKGVLELTVYGKKK
>AAT95008.1 Sol i 1; phospholipase A1 [Solenopsis invicta]
MRKFAAIFVVFVQCTHLYSLAQARAEPDPGVVEYLKQSCVYGNSSYINVYLYNSRFQ GK
NLGNQQSCQDINASLPVVFITHGFTSSAQVSTFKDLANAFVQKGHTAFIVDWSEAACTDG
LPGVQFAEYNAAASNTYDIGQLMAKYTVDL MNKCKIPLNNIQYVGHSLGSHVCGFAAKHV
KKLINKTMPYILALDPADPSFGSNKCGERICKSDAKRIVVFKTSILGIGENIIGHLLIVF
DGGKSQPACSWYDVPCHSESIYATGMVSGRCQH LAVPWAQQRINPIQWKFWRVFTSN
IPAYPTSDTTNCVVLNTNVFKNDNTFEGEYHAFPCARNLFKCRQQ
>AAC97370.1 Sol i 4; unknown function [Solenopsis invicta]
MKTFVLVSCLLVFTQIIYALDIKEISIMNRILEKCIKRTVPKRENDPINPLKNVNVLYCAF
TKRGIFTPKGVNTKQYINYCEKTIISPADIKLCKKIASKCVKKVYDRPGPIIERSKNLLS
CVLKKGLLELTVYGKKK
>P35775.1 Sol i 2; unknown function [Solenopsis invicta]
MKSFVLATCLLGFQIIYADNKEIKIIRKDVAECLRTL PKCGNQDDPLARVDVWHCAMA
KRGVYDNPDAVIKERSMKMCTKIITDPANVENCKKVASRCVDRETQGPKSNRQKAVNII
GCALRAGVAETT VLARKK
>AAB65434.1 Sol i 3; unknown function [Solenopsis invicta]
MELIVSILWLAITAENLANTLATNYCNLQSKRNNAIHTMCQYTSPTPGPMCLEYSNVGF
TDAEKDAIVNKHNELRQRVASGKEMRGTNGPQP PAVKMPNL TWDPELATIAQRWANQCTF
EHDACRNVERFAVGQNI AATSSSGKNKSTPNEMILLWYNEVKDFDNRWISSFPSDDNILM
KVGHYTQIVWAKTTKIGCGRIMFKEPDNWT KHYLV CNYPAGNVLGAPIYEIKK
>AAC97369.1 Sol i 4; unknown function [Solenopsis invicta]
MKTFVLVSCLLVFTQIIYALDIKEISIMNRILEKCIKRTVPKRENDPINPLRNVNVWYCAF
TKRGIFTPKGVNTKQYINYCEKTAISPADIKLCKKIASKCVKKVYDRPGPIIERSKNLLS
CVLKKGLLELTVYGKKK
>P35776.2 Sol r 2; unknown function [Solenopsis richteri]
DIEAQRVLRKDIAECARTLPKCVNQDDPLARVDVWHCAMS KRGVYDNPDAVVKEKNSK
MCPKIITDPADVENCKKVSRCVDRETQRPRSNRQKAINITGCILRAGVVEATVLAREK
>P35779.2 Sol r 3; unknown function [Solenopsis richteri]
TNYCNLQSKRNNAIHTMCQYTSPTPGPMCLEYSNVGFTDAEKDAIVNKHNELRQRVASG
KEMRGTNGPQP PAVKMPNL TWDPELATIAQRWANQCTFEHDACRNVERFAVGQNI AATSS
SGKNKSTLSDMILLWYNEVKDFDNRWISSFPSDGNILMHVGHY TQIVWAKTKKIGCGRIM

FKEDNWNKHVLCNYGPAGNVLGAQIYEIKK
>ADD74392.1 unknown function [*Solenopsis saevissima*]
MKTFVLVSCLLVFTQIIYALDIKEISIMNRILEKCIKRVPHENDPINPLRNVNVWYCAF
TKRGIFTPQKGVNTKQYINYCEKTAISPADIKLCKKIASKCVKKVYDRPGPIIERSKNLLS
CVLKKGLLELTVYGKKK
>AIL01316.1 Sor h 1; beta-expansin [*Sorghum halepense*]
MGVNMMSWSMQVALVVALAFLVGGAWCGPPKVAPGKNITATYGSWLEAKATWYGKPTGA
GPDDNGGACGYKDVNKAPFNSMGACGNLPIFKDGLGCGSCFEIKCDKPAECSGEAVVHI
TDMNYEQIAAYHFDLAGTAFGAMAKKGEELRKRAGIIDMKFRRVKCKYGEKVTFFHVEKG
SNPNYLALLVKYVDGDDVGVDIKEKGGDAYQPLKHSWGAIWRKDSKPIKFPVTVQIT
TEGGTKTAYEDVIPEGWKADTTYTAK
>AIL01317.1 Sor h 1; beta-expansin [*Sorghum halepense*]
MGSLANKIVAMAVALAALVTGGSCAPKKFPPGPNITTTNYNGQWLSARATWYGQPNGAGPD
DNGGACGKIKNVNLPYNGFTACGNVPIFKDGLGCGSCYEVRCCKEMPECSGNPITVFITDM
NYEPIAPYHFDGSGKAFGLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNP
NYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKPKVGPFSIRLTSES
GKKLVAPNVIPATWPKPDTLYNSNIQF
>AIL01320.1 Sor h 13; polygalacturonase [*Sorghum halepense*]
MALGSNAMRVFFLLAMVCAAAHAAGKAAPKEKEKGDGKSGGAPAEAPSGSAGGSDISKL
GAKGDGKTDSTKALNEAWAAACGKEGPQTLMIKPGDYLTGPLNFSGPCKGSVTIQLDGNL
LGTDLASAYKTNWIEIEHVDNLVISGKGLDGGQKQVWDNNKCAQKYDCKILPNSLVLDY
VNNGEVSGITLLNAKFFHMNVFQCKGVTIKDVTVTAPGDSPTDGIHIGDSSKVTITGTT
IGVGDDCISIGPGSTGINVTGVTGPGHGISVGLGRYKDEKDVTDINVKDCTLKKTSNG
VRIKSYEDAACVITASKLHYENIAMDDVANPIIIDMKYCPNKICTAKGDSKVTVKDVTFK
NITGTSSTPEAVSLLCSDKIPCSGVTMDNIKVEYKGTNNKTMAVCQNAKGSATGCLKELACF
>AIL01321.1 Sor h 13; polygalacturonase [*Sorghum halepense*]
MACTGNAMRAFFLLAFVCAAHAGKDAPAKDGAASGPGGSFDISKLGASGDGKKDSTK
AVQEAWTSACGGTQKQTLIPKGDYLVGPLNFTGPKGDVTIQVDGNLLATDLSQYKGN
WIEILRVDNLVITGKGLDGGQPAVWSKNSCAKQYDCKILPNSLVLDYVNNGEVSGITLL
NAKFFHMNVFQCKGVTIKDVTVTAPGDSPTDGIHIGDSSKVTITGTTIGVGDDCISIGP
GSTGINVTGVTGPGHGISVGLGRYKDEKDVTDINVKDCTLKKTSNGVRIKSYEDAACV
ITASKLHYENIAMDDVANPIIIDMKYCPNKICTAKGDSKVTVKDVTFKNITGTSSTPEAV
SLLCSDKIPCSGVTMDNIKVEYKGTNNKTMAVCQNAKGSATGCLKELACF
>ACT37324.1 Sta c 3; exodesoxyribonuclease [*Stachybotrys chartarum*]
ASVTFWTLDNVDRTLVTGNGPSAAIETITVGAENTTVEFPGSWVGNWYAYPTDAEDVP
GMLGEVQFGGWNLTYFDVSAIVNPTDHDNVKQMWPAESRKPMSGCEVFPDCNAYWLPDD
IQTKVTHEVDLWTTLGAGSTGLTF
>ACT37323.1 unknown function, partial [*Stachybotrys chartarum*]
AGPIASRQIVPNYPASSTSKGFHLVNVTDPSADFTPSINNFYVNSIHVGAALNYVGVT
VPGRIFYQNGTAEIIRYAQSTVISDGATPPVFPGLSLRPDEGSDVVSTARLDAGPGTTGV
RVSRLFPEPYRFLQPETFLACNESLAYYQGDYFTVIKQADVTVGDDGSIDYNVPDNCISVR
LIPECTELNELPEDAYASHEFAADTQCYDDVSALNWSYEGP
>P20723.1 enterotoxin [*Staphylococcus aureus*]
MKKFNILIALFFTSLSVPLNVKANENIDSVKEKELHKKSELSSTALNNMKHSYADKNP
IIGENKSTGDQFLENTLLYKFFFDLINFEDLLINFNSKEMAQHFKSKNVVYPIRYSIN
CYGGEIDRTACTYGGVTPHEGNLKERKKIPINLWINGVQKEVSLDKVQTDKKNVTVQEL
DAQARRYLQKDLKLYNNDTLGGKIQRGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSD
NKTLSSTEHLHIDIYLYEK
>P34071.1 enterotoxin [*Staphylococcus aureus*]

MNKSRLFISCVILIFALILVLFPTNVLAESQPDPTDELHKSSEFTGTMGMNKYLYDDHYV
SATKVMSVDKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYVNC
YFSSKDNVGVKVTGGKTCMYGGITKHEGNHFDNGNLQNVLIRVYENKRNTISFEVQTDKKS
VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKY
LMMYNDNKTVDSKSVKIEVHLTTKNG

>1ESF_B enterotoxin [Staphylococcus aureus]
SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHQFLQHTILFKGFFTD
HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT
EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVDFDGKVQ
RGLIVFHTSTEPSVNYDLFGAQQQYSNTLLRIYRDNKTINSEMHIDIYLYTS

>CAJ43561.1 enterotoxin [Staphylococcus aureus]
IFVLILVISTPNVLAESQPDPKDELHKASKFTGLMENMKVLYDDNHVSAINVKSIDQFL
YFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSH
QTDKRKTCMYGGVTEHNGNQLDKYRSITVRVFEDEGKNLLSFDVQTNKKKVTAQELDYLTR
HYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDS
KDKVIEVYLTTKK

>ADM53099.1 fibronectin-binding protein [Staphylococcus aureus]
MAYDGLFTKKMVESLQFLTTGRVHKINQPDNDTILMVRQNRQNHQLLSIHPNFSRLQL
TTKKYDNPFPNPFARVFRKHLEGGIIESIKQIGNDRRIEIDIKSKDEIGDTIYRTVILE
IMGKHSNLILVDENRKIIIEGFKHLTPNTNHYRTVMPGFNYEAPPTQHKINLYDITGAEVL
KYIDFNAGNIAKQLLNQFEGFSPLITNEIVSRRQFMTSSTLPEAFDEVMAETKLPPTPIF
HKNHETGKEDFYFIKLNQFNDDTVTYDSLNDLLDRFYDARGERERVKQRANDLVRVQQQ
LHKYQNKLAKLIEEYEQSKNKDTEQLYGELITANIYRIKQGDKEVTALNYTNEEVVIPL
NPTKSPSANAQYYYKQYNRMKTRERELQHQIQLTKDNIDYFSTIEQQLHHISVHIDEIR
DELAEQGFMKQRKNQTKKKAQIQLQHVVSTDGDDIYVGKNNKQNDYLTNKKAKKHTHWL
HTKDIPGSHVIFNDAPSDTTIKEAAMLAGYFSKAGNSGQIPVDYTLIKNVHKPSGAKPG
FVTYDNQKTLATPDYELIQMKQS

>P06886.1 toxic shock syndrome toxin [Staphylococcus aureus]
MNKLLMNFIVSPLLLATTATDFTPVPLSSNQIIKTAKASTNDNIKDLLDWYSSGSDTF
TNSEVLDNSLGMRIKNTDGSISLIIFSPYYSPAFTKGEKVDLNTKRTKKSQHTSEGTY
IHFQISGVTNTEKLPTPIELPLKVKVHGKDSPLKYGPKFDKKQLAISTLDFEIRHQLTQI
HGLYRSSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN

>XP_008286259.1 calcium-binding protein, parvalbumin [Stegastes partitus]
KAFAIIDQDKSGFIEEDELKFLQNFSAARA

>COMPARE152 Alt a 1-like, partial [Stemphylium botryosum]
KISEFYGRKPEGTYYNLSLGFNIKATNGGTLDFTCQAQADKLEDHKWYSCGENSFMSFSFD
SDRS

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

>ABS29033.1 Alt a 1-like [Stemphylium sp.]
LAAAAPFEARQADASCPVSTQGDYVWKISEFSGRKPEGTYYNLSFNKATNKGTLDFTC
SAQADKLEDDKFYSCGENSFMSFAFQSDRNGLLFRQDVSEITYVATATLPNYCHAGGNG
PKDFVCQGVSDAYFTLV

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

>AAD46493.1 unknown function [Strongyloides stercoralis]

NSARDENGLIYTYNGNDYDTKEAMEDAIQRDYPDKIFTFGGDNNNGKKRKIDISKWKGN
NTFSNKIFDEIWEGYNYDNDKAKNFKVMKTKLFNEQNKYRIAHGAKKLIKSKDLEKKAQA
YAEVIARLGRLEHDPKNRIEGTGENLAYGTTFIGHLAVKGWYDEIALYNFKKPGFSPATG
HFTQLVWKGTTTHAGFGVVEKGRVYVXKYSPPGNYPRQFXANVLQRKQ

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

>P00791.3 pepsin [Sus scrofa]
MKWLLLLSLVVLSECLVKVPLVRKKSRLRQNLIKNGKLDKDFLTKHKNPASKYFPEAAALI
GDEPLENYLDTEYFGTIGIGTPAQDFTVIFDGTSSNLWVPSVYCSSLACSDHNQFNPDSS
STFEATSQELSITYGTGSMGTGILGYDVTQVGGISDTNQIFGLSETEPGSFLLYAPFDGIL
GLAYPSISASGATPVFDNLWDQGLVSDQLFSVYLSNDDSGSVLLGGIDSSYYTGSLNW
VPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLTGPTSAIANIQSDIGASENS
DGEMVISCSSIDSLPDIIVFTINGVQYPLSPSAYILQDDSDCTSDFEGMDVPTSSGELWIL
GDVFIRQYYTVFDRANNKVGLAPVA

>NP_001005208 Sus s 1; serum albumin [Sus scrofa]
MKWVTFISLLFLFSSAYSRGVFRRTYKSEIAHRFKDLGEQYFKGLVLIASFQHLQQCPY
EEHVKLKLVREVFTEFAKTCVADESAENCDSIHTLFGDKLCAIPSLREHYGLADCCCEKEEP
ERNECFLLQHKNDNPDIKPKLPDVALCADFQEDEQKFWGKLYEIAARRHPYFYAPELLYY
AIIYKDVFSECCQAADKAACLLPKIEHLREKVL TSAAQRLKCAISIQKFGERAFKAWSLA
RLSQRFPKADFTEISKIVTDLAKVHKECCHGDLLCADDRADLAKYICENQDTISTKLKE
CCDKPLLEKSHCIAEAKRDEL PADLNPLEHDFVEDKEVCKNYKEAKHVFLGTFLEYESRR
HPDYSVSLLLRIAKIYEATLEDCCAKEDPPACYATVDFKQPLVDEPKNLIKQNCLEFEK
LGEYGFQNALIVRYTKKVPQVSTPTLVEVARKLGLVGSRCCKRPEEERLSCAEDYLSLVL
NRLCVLHEKTPVSEKVTKCCTESLVNRRPCFSALTPDETYKPKFVEGTFTFHADLCTLP
EDEKQIKKQTALVELLKHKPHATEEQLRVTLVGNFAAFVQKCCAAPDHEACFAVEGPKFVI
EIRGILA

>S43242 Syr v 1; Ole e 1-like [Syringa vulgaris]
EDVPQPPPIQFHIQGGVYCDTCRARFITESEFIPGASIRLQCKDRENGKITFTEIGYTR
AEGLYSMLVEGDHKNEFCEITLISSGREDCDEIPVEGWAKPSLKFKNLNTVNGTTRTINPI
GFFKKEALPKCTQVYNKLGMYPPNM

>S43243 Syr v 1; Ole e 1-like [Syringa vulgaris]
EDVPQPPVPIQFHIQGGVYCDTCRARFITESEFIPGASIRLQCKDGEHGKITFTEIGYTR
AEGLYSMLVEGDHKNEFCEITLISSSRKDCCEIPIEGWVKPSLKFILNTVNGTTRTINPL
GFFKKEVLPKCPQVFNKLGMYPPNM

>S43244 Syr v 1; Ole e 1-like [Syringa vulgaris]
EDVPQPPVPIQFHIQGGVYCDTCRARFITESEFIPGASIRLQCKDGENGKITFTEIGYTR
AEGLYSMLVEGDHKNEFCEITLISSGRKDCDEIPVEGWVKPSLKFKNLNTVNGTTRTINPI
GFFKKEALPKCTQVYNKLGMYPPNM

>P58171.1 Syr v 3; polcalcine [Syringa vulgaris]
MAEEVAELERIFKRFDANGDGKISSSELGETLKTLSVTPPEEQRMMAEIDTDGDFISF
EEFKDFARANSGLIKDVAKIF

>ADX78255.1 Tab y 1; apyrase [Tabanus yao]
MFKITVFIYVLQLILPSKVHSSVPDSDNGLREFPLSIVHINDFHARFEQTDELGGQCKP
TAKCVGGYARLVTTVKLKEEQNTIFLNAADNYQGLWYNLKGKWNVTAYFMNLLPADAM
TLGNHEFDDKIEGIVPFLVVIKTPIVVANIDDSLEPTFKGKYTKSVLLEGGGRKIGIVGV
IAQNTDNISSPGKLRFLDEIQSVKNESKRLREEEKVDIVIVLSHIGLDHHDYDLAEQAGDY
IDAIIGGHSFLWTDGNPPGKEKVVDPVVEIVQTSKKVLIQASAFARYVGNITLYF
GENNLIIRYAGAPVYLDSDVPEVPQIVEEMKAWEEFVHEKGNIEIAESRVVLSRENCRV

DCNIGNFFTDAYVHEVYVTSHTGPYWTPVSVGLMNVGGIRASVDRGNITFSQLITMAPFEN
TVDTFDLGSKHLLEAFEHAVTVPNRLGFNGQNMLQVSGVKLVYDVTKCEGQRVVSARKIRC
QKCDIPKYEPLDPEETYRIVTASFLANGGDGFTMIRDNKKNYKVGRKDYDVLINYAKYSS
PITIGEEGRIRIIQ

>ADM18346.1 Tab y 2; hyaluronidase [Tabanus yao]
MKLHQGLVCLSVLILLPTCILGDRKFEVYWNIPTFMCPDQNKTIMDLNKKHGVIQNTEDL
FRGDKISLLYHPGAFPAITRNKTTNTLIYENGGVQPQAGNLSLHLKLEKDINEQITDKNF
SGLAVIDFELWRPIFRQNGGSLSDYQNLSLKLEKDLHPEFNEDQLRKEAERRIEKFGRSF
IKQTLIKAKKLRPKAQWGYAFPYCFNGRRRYVDTCIPSAKIDNDRILYMFENSVDVIYPA
VYLQTDLAQKNQGLVKGRVDEAVRMAKMVKKPAKPPVLVYHRYVFTDTLEYISKENTTA
VFKAMKDNAGDGVIIWSSFDLNSKEKCAKFLDYLRVLPVIDEVKRS

>ADM18345.1 Tab y 5; unknown function, antigen 5 [Tabanus yao]
MAPIIVPCLLLVVLVLCQSVINSLDYCSLCRGGGEHVGCGSPGFSSDCGQKARTRKFTK
EHKKVILDKINDVRDHVAKGSWGLPVASRMKVIVWDEELAALAKRHTQGCVPEAYKCRHT
LRFWSPGQLNFEFYADKMPSTMSLISTAIKRHTQKHNITRDIIEKYQPAGPKGNVKELA
LAISDRVTAVGCGLTTWKLGGKARALLTCNFSSENDYNRPVYKGTNSPGEKCIKKDETFK
NLCSAQEPINPNEHNF

>QCI56574.1 tropomyosin [Tenebrio molitor]
AKLIAEEADKKYEEVARKLVLMEQDLERAEEAEQSESKIVELEEEELRVVGNLKSLEVS
EEKATLKEEEYSVTLKQVDQRLQEAERAEFAERSVQKLQKEVDRLEDDLLA

>QCI56575.1 tropomyosin [Tenebrio molitor]
RKLAMVEADLERAEERAEAGESKIVELEEEELRVVGNLKSLEVSEEKANQREEEYKNQIK
NLTTTLKEAEARAEFAERSVQKLQKEVDRLEEEELVAEKERYKEIGDDLDTAFVELIL

>P86360.1 Tha p 2; unknown function [Thaumetopoea pityocampa]
MKLLIFAILIALSSSVPQLSEKAEAEAVDLAYQEKNNLFDLGSVAGDILSRSGCHVSFGCH
KGYCWAGCGDPTNPWSWGENWCYTTKSYSQSYSYVQCTQDSECDGCWKCGGPCSA

>ADK47876.1 Tha p 1; unknown function [Thaumetopoea pityocampa]
MKLLILALTCAAHVWARPGETYSKDYDTIDVNEVLQSERLLKGYVECLLDKGRCTPDGKE
LKDTLPDALEHECSKCTEKQKSGADTVIRHLVNRPELWKE LAVKYDPENIYQERYKDRL
ESVKEH

>COMPARE158 Tha p 2; unknown function, partial [Thaumetopoea pityocampa]
SYSQSYSYVQCIQDSECNCGWK

>COMPARE159 Tha p 2; unknown function, partial [Thaumetopoea pityocampa]
KAEEAIDLTYQEK

>COMPARE160 Tha p 2; unknown function, partial [Thaumetopoea pityocampa]
NNLFNLGSAVAGDILSR

>CEE03318.1 unknown function [Thaumetopoea solitaria]
VPQLSEKAEKAVDLTYQEKNNLFELGSVVDIISKNGCHVSFGCHKGYCWAGCGNPTNPW
SWGENWCYTTKYSQSYSYVQCTQDSECDGCWKCGGPCSA

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

>AAK63089.1 calcium-binding protein, parvalbumin [Theragra chalcogramma]
MAFAGILKDAEVAALAEACKSAGSFDHTKFFKSCGLAGKSSDDVKKAFGIIDQDQSDFIE
EEELKFLQNFASARALSDAETKAFLKAGSDGDGKIGVDEFAAMVKA

>CAX62602.1 aldolase [Thunnus albacares]
MTHQFPSLSPEQKKELSDIAQRIVAPGKIGILAADESTGTMGKRLQKINVENNEENRRYFR
DLLFSSDASISNCGGVIFFHETLYQKADSGKLFQVQIKDKGIVVGIKVDKGTAGLNGTD
GETTTQGLDGLSERCAQYKKGDCDFAKWRCVVKISDGCPALGIAENANVLARYASICQQ
NGLVPIVEPEILPDGEHDLRLCQYVTEKVLAAVYKALSDHHVYLEGTLKPNMVTAGHSC

TKKYTPQEVAMATVTALRRTPAAVPGICFLSGGQSEEEASLNLNAINQVPLHRPWKLTFSYGRALQASALAAWQGAANKTAAQEAF CNRAKINGLAAGGEYKPSGSADKASMSLYTASYVY

>P86979.1 Thu a 3; aldolase [Thunnus albacares]

PHAFPFLTPEQKKELSDIAHKIVAPGKGILAADESTG

>CBL79145.1 enolase [Thunnus albacares]

MSILKIHAREIFDSRGNPTVEVDLYTKKGLFRAAVPSGASTGIYEALERDNDKTRYMGKGVKRAVKYINEFLAPALCNQDVTVIEQEKIDKMLDMDGTENKYKFGANAILGVSLAVCKAGAAEKGVPLRYRHADLAGNPEVILPVPAFNVINGGSHAGNKLAMQEFMILPVGASSFKDAMRIGAEVYHNLKNVIKEKYGDATNVGDEGGFAPNILENKEALKLLKNAIGKAGYTDKI VIGMDVAASEFYKGGKYDLDFKSPDDPSRYIPSDKLADLYKGFVKDYVVSIEDPFDQDDWEAWSKFTASTSIQVVGDDLTVTNPKRIAKGVAEKSCNCLLLKVNQIGSVTESLQACKMAQSSGWGMVSHRSGETEDTLISDLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEEELGAKAKFAGKNFRHPI

>P86978.1 Thu a 2; enolase [Thunnus albacares]

SITKIKAREILD

>BAE54431.1 tropomyosin [Todarodes pacificus]

MDAIKKKMLAMKMEKEVATDKAEQTEQSLRDLEAAKNTIEEDLSTLQKKYSNLENDFDNAKENLTVANTNLEASEKRVNECESEIQGLNRRIQLEEDLERSEERL TSAQSKLEDASKAADESERGRKVLNRSQGEERIDLLEKQLEEKWIAEDADRKFDEAARKLAITEVDLERAEARLEAAEAKIVELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTHRLKEAENRAEAERTVSKLQKEVDRLEDELLAEKERYKSISDELDTFAELAGY

>BAE46763.1 calcium-binding protein, parvalbumin [Trachurus japonicus]

MAFKGVLNDADVTAALDCKSAFDHKAFFKACGLAAKSADDIKKAFIIDDQDKSGFIEED ELKLFQNF CAGARALSDAETKAFKAGDSGDGKIGVDEFAAMVKH

>BAH10155.1 tropomyosin [Tresus keenae]

MDSIKKKMQAMKIEKENALDKAEQLDQKLDKDTEDSKAKIEEDLSSLQKKYTNLENEFDQVNEKYNDGVVVKLESSEKRVTECEDEIKGYTRRIQLEEDLERTQVKLEEATLKLEDATKTADESERGRKVLNRSIADDDRIDQLEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERAE TRLEAAEAKITELSEELSVVANCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRASEAERVVNKLQKEVDRLEDELLAEKEKYKQISDELDTFAELAGM

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

MKTFIVITFIGILSYAYADECENPEPMQGFSAQFYQGXWYVTHETSAXTLSECNILTTSNDNGKFTVKHKYTKDGXV GELICEGQASANNKF TYDCKFXGZTMEQVTRTAMDTDYNDYALYYLCTTYKXGPNAGKKEGHYILSRRQPNT EIPDALKT KTKDLNLKLCG

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

MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKDRPSGWNLNLKNGDISVLT TSDVSEITWLG DGTGVVYVNGTDSVEGGVGIWISDAKNFGNAYKAGSVNGAFSGLKLAKAGDKINFGYGGQSTTKGDLYNEAAAKEAVSSARIYDGLFVRHWDTYVGTQFNAVFSGLTKNGDKYSFDGKLNKLVQPVKYAESPYPPFGGSGDYDLSDDGKTVAFMSKAPELPKANLTTSYIFLVPHDGSRVAEPINKRNGPRTPQIEGASSSPVFPDGKRIAYLQMATKNYESDRRVIHIAEVGSNKPVQRIASSWDRSPEAVKWSSDGR TLYVTAEDHATGKLF TLPADARDNHKPSVVKHDGVS SFYF IGSSKSVLISGNSLWSNALYQVATPGRPNRKL FYANEHDP ELKGLPKDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFQKLTDDITNDWGGAPYKDLVKIWEHVRDHIKYIDTDNGIAAGASFGGFMVNIQGGQDLGRKFKALVSHDGT FVGSSKIGTDELFFI EHFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHNDDFRLSVAEGVGLFNVLQKEGIPSRFLNFPDETHWVTKPENSLVWHQQLGWINKWSGINKSNPKSIKLSDCPIEVIDHEAHSYFDY

>CAD23613.1 unknown function [Trichophyton benhamiae (Arthroderma benhamiae)]

NHDDVDYIEPDFVVRTSTNGTNLTRQENVPSWGLARVGSKKAGGTTYYYDSSAGKGV TAY
IIDTGIDINHEDFGGRAKWKGNFVDKMEDEDCNGHGHVAGTVGGTKYGLAKGVTLVAVKV
LDCDGSNSGVI EGM EWAMREASGGNGTAKAAGKAVMMSLGGPRSQASNDAAKAISD
AGIFMAVAAGNENMDAQHSSPASEPSVCTVAASTEDDGKAEFSNYGAVVDVYAPGKDITS
LKPGGSTDTLSGTSMASPHVCGLGAYLIGLGKQGGPGLCDTIKEMANEAIQR
>CAD23614.1 unknown function [Trichophyton benhamiae (Arthroderma benhamiae)]
FITKAIPVLAALSAVNGAKILEAGPHAETIPNKYIVVMKKDVSDEAFSTHTTWLSQNLN
RRLMRRSGSSKAMAGMQNKYSLGGIFRAYSGEFDDAMIKDISNHDDVDYIEPDFVVRTST
NGTNLTRQENVPSWGLARVGSKQAGGTTYYYDSSAGKGV TAYVIDTGIDIEHEDFGGRAK
WGNFVDQRDEDCNGHGHVAGTVGGTKYGLAKSVSLVAVKVLDCDGSNSGVI RGM EW
AMREASGGNGTAKAAGKSVMMSLGGPRSQASNDAARAI SEAGIFMAVAAGNENMDAQHS
SPASEPSVCTVAASTEDDGKAEFSNYGAVVDVYAPGKDITS LKPGGSTDTLSGTSMASPH
VCGLGAYLIGLGKQGGPGLCDTIKQMANEAIQRPGEGTTGKLIY
>BAH09387.1 dipeptidyl peptidase [Trichophyton mentagrophytes]
MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKKDRPSG
WNLNLLKNGDISVLT TSDVSEITWLG DGT KIVVNGTDSVKGGVGIWISDAKNFGNAYK
AGSVNGAFSGLKLAKSGDKINFGYQSTTKGDLYNEAAAKEAVSSARIYDSL FVRHWD T
YVGTQFNAVFSGALTKSGDKYSFDGKLNKLVHPVKYAESPYPFFGGSGDYDLS SDGKTVA
FMSKAPELPKANL TTTYIFVPHDGSRVAEPINKRNGPRTPQIEGASSSPV FSPDGKRI
AYLQMATKNYESDRRVIYIAEVGSNKPVQRIASNWD RSPEVVKWSSDGR TLYVTAEDHAT
GKLFTLPADARD SHKPAVVKHDG SVSSFYFVGS SKSVLISGNSLWSNALFQVATPGRPNR
KLFYANEHDP ELKGLGPNDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG
SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFGQKL TDDITNDWGGAPYKDLVKIWEHV
RDHIKYIDTDNGIAAGASFGGFMVNIQGHDLGRKFKALVSHDGT FVGS SKIGTDELFFI
EHDFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHND FDFRLSVAEGVGLFNVLQEKG
IPSRFLNFPDETHWVTKPENSLVWHQQVLGWINKW SGINKSNPKSIKLSDCPIE VVDHEA
HSYFDY
>AAD52013.1 Tri r 2; secreted alkaline protease [Trichophyton rubrum]
MGFITKAIPVLAALSTVNGARILEAGPHAEIPNKYIVVMKREVSDEAFNAHTTWLSQS
LNSRIMRRAGSSKPMAGMQDKYSLGGIFRAYSGEFDDAMIKDISSHDDVDFIEPDFVVRT
TTNGTNLTHQDNVPSWGLARVGSKKPGGTTYYYDPSAGKGV TAYIIDTGIDIDHEDFQGR
AKWGENFVDQQNTDCNGHGHVAGTVGGTKYGLAKGVSLVAVKVLDCDGSNSGVIKGM
EWAMRQASGGNGTAKAAGKSVMMSLGGPRSEASNQAAKAISDAGIFMAVAAGNENMDA
QHSSPASEPSVCTVAASTKDDGKADF SNYGAVVDVYAPGKDITS LKPGGSTDTLSGTSMA
SPHVCGLGAYLIGLGKQGGPGLCDTIKMANDVIQSPGEGTTGKLIYNGSGK
>AAD52012.1 Tri r 4; serine protease [Trichophyton rubrum]
MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKKDRPSG
WNLNLLKNGDINVL T TSDVSEITWLG DGT KV VYINGTDSVKGGVGIWISDAKNFGNAYK
AGSVNGAFSGLKLAKSGDKINFGYQSTTKGDLYNEAAAKEAVSSARIYDSL FVRHWD T
YVGTQFNAVFSGLTKSGDKYSFDGKLNKLVQPVKYAESPYPPFFGGSGDYDLS SDGKTVA
FMSKAPELPKANL TTSYIFLVPHDGSRVAEPINKRNGPRTPQIEGASSSPV FSPDGKRI
AYLQMAAKNYESDRRVIHIAEVGTNKPVQRIASNWD RSPEAVKWSSDGR TLYVTAEDHAT
GKLFTLPADARDNHKPAVVKHDG SVSSFYF IGSSKSVLISGNSLWSNALYQVATPDRPNR
KLFYANEHDP ELKGLGPNDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG
SWGDNWSTRWNPRVWADQGYVVVAPNPTGSTGFGQKL TDDITNDWGGAPYKDLVKIWEHV
HDHIKYIDTDNGIAAGASFGGFMVNIQGGDLGRKFKALVSHDGT FVGS SKIGTDELFFI
EHDFNGTFFEARQNYDRWDCSKPELVAKWSTPQLVHND FDFRLSVAEGVGLFNVLQEKG
VPSRFLNFPDETHWVTKPENSLVWHQQVLGWVKNW SGINKSNPKSIKLSDCPIE VVDHEA
HSYFDY
>Q8J077.1 dipeptidyl peptidase [Trichophyton schoenleinii]

FITKAIPIVLAALSAVNGAKILEAGPHAETIPNKYIVVMKKDVSDEAFSTHTTWLSQNLN
RRLMRRSGSSKAMAGMQNKYSLGGIFRAYSGEFDDAMIKDISNHDDVDYIEPDFVVRTST
NGTNLTRQENVPSWGLARVGSQAGGTTYYYDSSAGKGVTAVIDTGIDIEHEDFGGRAK
WGKNFVDQRDEDCNGHGTHVAGTVGGTKYGLAKSVSLVAVKVLDCDGSNSGIVIRGMEW
AMREASGGGNGTAKAAGKSVNMMSLGGPRSQASNDAARAISEAGIFMAVAAGNENMDAQH
SSPASEPSVCTVAASTEDDGKAIEFSNYGAVVDVYAPGKDITSLKPGGSTDTLSGTSMASP
HVCGLGAYLIGLGKQGGPGLCDTIKQMANEAIQRPGEGETTGKLIY

>CAD23374.1 unknown function [Trichophyton schoenleinii]
MAAAKWLIASLAFASSGLAFTPEDFISAPRRGEAIPDPKGELAVFHVSKYNFDKDRPSG
WNLNLKNGDISVLTTSDDVSEITWLGDTGVVYVNGTDSVEGGVGIWISDAKNFGNAYK
AGSVNGAFSGLKLAKAGDKINFGYQSTTKGDLYNEAAAKEAVSSARIYDGLFVRHWDT
YVGTQFNAVFSGLTKNGDKYSFDGKLNKLVQPVKYAESPYPPFGGSGDYDLSDDGKTVA
FMSKAPELPKANLTTSYIFLVPHDGSRVAEPINKRNGPRTPQIEGASSPVFSPDGKRI
AYLQMATKNYESDRRVIHIAEVGSNKPVQRIASSWDRSPEAVKWSDDGRTLVTAEHDAT
GKLFTLPADARDNHKPSVVKHDGVSFFYFIGSSKSVLISGNSLWSNALYQVATPGRPNR
KLFYANEHDPPELKGKLPKIDIEPLWVDGARTKIHSWIVKPTGFDKNKVYPLAFLIHGGPQG
SWGDSWSTRWNPRVWADQGYVVVAPNPTGSTGFGQKLTDDITNDWGGAPYKDLVKIWEHV
RDHIKYIDTDNGIAAGASFGGFMVNIQGGDLGRKFKALVSHDGTFFVSSKIGTDELFFI
EHDFTNGTFFEARQNYDRWDCSKPELVAKWSTPQLVIHNSDFRLSVAEGVGLFNVLQKEG
IPSRFLNFPDETHWVTKPENSLVWHQQLGWINKWSGINKSNPKSIKLSDCPIEVIDHEA
HSYFDY

>COMPARE138 Tri t 1; beta-glucosidase, partial [Trichophyton tonsurans]
NNMAFSLGVKGPDSVKQLVDFEQDFVAL

>C0HJM6 Trip s 1; chitinase [Triplochiton scleroxylon]
EQGGSQAGGSL

>CAA35598.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]
MASKSSISPLLLATVLVSVFAAATATGPYCYAGMGLPINPLEGCREYVAQQTCGISISGS
AVSTEPGNTPRDRCKELYDASQHCRCCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDFA
KVLVTSGHCNVMTVHNAPYCLGLDI

>CAA42453.1 Tri a 40; alpha-amylase inhibitor [Triticum aestivum]
MASKSNYNLLFTALLVFIFAAFAVAVGNECTPWTSTLITPLPSCRNYVEEQACRIEMPGP
PYLAKQECCEQLANIPQQCRQCALRYFMGPKSRPDQSGLMELPGCPREVQMNFPVILVTP
GYCNLTTVHNTPYCLGMEESQWS

>CAA35597.1 Tri a 30; alpha-amylase inhibitor [Triticum aestivum]
MACKSSCSLLLLAAVLLSVLAAASASGSCVPGVAFRTNLLPHCRDYVLQQTCTGFTPGSK
LPEWMTSASIYSPGKPYLAKLYCCQELAEISQQCRCEALRYFIALPVPSQPVDPRSGNVG
ESGLIDLPGCPREMQWDFVRLLVAPGQCENLATHNVRYCPAVEQPLWI

>ACG59281.1 Tri a 40; alpha-amylase inhibitor [Triticum aestivum]
MASESNCVLLLLAAVLVSIFAFAAIAIGNEDCTPWTSTLITPLPSCRDYVEEQACRIETPGS
PYLAKQQCCGELANIPQQCRQCALRYFMGPKSRPDQSGLMELPGCPREVQMDVFRILVTP
GYCNLTTVHNTPYCLAMEESQWS

>CAZ76052.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]
TGPYCYAGMGLPINPLEGCREYVAQQTCGISISGS AVSTEPGNTPRDRCKELYDASQHC
RCEAVRYFIGRRSDPNSSVLKDLPGCPREPQRDFAKVLVTPGHCVMTVHNAPYCLGLDI

>CBA13559.1 Tri a 29; alpha-amylase inhibitor [Triticum aestivum]
TGPYCYPGMGLPSNPLEGCREYVAQQTCGVGIVGSPVSTEPGNTPRDRCKELYDASQHC
WCEAVRYFIGRTSDPNSSVLKDLPGCPREPQRDS AKVLVTPGHCVMTVHNTPYCLGLDI

>CBA13560.1 Tri a 15; alpha-amylase inhibitor [Triticum aestivum]
SGPWSWCDPATGYKVSALTGCRAMVKLQCVGSQVPEAVLRDCCQQLADVNNNEWCRCEDLS
SMLRSVYQELGAREGKEVLPGRCKEVMKLTAAASVPEVRKVPINPNSGDRAGVCYWAAYPD

V

>AAV39514.1 Tri a 28; alpha-amylase inhibitor [Triticum aestivum]
SGPWCYPGQAFQVPALPACRPLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSM
LDSMYKEHGAQEGQAGTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAA
YPDA

>COMPARE220 Tri a 28; alpha-amylase inhibitor, partial [Triticum aestivum]
EHGVSEGGAGTGAFPSR

>COMPARE222 alpha-amylase inhibitor, partial from P16347.1 [Triticum aestivum]
STEWIHIDSELVSGR

>CAA65313.1 Tri a 37; alpha-purothionin [Triticum aestivum]
MGSKGFKGVIVCLLILGLVLEQLQVEGKSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKI
SSGLSCPFGPKLALESNSDEPDTIEYCNLGRSSVCDYMVNAAAADDEEMKLYVENCADA
CVSFCNGDAGLPSLDAY

>CAA67128.1 Tri a 17; beta-amylase [Triticum aestivum]
MAGNMLANYVQVYVMLPLDVVSVDNKFEGKDEIRAQLKKLLEAGVDGVMIDVWGLVEGK
GPKAYDWSAYKQVFDLVHEAGLKLQAIMSFHQCGGNVGDVNIPIQWVRDVGATDPDIF
YTNRGGTRNIEYLTLGVDDQPLFHGRTAVQMYADYMASFRENMKKFLDAGTIVDIEVGLG
PAGEMRYPSPYQSQGWVFPGIGEFICYDKYLEADFKAAAAKAGHPEWELPDDAGEYNDTP
EKTQFFKDNQTYLTEKGFFLSWYSNKLKIHGDKILDEANKVFLGCRVQLAIKISGIHWW
YRVPNHAAELTAGYYNLDDRDGYRTIARMLTRHHASMNFTCAEMRDSEQSEEAKSAPEEL
VQQVLSAGWREGLHVACENALGRYDATAYNTILRNARPKGINKNGPPEHKLFGFTYLRLS
NELLEGQNYATFQTFVEKMHANLGHDPVDPVAPLERSKPEMPIEMILKAAQPKLEPPFP
DKNTDLPVKDHTDVGDEVLVAPV

>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

>CAY85463.1 Tri a 35; dehydrin [Triticum aestivum]
MEHQGHGAGEKKGVESITEKLPGGHGDHQQATGGTYGQQGHAGVTGENIKEKLPGGHGD
HQQTGMTGSETHATTATTDGNYGKSGHTGTDGTGENKSIMDKIKDKLPGQH

>AKJ77985.1 Tri a 45; elongation factor [Triticum aestivum]
MGKRKAAAKPPPRKGMKLDLTVFSCPCFNHGSSVECRIDLKLNLI GEANCQICQESFSTTA
NALTEAIDVYSEWIDECERVNTVEGDDGA

>AKJ77990.1 Tri a 44; endosperm transfer cell specific PR60 [Triticum aestivum]
MAKLMCLCFIILTIIVVSADECEGDRQEMIKQCAKYQQWPANPKVNPSDACCAVWQKAN
IPCLCAGVTKEKEKIWCMEKVAYVANFCKKPFPHGYKCGSYTFPPLA

>Q4W1F8 expansin [Triticum aestivum]
MASSSIAVAAAALILCILVAHAHGCYAKHHAAPSATNSSWLDAKATWYGPPHGAGPDDNGG
ACGFKNVNLPFFSSMTSCGNQPLFKDGGKCGSCYQIRCLKSDHPACSGVPKTVIITDMNY
YPVSRYHFDLSGTAFGAMAKDGRNDEL RHAGMINMQFKRVPCQYPGLTVTFHVEEGSNPF
YMAILVEYENGDDVNQLDIMESRPNGGKMAPTGQWVPMKESWGS IWRMDAHHMPKAPFS
LRITNESGKTLVAEQVIPIDWKPNKTYSSLVQFH

>AAA34272.1 Tri a 20; gamma-gliadin [Triticum aestivum]
MKTLILITILAMATTIATANMQVDPSSGQVQWPQQQPFQPPQPPFCQQPQRTIPQPHQTFH
HQPQQTFPQPQQTYPHQPQQQFPQTQQPQQPFPQPQQTFPQQPQLPFPQQPQQPFPQPQQ
PQQPFPQSQQPQQPFPQPQQQFPQPQQPQQSFPQQQQPAIQSFLQQQMNPKNFLLQQCN
HVSLSVSSLVSIILPRSDCQVMQQCCQQLAQIPQQLQCAAHSVAHSIIMQQEQQQGVPI
LRPLFQLAQGLGIIQPQQAQLEGIRSLVLKTLPTMCNVVYVPPDCSTINVPYANIDAGIG
GQ

>AAA34274.1 Tri a 20; gamma-gliadin [Triticum aestivum]
MKTLILITILAMAITIATANMQADPSGQVQWPQQQPFLLQPHQPFSSQQPQQIFPQPQQTFP
HQPQQQFPQPQQPQQQLFQPRQFPQPQQPYPQQPQQPFPQTQQPQQPFPQSKQPQQPF
PQPQQPQQSFPQQPSLIQQSLQQQLNPKNFLLQQCKPVSLVSSLWSIILPPSDCQVMR
QQCCQQLAQIPQQLQCAAHSVHHSIIMQQEQEQQLQGVQILVPLSQQQQVGGIILVQGG
GIIQPQQAQLEVIRSLVLQTLPTMCNVVYVPPYCSITIRAPFASIVASIGGQ

>AAA34285.1 gamma-gliadin [Triticum aestivum]
MKTFVLVFAIAVATSIAIAQMETSCISGLERPWQQQLPQQSFSQQPPFSQQQQQPLPQ
QPSFSQQQPPFSQQQPILSQPPFSQQQPVLPPQQSPFSQQQLVLPPQQQQQLLVQQQI
PIVQPSVLQQLNPKVFLQQQCSVPAMPQRLARSQMWQQSSCHVMQQCCQQLQQIPEQS
RYEAIRAIIYSIILQEQQQGFVQPQQQQPQQSGQGVSSQSQSQQLGQCSFQQPQQQLG
QQPQQQQQQVLQGTFLQPHQIAHLEAVTSIALRTLPTMCSVNVPLYSATTSVPFGVGTG
VGAY

>AAA34286.1 gamma-gliadin [Triticum aestivum]
TITRTFPIPTISSNNHHFRSNSNHFFHSNMQFYRNNSPGHNNPLNNNSPNNNSPSN
HHNSPNNNFQYHTHPSNHKNLPHTNMIQQQPPFSQQQQPPFSQQQQPVLPPQQSPPFSQQ
QQLVLPPQQQQQLLVQQQIPIVQPSVLQQLNPKVFLQQQCSVPAMPQRLARSQMWQQSS
CHVMQQCCQQLQQIPEQSRYEAIRAIIYSIILQEQQQGFVQPQQQQPQQSGQGVSSQSQ
QSQQQLGQCSFQQPQQQLGQQPQQQQQQVLQGTFLQPHQIAHLEAVTSIALRTLPTMCS
VNVPLYSATTSVPFGVGTG

>AAA34287.1 gamma-gliadin [Triticum aestivum]
PQQPFLPQQSFLWQSQQPFLQQPQQPSPQPQQVQIISPATPTTIPSAGKPTSAPFPQ
QQQQHQQLAQQQIPVVQPSILQQLNPKVFLQQQCSVPAMPQRLARSQMLQQSSCHVMQQ
QCCQQLPQIPQQSRYQAIRAIIYSIILQEQQVQGSIQSQQQPQQQLGQCVSQPQQQSQQ
QLGQQPQQQLAQGTFLQPHQIAQLEVMTSIALRILPTMCSVNVPLYRTTTSVPFGVGTG
VGAY

>AAA34288.1 Tri a 20; gamma-gliadin [Triticum aestivum]
MKTLILITILAMAITIGTANMQVDPSSQVQWPQQQPVQPHQPFSSQQPQQTFPQPQQTFP
HQPQQQFPQPQQPQQQLFQPPQFPQPQQPYPQQPQQPFPQTQQPQQLFQPSQQPQQQF
SQPQQQFPQPQQPQQSFPQQPPFIQPSLQQQVNPCKNFLLQQCKPVSLVSSLWSMIWPQ
SDCQVMRQQCCQQLAQIPQQLQCAAHTIHSIIMQQEQEQQGMHILLPLYQQQQVGG
GTLVQGGIIQ

>AAA34289.1 Tri a 20; gamma-gliadin [Triticum aestivum]
MKTLILITILAMAITIGTANIQVDPSSGQVQWLQQQLVPQLQQPLSQPPQQTFPQPQQTFP
HQPQQQVPQPQQPQQPFLQPPQFPQPQQPFPQTQQPQQPFPQQPQQPFPQTQQPQQPF
PQQPQQPFPQTQQPQQPFPQLQQPQQPFPQPQQQLPQPQQPQQSFPQQQRPFIQPSLQQ
LNPKNILLQQSKPASLVSSLWSIWPQSDCQVMRQQCCQQLAQIPQQLQCAAHSVHHS
IIMQQQQQQQQGIDIFLPLSQHEQVGGSLVQGGIIPQQAQLEAIRSLVLQTLPS
MCNVVYVPECSIMRAPFASIVAGIGGQ

>BAA11251.1 Tri a 20; gamma-gliadin [Triticum aestivum]
NIQVDPSSGQVQWPQQQPFQPHQPFSSQQPQQTFPQPQQTFPQPHQPPQFSQPQQPQQFIQ
PQQPFPQPQQTYPQRPPQFPQTQQPQQPFPQSQQPQQPFPQPQQQFPQPQQPQQSFPQ
QQPSLIQQSLQQQLNPKNFLLQQCKPVSLVSSLWSMILPRSDCQVMRQQCCQQLAQIPQ

QLQCAAIHSIVHSIIMQQEQEQEQRQGVQILVPLSQQQVVGQGLVQGGIIPQPPAQL
VIRSSVLQTLATMCNVYVPPYCSTIRAPFASIVAGIGGQ
>CAI78902.1 gamma-gliadin [Triticum aestivum]
MQVNPSVQVQPTQQQYPPESSQPPFISQSQQQFPQPQQPFPQQPFPQSQQQCLQQPQH
QFPQPTQQFPQRPLLPFTHPFLTFPDQLLPQPPHQSFQPPQSYPPQLPFPQPPQKY
PEQPQQPFPWQQPTIQLYLQQQLNPKCEFLQCRPVSLLSYLWSKIVQQSSCRMQQQC
CLQLAQIPEQYKCTAIDSIVHAIIFMQQGRQGVQIVQQQPQPQQVGGCVLVQGGVVPQ
QLAQMEAIRTLVLQSVPSMCFNVPNCSTIKAPFVGVVTGVGGQ
>BAN29066.1 Tri a 20; gamma-gliadin [Triticum aestivum]
NMQVDPSSQVQWPQQPVPQPHQPFSSQPPQTFPQPQQTFPHQPPQFPQPQQPQQFLQ
PQQPFPQQPQQPYPQQPQQPFPQTQQPQQLFQSSQPPQQFSQPQQQFPQPQQPQSFQ
QQPFIQPSLQQQVNPCKNFLQCKPVSLVSSLWSMIWPQSDCQVMRQQCCQQLAQIPQ
QLQCAAIHTIIHSIIMQQEQEQEQGMHILLPLYQQQVVGQGLVQGGIIPQPPAQL
AIRSLVLQTLPTMCNVYVPPYECSTIKAPFSSVWVAGIGGQ
>CAA35238.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILALLAIVATTARIAVRVPVPLQPPQNPSSQQQPQEQVPLVQQQQFPGQQQFPFPQ
QPYPQPQPFPSQQPYLQLQPFQPPQLPYPQPQLPYPQPQLPYPQPQFRPQQPYPQSQPQ
YSQPQQPISQQQQQQQQQQKQQQQQQQILQQILQQQLIPCRDVVLQQHSIAYGSSQV
LQQSTYQLVQQLCCQQLWQIPEQSRCAIHNVVHAIILHQQQQQQQQQQQPLSQVVFQ
PQQQYPSGQGSFQPSQQNPQAQGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAP
VGIFGTN
>CAA25593.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILVLLAIVATTATTAVRFPVPLQPPQNPSSQQQPQEQVPLVQQQQFLGQQQFPFPQ
QPYPQPQPFPSQLPYLQLQPFQPPQLPYSQPQFRPQQPYPQPQPYSQPQQPISQQQQQ
QQQQQQQQQQQQQILQQILQQQLIPCMDVVLQQHNIHAGRSQVLQQSTYQLLQELCCQHL
WQIPEQSQCAIHKVVHAIILHQQQKQQQPSSQVVFQPLQQYPLGQGSFRPSQQNPQA
QGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN
>CAA26383.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILALLAIVATTATTAVRFPVPLQPPQNPSSQPPQEQVPLVQQQQFPGQQQFPFPQ
QPYPQPQPFPSQQPYLQLQPFQPPQLPYPQPQPPFSPQQPYPQPQPYPQPQQPIS
QQQAQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHNIHARSQVLQQSTYQP
LQQLCCQQLWQIPEQSRCAIHNVVHAIILHQQQRQQQPSSQVSLQQPQQYPSGQGFQ
PSQQNPQAQGSVQPQQLPQFEEIRNLALQTLPRMCNVYIPPYCSTTIAPFGIFGTN
>CAA26384.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILVLLAIVATTATTAVRFPVPLQPPQNPSSQQQPQEQVPLVQQQQFLGQQQFPFPQ
QPYPQPQPFPSQLPYLQLQPFQPPQLPYSQPQFRPQQPYPQPQPYSQPQQPISQQQQQ
QQQQQQQQQQQQQILQQILQQQLIPCMDVVLQQHNIHAGRSQVLQQSTYQLLQELCCQHL
WQIPEQSQCAIHNVVHAIILHQQQKQQQPSSQVVFQPLQQYPLGQGSFRPSQQNPQA
QGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN
>CAA26385.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILALVATTATTAVRVPVPLQPKNPSSQQQPQEQVPLVQQQQFPGQQQFPFPQPY
PQPQPFPSQQPYLQLQPFQPPQLPYPQPQSFPPQQPYPQQRPMYLPQQPISQQQ
AQQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHNIHASSQVLQQSTYQLLQQL
CCQQLLQIPEQSRCAIHNVVHAIIMHQEQQQQLQQQQQQQLQQQQQQQQQQQPSQV
SFQQPQQYPSQGSFQPSQQNPQAQGSVQPQQLPQFAEIRNLALQTLPAMCNVYIPPHC
STTIAPFGIFGTN
>AAA34275.1 Tri a 21; gliadin [Triticum aestivum]
MKTFLILALLAIVATTATTAVRFPVPLQPPQNPSSQQQPQEQVPLVQQQQFPGQQQFPFPQ
QPYPQPQPFPSQQPYLQLQPFQPPQLPYPQPQSFPPQQPYPQQPQYLQPQQPISQ
QQAQQQQQQQQQQQQQQQQQILQQILQQQLIPCRDVVLQQHNIHASSQVLQQSTYQLLQQL

CCQQLLQIPEQSQCQAIHNVHAHAIIMHQOQQQQQEQKQQLQQOQQQQQQQLQQOQQQQQQQ
PSSQVVSFQQPQQYPSQVVSFQPSQLNPQAQGSVQPQQLPQFAEIRNLALQTLPAMCNVY
IPPHCSTTIAPFGISGTN

>AAA34276.1 Tri a 21; gliadin [Triticum aestivum]
MKTFPILALLAIVATTATTAVRVPVPLQQLQNPSSQQQPQEQVPLVQEQFQGGQQPFPQQ
QPYPQPQPFPSQQPYLQLQPFQPPQLPYPQPQFRPQQPYPQPQYSPQQPISQQQQQ
QQOQQQQQQQILQQILQQQLIPCRDVLQOHNIAHGSSQVLQESTYQLVQQLCCQQLWQI
PEQSRCQAIHNVVHAIILHQHHHQOQQQQQQQPLSQVVSFQQPQQYPSGGQFFQPSQ
QNPQAQGSFQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN

>AAA34279.1 Tri a 21; gliadin [Triticum aestivum]
MKTFILILALVATTATTAVRVPVPLQPKNPSQQQPQEQVPLVQQQFPGQQQQPFPQQPY
PQPQPFPSQQPYLQLQPFQPPQLPYPQPQSFPPQQPYPQQRPKYLQPPQISQQQ
AQOQQQQQQQQQQQQQQQILQQILQQQLIPCRDVLQOHNIAHASSQVLQQSTYQLLQQL
CCQQLLQIPEQSQCQAIHNVVHAIIMHQEQOQQQLQQOQQQQQLQQOQQQQQQQQPSSQV
SFQQPQQYPSQGSFQPSQQNPQAQGSVQPQQLPQFAEIRNLALQTLPAMCNVYIPPHC
STTIAPFGIFGTN

>AAA34280.1 Tri a 21; gliadin [Triticum aestivum]
MKTFILILVLLAIVATTATTAVRFPVPLQPPQNPSSQQQPQEQVPLVQQQFLGQQQPFPQQ
QPYPQPQPFPSQLPYLQLQPFQPPQLPYSQPQFRPQQPYPQPQYSPQQPISQQQQQ
QQOQQQQQQQQQQQILQQILQQQLIPCMDVVLQOHNIAHGRSQVLQQSTYQLLQELCCQHL
WQIPEQSQCQAIHNVVHAIILHQOQKQQQQPSSQVVSFQQPLQQYPLGQGSFRPSQQNPQA
QGSVQPQQLPQFEEIRNLALQTLPAMCNVYIPPYCTIAPFGIFGTN

>AAA34281.1 Tri a 21; gliadin [Triticum aestivum]
MKTFILILALLAIVATTATTAVRVPVPLQPPQNPSSQQQPQEQVPLVQQQFLGQQQPFPQQ
QPYPQPQPFPSQQPYLQLQPFQPPQLPYSQPQFRPQQPYPQPQYSPQQPISQQQQQ
QQOQQQQQQQQQQQIIQQILQQQLIPCMDVVLQOHNIVHGKSQVLQQSTYQLLQELCCQH
LWQIPEQSQCQAIHNVVHAIILHQOQKQQQQPSSQVVSFQQPLQQYPLGQGSFRPSQQNPQ
AQGSVQPQQLPQFEEIRNLARK

>AAA34282.1 Tri a 21; gliadin [Triticum aestivum]
MKTFILILALRAIVATTATIARVPVPLQPPQNPSSQQQPQKQVPLVQQQFPGQQQPFPQQ
QPYPQQQPFPSQQPYMQLPFQPPQLPYPQPQLPYPQPQFRPQQSYPPQPQYSPQQP
ISQQOQQQQQQQQQQQILQQILQQQLIPCRDVLQOHSIAHGSSQVLQQSTYQLVQQFC
CQQLWQIPEQSQCQAIHNVVHAIILHQOQQQQQQQQQQQPLSQVCFQSSQQYPSGGG
SFQPSQQNPQAQGSVQPQQLPQFEEIRNLAETLPAMCNVYIPPYCTIAPVGFIFGTN

>AAA34283.1 Tri a 21; gliadin [Triticum aestivum]
MKTFILILALLAIVATTATSARVPVPLQPPQNPSSQQQPQEQVPLMQQQQFPGQQEQFPP
QQPYPHQQPFPSQQPYPQPQFPFPQLPYPQTPFPQQPYPQPQYSPQQPISQQQAQ
QQOQQQQTLQQILQQQLIPCRDVLQOHNIAHASSQVLQQSSYQLLQQLCCQQLFQIPEQ
SRCQAIHNVVHAIILHHHQOQQQQPSSQVSYQQPQEQYPSGQVVSFQSSQQNPQAQGSVQP
QQLPQFQEIRNLALQTLPAMCNVYIPPYCSTTIAPFGIFGTN

>BAA12318.1 Tri a 21; gliadin [Triticum aestivum]
VRVPVPLQPPQNPSSQQQPQEQVPLVQQQFLGQQQFPPQQPYPQPQPFPSQQPYLQLQ
FPQPQLPYSQPQFRPQQPYPQPQYSPQEPISQQOQQQQQQQILQQILQQQLIPCM
DVLQOHNIAHGRSQVLQQSTYQLLQELCCQHLWQIPEQSQCQAIQNVVHAIILHQOQK
QQQPSQVVSFQQPLQQYPLGQGSFRPSQQNPQDQGSVQPQQLPQFEEIRNLALQTLPAMC
NVYIPPYCTIAPFGIFGTN

>CAY54134.1 Tri a 21; gliadin [Triticum aestivum]
VRVPVPLQPPQNPSSQQQPQEQVPLVQQQFLGQQQHFPQQQFPPQQPYPQPQFPPLQ
LPYPQPQFPQQSYPPQPQYSPQPPISQQQAQLQQOQQQQQQQILQQILQQQLIPCR
DVLQOQPNIAHASSQVSSYQLLQQLCCQQLWQTPEQSRCQAIHNVHAIILHHQQQQQ

QQQQQQQQQQQQQQQQQQQQQQQQPSSQVSYQQPQQQYPSGQGSFQPSQQNPQAQGFVQPQ
QLPQFEEIRNLALQTL PAMCNVYIPPYCSTTIAPFGIFSTN

>AAA34284.1 Tri a 21; gliadin, partial [Triticum aestivum]
PQPQPQYSQPQQPISQQQQQQQQQQQQQQQEQQILQQILQQQLIPCMDVVLQQHNIHGR
SQVLQQSTYQLLQELCCQHLWQIPEQSQCQAIHNVVHAILHQQQQKQQQQPSSQFSFQQ
PLQQYPLGQGSFRPSQQNPQAQGSVQPQQLPQFEEIRNLALQTL PAMCNVYIPPYCTIAPF
GIFGTN

>ACE82289.1 glutathione S-transferase [Triticum aestivum]
MAGEKGLVLLDFWVSPFGQRVRIALAEKGLPYEYAEEDLMAGKSDRLLRANPVHKKIPVL
LHDGRPVNESLIILQYLEDAFPDAPALLSPDPYARAQARFWADYVDKVVYDCGSRLWKLK
GEPQAQARAEMLDILKTLDGALGDKPFFGGDKFGFVDAAFAPFTAWFHSYERYGEFSLPE
VAPKIAAWAKRCGERESVAKSLYSPDKVYDFIGLLKKKYGIE

>CAZ76054.1 Tri a 34; glyceraldehyde-3-phosphate-dehydrogenase [Triticum aestivum]
MGKIKIGINGFGRIGRLVARVALQSDDELVAVNDPFITTEYMTYMFKYDTHVGHWKHSD
IKLKDDKTLFGEKPVTVFVGRNPEEIPWGEAGADYVVESTGVFTDKDKAAAHKGGAKK
VVISAPSKDAPMFVGVNEDKYTSDVNIVSNASCTTNCLAPLAKIINDNFGIIEGLMTTV
HAITATQKTVDGPSSKDWRRGGAASFNIIPSSTGAAKAVGKVLPELNGKLTGMSFRVPTV
DVSVDLTVRTEKAASYDDIKKAIKAASEGKLGKIMGYVEEDLVSTDFVGDSSIFDAK
AGIALNDHFVKLVSWYDNEWGYSNRVVDLIRHMAKTQ

>CAA43331.1 Tri a 26; HMW glutenin [Triticum aestivum]
MTKRLVLF AAVVALVALTAAEGEASGQLQCERELQEHSKACRQVVDQQLRDVSPECQP
VGGGPVARQYEQQVVVPPKGGSFYPPGETTPPQQQQSILWGIPALLRRYYLSVTSPQQVS
YYPGQASSQRPGQGQQPGQGQQEYLLTSPQQSGQWQQPGQGQAGYYPTSPQQSGQEPPGY
YPTSPWQPEQLQQPTQGQQRQQPGQGQQLRQGQQGQQSGQGQPRYYPTSSQQPGQLQQLA
QGQQGQQPERGQQGQQSGQGQQLGQGQQGQQPGQKQQSGQGQQGYYPISPQQLGQGQQSG
QGQLGYPTSPQQSGQGQSGYYPTSAQQPGQLQQSTQEQQLGQEQDQQSGQGRQGQQSG
QRQQDQQSGQGQQPGQRQPGYYSTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQ
QGQQPEQGQQGQQPGQGEQGQQPGQGQQGQQPGQGQPGYYPTSPQQSGQGQPGYYPTSPQ
QSGQLQQPAQGQQPGQEQQGQQPGQGQQGQQPGQGQPGQGQPGYYPTSPQQSGQEQQLE
QWQQSGQGQPGHYPTSPLQPGQGQPGYYPTSPQQIGQGQQPGQLQQPTQGQQGQQPGQGQ
QGQQPGQGQQGQQPGQGQQPGQGQPGYYPTSLQQSGQGQQPGQWQQPGQLPGYYPTSSL
QPEQGQQGYPTSPQQPGQPGQWQQSGQGQQGYPTSPQQSGQGQQPGQWLQPGQWL
QSGYYLTSPQQLGQGQQPRQWLQPRQGQQGYPTSPQQSGQGQQLGQGQQGYPTSPQQS
GGQGQQGYDSPYHVS AEHQAASLKVAKAQQQLAAQLPAMCRLEGGDALLASQ

>CAA31396.1 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLF AAVVIALVALTTAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG
LQMRCCQQLRDVSAKCRSVAVSQVARQYEQTVVPPKGGSFYPPGETTLPQQQLQQGIFWGTS
SQTVQGYYPGVTS PRQGSYYPGQASPPQPGQGQQPGKWQEPGQGQQWYYPTSLQQPGQGQ
QIGKGGQQGYPTSLQQPGQGQQGYPTSLQHTGQRQQPVQGGQPEQGQQPGQWQQGYPT
SPQQLGQGQQPRQWQQSGQGQQGHYPTSLQQPGQGQQGHYLASQQPGQGQQGHYPASQQ
QPGQGQQGHYPASQQPGQGQQGHYPASQQEPGQGQQGQIPASQQPGQGQQGHYPASLQ
QPGQGQQGHYPTSLQQLGQGQQTGQPGQKQQPGQGQQTGQGQQPEQEQQPGQGQQGYPT
SLQQPGQGQQGQQGQQGYPTSLQQPGQGQQGHYPASLQQPGQGQPGQRQQPGQGQHPEQ
GKQPGQGQQGYPTSPQQPGQGQQLGQGQQGYPTSPQQPGQGQQPGQGQQGHCPTSPQQ
SGQAQQPGQGQQIGQVQQPGQGQQGYPTSVQQPGQGQQSGQGQQSGQGHPGQGQQSGQ
EQQGYDSPYHVS AEQAASPMVAKAQQPATQLPTVCRMEGGDALSASQ

>CAA26847.1 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLF AAVVIALVALTTAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG
LQMRCCQQLRDVSAKCRSVAVSQVARQYEQTVVPPKGGSFYPPGETTLPQQQLQQGIFWGTS
SQTVQGYYPVTS PRQGSYYPGQASPPQPGQGQQPGKWQEPGQGQQWYYPTSLQQPGQGQ

QIGKKGQGYPTSLQQPGGQQIGQGQQGYPTSPQHTGQRQQPVQGGQIGQGQQPEQGG
QPGQWQQGYPTSPQQLGQGQQPGWQQSGQGQQGHYPTSLQQPGGQQGHYLASQQQPA
QGQQGHYPASQQPGQGQQGHYPASQQPGQGQQGHYPASQQEPGGQQGQIPASQQQPG
QGQQGHYPASLQQPGQQGHYPTSLQQLGQGQQIGQPGQKQQPGGQQTGQQQQPEQEQQP
GGQQGYPTSLQQPGGQQQQGGQQGYPTSLQQPGGQQGHYPASLQQPGGQQGQPGQ
RQQPGGQHPEQGQQPGQGQQGYPTSPQQPGGQQLGQGQQGYPTSPQQPGGQQPGQ
GGQGHCPMSPQQTGAQQLGQGQQIGQVQQPGQGQQGYPTSLQQPGGQQSGQGQQSGQ
GHQPGGQQSGQEKGQYDSPYHVSAAEQQAASPMVAKAQQPATQLPTVCRMEGGDALSASQ
>CAA43361.1 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLFATVVITLVALTAAEGEASRQLQCERELQESSLEACRQVVDQQLAGRLPWSTG
LQMRCQQLRDVSAKCRPVAVSQVVRQYEQTVPKGGSFYPGETTPLLQQLQQVIFWGT
SQTVQGYPSVSSPQQGPPYYPGQASPPQPGQGQQPGKWQELGQGQQGYPTSLHQSGQGQ
QGYYPSSLQQPGGQQIGQGQQGYPTSLQQPGGQQIGQGQQGYPTSPQHPGQRQQPG
QGQQIGQGQQLGQGRQIGQGQQSGQGQQGYPTSPQQLGQGQQPGWQQSGQGQQGYPT
SQQQPGGQQGQYPASQQPGQGQQGQYPASQQPGQGQQGQYPASQQPGQGQQGHYLA
SQQQPGGQQRHYPASLQQPGGQQGHYASLQQPGGQQGHYPASLQQVGGQQIGQLG
QRQQPGGQQTRQGQLEQGQQPGGQQTRQGQLEQGQQPGGQQGYPTSPQQSGQGQ
QPGQSQQPGGQQGYSSSLQQPGGQLQGHYPASLQQPGGHPGQRQQPGGQQPEQGQQ
PGGQQGYPTSPQQPGGKQLGQGQQGYPTSPQQPGGQQPGGQQGHCPTSPQQTGQ
AQPPGGQQIGQVQQPGQGQQGYPTSLQQSGQGQQSGQGQQSGQHQLGQGQQSGEQQ
GYDNPYHVNTEQQTASPKVAKVQQPATQLPIMCRMEGGDALSASQ
>AAB02788.1 Tri a 26; HMW glutenin [Triticum aestivum]
MTKRLVLFVAVVVALVALTAAEGEASGQLQCERELQEHSLKACRQVVDQQLRDVSPECQP
VGGGPPVARQYEQVVVPPKGGSFYPGETTTPPQQLQQSILWIPALLRRYYLSVTSPQQVS
YYPGQASSQRPGGQQEYLLTSPQQSGQWQQPGGQSGYPTSPQQSGQKQPGYPTSPW
QPEQLQQPTQGQRQQPGGQQLRQGQQGQQSGQGQPRYYPTSSQQPGQLQQLAQGQQGQ
QPERGQQGQQSGGQQLGQGQQGQQPGQKQQSGQGQQGYPTSPQQLGQGQQSGGQLGY
YPTSPQQSGGQSGYPTSAQQPGQLQOSTQEQQLGQEQDQSGQGRQGQQSGRQQDQ
QSGGQQPGQRQPGYYTSPQQLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQQGQQPE
QGQQGQQQRQGEQGQQPGGQQGQQPGGQPGYPTSPQQSGGQPGYPTSPQQSGQLQ
QPAQGQQPGQEQQGQQPGGQQPGGQPGYPTSPQQSGQEQQLEQWQQSGGQPGHYPT
SPLQPGGQPGYPTSPQQIGQGQQPGQLQQPTQGQQGQQPGGQQGQQPGEGQQGQQPG
QGQQPGGQPGYPTSLQQSGGQQPGWQQPGGQPGYPTSSLQPEQGQQGYPTSQQ
QPGGQPGQWQQSGGQQGYPTSPQQSGGQQPGQWLQPGQWLQSGYYLTSPQQLGQG
QQPRQWLQPRQGQQGYPTSPQQSGGQQLGQGQQGYPTSPQQSGGQQGYDSPYHVSA
EHQAASLKVAKAQQLAQLPAMCRLEGGDALLASQ
>CAA27052.1 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLFVAVVVALVALTAAEGEASEQLQCERELQELQERELKACQQVMDQQLRDISPE
CHPVVVPVAGQYEQIIVPKGGSFYPGETTTPPQQLQQRIFWIPALLKRYPSVTSPQQ
VSYYPGQASPRPGGQQPGGQQSGGQQGYPTSPQQPGWQQPEQGQPGYPTSPQQ
PGQLQQAQGGQQPGGQQGRQPGGQPGYPTSSQLQPGQLQQAQGGQQPGGQQGQ
QPGGQQPGGQQGQQPGGQQPGGQQGQLGQGQQGYPTSLQQSGGQPGYPTSLQ
QLGQGQSGYPTSPQQPGGQQPGQLQQAQGGQPEQGQQGQQPGGQQGQQPGGQQPG
QGQPGYPTSPQQSGGQPGYPTSSQQPTQSQQPGGQQGQQVGGQQAQPPGGQQPG
QGQPGYPTSPQLSGGQPGYLLTSPQQSGGQQPGQLQQAQGGQKGGQPGGQQPGGQ
QGQQPGGQQGQQPGGQPGYPTSPQQSGGQQPGWQQPGGQPGYPTSPQLQPGGQ
PGYDPTSPQQPGGQQPGQLQQAQGGQQGQLAQGGQQPAQVQQGQQPAQGGQQGQLG
QGQQGQQPGGQQPAQGGQQGQQPGGQQGQQPGGQQPGGQPWYPTSPQESGGQQPG
QWQQPGWQQPGGQPGYLLTSPQLGQGQQGYPTSLQQPGGQQPGWQQSGGQHGY
YPTSPQLSGGQRPGQWLQPGGQQGYPTSPQQSGGQQLGQWLQPGGQQGYPTSLQ

QTGQGQSGQGQGGYSSYHVSVEHQAASLKVAKAQQLAAQLPAMCRLEGGDALSASQ
>AAZ23584.1 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLFVAVVVALVALTAAEGEASGQLQCEHELEACQQVVDQQLRDVSPGCRPITVSP
GTRQYEQPVVPSKAGSFYPSSETTPSQQLQQMIFWGIPIALLRRYYPSVTSSQQGSYYPGQ
ASPQQSGQGQPPGQEQQPGQGQDQDPGQRQQGYPTSPQQPGQGQQLGQGQPGYYPTSQ
QPGQKQAGQGQSGQGQGGYPTSPQQSGQGQPPGQPGYYPTSPQQSGQWQPPGQGQ
QPGQGQSGQGQGGQPPGQGRPGQGQGGYPTSPQQPGQGQSGQGQPGYYPTSLRQPG
QWQPPGQGQPPGQGQGGQPPGQGQSGQGQGGYPTSLQQPGQGQQLGQGQPGYYPTSQQ
SEQGQPPGQKQPGQGQGGYPTSPQQSGQGQQLGQGQPGYYPTSPQQSGQGQSGQGQ
GYYPTSPQQSGQGQPPGQGQSGYFPTSRQQSGQGQPPGQGQSGQGQGGQPPGQGQAYY
PTSSQQSRQRQAGQWQRPQGQPPGYYPTSPQQPGQEQQSGQAQQSGQWQLVYYPTSPQQ
PGQLQPPAQGQPPAQGQSAEQPPGQAQQSGQWQLVYYPTSPQQPGQLQPPAQGQGGY
PTSPQQSGQGQGGYPTSPQQSGQGQGGYPTSPQQSGQGQPPGQGQPPRQGQGGYPTSP
PQQSGQGQPPGQGQGGYPTSPQQSGQGQPPGHEQQPGQWLQPGQGQGGYPTSSQQSGQ
GHQSGQGQGGYPTSLWQPGQGQPPGQGQGGYASPYHVS AEYQAARLKVAKAQQLAAQLP
AMCRLEGS DALSTRQ

>CAA31395.4 Tri a 26; HMW glutenin [Triticum aestivum]
MAKRLVLFVAVVVALVALTVAEGEASEQLQCERELQELQERELKACQQVMDQQLRDISPE
CHPVVVPVAGQYEQIVVPPKGGSFYPGETTPPQQLQQRIFWGIPIALLKRYPSVTCPQ
QVSYYPGQASPRPGQGQPPGQGQGGYPTSPQQPGQWQPEQGQPRYYPTSPQQSGQLQ
QPAQGQPPGQGQGGQPPGQGQPGYYPTSSQLQPGQLQPPAQGQGGQPPGQAQQGQPPGQ
QQPGQGQGGQPPGQGQGGQPPGQGQGGQQLGQGQGGYPTSLQQSGQGQPGYYPTSLQQLGQG
QSGYYPTSPQQPGQGQPPGQLQPPAQGQPPGQGQGGQPPGQGQGGQPPGQGQPPGQGQPPG
YYPTSPQQSGQGQPGYYPTSSQQPTQSQQPGQGQGGQVVGQQAQQPGQGQPPGQGQPPG
YYPTSPQQSGQGQPGYYLTSPQQSGQGQPPGQLQQSAQGQKGGQPPGQGQPPGQGQGGQPP
GGQGGQPPGQGQPPGYYPTSPQQSGQGQPPGQWQPPGQGQPGYYPTSP LQPGQGQPPGYDP
TSPQQPGQGQPPGQLQPPAQGQGGQQLAQGQGGQPPAQVQQGQPPAQGQGGQPPGQGQGG
QQLGQGQGGQPPGQGQGGQPPAQGQGGQPPGQGQGGQPPGQGQGGQPPGQGQPPGQGQPPW
YYPTSPQESGQGQPPGQWQPPGQGQPGYYLTSP LQLGQGQGGYPTSLQQPGQGQPPGQW
QQSGQGQHYYPTSPQLSGQGQPPGQWLQPPGQGQGGYPTSPQQPGQGQQLGQWLQPPGQ
QQGGYPTSLQQTGQGQSGQGQGGYSSYHVSVEHQAASLKVAKAQQLAAQLPAMCRLEG
GDALSASQ

>BAN29068.1 Tri a 26; HMW glutenin [Triticum aestivum]
EGEASEQLQCERELQEHSLKACRQVVDQQLRDVSPQCQVGGPVARQYEQVVVPPKGG
SFYPGETTPPQQLQQSILWGIPIALLRRYYLSVTSPQQVSYYPGQASSQRPGQGQGEYLLT
SPQQSGQWQPPGQGQSGYPTSPQQSGQKQPGYYPTSPWQPEQLQPTQGGQRQQPGQGQ
QLRQGQGGQSGQGQPRYYPTSSQQPGQLQQLAQGQGGQPPERGQGGQSGQGQQLGQGQ
QGQPPGQKQSGQGQGGYPTSPQQLGQGQSGQGQLGYYPTSPQQSGQGQSGYYPTSAQ
QPGQLQQSTQEQLGQEQQDQSGQGRQGQSGQRQQDQSGQGQPPGQRQPGYYSTSPQ
QLGQGQPRYYPTSPQQPGQEQQPRQLQQPEQGQGGQPPGQGQGGQPPGQGQGGQPPGQGQ
QGQPPGQGQPGYYPTSPQQSGQGQPGYYPTSPQQSGQLQPPAQGQPPGQEQQGQPPGQGQ
QPGQGQPGYYPTSPQQSGQEQQLEQWQSGQGQPPGHYPTSP LQPGQGQPGYYPTSPQQIG
QGQPPGQLQPTQGGQGGQPPGQGQGGQPPGEGQGGQPPGQGQPPGQGQPGYYPTSLQQSG
QGQPPGQWQPPGQGQPGYYPTSSLPQEQQGGYPTSPQQPGQPPGQWQSGQGQGGY
YPTSPQQSGQGQPPGQWLQPPGQWLQSGYYLTSPQQLGQGQPPRQWLQPPRQGQGGYPTSP
QQSGQGQQLGQGQGGYPTSPQQSGQGQGGYDSPYHVS AEHQAASLKVAKAQQLAAQLPA
MCRLEGGDALSASQ

>CAA24934.1 Tri a 26; HMW glutenin, partial [Triticum aestivum]
LVSVEHQAARLKVAKAQQLAAQLPAMCRLEGGDALSASQ

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

EKLGQGGQPRQWLQPRQGQGGYYPTSPQQSGGQQLGQGGQGGYYPTSPQQSGGQGGYDS
PYHVSAEHQAASLKVAKAQQQLAAQLPAMCRLEGGDALLASQ
>P24296.2 lipid transfer protein [Triticum aestivum]
AQVMLMAVALVLMLAAPRAAVIDCGHVDLSLRPCLSYVQGGPGPSGQCCDGVKNLHNQ
ARSQSDRQSACNCLKGIARGIHNLNEDNARSIPPKCGVNLPTYISLNIIDCSR
>CAI64398.1 Tri a 44; lipid transfer protein [Triticum aestivum]
IAVAVSADECEGDRRAMIKECAKYQQWPANPKLDPSDACCVAWQKANIPCLCAGVTKEKE
KIYCMKVVAVANFCKKPFPHGYKCGSYTFPPLA
>D2T2K2 Tri a 14; lipid transfer protein [Triticum aestivum]
ISCSQVDSTLMPCLQYVQGGSPARGCCTGIQNLLAEANNSPDRRTICGCLKNVANGASG
GPYITRAAALPSKCNVALPYKISPSVDCNTVH
>CAA31685.1 Tri a 36; LMW glutenin [Triticum aestivum]
MKTFLV FALLAVAATSAIAQMETRCIPGLERPWQQQLPQQTFPQQPLFSQQQQQLFP
QQPSFSQQQPPFWQQQPPFSQQQPILPQQPPFSQQQLVLPQQPPFSQQQPVLPPQQSP
FPQQQQHQQLVQQQIPVVQPSILQQLNPCKVFLQQCSPVAMPQRLARSQMLQQSSCHV
MQQQCCQQLPQIPQQSRYEAIRAIYSIILQEQQVQGSIQSQQQPQQLGQCVSQPQQ
SQQQLGQQPQQQLAQGTFLQPHQIAQLEVMTSIALRILPTMCSNVNPLYRRTTTSVPFGV
GTGVGAY
>CAA30570.1 Tri a 36; LMW glutenin [Triticum aestivum]
MKTFLV FALLALAAASAVAQISQQQAPPFSQQQPPFSQQQPPFSQQQSPFSQQQQ
PPFAQQQPPFSQQPPISQQQPPFSQQQPPFSQQQPPFSQQQPPFSQQQPPFSQQ
QQPPFSQQQPPFTQQQQQQQQPPFTQQQPPFSQQPPISQQQPPFLQQRPPFSRQ
QQIPVIHPSVLQQLNPCKVFLQQCIPVAMQRLARSQMLQQSICHVMQQQCCQLRQIP
EQSRHESIRAIYSIILQQQQQQQQQQQQGQSIIQYQQQPQQLGQCVSQPLQQLQQ
LGQQPQQQLAHQIAQLEVMTSIALRILPTMCSNVNPLYRRTTTSVPLGVGIGVGY
>CAA59338.1 Tri a 36; LMW glutenin [Triticum aestivum]
FALIAVATSTIAQMETSCIPGLERPWQQQLPQQTLFPQQPFPQQPPFSQQQPSFS
QQQPPFSQQQPILPEPPFSLQQQPVLPPQQSPFSQQQLVLPQQQQQLPQQQISIVQPSVL
QQLNPCKVFLQQCSPVAMPQRLARSQMWQSRCHVMQQQCCQLSQIPEQSRDAICAI
TYSIILQEQQGQFVQAQQQPQQSGQVVSQSQQSQQQLGQCSFQQPQQ
>CAA59339.1 Tri a 36; LMW glutenin [Triticum aestivum]
HIPSLEKPLQQPLPLQQLLWYQQQPIQQQPQPFQPPCSQQQPPLSQQQPPFSQQ
QPPFSQQQPILPQQPPFSQQQQFPQQQPLLPPQQPPFSQQQPPFSQQQPPFSQQQ
QPILLQPPFSQHQQPVLPPQQIPSVQPSILQQLNPCKVFLQQCSPVAMPQSLARSQML
WQSSCHVMQQCCRQLPQIPEQSRDAIRAIYSIVLQEQQHGQLNQPQQQPQQSVQG
VSQPQQQKQLGQCSFQQPQQ
>CAA59340.1 Tri a 36; LMW glutenin [Triticum aestivum]
HIPSLEKPSQQPLPLQQLLWYHQQPIQQQPQPFQPPCSQQQPPLSQQQPPFSQQ
QPPFSQQELPILPQQPPFSQQQPQFSQQQPFPQQQPLLQPPFSQQRPPFSQQQQ
PVLPPQQPPFSQQQQQPILPQQPPFSLHQQPVLPPQQIPYVQPSILQQLNPCKVFLQQC
SPVAMPQSLARSQMLWQSSCHVMQQCCQQLPRIPEQSRDAIRAIYSIVLQEQQHGQ
FNQPQQQPQQSVQGVSQPQQQKQLGQCSFQQPQQ
>CAI79052.1 Tri a 36; LMW glutenin [Triticum aestivum]
MSHIPGLERPSQQPLRPQQLSHHHHQPIQQQPQFPQQQPCSQQQQPPLSQQQPP
FSQQQPPFSQQQPVLPPQPSFSQQQLPPFSQQQPPFSQQQPVLPPQPSFSQQQLPP
FSQQLPPFSQQQPVLQQQIPFVHPSILQQLNPCKVFLQQCSPVAMPQSLARSQMLQQ
SSCHVMQQCCQQLPQIPQQSRYEAIRAIVYSIILQEQQVQGSIQTQQQPQQLGQCVS
QPQQSQQQLGQCSFQQPQQLQQLGQQPQQQIPQGIQFLQPHQISQLEVMTSIALRILPT
MCGVNVPLYSSSTIMPFSIGTGVGGY
>O22108 Tri a 36; LMW glutenin [Triticum aestivum]

RCIPGLERPWQQQLPQQPQTFPQQPLFSQQQQQLFPQQPSFSQQQPPFWQQQPPFSQQQ
PILPQQPPFSQQQLVLPQQSPFSQQQLLILPPQQQQLPQQQISIVQPSVLQQLNPKV
FLQQQCSPVAMPQRLARSQMWQQSSCHVMQQCCQQLSQIPEQSRYDAIRAITYSIILQE
QQQGFVQAQQQPQQSGQVQSQQQSQQQLGQCSFQQPQQQLGQQPQQQVQQGTFLQP
HQIAHLEVMTSIALRTLPMCSNVNPLYSTTSVFPFGVGTGVGAY

>O22116 Tri a 36; LMW glutenin [Triticum aestivum]
ASAVAQISQQQPPPPFSQQQPPFSQQQPPFSQQQSPFSQQQPPFSQQQPPFSQQQPPFSQQ
PLISQQQQLPFSQQQPPFSQQQPPYSQQQPPYSQQQPPFSQQQPPFSQQQPPFSQQQPSFS
QQQPPFTQQQPPFSQQSPIQQQQQQQQQQPPFTQQQPPFSQQPPISQQQPPFS
QQQPPFSQQQIPVIHPSVLQQLNPKMVFLLQQCIPVAMQRCLARSQMLQQSICHVMQR
QCCQLRQIPEQSRHESIRAIYSIILQQQQQQQQQQQQGQSIIQYQQQPPQQLGQCV
SQPQQQLQQQLGQQPQQQLAHGTFLLQPHKIAQLEVMTSIALRTLPRMCSNVNPLYETTT
SVPLGVGIGVGVY

>CAR82265.1 LMW glutenin [Triticum aestivum]
MARQLNPSNKLQSPQQSFSHQQPFPQQPYPQPPYPSQQPYPSPQPFPTPQPQFPQQSQ
QPFTQPQQPTLPQQPFPQQPQQPFPQPPFPWQPQQPFPQTQQSFPLQPQQPFP
QQPQQPFPQQLQFPQQPEQIIPQQPQQPFLLESQQPFPQQPQQPFPQPPQLIPMQPQQP
FPQQSQSQPFPQPPQLFPELQQPQPQQPFPQPPFPQQSQPFPQQPQQPCPL
QPQQPFPQQPQQPFPQQPQQPFPQPPFPQPPFPQQPQQSQQSFPQPQQPQQPQQP
SILQPQQPFPQQQLSQLEQTISQQPQQPFPQQPHQPQQPYPQQQPYGSSLTSIDGQ

>CAR82266.1 LMW glutenin [Triticum aestivum]
MGRLLSPRGKELHTPQEFPQQQFPQPQQFPQQILQHQIPQQPQQFPQQQFLQQQ
IPQQIPQQHQIPQQPQQFPQQFPQQFPQQHQSPQQFPQQFPQQLPQQEFSQQ
ISQQPQLPQQQIPQQPQQFLQQQFPQQPPQQHQFPQQLPQQQIPQQQIPQQPQ
QIPQQQIPQQPKQFPQQFPQQFPQQFPQQFPQQFPQQIAQQPQQLPQQQFPI
PYPPQSQEPSYQQYPQQQPSGSDVISICGL

>CAR82267.1 LMW glutenin [Triticum aestivum]
MGRLLSPRGKELHTPQEFPQQQFPQPQQFPQQILQHQIPQQPQQFPQQQFLQQQ
IPQQIPQQHQIPQQPQQFPQQFPQQFPQQHQSPQQFPQQFPQQLPQQEFSQQ
ISQQPQLPQQQIPQQPQQFLQQQFPQQPPQQHQFPQQLPQQQIPQQQIPQQPQ
QIPQQQIPQQPKQFPQQFPQQFPQQFPQQFPQQFPQQIAQQPQQLPQQQIP
QQPQLFPQQQFPQQSPQQQFPQQFPQQQLPQQFPQPQQIPQQQIPQQPQQFPQ
QQFPQQQFPQQQFPQQFPQQFHQQQLPQQQPSGSDVISICGL

>AEH31546.1 Tri a 36; LMW glutenin [Triticum aestivum]
MKTFLIFALLAIVATSAIAQMENSHIPGLERPSQQQLPQQQLSHHQQQQPIQQPQPF
SQQQPCSQQQQPLSQQQPPFSQQQPPFSQQQQPLSQQQPPFSQQQPPFSQQQPPF
SQQQPPFSQQQPVLPQQPSPFSQQQLPPFSQQQSPFSQQQIVLQQQPPFLQQQPSLPQ
QPPFSQQQQLVLPQQQIPFVHPSILQQLNPKVFLQQQCSPVAMPQSLARSQMLQQSSC
HVMQQCCQQLPQIPQQSRYEAIRAIYSIILQEQQQVQGSIQTPQQPQQLGQCVSQPQ
QQSQQLGQQPQQQLAQGTFLQPHQIAQLEVMTSIALRTLPTMCRNVNPLYRTTTSVFP
GVGTGVGSY

>BAN29069.1 Tri a 36; LMW glutenin [Triticum aestivum]
ENSHIPGLERPWQQQLPQQPQTFPQQPLFSQQQLFPQQPSFSQQQPPFWQQQPPFSQQQ
PILPQQPPFSQQQLVLPQQPPFSQQQPVLPQQSPFPQQQHQQLVQQQIPVVQPSIL
QQLNPKLFLQQQCSPVAMPQRLARSQMLQQSSCHVMQQCCQQLPQIPQQSRYEAIRAI
IYSIILQEQQQVQGSIQSQQQPQQLGQCVSQPQQQSQQQLGQQPQQQQLAQGTFLQPHQ
IAQLEVMTSIALRTLPTMCRNVNPLYRTTTSVFPFGVGTGVGGY

>AKJ77988.1 Tri a 41; mitochondrial ubiquitin ligase activator of NFKB 1 [Triticum
aestivum]

EMGDGQLCVICLRKRRRAAFVPCGHLVCCCNCAKRVELMDEPLCPVCRQDIQYMLRVYDS

>BAE20328.1 Tri a 19; omega-5 gliadin [Triticum aestivum]
MKTFFIIFVLLAMAMNIASARLLSPRGKELHTPQEQFPQQQFPQPQQFPQQIPQQHQI
PQQPQQFPQQQFLQQQIPQQQIPQQHQIPQQPQQFPQQQFPQQHQSPQQQFPQQQFP
QQKLPQQEFPPQQISQQPQQLPQQQQIPQQPQQFLQQQFPQQQPPQQHQFPQQQLPQQQ
QIPQQQQIPQQPQQIPQQQQIPQQPQQFPQQQFPQQQFPQQQFPQQQFPQQQFPQQQIA
RQPQQLPQQQQIPQQPQQFPQQQFPQQQSPQQQFPQQQFPQQQQLPQKQFPQPQQIPQ
QQQIPQQPQQFPQQQFPQQQFPQQQFPQQQFPQQQFPQQQFHQQQLPQQQFPQQQFPQQQFPQ
QQQFPQQQQLTQQQFPRPQQSPEQQQFPQQQFPQQPPQQFPQQQFPQQQFPQQQFPQQQSEEPSY
QQYPQQQPSGSDVISISGL

>BAN29067.1 omega-5 gliadin, partial [Triticum aestivum]
ARELNPSNKLQSPQQSFHQQQPFPQQPYPQQPYPSQQPYPSQQPFPTPQQQFPQQSQQ
PFTQPQQPTPLQPQQPFPQQPQQPQQPFPQPQQPFPWQPQQPFPQTQQSFPLQPQQPFPQ
QPQQPFPQPQLPFPQQSEQIIPQQPQQPFPPLQPQQPFPQQPQQPFPQPQQPQPQQPQQSFPQQ
PQQSQQSQQPFAQPQQLFPELQQPQQPQQPFPPLQPQQPFPQQPQQPFPQPQQSFPQQ
PQQPFPQQPQQPFPQQPQQPFPQQPQQPFPPLRPQQPFPQQPQQSQQSFPQPQPQQPQQPS
ILQPQQPLPQQPQQPFPQQPQQLSQQPEQTISQQPQQPFPQQPHQPQQPYPQQQPYGSSL
TSIGGQ

>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

>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

>Q6W8Q2.1 Tri a 32; peroxiredoxin [Triticum aestivum]
MPGLTIGDTPVNLLELDSTHGKIRIHDYVGNQYVILFSHPGDFTPVCTTELAAMANYAKEF
EKRGVKLLGISCDVQSHKEWTKDIEAYKPGSKVTYPIMADPDRSAIKQLNMVDPDEKDA
EGQLPSRTLHIVGPKKVKLSFLYPSCTGRNMDEVVRAVDSLLTAAKHKVATPANWNPGE
CVVIAPGVSDDEAKKMFQGFETADLPSKKGYLRFKTV

>ACE82290.1 Tri a 32; peroxiredoxin [Triticum aestivum]
MPGLTIGDTPVNLLELDSTHGKIRIHDYVGNQYVILFSHPGDFTPVCTTELAAMANYAKEF
EKRGVKLLGISCDVQSHKEWTKDIEAYKPGSRVTYPIMADPDRSAIKQLNMVDPDEKDG
QGQLPSRTLHIVGPKKVKLSFLYPSCTGRNMDEVVRAVDSLLTAAKHKVATPANWKPGE
CVVIAPGVSDDEAKKMFQGFETADLPSKKGYLRFKTV

>ACE82291.1 Tri a 12; profilin [Triticum aestivum]
MSWQTYVDDHLCCEIDGQHLTSAAILGHDGSVWAESPFPKFKPEEIAIGIVKDFEEPGHL
APTGLFLGGTKYMIQGEVIRGKKGTTGGITIKKTMALILGIYDEPMTPGQCNLVVE
RLGDYPVEQGF

>CAQ57979.1 Tri a 12; profilin [Triticum aestivum]

MSWKAYVDDHLCCEIDGQHLTSAAILGHDGSVWAQSPNFPQFKPEEIAGIVKDFEEPGHL
APTGLFLGGTKYMVIQGEPCVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE
RLGDYLIDQGY
>CAA61943.2 Tri a 12; profilin, partial [Triticum aestivum]
MSWQTYVDDHLCCEIDGQHLTSAAILGHDGSVWTESPNFPKFKPEEIAGIVKDFEEPGHL
APTGLFLGGTKYMVIQGEPCVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE
RLGDYLIDQGY
>CAA61944.2 Tri a 12; profilin, partial [Triticum aestivum]
MSWQAYVDDHLCCEIDGQHLTSAAILGHDGSVWAESPFPKFKPEEIAGIVKDFEEPGHL
APTGLFLGGTKYMVIQGEPCVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE
RLGDYLIDQGY
>CAA61945.2 Tri a 12; profilin, partial [Triticum aestivum]
MSWKAYVDDHLCCEIDGQHLTSAAILGHDGSVWAQSPNFPQFKPEENAGIVKDFEEPGHL
APTGLFLGGTKYMVIQGEPCVIRGKKGTGGITIKKTGMALILGIYDEPMTPGQCNLVE
RLGDYLIDQGY
>CAI64396.1 serine carboxypeptidase [Triticum aestivum]
GNGLIDDYHDYVGTFFFWNHGLVSDDTYQRLREACLHDSFIHPSACDAATDVATAEQG
NIDMYSLYTPVCNITSSSSSSSSLSQQRSSRGRYPWLTGSYDPCTERYSTAYNRRDVQ
TALHANVTGAMNYTWSTCSDTINTHWHADAPRSMLPIYRELIAAGLRIWVFSGDTDAVPL
TATRYSIGALGLPTTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRPRQALVL
FQYFLQGKPMGPQATNATVA
>P08819.2 serine carboxypeptidase [Triticum aestivum]
VEPSGHAADRIARLPQPAVDFDMSYGYITVDEGAGRSFYLLQEAPEDAQPAPLVLWLN
GGPGCSSVAYGASEELGAFRVKPRGAGLVLNEYRWKVANVLF LDSPAGVGFSTNTSSD
IYTSNGNRTAHDYAFYAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVIN
LKGFMVGNGLIDDYHDYVGTFFFWNHGIVSDDTYRRLKEACLHDSFIHPSACDAATDV
ATAEQGNIDMYSLYTPVCNITSSSSSSSSLSQQRSSRGRYPWLTGSYDPCTERYSTAYY
NRRDVQMALHANVTGAMNYTWATCSDTINTHWHADAPRSMLPIYRELIAAGLRIWVFSGDT
DAVPLTATRYSIGALGLPTTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRP
RQALVLFQYFLQGKPMGPQTKNAT
>P82977.2 Tri a 39; serine protease inhibitor [Triticum aestivum]
MSSVKKPLGGNTDTGDHNNQKTEWPELVGKSVVEAKKVILQDKSEAQIVVLPVGTIVTM
EYRIDRVRLFVDSLKDIAQVPRVG
>ABS58503.1 Tri a 39; serine protease inhibitor [Triticum aestivum]
MSPVKKPEGGNTDTGDHNNQKTEWPELVGKSVVEAKKVIMQDKSEAQIVVLPVGTIVTM
EYRIDRVRLFVDSLKDIAQVPRVG
>CCK33471.1 Tri a 39; serine protease inhibitor [Triticum aestivum]
MSPVKKPEGRNTDTSDDHNNQKTEWPELVGKSVVEAKKVILQDKSEAQIVVLPVGTIVTM
EYRIDRVRLFVDSLKDIAQVPRVG
>CAA72273.1 Tri a 33; serpin [Triticum aestivum]
MATTLATDVRLSIAHQTRFALRLASTISSNPKSAASNAAFSPVSLHSALSLLAAGAGSAT
RDQLVATLGTGEVEGGHALAEQVVQFVLADASSAGGPRVAFANGVFVDASLLLKPSFQEL
AVCKYKAETQSVDFQTKAAEVTTQVNSWVEKVTSGRIKNILPSGSVDNTTKLVLANALYF
KGAWTDQFDSYGTKNDFYLLDGSSVQTPFMSSMDDDQYISSSDGLKVLKLPYKQGGDNR
QFSMYILLPEAPGGLSSLAEKLSAEPDFLERHIPRQRVAIRQFKLPKFKISFGMEASDLL
KCLGLQLPFSDEADFSEMVDSPMPQGLRVSSVFHQAFVEVNEQGTAAAATAIKMVPQQA
RPPSVMDFIADHPFLFLLREDISGVVLFMGHVNPILLSS
>CAB52710.1 Tri a 33; serpin [Triticum aestivum]
MATTLATDVRLSIAHQTRFGFRLASTISSNPESTANNVAFSPVSLHVALSLITAGAGGAT
RDQLVATLGEGERLHALAEQVVQFVLADASYADSPRVTFANGVFVDASLPLKPSFQEL

AVCKYKAEAQSVDFQTKAAEVTAQVNSWVEKVTTGLIKDILPAGSISNTTRLVLGNALYF
KGAWTDQFDSRVTKSDYFYLLDGSSIQTPFMYSSSEQYISSSDGLKVLKLPYKQGGDKRQ
FSMYILLPEAPSGIWSLAEKLSAEPELLERHIPRQKVALRQFKLPKFKISFGIEASDLLK
HLGLQLPFSDEADLSEMVDSPMPQGLRISSVFHKTFVEVNETGTEAAAATIAKAVLLSAS
PPSDMDFIADHPFLFLIREDTSGVWLFIGHVWNPLRSL
>P27357.1 thaumatin-like [Triticum aestivum]
MATSPVLFLLLAVFAAGASAATFNIKNNCGFTIWPAGIPVGGGFALGSGQTSSINVPAGT
QAGRIWARTGCSFNNGSGSCQTGDCCGQLSCSLSGRPPATLAEYTIGGGSTQDFYDISVI
DGFNLAMDFSCSTGDALQCRDPSCPPPQAYQHPNDVATHACSGNNNYQITFCP
>BAC76688.1 Tri a 27; thiol reductase [Triticum aestivum]
GDVATGRGSEKVVHVAIYYESLCPYSRVFVANHLFKAYRDGLLDAANLTLVPYGNVVRND
GTISCQHGPPEECLLNTVEACAIDAWPDVKVHLGFIYCVSDLVLKKNHREWESCFQKQGLD
PKPVTECYKGERGHNLSLEYGRQTAELVPPHQFVPPWVVDGKPLYNDYGNFKAYICKAYK
GYPLLEACRSLGLEAHDVVYGR
>CAB96931.1 Tri a 25; thioredoxin [Triticum aestivum]
MAASAATATAAAVGAAGEVISVHSLEQWTMQIEEANAACKLVVIDFTASWCGPCRIMAPIF
ADLAKKFPAAVFLKVDVDELKSIAEQFSVEAMPTFLFMKEGDVKDRVVGAIKEELTNKVG
LHAAQ
>CAC14917.1 Tri a 31; triosephosphate isomerase [Triticum aestivum]
MGRKFFVGGNWKCNVTVEQVESIVNTLNAGQIASTDVVEVVVSPPYVFLPTVKGKLRPEI
QVAAQNCWVKKGGAFTEVSAEMLVNLGVPWVILGHSERRSLMGESSEFVGEKVAYALAQ
GLKVIACVGETLEQREAGSTMAVVAEQTKAIADKIKDWTNWWWAYEPVWAIGTGKVASPA
QAQEVHANLRDWLKTNVSPEVAESTRIIYGGSVTGASCKELAAQPDVDGFLVGGASLKPE
FIDIINAAAVKSA
>CAI64397.1 unknown function [Triticum aestivum]
KPVAANQDVALSALRRGLQDPNGELKNWDANLVDACTWSHITCDRDNNRVTRIDLNKMN
LSGPLAPELGKLDRLQYLEIDHNRLTGPIPRELAGLSNLKHADFSNNNLGPIPTTGAFQ
RIPRSSFANNPRLGRKC
>AKJ77986.1 Tri a 42; unknown function [Triticum aestivum]
EFTNTCMECLVCDVHVACGDFASNDVIDPAKFRRLGINDCLVNDGKSIEPSFPVSFQYGN
SFPYPMTVASASDCDN
>AKJ77987.1 Tri a 43; unknown function [Triticum aestivum]
MTLVASSSLDPVWVEVLGDPLLRLLLRIFIFCRATLSLFKASNDKAECLPSCVPPLPESV
GGESMLSQCCVMRVASFLGAADQFSFAEVTTWPDIDEPTSSGGVDKEL
>Q4W1G2 unknown function [Triticum aestivum]
ANGDTAFKASGKNKTATGGVAKPKRAPTPFFAFLAEFRPQYMEKHPEAKGVAAVTKAAGE
KWRMSDEEKAKYGGKKADAPASKAVNKKESTSSKKAKTGSVDVEDDGEEDDEE
>P81496.1 unknown function, partial [Triticum aestivum]
SFREQCVGREITYECLNACAEYAVRQ
>CAA34709.1 alpha-amylase inhibitor [Triticum turgidum]
MASKSNCVLLLA AVLVSIFA AVAAI GNE DCTP WMSTLITPLPSCR DYVEQQACRIETPGS
PYLAKQQCCGELANIPQQCRCQALRYFMGPKSRPDQSGLMELPGCPREVQMDFVRILVTP
GYCNLTTVHNTPYCLAMEESQWS
>CAA39099.1 alpha-amylase inhibitor [Triticum turgidum]
MASKSSITHLLLA AVLVSVFAAAAATGPYCYPGMGLPSNPLEGCREYVAQQTCGVGIVGS
PVSTEPGNTPRDRCKELYDASQHRCCEAVRYFIGRTSDPNSGVLKDLPGCPREPQRDFA
KVLVTPGHCVMTVHNTPYCLGLDI
>CAA36063.1 glutenin [Triticum turgidum]
MKTFLV FALLAVVATSTIAQMETS SCIPGLERPWQEQLPPQH TLFPPQQQPFPPQQQPPFS
QQQPSFLQQQPILPQLPFSQQQPVLPPQSPFSQQQLVLPQQQYQQVLQQQIPIVQPSV

LQQLNPCKVFLQQQCNPVAMPQRLARSQMLQQSSCHVMQQCCQQLPQIPEQSRVDVIRA
ITYSIIILQEQQQGFVQAQQQQPQQLGQGVVSQSQQQSQQQLGQCSFQQPQQQLGQQPQQQQ
VLQGTFLQPHQIAHLEVMTSIALRTLPTMCSVNVPLYSSSTTSVPSVGTGVGAYL
>AEG47274.1 Tri tu 14; lipid transfer protein [Triticum turgidum]
MARSAVAQVVLVAVVAAMLLAVTEAAVSCGQVSSALSPCISYARGNGASPSAACCSSGVRS
LASSARSTADKQAACKCIKSAAAGLNAGKAAGIPTKCGVSVPYAIISSSVDCSKIR
>CAA44473.1 LMW glutenin [Triticum turgidum]
MKTFLV FALLAVVATSAIAQMDTSCIPGLERPWQQQLPQQPQTFPQQPPFSQQQQQQPFP
QQPSFSQQQPILPQGPFPQQTQPVLQQSPFSQQQLLILPPQQQQQLPQQQISIVQPSV
LQQLNPCKVFLQQQCSVAIPQRLARSQMWQQSSCHVMQQCCQQLSQIPEQSRVDVIRA
ITYSIIILQEQQQGSQQQQPQQSGQGVVSQSQQQSQQQLGQCSFQQPQQQLGQQPQQQQVQ
QGTFLQPHQIAHLEVMTSIALRTLPTMCSVNVPLYSSSTTSVPSVGTGVGAYL
>AAA34290.1 gliadin [Triticum urartu]
MKTFLILALLAIVATTATTAVRVPVPPQPPQNPSPQPPQPPQVPLVQQQQFPQQQQPFPQ
QPYPQPQPPFSQQPYLQLQPFPPQPPFPQLPYPQPPPFSPQQPYPQPQPYPQPQPIS
QQQAQQQQQQQQQQQQQQQQQQILPQILQQQLIPCRDVLQQHNIHARSQVLQQSTYQP
LQQLCCQQLWQIPEQSRCAIHNVVAIILHQQQQQQPSSQVSLQQPQQQYPSGQGFQ
PSQQNPQAQGSVPPQQLPQFEEIRNLALQTLPRMCNVYIPPYCSTTTAPFGIFGTN
>BAH10149.1 tropomyosin [Turbo cornutus]
MDAIIKKMLAMKMEKENALDRAEQLEQKLRDTEEQKAKIEEDLNNLQKCCANLENDFDNV
NEQLQDALSKLENSEKRVTEMEQEVSGTTRKITLLEEDLERNEEGLQTATERLEEASKAA
NESERGLSADDERIDQLEAQLKEAKYIAEDAKYIAEDAERKYDEAARKLAITEVDLERAE
ARLEAAEAKILELEEEELKVVGNMMSLEISEQEASQREDSYEETIRDLTQRLKDAENRAT
EAERTVSKLQKEVDRLEDELLAEKEKYKAISDELDTFAELAGY
>AAX84656.1 alpha-tubulin [Tyrophagus putrescentiae]
MRECISVHVQGAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGTGDDSFNTFFSETGSGK
HVPRAVYVDLEPTVWDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIVDVVLD
RIRKLSDQCTGLQGFLIFHSFGGGTSGSFTSLLMERLSVDYGGKSKLEFAVYPAPQVSTA
VVEPYNSILTTHTLEHSDCAFMDNEAIYDICRRNLDIERPTYTNLNLIGQIVSSITA
SLRFDGALNVELTEFQTNLVPYPRIFPLVTYSPVISA EKAYHEQLTVAEITNTCFEPQN
QMVKCDPRHGKYMACL LLYRGDVVPKDVNAAIAGIKTKRSIQFVDWCPTGFKVGINYP
TVVPGDLAKVQRAVCMLSNTTAAIAEAWARLDHKFDL MYAKRAVHWYVGE GMEEGEFSE
AREDLAALEKDYEEVGLDSTEAE GGDGEEF
>QOI58528.1 Tyr p 20; arginine kinase [Tyrophagus putrescentiae]
MVDQATLDKLEAGFKKLQSSGDACHSLLKKYLTEDVFNKLDKKTGMGATLLDVIQSGVE
NLDSGVGLYAPDAEAYTLFADLFNPVIEGYHGGFKSTDKHPPSDFGDINQLVNVDPNNEF
VISTRVRCGRSLQGYFPNCLTEAQYKEMEEKVKAQLESFEGELKGTYYPLTGMDKATQQ
QLIDDHFLFKEGDRFLQAANACRFWPTGRGIFHNASKTF LMWVNEEDHLRIISMQKGGDL
KEVFGRLVKAVQHIEKKIPFSRDDRLGFLTFCPTNLGTTIRASVHIKLPKLAADRKKLEE
VAAKYNLQVRGTAGEHTESVGGVYDISNKRMRGLTEYQAVKEMQDGILELIKIEKSL
>ABM53750 Tyr p 7; bactericidal permeability-increasing like [Tyrophagus
putrescentiae]
MKSAVLVLVACFAGIADVADNGNANQFVDQIVTALKTQKNFDPLVIPP HHMNIDRKIGAIH
LKGTADLKETKITGLSHVRRVGDALLKNENGSFTAKLHLGDDNVKLFSDISLHFLHNIIH
PNLKVEIDIGNIGVGFVGTIGADGPKALKDFDIEEFKHVKIHVHGLGPLDHLVLDLIGEAY
ISLANTQARHMITGIVRPILDQELKNFKMGGF
>ABM53753 Tyr p 1; cysteine protease [Tyrophagus putrescentiae]
MALLFYILFLFFTFIQRHLEKVP TWEQYKVKFGKNYLTINEENFRKNNYFNLSLTKIVKN
NGKNGVTLGLNDMSDWSDEEFFSLNSKSPSSVFVSARPTSTVNTSPFPKSWDWRNIIAFN
SIEQQGRCS SCWAF AAATTVEAAYAHQKNKHNHLHSRQELVDC TNRTFDQHLYLNYGCKGG

WPTEAYKYIMDHGVYEDKLYHYTETFNEVCYADKVAHDKGHPVKYYISNYGRLAYNDTDE
AIMAMLVTYGPVTVDIHGTSDFRFYKGGIMRNVMPNSAYTNHIVVVVGYGTDSSGVDYW
IIRNSWGKTWGEHGYRRLERHPNLLGFNNKYNYPIL
>AAU11502.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]
MVQLNGSYKLEKSDNFDAFLKELGVNFVTRNLAKSASPTVEIVDGDSTYIKTSSTLKNS
EIKFKLGEFEEDRADGKKVQTSVTKEGDNKLVQVQKGDKPVTIVREFSEEGLTVTATVN
GVTSVRFYKRQ
>ABM53751.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]
MTIEGKYKLEKSENFDAFLDKLGVGFMVKTAAKTLKPTLEVEVAGDITYTLRSLSTFKNTE
IKFKLGEFEEDRADGKKVKTVWNKEGDNKLVQVQFGDKEVKIIREFNGDDVVVTASVDG
VTSVRSYKRI
>ABU97480.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]
MVQLNGSYKLEKSDNFDAFLKELGVNFVTRNLAKSASPTVEIVDGDSTYIKTSSTLKNS
EIKFKLGEFEEDRADGKKVQTSVTKEGDNKLVQVQKGDKPVTIVREFSEEGLTVTATVN
GATSVRFYKRQ
>ABM53752.1 Tyr p 13; fatty acid-binding protein [Tyrophagus putrescentiae]
MANKLLLALALVLAATTSVLAEDIDFSGRYKMTVADTSNYKDLLYELGIGYFKRLAAGA
SGSEYVITRNEAGTYTLQTVTTFSTAATFKSGEEFDEPRADGQTVKSTIVIAGNKWTH
VQKGSPTVTIERTFQGGNPPTYIDVITKCNAPVTRKYERQ
>AGG10560.1 Tyr p 8; glutathione S-transferase [Tyrophagus putrescentiae]
MSSKPVLGYWDIRGLAQPIRLLLAYLDVDYEDKRYQLGANFDRSAWLTEKFNGLDFPNL
PYYIDGNVKLSQTLAILRYIGRKYKLTGANPEELRVSLVEQQVVDGNQSLSRVAYDPNA
DKLKPDLKTLPSVQKLSHFLGNSPFVAGTSITYVDFWLYEYLVKLSVLVPEVFGQFDN
LKKFVERIESLPRVSVYIKAQQPKLFNGPMAKWNGQYA
>CAA73221.1 Tyr p 2; NPC2-like [Tyrophagus putrescentiae]
MKFLILFALVAVAAAGQVKFTDCGKKEIASVAVDGCEGDLCVIHKSKPVHVIAEFTANQD
TCKIEVKVTGQLNGLEVPIPIGIETDGCKVLKCPKKGTKYTMNYSVNVPSVVPNIKTVVK
LLATGEHGVLAGAVNTDVKP
>AAT40866.1 Tyr p 10; tropomyosin [Tyrophagus putrescentiae]
MDAIAKMKQAMKLEEDNAIDRAEIAEQKARDANLKSEKTEEEVRALQKKIQQIENELDQV
QENLTQATTKLEEKALQTAADVAALNRRIQLIEEDLERSEERLKVATAKLEEASHSA
DESERMKMLEHRSITDEERMDGLESQKLEARLMAEDADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKAQQREEAYEQQIRIMTSKLKEAEARAE
FAERSVQKLQKEVDRLDEDELVHEKEKEYESISDELDTFAELTGY
>ABQ96644.1 Tyr p 10; tropomyosin [Tyrophagus putrescentiae]
MEAIKKMKQAMKLEKDNAIDRADTLEQQNKEANNRAEKSEEEVHNLQKRMQQLGNDLDQV
QESLLKANIQLVEKDRALSNAEGEVAALNRRIQLLEEDLERSEERLNTATTKLAEASQAA
DESERMKRVLENRSLSDEKRMDALENQLKEARFLAEEADRKYDEVARKLAMVEADLERAE
ERAETGESKIVELEELRVVGNLKSLEVSEEKANQREEAYKEQIKTLTNKLAEEARAE
FAERSVQKLQKEVDRLDEDELVNEKEKEYKSITDELDTFSELTGY
>ABU97479.1 Tyr p 10; tropomyosin [Tyrophagus putrescentiae]
MEAIKKMKQAMKLEKDNAIDRAEIAEQKARDANLKSEKTEEEVRALQKKIQQIENELDQV
QENLTQATTKLEEKALQTAADVAALNRRIQLIEEDLERSEERLKVATAKLEEASHSA
DESERMKMLEHRSIPDEERMDGLESQKLEARLMAEDADRKYDEVARKLGMVEAHLERAE
ERAQLGIXIAKLERTARLRHT
>ACL36923.1 Tyr p 34; troponin C [Tyrophagus putrescentiae]
MSVEELSKEQVQMLRKAFFDMFRDKKGYIHTNMVSTILRTLQQTFFENDLQQLIIEIDAD
GSGELEFDEFLLTARFLVEEDTEAMQEELREAFRMYDKEGNGYIPTSALREILRALDDK
LTEDELDEMIAEIDTDGSGTVDFDEFMEMMTGD
>ABZ81991.1 Tyr p 3; trypsin [Tyrophagus putrescentiae]

MKILLFLCFLVSVAFAPPTIQLKSNTKSQNGFIVGGTEAVDGDAPHQVSLQHTSHFCGG
SIISERWILTAACIDADDLSNPGGMSVRYNTLNLKSGTLVKVKSIVHEQYSNVTSNDND
IALLETVASMNLNQTNAVAALPAKGNPDQDGLFLSGWGLHSGDTTIPTNLQKVTVPPL
TNRVCAEAYTGIVNITENMFCAGKMGIGGVDSQGDSSGGGAMLNKELVGVVSVFVGVGCGD
PKYPGVYTRVSQYLDWIELSAKSSATTLVAVNITLFLTLFIGAIW

>AAX34057.1 unknown function [Tyrophagus putrescentiae]
MKFAILALAF LGAVMAQGGPKVPAKGDFRNEFDHLLVSTLMEGMYKGEQHLLRLSEEIAH
LESTKTKVEQDRIVREIEVTVAFIEGGVVRVVEQELKRTDLNILERFNFEVQALS KLLVK
DLKEAEVKVKAVKTR

>AAX34059.1 unknown function [Tyrophagus putrescentiae]
MKFVIALAALLAVACAAPT PKPARPTAKGDFRNEFDHLIVAAVQRFHDL EEFLLKLSE
QVADLEKTKNREEKAKILREITIADGLVVGGRTYFEKELKRTDLDLVEKFNFEAVLATIG
ILDRDLKALATRVNAIKV

>COMPARE150 Alt a 1-like [Ulocladium botrytis]
MQFTTIASLFAAAGLAAAAPLESRQDNASCPVTTKGDYVWKISEFYGRKPEGTYYNLSLGF
NIKATNGGTLDFTCQAQADKLEGHKWYSCGENSFMDFSFSDSDRSGLLLKQKVSDE

>QCB92083.1 beta-expansin [Urochloa mutica]
MLAVVAVVLASVMGGALCAMGDKPGPNITATYGDKWLDKATFYGSDPRGAAPDDHGGAC
GYKDVKAPFDSMTGCGNEPIFKDGLGCGSCYEIKCKEPAECSGEPVLIKITDKNYEHIA
AYHFDLSGKAFGAMAKKGEEDKLKAGELMLQFRRVKCEYPSDTKIAFHVEKGSNPNYLA
LLVKYAAGDGNIVSVDIKSKGSDEF LPMKQSWGAIWRIDPPKPLKGPFTIRLTSESGGHV
EQEDVIPEDWKPDTVYKSKIQF

>QCB92082.1 Uro m 1; beta-expansin [Urochloa mutica]
DGKWLDAKATWYGKPTGAGPDDNGGACGYKDVNKAPFNSMGACGNPPIFKDGLGCGSCYE
IKCDKPAECSGEPVIVHITDQNYEPIAAYHFDLAGTAFGAMAKKGE EELKLRKAGIIDMQF
RRVKCKYPANTKIAFHVEKGCNPNYFALLIKYAAGGDIVAVDIKEKGSEEF IPLKHSWG
AIWRIDSPKPIKGP IAVRLTSEGTTLVQDDAIPEGWKADTVYTSK LQF

>QCB92084.1 beta-expansin [Urochloa mutica]
MGS LANIVAVAAVLAALVGGGSCGPPKVP PGP NITANYNGKWLPARATWYGKPTGAGPDD
NGGACGIKDVNLPPYSGMTACGNIPFKDGKGCSCYEIRCKAPVECSNPNVTFITDMN
YEPIAPYHFDLSGKAFGALAKPGLNDKLRHAGIMDIEFRRVRCKYTGGQKIVFHVEKACN
PNYLAVLVK FVADDGDIVNMELEKASAEWKPMKLSWGAIWRVDTPKALKGPF S IRTSE
SGKKLVANDVIPANWKANTAYPSNIQF

>AIV43662.1 Aca f 2; profilin [Vachellia farnesiana]
MCWQTYVDDHLMCEIEGTNNHLSGAAILGVDGSVWAQSASFQFKPDEIAAVVKDFDGP
TLAPTGLHLGGTKYMIQGEPRFIRGKKGPGGICVKKTGQALVFGIYDEPVT PGQC NMI
VERLGDYLVEQGM

>BAH10157.1 tropomyosin [Venerupis philippinarum]
MDAIKKKMQAMKLEKENALDKAEQLEQLRDVEETKAKAEEDLTLLQKKYTNLENEFDQV
NEKYNEGVNKLEVSEKRVTEAEDEIKGYTRRIQLLEDDLERTQVKLDEATSKLEDATKTA
DESERGRKVLERSIADDDRIDALEKQVKDAKYVAEEADRKYDEAARKLAITEVDLERSE
TRLEAAEAKITELSEELAVVGNCKALQNAVDQASQREDSYEETIRDLTQRLKDAENRAA
EAERVVNKLQKEVDRL EDELLAEKEYKAISDELDTFAELAGM

>P0DMB4.1 phospholipase A1 [Vespa affinis]
MMNLKYL LFFCLVQALHYCYAYGDPSLSNELDRFNPCPYSDDTVKMIIL TRENK K H D F Y T
LNTIKNHNEFKKSTIKHQVVFITHGFTSTATAENFLAMAEALLDKGNYLVLIDWRVAAC
TNEMAGVKLAYYSYAASNTRLVGN IATVTKMLVQQYNVPMANIRLIGHSLGAHTSGFAG
KKVQELRLGKYSEIIGLDPAGPSFKSQECSQRICETDANYVQI IHTSNHLGTLVTLGTVD
FYMNNGYNQPGCGLPIIGETCSHTRAVKYFTECIRHECCLIGVPQSKNPQPVSKCTRNEC
VCVGLNAKTYPKTGSFYVPVESKAPYCNKKGKII

>P0DMB5.1 phospholipase A1 [Vespa affinis]
MMNLKYLFFCLVQALHYCYAYGDPSPSLNELDRFNPCPYSDDTVKMIILTRENKKHDFYT
LNTIKNHNEFKKSTIKHQVVFITHGFTSTATAENFLAMAEALLDKGNLVLILIDWRVAAC
TNEMAGVKLAYYSYAASNTRLVGNLIATVTKMLVQQYNVPMANIRLVGHSLGAHTSGFAG
KKVQELRLGKYSEIIGLDPAGPSFKSQEQSRICETDANYVQIIHTSNHLGTLVTLGTVD
FYMNGYNQPGCGLPIIGETCSHTRAVKYFTECIRHECCLIGVPQSKNPQVSKCTRNQC
VCVGLNAKTYPKTGSFYVPVESKAPYCNNKGKII

>P0CH87.1 Vesp c 1; phospholipase A1 [Vespa crabro]
FNPCPYSDDTVKMIIVLTRENKKYDFYTLDTIKNHNEFKDTITLKPVVFITHGFTSSATAE
NFVVMKALLDKGNLVLILTDWRMAACTNEIAGLKLAYYPYAASNTRLVGNLIATVTKML
VQKYNVPMANIRLIGHSLGAHISGFAGKKVQELGLGKYPEIIGLDPAGPSFKSNDCSQRI
CETDANYVQIIHTSNRLGTERTLGTVDVFMNGYNQPGCGLPIIGETCSHTRAVKYFTEC
IKHECCLIGVPKSKNPQVSKCTRNECVGLNAKTYPKTGSFYVPVESKAPYCNNKGKI
I

>P35781.1 Vesp c 5; unknown function, antigen 5 [Vespa crabro]
NNYCKIKCRSGIHTLCKYGTSTKPNCGKNVVKASGLTKQENLEILKQHNEFRQKVARGLE
TRGNPGPQPPAKSMNTLVWNEDELAQIAQVWANQCNYGHDNCRNSAKYSVGQNI AEGSTTA
DNFGSVSNMVKMWEDEVKDYQYGSPKNKLNKVGHYTQMVAKTKEIGCGSIKYIENGWHR
HYLVCNYGPAGNVGNEPIYERK

>P35782.1 Vesp c 5; unknown function, antigen 5 [Vespa crabro]
NNYCKIKCRSGIHTLCKYGTSTKPNCGKNVVKASGLTKQENLEILKQHNEFRQKVARGLE
TRGNPGPQPPAKSMNTLVWNEDELAQIAQVWANQCNYGHDNCRNSAKYSVGQNI AEGSTSA
DNFVNVSNMVKMWEDEVKDYQYGSPKNKLNKVGHYTQMVAKTKEIGCGSEDIYEDGWHR
HYLVCNYGPAGNVGNEPIYERK

>CBY83816.1 Vesp ma 2; hyaluronidase [Vespa magnifica]
MLLVTLFLFFLQALVNGDSCGSNCEKSERPKRVFNIIYWNVPTFMCHQYGLYFDEVTFNFI
KHNSKDNFQGDKIAIFYDPGEFPALLPLNYGKYKIRNGGVPQEGNITIHQRFIEYLDKT
YPNRNFSGIGVIDFERWRPIFRQNWGNMKIYKNFSIDLVRKEHPFWNKKMIELEASKRFE
KYARLFMEETLKLAKKTRKQADWGYGYGYPCFNMSPTNFVPDCDVTARDENNEMSWLFNN
QNVLLPSVYIRRELTDPQRIGLVQGRVKEAVRISNKLKHSKPVFSYWWYVYQDETNTFLT
ETDVKKTQEIIVINGGDGIIIWGSSDVNSLSKCTRLREYLLTVLGP IAVNVTEAVN

>CBY93636.1 Vesp ma 5; unknown function, antigen 5 [Vespa magnifica]
MKISGFVYLILITTIINLSFSEANNYCKIKCRSGIHTLCKFGISTKPNCGKNVVKGSGLT
KAEKLEILKQHNEFRQKVARGLETRGKPGPQPPAKSMNTLVWNEDELAQIAQVWASQCKYG
HDDCRNTAKHSVGQNI AQQSTTAASFGSVSNMVQMWAVEVKNYQYGSTKNK LIEVGHYTQ
MVWAKTKEIGCGSIKYIENGWHRHYLVCNYGPAGNIGNEPIYEKK

>P81657.1 Vesp m 5; unknown function, antigen 5 [Vespa mandarinia]
NNYCKIKCRSGIHTLCKFGISTKPNCGKNVVKASGLTKAEKLEILKQHNEFRQKVARGLE
TRGKPGPQPPAKSMNTLVWNEDELAQIAQVWAGQCDYGHVCRNTAKYSVGQNI AENGSTA
ASFASVSNMVQMWAVEVKNYQYGSTKNK LIEVGHYTQMVAKTKEIGCGSIKYIENGWHR
HYLVCNYGPAGNIGNEPIYERK

>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]
ALLEKNDCMVISIDWRNGACTNEFQILKFIGYPAVENTR

>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]
ICETDAHVVQIIHTSNLGTTER

>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]

GLETRGNPGPQPPAKSMNTLVWDELQAQVWASQCK

>COMPARE00314 Vesp v 5; unknown function, antigen 5, partial from P0DMB9.2 [Vespa velutina]

NTAKYLVGQNIAEQSTTAASFEPVSNMVKMWSDEVKDYQYGSSKNKLNDVGHYTQMVWAK

TKEIGCGNIKYIENGWHHHYLVCNYGPAGNIGNEPIYEKK

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

NNYCKIKCLKGGVHTACKYGLKPCNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE

TRGNPGPQPPAKNMKNLVWDELAYVAQVWANQCQYGHDTCRDIAKYQVGGQNVALTGSTA

AKYDDPVKLVKMWEDVKDYNPKKFKSGNFKLTGHYTQMVWANTKEVGCSSIKFIQEKW

HKHYLVCNYGPSGNFQNEELYQTK

>CAL59818.1 hyaluronidase [Vespula germanica]

SERPKRVFNIYWNVPTFMCHQYDLYFDEVTNFNINIKRNSKDDFQGDKIAIFYDPGEFPALL

SLKDGKYYKRNKGGVPEGNITIHQKFIENLDKTYPNRNFSGIGVIDFERWRPIFRQNWG

NMKIHKNFIDLVRNEHPTWNKKMIELEASKRFKRYARFFMEETLKLAKKTRKQADWGY

GYPYCFNMSPNLVPEDVTAMHENDKMSWLFNQNQVLLPSVYVRQELTPDQRIGLVQGR

VKEAVRISNLLKHSPKVLVSYWVYVYQDETNTYLTETDVKKTFQEIVINGGDGIIIWSSS

DVNSLSKCKRLQDYLLTVLGPVAVNVTEAVN

>CAL59819.1 phospholipase A1 [Vespula germanica]

VITIWPKKGFSIYWNIPTHFCHNFGVYFKELKQFNINIKYNSMNNFRGETISLFYDPGNFPS

MVLLKNGTYEIRNEGVPQKGNLTIHLEQFTKELDEIYPKKIAGGIGVIHFHNWRPIFRN

VDNLKINKDISIDLVRKEHPKWDKSMIEKEASNRFFETSIFMEKTLKLAKEIRKKTTEWG

YHGYPHCLSGSTDKPSFDCDALSMSSENDKMSWLFNQNQVLLPSIYLKKNLKPDEKIHVLVQ

ERLKEAIRISKNLKHLPKVLPYWVYTYQDKESIFLTEADVKNFTKEILTNGADGIIIWGV

SYELTDRKRCEKLKEYLMKILGP

>CAJ28931.1 unknown function [Vespula germanica]

GPKCFNTDTVSMIETRENRRDLTYLQTLQNHPEFKEKTITRPVVFITHGFTSSASET

NFINLSKALVDKDNMVISIDWQTAECTNEAAGLKLYYPTAASNTRLVGGYIATITQKL

VKQYKISMANIRLIGHSLGAHVSGFAGKVKQELKLGKYEIIGLDPAGPSFSSNKCSDR

CETDAEYVQILHTSNHLGTERILGTVDYFMMNGKNQPGCGRFFTEVCSHSRAVIYMAECI

KHECCLIGIPKSKSSQPISSCTKQECVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII

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

NNYCKIKCLKGGVHTACKYESLKPNCANKKVVAYGLTKQEKQDILKEHNDFRQKIARGLE

TRGNPGPQPPAKNMKNLVWDELAYIAQVWANQCQYGHDTCRDVAKYPVGGQNVALTGSTA

AKYDNPVKLVKMWEDVVDKYNPKKKFSENNFLKIGHYTMVWANTKEVCGGSIKYIQDKW
HKHYLVCNYGSPGNFGNEELYQTK
>CAJ28930.1 Ves g 5; unknown function, antigen 5 [*Vespula germanica*]
NNYCKIKCLKGGVHTACKYESLKPNCANKKVVAYGLTKQEKQDILKEHNDFRQKIARGLE
TRGNPGPQPPAKNMKNLWVNDLAYIAQVWANQCQYGHDTCDVAKYPVGQNVALTGSTA
AKYDNPVKLVKMWEDVVDKYNPKKKFSENNFLKIGHYTMVWANTKEVCGGSIKYIQDKW
HKHYLVCNYGSPGNFGNEELYQTK
>P0CH89.1 Ves m 2; hyaluronidase [*Vespula maculifrons*]
DRCIWPKEGFSIYWNIPTHFCHNFGVYFKEL
>P51528.1 Ves m 1; phospholipase A1 [*Vespula maculifrons*]
GPKCFNSDTSIIIETRENRRDLYTLQTLQNHPEFKKKTITRPVVFITHGFTSSASEK
NFINLAKALVDKDNMVISIDWQTAECTNEYPGLKYAYYPTAASNTRLVGGYIATITQKL
VKDYKISMANIRLIGHSLGAHVSGFAGKRVQELKLGKYSEIIGLDPARPSFDSNHCSERL
CETDAEYVQIIHTSNYLGTTEKILGTVDYFNMNGKNNPGCGRFFSEVCSHTRAVIYMAECI
KHECCLIGIPRSKSSQPISRCTKQECVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII
>P35760.1 Ves m 5; unknown function, antigen 5 [*Vespula maculifrons*]
NNYCKIKCLKGGVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHNDFRQKIARGLE
TRGNPGPQPPAKNMKNLWVSDLAYIAQVWANQCQYGHDTCDVAKYQVVGQNVALTGSTA
AVYNDPVKLVKMWEDVVDKYNPKKKFSENNFLKIGHYTMVWANTKEVCGGSIKYIQENW
HKHYLVCNYGSPGNFGNEELYQTK
>ABC73068.1 unknown function, antigen 5 [*Vespula maculifrons*]
MEISGLVYLIIIVTIIDLPGKANNYCKIKCLKGGVHTACKYGLKPNCGNKVVSYGLT
KQEKQDILKEHNDFRQKVARGLETRGNPGPQPPAKNMKNLWVNDLAYVAQVWANQCQY
HDTCRDVAKYQVVGQNVALTGSTAAKYENPVNLVKMWENEVDKYNPKKKFSENNFIKIGHY
TMVWANTKEIGCGSMKYTENKWHYHYLVCNYGSPGNFGNEELYQTK
>P35785.1 Ves p 5; unknown function, antigen 5 [*Vespula pensylvanica*]
NNYCKIKCLKGGVHTACKYGLKPNCGNKIVSYGLTKEEKQDILKEHNDFRQKIARGLE
TRGNPGPQPPAKNMKNLWVNDLAYVAQVWANQCQYGHDTCDVAKYPVGQNVALTGSTA
DKYDNPVKLVKMWEDVVDKYNPKKKFSENNFNKIGHYTMVWANTKEIGCGSIKYIQNEW
HKHYLVCNYGSPGNFGNEELYQTK
>P0CH86.1 Ves s 1; phospholipase A1 [*Vespula squamosa*]
GSKCFSDDTVAMVIVTRENRRDFYTLQTLRNHDEFKKAITRPVVFITHGFTSSATVE
SFVDLQTAILEXXXXKVTVSDWRVAACNRTTGLLYVTVAVSNTRLVGRYIATVTKKLVTD
YNVSMADIRLIGHSLGAHVSGFAGKEVQKLEKYSEIIGLDPAGPSFESNDCAERLCKT
DAHVVQIIHTSKKFGIEKSIGHVDFYVNOGNNQPGCGIIPKDVCSHSRAITYMTECIKR
ECCLIGIPQSKSSKSISSCTRQECVGLKAKSYPNTGSFYVPVESTAPFCNNKGKII
>P35786.1 Ves s 5; unknown function, antigen 5 [*Vespula squamosa*]
VDYCKIKCLKGGVHTACKYGTSTKPNCGMMVKSQYVGTQAEKQEILKIHNDFRNKVARGL
ETRGNPGPQPPAKNMKNLWVNNELANIAQIWAQCYGHDTCKDITKYNVQNIIVSSST
AAVYENVGNLVKAWENEVDKFNPTISWEQNEFKKIGHYTMVWAKTKEIGCGSIKYVDNN
WYTHYLVCNYGPAGNFGNQEVYERK
>P35787.1 Ves vi 5; unknown function, antigen 5 [*Vespula vidua*]
KVNYSKIKCLKGGVHTACKYGTSTKPNCGKMWKAYGLTEAEKQEILKVHNDFRQKVAKG
LETRGNPGPQPPAKNMKNLWVNDLAYIAQVWASQCNQYGHDTCKDTEKYPVGQNIKRST
TAALFDSPGKLVKMWENEVDKFNPNIEWSKNNLKKTGHYTMVWAKTKEIGCGSVKYVKD
EWYTHYLVCNYGSPGNFRNEKLYEKK
>ACA00159.1 Ves v 3; dipeptidyl peptidase [*Vespula vulgaris*]
MVPLRSFVLLNSLFLVLLAARTVVTRVIDKDNSDRIVKTQNDQNLKVPFNLEETYTADF
LAYVFNGTWTSDTTIVYTDRTGDILQFDVIKQRSTLIVDSSVMDAYIVSNVYVLSPKGRY
LLIGYDLKKGRYSTFMRYVIYDIEHRAYHKIGNDMHIALAKWAPLTDDLIYILDNDIYY

MRFSNNGFNDVQRVTYDGISGIVYNGVPDWYEEVLQDSSAIWFSPDGNHLAYASFDDR
NVQEILYLHYGEPGNLDDQYPTVEVKKIKYPKVGTLPVVSLLVLDLHDPTLNKIDLKAPHY
AVGTDNLLYNVQWKDFDHVVVWTSNRVQNKTEIVWYNMYGEIVKTLHVVEHKGWLDIKHL
FFYKGSVYIRKLQPSGKTAGRFHHVTRYDETFKQSPTQMDLTPDAIEVQNICTIDQSNGR
IYYLASGLGKPSQKNLYSVPADGSEKPTCISCNVLTPEGNVCTYADAI FSPLGQYYVLVC
HGPDPAFVSIFNNAHQKVYSWENNL SLRKKLAKRHLPLVKDL DVRANGYESKVRLFLPHN
FDESKSYPMMLVNVYAGPNTLKIIDAASYGHQVYMTTNRSVIYAYIDGRGSSNKGSKMLFS
IYRKLGTVEVEDQITVTRQLQEMFPWIDSKRTGVWGW SYGGFSTAMILAKDTSFVFKCGI
AIAPVSSWIYYDSIYTERFMGFPTPEDNLSGYNEDVSRVEDIRGKKFMLIHGSGDDNV
HYQQSLALAKALEKADVMFEQITYTDEAHALFGVLP HLYHTMDRFWSDCFSLSHAH

>P49370.1 Ves v 2; hyaluronidase [*Vespula vulgaris*]
SERPKRVFNIIYWNVPTFMCHQYDLYFDEVTFNFIKRNKSKDDFQGDKIAIFYDPGEFPALL
SLKDGYKRRNGGVPQEGNITIHQKFIENLDKIYPNRNFSGIGVIDFERWRPIFRQNWG
NMKIHKNFSIDLVRNEHPTWNKKMIELEASKRFEKYARFFMEETLKLAKKTRKQADWGY
GYPYCFNMSPNNLVPECDVTAMHENDKMSWL FNNQNVLLPSVYVRQELTPDQRIGLVQGR
VKEAVRISNNLKHSPKVL SYWVYVYQDETNTFLTETDVKKTFQEIVINGGDGIIIWSSS
DVNSLSKCKRLQDYLLTVLGPIAINVTEAVN

>CAI77218.1 Ves v 2; hyaluronidase [*Vespula vulgaris*]
DRTIWPKKGFSIYWNIPTHFCHNFGVYFKELKQFNIIKYNMNNFRGETISLFYDPGNFPS
MVLKNGTYEIRNEGVPQKGNLTIHLEQFTKELDEIYPKKIAGGIGVIHFHNWRPIFRRN
VDNLKINKDISIDLVRKEHPKWDKSMIEKEASNRFETS AKIFMEKTLKLAKKTRKQADWGY
YHGYPHCLSGSTDKPSFDCDALSMSSENDKMSWL FNNQNVLLPSIYLKNVLPDEKIHVQ
ERLKEAIRISKNFKHLPKVLPYWVYTYQDKESIFL TEADVKNTFKEILTNGADGIIIWGV
SYELTDRKRCEKLKEYLKMILGPIAFKVTKAVKENTPLNF

>AAB48072.1 Ves v 1; phospholipase A1 [*Vespula vulgaris*]
MEENMNLKYL L LFVYFVQVLNCCYGHGDP LSYELDRGPKCFNSD TVSIIIETRENRRND
LYTLQTLQNHPEFKKKTITRPVWFITHGFTSSASETNFINLAKALVDKDNMVISIDWQT
AACTNEAAGLKYLYPTAARNTRLVGOYIATITQKLVKHYKISMANIRLIGHSLGAHASG
FAGKKVQELKLGKYEIIGLDPARPSFDSNHCSERLCETDAEYVQIIHTSNYLGTEKTLG
TVDFYMNNGKNQPGCGRFFSEVCSHRAVIYMAECIKHECCLIGIPKSKSSQPISSTKQ
ECVCVGLNAKKYPSRGSFYVPVESTAPFCNNKGKII

>AAA30333.1 Ves v 5; unknown function, antigen 5 [*Vespula vulgaris*]
MEISGLVYLIIIVTIIIDLPGKANNYCKIKCLKGGVHTACKYGS LKPNCGNKVVVSYGLT
KQEKQDILKEHNDFRQKIARGLETRGNPGPQPPAKNMKNLVW NDELAYVAQVWANQCQYG
HDTCRDVAKYQVGQVVALTGSTA AKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHY
TQM V WANTKEVGC GSIKYIQEKWHKHHLVCNYGPSGNFMNEELYQTK

>CAB42887.1 Ves v 5; unknown function, antigen 5 [*Vespula vulgaris*]
NNYCKIKCLKGGVHTACKYGS LKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE
TRGNPGPQPPAKNMKNLVW NDELAYIAQVWANQCEYGHDTCRDVAKYQVGQVVALTGSTA
AKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQM V WANTKEVGC GSIKYIQEKW
HKHYLVCNYGPSGNFKNEELYQTK

>1QNX_A Ves v 5; unknown function, antigen 5 [*Vespula vulgaris*]
AEAEFNKYCKIKCLKGGVHTACKYGS LKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKI
ARGLETRGNPGPQPPAKNMKNLVW NDELAYVAQVWANQCQYGHDTCRDVAKYQVGQVVAL
TGSTA AKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQM V WANTKEVGC GSIKY
IQEKWHKHHLVCNYGPSGNFKNEELYQTK

>AER70365.1 Ves v 6; vitellogenin [*Vespula vulgaris*]
MRSRFILL L LGVAVSNLDN NIEHGKVKGE EYQYLVR SRTL TGLQTLSDQYAGILMKATLR
IQCNSPDTLRAQLLKPQYAIHKKLPDGWDSRISDQMLEHKHLP LSNEPFVIK LKHGVIR
DLIVSKNVPTWEVNI IKSII SQFQADTQGENLKG NKNTQIPEDDNP FATFRVMEDCVSGK

CEVLYDVVPLTEDVLQHRPHILPKPELRNGEHIYITKTRNYDKCEQRMDYYFGISGNAN
WESDIRNNDKIMKKSSTSNMVISGNLKNFVIQTAVTTTEIIMKPRLVDDQESIVISKMN
TLVSVNKVSSPIAPANNPESTGNLVYTYNDPFSKTVQRRLGRPSVSPNSMSNELDSSADS
DEDLRLMREKYGKSDKMNVSDEDKAFRQMKPTLHEAPKNPMLPLFIGNNGKAVVMSDKI
NSGKMVMTLVQEIASEMEDPNVMPDRETLEKFTIVSRLISSMSLEQINKAEGSLHVS
WNEIGSDETNRMKKENARAVFRDAIANAGTGPALMTIKRWIEKKEIEGCEAADVLASIPK
TAR TPTAEYVDAFFSLASNPEVQKQTCLNSSAVLSFAELVHRAQVSNSSIYNHYPVNVFGR
LS SRRNDAVLRKYIPFFAEELKKAIKDGDSPRIQVYILALGLTGHPKILNVLEPYLEGK
ERVSTYQRFLMVMSLRKLCCEVKPSLARSVLYKIYLNWVHQIRCAAVNLIMRTNPPLDML
TRMAQFTNTDFSGQVNSAVKSAIESAANLNYPEWEELTRNARKVLHLMNTESDKYYS
ESHFTEMEENDQLSYRMMLNYIGSDNVIPLSTHFALQPSYNGFLSPVYELDMSISSV
KSLLEM YWHKSEKGDTEESFAEKTAKMLHIESDNVEQVEGNVFFKTPYLNRYFSFDNHT
IERILHDMVSPRSHSHVNMNKL LSYDITLSFPTETGLPFVYSLHVPTIKKFSVISKPDM
KSKFDVRLTSTKHQGRVGFITPFDHQAF LSGIDNNMQVFLPCKLDFHLNNEKSR
LDAALQPLKHNSKTRLGHFVPIPYTSQYEIMSLRPLLEKNTHRIQEKKTTHIRIPQNP
NSIFSVEVEADNLA EKIQQWLRSENKWEDMLSPSSALGTYEKIDLFVKPDLQENEAVK
FTATLDTKEIRSNNLDTNDESWKSGNKVLKTMHQALDSPARRKEFLQEVVKGINS
GKAYVIDAGLEVPGLWKS NHACTLCLASSNDENKFRSIFYWYTNIPSQDITYQMCVNG
QTRSSPTTPFDYKKILDSNPTN EFSINIQSGRTCTDNSLVTIKGQIKQSE
DYKTYVQESRIVKRCDENVRNSVKDCQKAAEM AKNLNEIDMTITKHNSAEESDTELEK
IFHGTKKMLTGLNVRVSEIQEHSDVNDNDIRVQ IKLSPNMTSAEGMASKSGQILTFSDI
HIDMGIDNDEMNEIEKGILHGATCTLRNNEAETFDGKVYPLKLGKCAHVLFTTYPRNAP
NEPNKRMSIPENMKVTVIAEETENKKELQILLGNDEILFKSSGTEVSAWVNGQVKVCSQ
KESYQHIKNDETLFEIFELPGPAIKLISDKYDIKLAYDTHVQIEVPHTYQQSVRGLCGDFD
GRSENFVTPKNCMLQKPEEFAATYILKERCEGPALNNAKKAERSKCIRKVLRFSDVISDGE
AGRYPVNWQWGYHKKENKKQCNTYRTQII TKDDNICFTIRPVPTCSSGCKSVVTKLKEYQ
LYCLPKNDSSLGMKKRIEQGANPDL SRTPTDNAMISVPLECVAT

>CAA50008.1 Vig r 4; 2S albumin, conglutin [Vigna radiata]
MSNLPIYINAAFRFSSRDYEVYFFAKNKYVRLQYTPGKTEDKILTNLRLISSGFPSLAGTP
FAEPGIDSAFHTEASEAYVFSANNRAYIDYAPGTTNDKILAGPTTIAEMFPVLRNTVFAD
SIDSAFRSTKGKEVYLFKGNKYVRIDYDSKQLVGSIRNISDGFVPLNGTGFESGIDASFA
SHKEPEAYLFGDKYVRIHFTPGKTDDTLVGDVVRPILDGWPVLKAFCLCELNKPSLSCIN
HLSLVTINKAFISNVCLFFFNVTLGLEACFLS

>ABG02262.1 Vig r 2; 8S globulin, vicilin [Vigna radiata]
MVRARVQLLLGILFLASLSVSGIVHREHQESQEESDSRGQNNPFYFNSDRRFHTLFKNQ
YGHRLVIRHFDQRSKQIQNLENYRVVEFKSKPNTLLLPHHADADFLVVLNGRAILTLVN
PDGRDSYILEQGHAKIPAGTTFFLVNPNDDNLRRIKLAIPVNNPHRFQNFLLSSTEAAQ
QSYLRGFSKNILEASFDSDFEIDRVLFGEERQQQHGEESQEEGVIVELKREQUIRELIK
HAKSSSRKELSSQDEPFNLNRNSNPIYSNKFGRWYEITPEKNPQLKDLDFISSVDMKEGGL
LLPHYNSKAIVILVINEGEAKIELVGPSSDQQQQDESLEVQRYRAELSEDDVFVIPAAYPV
AINATSNLNF FAFGINAENNRNFLAGEKDNVMSEIPTEVL DVSF PASGNKVEKLIKQ
QSESHFVDAQPEQQQREEGHKGRKGSLSLILGSLY

>ABW23574.1 Vig r 2; 8S globulin, vicilin [Vigna radiata]
MVRARIPLLLLLGILFLASLSVSGIVHRENIDGAEVSVSRGKNNPFYFNSDRWFHTLFR
NQFGHLRVLQRFDRSKQMQNLENYRVVLEMSKPNTLLLPHHADADFLVVLNGRAVLT
LVNPDGRDSNILEQGHAKIPAGTTFFLVNPDNDNLRRIKLAIPVNNPHRFQDFLLSSTE
AAQQSYLQGFKNILEASFDSDIKEISRVLFGEEGQQQQQGESQQEGVIVELKREQUIREL
TKHAKSSSKKLSLSEDPFNLRNQKPIYSNKLGRWFEITPEKNPQLRDLDMFIRSVD
MKEGSLLLPHYNSKAIVILVINEGKANI ELVGQREQKQEEQEESWEVQRYRAELSEDDVFI
IPATYPVAINATSNLNF FAFGINAENNRNFLAGEKDNVISEIPTEVL DVTF PASGEKVK

KLIKKQSESQFVDAQPEQQEREEARKGGKGPFFVY
>BAA74451.1 Vig r 6; pathogenesis related protein, PR-10, Bet v 1-like [Vigna radiata]
MVKEFNTQTELSVRLEALWAVLSKDFITVVPKVLPHIVKDVQLIEGDGGVGTILIFNFLP
EVSPSYQREIEITFEDESSHEIGLQVIEGGYLNQGLSYYKTTFKLSEIEEDKTLVNVKISY
DHDSIEEEKVTPTKTSQSTLMYLRRLERYLSNGSA
>AAK19889.1 Vig r 1; pathogenesis related protein, PR-10, Bet v 1-like [Vigna radiata]
MAVFTFDDQATSPVAPATLYNALAKDADNIIPKAVGSFQSVEIVEGNGGPGTIKKISFVE
DGETKFLVHKIESVDEANLGYSYSIVGGVALPDTAEKITIDTKISDGADGGSLIKLTISY
HGKGDAPPNEDELKAGKAKSDALFKAVEAYLLANP
>P33556.1 lipid transfer protein, partial [Vitis sp.]
AITCGQVSSALSSCLGYLKNGGAVPPGSSCGIKNLNSA
>P80274.1 lipid transfer protein, partial [Vitis sp.]
TVTCGQVASALSPCIDYLQKDGAVPAGSCCXKLSSA
>P80273.2 lipid transfer protein, partial [Vitis sp.]
LSCGDVATQMASCINYLRGAGPLPAACNGVKLNKNSATTTQDRRTACKCLISASKTISG
VNFGLAAGLPAKCGVSIPIYKISPSTNCDQVN
>CAR48256.1 Xip g 1; calcium-binding protein, parvalbumin [Xiphias gladius]
MAFAGVLSADVAALAEACKDAGTFDYKFFKSCGLAAKSTDDVKKAFAIIDQDKSGFIE
EDELKFLQNFKAAARPLTDAETEAFKAGDSGDGKIGAEFFAALVTA
>AAK56124.1 Zea m 1; beta-expansin [Zea mays]
MGSLVNNIMVVGAVLAALVAGGSCGPPKVPPGPNITTTNYNGKWL TARATWYGQPNGAGAP
DNGGACGIKNVNLPPYSGMTACGNVPIFKDGKGCSCYEVRCKEKEPECSGNPVTVYITDM
NYEPIAPYHFDLSGKAFGLAKPGLNDKIRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGC
NPNYLAVLVKYVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPFSIRLTS
ESGKKVIAKDVIPANWRPDAVYTSNVQFY
>AA045607.1 Zea m 1; beta-expansin [Zea mays]
MGSLANNIMVVGAVLAALVVGSCGPPKVPPGPNITTTNYNGKWL TARATWYGQPNGAGAP
DNGGACGIKNVNLPPYSGMTACGNVPIFKDGKGCSCYEVRCKEKEPECSGNPVTVFITDM
NYEPIAPYHFDLSGKAFGLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGC
NPNYVAVLVKVFVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPFSIRLTS
ESGKKVIAKDIIPANWRPDAVYTSNVQFY
>AA045608.1 Zea m 1; beta-expansin [Zea mays]
MGSLANNIMVVGAVLAALVAGGSCGPPKVPPGPNITTTNYNGKWL TARATWYGQPNGAGAP
DNGGACGIKNVNLPPYSGMTACGNVPIFKDGKGCSCYEVRCKEKEPECSGNPVTVYITDM
NYEPIAPYHFDLSGKAFGLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGC
NPNYLAVLVKYVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKGPFSIRLTS
ESGKKVIAKDVIPANWRPDAVYTSNVQFY
>ABD79094.1 Zea m 1; beta-expansin [Zea mays]
MWSLMQAQVAMVVALSFLVSGAWCGPPKVPPGKNITATYGKDWLDAKATWYGKPTGAGPD
DNGGGCGYKDVNKPFFNSMGACGNIPIFKDGLGCGSCFEIKCDKPVCESGKPVVWHITDM
NYEPIAAYHFDLAGTAFGAMAKKGEEEKLRKAGIIDMQFRRVKCKFGSKVFSHLEKGC
NYLALLVKYVDGDGDIVPVDIKEKGSPTYEPLKHSWGAIWRKDSKPLKGPLTVRLTTEG
GTKTVYDDVIPANWKANTAYTAK
>ABD79095.1 Zea m 1; beta-expansin [Zea mays]
ARALVFLVSGAWCGPPKVPPGKNITATYGKDWLDAKATWYGKPTGAGPDDNGGGCGYKDV
NKPPFNSMGACGNIPIFKDGLGCGSCFEIKCDKPVCESGKPVVWHITDMNYEPIAAYHFD
LAGTAFGAMAKKGEEEKLRKAGIIDMQFRRVKCKYDSKVTFHLEKGCNPYLALLVKYVD
GDGDIVAVDVKEKGSPTYEPLKHSWGAIWRKDSKPLKGPLTVRLTTEGGTKSVYDDVIP

ANWKANTAYTAK

>ABF81661.1 Zea m 1; beta-expansin [Zea mays]
CKYGSKVTFHLEKGCNPNYLALLVKYVDGDGDIVAVDIKEKGSPTYEPLKHSWGAIWRKD
SDKPIKGPITVRLTTEGGTKTVYDDVIPAEWKPNNTAYTT

>ABF81662.1 Zea m 1; beta-expansin [Zea mays]
MTVVSIMWSLVQVQVLVAVALSFLVGGAWCGPPKVPPGKNITANYGSDWLDKATWYGKP
TGAGPDDNNGGGCGYKDVNKAPFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSGKPVV
VYITDMNYEPIAAYHFDLAGTAFGAMAKKGEELRKAAGIIMQFRRVKCKYGSKVTFHL
EKGCNPNYLALLVKYVDGDGDIVAVDIKEKGSPTYEPLKHSWGAIWRKDSKPIKGPITV
RLTTEGGTKTVYDDVIPTDWPNTAYTTK

>2HCZ_X Zea m 1; beta-expansin [Zea mays]
GPPKVPPGXNITTTNYNGKWL TARATWYQPNGAGAPDNGGACGIKNVNLPYSGMTACGN
VPIFKDGLGCGSCYEVRCCKEPECSGNPVTYITDMNYEPIAPYHFDLSGKAFGLAKPG
LNDKIRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYLAVLVKYVADDGDIVLMEIQ
DKLSAEWKPMKLSWGAIWRMDTAKALGPFISIRLTSESGKKVIAKDVIPANWRPDAVYTS
NVQFY

>Q1ZYQ8.2 Zea m 1; beta-expansin [Zea mays]
MAVNVRTMWSSMRAQVAMVVALVFLVRGAWCGPPKVPPGKNITATYKGDWLDKATWYGK
PTGAGPDDNNGGGCGYKDVNKPPFNSMGACGNIPFKDGLGCGSCFEIKCDKPVCECSGKPV
VVHITDMNYEPIAAYHFDLAGTAFGAMAKKGEELRKAAGIIMQFRRVKCKYDSKVTFH
LEKGCNPNYLALLVKYVDGDGDIVAVDVKEKGSPTYEPLKHSWGAIWRKDSKPLKGPLT
VRLTTEGGTKSVYDDVIPANWKANTAYTAK

>P0C1Y5.1 Zea m 1; beta-expansin [Zea mays]
MTVVSIMWSLVQVQVLVAVALFLVGGAWCGPPKVPPGKNITAKYGSWLDKATWYGKP
TGAGPDDNNGGGCGYKDVNKAPFNSMGACGNVPIFKDGLGCGSCFEIKCDKPAECSGKPVV
VYITDMNYEPIAAYHFDLAGTAFGAMAKKGEELRKAAGIIMQFRRVKCKYGSKVTFHL
EKGCNPNYLALLVKYVDGDGDIVAVDIKEKGSPTYEPLKHSWGAIWRKDSKPIKGPITV
QLTTEGGTKTVYDDVIPAGWPNNTAYTAK

>P29022 Zea m 8; chitinase [Zea mays]
MANAPRILALGLLALLCAAAGPAAAQNCGCQPNFCCSKFGYCGTTDAYCGDGCQSGPCRS
GGGGGGGGGGGGGGGGANVANVVTDAFFNGIKNQAGSGCEGKNFYTRSAFLSAVNAYPG
FAHGGTEVEGKREIAAFFAHVTHETGHFCYISEINKSNAYCDASNRQWPCAAGQKYGRG
PLQISWNYNYGPAGRDIGFNGLADPNRVAQDAVIAFKTALWFWMNNVHGVMPPQGFATIR
AINGALECNGNNAQMNARVGYKQYCCQLRVDPGPNLIC

>AAA33493.1 Zea m 14; lipid transfer protein [Zea mays]
MARTQQLAVVATAVVALVLLAAATSEAAISCGQVASAIAPCISYARGQSGGPSAGCCSGV
RSLNNAARTTADRRACNCLKNAAAGVSLNAGNAASIPSKCGVSIPYTISTSTDCSRVN

>AAA33494.1 Zea m 14; lipid transfer protein [Zea mays]
SCGQVASAIAPCISYARGQSGGPSAGCCSGVRSLNNAARTTADRRACNCLKNAAAGVSG
LNAGNAASIPSKCGVSIPYTISTSTDCSRYSRRMHASAD

>ABD79096.1 polygalacturonase [Zea mays]
MACIDNAMRALFLLALFCVVHGEKAKSKDNDKASGPGGSFDITKLGASGNGKTDSTKAV
QEAWASACGGTQKQITILIPKGDFLVGPLNFTGPCKGDVTIQVNGNLLATDLSQYKDHGN
WIEILRVDNLVITGKGLDQGPVWSKNSCVKDYCKILPNSLVMDFVNNGEVSGITLL
NSKFFHMNYKCKDMLIKDVNVTAPGDSPTDGIHMGDSSGVTITNTVIGVGDCCISIGP
GTSKVNITGVTCPGHGISIGSLGRYKDEKDVTDINVKDCTLKKTANGVRIKAYEDAASV
LTASKIHYENIKMEDSGYPIIIMDKYCPNKLCTANGASKVTVKDVTFKNITGTSSTPEAV
NLLCSAKIPCTGVTMDDVNIKYSGTNNKTMVAVCKNAKGSAGKCLKELACF

>ABD79097.1 polygalacturonase [Zea mays]
ARGALFLLALFCVVHGEKAKSKDNDKASGPGGSFDITKLGASGNGKTDSTKAVQEAWAS

ACGGTGKQITILIPKGDFLVGPLNFTGPCKGDVTIQVNGNLLATTDLSQYKD HGNWIEILR
VDNLVITGKGLDGGQPAVWSKNSCVKKYDCKILPNSLVMDFVNNGEVSGITLLNSKFFH
MNMKYCKDMLIKDVNVTAPGDSPTDGIHMGDSSGVTITNTVIGVGDDCISIGPGTFKVN
ITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKTANGVRIKAYEDAASVLTASKI
HYENIKMEDSGYPIIIDMKYCPNKLCTANGASKVTVKDVTFKNIPGTSSTPEAVNLLCSA
KIPCTGVTMDDVNIKYSGTNNKTMVCKNAKGSAGCLKELACF

>ABD79098.1 polygalacturonase [Zea mays]
ARACTDNAMRALFLLVLFIVHGEKEESKIDAKASGPGGFFDITKLGASNGKTDSTKA
VQEAWASACGGTGKQITILIPKGDFLVGQLNFTGPCKGDVTIQVDGNLLATTDLSQYKEHG
NWIEILRVDNLVITGKGLDGGQPAVWSKNFCTKKYDCKILPNSLVMDFVNNGEVSGITL
LNSKFFHMNMKYCKNMLIKDVTVTAPGDSPTDGIHMGDSSGVTITNTVIGVGDDCISIG
PGTSKVNITGVTCGPGHGISIGSLGRYKDEKDVTDINVKDCTLKKTAMFGVRIKAYEDAAS
VLTVSKIHYENIKMEDSANPIFIDMKYCPNKLCTANGASKVTVKDVTFKNITGTSSTPEA
ISLLCTAKVPCTGVTMDDVNVEYSGTNNKTMVCKNAKGSAGCLKELACF

>CAA51718.1 Zea m 12; profilin [Zea mays]
MSWQTYVDEHLMCEIEGHHLSAAIVGHDGATWAQSTAFPEFKPEEMAAIMKDFDEPGHL
APTGLILGGTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQSLIIGIYDEPMTPGQCNLVVE
RLGDYLLEQGM

>CAA51719.1 Zea m 12; profilin [Zea mays]
MSDRAKMSWQAYVDEHLMCEIEGHHLSAAIVGHDGAAWAQSTAFPEFKTEDMANIMKDF
DEPGHLAPTGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVVGIYDEPMTPGQ
CNMVVERLGDYLLEQGM

>CAA51720.1 Zea m 12; profilin [Zea mays]
MSWQTYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFPEFKPEEMTNIIMKDFDEPGFL
APIGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE
RLGDYLVEQGL

>AAB86960.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGQHLSSAAIVGHDGVSVAQSESFPELKPEEVAGIIMKDFDEPGTL
APTGLFVGGTKYMVIQGEPEGVIRGKKKGTGGITIKKTGMSLIIGVYDEPMTPGQCNMVVE
RLGDYLIEQGF

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

>ABG81312.1 Zea m 12; profilin [Zea mays]
MSWQTYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFPEFKPEEMTNIIMKDFDEPGFL
APIGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE
RLGDYLVKQGL

>ABG81313.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFPEFKTEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQAMVVGIYDEPMTPGQCNMVVE
RLGDYLLEQGL

>ABG81314.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAAWAQSTAFPEFKTEDMANIMKDFDEPGHL
APTGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVVGIYDEPMTPGQCNMVVE
RLGDYLLKQGL

>ABG81315.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLSAAIVGHDGAVWAQSTAFPEFKTEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPEGAVIRGKKKSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE
RLGDYLLEQGM

>ABG81316.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLTSAAIVGHDGAVWAQSTAFPQFKTEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPAVIRGKKKSGGITVKKTGQALVIGIYDEPMTPGQCNMVVE
RLGDYLLEQGL

>ABG81317.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLTSAAIVGHDGAVWAQSTAFPQSKTEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPAVIRGKKKSGGITVKKTGQAMVVGIIYDEPMTPGQCNMVVE
RLGDYLLEQGL

>ABG81318.1 Zea m 12; profilin [Zea mays]
MSWQAYVDEHLMCEIEGHHLTSAAIVGHDGAVWAQSTAFPQFKTEEMTNIMKDFDEPGFL
APTGLFLGPTKYMVIQGEPAVIRGKKKSGGITVKKTGQAMVVGIIYDEPMTPGQCNMVVE
RLGDYLLNRA

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

>Q4W1F6 Zea m 25; thioredoxin [Zea mays]
MASEQGVVIACHSKAEFDAHMTKAQEAGKLVVIDFTAAWCGPCRAIAPLFVEHAKKFTQV
VFLKVDVDEVEKVTAAAYEVEAMPTFFHFVKNGKTVATIVGAKKDELLALIEKHAAPAPASA
SA

>2209273A unknown function [Zea mays]
MASVPAPATTTAAVILCLCVLSCAAADDPNLPDYVVIQGRVYCDTCRAGFVTNVTEYIAG
AKVRLECKHFGTGKLERAIIDGVTDATGTYTIELKDSHEEDICQVVLVASPRKDCDEVQAL
RDRAGVLLTRNVGISDSL PANPLGYFKDVPLPVCAALLKQLDSDDDDDDQ

>AAX40948.1 Ziz m 1; chitinase [Ziziphus mauritiana]
MVPQAKLVVASLILTSALIQTSEAVGGIATYWGQYTETEEGSLAEACASNLYSYINIAYL
NIFGEGRYLSL NISGHCS DCTFLGEEIKACQSQGVKIFLSLGGPYGDYHLTTDGDADRV
EQLWSSFLGGSKSTGVYQPLLGDVELDGDIDLDIQIGPPEEYDVLARNLKD LTKDRTRPFY
LSAAPKCSAYNDS DAYLWTAVETGLDFVWVKFYNDTSCQYNNDTAAGLDAFYRSWYDWT
VSLAEGNKLLIGIPASNETDNSPLGGYIPSDVLNDQIVSVIMTSSKFGGVNVWNRYYDLK
TNYSSSIILEYVNSGTKYLPLRRTKFMYQNA

>QCI56576.1 tropomyosin [Zophobas atratus]
EARFLAEADKKYDEVARKLAMVEADLERAEERAEAGESKIVELEEEELRVVGNLKSLE
VEEKANQREEEYKNQIKNL TTRLKEAEARAEFAERSVQKLQKEVDRL EDELVAEKERYKE
IGDDLDTAFVELIL

>COMPARE00353 7S globulin, vicilin, partial [Prosopis juliflora]
REQEQGSSSESRRQ

>COMPARE00354 7S globulin, vicilin, partial [Prosopis juliflora]
RRQSGDERRH

>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]
RVVLAIPINNPGRF

>COMPARE00361 7S globulin, vicilin, partial [Prosopis juliflora]

KFYDFYPSRTKD

>COMPARE00362 7S globulin, vicilin, partial [Prosopis juliflora]

RSNEPIYSNKF

>COMPARE00363 ATP synthase beta subunit, partial from XP_042978511.1,
XP_042985737.1 [Carya illinoensis]

RDAEGQDVLLFIDNIFRF

>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,
XP_042985737.1 [Carya illinoensis]

RFQEGLPPILTAEVLDNSIRL

>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 [Carya illinoensis]
RIMNVIGEPIDERG

>COMPARE00369 ATP synthase beta subunit, partial from XP_042978511.1,
XP_042985737.1 [Carya illinoensis]

KITDEFTGAGSIGVCQVIGAVVDVRF

>COMPARE00370 ATP synthase beta subunit, partial from XP_042978511.1,
XP_042985737.1 [Carya illinoensis]

KNLQDIIAILGMDSEDDKLTVARA

>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]

KLDLTAEEELTEEKA

>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]
KGAIPALPTETEVGLLKG

>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]
KDAGVLLSYDPNLR

>COMPARE00399 acyltransferase, transacylase, partial from XP_042956292.1 [Carya illinoensis]
KLDSTVISQPAIYVTSAAVELLRA

>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 from XP_042969845.1 [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

>COMPARE00414 Fag t 6; oleosin, partial from QZM06934.1 [Fagopyrum tataricum]
MADQHYYHQAKDHTNQAQQHGQQALSNNMAGYLQEK

>COMPARE00415 Fag t 6; oleosin, partial from QZM06934.1 [Fagopyrum tataricum]
AYDARAHEVGRTTA

>CAA77666.1 Asp f 13; alkaline serine protease [Aspergillus fumigatus]
ALTTQKGAPWGLGSIHKGQASTDYIYDTSAGAGTYAYVVDSGINVNHVEFESRASLAYN
AAGGSHVDSIGHGTHVAGTIGGKTYGVAKKTNLLSVKVFQGESSSTSIIILDGFNWAVNDI
VSKGRTKKAAINMSLGGGYSYAFNNAVENAFDEGVLSVVAAGNENSNDASNTSPASAPNAL
TVAAINKSNARASFSNYGSVVDIFAPGQDILSAWIGSTTATNTISGTSMATPHIVGLSVY
LMGLENLSGPAAVTARIKELATNGVVTNVKGSFNKLAYNGNA

>XP_018654157.1 unknown function [Schistosoma mansoni]
MATETKLSQMEEFIRAFLEIDADSNEMIDKQELIKYCQKYRLDMKLIDPWIARFDTDKDN
KISIEEFCRFGFLKVSEIRREKDELKKERDGGKFKLPPNIEIIAATMSKTKQYEICCCQFK
EYVDNTSRTGNDMREVANKMKSLLDNTYGRVWQVLLTGSYWMNFSHEPFLSIQFKYNNY
VCLAWRTPSQ

>XP_018649273.1 unknown function [Schistosoma mansoni]
MDSPMEKFIQTYLTLLRDGDETVETSKLSESCRKEKLDMKQVNEWIALFDVDKDKQITFE
EFCRGLGLKQEMRIERNHIKTVQSGREQSLPEGVSIIASTMPKPKQVEVTQLFKDIYNE
VKKDPDMNKVVKTFKSELERRYGRVWQVNAVTHSYWASFSHEPFQSIQFQYDNKIILAWR
TPSN

>XP_018649275.1 unknown function [Schistosoma mansoni]
MEPFVQVFFAIDRDGTETITVEELKKYVAENKLDMMVTKWKSLEDPKGTGRITFKTFCD

VLGLSPAQAVAMKTQHQQASSLKLHPDVVVIYEQLPLDRQVAISNKAIELLTSSKKFDEK
DQAVQLKQWLDITYGKAWHIVIVKGSFSSYSHSANKCFIFRVRDVSYLWVRTPDEEITS
A

>XP_018649276.1 unknown function [Schistosoma mansoni]
MEPFITTFGAIDKRGVNVITINELRNYVAENHLDKEMIPKWQALFDPEGTGKITFRRFCE
VLGVQPERHQAIINRPLYGIPTTGLRPEIFVIMQELPLQDQIKISEEAYRLTQPQDKFIE
KEASEKLRWLDTTYGRHWHTIVIRGSYWTTYTHIPNCSFHFKINQHSFIIYRTNA

>CCE94314.1 unknown function [Schistosoma mansoni]
MEPFVNIFFAIDEQQNETITRDELRRYVKHNHLDEGMITRWQSLFDPTNSGIITFQKFCD
VLGVKPEQARTLRKSVINNRPLPKDLQIISQNMSSDQFQIFEFVRSLLDNLSVQDMTQ
MIKQWLDKTFDPSRHVVIIDGSYWISYSHLPEQSLQFRLKEKCYLVWRTPKH

>CCE94321.1 unknown function [Schistosoma mansoni]
MQTIHKLDGFTEIYFMVDRKRRKGGWITMPELRKYMEENDVDEKMFERWKTLDPESTGRIT
LEKFCEVLGLQDEVINVQTAIQGNEMQDVHVIQTDMMNTKMKLTICGLIDEGILYQDDSK
LAEFLKNELDKYFGKLNVIIVIIYGRYWSRYCHETGYNFCFIKDDRIFLVYKIPDLE

>COMPARE00416 Hel a 6; pectate lyase, partial from XP_022025296.1 [Helianthus annuus]
RFGFFQVVNNNYDRWGTYAIGSSAPTILSQGNRFLAPDDAAKK

>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]
KQIWIDHCSFKA

>COMPARE00419 Hel a 6; pectate lyase, partial from XP_022025296.1 [Helianthus annuus]
KVEITNGGLTLM DVKN

>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

>AEN62318.1 unknown function [Polistes dominula]
LVTVLATIFFDTSSAEVCNERQDKPRFYTCQGVNLAQLDSL PDSVVGRLREKSTISRIP
ADAFSRFAASLIELRITGCSLESIEAHAFRRLDKLETLDLSNNRIQAI EASWVRGLFNLK
ELIVLRNRIARIEPEFYELLPKLETLDVAYNELVECITKDNFKKLKLNKLVLIASNPWSY
RCRSDMTYAFKTNHVNFIKDW SIGDLLIEECLAHEQGADSDDVILKHCVD RKS FESITPI
LPDLEKKVLELSNKVEELRNEVNNIKKR

>XP_015185303.1 endothelial growth factor [Polistes dominula]
MSYFEMKLAVFLLVCGIVFSQSDNRKIDNSERIVFPEHTDQDAIGNVKRSTVPSELDDNL
LMTSLEIAQKINSMSTYEEFLKFINVPPEKKVLIASRIGGGGEKSNAERP KPAGCIPENQ
TVSLRPENKFSTFYPSCTRVKRCGGCCGHYLLSCQPIETETRNFEVIVSELNADSTVSY
KNKEIPIIEHTKCKCDCKIKAQHCKKQAYRRNECSCVCMNIDEENKCKANKAVKIWDS
ETCTACRENEICSTGFYFDNNTCRCRQVPILSRFGDISRKS GYRFDQTERPESVPPVIV
HLDASDPRRQHKDDPEYK

>XP_015183815.1 phospholipase A2 [Polistes dominula]
MLTASLCILSVLWAQKTMASVLVADTTMSRMVELNAGEPICSLYNDRGVIQRMILGADPK
KVRQMPSNLVADLEETCLASKNRT PAGGLIYPGTKWCGPGNVASSYDDLQGHAAEDACCR
EHDHCPIAMSSQOCIHGICNNSPFRSHCDCAKFRRCLQNLNTEVANTIGALFFNVIQV

TCFKERRPCSQWRNGYDEAVSNRLCSQYKFRPSEKYVPLMPLNMNI
>QZP44316.1 Cra a 2; arginine kinase [Crassostrea angulata]
MSDLPKLLSEGESKSLKHKHCTKEVYEKLDKDKTKLGGTLADCIRSGALNLSGAGV
YACDPEGYEVFKELLDVIMDYHKVVKVEHPPCDFGPDQKLGFDPLDATGEFIVSTRVRV
GRSHEGYFPVSTDEQRKEMENKTIAALNTLEGEKLGKYYSLTMTPEENQQLIDDHFM
FKNDDKMLGDAGGYNGWPKARGIFFNDNKTFWCWINEEDHLRFISMQKGGDVGEVYKRLV
SAIKQLEKCLTFAYSKRHGYLTFPCPTNLGTTLRASVHIKVPKLAKNEEVLNKICADNKLQ
LRGIHGEHTESVGGVYDISNKRRLGLTEYQAMQEMYNGIKEIQAENAK
>NP_001037486.1 Bomb m 4; unknown function [Bombyx mori]
MRLTLFAFVLAVCALASNATLAPRTDDVLAEQLYMSVVIGEYETAIAKCSEYLKEKKGEV
IKEAVKRLIENGRNTMDFAYQLWTKDGKEIVKSYFPIQFRVIFTEQTVKLINKRDHHL
KLIDQONHNKIAFGDSKDKTSKKVSWKFTPVLENNRVYFKIMSTEDKQYLKLDNTKGSSD
DRIIYGDSTADTFKHHWYLEPSMYESDVMFFVYNREYNSVMTLDEDMAANEDREALGHSG
EVSQYPLFAWYIVPY
>Q0L10866.1 Que ac 1; pathogenesis related protein, PR-10, Bet v 1-like [Quercus
acutissima]
MGVYNYESQETSVIPARLFKAFVLDSNLIKVLPHAVKSTEIEGNGGPGTIKKFTFG
EASKVKYAKHRIDTLDPENCSYSFSVIEGEALTDIASISTEVKFBVSPDGGSIMKSTTKY
QTKGGFQLKEEQIAAVEKGTGLFKAVEAYLLAHPDLYN
>QVU02258.1 Que ac 2; profilin [Quercus acutissima]
MSWQTYVDEHLMCDIDGQGHAAAAIIGHDGSVWAQSSNFPQFKAEIISDIMKDFEEPG
HLAPTGLHLGGTKYMIQGEAGAVIRGKKKSGGVTIKKTSQALVFGIYEETVPGQCNMV
VERLGDYLVQGL
>QVU02259.1 calcium-binding protein, polcalcine [Quercus acutissima]
MATNSAPLNNSSTQNKSSPSLSNQSTEEVEKVFNRFDNNGDGKISVTELGAVFSSLGSS
FSDEEELRRIMDELSDHDGFISLTFEFAAFRCSSSAEDGGASELRDAFKLYDQDQNGLIS
ASELHLVLNRLGMNCSVEDCHRMIRSVSDSDGDNVNFEEFQKMMNTANTSNSNASPL
>COMPARE00422 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
LQQISVSQPR
>COMPARE00423 Mac i 2; 11s globulin, cupin, partial from XP_042518524.1 [Macadamia
integrifolia]
QRIQSEGGVTEFWDENEDQFQCTGVAAMR
>COMPARE00424 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
NIIQPNSLSLPNYSPPR
>COMPARE00425 Mac i 2; 11s globulin, cupin, partial from XP_042518524.1 [Macadamia
integrifolia]
GLLGVTFFGCPETYQSSRDEQSYR
>COMPARE00426 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
APGKMLVVLPAVAHWCLNDGK
>COMPARE00427 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
EDLVAVSVNNLNNQANQLNQK
>COMPARE00428 Mac i 2; 11s globulin, cupin, partial from XP_042518524.1 [Macadamia
integrifolia]
SYLAGSQNQESQR
>COMPARE00429 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
LCHGSWSNTYQNLSPFNQNLMDALNVDVETVR
>COMPARE00430 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
LDGGPQLHAGPHWLMNAHSLFYLTR
>COMPARE00431 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
LKDANVFVVR

>COMPARE00432 Mac i 2; 11s globulin, cupin, partial [Macadamia integrifolia]
MGPAQVLAQSYKSFAGEAQNLIK
>COMPARE00433 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
DNRESYNLECGDVIR
>COMPARE00436 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
EGVIISASQEQIR
>COMPARE00437 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
EILEAALNTQAER
>COMPARE00438 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
ELTRDDESERR
>COMPARE00439 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
ERNVLQQIEPQAMELAFAPR
>COMPARE00442 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
FLQTISTPGQYKEFFPAGGQNPEPYLSTFSK
>COMPARE00443 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
FRTEEGHISVLENFYGR
>COMPARE00445 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
GGSGRYEEGEEKQSDNPYYFDER
>COMPARE00446 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
GPYNLFNKRPLYSNK
>COMPARE00447 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
KEVEELFNSQDESIFPGPR
>COMPARE00448 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
LHIAKFLQTISTPGQYK
>COMPARE00449 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
IPAGTTFYLINR
>COMPARE00451 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
NVLQQIEPQAMELAFAPRK
>COMPARE00452 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
NYRLVLLLEANPNAFVLPHTLDADAILLVTGGR
>COMPARE00454 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia
integrifolia]
REAIVVPVGHVPVVFVSSGNENLLLFAFGINAQNNHENFLAGR
>COMPARE00455 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1
[Macadamia integrifolia]
RGGESSRGPYNLFNK

>COMPARE00456 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL4.1 [Macadamia integrifolia]
RHEEEEDVHVEQVKAR

>COMPARE00458 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1 [Macadamia integrifolia]
VVVVASGEADVEMACPHLSGR

>COMPARE00460 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1 [Macadamia integrifolia]
YQAYEVKPEDYR

>COMPARE00461 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1 [Macadamia integrifolia]
QCMQLETSGQMR

>COMPARE00462 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1, Q9SPL4.1 [Macadamia integrifolia]
RFEEDIDWSK

>COMPARE00464 Mac i 1; 7S globulin, vicilin-like, partial from Q9SPL3.1 [Macadamia integrifolia]
DPQQQYEQCQK

>CAD1459612.1 lipid transfer protein [Macadamia integrifolia]
MANSGVMKLVCLVLACMVVAAPLAEEAITCGQVSKLAPCLTYLRSGGAVPGTCCNAVKN
LNNSAKTTPDRQTACGCLKNAYNSISGINAAYAGGLPAKCGVNLPHYKISPSINCATYTLS
LYNF

>QEA69430.1 Sco m 5; unknown function, antigen 5 [Scolopendra mutilans]
MTIFLTSTLFVLLVFQILGKGMGCDMKVRGLDANMKKMILDLHNKKRQTVANGQQSGQPS
AANMKELHWDQIAANAQRS AETCVFQHTAKNLRKTSKYSYLGENIYMGSPDPPIPRSVN
AWYDEVKDVTPAVVKSFRSGGPMIGHYTQMVWANTEALGCGLVTASDKNTYIFCQYGPSG
NYPGEPIYKQGSPASDCKKKGKSSKYPGLCN

>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]
SLSDEERMDALENLK

>XP_025675300.1 Ara h 18; cyclophilin [Arachis hypogaea]
MANPRVFFDMTIGGQPAGRIIMELFADTTTPRTAENFRALCTGEKGVGRSGKPLHYKGSSF
HRVIPNFMCGGDFTAGNGTGGESIYGSKFADENFIKKHTGPGILSMANAGQNTNGSQFF
ICTAKTEWLDGKHVVFGQVVEGLDVVREIEKVGSSSGRTSKPVVADCGQLS

>ADK66280.1 Lit v 13; fatty acid-binding protein [Litopanaeus vannamei (Penaeus vannamei)]
MAKIEGKFKMESSENFDEFMKALGVGLVMRKMGNAATPTVEITKGDYTMKTTTTFKTT

EIKFKLGEEFEETTADGRVVKSTITLDGNKLVHKQVGDKEKKEKDESELLREFTDDKMLME
CKVDDVVCKRVYSRLE
>QEM21451.1 Cor a 15; oleosin [*Corylus avellana*]
MADYQHQQHQRPADAFKGMFPEKQQAQVQGPSASKVIAVVTLLPLGGFLLLLLAGLTFAG
TLIGLALSTPLFVLCSPVLVPAIIVIGLAVTGFLTSGAFGITGISSLSWILKYLRGTSVP
EQMEHAKRRAQDTAGHLGQKARETGQTVTGKGQEAGKTLEGGRGEEKKT
>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*]
IGAEVYHNLK
>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*]
EVILPVPAFNIVINGGSHAGNK
>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*]
FIHLDSLSDQDSV
>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

>COMPARE00501 glycerol dehydrogenase, partial [Aspergillus ochraceus]
GGNTLAQVLIWGLR

>ALQ56981.1 Coc n 1; 7S globulin, vicilin-like [Cocos nucifera]
MVSAMGDR TASAILALLSSWSLMVVMAYQGRGMEGREKRVEEKAPRSPEDRGLFILRR
SKEVLKTDAGEVRLMMGYRYRGNHSPMHIGFITMEPNTLYIPQYIDASLILFVRRGEAKV
GYIYKNKLVEKRLKSGYVDAIPAGSSFYIVNSDKSERLHIICSIDTLESMEYYGAYPQSF
YVGGGVLPRSVLSGFDASTLSAAFNVSSDQLEMILNSQRGGPIIRLNGEAAEQRDYLSI
MQLKERMVQEKEMSDDDDEAEQEEDDVWTRCLLKSLLGKGD CRVQRKHKLAHSPGSYN
LYDTEPSYQNDYGYSIAIDGHDYSALKHSNLGVYLVNLKAGAMLSPHVNPTATEYGIILR
GSGTIQVVPNGTAAAMNAKVSEGDVFWIPRYFPFCQIASDGAPLEFFGF TTSARKNRPQF
LVGKSSLLHSMRGP ELAAAFGVSEEQLERIVKAQREAVILPTSPHREMEEINGKKWKGEE
VLVMKRGLFA

>AGS43084.1 tropomyosin [Schistosoma mansoni]
MKLQIDQLKQELSSKQAILRKEEENKIKAEAEVASLQKRIRQLEDELESTETRLQEATVK
LEEASKAADESDRARRVLEARQTAEDERILHLESVVQETAKSVRDAETKYEEAARKLAIT
EVELERAESRLEAAESRLKELQSIHGTMGQLKSLEHQESQLNKQRS LHQSQLASLSKQL
IEAERRVKEASHQEEMKQIELCKLEETLEAEQLNHTNLRREMETMFTVENI

>AGS43085.1 tropomyosin [Schistosoma mansoni]
MEHIKKKMLAMKLDKENAVDEADQLEAKLREKELEMQTKDEEVAEVLKIKQVDTDKETA
QTQLAETNTKLEETDKRATEAEAEVASLQKRIRQLEDELESTETRLQEATVKLEEASKAA
DESDRGRKVLENRTFADEERINQLEEQLKESTFMAEDADRKYDEAARKLAITEVELERA
SRLEAAESKITELEEFELRIVGNNVKSLEISEQEAAQREEAYEENIRDLTERL KAAEDRAQ
ESERLVNTLQADADRLEDELVTEKEKYKALSEELDSTFAELTGN

>AGS43086.1 tropomyosin [Schistosoma mansoni]
MEEALSAVYLNSTGLIKMAIIGVELQNVIKVSLRKA AEAEVASLQKRIRQLEDELESTET
RQEATVKLEEASKAADESDRGRKVLENRTFADEERINQLEEQLKESTFMAEDADRKYDEA
ARKLAITEVELERAESRLEAAESKITELEEFELRIVGNNVKSLEISEQEAAQREEAYEENI
RDLTERL KAAEDRAQESERLVNTLQADADRLEDELVTEKEKYKALSEELDSTFAELTGN

>AGS43087.1 tropomyosin [Schistosoma mansoni]
MEHIKKKMLAMKLDKENAVDEADQLEAKLREKELEMQTKDEEVAEVLKIKQVDTDKETA
QTQLAETNTKLEETDKRATEAEAEVASLQKRIRQLEDELESTETRLQEATVKLEEASKAA
DESDRGRKVLENRTFADEERINQLEEQLKESTFMAEDADRKYDEVHF

>AWS00995.1 Cyp c 2; beta-enolase [Cyprinus carpio]
MSISKIHAREILDSRGNPTVEVDLYTAKGRFRAAVPSGASTGVHEALELRDGDKTRYLGK
GTQKAVDHVNKEIAPKLIKFKFSVVEQEKIDKFMLELDGTENKSKFGANAILGVSLAVCK
AGAAEKGVPLYRHIADLAGNKDVILPVPAFNVINGGSHAGNKLAMQEFMILPVGAKNFHE
AMRIGAEVYHNLNKVIKAKYKDATNVGDEGGFAPNILENNEALELLKSAIEKAGYDPKI
IIGMDVAASEFFKNGKYDLDFKSPDDPKRHITGDQLGDLYKSF IKNYPVQSIEDPFDQDD
WENWSKFTGSVDIQVVGDDLTVTNPKRIQQACEKKACNCLLLKVNQIGSVTESIQACKLA
QSNWGVMMVSHRSGETEDTFIADLVVGLCTGQIKTGAPCRSERLAKYNQLMRIEEELGDK
AKFAGKDFRHPKL

>QCX36431.1 Zoy m 1; beta-expansin [Zoysia matrella]
MASSSARRQAQLAAVAVLLSAMVGSALCEIGDKPGPNITATYNEEWQDAKATFYGSNPRG
AAPDDDDGGACGYKNVDKAPFFGMTGCGNEPIFKDGLGCGSCFEIKCKEPAECSDKPVLIR

ITDKNYEHIAAYHFDLSGKAFGSMKQGQEDNLRKAGELTLQFRRVKCEYPSKTKITFHV
EKGCNDNYLALLVEYAAGDGDIVAVDIKPKGSDEF LPMKPSWGAIWRIDPKKPLKGPFTV
RLTSESGAKLVQEDVIPADWKPNTAYTSNLQY
>COMPARE00502 gibberellin-regulated protein, partial from A0A498HTE5 [Malus domestica]
GSPFCDSKCGVRCCKAG
>AHM25029.1 Api m 10; icarapin, partial [Apis mellifera]
FPGAHDSDSKEERKNVDTVLVLP SIERDQMM AATFDFP SLSFEDSDEGSNWNWNTLLRPN
FLDGWYQTLQTHMKKVREQMAGILSRIPEQGVVWNKIPEGANTTSTTKIIDGHVVTINE
TTYTDGSDDYSTLIRVRVIDVRPQNETILTTSSEADSDVTTLPTLIGKNETSTQSSRSV
ESVEDFDNEIPKNQGDVLT A
>COMPARE00503 hexamerin, partial from ACU78069.1 [Locusta migratoria]
LLYHVQQPTLVKEEQEIAK
>COMPARE00504 hexamerin, partial from ACU78069.1 [Locusta migratoria]
VELFWKYYVDVGF LPK
>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]
SGLPLSVFTIIVTQASPDANKPILEHGDLHAAGFPFDR
>COMPARE00513 hexamerin, partial from ACU78069.1 [Locusta migratoria]
VVEFEFDV PNAHFDETFV V HRRVEDLNATA
>QUJ17885.1 Api g 7; defensin [Apium graveolens]
MAPKASSLTL SAI FLLFLVASYSVGVAQ GARAATEGEVWYPEALCEKPSQTWTGKCGNTK
NCDNQCIQWETARHGACHKRGGKWMCF CYFDRC
>AVQ67919.1 Per a 13; glyceraldehyde-3-phosphate-dehydrogenase [Periplaneta americana]
MSKIGINGFGRIGRLV LRAALEKGAQVVAINDPFI GLDYMVMFKYDSTHGRFKGEVSAE
GDQLVVNGQKISVFAERDPKAI PWGKAGADYVVESTGVFTTIDKASAHLEGGAKKVIISA
PSADAPMFVVGVNLEAYDPSLKIVSNASCTTNCLAPLAKVIHDNFEIVEGLMTTVHAVTA
TQKTVDGSPSGKLWRDGRGADQNIIPASTGAAKAVGKVIPALNGKLTGMAFRVPVPNVSVV
DLTVRLGKPASYDDIKAKVKEAATGPLKGILDYTEDDVVSSDFISDTHSSIFDAKAGIPL
NNNFVKLISWYDNEFGYSNRVIDLIKYMQSKD