



## **COMPARE 2025 Update Documentation**

The COMPARE Team is pleased to present the release of the COMPARE 2025 database, released on 01/27/2025 ([www.comparedatabase.org](http://www.comparedatabase.org)).

### **1. COMPARE 2025: General Overview**

#### **1.1. Database entries**

The COMPARE 2025 database consists of **2,836 sequence entries**. Overall updates to the 2025 COMPARE database include:

- **88 unique additions** to the COMPARE 2024 database.
  - 8 full-length proteins
  - 80 mass spectrometry (MS) additions

Therefore, COMPARE 2025 = 2,748 entries (COMPARE 2024) + 88 new unique entries = 2,836 sequence entries.

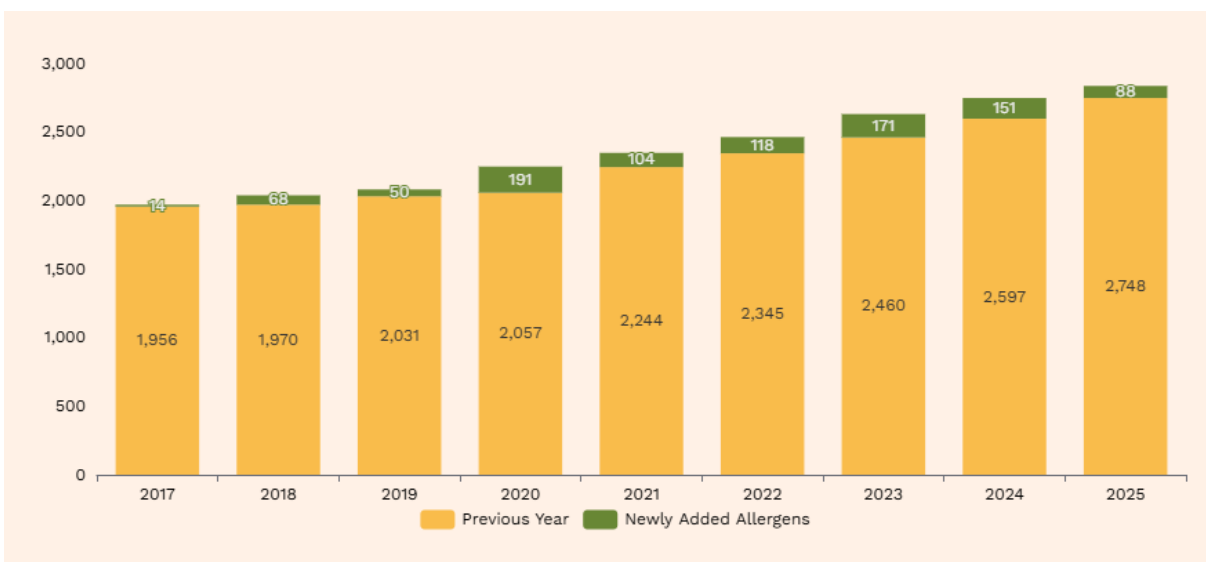




Figure 1: Constant and consistent growth of sequence entries in COMPARE. In 2020 a historical data review was undertaken, and MS sequences started to be included in the database.

All decisions result from the COMPARE Peer-Review Panel (PRP)'s review of sequence candidates with record dates ranging between May 15, 2023 – May 15, 2024, and associated literature. As in previous years, the candidate sequences were sourced from [NCBI Protein](#), [UniProt](#), [AllergenOnline](#), and [IUIS](#) databases, as well as a targeted literature search, for the same time window.

COMPARE 2025 has otherwise followed specifications set in 2019 - e.g., use of "COMPARE #" Accessions when no other public accession number is known for a specific sequence (see paragraph A in "[COMPARE 2019 Documentation](#)" file); information sharing via documentation and transparency files, available in the database page under the [Documentation tab](#).

## 1.2. Updates to past entries

QC checks conducted to verify the interoperability of sequences between COMPARE and NCBI Protein identified instances of partial sequences in the COMPARE database. To ensure consistency, the accessions in COMPARE were updated to reflect this.

### Accession updates:

<b>PAST COMPARE Accession</b>	<b>NEW COMPARE Accession</b>	<b>COMPARE Description</b>	<b>Reason</b>
XP_008286259.1	<b>COMPARE00967</b>	calcium-binding protein, parvalbumin, partial from XP_008286259.1	Sequence in COMPARE is not the full-length XP_008286259.1.
QOL11118.1	<b>COMPARE00968</b>	pectin methylesterase	Sequence did not match 100% to QOL11118.1.
Q9SPL5.1	<b>COMPARE00969</b>	7S globulin, vicilin-like, partial from AAD54244.1	Sequence in publication does not include N-terminal sequence
Q9SPL4.1	<b>COMPARE00970</b>	7S globulin, vicilin-like, partial from Q9SPL4.1	Sequence in publication does not include N-terminal sequence
GFG40850.1	<b>COMPARE00971</b>	arginine kinase, partial from GFG40850.1	Sequence in publication does not include N-terminal sequence



CAA77666.1	<b>COMPARE00972</b>	alkaline serine protease, partial from CAA77666.1	Sequence in publication does not include N-terminal sequence
UTE00285.1	<b>COMPARE00973</b>	7S globulin, vicilin, partial from UTE00285.1	Sequence in publication does not include N-terminal sequence
UTE00286.1	<b>COMPARE00974</b>	7S globulin, vicilin, partial from UTE00286.1	Sequence in publication does not include N-terminal sequence

### Species name and common name updates:

Species	Old Common Name	New Common Name
<i>Acheta domesticus</i>	Short ragweed	<b>House cricket</b>
<i>Betula platyphylla</i>	Japanese white birch	<b>Asian white birch</b>
Accession(s)	Old Species Name	New Species Name
UST29548.1, QZP44316.1, QIJ32297.1	<i>Crassostrea angulata</i>	<b><i>Crassostrea angulata</i></b> <b><i>(Magallana angulate)</i></b>

### Sequence updates:

Accession	Old Sequence	New Sequence	Reason
P81217.1	QDPQSETDYSQLSGEWNT	<b>X</b> QDPQSETDYSQLSGEWNT	For interoperability with NCBI Protein databases

### 1.3 NEW Data Download Form

As part of this year's updates, we have introduced a new process for downloading the complete COMPARE dataset and sequence file. Users are asked to complete a [short form](#) to help the COMPARE Team gather insights into how the database is being utilized. This information will shape our priorities for future enhancements. To sustain this valuable resource, we are also seeking financial contributions from industry users, either through donations or by participating in the Steering Team. Your support is crucial to keeping COMPARE freely accessible.



## REMINDER: bioinformatics companion tool, COMPASS (COMPare Analysis of Sequences with Software)



The COMPARE database is equipped with its companion tool, [COMPASS](#) (COMPare Analysis of Sequences with Software), as a built-in feature. COMPASS is a comparative sequence search software, incorporating the [open source FASTA software package](#) (FASTA v36). With this tool, COMPARE users can conduct website-based, real-time use of the COMPARE database to identify similarities between a protein sequence of interest and COMPARE's allergens via amino acid sequence alignments (between two or more amino acid sequences). COMPASS offers a visualization option to view results in a color-coded graphic display. To access the tool, go [www.comparedatabase.org](http://www.comparedatabase.org), click on the “[Database](#)” tab and click on the green button “[Run COMPASS](#).” For detailed information, instructions on how to use and supporting references, visit the [COMPASS’ “About” page](#).

As part of COMPARE 2025’s release, COMPASS is also updated to screen against COMPARE 2025 sequences.

### Your Feedback is Appreciated - Contact Us

The HESI COMPARE database program is committed to transparency and open dialog. Individuals or organizations are invited to submit feedback, questions, or inquiries via the “[Contact us](#)” portal in the COMPARE database website, or email to [comparedatabase@hesiglobal.org](mailto:comparedatabase@hesiglobal.org). HESI staff will respond if the information is readily available or will relay the inquiries to the Peer Review Panel if a more in-depth response is required.

### Licensing

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When using the database or referring to it in a publication, please cite the COMPARE publication:

van Ree et al., 2021. The COMPARE Database: A Public Resource for Allergen Identification, Adapted for Continuous Improvement. *Frontiers in Allergy*.  
<https://doi.org/10.3389/falgy.2021.700533>.



## Support COMPARE!

Is COMPARE useful as a resource and do you like its commitment to continuous improvement? If so, support COMPARE! We have other ideas to continue improving this resource and making it as comprehensive and thorough as possible. The COMPARE database is a collaborative HESI program. The annual update of the database is a resource intensive process that involves many more partners and collaborators, rolling on a steady annual cycle schedule. The execution of the program relies on scientific expertise and in-kind and direct financial support from both public sector and private sector scientific organizations to maintain this free, public resource. If you would like to learn more about how you or your organization can contribute, please contact us at [comparedatabase@hesiglobal.org](mailto:comparedatabase@hesiglobal.org).

**Your support is tax deductible in the US:** HESI is a non-profit, 501(c)(3) organization committed to generating science for a safer, more sustainable world. Financial support to HESI's scientific programs is considered a tax-deductible charitable donation in the United States. Your support to our mission, through funding and participation, makes our scientific collaborations and outreach possible, and helps improve both human and environmental health across the globe.

*We look forward to hearing from you!*

**About HESI ([www.hesiglobal.org](http://www.hesiglobal.org)):** The Health and Environmental Sciences Institute (HESI) is a non-profit institution whose mission is to collaboratively identify and help resolve global health and environmental challenges through the engagement of scientists from academia, government, industry, NGOs, and other strategic partners. Since 1989, HESI has provided the framework for scientists from public and private sectors to meaningfully collaborate in developing science for a safer, more sustainable world.



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