



## **COMPARE 2024 Update Documentation**

The COMPARE Team is pleased to present the release of the COMPARE 2024 database, released on 01/26/2024 ([www.comparedatabase.org](http://www.comparedatabase.org)).

### **1. COMPARE 2024: General Overview**

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

The COMPARE 2024 database consists of **2748 sequence entries**. Overall updates to the 2024 COMPARE database include:

- **151 unique additions** to the COMPARE 2023 database.
  - 35 full-length proteins
  - 116 mass spectrometry (MS) additions
- The **removal of 34 entries** from COMPARE 2023 (see table below).

Therefore, COMPARE 2024 = 2361 entries (COMPARE 2023) - 34 entries (removal from COMPARE 2023) + 151 new unique entries = 2748 sequence entries.

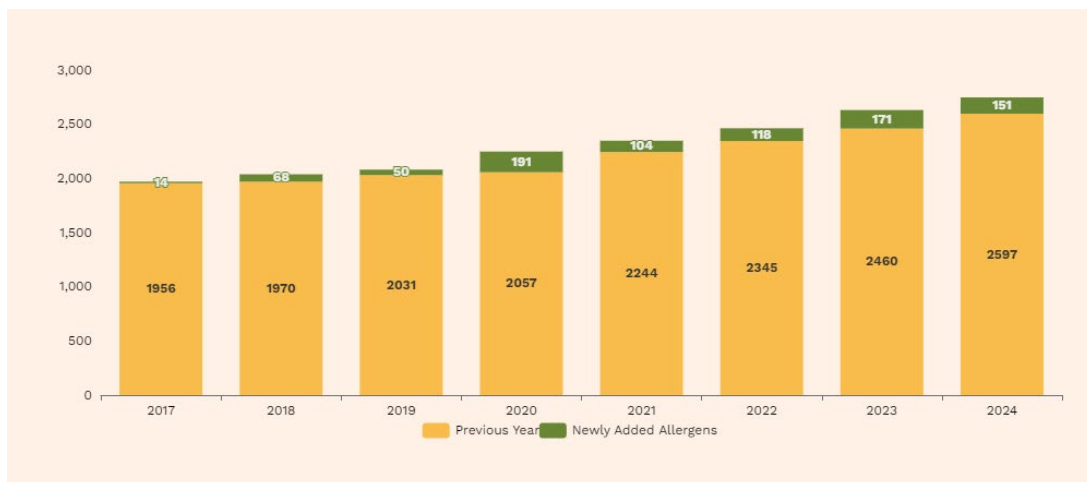


Figure 1: Constant and consistent growth of sequence entries in COMPARE. In 2020 a historical data review was undertaken, and MS sequences were included in the database.



All decisions result from the COMPARE Peer-Review Panel (PRP)'s review of sequence candidates with record dates ranging between May 15, 2022 – May 15, 2023, 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.

<b>Retired Sequence</b> (Removed from COMPARE 2023)	<b>Replacement Sequence</b> (new or updated sequence in COMPARE 2024)	<b>Justification</b>
<b>COMPARE167</b>	ALQ56981.1	Duplicate: COMPARE167 is fully contained in ALQ56981.1
<b>COMPARE227</b>	<i>(removed)</i>	Sequence does not contain 10 consecutive amino acids (criteria for inclusion)
<b>COMPARE00433</b>	Q9SPL3.1	Duplicate: COMPARE00433 is fully contained in Q9SPL3.1
<b>COMPARE00438</b>	Q9SPL3.1	Duplicate: COMPARE00438 is fully contained in Q9SPL3.1
<b>COMPARE00442</b>	Q9SPL3.1	Duplicate: COMPARE00442 is fully contained in Q9SPL3.1
<b>COMPARE00443</b>	Q9SPL3.1	Duplicate: COMPARE00443 is fully contained in Q9SPL3.1
<b>COMPARE00445</b>	Q9SPL3.1	Duplicate: COMPARE00445 is fully contained in Q9SPL3.1
<b>COMPARE00446</b>	Q9SPL3.1	Duplicate: COMPARE00446 is fully contained in Q9SPL3.1
<b>COMPARE00447</b>	Q9SPL3.1	Duplicate: COMPARE00447 is fully contained in Q9SPL3.1
<b>COMPARE00448</b>	Q9SPL3.1	Duplicate: COMPARE00448 is fully contained in Q9SPL3.1
<b>COMPARE00449</b>	Q9SPL3.1	Duplicate: COMPARE00449 is fully contained in Q9SPL3.1
<b>COMPARE00455</b>	Q9SPL3.1	Duplicate: COMPARE00455 is fully contained in Q9SPL3.1
<b>COMPARE00458</b>	Q9SPL3.1	Duplicate: COMPARE00458 is fully contained in Q9SPL3.1
<b>COMPARE00460</b>	Q9SPL3.1	Duplicate: COMPARE00460 is fully contained in Q9SPL3.1
<b>COMPARE00461</b>	Q9SPL3.1	Duplicate: COMPARE00461 is fully contained in Q9SPL3.1
<b>COMPARE00462</b>	Q9SPL3.1	Duplicate: COMPARE00462 is fully contained in Q9SPL3.1
<b>COMPARE00464</b>	Q9SPL3.1	Duplicate: COMPARE00464 is fully contained in Q9SPL3.1
<b>COMPARE00436</b>	Q9SPL4.1	Duplicate: COMPARE00436 is fully contained



		in Q9SPL4.1
<b>COMPARE00437</b>	Q9SPL4.1	Duplicate: COMPARE00437 is fully contained in Q9SPL4.1
<b>COMPARE00439</b>	Q9SPL4.1	Duplicate: COMPARE00439 is fully contained in Q9SPL4.1
<b>COMPARE00451</b>	Q9SPL4.1	Duplicate: COMPARE00451 is fully contained in Q9SPL4.1
<b>COMPARE00452</b>	Q9SPL4.1	Duplicate: COMPARE00452 is fully contained in Q9SPL4.1
<b>COMPARE00454</b>	Q9SPL4.1	Duplicate: COMPARE00454 is fully contained in Q9SPL4.1
<b>COMPARE00456</b>	Q9SPL4.1	Duplicate: COMPARE00456 is fully contained in Q9SPL4.1
<b>COMPARE00327</b>	QDO73345.1	Duplicate: COMPARE00327 is fully contained in QDO73345.1
<b>ABF21078.1</b>	AHM25029.1	Duplicate: ABF21078.1 is fully contained in AHM25029.1
<b>COMPARE105</b>	C0HLQ2	Duplicate: COMPARE105 is fully contained in C0HLQ2
<b>COMPARE106</b>	C0HLQ2	Duplicate: COMPARE106 is fully contained in C0HLQ2
<b>COMPARE00422</b>	XP_042518524.1	Duplicate: COMPARE00422 is fully contained in XP_042518524.1
<b>COMPARE00423</b>	XP_042518524.1	Duplicate: COMPARE00423 is fully contained in XP_042518524.1
<b>COMPARE00424</b>	XP_042518524.1	Duplicate: COMPARE00424 is fully contained in XP_042518524.1
<b>COMPARE00425</b>	XP_042518524.1	Duplicate: COMPARE00425 is fully contained in XP_042518524.1
<b>COMPARE00428</b>	XP_042518524.1	Duplicate: COMPARE00428 is fully contained in XP_042518524.1
<b>BAF47264.1</b>	CBY17558.1	Duplicate: Identical to CBY17558.1

COMPARE 2024 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. Accession number updates (past entries)

The “**Accession**” field was updated for **3** allergen entries.

<b>PAST COMPARE Accession</b>	<b>NEW COMPARE Accession</b>	<b>COMPARE Description</b>
MANUAL2	<b>COMPARE247</b>	cysteine protease
MANUAL3	<b>COMPARE248</b>	vitellogenin, partial
COMPARE022	<b>QFG58557.1</b>	7S globulin, vicilin, beta-conglutin

## 1.3. Description updates (past entries)

The “**Description**” field was updated for 13 entries.

<b>COMPARE Accession</b>	<b>PAST COMPARE Description</b>	<b>NEW COMPARE Description</b>
2MC9_A	peptidyl-prolyl isomerase	<b>cyclophilin/peptidyl-prolyl isomerase</b>
CAB44442.1	peptidyl-prolyl isomerase	<b>cyclophilin/peptidyl-prolyl isomerase</b>
CAC84116.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
CAI78448.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
AAP35065.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
AEY79726.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
ALM24136.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
AVV30163.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
CAA09884.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
P81531.2	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
XP_025675300.1	cyclophilin	<b>cyclophilin/peptidyl-prolyl isomerase</b>
ANQ43386.1	chitinase	<b>glyceraldehyde-3-phosphate-dehydrogenase</b>
CAA45085.1	alpha-amylase, partial	<b>alpha-amylase inhibitor, partial</b>



#### 1.4. Other updates to past entries

Accession	Old IUIS Name	New IUIS Name
ABM53752.1	Tyr p 13	None
Accession(s)	Old Species Name	New Species Name
P80273.2, P33556.1, P80274.1	Vitis sp.	Vitis vinifera
AKV72166.1	Acacia farnesiana	Acacia farnesiana (Vachellia farnesiana)
AIV43662.1	Vachellia farnesiana	Acacia farnesiana (Vachellia farnesiana)
BAH10157.1	Venerupis philippinarum	Ruditapes philippinarum (Venerupis philippinarum)
Accession	Old Sequence	New Sequence
COMPARE086	IEIESFYEGDQFSETLTR	IEIESFYEGDDFSETLTR

#### 1.5. **New!** Links to NCBI Protein database have been included on the allergen record page.

ADK66280.1

Accession	ADK66280.1
External DB Link	<a href="#">NCBI Protein</a> <span style="color: blue; font-size: 1.2em;">→</span>
Species	<a href="#">Litopanaeus vannamei (Penaeus vannamei)</a>
Common Name	<a href="#">white shrimp</a>
Description	fatty acid-binding protein
IUIS Name	<a href="#">Lit v 13</a>
Length	136
Year Adopted	2023
Sequence	>ADK66280.1 Lit v 13; fatty acid-binding protein [Litopanaeus vannamei (Penaeus vannamei)] MAKIEGKFKHESSENFDEFHKALGVGLVIRKIHGNAATPTVEITKDGDTYTHKTTTTFKTT EIKFKLGEEFEETTADGRVVKSTITLDGNKLVHKVQGDKEKKEKDSSELLREFTDDKMLHE CKVDDVVCKRVYSRLE

National Library of Medicine  
National Center for Biotechnology Information

Protein Protein ▾

[Advanced](#)

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GenPept =

Intracellular fatty acid-binding protein [Penaeus vannamei]

GenBank: ADK66280.1

[Identical Proteins](#) [FASTA](#) [Graphics](#)

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[Go to:](#) [⊞](#)

LOCUS ADK66280 136 aa linear DV 28-JUL-2010

DEFINITION Intracellular fatty acid-binding protein [Penaeus vannamei].

ACCESSION ADK66280

VERSION ADK66280.1

SOURCE accession [JFM33387.1](#)

KEYWORDS -

SOURCE Penaeus vannamei (Pacific white shrimp)

ORGANISM [Penaeus vannamei](#)  
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Crustacea;  
Multicrustacea; Malacostraca; Tanaulostraca; Eucarida; Decapoda;  
Dendrobranchiata; Penaeoidea; Penaeidae; Penaeus.



**1.6. New! A list of biochemical names in COMPARE has been included on the Documentation page.**

In 2021, the Peer Review Panel reviewed the description lines of all COMPARE entries to clean-up irrelevant wording from automated text imported from the source databases in order to generate meaningful description lines to the eyes of allergy experts. This list is now included in the Documentation tab [here](#).

**1.7. Enhanced visibility for Mass Spectrometry (MS) fragments: Visualization of MS fragments mapped to their Parent Accession has been incorporated.**

**New!** A visual representation of MS sequences mapped to their known full length parent sequence (even though the full-length parent protein sequence is not an entry in the database itself) has been included as part of our commitment to continuous improvement. An example is shown in Figure 2 below. COMPARE030 maps to parent sequence Q9FSH9.1. The graphic demonstrates where the peptide sequence is located on the parent and which other peptide sequences in COMPARE are associated with that parent sequence. This helps the user identify the portion of the parent sequence that has published IgE binding evidence.



## Allergen

### COMPARE030

Accession	<b>COMPARE030</b>
External DB Link	
Species	<a href="#">Lupinus albus</a>
Common Name	<a href="#">white lupine</a>
Description	7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1
IUIS Name	
Length	21
Year Adopted	2020H_MS
Sequence	>COMPARE030 7S globulin, vicilin, gamma-conglutin, partial from Q9FSH9.1 [Lupinus albus] AGIALGTHQLEENLVVFDLAR
Parent Accession	<a href="#">Q9FSH9.1</a>

### Related Sequences

Peptide sequences mapped to Parent Accession

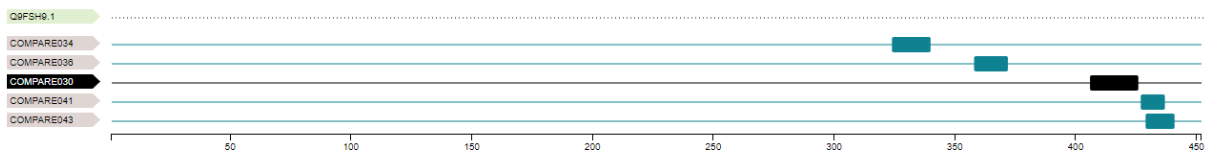


Figure 2: New visualization in COMPARE2024 for records with known Parent Accessions is now available. Allergen record page for [COMPARE030](#).





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



As of June 2019, 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 2024's release, COMPASS is also updated to screen against COMPARE 2024 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.

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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).

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