BIOPEP-UWM database of peptides from food – status in 2025

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Introduction

Peptides are extensively studied bioactive compounds of food origin. They are analyzed e.g. using in silico strategies. The BIOPEP-UWM database, launched in 2003, has become, a standard tool in peptide research. Number of visits since 2024.01.01 is c.a. 55 thousands (2025.07.09).

Database structure

BIOPEP-UWM database includes:

- Database of proteins [1; 4; 6]
- Database of bioactive peptides [1; 4; 6]
- Database of allergenic proteins and their epitopes [2; 6]
- Database of sensory peptides and amino acids [3; 6]
- Database of virtually bioactive peptides [5; 6]
- Repository of amino acids and modifications [6]

Encoding of proteins and peptides

Sequences of peptides and proteins are usually annotated using one-letter code utlizing capital letters for proteinogenic amino acids and small letters for D-amino acids. Modified or npn-proteinogenc amino acids and non-amino acid residues are annotated using multiletter symbols. Monomers, being building blocks for peptides and proteins are listed in the repository of amino acid and modifications. Rules for their encoding are available as .pdf file at the repository website.

Search options

Table 1. Search options in the BIOPEP-UWM database

Database or Search option	Proteins	Bioactive peptides	Allergens	Sensory peptides and amino acids	Virtually bioactive peptides	Amino acids
ID	+	+	+	+	+	+
Name	+	+	+	+	+	+
Latin name	+	-	-	-	-	-
Reference	+	+	+	+	+	-
Mass	+	+	+	+	+	-
Activity	-	+	-	+	+	-
Sequence	-	+	-	+	+	-
InChIKey	-	+	-	+	+	+
No of residues	-	+	+	+	+	-
Symbol	-	-	-	-	-	+
PubChem CID	-	-	-	-	-	+
Formula	-	-	-	-	-	+

- Search according to activity is restricted to activities listed in the database.
- Search based on sequence involves two options: exact match or finding all peptides containing query sequence as a fragment.
- Search based on sequence includes all monomers listed in the repository of amino acids and modifications.

Options and applications

- Profiles of potential biological and sensory activity of protein sand peptide sequences [4]
- Simulation of proteolysis [4]
- Calculation of quantiative parameters characterizing proteins as precursors of bioactive peptides [4]
- Conversion of amino acid sequences into SMILES code [4]
- Sorting of results according to peptide ID, activity and sequences
- Export of results to Excel (in the case of single sequence processing)

All options are available fro sequences annotated using entire set of symbols from the reopsitory of amino acids and modifications.

Database growth

Table 2. Number of compounds in particular parts of the BIOPEP-UWM database

Database	2023 [6]	2024	2025
Proteins	756	773	773
Bioactive peptides	4699	5141	5549
Allergens	136	136	136
Sensory peptides and amino acids	533	587	603
Virtually bioactive peptides	272	392	524
Amino acids and modifications	123	187	215

Conclusions

New options added to BIOPEP-UWM should facilitate in silico studies concerning enzymatic hydrolysis of proteins aimed on release peptides with various bioactivities. BIOPEP-UWM provides now opportunity for annotation of peptides and proteins containing modified amino acids.

References

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Availability

Website:
https://biochemia.uwm.edu.pl/en/biopep-uwm-2/
The database is free-accessible without registration.

This work was supported by designated subsidy of the Minister of Science and Higher Education Republic of Poland, task entitled: The Research Network of Life Sciences Universities for the Development of the Polish Dairy Industry – Research Project and by Minister of Science under "the Regional Initiative of Excellence Program".