Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Amino Acid Index Database

RRID:SCR_007044
Type: Tool

Proper Citation

Amino Acid Index Database (RRID:SCR_007044)

Resource Information

URL: http://www.genome.ad.jp/aaindex/

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Description: AAindex is a database of numerical indices representing various physicochemical and biochemical properties of amino acids and pairs of amino acids. AAindex consists of three sections now: AAindex1 for the amino acid index of 20 numerical values, AAindex2 for the amino acid mutation matrix and AAindex3 for the statistical protein contact potentials. All data are derived from published literature. An amino acid index is a set of 20 numerical values representing any of the different physicochemical and biological properties of amino acids. The AAindex1 section of the Amino Acid Index Database is a collection of published indices together with the result of cluster analysis using the correlation coefficient as the distance between two indices. This section currently contains 544 indices. Another important feature of amino acids that can be represented numerically is the similarity between amino acids. Thus, a similarity matrix, also called a mutation matrix, is a set of 210 numerical values, 20 diagonal and 20x19/2 off-diagonal elements, used for sequence alignments and similarity searches. The AAindex2 section of the Amino Acid Index Database is a collection of published amino acid mutation matrices together with the result of cluster analysis. This section currently contains 94 matrices. In the release 9.0, we added a collection of published protein pairwise contact potentials to AAindex as AAindex3. This section currently contains 47 contact potential matrices. Sponsors: This work was supported by grants and resources from the Ministry of Education, Culture, Sports, Science and Technology, and the Japan Science and Technology Agency, and the Bioinformatics Center, Institute for Chemical Research, Kyoto University and the Super Computer System, Human Genome Center, Institute of Medical Science, University of Tokyo.

Synonyms: AAindex

Resource Type: data or information resource, database

Defining Citation: PMID:3244698, PMID:9053899, PMID:9847231, PMID:10592278

Keywords: amino acid, biochemical property, mutation, physicochemical property, protein sequence, proteomics, FASEB list

Resource Name: Amino Acid Index Database

Resource ID: SCR_007044

Alternate IDs: nif-0000-02527

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260905T133137+0000

Ratings and Alerts

No rating or validation information has been found for Amino Acid Index Database.

No alerts have been found for Amino Acid Index Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 218 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Douglas GM, et al. (2026) DEX: a consensus-based amino acid exchangeability measure for improved codon substitution modelling. bioRxiv : the preprint server for biology.

Kong W, et al. (2026) A dual diffusion model-based representation learning framework for antimicrobial peptides classification. Bioinformatics (Oxford, England), 42(3).

Hao Y, et al. (2026) SLiMs prediction method based on enhanced attention mechanism and feature fusion. Bioinformatics advances, 6(1), vbaf240.

Polunina PV, et al. (2026) VEFill: accurate and generalizable deep mutational scanning score imputation across protein domains. Molecular systems biology, 22(6), 979.

Jia Y, et al. (2026) A Prediction Model for Uncoating Receptor Usage in Human Enteroviruses Based on Amino Acid Sequences and a Naive Bayes Algorithm. Viruses, 18(2).

Lee H, et al. (2026) Integrative Identification of Anti-Photoaging Peptides From Stress-Tolerant Microorganisms via Machine Learning and KEAP1-NRF2 Docking. Journal of peptide science : an official publication of the European Peptide Society, 32(8), e70115.

Li B, et al. (2026) A Proteogenomic Approach to Discover Novel lncRNA-Derived Microproteins and Their Potential Clinical Utility in Hepatocellular Carcinoma. Molecular &

cellular proteomics : MCP, 25(6), 101584.

Elreify HM, et al. (2026) BiGKbhb: a bi-directional gated recurrent unit model for predicting lysine ??-hydroxybutyrylation sites. BMC genomics, 27(1), 102.

Meng L, et al. (2026) Multi-ACPNet: A multi-scale sequence-structure feature fusion framework for anticancer peptide identification and functional prediction. PLoS computational biology, 22(3), e1014053.

Kan Y, et al. (2026) ProtDML: label-aware representation learning for broad-spectrum protein function prediction. Briefings in bioinformatics, 27(3).

Fadaei S, et al. (2026) Novel universal domain-centric method for protein classification. Scientific reports, 16(1).

Zhang Q, et al. (2025) Machine learning-guided evolution of pyrrolysyl-tRNA synthetase for improved incorporation efficiency of diverse noncanonical amino acids. Nature communications, 16(1), 6648.

Charoenkwan P, et al. (2025) PSR-MAPMS: A new approach for the interpretable prediction of myelin autoantigenic peptides in multiple sclerosis using multi-source propensity scores. Protein science : a publication of the Protein Society, 34(8), e70010.

Liang Y, et al. (2025) A deep learning model for prediction of lysine crotonylation sites by fusing multi-features based on multi-head self-attention mechanism. Scientific reports, 15(1), 18940.

Ahmed S, et al. (2025) Accurate identification of broadly neutralizing antibodies against dengue virus based on deep stacking strategy with multi-perspective features. Scientific reports, 16(1), 1720.

Shimizu I, et al. (2025) DARUMA: a gateway to fast and easy prediction of intrinsically disordered regions. PeerJ. Computer science, 11, e3343.

Keresztes L, et al. (2025) Navigating Homogeneous Graph Paths Through Amyloidogenic and Non-Amyloidogenic Hexapeptides. Journal of computational chemistry, 46(26), e70238.

Elreify HM, et al. (2025) An efficient machine-learning framework for predicting protein post-translational modification sites. Scientific reports, 15(1), 31179.

Pavesi A, et al. (2025) Covariation of Amino Acid Substitutions in the HIV-1 Envelope Glycoprotein gp120 and the Antisense Protein ASP Associated with Coreceptor Usage. Viruses, 17(3).

Liu T, et al. (2025) Effective Gene Expression Prediction and Optimization from Protein Sequences. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(8), e2407664.