Resource Summary Report

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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

Funding:

Resource Name: Amino Acid Index Database

Resource ID: SCR_007044

Alternate IDs: nif-0000-02527

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250521T061141+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 29 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Huang WL, et al. (2015) Prediction of linear B-cell epitopes of hepatitis C virus for vaccine development. BMC medical genomics, 8 Suppl 4(Suppl 4), S3.

Zhang SW, et al. (2014) Prediction of protein-protein interaction with pairwise kernel support vector machine. International journal of molecular sciences, 15(2), 3220.

Mazumder M, et al. (2014) Prediction and analysis of canonical EF hand loop and qualitative estimation of Ca²? binding affinity. PloS one, 9(4), e96202.

Qeli E, et al. (2014) Improved prediction of peptide detectability for targeted proteomics using a rank-based algorithm and organism-specific data. Journal of proteomics, 108, 269.

Kunda A, et al. (2014) Mapping the amino acid properties of constituent nucleoporins onto the yeast nuclear pore complex. Bioinformation, 10(2), 94.

Piatek MJ, et al. (2013) Simplified method for predicting a functional class of proteins in transcription factor complexes. PloS one, 8(7), e68857.

Zhang X, et al. (2013) TFPP: an SVM-based tool for recognizing flagellar proteins in Trypanosoma brucei. PloS one, 8(1), e54032.

Sharma A, et al. (2013) A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. BMC bioinformatics, 14, 233.

Hu L, et al. (2012) Cooperativity among short amyloid stretches in long amyloidogenic sequences. PloS one, 7(6), e39369.

Saethang T, et al. (2012) EpicCapo: epitope prediction using combined information of amino acid pairwise contact potentials and HLA-peptide contact site information. BMC bioinformatics, 13, 313.

Liu B, et al. (2012) Using amino acid physicochemical distance transformation for fast protein remote homology detection. PloS one, 7(9), e46633.

Pashley CL, et al. (2012) Conformational properties of the unfolded state of Im7 in nondenaturing conditions. Journal of molecular biology, 416(2), 300.

Xiao X, et al. (2012) iNR-PhysChem: a sequence-based predictor for identifying nuclear receptors and their subfamilies via physical-chemical property matrix. PloS one, 7(2), e30869.

Su CH, et al. (2012) Identification of amino acid propensities that are strong determinants of linear B-cell epitope using neural networks. PloS one, 7(2), e30617.

Saha I, et al. (2012) Fuzzy clustering of physicochemical and biochemical properties of amino acids. Amino acids, 43(2), 583.

Collingridge PW, et al. (2012) MergeAlign: improving multiple sequence alignment performance by dynamic reconstruction of consensus multiple sequence alignments. BMC bioinformatics, 13, 117.

Plewczynski D, et al. (2012) AMS 4.0: consensus prediction of post-translational modifications in protein sequences. Amino acids, 43(2), 573.

Xiong Y, et al. (2012) Prediction of heme binding residues from protein sequences with integrative sequence profiles. Proteome science, 10 Suppl 1(Suppl 1), S20.

Schmeier S, et al. (2011) Simplified method to predict mutual interactions of human transcription factors based on their primary structure. PloS one, 6(7), e21887.

Hu LL, et al. (2010) Prediction and analysis of protein hydroxyproline and hydroxylysine. PloS one, 5(12), e15917.