Resource Summary Report

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Prediction of Amyloid Structure Aggregation

RRID:SCR_001768
Type: Tool

Proper Citation

Prediction of Amyloid Structure Aggregation (RRID:SCR_001768)

Resource Information

URL: http://protein.bio.unipd.it/pasta2/

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Description: Online interface that utilizes an algorithm to predict the most aggregation-prone portions and the corresponding beta-strand inter-molecular pairing for a given input sequence. Users can paste the sequence into the interface and output the appropriate sequence.

Abbreviations: PASTA

Synonyms: PASTA 2.0, Prediction of amyloid structure aggregation

Resource Type: service resource, production service resource, web application, data analysis service, analysis service resource, software resource

Defining Citation: PMID:24848016

Keywords: protein aggregation, sequence, dna, rna, amyloid structure, protein analysis, bio.tools

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Availability: Acknowledgement requested, Free for academic use

Resource Name: Prediction of Amyloid Structure Aggregation

Resource ID: SCR_001768

Alternate IDs: biotools:pasta, OMICS_03861

Alternate URLs: https://bio.tools/pasta

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250429T054657+0000

Ratings and Alerts

No rating or validation information has been found for Prediction of Amyloid Structure Aggregation.

No alerts have been found for Prediction of Amyloid Structure Aggregation.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 175 mentions in open access literature.

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

Sarrazin-Gendron R, et al. (2025) Improving microbial phylogeny with citizen science within a mass-market video game. Nature biotechnology, 43(1), 76.

Schalch-Schuler M, et al. (2025) The planktonic freshwater ciliate Balanion planctonicum (Ciliophora, Prostomatea): A cryptic species complex or a "complex species"? The Journal of eukaryotic microbiology, 72(1), e13084.

Zhang T, et al. (2024) Phylogenomic profiles of whole-genome duplications in Poaceae and landscape of differential duplicate retention and losses among major Poaceae lineages. Nature communications, 15(1), 3305.

Baronait? I, et al. (2024) Formation of Calprotectin Inhibits Amyloid Aggregation of S100A8 and S100A9 Proteins. ACS chemical neuroscience, 15(9), 1915.

Gupta A, et al. (2024) Accurate, scalable, and fully automated inference of species trees from raw genome assemblies using ROADIES. bioRxiv : the preprint server for biology.

Xu YH, et al. (2024) Evolutionary Modes of wtf Meiotic Driver Genes in Schizosaccharomyces pombe. Genome biology and evolution, 16(10).

Villanueva A, et al. (2024) Identification of the Bioavailable Peptidome of Chia Protein

Hydrolysate and the In Silico Evaluation of Its Antioxidant and ACE Inhibitory Potential. Journal of agricultural and food chemistry, 72(6), 3189.

Aldrovandi S, et al. (2024) Expression of Random Sequences and de novo Evolved Genes From the Mouse in Human Cells Reveals Functional Diversity and Specificity. Genome biology and evolution, 16(12).

Nguyen TTT, et al. (2024) Effects of carbon source addition in rearing water on sediment characteristics, growth and health of cultured marron (Cherax cainii). Scientific reports, 14(1), 1349.

Rao NR, et al. (2024) Derailed protein turnover in the aging mammalian brain. Molecular systems biology, 20(2), 120.

Sharma K, et al. (2024) Cryo-EM observation of the amyloid key structure of polymorphic TDP-43 amyloid fibrils. Nature communications, 15(1), 486.

Chuang HY, et al. (2024) Engineered droplet-forming peptide as photocontrollable phase modulator for fused in sarcoma protein. Nature communications, 15(1), 5686.

Vakirlis N, et al. (2024) Large-scale investigation of species-specific orphan genes in the human gut microbiome elucidates their evolutionary origins. Genome research, 34(6), 888.

Lauterbach M, et al. (2024) Leaf transcriptomes from C3, C3-C4 intermediate, and C4Neurachne species give insights into C4 photosynthesis evolution. Plant physiology, 197(1).

Wong HL, et al. (2024) Ubiquitous genome streamlined Acidobacteriota in freshwater environments. ISME communications, 4(1), ycae124.

Malis V, et al. (2024) Aliphatic and Olefinic Fat Suppression in the Orbit Using Polarity-altered Spectral and Spatial Selective Acquisition (PASTA) with Opposed Phase. Magnetic resonance in medical sciences : MRMS : an official journal of Japan Society of Magnetic Resonance in Medicine, 23(2), 193.

Harkess A, et al. (2024) The unusual predominance of maintenance DNA methylation in Spirodela polyrhiza. G3 (Bethesda, Md.), 14(4).

Boukheloua R, et al. (2024) Global freshwater distribution of Telonemia protists. The ISME journal, 18(1).

von Rosen T, et al. (2023) ATP-independent substrate recruitment to proteasomal degradation in mycobacteria. Life science alliance, 6(10).

Shen C, et al. (2023) EMMA: a new method for computing multiple sequence alignments given a constraint subset alignment. Algorithms for molecular biology : AMB, 18(1), 21.