Resource Summary Report

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Aggrescan: The Hot Spot Finder

RRID:SCR_008403
Type: Tool

Proper Citation

Aggrescan: The Hot Spot Finder (RRID:SCR_008403)

Resource Information

URL: http://bioinf.uab.es/aggrescan/

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Description: Web-based tool for identifying hot spots of aggregation in polypeptides. Aggrescan uses an aggregation-propensity scale for natural amino acids derived from in vivo experiments and on the assumption that short and specific sequence stretches modulate protein aggregation. The algorithm is shown to identify a series of protein fragments involved in the aggregation of disease-related proteins and to predict the effect of genetic mutations on their deposition propensities. It also provides new insights into the differential aggregation properties displayed by globular proteins, natively unfolded polypeptides, amyloidogenic proteins and proteins found in bacterial inclusion bodies.

Abbreviations: Aggrescan

Resource Type: production service resource, analysis service resource, data analysis service, service resource

Defining Citation: PMID:17324296

Keywords: aggregation, amino acid, protein, mutation, polypeptide, amyloid, bacterial protein, protein aggregation, neurodegeneration

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Availability: Free, Acknowledgement requested

Resource Name: Aggrescan: The Hot Spot Finder

Resource ID: SCR_008403

Alternate IDs: nif-0000-30073

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250516T053911+0000

Ratings and Alerts

No rating or validation information has been found for Aggrescan: The Hot Spot Finder.

No alerts have been found for Aggrescan: The Hot Spot Finder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

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

Tarigan S, et al. (2024) Challenges and strategies in the soluble expression of CTA1-(S14P5)4-DD and CTA1-(S21P2)4-DD fusion proteins as candidates for COVID-19 intranasal vaccines. PloS one, 19(12), e0306153.

Kuri PR, et al. (2024) Unravelling aggregation propensity of rotavirus A VP6 expressed as E. coli inclusion bodies through in silico prediction. Scientific reports, 14(1), 21464.

Gilkes JM, et al. (2024) A new lysine biosynthetic enzyme from a bacterial endosymbiont shaped by genetic drift and genome reduction. Protein science : a publication of the Protein Society, 33(7), e5083.

Izgilov R, et al. (2024) Advanced glycation end-products accelerate amyloid deposits in adipocyte's lipid droplets. Cell death & disease, 15(11), 846.

Li X, et al. (2023) Refinement of the Fusion Tag PagP for Effective Formation of Inclusion Bodies in Escherichia coli. Microbiology spectrum, 11(3), e0380322.

Nishide G, et al. (2023) Nanoscopic Elucidation of Spontaneous Self-Assembly of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Open Reading Frame 6 (ORF6) Protein. The journal of physical chemistry letters, 14(38), 8385.

Kreye J, et al. (2023) Preclinical safety and efficacy of a therapeutic antibody that targets SARS-CoV-2 at the sotrovimab face but is escaped by Omicron. iScience, 26(4), 106323.

Lenin KLD, et al. (2023) In silico molecular and functional characterization of a dual function antimicrobial peptide, hepcidin (GIFT-Hep), isolated from genetically improved farmed tilapia (GIFT, Oreochromis niloticus). Journal, genetic engineering & biotechnology, 21(1), 130.

Kravchenko SV, et al. (2022) Multiple Antimicrobial Effects of Hybrid Peptides Synthesized Based on the Sequence of Ribosomal S1 Protein from Staphylococcus aureus. International journal of molecular sciences, 23(1).

Berdy?ski M, et al. (2022) SOD1 mutations associated with amyotrophic lateral sclerosis analysis of variant severity. Scientific reports, 12(1), 103.

Khetan R, et al. (2022) Current advances in biopharmaceutical informatics: guidelines, impact and challenges in the computational developability assessment of antibody therapeutics. mAbs, 14(1), 2020082.

Neelima S, et al. (2021) Molecular characterization of a novel ?-defensin isoform from the red-toothed trigger fish, Odonus niger (Ruppel, 1836). Journal, genetic engineering & biotechnology, 19(1), 71.

Langyan S, et al. (2021) In silico proteolysis and analysis of bioactive peptides from sequences of fatty acid desaturase 3 (FAD3) of flaxseed protein. Saudi journal of biological sciences, 28(10), 5480.

Gour S, et al. (2021) Aggregation hot spots in the SARS-CoV-2 proteome may constitute potential therapeutic targets for the suppression of the viral replication and multiplication. Journal of proteins and proteomics, 12(1), 1.

Salladini E, et al. (2021) Identification of a Region in the Common Amino-terminal Domain of Hendra Virus P, V, and W Proteins Responsible for Phase Transition and Amyloid Formation. Biomolecules, 11(9).

Thues C, et al. (2021) MAPRE2 mutations result in altered human cranial neural crest migration, underlying craniofacial malformations in CSC-KT syndrome. Scientific reports, 11(1), 4976.

Sannigrahi A, et al. (2021) The metal cofactor zinc and interacting membranes modulate SOD1 conformation-aggregation landscape in an in vitro ALS model. eLife, 10.

Surin AK, et al. (2020) Determination of amyloid core regions of insulin analogues fibrils. Prion, 14(1), 149.

Fields FR, et al. (2020) Algorithmic assessment of missense mutation severity in the Von-Hippel Lindau protein. PloS one, 15(11), e0234100.

Ridgway Z, et al. (2020) Analysis of Baboon IAPP Provides Insight into Amyloidogenicity and Cytotoxicity of Human IAPP. Biophysical journal, 118(5), 1142.