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: analysis service resource, data analysis service, production service resource, 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: 20260821T042808+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 65 mentions in open access literature.

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

Anderson H, et al. (2026) Ultrastructural expansion microscopy reveals unexpected levels of glycosome heterogeneity in African trypanosomes. Journal of microscopy, 301(2), 222.

Harrass S, et al. (2026) Lactobacilli Probiotics Prevent Amyloid-Beta Fibril Formation In Vitro. Probiotics and antimicrobial proteins, 18(3), 4640.

Pesce G, et al. (2026) AGGRESCAN and its evolution: A two-decade perspective on protein aggregation prediction. Biophysical reviews, 18(1), 83.

Ali M, et al. (2025) A Computational Approach for Designing a Peptide-Based Acetyl-CoA Synthetase 2 Inhibitor: A New Horizon for Anticancer Development. Cell biochemistry and biophysics, 83(3), 3465.

Errico S, et al. (2025) Structural commonalities determined by physicochemical principles in the complex polymorphism of the amyloid state of proteins. The Biochemical journal, 482(2), 87.

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

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.

Galliamov AA, et al. (2024) Mapping of Prion Structures in the Yeast Rnq1. International journal of molecular sciences, 25(6).

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. (2023) Enhancing the Antimicrobial Properties of Peptides through Cell-Penetrating Peptide Conjugation: A Comprehensive Assessment. International journal of molecular sciences, 24(23).

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.

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.

Nicy , et al. (2023) Energy Landscapes and Heat Capacity Signatures for Monomers and Dimers of Amyloid-Forming Hexapeptides. International journal of molecular sciences, 24(13).

Anju MV, et al. (2023) A novel anti-lipopolysaccharide factor from blue swimmer crab Portunus pelagicus and its cytotoxic effect on the prokaryotic expression host, E. coli on heterologous expression. Journal, genetic engineering & biotechnology, 21(1), 22.

Paz MM, et al. (2023) PRIMA-1 inhibits Y220C p53 amyloid aggregation and synergizes with cisplatin in hepatocellular carcinoma. Frontiers in molecular biosciences, 10, 1165132.

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.

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.

Alsowayeh N, et al. (2022) Designing a novel chimeric multi-epitope vaccine against Burkholderia pseudomallei, a causative agent of melioidosis. Frontiers in medicine, 9, 945938.