

# 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/>

**Proper Citation:** Aggrescan: The Hot Spot Finder (RRID:SCR\_008403)

**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

**Funding:** Ministerio de Educacion y Ciencia BIO2004-05879;  
Ministerio de Educacion y Ciencia BIO2003-02848;  
Spain Generalitat de Catalunya SGR2005-00037;  
Spain Generalitat de Catalunya SGR2005-01037

**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:** 20260808T190415+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 65 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#).

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) AGGRESKAN 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.

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).
- 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.
- 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).
- 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.
- 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).
- 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.
- 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.