Resource Summary Report

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SAS - Sequence Annotated by Structure

RRID:SCR_004635
Type: Tool

Proper Citation

SAS - Sequence Annotated by Structure (RRID:SCR_004635)

Resource Information

URL: http://www.ebi.ac.uk/thornton-srv/databases/sas/

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Description: SAS is a tool for applying structural information to a given protein sequence. It uses FASTA to scan a given protein sequence against all the proteins of known 3D structure in the Protein Data Bank (PDB). The resultant multiple alignment can be colored according to different structural features and the matching 3D structures can be superimposed and viewed in RasMol. Use the form to identify your protein sequence of interest by: a) providing a PDB code, b) providing a UniProt code or accession number, c) pasting in your sequence, or d) uploading a PDB file. By default the whole PDB will be searched, but you can restrict the search using the Search Option box at the bottom.

Abbreviations: SAS

Synonyms: Sequence Annotated by Structure

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

Keywords: gold standard

Funding:

Resource Name: SAS - Sequence Annotated by Structure

Resource ID: SCR_004635

Alternate IDs: nlx_63340

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250409T060417+0000

Ratings and Alerts

No rating or validation information has been found for SAS - Sequence Annotated by Structure.

No alerts have been found for SAS - Sequence Annotated by Structure.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Mascotti ML, et al. (2021) On the diversity of F420 -dependent oxidoreductases: A sequence- and structure-based classification. Proteins, 89(11), 1497.

Abdollahi S, et al. (2021) Physicochemical and structural characterization, epitope mapping and vaccine potential investigation of a new protein containing Tetratrico Peptide Repeats of Acinetobacter baumannii: An in-silico and in-vivo approach. Molecular immunology, 140, 22.

Zhang R, et al. (2021) Fungal effector SIB1 of Colletotrichum orbiculare has unique structural features and can suppress plant immunity in Nicotiana benthamiana. The Journal of biological chemistry, 297(6), 101370.

Chen PW, et al. (2020) Cataract and the increased risk of depression in general population: a 16-year nationwide population-based longitudinal study. Scientific reports, 10(1), 13421.

Laskowski RA, et al. (2018) PDBsum: Structural summaries of PDB entries. Protein science : a publication of the Protein Society, 27(1), 129.

Abdollahi S, et al. (2018) An in silico structural and physicochemical characterization of TonB-dependent copper receptor in A. baumannii. Microbial pathogenesis, 118, 18.

Agarwal AK, et al. (2017) Metabolic, Reproductive, and Neurologic Abnormalities in Agpat1-Null Mice. Endocrinology, 158(11), 3954.

Lionakis MS, et al. (2017) Inhibition of B Cell Receptor Signaling by Ibrutinib in Primary CNS Lymphoma. Cancer cell, 31(6), 833.

Diessler S, et al. (2017) Rai1 frees mice from the repression of active wake behaviors by light. eLife, 6.

Roa SLR, et al. (2017) Postnatal Ontogeny of the Circadian Expression of the Adrenal Clock Genes and Corticosterone Rhythm in Male Rats. Endocrinology, 158(5), 1339.

Korem T, et al. (2017) Bread Affects Clinical Parameters and Induces Gut Microbiome-Associated Personal Glycemic Responses. Cell metabolism, 25(6), 1243.

Mascotti ML, et al. (2016) Chopping and Changing: the Evolution of the Flavin-dependent Monooxygenases. Journal of molecular biology, 428(15), 3131.

Koh S, et al. (2015) Human Umbilical Tissue-Derived Cells Promote Synapse Formation and Neurite Outgrowth via Thrombospondin Family Proteins. The Journal of neuroscience : the official journal of the Society for Neuroscience, 35(47), 15649.

Chen YC, et al. (2014) Identifying RNA-binding residues based on evolutionary conserved structural and energetic features. Nucleic acids research, 42(3), e15.

Jorge SD, et al. (2013) Ligand-based design, synthesis, and experimental evaluation of novel benzofuroxan derivatives as anti-Trypanosoma cruzi agents. European journal of medicinal chemistry, 64, 200.

Chen YC, et al. (2012) DR_bind: a web server for predicting DNA-binding residues from the protein structure based on electrostatics, evolution and geometry. Nucleic acids research, 40(Web Server issue), W249.

Kurowska M, et al. (2011) TILLING: a shortcut in functional genomics. Journal of applied genetics, 52(4), 371.

Kariithi HM, et al. (2011) The salivary secretome of the tsetse fly Glossina pallidipes (Diptera: Glossinidae) infected by salivary gland hypertrophy virus. PLoS neglected tropical diseases, 5(11), e1371.

Chen H, et al. (2010) Identification and molecular characterization of a novel flavin-free NADPH preferred azoreductase encoded by azoB in Pigmentiphaga kullae K24. BMC biochemistry, 11, 13.