Resource Summary Report

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ESPript 2.2

RRID:SCR_006587
Type: Tool

Proper Citation

ESPript 2.2 (RRID:SCR_006587)

Resource Information

URL: http://espript.ibcp.fr/ESPript/ESPript/

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Description: A utility, whose output is a PostScript file of aligned sequences with graphical enhancements. Its main input is an ascii file of pre-aligned sequences. Optional files allow further rendering. The program calculates a similarity score for each residue of the aligned sequences. The output shows: * Secondary Structures * Aligned sequences * Similarities * Accessibility * Hydropathy * User-supplied markers * Intermolecular contacts In addition, similarity score can be written in the bfactor column of a pdb file, to enable direct display of highly conserved areas. You can run ESPript from this server with the HTML interface. It is configured for a maximum of 1,000 sequences. Links to webESPript * ENDscript: you can upload a PDB file or enter a PDB code such as 1M85. The programs DSSP and CNS are executed via the interface, so as to obtain an ESPript figure with a lot of structural information (secondary structure elements, intermolecular contacts). You can also find homologous sequences with a BLAST search, perform multiple sequence alignments with MULTALIN or CLUSTALW and create an image with BOBSCRIPT or MOLSCRIPT to show similarities on your 3D structure. * ProDom: you can enter a sequence identifier to find homologous domains, perform multiple sequence alignments with MULTALIN and click on the link to ESPript. * Predict Protein: you can receive a mail in text (do not use the HTML option when you submit your request in Predict Protein) with aligned sequences and numerous information including secondary structure prediction. Click on a special html link to upload your mail in ESPript. * NPS(at): you can execute the programs BLAST and CLUSTALW to obtain multiple alignments. You can predict secondary structure elements and click on the link to ESPript. This program started in the laboratory of Dr Richard Wade at the Institut de Biologie Structurale, Grenoble. It moved later to the Laboratory of Molecular Biophysics in Oxford, then to the Institut de Pharmacologie et de Biologie Structurale in Toulouse. It is now developed in the Laboratoire de BioCristallographie of Dr Richard Haser, Institut de Biologie et de Chimie des Prot????????ines, Lyon and in the Laboratoire de

Biologie Mol????????culaire et de Relations Plantes-Organismes, group of Dr Daniel Kahn, Institut National de la Recherche Agronomique de Toulouse.

Abbreviations: ESPript

Synonyms: Easy Sequencing in Postscript

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

Defining Citation: PMID:10320398, PMID:12824317

Keywords: postscript, aligned sequence, sequencing, blast, protein

Funding:

Availability: Free for academic use, Fee for commercial users, Licenses for accompanying programs used in ENDscript must be requested separately.

Resource Name: ESPript 2.2

Resource ID: SCR_006587

Alternate IDs: nif-0000-30499

Alternate URLs: http://genopole.toulouse.inra.fr/ESPript

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250412T055108+0000

Ratings and Alerts

No rating or validation information has been found for ESPript 2.2.

No alerts have been found for ESPript 2.2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 347 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Betz R, et al. (2024) Alternative splicing regulation in plants by SP7-like effectors from

symbiotic arbuscular mycorrhizal fungi. Nature communications, 15(1), 7107.

Miao Y, et al. (2024) RETINOBLASTOMA RELATED 1 switches mitosis to meiosis in rice. Plant communications, 5(6), 100857.

Salvador-Garcia D, et al. (2024) A force-sensitive mutation reveals a non-canonical role for dynein in anaphase progression. The Journal of cell biology, 223(10).

Tanaka N, et al. (2024) Functional and structural analysis of a cyclization domain in a cyclic ?-1,2-glucan synthase. Applied microbiology and biotechnology, 108(1), 187.

Yang H, et al. (2024) The Molecular and Functional Characterization of Sensory Neuron Membrane Protein 1b (SNMP1b) from Cyrtotrachelus buqueti (Coleoptera: Curculionidae). Insects, 15(2).

Bono M, et al. (2024) Chemical activation of ABA signaling in grapevine through the iSB09 and AMF4 ABA receptor agonists enhances water use efficiency. Physiologia plantarum, 176(6), e14635.

Chen Q, et al. (2024) Single-Nucleus and Spatial Transcriptomics Revealing Host Response Differences Triggered by Mutated Virus in Severe Dengue. Viruses, 16(11).

Liu Z, et al. (2024) Cytochrome P450 enzymes in the black-spotted frog (Pelophylax nigromaculatus): molecular characterization and upregulation of expression by sulfamethoxazole. Frontiers in physiology, 15, 1412943.

Zhao Y, et al. (2024) SCC3 is an axial element essential for homologous chromosome pairing and synapsis. eLife, 13.

Zhang L, et al. (2024) Evaluation of human antibodies from vaccinated volunteers for protection against Yersinia pestis infection. Microbiology spectrum, 12(10), e0105424.

Ding M, et al. (2024) Catalase-peroxidase StKatG2 from Salinicola tamaricis: a versatile Mn(II) oxidase that decolorizes malachite green. Frontiers in microbiology, 15, 1478305.

Mills KB, et al. (2024) Staphylococcus aureus skin colonization is mediated by SasG lectin variation. Cell reports, 43(4), 114022.

Jones ML, et al. (2023) How Pol ?-primase is targeted to replisomes to prime eukaryotic DNA replication. Molecular cell, 83(16), 2911.

Kikuchi M, et al. (2023) Epigenetic mechanisms to propagate histone acetylation by p300/CBP. Nature communications, 14(1), 4103.

Martin-Morales L, et al. (2023) Germline gain-of-function MMP11 variant results in an aggressive form of colorectal cancer. International journal of cancer, 152(2), 283.

Nakagawa R, et al. (2023) Cryo-EM structure of the transposon-associated TnpB enzyme. Nature, 616(7956), 390.

Liang Q, et al. (2023) A Recombinant Alginate Lyase Algt1 with Potential in Preparing Alginate Oligosaccharides at High-Concentration Substrate. Foods (Basel, Switzerland), 12(21).

Song J, et al. (2023) A candidate nanoparticle vaccine comprised of multiple epitopes of the African swine fever virus elicits a robust immune response. Journal of nanobiotechnology, 21(1), 424.

Zhu X, et al. (2023) An atypical GdpP enzyme linking cyclic nucleotide metabolism to osmotic tolerance and gene regulation in Mycoplasma bovis. Frontiers in microbiology, 14, 1250368.

Motouchi S, et al. (2023) Identification of enzymatic functions of osmo-regulated periplasmic glucan biosynthesis proteins from Escherichia coli reveals a novel glycoside hydrolase family. Communications biology, 6(1), 961.