

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

ESPrpt 2.2

RRID:SCR_006587

Type: Tool

Proper Citation

ESPrpt 2.2 (RRID:SCR_006587)

Resource Information

URL: <http://esprpt.ibcp.fr/ESPrpt/ESPrpt/>

Proper Citation: ESPrpt 2.2 (RRID:SCR_006587)

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 ESPrpt from this server with the HTML interface. It is configured for a maximum of 1,000 sequences. Links to webESPrpt * 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 ESPrpt 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 ESPrpt. * 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 ESPrpt. * 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 ESPrpt. 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 Protéines, Lyon and in the Laboratoire de Biologie Moléculaire 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: production service resource, data analysis service, software application, data processing software, analysis service resource, service resource, software resource

Defining Citation: [PMID:10320398](#), [PMID:12824317](#)

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

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: 20260804T043305+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 361 mentions in open access literature.

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

Haase J, et al. (2025) Cohesin-mediated stabilization of the CCAN complex at kinetochores in mitosis. Current biology : CB, 35(16), 3943.

Wang N, et al. (2025) Structural Homology Fails to Predict Secretion Efficiency in Pichia pastoris: Divergent Responses of Architecturally Similar scFvs to Multi-Parametric Genetic Engineering. International journal of molecular sciences, 26(10).

Jin J-q, et al. (2025) SmsB-SmsC machinery in Thermococcus kodakarensis functions as an archaeal scaffold mediating Fe-S cluster assembly. Applied and environmental

microbiology, 91(9), e0143825.

Jin JQ, et al. (2025) Biochemical characterization of phosphoenolpyruvate carboxykinases from multiple species of brown algae. *Journal of phycology*, 61(5), 1321.

Zhang C, et al. (2025) OsPRDA1 Interacts With OsFSD2 To Promote Chloroplast Development by Regulating Chloroplast Gene Expression in Rice. *Rice (New York, N.Y.)*, 18(1), 14.

Wang K, et al. (2025) Structural basis for antibiotic resistance by chloramphenicol acetyltransferase type A in *Staphylococcus aureus*. *Scientific reports*, 15(1), 37020.

Gong X, et al. (2025) Identification and functional study of a novel FOXC1 missense mutation in a Chinese family with Axenfeld-Rieger syndrome. *Scientific reports*, 15(1), 19957.

Wei X, et al. (2025) Exploring and expanding the natural chemical space of bacterial diterpenes. *Nature communications*, 16(1), 3721.

Ye Y, et al. (2025) The Identification and Characterization of a Novel Alginate Lyase from *Mesonia hitae* R32 Exhibiting High Thermal Stability and Potent Antioxidant Oligosaccharide Production. *Marine drugs*, 23(4).

Nakajima M, et al. (2025) New glycoside hydrolase families of β -1,2-glucanases. *Protein science : a publication of the Protein Society*, 34(6), e70147.

Lei M, et al. (2025) An Apple Susceptibility-Related LRR Receptor-Like Kinase MdRLKT21 Activates Plant Immunity by Hijacking a Trans-Kingdom Fungal microRNA-Like RNA. *Advanced science (Weinheim, Baden-Wurtemberg, Germany)*, 12(38), e17426.

Arnold CJ, et al. (2025) Resistance of ERG24 sterol C-14 reductase to heterocyclic amine antifungals. *npj antimicrobials and resistance*, 3(1), 83.

Jiang X, et al. (2025) The hook-like adaptor and cargo-binding (HAC) domain in the kinesin-2 tail enables adaptor assembly and cargo recognition. *Science advances*, 11(43), eady5861.

Lei P, et al. (2025) HLS1 interacts with ATG8 to negatively regulate the ABS3-mediated plant senescence pathway. *Cell reports*, 44(4), 115507.

Betz R, et al. (2024) Alternative splicing regulation in plants by SP7-like effectors from symbiotic arbuscular mycorrhizal fungi. *Nature communications*, 15(1), 7107.

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 β -1,2-glucan synthase. *Applied microbiology and biotechnology*, 108(1), 187.

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

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

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).