

Resource Summary Report

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Clustal Omega

RRID:SCR_001591

Type: Tool

Proper Citation

Clustal Omega (RRID:SCR_001591)

Resource Information

URL: <https://www.ebi.ac.uk/jdispatcher/msa/clustalo?type=protein>

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Description: Software package as multiple sequence alignment tool that uses seeded guide trees and HMM profile-profile techniques to generate alignments between three or more sequences. Accepts nucleic acid or protein sequences in multiple sequence formats NBRF/PIR, EMBL/UniProt, Pearson (FASTA), GDE, ALN/Clustal, GCG/MSF, RSF.

Abbreviations: Clustal Omega, Clustalo

Resource Type: software application, service resource, software resource, data processing software, alignment software, image analysis software

Defining Citation: [PMID:21988835](#), [PMID:20439314](#), [DOI:10.1038/msb.2011.75](#)

Keywords: multiple, sequence, alignment, DNA, RNA, protein, generate, bio.tools

Funding: Science Foundation Ireland

Availability: Free, Available for download, Freely available

Resource Name: Clustal Omega

Resource ID: SCR_001591

Alternate IDs: OMICS_00972, SCR_016062, biotools:clustalo, nlx_153836

Alternate URLs: <https://sources.debian.org/src/clustalo/>, <http://www.clustal.org/omega/>, <http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::clustalO-multialign>, <https://bio.tools/clustalo>, <https://sources.debian.org/src/clustalo/>

License: GNU lesser GPL

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260729T044019+0000

Ratings and Alerts

No rating or validation information has been found for Clustal Omega.

No alerts have been found for Clustal Omega.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9956 mentions in open access literature.

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

Mazny BE, et al. (2026) Evolved formate assimilation in phototrophic *Rhodopseudomonas palustris* indicates the need for a CO₂-concentrating mechanism. *Current biology : CB*, 36(1), 110.

Parnandi VA, et al. (2026) A small *Candida glabrata* protein promotes hyphal growth in *C. albicans* during mixed-species invasive candidiasis. *Current biology : CB*, 36(1), 1.

Marted?? R, et al. (2026) De novo cysteine biosynthesis in *Pseudomonas aeruginosa*: Characterization of the two main cysteine synthase isoforms. *iScience*, 29(1), 114304.

Strijbis VJF, et al. (2026) Modifications of the Prothrombin Active Site S4 Subpocket Confer Resistance to Dabigatran. *Thrombosis and haemostasis*, 126(1), 23.

Sun R, et al. (2026) Detoxification of conifer antimicrobial defenses promotes entomopathogenic fungus infection of bark beetles. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2525513122.

Markkanen M, et al. (2026) Sulfonamide resistance gene *sul4* is hosted by common wastewater sludge bacteria and found in various newly described contexts and hosts. *Microbiology spectrum*, 14(1), e0085725.

Contreras-Moreira B, et al. (2026) The PanOryza pangene catalog of Asian cultivated rice. *Genome research*, 36(1), 226.

Xu H, et al. (2026) Teleost GSDMEc regulates GSDMEa-mediated pyroptosis. *Journal of advanced research*, 79, 105.

Miao J, et al. (2026) Clathrins Are Involved in the Endocytosis of Host Cytosol in the Malaria Parasite. *Traffic (Copenhagen, Denmark)*, 27(1), e70025.

Riley SE, et al. (2026) In vivo screen reveals specific roles of Hippo pathway components in development and regeneration. *Life science alliance*, 9(3).

Sebastian PJ, et al. (2026) Apparent expansion of virulent *Vibrio parahaemolyticus* in humans and sea otters. *Virulence*, 17(1), 2603698.

Grieben M, et al. (2026) Cloning, expression, purification, and structural modeling of the Chandipura virus matrix protein. *FEBS open bio*, 16(1), 41.

Juanpere-Borras M, et al. (2026) Genome-wide Identification of conditionally essential genes supporting *Streptococcus suis* growth in serum and cerebrospinal fluid. *Virulence*, 17(1), 2600145.

Tseduliak V-M, et al. (2026) Probing the function of *Streptomyces albidoflavus* J1074 gene XNR_5296 for SPOUT family ribose methyltransferase. *Microbiology spectrum*, 14(1), e0219225.

Garg P, et al. (2026) Emerging genetic diversity and molecular epidemiology of *Entamoeba moshkovskii* among patients with acute diarrhoea in Northern India. *Tropical medicine and health*, 54(1), 3.

Boegli A, et al. (2026) The NLRP6 inflammasome is activated by sterile or pathogen-induced endolysosomal damage. *The EMBO journal*, 45(1), 30.

Fischer MC, et al. (2026) Splicing and frameshift variants in QSER1 may be involved in developmental phenotypes. *HGG advances*, 7(1), 100539.

Sueasuay J, et al. (2026) Evaluation of the conserved subunit of the pathogenic *Leptospira* FlaB protein-based immunochromatographic test for the diagnosis of acute leptospirosis. *Microbiology spectrum*, 14(1), e0030725.

Kamran Z, et al. (2026) In silico design of a matrix (M) protein-based vaccine candidate against Newcastle disease virus. *Poultry science*, 105(1), 106101.

Nath VR, et al. (2025) Ca²⁺ binding to Esyt modulates membrane contact site density in *Drosophila* photoreceptors. *The Journal of cell biology*, 224(5).