

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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://mobyli.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: 20260905T132436+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 10580 mentions in open access literature.

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

Le DM, et al. (2026) Distinct Associations of GTF2I, TP53, and NOTCH1 Variants with Indolent and Aggressive Thymic Epithelial Tumors in Vietnamese Patients. *Genes*, 17(5).

Hoshina N, et al. (2026) Complementary ?2-protocadherin expression delineates parallel basal ganglia circuits in primates. *iScience*, 29(7), 116598.

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.

Gadad SS, et al. (2026) X-linked cancer-associated polypeptide (XCP) from lncRNA1456 modulates PHF8 histone demethylase activity to regulate the epigenome, gene expression, and cellular pathways in breast cancer. *Oncogene*, 45(17), 1557.

Yu L, et al. (2026) Systematic characterization of PBP2 as the primary siderophore recognizer in Actinomycetes and other Gram-positive bacteria. *Microbial genomics*, 12(4).

Yang K, et al. (2026) Structural mechanism of Borna disease virus 1 RNA polymerase autoinhibition and suramin-mediated inhibition. *Cell reports*, 45(6), 117462.

Harris Snell P, et al. (2026) Coordinated regulation of mRNA translation and stability by ZC3H7A and ZC3H7B RNA-binding proteins. *Cell reports*, 45(6), 117511.

Kim S, et al. (2026) Gut microbiota transfer from autoimmune dry eye mice imprints stereotypic B cell receptor repertoires in the lacrimal gland and induces disease. *Frontiers in immunology*, 17, 1827057.

Niu B, et al. (2026) Oligomerization-Dependent Regulation of LrhA Controls Bacterial Flagellar Biosynthesis. *Journal of molecular biology*, 438(7), 169682.

Mrkacek M, et al. (2026) ORMDL Proteins Turnover via Proteasome and Autophagy Is Cell-Type Dependent and Tied to Ceramide Homeostasis. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 40(6), e71655.

Savani MR, et al. (2026) Nitrogen metabolism profiling reveals cell state-specific pyrimidine synthesis pathway choice. *Nature metabolism*, 8(5), 1124.

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.

Jiang X, et al. (2026) The KIF3B/B/KAP3 tail domain specifically facilitates TRIM46 transport to the axon initial segment. *The Journal of cell biology*, 225(5).

Ghasemi F, et al. (2026) Expansion, functional diversification, and gene fusion events in the Ato protein family. *iScience*, 29(7), 116467.

Muñoz-Sánchez S, et al. (2026) PIKfyve mediates the maturation of mycobacteria-containing vesicles. *Frontiers in cellular and infection microbiology*, 16, 1792069.

Yang K, et al. (2026) Double-ring assembly of mpox virus I3L reveals an unconventional mechanism for ssDNA engagement. *Cell reports*, 45(7), 117659.

Orkwis JA, et al. (2026) Helminth proteins recapitulate key structural motifs of MIF to facilitate immunomodulation of host receptors. *iScience*, 29(7), 116513.

Squair DR, et al. (2026) ZNFX1 uses two-component ubiquitin circuitry to quarantine viral RNA. *Molecular cell*, 86(6), 1164.

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

Senti KA, et al. (2026) Co-evolving infectivity and expression patterns drive the diversification of endogenous retroviruses. *The EMBO journal*, 45(6), 1889.