**Clustal Omega**

RRID:SCR_001591  
Type: Tool

**Proper Citation**

Clustal Omega (RRID:SCR_001591)

**Resource Information**

**URL:** [http://www.ebi.ac.uk/Tools/msa/clustalo/](http://www.ebi.ac.uk/Tools/msa/clustalo/)

**Proper Citation:** Clustal Omega (RRID:SCR_001591)

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

**Defining Citation:** [PMID:21988835](https://www.ncbi.nlm.nih.gov/pubmed/21988835), [PMID:20439314](https://www.ncbi.nlm.nih.gov/pubmed/20439314), [DOI:10.1038/msb.2011.75](https://doi.org/10.1038/msb.2011.75)

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

**Funding Agency:** Science Foundation Ireland

**Availability:** Free, Available for download, Freely available, Acknowledgement requested

**Resource Name:** Clustal Omega

**Resource ID:** SCR_001591

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

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 7271 mentions in open access literature.

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

Jahun AS, et al. (2023) Leaked genomic and mitochondrial DNA contribute to the host response to noroviruses in a STING-dependent manner. Cell reports, 42(3), 112179.


Meyer S, et al. (2023) Prevalent and immunodominant CD8 T cell epitopes are conserved in SARS-CoV-2 variants. Cell reports, 42(1), 111995.

Chen J, et al. (2023) Integrative transcriptomics and cell systems analyses reveal protective pathways controlled by Igfbp-3 in anthracycline-induced cardiotoxicity. FASEB journal: official publication of the Federation of American Societies for Experimental Biology, 37(6), e22977.


Yang Q, et al. (2023) X-chromosome target specificity diverged between dosage compensation mechanisms of two closely related Caenorhabditis species. eLife, 12.


Casas-Sanchez A, et al. (2023) The Trypanosoma brucei MISP family of invariant proteins is co-expressed with BARP as triple helical bundle structures on the surface of salivary gland forms, but is dispensable for parasite development within the tsetse vector. PLoS pathogens, 19(3), e1011269.


Baranowska E, et al. (2023) Probing the pathogenicity of patient-derived variants of MT-ATP6 in yeast. Disease models & mechanisms, 16(4).