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/

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.

Resource Name: Clustal Omega

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

Keywords: multiple, sequence, alignment, DNA, RNA, protein, generate

Resource ID: SCR_001591

Parent Organization: European Bioinformatics Institute, University College Dublin; Dublin; Ireland

Funding Agency: Science Foundation Ireland

Related resources: ClustalW2, ClustalW2, Clustal X

References: PMID:21988835, PMID:20439314

Availability: Free, Available for download, Freely available, Acknowledgement requested
**Website Status:** Last checked up

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

**Alternate URLs:** http://www.clustal.org/omega/, http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::clustalO-multialign

**Abbreviations:** Clustal Omega, Clustalo

**Mentions Count:** 3534

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**Ratings and Alerts**

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

No alerts have been found for Clustal Omega.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 3534 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](https://www.sciencedirect.com).


