

Resource Summary Report

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Clustal W2

RRID:SCR_002909

Type: Tool

Proper Citation

Clustal W2 (RRID:SCR_002909)

Resource Information

URL: <http://www.ebi.ac.uk/Tools/msa/clustalw2/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on January 19, 2022. Command line version of multiple sequence alignment program Clustal for DNA or proteins. Alignment is progressive and considers sequence redundancy. No longer being maintained. Please consider using Clustal Omega instead which accepts nucleic acid or protein sequences in multiple sequence formats NBRF/PIR, EMBL/UniProt, Pearson (FASTA), GDE, ALN/ClustalW, GCG/MSF, RSF.

Synonyms: European Bioinformatics Institute - ClustalW2

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

Defining Citation: [PMID:17846036](#), [PMID:20439314](#), [DOI:10.1093/bioinformatics/btm404](#)

Keywords: multiple, sequence, alignment, cladogram, phylogram, evolution, phylogenetic, tree, protein, nucleic, acid, bio.tools

Funding Agency: Science Foundation Ireland

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Clustal W2

Resource ID: SCR_002909

Alternate IDs: OMICS_02562, nif-0000-30076

Alternate URLs: <http://www.ch.embnet.org/software/ClustalW.html>,
<https://sources.debian.org/src/clustalx/>

Old URLs: <http://www.ebi.ac.uk/tools/clustalw/>

Ratings and Alerts

No rating or validation information has been found for Clustal W2.

No alerts have been found for Clustal W2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7790 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Jiao X, et al. (2024) A cyclin D1 intrinsically disordered domain accesses modified histone motifs to govern gene transcription. *Oncogenesis*, 13(1), 4.

Vellas C, et al. (2024) Intact proviruses are enriched in the colon and associated with PD-1+TIGIT- mucosal CD4+ T cells of people with HIV-1 on antiretroviral therapy. *EBioMedicine*, 100, 104954.

Tabassum N, et al. (2024) Genome-wide in-silico analysis of ethylene biosynthesis gene family in *Musa acuminata* L. and their response under nutrient stress. *Scientific reports*, 14(1), 558.

Ibrahim MM, et al. (2024) First report of *Kudoa* species (Myxozoa, Multivalvulida) infection in purple-spotted Bigeye (*Priacanthus tayenus*) from the Saudi Arabian Gulf. *PloS one*, 19(1), e0295668.

Zhang A, et al. (2024) Molecular Characterization and Expression Changes of the *bcl2l13* Gene in Response to Hypoxia in *Megalobrama amblycephala*. *Current issues in molecular biology*, 46(2), 1136.

Gheybi E, et al. (2023) In silico designing and expression of novel recombinant construct containing the variable part of CD44 extracellular domain for prediagnostic breast cancer. *Cancer reports (Hoboken, N.J.)*, 6(3), e1745.

Quaglia G, et al. (2023) Turkey adenovirus 3: ORF1 gene sequence comparison between vaccine-like and field strains. *Veterinary research communications*, 47(4), 2307.

Alves LA, et al. (2023) PepO and CppA modulate *Streptococcus sanguinis* susceptibility to complement immunity and virulence. *Virulence*, 14(1), 2239519.

Ibrahim YM, et al. (2023) Molecular characterization and pathogenicity evaluation of enterovirus G isolated from diarrheic piglets. *Microbiology spectrum*, 11(6), e0264323.

Yan J, et al. (2023) Identification of FtfL as a novel target of berberine in intestinal bacteria. *BMC biology*, 21(1), 280.

Xiao Y, et al. (2023) Biochemical Characterization and Functional Analysis of Glucose Regulated Protein 78 from the Silkworm *Bombyx mori*. *International journal of molecular sciences*, 24(4).

Guo L, et al. (2023) Disruption of ER ion homeostasis maintained by an ER anion channel CLCC1 contributes to ALS-like pathologies. *Cell research*, 33(7), 497.

Dong C, et al. (2023) A Small Subunit of Geranylgeranyl Diphosphate Synthase Functions as an Active Regulator of Carotenoid Synthesis in *Nicotiana tabacum*. *International journal of molecular sciences*, 24(2).

Moura-Mendes J, et al. (2023) Species Identification and Mycotoxigenic Potential of *Aspergillus* Section *Flavi* Isolated from Maize Marketed in the Metropolitan Region of Asunción, Paraguay. *Microorganisms*, 11(8).

Kuan JE, et al. (2023) Enzymatic Characterization of a Novel HSL Family IV Esterase EstD04 from *Pseudomonas* sp. D01 in Mealworm Gut Microbiota. *Molecules* (Basel, Switzerland), 28(14).

Xie R, et al. (2023) Host-Specific Diversity of Culturable Bacteria in the Gut Systems of Fungus-Growing Termites and Their Potential Functions towards Lignocellulose Bioconversion. *Insects*, 14(4).

Li Y, et al. (2023) The Endophytic Root Microbiome Is Different in Healthy and *Ralstonia solanacearum*-Infected Plants and Is Regulated by a Consortium Containing Beneficial Endophytic Bacteria. *Microbiology spectrum*, 11(1), e0203122.

do Lago BV, et al. (2023) Genetic diversity of hepatitis B virus quasispecies in different biological compartments reveals distinct genotypes. *Scientific reports*, 13(1), 17023.

Hauvermale AL, et al. (2023) Development of Novel Monoclonal Antibodies to Wheat Alpha-Amylases Associated with Grain Quality Problems That Are Increasing with Climate Change. *Plants* (Basel, Switzerland), 12(22).

Mishra S, et al. (2023) Genome-wide identification and expression analysis of the GRAS gene family under abiotic stresses in wheat (*Triticum aestivum* L.). *Scientific reports*, 13(1), 18705.