

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

T-Coffee

RRID:SCR_011818

Type: Tool

Proper Citation

T-Coffee (RRID:SCR_011818)

Resource Information

URL: <http://tcoffee.crg.cat/apps/tcoffee/do:regular>

Proper Citation: T-Coffee (RRID:SCR_011818)

Description: A multiple sequence alignment server which can align Protein, DNA and RNA sequences.

Abbreviations: T-Coffee

Synonyms: T-Coffee: Aligns DNA RNA or Proteins using the default T-Coffee

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:10964570](#), [DOI:10.1006/jmbi.2000.4042](#)

Keywords: bio.tools

Resource Name: T-Coffee

Resource ID: SCR_011818

Alternate IDs: biotools:tcoffee, OMICS_00989

Alternate URLs: <https://bio.tools/tcoffee>, <https://sources.debian.org/src/t-coffee/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260808T190422+0000

Ratings and Alerts

No rating or validation information has been found for T-Coffee.

No alerts have been found for T-Coffee.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1157 mentions in open access literature.

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

Lima AR, et al. (2026) Ancestral Protein Reconstruction Uncovers a Thermotolerant Rieske Oxygenase with Enhanced O-Demethylation Activity toward 3-O-Methylgallate. *ACS synthetic biology*, 15(6), 2660.

Fontenla-Iglesias F, et al. (2026) Ancient IL-6-STAT5 signaling orchestrates inflammation in jawless vertebrates. *bioRxiv : the preprint server for biology*.

Hoang M, et al. (2026) Fast, accurate construction of multiple sequence alignments from protein language embeddings. *bioRxiv : the preprint server for biology*.

El-Awadi R, et al. (2026) Interrelational Proteomic Sequence Features Enhance Predictive Modeling: Application to COVID-19 Severity. *Biomedicines*, 14(2).

Sun M, et al. (2026) Unambiguous chromosome identification by multicolour fluorescence in situ hybridisation reveals the genome organisation and evolution of sheepgrass (*Leymus chinensis*). *BMC plant biology*, 26(1).

Hu H, et al. (2026) Cryo-electron microscopy structure of the budding yeast telomerase holoenzyme. *Science (New York, N.Y.)*, 391(6792), eadz5344.

Zhang X, et al. (2026) Evolutionary Complexity of Primate Immune System Uncovered by the Extensive Phylogenomic Sampling. *Genome biology and evolution*, 18(4).

Gao Q, et al. (2026) ERBB2 I655V mutation correlates with efficacy of immunotherapy in gallbladder cancer. *World journal of surgical oncology*, 24(1).

Correia PD, et al. (2026) Injury-induced KIF4A neural expression and its role in Schwann cell proliferation suggest a dual function for this kinesin in neural regeneration. *Neural regeneration research*, 21(4), 1607.

Polonio P, et al. (2026) Solution NMR reveals micelle-stabilized α -helical segments flanking the RIPK1 RHIM amyloid core. *Biochemical and biophysical research communications*, 809, 153513.

Favre S, et al. (2026) Exploration of the proxiOME of large subunit ribosomal proteins reveals Acl1 and Bcl1 as cooperating dedicated chaperones of Rpl1. *Nucleic acids research*, 54(6).

Ogunshola FJ, et al. (2026) Duration of Initial Viremia Modulates Functional Properties of HIV-specific T Cell Receptors. Research square.

Rabuffetti M, et al. (2026) Structure-Guided Prioritization and Synthesis of New Ligands for GPR17 Receptor. ACS omega, 11(24), 35411.

Wang S, et al. (2026) Predicted protein 3D structures provide essential insights into the genetic architecture underlying phenotypic diversity in maize. Genome research, 36(1), 214.

Jin ZR, et al. (2026)

Echinacoside alleviates asthenozoospermia by upregulating Sox5-mediated transcriptional activation of the CatSper gene

. Molecular medicine reports, 33(3).

Krzynowek A, et al. (2026) PlasticEnz: An integrated database and screening tool combining homology and machine learning to identify plastic-degrading enzymes in meta-omics datasets. PLoS computational biology, 22(1), e1013892.

Kim K, et al. (2026) Differential targeting of human pyroptotic caspase-5 and caspase-4 by Shigella OspC2 and OspC3. mBio, 17(3), e0385525.

Zhao M, et al. (2026) G521 is the gatekeeper and a key transmembrane domain contact residue of Candida albicans Cdr1. mBio, 17(4), e0374625.

Ortiz Galeano LS, et al. (2026) Technological potential of Bacillus megaterium in Cacao bean fermentation. International microbiology : the official journal of the Spanish Society for Microbiology, 29(4), 485.

Payliss BJ, et al. (2026) Dual-site phosphorylation of SLX4 stabilizes the SLX4-MUS81 interface to promote mitotic SMX assembly and genome protection. Nucleic acids research, 54(9).