

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T133201+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 [Kravitz](#) .

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.

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

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).

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.

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).

Bajunaid W, et al. (2026) A bacterial family of fatty acid acyltransferases related to the *Shigella* effector IcsB. *mBio*, 17(4), e0389025.

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

Okoye IC, et al. (2026) ATAD3 megadalton complex in *Plasmodium falciparum* is essential for mitochondrial and cellular viability. *PLoS pathogens*, 22(6), e1014317.

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