

Resource Summary Report

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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, service resource, data analysis service, production 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: 20260728T043400+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 1121 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

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.

Chen W, et al. (2025) FAM50A drives breast cancer brain metastasis through interaction with C9ORF78 to enhance ??-asparagine production. *Science advances*, 11(25), eadt3075.

Ogbu CP, et al. (2025) Biophysical basis of tight junction barrier modulation by a pan-claudin-binding molecule. *PNAS nexus*, 4(6), pgaf189.

Cossio LA, et al. (2025) Genome-wide identification of lipid transfer proteins in Sorghum bicolor and discovery of flower-specific promoters. *Scientific reports*, 15(1), 25710.

Kjeldsen CMN, et al. (2025) The Proteinase PAPP-A has Deep Evolutionary Roots Outside of the IGF System. *Genome biology and evolution*, 17(3).

Smith NT, et al. (2025) Taxonomic distribution of SbmA/BacA and BacA-like antimicrobial peptide transporters suggests independent recruitment and convergent evolution in host-microbe interactions. *Microbial genomics*, 11(4).

Paesen GC, et al. (2025) Structure and stabilization of the antigenic glycoprotein building blocks of the New World mammarenavirus spike complex. *mBio*, 16(7), e0107625.

Prigge MJ, et al. (2025) Comparative mutant analyses reveal a novel mechanism of ARF regulation in land plants. *Nature plants*, 11(4), 821.

De Maayer P, et al. (2025) Pan-genome analysis of the *Enterobacter hormaechei* complex highlights its genomic flexibility and pertinence as a multidrug resistant pathogen. *BMC genomics*, 26(1), 408.

Resende BC, et al. (2025) Mismatch uracil DNA glycosylase (Mug) is maintained in the *Corynebacterium pseudotuberculosis* genome and exhibits affinity for uracil but not other types of damage. *Genetics and molecular biology*, 48(2), e20230353.

Kondo T, et al. (2025) Determinants of susceptibility to SARS-CoV-2 infection in murine ACE2. *Journal of virology*, 99(6), e0054325.

Chagny E, et al. (2025) Wide Diversity and Complex Evolution of M42 Aminopeptidases With Contrasted Functional Properties in Archaea. *Molecular biology and evolution*, 42(10).

Haque MS, et al. (2025) Identification and knockdown effect of disulfide isomerase in the *Haemaphysalis longicornis* (Acari: Ixodidae). *Revista brasileira de parasitologia veterinaria = Brazilian journal of veterinary parasitology : Orgao Oficial do Colegio Brasileiro de Parasitologia Veterinaria*, 34(4), e009125.

Zhang X, et al. (2025) Harnessing eukaryotic retroelement proteins for transgene insertion into human safe-harbor loci. *Nature biotechnology*, 43(1), 42.

Waqar S, et al. (2025) Arsenic efflux and bioremediation potential of *Klebsiella oxytoca* via the *arsB* gene. *PloS one*, 20(1), e0307918.

Magyar LB, et al. (2025) Pore-Forming Toxin-Like Proteins in the Anti-Parasitoid Immune Response of *Drosophila*. *Journal of innate immunity*, 17(1), 10.

De Pablo-Moreno JA, et al. (2025) Development of a novel and viable knock-in factor V deficiency murine model: Utility for an ultra-rare disease. *PloS one*, 20(6), e0321864.

Castellanos-Labarcena J, et al. (2025) Single specimen genome assembly of *Culicoides stellifer* shows evidence of a non-retroviral endogenous viral element. *BMC genomics*, 26(1), 247.

Lacoursiere RE, et al. (2025) RNF114 and RNF166 exemplify reader-writer E3 ligases that extend K11 polyubiquitin onto sites of MARUbylation. *The EMBO journal*, 44(21), 5993.

Saharan K, et al. (2025) Structure-function studies of a nucleoplasmin isoform from *Plasmodium falciparum*. *The Journal of biological chemistry*, 301(4), 108379.