

# Resource Summary Report

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## Transeq

RRID:SCR\_015647

Type: Tool

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### Proper Citation

Transeq (RRID:SCR\_015647)

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### Resource Information

**URL:** [http://www.ebi.ac.uk/Tools/st/emboss\\_transeq/](http://www.ebi.ac.uk/Tools/st/emboss_transeq/)

**Proper Citation:** Transeq (RRID:SCR\_015647)

**Description:** Software that translates nucleic acid sequences to their corresponding peptide sequences. It can translate to the three forward and three reverse frames, and output multiple frame translations at once.

**Synonyms:** EMBOSS Transeq

**Resource Type:** web application, software resource

**Defining Citation:** [PMID:10827456](#)

**Keywords:** peptide sequence, frame translation, nucleic acid, protein identification

**Availability:** Freely Available, Available for download

**Resource Name:** Transeq

**Resource ID:** SCR\_015647

**Alternate URLs:** <http://emboss.sourceforge.net/apps/cvs/emboss/apps/transeq.html>

**Record Creation Time:** 20220129T080326+0000

**Record Last Update:** 20260815T182514+0000

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### Ratings and Alerts

No rating or validation information has been found for Transeq.

No alerts have been found for Transeq.

## Data and Source Information

**Source:** [SciCrunch Registry](#)

## Usage and Citation Metrics

We found 200 mentions in open access literature.

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

Barrera-Duarte CC, et al. (2026) Regulatory network rewiring drives strain-specific lipid accumulation response in *Chlorella sorokiniana* under nutrient starvation. *The Plant journal : for cell and molecular biology*, 125(1), e70644.

Carofano I, et al. (2026) Detection of a Conserved Bacterial Symbiosis in non-frugivorous Australian Fruit Flies (Diptera, Tephritidae, Tephritinae) Supports its Widespread Association. *Microbial ecology*, 89(1), 38.

Buetas E, et al. (2026) Metatranscriptomic analysis of the microbiota of tumor tissue in colon cancer. *Microbiome*, 14(1).

Barua A, et al. (2026) Estimates of molecular convergence reveal multiple genes with adaptive variation across teleost fish. *Molecular biology and evolution*, 43(1).

Chen J, et al. (2026) De Novo Assembly and Characterization of Venom Gland Transcriptome for *Rhabdophis lateralis*. *Toxins*, 18(4).

Lei Y, et al. (2025) Deciphering functional landscapes of rumen microbiota unveils the role of *Prevotella bryantii* in milk fat synthesis in goats. *Genome biology*, 26(1), 311.

Duan C, et al. (2025) FGeneBERT: function-driven pre-trained gene language model for metagenomics. *Briefings in bioinformatics*, 26(2).

Gomaa F, et al. (2025) Array of metabolic pathways in a kleptoplastidic foraminiferan protist supports chemoautotrophy in dark, euxinic seafloor sediments. *The ISME journal*, 19(1).

Song B, et al. (2025) Prokaryotic cellulase gene clusters derived from 2,305 metagenomes. *Scientific data*, 12(1), 218.

Lu W, et al. (2025) Metagenomic sequencing reveals the taxonomic and functional characteristics of rumen microorganisms in Dongliu buffalo. *Scientific reports*, 15(1), 18398.

Chatterjee R, et al. (2025) Sensitizing Immune-Refractory Ovarian Tumors via p53 Mutation-Tailored Immunotherapy. *bioRxiv : the preprint server for biology*.

Duan C, et al. (2025) FGeneBERT: function-driven pre-trained gene language model for metagenomics. *Briefings in bioinformatics*, 26(6).

Wang L, et al. (2024) A novel esterase regulates *Klebsiella pneumoniae* hypermucoviscosity and virulence. *PLoS pathogens*, 20(10), e1012675.

Isla A, et al. (2024) Advancements in rapid diagnostics and genotyping of *Piscirickettsia salmonis* using Loop-mediated Isothermal Amplification. *Frontiers in microbiology*, 15, 1392808.

Zhao H, et al. (2024) Transcriptomics and metabolomics of blood, urine and ovarian follicular fluid of yak at induced estrus stage. *BMC genomics*, 25(1), 201.

Santos LGC, et al. (2024) SpliceProt 2.0: A Sequence Repository of Human, Mouse, and Rat Proteoforms. *International journal of molecular sciences*, 25(2).

Montfort J, et al. (2024) FEVER: an interactive web-based resource for evolutionary transcriptomics across fishes. *Nucleic acids research*, 52(W1), W65.

Gomathinayagam S, et al. (2024) Millennial-scale microbiome analysis reveals ancient antimicrobial resistance conserved despite modern selection pressures. *Environmental microbiome*, 19(1), 110.

Shao J, et al. (2024) AGRAMP: machine learning models for predicting antimicrobial peptides against phytopathogenic bacteria. *Frontiers in microbiology*, 15, 1304044.

Tripathi S, et al. (2023) Defining the condensate landscape of fusion oncoproteins. *Nature communications*, 14(1), 6008.