

Resource Summary Report

Generated by [NIF](#) on Aug 19, 2026

ProTISA

RRID:SCR_002138

Type: Tool

Proper Citation

ProTISA (RRID:SCR_002138)

Resource Information

URL: <http://mech.ctb.pku.edu.cn/protisa/>

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Description: Database of confirmed translation initiation sites (TISs) for prokaryotic genomes. The confirmed data has supporting evidence from different sources, including experiments records in the public protein database Swiss-Prot, literature, conserved domain search and sequence alignment among orthologous genes. Combing with predictions from the-state-of-the-art TIS predictor MED-Start/MED-StartPlus (in release 1.0 & 1.2) and TriTISA (since release 1.4) and annotations on potential regulatory signals, the database can serve as a refined annotation resource for the public database RefSeq.

Abbreviations: ProTISA

Resource Type: database, data or information resource

Defining Citation: [PMID:17942412](#)

Keywords: translation initiation site, annotation, genome

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ProTISA

Resource ID: SCR_002138

Alternate IDs: OMICS_01871

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260819T044040+0000

Ratings and Alerts

No rating or validation information has been found for ProTISA.

No alerts have been found for ProTISA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Wang P, et al. (2025) Deciphering gene redundancy in prokaryotic genomes provides evolutionary insights for pathogenicity and its roles in clinical infections. Nature communications, 16(1), 10797.