

# Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

## ProTISA

RRID:SCR\_002138

Type: Tool

### Proper Citation

ProTISA (RRID:SCR\_002138)

### Resource Information

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

**Proper Citation:** ProTISA (RRID:SCR\_002138)

**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:** data or information resource, database

**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:** 20260821T193637+0000

### Ratings and Alerts

No rating or validation information has been found for ProTISA.

No alerts have been found for ProTISA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.