

Resource Summary Report

Generated by [dkNET](#) on Aug 15, 2026

LEGER: the post-genome Database for Listeria Research

RRID:SCR_007760

Type: Tool

Proper Citation

LEGER: the post-genome Database for Listeria Research (RRID:SCR_007760)

Resource Information

URL: <https://leger2.helmholtz-hzi.de/cgi-bin/expLeger.pl>

Proper Citation: LEGER: the post-genome Database for Listeria Research (RRID:SCR_007760)

Description: Knowledge database and visualization tool for comparative genomics of pathogenic and non-pathogenic Listeria species. Provides information on gene functions (as annotated or supposed by literature from homologous organisms), protein expression levels under defined experimental conditions, subcellular localization of proteins (expected and/or experimentally validated), biological meaning of genes and proteins based on KEGG, InterPro and Gene Ontology.

Synonyms: Proteome Database LEGER

Resource Type: data or information resource, database

Defining Citation: [PMID:16381897](#)

Keywords: Proteome, functional, genome, data, protein, expression, subcellular, localization

Funding: German Bundesministerium für Bildung und Forschung (BMBF)

Availability: Free, Freely available

Resource Name: LEGER: the post-genome Database for Listeria Research

Resource ID: SCR_007760

Alternate IDs: nif-0000-03077

Record Creation Time: 20220129T080243+0000

Ratings and Alerts

No rating or validation information has been found for LEGER: the post-genome Database for Listeria Research.

No alerts have been found for LEGER: the post-genome Database for Listeria Research.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

McLaughlin HP, et al. (2012) A putative P-type ATPase required for virulence and resistance to haem toxicity in *Listeria monocytogenes*. PloS one, 7(2), e30928.

Dieterich G, et al. (2006) LEGER: knowledge database and visualization tool for comparative genomics of pathogenic and non-pathogenic *Listeria* species. Nucleic acids research, 34(Database issue), D402.