

# Resource Summary Report

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## DOLOP: A Database of Bacterial Lipoproteins

RRID:SCR\_013487

Type: Tool

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### Proper Citation

DOLOP: A Database of Bacterial Lipoproteins (RRID:SCR\_013487)

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### Resource Information

**URL:** <http://www.mrc-lmb.cam.ac.uk/genomes/dolop/>

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**Description:** DOLOP is an exclusive knowledge base for bacterial lipoproteins by processing information from 510 entries to provide a list of 199 distinct lipoproteins with relevant links to molecular details. Features include functional classification, predictive algorithm for query sequences, primary sequence analysis and lists of predicted lipoproteins from 43 completed bacterial genomes along with interactive information exchange facility. This website along will have additional information on the biosynthetic pathway, supplementary material and other related figures. DOLOP also contains information and links to molecular details for about 278 distinct lipoproteins and predicted lipoproteins from 234 completely sequenced bacterial genomes. Additionally, the website features a tool that applies a predictive algorithm to identify the presence or absence of the lipoprotein signal sequence in a user-given sequence. The experimentally verified lipoproteins have been classified into different functional classes and more importantly functional domain assignments using hidden Markov models from the SUPERFAMILY database that have been provided for the predicted lipoproteins. Other features include: primary sequence analysis, signal sequence analysis, and search facility and information exchange facility to allow researchers to exchange results on newly characterized lipoproteins.

**Synonyms:** DOLOP

**Resource Type:** data or information resource, data repository, database, service resource, storage service resource

**Keywords:** figure, functional, algorithm, analysis, bacterial, biosynthetic, classification, genome, lipid, lipoprotein, modification, molecular, molecule, pathogenesis, predictive, primary, prokaryote, query, sequence, signal

**Resource Name:** DOLOP: A Database of Bacterial Lipoproteins

**Resource ID:** SCR\_013487

**Alternate IDs:** nif-0000-21124

**Record Creation Time:** 20220129T080316+0000

**Record Last Update:** 20260905T132736+0000

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## Ratings and Alerts

No rating or validation information has been found for DOLOP: A Database of Bacterial Lipoproteins.

No alerts have been found for DOLOP: A Database of Bacterial Lipoproteins.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Nicchi S, et al. (2021) Decorating the surface of Escherichia coli with bacterial lipoproteins: a comparative analysis of different display systems. Microbial cell factories, 20(1), 33.

Knoppová J, et al. (2021) The Photosystem II Assembly Factor Ycf48 from the Cyanobacterium Synechocystis sp. PCC 6803 Is Lipidated Using an Atypical Lipobox Sequence. International journal of molecular sciences, 22(7).

Xue RY, et al. (2019) Synthetic Lipopeptide Enhances Protective Immunity Against Helicobacter pylori Infection. Frontiers in immunology, 10, 1372.

Acuña-Amador L, et al. (2018) Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of Porphyromonas gingivalis reference strains. BMC genomics, 19(1), 54.

Gasparini G, et al. (2018) Outer Membrane Vesicles (OMV)-based and Proteomics-driven Antigen Selection Identifies Novel Factors Contributing to Bordetella pertussis Adhesion to Epithelial Cells. Molecular & cellular proteomics : MCP, 17(2), 205.

Subedi R, et al. (2018) Genomic analyses reveal two distinct lineages of Corynebacterium ulcerans strains. New microbes and new infections, 25, 7.

Zhao L, et al. (2017) Deletion of the vacJ gene affects the biology and virulence in Haemophilus parasuis serovar 5. Gene, 603, 42.

González LJ, et al. (2016) Membrane anchoring stabilizes and favors secretion of New Delhi metallo- $\beta$ -lactamase. *Nature chemical biology*, 12(7), 516.

Scuotto A, et al. (2016) In silico mining and characterization of bifidobacterial lipoprotein with CHAP domain secreted in an aggregated form. *International journal of biological macromolecules*, 82, 653.

Méndez JA, et al. (2015) Quantitative proteomic analysis of host-pathogen interactions: a study of *Acinetobacter baumannii* responses to host airways. *BMC genomics*, 16(1), 422.

Hu X, et al. (2015) Identification and characterization of a novel stress-responsive outer membrane protein Lip40 from *Actinobacillus pleuropneumoniae*. *BMC biotechnology*, 15, 106.

Ercoli G, et al. (2015) LytM proteins play a crucial role in cell separation, outer membrane composition, and pathogenesis in nontypeable *Haemophilus influenzae*. *mBio*, 6(2), e02575.

Frye SA, et al. (2015) The Inner Membrane Protein PilG Interacts with DNA and the Secretin PilQ in Transformation. *PloS one*, 10(8), e0134954.

Karlsen OA, et al. (2011) *Methylococcus capsulatus* (Bath) from genome to protein function, and vice versa. *Methods in enzymology*, 495, 63.

Skultety L, et al. (2011) Proteomic comparison of virulent phase I and avirulent phase II of *Coxiella burnetii*, the causative agent of Q fever. *Journal of proteomics*, 74(10), 1974.

Callewaert L, et al. (2008) A new family of lysozyme inhibitors contributing to lysozyme tolerance in gram-negative bacteria. *PLoS pathogens*, 4(3), e1000019.