

Resource Summary Report

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Lipase Engineering Database

RRID:SCR_007762

Type: Tool

Proper Citation

Lipase Engineering Database (RRID:SCR_007762)

Resource Information

URL: <http://www.led.uni-stuttgart.de/>

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Description: Database that integrates information on sequence and structure of lipases and related proteins sharing the same a/b hydrolase fold to facilitate protein engineering. Users can browse the database by classification, organism, hierarchic tree, and structure. They can also perform homology searches against the lipase database, and query the Lipase Engineering Database using SQL.

Abbreviations: Lipase Engineering Database

Synonyms: The Lipase Engineering Database

Resource Type: data or information resource, database

Resource Name: Lipase Engineering Database

Resource ID: SCR_007762

Alternate IDs: nif-0000-03084

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260801T191006+0000

Ratings and Alerts

No rating or validation information has been found for Lipase Engineering Database.

No alerts have been found for Lipase Engineering Database.

Data and Source Information

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Zhao J-X, et al. (2025) Investigation of the genetic diversity of gut mycobiota of the wild and laboratory mice. *Microbiology spectrum*, 13(5), e0284024.

Sun G, et al. (2023) Comparative genomics of five *Valsa* species gives insights on their pathogenicity evolution. *G3 (Bethesda, Md.)*, 13(2).

Iwata M, et al. (2021) Omics analyses and biochemical study of *Phlebiopsis gigantea* elucidate its degradation strategy of wood extractives. *Scientific reports*, 11(1), 12528.

Tan Y, et al. (2021) An extracellular lipase from *Amycolatopsis mediterranei* is a cutinase with plastic degrading activity. *Computational and structural biotechnology journal*, 19, 869.

Ozketen AC, et al. (2020) In-depth secretome analysis of *Puccinia striiformis* f. sp. *tritici* in infected wheat uncovers effector functions. *Bioscience reports*, 40(12).

Sankar S, et al. (2020) Less explored plant lipases: Modeling and molecular dynamics simulations of plant lipases in different solvents and temperatures to understand structure-function relationship. *International journal of biological macromolecules*, 164, 3546.

Janfalk Carlsson Å, et al. (2018) Epoxide hydrolysis as a model system for understanding flux through a branched reaction scheme. *IUCrJ*, 5(Pt 3), 269.

Lopez D, et al. (2018) Genome-Wide Analysis of *Corynespora cassicola* Leaf Fall Disease Putative Effectors. *Frontiers in microbiology*, 9, 276.

Knapp DG, et al. (2018) Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. *Scientific reports*, 8(1), 6321.

Peter M, et al. (2016) Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus *Cenococcum geophilum*. *Nature communications*, 7, 12662.

Yang W, et al. (2015) A novel eurythermic and thermostable lipase LipM from *Pseudomonas moraviensis* M9 and its application in the partial hydrolysis of algal oil. *BMC biotechnology*, 15, 94.

Pellegrin C, et al. (2015) Comparative Analysis of Secretomes from Ectomycorrhizal Fungi with an Emphasis on Small-Secreted Proteins. *Frontiers in microbiology*, 6, 1278.

Ufarté L, et al. (2015) Discovery of new protein families and functions: new challenges in functional metagenomics for biotechnologies and microbial ecology. *Frontiers in microbiology*, 6, 563.

Jiménez DJ, et al. (2015) Compositional profile of α / β -hydrolase fold proteins in mangrove soil metagenomes: prevalence of epoxide hydrolases and haloalkane dehalogenases in oil-contaminated sites. *Microbial biotechnology*, 8(3), 604.

Borrelli GM, et al. (2015) Recombinant Lipases and Phospholipases and Their Use as Biocatalysts for Industrial Applications. *International journal of molecular sciences*, 16(9), 20774.

Vaquero ME, et al. (2015) A novel calb-type lipase discovered by fungal genomes mining. *PloS one*, 10(4), e0124882.

Yang Y, et al. (2014) The genome of the myxosporean *Thelohanellus kitauei* shows adaptations to nutrient acquisition within its fish host. *Genome biology and evolution*, 6(12), 3182.

Lai Y, et al. (2014) Comparative genomics and transcriptomics analyses reveal divergent lifestyle features of nematode endoparasitic fungus *Hirsutella minnesotensis*. *Genome biology and evolution*, 6(11), 3077.

Damon C, et al. (2012) Metatranscriptomics reveals the diversity of genes expressed by eukaryotes in forest soils. *PloS one*, 7(1), e28967.

Widmann M, et al. (2010) The isoelectric region of proteins: a systematic analysis. *PloS one*, 5(5), e10546.