

# Resource Summary Report

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## Proteome 2D-PAGE Database

RRID:SCR\_001678

Type: Tool

### Proper Citation

Proteome 2D-PAGE Database (RRID:SCR\_001678)

### Resource Information

**URL:** <https://protein.mpiib-berlin.mpg.de/cgi-bin/pdbs/2d-page/extern/index.cgi>

**Proper Citation:** Proteome 2D-PAGE Database (RRID:SCR\_001678)

**Description:** The Proteome 2D-PAGE Database system for microbial research is a curated database for storing and investigating proteomics data. Software tools are available and for data submission, please contact the Database Curator. Established at the Max Plank Institution for Infection Biology, this system contains four interconnected databases: i.) 2D-PAGE Database: Two dimensional electrophoresis (2-DE) and mass spectrometry of diverse microorganisms and other organisms. This database currently contains 4971 identified spots and 1228 mass peaklists in 44 reference maps representing experiments from 24 different organisms and strains. The data were submitted by 84 Submitters from 24 Institutes and 12 nations. It also contains various software tools that are important in formatting and analyzing gels and mass peaks; software include: \*TopSpot: Scanning the gel, editing the spots and saving the information \*Fragmentation: Fragmentation of the gel image into sections \*MS-Screener: Perl script to compare the similarity of MALDI-PMF peaklists \*MS-Screener update: MS-Screener can be used to compare mass spectra (MALDI-MS(/MS) as well as ESI-MS/MS spectra) on the basis of their peak lists (.dta, .pkm, .pkt, or .txt files), to recalibrate mass spectra, to determine and eliminate exogenous contaminant peaks, and to create matrices for cluster analyses. \*GelCali: Online calibration of the Mr- and pl-axis of 2-DE gels with mathematical regression methods ii.) Isotope Coded Affinity Tag (ICAT)-LC/MS database: Isotope Coded Affinity Tag (ICAT)-LC/MS data for Mycobacterium tuberculosis strain BCG versus H37Rv. iii.) FUNC\_CLASS database: Functional classification of diverse microorganism. This database also integrates genomic, proteomic, and metabolic data. iv.) DIFF database: Presentation of differently regulated proteins obtained by comparative proteomic experiments using computerized gel image analysis.

**Abbreviations:** 2D-PAGE

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

**Keywords:** microbial research, electrophoresis, mass spectrometry, mycobacterium tuberculosis, protein regulation

**Funding:** BMBF 031U107A;  
European Union QLRT-1999-31536;  
European Union QLK2-CT-2001-02018

**Availability:** Free, Freely Available

**Resource Name:** Proteome 2D-PAGE Database

**Resource ID:** SCR\_001678

**Alternate IDs:** nif-0000-02523

**Record Creation Time:** 20220129T080208+0000

**Record Last Update:** 20260807T042529+0000

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## Ratings and Alerts

No rating or validation information has been found for Proteome 2D-PAGE Database.

No alerts have been found for Proteome 2D-PAGE Database.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Jalan S, et al. (2015) Network Topologies Decoding Cervical Cancer. PloS one, 10(8), e0135183.

Magdeldin S, et al. (2014) Basics and recent advances of two dimensional-polyacrylamide gel electrophoresis. Clinical proteomics, 11(1), 16.

Lewinsohn DM, et al. (2013) Human Mycobacterium tuberculosis CD8 T Cell Antigens/Epitopes Identified by a Proteomic Peptide Library. PloS one, 8(6), e67016.

Wolfe LM, et al. (2010) Proteomic definition of the cell wall of Mycobacterium tuberculosis. Journal of proteome research, 9(11), 5816.

Rison SCG, et al. (2007) Experimental determination of translational starts using peptide mass mapping and tandem mass spectrometry within the proteome of Mycobacterium tuberculosis. Microbiology (Reading, England), 153(Pt 2), 521.