



the database for phenotypic data on prokaryotes

Lorenz Reimer, Joaquim Sardà Carbasse, Adam Podstawka, Jörg Overmann
Leibniz-Institut DSMZ - Deutsche Sammlung von Mikroorganismen und Zellkulturen

Short description of the project

BacDive - The Bacterial Diversity Metadatabase provides strain-linked information covering the multifarious aspects of microbial biodiversity:

- Taxonomic classification (213K entries)
- Morphology & physiology (349K entries)
- Cultivation & growth condition (133K entries)
- Origin & natural habitat (138K entries)
- Sequences (259K entries)
- Strain availability (83K entries)

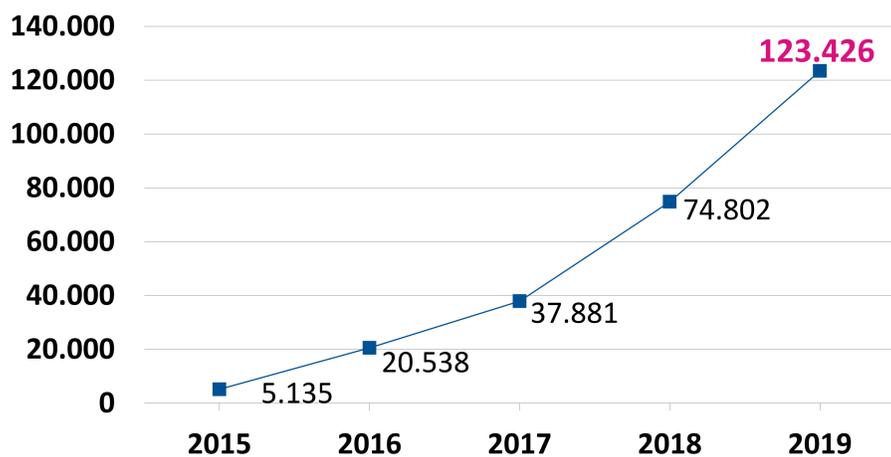
on **81.8K** bacterial and archaeal strains

de.NBI services

6640 manually annotated species descriptions enabling systematic analysis of phenotypic data.

World's largest API® test data collection with currently **27,634** API® tests providing physiological information for **15,357** bacterial strains.

Development of unique visitors per year



Web statistics collected and analyzed with Matomo Analytics

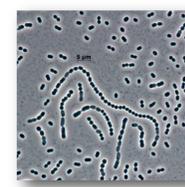
General information on the project

Joaquim Sardà Carbasse and Lorenz Reimer are funded by the de.NBI grant (100% FTE each). Up to four additional scientists and one technician are involved in this project with approx. 10% FTE each, without payment from the de.NBI grant.

Progress report

Content increase of 36%

- Data ingest of 19,505 strains from CCUG including
 - 19,877 API® tests
 - 4,614 fatty acid profiles
- Over **1500** new pictures showing colony morphology, cell arrangement and sporulation

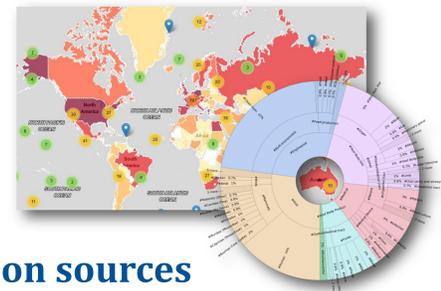


New interactive user feedback system

- Data field related feedback
- Proposal of database changes

Isolation Source Search

- Systematic analysis
- World map
- IS #tag distribution in Krona Plots



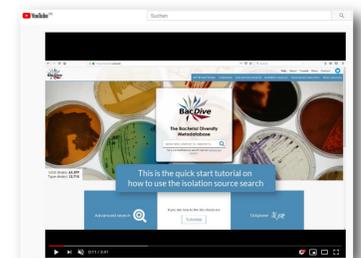
Σ 45,974 annotated isolation sources

de.NBI Training and education

Online video tutorials

Short introductions into functionalities of BacDive.

Watch our short online tutorials



Publications

1. Reimer, L. C., Vetcinova, A., Sardà Carbasse, J., Söhngen, C., Gleim, D., Ebeling, C., & Overmann, J. **BacDive in 2019: bacterial phenotypic data for High-throughput biodiversity analysis.** *Nucleic Acids Research (database issue 2018)*. <https://doi.org/10.1093/nar/gky879>
2. Reimer LC, Söhngen C, Vetcinova A, Overmann J. **Mobilization and integration of bacterial phenotypic data - Enabling next generation biodiversity analysis through the BacDive metadatabase.** *J Biotechnol* . 2017;(February); <http://dx.doi.org/10.1016/j.jbiotec.2017.05.004>