



Leibniz Institute
DSMZ-German Collection
of Microorganisms
and Cell Cultures GmbH



DIGITAL COLLECTION OF THE DSMZ

Access to well-structured digital information about living organisms is of central importance for the future of biological and medical science. As one of the biggest biological resource centres in the world, the Leibniz Institute DSMZ strives to improve the access to digital data by establishing a data centre for collection-associated research data.

- **Genomic, taxonomic and nomenclatural data for genome-based taxonomy (TYGS)**
- **Prokaryotic names (PNU/LPSN)**
- **Prokaryotic phenotypic data (BacDive)**

FUTURE EXTENSION OF THE DIGITAL COLLECTION

Still, a lot of valuable research data is hidden in the internal files of collections. Therefore the Leibniz Institute DSMZ has committed itself to the stepwise mobilization of these data and will establish a data centre for systematic access to standardized research data in biological resource centres. By further fostering the established BacDive, TYGS and PNU/LPSN services a plethora of new data will be made available for research in the respective areas of expertise such as high-quality phenotypic data on fungi, viruses, algae and cell lines, complex omics data and much more.

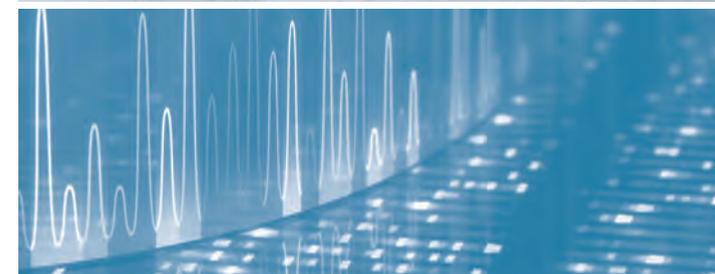
CONTACT

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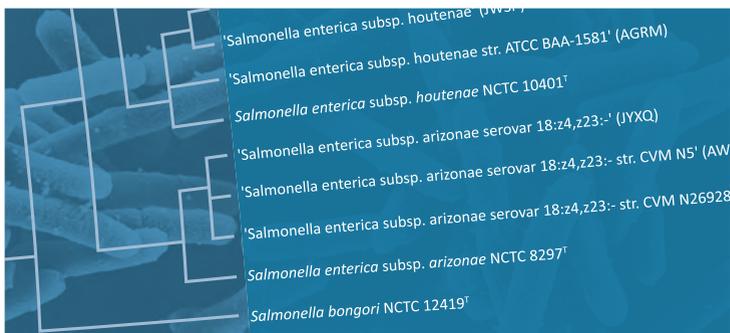
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home of more than 73,000 biological resources

DIGITAL COLLECTION



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GENOME-BASED TAXONOMY

The **Type (Strain) Genome Server (TYGS)**, released in 2019, is a user-friendly high-throughput **web server for genome-based prokaryotic taxonomy**, connected to a large, continuously growing database of genomic, taxonomic and nomenclatural information (Nat Commun 10:2182).

Nomenclatural types form the backbone of prokaryotic systematics, and comparisons with established types of species and subspecies are mandatory when classifying novel strains. However, even if a type (strain) genome sequence is publicly available, it might be difficult to verify its origin, especially in a complex situation of different synonyms and strain deposits.

Here, the TYGS database fills a gap by currently **providing already 11,000 type (strain) genomes and associated data** as the basis for its downstream bioinformatic analyses including state-of-the-art approaches for genome-based phylogenetic inference and (sub-)species delineation.

For more information visit: tygs.dsmz.de

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PROKARYOTIC NAMES

Since decades the Leibniz Institute DSMZ offers the service **Prokaryotic Nomenclature up-to-date (PNU)**, which provides a compilation of all names of Bacteria and Archaea that have been validly published according to the International Code of Nomenclature of Prokaryotes. In February 2020 this database was merged with the renowned **List of Prokaryotic names with Standing in Nomenclature (LPSN)**.

The combined database tracks all changes in the nomenclature of Prokaryotes by analysing publications in the International Journal of Systematic and Evolutionary Microbiology (IJSEM) and elsewhere. Data can be accessed by browsing the hierarchy, by using the advanced search, or by downloading a table containing the complete list of validly published names. **LPSN includes information on names, synonyms, publications, nomenclatural types and sequences.** For programmatic access, a web service is available, which is free after registration.

For more information visit: lpsn.dsmz.de

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PROKARYOTIC PHENOTYPIC DATA

The **Bacterial Metadatabase BacDive** is the worldwide largest database for standardized bacterial phenotypic information. *BacDive* offers data on over 80,000 bacterial and archaeal strains, including 14,091 type strains and thereby **covers approx. 90% of the described diversity.** Phenotypic data is mobilized from collections (e.g. CABI, CCUG, CIP, DSMZ) and enriched with data from so far over 6,000 species descriptions from literature.

Within over 600 data fields covering the topics taxonomy, morphology, physiology, origin, molecular data and cultivation conditions the database offers systematic access to over 970,000 data points. Thereby *BacDive* allows to **find bacterial strains based on their traits**, e.g. metabolite utilization, habitat or growth condition.

With currently 27,634 API® tests for 15,357 strains, *BacDive* offers the **worldwide largest API® test collection**, which can be queried using the API test finder tool.

For more information visit: bacdive.dsmz.de

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