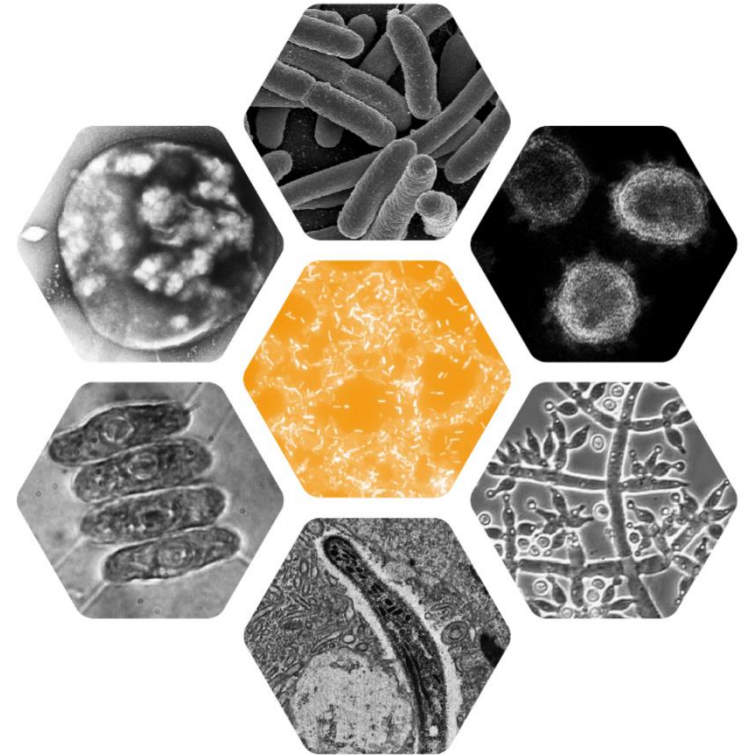


NFDI4Microbiota

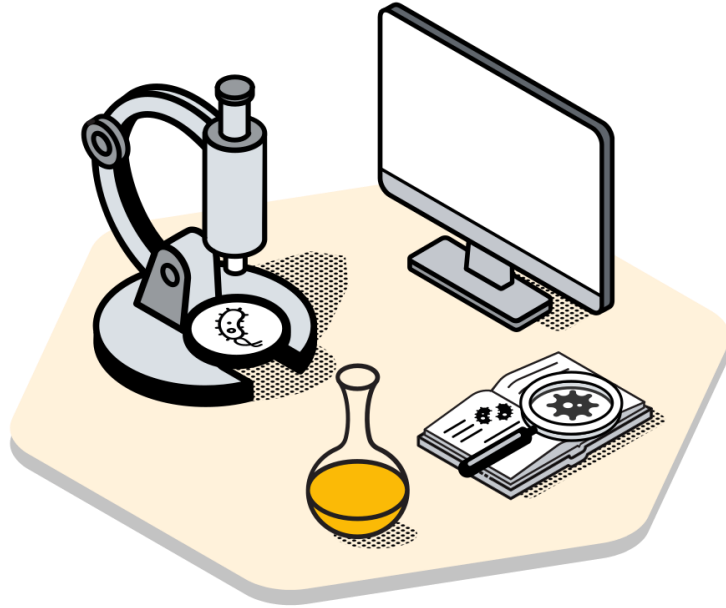
Making Microbiology Data FAIR and Open

Konrad Förstner

2024-06-05 VAAM & DGHM conference 2024, Würzburg

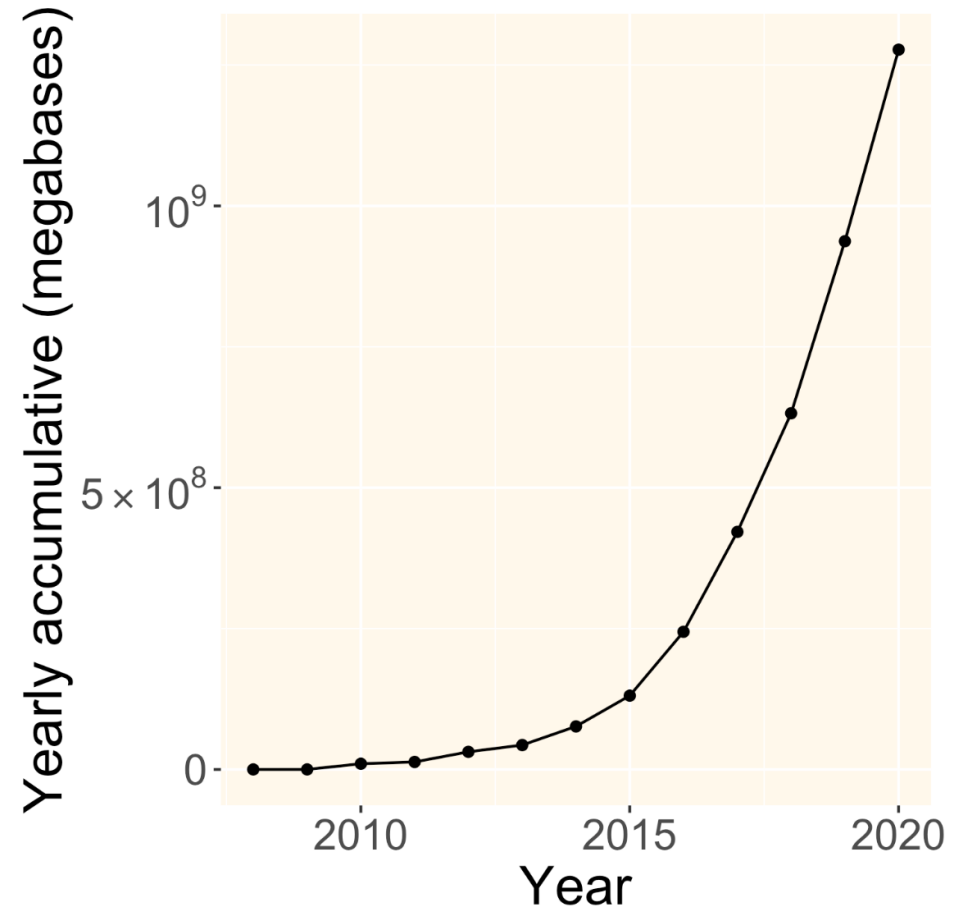


Situation in Microbiology – rapidly growing data production



Data types include:

- Omics
- Imaging
- Taxonomic data
- Subdomain-specific data, etc.



Metagenomic sequencing data submitted to SRA

SCIENTIFIC DATA

Amended: /

OPEN Comment: The FAIR Guiding Principles for scientific data management and stewardship

SUBJECT CATEGORIES
» Research data
» Publication characteristics

Mark D. Wilkinson *et al.*[#]

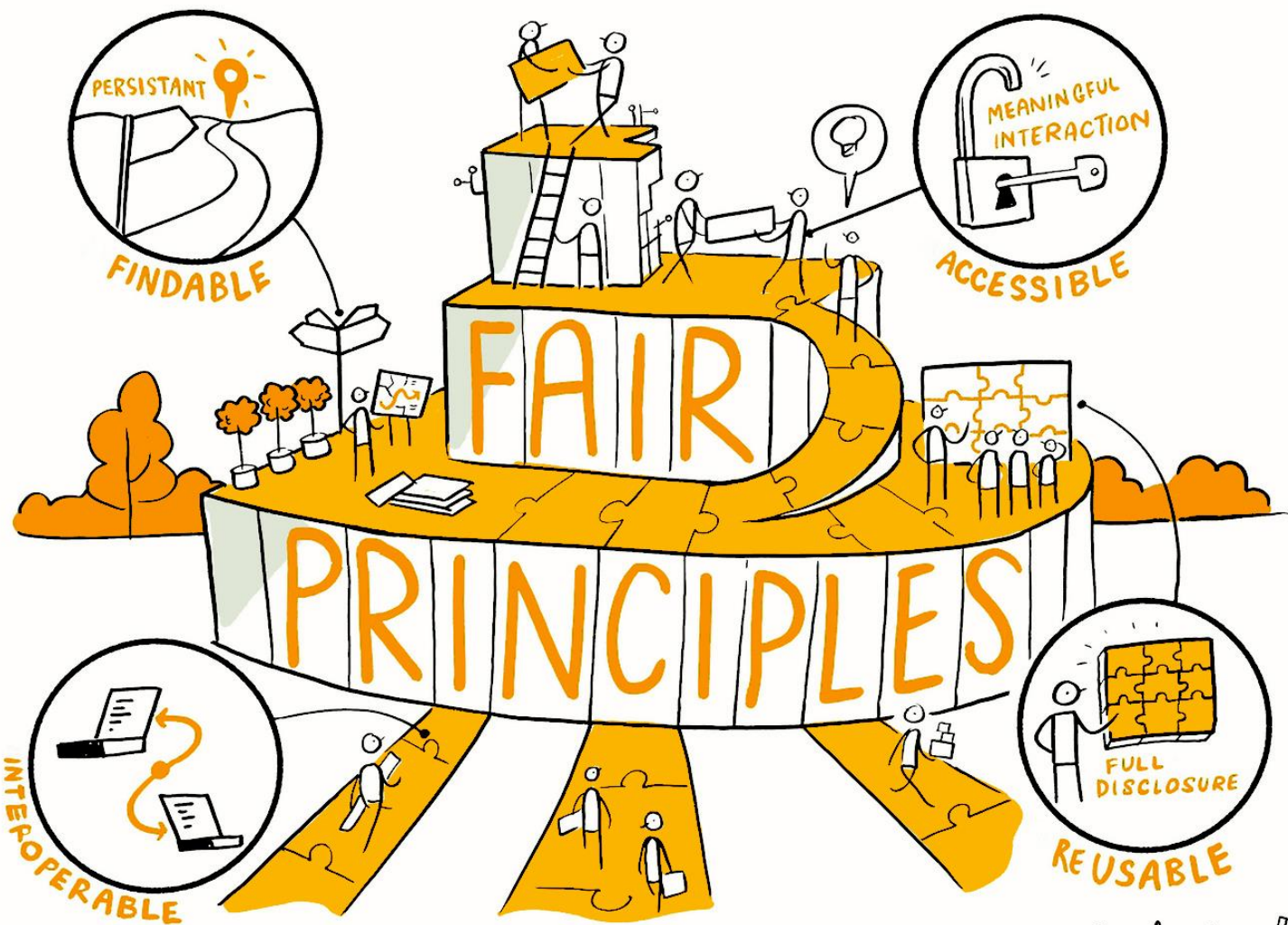
There is an urgent need to improve the infrastructure supporting the reuse of scholarly data set of stakeholders—representing academia, industry, funding agencies, and scholarly publishers—to as the FAIR Data Principles. The intent is that these may act as a guideline for those who enhance the reusability of their data holdings. Distinct from peer initiatives that focus on enhancing the reusability of their data holdings, the FAIR Principles put specific emphasis on enhancing the ability of machines to automatically find and use the data, in addition to supporting its reuse by individuals. This Comment is a formal publication of the FAIR Principles, and includes the rationale behind them, and some implementations in the community.

Received: 10 December 2015

Accepted: 12 February 2016

Published: 15 March 2016

Wilkinson, M., Dumontier, M., Aalbersberg, I. et al. The FAIR Guiding Principles for scientific data management and stewardship. *Sci Data* 3, 160018 (2016). <https://doi.org/10.1038/sdata.2016.18>



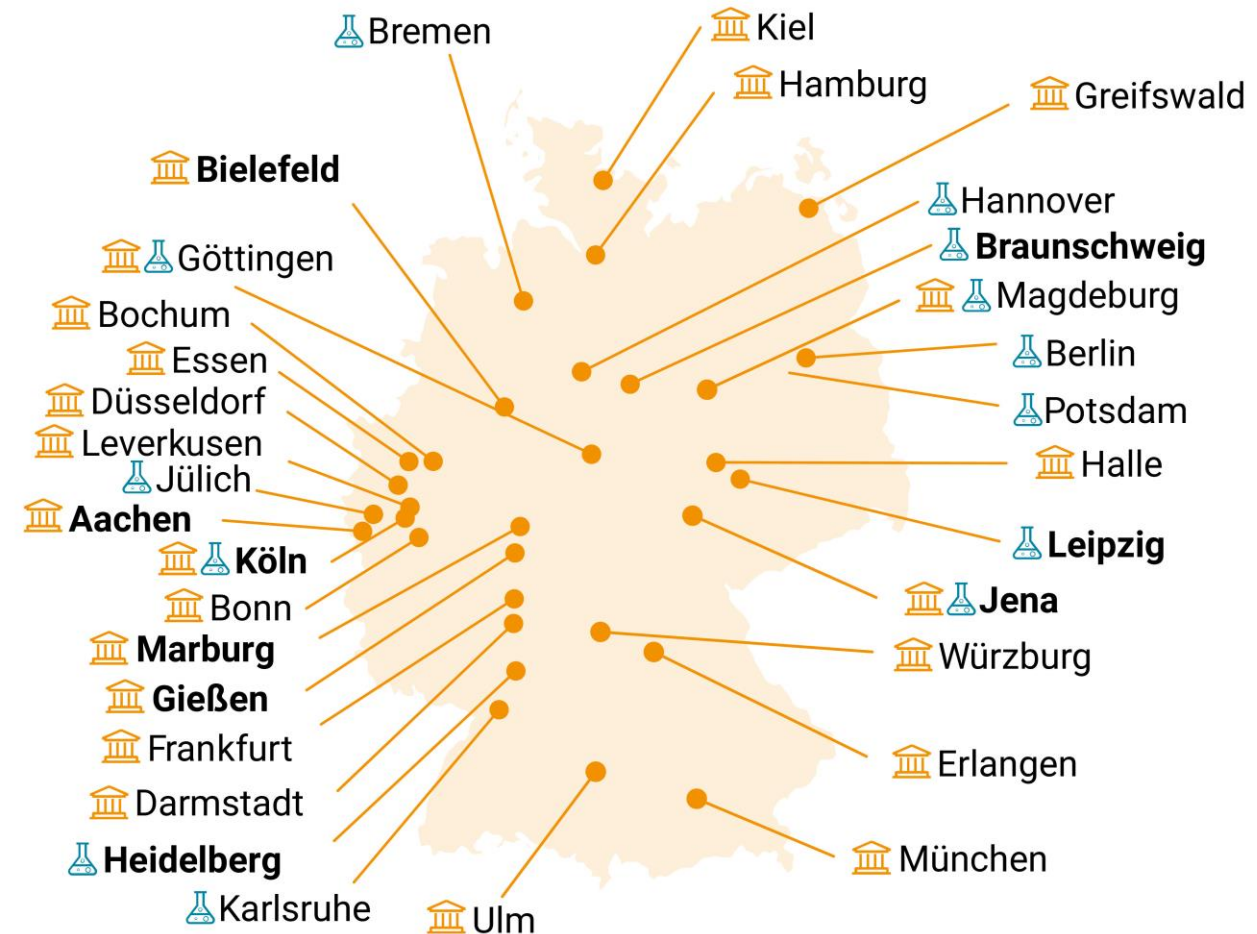
Scriberia

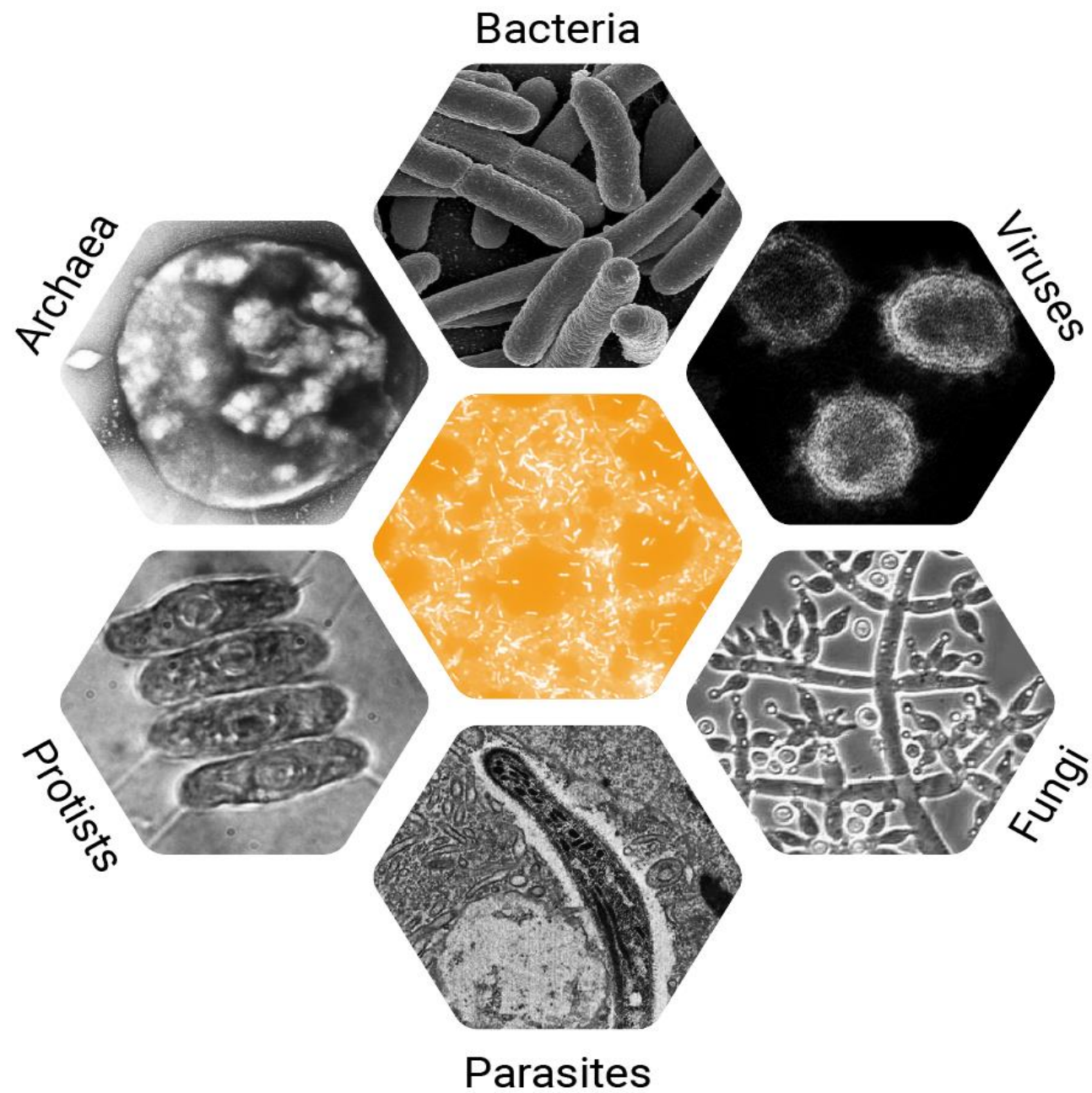
Adapted from:
The Turing Way Community, & Scriberia. (2022). Illustrations from The Turing Way: Shared under CC-BY 4.0 for reuse. Zenodo. <https://doi.org/10.5281/zenodo.6821117>

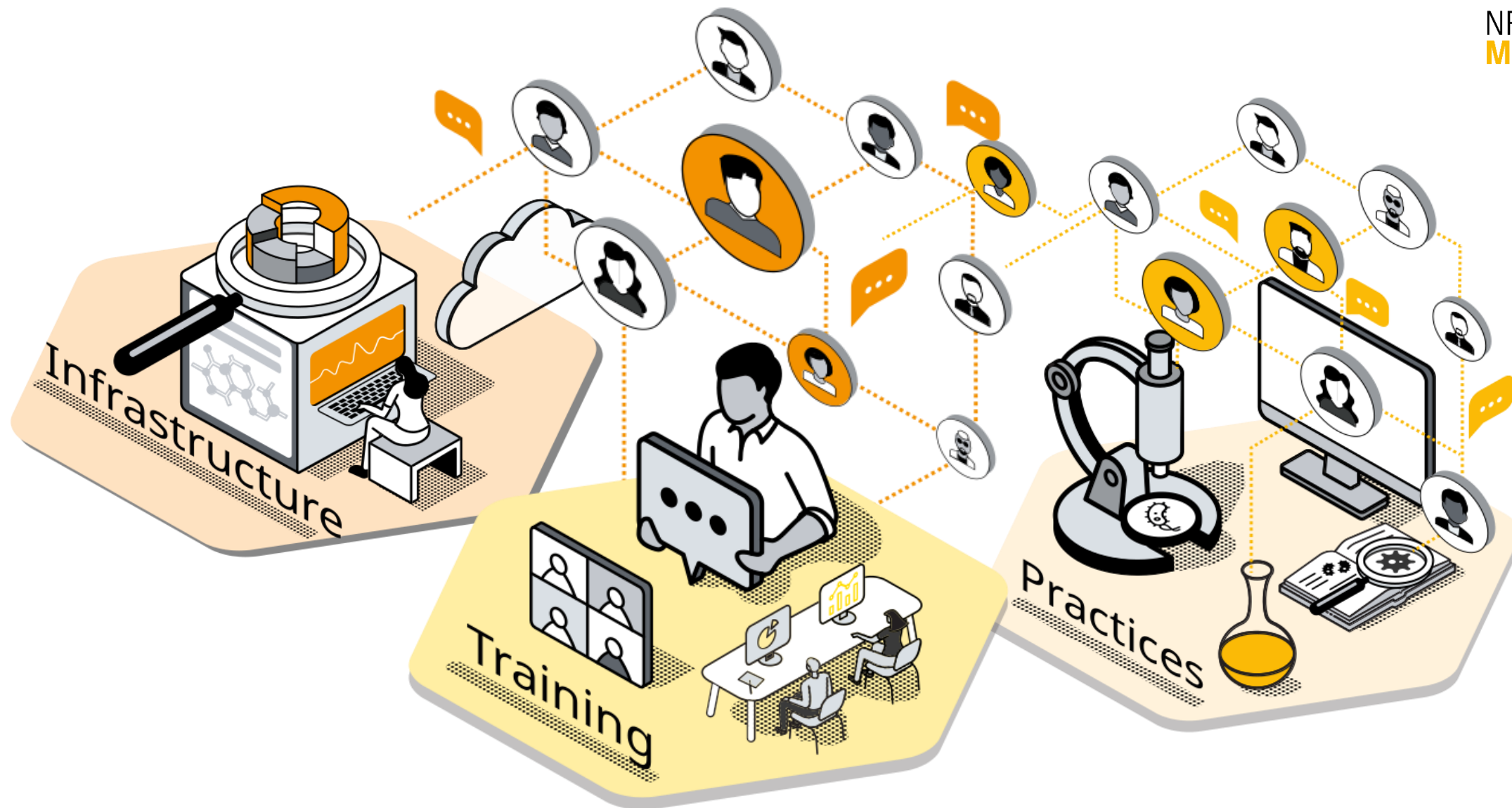
National Research Data Infrastructure for Microbiota Research

Vision: Enabling microbiologists to easily translate research data into a deep understanding of microbial species and their interactions on a molecular level

Mission: Becoming a central hub to support researchers from the German microbiology research community with data access, data analysis, (meta)data standards and training







For example:

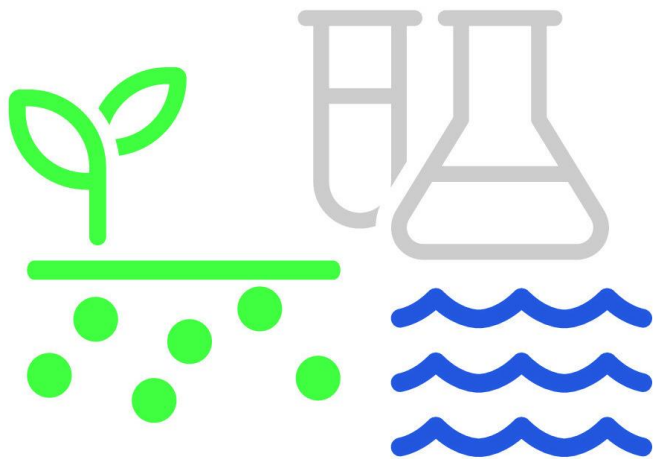
- Media composition
- pH value
- Temperature
- Geo location
- Sample depth

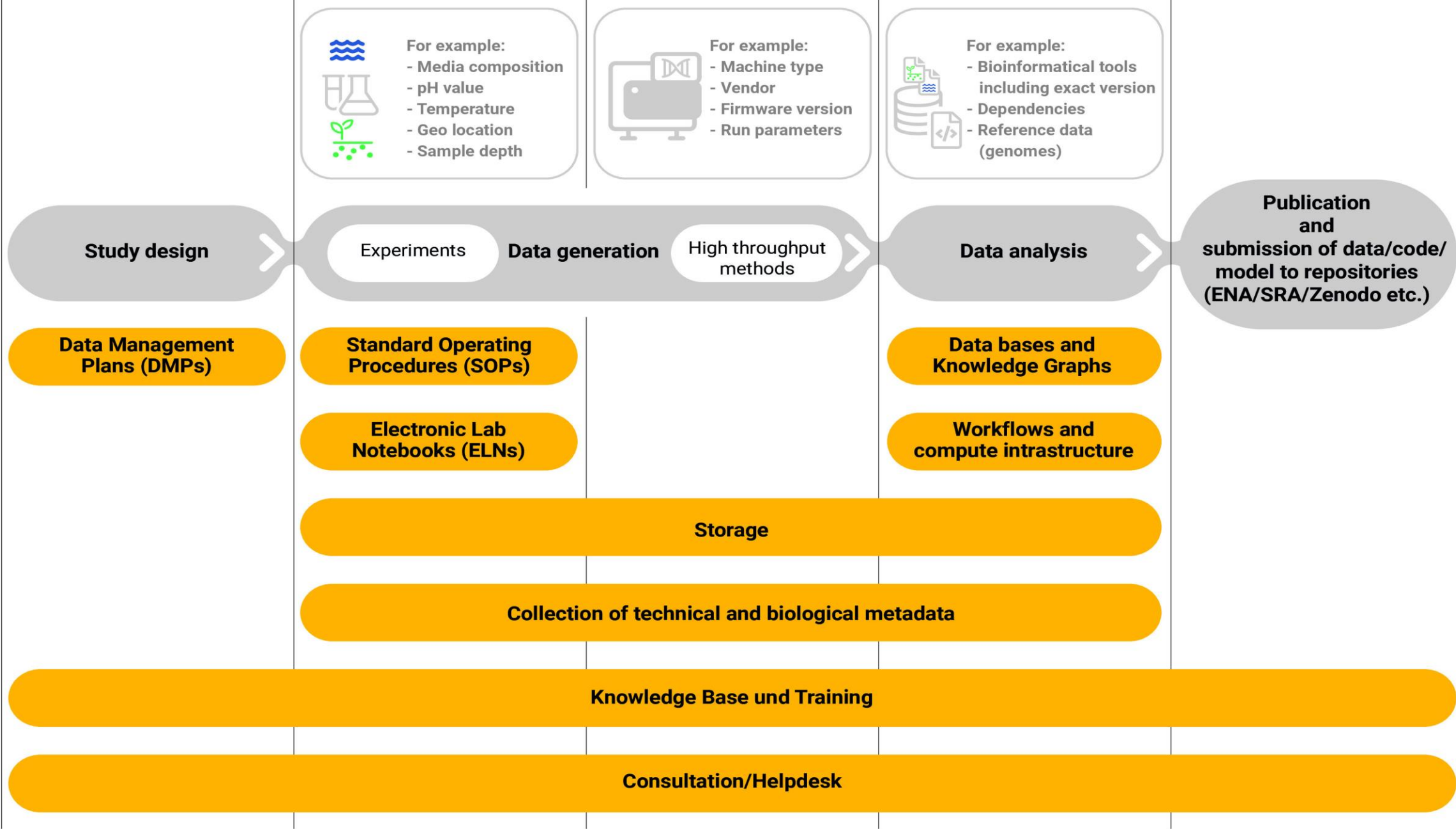
For example:

- Machine type
- Vendor
- Firmware version
- Run parameters

For example:

- Bioinformatical tools including exact version
- Dependencies
- Reference data (genomes)





NFDI4 MICROBIOTA



SAVE THE DATE Annual Conference

When? December 3-4, 2024

Where? Leipzig, Germany

What?

- Panel discussion
- Keynotes
- Workshops
- and much more

More information
and registration



[https://nfdi4microbiota.de/
newsroom/events.html](https://nfdi4microbiota.de/newsroom/events.html)

Thank you!

In collaboration with:



Funded by



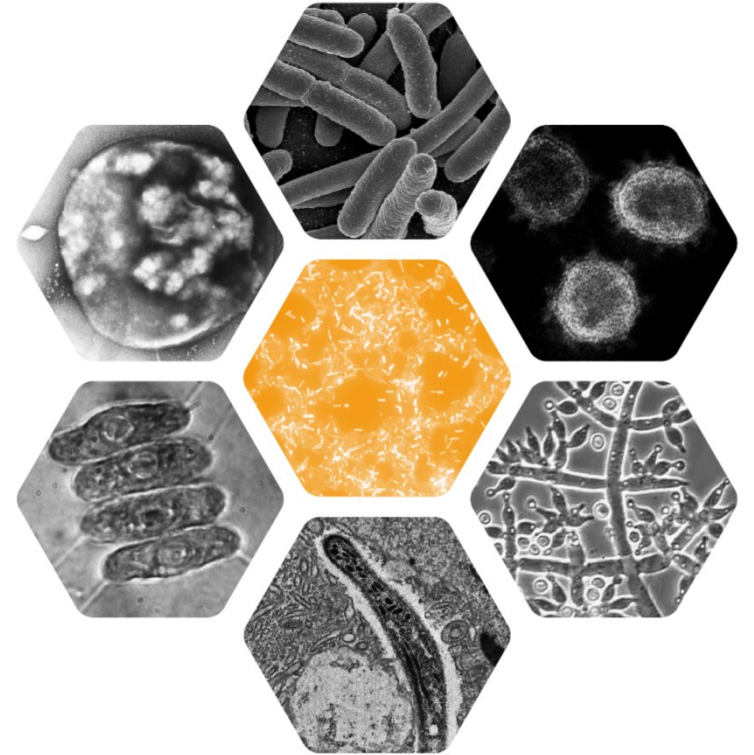
Funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) – Project number 460129525



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NFDI4**Microbiota**

N4M Analytical Services - generating high quality and FAIR computational microbiological data

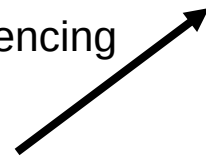
Common Data types in Microbiota research

- Microbial MetaOmics and Omics
 - (Meta)Genomics
 - (Meta)Transcriptomics
 - (Meta)Proteomics
 - (Meta)Metabolomics
- Amplicon (16S, 18S, ITS,...)
- Imaging data

Computational Metagenomics



Sequencing



GAGAGATATTTAGACCCACGATGATCC
AGCGATTTGACACGATGATAG
AGCGATTTGACACGGAGAGTATAGAA
AGCGATTTGTAGTATATCGAGGGG

Profiling



Bacteria 0.7
Archaea 0.3
Proteobacteria 0.2
Firmicutes 0.05
...

Assembly



```
[...]sdATGACGATTCCGAAACACGAGCCGCGGAGGCTTCGATCGGGCGATCGAGCATACGGGGGCGTTTCCC
CGGCCACTTTCGATCAGTGGTTTCGGGGAGTTCAGTTTCGATGATTCGACGACGGCTCTCGACGCTCGG
CGAGCAGCAGCGGCCATAGCGCCGACGACCTCGCGGGCCCGCCATCGCCCTCGCCGCTCGCTC
GGATCCCGTGAAGATGAGCACGAGCGCGCTGACCTCGCCGCTCGC
```

```
CCTCGACGGGGTGCCTCGTTGGCCCGTTCGGCTCCTTTGGAGCACGGCGCTCGCTGGATCTCGGC
```

```
GCTCTTCTCTCGTGAACGGCTCAGGAAATCGGGAGGTCGTTCCGCCGAAACCGCTCGCCGCTCGG
TAGAAGAACCGGAGGAGCCTCGTTCGACCGCCCGGCTCGGGGAAACGATCTCCGGGTTCTTCGGA
GATCGTCTCAGACGCTGCGGAGCGACCGGGCACCTCGGGGCGCACGAGCGGAGCGGGATACTC
```

```
GCTCGCTCGACGCCCGCATGATCTCGAACCGCTCGGCGCCGAAACGGTTTCGACCCGGGAGCATC
GATGGTGTGTTCCGGGGATGAGCTTGAAGCTACGCGCCCGCGGTTCTCGACCGCAAGCGACGCGGC
```

```
GTACGTCGAGGAGCAGCACCTCGTCCACTGCGGGAGAGCGGGCCCTCGACGCGACGCCGACCG
CGACGACCTGTGGGGTTGACGCCCTTGTGGCTCCGGCCGAAAGAACTCGGCGCCGCGCTCGAC
CGGGGATCCGGGTCATGCCGCCGACGAGGACACCGTGTGACGCGGAGACGGGAGCTTGGCGTC
CCGAGCTCGCGCGACAGACGTCGATGGTCCGGCGATGAGGCCCTCGACAGCATCTCGAGCTCTTGC
GCCGATCGTCCGCTCGAGGTGGAGCGGCCCTCGCCGGGGCCGACGGCGATGAAGGGATGTGTATCTC
```

```
GGTCTCGAGCGACGAGAGCTCGTCTCGCTTCCGCTTCCGGCCGCTTTCGAGCCGCTCGAGCCCATG
CGATCCGGGCGAGATCGATCGCGCTTCCCTCGAACTCGTCGCGAGCAGGTCGATGATCCGCTGGT
CGAAGTCTCGCCGCGAGGTGGTGGTCCGCCGCTCGCTTGAAGCTGAAAGACCCGCTCGGATCTC
GAGGATCGAGATATCGAACGTGCTCCGCCGAGATGAGACCGGATGCTCGGCTTCACTTGTG [...]x'
```

Genome & Taxonomic 'binning'



```
[...]sdATGACGATTCCGAAACACGAGCCGCGGAGGCTTCGATCGGGCGATCGAGCATACGGGGGCGTTTCCC
CGGCCACTTTCGATCAGTGGTTTCGGGGAGTTCAGTTTCGATGATTCGACGACGGCTCTCGACGCTCGG
CGAGCAGCAGCGGCCATAGGGGGCCAGACGCTCGCGGGGCCGCGCATGCGCTCGCCGCTCGCTCCTC
GGATCCCGTGAAGATGAGCACGAGCGCGCTGACCTCGCGCGCTCGC
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```
CCTCGACGGGGTGCCTCGTTGGCCCGTTCGGCTCCTTTGGAGCACGGCGCTCGCTGGATCTCGGC
```

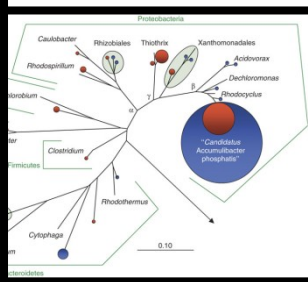
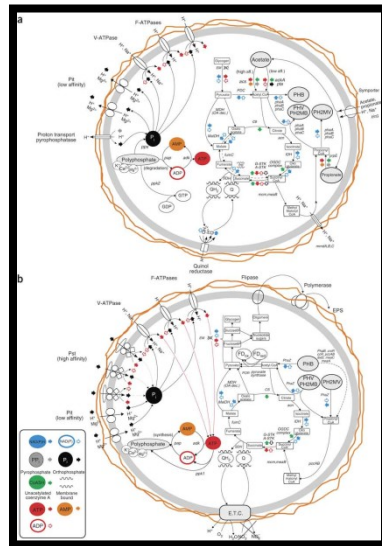
```
GCTCTTCTCTCGTGAACGGCTCAGGAAATCGGGAGGTCGTTCCGCCGAAACCGCTCGCCGCTCGG
TAGAAGAACCGGAGGAGCCTCGTTCGACCGCCGCGGAAAGAACTCGGCGCCGCTCGAC
GATCGTCTCAGACGCTCGCGGAGCGACCGGGCACCTCGGGGCGCACGAGCGGAGCGGGGATACTC
```

```
GCTCGCTCGACGCCCGCATGATCTCGAACCGCTCGGCGCCGAAACGGTTTCGACCCGGGAGCATC
GATGGTGTGTTCCGGGGATGAGCTTGAAGCTACGCGCCCGCGGTTCTCGACCGCAAGCGACGCGGC
```

```
GTACGTCGAGGAGCAGCACCTCGTCCACTGCGGGAGAGCGGGCCCTCGACGCGACGCCGACCG
CGAGCAGCTGTGGGGTTGACGCCCTTGTGGCTCCGGCCGAAAGAACTCGGCGCCGCGCTCGAC
CGGGGATCCGGGTCATGCCGCCGAGGACACCGTGTGACGCGGAGACGGGAGCTTGGCGTCC
CCGAGCTCGCGCGACAGACGTCGATGGTCCGGCGATGAGGCCCTCGACAGCATCTCGAGCTCTTGC
CGCGATCGTCCGCTCGAGGTGGAGCGGCCCTCGCCGGGGCGACGGCGATGAAGGGATGTGTATCTC
```

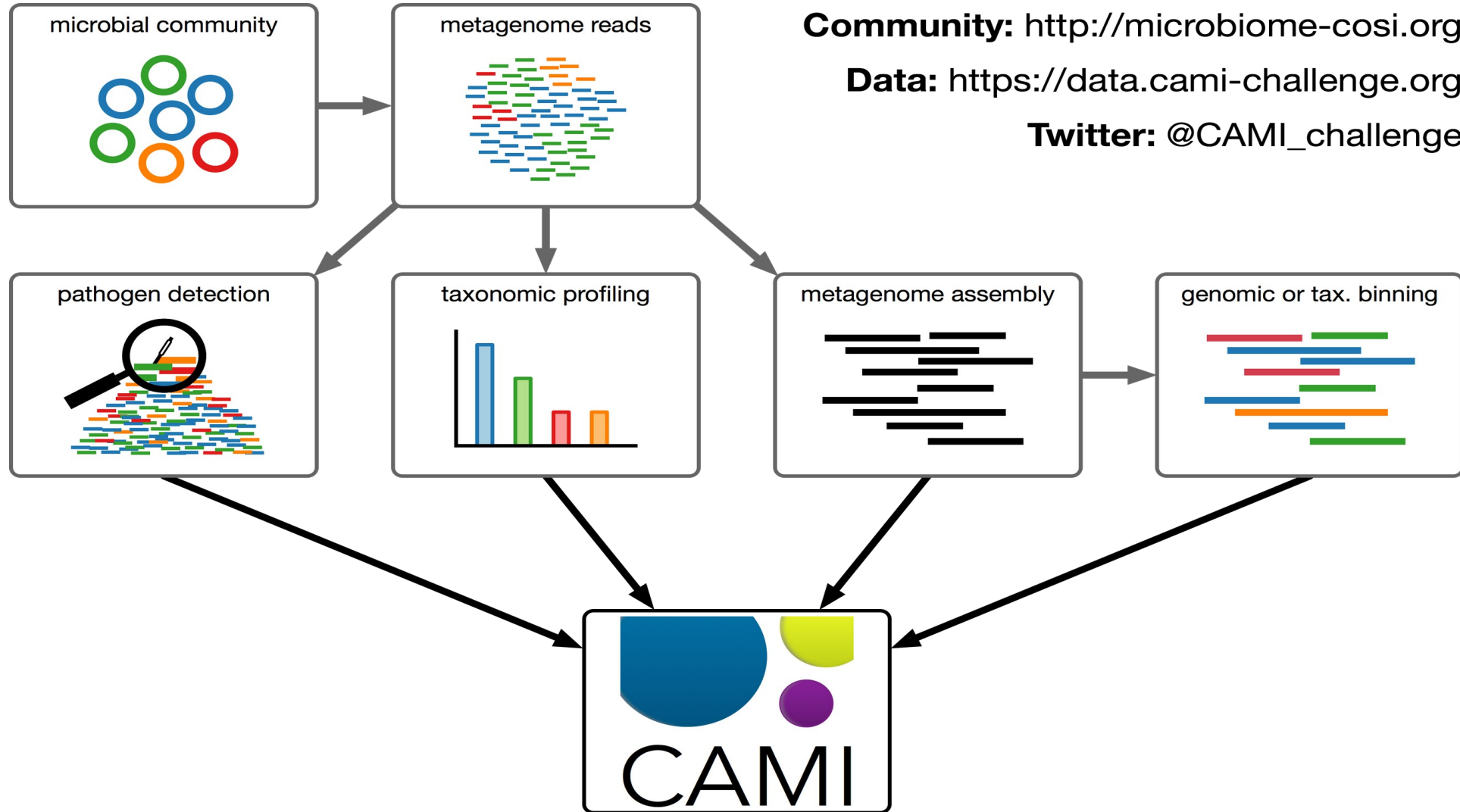
```
GGTCTCGAGCGACGAGAGCTCGTCTCGCTTCCGCTTCCGGCCGCTTTCGAGCCGCTCGACGCCCATG
CGATCCGGGCGAGATCGATCGCGCTTCCCTCGAACTCGTCGCGAGCAGGTCGATGATCCGCTGGT
CGAAGTCTCGCCGCGAGGTGGTGTCCGCCGCTCGCTTGAAGCTGAGCTGAAAGACCCCGCTCGGATCTC
GAGGATCGAGATATCGAACGTGCTCCGCCGAGATGAGACCGGATGCTCGGCTTCACTTGTG [...]
```

Annotation



From Garcia
Martin *et al.*
Nature Biotech.
2006

CAMI Benchmarking Contests Identify Best Practices and Challenges in Metagenome Data Processing



- **Training** (which tools, how to run tools, how to interpret results)
- Environment for installing and running computational workflows (**CloWM**, de.NBI)
- Identifying and Implementing best practice computational workflows
 - **CAMI II**
- System for assessing computational workflows (**CAMI 2 benchmarking platform**)
- **Help desk**

- Hands-on computational workflows for metagenome data analysis
- Nextflow Workshop organized by de.NBI for NFDI4Microbiota in EMBL Heidelberg (November 2023)
- Joint NFDI & de.NBI Metagenomics training course in Bielefeld University (February 2024)
- Joint NFDI & de.NBI Metagenomics training course in HZI Braunschweig (November 2024)



Best Practice Computational workflows

- **nf-core/MAG** workflow including all **CAMI 2 best practice** methods: Flye, MetaHipMer, Metabinner, MetaWRAP, and Ultrabinner

- **Availability:** Available on CloWM, June 2024
- **GitHub:** <https://github.com/hzi-bifo/mag>

nf-core/ 
mag

- **nf-core/Taxprofiler** workflow for taxonomic classification and profiling of shotgun metagenomic data including all CAMI2 best practices

- **Availability:** Available on CloWM, April 2024
- **GitHub:** <https://github.com/nf-core/taxprofiler>

nf-core/ 
taxprofiler

Cloud Workflow Management System



CloWM



CloWM Files Workflows Resources Hesham Almessady

Select Workflow

Filter Workflows Sort Workflows By Alphabetical Latest Release

Test my Workflow

Bismark methylome analysis

Analysis of mouse bisulfite treated, paired end reads using Bismark. 1.0.6 Last Update: 2 days ago

MetaTree

MegaTree is a workflow that creates a Multiple Sequence Alignment (MSA) of amino sequences using Clustal Omega, computes an evolutionary tree with IQ-TREE 2 and finally visualizes the tree and MSA using R/ggtree. 1.0.6 Last Update: a month ago

Meta-Omics-Toolkit

Full pipeline of assembly, binning and many other downstream analysis tasks or individual modules. 0.3.13 Last Update: a month ago

Eggnog mapper

Eggnogmapper is a bioinformatics pipeline for fast functional annotation of novel sequences. It uses precomputed orthologous groups and phylogenies from the eggNOG database to transfer functional information from fine-grained orthologs only. 0.1.2 Last Update: 2 months ago

SPiRE

Workflow used to produce data available on <https://spire.embl.de/> 1.0.2 Last Update: 2 months ago

nf-core/mag + CAMI 2 Best Practices

This pipeline is a modified version of the renowned nf-core/mag workflow, meticulously refined to incorporate best practice tools recognized for their performance in the CAMI2 benchmark. 1.0.3 Last Update: 2 months ago

nf-core/taxprofiler

Bioinformatics best-practice analysis pipeline for taxonomic classification and profiling of shotgun metagenomic data. 1.0.1 Last Update: 2 months ago

Official nf-core taxprofiler workflow

Latest version of the nf-core taxprofiler workflow with updated nextflow_schema.json. Less non working defaults. v1.1.5 Last Update: 2 months ago

CAMISIM

CAMISIM is a software to model abundance distributions of microbial communities and to simulate corresponding shotgun metagenome datasets. 1.0.1 Last Update: 2 months ago

Apscale

Executes Apscale for a folder of .fastq.gz-files. Writes the complete project into the output v0.0.4 Last Update: 2 months ago

DivAssociate

DivAssociate is a workflow implemented in Nextflow to perform a GWAS using GEMMA's [1] Linear Mixed Model algorithm. It uses genotyping data in VCF format and phenotyping data in ISA Tab format compliant to the MIAPPE [2] data model. 0.5.1 Last Update: 5 months ago

GUNC

Genome UNClutterer (GUNC) is a tool for detection of chimerism and contamination in prokaryotic genomes resulting from mis-binning of genomic contigs from unrelated lineages. It does so by applying an entropy based score on taxonomic assignment and contig 0.2.0 Last Update: 5 months ago

CloWM Files Workflows Resources Hesham Almessady

Available Resources

Filter Resources Show private resources

CheckM2 Reference

DIAMOND database that CheckM2 relies on for rapid annotation Source: <https://zenodo.org/records/4626519> 1.0.0 - Resource available Maintainer: Anthony Fullam

GTDB

The Genome Taxonomy Database (GTDB) is an initiative to establish a standardised microbial taxonomy based on genome phylogeny. Source: <https://gtdb.ecogenomic.org/> r214 - Resource available (latest) Maintainer: Daniel Göbel

GUNC GTDB database

GUNC GTDB database Source: https://swifter.embl.de/~fullam/gunc/gunc_db_gtdb95.dmdn.gz r95 - Resource available Maintainer: Mahdi Robbani

GUNC Progenomes database

GUNC Progenomes database Source: https://swifter.embl.de/~fullam/gunc/gunc_db_progenomes2.1.dmdn.gz 2.1 - Resource available Maintainer: Mahdi Robbani

Human/mouse Bismark indices

Bismark bisulfite aligner indices for Ensembl GRCh37 and GRCh38 genomes taken from Illumina Igenomes collection Source: https://support.illumina.com/sequencing/sequencing_software/igenome.html 1.0.0 - Resource available Maintainer: Michael Beckstette

Igenomes_human

The IGenomes are a collection of reference sequences and annotation files for commonly analyzed organisms. This is the Homo_sapiens subset of the collection, containing UCSC/hg19/ UCSC/hg38/ Ensembl/GRCh37/ Ensembl/GRCh38/ Source: https://support.illumina.com/sequencing/sequencing_software/igenome.html 1.0.0 - Resource available Maintainer: Michael Beckstette

UniProtKB/Swiss-Prot sequences

UniProtKB/Swiss-Prot protein sequences in FASTA format. UniProtKB/Swiss-Prot is the expertly curated component of UniProtKB (produced by the UniProt consortium). Source: https://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/complete/uniprot_sprot.fasta.gz 1.0.0 - Resource available (latest)

checkm

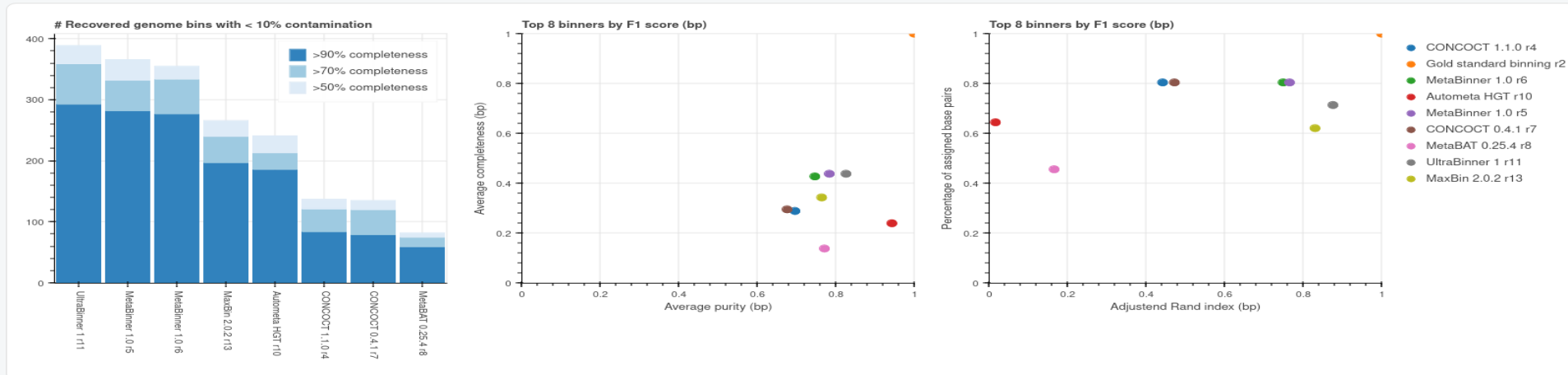
checkm database for the metagenomics-toolkit Source: https://openstack.cebitec.uni-bielefeld.de:8080/databases/checkm_data_2015_01_16.tar.gz 2015_01_16 - Resource available (latest)

CAMI II Benchmarking Platform



Genome binning: Marine

Sample: marmgCAMI2_short_read_pooled_gold_standard_assembly



Genome binning	Metrics per bin	Quality of bins: all bins have the same weight						Quality for sample				
		Average purity (bp)	Average purity (seq)	Average completeness (bp)	Average completeness (seq)	F1 score (bp) ▼	F1 score (seq)	Accuracy (bp)	Accuracy (seq)	Misclassification rate (bp)	Misclassification rate (seq)	Pu
Gold standard binning	976	1.000 ± 0.000	1.000 ±	1.000 ± 0.000	1.000 ±	1.000	1.000	1.000	1.000	0.000	0.000	1.000
UltraBinner 1	596	0.826 ± 0.073	0.527 ±	0.438 ± 0.201	0.362 ±	0.572	0.429	0.632	0.115	0.114	0.305	0.8
MetaBinner 1.0	653	0.784 ± 0.079	0.455 ±	0.438 ± 0.193	0.365 ±	0.562	0.405	0.657	0.123	0.183	0.443	0.8
MetaBinner 1.0	660	0.747 ± 0.099	0.450 ±	0.427 ± 0.196	0.358 ±	0.543	0.399	0.644	0.115	0.199	0.477	0.8
MaxBin 2.0.2	516	0.764 ± 0.089	0.481 ±	0.343 ± 0.181	0.296 ±	0.473	0.367	0.511	0.083	0.177	0.473	0.8
CONCOCT 0.4.1	373	0.676 ± 0.093	0.614 ±	0.295 ± 0.174	0.239 ±	0.410	0.344	0.429	0.117	0.467	0.469	0.8
CONCOCT 1.1.0	373	0.696 ± 0.088	0.596 ±	0.289 ± 0.173	0.236 ±	0.408	0.338	0.431	0.118	0.464	0.467	0.8
Autometa HGT	427	0.943 ± 0.020	0.789 ±	0.239 ± 0.152	0.203 ±	0.381	0.322	0.360	0.012	0.441	0.807	0.8
MetaBAT 0.25.4	232	0.771 ± 0.083	0.642 ±	0.138 ± 0.098	0.115 ±	0.234	0.195	0.204	0.013	0.552	0.657	0.4

NATURE METHODS | METHAGORA

The Critical Assessment of Metagenome Interpretation (CAMI) competition

27 Jun 2014 | 6:36 PM | Posted by Tal Nawy | Category: Bioinformatics, Computational, Guest Post, Metagenomics

Alice McHardy, Alex Sczyrba and Thomas Rattei announce a new initiative for assessing metagenomics methods in this guest post.



Alice McHardy
FOLKER MEYER



Alex Sczyrba
A. SCZYRBA



Thomas Rattei
ANJA VENIER

In just over a decade, metagenomics has developed into a powerful and productive method in microbiology and microbial ecology. The ability to retrieve and organize bits and pieces of genomic DNA from any natural context has opened a window into the vast universe of uncultivated microbes. Tremendous progress has been made in computational approaches to interpret this sequence data but none can completely recover the complex information encoded in metagenomes.

A number of challenges stand in the way. Simplifying

Summary and Outlook

- **Support High Quality Research Data Management:**
 - Adhering to best practices and continuous benchmarking
- **FAIR Principles:**
 - Maximize the scientific value and use of microbiome data

Principle	Status	Explanation
Findable	[✓] Achieved	Assigning computational workflows in searchable repositories.
Accessible	[🖨] Plan	Depositing computational data in a public repository like ENA
Interoperable	[✓] Achieved	Using workflows standards and combining outputs data with other datasets and usable across different systems
Reusable	[✓] Achieved	Providing rich metadata, clear Data usage licenses , and detailed provenance .

- **Helmholtz Center for Infection Research (HZI)**
 - Fernando Meyer
 - Adrian Fritz
 - Zhi-luo Deng
 - Gary Robertson
 - Alice Carolyn McHardy

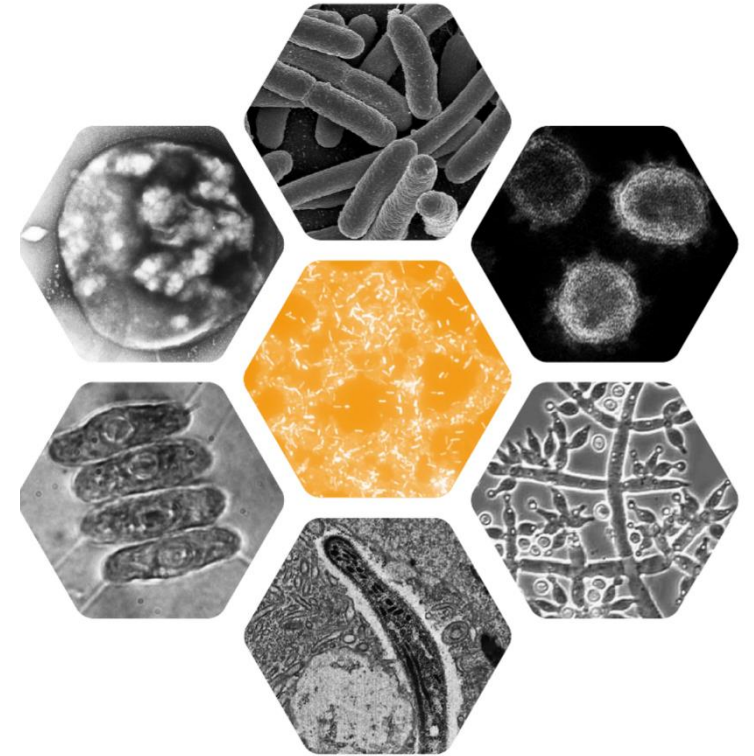
- **Bielefeld Institute for Bioinformatics Infrastructure (BIBI)**
 - Michael Beckstette
 - Daniel Goebel
 - Alex Sczyrba

Thank
you!

NFDI4Microbiota

Use Case: MetaProt

05.06.2024, Kay Schallert



What is Metaproteomics

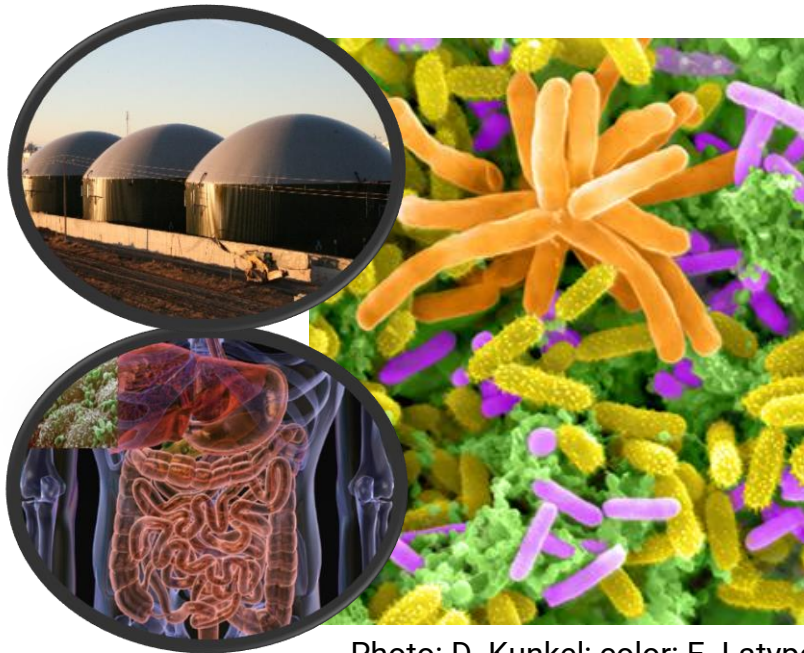
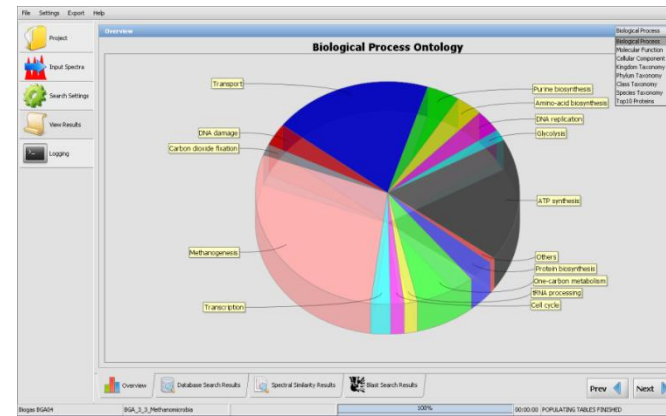


Photo: D. Kunkel; color: E. Latypova



- Shotgun Proteomics: detect proteome with liquid chromatography tandem mass spectrometry

- Shotgun proteomics for microbial communities
- Detects actual abundance of proteins, proteoforms, Post-Translational modifications
- Issues: Complex data analysis, homologous proteins, low abundance proteins


What are the goals of MetProt Use Case?

- Standardization in particular in gut metaproteomics
- Expand existing standards with meta data for metaproteomics
- Create Metadata annotation tool
- Workflow for research data management in metaproteomics (openBis)
- Create reference protein sequence database for human gut based on metagenomics

Starting point is proteomics SDRF that will be extended with metaproteomics-related meta data

Perspective | [Open Access](#) | [Published: 06 October 2021](#)

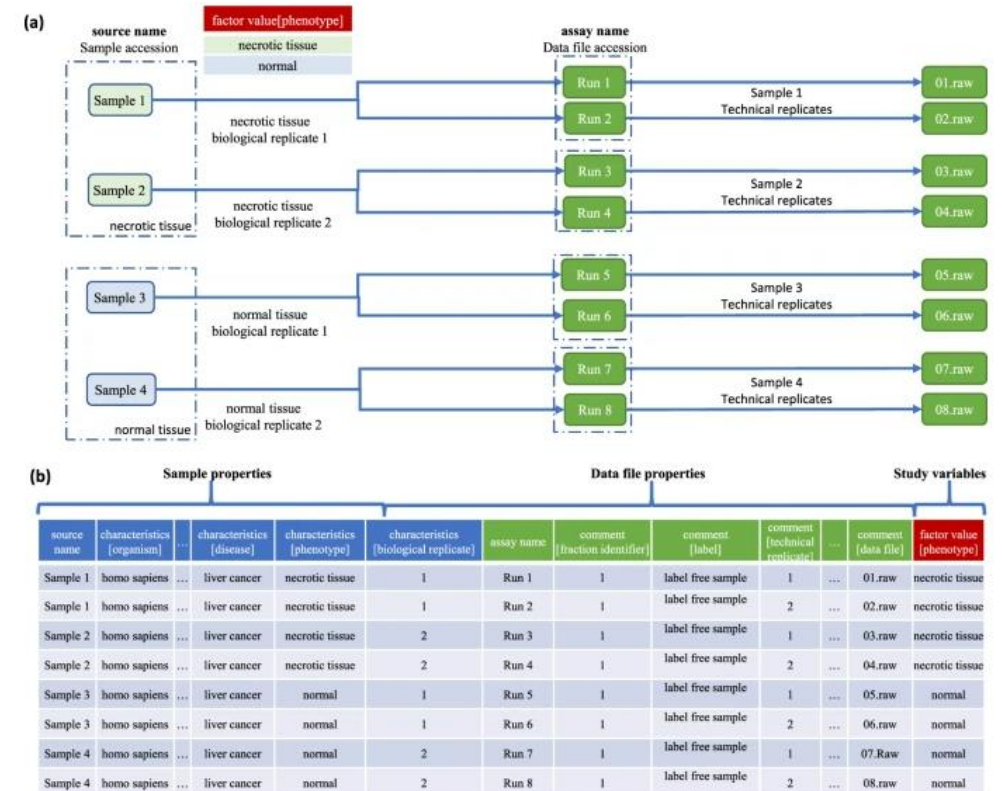
A proteomics sample metadata representation for multiomics integration and big data analysis

[Chengxin Dai](#), [Anja Füllgrabe](#), [Julianus Pfeuffer](#), [Elizaveta M. Solovyeva](#), [Jingwen Deng](#), [Pablo Moreno](#), [Selvakumar Kamatchinathan](#), [Deepti Jaiswal Kundu](#), [Nancy George](#), [Silvie Fexova](#), [Björn Grüning](#), [Melanie Christine Föll](#), [Johannes Griss](#), [Marc Vaudel](#), [Enrique Audain](#), [Marie Locard-Paulet](#), [Michael Turewicz](#), [Martin Eisenacher](#), [Julian Uszkoreit](#), [Tim Van Den Bossche](#), [Veit Schwämmle](#), [Henry Webel](#), [Stefan Schulze](#), [David Bouyssie](#), ... [Yasset Perez-Riverol](#)  [+ Show authors](#)

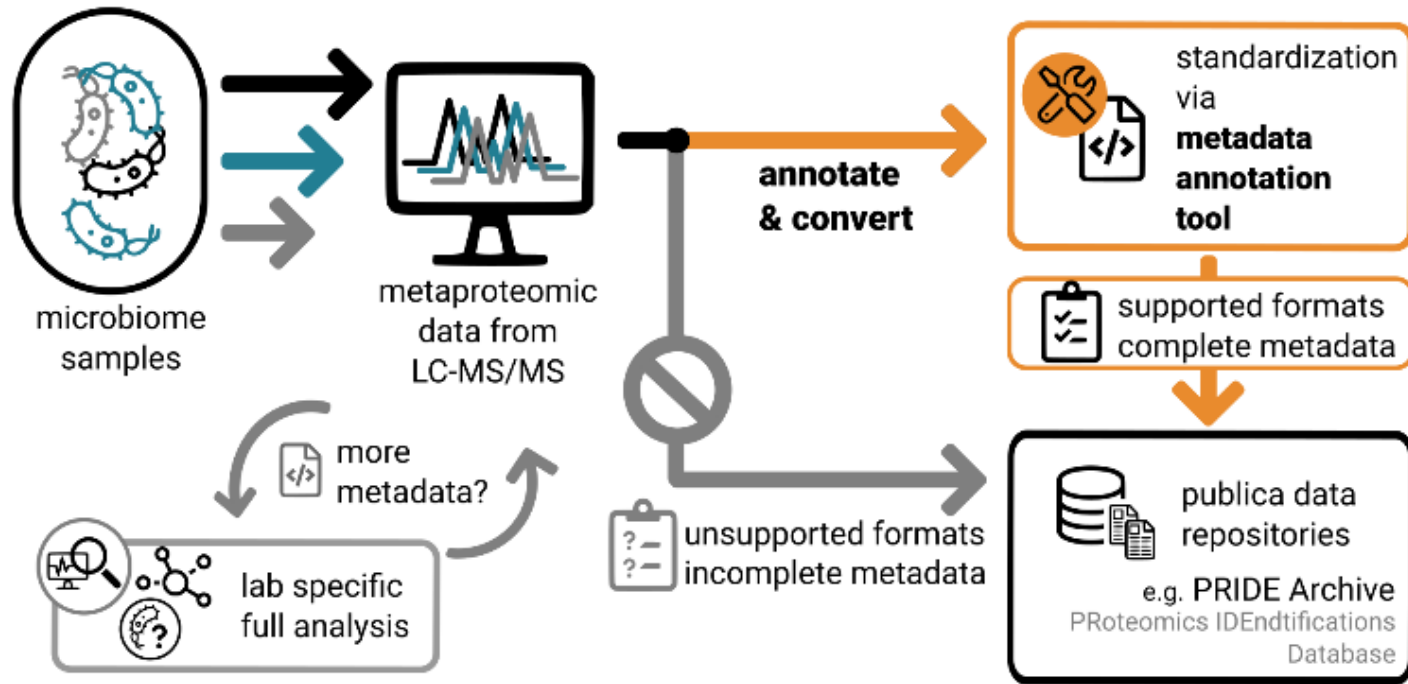
[Nature Communications](#) **12**, Article number: 5854 (2021) | [Cite this article](#)

9007 Accesses | 23 Citations | 28 Altmetric | [Metrics](#)

Fig. 1: SDRF-Proteomics representation for a label-free-based experiment without fractionation.



a Experimental design, including two biological replicates and two technical replicates per biological replicate. The biological and technical replicates are defined by the variable under study (e.g., phenotype). **b** The SDRF tab-delimited file, including the three main sections highlighted: sample metadata, data file properties, and the variables under study (factor values).



- Easy-to-use web service
- File conversion to supported standard formats
- Different approaches to add metadata

Use Case MetaProt

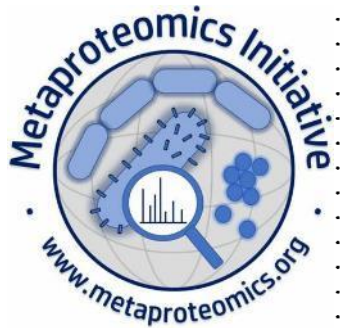


Use Case MetaProt by Dirk Benndorf, Robert Heyer & Kay Schallert with visual adaptation by Maja Magel is licensed under CC BY 4.0

- Test and publish MetaForge
- LLMs to extract metadata from full text
- openBis for research data management
 - Electronic lab notebook
 - Entity model for chemicals, samples, data files, etc.
 - Integration/Automation of workflows

The screenshot displays the MetaForge Workflow interface. At the top, there is a navigation bar with the MetaForge logo and the text "MetaForge Workflow". Below this, a vertical sidebar on the left lists five steps: 1. Choose Pipeline, 2. Upload Files, 3. Metadata Questions (highlighted), 4. Metadata Table, and 5. Download. The main content area shows the "Metadata Questions" step, which includes a progress indicator with five numbered steps: 1. Experiment Setti..., 2. Measurement Sett..., 3. Questions for Experi..., 4. About the Pro..., and 5. Variable Under Investigation (Factor...). Below the progress indicator, there are two dropdown menus. The first is labeled "Experiment Type" and has "Metaproteomics" selected. The second is labeled "What kind of experiment was done?" and has "Synthetic" selected. A "Next" button is located below the second dropdown menu.

Thank you!



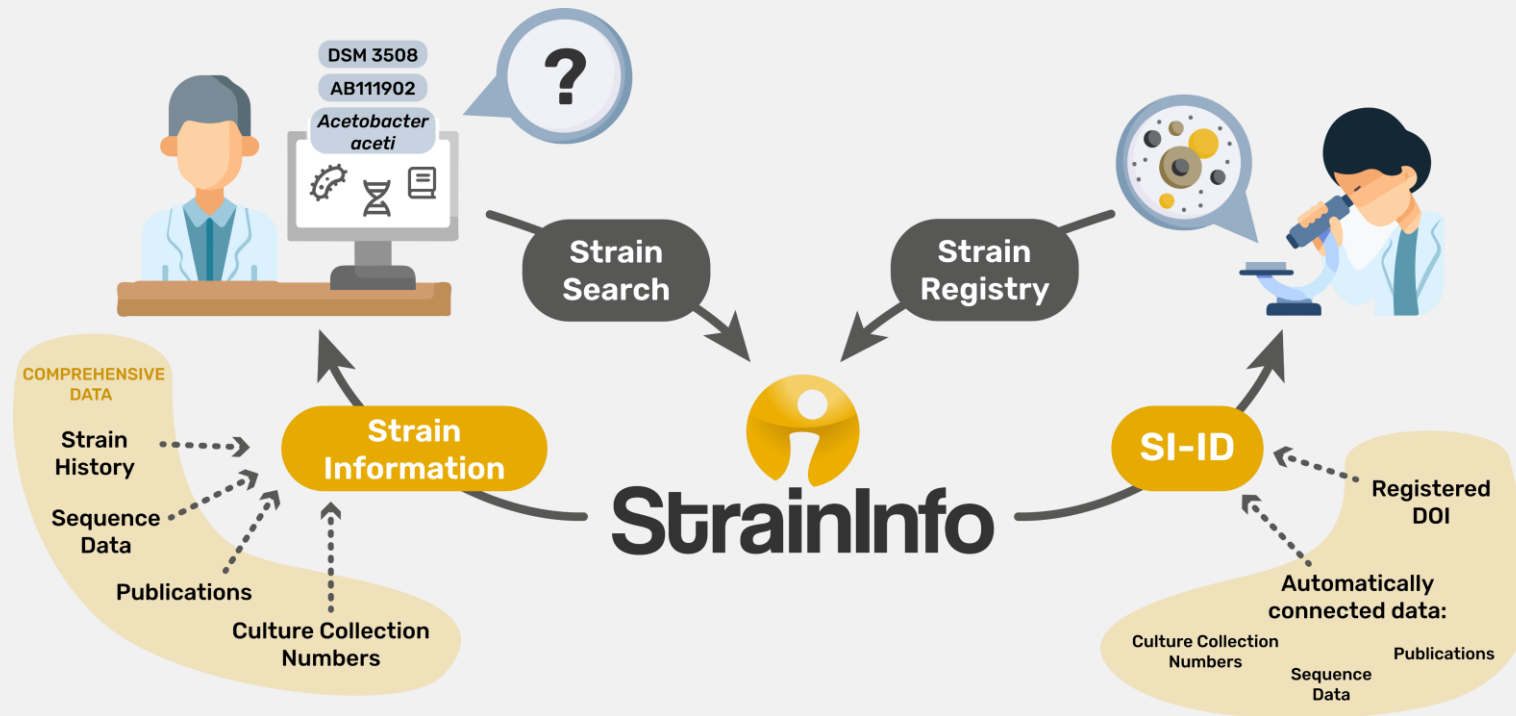
Contributors

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- Robert Heyer
- Nico Jehmlich
- Jana Seifert
- Dörte Becher
- Kay Schallert
- Daniel Kautzner

www.nfdi4microbiota.de
[@nfdi4microbiota](https://twitter.com/nfdi4microbiota)

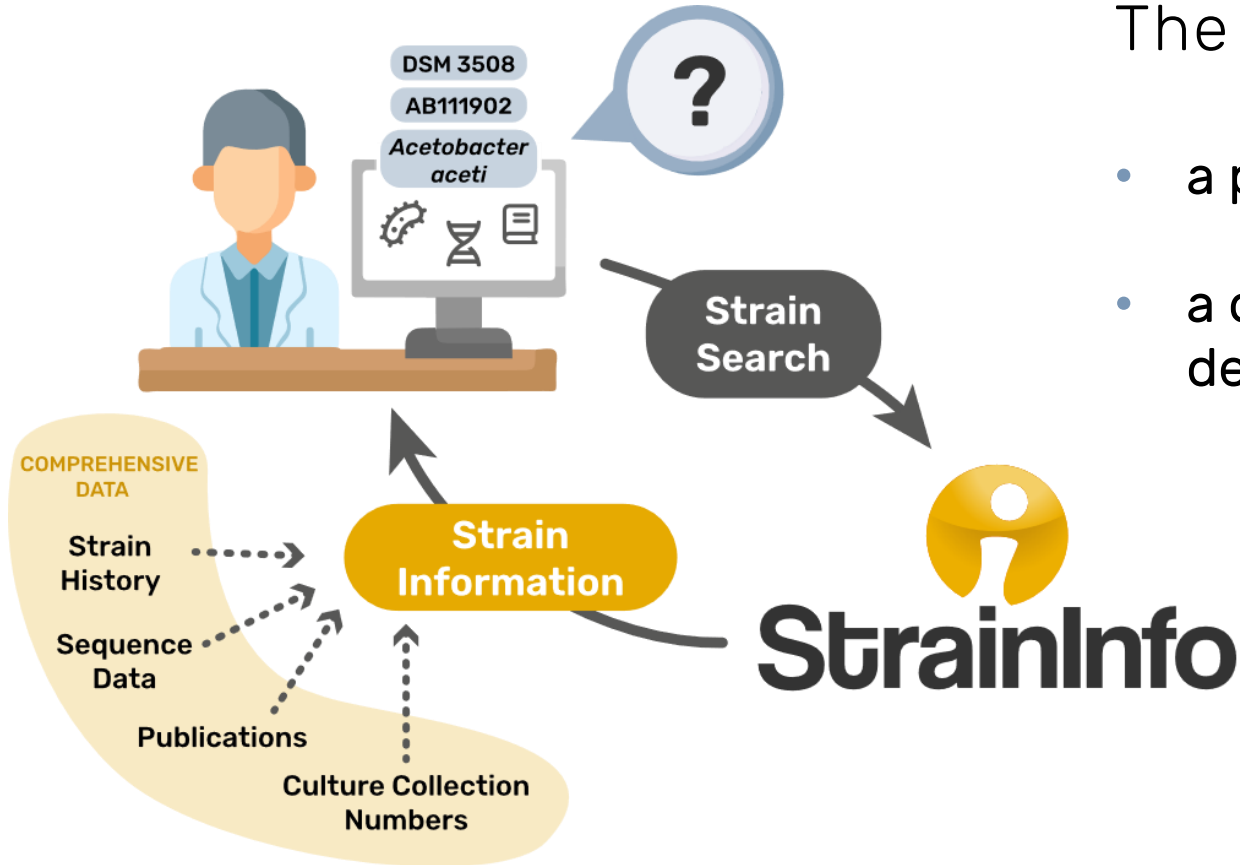
A central database for resolving microbial strain identifiers

Isabel Schober, Artur Lissin, Julius Witte, Adam Podstawka, Lorenz C. Reimer, Julia Koblitz, Boyke Bunk and Jörg Overmann



The StrainInfo database

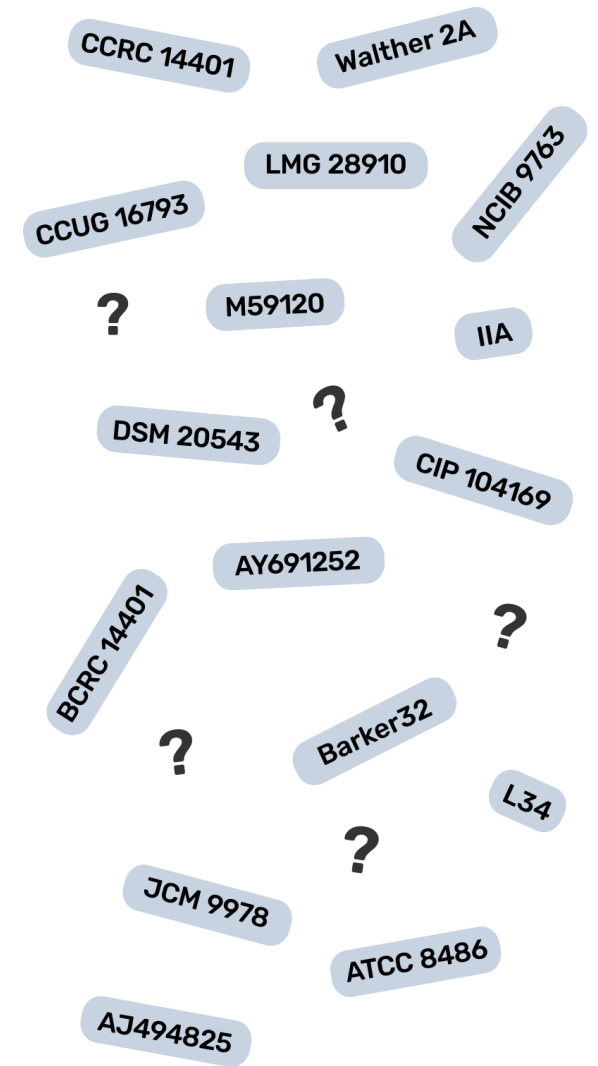
- a place for strain identity information
- a collection of strain identifiers and culture details from multiple resources



- based on the now defunct StrainInfo.net bioportal
- developed by BCCM/LMG between 2005 and 2015

Microbial strain identifiers

- designations
- culture collection numbers
- sequence accessions

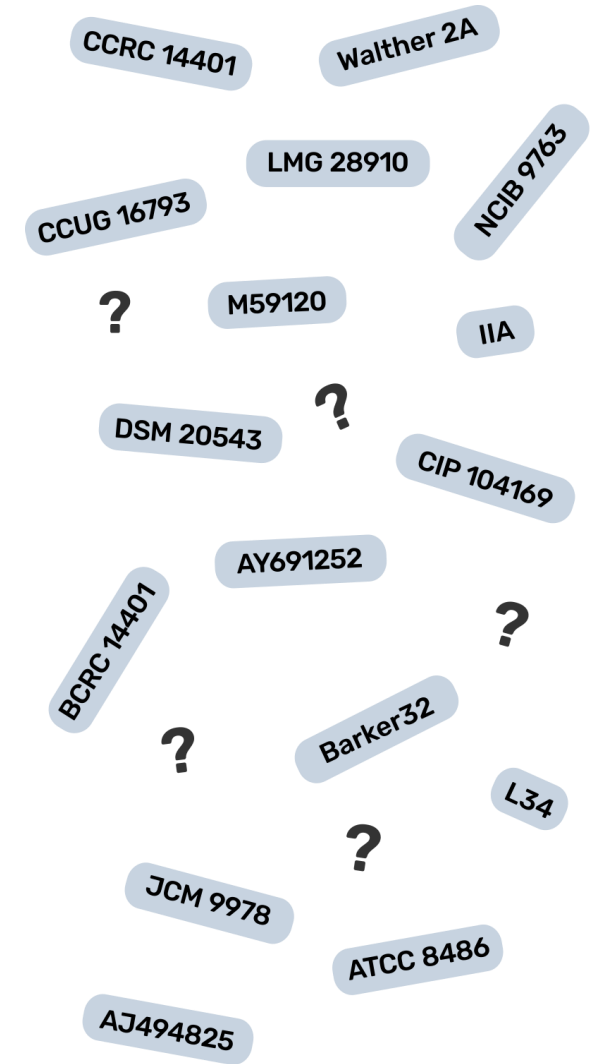


Microbial strain identifiers

- designations
- culture collection numbers
- sequence accessions

Culture collection numbers

→ most widely used strain identifiers



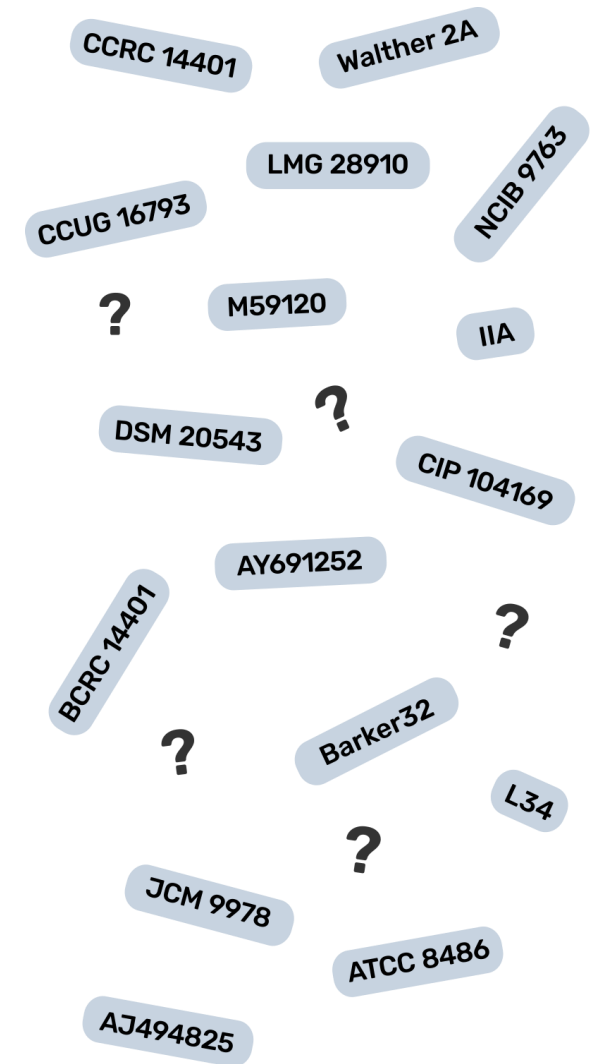
Microbial strain identifiers

- designations
- culture collection numbers
- sequence accessions

Culture collection numbers

→ most widely used strain identifiers

Advantage: unique, stable and reliable



Microbial strain identifiers

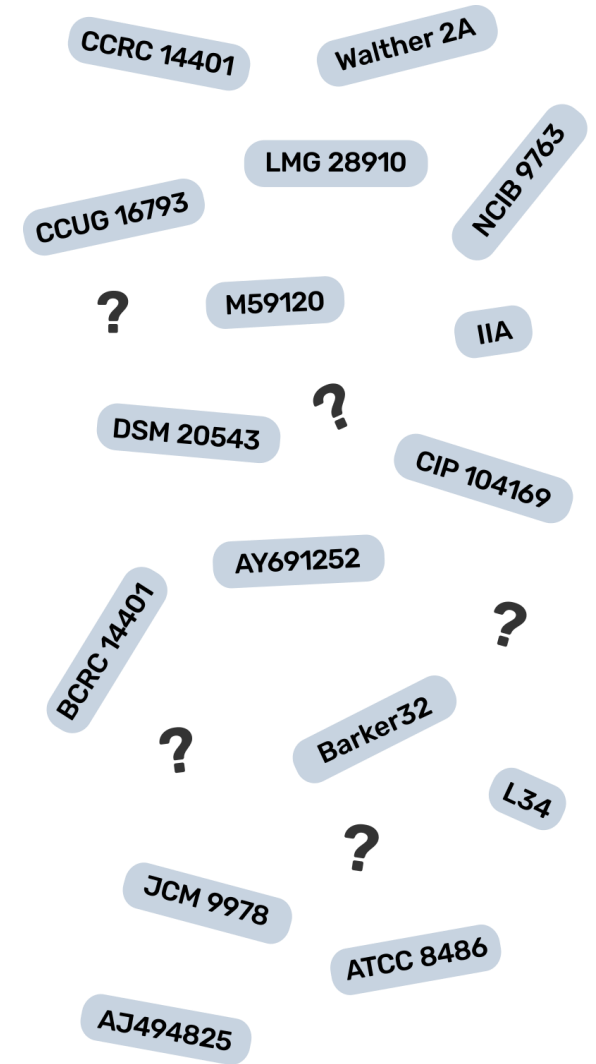
- designations
- culture collection numbers
- sequence accessions

Culture collection numbers

→ most widely used strain identifiers

Advantage: unique, stable and reliable

Disadvantage: each collection assigns their own number



Microbial strain identifiers

- designations
- culture collection numbers
- sequence accessions

Culture collection numbers

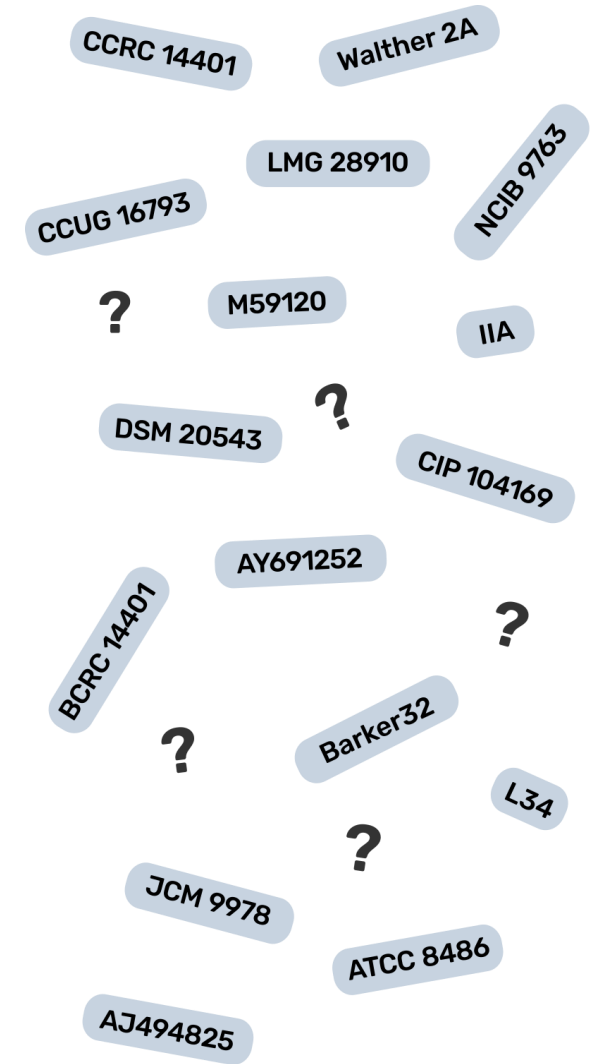
→ most widely used strain identifiers

Advantage: unique, stable and reliable

Disadvantage: each collection assigns their own number

Use of different designations challenges

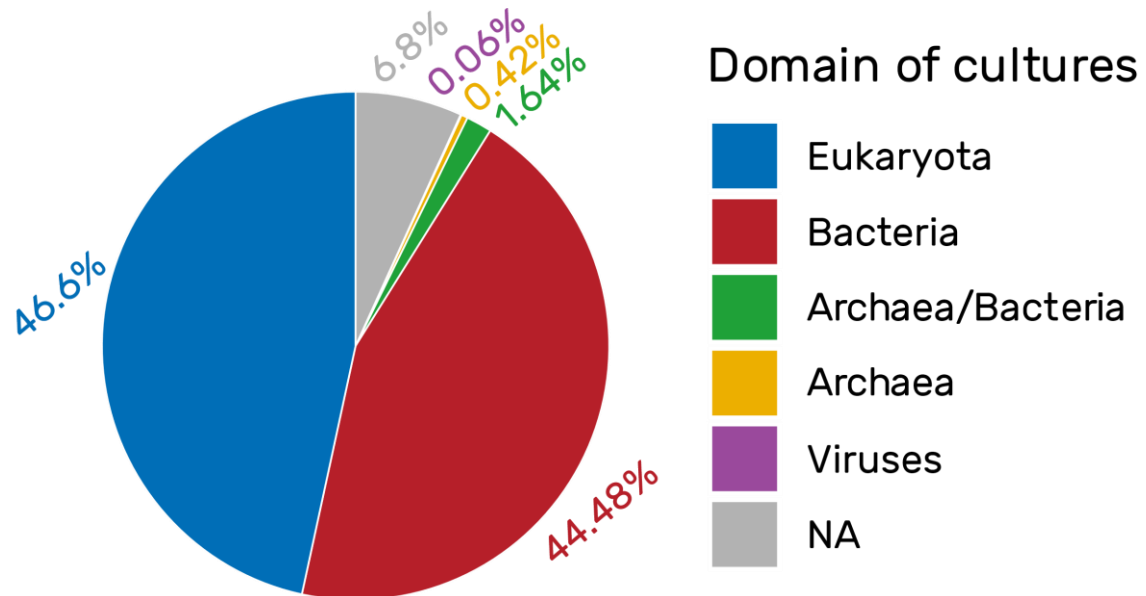
- communication of research findings
- comparison and reuse of data.



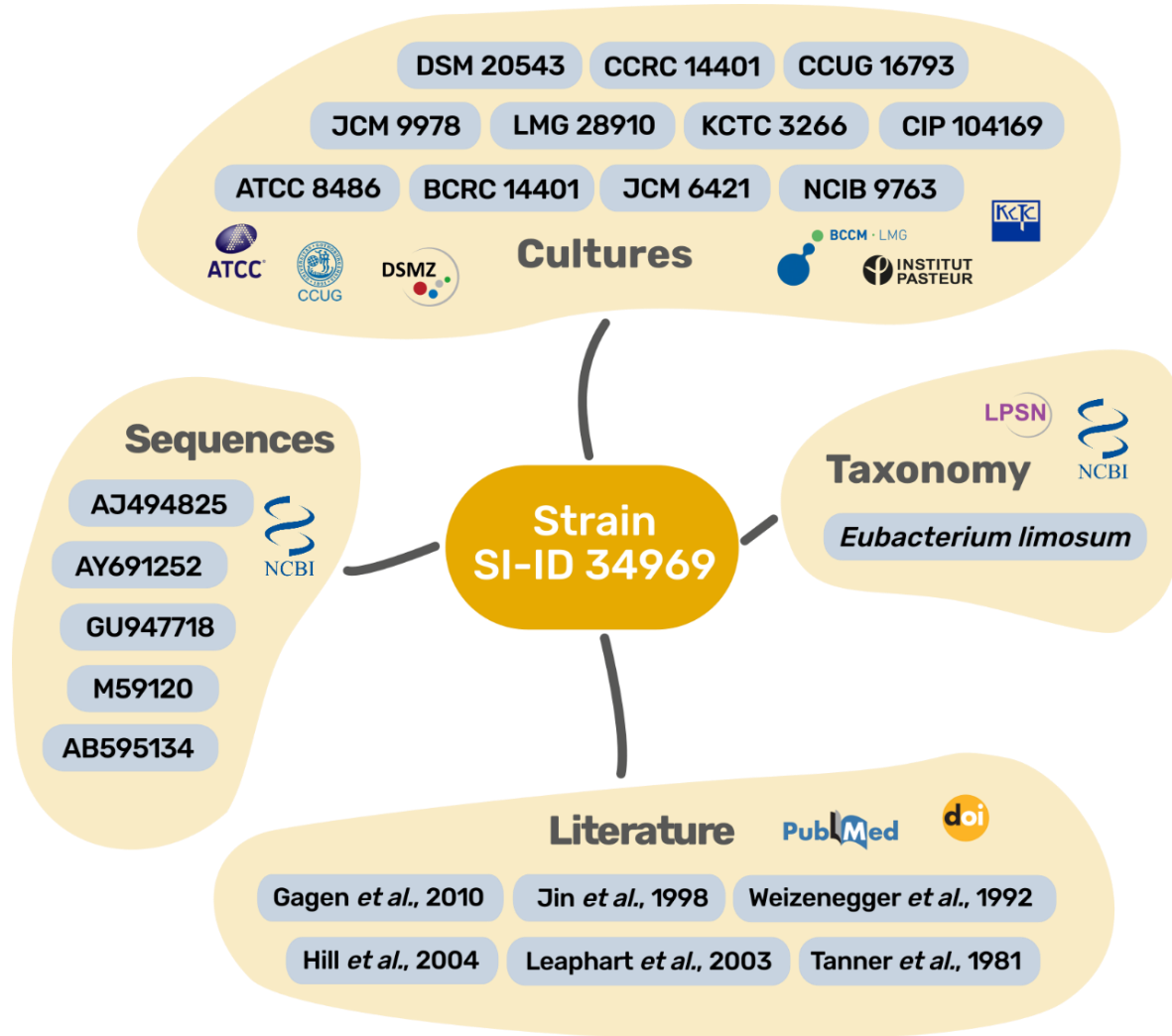
Database content

449,715 cultures of 290,238 strains
from all domains of life

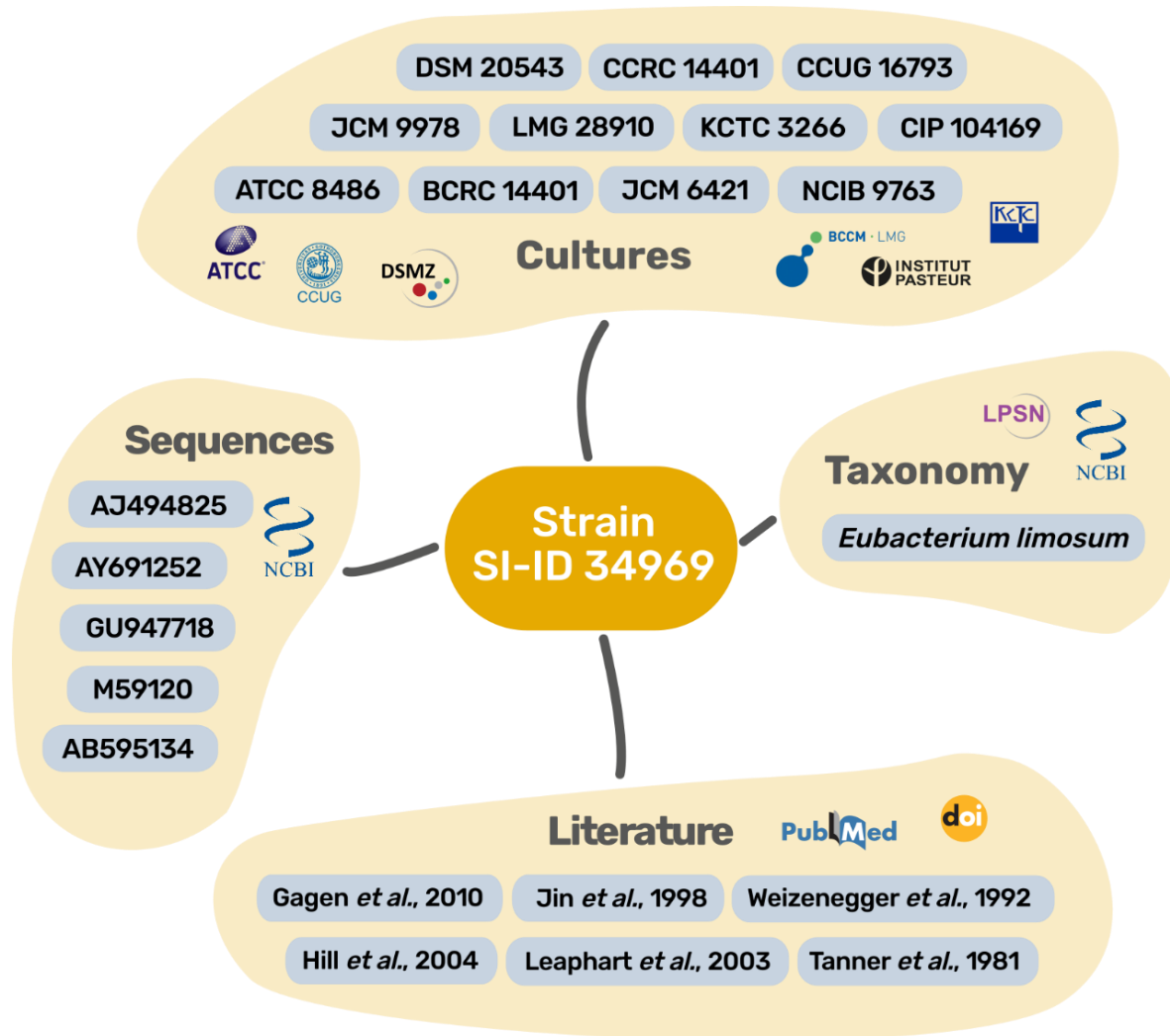
Culture:
An instance of a strain with
a designation that is
cultured in one laboratory.



Linking data

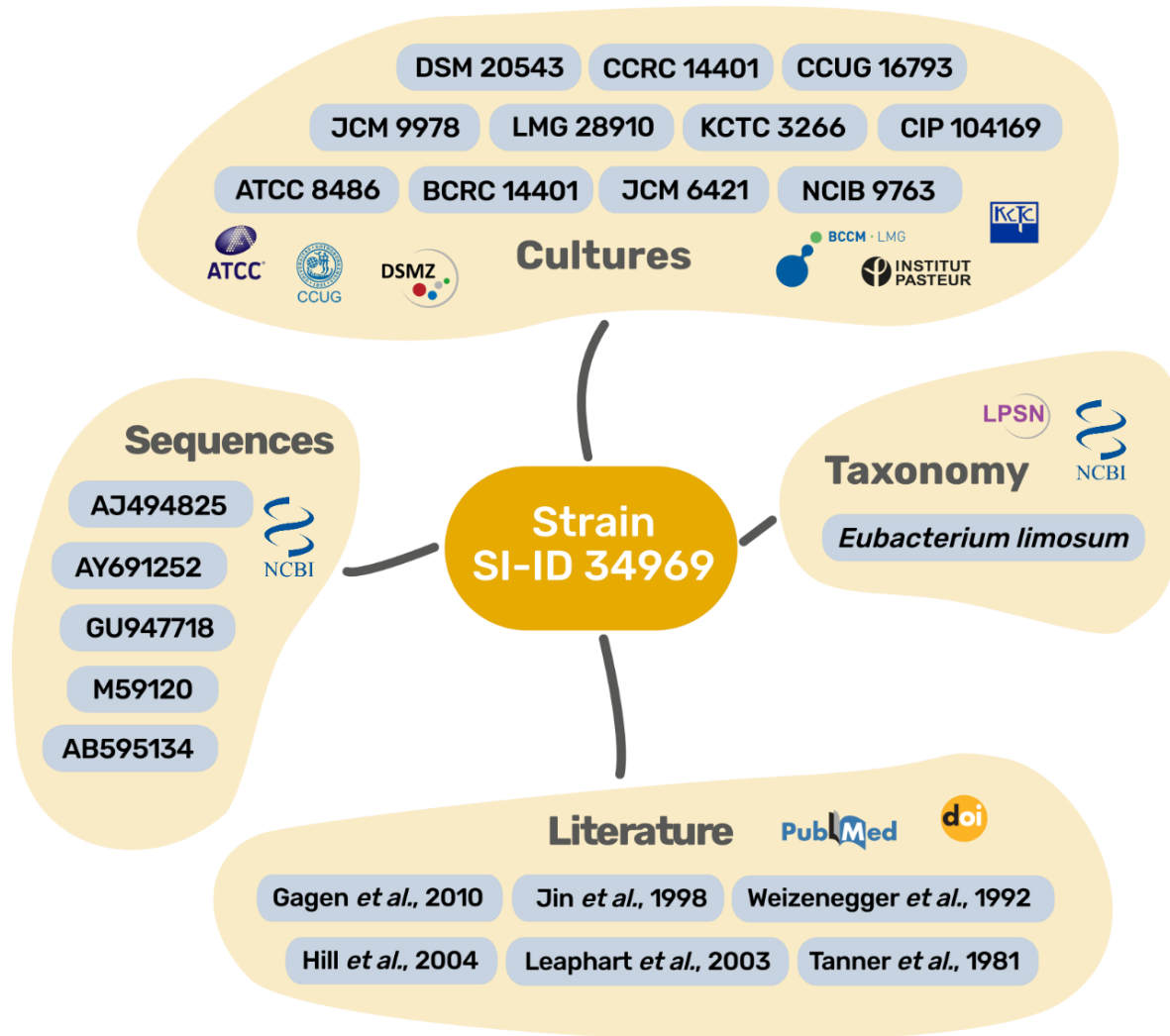


Linking data



- linking strain identifiers with taxonomy, sequences and publications

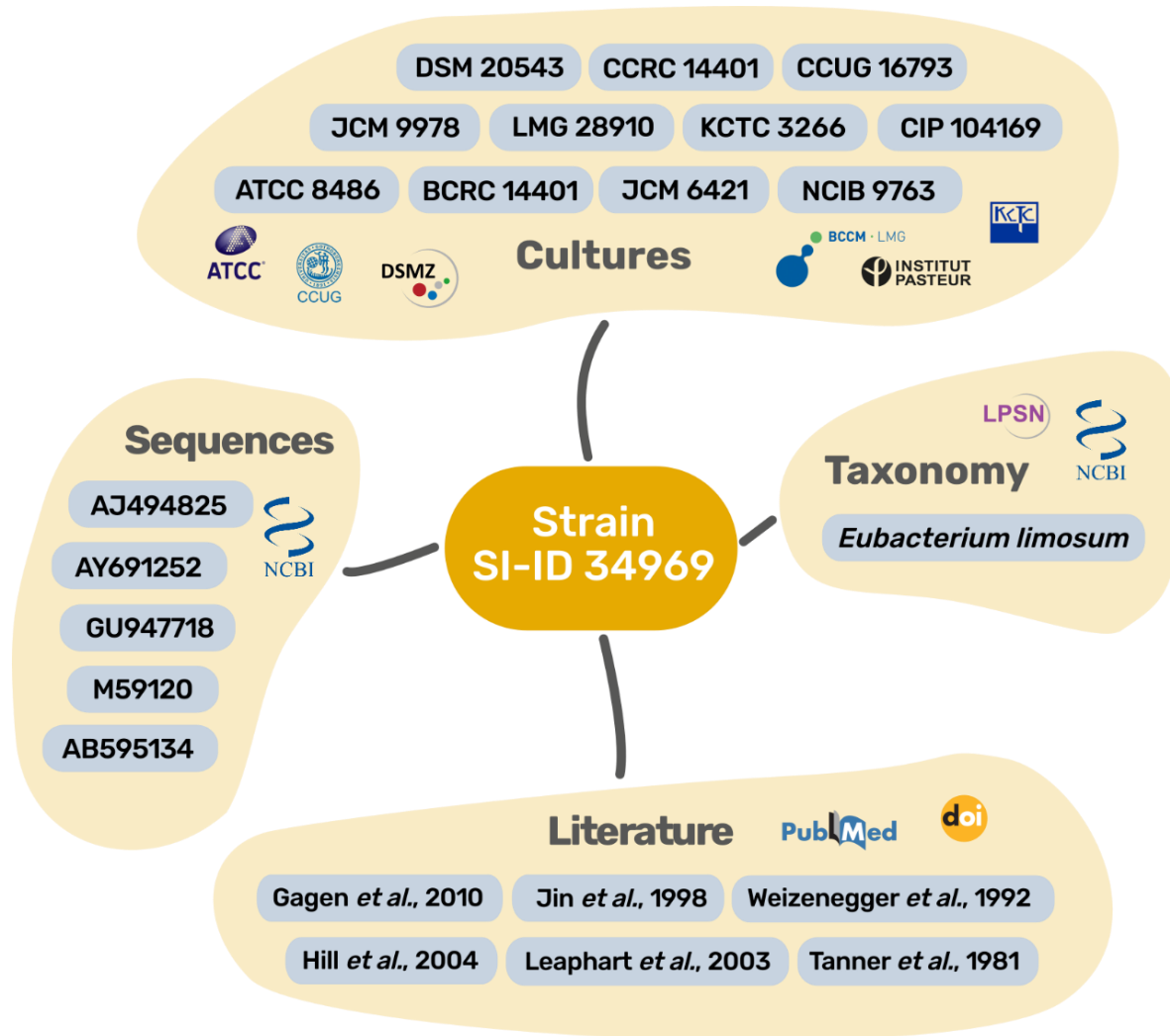
Linking data



- linking strain identifiers with taxonomy, sequences and publications

→ increased findability

Linking data

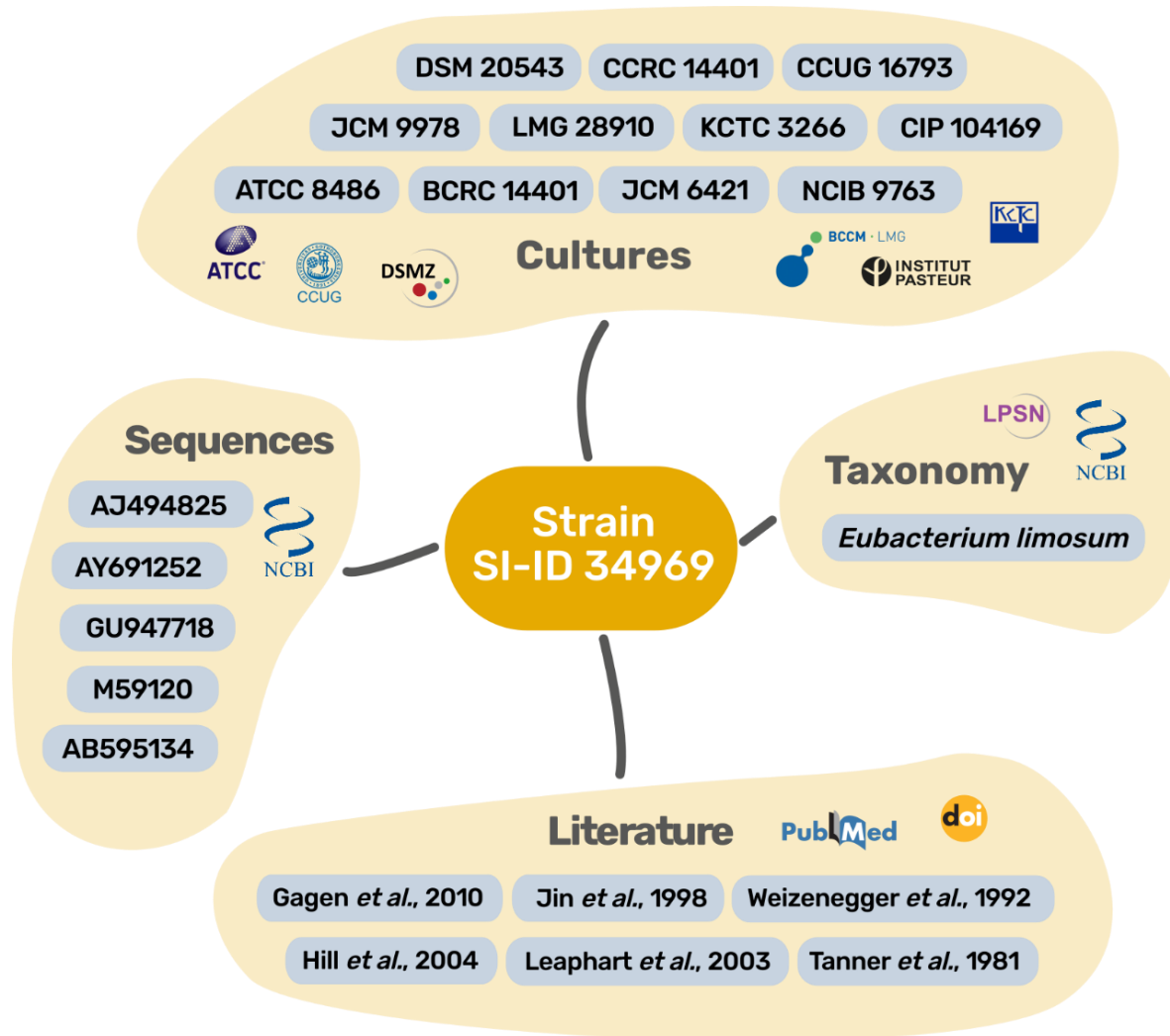


- linking strain identifiers with taxonomy, sequences and publications

→ increased findability

→ enables comparison and reuse of data

Linking data



- linking strain identifiers with taxonomy, sequences and publications

→ increased findability

→ enables comparison and reuse of data

Making strain data FAIR!

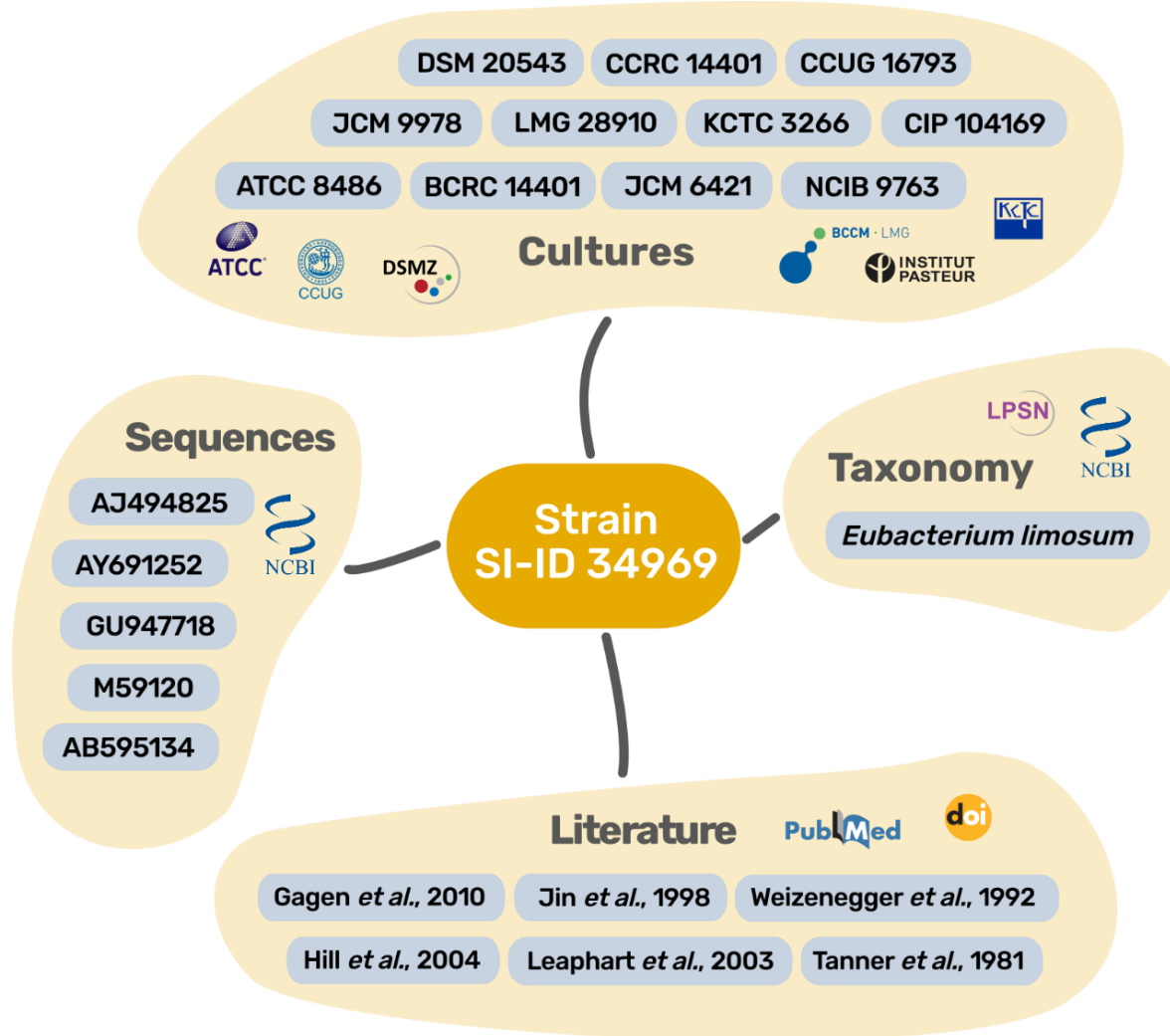
Linking data

Berberine-microbiota interplay: orchestrating gut health through modulation of the gut microbiota and metabolic transformation into bioactive metabolites

Tessa Dehau,¹ Marc Cherlet,² Siska Croubels,² Michiel Van De Vliet,³ Evy Goossens,¹ and Filip Van Immerseel^{1,*}

• Author information • Article notes • Copyright and License information • [PMC Disclaimer](#)

([Eeckhaut et al., 2011](#))). *Eubacterium limosum* (LMG 28910) was also included as it previously showed to carry O-demethylation ([Possemiers et al., 2008](#); [Rich et al., 2022](#)), a reaction involved in the transformation of berberine to berberrubine or thalifendine. Strains were sub-cultured



Eubacterium limosum strain ATCC 8486 16S ribosomal RNA gene, partial sequence

GenBank: M59120.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS	EUBRR16SA	1525 bp	DNA	linear	BCT 19-SEP-2013
DEFINITION	Eubacterium limosum strain ATCC 8486 16S ribosomal RNA gene, partial sequence.				
ACCESSION	M59120				
VERSION	M59120.1				
KEYWORDS	.				
SOURCE	Eubacterium limosum				
ORGANISM	Eubacterium limosum Bacteria; Bacillota; Clostridia; Eubacteriales; Eubacteriaceae; Eubacterium.				
REFERENCE	1 (bases 1 to 1525)				
AUTHORS	Woese,C.R., Yang,D. and Mandelco,L.				
TITLE	Phylogenetic analysis of some clostridia and their relatives				
JOURNAL	Unpublished				
FEATURES	Location/Qualifiers				
source	1..1525 /organism="Eubacterium limosum" /mol_type="genomic DNA" /strain="ATCC 8486" /culture_collection="ATCC:8486" /type_material="type strain of Eubacterium limosum" /db_xref="taxon:1736" /note="type strain of Eubacterium limosum"				
rRNA	<1..>1525 /product="16S ribosomal RNA"				

Welcome to StrainInfo

Live Demo

Microbial Strains

DSM 20543

Search examples

Designation	DSM 20543
Taxonomy	Eubacterium limosum
Seq. accession number	M59120
Strain id	SI-ID 34969
Culture id	SI-CU 901889

Ab



In microbial strain designations and data is often complicated by the existence of a number of different designation and identifiers for the same strain. StrainInfo is a service developed to provide a resolution of microbial strain identifiers by storing culture collection numbers, their relations, and culture-associated data.

StrainInfo was initially created by [BCCM/LMG](#) between the years 2005 and 2015 and is currently being developed by [DSMZ](#).

Related cultures

- ATCC 8486
- BCRC 14401
- CCRC 14401
- CCUG 16793
- CIP 104169
- DSM 20543**
- JCM 6421
- JCM 9978
- KCTC 3266
- LMG 28910
- NCIB 9763
- NCIMB 9763
- STAFF 1027

Culture details: DSM 20543

Available at		DSMZ - DSMZ-German Collection of Microorganisms and Cell Cultures			Location DE
Culture id	Registered	Information collected	Type culture	Culture - Type strain	
SI-CU 134886	2023-08-17	2023-08-03	✗	✓	
Identifier	Culture - Taxonomy		DSM 20543 Eubacterium limosum  		
Sample source	-		Sampling date	1990-01-01	
Depositor	-		Deposit designation	ATCC 8486	
Depositor - institute	ATCC		Deposit year	-	
Culture exchange					
<div style="display: flex; align-items: center; gap: 10px;"> ATCC 8486 > DSM 20543 > CCRC 14401 CCUG 16793 </div>					

On this page

- Related cultures
- Culture details
- Sequences
- Publications
- Archive

Other strains of Eubacterium limosum

- SI-ID 35290:**
ATCC 10825, KCTC 3244, ...
- SI-ID 47635:**
CCUG 16794, DSM 2593, ...
- SI-ID 47636:**
DSM 2594
- SI-ID 53956:**
CCUG 17367
- SI-ID 107970:**
CCUG 2228

Sequences

search in table

Accession number	Culture	Description	Year	Length
AJ494825	ATCC 8486	Eubacterium limosum partial FTHFS gene for formyltetrahydrofolate synthetase	2002	1311



SI-ID
34969

Type strain
✓

Taxonomy
Eubacterium limosum

More about this strain

Persistent link
 10.60712/SI-ID34969.1

Sample source -	Sampling date 1990-01-01	Location -
Depositor -	Deposit designation ATCC 8486	
Depositor - institute ATCC	Deposit year -	
Culture exchange ATCC 8486 > DSM 20543 > CCRC 14401 CCUG 16793		

On this page

- [Related cultures](#)
- [Culture details](#)
- [Sequences](#)
- [Publications](#)
- [Archive](#)

Other strains of Eubacterium limosum

- SI-ID 35290:**
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DSM 2594
- SI-ID 53956:**
CCUG 17367
- SI-ID 107970:**
CCUG 2228

Sequences

search in table

Accession number	Culture	Description	Year	Length
AJ494825	ATCC 8486	Eubacterium limosum partial FTHFS gene for formyltetrahydrofolate synthetase	2002	1311
GU947718	ATCC 8486	Eubacterium limosum clone ELacs acetyl-CoA synthase gene, partial cds	2010	1685
M59120	ATCC 8486	Eubacterium limosum strain ATCC 8486 16S ribosomal RNA gene, partial sequence	1991	1525
AY691252	ATCC 8486	Eubacterium limosum strain ATCC 8486 60 kDa chaperonin (cpn60) gene, partial cds	2004	552
AB595134	JCM 6421	Eubacterium limosum gene for 16S ribosomal RNA, partial sequence, strain: JCM 6421	2010	1484

Publications

search in table



SI-ID
34969

Type strain
✓

Taxonomy
Eubacterium limosum

More about this strain

Persistent link
 10.60712/SI-ID34969.1

Publications

search in table

Title	Authors	Publisher	Year
The Gram-positive Non-spore-bearing Anaerobic Bacilli of Human Feces [link]	Eggerth AH	American Society for Microbiology	1935
PCR detection and quantitation of predominant anaerobic bacteria in human and animal fecal samples. [link]	Wang RF,Cao WW,Cerniglia CE	Applied and environmental microbiology	1996
Genetic Relationships among Eubacterium Species [link]	Nakazawa F,Hoshino E	Microbiology Society	1994
Formation of N,N-Dimethylglycine, Acetic Acid, and Butyric Acid from Betaine by Eubacterium limosum. [link]	Müller E,Gottschalk G,Walther R,Fahlbusch K	Applied and environmental microbiology	1981
Biotransformation of the isoflavonoids biochanin A, formononetin, and glycitein by Eubacterium limosum. [link]	Hur H,Rafii F	FEMS microbiology letters	2000

On this page

- Related cultures
- Culture details
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- Publications
- Archive

Other strains of Eubacterium limosum

- SI-ID 35290:**
ATCC 10825, KCTC 3244, ...
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- SI-ID 47636:**
DSM 2594
- SI-ID 53956:**
CCUG 17367
- SI-ID 107970:**
CCUG 2228

Archive

search in table

DOI	Title	Date
10.60712/SI-ID34969.1	StrainInfo SI-ID 34969.1	2023-08-25

StrainInfo
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Help
[Manual](#)

Social Media
[@NFD14Microbiota](#)

Funded by
 Deutsche Forschungsgemeinschaft

StrainInfo - API 1.0.0 OAS 3.1

Notice

The current stable version of the web service is v1. We take the liberty to add more features and to add more information to the responses. If we make any breaking changes we will publish those in a new version.

Privacy Policy

We are collecting anonymized data and use it to evaluate the website performance and use. You may choose to prevent this website from aggregating and analyzing the actions you take here. To opt out please add 'do_not_track' argument to your API request.

Terms of use

All information provided by this web service is carefully checked for accuracy and is continuously up-dated. However, we cannot guarantee the completeness, the correctness and the topicality. Liability claims regarding damage caused by the use of any information provided, including any kind of information which is incomplete or incorrect, will therefore be rejected. According to the verdict passed by the District Court in Hamburg the owner of a website is responsible for the contents which appear in the links. This can only be prevented when the owner explicitly dissociates itself to these contents. We offer links to other homepages in the internet and we would like to emphasize that we have no influence on the contents and design of these pages. Therefore, herewith we explicitly dissociate ourselves from all the contents linked through our web service and that we take no responsibility for these contents. This statement applies to all the links offered by our web service.

[CC BY 4.0](#)

Servers

/v1

Filter by tag

Statistic

GET `/count/strains` Count of all strains

GET `/count/type_strains` Count of all type strains



type strain

Usually the original isolate used as a reference for the formal description of the species.

API requests in Python

In Python, API requests can be made using a package called "requests".

```
# load requests package to make API requests
import requests
```

The get method of the requests package can be used on the URL for an API call. In this example a strain designation is stored in a variable, which is then used as the variable in a request to the /search/culture/str_des endpoint. The response to the request is stored in a variable.

```
# Example strain Prevotella bivia 653C
designation="653C"

# make API request to search cultures connected
# with the designation using the requests.get()
# method and saving the response to a
# variable called 'response'
response=requests.get("https://api.straininfo.dsmz.de/v1/search/culture/str_des/"+designation)
```

The response can be transformed to a Python object using the json decoder from the requests package. In this case, the response is a list of culture IDs of the cultures connected to the designation.

```
# print 'response' using the json decoder
# from the requests package
print(response.json())
```

One of the SI-CUs can then be used to request detailed culture information.

```
# store the first culture ID of the list
si_cu=response.json()[0]
print(si_cu)

# make API request to search information on the culture with the SI-CU
response=requests.get("https://api.straininfo.dsmz.de/v1/data/culture/max/"+str(si_cu))
```

On this page

- [Terminology](#)
- [API requests in Python](#)
- [Voting on Strain Identity](#)

Tracking culture distribution

- reconstruction of the exchange history of strains

Tracking culture distribution

- reconstruction of the exchange history of strains
- currently displayed:
 - immediate ancestor
 - descendants

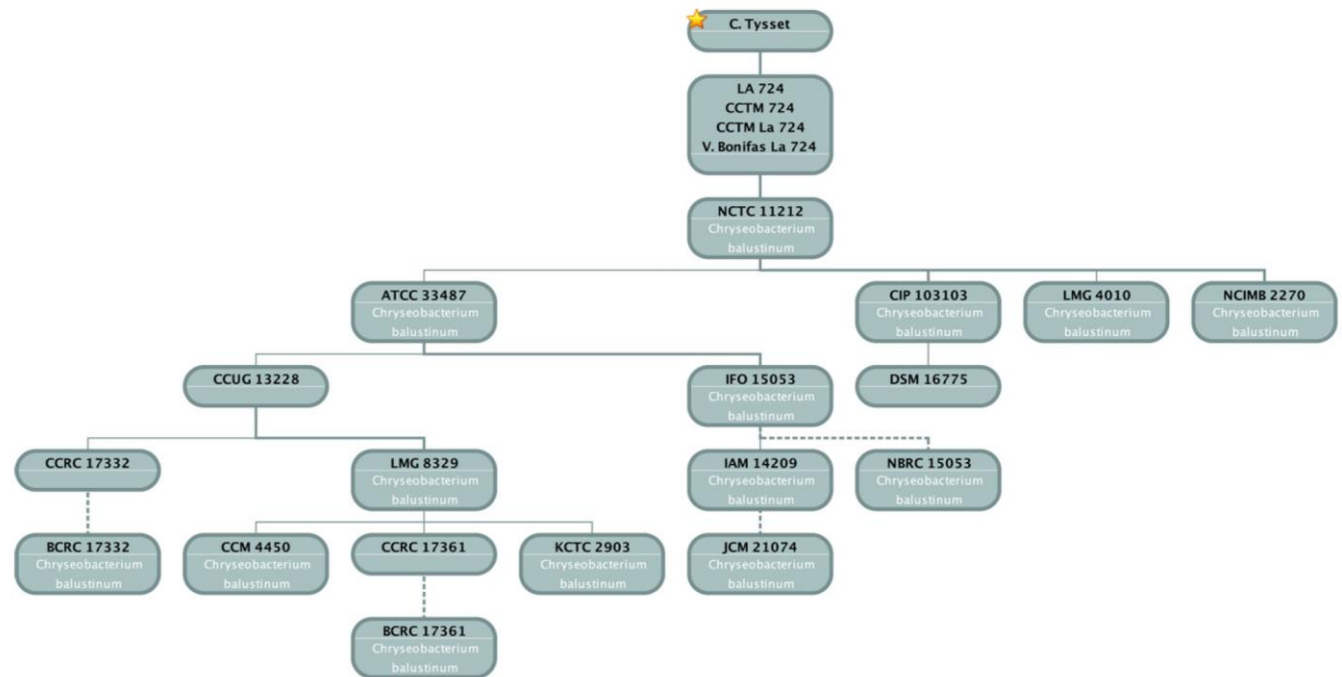


Tracking culture distribution

- reconstruction of the exchange history of strains
- currently displayed:
 - immediate ancestor
 - descendants



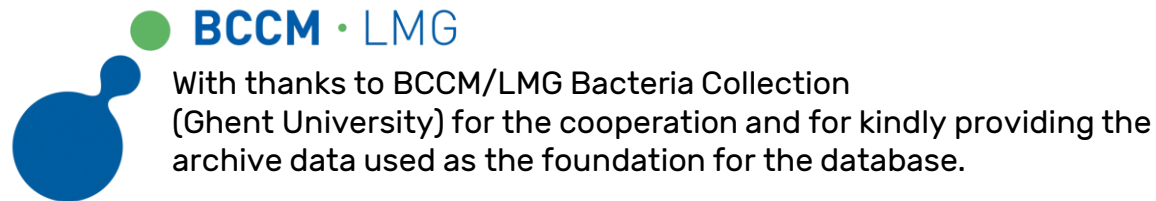
A full visualization of strain histories as rooted trees is planned in the future.



StrainInfo

A central database for resolving microbial strain identifiers

Isabel Schober, Artur Lissin, Julius Witte, Adam Podstawka, Lorenz C. Reimer,
Julia Koblitz, Boyke Bunk and Jörg Overmann

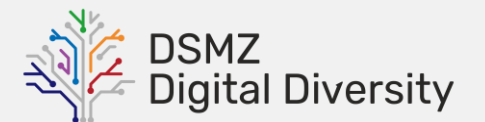


Visit

 StrainInfo



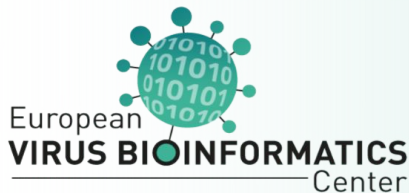
straininfo.dsmz.de



hub.dsmz.de



FRIEDRICH-SCHILLER-
UNIVERSITÄT
JENA



Funded by
DFG Deutsche
Forschungsgemeinschaft
German Research Foundation

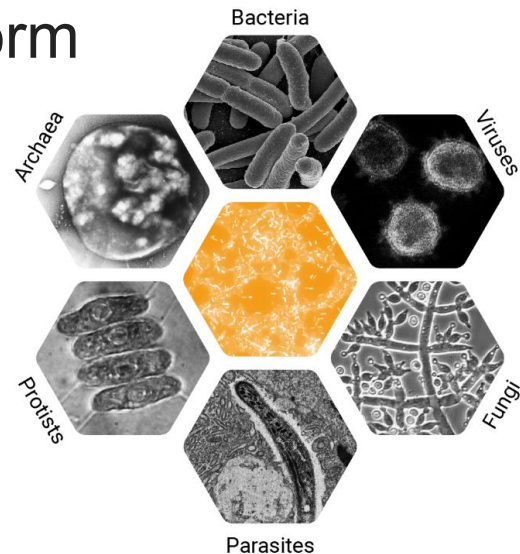
VirJenDB: toward a community-curated and open-source virus meta(data) analysis platform



virjendb.org

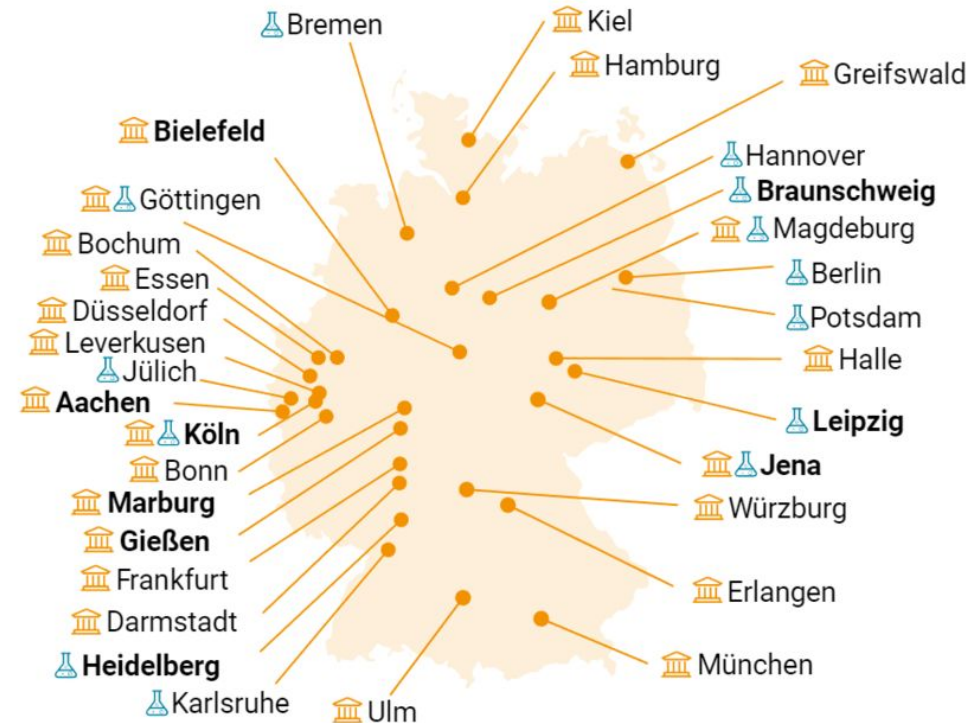
Special session at DGHM & VAAM 2024
7th Joint Microbiology & Infection Conference
2-5 June | Würzburg

Dr. Noriko Cassman
5 June 2024



NFDI4M Work Program: 5 Task Areas

1. Community, networking and training
2. Standards and policies
3. Services
4. Technical infrastructure
5. Coordination and communication



nfdi4microbiota.de

NFDI4M Work Program



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

1. Community, networking and training
2. Standards and policies
3. **Services & Use Cases**
4. Technical infrastructure
5. Coordination and communication



virjendb.org

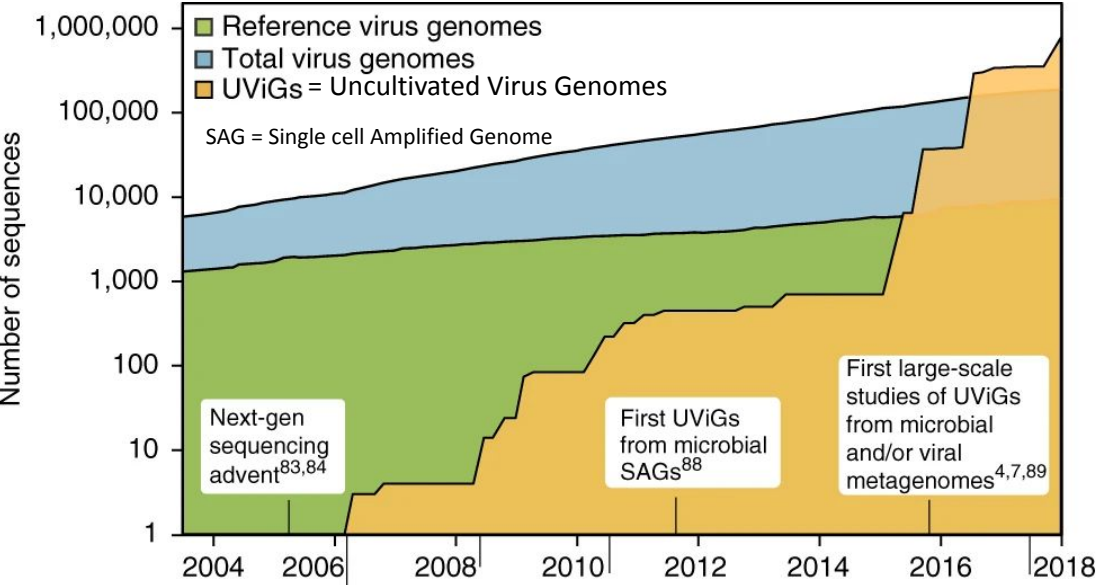
straininfo.dsmz.de



Since 2022: a virus database
for and by virus researchers



Background: (virus) sequencing data volume only increasing



Modified from Roux et al 2019 *Nat Biotechnol*

- Currently >24 active virus databases (Ritsch et al 2023 Viruses)
- >12K virus genomes in NCBI RefSeq
 - Represent only a fraction of available virus sequences
 - IMG/VR contains >15M UViGs
 - VirusDIP reports >30M sequences
- Need for efficient and organized storage of sequencing data and downstream datasets (alignments, predicted structures)
- Also a need for FAIR and Open and well-curated options for data re-use



Aims



Develop user-friendly database to lower barriers for virus -omics data analysis

Focus global efforts to curate and correct virus metadata



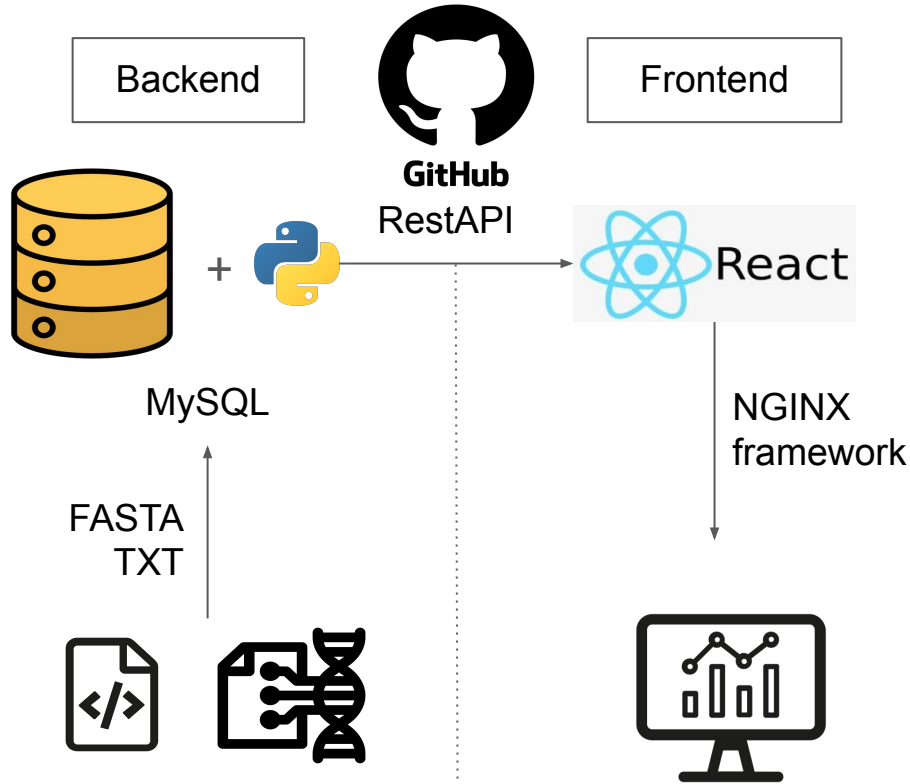
Support (German) virologists to deposit their virus sequences with rich metadata and train on RDM topics

FAIR and Open solutions: integration of tools and API development



FAIR Principles: Wilkinson et al 2016 *Sci Data*
Open Science: <https://unesdoc.unesco.org/ark:/48223/pf0000379949>

Developing the foundation: architecture and data flows



virjendb.org

Beta v0.1
~12M sequences and
30 metadata fields

Static demo start

Welcome to VirJenDB! We are a central hub connecting virus researchers to publicly available virus resources, metadata and sequences. Find and download data using the keyword search below.
We are in beta version and are looking for your input! Please direct your feedback and comments to our [feedback](#) page. For more info see the [FAQ](#) page.

Search

[Advanced Search](#)

Suggested Searches

SARS-CoV-2

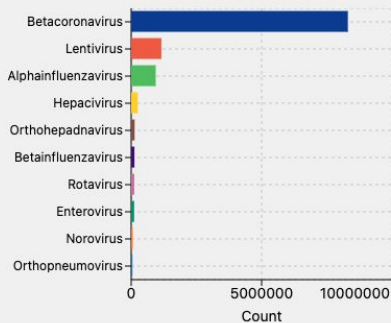
NonSARS-Cov-2

Bacteriophages

Influenza A virus

Archaea Viruses

Top 10 Genera



Families

9

Genera

177

Species

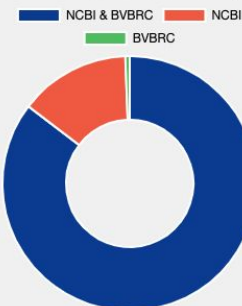
10,405

Total records

12,576,545

Data Sources

(To remove a data source click on legend)



Welcome to VirJenDB! We are a central hub connecting virus researchers to publicly available virus resources, metadata and sequences. Find and download data using the keyword search below.
We are in beta version and are looking for your input! Please direct your feedback and comments to our [feedback](#) page. For more info see the [FAQ](#) page.

Virus name, Host, Abbreviation ...

Search

Advanced Search

Suggested Searches

SARS-CoV-2

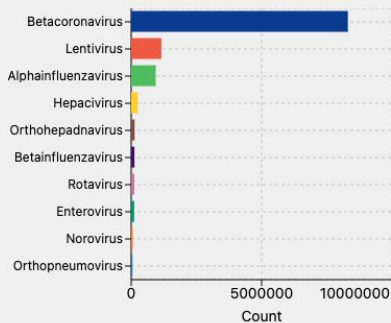
NonSARS-Cov-2

Bacteriophages

Influenza A virus

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Top 10 Genera



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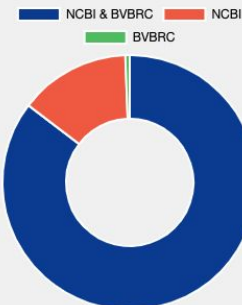
10,405

Total records

12,576,545

Data Sources

(To remove a data source click on legend)



Name	NCBI Accession ID	Abbreviation	Molecule Ty...	BVBRC ID	BioProject ID	Collection Country	Completen...	DB Source	GC%	Host Group	Host Name
Severe acute respira...	NC_004718.3	SARS-CoV	ssRNA+	227984.88	PRJNA485481	Canada	complete	NCBI Virus & BVBRC	40.7617	vertebrates	Homo sapiens
Severe acute respira...	AY274119.3	SARS-CoV	ssRNA+	227984.87		Canada	complete	NCBI Virus & BVBRC	40.7617	vertebrates	Homo sapiens
Severe acute respira...	AY269391.1	SARS-CoV	ssRNA+	227860.6		Viet Nam	partial	NCBI Virus & BVBRC	41.2346	vertebrates	
Severe acute respira...	AY278554.2	SARS-CoV	ssRNA+	228415.13		China	complete	NCBI Virus & BVBRC	40.7822	vertebrates	
Severe acute respira...	AY278491.2	SARS-CoV	ssRNA+	228404.25			complete	NCBI Virus & BVBRC	40.7673	vertebrates	
Severe acute respira...	AY268049.1	SARS-CoV	ssRNA+	227861.6			partial	NCBI Virus & BVBRC	40.9722	vertebrates	
Severe acute respira...	AY278487.3	SARS-CoV	ssRNA+	228406.6			complete	NCBI Virus & BVBRC	40.7699	vertebrates	
Severe acute respira...	AY278488.2	SARS-CoV	ssRNA+	228407.30			complete	NCBI Virus & BVBRC	40.7939	vertebrates	
Severe acute respira...	AY278489.2	SARS-CoV	ssRNA+	233044.12			complete	NCBI Virus & BVBRC	40.8038	vertebrates	
Severe acute respira...	AY278490.3	SARS-CoV	ssRNA+	228409.6			complete	NCBI Virus & BVBRC	40.8003	vertebrates	
Severe acute respira...	AY278741.1	SARS-CoV	ssRNA+	228330.73			complete	NCBI Virus & BVBRC	40.7979	vertebrates	
Severe acute respira...	AY279354.2	SARS-CoV	ssRNA+	228607.5			complete	NCBI Virus & BVBRC	40.7877	vertebrates	
Severe acute respira...	AY268070.1	SARS-CoV	ssRNA+	227998.5			partial	NCBI Virus & BVBRC	40.8669	vertebrates	
Severe acute respira...	AY282752.2	SARS-CoV	ssRNA+	229206.11			complete	NCBI Virus & BVBRC	40.7721	vertebrates	
Severe acute respira...	AY283794.1	SARS-CoV	ssRNA+	235414.5		Singapore	complete	NCBI Virus & BVBRC	40.7963	vertebrates	
Severe acute respira...	AY283795.1	SARS-CoV	ssRNA+	235413.6		Singapore	complete	NCBI Virus & BVBRC	40.8113	vertebrates	
Severe acute respira...	AY283796.1	SARS-CoV	ssRNA+	235412.6		Singapore	complete	NCBI Virus & BVBRC	40.7963	vertebrates	
Severe acute respira...	AY283797.1	SARS-CoV	ssRNA+	235411.6		Singapore	complete	NCBI Virus & BVBRC	40.7978	vertebrates	

<input type="checkbox"/>	<input type="checkbox"/>	NCBI Accession ID	Abbreviation	Molecule Ty...	BVBRC ID	BioProject ID	Collection Country	Completen...	DB Source	GC%	Host Group	Host Name	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	NC_004718.3	SARS-CoV	ssRNA+	227984.88	PRJNA485481	Canada	complete	NCBI Virus & BVBRC	40.7617	vertebrates	Homo sapiens
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY274119.3	SARS-CoV	ssRNA+	227984.87		Canada	complete	NCBI Virus & BVBRC	40.7617	vertebrates	Homo sapiens
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY269391.1	SARS-CoV	ssRNA+	227860.6		Viet Nam	partial	NCBI Virus & BVBRC	41.2346	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278554.2	SARS-CoV	ssRNA+	228415.13		China	complete	NCBI Virus & BVBRC	40.7822	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278491.2	SARS-CoV	ssRNA+	228404.25			complete	NCBI Virus & BVBRC	40.7673	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY268049.1	SARS-CoV	ssRNA+	227861.6			partial	NCBI Virus & BVBRC	40.9722	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278487.3	SARS-CoV	ssRNA+	228406.6			complete	NCBI Virus & BVBRC	40.7699	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278488.2	SARS-CoV	ssRNA+	228407.30			complete	NCBI Virus & BVBRC	40.7939	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278489.2	SARS-CoV	ssRNA+	233044.12			complete	NCBI Virus & BVBRC	40.8038	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278490.3	SARS-CoV	ssRNA+	228409.6			complete	NCBI Virus & BVBRC	40.8003	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY278741.1	SARS-CoV	ssRNA+	228330.73			complete	NCBI Virus & BVBRC	40.7979	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY279354.2	SARS-CoV	ssRNA+	228607.5			complete	NCBI Virus & BVBRC	40.7877	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY268070.1	SARS-CoV	ssRNA+	227998.5			partial	NCBI Virus & BVBRC	40.8669	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY282752.2	SARS-CoV	ssRNA+	229206.11			complete	NCBI Virus & BVBRC	40.7721	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY283794.1	SARS-CoV	ssRNA+	235414.5		Singapore	complete	NCBI Virus & BVBRC	40.7963	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY283795.1	SARS-CoV	ssRNA+	235413.6		Singapore	complete	NCBI Virus & BVBRC	40.8113	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY283796.1	SARS-CoV	ssRNA+	235412.6		Singapore	complete	NCBI Virus & BVBRC	40.7963	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	AY283797.1	SARS-CoV	ssRNA+	235411.6		Singapore	complete	NCBI Virus & BVBRC	40.7978	vertebrates	

Searched term: SARS-Cov-2

Reset Filters

Apply Filters

GC

55 - 100



- > Abbreviation
- > Collection Country
- > Collection Tissue
- ▼ Collection Year

Start year → End year



▼ Completeness

complete partial

> DB Source

▼ GC

0% 100%

- > Genome Structure
- > Host Group
- > Host Name
- > Host Tax ID
- > Length

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Add / Remove Columns

Abbreviation	Molecule Ty...	BVBRC ID	BioProject ID	Collection Country	Completen...	DB Source	GC%	Host Group	Host Name
SARS-CoV	ssRNA+	694009.2718			partial	NCBI Virus & BVBRC	65.625	vertebrates	Patent
SARS-CoV	ssRNA+	742000.8			partial	NCBI Virus & BVBRC	56.5217	vertebrates	
SARS-CoV	ssRNA+	258445.86			partial	NCBI Virus & BVBRC	58.3333	vertebrates	Patent
SARS-CoV	ssRNA+	258445.84			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
SARS-CoV	ssRNA+	258445.81			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
SARS-CoV	ssRNA+	258445.80			partial	NCBI Virus & BVBRC	60.5263	vertebrates	Patent
SARS-CoV	ssRNA+	258445.78			partial	NCBI Virus & BVBRC	67.5	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2491			partial	NCBI Virus & BVBRC	63.1579	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2482			partial	NCBI Virus & BVBRC	55	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2479			partial	NCBI Virus & BVBRC	63.1579	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2478			partial	NCBI Virus & BVBRC	61.1111	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2477			partial	NCBI Virus & BVBRC	57.8947	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2476			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2473			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
SARS-CoV	ssRNA+	694009.2472			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
SARS-CoV	ssRNA+	258445.76			partial	NCBI Virus & BVBRC	58.3333	vertebrates	Patent
SARS-CoV	ssRNA+	258445.74			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
SARS-CoV	ssRNA+	258445.72			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent



<input type="checkbox"/>	<input type="checkbox"/>	Name	NCBI Accession ID	Abbreviation	Molecule Ty...	BVBRC ID	BioProject ID	Collection Country	Completen...	DB Source	GC%	Host Group	Host Name
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute	CQ918600.1	SARS-CoV	ssRNA+	694009.2718			partial	NCBI Virus & BVBRC	65.625	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	1XJR_A	SARS-CoV	ssRNA+	742000.8			partial	NCBI Virus & BVBRC	56.5217	vertebrates	
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	CS050821.1	SARS-CoV	ssRNA+	258445.86			partial	NCBI Virus & BVBRC	58.3333	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	CS050841.1	SARS-CoV	ssRNA+	258445.84			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	CS050862.1	SARS-CoV	ssRNA+	258445.81			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	CS050883.1	SARS-CoV	ssRNA+	258445.80			partial	NCBI Virus & BVBRC	60.5263	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	CS050891.1	SARS-CoV	ssRNA+	258445.78			partial	NCBI Virus & BVBRC	67.5	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456901.1	SARS-CoV	ssRNA+	694009.2491			partial	NCBI Virus & BVBRC	63.1579	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456909.1	SARS-CoV	ssRNA+	694009.2482			partial	NCBI Virus & BVBRC	55	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456912.1	SARS-CoV	ssRNA+	694009.2479			partial	NCBI Virus & BVBRC	63.1579	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456913.1	SARS-CoV	ssRNA+	694009.2478			partial	NCBI Virus & BVBRC	61.1111	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456914.1	SARS-CoV	ssRNA+	694009.2477			partial	NCBI Virus & BVBRC	57.8947	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456915.1	SARS-CoV	ssRNA+	694009.2476			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456918.1	SARS-CoV	ssRNA+	694009.2473			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DD456919.1	SARS-CoV	ssRNA+	694009.2472			partial	NCBI Virus & BVBRC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DJ011594.1	SARS-CoV	ssRNA+	258445.76			partial	NCBI Virus & BVBRC	58.3333	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DJ011614.1	SARS-CoV	ssRNA+	258445.74			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent
<input type="checkbox"/>	<input type="checkbox"/>	Severe acute respira...	DJ011635.1	SARS-CoV	ssRNA+	258445.72			partial	NCBI Virus & BVBRC	55.2632	vertebrates	Patent

[Severe acute respiratory syndrome-related coronavirus Isolate:Tor2](#) [Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens](#)

NCBI Accession Number: **NC_004718.3** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 

[Severe acute respiratory syndrome-related coronavirus Isolate:Tor2](#) [Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens](#)

NCBI Accession Number: **AY274119.3** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 

[Severe acute respiratory syndrome-related coronavirus](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

NCBI Accession Number: **AY269391.1** Genome Coverage: **partial**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information

[Severe acute respiratory syndrome-related coronavirus Isolate:CUHK-W1](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

NCBI Accession Number: **AY278554.2** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 

[Severe acute respiratory syndrome-related coronavirus Isolate:HKU-39849](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

[Severe acute respiratory syndrome-related coronavirus Isolate:Tor2](#) [Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens](#)

NCBI Accession Number: **NC_004718.3** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 



[Severe acute respiratory syndrome-related coronavirus Isolate:Tor2](#) [Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens](#)

NCBI Accession Number: **AY274119.3** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 

[Severe acute respiratory syndrome-related coronavirus](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

NCBI Accession Number: **AY269391.1** Genome Coverage: **partial**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information

[Severe acute respiratory syndrome-related coronavirus Isolate:CUHK-W1](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

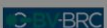


NCBI Accession Number: **AY278554.2** Genome Coverage: **complete**

Baltimore Class: -  National Library of Medicine
National Center for Biotechnology Information 

[Severe acute respiratory syndrome-related coronavirus Isolate:HKU-39849](#) [Severe acute respiratory syndrome-related coronavirus vertebrates](#)

[Results](#)[Card view](#)[Table View](#)[Download All Results](#)

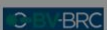

Severe acute respiratory syndrome-related coronavirus Isolate:Tor2 Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens

NCBI Accession Number: [NC_004718.3](#) Genome Coverage: **complete**Baltimore Class: -   National Library of Medicine
National Center for Biotechnology Information 

Severe acute respiratory syndrome-related coronavirus Isolate:Tor2 Severe acute respiratory syndrome-related coronavirus vertebrates Homo sapiens

NCBI Accession Number: [AY274119.3](#) Genome Coverage: **complete**Baltimore Class: -   National Library of Medicine
National Center for Biotechnology Information 

Severe acute respiratory syndrome-related coronavirus Severe acute respiratory syndrome-related coronavirus vertebrates

NCBI Accession Number: [AY269391.1](#) Genome Coverage: **partial**Baltimore Class: -   National Library of Medicine
National Center for Biotechnology Information

Severe acute respiratory syndrome-related coronavirus Isolate:CUHK-W1 Severe acute respiratory syndrome-related coronavirus vertebrates

NCBI Accession Number: [AY278554.2](#) Genome Coverage: **complete**Baltimore Class: -   National Library of Medicine
National Center for Biotechnology Information 

Severe acute respiratory syndrome-related coronavirus Isolate:HKU-39849 Severe acute respiratory syndrome-related coronavirus vertebrates

X Overview

Genbank accession number:
[NC_004718.3](#)Sample name: **Severe acute respiratory
syndrome-related coronavirus**Genome coverage: **complete**Sequence length: **29,751 bp**Host name: **Homo sapiens**Coordination: **Canada: Toronto**Submitter: **He;R.; Dobie;F.; Ballantine;M.;
Leeson;A.; Li;Y.; Bastien;N.; Cutts;T.;
Andonov;A.; Cao;J.; Booth;T.F.;
Plummer;F.A.; Tyler;S.; Baker;L.; Li;X.**Organization: **National Center for
Biotechnology Information; NIH**Taxonomy id: **227984**

Copy

Print

<input type="checkbox"/>	<i>i</i> Name	NCBI Accession ID	Abbreviation	Molecule Ty...	BV...	BioProject ID	Collection Country	Completen...	DB Source	GC%	Host Group	Host Name
<input type="checkbox"/>	<i>i</i> Severe acute respira...	CQ918600.1	SARS-CoV	ssRNA+	694009.2482			partial	NCBI Virus & BVBC	65.625	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	1XJR_A	SARS-CoV	ssRNA+	742000.8			partial	NCBI Virus & BVBC	56.5217	vertebrates	
<input type="checkbox"/>	<i>i</i> Severe acute respira...	CS050821.1	SARS-CoV	ssRNA+	258445.86			partial	NCBI Virus & BVBC	58.3333	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	CS050841.1	SARS-CoV	ssRNA+	258445.84			partial	NCBI Virus & BVBC	55.2632	vertebrates	Patent
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<input type="checkbox"/>	<i>i</i> Severe acute respira...	CS050883.1	SARS-CoV	ssRNA+	258445.80			partial	NCBI Virus & BVBC	60.5263	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	CS050891.1	SARS-CoV	ssRNA+	258445.78			partial	NCBI Virus & BVBC	67.5	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456901.1	SARS-CoV	ssRNA+	694009.2491			partial	NCBI Virus & BVBC	63.1579	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456909.1	SARS-CoV	ssRNA+	694009.2482			partial	NCBI Virus & BVBC	55	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456912.1	SARS-CoV	ssRNA+	694009.2479			partial	NCBI Virus & BVBC	63.1579	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456913.1	SARS-CoV	ssRNA+	694009.2478			partial	NCBI Virus & BVBC	61.1111	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456914.1	SARS-CoV	ssRNA+	694009.2477			partial	NCBI Virus & BVBC	57.8947	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456915.1	SARS-CoV	ssRNA+	694009.2476			partial	NCBI Virus & BVBC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456918.1	SARS-CoV	ssRNA+	694009.2473			partial	NCBI Virus & BVBC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DD456919.1	SARS-CoV	ssRNA+	694009.2472			partial	NCBI Virus & BVBC	55.5556	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DJ011594.1	SARS-CoV	ssRNA+	258445.76			partial	NCBI Virus & BVBC	58.3333	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DJ011614.1	SARS-CoV	ssRNA+	258445.74			partial	NCBI Virus & BVBC	55.2632	vertebrates	Patent
<input type="checkbox"/>	<i>i</i> Severe acute respira...	DJ011635.1	SARS-CoV	ssRNA+	258445.72			partial	NCBI Virus & BVBC	55.2632	vertebrates	Patent

Choose Columns

 Check all Columns Abbreviation ⓘ BioProject ID ⓘ BioSample ID ⓘ BVBC ID ⓘ Collection Country ⓘ Collection Date ⓘ Collection Tissue ⓘ Collection Year ⓘ Completeness ⓘ DB Source ⓘ GC ⓘ Genome Quality ⓘ Host Age ⓘ Host Group ⓘ Host Name ⓘ Length ⓘ Molecule Type ⓘ Name ⓘ NCBI Accession ID ⓘ NCBI Assembly ID ⓘ NCBI Tax. ID ⓘ Number Of Contigs ⓘ Organization ⓘ PMID ⓘ Reference ⓘ Release Date ⓘ Representative ⓘ Sample ID ⓘ Segment Name ⓘ Sequencing Center ⓘ Species ⓘ Species Tax. ID ⓘ SRA Accession ⓘ Submitter ⓘ Variant ⓘ

Metadata Schema



<input type="checkbox"/>	Name	NCBI Accession ID
<input type="checkbox"/>	Severe acute respira...	NC_004718.3
<input type="checkbox"/>	Severe acute respira...	AY274119.3
<input type="checkbox"/>	Severe acute respira...	AY269391.1
<input type="checkbox"/>	Severe acute respira...	AY278554.2
<input type="checkbox"/>	Severe acute respira...	AY278491.2
<input type="checkbox"/>	Severe acute respira...	AY268049.1
<input type="checkbox"/>	Severe acute respira...	AY278487.3
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<input type="checkbox"/>	Severe acute respira...	AY283797.1

SARS-CoV	ssRNA+	227998.5			partial	NCBI Virus & BVBC	40.7978	vertebrates
SARS-CoV	ssRNA+	229206.11			complete	NCBI Virus & BVBC	40.7978	vertebrates
SARS-CoV	ssRNA+	235414.5		Singapore	complete	NCBI Virus & BVBC	40.7963	vertebrates
SARS-CoV	ssRNA+	235413.6		Singapore	complete	NCBI Virus & BVBC	40.8113	vertebrates
SARS-CoV	ssRNA+	235412.6		Singapore	complete	NCBI Virus & BVBC	40.7963	vertebrates
SARS-CoV	ssRNA+	235411.6		Singapore	complete	NCBI Virus & BVBC	40.7978	vertebrates

Welcome to the VirJenDB Download Page!

Archaeal Viruses

Download

Description: Compressed file containing all available metadata for archaeal viruses.

Version: 0.1

Release Date: 15.10.2023

Size: 17 KB

Format: CSV.gz

Linux/Mac: Open a terminal and download this file to your computer using the following command:

```
wget -c https://virjendb.org:8000/api/downloads/vj.s/vj.v0.1_archaeal_virus.csv.gz --no-check-certificate
```

For MacOS, if wget is not installed, use the following command:

```
curl -Ok https://virjendb.org:8000/api/downloads/vj.v0.1_archaeal_virus.csv.gz
```

SARS-CoV-2

Download

Description: Compressed file containing all available metadata for SARS-CoV-2.

Version: 0.1

Release Date: 15.10.2023

Size: 43 MB

Format: CSV.gz

Linux/Mac: Open a terminal and download this file to your computer using the following command:

```
wget -c https://virjendb.org:8000/api/downloads/s/vj.v0.1_sars_cov_2.csv.gz --no-check-certificate
```

For MacOS, if wget is not installed, use the following command:

```
curl -Ok https://virjendb.org:8000/api/downloads/vj.v0.1_sars_cov_2.csv.gz
```

Non-SARS-CoV-2

Download

Description: Compressed file containing all available metadata of samples that are not SARS-CoV-2.

Version: 0.1

Release Date: 15.10.2023

Size: 245 MB

Format: CSV.gz

Linux/Mac: Open a terminal and download this file to your computer using the following command:

```
wget -c https://virjendb.org:8000/api/downloads/s/vj.v0.1_non_sars_cov_2.csv.gz --no-check-certificate
```

For MacOS, if wget is not installed, use the following command:

```
curl -Ok https://virjendb.org:8000/api/downloads/vj.v0.1_non_sars_cov_2.csv.gz
```

Influenza A virus

Download

Description: Compressed file containing all available metadata for Influenza A virus.

Version: 0.1

Release Date: 15.10.2023

Size: 12 MB

Format: CSV.gz

Linux/Mac: Open a terminal and download this file to your computer using the following command:

```
wget -c https://virjendb.org:8000/api/downloads/s/vj.v0.1_influenza_A_virus.csv.gz --no-check-certificate
```

For MacOS, if wget is not installed, use the following command:

```
curl -Ok https://virjendb.org:8000/api/downloads/vj.v0.1_influenza_A_virus.csv.gz
```

Bacteriophages

Download

Description: Compressed file containing all available metadata for Bacteriophages.

Version: 0.1

Release Date: 15.10.2023

Download All Metadata

Download All

Description: Compressed file containing all available metadata for all viruses.

Version: 0.1

Release Date: 15.10.2023 (Last updated)

Advanced search:

Construct a complex query by combining multiple fields using logical operators. To start, select a field to search through and enter your search term in the adjacent text box. Then, choose a logical operator (AND, OR, NOT, NOR, NAND) to connect it to the existing query and click "ADD". If there is no query in the query box, it will display the recently added field and search term. To reset your query, click "Reset".

Use Boolean terms to build a complex query and click **ADD**. Click **Reset** to reset your query.

AND

OR

NOT

NOR

NAND

ADD

Reset

Your search terms will appear here!

Click the **Search** below to submit your query.

Search

Write your query as text with the following syntax: OPERATOR1 TERM1[FIELD1] OPERATOR2

Search history:

Click **Insert** to copy and Insert your keywords in the search term box.

(Germany[Collection Country]) AND (Complete[Completeness])

04/06/2024 - 23:38:35


Insert



Virus Taxonomy Browsing

Browse to access virus records based on the latest Masters Species List (MSL 38v3, see <https://ictv.global/msl>) from the International Committee on Taxonomy of Viruses (ICTV).

How to browse:

Click each rank to expand the connected subranks. Use the breadcrumb trail (e.g., Viruses/.../.../... etc) or your browser back button to navigate backward. Click on the  next to a taxa rank to perform a search of all the records in that taxonomy rank at the species level.

The number of ranks in the current level are shown out of the total number of ranks for that level. For example, there are 7 out of 7 Realms [Realms (7/7)] while within the Monodnaviria realm there are 4 kingdoms out of the total number of 10 kingdoms [shown as Kingdom (4/10)] in the virus taxonomy.

Virus 

Realm (7 / 7)

Adnaviria



Duplodnaviria



Monodnaviria



Riboviria



Ribozyviria



Varidnaviria



Undefined



[Search](#)

Results For: pox

Family (1)

Poxviridae



Sub

Centapoxvirus

(taxid:200550)

VIRION

EV envelop

MV memb

Lateral bo

Core wal



Avipoxvirus



Capripoxvirus



Centapoxvirus



Cervidpoxvirus



Crocodylidpoxvirus



Leporipoxvirus



Macropopoxvirus



Molluscipoxvirus



Static demo end

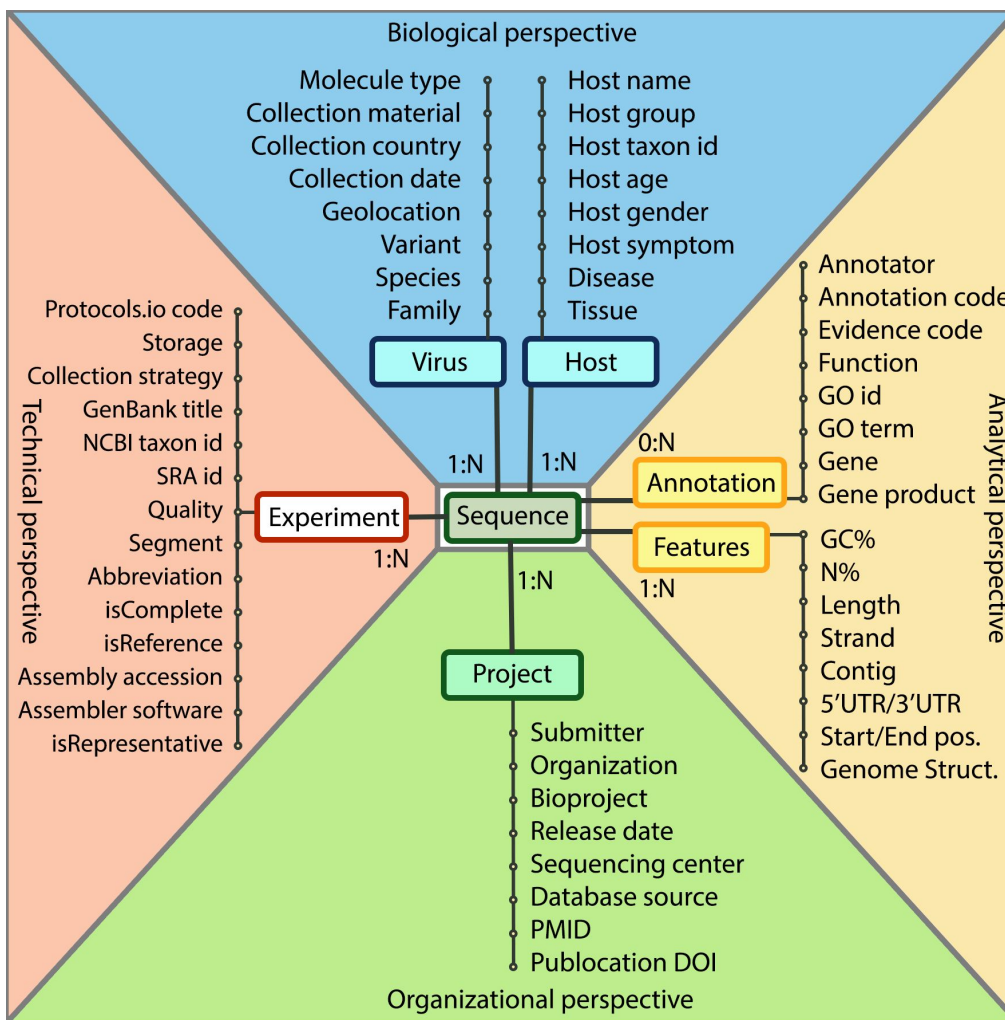
Virus metadata schema development



ROBERT KOCH INSTITUT



VJDB v0.1 metadata schema. Colors inspired by Bernasconi et al 2023



- Access, browse, download VJDB schemas & templates
- Expand the metadata schemas for specific viruses
- Pipeline for quality checking and correction of metadata

Summary of the VirJenDB Service and Use Case

- Pilot project connecting NFDI4Microbiota infrastructure
- Integrated dataset of virus metadata and (soon) genomic sequences
- Resource for data management of virus metadata and (soon) analysis
- Support to guide researchers to additional relevant virus resources



[virjendb.org](https://www.virjendb.org)



We welcome your input!

- Add your tool via nextflow on CloWM (de.NBI)
- **Become a beta tester** for the community curation feature
- Become an advisor or Ambassador

Stay tuned!

Planned release schedule for 2024 - 2026:



Helpdesk

Need help? Contact us!

The Helpdesk answers all kinds of questions and issues regarding data management and data analysis as well as queries about the NFDI4Microbiota consortium, services, outreach, community activities, and more.

Fill out the contact form or send us an email at helpdesk@nfdi4microbiota.de

Full Name

Contact Email Address

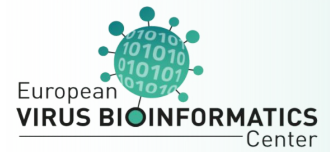
Issue type

Message

Please describe the problem here.

Security question: Please type the current year (YYYY).

The VirJenDB Team:



Dr. Noriko Cassman
Junior Group Leader (f/t)

Project manager
Coordinator + content
Data curator
Outreach



Shahram Saghaei
PhD Candidate (f/t)

Backend developer
Server architect
Data ingestor
Outreach



Prof. Dr. Manja Marz +
group
Principal Investigator

Coordinator + content
Outreach

Sarah Krautwurst
PhD Candidate -
Parttime outreach

Hamed Ziraksaz
Assistant - Parttime
Frontend developer

Soon to join:

- 1 f/t frontend developer (2024-2026)



FRIEDRICH-SCHILLER-
UNIVERSITÄT
JENA



NFDI4
MICROBIOTA

<https://nfdi4microbiota.de/contact-form/>

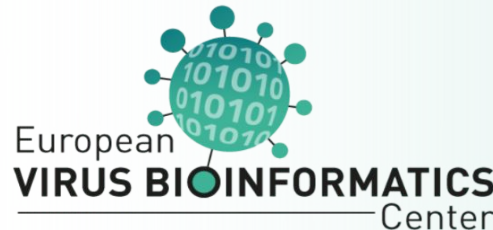
Thanks for your attention!

Web:

<https://virjendb.org>

Email:

virjendb@uni-jena.de



The NFDI4Microbiota Webportal and Helpdesk

Get in touch!

The Helpdesk can answer your questions on

- NFDI4Microbiota services
- Research Data Management
- FAIR Data Principles
- Data Management Plans
- Electronic Lab Notebooks
- Reproducible data analysis
- Data discovery and reuse
- Training
- ... and more



Send us an email at helpdesk@nfdi4microbiota.de or fill out the contact form

A screenshot of the NFDI4Microbiota website. The top navigation bar includes 'Services', 'Community', 'Helpdesk', 'Newsroom', and 'About Us'. The 'Helpdesk' link is highlighted with a black underline. Below the navigation, there is a main content area with the text 'Democratize access to microbiota data and high-end computational analyzes' and a 'Learn more' button. To the right, there is a megaphone icon and the NFDI4Microbiota logo. A yellow banner at the bottom right says 'The second Newsletter for 2024 is out! Read it here.' Below this, there are three columns: 'Training' with a description, 'Events' with a 'May' event 'NFDI4Microbiota Ambassador', and 'News' with a 'NFDI4Microbiota Symposium and...'. On the far right, there are four circular icons: a mail icon, a speech bubble icon, a refresh icon, and a search icon.

<https://nfdi4microbiota.de/>

Upcoming Training Events

June 17 Online

NFDI4Microbiota Online Seminar on Electronic Lab Notebooks (ELNs)

July 8 – 26 Leipzig

Summer - School Trends in multi-omics data analysis for Microbial Ecology and Biotechnology – UFZ Leipzig

October 9 – 10 Giessen

NFDI4Microbiota 16S amplicon training course

And much more...



Scan here for more info!

NFDI4 MICROBIOTA

SAVE THE DATE Annual Conference

When? December 3-4, 2024

Where? Leipzig, Germany

What?

- Panel discussion
- Keynotes
- Workshops
- and much more

More information
and registration



[https://nfdi4microbiota.de/
newsroom/events.html](https://nfdi4microbiota.de/newsroom/events.html)

Thank you!

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