Resource Summary Report

Generated by NIF on May 16, 2025

SEED

RRID:SCR_002129
Type: Tool

Proper Citation

SEED (RRID:SCR_002129)

Resource Information

URL: http://www.theseed.org/wiki/Home_of_the_SEED

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Description: The SEED is a framework to support comparative analysis and annotation of genomes. The cooperative effort focuses on the development of the comparative genomics environment and, more importantly, on the development of curated genomic data. Curation of genomic data (annotation) is done via the curation of subsystems by an expert annotator across many genomes, not on a gene by gene basis. From the curated subsystems we extract a set of freely available protein families (FIGfams). These FIGfams form the core component of our RAST automated annotation technology. Answering numerous requests for automatic Seed-Quality annotations for more or less complete bacterial and archaeal genomes, we have established the free RAST-Server (RAST=Rapid Annotation using Subsytems Technology). Using similar technology, we make the Metagenomics-RAST-Server freely available. We also provide a SEED-Viewer that allows read-only access to the latest curated data sets. We currently have 58 Archaea, 902 Bacteria, 562 Eukaryota, 1254 Plasmids and 1713 Viruses in our database. All tools and datasets that make up the SEED are in the public domain and can be downloaded at ftp://ftp.theseed.org

Abbreviations: SEED

Synonyms: The SEED

Resource Type: data set, service resource, production service resource, data or information resource, data analysis service, database, analysis service resource

Defining Citation: PMID:16214803

Keywords: environmental genome, eukaryal, archaeal, bacterial, viral, FASEB list

Funding:

Resource Name: SEED

Resource ID: SCR_002129

Alternate IDs: nif-0000-20923

Alternate URLs: http://www.theseed.org/wiki/Main_Page

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250516T053627+0000

Ratings and Alerts

No rating or validation information has been found for SEED.

No alerts have been found for SEED.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 467 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Kambach S, et al. (2025) Putting seedlings on the map: Trade-offs in demographic rates between ontogenetic size classes in five tropical forests. Ecology, 106(1), e4527.

Mašková Z, et al. (2025) Hermetia illucens in the Process of Kitchen Waste Biodegradation: The Effect of Different Approaches to Waste Storage on the Microbiological Profile and Nutritional Parameters of the Larvae. Insects, 16(1).

Dai W, et al. (2025) Metagenomic Insights into Pigeon Gut Microbiota Characteristics and Antibiotic-Resistant Genes. Biology, 14(1).

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Zhao J, et al. (2024) PhageGE: an interactive web platform for exploratory analysis and

visualization of bacteriophage genomes. GigaScience, 13.

Derikvand P, et al. (2024) Inoculum and pH effects on ammonium removal and microbial community dynamics in aquaponics systems. iScience, 27(3), 109073.

Zmuda AJ, et al. (2024) A universal metabolite repair enzyme removes a strong inhibitor of the TCA cycle. Nature communications, 15(1), 846.

Amin MHF, et al. (2024) A simple and cost-effective extraction for piscine environmental DNA metabarcoding using guanidine hydrochloride method. MethodsX, 13, 103020.

Price MN, et al. (2024) Interactive tools for functional annotation of bacterial genomes. Database : the journal of biological databases and curation, 2024.

Wu X, et al. (2024) Multi-source domain adaptation for EEG emotion recognition based on inter-domain sample hybridization. Frontiers in human neuroscience, 18, 1464431.

Lee S, et al. (2024) Plant growth-promoting rhizobacterium Bacillus megaterium modulates the expression of antioxidant-related and drought-responsive genes to protect rice (Oryza sativa L.) from drought. Frontiers in microbiology, 15, 1430546.

Richy E, et al. (2024) Long-read sequencing sheds light on key bacteria contributing to deadwood decomposition processes. Environmental microbiome, 19(1), 99.

Sharma N, et al. (2024) Metagenomic insights into microbial community, functional annotation, and antibiotic resistance genes in Himalayan Brahmaputra River sediment, India. Frontiers in microbiology, 15, 1426463.

Arzamasov AA, et al. (2024) Integrative genomic reconstruction of carbohydrate utilization networks in bifidobacteria: global trends, local variability, and dietary adaptation. bioRxiv : the preprint server for biology.

He F, et al. (2024) Development and External Validation of Machine Learning Models for Diabetic Microvascular Complications: Cross-Sectional Study With Metabolites. Journal of medical Internet research, 26, e41065.

Mingers T, et al. (2024) The alternative coproporphyrinogen III oxidase (CgoN) catalyzes the oxygen-independent conversion of coproporphyrinogen III into coproporphyrin III. Frontiers in microbiology, 15, 1378989.

Luo B, et al. (2024) Ethnobotanical insights into the traditional food plants of the Baiku Yao community: a study of cultural significance, utilization, and conservation. Journal of ethnobiology and ethnomedicine, 20(1), 52.

Liu ZT, et al. (2024) Organic fertilization co-selects genetically linked antibiotic and metal(loid) resistance genes in global soil microbiome. Nature communications, 15(1), 5168.

Geng J, et al. (2024) Impact of Incorporating Shiitake Mushrooms (Lentinula edodes) on Microbial Community and Flavor Volatiles in Traditional Jiuqu. Foods (Basel, Switzerland), 13(7).

Partipilo M, et al. (2024) The S-component fold: a link between bacterial transporters and receptors. Communications biology, 7(1), 610.