

Resource Summary Report

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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 Subsystems 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: analysis service resource, data analysis service, data or information resource, data set, database, production service resource, service resource

Defining Citation: [PMID:16214803](#)

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

Availability: Free, Freely Available

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: 20260821T193635+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 512 mentions in open access literature.

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

Martedì R, et al. (2026) De novo cysteine biosynthesis in *Pseudomonas aeruginosa*: Characterization of the two main cysteine synthase isoforms. *iScience*, 29(1), 114304.

Khurajog B, et al. (2026) Effectiveness of probiotic supplementation on growth performance, gut microbiota, and *Salmonella* reduction in broiler chicks challenged with *Salmonella Typhimurium*. *Scientific reports*, 16(1), 6983.

Chesneau G, et al. (2026) Lactuchelins represent lipopeptide siderophores produced by *Pseudomonas lactucae* that inhibit *Xanthomonas campestris*. *The ISME journal*, 20(1).

Margaret MJ, et al. (2026) On the prediction models for brain signal-based emotion recognition. *Scientific reports*, 16(1).

Goodall T, et al. (2026) Taxonomic filtering accompanies functional expansion during long-term soil restoration. *The ISME journal*, 20(1).

Enebe MC, et al. (2026) Microbial membrane transport genes in maize rhizosphere under fertilization - a preliminary study. *Scientific reports*, 16(1).

Pantoja L, et al. (2026) Genomic Analysis of Gut Bacteria in *Tecia Solanivora*: Insights into Host Functions and Their Potential in Biocontrol. *Current microbiology*, 83(8).

Jenab K, et al. (2026) Arbuscular mycorrhizal fungal families and exploration-based guilds exhibit distinct responses to long-term N, P and K deficiencies and imbalances. *The New phytologist*, 250(3), 1846.

Nosalova L, et al. (2026) *Pollutimonas rozaliensis* sp. nov., a novel bacterium isolated from gold ore of the active Rozalia mine (Central Europe, Slovakia). *Archives of microbiology*, 208(6).

Han S, et al. (2026) Functional Genome Annotation of *Lactiplantibacillus pentosus* KMU32 Reveals Its Dual Potential as a Starter Culture and Probiotic from Traditional Korean Kimchi. *Journal of microbiology and biotechnology*, 36, e2603032.

Vazquez-Cruz C, et al. (2026) *Actinobacillus seminis* DnaK interacts with bovine transferrin, lactoferrin, and hemoglobin as a putative iron acquisition mechanism. *Folia microbiologica*, 71(2), 369.

Kohl MP, et al. (2026) Extended Shine-Dalgarno motifs govern translation initiation in *Staphylococcus aureus*. *Nature communications*, 17(1).

Wang F, et al. (2026) Residual eDNA in eRNA Extracts Skews eRNA-Based Biodiversity Assessment: Call for Optimised DNase Treatment. *Molecular ecology resources*, 26(2), e70102.

Ravi A, et al. (2026) Cattle feces are a reservoir of diverse *Acinetobacter* species with potential to spread antibiotic resistance genes. *Animal microbiome*, 8(1).

Brestovi?ová S, et al. (2026) *Idiomarina solivarensis* sp. nov., halophilic bacterium isolated from brine of the former subsurface salt mine in Solivar (Slovakia) showing a unique fatty acids profile. *Archives of microbiology*, 208(9).

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).

Nagy B, et al. (2025) Effects of light exposure during IVF: transcriptomic analysis of murine embryos and embryo-derived EVs. *Frontiers in immunology*, 16, 1429252.

Howerton EM, et al. (2025) An epigenome-wide association study in the case-control study to explore early development identifies differential DNA methylation near ZFP57 as associated with autistic traits. *Journal of neurodevelopmental disorders*, 17(1), 49.

Thomsen T, et al. (2025) Arctic Soil C and N Cycling Are Linked With Microbial Adaptations During Drought. *Global change biology*, 31(9), e70502.