

Resource Summary Report

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JSpeciesWS

RRID:SCR_022059

Type: Tool

Proper Citation

JSpeciesWS (RRID:SCR_022059)

Resource Information

URL: <http://jspecies.ribohost.com/jspeciesws/#analyse>

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Description: Web server for prokaryotic species circumscription based on pairwise genome comparison. Service for in silico calculating extent of identity between two genomes, parameter routinely used in process of polyphasic microbial species circumscription. Service measures average nucleotide identity.

Synonyms: JSpecies Web Server

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:26576653](#)

Keywords: prokaryotic species circumscription, pairwise genome comparison, average nucleotide identity measurement

Funding: European Community Seventh Framework Programme

Availability: Free, Freely available

Resource Name: JSpeciesWS

Resource ID: SCR_022059

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260912T200004+0000

Ratings and Alerts

No rating or validation information has been found for JSpeciesWS.

No alerts have been found for JSpeciesWS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Oubassou EZ, et al. (2026) Genome sequencing and comparative analysis of *Nocardiosis moroccensis* sp. nov., a halotolerant Actinomycetota from Moroccan hypersaline ecosystem. BMC microbiology, 26(1).

Xia Y, et al. (2025) Conserved marseilleviruses harboring diverse antibiotic resistance genes isolated from the Yangtze river Delta and the Pearl river delta, China. Scientific reports, 15(1), 10663.

Goodman RN, et al. (2025) Comparative genomics of blood and faecal *E. coli* and *K. pneumoniae* isolates from neonates with bloodstream infections in Tanzania. Communications biology, 8(1), 1603.

Muema EK, et al. (2025) *Mesorhizobium salmacidum* sp. nov. and *Mesorhizobium argentiipisi* sp. nov. are symbionts of the dry-land forage legumes *Lessertia diffusa* and *Calobota sericea*. Antonie van Leeuwenhoek, 118(3), 54.

Núñez M, et al. (2025) Adapting to UV: Integrative Genomic and Structural Analysis in Bacteria from Chilean Extreme Environments. International journal of molecular sciences, 26(12).

Olana MD, et al. (2025) Molecular characterization of serotype and virulence genes of *Pseudomonas aeruginosa* isolated from patients admitted at two hospitals in Addis Ababa, Ethiopia. Journal of medical microbiology, 74(6).

Azam SM, et al. (2025) Isolation and Genome Analysis of *Serratia ureilytica* T6, a Heavy Metal(Ioid)-Resistant and Plant Growth-Promoting Bacterium, from Rice Soil. Microorganisms, 13(12).

Tizabi D, et al. (2025) Nanopore Sequencing of *Amoebophrya* Species Reveals Novel Collection of Bacteria Putatively Associated With *Karlodinium veneficum*. Genome biology and evolution, 17(3).

Wang X, et al. (2024) *Sphingomonas lacusdianchii* sp. nov., an attached bacterium inhibited by metabolites from its symbiotic cyanobacterium. Applied microbiology and biotechnology, 108(1), 309.

Rojas-Vargas J, et al. (2024) A comparative genomic study of a hydrocarbon-degrading marine bacterial consortium. PloS one, 19(8), e0303363.

Alnaimat SM, et al. (2024) Comparative genomic characterization of *Cellulosimicrobium funkei* isolate RVMD1 from Ma'an desert rock varnish challenges *Cellulosimicrobium* systematics. *Frontiers in microbiology*, 15, 1445943.

Skwor T, et al. (2024) First Report and Characterization of a Plasmid-Encoded blaSFO-1 in a Multi-Drug-Resistant *Aeromonas hydrophila* Clinical Isolate. *Microorganisms*, 12(3).

Irimajiri R, et al. (2024) Complete genome sequence of *Lentilactobacillus buchneri* subsp. *silagei* MGR2-32 isolated from guinea grass silage in Okinawa, Japan. *Microbiology resource announcements*, 13(4), e0069523.

Xu G, et al. (2024) Whole Genome Sequencing and Biocontrol Potential of *Streptomyces luteireticuli* ASG80 Against *Phytophthora* Diseases. *Microorganisms*, 12(11).

Shen C, et al. (2023) Molecular epidemiology and genomic dynamics of *Pseudomonas aeruginosa* isolates causing relapse infections. *Microbiology spectrum*, 11(5), e0531222.

Kuwabara M, et al. (2023) Complete Genome Sequence of the Thermophilic *Enterococcus faecalis* Strain K-4, Isolated from a Grass Silage in Thailand. *Microbiology resource announcements*, 12(4), e0081422.

Sun Y, et al. (2023) Complete genome sequence of the *Pogostemon cablin* bacterial wilt pathogen *Ralstonia solanacearum* strain SY1. *Genes & genomics*, 45(1), 123.

Liu W, et al. (2022) Complete genome sequencing and comparison of two nitrogen-metabolizing bacteria isolated from Antarctic deep-sea sediment. *BMC genomics*, 23(1), 713.

Altimira F, et al. (2022) Genomic and Experimental Analysis of the Insecticidal Factors Secreted by the Entomopathogenic Fungus *Beauveria pseudobassiana* RGM 2184. *Journal of fungi* (Basel, Switzerland), 8(3).

Ma K, et al. (2022) Genome mining reveals polysaccharide-degrading potential and new antimicrobial gene clusters of novel intestinal bacterium *Paenibacillus jilinensis* sp. nov. *BMC genomics*, 23(1), 380.