

Resource Summary Report

Generated by [NIF](#) on Sep 9, 2026

OrthoANlu

RRID:SCR_022562

Type: Tool

Proper Citation

OrthoANlu (RRID:SCR_022562)

Resource Information

URL: <https://www.ezbiocloud.net/tools/orthoaniu>

Proper Citation: OrthoANlu (RRID:SCR_022562)

Description: Software tool for calculating average nucleotide identity.

Synonyms: Average Nucleotide Identity

Resource Type: data analytics software, software application, software resource

Defining Citation: [PMID:26585518](#)

Keywords: calculating average nucleotide identity, nucleotide identity

Funding: NSF NRF-2014M3C9A3063541;
NSF NRF-2015R1A2A2A01008404

Resource Name: OrthoANlu

Resource ID: SCR_022562

Record Creation Time: 20220716T050142+0000

Record Last Update: 20260905T133311+0000

Ratings and Alerts

No rating or validation information has been found for OrthoANlu.

No alerts have been found for OrthoANlu.

Data and Source Information

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Sabri M, et al. (2026) Identification and characterization of Phi1 and Phi3 bacteriophages targeting *Xylella fastidiosa* subsp. *pauca*, the causal agent of olive quick decline in Italy. *Scientific reports*, 16(1).

Tenea GN, et al. (2026) Genomic and metabolomic insights into the antimicrobial and therapeutic potential of *Lactiplantibacillus plantarum* UTNGt28L isolated from Amazonian star apple. *Frontiers in microbiology*, 17, 1771106.

Galani A, et al. (2026) Comparative Physiology and Genomics of *Thermincola* and *Carboxydocella* Strains and Description of Two Novel Isolates. *Environmental microbiology*, 28(3), e70283.

Intarapakit N, et al. (2026) Genomic insights into a novel species, *Dyella thailandensis* sp. nov., a cellulolytic and xylanolytic bacterium isolated from soil associated with leaf compost. *Scientific reports*, 16(1), 1287.

Ghevondyan D, et al. (2026) Genomic and chemical insights into a human lectin-binding extracellular polysaccharides from *Parageobacillus toebii* strain H-70. *PloS one*, 21(1), e0340423.

Mori H, et al. (2026) Microbiome Datahub: an open-access platform integrating environmental metadata, taxonomy, and functional annotation for comprehensive metagenome-assembled genome datasets. *Microbiome*, 14(1).

Boisram?? A, et al. (2026) Genomic and transcriptomic insights into *Trichomonascus vanleenenianus*, a xylan-degrading yeast isolated from saproxylic insect larvae. *BMC genomics*, 27(1).

Salengros A, et al. (2026) Uncovering the ecophysiological potential of *Motilimonas* through genomic profiling analysis. *BMC genomics*, 27(1).

Ercole TG, et al. (2026) Integrated genome mining and phytohormone profiling of six plant growth-promoting elite bacterial strains. *Archives of microbiology*, 208(3), 152.

Masum MHU, et al. (2026) Whole genome and phylogenomic insights into *Vibrio parahaemolyticus* from Pacific White Shrimp reveal resistance and virulence traits in Bangladeshi aquaculture. *PloS one*, 21(4), e0346962.

Shaaban MT, et al. (2026) Comparative morphological, genomic, and functional characterization of two newly isolated lytic caudoviricetes phages targeting *Escherichia coli* and *Salmonella*. *Scientific reports*, 16(1).

Sotiropoulos AG, et al. (2026) Combining pangenomics and population genetics finds chromosomal re-arrangements, diversified chromosome segments, copy number variations and transposon polymorphisms in wheat and rye powdery mildew. *PLoS pathogens*, 22(4), e1013196.

Brierley S, et al. (2026) Description of *Bartonella bennetti* sp. nov., a novel rodent-associated species, with comparative genomics of the *Bartonella* genus. *International journal of systematic and evolutionary microbiology*, 76(3).

Sun L, et al. (2026) Isolation, Identification, and Genomic Characterization of a Cellulolytic *Bacillus subtilis* A2 from Goose Ileum. *Microorganisms*, 14(6).

Jihnaoui N, et al. (2026) *Bradyrhizobium cedriense* sp. nov., a novel rhizobial species isolated from *Acacia saligna* nodules grown in polluted soils in Tunisia. *International journal of systematic and evolutionary microbiology*, 76(4).

Kurmangali D, et al. (2026) High-quality draft genome sequence data of *Levilactobacillus brevis* 3LB isolated from fermented milk koumiss. *Data in brief*, 67, 112985.

Komorowski AS, et al. (2025) Molecular Epidemiology of Clinical Infections Caused by *Serratia marcescens* Complex in a Tertiary Care Hospital System: Insights From Whole-Genome Sequencing. *The Journal of infectious diseases*, 232(4), e589.

Alexyuk PG, et al. (2025) Genomic and Drug Resistance Profile of Bovine Multidrug-Resistant *Escherichia coli* Isolated in Kazakhstan. *Pathogens (Basel, Switzerland)*, 14(1).

Plangsangmas T, et al. (2025) Molecular Characterization and Clinicopathological Findings of *Mycoplasma pogonae* Infection in Captive Central Bearded Dragons (*Pogona vitticeps*). *Animals : an open access journal from MDPI*, 16(1).

Shu W, et al. (2025) Description of *Streptomyces explomaris* sp. nov., isolated from the coastal soil rhizosphere of *Juniperus excelsa* and reclassification of *Streptomyces libani* as a later heterotypic synonym of *Streptomyces nigrescens*. *International journal of systematic and evolutionary microbiology*, 75(5).