

Resource Summary Report

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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: software application, software resource, data analytics software

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: 20260731T043129+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 70 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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

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.

Tang T, et al. (2025) Bacteriocin Antagonistic Potentials of *Lactococcus cremoris* and *Lactococcus lactis* Isolates from Different Habitats. *Probiotics and antimicrobial proteins*, 17(6), 4203.

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).

Plomp N, et al. (2025) Synergy between culturomics and metagenomics of health status-associated gut bacteria originating from non-IBD and IBD populations. *Scientific reports*, 15(1), 45469.

Morohoshi T, et al. (2025) Distribution and Characterization of the Novel Quorum-quenching Enzyme AiiB in *Priestia megaterium* Isolated from a Natural Environment. *Microbes and environments*, 40(3).

Schultz Marcolla C, et al. (2025) Impact of a defined bacterial community including and excluding *Megamonas hypermegale* on broiler cecal microbiota and resistance to *Salmonella* infection. *Applied and environmental microbiology*, 91(9), e0094825.

Patil N, et al. (2025) Deletion or overexpression of *tpx* gene alters doubling time and response to stress agents and affects asphaltene biotransformation in *Micrococcus* sp. IITD107. *Applied microbiology and biotechnology*, 109(1), 269.

Sedlářek I, et al. (2025) Psychrotolerant *Erwinia psychrophila* sp. nov. and *Erwinia magellanica* sp. nov. Isolated from Penguin Faeces. *Current microbiology*, 83(2), 93.

Fan C, et al. (2025) A plasmid-borne *gadRCB* operon contributes to acid tolerance in *Lactiplantibacillus plantarum* ZR79. *Applied microbiology and biotechnology*, 109(1), 251.

Hsouna J, et al. (2025) *Bradyrhizobium tunisiense* sp. nov., a novel rhizobial species isolated from *Acacia saligna* nodules. *International journal of systematic and evolutionary microbiology*, 75(6).

Bryant JL, et al. (2025) Phenotypic and Complete Reference Whole Genome Sequence Analyses of Two *Paenibacillus* spp. Isolates from a Gray Wolf (*Canis lupus*) Gastrointestinal Tract. *Veterinary sciences*, 12(1).

Traversa D, et al. (2025) De Novo Assembly of the Polyhydroxybutyrate (PHB) Producer *Azohydromonas lata* Strain H1 Genome and Genomic Analysis of PHB Production Machinery. *Microorganisms*, 13(1).

Kim KM, et al. (2025) Genetic isolation and metabolic complexity of an Antarctic subglacial microbiome. *Nature communications*, 16(1), 7501.

Coelho MA, et al. (2025) Genomic and phenotypic insights into the expanding phylogenetic landscape of the *Cryptococcus* genus. *PLoS genetics*, 21(11), e1011945.

Fu Z, et al. (2024) Characterization of Endophytic *Streptomyces rhizosphaericola* Ahn75 and Its Potential for Biocontrol against Rice Blast. *Journal of microbiology and biotechnology*, 34(12), 2516.

Luo H, et al. (2024) Intraspecific cooperation allows the survival of *Staphylococcus aureus* staff: a novel strategy for disease relapse. *BMC infectious diseases*, 24(1), 1092.

Straková D, et al. (2024) Decoding the Genomic Profile of the *Halomicroarcula* Genus: Comparative Analysis and Characterization of Two Novel Species. *Microorganisms*, 12(2).

Commans F, et al. (2024) Whole-genome sequence and resistance determinants of four *Elizabethkingia anophelis* clinical isolates collected in Hanoi, Vietnam. *Scientific reports*, 14(1), 7241.

Straková D, et al. (2024) Reclassification of *Halomicroarcula saliterrae* Straková et al. 2024 and *Halomicroarcula onubensis* Straková et al. 2024 into the genus *Haloarcula*, as *Haloarcula saliterrae* comb. nov. and *Haloarcula onubensis* comb. nov., respectively. *International journal of systematic and evolutionary microbiology*, 74(9).