

# 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;  
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**Resource Name:** OrthoANlu

**Resource ID:** SCR\_022562

**Record Creation Time:** 20220716T050142+0000

**Record Last Update:** 20260805T044506+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 [RRID](#) .

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.

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.

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.

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.

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.

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.

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).