

Resource Summary Report

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Newbler

RRID:SCR_011916

Type: Tool

Proper Citation

Newbler (RRID:SCR_011916)

Resource Information

URL:

http://swes.cals.arizona.edu/maier_lab/kartchner/documentation/index.php/home/docs/newbler

Proper Citation: Newbler (RRID:SCR_011916)

Description: A software package for de novo DNA sequence assembly.

Abbreviations: Newbler

Resource Type: software resource

Resource Name: Newbler

Resource ID: SCR_011916

Alternate IDs: OMICS_01428

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190725+0000

Ratings and Alerts

No rating or validation information has been found for Newbler.

No alerts have been found for Newbler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1336 mentions in open access literature.

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

Washington JM, et al. (2025) Expanding the Diversity of Actinobacterial Tectiviridae: A Novel Genus from Microbacterium. *Viruses*, 17(1).

Stribling W, et al. (2025) Detecting, mapping, and suppressing the spread of a decade-long *Pseudomonas aeruginosa* nosocomial outbreak with genomics. *eLife*, 13.

Li X, et al. (2025) Systematic evaluation of phenotypic variations induced by prophages in a clinical isolate of *Pseudomonas aeruginosa*. *mSystems*, 10(9), e0042825.

Zamostiano R, et al. (2025) The snakehead retrovirus promoter functions independently of the 3'ORF protein and its products are maternally inherited in transgenic zebrafish. *PLoS pathogens*, 21(6), e1013243.

Wan S, et al. (2025) Biological Characteristics and Whole-Genome Analysis of a Porcine *E. coli* Phage. *Veterinary sciences*, 12(1).

Culot A, et al. (2025) High-Performance Genome Annotation for a Safer and Faster-Developing Phage Therapy. *Viruses*, 17(3).

Castelo-Branco R, et al. (2025) Phosphorylation of peptides by a kinase domain in cyanobactin pathways. *Nature communications*, 16(1), 10279.

Mori K, et al. (2025) Isolation and characterization of a bacterium affiliated with the hitherto uncultured candidate phylum WOR-3 from a deep-sea hydrothermal fluid. *Applied and environmental microbiology*, 91(7), e0018825.

Chen Z-Y, et al. (2025) Characteristics of viral ovarian tumor domain protease from two emerging orthornairoviruses and identification of Yezo virus human infections in northeastern China as early as 2012. *Journal of virology*, 99(2), e0172724.

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).

Matsuda N, et al. (2025) Analysis of gene expression of *Babesia gibsoni* cultured with diminazene aceturate using RNA sequencing. *The Journal of veterinary medical science*, 87(2), 181.

Safronov O, et al. (2025) Independent evolution of betulin biosynthesis in *Inonotus obliquus*. *Scientific reports*, 15(1), 21319.

Xie P, et al. (2025) Evolution and characteristics of tetracycline resistance in *Mycoplasma pneumoniae*. *Microbiology spectrum*, 13(7), e0339824.

Li X, et al. (2025) Understanding phage BX-1 resistance in *Vibrio alginolyticus* AP-1 and the role of quorum-sensing regulation. *Microbiology spectrum*, 13(2), e0243524.

Jung D, et al. (2025) Comparative genomic analysis of *Escherichia coli* isolated from cases of bovine clinical mastitis and the dairy farm environment. *Microbial genomics*, 11(6).

Xu C, et al. (2025) Assembly and comparative analysis of the complete mitochondrial of *Spodiopogon sagittifolius*, an endemic and protective species from Yunnan, China. *BMC plant biology*, 25(1), 373.

Aldaroub J, et al. (2025) Isolation and characterization of four novel *Vibrio parahaemolyticus* bacteriophages from oysters. *PloS one*, 20(12), e0339894.

Tobin LA, et al. (2025) Genomic analysis of early ST32 *Acinetobacter baumannii* strains recovered in US military treatment facilities reveals distinct lineages and links to the origins of the Tn6168 *ampC* transposon. *The Journal of antimicrobial chemotherapy*, 80(3), 666.

Xi Y, et al. (2025) Stability of gut microbiota in non-small cell lung cancer patients during chemoradiotherapy and its association with radiation pneumonitis. *iScience*, 28(8), 113163.

Shu W, et al. (2025) Metabolic engineering of *Streptomyces explomaris* for increased production of the reverse antibiotic nybomycin. *Microbial cell factories*, 24(1), 227.