

# Resource Summary Report

Generated by [dkNET](#) on Aug 30, 2026

## 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](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:** 20260829T182408+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 1343 mentions in open access literature.

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

Eroshenko GA, et al. (2026) The Role of the Caspian, Aral and Balkhash Lakes in the Spread and Preservation of *Yersinia pestis* in Eastern Europe and Central Asia in the 20th and 21st Centuries. *Pathogens* (Basel, Switzerland), 15(6).

Konno Y, et al. (2026) Symbiosis Islands of *Bradyrhizobium* Determine Relationships with Host Legumes *Lespedeza cuneata* and *Glycine max*. *Microbes and environments*, 41(1).

Lebreton F, et al. (2026) Preferred evolutionary routes of convergence in *Klebsiella pneumoniae* favor siderophore acquisition over hypervirulence. *Research square*.

Pereira MF, et al. (2026) Genomics of Hospital-Associated Brazilian Multidrug-Resistant *Klebsiella pneumoniae*: Abundance of Resistance and Virulence Genes and Mosaicism of the blaKPC-2 Genetic Context Among Enterobacterales. *Current microbiology*, 83(8).

Wei X, et al. (2026) Characterization and antibacterial efficacy of the broad-host-range phage P108 against biofilm-forming and methicillin-resistant *Staphylococcus aureus*. *Virus research*, 368, 199745.

Schulz K, et al. (2026) African swine fever outbreaks in German pig holdings - experiences, epidemiological considerations and genome sequences. *Scientific reports*, 16(1), 4350.

Chen D, et al. (2026) Analysis of mobile genetic elements carrying mcr genes in clinical *Leclercia* spp. isolates. *BMC microbiology*, 26(1).

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.

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

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

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

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

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

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

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

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.

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.