

Resource Summary Report

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Phrap

RRID:SCR_011917

Type: Tool

Proper Citation

Phrap (RRID:SCR_011917)

Resource Information

URL: <http://www.phrap.org/phredphrapconsed.html>

Proper Citation: Phrap (RRID:SCR_011917)

Description: A software program for assembling shotgun DNA sequence data.

Abbreviations: Phrap

Resource Type: software resource

Availability: Free to academic users

Resource Name: Phrap

Resource ID: SCR_011917

Alternate IDs: OMICS_01429

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260725T190727+0000

Ratings and Alerts

No rating or validation information has been found for Phrap.

No alerts have been found for Phrap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 370 mentions in open access literature.

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

Fechtner S, et al. (2025) 3,3-Dimethyl-1-Butanol and its Metabolite 3,3-Dimethylbutyrate Ameliorate Collagen-induced Arthritis Independent of Choline Trimethylamine Lyase Activity. *Inflammation*, 48(3), 1350.

Hartley GA, et al. (2025) Centromeric transposable elements and epigenetic status drive karyotypic variation in the eastern hoolock gibbon. *Cell genomics*, 5(4), 100808.

Mu W, et al. (2025) Characterization of the complete mitochondrial genomes of two sea cucumbers, *Deima validum* and *Oneirophanta mutabilis* (Holothuroidea, Synallactida, Deimatidae): Insight into deep-sea adaptive evolution of Deimatidae. *PloS one*, 20(5), e0323612.

Danbaki AS, et al. (2025) Pathogenic FANCC Variants Are Associated with Accessory Breasts in a Sub-Saharan African Multiplex Family. *Current issues in molecular biology*, 47(11).

W??hlbrand L, et al. (2025) Key role of Desulfobacteraceae in C/S cycles of marine sediments is based on congeneric catabolic-regulatory networks. *Science advances*, 11(10), eads5631.

Xiao R, et al. (2025) Phylogeographic and genetic insights into *Sinonychia martensi*: an endemic cave-dwelling harvestman in Beijing. *BMC ecology and evolution*, 25(1), 5.

Rivera J, et al. (2024) Phylogenomic, structural, and cell biological analyses reveal that *Stenotrophomonas maltophilia* replicates in acidified Rab7A-positive vacuoles of *Acanthamoeba castellanii*. *Microbiology spectrum*, 12(3), e0298823.

Cai Z, et al. (2024) Transcriptomic and Metatranscriptomic Analyses Provide New Insights into the Response of the Pea Aphid *Acyrtosiphon pisum* (Hemiptera: Aphididae) to Acetamiprid. *Insects*, 15(4).

Paulat NS, et al. (2023) Chiropterans Are a Hotspot for Horizontal Transfer of DNA Transposons in Mammalia. *Molecular biology and evolution*, 40(5).

Martinez-Hernandez F, et al. (2023) Genetic Variability of the Internal Transcribed Spacer and Pyruvate:Ferredoxin Oxidoreductase Partial Gene of *Trichomonas vaginalis* from Female Patients. *Microorganisms*, 11(9).

Butterfield RJ, et al. (2023) Deciphering D4Z4 CpG methylation gradients in fascioscapulohumeral muscular dystrophy using nanopore sequencing. *Genome research*, 33(9), 1439.

Mishina K, et al. (2023) Wheat Ym2 originated from *Aegilops sharonensis* and confers resistance to soil-borne Wheat yellow mosaic virus infection to the roots. *Proceedings of the National Academy of Sciences of the United States of America*, 120(11), e2214968120.

Tan CH, et al. (2023) De Novo Venom Gland Transcriptome Assembly and Characterization for *Calloselasma rhodostoma* (Kuhl, 1824), the Malayan Pit Viper from Malaysia: Unravelling Toxin Gene Diversity in a Medically Important Basal Crotaline. *Toxins*, 15(5).

Fechtner S, et al. (2023) 3,3-dimethyl-1-butanol and its metabolite 3,3-dimethylbutyrate ameliorate collagen-induced arthritis independent of choline trimethylamine lyase activity. *Research square*.

Tan CH, et al. (2023) De Novo Assembly of Venom Gland Transcriptome of *Tropidolaemus wagleri* (Temple Pit Viper, Malaysia) and Insights into the Origin of Its Major Toxin, Waglerin. *Toxins*, 15(9).

Iwanicki NSA, et al. (2022) Genomic signatures and insights into host niche adaptation of the entomopathogenic fungus *Metarhizium humberi*. *G3 (Bethesda, Md.)*, 12(2).

Crane CF, et al. (2022) slag: A program for seeded local assembly of genes in complex genomes. *Molecular ecology resources*, 22(5), 1999.

Storer JM, et al. (2022) Owl Monkey Alu Insertion Polymorphisms and Aotus Phylogenetics. *Genes*, 13(11).

Plassais J, et al. (2022) Natural and human-driven selection of a single non-coding body size variant in ancient and modern canids. *Current biology : CB*, 32(4), 889.

Jackson CL, et al. (2022) Evolution of the Gut Microbiome in HIV-Exposed Uninfected and Unexposed Infants during the First Year of Life. *mBio*, 13(5), e0122922.