

Resource Summary Report

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Staden Package

RRID:SCR_005629

Type: Tool

Proper Citation

Staden Package (RRID:SCR_005629)

Resource Information

URL: <http://staden.sourceforge.net/>

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Description: A fully developed set of DNA sequence assembly (Gap4 and Gap5), editing and analysis tools (Spin) for Unix, Linux, MacOSX and MS Windows.

Synonyms: Staden Package

Resource Type: software resource

Defining Citation: [PMID:20513662](#), [DOI:10.1093/bioinformatics/btq268](#)

Keywords: c, unix/linux, sequence assembly, dna/protein analysis, spin, sequence alignment, genome, genome viewer, c++, fortran, tcl, bio.tools

Availability: BSD License

Resource Name: Staden Package

Resource ID: SCR_005629

Alternate IDs: OMICS_00894, biotools:staden

Alternate URLs: <https://bio.tools/staden>, <https://sources.debian.org/src/staden/>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260821T193746+0000

Ratings and Alerts

No rating or validation information has been found for Staden Package.

No alerts have been found for Staden Package.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Yaikwawong M, et al. (2026) Associations of tumor necrosis factor alpha genetic variants with metabolic syndrome and type 2 diabetes mellitus in a Thai population. PloS one, 21(4), e0346147.

Acuña DC, et al. (2025) ?Taxonomic revalidation of *Selenobrachys* Schmidt, 1999 and *Chilocosmia* Schmidt & von Wirth, 1992 based on morphological and molecular analyses (Araneae, Theraphosidae), with the description of a new species from Romblon Island, Philippines. ZooKeys, 1233, 139.

Amr RM, et al. (2025) Correlation between the antibiotic resistance and virulence determinants of vancomycin-resistant enterococci: paradoxical involvement of *vanA* in phenotypic resistance to teicoplanin. Gut pathogens, 17(1), 110.

Troskie M, et al. (2025) Occurrence of tick-borne haemoparasites in South African rodent species evidence of *Babesia microti*-like sequence variants in two *Rhabdomys* species. International journal for parasitology. Parasites and wildlife, 26, 101051.

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. Cell genomics, 4(2), 100484.

Xie J, et al. (2024) Retrospective research: identifying and conducting phylogenetic analyses on four Orf virus strains isolated in Yunnan province between 2021 and 2023-revealing their significance and characteristic features. Frontiers in veterinary science, 11, 1481809.

Barry B, et al. (2024) Partial Sequence Analysis of Commercial Peste des Petits Ruminants Vaccines Produced in Africa. Veterinary sciences, 11(10).

Bueno-Marí R, et al. (2023) [*Wolbachia pipientis* infections in populations of *Aedes albopictus* in the city of València (Spain): implications for mosquito control]. Revista espanola de salud publica, 97.

Sacco JC, et al. (2023) Resequencing of the TMF-1 (TATA Element Modulatory Factor) regulated protein (TRNP1) gene in domestic and wild canids. Canine medicine and genetics, 10(1), 10.

Elshamy AA, et al. (2023) Transferable IncX3 plasmid harboring *bla*NDM-1, *ble*MBL, and *aph*(3')-VI genes from *Klebsiella pneumoniae* conferring phenotypic carbapenem resistance in *E. coli*. Molecular biology reports, 50(6), 4945.

Pena R, et al. (2023) Mycorrhizal C/N ratio determines plant-derived carbon and nitrogen allocation to symbiosis. *Communications biology*, 6(1), 1230.

Masembe C, et al. (2023) Diversity and emergence of new variants of African swine fever virus Genotype I circulating in domestic pigs in Nigeria (2016-2018). *Veterinary medicine and science*, 9(2), 819.

Bamford C, et al. (2023) Neoehrlichiosis in Symptomatic Immunocompetent Child, South Africa. *Emerging infectious diseases*, 29(2), 407.

Cabrera Mederos D, et al. (2022) An Unwanted Association: The Threat to Papaya Crops by a Novel Potexvirus in Northwest Argentina. *Viruses*, 14(10).

Yang N, et al. (2022) Soil nutrients and plant diversity affect ectomycorrhizal fungal community structure and functional traits across three subalpine coniferous forests. *Frontiers in microbiology*, 13, 1016610.

Molini U, et al. (2022) Molecular characterization of avipoxviruses circulating in Windhoek district, Namibia 2021. *The Journal of veterinary medical science*, 84(5), 707.

Daniels RS, et al. (2022) Temporal and Gene Reassortment Analysis of Influenza C Virus Outbreaks in Hong Kong, SAR, China. *Journal of virology*, 96(3), e0192821.

Isaac S, et al. (2022) Microbiome-mediated fructose depletion restricts murine gut colonization by vancomycin-resistant *Enterococcus*. *Nature communications*, 13(1), 7718.

Ouchene R, et al. (2022) Integrated Metabolomic, Molecular Networking, and Genome Mining Analyses Uncover Novel Angucyclines From *Streptomyces* sp. RO-S4 Strain Isolated From Bejaia Bay, Algeria. *Frontiers in microbiology*, 13, 906161.

Zhao Y, et al. (2022) Gene *sdaB* Is Involved in the Nematocidal Activity of *Enterobacter ludwigii* AA4 Against the Pine Wood Nematode *Bursaphelenchus xylophilus*. *Frontiers in microbiology*, 13, 870519.