

Resource Summary Report

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SSPACE

RRID:SCR_005056

Type: Tool

Proper Citation

SSPACE (RRID:SCR_005056)

Resource Information

URL: <http://www.baseclear.com/landingpages/basetools-a-wide-range-of-bioinformatics-solutions/sspacev12/>

Proper Citation: SSPACE (RRID:SCR_005056)

Description: A stand-alone software program for scaffolding pre-assembled contigs using paired-read data. Main features are: a short runtime, multiple library input of paired-end and/or mate pair datasets and possible contig extension with unmapped sequence reads.

Abbreviations: SSPACE

Resource Type: software resource

Defining Citation: [PMID:21149342](#), [DOI:10.1093/bioinformatics/btq683](#)

Keywords: scaffolding, contig, genome, bio.tools

Availability: GNU General Public License, Registration required

Resource Name: SSPACE

Resource ID: SCR_005056

Alternate IDs: biotools:sspace, OMICS_00050

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

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260801T190253+0000

Ratings and Alerts

No rating or validation information has been found for SSPACE.

No alerts have been found for SSPACE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 426 mentions in open access literature.

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

Chen SH, et al. (2025) Pathways to Recovery: Genomics and Resistance Assays for Tree Species Devastated by the Myrtle Rust Pathogen. *Molecular ecology*, 34(16), e70030.

Xu Y, et al. (2025) Genome analysis of viral hemorrhagic septicemia virus isolated from *Paralichthys olivaceus* in China. *Scientific reports*, 15(1), 32976.

Zhang H, et al. (2025) Mitochondrial Genome Comparison and Phylogenetic Analysis of Four Species of Dung Beetles (Coleoptera: Scarabaeidae: Scarabaeinae). *Ecology and evolution*, 15(8), e71906.

Zou T, et al. (2025) Chloroplast whole genome assembly and phylogenetic analysis of *Persicaria criopolitana* reveals its new taxonomic status. *Scientific reports*, 15(1), 19890.

Zheng HZ, et al. (2025) Comparative and evolutionary analysis of chloroplast genomes from five rare *Styrax* species. *BMC genomics*, 26(1), 450.

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte (Hong Kong, China)*, 2025, gigabyte155.

Rühlemann M, et al. (2025) Convergent genomic responses of human gut bacteria to variations in industrialization. *bioRxiv : the preprint server for biology*.

Carrier TJ, et al. (2025) Symbiont-Mediated Metabolic Shift in the Sea Anemone *Anthopleura elegantissima*. *Molecular ecology*, 34(8), e17722.

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Meng Y, et al. (2025) ?Complete mitochondrial genomes of *Sinonovacularivularis* and *Novaculinachinensis* and their phylogenetic relationships within family Pharidae. *ZooKeys*, 1232, 249.

Roberts WR, et al. (2025) Three reference genomes for freshwater diatom ecology and evolution. *Journal of phycology*, 61(2), 267.

Dittmer J, et al. (2025) The Endosymbiont Consortia of Two Cixiidae Planthoppers Reveal an Ancient Symbiosis With 'Candidatus Mirabilia Symbiotica'. *Environmental microbiology reports*, 17(5), e70204.

Boss A, et al. (2025) Genetic architecture of resistance to plant secondary metabolites in *Photorhabdus* entomopathogenic bacteria. *BMC genomics*, 26(1), 975.

Ribeyre Z, et al. (2025) De novo transcriptome assembly and discovery of drought-responsive genes in white spruce (*Picea glauca*). *PloS one*, 20(1), e0316661.

Mahillon M, et al. (2025) From insect endosymbiont to phloem colonizer: comparative genomics unveils the lifestyle transition of phytopathogenic *Arsenophonus* strains. *mSystems*, 10(5), e0149624.

Fang ?? Y, et al. (2025) Duckweed Evolution: from Land back to Water. *Genomics, proteomics & bioinformatics*, 23(4).

Durán-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPlib library. *BMC genomics*, 26(1), 473.

Zhang C, et al. (2024) Characterization and genomic analysis of a broad-spectrum lytic phage PG288: A potential natural therapy candidate for *Vibrio* infections. *Virus research*, 341, 199320.

White RT, et al. (2024) Genomic epidemiology reveals geographical clustering of multidrug-resistant *Escherichia coli* ST131 associated with bacteraemia in Wales. *Nature communications*, 15(1), 1371.

Wang W, et al. (2024) The complete chloroplast genome sequence of *Melochia corchorifolia* Linnaeus, 1753 (Sterculiaceae). *Mitochondrial DNA. Part B, Resources*, 9(1), 153.