

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: 20260821T193732+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 435 mentions in open access literature.

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

Kiran S, et al. (2026) Segmented filamentous bacteria are worldwide human gut commensals. *Nature communications*, 17(1).

Wilson HJ, et al. (2026) Whole-genome sequencing to investigate the prevalence and transmission of multidrug-resistant Gram-negative pathogens in an adult intensive care unit in the UK. *Microbial genomics*, 12(5).

da Silva FR, et al. (2026) Whole-Genome Sequencing and Comparative Genomic Analysis of *Leishmania (Viannia) naiffi* and *L. (Viannia) shawi* Reveal Species-Specific Genes and Novel Potential Drug Targets. *Microorganisms*, 14(2).

Boripun R, et al. (2026) Whole-Genome Sequence Analysis of Colistin-Resistant, mcr-Harboring *Escherichia coli* Isolated from a Swine Slaughterhouse in Thailand. *Antibiotics (Basel, Switzerland)*, 15(2).

Feng L, et al. (2026) Comprehensive analysis of the complete chloroplast genome of white pomegranate and phylogenetic relationships within Myrtales. *BMC genomics*, 27(1), 220.

Long W, et al. (2026) Comprehensive Analysis of Wild Rice Mitochondrial Genomes Reveals Structural Variation, Repeat Dynamics, and the Evolution of orf182. *Plants (Basel, Switzerland)*, 15(7).

Zhang Z, et al. (2026) A novel phage preparation capable of simultaneously inhibiting both K1 and K2 serotypes of *Klebsiella pneumoniae*. *Applied and environmental microbiology*, 92(3), e0242325.

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.

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.

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

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

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.

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.

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

Wang B, et al. (2025) Epidemiology, genetic dynamics, and transmission of the *mcr-1* gene in China. *Emerging microbes & infections*, 14(1), 2595798.

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

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).

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.