

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](https://pubmed.ncbi.nlm.nih.gov/21149342/), [DOI:10.1093/bioinformatics/btq683](https://doi.org/10.1093/bioinformatics/btq683)

Keywords: scaffolding, contig, genome, bio.tools

Funding:

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: 20250214T183116+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 410 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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.

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.

Errbii M, et al. (2024) Evolutionary genomics of socially polymorphic populations of *Pogonomyrmex californicus*. *BMC biology*, 22(1), 109.

Vargas AM, et al. (2024) Morphological and dietary changes encoded in the genome of *Beroe ovata*, a ctenophore-eating ctenophore. *NAR genomics and bioinformatics*, 6(2), lqae072.

Duan Y, et al. (2024) Comparative and phylogenetic analysis of the chloroplast genomes of four commonly used medicinal cultivars of *Chrysanthemums morifolium*. *BMC plant biology*, 24(1), 992.

He Q, et al. (2024) Complete mitochondrial genome sequencing and phylogenetic analysis of *Phellinus igniarius*. *Scientific reports*, 14(1), 31109.

Tathode MS, et al. (2024) Whole-genome analysis suggesting probiotic potential and safety properties of *Pediococcus pentosaceus* DSPZPP1, a promising LAB strain isolated from traditional fermented sausages of the Basilicata region (Southern Italy). *Frontiers in microbiology*, 15, 1268216.

Andradi-Brown C, et al. (2024) A novel computational pipeline for var gene expression augments the discovery of changes in the *Plasmodium falciparum* transcriptome during transition from in vivo to short-term in vitro culture. *eLife*, 12.

Belman S, et al. (2024) Geographical migration and fitness dynamics of *Streptococcus pneumoniae*. *Nature*, 631(8020), 386.

Du K, et al. (2024) Phylogenomic analyses of all species of swordtail fishes (genus *Xiphophorus*) show that hybridization preceded speciation. *Nature communications*, 15(1), 6609.

Miao H, et al. (2024) Genomic evolution and insights into agronomic trait innovations of *Sesamum* species. *Plant communications*, 5(1), 100729.

He J, et al. (2024) Novel Plastid Genome Characteristics in *Fugacium kawagutii* and the Trend of Accelerated Evolution of Plastid Proteins in Dinoflagellates. *Genome biology and evolution*, 16(1).

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, *Pectobacterium cacticida* and proposal for reclassification as *Alcorniella cacticida* comb. nov. *Frontiers in plant science*, 15, 1323790.

Hu J, et al. (2024) Comparative analysis of chloroplast genomes in ten holly (*Ilex*) species: insights into phylogenetics and genome evolution. *BMC ecology and evolution*, 24(1), 133.

Yang L, et al. (2024) Genomic analysis based on chromosome-level genome assembly reveals Myrtaceae evolution and terpene biosynthesis of rose myrtle. *BMC genomics*, 25(1), 578.

Nagasaki H, et al. (2024) Genomic variation across distribution of Micro-Tom, a model cultivar of tomato (*Solanum lycopersicum*). *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(5).

Zhao D, et al. (2024) Genomic Differences and Mutations in Epidemic Orf Virus and Vaccine Strains: Implications for Improving Orf Virus Vaccines. *Veterinary sciences*, 11(12).

Guizar Amador MF, et al. (2024) The *Gongora gibba* genome assembly provides new insights into the evolution of floral scent in male euglossine bee-pollinated orchids. *G3 (Bethesda, Md.)*, 14(11).