## SSPACE

**RRID:** SCR_005056  
**Type:** Tool

### Proper Citation

SSPACE (RRID:SCR_005056)

### Resource Information


**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.

**Resource Name:** SSPACE  
**Proper Citation:** SSPACE (RRID:SCR_005056)  
**Resource Type:** Resource, software resource  
**Keywords:** scaffolding, contig, genome  
**Resource ID:** SCR_005056  
**References:** PMID:21149342  
**Availability:** GNU General Public License, Registration required  
**Website Status:** Last checked up  
**Alternate IDs:** OMICS_00050

**Abbreviations:** SSPACE

**Mentions Count:** 239

### 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 239 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Alioto T, et al. (2020) Transposons played a major role in the diversification between the closely related almond and peach genomes: results from the almond genome sequence. The Plant journal : for cell and molecular biology, 101(2), 455-472.


Chen L, et al. (2019) The genomic basis for colonizing the freezing Southern Ocean revealed
by Antarctic toothfish and Patagonian robalo genomes. GigaScience, 8(4).


Wheeler NE, et al. (2019) Genomic correlates of extraintestinal infection are linked with changes in cell morphology in Campylobacter jejuni. Microbial genomics, 5(2).