

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## Scaffold builder

RRID:SCR\_000556

Type: Tool

---

### Proper Citation

Scaffold builder (RRID:SCR\_000556)

---

### Resource Information

**URL:** [http://edwards.sdsu.edu/scaffold\\_builder/](http://edwards.sdsu.edu/scaffold_builder/)

**Proper Citation:** Scaffold builder (RRID:SCR\_000556)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 6,2023. Tool designed to generate scaffolds (super contigs of sequences joined by N-bases) using the homology provided by a closely related reference sequence. Scaffold\_builder is an advanced wrapper for Nucmer, written in Python that resolves several situations that may arise when mapping contigs to the reference genome.

**Abbreviations:** scaffold\_builder

**Resource Type:** data analysis service, service resource, production service resource, analysis service resource

**Defining Citation:** [PMID:24267787](#)

**Keywords:** scaffolding

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Scaffold builder

**Resource ID:** SCR\_000556

**Alternate IDs:** OMICS\_00046

**Record Creation Time:** 20220129T080202+0000

**Record Last Update:** 20260801T190124+0000

---

### Ratings and Alerts

No rating or validation information has been found for Scaffold builder.

No alerts have been found for Scaffold builder.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We have not found any literature mentions for this resource.