## **Resource Summary Report**

Generated by dkNET on Apr 30, 2025

# Scaffold builder

RRID:SCR\_000556

Type: Tool

### **Proper Citation**

Scaffold builder (RRID:SCR\_000556)

#### Resource Information

URL: 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: analysis service resource, production service resource, data analysis

service, service resource

**Defining Citation: PMID:24267787** 

Keywords: scaffolding

**Funding:** 

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:** 20250430T055026+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.