## **Resource Summary Report**

Generated by <u>dkNET</u> on May 19, 2025

# SuperSegger

RRID:SCR\_018532 Type: Tool

**Proper Citation** 

SuperSegger (RRID:SCR\_018532)

#### **Resource Information**

URL: http://mtshasta.phys.washington.edu/website/SuperSegger.php

Proper Citation: SuperSegger (RRID:SCR\_018532)

**Description:** Software package as automated MATLAB based trainable image cell segmentation, fluorescence quantification and analysis suite. Used for high throughput time lapse fluorescence microscopy of in vivo bacterial cells. Robust image segmentation, analysis and lineage tracking of bacterial cells.

**Resource Type:** software application, software toolkit, data processing software, image analysis software, software resource

Defining Citation: PMID:27569113

**Keywords:** Image cell segmentation, fluorescence quantification, data analysis, high throughput, time lapse, fluorescence microscopy, bacteria cell, image segmentation

**Funding:** University of Washington Royalty Research Fund ; Sloan BR2011?110; NSF PHY?084845; NSF MCB?1151043?CAREER; Danish National Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: SuperSegger

Resource ID: SCR\_018532

Alternate URLs: https://github.com/wiggins-lab/SuperSegger

Record Creation Time: 20220129T080340+0000

Record Last Update: 20250517T060400+0000

#### **Ratings and Alerts**

No rating or validation information has been found for SuperSegger.

No alerts have been found for SuperSegger.

### Data and Source Information

Source: <u>SciCrunch Registry</u>

#### **Usage and Citation Metrics**

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Fisher GL, et al. (2021) Competitive binding of MatP and topoisomerase IV to the MukB hinge domain. eLife, 10.

Jeckel H, et al. (2021) Advances and opportunities in image analysis of bacterial cells and communities. FEMS microbiology reviews, 45(4).

Ting SY, et al. (2020) Targeted Depletion of Bacteria from Mixed Populations by Programmable Adhesion with Antagonistic Competitor Cells. Cell host & microbe, 28(2), 313.