

Resource Summary Report

Generated by T1D on Aug 3, 2026

Velvet-SC

RRID:SCR_004377

Type: Tool

Proper Citation

Velvet-SC (RRID:SCR_004377)

Resource Information

URL: <http://bix.ucsd.edu/projects/singlecell/>

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Description: Software package for short read data from single cells that improves assembly through use of progressively increasing coverage cutoff. Used for single cell Illumina sequences, allows variable coverage datasets to be utilized with assembly of E. coli and S. aureus single cell reads. Assembles single cell genome of uncultivated SAR324 clade of Deltaproteobacteria.

Abbreviations: Velvet SC

Synonyms: Velvet Single Cell

Resource Type: software resource, data processing software, sequence analysis software, software application, data analysis software

Defining Citation: [PMID:21926975](#)

Keywords: genome, single, cell, short, read, assembly

Funding: NHGRI R01 HG003647;
Sloan Foundation ;
NCRR P41 RR024851

Availability: Free, Available for download, Freely available

Resource Name: Velvet-SC

Resource ID: SCR_004377

Alternate IDs: OMICS_01504

Record Creation Time: 20220129T080224+0000

Ratings and Alerts

No rating or validation information has been found for Velvet-SC.

No alerts have been found for Velvet-SC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Wedemeyer A, et al. (2017) An improved filtering algorithm for big read datasets and its application to single-cell assembly. BMC bioinformatics, 18(1), 324.

Utturkar SM, et al. (2016) Enrichment of Root Endophytic Bacteria from Populus deltoides and Single-Cell-Genomics Analysis. Applied and environmental microbiology, 82(18), 5698.

Treangen TJ, et al. (2016) Identification and Genomic Analysis of a Novel Group C Orthobunyavirus Isolated from a Mosquito Captured near Iquitos, Peru. PLoS neglected tropical diseases, 10(4), e0004440.

Swan BK, et al. (2014) Genomic and metabolic diversity of Marine Group I Thaumarchaeota in the mesopelagic of two subtropical gyres. PloS one, 9(4), e95380.

Lo WS, et al. (2013) Comparative genome analysis of Spiroplasma melliferum IPMB4A, a honeybee-associated bacterium. BMC genomics, 14, 22.