**Velvet**

RRID:SCR_010755  
Type: Tool

**Proper Citation**

Velvet (RRID:SCR_010755)

**Resource Information**

**URL:** [http://www.molecularevolution.org/software/genomics/velvet](http://www.molecularevolution.org/software/genomics/velvet)

**Description:** Software package as de novo genomic assembler for short read sequencing technologies using de Bruijn graphs. Takes in short read sequences, removes errors, then produces high quality unique contigs, retrieves repeated areas between contigs. Can leverage very short reads in combination with read pairs to produce useful assemblies. Operating system Unix/Linux.

**Resource Name:** Velvet  
**Proper Citation:** Velvet (RRID:SCR_010755)  
**Resource Type:** Resource, software resource, data processing software, data analysis software, sequence analysis software, software application  
**Keywords:** de novo, genomic, assembly, short, read, sequencing, de Bruijn, graph  
**Resource ID:** SCR_010755  
**Parent Organization:** European Bioinformatics Institute  
**Funding Agency:** EMBL  
**Related resources:** Velvet-SC, shovill  
**References:** PMID:18349386  
**Availability:** Free, Available for download, Freely available
Website Status: Last checked up

Alternate IDs: OMICS_00038

Alternate URLs: https://www.ebi.ac.uk/~zerbino/velvet/

Abbreviations: Velvet

Mentions Count: 775

Ratings and Alerts

No rating or validation information has been found for Velvet.

No alerts have been found for Velvet.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 775 mentions in open access literature.

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


Kohl C, et al. (2020) Zwiesel bat banyangvirus, a potentially zoonotic Huaiyangshan banyangvirus (Formerly known as SFTS)-like banyangvirus in Northern bats from Germany. Scientific reports, 10(1), 1370.


Park S, et al. (2020) Recurrent gene duplication in the angiosperm tribe Delphinieae (Ranunculaceae) inferred from intracellular gene transfer events and heteroplasmic mutations in the plastid matK gene. Scientific reports, 10(1), 2720.


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