

Resource Summary Report

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Genovo

RRID:SCR_011911

Type: Tool

Proper Citation

Genovo (RRID:SCR_011911)

Resource Information

URL: <http://cs.stanford.edu/group/genovo/>

Proper Citation: Genovo (RRID:SCR_011911)

Description: Software for a novel de novo sequence assembler that discovers likely sequence reconstructions under the model.

Abbreviations: Genovo

Synonyms: Genovo - Metagenomic de novo Sequencing

Resource Type: software resource

Resource Name: Genovo

Resource ID: SCR_011911

Alternate IDs: OMICS_01422

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190431+0000

Ratings and Alerts

No rating or validation information has been found for Genovo.

No alerts have been found for Genovo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 227 mentions in open access literature.

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

Bethune J, et al. (2022) A method to build extended sequence context models of point mutations and indels. *Nature communications*, 13(1), 7884.

Wang PX, et al. (2021) Circulating tumor cell detection and single-cell analysis using an integrated workflow based on ChimeraX® -i120 Platform: A prospective study. *Molecular oncology*, 15(9), 2345.

Kumar S, et al. (2015) Metagenomics: Retrospect and Prospects in High Throughput Age. *Biotechnology research international*, 2015, 121735.

Klimm F, et al. (2014) Resolving structural variability in network models and the brain. *PLoS computational biology*, 10(3), e1003491.

Kojima M, et al. (2014) Human subperitoneal fibroblast and cancer cell interaction creates microenvironment that enhances tumor progression and metastasis. *PloS one*, 9(2), e88018.

Luz M, et al. (2014) Dynamic association with donor cell filopodia and lipid-modification are essential features of Wnt8a during patterning of the zebrafish neuroectoderm. *PloS one*, 9(1), e84922.

Syam N, et al. (2014) Glycosylation of TRPM4 and TRPM5 channels: molecular determinants and functional aspects. *Frontiers in cellular neuroscience*, 8, 52.

Mohamadlou H, et al. (2014) Maximizing Kolmogorov Complexity for accurate and robust bright field cell segmentation. *BMC bioinformatics*, 15, 32.

Lyashchenko AK, et al. (2014) cAMP control of HCN2 channel Mg²⁺ block reveals loose coupling between the cyclic nucleotide-gating ring and the pore. *PloS one*, 9(7), e101236.

Liu Z, et al. (2014) Changes in topological organization of functional PET brain network with normal aging. *PloS one*, 9(2), e88690.

Challis C, et al. (2014) Optogenetic modulation of descending prefrontocortical inputs to the dorsal raphe bidirectionally bias socioaffective choices after social defeat. *Frontiers in behavioral neuroscience*, 8, 43.

Patron M, et al. (2014) MICU1 and MICU2 finely tune the mitochondrial Ca²⁺ uniporter by exerting opposite effects on MCU activity. *Molecular cell*, 53(5), 726.

Xiong TC, et al. (2014) Imaging long distance propagating calcium signals in intact plant leaves with the BRET-based GFP-aequorin reporter. *Frontiers in plant science*, 5, 43.

Azagury DE, et al. (2014) Patient safety and surgical innovation-complementary or mutually exclusive? *Patient safety in surgery*, 8(1), 17.

Ng OH, et al. (2014) Deregulated WNT signaling in childhood T-cell acute lymphoblastic leukemia. *Blood cancer journal*, 4(3), e192.

You P, et al. (2014) Dynamic compressed HRRP generation for random stepped-frequency radar based on complex-valued fast sequential homotopy. *Sensors (Basel, Switzerland)*, 14(5), 8283.

Zhao C, et al. (2014) Recombinase-mediated reprogramming and dystrophin gene addition in mdx mouse induced pluripotent stem cells. *PloS one*, 9(4), e96279.

Herbst A, et al. (2014) Comprehensive analysis of β -catenin target genes in colorectal carcinoma cell lines with deregulated Wnt/ β -catenin signaling. *BMC genomics*, 15, 74.

Karimova M, et al. (2013) Vika/vox, a novel efficient and specific Cre/loxP-like site-specific recombination system. *Nucleic acids research*, 41(2), e37.

Gokcumen O, et al. (2013) Balancing selection on a regulatory region exhibiting ancient variation that predates human-neandertal divergence. *PLoS genetics*, 9(4), e1003404.