Resource Summary Report

Generated by RRID on Apr 8, 2025

HugeSeq

RRID:SCR_010803
Type: Tool

Proper Citation

HugeSeq (RRID:SCR_010803)

Resource Information

URL: http://hugeseq.snyderlab.org/

Proper Citation: HugeSeq (RRID:SCR_010803)

Description: An automated pipeline for detecting genetic variants from High-throUghput GEnome SEQuencing.

Abbreviations: HugeSeq

Resource Type: software resource

Funding:

Resource Name: HugeSeq

Resource ID: SCR_010803

Alternate IDs: OMICS_00288

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250214T183138+0000

Ratings and Alerts

No rating or validation information has been found for HugeSeq.

No alerts have been found for HugeSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Sailani MR, et al. (2020) Candidate variants in TUB are associated with familial tremor. PLoS genetics, 16(9), e1009010.

Wang GD, et al. (2019) Structural variation during dog domestication: insights from gray wolf and dhole genomes. National science review, 6(1), 110.

Velicky P, et al. (2018) Genome amplification and cellular senescence are hallmarks of human placenta development. PLoS genetics, 14(10), e1007698.

Rego S, et al. (2018) High-frequency actionable pathogenic exome variants in an average-risk cohort. Cold Spring Harbor molecular case studies, 4(6).

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Priest JR, et al. (2016) De Novo and Rare Variants at Multiple Loci Support the Oligogenic Origins of Atrioventricular Septal Heart Defects. PLoS genetics, 12(4), e1005963.

Kelly BJ, et al. (2015) Churchill: an ultra-fast, deterministic, highly scalable and balanced parallelization strategy for the discovery of human genetic variation in clinical and population-scale genomics. Genome biology, 16(1), 6.

John SE, et al. (2015) Kuwaiti population subgroup of nomadic Bedouin ancestry-Whole genome sequence and analysis. Genomics data, 3, 116.

Song G, et al. (2015) AGAPE (Automated Genome Analysis PipelinE) for pan-genome analysis of Saccharomyces cerevisiae. PloS one, 10(3), e0120671.

Thareja G, et al. (2015) Sequence and analysis of a whole genome from Kuwaiti population subgroup of Persian ancestry. BMC genomics, 16(1), 92.