Resource Summary Report

Generated by RRID on May 10, 2025

NGSANE

RRID:SCR_003478
Type: Tool

Proper Citation

NGSANE (RRID:SCR_003478)

Resource Information

URL: https://github.com/BauerLab/ngsane

Proper Citation: NGSANE (RRID:SCR_003478)

Description: Software providing a Linux-based High Performance Computing (HPC) enabled framework for high-throughput data analysis that minimizes overhead for set up and processing of new projects yet maintains full flexibility of custom scripting when processing raw sequence data.

Abbreviations: NGSANE

Synonyms: Next Generation Sequencing ANalysis for Enterprises

Resource Type: software resource

Defining Citation: PMID:24470576

Keywords: next generation sequencing

Funding:

Availability: BSD License, v3

Resource Name: NGSANE

Resource ID: SCR_003478

Alternate IDs: OMICS_02298

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250420T014144+0000

Ratings and Alerts

No rating or validation information has been found for NGSANE.

No alerts have been found for NGSANE.

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.

Skvortsova K, et al. (2022) Active DNA demethylation of developmental cis-regulatory regions predates vertebrate origins. Science advances, 8(48), eabn2258.

Giles KA, et al. (2021) BRG1 knockdown inhibits proliferation through multiple cellular pathways in prostate cancer. Clinical epigenetics, 13(1), 37.

Khoury A, et al. (2020) Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. Nature communications, 11(1), 54.

Achinger-Kawecka J, et al. (2020) Epigenetic reprogramming at estrogen-receptor binding sites alters 3D chromatin landscape in endocrine-resistant breast cancer. Nature communications, 11(1), 320.

Giles KA, et al. (2019) Integrated epigenomic analysis stratifies chromatin remodellers into distinct functional groups. Epigenetics & chromatin, 12(1), 12.

Talseth-Palmer BA, et al. (2016) Targeted next-generation sequencing of 22 mismatch repair genes identifies Lynch syndrome families. Cancer medicine, 5(5), 929.

Taberlay PC, et al. (2016) Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. Genome research, 26(6), 719.

Bauer DC, et al. (2015) Genome-wide analysis of chemically induced mutations in mouse in phenotype-driven screens. BMC genomics, 16, 866.

Barry G, et al. (2015) Long Non-Coding RNA Expression during Aging in the Human Subependymal Zone. Frontiers in neurology, 6, 45.

Buske FA, et al. (2014) NGSANE: a lightweight production informatics framework for high-

throughput data analysis. Bioinformatics (Oxford, England), 30(10), 1471.