

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

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

Availability: BSD License, v3

Resource Name: NGSANE

Resource ID: SCR_003478

Alternate IDs: OMICS_02298

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260912T195558+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 [PRECISE-TBI](#) .

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.

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.

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

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.