

Resource Summary Report

Generated by [NIF](#) on Aug 11, 2026

Computational Genomics Analysis Tools

RRID:SCR_006390

Type: Tool

Proper Citation

Computational Genomics Analysis Tools (RRID:SCR_006390)

Resource Information

URL: <http://www.cgat.org/~andreas/documentation/cgat/cgat.html>

Proper Citation: Computational Genomics Analysis Tools (RRID:SCR_006390)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 3, 2023. A collection of tools for the computational genomicist written in the python language to assist in the analysis of genome scale data from a range of standard file formats. The toolkit enables filtering, comparison, conversion, summarization and annotation of genomic intervals, gene sets and sequences. The tools can both be run from the Unix command line and installed into visual workflow builders, such as Galaxy. Please note that the tools are part of a larger code base also including genomics and NGS pipelines. Everyone who uses parts of the CGAT code collection is encouraged to contribute. Contributions can take many forms: bugreports, bugfixes, new scripts and pipelines, documentation, tests, etc. All contributions are welcome.

Abbreviations: CGAT

Synonyms: Computational Genomics Analysis Toolkit, CGAT - Computational Genomics Analysis Tools

Resource Type: software toolkit, software resource

Defining Citation: [PMID:24395753](#)

Keywords: computational genomics, genomics, command-line, next-generation sequencing, python, pipeline, functional enrichment, clustering, metagenomic, contig, variant, analysis, filter, compare, conversion, summarization, annotation

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Computational Genomics Analysis Tools

Resource ID: SCR_006390

Alternate IDs: OMICS_02209

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260810T040428+0000

Ratings and Alerts

No rating or validation information has been found for Computational Genomics Analysis Tools.

No alerts have been found for Computational Genomics Analysis Tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the Drosophila brain. Cell genomics, 101125.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. Cell genomics, 101103.

Fatalska A, et al. (2024) Recruitment of trimeric eIF2 by phosphatase non-catalytic subunit PPP1R15B. Molecular cell, 84(3), 506.

Sigeman H, et al. (2024) The rate of W chromosome degeneration across multiple avian neo-sex chromosomes. Scientific reports, 14(1), 16548.

Fléchon A, et al. (2024) Association of Tumor Mutational Burden and PD-L1 with the Efficacy of Pembrolizumab with or without Chemotherapy versus Chemotherapy in Advanced Urothelial Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(23), 5353.

Ngo Bebe D, et al. (2023) Making health insurance responsive to citizens: the management of members' complaints by mutual health organisations in Kinshasa, Democratic Republic of Congo. BMJ global health, 7(Suppl 6).

Liu L, et al. (2023) RNA-binding protein DHX9 promotes glioma growth and tumor-associated macrophages infiltration via TCF12. CNS neuroscience & therapeutics, 29(4), 988.

Bhin J, et al. (2023) MYC is a clinically significant driver of mTOR inhibitor resistance in breast cancer. The Journal of experimental medicine, 220(11).

- Law STS, et al. (2023) The genome of the deep-sea anemone *Actinernus* sp. contains a mega-array of ANTP-class homeobox genes. *Proceedings. Biological sciences*, 290(2009), 20231563.
- Kong BL, et al. (2022) Chromosomal level genome of *Ilex asprella* and insight into antiviral triterpenoid pathway. *Genomics*, 114(3), 110366.
- Larrouture QC, et al. (2021) Loss of mutual protection between human osteoclasts and chondrocytes in damaged joints initiates osteoclast-mediated cartilage degradation by MMPs. *Scientific reports*, 11(1), 22708.
- Baranwal M, et al. (2021) CGAT: Cell Graph ATtention Network for Grading of Pancreatic Disease Histology Images. *Frontiers in immunology*, 12, 727610.
- Cribbs AP, et al. (2021) Dissecting the Role of BET Bromodomain Proteins BRD2 and BRD4 in Human NK Cell Function. *Frontiers in immunology*, 12, 626255.
- Tarazona E, et al. (2020) Gene expression in diapausing rotifer eggs in response to divergent environmental predictability regimes. *Scientific reports*, 10(1), 21366.
- Gazanion E, et al. (2020) Genome wide distribution of G-quadruplexes and their impact on gene expression in malaria parasites. *PLoS genetics*, 16(7), e1008917.
- Cribbs AP, et al. (2020) Histone H3K27me3 demethylases regulate human Th17 cell development and effector functions by impacting on metabolism. *Proceedings of the National Academy of Sciences of the United States of America*, 117(11), 6056.
- Bellieny-Rabelo D, et al. (2020) Horizontally Acquired Quorum-Sensing Regulators Recruited by the PhoP Regulatory Network Expand the Host Adaptation Repertoire in the Phytopathogen *Pectobacterium brasiliense*. *mSystems*, 5(1).
- Jan HM, et al. (2020) Cholesteryl β -D-glucoside 6-acyltransferase enhances the adhesion of *Helicobacter pylori* to gastric epithelium. *Communications biology*, 3(1), 120.
- Coe EA, et al. (2019) The MITF-SOX10 regulated long non-coding RNA DIRC3 is a melanoma tumour suppressor. *PLoS genetics*, 15(12), e1008501.
- Viphakone N, et al. (2019) Co-transcriptional Loading of RNA Export Factors Shapes the Human Transcriptome. *Molecular cell*, 75(2), 310.