

Resource Summary Report

Generated by [NIF](#) on Sep 15, 2026

PiGx

RRID:SCR_016476

Type: Tool

Proper Citation

PiGx (RRID:SCR_016476)

Resource Information

URL: <http://bioinformatics.mdc-berlin.de/pigx/>

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Description: Software application as a collection of genomic pipelines used for raw fastq read data of bisulfite experiments, RNAseq samples, single cell dropseq analysis, reads from ChIPseq experiments, analysis of sequence mutations in CRISPR-CAS9 targeted amplicon sequencing data.

Abbreviations: PiGx

Synonyms: Pipelines in Genomics

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, software toolkit

Keywords: collection, genomic, pipeline, bisulfite, sequencing, rnaseq, chipseq, single, cell, reproducibility, sample, analysis, mutation, data

Funding: European Union Horizon 2020 No 654248;
German Federal Ministry of Education and Research (BMBF) 031 A538C RBC (de.NBI)

Availability: Free, Available for download, Freely available

Resource Name: PiGx

Resource ID: SCR_016476

Alternate URLs: <https://github.com/BIMSBbioinfo/pigx>

License: GNU GPL

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260912T195840+0000

Ratings and Alerts

No rating or validation information has been found for PiGx.

No alerts have been found for PiGx.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Mendonsa S, et al. (2023) Massively parallel identification of mRNA localization elements in primary cortical neurons. *Nature neuroscience*, 26(3), 394.

Schumann VF, et al. (2022) SARS-CoV-2 infection dynamics revealed by wastewater sequencing analysis and deconvolution. *The Science of the total environment*, 853, 158931.

Appel LM, et al. (2021) PHF3 regulates neuronal gene expression through the Pol II CTD reader domain SPOC. *Nature communications*, 12(1), 6078.

Wesolowski R, et al. (2021) Myeloid transformation by MLL-ENL depends strictly on C/EBP. *Life science alliance*, 4(1).

M??thel S, et al. (2019) The conserved histone chaperone LIN-53 is required for normal lifespan and maintenance of muscle integrity in *Caenorhabditis elegans*. *Aging cell*, 18(6), e13012.

Wurmus R, et al. (2018) PiGx: reproducible genomics analysis pipelines with GNU Guix. *GigaScience*, 7(12).