

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

AffyPipe

RRID:SCR_002032

Type: Tool

Proper Citation

AffyPipe (RRID:SCR_002032)

Resource Information

URL: <https://github.com/nicolazzie/AffyPipe>

Proper Citation: AffyPipe (RRID:SCR_002032)

Description: An open-source software pipeline for Affymetrix Axiom genotyping workflow.

Synonyms: AffyPipe: an open-source pipeline for Affymetrix Axiom genotyping workflow

Resource Type: software resource

Defining Citation: [PMID:25028724](#)

Keywords: affymetrix, bio.tools

Funding: Italian Ministry of Education University and Research 505/Ric;
project GenHome ;
European Union FP7 project Gene2Farm 289592

Availability: Free, Available for download, Freely available

Resource Name: AffyPipe

Resource ID: SCR_002032

Alternate IDs: biotools:affypipe, OMICS_05203

Alternate URLs: <https://bio.tools/affypipe>

License: GNU General Public License

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260808T185746+0000

Ratings and Alerts

No rating or validation information has been found for AffyPipe.

No alerts have been found for AffyPipe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Díaz-de Usera A, et al. (2022) Developing CIRdb as a catalog of natural genetic variation in the Canary Islanders. Scientific reports, 12(1), 16132.

Hernández-Beeftink T, et al. (2021) Whole-Blood Mitochondrial DNA Copies Are Associated With the Prognosis of Acute Respiratory Distress Syndrome After Sepsis. Frontiers in immunology, 12, 737369.

Ghoreishifar SM, et al. (2020) Genomic measures of inbreeding coefficients and genome-wide scan for runs of homozygosity islands in Iranian river buffalo, Bubalus bubalis. BMC genetics, 21(1), 16.

Mokhber M, et al. (2019) Study of whole genome linkage disequilibrium patterns of Iranian water buffalo breeds using the Axiom Buffalo Genotyping 90K Array. PloS one, 14(5), e0217687.

Mokhber M, et al. (2018) A genome-wide scan for signatures of selection in Azeri and Khuzestani buffalo breeds. BMC genomics, 19(1), 449.