

Resource Summary Report

Generated by SPARC SAWG on Sep 20, 2026

HiPipe

RRID:SCR_001215

Type: Tool

Proper Citation

HiPipe (RRID:SCR_001215)

Resource Information

URL: <http://hipipe.ncgm.sinica.edu.tw/>

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Description: Tool that provides high performance NGS (next-generation sequencing) data analysis pipelines so that researchers with minimum IT or bioinformatics knowledge can perform common analyses on NGS data. 3 TB of storage space is reserved for each task.

Abbreviations: HiPipe

Synonyms: HiPipe - High Performance Pipelines for NGS Data Analysis

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: next-generation sequencing, dna, rna, differential expression, mirna, gene fusion, variant, genome, exome, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HiPipe

Resource ID: SCR_001215

Alternate IDs: OMICS_02128, biotools:hipipe

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260919T195629+0000

Ratings and Alerts

No rating or validation information has been found for HiPipe.

No alerts have been found for HiPipe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Yang CF, et al. (2018) Loss of GPNMB Causes Autosomal-Recessive Amyloidosis Cutis Dyschromica in Humans. American journal of human genetics, 102(2), 219.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.