

# Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

## HiPipe

RRID:SCR\_001215

Type: Tool

### Proper Citation

HiPipe (RRID:SCR\_001215)

### Resource Information

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

**Proper Citation:** HiPipe (RRID:SCR\_001215)

**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:** 20260829T182917+0000

### Ratings and Alerts

No rating or validation information has been found for HiPipe.

No alerts have been found for HiPipe.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.