

# Resource Summary Report

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## SigFlow

RRID:SCR\_028486

Type: Tool

### Proper Citation

SigFlow (RRID:SCR\_028486)

### Resource Information

**URL:** <https://github.com/ShixiangWang/sigflow>

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**Description:** Software automated and comprehensive pipeline for cancer genome mutational signature analysis. Provides one-stop solution for de novo signature extraction, reference signature fitting, signature stability analysis, sample clustering based on signature exposure in different types of genome DNA alterations including single base substitution, doublet base substitution, small insertion and deletion and copy number alteration. It can auto-extract mutational signatures, fit mutation data to all/specified COSMIC reference signatures (SBS/DBS/INDEL) and run bootstrapping analysis for studying signature stability.

**Synonyms:** , sigflow, Sigflow

**Resource Type:** software resource, software toolkit, source code

**Defining Citation:** [PMID:33270873](#)

**Keywords:** cancer genome mutational signature analysis, cancer genome, mutational signature analysis,

**Funding:** National Natural Science Foundation of China

**Availability:** Free, Available for download, Freely available

**Resource Name:** SigFlow

**Resource ID:** SCR\_028486

**License:** GNU GPL

**Record Creation Time:** 20260529T042811+0000

**Record Last Update:** 20260805T044626+0000

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## Ratings and Alerts

No rating or validation information has been found for SigFlow.

No alerts have been found for SigFlow.

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## Data and Source Information

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

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.