

Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

S-MART

RRID:SCR_001908

Type: Tool

Proper Citation

S-MART (RRID:SCR_001908)

Resource Information

URL: <https://urgi.versailles.inra.fr/Tools/S-Mart>

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Description: Software toolbox that manages your RNA-Seq and ChIP-Seq data and also produces many different plots to visualize your data. It performs several tasks that are usually required during the analysis of mapped RNA-Seq and ChIP-Seq reads, including data selection and data visualization. It includes the selection (or the exclusion) of the data that overlaps with a reference set, clustering and comparative analysis. It also provides many ways to visualize data: size of the reads, density on the genome, distance with respect to a reference set, and the correlation of two data sets (with cloud plots). A computer science background is not required to run it through a graphical interface and it can be run on any personal computer, yielding results within an hour for most queries.

Abbreviations: S-MART

Resource Type: software resource

Defining Citation: [PMID:21998740](#)

Keywords: high throughput sequencing, rna-seq, chip-seq, python, linux, ms windows, mac, short-read, selection, visualization, bio.tools, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: S-MART

Resource ID: SCR_001908

Alternate IDs: OMICS_01937, biotools:mapperanalyzer, biotools:s-mart

Alternate URLs: <https://bio.tools/s-mart>, <https://bio.tools/mapperanalyzer>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20261017T202503+0000

Ratings and Alerts

No rating or validation information has been found for S-MART.

No alerts have been found for S-MART.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.