

Resource Summary Report

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Semi-Automated MEA Spike Sorting (SAMS)

RRID:SCR_027843

Type: Tool

Proper Citation

Semi-Automated MEA Spike Sorting (SAMS) (RRID:SCR_027843)

Resource Information

URL: <https://github.com/Zhao-Lab-UW/SAMS-Semi-Automatic-MEA-Spike-sorting-pipeline->

Proper Citation: Semi-Automated MEA Spike Sorting (SAMS) (RRID:SCR_027843)

Description: Software MATLAB-based application for spike sorting multi-electrode array (MEA) recordings. Used for efficient, reproducible spike sorting in high-throughput neuronal culture experiments. SAMS performs batched automated spike sorting processes and also allows the users to review and correct any clusters or spike assignments.

Synonyms: Semi-Automated MEA Spike Sorting

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:39975344](#)

Keywords: spike sorting, spike sorting multi-electrode array recordings, review and correct, clusters, spike assignments,

Availability: Free, Available for download, Freely available

Resource Name: Semi-Automated MEA Spike Sorting (SAMS)

Resource ID: SCR_027843

License: MIT license

Record Creation Time: 20260103T054312+0000

Record Last Update: 20260815T183309+0000

Ratings and Alerts

No rating or validation information has been found for Semi-Automated MEA Spike Sorting (SAMS).

No alerts have been found for Semi-Automated MEA Spike Sorting (SAMS).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Ren X, et al. (2026) A semi-automated MEA spike sorting method for high-throughput assessment of cultured neurons. Stem cell reports, 21(4), 102872.