

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

MS Amanda

RRID:SCR_018396

Type: Tool

Proper Citation

MS Amanda (RRID:SCR_018396)

Resource Information

URL: <http://bioinformatics.fh-hagenberg.at/site/index.php?id=17>

Proper Citation: MS Amanda (RRID:SCR_018396)

Description: Software scoring system to identify peptides out of tandem mass spectrometry data using database of known proteins. Universal identification algorithm optimized for high resolution and high accuracy tandem mass spectra. Software tool as peptide and protein identification algorithm developed by Bioinformatics Research Group University of Applied Sciences Upper Austria in close cooperation with group of Karl Mechtler at IMP Vienna, Austria.

Synonyms: MS Amanda 2.0, Universal Identification Algorithm Optimized for High Accuracy Tandem Mass Spectra

Resource Type: data analysis software, software resource, software application, algorithm resource, data processing software

Defining Citation: [PMID:24909410](#)

Keywords: Tandem mass spectrometry, protein database, scoring system, peptide identification, data, search algorithm, protein identification algorithm, peptide identification, proteomic

Funding: Austrian Science Fund ;
European Community Seventh Framework Programme ;
MeioSys

Availability: Free, Available for download, Freely available

Resource Name: MS Amanda

Resource ID: SCR_018396

Alternate URLs: <https://ms.imp.ac.at/?goto=msamanda>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260728T043551+0000

Ratings and Alerts

No rating or validation information has been found for MS Amanda.

No alerts have been found for MS Amanda.

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 [nidm-terms](#) .

Collado A, et al. (2025) Erythrocyte-derived extracellular vesicles induce endothelial dysfunction through arginase-1 and oxidative stress in type 2 diabetes. The Journal of clinical investigation, 135(10).

Ahel J, et al. (2020) Moyamoya disease factor RNF213 is a giant E3 ligase with a dynein-like core and a distinct ubiquitin-transfer mechanism. eLife, 9.