

# Resource Summary Report

Generated by [NIF](#) on Aug 10, 2026

## MS Amanda

RRID:SCR\_018396

Type: Tool

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### Proper Citation

MS Amanda (RRID:SCR\_018396)

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### 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, data processing software, software application, software resource, algorithm resource

**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:** 20260810T040741+0000

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## Ratings and Alerts

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

No alerts have been found for MS Amanda.

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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](#) .

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.