

Resource Summary Report

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Mascot

RRID:SCR_014322

Type: Tool

Proper Citation

Mascot (RRID:SCR_014322)

Resource Information

URL: <http://www.matrixscience.com/server.html>

Proper Citation: Mascot (RRID:SCR_014322)

Description: A software package and server used to identify and characterize proteins from primary sequence databases using mass spectrometry data. Mascot integrates peptide mass fingerprinting, sequence querying, and MS/MS ion searching in order to search for proteins in databases like SwissProt, NCBIInr, EMBL EST divisions, contaminants, and cRAP. If a license is purchased, users may: search data sets that exceed the 1200 spectrum limit of the free version; set up automated, high throughput work; add and edit proteins and quantification methods; and search a preferred collection of sequence databases. The software package works with instruments from AB Sciex, Agilent, Bruker, Jeol, Shimadzu, Thermo Scientific, and Waters.

Synonyms: Mascot Server

Resource Type: software application, data processing software, software resource, signal processing software, standalone software

Keywords: server, software package, mass spectrometry, protein, identify, characterize, bio.tools

Availability: Free, Can be licensed for in-house use, Available for download

Resource Name: Mascot

Resource ID: SCR_014322

Alternate IDs: biotools:MASCOT

Alternate URLs: http://www.matrixscience.com/search_intro.html,
<https://bio.tools/MASCOT>

License: License cost is based on number of processors used by Mascot, <http://www.matrixscience.com/licensing.html>

License URLs: <http://www.matrixscience.com/legal.html>

Record Creation Time: 20220129T080320+0000

Record Last Update: 20260801T190510+0000

Ratings and Alerts

No rating or validation information has been found for Mascot.

No alerts have been found for Mascot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6896 mentions in open access literature.

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

Cai Z, et al. (2026) The Cullin3-Ring E3 ubiquitin ligase complex and USP14 regulate spastin-mediated microtubule severing and promotion of neurite outgrowth. *Neural regeneration research*, 21(4), 1641.

Park YJ, et al. (2026) Spatiotemporal translation of sperm acrosome associated proteins during early capacitation modulates sperm fertilizing ability. *Journal of advanced research*, 79, 313.

Minchaca AZ, et al. (2026) Surface Proteomic Analysis Reveals the Presence of Noncanonical Cell Membrane Endoplasmic Reticulum Chaperones in High-Grade Gliomas. *Journal of proteome research*, 25(1), 169.

Rasslan R, et al. (2026) Peptidomics in Different Phases of Severe Acute Pancreatitis Model. *Proteomics. Clinical applications*, 20(1), e70035.

Zhang B, et al. (2026) Human papillomavirus E7 inhibits immune responses in keratinocytes by activating HTRA1-mediated mitophagy. *International journal of molecular medicine*, 57(1).

Du Y, et al. (2026) Insect I-Type Lysozymes Function as Antiviral Proteases by Forming Biomolecular Condensates. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e14408.

Lemaire ON, et al. (2026) Carbon-monoxide-driven bioethanol production operates through a tungsten-dependent catalyst. *Nature chemical biology*, 22(1), 28.

Kanli A, et al. (2026) Dysregulation of ERAD and Stress Response Proteins by V493F FTO Over-expression: A Proteomic Perspective. *In vivo* (Athens, Greece), 40(1), 249.

Kama Y, et al. (2026) Notch interaction with RUNX factors regulates initiation of the T-lineage program. *The Journal of experimental medicine*, 223(2).

Su J, et al. (2026) TAF1 acetyltransferase promotes colorectal carcinoma metastasis by catalyzing γ -hydroxybutyrylation of KCTD9. *Oncogene*, 45(1), 87.

Latini C, et al. (2025) Cytoplasmic DIS3 is an exosome-independent endoribonuclease with catalytic activity toward circular RNAs. *Cell reports*, 44(6), 115769.

Voigt O, et al. (2025) Genetic parallels in biomineralization of the calcareous sponge *Sycon ciliatum* and stony corals. *eLife*, 14.

Breunig K, et al. (2025) SERBP1 interacts with PARP1 and is present in PARylation-dependent protein complexes regulating splicing, cell division, and ribosome biogenesis. *eLife*, 13.

Kim DG, et al. (2025) Genetic characteristics of novel extreme alkaline-inducible promoter located in five prime upstream region of peptidyl-prolyl cis/trans isomerase from *Vibrio anguillarum*. *Scientific reports*, 15(1), 21372.

Welti J, et al. (2025) NXP800 Activates the Unfolded Protein Response, Altering AR and E2F Function to Impact Castration-Resistant Prostate Cancer Growth. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(6), 1109.

Bergheim BG, et al. (2025) Molecular dynamics of the matrisome across sea anemone life history. *eLife*, 14.

O'Hern C, et al. (2025) Human heart-macrophage assembloids mimic immune-cardiac interactions and enable arrhythmia disease modeling. *Cell stem cell*, 32(11), 1671.

Chen K, et al. (2025) Tumor-Derived CCL16 Normalizes Tumor Vasculature through Macrophage ICAM-1 Receptor and Enhances Immunotherapy Efficacy in Hepatocellular Carcinoma. *Cancer research*, 85(19), 3633.

Blidner AG, et al. (2025) Glycosylation-driven programs coordinate immunoregulatory and pro-angiogenic functions of myeloid-derived suppressor cells. *Immunity*, 58(6), 1553.

Fujimoto M, et al. (2025) Neofunctionalization of VAMP7 opened up a plant-unique vacuolar transport pathway. *Current biology : CB*, 35(11), 2630.