

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, standalone software, data processing software, signal processing software, software resource

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: 20260804T043536+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 [ASWG](#) .

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.

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.

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).

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.

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.

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

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.

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.

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.

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.

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.

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.