Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 22, 2025

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, NCBInr, 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 resource, standalone software, data processing software, software application, signal processing software

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

Funding:

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: 20250422T055758+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 6476 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Eadsforth TC, et al. (2025) Pharmacological and structural understanding of the Trypanosoma cruzi proteasome provides key insights for developing site-specific inhibitors. The Journal of biological chemistry, 301(1), 108049.

Zhou YQ, et al. (2025) Proteomic characterization of molecular mechanisms of paraquat-induced lung injury in a mouse model. Respiratory research, 26(1), 1.

Yang ZZ, et al. (2025) DCAF13-mediated K63-linked ubiquitination of RNA polymerase I promotes uncontrolled proliferation in Breast Cancer. Nature communications, 16(1), 557.

Lauer SM, et al. (2025) The proline-rich antimicrobial peptide Api137 disrupts large ribosomal subunit assembly and induces misfolding. Nature communications, 16(1), 567.

Clancy SM, et al. (2025) The Calicophoron daubneyi genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. BMC biology, 23(1), 11.

Makhammajanov Z, et al. (2025) Urinary Proteomic Shifts over Time and Their Associations with eGFR Decline in Chronic Kidney Disease. Biomolecules, 15(1).

Cho HS, et al. (2025) Two Cysteines in Raf Kinase Inhibitor Protein Make Differential Contributions to Structural Dynamics In Vitro. Molecules (Basel, Switzerland), 30(2).

Meng X, et al. (2025) A novel peptide encoded by circSRCAP confers resistance to enzalutamide by inhibiting the ubiquitin-dependent degradation of AR-V7 in castration-resistant prostate cancer. Journal of translational medicine, 23(1), 108.

Tan T, et al. (2025) Revisiting phosphoregulation of Cdc25C during M-phase induction. iScience, 28(1), 111603.

Bollen C, et al. (2025) Composition and liquid-to-solid maturation of protein aggregates contribute to bacterial dormancy development and recovery. Nature communications, 16(1), 1046.

Wang X, et al. (2025) Micropillar-induced changes in cell nucleus morphology enhance bone regeneration by modulating the secretome. Research square.

Flottes Y, et al. (2025) Proteomic Analysis of Fibroblasts Exposed to Resin Composite Release. Proteomics. Clinical applications, 19(1), e202400049.

Xiao J, et al. (2025) L3MBTL3 and STAT3 collaboratively upregulate SNAIL expression to promote metastasis in female breast cancer. Nature communications, 16(1), 231.

Wang F, et al. (2025) Human epicardial organoids from pluripotent stem cells resemble fetal stage with potential cardiomyocyte- transdifferentiation. Cell & bioscience, 15(1), 4.

Fay CX, et al. (2025) Global proteomics and affinity mass spectrometry analysis of human Schwann cells indicates that variation in and loss of neurofibromin (NF1) alters protein expression and cellular and mitochondrial metabolism. Scientific reports, 15(1), 3883.

Shiraz MG, et al. (2025) Young rat microbiota extracts strongly inhibit fibrillation of ?-synuclein and protect neuroblastoma cells and zebrafish against ?-synuclein toxicity. Molecules and cells, 48(1), 100161.

Sakari M, et al. (2025) ADP-ribosyltransferase-based biocatalysis of nonhydrolyzable NAD+ analogs. The Journal of biological chemistry, 301(1), 108106.

Wei X, et al. (2025) Disruption of tumor-intrinsic PGAM5 increases anti-PD-1 efficacy through the CCL2 signaling pathway. Journal for immunotherapy of cancer, 13(1).

Tarr GAM, et al. (2025) Persistent cross-species transmission systems dominate Shiga toxin-producing Escherichia coli O157:H7 epidemiology in a high incidence region: A genomic epidemiology study. eLife, 13.

Marczak M, et al. (2025) The HECT ubiquitin-protein ligases UPL1 and UPL2 are involved in degradation of Arabidopsis thaliana ACC synthase 7. Physiologia plantarum, 177(1),

e70030.