

Resource Summary Report

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MascotScan

RRID:SCR_018201

Type: Tool

Proper Citation

MascotScan (RRID:SCR_018201)

Resource Information

URL: <http://proteom.ibb.waw.pl/mscan/>

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Description: Software tool for analysis of qualitative data, operating on basis of lists of peptides and proteins identified in samples generated by Mascot database system. Responsible for preparing data for quantitative analysis of proteins both with use of stable isotope labeling and without isotope labeling.

Synonyms: MScan

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

Keywords: Data analysis, qualitative data, peptide, protein, Mascot database system, stable isotope labeling, no isotope labeling

Availability: Free, Freely available

Resource Name: MascotScan

Resource ID: SCR_018201

Record Creation Time: 20220129T080339+0000

Record Last Update: 20260905T132832+0000

Ratings and Alerts

No rating or validation information has been found for MascotScan.

No alerts have been found for MascotScan.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Gryciuk A, et al. (2026) Characteristics of Two *Saccharomyces cerevisiae* Strains and Their Extracellular Vesicles as New Candidates for Probiotics. *Probiotics and antimicrobial proteins*, 18(1), 1338.

Kodzik N, et al. (2024) Comparative proteomic analysis of the ovarian fluid and eggs of Siberian sturgeon. *BMC genomics*, 25(1), 451.

Shi L, et al. (2024) Low frequency ultrasound elicits broad cortical responses inhibited by ketamine in mice. *Communications engineering*, 3(1), 120.

Gregorczyk P, et al. (2023) N-glycosylation acts as a switch for FGFR1 trafficking between the plasma membrane and nuclear envelope. *Cell communication and signaling : CCS*, 21(1), 177.

Pabian-Jewu?a S, et al. (2023) Identification of Molecular Mechanisms Responsible for the MMP-9-1562C/T Dependent Differential Regulation of Matrix Metalloproteinase-9 Expression in Human Neuron-like Cells. *Genes*, 14(11).

Nowicka-Bauer K, et al. (2023) Proteomic approach towards identification of seminal fluid biomarkers from individuals with severe oligozoospermia, cryptozoospermia and non-obstructive azoospermia: a pilot study. *Translational andrology and urology*, 12(10), 1497.

Mucha O, et al. (2023) Proteome Profiling of the Dystrophic mdx Mice Diaphragm. *Biomolecules*, 13(11).

Sochacka M, et al. (2022) FGF12 is a novel component of the nucleolar NOLC1/TCOF1 ribosome biogenesis complex. *Cell communication and signaling : CCS*, 20(1), 182.

Szpotkowska J, et al. (2022) Structural Characteristics of the 5'-Terminal Region of Mouse p53 mRNA and Identification of Proteins That Bind to This mRNA Region. *International journal of molecular sciences*, 23(17).

Bana? AM, et al. (2021) Interplay between DsbA1, DsbA2 and C8J_1298 Periplasmic Oxidoreductases of *Campylobacter jejuni* and Their Impact on Bacterial Physiology and Pathogenesis. *International journal of molecular sciences*, 22(24).

Joachimia?k E, et al. (2021) Composition and function of the C1b/C1f region in the ciliary central apparatus. *Scientific reports*, 11(1), 11760.

Ziemli?ska E, et al. (2021) Palm Oil-Rich Diet Affects Murine Liver Proteome and S-Palmitoylome. *International journal of molecular sciences*, 22(23).

Zarba-Kozio M, et al. (2021) S-Palmitoylation of Synaptic Proteins as a Novel Mechanism Underlying Sex-Dependent Differences in Neuronal Plasticity. *International journal of molecular sciences*, 22(12).

Wakula M, et al. (2020) The interactome of multifunctional HAX1 protein suggests its role in the regulation of energy metabolism, de-aggregation, cytoskeleton organization and RNA-processing. *Bioscience reports*, 40(11).

Gorinski N, et al. (2020) DHHC7-mediated palmitoylation of the accessory protein barttin critically regulates the functions of ClC-K chloride channels. *The Journal of biological chemistry*, 295(18), 5970.