

Resource Summary Report

Generated by [RRID](#) on May 14, 2025

MSTools

RRID:SCR_018657

Type: Tool

Proper Citation

MSTools (RRID:SCR_018657)

Resource Information

URL: <http://peterslab.org/MSTools/>

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Description: Web based application for visualization and presentation of HXMS data. Comprises tools helping in preparation of H/D experiments as well as tools for turning simple tables with data on H/D exchange into different ways of representation.

Resource Type: software resource, service resource, data access protocol, web service

Defining Citation: [DOI:10.1016/j.ijms.2010.07.030](https://doi.org/10.1016/j.ijms.2010.07.030)

Keywords: Hydrogen, deuterium, exchange data, data visualization, HXMS data, data calculation, graphical representation

Funding:

Availability: Free, Freely available

Resource Name: MSTools

Resource ID: SCR_018657

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250514T061840+0000

Ratings and Alerts

No rating or validation information has been found for MSTools.

No alerts have been found for MSTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Honzejkova K, et al. (2024) The cryo-EM structure of ASK1 reveals an asymmetric architecture allosterically modulated by TRX1. *eLife*, 13.

Lepesheva A, et al. (2024) Modification of the RTX domain cap by acyl chains of adapted length rules the formation of functional hemolysin pores. *Biochimica et biophysica acta. Biomembranes*, 1866(5), 184311.

Osickova A, et al. (2023) A conserved tryptophan in the acylated segment of RTX toxins controls their β 2 integrin-independent cell penetration. *The Journal of biological chemistry*, 299(8), 104978.

Filandrová R, et al. (2021) Motif orientation matters: Structural characterization of TEAD1 recognition of genomic DNA. *Structure (London, England : 1993)*, 29(4), 345.

Pacheco-Garcia JL, et al. (2021) Structural basis of the pleiotropic and specific phenotypic consequences of missense mutations in the multifunctional NAD(P)H:quinone oxidoreductase 1 and their pharmacological rescue. *Redox biology*, 46, 102112.

Espinosa-Vinals CA, et al. (2021) Almost half of the RTX domain is dispensable for complement receptor 3 binding and cell-invasive activity of the *Bordetella* adenylate cyclase toxin. *The Journal of biological chemistry*, 297(1), 100833.

Lepesheva A, et al. (2021) Different roles of conserved tyrosine residues of the acylated domains in folding and activity of RTX toxins. *Scientific reports*, 11(1), 19814.

Felice AKG, et al. (2021) Chimeric Cellobiose Dehydrogenases Reveal the Function of Cytochrome Domain Mobility for the Electron Transfer to Lytic Polysaccharide Monooxygenase. *ACS catalysis*, 11(2), 517.

Osickova A, et al. (2020) Acyltransferase-mediated selection of the length of the fatty acyl chain and of the acylation site governs activation of bacterial RTX toxins. *The Journal of biological chemistry*, 295(28), 9268.

Masin J, et al. (2020) Retargeting from the CR3 to the LFA-1 receptor uncovers the adenylyl cyclase enzyme-translocating segment of *Bordetella* adenylate cyclase toxin. *The Journal of biological chemistry*, 295(28), 9349.