

Resource Summary Report

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StavroX

RRID:SCR_014957

Type: Tool

Proper Citation

StavroX (RRID:SCR_014957)

Resource Information

URL: <http://www.stavroX.com>

Proper Citation: StavroX (RRID:SCR_014957)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on June 29, 2023. Software tool for analyzing cross-linking/mass spectrometry datasets using any bifunctional cross-linker. It can be used to identify cross links of peptides – such as DSS, BS3, Disulfides, and zero-length – in complex mixtures.

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

Defining Citation: [PMID:22038510](#), [DOI:10.1007/s13361-011-0261-2](#)

Keywords: sequence analysis software, peptide, cross linking, mass spectrometry, bifunctional cross linker, complex mixture

Funding: DFG Si 867/13-1;
DFG Si 867/15-1;
BMBF ProNet-T3;
BMBF Project To-06

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: StavroX

Resource ID: SCR_014957

License: Freeware License

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260905T132752+0000

Ratings and Alerts

No rating or validation information has been found for StavroX.

No alerts have been found for StavroX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 75 mentions in open access literature.

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

Tian Y, et al. (2023) Oligomer-to-monomer transition underlies the chaperone function of AAGAB in AP1/AP2 assembly. *Proceedings of the National Academy of Sciences of the United States of America*, 120(2), e2205199120.

Kolhe JA, et al. (2023) Protocol for establishing a protein interactome based on close physical proximity to a target protein within live budding yeast. *STAR protocols*, 4(4), 102663.

Hani? M, et al. (2023) Dimerization of European Robin Cryptochrome 4a. *The journal of physical chemistry. B*, 127(28), 6251.

Cabello-Lobato MJ, et al. (2022) Microarray screening reveals two non-conventional SUMO-binding modules linked to DNA repair by non-homologous end-joining. *Nucleic acids research*, 50(8), 4732.

Bueno-Carrasco MT, et al. (2022) Structural mechanism for tyrosine hydroxylase inhibition by dopamine and reactivation by Ser40 phosphorylation. *Nature communications*, 13(1), 74.

Cuéllar J, et al. (2022) The Molecular Chaperone CCT Sequesters Gelsolin and Protects it from Cleavage by Caspase-3. *Journal of molecular biology*, 434(5), 167399.

Sharpen JDA, et al. (2022) Transglutaminase 3 crosslinks the secreted gel-forming mucus component Mucin-2 and stabilizes the colonic mucus layer. *Nature communications*, 13(1), 45.

Zhang S, et al. (2022) Scaffolding Protein GspB/OutB Facilitates Assembly of the *Dickeya dadantii* Type 2 Secretion System by Anchoring the Outer Membrane Secretin Pore to the Inner Membrane and to the Peptidoglycan Cell Wall. *mBio*, 13(3), e0025322.

Paluda A, et al. (2022) Ubiquitin and a charged loop regulate the ubiquitin E3 ligase activity of Ark2C. *Nature communications*, 13(1), 1181.

Iacobucci I, et al. (2021) From classical to new generation approaches: An excursus of -omics methods for investigation of protein-protein interaction networks. *Journal of proteomics*, 230, 103990.

Bragantini B, et al. (2021) The box C/D snoRNP assembly factor Bcd1 interacts with the histone chaperone Rtt106 and controls its transcription dependent activity. *Nature communications*, 12(1), 1859.

Horvath M, et al. (2021) 14-3-3 proteins inactivate DAPK2 by promoting its dimerization and protecting key regulatory phosphosites. *Communications biology*, 4(1), 986.

González LJ, et al. (2021) Synthesis, LC-MS/MS analysis, and biological evaluation of two vaccine candidates against ticks based on the antigenic P0 peptide from *R. sanguineus* linked to the p64K carrier protein from *Neisseria meningitidis*. *Analytical and bioanalytical chemistry*, 413(23), 5885.

Pohl P, et al. (2021) 14-3-3-protein regulates Nedd4-2 by modulating interactions between HECT and WW domains. *Communications biology*, 4(1), 899.

Shen S, et al. (2021) Photo-activatable Ub-PCNA probes reveal new structural features of the *Saccharomyces cerevisiae* Pol η /PCNA complex. *Nucleic acids research*, 49(16), 9374.

Liang LY, et al. (2021) The intracellular domains of the EphB6 and EphA10 receptor tyrosine pseudokinases function as dynamic signalling hubs. *The Biochemical journal*, 478(17), 3351.

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

Piróg A, et al. (2021) Two Bacterial Small Heat Shock Proteins, IbpA and IbpB, Form a Functional Heterodimer. *Journal of molecular biology*, 433(15), 167054.

Del Amo-Maestro L, et al. (2021) An Integrative Structural Biology Analysis of Von Willebrand Factor Binding and Processing by ADAMTS-13 in Solution. *Journal of molecular biology*, 433(13), 166954.

Moysa A, et al. (2021) A model of full-length RAGE in complex with S100B. *Structure (London, England : 1993)*, 29(9), 989.