

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: 20260821T194010+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 [dkNET](#) .

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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

Steimle S, et al. (2021) Cryo-EM structures of engineered active bc1-cbb3 type CIII2CIV super-complexes and electronic communication between the complexes. *Nature communications*, 12(1), 929.

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