Analyzing Proteinâ€Protein Interactions from Affinity with SAINT

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Citation Report

#	Article	IF	CITATIONS
1	The CRAPome: a contaminant repository for affinity purification–mass spectrometry data. Nature Methods, 2013, 10, 730-736.	9.0	1,353
2	Dynamic trans-Acting Factor Colocalization in Human Cells. Cell, 2013, 155, 713-724.	13.5	142
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5	Identification of Protein Interactions Involved in Cellular Signaling. Molecular and Cellular Proteomics, 2013, 12, 1752-1763.	2.5	84
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7	Detecting Protein–Protein Interactions/Complex Components Using Mass Spectrometry Coupled Techniques. Methods in Molecular Biology, 2014, 1164, 1-13.	0.4	9
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16	TRAF1 Coordinates Polyubiquitin Signaling to Enhance Epstein-Barr Virus LMP1-Mediated Growth and Survival Pathway Activation. PLoS Pathogens, 2015, 11, e1004890.	2.1	67
17	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human neuroblastoma cells. Journal of Proteomics, 2015, 123, 42-53.	1.2	62
18	Potato leafroll virus structural proteins manipulate overlapping, yet distinct protein interaction networks during infection. Proteomics, 2015, 15, 2098-2112.	1.3	22

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20	Model System-Guided Protein Interaction Mapping for Virus Isolated from Phloem Tissue. Journal of Proteome Research, 2016, 15, 4601-4611.	1.8	12
21	ARiBo pull-down for riboproteomic studies based on label-free quantitative mass spectrometry. Rna, 2016, 22, 1760-1770.	1.6	6
22	Data Independent Acquisition analysis in ProHits 4.0. Journal of Proteomics, 2016, 149, 64-68.	1.2	66
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54	Functional Proteomics of Nuclear Proteins in Tetrahymena thermophila: A Review. Genes, 2019, 10, 333.	1.0	11

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