

# Scoring Large-Scale Affinity Purification Mass Spectro

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Meta- and Orthogonal Integration of Influenza $\alpha$ OMICs Data Defines a Role for UBR4 in Virus Budding. <i>Cell Host and Microbe</i> , 2015, 18, 723-735.	5.1	868
2	Global Mapping of the Inc-Human Interactome Reveals that Retromer Restricts Chlamydia Infection. <i>Cell Host and Microbe</i> , 2015, 18, 109-121.	5.1	174
3	CDK11 in TREX/THOC Regulates HIV mRNA 3' End Processing. <i>Cell Host and Microbe</i> , 2015, 18, 560-570.	5.1	53
4	The Dengue Virus NS5 Protein Intrudes in the Cellular Spliceosome and Modulates Splicing. <i>PLoS Pathogens</i> , 2016, 12, e1005841.	2.1	176
5	A scaffold protein connects type IV pili with the Chp chemosensory system to mediate activation of virulence signaling in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2016, 101, 590-605.	1.2	69
6	Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF- $\beta$ Signaling. <i>Journal of Proteome Research</i> , 2017, 16, 14-33.	1.8	11
7	Systems-based analysis of RIG-I-dependent signalling identifies KHSRP as an inhibitor of RIG-I receptor activation. <i>Nature Microbiology</i> , 2017, 2, 17022.	5.9	25
8	Quantitative Assessment of the Effects of Trypsin Digestion Methods on Affinity Purification-Mass Spectrometry-based Protein-Protein Interaction Analysis. <i>Journal of Proteome Research</i> , 2017, 16, 3068-3082.	1.8	39
9	A Global Interactome Map of the Dengue Virus NS1 Identifies Virus Restriction and Dependency Host Factors. <i>Cell Reports</i> , 2017, 21, 3900-3913.	2.9	90
10	Inference of a Geminivirus-Host Protein-Protein Interaction Network through Affinity Purification and Mass Spectrometry Analysis. <i>Viruses</i> , 2017, 9, 275.	1.5	35
11	Comparative Flavivirus-Host Protein Interaction Mapping Reveals Mechanisms of Dengue and Zika Virus Pathogenesis. <i>Cell</i> , 2018, 175, 1931-1945.e18.	13.5	252
12	Multiple Routes to Oncogenesis Are Promoted by the Human Papillomavirus-Host Protein Network. <i>Cancer Discovery</i> , 2018, 8, 1474-1489.	7.7	67
13	An Mtb-Human Protein-Protein Interaction Map Identifies a Switch between Host Antiviral and Antibacterial Responses. <i>Molecular Cell</i> , 2018, 71, 637-648.e5.	4.5	100
14	Inferring Protein-Protein Interaction Networks From Mass Spectrometry-Based Proteomic Approaches: A Mini-Review. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 805-811.	1.9	39
15	Mapping Interactome Networks of DNAJC11, a Novel Mitochondrial Protein Causing Neuromuscular Pathology in Mice. <i>Journal of Proteome Research</i> , 2019, 18, 3896-3912.	1.8	6
16	Experimental Analysis of Viral-Host Interactions. <i>Frontiers in Physiology</i> , 2019, 10, 425.	1.3	22
17	Identification of antiviral roles for the exon-junction complex and nonsense-mediated decay in flaviviral infection. <i>Nature Microbiology</i> , 2019, 4, 985-995.	5.9	52
18	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	5.8	32

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19	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	5.9	51
20	Virus and host interactions critical for filoviral RNA synthesis as therapeutic targets. <i>Antiviral Research</i> , 2019, 162, 90-100.	1.9	12
21	Modelling of pathogen-host systems using deeper ORF annotations and transcriptomics to inform proteomics analyses. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2836-2850.	1.9	7
22	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing. <i>Nature</i> , 2020, 583, 459-468.	13.7	3,542
23	Methods of Computational Interactomics for Investigating Interactions of Human Proteoforms. <i>Biochemistry (Moscow)</i> , 2020, 85, 68-79.	0.7	1
24	Structural proteomics, electron cryo-microscopy and structural modeling approaches in bacteria-human protein interactions. <i>Medical Microbiology and Immunology</i> , 2020, 209, 265-275.	2.6	13
25	Virus-Host Interactome and Proteomic Survey Reveal Potential Virulence Factors Influencing SARS-CoV-2 Pathogenesis. <i>Med</i> , 2021, 2, 99-112.e7.	2.2	252
26	Identification of Required Host Factors for SARS-CoV-2 Infection in Human Cells. <i>Cell</i> , 2021, 184, 92-105.e16.	13.5	480
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28	Mapping the SARS-CoV-2 Host Protein-Protein Interactome by Affinity Purification Mass Spectrometry and Proximity-Dependent Biotin Labeling: A Rational and Straightforward Route to Discover Host-Directed Anti-SARS-CoV-2 Therapeutics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 532.	1.8	38
29	The CD147 Protein Complex Is Involved in Entry of Chikungunya Virus and Related Alphaviruses in Human Cells. <i>Frontiers in Microbiology</i> , 2021, 12, 615165.	1.5	17
30	Mapping the plant proteome: tools for surveying coordinating pathways. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 203-220.	1.1	9
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33	The peripheral and core regions of virus-host network of COVID-19. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
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40	The impact of the suppression of highly connected protein interactions on the corona virus infection. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
41	Distinct nuclear and cytoplasmic assemblies and interactomes of the mammalian CTLH E3 ligase complex. <i>Journal of Cell Science</i> , 2022, 135, .	1.2	4

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42	A proteinâ€“protein interaction map reveals that the <i>Coxiella burnetii</i> effector CirB inhibits host proteasome activity. <i>PLoS Pathogens</i> , 2022, 18, e1010660.	2.1	12
45	Deciphering Spatial Proteinâ€“Protein Interactions in Brain Using Proximity Labeling. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100422.	2.5	12
46	Open Modification Searching of SARS-CoV-2â€“Human Protein Interaction Data Reveals Novel Viral Modification Sites. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100425.	2.5	5
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48	Systems biology in COVID-19. , 2023, , 301-320.		0
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