

SAINT: probabilistic scoring of affinity purification“n

Nature Methods

8, 70-73

DOI: [10.1038/nmeth.1541](https://doi.org/10.1038/nmeth.1541)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Profiling of Protein Interaction Networks of Protein Complexes Using Affinity Purification and Quantitative Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1650-1665.	2.5	89
2	Sequence, Structure, and Network Evolution of Protein Phosphorylation Meeting information: Keystone Symposium: The Evolution of Protein Phosphorylation, 23 to 27 January 2011, Keystone, CO, USA. <i>Science Signaling</i> , 2011, 4, mr6.	1.6	17
3	A Protein Complex Network of <i>Drosophila melanogaster</i> . <i>Cell</i> , 2011, 147, 690-703.	13.5	593
4	Unraveling the dynamics of protein interactions with quantitative mass spectrometry. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011, 46, 216-228.	2.3	25
5	Technologies and Approaches to Elucidate and Model the Virulence Program of <i>Salmonella</i> . <i>Frontiers in Microbiology</i> , 2011, 2, 121.	1.5	18
6	A cost-benefit analysis of multidimensional fractionation of affinity purification-mass spectrometry samples. <i>Proteomics</i> , 2011, 11, 2603-2612.	1.3	29
7	Abacus: A computational tool for extracting and pre-processing spectral count data for label-free quantitative proteomic analysis. <i>Proteomics</i> , 2011, 11, 1340-1345.	1.3	93
8	Label-free quantitative proteomics and SAINT analysis enable interactome mapping for the human Ser/Thr protein phosphatase 5. <i>Proteomics</i> , 2011, 11, 1508-1516.	1.3	63
9	Modularity and hormone sensitivity of the <i>Drosophila melanogaster</i> insulin receptor/target of rapamycin interaction proteome. <i>Molecular Systems Biology</i> , 2011, 7, 547.	3.2	60
10	Computational Mass Spectrometry-Based Proteomics. <i>PLoS Computational Biology</i> , 2011, 7, e1002277.	1.5	55
11	Structure-Function Analysis of Core STRIPAK Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 25065-25075.	1.6	136
12	Proteomic Profiling of the TRAF3 Interactome Network Reveals a New Role for the ER-to-Golgi Transport Compartments in Innate Immunity. <i>PLoS Pathogens</i> , 2012, 8, e1002747.	2.1	48
13	Proteomic Profiling of the Human Cytomegalovirus UL35 Gene Products Reveals a Role for UL35 in the DNA Repair Response. <i>Journal of Virology</i> , 2012, 86, 806-820.	1.5	64
14	Mass spectrometry approaches to study mammalian kinase and phosphatase associated proteins. <i>Methods</i> , 2012, 57, 400-408.	1.9	66
15	An advanced method for identifying protein-protein interaction by analyzing TAP/MS data. , 2012, , .		0
16	Triple SILAC to Determine Stimulus Specific Interactions in the Wnt Pathway. <i>Journal of Proteome Research</i> , 2012, 11, 982-994.	1.8	63
17	Mapping the Protein Interaction Network of the Human COP9 Signalosome Complex Using a Label-free QTAX Strategy. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 138-147.	2.5	40
18	SAINT-MS1: Protein-Protein Interaction Scoring Using Label-free Intensity Data in Affinity Purification-Mass Spectrometry Experiments. <i>Journal of Proteome Research</i> , 2012, 11, 2619-2624.	1.8	62

#	ARTICLE	IF	CITATIONS
19	Beyond hairballs: The use of quantitative mass spectrometry data to understand protein-protein interactions. <i>FEBS Letters</i> , 2012, 586, 2723-2731.	1.3	31
20	Analyzing Protein-Protein Interactions from Affinity Purification-Mass Spectrometry Data with SAINT. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.15.	25.8	114
21	Quantitative mass spectrometry in proteomics: critical review update from 2007 to the present. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 939-965.	1.9	695
22	Comparative Interaction Networks: Bridging Genotype to Phenotype. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 139-156.	0.8	9
23	Using ProHits to Store, Annotate, and Analyze Affinity Purification-Mass Spectrometry (AP-MS) Data. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.16.	25.8	19
24	ROCS: a Reproducibility Index and Confidence Score for Interaction Proteomics Studies. <i>BMC Bioinformatics</i> , 2012, 13, 128.	1.2	9
25	A computational framework for boosting confidence in high-throughput protein-protein interaction datasets. <i>Genome Biology</i> , 2012, 13, R76.	13.9	44
26	Resolving protein interactions and complexes by affinity purification followed by label-based quantitative mass spectrometry. <i>Proteomics</i> , 2012, 12, 1623-1638.	1.3	48
27	Computational detection of protein complexes in AP-MS experiments. <i>Proteomics</i> , 2012, 12, 1663-1668.	1.3	9
28	Two steps forward-one step back: Advances in affinity purification mass spectrometry of macromolecular complexes. <i>Proteomics</i> , 2012, 12, 1591-1608.	1.3	48
29	Affinity-purification coupled to mass spectrometry: Basic principles and strategies. <i>Proteomics</i> , 2012, 12, 1576-1590.	1.3	292
30	Computational and informatics strategies for identification of specific protein interaction partners in affinity purification mass spectrometry experiments. <i>Proteomics</i> , 2012, 12, 1639-1655.	1.3	84
31	History of protein-protein interactions: From egg-white to complex networks. <i>Proteomics</i> , 2012, 12, 1478-1498.	1.3	214
32	High-throughput analysis of peptide-binding modules. <i>Proteomics</i> , 2012, 12, 1527-1546.	1.3	41
33	Identifying true protein complex constituents in interaction proteomics: The example of the DMXL2 protein complex. <i>Proteomics</i> , 2012, 12, 2428-2432.	1.3	27
34	Mass Spectrometry-Based Proteomics and Network Biology. <i>Annual Review of Biochemistry</i> , 2012, 81, 379-405.	5.0	382
35	Global landscape of HIV-human protein complexes. <i>Nature</i> , 2012, 481, 365-370.	13.7	651
36	Computational Framework for Analysis of Prey-Prey Associations in Interaction Proteomics Identifies Novel Human Protein-Protein Interactions and Networks. <i>Journal of Proteome Research</i> , 2012, 11, 4476-4487.	1.8	3

#	ARTICLE	IF	CITATIONS
37	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
38	A revolution coming to a classic model organism. <i>Nature Methods</i> , 2013, 10, 303-306.	9.0	3
39	Virus-Host Interactions. <i>Methods in Molecular Biology</i> , 2013, , .	0.4	2
40	Protein-protein interaction networks: the puzzling riches. <i>Current Opinion in Structural Biology</i> , 2013, 23, 941-953.	2.6	93
41	Insulin Biosynthetic Interaction Network Component, TMEM24, Facilitates Insulin Reserve Pool Release. <i>Cell Reports</i> , 2013, 4, 921-930.	2.9	38
42	Protein Interaction Network of the Mammalian Hippo Pathway Reveals Mechanisms of Kinase-Phosphatase Interactions. <i>Science Signaling</i> , 2013, 6, rs15.	1.6	411
43	The functional interactome landscape of the human histone deacetylase family. <i>Molecular Systems Biology</i> , 2013, 9, 672.	3.2	247
44	A global <i>S. cerevisiae</i> small ubiquitin-related modifier (SUMO) system interactome. <i>Molecular Systems Biology</i> , 2013, 9, 668.	3.2	46
45	Proteomic approaches to the study of papillomavirus-host interactions. <i>Virology</i> , 2013, 435, 57-69.	1.1	60
46	Proteomics-Based Methods for Discovery, Quantification, and Validation of Protein-Protein Interactions. <i>Analytical Chemistry</i> , 2013, 85, 749-768.	3.2	85
47	NANOG-dependent function of TET1 and TET2 in establishment of pluripotency. <i>Nature</i> , 2013, 495, 370-374.	13.7	376
48	Conserved Asf1-importin $\beta^2$ physical interaction in growth and sexual development in the ciliate <i>Tetrahymena thermophila</i> . <i>Journal of Proteomics</i> , 2013, 94, 311-326.	1.2	20
49	The Hippo Signaling Pathway Interactome. <i>Science</i> , 2013, 342, 737-740.	6.0	151
50	A Proteomic Perspective of Inbuilt Viral Protein Regulation: pUL46 Tegument Protein is Targeted for Degradation by ICPO during Herpes Simplex Virus Type 1 Infection. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3237-3252.	2.5	37
51	Interactome Networks. , 2013, , 45-63.		5
52	Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS. <i>Nature Methods</i> , 2013, 10, 307-314.	9.0	192
53	The linear ubiquitin-specific deubiquitinase gumby regulates angiogenesis. <i>Nature</i> , 2013, 498, 318-324.	13.7	234
54	The Protein Interaction Landscape of the Human CMGC Kinase Group. <i>Cell Reports</i> , 2013, 3, 1306-1320.	2.9	178

#	ARTICLE	IF	CITATIONS
55	Protein interaction networks in innate immunity. <i>Trends in Immunology</i> , 2013, 34, 610-619.	2.9	26
56	PPIRank - an advanced method for ranking protein-protein interactions in TAP/MS data. <i>Proteome Science</i> , 2013, 11, S16.	0.7	6
57	Identification of Protein Interactions Involved in Cellular Signaling. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1752-1763.	2.5	84
58	Histone Deacetylases in Herpesvirus Replication and Virus-Stimulated Host Defense. <i>Viruses</i> , 2013, 5, 1607-1632.	1.5	30
59	Popular Computational Methods to Assess Multiprotein Complexes Derived From Label-Free Affinity Purification and Mass Spectrometry (AP-MS) Experiments. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1-13.	2.5	46
60	Predicting Physical Interactions between Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1723-1734.	2.5	21
61	Molecular interaction networks for the analysis of human disease: Utility, limitations, and considerations. <i>Proteomics</i> , 2013, 13, 3393-3405.	1.3	17
62	Reproducibility restored—on toward the human interactome. <i>Nature Methods</i> , 2013, 10, 301-303.	9.0	6
63	A sampling framework for incorporating quantitative mass spectrometry data in protein interaction analysis. <i>BMC Bioinformatics</i> , 2013, 14, 299.	1.2	4
64	Mass spectrometry-based proteomic approaches for discovery of HIV—host interactions. <i>Future Virology</i> , 2014, 9, 979-992.	0.9	14
65	A Mass Spectrometry View of Stable and Transient Protein Interactions. <i>Advances in Experimental Medicine and Biology</i> , 2014, 806, 263-282.	0.8	31
66	Detecting Protein—Protein Interactions/Complex Components Using Mass Spectrometry Coupled Techniques. <i>Methods in Molecular Biology</i> , 2014, 1164, 1-13.	0.4	9
67	A systems-wide screen identifies substrates of the SCF <sup>TrCP</sup> ubiquitin ligase. <i>Science Signaling</i> , 2014, 7, rs8.	1.6	49
68	Pepper: cytoscape app for protein complex expansion using protein—protein interaction networks. <i>Bioinformatics</i> , 2014, 30, 3419-3420.	1.8	7
69	BiOLD data of c-MYC interacting protein partners in cultured cells and xenograft tumors. <i>Data in Brief</i> , 2014, 1, 76-78.	0.5	8
70	Sirtuin 4 Is a Lipoamidase Regulating Pyruvate Dehydrogenase Complex Activity. <i>Cell</i> , 2014, 159, 1615-1625.	13.5	356
71	The Impact of Mass Spectrometry—Based Proteomics on Fundamental Discoveries in Virology. <i>Annual Review of Virology</i> , 2014, 1, 581-604.	3.0	55
72	Spotlite: Web Application and Augmented Algorithms for Predicting Co-Complexed Proteins from Affinity Purification — Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2014, 13, 5944-5955.	1.8	18

#	ARTICLE	IF	CITATIONS
73	Systems Analysis of Chromatin-Related Protein Complexes in Cancer. , 2014, , .		0
74	Studying post-translational modifications with protein interaction networks. Current Opinion in Structural Biology, 2014, 24, 34-44.	2.6	51
75	CoreFlow: A computational platform for integration, analysis and modeling of complex biological data. Journal of Proteomics, 2014, 100, 167-173.	1.2	10
76	Fine Tuning of Proteomic Technologies to Improve Biological Findings: Advancements in 2011â€“2013. Analytical Chemistry, 2014, 86, 176-195.	3.2	18
77	Incorporating DNA shearing in standard affinity purification allows simultaneous identification of both soluble and chromatin-bound interaction partners. Journal of Proteomics, 2014, 100, 55-59.	1.2	28
78	From proteomes to complexomes in the era of systems biology. Proteomics, 2014, 14, 24-41.	1.3	35
79	Exploring intercellular signaling by proteomic approaches. Proteomics, 2014, 14, 498-512.	1.3	14
80	A Proteomic Perspective of Sirtuin 6 (SIRT6) Phosphorylation and Interactions and Their Dependence on Its Catalytic Activity. Molecular and Cellular Proteomics, 2014, 13, 168-183.	2.5	48
81	Proteomic Analysis of the Human Cyclin-dependent Kinase Family Reveals a Novel CDK5 Complex Involved in Cell Growth and Migration. Molecular and Cellular Proteomics, 2014, 13, 2986-3000.	2.5	34
82	PSEA-Quant: A Protein Set Enrichment Analysis on Label-Free and Label-Based Protein Quantification Data. Journal of Proteome Research, 2014, 13, 5496-5509.	1.8	57
83	Affinity purificationâ€“mass spectrometry and network analysis to understand protein-protein interactions. Nature Protocols, 2014, 9, 2539-2554.	5.5	169
84	The interactome of the atypical phosphatase Rtr1 in Saccharomyces cerevisiae. Molecular BioSystems, 2014, 10, 1730-1741.	2.9	36
85	Advancements of Mass Spectrometry in Biomedical Research. Advances in Experimental Medicine and Biology, 2014, , .	0.8	6
86	Modulation of the Chromatin Phosphoproteome by the Haspin Protein Kinase. Molecular and Cellular Proteomics, 2014, 13, 1724-1740.	2.5	37
87	The lysine methyltransferase SMYD3 interacts with hepatitis C virus NS5A and is a negative regulator of viral particle production. Virology, 2014, 462-463, 34-41.	1.1	18
88	Human-Chromatin-Related Protein Interactions Identify a Demethylase Complex Required for Chromosome Segregation. Cell Reports, 2014, 8, 297-310.	2.9	72
89	A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. Cell, 2014, 158, 434-448.	13.5	335
90	Pre- and Post-Processing Workflow for Affinity Purification Mass Spectrometry Data. Journal of Proteome Research, 2014, 13, 2239-2249.	1.8	8

#	ARTICLE	IF	CITATIONS
91	ZNF750 interacts with KLF4 and RCOR1, KDM1A, and CTBP1/2 chromatin regulators to repress epidermal progenitor genes and induce differentiation genes. <i>Genes and Development</i> , 2014, 28, 2013-2026.	2.7	122
92	Exploring mitochondrial system properties of neurodegenerative diseases through interactome mapping. <i>Journal of Proteomics</i> , 2014, 100, 8-24.	1.2	13
93	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	1.6	6
94	Building and exploring an integrated human kinase network: Global organization and medical entry points. <i>Journal of Proteomics</i> , 2014, 107, 113-127.	1.2	16
95	SAINTexpress: Improvements and additional features in Significance Analysis of INteractome software. <i>Journal of Proteomics</i> , 2014, 100, 37-43.	1.2	501
96	Defining the Protein-Protein Interaction Network of the Human Hippo Pathway. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 119-131.	2.5	126
97	Probing phosphorylation-dependent protein interactions within functional domains of histone deacetylase 5 (<sc>HDAC</sc>5). <i>Proteomics</i> , 2014, 14, 2156-2166.	1.3	13
99	GSK3 $\beta$ controls epithelial-mesenchymal transition and tumor metastasis by CHIP-mediated degradation of Slug. <i>Oncogene</i> , 2014, 33, 3172-3182.	2.6	118
102	21st Century Genetics: Mass Spectrometry of Yeast Telomerase. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 111-116.	2.0	2
103	Mapping the H <sup>+</sup> (V)-ATPase interactome: identification of proteins involved in trafficking, folding, assembly and phosphorylation. <i>Scientific Reports</i> , 2015, 5, 14827.	1.6	98
105	Fundamentals of protein interaction network mapping. <i>Molecular Systems Biology</i> , 2015, 11, 848.	3.2	226
106	Inferring genetic architecture from systems genetics studies. , 0, , 139-160.		0
107	EBprot: Statistical analysis of labeling-based quantitative proteomics data. <i>Proteomics</i> , 2015, 15, 2580-2591.	1.3	14
108	TRIM32 Senses and Restricts Influenza A Virus by Ubiquitination of PB1 Polymerase. <i>PLoS Pathogens</i> , 2015, 11, e1004960.	2.1	123
109	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1820-1826.	1.2	17
110	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015, 27, 864-876.	7.7	265
111	Scoring Large-Scale Affinity Purification Mass Spectrometry Datasets with MiST. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.19.1-8.19.16.	25.8	58
112	The functional interactome of <sc>PYHIN</sc> immune regulators reveals <sc>IFIX</sc> is a sensor of viral <sc>DNA</sc>. <i>Molecular Systems Biology</i> , 2015, 11, 787.	3.2	74

#	ARTICLE	IF	CITATIONS
113	Proteomic Analyses Uncover a New Function and Mode of Action for Mouse Homolog of Diaphanous 2 (mDia2)*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1064-1078.	2.5	20
114	CALML5 is a ZNF750- and TINCR-induced protein that binds stratifin to regulate epidermal differentiation. <i>Genes and Development</i> , 2015, 29, 2225-2230.	2.7	61
115	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. <i>Cell</i> , 2015, 163, 1484-1499.	13.5	446
116	Relevance Rank Platform (RRP) for Functional Filtering of High Content Protein-Protein Interaction Data*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3274-3283.	2.5	19
117	Understanding the role of chromatin remodeling in the regulation of circadian transcription in <i>Drosophila</i> . <i>Fly</i> , 2015, 9, 145-154.	0.9	8
118	Identifying binary protein-protein interactions from affinity purification mass spectrometry data. <i>BMC Genomics</i> , 2015, 16, 745.	1.2	11
119	A Role for Widely Interspaced Zinc Finger (WIZ) in Retention of the G9a Methyltransferase on Chromatin. <i>Journal of Biological Chemistry</i> , 2015, 290, 26088-26102.	1.6	29
120	The <i>S. cerevisiae</i> SUMO stress response is a conjugation-deconjugation cycle that targets the transcription machinery. <i>Journal of Proteomics</i> , 2015, 118, 39-48.	1.2	41
121	SLC38A9 is a component of the lysosomal amino acid sensing machinery that controls mTORC1. <i>Nature</i> , 2015, 519, 477-481.	13.7	561
122	Conserved abundance and topological features in chromatin-remodeling protein interaction networks. <i>EMBO Reports</i> , 2015, 16, 116-126.	2.0	17
123	Interactions of the Antiviral Factor Interferon Gamma-Inducible Protein 16 (IFI16) Mediate Immune Signaling and Herpes Simplex Virus-1 Immunosuppression. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2341-2356.	2.5	84
124	Incorporating computational resources in a cancer research program. <i>Human Genetics</i> , 2015, 134, 467-478.	1.8	2
125	The RNA-binding protein HuR/ELAVL1 regulates IFN- $\beta$ mRNA abundance and the type I IFN response. <i>European Journal of Immunology</i> , 2015, 45, 1500-1511.	1.6	49
126	Post-translational Modifications Regulate Class IIa Histone Deacetylase (HDAC) Function in Health and Disease. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 456-470.	2.5	72
127	Interactome analysis of AMP-activated protein kinase (AMPK)- $\alpha$ 1 and - $\beta$ 1 in INS-1 pancreatic beta-cells by affinity purification-mass spectrometry. <i>Scientific Reports</i> , 2014, 4, 4376.	1.6	36
128	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. <i>Nature Methods</i> , 2015, 12, 258-264.	9.0	561
129	Myotubularin-related Proteins 3 and 4 Interact with Polo-like Kinase 1 and Centrosomal Protein of 55 kDa to Ensure Proper Abscission. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 946-960.	2.5	17
130	A web-tool for visualizing quantitative protein-protein interaction data. <i>Proteomics</i> , 2015, 15, 1432-1436.	1.3	30



#	ARTICLE	IF	CITATIONS
131	PPI network inference from AP-MS data. , 2015, , 51-59.		1
132	The Ecdysone Receptor Coactivator Taiman Links Yorkie to Transcriptional Control of Germline Stem Cell Factors in Somatic Tissue. <i>Developmental Cell</i> , 2015, 34, 168-180.	3.1	56
133	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	9.0	109
134	TRAF1 Coordinates Polyubiquitin Signaling to Enhance Epstein-Barr Virus LMP1-Mediated Growth and Survival Pathway Activation. <i>PLoS Pathogens</i> , 2015, 11, e1004890.	2.1	67
135	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human neuroblastoma cells. <i>Journal of Proteomics</i> , 2015, 123, 42-53.	1.2	62
136	Extracting high confidence protein interactions from affinity purification data: At the crossroads. <i>Journal of Proteomics</i> , 2015, 118, 63-80.	1.2	30
137	Potato leafroll virus structural proteins manipulate overlapping, yet distinct protein interaction networks during infection. <i>Proteomics</i> , 2015, 15, 2098-2112.	1.3	22
138	Validation of a Novel Shotgun Proteomic Workflow for the Discovery of Protein-Protein Interactions: Focus on ZNF521. <i>Journal of Proteome Research</i> , 2015, 14, 1888-1899.	1.8	22
139	CHCHD2 Is Coamplified with EGFR in NSCLC and Regulates Mitochondrial Function and Cell Migration. <i>Molecular Cancer Research</i> , 2015, 13, 1119-1129.	1.5	43
140	Proteomics methods for discovering viral-host interactions. <i>Methods</i> , 2015, 90, 21-27.	1.9	6
141	BioID-based Identification of Skp Cullin F-box (SCF) <sup>2</sup> -TrCP1/2 E3 Ligase Substrates*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1781-1795.	2.5	148
142	Identification of Regulatory and Cargo Proteins of Endosomal and Secretory Pathways in <i>Arabidopsis thaliana</i> by Proteomic Dissection*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1796-1813.	2.5	101
143	Multidimensional proteomics for cell biology. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 269-280.	16.1	375
144	Proteomics of yeast telomerase identified Cdc48-Npl4-Ufd1 and Ufd4 as regulators of Est1 and telomere length. <i>Nature Communications</i> , 2015, 6, 8290.	5.8	32
145	The Human Adenovirus Type 5 E4orf4 Protein Targets Two Phosphatase Regulators of the Hippo Signaling Pathway. <i>Journal of Virology</i> , 2015, 89, 8855-8870.	1.5	10
146	Proteomic analyses reveal distinct chromatin-associated and soluble transcription factor complexes. <i>Molecular Systems Biology</i> , 2015, 11, 775.	3.2	121
147	Lineage-Specific Viral Hijacking of Non-canonical E3 Ubiquitin Ligase Cofactors in the Evolution of Vif Anti-APOBEC3 Activity. <i>Cell Reports</i> , 2015, 11, 1236-1250.	2.9	42
148	Biochemical Large-Scale Interaction Analysis of Murine Olfactory Receptors and Associated Signaling Proteins with Post-Synaptic Density 95, <i>Drosophila</i> Discs Large, Zona-Occludens 1 (PDZ) Domains. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2072-2084.	2.5	5

#	ARTICLE	IF	CITATIONS
149	Quantitative analysis of PPT1 interactome in human neuroblastoma cells. <i>Data in Brief</i> , 2015, 4, 207-216.	0.5	11
150	Network Analysis Identifies Mitochondrial Regulation of Epidermal Differentiation by MPZL3 and FDXR. <i>Developmental Cell</i> , 2015, 35, 444-457.	3.1	50
151	Insights Into the <i>Polevirus</i> Plant Interactome Revealed by Coimmunoprecipitation and Mass Spectrometry. <i>Molecular Plant-Microbe Interactions</i> , 2015, 28, 467-481.	1.4	45
152	The GTPase Regulatory Proteins Pix and Git Control Tissue Growth via the Hippo Pathway. <i>Current Biology</i> , 2015, 25, 124-130.	1.8	24
153	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. <i>Journal of Proteomics</i> , 2015, 118, 95-111.	1.2	112
154	Raw data for the identification of SUMOylated proteins in <i>S. cerevisiae</i> subjected to two types of osmotic shock, using affinity purification coupled with mass spectrometry. <i>Data in Brief</i> , 2015, 2, 29-31.	0.5	0
155	Identification of SUMO-2/3-modified proteins associated with mitotic chromosomes. <i>Proteomics</i> , 2015, 15, 763-772.	1.3	32
156	Network inference from AP-MS data: computational challenges and solutions. <i>Briefings in Bioinformatics</i> , 2015, 16, 658-674.	3.2	21
157	Substrate Trapping Proteomics Reveals Targets of the $\hat{2}$ TrCP2/FBXW11 Ubiquitin Ligase. <i>Molecular and Cellular Biology</i> , 2015, 35, 167-181.	1.1	55
158	From pathways to networks: Connecting dots by establishing protein-protein interaction networks in signaling pathways using affinity purification and mass spectrometry. <i>Proteomics</i> , 2015, 15, 188-202.	1.3	20
159	PIPINO: A Software Package to Facilitate the Identification of Protein-Protein Interactions from Affinity Purification Mass Spectrometry Data. <i>BioMed Research International</i> , 2016, 2016, 1-13.	0.9	0
160	Association of Cell Adhesion Molecules Contactin-6 and Latrophilin-1 Regulates Neuronal Apoptosis. <i>Frontiers in Molecular Neuroscience</i> , 2016, 9, 143.	1.4	28
161	A tissue-specific protein purification approach in <i>Caenorhabditis elegans</i> identifies novel interaction partners of DLG-1/Discs large. <i>BMC Biology</i> , 2016, 14, 66.	1.7	40
162	Pfh1 Is an Accessory Replicative Helicase that Interacts with the Replisome to Facilitate Fork Progression and Preserve Genome Integrity. <i>PLoS Genetics</i> , 2016, 12, e1006238.	1.5	35
163	Interrogating the Plasmodium Sporozoite Surface: Identification of Surface-Exposed Proteins and Demonstration of Glycosylation on CSP and TRAP by Mass Spectrometry-Based Proteomics. <i>PLoS Pathogens</i> , 2016, 12, e1005606.	2.1	159
164	SAINTq: Scoring protein-protein interactions in affinity purification mass spectrometry experiments with fragment or peptide intensity data. <i>Proteomics</i> , 2016, 16, 2238-2245.	1.3	45
165	Model System-Guided Protein Interaction Mapping for Virus Isolated from Phloem Tissue. <i>Journal of Proteome Research</i> , 2016, 15, 4601-4611.	1.8	12
166	Identification of Novel Host Interactors of Effectors Secreted by <i>Salmonella</i> and <i>Citrobacter</i> . <i>MSystems</i> , 2016, 1, .	1.7	22

#	ARTICLE	IF	CITATIONS
167	SAFER, an Analysis Method of Quantitative Proteomic Data, Reveals New Interactors of the <i>C. elegans</i> Autophagic Protein LGG-1. <i>Journal of Proteome Research</i> , 2016, 15, 1515-1523.	1.8	1
168	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	1.2	66
169	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1539-1555.	2.5	16
170	Quantitative Analysis of Dynamic Protein Interactions during Transcription Reveals a Role for Casein Kinase II in Polymerase-associated Factor (PAF) Complex Phosphorylation and Regulation of Histone H2B Monoubiquitylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 13410-13420.	1.6	15
171	Computational Proteomics. , 2016, , 11-20.		0
172	Sample Preparation for Mass Spectrometry Analysis of Proteinâ€“Protein Interactions in Cancer Cell Lines and Tissues. <i>Methods in Molecular Biology</i> , 2016, 1458, 339-347.	0.4	14
173	Minibrain and Wings apart control organ growth and tissue patterning through down-regulation of Capicua. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10583-10588.	3.3	26
174	Prenylated retinal ciliopathy protein RPGR interacts with PDE6Î³ and regulates ciliary localization of Joubert syndrome-associated protein INPP5E. <i>Human Molecular Genetics</i> , 2016, 25, ddw281.	1.4	29
175	Depot specific differences in the adipogenic potential of precursors are mediated by collagenous extracellular matrix and Flotillin 2â€“dependent signaling. <i>Molecular Metabolism</i> , 2016, 5, 937-947.	3.0	29
176	APOSTL: An Interactive Galaxy Pipeline for Reproducible Analysis of Affinity Proteomics Data. <i>Journal of Proteome Research</i> , 2016, 15, 4747-4754.	1.8	16
177	Interactomic landscape of PA-X-chicken protein complexes of H5N1 influenza A virus. <i>Journal of Proteomics</i> , 2016, 148, 20-25.	1.2	16
178	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. <i>Nature Chemical Biology</i> , 2016, 12, 867-875.	3.9	79
180	Mass-spectrometric exploration of proteome structure and function. <i>Nature</i> , 2016, 537, 347-355.	13.7	1,573
181	An Integrative Analysis of the InR/PI3K/Akt Network Identifies the Dynamic Response to Insulin Signaling. <i>Cell Reports</i> , 2016, 16, 3062-3074.	2.9	78
182	Basic Concepts in Mass Spectrometry and Protein Quantitation. , 2016, , 15-32.		0
183	Intelligent Mixing of Proteomes for Elimination of False Positives in Affinity Purification-Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 3929-3937.	1.8	8
184	Defining the Protein-Protein Interaction Network of the Human Protein Tyrosine Phosphatase Family. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3030-3044.	2.5	41
185	Expanding the Interactome of the Noncanonical NF-Î²B Signaling Pathway. <i>Journal of Proteome Research</i> , 2016, 15, 2900-2909.	1.8	8

#	ARTICLE	IF	CITATIONS
186	Germline missense pathogenic variants in the BRCA1 BRCT domain, p.Gly1706Glu and p.Ala1708Glu, increase cellular sensitivity to PARP inhibitor olaparib by a dominant negative effect. <i>Human Molecular Genetics</i> , 2016, 25, ddw343.	1.4	4
187	Deep interactome profiling of membrane proteins by co-interacting protein identification technology. <i>Nature Protocols</i> , 2016, 11, 2515-2528.	5.5	54
188	C9orf72 Dipeptide Repeats Impair the Assembly, Dynamics, and Function of Membrane-Less Organelles. <i>Cell</i> , 2016, 167, 774-788.e17.	13.5	577
189	Heme drives hemolysis-induced susceptibility to infection via disruption of phagocyte functions. <i>Nature Immunology</i> , 2016, 17, 1361-1372.	7.0	114
190	An Inducible Retroviral Expression System for Tandem Affinity Purification Mass-Spectrometry-Based Proteomics Identifies Mixed Lineage Kinase Domain-like Protein (MLKL) as an Heat Shock Protein 90 (HSP90) Client. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1139-1150.	2.5	23
191	Assembly Dynamics and Stoichiometry of the Apoptosis Signal-regulating Kinase (ASK) Signalosome in Response to Electrophile Stress. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1947-1961.	2.5	29
193	Identification of Sirtuin4 (SIRT4) Protein Interactions: Uncovering Candidate Acyl-Modified Mitochondrial Substrates and Enzymatic Regulators. <i>Methods in Molecular Biology</i> , 2016, 1436, 213-239.	0.4	11
194	Stable association of RNAi machinery is conserved between the cytoplasm and nucleus of human cells. <i>Rna</i> , 2016, 22, 1085-1098.	1.6	56
195	HELB Is a Feedback Inhibitor of DNA End Resection. <i>Molecular Cell</i> , 2016, 61, 405-418.	4.5	119
196	The Proteomic Profile of Deleted in Breast Cancer 1 (DBC1) Interactions Points to a Multifaceted Regulation of Gene Expression. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 791-809.	2.5	14
197	Characterizing Protein-Protein Interactions Using Mass Spectrometry: Challenges and Opportunities. <i>Trends in Biotechnology</i> , 2016, 34, 825-834.	4.9	131
198	Time-dependent, glucose-regulated Arabidopsis Regulator of G-protein Signaling 1 network. <i>Current Plant Biology</i> , 2016, 5, 25-35.	2.3	10
199	Proteomic approaches to uncovering virus-host protein interactions during the progression of viral infection. <i>Expert Review of Proteomics</i> , 2016, 13, 325-340.	1.3	76
200	Axin cancer mutants form nanoaggregates to rewire the Wnt signaling network. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 324-332.	3.6	31
201	SFINX: Straightforward Filtering Index for Affinity Purification-Mass Spectrometry Data Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 332-338.	1.8	20
202	Identification of Evening Complex Associated Proteins in Arabidopsis by Affinity Purification and Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 201-217.	2.5	170
203	Decoding protein networks during virus entry by quantitative proteomics. <i>Virus Research</i> , 2016, 218, 25-39.	1.1	24
204	UbE2E1/UBCH6 Is a Critical in Vivo E2 for the PRC1-catalyzed Ubiquitination of H2A at Lys-119. <i>Journal of Biological Chemistry</i> , 2017, 292, 2893-2902.	1.6	24

#	ARTICLE	IF	CITATIONS
205	Human Antiviral Protein IFIX Suppresses Viral Gene Expression during Herpes Simplex Virus 1 (HSV-1) Infection and Is Counteracted by Virus-induced Proteasomal Degradation. <i>Molecular and Cellular Proteomics</i> , 2017, 16, S200-S214.	2.5	27
206	Parallel Exploration of Interaction Space by BioID and Affinity Purification Coupled to Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1550, 115-136.	0.4	66
207	Small-Molecule Stabilization of 14-3-3 Protein-Protein Interactions Stimulates Axon Regeneration. <i>Neuron</i> , 2017, 93, 1082-1093.e5.	3.8	66
208	Identification of Topological Network Modules in Perturbed Protein Interaction Networks. <i>Scientific Reports</i> , 2017, 7, 43845.	1.6	29
209	ZMPSTE24 defends against influenza and other pathogenic viruses. <i>Journal of Experimental Medicine</i> , 2017, 214, 919-929.	4.2	61
210	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017, 18, 1527-1542.	2.9	79
211	Clustered, Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9-coupled Affinity Purification/Mass Spectrometry Analysis Revealed a Novel Role of Neurofibromin in mTOR Signaling. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 594-607.	2.5	13
212	MSFragger: ultrafast and comprehensive peptide identification in mass spectrometry-based proteomics. <i>Nature Methods</i> , 2017, 14, 513-520.	9.0	1,099
213	Transcriptional Elongation of HSV Immediate Early Genes by the Super Elongation Complex Drives Lytic Infection and Reactivation from Latency. <i>Cell Host and Microbe</i> , 2017, 21, 507-517.e5.	5.1	32
214	Plant Genomics. <i>Methods in Molecular Biology</i> , 2017, , .	0.4	2
215	MK2 Phosphorylates RIPK1 to Prevent TNF-Induced Cell Death. <i>Molecular Cell</i> , 2017, 66, 698-710.e5.	4.5	242
216	sfinx: an R package for the elimination of false positives from affinity purification-based mass spectrometry datasets. <i>Bioinformatics</i> , 2017, 33, 1902-1904.	1.8	3
217	Mapping Protein-Protein Interactions Using Affinity Purification and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1610, 231-249.	0.4	20
218	Artemisinin Target GABAA Receptor Signaling and Impair $\pm$ Cell Identity. <i>Cell</i> , 2017, 168, 86-100.e15.	13.5	330
219	Agonist-specific Protein Interactomes of Glucocorticoid and Androgen Receptor as Revealed by Proximity Mapping. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1462-1474.	2.5	55
220	The Plasmodium falciparum exported protein PF3D7_0402000 binds to erythrocyte ankyrin and band 4.1. <i>Molecular and Biochemical Parasitology</i> , 2017, 216, 5-13.	0.5	7
221	ZMPSTE24 Is Downstream Effector of Interferon-Induced Transmembrane Antiviral Activity. <i>DNA and Cell Biology</i> , 2017, 36, 513-517.	0.9	23
222	Characterization of the CLASP2 Protein Interaction Network Identifies SOGA1 as a Microtubule-Associated Protein. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1718-1735.	2.5	41

#	ARTICLE	IF	CITATIONS
223	Red Blood Cell Invasion by the Malaria Parasite Is Coordinated by the PfAP2-I Transcription Factor. <i>Cell Host and Microbe</i> , 2017, 21, 731-741.e10.	5.1	106
224	Proteomics and integrative omic approaches for understanding host-pathogen interactions and infectious diseases. <i>Molecular Systems Biology</i> , 2017, 13, 922.	3.2	164
225	An Approach to Spatiotemporally Resolve Protein Interaction Networks in Living Cells. <i>Cell</i> , 2017, 169, 350-360.e12.	13.5	322
226	Analyzing trapped protein complexes by Virotrap and SFINX. <i>Nature Protocols</i> , 2017, 12, 881-898.	5.5	15
227	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017, 4, 430-444.e5.	2.9	65
228	Single-Step Affinity Purification of ERK Signaling Complexes Using the Streptavidin-Binding Peptide (SBP) Tag. <i>Methods in Molecular Biology</i> , 2017, 1487, 113-126.	0.4	13
229	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. <i>Science Signaling</i> , 2017, 10, .	1.6	52
230	Recent progress in mass spectrometry proteomics for biomedical research. <i>Science China Life Sciences</i> , 2017, 60, 1093-1113.	2.3	97
231	The <i>Candida albicans</i> transcription factor Cas5 couples stress responses, drug resistance and cell cycle regulation. <i>Nature Communications</i> , 2017, 8, 499.	5.8	49
232	Unravelling the biology of chromatin in health and cancer using proteomic approaches. <i>Expert Review of Proteomics</i> , 2017, 14, 905-915.	1.3	5
233	Comparative influenza protein interactomes identify the role of plakophilin 2 in virus restriction. <i>Nature Communications</i> , 2017, 8, 13876.	5.8	58
234	Function of inhibitor of Bruton's tyrosine kinase isoform $I\beta$ (IBTK $I\beta$ ) in nonalcoholic steatohepatitis links autophagy and the unfolded protein response. <i>Journal of Biological Chemistry</i> , 2017, 292, 14050-14065.	1.6	14
235	ALBA4 modulates its stage-specific interactions and specific mRNA fates during <i>Plasmodium yoelii</i> growth and transmission. <i>Molecular Microbiology</i> , 2017, 106, 266-284.	1.2	40
236	Identification of the SOX2 Interactome by BioID Reveals EP300 as a Mediator of SOX2-dependent Squamous Differentiation and Lung Squamous Cell Carcinoma Growth. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1864-1888.	2.5	32
237	RNAi Screen and Proteomics Reveal NXF1 as a Novel Regulator of IRF5 Signaling. <i>Scientific Reports</i> , 2017, 7, 2683.	1.6	10
238	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. <i>Nature Methods</i> , 2017, 14, 645-646.	9.0	160
239	PIQED: automated identification and quantification of protein modifications from DIA-MS data. <i>Nature Methods</i> , 2017, 14, 646-647.	9.0	52
240	compleXView: a server for the interpretation of protein abundance and connectivity information to identify protein complexes. <i>Nucleic Acids Research</i> , 2017, 45, W276-W284.	6.5	6

#	ARTICLE	IF	CITATIONS
241	A proteomics view on integrin-mediated adhesions. <i>Proteomics</i> , 2017, 17, 1600022.	1.3	57
242	Combinatorial Drug Screening Identifies Ewing Sarcoma-specific Sensitivities. <i>Molecular Cancer Therapeutics</i> , 2017, 16, 88-101.	1.9	17
243	Endogenous Protein Interactome of Human UDP-Glucuronosyltransferases Exposed by Untargeted Proteomics. <i>Frontiers in Pharmacology</i> , 2017, 8, 23.	1.6	14
244	Influenza A Virus-Host Protein Interactions Control Viral Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1673.	1.8	45
245	Evaluation of a Bead-Free Coimmunoprecipitation Technique for Identification of Virus-Host Protein Interactions Using High-Resolution Mass Spectrometry. <i>Journal of Biomolecular Techniques</i> , 2017, 28, 111-121.	0.8	4
246	A two-step framework for inferring direct protein-protein interaction network from AP-MS data. <i>BMC Systems Biology</i> , 2017, 11, 82.	3.0	8
247	A rapid and accurate approach for prediction of interactomes from co-elution data (PrInCE). <i>BMC Bioinformatics</i> , 2017, 18, 457.	1.2	54
248	Sustained activation of the AKT/mTOR and MAP kinase pathways mediate resistance to the Src inhibitor, dasatinib, in thyroid cancer. <i>Oncotarget</i> , 2017, 8, 103014-103031.	0.8	9
249	Characterization of gene regulation and protein interaction networks for Matrin 3 encoding mutations linked to amyotrophic lateral sclerosis and myopathy. <i>Scientific Reports</i> , 2018, 8, 4049.	1.6	30
250	The MYO6 interactome reveals adaptor complexes coordinating early endosome and cytoskeletal dynamics. <i>EMBO Reports</i> , 2018, 19, .	2.0	49
251	Molecular Interaction Search Tool (MIST): an integrated resource for mining gene and protein interaction data. <i>Nucleic Acids Research</i> , 2018, 46, D567-D574.	6.5	66
252	An AP-MS- and BioID-compatible MAC-tag enables comprehensive mapping of protein interactions and subcellular localizations. <i>Nature Communications</i> , 2018, 9, 1188.	5.8	191
253	The Interaction Dynamics of Two Potato Leafroll Virus Movement Proteins Affects Their Localization to the Outer Membranes of Mitochondria and Plastids. <i>Viruses</i> , 2018, 10, 585.	1.5	22
254	Interactome and Proteome Dynamics Uncover Immune Modulatory Associations of the Pathogen Sensing Factor cGAS. <i>Cell Systems</i> , 2018, 7, 627-642.e6.	2.9	34
255	MYC Protein Interactome Profiling Reveals Functionally Distinct Regions that Cooperate to Drive Tumorigenesis. <i>Molecular Cell</i> , 2018, 72, 836-848.e7.	4.5	121
256	Casein Kinase II Phosphorylation of Spt6 Enforces Transcriptional Fidelity by Maintaining Spn1-Spt6 Interaction. <i>Cell Reports</i> , 2018, 25, 3476-3489.e5.	2.9	20
257	A Hippo-like Signaling Pathway Controls Tracheal Morphogenesis in <i>Drosophila melanogaster</i> . <i>Developmental Cell</i> , 2018, 47, 564-575.e5.	3.1	24
258	Human MARF1 is an endoribonuclease that interacts with the DCP1:2 decapping complex and degrades target mRNAs. <i>Nucleic Acids Research</i> , 2018, 46, 12008-12021.	6.5	22

#	ARTICLE	IF	CITATIONS
259	MYC dephosphorylation by the PP1/PNUTS phosphatase complex regulates chromatin binding and protein stability. <i>Nature Communications</i> , 2018, 9, 3502.	5.8	43
260	<scp>SHLD</scp> 2/ <scp>FAM</scp> 35A coöperates with <scp>REV</scp> 7 to coordinate <scp>DNA</scp> doubleâ€strand break repair pathway choice. <i>EMBO Journal</i> , 2018, 37, .	3.5	111
261	Aurora B opposes PP1 function in mitosis by phosphorylating the conserved PP1-binding RVxF motif in PP1 regulatory proteins. <i>Science Signaling</i> , 2018, 11, .	1.6	64
262	Global assessment of its network dynamics reveals that the kinase Plk1 inhibits the phosphatase PP6 to promote Aurora A activity. <i>Science Signaling</i> , 2018, 11, .	1.6	25
263	Identification of TOEFAZ1â€™interacting proteins reveals key regulators of <i>Trypanosoma brucei</i> cytokinesis. <i>Molecular Microbiology</i> , 2018, 109, 306-326.	1.2	42
264	Cooperative binding of ApiAP2 transcription factors is crucial for the expression of virulence genes in <i>Toxoplasma gondii</i> . <i>Nucleic Acids Research</i> , 2018, 46, 6057-6068.	6.5	41
265	Ciliary dynein motor preassembly is regulated by Wdr92 in association with HSP90 co-chaperone, R2TP. <i>Journal of Cell Biology</i> , 2018, 217, 2583-2598.	2.3	53
266	The multi-subunit GID/CTLH E3 ubiquitin ligase promotes cell proliferation and targets the transcription factor Hbp1 for degradation. <i>ELife</i> , 2018, 7, .	2.8	76
267	Mapping of Plasma Membrane Proteins Interacting With <i>Arabidopsis thaliana</i> Flotillin 2. <i>Frontiers in Plant Science</i> , 2018, 9, 991.	1.7	29
268	A widespread alternate form of cap-dependent mRNA translation initiation. <i>Nature Communications</i> , 2018, 9, 3068.	5.8	121
269	Large Scale Proteomic Data and Network-Based Systems Biology Approaches to Explore the Plant World. <i>Proteomes</i> , 2018, 6, 27.	1.7	18
270	p38-mediated phosphorylation at T367 induces EZH2 cytoplasmic localization to promote breast cancer metastasis. <i>Nature Communications</i> , 2018, 9, 2801.	5.8	87
271	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121.	18.7	445
272	Proteomic Analysis of NCK1/2 Adaptors Uncovers Paralog-specific Interactions That Reveal a New Role for NCK2 in Cell Abscission During Cytokinesis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1979-1990.	2.5	21
273	Regulation of KIF1A-Driven Dense Core Vesicle Transport: Ca <sup>2+</sup> /CaM Controls DCV Binding and Liprin-1/TANC2 Recruits DCVs to Postsynaptic Sites. <i>Cell Reports</i> , 2018, 24, 685-700.	2.9	64
274	Changes in proteome solubility indicate widespread proteostatic disruption in mouse models of neurodegenerative disease. <i>Acta Neuropathologica</i> , 2018, 136, 919-938.	3.9	27
275	Comprehensive evaluation of coding region point mutations in microsatelliteâ€™unstable colorectal cancer. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	10
276	Structural Analysis of Hippocampal Kinase Signal Transduction. <i>ACS Chemical Neuroscience</i> , 2018, 9, 3072-3085.	1.7	6



#	ARTICLE	IF	CITATIONS
277	Lgl reduces endosomal vesicle acidification and Notch signaling by promoting the interaction between Vap33 and the V-ATPase complex. <i>Science Signaling</i> , 2018, 11, .	1.6	21
278	In planta proximity dependent biotin identification (BioID). <i>Scientific Reports</i> , 2018, 8, 9212.	1.6	70
279	Discovering cellular protein-protein interactions: Technological strategies and opportunities. <i>Mass Spectrometry Reviews</i> , 2019, 38, 79-111.	2.8	70
280	Mining cancer biology through bioinformatic analysis of proteomic data. <i>Expert Review of Proteomics</i> , 2019, 16, 733-747.	1.3	21
281	Machine-learning techniques for the prediction of protein-protein interactions. <i>Journal of Biosciences</i> , 2019, 44, 1.	0.5	53
282	A Key Role for the Ubiquitin Ligase UBR4 in Myofiber Hypertrophy in Drosophila and Mice. <i>Cell Reports</i> , 2019, 28, 1268-1281.e6.	2.9	56
283	<i>Chlamydia trachomatis</i> . <i>Methods in Molecular Biology</i> , 2019, , .	0.4	1
284	Global proteomic analyses define an environmentally contingent Hsp90 interactome and reveal chaperone-dependent regulation of stress granule proteins and the R2TP complex in a fungal pathogen. <i>PLoS Biology</i> , 2019, 17, e3000358.	2.6	34
285	Non-coding RNA Transcription in Tetrahymena Meiotic Nuclei Requires Dedicated Mediator Complex-Associated Proteins. <i>Current Biology</i> , 2019, 29, 2359-2370.e5.	1.8	9
286	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. <i>Cell Host and Microbe</i> , 2019, 26, 86-99.e7.	5.1	42
287	Charge-Mediated Pyrin Oligomerization Nucleates Antiviral IFI16 Sensing of Herpesvirus DNA. <i>MBio</i> , 2019, 10, .	1.8	25
288	Protein interactions study through proximity-labeling. <i>Expert Review of Proteomics</i> , 2019, 16, 717-726.	1.3	7
289	Proximity labeling reveals novel interactomes in live Drosophila tissue. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	32
290	Regulation of the ER stress response by a mitochondrial microprotein. <i>Nature Communications</i> , 2019, 10, 4883.	5.8	115
291	Rapid Identification of Protein-Protein Interactions in Plants. <i>Current Protocols in Plant Biology</i> , 2019, 4, e20099.	2.8	22
292	ZEB1/NuRD complex suppresses TBC1D2b to stimulate E-cadherin internalization and promote metastasis in lung cancer. <i>Nature Communications</i> , 2019, 10, 5125.	5.8	72
293	Global Interactome Mapping of Mitochondrial Intermembrane Space Proteases Identifies a Novel Function for HTRA2. <i>Proteomics</i> , 2019, 19, e1900139.	1.3	22
294	Splice variants of DOMINO control Drosophila circadian behavior and pacemaker neuron maintenance. <i>PLoS Genetics</i> , 2019, 15, e1008474.	1.5	9

#	ARTICLE	IF	CITATIONS
295	Proteomic and Interactome Approaches Reveal PAK4, PHB-2, and 14-3-3 $\beta$ as Targets of Overactivated Cdc42 in Cellular Responses to Genomic Instability. <i>Journal of Proteome Research</i> , 2019, 18, 3597-3614.	1.8	10
296	Delineating the role of FANCA in glucose-stimulated insulin secretion in $\beta$ 2 cells through its protein interactome. <i>PLoS ONE</i> , 2019, 14, e0220568.	1.1	7
297	Systematic Identification of Host Cell Regulators of <i>Legionella pneumophila</i> Pathogenesis Using a Genome-wide CRISPR Screen. <i>Cell Host and Microbe</i> , 2019, 26, 551-563.e6.	5.1	62
298	Recurrent GNAQ mutation encoding T96S in natural killer/T cell lymphoma. <i>Nature Communications</i> , 2019, 10, 4209.	5.8	25
299	Off-target based drug repurposing opportunities for tivantinib in acute myeloid leukemia. <i>Scientific Reports</i> , 2019, 9, 606.	1.6	21
300	Plasmodium male gametocyte development and transmission are critically regulated by the two putative deadenylases of the CAF1/CCR4/NOT complex. <i>PLoS Pathogens</i> , 2019, 15, e1007164.	2.1	28
301	CTDP1 regulates breast cancer survival and DNA repair through BRCT-specific interactions with FANCI. <i>Cell Death Discovery</i> , 2019, 5, 105.	2.0	14
302	Functional Proteomics of Nuclear Proteins in <i>Tetrahymena thermophila</i> : A Review. <i>Genes</i> , 2019, 10, 333.	1.0	11
303	The Galaxy Platform for Reproducible Affinity Proteomic Mass Spectrometry Data Analysis. <i>Methods in Molecular Biology</i> , 2019, 1977, 249-261.	0.4	4
304	Considerations for Identifying Endogenous Protein Complexes from Tissue via Immunoaffinity Purification and Quantitative Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1977, 115-143.	0.4	5
305	Hdac4 Interactions in Huntington's Disease Viewed Through the Prism of Multiomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S92-S113.	2.5	28
306	Experimental Analysis of Viral-Host Interactions. <i>Frontiers in Physiology</i> , 2019, 10, 425.	1.3	22
307	Genome-Wide CRISPR-Cas9 Screens Expose Genetic Vulnerabilities and Mechanisms of Temozolomide Sensitivity in Glioblastoma Stem Cells. <i>Cell Reports</i> , 2019, 27, 971-986.e9.	2.9	139
308	LLGL2 rescues nutrient stress by promoting leucine uptake in ER+ breast cancer. <i>Nature</i> , 2019, 569, 275-279.	13.7	99
309	Insulin Induces Microtubule Stabilization and Regulates the Microtubule Plus-end Tracking Protein Network in Adipocytes. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1363-1381.	2.5	43
310	Gfi1b regulates the level of Wnt/ $\beta$ -catenin signaling in hematopoietic stem cells and megakaryocytes. <i>Nature Communications</i> , 2019, 10, 1270.	5.8	31
311	Methods review: Mass spectrometry analysis of RNAPII complexes. <i>Methods</i> , 2019, 159-160, 105-114.	1.9	4
312	Chromatin capture links the metabolic enzyme AHCY to stem cell proliferation. <i>Science Advances</i> , 2019, 5, eaav2448.	4.7	38

#	ARTICLE	IF	CITATIONS
313	A threonyl-tRNA synthetase-mediated translation initiation machinery. <i>Nature Communications</i> , 2019, 10, 1357.	5.8	52
314	Topological scoring of protein interaction networks. <i>Nature Communications</i> , 2019, 10, 1118.	5.8	32
315	Mass Spectrometry of Proteins. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	0
316	The Gag protein PEG10 binds to RNA and regulates trophoblast stem cell lineage specification. <i>PLoS ONE</i> , 2019, 14, e0214110.	1.1	48
318	Host cell interactome of PB1 N40 protein of H5N1 influenza A virus in chicken cells. <i>Journal of Proteomics</i> , 2019, 197, 34-41.	1.2	14
319	The interactome of <sc>KRAB</sc> zinc finger proteins reveals the evolutionary history of their functional diversification. <i>EMBO Journal</i> , 2019, 38, e101220.	3.5	67
320	Proximity Labeling To Map Host-Pathogen Interactions at the Membrane of a Bacterium-Containing Vacuole in <i>Chlamydia trachomatis</i> -Infected Human Cells. <i>Infection and Immunity</i> , 2019, 87, .	1.0	24
321	Label-Free Immunoprecipitation Mass Spectrometry Workflow for Large-scale Nuclear Interactome Profiling. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	7
322	Enterovirus pathogenesis requires the host methyltransferase SETD3. <i>Nature Microbiology</i> , 2019, 4, 2523-2537.	5.9	51
323	BioID Performed on Golgi Enriched Fractions Identify C10orf76 as a GBF1 Binding Protein Essential for Golgi Maintenance and Secretion. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2285-2297.	2.5	20
324	Mapping the Ku Interactome Using Proximity-Dependent Biotin Identification in Human Cells. <i>Journal of Proteome Research</i> , 2019, 18, 1064-1077.	1.8	33
325	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. <i>Molecular Cell</i> , 2019, 73, 621-638.e17.	4.5	135
326	RIPK1 and Caspase-8 Ensure Chromosome Stability Independently of Their Role in Cell Death and Inflammation. <i>Molecular Cell</i> , 2019, 73, 413-428.e7.	4.5	50
327	A Sam68â€dependent alternative splicing program shapes postsynaptic protein complexes. <i>European Journal of Neuroscience</i> , 2019, 49, 1436-1453.	1.2	12
328	Getting to know the neighborhood: using proximity-dependent biotinylation to characterize protein complexes and map organelles. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 44-54.	2.8	218
329	Interactome mapping defines BRG1, a component of the SWI/SNF chromatin remodeling complex, as a new partner of the transcriptional regulator CTCF. <i>Journal of Biological Chemistry</i> , 2019, 294, 861-873.	1.6	38
330	APEX2â€mediated RAB proximity labeling identifies a role for RAB21 in clathrinâ€independent cargo sorting. <i>EMBO Reports</i> , 2019, 20, .	2.0	44
331	The Functional Proximal Proteome of Oncogenic Ras Includes mTORC2. <i>Molecular Cell</i> , 2019, 73, 830-844.e12.	4.5	104

#	ARTICLE	IF	CITATIONS
332	TgDrpC, an atypical dynamin-related protein in <i>Toxoplasma gondii</i> , is associated with vesicular transport factors and parasite division. <i>Molecular Microbiology</i> , 2019, 111, 46-64.	1.2	35
333	Reinforce: An Ensemble Approach for Inferring PPI Network from AP-MS Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 365-376.	1.9	2
334	The apical annuli of <i>Toxoplasma gondii</i> are composed of coiled-coil and signalling proteins embedded in the inner membrane complex sutures. <i>Cellular Microbiology</i> , 2020, 22, e13112.	1.1	38
335	Non-proteolytic ubiquitination of OTULIN regulates NF- $\kappa$ B signaling pathway. <i>Journal of Molecular Cell Biology</i> , 2020, 12, 163-175.	1.5	23
336	The MyMOMA domain of MYO19 encodes for distinct Miro-dependent and Miro-independent mechanisms of interaction with mitochondrial membranes. <i>Cytoskeleton</i> , 2020, 77, 149-166.	1.0	28
337	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. <i>Nature Communications</i> , 2020, 11, 157.	5.8	218
338	Automated Spatially Targeted Optical Microproteomics (autoSTOMP) to Determine Protein Complexity of Subcellular Structures. <i>Analytical Chemistry</i> , 2020, 92, 2005-2010.	3.2	13
339	Connecting proteins: shareable tools for reproducible interaction mapping. <i>Biochemistry and Cell Biology</i> , 2020, 98, 309-313.	0.9	0
340	TFIIIC Binding to Alu Elements Controls Gene Expression via Chromatin Looping and Histone Acetylation. <i>Molecular Cell</i> , 2020, 77, 475-487.e11.	4.5	65
341	A meta-analysis of affinity purification-mass spectrometry experimental systems used to identify eukaryotic and chlamydial proteins at the <i>Chlamydia trachomatis</i> inclusion membrane. <i>Journal of Proteomics</i> , 2020, 212, 103595.	1.2	5
342	Nucleotide Binding, Evolutionary Insights, and Interaction Partners of the Pseudokinase Unc-51-like Kinase 4. <i>Structure</i> , 2020, 28, 1184-1196.e6.	1.6	22
343	Precise Temporal Regulation of Post-transcriptional Repressors Is Required for an Orderly <i>Drosophila</i> Maternal-to-Zygotic Transition. <i>Cell Reports</i> , 2020, 31, 107783.	2.9	35
344	Kir2.1 Interactome Mapping Uncovers PKP4 as a Modulator of the Kir2.1-Regulated Inward Rectifier Potassium Currents. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1436-1449.	2.5	18
345	Proximal Protein Interaction Landscape of RAS Paralogs. <i>Cancers</i> , 2020, 12, 3326.	1.7	6
346	A Novel Proximity Biotinylation Assay Based on the Self-Associating Split GFP10/11. <i>Proteomes</i> , 2020, 8, 37.	1.7	3
347	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. <i>Cell Systems</i> , 2020, 11, 589-607.e8.	2.9	26
348	The Zika Virus Capsid Disrupts Corticogenesis by Suppressing Dicer Activity and miRNA Biogenesis. <i>Cell Stem Cell</i> , 2020, 27, 618-632.e9.	5.2	48
349	Combined proximity labeling and affinity purification-mass spectrometry workflow for mapping and visualizing protein interaction networks. <i>Nature Protocols</i> , 2020, 15, 3182-3211.	5.5	75

#	ARTICLE	IF	CITATIONS
350	Structure of the essential inner membrane lipopolysaccharideâ€PbgA complex. <i>Nature</i> , 2020, 584, 479-483.	13.7	58
351	Mitochondria and Peroxisome Remodeling across Cytomegalovirus Infection Time Viewed through the Lens of Inter-ViSTA. <i>Cell Reports</i> , 2020, 32, 107943.	2.9	21
352	Chromatin-Bound Proteome Profiling by Genome Capture. <i>STAR Protocols</i> , 2020, 1, 100014.	0.5	6
353	A Novel Proteomic Method Reveals NLS Tagging of T-DM1 Contravenes Classical Nuclear Transport in a Model of HER2-Positive Breast Cancer. <i>Molecular Therapy - Methods and Clinical Development</i> , 2020, 19, 99-119.	1.8	8
354	Computational Identification of Human Biological Processes and Protein Sequence Motifs Putatively Targeted by SARS-CoV-2 Proteins Using Proteinâ€Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2020, 19, 4553-4566.	1.8	13
355	The adenoviral protein E4orf4: a probing tool to decipher mechanical stress-induced nuclear envelope remodeling in tumor cells. <i>Cell Cycle</i> , 2020, 19, 2963-2981.	1.3	0
356	The Genetic and Physical Interactomes of the <i>Saccharomyces cerevisiae</i> Hrq1 Helicase. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4347-4357.	0.8	4
357	Multiplexed Proximity Biotinylation Coupled to Mass Spectrometry for Defining Integrin Adhesion Complexes. <i>Current Protocols in Cell Biology</i> , 2020, 88, e113.	2.3	4
358	<i>Mycobacterium tuberculosis</i> Rv0991c Is a Redox-Regulated Molecular Chaperone. <i>MBio</i> , 2020, 11, .	1.8	7
359	Phosphorylated tau interactome in the human Alzheimerâ€™s disease brain. <i>Brain</i> , 2020, 143, 2803-2817.	3.7	171
360	Human VAPome Analysis Reveals MOSPD1 and MOSPD3 as Membrane Contact Site Proteins Interacting with FFAT-Related FFNT Motifs. <i>Cell Reports</i> , 2020, 33, 108475.	2.9	48
361	Guanine Nucleotide-Binding Protein-Like 1 (GNL1) binds RNA G-quadruplex structures in genes associated with Parkinsonâ€™s disease. <i>RNA Biology</i> , 2021, 18, 1-15.	1.5	11
362	NF45 and NF90 Regulate Mitotic Gene Expression by Competing with Staufen-Mediated mRNA Decay. <i>Cell Reports</i> , 2020, 31, 107660.	2.9	19
363	Bait Correlation Improves Interactor Identification by Tandem Mass Tag-Affinity Purification-Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 1565-1573.	1.8	9
364	The RNA-Binding Protein Rasputin/G3BP Enhances the Stability and Translation of Its Target mRNAs. <i>Cell Reports</i> , 2020, 30, 3353-3367.e7.	2.9	33
365	Comparative Interactome Analysis of Emerin, MAN1 and LEM2 Reveals a Unique Role for LEM2 in Nucleotide Excision Repair. <i>Cells</i> , 2020, 9, 463.	1.8	16
366	RNA Polymerase II CTD phosphatase Rtr1 fine-tunes transcription termination. <i>PLoS Genetics</i> , 2020, 16, e1008317.	1.5	12
367	Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. <i>Nature Cell Biology</i> , 2020, 22, 498-511.	4.6	154

#	ARTICLE	IF	CITATIONS
368	The mitochondrial peptidase, neurolysin, regulates respiratory chain supercomplex formation and is necessary for AML viability. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	33
369	RNA aptamer capture of macromolecular complexes for mass spectrometry analysis. <i>Nucleic Acids Research</i> , 2020, 48, e90-e90.	6.5	2
370	<p>Proteomic Applications in Antimicrobial Resistance and Clinical Microbiology Studies</p>. <i>Infection and Drug Resistance</i> , 2020, Volume 13, 1785-1806.	1.1	18
371	TBL1XR1 Mutations Drive Extranodal Lymphoma by Inducing a Pro-tumorigenic Memory Fate. <i>Cell</i> , 2020, 182, 297-316.e27.	13.5	63
372	FKBP5 Regulates RIG-I-Mediated NF- $\kappa$ B Activation and Influenza A Virus Infection. <i>Viruses</i> , 2020, 12, 672.	1.5	16
373	Fast Quantitative Analysis of timsTOF PASEF Data with MSFragger and IonQuant. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1575-1585.	2.5	152
374	Variability in Streptavidinâ€™Sepharose Matrix Quality Can Significantly Affect Proximity-Dependent Biotinylation (BioID) Data. <i>Journal of Proteome Research</i> , 2020, 19, 3554-3561.	1.8	11
375	Targeted Identification of Protein Interactions in Eukaryotic mRNA Translation. <i>Proteomics</i> , 2020, 20, 1900177.	1.3	2
376	Methods of Computational Interactomics for Investigating Interactions of Human Proteoforms. <i>Biochemistry (Moscow)</i> , 2020, 85, 68-79.	0.7	1
377	Protein interactome of the Cancerous Inhibitor of protein phosphatase 2A (CIP2A) in Th17 cells. <i>Current Research in Immunology</i> , 2020, 1, 10-22.	1.2	6
378	PIKES Analysis Reveals Response to Degradors and Key Regulatory Mechanisms of the CRL4 Network. <i>Molecular Cell</i> , 2020, 77, 1092-1106.e9.	4.5	56
379	Probing Protein Interaction Networks by Combining MS-Based Proteomics and Structural Data Integration. <i>Journal of Proteome Research</i> , 2020, 19, 2807-2820.	1.8	6
380	Polypharmacological Perturbation of the 14-3-3 Adaptor Protein Interactome Stimulates Neurite Outgrowth. <i>Cell Chemical Biology</i> , 2020, 27, 657-667.e6.	2.5	24
381	The SHCA adapter protein cooperates with lipoma-preferred partner in the regulation of adhesion dynamics and invadopodia formation. <i>Journal of Biological Chemistry</i> , 2020, 295, 10535-10559.	1.6	10
382	Emerging proteomic approaches to identify the underlying pathophysiology of neurodevelopmental and neurodegenerative disorders. <i>Molecular Autism</i> , 2020, 11, 27.	2.6	15
383	Diversity in A $\beta$ 2 deposit morphology and secondary proteome insolubility across models of Alzheimer-type Amyloidosis. <i>Acta Neuropathologica Communications</i> , 2020, 8, 43.	2.4	16
384	Mass Spectrometry-Based Protein Complex Profiling in Time and Space. <i>Analytical Chemistry</i> , 2021, 93, 598-619.	3.2	17
385	Protein Interaction Network Biology in Neuroscience. <i>Proteomics</i> , 2021, 21, e1900311.	1.3	13

#	ARTICLE	IF	CITATIONS
386	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatographyâ€“Mass Spectrometry (SECâ€“MS). <i>Methods in Molecular Biology</i> , 2021, 2259, 269-294.	0.4	11
387	Identifying and Validating MYC:Protein Interactors in Pursuit of Novel Anti-MYC Therapies. <i>Methods in Molecular Biology</i> , 2021, 2318, 45-67.	0.4	0
388	Affinity Proteomics and Deglycoproteomics Uncover Novel EDEM2 Endogenous Substrates and an Integrative ERAD Network. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100125.	2.5	7
389	Mass spectrometryâ€“based proteinâ€“protein interaction networks for the study of human diseases. <i>Molecular Systems Biology</i> , 2021, 17, e8792.	3.2	96
390	Proximity-dependent Mapping of the Androgen Receptor Identifies Kruppel-like Factor 4 as a Functional Partner. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100064.	2.5	11
392	Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2021, 20, 1464-1475.	1.8	11
394	Mapping the plant proteome: tools for surveying coordinating pathways. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 203-220.	1.1	9
396	The PfAP2â€“2 transcription factor is a critical regulator of gametocyte maturation. <i>Molecular Microbiology</i> , 2021, 115, 1005-1024.	1.2	36
397	SUMOylation regulates the protein network and chromatin accessibility at glucocorticoid receptor-binding sites. <i>Nucleic Acids Research</i> , 2021, 49, 1951-1971.	6.5	23
399	Identification of Ku70 Domain-Specific Interactors Using BioID2. <i>Cells</i> , 2021, 10, 646.	1.8	2
400	mTORC1-chaperonin CCT signaling regulates m <sup>6</sup> A RNA methylation to suppress autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	49
401	STAU2 protein level is controlled by caspases and the CHK1 pathway and regulates cell cycle progression in the non-transformed hTERT-RPE1 cells. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 16.	1.0	1
402	ORF10â€“Cullin-2â€“ZYG11B complex is not required for SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	26
404	The antiviral sirtuin 3 bridges protein acetylation to mitochondrial integrity and metabolism during human cytomegalovirus infection. <i>PLoS Pathogens</i> , 2021, 17, e1009506.	2.1	20
405	Viralâ€“Host Interactome Analysis Reveals Chicken STAU2 Interacts With Non-structural Protein 1 and Promotes the Replication of H5N1 Avian Influenza Virus. <i>Frontiers in Immunology</i> , 2021, 12, 590679.	2.2	5
406	Same but different â€” Molecular comparison of human KTI12 and PSTK. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021, 1868, 118945.	1.9	1
407	TAZ-CAMTA1 and YAP-TFE3 alter the TAZ/YAP transcriptome by recruiting the ATAC histone acetyltransferase complex. <i>ELife</i> , 2021, 10, .	2.8	27
408	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	159

#	ARTICLE	IF	CITATIONS
409	Recent progress in mass spectrometry-based strategies for elucidating protein-protein interactions. Cellular and Molecular Life Sciences, 2021, 78, 5325-5339.	2.4	53
410	Affinity Purification-Mass Spectrometry Identifies a Novel Interaction between a Poliovirus and a Conserved Innate Immunity Aphid Protein that Regulates Transmission Efficiency. Journal of Proteome Research, 2021, 20, 3365-3387.	1.8	8
411	Phase separation of OCT4 controls TAD reorganization to promote cell fate transitions. Cell Stem Cell, 2021, 28, 1868-1883.e11.	5.2	66
413	Selective and noncovalent targeting of RAS mutants for inhibition and degradation. Nature Communications, 2021, 12, 2656.	5.8	51
415	ALS-linked PFN1 variants exhibit loss and gain of functions in the context of formin-induced actin polymerization. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	19
416	BBLN-1 is essential for intermediate filament organization and apical membrane morphology. Current Biology, 2021, 31, 2334-2346.e9.	1.8	13
417	Proline/arginine dipeptide repeat polymers derail protein folding in amyotrophic lateral sclerosis. Nature Communications, 2021, 12, 3396.	5.8	14
418	Long noncoding RNA HOTAIR interacts with Y-Box Protein-1 (YBX1) to regulate cell proliferation. Life Science Alliance, 2021, 4, e202101139.	1.3	16
419	The antiviral enzyme viperin inhibits cholesterol biosynthesis. Journal of Biological Chemistry, 2021, 297, 100824.	1.6	10
420	Interactome Analysis of KIN (Kin17) Shows New Functions of This Protein. Current Issues in Molecular Biology, 2021, 43, 767-781.	1.0	6
421	Shifting proteomes: limitations in using the BioID proximity labeling system to study SNARE protein trafficking during infection with intracellular pathogens. Pathogens and Disease, 2021, 79, .	0.8	4
422	Reciprocal interaction between SIRT6 and APC/C regulates genomic stability. Scientific Reports, 2021, 11, 14253.	1.6	4
423	FIP200 restricts RNA virus infection by facilitating RIG-I activation. Communications Biology, 2021, 4, 921.	2.0	4
424	From Affinity to Proximity Techniques to Investigate Protein Complexes in Plants. International Journal of Molecular Sciences, 2021, 22, 7101.	1.8	10
425	The human cytomegalovirus protein pUL13 targets mitochondrial cristae architecture to increase cellular respiration during infection. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
426	CANVS: an easy-to-use application for the analysis and visualization of mass spectrometry-based protein-protein interaction/association data. Molecular Biology of the Cell, 2021, 32, br9.	0.9	0
428	Characterizing Endogenous Protein Complexes with Biological Mass Spectrometry. Chemical Reviews, 2022, 122, 7386-7414.	23.0	24
429	Proximity labeling reveals non-centrosomal microtubule-organizing center components required for microtubule growth and localization. Current Biology, 2021, 31, 3586-3600.e11.	1.8	31



#	ARTICLE	IF	CITATIONS
431	Proximity Interactome Map of the Vac14â€‘Fig4 Complex Using BioID. Journal of Proteome Research, 2021, 20, 4959-4973.	1.8	4
433	Leaked Mitochondrial C1QBP Inhibits Activation of the DNA Sensor cGAS. Journal of Immunology, 2021, 207, ji2100392.	0.4	6
434	The proximal proteome of 17 SARS-CoV-2 proteins links to disrupted antiviral signaling and host translation. PLoS Pathogens, 2021, 17, e1009412.	2.1	27
437	The comprehensive interactomes of human adenosine RNA methyltransferases and demethylases reveal distinct functional and regulatory features. Nucleic Acids Research, 2021, 49, 10895-10910.	6.5	26
438	Exploring Chromatin Readers Using High-Accuracy Quantitative Mass Spectrometry-Based Proteomics. , 2014, , 133-148.		2
439	Proteomic Analysis of the Notch Interactome. Methods in Molecular Biology, 2014, 1187, 181-192.	0.4	6
440	Simple and Effective Affinity Purification Procedures for Mass Spectrometry-Based Identification of Protein-Protein Interactions in Cell Signaling Pathways. Methods in Molecular Biology, 2016, 1394, 181-187.	0.4	2
441	Determining the Composition and Stability of Protein Complexes Using an Integrated Label-Free and Stable Isotope Labeling Strategy. Methods in Molecular Biology, 2016, 1410, 39-63.	0.4	10
442	Proximity Labeling of the Chlamydia trachomatis Inclusion Membrane. Methods in Molecular Biology, 2019, 2042, 245-278.	0.4	3
443	Discovery of Hostâ€‘Viral Protein Complexes During Infection. Methods in Molecular Biology, 2013, 1064, 43-70.	0.4	15
444	Adenoviral protein E4orf4 interacts with the polarity protein Par3 to induce nuclear rupture and tumor cell death. Journal of Cell Biology, 2020, 219, .	2.3	9
445	The chromatin bound proteome of the human malaria parasite. Microbial Genomics, 2020, 6, .	1.0	13
458	Constructing Reliable Protein-Protein Interaction (PPI) Networks. , 2017, , 15.		4
459	Reinvestigation of Aminoacyl-TRNA Synthetase Core Complex by Affinity Purification-Mass Spectrometry Reveals TARSL2 as a Potential Member of the Complex. PLoS ONE, 2013, 8, e81734.	1.1	18
460	The <i>FUS</i> gene is dualâ€‘coding with both proteins contributing to <i>FUS</i> â€‘mediated toxicity. EMBO Reports, 2021, 22, e50640.	2.0	31
461	PAF1 complex interactions with SETDB1 mediate promoter H3K9 methylation and transcriptional repression of <i>Hoxa9</i> and <i>Meis1</i> in acute myeloid leukemia. Oncotarget, 2018, 9, 22123-22136.	0.8	22
462	Mass spectrometry-based shotgun proteomic analysis of C. elegans protein complexes. WormBook, 2014, , 1-18.	5.3	17
463	The deca-CX3 proteins Yae1-Lto1 function as adaptors recruiting the ABC protein Rli1 for iron-sulfur cluster insertion. ELife, 2015, 4, e08231.	2.8	62

#	ARTICLE	IF	CITATIONS
464	Determining composition of micron-scale protein deposits in neurodegenerative disease by spatially targeted optical microproteomics. <i>ELife</i> , 2015, 4, .	2.8	38
465	AIRE is a critical spindle-associated protein in embryonic stem cells. <i>ELife</i> , 2017, 6, .	2.8	19
466	Proteomic identification of galectin-11 and 14 ligands from <i>Haemonchus contortus</i> . <i>PeerJ</i> , 2018, 6, e4510.	0.9	7
468	The androgen receptor depends on ligand-binding domain dimerization for transcriptional activation. <i>EMBO Reports</i> , 2021, 22, e52764.	2.0	20
469	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPS cell-derived neural progenitor cells. <i>IScience</i> , 2021, 24, 103321.	1.9	2
470	Dataset of human EDEM2 melanoma cells proteomics, affinity proteomics and deglycoproteomics. <i>Data in Brief</i> , 2021, 39, 107471.	0.5	3
471	Analysis of Chaperone Network Throughput. , 2014, , 3-23.		1
472	Sphingoproteomics: Proteomic Strategies to Examine Sphingolipid Biology. , 2015, , 359-384.		0
490	Endogenous Bioid Elucidates TCF7L1 Interactome Modulation Upon GSK-3 Inhibition in Mouse ESCs. <i>SSRN Electronic Journal</i> , 0, , .	0.4	1
505	SARS-CoV-2 host proteome interactions for antiviral drug discovery. <i>Molecular Systems Biology</i> , 2021, 17, e10396.	3.2	53
507	The axonal sorting activity of pseudorabies virus Us9 protein depends on the state of neuronal maturation. <i>PLoS Pathogens</i> , 2020, 16, e1008861.	2.1	4
511	The F-box protein Bard (CG14317) targets the Smaug RNA-binding protein for destruction during the <i>Drosophila</i> maternal-to-zygotic transition. <i>Genetics</i> , 2021, , .	1.2	5
515	Transcriptomic taxonomy and neurogenic trajectories of adult human, macaque, and pig hippocampal and entorhinal cells. <i>Neuron</i> , 2022, 110, 452-469.e14.	3.8	142
517	GFI1 tethers the NuRD complex to open and transcriptionally active chromatin in myeloid progenitors. <i>Communications Biology</i> , 2021, 4, 1356.	2.0	6
518	Defining the interactomes of proteins involved in cytoskeletal dynamics using high-throughput proximity-dependent biotinylation in cellulo. <i>STAR Protocols</i> , 2022, 3, 101075.	0.5	4
520	Selective autophagy controls innate immune response through a TAK1/TAB2/SH3PX1 axis. <i>Cell Reports</i> , 2022, 38, 110286.	2.9	19
522	Interactome Analysis of Human Phospholipase D and Phosphatidic Acid-Associated Protein Network. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100195.	2.5	13
523	Human transcription factor protein interaction networks. <i>Nature Communications</i> , 2022, 13, 766.	5.8	59

#	ARTICLE	IF	CITATIONS
524	Dynamics of huntingtin protein interactions in the striatum identifies candidate modifiers of Huntington disease. <i>Cell Systems</i> , 2022, 13, 304-320.e5.	2.9	15
525	Machine-learning techniques for the prediction of protein-protein interactions. <i>Journal of Biosciences</i> , 2019, 44, .	0.5	7
526	Proximity Profiling of the CFTR Interaction Landscape in Response to Orkambi. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2442.	1.8	4
528	PCBP2 maintains antiviral signaling homeostasis by regulating cGAS enzymatic activity via antagonizing its condensation. <i>Nature Communications</i> , 2022, 13, 1564.	5.8	15
530	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>IScience</i> , 2022, 25, 104137.	1.9	20
531	Physical and functional interactome atlas of human receptor tyrosine kinases. <i>EMBO Reports</i> , 2022, 23, e54041.	2.0	18
532	RNAmetasome network for macromolecule biogenesis in human cells. <i>Communications Biology</i> , 2021, 4, 1399.	2.0	2
533	Structural dynamics shape the fitness window of alanine:glyoxylate aminotransferase. <i>Protein Science</i> , 2022, 31, e4303.	3.1	6
537	Human pluripotent stem cell-derived cells endogenously expressing follicle-stimulating hormone receptors: modeling the function of an inactivating receptor mutation. <i>Molecular Human Reproduction</i> , 2022, 28, .	1.3	1
538	Reovirus $\sigma 2$ protein modulates host cell alternative splicing by reducing protein levels of U5 snRNP core components. <i>Nucleic Acids Research</i> , 2022, 50, 5263-5281.	6.5	14
539	Protein proximity networks and functional evaluation of the casein kinase 1 gamma family reveal unique roles for CK1 $\beta$ 3 in WNT signaling. <i>Journal of Biological Chemistry</i> , 2022, 298, 101986.	1.6	5
540	Systems Biology of Virus-Host Protein Interactions: From Hypothesis Generation to Mechanisms of Replication and Pathogenesis. <i>Annual Review of Virology</i> , 2022, 9, .	3.0	5
541	Gibbin mesodermal regulation patterns epithelial development. <i>Nature</i> , 2022, 606, 188-196.	13.7	9
542	Protein interaction networks in neurodegenerative diseases: From physiological function to aggregation. <i>Journal of Biological Chemistry</i> , 2022, 298, 102062.	1.6	30
543	Complementary omics strategies to dissect p53 signaling networks under nutrient stress. <i>Cellular and Molecular Life Sciences</i> , 2022, 79, .	2.4	4
544	Hypomorphic GINS3 variants alter DNA replication and cause Meier-Gorlin syndrome. <i>JCI Insight</i> , 2022, 7, .	2.3	6
546	Developing antisense oligonucleotides for a TECPR2 mutation-induced, ultra-rare neurological disorder using patient-derived cellular models. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 29, 189-203.	2.3	4
547	DLX1 and the NuRD complex cooperate in enhancer decommissioning and transcriptional repression. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	6

#	ARTICLE	IF	CITATIONS
548	The metabolic enzyme hexokinase 2 localizes to the nucleus in AML and normal haematopoietic stem and progenitor cells to maintain stemness. <i>Nature Cell Biology</i> , 2022, 24, 872-884.	4.6	25
551	Mapping Protein-Protein Interactions Using Data-Dependent Acquisition without Dynamic Exclusion. <i>Analytical Chemistry</i> , 2022, 94, 10579-10583.	3.2	3
552	The amino acid sensor GCN2 suppresses terminal oligopyrimidine (TOP) mRNA translation via La-related protein 1 (LARP1). <i>Journal of Biological Chemistry</i> , 2022, 298, 102277.	1.6	5
553	Endosomal LC3C-pathway selectively targets plasma membrane cargo for autophagic degradation. <i>Nature Communications</i> , 2022, 13, .	5.8	12
554	Identification of Exported <i>Plasmodium falciparum</i> Proteins That Bind to the Erythrocyte Cytoskeleton. <i>Microorganisms</i> , 2022, 10, 1438.	1.6	1
555	Protocol for establishing a protein-protein interaction network using tandem affinity purification followed by mass spectrometry in mammalian cells. <i>STAR Protocols</i> , 2022, 3, 101569.	0.5	6
556	N/C Interactions Are Dispensable for Normal In Vivo Functioning of the Androgen Receptor in Male Mice. <i>Endocrinology</i> , 2022, 163, .	1.4	5
557	Design, synthesis and biological evaluation of quinoline-1,2,4-triazine hybrids as antimalarial agents. <i>Journal of Molecular Structure</i> , 2022, , 133982.	1.8	4
558	The centriolar satellite protein Cfap53 facilitates formation of the zygotic microtubule organizing center in the zebrafish embryo. <i>Development (Cambridge)</i> , 2022, 149, .	1.2	1
559	HTT-OMNI: A Web-based Platform for Huntingtin Interaction Exploration and Multi-omics Data Integration. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100275.	2.5	3
560	Proteomic characterization of the <i>Toxoplasma gondii</i> cytokinesis machinery portrays an expanded hierarchy of its assembly and function. <i>Nature Communications</i> , 2022, 13, .	5.8	17
561	Differential CFTR-Interactome Proximity Labeling Procedures Identify Enrichment in Multiple SLC Transporters. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8937.	1.8	6
562	Mitochondrially targeted proximity biotinylation and proteomic analysis in <i>Plasmodium falciparum</i> . <i>PLoS ONE</i> , 2022, 17, e0273357.	1.1	9
563	FASN inhibitor TVB-3166 prevents S-acylation of the spike protein of human coronaviruses. <i>Journal of Lipid Research</i> , 2022, 63, 100256.	2.0	5
565	MAB21L4 Deficiency Drives Squamous Cell Carcinoma via Activation of RET. <i>Cancer Research</i> , 2022, 82, 3143-3157.	0.4	3
566	Failure of human rhombic lip differentiation underlies medulloblastoma formation. <i>Nature</i> , 2022, 609, 1021-1028.	13.7	52
568	Newfound Coding Potential of Transcripts Unveils Missing Members of Human Protein Communities. <i>Genomics, Proteomics and Bioinformatics</i> , 2023, 21, 515-534.	3.0	2
569	Structure-function analysis of enterovirus protease 2A in complex with its essential host factor SETD3. <i>Nature Communications</i> , 2022, 13, .	5.8	2

#	ARTICLE	IF	CITATIONS
570	Novel biochemical, structural, and systems insights into inflammatory signaling revealed by contextual interaction proteomics. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
571	The inÂvivo Interaction Landscape of Histones H3.1 and H3.3. Molecular and Cellular Proteomics, 2022, 21, 100411.	2.5	6
572	Deciphering Spatial Proteinâ€Protein Interactions in Brain Using Proximity Labeling. Molecular and Cellular Proteomics, 2022, 21, 100422.	2.5	12
573	Synthesis, Characterization, Crystal Structure, and Antitumor Activity of 2-Phenylthiazoleâ€Coumarin Derivatives. Russian Journal of Organic Chemistry, 2022, 58, 1341-1347.	0.3	0
575	USP7 targets XIAP for cancer progression: Establishment of a p53-independent therapeutic avenue for glioma. Oncogene, 2022, 41, 5061-5075.	2.6	16
576	CDK12 is hyperactivated and a synthetic-lethal target in BRAF-mutated melanoma. Nature Communications, 2022, 13, .	5.8	9
577	Essential Functions of Calmodulin and Identification of Its Proximal Interacting Proteins in Tachyzoite-Stage Toxoplasma gondii via BioID Technology. Microbiology Spectrum, 2022, 10, .	1.2	2
578	The Autophagy Receptor <sc>TAX1BP1</sc> ( <sc>T6BP</sc> ) improves antigen presentation by <sc>MHCâ€I</sc> molecules. EMBO Reports, 2022, 23, .	2.0	4
580	RAD51AP1 regulates ALT-HDR through chromatin-directed homeostasis of TERRA. Molecular Cell, 2022, 82, 4001-4017.e7.	4.5	20
581	<sc>TMBIM5</sc> is the Ca <sup>2+</sup> /H <sup>+</sup> antiporter of mammalian mitochondria. EMBO Reports, 2022, 23, .	2.0	23
582	Histone chaperone ASF1 mediates H3.3-H4 deposition in Arabidopsis. Nature Communications, 2022, 13, .	5.8	8
583	Use of Affinity Purificationâ€Mass Spectrometry to Identify Phosphorylated Tau Interactors in Alzheimerâ€™s Disease. Methods in Molecular Biology, 2023, , 263-277.	0.4	5
584	In silico and in vitro approaches allow the identification of the Prosystemin molecular network. Computational and Structural Biotechnology Journal, 2023, 21, 212-223.	1.9	1
585	Proteomic analysis of antiviral innate immunity. Current Opinion in Virology, 2023, 58, 101291.	2.6	1
586	Evaluation of affinity-purification coupled to mass spectrometry approaches for capture of short linear motif-based interactions. Analytical Biochemistry, 2023, 663, 115017.	1.1	5
587	Proximity-dependent biotin labeling in testicular germ cells identified TESMIN-associated proteins. Scientific Reports, 2022, 12, .	1.6	2
588	Impaired OTUD7A-dependent Ankyrin regulation mediates neuronal dysfunction in mouse and human models of the 15q13.3 microdeletion syndrome. Molecular Psychiatry, 0, , .	4.1	3
589	Protein network analysis and functional enrichment via computational biotechnology unravel molecular and pathogenic mechanisms of kidney stone disease. Biomedical Journal, 2023, 46, 100577.	1.4	4

#	ARTICLE	IF	CITATIONS
590	Trans-Proteomic Pipeline: Robust Mass Spectrometry-Based Proteomics Data Analysis Suite. <i>Journal of Proteome Research</i> , 2023, 22, 615-624.	1.8	21
591	NDR kinase <i>tricorned</i> genetically interacts with <i>Ccm3</i> and metabolic enzymes in <i>Drosophila melanogaster</i> tracheal development. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	0
592	Analysis of affinity purification-related proteomic data for studying protein-protein interaction networks in cells. <i>Briefings in Bioinformatics</i> , 2023, 24, .	3.2	1
593	Hippo pathway and Bonus control developmental cell fate decisions in the <i>Drosophila</i> eye. <i>Developmental Cell</i> , 2023, 58, 416-434.e12.	3.1	5
594	Identification of Proximity Interactors of Mammalian Nucleoid Proteins by BioID. <i>Methods in Molecular Biology</i> , 2023, , 153-172.	0.4	0
595	Investigating the dynamics of protein-protein interactions in plants. <i>Plant Journal</i> , 0, , .	2.8	2
599	NUSAP1 Binds ILF2 to Modulate R-Loop Accumulation and DNA Damage in Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2023, 24, 6258.	1.8	5
600	Identification of an Essential Lold-Like Protein in <i>Helicobacter pylori</i> . <i>Journal of Bacteriology</i> , 0, , .	1.0	3
604	Comprehensive Interactome Mapping of the DNA Repair Scaffold SLX4 Using Proximity Labeling and Affinity Purification. <i>Journal of Proteome Research</i> , 2023, 22, 1660-1681.	1.8	1
610	Analyzing Protein Interactions by MAC-Tag Approaches. <i>Methods in Molecular Biology</i> , 2023, , 281-297.	0.4	1
611	Identification and Quantification of Affinity-Purified Proteins with MaxQuant, Followed by the Discrimination of Nonspecific Interactions with the CRAPome Interface. <i>Methods in Molecular Biology</i> , 2023, , 299-310.	0.4	1
621	Studying Cellular Dynamics Using Proximity-Dependent Biotinylation: Somatic Cell Reprogramming. <i>Methods in Molecular Biology</i> , 2023, , 23-52.	0.4	0
627	Proximity Mapping of Ciliary Proteins by BioID. <i>Methods in Molecular Biology</i> , 2024, , 181-198.	0.4	0