

# Anne-Claude Gingras

## List of Publications by Year in descending order

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307  
papers

44,501  
citations

2426

97  
h-index

2567

195  
g-index

359  
all docs

359  
docs citations

359  
times ranked

48993  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genetic Landscape of a Cell. <i>Science</i> , 2010, 327, 425-431.	6.0	1,937
2	eIF4 Initiation Factors: Effectors of mRNA Recruitment to Ribosomes and Regulators of Translation. <i>Annual Review of Biochemistry</i> , 1999, 68, 913-963.	5.0	1,934
3	Histone Recognition and Large-Scale Structural Analysis of the Human Bromodomain Family. <i>Cell</i> , 2012, 149, 214-231.	13.5	1,368
4	Regulation of translation initiation by FRAP/mTOR. <i>Genes and Development</i> , 2001, 15, 807-826.	2.7	1,363
5	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
6	Insulin-dependent stimulation of protein synthesis by phosphorylation of a regulator of 5'-cap function. <i>Nature</i> , 1994, 371, 762-767.	13.7	1,192
7	Regulation of 4E-BP1 phosphorylation: a novel two-step mechanism. <i>Genes and Development</i> , 1999, 13, 1422-1437.	2.7	1,104
8	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016, 353, .	6.0	979
9	4E-BP1, a repressor of mRNA translation, is phosphorylated and inactivated by the Akt(PKB) signaling pathway. <i>Genes and Development</i> , 1998, 12, 502-513.	2.7	771
10	Persistence of serum and saliva antibody responses to SARS-CoV-2 spike antigens in COVID-19 patients. <i>Science Immunology</i> , 2020, 5, .	5.6	714
11	Hierarchical phosphorylation of the translation inhibitor 4E-BP1. <i>Genes and Development</i> , 2001, 15, 2852-2864.	2.7	703
12	A rapamycin-sensitive signaling pathway contributes to long-term synaptic plasticity in the hippocampus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 467-472.	3.3	680
13	SAINT: probabilistic scoring of affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2011, 8, 70-73.	9.0	647
14	Cocrystal Structure of the Messenger RNA 5 <sup>â€²</sup> Cap-Binding Protein (eIF4E) Bound to 7-methyl-GDP. <i>Cell</i> , 1997, 89, 951-961.	13.5	635
15	Analysis of protein complexes using mass spectrometry. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 645-654.	16.1	634
16	A Global Protein Kinase and Phosphatase Interaction Network in Yeast. <i>Science</i> , 2010, 328, 1043-1046.	6.0	608
17	Human eukaryotic translation initiation factor 4G (eIF4G) recruits Mnk1 to phosphorylate eIF4E. <i>EMBO Journal</i> , 1999, 18, 270-279.	3.5	584
18	High-Density Proximity Mapping Reveals the Subcellular Organization of mRNA-Associated Granules and Bodies. <i>Molecular Cell</i> , 2018, 69, 517-532.e11.	4.5	583

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19	The mRNA 5' cap-binding protein eIF4E and control of cell growth. <i>Current Opinion in Cell Biology</i> , 1998, 10, 268-275.	2.6	568
20	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. <i>Nature Methods</i> , 2015, 12, 258-264.	9.0	561
21	The target of rapamycin (TOR) proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 7037-7044.	3.3	543
22	SAINTexpress: Improvements and additional features in Significance Analysis of INteractome software. <i>Journal of Proteomics</i> , 2014, 100, 37-43.	1.2	501
23	Cap-Dependent Translation Initiation in Eukaryotes Is Regulated by a Molecular Mimic of eIF4G. <i>Molecular Cell</i> , 1999, 3, 707-716.	4.5	457
24	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. <i>Cell</i> , 2015, 163, 1484-1499.	13.5	446
25	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121.	13.7	445
26	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	5.8	423
27	Protein Interaction Network of the Mammalian Hippo Pathway Reveals Mechanisms of Kinase-Phosphatase Interactions. <i>Science Signaling</i> , 2013, 6, rs15.	1.6	411
28	Phosphorylation of eucaryotic translation initiation factor 4B Ser422 is modulated by S6 kinases. <i>EMBO Journal</i> , 2004, 23, 1761-1769.	3.5	397
29	Wilms Tumor Suppressor WTX Negatively Regulates WNT/ $\beta$ -Catenin Signaling. <i>Science</i> , 2007, 316, 1043-1046.	6.0	379
30	Biophysical Studies of eIF4E Cap-binding Protein: Recognition of mRNA 5' Cap Structure and Synthetic Fragments of eIF4G and 4E-BP1 Proteins. <i>Journal of Molecular Biology</i> , 2002, 319, 615-635.	2.0	353
31	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. <i>Nature Biotechnology</i> , 2011, 29, 361-367.	9.4	352
32	Structure of translation factor eIF4E bound to m7GDP and interaction with 4E-binding protein. <i>Nature Structural Biology</i> , 1997, 4, 717-724.	9.7	347
33	Adipose tissue reduction in mice lacking the translational inhibitor 4E-BP1. <i>Nature Medicine</i> , 2001, 7, 1128-1132.	15.2	341
34	A Quantitative Chaperone Interaction Network Reveals the Architecture of Cellular Protein Homeostasis Pathways. <i>Cell</i> , 2014, 158, 434-448.	13.5	335
35	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. <i>Nature Methods</i> , 2010, 7, 1017-1024.	9.0	319
36	Non-canonical inhibition of DNA damage-dependent ubiquitination by OTUB1. <i>Nature</i> , 2010, 466, 941-946.	13.7	316

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37	A PP2A Phosphatase High Density Interaction Network Identifies a Novel Striatin-interacting Phosphatase and Kinase Complex Linked to the Cerebral Cavernous Malformation 3 (CCM3) Protein. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 157-171.	2.5	315
38	Affinityâ€purification coupled to mass spectrometry: Basic principles and strategies. <i>Proteomics</i> , 2012, 12, 1576-1590.	1.3	292
39	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. <i>Nature Methods</i> , 2013, 10, 1239-1245.	9.0	277
40	A proximity-dependent biotinylation map of a human cell. <i>Nature</i> , 2021, 595, 120-124.	13.7	263
41	4E-BP3, a New Member of the Eukaryotic Initiation Factor 4E-binding Protein Family. <i>Journal of Biological Chemistry</i> , 1998, 273, 14002-14007.	1.6	260
42	Properties of Stress Granule and P-Body Proteomes. <i>Molecular Cell</i> , 2019, 76, 286-294.	4.5	258
43	Temporal regulation of EGF signalling networks by the scaffold protein Shc1. <i>Nature</i> , 2013, 499, 166-171.	13.7	257
44	eIF4E activity is regulated at multiple levels. <i>International Journal of Biochemistry and Cell Biology</i> , 1999, 31, 43-57.	1.2	251
45	Activation of GCN2 in UV-Irradiated Cells Inhibits Translation. <i>Current Biology</i> , 2002, 12, 1279-1286.	1.8	245
46	4E-BP1 phosphorylation is mediated by the FRAP-p70s6k pathway and is independent of mitogen-activated protein kinase.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 4076-4080.	3.3	238
47	Serum-stimulated, rapamycin-sensitive phosphorylation sites in the eukaryotic translation initiation factor 4G1. <i>EMBO Journal</i> , 2000, 19, 434-444.	3.5	237
48	The linear ubiquitin-specific deubiquitinase gumby regulates angiogenesis. <i>Nature</i> , 2013, 498, 318-324.	13.7	234
49	Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes. <i>Journal of Proteomics</i> , 2015, 118, 81-94.	1.2	234
50	HAUS, the 8-Subunit Human Augmin Complex, Regulates Centrosome and Spindle Integrity. <i>Current Biology</i> , 2009, 19, 816-826.	1.8	231
51	The Insulin-Induced Signalling Pathway Leading to S6 and Initiation Factor 4E Binding Protein 1 Phosphorylation Bifurcates at a Rapamycin-Sensitive Point Immediately Upstream of p70<sup>s6k</sup>. <i>Molecular and Cellular Biology</i> , 1997, 17, 5426-5436.	1.1	224
52	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
53	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LCâ€MS/MS. <i>Nature Communications</i> , 2020, 11, 157.	5.8	218
54	Activation of the translational suppressor 4E-BP1 following infection with encephalomyocarditis virus and poliovirus.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1996, 93, 5578-5583.	3.3	215

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55	History of protein-protein interactions: From egg-white to complex networks. <i>Proteomics</i> , 2012, 12, 1478-1498.	1.3	214
56	ProHits: integrated software for mass spectrometry-based interaction proteomics. <i>Nature Biotechnology</i> , 2010, 28, 1015-1017.	9.4	202
57	The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. <i>Molecular Cell</i> , 2016, 62, 409-421.	4.5	198
58	A simple protein-based surrogate neutralization assay for SARS-CoV-2. <i>JCI Insight</i> , 2020, 5, .	2.3	193
59	Topoisomerase II beta interacts with cohesin and CTCF at topological domain borders. <i>Genome Biology</i> , 2016, 17, 182.	3.8	190
60	Rare driver mutations in head and neck squamous cell carcinomas converge on NOTCH signaling. <i>Science</i> , 2020, 367, 1264-1269.	6.0	190
61	Global Gene Deletion Analysis Exploring Yeast Filamentous Growth. <i>Science</i> , 2012, 337, 1353-1356.	6.0	186
62	The eIF4E-binding proteins 1 and 2 are negative regulators of cell growth. <i>Oncogene</i> , 1996, 13, 2415-20.	2.6	182
63	PP4 is a $\gamma$ -H2AX phosphatase required for recovery from the DNA damage checkpoint. <i>EMBO Reports</i> , 2008, 9, 1019-1026.	2.0	179
64	$\mu$ -Opioid Receptor Activates Signaling Pathways Implicated in Cell Survival and Translational Control. <i>Journal of Biological Chemistry</i> , 1998, 273, 23534-23541.	1.6	177
65	A Novel, Evolutionarily Conserved Protein Phosphatase Complex Involved in Cisplatin Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1725-1740.	2.5	173
66	Advances in protein complex analysis using mass spectrometry. <i>Journal of Physiology</i> , 2005, 563, 11-21.	1.3	164
67	A Novel 4EHP-GIGYF2 Translational Repressor Complex Is Essential for Mammalian Development. <i>Molecular and Cellular Biology</i> , 2012, 32, 3585-3593.	1.1	164
68	Regulation of CD133 by HDAC6 Promotes $\beta$ -Catenin Signaling to Suppress Cancer Cell Differentiation. <i>Cell Reports</i> , 2012, 2, 951-963.	2.9	161
69	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. <i>Nature Methods</i> , 2017, 14, 645-646.	9.0	160
70	Subcellular proteomics. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	159
71	Eukaryotic Translation Initiation Factor 4E Availability Controls the Switch between Cap-Dependent and Internal Ribosomal Entry Site-Mediated Translation. <i>Molecular and Cellular Biology</i> , 2005, 25, 10556-10565.	1.1	158
72	( <i>SMN2</i> )-PFI-2 is a potent and selective inhibitor of SETD7 methyltransferase activity in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 12853-12858.	3.3	158

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73	Exploring genetic suppression interactions on a global scale. <i>Science</i> , 2016, 354, .	6.0	157
74	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
75	Construction of human activity-based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	3.2	153
76	FRAP/mTOR is required for proliferation and patterning during embryonic development in the mouse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13796-13801.	3.3	152
77	Systemic and mucosal IgA responses are variably induced in response to SARS-CoV-2 mRNA vaccination and are associated with protection against subsequent infection. <i>Mucosal Immunology</i> , 2022, 15, 799-808.	2.7	152
78	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. <i>Journal of Proteomics</i> , 2015, 129, 108-120.	1.2	149
79	BioID-based Identification of Skp Cullin F-box (SCF) <sup>12</sup> -TrCP1/2 E3 Ligase Substrates*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1781-1795.	2.5	148
80	<i>SLC25A46</i> is required for mitochondrial lipid homeostasis and cristae maintenance and is responsible for Leigh syndrome. <i>EMBO Molecular Medicine</i> , 2016, 8, 1019-1038.	3.3	141
81	Structure-Function Analysis of Core STRIPAK Proteins. <i>Journal of Biological Chemistry</i> , 2011, 286, 25065-25075.	1.6	136
82	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. <i>Molecular Cell</i> , 2019, 73, 621-638.e17.	4.5	135
83	Proximity Dependent Biotinylation: Key Enzymes and Adaptation to Proteomics Approaches. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 757-773.	2.5	135
84	A Global Regulatory Mechanism for Activating an Exon Network Required for Neurogenesis. <i>Molecular Cell</i> , 2014, 56, 90-103.	4.5	131
85	Control of the Hippo Pathway by Set7-Dependent Methylation of Yap. <i>Developmental Cell</i> , 2013, 26, 188-194.	3.1	130
86	An alternative splicing event amplifies evolutionary differences between vertebrates. <i>Science</i> , 2015, 349, 868-873.	6.0	128
87	Phosphorylation of eIF4E attenuates its interaction with mRNA 5' cap analogs by electrostatic repulsion: Intein-mediated protein ligation strategy to obtain phosphorylated protein. <i>Rna</i> , 2003, 9, 52-61.	1.6	124
88	A High-Density Human Mitochondrial Proximity Interaction Network. <i>Cell Metabolism</i> , 2020, 32, 479-497.e9.	7.2	124
89	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. <i>Molecular Cell</i> , 2017, 65, 347-360.	4.5	123
90	Mapping the proximity interaction network of the Rho-family GTPases reveals signalling pathways and regulatory mechanisms. <i>Nature Cell Biology</i> , 2020, 22, 120-134.	4.6	123

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91	Cloning and Characterization of 4EHP, a Novel Mammalian eIF4E-related Cap-binding Protein. <i>Journal of Biological Chemistry</i> , 1998, 273, 13104-13109.	1.6	122
92	A pseudouridine synthase module is essential for mitochondrial protein synthesis and cell viability. <i>EMBO Reports</i> , 2017, 18, 28-38.	2.0	120
93	HELB Is a Feedback Inhibitor of DNA End Resection. <i>Molecular Cell</i> , 2016, 61, 405-418.	4.5	119
94	Regulatory Expansion in Mammals of Multivalent hnRNP Assemblies that Globally Control Alternative Splicing. <i>Cell</i> , 2017, 170, 324-339.e23.	13.5	119
95	4E Binding Proteins Inhibit the Translation Factor eIF4E without Folded Structure. <i>Biochemistry</i> , 1998, 37, 9-15.	1.2	116
96	Plk4 Promotes Cancer Invasion and Metastasis through Arp2/3 Complex Regulation of the Actin Cytoskeleton. <i>Cancer Research</i> , 2017, 77, 434-447.	0.4	116
97	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
98	MSPLIT-DIA: sensitive peptide identification for data-independent acquisition. <i>Nature Methods</i> , 2015, 12, 1106-1108.	9.0	113
99	Global Interactomics Uncovers Extensive Organellar Targeting by Zika Virus. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2242-2255.	2.5	112
100	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
101	The MMS22L-TONSL Complex Mediates Recovery from Replication Stress and Homologous Recombination. <i>Molecular Cell</i> , 2010, 40, 619-631.	4.5	106
102	Control of eIF4E cellular localization by eIF4E-binding proteins, 4E-BPs. <i>Rna</i> , 2008, 14, 1318-1327.	1.6	104
103	Two phosphatidylinositol 4-kinases control lysosomal delivery of the Gaucher disease enzyme, $\beta$ -glucocerebrosidase. <i>Molecular Biology of the Cell</i> , 2012, 23, 1533-1545.	0.9	103
104	Protein analysis by mass spectrometry and sequence database searching: Tools for cancer research in the post-genomic era. <i>Electrophoresis</i> , 1999, 20, 310-319.	1.3	100
105	Affinity-purification mass spectrometry (AP-MS) of serine/threonine phosphatases. <i>Methods</i> , 2007, 42, 298-305.	1.9	100
106	Translational Homeostasis: Eukaryotic Translation Initiation Factor 4E Control of 4E-Binding Protein 1 and p70 S6 Kinase Activities. <i>Molecular and Cellular Biology</i> , 1999, 19, 4302-4310.	1.1	99
107	<sc>BRPF</sc> 3<sc>HBO</sc> 1 regulates replication origin activation and histone H3K14 acetylation. <i>EMBO Journal</i> , 2016, 35, 176-192.	3.5	97
108	Translational Control of Cell Fate: Availability of Phosphorylation Sites on Translational Repressor 4E-BP1 Governs Its Proapoptotic Potency. <i>Molecular and Cellular Biology</i> , 2002, 22, 2853-2861.	1.1	96

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109	Postnatal Deamidation of 4E-BP2 in Brain Enhances Its Association with Raptor and Alters Kinetics of Excitatory Synaptic Transmission. <i>Molecular Cell</i> , 2010, 37, 797-808.	4.5	96
110	Translational Control of the Antiapoptotic Function of Ras. <i>Journal of Biological Chemistry</i> , 2000, 275, 24776-24780.	1.6	95
111	Expression of a translationally regulated, dominant-negative CCAAT/enhancer-binding protein beta isoform and up-regulation of the eukaryotic translation initiation factor 2alpha are correlated with neoplastic transformation of mammary epithelial cells. <i>Cancer Research</i> , 1996, 56, 4382-6.	0.4	94
112	Cap-binding protein 4EHP effects translation silencing by microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5425-5430.	3.3	93
113	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. <i>Science Advances</i> , 2016, 2, e1600760.	4.7	90
114	Phosphorylation of eIF-4E on Serine 209 by Protein Kinase C Is Inhibited by the Translational Repressors, 4E-binding Proteins. <i>Journal of Biological Chemistry</i> , 1996, 271, 11831-11837.	1.6	88
115	Requirement for Akt (Protein Kinase B) in Insulin-induced Activation of Glycogen Synthase and Phosphorylation of 4E-BP1 (PHAS-1). <i>Journal of Biological Chemistry</i> , 1999, 274, 20611-20618.	1.6	86
116	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. <i>Cell Reports</i> , 2016, 17, 2724-2737.	2.9	86
117	Genome-wide CRISPR-Cas9 Interrogation of Splicing Networks Reveals a Mechanism for Recognition of Autism-Misregulated Neuronal Microexons. <i>Molecular Cell</i> , 2018, 72, 510-524.e12.	4.5	86
118	CCM-3/STRIPAK promotes seamless tube extension through endocytic recycling. <i>Nature Communications</i> , 2015, 6, 6449.	5.8	85
119	Control of Translation by the Target of Rapamycin Proteins. <i>Progress in Molecular and Subcellular Biology</i> , 2001, 27, 143-174.	0.9	85
120	A Lentiviral Functional Proteomics Approach Identifies Chromatin Remodeling Complexes Important for the Induction of Pluripotency. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 811-823.	2.5	83
121	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
122	Phenotypic and Interaction Profiling of the Human Phosphatases Identifies Diverse Mitotic Regulators. <i>Cell Reports</i> , 2016, 17, 2488-2501.	2.9	81
123	PP4R4/KIAA1622 Forms a Novel Stable Cytosolic Complex with Phosphoprotein Phosphatase 4. <i>Journal of Biological Chemistry</i> , 2008, 283, 29273-29284.	1.6	80
124	Functional characterization of a PROTAC directed against BRAF mutant V600E. <i>Nature Chemical Biology</i> , 2020, 16, 1170-1178.	3.9	80
125	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. <i>Nature Chemical Biology</i> , 2016, 12, 867-875.	3.9	79
126	The RhoGEF GEF-H1 Is Required for Oncogenic RAS Signaling via KSR-1. <i>Cancer Cell</i> , 2014, 25, 181-195.	7.7	76



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127	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. <i>Nature Communications</i> , 2018, 9, 3510.	5.8	75
128	Insulin regulation of protein translation repressor 4E-BP1, an eIF4E-binding protein, in renal epithelial cells. <i>Kidney International</i> , 2001, 59, 866-875.	2.6	73
129	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. <i>Nature Metabolism</i> , 2020, 2, 499-513.	5.1	72
130	The cargo receptor SURF4 promotes the efficient cellular secretion of PCSK9. <i>ELife</i> , 2018, 7, .	2.8	72
131	Role of the SIK2-p35-PJA2 complex in pancreatic $\beta$ -cell functional compensation. <i>Nature Cell Biology</i> , 2014, 16, 234-244.	4.6	71
132	The eIF4E-Binding Protein 4E-T Is a Component of the mRNA Decay Machinery that Bridges the 5' and 3' Termini of Target mRNAs. <i>Cell Reports</i> , 2015, 11, 1425-1436.	2.9	70
133	In planta proximity dependent biotin identification (BioID). <i>Scientific Reports</i> , 2018, 8, 9212.	1.6	70
134	LuciPHOR: Algorithm for Phosphorylation Site Localization with False Localization Rate Estimation Using Modified Target-Decoy Approach. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3409-3419.	2.5	69
135	Assessing cellular efficacy of bromodomain inhibitors using fluorescence recovery after photobleaching. <i>Epigenetics and Chromatin</i> , 2014, 7, 14.	1.8	69
136	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. <i>Molecular Cell</i> , 2020, 77, 1176-1192.e16.	4.5	69
137	CCM3/PDCD10 Heterodimerizes with Germinal Center Kinase III (GCKIII) Proteins Using a Mechanism Analogous to CCM3 Homodimerization. <i>Journal of Biological Chemistry</i> , 2011, 286, 25056-25064.	1.6	67
138	Mass spectrometry approaches to study mammalian kinase and phosphatase associated proteins. <i>Methods</i> , 2012, 57, 400-408.	1.9	66
139	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	1.2	66
140	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
141	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1594-603.	3.3	65
142	A scalable serology solution for profiling humoral immune responses to SARS-CoV-2 infection and vaccination. <i>Clinical and Translational Immunology</i> , 2022, 11, e1380.	1.7	65
143	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. <i>Journal of Proteomics</i> , 2015, 118, 49-62.	1.2	64
144	Identification and functional characterization of transcriptional activators in human cells. <i>Molecular Cell</i> , 2022, 82, 677-695.e7.	4.5	64

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145	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
146	A novel protein domain in an ancestral splicing factor drove the evolution of neural microexons. <i>Nature Ecology and Evolution</i> , 2019, 3, 691-701.	3.4	63
147	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
148	Neutralization against Omicron variant in transplant recipients after three doses of mRNA vaccine. <i>American Journal of Transplantation</i> , 2022, 22, 2089-2093.	2.6	61
149	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. <i>Nature Communications</i> , 2020, 11, 2396.	5.8	59
150	Functions of the COPII gene paralogs SEC23A and SEC23B are interchangeable in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7748-E7757.	3.3	58
151	Interaction Proteomics Identify NEURL4 and the HECT E3 Ligase HERC2 as Novel Modulators of Centrosome Architecture. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014233.	2.5	57
152	Regulation of the Rapamycin and FKBP-Target 1/Mammalian Target of Rapamycin and Cap-dependent Initiation of Translation by the c-Abl Protein-tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 2000, 275, 10779-10787.	1.6	55
153	Label-free quantitative proteomics trends for protein-protein interactions. <i>Journal of Proteomics</i> , 2013, 81, 91-101.	1.2	55
154	Tissue Distribution, Genomic Structure, and Chromosome Mapping of Mouse and Human Eukaryotic Initiation Factor 4E-Binding Proteins 1 and 2. <i>Genomics</i> , 1996, 38, 353-363.	1.3	54
155	The GATOR-Rag GTPase pathway inhibits mTORC1 activation by lysosome-derived amino acids. <i>Science</i> , 2020, 370, 351-356.	6.0	53
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