

Brian Raught

List of Publications by Year in descending order

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Version: 2024-02-01

140
papers

19,557
citations

26567

56
h-index

12233

133
g-index

147
all docs

147
docs citations

147
times ranked

26599
citing authors

#	ARTICLE	IF	CITATIONS
1	eIF4 Initiation Factors: Effectors of mRNA Recruitment to Ribosomes and Regulators of Translation. Annual Review of Biochemistry, 1999, 68, 913-963.	5.0	1,934
2	Regulation of translation initiation by FRAP/mTOR. Genes and Development, 2001, 15, 807-826.	2.7	1,363
3	The CRAPome: a contaminant repository for affinity purificationâ€“mass spectrometry data. Nature Methods, 2013, 10, 730-736.	9.0	1,353
4	A global genetic interaction network maps a wiring diagram of cellular function. Science, 2016, 353, .	6.0	979
5	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
6	Hierarchical phosphorylation of the translation inhibitor 4E-BP1. Genes and Development, 2001, 15, 2852-2864.	2.7	703
7	Computational prediction of proteotypic peptides for quantitative proteomics. Nature Biotechnology, 2007, 25, 125-131.	9.4	653
8	Arsenic degrades PML or PMLâ€“RARÎ± through a SUMO-triggered RNF4/ubiquitin-mediated pathway. Nature Cell Biology, 2008, 10, 547-555.	4.6	637
9	Analysis of protein complexes using mass spectrometry. Nature Reviews Molecular Cell Biology, 2007, 8, 645-654.	16.1	634
10	The mTOR/PI3K and MAPK pathways converge on eIF4B to control its phosphorylation and activity. EMBO Journal, 2006, 25, 2781-2791.	3.5	459
11	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. Cell, 2015, 163, 1484-1499.	13.5	446
12	Phosphorylation of eucaryotic translation initiation factor 4B Ser422 is modulated by S6 kinases. EMBO Journal, 2004, 23, 1761-1769.	3.5	397
13	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. Molecular and Cellular Proteomics, 2009, 8, 157-171.	2.5	315
14	PML/RARA Oxidation and Arsenic Binding Initiate the Antileukemia Response of As2O3. Cancer Cell, 2010, 18, 88-98.	7.7	301
15	miRNA-mediated deadenylation is orchestrated by GW182 through two conserved motifs that interact with CCR4â€“NOT. Nature Structural and Molecular Biology, 2011, 18, 1211-1217.	3.6	286
16	A Novel Functional Human Eukaryotic Translation Initiation Factor 4G. Molecular and Cellular Biology, 1998, 18, 334-342.	1.1	281
17	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. Cancer Cell, 2015, 27, 864-876.	7.7	265
18	A proximity-dependent biotinylation map of a human cell. Nature, 2021, 595, 120-124.	13.7	263

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19	A Strategy for Modulation of Enzymes in the Ubiquitin System. <i>Science</i> , 2013, 339, 590-595.	6.0	257
20	eIF4E activity is regulated at multiple levels. <i>International Journal of Biochemistry and Cell Biology</i> , 1999, 31, 43-57.	1.2	251
21	Activation of GCN2 in UV-Irradiated Cells Inhibits Translation. <i>Current Biology</i> , 2002, 12, 1279-1286.	1.8	245
22	The linear ubiquitin-specific deubiquitinase gumbly regulates angiogenesis. <i>Nature</i> , 2013, 498, 318-324.	13.7	234
23	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
24	VAPs and ACBD5 tether peroxisomes to the ER for peroxisome maintenance and lipid homeostasis. <i>Journal of Cell Biology</i> , 2017, 216, 367-377.	2.3	214
25	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019, 35, 721-737.e9.	7.7	206
26	ProHits: integrated software for mass spectrometry-based interaction proteomics. <i>Nature Biotechnology</i> , 2010, 28, 1015-1017.	9.4	202
27	Phosphorylation of Eukaryotic Translation Initiation Factor 4E Is Critical for Growth. <i>Molecular and Cellular Biology</i> , 2002, 22, 1656-1663.	1.1	175
28	A Novel, Evolutionarily Conserved Protein Phosphatase Complex Involved in Cisplatin Sensitivity. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1725-1740.	2.5	173
29	Inhibition of SHP2-mediated dephosphorylation of Ras suppresses oncogenesis. <i>Nature Communications</i> , 2015, 6, 8859.	5.8	173
30	Advances in protein complex analysis using mass spectrometry. <i>Journal of Physiology</i> , 2005, 563, 11-21.	1.3	164
31	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. <i>Nature Methods</i> , 2017, 14, 645-646.	9.0	160
32	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
33	CEP120 and SPICE1 Cooperate with CPAP in Centriole Elongation. <i>Current Biology</i> , 2013, 23, 1360-1366.	1.8	153
34	BioID-based Identification of Skp Cullin F-box (SCF) ¹² -TrCP1/2 E3 Ligase Substrates*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1781-1795.	2.5	148
35	MYC protein interactors in gene transcription and cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 579-591.	12.8	136
36	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

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37	Increased quantitative proteome coverage with ¹³ C/ ¹² C-based, acid-cleavable isotope-coded affinity tag reagent and modified data acquisition scheme. <i>Proteomics</i> , 2005, 5, 380-387.	1.3	118
38	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
39	Global Interactomics Uncovers Extensive Organellar Targeting by Zika Virus. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2242-2255.	2.5	112
40	Automated identification of SUMOylation sites using mass spectrometry and SUMmOn pattern recognition software. <i>Nature Methods</i> , 2006, 3, 533-539.	9.0	111
41	Global Map of SUMO Function Revealed by Protein-Protein Interaction and Genetic Networks. <i>Molecular Cell</i> , 2009, 33, 124-135.	4.5	109
42	Palmitoylation of NOD1 and NOD2 is required for bacterial sensing. <i>Science</i> , 2019, 366, 460-467.	6.0	109
43	Myc and its interactors take shape. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015, 1849, 469-483.	0.9	102
44	Integrating high-throughput genetic interaction mapping and high-content screening to explore yeast spindle morphogenesis. <i>Journal of Cell Biology</i> , 2010, 188, 69-81.	2.3	100
45	LLGL2 rescues nutrient stress by promoting leucine uptake in ER+ breast cancer. <i>Nature</i> , 2019, 569, 275-279.	13.7	99
46	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
47	A Human Ubiquitin Conjugating Enzyme (E2)-HECT E3 Ligase Structure-function Screen. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 329-341.	2.5	95
48	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , 2018, 34, 579-595.e8.	7.7	94
49	A Pathogen Type III Effector with a Novel E3 Ubiquitin Ligase Architecture. <i>PLoS Pathogens</i> , 2013, 9, e1003121.	2.1	82
50	Src promotes GTPase activity of Ras via tyrosine 32 phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3785-94.	3.3	81
51	RNF168 ubiquitylates 53BP1 and controls its response to DNA double-strand breaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20982-20987.	3.3	73
52	Spatial and proteomic profiling reveals centrosome-independent features of centriolar satellites. <i>EMBO Journal</i> , 2019, 38, e101109.	3.5	73
53	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
54	The Dynamics and Mechanism of SUMO Chain Deconjugation by SUMO-specific Proteases. <i>Journal of Biological Chemistry</i> , 2011, 286, 10238-10247.	1.6	71

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55	The Catalytic Subunit of Shiga-like Toxin 1 Interacts with Ribosomal Stalk Proteins and is Inhibited by Their Conserved C-Terminal Domain. <i>Journal of Molecular Biology</i> , 2008, 378, 375-386.	2.0	69
56	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	1.2	66
57	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
58	Tyrosyl phosphorylation of KRAS stalls GTPase cycle via alteration of switch I and II conformation. <i>Nature Communications</i> , 2019, 10, 224.	5.8	66
59	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
60	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006, 7, R106.	13.9	60
61	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. <i>Journal of Cell Biology</i> , 2013, 201, 145-163.	2.3	58
62	An ATG16L1-dependent pathway promotes plasma membrane repair and limits <i>Listeria monocytogenes</i> cell-to-cell spread. <i>Nature Microbiology</i> , 2018, 3, 1472-1485.	5.9	57
63	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. <i>Science Signaling</i> , 2017, 10, .	1.6	52
64	A Comprehensive, Flexible Collection of SARS-CoV-2 Coding Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 3399-3402.	0.8	48
65	Using mass spectrometry to identify ubiquitin and ubiquitin-like protein conjugation sites. <i>Proteomics</i> , 2009, 9, 922-934.	1.3	47
66	Multiple direct interactions of TBP with the MYC oncoprotein. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1035-1043.	3.6	47
67	A global <i>S. cerevisiae</i> small ubiquitin-related modifier (SUMO) system interactome. <i>Molecular Systems Biology</i> , 2013, 9, 668.	3.2	46
68	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
69	MYC dephosphorylation by the PP1/PNUTS phosphatase complex regulates chromatin binding and protein stability. <i>Nature Communications</i> , 2018, 9, 3502.	5.8	43
70	FKBP4 connects mTORC2 and PI3K to activate the PDK1/Akt-dependent cell proliferation signaling in breast cancer. <i>Theranostics</i> , 2019, 9, 7003-7015.	4.6	43
71	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
72	BioID screen of <i>Salmonella</i> type 3 secreted effectors reveals host factors involved in vacuole positioning and stability during infection. <i>Nature Microbiology</i> , 2019, 4, 2511-2522.	5.9	39

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73	The Ion Transporter NKCC1 Links Cell Volume to Cell Mass Regulation by Suppressing mTORC1. <i>Cell Reports</i> , 2019, 27, 1886-1896.e6.	2.9	39
74	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	38
75	A Novel Mechanism for SUMO System Control: Regulated Ulp1 Nucleolar Sequestration. <i>Molecular and Cellular Biology</i> , 2010, 30, 4452-4462.	1.1	37
76	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. <i>Cell Cycle</i> , 2016, 15, 1693-1705.	1.3	37
77	RNF168 and USP10 regulate topoisomerase II \pm function via opposing effects on its ubiquitylation. <i>Nature Communications</i> , 2016, 7, 12638.	5.8	35
78	Proteomic analyses of CSF aimed at biomarker development for pediatric brain tumors. <i>Journal of Neuro-Oncology</i> , 2014, 118, 225-238.	1.4	34
79	The Deubiquitinase USP37 Regulates Chromosome Cohesion and Mitotic Progression. <i>Current Biology</i> , 2015, 25, 2290-2299.	1.8	34
80	MYC Phosphorylation at Novel Regulatory Regions Suppresses Transforming Activity. <i>Cancer Research</i> , 2013, 73, 6504-6515.	0.4	33
81	Oxygen-dependent Regulation of Erythropoietin Receptor Turnover and Signaling. <i>Journal of Biological Chemistry</i> , 2016, 291, 7357-7372.	1.6	33
82	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
83	Structural and Functional Comparison of the RING Domains of Two p53 E3 Ligases, Mdm2 and Pirh2. <i>Journal of Biological Chemistry</i> , 2011, 286, 4796-4808.	1.6	32
84	Identification of SUMO-2/3-modified proteins associated with mitotic chromosomes. <i>Proteomics</i> , 2015, 15, 763-772.	1.3	32
85	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
86	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018, 9, 1731.	5.8	32
87	Beyond hairballs: The use of quantitative mass spectrometry data to understand proteinâ€“protein interactions. <i>FEBS Letters</i> , 2012, 586, 2723-2731.	1.3	31
88	KCMF1 (potassium channel modulatory factor 1) Links RAD6 to UBR4 (ubiquitin N-recognin) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 T <i>Proteomics</i> , 2015, 14, 674-685.	2.5	31
89	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. <i>Genome Biology</i> , 2016, 17, 82.	3.8	31
90	EXD2 governs germ stem cell homeostasis and lifespan by promoting mitoribosome integrity and translation. <i>Nature Cell Biology</i> , 2018, 20, 162-174.	4.6	31

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91	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. <i>Journal of Clinical Investigation</i> , 2018, 128, 4525-4542.	3.9	31
92	PPP1R35 is a novel centrosomal protein that regulates centriole length in concert with the microcephaly protein RTTN. <i>ELife</i> , 2018, 7, .	2.8	30
93	An improved SUMmOn-based methodology for the identification of ubiquitin and ubiquitin-like protein conjugation sites identifies novel ubiquitin-like protein chain linkages. <i>Proteomics</i> , 2010, 10, 254-265.	1.3	27
94	Phosphorylation Screening Identifies Translational Initiation Factor 4GII as an Intracellular Target of Ca ²⁺ /Calmodulin-dependent Protein Kinase I. <i>Journal of Biological Chemistry</i> , 2003, 278, 48570-48579.	1.6	26
95	A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness. <i>Nature Immunology</i> , 2021, 22, 723-734.	7.0	26
96	USP7 Regulates Cytokinesis through FBXO38 and KIF20B. <i>Scientific Reports</i> , 2019, 9, 2724.	1.6	25
97	Mutations of the Transcriptional Corepressor ZMYM2 Cause Syndromic Urinary Tract Malformations. <i>American Journal of Human Genetics</i> , 2020, 107, 727-742.	2.6	25
98	LUZP1 and the tumor suppressor EPLIN modulate actin stability to restrict primary cilia formation. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	25
99	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
100	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
101	The dynamic interacting landscape of MAPL reveals essential functions for SUMOylation in innate immunity. <i>Scientific Reports</i> , 2017, 7, 107.	1.6	22
102	Spatiotemporal distribution of small ubiquitin-like modifiers during human placental development and in response to oxidative and inflammatory stress. <i>Journal of Physiology</i> , 2018, 596, 1587-1600.	1.3	22
103	<i>Salmonella</i> exploits host Rho GTPase signalling pathways through the phosphatase activity of SopB. <i>Cellular Microbiology</i> , 2018, 20, e12938.	1.1	22
104	Global Interactome Mapping of Mitochondrial Intermembrane Space Proteases Identifies a Novel Function for HTRA2. <i>Proteomics</i> , 2019, 19, e1900139.	1.3	22
105	Deficiency of the autophagy gene ATG16L1 induces insulin resistance through KLHL9/KLHL13/CUL3-mediated IRS1 degradation. <i>Journal of Biological Chemistry</i> , 2019, 294, 16172-16185.	1.6	22
106	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
107	Comparative Super-Resolution Mapping of Basal Feet Reveals a Modular but Distinct Architecture in Primary and Motile Cilia. <i>Developmental Cell</i> , 2020, 55, 209-223.e7.	3.1	21
108	C5orf51 is a component of the MON1-CCZ1 complex and controls RAB7A localization and stability during mitophagy. <i>Autophagy</i> , 2022, 18, 829-840.	4.3	21

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109	Differential requirements for Torsled-like kinases 1 and 2 in mammalian development. <i>Cell Death and Differentiation</i> , 2017, 24, 1872-1885.	5.0	20
110	Proximity interactions of the ubiquitin ligase Mind bomb 1 reveal a role in regulation of epithelial polarity complex proteins. <i>Scientific Reports</i> , 2019, 9, 12471.	1.6	20
111	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
112	Using ProHits to Store, Annotate, and Analyze Affinity Purificationâ€“Mass Spectrometry (APâ€“MS) Data. <i>Current Protocols in Bioinformatics</i> , 2012, 39, Unit8.16.	25.8	19
113	Haploinsufficiency of RREB1 causes a Noonan-like RASopathy via epigenetic reprogramming of RAS-MAPK pathway genes. <i>Nature Communications</i> , 2020, 11, 4673.	5.8	19
114	Cancer proteome and metabolite changes linked to SHMT2. <i>PLoS ONE</i> , 2020, 15, e0237981.	1.1	18
115	Identification of c-MYC SUMOylation by Mass Spectrometry. <i>PLoS ONE</i> , 2014, 9, e115337.	1.1	18
116	Aggresome assembly at the centrosome is driven by CP110â€“CEP97â€“CEP290 and centriolar satellites. <i>Nature Cell Biology</i> , 2022, 24, 483-496.	4.6	18
117	A ubiquitin and ubiquitin-like protein spectral library. <i>Proteomics</i> , 2010, 10, 337-342.	1.3	17
118	Atypical Cadherin Dachous1b Interacts with Ttc28 and Aurora B to Control Microtubule Dynamics in Embryonic Cleavages. <i>Developmental Cell</i> , 2018, 45, 376-391.e5.	3.1	15
119	ARID1a Associates with Lymphoid-Restricted Transcription Factors and Has an Essential Role in T Cell Development. <i>Journal of Immunology</i> , 2020, 205, 1419-1432.	0.4	15
120	Characterizing the mitochondrial DNA polymerase gamma interactome by BioID identifies Ruvbl2 localizes to the mitochondria. <i>Mitochondrion</i> , 2017, 32, 31-35.	1.6	13
121	The use of ubiquitin lysine mutants to characterize E2-E3 linkage specificity: Mass spectrometry offers a cautionary â€œtailâ€“. <i>Proteomics</i> , 2015, 15, 2910-2915.	1.3	11
122	The SUMO-specific isopeptidase SENP2 is targeted to intracellular membranes via a predicted N-terminal amphipathic Î±-helix. <i>Molecular Biology of the Cell</i> , 2018, 29, 1878-1890.	0.9	11
123	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
124	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. <i>Structure</i> , 2019, 27, 1000-1012.e6.	1.6	10
125	Global Proximity Interactome of the Human Macroautophagy Pathway. <i>Autophagy</i> , 2022, 18, 1174-1186.	4.3	9
126	BioID 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

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127	Salmonella effector SopD promotes plasma membrane scission by inhibiting Rab10. <i>Nature Communications</i> , 2021, 12, 4707.	5.8	8
128	Proximal Protein Interaction Landscape of RAS Paralogs. <i>Cancers</i> , 2020, 12, 3326.	1.7	6
129	Tankyrase regulates epithelial lumen formation via suppression of Rab11 GEFs. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	6
130	Loss of Acot12 contributes to NAFLD independent of lipolysis of adipose tissue. <i>Experimental and Molecular Medicine</i> , 2021, 53, 1159-1169.	3.2	6
131	A SARS-CoV-2 Peptide Spectral Library Enables Rapid, Sensitive Identification of Virus Peptides in Complex Biological Samples. <i>Journal of Proteome Research</i> , 2021, 20, 2187-2194.	1.8	5
132	Proximity Profiling of the CFTR Interaction Landscape in Response to Orkambi. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2442.	1.8	4
133	The long form of pVHL is artifactually modified by serine protease inhibitor AEBSF. <i>Protein Science</i> , 2020, 29, 1843-1850.	3.1	1
134	The Mitochondrial Protease, Neurolysin (NLN), Regulates Respiratory Chain Complex and Supercomplex Formation and Is Necessary for AML Viability. <i>Blood</i> , 2019, 134, 729-729.	0.6	1
135	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
136	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
137	SLAP2 Adaptor Binding Disrupts c-CBL Autoinhibition to Activate Ubiquitin Ligase Function. <i>Journal of Molecular Biology</i> , 2021, 433, 166880.	2.0	0
138	Targeting The Mitochondrial ClpP As a Novel Therapeutic Strategy For Acute Myeloid Leukemia. <i>Blood</i> , 2013, 122, 3937-3937.	0.6	0
139	2017 "A DISTINCT SUBSET OF LATENT LONG-TERM HUMAN HEMATOPOIETIC STEM CELLS RESISTS REGENERATIVE STRESS TO PRESERVES STEMNESS. <i>Experimental Hematology</i> , 2020, 88, S43.	0.2	0
140	IPO11 Regulates the Nuclear Import of BZW1/2 and Is Necessary for AML Cells and Stem Cells. <i>Blood</i> , 2020, 136, 22-23.	0.6	0