

Brian Raught

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

140
papers

14,902
citations

52
h-index

121
g-index

147
ext. papers

17,641
ext. citations

12.6
avg. IF

6.14
L-index

#	Paper	IF	Citations
140	SLAP2 Adaptor Binding Disrupts c-CBL Autoinhibition to Activate Ubiquitin Ligase Function. <i>Journal of Molecular Biology</i> , 2021 , 433, 166880	6.5	
139	A latent subset of human hematopoietic stem cells resists regenerative stress to preserve stemness. <i>Nature Immunology</i> , 2021 , 22, 723-734	19.1	1
138	MYC protein interactors in gene transcription and cancer. <i>Nature Reviews Cancer</i> , 2021 , 21, 579-591	31.3	17
137	A proximity-dependent biotinylation map of a human cell. <i>Nature</i> , 2021 , 595, 120-124	50.4	60
136	Identifying and Validating MYC:Protein Interactors in Pursuit of Novel Anti-MYC Therapies. <i>Methods in Molecular Biology</i> , 2021 , 2318, 45-67	1.4	
135	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	11
134	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	5.6	2
133	Loss of Acot12 contributes to NAFLD independent of lipolysis of adipose tissue. <i>Experimental and Molecular Medicine</i> , 2021 , 53, 1159-1169	12.8	0
132	Salmonella effector SopD promotes plasma membrane scission by inhibiting Rab10. <i>Nature Communications</i> , 2021 , 12, 4707	17.4	1
131	C5orf51 is a component of the MON1-CCZ1 complex and controls RAB7A localization and stability during mitophagy. <i>Autophagy</i> , 2021 , 1-12	10.2	3
130	Global Proximity Interactome of the Human Macroautophagy Pathway. <i>Autophagy</i> , 2021 , 1-13	10.2	4
129	Mutations of the Transcriptional Corepressor ZMYM2 Cause Syndromic Urinary Tract Malformations. <i>American Journal of Human Genetics</i> , 2020 , 107, 727-742	11	2
128	The long form of pVHL is artifactually modified by serine protease inhibitor AEBSF. <i>Protein Science</i> , 2020 , 29, 1843-1850	6.3	1
127	The mitochondrial peptidase, neurolysin, regulates respiratory chain supercomplex formation and is necessary for AML viability. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	22
126	Variability in Streptavidin-Sepharose Matrix Quality Can Significantly Affect Proximity-Dependent Biotinylation (BioID) Data. <i>Journal of Proteome Research</i> , 2020 , 19, 3554-3561	5.6	3
125	IPO11 Regulates the Nuclear Import of BZW1/2 and Is Necessary for AML Cells and Stem Cells. <i>Blood</i> , 2020 , 136, 22-23	2.2	
124	LUZP1 and the tumor suppressor EPLIN modulate actin stability to restrict primary cilia formation. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	10

123	Nucleotide Binding, Evolutionary Insights, and Interaction Partners of the Pseudokinase Unc-51-like Kinase 4. <i>Structure</i> , 2020 , 28, 1184-1196.e6	5.2	9
122	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	10.2	9
121	Proximal Protein Interaction Landscape of RAS Paralogs. <i>Cancers</i> , 2020 , 12,	6.6	5
120	A Comprehensive, Flexible Collection of SARS-CoV-2 Coding Regions. <i>G3: Genes, Genomes, Genetics</i> , 2020 , 10, 3399-3402	3.2	22
119	Haploinsufficiency of RREB1 causes a Noonan-like RASopathy via epigenetic reprogramming of RAS-MAPK pathway genes. <i>Nature Communications</i> , 2020 , 11, 4673	17.4	8
118	Cancer proteome and metabolite changes linked to SHMT2. <i>PLoS ONE</i> , 2020 , 15, e0237981	3.7	7
117	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	5.3	2
116	Palmitoylation of NOD1 and NOD2 is required for bacterial sensing. <i>Science</i> , 2019 , 366, 460-467	33.3	45
115	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	4.9	8
114	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 ^{5.4}	5.4	12
113	Spatial and proteomic profiling reveals centrosome-independent features of centriolar satellites. <i>EMBO Journal</i> , 2019 , 38, e101109	13	33
112	The Ion Transporter NKCC1 Links Cell Volume to Cell Mass Regulation by Suppressing mTORC1. <i>Cell Reports</i> , 2019 , 27, 1886-1896.e6	10.6	15
111	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. <i>Structure</i> , 2019 , 27, 1000-1012.e6	5.2	5
110	Mitochondrial ClpP-Mediated Proteolysis Induces Selective Cancer Cell Lethality. <i>Cancer Cell</i> , 2019 , 35, 721-737.e9	24.3	108
109	LLGL2 rescues nutrient stress by promoting leucine uptake in ER breast cancer. <i>Nature</i> , 2019 , 569, 275-279.4	30.4	58
108	USP7 Regulates Cytokinesis through FBXO38 and KIF20B. <i>Scientific Reports</i> , 2019 , 9, 2724	4.9	10
107	BioID screen of Salmonella type 3 secreted effectors reveals host factors involved in vacuole positioning and stability during infection. <i>Nature Microbiology</i> , 2019 , 4, 2511-2522	26.6	18
106	Multiple direct interactions of TBP with the MYC oncoprotein. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1035-1043	17.6	20

105	FKBP4 connects mTORC2 and PI3K to activate the PDK1/Akt-dependent cell proliferation signaling in breast cancer. <i>Theranostics</i> , 2019 , 9, 7003-7015	12.1	23
104	ZEB1/NuRD complex suppresses TBC1D2b to stimulate E-cadherin internalization and promote metastasis in lung cancer. <i>Nature Communications</i> , 2019 , 10, 5125	17.4	35
103	Global Interactome Mapping of Mitochondrial Intermembrane Space Proteases Identifies a Novel Function for HTRA2. <i>Proteomics</i> , 2019 , 19, e1900139	4.8	9
102	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	2.2	
101	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	7.6	9
100	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	9.7	122
99	Tyrosyl phosphorylation of KRAS stalls GTPase cycle via alteration of switch I and II conformation. <i>Nature Communications</i> , 2019 , 10, 224	17.4	43
98	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	3.9	11
97	EXD2 governs germ stem cell homeostasis and lifespan by promoting mitoribosome integrity and translation. <i>Nature Cell Biology</i> , 2018 , 20, 162-174	23.4	20
96	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018 , 9, 1731	17.4	24
95	The SUMO-specific isopeptidase SENP2 is targeted to intracellular membranes via a predicted N-terminal amphipathic helix. <i>Molecular Biology of the Cell</i> , 2018 , 29, 1878-1890	3.5	6
94	Global Interactomics Uncovers Extensive Organellar Targeting by Zika Virus. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2242-2255	7.6	78
93	Salmonella exploits host Rho GTPase signalling pathways through the phosphatase activity of SopB. <i>Cellular Microbiology</i> , 2018 , 20, e12938	3.9	11
92	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	10.2	8
91	Ubiquitin ligase RNF8 suppresses Notch signaling to regulate mammary development and tumorigenesis. <i>Journal of Clinical Investigation</i> , 2018 , 128, 4525-4542	15.9	14
90	PPP1R35 is a novel centrosomal protein that regulates centriole length in concert with the microcephaly protein RTTN. <i>ELife</i> , 2018 , 7,	8.9	19
89	An ATG16L1-dependent pathway promotes plasma membrane repair and limits Listeria monocytogenes cell-to-cell spread. <i>Nature Microbiology</i> , 2018 , 3, 1472-1485	26.6	40
88	MYC Protein Interactome Profiling Reveals Functionally Distinct Regions that Cooperate to Drive Tumorigenesis. <i>Molecular Cell</i> , 2018 , 72, 836-848.e7	17.6	62

87	MYC Interacts with the G9a Histone Methyltransferase to Drive Transcriptional Repression and Tumorigenesis. <i>Cancer Cell</i> , 2018 , 34, 579-595.e8	24.3	52
86	MYC dephosphorylation by the PP1/PNUTS phosphatase complex regulates chromatin binding and protein stability. <i>Nature Communications</i> , 2018 , 9, 3502	17.4	23
85	VAPs and ACBD5 tether peroxisomes to the ER for peroxisome maintenance and lipid homeostasis. <i>Journal of Cell Biology</i> , 2017 , 216, 367-377	7.3	142
84	Ube2E1/UBCH6 Is a Critical E2 For the PRC1-catalyzed Ubiquitination of H2A at Lys-119. <i>Journal of Biological Chemistry</i> , 2017 , 292, 2893-2902	5.4	15
83	Parallel Exploration of Interaction Space by BioID and Affinity Purification Coupled to Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017 , 1550, 115-136	1.4	39
82	The dynamic interacting landscape of MAPL reveals essential functions for SUMOylation in innate immunity. <i>Scientific Reports</i> , 2017 , 7, 107	4.9	15
81	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. <i>Science Signaling</i> , 2017 , 10,	8.8	28
80	Differential requirements for Tausled-like kinases 1 and 2 in mammalian development. <i>Cell Death and Differentiation</i> , 2017 , 24, 1872-1885	12.7	14
79	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	7.6	20
78	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. <i>Nature Methods</i> , 2017 , 14, 645-646	21.6	90
77	Characterizing the mitochondrial DNA polymerase gamma interactome by BioID identifies Ruvbl2 localizes to the mitochondria. <i>Mitochondrion</i> , 2017 , 32, 31-35	4.9	10
76	RNF168 and USP10 regulate topoisomerase II β function via opposing effects on its ubiquitylation. <i>Nature Communications</i> , 2016 , 7, 12638	17.4	28
75	MYC interaction with the tumor suppressive SWI/SNF complex member INI1 regulates transcription and cellular transformation. <i>Cell Cycle</i> , 2016 , 15, 1693-705	4.7	29
74	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016 , 149, 64-68	3.9	37
73	Oxygen-dependent Regulation of Erythropoietin Receptor Turnover and Signaling. <i>Journal of Biological Chemistry</i> , 2016 , 291, 7357-72	5.4	24
72	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. <i>Genome Biology</i> , 2016 , 17, 82	18.3	26
71	A global genetic interaction network maps a wiring diagram of cellular function. <i>Science</i> , 2016 , 353,	33.3	626
70	CHCHD2 Is Coamplified with EGFR in NSCLC and Regulates Mitochondrial Function and Cell Migration. <i>Molecular Cancer Research</i> , 2015 , 13, 1119-29	6.6	30

69	BioID-based Identification of Skp Cullin F-box (SCF) E3 Ligase Substrates. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1781-95	7.6	108
68	The Deubiquitinase USP37 Regulates Chromosome Cohesion and Mitotic Progression. <i>Current Biology</i> , 2015 , 25, 2290-9	6.3	26
67	Inhibition of SHP2-mediated dephosphorylation of Ras suppresses oncogenesis. <i>Nature Communications</i> , 2015 , 6, 8859	17.4	112
66	BioID identifies novel c-MYC interacting partners in cultured cells and xenograft tumors. <i>Journal of Proteomics</i> , 2015 , 118, 95-111	3.9	83
65	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	1.2	
64	Identification of SUMO-2/3-modified proteins associated with mitotic chromosomes. <i>Proteomics</i> , 2015 , 15, 763-72	4.8	26
63	Myc and its interactors take shape. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2015 , 1849, 469-83	6	77
62	The use of ubiquitin lysine mutants to characterize E2-E3 linkage specificity: Mass spectrometry offers a cautionary "tail". <i>Proteomics</i> , 2015 , 15, 2910-5	4.8	10
61	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015 , 27, 864-76	24.3	191
60	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. <i>Cell</i> , 2015 , 163, 1484-99	56.2	316
59	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	3.9	35
58	KCMF1 (potassium channel modulatory factor 1) Links RAD6 to UBR4 (ubiquitin N-recognition domain-containing E3 ligase 4) and lysosome-mediated degradation. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 674-85	7.6	17
57	Proteomic analyses of CSF aimed at biomarker development for pediatric brain tumors. <i>Journal of Neuro-Oncology</i> , 2014 , 118, 225-238	4.8	23
56	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	11.5	59
55	BioID data of c-MYC interacting protein partners in cultured cells and xenograft tumors. <i>Data in Brief</i> , 2014 , 1, 76-8	1.2	8
54	Identification of c-MYC SUMOylation by mass spectrometry. <i>PLoS ONE</i> , 2014 , 9, e115337	3.7	16
53	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013 , 10, 730-6	21.6	894
52	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, 20982-7	11.5	61

51	CEP120 and SPICE1 cooperate with CPAP in centriole elongation. <i>Current Biology</i> , 2013 , 23, 1360-6	6.3	113
50	A global <i>S. cerevisiae</i> small ubiquitin-related modifier (SUMO) system interactome. <i>Molecular Systems Biology</i> , 2013 , 9, 668	12.2	35
49	A strategy for modulation of enzymes in the ubiquitin system. <i>Science</i> , 2013 , 339, 590-5	33.3	199
48	The linear ubiquitin-specific deubiquitinase gumbly regulates angiogenesis. <i>Nature</i> , 2013 , 498, 318-24	50.4	184
47	A pathogen type III effector with a novel E3 ubiquitin ligase architecture. <i>PLoS Pathogens</i> , 2013 , 9, e1003121	12.1	64
46	MYC phosphorylation at novel regulatory regions suppresses transforming activity. <i>Cancer Research</i> , 2013 , 73, 6504-15	10.1	22
45	Global analysis of SUMO chain function reveals multiple roles in chromatin regulation. <i>Journal of Cell Biology</i> , 2013 , 201, 145-63	7.3	47
44	Targeting The Mitochondrial ClpP As a Novel Therapeutic Strategy For Acute Myeloid Leukemia. <i>Blood</i> , 2013 , 122, 3937-3937	2.2	
43	A human ubiquitin conjugating enzyme (E2)-HECT E3 ligase structure-function screen. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 329-41	7.6	81
42	Beyond hairballs: The use of quantitative mass spectrometry data to understand protein-protein interactions. <i>FEBS Letters</i> , 2012 , 586, 2723-31	3.8	23
41	Using ProHits to store, annotate, and analyze affinity purification-mass spectrometry (AP-MS) data. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 8, Unit8.16	24.2	17
40	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, 806-20	6.6	57
39	miRNA-mediated deadenylation is orchestrated by GW182 through two conserved motifs that interact with CCR4-NOT. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1211-7	17.6	238
38	The dynamics and mechanism of SUMO chain deconjugation by SUMO-specific proteases. <i>Journal of Biological Chemistry</i> , 2011 , 286, 10238-47	5.4	56
37	Structural and functional comparison of the RING domains of two p53 E3 ligases, Mdm2 and Pirh2. <i>Journal of Biological Chemistry</i> , 2011 , 286, 4796-808	5.4	29
36	ProHits: integrated software for mass spectrometry-based interaction proteomics. <i>Nature Biotechnology</i> , 2010 , 28, 1015-7	44.5	156
35	A novel mechanism for SUMO system control: regulated Ulp1 nucleolar sequestration. <i>Molecular and Cellular Biology</i> , 2010 , 30, 4452-62	4.8	33
34	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	7.3	81

33	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	17.6	66
32	PML/RARA oxidation and arsenic binding initiate the antileukemia response of As ₂ O ₃ . <i>Cancer Cell</i> , 2010 , 18, 88-98	24.3	235
31	A ubiquitin and ubiquitin-like protein spectral library. <i>Proteomics</i> , 2010 , 10, 337-42	4.8	15
30	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, 254-65	4.8	27
29	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, 157-71	7.6	257
28	Using mass spectrometry to identify ubiquitin and ubiquitin-like protein conjugation sites. <i>Proteomics</i> , 2009 , 9, 922-34	4.8	46
27	Global map of SUMO function revealed by protein-protein interaction and genetic networks. <i>Molecular Cell</i> , 2009 , 33, 124-35	17.6	99
26	Arsenic degrades PML or PML-RARalpha through a SUMO-triggered RNF4/ubiquitin-mediated pathway. <i>Nature Cell Biology</i> , 2008 , 10, 547-55	23.4	544
25	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, 375-86	6.5	65
24	Computational prediction of proteotypic peptides for quantitative proteomics. <i>Nature Biotechnology</i> , 2007 , 25, 125-31	44.5	582
23	Analysis of protein complexes using mass spectrometry. <i>Nature Reviews Molecular Cell Biology</i> , 2007 , 8, 645-54	48.7	553
22	Analysis of the <i>Saccharomyces cerevisiae</i> proteome with PeptideAtlas. <i>Genome Biology</i> , 2006 , 7, R106	18.3	51
21	Automated identification of SUMOylation sites using mass spectrometry and SUMmOn pattern recognition software. <i>Nature Methods</i> , 2006 , 3, 533-9	21.6	106
20	The mTOR/PI3K and MAPK pathways converge on eIF4B to control its phosphorylation and activity. <i>EMBO Journal</i> , 2006 , 25, 2781-91	13	391
19	Advances in protein complex analysis using mass spectrometry. <i>Journal of Physiology</i> , 2005 , 563, 11-21	3.9	148
18	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, 380-7	4.8	105
17	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, 10556-65	4.8	143
16	A novel, evolutionarily conserved protein phosphatase complex involved in cisplatin sensitivity. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1725-40	7.6	148

15	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004 , 22, 1459-66	44.5	632
14	Phosphorylation of eucaryotic translation initiation factor 4B Ser422 is modulated by S6 kinases. <i>EMBO Journal</i> , 2004 , 23, 1761-9	13	363
13	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, 48570-9	5.4	26
12	Activation of GCN2 in UV-irradiated cells inhibits translation. <i>Current Biology</i> , 2002 , 12, 1279-86	6.3	209
11	Phosphorylation of eukaryotic translation initiation factor 4E is critical for growth. <i>Molecular and Cellular Biology</i> , 2002 , 22, 1656-63	4.8	152
10	Regulation of translation initiation by FRAP/mTOR. <i>Genes and Development</i> , 2001 , 15, 807-26	12.6	1230
9	Hierarchical phosphorylation of the translation inhibitor 4E-BP1. <i>Genes and Development</i> , 2001 , 15, 2852-66	16.6	595
8	eIF4E activity is regulated at multiple levels. <i>International Journal of Biochemistry and Cell Biology</i> , 1999 , 31, 43-57	5.6	241
7	eIF4 initiation factors: effectors of mRNA recruitment to ribosomes and regulators of translation. <i>Annual Review of Biochemistry</i> , 1999 , 68, 913-63	29.1	1729
6	A novel functional human eukaryotic translation initiation factor 4G. <i>Molecular and Cellular Biology</i> , 1998 , 18, 334-42	4.8	252
5	A SARS-CoV-2 BioID-based virus-host membrane protein interactome and virus peptide compendium: new proteomics resources for COVID-19 research		11
4	A SARS-CoV-2 host proximity interactome		34
3	Super-resolution Molecular Map of Basal Foot Reveals Novel Cilium in Airway Multiciliated Cells		3
2	LUZP1 and the tumour suppressor EPLIN are negative regulators of primary cilia formation		2
1	A proximity-dependent biotinylation map of a human cell: an interactive web resource		28