Jeffrey W Harper

List of Publications by Year
in descending order

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226 papers	61,329 citations	1371 108 h-index	1284 225 g-index
251 all docs	251 docs citations	251 times ranked	71485 citing authors

#	Article	IF	Citations
1	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). Autophagy, 2016, 12, 1-222.	9.1	4,701
2	Guidelines for the use and interpretation of assays for monitoring autophagy. Autophagy, 2012, 8, 445-544.	9.1	3,122
3	A Map of the Interactome Network of the Metazoan C. elegans. Science, 2004, 303, 540-543.	12.6	1,587
4	The DNA Damage Response: Ten Years After. Molecular Cell, 2007, 28, 739-745.	9.7	1,494
5	Systematic and Quantitative Assessment of the Ubiquitin-Modified Proteome. Molecular Cell, 2011, 44, 325-340.	9.7	1,406
6	Network organization of the human autophagy system. Nature, 2010, 466, 68-76.	27.8	1,383
7	Defining the Human Deubiquitinating Enzyme Interaction Landscape. Cell, 2009, 138, 389-403.	28.9	1,354
8	SKP1 Connects Cell Cycle Regulators to the Ubiquitin Proteolysis Machinery through a Novel Motif, the F-Box. Cell, 1996, 86, 263-274.	28.9	1,336
9	Structure of the Cul1â€“Rbx1â€“Skp1â€“F boxSkp2 SCF ubiquitin ligase complex. Nature, 2002, 416, 703-709.	27.8	1,322
10	The BioPlex Network: A Systematic Exploration of the Human Interactome. Cell, 2015, 162, 425-440.	28.9	1,241
11	Molecular definitions of autophagy and related processes. EMBO Journal, 2017, 36, 1811-1836.	7.8	1,230
12	Architecture of the human interactome defines protein communities and disease networks. Nature, 2017, 545, 505-509.	27.8	1,190
13	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. Nature, 2014, 509, 105-109.	27.8	1,169
14	F-Box Proteins Are Receptors that Recruit Phosphorylated Substrates to the SCF Ubiquitin-Ligase Complex. Cell, 1997, 91, 209-219.	28.9	1,166
15	Inhibition of cyclin-dependent kinases by p21.. Molecular Biology of the Cell, 1995, 6, 387-400.	2.1	914
16	The Keap1-BTB Protein Is an Adaptor That Bridges Nrf2 to a Cul3-Based E3 Ligase: Oxidative Stress Sensing by a Cul3-Keap1 Ligase. Molecular and Cellular Biology, 2004, 24, 8477-8486.	2.3	858
17	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. Nature, 2013, 496, 372-376.	27.8	851
18	The SCFbeta -TRCP-ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in Ikappa Balpha and beta -catenin and stimulates Ikappa Balpha ubiquitination in vitro. Genes and Development, 1999, 13, 270-283.	5.9	845

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19	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. Science, 2015, 347, 1436-1441.	12.6	823
20	The Fbw7 tumor suppressor regulates glycogen synthase kinase 3 phosphorylation-dependent c-Myc protein degradation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9085-9090.	7.1	785
21	Structure of the DDB1â€“CRBN E3 ubiquitin ligase in complex with thalidomide. Nature, 2014, 512, 49-53.	27.8	745
22	Altered cell differentiation and proliferation in mice lacking p57KIP2 indicates a role in Beckwithâ€“Wiedemann syndrome. Nature, 1997, 387, 151-158.	27.8	721
23	Phosphorylation-Dependent Ubiquitination of Cyclin E by the SCF ^{Fbw7} Ubiquitin Ligase. Science, 2001, 294, 173-177.	12.6	718
24	Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. Nature Reviews Molecular Cell Biology, 2009, 10, 319-331.	37.0	703
25	The PINK1-PARKIN Mitochondrial Ubiquitylation Pathway Drives a Program of OPTN/NDP52 Recruitment and TBK1 Activation to Promote Mitophagy. Molecular Cell, 2015, 60, 7-20.	9.7	658
26	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. Cell, 2016, 165, 153-164.	28.9	598
27	Systematic analysis and nomenclature of mammalian F-box proteins. Genes and Development, 2004, 18, 2573-2580.	5.9	589
28	Structure of a Î²-TrCP1-Skp1-Î²-Catenin Complex. Molecular Cell, 2003, 11, 1445-1456.	9.7	560
29	A Family of Diverse Cul4-Ddb1-Interacting Proteins Includes Cdt2, which Is Required for S Phase Destruction of the Replication Factor Cdt1. Molecular Cell, 2006, 23, 709-721.	9.7	551
30	Insights into SCF ubiquitin ligases from the structure of the Skp1â€“Skp2 complex. Nature, 2000, 408, 381-386.	27.8	550
31	Quantitative Proteomics Reveal a Feedforward Mechanism for Mitochondrial PARKIN Translocation and Ubiquitin Chain Synthesis. Molecular Cell, 2014, 56, 360-375.	9.7	550
32	Drug discovery in the ubiquitinâ€“proteasome system. Nature Reviews Drug Discovery, 2006, 5, 596-613.	46.4	548
33	Building and decoding ubiquitin chains for mitophagy. Nature Reviews Molecular Cell Biology, 2018, 19, 93-108.	37.0	458
34	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. Cell, 2021, 184, 3022-3040.e28.	28.9	455
35	The Brd4 Extraterminal Domain Confers Transcription Activation Independent of pTEFb by Recruiting Multiple Proteins, Including NSD3. Molecular and Cellular Biology, 2011, 31, 2641-2652.	2.3	450
36	BTB proteins are substrate-specific adaptors in an SCF-like modular ubiquitin ligase containing CUL-3. Nature, 2003, 425, 316-321.	27.8	445

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37	Defining human ERAD networks through an integrative mapping strategy. Nature Cell Biology, 2012, 14, 93-105.	10.3	439
38	The anaphase-promoting complex: it's not just for mitosis any more. Genes and Development, 2002, 16, 2179-2206.	5.9	435
39	How the Cyclin Became a Cyclin. Cell, 1999, 97, 431-434.	28.9	427
40	A Calcium-Regulated MEF2 Sumoylation Switch Controls Postsynaptic Differentiation. Science, 2006, 311, 1012-1017.	12.6	411
41	Mammalian BTBD12/SLX4 Assembles A Holliday Junction Resolvase and Is Required for DNA Repair. Cell, 2009, 138, 63-77.	28.9	403
42	Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases. Molecular Cell, 2009, 36, 39-50.	9.7	403
43	Structure of a Fbw7-Skp1-Cyclin E Complex: Multisite-Phosphorylated Substrate Recognition by SCF Ubiquitin Ligases. Molecular Cell, 2007, 26, 131-143.	9.7	400
44	SAMTOR is an S -adenosylmethionine sensor for the mTORC1 pathway. Science, 2017, 358, 813-818.	12.6	384
45	The v-Jun point mutation allows c-Jun to escape GSK3-dependent recognition and destruction by the Fbw7 ubiquitin ligase. Cancer Cell, 2005, 8, 25-33.	16.8	370
46	Control of lipid metabolism by phosphorylation-dependent degradation of the SREBP family of transcription factors by SCFFbw7. Cell Metabolism, 2005, 1, 379-391.	16.2	368
47	Anticancer drug targets: cell cycle and checkpoint control. Journal of Clinical Investigation, 1999, 104, 1645-1653.	8.2	367
48	Cancer Proliferation Gene Discovery Through Functional Genomics. Science, 2008, 319, 620-624.	12.6	365
49	Excessive Cell Growth Causes Cytoplasm Dilution And Contributes to Senescence. Cell, 2019, 176, 1083-1097.e18.	28.9	347
50	A family of mammalian F-box proteins. Current Biology, 1999, 9, 1180-S3.	3.9	342
51	Anaphase initiation is regulated by antagonistic ubiquitination and deubiquitination activities. Nature, 2007, 446, 876-881.	27.8	333
52	Dynamics of Cullin-RING Ubiquitin Ligase Network Revealed by Systematic Quantitative Proteomics. Cell, 2010, 143, 951-965.	28.9	328
53	Phosphorylation-Dependent Ubiquitination of Cyclin D1 by the SCFFBX4-Î±B Crystallin Complex. Molecular Cell, 2006, 24, 355-366.	9.7	321
54	Dual E1 activation systems for ubiquitin differentially regulate E2 enzyme charging. Nature, 2007, 447, 1135-1138.	27.8	318

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55	Endosome-ER Contacts Control Actin Nucleation and Retromer Function through VAP-Dependent Regulation of PI4P. Cell, 2016, 166, 408-423.	28.9	315
56	Ferritinophagy via NCOA4 is required for erythropoiesis and is regulated by iron dependent HERC2-mediated proteolysis. ELife, 2015, 4, .	6.0	309
57	A Genetic Screen Identifies FAN1, a Fanconi Anemia-Associated Nuclease Necessary for DNA Interstrand Crosslink Repair. Molecular Cell, 2010, 39, 36-47.	9.7	306
58	SCFÂ-TRCP links Chk1 signaling to degradation of the Cdc25A protein phosphatase. Genes and Development, 2003, 17, 3062-3074.	5.9	299
59	SCFÎ²-TRCP controls oncogenic transformation and neural differentiation through REST degradation. Nature, 2008, 452, 370-374.	27.8	289
60	Endogenous Parkin Preserves Dopaminergic Substantia Nigral Neurons following Mitochondrial DNA Mutagenic Stress. Neuron, 2015, 87, 371-381.	8.1	277
61	Building and remodelling Cullinâ€“RING E3 ubiquitin ligases. EMBO Reports, 2013, 14, 1050-1061.	4.5	275
62	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. Cell, 2016, 167, 985-1000.e21.	28.9	259
63	N-Terminal Acetylation Acts as an Avidity Enhancer Within an Interconnected Multiprotein Complex. Science, 2011, 334, 674-678.	12.6	248
64	SCFÎ²-TRCP Controls Clock-dependent Transcription via Casein Kinase 1-dependent Degradation of the Mammalian Period-1 (Per1) Proteinm. Journal of Biological Chemistry, 2005, 280, 26863-26872.	3.4	240
65	Human Papillomavirus Type 16 E7 Oncoprotein Associates with the Cullin 2 Ubiquitin Ligase Complex, Which Contributes to Degradation of the Retinoblastoma Tumor Suppressor. Journal of Virology, 2007, 81, 9737-9747.	3.4	240
66	Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6637-6642.	7.1	240
67	Mitochondrial unfolded protein response controls matrix pre-RNA processing and translation. Nature, 2016, 534, 710-713.	27.8	231
68	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. Nature Communications, 2017, 8, 15965.	12.8	231
69	Defective cardiovascular development and elevated cyclin E and Notch proteins in mice lacking the Fbw7 F-box protein. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 3338-3345.	7.1	228
70	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. Cancer Cell, 2019, 36, 369-384.e13.	16.8	224
71	mTOR Drives Its Own Activation via SCFÎ²TrCP-Dependent Degradation of the mTOR Inhibitor DEPTOR. Molecular Cell, 2011, 44, 290-303.	9.7	212
72	Cyclin-Dependent Kinases. Chemical Reviews, 2001, 101, 2511-2526.	47.7	206

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73	The Prp19 complex and the Usp4^{Sart3} deubiquitinating enzyme control reversible ubiquitination at the spliceosome. Genes and Development, 2010, 24, 1434-1447.	5.9	196
74	Constructing and decoding unconventional ubiquitin chains. Nature Structural and Molecular Biology, 2011, 18, 520-528.	8.2	196
75	Proteome complexity and the forces that drive proteome imbalance. Nature, 2016, 537, 328-338.	27.8	195
76	A DNA Damage Response Screen Identifies RHINO, a 9-1-1 and TopBP1 Interacting Protein Required for ATR Signaling. Science, 2011, 332, 1313-1317.	12.6	194
77	TEX264 Is an Endoplasmic Reticulum-Resident ATG8-Interacting Protein Critical for ER Remodeling during Nutrient Stress. Molecular Cell, 2019, 74, 891-908.e10.	9.7	193
78	The SIOD disorder protein SMARCAL1 is an RPA-interacting protein involved in replication fork restart. Genes and Development, 2009, 23, 2415-2425.	5.9	183
79	Phosphorylation by Casein Kinase I Promotes the Turnover of the Mdm2 Oncoprotein via the SCFÎ²-TRCP Ubiquitin Ligase. Cancer Cell, 2010, 18, 147-159.	16.8	182
80	Systematic identification of interactions between host cell proteins and E7 oncoproteins from diverse human papillomaviruses. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E260-7.	7.1	182
81	Comprehensive Analysis of Host Cellular Interactions with Human Papillomavirus E6 Proteins Identifies New E6 Binding Partners and Reflects Viral Diversity. Journal of Virology, 2012, 86, 13174-13186.	3.4	178
82	Doc1 mediates the activity of the anaphase-promoting complex by contributing to substrate recognition. EMBO Journal, 2003, 22, 786-796.	7.8	176
83	Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. Cell, 2016, 166, 1198-1214.e24.	28.9	172
84	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. Molecular Cell, 2019, 74, 32-44.e8.	9.7	170
85	DNA Unwinding by ASCC3 Helicase Is Coupled to ALKBH3-Dependent DNA Alkylation Repair and Cancer Cell Proliferation. Molecular Cell, 2011, 44, 373-384.	9.7	166
86	Uba1 functions in Atg7- and Atg3-independent autophagy. Nature Cell Biology, 2013, 15, 1067-1078.	10.3	165
87	Structure of a RING E3 Trapped in Action Reveals Ligation Mechanism for the Ubiquitin-like Protein NEDD8. Cell, 2014, 157, 1671-1684.	28.9	163
88	Rab GTPase-Activating Proteins in Autophagy: Regulation of Endocytic and Autophagy Pathways by Direct Binding to Human ATG8 Modifiers. Molecular and Cellular Biology, 2012, 32, 1733-1744.	2.3	161
89	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. Cell Systems, 2016, 3, 395-403.e4.	6.2	153
90	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. Molecular Cell, 2018, 70, 211-227.e8.	9.7	145

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91	Genome-wide siRNA screen identifies SMCX, EP400, and Brd4 as E2-dependent regulators of human papillomavirus oncogene expression. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3752-3757.	7.1	143
92	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. Molecular Cell, 2020, 77, 1124-1142.e10.	9.7	143
93	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. Molecular Cell, 2016, 62, 121-136.	9.7	142
94	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. ELife, 2015, 4, .	6.0	141
95	TRAF2 and OTUD7B govern a ubiquitin-dependent switch that regulates mTORC2 signalling. Nature, 2017, 545, 365-369.	27.8	136
96	Deletion of the Cul1 gene in mice causes arrest in early embryogenesis and accumulation of cyclin E. Current Biology, 1999, 9, 1191-S2.	3.9	134
97	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. Cell Reports, 2015, 11, 1486-1500.	6.4	134
98	Systematic analysis of ribophagy in human cells reveals bystander flux during selective autophagy. Nature Cell Biology, 2018, 20, 135-143.	10.3	131
99	A glycine-specific N-degron pathway mediates the quality control of protein N -myristoylation. Science, 2019, 365, .	12.6	131
100	Structural Complexity in Ubiquitin Recognition. Cell, 2006, 124, 1133-1136.	28.9	129
101	RAB7A phosphorylation by TBK1 promotes mitophagy via the PINK-PARKIN pathway. Science Advances, 2018, 4, eaav0443.	10.3	128
102	Biallelic Mutations in DNAJC12 Cause Hyperphenylalaninemia, Dystonia, and Intellectual Disability. American Journal of Human Genetics, 2017, 100, 257-266.	6.2	127
103	The role of Cdk7 in CAK function, aÂretro-retrospective. Genes and Development, 1998, 12, 285-289.	5.9	126
104	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	28.9	126
105	Cyclin C is a haploinsufficient tumour suppressor. Nature Cell Biology, 2014, 16, 1080-1091.	10.3	124
106	Quantifying Ubiquitin Signaling. Molecular Cell, 2015, 58, 660-676.	9.7	124
107	The tumor suppressor CYLD regulates entry into mitosis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8869-8874.	7.1	123
108	Cutaneous Î²-human papillomavirus E6 proteins bind Mastermind-like coactivators and repress Notch signaling. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1473-80.	7.1	119

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109	Recognition of Phosphodegron Motifs in Human Cyclin E by the SCFFbw7 Ubiquitin Ligase. Journal of Biological Chemistry, 2004, 279, 50110-50119.	3.4	116
110	Identification and Functional Evaluation of Cellular and Viral Factors Involved in the Alteration of Nuclear Architecture during Herpes Simplex Virus 1 Infection. Journal of Virology, 2005, 79, 12840-12851.	3.4	116
111	Microcephaly Proteins Wdr62 and Aspm Define a Mother Centriole Complex Regulating Centriole Biogenesis, Apical Complex, and Cell Fate. Neuron, 2016, 92, 813-828.	8.1	116
112	Endosomal Rab cycles regulate Parkin-mediated mitophagy. ELife, 2018, 7, .	6.0	113
113	The histone demethylase LSD1/KDM1A promotes the DNA damage response. Journal of Cell Biology, 2013, 203, 457-470.	5.2	112
114	Ubiquitin proteasome system (UPS): what can chromatin do for you?. Current Opinion in Cell Biology, 2007, 19, 206-214.	5.4	111
115	Cullin-RING Ubiquitin Ligase Regulatory Circuits: A Quarter Century Beyond the F-Box Hypothesis. Annual Review of Biochemistry, 2021, 90, 403-429.	11.1	108
116	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. Nature Cell Biology, 2017, 19, 177-188.	10.3	107
117	A Genome-wide Screen Identifies p97 as an Essential Regulator of DNA Damage-Dependent CDT1 Destruction. Molecular Cell, 2011, 44, 72-84.	9.7	106
118	The endoplasmic reticulum P5A-ATPase is a transmembrane helix dislocase. Science, 2020, 369, .	12.6	104
119	An FTS/Hook/p107^{FHIP}Complex Interacts with and Promotes Endosomal Clustering by the Homotypic Vacuolar Protein Sorting Complex. Molecular Biology of the Cell, 2008, 19, 5059-5071.	2.1	101
120	Structural Conservation of Distinctive N-terminal Acetylation-Dependent Interactions across a Family of Mammalian NEDD8 Ligation Enzymes. Structure, 2013, 21, 42-53.	3.3	101
121	A Genome-wide Camptothecin Sensitivity Screen Identifies a Mammalian MMS22L-NFKBIL2 Complex Required for Genomic Stability. Molecular Cell, 2010, 40, 645-657.	9.7	99
122	A premature-termination mutation in the Mus musculus cyclin-dependent kinase 3 gene. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1682-1686.	7.1	98
123	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. Nature, 2017, 543, 211-216.	27.8	96
124	EDF1 coordinates cellular responses to ribosome collisions. ELife, 2020, 9, .	6.0	96
125	A functional genomic screen identifies a role for TAO1 kinase in spindle-checkpoint signalling. Nature Cell Biology, 2007, 9, 556-564.	10.3	95
126	Systematic Analysis of Human Cells Lacking ATG8 Proteins Uncovers Roles for GABARAPs and the CCZ1/MON1 Regulator C18orf8/RMC1 in Macroautophagic and Selective Autophagic Flux. Molecular and Cellular Biology, 2018, 38, .	2.3	95

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127	M phase phosphorylation of the epigenetic regulator UHRF1 regulates its physical association with the deubiquitylase USP7 and stability. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4828-4833.	7.1	94
128	Protein destruction: Adapting roles for Cks proteins. Current Biology, 2001, 11, R431-R435.	3.9	92
129	Treacher Collins syndrome TCOF1 protein cooperates with NBS1 in the DNA damage response. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18631-18636.	7.1	92
130	Identification and Proteomic Analysis of Distinct UBE3A/E6AP Protein Complexes. Molecular and Cellular Biology, 2012, 32, 3095-3106.	2.3	91
131	Parallel SCF Adaptor Capture Proteomics Reveals a Role for SCFFBXL17 in NRF2 Activation via BACH1 Repressor Turnover. Molecular Cell, 2013, 52, 9-24.	9.7	91
132	DNA damage: ubiquitin marks the spot. Nature Structural and Molecular Biology, 2008, 15, 20-22.	8.2	90
133	The X-Linked Intellectual Disability Protein PHF6 Associates with the PAF1 Complex and Regulates Neuronal Migration in the Mammalian Brain. Neuron, 2013, 78, 986-993.	8.1	89
134	HiNF-P Directly Links the Cyclin E/CDK2/p220NPAT Pathway to Histone H4 Gene Regulation at the G1/S Phase Cell Cycle Transition. Molecular and Cellular Biology, 2005, 25, 6140-6153.	2.3	88
135	The F-box Protein FBX4 Targets PIN2/TRF1 for Ubiquitin-mediated Degradation and Regulates Telomere Maintenance. Journal of Biological Chemistry, 2006, 281, 759-768.	3.4	88
136	Induction of human Cdc37 in prostate cancer correlates with the ability of targeted Cdc37 expression to promote prostatic hyperplasia. Oncogene, 2000, 19, 2186-2193.	5.9	87
137	An Oriented Peptide Array Library (OPAL) Strategy to Study Protein-Protein Interactions. Journal of Biological Chemistry, 2004, 279, 8802-8807.	3.4	84
138	GEN1/Yen1 and the SLX4 complex: solutions to the problem of Holliday junction resolution. Genes and Development, 2010, 24, 521-536.	5.9	84
139	Rictor Forms a Complex with Cullin-1 to Promote SGK1 Ubiquitination and Destruction. Molecular Cell, 2010, 39, 797-808.	9.7	84
140	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. Genes and Development, 2019, 33, 1031-1047.	5.9	83
141	An OBSL1-Cul7Fbxw8 Ubiquitin Ligase Signaling Mechanism Regulates Golgi Morphology and Dendrite Patterning. PLoS Biology, 2011, 9, e1001060.	5.6	82
142	Systematic proteomics of the VCPâ€“UBXD adaptor network identifies a role for UBXN10 in regulating ciliogenesis. Nature Cell Biology, 2015, 17, 1356-1369.	10.3	82
143	SCF^{FBXO22} Regulates Histone H3 Lysine 9 and 36 Methylation Levels by Targeting Histone Demethylase KDM4A for Ubiquitin-Mediated Proteasomal Degradation. Molecular and Cellular Biology, 2011, 31, 3687-3699.	2.3	81
144	Blocking an N-terminal acetylationâ€“dependent protein interaction inhibits an E3 ligase. Nature Chemical Biology, 2017, 13, 850-857.	8.0	80

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145	TIMMDC1/C3orf1 Functions as a Membrane-Embedded Mitochondrial Complex I Assembly Factor through Association with the MCIA Complex. Molecular and Cellular Biology, 2014, 34, 847-861.	2.3	78
146	Systematic quantitative analysis of ribosome inventory during nutrient stress. Nature, 2020, 583, 303-309.	27.8	78
147	Staged assembly of histone gene expression machinery at subnuclear foci in the abbreviated cell cycle of human embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16964-16969.	7.1	76
148	Cyclin/CDK Regulates the Nucleocytoplasmic Localization of the Human Papillomavirus E1 DNA Helicase. Journal of Virology, 2004, 78, 13954-13965.	3.4	70
149	Phosphorylation of Atg9 regulates movement to the phagophore assembly site and the rate of autophagosome formation. Autophagy, 2016, 12, 648-658.	9.1	68
150	Alternative Ubiquitin Activation/Conjugation Cascades Interact with N-End Rule Ubiquitin Ligases to Control Degradation of RGS Proteins. Molecular Cell, 2011, 43, 392-405.	9.7	65
151	Understanding Cullin-RING E3 Biology through Proteomics-based Substrate Identification. Molecular and Cellular Proteomics, 2012, 11, 1541-1550.	3.8	65
152	Cell cycle dependent phosphorylation and subnuclear organization of the histone gene regulator p220NPAT in human embryonic stem cells. Journal of Cellular Physiology, 2007, 213, 9-17.	4.1	62
153	Ribosome Abundance Control Via the Ubiquitinâ€“Proteasome System and Autophagy. Journal of Molecular Biology, 2020, 432, 170-184.	4.2	62
154	BioPlex Display: An Interactive Suite for Large-Scale APâ€“MS Proteinâ€–Protein Interaction Data. Journal of Proteome Research, 2018, 17, 722-726.	3.7	59
155	Quantitative proteomics reveals the selectivity of ubiquitin-binding autophagy receptors in the turnover of damaged lysosomes by lysophagy. ELife, 2021, 10, .	6.0	59
156	A High-Confidence Interaction Map Identifies SIRT1 as a Mediator of Acetylation of USP22 and the SAGA Coactivator Complex. Molecular and Cellular Biology, 2013, 33, 1487-1502.	2.3	58
157	The Tumor-specific Hyperactive Forms of Cyclin E Are Resistant to Inhibition by p21 and p27. Journal of Biological Chemistry, 2005, 280, 15148-15157.	3.4	57
158	Hook3 is a scaffold for the opposite-polarity microtubule-based motors cytoplasmic dynein-1 and KIF1C. Journal of Cell Biology, 2019, 218, 2982-3001.	5.2	57
159	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. Science Advances, 2019, 5, eaay4624.	10.3	55
160	Regulation of Postsynaptic RapGAP SPAR by Polo-like Kinase 2 and the SCFÎ²-TRCP Ubiquitin Ligase in Hippocampal Neurons. Journal of Biological Chemistry, 2008, 283, 29424-29432.	3.4	53
161	Cytokinesis involves a nontranscriptional function of the Hippo pathway effector YAP. Science Signaling, 2016, 9, ra23.	3.6	53
162	Temporal proteomics during neurogenesis reveals large-scale proteome and organelle remodeling via selective autophagy. Molecular Cell, 2021, 81, 5082-5098.e11.	9.7	52

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163	SLX-1 Is Required for Maintaining Genomic Integrity and Promoting Meiotic Noncrossovers in the Caenorhabditis elegans Germline. PLoS Genetics, 2012, 8, e1002888.	3.5	51
164	Implications for the Ubiquitination Reaction of the Anaphase-promoting Complex from the Crystal Structure of the Doc1/Apc10 Subunit. Journal of Molecular Biology, 2002, 316, 955-968.	4.2	48
165	The PINK1 kinase-driven ubiquitin ligase Parkin promotes mitochondrial protein import through the presequence pathway in living cells. Scientific Reports, 2019, 9, 11829.	3.3	48
166	Skipping into the E2F1-destruction pathway. Nature Cell Biology, 1999, 1, E5-E7.	10.3	47
167	Differential Roles for Checkpoint Kinases in DNA Damage-dependent Degradation of the Cdc25A Protein Phosphatase. Journal of Biological Chemistry, 2008, 283, 19322-19328.	3.4	47
168	Altered Social Behavior and Neuronal Development in Mice Lacking the Uba6-Use1ÂUbiquitin Transfer System. Molecular Cell, 2013, 50, 172-184.	9.7	47
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