

Jeffrey W Harper

List of Publications by Year in descending order

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Version: 2024-02-01

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	Brain-derived autophagosome profiling reveals the engulfment of nucleoid-enriched mitochondrial fragments by basal autophagy in neurons. <i>Neuron</i> , 2022, 110, 967-976.e8.	8.1	43
2	Targeted protein degradation: from small molecules to complex organelles—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2022, 1510, 79-99.	3.8	5
3	Mechanisms underlying ubiquitin-driven selective mitochondrial and bacterial autophagy. <i>Molecular Cell</i> , 2022, 82, 1501-1513.	9.7	46
4	Functional conservation and divergence of the helix-turn-helix motif of E2 ubiquitin-conjugating enzymes. <i>EMBO Journal</i> , 2022, 41, e108823.	7.8	8
5	Quantitative intravital imaging in zebrafish reveals <i>in vivo</i> dynamics of physiological-stress-induced mitophagy. <i>Journal of Cell Science</i> , 2021, 134, .	2.0	35
6	Super Heavy TMTpro Labeling Reagent: An Alternative and Higher-Charge-State-Amenable Stable-Isotope-Labeled TMTpro Variant. <i>Journal of Proteome Research</i> , 2021, 20, 3009-3013.	3.7	1
7	ORF10—Cullin-2—ZYG11B complex is not required for SARS-CoV-2 infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
8	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , 2021, 184, 3022-3040.e28.	28.9	455
9	Cullin-RING Ubiquitin Ligase Regulatory Circuits: A Quarter Century Beyond the F-Box Hypothesis. <i>Annual Review of Biochemistry</i> , 2021, 90, 403-429.	11.1	108
10	iRQC, a surveillance pathway for 40S ribosomal quality control during mRNA translation initiation. <i>Cell Reports</i> , 2021, 36, 109642.	6.4	30
11	Quantitative proteomics reveals the selectivity of ubiquitin-binding autophagy receptors in the turnover of damaged lysosomes by lysophagy. <i>ELife</i> , 2021, 10, .	6.0	59
12	Temporal proteomics during neurogenesis reveals large-scale proteome and organelle remodeling via selective autophagy. <i>Molecular Cell</i> , 2021, 81, 5082-5098.e11.	9.7	52
13	A multi-scale map of cell structure fusing protein images and interactions. <i>Nature</i> , 2021, 600, 536-542.	27.8	43
14	Global ubiquitylation analysis of mitochondria in primary neurons identifies endogenous Parkin targets following activation of PINK1. <i>Science Advances</i> , 2021, 7, eabj0722.	10.3	29
15	Ribosome Abundance Control Via the Ubiquitin—Proteasome System and Autophagy. <i>Journal of Molecular Biology</i> , 2020, 432, 170-184.	4.2	62
16	Pathogenic Pathways in Early-Onset Autosomal Recessive Parkinson's Disease Discovered Using Isogenic Human Dopaminergic Neurons. <i>Stem Cell Reports</i> , 2020, 14, 75-90.	4.8	37
17	The endoplasmic reticulum P5A-ATPase is a transmembrane helix dislocase. <i>Science</i> , 2020, 369, .	12.6	104
18	Ubiquitin chain-elongating enzyme UBE2S activates the RING E3 ligase APC/C for substrate priming. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 550-560.	8.2	26

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19	Global Landscape and Dynamics of Parkin and USP30-Dependent Ubiquitylomes in iNeurons during Mitophagic Signaling. <i>Molecular Cell</i> , 2020, 77, 1124-1142.e10.	9.7	143
20	Systematic quantitative analysis of ribosome inventory during nutrient stress. <i>Nature</i> , 2020, 583, 303-309.	27.8	78
21	Inhibition of sphingolipid synthesis improves outcomes and survival in GARP mutant <i>wobbler</i> mice, a model of motor neuron degeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10565-10574.	7.1	33
22	EDF1 coordinates cellular responses to ribosome collisions. <i>ELife</i> , 2020, 9, .	6.0	96
23	The PINK1 kinase-driven ubiquitin ligase Parkin promotes mitochondrial protein import through the presequence pathway in living cells. <i>Scientific Reports</i> , 2019, 9, 11829.	3.3	48
24	Mutations in RABL3 alter KRAS prenylation and are associated with hereditary pancreatic cancer. <i>Nature Genetics</i> , 2019, 51, 1308-1314.	21.4	47
25	Hook3 is a scaffold for the opposite-polarity microtubule-based motors cytoplasmic dynein-1 and KIF1C. <i>Journal of Cell Biology</i> , 2019, 218, 2982-3001.	5.2	57
26	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. <i>Cell Host and Microbe</i> , 2019, 26, 86-99.e7.	11.0	42
27	A glycine-specific N-degron pathway mediates the quality control of protein N-myristoylation. <i>Science</i> , 2019, 365, .	12.6	131
28	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	16.8	224
29	Protein aggregation mediates stoichiometry of protein complexes in aneuploid cells. <i>Genes and Development</i> , 2019, 33, 1031-1047.	5.9	83
30	TEX264 Is an Endoplasmic Reticulum-Resident ATG8-Interacting Protein Critical for ER Remodeling during Nutrient Stress. <i>Molecular Cell</i> , 2019, 74, 891-908.e10.	9.7	193
31	Probing the Global Cellular Responses to Lipotoxicity Caused by Saturated Fatty Acids. <i>Molecular Cell</i> , 2019, 74, 32-44.e8.	9.7	170
32	Excessive Cell Growth Causes Cytoplasm Dilution And Contributes to Senescence. <i>Cell</i> , 2019, 176, 1083-1097.e18.	28.9	347
33	The role of nuclear receptor co-activator 4 in erythropoiesis (Reply to Nai et al.). <i>Haematologica</i> , 2019, 104, e585-e586.	3.5	1
34	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. <i>Science Advances</i> , 2019, 5, eaay4624.	10.3	55
35	Mitotic regulators TPX2 and Aurora A protect DNA forks during replication stress by counteracting 53BP1 function. <i>Journal of Cell Biology</i> , 2019, 218, 422-432.	5.2	39
36	NCOA4 maintains murine erythropoiesis via cell autonomous and non-autonomous mechanisms. <i>Haematologica</i> , 2019, 104, 1342-1354.	3.5	38

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37	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. <i>Molecular Cell</i> , 2018, 70, 211-227.e8.	9.7	145
38	Building and decoding ubiquitin chains for mitophagy. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 93-108.	37.0	458
39	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. <i>Molecular and Cellular Biology</i> , 2018, 38, .	2.3	95
40	BioPlex Display: An Interactive Suite for Large-Scale APâ€‘MS Proteinâ€‘Protein Interaction Data. <i>Journal of Proteome Research</i> , 2018, 17, 722-726.	3.7	59
41	Systematic analysis of ribophagy in human cells reveals bystander flux during selective autophagy. <i>Nature Cell Biology</i> , 2018, 20, 135-143.	10.3	131
42	RAB7A phosphorylation by TBK1 promotes mitophagy via the PINK-PARKIN pathway. <i>Science Advances</i> , 2018, 4, eaav0443.	10.3	128
43	Angelman syndromeâ€‘associated point mutations in the Zn ²⁺ -binding N-terminal (AZUL) domain of UBE3A ubiquitin ligase inhibit binding to the proteasome. <i>Journal of Biological Chemistry</i> , 2018, 293, 18387-18399.	3.4	29
44	Endosomal Rab cycles regulate Parkin-mediated mitophagy. <i>ELife</i> , 2018, 7, .	6.0	113
45	Biallelic Mutations in DNAJC12 Cause Hyperphenylalaninemia, Dystonia, and Intellectual Disability. <i>American Journal of Human Genetics</i> , 2017, 100, 257-266.	6.2	127
46	TIRR regulates 53BP1 by masking its histone methyl-lysine binding function. <i>Nature</i> , 2017, 543, 211-216.	27.8	96
47	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. <i>Nature Cell Biology</i> , 2017, 19, 177-188.	10.3	107
48	TRAF2 and OTUD7B govern a ubiquitin-dependent switch that regulates mTORC2 signalling. <i>Nature</i> , 2017, 545, 365-369.	27.8	136
49	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , 2017, 545, 505-509.	27.8	1,190
50	Molecular definitions of autophagy and related processes. <i>EMBO Journal</i> , 2017, 36, 1811-1836.	7.8	1,230
51	Quantitative Phospho-proteomic Analysis of TNF α /NF κ B Signaling Reveals a Role for RIPK1 Phosphorylation in Suppressing Necrotic Cell Death. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1200-1216.	3.8	18
52	SAMTOR is an <i>S</i> -adenosylmethionine sensor for the mTORC1 pathway. <i>Science</i> , 2017, 358, 813-818.	12.6	384
53	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. <i>Nature Communications</i> , 2017, 8, 15965.	12.8	231
54	Blocking an N-terminal acetylationâ€‘dependent protein interaction inhibits an E3 ligase. <i>Nature Chemical Biology</i> , 2017, 13, 850-857.	8.0	80

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55	A protein interaction map for cell-cell adhesion regulators identifies DUSP23 as a novel phosphatase for β -catenin. <i>Scientific Reports</i> , 2016, 6, 27114.	3.3	13
56	Phosphorylation of Atg9 regulates movement to the phagophore assembly site and the rate of autophagosome formation. <i>Autophagy</i> , 2016, 12, 648-658.	9.1	68
57	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. <i>Cell Systems</i> , 2016, 3, 395-403.e4.	6.2	153
58	Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. <i>Cell</i> , 2016, 166, 1198-1214.e24.	28.9	172
59	Proteome complexity and the forces that drive proteome imbalance. <i>Nature</i> , 2016, 537, 328-338.	27.8	195
60	Endosome-ER Contacts Control Actin Nucleation and Retromer Function through VAP-Dependent Regulation of PI4P. <i>Cell</i> , 2016, 166, 408-423.	28.9	315
61	Cytokinesis involves a nontranscriptional function of the Hippo pathway effector YAP. <i>Science Signaling</i> , 2016, 9, ra23.	3.6	53
62	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. <i>Cell</i> , 2016, 167, 985-1000.e21.	28.9	259
63	Microcephaly Proteins Wdr62 and Aspm Define a Mother Centriole Complex Regulating Centriole Biogenesis, Apical Complex, and Cell Fate. <i>Neuron</i> , 2016, 92, 813-828.	8.1	116
64	Mitochondrial unfolded protein response controls matrix pre-RNA processing and translation. <i>Nature</i> , 2016, 534, 710-713.	27.8	231
65	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. <i>Cell</i> , 2016, 165, 1440-1453.	28.9	126
66	Guidelines for the use and interpretation of assays for monitoring autophagy (3rd edition). <i>Autophagy</i> , 2016, 12, 1-222.	9.1	4,701
67	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. <i>Molecular Cell</i> , 2016, 62, 121-136.	9.7	142
68	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. <i>Cell</i> , 2016, 165, 153-164.	28.9	598
69	The MAP kinase pathway coordinates crossover designation with disassembly of synaptonemal complex proteins during meiosis. <i>ELife</i> , 2016, 5, e12039.	6.0	36
70	QIL1 mutation causes MICOS disassembly and early onset fatal mitochondrial encephalopathy with liver disease. <i>ELife</i> , 2016, 5, .	6.0	46
71	Ferritinophagy via NCOA4 is required for erythropoiesis and is regulated by iron dependent HERC2-mediated proteolysis. <i>ELife</i> , 2015, 4, .	6.0	309
72	Quantifying Ubiquitin Signaling. <i>Molecular Cell</i> , 2015, 58, 660-676.	9.7	124

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73	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. <i>Cell Reports</i> , 2015, 11, 1486-1500.	6.4	134
74	Exome sequencing in amyotrophic lateral sclerosis identifies risk genes and pathways. <i>Science</i> , 2015, 347, 1436-1441.	12.6	823
75	Identification of TRIM27 as a Novel Degradation Target of Herpes Simplex Virus 1 ICPO. <i>Journal of Virology</i> , 2015, 89, 220-229.	3.4	36
76	Endogenous Parkin Preserves Dopaminergic Substantia Nigral Neurons following Mitochondrial DNA Mutagenic Stress. <i>Neuron</i> , 2015, 87, 371-381.	8.1	277
77	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , 2015, 162, 425-440.	28.9	1,241
78	Defining roles of PARKIN and ubiquitin phosphorylation by PINK1 in mitochondrial quality control using a ubiquitin replacement strategy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6637-6642.	7.1	240
79	Systematic proteomics of the VCP/UBXD adaptor network identifies a role for UBXN10 in regulating ciliogenesis. <i>Nature Cell Biology</i> , 2015, 17, 1356-1369.	10.3	82
80	The PINK1-PARKIN Mitochondrial Ubiquitylation Pathway Drives a Program of OPTN/NDP52 Recruitment and TBK1 Activation to Promote Mitophagy. <i>Molecular Cell</i> , 2015, 60, 7-20.	9.7	658
81	Proteomic Analysis and Identification of Cellular Interactors of the Giant Ubiquitin Ligase HERC2. <i>Journal of Proteome Research</i> , 2015, 14, 953-966.	3.7	45
82	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. <i>ELife</i> , 2015, 4, .	6.0	141
83	TIF1 β Protein Regulates Epithelial-Mesenchymal Transition by Operating as a Small Ubiquitin-like Modifier (SUMO) E3 Ligase for the Transcriptional Regulator SnoN1. <i>Journal of Biological Chemistry</i> , 2014, 289, 25067-25078.	3.4	32
84	Treacher Collins syndrome TCOF1 protein cooperates with NBS1 in the DNA damage response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18631-18636.	7.1	92
85	TIMMDC1/C3orf1 Functions as a Membrane-Embedded Mitochondrial Complex I Assembly Factor through Association with the MCIA Complex. <i>Molecular and Cellular Biology</i> , 2014, 34, 847-861.	2.3	78
86	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. <i>Nature</i> , 2014, 509, 105-109.	27.8	1,169
87	Spindle Assembly Factor Protection. <i>Molecular Cell</i> , 2014, 53, 165-166.	9.7	2
88	Cyclin C is a haploinsufficient tumour suppressor. <i>Nature Cell Biology</i> , 2014, 16, 1080-1091.	10.3	124
89	Structure of the DDB1/CRBN E3 ubiquitin ligase in complex with thalidomide. <i>Nature</i> , 2014, 512, 49-53.	27.8	745
90	Balancing act. <i>Nature</i> , 2014, 510, 347-348.	27.8	6

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91	Quantitative Proteomics Reveal a Feedforward Mechanism for Mitochondrial PARKIN Translocation and Ubiquitin Chain Synthesis. <i>Molecular Cell</i> , 2014, 56, 360-375.	9.7	550
92	Structure of a RING E3 Trapped in Action Reveals Ligation Mechanism for the Ubiquitin-like Protein NEDD8. <i>Cell</i> , 2014, 157, 1671-1684.	28.9	163
93	Uba1 functions in Atg7- and Atg3-independent autophagy. <i>Nature Cell Biology</i> , 2013, 15, 1067-1078.	10.3	165
94	Structural Conservation of Distinctive N-terminal Acetylation-Dependent Interactions across a Family of Mammalian NEDD8 Ligation Enzymes. <i>Structure</i> , 2013, 21, 42-53.	3.3	101
95	The histone demethylase LSD1/KDM1A promotes the DNA damage response. <i>Journal of Cell Biology</i> , 2013, 203, 457-470.	5.2	112
96	A Novel Hap1- τ sc1 Interaction Regulates Neuronal mTORC1 Signaling and Morphogenesis in the Brain. <i>Journal of Neuroscience</i> , 2013, 33, 18015-18021.	3.6	16
97	Parallel SCF Adaptor Capture Proteomics Reveals a Role for SCFFBXL17 in NRF2 Activation via BACH1 Repressor Turnover. <i>Molecular Cell</i> , 2013, 52, 9-24.	9.7	91
98	Building and remodelling Cullin-RING E3 ubiquitin ligases. <i>EMBO Reports</i> , 2013, 14, 1050-1061.	4.5	275
99	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. <i>Nature</i> , 2013, 496, 372-376.	27.8	851
100	Altered Social Behavior and Neuronal Development in Mice Lacking the Uba6-Use1 Ubiquitin Transfer System. <i>Molecular Cell</i> , 2013, 50, 172-184.	9.7	47
101	The X-Linked Intellectual Disability Protein PHF6 Associates with the PAF1 Complex and Regulates Neuronal Migration in the Mammalian Brain. <i>Neuron</i> , 2013, 78, 986-993.	8.1	89
102	A High-Confidence Interaction Map Identifies SIRT1 as a Mediator of Acetylation of USP22 and the SAGA Coactivator Complex. <i>Molecular and Cellular Biology</i> , 2013, 33, 1487-1502.	2.3	58
103	Landscape of the PARKIN-dependent ubiquitin modified proteome in response to mitochondrial depolarization defined through quantitative proteomics. <i>FASEB Journal</i> , 2013, 27, 553.17.	0.5	0
104	SLX-1 Is Required for Maintaining Genomic Integrity and Promoting Meiotic Noncrossovers in the <i>Caenorhabditis elegans</i> Germline. <i>PLoS Genetics</i> , 2012, 8, e1002888.	3.5	51
105	Cutaneous β -human papillomavirus E6 proteins bind Mastermind-like coactivators and repress Notch signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1473-80.	7.1	119
106	Identification and Proteomic Analysis of Distinct UBE3A/E6AP Protein Complexes. <i>Molecular and Cellular Biology</i> , 2012, 32, 3095-3106.	2.3	91
107	M phase phosphorylation of the epigenetic regulator UHRF1 regulates its physical association with the deubiquitylase USP7 and stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4828-4833.	7.1	94
108	Understanding Cullin-RING E3 Biology through Proteomics-based Substrate Identification. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1541-1550.	3.8	65

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109	Defining human ERAD networks through an integrative mapping strategy. <i>Nature Cell Biology</i> , 2012, 14, 93-105.	10.3	439
110	Rab GTPase-Activating Proteins in Autophagy: Regulation of Endocytic and Autophagy Pathways by Direct Binding to Human ATG8 Modifiers. <i>Molecular and Cellular Biology</i> , 2012, 32, 1733-1744.	2.3	161
111	Comprehensive Analysis of Host Cellular Interactions with Human Papillomavirus E6 Proteins Identifies New E6 Binding Partners and Reflects Viral Diversity. <i>Journal of Virology</i> , 2012, 86, 13174-13186.	3.4	178
112	Emerging Anatomy of the BAP1 Tumor Suppressor System. <i>Science</i> , 2012, 337, 1463-1464.	12.6	35
113	Guidelines for the use and interpretation of assays for monitoring autophagy. <i>Autophagy</i> , 2012, 8, 445-544.	9.1	3,122
114	Systematic identification of interactions between host cell proteins and E7 oncoproteins from diverse human papillomaviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E260-7.	7.1	182
115	A DNA Damage Response Screen Identifies RHINO, a 9-1-1 and TopBP1 Interacting Protein Required for ATR Signaling. <i>Science</i> , 2011, 332, 1313-1317.	12.6	194
116	Stuck in the Middle: Drugging the Ubiquitin System at the E2 Step. <i>Cell</i> , 2011, 145, 1007-1009.	28.9	9
117	DNA Unwinding by ASCC3 Helicase Is Coupled to ALKBH3-Dependent DNA Alkylation Repair and Cancer Cell Proliferation. <i>Molecular Cell</i> , 2011, 44, 373-384.	9.7	166
118	Alternative Ubiquitin Activation/Conjugation Cascades Interact with N-End Rule Ubiquitin Ligases to Control Degradation of RGS Proteins. <i>Molecular Cell</i> , 2011, 43, 392-405.	9.7	65
119	A Genome-wide Screen Identifies p97 as an Essential Regulator of DNA Damage-Dependent CDT1 Destruction. <i>Molecular Cell</i> , 2011, 44, 72-84.	9.7	106
120	Systematic and Quantitative Assessment of the Ubiquitin-Modified Proteome. <i>Molecular Cell</i> , 2011, 44, 325-340.	9.7	1,406
121	mTOR Drives Its Own Activation via SCF ^{TrCP} -Dependent Degradation of the mTOR Inhibitor DEPTOR. <i>Molecular Cell</i> , 2011, 44, 290-303.	9.7	212
122	Constructing and decoding unconventional ubiquitin chains. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 520-528.	8.2	196
123	N-Terminal Acetylation Acts as an Avidity Enhancer Within an Interconnected Multiprotein Complex. <i>Science</i> , 2011, 334, 674-678.	12.6	248
124	SCF ^{FBXO22} Regulates Histone H3 Lysine 9 and 36 Methylation Levels by Targeting Histone Demethylase KDM4A for Ubiquitin-Mediated Proteasomal Degradation. <i>Molecular and Cellular Biology</i> , 2011, 31, 3687-3699.	2.3	81
125	Simply quantifying ubiquitin complexity. <i>Nature Methods</i> , 2011, 8, 630-631.	19.0	0
126	The Brd4 Extraterminal Domain Confers Transcription Activation Independent of pTEFb by Recruiting Multiple Proteins, Including NSD3. <i>Molecular and Cellular Biology</i> , 2011, 31, 2641-2652.	2.3	450

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127	An OBSL1-Cul7Fbxw8 Ubiquitin Ligase Signaling Mechanism Regulates Golgi Morphology and Dendrite Patterning. <i>PLoS Biology</i> , 2011, 9, e1001060.	5.6	82
128	Phosphorylation by Casein Kinase I Promotes the Turnover of the Mdm2 Oncoprotein via the SCF ^{β2} -TRCP Ubiquitin Ligase. <i>Cancer Cell</i> , 2010, 18, 147-159.	16.8	182
129	Network organization of the human autophagy system. <i>Nature</i> , 2010, 466, 68-76.	27.8	1,383
130	Inhibitors for E3 ubiquitin ligases. <i>Nature Biotechnology</i> , 2010, 28, 682-684.	17.5	15
131	Cdc25A and Dub3 in a high-stakes balancing act. <i>Nature Cell Biology</i> , 2010, 12, 311-313.	10.3	8
132	GEN1/Yen1 and the SLX4 complex: solutions to the problem of Holliday junction resolution. <i>Genes and Development</i> , 2010, 24, 521-536.	5.9	84
133	NCoR1 Mediates Papillomavirus E8 ^{E2C} Transcriptional Repression. <i>Journal of Virology</i> , 2010, 84, 4451-4460.	3.4	39
134	Genome-wide siRNA screen identifies SMCX, EP400, and Brd4 as E2-dependent regulators of human papillomavirus oncogene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3752-3757.	7.1	143
135	A Genetic Screen Identifies FAN1, a Fanconi Anemia-Associated Nuclease Necessary for DNA Interstrand Crosslink Repair. <i>Molecular Cell</i> , 2010, 39, 36-47.	9.7	306
136	Rictor Forms a Complex with Cullin-1 to Promote SGK1 Ubiquitination and Destruction. <i>Molecular Cell</i> , 2010, 39, 797-808.	9.7	84
137	A Genome-wide Camptothecin Sensitivity Screen Identifies a Mammalian MMS22L-NFKBIL2 Complex Required for Genomic Stability. <i>Molecular Cell</i> , 2010, 40, 645-657.	9.7	99
138	Telomeric TurF1 Wars. <i>Developmental Cell</i> , 2010, 18, 167-168.	7.0	3
139	Ubiquitin Gets CARDed. <i>Cell</i> , 2010, 141, 220-222.	28.9	4
140	Dynamics of Cullin-RING Ubiquitin Ligase Network Revealed by Systematic Quantitative Proteomics. <i>Cell</i> , 2010, 143, 951-965.	28.9	328
141	The Prp19 complex and the Usp4 ^{Sart3} deubiquitinating enzyme control reversible ubiquitination at the spliceosome. <i>Genes and Development</i> , 2010, 24, 1434-1447.	5.9	196
142	Brd4 Regulation of Papillomavirus Protein E2 Stability. <i>Journal of Virology</i> , 2009, 83, 8683-8692.	3.4	40
143	The SIOD disorder protein SMARCAL1 is an RPA-interacting protein involved in replication fork restart. <i>Genes and Development</i> , 2009, 23, 2415-2425.	5.9	183
144	CDK inhibitors selectively diminish cell cycle controlled activation of the histone H4 gene promoter by p220 ^{NPAT} and HiNF ^ε . <i>Journal of Cellular Physiology</i> , 2009, 219, 438-448.	4.1	14

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145	Stairway to the proteasome. <i>Nature</i> , 2009, 462, 585-586.	27.8	2
146	A road map of cellular protein homeostasis. <i>Nature Chemical Biology</i> , 2009, 5, 9-11.	8.0	3
147	Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 319-331.	37.0	703
148	Perturbation of vacuolar maturation promotes listeriolysin O-independent vacuolar escape during <i>Listeria monocytogenes</i> infection of human cells. <i>Cellular Microbiology</i> , 2009, 11, 1382-1398.	2.1	33
149	Defining the Human Deubiquitinating Enzyme Interaction Landscape. <i>Cell</i> , 2009, 138, 389-403.	28.9	1,354
150	Mammalian BTBD12/SLX4 Assembles A Holliday Junction Resolvase and Is Required for DNA Repair. <i>Cell</i> , 2009, 138, 63-77.	28.9	403
151	Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases. <i>Molecular Cell</i> , 2009, 36, 39-50.	9.7	403
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