Brenda A Schulman

List of Publications by Year
in descending order

107 papers	14,427 citations	23500 58 h-index	30010 103 g-index
126 all docs	126 docs citations	126 times ranked	16623 citing authors

#	Article	IF	Citations
1	Structure of the Cul1â€"Rbx1â€"Skp1â€"F boxSkp2 SCF ubiquitin ligase complex. Nature, 2002, 416, 703-709.	13.7	1,322
2	Papain-like protease regulates SARS-CoV-2 viral spread and innate immunity. Nature, 2020, 587, 657-662.	13.7	818
3	Ubiquitin-like protein activation by E1 enzymes: the apex for downstream signalling pathways. Nature Reviews Molecular Cell Biology, 2009, 10, 319-331.	16.1	703
4	Structural Insights into NEDD8 Activation of Cullin-RING Ligases: Conformational Control of Conjugation. Cell, 2008, 134, 995-1006.	13.5	659
5	Structure of a Î²-TrCP1-Skp1-Î²-Catenin Complex. Molecular Cell, 2003, 11, 1445-1456.	4.5	560
6	Insights into SCF ubiquitin ligases from the structure of the Skp1â€"Skp2 complex. Nature, 2000, 408, 381-386.	13.7	550
7	Quantitative Proteomics Reveal a Feedforward Mechanism for Mitochondrial PARKIN Translocation and Ubiquitin Chain Synthesis. Molecular Cell, 2014, 56, 360-375.	4.5	550
8	Protein neddylation: beyond cullinâ€"RING ligases. Nature Reviews Molecular Cell Biology, 2015, 16, 30-44.	16.1	417
9	Structures of SPOP-Substrate Complexes: Insights into Molecular Architectures of BTB-Cul3 Ubiquitin Ligases. Molecular Cell, 2009, 36, 39-50.	4.5	403
10	Cancer Mutations of the Tumor Suppressor SPOP Disrupt the Formation of Active, Phase-Separated Compartments. Molecular Cell, 2018, 72, 19-36.e8.	4.5	286
11	Building and remodelling Cullinâ€"RING E3 ubiquitin ligases. EMBO Reports, 2013, 14, 1050-1061.	2.0	275
12	biGBac enables rapid gene assembly for the expression of large multisubunit protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2564-9.	3.3	263
13	Structural Basis of the Cks1-Dependent Recognition of p27Kip1 by the SCFSkp2 Ubiquitin Ligase. Molecular Cell, 2005, 20, 9-19.	4.5	255
14	N-Terminal Acetylation Acts as an Avidity Enhancer Within an Interconnected Multiprotein Complex. Science, 2011, 334, 674-678.	6.0	248
15	Insights into Ubiquitin Transfer Cascades from a Structure of a UbcH5Bâˆ¼Ubiquitin-HECTNEDD4L Complex. Molecular Cell, 2009, 36, 1095-1102.	4.5	246
16	The Structure of the APPBP1-UBA3-NEDD8-ATP Complex Reveals the Basis for Selective Ubiquitin-like Protein Activation by an E1. Molecular Cell, 2003, 12, 1427-1437.	4.5	241
17	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.	3.3	240
18	A residue-specific NMR view of the non-cooperative unfolding of a molten globule. Nature Structural Biology, 1997, 4, 630-634.	9.7	236

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19	Dynamic regulation of macroautophagy by distinctive ubiquitin-like proteins. Nature Structural and Molecular Biology, 2014, 21, 336-345.	3.6	235
20	E2-RING Expansion of the NEDD8 Cascade Confers Specificity to Cullin Modification. Molecular Cell, 2009, 33, 483-495.	4.5	228
21	Basis for a ubiquitin-like protein thioester switch toggling E1â€“E2 affinity. Nature, 2007, 445, 394-398.	13.7	191
22	NEDD8Ânucleates a multivalent cullinâ€“RINGâ€“UBE2D ubiquitin ligation assembly. Nature, 2020, 578, 461-466.	13.7	178
23	Atomistic Autophagy: The Structures of Cellular Self-Digestion. Cell, 2014, 157, 300-311.	13.5	173
24	Two Distinct Types of E3 Ligases Work in Unison to Regulate Substrate Ubiquitylation. Cell, 2016, 166, 1198-1214.e24.	13.5	172
25	Structure of a RING E3 Trapped in Action Reveals Ligation Mechanism for the Ubiquitin-like Protein NEDD8. Cell, 2014, 157, 1671-1684.	13.5	163
26	Mutation in ATG5 reduces autophagy and leads to ataxia with developmental delay. ELife, 2016, 5, .	2.8	161
27	SPOP Promotes Tumorigenesis by Acting as a Key Regulatory Hub in Kidney Cancer. Cancer Cell, 2014, 25, 455-468.	7.7	154
28	Quantifying the heterogeneity of macromolecular machines by mass photometry. Nature Communications, 2020, 11, 1772.	5.8	146
29	Structural Basis for a Reciprocal Regulation between SCF and CSN. Cell Reports, 2012, 2, 616-627.	2.9	145
30	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. Molecular Cell, 2016, 62, 121-136.	4.5	142
31	Atg8 Transfer from Atg7 to Atg3: A Distinctive E1-E2 Architecture and Mechanism in the Autophagy Pathway. Molecular Cell, 2011, 44, 451-461.	4.5	135
32	Mechanism of ubiquitin ligation and lysine prioritization by a HECT E3. ELife, 2013, 2, e00828.	2.8	130
33	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	13.5	126
34	Cryo-EM of Mitotic Checkpoint Complex-Bound APC/C Reveals Reciprocal and Conformational Regulation of Ubiquitin Ligation. Molecular Cell, 2016, 63, 593-607.	4.5	123
35	A cascading activity-based probe sequentially targets E1â€“E2â€“E3 ubiquitin enzymes. Nature Chemical Biology, 2016, 12, 523-530.	3.9	122
36	Alpha-lactalbumin forms a compact molten globule in the absence of disulfide bonds. Nature Structural Biology, 1999, 6, 948-952.	9.7	121

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37	APC15 mediates CDC20 autoubiquitylation by APC/CMCC and disassembly of the mitotic checkpoint complex. Nature Structural and Molecular Biology, 2012, 19, 1116-1123.	3.6	118
38	Structure of HHARI, a RING-IBR-RING Ubiquitin Ligase: Autoinhibition of an Ariadne-Family E3 and Insights into Ligation Mechanism. Structure, 2013, 21, 1030-1041.	1.6	116
39	Mechanism of APC/C ^{CDC20} activation by mitotic phosphorylation. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2570-8.	3.3	112
40	Cullin-RING Ubiquitin Ligase Regulatory Circuits: A Quarter Century Beyond the F-Box Hypothesis. Annual Review of Biochemistry, 2021, 90, 403-429.	5.0	108
41	Structural Conservation of Distinctive N-terminal Acetylation-Dependent Interactions across a Family of Mammalian NEDD8 Ligation Enzymes. Structure, 2013, 21, 42-53.	1.6	101
42	Posing the APC/C E3 Ubiquitin Ligase to Orchestrate Cell Division. Trends in Cell Biology, 2019, 29, 117-134.	3.6	101
43	Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. Molecular Cell, 2014, 56, 246-260.	4.5	98
44	Ubiquitin ligation to F-box protein targets by SCFâ€“RBR E3â€“E3 super-assembly. Nature, 2021, 590, 671-676.	13.7	97
45	Proline scanning mutagenesis of a molten globule reveals non-cooperative formation of a protein's overall topology. Nature Structural and Molecular Biology, 1996, 3, 682-687.	3.6	96
46	A Dual E3 Mechanism for Rub1 Ligation to Cdc53. Molecular Cell, 2010, 39, 784-796.	4.5	93
47	Noncanonical E2 recruitment by the autophagy E1 revealed by Atg7â€“Atg3 and Atg7â€“Atg10 structures. Nature Structural and Molecular Biology, 2012, 19, 1242-1249.	3.6	92
48	NEDD8 and ubiquitin ligation by cullin-RING E3 ligases. Current Opinion in Structural Biology, 2021, 67, 101-109.	2.6	92
49	ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nature Methods, 2015, 12, 859-865.	9.0	87
50	TRIAD1 and HHARI bind to and are activated by distinct neddylated Cullin-RING ligase complexes. EMBO Journal, 2013, 32, 2848-2860.	3.5	84
51	Electron microscopy structure of human APC/CCDH1â€“EMI1 reveals multimodal mechanism of E3 ligase shutdown. Nature Structural and Molecular Biology, 2013, 20, 827-835.	3.6	82
52	A Selective Autophagy Pathway for Phase-Separated Endocytic Protein Deposits. Molecular Cell, 2020, 80, 764-778.e7.	4.5	82
53	RING E3 mechanism for ubiquitin ligation to a disordered substrate visualized for human anaphase-promoting complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5272-5279.	3.3	80
54	Blocking an N-terminal acetylationâ€“dependent protein interaction inhibits an E3 ligase. Nature Chemical Biology, 2017, 13, 850-857.	3.9	80

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55	PAX5 is a tumor suppressor in mouse mutagenesis models of acute lymphoblastic leukemia. Blood, 2015, 125, 3609-3617.	0.6	72
56	Structure of a Glomulin-RBX1-CUL1 Complex: Inhibition of a RING E3 Ligase through Masking of Its E2-Binding Surface. Molecular Cell, 2012, 47, 371-382.	4.5	71
57	Data-independent acquisition method for ubiquitinome analysis reveals regulation of circadian biology. Nature Communications, 2021, 12, 254.	5.8	71
58	Pathogenic Bacteria Target NEDD8-Conjugated Cullins to Hijack Host-Cell Signaling Pathways. PLoS Pathogens, 2010, 6, e1001128.	2.1	66
59	Structural and mechanistic basis of the EMC-dependent biogenesis of distinct transmembrane clients. ELife, 2020, 9, .	2.8	66
60	Disulfide Determinants of Calcium-Induced Packing in Î±-Lactalbuminâ€. Biochemistry, 1996, 35, 859-863.	1.2	63
61	The Glomuvenous Malformation Protein Glomulin Binds Rbx1 and Regulates Cullin RING Ligase-Mediated Turnover of Fbw7. Molecular Cell, 2012, 46, 67-78.	4.5	59
62	Interconversion between Anticipatory and Active GID E3ÂUbiquitin Ligase Conformations via Metabolically Driven Substrate Receptor Assembly. Molecular Cell, 2020, 77, 150-163.e9.	4.5	50
63	The structural context of posttranslational modifications at a proteome-wide scale. PLoS Biology, 2022, 20, e3001636.	2.6	50
64	Insights into anaphase promoting complex TPR subdomain assembly from a CDC26â€"APC6 structure. Nature Structural and Molecular Biology, 2009, 16, 987-989.	3.6	45
65	Structural Studies of HHARI/UbcH7âˆ¼Ub Reveal Unique E2âˆ¼Ub Conformational Restriction by RBR RING1. Structure, 2017, 25, 890-900.e5.	1.6	45
66	Multiple Weak Linear Motifs Enhance Recruitment and Processivity in SPOP-Mediated Substrate Ubiquitination. Journal of Molecular Biology, 2016, 428, 1256-1271.	2.0	44
67	GID E3 ligase supramolecular chelate assembly configures multipronged ubiquitin targeting of an oligomeric metabolic enzyme. Molecular Cell, 2021, 81, 2445-2459.e13.	4.5	44
68	ARIH2 Is a Vif-Dependent Regulator of CUL5-Mediated APOBEC3G Degradation in HIV Infection. Cell Host and Microbe, 2019, 26, 86-99.e7.	5.1	42
69	Discovery of an Orally Bioavailable Inhibitor of Defective in Cullin Neddylation 1 (DCN1)-Mediated Cullin Neddylation. Journal of Medicinal Chemistry, 2018, 61, 2694-2706.	2.9	41
70	Twists and turns in ubiquitinâ€like protein conjugation cascades. Protein Science, 2011, 20, 1941-1954.	3.1	39
71	Molecular glue concept solidifies. Nature Chemical Biology, 2020, 16, 2-3.	3.9	39
72	The IMiD target CRBN determines HSP90 activity toward transmembrane proteins essential in multiple myeloma. Molecular Cell, 2021, 81, 1170-1186.e10.	4.5	39

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73	How the ends signal the end: Regulation by E3 ubiquitin ligases recognizing protein termini. Molecular Cell, 2022, 82, 1424-1438.	4.5	39
74	A switch element in the autophagy E2 Atg3 mediates allosteric regulation across the lipidation cascade. Nature Communications, 2019, 10, 3600.	5.8	36
75	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. ELife, 2019, 8, .	2.8	36
76	Structure of an APC3â€"APC16 Complex: Insights into Assembly of the Anaphase-Promoting Complex/Cyclosome. Journal of Molecular Biology, 2015, 427, 1748-1764.	2.0	35
77	Piperidinyl Ureas Chemically Control Defective in Cullin Neddylation 1 (DCN1)-Mediated Cullin Neddylation. Journal of Medicinal Chemistry, 2018, 61, 2680-2693.	2.9	34
78	Structures of Atg7-Atg3 and Atg7-Atg10 reveal noncanonical mechanisms of E2 recruitment by the autophagy E1. Autophagy, 2013, 9, 778-780.	4.3	32
79	Decoding the messaging of the ubiquitin system using chemical and protein probes. Cell Chemical Biology, 2021, 28, 889-902.	2.5	32
80	CUL5-ARIH2 E3-E3 ubiquitin ligase structure reveals cullin-specific NEDD8 activation. Nature Chemical Biology, 2021, 17, 1075-1083.	3.9	30
81	Linkage-specific ubiquitin chain formation depends on a lysine hydrocarbon ruler. Nature Chemical Biology, 2021, 17, 272-279.	3.9	26
82	The UBA domain of conjugating enzyme Ubc1/Ube2K facilitates assembly of K48/K63â€branched ubiquitin chains. EMBO Journal, 2021, 40, e106094.	3.5	25
83	Discovery of Novel Pyrazolo-pyridone DCN1 Inhibitors Controlling Cullin Neddylation. Journal of Medicinal Chemistry, 2019, 62, 8429-8442.	2.9	24
84	Protein engineering of a ubiquitin-variant inhibitor of APC/C identifies a cryptic K48 ubiquitin chain binding site. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17280-17289.	3.3	22
85	FBXO11-mediated proteolysis of BAHD1 relieves PRC2-dependent transcriptional repression in erythropoiesis. Blood, 2021, 137, 155-167.	0.6	22
86	Integrative proteomics reveals principles of dynamic phosphosignaling networks in human erythropoiesis. Molecular Systems Biology, 2020, 16, e9813.	3.2	21
87	Binding to E1 and E3 is mutually exclusive for the human autophagy E2 Atg3. Protein Science, 2013, 22, 1691-1697.	3.1	20
88	Hydrogen exchange in BPTI variants that do not share a common disulfide bond. Protein Science, 1994, 3, 2226-2232.	3.1	19
89	Insights into links between autophagy and the ubiquitin system from the structure of LC3B bound to the LIR motif from the E3 ligase NEDD4. Protein Science, 2017, 26, 1674-1680.	3.1	18
90	Protein Ubiquitination: CHIPping Away the Symmetry. Molecular Cell, 2005, 20, 653-655.	4.5	17

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91	DIA-based systems biology approach unveils E3 ubiquitin ligase-dependent responses to a metabolic shift. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32806-32815.	3.3	17
92	Paradoxical mitotic exit induced by a small molecule inhibitor of APC/CCdc20. Nature Chemical Biology, 2020, 16, 546-555.	3.9	16
93	Multifaceted N-Degron Recognition and Ubiquitylation by GID/CTLH E3 Ligases. Journal of Molecular Biology, 2022, 434, 167347.	2.0	15
94	Measuring APC/C-Dependent Ubiquitylation In Vitro. Methods in Molecular Biology, 2016, 1342, 287-303.	0.4	12
95	New classes of E3 ligases illuminated by chemical probes. Current Opinion in Structural Biology, 2022, 73, 102341.	2.6	11
96	Allosteric regulation through a switch element in the autophagy E2, Atg3. Autophagy, 2020, 16, 183-184.	4.3	10
97	A GID E3 ligase assembly ubiquitinates an Rsp5 E3 adaptor and regulates plasma membrane transporters. EMBO Reports, 2022, 23, e53835.	2.0	9
98	Improvement of Oral Bioavailability of Pyrazolo-Pyridone Inhibitors of the Interaction of DCN1/2 and UBE2M. Journal of Medicinal Chemistry, 2021, 64, 5850-5862.	2.9	8
99	Targeted protein degradation: from small molecules to complex organellesâ€"a Keystone Symposia report. Annals of the New York Academy of Sciences, 2022, 1510, 79-99.	1.8	5
100	Dual-color pulse-chase ubiquitination assays to simultaneously monitor substrate priming and extension. Methods in Enzymology, 2019, 618, 29-48.	0.4	4
101	APC7 mediates ubiquitin signaling in constitutive heterochromatin in the developing mammalian brain. Molecular Cell, 2022, 82, 90-105.e13.	4.5	4
102	SCF E3 Ligase Substrates Switch from CAN-D to Can-ubiquitylate. Molecular Cell, 2018, 69, 721-723.	4.5	3
103	Cryo-EM structures of Gid12-bound GID E3 reveal steric blockade as a mechanism inhibiting substrate ubiquitylation. Nature Communications, 2022, 13, .	5.8	3
104	A role of autophagy in spinocerebellar ataxiaâ€"Rare exception or general principle?. Autophagy, 2016, 12, 1208-1209.	4.3	0
105	Mechanistic Insights into the NEDD8 Conjugation Cascade. FASEB Journal, 2008, 22, 98.1.	0.2	0
106	IDH1 and IDH2 Mutations In Pediatric Acute Myeloid Leukemia. Blood, 2010, 116, 1699-1699.	0.6	0
107	The GID E3 Ubiquitin Ligase Converts Between Anticipatory and Active States Through the Incorporation of Swappable Substrate Receptors. FASEB Journal, 2020, 34, 1-1.	0.2	0