Catherine L Day

List of Publications by Year
in descending order

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64 papers	7,584 citations	101543 36 h-index	123424 61 g-index
67 all docs	67 docs citations	67 times ranked	8066 citing authors

#	Article	IF	Citations
1	Ubiquitin and a charged loop regulate the ubiquitin E3 ligase activity of Ark2C. Nature Communications, 2022, 13, 1181.	12.8	8
2	The Structure and Ubiquitin Binding Properties of TRAF RING Heterodimers. Journal of Molecular Biology, 2021, 433, 166844.	4.2	20
3	Identification of Ubiquitin Variants That Inhibit the E2 Ubiquitin Conjugating Enzyme, Ube2k. ACS Chemical Biology, 2021, 16, 1745-1756.	3.4	12
4	A cryptic tubulin-binding domain links MEKK1 to curved tubulin protomers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21308-21318.	7.1	12
5	Collaborative networks enable the rapid establishment of serological assays for SARS-CoV-2 during nationwide lockdown in New Zealand. PeerJ, 2020, 8, e9863.	2.0	12
6	Ubiquitin Variant Inhibitors Meet the Deubiquitinase USP15. Structure, 2019, 27, 564-565.	3.3	1
7	E2 enzymes: lessons in ubiquitin transfer from XLID patients. Nature Chemical Biology, 2019, 15, 6-7.	8.0	2
8	The RING domain of RING Finger 11 (RNF 11) protein binds Ubc13 and inhibits formation of polyubiquitin chains. FEBS Letters, 2018, 592, 1434-1444.	2.8	9
9	A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. Nature Communications, 2018, 9, 3932.	12.8	25
10	Regulation of E2s: A Role for Additional Ubiquitin Binding Sites?. Journal of Molecular Biology, 2017, 429, 3430-3440.	4.2	17
11	The activity of TRAF RING homo- and heterodimers is regulated by zinc finger 1. Nature Communications, 2017, 8, 1788.	12.8	42
12	Structure and Function of the RING Domains of RNF20 and RNF40, Dimeric E3 Ligases that Monoubiquitylate Histone H2B. Journal of Molecular Biology, 2016, 428, 4073-4086.	4.2	23
13	Noncovalent Ubiquitin Interactions Regulate the Catalytic Activity of Ubiquitin Writers. Trends in Biochemical Sciences, 2016, 41, 924-937.	7.5	27
14	Secondary ubiquitin-RING docking enhances Arkadia and Ark2C E3 ligase activity. Nature Structural and Molecular Biology, 2016, 23, 45-52.	8.2	46
15	The molecular basis of lysine 48 ubiquitin chain synthesis by Ube2K. Scientific Reports, 2015, 5, 16793.	3.3	43
16	IAPs: Modular regulators of cell signalling. Seminars in Cell and Developmental Biology, 2015, 39, 80-90.	5.0	43
17	Enhancing the peroxidase activity of cytochrome c by mutation of residue 41: implications for the peroxidase mechanism and cytochrome c release. Biochemical Journal, 2014, 458, 259-265.	3.7	38
18	Structure of the bacterial type <scp>II NADH</scp> dehydrogenase: a monotopic membrane protein with an essential role in energy generation. Molecular Microbiology, 2014, 91, 950-964.	2.5	103

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19	The Ubiquitin-associated Domain of Cellular Inhibitor of Apoptosis Proteins Facilitates Ubiquitylation. Journal of Biological Chemistry, 2014, 289, 25721-25736.	3.4	10
20	Birinapant, a Smac-Mimetic with Improved Tolerability for the Treatment of Solid Tumors and Hematological Malignancies. Journal of Medicinal Chemistry, 2014, 57, 3666-3677.	6.4	146
21	Use of E2~Ubiquitin Conjugates for the Characterization of Ubiquitin Transfer by RING E3 Ligases Such as the Inhibitor of Apoptosis Proteins. Methods in Enzymology, 2014, 545, 243-263.	1.0	23
22	The N-Terminal Extension of UBE2E Ubiquitin-Conjugating Enzymes Limits Chain Assembly. Journal of Molecular Biology, 2013, 425, 4099-4111.	4.2	39
23	Regulation of ubiquitin transfer by XIAP, a dimeric RING E3 ligase. Biochemical Journal, 2013, 450, 629-638.	3.7	50
24	Solution Structure and Physiological Requirements for Psb27 in Synechocystis sp. PCC 6803. Advanced Topics in Science and Technology in China, 2013, , 432-435.	0.1	0
25	RINGs hold the key to ubiquitin transfer. Trends in Biochemical Sciences, 2012, 37, 58-65.	7.5	168
26	CARD-Mediated Autoinhibition of cIAP1's E3 Ligase Activity Suppresses Cell Proliferation and Migration. Molecular Cell, 2011, 42, 569-583.	9.7	89
27	Smac Mimetics Activate the E3 Ligase Activity of cIAP1 Protein by Promoting RING Domain Dimerization. Journal of Biological Chemistry, 2011, 286, 17015-17028.	3.4	142
28	RING domain dimerization is essential for RNF4 function. Biochemical Journal, 2010, 431, 23-29.	3.7	80
29	FRIGIDA and related proteins have a conserved central domain and family specific N- and C- terminal regions that are functionally important. Plant Molecular Biology, 2010, 73, 493-505.	3.9	29
30	The structure of Boo/Diva reveals a divergent Bcl-2 protein. Proteins: Structure, Function and Bioinformatics, 2010, 78, NA-NA.	2.6	24
31	Tumor Necrosis Factor (TNF) Signaling, but Not TWEAK (TNF-like Weak Inducer of Apoptosis)-triggered cIAP1 (Cellular Inhibitor of Apoptosis Protein 1) Degradation, Requires cIAP1 RING Dimerization and E2 Binding. Journal of Biological Chemistry, 2010, 285, 17525-17536.	3.4	37
32	Intrinsically Disordered Proteins in Bcl-2 Regulated Apoptosis. International Journal of Molecular Sciences, 2010, 11, 1808-1824.	4.1	69
33	Asymmetric Recruitment of cIAPs by TRAF2. Journal of Molecular Biology, 2010, 400, 8-15.	4.2	72
34	A Direct Interaction with NEDD1 Regulates Î³-Tubulin Recruitment to the Centrosome. PLoS ONE, 2010, 5, e9618.	2.5	36
35	TRAF2 Must Bind to Cellular Inhibitors of Apoptosis for Tumor Necrosis Factor (TNF) to Efficiently Activate NF-Î¹B and to Prevent TNF-induced Apoptosis. Journal of Biological Chemistry, 2009, 284, 35906-35915.	3.4	202
36	Reevaluation of Abscisic Acid-Binding Assays Shows That G-Protein-Coupled Receptor2 Does Not Bind Abscisic Acid. Plant Physiology, 2009, 150, 6-11.	4.8	48

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37	Solution Structure of Psb27 from Cyanobacterial Photosystem II,. Biochemistry, 2009, 48, 8771-8773.	2.5	40
38	Bak Activation for Apoptosis Involves Oligomerization of Dimers via Their Î±6 Helices. Molecular Cell, 2009, 36, 696-703.	9.7	200
39	FCA does not bind abscisic acid. Nature, 2008, 456, E5-E6.	27.8	40
40	Structural Plasticity Underpins Promiscuous Binding of the Prosurvival Protein A1. Structure, 2008, 16, 818-829.	3.3	97
41	Structure of the BH3 Domains from the p53-Inducible BH3-Only Proteins Noxa and Puma in Complex with Mcl-1. Journal of Molecular Biology, 2008, 380, 958-971.	4.2	178
42	Structures of the cIAP2 RING Domain Reveal Conformational Changes Associated with Ubiquitin-conjugating Enzyme (E2) Recruitment. Journal of Biological Chemistry, 2008, 283, 31633-31640.	3.4	153
43	Structural insights into the degradation of Mcl-1 induced by BH3 domains. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6217-6222.	7.1	397
44	Solution structure of Mclâ€‡1 and its complexes. FASEB Journal, 2007, 21, A638.	0.5	0
45	The BH3 mimetic ABT-737 targets selective Bcl-2 proteins and efficiently induces apoptosis via Bak/Bax if Mcl-1 is neutralized. Cancer Cell, 2006, 10, 389-399.	16.8	1,149
46	Regulation of apoptosis: uncovering the binding determinants. Current Opinion in Structural Biology, 2005, 15, 690-699.	5.7	63
47	Determination of cell survival by RING-mediated regulation of inhibitor of apoptosis (IAP) protein abundance. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16182-16187.	7.1	133
48	Solution Structure of Prosurvival Mcl-1 and Characterization of Its Binding by Proapoptotic BH3-only Ligands. Journal of Biological Chemistry, 2005, 280, 4738-4744.	3.4	187
49	Differential Targeting of Prosurvival Bcl-2 Proteins by Their BH3-Only Ligands Allows Complementary Apoptotic Function. Molecular Cell, 2005, 17, 393-403.	9.7	1,639
50	Localization of dynein light chains 1 and 2 and their pro-apoptotic ligands. Biochemical Journal, 2004, 377, 597-605.	3.7	65
51	The structure of Bcl-w reveals a role for the C-terminal residues in modulating biological activity. EMBO Journal, 2003, 22, 1497-1507.	7.8	151
52	Proapoptotic BH3-only proteins trigger membrane integration of prosurvival Bcl-w and neutralize its activity. Journal of Cell Biology, 2003, 162, 877-888.	5.2	104
53	The Bcl-2-regulated apoptotic pathway. Journal of Cell Science, 2003, 116, 4053-4056.	2.0	206
54	HtrA2 Promotes Cell Death through Its Serine Protease Activity and Its Ability to Antagonize Inhibitor of Apoptosis Proteins. Journal of Biological Chemistry, 2002, 277, 445-454.	3.4	484

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55	The anti-apoptotic activity of XIAP is retained upon mutation of both the caspase 3â€“ and caspase 9â€“interacting sites. Journal of Cell Biology, 2002, 157, 115-124.	5.2	124
56	HtrAâ€”A Renaissance Protein. Structure, 2002, 10, 737-739.	3.3	10
57	Structure of a domain-opened mutant (R121D) of the human lactoferrin N-lobe refined from a merohedrally twinned crystal form. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 955-962.	2.5	10
58	Crystal structure of the amino-terminal coiled-coil domain of the APC tumor suppressor 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2000, 301, 147-156.	4.2	50
59	Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat. Nature Structural Biology, 1999, 6, 648-651.	9.7	165
60	Altered Domain Closure and Iron Binding in Lactoferrin Mutants. , 1997, , 25-38.		0
61	Mutation of Arginine 121 in Lactoferrin Destabilizes Iron Binding by Disruption of Anion Binding:Â Crystal Structures of R121S and R121E Mutantsâ€,â€¡. Biochemistry, 1996, 35, 14473-14479.	2.5	34
62	Altered Domain Closure and Iron Binding in Transferrins: The Crystal Structure of the Asp60Ser Mutant of the Amino-terminal Half-molecule of Human Lactoferrin. Journal of Molecular Biology, 1996, 256, 352-363.	4.2	62
63	Structure of the Recombinant N-Terminal Lobe of Human Lactoferrin at 2Â·0 Ã... Resolution. Journal of Molecular Biology, 1993, 232, 1084-1100.	4.2	83
64	Preliminary crystallographic studies of the amino terminal half of human lactoferrin in its iron-saturated and iron-free forms. Journal of Molecular Biology, 1992, 228, 973-974.	4.2	13