

Catherine L Day

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7933428/publications.pdf>

Version: 2024-02-01

64
papers

7,584
citations

101384

36
h-index

123241

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. <i>Nature Communications</i> , 2022, 13, 1181.	5.8	8
2	The Structure and Ubiquitin Binding Properties of TRAF RING Heterodimers. <i>Journal of Molecular Biology</i> , 2021, 433, 166844.	2.0	20
3	Identification of Ubiquitin Variants That Inhibit the E2 Ubiquitin Conjugating Enzyme, Ube2k. <i>ACS Chemical Biology</i> , 2021, 16, 1745-1756.	1.6	12
4	A cryptic tubulin-binding domain links MEKK1 to curved tubulin protomers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21308-21318.	3.3	12
5	Collaborative networks enable the rapid establishment of serological assays for SARS-CoV-2 during nationwide lockdown in New Zealand. <i>PeerJ</i> , 2020, 8, e9863.	0.9	12
6	Ubiquitin Variant Inhibitors Meet the Deubiquitinase USP15. <i>Structure</i> , 2019, 27, 564-565.	1.6	1
7	E2 enzymes: lessons in ubiquitin transfer from XLID patients. <i>Nature Chemical Biology</i> , 2019, 15, 6-7.	3.9	2
8	The RING domain of RING Finger 11 (RNF 11) protein binds Ubc13 and inhibits formation of polyubiquitin chains. <i>FEBS Letters</i> , 2018, 592, 1434-1444.	1.3	9
9	A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. <i>Nature Communications</i> , 2018, 9, 3932.	5.8	25
10	Regulation of E2s: A Role for Additional Ubiquitin Binding Sites?. <i>Journal of Molecular Biology</i> , 2017, 429, 3430-3440.	2.0	17
11	The activity of TRAF RING homo- and heterodimers is regulated by zinc finger 1. <i>Nature Communications</i> , 2017, 8, 1788.	5.8	42
12	Structure and Function of the RING Domains of RNF20 and RNF40, Dimeric E3 Ligases that Monoubiquitylate Histone H2B. <i>Journal of Molecular Biology</i> , 2016, 428, 4073-4086.	2.0	23
13	Noncovalent Ubiquitin Interactions Regulate the Catalytic Activity of Ubiquitin Writers. <i>Trends in Biochemical Sciences</i> , 2016, 41, 924-937.	3.7	27
14	Secondary ubiquitin-RING docking enhances Arkadia and Ark2C E3 ligase activity. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 45-52.	3.6	46
15	The molecular basis of lysine 48 ubiquitin chain synthesis by Ube2K. <i>Scientific Reports</i> , 2015, 5, 16793.	1.6	43
16	IAPs: Modular regulators of cell signalling. <i>Seminars in Cell and Developmental Biology</i> , 2015, 39, 80-90.	2.3	43
17	Enhancing the peroxidase activity of cytochrome <i>c</i> by mutation of residue 41: implications for the peroxidase mechanism and cytochrome <i>c</i> release. <i>Biochemical Journal</i> , 2014, 458, 259-265.	1.7	38
18	Structure of the bacterial type II NADH dehydrogenase: a monotopic membrane protein with an essential role in energy generation. <i>Molecular Microbiology</i> , 2014, 91, 950-964.	1.2	103

#	ARTICLE	IF	CITATIONS
19	The Ubiquitin-associated Domain of Cellular Inhibitor of Apoptosis Proteins Facilitates Ubiquitylation. <i>Journal of Biological Chemistry</i> , 2014, 289, 25721-25736.	1.6	10
20	Birinapant, a Smac-Mimetic with Improved Tolerability for the Treatment of Solid Tumors and Hematological Malignancies. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 3666-3677.	2.9	146
21	Use of E2-Ubiquitin Conjugates for the Characterization of Ubiquitin Transfer by RING E3 Ligases Such as the Inhibitor of Apoptosis Proteins. <i>Methods in Enzymology</i> , 2014, 545, 243-263.	0.4	23
22	The N-Terminal Extension of UBE2E Ubiquitin-Conjugating Enzymes Limits Chain Assembly. <i>Journal of Molecular Biology</i> , 2013, 425, 4099-4111.	2.0	39
23	Regulation of ubiquitin transfer by XIAP, a dimeric RING E3 ligase. <i>Biochemical Journal</i> , 2013, 450, 629-638.	1.7	50
24	Solution Structure and Physiological Requirements for Psb27 in <i>Synechocystis</i> sp. PCC 6803. <i>Advanced Topics in Science and Technology in China</i> , 2013, , 432-435.	0.0	0
25	RINGs hold the key to ubiquitin transfer. <i>Trends in Biochemical Sciences</i> , 2012, 37, 58-65.	3.7	168
26	CARD-Mediated Autoinhibition of cIAP1's E3 Ligase Activity Suppresses Cell Proliferation and Migration. <i>Molecular Cell</i> , 2011, 42, 569-583.	4.5	89
27	Smac Mimetics Activate the E3 Ligase Activity of cIAP1 Protein by Promoting RING Domain Dimerization. <i>Journal of Biological Chemistry</i> , 2011, 286, 17015-17028.	1.6	142
28	RING domain dimerization is essential for RNF4 function. <i>Biochemical Journal</i> , 2010, 431, 23-29.	1.7	80
29	FRIGIDA and related proteins have a conserved central domain and family specific N- and C-terminal regions that are functionally important. <i>Plant Molecular Biology</i> , 2010, 73, 493-505.	2.0	29
30	The structure of Boo/Diva reveals a divergent Bcl-2 protein. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, NA-NA.	1.5	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. <i>Journal of Biological Chemistry</i> , 2010, 285, 17525-17536.	1.6	37
32	Intrinsically Disordered Proteins in Bcl-2 Regulated Apoptosis. <i>International Journal of Molecular Sciences</i> , 2010, 11, 1808-1824.	1.8	69
33	Asymmetric Recruitment of cIAPs by TRAF2. <i>Journal of Molecular Biology</i> , 2010, 400, 8-15.	2.0	72
34	A Direct Interaction with NEDD1 Regulates β -Tubulin Recruitment to the Centrosome. <i>PLoS ONE</i> , 2010, 5, e9618.	1.1	36
35	TRAF2 Must Bind to Cellular Inhibitors of Apoptosis for Tumor Necrosis Factor (TNF) to Efficiently Activate NF- κ B and to Prevent TNF-induced Apoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 35906-35915.	1.6	202
36	Reevaluation of Abscisic Acid-Binding Assays Shows That G-Protein-Coupled Receptor2 Does Not Bind Abscisic Acid. <i>Plant Physiology</i> , 2009, 150, 6-11.	2.3	48

#	ARTICLE	IF	CITATIONS
37	Solution Structure of Psb27 from Cyanobacterial Photosystem II. <i>Biochemistry</i> , 2009, 48, 8771-8773.	1.2	40
38	Bak Activation for Apoptosis Involves Oligomerization of Dimers via Their $\alpha 6$ Helices. <i>Molecular Cell</i> , 2009, 36, 696-703.	4.5	200
39	FCA does not bind abscisic acid. <i>Nature</i> , 2008, 456, E5-E6.	13.7	40
40	Structural Plasticity Underpins Promiscuous Binding of the Prosurvival Protein A1. <i>Structure</i> , 2008, 16, 818-829.	1.6	97
41	Structure of the BH3 Domains from the p53-Inducible BH3-Only Proteins Noxa and Puma in Complex with Mcl-1. <i>Journal of Molecular Biology</i> , 2008, 380, 958-971.	2.0	178
42	Structures of the cIAP2 RING Domain Reveal Conformational Changes Associated with Ubiquitin-conjugating Enzyme (E2) Recruitment. <i>Journal of Biological Chemistry</i> , 2008, 283, 31633-31640.	1.6	153
43	Structural insights into the degradation of Mcl-1 induced by BH3 domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6217-6222.	3.3	397
44	Solution structure of Mcl-1 and its complexes. <i>FASEB Journal</i> , 2007, 21, A638.	0.2	0
45	The BH3 mimetic ABT-737 targets selective Bcl-2 proteins and efficiently induces apoptosis via Bak/Bax if Mcl-1 is neutralized. <i>Cancer Cell</i> , 2006, 10, 389-399.	7.7	1,149
46	Regulation of apoptosis: uncovering the binding determinants. <i>Current Opinion in Structural Biology</i> , 2005, 15, 690-699.	2.6	63
47	Determination of cell survival by RING-mediated regulation of inhibitor of apoptosis (IAP) protein abundance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16182-16187.	3.3	133
48	Solution Structure of Prosurvival Mcl-1 and Characterization of Its Binding by Proapoptotic BH3-only Ligands. <i>Journal of Biological Chemistry</i> , 2005, 280, 4738-4744.	1.6	187
49	Differential Targeting of Prosurvival Bcl-2 Proteins by Their BH3-Only Ligands Allows Complementary Apoptotic Function. <i>Molecular Cell</i> , 2005, 17, 393-403.	4.5	1,639
50	Localization of dynein light chains 1 and 2 and their pro-apoptotic ligands. <i>Biochemical Journal</i> , 2004, 377, 597-605.	1.7	65
51	The structure of Bcl-w reveals a role for the C-terminal residues in modulating biological activity. <i>EMBO Journal</i> , 2003, 22, 1497-1507.	3.5	151
52	Proapoptotic BH3-only proteins trigger membrane integration of prosurvival Bcl-w and neutralize its activity. <i>Journal of Cell Biology</i> , 2003, 162, 877-888.	2.3	104
53	The Bcl-2-regulated apoptotic pathway. <i>Journal of Cell Science</i> , 2003, 116, 4053-4056.	1.2	206
54	HtrA2 Promotes Cell Death through Its Serine Protease Activity and Its Ability to Antagonize Inhibitor of Apoptosis Proteins. <i>Journal of Biological Chemistry</i> , 2002, 277, 445-454.	1.6	484

#	ARTICLE	IF	CITATIONS
55	The anti-apoptotic activity of XIAP is retained upon mutation of both the caspase 3 and caspase 9 interacting sites. <i>Journal of Cell Biology</i> , 2002, 157, 115-124.	2.3	124
56	HtrA Renaissance Protein. <i>Structure</i> , 2002, 10, 737-739.	1.6	10
57	Structure of a domain-opened mutant (R121D) of the human lactoferrin N-lobe refined from a merohedrally twinned crystal form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 955-962.	2.5	10
58	Crystal structure of the amino-terminal coiled-coil domain of the APC tumor suppressor 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 2000, 301, 147-156.	2.0	50
59	Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat. <i>Nature Structural Biology</i> , 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: Crystal Structures of R121S and R121E Mutants. <i>Biochemistry</i> , 1996, 35, 14473-14479.	1.2	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. <i>Journal of Molecular Biology</i> , 1996, 256, 352-363.	2.0	62
63	Structure of the Recombinant N-Terminal Lobe of Human Lactoferrin at 2.0 Å Resolution. <i>Journal of Molecular Biology</i> , 1993, 232, 1084-1100.	2.0	83
64	Preliminary crystallographic studies of the amino terminal half of human lactoferrin in its iron-saturated and iron-free forms. <i>Journal of Molecular Biology</i> , 1992, 228, 973-974.	2.0	13