# 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 | Differential Targeting of Prosurvival Bcl-2 Proteins by Their BH3-Only Ligands Allows Complementary Apoptotic Function. Molecular Cell, 2005, 17, 393-403. | 4.5 | 1,639 |
| 2 | 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. | 7.7 | 1,149 |
| 3 | 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. | 1.6 | 484 |
| 4 | 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. | 3.3 | 397 |
| 5 | The Bcl-2-regulated apoptotic pathway. Journal of Cell Science, 2003, 116, 4053-4056. | 1.2 | 206 |
| 6 | TRAF2 Must Bind to Cellular Inhibitors of Apoptosis for Tumor Necrosis Factor (TNF) to Efficiently Activate NF-Î ºB and to Prevent TNF-induced Apoptosis. Journal of Biological Chemistry, 2009, 284, 35906-35915. | 1.6 | 202 |
| 7 | Bak Activation for Apoptosis Involves Oligomerization of Dimers via Their Î±6 Helices. Molecular Cell, 2009, 36, 696-703. | 4.5 | 200 |
| 8 | Solution Structure of Prosurvival Mcl-1 and Characterization of Its Binding by Proapoptotic BH3-only Ligands. Journal of Biological Chemistry, 2005, 280, 4738-4744. | 1.6 | 187 |
| 9 | 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. | 2.0 | 178 |
| 10 | RINGs hold the key to ubiquitin transfer. Trends in Biochemical Sciences, 2012, 37, 58-65. | 3.7 | 168 |
| 11 | Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat. Nature Structural Biology, 1999, 6, 648-651. | 9.7 | 165 |
| 12 | Structures of the cIAP2 RING Domain Reveal Conformational Changes Associated with Ubiquitin-conjugating Enzyme (E2) Recruitment. Journal of Biological Chemistry, 2008, 283, 31633-31640. | 1.6 | 153 |
| 13 | The structure of Bcl-w reveals a role for the C-terminal residues in modulating biological activity. EMBO Journal, 2003, 22, 1497-1507. | 3.5 | 151 |
| 14 | Birinapant, a Smac-Mimetic with Improved Tolerability for the Treatment of Solid Tumors and Hematological Malignancies. Journal of Medicinal Chemistry, 2014, 57, 3666-3677. | 2.9 | 146 |
| 15 | Smac Mimetics Activate the E3 Ligase Activity of cIAP1 Protein by Promoting RING Domain Dimerization. Journal of Biological Chemistry, 2011, 286, 17015-17028. | 1.6 | 142 |
| 16 | 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. | 3.3 | 133 |
| 17 | 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. | 2.3 | 124 |
| 18 | Proapoptotic BH3-only proteins trigger membrane integration of prosurvival Bcl-w and neutralize its activity. Journal of Cell Biology, 2003, 162, 877-888. | 2.3 | 104 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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. | 1.2 | 103 |
| 20 | Structural Plasticity Underpins Promiscuous Binding of the Prosurvival Protein A1. Structure, 2008, 16, 818-829. | 1.6 | 97 |
| 21 | CARD-Mediated Autoinhibition of cIAP1's E3 Ligase Activity Suppresses Cell Proliferation and Migration. Molecular Cell, 2011, 42, 569-583. | 4.5 | 89 |
| 22 | Structure of the Recombinant N-Terminal Lobe of Human Lactoferrin at 2Â·0 Ã... Resolution. Journal of Molecular Biology, 1993, 232, 1084-1100. | 2.0 | 83 |
| 23 | RING domain dimerization is essential for RNF4 function. Biochemical Journal, 2010, 431, 23-29. | 1.7 | 80 |
| 24 | Asymmetric Recruitment of cIAPs by TRAF2. Journal of Molecular Biology, 2010, 400, 8-15. | 2.0 | 72 |
| 25 | Intrinsically Disordered Proteins in Bcl-2 Regulated Apoptosis. International Journal of Molecular Sciences, 2010, 11, 1808-1824. | 1.8 | 69 |
| 26 | Localization of dynein light chains 1 and 2 and their pro-apoptotic ligands. Biochemical Journal, 2004, 377, 597-605. | 1.7 | 65 |
| 27 | Regulation of apoptosis: uncovering the binding determinants. Current Opinion in Structural Biology, 2005, 15, 690-699. | 2.6 | 63 |
| 28 | 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. | 2.0 | 62 |
| 29 | 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. | 2.0 | 50 |
| 30 | Regulation of ubiquitin transfer by XIAP, a dimeric RING E3 ligase. Biochemical Journal, 2013, 450, 629-638. | 1.7 | 50 |
| 31 | Reevaluation of Abscisic Acid-Binding Assays Shows That G-Protein-Coupled Receptor2 Does Not Bind Abscisic Acid. Plant Physiology, 2009, 150, 6-11. | 2.3 | 48 |
| 32 | Secondary ubiquitin-RING docking enhances Arkadia and Ark2C E3 ligase activity. Nature Structural and Molecular Biology, 2016, 23, 45-52. | 3.6 | 46 |
| 33 | The molecular basis of lysine 48 ubiquitin chain synthesis by Ube2K. Scientific Reports, 2015, 5, 16793. | 1.6 | 43 |
| 34 | IAPs: Modular regulators of cell signalling. Seminars in Cell and Developmental Biology, 2015, 39, 80-90. | 2.3 | 43 |
| 35 | The activity of TRAF RING homo- and heterodimers is regulated by zinc finger 1. Nature Communications, 2017, 8, 1788. | 5.8 | 42 |
| 36 | FCA does not bind abscisic acid. Nature, 2008, 456, E5-E6. | 13.7 | 40 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Solution Structure of Psb27 from Cyanobacterial Photosystem II,. Biochemistry, 2009, 48, 8771-8773. | 1.2 | 40 |
| 38 | The N-Terminal Extension of UBE2E Ubiquitin-Conjugating Enzymes Limits Chain Assembly. Journal of Molecular Biology, 2013, 425, 4099-4111. | 2.0 | 39 |
| 39 | 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. | 1.7 | 38 |
| 40 | 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. | 1.6 | 37 |
| 41 | A Direct Interaction with NEDD1 Regulates Î³-Tubulin Recruitment to the Centrosome. PLoS ONE, 2010, 5, e9618. | 1.1 | 36 |
| 42 | 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. | 1.2 | 34 |
| 43 | 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. | 2.0 | 29 |
| 44 | Noncovalent Ubiquitin Interactions Regulate the Catalytic Activity of Ubiquitin Writers. Trends in Biochemical Sciences, 2016, 41, 924-937. | 3.7 | 27 |
| 45 | A bidentate Polycomb Repressive-Deubiquitinase complex is required for efficient activity on nucleosomes. Nature Communications, 2018, 9, 3932. | 5.8 | 25 |
| 46 | The structure of Boo/Diva reveals a divergent Bcl-2 protein. Proteins: Structure, Function and Bioinformatics, 2010, 78, NA-NA. | 1.5 | 24 |
| 47 | 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. | 0.4 | 23 |
| 48 | 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. | 2.0 | 23 |
| 49 | The Structure and Ubiquitin Binding Properties of TRAF RING Heterodimers. Journal of Molecular Biology, 2021, 433, 166844. | 2.0 | 20 |
| 50 | Regulation of E2s: A Role for Additional Ubiquitin Binding Sites?. Journal of Molecular Biology, 2017, 429, 3430-3440. | 2.0 | 17 |
| 51 | 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. | 2.0 | 13 |
| 52 | 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. | 3.3 | 12 |
| 53 | Identification of Ubiquitin Variants That Inhibit the E2 Ubiquitin Conjugating Enzyme, Ube2k. ACS Chemical Biology, 2021, 16, 1745-1756. | 1.6 | 12 |
| 54 | Collaborative networks enable the rapid establishment of serological assays for SARS-CoV-2 during nationwide lockdown in New Zealand. PeerJ, 2020, 8, e9863. | 0.9 | 12 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | HtrAâ€”A Renaissance Protein. Structure, 2002, 10, 737-739. | 1.6 | 10 |
| 56 | 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 |
| 57 | The Ubiquitin-associated Domain of Cellular Inhibitor of Apoptosis Proteins Facilitates Ubiquitylation. Journal of Biological Chemistry, 2014, 289, 25721-25736. | 1.6 | 10 |
| 58 | The RING domain of RING Finger 11 ( RNF 11) protein binds Ubc13 and inhibits formation of polyubiquitin chains. FEBS Letters, 2018, 592, 1434-1444. | 1.3 | 9 |
| 59 | Ubiquitin and a charged loop regulate the ubiquitin E3 ligase activity of Ark2C. Nature Communications, 2022, 13, 1181. | 5.8 | 8 |
| 60 | E2 enzymes: lessons in ubiquitin transfer from XLID patients. Nature Chemical Biology, 2019, 15, 6-7. | 3.9 | 2 |
| 61 | Ubiquitin Variant Inhibitors Meet the Deubiquitinase USP15. Structure, 2019, 27, 564-565. | 1.6 | 1 |
| 62 | Solution structure of Mclâ€1 and its complexes. FASEB Journal, 2007, 21, A638. | 0.2 | 0 |
| 63 | Solution Structure and Physiological Requirements for Psb27 in Synechocystis sp. PCC 6803. Advanced Topics in Science and Technology in China, 2013, , 432-435. | 0.0 | 0 |
| 64 | Altered Domain Closure and Iron Binding in Lactoferrin Mutants. , 1997, , 25-38. | | 0 |