Danette L Daniels

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Modeling the CRL4A ligase complex to predict target protein ubiquitination induced by cereblon-recruiting PROTACs. Journal of Biological Chemistry, 2022, 298, 101653.	3.4	37
2	Degrading boundaries to break new ground in chemical biology. Current Research in Chemical Biology, 2022, 2, 100033.	2.9	1
3	The importance of cellular degradation kinetics for understanding mechanisms in targeted protein degradation. Chemical Society Reviews, 2022, 51, 6210-6221.	38.1	12
4	CDK Family PROTAC Profiling Reveals Distinct Kinetic Responses and Cell Cycle–Dependent Degradation of CDK2. SLAS Discovery, 2021, 26, 560-569.	2.7	21
5	Kinetic Detection of E3:PROTAC:Target Ternary Complexes Using NanoBRET Technology in Live Cells. Methods in Molecular Biology, 2021, 2365, 151-171.	0.9	8
6	Discovery and resistance mechanism of a selective CDK12 degrader. Nature Chemical Biology, 2021, 17, 675-683.	8.0	69
7	Translating PROTAC chemical series optimization into functional outcomes underlying BRD7 and BRD9 protein degradation. Current Research in Chemical Biology, 2021, 1, 100009.	2.9	11
8	Trivalent PROTACs enhance protein degradation via combined avidity and cooperativity. Nature Chemical Biology, 2021, 17, 1157-1167.	8.0	108
9	Targeted Protein Degradation Phenotypic Studies Using HaloTag CRISPR/Cas9 Endogenous Tagging Coupled with HaloPROTAC3. Current Protocols in Pharmacology, 2020, 91, e81.	4.0	21
10	Selective targeting of BD1 and BD2 of the BET proteins in cancer and immunoinflammation. Science, 2020, 368, 387-394.	12.6	274
11	High-Throughput Cellular Profiling of Targeted Protein Degradation Compounds using HiBiT CRISPR Cell Lines. Journal of Visualized Experiments, 2020, , .	0.3	10
12	Monitoring and deciphering protein degradation pathways inside cells. Drug Discovery Today: Technologies, 2019, 31, 61-68.	4.0	45
13	Iterative Design and Optimization of Initially Inactive Proteolysis Targeting Chimeras (PROTACs) Identify VZ185 as a Potent, Fast, and Selective von Hippel–Lindau (VHL) Based Dual Degrader Probe of BRD9 and BRD7. Journal of Medicinal Chemistry, 2019, 62, 699-726.	6.4	230
14	Quantitative Live-Cell Kinetic Degradation and Mechanistic Profiling of PROTAC Mode of Action. ACS Chemical Biology, 2018, 13, 2758-2770.	3.4	194
15	Selective Targeting of Bromodomains of the Bromodomain-PHD Fingers Family Impairs Osteoclast Differentiation. ACS Chemical Biology, 2017, 12, 2619-2630.	3.4	41
16	SONAR Discovers RNA-Binding Proteins from Analysis of Large-Scale Protein-Protein Interactomes. Molecular Cell, 2016, 64, 282-293.	9.7	155
17	Potent and selective bivalent inhibitors of BET bromodomains. Nature Chemical Biology, 2016, 12, 1097-1104.	8.0	109
18	Pharmacological Inhibition of the Histone Lysine Demethylase KDM1A Suppresses the Growth of Multiple Acute Myeloid Leukemia Subtypes. Cancer Research, 2016, 76, 1975-1988.	0.9	89

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19	Target engagement and drug residence time can be observed in living cells with BRET. Nature Communications, 2015, 6, 10091.	12.8	208
20	Phosphorylation of FADD by the kinase CK1α promotes KRAS ^{G12D} -induced lung cancer. Science Signaling, 2015, 8, ra9.	3.6	40
21	NanoBRET—A Novel BRET Platform for the Analysis of Protein–Protein Interactions. ACS Chemical Biology, 2015, 10, 1797-1804.	3.4	360
22	LP99: Discovery and Synthesis of the First Selective BRD7/9 Bromodomain Inhibitor. Angewandte Chemie - International Edition, 2015, 54, 6217-6221.	13.8	137
23	9 <i>H</i> -Purine Scaffold Reveals Induced-Fit Pocket Plasticity of the BRD9 Bromodomain. Journal of Medicinal Chemistry, 2015, 58, 2718-2736.	6.4	63
24	Generation of a Selective Small Molecule Inhibitor of the CBP/p300 Bromodomain for Leukemia Therapy. Cancer Research, 2015, 75, 5106-5119.	0.9	193
25	EZH2 Inhibitor Efficacy in Non-Hodgkin's Lymphoma Does Not Require Suppression of H3K27 Monomethylation. Chemistry and Biology, 2014, 21, 1463-1475.	6.0	128
26	Discovering Protein Interactions and Characterizing Protein Function Using HaloTag Technology. Journal of Visualized Experiments, 2014, , .	0.3	6
27	KDM4A Lysine Demethylase Induces Site-Specific Copy Gain and Rereplication of Regions Amplified in Tumors. Cell, 2013, 154, 541-555.	28.9	189
28	Isolation of Intracellular Protein – DNA Complexes Using HaloCHIP, an Antibody-Free Alternative to Chromatin Immunoprecipitation. Methods in Molecular Biology, 2013, 977, 111-124.	0.9	4
29	Structural Studies of Wnts and Identification of an LRP6 Binding Site. Structure, 2013, 21, 1235-1242.	3.3	73
30	HIF1A Employs CDK8-Mediator to Stimulate RNAPII Elongation in Response to Hypoxia. Cell, 2013, 153, 1327-1339.	28.9	300
31	TET2 and TET3 regulate GlcNAcylation and H3K4 methylation through OGT and SET1/COMPASS. EMBO Journal, 2013, 32, 645-655.	7.8	411
32	Development of a Dehalogenase-Based Protein Fusion Tag Capable of Rapid, Selective and Covalent Attachment to Customizable Ligands. Current Chemical Genomics, 2013, 6, 55-71.	2.0	107
33	Examining the Complexity of Human RNA Polymerase Complexes using HaloTag Technology Coupled to Label Free Quantitative Proteomics. Journal of Proteome Research, 2012, 11, 564-575.	3.7	27
34	Highly Efficient Protein and Complex Purification from Mammalian Cells Using the HaloTag® Technology. BioTechniques, 2011, 51, 276-277.	1.8	4
35	β-catenin directly displaces Groucho/TLE repressors from Tcf/Lef in Wnt-mediated transcription activation. Nature Structural and Molecular Biology, 2005, 12, 364-371.	8.2	476
36	ICAT Inhibits β-Catenin Binding to Tcf/Lef-Family Transcription Factors and the General Coactivator p300 Using Independent Structural Modules. Molecular Cell, 2002, 10, 573-584.	9.7	159

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37	β-catenin: molecular plasticity and drug design. Trends in Biochemical Sciences, 2001, 26, 672-678.	7.5	80
38	Crystal structure of the hCASK PDZ domain reveals the structural basis of class II PDZ domain target recognition. Nature Structural Biology, 1998, 5, 317-325.	9.7	172
39	Two Competing Pathways for Self-splicing by Group II Introns: A Quantitative Analysis ofin VitroReaction Rates and Products. Journal of Molecular Biology, 1996, 256, 31-49.	4.2	121