Frank Sicheri

List of Publications by Year
in descending order

63 papers	5,576 citations	147801 31 h-index	138484 58 g-index
66 all docs	66 docs citations	66 times ranked	9098 citing authors

#	Article	IF	Citations
1	Panel of Engineered Ubiquitin Variants Targeting the Family of Human Ubiquitin Interacting Motifs. ACS Chemical Biology, 2022, 17, 941-956.	3.4	5
2	A suite of in vitro and in vivo assays for monitoring the activity of the pseudokinase Bud32. Methods in Enzymology, 2022, 667, 729-773.	1.0	0
3	Firstâ€inâ€class Deubiquitylase Inhibitors Reveal New Enzyme Conformations. FASEB Journal, 2022, 36, .	0.5	0
4	Bora phosphorylation substitutes in trans for T-loop phosphorylation in Aurora A to promote mitotic entry. Nature Communications, 2021, 12, 1899.	12.8	18
5	Aurora A kinase activation: Different means to different ends. Journal of Cell Biology, 2021, 220, .	5.2	19
6	Comprehensive Assessment of the Relationship Between Siteâ^'2 Specificity and Helix Î±2 in the Erbin PDZ Domain. Journal of Molecular Biology, 2021, 433, 167115.	4.2	0
7	Bipartite binding of the N terminus of Skp2 to cyclin A. Structure, 2021, 29, 975-988.e5.	3.3	2
8	The structural and functional workings of KEOPS. Nucleic Acids Research, 2021, 49, 10818-10834.	14.5	23
9	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzymeâ€“ubiquitin complex. Science Advances, 2021, 7, eabi5797.	10.3	17
10	Structural and Functional Analysis of Ubiquitin-based Inhibitors That Target the Backsides of E2 Enzymes. Journal of Molecular Biology, 2020, 432, 952-966.	4.2	22
11	Comprehensive analysis of all evolutionary paths between two divergent PDZ domain specificities. Protein Science, 2020, 29, 433-442.	7.6	17
12	Persistence of serum and saliva antibody responses to SARS-CoV-2 spike antigens in COVID-19 patients. Science Immunology, 2020, 5, .	11.9	714
13	A phenolic small molecule inhibitor of RNase L prevents cell death from ADAR1 deficiency. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 24802-24812.	7.1	17
14	Functional characterization of a PROTAC directed against BRAF mutant V600E. Nature Chemical Biology, 2020, 16, 1170-1178.	8.0	80
15	A substrate binding model for the KEOPS tRNA modifying complex. Nature Communications, 2020, 11, 6233.	12.8	21
16	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. Structure, 2019, 27, 590-605.e5.	3.3	47
17	Rigidification Dramatically Improves Inhibitor Selectivity for RAF Kinases. ACS Medicinal Chemistry Letters, 2019, 10, 1074-1080.	2.8	10
18	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. Structure, 2019, 27, 1000-1012.e6.	3.3	10

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19	The ubiquitin interacting motifs of USP37 act on the proximal Ub of a di-Ub chain to enhance catalytic efficiency. Scientific Reports, 2019, 9, 4119.	3.3	11
20	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. Protein Science, 2019, 28, 848-856.	7.6	9
21	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. Journal of Molecular Biology, 2019, 431, 1160-1171.	4.2	6
22	OAS-RNase L innate immune pathway mediates the cytotoxicity of a DNA-demethylating drug. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5071-5076.	7.1	58
23	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. ELife, 2019, 8, .	6.0	36
24	Effects of rigidity on the selectivity of protein kinase inhibitors. European Journal of Medicinal Chemistry, 2018, 146, 519-528.	5.5	11
25	MEK drives BRAF activation through allosteric control of KSR proteins. Nature, 2018, 554, 549-553.	27.8	105
26	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. Nature Communications, 2018, 9, 3510.	12.8	75
27	Structural Basis for Auto-Inhibition of the NDR1 Kinase Domain by an Atypically Long Activation Segment. Structure, 2018, 26, 1101-1115.e6.	3.3	17
28	A Structure-Based Strategy for Engineering Selective Ubiquitin Variant Inhibitors of Skp1-Cul1-F-Box Ubiquitin Ligases. Structure, 2018, 26, 1226-1236.e3.	3.3	27
29	Metformin reduces liver glucose production by inhibition of fructose-1-6-bisphosphatase. Nature Medicine, 2018, 24, 1395-1406.	30.7	212
30	Mechanism of catalysis, E2 recognition, and autoinhibition for the IpaH family of bacterial E3 ubiquitin ligases. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1311-1316.	7.1	27
31	Structural and functional characterization of a ubiquitin variant engineered for tight and specific binding to an alphaâ€helical ubiquitin interacting motif. Protein Science, 2017, 26, 1060-1069.	7.6	20
32	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Communications, 2017, 8, 13943.	12.8	33
33	Inhibition of RAS function through targeting an allosteric regulatory site. Nature Chemical Biology, 2017, 13, 62-68.	8.0	237
34	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. Nucleic Acids Research, 2017, 45, 805-817.	14.5	49
35	Inhibition of SCF ubiquitin ligases by engineered ubiquitin variants that target the Cul1 binding site on the Skp1â€“F-box interface. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3527-3532.	7.1	61
36	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t⁶A biosynthesis. Nucleic Acids Research, 2016, 44, 6971-6980.	14.5	26

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37	Expression and purification of functional human glycogen synthase-1:glycogenin-1 complex in insect cells. Protein Expression and Purification, 2015, 108, 23-29.	1.3	12
38	Getting a handle on glycogen synthase â€“ Its interaction with glycogenin. Molecular Aspects of Medicine, 2015, 46, 63-69.	6.4	25
39	Baculovirus protein PK2 subverts eIF2Î± kinase function by mimicry of its kinase domain C-lobe. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4364-73.	7.1	14
40	Higher-Order Assembly of BRCC36â€“KIAA0157 Is Required for DUB Activity and Biological Function. Molecular Cell, 2015, 59, 970-983.	9.7	44
41	Crystal structure of a BRAF kinase domain monomer explains basis for allosteric regulation. Nature Structural and Molecular Biology, 2015, 22, 37-43.	8.2	121
42	Structural basis for the recruitment of glycogen synthase by glycogenin. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E2831-40.	7.1	43
43	Dimeric Structure of Pseudokinase RNase L Bound to 2-5A Reveals a Basis for Interferon-Induced Antiviral Activity. Molecular Cell, 2014, 53, 221-234.	9.7	123
44	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. Nature Chemical Biology, 2014, 10, 156-163.	8.0	81
45	Structure and mechanism of action of the hydroxyâ€“arylâ€“aldehyde class of IRE1 endoribonuclease inhibitors. Nature Communications, 2014, 5, 4202.	12.8	108
46	Dimerization-induced allostery in protein kinase regulation. Trends in Biochemical Sciences, 2014, 39, 475-486.	7.5	80
47	Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. Cellular Signalling, 2014, 26, 1825-1836.	3.6	16
48	A Strategy for Modulation of Enzymes in the Ubiquitin System. Science, 2013, 339, 590-595.	12.6	257
49	Inhibitors that stabilize a closed RAF kinase domain conformation induce dimerization. Nature Chemical Biology, 2013, 9, 428-436.	8.0	140
50	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. Nucleic Acids Research, 2013, 41, 6332-6346.	14.5	68
51	Conserved Structural Mechanisms for Autoinhibition in IpaH Ubiquitin Ligases. Journal of Biological Chemistry, 2012, 287, 268-275.	3.4	39
52	Structural basis for specificity of TGFÎ² family receptor small molecule inhibitors. Cellular Signalling, 2012, 24, 476-483.	3.6	50
53	An Allosteric Inhibitor of the Human Cdc34ÂUbiquitin-Conjugating Enzyme. Cell, 2011, 145, 1075-1087.	28.9	203
54	Putting the brakes on the unfolded protein response. Journal of Cell Biology, 2011, 193, 17-19.	5.2	6

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55	An allosteric inhibitor of substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Biotechnology, 2010, 28, 733-737.	17.5	136
56	A dimerization-dependent mechanism drives RAF catalytic activation. Nature, 2009, 461, 542-545.	27.8	420
57	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. Molecular Cell, 2008, 32, 259-275.	9.7	87
58	The Eukaryotic Protein Kinase Domain. , 2005, , 181-209.		2
59	Higher-Order Substrate Recognition of eIF2Î± by the RNA-Dependent Protein Kinase PKR. Cell, 2005, 122, 887-900.	28.9	351
60	Structural and biochemical characterization of the type III secretion chaperones CesT and SigE. Nature Structural Biology, 2001, 8, 1031-1036.	9.7	122
61	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. Nature, 2001, 414, 514-521.	27.8	710
62	The crystal structure of an Eph receptor SAM domain reveals a mechanism for modular dimerization. Nature Structural Biology, 1999, 6, 44-49.	9.7	229
63	Engineered SH2 Domains for Targeted Phosphoproteomics. ACS Chemical Biology, 0, , .	3.4	6