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	Persistence of serum and saliva antibody responses to SARS-CoV-2 spike antigens in COVID-19 patients. Science Immunology, 2020, 5, .	11.9	714
2	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. Nature, 2001, 414, 514-521.	27.8	710
3	A dimerization-dependent mechanism drives RAF catalytic activation. Nature, 2009, 461, 542-545.	27.8	420
4	Higher-Order Substrate Recognition of eIF2Î± by the RNA-Dependent Protein Kinase PKR. Cell, 2005, 122, 887-900.	28.9	351
5	A Strategy for Modulation of Enzymes in the Ubiquitin System. Science, 2013, 339, 590-595.	12.6	257
6	Inhibition of RAS function through targeting an allosteric regulatory site. Nature Chemical Biology, 2017, 13, 62-68.	8.0	237
7	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
8	Metformin reduces liver glucose production by inhibition of fructose-1-6-bisphosphatase. Nature Medicine, 2018, 24, 1395-1406.	30.7	212
9	An Allosteric Inhibitor of the Human Cdc34ÂUbiquitin-Conjugating Enzyme. Cell, 2011, 145, 1075-1087.	28.9	203
10	Inhibitors that stabilize a closed RAF kinase domain conformation induce dimerization. Nature Chemical Biology, 2013, 9, 428-436.	8.0	140
11	An allosteric inhibitor of substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Biotechnology, 2010, 28, 733-737.	17.5	136
12	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
13	Structural and biochemical characterization of the type III secretion chaperones CesT and SigE. Nature Structural Biology, 2001, 8, 1031-1036.	9.7	122
14	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
15	Structure and mechanism of action of the hydroxyâ€“arylâ€“aldehyde class of IRE1 endoribonuclease inhibitors. Nature Communications, 2014, 5, 4202.	12.8	108
16	MEK drives BRAF activation through allosteric control of KSR proteins. Nature, 2018, 554, 549-553.	27.8	105
17	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. Molecular Cell, 2008, 32, 259-275.	9.7	87
18	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. Nature Chemical Biology, 2014, 10, 156-163.	8.0	81

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19	Dimerization-induced allostery in protein kinase regulation. Trends in Biochemical Sciences, 2014, 39, 475-486.	7.5	80
20	Functional characterization of a PROTAC directed against BRAF mutant V600E. Nature Chemical Biology, 2020, 16, 1170-1178.	8.0	80
21	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. Nature Communications, 2018, 9, 3510.	12.8	75
22	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. Nucleic Acids Research, 2013, 41, 6332-6346.	14.5	68
23	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
24	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
25	Structural basis for specificity of TGFÎ² family receptor small molecule inhibitors. Cellular Signalling, 2012, 24, 476-483.	3.6	50
26	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
27	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. Structure, 2019, 27, 590-605.e5.	3.3	47
28	Higher-Order Assembly of BRCC36â€“KIAA0157 Is Required for DUB Activity and Biological Function. Molecular Cell, 2015, 59, 970-983.	9.7	44
29	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
30	Conserved Structural Mechanisms for Autoinhibition in IpaH Ubiquitin Ligases. Journal of Biological Chemistry, 2012, 287, 268-275.	3.4	39
31	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. ELife, 2019, 8, .	6.0	36
32	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. Nature Communications, 2017, 8, 13943.	12.8	33
33	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
34	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
35	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
36	Getting a handle on glycogen synthase â€“ Its interaction with glycogenin. Molecular Aspects of Medicine, 2015, 46, 63-69.	6.4	25

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37	The structural and functional workings of KEOPS. Nucleic Acids Research, 2021, 49, 10818-10834.	14.5	23
38	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
39	A substrate binding model for the KEOPS tRNA modifying complex. Nature Communications, 2020, 11, 6233.	12.8	21
40	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
41	Aurora A kinase activation: Different means to different ends. Journal of Cell Biology, 2021, 220, .	5.2	19
42	Bora phosphorylation substitutes in trans for T-loop phosphorylation in Aurora A to promote mitotic entry. Nature Communications, 2021, 12, 1899.	12.8	18
43	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
44	Comprehensive analysis of all evolutionary paths between two divergent PDZ domain specificities. Protein Science, 2020, 29, 433-442.	7.6	17
45	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
46	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzymeâ€“ubiquitin complex. Science Advances, 2021, 7, eabi5797.	10.3	17
47	Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. Cellular Signalling, 2014, 26, 1825-1836.	3.6	16
48	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
49	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
50	Effects of rigidity on the selectivity of protein kinase inhibitors. European Journal of Medicinal Chemistry, 2018, 146, 519-528.	5.5	11
51	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
52	Rigidification Dramatically Improves Inhibitor Selectivity for RAF Kinases. ACS Medicinal Chemistry Letters, 2019, 10, 1074-1080.	2.8	10
53	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. Structure, 2019, 27, 1000-1012.e6.	3.3	10
54	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. Protein Science, 2019, 28, 848-856.	7.6	9

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55	Putting the brakes on the unfolded protein response. Journal of Cell Biology, 2011, 193, 17-19.	5.2	6
56	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. Journal of Molecular Biology, 2019, 431, 1160-1171.	4.2	6
57	Engineered SH2 Domains for Targeted Phosphoproteomics. ACS Chemical Biology, 0, , .	3.4	6
58	Panel of Engineered Ubiquitin Variants Targeting the Family of Human Ubiquitin Interacting Motifs. ACS Chemical Biology, 2022, 17, 941-956.	3.4	5
59	The Eukaryotic Protein Kinase Domain. , 2005, , 181-209.		2
60	Bipartite binding of the N terminus of Skp2 to cyclin A. Structure, 2021, 29, 975-988.e5.	3.3	2
61	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
62	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
63	Firstâ€inâ€class Deubiquitylase Inhibitors Reveal New Enzyme Conformations. FASEB Journal, 2022, 36, .	0.5	0