

Frank Sicheri

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

5,576
citations

147566

31
h-index

138251

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. <i>Science Immunology</i> , 2020, 5, .	5.6	714
2	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. <i>Nature</i> , 2001, 414, 514-521.	13.7	710
3	A dimerization-dependent mechanism drives RAF catalytic activation. <i>Nature</i> , 2009, 461, 542-545.	13.7	420
4	Higher-Order Substrate Recognition of eIF2 γ by the RNA-Dependent Protein Kinase PKR. <i>Cell</i> , 2005, 122, 887-900.	13.5	351
5	A Strategy for Modulation of Enzymes in the Ubiquitin System. <i>Science</i> , 2013, 339, 590-595.	6.0	257
6	Inhibition of RAS function through targeting an allosteric regulatory site. <i>Nature Chemical Biology</i> , 2017, 13, 62-68.	3.9	237
7	The crystal structure of an Eph receptor SAM domain reveals a mechanism for modular dimerization. <i>Nature Structural Biology</i> , 1999, 6, 44-49.	9.7	229
8	Metformin reduces liver glucose production by inhibition of fructose-1-6-bisphosphatase. <i>Nature Medicine</i> , 2018, 24, 1395-1406.	15.2	212
9	An Allosteric Inhibitor of the Human Cdc34 Ubiquitin-Conjugating Enzyme. <i>Cell</i> , 2011, 145, 1075-1087.	13.5	203
10	Inhibitors that stabilize a closed RAF kinase domain conformation induce dimerization. <i>Nature Chemical Biology</i> , 2013, 9, 428-436.	3.9	140
11	An allosteric inhibitor of substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Biotechnology</i> , 2010, 28, 733-737.	9.4	136
12	Dimeric Structure of Pseudokinase RNase L Bound to 2-5A Reveals a Basis for Interferon-Induced Antiviral Activity. <i>Molecular Cell</i> , 2014, 53, 221-234.	4.5	123
13	Structural and biochemical characterization of the type III secretion chaperones CesT and SigE. <i>Nature Structural Biology</i> , 2001, 8, 1031-1036.	9.7	122
14	Crystal structure of a BRAF kinase domain monomer explains basis for allosteric regulation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 37-43.	3.6	121
15	Structure and mechanism of action of the hydroxyaryl aldehyde class of IRE1 endoribonuclease inhibitors. <i>Nature Communications</i> , 2014, 5, 4202.	5.8	108
16	MEK drives BRAF activation through allosteric control of KSR proteins. <i>Nature</i> , 2018, 554, 549-553.	13.7	105
17	Atomic Structure of the KEOPS Complex: An Ancient Protein Kinase-Containing Molecular Machine. <i>Molecular Cell</i> , 2008, 32, 259-275.	4.5	87
18	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. <i>Nature Chemical Biology</i> , 2014, 10, 156-163.	3.9	81

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19	Dimerization-induced allostery in protein kinase regulation. <i>Trends in Biochemical Sciences</i> , 2014, 39, 475-486.	3.7	80
20	Functional characterization of a PROTAC directed against BRAF mutant V600E. <i>Nature Chemical Biology</i> , 2020, 16, 1170-1178.	3.9	80
21	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. <i>Nature Communications</i> , 2018, 9, 3510.	5.8	75
22	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. <i>Nucleic Acids Research</i> , 2013, 41, 6332-6346.	6.5	68
23	Inhibition of SCF ubiquitin ligases by engineered ubiquitin variants that target the Cul1 binding site on the Skp1-F-box interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3527-3532.	3.3	61
24	OAS-RNase L innate immune pathway mediates the cytotoxicity of a DNA-demethylating drug. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 5071-5076.	3.3	58
25	Structural basis for specificity of TGF β family receptor small molecule inhibitors. <i>Cellular Signalling</i> , 2012, 24, 476-483.	1.7	50
26	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. <i>Nucleic Acids Research</i> , 2017, 45, 805-817.	6.5	49
27	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. <i>Structure</i> , 2019, 27, 590-605.e5.	1.6	47
28	Higher-Order Assembly of BRCC36-KIAA0157 Is Required for DUB Activity and Biological Function. <i>Molecular Cell</i> , 2015, 59, 970-983.	4.5	44
29	Structural basis for the recruitment of glycogen synthase by glycogenin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2831-40.	3.3	43
30	Conserved Structural Mechanisms for Autoinhibition in IpaH Ubiquitin Ligases. <i>Journal of Biological Chemistry</i> , 2012, 287, 268-275.	1.6	39
31	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , 2019, 8, .	2.8	36
32	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCFCdc4 ubiquitin ligase. <i>Nature Communications</i> , 2017, 8, 13943.	5.8	33
33	Mechanism of catalysis, E2 recognition, and autoinhibition for the IpaH family of bacterial E3 ubiquitin ligases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1311-1316.	3.3	27
34	A Structure-Based Strategy for Engineering Selective Ubiquitin Variant Inhibitors of Skp1-Cul1-F-Box Ubiquitin Ligases. <i>Structure</i> , 2018, 26, 1226-1236.e3.	1.6	27
35	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t ^{sup>6</sup>A biosynthesis. <i>Nucleic Acids Research</i>, 2016, 44, 6971-6980.}	6.5	26
36	Getting a handle on glycogen synthase - Its interaction with glycogenin. <i>Molecular Aspects of Medicine</i> , 2015, 46, 63-69.	2.7	25

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37	The structural and functional workings of KEOPS. <i>Nucleic Acids Research</i> , 2021, 49, 10818-10834.	6.5	23
38	Structural and Functional Analysis of Ubiquitin-based Inhibitors That Target the Backsides of E2 Enzymes. <i>Journal of Molecular Biology</i> , 2020, 432, 952-966.	2.0	22
39	A substrate binding model for the KEOPS tRNA modifying complex. <i>Nature Communications</i> , 2020, 11, 6233.	5.8	21
40	Structural and functional characterization of a ubiquitin variant engineered for tight and specific binding to an alpha-helical ubiquitin interacting motif. <i>Protein Science</i> , 2017, 26, 1060-1069.	3.1	20
41	Aurora A kinase activation: Different means to different ends. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	19
42	Bora phosphorylation substitutes in trans for T-loop phosphorylation in Aurora A to promote mitotic entry. <i>Nature Communications</i> , 2021, 12, 1899.	5.8	18
43	Structural Basis for Auto-Inhibition of the NDR1 Kinase Domain by an Atypically Long Activation Segment. <i>Structure</i> , 2018, 26, 1101-1115.e6.	1.6	17
44	Comprehensive analysis of all evolutionary paths between two divergent PDZ domain specificities. <i>Protein Science</i> , 2020, 29, 433-442.	3.1	17
45	A phenolic small molecule inhibitor of RNase L prevents cell death from ADAR1 deficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 24802-24812.	3.3	17
46	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzyme-ubiquitin complex. <i>Science Advances</i> , 2021, 7, eabi5797.	4.7	17
47	Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. <i>Cellular Signalling</i> , 2014, 26, 1825-1836.	1.7	16
48	Baculovirus protein PK2 subverts eIF2 γ kinase function by mimicry of its kinase domain C-lobe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4364-73.	3.3	14
49	Expression and purification of functional human glycogen synthase-1:glycogenin-1 complex in insect cells. <i>Protein Expression and Purification</i> , 2015, 108, 23-29.	0.6	12
50	Effects of rigidity on the selectivity of protein kinase inhibitors. <i>European Journal of Medicinal Chemistry</i> , 2018, 146, 519-528.	2.6	11
51	The ubiquitin interacting motifs of USP37 act on the proximal Ub of a di-Ub chain to enhance catalytic efficiency. <i>Scientific Reports</i> , 2019, 9, 4119.	1.6	11
52	Rigidification Dramatically Improves Inhibitor Selectivity for RAF Kinases. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1074-1080.	1.3	10
53	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. <i>Structure</i> , 2019, 27, 1000-1012.e6.	1.6	10
54	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. <i>Protein Science</i> , 2019, 28, 848-856.	3.1	9

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55	Putting the brakes on the unfolded protein response. <i>Journal of Cell Biology</i> , 2011, 193, 17-19.	2.3	6
56	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. <i>Journal of Molecular Biology</i> , 2019, 431, 1160-1171.	2.0	6
57	Engineered SH2 Domains for Targeted Phosphoproteomics. <i>ACS Chemical Biology</i> , 0, , .	1.6	6
58	Panel of Engineered Ubiquitin Variants Targeting the Family of Human Ubiquitin Interacting Motifs. <i>ACS Chemical Biology</i> , 2022, 17, 941-956.	1.6	5
59	The Eukaryotic Protein Kinase Domain. , 2005, , 181-209.		2
60	Bipartite binding of the N terminus of Skp2 to cyclin A. <i>Structure</i> , 2021, 29, 975-988.e5.	1.6	2
61	Comprehensive Assessment of the Relationship Between Site ² Specificity and Helix ± 2 in the Erbin PDZ Domain. <i>Journal of Molecular Biology</i> , 2021, 433, 167115.	2.0	0
62	A suite of in vitro and in vivo assays for monitoring the activity of the pseudokinase Bud32. <i>Methods in Enzymology</i> , 2022, 667, 729-773.	0.4	0
63	First-class Deubiquitylase Inhibitors Reveal New Enzyme Conformations. <i>FASEB Journal</i> , 2022, 36, .	0.2	0