

# Frank Sicheiri

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

62

papers

4,081

citations

30

h-index

63

g-index

66

ext. papers

4,971

ext. citations

15.2

avg, IF

4.98

L-index

#	Paper	IF	Citations
62	Panel of Engineered Ubiquitin Variants Targeting the Family of Human Ubiquitin Interacting Motifs.. <i>ACS Chemical Biology</i> , <b>2022</b> ,	4.9	1
61	A suite of in vitro and in vivo assays for monitoring the activity of the pseudokinase Bud32.. <i>Methods in Enzymology</i> , <b>2022</b> , 667, 729-773	1.7	
60	The structural and functional workings of KEOPS. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, 10818-10834	20.1	4
59	Identification and optimization of molecular glue compounds that inhibit a noncovalent E2 enzyme-ubiquitin complex. <i>Science Advances</i> , <b>2021</b> , 7, eabi5797	14.3	4
58	Bora phosphorylation substitutes in trans for T-loop phosphorylation in Aurora A to promote mitotic entry. <i>Nature Communications</i> , <b>2021</b> , 12, 1899	17.4	8
57	Aurora A kinase activation: Different means to different ends. <i>Journal of Cell Biology</i> , <b>2021</b> , 220,	7.3	4
56	Comprehensive Assessment of the Relationship Between Site Specificity and Helix $\alpha$ in the Erbin PDZ Domain. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 167115	6.5	
55	Bipartite binding of the N terminus of Skp2 to cyclin A. <i>Structure</i> , <b>2021</b> , 29, 975-988.e5	5.2	0
54	A substrate binding model for the KEOPS tRNA modifying complex. <i>Nature Communications</i> , <b>2020</b> , 11, 6233	17.4	6
53	Comprehensive analysis of all evolutionary paths between two divergent PDZ domain specificities. <i>Protein Science</i> , <b>2020</b> , 29, 433-442	6.3	6
52	Persistence of serum and saliva antibody responses to SARS-CoV-2 spike antigens in COVID-19 patients. <i>Science Immunology</i> , <b>2020</b> , 5,	28	396
51	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> , <b>2020</b> , 117, 24802-24812	11.5	3
50	Functional characterization of a PROTAC directed against BRAF mutant V600E. <i>Nature Chemical Biology</i> , <b>2020</b> , 16, 1170-1178	11.7	34
49	Structural and Functional Analysis of Ubiquitin-based Inhibitors That Target the Backsides of E2 Enzymes. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 952-966	6.5	12
48	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. <i>Structure</i> , <b>2019</b> , 27, 590-605.e5	5.2	32
47	Rigidification Dramatically Improves Inhibitor Selectivity for RAF Kinases. <i>ACS Medicinal Chemistry Letters</i> , <b>2019</b> , 10, 1074-1080	4.3	7
46	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. <i>Structure</i> , <b>2019</b> , 27, 1000-1012.e6	5.2	5

45	The ubiquitin interacting motifs of USP37 act on the proximal Ub of a di-Ub chain to enhance catalytic efficiency. <i>Scientific Reports</i> , <b>2019</b> , 9, 4119	4.9	7
44	Dimerization of a ubiquitin variant leads to high affinity interactions with a ubiquitin interacting motif. <i>Protein Science</i> , <b>2019</b> , 28, 848-856	6.3	7
43	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 1160-1171	6.5	2
42	Robust cullin-RING ligase function is established by a multiplicity of poly-ubiquitylation pathways. <i>ELife</i> , <b>2019</b> , 8,	8.9	20
41	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> , <b>2019</b> , 116, 5071-5076	11.5	32
40	Effects of rigidity on the selectivity of protein kinase inhibitors. <i>European Journal of Medicinal Chemistry</i> , <b>2018</b> , 146, 519-528	6.8	8
39	MEK drives BRAF activation through allosteric control of KSR proteins. <i>Nature</i> , <b>2018</b> , 554, 549-553	50.4	64
38	A Structure-Based Strategy for Engineering Selective Ubiquitin Variant Inhibitors of Skp1-Cul1-F-Box Ubiquitin Ligases. <i>Structure</i> , <b>2018</b> , 26, 1226-1236.e3	5.2	15
37	Metformin reduces liver glucose production by inhibition of fructose-1-6-bisphosphatase. <i>Nature Medicine</i> , <b>2018</b> , 24, 1395-1406	50.5	113
36	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. <i>Nature Communications</i> , <b>2018</b> , 9, 3510	17.4	37
35	Structural Basis for Auto-Inhibition of the NDR1 Kinase Domain by an Atypically Long Activation Segment. <i>Structure</i> , <b>2018</b> , 26, 1101-1115.e6	5.2	12
34	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> , <b>2017</b> , 114, 1311-1316	11.5	14
33	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> , <b>2017</b> , 26, 1060-1069	6.3	17
32	An allosteric conduit facilitates dynamic multisite substrate recognition by the SCF ubiquitin ligase. <i>Nature Communications</i> , <b>2017</b> , 8, 13943	17.4	28
31	Inhibition of RAS function through targeting an allosteric regulatory site. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 62-68	11.7	177
30	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 805-817	20.1	31
29	Structural and functional characterization of KEOPS dimerization by Pcc1 and its role in t6A biosynthesis. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 6971-80	20.1	17
28	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> , <b>2016</b> , 113, 3527-32	11.5	47

27	Getting a handle on glycogen synthase - Its interaction with glycogenin. <i>Molecular Aspects of Medicine</i> , <b>2015</b> , 46, 63-9	16.7	15
26	Baculovirus protein PK2 subverts eIF2 $\alpha$ 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> , <b>2015</b> , 112, E4364-73	11.5	11
25	Higher-Order Assembly of BRCC36-KIAA0157 Is Required for DUB Activity and Biological Function. <i>Molecular Cell</i> , <b>2015</b> , 59, 970-83	17.6	31
24	Crystal structure of a BRAF kinase domain monomer explains basis for allosteric regulation. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 37-43	17.6	94
23	Expression and purification of functional human glycogen synthase-1:glycogenin-1 complex in insect cells. <i>Protein Expression and Purification</i> , <b>2015</b> , 108, 23-29	2	5
22	E2 enzyme inhibition by stabilization of a low-affinity interface with ubiquitin. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 156-163	11.7	58
21	Structure and mechanism of action of the hydroxy-aryl-aldehyde class of IRE1 endoribonuclease inhibitors. <i>Nature Communications</i> , <b>2014</b> , 5, 4202	17.4	78
20	Dimerization-induced allostery in protein kinase regulation. <i>Trends in Biochemical Sciences</i> , <b>2014</b> , 39, 475-86	10.3	65
19	Structural basis of Rad53 kinase activation by dimerization and activation segment exchange. <i>Cellular Signalling</i> , <b>2014</b> , 26, 1825-36	4.9	10
18	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> , <b>2014</b> , 111, E2831-40	11.5	33
17	Dimeric structure of pseudokinase RNase L bound to 2-5A reveals a basis for interferon-induced antiviral activity. <i>Molecular Cell</i> , <b>2014</b> , 53, 221-34	17.6	90
16	A strategy for modulation of enzymes in the ubiquitin system. <i>Science</i> , <b>2013</b> , 339, 590-5	33.3	199
15	Inhibitors that stabilize a closed RAF kinase domain conformation induce dimerization. <i>Nature Chemical Biology</i> , <b>2013</b> , 9, 428-36	11.7	120
14	Reconstitution and characterization of eukaryotic N6-threonylcarbamoylation of tRNA using a minimal enzyme system. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 6332-46	20.1	50
13	Structural basis for specificity of TGF $\beta$ family receptor small molecule inhibitors. <i>Cellular Signalling</i> , <b>2012</b> , 24, 476-483	4.9	33
12	Conserved structural mechanisms for autoinhibition in IpaH ubiquitin ligases. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 268-275	5.4	33
11	An allosteric inhibitor of the human Cdc34 ubiquitin-conjugating enzyme. <i>Cell</i> , <b>2011</b> , 145, 1075-87	56.2	172
10	Putting the brakes on the unfolded protein response. <i>Journal of Cell Biology</i> , <b>2011</b> , 193, 17-9	7.3	6

9	An allosteric inhibitor of substrate recognition by the SCF(Cdc4) ubiquitin ligase. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 733-7	44.5	118
8	A dimerization-dependent mechanism drives RAF catalytic activation. <i>Nature</i> , <b>2009</b> , 461, 542-5	50.4	345
7	Atomic structure of the KEOPS complex: an ancient protein kinase-containing molecular machine. <i>Molecular Cell</i> , <b>2008</b> , 32, 259-75	17.6	72
6	Higher-order substrate recognition of eIF2alpha by the RNA-dependent protein kinase PKR. <i>Cell</i> , <b>2005</b> , 122, 887-900	56.2	291
5	The Eukaryotic Protein Kinase Domain <b>2005</b> , 181-209		2
4	Structural and biochemical characterization of the type III secretion chaperones CseT and SigE. <i>Nature Structural Biology</i> , <b>2001</b> , 8, 1031-6		112
3	Multisite phosphorylation of a CDK inhibitor sets a threshold for the onset of DNA replication. <i>Nature</i> , <b>2001</b> , 414, 514-21	50.4	639
2	The crystal structure of an Eph receptor SAM domain reveals a mechanism for modular dimerization. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 44-9		199
1	Mucosal versus systemic antibody responses to SARS-CoV-2 antigens in COVID-19 patients		30