Igor Kurinov

List of Publications by Year
in descending order

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24 papers	1,016 citations	516710 16 h-index	642732 23 g-index
26 all docs	26 docs citations	26 times ranked	1748 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	Structural and biochemical analysis of human ADP-ribosyl-acceptor hydrolase 3 reveals the basis of metal selectivity and different roles for the two magnesium ions. Journal of Biological Chemistry, 2021, 296, 100692.	3.4	1
3	Crystal structure of human PACRG in complex with MEIG1 reveals roles in axoneme formation and tubulin binding. Structure, 2021, 29, 572-586.e6.	3.3	19
4	Bipartite binding of the N terminus of Skp2 to cyclin A. Structure, 2021, 29, 975-988.e5.	3.3	2
5	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
6	Functional characterization of a PROTAC directed against BRAF mutant V600E. Nature Chemical Biology, 2020, 16, 1170-1178.	8.0	80
7	Conformation-specific inhibitors of activated Ras GTPases reveal limited Ras dependency of patient-derived cancer organoids. Journal of Biological Chemistry, 2020, 295, 4526-4540.	3.4	19
8	Rigidification Dramatically Improves Inhibitor Selectivity for RAF Kinases. ACS Medicinal Chemistry Letters, 2019, 10, 1074-1080.	2.8	10
9	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. Structure, 2019, 27, 1000-1012.e6.	3.3	10
10	Structural basis for auxiliary subunit KCTD16 regulation of the GABA _B receptor. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8370-8379.	7.1	32
11	Structural Insights into the Induced-fit Inhibition of Fascin by a Small-Molecule Inhibitor. Journal of Molecular Biology, 2018, 430, 1324-1335.	4.2	28
12	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
13	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
14	Structure of human ADP-ribosyl-acceptor hydrolase 3 bound to ADP-ribose reveals a conformational switch that enables specific substrate recognition. Journal of Biological Chemistry, 2018, 293, 12350-12359.	3.4	27
15	Crystal structure of the human Polϊμ B-subunit in complex with the C-terminal domain of the catalytic subunit. Journal of Biological Chemistry, 2017, 292, 15717-15730.	3.4	30
16	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
17	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
18	Structural mechanism of ligand activation in human calcium-sensing receptor. ELife, 2016, 5, .	6.0	189

#	Article	IF	Citations
19	Higher-Order Assembly of BRCC36â€“KIAA0157 Is Required for DUB Activity and Biological Function. Molecular Cell, 2015, 59, 970-983.	9.7	44
20	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
21	Structures of CRISPR Cas3 offer mechanistic insights into Cascade-activated DNA unwinding and degradation. Nature Structural and Molecular Biology, 2014, 21, 771-777.	8.2	167
22	Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. Molecular Cell, 2014, 56, 246-260.	9.7	98
23	Crystal Structure of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated Csn2 Protein Revealed Ca2+-dependent Double-stranded DNA Binding Activity*. Journal of Biological Chemistry, 2011, 286, 30759-30768.	3.4	49
24	Engineered SH2 Domains for Targeted Phosphoproteomics. ACS Chemical Biology, 0, , .	3.4	6