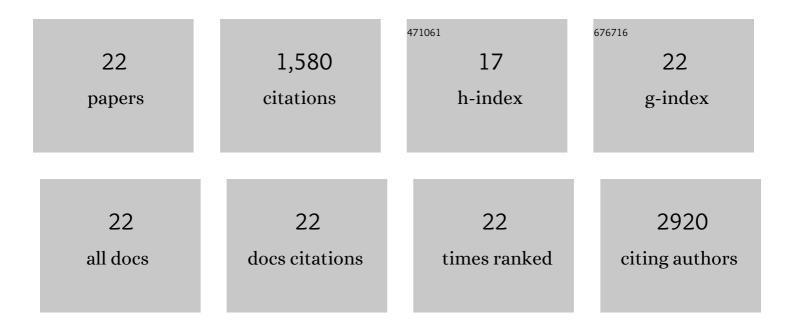
## Zhizhi Wang

List of Publications by Year in descending order

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<u> 7нігні Шліс</u>

#	Article	IF	CITATIONS
1	Inactivation of PP2A by a recurrent mutation drives resistance to MEK inhibitors. Oncogene, 2020, 39, 703-717.	2.6	24
2	Crystal structure of human LDB1 in complex with SSBP2. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1042-1048.	3.3	18
3	Selective PP2A Enhancement through Biased Heterotrimer Stabilization. Cell, 2020, 181, 688-701.e16.	13.5	107
4	Crystal structure of the LUFS domain of human singleâ€stranded DNA binding Protein 2 (SSBP2). Protein Science, 2019, 28, 788-793.	3.1	8
5	The Highly Recurrent PP2A Aα-Subunit Mutation P179R Alters Protein Structure and Impairs PP2A Enzyme Function to Promote Endometrial Tumorigenesis. Cancer Research, 2019, 79, 4242-4257.	0.4	37
6	Crystal structure of a membrane-bound O-acyltransferase. Nature, 2018, 562, 286-290.	13.7	87
7	Identification of ICAT as an APC Inhibitor, Revealing Wnt-Dependent Inhibition of APC-Axin Interaction. Molecular Cell, 2018, 72, 37-47.e4.	4.5	24
8	Biochemical and Biophysical Assays of PAR-WWE Domain Interactions and Production of iso-ADPr for PAR-Binding Analysis. Methods in Molecular Biology, 2018, 1813, 65-73.	0.4	3
9	Oncoprotein <scp>CIP</scp> 2A is stabilized via interaction with tumor suppressor <scp>PP</scp> 2A/B56. EMBO Reports, 2017, 18, 437-450.	2.0	84
10	Small molecule Photoregulin3 prevents retinal degeneration in the RhoP23H mouse model of retinitis pigmentosa. ELife, 2017, 6, .	2.8	19
11	Activation of tumor suppressor protein PP2A inhibits KRAS-driven tumor growth. Journal of Clinical Investigation, 2017, 127, 2081-2090.	3.9	155
12	Crystal structure of a tankyrase 1–telomere repeat factor 1 complex. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 320-327.	0.4	19
13	Crystal structure of a PP2A B56-BubR1 complex and its implications for PP2A substrate recruitment and localization. Protein and Cell, 2016, 7, 516-526.	4.8	70
14	Structural Basis of the Interaction between Tuberous Sclerosis Complex 1 (TSC1) and Tre2-Bub2-Cdc16 Domain Family Member 7 (TBC1D7). Journal of Biological Chemistry, 2016, 291, 8591-8601.	1.6	31
15	Structural basis of the Norrin-Frizzled 4 interaction. Cell Research, 2015, 25, 1078-1081.	5.7	33
16	Allosteric activation of the RNF146 ubiquitin ligase by a poly(ADP-ribosyl)ation signal. Nature, 2015, 517, 223-226.	13.7	177
17	Crystallographic and Biochemical Analysis of the Mouse Poly(ADP-Ribose) Glycohydrolase. PLoS ONE, 2014, 9, e86010.	1.1	24
18	MeCP2 Suppresses Nuclear MicroRNA Processing and Dendritic Growth by Regulating the DGCR8/Drosha Complex. Developmental Cell, 2014, 28, 547-560.	3.1	211

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#	Article	IF	CITATIONS
19	Crystal structure of the yeast TSC1 core domain and implications for tuberous sclerosis pathological mutations. Nature Communications, 2013, 4, 2135.	5.8	24
20	Recognition of the <i>iso</i> -ADP-ribose moiety in poly(ADP-ribose) by WWE domains suggests a general mechanism for poly(ADP-ribosyl)ation-dependent ubiquitination. Genes and Development, 2012, 26, 235-240.	2.7	205
21	Robust design and optimization of retroaldol enzymes. Protein Science, 2012, 21, 717-726.	3.1	137
22	Streptavidin and its biotin complex at atomic resolution. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 813-821.	2.5	83