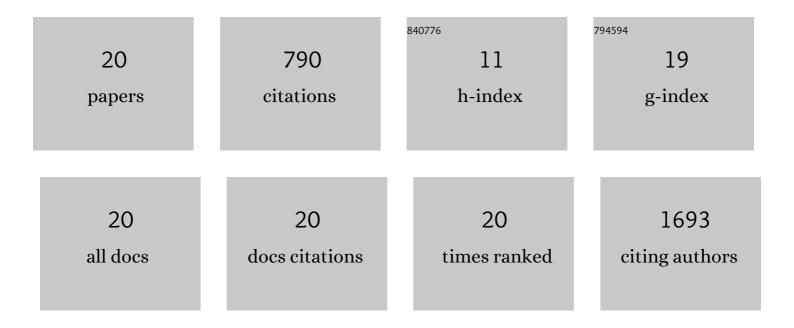
## Sheng Ye

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structure-based discovery of Middle East respiratory syndrome coronavirus fusion inhibitor. Nature Communications, 2014, 5, 3067.	12.8	324
2	Structural basis of ligand binding modes at the neuropeptide YY1 receptor. Nature, 2018, 556, 520-524.	27.8	100
3	Munc18 and Munc13 serve as a functional template to orchestrate neuronal SNARE complex assembly. Nature Communications, 2019, 10, 69.	12.8	80
4	BubR1 phosphorylates CENP-E as a switch enabling the transition from lateral association to end-on capture of spindle microtubules. Cell Research, 2019, 29, 562-578.	12.0	46
5	Improved Pharmacological and Structural Properties of HIV Fusion Inhibitor AP3 over Enfuvirtide: Highlighting Advantages of Artificial Peptide Strategy. Scientific Reports, 2015, 5, 13028.	3.3	33
6	Characterization by high-resolution crystal structure analysis of a triple-helix region of human collagen type III with potent cell adhesion activity. Biochemical and Biophysical Research Communications, 2019, 508, 1018-1023.	2.1	33
7	Crystal structure of kindlin-2 PH domain reveals a conformational transition for its membrane anchoring and regulation of integrin activation. Protein and Cell, 2012, 3, 434-440.	11.0	32
8	Creating an Artificial Tail Anchor as a Novel Strategy To Enhance the Potency of Peptide-Based HIV Fusion Inhibitors. Journal of Virology, 2017, 91, .	3.4	25
9	A critical epitope in CD147 facilitates memory CD4+ T-cell hyper-activation in rheumatoid arthritis. Cellular and Molecular Immunology, 2019, 16, 568-579.	10.5	25
10	Structure of iridoid synthase in complex with NADP + /8-oxogeranial reveals the structural basis of its substrate specificity. Journal of Structural Biology, 2016, 194, 224-230.	2.8	16
11	Rational improvement of gp41-targeting HIV-1 fusion inhibitors: an innovatively designed lle-Asp-Leu tail with alternative conformations. Scientific Reports, 2016, 6, 31983.	3.3	12
12	Structure of Escherichia coli Arginyl-tRNA Synthetase in Complex with tRNAArg: Pivotal Role of the D-loop. Journal of Molecular Biology, 2018, 430, 1590-1606.	4.2	12
13	Crystal Structure of Refolding Fusion Core of Lassa Virus GP2 and Design of Lassa Virus Fusion Inhibitors. Frontiers in Microbiology, 2019, 10, 1829.	3.5	11
14	Junctional and somatic hypermutation-induced CX4C motif is critical for the recognition of a highly conserved epitope on HCV E2 by a human broadly neutralizing antibody. Cellular and Molecular Immunology, 2021, 18, 675-685.	10.5	10
15	The crystal structure of ORP3 reveals the conservative PI4P binding pattern. Biochemical and Biophysical Research Communications, 2020, 529, 1005-1010.	2.1	9
16	Structure of the DNA-binding domain of human myelin-gene regulatory factor reveals its potential protein-DNA recognition mode. Journal of Structural Biology, 2018, 203, 170-178.	2.8	8
17	Structure of thrombospondin type 3 repeats in bacterial outer membrane protein A reveals its intra-repeat disulfide bond-dependent calcium-binding capability. Cell Calcium, 2017, 66, 78-89.	2.4	7
18	Structure of a prokaryotic SEFIR domain reveals two novel SEFIR-SEFIR interaction modes. Journal of Structural Biology, 2018, 203, 81-89.	2.8	4

#	Article	IF	CITATIONS
19	Structure of a double-domain phosphagen kinase reveals an asymmetric arrangement of the tandem domains. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 779-789.	2.5	3
20	Crystallization and preliminary X-ray analysis of SNR 141. Science Bulletin, 1997, 42, 957-959.	1.7	0