

Ke Shi

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.

71
papers

3,521
citations

21
h-index

59
g-index

74
ext. papers

4,657
ext. citations

9.6
avg, IF

5.97
L-index

#	Paper	IF	Citations
71	A Structure-based Design Approach for Generating High Affinity BRD4 D1-Selective Chemical Probes.. <i>Journal of Medicinal Chemistry</i> , 2022 ,	8.3	1
70	Structure and dynamics of SARS-CoV-2 proofreading exoribonuclease ExoN.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	9
69	Cryo-EM structure of the EBV ribonucleotide reductase BORF2 and mechanism of APOBEC3B inhibition.. <i>Science Advances</i> , 2022 , 8, eabm2827	14.3	1
68	Mechanisms of SARS-CoV-2 neutralization by shark variable new antigen receptors elucidated through X-ray crystallography.. <i>Nature Communications</i> , 2021 , 12, 7325	17.4	4
67	Structural basis for recognition of distinct deaminated DNA lesions by endonuclease Q. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
66	Cryo-EM structure of the Rous sarcoma virus octameric cleaved synaptic complex intasome. <i>Communications Biology</i> , 2021 , 4, 330	6.7	4
65	Soluble Methane Monooxygenase Component Interactions Monitored by F NMR. <i>Biochemistry</i> , 2021 , 60, 1995-2010	3.2	1
64	Selective N-Terminal BET Bromodomain Inhibitors by Targeting Non-Conserved Residues and Structured Water Displacement**. <i>Angewandte Chemie</i> , 2021 , 133, 1240-1246	3.6	
63	Selective N-Terminal BET Bromodomain Inhibitors by Targeting Non-Conserved Residues and Structured Water Displacement*. <i>Angewandte Chemie - International Edition</i> , 2021 , 60, 1220-1226	16.4	13
62	Molecular underpinnings of ssDNA specificity by Rep HUH-endonucleases and implications for HUH-tag multiplexing and engineering. <i>Nucleic Acids Research</i> , 2021 , 49, 1046-1064	20.1	6
61	4-Methyl-1,2,3-Triazoles as -Acetyl-Lysine Mimics Afford Potent BET Bromodomain Inhibitors with Improved Selectivity. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 10497-10511	8.3	3
60	The development of - as anti-SARS-CoV-2 nanobody drug candidates. <i>ELife</i> , 2021 , 10,	8.9	10
59	New Design Rules for Developing Potent Cell-Active Inhibitors of the Nucleosome Remodeling Factor (NURF) via BPTF Bromodomain Inhibition. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 13902-13917	8.3	0
58	Structural basis of receptor recognition by SARS-CoV-2. <i>Nature</i> , 2020 , 581, 221-224	50.4	2085
57	Structural Characterization of the Helicase nsp10 Encoded by Porcine Reproductive and Respiratory Syndrome Virus. <i>Journal of Virology</i> , 2020 , 94,	6.6	2
56	Structural basis for receptor recognition by the novel coronavirus from Wuhan 2020 ,		14
55	DNA aptamers against the DUX4 protein reveal novel therapeutic implications for FSHD. <i>FASEB Journal</i> , 2020 , 34, 4573-4590	0.9	10

54	Structural insights into the promiscuous DNA binding and broad substrate selectivity of fowlpox virus resolvase. <i>Scientific Reports</i> , 2020 , 10, 393	4.9	1
53	Structural basis of host protein hijacking in human T-cell leukemia virus integration. <i>Nature Communications</i> , 2020 , 11, 3121	17.4	16
52	Structural basis of superinfection exclusion by bacteriophage T4 Spackle. <i>Communications Biology</i> , 2020 , 3, 691	6.7	8
51	Structural Studies of the OB3b Soluble Methane Monooxygenase Hydroxylase and Regulatory Component Complex Reveal a Transient Substrate Tunnel. <i>Biochemistry</i> , 2020 , 59, 2946-2961	3.2	13
50	Crystal structure of bacteriophage T4 Spackle as determined by native SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020 , 76, 899-904	5.5	2
49	Enhancing subtilisin thermostability through a modified normalized B-factor analysis and loop-grafting strategy. <i>Journal of Biological Chemistry</i> , 2019 , 294, 18398-18407	5.4	8
48	Selectivity, ligand deconstruction, and cellular activity analysis of a BPTF bromodomain inhibitor. <i>Organic and Biomolecular Chemistry</i> , 2019 , 17, 2020-2027	3.9	15
47	Insight into subtilisin E-S7 cleavage pattern based on crystal structure and hydrolysates peptide analysis. <i>Biochemical and Biophysical Research Communications</i> , 2019 , 512, 623-628	3.4	1
46	Crystal structures of Moorella thermoacetica cyanuric acid hydrolase reveal conformational flexibility and asymmetry important for catalysis. <i>PLoS ONE</i> , 2019 , 14, e0216979	3.7	1
45	The Role of RNA in HIV-1 Vif-Mediated Degradation of APOBEC3H. <i>Journal of Molecular Biology</i> , 2019 , 431, 5019-5031	6.5	2
44	Crystal structure of the Wheat dwarf virus Rep domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 744-749	1.1	3
43	Crystal structure of lipid A disaccharide synthase LpxB from Escherichia coli. <i>Nature Communications</i> , 2018 , 9, 377	17.4	14
42	The Antiviral and Cancer Genomic DNA Deaminase APOBEC3H Is Regulated by an RNA-Mediated Dimerization Mechanism. <i>Molecular Cell</i> , 2018 , 69, 75-86.e9	17.6	47
41	Structures of chaperone-substrate complexes docked onto the export gate in a type III secretion system. <i>Nature Communications</i> , 2018 , 9, 1773	17.4	41
40	The substrate-binding cap of the UDP-diacetylglucosamine pyrophosphatase LpxH is highly flexible, enabling facile substrate binding and product release. <i>Journal of Biological Chemistry</i> , 2018 , 293, 7969-7981	5.4	10
39	New fluorescence-based high-throughput screening assay for small molecule inhibitors of tyrosyl-DNA phosphodiesterase 2 (TDP2). <i>European Journal of Pharmaceutical Sciences</i> , 2018 , 118, 67-79	5.1	11
38	Dimerization of Coronavirus nsp9 with Diverse Modes Enhances Its Nucleic Acid Binding Affinity. <i>Journal of Virology</i> , 2018 , 92,	6.6	42
37	Comment on structural basis of DUX4/IGH-driven transactivation. <i>Leukemia</i> , 2018 , 32, 2090-2092	10.7	1

36	T4 DNA ligase structure reveals a prototypical ATP-dependent ligase with a unique mode of sliding clamp interaction. <i>Nucleic Acids Research</i> , 2018 , 46, 10474-10488	20.1	24
35	Crystal Structure of the Double Homeodomain of DUX4 in Complex with DNA. <i>Cell Reports</i> , 2018 , 25, 2955-2962.e3	10.6	14
34	Crystal Structure of Cdc45 Suggests a Conformational Switch that May Regulate DNA Replication. <i>iScience</i> , 2018 , 3, 102-109	6.1	1
33	A C-terminal "Tail" Region in the Rous Sarcoma Virus Integrase Provides High Plasticity of Functional Integrase Oligomerization during Intasome Assembly. <i>Journal of Biological Chemistry</i> , 2017 , 292, 5018-5030	5.4	4
32	Five Fatty Aldehyde Dehydrogenase Enzymes from <i>Marinobacter</i> and <i>Acinetobacter</i> spp. and Structural Insights into the Aldehyde Binding Pocket. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	3
31	Structural basis for targeted DNA cytosine deamination and mutagenesis by APOBEC3A and APOBEC3B. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 131-139	17.6	141
30	Conformational Switch Regulates the DNA Cytosine Deaminase Activity of Human APOBEC3B. <i>Scientific Reports</i> , 2017 , 7, 17415	4.9	21
29	Crystal structure of the Rous sarcoma virus intasome. <i>Nature</i> , 2016 , 530, 362-6	50.4	65
28	Structures of Rpn1 T1:Rad23 and hRpn13:hPLIC2 Reveal Distinct Binding Mechanisms between Substrate Receptors and Shuttle Factors of the Proteasome. <i>Structure</i> , 2016 , 24, 1257-1270	5.2	46
27	1.92 Angstrom Zinc-Free APOBEC3F Catalytic Domain Crystal Structure. <i>Journal of Molecular Biology</i> , 2016 , 428, 2307-2316	6.5	30
26	Crystal Structure of the DNA Deaminase APOBEC3B Catalytic Domain. <i>Journal of Biological Chemistry</i> , 2015 , 290, 28120-28130	5.4	71
25	Cyanuric acid hydrolase from <i>Azorhizobium caulinodans</i> ORS 571: crystal structure and insights into a new class of Ser-Lys dyad proteins. <i>PLoS ONE</i> , 2014 , 9, e99349	3.7	8
24	Structural asymmetry in the <i>Thermus thermophilus</i> RuvC dimer suggests a basis for sequential strand cleavages during Holliday junction resolution. <i>Nucleic Acids Research</i> , 2013 , 41, 648-56	20.1	26
23	Crystallization and preliminary X-ray diffraction studies of cyanuric acid hydrolase from <i>Azorhizobium caulinodans</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013 , 69, 880-3		3
22	An enzyme-catalyzed multistep DNA refolding mechanism in hairpin telomere formation. <i>PLoS Biology</i> , 2013 , 11, e1001472	9.7	12
21	A possible role for the asymmetric C-terminal domain dimer of Rous sarcoma virus integrase in viral DNA binding. <i>PLoS ONE</i> , 2013 , 8, e56892	3.7	10
20	Structural basis for recognition of 5Tphosphotyrosine adducts by Tdp2. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1372-7	17.6	48
19	Linear chromosome-generating system of <i>Agrobacterium tumefaciens</i> C58: protelomerase generates and protects hairpin ends. <i>Journal of Biological Chemistry</i> , 2012 , 287, 25551-63	5.4	16

18	Structure of a mutant β -toxin from <i>Staphylococcus aureus</i> reveals domain swapping and conformational flexibility. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011 , 67, 438-41		2
17	Structure and biological activities of beta toxin from <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2007 , 189, 8719-26	3.5	103
16	Base-tetrad swapping results in dimerization of RNA quadruplexes: implications for formation of the i-motif RNA octaplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 3130-4	11.5	38
15	Crystal structure of an RNA quadruplex containing inosine tetrad: implications for the roles of NH ₂ group in purine tetrads. <i>Journal of Molecular Biology</i> , 2006 , 363, 451-9	6.5	37
14	Molecular basis for control of conjugation by bacterial pheromone and inhibitor peptides. <i>Molecular Microbiology</i> , 2006 , 62, 958-69	4.1	69
13	Structure of peptide sex pheromone receptor PrgX and PrgX/pheromone complexes and regulation of conjugation in <i>Enterococcus faecalis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 18596-601	11.5	102
12	Solution structure of 2T5Td(G4C4). Relevance to topological restrictions and nature's choice of phosphodiester links. <i>FEBS Journal</i> , 2004 , 271, 2956-66		13
11	Synthesis, Purification and Crystallization of Guanine-rich RNA Oligonucleotides. <i>Biological Procedures Online</i> , 2004 , 6, 257-262	8.3	5
10	Structures of d(Gm5)CGm5CGCGC and d(GCGCGm5CGm5C): effects of methylation on alternating DNA octamers. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 61-5		2
9	The crystal structure of an alternating RNA heptamer r(GUAUACA) forming a six base-paired duplex with 3T _{end} adenine overhangs. <i>Nucleic Acids Research</i> , 2003 , 31, 1392-7	20.1	
8	Crystal structure of an RNA purine-rich tetraplex containing adenine tetrads: implications for specific binding in RNA tetraplexes. <i>Structure</i> , 2003 , 11, 815-23	5.2	71
7	An eight-stranded helical fragment in RNA crystal structure: implications for tetraplex interaction. <i>Structure</i> , 2003 , 11, 825-31	5.2	43
6	Crystal structure of a bulged RNA tetraplex at 1.1 Å resolution: implications for a novel binding site in RNA tetraplex. <i>Structure</i> , 2003 , 11, 1423-30	5.2	45
5	Structure of a B-form DNA/RNA chimera (dC)(rG)d(ATCG) complexed with daunomycin at 1.5 Å resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 1377-83		4
4	Structure of the 1:1 netropsin-decamer d(CCIICICCI) ₂ complex with a single bound netropsin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002 , 58, 601-6		4
3	The crystal structure of the octamer [r(guauaca)dC] ₂ with six Watson-Crick base-pairs and two 3T _{end} overhang residues. <i>Journal of Molecular Biology</i> , 2000 , 299, 113-22	6.5	10
2	Crystal Structure of an RNA Duplex [r(gugcaca)dC] ₂ with 3T _{end} Dinucleoside Overhangs Forming a Superhelix. <i>Journal of Biomolecular Structure and Dynamics</i> , 2000 , 17 Suppl 1, 189-94	3.6	3
1	Crystal structure of an RNA duplex r(G GCGC CC) ₂ with non-adjacent G*U base pairs. <i>Nucleic Acids Research</i> , 1999 , 27, 2196-201	20.1	25

