

Dinshaw J Patel

List of Publications by Year in descending order

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140
papers

18,890
citations

17440

63
h-index

13771

129
g-index

149
all docs

149
docs citations

149
times ranked

20911
citing authors

#	ARTICLE	IF	CITATIONS
1	How chromatin-binding modules interpret histone modifications: lessons from professional pocket pickers. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1025-1040.	8.2	1,288
2	Human telomere, oncogenic promoter and 5'-UTR G-quadruplexes: diverse higher order DNA and RNA targets for cancer therapeutics. <i>Nucleic Acids Research</i> , 2007, 35, 7429-7455.	14.5	812
3	Cyclic [G(2â€²,5â€²) pA(3â€²,5â€²) p] Is the Metazoan Second Messenger Produced by DNA-Activated Cyclic GMP-AMP Synthase. <i>Cell</i> , 2013, 153, 1094-1107.	28.9	795
4	DNA methylation pathways and their crosstalk with histone methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 519-532.	37.0	779
5	Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 64-72.	8.2	690
6	Structural basis for overhang-specific small interfering RNA recognition by the PAZ domain. <i>Nature</i> , 2004, 429, 318-322.	27.8	647
7	Structure of an argonaute silencing complex with a seed-containing guide DNA and target RNA duplex. <i>Nature</i> , 2008, 456, 921-926.	27.8	512
8	Nucleation, propagation and cleavage of target RNAs in Ago silencing complexes. <i>Nature</i> , 2009, 461, 754-761.	27.8	483
9	Structure of the guide-strand-containing argonaute silencing complex. <i>Nature</i> , 2008, 456, 209-213.	27.8	481
10	PRMT5-mediated methylation of histone H4R3 recruits DNMT3A, coupling histone and DNA methylation in gene silencing. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 304-311.	8.2	451
11	Dual Binding of Chromomethylase Domains to H3K9me2-Containing Nucleosomes Directs DNA Methylation in Plants. <i>Cell</i> , 2012, 151, 167-180.	28.9	446
12	Histone chaperone networks shaping chromatin function. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 141-158.	37.0	401
13	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 743-753.	8.2	400
14	DNA-guided DNA interference by a prokaryotic Argonaute. <i>Nature</i> , 2014, 507, 258-261.	27.8	373
15	Structure of DNMT1-DNA Complex Reveals a Role for Autoinhibition in Maintenance DNA Methylation. <i>Science</i> , 2011, 331, 1036-1040.	12.6	363
16	The BAH domain of ORC1 links H4K20me2 to DNA replication licensing and Meierâ€™Gorlin syndrome. <i>Nature</i> , 2012, 484, 115-119.	27.8	314
17	Structure of yeast Argonaute with guide RNA. <i>Nature</i> , 2012, 486, 368-374.	27.8	314
18	Readout of Epigenetic Modifications. <i>Annual Review of Biochemistry</i> , 2013, 82, 81-118.	11.1	285

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19	Yng1 PHD Finger Binding to H3 Trimethylated at K4 Promotes NuA3 HAT Activity at K14 of H3 and Transcription at a Subset of Targeted ORFs. <i>Molecular Cell</i> , 2006, 24, 785-796.	9.7	283
20	Structure-Based Mechanistic Insights into DNMT1-Mediated Maintenance DNA Methylation. <i>Science</i> , 2012, 335, 709-712.	12.6	283
21	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014, 507, 124-128.	27.8	271
22	A Poised Chromatin Platform for TGF- β Access to Master Regulators. <i>Cell</i> , 2011, 147, 1511-1524.	28.9	251
23	Molecular Mechanism of Action of Plant DRM De Novo DNA Methyltransferases. <i>Cell</i> , 2014, 157, 1050-1060.	28.9	245
24	Uridylation by TUT4 and TUT7 Marks mRNA for Degradation. <i>Cell</i> , 2014, 159, 1365-1376.	28.9	243
25	<i>RNA-Puzzles</i> : A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	3.5	241
26	Polycomb-like proteins link the PRC2 complex to CpG islands. <i>Nature</i> , 2017, 549, 287-291.	27.8	238
27	An H3K36 Methylation-Engaging Tudor Motif of Polycomb-like Proteins Mediates PRC2 Complex Targeting. <i>Molecular Cell</i> , 2013, 49, 571-582.	9.7	221
28	DAXX envelops a histone H3-H4 dimer for H3.3-specific recognition. <i>Nature</i> , 2012, 491, 560-565.	27.8	220
29	Small molecule inhibition of cGAS reduces interferon expression in primary macrophages from autoimmune mice. <i>Nature Communications</i> , 2017, 8, 750.	12.8	202
30	Structure-based cleavage mechanism of <i>Thermus thermophilus</i> Argonaute DNA guide strand-mediated DNA target cleavage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 652-657.	7.1	194
31	A unique binding mode enables MCM2 to chaperone histones H3-H4 at replication forks. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 618-626.	8.2	192
32	Mechanism of DNA Methylation-Directed Histone Methylation by KRYPTONITE. <i>Molecular Cell</i> , 2014, 55, 495-504.	9.7	186
33	Type V CRISPR-Cas Cpf1 endonuclease employs a unique mechanism for crRNA-mediated target DNA recognition. <i>Cell Research</i> , 2016, 26, 901-913.	12.0	180
34	H4K20me0 marks post-replicative chromatin and recruits the TONSL-MMS22L DNA repair complex. <i>Nature</i> , 2016, 534, 714-718.	27.8	172
35	PHD Finger Recognition of Unmodified Histone H3R2 Links UHRF1 to Regulation of Euchromatic Gene Expression. <i>Molecular Cell</i> , 2011, 43, 275-284.	9.7	170
36	Crystal structure reveals specific recognition of a G-quadruplex RNA by a β -turn in the RGG motif of FMRP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5391-400.	7.1	168

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37	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
38	Cryo-EM Structures Reveal Mechanism and Inhibition of DNA Targeting by a CRISPR-Cas Surveillance Complex. <i>Cell</i> , 2017, 171, 414-426.e12.	28.9	158
39	Inhibition Mechanism of an Anti-CRISPR Suppressor AcrIIA4 Targeting SpyCas9. <i>Molecular Cell</i> , 2017, 67, 117-127.e5.	9.7	143
40	Development of human cGAS-specific small-molecule inhibitors for repression of dsDNA-triggered interferon expression. <i>Nature Communications</i> , 2019, 10, 2261.	12.8	134
41	Human cGAS catalytic domain has an additional DNA-binding interface that enhances enzymatic activity and liquid-phase condensation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11946-11955.	7.1	129
42	Cutoff Suppresses RNA Polymerase II Termination to Ensure Expression of piRNA Precursors. <i>Molecular Cell</i> , 2016, 63, 97-109.	9.7	116
43	A Phosphate-Binding Pocket within the Platform-PAZ-Connector Helix Cassette of Human Dicer. <i>Molecular Cell</i> , 2014, 53, 606-616.	9.7	111
44	N6-Methyladenosine on mRNA facilitates a phase-separated nuclear body that suppresses myeloid leukemic differentiation. <i>Cancer Cell</i> , 2021, 39, 958-972.e8.	16.8	108
45	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
46	c-di-AMP binds the ydaO riboswitch in two pseudo-symmetry-related pockets. <i>Nature Chemical Biology</i> , 2014, 10, 780-786.	8.0	98
47	Aub and Ago3 Are Recruited to Nuage through Two Mechanisms to Form a Ping-Pong Complex Assembled by Krimper. <i>Molecular Cell</i> , 2015, 59, 564-575.	9.7	98
48	<scp>TUT</scp> 7 controls the fate of precursor micro <scp>RNA</scp> s by using three different uridylation mechanisms. <i>EMBO Journal</i> , 2015, 34, 1801-1815.	7.8	97
49	Small-molecule targeting of MUSASHI RNA-binding activity in acute myeloid leukemia. <i>Nature Communications</i> , 2019, 10, 2691.	12.8	93
50	Structural basis for piRNA 2'-O-methylated 3'-end recognition by Piwi PAZ (Piwi/Argonaute/Zwille) domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 903-910.	7.1	91
51	Eukaryote-Specific Insertion Elements Control Human ARGONAUTE Slicer Activity. <i>Cell Reports</i> , 2013, 3, 1893-1900.	6.4	91
52	CRISPR-Cas III-A Csm6 CARF Domain Is a Ring Nuclease Triggering Stepwise cA4 Cleavage with ApA>p Formation Terminating RNase Activity. <i>Molecular Cell</i> , 2019, 75, 944-956.e6.	9.7	90
53	REC114 Partner ANKRD31 Controls Number, Timing, and Location of Meiotic DNA Breaks. <i>Molecular Cell</i> , 2019, 74, 1053-1068.e8.	9.7	89
54	Binding-Pocket and Lid-Region Substitutions Render Human STING Sensitive to the Species-Specific Drug DMXAA. <i>Cell Reports</i> , 2014, 8, 1668-1676.	6.4	87

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55	Adenylation of Maternally Inherited MicroRNAs by Wispy. <i>Molecular Cell</i> , 2014, 56, 696-707.	9.7	87
56	Structural Basis for Molecular Discrimination by a 3â€²,3â€²-cGAMP Sensing Riboswitch. <i>Cell Reports</i> , 2015, 11, 1-12.	6.4	87
57	Molecular basis of nucleosomal H3K36 methylation by NSD methyltransferases. <i>Nature</i> , 2021, 590, 498-503.	27.8	85
58	In-line alignment and Mg ²⁺ coordination at the cleavage site of the env22 twister ribozyme. <i>Nature Communications</i> , 2014, 5, 5534.	12.8	84
59	Structural and mechanistic insights into ATRX-dependent and -independent functions of the histone chaperone DAXX. <i>Nature Communications</i> , 2017, 8, 1193.	12.8	84
60	A molecular threading mechanism underlies Jumonji lysine demethylase KDM2A regulation of methylated H3K36. <i>Genes and Development</i> , 2014, 28, 1758-1771.	5.9	83
61	A Structural Perspective on Readout of Epigenetic Histone and DNA Methylation Marks. <i>Cold Spring Harbor Perspectives in Biology</i> , 2016, 8, a018754.	5.5	79
62	The PZP Domain of AF10 Senses Unmodified H3K27 to Regulate DOT1L-Mediated Methylation of H3K79. <i>Molecular Cell</i> , 2015, 60, 319-327.	9.7	78
63	Pistol ribozyme adopts a pseudoknot fold facilitating site-specific in-line cleavage. <i>Nature Chemical Biology</i> , 2016, 12, 702-708.	8.0	78
64	Type III-A CRISPR-Cas Csm Complexes: Assembly, Periodic RNA Cleavage, DNase Activity Regulation, and Autoimmunity. <i>Molecular Cell</i> , 2019, 73, 264-277.e5.	9.7	77
65	A phage-encoded anti-CRISPR enables complete evasion of type VI-A CRISPR-Cas immunity. <i>Science</i> , 2020, 369, 54-59.	12.6	77
66	The Card1 nuclease provides defence during type III CRISPR immunity. <i>Nature</i> , 2021, 590, 624-629.	27.8	76
67	The nascent RNA binding complex SFINX licenses piRNA-guided heterochromatin formation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 720-731.	8.2	75
68	Structure and function of the bacterial decapping enzyme NudC. <i>Nature Chemical Biology</i> , 2016, 12, 730-734.	8.0	74
69	DNA-driven condensation assembles the meiotic DNA break machinery. <i>Nature</i> , 2021, 592, 144-149.	27.8	71
70	Arabidopsis Accelerated Cell Death 11, ACD11, Is a Ceramide-1-Phosphate Transfer Protein and Intermediary Regulator of Phytoceramide Levels. <i>Cell Reports</i> , 2014, 6, 388-399.	6.4	69
71	Solution Structure of the Aminofluorene [AF]-Intercalated Conformer of the syn-[AF]-C8-dG Adduct Opposite dC in a DNA Duplex. <i>Biochemistry</i> , 1998, 37, 81-94.	2.5	68
72	<i>In vitro</i> antiviral activity of the anti-HCV drugs daclatasvir and sofosbuvir against SARS-CoV-2, the aetiological agent of COVID-19. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1874-1885.	3.0	65

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73	TRF2 binds branched DNA to safeguard telomere integrity. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 734-742.	8.2	63
74	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021, 12, 2490.	12.8	63
75	Solution Structure of the Aminofluorene [AF]-External Conformer of the anti-[AF]-C8-dG Adduct Opposite dC in a DNA Duplex. <i>Biochemistry</i> , 1998, 37, 95-106.	2.5	62
76	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18439-18447.	7.1	62
77	Structure-based mechanistic insights into catalysis by small self-cleaving ribozymes. <i>Current Opinion in Chemical Biology</i> , 2017, 41, 71-83.	6.1	56
78	Structure-based functional mechanisms and biotechnology applications of anti-CRISPR proteins. <i>Nature Reviews Molecular Cell Biology</i> , 2021, 22, 563-579.	37.0	56
79	Solution Conformation of the N-(Deoxyguanosin-8-yl)-1-aminopyrene ([AP]dG) Adduct Opposite dC in a DNA Duplex. <i>Biochemistry</i> , 1996, 35, 12659-12670.	2.5	55
80	A Mini-Twister Variant and Impact of Residues/Cations on the Phosphodiester Cleavage of this Ribozyme Class. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 15128-15133.	13.8	51
81	Structural and Dynamic Basis for Low-Affinity, High-Selectivity Binding of L-Glutamine by the Glutamine Riboswitch. <i>Cell Reports</i> , 2015, 13, 1800-1813.	6.4	50
82	Structure-function studies of nucleocytoplasmic transport of retroviral genomic RNA by mRNA export factor TAP. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 990-998.	8.2	47
83	Accommodation of Helical Imperfections in <i>Rhodobacter sphaeroides</i> Argonaute Ternary Complexes with Guide RNA and Target DNA. <i>Cell Reports</i> , 2018, 24, 453-462.	6.4	47
84	Structure-function studies of histone H3/H4 tetramer maintenance during transcription by chaperone Spt2. <i>Genes and Development</i> , 2015, 29, 1326-1340.	5.9	46
85	The CENP-T/W complex is a binding partner of the histone chaperone FACT. <i>Genes and Development</i> , 2016, 30, 1313-1326.	5.9	45
86	Structural basis underlying CAC RNA recognition by the RRM domain of dimeric RNA-binding protein RBPMS. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e1.	5.7	42
87	Mouse MORC3 is a GHKL ATPase that localizes to H3K4me3 marked chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5108-16.	7.1	41
88	Combination of antiviral drugs inhibits SARS-CoV-2 polymerase and exonuclease and demonstrates COVID-19 therapeutic potential in viral cell culture. <i>Communications Biology</i> , 2022, 5, 154.	4.4	40
89	Second Messenger cA4 Formation within the Composite Csm1 Palm Pocket of Type III-A CRISPR-Cas Csm Complex and Its Release Path. <i>Molecular Cell</i> , 2019, 75, 933-943.e6.	9.7	37
90	Control of a neuronal morphology program by an RNA-binding zinc finger protein, Unkempt. <i>Genes and Development</i> , 2015, 29, 501-512.	5.9	35

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91	Integrative analysis reveals unique structural and functional features of the Smc5/6 complex. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	35
92	Structural basis for self-cleavage prevention by tag:anti-tag pairing complementarity in type VI Cas13 CRISPR systems. Molecular Cell, 2021, 81, 1100-1115.e5.	9.7	34
93	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. Molecular Cell, 2021, 81, 2533-2548.e9.	9.7	31
94	Structural basis of phosphatidylcholine recognition by the C2 domain of cytosolic phospholipase A2. eLife, 2019, 8, .	6.0	31
95	Global RNA Fold and Molecular Recognition for a pfl Riboswitch Bound to ZMP, a Master Regulator of One-Carbon Metabolism. Structure, 2015, 23, 1375-1381.	3.3	30
96	Sphingolipid transfer proteins defined by the GLTP-fold. Quarterly Reviews of Biophysics, 2015, 48, 281-322.	5.7	30
97	Structure-based insights into self-cleavage by a four-way junctional twister-sister ribozyme. Nature Communications, 2017, 8, 1180.	12.8	30
98	Structure-function insights into the initial step of DNA integration by a CRISPR-Cas Transposon complex. Cell Research, 2020, 30, 182-184.	12.0	30
99	Atom-specific Mutagenesis Reveals Structural and Catalytic Roles for an Active Site Adenosine and Hydrated Mg ²⁺ in Pistol Ribozymes. Angewandte Chemie - International Edition, 2017, 56, 15954-15958.	13.8	29
100	Structure/cleavage-based insights into helical perturbations at bulge sites within T. thermophilus Argonaute silencing complexes. Nucleic Acids Research, 2017, 45, 9149-9163.	14.5	29
101	Glycolipid Acquisition by Human Glycolipid Transfer Protein Dramatically Alters Intrinsic Tryptophan Fluorescence. Journal of Biological Chemistry, 2009, 284, 13620-13628.	3.4	28
102	Hatchet ribozyme structure and implications for cleavage mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10783-10791.	7.1	28
103	Structural biology-based insights into combinatorial readout and crosstalk among epigenetic marks. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2014, 1839, 719-727.	1.9	27
104	Structural basis underlying viral hijacking of a histone chaperone complex. Nature Communications, 2016, 7, 12707.	12.8	27
105	Cryo-EM structure of DNA-bound Smc5/6 reveals DNA clamping enabled by multi-subunit conformational changes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	27
106	Crucial Roles of Two Hydrated Mg ²⁺ Ions in Reaction Catalysis of the Pistol Ribozyme. Angewandte Chemie - International Edition, 2020, 59, 2837-2843.	13.8	24
107	Recognition of distinct RNA motifs by the clustered CCCH zinc fingers of neuronal protein Unkempt. Nature Structural and Molecular Biology, 2016, 23, 16-23.	8.2	23
108	Molecular principles of Piwi-mediated cotranscriptional silencing through the dimeric SFiNX complex. Genes and Development, 2021, 35, 392-409.	5.9	23

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109	Phosphatidylserine Stimulates Ceramide 1-Phosphate (C1P) Intermembrane Transfer by C1P Transfer Proteins. <i>Journal of Biological Chemistry</i> , 2017, 292, 2531-2541.	3.4	20
110	Transcriptional elongation factor Paf1 core complex adopts a spirally wrapped solenoidal topology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9998-10003.	7.1	20
111	Structural Basis for the Unique Multivalent Readout of Unmodified H3 Tail by Arabidopsis ORC1b BAH-PHD Cassette. <i>Structure</i> , 2016, 24, 486-494.	3.3	19
112	How α -Helical Motifs Form Functionally Diverse Lipid-Binding Compartments. <i>Annual Review of Biochemistry</i> , 2017, 86, 609-636.	11.1	19
113	CasX: a new and small CRISPR gene-editing protein. <i>Cell Research</i> , 2019, 29, 345-346.	12.0	19
114	Panoramix SUMOylation on chromatin connects the piRNA pathway to the cellular heterochromatin machinery. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 130-142.	8.2	19
115	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. <i>PLoS Genetics</i> , 2020, 16, e1008422.	3.5	17
116	Structures and single-molecule analysis of bacterial motor nuclease AdnAB illuminate the mechanism of DNA double-strand break resection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24507-24516.	7.1	16
117	Molecular mechanisms of assembly and TRIP13-mediated remodeling of the human Shieldin complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2024512118.	7.1	16
118	The transcriptional regulator HDP1 controls expansion of the inner membrane complex during early sexual differentiation of malaria parasites. <i>Nature Microbiology</i> , 2022, 7, 289-299.	13.3	15
119	Distinct structural bases for sequence-specific DNA binding by mammalian BEN domain proteins. <i>Genes and Development</i> , 2022, 36, 225-240.	5.9	13
120	Binding of guide piRNA triggers methylation of the unstructured N-terminal region of Aub leading to assembly of the piRNA amplification complex. <i>Nature Communications</i> , 2021, 12, 4061.	12.8	11
121	Structural insights into DNMT5-mediated ATP-dependent high-fidelity epigenome maintenance. <i>Molecular Cell</i> , 2022, 82, 1186-1198.e6.	9.7	11
122	Structural analyses of 4-phosphate adaptor protein 2 yield mechanistic insights into sphingolipid recognition by the glycolipid transfer protein family. <i>Journal of Biological Chemistry</i> , 2018, 293, 16709-16723.	3.4	9
123	Structure-function analysis of microRNA 3'-end trimming by Nibbler. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30370-30379.	7.1	9
124	Ceramide-1-phosphate transfer protein (CPTP) regulation by phosphoinositides. <i>Journal of Biological Chemistry</i> , 2021, 296, 100600.	3.4	8
125	V-cGAPs: attenuators of β -cGAMP signaling. <i>Cell Research</i> , 2015, 25, 529-530.	12.0	5
126	New CRISPR-Cas systems discovered. <i>Cell Research</i> , 2017, 27, 313-314.	12.0	4

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127	Atom-specific Mutagenesis Reveals Structural and Catalytic Roles for an Active-Site Adenosine and Hydrated Mg ²⁺ in Pistol Ribozymes. <i>Angewandte Chemie</i> , 2017, 129, 16170-16174.	2.0	4
128	Oligomeric quaternary structure of <i>Escherichia coli</i> and <i>Mycobacterium smegmatis</i> Lhr helicases is nucleated by a novel C-terminal domain composed of five winged-helix modules. <i>Nucleic Acids Research</i> , 2021, 49, 3876-3887.	14.5	4
129	Ceramide-1-Phosphate Transfer Protein Promotes Sphingolipid Reorientation Needed for Binding during Membrane Interaction. <i>Journal of Lipid Research</i> , 2021, , 100151.	4.2	4
130	Structure-activity relationships at a nucleobase-stacking tryptophan required for chemomechanical coupling in the DNA resecting motor-nuclease AdnAB. <i>Nucleic Acids Research</i> , 2022, 50, 952-961.	14.5	2
131	Complete pairing not needed. <i>Science</i> , 2014, 346, 542-543.	12.6	1
132	Keeping innate immune response in check: when cGAS meets the nucleosome. <i>Cell Research</i> , 2020, 30, 1055-1056.	12.0	1
133	Purification of Cytosolic Phospholipase A2± C2-domain after Expression in Soluble Form in <i>Escherichia coli</i> . <i>Bio-protocol</i> , 2021, 11, e3906.	0.4	0
134	What makes Phosphatidylserine a Novel Regulator of Ceramide-1-Phosphate Transfer Proteins?. <i>FASEB Journal</i> , 2015, 29, 886.23.	0.5	0
135	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
136	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
137	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
138	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
139	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
140	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0