

# Dinshaw J Patel

## List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	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
4	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
5	Structural insights into DNMT5-mediated ATP-dependent high-fidelity epigenome maintenance. <i>Molecular Cell</i> , 2022, 82, 1186-1198.e6.	9.7	11
6	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
7	Cryo-EM structure of DNA-bound Smc5/6 reveals DNA clamping enabled by multi-subunit conformational changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	27
8	Molecular basis of nucleosomal H3K36 methylation by NSD methyltransferases. <i>Nature</i> , 2021, 590, 498-503.	27.8	85
9	The Card1 nuclease provides defence during type III CRISPR immunity. <i>Nature</i> , 2021, 590, 624-629.	27.8	76
10	Purification of Cytosolic Phospholipase A2± C2-domain after Expression in Soluble Form in Escherichia coli. <i>Bio-protocol</i> , 2021, 11, e3906.	0.4	0
11	Molecular principles of Piwi-mediated cotranscriptional silencing through the dimeric SFiNX complex. <i>Genes and Development</i> , 2021, 35, 392-409.	5.9	23
12	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
13	Structural basis for self-cleavage prevention by tag:anti-tag pairing complementarity in type VI Cas13 CRISPR systems. <i>Molecular Cell</i> , 2021, 81, 1100-1115.e5.	9.7	34
14	DNA-driven condensation assembles the meiotic DNA break machinery. <i>Nature</i> , 2021, 592, 144-149.	27.8	71
15	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
16	<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
17	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. <i>Nature Communications</i> , 2021, 12, 2490.	12.8	63
18	Integrative analysis reveals unique structural and functional features of the Smc5/6 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35

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19	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
20	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021, 81, 2533-2548.e9.	9.7	31
21	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
22	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
23	Ceramide-1-phosphate transfer protein (CPTP) regulation by phosphoinositides. <i>Journal of Biological Chemistry</i> , 2021, 296, 100600.	3.4	8
24	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
25	Structure-function insights into the initial step of DNA integration by a CRISPR-Cas Transposon complex. <i>Cell Research</i> , 2020, 30, 182-184.	12.0	30
26	Crucial Roles of Two Hydrated Mg <sup>2+</sup> Ions in Reaction Catalysis of the Pistol Ribozyme. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2837-2843.	13.8	24
27	Keeping innate immune response in check: when cGAS meets the nucleosome. <i>Cell Research</i> , 2020, 30, 1055-1056.	12.0	1
28	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
29	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
30	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
31	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. <i>PLoS Genetics</i> , 2020, 16, e1008422.	3.5	17
32	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
33	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
34	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
35	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
36	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0

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37	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
38	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
39	The nascent RNA binding complex SFiNX licenses piRNA-guided heterochromatin formation. Nature Structural and Molecular Biology, 2019, 26, 720-731.	8.2	75
40	Second Messenger cA4 Formation within the Composite Csm1 Palm Pocket of Type III-A CRISPR-Cas Csm Complex and Its Release Path. Molecular Cell, 2019, 75, 933-943.e6.	9.7	37
41	CRISPR-Cas III-A Csm6 CARF Domain Is a Ring Nuclease Triggering Stepwise cA4 Cleavage with ApA&gt;p Formation Terminating RNase Activity. Molecular Cell, 2019, 75, 944-956.e6.	9.7	90
42	Small-molecule targeting of MUSASHI RNA-binding activity in acute myeloid leukemia. Nature Communications, 2019, 10, 2691.	12.8	93
43	Human cGAS catalytic domain has an additional DNA-binding interface that enhances enzymatic activity and liquid-phase condensation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11946-11955.	7.1	129
44	Development of human cGAS-specific small-molecule inhibitors for repression of dsDNA-triggered interferon expression. Nature Communications, 2019, 10, 2261.	12.8	134
45	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
46	CasX: a new and small CRISPR gene-editing protein. Cell Research, 2019, 29, 345-346.	12.0	19
47	REC114 Partner ANKRD31 Controls Number, Timing, and Location of Meiotic DNA Breaks. Molecular Cell, 2019, 74, 1053-1068.e8.	9.7	89
48	Structures and single-molecule analysis of bacterial motor nuclease AdnAB illuminate the mechanism of DNA double-strand break resection. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24507-24516.	7.1	16
49	Type III-A CRISPR-Cas Csm Complexes: Assembly, Periodic RNA Cleavage, DNase Activity Regulation, and Autoimmunity. Molecular Cell, 2019, 73, 264-277.e5.	9.7	77
50	Structural basis of phosphatidylcholine recognition by the C2&acirc; domain of cytosolic phospholipase A2&plus. ELife, 2019, 8, .	6.0	31
51	Structural analyses of 4-phosphate adaptor protein 2 yield mechanistic insights into sphingolipid recognition by the glycolipid transfer protein family. Journal of Biological Chemistry, 2018, 293, 16709-16723.	3.4	9
52	Transcriptional elongation factor Paf1 core complex adopts a spirally wrapped solenoidal topology. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 9998-10003.	7.1	20
53	Accommodation of Helical Imperfections in Rhodobacter sphaeroides Argonaute Ternary Complexes with Guide RNA and Target DNA. Cell Reports, 2018, 24, 453-462.	6.4	47
54	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158

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55	New CRISPR-Cas systems discovered. <i>Cell Research</i> , 2017, 27, 313-314.	12.0	4
56	Inhibition Mechanism of an Anti-CRISPR Suppressor AcrIIA4 Targeting SpyCas9. <i>Molecular Cell</i> , 2017, 67, 117-127.e5.	9.7	143
57	How $\pm$ -Helical Motifs Form Functionally Diverse Lipid-Binding Compartments. <i>Annual Review of Biochemistry</i> , 2017, 86, 609-636.	11.1	19
58	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
59	Histone chaperone networks shaping chromatin function. <i>Nature Reviews Molecular Cell Biology</i> , 2017, 18, 141-158.	37.0	401
60	Structure-based insights into self-cleavage by a four-way junctional twister-sister ribozyme. <i>Nature Communications</i> , 2017, 8, 1180.	12.8	30
61	Small molecule inhibition of cGAS reduces interferon expression in primary macrophages from autoimmune mice. <i>Nature Communications</i> , 2017, 8, 750.	12.8	202
62	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
63	Atom-specific Mutagenesis Reveals Structural and Catalytic Roles for an Active-site Adenosine and Hydrated Mg <sup>2+</sup> in Pistol Ribozymes. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 15954-15958.	13.8	29
64	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
65	Polycomb-like proteins link the PRC2 complex to CpG islands. <i>Nature</i> , 2017, 549, 287-291.	27.8	238
66	TRF2 binds branched DNA to safeguard telomere integrity. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 734-742.	8.2	63
67	Atom-specific Mutagenesis Reveals Structural and Catalytic Roles for an Active-site Adenosine and Hydrated Mg <sup>2+</sup> in Pistol Ribozymes. <i>Angewandte Chemie</i> , 2017, 129, 16170-16174.	2.0	4
68	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
69	Structure/cleavage-based insights into helical perturbations at bulge sites within <i>T. thermophilus</i> Argonaute silencing complexes. <i>Nucleic Acids Research</i> , 2017, 45, 9149-9163.	14.5	29
70	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
71	Structural basis underlying viral hijacking of a histone chaperone complex. <i>Nature Communications</i> , 2016, 7, 12707.	12.8	27
72	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

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73	Pistol ribozyme adopts a pseudoknot fold facilitating site-specific in-line cleavage. <i>Nature Chemical Biology</i> , 2016, 12, 702-708.	8.0	78
74	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
75	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
76	Structure and function of the bacterial decapping enzyme NudC. <i>Nature Chemical Biology</i> , 2016, 12, 730-734.	8.0	74
77	H4K20me0 marks post-replicative chromatin and recruits the TONSL-MMS22L DNA repair complex. <i>Nature</i> , 2016, 534, 714-718.	27.8	172
78	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
79	Cutoff Suppresses RNA Polymerase II Termination to Ensure Expression of piRNA Precursors. <i>Molecular Cell</i> , 2016, 63, 97-109.	9.7	116
80	Recognition of distinct RNA motifs by the clustered CCCH zinc fingers of neuronal protein Unkempt. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 16-23.	8.2	23
81	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
82	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
83	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
84	<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
85	Structural Basis for Molecular Discrimination by a 3'-cGAMP Sensing Riboswitch. <i>Cell Reports</i> , 2015, 11, 1-12.	6.4	87
86	V-cGAPs: attenuators of 3'-cGAMP signaling. <i>Cell Research</i> , 2015, 25, 529-530.	12.0	5
87	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
88	DNA methylation pathways and their crosstalk with histone methylation. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 519-532.	37.0	779
89	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
90	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

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91	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
92	Global RNA Fold and Molecular Recognition for a pfl Riboswitch Bound to ZMP, a Master Regulator of One-Carbon Metabolism. <i>Structure</i> , 2015, 23, 1375-1381.	3.3	30
93	Sphingolipid transfer proteins defined by the GLTP-fold. <i>Quarterly Reviews of Biophysics</i> , 2015, 48, 281-322.	5.7	30
94	Crystal structure reveals specific recognition of a G-quadruplex RNA by a $\hat{2}$ -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
95	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
96	What makes Phosphatidylserine a Novel Regulator of Ceramide&Phosphate Transfer Proteins?. <i>FASEB Journal</i> , 2015, 29, 886.23.	0.5	0
97	In-line alignment and Mg <sup>2+</sup> coordination at the cleavage site of the env22 twister ribozyme. <i>Nature Communications</i> , 2014, 5, 5534.	12.8	84
98	Uridylation by TUT4 and TUT7 Marks mRNA for Degradation. <i>Cell</i> , 2014, 159, 1365-1376.	28.9	243
99	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
100	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
101	DNA-guided DNA interference by a prokaryotic Argonaute. <i>Nature</i> , 2014, 507, 258-261.	27.8	373
102	SRA- and SET-domain-containing proteins link RNA polymerase V occupancy to DNA methylation. <i>Nature</i> , 2014, 507, 124-128.	27.8	271
103	Structural biology-based insights into combinatorial readout and crosstalk among epigenetic marks. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 719-727.	1.9	27
104	Non-CG methylation patterns shape the epigenetic landscape in Arabidopsis. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 64-72.	8.2	690
105	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
106	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
107	Adenylation of Maternally Inherited MicroRNAs by Wispy. <i>Molecular Cell</i> , 2014, 56, 696-707.	9.7	87
108	Complete pairing not needed. <i>Science</i> , 2014, 346, 542-543.	12.6	1

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109	The evolutionary journey of Argonaute proteins. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 743-753.	8.2	400
110	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
111	Mechanism of DNA Methylation-Directed Histone Methylation by KRYPTONITE. <i>Molecular Cell</i> , 2014, 55, 495-504.	9.7	186
112	Molecular Mechanism of Action of Plant DRM De Novo DNA Methyltransferases. <i>Cell</i> , 2014, 157, 1050-1060.	28.9	245
113	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
114	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
115	Eukaryote-Specific Insertion Elements Control Human ARGONAUTE Slicer Activity. <i>Cell Reports</i> , 2013, 3, 1893-1900.	6.4	91
116	Cyclic [G(2'5'-ppA(3'5'-pp)] Is the Metazoan Second Messenger Produced by DNA-Activated Cyclic GMP-AMP Synthase. <i>Cell</i> , 2013, 153, 1094-1107.	28.9	795
117	Readout of Epigenetic Modifications. <i>Annual Review of Biochemistry</i> , 2013, 82, 81-118.	11.1	285
118	<i>RNA-Puzzles</i>: A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	3.5	241
119	The BAH domain of ORC1 links H4K20me2 to DNA replication licensing and Meier's Gorlin syndrome. <i>Nature</i> , 2012, 484, 115-119.	27.8	314
120	DAXX envelops a histone H3.3-H4 dimer for H3.3-specific recognition. <i>Nature</i> , 2012, 491, 560-565.	27.8	220
121	Dual Binding of Chromomethylase Domains to H3K9me2-Containing Nucleosomes Directs DNA Methylation in Plants. <i>Cell</i> , 2012, 151, 167-180.	28.9	446
122	Structure-Based Mechanistic Insights into DNMT1-Mediated Maintenance DNA Methylation. <i>Science</i> , 2012, 335, 709-712.	12.6	283
123	Structure of yeast Argonaute with guide RNA. <i>Nature</i> , 2012, 486, 368-374.	27.8	314
124	Structure of DNMT1-DNA Complex Reveals a Role for Autoinhibition in Maintenance DNA Methylation. <i>Science</i> , 2011, 331, 1036-1040.	12.6	363
125	A Poised Chromatin Platform for TGF- $\beta^2$ Access to Master Regulators. <i>Cell</i> , 2011, 147, 1511-1524.	28.9	251
126	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



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127	Structural basis for piRNA 2'-O-methylated 3'-end recognition by Piwi PAZ (Piwi/Argonaute/Zwille) domains. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 903-910.	7.1	91
128	Structure-function studies of nucleocytoplasmic transport of retroviral genomic RNA by mRNA export factor TAP. Nature Structural and Molecular Biology, 2011, 18, 990-998.	8.2	47
129	Glycolipid Acquisition by Human Glycolipid Transfer Protein Dramatically Alters Intrinsic Tryptophan Fluorescence. Journal of Biological Chemistry, 2009, 284, 13620-13628.	3.4	28
130	Nucleation, propagation and cleavage of target RNAs in Ago silencing complexes. Nature, 2009, 461, 754-761.	27.8	483
131	PRMT5-mediated methylation of histone H4R3 recruits DNMT3A, coupling histone and DNA methylation in gene silencing. Nature Structural and Molecular Biology, 2009, 16, 304-311.	8.2	451
132	Structure of the guide-strand-containing argonaute silencing complex. Nature, 2008, 456, 209-213.	27.8	481
133	Structure of an argonaute silencing complex with a seed-containing guide DNA and target RNA duplex. Nature, 2008, 456, 921-926.	27.8	512
134	Human telomere, oncogenic promoter and 5'-UTR G-quadruplexes: diverse higher order DNA and RNA targets for cancer therapeutics. Nucleic Acids Research, 2007, 35, 7429-7455.	14.5	812
135	How chromatin-binding modules interpret histone modifications: lessons from professional pocket pickers. Nature Structural and Molecular Biology, 2007, 14, 1025-1040.	8.2	1,288
136	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. Molecular Cell, 2006, 24, 785-796.	9.7	283
137	Structural basis for overhang-specific small interfering RNA recognition by the PAZ domain. Nature, 2004, 429, 318-322.	27.8	647
138	Solution Structure of the Aminofluorene [AF]-Intercalated Conformer of the syn-[AF]-C8-dG Adduct Opposite dC in a DNA Duplex. Biochemistry, 1998, 37, 81-94.	2.5	68
139	Solution Structure of the Aminofluorene [AF]-External Conformer of the anti-[AF]-C8-dG Adduct Opposite dC in a DNA Duplex. Biochemistry, 1998, 37, 95-106.	2.5	62
140	Solution Conformation of the N-(Deoxyguanosin-8-yl)-1-aminopyrene ([AP]dG) Adduct Opposite dC in a DNA Duplex. Biochemistry, 1996, 35, 12659-12670.	2.5	55