Patrick Cramer

List of Publications by Year
in descending order

200 papers	28,532 citations	5574 82 h-index	7348 152 g-index
236 all docs	236 docs citations	236 times ranked	25622 citing authors

#	Article	IF	Citations
1	Distinct transcription kinetics of pluripotent cell states. Molecular Systems Biology, 2022, 18, e10407.	7.2	4
2	Sequence determinants of human gene regulatory elements. Nature Genetics, 2022, 54, 283-294.	21.4	87
3	RNA transcription and degradation of Alu retrotransposons depends on sequence features and evolutionary history. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	1
4	Histone H1 binding to nucleosome arrays depends on linker DNA length and trajectory. Nature Structural and Molecular Biology, 2022, 29, 493-501.	8.2	32
5	Permissive epigenomes endow reprogramming competence to transcriptional regulators. Nature Chemical Biology, 2021, 17, 47-56.	8.0	35
6	The Cdk8 kinase module regulates interaction of the mediator complex with RNA polymerase II. Journal of Biological Chemistry, 2021, 296, 100734.	3.4	33
7	Structure of a transcribing RNA polymerase IIâ€"U1 snRNP complex. Science, 2021, 371, 305-309.	12.6	71
8	Transcriptionally active enhancers in human cancer cells. Molecular Systems Biology, 2021, 17, e9873.	7.2	28
9	Ubiquitylation of MYC couples transcription elongation with double-strand break repair at active promoters. Molecular Cell, 2021, 81, 830-844.e13.	9.7	28
10	Integrator is a genome-wide attenuator of non-productive transcription. Molecular Cell, 2021, 81, 514-529.e6.	9.7	82
11	Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.5â€‰Ã… in cells. Nature Methods, 2021, 18, 186-193.	19.0	265
12	Transcription activation depends on the length of the RNA polymerase II Câ€terminal domain. EMBO Journal, 2021, 40, e107015.	7.8	11
13	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. ELife, 2021, 10, .	6.0	64
14	Stress-induced nuclear condensation of NELF drives transcriptional downregulation. Molecular Cell, 2021, 81, 1013-1026.e11.	9.7	83
15	Structure of the human Mediatorâ€"RNA polymerase II pre-initiation complex. Nature, 2021, 594, 129-133.	27.8	73
16	Structures of mammalian RNA polymerase II pre-initiation complexes. Nature, 2021, 594, 124-128.	27.8	63
17	The pentatricopeptide repeat protein Rmd9 recognizes the dodecameric element in the 3â€²-UTRs of yeast mitochondrial mRNAs. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
18	Structural basis of nucleosome transcription mediated by Chd1 and FACT. Nature Structural and Molecular Biology, 2021, 28, 382-387.	8.2	72

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19	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. Nature Communications, 2021, 12, 3232.	12.8	34
20	Efficient RNA polymerase II pause release requires U2 snRNP function. Molecular Cell, 2021, 81, 1920-1934.e9.	9.7	45
21	Cryo-EM structure of mammalian RNA polymerase II in complex with human RPAP2. Communications Biology, 2021, 4, 606.	4.4	11
22	Structures and implications of TBPâ€“nucleosome complexes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	21
23	The total mRNA concentration buffering system in yeast is global rather than gene-specific. Rna, 2021, 27, 1281-1290.	3.5	11
24	Structure of RNA polymerase II pre-initiation complex at 2.9ÂÃ… defines initial DNA opening. Cell, 2021, 184, 4064-4072.e28.	28.9	42
25	The structure of a dimeric form of SARS-CoV-2 polymerase. Communications Biology, 2021, 4, 999.	4.4	9
26	Two distinct mechanisms of RNA polymerase II elongation stimulation inÂvivo. Molecular Cell, 2021, 81, 3096-3109.e8.	9.7	53
27	Allosteric transcription stimulation by RNA polymerase II super elongation complex. Molecular Cell, 2021, 81, 3386-3399.e10.	9.7	17
28	AlphaFold2 and the future of structural biology. Nature Structural and Molecular Biology, 2021, 28, 704-705.	8.2	192
29	Mechanism of molnupiravir-induced SARS-CoV-2 mutagenesis. Nature Structural and Molecular Biology, 2021, 28, 740-746.	8.2	450
30	Structural basis of human transcriptionâ€“DNA repair coupling. Nature, 2021, 598, 368-372.	27.8	59
31	Structure of an inactive RNA polymerase II dimer. Nucleic Acids Research, 2021, 49, 10747-10755.	14.5	8
32	Structural basis of RNA processing by human mitochondrial RNase P. Nature Structural and Molecular Biology, 2021, 28, 713-723.	8.2	48
33	Mechanism of SARS-CoV-2 polymerase stalling by remdesivir. Nature Communications, 2021, 12, 279.	12.8	412
34	Structural basis of Integrator-mediated transcription regulation. Science, 2021, 374, 883-887.	12.6	78
35	Structure of H3K36-methylated nucleosomeâ€“PWWP complex reveals multivalent cross-gyre binding. Nature Structural and Molecular Biology, 2020, 27, 8-13.	8.2	57
36	Rosalind Franklin and the Advent of Molecular Biology. Cell, 2020, 182, 787-789.	28.9	3

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37	In-cell architecture of an actively transcribing-translating expressome. Science, 2020, 369, 554-557.	12.6	192
38	CDK12 globally stimulates RNA polymerase II transcription elongation and carboxyl-terminal domain phosphorylation. Nucleic Acids Research, 2020, 48, 7712-7727.	14.5	58
39	Structure of replicating SARS-CoV-2 polymerase. Nature, 2020, 584, 154-156.	27.8	627
40	Native molecule sequencing by nano-ID reveals synthesis and stability of RNA isoforms. Genome Research, 2020, 30, 1332-1344.	5.5	29
41	Structural Biology of RNA Polymerase II Transcription: 20 Years On. Annual Review of Cell and Developmental Biology, 2020, 36, 1-34.	9.4	76
42	Small-molecule inhibitors of human mitochondrial DNA transcription. Nature, 2020, 588, 712-716.	27.8	115
43	Selective Mediator dependence of cell-type-specifying transcription. Nature Genetics, 2020, 52, 719-727.	21.4	84
44	Structure of complete Pol IIâ€“DSIFâ€“PAFâ€“SPT6 transcription complex reveals RTF1 allosteric activation. Nature Structural and Molecular Biology, 2020, 27, 668-677.	8.2	98
45	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. Nature Genetics, 2020, 52, 655-661.	21.4	98
46	Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. Nature, 2020, 579, 448-451.	27.8	106
47	500 years after the first circumnavigation of the world: the efforts, rewards and drawbacks of exploration. FEBS Letters, 2020, 594, 207-208.	2.8	0
48	Structure of the transcription coactivator SAGA. Nature, 2020, 577, 717-720.	27.8	112
49	Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. Nature, 2020, 580, 669-672.	27.8	177
50	Nucleosome-CHD4 chromatin remodeler structure maps human disease mutations. ELife, 2020, 9, .	6.0	52
51	The pause-initiation limit restricts transcription activation in human cells. Nature Communications, 2019, 10, 3603.	12.8	60
52	NASC-seq monitors RNA synthesis in single cells. Nature Communications, 2019, 10, 3138.	12.8	75
53	Global donor and acceptor splicing site kinetics in human cells. ELife, 2019, 8, .	6.0	51
54	Structural basis of TFIIH activation for nucleotide excision repair. Nature Communications, 2019, 10, 2885.	12.8	112

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55	Eukaryotic Transcription Turns 50. Cell, 2019, 179, 808-812.	28.9	35
56	Organization and regulation of gene transcription. Nature, 2019, 573, 45-54.	27.8	431
57	Structure of the super-elongation complex subunit AFF4 C-terminal homology domain reveals requirements for AFF homo- and heterodimerization. Journal of Biological Chemistry, 2019, 294, 10663-10673.	3.4	24
58	MYC Recruits SPT5 to RNA Polymerase II to Promote Processive Transcription Elongation. Molecular Cell, 2019, 74, 674-687.e11.	9.7	89
59	Yeast mitochondrial protein Pet111p binds directly to two distinct targets in COX2 mRNA, suggesting a mechanism of translational activation. Journal of Biological Chemistry, 2019, 294, 7528-7536.	3.4	14
60	Real-time cryo-electron microscopy data preprocessing with Warp. Nature Methods, 2019, 16, 1146-1152.	19.0	833
61	Structural Basis of Poxvirus Transcription: Transcribing and Capping Vaccinia Complexes. Cell, 2019, 179, 1525-1536.e12.	28.9	37
62	Structural Basis of Poxvirus Transcription: Vaccinia RNA Polymerase Complexes. Cell, 2019, 179, 1537-1550.e19.	28.9	41
63	The Implication of Early Chromatin Changes in X Chromosome Inactivation. Cell, 2019, 176, 182-197.e23.	28.9	207
64	Promoter Distortion and Opening in the RNA Polymerase II Cleft. Molecular Cell, 2019, 73, 97-106.e4.	9.7	65
65	Transcriptome maps of general eukaryotic RNA degradation factors. ELife, 2019, 8, .	6.0	23
66	Cryo-EM structure of a mammalian RNA polymerase II elongation complex inhibited by Î±-amanitin. Journal of Biological Chemistry, 2018, 293, 7189-7194.	3.4	37
67	Structure of transcribing RNA polymerase II-nucleosome complex. Nature Communications, 2018, 9, 5432.	12.8	85
68	The APT complex is involved in non-coding RNA transcription and is distinct from CPF. Nucleic Acids Research, 2018, 46, 11528-11538.	14.5	17
69	The interaction landscape between transcription factors and the nucleosome. Nature, 2018, 562, 76-81.	27.8	259
70	Structural basis of mitochondrial transcription. Nature Structural and Molecular Biology, 2018, 25, 754-765.	8.2	67
71	Distinct Mechanisms of Transcription Initiation by RNA Polymerases I and II. Annual Review of Biophysics, 2018, 47, 425-446.	10.0	63
72	RNA polymerase II clustering through carboxy-terminal domain phase separation. Nature Structural and Molecular Biology, 2018, 25, 833-840.	8.2	456

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73	RNA velocity of single cells. Nature, 2018, 560, 494-498.	27.8	2,602
74	Structure of activated transcription complex Pol IIâ€“DSIFâ€“PAFâ€“SPT6. Nature, 2018, 560, 607-612.	27.8	300
75	Structure of paused transcription complex Pol IIâ€“DSIFâ€“NELF. Nature, 2018, 560, 601-606.	27.8	262
76	Architecture of a transcribing-translating expressome. Science, 2017, 356, 194-197.	12.6	163
77	Structural Molecular Biologyâ€”A Personal Reflection on the Occasion of John Kendrew's 100th Birthday. Journal of Molecular Biology, 2017, 429, 2603-2610.	4.2	2
78	Core Mediator structure at 3.4 Ã… extends model of transcription initiation complex. Nature, 2017, 545, 248-251.	27.8	100
79	Conserved RNA polymerase II initiation complex structure. Current Opinion in Structural Biology, 2017, 47, 17-22.	5.7	46
80	Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex. Nature Communications, 2017, 8, 15741.	12.8	80
81	The conserved protein Seb1 drives transcription termination by binding RNA polymerase II and nascent RNA. Nature Communications, 2017, 8, 14861.	12.8	48
82	Structural Basis of RNA Polymerase I Transcription Initiation. Cell, 2017, 169, 120-131.e22.	28.9	101
83	Spt5 Plays Vital Roles in the Control of Sense and Antisense Transcription Elongation. Molecular Cell, 2017, 66, 77-88.e5.	9.7	90
84	TTâ€seq captures enhancer landscapes immediately after Tâ€cell stimulation. Molecular Systems Biology, 2017, 13, 920.	7.2	44
85	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. Molecular Cell, 2017, 66, 38-49.e6.	9.7	100
86	Structures of transcription pre-initiation complex with TFIIH and Mediator. Nature, 2017, 551, 204-209.	27.8	219
87	Nucleosomeâ€“Chd1 structure and implications for chromatin remodelling. Nature, 2017, 550, 539-542.	27.8	205
88	Mechanism of Transcription Anti-termination in Human Mitochondria. Cell, 2017, 171, 1082-1093.e13.	28.9	68
89	Structure of a transcribing RNA polymerase IIâ€“DSIF complex reveals a multidentate DNAâ€“RNA clamp. Nature Structural and Molecular Biology, 2017, 24, 809-815.	8.2	130
90	Structural Basis of Mitochondrial Transcription Initiation. Cell, 2017, 171, 1072-1081.e10.	28.9	131

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91	Mechanism of RNA polymerase II stalling by DNA alkylation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12172-12177.	7.1	18
92	CDK9-dependent RNA polymerase II pausing controls transcription initiation. ELife, 2017, 6, .	6.0	179
93	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. PLoS ONE, 2017, 12, e0169249.	2.5	73
94	RNA-dependent chromatin association of transcription elongation factors and Pol II CTD kinases. ELife, 2017, 6, .	6.0	48
95	Inference of gene regulation functions from dynamic transcriptome data. ELife, 2016, 5, .	6.0	12
96	Determinants of <scp>RNA</scp> metabolism in the Schizosaccharomyces pombe genome. Molecular Systems Biology, 2016, 12, 857.	7.2	81
97	Mechanisms of backtrack recovery by RNA polymerases I and II. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2946-2951.	7.1	98
98	Structure of GPN-Loop GTPase Npa3 and Implications for RNA Polymerase II Assembly. Molecular and Cellular Biology, 2016, 36, 820-831.	2.3	37
99	Transcription initiation complex structures elucidate DNA opening. Nature, 2016, 533, 353-358.	27.8	250
100	Structure determination of transient transcription complexes. Biochemical Society Transactions, 2016, 44, 1177-1182.	3.4	3
101	Nucleosomal arrangement affects single-molecule transcription dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 12733-12738.	7.1	13
102	RNA polymerase Iâ€“Rrn3 complex at 4.8 Ã… resolution. Nature Communications, 2016, 7, 12129.	12.8	58
103	TT-seq maps the human transient transcriptome. Science, 2016, 352, 1225-1228.	12.6	384
104	Structure of transcribing mammalian RNA polymerase II. Nature, 2016, 529, 551-554.	27.8	174
105	Heptad-Specific Phosphorylation of RNA PolymeraseÂII CTD. Molecular Cell, 2016, 61, 305-314.	9.7	118
106	Mediator Architecture and RNA Polymerase II Interaction. Journal of Molecular Biology, 2016, 428, 2569-2574.	4.2	50
107	Architecture and RNA binding of the human negative elongation factor. ELife, 2016, 5, .	6.0	54
108	Structure of Ctk3, a subunit of the RNA polymerase II CTD kinase complex, reveals a noncanonical CTD-interacting domain fold. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1849-1858.	2.6	4

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109	Architecture of the RNA polymerase IIâ€“Mediator core initiation complex. Nature, 2015, 518, 376-380.	27.8	259
110	Structural basis of transcription initiation by RNA polymerase II. Nature Reviews Molecular Cell Biology, 2015, 16, 129-143.	37.0	322
111	BRF1 mutations alter RNA polymerase IIIâ€“dependent transcription and cause neurodevelopmental anomalies. Genome Research, 2015, 25, 155-166.	5.5	85
112	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. Molecular Cell, 2015, 58, 1079-1089.	9.7	109
113	An alternative RNA polymerase I structure reveals a dimer hinge. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 1850-1855.	2.5	16
114	A model for transcription initiation in human mitochondria. Nucleic Acids Research, 2015, 43, 3726-3735.	14.5	60
115	Structure-Based Prediction of Asparagine and Aspartate Degradation Sites in Antibody Variable Regions. PLoS ONE, 2014, 9, e100736.	2.5	128
116	Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle. Molecular Systems Biology, 2014, 10, 768.	7.2	21
117	Periodic <scp>mRNA</scp> synthesis and degradation coâ€operate during cell cycle gene expression. Molecular Systems Biology, 2014, 10, 717.	7.2	80
118	A novel intermediate in transcription initiation by human mitochondrial RNA polymerase. Nucleic Acids Research, 2014, 42, 3884-3893.	14.5	60
119	Conserved architecture of the core RNA polymerase II initiation complex. Nature Communications, 2014, 5, 4310.	12.8	37
120	A Tale of Chromatin and Transcription in 100 Structures. Cell, 2014, 159, 985-994.	28.9	25
121	RNA polymerase II termination involves C-terminal-domain tyrosine dephosphorylation by CPF subunit Glc7. Nature Structural and Molecular Biology, 2014, 21, 175-179.	8.2	77
122	Rpb4 Subunit Functions Mainly in mRNA Synthesis by RNA Polymerase II. Journal of Biological Chemistry, 2014, 289, 17446-17452.	3.4	41
123	Molecular Basis for Coordinating Transcription Termination with Noncoding RNA Degradation. Molecular Cell, 2014, 55, 467-481.	9.7	99
124	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. Molecular Cell, 2014, 55, 745-757.	9.7	99
125	RNA polymerase I structure and transcription regulation. Nature, 2013, 502, 650-655.	27.8	193
126	Structure of human mitochondrial RNA polymerase elongation complex. Nature Structural and Molecular Biology, 2013, 20, 1298-1303.	8.2	67

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127	Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. Cell, 2013, 155, 1075-1087.	28.9	201
128	Structural basis of transcription elongation. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 9-19.	1.9	79
129	Structure and function of the initially transcribing RNA polymerase IIâ€"TFIIB complex. Nature, 2013, 493, 437-440.	27.8	170
130	The RNA Polymerase II C-terminal Domain-interacting Domain of Yeast Nrd1 Contributes to the Choice of Termination Pathway and Couples to RNA Processing by the Nuclear Exosome. Journal of Biological Chemistry, 2013, 288, 36676-36690.	3.4	21
131	Global Analysis of Eukaryotic mRNA Degradation Reveals Xrn1-Dependent Buffering of Transcript Levels. Molecular Cell, 2013, 52, 52-62.	9.7	218
132	Cap Completion and C-Terminal Repeat Domain Kinase Recruitment Underlie the Initiation-Elongation Transition of RNA Polymerase II. Molecular and Cellular Biology, 2013, 33, 3805-3816.	2.3	53
133	Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. Genome Research, 2012, 22, 1350-1359.	5.5	255
134	Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). Bioinformatics, 2012, 28, 884-885.	4.1	24
135	Structure of the Mediator head module. Nature, 2012, 492, 448-451.	27.8	89
136	The Spt5 C-Terminal Region Recruits Yeast 3â€² RNA Cleavage Factor I. Molecular and Cellular Biology, 2012, 32, 1321-1331.	2.3	56
137	Conservation between the RNA Polymerase I, II, and III Transcription Initiation Machineries. Molecular Cell, 2012, 45, 439-446.	9.7	357
138	Mechanism of Translesion Transcription by RNA Polymerase II and Its Role in Cellular Resistance to DNA Damage. Molecular Cell, 2012, 46, 18-29.	9.7	104
139	A Movie of RNA Polymerase II Transcription. Cell, 2012, 149, 1431-1437.	28.9	105
140	CTD Tyrosine Phosphorylation Impairs Termination Factor Recruitment to RNA Polymerase II. Science, 2012, 336, 1723-1725.	12.6	215
141	A structural perspective on Mediator function. Current Opinion in Cell Biology, 2012, 24, 305-313.	5.4	70
142	Biogenesis of multisubunit RNA polymerases. Trends in Biochemical Sciences, 2012, 37, 99-105.	7.5	83
143	Structure of human mitochondrial RNA polymerase. Nature, 2011, 478, 269-273.	27.8	175
144	Iwr1 Directs RNA Polymerase II Nuclear Import. Molecular Cell, 2011, 42, 261-266.	9.7	82

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145	Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Molecular Systems Biology, 2011, 7, 458.	7.2	333
146	Structure and VP16 binding of the Mediator Med25 activator interaction domain. Nature Structural and Molecular Biology, 2011, 18, 404-409.	8.2	103
147	Architecture of the RNA polymerase-Spt4/5 complex and basis of universal transcription processivity. EMBO Journal, 2011, 30, 1302-1310.	7.8	209
148	Structural basis of RNA polymerase II backtracking, arrest and reactivation. Nature, 2011, 471, 249-253.	27.8	310
149	Mediator head subcomplex Med11/22 contains a common helix bundle building block with a specific function in transcription initiation complex stabilization. Nucleic Acids Research, 2011, 39, 6291-6304.	14.5	38
150	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. Genes and Development, 2011, 25, 2093-2105.	5.9	87
151	A Cytoplasmic Complex Mediates Specific mRNA Recognition and Localization in Yeast. PLoS Biology, 2011, 9, e1000611.	5.6	72
152	Structural basis of initial RNA polymerase II transcription. EMBO Journal, 2011, 30, 4755-4763.	7.8	82
153	Uniform transitions of the general RNA polymerase II transcription complex. Nature Structural and Molecular Biology, 2010, 17, 1272-1278.	8.2	399
154	Architecture of the RNA polymerase IIâ€“TFIIF complex revealed by cross-linking and mass spectrometry. EMBO Journal, 2010, 29, 717-726.	7.8	355
155	A Tandem SH2 Domain in Transcription Elongation Factor Spt6 Binds the Phosphorylated RNA Polymerase II C-terminal Repeat Domain (CTD). Journal of Biological Chemistry, 2010, 285, 41597-41603.	3.4	76
156	Spt4/5 stimulates transcription elongation through the RNA polymerase clamp coiled-coil motif. Nucleic Acids Research, 2010, 38, 4040-4051.	14.5	150
157	Towards molecular systems biology of gene transcription and regulation. Biological Chemistry, 2010, 391, 731-5.	2.5	3
158	RNA Polymerase I Contains a TFIIF-Related DNA-Binding Subcomplex. Molecular Cell, 2010, 39, 583-594.	9.7	120
159	Molecular Basis of RNA Polymerase III Transcription Repression by Maf1. Cell, 2010, 143, 59-70.	28.9	156
160	Nano positioning system reveals the course of upstream and nontemplate DNA within the RNA polymerase II elongation complex. Nucleic Acids Research, 2009, 37, 5803-5809.	14.5	80
161	RNA polymerase IIâ€“TFIIB structure and mechanism of transcription initiation. Nature, 2009, 462, 323-330.	27.8	266
162	Structure and in Vivo Requirement of the Yeast Spt6 SH2 Domain. Journal of Molecular Biology, 2009, 389, 211-225.	4.2	47

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163	Structural Basis of Transcription: Mismatch-Specific Fidelity Mechanisms and Paused RNA Polymerase II with Frayed RNA. Molecular Cell, 2009, 34, 710-721.	9.7	161
164	Structural basis of transcription inhibition by Î±-amanitin and implications for RNA polymerase II translocation. Nature Structural and Molecular Biology, 2008, 15, 811-818.	8.2	223
165	A nano-positioning system for macromolecular structural analysis. Nature Methods, 2008, 5, 965-971.	19.0	183
166	Structure of Eukaryotic RNA Polymerases. Annual Review of Biophysics, 2008, 37, 337-352.	10.0	251
167	Single-molecule tracking of mRNA exiting from RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 135-140.	7.1	102
168	CPD Damage Recognition by Transcribing RNA Polymerase II. Science, 2007, 315, 859-862.	12.6	209
169	Functional Architecture of RNA Polymerase I. Cell, 2007, 131, 1260-1272.	28.9	192
170	Mechanism of transcriptional stalling at cisplatin-damaged DNA. Nature Structural and Molecular Biology, 2007, 14, 1127-1133.	8.2	149
171	Molecular basis of RNA-dependent RNA polymerase II activity. Nature, 2007, 450, 445-449.	27.8	125
172	Structural Biology of RNA Polymerase III: Mass Spectrometry Elucidates Subcomplex Architecture. Structure, 2007, 15, 1237-1245.	3.3	85
173	MOLECULAR BIOLOGY: Self-Correcting Messages. Science, 2006, 313, 447-448.	12.6	7
174	Structural Biology of RNA Polymerase III: Subcomplex C17/25 X-Ray Structure and 11 Subunit Enzyme Model. Molecular Cell, 2006, 23, 71-81.	9.7	80
175	Recent structural studies of RNA polymerases II and III. Biochemical Society Transactions, 2006, 34, 1058-1061.	3.4	10
176	Structure and TBP binding of the Mediator head subcomplex Med8â€“Med18â€“Med20. Nature Structural and Molecular Biology, 2006, 13, 895-901.	8.2	96
177	Deciphering the RNA polymerase II structure: a personal perspective. Nature Structural and Molecular Biology, 2006, 13, 1042-1044.	8.2	3
178	Structure and Carboxyl-terminal Domain (CTD) Binding of the Set2 SRI Domain That Couples Histone H3 Lys36 Methylation to Transcription*. Journal of Biological Chemistry, 2006, 281, 13-15.	3.4	76
179	Mechanistic studies of the mRNA transcription cycle. Biochemical Society Symposia, 2006, 73, 41-47.	2.7	4
180	A structural perspective of CTD function. Genes and Development, 2005, 19, 1401-1415.	5.9	276

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181	Structures of Complete RNA Polymerase II and Its Subcomplex, Rpb4/7. Journal of Biological Chemistry, 2005, 280, 7131-7134.	3.4	201
182	A Conserved Mediator Hinge Revealed in the Structure of the MED7Â·MED21 (Med7Â·Srb7) Heterodimer. Journal of Biological Chemistry, 2005, 280, 18171-18178.	3.4	59
183	Structure and Function of RNA Polymerase II. Advances in Protein Chemistry, 2004, 67, 1-42.	4.4	32
184	Structure of a bifunctional DNA primase-polymerase. Nature Structural and Molecular Biology, 2004, 11, 157-162.	8.2	92
185	Recognition of RNA polymerase II carboxy-terminal domain by 3â€²-RNA-processing factors. Nature, 2004, 430, 223-226.	27.8	260
186	RNA polymerase II structure: from core to functional complexes. Current Opinion in Genetics and Development, 2004, 14, 218-226.	3.3	72
187	Structure and Mechanism of RNA Polymerase II CTD Phosphatases. Molecular Cell, 2004, 15, 399-407.	9.7	121
188	Complete RNA Polymerase II Elongation Complex Structure and Its Interactions with NTP and TFIIS. Molecular Cell, 2004, 16, 955-965.	9.7	384
189	Architecture of the RNA Polymerase II-TFIIS Complex and Implications for mRNA Cleavage. Cell, 2003, 114, 347-357.	28.9	298
190	Architecture of initiation-competent 12-subunit RNA polymerase II. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6964-6968.	7.1	218
191	An Extended Winged Helix Domain in General Transcription Factor E/IIEÎ±. Journal of Biological Chemistry, 2003, 278, 48267-48274.	3.4	80
192	Multisubunit RNA polymerases. Current Opinion in Structural Biology, 2002, 12, 89-97.	5.7	224
193	Common structural features of nucleic acid polymerases. BioEssays, 2002, 24, 724-729.	2.5	37
194	Structural basis of transcription: Â-Amanitin-RNA polymerase II cocrystal at 2.8 A resolution. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1218-1222.	7.1	273
195	Structural Basis of Transcription: An RNA Polymerase II Elongation Complex at 3.3 A Resolution. Science, 2001, 292, 1876-1882.	12.6	834
196	Structural Basis of Transcription: RNA Polymerase II at 2.8 Angstrom Resolution. Science, 2001, 292, 1863-1876.	12.6	1,118
197	Architecture of RNA Polymerase II and Implications for the Transcription Mechanism. Science, 2000, 288, 640-649.	12.6	570
198	Coupling of Transcription with Alternative Splicing. Molecular Cell, 1999, 4, 251-258.	9.7	274

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199	Structure of the human NF-kappa B p52 homodimer-DNA complex at 2.1Aresolution. EMBO Journal, 1997, 16, 7078-7090.	7.8	126
200	Oct4 differentially regulates chromatin opening and enhancer transcription in pluripotent stem cells. ELife, 0, 11, .	6.0	15