

Patrick Cramer

List of Publications by Year in descending order

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Version: 2024-02-01

200
papers

28,532
citations

5558

82
h-index

7333

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. <i>Molecular Systems Biology</i> , 2022, 18, e10407.	3.2	4
2	Sequence determinants of human gene regulatory elements. <i>Nature Genetics</i> , 2022, 54, 283-294.	9.4	87
3	RNA transcription and degradation of Alu retrotransposons depends on sequence features and evolutionary history. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	1
4	Histone H1 binding to nucleosome arrays depends on linker DNA length and trajectory. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 493-501.	3.6	32
5	Permissive epigenomes endow reprogramming competence to transcriptional regulators. <i>Nature Chemical Biology</i> , 2021, 17, 47-56.	3.9	35
6	The Cdk8 kinase module regulates interaction of the mediator complex with RNA polymerase II. <i>Journal of Biological Chemistry</i> , 2021, 296, 100734.	1.6	33
7	Structure of a transcribing RNA polymerase II-U1 snRNP complex. <i>Science</i> , 2021, 371, 305-309.	6.0	71
8	Transcriptionally active enhancers in human cancer cells. <i>Molecular Systems Biology</i> , 2021, 17, e9873.	3.2	28
9	Ubiquitylation of MYC couples transcription elongation with double-strand break repair at active promoters. <i>Molecular Cell</i> , 2021, 81, 830-844.e13.	4.5	28
10	Integrator is a genome-wide attenuator of non-productive transcription. <i>Molecular Cell</i> , 2021, 81, 514-529.e6.	4.5	82
11	Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.5Å in cells. <i>Nature Methods</i> , 2021, 18, 186-193.	9.0	265
12	Transcription activation depends on the length of the RNA polymerase II C-terminal domain. <i>EMBO Journal</i> , 2021, 40, e107015.	3.5	11
13	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. <i>ELife</i> , 2021, 10, .	2.8	64
14	Stress-induced nuclear condensation of NELF drives transcriptional downregulation. <i>Molecular Cell</i> , 2021, 81, 1013-1026.e11.	4.5	83
15	Structure of the human Mediator-RNA polymerase II pre-initiation complex. <i>Nature</i> , 2021, 594, 129-133.	13.7	73
16	Structures of mammalian RNA polymerase II pre-initiation complexes. <i>Nature</i> , 2021, 594, 124-128.	13.7	63
17	The pentatricopeptide repeat protein Rmd9 recognizes the dodecameric element in the 3'-UTRs of yeast mitochondrial mRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
18	Structural basis of nucleosome transcription mediated by Chd1 and FACT. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 382-387.	3.6	72

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19	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021, 12, 3232.	5.8	34
20	Efficient RNA polymerase II pause release requires U2 snRNP function. <i>Molecular Cell</i> , 2021, 81, 1920-1934.e9.	4.5	45
21	Cryo-EM structure of mammalian RNA polymerase II in complex with human RPAP2. <i>Communications Biology</i> , 2021, 4, 606.	2.0	11
22	Structures and implications of TBP nucleosome complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
23	The total mRNA concentration buffering system in yeast is global rather than gene-specific. <i>Rna</i> , 2021, 27, 1281-1290.	1.6	11
24	Structure of RNA polymerase II pre-initiation complex at 2.9 Å defines initial DNA opening. <i>Cell</i> , 2021, 184, 4064-4072.e28.	13.5	42
25	The structure of a dimeric form of SARS-CoV-2 polymerase. <i>Communications Biology</i> , 2021, 4, 999.	2.0	9
26	Two distinct mechanisms of RNA polymerase II elongation stimulation in vivo. <i>Molecular Cell</i> , 2021, 81, 3096-3109.e8.	4.5	53
27	Allosteric transcription stimulation by RNA polymerase II super elongation complex. <i>Molecular Cell</i> , 2021, 81, 3386-3399.e10.	4.5	17
28	AlphaFold2 and the future of structural biology. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 704-705.	3.6	192
29	Mechanism of molnupiravir-induced SARS-CoV-2 mutagenesis. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 740-746.	3.6	450
30	Structural basis of human transcription DNA repair coupling. <i>Nature</i> , 2021, 598, 368-372.	13.7	59
31	Structure of an inactive RNA polymerase II dimer. <i>Nucleic Acids Research</i> , 2021, 49, 10747-10755.	6.5	8
32	Structural basis of RNA processing by human mitochondrial RNase P. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 713-723.	3.6	48
33	Mechanism of SARS-CoV-2 polymerase stalling by remdesivir. <i>Nature Communications</i> , 2021, 12, 279.	5.8	412
34	Structural basis of Integrator-mediated transcription regulation. <i>Science</i> , 2021, 374, 883-887.	6.0	78
35	Structure of H3K36-methylated nucleosome PWWP complex reveals multivalent cross-gyre binding. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 8-13.	3.6	57
36	Rosalind Franklin and the Advent of Molecular Biology. <i>Cell</i> , 2020, 182, 787-789.	13.5	3

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37	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020, 369, 554-557.	6.0	192
38	CDK12 globally stimulates RNA polymerase II transcription elongation and carboxyl-terminal domain phosphorylation. <i>Nucleic Acids Research</i> , 2020, 48, 7712-7727.	6.5	58
39	Structure of replicating SARS-CoV-2 polymerase. <i>Nature</i> , 2020, 584, 154-156.	13.7	627
40	Native molecule sequencing by nano-ID reveals synthesis and stability of RNA isoforms. <i>Genome Research</i> , 2020, 30, 1332-1344.	2.4	29
41	Structural Biology of RNA Polymerase II Transcription: 20 Years On. <i>Annual Review of Cell and Developmental Biology</i> , 2020, 36, 1-34.	4.0	76
42	Small-molecule inhibitors of human mitochondrial DNA transcription. <i>Nature</i> , 2020, 588, 712-716.	13.7	115
43	Selective Mediator dependence of cell-type-specifying transcription. <i>Nature Genetics</i> , 2020, 52, 719-727.	9.4	84
44	Structure of complete Pol IIâ€“DSIFâ€“PAFâ€“SPT6 transcription complex reveals RTF1 allosteric activation. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 668-677.	3.6	98
45	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. <i>Nature Genetics</i> , 2020, 52, 655-661.	9.4	98
46	Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. <i>Nature</i> , 2020, 579, 448-451.	13.7	106
47	500 years after the first circumnavigation of the world: the efforts, rewards and drawbacks of exploration. <i>FEBS Letters</i> , 2020, 594, 207-208.	1.3	0
48	Structure of the transcription coactivator SAGA. <i>Nature</i> , 2020, 577, 717-720.	13.7	112
49	Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. <i>Nature</i> , 2020, 580, 669-672.	13.7	177
50	Nucleosome-CHD4 chromatin remodeler structure maps human disease mutations. <i>ELife</i> , 2020, 9, .	2.8	52
51	The pause-initiation limit restricts transcription activation in human cells. <i>Nature Communications</i> , 2019, 10, 3603.	5.8	60
52	NASC-seq monitors RNA synthesis in single cells. <i>Nature Communications</i> , 2019, 10, 3138.	5.8	75
53	Global donor and acceptor splicing site kinetics in human cells. <i>ELife</i> , 2019, 8, .	2.8	51
54	Structural basis of TFIIH activation for nucleotide excision repair. <i>Nature Communications</i> , 2019, 10, 2885.	5.8	112

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55	Eukaryotic Transcription Turns 50. <i>Cell</i> , 2019, 179, 808-812.	13.5	35
56	Organization and regulation of gene transcription. <i>Nature</i> , 2019, 573, 45-54.	13.7	431
57	Structure of the super-elongation complex subunit AFF4 C-terminal homology domain reveals requirements for AFF homo- and heterodimerization. <i>Journal of Biological Chemistry</i> , 2019, 294, 10663-10673.	1.6	24
58	MYC Recruits SPT5 to RNA Polymerase II to Promote Processive Transcription Elongation. <i>Molecular Cell</i> , 2019, 74, 674-687.e11.	4.5	89
59	Yeast mitochondrial protein Pet111p binds directly to two distinct targets in COX2 mRNA, suggesting a mechanism of translational activation. <i>Journal of Biological Chemistry</i> , 2019, 294, 7528-7536.	1.6	14
60	Real-time cryo-electron microscopy data preprocessing with Warp. <i>Nature Methods</i> , 2019, 16, 1146-1152.	9.0	833
61	Structural Basis of Poxvirus Transcription: Transcribing and Capping Vaccinia Complexes. <i>Cell</i> , 2019, 179, 1525-1536.e12.	13.5	37
62	Structural Basis of Poxvirus Transcription: Vaccinia RNA Polymerase Complexes. <i>Cell</i> , 2019, 179, 1537-1550.e19.	13.5	41
63	The Implication of Early Chromatin Changes in X Chromosome Inactivation. <i>Cell</i> , 2019, 176, 182-197.e23.	13.5	207
64	Promoter Distortion and Opening in the RNA Polymerase II Cleft. <i>Molecular Cell</i> , 2019, 73, 97-106.e4.	4.5	65
65	Transcriptome maps of general eukaryotic RNA degradation factors. <i>ELife</i> , 2019, 8, .	2.8	23
66	Cryo-EM structure of a mammalian RNA polymerase II elongation complex inhibited by Î±-amanitin. <i>Journal of Biological Chemistry</i> , 2018, 293, 7189-7194.	1.6	37
67	Structure of transcribing RNA polymerase II-nucleosome complex. <i>Nature Communications</i> , 2018, 9, 5432.	5.8	85
68	The APT complex is involved in non-coding RNA transcription and is distinct from CPF. <i>Nucleic Acids Research</i> , 2018, 46, 11528-11538.	6.5	17
69	The interaction landscape between transcription factors and the nucleosome. <i>Nature</i> , 2018, 562, 76-81.	13.7	259
70	Structural basis of mitochondrial transcription. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 754-765.	3.6	67
71	Distinct Mechanisms of Transcription Initiation by RNA Polymerases I and II. <i>Annual Review of Biophysics</i> , 2018, 47, 425-446.	4.5	63
72	RNA polymerase II clustering through carboxy-terminal domain phase separation. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 833-840.	3.6	456

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73	RNA velocity of single cells. <i>Nature</i> , 2018, 560, 494-498.	13.7	2,602
74	Structure of activated transcription complex Pol IIâ€“DSIFâ€“PAFâ€“SPT6. <i>Nature</i> , 2018, 560, 607-612.	13.7	300
75	Structure of paused transcription complex Pol IIâ€“DSIFâ€“NELF. <i>Nature</i> , 2018, 560, 601-606.	13.7	262
76	Architecture of a transcribing-translating expressome. <i>Science</i> , 2017, 356, 194-197.	6.0	163
77	Structural Molecular Biologyâ€“A Personal Reflection on the Occasion of John Kendrew's 100th Birthday. <i>Journal of Molecular Biology</i> , 2017, 429, 2603-2610.	2.0	2
78	Core Mediator structure at 3.4 Å... extends model of transcription initiation complex. <i>Nature</i> , 2017, 545, 248-251.	13.7	100
79	Conserved RNA polymerase II initiation complex structure. <i>Current Opinion in Structural Biology</i> , 2017, 47, 17-22.	2.6	46
80	Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex. <i>Nature Communications</i> , 2017, 8, 15741.	5.8	80
81	The conserved protein Seb1 drives transcription termination by binding RNA polymerase II and nascent RNA. <i>Nature Communications</i> , 2017, 8, 14861.	5.8	48
82	Structural Basis of RNA Polymerase I Transcription Initiation. <i>Cell</i> , 2017, 169, 120-131.e22.	13.5	101
83	Spt5 Plays Vital Roles in the Control of Sense and Antisense Transcription Elongation. <i>Molecular Cell</i> , 2017, 66, 77-88.e5.	4.5	90
84	TTâ€“seq captures enhancer landscapes immediately after Tâ€“cell stimulation. <i>Molecular Systems Biology</i> , 2017, 13, 920.	3.2	44
85	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. <i>Molecular Cell</i> , 2017, 66, 38-49.e6.	4.5	100
86	Structures of transcription pre-initiation complex with TFIID and Mediator. <i>Nature</i> , 2017, 551, 204-209.	13.7	219
87	Nucleosomeâ€“Chd1 structure and implications for chromatin remodelling. <i>Nature</i> , 2017, 550, 539-542.	13.7	205
88	Mechanism of Transcription Anti-termination in Human Mitochondria. <i>Cell</i> , 2017, 171, 1082-1093.e13.	13.5	68
89	Structure of a transcribing RNA polymerase IIâ€“DSIF complex reveals a multidentate DNAâ€“RNA clamp. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 809-815.	3.6	130
90	Structural Basis of Mitochondrial Transcription Initiation. <i>Cell</i> , 2017, 171, 1072-1081.e10.	13.5	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.	3.3	18
92	CDK9-dependent RNA polymerase II pausing controls transcription initiation. ELife, 2017, 6, .	2.8	179
93	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. PLoS ONE, 2017, 12, e0169249.	1.1	73
94	RNA-dependent chromatin association of transcription elongation factors and Pol II CTD kinases. ELife, 2017, 6, .	2.8	48
95	Inference of gene regulation functions from dynamic transcriptome data. ELife, 2016, 5, .	2.8	12
96	Determinants of <sc>RNA</sc> metabolism in the <i>Schizosaccharomyces pombe</i> genome. Molecular Systems Biology, 2016, 12, 857.	3.2	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.	3.3	98
98	Structure of GPN-Loop GTPase Npa3 and Implications for RNA Polymerase II Assembly. Molecular and Cellular Biology, 2016, 36, 820-831.	1.1	37
99	Transcription initiation complex structures elucidate DNA opening. Nature, 2016, 533, 353-358.	13.7	250
100	Structure determination of transient transcription complexes. Biochemical Society Transactions, 2016, 44, 1177-1182.	1.6	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.	3.3	13
102	RNA polymerase “Rn3 complex at 4.8 Å... resolution. Nature Communications, 2016, 7, 12129.	5.8	58
103	TT-seq maps the human transient transcriptome. Science, 2016, 352, 1225-1228.	6.0	384
104	Structure of transcribing mammalian RNA polymerase II. Nature, 2016, 529, 551-554.	13.7	174
105	Heptad-Specific Phosphorylation of RNA Polymerase“II CTD. Molecular Cell, 2016, 61, 305-314.	4.5	118
106	Mediator Architecture and RNA Polymerase II Interaction. Journal of Molecular Biology, 2016, 428, 2569-2574.	2.0	50
107	Architecture and RNA binding of the human negative elongation factor. ELife, 2016, 5, .	2.8	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.	1.5	4

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109	Architecture of the RNA polymerase II "Mediator core initiation complex. <i>Nature</i> , 2015, 518, 376-380.	13.7	259
110	Structural basis of transcription initiation by RNA polymerase II. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 129-143.	16.1	322
111	<i>BRF1</i> mutations alter RNA polymerase III-dependent transcription and cause neurodevelopmental anomalies. <i>Genome Research</i> , 2015, 25, 155-166.	2.4	85
112	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	4.5	109
113	An alternative RNA polymerase I structure reveals a dimer hinge. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1850-1855.	2.5	16
114	A model for transcription initiation in human mitochondria. <i>Nucleic Acids Research</i> , 2015, 43, 3726-3735.	6.5	60
115	Structure-Based Prediction of Asparagine and Aspartate Degradation Sites in Antibody Variable Regions. <i>PLoS ONE</i> , 2014, 9, e100736.	1.1	128
116	Annotation of genomics data using bidirectional hidden Markov models unveils variations in Pol II transcription cycle. <i>Molecular Systems Biology</i> , 2014, 10, 768.	3.2	21
117	Periodic mRNA synthesis and degradation cooperate during cell cycle gene expression. <i>Molecular Systems Biology</i> , 2014, 10, 717.	3.2	80
118	A novel intermediate in transcription initiation by human mitochondrial RNA polymerase. <i>Nucleic Acids Research</i> , 2014, 42, 3884-3893.	6.5	60
119	Conserved architecture of the core RNA polymerase II initiation complex. <i>Nature Communications</i> , 2014, 5, 4310.	5.8	37
120	A Tale of Chromatin and Transcription in 100 Structures. <i>Cell</i> , 2014, 159, 985-994.	13.5	25
121	RNA polymerase II termination involves C-terminal-domain tyrosine dephosphorylation by CPF subunit G1c7. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 175-179.	3.6	77
122	Rpb4 Subunit Functions Mainly in mRNA Synthesis by RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2014, 289, 17446-17452.	1.6	41
123	Molecular Basis for Coordinating Transcription Termination with Noncoding RNA Degradation. <i>Molecular Cell</i> , 2014, 55, 467-481.	4.5	99
124	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. <i>Molecular Cell</i> , 2014, 55, 745-757.	4.5	99
125	RNA polymerase I structure and transcription regulation. <i>Nature</i> , 2013, 502, 650-655.	13.7	193
126	Structure of human mitochondrial RNA polymerase elongation complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1298-1303.	3.6	67

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127	Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. <i>Cell</i> , 2013, 155, 1075-1087.	13.5	201
128	Structural basis of transcription elongation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 9-19.	0.9	79
129	Structure and function of the initially transcribing RNA polymerase II-TFIIB complex. <i>Nature</i> , 2013, 493, 437-440.	13.7	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. <i>Journal of Biological Chemistry</i> , 2013, 288, 36676-36690.	1.6	21
131	Global Analysis of Eukaryotic mRNA Degradation Reveals Xrn1-Dependent Buffering of Transcript Levels. <i>Molecular Cell</i> , 2013, 52, 52-62.	4.5	218
132	Cap Completion and C-Terminal Repeat Domain Kinase Recruitment Underlie the Initiation-Elongation Transition of RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2013, 33, 3805-3816.	1.1	53
133	Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. <i>Genome Research</i> , 2012, 22, 1350-1359.	2.4	255
134	Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). <i>Bioinformatics</i> , 2012, 28, 884-885.	1.8	24
135	Structure of the Mediator head module. <i>Nature</i> , 2012, 492, 448-451.	13.7	89
136	The Spt5 C-Terminal Region Recruits Yeast 3' RNA Cleavage Factor I. <i>Molecular and Cellular Biology</i> , 2012, 32, 1321-1331.	1.1	56
137	Conservation between the RNA Polymerase I, II, and III Transcription Initiation Machineries. <i>Molecular Cell</i> , 2012, 45, 439-446.	4.5	357
138	Mechanism of Translesion Transcription by RNA Polymerase II and Its Role in Cellular Resistance to DNA Damage. <i>Molecular Cell</i> , 2012, 46, 18-29.	4.5	104
139	A Movie of RNA Polymerase II Transcription. <i>Cell</i> , 2012, 149, 1431-1437.	13.5	105
140	CTD Tyrosine Phosphorylation Impairs Termination Factor Recruitment to RNA Polymerase II. <i>Science</i> , 2012, 336, 1723-1725.	6.0	215
141	A structural perspective on Mediator function. <i>Current Opinion in Cell Biology</i> , 2012, 24, 305-313.	2.6	70
142	Biogenesis of multisubunit RNA polymerases. <i>Trends in Biochemical Sciences</i> , 2012, 37, 99-105.	3.7	83
143	Structure of human mitochondrial RNA polymerase. <i>Nature</i> , 2011, 478, 269-273.	13.7	175
144	Iwr1 Directs RNA Polymerase II Nuclear Import. <i>Molecular Cell</i> , 2011, 42, 261-266.	4.5	82

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145	Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. <i>Molecular Systems Biology</i> , 2011, 7, 458.	3.2	333
146	Structure and VP16 binding of the Mediator Med25 activator interaction domain. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 404-409.	3.6	103
147	Architecture of the RNA polymerase-Spt4/5 complex and basis of universal transcription processivity. <i>EMBO Journal</i> , 2011, 30, 1302-1310.	3.5	209
148	Structural basis of RNA polymerase II backtracking, arrest and reactivation. <i>Nature</i> , 2011, 471, 249-253.	13.7	310
149	Mediator head subcomplex Med11/22 contains a common helix bundle building block with a specific function in transcription initiation complex stabilization. <i>Nucleic Acids Research</i> , 2011, 39, 6291-6304.	6.5	38
150	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011, 25, 2093-2105.	2.7	87
151	A Cytoplasmic Complex Mediates Specific mRNA Recognition and Localization in Yeast. <i>PLoS Biology</i> , 2011, 9, e1000611.	2.6	72
152	Structural basis of initial RNA polymerase II transcription. <i>EMBO Journal</i> , 2011, 30, 4755-4763.	3.5	82
153	Uniform transitions of the general RNA polymerase II transcription complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1272-1278.	3.6	399
154	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. <i>EMBO Journal</i> , 2010, 29, 717-726.	3.5	355
155	A Tandem SH2 Domain in Transcription Elongation Factor Spt6 Binds the Phosphorylated RNA Polymerase II C-terminal Repeat Domain (CTD). <i>Journal of Biological Chemistry</i> , 2010, 285, 41597-41603.	1.6	76
156	Spt4/5 stimulates transcription elongation through the RNA polymerase clamp coiled-coil motif. <i>Nucleic Acids Research</i> , 2010, 38, 4040-4051.	6.5	150
157	Towards molecular systems biology of gene transcription and regulation. <i>Biological Chemistry</i> , 2010, 391, 731-5.	1.2	3
158	RNA Polymerase I Contains a TFIIF-Related DNA-Binding Subcomplex. <i>Molecular Cell</i> , 2010, 39, 583-594.	4.5	120
159	Molecular Basis of RNA Polymerase III Transcription Repression by Maf1. <i>Cell</i> , 2010, 143, 59-70.	13.5	156
160	Nano positioning system reveals the course of upstream and nontemplate DNA within the RNA polymerase II elongation complex. <i>Nucleic Acids Research</i> , 2009, 37, 5803-5809.	6.5	80
161	RNA polymerase II-TFIIB structure and mechanism of transcription initiation. <i>Nature</i> , 2009, 462, 323-330.	13.7	266
162	Structure and in Vivo Requirement of the Yeast Spt6 SH2 Domain. <i>Journal of Molecular Biology</i> , 2009, 389, 211-225.	2.0	47

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163	Structural Basis of Transcription: Mismatch-Specific Fidelity Mechanisms and Paused RNA Polymerase II with Frayed RNA. <i>Molecular Cell</i> , 2009, 34, 710-721.	4.5	161
164	Structural basis of transcription inhibition by Î±-amanitin and implications for RNA polymerase II translocation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 811-818.	3.6	223
165	A nano-positioning system for macromolecular structural analysis. <i>Nature Methods</i> , 2008, 5, 965-971.	9.0	183
166	Structure of Eukaryotic RNA Polymerases. <i>Annual Review of Biophysics</i> , 2008, 37, 337-352.	4.5	251
167	Single-molecule tracking of mRNA exiting from RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 135-140.	3.3	102
168	CPD Damage Recognition by Transcribing RNA Polymerase II. <i>Science</i> , 2007, 315, 859-862.	6.0	209
169	Functional Architecture of RNA Polymerase I. <i>Cell</i> , 2007, 131, 1260-1272.	13.5	192
170	Mechanism of transcriptional stalling at cisplatin-damaged DNA. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1127-1133.	3.6	149
171	Molecular basis of RNA-dependent RNA polymerase II activity. <i>Nature</i> , 2007, 450, 445-449.	13.7	125
172	Structural Biology of RNA Polymerase III: Mass Spectrometry Elucidates Subcomplex Architecture. <i>Structure</i> , 2007, 15, 1237-1245.	1.6	85
173	MOLECULAR BIOLOGY: Self-Correcting Messages. <i>Science</i> , 2006, 313, 447-448.	6.0	7
174	Structural Biology of RNA Polymerase III: Subcomplex C17/25 X-Ray Structure and 11 Subunit Enzyme Model. <i>Molecular Cell</i> , 2006, 23, 71-81.	4.5	80
175	Recent structural studies of RNA polymerases II and III. <i>Biochemical Society Transactions</i> , 2006, 34, 1058-1061.	1.6	10
176	Structure and TBP binding of the Mediator head subcomplex Med8â€“Med18â€“Med20. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 895-901.	3.6	96
177	Deciphering the RNA polymerase II structure: a personal perspective. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 1042-1044.	3.6	3
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