

Patrick Cramer

List of Publications by Year in descending order

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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	RNA velocity of single cells. Nature, 2018, 560, 494-498.	13.7	2,602
2	Structural Basis of Transcription: RNA Polymerase II at 2.8 Angstrom Resolution. Science, 2001, 292, 1863-1876.	6.0	1,118
3	Structural Basis of Transcription: An RNA Polymerase II Elongation Complex at 3.3 A Resolution. Science, 2001, 292, 1876-1882.	6.0	834
4	Real-time cryo-electron microscopy data preprocessing with Warp. Nature Methods, 2019, 16, 1146-1152.	9.0	833
5	Structure of replicating SARS-CoV-2 polymerase. Nature, 2020, 584, 154-156.	13.7	627
6	Architecture of RNA Polymerase II and Implications for the Transcription Mechanism. Science, 2000, 288, 640-649.	6.0	570
7	RNA polymerase II clustering through carboxy-terminal domain phase separation. Nature Structural and Molecular Biology, 2018, 25, 833-840.	3.6	456
8	Mechanism of molnupiravir-induced SARS-CoV-2 mutagenesis. Nature Structural and Molecular Biology, 2021, 28, 740-746.	3.6	450
9	Organization and regulation of gene transcription. Nature, 2019, 573, 45-54.	13.7	431
10	Mechanism of SARS-CoV-2 polymerase stalling by remdesivir. Nature Communications, 2021, 12, 279.	5.8	412
11	Uniform transitions of the general RNA polymerase II transcription complex. Nature Structural and Molecular Biology, 2010, 17, 1272-1278.	3.6	399
12	Complete RNA Polymerase II Elongation Complex Structure and Its Interactions with NTP and TFIIIS. Molecular Cell, 2004, 16, 955-965.	4.5	384
13	TT-seq maps the human transient transcriptome. Science, 2016, 352, 1225-1228.	6.0	384
14	Conservation between the RNA Polymerase I, II, and III Transcription Initiation Machineries. Molecular Cell, 2012, 45, 439-446.	4.5	357
15	Architecture of the RNA polymerase II-TFIIF complex revealed by cross-linking and mass spectrometry. EMBO Journal, 2010, 29, 717-726.	3.5	355
16	Dynamic transcriptome analysis measures rates of mRNA synthesis and decay in yeast. Molecular Systems Biology, 2011, 7, 458.	3.2	333
17	Structural basis of transcription initiation by RNA polymerase II. Nature Reviews Molecular Cell Biology, 2015, 16, 129-143.	16.1	322
18	Structural basis of RNA polymerase II backtracking, arrest and reactivation. Nature, 2011, 471, 249-253.	13.7	310

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19	Structure of activated transcription complex Pol IIâ€“DSIFâ€“PAFâ€“SPT6. <i>Nature</i> , 2018, 560, 607-612.	13.7	300
20	Architecture of the RNA Polymerase II-TFIIS Complex and Implications for mRNA Cleavage. <i>Cell</i> , 2003, 114, 347-357.	13.5	298
21	A structural perspective of CTD function. <i>Genes and Development</i> , 2005, 19, 1401-1415.	2.7	276
22	Coupling of Transcription with Alternative Splicing. <i>Molecular Cell</i> , 1999, 4, 251-258.	4.5	274
23	Structural basis of transcription: \hat{A} -Amanitin-RNA polymerase II cocrystal at 2.8 Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 1218-1222.	3.3	273
24	RNA polymerase IIâ€“TFIIB structure and mechanism of transcription initiation. <i>Nature</i> , 2009, 462, 323-330.	13.7	266
25	Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.5â€“Å... in cells. <i>Nature Methods</i> , 2021, 18, 186-193.	9.0	265
26	Structure of paused transcription complex Pol IIâ€“DSIFâ€“NELF. <i>Nature</i> , 2018, 560, 601-606.	13.7	262
27	Recognition of RNA polymerase II carboxy-terminal domain by 3â€“RNA-processing factors. <i>Nature</i> , 2004, 430, 223-226.	13.7	260
28	Architecture of the RNA polymerase IIâ€“Mediator core initiation complex. <i>Nature</i> , 2015, 518, 376-380.	13.7	259
29	The interaction landscape between transcription factors and the nucleosome. <i>Nature</i> , 2018, 562, 76-81.	13.7	259
30	Comparative dynamic transcriptome analysis (cDTA) reveals mutual feedback between mRNA synthesis and degradation. <i>Genome Research</i> , 2012, 22, 1350-1359.	2.4	255
31	Structure of Eukaryotic RNA Polymerases. <i>Annual Review of Biophysics</i> , 2008, 37, 337-352.	4.5	251
32	Transcription initiation complex structures elucidate DNA opening. <i>Nature</i> , 2016, 533, 353-358.	13.7	250
33	Multisubunit RNA polymerases. <i>Current Opinion in Structural Biology</i> , 2002, 12, 89-97.	2.6	224
34	Structural basis of transcription inhibition by \hat{A} -amanitin and implications for RNA polymerase II translocation. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 811-818.	3.6	223
35	Structures of transcription pre-initiation complex with TFIIF and Mediator. <i>Nature</i> , 2017, 551, 204-209.	13.7	219
36	Architecture of initiation-competent 12-subunit RNA polymerase II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 6964-6968.	3.3	218

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37	Global Analysis of Eukaryotic mRNA Degradation Reveals Xrn1-Dependent Buffering of Transcript Levels. <i>Molecular Cell</i> , 2013, 52, 52-62.	4.5	218
38	CTD Tyrosine Phosphorylation Impairs Termination Factor Recruitment to RNA Polymerase II. <i>Science</i> , 2012, 336, 1723-1725.	6.0	215
39	CPD Damage Recognition by Transcribing RNA Polymerase II. <i>Science</i> , 2007, 315, 859-862.	6.0	209
40	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
41	The Implication of Early Chromatin Changes in X Chromosome Inactivation. <i>Cell</i> , 2019, 176, 182-197.e23.	13.5	207
42	Nucleosome- α Chd1 structure and implications for chromatin remodelling. <i>Nature</i> , 2017, 550, 539-542.	13.7	205
43	Structures of Complete RNA Polymerase II and Its Subcomplex, Rpb4/7. <i>Journal of Biological Chemistry</i> , 2005, 280, 7131-7134.	1.6	201
44	Transcriptome Surveillance by Selective Termination of Noncoding RNA Synthesis. <i>Cell</i> , 2013, 155, 1075-1087.	13.5	201
45	RNA polymerase I structure and transcription regulation. <i>Nature</i> , 2013, 502, 650-655.	13.7	193
46	Functional Architecture of RNA Polymerase I. <i>Cell</i> , 2007, 131, 1260-1272.	13.5	192
47	In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , 2020, 369, 554-557.	6.0	192
48	AlphaFold2 and the future of structural biology. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 704-705.	3.6	192
49	A nano-positioning system for macromolecular structural analysis. <i>Nature Methods</i> , 2008, 5, 965-971.	9.0	183
50	CDK9-dependent RNA polymerase II pausing controls transcription initiation. <i>ELife</i> , 2017, 6, .	2.8	179
51	Nucleosome-bound SOX2 and SOX11 structures elucidate pioneer factor function. <i>Nature</i> , 2020, 580, 669-672.	13.7	177
52	Structure of human mitochondrial RNA polymerase. <i>Nature</i> , 2011, 478, 269-273.	13.7	175
53	Structure of transcribing mammalian RNA polymerase II. <i>Nature</i> , 2016, 529, 551-554.	13.7	174
54	Structure and function of the initially transcribing RNA polymerase II- α TFIIB complex. <i>Nature</i> , 2013, 493, 437-440.	13.7	170

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55	Architecture of a transcribing-translating expressome. <i>Science</i> , 2017, 356, 194-197.	6.0	163
56	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
57	Molecular Basis of RNA Polymerase III Transcription Repression by Maf1. <i>Cell</i> , 2010, 143, 59-70.	13.5	156
58	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
59	Mechanism of transcriptional stalling at cisplatin-damaged DNA. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 1127-1133.	3.6	149
60	Structural Basis of Mitochondrial Transcription Initiation. <i>Cell</i> , 2017, 171, 1072-1081.e10.	13.5	131
61	Structure of a transcribing RNA polymerase II-DSIF complex reveals a multidentate DNA-RNA clamp. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 809-815.	3.6	130
62	Structure-Based Prediction of Asparagine and Aspartate Degradation Sites in Antibody Variable Regions. <i>PLoS ONE</i> , 2014, 9, e100736.	1.1	128
63	Structure of the human NF-kappa B p52 homodimer-DNA complex at 2.1 Å resolution. <i>EMBO Journal</i> , 1997, 16, 7078-7090.	3.5	126
64	Molecular basis of RNA-dependent RNA polymerase II activity. <i>Nature</i> , 2007, 450, 445-449.	13.7	125
65	Structure and Mechanism of RNA Polymerase II CTD Phosphatases. <i>Molecular Cell</i> , 2004, 15, 399-407.	4.5	121
66	RNA Polymerase I Contains a TFIIF-Related DNA-Binding Subcomplex. <i>Molecular Cell</i> , 2010, 39, 583-594.	4.5	120
67	Heptad-Specific Phosphorylation of RNA Polymerase II CTD. <i>Molecular Cell</i> , 2016, 61, 305-314.	4.5	118
68	Small-molecule inhibitors of human mitochondrial DNA transcription. <i>Nature</i> , 2020, 588, 712-716.	13.7	115
69	Structural basis of TFIIH activation for nucleotide excision repair. <i>Nature Communications</i> , 2019, 10, 2885.	5.8	112
70	Structure of the transcription coactivator SAGA. <i>Nature</i> , 2020, 577, 717-720.	13.7	112
71	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	4.5	109
72	Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. <i>Nature</i> , 2020, 579, 448-451.	13.7	106

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73	A Movie of RNA Polymerase II Transcription. <i>Cell</i> , 2012, 149, 1431-1437.	13.5	105
74	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
75	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
76	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
77	Structural Basis of RNA Polymerase I Transcription Initiation. <i>Cell</i> , 2017, 169, 120-131.e22.	13.5	101
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	Genome-wide Analysis of RNA Polymerase II Termination at Protein-Coding Genes. <i>Molecular Cell</i> , 2017, 66, 38-49.e6.	4.5	100
80	Molecular Basis for Coordinating Transcription Termination with Noncoding RNA Degradation. <i>Molecular Cell</i> , 2014, 55, 467-481.	4.5	99
81	Transcriptome Maps of mRNP Biogenesis Factors Define Pre-mRNA Recognition. <i>Molecular Cell</i> , 2014, 55, 745-757.	4.5	99
82	Mechanisms of backtrack recovery by RNA polymerases I and II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2946-2951.	3.3	98
83	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
84	CTCF is dispensable for immune cell transdifferentiation but facilitates an acute inflammatory response. <i>Nature Genetics</i> , 2020, 52, 655-661.	9.4	98
85	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
86	Structure of a bifunctional DNA primase-polymerase. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 157-162.	3.6	92
87	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
88	Structure of the Mediator head module. <i>Nature</i> , 2012, 492, 448-451.	13.7	89
89	MYC Recruits SPT5 to RNA Polymerase II to Promote Processive Transcription Elongation. <i>Molecular Cell</i> , 2019, 74, 674-687.e11.	4.5	89
90	Molecular basis of Rrn3-regulated RNA polymerase I initiation and cell growth. <i>Genes and Development</i> , 2011, 25, 2093-2105.	2.7	87

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91	Sequence determinants of human gene regulatory elements. <i>Nature Genetics</i> , 2022, 54, 283-294.	9.4	87
92	Structural Biology of RNA Polymerase III: Mass Spectrometry Elucidates Subcomplex Architecture. <i>Structure</i> , 2007, 15, 1237-1245.	1.6	85
93	<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
94	Structure of transcribing RNA polymerase II-nucleosome complex. <i>Nature Communications</i> , 2018, 9, 5432.	5.8	85
95	Selective Mediator dependence of cell-type-specifying transcription. <i>Nature Genetics</i> , 2020, 52, 719-727.	9.4	84
96	Biogenesis of multisubunit RNA polymerases. <i>Trends in Biochemical Sciences</i> , 2012, 37, 99-105.	3.7	83
97	Stress-induced nuclear condensation of NELF drives transcriptional downregulation. <i>Molecular Cell</i> , 2021, 81, 1013-1026.e11.	4.5	83
98	<i>Iwr1</i> Directs RNA Polymerase II Nuclear Import. <i>Molecular Cell</i> , 2011, 42, 261-266.	4.5	82
99	Structural basis of initial RNA polymerase II transcription. <i>EMBO Journal</i> , 2011, 30, 4755-4763.	3.5	82
100	Integrator is a genome-wide attenuator of non-productive transcription. <i>Molecular Cell</i> , 2021, 81, 514-529.e6.	4.5	82
101	Determinants of <i>scp</i> RNA metabolism in the <i>Schizosaccharomyces pombe</i> genome. <i>Molecular Systems Biology</i> , 2016, 12, 857.	3.2	81
102	An Extended Winged Helix Domain in General Transcription Factor E/IF4. <i>Journal of Biological Chemistry</i> , 2003, 278, 48267-48274.	1.6	80
103	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
104	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
105	Periodic <i>scp</i> mRNA synthesis and degradation cooperate during cell cycle gene expression. <i>Molecular Systems Biology</i> , 2014, 10, 717.	3.2	80
106	Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex. <i>Nature Communications</i> , 2017, 8, 15741.	5.8	80
107	Structural basis of transcription elongation. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 9-19.	0.9	79
108	Structural basis of Integrator-mediated transcription regulation. <i>Science</i> , 2021, 374, 883-887.	6.0	78

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109	RNA polymerase II termination involves C-terminal-domain tyrosine dephosphorylation by CPF subunit Glc7. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 175-179.	3.6	77
110	Structure and Carboxyl-terminal Domain (CTD) Binding of the Set2 SRI Domain That Couples Histone H3 Lys36 Methylation to Transcription*. <i>Journal of Biological Chemistry</i> , 2006, 281, 13-15.	1.6	76
111	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
112	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
113	NASC-seq monitors RNA synthesis in single cells. <i>Nature Communications</i> , 2019, 10, 3138.	5.8	75
114	Accurate Promoter and Enhancer Identification in 127 ENCODE and Roadmap Epigenomics Cell Types and Tissues by GenoSTAN. <i>PLoS ONE</i> , 2017, 12, e0169249.	1.1	73
115	Structure of the human Mediator-RNA polymerase II pre-initiation complex. <i>Nature</i> , 2021, 594, 129-133.	13.7	73
116	RNA polymerase II structure: from core to functional complexes. <i>Current Opinion in Genetics and Development</i> , 2004, 14, 218-226.	1.5	72
117	A Cytoplasmic Complex Mediates Specific mRNA Recognition and Localization in Yeast. <i>PLoS Biology</i> , 2011, 9, e1000611.	2.6	72
118	Structural basis of nucleosome transcription mediated by Chd1 and FACT. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 382-387.	3.6	72
119	Structure of a transcribing RNA polymerase II-U1 snRNP complex. <i>Science</i> , 2021, 371, 305-309.	6.0	71
120	A structural perspective on Mediator function. <i>Current Opinion in Cell Biology</i> , 2012, 24, 305-313.	2.6	70
121	Mechanism of Transcription Anti-termination in Human Mitochondria. <i>Cell</i> , 2017, 171, 1082-1093.e13.	13.5	68
122	Structure of human mitochondrial RNA polymerase elongation complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1298-1303.	3.6	67
123	Structural basis of mitochondrial transcription. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 754-765.	3.6	67
124	Promoter Distortion and Opening in the RNA Polymerase II Cleft. <i>Molecular Cell</i> , 2019, 73, 97-106.e4.	4.5	65
125	Evidence for additive and synergistic action of mammalian enhancers during cell fate determination. <i>ELife</i> , 2021, 10, .	2.8	64
126	Distinct Mechanisms of Transcription Initiation by RNA Polymerases I and II. <i>Annual Review of Biophysics</i> , 2018, 47, 425-446.	4.5	63

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127	Structures of mammalian RNA polymerase II pre-initiation complexes. <i>Nature</i> , 2021, 594, 124-128.	13.7	63
128	A novel intermediate in transcription initiation by human mitochondrial RNA polymerase. <i>Nucleic Acids Research</i> , 2014, 42, 3884-3893.	6.5	60
129	A model for transcription initiation in human mitochondria. <i>Nucleic Acids Research</i> , 2015, 43, 3726-3735.	6.5	60
130	The pause-initiation limit restricts transcription activation in human cells. <i>Nature Communications</i> , 2019, 10, 3603.	5.8	60
131	A Conserved Mediator Hinge Revealed in the Structure of the MED7-MED21 (Med7-Srb7) Heterodimer. <i>Journal of Biological Chemistry</i> , 2005, 280, 18171-18178.	1.6	59
132	Structural basis of human transcription-DNA repair coupling. <i>Nature</i> , 2021, 598, 368-372.	13.7	59
133	RNA polymerase Rn3 complex at 4.8 Å resolution. <i>Nature Communications</i> , 2016, 7, 12129.	5.8	58
134	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
135	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
136	The Spt5 C-Terminal Region Recruits Yeast RNA Cleavage Factor I. <i>Molecular and Cellular Biology</i> , 2012, 32, 1321-1331.	1.1	56
137	Architecture and RNA binding of the human negative elongation factor. <i>ELife</i> , 2016, 5, .	2.8	54
138	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
139	Two distinct mechanisms of RNA polymerase II elongation stimulation in vivo. <i>Molecular Cell</i> , 2021, 81, 3096-3109.e8.	4.5	53
140	Nucleosome-CHD4 chromatin remodeler structure maps human disease mutations. <i>ELife</i> , 2020, 9, .	2.8	52
141	Global donor and acceptor splicing site kinetics in human cells. <i>ELife</i> , 2019, 8, .	2.8	51
142	Mediator Architecture and RNA Polymerase II Interaction. <i>Journal of Molecular Biology</i> , 2016, 428, 2569-2574.	2.0	50
143	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
144	Structural basis of RNA processing by human mitochondrial RNase P. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 713-723.	3.6	48

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145	RNA-dependent chromatin association of transcription elongation factors and Pol II CTD kinases. <i>ELife</i> , 2017, 6, .	2.8	48
146	Structure and in Vivo Requirement of the Yeast Spt6 SH2 Domain. <i>Journal of Molecular Biology</i> , 2009, 389, 211-225.	2.0	47
147	Conserved RNA polymerase II initiation complex structure. <i>Current Opinion in Structural Biology</i> , 2017, 47, 17-22.	2.6	46
148	Efficient RNA polymerase II pause release requires U2 snRNP function. <i>Molecular Cell</i> , 2021, 81, 1920-1934.e9.	4.5	45
149	TTâ€seq captures enhancer landscapes immediately after Tâ€cell stimulation. <i>Molecular Systems Biology</i> , 2017, 13, 920.	3.2	44
150	Structure of RNA polymerase II pre-initiation complex at 2.9Å... defines initial DNA opening. <i>Cell</i> , 2021, 184, 4064-4072.e28.	13.5	42
151	Rpb4 Subunit Functions Mainly in mRNA Synthesis by RNA Polymerase II. <i>Journal of Biological Chemistry</i> , 2014, 289, 17446-17452.	1.6	41
152	Structural Basis of Poxvirus Transcription: Vaccinia RNA Polymerase Complexes. <i>Cell</i> , 2019, 179, 1537-1550.e19.	13.5	41
153	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
154	Common structural features of nucleic acid polymerases. <i>BioEssays</i> , 2002, 24, 724-729.	1.2	37
155	Conserved architecture of the core RNA polymerase II initiation complex. <i>Nature Communications</i> , 2014, 5, 4310.	5.8	37
156	Structure of GPN-Loop GTPase Npa3 and Implications for RNA Polymerase II Assembly. <i>Molecular and Cellular Biology</i> , 2016, 36, 820-831.	1.1	37
157	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
158	Structural Basis of Poxvirus Transcription: Transcribing and Capping Vaccinia Complexes. <i>Cell</i> , 2019, 179, 1525-1536.e12.	13.5	37
159	Eukaryotic Transcription Turns 50. <i>Cell</i> , 2019, 179, 808-812.	13.5	35
160	Permissive epigenomes endow reprogramming competence to transcriptional regulators. <i>Nature Chemical Biology</i> , 2021, 17, 47-56.	3.9	35
161	Ruler elements in chromatin remodelers set nucleosome array spacing and phasing. <i>Nature Communications</i> , 2021, 12, 3232.	5.8	34
162	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

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163	Structure and Function of RNA Polymerase II. <i>Advances in Protein Chemistry</i> , 2004, 67, 1-42.	4.4	32
164	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
165	Native molecule sequencing by nano-ID reveals synthesis and stability of RNA isoforms. <i>Genome Research</i> , 2020, 30, 1332-1344.	2.4	29
166	Transcriptionally active enhancers in human cancer cells. <i>Molecular Systems Biology</i> , 2021, 17, e9873.	3.2	28
167	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
168	A Tale of Chromatin and Transcription in 100 Structures. <i>Cell</i> , 2014, 159, 985-994.	13.5	25
169	Measurement of genome-wide RNA synthesis and decay rates with Dynamic Transcriptome Analysis (DTA). <i>Bioinformatics</i> , 2012, 28, 884-885.	1.8	24
170	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
171	Transcriptome maps of general eukaryotic RNA degradation factors. <i>ELife</i> , 2019, 8, .	2.8	23
172	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
173	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
174	Structures and implications of TBP- ϵ nucleosome complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	21
175	Mechanism of RNA polymerase II stalling by DNA alkylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12172-12177.	3.3	18
176	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
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