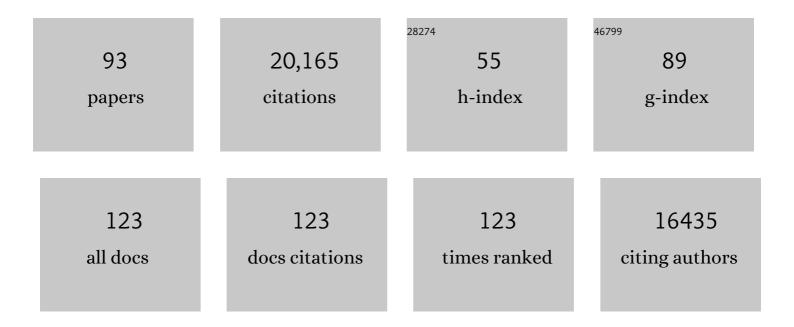
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Transcriptional Regulation in Mammalian Cells by Sequence-Specific DNA Binding Proteins. Science, 1989, 245, 371-378.	12.6	3,446
2	Analysis of Sp1 in vivo reveals mutiple transcriptional domains, including a novel glutamine-rich activation motif. Cell, 1988, 55, 887-898.	28.9	1,753
3	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. Nature, 2016, 538, 270-273.	27.8	854
4	A family of human CCAAT-box-binding proteins active in transcription and DNA replication: cloning and expression of multiple cDNAs. Nature, 1988, 334, 218-224.	27.8	802
5	Imaging dynamic and selective low-complexity domain interactions that control gene transcription. Science, 2018, 361, .	12.6	750
6	Nucleolar transcription factor hUBF contains a DNA-binding motif with homology to HMG proteins. Nature, 1990, 344, 830-836.	27.8	691
7	Single-Molecule Dynamics of Enhanceosome Assembly in Embryonic Stem Cells. Cell, 2014, 156, 1274-1285.	28.9	532
8	A glutamine-rich hydrophobic patch in transcription factor Sp1 contacts the dTAFII110 component of the Drosophila TFIID complex and mediates transcriptional activation Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 192-196.	7.1	526
9	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. ELife, 2017, 6, .	6.0	476
10	Overcoming the bottleneck to widespread testing: a rapid review of nucleic acid testing approaches for COVID-19 detection. Rna, 2020, 26, 771-783.	3.5	426
11	Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. Genes and Development, 2019, 33, 1619-1634.	5.9	424
12	Looping Back to Leap Forward: Transcription Enters a New Era. Cell, 2014, 157, 13-25.	28.9	423
13	Composite co-activator ARC mediates chromatin-directed transcriptional activation. Nature, 1999, 398, 828-832.	27.8	408
14	Distinct regions of Sp1 modulate DNA binding and transcriptional activation. Science, 1988, 242, 1566-1570.	12.6	382
15	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. Molecular Cell, 2020, 78, 539-553.e8.	9.7	380
16	DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1 Genes and Development, 1991, 5, 820-826.	5.9	354
17	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. ELife, 2016, 5, .	6.0	349
18	The transcriptional cofactor complex CRSP is required for activity of the enhancer-binding protein Sp1. Nature, 1999, 397, 446-450.	27.8	322

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19	Dynamics of CRISPR-Cas9 genome interrogation in living cells. Science, 2015, 350, 823-826.	12.6	301
20	Near-atomic resolution visualization of human transcription promoter opening. Nature, 2016, 533, 359-365.	27.8	256
21	Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation. Nature, 1993, 362, 175-179.	27.8	254
22	CASFISH: CRISPR/Cas9-mediated in situ labeling of genomic loci in fixed cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11870-11875.	7.1	243
23	Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. Nature, 2001, 414, 924-928.	27.8	238
24	TBP-TAF complexes: selectivity factors for eukaryotic transcription. Current Opinion in Cell Biology, 1994, 6, 403-409.	5.4	236
25	Structure, Function, and Activator-Induced Conformations of the CRSP Coactivator. Science, 2002, 295, 1058-1062.	12.6	230
26	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. ELife, 2019, 8, .	6.0	222
27	Bromodomains Mediate an Acetyl-Histone Encoded Antisilencing Function at Heterochromatin Boundaries. Molecular Cell, 2003, 11, 365-376.	9.7	219
28	A dynamic mode of mitotic bookmarking by transcription factors. ELife, 2016, 5, .	6.0	216
29	Robust model-based analysis of single-particle tracking experiments with Spot-On. ELife, 2018, 7, .	6.0	213
30	Structure and functional properties of human general transcription factor IIE. Nature, 1991, 354, 369-373.	27.8	209
31	3D imaging of Sox2 enhancer clusters in embryonic stem cells. ELife, 2014, 3, e04236.	6.0	204
32	Recent evidence that TADs and chromatin loops are dynamic structures. Nucleus, 2018, 9, 20-32.	2.2	188
33	Unexpected roles for core promoter recognition factors in cell-type-specific transcription and gene regulation. Nature Reviews Genetics, 2010, 11, 549-558.	16.3	184
34	Largest subunit of Drosophila transcription factor IID directs assembly of a complex containing TBP and a coactivator. Nature, 1993, 362, 511-517.	27.8	180
35	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. Molecular Cell, 2019, 76, 395-411.e13.	9.7	172
36	Visualizing transcription factor dynamics in living cells. Journal of Cell Biology, 2018, 217, 1181-1191.	5.2	159

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37	Temporal pattern of alcohol dehydrogenase gene transcription reproduced by Drosophila stage-specific embryonic extracts. Nature, 1988, 331, 410-415.	27.8	142
38	The dTAFII80 subunit of Drosophila TFIID contains \hat{I}^2 -transducin repeats. Nature, 1993, 363, 176-179.	27.8	134
39	Three-Dimensional Structure of the Human TFIID-IIA-IIB Complex. Science, 1999, 286, 2153-2156.	12.6	131
40	ecDNA hubs drive cooperative intermolecular oncogene expression. Nature, 2021, 600, 731-736.	27.8	123
41	A new factor related to TATA-binding protein has highly restricted expression patterns in Drosophila. Nature, 1993, 361, 557-561.	27.8	120
42	Guided nuclear exploration increases CTCF target search efficiency. Nature Chemical Biology, 2020, 16, 257-266.	8.0	113
43	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. ELife, 2019, 8, .	6.0	103
44	Promoter-Selective Properties of the TBP-Related Factor TRF1. Science, 2000, 288, 867-870.	12.6	97
45	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. ELife, 2018, 7,	6.0	92
46	Structure of the human Mediator-bound transcription preinitiation complex. Science, 2021, 372, 52-56.	12.6	91
47	Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription. Molecular Cell, 2022, 82, 2084-2097.e5.	9.7	89
48	v-Src and EJ Ras alleviate repression of c-Jun by a cell-specific inhibitor. Nature, 1991, 352, 165-168.	27.8	87
49	Impaired cell fate through gain-of-function mutations in a chromatin reader. Nature, 2020, 577, 121-126.	27.8	84
50	The transcription factor activity gradient (TAG) model: contemplating a contact-independent mechanism for enhancer–promoter communication. Genes and Development, 2022, 36, 7-16.	5.9	80
51	Transcription initiation by human RNA polymerase II visualized at single-molecule resolution. Genes and Development, 2012, 26, 1691-1702.	5.9	75
52	Real-time imaging of Huntingtin aggregates diverting target search and gene transcription. ELife, 2016, 5, .	6.0	74
53	Sewage, Salt, Silica, and SARS-CoV-2 (4S): An Economical Kit-Free Method for Direct Capture of SARS-CoV-2 RNA from Wastewater. Environmental Science & Technology, 2021, 55, 4880-4888.	10.0	72
54	Single-molecule tracking of the transcription cycle by sub-second RNA detection. ELife, 2014, 3, e01775.	6.0	70

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55	Genomes in Focus: Development and Applications of CRISPR as9 Imaging Technologies. Angewandte Chemie - International Edition, 2018, 57, 4329-4337.	13.8	67
56	3D ATAC-PALM: super-resolution imaging of the accessible genome. Nature Methods, 2020, 17, 430-436.	19.0	62
57	Structure and Function of CRSP/Med2. Molecular Cell, 2004, 14, 675-683.	9.7	61
58	Rapid dynamics of general transcription factor TFIIB binding during preinitiation complex assembly revealed by single-molecule analysis. Genes and Development, 2016, 30, 2106-2118.	5.9	60
59	The biochemistry of transcription in eukaryotes: a paradigm for multisubunit regulatory complexes. Philosophical Transactions of the Royal Society B: Biological Sciences, 1996, 351, 491-499.	4.0	52
60	A dynamic interplay of enhancer elements regulates <i>Klf4</i> expression in naÃ ⁻ ve pluripotency. Genes and Development, 2017, 31, 1795-1808.	5.9	49
61	dCas9-targeted locus-specific protein isolation method identifies histone gene regulators. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2734-E2741.	7.1	44
62	The dyskerin ribonucleoprotein complex as an OCT4/SOX2 coactivator in embryonic stem cells. ELife, 2014, 3, .	6.0	43
63	Imaging Transcription: Past, Present, and Future. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 1-8.	1.1	41
64	Functional and mechanistic studies of XPC DNA-repair complex as transcriptional coactivator in embryonic stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E2317-26.	7.1	38
65	Core promoter factor TAF9B regulates neuronal gene expression. ELife, 2014, 3, e02559.	6.0	37
66	Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. ELife, 2015, 4, .	6.0	35
67	The tell-tail trigger. Nature, 1992, 358, 620-621.	27.8	34
68	MEF2C and EBF1 Co-regulate B Cell-Specific Transcription. PLoS Genetics, 2016, 12, e1005845.	3.5	33
69	MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. ELife, 2019, 8, .	6.0	29
70	BRD2 compartmentalizes the accessible genome. Nature Genetics, 2022, 54, 481-491.	21.4	29
71	Architecture of the human XPC DNA repair and stem cell coactivator complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14817-14822.	7.1	28
72	A specific E3 ligase/deubiquitinase pair modulates TBP protein levels during muscle differentiation. ELife, 2015, 4, e08536.	6.0	28

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73	TAF7L modulates brown adipose tissue formation. ELife, 2014, 3, .	6.0	27
74	Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. PLoS ONE, 2021, 16, e0246647.	2.5	27
75	Structure of the human SAGA coactivator complex. Nature Structural and Molecular Biology, 2021, 28, 989-996.	8.2	27
76	Evidence for an Integrated Gene Repression Mechanism Based on mRNA Isoform Toggling in Human Cells. G3: Genes, Genomes, Genetics, 2019, 9, 1045-1053.	1.8	25
77	Regulation of DNA demethylation by the XPC DNA repair complex in somatic and pluripotent stem cells. Genes and Development, 2017, 31, 830-844.	5.9	21
78	Transcriptional regulation in Drosophila : the post-genome challenge. Functional and Integrative Genomics, 2001, 1, 223-234.	3.5	18
79	Weak multivalent biomolecular interactions: a strength versus numbers tug of war with implications for phase partitioning. Rna, 2022, 28, 48-51.	3.5	17
80	Measuring dynamics of eukaryotic transcription initiation: Challenges, insights and opportunities. Transcription, 2018, 9, 159-165.	3.1	16
81	A Single-Molecule Surface-Based Platform to Detect the Assembly and Function of the Human RNA Polymerase II Transcription Machinery. Structure, 2020, 28, 1337-1343.e4.	3.3	11
82	Genome im Fokus: Entwicklung und Anwendungen von CRISPR as9â€Bildgebungstechnologien. Angewandte Chemie, 2018, 130, 4412-4420.	2.0	7
83	Simple, Inexpensive RNA Isolation and Oneâ€Step RTâ€qPCR Methods for SARS oVâ€2 Detection and General Use. Current Protocols, 2021, 1, e130.	2.9	7
84	Sub-nuclear compartmentalization of core promoter factors and target genes. Cell Cycle, 2011, 10, 2405-2406.	2.6	6
85	Supporting Biomedical Research. JAMA - Journal of the American Medical Association, 2015, 313, 133.	7.4	6
86	Dual Mechanism of <i>Rag</i> Gene Repression by c-Myb during Pre-B Cell Proliferation. Molecular and Cellular Biology, 2017, 37, .	2.3	6
87	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. Bio-protocol, 2020, 10, e3527.	0.4	4
88	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. Bio-protocol, 2020, 10, e3526.	0.4	3
89	The biochemistry of transcription and gene regulation. Harvey Lectures, 1994, 90, 19-39.	0.2	3
90	Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. SSRN Electronic Journal, 0, , .	0.4	2

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91	Dissecting the Macromolecular Machine that Decodes the Genome. Biochemical Society Transactions, 2000, 28, A105-A105.	3.4	0
92	Daniel E. Koshland, Jr. (1920–2007). ACS Chemical Biology, 2007, 2, 586-588.	3.4	0
93	Distinct Handoff Mechanism for TBP-TATA DNA Engagement Revealed by SAGA Structures. Biochemistry, 2020, 59, 1647-1649.	2.5	0