Robert Tjian

List of Publications by Citations

103 papers	15,772 citations	48 h-index	123 g-index
123 ext. papers	18,180 ext. citations	20.4 avg, IF	6.79 L-index

#	Paper	IF	Citations
103	Transcriptional regulation in mammalian cells by sequence-specific DNA binding proteins. *Science*, **1989**, 245, 371-8	33.3	3153
102	Analysis of Sp1 in vivo reveals multiple transcriptional domains, including a novel glutamine-rich activation motif. *Cell*, **1988**, 55, 887-98	56.2	1600
101	A family of human CCAAT-box-binding proteins active in transcription and DNA replication: cloning and expression of multiple cDNAs. *Nature*, **1988**, 334, 218-24	50.4	749
100	Nucleolar transcription factor hUBF contains a DNA-binding motif with homology to HMG proteins. *Nature*, **1990**, 344, 830-6	50.4	645
99	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. *Nature*, **2016**, 538, 270-273	50.4	527
98	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, 192-6	11.5	501
97	Imaging dynamic and selective low-complexity domain interactions that control gene transcription. *Science*, **2018**, 361,	33.3	454
96	Single-molecule dynamics of enhanceosome assembly in embryonic stem cells. *Cell*, **2014**, 156, 1274-1285	56.2	390
95	Composite co-activator ARC mediates chromatin-directed transcriptional activation. *Nature*, **1999**, 398, 828-32	50.4	389
94	Distinct regions of Sp1 modulate DNA binding and transcriptional activation. *Science*, **1988**, 242, 1566-70	33.3	342
93	Looping back to leap forward: transcription enters a new era. *Cell*, **2014**, 157, 13-25	56.2	333
92	The transcriptional cofactor complex CRSP is required for activity of the enhancer-binding protein Sp1. *Nature*, **1999**, 397, 446-50	50.4	307
91	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. *ELife*, **2017**, 6,	8.9	299
90	DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1. *Genes and Development*, **1991**, 5, 820-6	12.6	289
89	Overcoming the bottleneck to widespread testing: a rapid review of nucleic acid testing approaches for COVID-19 detection. *Rna*, **2020**, 26, 771-783	5.8	281
88	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. *ELife*, **2016**, 5,	8.9	243
87	Dynamics of CRISPR-Cas9 genome interrogation in living cells. *Science*, **2015**, 350, 823-6	33.3	241

86	Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation. *Nature*, **1993**, 362, 175-9	50.4	231
85	Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. *Genes and Development*, **2019**, 33, 1619-1634	12.6	221
84	Structure, function, and activator-induced conformations of the CRSP coactivator. *Science*, **2002**, 295, 1058-62	33.3	219
83	Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. *Nature*, **2001**, 414, 924-8	50.4	215
82	TBP-TAF complexes: selectivity factors for eukaryotic transcription. *Current Opinion in Cell Biology*, **1994**, 6, 403-9	9	214
81	Bromodomains mediate an acetyl-histone encoded antisilencing function at heterochromatin boundaries. *Molecular Cell*, **2003**, 11, 365-76	17.6	201
80	Structure and functional properties of human general transcription factor IIE. *Nature*, **1991**, 354, 369-73	50.4	198
79	Near-atomic resolution visualization of human transcription promoter opening. *Nature*, **2016**, 533, 359-65	50.4	197
78	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, 11870-5	11.5	166
77	Largest subunit of Drosophila transcription factor IID directs assembly of a complex containing TBP and a coactivator. *Nature*, **1993**, 362, 511-7	50.4	165
76	Unexpected roles for core promoter recognition factors in cell-type-specific transcription and gene regulation. *Nature Reviews Genetics*, **2010**, 11, 549-58	30.1	152
75	A dynamic mode of mitotic bookmarking by transcription factors. *ELife*, **2016**, 5,	8.9	148
74	3D imaging of Sox2 enhancer clusters in embryonic stem cells. *ELife*, **2014**, 3, e04236	8.9	146
73	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. *Molecular Cell*, **2020**, 78, 539-553.e8	17.6	143
72	Temporal pattern of alcohol dehydrogenase gene transcription reproduced by Drosophila stage-specific embryonic extracts. *Nature*, **1988**, 331, 410-5	50.4	136
71	The dTAFII80 subunit of Drosophila TFIID contains beta-transducin repeats. *Nature*, **1993**, 363, 176-9	50.4	130
70	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. *ELife*, **2019**, 8,	8.9	128
69	Three-dimensional structure of the human TFIID-IIA-IIB complex. *Science*, **1999**, 286, 2153-6	33.3	120

68	Recent evidence that TADs and chromatin loops are dynamic structures. *Nucleus*, **2018**, 9, 20-32	3.9	116
67	A new factor related to TATA-binding protein has highly restricted expression patterns in Drosophila. *Nature*, **1993**, 361, 557-61	50.4	114
66	Robust model-based analysis of single-particle tracking experiments with Spot-On. *ELife*, **2018**, 7,	8.9	104
65	Visualizing transcription factor dynamics in living cells. *Journal of Cell Biology*, **2018**, 217, 1181-1191	7.3	102
64	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. *Molecular Cell*, **2019**, 76, 395-411.e13	17.6	97
63	Promoter-selective properties of the TBP-related factor TRF1. *Science*, **2000**, 288, 867-70	33.3	92
62	v-Src and EJ Ras alleviate repression of c-Jun by a cell-specific inhibitor. *Nature*, **1991**, 352, 165-8	50.4	83
61	Transcription initiation by human RNA polymerase II visualized at single-molecule resolution. *Genes and Development*, **2012**, 26, 1691-702	12.6	64
60	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. *ELife*, **2019**, 8,	8.9	59
59	Structure and function of CRSP/Med2; a promoter-selective transcriptional coactivator complex. *Molecular Cell*, **2004**, 14, 675-83	17.6	58
58	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. *ELife*, **2018**, 7,	8.9	58
57	Single-molecule tracking of the transcription cycle by sub-second RNA detection. *ELife*, **2014**, 3, e01775	8.9	50
56	Guided nuclear exploration increases CTCF target search efficiency. *Nature Chemical Biology*, **2020**, 16, 257-266	11.7	50
55	The biochemistry of transcription in eukaryotes: a paradigm for multisubunit regulatory complexes. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **1996**, 351, 491-9	5.8	47
54	Real-time imaging of Huntingtin aggregates diverting target search and gene transcription. *ELife*, **2016**, 5,	8.9	47
53	Genomes in Focus: Development and Applications of CRISPR-Cas9 Imaging Technologies. *Angewandte Chemie - International Edition*, **2018**, 57, 4329-4337	16.4	46
52	Structure of the human Mediator-bound transcription preinitiation complex. *Science*, **2021**, 372, 52-56	33.3	39
51	Impaired cell fate through gain-of-function mutations in a chromatin reader. *Nature*, **2020**, 577, 121-126	50.4	36

50	Rapid dynamics of general transcription factor TFIIB binding during preinitiation complex assembly revealed by single-molecule analysis. *Genes and Development*, **2016**, 30, 2106-2118	12.6	34
49	The dyskerin ribonucleoprotein complex as an OCT4/SOX2 coactivator in embryonic stem cells. *ELife*, **2014**, 3,	8.9	33
48	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	11.5	32
47	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	11.5	32
46	A dynamic interplay of enhancer elements regulates expression in naïve pluripotency. *Genes and Development*, **2017**, 31, 1795-1808	12.6	31
45	Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. *ELife*, **2015**, 4,	8.9	29
44	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	10.3	29
43	Imaging Transcription: Past, Present, and Future. *Cold Spring Harbor Symposia on Quantitative Biology*, **2015**, 80, 1-8	3.9	28
42	3D ATAC-PALM: super-resolution imaging of the accessible genome. *Nature Methods*, **2020**, 17, 430-436	21.6	24
41	A specific E3 ligase/deubiquitinase pair modulates TBP protein levels during muscle differentiation. *ELife*, **2015**, 4, e08536	8.9	23
40	Core promoter factor TAF9B regulates neuronal gene expression. *ELife*, **2014**, 3, e02559	8.9	22
39	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, 14817-22	11.5	20
38	TAF7L modulates brown adipose tissue formation. *ELife*, **2014**, 3,	8.9	20
37	MEF2C and EBF1 Co-regulate B Cell-Specific Transcription. *PLoS Genetics*, **2016**, 12, e1005845	6	19
36	ecDNA hubs drive cooperative intermolecular oncogene expression. *Nature*, **2021**,	50.4	18
35	Regulation of DNA demethylation by the XPC DNA repair complex in somatic and pluripotent stem cells. *Genes and Development*, **2017**, 31, 830-844	12.6	17
34	Transcriptional regulation in Drosophila: the post-genome challenge. *Functional and Integrative Genomics*, **2001**, 1, 223-34	3.8	17
33	Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. *PLoS ONE*, **2021**, 16, e0246647	3.6	14

32	MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. *ELife*, **2019**, 8,	8.9	13
31	An RNA-binding region regulates CTCF clustering and chromatin looping		12
30	Evidence for an Integrated Gene Repression Mechanism Based on mRNA Isoform Toggling in Human Cells. *G3: Genes, Genomes, Genetics*, **2019**, 9, 1045-1053	3.2	11
29	Measuring dynamics of eukaryotic transcription initiation: Challenges, insights and opportunities. *Transcription*, **2018**, 9, 159-165	4.8	10
28	Sewage, Salt, Silica and SARS-CoV-2 (4S): An economical kit-free method for direct capture of SARS-CoV-2 RNA from wastewater **2020**,		10
27	Resolving the 3D landscape of transcription-linked mammalian chromatin folding		10
26	Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription.. *Molecular Cell*, **2022**,	17.6	10
25	Enhancer-promoter interactions and transcription are maintained upon acute loss of CTCF, cohesin, WAPL, and YY1		8
24	The transcription factor activity gradient (TAG) model: contemplating a contact-independent mechanism for enhancer-promoter communication.. *Genes and Development*, **2021**,	12.6	7
23	Inexpensive, versatile and open-source methods for SARS-CoV-2 detection		7
22	Dual Mechanism of Gene Repression by c-Myb during Pre-B Cell Proliferation. *Molecular and Cellular Biology*, **2017**, 37,	4.8	5
21	Sub-nuclear compartmentalization of core promoter factors and target genes. *Cell Cycle*, **2011**, 10, 2405-67		5
20	Guided nuclear exploration increases CTCF target search efficiency		5
19	Simple, Inexpensive RNA Isolation and One-Step RT-qPCR Methods for SARS-CoV-2 Detection and General Use. *Current Protocols*, **2021**, 1, e130		5
18	Structure of the human SAGA coactivator complex. *Nature Structural and Molecular Biology*, **2021**, 28, 989-996	17.6	4
17	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	5.2	4
16	Supporting biomedical research: meeting challenges and opportunities at HHMI. *JAMA - Journal of the American Medical Association*, **2015**, 313, 133-4	27.4	3
15	EcDNA hubs drive cooperative intermolecular oncogene expression		3

14	Super-resolution Imaging Reveals 3D Structure and Organizing Mechanism of Accessible Chromatin		3
13	CTCF and Cohesin Regulate Chromatin Loop Stability with Distinct Dynamics		3
12	Recovering mixtures of fast diffusing states from short single particle trajectories		3
11	Structure of the human SAGA coactivator complex: The divergent architecture of human SAGA allows modular coordination of transcription activation and co-transcriptional splicing		3
10	The biochemistry of transcription and gene regulation. *Harvey Lectures*, **1994**, 90, 19-39		3
9	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. *Bio-protocol*, **2020**, 10, e3527	0.9	2
8	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. *Bio-protocol*, **2020**, 10, e3526	0.9	2
7	Spot-On: robust model-based analysis of single-particle tracking experiments		2
6	Transient DNA Binding Induces RNA Polymerase II Compartmentalization During Herpesviral Infection Distinct From Phase Separation		2
5	Genome im Fokus: Entwicklung und Anwendungen von CRISPR-Cas9-Bildgebungstechnologien. *Angewandte Chemie*, **2018**, 130, 4412-4420	3.6	2
4	Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. *SSRN Electronic Journal*,	1	1
3	Daniel E. Koshland, Jr. (1920-2007). *ACS Chemical Biology*, **2007**, 2, 586-8	4.9	
2	Dissecting the Macromolecular Machine that Decodes the Genome. *Biochemical Society Transactions*, **2000**, 28, A105-A105	5.1	
1	Distinct Handoff Mechanism for TBP-TATA DNA Engagement Revealed by SAGA Structures. *Biochemistry*, **2020**, 59, 1647-1649	3.2	