

Robert Tjian

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

20,165
citations

28190

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46693

89
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123
all docs

123
docs citations

123
times ranked

16435
citing authors

#	ARTICLE	IF	CITATIONS
1	Weak multivalent biomolecular interactions: a strength versus numbers tug of war with implications for phase partitioning. <i>Rna</i> , 2022, 28, 48-51.	1.6	17
2	The transcription factor activity gradient (TAG) model: contemplating a contact-independent mechanism for enhancer-promoter communication. <i>Genes and Development</i> , 2022, 36, 7-16.	2.7	80
3	BRD2 compartmentalizes the accessible genome. <i>Nature Genetics</i> , 2022, 54, 481-491.	9.4	29
4	Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription. <i>Molecular Cell</i> , 2022, 82, 2084-2097.e5.	4.5	89
5	Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. <i>PLoS ONE</i> , 2021, 16, e0246647.	1.1	27
6	Sewage, Salt, Silica, and SARS-CoV-2 (4S): An Economical Kit-Free Method for Direct Capture of SARS-CoV-2 RNA from Wastewater. <i>Environmental Science & Technology</i> , 2021, 55, 4880-4888.	4.6	72
7	Simple, Inexpensive RNA Isolation and One-Step RT-qPCR Methods for SARS-CoV-2 Detection and General Use. <i>Current Protocols</i> , 2021, 1, e130.	1.3	7
8	Structure of the human Mediator-bound transcription preinitiation complex. <i>Science</i> , 2021, 372, 52-56.	6.0	91
9	Structure of the human SAGA coactivator complex. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 989-996.	3.6	27
10	ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021, 600, 731-736.	13.7	123
11	Impaired cell fate through gain-of-function mutations in a chromatin reader. <i>Nature</i> , 2020, 577, 121-126.	13.7	84
12	Guided nuclear exploration increases CTCF target search efficiency. <i>Nature Chemical Biology</i> , 2020, 16, 257-266.	3.9	113
13	A Single-Molecule Surface-Based Platform to Detect the Assembly and Function of the Human RNA Polymerase II Transcription Machinery. <i>Structure</i> , 2020, 28, 1337-1343.e4.	1.6	11
14	Overcoming the bottleneck to widespread testing: a rapid review of nucleic acid testing approaches for COVID-19 detection. <i>Rna</i> , 2020, 26, 771-783.	1.6	426
15	3D ATAC-PALM: super-resolution imaging of the accessible genome. <i>Nature Methods</i> , 2020, 17, 430-436.	9.0	62
16	Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. <i>Molecular Cell</i> , 2020, 78, 539-553.e8.	4.5	380
17	Distinct Handoff Mechanism for TBP-TATA DNA Engagement Revealed by SAGA Structures. <i>Biochemistry</i> , 2020, 59, 1647-1649.	1.2	0
18	Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. <i>Bio-protocol</i> , 2020, 10, e3526.	0.2	3

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19	Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. <i>Bio-protocol</i> , 2020, 10, e3527.	0.2	4
20	Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. <i>Genes and Development</i> , 2019, 33, 1619-1634.	2.7	424
21	Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. <i>Molecular Cell</i> , 2019, 76, 395-411.e13.	4.5	172
22	Evidence for an Integrated Gene Repression Mechanism Based on mRNA Isoform Toggling in Human Cells. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1045-1053.	0.8	25
23	Determining cellular CTCF and cohesin abundances to constrain 3D genome models. <i>ELife</i> , 2019, 8, .	2.8	103
24	Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. <i>ELife</i> , 2019, 8, .	2.8	222
25	MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. <i>ELife</i> , 2019, 8, .	2.8	29
26	dCas9-targeted locus-specific protein isolation method identifies histone gene regulators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2734-E2741.	3.3	44
27	Visualizing transcription factor dynamics in living cells. <i>Journal of Cell Biology</i> , 2018, 217, 1181-1191.	2.3	159
28	Recent evidence that TADs and chromatin loops are dynamic structures. <i>Nucleus</i> , 2018, 9, 20-32.	0.6	188
29	Genomes in Focus: Development and Applications of CRISPR-Cas9 Imaging Technologies. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 4329-4337.	7.2	67
30	Measuring dynamics of eukaryotic transcription initiation: Challenges, insights and opportunities. <i>Transcription</i> , 2018, 9, 159-165.	1.7	16
31	Genome im Fokus: Entwicklung und Anwendungen von CRISPR-Cas9-Bildgebungstechnologien. <i>Angewandte Chemie</i> , 2018, 130, 4412-4420.	1.6	7
32	Imaging dynamic and selective low-complexity domain interactions that control gene transcription. <i>Science</i> , 2018, 361, .	6.0	750
33	Robust model-based analysis of single-particle tracking experiments with Spot-On. <i>ELife</i> , 2018, 7, .	2.8	213
34	A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. <i>ELife</i> , 2018, 7, .	2.8	92
35	Regulation of DNA demethylation by the XPC DNA repair complex in somatic and pluripotent stem cells. <i>Genes and Development</i> , 2017, 31, 830-844.	2.7	21
36	Dual Mechanism of <i>Rag</i> Gene Repression by c-Myb during Pre-B Cell Proliferation. <i>Molecular and Cellular Biology</i> , 2017, 37, .	1.1	6

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37	A dynamic interplay of enhancer elements regulates <i>Klf4</i> expression in naïve pluripotency. <i>Genes and Development</i> , 2017, 31, 1795-1808.	2.7	49
38	CTCF and cohesin regulate chromatin loop stability with distinct dynamics. <i>ELife</i> , 2017, 6, .	2.8	476
39	Near-atomic resolution visualization of human transcription promoter opening. <i>Nature</i> , 2016, 533, 359-365.	13.7	256
40	Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. <i>Nature</i> , 2016, 538, 270-273.	13.7	854
41	Rapid dynamics of general transcription factor TFIIB binding during preinitiation complex assembly revealed by single-molecule analysis. <i>Genes and Development</i> , 2016, 30, 2106-2118.	2.7	60
42	MEF2C and EBF1 Co-regulate B Cell-Specific Transcription. <i>PLoS Genetics</i> , 2016, 12, e1005845.	1.5	33
43	Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016, 5, .	2.8	349
44	Real-time imaging of Huntingtin aggregates diverting target search and gene transcription. <i>ELife</i> , 2016, 5, .	2.8	74
45	A dynamic mode of mitotic bookmarking by transcription factors. <i>ELife</i> , 2016, 5, .	2.8	216
46	Architecture of the human XPC DNA repair and stem cell coactivator complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14817-14822.	3.3	28
47	Dynamics of CRISPR-Cas9 genome interrogation in living cells. <i>Science</i> , 2015, 350, 823-826.	6.0	301
48	Imaging Transcription: Past, Present, and Future. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015, 80, 1-8.	2.0	41
49	Supporting Biomedical Research. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 133.	3.8	6
50	Functional and mechanistic studies of XPC DNA-repair complex as transcriptional coactivator in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2317-26.	3.3	38
51	CASFISH: CRISPR/Cas9-mediated in situ labeling of genomic loci in fixed cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11870-11875.	3.3	243
52	Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. <i>ELife</i> , 2015, 4, .	2.8	35
53	A specific E3 ligase/deubiquitinase pair modulates TBP protein levels during muscle differentiation. <i>ELife</i> , 2015, 4, e08536.	2.8	28
54	TAF7L modulates brown adipose tissue formation. <i>ELife</i> , 2014, 3, .	2.8	27

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55	The dyskerin ribonucleoprotein complex as an OCT4/SOX2 coactivator in embryonic stem cells. <i>ELife</i> , 2014, 3, .	2.8	43
56	Single-Molecule Dynamics of Enhanceosome Assembly in Embryonic Stem Cells. <i>Cell</i> , 2014, 156, 1274-1285.	13.5	532
57	Looping Back to Leap Forward: Transcription Enters a New Era. <i>Cell</i> , 2014, 157, 13-25.	13.5	423
58	Single-molecule tracking of the transcription cycle by sub-second RNA detection. <i>ELife</i> , 2014, 3, e01775.	2.8	70
59	Core promoter factor TAF9B regulates neuronal gene expression. <i>ELife</i> , 2014, 3, e02559.	2.8	37
60	3D imaging of Sox2 enhancer clusters in embryonic stem cells. <i>ELife</i> , 2014, 3, e04236.	2.8	204
61	Transcription initiation by human RNA polymerase II visualized at single-molecule resolution. <i>Genes and Development</i> , 2012, 26, 1691-1702.	2.7	75
62	Sub-nuclear compartmentalization of core promoter factors and target genes. <i>Cell Cycle</i> , 2011, 10, 2405-2406.	1.3	6
63	Unexpected roles for core promoter recognition factors in cell-type-specific transcription and gene regulation. <i>Nature Reviews Genetics</i> , 2010, 11, 549-558.	7.7	184
64	Daniel E. Koshland, Jr. (1920–2007). <i>ACS Chemical Biology</i> , 2007, 2, 586-588.	1.6	0
65	Structure and Function of CRSP/Med2. <i>Molecular Cell</i> , 2004, 14, 675-683.	4.5	61
66	Bromodomains Mediate an Acetyl-Histone Encoded Antisilencing Function at Heterochromatin Boundaries. <i>Molecular Cell</i> , 2003, 11, 365-376.	4.5	219
67	Structure, Function, and Activator-Induced Conformations of the CRSP Coactivator. <i>Science</i> , 2002, 295, 1058-1062.	6.0	230
68	Transcriptional regulation in <i>Drosophila</i> : the post-genome challenge. <i>Functional and Integrative Genomics</i> , 2001, 1, 223-234.	1.4	18
69	Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. <i>Nature</i> , 2001, 414, 924-928.	13.7	238
70	Dissecting the Macromolecular Machine that Decodes the Genome. <i>Biochemical Society Transactions</i> , 2000, 28, A105-A105.	1.6	0
71	Promoter-Selective Properties of the TBP-Related Factor TRF1. <i>Science</i> , 2000, 288, 867-870.	6.0	97
72	Composite co-activator ARC mediates chromatin-directed transcriptional activation. <i>Nature</i> , 1999, 398, 828-832.	13.7	408

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73	The transcriptional cofactor complex CRSP is required for activity of the enhancer-binding protein Sp1. <i>Nature</i> , 1999, 397, 446-450.	13.7	322
74	Three-Dimensional Structure of the Human TFIID-IIA-IIB Complex. <i>Science</i> , 1999, 286, 2153-2156.	6.0	131
75	The biochemistry of transcription in eukaryotes: a paradigm for multisubunit regulatory complexes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 1996, 351, 491-499.	1.8	52
76	TBP-TAF complexes: selectivity factors for eukaryotic transcription. <i>Current Opinion in Cell Biology</i> , 1994, 6, 403-409.	2.6	236
77	A glutamine-rich hydrophobic patch in transcription factor Sp1 contacts the dTAFII110 component of the Drosophila TFIID complex and mediates transcriptional activation.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 192-196.	3.3	526
78	The biochemistry of transcription and gene regulation. <i>Harvey Lectures</i> , 1994, 90, 19-39.	0.2	3
79	The dTAFII80 subunit of Drosophila TFIID contains \hat{I}^2 -transducin repeats. <i>Nature</i> , 1993, 363, 176-179.	13.7	134
80	A new factor related to TATA-binding protein has highly restricted expression patterns in Drosophila. <i>Nature</i> , 1993, 361, 557-561.	13.7	120
81	Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation. <i>Nature</i> , 1993, 362, 175-179.	13.7	254
82	Largest subunit of Drosophila transcription factor IID directs assembly of a complex containing TBP and a coactivator. <i>Nature</i> , 1993, 362, 511-517.	13.7	180
83	The tell-tail trigger. <i>Nature</i> , 1992, 358, 620-621.	13.7	34
84	v-Src and EJ Ras alleviate repression of c-Jun by a cell-specific inhibitor. <i>Nature</i> , 1991, 352, 165-168.	13.7	87
85	Structure and functional properties of human general transcription factor IIE. <i>Nature</i> , 1991, 354, 369-373.	13.7	209
86	DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1.. <i>Genes and Development</i> , 1991, 5, 820-826.	2.7	354
87	Nucleolar transcription factor hUBF contains a DNA-binding motif with homology to HMG proteins. <i>Nature</i> , 1990, 344, 830-836.	13.7	691
88	Transcriptional regulation in mammalian cells by sequence-specific DNA binding proteins. <i>Science</i> , 1989, 245, 371-378.	6.0	3,446
89	Temporal pattern of alcohol dehydrogenase gene transcription reproduced by Drosophila stage-specific embryonic extracts. <i>Nature</i> , 1988, 331, 410-415.	13.7	142
90	A family of human CCAAT-box-binding proteins active in transcription and DNA replication: cloning and expression of multiple cDNAs. <i>Nature</i> , 1988, 334, 218-224.	13.7	802

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91	Analysis of Sp1 in vivo reveals multiple transcriptional domains, including a novel glutamine-rich activation motif. Cell, 1988, 55, 887-898.	13.5	1,753
92	Distinct regions of Sp1 modulate DNA binding and transcriptional activation. Science, 1988, 242, 1566-1570.	6.0	382
93	Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. SSRN Electronic Journal, 0, , .	0.4	2