

Robert Tjian

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription.. <i>Molecular Cell</i> , 2022 , | 17.6 | 10 |
| 102 | The transcription factor activity gradient (TAG) model: contemplating a contact-independent mechanism for enhancer-promoter communication.. <i>Genes and Development</i> , 2021 , | 12.6 | 7 |
| 101 | Structure of the human SAGA coactivator complex. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 989-996 | 17.6 | 4 |
| 100 | ecDNA hubs drive cooperative intermolecular oncogene expression. <i>Nature</i> , 2021 , | 50.4 | 18 |
| 99 | 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 | 10.3 | 29 |
| 98 | 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 | | 5 |
| 97 | Structure of the human Mediator-bound transcription preinitiation complex. <i>Science</i> , 2021 , 372, 52-56 | 33.3 | 39 |
| 96 | Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. <i>PLoS ONE</i> , 2021 , 16, e0246647 | 5.7 | 14 |
| 95 | 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 | 5.8 | 281 |
| 94 | 3D ATAC-PALM: super-resolution imaging of the accessible genome. <i>Nature Methods</i> , 2020 , 17, 430-436 | 21.6 | 24 |
| 93 | Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. <i>Molecular Cell</i> , 2020 , 78, 539-553.e8 | 17.6 | 143 |
| 92 | Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. <i>Bio-protocol</i> , 2020 , 10, e3527 | 0.9 | 2 |
| 91 | Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. <i>Bio-protocol</i> , 2020 , 10, e3526 | 0.9 | 2 |
| 90 | 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 |
| 89 | Impaired cell fate through gain-of-function mutations in a chromatin reader. <i>Nature</i> , 2020 , 577, 121-126 | 50.4 | 36 |
| 88 | Guided nuclear exploration increases CTCF target search efficiency. <i>Nature Chemical Biology</i> , 2020 , 16, 257-266 | 11.7 | 50 |
| 87 | 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 | 5.2 | 4 |

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| 86 | Distinct Handoff Mechanism for TBP-TATA DNA Engagement Revealed by SAGA Structures. <i>Biochemistry</i> , 2020 , 59, 1647-1649 | 3.2 | |
| 85 | Distinct Classes of Chromatin Loops Revealed by Deletion of an RNA-Binding Region in CTCF. <i>Molecular Cell</i> , 2019 , 76, 395-411.e13 | 17.6 | 97 |
| 84 | 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 | 3.2 | 11 |
| 83 | Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. <i>Genes and Development</i> , 2019 , 33, 1619-1634 | 12.6 | 221 |
| 82 | Determining cellular CTCF and cohesin abundances to constrain 3D genome models. <i>ELife</i> , 2019 , 8, | 8.9 | 59 |
| 81 | Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. <i>ELife</i> , 2019 , 8, | 8.9 | 128 |
| 80 | MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. <i>ELife</i> , 2019 , 8, | 8.9 | 13 |
| 79 | 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 ^{11.5} | | 32 |
| 78 | Visualizing transcription factor dynamics in living cells. <i>Journal of Cell Biology</i> , 2018 , 217, 1181-1191 | 7.3 | 102 |
| 77 | Recent evidence that TADs and chromatin loops are dynamic structures. <i>Nucleus</i> , 2018 , 9, 20-32 | 3.9 | 116 |
| 76 | Genomes in Focus: Development and Applications of CRISPR-Cas9 Imaging Technologies. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 4329-4337 | 16.4 | 46 |
| 75 | Measuring dynamics of eukaryotic transcription initiation: Challenges, insights and opportunities. <i>Transcription</i> , 2018 , 9, 159-165 | 4.8 | 10 |
| 74 | Genome im Fokus: Entwicklung und Anwendungen von CRISPR-Cas9-Bildgebungstechnologien. <i>Angewandte Chemie</i> , 2018 , 130, 4412-4420 | 3.6 | 2 |
| 73 | Imaging dynamic and selective low-complexity domain interactions that control gene transcription. <i>Science</i> , 2018 , 361, | 33.3 | 454 |
| 72 | Robust model-based analysis of single-particle tracking experiments with Spot-On. <i>ELife</i> , 2018 , 7, | 8.9 | 104 |
| 71 | A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. <i>ELife</i> , 2018 , 7, | 8.9 | 58 |
| 70 | 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 | 12.6 | 17 |
| 69 | Dual Mechanism of Gene Repression by c-Myb during Pre-B Cell Proliferation. <i>Molecular and Cellular Biology</i> , 2017 , 37, | 4.8 | 5 |

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| 68 | A dynamic interplay of enhancer elements regulates expression in naïve pluripotency. <i>Genes and Development</i> , 2017 , 31, 1795-1808 | 12.6 | 31 |
| 67 | CTCF and cohesin regulate chromatin loop stability with distinct dynamics. <i>ELife</i> , 2017 , 6, | 8.9 | 299 |
| 66 | MEF2C and EBF1 Co-regulate B Cell-Specific Transcription. <i>PLoS Genetics</i> , 2016 , 12, e1005845 | 6 | 19 |
| 65 | Nucleosomes impede Cas9 access to DNA in vivo and in vitro. <i>ELife</i> , 2016 , 5, | 8.9 | 243 |
| 64 | Real-time imaging of Huntingtin aggregates diverting target search and gene transcription. <i>ELife</i> , 2016 , 5, | 8.9 | 47 |
| 63 | A dynamic mode of mitotic bookmarking by transcription factors. <i>ELife</i> , 2016 , 5, | 8.9 | 148 |
| 62 | Near-atomic resolution visualization of human transcription promoter opening. <i>Nature</i> , 2016 , 533, 359-650.4 | 50.4 | 197 |
| 61 | Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. <i>Nature</i> , 2016 , 538, 270-273 | 50.4 | 527 |
| 60 | 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 | 12.6 | 34 |
| 59 | Supporting biomedical research: meeting challenges and opportunities at HHMI. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 133-4 | 27.4 | 3 |
| 58 | 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 | 11.5 | 32 |
| 57 | 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, 11870-5 | 11.5 | 166 |
| 56 | 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, 14817-22 | 11.5 | 20 |
| 55 | Dynamics of CRISPR-Cas9 genome interrogation in living cells. <i>Science</i> , 2015 , 350, 823-6 | 33.3 | 241 |
| 54 | Imaging Transcription: Past, Present, and Future. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2015 , 80, 1-8 | 3.9 | 28 |
| 53 | Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. <i>ELife</i> , 2015 , 4, | 8.9 | 29 |
| 52 | A specific E3 ligase/deubiquitinase pair modulates TBP protein levels during muscle differentiation. <i>ELife</i> , 2015 , 4, e08536 | 8.9 | 23 |
| 51 | Single-molecule dynamics of enhanceosome assembly in embryonic stem cells. <i>Cell</i> , 2014 , 156, 1274-12856.2 | 56.2 | 390 |

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|----|---|------|-----|
| 50 | Looping back to leap forward: transcription enters a new era. <i>Cell</i> , 2014 , 157, 13-25 | 56.2 | 333 |
| 49 | TAF7L modulates brown adipose tissue formation. <i>ELife</i> , 2014 , 3, | 8.9 | 20 |
| 48 | The dyskerin ribonucleoprotein complex as an OCT4/SOX2 coactivator in embryonic stem cells. <i>ELife</i> , 2014 , 3, | 8.9 | 33 |
| 47 | Single-molecule tracking of the transcription cycle by sub-second RNA detection. <i>ELife</i> , 2014 , 3, e01775 | 8.9 | 50 |
| 46 | Core promoter factor TAF9B regulates neuronal gene expression. <i>ELife</i> , 2014 , 3, e02559 | 8.9 | 22 |
| 45 | 3D imaging of Sox2 enhancer clusters in embryonic stem cells. <i>ELife</i> , 2014 , 3, e04236 | 8.9 | 146 |
| 44 | Transcription initiation by human RNA polymerase II visualized at single-molecule resolution. <i>Genes and Development</i> , 2012 , 26, 1691-702 | 12.6 | 64 |
| 43 | Sub-nuclear compartmentalization of core promoter factors and target genes. <i>Cell Cycle</i> , 2011 , 10, 2405-17 | 4.7 | 5 |
| 42 | Unexpected roles for core promoter recognition factors in cell-type-specific transcription and gene regulation. <i>Nature Reviews Genetics</i> , 2010 , 11, 549-58 | 30.1 | 152 |
| 41 | Daniel E. Koshland, Jr. (1920-2007). <i>ACS Chemical Biology</i> , 2007 , 2, 586-8 | 4.9 | |
| 40 | Structure and function of CRSP/Med2; a promoter-selective transcriptional coactivator complex. <i>Molecular Cell</i> , 2004 , 14, 675-83 | 17.6 | 58 |
| 39 | Bromodomains mediate an acetyl-histone encoded antisilencing function at heterochromatin boundaries. <i>Molecular Cell</i> , 2003 , 11, 365-76 | 17.6 | 201 |
| 38 | Structure, function, and activator-induced conformations of the CRSP coactivator. <i>Science</i> , 2002 , 295, 1058-62 | 33.3 | 219 |
| 37 | Transcriptional regulation in Drosophila: the post-genome challenge. <i>Functional and Integrative Genomics</i> , 2001 , 1, 223-34 | 3.8 | 17 |
| 36 | Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. <i>Nature</i> , 2001 , 414, 924-8 | 50.4 | 215 |
| 35 | Dissecting the Macromolecular Machine that Decodes the Genome. <i>Biochemical Society Transactions</i> , 2000 , 28, A105-A105 | 5.1 | |
| 34 | Promoter-selective properties of the TBP-related factor TRF1. <i>Science</i> , 2000 , 288, 867-70 | 33.3 | 92 |
| 33 | Composite co-activator ARC mediates chromatin-directed transcriptional activation. <i>Nature</i> , 1999 , 398, 828-32 | 50.4 | 389 |

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|----|---|------|------|
| 32 | The transcriptional cofactor complex CRSP is required for activity of the enhancer-binding protein Sp1. <i>Nature</i> , 1999 , 397, 446-50 | 50.4 | 307 |
| 31 | Three-dimensional structure of the human TFIID-IIA-IIB complex. <i>Science</i> , 1999 , 286, 2153-6 | 33.3 | 120 |
| 30 | 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, 491-9 | 5.8 | 47 |
| 29 | TBP-TAF complexes: selectivity factors for eukaryotic transcription. <i>Current Opinion in Cell Biology</i> , 1994 , 6, 403-9 | 9 | 214 |
| 28 | 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, 192-6 | 11.5 | 501 |
| 27 | The biochemistry of transcription and gene regulation. <i>Harvey Lectures</i> , 1994 , 90, 19-39 | | 3 |
| 26 | The dTAFII80 subunit of Drosophila TFIID contains beta-transducin repeats. <i>Nature</i> , 1993 , 363, 176-9 | 50.4 | 130 |
| 25 | A new factor related to TATA-binding protein has highly restricted expression patterns in Drosophila. <i>Nature</i> , 1993 , 361, 557-61 | 50.4 | 114 |
| 24 | Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation. <i>Nature</i> , 1993 , 362, 175-9 | 50.4 | 231 |
| 23 | Largest subunit of Drosophila transcription factor IID directs assembly of a complex containing TBP and a coactivator. <i>Nature</i> , 1993 , 362, 511-7 | 50.4 | 165 |
| 22 | v-Src and EJ Ras alleviate repression of c-Jun by a cell-specific inhibitor. <i>Nature</i> , 1991 , 352, 165-8 | 50.4 | 83 |
| 21 | Structure and functional properties of human general transcription factor IIE. <i>Nature</i> , 1991 , 354, 369-73 | 50.4 | 198 |
| 20 | DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1. <i>Genes and Development</i> , 1991 , 5, 820-6 | 12.6 | 289 |
| 19 | Nucleolar transcription factor hUBF contains a DNA-binding motif with homology to HMG proteins. <i>Nature</i> , 1990 , 344, 830-6 | 50.4 | 645 |
| 18 | Transcriptional regulation in mammalian cells by sequence-specific DNA binding proteins. <i>Science</i> , 1989 , 245, 371-8 | 33.3 | 3153 |
| 17 | Temporal pattern of alcohol dehydrogenase gene transcription reproduced by Drosophila stage-specific embryonic extracts. <i>Nature</i> , 1988 , 331, 410-5 | 50.4 | 136 |
| 16 | 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, 218-24 | 50.4 | 749 |
| 15 | Analysis of Sp1 in vivo reveals multiple transcriptional domains, including a novel glutamine-rich activation motif. <i>Cell</i> , 1988 , 55, 887-98 | 56.2 | 1600 |

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|----|---|------|-----|
| 14 | Distinct regions of Sp1 modulate DNA binding and transcriptional activation. <i>Science</i> , 1988 , 242, 1566-70 | 33.3 | 342 |
| 13 | Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. <i>SSRN Electronic Journal</i> , | 1 | 1 |
| 12 | Spot-On: robust model-based analysis of single-particle tracking experiments | | 2 |
| 11 | Inexpensive, versatile and open-source methods for SARS-CoV-2 detection | | 7 |
| 10 | EcDNA hubs drive cooperative intermolecular oncogene expression | | 3 |
| 9 | Transient DNA Binding Induces RNA Polymerase II Compartmentalization During Herpesviral Infection Distinct From Phase Separation | | 2 |
| 8 | An RNA-binding region regulates CTCF clustering and chromatin looping | | 12 |
| 7 | Guided nuclear exploration increases CTCF target search efficiency | | 5 |
| 6 | Resolving the 3D landscape of transcription-linked mammalian chromatin folding | | 10 |
| 5 | Super-resolution Imaging Reveals 3D Structure and Organizing Mechanism of Accessible Chromatin | | 3 |
| 4 | CTCF and Cohesin Regulate Chromatin Loop Stability with Distinct Dynamics | | 3 |
| 3 | Recovering mixtures of fast diffusing states from short single particle trajectories | | 3 |
| 2 | Structure of the human SAGA coactivator complex: The divergent architecture of human SAGA allows modular coordination of transcription activation and co-transcriptional splicing | | 3 |
| 1 | Enhancer-promoter interactions and transcription are maintained upon acute loss of CTCF, cohesin, WAPL, and YY1 | | 8 |