List of Publications by Year in descending order

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| # | Article | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Weak multivalent biomolecular interactions: a strength versus numbers tug of war with implications for phase partitioning. Rna, 2022, 28, 48-51. | 3.5 | 17 |
| 2 | 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 |
| 3 | BRD2 compartmentalizes the accessible genome. Nature Genetics, 2022, 54, 481-491. | 21.4 | 29 |
| 4 | Tuning levels of low-complexity domain interactions to modulate endogenous oncogenic transcription. Molecular Cell, 2022, 82, 2084-2097.e5. | 9.7 | 89 |
| 5 | Open-source RNA extraction and RT-qPCR methods for SARS-CoV-2 detection. PLoS ONE, 2021, 16, e0246647. | 2.5 | 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. Environmental Science & Technology, 2021, 55, 4880-4888. | 10.0 | 72 |
| 7 | Simple, Inexpensive RNA Isolation and Oneâ€Step RTâ€qPCR Methods for SARSâ€CoVâ€2 Detection and General Use. Current Protocols, 2021, 1, e130. | 2.9 | 7 |
| 8 | Structure of the human Mediator-bound transcription preinitiation complex. Science, 2021, 372, 52-56. | 12.6 | 91 |
| 9 | Structure of the human SAGA coactivator complex. Nature Structural and Molecular Biology, 2021, 28, 989-996. | 8.2 | 27 |
| 10 | ecDNA hubs drive cooperative intermolecular oncogene expression. Nature, 2021, 600, 731-736. | 27.8 | 123 |
| 11 | Impaired cell fate through gain-of-function mutations in a chromatin reader. Nature, 2020, 577, 121-126. | 27.8 | 84 |
| 12 | Guided nuclear exploration increases CTCF target search efficiency. Nature Chemical Biology, 2020, 16, 257-266. | 8.0 | 113 |
| 13 | 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 |
| 14 | 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 |
| 15 | 3D ATAC-PALM: super-resolution imaging of the accessible genome. Nature Methods, 2020, 17, 430-436. | 19.0 | 62 |
| 16 | Resolving the 3D Landscape of Transcription-Linked Mammalian Chromatin Folding. Molecular Cell, 2020, 78, 539-553.e8. | 9.7 | 380 |
| 17 | Distinct Handoff Mechanism for TBP-TATA DNA Engagement Revealed by SAGA Structures. Biochemistry, 2020, 59, 1647-1649. | 2.5 | 0 |
| 18 | Assessing Self-interaction of Mammalian Nuclear Proteins by Co-immunoprecipitation. Bio-protocol, 2020, 10, e3526. | 0.4 | 3 |

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|----|--|------|-----------|
| 19 | Estimating Cellular Abundances of Halo-tagged Proteins in Live Mammalian Cells by Flow Cytometry. Bio-protocol, 2020, 10, e3527. | 0.4 | 4 |
| 20 | Evaluating phase separation in live cells: diagnosis, caveats, and functional consequences. Genes and Development, 2019, 33, 1619-1634. | 5.9 | 424 |
| 21 | 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 |
| 22 | 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 |
| 23 | Determining cellular CTCF and cohesin abundances to constrain 3D genome models. ELife, 2019, 8, . | 6.0 | 103 |
| 24 | Evidence for DNA-mediated nuclear compartmentalization distinct from phase separation. ELife, 2019, 8, . | 6.0 | 222 |
| 25 | MeCP2 nuclear dynamics in live neurons results from low and high affinity chromatin interactions. ELife, 2019, 8, . | 6.0 | 29 |
| 26 | 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 |
| 27 | Visualizing transcription factor dynamics in living cells. Journal of Cell Biology, 2018, 217, 1181-1191. | 5.2 | 159 |
| 28 | Recent evidence that TADs and chromatin loops are dynamic structures. Nucleus, 2018, 9, 20-32. | 2.2 | 188 |
| 29 | Genomes in Focus: Development and Applications of CRISPR as9 Imaging Technologies. Angewandte Chemie - International Edition, 2018, 57, 4329-4337. | 13.8 | 67 |
| 30 | Measuring dynamics of eukaryotic transcription initiation: Challenges, insights and opportunities. Transcription, 2018, 9, 159-165. | 3.1 | 16 |
| 31 | Genome im Fokus: Entwicklung und Anwendungen von CRISPR as9â€Bildgebungstechnologien. Angewandte Chemie, 2018, 130, 4412-4420. | 2.0 | 7 |
| 32 | Imaging dynamic and selective low-complexity domain interactions that control gene transcription. Science, 2018, 361, . | 12.6 | 750 |
| 33 | Robust model-based analysis of single-particle tracking experiments with Spot-On. ELife, 2018, 7, . | 6.0 | 213 |
| 34 | A stable mode of bookmarking by TBP recruits RNA polymerase II to mitotic chromosomes. ELife, 2018, 7, | 6.0 | 92 |
| 35 | 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 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | CTCF and cohesin regulate chromatin loop stability with distinct dynamics. ELife, 2017, 6, . | 6.0 | 476 |
| 39 | Near-atomic resolution visualization of human transcription promoter opening. Nature, 2016, 533, 359-365. | 27.8 | 256 |
| 40 | Two distinct RNase activities of CRISPR-C2c2 enable guide-RNA processing and RNA detection. Nature, 2016, 538, 270-273. | 27.8 | 854 |
| 41 | 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 |
| 42 | MEF2C and EBF1 Co-regulate B Cell-Specific Transcription. PLoS Genetics, 2016, 12, e1005845. | 3.5 | 33 |
| 43 | Nucleosomes impede Cas9 access to DNA in vivo and in vitro. ELife, 2016, 5, . | 6.0 | 349 |
| 44 | Real-time imaging of Huntingtin aggregates diverting target search and gene transcription. ELife, 2016, 5, . | 6.0 | 74 |
| 45 | A dynamic mode of mitotic bookmarking by transcription factors. ELife, 2016, 5, . | 6.0 | 216 |
| 46 | 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 |
| 47 | Dynamics of CRISPR-Cas9 genome interrogation in living cells. Science, 2015, 350, 823-826. | 12.6 | 301 |
| 48 | Imaging Transcription: Past, Present, and Future. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 1-8. | 1.1 | 41 |
| 49 | Supporting Biomedical Research. JAMA - Journal of the American Medical Association, 2015, 313, 133. | 7.4 | 6 |
| 50 | 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 |
| 51 | 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 |
| 52 | Chemical perturbation of an intrinsically disordered region of TFIID distinguishes two modes of transcription initiation. ELife, 2015, 4, . | 6.0 | 35 |
| 53 | A specific E3 ligase/deubiquitinase pair modulates TBP protein levels during muscle differentiation. ELife, 2015, 4, e08536. | 6.0 | 28 |
| 54 | TAF7L modulates brown adipose tissue formation. ELife, 2014, 3, . | 6.0 | 27 |

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|----|---|------|-----------|
| 55 | The dyskerin ribonucleoprotein complex as an OCT4/SOX2 coactivator in embryonic stem cells. ELife, 2014, 3, . | 6.0 | 43 |
| 56 | Single-Molecule Dynamics of Enhanceosome Assembly in Embryonic Stem Cells. Cell, 2014, 156, 1274-1285. | 28.9 | 532 |
| 57 | Looping Back to Leap Forward: Transcription Enters a New Era. Cell, 2014, 157, 13-25. | 28.9 | 423 |
| 58 | Single-molecule tracking of the transcription cycle by sub-second RNA detection. ELife, 2014, 3, e01775. | 6.0 | 70 |
| 59 | Core promoter factor TAF9B regulates neuronal gene expression. ELife, 2014, 3, e02559. | 6.0 | 37 |
| 60 | 3D imaging of Sox2 enhancer clusters in embryonic stem cells. ELife, 2014, 3, e04236. | 6.0 | 204 |
| 61 | Transcription initiation by human RNA polymerase II visualized at single-molecule resolution. Genes and Development, 2012, 26, 1691-1702. | 5.9 | 75 |
| 62 | Sub-nuclear compartmentalization of core promoter factors and target genes. Cell Cycle, 2011, 10, 2405-2406. | 2.6 | 6 |
| 63 | 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 |
| 64 | Daniel E. Koshland, Jr. (1920–2007). ACS Chemical Biology, 2007, 2, 586-588. | 3.4 | 0 |
| 65 | Structure and Function of CRSP/Med2. Molecular Cell, 2004, 14, 675-683. | 9.7 | 61 |
| 66 | Bromodomains Mediate an Acetyl-Histone Encoded Antisilencing Function at Heterochromatin Boundaries. Molecular Cell, 2003, 11, 365-376. | 9.7 | 219 |
| 67 | Structure, Function, and Activator-Induced Conformations of the CRSP Coactivator. Science, 2002, 295, 1058-1062. | 12.6 | 230 |
| 68 | Transcriptional regulation in Drosophila : the post-genome challenge. Functional and Integrative Genomics, 2001, 1, 223-234. | 3.5 | 18 |
| 69 | Selectivity of chromatin-remodelling cofactors for ligand-activated transcription. Nature, 2001, 414, 924-928. | 27.8 | 238 |
| 70 | Dissecting the Macromolecular Machine that Decodes the Genome. Biochemical Society Transactions, 2000, 28, A105-A105. | 3.4 | 0 |
| 71 | Promoter-Selective Properties of the TBP-Related Factor TRF1. Science, 2000, 288, 867-870. | 12.6 | 97 |
| 72 | Composite co-activator ARC mediates chromatin-directed transcriptional activation. Nature, 1999, 398, 828-832. | 27.8 | 408 |

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|----|---|------|-----------|
| 73 | The transcriptional cofactor complex CRSP is required for activity of the enhancer-binding protein Sp1. Nature, 1999, 397, 446-450. | 27.8 | 322 |
| 74 | Three-Dimensional Structure of the Human TFIID-IIA-IIB Complex. Science, 1999, 286, 2153-2156. | 12.6 | 131 |
| 75 | 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 |
| 76 | TBP-TAF complexes: selectivity factors for eukaryotic transcription. Current Opinion in Cell Biology, 1994, 6, 403-409. | 5.4 | 236 |
| 77 | 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 |
| 78 | The biochemistry of transcription and gene regulation. Harvey Lectures, 1994, 90, 19-39. | 0.2 | 3 |
| 79 | The dTAFII80 subunit of Drosophila TFIID contains β-transducin repeats. Nature, 1993, 363, 176-179. | 27.8 | 134 |
| 80 | A new factor related to TATA-binding protein has highly restricted expression patterns in Drosophila. Nature, 1993, 361, 557-561. | 27.8 | 120 |
| 81 | Cloning and expression of human TAFII250: a TBP-associated factor implicated in cell-cycle regulation. Nature, 1993, 362, 175-179. | 27.8 | 254 |
| 82 | 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 |
| 83 | The tell-tail trigger. Nature, 1992, 358, 620-621. | 27.8 | 34 |
| 84 | v-Src and EJ Ras alleviate repression of c-Jun by a cell-specific inhibitor. Nature, 1991, 352, 165-168. | 27.8 | 87 |
| 85 | Structure and functional properties of human general transcription factor IIE. Nature, 1991, 354, 369-373. | 27.8 | 209 |
| 86 | DNA looping between sites for transcriptional activation: self-association of DNA-bound Sp1 Genes and Development, 1991, 5, 820-826. | 5.9 | 354 |
| 87 | Nucleolar transcription factor hUBF contains a DNA-binding motif with homology to HMG proteins. Nature, 1990, 344, 830-836. | 27.8 | 691 |
| 88 | Transcriptional Regulation in Mammalian Cells by Sequence-Specific DNA Binding Proteins. Science, 1989, 245, 371-378. | 12.6 | 3,446 |
| 89 | Temporal pattern of alcohol dehydrogenase gene transcription reproduced by Drosophila stage-specific embryonic extracts. Nature, 1988, 331, 410-415. | 27.8 | 142 |
| 90 | 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 |

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|----|--|------|-----------|
| 91 | 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 |
| 92 | Distinct regions of Sp1 modulate DNA binding and transcriptional activation. Science, 1988, 242, 1566-1570. | 12.6 | 382 |
| 93 | Mecp2 Nuclear Dynamics in Live Neurons Results from Low and High Affinity Chromatin Interactions. SSRN Electronic Journal, 0, , . | 0.4 | 2 |