

Richard A Young

List of Publications by Citations

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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.

268
papers

85,396
citations

139
h-index

278
g-index

278
ext. papers

97,916
ext. citations

25.3
avg, IF

7.92
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 268 | Core transcriptional regulatory circuitry in human embryonic stem cells. <i>Cell</i> , 2005 , 122, 947-56 | 56.2 | 3494 |
| 267 | Histone H3K27ac separates active from poised enhancers and predicts developmental state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 21931-6 | 11.5 | 2453 |
| 266 | Transcriptional regulatory networks in <i>Saccharomyces cerevisiae</i> . <i>Science</i> , 2002 , 298, 799-804 | 33.3 | 2329 |
| 265 | Master transcription factors and mediator establish super-enhancers at key cell identity genes. <i>Cell</i> , 2013 , 153, 307-19 | 56.2 | 2252 |
| 264 | Super-enhancers in the control of cell identity and disease. <i>Cell</i> , 2013 , 155, 934-47 | 56.2 | 2053 |
| 263 | BET bromodomain inhibition as a therapeutic strategy to target c-Myc. <i>Cell</i> , 2011 , 146, 904-17 | 56.2 | 2045 |
| 262 | Polycomb complexes repress developmental regulators in murine embryonic stem cells. <i>Nature</i> , 2006 , 441, 349-53 | 50.4 | 2008 |
| 261 | Control of developmental regulators by Polycomb in human embryonic stem cells. <i>Cell</i> , 2006 , 125, 301-13 | 56.2 | 1882 |
| 260 | Selective inhibition of tumor oncogenes by disruption of super-enhancers. <i>Cell</i> , 2013 , 153, 320-34 | 56.2 | 1744 |
| 259 | Transcriptional regulatory code of a eukaryotic genome. <i>Nature</i> , 2004 , 431, 99-104 | 50.4 | 1732 |
| 258 | Genome-wide location and function of DNA binding proteins. <i>Science</i> , 2000 , 290, 2306-9 | 33.3 | 1679 |
| 257 | Dissecting the regulatory circuitry of a eukaryotic genome. <i>Cell</i> , 1998 , 95, 717-28 | 56.2 | 1621 |
| 256 | A chromatin landmark and transcription initiation at most promoters in human cells. <i>Cell</i> , 2007 , 130, 77-88 | 56.2 | 1541 |
| 255 | Mediator and cohesin connect gene expression and chromatin architecture. <i>Nature</i> , 2010 , 467, 430-5 | 50.4 | 1410 |
| 254 | Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. <i>Cell</i> , 2008 , 134, 521-33 | 56.2 | 1228 |
| 253 | Stem cells, the molecular circuitry of pluripotency and nuclear reprogramming. <i>Cell</i> , 2008 , 132, 567-82 | 56.2 | 1126 |
| 252 | Genome-wide map of nucleosome acetylation and methylation in yeast. <i>Cell</i> , 2005 , 122, 517-27 | 56.2 | 1102 |

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|-----|--|------|------|
| 251 | Remodeling of yeast genome expression in response to environmental changes. <i>Molecular Biology of the Cell</i> , 2001 , 12, 323-37 | 3.5 | 1091 |
| 250 | Control of pancreas and liver gene expression by HNF transcription factors. <i>Science</i> , 2004 , 303, 1378-81 | 33.3 | 1071 |
| 249 | Transcriptional amplification in tumor cells with elevated c-Myc. <i>Cell</i> , 2012 , 151, 56-67 | 56.2 | 996 |
| 248 | Coactivator condensation at super-enhancers links phase separation and gene control. <i>Science</i> , 2018 , 361, | 33.3 | 951 |
| 247 | c-Myc regulates transcriptional pause release. <i>Cell</i> , 2010 , 141, 432-45 | 56.2 | 930 |
| 246 | Targeted recruitment of Set1 histone methylase by elongating Pol II provides a localized mark and memory of recent transcriptional activity. <i>Molecular Cell</i> , 2003 , 11, 709-19 | 17.6 | 865 |
| 245 | A Phase Separation Model for Transcriptional Control. <i>Cell</i> , 2017 , 169, 13-23 | 56.2 | 856 |
| 244 | Control of the embryonic stem cell state. <i>Cell</i> , 2011 , 144, 940-54 | 56.2 | 853 |
| 243 | E2F integrates cell cycle progression with DNA repair, replication, and G(2)/M checkpoints. <i>Genes and Development</i> , 2002 , 16, 245-56 | 12.6 | 841 |
| 242 | Transcriptional regulation and its misregulation in disease. <i>Cell</i> , 2013 , 152, 1237-51 | 56.2 | 805 |
| 241 | Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 4459-64 | 11.5 | 756 |
| 240 | Divergent transcription from active promoters. <i>Science</i> , 2008 , 322, 1849-51 | 33.3 | 695 |
| 239 | Editing DNA Methylation in the Mammalian Genome. <i>Cell</i> , 2016 , 167, 233-247.e17 | 56.2 | 690 |
| 238 | Densely interconnected transcriptional circuits control cell states in human hematopoiesis. <i>Cell</i> , 2011 , 144, 296-309 | 56.2 | 655 |
| 237 | The plasticity of dendritic cell responses to pathogens and their components. <i>Science</i> , 2001 , 294, 870-5 | 33.3 | 652 |
| 236 | NOTCH1 directly regulates c-MYC and activates a feed-forward-loop transcriptional network promoting leukemic cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 18261-6 | 11.5 | 639 |
| 235 | Transcription Factors Activate Genes through the Phase-Separation Capacity of Their Activation Domains. <i>Cell</i> , 2018 , 175, 1842-1855.e16 | 56.2 | 636 |
| 234 | Transcription of eukaryotic protein-coding genes. <i>Annual Review of Genetics</i> , 2000 , 34, 77-137 | 14.5 | 629 |

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|-----|--|------|-----|
| 233 | Poised chromatin at the ZEB1 promoter enables breast cancer cell plasticity and enhances tumorigenicity. <i>Cell</i> , 2013 , 154, 61-74 | 56.2 | 608 |
| 232 | Control of cell identity genes occurs in insulated neighborhoods in mammalian chromosomes. <i>Cell</i> , 2014 , 159, 374-387 | 56.2 | 605 |
| 231 | Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016 , 351, 1454-1458 | 55.8 | 600 |
| 230 | RNA polymerase stalling at developmental control genes in the <i>Drosophila melanogaster</i> embryo. <i>Nature Genetics</i> , 2007 , 39, 1512-6 | 36.3 | 589 |
| 229 | Chromatin immunoprecipitation and microarray-based analysis of protein location. <i>Nature Protocols</i> , 2006 , 1, 729-48 | 18.8 | 581 |
| 228 | Foxp3 occupancy and regulation of key target genes during T-cell stimulation. <i>Nature</i> , 2007 , 445, 931-5 | 50.4 | 577 |
| 227 | Human macrophage activation programs induced by bacterial pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 1503-8 | 11.5 | 560 |
| 226 | An RNA polymerase II holoenzyme responsive to activators. <i>Nature</i> , 1994 , 368, 466-9 | 50.4 | 553 |
| 225 | Serial regulation of transcriptional regulators in the yeast cell cycle. <i>Cell</i> , 2001 , 106, 697-708 | 56.2 | 532 |
| 224 | Insights into host responses against pathogens from transcriptional profiling. <i>Nature Reviews Microbiology</i> , 2005 , 3, 281-94 | 22.2 | 524 |
| 223 | Targeting transcription regulation in cancer with a covalent CDK7 inhibitor. <i>Nature</i> , 2014 , 511, 616-20 | 50.4 | 507 |
| 222 | Systematic identification of culture conditions for induction and maintenance of naive human pluripotency. <i>Cell Stem Cell</i> , 2014 , 15, 471-487 | 18 | 506 |
| 221 | Transcriptional Addiction in Cancer. <i>Cell</i> , 2017 , 168, 629-643 | 56.2 | 491 |
| 220 | Discovery and characterization of super-enhancer-associated dependencies in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2013 , 24, 777-90 | 24.3 | 491 |
| 219 | Oncogene regulation. An oncogenic super-enhancer formed through somatic mutation of a noncoding intergenic element. <i>Science</i> , 2014 , 346, 1373-7 | 33.3 | 484 |
| 218 | Epitope tagging and protein surveillance. <i>Methods in Enzymology</i> , 1991 , 194, 508-19 | 1.7 | 461 |
| 217 | Master transcription factors determine cell-type-specific responses to TGF- β signaling. <i>Cell</i> , 2011 , 147, 565-76 | 56.2 | 447 |
| 216 | YY1 Is a Structural Regulator of Enhancer-Promoter Loops. <i>Cell</i> , 2017 , 171, 1573-1588.e28 | 56.2 | 444 |

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|-----|--|------|-----|
| 215 | Stress proteins, infection, and immune surveillance. <i>Cell</i> , 1989 , 59, 5-8 | 56.2 | 444 |
| 214 | Computational discovery of gene modules and regulatory networks. <i>Nature Biotechnology</i> , 2003 , 21, 1337-42 | 44.5 | 442 |
| 213 | Enhancer decommissioning by LSD1 during embryonic stem cell differentiation. <i>Nature</i> , 2012 , 482, 221-5 | 50.4 | 436 |
| 212 | Evidence for an instructive mechanism of de novo methylation in cancer cells. <i>Nature Genetics</i> , 2006 , 38, 149-53 | 36.3 | 419 |
| 211 | A multisubunit complex associated with the RNA polymerase II CTD and TATA-binding protein in yeast. <i>Cell</i> , 1993 , 73, 1361-75 | 56.2 | 414 |
| 210 | Revisiting global gene expression analysis. <i>Cell</i> , 2012 , 151, 476-82 | 56.2 | 410 |
| 209 | The histone methyltransferase SETDB1 is recurrently amplified in melanoma and accelerates its onset. <i>Nature</i> , 2011 , 471, 513-7 | 50.4 | 405 |
| 208 | Stress proteins and immunology. <i>Annual Review of Immunology</i> , 1990 , 8, 401-20 | 34.7 | 404 |
| 207 | RNA polymerase II. <i>Annual Review of Biochemistry</i> , 1991 , 60, 689-715 | 29.1 | 403 |
| 206 | BRCA1 is a component of the RNA polymerase II holoenzyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997 , 94, 5605-10 | 11.5 | 398 |
| 205 | CDK7 inhibition suppresses super-enhancer-linked oncogenic transcription in MYCN-driven cancer. <i>Cell</i> , 2014 , 159, 1126-1139 | 56.2 | 386 |
| 204 | Tcf3 is an integral component of the core regulatory circuitry of embryonic stem cells. <i>Genes and Development</i> , 2008 , 22, 746-55 | 12.6 | 384 |
| 203 | A kinase-cyclin pair in the RNA polymerase II holoenzyme. <i>Nature</i> , 1995 , 374, 193-6 | 50.4 | 378 |
| 202 | Response and resistance to BET bromodomain inhibitors in triple-negative breast cancer. <i>Nature</i> , 2016 , 529, 413-417 | 50.4 | 363 |
| 201 | Parkinson-associated risk variant in distal enhancer of β synuclein modulates target gene expression. <i>Nature</i> , 2016 , 533, 95-9 | 50.4 | 360 |
| 200 | Wnt signaling promotes reprogramming of somatic cells to pluripotency. <i>Cell Stem Cell</i> , 2008 , 3, 132-5 | 18 | 357 |
| 199 | Temporal regulation of RNA polymerase II by Srb10 and Kin28 cyclin-dependent kinases. <i>Molecular Cell</i> , 1998 , 2, 43-53 | 17.6 | 348 |
| 198 | Chromatin structure and gene expression programs of human embryonic and induced pluripotent stem cells. <i>Cell Stem Cell</i> , 2010 , 7, 249-57 | 18 | 347 |

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|-----|--|------|-----|
| 197 | Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 2876-81 | 11.5 | 345 |
| 196 | Genome-wide distribution of ORC and MCM proteins in <i>S. cerevisiae</i> : high-resolution mapping of replication origins. <i>Science</i> , 2001 , 294, 2357-60 | 33.3 | 342 |
| 195 | Association of Cdk-activating kinase subunits with transcription factor TFIIH. <i>Nature</i> , 1995 , 374, 280-2 | 50.4 | 335 |
| 194 | RNA polymerase II holoenzyme contains SWI/SNF regulators involved in chromatin remodeling. <i>Cell</i> , 1996 , 84, 235-44 | 56.2 | 333 |
| 193 | DHODH modulates transcriptional elongation in the neural crest and melanoma. <i>Nature</i> , 2011 , 471, 518-24 | 32.4 | 329 |
| 192 | Chromosomal landscape of nucleosome-dependent gene expression and silencing in yeast. <i>Nature</i> , 1999 , 402, 418-21 | 50.4 | 328 |
| 191 | Biomedical discovery with DNA arrays. <i>Cell</i> , 2000 , 102, 9-15 | 56.2 | 316 |
| 190 | Short RNAs are transcribed from repressed polycomb target genes and interact with polycomb repressive complex-2. <i>Molecular Cell</i> , 2010 , 38, 675-88 | 17.6 | 312 |
| 189 | Redundant roles for the TFIID and SAGA complexes in global transcription. <i>Nature</i> , 2000 , 405, 701-4 | 50.4 | 311 |
| 188 | Derivation of pre-X inactivation human embryonic stem cells under physiological oxygen concentrations. <i>Cell</i> , 2010 , 141, 872-83 | 56.2 | 306 |
| 187 | Role of SWI/SNF in acute leukemia maintenance and enhancer-mediated Myc regulation. <i>Genes and Development</i> , 2013 , 27, 2648-62 | 12.6 | 300 |
| 186 | Targeting transcriptional addictions in small cell lung cancer with a covalent CDK7 inhibitor. <i>Cancer Cell</i> , 2014 , 26, 909-922 | 24.3 | 294 |
| 185 | Rapid analysis of the DNA-binding specificities of transcription factors with DNA microarrays. <i>Nature Genetics</i> , 2004 , 36, 1331-9 | 36.3 | 294 |
| 184 | Functional redundancy and structural polymorphism in the large subunit of RNA polymerase II. <i>Cell</i> , 1987 , 50, 909-15 | 56.2 | 291 |
| 183 | Dissection of Mycobacterium tuberculosis antigens using recombinant DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1985 , 82, 2583-7 | 11.5 | 290 |
| 182 | Genes for the major protein antigens of the leprosy parasite Mycobacterium leprae. <i>Nature</i> , 1985 , 316, 450-2 | 50.4 | 290 |
| 181 | Convergence of developmental and oncogenic signaling pathways at transcriptional super-enhancers. <i>Molecular Cell</i> , 2015 , 58, 362-70 | 17.6 | 287 |
| 180 | Mir-214-dependent regulation of the polycomb protein Ezh2 in skeletal muscle and embryonic stem cells. <i>Molecular Cell</i> , 2009 , 36, 61-74 | 17.6 | 285 |

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| 179 | The RNA polymerase II holoenzyme and its implications for gene regulation. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 113-6 | 10.3 | 282 |
| 178 | Global and Hox-specific roles for the MLL1 methyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 8603-8 | 11.5 | 281 |
| 177 | 3D Chromosome Regulatory Landscape of Human Pluripotent Cells. <i>Cell Stem Cell</i> , 2016 , 18, 262-75 | 18 | 271 |
| 176 | CDK7-dependent transcriptional addiction in triple-negative breast cancer. <i>Cell</i> , 2015 , 163, 174-86 | 56.2 | 268 |
| 175 | Transcription factor trapping by RNA in gene regulatory elements. <i>Science</i> , 2015 , 350, 978-81 | 33.3 | 267 |
| 174 | Exchange of RNA polymerase II initiation and elongation factors during gene expression in vivo. <i>Molecular Cell</i> , 2002 , 9, 799-809 | 17.6 | 267 |
| 173 | H2AZ is enriched at polycomb complex target genes in ES cells and is necessary for lineage commitment. <i>Cell</i> , 2008 , 135, 649-61 | 56.2 | 264 |
| 172 | Insulated Neighborhoods: Structural and Functional Units of Mammalian Gene Control. <i>Cell</i> , 2016 , 167, 1188-1200 | 56.2 | 261 |
| 171 | PolII phosphorylation regulates a switch between transcriptional and splicing condensates. <i>Nature</i> , 2019 , 572, 543-548 | 50.4 | 255 |
| 170 | Negative regulation of Gcn4 and Msn2 transcription factors by Srb10 cyclin-dependent kinase. <i>Genes and Development</i> , 2001 , 15, 1078-92 | 12.6 | 254 |
| 169 | Pharmacological perturbation of CDK9 using selective CDK9 inhibition or degradation. <i>Nature Chemical Biology</i> , 2018 , 14, 163-170 | 11.7 | 243 |
| 168 | Rescue of Fragile X Syndrome Neurons by DNA Methylation Editing of the FMR1 Gene. <i>Cell</i> , 2018 , 172, 979-992.e6 | 56.2 | 239 |
| 167 | Lineage regulators direct BMP and Wnt pathways to cell-specific programs during differentiation and regeneration. <i>Cell</i> , 2011 , 147, 577-89 | 56.2 | 234 |
| 166 | Whole-genome ChIP-chip analysis of Dorsal, Twist, and Snail suggests integration of diverse patterning processes in the Drosophila embryo. <i>Genes and Development</i> , 2007 , 21, 385-90 | 12.6 | 232 |
| 165 | SetDB1 contributes to repression of genes encoding developmental regulators and maintenance of ES cell state. <i>Genes and Development</i> , 2009 , 23, 2484-9 | 12.6 | 228 |
| 164 | A zebrafish melanoma model reveals emergence of neural crest identity during melanoma initiation. <i>Science</i> , 2016 , 351, aad2197 | 33.3 | 223 |
| 163 | Global transcriptional and translational repression in human-embryonic-stem-cell-derived Rett syndrome neurons. <i>Cell Stem Cell</i> , 2013 , 13, 446-58 | 18 | 217 |
| 162 | Transcriptional role of cyclin D1 in development revealed by a genetic-proteomic screen. <i>Nature</i> , 2010 , 463, 374-8 | 50.4 | 217 |

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|-----|--|------|-----|
| 161 | Genome-wide location and regulated recruitment of the RSC nucleosome-remodeling complex. <i>Genes and Development</i> , 2002 , 16, 806-19 | 12.6 | 209 |
| 160 | Activated signal transduction kinases frequently occupy target genes. <i>Science</i> , 2006 , 313, 533-6 | 33.3 | 208 |
| 159 | Small-molecule ROR β antagonists inhibit T helper 17 cell transcriptional network by divergent mechanisms. <i>Immunity</i> , 2014 , 40, 477-89 | 32.3 | 207 |
| 158 | Aberrant chromatin at genes encoding stem cell regulators in human mixed-lineage leukemia. <i>Genes and Development</i> , 2008 , 22, 3403-8 | 12.6 | 204 |
| 157 | Core transcriptional regulatory circuit controlled by the TAL1 complex in human T cell acute lymphoblastic leukemia. <i>Cancer Cell</i> , 2012 , 22, 209-21 | 24.3 | 202 |
| 156 | Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. <i>Nature</i> , 2015 , 528, 418-21 | 50.4 | 201 |
| 155 | Global position and recruitment of HATs and HDACs in the yeast genome. <i>Molecular Cell</i> , 2004 , 16, 199-209 | 27.6 | 199 |
| 154 | Program-specific distribution of a transcription factor dependent on partner transcription factor and MAPK signaling. <i>Cell</i> , 2003 , 113, 395-404 | 56.2 | 193 |
| 153 | HIV-1 Tat reprograms immature dendritic cells to express chemoattractants for activated T cells and macrophages. <i>Nature Medicine</i> , 2003 , 9, 191-7 | 50.5 | 189 |
| 152 | The ribonuclease III site flanking 23S sequences in the 30S ribosomal precursor RNA of E. coli. <i>Cell</i> , 1980 , 19, 393-401 | 56.2 | 189 |
| 151 | Global and gene-specific analyses show distinct roles for MyoD and MyoG at a common set of promoters. <i>EMBO Journal</i> , 2006 , 25, 502-11 | 13 | 188 |
| 150 | Binding of pRB to the PHD protein RBP2 promotes cellular differentiation. <i>Molecular Cell</i> , 2005 , 18, 623-35 | 35.6 | 187 |
| 149 | An activator target in the RNA polymerase II holoenzyme. <i>Molecular Cell</i> , 1998 , 1, 895-904 | 17.6 | 178 |
| 148 | An unusual eukaryotic protein phosphatase required for transcription by RNA polymerase II and CTD dephosphorylation in <i>S. cerevisiae</i> . <i>Molecular Cell</i> , 1999 , 4, 55-62 | 17.6 | 176 |
| 147 | Recurrent somatic mutations in POLR2A define a distinct subset of meningiomas. <i>Nature Genetics</i> , 2016 , 48, 1253-9 | 36.3 | 173 |
| 146 | Super-Enhancer-Mediated RNA Processing Revealed by Integrative MicroRNA Network Analysis. <i>Cell</i> , 2017 , 168, 1000-1014.e15 | 56.2 | 167 |
| 145 | The long noncoding RNA controls cardiac fibrosis and remodeling. <i>Science Translational Medicine</i> , 2017 , 9, | 17.5 | 167 |
| 144 | RNA polymerase II holoenzymes and subcomplexes. <i>Journal of Biological Chemistry</i> , 1998 , 273, 27757-60 | 5.4 | 167 |

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|-----|--|-------|-----|
| 143 | RNA polymerase II C-terminal repeat influences response to transcriptional enhancer signals. <i>Nature</i> , 1990 , 347, 491-4 | 50.4 | 167 |
| 142 | A novel transcription factor reveals a functional link between the RNA polymerase II CTD and TFIID. <i>Cell</i> , 1992 , 69, 883-94 | 56.2 | 163 |
| 141 | Covalent targeting of remote cysteine residues to develop CDK12 and CDK13 inhibitors. <i>Nature Chemical Biology</i> , 2016 , 12, 876-84 | 11.7 | 162 |
| 140 | The transcription factors T-bet and GATA-3 control alternative pathways of T-cell differentiation through a shared set of target genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 17876-81 | 11.5 | 161 |
| 139 | Genome-wide maps of histone modifications unwind in vivo chromatin states of the hair follicle lineage. <i>Cell Stem Cell</i> , 2011 , 9, 219-32 | 18 | 159 |
| 138 | Enhancer Features that Drive Formation of Transcriptional Condensates. <i>Molecular Cell</i> , 2019 , 75, 549-561 | 11.67 | 155 |
| 137 | Core transcriptional regulatory circuitry in human hepatocytes. <i>Molecular Systems Biology</i> , 2006 , 2, 2006.0017 | 10.17 | 155 |
| 136 | Models of human core transcriptional regulatory circuitries. <i>Genome Research</i> , 2016 , 26, 385-96 | 9.7 | 153 |
| 135 | Identification of the gal4 suppressor Sug1 as a subunit of the yeast 26S proteasome. <i>Nature</i> , 1996 , 379, 655-7 | 50.4 | 153 |
| 134 | Gene isolation by screening lambda gt11 libraries with antibodies. <i>Methods in Enzymology</i> , 1987 , 152, 458-69 | 1.7 | 147 |
| 133 | Deciphering gene expression regulatory networks. <i>Current Opinion in Genetics and Development</i> , 2002 , 12, 130-6 | 4.9 | 146 |
| 132 | Human T-cell clones recognize a major M. leprae protein antigen expressed in E. coli. <i>Nature</i> , 1986 , 319, 63-6 | 50.4 | 145 |
| 131 | Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016 , 17, 11 | 18.3 | 141 |
| 130 | Aire unleashes stalled RNA polymerase to induce ectopic gene expression in thymic epithelial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 535-40 | 11.5 | 139 |
| 129 | Genome-wide localization of small molecules. <i>Nature Biotechnology</i> , 2014 , 32, 92-6 | 44.5 | 138 |
| 128 | X-linked H3K27me3 demethylase Utx is required for embryonic development in a sex-specific manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13004-9 | 11.5 | 137 |
| 127 | Tandem promoters direct E. coli ribosomal RNA synthesis. <i>Cell</i> , 1979 , 17, 225-34 | 56.2 | 137 |
| 126 | Increased antimycobacterial immunity in interleukin-10-deficient mice. <i>Infection and Immunity</i> , 1999 , 67, 3087-95 | 3.7 | 137 |

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|-----|--|------|-----|
| 125 | Coordinated binding of NF-kappaB family members in the response of human cells to lipopolysaccharide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 5899-904 | 11.5 | 135 |
| 124 | Lambda gt 11: gene isolation with antibody probes and other applications. <i>Methods in Enzymology</i> , 1987 , 154, 107-28 | 1.7 | 132 |
| 123 | A mammalian SRB protein associated with an RNA polymerase II holoenzyme. <i>Nature</i> , 1996 , 380, 82-5 | 50.4 | 129 |
| 122 | A proposed mechanism for the induction of cytotoxic T lymphocyte production by heat shock fusion proteins. <i>Immunity</i> , 2000 , 12, 263-72 | 32.3 | 123 |
| 121 | Partitioning of cancer therapeutics in nuclear condensates. <i>Science</i> , 2020 , 368, 1386-1392 | 33.3 | 120 |
| 120 | The genome-wide localization of Rsc9, a component of the RSC chromatin-remodeling complex, changes in response to stress. <i>Molecular Cell</i> , 2002 , 9, 563-73 | 17.6 | 119 |
| 119 | In vivo cytotoxic T lymphocyte elicitation by mycobacterial heat shock protein 70 fusion proteins maps to a discrete domain and is CD4(+) T cell independent. <i>Journal of Experimental Medicine</i> , 2000 , 191, 403-8 | 16.6 | 116 |
| 118 | The developmental potential of iPSCs is greatly influenced by reprogramming factor selection. <i>Cell Stem Cell</i> , 2014 , 15, 295-309 | 18 | 112 |
| 117 | Global control of motor neuron topography mediated by the repressive actions of a single hox gene. <i>Neuron</i> , 2010 , 67, 781-96 | 13.9 | 107 |
| 116 | A set of genes critical to development is epigenetically poised in mouse germ cells from fetal stages through completion of meiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 16061-6 | 11.5 | 106 |
| 115 | Genome-wide analysis of the H3K4 histone demethylase RBP2 reveals a transcriptional program controlling differentiation. <i>Molecular Cell</i> , 2008 , 31, 520-530 | 17.6 | 105 |
| 114 | Saltatory remodeling of Hox chromatin in response to rostrocaudal patterning signals. <i>Nature Neuroscience</i> , 2013 , 16, 1191-1198 | 25.5 | 103 |
| 113 | Biomolecular Condensates in the Nucleus. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 961-977 | 10.3 | 103 |
| 112 | A CD47-associated super-enhancer links pro-inflammatory signalling to CD47 upregulation in breast cancer. <i>Nature Communications</i> , 2017 , 8, 14802 | 17.4 | 101 |
| 111 | Ligand-dependent dynamics of retinoic acid receptor binding during early neurogenesis. <i>Genome Biology</i> , 2011 , 12, R2 | 18.3 | 101 |
| 110 | Functional association of Gdown1 with RNA polymerase II poised on human genes. <i>Molecular Cell</i> , 2012 , 45, 38-50 | 17.6 | 99 |
| 109 | RNA-Mediated Feedback Control of Transcriptional Condensates. <i>Cell</i> , 2021 , 184, 207-225.e24 | 56.2 | 99 |
| 108 | Drives a Subset of High-Risk Pediatric Neuroblastomas and Is Activated through Mechanisms Including Enhancer Hijacking and Focal Enhancer Amplification. <i>Cancer Discovery</i> , 2018 , 8, 320-335 | 24.4 | 98 |

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|-----|---|------|----|
| 107 | Integrated genomic analyses of de novo pathways underlying atypical meningiomas. <i>Nature Communications</i> , 2017 , 8, 14433 | 17.4 | 95 |
| 106 | Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018 , 50, 1240-1246 | 36.3 | 94 |
| 105 | A Systematic Approach to Identify Candidate Transcription Factors that Control Cell Identity. <i>Stem Cell Reports</i> , 2015 , 5, 763-775 | 8 | 93 |
| 104 | A strategy for rapid, high-confidence protein identification. <i>Analytical Chemistry</i> , 1997 , 69, 3995-4001 | 7.8 | 93 |
| 103 | The polycomb group protein L3mbtl2 assembles an atypical PRC1-family complex that is essential in pluripotent stem cells and early development. <i>Cell Stem Cell</i> , 2012 , 11, 319-32 | 18 | 91 |
| 102 | The TAL1 complex targets the FBXW7 tumor suppressor by activating miR-223 in human T cell acute lymphoblastic leukemia. <i>Journal of Experimental Medicine</i> , 2013 , 210, 1545-57 | 16.6 | 90 |
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