

# John L Rinn

## List of Publications by Year in descending order

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155  
papers

80,166  
citations

4146

87  
h-index

6654

156  
g-index

190  
all docs

190  
docs citations

190  
times ranked

85379  
citing authors

#	ARTICLE	IF	CITATIONS
1	From genotype to phenotype: genetics of mammalian long non-coding RNAs in vivo. <i>Nature Reviews Genetics</i> , 2022, 23, 229-243.	16.3	53
2	Mosaic cis-regulatory evolution drives transcriptional partitioning of HERVH endogenous retrovirus in the human embryo. <i>ELife</i> , 2022, 11, .	6.0	31
3	Evolutionary divergence of Firre localization and expression. <i>Rna</i> , 2022, , rna.079070.121.	3.5	8
4	An in vivo screen of noncoding loci reveals that <i>Daedalus</i> is a gatekeeper of an Ikaros-dependent checkpoint during haematopoiesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	2
5	Identification of human long noncoding RNAs associated with nonalcoholic fatty liver disease and metabolic homeostasis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	23
6	Myosin 7b is a regulatory long noncoding RNA (lncMYH7b) in the human heart. <i>Journal of Biological Chemistry</i> , 2021, 296, 100694.	3.4	11
7	Defective insulin receptor signaling in hPSCs skews pluripotency and negatively perturbs neural differentiation. <i>Journal of Biological Chemistry</i> , 2021, 296, 100495.	3.4	2
8	Nuclear compartmentalization of TERT mRNA and TUG1 lncRNA is driven by intron retention. <i>Nature Communications</i> , 2021, 12, 3308.	12.8	25
9	Genome-wide binding analysis of 195 DNA binding proteins reveals a reservoir of promoters and human specific SVA-repeat family regulation. <i>PLoS ONE</i> , 2021, 16, e0237055.	2.5	2
10	Genome-wide CRISPR interference screen identifies long non-coding RNA loci required for differentiation and pluripotency. <i>PLoS ONE</i> , 2021, 16, e0252848.	2.5	12
11	Diverse epigenetic mechanisms maintain parental imprints within the embryonic and extraembryonic lineages. <i>Developmental Cell</i> , 2021, 56, 2995-3005.e4.	7.0	33
12	Noncoding RNAs: biology and applications—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 118-141.	3.8	13
13	Common variants in signaling transcription-factor-binding sites drive phenotypic variability in red blood cell traits. <i>Nature Genetics</i> , 2020, 52, 1333-1345.	21.4	24
14	Mitoregulin Controls $\beta^2$ -Oxidation in Human and Mouse Adipocytes. <i>Stem Cell Reports</i> , 2020, 14, 590-602.	4.8	31
15	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	27.8	1,252
16	The Tug1 lncRNA locus is essential for male fertility. <i>Genome Biology</i> , 2020, 21, 237.	8.8	61
17	Cis and trans effects differentially contribute to the evolution of promoters and enhancers. <i>Genome Biology</i> , 2020, 21, 210.	8.8	35
18	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. <i>Nature Communications</i> , 2020, 11, 6053.	12.8	33

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19	Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics. <i>Cell</i> , 2020, 183, 1383-1401.e19.	28.9	79
20	Long Noncoding RNAs: Molecular Modalities to Organismal Functions. <i>Annual Review of Biochemistry</i> , 2020, 89, 283-308.	11.1	183
21	RNA is essential for PRC2 chromatin occupancy and function in human pluripotent stem cells. <i>Nature Genetics</i> , 2020, 52, 931-938.	21.4	99
22	The Sox2 transcription factor binds RNA. <i>Nature Communications</i> , 2020, 11, 1805.	12.8	77
23	Resolving mechanisms of immune-mediated disease in primary CD4 T cells. <i>EMBO Molecular Medicine</i> , 2020, 12, e12112.	6.9	30
24	The Firre locus produces a trans-acting RNA molecule that functions in hematopoiesis. <i>Nature Communications</i> , 2019, 10, 5137.	12.8	60
25	Linking long noncoding RNA to drug resistance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21963-21965.	7.1	11
26	Single-cell imaging reveals unexpected heterogeneity of telomerase reverse transcriptase expression across human cancer cell lines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 18488-18497.	7.1	27
27	RNA-seq as a tool for evaluating human embryo competence. <i>Genome Research</i> , 2019, 29, 1705-1718.	5.5	31
28	High-throughput functional analysis of lncRNA core promoters elucidates rules governing tissue specificity. <i>Genome Research</i> , 2019, 29, 344-355.	5.5	100
29	Illuminating Genomic Dark Matter with RNA Imaging. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032094.	5.5	17
30	Interchromosomal interactions: A genomic love story of kissing chromosomes. <i>Journal of Cell Biology</i> , 2019, 218, 27-38.	5.2	98
31	Differential contribution of steady-state RNA and active transcription in chromatin organization. <i>EMBO Reports</i> , 2019, 20, e48068.	4.5	61
32	In vivo Firre and Dxz4 deletion elucidates roles for autosomal gene regulation. <i>ELife</i> , 2019, 8, .	6.0	18
33	Inter-chromosomal Contact Properties in Live-Cell Imaging and in Hi-C. <i>Molecular Cell</i> , 2018, 69, 1039-1045.e3.	9.7	60
34	A TAD boundary is preserved upon deletion of the CTCF-rich Firre locus. <i>Nature Communications</i> , 2018, 9, 1444.	12.8	97
35	An Integrated Genome-wide CRISPRa Approach to Functionalize lncRNAs in Drug Resistance. <i>Cell</i> , 2018, 173, 649-664.e20.	28.9	238
36	A CLK3-HMGA2 Alternative Splicing Axis Impacts Human Hematopoietic Stem Cell Molecular Identity throughout Development. <i>Cell Stem Cell</i> , 2018, 22, 575-588.e7.	11.1	40

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37	High-throughput identification of <i>scp</i> RNA nuclear enrichment sequences. EMBO Journal, 2018, 37, .	7.8	99
38	Genetic determinants and epigenetic effects of pioneer-factor occupancy. Nature Genetics, 2018, 50, 250-258.	21.4	139
39	Spatiotemporal allele organization by allele-specific CRISPR live-cell imaging (SNP-CLING). Nature Structural and Molecular Biology, 2018, 25, 176-184.	8.2	75
40	Genetic Models Reveal cis and trans Immune-Regulatory Activities for lincRNA-Cox2. Cell Reports, 2018, 25, 1511-1524.e6.	6.4	73
41	Enhancers in the Peril lincRNA locus regulate distant but not local genes. Genome Biology, 2018, 19, 219.	8.8	20
42	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. Cell Systems, 2018, 7, 258-268.e3.	6.2	65
43	Reorganization of <i>inter</i> chromosomal interactions in the 2q37 deletion syndrome. EMBO Journal, 2018, 37, .	7.8	13
44	Dynamic changes during the treatment of pancreatic cancer. Oncotarget, 2018, 9, 14764-14790.	1.8	21
45	Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs. Genome Research, 2017, 27, 27-37.	5.5	207
46	Group 1 Innate Lymphoid Cell Lineage Identity Is Determined by a cis-Regulatory Element Marked by a Long Non-coding RNA. Immunity, 2017, 47, 435-449.e8.	14.3	57
47	p53 regulates enhancer accessibility and activity in response to DNA damage. Nucleic Acids Research, 2017, 45, 9889-9900.	14.5	61
48	<i>Neat1</i> is a p53-inducible lincRNA essential for transformation suppression. Genes and Development, 2017, 31, 1095-1108.	5.9	179
49	lncRNA requirements for mouse acute myeloid leukemia and normal differentiation. ELife, 2017, 6, .	6.0	54
50	Live-cell mapping of organelle-associated RNAs via proximity biotinylation combined with protein-RNA crosslinking. ELife, 2017, 6, .	6.0	143
51	LINC00520 is induced by Src, STAT3, and PI3K and plays a functional role in breast cancer. Oncotarget, 2016, 7, 81981-81994.	1.8	48
52	Function and evolution of local repeats in the Firre locus. Nature Communications, 2016, 7, 11021.	12.8	75
53	A distant trophoblast-specific enhancer controls HLA-G expression at the maternal-fetal interface. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5364-5369.	7.1	90
54	The long non-coding RNA Morrbid regulates Bim and short-lived myeloid cell lifespan. Nature, 2016, 537, 239-243.	27.8	234

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55	InÂVivo Characterization of Linc-p21 Reveals Functional cis -Regulatory DNA Elements. <i>Cell Reports</i> , 2016, 16, 2178-2186.	6.4	94
56	Integrative analyses reveal a long noncoding RNA-mediated sponge regulatory network in prostate cancer. <i>Nature Communications</i> , 2016, 7, 10982.	12.8	267
57	Widespread RNA binding by chromatin-associated proteins. <i>Genome Biology</i> , 2016, 17, 28.	8.8	197
58	Basset: learning the regulatory code of the accessible genome with deep convolutional neural networks. <i>Genome Research</i> , 2016, 26, 990-999.	5.5	790
59	â€œCatâ€™s Cradlingâ€™the 3D Genome by the Act of LncRNA Transcription. <i>Molecular Cell</i> , 2016, 62, 657-664.	9.7	128
60	Transcriptional silencing of long noncoding RNA GNG12-AS1 uncouples its transcriptional and product-related functions. <i>Nature Communications</i> , 2016, 7, 10406.	12.8	77
61	Diverse Phenotypes and Specific Transcription Patterns in Twenty Mouse Lines with Ablated LincRNAs. <i>PLoS ONE</i> , 2015, 10, e0125522.	2.5	51
62	Multiplexable, locus-specific targeting of long RNAs with CRISPR-Display. <i>Nature Methods</i> , 2015, 12, 664-670.	19.0	268
63	The histone chaperone CAF-1 safeguards somatic cell identity. <i>Nature</i> , 2015, 528, 218-224.	27.8	244
64	Discovery and annotation of long noncoding RNAs. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 5-7.	8.2	581
65	DeCoN: Genome-wide Analysis of InÂVivo Transcriptional Dynamics during Pyramidal Neuron Fate Selection in Neocortex. <i>Neuron</i> , 2015, 85, 275-288.	8.1	248
66	Visualization of lncRNA by Single-Molecule Fluorescence In Situ Hybridization. <i>Methods in Molecular Biology</i> , 2015, 1262, 3-19.	0.9	68
67	Strand-specific RNA sequencing in <i>Plasmodium falciparum</i> malaria identifies developmentally regulated long non-coding RNA and circular RNA. <i>BMC Genomics</i> , 2015, 16, 454.	2.8	160
68	Spatiotemporal expression and transcriptional perturbations by long noncoding RNAs in the mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6855-6862.	7.1	152
69	Integrative genomic analysis reveals widespread enhancer regulation by p53 in response to DNA damage. <i>Nucleic Acids Research</i> , 2015, 43, 4447-4462.	14.5	84
70	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015, 162, 412-424.	28.9	206
71	Localization and abundance analysis of human lncRNAs at single-cell and single-molecule resolution. <i>Genome Biology</i> , 2015, 16, 20.	8.8	565
72	Targeted disruption of DNMT1, DNMT3A and DNMT3B in human embryonic stem cells. <i>Nature Genetics</i> , 2015, 47, 469-478.	21.4	409

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73	Linking RNA biology to lncRNAs. <i>Genome Research</i> , 2015, 25, 1456-1465.	5.5	158
74	A comparison of genetically matched cell lines reveals the equivalence of human iPSCs and ESCs. <i>Nature Biotechnology</i> , 2015, 33, 1173-1181.	17.5	235
75	Genome-wide RNA-Seq of Human Motor Neurons Implicates Selective ER Stress Activation in Spinal Muscular Atrophy. <i>Cell Stem Cell</i> , 2015, 17, 569-584.	11.1	108
76	Mechanisms of Long Non-coding RNAs in Mammalian Nervous System Development, Plasticity, Disease, and Evolution. <i>Neuron</i> , 2015, 88, 861-877.	8.1	366
77	Silent pericentromeric repeats speak out. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15008-15009.	7.1	8
78	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	27.8	172
79	Transposable elements modulate human RNA abundance and splicing via specific RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 537.	8.8	88
80	'Lnc'-ing enhancers to MYC regulation. <i>Cell Research</i> , 2014, 24, 643-644.	12.0	23
81	Gene co-regulation by Fezf2 selects neurotransmitter identity and connectivity of corticospinal neurons. <i>Nature Neuroscience</i> , 2014, 17, 1046-1054.	14.8	121
82	RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome. <i>Genome Biology</i> , 2014, 15, R3.	9.6	76
83	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. <i>Nature Biotechnology</i> , 2014, 32, 381-386.	17.5	4,652
84	'Oming in on RNA-protein interactions. <i>Genome Biology</i> , 2014, 15, 401.	9.6	32
85	Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 198-206.	8.2	565
86	The multilayered complexity of ceRNA crosstalk and competition. <i>Nature</i> , 2014, 505, 344-352.	27.8	3,223
87	lncRNAs: Linking RNA to Chromatin. <i>Cold Spring Harbor Perspectives in Biology</i> , 2014, 6, a018614-a018614.	5.5	118
88	RNA and dynamic nuclear organization. <i>Science</i> , 2014, 345, 1240-1241.	12.6	119
89	DNMT1-interacting RNAs block gene-specific DNA methylation. <i>Nature</i> , 2013, 503, 371-376.	27.8	446
90	Poly-combing the genome for RNA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1344-1346.	8.2	6

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91	Scaffold function of long non-coding RNA HOTAIR in protein ubiquitination. <i>Nature Communications</i> , 2013, 4, 2939.	12.8	382
92	Sixty years of genome biology. <i>Genome Biology</i> , 2013, 14, 113.	9.6	6
93	Differential analysis of gene regulation at transcript resolution with RNA-seq. <i>Nature Biotechnology</i> , 2013, 31, 46-53.	17.5	3,256
94	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	27.8	810
95	Peptidomic discovery of short open reading frame-encoded peptides in human cells. <i>Nature Chemical Biology</i> , 2013, 9, 59-64.	8.0	529
96	Identifying Recent Adaptations in Large-Scale Genomic Data. <i>Cell</i> , 2013, 152, 703-713.	28.9	325
97	Long noncoding RNAs regulate adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3387-3392.	7.1	371
98	Ribosome profiling reveals resemblance between long non-coding RNAs and 5' leaders of coding RNAs. <i>Development (Cambridge)</i> , 2013, 140, 2828-2834.	2.5	237
99	Transcriptional and Epigenetic Dynamics during Specification of Human Embryonic Stem Cells. <i>Cell</i> , 2013, 153, 1149-1163.	28.9	419
100	Pint lincRNA connects the p53 pathway with epigenetic silencing by the Polycomb repressive complex 2. <i>Genome Biology</i> , 2013, 14, R104.	9.6	224
101	<i>linc-HOXA1</i> is a noncoding RNA that represses <i>Hoxa1</i> transcription in <i>cis</i> . <i>Genes and Development</i> , 2013, 27, 1260-1271.	5.9	120
102	Multiple knockout mouse models reveal lincRNAs are required for life and brain development. <i>ELife</i> , 2013, 2, e01749.	6.0	609
103	Suppression of progenitor differentiation requires the long noncoding RNA ANCR. <i>Genes and Development</i> , 2012, 26, 338-343.	5.9	391
104	Systematic identification of long noncoding RNAs expressed during zebrafish embryogenesis. <i>Genome Research</i> , 2012, 22, 577-591.	5.5	809
105	Computational analysis of noncoding RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 759-778.	6.4	50
106	Identification of proteins binding coding and non-coding human RNAs using protein microarrays. <i>BMC Genomics</i> , 2012, 13, 633.	2.8	35
107	Programming human pluripotent stem cells into white and brown adipocytes. <i>Nature Cell Biology</i> , 2012, 14, 209-219.	10.3	209
108	Transposable elements reveal a stem cell-specific class of long noncoding RNAs. <i>Genome Biology</i> , 2012, 13, R107.	9.6	462

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109	Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. <i>Nature Protocols</i> , 2012, 7, 562-578.	12.0	11,433
110	Modular regulatory principles of large non-coding RNAs. <i>Nature</i> , 2012, 482, 339-346.	27.8	2,036
111	Genome Regulation by Long Noncoding RNAs. <i>Annual Review of Biochemistry</i> , 2012, 81, 145-166.	11.1	3,665
112	Targeted RNA sequencing reveals the deep complexity of the human transcriptome. <i>Nature Biotechnology</i> , 2012, 30, 99-104.	17.5	437
113	As we come to the end of 2011, several members of the Genome Biology Editorial Board give their views on the state of play in genomics. <i>Genome Biology</i> , 2011, 12, 137.	9.6	0
114	Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. <i>Genes and Development</i> , 2011, 25, 1915-1927.	5.9	3,208
115	RNA-protein interactions in human health and disease. <i>Seminars in Cell and Developmental Biology</i> , 2011, 22, 359-365.	5.0	131
116	Improving RNA-Seq expression estimates by correcting for fragment bias. <i>Genome Biology</i> , 2011, 12, R22.	9.6	1,164
117	A global transcriptional analysis of <i>Plasmodium falciparum</i> malaria reveals a novel family of telomere-associated lincRNAs. <i>Genome Biology</i> , 2011, 12, R56.	9.6	124
118	lincRNAs act in the circuitry controlling pluripotency and differentiation. <i>Nature</i> , 2011, 477, 295-300.	27.8	1,749
119	Non-coding RNAs as regulators of embryogenesis. <i>Nature Reviews Genetics</i> , 2011, 12, 136-149.	16.3	558
120	To repress or not to repress: This is the guardian's question. <i>Trends in Cell Biology</i> , 2011, 21, 344-353.	7.9	52
121	The Reality of Pervasive Transcription. <i>PLoS Biology</i> , 2011, 9, e1000625.	5.6	380
122	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010, 464, 922-926.	27.8	340
123	Long non-coding RNA HOTAIR reprograms chromatin state to promote cancer metastasis. <i>Nature</i> , 2010, 464, 1071-1076.	27.8	4,648
124	Genome-wide measurement of RNA secondary structure in yeast. <i>Nature</i> , 2010, 467, 103-107.	27.8	713
125	Ab initio reconstruction of cell type-specific transcriptomes in mouse reveals the conserved multi-exonic structure of lincRNAs. <i>Nature Biotechnology</i> , 2010, 28, 503-510.	17.5	1,251
126	Large intergenic non-coding RNA-RoR modulates reprogramming of human induced pluripotent stem cells. <i>Nature Genetics</i> , 2010, 42, 1113-1117.	21.4	902



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127	DNA methylation and epigenetic control of cellular differentiation. <i>Cell Cycle</i> , 2010, 9, 3880-3883.	2.6	127
128	The Emerging Non-Coding RNA World. <i>Molecular Medicine and Biotechnology</i> , 2010, , 17-49.	0.4	1
129	Large non-coding RNAs: missing links in cancer?. <i>Human Molecular Genetics</i> , 2010, 19, R152-R161.	2.9	466
130	RNA traffic control of chromatin complexes. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 142-148.	3.3	161
131	A Large Intergenic Noncoding RNA Induced by p53 Mediates Global Gene Repression in the p53 Response. <i>Cell</i> , 2010, 142, 409-419.	28.9	1,919
132	Lin28a transgenic mice manifest size and puberty phenotypes identified in human genetic association studies. <i>Nature Genetics</i> , 2010, 42, 626-630.	21.4	282
133	Unbiased Reconstruction of a Mammalian Transcriptional Network Mediating Pathogen Responses. <i>Science</i> , 2009, 326, 257-263.	12.6	473
134	HOXA3 Modulates Injury-Induced Mobilization and Recruitment of Bone Marrow-Derived Cells. <i>Stem Cells</i> , 2009, 27, 1654-1665.	3.2	37
135	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	27.8	3,801
136	Many human large intergenic noncoding RNAs associate with chromatin-modifying complexes and affect gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 11667-11672.	7.1	2,709
137	Hierarchical Maintenance of MLL Myeloid Leukemia Stem Cells Employs a Transcriptional Program Shared with Embryonic Rather Than Adult Stem Cells. <i>Cell Stem Cell</i> , 2009, 4, 129-140.	11.1	326
138	A Systems Biology Approach to Anatomic Diversity of Skin. <i>Journal of Investigative Dermatology</i> , 2008, 128, 776-782.	0.7	78
139	Myo2p, a class V myosin in budding yeast, associates with a large ribonucleic acid-protein complex that contains mRNAs and subunits of the RNA-processing body. <i>Rna</i> , 2008, 14, 491-502.	3.5	29
140	A dermal <i>HOX</i> transcriptional program regulates site-specific epidermal fate. <i>Genes and Development</i> , 2008, 22, 303-307.	5.9	165
141	Mechanisms of an autoimmunity syndrome in mice caused by a dominant mutation in Aire. <i>Journal of Clinical Investigation</i> , 2008, 118, 1712-1726.	8.2	143
142	Genome-Wide Analysis of KAP1 Binding Suggests Autoregulation of KRAB-ZNFs. <i>PLoS Genetics</i> , 2007, 3, e89.	3.5	166
143	Ras/Erk MAPK Signaling in Epidermal Homeostasis and Neoplasia. <i>Cell Cycle</i> , 2007, 6, 2928-2931.	2.6	119
144	Functional Demarcation of Active and Silent Chromatin Domains in Human HOX Loci by Noncoding RNAs. <i>Cell</i> , 2007, 129, 1311-1323.	28.9	3,835

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145	A histone H3 lysine 27 demethylase regulates animal posterior development. <i>Nature</i> , 2007, 449, 689-694.	27.8	718
146	Spontaneous autoimmunity prevented by thymic expression of a single self-antigen. <i>Journal of Experimental Medicine</i> , 2006, 203, 2727-2735.	8.5	240
147	Anatomic Demarcation by Positional Variation in Fibroblast Gene Expression Programs. <i>PLoS Genetics</i> , 2006, 2, e119.	3.5	413
148	Design Issues in Implementing a Portable Sample Tracking and Analysis Research Support (STARS) System for PCR Based Microarray Research. , 2006, , .		0
149	Sexual dimorphism in mammalian gene expression. <i>Trends in Genetics</i> , 2005, 21, 298-305.	6.7	231
150	CREB Binds to Multiple Loci on Human Chromosome 22. <i>Molecular and Cellular Biology</i> , 2004, 24, 3804-3814.	2.3	160
151	Global Identification of Human Transcribed Sequences with Genome Tiling Arrays. <i>Science</i> , 2004, 306, 2242-2246.	12.6	983
152	Major Molecular Differences between Mammalian Sexes Are Involved in Drug Metabolism and Renal Function. <i>Developmental Cell</i> , 2004, 6, 791-800.	7.0	151
153	The transcriptional activity of human Chromosome 22. <i>Genes and Development</i> , 2003, 17, 529-540.	5.9	253
154	Distribution of NF- $\kappa$ B-binding sites across human chromosome 22. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12247-12252.	7.1	298
155	Expression of Shal potassium channel subunits in the adult and developing cochlear nucleus of the mouse. <i>Hearing Research</i> , 2000, 147, 31-45.	2.0	18