

# Manolis Kellis

## List of Publications by Year in descending order

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Version: 2024-02-01

259  
papers

131,673  
citations

902

116  
h-index

631

257  
g-index

334  
all docs

334  
docs citations

334  
times ranked

126801  
citing authors

#	ARTICLE	IF	CITATIONS
1	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. <i>Nature Biotechnology</i> , 2022, 40, 209-217.	9.4	127
2	Single-cell dissection of the human brain vasculature. <i>Nature</i> , 2022, 603, 893-899.	13.7	135
3	Immune genes outside immune cells for multiple sclerosis. <i>Neuron</i> , 2022, 110, 1090-1092.	3.8	2
4	Evolution of enhanced innate immune evasion by SARS-CoV-2. <i>Nature</i> , 2022, 602, 487-495.	13.7	237
5	BACE-1 inhibition facilitates the transition from homeostatic microglia to DAM-1. <i>Science Advances</i> , 2022, 8, .	4.7	27
6	Standardized annotation of translated open reading frames. <i>Nature Biotechnology</i> , 2022, 40, 994-999.	9.4	86
7	GENCODE 2021. <i>Nucleic Acids Research</i> , 2021, 49, D916-D923.	6.5	633
8	Genus-Wide Characterization of Bumblebee Genomes Provides Insights into Their Evolution and Variation in Ecological and Behavioral Traits. <i>Molecular Biology and Evolution</i> , 2021, 38, 486-501.	3.5	58
9	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimer's disease. <i>Translational Psychiatry</i> , 2021, 11, 146.	2.4	13
10	Regulatory genomic circuitry of human disease loci by integrative epigenomics. <i>Nature</i> , 2021, 590, 300-307.	13.7	232
11	<i>APOE4</i> disrupts intracellular lipid homeostasis in human iPSC-derived glia. <i>Science Translational Medicine</i> , 2021, 13, .	5.8	141
12	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. <i>Nature Communications</i> , 2021, 12, 2642.	5.8	136
13	NEBULA is a fast negative binomial mixed model for differential or co-expression analysis of large-scale multi-subject single-cell data. <i>Communications Biology</i> , 2021, 4, 629.	2.0	50
14	Evolution of delayed resistance to immunotherapy in a melanoma responder. <i>Nature Medicine</i> , 2021, 27, 985-992.	15.2	67
15	Conflicting and ambiguous names of overlapping ORFs in the SARS-CoV-2 genome: A homology-based resolution. <i>Virology</i> , 2021, 558, 145-151.	1.1	40
16	High-throughput 5' UTR engineering for enhanced protein production in non-viral gene therapies. <i>Nature Communications</i> , 2021, 12, 4138.	5.8	55
17	Genetic drivers of m6A methylation in human brain, lung, heart and muscle. <i>Nature Genetics</i> , 2021, 53, 1156-1165.	9.4	57
18	CoCoA-diff: counterfactual inference for single-cell gene expression analysis. <i>Genome Biology</i> , 2021, 22, 228.	3.8	9

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19	Distinct metabolic programs established in the thymus control effector functions of $\hat{\alpha}\hat{\beta}$ T cell subsets in tumor microenvironments. <i>Nature Immunology</i> , 2021, 22, 179-192.	7.0	99
20	MEF2 is a key regulator of cognitive potential and confers resilience to neurodegeneration. <i>Science Translational Medicine</i> , 2021, 13, eabd7695.	5.8	37
21	Spectral Alignment of Graphs. <i>IEEE Transactions on Network Science and Engineering</i> , 2020, 7, 1182-1197.	4.1	27
22	Improved haplotype inference by exploiting long-range linking and allelic imbalance in RNA-seq datasets. <i>Nature Communications</i> , 2020, 11, 4662.	5.8	14
23	Evidence for secondary-variant genetic burden and non-random distribution across biological modules in a recessive ciliopathy. <i>Nature Genetics</i> , 2020, 52, 1145-1150.	9.4	22
24	Mapping the epigenomic and transcriptomic interplay during memory formation and recall in the hippocampal engram ensemble. <i>Nature Neuroscience</i> , 2020, 23, 1606-1617.	7.1	89
25	Cell Type-Specific Transcriptomics Reveals that Mutant Huntingtin Leads to Mitochondrial RNA Release and Neuronal Innate Immune Activation. <i>Neuron</i> , 2020, 107, 891-908.e8.	3.8	147
26	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. <i>Cell Systems</i> , 2020, 11, 625-639.e13.	2.9	31
27	Plasma-derived extracellular vesicle analysis and deconvolution enable prediction and tracking of melanoma checkpoint blockade outcome. <i>Science Advances</i> , 2020, 6, .	4.7	37
28	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
29	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , 2020, 583, 699-710.	13.7	1,252
30	Translation Initiation Site Profiling Reveals Widespread Synthesis of Non-AUG-Initiated Protein Isoforms in Yeast. <i>Cell Systems</i> , 2020, 11, 145-160.e5.	2.9	41
31	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. <i>Cell Reports</i> , 2020, 31, 107716.	2.9	44
32	Single-Nucleus Transcriptomic Analysis of PTSD and MDD in Human Post-Mortem DLPFC. <i>Biological Psychiatry</i> , 2020, 87, S25.	0.7	0
33	A multiresolution framework to characterize single-cell state landscapes. <i>Nature Communications</i> , 2020, 11, 5399.	5.8	35
34	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , 2020, 183, 269-283.e19.	13.5	243
35	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.	3.8	68
36	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	4.5	255

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37	Inferring multimodal latent topics from electronic health records. <i>Nature Communications</i> , 2020, 11, 2536.	5.8	40
38	Reconstruction of the human blood–brain barrier in vitro reveals a pathogenic mechanism of APOE4 in pericytes. <i>Nature Medicine</i> , 2020, 26, 952-963.	15.2	173
39	Few SINEs of life: Alu elements have little evidence for biological relevance despite elevated translation. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqz023.	1.5	12
40	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. <i>BMC Genetics</i> , 2020, 21, 25.	2.7	30
41	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.	13.5	147
42	Genome-wide In Vivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. <i>Neuron</i> , 2020, 106, 76-89.e8.	3.8	62
43	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
44	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
45	Interleukin-6 deficiency exacerbates Huntington's disease model phenotypes. <i>Molecular Neurodegeneration</i> , 2020, 15, 29.	4.4	20
46	Network Infusion to Infer Information Sources in Networks. <i>IEEE Transactions on Network Science and Engineering</i> , 2019, 6, 402-417.	4.1	13
47	ncdDetect2: improved models of the site-specific mutation rate in cancer and driver detection with robust significance evaluation. <i>Bioinformatics</i> , 2019, 35, 189-199.	1.8	6
48	Joint profiling of DNA methylation and chromatin architecture in single cells. <i>Nature Methods</i> , 2019, 16, 991-993.	9.0	155
49	Integrative construction of regulatory region networks in 127 human reference epigenomes by matrix factorization. <i>Nucleic Acids Research</i> , 2019, 47, 7235-7246.	6.5	2
50	A high-throughput screening and computation platform for identifying synthetic promoters with enhanced cell-state specificity (SPECS). <i>Nature Communications</i> , 2019, 10, 2880.	5.8	42
51	Single-cell transcriptomic atlas of the human retina identifies cell types associated with age-related macular degeneration. <i>Nature Communications</i> , 2019, 10, 4902.	5.8	203
52	Elucidation of Codon Usage Signatures across the Domains of Life. <i>Molecular Biology and Evolution</i> , 2019, 36, 2328-2339.	3.5	54
53	Single-cell transcriptomic analysis of Alzheimer's disease. <i>Nature</i> , 2019, 570, 332-337.	13.7	1,528
54	200. Dissecting the Transcriptomic and Phenotypic Complexity of PTSD With Transcriptomic Imputation and Bayesian Machine Learning. <i>Biological Psychiatry</i> , 2019, 85, S83.	0.7	0

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55	Challenges in IBD Research: Environmental Triggers. <i>Inflammatory Bowel Diseases</i> , 2019, 25, S13-S23.	0.9	62
56	A gene expression atlas of embryonic neurogenesis in <i>Drosophila</i> reveals complex spatiotemporal regulation of lncRNAs. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	21
57	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. <i>Cell Reports</i> , 2019, 29, 4568-4582.e5.	2.9	114
58	Reconstruction of Cell-type-Specific Interactomes at Single-Cell Resolution. <i>Cell Systems</i> , 2019, 9, 559-568.e4.	2.9	51
59	Discovery of high-confidence human protein-coding genes and exons by whole-genome PhyloCSF helps elucidate 118 GWAS loci. <i>Genome Research</i> , 2019, 29, 2073-2087.	2.4	52
60	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019, 29, 223-235.	2.4	46
61	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	9.4	1,307
62	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , 2019, 47, D766-D773.	6.5	2,350
63	Abstract 948: Epigenomic correlates of checkpoint blockade immunotherapy resistance. <i>Cancer Research</i> , 2019, 79, 948-948.	0.4	3
64	Rate of brain aging and <i>APOE</i> $\epsilon 4$ are synergistic risk factors for Alzheimer's disease. <i>Life Science Alliance</i> , 2019, 2, e201900303.	1.3	10
65	Abstract 4533: Plasma and exosome proteomic profiling for prediction of immunotherapy response and toxicity. , 2019, , .		0
66	Abstract 3013: Acquired resistance to immune checkpoint inhibition by melanoma phenotypic transformation. , 2019, , .		0
67	Pan-cancer screen for mutations in non-coding elements with conservation and cancer specificity reveals correlations with expression and survival. <i>Npj Genomic Medicine</i> , 2018, 3, 1.	1.7	79
68	Stop codon readthrough generates a C-terminally extended variant of the human vitamin D receptor with reduced calcitriol response. <i>Journal of Biological Chemistry</i> , 2018, 293, 4434-4444.	1.6	59
69	N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. <i>Nature Neuroscience</i> , 2018, 21, 195-206.	7.1	317
70	RANGER-DTL 2.0: rigorous reconstruction of gene-family evolution by duplication, transfer and loss. <i>Bioinformatics</i> , 2018, 34, 3214-3216.	1.8	64
71	Target site specificity and in vivo complexity of the mammalian arginylome. <i>Scientific Reports</i> , 2018, 8, 16177.	1.6	25
72	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. <i>Nature Communications</i> , 2018, 9, 5380.	5.8	117

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73	Loss of <i>LDAH</i> associated with prostate cancer and hearing loss. <i>Human Molecular Genetics</i> , 2018, 27, 4194-4203.	1.4	14
74	Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , 2018, 50, 956-967.	9.4	389
75	Analyses of mRNA structure dynamics identify embryonic gene regulatory programs. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 677-686.	3.6	90
76	Loose ends: almost one in five human genes still have unresolved coding status. <i>Nucleic Acids Research</i> , 2018, 46, 7070-7084.	6.5	62
77	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	5.8	79
78	Chromatin Accessibility Impacts Transcriptional Reprogramming in Oocytes. <i>Cell Reports</i> , 2018, 24, 304-311.	2.9	50
79	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. <i>Science</i> , 2018, 361, .	6.0	87
80	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.	5.8	140
81	Abstract 4282: Deconvolution of plasma-derived exosomes for tracking and prediction of immunotherapy across multiple tissues. <i>Cancer Research</i> , 2018, 78, 4282-4282.	0.4	9
82	Abstract A35: BRAF inhibition increases exosomal PD-L1 protein expression in melanoma. , 2018, , .		2
83	Phylogenetic analysis of longitudinal melanoma samples to reveal convergent evolution and markers of immunotherapy resistance.. <i>Journal of Clinical Oncology</i> , 2018, 36, 9581-9581.	0.8	0
84	Predicting gene expression in massively parallel reporter assays: A comparative study. <i>Human Mutation</i> , 2017, 38, 1240-1250.	1.1	39
85	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
86	Network Maximal Correlation. <i>IEEE Transactions on Network Science and Engineering</i> , 2017, 4, 229-247.	4.1	9
87	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. <i>Nature Communications</i> , 2017, 8, 15011.	5.8	40
88	Dynamic landscape and regulation of RNA editing in mammals. <i>Nature</i> , 2017, 550, 249-254.	13.7	495
89	Landscape of X chromosome inactivation across human tissues. <i>Nature</i> , 2017, 550, 244-248.	13.7	764
90	Genetic effects on gene expression across human tissues. <i>Nature</i> , 2017, 550, 204-213.	13.7	3,500

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91	Chromatin-state discovery and genome annotation with ChromHMM. <i>Nature Protocols</i> , 2017, 12, 2478-2492.	5.5	613
92	Evidence of reduced recombination rate in human regulatory domains. <i>Genome Biology</i> , 2017, 18, 193.	3.8	38
93	Abstract A14: Convergence analysis of regulatory mutations into immuno-modulatory pathways across 14 tumor types. , 2017, , .		1
94	Abstract A15: Deconvolution of diverse cell types in the tumor microenvironment by jointly modeling transcriptomic and epigenomic information. , 2017, , .		0
95	Abstract 5689: Identify tissue-of-origin in cancer cfDNA by whole genome sequencing. , 2017, , .		1
96	Abstract B20: Discovery of combination therapies in a pan-cancer context through functional complementarity and convergence analysis of oncogenic drivers. , 2017, , .		0
97	SwiSpot: modeling riboswitches by spotting out switching sequences. <i>Bioinformatics</i> , 2016, 32, 3252-3259.	1.8	11
98	HaploReg v4: systematic mining of putative causal variants, cell types, regulators and target genes for human complex traits and disease. <i>Nucleic Acids Research</i> , 2016, 44, D877-D881.	6.5	796
99	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , 2016, 34, 1180-1190.	9.4	132
100	Joint Bayesian inference of risk variants and tissue-specific epigenomic enrichments across multiple complex human diseases. <i>Nucleic Acids Research</i> , 2016, 44, e144-e144.	6.5	76
101	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
102	Evolutionary Dynamics of Abundant Stop Codon Readthrough. <i>Molecular Biology and Evolution</i> , 2016, 33, 3108-3132.	3.5	53
103	Soft X-Ray Tomography Reveals Gradual Chromatin Compaction and Reorganization during Neurogenesis In Vivo. <i>Cell Reports</i> , 2016, 17, 2125-2136.	2.9	85
104	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	6.0	114
105	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. <i>Analytical Chemistry</i> , 2016, 88, 3967-3975.	3.2	119
106	MicroRNA and gene expression changes in unruptured human cerebral aneurysms. <i>Journal of Neurosurgery</i> , 2016, 125, 1390-1399.	0.9	38
107	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. <i>Nature Methods</i> , 2016, 13, 366-370.	9.0	306
108	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. <i>PLoS Genetics</i> , 2016, 12, e1006034.	1.5	34

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109	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. <i>ELife</i> , 2016, 5, .	2.8	115
110	Alzheimer's loci: epigenetic associations and interaction with genetic factors. <i>Annals of Clinical and Translational Neurology</i> , 2015, 2, 636-647.	1.7	57
111	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. <i>Nature Genetics</i> , 2015, 47, 381-386.	9.4	589
112	Activity-Induced DNA Breaks Govern the Expression of Neuronal Early-Response Genes. <i>Cell</i> , 2015, 161, 1592-1605.	13.5	566
113	Improved gene tree error correction in the presence of horizontal gene transfer. <i>Bioinformatics</i> , 2015, 31, 1211-1218.	1.8	64
114	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. <i>Molecular Cell</i> , 2015, 57, 636-647.	4.5	363
115	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. <i>Nature Biotechnology</i> , 2015, 33, 364-376.	9.4	354
116	Intermediate DNA methylation is a conserved signature of genome regulation. <i>Nature Communications</i> , 2015, 6, 6363.	5.8	91
117	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimer's disease. <i>Nature</i> , 2015, 518, 365-369.	13.7	526
118	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
119	Deep learning for regulatory genomics. <i>Nature Biotechnology</i> , 2015, 33, 825-826.	9.4	140
120	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. <i>PLoS Computational Biology</i> , 2015, 11, e1004220.	1.5	158
121	Context influences on TALE-DNA binding revealed by quantitative profiling. <i>Nature Communications</i> , 2015, 6, 7440.	5.8	30
122	FRESCO: finding regions of excess synonymous constraint in diverse viruses. <i>Genome Biology</i> , 2015, 16, 38.	3.8	35
123	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. <i>Science</i> , 2015, 348, 648-660.	6.0	4,659
124	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	6.0	252
125	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. <i>Biopreservation and Biobanking</i> , 2015, 13, 311-319.	0.5	674
126	Systematic chromatin state comparison of epigenomes associated with diverse properties including sex and tissue type. <i>Nature Communications</i> , 2015, 6, 7973.	5.8	57



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127	<i>FTO</i> Obesity Variant Circuitry and Adipocyte Browning in Humans. <i>New England Journal of Medicine</i> , 2015, 373, 895-907.	13.9	1,105
128	PRC2 Is Required to Maintain Expression of the Maternal <i>Gtl2-Rian-Mirg</i> Locus by Preventing De Novo DNA Methylation in Mouse Embryonic Stem Cells. <i>Cell Reports</i> , 2015, 12, 1456-1470.	2.9	64
129	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
130	The Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. <i>FASEB Journal</i> , 2015, 29, 567-21.	0.2	0
131	Evidence of efficient stop codon readthrough in four mammalian genes. <i>Nucleic Acids Research</i> , 2014, 42, 8928-8938.	6.5	184
132	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6131-6138.	3.3	635
133	Pareto-optimal phylogenetic tree reconciliation. <i>Bioinformatics</i> , 2014, 30, i87-i95.	1.8	59
134	Most parsimonious reconciliation in the presence of gene duplication, loss, and deep coalescence using labeled coalescent trees. <i>Genome Research</i> , 2014, 24, 475-486.	2.4	69
135	Core and region-enriched networks of behaviorally regulated genes and the singing genome. <i>Science</i> , 2014, 346, 1256780.	6.0	97
136	Diverse patterns of genomic targeting by transcriptional regulators in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2014, 24, 1224-1235.	2.4	31
137	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. <i>Nucleic Acids Research</i> , 2014, 42, 2976-2987.	6.5	421
138	The NF- $\kappa$ B Genomic Landscape in Lymphoblastoid B Cells. <i>Cell Reports</i> , 2014, 8, 1595-1606.	2.9	147
139	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2051-2063.	0.8	39
140	Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. <i>Journal of Proteome Research</i> , 2014, 13, 1757-1765.	1.8	149
141	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980.	6.0	391
142	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. <i>Nature</i> , 2014, 505, 701-705.	13.7	753
143	Evolutionary dynamics and tissue specificity of human long noncoding RNAs in six mammals. <i>Genome Research</i> , 2014, 24, 616-628.	2.4	318
144	RECOMB/ISCB Systems Biology, Regulatory Genomics, and DREAM 2013 Special Issue. <i>Journal of Computational Biology</i> , 2014, 21, 371-372.	0.8	1

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145	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
146	Comparative analysis of regulatory information and circuits across distant species. <i>Nature</i> , 2014, 512, 453-456.	13.7	184
147	Comparative analysis of metazoan chromatin organization. <i>Nature</i> , 2014, 512, 449-452.	13.7	363
148	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3366.	3.3	25
149	Comparative validation of the <i>D. melanogaster</i> modENCODE transcriptome annotation. <i>Genome Research</i> , 2014, 24, 1209-1223.	2.4	147
150	<i>CHD8</i> regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4468-77.	3.3	297
151	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	7.1	800
152	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
153	Energy-Based RNA Consensus Secondary Structure Prediction in Multiple Sequence Alignments. <i>Methods in Molecular Biology</i> , 2014, 1097, 125-141.	0.4	3
154	Genomic evidence for ameiotic evolution in the bdelloid rotifer <i>Adineta vaga</i> . <i>Nature</i> , 2013, 500, 453-457.	13.7	352
155	Network deconvolution as a general method to distinguish direct dependencies in networks. <i>Nature Biotechnology</i> , 2013, 31, 726-733.	9.4	223
156	Extensive Variation in Chromatin States Across Humans. <i>Science</i> , 2013, 342, 750-752.	6.0	338
157	Spatial expression of transcription factors in <i>Drosophila</i> embryonic organ development. <i>Genome Biology</i> , 2013, 14, R140.	13.9	135
158	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. <i>Journal of Computational Biology</i> , 2013, 20, 738-754.	0.8	55
159	Integrative annotation of chromatin elements from ENCODE data. <i>Nucleic Acids Research</i> , 2013, 41, 827-841.	6.5	490
160	Long noncoding RNAs regulate adipogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3387-3392.	3.3	371
161	Constitutive nuclear lamina-genome interactions are highly conserved and associated with A/T-rich sequence. <i>Genome Research</i> , 2013, 23, 270-280.	2.4	377
162	The Tissue-Specific lncRNA <i>Fendrr</i> Is an Essential Regulator of Heart and Body Wall Development in the Mouse. <i>Developmental Cell</i> , 2013, 24, 206-214.	3.1	866

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163	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. <i>Genome Research</i> , 2013, 23, 2136-2148.	2.4	51
164	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013, 23, 800-811.	2.4	298
165	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. <i>Genome Research</i> , 2013, 23, 1142-1154.	2.4	84
166	Arboretum: Reconstruction and analysis of the evolutionary history of condition-specific transcriptional modules. <i>Genome Research</i> , 2013, 23, 1039-1050.	2.4	60
167	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. <i>Systematic Biology</i> , 2013, 62, 110-120.	2.7	101
168	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2012 Special Issue. <i>Journal of Computational Biology</i> , 2013, 20, 373-374.	0.8	0
169	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , 2013, 45, 580-585.	9.4	6,815
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