Manolis Kellis

List of Publications by Year
in descending order

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259 papers	131,673 citations	1070 116 h-index	738 257 g-index
334 all docs	334 docs citations	334 times ranked	139749 citing authors

#	Article	IF	Citations
1	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	9.4	127
2	Single-cell dissection of the human brain vasculature. Nature, 2022, 603, 893-899.	13.7	135
3	Immune genes outside immune cells for multiple sclerosis. Neuron, 2022, 110, 1090-1092.	3.8	2
4	Evolution of enhanced innate immune evasion by SARS-CoV-2. Nature, 2022, 602, 487-495.	13.7	237
5	BACE-1 inhibition facilitates the transition from homeostatic microglia to DAM-1. Science Advances, 2022, 8, .	4.7	27
6	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
7	GENCODE 2021. Nucleic Acids Research, 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. Molecular Biology and Evolution, 2021, 38, 486-501.	3.5	58
9	Exome-wide age-of-onset analysis reveals exonic variants in ERN1 and SPPL2C associated with Alzheimerâ€™s disease. Translational Psychiatry, 2021, 11, 146.	2.4	13
10	Regulatory genomic circuitry of human disease loci by integrative epigenomics. Nature, 2021, 590, 300-307.	13.7	232
11	APOE4 disrupts intracellular lipid homeostasis in human iPSC-derived glia. Science Translational Medicine, 2021, 13, .	5.8	141
12	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. Nature Communications, 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. Communications Biology, 2021, 4, 629.	2.0	50
14	Evolution of delayed resistance to immunotherapy in a melanoma responder. Nature Medicine, 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. Virology, 2021, 558, 145-151.	1.1	40
16	High-throughput 5â€² UTR engineering for enhanced protein production in non-viral gene therapies. Nature Communications, 2021, 12, 4138.	5.8	55
17	Genetic drivers of m6A methylation in human brain, lung, heart and muscle. Nature Genetics, 2021, 53, 1156-1165.	9.4	57
18	CoCoA-diff: counterfactual inference for single-cell gene expression analysis. Genome Biology, 2021, 22, 228.	3.8	9

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19	Distinct metabolic programs established in the thymus control effector functions of Î³Î´ T cell subsets in tumor microenvironments. Nature Immunology, 2021, 22, 179-192.	7.0	99
20	MEF2 is a key regulator of cognitive potential and confers resilience to neurodegeneration. Science Translational Medicine, 2021, 13, eabd7695.	5.8	37
21	Spectral Alignment of Graphs. IEEE Transactions on Network Science and Engineering, 2020, 7, 1182-1197.	4.1	27
22	Improved haplotype inference by exploiting long-range linking and allelic imbalance in RNA-seq datasets. Nature Communications, 2020, 11, 4662.	5.8	14
23	Evidence for secondary-variant genetic burden and non-random distribution across biological modules in a recessive ciliopathy. Nature Genetics, 2020, 52, 1145-1150.	9.4	22
24	Mapping the epigenomic and transcriptomic interplay during memory formation and recall in the hippocampal engram ensemble. Nature Neuroscience, 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. Neuron, 2020, 107, 891-908.e8.	3.8	147
26	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. Cell Systems, 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. Science Advances, 2020, 6, .	4.7	37
28	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
29	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
30	Translation Initiation Site Profiling Reveals Widespread Synthesis of Non-AUG-Initiated Protein Isoforms in Yeast. Cell Systems, 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. Cell Reports, 2020, 31, 107716.	2.9	44
32	Single-Nucleus Transcriptomic Analysis of PTSD and MDD in Human Post-Mortem DLPFC. Biological Psychiatry, 2020, 87, S25.	0.7	0
33	A multiresolution framework to characterize single-cell state landscapes. Nature Communications, 2020, 11, 5399.	5.8	35
34	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
35	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
36	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. Molecular Cell, 2020, 80, 1078-1091.e6.	4.5	255

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37	Inferring multimodal latent topics from electronic health records. Nature Communications, 2020, 11, 2536.	5.8	40
38	Reconstruction of the human bloodâ€“brain barrier in vitro reveals a pathogenic mechanism of APOE4 in pericytes. Nature Medicine, 2020, 26, 952-963.	15.2	173
39	Few SINEs of life: Alu elements have little evidence for biological relevance despite elevated translation. NAR Genomics and Bioinformatics, 2020, 2, lqz023.	1.5	12
40	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. BMC Genetics, 2020, 21, 25.	2.7	30
41	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	13.5	147
42	Genome-wide InÂVivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. Neuron, 2020, 106, 76-89.e8.	3.8	62
43	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
44	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
45	Interleukin-6 deficiency exacerbates Huntingtonâ€™s disease model phenotypes. Molecular Neurodegeneration, 2020, 15, 29.	4.4	20
46	Network Infusion to Infer Information Sources in Networks. IEEE Transactions on Network Science and Engineering, 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. Bioinformatics, 2019, 35, 189-199.	1.8	6
48	Joint profiling of DNA methylation and chromatin architecture in single cells. Nature Methods, 2019, 16, 991-993.	9.0	155
49	Integrative construction of regulatory region networks in 127 human reference epigenomes by matrix factorization. Nucleic Acids Research, 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). Nature Communications, 2019, 10, 2880.	5.8	42
51	Single-cell transcriptomic atlas of the human retina identifies cell types associated with age-related macular degeneration. Nature Communications, 2019, 10, 4902.	5.8	203
52	Elucidation of Codon Usage Signatures across the Domains of Life. Molecular Biology and Evolution, 2019, 36, 2328-2339.	3.5	54
53	Single-cell transcriptomic analysis of Alzheimerâ€™s disease. Nature, 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. Biological Psychiatry, 2019, 85, S83.	0.7	0

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55	Challenges in IBD Research: Environmental Triggers. Inflammatory Bowel Diseases, 2019, 25, S13-S23.	0.9	62
56	A gene expression atlas of embryonic neurogenesis in Drosophila reveals complex spatiotemporal regulation of lncRNAs. Development (Cambridge), 2019, 146, .	1.2	21
57	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. Cell Reports, 2019, 29, 4568-4582.e5.	2.9	114
58	Reconstruction of Cell-type-Specific Interactomes at Single-Cell Resolution. Cell Systems, 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. Genome Research, 2019, 29, 2073-2087.	2.4	52
60	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. Genome Research, 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. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
62	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
63	Abstract 948: Epigenomic correlates of checkpoint blockade immunotherapy resistance. Cancer Research, 2019, 79, 948-948.	0.4	3
64	Rate of brain aging and APOE Îµ4 are synergistic risk factors for Alzheimerâ€™s disease. Life Science Alliance, 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. Npj Genomic Medicine, 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. Journal of Biological Chemistry, 2018, 293, 4434-4444.	1.6	59
69	N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. Nature Neuroscience, 2018, 21, 195-206.	7.1	317
70	RANGER-DTL 2.0: rigorous reconstruction of gene-family evolution by duplication, transfer and loss. Bioinformatics, 2018, 34, 3214-3216.	1.8	64
71	Target site specificity and in vivo complexity of the mammalian arginylome. Scientific Reports, 2018, 8, 16177.	1.6	25
72	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. Nature Communications, 2018, 9, 5380.	5.8	117

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73	Loss of LDAH associated with prostate cancer and hearing loss. Human Molecular Genetics, 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. Nature Genetics, 2018, 50, 956-967.	9.4	389
75	Analyses of mRNA structure dynamics identify embryonic gene regulatory programs. Nature Structural and Molecular Biology, 2018, 25, 677-686.	3.6	90
76	Loose ends: almost one in five human genes still have unresolved coding status. Nucleic Acids Research, 2018, 46, 7070-7084.	6.5	62
77	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
78	Chromatin Accessibility Impacts Transcriptional Reprogramming in Oocytes. Cell Reports, 2018, 24, 304-311.	2.9	50
79	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	6.0	87
80	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
81	Abstract 4282: Deconvolution of plasma-derived exosomes for tracking and prediction of immunotherapy across multiple tissues. Cancer Research, 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.. Journal of Clinical Oncology, 2018, 36, 9581-9581.	0.8	0
84	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 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. Nature Genetics, 2017, 49, 834-841.	9.4	426
86	Network Maximal Correlation. IEEE Transactions on Network Science and Engineering, 2017, 4, 229-247.	4.1	9
87	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. Nature Communications, 2017, 8, 15011.	5.8	40
88	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	13.7	495
89	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
90	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500

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91	Chromatin-state discovery and genome annotation with ChromHMM. Nature Protocols, 2017, 12, 2478-2492.	5.5	613
92	Evidence of reduced recombination rate in human regulatory domains. Genome Biology, 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. Bioinformatics, 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. Nucleic Acids Research, 2016, 44, D877-D881.	6.5	796
99	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. Nature Biotechnology, 2016, 34, 1180-1190.	9.4	132
100	Joint Bayesian inference of risk variants and tissue-specific epigenomic enrichments across multiple complex human diseases. Nucleic Acids Research, 2016, 44, e144-e144.	6.5	76
101	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
102	Evolutionary Dynamics of Abundant Stop Codon Readthrough. Molecular Biology and Evolution, 2016, 33, 3108-3132.	3.5	53
103	Soft X-Ray Tomography Reveals Gradual Chromatin Compaction and Reorganization during Neurogenesis InÂVivo. Cell Reports, 2016, 17, 2125-2136.	2.9	85
104	Survey of variation in human transcription factors reveals prevalent DNA binding changes. Science, 2016, 351, 1450-1454.	6.0	114
105	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. Analytical Chemistry, 2016, 88, 3967-3975.	3.2	119
106	MicroRNA and gene expression changes in unruptured human cerebral aneurysms. Journal of Neurosurgery, 2016, 125, 1390-1399.	0.9	38
107	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. Nature Methods, 2016, 13, 366-370.	9.0	306
108	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. PLoS Genetics, 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. ELife, 2016, 5, .	2.8	115
110	Alzheimer's loci: epigenetic associations and interaction with genetic factors. Annals of Clinical and Translational Neurology, 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. Nature Genetics, 2015, 47, 381-386.	9.4	589
112	Activity-Induced DNA Breaks Govern the Expression of Neuronal Early-Response Genes. Cell, 2015, 161, 1592-1605.	13.5	566
113	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	1.8	64
114	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. Molecular Cell, 2015, 57, 636-647.	4.5	363
115	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. Nature Biotechnology, 2015, 33, 364-376.	9.4	354
116	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	5.8	91
117	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimerâ€™s disease. Nature, 2015, 518, 365-369.	13.7	526
118	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
119	Deep learning for regulatory genomics. Nature Biotechnology, 2015, 33, 825-826.	9.4	140
120	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	1.5	158
121	Context influences on TALEâ€“DNA binding revealed by quantitative profiling. Nature Communications, 2015, 6, 7440.	5.8	30
122	FRESCo: finding regions of excess synonymous constraint in diverse viruses. Genome Biology, 2015, 16, 38.	3.8	35
123	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
124	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
125	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. Biopreservation and Biobanking, 2015, 13, 311-319.	0.5	674
126	Systematic chromatin state comparison of epigenomes associated with diverse properties including sex and tissue type. Nature Communications, 2015, 6, 7973.	5.8	57

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127	FTO Obesity Variant Circuitry and Adipocyte Browning in Humans. New England Journal of Medicine, 2015, 373, 895-907.	13.9	1,105
128	PRC2 Is Required to Maintain Expression of the Maternal Gtl2-Rian-Mirg Locus by Preventing De Novo DNA Methylation in Mouse Embryonic Stem Cells. Cell Reports, 2015, 12, 1456-1470.	2.9	64
129	Highly evolvable malaria vectors: The genomes of 16 Anopheles mosquitoes. Science, 2015, 347, 1258522.	6.0	492
130	The Discovery of Human sORFâ€Encoded Polypeptides (SEPs) in Cell Lines and Tissue. FASEB Journal, 2015, 29, 567.21.	0.2	0
131	Evidence of efficient stop codon readthrough in four mammalian genes. Nucleic Acids Research, 2014, 42, 8928-8938.	6.5	184
132	Defining functional DNA elements in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6131-6138.	3.3	635
133	Pareto-optimal phylogenetic tree reconciliation. Bioinformatics, 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. Genome Research, 2014, 24, 475-486.	2.4	69
135	Core and region-enriched networks of behaviorally regulated genes and the singing genome. Science, 2014, 346, 1256780.	6.0	97
136	Diverse patterns of genomic targeting by transcriptional regulators in Drosophila melanogaster. Genome Research, 2014, 24, 1224-1235.	2.4	31
137	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. Nucleic Acids Research, 2014, 42, 2976-2987.	6.5	421
138	The NF-ÎºB Genomic Landscape in Lymphoblastoid B Cells. Cell Reports, 2014, 8, 1595-1606.	2.9	147
139	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	0.8	39
140	Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. Journal of Proteome Research, 2014, 13, 1757-1765.	1.8	149
141	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
142	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. Nature, 2014, 505, 701-705.	13.7	753
143	Evolutionary dynamics and tissue specificity of human long noncoding RNAs in six mammals. Genome Research, 2014, 24, 616-628.	2.4	318
144	RECOMB/ISCB Systems Biology, Regulatory Genomics, and DREAM 2013 Special Issue. Journal of Computational Biology, 2014, 21, 371-372.	0.8	1

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145	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
146	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
147	Comparative analysis of metazoan chromatin organization. Nature, 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. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3366.	3.3	25
149	Comparative validation of the D. melanogaster modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	2.4	147
150	CHD8 regulates neurodevelopmental pathways associated with autism spectrum disorder in neural progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4468-77.	3.3	297
151	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	7.1	800
152	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
153	Energy-Based RNA Consensus Secondary Structure Prediction in Multiple Sequence Alignments. Methods in Molecular Biology, 2014, 1097, 125-141.	0.4	3
154	Genomic evidence for ameiotic evolution in the bdelloid rotifer Adineta vaga. Nature, 2013, 500, 453-457.	13.7	352
155	Network deconvolution as a general method to distinguish direct dependencies in networks. Nature Biotechnology, 2013, 31, 726-733.	9.4	223
156	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	6.0	338
157	Spatial expression of transcription factors in Drosophila embryonic organ development. Genome Biology, 2013, 14, R140.	13.9	135
158	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. Journal of Computational Biology, 2013, 20, 738-754.	0.8	55
159	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
160	Long noncoding RNAs regulate adipogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3387-3392.	3.3	371
161	Constitutive nuclear laminaâ€“genome interactions are highly conserved and associated with A/T-rich sequence. Genome Research, 2013, 23, 270-280.	2.4	377
162	The Tissue-Specific lncRNA Fendrr Is an Essential Regulator of Heart and Body Wall Development in the Mouse. Developmental Cell, 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. Genome Research, 2013, 23, 2136-2148.	2.4	51
164	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. Genome Research, 2013, 23, 800-811.	2.4	298
165	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. Genome Research, 2013, 23, 1142-1154.	2.4	84
166	Arboretum: Reconstruction and analysis of the evolutionary history of condition-specific transcriptional modules. Genome Research, 2013, 23, 1039-1050.	2.4	60
167	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. Systematic Biology, 2013, 62, 110-120.	2.7	101
168	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2012 Special Issue. Journal of Computational Biology, 2013, 20, 373-374.	0.8	0
169	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
170	Response to Comment on â€œEvidence of Abundant Purifying Selection in Humans for Recently Acquired Regulatory Functionsâ€• Science, 2013, 340, 682-682.	6.0	12
171	Multiple knockout mouse models reveal lincRNAs are required for life and brain development. ELife, 2013, 2, e01749.	2.8	609
172	RFECS: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. PLoS Computational Biology, 2013, 9, e1002968.	1.5	205
173	Heterologous Stop Codon Readthrough of Metazoan Readthrough Candidates in Yeast. PLoS ONE, 2013, 8, e59450.	1.1	8
174	Evolutionary principles of modular gene regulation in yeasts. ELife, 2013, 2, e00603.	2.8	73
175	Common Variants at 9p21 and 8q22 Are Associated with Increased Susceptibility to Optic Nerve Degeneration in Glaucoma. PLoS Genetics, 2012, 8, e1002654.	1.5	276
176	Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. Bioinformatics, 2012, 28, i283-i291.	1.8	188
177	Unified modeling of gene duplication, loss, and coalescence using a locus tree. Genome Research, 2012, 22, 755-765.	2.4	153
178	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2011 Special Issue. Journal of Computational Biology, 2012, 19, 101-101.	0.8	2
179	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. Nucleic Acids Research, 2012, 40, 4261-4272.	6.5	106
180	Evolution at the Subgene Level: Domain Rearrangements in the Drosophila Phylogeny. Molecular Biology and Evolution, 2012, 29, 689-705.	3.5	42

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181	HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. Nucleic Acids Research, 2012, 40, D930-D934.	6.5	2,020
182	Interpreting noncoding genetic variation in complex traits and human disease. Nature Biotechnology, 2012, 30, 1095-1106.	9.4	445
183	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	13.9	83
184	Linking DNA Methyltransferases to Epigenetic Marks and Nucleosome Structure Genome-wide in Human Tumor Cells. Cell Reports, 2012, 2, 1411-1424.	2.9	96
185	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
186	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
187	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
188	Wisdom of crowds for robust gene network inference. Nature Methods, 2012, 9, 796-804.	9.0	1,481
189	Evidence of Abundant Purifying Selection in Humans for Recently Acquired Regulatory Functions. Science, 2012, 337, 1675-1678.	6.0	193
190	Computational analysis of noncoding RNAs. Wiley Interdisciplinary Reviews RNA, 2012, 3, 759-778.	3.2	50
191	High depth, whole-genome sequencing of cholera isolates from Haiti and the Dominican Republic. BMC Genomics, 2012, 13, 468.	1.2	16
192	Disruption of a Large Intergenic Noncoding RNA in Subjects with Neurodevelopmental Disabilities. American Journal of Human Genetics, 2012, 91, 1128-1134.	2.6	61
193	Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. Nature Biotechnology, 2012, 30, 271-277.	9.4	602
194	ChromHMM: automating chromatin-state discovery and characterization. Nature Methods, 2012, 9, 215-216.	9.0	2,127
195	Predictive regulatory models in Drosophila melanogaster by integrative inference of transcriptional networks. Genome Research, 2012, 22, 1334-1349.	2.4	104
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