Manolis Kellis

List of Publications by Year
in descending order

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259	131,673	902 116	631 257
papers	citations	h-index	g-index

334	334	334	126801
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
2	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
3	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	13.7	5,653
4	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
5	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
6	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	13.7	3,801
7	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
8	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 2011, 473, 43-49.	13.7	2,630
9	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
10	Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature, 2009, 459, 108-112.	13.7	2,225
11	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
12	Discrete Small RNA-Generating Loci as Master Regulators of Transposon Activity in Drosophila. Cell, 2007, 128, 1089-1103.	13.5	2,215
13	ChromHMM: automating chromatin-state discovery and characterization. Nature Methods, 2012, 9, 215-216.	9.0	2,127
14	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
15	Transcriptional regulatory code of a eukaryotic genome. Nature, 2004, 431, 99-104.	13.7	1,969
16	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
17	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	13.7	1,886
18	Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature, 2004, 431, 946-957.	13.7	1,801

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19	Systematic discovery of regulatory motifs in human promoters and 3â€² UTRs by comparison of several mammals. Nature, 2005, 434, 338-345.	13.7	1,744
20	ChIP-seq guidelines and practices of the ENCODE and modENCODE consortia. Genome Research, 2012, 22, 1813-1831.	2.4	1,708
21	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	9.4	1,705
22	Sequencing and comparison of yeast species to identify genes and regulatory elements. Nature, 2003, 423, 241-254.	13.7	1,654
23	The genome sequence of the filamentous fungus Neurospora crassa. Nature, 2003, 422, 859-868.	13.7	1,528
24	Single-cell transcriptomic analysis of Alzheimerâ€™s disease. Nature, 2019, 570, 332-337.	13.7	1,528
25	Wisdom of crowds for robust gene network inference. Nature Methods, 2012, 9, 796-804.	9.0	1,481
26	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
27	Proof and evolutionary analysis of ancient genome duplication in the yeast Saccharomyces cerevisiae. Nature, 2004, 428, 617-624.	13.7	1,357
28	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
29	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
30	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
31	Identification of Functional Elements and Regulatory Circuits by Drosophila modENCODE. Science, 2010, 330, 1787-1797.	6.0	1,124
32	FTO Obesity Variant Circuitry and Adipocyte Browning in Humans. New England Journal of Medicine, 2015, 373, 895-907.	13.9	1,105
33	Extensive and coordinated transcription of noncoding RNAs within cell-cycle promoters. Nature Genetics, 2011, 43, 621-629.	9.4	1,080
34	A high-resolution map of human evolutionary constraint using 29 mammals. Nature, 2011, 478, 476-482.	13.7	1,016
35	Evolution of pathogenicity and sexual reproduction in eight Candida genomes. Nature, 2009, 459, 657-662.	13.7	963
36	Discovery and characterization of chromatin states for systematic annotation of the human genome. Nature Biotechnology, 2010, 28, 817-825.	9.4	947

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37	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
38	PhyloCSF: a comparative genomics method to distinguish protein coding and non-coding regions. Bioinformatics, 2011, 27, i275-i282.	1.8	864
39	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
40	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
41	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. Nature, 2011, 471, 480-485.	13.7	781
42	Landscape of X chromosome inactivation across human tissues. Nature, 2017, 550, 244-248.	13.7	764
43	Genome-wide probing of RNA structure reveals active unfolding of mRNA structures in vivo. Nature, 2014, 505, 701-705.	13.7	753
44	Unlocking the secrets of the genome. Nature, 2009, 459, 927-930.	13.7	744
45	A Novel Approach to High-Quality Postmortem Tissue Procurement: The GTEx Project. Biopreservation and Biobanking, 2015, 13, 311-319.	0.5	674
46	RNA polymerase stalling at developmental control genes in the Drosophila melanogaster embryo. Nature Genetics, 2007, 39, 1512-1516.	9.4	671
47	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	13.7	657
48	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
49	An endogenous small interfering RNA pathway in Drosophila. Nature, 2008, 453, 798-802.	13.7	633
50	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
51	Chromatin-state discovery and genome annotation with ChromHMM. Nature Protocols, 2017, 12, 2478-2492.	5.5	613
52	Multiple knockout mouse models reveal lincRNAs are required for life and brain development. ELife, 2013, 2, e01749.	2.8	609
53	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
54	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

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55	Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures. Nature, 2007, 450, 219-232.	13.7	573
56	Activity-Induced DNA Breaks Govern the Expression of Neuronal Early-Response Genes. Cell, 2015, 161, 1592-1605.	13.5	566
57	Evolution, biogenesis, expression, and target predictions of a substantially expanded set of Drosophila microRNAs. Genome Research, 2007, 17, 1850-1864.	2.4	540
58	Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimerâ€™s disease. Nature, 2015, 518, 365-369.	13.7	526
59	Distinguishing protein-coding and noncoding genes in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 19428-19433.	3.3	503
60	Dynamic landscape and regulation of RNA editing in mammals. Nature, 2017, 550, 249-254.	13.7	495
61	Highly evolvable malaria vectors: The genomes of 16 Anopheles mosquitoes. Science, 2015, 347, 1258522.	6.0	492
62	Integrative annotation of chromatin elements from ENCODE data. Nucleic Acids Research, 2013, 41, 827-841.	6.5	490
63	A cis-regulatory map of the Drosophila genome. Nature, 2011, 471, 527-531.	13.7	477
64	The consensus coding sequence (CCDS) project: Identifying a common protein-coding gene set for the human and mouse genomes. Genome Research, 2009, 19, 1316-1323.	2.4	476
65	Comparative Functional Genomics of the Fission Yeasts. Science, 2011, 332, 930-936.	6.0	458
66	Interpreting noncoding genetic variation in complex traits and human disease. Nature Biotechnology, 2012, 30, 1095-1106.	9.4	445
67	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
68	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
69	Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. Nucleic Acids Research, 2014, 42, 2976-2987.	6.5	421
70	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. Science, 2014, 343, 1246980.	6.0	391
71	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
72	Constitutive nuclear laminaâ€“genome interactions are highly conserved and associated with A/T-rich sequence. Genome Research, 2013, 23, 270-280.	2.4	377

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73	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
74	Comparative analysis of metazoan chromatin organization. Nature, 2014, 512, 449-452.	13.7	363
75	BRCA1 Recruitment to Transcriptional Pause Sites Is Required for R-Loop-Driven DNA Damage Repair. Molecular Cell, 2015, 57, 636-647.	4.5	363
76	Large-scale imputation of epigenomic datasets for systematic annotation of diverse human tissues. Nature Biotechnology, 2015, 33, 364-376.	9.4	354
77	Genomic evidence for ameiotic evolution in the bdelloid rotifer Adineta vaga. Nature, 2013, 500, 453-457.	13.7	352
78	Extensive Variation in Chromatin States Across Humans. Science, 2013, 342, 750-752.	6.0	338
79	Evolutionary dynamics and tissue specificity of human long noncoding RNAs in six mammals. Genome Research, 2014, 24, 616-628.	2.4	318
80	N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. Nature Neuroscience, 2018, 21, 195-206.	7.1	317
81	Tissue-specific regulatory circuits reveal variable modular perturbations across complex diseases. Nature Methods, 2016, 13, 366-370.	9.0	306
82	A Comprehensive Map of Insulator Elements for the Drosophila Genome. PLoS Genetics, 2010, 6, e1000814.	1.5	305
83	Combinatorial Patterning of Chromatin Regulators Uncovered by Genome-wide Location Analysis in Human Cells. Cell, 2011, 147, 1628-1639.	13.5	303
84	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
85	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
86	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
87	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
88	Whole-genome ChIP-chip analysis of Dorsal, Twist, and Snail suggests integration of diverse patterning processes in the Drosophila embryo. Genes and Development, 2007, 21, 385-390.	2.7	274
89	Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7145-7150.	3.3	272
90	An Epigenetic Signature for Monoallelic Olfactory Receptor Expression. Cell, 2011, 145, 555-570.	13.5	257

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91	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. Molecular Cell, 2020, 80, 1078-1091.e6.	4.5	255
92	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
93	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
94	Evolution of enhanced innate immune evasion by SARS-CoV-2. Nature, 2022, 602, 487-495.	13.7	237
95	Regulatory genomic circuitry of human disease loci by integrative epigenomics. Nature, 2021, 590, 300-307.	13.7	232
96	Network deconvolution as a general method to distinguish direct dependencies in networks. Nature Biotechnology, 2013, 31, 726-733.	9.4	223
97	The Tasmanian Devil Transcriptome Reveals Schwann Cell Origins of a Clonally Transmissible Cancer. Science, 2010, 327, 84-87.	6.0	222
98	A single Hox locus in Drosophila produces functional microRNAs from opposite DNA strands. Genes and Development, 2008, 22, 8-13.	2.7	205
99	RFECS: A Random-Forest Based Algorithm for Enhancer Identification from Chromatin State. PLoS Computational Biology, 2013, 9, e1002968.	1.5	205
100	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
101	Evidence of abundant stop codon readthrough in Drosophila and other metazoa. Genome Research, 2011, 21, 2096-2113.	2.4	196
102	Evidence of Abundant Purifying Selection in Humans for Recently Acquired Regulatory Functions. Science, 2012, 337, 1675-1678.	6.0	193
103	Efficient algorithms for the reconciliation problem with gene duplication, horizontal transfer and loss. Bioinformatics, 2012, 28, i283-i291.	1.8	188
104	Evidence of efficient stop codon readthrough in four mammalian genes. Nucleic Acids Research, 2014, 42, 8928-8938.	6.5	184
105	Comparative analysis of regulatory information and circuits across distant species. Nature, 2014, 512, 453-456.	13.7	184
106	Systematic discovery and characterization of fly microRNAs using 12 Drosophila genomes. Genome Research, 2007, 17, 1865-1879.	2.4	182
107	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
108	Network Motif Discovery Using Subgraph Enumeration and Symmetry-Breaking. , 2007, , 92-106.		166

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109	Sharing and Specificity of Co-expression Networks across 35 Human Tissues. PLoS Computational Biology, 2015, 11, e1004220.	1.5	158
110	Joint profiling of DNA methylation and chromatin architecture in single cells. Nature Methods, 2019, 16, 991-993.	9.0	155
111	Unified modeling of gene duplication, loss, and coalescence using a locus tree. Genome Research, 2012, 22, 755-765.	2.4	153
112	Discovery of Human sORF-Encoded Polypeptides (SEPs) in Cell Lines and Tissue. Journal of Proteome Research, 2014, 13, 1757-1765.	1.8	149
113	The NF-Î¹B Genomic Landscape in Lymphoblastoid B Cells. Cell Reports, 2014, 8, 1595-1606.	2.9	147
114	Comparative validation of the D. melanogaster modENCODE transcriptome annotation. Genome Research, 2014, 24, 1209-1223.	2.4	147
115	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
116	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	13.5	147
117	Reliable prediction of regulator targets using 12 Drosophila genomes. Genome Research, 2007, 17, 1919-1931.	2.4	141
118	APOE4 disrupts intracellular lipid homeostasis in human iPSC-derived glia. Science Translational Medicine, 2021, 13, .	5.8	141
119	Deep learning for regulatory genomics. Nature Biotechnology, 2015, 33, 825-826.	9.4	140
120	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
121	SARS-CoV-2 gene content and COVID-19 mutation impact by comparing 44 Sarbecovirus genomes. Nature Communications, 2021, 12, 2642.	5.8	136
122	Revisiting the protein-coding gene catalog of Drosophila melanogaster using 12 fly genomes. Genome Research, 2007, 17, 1823-1836.	2.4	135
123	Spatial expression of transcription factors in Drosophila embryonic organ development. Genome Biology, 2013, 14, R140.	13.9	135
124	Single-cell dissection of the human brain vasculature. Nature, 2022, 603, 893-899.	13.7	135
125	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. Nature Biotechnology, 2016, 34, 1180-1190.	9.4	132
126	Position specific variation in the rate of evolution in transcription factor binding sites. BMC Evolutionary Biology, 2003, 3, 19.	3.2	130

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127	Three Periods of Regulatory Innovation During Vertebrate Evolution. Science, 2011, 333, 1019-1024.	6.0	127
128	Unannotated proteins expand the MHC-I-restricted immunopeptidome in cancer. Nature Biotechnology, 2022, 40, 209-217.	9.4	127
129	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
130	Improved Identification and Analysis of Small Open Reading Frame Encoded Polypeptides. Analytical Chemistry, 2016, 88, 3967-3975.	3.2	119
131	High-resolution genome-wide functional dissection of transcriptional regulatory regions and nucleotides in human. Nature Communications, 2018, 9, 5380.	5.8	117
132	Discovery and validation of sub-threshold genome-wide association study loci using epigenomic signatures. ELife, 2016, 5, .	2.8	115
133	Survey of variation in human transcription factors reveals prevalent DNA binding changes. Science, 2016, 351, 1450-1454.	6.0	114
134	Human Primordial Germ Cells Are Specified from Lineage-Primed Progenitors. Cell Reports, 2019, 29, 4568-4582.e5.	2.9	114
135	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	1.2	113
136	A Bayesian Approach for Fast and Accurate Gene Tree Reconstruction. Molecular Biology and Evolution, 2011, 28, 273-290.	3.5	110
137	Dynamics of the epigenetic landscape during erythroid differentiation after GATA1 restoration. Genome Research, 2011, 21, 1659-1671.	2.4	110
138	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. Nucleic Acids Research, 2012, 40, 4261-4272.	6.5	106
139	Predictive regulatory models in Drosophila melanogaster by integrative inference of transcriptional networks. Genome Research, 2012, 22, 1334-1349.	2.4	104
140	TreeFix: Statistically Informed Gene Tree Error Correction Using Species Trees. Systematic Biology, 2013, 62, 110-120.	2.7	101
141	New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. Genome Research, 2011, 21, 1929-1943.	2.4	100
142	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
143	Core and region-enriched networks of behaviorally regulated genes and the singing genome. Science, 2014, 346, 1256780.	6.0	97
144	Linking DNA Methyltransferases to Epigenetic Marks and Nucleosome Structure Genome-wide in Human Tumor Cells. Cell Reports, 2012, 2, 1411-1424.	2.9	96

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145	Intermediate DNA methylation is a conserved signature of genome regulation. Nature Communications, 2015, 6, 6363.	5.8	91
146	Analyses of mRNA structure dynamics identify embryonic gene regulatory programs. Nature Structural and Molecular Biology, 2018, 25, 677-686.	3.6	90
147	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
148	Methods in Comparative Genomics: Genome Correspondence, Gene Identification and Regulatory Motif Discovery. Journal of Computational Biology, 2004, 11, 319-355.	0.8	88
149	Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. Science, 2018, 361, .	6.0	87
150	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
151	Soft X-Ray Tomography Reveals Gradual Chromatin Compaction and Reorganization during Neurogenesis InAVivo. Cell Reports, 2016, 17, 2125-2136.	2.9	85
152	Interplay between chromatin state, regulator binding, and regulatory motifs in six human cell types. Genome Research, 2013, 23, 1142-1154.	2.4	84
153	Locating protein-coding sequences under selection for additional, overlapping functions in 29 mammalian genomes. Genome Research, 2011, 21, 1916-1928.	2.4	83
154	Analysis of variation at transcription factor binding sites in Drosophila and humans. Genome Biology, 2012, 13, R49.	13.9	83
155	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
156	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
157	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
158	Accurate gene-tree reconstruction by learning gene- and species-specific substitution rates across multiple complete genomes. Genome Research, 2007, 17, 1932-1942.	2.4	73
159	Evolutionary principles of modular gene regulation in yeasts. ELife, 2013, 2, e00603.	2.8	73
160	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
161	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
162	Evolution of delayed resistance to immunotherapy in a melanoma responder. Nature Medicine, 2021, 27, 985-992.	15.2	67

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163	SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings. Journal of Computational Biology, 2011, 18, 219-235.	0.8	66
164	Improved gene tree error correction in the presence of horizontal gene transfer. Bioinformatics, 2015, 31, 1211-1218.	1.8	64
165	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
166	RANGER-DTL 2.0: rigorous reconstruction of gene-family evolution by duplication, transfer and loss. Bioinformatics, 2018, 34, 3214-3216.	1.8	64
167	Loose ends: almost one in five human genes still have unresolved coding status. Nucleic Acids Research, 2018, 46, 7070-7084.	6.5	62
168	Challenges in IBD Research: Environmental Triggers. Inflammatory Bowel Diseases, 2019, 25, S13-S23.	0.9	62
169	Genome-wide InÂVivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. Neuron, 2020, 106, 76-89.e8.	3.8	62
170	Disruption of a Large Intergenic Noncoding RNA in Subjects with Neurodevelopmental Disabilities. American Journal of Human Genetics, 2012, 91, 1128-1134.	2.6	61
171	Arboretum: Reconstruction and analysis of the evolutionary history of condition-specific transcriptional modules. Genome Research, 2013, 23, 1039-1050.	2.4	60
172	Pareto-optimal phylogenetic tree reconciliation. Bioinformatics, 2014, 30, i87-i95.	1.8	59
173	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
174	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
175	Alzheimer's loci: epigenetic associations and interaction with genetic factors. Annals of Clinical and Translational Neurology, 2015, 2, 636-647.	1.7	57
176	Systematic chromatin state comparison of epigenomes associated with diverse properties including sex and tissue type. Nature Communications, 2015, 6, 7973.	5.8	57
177	Genetic drivers of m6A methylation in human brain, lung, heart and muscle. Nature Genetics, 2021, 53, 1156-1165.	9.4	57
178	Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss. Journal of Computational Biology, 2013, 20, 738-754.	0.8	55
179	High-throughput 5â€² UTR engineering for enhanced protein production in non-viral gene therapies. Nature Communications, 2021, 12, 4138.	5.8	55
180	Elucidation of Codon Usage Signatures across the Domains of Life. Molecular Biology and Evolution, 2019, 36, 2328-2339.	3.5	54

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181	Evolutionary Dynamics of Abundant Stop Codon Readthrough. Molecular Biology and Evolution, 2016, 33, 3108-3132.	3.5	53
182	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
183	The evolutionary dynamics of the Saccharomyces cerevisiae protein interaction network after duplication. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 950-954.	3.3	51
184	Integrating and mining the chromatin landscape of cell-type specificity using self-organizing maps. Genome Research, 2013, 23, 2136-2148.	2.4	51
185	Reconstruction of Cell-type-Specific Interactomes at Single-Cell Resolution. Cell Systems, 2019, 9, 559-568.e4.	2.9	51
186	Computational analysis of noncoding RNAs. Wiley Interdisciplinary Reviews RNA, 2012, 3, 759-778.	3.2	50
187	Chromatin Accessibility Impacts Transcriptional Reprogramming in Oocytes. Cell Reports, 2018, 24, 304-311.	2.9	50
188	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
189	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. Genome Research, 2019, 29, 223-235.	2.4	46
190	Performance and Scalability of Discriminative Metrics for Comparative Gene Identification in 12 Drosophila Genomes. PLoS Computational Biology, 2008, 4, e1000067.	1.5	45
191	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. Genome Biology, 2003, 4, R43.	13.9	44
192	Analysis of Genetically Regulated Gene Expression Identifies a Prefrontal PTSD Gene, SNRNP35, Specific to Military Cohorts. Cell Reports, 2020, 31, 107716.	2.9	44
193	Optimization of parameters for coverage of low molecular weight proteins. Analytical and Bioanalytical Chemistry, 2010, 398, 2867-2881.	1.9	43
194	Evolution at the Subgene Level: Domain Rearrangements in the Drosophila Phylogeny. Molecular Biology and Evolution, 2012, 29, 689-705.	3.5	42
195	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
196	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
197	Multi-scale chromatin state annotation using a hierarchical hidden Markov model. Nature Communications, 2017, 8, 15011.	5.8	40
198	Inferring multimodal latent topics from electronic health records. Nature Communications, 2020, 11, 2536.	5.8	40

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199	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
200	Conservation of small RNA pathways in platypus. Genome Research, 2008, 18, 995-1004.	2.4	39
201	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	0.8	39
202	Predicting gene expression in massively parallel reporter assays: A comparative study. Human Mutation, 2017, 38, 1240-1250.	1.1	39
203	MicroRNA and gene expression changes in unruptured human cerebral aneurysms. Journal of Neurosurgery, 2016, 125, 1390-1399.	0.9	38
204	Evidence of reduced recombination rate in human regulatory domains. Genome Biology, 2017, 18, 193.	3.8	38
205	Plasma-derived extracellular vesicle analysis and deconvolution enable prediction and tracking of melanoma checkpoint blockade outcome. Science Advances, 2020, 6, .	4.7	37
206	MEF2 is a key regulator of cognitive potential and confers resilience to neurodegeneration. Science Translational Medicine, 2021, 13, eabd7695.	5.8	37
207	FRESCo: finding regions of excess synonymous constraint in diverse viruses. Genome Biology, 2015, 16, 38.	3.8	35
208	A multiresolution framework to characterize single-cell state landscapes. Nature Communications, 2020, 11, 5399.	5.8	35
209	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. PLoS Genetics, 2016, 12, e1006034.	1.5	34
210	Error and Error Mitigation in Low-Coverage Genome Assemblies. PLoS ONE, 2011, 6, e17034.	1.1	33
211	Diverse patterns of genomic targeting by transcriptional regulators in Drosophila melanogaster. Genome Research, 2014, 24, 1224-1235.	2.4	31
212	Conserved Epigenetic Regulatory Logic Infers Genes Governing Cell Identity. Cell Systems, 2020, 11, 625-639.e13.	2.9	31
213	Context influences on TALEâ€“DNA binding revealed by quantitative profiling. Nature Communications, 2015, 6, 7440.	5.8	30
214	Evidence for a novel overlapping coding sequence in POLG initiated at a CUG start codon. BMC Genetics, 2020, 21, 25.	2.7	30
215	Motif discovery in physiological datasets. ACM Transactions on Knowledge Discovery From Data, 2010, 4, 1-23.	2.5	28
216	Spectral Alignment of Graphs. IEEE Transactions on Network Science and Engineering, 2020, 7, 1182-1197.	4.1	27

#	Article	IF	Citations
217	BACE-1 inhibition facilitates the transition from homeostatic microglia to DAM-1. Science Advances, 2022, 8, .	4.7	27
218	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
219	Target site specificity and in vivo complexity of the mammalian arginylome. Scientific Reports, 2018, 8, 16177.	1.6	25
220	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
221	A gene expression atlas of embryonic neurogenesis in Drosophila reveals complex spatiotemporal regulation of lncRNAs. Development (Cambridge), 2019, 146, .	1.2	21
222	Interleukin-6 deficiency exacerbates Huntingtonâ€™s disease model phenotypes. Molecular Neurodegeneration, 2020, 15, 29.	4.4	20
223	High depth, whole-genome sequencing of cholera isolates from Haiti and the Dominican Republic. BMC Genomics, 2012, 13, 468.	1.2	16
224	Loss of LDAH associated with prostate cancer and hearing loss. Human Molecular Genetics, 2018, 27, 4194-4203.	1.4	14
225	Improved haplotype inference by exploiting long-range linking and allelic imbalance in RNA-seq datasets. Nature Communications, 2020, 11, 4662.	5.8	14
226	Network Infusion to Infer Information Sources in Networks. IEEE Transactions on Network Science and Engineering, 2019, 6, 402-417.	4.1	13
227	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
228	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
229	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
230	SwiSpot: modeling riboswitches by spotting out switching sequences. Bioinformatics, 2016, 32, 3252-3259.	1.8	11
231	Rate of brain aging and APOE Îµ4 are synergistic risk factors for Alzheimerâ€™s disease. Life Science Alliance, 2019, 2, e201900303.	1.3	10
232	Network Maximal Correlation. IEEE Transactions on Network Science and Engineering, 2017, 4, 229-247.	4.1	9
233	CoCoA-diff: counterfactual inference for single-cell gene expression analysis. Genome Biology, 2021, 22, 228.	3.8	9
234	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

#	Article	IF	Citations
235	Heterologous Stop Codon Readthrough of Metazoan Readthrough Candidates in Yeast. PLoS ONE, 2013, 8, e59450.	1.1	8
236	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
237	Abstract 948: Epigenomic correlates of checkpoint blockade immunotherapy resistance. Cancer Research, 2019, 79, 948-948.	0.4	3
238	Energy-Based RNA Consensus Secondary Structure Prediction in Multiple Sequence Alignments. Methods in Molecular Biology, 2014, 1097, 125-141.	0.4	3
239	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2011 Special Issue. Journal of Computational Biology, 2012, 19, 101-101.	0.8	2
240	Integrative construction of regulatory region networks in 127 human reference epigenomes by matrix factorization. Nucleic Acids Research, 2019, 47, 7235-7246.	6.5	2
241	Abstract A35: BRAF inhibition increases exosomal PD-L1 protein expression in melanoma. , 2018, , .		2
242	Immune genes outside immune cells for multiple sclerosis. Neuron, 2022, 110, 1090-1092.	3.8	2
243	PhyloCSF: a comparative genomics method to distinguish protein-coding and non-coding regions. Nature Precedings, 2010, , .	0.1	1
244	Preface. Journal of Computational Biology, 2011, 18, 131-131.	0.8	1
245	RECOMB/ISCB Systems Biology, Regulatory Genomics, and DREAM 2013 Special Issue. Journal of Computational Biology, 2014, 21, 371-372.	0.8	1
246	HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. , 0, .		1
247	Abstract A14: Convergence analysis of regulatory mutations into immuno-modulatory pathways across 14 tumor types. , 2017, , .		1
248	Abstract 5689: Identify tissue-of-origin in cancer cfDNA by whole genome sequencing. , 2017, , .		1
249	The changing face of genomics. Genome Biology, 2004, 5, 324.	13.9	0
250	Gene finding using multiple related species: a classification approach. , 2005, , .		0
251	Preface: RECOMB Systems Biology, Regulatory Genomics, and DREAM 2012 Special Issue. Journal of Computational Biology, 2013, 20, 373-374.	0.8	0
252	200. Dissecting the Transcriptomic and Phenotypic Complexity of PTSD With Transcriptomic Imputation and Bayesian Machine Learning. Biological Psychiatry, 2019, 85, S83.	0.7	0

#	Article	IF	Citations
253	Single-Nucleus Transcriptomic Analysis of PTSD and MDD in Human Post-Mortem DLPFC. Biological Psychiatry, 2020, 87, S25.	0.7	0
254	The Discovery of Human sORFâ€Encoded Polypeptides (SEPs) in Cell Lines and Tissue. FASEB Journal, 2015, 29, 567.21.	0.2	0
255	Abstract A15: Deconvolution of diverse cell types in the tumor microenvironment by jointly modeling transcriptomic and epigenomic information. , 2017, , .		0
256	Abstract B20: Discovery of combination therapies in a pan-cancer context through functional complementarity and convergence analysis of oncogenic drivers. , 2017, , .		0
257	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
258	Abstract 4533: Plasma and exosome proteomic profiling for prediction of immunotherapy response and toxicity. , 2019, , .		0
259	Abstract 3013: Acquired resistance to immune checkpoint inhibition by melanoma phenotypic transformation. , 2019, , .		0