Roderic Guigo

List of Publications by Year
in descending order

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266 papers	130,567 citations	1463 107 h-index	677 254 g-index
325 all docs	325 docs citations	325 times ranked	129006 citing authors

#	Article	IF	Citations
1	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
2	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
3	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	21.4	6,815
4	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
5	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
6	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	12.6	4,659
7	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	27.8	4,484
8	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	5.5	4,428
9	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	5.5	4,217
10	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	27.8	3,500
11	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	27.8	2,860
12	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004, 432, 695-716.	27.8	2,421
13	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	12.6	2,385
14	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	14.5	2,350
15	International network of cancer genome projects. Nature, 2010, 464, 993-998.	27.8	2,114
16	Characterization of Mammalian Selenoproteomes. Science, 2003, 300, 1439-1443.	12.6	2,019
17	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
18	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886

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19	The Genome Sequence of the Malaria Mosquito Anopheles gambiae. Science, 2002, 298, 129-149.	12.6	1,859
20	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	27.8	1,857
21	Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. Nature, 2004, 431, 946-957.	27.8	1,801
22	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	28.9	1,664
23	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	27.8	1,444
24	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
25	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	27.8	1,252
26	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	12.6	1,127
27	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
28	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	12.6	1,038
29	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	5.6	913
30	Transcriptome genetics using second generation sequencing in a Caucasian population. Nature, 2010, 464, 773-777.	27.8	782
31	Global trends of whole-genome duplications revealed by the ciliate Paramecium tetraurelia. Nature, 2006, 444, 171-178.	27.8	744
32	Evaluation of Gene Structure Prediction Programs. Genomics, 1996, 34, 353-367.	2.9	682
33	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	19.0	679
34	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	7.1	654
35	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.	7.1	635
36	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	14.5	633

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37	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
38	GENCODE: producing a reference annotation for ENCODE. Genome Biology, 2006, 7, S4.	9.6	533
39	The GEM mapper: fast, accurate and versatile alignment by filtration. Nature Methods, 2012, 9, 1185-1188.	19.0	500
40	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	19.0	467
41	Fast Computation and Applications of Genome Mappability. PLoS ONE, 2012, 7, e30377.	2.5	458
42	Towards a complete map of the human long non-coding RNA transcriptome. Nature Reviews Genetics, 2018, 19, 535-548.	16.3	451
43	Sequencing of Culex quinquefasciatus Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	12.6	424
44	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	9.6	410
45	Nucleosome positioning as a determinant of exon recognition. Nature Structural and Molecular Biology, 2009, 16, 996-1001.	8.2	406
46	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
47	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. Genome Research, 2012, 22, 1616-1625.	5.5	401
48	Insights into evolution of multicellular fungi from the assembled chromosomes of the mushroom Coprinopsis cinerea (Coprinus cinereus). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 11889-11894.	7.1	389
49	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	2.8	375
50	A Combinatorial Code for CPE-Mediated Translational Control. Cell, 2008, 132, 434-448.	28.9	360
51	GeneID in Drosophila. Genome Research, 2000, 10, 511-515.	5.5	331
52	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	8.8	330
53	Genome of Rhodnius prolixus , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14936-14941.	7.1	329
54	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329

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55	Are splicing mutations the most frequent cause of hereditary disease?. FEBS Letters, 2005, 579, 1900-1903.	2.8	327
56	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	17.5	323
57	Prediction of gene structure. Journal of Molecular Biology, 1992, 226, 141-157.	4.2	317
58	Regulation of Fas Alternative Splicing by Antagonistic Effects of TIA-1 and PTB on Exon Definition. Molecular Cell, 2005, 19, 475-484.	9.7	307
59	Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. Nature, 2014, 508, 345-350.	27.8	298
60	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	27.8	289
61	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. Genome Research, 2010, 20, 1411-1419.	5.5	284
62	Using geneid to Identify Genes. , 2007, Chapter 4, Unit 4.3.		281
63	Modelling and simulating generic RNA-Seq experiments with the flux simulator. Nucleic Acids Research, 2012, 40, 10073-10083.	14.5	264
64	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
65	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	12.6	252
66	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	17.5	251
67	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. Rna, 2014, 20, 959-976.	3.5	246
68	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. European Heart Journal, 2015, 36, 353-368.	2.2	244
69	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	28.9	243
70	A General Definition and Nomenclature for Alternative Splicing Events. PLoS Computational Biology, 2008, 4, e1000147.	3.2	232
71	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	9.6	231
72	LncATLAS database for subcellular localization of long noncoding RNAs. Rna, 2017, 23, 1080-1087.	3.5	230

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73	EGASP: the human ENCODE Genome Annotation Assessment Project. Genome Biology, 2006, 7, S2.	9.6	228
74	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. Nature Genetics, 2017, 49, 1731-1740.	21.4	227
75	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. Journal of Molecular and Cellular Cardiology, 2015, 89, 98-112.	1.9	223
76	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	5.6	221
77	Composition and Evolution of the Vertebrate and Mammalian Selenoproteomes. PLoS ONE, 2012, 7, e33066.	2.5	211
78	Reconstruction of Ancient Molecular Phylogeny. Molecular Phylogenetics and Evolution, 1996, 6, 189-213.	2.7	210
79	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
80	Selenoprotein Gene Nomenclature. Journal of Biological Chemistry, 2016, 291, 24036-24040.	3.4	207
81	The implications of alternative splicing in the ENCODE protein complement. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5495-5500.	7.1	206
82	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	12.8	198
83	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. Rna, 2016, 22, 867-882.	3.5	194
84	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	7.1	192
85	Pseudogenes in the ENCODE regions: Consensus annotation, analysis of transcription, and evolution. Genome Research, 2007, 17, 839-851.	5.5	191
86	Comparative Gene Prediction in Human and Mouse. Genome Research, 2003, 13, 108-117.	5.5	183
87	An Assessment of Gene Prediction Accuracy in Large DNA Sequences. Genome Research, 2000, 10, 1631-1642.	5.5	179
88	Tandem chimerism as a means to increase protein complexity in the human genome. Genome Research, 2005, 16, 37-44.	5.5	177
89	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. Nature, 2002, 418, 79-85.	27.8	176
90	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	5.5	175

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91	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. Genome Research, 2007, 17, 746-759.	5.5	173
92	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	21.4	172
93	Comparative transcriptomics in human and mouse. Nature Reviews Genetics, 2017, 18, 425-440.	16.3	168
94	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
95	The histone variant macroH2A is an epigenetic regulator of key developmental genes. Nature Structural and Molecular Biology, 2009, 16, 1074-1079.	8.2	166
96	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	5.5	166
97	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. Genome Biology, 2016, 17, 32.	8.8	166
98	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. PLoS Computational Biology, 2018, 14, e1006360.	3.2	159
99	Improving gene annotation using peptide mass spectrometry. Genome Research, 2007, 17, 231-239.	5.5	157
100	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	30.7	157
101	CPEB1 coordinates alternative 3â€²-UTR formation with translational regulation. Nature, 2013, 495, 121-125.	27.8	156
102	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	5.5	150
103	Whole genome sequencing of turbot (Scophthalmus maximus; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	3.4	150
104	Comparative Analysis of Amino Acid Repeats in Rodents and Humans. Genome Research, 2004, 14, 549-554.	5.5	149
105	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. Genome Research, 2012, 22, 1231-1242.	5.5	143
106	Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology, 2017, 18, 60.	8.8	142
107	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. Genome Biology, 2013, 14, R20.	9.6	139
108	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	8.8	131

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109	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	27.8	123
110	Hnf1Î± (MODY3) Controls Tissue-Specific Transcriptional Programs and Exerts Opposed Effects on Cell Growth in Pancreatic Islets and Liver. Molecular and Cellular Biology, 2009, 29, 2945-2959.	2.3	122
111	Identification of genetic variants associated with alternative splicing using sQTLseekeR. Nature Communications, 2014, 5, 4698.	12.8	121
112	Recent advances in gene structure prediction. Current Opinion in Structural Biology, 2004, 14, 264-272.	5.7	119
113	The Long Non-Coding RNAs: A New (P)layer in the â€œDark Matterâ€• Frontiers in Genetics, 2011, 2, 107.	2.3	113
114	Using geneid to Identify Genes. Current Protocols in Bioinformatics, 2018, 64, e56.	25.8	112
115	In silico identification of novel selenoproteins in the Drosophila melanogaster genome. EMBO Reports, 2001, 2, 697-702.	4.5	110
116	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	5.5	109
117	Comparison of mouse and human genomes followed by experimental verification yields an estimated 1,019 additional genes. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1140-1145.	7.1	106
118	Genomic analysis of a migratory divide reveals candidate genes for migration and implicates selective sweeps in generating islands of differentiation. Molecular Ecology, 2015, 24, 1873-1888.	3.9	106
119	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	27.8	105
120	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. BMC Genomics, 2015, 16, 846.	2.8	100
121	Reconsidering the evolution of eukaryotic selenoproteins: a novel nonmammalian family with scattered phylogenetic distribution. EMBO Reports, 2004, 5, 71-77.	4.5	99
122	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. Scientific Reports, 2017, 7, 41544.	3.3	98
123	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. Nature Structural and Molecular Biology, 2011, 18, 708-714.	8.2	95
124	Diversity and functional plasticity of eukaryotic selenoproteins: Identification and characterization of the SelJ family. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 16188-16193.	7.1	94
125	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	28.9	94
126	Exon structure conservation despite low sequence similarity: a relic of dramatic events in evolution?. EMBO Journal, 2001, 20, 5354-5360.	7.8	93

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127	Assembling Genes from Predicted Exons in Linear Time with Dynamic Programming. Journal of Computational Biology, 1998, 5, 681-702.	1.6	92
128	Intron-centric estimation of alternative splicing from RNA-seq data. Bioinformatics, 2013, 29, 273-274.	4.1	92
129	Fusion of the Human Gene for the Polyubiquitination Coeffector UEV1 with Kua, a Newly Identified Gene. Genome Research, 2000, 10, 1743-1756.	5.5	91
130	SGP-1: Prediction and Validation of Homologous Genes Based on Sequence Alignments. Genome Research, 2001, 11, 1574-1583.	5.5	91
131	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	6.5	91
132	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	8.8	89
133	Comparison of splice sites in mammals and chicken. Genome Research, 2005, 15, 111-119.	5.5	88
134	ASTD: The Alternative Splicing and Transcript Diversity database. Genomics, 2009, 93, 213-220.	2.9	87
135	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. Nature Communications, 2021, 12, 727.	12.8	83
136	Identifying protein-coding genes in genomic sequences. Genome Biology, 2009, 10, 201.	9.6	82
137	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. BMC Genomics, 2015, 16, S2.	2.8	80
138	SECISearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins. Nucleic Acids Research, 2013, 41, e149-e149.	14.5	79
139	Nematode selenoproteome: the use of the selenocysteine insertion system to decode one codon in an animal genome?. Nucleic Acids Research, 2005, 33, 2227-2238.	14.5	76
140	Absence of canonical marks of active chromatin in developmentally regulated genes. Nature Genetics, 2015, 47, 1158-1167.	21.4	75
141	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. Molecular Biology and Evolution, 2011, 28, 2949-2959.	8.9	74
142	A Snapshot of the Emerging Tomato Genome Sequence. Plant Genome, 2009, 2, .	2.8	73
143	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	12.8	73
144	Long Noncoding RNAs as Enhancers of Gene Expression. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 325-331.	1.1	72

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145	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). Nature Communications, 2016, 7, 12339.	12.8	69
146	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
147	A comparison of random sequence reads versus 16S rDNA sequences for estimating the biodiversity of a metagenomic library. Nucleic Acids Research, 2008, 36, 5180-5188.	14.5	66
148	Relaxation of Selective Constraints Causes Independent Selenoprotein Extinction in Insect Genomes. PLoS ONE, 2008, 3, e2968.	2.5	66
149	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. PLoS Computational Biology, 2017, 13, e1005341.	3.2	64
150	Autoimmune response in AIDS. Nature, 1990, 345, 26-26.	27.8	61
151	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	2.5	61
152	Estimation of alternative splicing variability in human populations. Genome Research, 2012, 22, 528-538.	5.5	59
153	ABS: a database of Annotated regulatory Binding Sites from orthologous promoters. Nucleic Acids Research, 2006, 34, D63-D67.	14.5	56
154	SelenoDB 1.0 : a database of selenoprotein genes, proteins and SECIS elements. Nucleic Acids Research, 2008, 36, D332-D338.	14.5	54
155	Damage-responsive elements in Drosophila regeneration. Genome Research, 2018, 28, 1852-1866.	5.5	52
156	Transcription Factor Map Alignment of Promoter Regions. PLoS Computational Biology, 2006, 2, e49.	3.2	50
157	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. Genome Research, 2012, 22, 1698-1710.	5.5	50
158	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. Nucleic Acids Research, 2019, 47, 5293-5306.	14.5	49
159	Dynamic changes in intron retention are tightly associated with regulation of splicing factors and proliferative activity during B-cell development. Nucleic Acids Research, 2020, 48, 1327-1340.	14.5	49
160	Computational gene identification: an open problem. Computers & Chemistry, 1997, 21, 215-222.	1.2	48
161	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. Genome Research, 2015, 25, 1256-1267.	5.5	46
162	Distinctive Sequence Features in Protein Coding Genic Non-coding, and Intergenic Human DNA. Journal of Molecular Biology, 1995, 253, 51-60.	4.2	44

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163	Improving data and knowledge management to better integrate health care and research. Journal of Internal Medicine, 2013, 274, 321-328.	6.0	44
164	Computational identification of the selenocysteine tRNA (tRNASec) in genomes. PLoS Computational Biology, 2017, 13, e1005383.	3.2	44
165	A short motif in Drosophila SECIS Binding Protein 2 provides differential binding affinity to SECIS RNA hairpins. Nucleic Acids Research, 2009, 37, 2126-2141.	14.5	42
166	Splice site identification by idlBNs. Bioinformatics, 2004, 20, i69-i76.	4.1	41
167	Efficient targeted transcript discovery via array-based normalization of RACE libraries. Nature Methods, 2008, 5, 629-635.	19.0	41
168	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. BMC Biology, 2020, 18, 90.	3.8	40
169	Exact Transcriptome Reconstruction from Short Sequence Reads. Lecture Notes in Computer Science, 2008, , 50-63.	1.3	40
170	LokiarchaeotaMarks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. Molecular Biology and Evolution, 2016, 33, 2441-2453.	8.9	39
171	Low Exchangeability of Selenocysteine, the 21st Amino Acid, in Vertebrate Proteins. Molecular Biology and Evolution, 2009, 26, 2031-2040.	8.9	38
172	Using geneid to Identify Genes. Current Protocols in Bioinformatics, 2003, 00, 4.3.1.	25.8	37
173	SECISaln, a web-based tool for the creation of structure-based alignments of eukaryotic SECIS elements. Bioinformatics, 2009, 25, 674-675.	4.1	35
174	SelenoDB 2.0: annotation of selenoprotein genes in animals and their genetic diversity in humans. Nucleic Acids Research, 2014, 42, D437-D443.	14.5	35
175	Comparative transcriptomics across 14 Drosophila species reveals signatures of longevity. Aging Cell, 2018, 17, e12740.	6.7	35
176	Gene finding in the chicken genome. BMC Bioinformatics, 2005, 6, 131.	2.6	34
177	DNA Composition, Codon Usage and Exon Prediction. , 1997, , 53-80.		33
178	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. Genome Biology, 2015, 16, 236.	8.8	32
179	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	5.5	32
180	EGASP: collaboration through competition to find human genes. Nature Methods, 2005, 2, 575-577.	19.0	30

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181	Grape RNA-Seq analysis pipeline environment. Bioinformatics, 2013, 29, 614-621.	4.1	30
182	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	2.8	30
183	PyHIST: A Histological Image Segmentation Tool. PLoS Computational Biology, 2020, 16, e1008349.	3.2	30
184	Perivascular spaces are associated with tau pathophysiology and synaptic dysfunction in early Alzheimerâ€™s continuum. Alzheimer's Research and Therapy, 2021, 13, 135.	6.2	30
185	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	3.3	28
186	Mutation patterns of amino acid tandem repeats in the human proteome. Genome Biology, 2006, 7, R33.	9.6	27
187	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	3.8	27
188	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. Nature Communications, 2021, 12, 2300.	12.8	27
189	Islands of euchromatin-like sequence and expressed polymorphic sequences within the short arm of human chromosome 21. Genome Research, 2007, 17, 1690-1696.	5.5	25
190	The DART classification of unannotated transcription within the ENCODE regions: Associating transcription with known and novel loci. Genome Research, 2007, 17, 732-745.	5.5	25
191	CROC: finding chromosomal clusters in eukaryotic genomes. Bioinformatics, 2009, 25, 1552-1553.	4.1	25
192	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.	7.1	25
193	The rate and spectrum of mosaic mutations during embryogenesis revealed by RNA sequencing of 49 tissues. Genome Medicine, 2020, 12, 49.	8.2	25
194	Functional Targets of the Monogenic Diabetes Transcription Factors HNF-1Î± and HNF-4Î± Are Highly Conserved Between Mice and Humans. Diabetes, 2009, 58, 1245-1253.	0.6	24
195	From chromatin to splicing: RNA-processing as a total artwork. Epigenetics, 2010, 5, 180-184.	2.7	24
196	Gene Organization Features in A/T-Rich Organisms. Journal of Molecular Evolution, 2005, 60, 90-98.	1.8	22
197	Transcriptional network controlled by the trithorax-group gene ash2 in Drosophila melanogaster. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3293-3298.	7.1	21
198	Dynamics of microRNA expression during mouse prenatal development. Genome Research, 2019, 29, 1900-1909.	5.5	21

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199	Enhancers with tissue-specific activity are enriched in intronic regions. Genome Research, 2021, 31, 1325-1336.	5.5	21
200	The human CD6 gene is transcriptionally regulated by RUNX and Ets transcription factors in T cells. Molecular Immunology, 2009, 46, 2226-2235.	2.2	19
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