Roderic Guigo

List of Publications by Year
in descending order

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266	130,567	1457 107	677 254
papers	citations	h-index	g-index

325	325	325	129006
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and functional conservation of lncRNAs: lessons from flies. Mammalian Genome, 2022, 33, 328-342.	1.0	18
2	Paired guide RNA CRISPR-Cas9 screening for protein-coding genes and lncRNAs involved in transdifferentiation of human B-cells to macrophages. BMC Genomics, 2022, 23, .	1.2	7
3	GENCODE 2021. Nucleic Acids Research, 2021, 49, D916-D923.	6.5	633
4	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. Nature Communications, 2021, 12, 727.	5.8	83
5	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. Nature Communications, 2021, 12, 2300.	5.8	27
6	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	2.4	17
7	Genetic Influences on Hippocampal Subfields. Neurology: Genetics, 2021, 7, e591.	0.9	8
8	Genetic Predisposition to Alzheimerâ€™s Disease Is Associated with Enlargement of Perivascular Spaces in Centrum Semiovale Region. Genes, 2021, 12, 825.	1.0	7
9	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
10	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
11	Enhancers with tissue-specific activity are enriched in intronic regions. Genome Research, 2021, 31, 1325-1336.	2.4	21
12	Perivascular spaces are associated with tau pathophysiology and synaptic dysfunction in early Alzheimerâ€™s continuum. Alzheimer's Research and Therapy, 2021, 13, 135.	3.0	30
13	Annotation of Full-Length Long Noncoding RNAs with Capture Long-Read Sequencing (CLS). Methods in Molecular Biology, 2021, 2254, 133-159.	0.4	3
14	FA-nf: A Functional Annotation Pipeline for Proteins from Non-Model Organisms Implemented in Nextflow. Genes, 2021, 12, 1645.	1.0	2
15	Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Letâ€™s MAMBO!. Computational and Structural Biotechnology Journal, 2021, 19, 5800-5810.	1.9	4
16	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.	6.5	49
17	The abundance of the long intergenic non-coding RNA 01087 differentiates between luminal and triple-negative breast cancers and predicts patient outcome. Pharmacological Research, 2020, 161, 105249.	3.1	13
18	PyHIST: A Histological Image Segmentation Tool. PLoS Computational Biology, 2020, 16, e1008349.	1.5	30

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19	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.	1.7	40
20	Perspectives on ENCODE. Nature, 2020, 583, 693-698.	13.7	123
21	Expanded encyclopaedias of DNA elements in the human and mouse genomes. Nature, 2020, 583, 699-710.	13.7	1,252
22	A limited set of transcriptional programs define major cell types. Genome Research, 2020, 30, 1047-1059.	2.4	32
23	The tuatara genome reveals ancient features of amniote evolution. Nature, 2020, 584, 403-409.	13.7	105
24	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	2.4	109
25	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
26	The GTEx Consortium atlas of genetic regulatory effects across human tissues. Science, 2020, 369, 1318-1330.	6.0	2,385
27	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	6.0	210
28	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	6.0	329
29	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	3.8	68
30	Effect of BDNF Val66Met on hippocampal subfields volumes and compensatory interaction with APOE-Îµ4 in middle-age cognitively unimpaired individuals from the ALFA study. Brain Structure and Function, 2020, 225, 2331-2345.	1.2	5
31	The rate and spectrum of mosaic mutations during embryogenesis revealed by RNA sequencing of 49 tissues. Genome Medicine, 2020, 12, 49.	3.6	25
32	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. Non-coding RNA, 2020, 6, 11.	1.3	11
33	Gene duplications, divergence and recombination shape adaptive evolution of the fish ectoparasite Gyrodactylus bullatarudis. Molecular Ecology, 2020, 29, 1494-1507.	2.0	11
34	Enteric infection induces Lark-mediated intron retention at the 5â€² end of Drosophila genes. Genome Biology, 2020, 21, 4.	3.8	4
35	bsAS, an antisense long non-coding RNA, essential for correct wing development through regulation of blistered/DSRF isoform usage. PLoS Genetics, 2020, 16, e1009245.	1.5	7
36	PyHIST: A Histological Image Segmentation Tool. , 2020, 16, e1008349.		0

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37	PyHIST: A Histological Image Segmentation Tool. , 2020, 16, e1008349.		0
38	PyHIST: A Histological Image Segmentation Tool. , 2020, 16, e1008349.		0
39	PyHIST: A Histological Image Segmentation Tool. , 2020, 16, e1008349.		0
40	Title is missing!. , 2020, 16, e1009245.		0
41	Title is missing!. , 2020, 16, e1009245.		0
42	Title is missing!. , 2020, 16, e1009245.		0
43	Title is missing!. , 2020, 16, e1009245.		0
44	Title is missing!. , 2020, 16, e1009245.		0
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46	Dynamics of microRNA expression during mouse prenatal development. Genome Research, 2019, 29, 1900-1909.	2.4	21
47	Processive Recoding and MetazoanÂEvolution of SelenoproteinÂP: Up to 132 UGAs in Molluscs. Journal of Molecular Biology, 2019, 431, 4381-4407.	2.0	18
48	The Origins and the Biological Consequences of the Pur/Pyr DNAÂ·RNA Asymmetry. CheM, 2019, 5, 1619-1631.	5.8	13
49	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. Nucleic Acids Research, 2019, 47, 5293-5306.	6.5	49
50	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in SCN1A. Npj Genomic Medicine, 2019, 4, 31.	1.7	27
51	GENCODE reference annotation for the human and mouse genomes. Nucleic Acids Research, 2019, 47, D766-D773.	6.5	2,350
52	Expression of the transcribed ultraconserved region 70 and the related long nonâ€coding <scp>RNA AC</scp>092652.2â€202 has prognostic value in Chronic Lymphocytic Leukaemia. British Journal of Haematology, 2019, 184, 1045-1050.	1.2	10
53	Comparative transcriptomics across 14 Drosophila species reveals signatures of longevity. Aging Cell, 2018, 17, e12740.	3.0	35
54	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. Nature Communications, 2018, 9, 490.	5.8	198

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55	The discovery potential of RNA processing profiles. Nucleic Acids Research, 2018, 46, e15-e15.	6.5	9
56	Selenoprofiles: A Computational Pipeline for Annotation of Selenoproteins. Methods in Molecular Biology, 2018, 1661, 17-28.	0.4	8
57	Recent advances in functional genome analysis. F1000Research, 2018, 7, 1968.	0.8	16
58	Damage-responsive elements in Drosophila regeneration. Genome Research, 2018, 28, 1852-1866.	2.4	52
59	Using geneid to Identify Genes. Current Protocols in Bioinformatics, 2018, 64, e56.	25.8	112
60	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. Nature Medicine, 2018, 24, 868-880.	15.2	157
61	Towards a complete map of the human long non-coding RNA transcriptome. Nature Reviews Genetics, 2018, 19, 535-548.	7.7	451
62	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. PLoS Computational Biology, 2018, 14, e1006360.	1.5	159
63	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	9.4	167
64	Data resources for human functional genomics. Current Opinion in Systems Biology, 2017, 1, 75-79.	1.3	5
65	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. Scientific Reports, 2017, 7, 41544.	1.6	98
66	Comparative transcriptomics in human and mouse. Nature Reviews Genetics, 2017, 18, 425-440.	7.7	168
67	LncATLAS database for subcellular localization of long noncoding RNAs. Rna, 2017, 23, 1080-1087.	1.6	230
68	Genetic effects on gene expression across human tissues. Nature, 2017, 550, 204-213.	13.7	3,500
69	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. Nature Genetics, 2017, 49, 1731-1740.	9.4	227
70	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. BMC Genomics, 2017, 18, 7.	1.2	30
71	Genomic history of the origin and domestication of common bean unveils its closest sister species. Genome Biology, 2017, 18, 60.	3.8	142
72	Brain Transcriptome Sequencing of a Natural Model of Alzheimer's Disease. Frontiers in Aging Neuroscience, 2017, 9, 64.	1.7	14

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73	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. PLoS Computational Biology, 2017, 13, e1005341.	1.5	64
74	Ten Simple Rules on How to Organize a Scientific Retreat. PLoS Computational Biology, 2017, 13, e1005344.	1.5	3
75	Computational identification of the selenocysteine tRNA (tRNASec) in genomes. PLoS Computational Biology, 2017, 13, e1005383.	1.5	44
76	Gene-specific patterns of expression variation across organs and species. Genome Biology, 2016, 17, 151.	3.8	89
77	Human selenoprotein P and S variant mRNAs with different numbers of SECIS elements and inferences from mutant mice of the roles of multiple SECIS elements. Open Biology, 2016, 6, 160241.	1.5	12
78	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
79	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.	3.8	166
80	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. Rna, 2016, 22, 867-882.	1.6	194
81	LokiarchaeotaMarks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. Molecular Biology and Evolution, 2016, 33, 2441-2453.	3.5	39
82	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). Nature Communications, 2016, 7, 12339.	5.8	69
83	Selenoprotein Gene Nomenclature. Journal of Biological Chemistry, 2016, 291, 24036-24040.	1.6	207
84	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	13.5	1,052
85	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
86	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	13.5	573
87	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. Scientific Reports, 2016, 6, 32406.	1.6	28
88	Whole genome sequencing of turbot (Scophthalmus maximus; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	1.5	150
89	Spatiotemporal Control of Forkhead Binding to DNA Regulates the Meiotic Gene Expression Program. Cell Reports, 2016, 14, 885-895.	2.9	12
90	Identification of a selenium-dependent glutathione peroxidase in the blood-sucking insect Rhodnius prolixus. Insect Biochemistry and Molecular Biology, 2016, 69, 105-114.	1.2	15

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91	Evolution of Selenophosphate Synthetase. , 2016, , 85-99.		0
92	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. BMC Genomics, 2015, 16, 846.	1.2	100
93	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. Genome Biology, 2015, 16, 236.	3.8	32
94	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. BMC Genomics, 2015, 16, S2.	1.2	80
95	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.	2.0	106
96	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.	3.3	329
97	Prescribing splicing. Science, 2015, 347, 124-125.	6.0	8
98	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	5.8	73
99	Role of six single nucleotide polymorphisms, risk factors in coronary disease, inOLR1alternative splicing. Rna, 2015, 21, 1187-1202.	1.6	14
100	The genomes of two key bumblebee species with primitive eusocial organization. Genome Biology, 2015, 16, 76.	3.8	330
101	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	6.0	1,127
102	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
103	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
104	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.	3.3	192
105	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.	0.9	223
106	Absence of canonical marks of active chromatin in developmentally regulated genes. Nature Genetics, 2015, 47, 1158-1167.	9.4	75
107	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. Genome Research, 2015, 25, 1256-1267.	2.4	46
108	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.	1.0	244

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109	Active transcription without histone modifications. Oncotarget, 2015, 6, 41401-41401.	0.8	4
110	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
111	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	2.6	221
112	Identification of genetic variants associated with alternative splicing using sQTLseekeR. Nature Communications, 2014, 5, 4698.	5.8	121
113	SelenoDB 2.0: annotation of selenoprotein genes in animals and their genetic diversity in humans. Nucleic Acids Research, 2014, 42, D437-D443.	6.5	35
114	Finding the missing honey bee genes: lessons learned from a genome upgrade. BMC Genomics, 2014, 15, 86.	1.2	375
115	Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. Nature, 2014, 508, 345-350.	13.7	298
116	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	2.4	175
117	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
118	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. AIDS Research and Human Retroviruses, 2014, 30, A64-A64.	0.5	1
119	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. Rna, 2014, 20, 959-976.	1.6	246
120	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
121	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
122	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
123	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.	13.9	139
124	Assessment of transcript reconstruction methods for RNA-seq. Nature Methods, 2013, 10, 1177-1184.	9.0	679
125	Systematic evaluation of spliced alignment programs for RNA-seq data. Nature Methods, 2013, 10, 1185-1191.	9.0	467
126	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. Nature Biotechnology, 2013, 31, 1015-1022.	9.4	251

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127	Transcriptome and genome sequencing uncovers functional variation in humans. Nature, 2013, 501, 506-511.	13.7	1,857
128	The Coding and the Non-coding Transcriptome. , 2013, , 27-41.		3
129	CPEB1 coordinates alternative 3â€²-UTR formation with translational regulation. Nature, 2013, 495, 121-125.	13.7	156
130	SECISearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins. Nucleic Acids Research, 2013, 41, e149-e149.	6.5	79
131	ASPic-GeneID: A Lightweight Pipeline for Gene Prediction and Alternative Isoforms Detection. BioMed Research International, 2013, 2013, 1-11.	0.9	8
132	Grape RNA-Seq analysis pipeline environment. Bioinformatics, 2013, 29, 614-621.	1.8	30
133	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. Nucleic Acids Research, 2013, 41, 7220-7230.	6.5	13
134	Topoisomerase II regulates yeast genes with singular chromatin architectures. Nucleic Acids Research, 2013, 41, 9243-9256.	6.5	14
135	Intron-centric estimation of alternative splicing from RNA-seq data. Bioinformatics, 2013, 29, 273-274.	1.8	92
136	Improving data and knowledge management to better integrate health care and research. Journal of Internal Medicine, 2013, 274, 321-328.	2.7	44
137	The Genotype-Tissue Expression (GTEx) project. Nature Genetics, 2013, 45, 580-585.	9.4	6,815
138	Estimation of alternative splicing variability in human populations. Genome Research, 2012, 22, 528-538.	2.4	59
139	SPIn: Model Selection for Phylogenetic Mixtures via Linear Invariants. Molecular Biology and Evolution, 2012, 29, 929-937.	3.5	12
140	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. Genome Research, 2012, 22, 1698-1710.	2.4	50
141	Modelling and simulating generic RNA-Seq experiments with the flux simulator. Nucleic Acids Research, 2012, 40, 10073-10083.	6.5	264
142	An encyclopedia of mouse DNA elements (Mouse ENCODE). Genome Biology, 2012, 13, 418.	13.9	410
143	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	13.7	15,516
144	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217

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145	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.	2.4	401
146	Chimeras taking shape: Potential functions of proteins encoded by chimeric RNA transcripts. Genome Research, 2012, 22, 1231-1242.	2.4	143
147	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
148	Modeling gene expression using chromatin features in various cellular contexts. Genome Biology, 2012, 13, R53.	13.9	231
149	The GEM mapper: fast, accurate and versatile alignment by filtration. Nature Methods, 2012, 9, 1185-1188.	9.0	500
150	Composition and Evolution of the Vertebrate and Mammalian Selenoproteomes. PLoS ONE, 2012, 7, e33066.	1.1	211
151	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. Genome Research, 2012, 22, 1658-1667.	2.4	166
152	The tomato genome sequence provides insights into fleshy fruit evolution. Nature, 2012, 485, 635-641.	13.7	2,860
153	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
154	Evidence for Transcript Networks Composed of Chimeric RNAs in Human Cells. PLoS ONE, 2012, 7, e28213.	1.1	61
155	BLUEPRINT to decode the epigenetic signature written in blood. Nature Biotechnology, 2012, 30, 224-226.	9.4	323
156	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
157	Fast Computation and Applications of Genome Mappability. PLoS ONE, 2012, 7, e30377.	1.1	458
158	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	13.7	1,364
159	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.	3.6	95
160	Review of â€˜Capâ€analysis gene expressionâ€™. BioEssays, 2011, 33, 233-234.	1.2	0
161	The Origins, Evolution, and Functional Potential of Alternative Splicing in Vertebrates. Molecular Biology and Evolution, 2011, 28, 2949-2959.	3.5	74
162	The Long Non-Coding RNAs: A New (P)layer in the â€œDark Matterâ€• Frontiers in Genetics, 2011, 2, 107.	1.1	113

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163	Long Noncoding RNAs as Enhancers of Gene Expression. Cold Spring Harbor Symposia on Quantitative Biology, 2010, 75, 325-331.	2.0	72
164	Sequencing of Culex quinquefasciatus Establishes a Platform for Mosquito Comparative Genomics. Science, 2010, 330, 86-88.	6.0	424
165	Structural constraints revealed in consistent nucleosome positions in the genome of S. cerevisiae. Epigenetics and Chromatin, 2010, 3, 20.	1.8	19
166	Transcriptome genetics using second generation sequencing in a Caucasian population. Nature, 2010, 464, 773-777.	13.7	782
167	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
168	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. Genome Research, 2010, 20, 1411-1419.	2.4	284
169	Genome Sequence of the Pea Aphid Acyrthosiphon pisum. PLoS Biology, 2010, 8, e1000313.	2.6	913
170	From chromatin to splicing: RNA-processing as a total artwork. Epigenetics, 2010, 5, 180-184.	1.3	24
171	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.	3.3	389
172	Long Noncoding RNAs with Enhancer-like Function in Human Cells. Cell, 2010, 143, 46-58.	13.5	1,664
173	From identification to validation to gene count. Genome Biology, 2010, 11, .	3.8	1
174	A Snapshot of the Emerging Tomato Genome Sequence. Plant Genome, 2009, 2, .	1.6	73
175	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.	0.3	24
176	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.	1.1	122
177	SECISaln, a web-based tool for the creation of structure-based alignments of eukaryotic SECIS elements. Bioinformatics, 2009, 25, 674-675.	1.8	35
178	Low Exchangeability of Selenocysteine, the 21st Amino Acid, in Vertebrate Proteins. Molecular Biology and Evolution, 2009, 26, 2031-2040.	3.5	38
179	A short motif in Drosophila SECIS Binding Protein 2 provides differential binding affinity to SECIS RNA hairpins. Nucleic Acids Research, 2009, 37, 2126-2141.	6.5	42
180	CROC: finding chromosomal clusters in eukaryotic genomes. Bioinformatics, 2009, 25, 1552-1553.	1.8	25

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181	Variation in novel exons (RACEfrags) of theMECP2gene in Rett syndrome patients and controls. Human Mutation, 2009, 30, E866-E879.	1.1	1
182	Nucleosome positioning as a determinant of exon recognition. Nature Structural and Molecular Biology, 2009, 16, 996-1001.	3.6	406
183	The histone variant macroH2A is an epigenetic regulator of key developmental genes. Nature Structural and Molecular Biology, 2009, 16, 1074-1079.	3.6	166
184	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. Science, 2009, 324, 522-528.	6.0	1,038
185	ASTD: The Alternative Splicing and Transcript Diversity database. Genomics, 2009, 93, 213-220.	1.3	87
186	The human CD6 gene is transcriptionally regulated by RUNX and Ets transcription factors in T cells. Molecular Immunology, 2009, 46, 2226-2235.	1.0	19
187	Identifying protein-coding genes in genomic sequences. Genome Biology, 2009, 10, 201.	13.9	82
188	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
189	Efficient targeted transcript discovery via array-based normalization of RACE libraries. Nature Methods, 2008, 5, 629-635.	9.0	41
190	A Combinatorial Code for CPE-Mediated Translational Control. Cell, 2008, 132, 434-448.	13.5	360
191	Conserved chromosomal clustering of genes governed by chromatin regulators in Drosophila. Genome Biology, 2008, 9, R134.	13.9	16
192	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.	6.5	66
193	A General Definition and Nomenclature for Alternative Splicing Events. PLoS Computational Biology, 2008, 4, e1000147.	1.5	232
194	SelenoDB 1.0 : a database of selenoprotein genes, proteins and SECIS elements. Nucleic Acids Research, 2008, 36, D332-D338.	6.5	54
195	Interoperability with Moby 1.0--It's better than sharing your toothbrush!. Briefings in Bioinformatics, 2008, 9, 220-231.	3.2	91
196	Relaxation of Selective Constraints Causes Independent Selenoprotein Extinction in Insect Genomes. PLoS ONE, 2008, 3, e2968.	1.1	66
197	Bubbles: Alternative Splicing Events of Arbitrary Dimension in Splicing Graphs. , 2008, , 372-395.		6
198	Exact Transcriptome Reconstruction from Short Sequence Reads. Lecture Notes in Computer Science, 2008, , 50-63.	1.0	40

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199	Islands of euchromatin-like sequence and expressed polymorphic sequences within the short arm of human chromosome 21. Genome Research, 2007, 17, 1690-1696.	2.4	25
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