

# Roderic Guigo

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

276  
papers

96,777  
citations

100  
h-index

311  
g-index

325  
ext. papers

118,105  
ext. citations

17.2  
avg, IF

8.67  
L-index

#	Paper	IF	Citations
276	Genomic and functional conservation of lncRNAs: lessons from flies.. <i>Mammalian Genome</i> , <b>2022</b> , 1	3.2	2
275	Annotation of Full-Length Long Noncoding RNAs with Capture Long-Read Sequencing (CLS). <i>Methods in Molecular Biology</i> , <b>2021</b> , 2254, 133-159	1.4	1
274	Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO!. <i>Computational and Structural Biotechnology Journal</i> , <b>2021</b> , 19, 5800-5810	6.8	0
273	Day-night and seasonal variation of human gene expression across tissues <b>2021</b> ,		2
272	Conserved long-range base pairings are associated with pre-mRNA processing of human genes. <i>Nature Communications</i> , <b>2021</b> , 12, 2300	17.4	6
271	The genomic basis of evolutionary differentiation among honey bees. <i>Genome Research</i> , <b>2021</b> ,	9.7	1
270	Genetic Influences on Hippocampal Subfields: An Emerging Area of Neuroscience Research. <i>Neurology: Genetics</i> , <b>2021</b> , 7, e591	3.8	1
269	Genetic Predisposition to Alzheimer's Disease Is Associated with Enlargement of Perivascular Spaces in Centrum Semiovale Region. <i>Genes</i> , <b>2021</b> , 12,	4.2	1
268	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. <i>Cell</i> , <b>2021</b> , 184, 2633-2648.e19	56.2	20
267	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
266	Enhancers with tissue-specific activity are enriched in intronic regions. <i>Genome Research</i> , <b>2021</b> , 31, 1325-1336	13.36	1
265	GENCODE 2021. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D916-D923	20.1	82
264	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. <i>Nature Communications</i> , <b>2021</b> , 12, 727	17.4	13
263	Perivascular spaces are associated with tau pathophysiology and synaptic dysfunction in early Alzheimer's continuum. <i>Alzheimer's Research and Therapy</i> , <b>2021</b> , 13, 135	9	0
262	The rate and spectrum of mosaic mutations during embryogenesis revealed by RNA sequencing of 49 tissues. <i>Genome Medicine</i> , <b>2020</b> , 12, 49	14.4	10
261	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. <i>Non-coding RNA</i> , <b>2020</b> , 6,	7.1	4
260	Gene duplications, divergence and recombination shape adaptive evolution of the fish ectoparasite <i>Gyrodactylus bullatarudis</i> . <i>Molecular Ecology</i> , <b>2020</b> , 29, 1494-1507	5.7	6

259	Enteric infection induces Lark-mediated intron retention at the 5' end of Drosophila genes. <i>Genome Biology</i> , <b>2020</b> , 21, 4	18.3	2
258	bsAS, an antisense long non-coding RNA, essential for correct wing development through regulation of blistered/DSRF isoform usage. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009245	6	3
257	Dynamic changes in intron retention are tightly associated with regulation of splicing factors and proliferative activity during B-cell development. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 1327-1340	20.1	19
256	The abundance of the long intergenic non-coding RNA 01087 differentiates between luminal and triple-negative breast cancers and predicts patient outcome. <i>Pharmacological Research</i> , <b>2020</b> , 161, 105249	19.2	8
255	PyHIST: A Histological Image Segmentation Tool. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008349	5	8
254	The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. <i>BMC Biology</i> , <b>2020</b> , 18, 90	7.3	19
253	Perspectives on ENCODE. <i>Nature</i> , <b>2020</b> , 583, 693-698	50.4	61
252	Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , <b>2020</b> , 583, 699-710	10.4	360
251	A limited set of transcriptional programs define major cell types. <i>Genome Research</i> , <b>2020</b> , 30, 1047-1059	9.7	15
250	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , <b>2020</b> , 584, 403-409	50.4	49
249	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072	9.7	41
248	A Quantitative Proteome Map of the Human Body. <i>Cell</i> , <b>2020</b> , 183, 269-283.e19	56.2	73
247	The GTEx Consortium atlas of genetic regulatory effects across human tissues. <i>Science</i> , <b>2020</b> , 369, 1318-1330	33.3	589
246	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , <b>2020</b> , 369,	33.3	68
245	The impact of sex on gene expression across human tissues. <i>Science</i> , <b>2020</b> , 369,	33.3	100
244	A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , <b>2020</b> , 21, 234	18.3	18
243	Effect of BDNF Val66Met on hippocampal subfields volumes and compensatory interaction with APOE- $\epsilon$ 4 in middle-age cognitively unimpaired individuals from the ALFA study. <i>Brain Structure and Function</i> , <b>2020</b> , 225, 2331-2345	4	3
242	PyHIST: A Histological Image Segmentation Tool <b>2020</b> , 16, e1008349		

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238	bsAS, an antisense long non-coding RNA, essential for correct wing development through regulation of blistered/DSRF isoform usage <b>2020</b> , 16, e1009245		
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233	bsAS, an antisense long non-coding RNA, essential for correct wing development through regulation of blistered/DSRF isoform usage <b>2020</b> , 16, e1009245		
232	Dynamics of microRNA expression during mouse prenatal development. <i>Genome Research</i> , <b>2019</b> , 29, 1900-1909	9.7	9
231	Processive Recoding and Metazoan Evolution of Selenoprotein P: Up to 132 UGAs in Molluscs. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 4381-4407	6.5	12
230	The Origins and the Biological Consequences of the Pur/Pyr DNA/RNA Asymmetry. <i>Chem</i> , <b>2019</b> , 5, 1619-1631	6.3	6
229	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 5293-5306	20.1	22
228	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in. <i>Npj Genomic Medicine</i> , <b>2019</b> , 4, 31	6.2	12
227	GENCODE reference annotation for the human and mouse genomes. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D766-D773	20.1	1140
226	Expression of the transcribed ultraconserved region 70 and the related long non-coding RNA AC092652.2-202 has prognostic value in Chronic Lymphocytic Leukaemia. <i>British Journal of Haematology</i> , <b>2019</b> , 184, 1045-1050	4.5	7
225	Comparative transcriptomics across 14 Drosophila species reveals signatures of longevity. <i>Aging Cell</i> , <b>2018</b> , 17, e12740	9.9	19
224	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. <i>Nature Communications</i> , <b>2018</b> , 9, 490	17.4	108

223	The discovery potential of RNA processing profiles. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e15	20.1	7
222	Selenoprofiles: A Computational Pipeline for Annotation of Selenoproteins. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1661, 17-28	1.4	5
221	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1006360	5	59
220	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. <i>Nature Genetics</i> , <b>2018</b> , 50, 1327-1334	36.3	98
219	Recent advances in functional genome analysis. <i>F1000Research</i> , <b>2018</b> , 7,	3.6	10
218	Damage-responsive elements in regeneration. <i>Genome Research</i> , <b>2018</b> , 28, 1852-1866	9.7	24
217	Using geneid to Identify Genes. <i>Current Protocols in Bioinformatics</i> , <b>2018</b> , 64, e56	24.2	33
216	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. <i>Nature Medicine</i> , <b>2018</b> , 24, 868-880	50.5	103
215	Towards a complete map of the human long non-coding RNA transcriptome. <i>Nature Reviews Genetics</i> , <b>2018</b> , 19, 535-548	30.1	248
214	Data Resources for Human Functional Genomics. <i>Current Opinion in Systems Biology</i> , <b>2017</b> , 1, 75-79	3.2	2
213	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. <i>Scientific Reports</i> , <b>2017</b> , 7, 41544	4.9	58
212	Comparative transcriptomics in human and mouse. <i>Nature Reviews Genetics</i> , <b>2017</b> , 18, 425-440	30.1	99
211	LncATLAS database for subcellular localization of long noncoding RNAs. <i>Rna</i> , <b>2017</b> , 23, 1080-1087	5.8	140
210	Genetic effects on gene expression across human tissues. <i>Nature</i> , <b>2017</b> , 550, 204-213	50.4	2086
209	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005341	5	44
208	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. <i>Nature Genetics</i> , <b>2017</b> , 49, 1731-1740	36.3	140
207	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. <i>BMC Genomics</i> , <b>2017</b> , 18, 7	4.5	19
206	Genomic history of the origin and domestication of common bean unveils its closest sister species. <i>Genome Biology</i> , <b>2017</b> , 18, 60	18.3	79

205	Brain Transcriptome Sequencing of a Natural Model of Alzheimer's Disease. <i>Frontiers in Aging Neuroscience</i> , <b>2017</b> , 9, 64	5.3	8
204	Computational identification of the selenocysteine tRNA (tRNA <sup>Sec</sup> ) in genomes. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005383	5	34
203	Lokiarchaeota Marks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 2441-53	8.3	31
202	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). <i>Nature Communications</i> , <b>2016</b> , 7, 12339	17.4	47
201	Selenoprotein Gene Nomenclature. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 24036-24040	5.4	147
200	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , <b>2016</b> , 167, 1415-1429.e19	56.2	637
199	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , <b>2016</b> , 167, 1145-1149	56.2	232
198	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. <i>Cell</i> , <b>2016</b> , 167, 1398-1414.e24	56.2	334
197	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. <i>Scientific Reports</i> , <b>2016</b> , 6, 32406	4.9	21
196	Whole genome sequencing of turbot ( <i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. <i>DNA Research</i> , <b>2016</b> , 23, 181-92	4.5	103
195	Spatiotemporal Control of Forkhead Binding to DNA Regulates the Meiotic Gene Expression Program. <i>Cell Reports</i> , <b>2016</b> , 14, 885-895	10.6	8
194	Identification of a selenium-dependent glutathione peroxidase in the blood-sucking insect <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , <b>2016</b> , 69, 105-14	4.5	7
193	Evolution of Selenophosphate Synthetase <b>2016</b> , 85-99		
192	Gene-specific patterns of expression variation across organs and species. <i>Genome Biology</i> , <b>2016</b> , 17, 151	18.3	44
191	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. <i>Open Biology</i> , <b>2016</b> , 6,	7	10
190	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. <i>Genome Biology</i> , <b>2016</b> , 17, 251	18.3	85
189	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , <b>2016</b> , 17, 32	18.3	124
188	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. <i>Rna</i> , <b>2016</b> , 22, 867-82	5.8	132

187	Role of six single nucleotide polymorphisms, risk factors in coronary disease, in OLR1 alternative splicing. <i>Rna</i> , <b>2015</b> , 21, 1187-202	5.8	12
186	The genomes of two key bumblebee species with primitive eusocial organization. <i>Genome Biology</i> , <b>2015</b> , 16, 76	18.3	229
185	Human genomics. The human transcriptome across tissues and individuals. <i>Science</i> , <b>2015</b> , 348, 660-5	33.3	833
184	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , <b>2015</b> , 348, 648-60	33.3	3242
183	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , <b>2015</b> , 348, 666-9	33.3	170
182	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 13970-5	11.5	127
181	CARMEN, a human super enhancer-associated long noncoding RNA controlling cardiac specification, differentiation and homeostasis. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2015</b> , 89, 98-112	5.8	173
180	Absence of canonical marks of active chromatin in developmentally regulated genes. <i>Nature Genetics</i> , <b>2015</b> , 47, 1158-1167	36.3	58
179	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. <i>Genome Research</i> , <b>2015</b> , 25, 1256-67	9.7	39
178	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. <i>European Heart Journal</i> , <b>2015</b> , 36, 353-68a	9.5	199
177	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. <i>BMC Genomics</i> , <b>2015</b> , 16, 846	4.5	63
176	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. <i>Genome Biology</i> , <b>2015</b> , 16, 236	18.3	23
175	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 8, S2	4.5	53
174	Genomic analysis of a migratory divide reveals candidate genes for migration and implicates selective sweeps in generating islands of differentiation. <i>Molecular Ecology</i> , <b>2015</b> , 24, 1873-88	5.7	77
173	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 14936-41	11.5	220
172	RNA. Prescribing splicing. <i>Science</i> , <b>2015</b> , 347, 124-5	33.3	8
171	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , <b>2015</b> , 6, 5903	17.4	56
170	Finding the missing honey bee genes: lessons learned from a genome upgrade. <i>BMC Genomics</i> , <b>2014</b> , 15, 86	4.5	284

169	Domains of genome-wide gene expression dysregulation in Down's syndrome. <i>Nature</i> , <b>2014</b> , 508, 345-505	50.4	195
168	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , <b>2014</b> , 24, 212-26	9.7	143
167	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , <b>2014</b> , 515, 355-64	50.4	1026
166	Transcriptional Signatures of Viral Control in HIV-1 Infected South African Women. <i>AIDS Research and Human Retroviruses</i> , <b>2014</b> , 30, A64-A64	1.6	1
165	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. <i>Rna</i> , <b>2014</b> , 20, 959-76	5.8	183
164	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , <b>2014</b> , 512, 445-8	50.4	207
163	Reply to Brunet and Doolittle: Both selected effect and causal role elements can influence human biology and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E3366	11.5	22
162	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , <b>2014</b> , 345, 1251033	33.3	187
161	Defining functional DNA elements in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 6131-8	11.5	490
160	The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , <b>2014</b> , 12, e1002005	9.7	182
159	Identification of genetic variants associated with alternative splicing using sQTLseeker. <i>Nature Communications</i> , <b>2014</b> , 5, 4698	17.4	77
158	SelenoDB 2.0: annotation of selenoprotein genes in animals and their genetic diversity in humans. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D437-43	20.1	30
157	Transcriptome analyses of primitively eusocial wasps reveal novel insights into the evolution of sociality and the origin of alternative phenotypes. <i>Genome Biology</i> , <b>2013</b> , 14, R20	18.3	114
156	Assessment of transcript reconstruction methods for RNA-seq. <i>Nature Methods</i> , <b>2013</b> , 10, 1177-84	21.6	477
155	Systematic evaluation of spliced alignment programs for RNA-seq data. <i>Nature Methods</i> , <b>2013</b> , 10, 1185-91	21.6	371
154	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 1015-22	44.5	187
153	Transcriptome and genome sequencing uncovers functional variation in humans. <i>Nature</i> , <b>2013</b> , 501, 506-514	41.4	1323
152	The Coding and the Non-coding Transcriptome <b>2013</b> , 27-41		2



151	CPEB1 coordinates alternative 3'-UTR formation with translational regulation. <i>Nature</i> , <b>2013</b> , 495, 121-5	50.4	113
150	SECISearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e149	20.1	66
149	ASPic-GeneID: a lightweight pipeline for gene prediction and alternative isoforms detection. <i>BioMed Research International</i> , <b>2013</b> , 2013, 502827	3	6
148	Grape RNA-Seq analysis pipeline environment. <i>Bioinformatics</i> , <b>2013</b> , 29, 614-21	7.2	23
147	Unravelling the hidden DNA structural/physical code provides novel insights on promoter location. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 7220-30	20.1	11
146	Topoisomerase II regulates yeast genes with singular chromatin architectures. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 9243-56	20.1	10
145	Intron-centric estimation of alternative splicing from RNA-seq data. <i>Bioinformatics</i> , <b>2013</b> , 29, 273-4	7.2	56
144	The Genotype-Tissue Expression (GTEx) project. <i>Nature Genetics</i> , <b>2013</b> , 45, 580-5	36.3	4179
143	Analysis of RNA Transcripts by High-Throughput RNA Sequencing <b>2012</b> , 544-554		1
142	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , <b>2012</b> , 489, 57-74	50.4	11449
141	GENCODE: the reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , <b>2012</b> , 22, 1760-74	9.7	3142
140	Deep sequencing of subcellular RNA fractions shows splicing to be predominantly co-transcriptional in the human genome but inefficient for lncRNAs. <i>Genome Research</i> , <b>2012</b> , 22, 1616-25	9.7	317
139	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. <i>Genome Research</i> , <b>2012</b> , 22, 1231-42	9.7	101
138	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , <b>2012</b> , 22, 1775-89	9.7	3408
137	Modeling gene expression using chromatin features in various cellular contexts. <i>Genome Biology</i> , <b>2012</b> , 13, R53	18.3	182
136	The GEM mapper: fast, accurate and versatile alignment by filtration. <i>Nature Methods</i> , <b>2012</b> , 9, 1185-8	21.6	382
135	Composition and evolution of the vertebrate and mammalian selenoproteomes. <i>PLoS ONE</i> , <b>2012</b> , 7, e33066	9.7	172
134	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , <b>2012</b> , 22, 1658-67	9.7	133

133	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , <b>2012</b> , 485, 635-41	50.4	2138
132	Landscape of transcription in human cells. <i>Nature</i> , <b>2012</b> , 489, 101-8	50.4	3544
131	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , <b>2012</b> , 7, e28213	3.7	51
130	BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 224-6	44.5	261
129	The genome of melon ( <i>Cucumis melo</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 11872-7	11.5	462
128	Estimation of alternative splicing variability in human populations. <i>Genome Research</i> , <b>2012</b> , 22, 528-38	9.7	49
127	SPIn: model selection for phylogenetic mixtures via linear invariants. <i>Molecular Biology and Evolution</i> , <b>2012</b> , 29, 929-37	8.3	11
126	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. <i>Genome Research</i> , <b>2012</b> , 22, 1698-710	9.7	44
125	Modelling and simulating generic RNA-Seq experiments with the flux simulator. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 10073-83	20.1	200
124	An encyclopedia of mouse DNA elements (Mouse ENCODE). <i>Genome Biology</i> , <b>2012</b> , 13, 418	18.3	340
123	Fast computation and applications of genome mappability. <i>PLoS ONE</i> , <b>2012</b> , 7, e30377	3.7	357
122	The Long Non-Coding RNAs: A New (P)layer in the "Dark Matter". <i>Frontiers in Genetics</i> , <b>2011</b> , 2, 107	4.5	88
121	A Comparison of Random Sequence Reads Versus 16S rDNA Sequences for Estimating the Biodiversity of a Metagenomic Sample <b>2011</b> , 163-169		
120	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 708-14	17.6	77
119	Review of Cap-analysis gene expression <i>BioEssays</i> , <b>2011</b> , 33, 233-234	4.1	
118	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , <b>2011</b> , 475, 101-5	50.4	1206
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14	Conserved long-range base pairings are associated with pre-mRNA processing of human genes		1
13	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features		2
12	High-throughput annotation of full-length long noncoding RNAs with Capture Long-Read Sequencing		3
11	Modified penetrance of coding variants by cis-regulatory variation shapes human traits		4
10	Intronic enhancers regulate the expression of genes involved in tissue-specific functions and homeostasis		3
9	A systematic survey of human tissue-specific gene expression and splicing reveals new opportunities for therapeutic target identification and evaluation		12
8	Nearly all new protein-coding predictions in the CHES database are not protein-coding		8



7	Novel autoregulatory cases of alternative splicing coupled with nonsense-mediated mRNA decay	1
6	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping	6
5	Atlas of transcriptionally active transposable elements in human adult tissues	3
4	The GTEx Consortium atlas of genetic regulatory effects across human tissues	81
3	Cell type specific genetic regulation of gene expression across human tissues	7
2	A limited set of transcriptional programs define major cell types	3
1	LncATLAS database for subcellular localisation of long noncoding RNAs	1