Roderic Guigo

List of Publications by Citations

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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	An integrated encyclopedia of DNA elements in the human genome. *Nature*, **2012**, 489, 57-74	50.4	11449
275	The sequence of the human genome. *Science*, **2001**, 291, 1304-51	33.3	10609
274	Initial sequencing and comparative analysis of the mouse genome. *Nature*, **2002**, 420, 520-62	50.4	5376
273	The Genotype-Tissue Expression (GTEx) project. *Nature Genetics*, **2013**, 45, 580-5	36.3	4179
272	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature*, **2007**, 447, 799-816	50.4	4121
271	Landscape of transcription in human cells. *Nature*, **2012**, 489, 101-8	50.4	3544
270	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. *Genome Research*, **2012**, 22, 1775-89	9.7	3408
269	Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science*, **2015**, 348, 648-60	33.3	3242
268	GENCODE: the reference human genome annotation for The ENCODE Project. *Genome Research*, **2012**, 22, 1760-74	9.7	3142
267	Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature*, **2004**, 432, 695-716	50.4	2143
266	The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, **2012**, 485, 635-41	50.4	2138
265	Genetic effects on gene expression across human tissues. *Nature*, **2017**, 550, 204-213	50.4	2086
264	Characterization of mammalian selenoproteomes. *Science*, **2003**, 300, 1439-43	33.3	1741
263	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. *Nature*, **2004** , 428, 493-521	50.4	1689
262	The genome sequence of the malaria mosquito Anopheles gambiae. *Science*, **2002**, 298, 129-49	33.3	1622
261	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
260	Evolution of genes and genomes on the Drosophila phylogeny. *Nature*, **2007**, 450, 203-18	50.4	1586

259	Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype. *Nature*, **2004**, 431, 946-57	50.4	1543
258	Long noncoding RNAs with enhancer-like function in human cells. *Cell*, **2010**, 143, 46-58	56.2	1422
257	Transcriptome and genome sequencing uncovers functional variation in humans. *Nature*, **2013**, 501, 506-11	50.4	1323
256	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. *Nature* , **2011**, 475, 101-5	50.4	1206
255	GENCODE reference annotation for the human and mouse genomes. *Nucleic Acids Research*, **2019**, 47, D766-D773	20.1	1140
254	A comparative encyclopedia of DNA elements in the mouse genome. *Nature*, **2014**, 515, 355-64	50.4	1026
253	The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science*, **2009**, 324, 522-8	33.3	863
252	Human genomics. The human transcriptome across tissues and individuals. *Science*, **2015**, 348, 660-5	33.3	833
251	Genome sequence of the pea aphid Acyrthosiphon pisum. *PLoS Biology*, **2010**, 8, e1000313	9.7	732
250	Transcriptome genetics using second generation sequencing in a Caucasian population. *Nature*, **2010**, 464, 773-7	50.4	678
249	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. *Cell*, **2016**, 167, 1415-1429.e19	56.2	637
248	Global trends of whole-genome duplications revealed by the ciliate Paramecium tetraurelia. *Nature* , **2006**, 444, 171-8	50.4	633
247	The GTEx Consortium atlas of genetic regulatory effects across human tissues. *Science*, **2020**, 369, 1318-1330	33.3	589
246	Evaluation of gene structure prediction programs. *Genomics*, **1996**, 34, 353-67	4.3	563
245	Defining functional DNA elements in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 6131-8	11.5	490
244	Assessment of transcript reconstruction methods for RNA-seq. *Nature Methods*, **2013**, 10, 1177-84	21.6	477
243	The genome of melon (Cucumis melo L.). *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 11872-7	11.5	462
242	GENCODE: producing a reference annotation for ENCODE. *Genome Biology*, **2006**, 7 Suppl 1, S4.1-9	18.3	434

241	The GEM mapper: fast, accurate and versatile alignment by filtration. *Nature Methods*, **2012**, 9, 1185-8	21.6	382
240	Systematic evaluation of spliced alignment programs for RNA-seq data. *Nature Methods*, **2013**, 10, 1185-91	21.6	371
239	Expanded encyclopaedias of DNA elements in the human and mouse genomes. *Nature*, **2020**, 583, 699-710	50.4	360
238	Fast computation and applications of genome mappability. *PLoS ONE*, **2012**, 7, e30377	3.7	357
237	Sequencing of Culex quinquefasciatus establishes a platform for mosquito comparative genomics. *Science*, **2010**, 330, 86-8	33.3	352
236	An encyclopedia of mouse DNA elements (Mouse ENCODE). *Genome Biology*, **2012**, 13, 418	18.3	340
235	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. *Cell*, **2016**, 167, 1398-1414.e24	56.2	339
234	Nucleosome positioning as a determinant of exon recognition. *Nature Structural and Molecular Biology*, **2009**, 16, 996-1001	17.6	337
233	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, 11889-94	11.5	322
232	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, 1616-25	9.7	317
231	Finding the missing honey bee genes: lessons learned from a genome upgrade. *BMC Genomics*, **2014**, 15, 86	4.5	284
230	A combinatorial code for CPE-mediated translational control. *Cell*, **2008**, 132, 434-48	56.2	279
229	Regulation of Fas alternative splicing by antagonistic effects of TIA-1 and PTB on exon definition. *Molecular Cell*, **2005**, 19, 475-84	17.6	272
228	BLUEPRINT to decode the epigenetic signature written in blood. *Nature Biotechnology*, **2012**, 30, 224-6	44.5	261
227	Are splicing mutations the most frequent cause of hereditary disease?. *FEBS Letters*, **2005**, 579, 1900-3	3.8	260
226	Prediction of gene structure. *Journal of Molecular Biology*, **1992**, 226, 141-57	6.5	258
225	GeneID in Drosophila. *Genome Research*, **2000**, 10, 511-5	9.7	256
224	Towards a complete map of the human long non-coding RNA transcriptome. *Nature Reviews Genetics*, **2018**, 19, 535-548	30.1	248

223	Reshaping the gut microbiome with bacterial transplantation and antibiotic intake. *Genome Research*, **2010**, 20, 1411-9	9.7	235
222	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. *Cell*, **2016**, 167, 1145-1149	56.2	232
221	The genomes of two key bumblebee species with primitive eusocial organization. *Genome Biology*, **2015**, 16, 76	18.3	229
220	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, 14936-41	11.5	220
219	Comparative analysis of the transcriptome across distant species. *Nature*, **2014**, 512, 445-8	50.4	207
218	Modelling and simulating generic RNA-Seq experiments with the flux simulator. *Nucleic Acids Research*, **2012**, 40, 10073-83	20.1	200
217	Genome-wide profiling of the cardiac transcriptome after myocardial infarction identifies novel heart-specific long non-coding RNAs. *European Heart Journal*, **2015**, 36, 353-68a	9.5	199
216	Domains of genome-wide gene expression dysregulation in Down's syndrome. *Nature*, **2014**, 508, 345-50	50.4	195
215	Transcriptional diversity during lineage commitment of human blood progenitors. *Science*, **2014**, 345, 1251033	33.3	187
214	Reproducibility of high-throughput mRNA and small RNA sequencing across laboratories. *Nature Biotechnology*, **2013**, 31, 1015-22	44.5	187
213	EGASP: the human ENCODE Genome Annotation Assessment Project. *Genome Biology*, **2006**, 7 Suppl 1, S2.1-31	18.3	187
212	The RIDL hypothesis: transposable elements as functional domains of long noncoding RNAs. *Rna*, **2014**, 20, 959-76	5.8	183
211	The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede Strigamia maritima. *PLoS Biology*, **2014**, 12, e1002005	9.7	182
210	Modeling gene expression using chromatin features in various cellular contexts. *Genome Biology*, **2012**, 13, R53	18.3	182
209	Reconstruction of ancient molecular phylogeny. *Molecular Phylogenetics and Evolution*, **1996**, 6, 189-213	4.1	178
208	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, 5495-500	11.5	177
207	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	5.8	173
206	Composition and evolution of the vertebrate and mammalian selenoproteomes. *PLoS ONE*, **2012**, 7, e33066	3.7	172

205	Human genomics. Effect of predicted protein-truncating genetic variants on the human transcriptome. *Science*, **2015**, 348, 666-9	33.3	170
204	A general definition and nomenclature for alternative splicing events. *PLoS Computational Biology*, **2008**, 4, e1000147	5	165
203	Pseudogenes in the ENCODE regions: consensus annotation, analysis of transcription, and evolution. *Genome Research*, **2007**, 17, 839-51	9.7	158
202	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. *Nature*, **2002**, 418, 79-85	50.4	158
201	Tandem chimerism as a means to increase protein complexity in the human genome. *Genome Research*, **2006**, 16, 37-44	9.7	157
200	Prominent use of distal 5' transcription start sites and discovery of a large number of additional exons in ENCODE regions. *Genome Research*, **2007**, 17, 746-59	9.7	156
199	SNP and haplotype mapping for genetic analysis in the rat. *Nature Genetics*, **2008**, 40, 560-6	36.3	150
198	The histone variant macroH2A is an epigenetic regulator of key developmental genes. *Nature Structural and Molecular Biology*, **2009**, 16, 1074-9	17.6	148
197	Selenoprotein Gene Nomenclature. *Journal of Biological Chemistry*, **2016**, 291, 24036-24040	5.4	147
196	Improving gene annotation using peptide mass spectrometry. *Genome Research*, **2007**, 17, 231-9	9.7	144
195	Comparative gene prediction in human and mouse. *Genome Research*, **2003**, 13, 108-17	9.7	144
194	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. *Genome Research*, **2014**, 24, 212-26	9.7	143
193	LncATLAS database for subcellular localization of long noncoding RNAs. *Rna*, **2017**, 23, 1080-1087	5.8	140
192	High-throughput annotation of full-length long noncoding RNAs with capture long-read sequencing. *Nature Genetics*, **2017**, 49, 1731-1740	36.3	140
191	An assessment of gene prediction accuracy in large DNA sequences. *Genome Research*, **2000**, 10, 1631-42	9.7	140
190	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome Research*, **2012**, 22, 1658-67	9.7	133
189	Using geneid to identify genes. *Current Protocols in Bioinformatics*, **2007**, Chapter 4, Unit 4.3	24.2	133
188	Cytoplasmic long noncoding RNAs are frequently bound to and degraded at ribosomes in human cells. *Rna*, **2016**, 22, 867-82	5.8	132

187	Structured RNAs in the ENCODE selected regions of the human genome. *Genome Research*, **2007**, 17, 852-64	9.7	131
186	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, 13970-5	11.5	127
185	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	18.3	124
184	Comparative analysis of amino acid repeats in rodents and humans. *Genome Research*, **2004**, 14, 549-54	9.7	121
183	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	18.3	114
182	CPEB1 coordinates alternative 3'-UTR formation with translational regulation. *Nature*, **2013**, 495, 121-5	50.4	113
181	The effects of death and post-mortem cold ischemia on human tissue transcriptomes. *Nature Communications*, **2018**, 9, 490	17.4	108
180	Whole genome sequencing of turbot (Scophthalmus maximus; Pleuronectiformes): a fish adapted to demersal life. *DNA Research*, **2016**, 23, 181-92	4.5	103
179	The reference epigenome and regulatory chromatin landscape of chronic lymphocytic leukemia. *Nature Medicine*, **2018**, 24, 868-880	50.5	103
178	In silico identification of novel selenoproteins in the Drosophila melanogaster genome. *EMBO Reports*, **2001**, 2, 697-702	6.5	102
177	Chimeras taking shape: potential functions of proteins encoded by chimeric RNA transcripts. *Genome Research*, **2012**, 22, 1231-42	9.7	101
176	The impact of sex on gene expression across human tissues. *Science*, **2020**, 369,	33.3	100
175	Comparative transcriptomics in human and mouse. *Nature Reviews Genetics*, **2017**, 18, 425-440	30.1	99
174	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. *Nature Genetics*, **2018**, 50, 1327-1334	36.3	98
173	Recent advances in gene structure prediction. *Current Opinion in Structural Biology*, **2004**, 14, 264-72	8.1	97
172	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, 1140-5	11.5	95
171	Reconsidering the evolution of eukaryotic selenoproteins: a novel nonmammalian family with scattered phylogenetic distribution. *EMBO Reports*, **2004**, 5, 71-7	6.5	94
170	Hnf1alpha (MODY3) controls tissue-specific transcriptional programs and exerts opposed effects on cell growth in pancreatic islets and liver. *Molecular and Cellular Biology*, **2009**, 29, 2945-59	4.8	92

169	The Long Non-Coding RNAs: A New (P)layer in the "Dark Matter". *Frontiers in Genetics*, **2011**, 2, 107	4.5	88
168	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, 16188-93	11.5	85
167	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. *Genome Biology*, **2016**, 17, 251	18.3	85
166	GENCODE 2021. *Nucleic Acids Research*, **2021**, 49, D916-D923	20.1	82
165	The GTEx Consortium atlas of genetic regulatory effects across human tissues		81
164	ASTD: The Alternative Splicing and Transcript Diversity database. *Genomics*, **2009**, 93, 213-20	4.3	80
163	Genomic history of the origin and domestication of common bean unveils its closest sister species. *Genome Biology*, **2017**, 18, 60	18.3	79
162	Genomic analysis of a migratory divide reveals candidate genes for migration and implicates selective sweeps in generating islands of differentiation. *Molecular Ecology*, **2015**, 24, 1873-88	5.7	77
161	Identification of genetic variants associated with alternative splicing using sQTLseekeR. *Nature Communications*, **2014**, 5, 4698	17.4	77
160	Genome-wide CTCF distribution in vertebrates defines equivalent sites that aid the identification of disease-associated genes. *Nature Structural and Molecular Biology*, **2011**, 18, 708-14	17.6	77
159	Exon structure conservation despite low sequence similarity: a relic of dramatic events in evolution?. *EMBO Journal*, **2001**, 20, 5354-60	13	74
158	Interoperability with Moby 1.0--it's better than sharing your toothbrush!. *Briefings in Bioinformatics*, **2008**, 9, 220-31	13.4	73
157	Fusion of the human gene for the polyubiquitination coeffector UEV1 with Kua, a newly identified gene. *Genome Research*, **2000**, 10, 1743-56	9.7	73
156	A Quantitative Proteome Map of the Human Body. *Cell*, **2020**, 183, 269-283.e19	56.2	73
155	Nematode selenoproteome: the use of the selenocysteine insertion system to decode one codon in an animal genome?. *Nucleic Acids Research*, **2005**, 33, 2227-38	20.1	70
154	SGP-1: prediction and validation of homologous genes based on sequence alignments. *Genome Research*, **2001**, 11, 1574-83	9.7	69
153	Cell type-specific genetic regulation of gene expression across human tissues. *Science*, **2020**, 369,	33.3	68
152	SECISearch3 and Seblastian: new tools for prediction of SECIS elements and selenoproteins. *Nucleic Acids Research*, **2013**, 41, e149	20.1	66

151	Comparison of splice sites in mammals and chicken. *Genome Research*, **2005**, 15, 111-9	9.7	64
150	DECKO: Single-oligo, dual-CRISPR deletion of genomic elements including long non-coding RNAs. *BMC Genomics*, **2015**, 16, 846	4.5	63
149	Assembling genes from predicted exons in linear time with dynamic programming. *Journal of Computational Biology*, **1998**, 5, 681-702	1.7	63
148	A Snapshot of the Emerging Tomato Genome Sequence. *Plant Genome*, **2009**, 2,	4.4	62
147	Perspectives on ENCODE. *Nature*, **2020**, 583, 693-698	50.4	61
146	A comparison of random sequence reads versus 16S rDNA sequences for estimating the biodiversity of a metagenomic library. *Nucleic Acids Research*, **2008**, 36, 5180-8	20.1	60
145	ggsashimi: Sashimi plot revised for browser- and annotation-independent splicing visualization. *PLoS Computational Biology*, **2018**, 14, e1006360	5	59
144	Discovery of Cancer Driver Long Noncoding RNAs across 1112 Tumour Genomes: New Candidates and Distinguishing Features. *Scientific Reports*, **2017**, 7, 41544	4.9	58
143	Absence of canonical marks of active chromatin in developmentally regulated genes. *Nature Genetics*, **2015**, 47, 1158-1167	36.3	58
142	Identifying protein-coding genes in genomic sequences. *Genome Biology*, **2009**, 10, 201	18.3	58
141	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. *Nature Communications*, **2015**, 6, 5903	17.4	56
140	Intron-centric estimation of alternative splicing from RNA-seq data. *Bioinformatics*, **2013**, 29, 273-4	7.2	56
139	Relaxation of selective constraints causes independent selenoprotein extinction in insect genomes. *PLoS ONE*, **2008**, 3, e2968	3.7	56
138	The origins, evolution, and functional potential of alternative splicing in vertebrates. *Molecular Biology and Evolution*, **2011**, 28, 2949-59	8.3	55
137	Comparison of GENCODE and RefSeq gene annotation and the impact of reference geneset on variant effect prediction. *BMC Genomics*, **2015**, 16 Suppl 8, S2	4.5	53
136	Autoimmune response in AIDS. *Nature*, **1990**, 345, 26	50.4	53
135	Evidence for transcript networks composed of chimeric RNAs in human cells. *PLoS ONE*, **2012**, 7, e28213	3.7	51
134	ABS: a database of Annotated regulatory Binding Sites from orthologous promoters. *Nucleic Acids Research*, **2006**, 34, D63-7	20.1	51

133	SelenoDB 1.0 : a database of selenoprotein genes, proteins and SECIS elements. *Nucleic Acids Research*, **2008**, 36, D332-8	20.1	50
132	Estimation of alternative splicing variability in human populations. *Genome Research*, **2012**, 22, 528-38	9.7	49
131	The tuatara genome reveals ancient features of amniote evolution. *Nature*, **2020**, 584, 403-409	50.4	49
130	Extension of human lncRNA transcripts by RACE coupled with long-read high-throughput sequencing (RACE-Seq). *Nature Communications*, **2016**, 7, 12339	17.4	47
129	Transcription factor map alignment of promoter regions. *PLoS Computational Biology*, **2006**, 2, e49	5	46
128	Scalable Design of Paired CRISPR Guide RNAs for Genomic Deletion. *PLoS Computational Biology*, **2017**, 13, e1005341	5	44
127	Combining RT-PCR-seq and RNA-seq to catalog all genic elements encoded in the human genome. *Genome Research*, **2012**, 22, 1698-710	9.7	44
126	Long noncoding RNAs as enhancers of gene expression. *Cold Spring Harbor Symposia on Quantitative Biology*, **2010**, 75, 325-31	3.9	44
125	Gene-specific patterns of expression variation across organs and species. *Genome Biology*, **2016**, 17, 151	18.3	44
124	Distinctive sequence features in protein coding genic non-coding, and intergenic human DNA. *Journal of Molecular Biology*, **1995**, 253, 51-60	6.5	41
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122	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. *Genome Research*, **2015**, 25, 1256-67	9.7	39
121	A short motif in Drosophila SECIS Binding Protein 2 provides differential binding affinity to SECIS RNA hairpins. *Nucleic Acids Research*, **2009**, 37, 2126-41	20.1	39
120	Efficient targeted transcript discovery via array-based normalization of RACE libraries. *Nature Methods*, **2008**, 5, 629-35	21.6	35
119	Splice site identification by idlBNs. *Bioinformatics*, **2004**, 20 Suppl 1, i69-76	7.2	34
118	Computational identification of the selenocysteine tRNA (tRNASec) in genomes. *PLoS Computational Biology*, **2017**, 13, e1005383	5	34
117	Exact Transcriptome Reconstruction from Short Sequence Reads. *Lecture Notes in Computer Science* , **2008**, 50-63	0.9	34
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114	Using geneid to Identify Genes. *Current Protocols in Bioinformatics*, **2018**, 64, e56	24.2	33
113	SECISaln, a web-based tool for the creation of structure-based alignments of eukaryotic SECIS elements. *Bioinformatics*, **2009**, 25, 674-5	7.2	32
112	Lokiarchaeota Marks the Transition between the Archaeal and Eukaryotic Selenocysteine Encoding Systems. *Molecular Biology and Evolution*, **2016**, 33, 2441-53	8.3	31
111	Using geneid to Identify Genes. *Current Protocols in Bioinformatics*, **2003**, 00, 4.3.1	24.2	31
110	SelenoDB 2.0: annotation of selenoprotein genes in animals and their genetic diversity in humans. *Nucleic Acids Research*, **2014**, 42, D437-43	20.1	30
109	EGASP: collaboration through competition to find human genes. *Nature Methods*, **2005**, 2, 575-7	21.6	26
108	Gene finding in the chicken genome. *BMC Bioinformatics*, **2005**, 6, 131	3.6	26
107	Damage-responsive elements in regeneration. *Genome Research*, **2018**, 28, 1852-1866	9.7	24
106	Promoter-like epigenetic signatures in exons displaying cell type-specific splicing. *Genome Biology*, **2015**, 16, 236	18.3	23
105	Grape RNA-Seq analysis pipeline environment. *Bioinformatics*, **2013**, 29, 614-21	7.2	23
104	Integrative transcriptomic analysis suggests new autoregulatory splicing events coupled with nonsense-mediated mRNA decay. *Nucleic Acids Research*, **2019**, 47, 5293-5306	20.1	22
103	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	11.5	22
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100	Sequence variation between 462 human individuals fine-tunes functional sites of RNA processing. *Scientific Reports*, **2016**, 6, 32406	4.9	21
99	Islands of euchromatin-like sequence and expressed polymorphic sequences within the short arm of human chromosome 21. *Genome Research*, **2007**, 17, 1690-6	9.7	21
98	The DART classification of unannotated transcription within the ENCODE regions: associating transcription with known and novel loci. *Genome Research*, **2007**, 17, 732-45	9.7	21

97	Functional targets of the monogenic diabetes transcription factors HNF-1alpha and HNF-4alpha are highly conserved between mice and humans. *Diabetes*, **2009**, 58, 1245-53	0.9	20
96	Mutation patterns of amino acid tandem repeats in the human proteome. *Genome Biology*, **2006**, 7, R33	18.3	20
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94	Comparative transcriptomics across 14 Drosophila species reveals signatures of longevity. *Aging Cell*, **2018**, 17, e12740	9.9	19
93	ChimPipe: accurate detection of fusion genes and transcription-induced chimeras from RNA-seq data. *BMC Genomics*, **2017**, 18, 7	4.5	19
92	CROC: finding chromosomal clusters in eukaryotic genomes. *Bioinformatics*, **2009**, 25, 1552-3	7.2	19
91	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, 3293-8	11.5	19
90	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	20.1	19
89	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	7.3	19
88	A vast resource of allelic expression data spanning human tissues. *Genome Biology*, **2020**, 21, 234	18.3	18
87	Conserved chromosomal clustering of genes governed by chromatin regulators in Drosophila. *Genome Biology*, **2008**, 9, R134	18.3	15
86	EGASP: Introduction. *Genome Biology*, **2006**, 7 Suppl 1, S1.1-3	18.3	15
85	A limited set of transcriptional programs define major cell types. *Genome Research*, **2020**, 30, 1047-1059	9.7	15
84	The human CD6 gene is transcriptionally regulated by RUNX and Ets transcription factors in T cells. *Molecular Immunology*, **2009**, 46, 2226-35	4.3	14
83	Structural constraints revealed in consistent nucleosome positions in the genome of S. cerevisiae. *Epigenetics and Chromatin*, **2010**, 3, 20	5.8	14
82	Identification and analysis of splicing quantitative trait loci across multiple tissues in the human genome. *Nature Communications*, **2021**, 12, 727	17.4	13
81	Processive Recoding and Metazoan Evolution of Selenoprotein P: Up to 132 UGAs in Molluscs. *Journal of Molecular Biology*, **2019**, 431, 4381-4407	6.5	12
80	Role of six single nucleotide polymorphisms, risk factors in coronary disease, in OLR1 alternative splicing. *Rna*, **2015**, 21, 1187-202	5.8	12

79	BioMoby web services to support clustering of co-regulated genes based on similarity of promoter configurations. *Bioinformatics*, **2007**, 23, 1831-3	7.2	12
78	A systematic survey of human tissue-specific gene expression and splicing reveals new opportunities for therapeutic target identification and evaluation		12
77	Re-annotation of 191 developmental and epileptic encephalopathy-associated genes unmasks de novo variants in. *Npj Genomic Medicine*, **2019**, 4, 31	6.2	12
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