

Chris Paul Ponting

List of Publications by Citations

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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.

228 papers	68,810 citations	100 h-index	262 g-index
264 ext. papers	78,936 ext. citations	14.8 avg, IF	7.33 L-index

#	Paper	IF	Citations
228	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
227	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
226	Evolution and functions of long noncoding RNAs. <i>Cell</i> , 2009 , 136, 629-41	56.2	3721
225	Regulation of chromatin structure by site-specific histone H3 methyltransferases. <i>Nature</i> , 2000 , 406, 593-9	50.4	2193
224	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005 , 438, 803-19	50.4	1809
223	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004 , 428, 493-521	50.4	1689
222	Evolution of genes and genomes on the Drosophila phylogeny. <i>Nature</i> , 2007 , 450, 203-18	50.4	1586
221	Functional impact of global rare copy number variation in autism spectrum disorders. <i>Nature</i> , 2010 , 466, 368-72	50.4	1499
220	The obesity-associated FTO gene encodes a 2-oxoglutarate-dependent nucleic acid demethylase. <i>Science</i> , 2007 , 318, 1469-72	33.3	1119
219	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011 , 477, 289-94	50.4	1087
218	SMART: a web-based tool for the study of genetically mobile domains. <i>Nucleic Acids Research</i> , 2000 , 28, 231-4	20.1	939
217	The Human Cell Atlas. <i>ELife</i> , 2017 , 6,	8.9	937
216	Sequencing depth and coverage: key considerations in genomic analyses. <i>Nature Reviews Genetics</i> , 2014 , 15, 121-32	30.1	799
215	SMART 4.0: towards genomic data integration. <i>Nucleic Acids Research</i> , 2004 , 32, D142-4	20.1	764
214	The genomic substrate for adaptive radiation in African cichlid fish. <i>Nature</i> , 2014 , 513, 375-381	50.4	656
213	The genome of a songbird. <i>Nature</i> , 2010 , 464, 757-62	50.4	655
212	A ChIP-seq defined genome-wide map of vitamin D receptor binding: associations with disease and evolution. <i>Genome Research</i> , 2010 , 20, 1352-60	9.7	606

211	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
210	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
209	Genome analysis of the platypus reveals unique signatures of evolution. <i>Nature</i> , 2008 , 453, 175-83	50.4	545
208	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002 , 30, 242-4	20.1	535
207	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. <i>Genome Research</i> , 2007 , 17, 556-65	9.7	530
206	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
205	Mutations in genes encoding ribonuclease H2 subunits cause Aicardi-Goutières syndrome and mimic congenital viral brain infection. <i>Nature Genetics</i> , 2006 , 38, 910-6	36.3	505
204	Mutations in the fukutin-related protein gene (FKRP) cause a form of congenital muscular dystrophy with secondary laminin alpha2 deficiency and abnormal glycosylation of alpha-dystroglycan. <i>American Journal of Human Genetics</i> , 2001 , 69, 1198-209	11	498
203	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013 , 496, 311-6	50.4	488
202	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011 , 477, 587-91	50.4	478
201	Protein repeats: structures, functions, and evolution. <i>Journal of Structural Biology</i> , 2001 , 134, 117-31	3.4	471
200	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021 , 591, 92-98	50.4	451
199	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. <i>Nature Methods</i> , 2015 , 12, 519-22	22.6	443
198	Systematic identification of novel protein domain families associated with nuclear functions. <i>Genome Research</i> , 2002 , 12, 47-56	9.7	437
197	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431
196	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016 , 13, 229-232	21.6	430
195	The Tudor domain @Royal Family@Tudor, plant Agenet, Chromo, PWWP and MBT domains. <i>Trends in Biochemical Sciences</i> , 2003 , 28, 69-74	10.3	397
194	Lineage-specific biology revealed by a finished genome assembly of the mouse. <i>PLoS Biology</i> , 2009 , 7, e1000112	9.7	354

193	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012 , 486, 527-31	50.4	350
192	The RNA-editing enzyme ADAR1 controls innate immune responses to RNA. <i>Cell Reports</i> , 2014 , 9, 1482-94	46.6	348
191	EMSY links the BRCA2 pathway to sporadic breast and ovarian cancer. <i>Cell</i> , 2003 , 115, 523-35	56.2	345
190	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , 2004 , 432, 717-22	50.4	341
189	START: a lipid-binding domain in StAR, HD-ZIP and signalling proteins. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 130-2	10.3	337
188	The cytoplasmic helical linker domain of receptor histidine kinase and methyl-accepting proteins is common to many prokaryotic signalling proteins. <i>FEMS Microbiology Letters</i> , 1999 , 176, 111-6	2.9	326
187	The reality of pervasive transcription. <i>PLoS Biology</i> , 2011 , 9, e1000625; discussion e1001102	9.7	325
186	KDM2B links the Polycomb Repressive Complex 1 (PRC1) to recognition of CpG islands. <i>ELife</i> , 2012 , 1, e00205	8.9	318
185	Transcriptional regulatory functions of nuclear long noncoding RNAs. <i>Trends in Genetics</i> , 2014 , 30, 348-58	55.5	305
184	Genomic and transcriptional co-localization of protein-coding and long non-coding RNA pairs in the developing brain. <i>PLoS Genetics</i> , 2009 , 5, e1000617	6	305
183	Single-Cell Multiomics: Multiple Measurements from Single Cells. <i>Trends in Genetics</i> , 2017 , 33, 155-168	8.5	299
182	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , 2015 , 16, 712-24	18	286
181	Positional cloning of a novel gene influencing asthma from chromosome 2q14. <i>Nature Genetics</i> , 2003 , 35, 258-63	36.3	283
180	PAS: a multifunctional domain family comes to light. <i>Current Biology</i> , 1997 , 7, R674-7	6.3	278
179	Positional cloning of a quantitative trait locus on chromosome 13q14 that influences immunoglobulin E levels and asthma. <i>Nature Genetics</i> , 2003 , 34, 181-6	36.3	263
178	SMART: identification and annotation of domains from signalling and extracellular protein sequences. <i>Nucleic Acids Research</i> , 1999 , 27, 229-32	20.1	262
177	Coordination of structure-specific nucleases by human SLX4/BTBD12 is required for DNA repair. <i>Molecular Cell</i> , 2009 , 35, 116-27	17.6	259
176	Considerations when investigating lncRNA function in vivo. <i>ELife</i> , 2014 , 3, e03058	8.9	252

175	Rapid turnover of long noncoding RNAs and the evolution of gene expression. <i>PLoS Genetics</i> , 2012 , 8, e1002841	6	238
174	On the evolution of protein folds: are similar motifs in different protein folds the result of convergence, insertion, or relics of an ancient peptide world?. <i>Journal of Structural Biology</i> , 2001 , 134, 191-203	3.4	225
173	A transcriptomic atlas of mouse neocortical layers. <i>Neuron</i> , 2011 , 71, 605-16	13.9	224
172	The natural history of protein domains. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2002 , 31, 45-71		221
171	Transcribed dark matter: meaning or myth?. <i>Human Molecular Genetics</i> , 2010 , 19, R162-8	5.6	220
170	The protein composition of mitotic chromosomes determined using multiclassifier combinatorial proteomics. <i>Cell</i> , 2010 , 142, 810-21	56.2	217
169	Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness. <i>Genome Biology</i> , 2009 , 10, R124	18.3	208
168	Bias of selection on human copy-number variants. <i>PLoS Genetics</i> , 2006 , 2, e20	6	205
167	Accelerated evolution of the Prdm9 speciation gene across diverse metazoan taxa. <i>PLoS Genetics</i> , 2009 , 5, e1000753	6	203
166	JmjC: cupin metalloenzyme-like domains in jumonji, hairless and phospholipase A2beta. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 7-9	10.3	201
165	Mutations in BMP4 cause eye, brain, and digit developmental anomalies: overlap between the BMP4 and hedgehog signaling pathways. <i>American Journal of Human Genetics</i> , 2008 , 82, 304-19	11	198
164	Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. <i>Genome Research</i> , 2014 , 24, 1918-31	9.7	197
163	Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes. <i>Genome Biology</i> , 2010 , 11, R72	18.3	191
162	Natural genetic variation caused by small insertions and deletions in the human genome. <i>Genome Research</i> , 2011 , 21, 830-9	9.7	178
161	Identification of region-specific astrocyte subtypes at single cell resolution. <i>Nature Communications</i> , 2020 , 11, 1220	17.4	168
160	Homology-based method for identification of protein repeats using statistical significance estimates. <i>Journal of Molecular Biology</i> , 2000 , 298, 521-37	6.5	167
159	Identification and properties of 1,119 candidate lincRNA loci in the <i>Drosophila melanogaster</i> genome. <i>Genome Biology and Evolution</i> , 2012 , 4, 427-42	3.9	165
158	Stc1: a critical link between RNAi and chromatin modification required for heterochromatin integrity. <i>Cell</i> , 2010 , 140, 666-77	56.2	160

157	The long non-coding RNA Paupar regulates the expression of both local and distal genes. <i>EMBO Journal</i> , 2014 , 33, 296-311	13	154
156	EYS, encoding an ortholog of Drosophila spacemaker, is mutated in autosomal recessive retinitis pigmentosa. <i>Nature Genetics</i> , 2008 , 40, 1285-7	36.3	151
155	Comparison of the genomes of human and mouse lays the foundation of genome zoology. <i>Human Molecular Genetics</i> , 2003 , 12, 701-9	5.6	149
154	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. <i>ELife</i> , 2013 , 2, e00348	8.9	148
153	Genome-wide identification of human functional DNA using a neutral indel model. <i>PLoS Computational Biology</i> , 2006 , 2, e5	5	141
152	Elevated rates of protein secretion, evolution, and disease among tissue-specific genes. <i>Genome Research</i> , 2004 , 14, 54-61	9.7	141
151	Repo-Man coordinates chromosomal reorganization with nuclear envelope reassembly during mitotic exit. <i>Developmental Cell</i> , 2011 , 21, 328-42	10.2	139
150	TRAM, LAG1 and CLN8: members of a novel family of lipid-sensing domains?. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 381-3	10.3	139
149	Identification of a novel family of presenilin homologues. <i>Human Molecular Genetics</i> , 2002 , 11, 1037-44	5.6	139
148	High incidence of unrecognized visceral/neurological late-onset Niemann-Pick disease, type C1, predicted by analysis of massively parallel sequencing data sets. <i>Genetics in Medicine</i> , 2016 , 18, 41-8	8.1	138
147	RBFOX and PTBP1 proteins regulate the alternative splicing of micro-exons in human brain transcripts. <i>Genome Research</i> , 2015 , 25, 1-13	9.7	137
146	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35	13.4	137
145	GAT: a simulation framework for testing the association of genomic intervals. <i>Bioinformatics</i> , 2013 , 29, 2046-8	7.2	136
144	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. <i>Genome Biology</i> , 2013 , 14, R131	18.3	135
143	PIN domains in nonsense-mediated mRNA decay and RNAi. <i>Current Biology</i> , 2000 , 10, R888-90	6.3	131
142	Vitamin K epoxide reductase: homology, active site and catalytic mechanism. <i>Trends in Biochemical Sciences</i> , 2004 , 29, 289-92	10.3	125
141	8.2% of the Human genome is constrained: variation in rates of turnover across functional element classes in the human lineage. <i>PLoS Genetics</i> , 2014 , 10, e1004525	6	124
140	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. <i>Genome Biology</i> , 2012 , 13, R45	18.3	124

139	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. <i>Genome Biology</i> , 2012 , 13, 26	18.3	122
138	The long non-coding RNA Dali is an epigenetic regulator of neural differentiation. <i>ELife</i> , 2014 , 3, e045308.9		116
137	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. <i>Cell Reports</i> , 2019 , 29, 1832-1847.e8	10.6	115
136	Complexities of post-transcriptional regulation and the modeling of ceRNA crosstalk. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2018 , 53, 231-245	8.7	114
135	Regulation of DNA replication through Sld3-Dpb11 interaction is conserved from yeast to humans. <i>Current Biology</i> , 2011 , 21, 1152-7	6.3	110
134	Evolutionary rate analyses of orthologs and paralogs from 12 Drosophila genomes. <i>Genome Research</i> , 2007 , 17, 1837-49	9.7	110
133	Ki-67 is a PP1-interacting protein that organises the mitotic chromosome periphery. <i>ELife</i> , 2014 , 3, e016419	11.9	110
132	Phylogenetic reconstruction of orthology, paralogy, and conserved synteny for dog and human. <i>PLoS Computational Biology</i> , 2006 , 2, e133	5	108
131	Proteins of the endoplasmic-reticulum-associated degradation pathway: domain detection and function prediction. <i>Biochemical Journal</i> , 2000 , 351, 527-535	3.8	108
130	What fraction of the human genome is functional?. <i>Genome Research</i> , 2011 , 21, 1769-76	9.7	104
129	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. <i>Genome Biology</i> , 2004 , 5, R47	18.3	102
128	Next-generation sequencing of advanced prostate cancer treated with androgen-deprivation therapy. <i>European Urology</i> , 2014 , 66, 32-9	10.2	99
127	Foxn1 regulates key target genes essential for T cell development in postnatal thymic epithelial cells. <i>Nature Immunology</i> , 2016 , 17, 1206-1215	19.1	98
126	Death of PRDM9 coincides with stabilization of the recombination landscape in the dog genome. <i>Genome Research</i> , 2012 , 22, 51-63	9.7	97
125	Occurrence and consequences of coding sequence insertions and deletions in Mammalian genomes. <i>Genome Research</i> , 2004 , 14, 555-66	9.7	97
124	Identification of distant homologues of fibroblast growth factors suggests a common ancestor for all beta-trefoil proteins. <i>Journal of Molecular Biology</i> , 2000 , 302, 1041-7	6.5	97
123	A novel domain suggests a ciliary function for ASPM, a brain size determining gene. <i>Bioinformatics</i> , 2006 , 22, 1031-5	7.2	96
122	Novel domains and orthologues of eukaryotic transcription elongation factors. <i>Nucleic Acids Research</i> , 2002 , 30, 3643-52	20.1	93

121	Separation and parallel sequencing of the genomes and transcriptomes of single cells using G&T-seq. <i>Nature Protocols</i> , 2016 , 11, 2081-103	18.8	93
120	The functional repertoires of metazoan genomes. <i>Nature Reviews Genetics</i> , 2008 , 9, 689-98	30.1	91
119	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. <i>Genome Research</i> , 2015 , 25, 655-66	9.7	82
118	Predicting long non-coding RNAs using RNA sequencing. <i>Methods</i> , 2013 , 63, 50-9	4.6	82
117	Diagnostically relevant facial gestalt information from ordinary photos. <i>ELife</i> , 2014 , 3, e02020	8.9	81
116	Predicting protein cellular localization using a domain projection method. <i>Genome Research</i> , 2002 , 12, 1168-74	9.7	81
115	Long noncoding RNAs in B-cell development and activation. <i>Blood</i> , 2016 , 128, e10-9	2.2	79
114	Massive turnover of functional sequence in human and other mammalian genomes. <i>Genome Research</i> , 2010 , 20, 1335-43	9.7	76
113	Novel eIF4G domain homologues linking mRNA translation with nonsense-mediated mRNA decay. <i>Trends in Biochemical Sciences</i> , 2000 , 25, 423-6	10.3	75
112	Chlamydial homologues of the MACPF (MAC/perforin) domain. <i>Current Biology</i> , 1999 , 9, R911-3	6.3	73
111	Evolution and comparative genomics of odorant- and pheromone-associated genes in rodents. <i>Genome Research</i> , 2004 , 14, 591-602	9.7	72
110	Adult pallium transcriptomes surprise in not reflecting predicted homologies across diverse chicken and mouse pallial sectors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 13150-5	11.5	68
109	Evolution of primary microcephaly genes and the enlargement of primate brains. <i>Current Opinion in Genetics and Development</i> , 2005 , 15, 241-8	4.9	68
108	Meisetz and the birth of the KRAB motif. <i>Bioinformatics</i> , 2006 , 22, 2841-5	7.2	67
107	Mutations in CDC45, Encoding an Essential Component of the Pre-initiation Complex, Cause Meier-Gorlin Syndrome and Craniosynostosis. <i>American Journal of Human Genetics</i> , 2016 , 99, 125-38	11	67
106	Sialidase-like Asp-boxes: sequence-similar structures within different protein folds. <i>Protein Science</i> , 2001 , 10, 285-92	6.3	66
105	Intergenic lncRNAs and the evolution of gene expression. <i>Current Opinion in Genetics and Development</i> , 2014 , 27, 48-53	4.9	65
104	Assessing similarity to primary tissue and cortical layer identity in induced pluripotent stem cell-derived cortical neurons through single-cell transcriptomics. <i>Human Molecular Genetics</i> , 2016 , 25, 989-1000	5.6	64

103	Cross-talking noncoding RNAs contribute to cell-specific neurodegeneration in SCA7. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 955-961	17.6	64
102	Monoallelic and biallelic mutations in MAB21L2 cause a spectrum of major eye malformations. <i>American Journal of Human Genetics</i> , 2014 , 94, 915-23	11	64
101	Reduced purifying selection prevails over positive selection in human copy number variant evolution. <i>Genome Research</i> , 2008 , 18, 1711-23	9.7	64
100	Understanding functional miRNA-target interactions in vivo by site-specific genome engineering. <i>Nature Communications</i> , 2014 , 5, 4640	17.4	63
99	What are the genomic drivers of the rapid evolution of PRDM9?. <i>Trends in Genetics</i> , 2011 , 27, 165-71	8.5	61
98	Unexpected selection to retain high GC content and splicing enhancers within exons of multiexonic lncRNA loci. <i>Rna</i> , 2015 , 21, 333-46	5.8	58
97	Homology explains the functional similarities of Treslin/Ticrr and Sld3. <i>Current Biology</i> , 2010 , 20, R509-10	6.3	58
96	Evolution of domain families. <i>Advances in Protein Chemistry</i> , 2000 , 54, 185-244		57
95	Cytoplasmic signalling domains: the next generation. <i>Trends in Biochemical Sciences</i> , 1997 , 22, 296-8	10.3	56
94	Duplication and positive selection among hominin-specific PRAME genes. <i>BMC Genomics</i> , 2005 , 6, 120	4.5	54
93	A code for RanGDP binding in ankyrin repeats defines a nuclear import pathway. <i>Cell</i> , 2014 , 157, 1130-45	6.2	52
92	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. <i>Genome Biology</i> , 2012 , 13, R102	18.3	51
91	Genetic mechanisms of critical illness in Covid-19		51
90	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. <i>GigaScience</i> , 2014 , 3, 27	7.6	50
89	Cadherin-like domains in alpha-dystroglycan, alpha/epsilon-sarcoglycan and yeast and bacterial proteins. <i>Current Biology</i> , 2002 , 12, R197-9	6.3	50
88	Tuning the Transcriptional Response to Hypoxia by Inhibiting Hypoxia-inducible Factor (HIF) Prolyl and Asparaginyl Hydroxylases. <i>Journal of Biological Chemistry</i> , 2016 , 291, 20661-73	5.4	50
87	Protein families in multicellular organisms. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 408-15	8.1	48
86	Mutations within lncRNAs are effectively selected against in fruitfly but not in human. <i>Genome Biology</i> , 2013 , 14, R49	18.3	46

85	Protein fold irregularities that hinder sequence analysis. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 364-71	8.1	46
84	Comparative evolutionary genomics of androgen-binding protein genes. <i>Genome Research</i> , 2004 , 14, 1516-29	9.7	46
83	Domain homologues of dopamine beta-hydroxylase and ferric reductase: roles for iron metabolism in neurodegenerative disorders?. <i>Human Molecular Genetics</i> , 2001 , 10, 1853-8	5.6	46
82	Dynamic spatio-temporal contribution of single Bt+ cortical epithelial precursors to the thymus medulla. <i>European Journal of Immunology</i> , 2016 , 46, 846-56	6.1	45
81	CGAT: computational genomics analysis toolkit. <i>Bioinformatics</i> , 2014 , 30, 1290-1	7.2	44
80	An analysis of the gene complement of a marsupial, <i>Monodelphis domestica</i> : evolution of lineage-specific genes and giant chromosomes. <i>Genome Research</i> , 2007 , 17, 969-81	9.7	43
79	TM6SF2 and MAC30, new enzyme homologs in sterol metabolism and common metabolic disease. <i>Frontiers in Genetics</i> , 2014 , 5, 439	4.5	42
78	The Human Cell Atlas 2017 ,		41
77	Hotspots of mutation and breakage in dog and human chromosomes. <i>Genome Research</i> , 2005 , 15, 1787-97	9.7	40
76	Identification and function of long non-coding RNAs. <i>Essays in Biochemistry</i> , 2013 , 54, 113-26	7.6	39
75	Genome assembly quality: assessment and improvement using the neutral indel model. <i>Genome Research</i> , 2010 , 20, 675-84	9.7	39
74	Forging links between human mental retardation-associated CNVs and mouse gene knockout models. <i>PLoS Genetics</i> , 2009 , 5, e1000531	6	39
73	Temporal transcriptomics suggest that twin-peaking genes reset the clock. <i>ELife</i> , 2015 , 4,	8.9	38
72	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. <i>BMC Evolutionary Biology</i> , 2008 , 8, 46	3	38
71	More than 1,000 putative new human signalling proteins revealed by EST data mining. <i>Nature Genetics</i> , 2000 , 25, 201-4	36.3	38
70	Single cell RNA-seq reveals profound transcriptional similarity between Barrett's oesophagus and oesophageal submucosal glands. <i>Nature Communications</i> , 2018 , 9, 4261	17.4	37
69	Signatures of adaptive evolution within human non-coding sequence. <i>Human Molecular Genetics</i> , 2006 , 15 Spec No 2, R170-5	5.6	35
68	The long non-coding RNA promotes KAP1-dependent chromatin changes and regulates olfactory bulb neurogenesis. <i>EMBO Journal</i> , 2018 , 37,	13	33

67	Insights into the evolution of Darwin [®] finches from comparative analysis of the Geospiza magnirostris genome sequence. <i>BMC Genomics</i> , 2013 , 14, 95	4.5	33
66	Microglia recapitulate a hematopoietic master regulator network in the aging human frontal cortex. <i>Neurobiology of Aging</i> , 2015 , 36, 2443.e9-2443.e20	5.6	32
65	Eukaryotic domain evolution inferred from genome comparisons. <i>Current Opinion in Genetics and Development</i> , 2003 , 13, 623-8	4.9	31
64	Biologically indeterminate yet ordered promiscuous gene expression in single medullary thymic epithelial cells. <i>EMBO Journal</i> , 2020 , 39, e101828	13	29
63	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. <i>ELife</i> , 2020 , 9,	8.9	29
62	TMEM132: an ancient architecture of cohesin and immunoglobulin domains define a new family of neural adhesion molecules. <i>Bioinformatics</i> , 2018 , 34, 721-724	7.2	28
61	Disruption of Visc-2, a Brain-Expressed Conserved Long Noncoding RNA, Does Not Elicit an Overt Anatomical or Behavioral Phenotype. <i>Cerebral Cortex</i> , 2015 , 25, 3572-85	5.1	27
60	The phenotypic spectrum of Xia-Gibbs syndrome. <i>American Journal of Medical Genetics, Part A</i> , 2018 , 176, 1315-1326	2.5	25
59	Cofilin-1: a modulator of anxiety in mice. <i>PLoS Genetics</i> , 2012 , 8, e1002970	6	25
58	The long and the short of RNA maps. <i>BioEssays</i> , 2007 , 29, 1077-80	4.1	25
57	Diverse spatial, temporal, and sexual expression of recently duplicated androgen-binding protein genes in <i>Mus musculus</i> . <i>BMC Evolutionary Biology</i> , 2005 , 5, 40	3	25
56	Mammalian BEX, WEX and GASP genes: coding and non-coding chimaerism sustained by gene conversion events. <i>BMC Evolutionary Biology</i> , 2005 , 5, 54	3	25
55	Vasohibins: new transglutaminase-like cysteine proteases possessing a non-canonical Cys-His-Ser catalytic triad. <i>Bioinformatics</i> , 2016 , 32, 1441-5	7.2	25
54	Sequence variation and disease in the wake of the draft human genome. <i>Human Molecular Genetics</i> , 2001 , 10, 2209-14	5.6	24
53	OPTIC: orthologous and paralogous transcripts in clades. <i>Nucleic Acids Research</i> , 2008 , 36, D267-70	20.1	22
52	Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease. <i>Human Molecular Genetics</i> , 2017 , 26, 2164-2176	5.6	21
51	Wrangling for microRNAs provokes much crosstalk. <i>Genome Biology</i> , 2011 , 12, 132	18.3	21
50	A beta-propeller domain within TolB. <i>Molecular Microbiology</i> , 1999 , 31, 739-40	4.1	20

49	Biological function in the twilight zone of sequence conservation. <i>BMC Biology</i> , 2017 , 15, 71	7.3	19
48	The Cdk8/19-cyclin C transcription regulator functions in genome replication through metazoan Sld7. <i>PLoS Biology</i> , 2019 , 17, e2006767	9.7	18
47	Rapid turnover of functional sequence in human and other genomes. <i>Annual Review of Genomics and Human Genetics</i> , 2011 , 12, 275-99	9.7	17
46	The long non-coding RNA is a post transcriptional regulator of mitochondrial complex I catalytic activity. <i>ELife</i> , 2019 , 8,	8.9	17
45	Insights into the post-transcriptional regulation of the mitochondrial electron transport chain. <i>Biochemical Society Transactions</i> , 2016 , 44, 1491-1498	5.1	16
44	Transcriptional dynamics of pluripotent stem cell-derived endothelial cell differentiation revealed by single-cell RNA sequencing. <i>European Heart Journal</i> , 2020 , 41, 1024-1036	9.5	15
43	beta-propeller repeats and a PDZ domain in the tricorn protease: predicted self-compartmentalisation and C-terminal polypeptide-binding strategies of substrate selection. <i>FEMS Microbiology Letters</i> , 1999 , 179, 447-51	2.9	15
42	Identification of functional long non-coding RNAs in <i>C. elegans</i> . <i>BMC Biology</i> , 2019 , 17, 14	7.3	15
41	Zebrafish MITF-Low Melanoma Subtype Models Reveal Transcriptional Subclusters and MITF-Independent Residual Disease. <i>Cancer Research</i> , 2019 , 79, 5769-5784	10.1	14
40	No gene in the genome makes sense except in the light of evolution. <i>Annual Review of Genomics and Human Genetics</i> , 2014 , 15, 71-92	9.7	14
39	The role of ADP-ribosylation in regulating DNA interstrand crosslink repair. <i>Journal of Cell Science</i> , 2016 , 129, 3845-3858	5.3	13
38	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020 , 16, e1008785	6	12
37	Brain-expressed 3'UTR extensions strengthen miRNA cross-talk between ion channel/transporter encoding mRNAs. <i>Frontiers in Genetics</i> , 2014 , 5, 41	4.5	11
36	Separating derived from ancestral features of mouse and human genomes. <i>Biochemical Society Transactions</i> , 2009 , 37, 734-9	5.1	11
35	Genetic risk factors of ME/CFS: a critical review. <i>Human Molecular Genetics</i> , 2020 , 29, R117-R124	5.6	11
34	REC-1 and HIM-5 distribute meiotic crossovers and function redundantly in meiotic double-strand break formation in <i>Caenorhabditis elegans</i> . <i>Genes and Development</i> , 2015 , 29, 1969-79	12.6	10
33	Identification of molecular signatures specific for distinct cranial sensory ganglia in the developing chick. <i>Neural Development</i> , 2016 , 11, 3	3.9	10
32	Sequence analysis of multidomain proteins: past perspectives and future directions. <i>Advances in Protein Chemistry</i> , 2002 , 61, 75-98		10

31	Author response: The Human Cell Atlas 2017 ,		10
30	Comprehensively Profiling the Chromatin Architecture of Tissue Restricted Antigen Expression in Thymic Epithelial Cells Over Development. <i>Frontiers in Immunology</i> , 2018 , 9, 2120	8.4	10
29	Accelerated evolution of PAK3- and PIM1-like kinase gene families in the zebra finch, <i>Taeniopygia guttata</i> . <i>Molecular Biology and Evolution</i> , 2010 , 27, 1923-34	8.3	9
28	Whole genome sequencing reveals host factors underlying critical Covid-19.. <i>Nature</i> , 2022 ,	50.4	8
27	A gene expression signature in developing Purkinje cells predicts autism and intellectual disability co-morbidity status. <i>Scientific Reports</i> , 2019 , 9, 485	4.9	7
26	Accurate estimation of gene evolutionary rates using XRATE, with an application to transmembrane proteins. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1715-21	8.3	7
25	Genome-Wide Analysis of Human Long Noncoding RNAs: A Provocative Review.. <i>Annual Review of Genomics and Human Genetics</i> , 2022 ,	9.7	7
24	The Human Cell Atlas: making cell space for disease. <i>DMM Disease Models and Mechanisms</i> , 2019 , 12,	4.1	6
23	CGAT: a model for immersive personalized training in computational genomics. <i>Briefings in Functional Genomics</i> , 2016 , 15, 32-7	4.9	4
22	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. <i>F1000Research</i> , 2016 , 5,	3.6	4
21	Big knowledge from big data in functional genomics. <i>Emerging Topics in Life Sciences</i> , 2017 , 1, 245-248	3.5	3
20	Brain, know thy transcriptome, know thyself. <i>Neuron</i> , 2012 , 75, 543-5	13.9	3
19	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. <i>Human Genetics</i> , 2021 , 141, 147	6.3	3
18	The RFTS domain of Raf2 is required for Cul4 interaction and heterochromatin integrity in fission yeast. <i>PLoS ONE</i> , 2014 , 9, e104161	3.7	3
17	Biologically indeterminate yet ordered promiscuous gene expression in single medullary thymic epithelial cells		3
16	Functional RNA classes: a matter of time?. <i>Nature Structural and Molecular Biology</i> , 2017 , 24, 7-8	17.6	2
15	Violation of the 12/23 rule of genomic V(D)J recombination is common in lymphocytes. <i>Genome Research</i> , 2015 , 25, 226-34	9.7	2
14	Loaded dice for human genome mutation. <i>Cell</i> , 2012 , 151, 1399-400	56.2	2

13	No Sec7-homology domain in guanine-nucleotide-exchange factors that act on Ras and Rho. <i>Trends in Biochemical Sciences</i> , 1999 , 24, 177-8	10.3	2
12	Whole genome sequencing identifies multiple loci for critical illness caused by COVID-19		2
11	Hexa-Longin domain scaffolds for inter-Rab signalling. <i>Bioinformatics</i> , 2020 , 36, 990-993	7.2	1
10	Protein Sequence Analysis and Domain Identification 2005 , 527-541		1
9	THoR: a tool for domain discovery and curation of multiple alignments. <i>Genome Biology</i> , 2003 , 4, R52	18.3	1
8	A coming of age for bioinformatics. <i>Journal of Cell Science</i> , 2003 , 116, 6-7	5.3	1
7	Refining the domain architecture model of the replication origin firing factor Treslin/TICRR.. <i>Life Science Alliance</i> , 2022 , 5,	5.8	1
6	Identification of functional long non-coding RNAs in <i>C. elegans</i>		1
5	A new sequence motif linking lissencephaly, Treacher Collins and oral-facial-digital type 1 syndromes, microtubule dynamics and cell migration		1
4	FAM111A regulates replication origin activation and cell fitness		1
3	Protein citrullination was introduced into animals by horizontal gene transfer from cyanobacteria		1
2	Extending the Horizon of Homology Detection with Coevolution-based Structure Prediction. <i>Journal of Molecular Biology</i> , 2021 , 433, 167106	6.5	1
1	Genetics Needs Non-geneticists. <i>Trends in Genetics</i> , 2020 , 36, 629-630	8.5	