Chris Paul Ponting

List of Publications by Year
in descending order

225 papers	85,342 citations	1463 107 h-index	1347 223 g-index
264 all docs	264 docs citations	264 times ranked	90681 citing authors

#	Article	IF	Citations
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
3	Evolution and Functions of Long Noncoding RNAs. Cell, 2009, 136, 629-641.	28.9	4,480
4	Regulation of chromatin structure by site-specific histone H3 methyltransferases. Nature, 2000, 406, 593-599.	27.8	2,497
5	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215
6	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
7	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
8	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
9	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
10	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	27.8	1,461
11	The Obesity-AssociatedFTOGene Encodes a 2-Oxoglutarate-Dependent Nucleic Acid Demethylase. Science, 2007, 318, 1469-1472.	12.6	1,305
12	SMART: a web-based tool for the study of genetically mobile domains. Nucleic Acids Research, 2000, 28, 231-234.	14.5	1,159
13	Sequencing depth and coverage: key considerations in genomic analyses. Nature Reviews Genetics, 2014, 15, 121-132.	16.3	1,116
14	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
15	SMART 4.0: towards genomic data integration. Nucleic Acids Research, 2004, 32, 142D-144.	14.5	892
16	The genomic substrate for adaptive radiation in African cichlid fish. Nature, 2014, 513, 375-381.	27.8	874
17	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
18	A ChIP-seq defined genome-wide map of vitamin D receptor binding: Associations with disease and evolution. Genome Research, 2010, 20, 1352-1360.	5.5	737

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19	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
20	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
21	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
22	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	14.5	640
23	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. Nature Methods, 2015, 12, 519-522.	19.0	633
24	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. Genome Research, 2007, 17, 556-565.	5.5	632
25	Recent improvements to the SMART domain-based sequence annotation resource. Nucleic Acids Research, 2002, 30, 242-244.	14.5	613
26	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	27.8	612
27	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	19.0	602
28	Mutations in genes encoding ribonuclease H2 subunits cause Aicardi-GoutiÃ¨res syndrome and mimic congenital viral brain infection. Nature Genetics, 2006, 38, 910-916.	21.4	592
29	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
30	Mutations in the Fukutin-Related Protein Gene (FKRP) Cause a Form of Congenital Muscular Dystrophy with Secondary Laminin Î±2 Deficiency and Abnormal Glycosylation of Î±-Dystroglycan. American Journal of Human Genetics, 2001, 69, 1198-1209.	6.2	563
31	Protein Repeats: Structures, Functions, and Evolution. Journal of Structural Biology, 2001, 134, 117-131.	2.8	559
32	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
33	Systematic Identification of Novel Protein Domain Families Associated with Nuclear Functions. Genome Research, 2002, 12, 47-56.	5.5	527
34	The RNA-Editing Enzyme ADAR1 Controls Innate Immune Responses to RNA. Cell Reports, 2014, 9, 1482-1494.	6.4	508
35	The Tudor domain â€˜Royal Familyâ€™: Tudor, plant Agenet, Chromo, PWWP and MBT domains. Trends in Biochemical Sciences, 2003, 28, 69-74.	7.5	448
36	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	27.8	445

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37	Identification of region-specific astrocyte subtypes at single cell resolution. Nature Communications, 2020, 11, 1220.	12.8	444
38	Lineage-Specific Biology Revealed by a Finished Genome Assembly of the Mouse. PLoS Biology, 2009, 7, e1000112.	5.6	419
39	KDM2B links the Polycomb Repressive Complex 1 (PRC1) to recognition of CpG islands. ELife, 2012, 1, e00205.	6.0	414
40	Single-Cell Multiomics: Multiple Measurements from Single Cells. Trends in Genetics, 2017, 33, 155-168.	6.7	392
41	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	27.8	391
42	EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. Cell, 2003, 115, 523-535.	28.9	389
43	Transcriptional regulatory functions of nuclear long noncoding RNAs. Trends in Genetics, 2014, 30, 348-355.	6.7	381
44	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	5.6	380
45	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	11.1	376
46	START: a lipid-binding domain in StAR, HD-ZIP and signalling proteins. Trends in Biochemical Sciences, 1999, 24, 130-132.	7.5	364
47	Genomic and Transcriptional Co-Localization of Protein-Coding and Long Non-Coding RNA Pairs in the Developing Brain. PLoS Genetics, 2009, 5, e1000617.	3.5	354
48	The cytoplasmic helical linker domain of receptor histidine kinase and methyl-accepting proteins is common to many prokaryotic signalling proteins. FEMS Microbiology Letters, 1999, 176, 111-116.	1.8	352
49	Positional cloning of a novel gene influencing asthma from Chromosome 2q14. Nature Genetics, 2003, 35, 258-263.	21.4	326
50	PAS: a multifunctional domain family comes to light. Current Biology, 1997, 7, R674-R677.	3.9	319
51	Considerations when investigating lncRNA function in vivo. ELife, 2014, 3, e03058.	6.0	309
52	Population and single-cell genomics reveal the Aire dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. Genome Research, 2014, 24, 1918-1931.	5.5	308
53	Positional cloning of a quantitative trait locus on chromosome 13q14 that influences immunoglobulin E levels and asthma. Nature Genetics, 2003, 34, 181-186.	21.4	300
54	Coordination of Structure-Specific Nucleases by Human SLX4/BTBD12 Is Required for DNA Repair. Molecular Cell, 2009, 35, 116-127.	9.7	300

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55	SMART: identification and annotation of domains from signalling and extracellular protein sequences. Nucleic Acids Research, 1999, 27, 229-232.	14.5	291
56	The Natural History of Protein Domains. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 45-71.	18.3	286
57	Rapid Turnover of Long Noncoding RNAs and the Evolution of Gene Expression. PLoS Genetics, 2012, 8, e1002841.	3.5	284
58	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?. Journal of Structural Biology, 2001, 134, 191-203.	2.8	276
59	The Protein Composition of Mitotic Chromosomes Determined Using Multiclassifier Combinatorial Proteomics. Cell, 2010, 142, 810-821.	28.9	266
60	A Transcriptomic Atlas of Mouse Neocortical Layers. Neuron, 2011, 71, 605-616.	8.1	266
61	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. Cell Reports, 2019, 29, 1832-1847.e8.	6.4	261
62	Accelerated Evolution of the Prdm9 Speciation Gene across Diverse Metazoan Taxa. PLoS Genetics, 2009, 5, e1000753.	3.5	256
63	Transcribed dark matter: meaning or myth?. Human Molecular Genetics, 2010, 19, R162-R168.	2.9	253
64	Bias of Selection on Human Copy-Number Variants. PLoS Genetics, 2006, 2, e20.	3.5	237
65	Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness. Genome Biology, 2009, 10, R124.	9.6	232
66	Mutations in BMP4 Cause Eye, Brain, and Digit Developmental Anomalies: Overlap between the BMP4 and Hedgehog Signaling Pathways. American Journal of Human Genetics, 2008, 82, 304-319.	6.2	221
67	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	4.1	221
68	Identification and Properties of 1,119 Candidate LincRNA Loci in the Drosophila melanogaster Genome. Genome Biology and Evolution, 2012, 4, 427-442.	2.5	217
69	JmjC: cupin metalloenzyme-like domains in jumonji, hairless and phospholipase A2Î². Trends in Biochemical Sciences, 2001, 26, 7-9.	7.5	215
70	Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes. Genome Biology, 2010, 11, R72.	9.6	215
71	8.2% of the Human Genome Is Constrained: Variation in Rates of Turnover across Functional Element Classes in the Human Lineage. PLoS Genetics, 2014, 10, e1004525.	3.5	213
72	Natural genetic variation caused by small insertions and deletions in the human genome. Genome Research, 2011, 21, 830-839.	5.5	212

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73	Stc1: A Critical Link between RNAi and Chromatin Modification Required for Heterochromatin Integrity. Cell, 2010, 140, 666-677.	28.9	195
74	The long non-coding RNA Paupar regulates the expression of both local and distal genes. EMBO Journal, 2014, 33, 296-311.	7.8	195
75	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. ELife, 2013, 2, e00348.	6.0	192
76	Comparison of the genomes of human and mouse lays the foundation of genome zoology. Human Molecular Genetics, 2003, 12, 701-709.	2.9	191
77	RBFOX and PTBP1 proteins regulate the alternative splicing of micro-exons in human brain transcripts. Genome Research, 2015, 25, 1-13.	5.5	187
78	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. Genome Biology, 2013, 14, R131.	9.6	183
79	Homology-based method for identification of protein repeats using statistical significance estimates. Journal of Molecular Biology, 2000, 298, 521-537.	4.2	176
80	EYS, encoding an ortholog of Drosophila spacemaker, is mutated in autosomal recessive retinitis pigmentosa. Nature Genetics, 2008, 40, 1285-1287.	21.4	175
81	Complexities of post-transcriptional regulation and the modeling of ceRNA crosstalk. Critical Reviews in Biochemistry and Molecular Biology, 2018, 53, 231-245.	5.2	175
82	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
83	Repo-Man Coordinates Chromosomal Reorganization with Nuclear Envelope Reassembly during Mitotic Exit. Developmental Cell, 2011, 21, 328-342.	7.0	172
84	High incidence of unrecognized visceral/neurological late-onset Niemann-Pick disease, type C1, predicted by analysis of massively parallel sequencing data sets. Genetics in Medicine, 2016, 18, 41-48.	2.4	171
85	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. Genome Biology, 2012, 13, R45.	9.6	170
86	Ki-67 is a PP1-interacting protein that organises the mitotic chromosome periphery. ELife, 2014, 3, e01641.	6.0	167
87	Elevated Rates of Protein Secretion, Evolution, and Disease Among Tissue-Specific Genes. Genome Research, 2003, 14, 54-61.	5.5	160
88	Identification of a novel family of presenilin homologues. Human Molecular Genetics, 2002, 11, 1037-1044.	2.9	157
89	Genome-Wide Identification of Human Functional DNA Using a Neutral Indel Model. PLoS Computational Biology, 2006, 2, e5.	3.2	157
90	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155

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91	TRAM, LAG1 and CLN8: members of a novel family of lipid-sensing domains?. Trends in Biochemical Sciences, 2002, 27, 381-383.	7.5	152
92	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. Genome Biology, 2012, 13, R26.	9.6	149
93	The long non-coding RNA Dali is an epigenetic regulator of neural differentiation. ELife, 2014, 3, e04530.	6.0	144
94	Separation and parallel sequencing of the genomes and transcriptomes of single cells using G&T-seq. Nature Protocols, 2016, 11, 2081-2103.	12.0	142
95	Foxn1 regulates key target genes essential for T cell development in postnatal thymic epithelial cells. Nature Immunology, 2016, 17, 1206-1215.	14.5	142
96	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. European Urology, 2014, 66, 32-39.	1.9	139
97	PIN domains in nonsense-mediated mRNA decay and RNAi. Current Biology, 2000, 10, R888-R890.	3.9	138
98	Vitamin K epoxide reductase: homology, active site and catalytic mechanism. Trends in Biochemical Sciences, 2004, 29, 289-292.	7.5	138
99	Regulation of DNA Replication through Sld3-Dpb11 Interaction Is Conserved from Yeast to Humans. Current Biology, 2011, 21, 1152-1157.	3.9	135
100	What fraction of the human genome is functional?. Genome Research, 2011, 21, 1769-1776.	5.5	134
101	Evolutionary rate analyses of orthologs and paralogs from 12 Drosophila genomes. Genome Research, 2007, 17, 1837-1849.	5.5	131
102	Phylogenetic Reconstruction of Orthology, Paralogy, and Conserved Synteny for Dog and Human. PLoS Computational Biology, 2006, 2, e133.	3.2	130
103	Diagnostically relevant facial gestalt information from ordinary photos. ELife, 2014, 3, e02020.	6.0	129
104	Proteins of the endoplasmic-reticulum-associated degradation pathway: domain detection and function prediction. Biochemical Journal, 2000, 351, 527-535.	3.7	122
105	Predicting long non-coding RNAs using RNA sequencing. Methods, 2013, 63, 50-59.	3.8	117
106	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. Genome Biology, 2004, 5, R47.	9.6	116
107	Death ofPRDM9coincides with stabilization of the recombination landscape in the dog genome. Genome Research, 2012, 22, 51-63.	5.5	116
108	Long noncoding RNAs in B-cell development and activation. Blood, 2016, 128, e10-e19.	1.4	115

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109	Occurrence and Consequences of Coding Sequence Insertions and Deletions in Mammalian Genomes. Genome Research, 2004, 14, 555-566.	5.5	114
110	Identification of distant homologues of fibroblast growth factors suggests a common ancestor for all Î²-trefoil proteins 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 302, 1041-1047.	4.2	111
111	A novel domain suggests a ciliary function for ASPM, a brain size determining gene. Bioinformatics, 2006, 22, 1031-1035.	4.1	107
112	Novel domains and orthologues of eukaryotic transcription elongation factors. Nucleic Acids Research, 2002, 30, 3643-3652.	14.5	101
113	The functional repertoires of metazoan genomes. Nature Reviews Genetics, 2008, 9, 689-698.	16.3	100
114	Predicting Protein Cellular Localization Using a Domain Projection Method. Genome Research, 2002, 12, 1168-1174.	5.5	97
115	Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. Genome Research, 2004, 14, 591-602.	5.5	97
116	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. Genome Research, 2015, 25, 655-666.	5.5	95
117	Mutations in CDC45 , Encoding an Essential Component of the Pre-initiation Complex, Cause Meier-Gorlin Syndrome and Craniosynostosis. American Journal of Human Genetics, 2016, 99, 125-138.	6.2	92
118	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. ELife, 2020, 9, .	6.0	92
119	Tuning the Transcriptional Response to Hypoxia by Inhibiting Hypoxia-inducible Factor (HIF) Prolyl and Asparaginyl Hydroxylases. Journal of Biological Chemistry, 2016, 291, 20661-20673.	3.4	91
120	Meisetz and the birth of the KRAB motif. Bioinformatics, 2006, 22, 2841-2845.	4.1	90
121	Intergenic lncRNAs and the evolution of gene expression. Current Opinion in Genetics and Development, 2014, 27, 48-53.	3.3	87
122	Novel eIF4G domain homologues linking mRNA translation with nonsense-mediated mRNA decay. Trends in Biochemical Sciences, 2000, 25, 423-426.	7.5	86
123	Massive turnover of functional sequence in human and other mammalian genomes. Genome Research, 2010, 20, 1335-1343.	5.5	86
124	Understanding functional miRNAâ€“target interactions in vivo by site-specific genome engineering. Nature Communications, 2014, 5, 4640.	12.8	86
125	Assessing similarity to primary tissue and cortical layer identity in induced pluripotent stem cell-derived cortical neurons through single-cell transcriptomics. Human Molecular Genetics, 2016, 25, 989-1000.	2.9	86
126	Evolution of domain families. Advances in Protein Chemistry, 2000, 54, 185-244.	4.4	81

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127	Chlamydial homologues of the MACPF (MAC/perforin) domain. Current Biology, 1999, 9, R911-R913.	3.9	79
128	Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. Genome Research, 2004, 14, 1516-1529.	5.5	79
129	Cross-talking noncoding RNAs contribute to cell-specific neurodegeneration in SCA7. Nature Structural and Molecular Biology, 2014, 21, 955-961.	8.2	79
130	Monoallelic and Biallelic Mutations in MAB21L2 Cause a Spectrum of Major Eye Malformations. American Journal of Human Genetics, 2014, 94, 915-923.	6.2	79
131	Evolution of primary microcephaly genes and the enlargement of primate brains. Current Opinion in Genetics and Development, 2005, 15, 241-248.	3.3	78
132	Adult pallium transcriptomes surprise in not reflecting predicted homologies across diverse chicken and mouse pallial sectors. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13150-13155.	7.1	77
133	Unexpected selection to retain high GC content and splicing enhancers within exons of multiexonic lncRNA loci. Rna, 2015, 21, 320-332.	3.5	76
134	Reduced purifying selection prevails over positive selection in human copy number variant evolution. Genome Research, 2008, 18, 1711-1723.	5.5	73
135	What are the genomic drivers of the rapid evolution of PRDM9?. Trends in Genetics, 2011, 27, 165-171.	6.7	73
136	Two Antarctic penguin genomes reveal insights into their evolutionary history and molecular changes related to the Antarctic environment. GigaScience, 2014, 3, 27.	6.4	72
137	Sialidase-like Asp-boxes: Sequence-similar structures within different protein folds. Protein Science, 2001, 10, 285-292.	7.6	70
138	Homology explains the functional similarities of Treslin/Ticrr and Sld3. Current Biology, 2010, 20, R509-R510.	3.9	69
139	A Code for RanGDP Binding in Ankyrin Repeats Defines a Nuclear Import Pathway. Cell, 2014, 157, 1130-1145.	28.9	67
140	An analysis of the gene complement of a marsupial, Monodelphis domestica: Evolution of lineage-specific genes and giant chromosomes. Genome Research, 2007, 17, 969-981.	5.5	66
141	CGAT: computational genomics analysis toolkit. Bioinformatics, 2014, 30, 1290-1291.	4.1	65
142	Single cell RNA-seq reveals profound transcriptional similarity between Barrettâ€™s oesophagus and oesophageal submucosal glands. Nature Communications, 2018, 9, 4261.	12.8	65
143	Cytoplasmic signalling domains: the next generation. Trends in Biochemical Sciences, 1997, 22, 296-298.	7.5	64
144	Duplication and positive selection among hominin-specific PRAME genes. BMC Genomics, 2005, 6, 120.	2.8	64

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145	Temporal transcriptomics suggest that twin-peaking genes reset the clock. ELife, 2015, 4, .	6.0	64
146	Biologically indeterminate yet ordered promiscuous gene expression in single medullary thymic epithelial cells. EMBO Journal, 2020, 39, e101828.	7.8	63
147	Mutations within lncRNAs are effectively selected against in fruitfly but not in human. Genome Biology, 2013, 14, R49.	9.6	62
148	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. Genome Biology, 2012, 13, R102.	9.6	61
149	Protein families in multicellular organisms. Current Opinion in Structural Biology, 1999, 9, 408-415.	5.7	58
150	Cadherin-like domains in Î±-dystroglycan, Î±/Îµ-sarcoglycan and yeast and bacterial proteins. Current Biology, 2002, 12, R197-R199.	3.9	58
151	Dynamic spatioâ€temporal contribution of single Î²5t+ cortical epithelial precursors to the thymus medulla. European Journal of Immunology, 2016, 46, 846-856.	2.9	56
152	Domain homologues of dopamine beta-hydroxylase and ferric reductase: roles for iron metabolism in neurodegenerative disorders?. Human Molecular Genetics, 2001, 10, 1853-1858.	2.9	54
153	Genome-Wide Analysis of Human Long Noncoding RNAs: A Provocative Review. Annual Review of Genomics and Human Genetics, 2022, 23, 153-172.	6.2	53
154	Identification and function of long non-coding RNAs. Essays in Biochemistry, 2013, 54, 113-126.	4.7	50
155	TM6SF2 and MAC30, new enzyme homologs in sterol metabolism and common metabolic disease. Frontiers in Genetics, 2014, 5, 439.	2.3	50
156	Protein fold irregularities that hinder sequence analysis. Current Opinion in Structural Biology, 1998, 8, 364-371.	5.7	48
157	Hotspots of mutation and breakage in dog and human chromosomes. Genome Research, 2005, 15, 1787-1797.	5.5	47
158	Microglia recapitulate a hematopoietic master regulator network inÂthe aging human frontal cortex. Neurobiology of Aging, 2015, 36, 2443.e9-2443.e20.	3.1	46
159	Signatures of adaptive evolution within human non-coding sequence. Human Molecular Genetics, 2006, 15, R170-R175.	2.9	45
160	The long nonâ€coding <scp>RNA</scp> Paupar promotes <scp>KAP</scp> 1â€dependent chromatin changes and regulatesÂolfactory bulb neurogenesis. EMBO Journal, 2018, 37, .	7.8	45
161	Genome assembly quality: Assessment and improvement using the neutral indel model. Genome Research, 2010, 20, 675-684.	5.5	44
162	Transcriptional dynamics of pluripotent stem cell-derived endothelial cell differentiation revealed by single-cell RNA sequencing. European Heart Journal, 2020, 41, 1024-1036.	2.2	43

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163	The long non-coding RNA Cerox1 is a post transcriptional regulator of mitochondrial complex I catalytic activity. ELife, 2019, 8, .	6.0	42
164	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. BMC Evolutionary Biology, 2008, 8, 46.	3.2	41
165	More than 1,000 putative new human signalling proteins revealed by EST data mining. Nature Genetics, 2000, 25, 201-204.	21.4	40
166	Forging Links between Human Mental Retardationâ€“Associated CNVs and Mouse Gene Knockout Models. PLoS Genetics, 2009, 5, e1000531.	3.5	40
167	Biological function in the twilight zone of sequence conservation. BMC Biology, 2017, 15, 71.	3.8	40
168	Insights into the evolution of Darwinâ€™s finches from comparative analysis of the Geospiza magnirostris genome sequence. BMC Genomics, 2013, 14, 95.	2.8	38
169	TMEM132: an ancient architecture of cohesin and immunoglobulin domains define a new family of neural adhesion molecules. Bioinformatics, 2018, 34, 721-724.	4.1	38
170	Zebrafish MITF-Low Melanoma Subtype Models Reveal Transcriptional Subclusters and MITF-Independent Residual Disease. Cancer Research, 2019, 79, 5769-5784.	0.9	36
171	Vasohibins: new transglutaminase-like cysteine proteases possessing a non-canonical Cys-His-Ser catalytic triad. Bioinformatics, 2016, 32, 1441-1445.	4.1	35
172	The phenotypic spectrum of Xiaâ€Gibbs syndrome. American Journal of Medical Genetics, Part A, 2018, 176, 1315-1326.	1.2	34
173	Eukaryotic domain evolution inferred from genome comparisons. Current Opinion in Genetics and Development, 2003, 13, 623-628.	3.3	33
174	The Cdk8/19-cyclin C transcription regulator functions in genome replication through metazoan Sld7. PLoS Biology, 2019, 17, e2006767.	5.6	32
175	Sequence variation and disease in the wake of the draft human genome. Human Molecular Genetics, 2001, 10, 2209-2214.	2.9	30
176	Disruption ofVisc-2, a Brain-Expressed Conserved Long Noncoding RNA, Does Not Elicit an Overt Anatomical or Behavioral Phenotype. Cerebral Cortex, 2015, 25, 3572-3585.	2.9	30
177	Identification of functional long non-coding RNAs in C. elegans. BMC Biology, 2019, 17, 14.	3.8	30
178	The long and the short of RNA maps. BioEssays, 2007, 29, 1077-1080.	2.5	29
179	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. PLoS Genetics, 2020, 16, e1008785.	3.5	29
180	Cofilin-1: A Modulator of Anxiety in Mice. PLoS Genetics, 2012, 8, e1002970.	3.5	28

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181	Diverse spatial, temporal, and sexual expression of recently duplicated androgen-binding protein genes in Mus musculus. BMC Evolutionary Biology, 2005, 5, 40.	3.2	27
182	Wrangling for microRNAs provokes much crosstalk. Genome Biology, 2011, 12, 132.	9.6	27
183	Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease. Human Molecular Genetics, 2017, 26, 2164-2176.	2.9	27
184	Mammalian BEX, WEX and GASP genes: coding and non-coding chimaerism sustained by gene conversion events. BMC Evolutionary Biology, 2005, 5, 54.	3.2	26
185	Genetic risk factors of ME/CFS: a critical review. Human Molecular Genetics, 2020, 29, R117-R124.	2.9	24
186	Mapping the developing human cardiac endothelium at single-cell resolution identifies MECOM as a regulator of arteriovenous gene expression. Cardiovascular Research, 2022, 118, 2960-2972.	3.8	24
187	OPTIC: orthologous and paralogous transcripts in clades. Nucleic Acids Research, 2007, 36, D267-D270.	14.5	23
188	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	3.8	22
189	Rapid Turnover of Functional Sequence in Human and Other Genomes. Annual Review of Genomics and Human Genetics, 2011, 12, 275-299.	6.2	21
190	Insights into the post-transcriptional regulation of the mitochondrial electron transport chain. Biochemical Society Transactions, 2016, 44, 1491-1498.	3.4	21
191	A beta-propeller domain within TolB. Molecular Microbiology, 1999, 31, 739-740.	2.5	20
192	No Gene in the Genome Makes Sense Except in the Light of Evolution. Annual Review of Genomics and Human Genetics, 2014, 15, 71-92.	6.2	19
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