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	Citrullination Was Introduced into Animals by Horizontal Gene Transfer from Cyanobacteria. Molecular Biology and Evolution, 2022, 39, .	8.9	16
2	Refining the domain architecture model of the replication origin firing factor Treslin/TICRR. Life Science Alliance, 2022, 5, e202101088.	2.8	7
3	PERCC1, a new member of theYap/TAZ/FAM181transcriptional co-regulator family. Bioinformatics Advances, 2022, 2, .	2.4	2
4	Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human Genetics, 2022, 141, 147-173.	3.8	22
5	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
6	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
7	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
8	The genetics of ME: A commentary on Hajdarevic et al.. Brain, Behavior, and Immunity, 2022, 104, 181-182.	4.1	0
9	DecodeME: community recruitment for a large genetics study of myalgic encephalomyelitis / chronic fatigue syndrome. BMC Neurology, 2022, 22, .	1.8	6
10	Extending the Horizon of Homology Detection with Coevolution-based Structure Prediction. Journal of Molecular Biology, 2021, 433, 167106.	4.2	7
11	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
12	Hexa-Longin domain scaffolds for inter-Rab signalling. Bioinformatics, 2020, 36, 990-993.	4.1	5
13	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
14	Genetics Needs Non-geneticists. Trends in Genetics, 2020, 36, 629-630.	6.7	0
15	Genetic risk factors of ME/CFS: a critical review. Human Molecular Genetics, 2020, 29, R117-R124.	2.9	24
16	Identification of region-specific astrocyte subtypes at single cell resolution. Nature Communications, 2020, 11, 1220.	12.8	444
17	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
18	Biologically indeterminate yet ordered promiscuous gene expression in single medullary thymic epithelial cells. EMBO Journal, 2020, 39, e101828.	7.8	63

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19	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. ELife, 2020, 9, .	6.0	92
20	Single-Cell Transcriptomics Uncovers Zonation of Function in the Mesenchyme during Liver Fibrosis. Cell Reports, 2019, 29, 1832-1847.e8.	6.4	261
21	Zebrafish MITF-Low Melanoma Subtype Models Reveal Transcriptional Subclusters and MITF-Independent Residual Disease. Cancer Research, 2019, 79, 5769-5784.	0.9	36
22	The Human Cell Atlas: making â€˜cell spaceâ€™ for disease. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	9
23	A gene expression signature in developing Purkinje cells predicts autism and intellectual disability co-morbidity status. Scientific Reports, 2019, 9, 485.	3.3	14
24	The Cdk8/19-cyclin C transcription regulator functions in genome replication through metazoan Sld7. PLoS Biology, 2019, 17, e2006767.	5.6	32
25	Identification of functional long non-coding RNAs in C. elegans. BMC Biology, 2019, 17, 14.	3.8	30
26	The long non-coding RNA Cerox1 is a post transcriptional regulator of mitochondrial complex I catalytic activity. ELife, 2019, 8, .	6.0	42
27	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
28	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
29	The phenotypic spectrum of Xiaâ€Gibbs syndrome. American Journal of Medical Genetics, Part A, 2018, 176, 1315-1326.	1.2	34
30	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
31	Comprehensively Profiling the Chromatin Architecture of Tissue Restricted Antigen Expression in Thymic Epithelial Cells Over Development. Frontiers in Immunology, 2018, 9, 2120.	4.8	17
32	Single cell RNA-seq reveals profound transcriptional similarity between Barrettâ€™s oesophagus and oesophageal submucosal glands. Nature Communications, 2018, 9, 4261.	12.8	65
33	Single-Cell Multiomics: Multiple Measurements from Single Cells. Trends in Genetics, 2017, 33, 155-168.	6.7	392
34	Identification of genetic variants affecting vitamin D receptor binding and associations with autoimmune disease. Human Molecular Genetics, 2017, 26, 2164-2176.	2.9	27
35	Functional RNA classes: a matter of time?. Nature Structural and Molecular Biology, 2017, 24, 7-8.	8.2	4
36	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547

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37	Biological function in the twilight zone of sequence conservation. BMC Biology, 2017, 15, 71.	3.8	40
38	Big knowledge from big data in functional genomics. Emerging Topics in Life Sciences, 2017, 1, 245-248.	2.6	4
39	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
40	Insights into the post-transcriptional regulation of the mitochondrial electron transport chain. Biochemical Society Transactions, 2016, 44, 1491-1498.	3.4	21
41	Vasohibins: new transglutaminase-like cysteine proteases possessing a non-canonical Cys-His-Ser catalytic triad. Bioinformatics, 2016, 32, 1441-1445.	4.1	35
42	Long noncoding RNAs in B-cell development and activation. Blood, 2016, 128, e10-e19.	1.4	115
43	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
44	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
45	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
46	Foxn1 regulates key target genes essential for T cell development in postnatal thymic epithelial cells. Nature Immunology, 2016, 17, 1206-1215.	14.5	142
47	The role of ADP-ribosylation in regulating DNA interstrand crosslink repair. Journal of Cell Science, 2016, 129, 3845-3858.	2.0	15
48	Identification of molecular signatures specific for distinct cranial sensory ganglia in the developing chick. Neural Development, 2016, 11, 3.	2.4	18
49	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
50	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. Nature Methods, 2016, 13, 229-232.	19.0	602
51	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
52	An open and transparent process to select ELIXIR Node Services as implemented by ELIXIR-UK. F1000Research, 2016, 5, 2894.	1.6	6
53	Temporal transcriptomics suggest that twin-peaking genes reset the clock. ELife, 2015, 4, .	6.0	64
54	Unexpected selection to retain high GC content and splicing enhancers within exons of multiexonic lncRNA loci. Rna, 2015, 21, 320-332.	3.5	76

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55	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	11.1	376
56	CGAT: a model for immersive personalized training in computational genomics. Briefings in Functional Genomics, 2015, 15, 32-7.	2.7	4
57	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
58	RBFOX and PTBP1 proteins regulate the alternative splicing of micro-exons in human brain transcripts. Genome Research, 2015, 25, 1-13.	5.5	187
59	Microglia recapitulate a hematopoietic master regulator network inÂthe aging human frontal cortex. Neurobiology of Aging, 2015, 36, 2443.e9-2443.e20.	3.1	46
60	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. Nature Methods, 2015, 12, 519-522.	19.0	633
61	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. Genome Research, 2015, 25, 655-666.	5.5	95
62	Violation of the 12/23 rule of genomic V(D)J recombination is common in lymphocytes. Genome Research, 2015, 25, 226-234.	5.5	2
63	REC-1 and HIM-5 distribute meiotic crossovers and function redundantly in meiotic double-strand break formation in Caenorhabditis elegans. Genes and Development, 2015, 29, 1969-1979.	5.9	19
64	Diagnostically relevant facial gestalt information from ordinary photos. ELife, 2014, 3, e02020.	6.0	129
65	Brain-expressed 3â€²UTR extensions strengthen miRNA cross-talk between ion channel/transporter encoding mRNAs. Frontiers in Genetics, 2014, 5, 41.	2.3	16
66	TM6SF2 and MAC30, new enzyme homologs in sterol metabolism and common metabolic disease. Frontiers in Genetics, 2014, 5, 439.	2.3	50
67	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
68	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
69	Understanding functional miRNAâ€“target interactions in vivo by site-specific genome engineering. Nature Communications, 2014, 5, 4640.	12.8	86
70	The RNA-Editing Enzyme ADAR1 Controls Innate Immune Responses to RNA. Cell Reports, 2014, 9, 1482-1494.	6.4	508
71	CGAT: computational genomics analysis toolkit. Bioinformatics, 2014, 30, 1290-1291.	4.1	65
72	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

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73	The long non-coding RNA Paupar regulates the expression of both local and distal genes. EMBO Journal, 2014, 33, 296-311.	7.8	195
74	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
75	Sequencing depth and coverage: key considerations in genomic analyses. Nature Reviews Genetics, 2014, 15, 121-132.	16.3	1,116
76	Cross-talking noncoding RNAs contribute to cell-specific neurodegeneration in SCA7. Nature Structural and Molecular Biology, 2014, 21, 955-961.	8.2	79
77	Transcriptional regulatory functions of nuclear long noncoding RNAs. Trends in Genetics, 2014, 30, 348-355.	6.7	381
78	The genomic substrate for adaptive radiation in African cichlid fish. Nature, 2014, 513, 375-381.	27.8	874
79	Next-generation Sequencing of Advanced Prostate Cancer Treated with Androgen-deprivation Therapy. European Urology, 2014, 66, 32-39.	1.9	139
80	A Code for RanGDP Binding in Ankyrin Repeats Defines a Nuclear Import Pathway. Cell, 2014, 157, 1130-1145.	28.9	67
81	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
82	Intergenic lncRNAs and the evolution of gene expression. Current Opinion in Genetics and Development, 2014, 27, 48-53.	3.3	87
83	Considerations when investigating lncRNA function in vivo. ELife, 2014, 3, e03058.	6.0	309
84	The long non-coding RNA Dali is an epigenetic regulator of neural differentiation. ELife, 2014, 3, e04530.	6.0	144
85	The RFTS Domain of Raf2 Is Required for Cul4 Interaction and Heterochromatin Integrity in Fission Yeast. PLoS ONE, 2014, 9, e104161.	2.5	5
86	Ki-67 is a PP1-interacting protein that organises the mitotic chromosome periphery. ELife, 2014, 3, e01641.	6.0	167
87	Mutations within lncRNAs are effectively selected against in fruitfly but not in human. Genome Biology, 2013, 14, R49.	9.6	62
88	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
89	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
90	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	27.8	612

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91	Predicting long non-coding RNAs using RNA sequencing. Methods, 2013, 63, 50-59.	3.8	117
92	Identification and function of long non-coding RNAs. Essays in Biochemistry, 2013, 54, 113-126.	4.7	50
93	GAT: a simulation framework for testing the association of genomic intervals. Bioinformatics, 2013, 29, 2046-2048.	4.1	221
94	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
95	Epigenetic conservation at gene regulatory elements revealed by non-methylated DNA profiling in seven vertebrates. ELife, 2013, 2, e00348.	6.0	192
96	Cofilin-1: A Modulator of Anxiety in Mice. PLoS Genetics, 2012, 8, e1002970.	3.5	28
97	Rapid Turnover of Long Noncoding RNAs and the Evolution of Gene Expression. PLoS Genetics, 2012, 8, e1002841.	3.5	284
98	Death ofPRDM9coincides with stabilization of the recombination landscape in the dog genome. Genome Research, 2012, 22, 51-63.	5.5	116
99	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
100	KDM2B links the Polycomb Repressive Complex 1 (PRC1) to recognition of CpG islands. ELife, 2012, 1, e00205.	6.0	414
101	Evidence for conserved post-transcriptional roles of unitary pseudogenes and for frequent bifunctionality of mRNAs. Genome Biology, 2012, 13, R102.	9.6	61
102	High levels of RNA-editing site conservation amongst 15 laboratory mouse strains. Genome Biology, 2012, 13, R26.	9.6	149
103	The genomic landscape shaped by selection on transposable elements across 18 mouse strains. Genome Biology, 2012, 13, R45.	9.6	170
104	Loaded Dice for Human Genome Mutation. Cell, 2012, 151, 1399-1400.	28.9	3
105	Brain, Know Thy Transcriptome, Know Thyself. Neuron, 2012, 75, 543-545.	8.1	3
106	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	27.8	445
107	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	27.8	663
108	Wrangling for microRNAs provokes much crosstalk. Genome Biology, 2011, 12, 132.	9.6	27

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109	The genome of the green anole lizard and a comparative analysis with birds and mammals. Nature, 2011, 477, 587-591.	27.8	575
110	Rapid Turnover of Functional Sequence in Human and Other Genomes. Annual Review of Genomics and Human Genetics, 2011, 12, 275-299.	6.2	21
111	Repo-Man Coordinates Chromosomal Reorganization with Nuclear Envelope Reassembly during Mitotic Exit. Developmental Cell, 2011, 21, 328-342.	7.0	172
112	A Transcriptomic Atlas of Mouse Neocortical Layers. Neuron, 2011, 71, 605-616.	8.1	266
113	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	27.8	1,461
114	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	27.8	541
115	What are the genomic drivers of the rapid evolution of PRDM9?. Trends in Genetics, 2011, 27, 165-171.	6.7	73
116	Regulation of DNA Replication through Sld3-Dpb11 Interaction Is Conserved from Yeast to Humans. Current Biology, 2011, 21, 1152-1157.	3.9	135
117	What fraction of the human genome is functional?. Genome Research, 2011, 21, 1769-1776.	5.5	134
118	Natural genetic variation caused by small insertions and deletions in the human genome. Genome Research, 2011, 21, 830-839.	5.5	212
119	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	5.6	380
120	Homology explains the functional similarities of Treslin/Ticrr and Sld3. Current Biology, 2010, 20, R509-R510.	3.9	69
121	The genome of a songbird. Nature, 2010, 464, 757-762.	27.8	770
122	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
123	Transcribed dark matter: meaning or myth?. Human Molecular Genetics, 2010, 19, R162-R168.	2.9	253
124	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
125	Accelerated Evolution of PAK3- and PIM1-like Kinase Gene Families in the Zebra Finch, Taeniopygia guttata. Molecular Biology and Evolution, 2010, 27, 1923-1934.	8.9	12
126	Genome assembly quality: Assessment and improvement using the neutral indel model. Genome Research, 2010, 20, 675-684.	5.5	44

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127	Massive turnover of functional sequence in human and other mammalian genomes. Genome Research, 2010, 20, 1335-1343.	5.5	86
128	Stc1: A Critical Link between RNAi and Chromatin Modification Required for Heterochromatin Integrity. Cell, 2010, 140, 666-677.	28.9	195
129	The Protein Composition of Mitotic Chromosomes Determined Using Multiclassifier Combinatorial Proteomics. Cell, 2010, 142, 810-821.	28.9	266
130	Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes. Genome Biology, 2010, 11, R72.	9.6	215
131	Accurate Estimation of Gene Evolutionary Rates Using XRATE, with an Application to Transmembrane Proteins. Molecular Biology and Evolution, 2009, 26, 1715-1721.	8.9	9
132	Lineage-Specific Biology Revealed by a Finished Genome Assembly of the Mouse. PLoS Biology, 2009, 7, e1000112.	5.6	419
133	Forging Links between Human Mental Retardationâ€“Associated CNVs and Mouse Gene Knockout Models. PLoS Genetics, 2009, 5, e1000531.	3.5	40
134	Accelerated Evolution of the Prdm9 Speciation Gene across Diverse Metazoan Taxa. PLoS Genetics, 2009, 5, e1000753.	3.5	256
135	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
136	Evolution and Functions of Long Noncoding RNAs. Cell, 2009, 136, 629-641.	28.9	4,480
137	Coordination of Structure-Specific Nucleases by Human SLX4/BTBD12 Is Required for DNA Repair. Molecular Cell, 2009, 35, 116-127.	9.7	300
138	Catalogues of mammalian long noncoding RNAs: modest conservation and incompleteness. Genome Biology, 2009, 10, R124.	9.6	232
139	Separating derived from ancestral features of mouse and human genomes. Biochemical Society Transactions, 2009, 37, 734-739.	3.4	13
140	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
141	Genome analysis of the platypus reveals unique signatures of evolution. Nature, 2008, 453, 175-183.	27.8	657
142	EYS, encoding an ortholog of Drosophila spacemaker, is mutated in autosomal recessive retinitis pigmentosa. Nature Genetics, 2008, 40, 1285-1287.	21.4	175
143	The functional repertoires of metazoan genomes. Nature Reviews Genetics, 2008, 9, 689-698.	16.3	100
144	Rapid bursts of androgen-binding protein (Abp) gene duplication occurred independently in diverse mammals. BMC Evolutionary Biology, 2008, 8, 46.	3.2	41

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145	Reduced purifying selection prevails over positive selection in human copy number variant evolution. Genome Research, 2008, 18, 1711-1723.	5.5	73
146	OPTIC: orthologous and paralogous transcripts in clades. Nucleic Acids Research, 2007, 36, D267-D270.	14.5	23
147	Functionality or transcriptional noise? Evidence for selection within long noncoding RNAs. Genome Research, 2007, 17, 556-565.	5.5	632
148	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
149	Evolutionary rate analyses of orthologs and paralogs from 12 Drosophila genomes. Genome Research, 2007, 17, 1837-1849.	5.5	131
150	The Obesity-AssociatedFTOGene Encodes a 2-Oxoglutarate-Dependent Nucleic Acid Demethylase. Science, 2007, 318, 1469-1472.	12.6	1,305
151	The long and the short of RNA maps. BioEssays, 2007, 29, 1077-1080.	2.5	29
152	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
153	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
154	Signatures of adaptive evolution within human non-coding sequence. Human Molecular Genetics, 2006, 15, R170-R175.	2.9	45
155	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
156	Human brain gene wins genome race. Nature, 2006, 443, 149-150.	27.8	9
157	A novel domain suggests a ciliary function for ASPM, a brain size determining gene. Bioinformatics, 2006, 22, 1031-1035.	4.1	107
158	Meisetz and the birth of the KRAB motif. Bioinformatics, 2006, 22, 2841-2845.	4.1	90
159	Genome-Wide Identification of Human Functional DNA Using a Neutral Indel Model. PLoS Computational Biology, 2006, 2, e5.	3.2	157
160	Bias of Selection on Human Copy-Number Variants. PLoS Genetics, 2006, 2, e20.	3.5	237
161	Phylogenetic Reconstruction of Orthology, Paralogy, and Conserved Synteny for Dog and Human. PLoS Computational Biology, 2006, 2, e133.	3.2	130
162	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215

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163	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
164	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
165	Duplication and positive selection among hominin-specific PRAME genes. BMC Genomics, 2005, 6, 120.	2.8	64
166	Hotspots of mutation and breakage in dog and human chromosomes. Genome Research, 2005, 15, 1787-1797.	5.5	47
167	Evolution of primary microcephaly genes and the enlargement of primate brains. Current Opinion in Genetics and Development, 2005, 15, 241-248.	3.3	78
168	Comparative Evolutionary Genomics of Androgen-Binding Protein Genes. Genome Research, 2004, 14, 1516-1529.	5.5	79
169	Occurrence and Consequences of Coding Sequence Insertions and Deletions in Mammalian Genomes. Genome Research, 2004, 14, 555-566.	5.5	114
170	Evolution and Comparative Genomics of Odorant- and Pheromone-Associated Genes in Rodents. Genome Research, 2004, 14, 591-602.	5.5	97
171	SMART 4.0: towards genomic data integration. Nucleic Acids Research, 2004, 32, 142D-144.	14.5	892
172	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	27.8	1,943
173	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004, 432, 717-722.	27.8	391
174	Vitamin K epoxide reductase: homology, active site and catalytic mechanism. Trends in Biochemical Sciences, 2004, 29, 289-292.	7.5	138
175	Evolutionary conservation and selection of human disease gene orthologs in the rat and mouse genomes. Genome Biology, 2004, 5, R47.	9.6	116
176	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
177	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
178	Positional cloning of a novel gene influencing asthma from Chromosome 2q14. Nature Genetics, 2003, 35, 258-263.	21.4	326
179	Eukaryotic domain evolution inferred from genome comparisons. Current Opinion in Genetics and Development, 2003, 13, 623-628.	3.3	33
180	EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. Cell, 2003, 115, 523-535.	28.9	389

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181	THoR: a tool for domain discovery and curation of multiple alignments. Genome Biology, 2003, 4, R52.	9.6	3
182	A coming of age for bioinformatics. Journal of Cell Science, 2003, 116, 6-7.	2.0	1
183	Elevated Rates of Protein Secretion, Evolution, and Disease Among Tissue-Specific Genes. Genome Research, 2003, 14, 54-61.	5.5	160
184	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	14.5	640
185	Comparison of the genomes of human and mouse lays the foundation of genome zoology. Human Molecular Genetics, 2003, 12, 701-709.	2.9	191
186	Systematic Identification of Novel Protein Domain Families Associated with Nuclear Functions. Genome Research, 2002, 12, 47-56.	5.5	527
187	Novel domains and orthologues of eukaryotic transcription elongation factors. Nucleic Acids Research, 2002, 30, 3643-3652.	14.5	101
188	Recent improvements to the SMART domain-based sequence annotation resource. Nucleic Acids Research, 2002, 30, 242-244.	14.5	613
189	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155
190	Identification of a novel family of presenilin homologues. Human Molecular Genetics, 2002, 11, 1037-1044.	2.9	157
191	Predicting Protein Cellular Localization Using a Domain Projection Method. Genome Research, 2002, 12, 1168-1174.	5.5	97
192	Sequence analysis of multidomain proteins: Past perspectives and future directions. Advances in Protein Chemistry, 2002, 61, 75-98.	4.4	15
193	The Natural History of Protein Domains. Annual Review of Biophysics and Biomolecular Structure, 2002, 31, 45-71.	18.3	286
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