Martin S Taylor

List of Publications by Year
in descending order

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75	16,427	87843 38	76872 74
papers	citations	h-index	g-index

89	89	89	25390
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Transcriptional Landscape of the Mammalian Genome. Science, 2005, 309, 1559-1563.	6.0	3,227
2	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
3	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
4	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. Nature, 2002, 420, 563-573.	13.7	1,548
5	Genome-wide analysis of mammalian promoter architecture and evolution. Nature Genetics, 2006, 38, 626-635.	9.4	1,201
6	Disruption of two novel genes by a translocation co-segregating with schizophrenia. Human Molecular Genetics, 2000, 9, 1415-1423.	1.4	1,135
7	Genome-wide genetic association of complex traits in heterogeneous stock mice. Nature Genetics, 2006, 38, 879-887.	9.4	508
8	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. Nature Genetics, 2009, 41, 553-562.	9.4	408
9	Enzymatic Removal of Ribonucleotides from DNA Is Essential for Mammalian Genome Integrity and Development. Cell, 2012, 149, 1008-1022.	13.5	397
10	Conservation and divergence in Toll-like receptor 4-regulated gene expression in primary human versus mouse macrophages. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E944-53.	3.3	332
11	A High-Resolution Single Nucleotide Polymorphism Genetic Map of the Mouse Genome. PLoS Biology, 2006, 4, e395.	2.6	243
12	Lagging-strand replication shapes the mutational landscape of the genome. Nature, 2015, 518, 502-506.	13.7	213
13	CEP152 is a genome maintenance protein disrupted in Seckel syndrome. Nature Genetics, 2011, 43, 23-26.	9.4	201
14	Variant detection sensitivity and biases in whole genome and exome sequencing. BMC Bioinformatics, 2014, 15, 247.	1.2	197
15	Identification of a new gene mutated in Fraser syndrome and mouse myelencephalic blebs. Nature Genetics, 2005, 37, 520-525.	9.4	148
16	Genetic heterogeneity in Cornelia de Lange syndrome (CdLS) and CdLS-like phenotypes with observed and predicted levels of mosaicism. Journal of Medical Genetics, 2014, 51, 659-668.	1.5	141
17	The structure and evolution of the melanocortin and MCH receptors in fish and mammals. Genomics, 2003, 81, 184-191.	1.3	139
18	Identification of Common Genetic Variation That Modulates Alternative Splicing. PLoS Genetics, 2007, 3, e99.	1.5	139

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19	Genetic Analysis of Pathways Regulated by the von Hippel-Lindau Tumor Suppressor in Caenorhabditis elegans. PLoS Biology, 2004, 2, e289.	2.6	137
20	Characterization and comparative analysis of the EGLN gene family. Gene, 2001, 275, 125-132.	1.0	130
21	Occurrence and Consequences of Coding Sequence Insertions and Deletions in Mammalian Genomes. Genome Research, 2004, 14, 555-566.	2.4	114
22	Development and evaluation of a real-time PCR assay for detection of Pneumocystis jirovecii DNA in bronchoalveolar lavage fluid of HIV-infected patients. Thorax, 2007, 63, 154-159.	2.7	110
23	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	2.4	109
24	The extracellular matrix gene Frem1 is essential for the normal adhesion of the embryonic epidermis. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13560-13565.	3.3	108
25	Evolution of the human-specific microRNA miR-941. Nature Communications, 2012, 3, 1145.	5.8	103
26	Heterotachy in Mammalian Promoter Evolution. PLoS Genetics, 2006, 2, e30.	1.5	102
27	Heterozygous Loss-of-Function Mutations in YAP1 Cause Both Isolated and Syndromic Optic Fissure Closure Defects. American Journal of Human Genetics, 2014, 94, 295-302.	2.6	93
28	Evolutionary constraints on the Disrupted in Schizophrenia locus. Genomics, 2003, 81, 67-77.	1.3	83
29	Monoallelic and Biallelic Mutations in MAB21L2 Cause a Spectrum of Major Eye Malformations. American Journal of Human Genetics, 2014, 94, 915-923.	2.6	79
30	Mutational Biases Drive Elevated Rates of Substitution at Regulatory Sites across Cancer Types. PLoS Genetics, 2016, 12, e1006207.	1.5	75
31	Quantifying single nucleotide variant detection sensitivity in exome sequencing. BMC Bioinformatics, 2013, 14, 195.	1.2	74
32	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. Genome Research, 2009, 19, 1133-1140.	2.4	69
33	Pervasive haplotypic variation in the spliceo-transcriptome of the human major histocompatibility complex. Genome Research, 2011, 21, 1042-1054.	2.4	63
34	Codon Usage and Splicing Jointly Influence mRNA Localization. Cell Systems, 2020, 10, 351-362.e8.	2.9	61
35	Interaction of the Anaphase-promoting Complex/Cyclosome and Proteasome Protein Complexes with Multiubiquitin Chain-binding Proteins. Journal of Biological Chemistry, 2003, 278, 16791-16796.	1.6	60
36	Application of next generation qPCR and sequencing platforms to mRNA biomarker analysis. Methods, 2013, 59, 89-100.	1.9	55

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37	The frequent evolutionary birth and death of functional promoters in mouse and human. Genome Research, 2015, 25, 1546-1557.	2.4	55
38	Bidirectional transcription initiation marks accessible chromatin and is not specific to enhancers. Genome Biology, 2017, 18, 242.	3.8	52
39	Aberrant ribonucleotide incorporation and multiple deletions in mitochondrial DNA of the murine MPV17 disease model. Nucleic Acids Research, 2017, 45, 12808-12815.	6.5	43
40	Genome-wide mapping of embedded ribonucleotides and other noncanonical nucleotides using emRiboSeq and EndoSeq. Nature Protocols, 2015, 10, 1433-1444.	5.5	42
41	FRA2A Is a CGG Repeat Expansion Associated with Silencing of AFF3. PLoS Genetics, 2014, 10, e1004242.	1.5	41
42	Quantification of epigenetic biomarkers: an evaluation of established and emerging methods for DNA methylation analysis. BMC Genomics, 2014, 15, 1174.	1.2	40
43	Singleton SNPs in the human genome and implications for genome-wide association studies. European Journal of Human Genetics, 2008, 16, 506-515.	1.4	39
44	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. Nature, 2022, 602, 623-631.	13.7	38
45	Identification of a localized nonsense-mediated decay pathway at the endoplasmic reticulum. Genes and Development, 2020, 34, 1075-1088.	2.7	37
46	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
47	Sequence Characterization of Teleost Fish Melanocortin Receptors. Annals of the New York Academy of Sciences, 2003, 994, 319-330.	1.8	30
48	Genomic anatomy of the Tyrp1 (brown) deletion complex. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 3704-3709.	3.3	30
49	Comparative transcriptomics of primary cells in vertebrates. Genome Research, 2020, 30, 951-961.	2.4	29
50	A CGG-Repeat Expansion Mutation inZNF713Causes FRA7A: Association with Autistic Spectrum Disorder in two Families. Human Mutation, 2014, 35, n/a-n/a.	1.1	28
51	The severe G480C cystic fibrosis mutation, when replicated in the mouse, demonstrates mistrafficking, normal survival and organ-specific bioelectrics. Human Molecular Genetics, 2002, 11, 243-251.	1.4	27
52	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	1.4	27
53	Genomic Sequence Analysis of Fugu rubripes CFTR and Flanking Genes in a 60 kb Region Conserving Synteny with 800 kb of Human Chromosome 7. Genome Research, 2000, 10, 1194-1203.	2.4	26
54	Dynamic and Physical Clustering of Gene Expression during Epidermal Barrier Formation in Differentiating Keratinocytes. PLoS ONE, 2009, 4, e7651.	1.1	26

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55	Expression of the fras1/frem gene family during zebrafish development and fin morphogenesis. Developmental Dynamics, 2008, 237, 3295-3304.	0.8	20
56	Loss of <scp>ALDH</scp>18A1 function is associated with a cellular lipid droplet phenotype suggesting a link between autosomal recessive cutis laxa type 3A and Warburg Micro syndrome. Molecular Genetics & Genomic Medicine, 2014, 2, 319-325.	0.6	19
57	Rapidly evolving human promoter regions. Nature Genetics, 2008, 40, 1262-1263.	9.4	18
58	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	1.5	17
59	The (non)malignancy of cancerous amino acidic substitutions. Proteins: Structure, Function and Bioinformatics, 2010, 78, 518-529.	1.5	15
60	SuRFing the genomics wave: an R package for prioritising SNPs by functionality. Genome Medicine, 2014, 6, 79.	3.6	15
61	Isolation and characterization of the mouse translin-associated protein X (Trax) gene. Mammalian Genome, 2000, 11, 395-398.	1.0	12
62	Manipulation of Dipeptidylpeptidase 10 in mouse and human in vivo and in vitro models indicates a protective role in asthma. DMM Disease Models and Mechanisms, 2018, 11, .	1.2	11
63	In Vivo Modeling of Patient Genetic Heterogeneity Identifies New Ways to Target Cholangiocarcinoma. Cancer Research, 2022, 82, 1548-1559.	0.4	8
64	The Structure of Change. Science, 2009, 323, 347-348.	6.0	7
65	Functional analysis of a novel ENU-induced PHD finger 11 (Phf11) mouse mutant. Mammalian Genome, 2014, 25, 573-582.	1.0	7
66	Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study. Twin Research and Human Genetics, 2015, 18, 117-125.	0.3	7
67	Problems of Developing Molecular Diagnostic Tests for Opportunistic Pathogens: The Example of Pneumocystis jirovecii. Journal of Eukaryotic Microbiology, 2006, 53, S85-S86.	0.8	4
68	Management, presentation and interpretation of genome scans using GSCANDB. Bioinformatics, 2007, 23, 1545-1549.	1.8	4
69	Mutational bias in spermatogonia impacts the anatomy of regulatory sites in the human genome. Genome Research, 2021, 31, 1994-2007.	2.4	4
70	The contribution of evolutionarily volatile promoters to molecular phenotypes and human trait variation. Genome Biology, 2022, 23, 89.	3.8	4
71	Sushi gets serious: the draft genome sequence of the pufferfish Fugu rubripes. Genome Biology, 2002, 3, reviews1025.1.	13.9	1
72	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes: Authors' Reply. PLoS Biology, 2007, 5, e128.	2.6	1

#	Article	IF	Citations
73	Comparative Genomics. , 0, , 105-144.		0
74	Comparative Genomics and Mammalian Promoter Evolution. , 2009, , 209-226.		0
75	Evolutionary dependencies show paths to cancer development. Nature Genetics, 2020, 52, 1135-1136.	9.4	0