James G D Prendergast

List of Publications by Year
in descending order

52 papers	7,304 citations	257450 24 h-index	182427 51 g-index
61 all docs	61 docs citations	61 times ranked	13434 citing authors

#	Article	IF	Citations
1	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
2	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
3	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	21.4	542
4	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. Nature Genetics, 2008, 40, 623-630.	21.4	514
5	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
6	Abundant Pleiotropy in Human Complex Diseases and Traits. American Journal of Human Genetics, 2011, 89, 607-618.	6.2	478
7	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. Nature Genetics, 2010, 42, 973-977.	21.4	335
8	Transcription forms and remodels supercoiling domains unfolding large-scale chromatin structures. Nature Structural and Molecular Biology, 2013, 20, 387-395.	8.2	324
9	Germline Susceptibility to Colorectal Cancer Due to Base-Excision Repair Gene Defects. American Journal of Human Genetics, 2005, 77, 112-119.	6.2	268
10	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
11	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	9.6	200
12	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
13	Genome-wide methylation profiling in CrohnÊ¼s disease identifies altered epigenetic regulation of key host defense mechanisms including the Th17 pathway. Inflammatory Bowel Diseases, 2012, 18, 889-899.	1.9	152
14	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5289-5294.	7.1	111
15	Chromatin structure and evolution in the human genome. BMC Evolutionary Biology, 2007, 7, 72.	3.2	80
16	Sequencing Illustrates the Transcriptional Response of Legionella pneumophila during Infection and Identifies Seventy Novel Small Non-Coding RNAs. PLoS ONE, 2011, 6, e17570.	2.5	76
17	Sex differences in genetic architecture in the UK Biobank. Nature Genetics, 2021, 53, 1283-1289.	21.4	69
18	Widespread signatures of recent selection linked to nucleosome positioning in the human lineage. Genome Research, 2011, 21, 1777-1787.	5.5	65

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19	hapbin: An Efficient Program for Performing Haplotype-Based Scans for Positive Selection in Large Genomic Datasets: Fig. 1.. Molecular Biology and Evolution, 2015, 32, 3027-3029.	8.9	61
20	Fine-mapping of colorectal cancer susceptibility loci at 8q23.3, 16q22.1 and 19q13.11: refinement of association signals and use of in silico analysis to suggest functional variation and unexpected candidate target genes. Human Molecular Genetics, 2011, 20, 2879-2888.	2.9	56
21	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. Nature Communications, 2020, 11, 4739.	12.8	50
22	The host ubiquitin-dependent segregase VCP/p97 is required for the onset of human cytomegalovirus replication. PLoS Pathogens, 2017, 13, e1006329.	4.7	41
23	Sequencing and analysis of an Irish human genome. Genome Biology, 2010, 11, R91.	9.6	36
24	A cattle graph genome incorporating global breed diversity. Nature Communications, 2022, 13, 910.	12.8	35
25	Age-related gene expression changes, and transcriptome wide association study of physical and cognitive aging traits, in the Lothian Birth Cohort 1936. Aging, 2017, 9, 2489-2503.	3.1	33
26	Species-Specificity of Transcriptional Regulation and the Response to Lipopolysaccharide in Mammalian Macrophages. Frontiers in Cell and Developmental Biology, 2020, 8, 661.	3.7	29
27	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	2.9	27
28	Detailed analysis of chick optic fissure closure reveals Netrin-1 as an essential mediator of epithelial fusion. ELife, 2019, 8, .	6.0	27
29	Lossâ€ofâ€Function Mutations in the ALPL Gene Presenting with Adult Onset Osteoporosis and Low Serum Concentrations of Total Alkaline Phosphatase. Journal of Bone and Mineral Research, 2020, 35, 657-661.	2.8	23
30	A recurrent de novo mutation inACTG1causes isolated ocular coloboma. Human Mutation, 2017, 38, 942-946.	2.5	21
31	A genome-wide screen in human embryonic stem cells reveals novel sites of allele-specific histone modification associated with known disease loci. Epigenetics and Chromatin, 2012, 5, 6.	3.9	20
32	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. Genome Biology and Evolution, 2021, 13, .	2.5	20
33	Sequence-Level Mechanisms of Human Epigenome Evolution. Genome Biology and Evolution, 2014, 6, 1758-1771.	2.5	17
34	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	3.5	17
35	Shared regulatory sites are abundant in the human genome and shed light on genome evolution and disease pleiotropy. PLoS Genetics, 2017, 13, e1006673.	3.5	16
36	Local Exome Sequences Facilitate Imputation of Less Common Variants and Increase Power of Genome Wide Association Studies. PLoS ONE, 2013, 8, e68604.	2.5	13

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37	Reply to Webb et al.. American Journal of Human Genetics, 2006, 79, 771.	6.2	12
38	Arginine to Glutamine Variant in Olfactomedin Like 3 (OLFML3) Is a Candidate for Severe Goniodysgenesis and Glaucoma in the Border Collie Dog Breed. G3: Genes, Genomes, Genetics, 2019, 9, 943-954.	1.8	11
39	nf-LO: A Scalable, Containerized Workflow for Genome-to-Genome Lift Over. Genome Biology and Evolution, 2021, 13, .	2.5	10
40	Linked Mutations at Adjacent Nucleotides Have Shaped Human Population Differentiation and Protein Evolution. Genome Biology and Evolution, 2019, 11, 759-775.	2.5	9
41	Exome Sequencing to Detect Rare Variants Associated With General Cognitive Ability: A Pilot Study. Twin Research and Human Genetics, 2015, 18, 117-125.	0.6	7
42	Using regulatory variants to detect geneâ€“gene interactions identifies networks of genes linked to cell immortalisation. Nature Communications, 2020, 11, 343.	12.8	7
43	Rare Missense Functional Variants at COL4A1 and COL4A2 in Sporadic Intracerebral Hemorrhage. Neurology, 2021, 97, .	1.1	6
44	A locus conferring tolerance to Theileria infection in African cattle. PLoS Genetics, 2022, 18, e1010099.	3.5	6
45	Inherited Tolerance in Cattle to the Apicomplexan Protozoan Theileria parva is Associated with Decreased Proliferation of Parasite-Infected Lymphocytes. Frontiers in Cellular and Infection Microbiology, 2021, 11, 751671.	3.9	5
46	Inverted CD4+/CD8+ T cell ratio in Boran (Bos indicus) cattle. Veterinary Immunology and Immunopathology, 2020, 230, 110126.	1.2	4
47	Identification and functional modelling of plausibly causative cis-regulatory variants in a highly-selected cohort with X-linked intellectual disability. PLoS ONE, 2021, 16, e0256181.	2.5	3
48	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. Genetics, 2019, 212, 577-586.	2.9	2
49	Clinical Evaluation of Corridor Disease in Bos indicus (Boran) Cattle Naturally Infected With Buffalo-Derived Theileria parva. Frontiers in Veterinary Science, 2021, 8, 731238.	2.2	2
50	Side Effects: Substantial Non-Neutral Evolution Flanking Regulatory Sites. PLoS Genetics, 2013, 9, e1003528.	3.5	1
51	Investigating the origin and authenticity of Victoria Cross medals using X-ray fluorescence spectrometry. Scientific Reports, 2020, 10, 19953.	3.3	1
52	Using machine learning to detect the differential usage of novel gene isoforms. BMC Bioinformatics, 2022, 23, 45.	2.6	1