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	Using machine learning to detect the differential usage of novel gene isoforms. BMC Bioinformatics, 2022, 23, 45.	2.6	1
2	A cattle graph genome incorporating global breed diversity. Nature Communications, 2022, 13, 910.	12.8	35
3	A locus conferring tolerance to Theileria infection in African cattle. PLoS Genetics, 2022, 18, e1010099.	3.5	6
4	Whole-Genome Sequence Data Suggest Environmental Adaptation of Ethiopian Sheep Populations. Genome Biology and Evolution, 2021, 13, .	2.5	20
5	Rare Missense Functional Variants at COL4A1 and COL4A2 in Sporadic Intracerebral Hemorrhage. Neurology, 2021, 97, .	1.1	6
6	nf-LO: A Scalable, Containerized Workflow for Genome-to-Genome Lift Over. Genome Biology and Evolution, 2021, 13, .	2.5	10
7	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
8	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
9	Sex differences in genetic architecture in the UK Biobank. Nature Genetics, 2021, 53, 1283-1289.	21.4	69
10	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
11	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
12	Inverted CD4+/CD8+ T cell ratio in Boran (Bos indicus) cattle. Veterinary Immunology and Immunopathology, 2020, 230, 110126.	1.2	4
13	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
14	Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. Nature Communications, 2020, 11, 4739.	12.8	50
15	Investigating the origin and authenticity of Victoria Cross medals using X-ray fluorescence spectrometry. Scientific Reports, 2020, 10, 19953.	3.3	1
16	Using regulatory variants to detect geneâ€“gene interactions identifies networks of genes linked to cell immortalisation. Nature Communications, 2020, 11, 343.	12.8	7
17	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
18	Linked Mutations at Adjacent Nucleotides Have Shaped Human Population Differentiation and Protein Evolution. Genome Biology and Evolution, 2019, 11, 759-775.	2.5	9

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19	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
20	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	3.5	17
21	Detailed analysis of chick optic fissure closure reveals Netrin-1 as an essential mediator of epithelial fusion. ELife, 2019, 8, .	6.0	27
22	A recurrent de novo mutation inACTG1causes isolated ocular coloboma. Human Mutation, 2017, 38, 942-946.	2.5	21
23	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
24	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
25	The host ubiquitin-dependent segregase VCP/p97 is required for the onset of human cytomegalovirus replication. PLoS Pathogens, 2017, 13, e1006329.	4.7	41
26	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	2.9	27
27	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
28	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
29	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
30	Sequence-Level Mechanisms of Human Epigenome Evolution. Genome Biology and Evolution, 2014, 6, 1758-1771.	2.5	17
31	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	27.8	1,838
32	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	9.6	200
33	Transcription forms and remodels supercoiling domains unfolding large-scale chromatin structures. Nature Structural and Molecular Biology, 2013, 20, 387-395.	8.2	324
34	Side Effects: Substantial Non-Neutral Evolution Flanking Regulatory Sites. PLoS Genetics, 2013, 9, e1003528.	3.5	1
35	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
36	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210

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37	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
38	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
39	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
40	Abundant Pleiotropy in Human Complex Diseases and Traits. American Journal of Human Genetics, 2011, 89, 607-618.	6.2	478
41	Widespread signatures of recent selection linked to nucleosome positioning in the human lineage. Genome Research, 2011, 21, 1777-1787.	5.5	65
42	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
43	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
44	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
45	Sequencing and analysis of an Irish human genome. Genome Biology, 2010, 11, R91.	9.6	36
46	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
47	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
48	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
49	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
50	Chromatin structure and evolution in the human genome. BMC Evolutionary Biology, 2007, 7, 72.	3.2	80
51	Reply to Webb et al.. American Journal of Human Genetics, 2006, 79, 771.	6.2	12
52	Germline Susceptibility to Colorectal Cancer Due to Base-Excision Repair Gene Defects. American Journal of Human Genetics, 2005, 77, 112-119.	6.2	268