Oliver S Burren

List of Publications by Year
in descending order

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37	7,205	236925	289244
papers	citations	25 h-index	40 g-index

49	49	49	14327
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Prioritisation of Candidate Genes Underpinning COVID-19 Host Genetic Traits Based on High-Resolution 3D Chromosomal Topology. Frontiers in Genetics, 2021, 12, 745672.	2.3	5
2	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. Genome Medicine, 2020, 12, 106.	8.2	12
3	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. Nature, 2020, 583, 90-95.	27.8	148
4	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
5	Resolving mechanisms of immuneâ€mediated disease in primary <scp>CD</scp> 4 T cells. EMBO Molecular Medicine, 2020, 12, e12112.	6.9	30
6	Fine mapping chromatin contacts in capture Hi-C data. BMC Genomics, 2019, 20, 77.	2.8	16
7	Approaches and advances in the genetic causes of autoimmune disease and their implications. Nature Immunology, 2018, 19, 674-684.	14.5	58
8	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. Genome Biology, 2017, 18, 165.	8.8	68
9	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. Cell, 2016, 167, 1369-1384.e19.	28.9	863
10	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. European Journal of Immunology, 2015, 45, 3200-3203.	2.9	26
11	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. PLoS Genetics, 2015, 11, e1005272.	3.5	55
12	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386.	21.4	589
13	Detection and correction of artefacts in estimation of rare copy number variants and analysis of rare deletions in type 1 diabetes. Human Molecular Genetics, 2015, 24, 1774-1790.	2.9	20
14	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. Nature Genetics, 2015, 47, 839-846.	21.4	128
15	Integration of disease association and eQTL data using a Bayesian colocalisation approach highlights six candidate causal genes in immune-mediated diseases. Human Molecular Genetics, 2015, 24, 3305-3313.	2.9	134
16	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. Nature Communications, 2015, 6, 7000.	12.8	367
17	VSEAMS: a pipeline for variant set enrichment analysis using summary GWAS data identifies IKZF3, BATF and ESRRA as key transcription factors in type 1 diabetes. Bioinformatics, 2014, 30, 3342-3348.	4.1	14
18	A Type I Interferon Transcriptional Signature Precedes Autoimmunity in Children Genetically at Risk for Type 1 Diabetes. Diabetes, 2014, 63, 2538-2550.	0.6	261

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19	A Method for Geneâ€Based Pathway Analysis Using Genomewide Association Study Summary Statistics Reveals Nine New Type 1 Diabetes Associations. Genetic Epidemiology, 2014, 38, 661-670.	1.3	54
20	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. BMC Genomics, 2014, 15, 274.	2.8	12
21	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. Nature, 2013, 498, 232-235.	27.8	184
22	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. Human Molecular Genetics, 2012, 21, 322-333.	2.9	100
23	Seven newly identified loci for autoimmune thyroid disease. Human Molecular Genetics, 2012, 21, 5202-5208.	2.9	143
24	T1DBase: update 2011, organization and presentation of large-scale data sets for type 1 diabetes research. Nucleic Acids Research, 2011, 39, D997-D1001.	14.5	68
25	Evidence thatCd101Is an Autoimmune Diabetes Gene in Nonobese Diabetic Mice. Journal of Immunology, 2011, 187, 325-336.	0.8	26
26	Inherited Variation in Vitamin D Genes Is Associated With Predisposition to Autoimmune Disease Type 1 Diabetes. Diabetes, 2011, 60, 1624-1631.	0.6	260
27	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
28	Cell-specific protein phenotypes for the autoimmune locus IL2RA using a genotype-selectable human bioresource. Nature Genetics, 2009, 41, 1011-1015.	21.4	249
29	Chapter 6 Geneâ€“Gene Interactions in the NOD Mouse Model of Type 1 Diabetes. Advances in Immunology, 2008, 100, 151-175.	2.2	65
30	T1DBase: integration and presentation of complex data for type 1 diabetes research. Nucleic Acids Research, 2007, 35, D742-D746.	14.5	60
31	Sequencing and association analysis of the type 1 diabetes â€“ linked region on chromosome 10p12-q11. BMC Genetics, 2007, 8, 24.	2.7	10
32	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. Nature Genetics, 2007, 39, 857-864.	21.4	1,324
33	Discovery, linkage disequilibrium and association analyses of polymorphisms of the immune complement inhibitor, decay-accelerating factor gene (DAF/CD55) in type 1 diabetes. BMC Genetics, 2006, 7, 22.	2.7	11
34	A genome-wide association study of nonsynonymous SNPs identifies a type 1 diabetes locus in the interferon-induced helicase (IFIH1) region. Nature Genetics, 2006, 38, 617-619.	21.4	619
35	No evidence for association of the TATA-box binding protein glutamine repeat sequence or the flanking chromosome 6q27 region with type 1 diabetes. Biochemical and Biophysical Research Communications, 2005, 331, 435-441.	2.1	6
36	T1DBase, a community web-based resource for type 1 diabetes research. Nucleic Acids Research, 2004, 33, D544-D549.	14.5	44

#	Article	IF	Citations
37	Development of an integrated genome informatics, data management and workflow infrastructure: A toolbox for the study of complex disease genetics. Human Genomics, 2004, 1, 98.	2.9	15