

Oliver S Burren

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

7,205
citations

236925

25
h-index

289244

40
g-index

49
all docs

49
docs citations

49
times ranked

14327
citing authors

#	ARTICLE	IF	CITATIONS
1	Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes. <i>Nature Genetics</i> , 2007, 39, 857-864.	21.4	1,324
2	Lineage-Specific Genome Architecture Links Enhancers and Non-coding Disease Variants to Target Gene Promoters. <i>Cell</i> , 2016, 167, 1369-1384.e19.	28.9	863
3	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. <i>Nature</i> , 2010, 464, 713-720.	27.8	737
4	A genome-wide association study of nonsynonymous SNPs identifies a type 1 diabetes locus in the interferon-induced helicase (IFIH1) region. <i>Nature Genetics</i> , 2006, 38, 617-619.	21.4	619
5	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. <i>Nature Genetics</i> , 2015, 47, 381-386.	21.4	589
6	Widespread seasonal gene expression reveals annual differences in human immunity and physiology. <i>Nature Communications</i> , 2015, 6, 7000.	12.8	367
7	Whole-genome sequencing of patients with rare diseases in a national health system. <i>Nature</i> , 2020, 583, 96-102.	27.8	338
8	A Type I Interferon Transcriptional Signature Precedes Autoimmunity in Children Genetically at Risk for Type 1 Diabetes. <i>Diabetes</i> , 2014, 63, 2538-2550.	0.6	261
9	Inherited Variation in Vitamin D Genes Is Associated With Predisposition to Autoimmune Disease Type 1 Diabetes. <i>Diabetes</i> , 2011, 60, 1624-1631.	0.6	260
10	Cell-specific protein phenotypes for the autoimmune locus IL2RA using a genotype-selectable human bioresource. <i>Nature Genetics</i> , 2009, 41, 1011-1015.	21.4	249
11	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. <i>Nature</i> , 2013, 498, 232-235.	27.8	184
12	Whole-genome sequencing of a sporadic primary immunodeficiency cohort. <i>Nature</i> , 2020, 583, 90-95.	27.8	148
13	Seven newly identified loci for autoimmune thyroid disease. <i>Human Molecular Genetics</i> , 2012, 21, 5202-5208.	2.9	143
14	Integration of disease association and eQTL data using a Bayesian colocalisation approach highlights six candidate causal genes in immune-mediated diseases. <i>Human Molecular Genetics</i> , 2015, 24, 3305-3313.	2.9	134
15	Statistical colocalization of genetic risk variants for related autoimmune diseases in the context of common controls. <i>Nature Genetics</i> , 2015, 47, 839-846.	21.4	128
16	Long-range DNA looping and gene expression analyses identify DEXI as an autoimmune disease candidate gene. <i>Human Molecular Genetics</i> , 2012, 21, 322-333.	2.9	100
17	T1DBase: update 2011, organization and presentation of large-scale data sets for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2011, 39, D997-D1001.	14.5	68
18	Chromosome contacts in activated T cells identify autoimmune disease candidate genes. <i>Genome Biology</i> , 2017, 18, 165.	8.8	68

#	ARTICLE	IF	CITATIONS
19	Chapter 6 Gene–Gene Interactions in the NOD Mouse Model of Type 1 Diabetes. <i>Advances in Immunology</i> , 2008, 100, 151-175.	2.2	65
20	T1DBase: integration and presentation of complex data for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2007, 35, D742-D746.	14.5	60
21	Approaches and advances in the genetic causes of autoimmune disease and their implications. <i>Nature Immunology</i> , 2018, 19, 674-684.	14.5	58
22	Dissection of a Complex Disease Susceptibility Region Using a Bayesian Stochastic Search Approach to Fine Mapping. <i>PLoS Genetics</i> , 2015, 11, e1005272.	3.5	55
23	A Method for Gene–Based Pathway Analysis Using Genomewide Association Study Summary Statistics Reveals Nine New Type 1 Diabetes Associations. <i>Genetic Epidemiology</i> , 2014, 38, 661-670.	1.3	54
24	T1DBase, a community web-based resource for type 1 diabetes research. <i>Nucleic Acids Research</i> , 2004, 33, D544-D549.	14.5	44
25	Resolving mechanisms of immune–mediated disease in primary <sc>CD</sc> 4 T cells. <i>EMBO Molecular Medicine</i> , 2020, 12, e12112.	6.9	30
26	Evidence that <i>Cd101</i> is an Autoimmune Diabetes Gene in Nonobese Diabetic Mice. <i>Journal of Immunology</i> , 2011, 187, 325-336.	0.8	26
27	Epigenetic analysis of regulatory T cells using multiplex bisulfite sequencing. <i>European Journal of Immunology</i> , 2015, 45, 3200-3203.	2.9	26
28	Detection and correction of artefacts in estimation of rare copy number variants and analysis of rare deletions in type 1 diabetes. <i>Human Molecular Genetics</i> , 2015, 24, 1774-1790.	2.9	20
29	Fine mapping chromatin contacts in capture Hi-C data. <i>BMC Genomics</i> , 2019, 20, 77.	2.8	16
30	Development of an integrated genome informatics, data management and workflow infrastructure: A toolbox for the study of complex disease genetics. <i>Human Genomics</i> , 2004, 1, 98.	2.9	15
31	VSEAMS: a pipeline for variant set enrichment analysis using summary GWAS data identifies <i>IKZF3</i>, <i>BATF</i> and <i>ESRRA</i> as key transcription factors in type 1 diabetes. <i>Bioinformatics</i> , 2014, 30, 3342-3348.	4.1	14
32	A hybrid qPCR/SNP array approach allows cost efficient assessment of KIR gene copy numbers in large samples. <i>BMC Genomics</i> , 2014, 15, 274.	2.8	12
33	Genetic feature engineering enables characterisation of shared risk factors in immune-mediated diseases. <i>Genome Medicine</i> , 2020, 12, 106.	8.2	12
34	Discovery, linkage disequilibrium and association analyses of polymorphisms of the immune complement inhibitor, decay-accelerating factor gene (DAF/CD55) in type 1 diabetes. <i>BMC Genetics</i> , 2006, 7, 22.	2.7	11
35	Sequencing and association analysis of the type 1 diabetes – linked region on chromosome 10p12-q11. <i>BMC Genetics</i> , 2007, 8, 24.	2.7	10
36	No evidence for association of the TATA-box binding protein glutamine repeat sequence or the flanking chromosome 6q27 region with type 1 diabetes. <i>Biochemical and Biophysical Research Communications</i> , 2005, 331, 435-441.	2.1	6

#	ARTICLE	IF	CITATIONS
37	Prioritisation of Candidate Genes Underpinning COVID-19 Host Genetic Traits Based on High-Resolution 3D Chromosomal Topology. <i>Frontiers in Genetics</i> , 2021, 12, 745672.	2.3	5