

Colm O'dushlaine

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

11,113
citations

172386
29
h-index

377752
34
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all docs

34
docs citations

34
times ranked

20092
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. <i>Nature Genetics</i> , 2022, 54, 382-392.	9.4	97
2	Computationally efficient whole-genome regression for quantitative and binary traits. <i>Nature Genetics</i> , 2021, 53, 1097-1103.	9.4	457
3	Genome-wide association analysis of serum alanine and aspartate aminotransferase, and the modifying effects of BMI in 388k European individuals. <i>Genetic Epidemiology</i> , 2021, 45, 664-681.	0.6	9
4	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. <i>American Journal of Human Genetics</i> , 2021, 108, 1350-1355.	2.6	72
5	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. <i>Molecular Psychiatry</i> , 2020, 25, 2455-2467.	4.1	82
6	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. <i>Nature</i> , 2020, 586, 749-756.	13.7	369
7	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
8	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.1	2
9	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. <i>American Journal of Human Genetics</i> , 2018, 102, 103-115.	2.6	86
10	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. <i>American Journal of Human Genetics</i> , 2018, 102, 874-889.	2.6	58
11	A Protein-Truncating <i>HSD17B13</i> Variant and Protection from Chronic Liver Disease. <i>New England Journal of Medicine</i> , 2018, 378, 1096-1106.	13.9	556
12	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	9.4	547
13	Genetic inactivation of <i>ANGPTL4</i> improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018, 9, 2252.	5.8	99
14	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. <i>JAMA - Journal of the American Medical Association</i> , 2017, 317, 937.	3.8	148
15	Genetic and Pharmacologic Inactivation of <i>ANGPTL3</i> and Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 211-221.	13.9	633
16	Implication of <i>LRRC4C</i> and <i>DPP6</i> in neurodevelopmental disorders. <i>American Journal of Medical Genetics, Part A</i> , 2017, 173, 395-406.	0.7	40
17	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	9.4	838
18	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. <i>Science</i> , 2016, 354, .	6.0	464

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19	Genetic identification of familial hypercholesterolemia within a single U.S. health care system. <i>Science</i> , 2016, 354, .	6.0	349
20	Inactivating Variants in <i>ANGPTL4</i> and Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1123-1133.	13.9	411
21	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. <i>PLoS Genetics</i> , 2016, 12, e1006343.	1.5	24
22	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015, 44, 1706-1721.	0.9	53
23	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. <i>Human Molecular Genetics</i> , 2014, 23, 1669-1676.	1.4	82
24	A polygenic burden of rare disruptive mutations in schizophrenia. <i>Nature</i> , 2014, 506, 185-190.	13.7	1,305
25	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. <i>American Journal of Human Genetics</i> , 2014, 95, 454-461.	2.6	45
26	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013, 45, 1150-1159.	9.4	1,395
27	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013, 45, 984-994.	9.4	2,067
28	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. <i>Science Translational Medicine</i> , 2013, 5, 192ra86.	5.8	77
29	INRICH: interval-based enrichment analysis for genome-wide association studies. <i>Bioinformatics</i> , 2012, 28, 1797-1799.	1.8	218
30	The Genetic Structure of the Swedish Population. <i>PLoS ONE</i> , 2011, 6, e22547.	1.1	67
31	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. <i>European Journal of Human Genetics</i> , 2011, 19, 1082-1089.	1.4	39
32	Genes predict village of origin in rural Europe. <i>European Journal of Human Genetics</i> , 2010, 18, 1269-1270.	1.4	22
33	Genetic Differences between Five European Populations. <i>Human Heredity</i> , 2010, 70, 141-149.	0.4	29
34	The SNP ratio test: pathway analysis of genome-wide association datasets. <i>Bioinformatics</i> , 2009, 25, 2762-2763.	1.8	125