Colm O'dushlaine

List of Publications by Year
in descending order

34	11,113	172457 29	377865 34
papers	citations	h-index	g-index

34	34	34	20092
all docs	docs citations	times ranked	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. Nature Genetics, 2022, 54, 382-392.	21.4	97
2	Computationally efficient whole-genome regression for quantitative and binary traits. Nature Genetics, 2021, 53, 1097-1103.	21.4	457
3	Genomeâ€wide association analysis of serum alanine and aspartate aminotransferase, and the modifying effects of BMI in 388kÂEuropean individuals. Genetic Epidemiology, 2021, 45, 664-681.	1.3	9
4	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	6.2	72
5	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. Molecular Psychiatry, 2020, 25, 2455-2467.	7.9	82
6	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	27.8	369
7	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
8	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.7	2
9	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	6.2	86
10	Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. American Journal of Human Genetics, 2018, 102, 874-889.	6.2	58
11	A Protein-TruncatingHSD17B13Variant and Protection from Chronic Liver Disease. New England Journal of Medicine, 2018, 378, 1096-1106.	27.0	556
12	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
13	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99
14	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	7.4	148
15	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	27.0	633
16	Implication of LRRC4C and DPP6 in neurodevelopmental disorders. American Journal of Medical Genetics, Part A, 2017, 173, 395-406.	1.2	40
17	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
18	Distribution and clinical impact of functional variants in 50,726 whole-exome sequences from the DiscovEHR study. Science, 2016, 354, .	12.6	464

#	Article	IF	Citations
19	Genetic identification of familial hypercholesterolemia within a single U.S. health care system. Science, 2016, 354, .	12.6	349
20	Inactivating Variants in ANGPTL4 and Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 1123-1133.	27.0	411
21	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. PLoS Genetics, 2016, 12, e1006343.	3.5	24
22	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
23	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. Human Molecular Genetics, 2014, 23, 1669-1676.	2.9	82
24	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	27.8	1,305
25	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. American Journal of Human Genetics, 2014, 95, 454-461.	6.2	45
26	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
27	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
28	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. Science Translational Medicine, 2013, 5, 192ra86.	12.4	77
29	INRICH: interval-based enrichment analysis for genome-wide association studies. Bioinformatics, 2012, 28, 1797-1799.	4.1	218
30	The Genetic Structure of the Swedish Population. PLoS ONE, 2011, 6, e22547.	2.5	67
31	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. European Journal of Human Genetics, 2011, 19, 1082-1089.	2.8	39
32	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	2.8	22
33	Genetic Differences between Five European Populations. Human Heredity, 2010, 70, 141-149.	0.8	29
34	The SNP ratio test: pathway analysis of genome-wide association datasets. Bioinformatics, 2009, 25, 2762-2763.	4.1	125