Philip Awadalla

List of Publications by Year
in descending order

39	4,118	279798	302126
papers	citations	23 h-index	39 g-index

40	40	40	8673
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A Coalescent-Based Method for Detecting and Estimating Recombination From Gene Sequences. Genetics, 2002, 160, 1231-1241.	2.9	624
2	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
3	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
4	Variation in genome-wide mutation rates within and between human families. Nature Genetics, 2011, 43, 712-714.	21.4	525
5	Direct Measure of the De Novo Mutation Rate in Autism and Schizophrenia Cohorts. American Journal of Human Genetics, 2010, 87, 316-324.	6.2	222
6	Cohort profile of the CARTaGENE study: Quebecâ€™s population-based biobank for public health and personalized genomics. International Journal of Epidemiology, 2013, 42, 1285-1299.	1.9	172
7	Genetically encoded impairment of neuronal <scp>KCC</scp> 2 cotransporter function in human idiopathic generalized epilepsy. EMBO Reports, 2014, 15, 766-774.	4.5	163
8	High-Resolution Genomic Analysis of Human Mitochondrial RNA Sequence Variation. Science, 2014, 344, 413-415.	12.6	90
9	Evidence for additive and interaction effects of host genotype and infection in malaria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16786-16793.	7.1	89
10	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	5.5	88
11	Recombination affects accumulation of damaging and disease-associated mutations in human populations. Nature Genetics, 2015, 47, 400-404.	21.4	84
12	Gene-by-environment interactions in urban populations modulate risk phenotypes. Nature Communications, 2018, 9, 827.	12.8	84
13	Clonal hematopoiesis is associated with risk of severe Covid-19. Nature Communications, 2021, 12, 5975.	12.8	81
14	The Canadian Partnership for Tomorrow Project: a pan-Canadian platform for research on chronic disease prevention. Cmaj, 2018, 190, E710-E717.	2.0	71
15	Whole-Exome Sequencing Reveals a Rapid Change in the Frequency of Rare Functional Variants in a Founding Population of Humans. PLoS Genetics, 2013, 9, e1003815.	3.5	70
16	ARMC5 mutations in a large French-Canadian family with cortisol-secreting Î²-adrenergic/vasopressin responsive bilateral macronodular adrenal hyperplasia. European Journal of Endocrinology, 2016, 174, 85-96.	3.7	55
17	Replication study of MATR3 in familial and sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2016, 37, 209.e17-209.e21.	3.1	53
18	Relaxed Selection During a Recent Human Expansion. Genetics, 2018, 208, 763-777.	2.9	49

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19	Age-Dependent Recombination Rates in Human Pedigrees. PLoS Genetics, 2011, 7, e1002251.	3.5	48
20	Rare allelic forms of PRDM9 associated with childhood leukemogenesis. Genome Research, 2013, 23, 419-430.	5.5	45
21	Gain-of-function missense variant in SLC12A2, encoding the bumetanide-sensitive NKCC1 cotransporter, identified in human schizophrenia. Journal of Psychiatric Research, 2016, 77, 22-26.	3.1	40
22	Clinical, Genetic, and Urinary Factors Associated with Uromodulin Excretion. Clinical Journal of the American Society of Nephrology: CJASN, 2016, 11, 62-69.	4.5	33
23	The impact of recombination on human mutation load and disease. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160465.	4.0	31
24	Aberrant PRDM9 expression impacts the pan-cancer genomic landscape. Genome Research, 2018, 28, 1611-1620.	5.5	27
25	Polygenic risk scores predict diabetes complications and their response to intensive blood pressure and glucose control. Diabetologia, 2021, 64, 2012-2025.	6.3	24
26	Exploiting Gene Expression Variation to Capture Gene-Environment Interactions for Disease. Frontiers in Genetics, 2012, 3, 228.	2.3	21
27	Aortic Dilatation Associated With a De Novo Mutation inÂtheÂSOX18 Gene: Expanding the Clinical Spectrum ofÂHypotrichosis-Lymphedema-Telangiectasia Syndrome. Canadian Journal of Cardiology, 2016, 32, 135.e1-135.e7.	1.7	19
28	Normal sex and age-specific parameters in a multi-ethnic population: a cardiovascular magnetic resonance study of the Canadian Alliance for Healthy Hearts and Minds cohort. Journal of Cardiovascular Magnetic Resonance, 2022, 24, 2.	3.3	17
29	Building knowledge, optimising physical and mental health and setting up healthier life trajectories in South African women (Bukhali): a preconception randomised control trial part of the Healthy Life Trajectories Initiative (HeLTI). BMJ Open, 2022, 12, e059914.	1.9	17
30	Effect of Cognitive Reserve on the Association of Vascular Brain Injury With Cognition. Neurology, 2021, 97, e1707-e1716.	1.1	13
31	Genomic architecture of sickle cell disease in West African children. Frontiers in Genetics, 2014, 5, 26.	2.3	11
32	Diabetes, Brain Infarcts, Cognition, and Small Vessels in the Canadian Alliance for Healthy Hearts and Minds Study. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e891-e898.	3.6	11
33	Interacting evolutionary pressures drive mutation dynamics and health outcomes in aging blood. Nature Communications, 2021, 12, 4921.	12.8	11
34	Reduced Cognitive Assessment Scores Among Individuals With Magnetic Resonance Imagingâ€“Detected Vascular Brain Injury. Stroke, 2020, 51, 1158-1165.	2.0	9
35	A haplotype-based normalization technique for the analysis and detection of allele specific expression. BMC Bioinformatics, 2016, 17, 364.	2.6	7
36	Recombination affects allele-specific expression of deleterious variants in human populations. Science Advances, 2022, 8, eabl3819.	10.3	3

#	Article	IF	Citations
37	Inferring ongoing cancer evolution from single tumour biopsies using synthetic supervised learning. PLoS Computational Biology, 2022, 18, e1010007.	3.2	2
38	The Canadian Alliance for Healthy Hearts and Minds: How Well Does It Reflect the Canadian Population?. CJC Open, 2020, 2, 599-609.	1.5	1
39	Score tests for scale effects, with application toÂgenomic analysis. Statistics in Medicine, 2021, 40, 3808-3822.	1.6	0