

Gad Abraham

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

34
papers

1,756
citations

19
h-index

41
g-index

45
ext. papers

2,746
ext. citations

8.4
avg, IF

5.17
L-index

#	Paper	IF	Citations
34	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. <i>Nature Metabolism</i> , 2021 , 3, 1476-1483	14.6	6
33	The Polygenic Score Catalog as an open database for reproducibility and systematic evaluation. <i>Nature Genetics</i> , 2021 , 53, 420-425	36.3	58
32	Polygenic risk scores in cardiovascular risk prediction: A cohort study and modelling analyses. <i>PLoS Medicine</i> , 2021 , 18, e1003498	11.6	27
31	Predictive Performance of a Polygenic Risk Score for Incident Ischemic Stroke in a Healthy Older Population. <i>Stroke</i> , 2021 , 52, 2882-2891	6.7	3
30	Risk Prediction Using Polygenic Risk Scores for Prevention of Stroke and Other Cardiovascular Diseases. <i>Stroke</i> , 2021 , 52, 2983-2991	6.7	2
29	Prognostic Value of a Polygenic Risk Score for Coronary Heart Disease in Individuals Aged 70 Years and Older.. <i>Circulation Genomic and Precision Medicine</i> , 2021 , CIRCGEN121003429	5.2	0
28	Genomic risk scores for juvenile idiopathic arthritis and its subtypes. <i>Annals of the Rheumatic Diseases</i> , 2020 , 79, 1572-1579	2.4	3
27	Towards clinical utility of polygenic risk scores. <i>Human Molecular Genetics</i> , 2019 , 28, R133-R142	5.6	166
26	Multivariate Genome-wide Association Analysis of a Cytokine Network Reveals Variants with Widespread Immune, Haematological, and Cardiometabolic Pleiotropy. <i>American Journal of Human Genetics</i> , 2019 , 105, 1076-1090	11	16
25	Elevated serum alpha-1 antitrypsin is a major component of GlycA-associated risk for future morbidity and mortality. <i>PLoS ONE</i> , 2019 , 14, e0223692	3.7	10
24	Genomic risk score offers predictive performance comparable to clinical risk factors for ischaemic stroke. <i>Nature Communications</i> , 2019 , 10, 5819	17.4	54
23	Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention. <i>Journal of the American College of Cardiology</i> , 2018 , 72, 1883-1893	15.1	285
22	Interactions within the MHC contribute to the genetic architecture of celiac disease. <i>PLoS ONE</i> , 2017 , 12, e0172826	3.7	9
21	An interaction map of circulating metabolites, immune gene networks, and their genetic regulation. <i>Genome Biology</i> , 2017 , 18, 146	18.3	27
20	Genetic loci associated with coronary artery disease harbor evidence of selection and antagonistic pleiotropy. <i>PLoS Genetics</i> , 2017 , 13, e1006328	6	39
19	FlashPCA2: principal component analysis of Biobank-scale genotype datasets. <i>Bioinformatics</i> , 2017 , 33, 2776-2778	7.2	133
18	Genomic prediction of coronary heart disease. <i>European Heart Journal</i> , 2016 , 37, 3267-3278	9.5	184

17	A Scalable Permutation Approach Reveals Replication and Preservation Patterns of Network Modules in Large Datasets. <i>Cell Systems</i> , 2016 , 3, 71-82	10.6	28
16	Genomic risk prediction of complex human disease and its clinical application. <i>Current Opinion in Genetics and Development</i> , 2015 , 33, 10-6	4.9	65
15	The Biomarker GlycA Is Associated with Chronic Inflammation and Predicts Long-Term Risk of Severe Infection. <i>Cell Systems</i> , 2015 , 1, 293-301	10.6	113
14	Genomic prediction of celiac disease targeting HLA-positive individuals. <i>Genome Medicine</i> , 2015 , 7, 72	14.4	20
13	Towards a molecular systems model of coronary artery disease. <i>Current Cardiology Reports</i> , 2014 , 16, 488	4.2	16
12	Fast principal component analysis of large-scale genome-wide data. <i>PLoS ONE</i> , 2014 , 9, e93766	3.7	160
11	Accurate and robust genomic prediction of celiac disease using statistical learning. <i>PLoS Genetics</i> , 2014 , 10, e1004137	6	68
10	Look, no hands! Spectral biomarkers from genetic association studies. <i>Genome Medicine</i> , 2013 , 5, 14	14.4	
9	Performance and robustness of penalized and unpenalized methods for genetic prediction of complex human disease. <i>Genetic Epidemiology</i> , 2013 , 37, 184-95	2.6	78
8	SparSNP: fast and memory-efficient analysis of all SNPs for phenotype prediction. <i>BMC Bioinformatics</i> , 2012 , 13, 88	3.6	25
7	Meta-analysis of gene expression microarrays with missing replicates. <i>BMC Bioinformatics</i> , 2011 , 12, 84	3.6	2
6	Prediction of breast cancer prognosis using gene set statistics provides signature stability and biological context. <i>BMC Bioinformatics</i> , 2010 , 11, 277	3.6	64
5	Short-term forecasting of emergency inpatient flow. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2009 , 13, 380-8		56
4	FlashPCA2: principal component analysis of biobank-scale genotype datasets		4
3	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases		4
2	The Polygenic Score Catalog: an open database for reproducibility and systematic evaluation		14
1	Genomic risk prediction of coronary artery disease in nearly 500,000 adults: implications for early screening and primary prevention		17