

William J Astle

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

4,732
citations

331670

21
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

12133
citing authors

#	ARTICLE	IF	CITATIONS
1	G protein-coupled receptor kinase 5 regulates thrombin signaling in platelets via PAR-1. <i>Blood Advances</i> , 2022, 6, 2319-2330.	5.2	8
2	Advances in understanding the pathogenesis of hereditary macrothrombocytopenia. <i>British Journal of Haematology</i> , 2021, 195, 25-45.	2.5	9
3	Familial pseudohyperkalemia induces significantly higher levels of extracellular potassium in early storage of red cell concentrates without affecting other standard measures of quality: A case control and allele frequency study. <i>Transfusion</i> , 2021, 61, 2439-2449.	1.6	9
4	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
5	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. <i>Blood Advances</i> , 2020, 4, 3495-3506.	5.2	31
6	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. <i>Blood</i> , 2020, 136, 1956-1967.	1.4	34
7	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
8	Whole-genome sequencing of patients with rare diseases in a national health system. <i>Nature</i> , 2020, 583, 96-102.	27.8	338
9	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. <i>Nature Communications</i> , 2019, 10, 5120.	12.8	160
10	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599,912 current drinkers in 83 prospective studies. <i>Lancet</i> , 2018, 391, 1513-1523.	13.7	858
11	Nbeal2 interacts with Dock7, Sec16a, and Vac14. <i>Blood</i> , 2018, 131, 1000-1011.	1.4	29
12	Rare variants in GP1BB are responsible for autosomal dominant macrothrombocytopenia. <i>Blood</i> , 2017, 129, 520-524.	1.4	42
13	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. <i>Nature Communications</i> , 2017, 8, 16058.	12.8	50
14	Mutations in tropomyosin 4 underlie a rare form of human macrothrombocytopenia. <i>Journal of Clinical Investigation</i> , 2017, 127, 814-829.	8.2	57
15	SNP in human ARHGEF3 promoter is associated with DNase hypersensitivity, transcript level and platelet function, and Arhgef3 KO mice have increased mean platelet volume. <i>PLoS ONE</i> , 2017, 12, e0178095.	2.5	20
16	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016, 48, 1303-1312.	21.4	66
17	A gain-of-function variant in DIAPH1 causes dominant macrothrombocytopenia and hearing loss. <i>Blood</i> , 2016, 127, 2903-2914.	1.4	121
18	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. <i>Cell</i> , 2016, 167, 1415-1429.e19.	28.9	1,052

#	ARTICLE	IF	CITATIONS
19	Flexible analysis of RNA-seq data using mixed effects models. <i>Bioinformatics</i> , 2014, 30, 180-188.	4.1	73
20	Transcriptional diversity during lineage commitment of human blood progenitors. <i>Science</i> , 2014, 345, 1251033.	12.6	253
21	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. <i>Nature Protocols</i> , 2014, 9, 1416-1427.	12.0	167
22	The relationship between DXA-based and anthropometric measures of visceral fat and morbidity in women. <i>BMC Cardiovascular Disorders</i> , 2013, 13, 25.	1.7	50
23	BATMAN – an R package for the automated quantification of metabolites from nuclear magnetic resonance spectra using a Bayesian model. <i>Bioinformatics</i> , 2012, 28, 2088-2090.	4.1	142
24	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. <i>Journal of the American Statistical Association</i> , 2012, 107, 1259-1271.	3.1	41
25	Population Structure and Cryptic Relatedness in Genetic Association Studies. <i>Statistical Science</i> , 2009, 24, .	2.8	372