William J Astle

List of Publications by Year
in descending order

25	4,732	331670 21	580821 25
papers	citations	h-index	g-index

29	29	29	12133
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19.	28.9	1,052
2	Risk thresholds for alcohol consumption: combined analysis of individual-participant data for 599â€˜912 current drinkers in 83 prospective studies. Lancet, The, 2018, 391, 1513-1523.	13.7	858
3	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
4	Population Structure and Cryptic Relatedness in Genetic Association Studies. Statistical Science, 2009, 24, .	2.8	372
5	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
6	Whole-genome sequencing of patients with rare diseases in a national health system. Nature, 2020, 583, 96-102.	27.8	338
7	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
8	Bayesian deconvolution and quantification of metabolites in complex 1D NMR spectra using BATMAN. Nature Protocols, 2014, 9, 1416-1427.	12.0	167
9	Genome-wide association study of eosinophilic granulomatosis with polyangiitis reveals genomic loci stratified by ANCA status. Nature Communications, 2019, 10, 5120.	12.8	160
10	BATMANâ€”an R package for the automated quantification of metabolites from nuclear magnetic resonance spectra using a Bayesian model. Bioinformatics, 2012, 28, 2088-2090.	4.1	142
11	A gain-of-function variant in DIAPH1 causes dominant macrothrombocytopenia and hearing loss. Blood, 2016, 127, 2903-2914.	1.4	121
12	Flexible analysis of RNA-seq data using mixed effects models. Bioinformatics, 2014, 30, 180-188.	4.1	73
13	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
14	Mutations in tropomyosin 4 underlie a rare form of human macrothrombocytopenia. Journal of Clinical Investigation, 2017, 127, 814-829.	8.2	57
15	The relationship between DXA-based and anthropometric measures of visceral fat and morbidity in women. BMC Cardiovascular Disorders, 2013, 13, 25.	1.7	50
16	Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature Communications, 2017, 8, 16058.	12.8	50
17	Rare variants in GP1BB are responsible for autosomal dominant macrothrombocytopenia. Blood, 2017, 129, 520-524.	1.4	42
18	A Bayesian Model of NMR Spectra for the Deconvolution and Quantification of Metabolites in Complex Biological Mixtures. Journal of the American Statistical Association, 2012, 107, 1259-1271.	3.1	41

#	Article	IF	Citations
19	Novel manifestations of immune dysregulation and granule defects in gray platelet syndrome. Blood, 2020, 136, 1956-1967.	1.4	34
20	Development and validation of a universal blood donor genotyping platform: a multinational prospective study. Blood Advances, 2020, 4, 3495-3506.	5.2	31
21	Nbeal2 interacts with Dock7, Sec16a, and Vac14. Blood, 2018, 131, 1000-1011.	1.4	29
22	SNP in human ARHGEF3 promoter is associated with DNase hypersensitivity, transcript level and platelet function, and Arhgef3 KO mice have increased mean platelet volume. PLoS ONE, 2017, 12, e0178095.	2.5	20
23	Advances in understanding the pathogenesis of hereditary macrothrombocytopenia. British Journal of Haematology, 2021, 195, 25-45.	2.5	9
24	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. Transfusion, 2021, 61, 2439-2449.	1.6	9
25	G proteinâ€“coupled receptor kinase 5 regulates thrombin signaling in platelets via PAR-1. Blood Advances, 2022, 6, 2319-2330.	5.2	8