Andrew D Johnson

List of Publications by Year
in descending order

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		3159	3830
249	37,312	92	178
papers	citations	h-index	g-index

279	279	279	48047
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
2	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	21.4	1,748
3	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
4	SNAP: a web-based tool for identification and annotation of proxy SNPs using HapMap. Bioinformatics, 2008, 24, 2938-2939.	4.1	1,201
5	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
6	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
7	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
8	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
9	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
10	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
11	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
12	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
14	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
15	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
16	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
17	Allelic Expression Imbalance of Human mu Opioid Receptor (OPRM1) Caused by Variant A118G. Journal of Biological Chemistry, 2005, 280, 32618-32624.	3.4	490
18	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	21.4	452

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19	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
20	Multidrug resistance polypeptide 1 (MDR1, ABCB1) variant 3435C>T affects mRNA stability. Pharmacogenetics and Genomics, 2005, 15, 693-704.	1.5	419
21	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
22	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
23	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
24	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
25	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
26	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
27	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
28	Identification of Ciliary Localization Sequences within the Third Intracellular Loop of G Protein-coupled Receptors. Molecular Biology of the Cell, 2008, 19, 1540-1547.	2.1	322
29	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	5.5	313
30	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
31	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
32	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
33	An Open Access Database of Genome-wide Association Results. BMC Medical Genetics, 2009, 10, 6.	2.1	276
34	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
35	GRASP: analysis of genotypeâ€“phenotype results from 1390 genome-wide association studies and corresponding open access database. Bioinformatics, 2014, 30, i185-i194.	4.1	261
36	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260

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37	LTB4 promotes insulin resistance in obese mice by acting on macrophages, hepatocytes and myocytes. Nature Medicine, 2015, 21, 239-247.	30.7	252
38	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	21.4	247
39	Genome-Wide Association for Abdominal Subcutaneous and Visceral Adipose Reveals a Novel Locus for Visceral Fat in Women. PLoS Genetics, 2012, 8, e1002695.	3.5	245
40	Genome-wide association identifies OBFC1 as a locus involved in human leukocyte telomere biology. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9293-9298.	7.1	244
41	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	7.1	244
42	Genomeâ€wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. Nature Communications, 2018, 9, 3268.	12.8	221
43	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
44	Genome-wide association meta-analysis for total serum bilirubin levels. Human Molecular Genetics, 2009, 18, 2700-2710.	2.9	214
45	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
46	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
47	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
48	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
49	Common variation in PHACTR1 is associated with susceptibility to cervical artery dissection. Nature Genetics, 2015, 47, 78-83.	21.4	195
50	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
51	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
52	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	3.5	190
53	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
54	Dopamine receptor 1 localizes to neuronal cilia in a dynamic process that requires the Bardet-Biedl syndrome proteins. Cellular and Molecular Life Sciences, 2011, 68, 2951-2960.	5.4	187

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55	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	7.2	182
56	Association of Hypertension Drug Target Genes With Blood Pressure and Hypertension in 86 588 Individuals. Hypertension, 2011, 57, 903-910.	2.7	181
57	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
58	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
59	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
60	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
61	Multidrug resistance polypeptide 1 (MDR1, ABCB1) variant 3435C>T affects mRNA stability. Pharmacogenetics and Genomics, 2005, 15, 693-704.	1.5	166
62	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
63	Common genetic loci influencing plasma homocysteine concentrations and their effect on risk of coronary artery disease. American Journal of Clinical Nutrition, 2013, 98, 668-676.	4.7	161
64	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
65	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
66	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1427-1434.	2.4	157
67	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
68	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
69	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151
70	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. Genome Biology, 2017, 18, 16.	8.8	151
71	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
72	GRASP v2.0: an update on the Genome-Wide Repository of Associations between SNPs and phenotypes. Nucleic Acids Research, 2015, 43, D799-D804.	14.5	143

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73	70-year legacy of the Framingham Heart Study. Nature Reviews Cardiology, 2019, 16, 687-698.	13.7	143
74	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
75	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
76	Genome-wide identification of microRNA expression quantitative trait loci. Nature Communications, 2015, 6, 6601.	12.8	134
77	Whole-genome sequenceâ€"based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132
78	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	10.2	130
79	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
80	Imputation of Exome Sequence Variants into Population- Based Samples and Blood-Cell-Trait-Associated Loci in African Americans: NHLBI GO Exome Sequencing Project. American Journal of Human Genetics, 2012, 91, 794-808.	6.2	123
81	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
82	Relation of Platelet and Leukocyte Inflammatory Transcripts to Body Mass Index in the Framingham Heart Study. Circulation, 2010, 122, 119-129.	1.6	121
83	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	21.4	116
84	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
85	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112
86	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
87	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
88	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
89	Clinical and Genetic Correlates of Growth Differentiation Factor 15 in the Community. Clinical Chemistry, 2012, 58, 1582-1591.	3.2	106
90	Gene Expression Signatures of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1418-1426.	2.4	105

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91	Theta reset produces optimal conditions for long-term potentiation. Hippocampus, 2004, 14, 684-687.	1.9	103
92	Identification of common genetic variants controlling transcript isoform variation in human whole blood. Nature Genetics, 2015, 47, 345-352.	21.4	103
93	Characterization of the platelet transcriptome by RNA sequencing in patients with acute myocardial infarction. Platelets, 2016, 27, 230-239.	2.3	103
94	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
95	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. Molecular Systems Biology, 2015, 11, 799.	7.2	102
96	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
97	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	2.4	101
98	Dynamic Role of trans Regulation of Gene Expression in Relation to Complex Traits. American Journal of Human Genetics, 2017, 100, 571-580.	6.2	101
99	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. Journal of Clinical Investigation, 2013, 123, 4208-4218.	8.2	101
100	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	3.2	96
101	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	1.4	95
102	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
103	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. Nature Genetics, 2019, 51, 1580-1587.	21.4	92
104	Polymorphisms affecting gene transcription and mRNA processing in pharmacogenetic candidate genes: detection through allelic expression imbalance in human target tissues. Pharmacogenetics and Genomics, 2008, 18, 781-791.	1.5	90
105	Common Genetic Variation in the 3â€²- BCL11B Gene Desert Is Associated With Carotid-Femoral Pulse Wave Velocity and Excess Cardiovascular Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 81-90.	5.1	90
106	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
107	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
108	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88

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109	Association of Novel Genetic Loci With Circulating Fibrinogen Levels. Circulation: Cardiovascular Genetics, 2009, 2, 125-133.	5.1	86
110	Common variants in the calcium-sensing receptor gene are associated with total serum calcium levels. Human Molecular Genetics, 2010, 19, 4296-4303.	2.9	86
111	Evolution of the germ lineâ€“soma relationship in vertebrate embryos. Reproduction, 2011, 141, 291-300.	2.6	86
112	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	6.2	85
113	Transient Accumulation of 5-Carboxylcytosine Indicates Involvement of Active Demethylation in Lineage Specification of Neural Stem Cells. Cell Reports, 2014, 7, 1353-1361.	6.4	85
114	Polymorphisms affecting gene regulation and mRNA processing: Broad implications for pharmacogenetics. , 2005, 106, 19-38.		83
115	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Human Molecular Genetics, 2014, 23, 1957-1963.	2.9	82
116	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
117	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	1.3	74
118	Discovery and replication of novel blood pressure genetic loci in the Women's Genome Health Study. Journal of Hypertension, 2011, 29, 62-69.	0.5	73
119	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
120	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	6.7	72
121	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2560-2569.	7.1	71
122	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
123	Syntaxin-binding protein STXBP5 inhibits endothelial exocytosis and promotes platelet secretion. Journal of Clinical Investigation, 2014, 124, 4503-4516.	8.2	68
124	Sex- and age-interacting eQTLs in human complex diseases. Human Molecular Genetics, 2014, 23, 1947-1956.	2.9	66
125	Pharmacogenomics of the RNA World: Structural RNA Polymorphisms in Drug Therapy. Clinical Pharmacology and Therapeutics, 2011, 89, 355-365.	4.7	64
126	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64

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127	Stochastic specification of primordial germ cells from mesoderm precursors in axolotl embryos. Development (Cambridge), 2014, 141, 2429-2440.	2.5	64
128	An extended IUPAC nomenclature code for polymorphic nucleic acids. Bioinformatics, 2010, 26, 1386-1389.	4.1	63
129	PRIMe: a method for characterization and evaluation of pleiotropic regions from multiple genome-wide association studies. Bioinformatics, 2011, 27, 1201-1206.	4.1	63
130	Association of Single Nucleotide Polymorphisms on Chromosome 9p21.3 With Platelet Reactivity. Circulation: Cardiovascular Genetics, 2010, 3, 445-453.	5.1	61
131	Gene expression analysis of whole blood, peripheral blood mononuclear cells, and lymphoblastoid cell lines from the Framingham Heart Study. Physiological Genomics, 2012, 44, 59-75.	2.3	61
132	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
133	Primordial germ cells: the first cell lineage or the last cells standing?. Development (Cambridge), 2015, 142, 2730-2739.	2.5	60
134	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
135	Resequencing and Clinical Associations of the 9p21.3 Region. Circulation, 2013, 127, 799-810.	1.6	58
136	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
137	Six Novel Loci Associated with Circulating VEGF Levels Identified by a Meta-analysis of Genome-Wide Association Studies. PLoS Genetics, 2016, 12, e1005874.	3.5	56
138	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
139	Dissecting the Roles of MicroRNAs in Coronary Heart Disease via Integrative Genomic Analyses. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1011-1021.	2.4	53
140	Epigenetic reprogramming of breast cancer cells with oocyte extracts. Molecular Cancer, 2011, 10, 7.	19.2	52
141	Axolotl Nanog activity in mouse embryonic stem cells demonstrates that ground state pluripotency is conserved from urodele amphibians to mammals. Development (Cambridge), 2010, 137, 2973-2980.	2.5	51
142	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
143	ADP Platelet Hyperreactivity Predicts Cardiovascular Disease in the FHS (Framingham Heart Study). Journal of the American Heart Association, 2018, 7, .	3.7	51
144	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50

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145	Epigenetic marks in somatic chromatin are remodelled to resemble pluripotent nuclei by amphibian oocyte extracts. Epigenetics, 2009, 4, 194-202.	2.7	49
146	Expression ofDazlandVasain turtle embryos and ovaries: evidence for inductive specification of germ cells. Evolution & Development, 2009, 11, 525-534.	2.0	49
147	Single-Nucleotide Polymorphism Bioinformatics. Circulation: Cardiovascular Genetics, 2009, 2, 530-536.	5.1	49
148	Genetic associations with expression for genes implicated in GWAS studies for atherosclerotic cardiovascular disease and blood phenotypes. Human Molecular Genetics, 2014, 23, 782-795.	2.9	49
149	Synthesis of 53 tissue and cell line expression QTL datasets reveals master eQTLs. BMC Genomics, 2014, 15, 532.	2.8	49
150	Genome-Wide Association of Pericardial Fat Identifies a Unique Locus for Ectopic Fat. PLoS Genetics, 2012, 8, e1002705.	3.5	48
151	5-hydroxymethyl-cytosine enrichment of non-committed cells is not a universal feature of vertebrate development. Epigenetics, 2012, 7, 383-389.	2.7	48
152	Acquisition of Germ Plasm Accelerates Vertebrate Evolution. Science, 2014, 344, 200-203.	12.6	48
153	Caenorhabditis elegans orthologs of human genes differentially expressed with age are enriched for determinants of longevity. Aging Cell, 2017, 16, 672-682.	6.7	47
154	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
155	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. American Journal of Human Genetics, 2017, 100, 51-63.	6.2	45
156	The genetics of common variation affecting platelet development, function and pharmaceutical targeting. Journal of Thrombosis and Haemostasis, 2011, 9, 246-257.	3.8	44
157	The genetics of platelet count and volume in humans. Platelets, 2018, 29, 125-130.	2.3	44
158	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
159	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
160	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. Nature Genetics, 2016, 48, 867-876.	21.4	41
161	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	2.4	40
162	A conserved mechanism for vertebrate mesoderm specification in urodele amphibians and mammals. Developmental Biology, 2010, 343, 138-152.	2.0	39

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163	Cardiovascular correlates of platelet count and volume in the Framingham Heart Study. Annals of Epidemiology, 2015, 25, 492-498.	1.9	39
164	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	3.5	39
165	Association of Genetic Variation in the Mitochondrial Genome With Blood Pressure and Metabolic Traits. Hypertension, 2012, 60, 949-956.	2.7	38
166	Association of genomic loci from a cardiovascular gene SNP array with fibrinogen levels in European Americans and African-Americans from six cohort studies: the Candidate Gene Association Resource (CARe). Blood, 2011, 117, 268-275.	1.4	36
167	A systematic heritability analysis of the human whole blood transcriptome. Human Genetics, 2015, 134, 343-358.	3.8	35
168	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
169	Promoter Polymorphisms in ACE (Angiotensin Iâ€“Converting Enzyme) Associated With Clinical Outcomes in Hypertension. Clinical Pharmacology and Therapeutics, 2009, 85, 36-44.	4.7	33
170	The POU-er of gene nomenclature. Development (Cambridge), 2014, 141, 2921-2923.	2.5	33
171	5-Carboxylcytosine levels are elevated in human breast cancers and gliomas. Clinical Epigenetics, 2015, 7, 88.	4.1	33
172	The risk for developing a secondary cancer after breast radiation therapy: Comparison of photon and proton techniques. Radiotherapy and Oncology, 2020, 149, 212-218.	0.6	32
173	Evolution of germ cell development in tetrapods: comparison of urodeles and amniotes. Evolution & Development, 2009, 11, 603-609.	2.0	30
174	Integrative DNA, RNA, and Protein Evidence Connects TREML4 to Coronary Artery Calcification. American Journal of Human Genetics, 2014, 95, 66-76.	6.2	30
175	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
176	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
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