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	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
2	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88
3	Proton Radiotherapy for Patients With Oligometastatic Breast Cancer Involving the Sternum. International Journal of Particle Therapy, 2022, 8, 66-71.	1.8	4
4	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
5	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
6	A year of COVID-19 GWAS results from the GRASP portal reveals potential genetic risk factors. Human Genetics and Genomics Advances, 2022, 3, 100095.	1.7	21
7	Platelet Function Is Associated With Dementia Risk in the Framingham Heart Study. Journal of the American Heart Association, 2022, 11, e023918.	3.7	11
8	Relationship of travel distance with patient demographics, advance care planning, and survival in early-phase clinical trials (EP-CTs).. Journal of Clinical Oncology, 2022, 40, 6558-6558.	1.6	0
9	Protocol requirements and logistical intensity of early-phase clinical trials (EP-CTs).. Journal of Clinical Oncology, 2022, 40, e18609-e18609.	1.6	0
10	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	1.4	21
11	The Association Between Cardiac Mortality and Adjuvant Radiation Therapy Among Older Patients With Stage I Estrogen Positive Breast Cancer: A Surveillance, Epidemiology, and End Results (SEER)â€“Based Study on Cardiac Mortality and Radiation Therapy. Advances in Radiation Oncology, 2021, 6, 100633.	1.2	2
12	Genome-wide transcriptome study using deep RNA sequencing for myocardial infarction and coronary artery calcification. BMC Medical Genomics, 2021, 14, 45.	1.5	5
13	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
14	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	1.4	19
15	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
16	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
17	FGL1 as a modulator of plasma Dâ€dimer levels: Exomeâ€wide marker analysis of plasma tPA, PAIâ€1, and Dâ€dimer. Journal of Thrombosis and Haemostasis, 2021, 19, 2019-2028.	3.8	1
18	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	6.7	72

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19	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
20	Target coverage and cardiopulmonary sparing with the updated ESTRO-ACROP contouring guidelines for postmastectomy radiation therapy after breast reconstruction: a treatment planning study using VMAT and proton PBS techniques. Acta OncolÃ³gica, 2021, 60, 1440-1451.	1.8	5
21	ZBTB33 Is Mutated in Clonal Hematopoiesis and Myelodysplastic Syndromes and Impacts RNA Splicing. Blood Cancer Discovery, 2021, 2, 500-517.	5.0	17
22	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.7	2
23	Proton Radiation Therapy for Pediatric Craniopharyngioma. International Journal of Radiation Oncology Biology Physics, 2021, 110, 1480-1487.	0.8	27
24	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16
25	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	4.5	13
26	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
27	Identifying early-phase clinical trial (EP-CT) participants at risk for poor outcomes.. Journal of Clinical Oncology, 2021, 39, 301-301.	1.6	0
28	Time burden and logistical intensity of early-phase clinical trials (EP-CTs).. Journal of Clinical Oncology, 2021, 39, 84-84.	1.6	0
29	Supportive care services and goals of care in early phase clinical trials (EP-CTs).. Journal of Clinical Oncology, 2021, 39, 26-26.	1.6	2
30	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
31	The Neutrophil to Lymphocyte Ratio Is Associated With the Risk of Subsequent Dementia in the Framingham Heart Study. Frontiers in Aging Neuroscience, 2021, 13, 773984.	3.4	19
32	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
33	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
34	Platelet Measurements and Type 2 Diabetes: Investigations in Two Population-Based Cohorts. Frontiers in Cardiovascular Medicine, 2020, 7, 118.	2.4	16
35	Integrative Genomic Analysis Reveals Four Protein Biomarkers for Platelet Traits. Circulation Research, 2020, 127, 1182-1194.	4.5	7
36	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

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37	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
38	The adjuvant use of capecitabine for residual disease following pre-operative chemotherapy for breast cancer: Challenges applying CREATE-X to a US population. Journal of Oncology Pharmacy Practice, 2020, , 107815522097175.	0.9	2
39	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. Circulation Research, 2020, 127, 394-396.	4.5	3
40	Arms positioning in post-mastectomy proton radiation: Feasibility and development of a new arms down contouring atlas. Physics and Imaging in Radiation Oncology, 2020, 14, 6-11.	2.9	8
41	A Platelet Function Modulator of Thrombin Activation Is Causally Linked to Cardiovascular Disease and Affects PAR4 Receptor Signaling. American Journal of Human Genetics, 2020, 107, 211-221.	6.2	26
42	The Impact of an Introductory Radiation Oncology Curriculum (IROC) for Radiation Oncology Trainees Across the United States and Canada. International Journal of Radiation Oncology Biology Physics, 2020, 107, 408-416.	0.8	13
43	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
44	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
45	Oncologist experiences regarding patient-recorded clinical encounters: Implications for the patient-doctor relationship.. Journal of Clinical Oncology, 2020, 38, 290-290.	1.6	0
46	Involvement of social work services in patients with advanced cancer in early-phase clinical trials (EP-CTs).. Journal of Clinical Oncology, 2020, 38, 28-28.	1.6	0
47	Understanding the supportive care needs of early-phase cancer clinical trial (CT) participants.. Journal of Clinical Oncology, 2020, 38, 26-26.	1.6	3
48	Palliative care referrals in patients with advanced cancer on early-phase cancer clinical trials (EP-CTs).. Journal of Clinical Oncology, 2020, 38, 29-29.	1.6	6
49	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
50	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. Nature Genetics, 2019, 51, 1580-1587.	21.4	92
51	Genome-wide identification of DNA methylation QTLs in whole blood highlights pathways for cardiovascular disease. Nature Communications, 2019, 10, 4267.	12.8	139
52	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
53	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
54	70-year legacy of the Framingham Heart Study. Nature Reviews Cardiology, 2019, 16, 687-698.	13.7	143

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55	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
56	Platelet Genomics. , 2019, , 99-126.		0
57	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
58	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
59	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
60	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
61	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
62	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
63	ADP Platelet Hyperreactivity Predicts Cardiovascular Disease in the FHS (Framingham Heart Study). Journal of the American Heart Association, 2018, 7, .	3.7	51
64	Large-scale pharmacogenomic study of sulfonylureas and the QT, JT and QRS intervals: CHARGE Pharmacogenomics Working Group. Pharmacogenomics Journal, 2018, 18, 127-135.	2.0	12
65	The genetics of platelet count and volume in humans. Platelets, 2018, 29, 125-130.	2.3	44
66	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
67	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16
68	Reversal of Agingâ€Induced Increases in Aortic Stiffness by Targeting Cytoskeletal Proteinâ€Protein Interfaces. Journal of the American Heart Association, 2018, 7, .	3.7	17
69	Genomeâ€wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. Nature Communications, 2018, 9, 3268.	12.8	221
70	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
71	Novel Thrombotic Function of a Human SNP in STXBP5 Revealed by CRISPR/Cas9 Gene Editing in Mice. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 264-270.	2.4	24
72	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

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73	Integrated genome-wide analysis of expression quantitative trait loci aids interpretation of genomic association studies. Genome Biology, 2017, 18, 16.	8.8	151
74	Platelet function as a risk factor for venous thromboembolism in the Framingham Heart Study. Thrombosis Research, 2017, 151, 57-62.	1.7	24
75	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
76	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
77	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
78	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
79	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
80	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
81	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260
82	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
83	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
84	Mean platelet volume â€" A controversial marker of platelets that requires further unpacking. Thrombosis Research, 2017, 153, 118-119.	1.7	5
85	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
86	Mechanisms of Vertebrate Germ Cell Determination. Advances in Experimental Medicine and Biology, 2017, 953, 383-440.	1.6	13
87	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
88	D-Dimer in African Americans. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 2220-2227.	2.4	40
89	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
90	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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91	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	3.5	39
92	Whole exome sequencing in the Framingham Heart Study identifies rare variation in HYAL2 that influences platelet aggregation. Thrombosis and Haemostasis, 2017, 117, 1083-1092.	3.4	11
93	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
94	The complex genetics of gait speed: genome-wide meta-analysis approach. Aging, 2017, 9, 209-246.	3.1	21
95	Detection of Modified Forms of Cytosine Using Sensitive Immunohistochemistry. Journal of Visualized Experiments, 2016, , .	0.3	8
96	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
97	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
98	Genetic loci associated with ideal cardiovascular health: A meta-analysis of genome-wide association studies. American Heart Journal, 2016, 175, 112-120.	2.7	25
99	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
100	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
101	Pairing megakaryopoiesis methylation with PEAR1. Blood, 2016, 128, 890-892.	1.4	7
102	<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
103	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
104	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. Diabetes, 2016, 65, 3794-3804.	0.6	22
105	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
106	The role of dietary fat in obesity-induced insulin resistance. American Journal of Physiology - Endocrinology and Metabolism, 2016, 311, E989-E997.	3.5	21
107	KYNURENINE PATHWAY GENES INFLUENCE AGING THROUGH MULTIPLE DISTINCT MOLECULAR MECHANISMS. Gerontologist, The, 2016, 56, 110-111.	3.9	0
108	Stepwise evolution of Elkâ€1 in early deuterostomes. FEBS Journal, 2016, 283, 1025-1038.	4.7	5

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109	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
110	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
111	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
112	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
113	Replication and hematological characterization of human platelet reactivity genetic associations in men from the Caerphilly Prospective Study (CaPS). Journal of Thrombosis and Thrombolysis, 2016, 41, 343-350.	2.1	25
114	Lipids, obesity and gallbladder disease in women: insights from genetic studies using the cardiovascular gene-centric 50K SNP array. European Journal of Human Genetics, 2016, 24, 106-112.	2.8	23
115	Characterization of the platelet transcriptome by RNA sequencing in patients with acute myocardial infarction. Platelets, 2016, 27, 230-239.	2.3	103
116	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	3.2	96
117	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
118	Conditional entropy in variation-adjusted windows detects selection signatures associated with expression quantitative trait loci (eQTLs). BMC Genomics, 2015, 16, S8.	2.8	3
119	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
120	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
121	Primordial germ cells: the first cell lineage or the last cells standing?. Development (Cambridge), 2015, 142, 2730-2739.	2.5	60
122	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
123	Identification of common genetic variants controlling transcript isoform variation in human whole blood. Nature Genetics, 2015, 47, 345-352.	21.4	103
124	A systematic heritability analysis of the human whole blood transcriptome. Human Genetics, 2015, 134, 343-358.	3.8	35
125	LTB4 promotes insulin resistance in obese mice by acting on macrophages, hepatocytes and myocytes. Nature Medicine, 2015, 21, 239-247.	30.7	252
126	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107

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127	Cardiovascular correlates of platelet count and volume in the Framingham Heart Study. Annals of Epidemiology, 2015, 25, 492-498.	1.9	39
128	Genome-wide identification of microRNA expression quantitative trait loci. Nature Communications, 2015, 6, 6601.	12.8	134
129	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
130	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
131	Integrative network analysis reveals molecular mechanisms of blood pressure regulation. Molecular Systems Biology, 2015, 11, 799.	7.2	102
132	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	2.4	101
133	5-Carboxylcytosine levels are elevated in human breast cancers and gliomas. Clinical Epigenetics, 2015, 7, 88.	4.1	33
134	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	5.5	313
135	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
136	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
137	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112
138	Common variation in PHACTR1 is associated with susceptibility to cervical artery dissection. Nature Genetics, 2015, 47, 78-83.	21.4	195
139	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	2.5	13
140	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
141	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
142	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
143	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
144	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56

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145	Association of Levels of Fasting Glucose and Insulin With Rare Variants at the Chromosome 11p11.2-MADD Locus. Circulation: Cardiovascular Genetics, 2014, 7, 374-382.	5.1	12
146	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
147	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
148	Acquisition of Germ Plasm Accelerates Vertebrate Evolution. Science, 2014, 344, 200-203.	12.6	48
149	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
150	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
151	Common dysregulation network in the human prefrontal cortex underlies two neurodegenerative diseases. Molecular Systems Biology, 2014, 10, 743.	7.2	182
152	The POU-er of gene nomenclature. Development (Cambridge), 2014, 141, 2921-2923.	2.5	33
153	Integrative DNA, RNA, and Protein Evidence Connects TREML4 to Coronary Artery Calcification. American Journal of Human Genetics, 2014, 95, 66-76.	6.2	30
154	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
155	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
156	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
157	Synthesis of 53 tissue and cell line expression QTL datasets reveals master eQTLs. BMC Genomics, 2014, 15, 532.	2.8	49
158	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
159	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
160	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
161	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
162	Sex- and age-interacting eQTLs in human complex diseases. Human Molecular Genetics, 2014, 23, 1947-1956.	2.9	66

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163	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
164	Stochastic specification of primordial germ cells from mesoderm precursors in axolotl embryos. Development (Cambridge), 2014, 141, 2429-2440.	2.5	64
165	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
166	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
167	Syntaxin-binding protein STXBP5 inhibits endothelial exocytosis and promotes platelet secretion. Journal of Clinical Investigation, 2014, 124, 4503-4516.	8.2	68
168	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
169	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
170	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
171	Resequencing and Clinical Associations of the 9p21.3 Region. Circulation, 2013, 127, 799-810.	1.6	58
172	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
173	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
174	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132
175	A Systems Biology Framework Identifies Molecular Underpinnings of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1427-1434.	2.4	157
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