Lisa R Yanek

List of Publications by Year
in descending order

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143 papers	9,032 citations	47006 47 h-index	54911 84 g-index
157 all docs	157 docs citations	157 times ranked	16090 citing authors

#	Article	IF	Citations
1	Early Readmission following NICU Discharges among a National Sample: Associated Factors and Spending. American Journal of Perinatology, 2023, 40, 1437-1445.	1.4	3
2	Galectin-4 as a Novel Biomarker of Neonatal Intestinal Injury. Digestive Diseases and Sciences, 2022, 67, 863-871.	2.3	3
3	Factors associated with a change in disposition for mental health patients boarding in an urban Paediatric emergency department. Microbial Biotechnology, 2022, 16, 509-517.	1.7	2
4	Cardiovascular disease is a leading cause of mortality among TTP survivors in clinical remission. Blood Advances, 2022, 6, 1264-1270.	5.2	20
5	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
6	Obesity Partially Mediates the Diabetogenic Effect of Lowering LDL Cholesterol. Diabetes Care, 2022, 45, 232-240.	8.6	10
7	Obstructed defecation syndrome in the first week after pelvic reconstructive surgery. International Urogynecology Journal, 2022, 33, 2985-2992.	1.4	1
8	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
9	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
10	Mitochondrial Creatine Kinase Attenuates Pathologic Remodeling in Heart Failure. Circulation Research, 2022, , CIRCRESAHA121319648.	4.5	6
11	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
12	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
13	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
14	Predictors of new persistent opioid use after benign hysterectomy in the United States. American Journal of Obstetrics and Gynecology, 2022, 227, 68.e1-68.e24.	1.3	5
15	Secondary analyses for genomeâ€wide association studies using expression quantitative trait loci. Genetic Epidemiology, 2022, , .	1.3	2
16	Malnutrition Increases Hospital Length of Stay and Mortality among Adult Inpatients with COVID-19. Nutrients, 2022, 14, 1310.	4.1	20
17	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
18	Under-Enrollment of Obese Heart Failure with Preserved Ejection Fraction Patients in Major HFpEF Clinical Trials. Journal of Cardiac Failure, 2022, 28, 723-731.	1.7	3

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19	Whole blood transfusion for severe malarial anemia in a high Plasmodium falciparum transmission setting. Clinical Infectious Diseases, 2022, , .	5.8	2
20	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
21	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
22	Markers of endothelial cell activation are associated with the severity of pulmonary disease in COVID-19. PLoS ONE, 2022, 17, e0268296.	2.5	12
23	Association of Vascular Properties With the Brain White Matter Hyperintensity in Middleâ€Aged Population. Journal of the American Heart Association, 2022, 11, .	3.7	5
24	Disparities in Telemedicine Success and Their Association With Adverse Outcomes in Patients With Thoracic Cancer During the COVID-19 Pandemic. JAMA Network Open, 2022, 5, e2220543.	5.9	15
25	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
26	Transcriptional profile of platelets and iPSC-derived megakaryocytes from whole-genome and RNA sequencing. Blood, 2021, 137, 959-968.	1.4	21
27	White Matter Injury Is Associated with Reduced Manual Dexterity and Elevated Serum Ceramides in Subjects with Cerebral Small Vessel Disease. Cerebrovascular Diseases, 2021, 50, 100-107.	1.7	6
28	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
29	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
30	Factors associated with a lower chance of having gaps in care in adult congenital heart disease. Cardiology in the Young, 2021, 31, 1576-1581.	0.8	4
31	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18
32	Racial differences in platelet serotonin polymorphisms in acute coronary syndrome. Thrombosis Research, 2021, 200, 115-120.	1.7	1
33	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
34	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23
35	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
36	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

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37	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
38	Gene and protein expression in human megakaryocytes derived from induced pluripotent stem cells. Journal of Thrombosis and Haemostasis, 2021, 19, 1783-1799.	3.8	6
39	Heart rate trajectories in patients recovering from acute myocardial infarction: A longitudinal analysis of Apple Watch heart rate recordings. Cardiovascular Digital Health Journal, 2021, 2, 270-281.	1.3	4
40	Visceral adiposity, muscle composition, and exercise tolerance in heart failure with preserved ejection fraction. ESC Heart Failure, 2021, 8, 2535-2545.	3.1	21
41	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
42	Genome sequencing unveils a regulatory landscape of platelet reactivity. Nature Communications, 2021, 12, 3626.	12.8	29
43	Association of Coronary Artery Atherosclerosis With Brain White Matter Hyperintensity. Stroke, 2021, 52, 2594-2600.	2.0	13
44	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
45	Major adverse cardiovascular events in survivors of immuneâ€mediated thrombotic thrombocytopenic purpura. American Journal of Hematology, 2021, 96, 1587-1594.	4.1	9
46	Use of white cell count, age, and presence of other injuries in stratifying risk of intracranial injury in pediatric trauma. Journal of Investigative Medicine, 2021, 69, 408-410.	1.6	0
47	Spinal Anesthesia with Targeted Sedation Based on Bispectral Index Values Compared with General Anesthesia with Masked Bispectral Index Values to Reduce Delirium: The SHARP Randomized Controlled Trial. Anesthesiology, 2021, 135, 992-1003.	2.5	18
48	Opioid Dispensing After Hysteroscopy in the United States. Obstetrics and Gynecology, 2021, 138, 888-890.	2.4	3
49	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	4.8	2
50	Endomyocardial Biopsy Characterization of HeartÂFailure With Preserved EjectionÂFraction and Prevalence of Cardiac Amyloidosis. JACC: Heart Failure, 2020, 8, 712-724.	4.1	138
51	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
52	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
53	Whole genome sequence association analyses of brain volumes in the TOPMed program. Alzheimer's and Dementia, 2020, 16, e040627.	0.8	0
54	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89

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55	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
56	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
57	Characteristics of Mental Health Patients Boarding for Longer Than 24 Hours in a Pediatric Emergency Department. JAMA Pediatrics, 2020, 174, 1206.	6.2	9
58	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
59	Genomic integrity of human induced pluripotent stem cells across nine studies in the NHLBI NextGen program. Stem Cell Research, 2020, 46, 101803.	0.7	10
60	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
61	Using Mobile Health Tools to Assess Physical Activity Guideline Adherence and Smoking Urges: Secondary Analysis of mActive-Smoke. JMIR Cardio, 2020, 4, e14963.	1.7	0
62	The relationship of family history and risk of type 2 diabetes differs by ancestry. Diabetes and Metabolism, 2019, 45, 261-267.	2.9	1
63	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
64	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
65	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
66	Shaping anesthetic techniques to reduce post-operative delirium (SHARP) study: a protocol for a prospective pragmatic randomized controlled trial to evaluate spinal anesthesia with targeted sedation compared with general anesthesia in older adults undergoing lumbar spine fusion surgery. BMC Anesthesiology, 2019, 19, 192.	1.8	12
67	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
68	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
69	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
70	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
71	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
72	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112

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73	Evolution of Hominin Polyunsaturated Fatty Acid Metabolism: From Africa to the New World. Genome Biology and Evolution, 2019, 11, 1417-1430.	2.5	38
74	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
75	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
76	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
77	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
78	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
79	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
80	Targeted deep sequencing of the PEAR1 locus for platelet aggregation in European and African American families. Platelets, 2019, 30, 380-386.	2.3	19
81	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
82	Genome-Wide Association Study of Heavy Smoking and Daily/Nondaily Smoking in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Nicotine and Tobacco Research, 2018, 20, 448-457.	2.6	21
83	Hypertension Is Associated with White Matter Disruption in Apparently Healthy Middle-Aged Individuals. American Journal of Neuroradiology, 2018, 39, 2243-2248.	2.4	32
84	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
85	Diabetes and Platelet Response to Low-dose Aspirin. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 4599-4608.	3.6	8
86	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
87	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. Stroke, 2018, 49, 1812-1819.	2.0	17
88	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
89	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
90	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

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91	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
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	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
94	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
95	Integrity of Induced Pluripotent Stem Cell (iPSC) Derived Megakaryocytes as Assessed by Genetic and Transcriptomic Analysis. PLoS ONE, 2017, 12, e0167794.	2.5	9
96	Abstract TMP93: Hypertension is Associated with Disruption of White Matter Tracts in Healthy Middle-aged Persons at Risk for Vascular Disease. Stroke, 2017, 48, .	2.0	0
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	P1â€118: Association of Lowâ€Frequency and Rare Coding Variants with Information Processing Speed. Alzheimer's and Dementia, 2016, 12, P448.	0.8	0
99	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
100	SCARB1 Gene Variants Are Associated With the Phenotype of Combined High High-Density Lipoprotein Cholesterol and High Lipoprotein (a). Circulation: Cardiovascular Genetics, 2016, 9, 408-418.	5.1	29
101	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
102	Relation of Plasma Lipoprotein(a) to Subclinical Coronary Plaque Volumes, Three-Vessel and Left Main Coronary Disease, and Severe Coronary Stenoses in Apparently Healthy African-Americans With a Family History of Early-Onset Coronary Artery Disease. American Journal of Cardiology, 2016, 118, 656-661.	1.6	24
103	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
104	Impact of Self-Preference Community Fitness Interventions in High-Risk African Americans. Family and Community Health, 2016, 39, 251-262.	1.1	1
105	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
106	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
107	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
108	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73

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109	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
110	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
111	Meta-analysis of Correlated Traits via Summary Statistics from GWASs with an Application in Hypertension. American Journal of Human Genetics, 2015, 96, 21-36.	6.2	321
112	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
113	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
114	Age differences in periventricular and deep white matter lesions. Neurobiology of Aging, 2015, 36, 1653-1658.	3.1	38
115	Genome-wide association study of platelet aggregation in African Americans. BMC Genetics, 2015, 16, 58.	2.7	50
116	Greater Collagen-Induced Platelet Aggregation Following Cyclooxygenase 1 Inhibition Predicts Incident Acute Coronary Syndromes. Clinical and Translational Science, 2015, 8, 17-22.	3.1	13
117	Effect of white matter lesions on manual dexterity in healthy middle-aged persons. Neurology, 2015, 84, 1920-1926.	1.1	22
118	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
119	Extreme Deep White Matter Hyperintensity Volumes Are Associated with African American Race. Cerebrovascular Diseases, 2014, 37, 244-250.	1.7	47
120	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
121	Noncalcified Coronary Plaque Volumes in Healthy People With a Family History of Early Onset Coronary Artery Disease. Circulation: Cardiovascular Imaging, 2014, 7, 446-453.	2.6	47
122	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
123	Prospective Associations of Coronary Heart Disease Loci in African Americans Using the MetaboChip: The PAGE Study. PLoS ONE, 2014, 9, e113203.	2.5	27
124	A Simple Scalable Association Hypothesis Test Combining Gene-wide Evidence from Multiple Polymorphisms. British Journal of Medicine and Medical Research, 2014, 4, 1413-1422.	0.2	0
125	Abstract 18767: Association of Protein-Coding Genetic Variants with Coronary Arterial Calcification in 21,000 Individuals of European and African Ancestries. Circulation, 2014, 130, .	1.6	0
126	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

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127	Relation of Subclinical Coronary Artery Atherosclerosis to Cerebral White Matter Disease in Healthy Subjects From Families With Early-Onset Coronary Artery Disease. American Journal of Cardiology, 2013, 112, 747-752.	1.6	15
128	Effect of Positive Well-Being on Incidence of Symptomatic Coronary Artery Disease. American Journal of Cardiology, 2013, 112, 1120-1125.	1.6	19
129	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	21.4	232
130	Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. PLoS Genetics, 2013, 9, e1003681.	3.5	109
131	Genome-wide association analysis of red blood cell traits in African Americans: the COGENT Network. Human Molecular Genetics, 2013, 22, 2529-2538.	2.9	57
132	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
133	Targeted Deep Resequencing Identifies Coding Variants in the PEAR1 Gene That Play a Role in Platelet Aggregation. PLoS ONE, 2013, 8, e64179.	2.5	28
134	Genome-Wide Association Study of Platelet Function in African Americans. Blood, 2012, 120, 1068-1068.	1.4	0
135	Identification of a specific intronic PEAR1 gene variant associated with greater platelet aggregability and protein expression. Blood, 2011, 118, 3367-3375.	1.4	95
136	Silent myocardial ischaemia and long-term coronary artery disease outcomes in apparently healthy people from families with early-onset ischaemic heart disease. European Heart Journal, 2011, 32, 2766-2772.	2.2	15
137	Genome-Wide Association Study of White Blood Cell Count in 16,388 African Americans: the Continental Origins and Genetic Epidemiology Network (COGENT). PLoS Genetics, 2011, 7, e1002108.	3.5	133
138	Genome-wide meta-analyses identifies seven loci associated with platelet aggregation in response to agonists. Nature Genetics, 2010, 42, 608-613.	21.4	247
139	A Novel Variant in the Platelet Endothelial Aggregation Receptor-1 Gene Is Associated With Increased Platelet Aggregability. Arteriosclerosis, Thrombosis, and Vascular Biology, 2008, 28, 1484-1490.	2.4	100
140	Heritability of Platelet Responsiveness to Aspirin in Activation Pathways Directly and Indirectly Related to Cyclooxygenase-1. Circulation, 2007, 115, 2490-2496.	1.6	147
141	Incidence of Coronary Artery Disease in Siblings of Patients With Premature Coronary Artery Disease: 10 Years of Follow-up. American Journal of Cardiology, 2007, 100, 1410-1415.	1.6	46
142	Sex Differences in Platelet Reactivity and Response to Low-Dose Aspirin Therapy. JAMA - Journal of the American Medical Association, 2006, 295, 1420.	7.4	267
143	Dietary Counseling for High Blood Cholesterol in Families at Risk of Coronary Disease. Preventive Cardiology, 2001, 4, 158-164.	1.1	25