David A TrÃ©gouÃ«t

List of Publications by Year
in descending order

213 papers	22,304 citations	18482 62 h-index	10445 139 g-index
222 all docs	222 docs citations	222 times ranked	30799 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453.	27.0	1,865
3	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
4	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
5	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	13.7	686
6	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
7	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	21.4	440
8	Genome-wide haplotype association study identifies the SLC22A3-LPAL2-LPA gene cluster as a risk locus for coronary artery disease. Nature Genetics, 2009, 41, 283-285.	21.4	427
9	A Novel Channelopathy in Pulmonary Arterial Hypertension. New England Journal of Medicine, 2013, 369, 351-361.	27.0	412
10	Repeated Replication and a Prospective Meta-Analysis of the Association Between Chromosome 9p21.3 and Coronary Artery Disease. Circulation, 2008, 117, 1675-1684.	1.6	356
11	EIF2AK4 mutations cause pulmonary veno-occlusive disease, a recessive form of pulmonary hypertension. Nature Genetics, 2014, 46, 65-69.	21.4	351
12	Cytochrome P450 2C9 (CYP2C9) and vitamin K epoxide reductase (VKORC1) genotypes as determinants of acenocoumarol sensitivity. Blood, 2005, 106, 135-140.	1.4	335
13	A genome-wide association study identifies two loci associated with heart failure due to dilated cardiomyopathy. European Heart Journal, 2011, 32, 1065-1076.	2.2	292
14	Common susceptibility alleles are unlikely to contribute as strongly as the FV and ABO loci to VTE risk: results from a GWAS approach. Blood, 2009, 113, 5298-5303.	1.4	283
15	A new algorithm for haplotypeâ€based association analysis: the Stochasticâ€EM algorithm. Annals of Human Genetics, 2004, 68, 165-177.	0.8	258
16	Human herpesvirus 8 transmission from mother to child and between siblings in an endemic population. Lancet, The, 2000, 356, 1062-1065.	13.7	255
17	A new JAVA interface implementation of THESIAS: testing haplotype effects in association studies. Bioinformatics, 2007, 23, 1038-1039.	4.1	231
18	Thymidylate Synthase Gene Polymorphism Predicts Toxicity in Colorectal Cancer Patients Receiving 5-Fluorouracil-based Chemotherapy. Clinical Cancer Research, 2004, 10, 5880-5888.	7.0	228

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19	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	6.2	222
20	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	21.4	218
21	New Susceptibility Loci Associated with Kidney Disease in Type 1 Diabetes. PLoS Genetics, 2012, 8, e1002921.	3.5	216
22	Genetic Analysis of the Interleukin-18 System Highlights the Role of the Interleukin-18 Gene in Cardiovascular Disease. Circulation, 2005, 112, 643-650.	1.6	205
23	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
24	Activated thrombin activatable fibrinolysis inhibitor levels are associated with the risk of cardiovascular death in patients with coronary artery disease: the AtheroGene study. Journal of Thrombosis and Haemostasis, 2009, 7, 49-57.	3.8	169
25	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
26	Specific haplotypes of the P-selectin gene are associated with myocardial infarction. Human Molecular Genetics, 2002, 11, 2015-2023.	2.9	161
27	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	21.4	152
28	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	2.8	149
29	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	6.2	149
30	Pharmacogenetic Assessment of Toxicity and Outcome in Patients With Metastatic Colorectal Cancer Treated With LV5FU2, FOLFOX, and FOLFIRI: FFCD 2000-05. Journal of Clinical Oncology, 2010, 28, 2556-2564.	1.6	146
31	Genetics of Venous Thrombosis: Insights from a New Genome Wide Association Study. PLoS ONE, 2011, 6, e25581.	2.5	127
32	Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. PLoS Genetics, 2011, 7, e1002367.	3.5	126
33	Metabolic Determinants Are Much More Important Than Genetic Polymorphisms in Determining the PAI-1 Activity and Antigen Plasma Concentrations. Arteriosclerosis, Thrombosis, and Vascular Biology, 1998, 18, 84-91.	2.4	123
34	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
35	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. Lancet Respiratory Medicine,the, 2019, 7, 227-238.	10.7	122
36	Human CalDAG-GEFI gene (RASGRP2) mutation affects platelet function and causes severe bleeding. Journal of Experimental Medicine, 2014, 211, 1349-1362.	8.5	117

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37	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. Nature Communications, 2015, 6, 6326.	12.8	115
38	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	2.2	113
39	Genome-wide haplotype association study identifies the FRMD4A gene as a risk locus for Alzheimer's disease. Molecular Psychiatry, 2013, 18, 461-470.	7.9	103
40	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
41	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	2.4	101
42	Removing Batch Effects from Longitudinal Gene Expression - Quantile Normalization Plus ComBat as Best Approach for Microarray Transcriptome Data. PLoS ONE, 2016, 11, e0156594.	2.5	101
43	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99
44	In-Depth Haplotype Analysis of ABCA1 Gene Polymorphisms in Relation to Plasma ApoA1 Levels and Myocardial Infarction. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 775-781.	2.4	96
45	Genetic Variations at the Endocannabinoid Type 1 Receptor Gene (CNR1) Are Associated with Obesity Phenotypes in Men. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 2382-2386.	3.6	96
46	Genome-wide association analysis identifies a susceptibility locus for pulmonary arterial hypertension. Nature Genetics, 2013, 45, 518-521.	21.4	93
47	Testing Association between Candidate-Gene Markers and Phenotype in Related Individuals, by Use of Estimating Equations. American Journal of Human Genetics, 1997, 61, 189-199.	6.2	89
48	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
49	Merkel cell polyomavirus infection occurs during early childhood and is transmitted between siblings. Journal of Clinical Virology, 2013, 58, 288-291.	3.1	86
50	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
51	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
52	Shared genetic regulatory networks for cardiovascular disease and type 2 diabetes in multiple populations of diverse ethnicities in the United States. PLoS Genetics, 2017, 13, e1007040.	3.5	82
53	Genetic Markers Enhance Coronary Risk Prediction in Men: The MORGAM Prospective Cohorts. PLoS ONE, 2012, 7, e40922.	2.5	81
54	Genetics of Venous Thrombosis: update in 2015. Thrombosis and Haemostasis, 2015, 114, 910-919.	3.4	81

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55	Biological and genetic factors influencing plasma factor VIII levels in a healthy family population: results from the Stanislas cohort. British Journal of Haematology, 2005, 128, 91-99.	2.5	80
56	Haplotype Effect of the Matrix Metalloproteinase-1 Gene on Risk of Myocardial Infarction. Circulation Research, 2005, 97, 1070-1076.	4.5	77
57	Genderâ€Specific Association of a Perilipin Gene Haplotype with Obesity Risk in a White Population. Obesity, 2004, 12, 1758-1765.	4.0	75
58	Variation in USF1 shows haplotype effects, geneâ€…:â€…gene and geneâ€…:â€…environment associations with glucose and lipid parameters in the European Atherosclerosis Research Study II. Human Molecular Genetics, 2004, 13, 1587-1597.	2.9	74
59	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
60	Germline variants in ETV6 underlie reduced platelet formation, platelet dysfunction and increased levels of circulating CD34 ⁺ progenitors. Haematologica, 2017, 102, 282-294.	3.5	70
61	Identification of a KCNQ1 Polymorphism Acting as a Protective Modifier Against Arrhythmic Risk in Long-QT Syndrome. Circulation: Cardiovascular Genetics, 2013, 6, 354-361.	5.1	69
62	Combined Effects of Genetic and Environmental Factors on Insulin Resistance Associated With Reduced Fetal Growth. Diabetes, 2002, 51, 3473-3478.	0.6	66
63	Association of Plasminogen Activator Inhibitor (PAI)-1 (SERPINE1) SNPs With Myocardial Infarction, Plasma PAI-1, and Metabolic Parameters. Arteriosclerosis, Thrombosis, and Vascular Biology, 2007, 27, 2250-2257.	2.4	65
64	Association between Angiotensin-Converting Enzyme Gene Polymorphisms and Diabetic Nephropathy: Case-Control, Haplotype, and Family-Based Study in Three European Populations. Journal of the American Society of Nephrology: JASN, 2007, 18, 1284-1291.	6.1	64
65	Combined analysis of three genome-wide association studies on vWF and FVIII plasma levels. BMC Medical Genetics, 2011, 12, 102.	2.1	63
66	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
67	Cox proportional hazards survival regression in haplotype-based association analysis using the Stochastic-EM algorithm. European Journal of Human Genetics, 2004, 12, 971-974.	2.8	61
68	C4BPB/C4BPA is a new susceptibility locus for venous thrombosis with unknown protein Sâ€“independent mechanism: results from genome-wide association and gene expression analyses followed by case-control studies. Blood, 2010, 115, 4644-4650.	1.4	61
69	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
70	High prevalence of laminopathies among patients with metabolic syndrome. Human Molecular Genetics, 2011, 20, 3779-3786.	2.9	58
71	Multilocus Genetic Risk Scores for Venous Thromboembolism Risk Assessment. Journal of the American Heart Association, 2014, 3, e001060.	3.7	58
72	A Follow-Up Study of a Genome-wide Association Scan Identifies a Susceptibility Locus for Venous Thrombosis on Chromosome 6p24.1. American Journal of Human Genetics, 2010, 86, 592-595.	6.2	57

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73	The endothelial protein C receptor (PROCR) Ser219Gly variant and risk of common thrombotic disorders: a HuGE review and meta-analysis of evidence from observational studies. Blood, 2012, 119, 2392-2400.	1.4	56
74	Targeted panel sequencing in adult patients with left ventricular nonâ€compaction reveals a large genetic heterogeneity. Clinical Genetics, 2019, 95, 356-367.	2.0	56
75	miR-421 and miR-30c Inhibit SERPINE 1 Gene Expression in Human Endothelial Cells. PLoS ONE, 2012, 7, e44532.	2.5	56
76	TAFI gene haplotypes, TAFI plasma levels and future risk of coronary heart disease: the PRIME Study. Journal of Thrombosis and Haemostasis, 2005, 3, 1503-1510.	3.8	55
77	Genome wide association study for plasma levels of natural anticoagulant inhibitors and protein C anticoagulant pathway: the MARTHA project. British Journal of Haematology, 2012, 157, 230-239.	2.5	55
78	Effect of cytochrome P450 2C19 genotype on voriconazole exposure in cystic fibrosis lung transplant patients. European Journal of Clinical Pharmacology, 2011, 67, 253-260.	1.9	54
79	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.6	54
80	A rare Asian founder polymorphism of Raptor may explain the high prevalence of Moyamoya disease among East Asians and its low prevalence among Caucasians. Environmental Health and Preventive Medicine, 2010, 15, 94-104.	3.4	53
81	KNG1 Ile581Thr and susceptibility to venous thrombosis. Blood, 2011, 117, 3692-3694.	1.4	53
82	Genome-Wide Haplotype Analysis of Cis Expression Quantitative Trait Loci in Monocytes. PLoS Genetics, 2013, 9, e1003240.	3.5	53
83	Pharmacogenetics of acenocoumarol pharmacodynamics. Clinical Pharmacology and Therapeutics, 2004, 75, 403-414.	4.7	49
84	Genome-wide association analysis in dilated cardiomyopathy reveals two new players in systolic heart failure on chromosomes 3p25.1 and 22q11.23. European Heart Journal, 2021, 42, 2000-2011.	2.2	49
85	Effects of Genetically Determined Iron Status on Risk of Venous Thromboembolism and Carotid Atherosclerotic Disease: A Mendelian Randomization Study. Journal of the American Heart Association, 2019, 8, e012994.	3.7	45
86	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 586-594.	5.6	45
87	Reactivation of the Epicardium at the Origin of Myocardial Fibro-Fatty Infiltration During the Atrial Cardiomyopathy. Circulation Research, 2020, 126, 1330-1342.	4.5	45
88	Polymorphisms of the tumor necrosis factor-alpha (TNF) and the TNF-alpha converting enzyme (TACE/ADAM17) genes in relation to cardiovascular mortality: the AtheroGene study. Journal of Molecular Medicine, 2008, 86, 1153-1161.	3.9	44
89	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
90	SORBS1 gene, a new candidate for diabetic nephropathy: results from a multi-stage genome-wide association study in patients with type 1 diabetes. Diabetologia, 2015, 58, 543-548.	6.3	43

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91	SELPLG Gene Polymorphisms in Relation to Plasma SELPLG Levels and Coronary Artery Disease. Annals of Human Genetics, 2003, 67, 504-511.	0.8	42
92	Dissection of familial correlations in hepatitis C virus (HCV) seroprevalence suggests intrafamilial viral transmission and genetic predisposition to infection. Gut, 2008, 57, 1268-1274.	12.1	42
93	A multiâ€stage multiâ€design strategy provides strong evidence that the BAI3 locus is associated with earlyâ€onset venous thromboembolism. Journal of Thrombosis and Haemostasis, 2010, 8, 2671-2679.	3.8	42
94	Current knowledge on the genetics of incident venous thrombosis. Journal of Thrombosis and Haemostasis, 2013, 11, 111-121.	3.8	42
95	G/T Substitution in Intron 1 of the UNC13B Gene Is Associated With Increased Risk of Nephropathy in Patients With Type 1 Diabetes. Diabetes, 2008, 57, 2843-2850.	0.6	39
96	PDGFB, a new candidate plasma biomarker for venous thromboembolism: results from the VEREMA affinity proteomics study. Blood, 2016, 128, e59-e66.	1.4	39
97	Automated Detection of Informative Combined Effects in Genetic Association Studies of Complex Traits. Genome Research, 2003, 13, 1952-1960.	5.5	38
98	Fine mapping of quantitative trait nucleotides underlying thrombin-activatable fibrinolysis inhibitor antigen levels by a transethnic study. Blood, 2006, 108, 1562-1568.	1.4	37
99	Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. American Journal of Human Genetics, 2015, 97, 228-237.	6.2	37
100	Variations in Risk of End-Stage Renal Disease and Risk of Mortality in an International Study of Patients With Type 1 Diabetes and Advanced Nephropathy. Diabetes Care, 2019, 42, 93-101.	8.6	37
101	Lessons from genomeâ€wide association studies in venous thrombosis. Journal of Thrombosis and Haemostasis, 2011, 9, 258-264.	3.8	36
102	Single-Cell Study of Two Rat Models of Pulmonary Arterial Hypertension Reveals Connections to Human Pathobiology and Drug Repositioning. American Journal of Respiratory and Critical Care Medicine, 2021, 203, 1006-1022.	5.6	36
103	Graphical Modeling of Gene Expression in Monocytes Suggests Molecular Mechanisms Explaining Increased Atherosclerosis in Smokers. PLoS ONE, 2013, 8, e50888.	2.5	36
104	Risk factors for venous thromboembolism in women under combined oral contraceptive. Thrombosis and Haemostasis, 2016, 115, 135-142.	3.4	35
105	Genome-wide association study with additional genetic and post-transcriptional analyses reveals novel regulators of plasma factor XI levels. Human Molecular Genetics, 2017, 26, ddw401.	2.9	35
106	Association of vitronectin and plasminogen activator inhibitor-1 levels with the risk of metabolic syndrome and type 2 diabetes mellitus. Thrombosis and Haemostasis, 2011, 106, 416-422.	3.4	34
107	Macrothrombocytopenia and dense granule deficiency associated with FLI1 variants: ultrastructural and pathogenic features. Haematologica, 2017, 102, 1006-1016.	3.5	34
108	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	2.7	34

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109	What is currently known about the genetics of venous thromboembolism at the dawn of next generation sequencing technologies. British Journal of Haematology, 2018, 180, 335-345.	2.5	34
110	Whole-exome sequencing identifies rare variants in STAB2 associated with venous thromboembolic disease. Blood, 2020, 136, 533-541.	1.4	34
111	Combined segregation-linkage analysis of plasma thrombin activatable fibrinolysis inhibitor (TAFI) antigen levels with TAFI gene polymorphisms. Human Genetics, 2001, 109, 191-197.	3.8	33
112	Myeloperoxidase genetic polymorphisms modulate human neutrophil enzyme activity: Genetic determinants for atherosclerosis?. Atherosclerosis, 2006, 188, 150-154.	0.8	33
113	Human thymopoiesis is influenced by a common genetic variant within the TCRA-TCRD locus. Science Translational Medicine, 2018, 10, .	12.4	33
114	Robust validation of methylation levels association at CPT1A locus with lipid plasma levels. Journal of Lipid Research, 2014, 55, 1189-1191.	4.2	32
115	miR-322 regulates insulin signaling pathway and protects against metabolic syndrome-induced cardiac dysfunction in mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2016, 1862, 611-621.	3.8	32
116	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. Scientific Reports, 2017, 7, 11207.	3.3	32
117	Familial Aggregation of Fetal Growth Restriction in a French Cohort of 7,822 Term Births between 1971 and 1985. American Journal of Epidemiology, 2002, 156, 180-187.	3.4	31
118	Small platelet microparticle levels are increased in pulmonary arterial hypertension. European Journal of Clinical Investigation, 2013, 43, 64-71.	3.4	31
119	Association of Oral Contraceptives With Drug-Induced QT Interval Prolongation in Healthy Nonmenopausal Women. JAMA Cardiology, 2018, 3, 877.	6.1	30
120	Novel risk genes identified in a genome-wide association study for coronary artery disease in patients with type 1 diabetes. Cardiovascular Diabetology, 2018, 17, 61.	6.8	29
121	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. Diabetologia, 2019, 62, 292-305.	6.3	29
122	Anti-integrin Î±v therapy improves cardiac fibrosis after myocardial infarction by blunting cardiac PW1+ stromal cells. Scientific Reports, 2020, 10, 11404.	3.3	28
123	Single nucleotide polymorphisms in MMP1 and MMP3 gene promoters as risk factor in head and neck squamous cell carcinoma. Anticancer Research, 2004, 24, 2021-6.	1.1	28
124	A polymorphism in ACE2 is associated with a lower risk for fatal cardiovascular events in females: the MORGAM project. JRAAS - Journal of the Renin-Angiotensin-Aldosterone System, 2011, 12, 504-509.	1.7	27
125	A meta-analysis of genome-wide association studies identifies ORM1 as a novel gene controlling thrombin generation potential. Blood, 2014, 123, 777-785.	1.4	27
126	Fibrogenic Potential of PW1/Peg3 Expressing Cardiac Stem Cells. Journal of the American College of Cardiology, 2017, 70, 728-741.	2.8	27

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127	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
128	Mendelian randomisation analysis of red cell distribution width in pulmonary arterial hypertension. European Respiratory Journal, 2020, 55, 1901486.	6.7	26
129	A genome-wide search for common SNP x SNP interactions on the risk of venous thrombosis. BMC Medical Genetics, 2013, 14, 36.	2.1	25
130	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. Genomics, 2011, 98, 320-326.	2.9	23
131	The Choice of the Filtering Method in Microarrays Affects the Inference Regarding Dosage Compensation of the Active X-Chromosome. PLoS ONE, 2011, 6, e23956.	2.5	23
132	A Parametric Copula Model for Analysis of Familial Binary Data. American Journal of Human Genetics, 1999, 64, 886-893.	6.2	22
133	Family study of the relationship between height and cardiovascular risk factors in the STANISLAS cohort. International Journal of Epidemiology, 2003, 32, 607-614.	1.9	22
134	Influence of ghrelin gene polymorphisms on hypertension and atherosclerotic disease. Hypertension Research, 2010, 33, 155-160.	2.7	22
135	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	1.3	22
136	The Factor XII â^'4C>T Variant and Risk of Common Thrombotic Disorders: A HuGE Review and Meta-Analysis of Evidence From Observational Studies. American Journal of Epidemiology, 2011, 173, 136-144.	3.4	21
137	Familial resemblance of physical activity levels in the Portuguese population. Journal of Science and Medicine in Sport, 2014, 17, 381-386.	1.3	21
138	Whole-Blood miRNA Sequencing Profiling for Vasospasm in Patients With Aneurysmal Subarachnoid Hemorrhage. Stroke, 2018, 49, 2220-2223.	2.0	21
139	Plasma Biomarkers and Identification of Resilient Metabolic Disruptions in Patients With Venous Thromboembolism Using a Metabolic Systems Approach. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 2527-2538.	2.4	21
140	GoldVariants, a resource for sharing rare genetic variants detected in bleeding, thrombotic, and platelet disorders: Communication from the ISTH SSC Subcommittee on Genomics in Thrombosis and Hemostasis. Journal of Thrombosis and Haemostasis, 2021, 19, 2612-2617.	3.8	21
141	Investigation of the Human ANP Gene in Type 1 Diabetic Nephropathy: Case-Control and Follow-up Studies. Diabetes, 2004, 53, 1394-1398.	0.6	20
142	Impact on venous thrombosis risk of newly discovered gene variants associated with FVIII and VWF plasma levels. Journal of Thrombosis and Haemostasis, 2011, 9, 229-231.	3.8	20
143	Plasma levels of hsa-miR-152-3p are associated with diabetic nephropathy in patients with type 2 diabetes. Nephrology Dialysis Transplantation, 2018, 33, 2201-2207.	0.7	20
144	Bivariate familial correlation analysis of quantitative traits by use of estimating equations: Application to a familial analysis of the insulin resistance syndrome. , 1999, 16, 69-83.		19

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145	Applications of the estimating equations theory to genetic epidemiology: a review. Annals of Human Genetics, 2000, 64, 1-14.	0.8	19
146	ABO Blood Group and von Willebrand Factor Levels Partially Explained the Incomplete Penetrance of Congenital Thrombophilia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 2021-2028.	2.4	19
147	A systems-approach reveals human nestin is an endothelial-enriched, angiogenesis-independent intermediate filament protein. Scientific Reports, 2018, 8, 14668.	3.3	19
148	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	1.4	19
149	Lack of association between polymorphisms of the IL18R1 and IL18RAP genes and cardiovascular risk: the MORGAM Project. BMC Medical Genetics, 2009, 10, 44.	2.1	18
150	Influence of coronary artery disease-associated genetic variants on risk of venous thromboembolism. Thrombosis Research, 2014, 134, 426-432.	1.7	18
151	Association of soluble endothelial protein C receptor plasma levels and PROCR rs867186 with cardiovascular risk factors and cardiovascular events in coronary artery disease patients: The Athero Gene Study. BMC Medical Genetics, 2012, 13, 103.	2.1	17
152	Risk assessment of venous thrombosis in families with known hereditary thrombophilia: the MARseillesâ€NImes prediction model. Journal of Thrombosis and Haemostasis, 2014, 12, 138-146.	3.8	17
153	Caution in Interpreting Results from Imputation Analysis When Linkage Disequilibrium Extends over a Large Distance: A Case Study on Venous Thrombosis. PLoS ONE, 2012, 7, e38538.	2.5	17
154	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	1.4	16
155	Preservation Analysis of Macrophage Gene Coexpression Between Human and Mouse Identifies PARK2 as a Genetically Controlled Master Regulator of Oxidative Phosphorylation in Humans. G3: Genes, Genomes, Genetics, 2016, 6, 3361-3371.	1.8	15
156	Comparison of Cox Model Methods in A Low-dimensional Setting with Few Events. Genomics, Proteomics and Bioinformatics, 2016, 14, 235-243.	6.9	15
157	Deciphering the molecular basis of venous thromboembolism: where are we and where should we go?. British Journal of Haematology, 2010, 148, 495-506.	2.5	14
158	Protein S Heerlen mutation heterozygosity is associated with venous thrombosis risk. Scientific Reports, 2017, 7, 45507.	3.3	14
159	Automated detection of informative combined effects in genetic association studies of complex traits. Genome Research, 2003, 13, 1952-60.	5.5	14
160	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	4.5	13
161	GENomE wide analysis of sotalol-induced IKr inhibition during ventricular REPOLarization, â€œGENEREPOL studyâ€• Lack of common variants with large effect sizes. PLoS ONE, 2017, 12, e0181875.	2.5	13
162	Associations of PPARGC1A Haplotypes With Plaque Score but Not With Intima-Media Thickness of Carotid Arteries in Middle-Aged Subjects. Stroke, 2006, 37, 2260-2265.	2.0	12

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164	Adrenomedullin and Arterial Stiffness. Circulation: Cardiovascular Genetics, 2014, 7, 634-641.	5.1	12
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