David A TrÃ©gouÃ«t

List of Publications by Year
in descending order

213 papers	22,304 citations	18436 62 h-index	10424 139 g-index
222 all docs	222 docs citations	222 times ranked	30799 citing authors

#	Article	IF	Citations
1	NPTX1 mutations trigger endoplasmic reticulum stress and cause autosomal dominant cerebellar ataxia. Brain, 2022, 145, 1519-1534.	3.7	10
2	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	5.8	5
3	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	1.9	12
4	Common and Rare 5â€²UTR Variants Altering Upstream Open Reading Frames in Cardiovascular Genomics. Frontiers in Cardiovascular Medicine, 2022, 9, 841032.	1.1	9
5	Two SERPINC1 variants affecting N-glycosylation of Asn224 cause severe thrombophilia not detected by functional assays. Blood, 2022, 140, 140-151.	0.6	11
6	Genome-wide association study on coronary artery disease in type 1 diabetes suggests beta-defensin 127 as a risk locus. Cardiovascular Research, 2021, 117, 600-612.	1.8	12
7	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.	2.5	36
8	A rare coding mutation in the MAST2 gene causes venous thrombosis in a French family with unexplained thrombophilia: The Breizh MAST2 Arg89Gln variant. PLoS Genetics, 2021, 17, e1009284.	1.5	2
9	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. European Heart Journal, 2021, 42, 919-933.	1.0	113
10	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.	1.0	49
11	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	0.6	19
12	CRIP1 expression in monocytes related to hypertension. Clinical Science, 2021, 135, 911-924.	1.8	5
13	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.	1.9	1
14	An artificial neural network approach integrating plasma proteomics and genetic data identifies PLXNA4 as a new susceptibility locus for pulmonary embolism. Scientific Reports, 2021, 11, 14015.	1.6	8
15	Association of Coding Variants in Hydroxysteroid 17-beta Dehydrogenase 14 (HSD17B14) with Reduced Progression to End Stage Kidney Disease in Type 1 Diabetes. Journal of the American Society of Nephrology: JASN, 2021, 32, 2634-2651.	3.0	9
16	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.	1.9	21
17	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	2.4	13
18	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature Genetics, 2021, 53, 1311-1321.	9.4	218

#	ARTICLE	IF	CITATIONS
19	Small Open Reading Frames, How to Find Them and Determine Their Function. Frontiers in Genetics, 2021, 12, 796060.	1.1	10
20	Anti-integrin Î±v therapy improves cardiac fibrosis after myocardial infarction by blunting cardiac PW1+ stromal cells. Scientific Reports, 2020, 10, 11404.	1.6	28
21	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.	1.1	21
22	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
23	Whole-Blood RNA Profiles Associated with Pulmonary Arterial Hypertension and Clinical Outcome. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 586-594.	2.5	45
24	Whole-exome sequencing identifies rare variants in STAB2 associated with venous thromboembolic disease. Blood, 2020, 136, 533-541.	0.6	34
25	Bayesian network analysis of plasma microRNA sequencing data in patients with venous thrombosis. European Heart Journal Supplements, 2020, 22, C34-C45.	0.0	9
26	Reactivation of the Epicardium at the Origin of Myocardial Fibro-Fatty Infiltration During the Atrial Cardiomyopathy. Circulation Research, 2020, 126, 1330-1342.	2.0	45
27	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.	2.6	26
28	ABO blood group, glycosyltransferase activity and risk of venous thromboembolism. Thrombosis Research, 2020, 193, 31-35.	0.8	10
29	Design and Rationale of the ERA-CVD Consortium PREMED-CADâ€"Precision Medicine in Coronary Artery Disease. Biomolecules, 2020, 10, 125.	1.8	1
30	Mendelian randomisation analysis of red cell distribution width in pulmonary arterial hypertension. European Respiratory Journal, 2020, 55, 1901486.	3.1	26
31	A novel rare c.-39C>T mutation in the PROS1 5â€²UTR causing PS deficiency by creating a new upstream translation initiation codon. Clinical Science, 2020, 134, 1181-1190.	1.8	10
32	Multi-omic profiling in pulmonary arterial hypertension. , 2020, , .		0
33	High-Dimensional Multi-Block Analysis of Factors Associated with Thrombin Generation Potential. , 2019, , .		1
34	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
35	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.	1.6	45
36	A Genome Wide Association Study on plasma FV levels identified PLXDC2 as a new modifier of the coagulation process. Journal of Thrombosis and Haemostasis, 2019, 17, 1808-1814.	1.9	6

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37	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
38	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	9.4	152
39	A largeâ€scale exome array analysis of venous thromboembolism. Genetic Epidemiology, 2019, 43, 449-457.	0.6	22
40	OPTIMIR, a novel algorithm for integrating available genome-wide genotype data into miRNA sequence alignment analysis. Rna, 2019, 25, 657-668.	1.6	7
41	Minor allele of the factor V K858R variant protects from venous thrombosis only in non-carriers of factor V Leiden mutation. Scientific Reports, 2019, 9, 3750.	1.6	7
42	Genetic determinants of risk in pulmonary arterial hypertension: international genome-wide association studies and meta-analysis. Lancet Respiratory Medicine,the, 2019, 7, 227-238.	5.2	122
43	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.	2.9	29
44	Targeted panel sequencing in adult patients with left ventricular nonâ€compaction reveals a large genetic heterogeneity. Clinical Genetics, 2019, 95, 356-367.	1.0	56
45	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
46	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.	4.3	37
47	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.3	54
48	No prognostic role of a GWAS-derived genetic risk score in renal outcomes for patients from French cohorts with type 1 and type 2 diabetes. Diabetes and Metabolism, 2019, 45, 494-497.	1.4	5
49	Whole blood levels of S1PR4 mRNA associated with cerebral vasospasm after aneurysmal subarachnoid hemorrhage. Journal of Neurosurgery, 2019, , 1-5.	0.9	2
50	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.	0.4	20
51	MACARON: a python framework to identify and re-annotate multi-base affected codons in whole genome/exome sequence data. Bioinformatics, 2018, 34, 3396-3398.	1.8	5
52	Genome-Wide Association Study Identifies a Novel Genetic Risk Factor for Recurrent Venous Thrombosis. Circulation Genomic and Precision Medicine, 2018, 11, .	1.6	10
53	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.	1.2	34
54	A systems-approach reveals human nestin is an endothelial-enriched, angiogenesis-independent intermediate filament protein. Scientific Reports, 2018, 8, 14668.	1.6	19

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55	Human thymopoiesis is influenced by a common genetic variant within the TCRA-TCRD locus. Science Translational Medicine, 2018, 10, .	5.8	33
56	Association of Oral Contraceptives With Drug-Induced QT Interval Prolongation in Healthy Nonmenopausal Women. JAMA Cardiology, 2018, 3, 877.	3.0	30
57	Whole-Blood miRNA Sequencing Profiling for Vasospasm in Patients With Aneurysmal Subarachnoid Hemorrhage. Stroke, 2018, 49, 2220-2223.	1.0	21
58	DNA methylation age is associated with an altered hemostatic profile in a multiethnic meta-analysis. Blood, 2018, 132, 1842-1850.	0.6	16
59	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.	2.7	29
60	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
61	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.	1.4	35
62	Germline variants in ETV6 underlie reduced platelet formation, platelet dysfunction and increased levels of circulating CD34 ⁺ progenitors. Haematologica, 2017, 102, 282-294.	1.7	70
63	Leveraging cell type specific regulatory regions to detect SNPs associated with tissue factor pathway inhibitor plasma levels. Genetic Epidemiology, 2017, 41, 455-466.	0.6	1
64	Protein S Heerlen mutation heterozygosity is associated with venous thrombosis risk. Scientific Reports, 2017, 7, 45507.	1.6	14
65	Macrothrombocytopenia and dense granule deficiency associated with FLI1 variants: ultrastructural and pathogenic features. Haematologica, 2017, 102, 1006-1016.	1.7	34
66	Homocysteine levels associate with subtle changes in leukocyte DNA methylation: an epigenome-wide analysis. Epigenomics, 2017, 9, 1403-1422.	1.0	6
67	Blood triglyceride levels are associated with DNA methylation at the serine metabolism gene PHGDH. Scientific Reports, 2017, 7, 11207.	1.6	32
68	Fibrogenic Potential of PW1/Peg3 Expressing Cardiac Stem Cells. Journal of the American College of Cardiology, 2017, 70, 728-741.	1.2	27
69	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. Hypertension, 2017, 70, 743-750.	1.3	34
70	Genetic risk factors for venous thrombosis in women using combined oral contraceptives: update of the <scp>PILGRIM</scp> study. Clinical Genetics, 2017, 91, 131-136.	1.0	7
71	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.	1.5	82
72	Association of impaired renal function with venous thrombosis: A genetic risk score approach. Thrombosis Research, 2017, 158, 102-107.	0.8	2

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73	Sex-specific effect of CPB2 Ala147Thr but not Thr325Ile variants on the risk of venous thrombosis: A comprehensive meta-analysis. PLoS ONE, 2017, 12, e0177768.	1.1	5
74	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.	1.1	13
75	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	1.1	10
76	Removing Batch Effects from Longitudinal Gene Expression - Quantile Normalization Plus ComBat as Best Approach for Microarray Transcriptome Data. PLoS ONE, 2016, 11, e0156594.	1.1	101
77	Risk factors for venous thromboembolism in women under combined oral contraceptive. Thrombosis and Haemostasis, 2016, 115, 135-142.	1.8	35
78	Is there still room for additional common susceptibility alleles for venous thromboembolism?. Journal of Thrombosis and Haemostasis, 2016, 14, 1798-1802.	1.9	12
79	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.	0.8	15
80	PDGFB, a new candidate plasma biomarker for venous thromboembolism: results from the VEREMA affinity proteomics study. Blood, 2016, 128, e59-e66.	0.6	39
81	Comparison of Cox Model Methods in A Low-dimensional Setting with Few Events. Genomics, Proteomics and Bioinformatics, 2016, 14, 235-243.	3.0	15
82	Single nucleotide polymorphisms in an intergenic chromosome 2q region associated with tissue factor pathway inhibitor plasma levels and venous thromboembolism. Journal of Thrombosis and Haemostasis, 2016, 14, 1960-1970.	1.9	3
83	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.	1.8	32
84	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73
85	Genetics of Venous Thrombosis: update in 2015. Thrombosis and Haemostasis, 2015, 114, 910-919.	1.8	81
86	Genetic determinants of tissue factor pathway inhibitor plasma levels. Thrombosis and Haemostasis, 2015, 114, 245-257.	1.8	9
87	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	0.9	123
88	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
89	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.3	63
90	Runs of Homozygosity: Association with Coronary Artery Disease and Gene Expression in Monocytes and Macrophages. American Journal of Human Genetics, 2015, 97, 228-237.	2.6	37

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91	Thrombin Generation Potential and Whole-Blood DNA methylation. Thrombosis Research, 2015, 135, 561-564.	0.8	7
92	Long-range epigenetic regulation is conferred by genetic variation located at thousands of independent loci. Nature Communications, 2015, 6, 6326.	5.8	115
93	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.	2.6	222
94	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2207-2217.	1.1	101
95	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.	2.9	43
96	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	1.1	8
97	Adrenomedullin and Arterial Stiffness. Circulation: Cardiovascular Genetics, 2014, 7, 634-641.	5.1	12
98	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.	1.1	43
99	Robust validation of methylation levels association at CPT1A locus with lipid plasma levels. Journal of Lipid Research, 2014, 55, 1189-1191.	2.0	32
100	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.	1.9	17
101	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	2.6	149
102	Familial resemblance of physical activity levels in the Portuguese population. Journal of Science and Medicine in Sport, 2014, 17, 381-386.	0.6	21
103	DNA methylation and body-mass index: a genome-wide analysis. Lancet, The, 2014, 383, 1990-1998.	6.3	686
104	EIF2AK4 mutations cause pulmonary veno-occlusive disease, a recessive form of pulmonary hypertension. Nature Genetics, 2014, 46, 65-69.	9.4	351
105	Multilocus Genetic Risk Scores for Venous Thromboembolism Risk Assessment. Journal of the American Heart Association, 2014, 3, e001060.	1.6	58
106	Human CalDAG-GEFI gene (RASGRP2) mutation affects platelet function and causes severe bleeding. Journal of Experimental Medicine, 2014, 211, 1349-1362.	4.2	117
107	Influence of coronary artery disease-associated genetic variants on risk of venous thromboembolism. Thrombosis Research, 2014, 134, 426-432.	0.8	18
108	A meta-analysis of genome-wide association studies identifies ORM1 as a novel gene controlling thrombin generation potential. Blood, 2014, 123, 777-785.	0.6	27

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109	Genome-Wide Investigation of DNA Methylation Marks Associated with FV Leiden Mutation. PLoS ONE, 2014, 9, e108087.	1.1	7
110	A Novel Channelopathy in Pulmonary Arterial Hypertension. New England Journal of Medicine, 2013, 369, 351-361.	13.9	412
111	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
112	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
113	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.	0.6	99
114	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
115	Merkel cell polyomavirus infection occurs during early childhood and is transmitted between siblings. Journal of Clinical Virology, 2013, 58, 288-291.	1.6	86
116	Small platelet microparticle levels are increased in pulmonary arterial hypertension. European Journal of Clinical Investigation, 2013, 43, 64-71.	1.7	31
117	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
118	Genome-wide association analysis identifies a susceptibility locus for pulmonary arterial hypertension. Nature Genetics, 2013, 45, 518-521.	9.4	93
119	Familial Aggregation of Metabolic Syndrome Indicators in Portuguese Families. BioMed Research International, 2013, 2013, 1-7.	0.9	10
120	Genome-Wide Haplotype Analysis of Cis Expression Quantitative Trait Loci in Monocytes. PLoS Genetics, 2013, 9, e1003240.	1.5	53
121	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
122	Current knowledge on the genetics of incident venous thrombosis. Journal of Thrombosis and Haemostasis, 2013, 11, 111-121.	1.9	42
123	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
124	Genome-wide haplotype association study identifies the FRMD4A gene as a risk locus for Alzheimer's disease. Molecular Psychiatry, 2013, 18, 461-470.	4.1	103
125	Graphical Modeling of Gene Expression in Monocytes Suggests Molecular Mechanisms Explaining Increased Atherosclerosis in Smokers. PLoS ONE, 2013, 8, e50888.	1.1	36
126	New Susceptibility Loci Associated with Kidney Disease in Type 1 Diabetes. PLoS Genetics, 2012, 8, e1002921.	1.5	216

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127	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.	0.6	56
128	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.	1.2	149
129	Lack of association of non-synonymous FUT2 and ALPL polymorphisms with venous thrombosis. Journal of Thrombosis and Haemostasis, 2012, 10, 1693-1695.	1.9	2
130	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.	1.1	19
131	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.	2.6	85
132	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
133	MFGE8 Does Not Influence Chorio-Retinal Homeostasis or Choroidal Neovascularization in vivo. PLoS ONE, 2012, 7, e33244.	1.1	2
134	Genetic Markers Enhance Coronary Risk Prediction in Men: The MORGAM Prospective Cohorts. PLoS ONE, 2012, 7, e40922.	1.1	81
135	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.	1.2	55
136	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.	1.1	17
137	miR-421 and miR-30c Inhibit SERPINE 1 Gene Expression in Human Endothelial Cells. PLoS ONE, 2012, 7, e44532.	1.1	56
138	Comprehensive Exploration of the Effects of miRNA SNPs on Monocyte Gene Expression. PLoS ONE, 2012, 7, e45863.	1.1	8
139	A genome-wide association study identifies two loci associated with heart failure due to dilated cardiomyopathy. European Heart Journal, 2011, 32, 1065-1076.	1.0	292
140	Influence of sex and genetic variability on expression of X-linked genes in human monocytes. Genomics, 2011, 98, 320-326.	1.3	23
141	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.	1.8	34
142	The Choice of the Filtering Method in Microarrays Affects the Inference Regarding Dosage Compensation of the Active X-Chromosome. PLoS ONE, 2011, 6, e23956.	1.1	23
143	KNG1 Ile581Thr and susceptibility to venous thrombosis. Blood, 2011, 117, 3692-3694.	0.6	53
144	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.	1.9	20

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145	Lessons from genomeâ€wide association studies in venous thrombosis. Journal of Thrombosis and Haemostasis, 2011, 9, 258-264.	1.9	36
146	Effect of cytochrome P450 2C19 genotype on voriconazole exposure in cystic fibrosis lung transplant patients. European Journal of Clinical Pharmacology, 2011, 67, 253-260.	0.8	54
147	Combined analysis of three genome-wide association studies on vWF and FVIII plasma levels. BMC Medical Genetics, 2011, 12, 102.	2.1	63
148	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.	1.0	27
149	High prevalence of laminopathies among patients with metabolic syndrome. Human Molecular Genetics, 2011, 20, 3779-3786.	1.4	58
150	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.	1.6	21
151	Integrating Genome-Wide Genetic Variations and Monocyte Expression Data Reveals Trans-Regulated Gene Modules in Humans. PLoS Genetics, 2011, 7, e1002367.	1.5	126
152	Genetics of Venous Thrombosis: Insights from a New Genome Wide Association Study. PLoS ONE, 2011, 6, e25581.	1.1	127
153	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.	0.6	61
154	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.	2.6	57
155	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, 655.	2.6	0
156	Polymorphisms of the lamina maturation pathway and their association with the metabolic syndrome: the DESIR prospective study. Journal of Molecular Medicine, 2010, 88, 193-201.	1.7	5
157	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.	1.4	53
158	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.	1.9	42
159	Deciphering the molecular basis of venous thromboembolism: where are we and where should we go?. British Journal of Haematology, 2010, 148, 495-506.	1.2	14
160	Les facteurs deÂrisque gÃ©nÃ©tique deÂlaÂthrombose veineuse: oÃ¹ÂenÂsommes nous?. Sang Thrombose Vaisseaux, 2010, 22, 421-427.	0.1	0
161	Influence of ghrelin gene polymorphisms on hypertension and atherosclerotic disease. Hypertension Research, 2010, 33, 155-160.	1.5	22
162	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.	0.8	146

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163	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.	0.6	283
164	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
165	New susceptibility locus for coronary artery disease on chromosome 3q22.3. Nature Genetics, 2009, 41, 280-282.	9.4	440
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