Maria Sabater-Lleal

List of Publications by Year
in descending order

67	5,016	159585	123424
papers	citations	30 h-index	61 g-index

75	75	75	10910
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Elucidating mechanisms of genetic cross-disease associations at the PROCR vascular disease locus. Nature Communications, 2022, 13, 1222.	12.8	5
2	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
3	Integrated GWAS and Gene Expression Suggest ORM1 as a Potential Regulator of Plasma Levels of Cell-Free DNA and Thrombosis Risk. Thrombosis and Haemostasis, 2022, 122, 1027-1039.	3.4	6
4	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
5	Organ-on-a-chip technology: a novel approach to investigate cardiovascular diseases. Cardiovascular Research, 2021, 117, 2742-2754.	3.8	53
6	Association between ABO haplotypes and the risk of venous thrombosis: impact on disease risk estimation. Blood, 2021, 137, 2394-2402.	1.4	19
7	Association Between Hemostatic Profile and Migraine. Neurology, 2021, 96, e2481-e2487.	1.1	6
8	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
9	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	4.5	13
10	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
11	PCSK6 Is a Key Protease in the Control of Smooth Muscle Cell Function in Vascular Remodeling. Circulation Research, 2020, 126, 571-585.	4.5	38
12	The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. Nature Communications, 2020, 11, 3479.	12.8	43
13	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 41, 380-386.	2.4	14
14	Expression of microRNAs in human platelet-poor plasma: analysis of the factors affecting their expression and association with proximal genetic variants. Epigenetics, 2020, 15, 1396-1406.	2.7	1
15	The TAGA Study: A Study of Factors Determining Aortic Diameter in Families at High Risk of Abdominal Aortic Aneurysm Reveal Two New Candidate Genes. Journal of Clinical Medicine, 2020, 9, 1242.	2.4	3
16	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
17	Influence of ABO Locus on PFA-100 Collagen-ADP Closure Time Is Not Totally Dependent on the Von Willebrand Factor. Results of a GWAS on GAIT-2 Project Phenotypes. International Journal of Molecular Sciences, 2019, 20, 3221.	4.1	12
18	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84

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19	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
20	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
21	Genetically Determined FXI (Factor XI) Levels and Risk of Stroke. Stroke, 2018, 49, 2761-2763.	2.0	45
22	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
23	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
24	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
25	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	3.5	194
26	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	2.5	29
27	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
28	Phenotypic Modulation of Smooth Muscle Cells in Atherosclerosis Is Associated With Downregulation of LMOD1, SYNPO2, PDLIM7, PLN , and SYNM. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, 1947-1961.	2.4	64
29	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19
30	Genome-wide association analysis of self-reported events in 6135 individuals and 252 827 controls identifies 8 loci associated with thrombosis. Human Molecular Genetics, 2016, 25, 1867-1874.	2.9	103
31	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
32	Abstract 173: Proprotein Convertase Subtilisin/Kexin Type 6 is a Key Protease in the Control of Smooth Muscle Cell Function in Vascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, .	2.4	0
33	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
34	Predicting venous thrombosis in women using a combination of genetic markers and clinical risk factors. Journal of Thrombosis and Haemostasis, 2015, 13, 219-227.	3.8	50
35	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
36	Sexâ€Specific Effects of Adiponectin on Carotid Intimaâ€Media Thickness and Incident Cardiovascular Disease. Journal of the American Heart Association, 2015, 4, e001853.	3.7	33

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37	Abstract 367: Pcsk6 Is a Key Protease Modulating Smooth Muscle Cell Activation in Vascular Remodeling and Plaque Vulnerability. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, .	2.4	0
38	Abstract 150: Identification of SYNPO2, SYNM, LMOD1, PDLIM7 and PLN as Novel Markers of Smooth Muscle Cells in Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, .	2.4	0
39	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.	2.5	8
40	Human Genetic Evidence for Involvement of CD137 in Atherosclerosis. Molecular Medicine, 2014, 20, 456-465.	4.4	8
41	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
42	Influence of coronary artery disease-associated genetic variants on risk of venous thromboembolism. Thrombosis Research, 2014, 134, 426-432.	1.7	18
43	Common Genetic Determinants of Lung Function, Subclinical Atherosclerosis and Risk of Coronary Artery Disease. PLoS ONE, 2014, 9, e104082.	2.5	36
44	Abstract 467: PCSK6 Is Upregulated in Vascular Diseases Characterized by Inflammation and Smooth Muscle Cell Proliferation. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, .	2.4	0
45	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
46	Genetic determinants of plasma Î²2 -glycoproteinÂI levels: a genome-wide association study in extended pedigrees from Spain. Journal of Thrombosis and Haemostasis, 2013, 11, 521-528.	3.8	11
47	Genetic Variants from Lipid-Related Pathways and Risk for Incident Myocardial Infarction. PLoS ONE, 2013, 8, e60454.	2.5	8
48	Identification of the BCAR1-CFDP1-TMEM170A Locus as a Determinant of Carotid Intima-Media Thickness and Coronary Artery Disease Risk. Circulation: Cardiovascular Genetics, 2012, 5, 656-665.	5.1	47
49	Interleukin-6 receptor pathways in coronary heart disease: a collaborative meta-analysis of 82 studies. Lancet, The, 2012, 379, 1205-1213.	13.7	668
50	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
51	Lack of association of non-synonymous FUT2 and ALPL polymorphisms with venous thrombosis. Journal of Thrombosis and Haemostasis, 2012, 10, 1693-1695.	3.8	2
52	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
53	A Genome-Wide Association Study Identifies KNG1 as a Genetic Determinant of Plasma Factor XI Level and Activated Partial Thromboplastin Time. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 2008-2016.	2.4	33
54	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762

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55	Large-Scale Gene-Centric Analysis Identifies Novel Variants for Coronary Artery Disease. PLoS Genetics, 2011, 7, e1002260.	3.5	203
56	Sequence variation and genetic evolution at the human F12 locus: mapping quantitative trait nucleotides that influence FXII plasma levels. Human Molecular Genetics, 2010, 19, 517-525.	2.9	28
57	Novel Associations of Multiple Genetic Loci With Plasma Levels of Factor VII, Factor VIII, and von Willebrand Factor. Circulation, 2010, 121, 1382-1392.	1.6	311
58	Combined cis-regulator elements as important mechanism affecting FXII plasma levels. Thrombosis Research, 2010, 125, e55-e60.	1.7	10
59	A genome-wide exploration suggests an oligogenic model of inheritance for the TAFI activity and its antigen levels. Human Genetics, 2008, 124, 81-88.	3.8	9
60	Floating Feature Selection for multiloci association of quantitative traits in sib-pairs analysis. , 2008, , .		0
61	SNP sets selection under mutual information criterion, application to F7/FVII dataset. , 2008, 2008, 3783-6.		3
62	Clustering of individuals given SNPs similarity based on normalized mutual information: F7 SNPs in the GAIT sample. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 123-6.	0.5	2
63	Functional analysis of the genetic variability in the F7 gene promoter. Atherosclerosis, 2007, 195, 262-268.	0.8	24
64	Genetic architecture of the F7 gene in a Spanish population: implication for mapping complex diseases and for functional assays. Clinical Genetics, 2006, 69, 420-428.	2.0	5
65	Human F7 sequence is split into three deep clades that are related to FVII plasma levels. Human Genetics, 2006, 118, 741-751.	3.8	12
66	The F7 Gene and Clotting Factor VII Levels: Dissection of a Human Quantitative Trait Locus. Human Biology, 2005, 77, 561-575.	0.2	27
67	Complexity of the genetic contribution to factor VII deficiency in two Spanish families: clinical and biological implications. Haematologica, 2003, 88, 906-13.	3.5	7