

Johan L M Bjorkegren

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

8,299
citations

94433

37
h-index

71685

76
g-index

93
all docs

93
docs citations

93
times ranked

13173
citing authors

#	ARTICLE	IF	CITATIONS
1	<i>Cis</i> -epistasis at the <i>LPA</i> locus and risk of cardiovascular diseases. <i>Cardiovascular Research</i> , 2022, 118, 1088-1102.	3.8	14
2	Dynamic changes in chromatin accessibility are associated with the atherogenic transitioning of vascular smooth muscle cells. <i>Cardiovascular Research</i> , 2022, 118, 2792-2804.	3.8	17
3	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
4	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. <i>Basic Research in Cardiology</i> , 2022, 117, 6.	5.9	22
5	Integrative Prioritization of Causal Genes for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, CIRCGEN121003365.	3.6	11
6	The SARS-CoV-2 receptor ACE2 is expressed in mouse pericytes but not endothelial cells: Implications for COVID-19 vascular research. <i>Stem Cell Reports</i> , 2022, 17, 1089-1104.	4.8	41
7	A Transcriptional Regulation Bioinformatics Pipeline to Predict Co-regulated Genes in Vascular Smooth Muscle Cell Phenotypic Transitions During Atherosclerosis. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
8	Atherosclerosis: Recent developments. <i>Cell</i> , 2022, 185, 1630-1645.	28.9	311
9	Single-nucleus chromatin accessibility profiling highlights regulatory mechanisms of coronary artery disease risk. <i>Nature Genetics</i> , 2022, 54, 804-816.	21.4	51
10	The HDAC9-associated risk locus promotes coronary artery disease by governing TWIST1. <i>PLoS Genetics</i> , 2022, 18, e1010261.	3.5	2
11	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	12.8	35
12	Sex-Stratified Gene Regulatory Networks Reveal Female Key Driver Genes of Atherosclerosis Involved in Smooth Muscle Cell Phenotype Switching. <i>Circulation</i> , 2021, 143, 713-726.	1.6	61
13	Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. <i>European Heart Journal</i> , 2021, 42, 919-933.	2.2	113
14	Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. <i>Nature Communications</i> , 2021, 12, 1610.	12.8	118
15	Transcription Factor MAFF (MAF Basic Leucine Zipper Transcription Factor F) Regulates an Atherosclerosis Relevant Network Connecting Inflammation and Cholesterol Metabolism. <i>Circulation</i> , 2021, 143, 1809-1823.	1.6	28
16	Precision Medicine Approaches to Vascular Disease. <i>Journal of the American College of Cardiology</i> , 2021, 77, 2531-2550.	2.8	10
17	Sex-specific Genetic Regulation of Adipose Mitochondria and Their Relationship to Metabolic Syndrome. <i>FASEB Journal</i> , 2021, 35, .	0.5	0
18	Histone deacetylase 9 promotes endothelial-mesenchymal transition and an unfavorable atherosclerotic plaque phenotype. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	36

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19	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. <i>Journal of Human Genetics</i> , 2021, 66, 625-636.	2.3	40
20	Sex-specific genetic regulation of adipose mitochondria and metabolic syndrome by Ndufv2. <i>Nature Metabolism</i> , 2021, 3, 1552-1568.	11.9	32
21	Model-based clustering of multi-tissue gene expression data. <i>Bioinformatics</i> , 2020, 36, 1807-1813.	4.1	13
22	A plasma proteogenomic signature for fibromuscular dysplasia. <i>Cardiovascular Research</i> , 2020, 116, 63-77.	3.8	27
23	Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. <i>Genome Research</i> , 2020, 30, 1379-1392.	5.5	35
24	Genetic Regulation of Atherosclerosis-Relevant Phenotypes in Human Vascular Smooth Muscle Cells. <i>Circulation Research</i> , 2020, 127, 1552-1565.	4.5	60
25	Stem Cell Pluripotency Genes Klf4 and Oct4 Regulate Complex SMC Phenotypic Changes Critical in Late-Stage Atherosclerotic Lesion Pathogenesis. <i>Circulation</i> , 2020, 142, 2045-2059.	1.6	221
26	Functional investigation of the coronary artery disease gene SVEP1. <i>Basic Research in Cardiology</i> , 2020, 115, 67.	5.9	25
27	Single-cell analysis uncovers fibroblast heterogeneity and criteria for fibroblast and mural cell identification and discrimination. <i>Nature Communications</i> , 2020, 11, 3953.	12.8	316
28	Multiple independent mechanisms link gene polymorphisms in the region of ZEB2 with risk of coronary artery disease. <i>Atherosclerosis</i> , 2020, 311, 20-29.	0.8	9
29	Clonally expanding smooth muscle cells promote atherosclerosis by escaping efferocytosis and activating the complement cascade. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 15818-15826.	7.1	83
30	alona: a web server for single-cell RNA-seq analysis. <i>Bioinformatics</i> , 2020, 36, 3910-3912.	4.1	33
31	Integrative analysis of loss-of-function variants in clinical and genomic data reveals novel genes associated with cardiovascular traits. <i>BMC Medical Genomics</i> , 2019, 12, 108.	1.5	8
32	Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019, 10, 3834.	12.8	68
33	Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019, 39, 2386-2401.	2.4	36
34	Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019, 73, 2946-2957.	2.8	45
35	Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019, 51, 592-599.	21.4	592
36	PanglaoDB: a web server for exploration of mouse and human single-cell RNA sequencing data. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	762

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37	EnsembleCNV: an ensemble machine learning algorithm to identify and genotype copy number variation using SNP array data. <i>Nucleic Acids Research</i> , 2019, 47, e39-e39.	14.5	15
38	Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , 2019, 25, 1576-1588.	30.7	540
39	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018, 8, 3434.	3.3	43
40	A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. <i>Cell Metabolism</i> , 2018, 27, 1138-1155.e6.	16.2	58
41	HDL and atherosclerotic cardiovascular disease: genetic insights into complex biology. <i>Nature Reviews Cardiology</i> , 2018, 15, 9-19.	13.7	105
42	83â€¦The coronary artery disease associated gene JCAD regulates hippo signalling in endothelial cells. , 2018, , .		0
43	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018, 14, e1007799.	3.5	38
44	Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018, 14, e1007755.	3.5	30
45	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018, 9, 5141.	12.8	119
46	Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002115.	3.6	20
47	Macrophage Trafficking, Inflammatory Resolution, and Genomics in Atherosclerosis. <i>Journal of the American College of Cardiology</i> , 2018, 72, 2181-2197.	2.8	139
48	<i>JCAD</i>, a Gene at the 10p11 Coronary Artery Disease Locus, Regulates Hippo Signaling in Endothelial Cells. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 1711-1722.	2.4	36
49	CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. <i>Stem Cell Reports</i> , 2018, 11, 242-257.	4.8	26
50	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
51	Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018, 6, e4466.	2.0	21
52	Poliovirus Receptorâ€“Related 2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017, 37, 534-542.	2.4	23
53	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated Withâ€Coronary Arteryâ€Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	2.8	214
54	Functional Characterization of the <i>GUCY1A3</i> Coronary Artery Disease Risk Locus. <i>Circulation</i> , 2017, 136, 476-489.	1.6	84

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55	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017, 120, 341-353.	4.5	166
56	Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017, 100, 885-894.	6.2	91
57	Carbonyl reductase 1 catalyzes 20 β -reduction of glucocorticoids, modulating receptor activation and metabolic complications of obesity. <i>Scientific Reports</i> , 2017, 7, 10633.	3.3	15
58	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	21.4	571
59	Enabling Precision Cardiology Through Multiscale Biology and Systems Medicine. <i>JACC Basic To Translational Science</i> , 2017, 2, 311-327.	4.1	61
60	Preservation Analysis of Macrophage Gene Coexpression Between Human and Mouse Identifies PARK2 as a Genetically Controlled Master Regulator of Oxidative Phosphorylation in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3361-3371.	1.8	15
61	Systematic analysis of chromatin interactions at disease associated loci links novel candidate genes to inflammatory bowel disease. <i>Genome Biology</i> , 2016, 17, 247.	8.8	39
62	Human Validation of Genes Associated With a Murine Atherosclerotic Phenotype. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016, 36, 1240-1246.	2.4	44
63	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016, 353, 827-830.	12.6	241
64	Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016, 7, 12092.	12.8	123
65	Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016, 2, 196-208.	6.2	120
66	Genome-Wide Significant Loci: How Important Are They?. <i>Journal of the American College of Cardiology</i> , 2015, 65, 830-845.	2.8	129
67	Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 2207-2217.	2.4	101
68	Expression Quantitative Trait Loci Acting Across Multiple Tissues Are Enriched in Inherited Risk for Coronary Artery Disease. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 305-315.	5.1	39
69	Plasma Cholesterol-Induced Lesion Networks Activated before Regression of Early, Mature, and Advanced Atherosclerosis. <i>PLoS Genetics</i> , 2014, 10, e1004201.	3.5	64
70	kruX: matrix-based non-parametric eQTL discovery. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	39
71	Lim Domain Binding 2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 2068-2077.	2.4	17
72	NEW: Network-Enabled Wisdom in Biology, Medicine, and Health Care. <i>Science Translational Medicine</i> , 2012, 4, 115rv1.	12.4	115

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73	Systems and genome-wide approaches unite to provide a route to personalized medicine. <i>Genome Medicine</i> , 2012, 4, 29.	8.2	1
74	Carotid Plaque Age Is a Feature of Plaque Stability Inversely Related to Levels of Plasma Insulin. <i>PLoS ONE</i> , 2011, 6, e18248.	2.5	18
75	Multi-Organ Expression Profiling Uncovers a Gene Module in Coronary Artery Disease Involving Transendothelial Migration of Leukocytes and LIM Domain Binding 2: The Stockholm Atherosclerosis Gene Expression (STAGE) Study. <i>PLoS Genetics</i> , 2009, 5, e1000754.	3.5	118
76	Transcriptional Profiling Uncovers a Network of Cholesterol-Responsive Atherosclerosis Target Genes. <i>PLoS Genetics</i> , 2008, 4, e1000036.	3.5	67
77	Dual roles of apolipoprotein CI in the Formation of atherogenic remnants. <i>Current Atherosclerosis Reports</i> , 2006, 8, 1-2.	4.8	8
78	The Low Density Lipoprotein Receptor Prevents Secretion of Dense ApoB100-containing Lipoproteins from the Liver. <i>Journal of Biological Chemistry</i> , 2004, 279, 831-836.	3.4	52
79	Postprandial Enrichment of Remnant Lipoproteins With ApoC-I in Healthy Normolipidemic Men With Early Asymptomatic Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2002, 22, 1470-1474.	2.4	31