Johan L M Bjorkegren

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62 78 30 3,945 h-index g-index citations papers 6,296 5.36 12.5 93 L-index avg, IF ext. citations ext. papers

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 78 | 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 | 36.3 | 536 |
| 77 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391 | 36.3 | 361 |
| 76 | Opportunities and challenges for transcriptome-wide association studies. <i>Nature Genetics</i> , 2019 , 51, 592-599 | 36.3 | 266 |
| 75 | Single-cell immune landscape of human atherosclerotic plaques. <i>Nature Medicine</i> , 2019 , 25, 1576-1588 | 50.5 | 247 |
| 74 | 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, | 5 | 236 |
| 73 | Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissues and diseases. <i>Science</i> , 2016 , 353, 827-30 | 33.3 | 166 |
| 72 | Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 823-836 | 15.1 | 146 |
| 71 | Genome-wide significant loci: how important are they? Systems genetics to understand heritability of coronary artery disease and other common complex disorders. <i>Journal of the American College of Cardiology</i> , 2015 , 65, 830-845 | 15.1 | 108 |
| 70 | 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 | 15.7 | 97 |
| 69 | NEW: network-enabled wisdom in biology, medicine, and health care. <i>Science Translational Medicine</i> , 2012 , 4, 115rv1 | 17.5 | 97 |
| 68 | 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 | 6 | 89 |
| 67 | Single-cell analysis uncovers fibroblast heterogeneity and criteria for fibroblast and mural cell identification and discrimination. <i>Nature Communications</i> , 2020 , 11, 3953 | 17.4 | 82 |
| 66 | Cross-Tissue Regulatory Gene Networks in Coronary Artery Disease. <i>Cell Systems</i> , 2016 , 2, 196-208 | 10.6 | 81 |
| 65 | Macrophage Trafficking, Inflammatory Resolution, and Genomics in Atherosclerosis: JACC Macrophage in CVD Series (Part 2). <i>Journal of the American College of Cardiology</i> , 2018 , 72, 2181-2197 | 15.1 | 76 |
| 64 | Integrative functional genomics identifies regulatory mechanisms at coronary artery disease loci. <i>Nature Communications</i> , 2016 , 7, 12092 | 17.4 | 70 |
| 63 | 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 | 16.7 | 65 |
| 62 | HDL and atherosclerotic cardiovascular disease: genetic insights into complex biology. <i>Nature Reviews Cardiology</i> , 2018 , 15, 9-19 | 14.8 | 65 |

(2002-2015)

| 61 | Prediction of Causal Candidate Genes in Coronary Artery Disease Loci. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 2207-17 | 9.4 | 64 |
|----|---|------|----|
| 60 | GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018 , 9, 5141 | 17.4 | 64 |
| 59 | Functional Characterization of the Coronary Artery Disease Risk Locus. <i>Circulation</i> , 2017 , 136, 476-489 | 16.7 | 61 |
| 58 | Transcriptional profiling uncovers a network of cholesterol-responsive atherosclerosis target genes. <i>PLoS Genetics</i> , 2008 , 4, e1000036 | 6 | 59 |
| 57 | Large-Scale Identification of Common Trait and Disease Variants Affecting Gene Expression. <i>American Journal of Human Genetics</i> , 2017 , 100, 885-894 | 11 | 48 |
| 56 | The low density lipoprotein receptor prevents secretion of dense apoB100-containing lipoproteins from the liver. <i>Journal of Biological Chemistry</i> , 2004 , 279, 831-6 | 5.4 | 45 |
| 55 | Enabling Precision Cardiology Through Multiscale Biology and Systems Medicine. <i>JACC Basic To Translational Science</i> , 2017 , 2, 311-327 | 8.7 | 42 |
| 54 | Plasma cholesterol-induced lesion networks activated before regression of early, mature, and advanced atherosclerosis. <i>PLoS Genetics</i> , 2014 , 10, e1004201 | 6 | 38 |
| 53 | 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 | 11.5 | 36 |
| 52 | Human Validation of Genes Associated With a Murine Atherosclerotic Phenotype. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2016 , 36, 1240-6 | 9.4 | 34 |
| 51 | Expression quantitative trait Loci acting across multiple tissues are enriched in inherited risk for coronary artery disease. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 305-15 | | 33 |
| 50 | Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018 , 8, 3434 | 4.9 | 31 |
| 49 | A Strategy for Discovery of Endocrine Interactions with Application to Whole-Body Metabolism. <i>Cell Metabolism</i> , 2018 , 27, 1138-1155.e6 | 24.6 | 30 |
| 48 | Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits. <i>Nature Communications</i> , 2019 , 10, 3834 | 17.4 | 28 |
| 47 | Contribution of Gene Regulatory Networks to Heritability of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2019 , 73, 2946-2957 | 15.1 | 28 |
| 46 | Systematic analysis of chromatin interactions at disease associated loci links novel candidate genes to inflammatory bowel disease. <i>Genome Biology</i> , 2016 , 17, 247 | 18.3 | 28 |
| 45 | kruX: matrix-based non-parametric eQTL discovery. <i>BMC Bioinformatics</i> , 2014 , 15, 11 | 3.6 | 26 |
| 44 | 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, 1470-4 | 9.4 | 25 |

| 43 | Integration of Alzheimer's disease genetics and myeloid genomics identifies disease risk regulatory elements and genes. <i>Nature Communications</i> , 2021 , 12, 1610 | 17.4 | 25 |
|----|---|--------------|----|
| 42 | CD90 Identifies Adventitial Mesenchymal Progenitor Cells in Adult Human Medium- and Large-Sized Arteries. <i>Stem Cell Reports</i> , 2018 , 11, 242-257 | 8 | 21 |
| 41 | alona: a web server for single-cell RNA-seq analysis. <i>Bioinformatics</i> , 2020 , 36, 3910-3912 | 7.2 | 19 |
| 40 | JCAD, 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 | 9.4 | 19 |
| 39 | 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 | 16.7 | 18 |
| 38 | Atherosclerosis: Recent developments <i>Cell</i> , 2022 , 185, 1630-1645 | 56.2 | 18 |
| 37 | A plasma proteogenomic signature for fibromuscular dysplasia. Cardiovascular Research, 2020, 116, 63- | 73 .9 | 17 |
| 36 | Global analysis of A-to-I RNA editing reveals association with common disease variants. <i>PeerJ</i> , 2018 , 6, e4466 | 3.1 | 16 |
| 35 | Poliovirus Receptor-Related 2: A Cholesterol-Responsive Gene Affecting Atherosclerosis Development by Modulating Leukocyte Migration. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017 , 37, 534-542 | 9.4 | 15 |
| 34 | Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2019 , 39, 2386-2401 | 9.4 | 15 |
| 33 | Carotid plaque age is a feature of plaque stability inversely related to levels of plasma insulin. <i>PLoS ONE</i> , 2011 , 6, e18248 | 3.7 | 15 |
| 32 | Functional regulatory mechanism of smooth muscle cell-restricted LMOD1 coronary artery disease locus. <i>PLoS Genetics</i> , 2018 , 14, e1007755 | 6 | 15 |
| 31 | Genome-wide analysis identifies novel susceptibility loci for myocardial infarction. <i>European Heart Journal</i> , 2021 , 42, 919-933 | 9.5 | 14 |
| 30 | Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018 , 14, e1007799 | 6 | 13 |
| 29 | Lim domain binding 2: a key driver of transendothelial migration of leukocytes and atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014 , 34, 2068-77 | 9.4 | 12 |
| 28 | Transcriptome-wide association studies: opportunities and challenges | | 12 |
| 27 | Genetic Regulation of Atherosclerosis-Relevant Phenotypes in Human Vascular Smooth Muscle Cells. <i>Circulation Research</i> , 2020 , 127, 1552-1565 | 15.7 | 12 |
| 26 | An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021 , 12, 547 | 17.4 | 12 |

(2021-2021)

| 25 | 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 | 4.3 | 12 | |
|----|--|------|----|--|
| 24 | Carbonyl reductase 1 catalyzes 20F eduction of glucocorticoids, modulating receptor activation and metabolic complications of obesity. <i>Scientific Reports</i> , 2017 , 7, 10633 | 4.9 | 11 | |
| 23 | 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 | 3.2 | 11 | |
| 22 | Genetic Susceptibility Loci for Cardiovascular Disease and Their Impact on Atherosclerotic Plaques. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002115 | 5.2 | 11 | |
| 21 | 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 | 20.1 | 10 | |
| 20 | 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 | 16.7 | 10 | |
| 19 | Sex differences in human adipose tissue gene expression and genetic regulation involve adipogenesis. <i>Genome Research</i> , 2020 , 30, 1379-1392 | 9.7 | 9 | |
| 18 | Dual roles of apolipoprotein CI in the formation of atherogenic remnants. <i>Current Atherosclerosis Reports</i> , 2006 , 8, 1-2 | 6 | 7 | |
| 17 | Histone deacetylase 9 promotes endothelial-mesenchymal transition and an unfavorable atherosclerotic plaque phenotype. <i>Journal of Clinical Investigation</i> , 2021 , 131, | 15.9 | 7 | |
| 16 | Sex-specific genetic regulation of adipose mitochondria and metabolic syndrome by Ndufv2. <i>Nature Metabolism</i> , 2021 , 3, 1552-1568 | 14.6 | 6 | |
| 15 | Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular Research, 2021, | 9.9 | 6 | |
| 14 | Model-based clustering of multi-tissue gene expression data. <i>Bioinformatics</i> , 2020 , 36, 1807-1813 | 7.2 | 6 | |
| 13 | 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 | 3.7 | 5 | |
| 12 | A mechanistic framework for cardiometabolic and coronary artery diseases 2022 , 1, 85-100 | | 5 | |
| 11 | Functional investigation of the coronary artery disease gene SVEP1. <i>Basic Research in Cardiology</i> , 2020 , 115, 67 | 11.8 | 5 | |
| 10 | Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants | | 5 | |
| 9 | Multiple independent mechanisms link gene polymorphisms in the region of ZEB2 with risk of coronary artery disease. <i>Atherosclerosis</i> , 2020 , 311, 20-29 | 3.1 | 4 | |
| 8 | Precision Medicine Approaches to Vascular Disease: JACC Focus Seminar 2/5. <i>Journal of the American College of Cardiology</i> , 2021 , 77, 2531-2550 | 15.1 | 3 | |

| 7 | Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes <i>Basic Research in Cardiology</i> , 2022 , 117, 6 | 11.8 | 3 |
|---|--|------|---|
| 6 | Dynamic changes in chromatin accessibility are associated with the atherogenic transitioning of vascular smooth muscle cells. <i>Cardiovascular Research</i> , 2021 , | 9.9 | 2 |
| 5 | Integrative Prioritization of Causal Genes for Coronary Artery Disease <i>Circulation Genomic and Precision Medicine</i> , 2021 , CIRCGEN121003365 | 5.2 | 2 |
| 4 | Systems and genome-wide approaches unite to provide a route to personalized medicine. <i>Genome Medicine</i> , 2012 , 4, 29 | 14.4 | 1 |
| 3 | Integrative transcriptome imputation reveals tissue-specific and shared biological mechanisms mediating susceptibility to complex traits | | 1 |
| 2 | Cis-epistasis at the LPA locus and risk of coronary artery disease | | 1 |

Genetics and Pharmacogenetics in Interventional Cardiology **2016**, 459-468