Nathan Oliver Stitziel

List of Publications by Year
in descending order

62	9,683	87888 38	106344 65
papers	citations	h-index	g-index

71	71	71	16694
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
2	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
3	Genetic risk, coronary heart disease events, and the clinical benefit of statin therapy: an analysis of primary and secondary prevention trials. Lancet, The, 2015, 385, 2264-2271.	13.7	564
4	A general approach to single-nucleotide polymorphism discovery. Nature Genetics, 1999, 23, 452-456.	21.4	550
5	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
6	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
7	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
8	Polygenic Risk Score Identifies Subgroup With Higher Burden of Atherosclerosis and Greater Relative Benefit From Statin Therapy in the Primary Prevention Setting. Circulation, 2017, 135, 2091-2101.	1.6	403
9	Clinical Genetic Testing for FamilialÂHypercholesterolemia. Journal of the American College of Cardiology, 2018, 72, 662-680.	2.8	387
10	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
11	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
12	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	2.8	348
13	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340
14	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
15	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
16	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
17	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	27.8	194
18	Gain-of-function mutations in the mechanically activated ion channel PIEZO2 cause a subtype of Distal Arthrogryposis. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4667-4672.	7.1	193

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19	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
20	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
21	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	7.4	148
22	Loss of function mutation in LOX causes thoracic aortic aneurysm and dissection in humans. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8759-8764.	7.1	144
23	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	12.8	120
24	Computational and statistical approaches to analyzing variants identified by exome sequencing. Genome Biology, 2011, 12, 227.	9.6	116
25	Description of a Large Family with Autosomal Dominant Hypercholesterolemia Associated with theAPOEp.Leu167del Mutation. Human Mutation, 2013, 34, 83-87.	2.5	103
26	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. Genome Biology, 2014, 15, R53.	9.6	101
27	Exome Sequencing and Directed Clinical Phenotyping Diagnose Cholesterol Ester Storage Disease Presenting as Autosomal Recessive Hypercholesterolemia. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 2909-2914.	2.4	87
28	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232.	1.6	87
29	High-protein diets increase cardiovascular risk by activating macrophage mTOR to suppress mitophagy. Nature Metabolism, 2020, 2, 110-125.	11.9	85
30	APOE p.Leu167del mutation in familial hypercholesterolemia. Atherosclerosis, 2013, 231, 218-222.	0.8	84
31	topoSNP: a topographic database of non-synonymous single nucleotide polymorphisms with and without known disease association. Nucleic Acids Research, 2004, 32, 520D-522.	14.5	81
32	Clinical characteristics and plasma lipids in subjects with familial combined hypolipidemia: a pooled analysis. Journal of Lipid Research, 2013, 54, 3481-3490.	4.2	76
33	Structural Location of Disease-associated Single-nucleotide Polymorphisms. Journal of Molecular Biology, 2003, 327, 1021-1030.	4.2	74
34	Identification of Medically Actionable Secondary Findings in the 1000 Genomes. PLoS ONE, 2015, 10, e0135193.	2.5	74
35	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
36	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54

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37	Exome Sequencing in Suspected Monogenic Dyslipidemias. Circulation: Cardiovascular Genetics, 2015, 8, 343-350.	5.1	45
38	Prognostic value of diastolic filling parameters derived using a novel image processing technique in patients â‰¥70 years of age with congestive heart failure. American Journal of Cardiology, 1999, 84, 82-86.	1.6	39
39	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
40	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. American Journal of Human Genetics, 2020, 107, 46-59.	6.2	30
41	SVEP1 is a human coronary artery disease locus that promotes atherosclerosis. Science Translational Medicine, 2021, 13, .	12.4	28
42	Leveraging human genetics to guide drug target discovery. Trends in Cardiovascular Medicine, 2017, 27, 352-359.	4.9	26
43	New Sequencing technologies help revealing unexpected mutations in Autosomal Dominant Hypercholesterolemia. Scientific Reports, 2018, 8, 1943.	3.3	25
44	An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease gene discovery. Npj Genomic Medicine, 2018, 3, 21.	3.8	24
45	Coronary Artery Disease Risk and Lipidomic Profiles Are Similar in Hyperlipidemias With Family History and Populationâ€Ascertained Hyperlipidemias. Journal of the American Heart Association, 2019, 8, e012415.	3.7	24
46	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. European Journal of Preventive Cardiology, 2017, 24, 492-504.	1.8	22
47	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
48	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	6.2	22
49	Common and Rare Genetic Variation in CCR2 , CCR5 , or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. Circulation: Cardiovascular Genetics, 2016, 9, 250-258.	5.1	20
50	Diagnosis and management of adult hereditary cardio-neuromuscular disorders: A model for the multidisciplinary care of complex genetic disorders. Trends in Cardiovascular Medicine, 2017, 27, 51-58.	4.9	19
51	Membrane-Associated and Secreted Genes in Breast Cancer. Cancer Research, 2004, 64, 8682-8687.	0.9	17
52	Genetic association studies in cardiovascular diseases: Do we have enough power?. Trends in Cardiovascular Medicine, 2017, 27, 397-404.	4.9	17
53	Genetics of the extracellular matrix in aortic aneurysmal diseases. Matrix Biology, 2018, 71-72, 128-143.	3.6	17
54	A Clinical Approach to Inherited Premature Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 558-564.	5.1	16

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55	Emerging Targets for Cardiovascular Disease Prevention in Diabetes. Trends in Molecular Medicine, 2020, 26, 744-757.	6.7	15
56	Functional Characterization of LIPA (Lysosomal Acid Lipase) Variants Associated With Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 2480-2491.	2.4	13
57	Human genetic insights into lipoproteins and risk of cardiometabolic disease. Current Opinion in Lipidology, 2017, 28, 113-119.	2.7	12
58	Intracellular retention of mutant lysyl oxidase leads to aortic dilation in response to increased hemodynamic stress. JCI Insight, 2019, 4, .	5.0	12
59	Inherited CHST11/MIR3922 deletion is associated with a novel recessive syndrome presenting with skeletal malformation and malignant lymphoproliferative disease. Molecular Genetics & Genomic Medicine, 2015, 3, 413-423.	1.2	11
60	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.	2.9	7
61	Capitalizing on Insights from Human Genetics to Identify Novel Therapeutic Targets for Coronary Artery Disease. Annual Review of Medicine, 2019, 70, 19-32.	12.2	6
62	Reply. Journal of the American College of Cardiology, 2017, 70, 2099-2100.	2.8	1