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	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	12.8	63
2	SVEP1 is a human coronary artery disease locus that promotes atherosclerosis. Science Translational Medicine, 2021, 13, .	12.4	28
3	Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.	6.2	22
4	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
5	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. American Journal of Human Genetics, 2020, 107, 46-59.	6.2	30
6	Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583, 83-89.	27.8	194
7	Emerging Targets for Cardiovascular Disease Prevention in Diabetes. Trends in Molecular Medicine, 2020, 26, 744-757.	6.7	15
8	High-protein diets increase cardiovascular risk by activating macrophage mTOR to suppress mitophagy. Nature Metabolism, 2020, 2, 110-125.	11.9	85
9	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	27.8	161
10	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
11	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
12	Genetic architecture of human plasma lipidome and its link to cardiovascular disease. Nature Communications, 2019, 10, 4329.	12.8	120
13	Roadmap for a precision-medicine initiative in the Nordic region. Nature Genetics, 2019, 51, 924-930.	21.4	22
14	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
15	Intracellular retention of mutant lysyl oxidase leads to aortic dilation in response to increased hemodynamic stress. JCI Insight, 2019, 4, .	5.0	12
16	Genetics of the extracellular matrix in aortic aneurysmal diseases. Matrix Biology, 2018, 71-72, 128-143.	3.6	17
17	New Sequencing technologies help revealing unexpected mutations in Autosomal Dominant Hypercholesterolemia. Scientific Reports, 2018, 8, 1943.	3.3	25
18	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232.	1.6	87

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19	Clinical Genetic Testing for FamilialÂHypercholesterolemia. Journal of the American College of Cardiology, 2018, 72, 662-680.	2.8	387
20	An integrated clinical program and crowdsourcing strategy for genomic sequencing and Mendelian disease gene discovery. Npj Genomic Medicine, 2018, 3, 21.	3.8	24
21	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
22	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
23	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
24	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
25	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
26	Human genetic insights into lipoproteins and risk of cardiometabolic disease. Current Opinion in Lipidology, 2017, 28, 113-119.	2.7	12
27	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	2.8	348
28	Genetic association studies in cardiovascular diseases: Do we have enough power?. Trends in Cardiovascular Medicine, 2017, 27, 397-404.	4.9	17
29	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
30	Reply. Journal of the American College of Cardiology, 2017, 70, 2099-2100.	2.8	1
31	Leveraging human genetics to guide drug target discovery. Trends in Cardiovascular Medicine, 2017, 27, 352-359.	4.9	26
32	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
33	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
34	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
35	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
36	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

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37	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
38	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
39	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
40	Identification of Medically Actionable Secondary Findings in the 1000 Genomes. PLoS ONE, 2015, 10, e0135193.	2.5	74
41	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	2.9	36
42	Exome Sequencing in Suspected Monogenic Dyslipidemias. Circulation: Cardiovascular Genetics, 2015, 8, 343-350.	5.1	45
43	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
44	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
45	A Clinical Approach to Inherited Premature Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 558-564.	5.1	16
46	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
47	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
48	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
49	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
50	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
51	Description of a Large Family with Autosomal Dominant Hypercholesterolemia Associated with theAPOEp.Leu167del Mutation. Human Mutation, 2013, 34, 83-87.	2.5	103
52	APOE p.Leu167del mutation in familial hypercholesterolemia. Atherosclerosis, 2013, 231, 218-222.	0.8	84
53	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
54	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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55	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
56	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340
57	Computational and statistical approaches to analyzing variants identified by exome sequencing. Genome Biology, 2011, 12, 227.	9.6	116
58	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
59	Membrane-Associated and Secreted Genes in Breast Cancer. Cancer Research, 2004, 64, 8682-8687.	0.9	17
60	Structural Location of Disease-associated Single-nucleotide Polymorphisms. Journal of Molecular Biology, 2003, 327, 1021-1030.	4.2	74
61	A general approach to single-nucleotide polymorphism discovery. Nature Genetics, 1999, 23, 452-456.	21.4	550
62	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