Ãsa Johansson

List of Publications by Year
in descending order

116	32,432	29994 54	18075 120
papers	citations	h-index	g-index

136	136	136	38399
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
2	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
3	Contribution of rare whole-genome sequencing variants to plasma protein levels and the missing heritability. Nature Communications, 2022, 13, 2532.	5.8	9
4	Oral Contraceptives, Hormone Replacement Therapy, and Stroke Risk. Stroke, 2022, 53, 3107-3115.	1.0	20
5	Investigating the Effect of Estradiol Levels on the Risk of Breast, Endometrial, and Ovarian Cancer. Journal of the Endocrine Society, 2022, 6, .	0.1	10
6	DNA methylation in cord blood in association with prenatal depressive symptoms. Clinical Epigenetics, 2021, 13, 78.	1.8	14
7	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. Cellular and Molecular Life Sciences, 2021, 78, 4019-4033.	2.4	54
8	Inflammation-related plasma protein levels and association with adiposity measurements in young adults. Scientific Reports, 2021, 11, 11391.	1.6	10
9	Modification of Heritability for Educational Attainment and Fluid Intelligence by Socioeconomic Deprivation in the UK Biobank. American Journal of Psychiatry, 2021, 178, 625-634.	4.0	15
10	Genome-wide Association Study of Estradiol Levels and the Causal Effect of Estradiol on Bone Mineral Density. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e4471-e4486.	1.8	41
11	Characterization of the human <scp>ABO</scp> genotypes and their association to common inflammatory and cardiovascular diseases in the <scp>UK Biobank</scp>. American Journal of Hematology, 2021, 96, 1350-1362.	2.0	8
12	Time-Dependent Effects of Oral Contraceptive Use on Breast, Ovarian, and Endometrial Cancers. Cancer Research, 2021, 81, 1153-1162.	0.4	42
13	A combined genome-wide association and molecular study of age-related hearing loss in H. sapiens. BMC Medicine, 2021, 19, 302.	2.3	16
14	Causal effects of inflammatory protein biomarkers on inflammatory diseases. Science Advances, 2021, 7, eabl4359.	4.7	18
15	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
16	Genome-wide association analysis of 350â€‰000 Caucasians from the UK Biobank identifies novel loci for asthma, hay fever and eczema. Human Molecular Genetics, 2019, 28, 4022-4041.	1.4	110
17	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	3.1	49
18	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84

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19	Contribution of genetics to visceral adiposity and its relation to cardiovascular and metabolic disease. Nature Medicine, 2019, 25, 1390-1395.	15.2	172
20	Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects. Nature Communications, 2019, 10, 339.	5.8	163
21	Improved power and precision with whole genome sequencing data in genome-wide association studies of inflammatory biomarkers. Scientific Reports, 2019, 9, 16844.	1.6	43
22	Systemic and specific effects of antihypertensive and lipid-lowering medication on plasma protein biomarkers for cardiovascular diseases. Scientific Reports, 2018, 8, 5531.	1.6	29
23	Genetic variants influencing phenotypic variance heterogeneity. Human Molecular Genetics, 2018, 27, 799-810.	1.4	30
24	Breast-feeding and risk of asthma, hay fever, and eczema. Journal of Allergy and Clinical Immunology, 2018, 141, 1157-1159.e9.	1.5	17
25	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
26	A Meta-Analysis of Genome-Wide Association Studies of Growth Differentiation Factor-15 Concentration in Blood. Frontiers in Genetics, 2018, 9, 97.	1.1	26
27	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	0.9	19
28	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
29	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
30	Tea and coffee consumption in relation to DNA methylation in four European cohorts. Human Molecular Genetics, 2017, 26, 3221-3231.	1.4	25
31	Epigenome-wide DNA methylation study of IgE concentration in relation to self-reported allergies. Epigenomics, 2017, 9, 407-418.	1.0	17
32	SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population. European Journal of Human Genetics, 2017, 25, 1253-1260.	1.4	148
33	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
34	Gene-environment interaction study for BMI reveals interactions between genetic factors and physical activity, alcohol consumption and socioeconomic status. PLoS Genetics, 2017, 13, e1006977.	1.5	125
35	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
36	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194

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37	The relative contribution of DNA methylation and genetic variants on protein biomarkers for human diseases. PLoS Genetics, 2017, 13, e1007005.	1.5	54
38	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	3.3	208
39	Epigenome-wide association study reveals differential DNA methylation in individuals with a history of myocardial infarction. Human Molecular Genetics, 2016, 25, ddw302.	1.4	88
40	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. Human Molecular Genetics, 2016, 25, 817-827.	1.4	32
41	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
42	Genome-wide association and Mendelian randomization study of NT-proBNP in patients with acute coronary syndrome. Human Molecular Genetics, 2016, 25, 1447-1456.	1.4	41
43	A multiple-phenotype imputation method for genetic studies. Nature Genetics, 2016, 48, 466-472.	9.4	93
44	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
45	The role of DNA methylation in the pathogenesis of disease: what can epigenome-wide association studies tell?. Epigenomics, 2016, 8, 5-7.	1.0	6
46	Protein profiling reveals consequences of lifestyle choices on predicted biological aging. Scientific Reports, 2015, 5, 17282.	1.6	36
47	Genome-Wide Association Study Identifies That the ABO Blood Group System Influences Interleukin-10 Levels and the Risk of Clinical Events in Patients with Acute Coronary Syndrome. PLoS ONE, 2015, 10, e0142518.	1.1	21
48	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
49	Effect of genetic variations on ticagrelor plasma levels and clinical outcomes. European Heart Journal, 2015, 36, 1901-1912.	1.0	107
50	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	1.4	27
51	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
52	Effect of genetic and environmental factors on protein biomarkers for common non-communicable disease and use of personally normalized plasma protein profiles (PNPPP). Biomarkers, 2015, 20, 355-364.	0.9	16
53	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
54	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173

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55	NLRC4 Inflammasome Is an Important Regulator of Interleukin-18 Levels in Patients With Acute Coronary Syndromes. Circulation: Cardiovascular Genetics, 2015, 8, 498-506.	5.1	25
56	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
57	Strong effects of genetic and lifestyle factors on biomarker variation and use of personalized cutoffs. Nature Communications, 2014, 5, 4684.	5.8	152
58	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. Human Molecular Genetics, 2014, 23, 3054-3068.	1.4	90
59	Smoke-related DNA methylation changes in the etiology of human disease. Human Molecular Genetics, 2014, 23, 2290-2297.	1.4	155
60	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
61	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
62	Polymorphism of the cystatin C gene in patients with acute coronary syndromes: Results from the PLATelet inhibition and patient Outcomes study. American Heart Journal, 2014, 168, 96-102.e2.	1.2	17
63	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	2.6	60
64	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
65	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
66	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
67	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
68	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	3.0	33
69	Identification of genetic variants influencing the human plasma proteome. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4673-4678.	3.3	78
70	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
71	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
72	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371

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73	Animal source food intake and association with blood cholesterol, glycerophospholipids and sphingolipids in a northern Swedish population. International Journal of Circumpolar Health, 2013, 72, 21162.	0.5	27
74	Prevalence and sensitization of atopic allergy and coeliac disease in the Northern Sweden Population Health Study. International Journal of Circumpolar Health, 2013, 72, 21403.	0.5	19
75	Continuous Aging of the Human DNA Methylome Throughout the Human Lifespan. PLoS ONE, 2013, 8, e67378.	1.1	315
76	Differential Gene Expression at the Maternal-Fetal Interface in Preeclampsia Is Influenced by Gestational Age. PLoS ONE, 2013, 8, e69848.	1.1	13
77	Sequencing of high-complexity DNA pools for identification of nucleotide and structural variants in regions associated with complex traits. European Journal of Human Genetics, 2012, 20, 77-83.	1.4	10
78	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
79	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
80	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
81	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
82	Polymorphisms in sh2b1 and spns1 loci are associated with triglyceride levels in a healthy population in northern Sweden. Journal of Genetics, 2012, 91, 237-240.	0.4	5
83	Genetic Adaptation of Fatty-Acid Metabolism: A Human-Specific Haplotype Increasing the Biosynthesis of Long-Chain Omega-3 and Omega-6 Fatty Acids. American Journal of Human Genetics, 2012, 90, 809-820.	2.6	205
84	Identification of ACOX2 as a shared genetic risk factor for preeclampsia and cardiovascular disease. European Journal of Human Genetics, 2011, 19, 796-800.	1.4	37
85	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
86	Partial correlation network analyses to detect altered gene interactions in human disease: using preeclampsia as a model. Human Genetics, 2011, 129, 25-34.	1.8	20
87	Polymorphisms in B3GAT1, SLC9A9 and MGAT5 are associated with variation within the human plasma N-glycome of 3533 European adults. Human Molecular Genetics, 2011, 20, 5000-5011.	1.4	74
88	A Genome-Wide Screen for Interactions Reveals a New Locus on 4p15 Modifying the Effect of Waist-to-Hip Ratio on Total Cholesterol. PLoS Genetics, 2011, 7, e1002333.	1.5	29
89	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56
90	A meta-analysis of genome-wide data from five European isolates reveals an association of COL22A1, SYT1, and GABRR2with serum creatinine level. BMC Medical Genetics, 2010, 11, 41.	2.1	48

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91	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	1.4	22
92	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
93	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
94	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	9.4	518
95	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
96	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
97	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
98	Modeling of Environmental Effects in Genome-Wide Association Studies Identifies SLC2A2 and HP as Novel Loci Influencing Serum Cholesterol Levels. PLoS Genetics, 2010, 6, e1000798.	1.5	51
99	STOX2 but not STOX1 is differentially expressed in decidua from pre-eclamptic women: data from the Second Nord-Trondelag Health Study. Molecular Human Reproduction, 2010, 16, 960-968.	1.3	28
100	Linkage and Genomeâ€wide Association Analysis of Obesityâ€related Phenotypes: Association of Weight With the MGAT1 Gene. Obesity, 2010, 18, 803-808.	1.5	54
101	The Northern Swedish Population Health Study (NSPHS)–a paradigmatic study in a rural population combining community health and basic research. Rural and Remote Health, 2010, 10, 1363.	0.4	22
102	Adherence to a traditional lifestyle affects food and nutrient intake among modern swedish sami. International Journal of Circumpolar Health, 2009, 68, 372-385.	0.5	22
103	Extended Haplotypes in the Growth Hormone Releasing Hormone Receptor Gene (GHRHR) Are Associated with Normal Variation in Height. PLoS ONE, 2009, 4, e4464.	1.1	10
104	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	1.5	230
105	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	1.5	572
106	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	1.5	184
107	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Human Molecular Genetics, 2009, 18, 373-380.	1.4	88
108	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776

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109	Genetic origin of the Swedish Sami inferred from HLA class I and class II allele frequencies. European Journal of Human Genetics, 2008, 16, 1341-1349.	1.4	24
110	Identification of local selective sweeps in human populations since the exodus from Africa. Hereditas, 2008, 145, 126-137.	0.5	17
111	Evaluation of the SNP tagging approach in an independent population sampleâ€”array-based SNP discovery in Sami. Human Genetics, 2007, 122, 141-150.	1.8	10
112	Lifestyle, genetics, and disease in Sami. Croatian Medical Journal, 2006, 47, 553-65.	0.2	19
113	Linkage disequilibrium between microsatellite markers in the Swedish Sami relative to a worldwide selection of populations. Human Genetics, 2005, 116, 105-113.	1.8	22
114	A novel method for automatic genotyping of microsatellite markers based on parametric pattern recognition. Human Genetics, 2003, 113, 316-324.	1.8	14
115	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	11
116	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	1