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	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
3	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
4	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
5	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
6	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
7	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
8	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
9	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
10	Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. Nature Genetics, 2009, 41, 47-55.	9.4	776
11	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
12	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	9.4	710
13	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
14	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
15	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
16	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	9.4	518
17	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
18	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438

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19	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	5.8	412
20	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
21	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
22	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	5.1	327
23	Continuous Aging of the Human DNA Methylome Throughout the Human Lifespan. PLoS ONE, 2013, 8, e67378.	1.1	315
24	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
25	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
26	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
27	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
28	Mapping of 79 loci for 83 plasma protein biomarkers in cardiovascular disease. PLoS Genetics, 2017, 13, e1006706.	1.5	194
29	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	1.5	184
30	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	1.5	181
31	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
32	Contribution of genetics to visceral adiposity and its relation to cardiovascular and metabolic disease. Nature Medicine, 2019, 25, 1390-1395.	15.2	172
33	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
34	Genome-wide association study of body fat distribution identifies adiposity loci and sex-specific genetic effects. Nature Communications, 2019, 10, 339.	5.8	163
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	Smoke-related DNA methylation changes in the etiology of human disease. Human Molecular Genetics, 2014, 23, 2290-2297.	1.4	155

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37	Strong effects of genetic and lifestyle factors on biomarker variation and use of personalized cutoffs. Nature Communications, 2014, 5, 4684.	5.8	152
38	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
39	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
40	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
41	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
42	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
43	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
44	Effect of genetic variations on ticagrelor plasma levels and clinical outcomes. European Heart Journal, 2015, 36, 1901-1912.	1.0	107
45	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	1.6	98
46	A multiple-phenotype imputation method for genetic studies. Nature Genetics, 2016, 48, 466-472.	9.4	93
47	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
48	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
49	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
50	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
51	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
52	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
53	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
54	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

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55	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
56	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
57	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56
58	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
59	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. Cellular and Molecular Life Sciences, 2021, 78, 4019-4033.	2.4	54
60	The relative contribution of DNA methylation and genetic variants on protein biomarkers for human diseases. PLoS Genetics, 2017, 13, e1007005.	1.5	54
61	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
62	Epigenome-wide association study of lung function level and its change. European Respiratory Journal, 2019, 54, 1900457.	3.1	49
63	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
64	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
65	Time-Dependent Effects of Oral Contraceptive Use on Breast, Ovarian, and Endometrial Cancers. Cancer Research, 2021, 81, 1153-1162.	0.4	42
66	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
67	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
68	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
69	Protein profiling reveals consequences of lifestyle choices on predicted biological aging. Scientific Reports, 2015, 5, 17282.	1.6	36
70	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
71	Genome-wide DNA methylation study identifies genes associated with the cardiovascular biomarker GDF-15. Human Molecular Genetics, 2016, 25, 817-827.	1.4	32
72	Genetic variants influencing phenotypic variance heterogeneity. Human Molecular Genetics, 2018, 27, 799-810.	1.4	30

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73	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
74	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
75	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
76	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
77	Homozygous loss-of-function variants in European cosmopolitan and isolate populations. Human Molecular Genetics, 2015, 24, 5464-5474.	1.4	27
78	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
79	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
80	Tea and coffee consumption in relation to DNA methylation in four European cohorts. Human Molecular Genetics, 2017, 26, 3221-3231.	1.4	25
81	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
82	Genetic architecture of circulating lipid levels. European Journal of Human Genetics, 2011, 19, 813-819.	1.4	23
83	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
84	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
85	Genes predict village of origin in rural Europe. European Journal of Human Genetics, 2010, 18, 1269-1270.	1.4	22
86	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
87	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
88	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
89	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
90	Oral Contraceptives, Hormone Replacement Therapy, and Stroke Risk. Stroke, 2022, 53, 3107-3115.	1.0	20

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91	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
92	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	0.9	19
93	Lifestyle, genetics, and disease in Sami. Croatian Medical Journal, 2006, 47, 553-65.	0.2	19
94	Causal effects of inflammatory protein biomarkers on inflammatory diseases. Science Advances, 2021, 7, eabl4359.	4.7	18
95	Identification of local selective sweeps in human populations since the exodus from Africa. Hereditas, 2008, 145, 126-137.	0.5	17
96	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
97	Epigenome-wide DNA methylation study of IgE concentration in relation to self-reported allergies. Epigenomics, 2017, 9, 407-418.	1.0	17
98	Breast-feeding and risk of asthma, hay fever, and eczema. Journal of Allergy and Clinical Immunology, 2018, 141, 1157-1159.e9.	1.5	17
99	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
100	A combined genome-wide association and molecular study of age-related hearing loss in H. sapiens. BMC Medicine, 2021, 19, 302.	2.3	16
101	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
102	A novel method for automatic genotyping of microsatellite markers based on parametric pattern recognition. Human Genetics, 2003, 113, 316-324.	1.8	14
103	DNA methylation in cord blood in association with prenatal depressive symptoms. Clinical Epigenetics, 2021, 13, 78.	1.8	14
104	Differential Gene Expression at the Maternal-Fetal Interface in Preeclampsia Is Influenced by Gestational Age. PLoS ONE, 2013, 8, e69848.	1.1	13
105	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	11
106	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
107	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
108	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

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109	Inflammation-related plasma protein levels and association with adiposity measurements in young adults. Scientific Reports, 2021, 11, 11391.	1.6	10
110	A multi-omics study of circulating phospholipid markers of blood pressure. Scientific Reports, 2022, 12, 574.	1.6	10
111	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
112	Contribution of rare whole-genome sequencing variants to plasma protein levels and the missing heritability. Nature Communications, 2022, 13, 2532.	5.8	9
113	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
114	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
115	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
116	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	1