Ilja M Nolte

List of Publications by Year in descending order

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161 papers	27,460 citations	20817 60 h-index	7518 151 g-index
173 all docs	173 docs citations	173 times ranked	35160 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
3	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
5	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
6	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
7	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
8	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	21.4	709
9	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
10	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
11	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
12	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
13	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
14	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
15	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
16	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
17	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
18	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362

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19	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
20	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
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.	3.5	331
22	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
23	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
24	Genome-Wide Association Study of Blood Pressure Extremes Identifies Variant near UMOD Associated with Hypertension. PLoS Genetics, 2010, 6, e1001177.	3.5	312
25	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
26	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
27	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
28	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
29	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
30	Genetic evidence of assortative mating in humans. Nature Human Behaviour, 2017, 1, .	12.0	242
31	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
32	Validity of (Ultra-)Short Recordings for Heart Rate Variability Measurements. PLoS ONE, 2015, 10, e0138921.	2.5	225
33	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	3.5	194
34	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. American Journal of Human Genetics, 2015, 96, 377-385.	6.2	191
35	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. Nature Communications, 2018, 9, 4455.	12.8	181
36	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	21.4	177

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37	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
38	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
39	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
40	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
41	A genomeâ€wide approach to children's aggressive behavior: The EAGLE consortium. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 562-572.	1.7	153
42	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. PLoS Medicine, 2016, 13, e1001976.	8.4	150
43	Genome-Wide Association Study of Classical Hodgkin Lymphoma and Epsteinâ€“Barr Virus Statusâ€“Defined Subgroups. Journal of the National Cancer Institute, 2012, 104, 240-253.	6.3	141
44	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
45	Genome-wide association analysis identifies multiple loci related to resting heart rate. Human Molecular Genetics, 2010, 19, 3885-3894.	2.9	133
46	HLA-A*02 is associated with a reduced risk and HLA-A*01 with an increased risk of developing EBV+ Hodgkin lymphoma. Blood, 2007, 110, 3310-3315.	1.4	131
47	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
48	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	21.4	119
49	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
50	HLA Class II Expression by Hodgkin Reed-Sternberg Cells Is an Independent Prognostic Factor in Classical Hodgkin's Lymphoma. Journal of Clinical Oncology, 2007, 25, 3101-3108.	1.6	118
51	Genome-wide association study of kidney function decline in individuals of European descent. Kidney International, 2015, 87, 1017-1029.	5.2	113
52	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
53	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
54	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109

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55	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
56	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
57	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
58	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
59	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
60	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
61	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
62	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
63	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
64	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
65	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. European Journal of Human Genetics, 2017, 25, 877-885.	2.8	67
66	Lipid and lipoprotein reference values from 133,450 Dutch Lifelines participants: Age- and gender-specific baseline lipid values and percentiles. Journal of Clinical Lipidology, 2017, 11, 1055-1064.e6.	1.5	67
67	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
68	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
69	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
70	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
71	Common Genetic Variation Near the Phospholamban Gene Is Associated with Cardiac Repolarisation: Meta-Analysis of Three Genome-Wide Association Studies. PLoS ONE, 2009, 4, e6138.	2.5	53
72	HLA Associations in Classical Hodgkin Lymphoma: EBV Status Matters. PLoS ONE, 2012, 7, e39986.	2.5	52

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73	Genetic Associations in Classical Hodgkin Lymphoma: A Systematic Review and Insights into Susceptibility Mechanisms. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2737-2747.	2.5	52
74	Filling the Gap: Relationship Between the Serotonin-Transporter-Linked Polymorphic Region and Amygdala Activation. Psychological Science, 2014, 25, 2058-2066.	3.3	52
75	Novel childhood asthma genes interact with in utero and early-life tobacco smoke exposure. Journal of Allergy and Clinical Immunology, 2014, 133, 885-888.	2.9	47
76	miR-24-3p Is Overexpressed in Hodgkin Lymphoma and Protects Hodgkin and Reed-Sternberg Cells from Apoptosis. American Journal of Pathology, 2017, 187, 1343-1355.	3.8	46
77	C-Terminal Fibroblast Growth Factor 23, Iron Deficiency, and Mortality in Renal Transplant Recipients. Journal of the American Society of Nephrology: JASN, 2017, 28, 3639-3646.	6.1	46
78	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
79	The Human Leukocyte Antigen Class I Region Is Associated with EBV-Positive Hodgkin's Lymphoma: HLA-A and HLA Complex Group 9 Are Putative Candidate Genes. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2280-2284.	2.5	36
80	The association of depression and anxiety with cardiac autonomic activity: The role of confounding effects of antidepressants. Depression and Anxiety, 2019, 36, 1163-1172.	4.1	36
81	Association of different iron deficiency cutoffs with adverse outcomes in chronic kidney disease. BMC Nephrology, 2018, 19, 225.	1.8	35
82	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
83	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
84	Connecting the dots, genome-wide association studies in substance use. Molecular Psychiatry, 2016, 21, 733-735.	7.9	31
85	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
86	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.5	26
87	Consumption of fruits and vegetables and cardiovascular mortality in renal transplant recipients: a prospective cohort study. Nephrology Dialysis Transplantation, 2020, 35, 357-365.	0.7	25
88	In Silico Post Genome-Wide Association Studies Analysis of C-Reactive Protein Loci Suggests an Important Role for Interferons. Circulation: Cardiovascular Genetics, 2015, 8, 487-497.	5.1	24
89	Genetic regulation of IL1RL1 methylation and IL1RL1-a protein levels in asthma. European Respiratory Journal, 2018, 51, 1701377.	6.7	24
90	Genomeâ€wide association metaâ€analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	3.3	24

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91	QCGWAS: A flexible R package for automated quality control of genome-wide association results. Bioinformatics, 2014, 30, 1185-1186.	4.1	22
92	Sex and Gender-Related Differences in COVID-19 Diagnoses and SARS-CoV-2 Testing Practices During the First Wave of the Pandemic: The Dutch Lifelines COVID-19 Cohort Study. Journal of Women's Health, 2021, 30, 1686-1692.	3.3	20
93	Associations between genetic risk, functional brain network organization and neuroticism. Brain Imaging and Behavior, 2017, 11, 1581-1591.	2.1	19
94	The miR-26b-5p/KPNA2 Axis Is an Important Regulator of Burkitt Lymphoma Cell Growth. Cancers, 2020, 12, 1464.	3.7	19
95	Postoperative Recovery of Visual Function after Macula-Off Rhegmatogenous Retinal Detachment. PLoS ONE, 2014, 9, e99787.	2.5	19
96	Plasma cadmium is associated with increased risk of long-term kidney graft failure. Kidney International, 2021, 99, 1213-1224.	5.2	18
97	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
98	The effect of high compared with low dairy consumption on glucose metabolism, insulin sensitivity, and metabolic flexibility in overweight adults: a randomized crossover trial. American Journal of Clinical Nutrition, 2019, 109, 1555-1568.	4.7	17
99	Metasubtract: an R-package to analytically produce leave-one-out meta-analysis GWAS summary statistics. Bioinformatics, 2020, 36, 4521-4522.	4.1	17
100	Genetic Risk Scores for Complex Disease Traits in Youth. Circulation Genomic and Precision Medicine, 2020, 13, e002775.	3.6	17
101	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
102	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
103	Personality Polygenes, Positive Affect, and Life Satisfaction. Twin Research and Human Genetics, 2016, 19, 407-417.	0.6	16
104	Active Smoking and Hematocrit and Fasting Circulating Erythropoietin Concentrations in the General Population. Mayo Clinic Proceedings, 2018, 93, 337-343.	3.0	16
105	Iron deficiency, elevated erythropoietin, fibroblast growth factor 23, and mortality in the general population of the Netherlands: A cohort study. PLoS Medicine, 2019, 16, e1002818.	8.4	16
106	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
107	Postoperative Vision-Related Quality of Life in Macula-Off Rhegmatogenous Retinal Detachment Patients and Its Relation to Visual Function. PLoS ONE, 2014, 9, e114489.	2.5	14
108	A Comparison of Heritability Estimates by Classical Twin Modeling and Based on Genome-Wide Genetic Relatedness for Cardiac Conduction Traits. Twin Research and Human Genetics, 2017, 20, 489-498.	0.6	14

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109	Identifying Genetic Variants for Heart Rate Variability in the Acetylcholine Pathway. PLoS ONE, 2014, 9, e112476.	2.5	13
110	Does refining the phenotype improve replication rates? A review and replication of candidate gene studies on Major Depressive Disorder and Chronic Major Depressive Disorder. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 215-236.	1.7	13
111	Genetic and environmental influences on stability and change in baseline levels of C-reactive protein: A longitudinal twin study. Atherosclerosis, 2017, 265, 172-178.	0.8	13
112	Heritability and genetic correlations of heart rate variability at rest and during stress in the Oman Family Study. Journal of Hypertension, 2018, 36, 1477-1485.	0.5	13
113	Ethnic differences in prevalence of Dupuytren disease can partly be explained by known genetic risk variants. European Journal of Human Genetics, 2019, 27, 1876-1884.	2.8	13
114	Heritability and the Genetic Correlation of Heart Rate Variability and Blood Pressure in >29â€‰000 Families. Hypertension, 2020, 76, 1256-1262.	2.7	13
115	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
116	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. Behavior Genetics, 2021, 51, 592-606.	2.1	13
117	Mitochondrial Genome Study Identifies Association Between Primary Open-Angle Glaucoma and Variants in MT-CYB, MT-ND4 Genes and Haplogroups. Frontiers in Genetics, 2021, 12, 781189.	2.3	13
118	Association testing by haplotype-sharing methods applicable to whole-genome analysis. BMC Proceedings, 2007, 1, S129.	1.6	12
119	The association of single nucleotide polymorphisms of the maternal cystathionine-Î²-synthase gene with early-onset preeclampsia. Pregnancy Hypertension, 2016, 6, 60-65.	1.4	12
120	Novel genes for QTc interval. How much heritability is explained, and how much is left to find?. Genome Medicine, 2010, 2, 35.	8.2	11
121	Evaluation of a genetic risk score based on creatinine-estimated glomerular filtration rate and its association with kidney outcomes. Nephrology Dialysis Transplantation, 2018, 33, 1757-1764.	0.7	11
122	Switching iron sucrose to ferric carboxymaltose associates to better control of iron status in hemodialysis patients. BMC Nephrology, 2018, 19, 242.	1.8	11
123	GWASinspector: comprehensive quality control of genome-wide association study results. Bioinformatics, 2021, 37, 129-130.	4.1	11
124	Heritability and genetic correlations of obesity indices with ambulatory and office beat-to-beat blood pressure in the Oman Family Study. Journal of Hypertension, 2020, 38, 1474-1480.	0.5	10
125	Thyroid function and risk of all-cause and cardiovascular mortality: a prospective population-based cohort study. Endocrine, 2021, 71, 385-396.	2.3	10
126	Genetic pre-screening for glaucoma in population-based epidemiology: protocol for a double-blind prospective screening study within Lifelines (EyeLife). BMC Ophthalmology, 2021, 21, 18.	1.4	9

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127	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
128	A Weighted Genetic Risk Score Predicts Surgical Recurrence Independent of High-Risk Clinical Features in Dupuytrenâ€™s Disease. Plastic and Reconstructive Surgery, 2019, 143, 512-518.	1.4	8
129	Heritability and genetic and environmental correlations of heart rate variability and baroreceptor reflex sensitivity with ambulatory and beat-to-beat blood pressure. Scientific Reports, 2019, 9, 1664.	3.3	8
130	Spontaneous baroreflex sensitivity and its association with age, sex, obesity indices and hypertension: a population study. American Journal of Hypertension, 2021, 34, 1276-1283.	2.0	8
131	Galectin-3 and Risk of Late Graft Failure in Kidney Transplant Recipients: A 10-year Prospective Cohort Study. Transplantation, 2021, 105, 1106-1115.	1.0	8
132	Early increase in single-kidney glomerular filtration rate after living kidney donation predicts long-term kidney function. Kidney International, 2022, 101, 1251-1259.	5.2	8
133	Interactions between uncoupling protein 2 gene polymorphisms, obesity and alcohol intake on liver function: a large meta-analysed population-based study. European Journal of Endocrinology, 2015, 173, 863-872.	3.7	7
134	The narrow-sense and common single nucleotide polymorphism heritability of early repolarization. International Journal of Cardiology, 2019, 279, 135-140.	1.7	7
135	Altered Gut Microbial Fermentation and Colonization with Methanobrevibacter smithii in Renal Transplant Recipients. Journal of Clinical Medicine, 2020, 9, 518.	2.4	7
136	HLA expression and HLA type associations in relation to EBV status in Hispanic Hodgkin lymphoma patients. PLoS ONE, 2017, 12, e0174457.	2.5	7
137	Geneâ€“environment interplay in externalizing behavior from childhood through adulthood. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2022, 63, 1206-1213.	5.2	7
138	Validating the doubly weighted genetic risk score for the prediction of type 2 diabetes in the Lifelines and Estonian Biobank cohorts. Genetic Epidemiology, 2020, 44, 589-600.	1.3	6
139	Interaction between ERAP Alleles and HLA Class I Types Support a Role of Antigen Presentation in Hodgkin Lymphoma Development. Cancers, 2021, 13, 414.	3.7	6
140	The associations of CNR1 SNPs and haplotypes with vulnerability and treatment response phenotypes in Han Chinese with major depressive disorder: A caseâ€“control association study. Molecular Genetics & Genomic Medicine, 2021, 9, e1752.	1.2	6
141	Polygenic risk for aggressive behavior from late childhood through early adulthood. European Child and Adolescent Psychiatry, 2023, 32, 651-660.	4.7	6
142	Plasma Lead Concentration and Risk of Late Kidney Allograft Failure: Findings From the TransplantLines Biobank and Cohort Studies. American Journal of Kidney Diseases, 2022, 80, 87-97.e1.	1.9	6
143	lodGWAS: a software package for genome-wide association analysis of biomarkers with a limit of detection. Bioinformatics, 2016, 32, 1552-1554.	4.1	5
144	Genome-Wide Association Scan of Serum Urea in European Populations Identifies Two Novel Loci. American Journal of Nephrology, 2019, 49, 193-202.	3.1	5

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145	Meat intake and risk of mortality and graft failure in kidney transplant recipients. American Journal of Clinical Nutrition, 2021, 114, 1505-1517.	4.7	5
146	Using Polygenic Scores in Social Science Research: Unraveling Childlessness. Frontiers in Sociology, 2019, 4, 74.	2.0	4
147	Serum uric acid is associated with increased risk of posttransplantation diabetes in kidney transplant recipients: a prospective cohort study. Metabolism: Clinical and Experimental, 2021, 116, 154465.	3.4	4
148	Killer Cell Immunoglobulin-Like Receptor Haplotype B Modulates Susceptibility to EBV-Associated Classic Hodgkin Lymphoma. Frontiers in Immunology, 2022, 13, 829943.	4.8	4
149	A Population Based Study of the Genetic Association between Catecholamine Gene Variants and Spontaneous Low-Frequency Fluctuations in Reaction Time. PLoS ONE, 2015, 10, e0126461.	2.5	2
150	Plasma versus Erythrocyte Vitamin E in Renal Transplant Recipients, and Duality of Tocopherol Species. Nutrients, 2019, 11, 2821.	4.1	2
151	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
152	Lack of association of FKBP5 SNPs and haplotypes with susceptibility and treatment response phenotypes in Han Chinese with major depressive disorder. Medicine (United States), 2021, 100, e26983.	1.0	2
153	Plasma phosphate and all-cause mortality in individuals with and without type 2 diabetes: the Dutch population-based lifelines cohort study. Cardiovascular Diabetology, 2022, 21, 61.	6.8	2
154	Population Based Genotyping of Human Leukocyte Antigen (HLA) in Hodgkin Lymphoma: EBV Positive HL Is Associated with HLA Class I and EBV Negative HL Is Associated with HLA Class III.. Blood, 2004, 104, 432-432.	1.4	1
155	Protective and Predisposing HLA Alleles In Dutch Classical Hodgkin Lymphoma Patients. Blood, 2010, 116, 749-749.	1.4	1
156	HLA Expression in Relation to HLA Type in Classic Hodgkin Lymphoma Patients. Cancers, 2021, 13, 5833.	3.7	1
157	Influence of Receptor Polymorphisms on the Response to Î±-Adrenergic Receptor Blockers in Pheochromocytoma Patients. Biomedicines, 2022, 10, 896.	3.2	1
158	Erythropoietin, Fibroblast Growth Factor 23, and Death After Kidney Transplantation. Journal of Clinical Medicine, 2020, 9, 1737.	2.4	0
159	Duality of Tocopherol Isoforms and Novel Associations with Vitamins Involved in One-Carbon Metabolism: Results from an Elderly Sample of the LifeLines Cohort Study. Nutrients, 2020, 12, 580.	4.1	0
160	Haplotype-Based Sequencing To Delineate the Associated HLA Class I Region for EBV Positive Hodgkin Lymphoma.. Blood, 2005, 106, 971-971.	1.4	0
161	MO944: Persistent Microscopic Hematuria At Kidney Donor Screening and Long-Term Post-Donation Kidney Outcomes. Nephrology Dialysis Transplantation, 2022, 37, .	0.7	0