

Ozren Polasek

List of Publications by Year in descending order

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Version: 2024-02-01

354
papers

50,425
citations

2669

95
h-index

1974

206
g-index

403
all docs

403
docs citations

403
times ranked

54944
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
4	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
5	Worldwide trends in blood pressure from 1975 to 2015: a pooled analysis of 1479 population-based measurement studies with 19A.1 million participants. <i>Lancet</i> , The, 2017, 389, 37-55.	6.3	1,667
6	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
7	Runs of Homozygosity in European Populations. <i>American Journal of Human Genetics</i> , 2008, 83, 359-372.	2.6	958
8	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
9	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	9.4	870
10	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
11	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
12	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750
13	Large-scale association analyses identify new loci influencing glycaemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
14	New loci associated with kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 376-384.	9.4	710
15	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. <i>Nature Genetics</i> , 2008, 40, 437-442.	9.4	678
16	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675
17	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	9.4	581
18	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578

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19	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. <i>PLoS Genetics</i> , 2014, 10, e1004234.	1.5	553
20	International Photographic Classification and Grading System for Myopic Maculopathy. <i>American Journal of Ophthalmology</i> , 2015, 159, 877-883.e7.	1.7	549
21	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	9.4	549
22	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
23	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019, 51, 245-257.	9.4	536
24	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	9.4	518
25	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
26	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
27	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
28	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	9.4	445
29	High Throughput Isolation and Glycosylation Analysis of IgG—Variability and Heritability of the IgG Glycome in Three Isolated Human Populations. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010090.	2.5	443
30	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
31	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
32	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
33	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
34	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. <i>Nature Genetics</i> , 2013, 45, 314-318.	9.4	398
35	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.3	387
36	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383

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37	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
38	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
39	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
40	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. <i>Nature Genetics</i> , 2019, 51, 481-493.	9.4	350
41	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , 2015, 3, 769-781.	5.2	346
42	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53,949). <i>Molecular Psychiatry</i> , 2015, 20, 183-192.	4.1	344
43	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. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
44	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	9.4	341
45	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.3	335
46	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
47	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
48	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. <i>PLoS Genetics</i> , 2013, 9, e1003225.	1.5	323
49	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2014, 2, 719-729.	5.5	319
50	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. <i>Nature Genetics</i> , 2010, 42, 1068-1076.	9.4	308
51	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	9.4	303
52	Glycans Are a Novel Biomarker of Chronological and Biological Ages. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2014, 69, 779-789.	1.7	297
53	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	6.0	289
54	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	2.6	287

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55	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
56	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	9.4	284
57	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
58	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	9.4	281
59	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 2013, 45, 155-163.	9.4	269
60	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
61	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. <i>Nature Genetics</i> , 2017, 49, 416-425.	9.4	257
62	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
63	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
64	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	9.4	239
65	Genomics Meets Glycomics—The First GWAS Study of Human N-Glycome Identifies HNF1 α as a Master Regulator of Plasma Protein Fucosylation. <i>PLoS Genetics</i> , 2010, 6, e1001256.	1.5	213
66	Variability, Heritability and Environmental Determinants of Human Plasma N-Glycome. <i>Journal of Proteome Research</i> , 2009, 8, 694-701.	1.8	212
67	CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.	3.0	208
68	Effects of aging, body mass index, plasma lipid profiles, and smoking on human plasma N-glycans. <i>Glycobiology</i> , 2010, 20, 959-969.	1.3	207
69	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. <i>PLoS Genetics</i> , 2009, 5, e1000672.	1.5	184
70	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
71	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	1.5	181
72	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178

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73	Effects of genome-wide heterozygosity on a range of biomedically relevant human quantitative traits. <i>Human Molecular Genetics</i> , 2007, 16, 233-241.	1.4	176
74	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173
75	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
76	Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1598-1610.	2.5	169
77	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
78	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
79	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	1.5	166
80	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
81	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	5.8	147
82	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. <i>PLoS Genetics</i> , 2013, 9, e1003796.	1.5	142
83	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. <i>American Journal of Human Genetics</i> , 2013, 93, 264-277.	2.6	139
84	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. <i>Human Molecular Genetics</i> , 2010, 19, 4304-4311.	1.4	136
85	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	4.1	134
86	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
87	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.3	131
88	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. <i>Circulation</i> , 2013, 128, 1310-1324.	1.6	128
89	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
90	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	2.6	123

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91	52 Genetic Loci Influencing Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 2016, 68, 1435-1448.	1.2	113
92	Genome-wide association uncovers shared genetic effects among personality traits and mood states. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 684-695.	1.1	112
93	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. <i>PLoS Genetics</i> , 2018, 14, e1007601.	1.5	112
94	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	9.4	112
95	Gaps in policy-relevant information on burden of disease in children: a systematic review. <i>Lancet</i> , The, 2005, 365, 2031-2040.	6.3	110
96	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	3.3	110
97	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	5.8	108
98	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	1.5	107
99	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. <i>Nature Communications</i> , 2016, 7, 11008.	5.8	104
100	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	1.4	103
101	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. <i>Nature Communications</i> , 2017, 8, 447.	5.8	102
102	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
103	1000 Dalmatians: Croatia Launches Its National Biobank. <i>Croatian Medical Journal</i> , 2009, 50, 4-6.	0.2	99
104	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 100-112.	5.1	98
105	Mutations in <i>HNF1A</i> Result in Marked Alterations of Plasma Glycan Profile. <i>Diabetes</i> , 2013, 62, 1329-1337.	0.3	97
106	Have Lifestyle Habits and Psychological Well-Being Changed among Adolescents and Medical Students Due to COVID-19 Lockdown in Croatia?. <i>Nutrients</i> , 2021, 13, 97.	1.7	97
107	Ethical aspects of human biobanks: a systematic review. <i>Croatian Medical Journal</i> , 2011, 52, 262-279.	0.2	95
108	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94

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109	Impact analysis of a regional scientific journal (1980-2000): supporting promising local researchers pays the greatest dividends. <i>Collegium Antropologicum</i> , 2005, 29, 1-7.	0.1	94
110	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
111	Genetic determinants of heel bone properties: genome-wide association meta-analysis and replication in the GEFOS/GENOMOS consortium. <i>Human Molecular Genetics</i> , 2014, 23, 3054-3068.	1.4	90
112	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. <i>Science Advances</i> , 2020, 6, eaax0301.	4.7	90
113	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	89
114	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
115	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. <i>Human Molecular Genetics</i> , 2009, 18, 373-380.	1.4	88
116	The Effect of Intra-articular Injection of Autologous Microfragmented Fat Tissue on Proteoglycan Synthesis in Patients with Knee Osteoarthritis. <i>Genes</i> , 2017, 8, 270.	1.0	87
117	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
118	Common Variants in UMOD Associate with Urinary Uromodulin Levels. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 1869-1882.	3.0	85
119	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
120	The Association Between Glycosylation of Immunoglobulin G and Hypertension. <i>Medicine (United States)</i> , 2019, 98, 161-167.	0.4	84
121	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
122	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	1.5	80
123	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. <i>Scientific Reports</i> , 2016, 6, 25853.	1.6	80
124	Evidence of Inbreeding Depression on Human Height. <i>PLoS Genetics</i> , 2012, 8, e1002655.	1.5	79
125	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	6.2	79
126	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. <i>Human Molecular Genetics</i> , 2013, 22, 4857-4869.	1.4	77

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127	Estimating Human Inbreeding Coefficients: Comparison of Genealogical and Marker Heterozygosity Approaches. <i>Annals of Human Genetics</i> , 2006, 70, 666-676.	0.3	75
128	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	6.2	75
129	Polymorphisms in B3GAT1, SLC9A9 and MGAT5 are associated with variation within the human plasma N-glycome of 3533 European adults. <i>Human Molecular Genetics</i> , 2011, 20, 5000-5011.	1.4	74
130	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
131	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
132	Hypercoagulability in Cushing's syndrome: the role of specific haemostatic and fibrinolytic markers. <i>Endocrine</i> , 2009, 36, 70-74.	1.1	72
133	Genome-wide linkage analysis of serum creatinine in three isolated European populations. <i>Kidney International</i> , 2009, 76, 297-306.	2.6	71
134	Hearing function and thresholds: a genome-wide association study in European isolated populations identifies new loci and pathways. <i>Journal of Medical Genetics</i> , 2011, 48, 369-374.	1.5	71
135	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. <i>Archives of General Psychiatry</i> , 2012, 69, 854.	13.8	71
136	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	5.8	71
137	The Eysenck personality factors: Psychometric structure, reliability, heritability and phenotypic and genetic correlations with psychological distress in an isolated Croatian population. <i>Personality and Individual Differences</i> , 2007, 42, 123-133.	1.6	70
138	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. <i>American Journal of Human Genetics</i> , 2012, 91, 744-753.	2.6	69
139	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. <i>Lancet Respiratory Medicine</i> , 2020, 8, 696-708.	5.2	69
140	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012, 131, 1467-1480.	1.8	67
141	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	0.7	67
142	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. <i>Nature Communications</i> , 2017, 8, 1483.	5.8	67
143	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. <i>Lancet Respiratory Medicine</i> , 2015, 3, 782-795.	5.2	66
144	Contributions of mean and shape of blood pressure distribution to worldwide trends and variations in raised blood pressure: a pooled analysis of 1018 population-based measurement studies with 88.6 million participants. <i>International Journal of Epidemiology</i> , 2018, 47, 872-883i.	0.9	65

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145	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	1.4	64
146	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
147	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
148	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. <i>Molecular Psychiatry</i> , 2017, 22, 192-201.	4.1	63
149	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. <i>Nature Communications</i> , 2018, 9, 1864.	5.8	63
150	3000 years of solitude: extreme differentiation in the island isolates of Dalmatia, Croatia. <i>European Journal of Human Genetics</i> , 2006, 14, 478-487.	1.4	61
151	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. <i>Circulation</i> , 2011, 123, 1864-1872.	1.6	60
152	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	2.6	60
153	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in <i>RBFOX1</i> , a regulator of tissue-specific splicing, associated with refractive error. <i>Human Molecular Genetics</i> , 2013, 22, 2754-2764.	1.4	60
154	The role of host genetic factors in respiratory tract infectious diseases: systematic review, meta-analyses and field synopsis. <i>Scientific Reports</i> , 2015, 5, 16119.	1.6	59
155	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰%000 subjects. <i>Molecular Psychiatry</i> , 2015, 20, 735-743.	4.1	59
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