Ozren Polasek

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5155296/publications.pdf

Version: 2024-02-01

354 papers 50,425 citations

95 h-index 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. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
2	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
4	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
5	Worldwide trends in blood pressure from 1975 to 2015: a pooled analysis of 1479 population-based measurement studies with $19 \text{\AA} \cdot 1$ million participants. Lancet, The, 2017, 389, 37-55.	13.7	1,667
6	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
7	Runs of Homozygosity in European Populations. American Journal of Human Genetics, 2008, 83, 359-372.	6.2	958
8	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
9	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
10	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.	21.4	836
11	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
12	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
13	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
14	New loci associated with kidney function and chronic kidney disease. Nature Genetics, 2010, 42, 376-384.	21.4	710
15	SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. Nature Genetics, 2008, 40, 437-442.	21.4	678
16	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
17	Meta-analysis and imputation refines the association of $15q25$ with smoking quantity. Nature Genetics, $2010, 42, 436-440$.	21.4	581
18	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578

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19	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. PLoS Genetics, 2014, 10, e1004234.	3.5	553
20	International Photographic Classification and Grading System for Myopic Maculopathy. American Journal of Ophthalmology, 2015, 159, 877-883.e7.	3.3	549
21	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
22	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	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. Nature Genetics, 2019, 51, 245-257.	21.4	536
24	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
25	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
26	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
27	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
28	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
29	High Throughput Isolation and Glycosylation Analysis of IgG–Variability and Heritability of the IgG Glycome in Three Isolated Human Populations. Molecular and Cellular Proteomics, 2011, 10, M111.010090.	3.8	443
30	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
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. PLoS Genetics, 2012, 8, e1002607.	3.5	419
32	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
33	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
34	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
35	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
36	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383

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37	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
38	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
39	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
40	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	21.4	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. Lancet Respiratory Medicine, the, 2015, 3, 769-781.	10.7	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). Molecular Psychiatry, 2015, 20, 183-192.	7.9	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. PLoS Medicine, 2017, 14, e1002383.	8.4	341
44	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	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. Diabetes, 2011, 60, 2624-2634.	0.6	335
46	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
47	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. Nature Metabolism, 2020, 2, 1135-1148.	11.9	327
48	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. PLoS Genetics, 2013, 9, e1003225.	3.5	323
49	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
50	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. Nature Genetics, 2010, 42, 1068-1076.	21.4	308
51	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
52	Glycans Are a Novel Biomarker of Chronological and Biological Ages. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2014, 69, 779-789.	3.6	297
53	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	11.0	289
54	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287

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55	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
56	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
57	Identification of heart rate–associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
58	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
59	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	21.4	269
60	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
61	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
62	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
63	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
64	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
65	Genomics Meets Glycomics—The First GWAS Study of Human N-Glycome Identifies HNF1α as a Master Regulator of Plasma Protein Fucosylation. PLoS Genetics, 2010, 6, e1001256.	3.5	213
66	Variability, Heritability and Environmental Determinants of Human Plasma N-Glycome. Journal of Proteome Research, 2009, 8, 694-701.	3.7	212
67	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
68	Effects of aging, body mass index, plasma lipid profiles, and smoking on human plasma N-glycans. Glycobiology, 2010, 20, 959-969.	2.5	207
69	Genetic Determinants of Circulating Sphingolipid Concentrations in European Populations. PLoS Genetics, 2009, 5, e1000672.	3.5	184
70	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
71	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
72	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	2.1	178

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73	Effects of genome-wide heterozygosity on a range of biomedically relevant human quantitative traits. Human Molecular Genetics, 2007, 16, 233-241.	2.9	176
74	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
75	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
76	Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research. Molecular and Cellular Proteomics, 2014, 13, 1598-1610.	3.8	169
77	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
78	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
79	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	3.5	166
80	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
81	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
82	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
83	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	6.2	139
84	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. Human Molecular Genetics, 2010, 19, 4304-4311.	2.9	136
85	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
86	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
87	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	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. Circulation, 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. Hypertension, 2017, 70, .	2.7	123
90	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123

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91	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
92	Genomeâ€wide association uncovers shared genetic effects among personality traits and mood states. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 684-695.	1.7	112
93	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
94	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
95	Gaps in policy-relevant information on burden of disease in children: a systematic review. Lancet, The, 2005, 365, 2031-2040.	13.7	110
96	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
97	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015 , 6 , 8658 .	12.8	108
98	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. PLoS Genetics, 2015, 11, e1005035.	3.5	107
99	Meta-analysis of gene–environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
100	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. Behavior Genetics, 2014, 44, 295-313.	2.1	103
101	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. Nature Communications, 2017, 8, 447.	12.8	102
102	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 2019, 139, 620-635.	1.6	102
103	"10 001 Dalmatians:―Croatia Launches Its National Biobank. Croatian Medical Journal, 2009, 50, 4-6.	0.7	99
104	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
105	Mutations in <i>HNF1A</i> Result in Marked Alterations of Plasma Glycan Profile. Diabetes, 2013, 62, 1329-1337.	0.6	97
106	Have Lifestyle Habits and Psychological Well-Being Changed among Adolescents and Medical Students Due to COVID-19 Lockdown in Croatia?. Nutrients, 2021, 13, 97.	4.1	97
107	Ethical aspects of human biobanks: a systematic review. Croatian Medical Journal, 2011, 52, 262-279.	0.7	95
108	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

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109	Impact analysis of a regional scientific journal (1980-2000): supporting promising local researchers pays the greatest dividends. Collegium Antropologicum, 2005, 29, 1-7.	0.2	94
110	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
111	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.	2.9	90
112	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	10.3	90
113	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
114	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
115	Common variants in the JAZF1 gene associated with height identified by linkage and genome-wide association analysis. Human Molecular Genetics, 2009, 18, 373-380.	2.9	88
116	The Effect of Intra-articular Injection of Autologous Microfragmented Fat Tissue on Proteoglycan Synthesis in Patients with Knee Osteoarthritis. Genes, 2017, 8, 270.	2.4	87
117	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
118	Common Variants in UMOD Associate with Urinary Uromodulin Levels. Journal of the American Society of Nephrology: JASN, 2014, 25, 1869-1882.	6.1	85
119	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
120	The Association Between Glycosylation of Immunoglobulin G and Hypertension. Medicine (United) Tj ETQq0 0 0 r	gBT/Over	logk 10 Tf 50
121	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
122	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3 . 5	80
123	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. Scientific Reports, 2016, 6, 25853.	3.3	80
124	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
125	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
126	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. Human Molecular Genetics, 2013, 22, 4857-4869.	2.9	77

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127	Estimating Human Inbreeding Coefficients: Comparison of Genealogical and Marker Heterozygosity Approaches. Annals of Human Genetics, 2006, 70, 666-676.	0.8	7 5
128	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
129	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.	2.9	74
130	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
131	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	7 3
132	Hypercoagulability in Cushing's syndrome: the role of specific haemostatic and fibrinolytic markers. Endocrine, 2009, 36, 70-74.	2.3	72
133	Genome-wide linkage analysis of serum creatinine in three isolated European populations. Kidney International, 2009, 76, 297-306.	5.2	71
134	Hearing function and thresholds: a genome-wide association study in European isolated populations identifies new loci and pathways. Journal of Medical Genetics, 2011, 48, 369-374.	3.2	71
135	Increased Genetic Vulnerability to Smoking at CHRNA5 in Early-Onset Smokers. Archives of General Psychiatry, 2012, 69, 854.	12.3	71
136	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
137	The Eysenck personality factors: Psychometric structure, reliability, heritability and phenotypic and genetic correlations with psychological distress in an isolated Croatian population. Personality and Individual Differences, 2007, 42, 123-133.	2.9	70
138	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69
139	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine, the, 2020, 8, 696-708.	10.7	69
140	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67
141	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	1.3	67
142	Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. Nature Communications, 2017, 8, 1483.	12.8	67
143	Molecular mechanisms underlying variations in lung function: a systems genetics analysis. Lancet Respiratory Medicine, the, 2015, 3, 782-795.	10.7	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. International Journal of Epidemiology, 2018, 47, 872-883i.	1.9	65

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145	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	2.9	64
146	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
147	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
148	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	7.9	63
149	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
150	3000 years of solitude: extreme differentiation in the island isolates of Dalmatia, Croatia. European Journal of Human Genetics, 2006, 14, 478-487.	2.8	61
151	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
152	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
153	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
154	The role of host genetic factors in respiratory tract infectious diseases: systematic review, meta-analyses and field synopsis. Scientific Reports, 2015, 5, 16119.	3.3	59
155	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25 000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	7.9	59
156	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
157	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
158	Facial aging trajectories: A common shape pattern in male and female faces is disrupted after menopause. American Journal of Physical Anthropology, 2019, 169, 678-688.	2.1	56
159	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
160	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
161	Early results of intra-articular micro-fragmented lipoaspirate treatment in patients with late stages knee osteoarthritis: a prospective study. Croatian Medical Journal, 2019, 60, 227-236.	0.7	55
162	The association between galactosylation of immunoglobulin G and body mass index. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2014, 48, 20-25.	4.8	52

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163	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.	3.5	51
164	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. American Journal of Epidemiology, 2013, 178, 451-460.	3.4	51
165	A common biological basis of obesity and nicotine addiction. Translational Psychiatry, 2013, 3, e308-e308.	4.8	51
166	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
167	Concordant Association of Insulin Degrading Enzyme Gene (IDE) Variants with IDE mRNA, Aß, and Alzheimer's Disease. PLoS ONE, 2010, 5, e8764.	2.5	48
168	New Blood Pressure–Associated Loci Identified in Meta-Analyses of 475 000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
169	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
170	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
171	A 24-Month Follow-Up Study of the Effect of Intra-Articular Injection of Autologous Microfragmented Fat Tissue on Proteoglycan Synthesis in Patients with Knee Osteoarthritis. Genes, 2019, 10, 1051.	2.4	45
172	Common aberrations from the normal human plasma N-glycan profile. Glycobiology, 2010, 20, 970-975.	2. 5	44
173	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. PLoS Genetics, 2013, 9, e1003585.	3.5	43
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