List of Publications by Year in descending order

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HONG-HEE MON

#	Article	IF	CITATIONS
1	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
2	A comprehensive 1000 Genomes–based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
3	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
4	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	1.2	723
5	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
6	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
7	Coding Variation in <i>ANGPTL4,LPL,</i> and <i>SVEP1</i> and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
8	Inactivating Mutations in <i>NPC1L1</i> and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	13.9	386
9	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	13.7	292
10	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
11	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	9.4	209
12	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	1.2	186
13	SORL1 Is Genetically Associated with Late-Onset Alzheimer's Disease in Japanese, Koreans and Caucasians. PLoS ONE, 2013, 8, e58618.	1.1	149
14	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	3.8	148
15	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	1.2	147
16	Physical activity and the risk of SARS-CoV-2 infection, severe COVID-19 illness and COVID-19 related mortality in South Korea: a nationwide cohort study. British Journal of Sports Medicine, 2022, 56, 901-912.	3.1	120
17	Mutations in PRPS1, Which Encodes the Phosphoribosyl Pyrophosphate Synthetase Enzyme Critical for Nucleotide Biosynthesis, Cause Hereditary Peripheral Neuropathy with Hearing Loss and Optic Neuropathy (CMTX5). American Journal of Human Genetics, 2007, 81, 552-558.	2.6	116
18	Association between adiposity and cardiovascular outcomes: an umbrella review and meta-analysis of observational and Mendelian randomization studies. European Heart Journal, 2021, 42, 3388-3403.	1.0	114

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19	Predicting National Suicide Numbers with Social Media Data. PLoS ONE, 2013, 8, e61809.	1.1	102
20	No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725.	3.9	97
21	Cancer classification using ensemble of neural networks with multiple significant gene subsets. Applied Intelligence, 2007, 26, 243-250.	3.3	86
22	Myocardial Infarction–Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With <i>PHACTR1</i> Expression Levels in Human Coronary Arteries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1472-1479.	1.1	78
23	Polymorphic markers associated with severe oxaliplatinâ€induced, chronic peripheral neuropathy in colon cancer patients. Cancer, 2012, 118, 2828-2836.	2.0	76
24	Autoimmune inflammatory rheumatic diseases and COVID-19 outcomes in South Korea: a nationwide cohort study. Lancet Rheumatology, The, 2021, 3, e698-e706.	2.2	73
25	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	1.5	70
26	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	2.0	68
27	Moyamoya Disease and Spectrums of RNF213 Vasculopathy. Translational Stroke Research, 2020, 11, 580-589.	2.3	67
28	Association between Air Pollution and Suicide in South Korea: A Nationwide Study. PLoS ONE, 2015, 10, e0117929.	1.1	63
29	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	0.9	61
30	Rare Protein-Truncating Variants in <i>APOB</i> , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002376.	1.6	57
31	Systematic Cell-Based Phenotyping of Missense Alleles Empowers Rare Variant Association Studies: A Case for LDLR and Myocardial Infarction. PLoS Genetics, 2015, 11, e1004855.	1.5	50
32	Paraquat Prohibition and Change in the Suicide Rate and Methods in South Korea. PLoS ONE, 2015, 10, e0128980.	1.1	47
33	The 18p11.22 locus is associated with never smoker non-small cell lung cancer susceptibility in Korean populations. Human Genetics, 2012, 131, 365-372.	1.8	45
34	Evaluation of the effects of VKORC1 polymorphisms and haplotypes, CYP2C9 genotypes, and clinical factors on warfarin response in Sudanese patients. European Journal of Clinical Pharmacology, 2011, 67, 1119-1130.	0.8	38
35	NUDT15 genotype distributions in the Korean population. Pharmacogenetics and Genomics, 2017, 27, 197-200.	0.7	35
36	Genetic association study of individual symptoms in depression. Psychiatry Research, 2012, 198, 400-406.	1.7	34

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37	Burden of Intracranial Atherosclerosis Is Associated With Long-Term Vascular Outcome in Patients With Ischemic Stroke. Stroke, 2017, 48, 2819-2826.	1.0	34
38	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. Science Advances, 2020, 6, .	4.7	33
39	Founder effects in two predominant intronic mutations of UNC13D, c.118-308C>T and c.754-1G>C underlie the unusual predominance of type 3 familial hemophagocytic lymphohistiocytosis (FHL3) in Korea. Annals of Hematology, 2013, 92, 357-364.	0.8	32
40	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29
41	A genome-wide association study of antidepressant response in Koreans. Translational Psychiatry, 2015, 5, e633-e633.	2.4	29
42	A genome-wide association study identifies novel loci associated with susceptibility to chronic myeloid leukemia. Blood, 2011, 117, 6906-6911.	0.6	28
43	SNP Linkage Analysis and Whole Exome Sequencing Identify a Novel POU4F3 Mutation in Autosomal Dominant Late-Onset Nonsyndromic Hearing Loss (DFNA15). PLoS ONE, 2013, 8, e79063.	1.1	28
44	A Genome-Wide Scan for the Sasang Constitution in a Korean Family Suggests Significant Linkage at Chromosomes 8q11.22–23 and 11q22.1–3. Journal of Alternative and Complementary Medicine, 2009, 15, 765-769.	2.1	25
45	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	1.6	25
46	Association of the Choline Acetyltransferase Gene with Responsiveness to Acetylcholinesterase Inhibitors in Alzheimer's Disease. Pharmacopsychiatry, 2015, 48, 111-117.	1.7	24
47	DATA MINING FOR GENE EXPRESSION PROFILES FROM DNA MICROARRAY. International Journal of Software Engineering and Knowledge Engineering, 2003, 13, 593-608.	0.6	23
48	Association Between a Polymorphism in the Lymphotoxin?aPromoter Region and Migraine. Headache, 2007, 47, 1056-1062.	1.8	22
49	Subjective cognitive decline and subsequent dementia: a nationwide cohort study of 579,710 people aged 66 years in South Korea. Alzheimer's Research and Therapy, 2020, 12, 52.	3.0	22
50	EnsemPro: An ensemble approach to predicting transcription start sites in human genomic DNA sequences. Genomics, 2008, 91, 259-266.	1.3	20
51	Multiple Single-Nucleotide Polymorphism–Based Risk Model for Clinical Outcomes After Allogeneic Stem-Cell Transplantation, Especially for Acute Graft-Versus-Host Disease. Transplantation, 2012, 94, 1250-1257.	0.5	19
52	Associations between vascular risk factors and subsequent Alzheimer's disease in older adults. Alzheimer's Research and Therapy, 2020, 12, 117.	3.0	19
53	Risk stratification of organ-specific GVHD can be improved by single-nucleotide polymorphism-based risk models. Bone Marrow Transplantation, 2014, 49, 649-656.	1.3	18
54	GWAS Analysis of 17,019 Korean Women Identifies the Variants Associated with Facial Pigmented Spots. Journal of Investigative Dermatology, 2021, 141, 555-562.	0.3	18

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55	hnRNPK-regulated LINC00263 promotes malignant phenotypes through miR-147a/CAPN2. Cell Death and Disease, 2021, 12, 290.	2.7	18
56	Comprehensive characterization of distinct genetic alterations in metastatic breast cancer across various metastatic sites. Npj Breast Cancer, 2021, 7, 93.	2.3	17
57	Genetic Prediction of Antidepressant Drug Response and Nonresponse in Korean Patients. PLoS ONE, 2014, 9, e107098.	1.1	17
58	Evaluation of lysyl oxidase-like 1 gene polymorphisms in pseudoexfoliation syndrome in a Korean population. Molecular Vision, 2013, 19, 448-53.	1.1	17
59	Genome-wide association study in patients with pulmonary <i>Mycobacterium avium</i> complex disease. European Respiratory Journal, 2021, 58, 1902269.	3.1	16
60	Celebrity Suicides and Their Differential Influence on Suicides in the General Population: A National Population-Based Study in Korea. Psychiatry Investigation, 2015, 12, 204.	0.7	15
61	Whole exome sequencing combined with integrated variant annotation prediction identifies a causative myosin essential light chain variant in hypertrophic cardiomyopathy. Journal of Cardiology, 2016, 67, 133-139.	0.8	14
62	HMGCLL1 is a predictive biomarker for deep molecular response to imatinib therapy in chronic myeloid leukemia. Leukemia, 2019, 33, 1439-1450.	3.3	14
63	Machine learning-based diagnostic method of pre-therapeutic 18F-FDG PET/CT for evaluating mediastinal lymph nodes in non-small cell lung cancer. European Radiology, 2021, 31, 4184-4194.	2.3	14
64	Polygenic risk for type 2 diabetes, lifestyle, metabolic health, and cardiovascular disease: a prospective UK Biobank study. Cardiovascular Diabetology, 2022, 21, .	2.7	14
65	Interleukin 10 polymorphisms differentially influence the risk of gastric cancer in East Asians and Caucasians. Cytokine, 2010, 51, 73-77.	1.4	13
66	Contribution of SLC22A12 on hypouricemia and its clinical significance for screening purposes. Scientific Reports, 2019, 9, 14360.	1.6	13
67	Analysis of dementia-related gene variants in APOE lµ4 noncarrying Korean patients with early-onset Alzheimer's disease. Neurobiology of Aging, 2020, 85, 155.e5-155.e8.	1.5	13
68	Polygenic analysis of the effect of common and low-frequency genetic variants on serum uric acid levels in Korean individuals. Scientific Reports, 2020, 10, 9179.	1.6	13
69	Comparative analysis of the JAK/STAT signaling through erythropoietin receptor and thrombopoietin receptor using a systems approach. BMC Bioinformatics, 2009, 10, S53.	1.2	12
70	Genomeâ€widely significant evidence of linkage of schizophrenia to chromosomes 2p24.3 and 6q27 in an SNPâ€Based analysis of Korean families. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 647-652.	1.1	12
71	Cataloging Coding Sequence Variations in Human Genome Databases. PLoS ONE, 2008, 3, e3575.	1.1	12
72	Development and validation of a novel strong prognostic index for colon cancer through a robust combination of laboratory features for systemic inflammation: a prognostic immune nutritional index. British Journal of Cancer, 2022	2.9	12

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73	Pathogenesis and Management of Brugada Syndrome: Recent Advances and Protocol for Umbrella Reviews of Meta-Analyses in Major Arrhythmic Events Risk Stratification. Journal of Clinical Medicine, 2022, 11, 1912.	1.0	12
74	Comparison of identical single nucleotide polymorphisms genotyped by the GeneChip Targeted Genotyping 25K, Affymetrix 500K and Illumina 550K platforms. Genomics, 2009, 94, 89-93.	1.3	11
75	Genome-wide linkage scan of quantitative traits representing symptom dimensions in multiplex schizophrenia families. Psychiatry Research, 2013, 210, 756-760.	1.7	11
76	Breakpoint mapping by whole genome sequencing identifies <i>PTH2R</i> gene disruption in a patient with midline craniosynostosis and a de novo balanced chromosomal rearrangement. Journal of Medical Genetics, 2015, 52, 706-709.	1.5	10
77	The Association of Single-Nucleotide Polymorphisms in the <i>MMP-9</i> Gene with Normal Tension Glaucoma and Primary Open-Angle Glaucoma. Current Eye Research, 2018, 43, 534-538.	0.7	10
78	Shared Genetic Background between Parkinson's Disease and Schizophrenia: A Two-Sample Mendelian Randomization Study. Brain Sciences, 2021, 11, 1042.	1.1	10
79	Rare, Damaging DNA Variants in <i>CORIN</i> and Risk of Coronary Artery Disease: Insights From Functional Genomics and Large-Scale Sequencing Analyses. Circulation Genomic and Precision Medicine, 2021, 14, e003399.	1.6	10
80	Machine learning-based prediction model for responses of bDMARDs in patients with rheumatoid arthritis and ankylosing spondylitis. Arthritis Research and Therapy, 2021, 23, 254.	1.6	10
81	GWAS Identifies Multiple Genetic Loci for Skin Color in Korean Women. Journal of Investigative Dermatology, 2022, 142, 1077-1084.	0.3	10
82	Heritability estimates of individual psychological distress symptoms from genetic variation. Journal of Affective Disorders, 2019, 252, 413-420.	2.0	9
83	Correlation Between Hippocampal Enlarged Perivascular Spaces and Cognition in Non-dementic Elderly Population. Frontiers in Neurology, 2020, 11, 542511.	1.1	8
84	A deep learning model for screening type 2 diabetes from retinal photographs. Nutrition, Metabolism and Cardiovascular Diseases, 2022, 32, 1218-1226.	1.1	8
85	OUP accepted manuscript. Brain, 2021, , .	3.7	7
86	Identifying novel genetic variants for brain amyloid deposition: a genome-wide association study in the Korean population. Alzheimer's Research and Therapy, 2021, 13, 117.	3.0	7
87	Differentially expressed genes in human peripheral blood as potential markers for statin response. Journal of Molecular Medicine, 2012, 90, 201-211.	1.7	6
88	Neural Network Ensemble with Negatively Correlated Features for Cancer Classification. Lecture Notes in Computer Science, 2003, , 1143-1150.	1.0	6
89	Two-sample Mendelian randomization study for schizophrenia and breast cancer. Precision and Future Medicine, 2020, 4, 21-30.	0.5	6
90	Sequence Variations and Haplotypes of the <i>GJB2</i> Gene Revealed by Resequencing of 192 Chromosomes from the General Population in Korea. Clinical and Experimental Otorhinolaryngology, 2010, 3, 65.	1.1	6

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91	DBC1 is a key positive regulator of enhancer epigenomic writers KMT2D and p300. Nucleic Acids Research, 2022, 50, 7873-7888.	6.5	6
92	A Bayesian ensemble approach with a disease gene network predicts damaging effects of missense variants of human cancers. Human Genetics, 2013, 132, 15-27.	1.8	4
93	Risk of Second Primary Malignancies among Patients with Early Gastric Cancer Exposed to Recurrent Computed Tomography Scans. Cancers, 2021, 13, 1144.	1.7	4
94	Dissecting the genetic architecture of suicide attempt and repeated attempts in Korean patients with bipolar disorder using polygenic risk scores. International Journal of Bipolar Disorders, 2022, 10, 3.	0.8	4
95	Genetic Variants Associated with Supernormal Coronary Arteries. Journal of Atherosclerosis and Thrombosis, 2023, 30, 467-480.	0.9	4
96	Paired neural network with negatively correlated features for cancer classification in DNA gene expression profiles. , 0, , .		3
97	Atypical Antipsychotics Augmentation in Patients with Depressive Disorder and Risk of Subsequent Dementia: A Nationwide Population-Based Cohort Study. Journal of Alzheimer's Disease, 2021, 80, 197-207.	1.2	3
98	Shared Genetic Background Between Cerebrospinal Fluid Biomarkers and Risk for Alzheimer's Disease: A Two-Sample Mendelian Randomization Study. Journal of Alzheimer's Disease, 2021, 80, 1197-1207.	1.2	3
99	Genetic pleiotropy of <i>ERCC6</i> lossâ€ofâ€function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. Human Mutation, 2021, 42, 969-977.	1.1	3
100	Ethnic differences in the frequency of \hat{l}^2 -amyloid deposition in cognitively normal individuals. Neurobiology of Aging, 2022, 114, 27-37.	1.5	3
101	The association of single nucleotide polymorphisms in the connective tissue growth factor gene with pseudoexfoliation syndrome/glaucoma. Acta Ophthalmologica, 2015, 93, e682-e683.	0.6	2
102	Identification of Genetic Loci Associated with Facial Wrinkles in a Large Korean Population. Journal of Investigative Dermatology, 2022, 142, 2824-2827.	0.3	2
103	Shared genetic architectures of subjective well-being in East Asian and European ancestry populations. Nature Human Behaviour, 2022, 6, 1014-1026.	6.2	2
104	Effectiveness of <i>in silico</i> tagSNP selection methods: virtual analysis of the genotypes of pharmacogenetic genes. Pharmacogenomics, 2007, 8, 1347-1357.	0.6	1
105	Distinct Linkage Disequilibrium (LD) Runs of Single Nucleotide Polymorphisms and Microsatellite Markers; Implications for Use of Mixed Marker Haplotypes in LD-based Mapping. Journal of Korean Medical Science, 2007, 22, 425.	1.1	1
106	RARE PROTEIN-TRUNCATING VARIANTS IN APOB ASSOCIATE WITH LOWER LOW-DENSITY LIPOPROTEIN CHOLESTEROL, LOWER TRIGLYCERIDES, AND REDUCED RISK OF CORONARY HEART DISEASE. Journal of the American College of Cardiology, 2019, 73, 1716.	1.2	1
107	Genetic risk prediction of lateâ€onset Alzheimer's disease based on tissueâ€specific transcriptomic analysis and polygenic risk scores. Alzheimer's and Dementia, 2020, 16, e045184.	0.4	1
108	Ethnic differences in the frequency of βâ€amyloid deposition in cognitively normal individuals. Alzheimer's and Dementia, 2021, 17, .	0.4	1

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109	Genetic Characteristics of Polycythemia Vera and Essential Thrombocythemia in Korean Patients. Journal of Clinical Laboratory Analysis, 2016, 30, 1061-1070.	0.9	0
110	In Silico Functional Assessment of Sequence Variations: Predicting Phenotypic Functions of Novel Variations. Genomics and Informatics, 2008, 6, 166-172.	0.4	0
111	The Risk of Organ Specific Graft-Versus-Host Disease Can Be Predicted by the Multiple Single Nucleotide Polymorphism Based Predictive Models Blood, 2012, 120, 3056-3056.	0.6	0
112	Bioinformatics challenges in molecular epidemiology of cancers. Precision and Future Medicine, 2017, 1, 69-76.	0.5	0
113	Dreaming of the future of stroke: translation of bench to bed. Precision and Future Medicine, 2017, 1, 143-151.	0.5	0
114	A cluster analysis of patients with axial spondyloarthritis using tumour necrosis factor alpha inhibitors based on clinical characteristics. Arthritis Research and Therapy, 2021, 23, 284.	1.6	0
115	netCRS: Network-based comorbidity risk score for prediction of myocardial infarction using biobank-scaled PheWAS data. , 2021, , .		0
116	netCRS: Network-based comorbidity risk score for prediction of myocardial infarction using biobank-scaled PheWAS data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 325-336.	0.7	0
117	Novel polygenic risk score approach with transcriptome-based weighting for genetic risk prediction of late-onset Alzheimer's disease Alzheimer's and Dementia, 2021, 17 Suppl 3, e053960.	0.4	0