Hong-Hee Won

List of Publications by Year
in descending order

117	18,733	109321 35	25787 108
papers	citations	h-index	g-index

126	126	126	40884
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic Variants Associated with Supernormal Coronary Arteries. Journal of Atherosclerosis and Thrombosis, 2023, 30, 467-480.	2.0	4
2	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.	6.7	120
3	GWAS Identifies Multiple Genetic Loci for Skin Color in Korean Women. Journal of Investigative Dermatology, 2022, 142, 1077-1084.	0.7	10
4	A deep learning model for screening type 2 diabetes from retinal photographs. Nutrition, Metabolism and Cardiovascular Diseases, 2022, 32, 1218-1226.	2.6	8
5	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.	2.2	4
6	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
7	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, , .	6.4	12
8	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.	2.4	12
9	Ethnic differences in the frequency of Î²-amyloid deposition in cognitively normal individuals. Neurobiology of Aging, 2022, 114, 27-37.	3.1	3
10	Identification of Genetic Loci Associated with Facial Wrinkles in a Large Korean Population. Journal of Investigative Dermatology, 2022, 142, 2824-2827.	0.7	2
11	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	21.4	209
12	Shared genetic architectures of subjective well-being in East Asian and European ancestry populations. Nature Human Behaviour, 2022, 6, 1014-1026.	12.0	2
13	Polygenic risk for type 2 diabetes, lifestyle, metabolic health, and cardiovascular disease: a prospective UK Biobank study. Cardiovascular Diabetology, 2022, 21, .	6.8	14
14	DBC1 is a key positive regulator of enhancer epigenomic writers KMT2D and p300. Nucleic Acids Research, 2022, 50, 7873-7888.	14.5	6
15	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.	4.5	14
16	GWAS Analysis of 17,019 Korean Women Identifies the Variants Associated with Facial Pigmented Spots. Journal of Investigative Dermatology, 2021, 141, 555-562.	0.7	18
17	OUP accepted manuscript. Brain, 2021, , .	7.6	7
18	Genome-wide association study in patients with pulmonary Mycobacterium avium complex disease. European Respiratory Journal, 2021, 58, 1902269.	6.7	16

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19	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.	2.6	3
20	hnRNPK-regulated LINC00263 promotes malignant phenotypes through miR-147a/CAPN2. Cell Death and Disease, 2021, 12, 290.	6.3	18
21	Risk of Second Primary Malignancies among Patients with Early Gastric Cancer Exposed to Recurrent Computed Tomography Scans. Cancers, 2021, 13, 1144.	3.7	4
22	Shared Genetic Background Between Cerebrospinal Fluid Biomarkers and Risk for Alzheimerâ€™s Disease: A Two-Sample Mendelian Randomization Study. Journal of Alzheimer's Disease, 2021, 80, 1197-1207.	2.6	3
23	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.	21.4	629
24	Genetic pleiotropy of ERCC6 lossâ€ofâ€function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. Human Mutation, 2021, 42, 969-977.	2.5	3
25	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.	6.2	7
26	Comprehensive characterization of distinct genetic alterations in metastatic breast cancer across various metastatic sites. Npj Breast Cancer, 2021, 7, 93.	5.2	17
27	Shared Genetic Background between Parkinsonâ€™s Disease and Schizophrenia: A Two-Sample Mendelian Randomization Study. Brain Sciences, 2021, 11, 1042.	2.3	10
28	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.	2.2	114
29	Rare, Damaging DNA Variants in CORIN and Risk of Coronary Artery Disease: Insights From Functional Genomics and Large-Scale Sequencing Analyses. Circulation Genomic and Precision Medicine, 2021, 14, e003399.	3.6	10
30	Autoimmune inflammatory rheumatic diseases and COVID-19 outcomes in South Korea: a nationwide cohort study. Lancet Rheumatology, The, 2021, 3, e698-e706.	3.9	73
31	Machine learning-based prediction model for responses of bDMARDs in patients with rheumatoid arthritis and ankylosing spondylitis. Arthritis Research and Therapy, 2021, 23, 254.	3.5	10
32	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.	3.5	0
33	netCRS: Network-based comorbidity risk score for prediction of myocardial infarction using biobank-scaled PheWAS data. , 2021, , .		0
34	Ethnic differences in the frequency of Î²â€amyloid deposition in cognitively normal individuals. Alzheimer's and Dementia, 2021, 17, .	0.8	1
35	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.	0.8	0
36	Analysis of dementia-related gene variants in APOE Îµ4 noncarrying Korean patients with early-onset Alzheimer's disease. Neurobiology of Aging, 2020, 85, 155.e5-155.e8.	3.1	13

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37	Moyamoya Disease and Spectrums of RNF213 Vasculopathy. Translational Stroke Research, 2020, 11, 580-589.	4.2	67
38	Associations between vascular risk factors and subsequent Alzheimerâ€™s disease in older adults. Alzheimer's Research and Therapy, 2020, 12, 117.	6.2	19
39	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. Science Advances, 2020, 6, .	10.3	33
40	Genetic risk prediction of lateâ€onset Alzheimerâ€™s disease based on tissueâ€specific transcriptomic analysis and polygenic risk scores. Alzheimer's and Dementia, 2020, 16, e045184.	0.8	1
41	Correlation Between Hippocampal Enlarged Perivascular Spaces and Cognition in Non-dementic Elderly Population. Frontiers in Neurology, 2020, 11, 542511.	2.4	8
42	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.	6.2	22
43	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.	3.3	13
44	Two-sample Mendelian randomization study for schizophrenia and breast cancer. Precision and Future Medicine, 2020, 4, 21-30.	1.6	6
45	Contribution of SLC22A12 on hypouricemia and its clinical significance for screening purposes. Scientific Reports, 2019, 9, 14360.	3.3	13
46	Rare Protein-Truncating Variants in APOB , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002376.	3.6	57
47	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.	2.8	1
48	Heritability estimates of individual psychological distress symptoms from genetic variation. Journal of Affective Disorders, 2019, 252, 413-420.	4.1	9
49	HMGCLL1 is a predictive biomarker for deep molecular response to imatinib therapy in chronic myeloid leukemia. Leukemia, 2019, 33, 1439-1450.	7.2	14
50	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
51	No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725.	8.4	97
52	The Association of Single-Nucleotide Polymorphisms in the MMP-9 Gene with Normal Tension Glaucoma and Primary Open-Angle Glaucoma. Current Eye Research, 2018, 43, 534-538.	1.5	10
53	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.	7.4	148
54	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214

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55	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	27.8	292
56	NUDT15 genotype distributions in the Korean population. Pharmacogenetics and Genomics, 2017, 27, 197-200.	1.5	35
57	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	4.5	68
58	Burden of Intracranial Atherosclerosis Is Associated With Long-Term Vascular Outcome in Patients With Ischemic Stroke. Stroke, 2017, 48, 2819-2826.	2.0	34
59	Bioinformatics challenges in molecular epidemiology of cancers. Precision and Future Medicine, 2017, 1, 69-76.	1.6	0
60	Dreaming of the future of stroke: translation of bench to bed. Precision and Future Medicine, 2017, 1, 143-151.	1.6	0
61	Genetic Characteristics of Polycythemia Vera and Essential Thrombocythemia in Korean Patients. Journal of Clinical Laboratory Analysis, 2016, 30, 1061-1070.	2.1	0
62	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	2.8	186
63	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.	2.8	723
64	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
65	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	27.8	9,051
66	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
67	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.	1.9	14
68	The association of single nucleotide polymorphisms in the connective tissue growth factor gene with pseudoexfoliation syndrome/glaucoma. Acta Ophthalmologica, 2015, 93, e682-e683.	1.1	2
69	Association between Air Pollution and Suicide in South Korea: A Nationwide Study. PLoS ONE, 2015, 10, e0117929.	2.5	63
70	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	3.5	70
71	Celebrity Suicides and Their Differential Influence on Suicides in the General Population: A National Population-Based Study in Korea. Psychiatry Investigation, 2015, 12, 204.	1.6	15
72	Association of the Choline Acetyltransferase Gene with Responsiveness to Acetylcholinesterase Inhibitors in Alzheimerâ€™s Disease. Pharmacopsychiatry, 2015, 48, 111-117.	3.3	24

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73	Breakpoint mapping by whole genome sequencing identifiesPTH2Rgene disruption in a patient with midline craniosynostosis and a de novo balanced chromosomal rearrangement. Journal of Medical Genetics, 2015, 52, 706-709.	3.2	10
74	Systematic Cell-Based Phenotyping of Missense Alleles Empowers Rare Variant Association Studies: A Case for LDLR and Myocardial Infarction. PLoS Genetics, 2015, 11, e1004855.	3.5	50
75	Myocardial Infarctionâ€“Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1472-1479.	2.4	78
76	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
77	A genome-wide association study of antidepressant response in Koreans. Translational Psychiatry, 2015, 5, e633-e633.	4.8	29
78	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
79	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	1.9	61
80	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
81	Paraquat Prohibition and Change in the Suicide Rate and Methods in South Korea. PLoS ONE, 2015, 10, e0128980.	2.5	47
82	Risk stratification of organ-specific GVHD can be improved by single-nucleotide polymorphism-based risk models. Bone Marrow Transplantation, 2014, 49, 649-656.	2.4	18
83	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
84	Multiple Associated Variants Increase the Heritability Explained for Plasma Lipids and Coronary Artery Disease. Circulation: Cardiovascular Genetics, 2014, 7, 583-587.	5.1	29
85	Genetic Prediction of Antidepressant Drug Response and Nonresponse in Korean Patients. PLoS ONE, 2014, 9, e107098.	2.5	17
86	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.	1.8	32
87	Genome-wide linkage scan of quantitative traits representing symptom dimensions in multiplex schizophrenia families. Psychiatry Research, 2013, 210, 756-760.	3.3	11
88	A Bayesian ensemble approach with a disease gene network predicts damaging effects of missense variants of human cancers. Human Genetics, 2013, 132, 15-27.	3.8	4
89	Predicting National Suicide Numbers with Social Media Data. PLoS ONE, 2013, 8, e61809.	2.5	102
90	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.	2.5	28

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91	SORL1 Is Genetically Associated with Late-Onset Alzheimerâ€™s Disease in Japanese, Koreans and Caucasians. PLoS ONE, 2013, 8, e58618.	2.5	149
92	Evaluation of lysyl oxidase-like 1 gene polymorphisms in pseudoexfoliation syndrome in a Korean population. Molecular Vision, 2013, 19, 448-53.	1.1	17
93	Multiple Single-Nucleotide Polymorphismâ€“Based Risk Model for Clinical Outcomes After Allogeneic Stem-Cell Transplantation, Especially for Acute Graft-Versus-Host Disease. Transplantation, 2012, 94, 1250-1257.	1.0	19
94	Genetic association study of individual symptoms in depression. Psychiatry Research, 2012, 198, 400-406.	3.3	34
95	Polymorphic markers associated with severe oxaliplatinâ€induced, chronic peripheral neuropathy in colon cancer patients. Cancer, 2012, 118, 2828-2836.	4.1	76
96	Differentially expressed genes in human peripheral blood as potential markers for statin response. Journal of Molecular Medicine, 2012, 90, 201-211.	3.9	6
97	The 18p11.22 locus is associated with never smoker non-small cell lung cancer susceptibility in Korean populations. Human Genetics, 2012, 131, 365-372.	3.8	45
98	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.	1.4	0
99	A genome-wide association study identifies novel loci associated with susceptibility to chronic myeloid leukemia. Blood, 2011, 117, 6906-6911.	1.4	28
100	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.	1.9	38
101	Interleukin 10 polymorphisms differentially influence the risk of gastric cancer in East Asians and Caucasians. Cytokine, 2010, 51, 73-77.	3.2	13
102	Sequence Variations and Haplotypes of theGJB2Gene Revealed by Resequencing of 192 Chromosomes from the General Population in Korea. Clinical and Experimental Otorhinolaryngology, 2010, 3, 65.	2.1	6
103	A Genome-Wide Scan for the Sasang Constitution in a Korean Family Suggests Significant Linkage at Chromosomes 8q11.22â€“23 and 11q22.1â€“3. Journal of Alternative and Complementary Medicine, 2009, 15, 765-769.	2.1	25
104	Comparative analysis of the JAK/STAT signaling through erythropoietin receptor and thrombopoietin receptor using a systems approach. BMC Bioinformatics, 2009, 10, S53.	2.6	12
105	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.	1.7	12
106	Comparison of identical single nucleotide polymorphisms genotyped by the GeneChip Targeted Genotyping 25K, Affymetrix 500K and Illumina 550K platforms. Genomics, 2009, 94, 89-93.	2.9	11
107	EnsemPro: An ensemble approach to predicting transcription start sites in human genomic DNA sequences. Genomics, 2008, 91, 259-266.	2.9	20
108	Cataloging Coding Sequence Variations in Human Genome Databases. PLoS ONE, 2008, 3, e3575.	2.5	12

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109	In Silico Functional Assessment of Sequence Variations: Predicting Phenotypic Functions of Novel Variations. Genomics and Informatics, 2008, 6, 166-172.	0.8	0
110	Effectiveness of in silico tagSNP selection methods: virtual analysis of the genotypes of pharmacogenetic genes. Pharmacogenomics, 2007, 8, 1347-1357.	1.3	1
111	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.	6.2	116
112	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.	2.5	1
113	Association Between a Polymorphism in the Lymphotoxin?aPromoter Region and Migraine. Headache, 2007, 47, 1056-1062.	3.9	22
114	Cancer classification using ensemble of neural networks with multiple significant gene subsets. Applied Intelligence, 2007, 26, 243-250.	5.3	86
115	DATA MINING FOR GENE EXPRESSION PROFILES FROM DNA MICROARRAY. International Journal of Software Engineering and Knowledge Engineering, 2003, 13, 593-608.	0.8	23
116	Neural Network Ensemble with Negatively Correlated Features for Cancer Classification. Lecture Notes in Computer Science, 2003, , 1143-1150.	1.3	6
117	Paired neural network with negatively correlated features for cancer classification in DNA gene expression profiles. , 0, , .		3