

Hae-Won Uh

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

9,127
citations

147566

31
h-index

133063

59
g-index

65
all docs

65
docs citations

65
times ranked

18246
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical integration of two omics datasets using GO2PLS. BMC Bioinformatics, 2021, 22, 131.	1.2	6
2	Statistical method for modeling sequencing data from different technologies in longitudinal studies with application to Huntington disease. Biometrical Journal, 2021, 63, 745-760.	0.6	1
3	Joint Models for Repeatedly Measured Compositional and Normally Distributed Outcomes. Frontiers in Probability and the Statistical Sciences, 2021, , 131-173.	0.1	0
4	Prediction of vascular aging based on smartphone acquired PPG signals. Scientific Reports, 2020, 10, 19756.	1.6	37
5	Choosing proper normalization is essential for discovery of sparse glycan biomarkers. Molecular Omics, 2020, 16, 231-242.	1.4	13
6	Low IgA Associated With Oropharyngeal Microbiota Changes and Lung Disease in Primary Antibody Deficiency. Frontiers in Immunology, 2020, 11, 1245.	2.2	25
7	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	4.7	90
8	Roux-Y Gastric Bypass and Sleeve Gastrectomy directly change gut microbiota composition independent of surgery type. Scientific Reports, 2019, 9, 10979.	1.6	55
9	The mixed model for the analysis of a repeated measurement multivariate count data. Statistics in Medicine, 2019, 38, 2248-2268.	0.8	15
10	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.5	30
11	Facial Wrinkles in Europeans: A Genome-Wide Association Study. Journal of Investigative Dermatology, 2018, 138, 1877-1880.	0.3	8
12	Integrating omics datasets with the OmicsPLS package. BMC Bioinformatics, 2018, 19, 371.	1.2	50
13	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
14	Probabilistic partial least squares model: Identifiability, estimation and application. Journal of Multivariate Analysis, 2018, 167, 331-346.	0.5	10
15	Human Plasma N-glycosylation as Analyzed by Matrix-Assisted Laser Desorption/Ionization-Fourier Transform Ion Cyclotron Resonance-MS Associates with Markers of Inflammation and Metabolic Health. Molecular and Cellular Proteomics, 2017, 16, 228-242.	2.5	58
16	Subclass-specific IgG glycosylation is associated with markers of inflammation and metabolic health. Scientific Reports, 2017, 7, 12325.	1.6	123
17	Estimation of metabolite networks with regard to a specific covariable: applications to plant and human data. Metabolomics, 2017, 13, 129.	1.4	9
18	Statistical Analysis of Lipidomics Data in a Case-Control Study. , 2017, , 277-295.		1

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19	Classification for Longevity Potential: The Use of Novel Biomarkers. <i>Frontiers in Public Health</i> , 2016, 4, 233.	1.3	8
20	The MC1R Gene and Youthful Looks. <i>Current Biology</i> , 2016, 26, 1213-1220.	1.8	64
21	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	3.0	83
22	Gene coexpression network analysis for family studies based on a meta-analytic approach. <i>BMC Proceedings</i> , 2016, 10, 119-123.	1.8	1
23	Evaluation of O2PLS in Omics data integration. <i>BMC Bioinformatics</i> , 2016, 17, 11.	1.2	113
24	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	5.8	153
25	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
26	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
27	A Genome-Wide Association Study Identifies the Skin Color Genes IRF4, MC1R, ASIP, and BNC2 Influencing Facial Pigmented Spots. <i>Journal of Investigative Dermatology</i> , 2015, 135, 1735-1742.	0.3	117
28	Genotype-Based Score Test for Association Testing in Families. <i>Statistics in Biosciences</i> , 2015, 7, 394-416.	0.6	24
29	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.	5.1	162
30	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , 2015, 6, 6065.	5.8	45
31	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014, 23, 4420-4432.	1.4	227
32	Combining information from linkage and association mapping for next-generation sequencing longitudinal family data. <i>BMC Proceedings</i> , 2014, 8, S34.	1.8	2
33	Gene analysis for longitudinal family data using random-effects models. <i>BMC Proceedings</i> , 2014, 8, S88.	1.8	3
34	Total Plasma N-Glycome Changes during Pregnancy. <i>Journal of Proteome Research</i> , 2014, 13, 1657-1668.	1.8	51
35	Schistosome infection is negatively associated with mite atopy, but not wheeze and asthma in Ghanaian schoolchildren. <i>Clinical and Experimental Allergy</i> , 2014, 44, 965-975.	1.4	24
36	Gene set analysis of GWAS data for human longevity highlights the relevance of the insulin/IGF-1 signaling and telomere maintenance pathways. <i>Age</i> , 2013, 35, 235-249.	3.0	105

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37	Lipidomics of familial longevity. <i>Aging Cell</i> , 2013, 12, 426-434.	3.0	157
38	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
39	Targeted Biomarker Discovery by High Throughput Glycosylation Profiling of Human Plasma Alpha1-Antitrypsin and Immunoglobulin A. <i>PLoS ONE</i> , 2013, 8, e73082.	1.1	43
40	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
41	How to deal with the early GWAS data when imputing and combining different arrays is necessary. <i>European Journal of Human Genetics</i> , 2012, 20, 572-576.	1.4	26
42	Quantitative Polymerase Chain Reaction-Based Analysis of Podocyturia Is a Feasible Diagnostic Tool in Preeclampsia. <i>Hypertension</i> , 2012, 60, 1538-1544.	1.3	39
43	Plasma protein N-glycan profiles are associated with calendar age, familial longevity and health. <i>Journal of Proteome Research</i> , 2011, 10, 1667-1674.	1.8	87
44	Haplotype Estimation from Fuzzy Genotypes Using Penalized Likelihood. <i>PLoS ONE</i> , 2011, 6, e24219.	1.1	0
45	Genome-wide association study identifies a single major locus contributing to survival into old age; the <i>APOE</i> locus revisited. <i>Aging Cell</i> , 2011, 10, 686-698.	3.0	249
46	Pathway analysis for family data using nested random-effects models. <i>BMC Proceedings</i> , 2011, 5, S22.	1.8	6
47	Does pathway analysis make it easier for common variants to tag rare ones?. <i>BMC Proceedings</i> , 2011, 5, S90.	1.8	9
48	Decreased Levels of Bisecting GlcNAc Glycoforms of IgG Are Associated with Human Longevity. <i>PLoS ONE</i> , 2010, 5, e12566.	1.1	104
49	A Meta-analysis of Four Genome-Wide Association Studies of Survival to Age 90 Years or Older: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010, 65A, 478-487.	1.7	117
50	Testing for genetic association taking into account phenotypic information of relatives. <i>BMC Proceedings</i> , 2009, 3, S123.	1.8	17
51	Single nucleotide polymorphisms in antigen processing machinery component ERAP1 significantly associate with clinical outcome in cervical carcinoma. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 410-418.	1.5	79
52	Assessment of global phase uncertainty in case-control studies. <i>BMC Genetics</i> , 2009, 10, 54.	2.7	5
53	Evaluation of regression methods when immunological measurements are constrained by detection limits. <i>BMC Immunology</i> , 2008, 9, 59.	0.9	103
54	Model selection based on logistic regression in a highly correlated candidate gene region. <i>BMC Proceedings</i> , 2007, 1, S114.	1.8	17

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55	Genetic variation of antigen processing machinery components and association with cervical carcinoma. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 577-586.	1.5	82
56	Asymptotic Normality of Kernel-Type Deconvolution Estimators. <i>Scandinavian Journal of Statistics</i> , 2005, 32, 467-483.	0.9	30
57	How to quantify information loss due to phase ambiguity in haplotype case-control studies. <i>BMC Genetics</i> , 2005, 6, S108.	2.7	5
58	Modeling the effect of an associated single-nucleotide polymorphism in linkage studies. <i>BMC Genetics</i> , 2005, 6, S46.	2.7	5
59	Locally weighted transmission/disequilibrium test for genetic association analysis. <i>BMC Genetics</i> , 2005, 6, S60.	2.7	3
60	Multi bandwidth kernel estimators for nonparametric deconvolution problems: asymptotics and finite sample performance. <i>Journal of Nonparametric Statistics</i> , 2000, 13, 107-128.	0.4	3