Peng Wei

List of Publications by Year
in descending order

92 papers	3,562 citations	218592 26 h-index	155592 55 g-index
98 all docs	98 docs citations	98 times ranked	8826 citing authors

#	Article	IF	Citations
1	Identification of novel susceptibility methylation loci for pancreatic cancer in a two-phase epigenome-wide association study. Epigenetics, 2022, 17, 1357-1372.	1.3	4
2	TP53 copy number and protein expression inform mutation status across risk categories in acute myeloid leukemia. Blood, 2022, 140, 58-72.	0.6	46
3	A model combining pretreatment MRI radiomic features and tumor-infiltrating lymphocytes to predict response to neoadjuvant systemic therapy in triple-negative breast cancer. European Journal of Radiology, 2022, 149, 110220.	1.2	13
4	Predicting outcomes of phase III oncology trials with Bayesian mediation modeling of tumor response. Statistics in Medicine, 2022, 41, 751-768.	0.8	3
5	Whole-exome sequencing of 14â€‰389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors. Human Molecular Genetics, 2022, 31, 3120-3132.	1.4	3
6	The origin of bladder cancer from mucosal field effects. IScience, 2022, 25, 104551.	1.9	12
7	Functional principal component based landmark analysis for the effects of longitudinal cholesterol profiles on the risk of coronary heart disease. Statistics in Medicine, 2021, 40, 650-667.	0.8	2
8	Integrative analysis of multi-omics data for discovering low-frequency variants associated with low-density lipoprotein cholesterol levels. Bioinformatics, 2021, 36, 5223-5228.	1.8	3
9	IMIX: a multivariate mixture model approach to association analysis through multi-omics data integration. Bioinformatics, 2021, 36, 5439-5447.	1.8	4
10	Myelodysplastic syndrome with t(6;9)(p22;q34.1)/DEK-NUP214 better classified as acute myeloid leukemia? A multicenter study of 107 cases. Modern Pathology, 2021, 34, 1143-1152.	2.9	12
11	Abstract PD6-06: Radiomic phenotypes from dynamic contrast-enhanced MRI (DCE-MRI) parametric maps for early prediction of response to neoadjuvant systemic therapy (NAST) in triple negative breast cancer (TNBC) patients. , 2021, , .		1
12	Functional Tumor Volume by Fast Dynamic<scp>Contrastâ€Enhanced MRI</scp>for Predicting Neoadjuvant Systemic Therapy Response in<scp>Tripleâ€Negative</scp>Breast Cancer. Journal of Magnetic Resonance Imaging, 2021, 54, 251-260.	1.9	18
13	A Deep-Learning Approach to Recreate Raw Full-Field Digital Mammograms for Breast Density and Texture Analysis. Radiology: Artificial Intelligence, 2021, 3, e200097.	3.0	5
14	Lipidomic Profiles of Plasma Exosomes Identify Candidate Biomarkers for Early Detection of Hepatocellular Carcinoma in Patients with Cirrhosis. Cancer Prevention Research, 2021, 14, 955-962.	0.7	22
15	Estimation of total mediation effect for high-dimensional omics mediators. BMC Bioinformatics, 2021, 22, 414.	1.2	6
16	A survival mediation model with Bayesian model averaging. Statistical Methods in Medical Research, 2021, 30, 2413-2427.	0.7	4
17	Assessment of Early Response to Neoadjuvant Systemic Therapy in Triple-Negative Breast Cancer Using Amide Proton Transferâ€“weighted Chemical Exchange Saturation Transfer MRI: A Pilot Study. Radiology Imaging Cancer, 2021, 3, e200155.	0.7	12
18	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	1.6	2

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19	Radiomics, deep learning and early diagnosis in oncology. Emerging Topics in Life Sciences, 2021, 5, 829-835.	1.1	6
20	An adaptive test for metaâ€analysis of rare variant association studies. Genetic Epidemiology, 2020, 44, 104-116.	0.6	2
21	Urothelial-to-Neural Plasticity Drives Progression to Small Cell Bladder Cancer. IScience, 2020, 23, 101201.	1.9	18
22	Abnormal Endothelial Gene Expression Associated With Early Coronary Atherosclerosis. Journal of the American Heart Association, 2020, 9, e016134.	1.6	21
23	Incorporating multiple sets of eQTL weights into geneâ€byâ€environment interaction analysis identifies novel susceptibility loci for pancreatic cancer. Genetic Epidemiology, 2020, 44, 880-892.	0.6	0
24	Clinicopathological characterization of chronic lymphocytic leukemia with MYD88 mutations: L265P and non-L265P mutations are associated with different features. Blood Cancer Journal, 2020, 10, 86.	2.8	10
25	Assessment of Luminal and Basal Phenotypes in Bladder Cancer. Scientific Reports, 2020, 10, 9743.	1.6	83
26	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5
27	Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. Human Molecular Genetics, 2020, 29, 515-526.	1.4	7
28	A genetic variant within MDM4 3â€²UTR miRNA binding site is associated with HPV16â€positive tumors and survival of oropharyngeal cancer. Molecular Carcinogenesis, 2019, 58, 2276-2285.	1.3	5
29	Dysregulation of EMT Drives the Progression to Clinically Aggressive Sarcomatoid Bladder Cancer. Cell Reports, 2019, 27, 1781-1793.e4.	2.9	102
30	Vitamin C and Vitamin E Mitigate the Risk of Pancreatic Ductal Adenocarcinoma from Meat-Derived Mutagen Exposure in Adults in a Case-Control Study. Journal of Nutrition, 2019, 149, 1443-1450.	1.3	9
31	FunSPU: A versatile and adaptive multiple functional annotation-based association test of whole-genome sequencing data. PLoS Genetics, 2019, 15, e1008081.	1.5	16
32	Whole-Organ Genomic Characterization of Mucosal Field Effects Initiating Bladder Carcinogenesis. Cell Reports, 2019, 26, 2241-2256.e4.	2.9	31
33	Persistent IDH1/2 mutations in remission can predict relapse in patients with acute myeloid leukemia. Haematologica, 2019, 104, 305-311.	1.7	56
34	A powerful and dataâ€adaptive test for rareâ€variantâ€“based geneâ€environment interaction analysis. Statistics in Medicine, 2019, 38, 1230-1244.	0.8	15
35	Validation of the 2017 revision of the WHO chronic myelomonocytic leukemia categories. Blood Advances, 2018, 2, 1807-1816.	2.5	34
36	Association between VEGF genetic variants and diabetic foot ulcer in Chinese Han population. Medicine (United States), 2018, 97, e10672.	0.4	16

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37	Non-Native Conformational Isomers of the Catalytic Domain of PCSK9 Induce an Immune Response, Reduce Lipids and Increase LDL Receptor Levels. International Journal of Molecular Sciences, 2018, 19, 640.	1.8	3
38	Overexpression of miRNA 4451 is Associated With a Poor Survival of Patients With Hypopharyngeal Cancer After Surgery With Postoperative Radiotherapy. Translational Oncology, 2018, 11, 1244-1250.	1.7	4
39	Caffeine, creatine, GRIN2A and Parkinson's disease progression. Journal of the Neurological Sciences, 2017, 375, 355-359.	0.3	23
40	Circularly permuted TRAIL plus thalidomide and dexamethasone versus thalidomide and dexamethasone for relapsed/refractory multiple myeloma: a phase 2 study. Cancer Chemotherapy and Pharmacology, 2017, 79, 1141-1149.	1.1	25
41	Genetic polymorphisms associated with pancreatic cancer survival: a genomeâ€wide association study. International Journal of Cancer, 2017, 141, 678-686.	2.3	23
42	Association between miRNA-binding site polymorphisms in double-strand break repair genes and risk of recurrence in patients with squamous cell carcinomas of the non-oropharynx. Carcinogenesis, 2017, 38, 432-438.	1.3	6
43	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 771-777.	1.6	23
44	A Powerful Framework for Integrating eQTL and GWAS Summary Data. Genetics, 2017, 207, 893-902.	1.2	72
45	A Semiparametric Model for VQTL Mapping. Biometrics, 2017, 73, 571-581.	0.8	12
46	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	1.6	150
47	Identification of an Association of TNFAIP3 Polymorphisms With Matrix Metalloproteinase Expression in Fibroblasts in an Integrative Study of Systemic Sclerosisâ€“Associated Genetic and Environmental Factors. Arthritis and Rheumatology, 2016, 68, 749-760.	2.9	24
48	An adaptive two-sample test for high-dimensional means. Biometrika, 2016, 103, 609-624.	1.3	55
49	On Robust Association Testing for Quantitative Traits and Rare Variants. G3: Genes, Genomes, Genetics, 2016, 6, 3941-3950.	0.8	11
50	Mendelian randomization analysis of a timeâ€varying exposure for binary disease outcomes using functional data analysis methods. Genetic Epidemiology, 2016, 40, 744-755.	0.6	13
51	Incorporating ENCODE information into association analysis of whole genome sequencing data. BMC Proceedings, 2016, 10, 257-261.	1.8	9
52	The impact of multiple single day blood pressure readings on cardiovascular risk estimation: The Atherosclerosis Risk in Communities study. European Journal of Preventive Cardiology, 2016, 23, 1529-1536.	0.8	5
53	FLAGS: A Flexible and Adaptive Association Test for Gene Sets Using Summary Statistics. Genetics, 2016, 202, 919-929.	1.2	11
54	Hydroxycarbamide versus chronic transfusion for maintenance of transcranial doppler flow velocities in children with sickle cell anaemiaâ€”TCD With Transfusions Changing to Hydroxyurea (TWiTCH): a multicentre, open-label, phase 3, non-inferiority trial. Lancet, The, 2016, 387, 661-670.	6.3	375

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55	WGSA: an annotation pipeline for human genome sequencing studies. Journal of Medical Genetics, 2016, 53, 111-112.	1.5	96
56	Powerful Tukey's One Degree-of-Freedom Test for Detecting Gene-Gene and Gene-Environment Interactions. Cancer Informatics, 2015, 14s2, CIN.S17305.	0.9	4
57	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	1.4	36
58	Comparison and integration of deleteriousness prediction methods for nonsynonymous SNVs in whole exome sequencing studies. Human Molecular Genetics, 2015, 24, 2125-2137.	1.4	892
59	A Powerful Pathway-Based Adaptive Test for Genetic Association with Common or Rare Variants. American Journal of Human Genetics, 2015, 97, 86-98.	2.6	61
60	Testing for Polygenic Effects in Genomeâ€Wide Association Studies. Genetic Epidemiology, 2015, 39, 306-316.	0.6	14
61	A Family-Based Joint Test for Mean and Variance Heterogeneity for Quantitative Traits. Annals of Human Genetics, 2015, 79, 46-56.	0.3	10
62	Association of Rare Loss-Of-Function Alleles in HAL , Serum Histidine. Circulation: Cardiovascular Genetics, 2015, 8, 351-355.	5.1	41
63	TCD with Transfusions Changing to Hydroxyurea (TWiTCH): Hydroxyurea Therapy As an Alternative to Transfusions for Primary Stroke Prevention in Children with Sickle Cell Anemia. Blood, 2015, 126, 3-3.	0.6	19
64	Genetic Variants in DNA Double-Strand Break Repair Genes and Risk of Salivary Gland Carcinoma: A Case-Control Study. PLoS ONE, 2015, 10, e0128753.	1.1	4
65	Genesâ€"Environment Interactions in Obesity- and Diabetes-Associated Pancreatic Cancer: A GWAS Data Analysis. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 98-106.	1.1	32
66	Genetic variants inTNF-Î± promoter are predictors of recurrence in patients with squamous cell carcinoma of oropharynx after definitive radiotherapy. International Journal of Cancer, 2014, 134, 1907-1915.	2.3	14
67	A Versatile Omnibus Test for Detecting Mean and Variance Heterogeneity. Genetic Epidemiology, 2014, 38, 51-59.	0.6	52
68	A multicenter, openâ€label phase II study of recombinant CPT (Circularly Permuted TRAIL) plus thalidomide in patients with relapsed and refractory multiple myeloma. American Journal of Hematology, 2014, 89, 1037-1042.	2.0	36
69	Axonal guidance signaling pathway interacting with smoking in modifying the risk of pancreatic cancer: a gene- and pathway-based interaction analysis of GWAS data. Carcinogenesis, 2014, 35, 1039-1045.	1.3	41
70	Functional Logistic Regression Approach to Detecting Gene by Longitudinal Environmental Exposure Interaction in a Caseâ€Control Study. Genetic Epidemiology, 2014, 38, 638-651.	0.6	16
71	A Powerful and Adaptive Association Test for Rare Variants. Genetics, 2014, 197, 1081-1095.	1.2	150
72	miR-155 mediates drug resistance in osteosarcoma cells via inducing autophagy. Experimental and Therapeutic Medicine, 2014, 8, 527-532.	0.8	46

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73	Transiently Elevated AST/LDH Are Associated with Clinical Response to Recombinant Circularly Permuted TRAIL (CPT) Plus Thalidomide in Patients with Relapsed and/or Refractory Multiple Myeloma. Blood, 2014, 124, 3478-3478.	0.6	4
74	Differentially regulated gene expression associated with hepatitis C virus clearance. Journal of General Virology, 2013, 94, 534-542.	1.3	8
75	Genetic variants in p53-related genes confer susceptibility to second primary malignancy in patients with index squamous cell carcinoma of head and neck. Carcinogenesis, 2013, 34, 1551-1557.	1.3	14
76	Bayesian Inference on Risk Differences: An Application to Multivariate Meta-Analysis of Adverse Events in Clinical Trials. Statistics in Biopharmaceutical Research, 2013, 5, 142-155.	0.6	2
77	Long-term Expression of Apolipoprotein B mRNA-specific Hammerhead Ribozyme via scAAV8.2 Vector Inhibits Atherosclerosis in Mice. Molecular Therapy - Nucleic Acids, 2013, 2, e125.	2.3	4
78	Common and rare von Willebrand factor (VWF) coding variants, VWF levels, and factor VIII levels in African Americans: the NHLBI Exome Sequencing Project. Blood, 2013, 122, 590-597.	0.6	70
79	Bayesian joint modeling of multiple gene networks and diverse genomic data to identify target genes of a transcription factor. Annals of Applied Statistics, 2012, 6, 334-355.	0.5	15
80	Insights into Pancreatic Cancer Etiology from Pathway Analysis of Genome-Wide Association Study Data. PLoS ONE, 2012, 7, e46887.	1.1	68
81	Differential endothelial cell gene expression by African Americans versusCaucasian Americans: a possible contribution to health disparity in vascular disease and cancer. BMC Medicine, 2011, 9, 2.	2.3	37
82	Incorporating predicted functions of nonsynonymous variants into gene-based analysis of exome sequencing data: a comparative study. BMC Proceedings, 2011, 5, S20.	1.8	18
83	Incorporating biological information into association studies of sequencing data. Genetic Epidemiology, 2011, 35, S29-34.	0.6	4
84	Proinflammatory phenotype with imbalance of KLF2 and RelA: Risk of childhood stroke with sickle cell anemia. American Journal of Hematology, 2010, 85, 18-23.	2.0	15
85	Network-based genomic discovery: application and comparison of Markov random-field models. Journal of the Royal Statistical Society Series C: Applied Statistics, 2010, 59, 105-125.	0.5	19
86	Activation of Endothelial and Coagulation Systems in Left Ventricular Assist Device Recipients. Annals of Thoracic Surgery, 2009, 88, 1171-1179.	0.7	101
87	Incorporating Gene Functions into Regression Analysis of DNA-Protein Binding Data and Gene Expression Data to Construct Transcriptional Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 401-415.	1.9	5
88	Incorporating gene networks into statistical tests for genomic data via a spatially correlated mixture model. Bioinformatics, 2008, 24, 404-411.	1.8	75
89	Genetic endothelial systems biology of sickle stroke risk. Blood, 2008, 111, 3872-3879.	0.6	54
90	A parametric joint model of DNA-protein binding, gene expression and DNA sequence data to detect target genes of a transcription factor. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 465-76.	0.7	4

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91	A PARAMETRIC JOINT MODEL OF DNA-PROTEIN BINDING, GENE EXPRESSION AND DNA SEQUENCE DATA TO DETECT TARGET GENES OF A TRANSCRIPTION FACTOR. , 2007, , .		1
92	Combining Gene Annotations and Gene Expression Data in Model-Based Clustering: Weighted Method. OMICS A Journal of Integrative Biology, 2006, 10, 28.	1.0	15