

Heather E Wheeler

List of Publications by Year in descending order

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Version: 2024-02-01

70
papers

5,263
citations

186265
28
h-index

123424
61
g-index

84
all docs

84
docs citations

84
times ranked

10835
citing authors

#	ARTICLE	IF	CITATIONS
1	A gene-based association method for mapping traits using reference transcriptome data. <i>Nature Genetics</i> , 2015, 47, 1091-1098.	21.4	1,473
2	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. <i>Nature Communications</i> , 2018, 9, 1825.	12.8	748
3	Integrating predicted transcriptome from multiple tissues improves association detection. <i>PLoS Genetics</i> , 2019, 15, e1007889.	3.5	239
4	Association of an Inherited Genetic Variant With Vincristine-Related Peripheral Neuropathy in Children With Acute Lymphoblastic Leukemia. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 815.	7.4	234
5	Comprehensive Audiometric Analysis of Hearing Impairment and Tinnitus After Cisplatin-Based Chemotherapy in Survivors of Adult-Onset Cancer. <i>Journal of Clinical Oncology</i> , 2016, 34, 2712-2720.	1.6	197
6	Cancer pharmacogenomics: strategies and challenges. <i>Nature Reviews Genetics</i> , 2013, 14, 23-34.	16.3	192
7	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. <i>PLoS Genetics</i> , 2012, 8, e1002584.	3.5	166
8	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. <i>PLoS Genetics</i> , 2016, 12, e1006423.	3.5	143
9	Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.	3.5	117
10	Lymphoblastoid cell lines in pharmacogenomic discovery and clinical translation. <i>Pharmacogenomics</i> , 2012, 13, 55-70.	1.3	101
11	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. <i>Science</i> , 2019, 366, 351-356.	12.6	99
12	Modeling Chemotherapeutic Neurotoxicity with Human Induced Pluripotent Stem Cell-Derived Neuronal Cells. <i>PLoS ONE</i> , 2015, 10, e0118020.	2.5	88
13	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.	12.8	85
14	Relating human genetic variation to variation in drug responses. <i>Trends in Genetics</i> , 2012, 28, 487-495.	6.7	76
15	Variants in <i>WFS1</i> and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. <i>Clinical Cancer Research</i> , 2017, 23, 3325-3333.	7.0	65
16	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. <i>Human Molecular Genetics</i> , 2012, 21, 5329-5343.	2.9	64
17	Genetics and genomics of human ageing. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 43-50.	4.0	63
18	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 5757-5768.	7.0	63

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19	Regulatory Polymorphisms in β -Tubulin IIa Are Associated with Paclitaxel-Induced Peripheral Neuropathy. <i>Clinical Cancer Research</i> , 2012, 18, 4441-4448.	7.0	61
20	Application of stem cell derived neuronal cells to evaluate neurotoxic chemotherapy. <i>Stem Cell Research</i> , 2017, 22, 79-88.	0.7	56
21	Integration of Cell Line and Clinical Trial Genome-Wide Analyses Supports a Polygenic Architecture of Paclitaxel-Induced Sensory Peripheral Neuropathy. <i>Clinical Cancer Research</i> , 2013, 19, 491-499.	7.0	55
22	Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. <i>PLoS Genetics</i> , 2009, 5, e1000685.	3.5	50
23	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. <i>Pharmacogenomics Journal</i> , 2013, 13, 35-43.	2.0	49
24	Pharmacogenetic Discovery in CALGB (Alliance) 90401 and Mechanistic Validation of a <i>VAC14</i> Polymorphism that Increases Risk of Docetaxel-Induced Neuropathy. <i>Clinical Cancer Research</i> , 2016, 22, 4890-4900.	7.0	46
25	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. <i>Blood</i> , 2013, 121, 4366-4376.	1.4	42
26	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. <i>Genome Biology</i> , 2022, 23, 23.	8.8	42
27	Poly-Omic Prediction of Complex Traits: OmicKriging. <i>Genetic Epidemiology</i> , 2014, 38, 402-415.	1.3	41
28	Pharmacoethnicity in Paclitaxel-Induced Sensory Peripheral Neuropathy. <i>Clinical Cancer Research</i> , 2015, 21, 4337-4346.	7.0	39
29	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2013, 24, 2105-2117.	6.1	33
30	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. <i>Pharmacogenetics and Genomics</i> , 2012, 22, 498-507.	1.5	28
31	Fine-mapping and QTL tissue-sharing information improves the reliability of causal gene identification. <i>Genetic Epidemiology</i> , 2020, 44, 854-867.	1.3	28
32	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. <i>Clinical Cancer Research</i> , 2019, 25, 4104-4116.	7.0	27
33	Identification of novel germline polymorphisms governing capecitabine sensitivity. <i>Cancer</i> , 2012, 118, 4063-4073.	4.1	25
34	Genome-Wide Local Ancestry Approach Identifies Genes and Variants Associated with Chemotherapeutic Susceptibility in African Americans. <i>PLoS ONE</i> , 2011, 6, e21920.	2.5	25
35	Clinical Translation of Cell-Based Pharmacogenomic Discovery. <i>Clinical Pharmacology and Therapeutics</i> , 2012, 92, 425-427.	4.7	24
36	Pharmacokinetics and pharmacogenomics of daunorubicin in children: a report from the Children's Oncology Group. <i>Cancer Chemotherapy and Pharmacology</i> , 2014, 74, 831-838.	2.3	21

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37	Chemotherapeutic-induced apoptosis. <i>Pharmacogenetics and Genomics</i> , 2011, 21, 476-488.	1.5	19
38	Imputed gene associations identify replicable <i>transacting</i> genes enriched in transcription pathways and complex traits. <i>Genetic Epidemiology</i> , 2019, 43, 596-608.	1.3	19
39	Genetic and epigenetic variants contributing to clofarabine cytotoxicity. <i>Human Molecular Genetics</i> , 2013, 22, 4007-4020.	2.9	18
40	Chronic circadian misalignment results in reduced longevity and large-scale changes in gene expression in <i>Drosophila</i> . <i>BMC Genomics</i> , 2019, 20, 14.	2.8	17
41	Comparing local ancestry inference models in populations of two- and three-way admixture. <i>PeerJ</i> , 2020, 8, e10090.	2.0	17
42	Clinical and Genome-Wide Analysis of Serum Platinum Levels after Cisplatin-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 5913-5924.	7.0	16
43	Population-Matched Transcriptome Prediction Increases TWAS Discovery and Replication Rate. <i>IScience</i> , 2020, 23, 101850.	4.1	16
44	EPS8 Inhibition Increases Cisplatin Sensitivity in Lung Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e82220.	2.5	16
45	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. <i>PLoS ONE</i> , 2019, 14, e0220827.	2.5	14
46	Transcriptome prediction performance across machine learning models and diverse ancestries. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100019.	1.7	14
47	Gene-based association study for lipid traits in diverse cohorts implicates <i>BACE1</i> and <i>SIDT2</i> regulation in triglyceride levels. <i>PeerJ</i> , 2018, 6, e4314.	2.0	14
48	Multi-ethnic transcriptome-wide association study of prostate cancer. <i>PLoS ONE</i> , 2020, 15, e0236209.	2.5	13
49	Protein prediction for trait mapping in diverse populations. <i>PLoS ONE</i> , 2022, 17, e0264341.	2.5	13
50	Transcriptome association studies of neuropsychiatric traits in African Americans implicate <i>PRMT7</i> in schizophrenia. <i>PeerJ</i> , 2019, 7, e7778.	2.0	12
51	Identification of genetic variants associated with capecitabine-induced hand-foot syndrome through integration of patient and cell line genomic analyses. <i>Pharmacogenetics and Genomics</i> , 2014, 24, 231-237.	1.5	10
52	Clinical and Genome-Wide Analysis of Multiple Severe Cisplatin-Induced Neurotoxicities in Adult-Onset Cancer Survivors. <i>Clinical Cancer Research</i> , 2020, 26, 6550-6558.	7.0	9
53	Genetically regulated expression underlies cellular sensitivity to chemotherapy in diverse populations. <i>Human Molecular Genetics</i> , 2021, 30, 305-317.	2.9	8
54	Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. <i>Human Molecular Genetics</i> , 2012, 21, 4348-4355.	2.9	7

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55	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. <i>American Journal of Human Genetics</i> , 2022, 109, 857-870.	6.2	7
56	Clinical and genetic risk factors for radiation-associated ototoxicity: A report from the Childhood Cancer Survivor Study and the St. Jude Lifetime Cohort. <i>Cancer</i> , 2021, 127, 4091-4102.	4.1	6
57	Genetic Variants Contributing to Colistin Cytotoxicity: Identification of TGIF1 and HOXD10 Using a Population Genomics Approach. <i>International Journal of Molecular Sciences</i> , 2017, 18, 661.	4.1	2
58	Comprehensive characterization of cisplatin-related hearing loss in U.S. and Canadian Testicular Cancer Survivors (TCS).. <i>Journal of Clinical Oncology</i> , 2015, 33, 9570-9570.	1.6	2
59	Genome-wide association study of cisplatin-induced peripheral neuropathy (CIPN) in testicular cancer survivors.. <i>Journal of Clinical Oncology</i> , 2016, 34, 4543-4543.	1.6	2
60	Genome-wide association study (GWAS) of cisplatin-related hearing loss in testicular cancer survivors (TCS) to reveal associated variant in Wolfram syndrome 1 (WFS1) gene.. <i>Journal of Clinical Oncology</i> , 2016, 34, 10015-10015.	1.6	1
61	Variation in protein-coding sequence and the genetic basis of cisplatin-induced toxicities among testicular cancer survivors (TCS) in the Platinum Study.. <i>Journal of Clinical Oncology</i> , 2016, 34, 1537-1537.	1.6	1
62	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. <i>Pharmacogenomics Journal</i> , 2019, 19, 178-190.	2.0	0
63	Identification of pharmacogenetic target genes associated with chemotherapy-induced peripheral neuropathy.. <i>Journal of Clinical Oncology</i> , 2013, 31, e13541-e13541.	1.6	0
64	Genome-wide association study (GWAS) of chemotherapy-induced Raynaud's phenomenon (RP) to reveal shared pathways with cardiovascular disease (CVD).. <i>Journal of Clinical Oncology</i> , 2017, 35, e18162-e18162.	1.6	0
65	Diverse Populations Are Needed To Understand The Genetics Of Complex Traits. , 2018, , .		0
66	Clinical and genetic risk factors for radiation-associated ototoxicity: A report from the childhood cancer survivor study and the St. Jude Lifetime Cohort.. <i>Journal of Clinical Oncology</i> , 2020, 38, 10550-10550.	1.6	0
67	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
68	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
69	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
70	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0