Heather E Wheeler

List of Publications by Year
in descending order

70	5,263	185998 28	123241 61
papers	citations	h-index	g-index

84	84	84	10835
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	9.4	1,473
2	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
3	Integrating predicted transcriptome from multiple tissues improves association detection. PLoS Genetics, 2019, 15, e1007889.	1.5	239
4	Association of an Inherited Genetic Variant With Vincristine-Related Peripheral Neuropathy in Children With Acute Lymphoblastic Leukemia. JAMA - Journal of the American Medical Association, 2015, 313, 815.	3.8	234
5	Comprehensive Audiometric Analysis of Hearing Impairment and Tinnitus After Cisplatin-Based Chemotherapy in Survivors of Adult-Onset Cancer. Journal of Clinical Oncology, 2016, 34, 2712-2720.	0.8	197
6	Cancer pharmacogenomics: strategies and challenges. Nature Reviews Genetics, 2013, 14, 23-34.	7.7	192
7	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
8	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	1.5	143
9	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	1.5	117
10	Lymphoblastoid cell lines in pharmacogenomic discovery and clinical translation. Pharmacogenomics, 2012, 13, 55-70.	0.6	101
11	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	6.0	99
12	Modeling Chemotherapeutic Neurotoxicity with Human Induced Pluripotent Stem Cell-Derived Neuronal Cells. PLoS ONE, 2015, 10, e0118020.	1.1	88
13	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
14	Relating human genetic variation to variation in drug responses. Trends in Genetics, 2012, 28, 487-495.	2.9	76
15	Variants in WFS1 and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. Clinical Cancer Research, 2017, 23, 3325-3333.	3.2	65
16	Integration of genome-wide association studies with biological knowledge identifies six novel genes related to kidney function. Human Molecular Genetics, 2012, 21, 5329-5343.	1.4	64
17	Genetics and genomics of human ageing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 43-50.	1.8	63
18	Clinical and Genome-Wide Analysis of Cisplatin-Induced Peripheral Neuropathy in Survivors of Adult-Onset Cancer. Clinical Cancer Research, 2017, 23, 5757-5768.	3.2	63

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19	Regulatory Polymorphisms in Î²-Tubulin IIa Are Associated with Paclitaxel-Induced Peripheral Neuropathy. Clinical Cancer Research, 2012, 18, 4441-4448.	3.2	61
20	Application of stem cell derived neuronal cells to evaluate neurotoxic chemotherapy. Stem Cell Research, 2017, 22, 79-88.	0.3	56
21	Integration of Cell Line and Clinical Trial Genome-Wide Analyses Supports a Polygenic Architecture of Paclitaxel-Induced Sensory Peripheral Neuropathy. Clinical Cancer Research, 2013, 19, 491-499.	3.2	55
22	Sequential Use of Transcriptional Profiling, Expression Quantitative Trait Mapping, and Gene Association Implicates MMP20 in Human Kidney Aging. PLoS Genetics, 2009, 5, e1000685.	1.5	50
23	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. Pharmacogenomics Journal, 2013, 13, 35-43.	0.9	49
24	Pharmacogenetic Discovery in CALGB (Alliance) 90401 and Mechanistic Validation of a VAC14 Polymorphism that Increases Risk of Docetaxel-Induced Neuropathy. Clinical Cancer Research, 2016, 22, 4890-4900.	3.2	46
25	Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. Blood, 2013, 121, 4366-4376.	0.6	42
26	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. Genome Biology, 2022, 23, 23.	3.8	42
27	Poly-Omic Prediction of Complex Traits: OmicKriging. Genetic Epidemiology, 2014, 38, 402-415.	0.6	41
28	Pharmacoethnicity in Paclitaxel-Induced Sensory Peripheral Neuropathy. Clinical Cancer Research, 2015, 21, 4337-4346.	3.2	39
29	Common Variants in Mendelian Kidney Disease Genes and Their Association with Renal Function. Journal of the American Society of Nephrology: JASN, 2013, 24, 2105-2117.	3.0	33
30	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. Pharmacogenetics and Genomics, 2012, 22, 498-507.	0.7	28
31	Fineâ€mapping and QTL tissueâ€sharing information improves the reliability of causal gene identification. Genetic Epidemiology, 2020, 44, 854-867.	0.6	28
32	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. Clinical Cancer Research, 2019, 25, 4104-4116.	3.2	27
33	Identification of novel germline polymorphisms governing capecitabine sensitivity. Cancer, 2012, 118, 4063-4073.	2.0	25
34	Genome-Wide Local Ancestry Approach Identifies Genes and Variants Associated with Chemotherapeutic Susceptibility in African Americans. PLoS ONE, 2011, 6, e21920.	1.1	25
35	Clinical Translation of Cell-Based Pharmacogenomic Discovery. Clinical Pharmacology and Therapeutics, 2012, 92, 425-427.	2.3	24
36	Pharmacokinetics and pharmacogenomics of daunorubicin in children: a report from the Childrenâ€™s Oncology Group. Cancer Chemotherapy and Pharmacology, 2014, 74, 831-838.	1.1	21

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37	Chemotherapeutic-induced apoptosis. Pharmacogenetics and Genomics, 2011, 21, 476-488.	0.7	19
38	Imputed gene associations identify replicable transâ€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608.	0.6	19
39	Genetic and epigenetic variants contributing to clofarabine cytotoxicity. Human Molecular Genetics, 2013, 22, 4007-4020.	1.4	18
40	Chronic circadian misalignment results in reduced longevity and large-scale changes in gene expression in Drosophila. BMC Genomics, 2019, 20, 14.	1.2	17
41	Comparing local ancestry inference models in populations of two- and three-way admixture. PeerJ, 2020, 8, e10090.	0.9	17
42	Clinical and Genome-Wide Analysis of Serum Platinum Levels after Cisplatin-Based Chemotherapy. Clinical Cancer Research, 2019, 25, 5913-5924.	3.2	16
43	Population-Matched Transcriptome Prediction Increases TWAS Discovery and Replication Rate. IScience, 2020, 23, 101850.	1.9	16
44	EPS8 Inhibition Increases Cisplatin Sensitivity in Lung Cancer Cells. PLoS ONE, 2013, 8, e82220.	1.1	16
45	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. PLoS ONE, 2019, 14, e0220827.	1.1	14
46	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.0	14
47	Gene-based association study for lipid traits in diverse cohorts implicates BACE1 and SIDT2 regulation in triglyceride levels. PeerJ, 2018, 6, e4314.	0.9	14
48	Multi-ethnic transcriptome-wide association study of prostate cancer. PLoS ONE, 2020, 15, e0236209.	1.1	13
49	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	1.1	13
50	Transcriptome association studies of neuropsychiatric traits in African Americans implicate PRMT7 in schizophrenia. PeerJ, 2019, 7, e7778.	0.9	12
51	Identification of genetic variants associated with capecitabine-induced handâ€“foot syndrome through integration of patient and cell line genomic analyses. Pharmacogenetics and Genomics, 2014, 24, 231-237.	0.7	10
52	Clinical and Genome-Wide Analysis of Multiple Severe Cisplatin-Induced Neurotoxicities in Adult-Onset Cancer Survivors. Clinical Cancer Research, 2020, 26, 6550-6558.	3.2	9
53	Genetically regulated expression underlies cellular sensitivity to chemotherapy in diverse populations. Human Molecular Genetics, 2021, 30, 305-317.	1.4	8
54	Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. Human Molecular Genetics, 2012, 21, 4348-4355.	1.4	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. American Journal of Human Genetics, 2022, 109, 857-870.	2.6	7
56	Clinical and genetic risk factors for radiationâ€associated ototoxicity: A report from the Childhood Cancer Survivor Study and the St. Jude Lifetime Cohort. Cancer, 2021, 127, 4091-4102.	2.0	6
57	Genetic Variants Contributing to Colistin Cytotoxicity: Identification of TGIF1 and HOXD10 Using a Population Genomics Approach. International Journal of Molecular Sciences, 2017, 18, 661.	1.8	2
58	Comprehensive characterization of cisplatin-related hearing loss in U.S. and Canadian Testicular Cancer Survivors (TCS).. Journal of Clinical Oncology, 2015, 33, 9570-9570.	0.8	2
59	Genome-wide association study of cisplatin-induced peripheral neuropathy (CIPN) in testicular cancer survivors.. Journal of Clinical Oncology, 2016, 34, 4543-4543.	0.8	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.. Journal of Clinical Oncology, 2016, 34, 10015-10015.	0.8	1
61	Variation in protein-coding sequence and the genetic basis of cisplatin-induced toxicities among testicular cancer survivors (TCS) in the Platinum Study.. Journal of Clinical Oncology, 2016, 34, 1537-1537.	0.8	1
62	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. Pharmacogenomics Journal, 2019, 19, 178-190.	0.9	0
63	Identification of pharmacogenetic target genes associated with chemotherapy-induced peripheral neuropathy.. Journal of Clinical Oncology, 2013, 31, e13541-e13541.	0.8	0
64	Genome-wide association study (GWAS) of chemotherapy-induced Raynaud's phenomenon (RP) to reveal shared pathways with cardiovascular disease (CVD).. Journal of Clinical Oncology, 2017, 35, e18162-e18162.	0.8	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.. Journal of Clinical Oncology, 2020, 38, 10550-10550.	0.8	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