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	Polygenic transcriptome risk scores (PTRS) can improve portability of polygenic risk scores across ancestries. Genome Biology, 2022, 23, 23.	3.8	42
2	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	1.1	13
3	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
4	Genetically regulated expression underlies cellular sensitivity to chemotherapy in diverse populations. Human Molecular Genetics, 2021, 30, 305-317.	1.4	8
5	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.0	14
6	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
7	Fineâ€mapping and QTL tissueâ€sharing information improves the reliability of causal gene identification. Genetic Epidemiology, 2020, 44, 854-867.	0.6	28
8	Population-Matched Transcriptome Prediction Increases TWAS Discovery and Replication Rate. IScience, 2020, 23, 101850.	1.9	16
9	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
10	Multi-ethnic transcriptome-wide association study of prostate cancer. PLoS ONE, 2020, 15, e0236209.	1.1	13
11	Comparing local ancestry inference models in populations of two- and three-way admixture. PeerJ, 2020, 8, e10090.	0.9	17
12	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
13	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
14	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
15	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
16	Multi-ethnic transcriptome-wide association study of prostate cancer. , 2020, 15, e0236209.		0
17	Integration of genetic and functional genomics data to uncover chemotherapeutic induced cytotoxicity. Pharmacogenomics Journal, 2019, 19, 178-190.	0.9	0
18	Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. PLoS ONE, 2019, 14, e0220827.	1.1	14

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19	Clinical and Genome-Wide Analysis of Serum Platinum Levels after Cisplatin-Based Chemotherapy. Clinical Cancer Research, 2019, 25, 5913-5924.	3.2	16
20	Genetic regulatory variation in populations informs transcriptome analysis in rare disease. Science, 2019, 366, 351-356.	6.0	99
21	Integrating predicted transcriptome from multiple tissues improves association detection. PLoS Genetics, 2019, 15, e1007889.	1.5	239
22	Clinical and Genome-wide Analysis of Cisplatin-induced Tinnitus Implicates Novel Ototoxic Mechanisms. Clinical Cancer Research, 2019, 25, 4104-4116.	3.2	27
23	Imputed gene associations identify replicable transâ€acting genes enriched in transcription pathways and complex traits. Genetic Epidemiology, 2019, 43, 596-608.	0.6	19
24	Chronic circadian misalignment results in reduced longevity and large-scale changes in gene expression in Drosophila. BMC Genomics, 2019, 20, 14.	1.2	17
25	Transcriptome association studies of neuropsychiatric traits in African Americans implicate PRMT7 in schizophrenia. PeerJ, 2019, 7, e7778.	0.9	12
26	Exploring the phenotypic consequences of tissue specific gene expression variation inferred from GWAS summary statistics. Nature Communications, 2018, 9, 1825.	5.8	748
27	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	1.5	117
28	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
29	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
30	Diverse Populations Are Needed To Understand The Genetics Of Complex Traits. , 2018, , .		0
31	Variants in WFS1 and Other Mendelian Deafness Genes Are Associated with Cisplatin-Associated Ototoxicity. Clinical Cancer Research, 2017, 23, 3325-3333.	3.2	65
32	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
33	Application of stem cell derived neuronal cells to evaluate neurotoxic chemotherapy. Stem Cell Research, 2017, 22, 79-88.	0.3	56
34	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
35	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
36	Survey of the Heritability and Sparse Architecture of Gene Expression Traits across Human Tissues. PLoS Genetics, 2016, 12, e1006423.	1.5	143

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37	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
38	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
39	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
40	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
41	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
42	Modeling Chemotherapeutic Neurotoxicity with Human Induced Pluripotent Stem Cell-Derived Neuronal Cells. PLoS ONE, 2015, 10, e0118020.	1.1	88
43	Pharmacoethnicity in Paclitaxel-Induced Sensory Peripheral Neuropathy. Clinical Cancer Research, 2015, 21, 4337-4346.	3.2	39
44	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
45	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	9.4	1,473
46	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
47	Poly-Omic Prediction of Complex Traits: OmicKriging. Genetic Epidemiology, 2014, 38, 402-415.	0.6	41
48	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
49	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
50	Cancer pharmacogenomics: strategies and challenges. Nature Reviews Genetics, 2013, 14, 23-34.	7.7	192
51	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
52	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
53	Genetic and epigenetic variants contributing to clofarabine cytotoxicity. Human Molecular Genetics, 2013, 22, 4007-4020.	1.4	18
54	Genome-wide meta-analysis identifies variants associated with platinating agent susceptibility across populations. Pharmacogenomics Journal, 2013, 13, 35-43.	0.9	49

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55	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
56	EPS8 Inhibition Increases Cisplatin Sensitivity in Lung Cancer Cells. PLoS ONE, 2013, 8, e82220.	1.1	16
57	Identification of pharmacogenetic target genes associated with chemotherapy-induced peripheral neuropathy.. Journal of Clinical Oncology, 2013, 31, e13541-e13541.	0.8	0
58	Genome-Wide Association and Functional Follow-Up Reveals New Loci for Kidney Function. PLoS Genetics, 2012, 8, e1002584.	1.5	166
59	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
60	Lymphoblastoid cell lines in pharmacogenomic discovery and clinical translation. Pharmacogenomics, 2012, 13, 55-70.	0.6	101
61	Regulatory Polymorphisms in Î²-Tubulin IIa Are Associated with Paclitaxel-Induced Peripheral Neuropathy. Clinical Cancer Research, 2012, 18, 4441-4448.	3.2	61
62	Whole-genome studies identify solute carrier transporters in cellular susceptibility to paclitaxel. Pharmacogenetics and Genomics, 2012, 22, 498-507.	0.7	28
63	Clinical Translation of Cell-Based Pharmacogenomic Discovery. Clinical Pharmacology and Therapeutics, 2012, 92, 425-427.	2.3	24
64	Relating human genetic variation to variation in drug responses. Trends in Genetics, 2012, 28, 487-495.	2.9	76
65	Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. Human Molecular Genetics, 2012, 21, 4348-4355.	1.4	7
66	Identification of novel germline polymorphisms governing capecitabine sensitivity. Cancer, 2012, 118, 4063-4073.	2.0	25
67	Genetics and genomics of human ageing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2011, 366, 43-50.	1.8	63
68	Chemotherapeutic-induced apoptosis. Pharmacogenetics and Genomics, 2011, 21, 476-488.	0.7	19
69	Genome-Wide Local Ancestry Approach Identifies Genes and Variants Associated with Chemotherapeutic Susceptibility in African Americans. PLoS ONE, 2011, 6, e21920.	1.1	25
70	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