Wenyi Wang

List of Publications by Year in Descending Order

61 papers	6,197 citations	24 h-index	75 g-index
75 ext. papers	7,849 ext. citations	12.6 avg, IF	6.6 L-index

#	Paper	IF	Citations
61	MuSE: A Novel Approach to Mutation Calling with Sample-Specific Error Modeling. *Methods in Molecular Biology*, **2022**, 21-27	1.4	
60	HepatoScore-14: Measures of Biological Heterogeneity Significantly Improve Prediction of Hepatocellular Carcinoma Risk. *Hepatology*, **2021**, 73, 2278-2292	11.2	5
59	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. *Cell*, **2021**, 184, 2239-2254.e39	56.2	57
58	Single-cell ATAC and RNA sequencing reveal pre-existing and persistent cells associated with prostate cancer relapse. *Nature Communications*, **2021**, 12, 5307	17.4	9
57	Cardelino: computational integration of somatic clonal substructure and single-cell transcriptomes. *Nature Methods*, **2020**, 17, 414-421	21.6	17
56	Immuno-genomic landscape of osteosarcoma. *Nature Communications*, **2020**, 11, 1008	17.4	77
55	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
54	BAYESIAN VARIABLE SELECTION FOR SURVIVAL DATA USING INVERSE MOMENT PRIORS. *Annals of Applied Statistics*, **2020**, 14, 809-828	2.1	8
53	Penetrance of Different Cancer Types in Families with Li-Fraumeni Syndrome: A Validation Study Using Multicenter Cohorts. *Cancer Research*, **2020**, 80, 354-360	10.1	9
52	Penetrance Estimates Over Time to First and Second Primary Cancer Diagnosis in Families with Li-Fraumeni Syndrome: A Single Institution Perspective. *Cancer Research*, **2020**, 80, 347-353	10.1	3
51	Systematic Assessment of Tumor Purity and Its Clinical Implications. *JCO Precision Oncology*, **2020**, 4,	3.6	7
50	A pedigree-based prediction model identifies carriers of deleterious de novo mutations in families with Li-Fraumeni syndrome. *Genome Research*, **2020**, 30, 1170-1180	9.7	1
49	Bayesian estimation of a semiparametric recurrent event model with applications to the penetrance estimation of multiple primary cancers in Li-Fraumeni syndrome. *Biostatistics*, **2020**, 21, 467-482	3.7	1
48	Integration of transcriptional and mutational data simplifies the stratification of peripheral T-cell lymphoma. *American Journal of Hematology*, **2019**, 94, 628-634	7.1	7
47	Bayesian Semiparametric Estimation of Cancer-specific Age-at-onset Penetrance with Application to Li-Fraumeni Syndrome. *Journal of the American Statistical Association*, **2019**, 114, 541-552	2.8	3
46	Bayesian analysis of longitudinal dyadic data with informative missing data using a dyadic shared-parameter model. *Statistical Methods in Medical Research*, **2019**, 28, 70-83	2.3	2
45	Abstract 3000: Pervasive intra-tumour heterogeneity and subclonal selection across cancer types **2018**,		6

44	Accurate RNA Sequencing From Formalin-Fixed Cancer Tissue To Represent High-Quality Transcriptome From Frozen Tissue. *JCO Precision Oncology*, **2018**, 2018,	3.6	26
43	Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. *IScience*, **2018**, 9, 451-460	6.1	36
42	Neutral tumor evolution?. *Nature Genetics*, **2018**, 50, 1630-1633	36.3	38
41	RNA-seq mixology: designing realistic control experiments to compare protocols and analysis methods. *Nucleic Acids Research*, **2017**, 45, e30	20.1	19
40	Estimating Mutation Carrier Probability in Families with Li-Fraumeni Syndrome Using LFSPRO. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 837-844	4	7
39	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. *Genome Biology*, **2016**, 17, 178	18.3	120
38	Bayesian variable selection for binary outcomes in high-dimensional genomic studies using non-local priors. *Bioinformatics*, **2016**, 32, 1338-45	7.2	21
37	Next-Generation Molecular Testing of Newborn Dried Blood Spots for Cystic Fibrosis. *Journal of Molecular Diagnostics*, **2016**, 18, 267-82	5.1	21
36	Identification of germline DICER1 mutations and loss of heterozygosity in familial Wilms tumour. *Journal of Medical Genetics*, **2016**, 53, 385-8	5.8	19
35	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
34	An ensemble approach to accurately detect somatic mutations using SomaticSeq. *Genome Biology*, **2015**, 16, 197	18.3	64
33	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
32	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
31	FamSeq: a variant calling program for family-based sequencing data using graphics processing units. *PLoS Computational Biology*, **2014**, 10, e1003880	5	10
30	Multiplex target capture with double-stranded DNA probes. *Genome Medicine*, **2013**, 5, 50	14.4	15
29	Integrating multi-platform genomic data using hierarchical Bayesian relevance vector machines. *Eurasip Journal on Bioinformatics and Systems Biology*, **2013**, 2013, 9		4
28	DeMix: deconvolution for mixed cancer transcriptomes using raw measured data. *Bioinformatics*, **2013**, 29, 1865-71	7.2	72
27	Rare variant detection using family-based sequencing analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 3985-90	11.5	42

26	Bayesian latent-class mixed-effect hybrid models for dyadic longitudinal data with non-ignorable dropouts. *Biometrics*, **2013**, 69, 914-24	1.8	2
25	A DNA resequencing array for genes involved in Parkinson\'s disease. *Parkinsonism and Related Disorders*, **2012**, 18, 386-90	3.6	7
24	Slow down to stay alive: HER4 protects against cellular stress and confers chemoresistance in neuroblastoma. *Cancer*, **2012**, 118, 5140-54	6.4	18
23	SRMA: an R package for resequencing array data analysis. *Bioinformatics*, **2012**, 28, 1928-30	7.2	1
22	Identification of rare DNA variants in mitochondrial disorders with improved array-based sequencing. *Nucleic Acids Research*, **2011**, 39, 44-58	20.1	26
21	High-quality DNA sequence capture of 524 disease candidate genes. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 6549-54	11.5	47
20	Estimating CDKN2A carrier probability and personalizing cancer risk assessments in hereditary melanoma using MelaPRO. *Cancer Research*, **2010**, 70, 552-9	10.1	31
19	A molecular inversion probe assay for detecting alternative splicing. *BMC Genomics*, **2010**, 11, 712	4.5	6
18	Evaluation of school-based smoking-cessation interventions for self-described adolescent smokers. *Pediatrics*, **2009**, 124, e187-94	7.4	18
17	Estimating genome-wide copy number using allele-specific mixture models. *Journal of Computational Biology*, **2008**, 15, 857-66	1.7	17
16	PancPRO: risk assessment for individuals with a family history of pancreatic cancer. *Journal of Clinical Oncology*, **2007**, 25, 1417-22	2.2	150
15	Estimating Genome-Wide Copy Number Using Allele Specific Mixture Models. *Lecture Notes in Computer Science*, **2007**, 137-150	0.9	1
14	A recessive Mendelian model to predict carrier probabilities of DFNB1 for nonsyndromic deafness. *Human Mutation*, **2006**, 27, 1135-42	4.7	4
13	Prediction of germline mutations and cancer risk in the Lynch syndrome. *JAMA - Journal of the American Medical Association*, **2006**, 296, 1479-87	27.4	271
12	Siah1 interacts with the scaffold protein POSH to promote JNK activation and apoptosis. *Journal of Biological Chemistry*, **2006**, 281, 303-12	5.4	53
11	Inference of combinatorial regulation in yeast transcriptional networks: a case study of sporulation. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 1998-2003	11.5	87
10	BayesMendel: an R environment for Mendelian risk prediction. *Statistical Applications in Genetics and Molecular Biology*, **2004**, 3, Article21	1.2	56
9	A systematic approach to reconstructing transcription networks in Saccharomycescerevisiae. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 16893-8	11.5	71

List of Publications

8	Mammalian Sug1 and c-Fos in the nuclear 26S proteasome. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 8236-40	11.5	53
7	DNA Variant Calling in Targeted Sequencing Data54-76		
6	Bayesian Edge Regression in Undirected Graphical Models to Characterize Interpatient Heterogeneity in Cancer. *Journal of the American Statistical Association*,1-31	2.8	1
5	Tumor cell total mRNA expression shapes the molecular and clinical phenotype of cancer		2
4	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes		25
3	Cardelino: Integrating whole exomes and single-cell transcriptomes to reveal phenotypic impact of somatic variants		12
2	Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration		2
1	Single-cell ATAC and RNA sequencing reveal pre-existing and persistent subpopulations of cells associated with relapse of prostate cancer		1