Qinying Xu

List of Publications by Year
in descending order

23 papers	10,844 citations	430874 18 h-index	677142 22 g-index
23 all docs	23 docs citations	23 times ranked	18179 citing authors

#	Article	IF	Citations
1	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	2.4	5
2	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	8.2	24
3	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	12.8	102
4	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	5.2	19
5	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	12.8	205
6	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	1.5	19
7	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. International Journal of Cancer, 2019, 144, 1049-1060.	5.1	54
8	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	4.5	73
9	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	2.5	57
10	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	27.8	716
11	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	27.8	1,068
12	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	1.3	174
13	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	27.8	2,700
14	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	4.5	98
15	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	27.8	1,206
16	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	27.8	2,132
17	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	1.8	0
18	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	12.8	236

#	Article	IF	Citations
19	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	2.5	67
20	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	27.8	1,741
21	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	2.5	92
22	X-MATE: a flexible system for mapping short read data. Bioinformatics, 2011, 27, 580-581.	4.1	11
23	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. Bioinformatics, 2009, 25, 2615-2616.	4.1	45