Qinying Xu

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/5714146/publications.pdf

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23 papers	10,844 citations	430754 18 h-index	677027 22 g-index
23 all docs	23 docs citations	23 times ranked	18179 citing authors

#	Article	IF	Citations
1	Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 2016, 531, 47-52.	13.7	2,700
2	Whole genomes redefine the mutational landscape of pancreatic cancer. Nature, 2015, 518, 495-501.	13.7	2,132
3	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. Nature, 2012, 491, 399-405.	13.7	1,741
4	Wholeâ€“genome characterization of chemoresistant ovarian cancer. Nature, 2015, 521, 489-494.	13.7	1,206
5	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
6	Whole-genome landscape of pancreatic neuroendocrine tumours. Nature, 2017, 543, 65-71.	13.7	716
7	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. Nature Communications, 2014, 5, 5224.	5.8	236
8	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. Nature Communications, 2019, 10, 3163.	5.8	205
9	Hypermutation In Pancreatic Cancer. Gastroenterology, 2017, 152, 68-74.e2.	0.6	174
10	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. Nature Communications, 2020, 11, 5259.	5.8	102
11	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	2.1	98
12	qpure: A Tool to Estimate Tumor Cellularity from Genome-Wide Single-Nucleotide Polymorphism Profiles. PLoS ONE, 2012, 7, e45835.	1.1	92
13	Phenotypic and molecular dissection of metaplastic breast cancer and the prognostic implications. Journal of Pathology, 2019, 247, 214-227.	2.1	73
14	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
15	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. PLoS ONE, 2018, 13, e0190264.	1.1	57
16	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.	2.3	54
17	RNA-MATE: a recursive mapping strategy for high-throughput RNA-sequencing data. Bioinformatics, 2009, 25, 2615-2616.	1.8	45
18	Comprehensive genomic and tumour immune profiling reveals potential therapeutic targets in malignant pleural mesothelioma. Genome Medicine, 2022, 14, .	3.6	24

#	Article	IF	Citations
19	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	0.7	19
20	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
21	X-MATE: a flexible system for mapping short read data. Bioinformatics, 2011, 27, 580-581.	1.8	11
22	qmotif: determination of telomere content from whole-genome sequence data. Bioinformatics Advances, 2022, 2, .	0.9	5
23	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0