

Felicity Newell

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

11,043
citations

304368

22
h-index

454577

30
g-index

34
all docs

34
docs citations

34
times ranked

18305
citing authors

#	ARTICLE	IF	CITATIONS
1	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. <i>Genome Medicine</i> , 2022, 14, 3.	3.6	16
2	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. <i>Cancer Cell</i> , 2022, 40, 88-102.e7.	7.7	64
3	Anatomic position determines oncogenic specificity in melanoma. <i>Nature</i> , 2022, 604, 354-361.	13.7	44
4	Classification of esophageal adenocarcinoma into subgroups that are associated with patient survival using RNA-seq and immunohistochemistry.. <i>Journal of Clinical Oncology</i> , 2022, 40, e16028-e16028.	0.8	0
5	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	2.0	26
6	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. <i>Molecular Cancer Research</i> , 2021, 19, 991-1004.	1.5	19
7	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. <i>Human Mutation</i> , 2021, 42, 530-536.	1.1	8
8	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. <i>Cancers</i> , 2021, 13, 1762.	1.7	5
9	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021, 12, 1137.	5.8	33
10	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	5.8	102
11	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. <i>Cancer Immunology Research</i> , 2020, 8, 1346-1353.	1.6	13
12	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	2.3	19
13	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. <i>Nature Communications</i> , 2020, 11, 2408.	5.8	86
14	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	5.8	205
15	Molecular Genomic Profiling of Melanocytic Nevus. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1762-1768.	0.3	55
16	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	0.7	19
17	Whole genome sequencing of melanomas in adolescent and young adults reveals distinct mutation landscapes and the potential role of germline variants in disease susceptibility. <i>International Journal of Cancer</i> , 2019, 144, 1049-1060.	2.3	54
18	Comprehensive molecular profiling of metastatic melanoma to predict response to monotherapy and combination immunotherapy.. <i>Journal of Clinical Oncology</i> , 2019, 37, 9511-9511.	0.8	3

#	ARTICLE	IF	CITATIONS
19	Mixed ductal–lobular carcinomas: evidence for progression from ductal to lobular morphology. <i>Journal of Pathology</i> , 2018, 244, 460-468.	2.1	31
20	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0190264.	1.1	57
21	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	13.7	716
22	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	13.7	1,068
23	Hypermethylation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	0.6	174
24	Genomic analyses identify molecular subtypes of pancreatic cancer. <i>Nature</i> , 2016, 531, 47-52.	13.7	2,700
25	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	2.1	98
26	Whole“genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	13.7	1,206
27	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	13.7	2,132
28	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0126911.	1.1	42
29	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , 2014, 57, 31-38.	0.8	0
30	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	5.8	236
31	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	1.1	67
32	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	13.7	1,741