Felicity Newell

List of Publications by Year
in descending order

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	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	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. Nature Communications, 2020, 11, 2408.	5.8	86
13	Somatic Point Mutation Calling in Low Cellularity Tumors. PLoS ONE, 2013, 8, e74380.	1.1	67
14	Multiomic profiling of checkpoint inhibitor-treated melanoma: Identifying predictors of response and resistance, and markers of biological discordance. Cancer Cell, 2022, 40, 88-102.e7.	7.7	64
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	Molecular Genomic Profiling of MelanocyticÂNevi. Journal of Investigative Dermatology, 2019, 139, 1762-1768.	0.3	55
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. International Journal of Cancer, 2019, 144, 1049-1060.	2.3	54
18	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44

#	Article	IF	Citations
19	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. PLoS ONE, 2015, 10, e0126911.	1.1	42
20	Tumour gene expression signature in primary melanoma predicts long-term outcomes. Nature Communications, 2021, 12, 1137.	5.8	33
21	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	2.1	31
22	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. Communications Biology, 2021, 4, 155.	2.0	26
23	Complex structural rearrangements are present in high-grade dysplastic Barrettâ€™s oesophagus samples. BMC Medical Genomics, 2019, 12, 31.	0.7	19
24	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
25	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. Molecular Cancer Research, 2021, 19, 991-1004.	1.5	19
26	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. Genome Medicine, 2022, 14, 3.	3.6	16
27	Tumor Mutation Burden and Structural Chromosomal Aberrations Are Not Associated with T-cell Density or Patient Survival in Acral, Mucosal, and Cutaneous Melanomas. Cancer Immunology Research, 2020, 8, 1346-1353.	1.6	13
28	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. Human Mutation, 2021, 42, 530-536.	1.1	8
29	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. Cancers, 2021, 13, 1762.	1.7	5
30	Comprehensive molecular profiling of metastatic melanoma to predict response to monotherapy and combination immunotherapy.. Journal of Clinical Oncology, 2019, 37, 9511-9511.	0.8	3
31	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	0
32	Classification of esophageal adenocarcinoma into subgroups that are associated with patient survival using RNA-seq and immunohistochemistry.. Journal of Clinical Oncology, 2022, 40, e16028-e16028.	0.8	0