

# Felicity Newell

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

11,043  
citations

304743

22  
h-index

454955

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. <i>Nature</i> , 2016, 531, 47-52.	27.8	2,700
2	Whole genomes redefine the mutational landscape of pancreatic cancer. <i>Nature</i> , 2015, 518, 495-501.	27.8	2,132
3	Pancreatic cancer genomes reveal aberrations in axon guidance pathway genes. <i>Nature</i> , 2012, 491, 399-405.	27.8	1,741
4	Whole-genome characterization of chemoresistant ovarian cancer. <i>Nature</i> , 2015, 521, 489-494.	27.8	1,206
5	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017, 545, 175-180.	27.8	1,068
6	Whole-genome landscape of pancreatic neuroendocrine tumours. <i>Nature</i> , 2017, 543, 65-71.	27.8	716
7	Genomic catastrophes frequently arise in esophageal adenocarcinoma and drive tumorigenesis. <i>Nature Communications</i> , 2014, 5, 5224.	12.8	236
8	Whole-genome landscape of mucosal melanoma reveals diverse drivers and therapeutic targets. <i>Nature Communications</i> , 2019, 10, 3163.	12.8	205
9	Hypermutation In Pancreatic Cancer. <i>Gastroenterology</i> , 2017, 152, 68-74.e2.	1.3	174
10	Whole-genome sequencing of acral melanoma reveals genomic complexity and diversity. <i>Nature Communications</i> , 2020, 11, 5259.	12.8	102
11	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. <i>Journal of Pathology</i> , 2015, 237, 363-378.	4.5	98
12	Whole genome landscapes of uveal melanoma show an ultraviolet radiation signature in iris tumours. <i>Nature Communications</i> , 2020, 11, 2408.	12.8	86
13	Somatic Point Mutation Calling in Low Cellularity Tumors. <i>PLoS ONE</i> , 2013, 8, e74380.	2.5	67
14	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.	16.8	64
15	Germline and somatic variant identification using BGISEQ-500 and HiSeq X Ten whole genome sequencing. <i>PLoS ONE</i> , 2018, 13, e0190264.	2.5	57
16	Molecular Genomic Profiling of Melanocytic Nevus. <i>Journal of Investigative Dermatology</i> , 2019, 139, 1762-1768.	0.7	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. <i>International Journal of Cancer</i> , 2019, 144, 1049-1060.	5.1	54
18	Anatomic position determines oncogenic specificity in melanoma. <i>Nature</i> , 2022, 604, 354-361.	27.8	44

#	ARTICLE	IF	CITATIONS
19	Recommendations for Accurate Resolution of Gene and Isoform Allele-Specific Expression in RNA-Seq Data. <i>PLoS ONE</i> , 2015, 10, e0126911.	2.5	42
20	Tumour gene expression signature in primary melanoma predicts long-term outcomes. <i>Nature Communications</i> , 2021, 12, 1137.	12.8	33
21	Mixed ductal&lobular carcinomas: evidence for progression from ductal to lobular morphology. <i>Journal of Pathology</i> , 2018, 244, 460-468.	4.5	31
22	DNA methylation patterns identify subgroups of pancreatic neuroendocrine tumors with clinical association. <i>Communications Biology</i> , 2021, 4, 155.	4.4	26
23	Complex structural rearrangements are present in high-grade dysplastic Barrett's oesophagus samples. <i>BMC Medical Genomics</i> , 2019, 12, 31.	1.5	19
24	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. <i>Npj Breast Cancer</i> , 2020, 6, 33.	5.2	19
25	Meta-Analysis and Systematic Review of the Genomics of Mucosal Melanoma. <i>Molecular Cancer Research</i> , 2021, 19, 991-1004.	3.4	19
26	Patient-derived xenograft models capture genomic heterogeneity in endometrial cancer. <i>Genome Medicine</i> , 2022, 14, 3.	8.2	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. <i>Cancer Immunology Research</i> , 2020, 8, 1346-1353.	3.4	13
28	Considerations for using population frequency data in germline variant interpretation: Cancer syndrome genes as a model. <i>Human Mutation</i> , 2021, 42, 530-536.	2.5	8
29	Tumor Signature Analysis Implicates Hereditary Cancer Genes in Endometrial Cancer Development. <i>Cancers</i> , 2021, 13, 1762.	3.7	5
30	Comprehensive molecular profiling of metastatic melanoma to predict response to monotherapy and combination immunotherapy.. <i>Journal of Clinical Oncology</i> , 2019, 37, 9511-9511.	1.6	3
31	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. <i>BioTechniques</i> , 2014, 57, 31-38.	1.8	0
32	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.	1.6	0