Stephen-John Sammut

List of Publications by Year
in descending order

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27 papers	14,667 citations	331670 21 h-index	501196 28 g-index
28 all docs	28 docs citations	28 times ranked	27245 citing authors

#	Article	IF	Citations
1	Residual cancer burden after neoadjuvant chemotherapy and long-term survival outcomes in breast cancer: a multicentre pooled analysis of 5161 patients. Lancet Oncology, The, 2022, 23, 149-160.	10.7	148
2	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	27.8	187
3	AACR Project GENIE: 100,000 Cases and Beyond. Cancer Discovery, 2022, 12, 2044-2057.	9.4	27
4	The temporal mutational and immune tumour microenvironment remodelling of HER2-negative primary breast cancers. Npj Breast Cancer, 2021, 7, 73.	5.2	2
5	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. Nature Communications, 2021, 12, 5406.	12.8	29
6	The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. Nature Communications, 2020, 11, 6433.	12.8	37
7	Personalized circulating tumor DNA analysis to detect residual disease after neoadjuvant therapy in breast cancer. Science Translational Medicine, 2019, 11, .	12.4	197
8	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	6.4	95
9	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	27.8	239
10	T-cell bispecific antibodies in node-positive breast cancer: novel therapeutic avenue for MHC class I loss variants. Annals of Oncology, 2019, 30, 934-944.	1.2	20
11	Next Generation-Targeted Amplicon Sequencing (NG-TAS): an optimised protocol and computational pipeline for cost-effective profiling of circulating tumour DNA. Genome Medicine, 2019, 11, 1.	8.2	84
12	Shallow whole genome sequencing for robust copy number profiling of formalin-fixed paraffin-embedded breast cancers. Experimental and Molecular Pathology, 2018, 104, 161-169.	2.1	25
13	Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. BMC Genomics, 2018, 19, 19.	2.8	55
14	Big data in cancer genomics. Current Opinion in Systems Biology, 2017, 4, 78-84.	2.6	12
15	Intersect-then-combine approach: improving the performance of somatic variant calling in whole exome sequencing data using multiple aligners and callers. Genome Medicine, 2017, 9, 35.	8.2	48
16	New Model for Estimating Glomerular Filtration Rate in Patients With Cancer. Journal of Clinical Oncology, 2017, 35, 2798-2805.	1.6	78
17	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. Scientific Reports, 2016, 6, 18517.	3.3	143
18	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	28.9	376

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19	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	12.8	1,221
20	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	4.6	38
21	Pyogenic Granuloma as a Cutaneous Adverse Effect of Vemurafenib. New England Journal of Medicine, 2014, 371, 1265-1267.	27.0	20
22	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
23	Management of febrile neutropenia in an acute oncology service. QJM - Monthly Journal of the Association of Physicians, 2012, 105, 327-336.	0.5	18
24	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
25	ApiNATOMY: A novel toolkit for visualizing multiscale anatomy schematics with phenotype-related information. Human Mutation, 2012, 33, 837-848.	2.5	25
26	Pfam 10 years on: 10 000 families and still growing. Briefings in Bioinformatics, 2008, 9, 210-219.	6.5	114
27	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	14.5	6,372