Stephen-John Sammut

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9323035/publications.pdf

Version: 2024-02-01

27 papers

14,667 citations

331670 21 h-index 501196 28 g-index

28 all docs

 $\begin{array}{c} 28 \\ \text{docs citations} \end{array}$

times ranked

28

27245 citing authors

#	Article	IF	CITATIONS
1	The Pfam protein families database. Nucleic Acids Research, 2007, 36, D281-D288.	14.5	6,372
2	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
3	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	12.8	1,221
4	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	28.9	376
5	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
6	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	27.8	239
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	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	27.8	187
9	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
10	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
11	Pfam 10 years on: 10 000 families and still growing. Briefings in Bioinformatics, 2008, 9, 210-219.	6.5	114
12	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	6.4	95
13	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
14	New Model for Estimating Glomerular Filtration Rate in Patients With Cancer. Journal of Clinical Oncology, 2017, 35, 2798-2805.	1.6	78
15	Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. BMC Genomics, 2018, 19, 19.	2.8	55
16	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
17	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
18	The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. Nature Communications, 2020, 11, 6433.	12.8	37

#	Article	IF	CITATIONS
19	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
20	AACR Project GENIE: 100,000 Cases and Beyond. Cancer Discovery, 2022, 12, 2044-2057.	9.4	27
21	ApiNATOMY: A novel toolkit for visualizing multiscale anatomy schematics with phenotype-related information. Human Mutation, 2012, 33, 837-848.	2.5	25
22	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
23	Pyogenic Granuloma as a Cutaneous Adverse Effect of Vemurafenib. New England Journal of Medicine, 2014, 371, 1265-1267.	27.0	20
24	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
25	Management of febrile neutropenia in an acute oncology service. QJM - Monthly Journal of the Association of Physicians, 2012, 105, 327-336.	0.5	18
26	Big data in cancer genomics. Current Opinion in Systems Biology, 2017, 4, 78-84.	2.6	12
27	The temporal mutational and immune tumour microenvironment remodelling of HER2-negative primary breast cancers. Npj Breast Cancer, 2021, 7, 73.	5.2	2