

Sarah A Killcoyne

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,246
citations

516215

16
h-index

500791

28
g-index

32
all docs

32
docs citations

32
times ranked

7510
citing authors

#	ARTICLE	IF	CITATIONS
1	Limitations of Heartburn and Other Societiesâ€™ Criteria in Barrettâ€™s Screening for Detecting De Novo Esophageal Adenocarcinoma. <i>Clinical Gastroenterology and Hepatology</i> , 2022, 20, 1709-1718.	2.4	17
2	Use of a Cytosponge biomarker panel to prioritise endoscopic Barrett's oesophagus surveillance: a cross-sectional study followed by a real-world prospective pilot. <i>Lancet Oncology</i> , The, 2022, 23, 270-278.	5.1	28
3	Rearrangement processes and structural variations show evidence of selection in oesophageal adenocarcinomas. <i>Communications Biology</i> , 2022, 5, 335.	2.0	8
4	Practical early cancer detection: distinguishing stable from unstable genomes in pre-cancerous tissues. <i>British Journal of Cancer</i> , 2021, 124, 683-685.	2.9	1
5	Genomic instability signals offer diagnostic possibility in early cancer detection. <i>Trends in Genetics</i> , 2021, 37, 966-972.	2.9	11
6	Evolution and progression of Barrettâ€™s oesophagus to oesophageal cancer. <i>Nature Reviews Cancer</i> , 2021, 21, 731-741.	12.8	32
7	Comparison of Phenotypes and Risk Factors for Esophageal Adenocarcinoma at Present vs Prior Decades. <i>Clinical Gastroenterology and Hepatology</i> , 2020, 18, 2710-2716.e1.	2.4	5
8	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	9.4	79
9	Genomic copy number predicts esophageal cancer years before transformation. <i>Nature Medicine</i> , 2020, 26, 1726-1732.	15.2	86
10	Aneuploidy in targeted endoscopic biopsies outperforms other tissue biomarkers in the prediction of histologic progression of Barrett's oesophagus: A multi-centre prospective cohort study. <i>EBioMedicine</i> , 2020, 56, 102765.	2.7	19
11	Identification of Subtypes of Barrettâ€™s Esophagus and Esophageal Adenocarcinoma Based on DNA Methylation Profiles and Integration of Transcriptome and Genome Data. <i>Gastroenterology</i> , 2020, 158, 1682-1697.e1.	0.6	58
12	Managing Chaos: Bridging the cultural divide between engineers and scientists working within the life sciences. <i>Computing in Science and Engineering</i> , 2019, , 1-1.	1.2	2
13	The landscape of selection in 551 esophageal adenocarcinomas defines genomic biomarkers for the clinic. <i>Nature Genetics</i> , 2019, 51, 506-516.	9.4	166
14	Identification of Prognostic Phenotypes of Esophageal Adenocarcinoma in 2 Independent Cohorts. <i>Gastroenterology</i> , 2018, 155, 1720-1728.e4.	0.6	67
15	Shallow Whole Genome Sequencing can Detect Copy Number Changes in FFPE Material in the Progression of Barrett's Esophagus. <i>Gastroenterology</i> , 2017, 152, S106.	0.6	0
16	Identification of large-scale genomic variation in cancer genomes using <i>in silico</i> reference models. <i>Nucleic Acids Research</i> , 2016, 44, e5-e5.	6.5	4
17	FIGG: Simulating populations of whole genome sequences for heterogeneous data analyses. <i>BMC Bioinformatics</i> , 2014, 15, 149.	1.2	9
18	Mining PeptideAtlas for Biomarkers and Therapeutics in Human Disease. <i>Current Pharmaceutical Design</i> , 2012, 18, 748-754.	0.9	2

#	ARTICLE	IF	CITATIONS
19	Interfaces to PeptideAtlas: a case study of standard data access systems. Briefings in Bioinformatics, 2012, 13, 615-626.	3.2	1
20	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. BMC Bioinformatics, 2012, 13, 324.	1.2	48
21	Methods for visual mining of genomic and proteomic data atlases. BMC Bioinformatics, 2012, 13, 58.	1.2	8
22	SAMQA: error classification and validation of high-throughput sequenced read data. BMC Genomics, 2011, 12, 419.	1.2	13
23	SEQADAPT: an adaptable system for the tracking, storage and analysis of high throughput sequencing experiments. BMC Bioinformatics, 2010, 11, 377.	1.2	0
24	Howdah - A Flexible Pipeline Framework for Analyzing Genomic Data. , 2010, , .		0
25	An Integration Architecture Designed to Deal with the Issues of Biological Scope, Scale and Complexity. Lecture Notes in Computer Science, 2010, , 179-191.	1.0	1
26	Adaptable data management for systems biology investigations. BMC Bioinformatics, 2009, 10, 79.	1.2	18
27	Cytoscape: A Community-Based Framework for Network Modeling. Methods in Molecular Biology, 2009, 563, 219-239.	0.4	191
28	Managing Chaos: Lessons Learned Developing Software in the Life Sciences. Computing in Science and Engineering, 2009, 11, 20-29.	1.2	17
29	Systems biology driven software design for the research enterprise. BMC Bioinformatics, 2008, 9, 295.	1.2	19
30	T1DBase: integration and presentation of complex data for type 1 diabetes research. Nucleic Acids Research, 2007, 35, D742-D746.	6.5	60
31	Integration of biological networks and gene expression data using Cytoscape. Nature Protocols, 2007, 2, 2366-2382.	5.5	2,275