Sarah Sandmann

List of Publications by Year
in descending order

27	636	933447 10	642732 23
papers	citations	h-index	g-index

30	30	30	1370
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Evaluating Variant Calling Tools for Non-Matched Next-Generation Sequencing Data. Scientific Reports, 2017, 7, 43169.	3.3	185
2	Clonal evolution in myelodysplastic syndromes. Nature Communications, 2017, 8, 15099.	12.8	118
3	Effects of computerized decision support system implementations on patient outcomes in inpatient care: a systematic review. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 593-602.	4.4	98
4	Persistent symptoms and lab abnormalities in patients who recovered from COVID-19. Scientific Reports, 2021, 11, 12775.	3.3	36
5	Integrative genomic analysis of pediatric T-cell lymphoblastic lymphoma reveals candidates of clinical significance. Blood, 2021, 137, 2347-2359.	1.4	31
6	Clinical relevance of molecular characteristics in Burkitt lymphoma differs according to age. Nature Communications, 2022, 13, .	12.8	28
7	appreci8: a pipeline for precise variant calling integrating 8 tools. Bioinformatics, 2018, 34, 4205-4212.	4.1	26
8	Machine learning in the detection and management of atrial fibrillation. Clinical Research in Cardiology, 2022, 111, 1010-1017.	3.3	23
9	Reconstructing clonal evolution in relapsed and non-relapsed Burkitt lymphoma. Leukemia, 2021, 35, 639-643.	7.2	16
10	Genetic alterations in human papillomavirus-associated oropharyngeal squamous cell carcinoma of patients with treatment failure. Oral Oncology, 2019, 93, 59-65.	1.5	10
11	Mutation patterns in recurrent and/or metastatic oropharyngeal squamous cell carcinomas in relation to human papillomavirus status. Cancer Medicine, 2021, 10, 1347-1356.	2.8	9
12	Calcitonin receptor-like (CALCRL) is a marker of stemness and an independent predictor of outcome in pediatric AML. Blood Advances, 2021, 5, 4413-4421.	5.2	9
13	GLM-based optimization of NGS data analysis: A case study of Roche 454, Ion Torrent PGM and Illumina NextSeq sequencing data. PLoS ONE, 2017, 12, e0171983.	2.5	7
14	Comparison of Open-access Databases for Clinical Variant Interpretation in Cancer: A Case Study of MDS/AML. Cancer Genomics and Proteomics, 2021, 18, 157-166.	2.0	6
15	Divergent Effects of EZH1 and EZH2 Protein Expression on the Prognosis of Patients with T-Cell Lymphomas. Biomedicines, 2021, 9, 1842.	3.2	6
16	CopyDetective: Detection thresholdâ€“aware copy number variant calling in whole-exome sequencing data. GigaScience, 2020, 9, .	6.4	5
17	Online Information Infrastructure Increases Inter-Rater Reliability of Medical Coders: A Quasi-Experimental Study (Preprint). Journal of Medical Internet Research, 2018, 20, e274.	4.3	5
18	SimFFPE and FilterFFPE: improving structural variant calling in FFPE samples. GigaScience, 2021, 10, .	6.4	4

#	Article	IF	Citations
19	Mutation Profiles Identify Distinct Clusters of Lower Risk Myelodysplastic Syndromes with Unique Clinical and Biological Features and Clinical Endpoints. Blood, 2020, 136, 29-29.	1.4	2
20	Design of a targeted nextâ€generation DNA sequencing panel for pediatric Tâ€cell lymphoblastic lymphoma to unravel biology and optimize treatment. Genes Chromosomes and Cancer, 2022, 61, 459-470.	2.8	2
21	Clonal Evolution at First Sight: A Combined Visualization of Diverse Diagnostic Methods Improves Understanding of Leukemic Progression. Frontiers in Oncology, 0, 12, .	2.8	2
22	Multicenter Next-Generation Sequencing Studies between Theory and Practice. Journal of Molecular Diagnostics, 2021, 23, 347-357.	2.8	1
23	Medical Effect of Venous Thromboembolism Prophylaxis Systems and Common Input Categories: Preliminary Findings from a Systematic Review. Studies in Health Technology and Informatics, 2017, 245, 1175-1179.	0.3	1
24	Exploring Current Challenges and Perspectives for Automatic Reconstruction of Clonal Evolution. Cancer Genomics and Proteomics, 2022, 19, 194-204.	2.0	1
25	MEDB-67. Subgroup specific analysis of cellular metabolism in medulloblastoma. Neuro-Oncology, 2022, 24, i122-i122.	1.2	1
26	BBCAnalyzer: a visual approach to facilitate variant calling. BMC Bioinformatics, 2017, 18, 133.	2.6	0
27	Clonal Evolution at First Sight: A Combined Visualization of Diverse Diagnostic Methods Improves Understanding of Leukemia Progression. Blood, 2021, 138, 1293-1293.	1.4	0