

Mara Rosenberg

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

13,261
citations

172386

29
h-index

345118

36
g-index

38
all docs

38
docs citations

38
times ranked

27181
citing authors

#	ARTICLE	IF	CITATIONS
1	Implementation of a prostate cancer-specific targeted sequencing panel for credentialing of patient-derived cell lines and genomic characterization of patient samples. <i>Prostate</i> , 2022, , .	1.2	1
2	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , 2020, 11, 5040.	5.8	5
3	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020, 38, 288-292.	9.4	11
4	Geographic differences in the unpaid caregiver experience from the National Study of Caregiving (NSOC). <i>Rural and Remote Health</i> , 2020, 20, 6062.	0.4	4
5	The combination of NPM1, DNMT3A, and IDH1/2 mutations leads to inferior overall survival in AML. <i>American Journal of Hematology</i> , 2019, 94, 913-920.	2.0	31
6	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. <i>Clinical Cancer Research</i> , 2019, 25, 5135-5142.	3.2	14
7	The TP53 Apoptotic Network Is a Primary Mediator of Resistance to BCL2 Inhibition in AML Cells. <i>Cancer Discovery</i> , 2019, 9, 910-925.	7.7	215
8	CSF1R inhibitors exhibit antitumor activity in acute myeloid leukemia by blocking paracrine signals from support cells. <i>Blood</i> , 2019, 133, 588-599.	0.6	80
9	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018, 24, 679-690.	15.2	1,224
10	DeTiN: overcoming tumor-in-normal contamination. <i>Nature Methods</i> , 2018, 15, 531-534.	9.0	71
11	Sporadic Early-Onset Diffuse Gastric Cancers Have High Frequency of Somatic CDH1 Alterations, but Low Frequency of Somatic RHOA Mutations Compared With Late-Onset Cancers. <i>Gastroenterology</i> , 2017, 153, 536-549.e26.	0.6	90
12	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
13	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.	5.8	584
14	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017, 547, 55-60.	13.7	269
15	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. <i>Cell Reports</i> , 2016, 15, 857-865.	2.9	671
16	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
17	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016, 48, 848-855.	9.4	174
18	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. <i>Oncotarget</i> , 2016, 7, 52888-52899.	0.8	18

#	ARTICLE	IF	CITATIONS
19	Near universal detection of alterations in <i>CTNNB1</i> and Wnt pathway regulators in desmoid-type fibromatosis by whole-exome sequencing and genomic analysis. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 606-615.	1.5	138
20	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015, 5, 1164-1177.	7.7	821
21	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. <i>Genome Research</i> , 2015, 25, 1634-1645.	2.4	96
22	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015, 526, 525-530.	13.7	868
23	The genomic landscape of juvenile myelomonocytic leukemia. <i>Nature Genetics</i> , 2015, 47, 1326-1333.	9.4	233
24	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. <i>PLoS ONE</i> , 2014, 9, e87361.	1.1	168
25	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. <i>Cancer Discovery</i> , 2014, 4, 94-109.	7.7	782
26	The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.	7.7	415
27	MAP Kinase Pathway Alterations in <i>BRAF</i> -Mutant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. <i>Cancer Discovery</i> , 2014, 4, 61-68.	7.7	419
28	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	7.7	847
29	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.	9.4	495
30	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. <i>Nature Medicine</i> , 2014, 20, 682-688.	15.2	508
31	Comprehensive Genomic Analysis of Rhabdomyosarcoma Reveals a Landscape of Alterations Affecting a Common Genetic Axis in Fusion-Positive and Fusion-Negative Tumors. <i>Cancer Discovery</i> , 2014, 4, 216-231.	7.7	596
32	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. <i>New England Journal of Medicine</i> , 2014, 371, 1426-1433.	13.9	290
33	Whole-exome sequencing identifies a recurrent NAB2-STAT6 fusion in solitary fibrous tumors. <i>Nature Genetics</i> , 2013, 45, 131-132.	9.4	500
34	Depth-resolved optical imaging of hemodynamic response in mouse brain with microcirculatory beds. , 2011, , .		1