Mara Rosenberg

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/669920/publications.pdf

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34 papers 13,261 citations

172386 29 h-index 36 g-index

38 all docs

38 docs citations

38 times ranked 27181 citing authors

#	Article	IF	Citations
1	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
2	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	15.2	1,224
3	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
4	Mutations driving CLL and their evolution in progression and relapse. Nature, 2015, 526, 525-530.	13.7	868
5	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	7.7	847
6	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. Cancer Discovery, 2015, 5, 1164-1177.	7.7	821
7	The Genetic Landscape of Clinical Resistance to RAF Inhibition in Metastatic Melanoma. Cancer Discovery, 2014, 4, 94-109.	7.7	782
8	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. Cell Reports, 2016, 15, 857-865.	2.9	671
9	Comprehensive Genomic Analysis of Rhabdomyosarcoma Reveals a Landscape of Alterations Affecting a Common Genetic Axis in Fusion-Positive and Fusion-Negative Tumors. Cancer Discovery, 2014, 4, 216-231.	7.7	596
10	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	5.8	584
11	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. Nature Medicine, 2014, 20, 682-688.	15.2	508
12	Whole-exome sequencing identifies a recurrent NAB2-STAT6 fusion in solitary fibrous tumors. Nature Genetics, 2013, 45, 131-132.	9.4	500
13	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	9.4	495
14	MAP Kinase Pathway Alterations in <i>BRAF</i> Houtant Melanoma Patients with Acquired Resistance to Combined RAF/MEK Inhibition. Cancer Discovery, 2014, 4, 61-68.	7.7	419
15	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	7.7	415
16	Response and Acquired Resistance to Everolimus in Anaplastic Thyroid Cancer. New England Journal of Medicine, 2014, 371, 1426-1433.	13.9	290
17	Recurrent and functional regulatory mutations in breast cancer. Nature, 2017, 547, 55-60.	13.7	269
18	The genomic landscape of juvenile myelomonocytic leukemia. Nature Genetics, 2015, 47, 1326-1333.	9.4	233

#	Article	IF	CITATIONS
19	The TP53 Apoptotic Network Is a Primary Mediator of Resistance to BCL2 Inhibition in AML Cells. Cancer Discovery, 2019, 9, 910-925.	7.7	215
20	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. Nature Genetics, 2016, 48, 848-855.	9.4	174
21	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. PLoS ONE, 2014, 9, e87361.	1.1	168
22	Near universal detection of alterations in <scp><i>CTNNB1</i></scp> and <scp>Wnt</scp> pathway regulators in desmoidâ€type fibromatosis by wholeâ€exome sequencing and genomic analysis. Genes Chromosomes and Cancer, 2015, 54, 606-615.	1.5	138
23	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	2.4	96
24	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. Gastroenterology, 2017, 153, 536-549.e26.	0.6	90
25	CSF1R inhibitors exhibit antitumor activity in acute myeloid leukemia by blocking paracrine signals from support cells. Blood, 2019, 133, 588-599.	0.6	80
26	DeTiN: overcoming tumor-in-normal contamination. Nature Methods, 2018, 15, 531-534.	9.0	71
27	The combination of NPM1, DNMT3A, and IDH1/2 mutations leads to inferior overall survival in AML. American Journal of Hematology, 2019, 94, 913-920.	2.0	31
28	A comparative assessment of clinical whole exome and transcriptome profiling across sequencing centers: implications for precision cancer medicine. Oncotarget, 2016, 7, 52888-52899.	0.8	18
29	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. Clinical Cancer Research, 2019, 25, 5135-5142.	3.2	14
30	Butler enables rapid cloud-based analysis of thousands of human genomes. Nature Biotechnology, 2020, 38, 288-292.	9.4	11
31	Framework for quality assessment of whole genome cancer sequences. Nature Communications, 2020, 11, 5040.	5.8	5
32	Geographic differences in the unpaid caregiver experience from the National Study of Caregiving (NSOC). Rural and Remote Health, 2020, 20, 6062.	0.4	4
33	Depth-resolved optical imaging of hemodynamic response in mouse brain with microcirculatory beds. , $2011,$, .		1
34	Implementation of a prostate cancerâ€specific targeted sequencing panel for credentialing of patientâ€derived cell lines and genomic characterization of patient samples. Prostate, 2022, , .	1.2	1