

Mara Rosenberg

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

33 papers	9,188 citations	28 h-index	38 g-index
38 ext. papers	11,633 ext. citations	23.8 avg, IF	4.77 L-index

#	Paper	IF	Citations
33	Geographic differences in the unpaid caregiver experience from the National Study of Caregiving (NSOC). <i>Rural and Remote Health</i> , 2020 , 20, 6062	1.3	1
32	Butler enables rapid cloud-based analysis of thousands of human genomes. <i>Nature Biotechnology</i> , 2020 , 38, 288-292	44.5	9
31	Framework for quality assessment of whole genome cancer sequences. <i>Nature Communications</i> , 2020 , 11, 5040	17.4	1
30	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	7.1	19
29	Genomic Evolutionary Patterns of Leiomyosarcoma and Liposarcoma. <i>Clinical Cancer Research</i> , 2019 , 25, 5135-5142	12.9	11
28	The TP53 Apoptotic Network Is a Primary Mediator of Resistance to BCL2 Inhibition in AML Cells. <i>Cancer Discovery</i> , 2019 , 9, 910-925	24.4	98
27	CSF1R inhibitors exhibit antitumor activity in acute myeloid leukemia by blocking paracrine signals from support cells. <i>Blood</i> , 2019 , 133, 588-599	2.2	53
26	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018 , 24, 679-690	50.5	659
25	DeTiN: overcoming tumor-in-normal contamination. <i>Nature Methods</i> , 2018 , 15, 531-534	21.6	32
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. <i>Gastroenterology</i> , 2017 , 153, 536-549.e26	13.3	63
23	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	24.9	13896
22	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017 , 8, 1324	17.4	314
21	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017 , 547, 55-60	50.4	192
20	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. <i>Nature Genetics</i> , 2016 , 48, 848-55	36.3	135
19	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	3.3	14
18	Genomic Correlates of Immune-Cell Infiltrates in Colorectal Carcinoma. <i>Cell Reports</i> , 2016 , 15, 857-865	10.6	422
17	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16	36.3	613

16	Genomic Characterization of Brain Metastases Reveals Branched Evolution and Potential Therapeutic Targets. <i>Cancer Discovery</i> , 2015 , 5, 1164-1177	24.4	581
15	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. <i>Genome Research</i> , 2015 , 25, 1634-45	9.7	56
14	Mutations driving CLL and their evolution in progression and relapse. <i>Nature</i> , 2015 , 526, 525-30	50.4	658
13	The genomic landscape of juvenile myelomonocytic leukemia. <i>Nature Genetics</i> , 2015 , 47, 1326-1333	36.3	166
12	Near universal detection of alterations in CTNNB1 and Wnt pathway regulators in desmoid-type fibromatosis by whole-exome sequencing and genomic analysis. <i>Genes Chromosomes and Cancer</i> , 2015 , 54, 606-15	5	84
11	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. <i>Cancer Cell</i> , 2014 , 25, 91-101	24.3	657
10	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014 , 32, 479-84	44.5	434
9	Whole-exome sequencing and clinical interpretation of formalin-fixed, paraffin-embedded tumor samples to guide precision cancer medicine. <i>Nature Medicine</i> , 2014 , 20, 682-8	50.5	406
8	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, 216-31	24.4	417
7	Response and acquired resistance to everolimus in anaplastic thyroid cancer. <i>New England Journal of Medicine</i> , 2014 , 371, 1426-33	59.2	237
6	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	3.7	112
5	The genetic landscape of clinical resistance to RAF inhibition in metastatic melanoma. <i>Cancer Discovery</i> , 2014 , 4, 94-109	24.4	626
4	The genomic landscape of pediatric Ewing sarcoma. <i>Cancer Discovery</i> , 2014 , 4, 1326-41	24.4	302
3	MAP kinase pathway alterations in BRAF-mutant melanoma patients with acquired resistance to combined RAF/MEK inhibition. <i>Cancer Discovery</i> , 2014 , 4, 61-8	24.4	351
2	Whole-exome sequencing identifies a recurrent NAB2-STAT6 fusion in solitary fibrous tumors. <i>Nature Genetics</i> , 2013 , 45, 131-2	36.3	386
1	Depth-resolved optical imaging of hemodynamic response in mouse brain with microcirculatory beds 2011 ,		1