Jeremiah A Wala

List of Publications by Year
in descending order

22 papers	6,942 citations	430874 18 h-index	580821 25 g-index
32 all docs	32 docs citations	32 times ranked	15144 citing authors

#	Article	IF	Citations
1	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	21.4	1,616
2	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	30.7	1,224
3	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	21.4	933
4	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	27.8	560
5	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
6	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
7	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
8	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	28.9	258
9	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
10	MYB-QKI rearrangements in angiocentric glioma drive tumorigenicity through a tripartite mechanism. Nature Genetics, 2016, 48, 273-282.	21.4	214
11	The genomic landscape and evolution of endometrial carcinoma progression and abdominopelvic metastasis. Nature Genetics, 2016, 48, 848-855.	21.4	174
12	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	28.9	141
13	Genomic landscape of high-grade meningiomas. Npj Genomic Medicine, 2017, 2, .	3.8	130
14	Multicriteria VMAT optimization. Medical Physics, 2012, 39, 686-696.	3.0	97
15	Renal medullary carcinomas depend upon SMARCB1 loss and are sensitive to proteasome inhibition. ELife, 2019, 8, .	6.0	32
16	Maximizing dosimetric benefits of IMRT in the treatment of localized prostate cancer through multicriteria optimization planning. Medical Dosimetry, 2013, 38, 298-303.	0.9	27
17	VariantBam: filtering and profiling of next-generational sequencing data using region-specific rules. Bioinformatics, 2016, 32, 2029-2031.	4.1	25
18	Genomic Heterogeneity and Exceptional Response to Dual Pathway Inhibition in Anaplastic Thyroid Cancer. Clinical Cancer Research, 2017, 23, 2367-2373.	7.0	24

#	Article	IF	Citations
19	Structural variants shape driver combinations and outcomes in pediatric high-grade glioma. Nature Cancer, 2022, 3, 994-1011.	13.2	20
20	SeqLib: a Câ€‰++ API for rapid BAM manipulation, sequence alignment and sequence assembly. Bioinformatics, 2017, 33, 751-753.	4.1	12
21	Haplotype-resolved germline and somatic alterations in renal medullary carcinomas. Genome Medicine, 2021, 13, 114.	8.2	5
22	The oncogene makes its escape. Science, 2016, 351, 1398-1399.	12.6	4