

Robin M Meyers

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

6,498
citations

361413

20
h-index

713466

21
g-index

23
all docs

23
docs citations

23
times ranked

11214
citing authors

#	ARTICLE	IF	CITATIONS
1	A genome-wide atlas of co-essential modules assigns function to uncharacterized genes. <i>Nature Genetics</i> , 2021, 53, 638-649.	21.4	86
2	Multimodal Analysis of Composition and Spatial Architecture in Human Squamous Cell Carcinoma. <i>Cell</i> , 2020, 182, 497-514.e22.	28.9	508
3	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. <i>Cell Reports</i> , 2019, 28, 2331-2344.e8.	6.4	24
4	Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. <i>Cell Systems</i> , 2018, 6, 555-568.e7.	6.2	126
5	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. <i>Nature Communications</i> , 2018, 9, 2024.	12.8	80
6	Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , 2017, 49, 1779-1784.	21.4	1,436
7	Defining a Cancer Dependency Map. <i>Cell</i> , 2017, 170, 564-576.e16.	28.9	1,794
8	Sequence intrinsic somatic mutation mechanisms contribute to affinity maturation of VRC01-class HIV-1 broadly neutralizing antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8614-8619.	7.1	42
9	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2017, 128, 446-462.	8.2	117
10	Detecting DNA double-stranded breaks in mammalian genomes by linear amplification-mediated high-throughput genome-wide translocation sequencing. <i>Nature Protocols</i> , 2016, 11, 853-871.	12.0	213
11	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016, 6, 914-929.	9.4	485
12	Transcription-associated processes cause DNA double-strand breaks and translocations in neural stem/progenitor cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2258-2263.	7.1	88
13	Long Neural Genes Harbor Recurrent DNA Break Clusters in Neural Stem/Progenitor Cells. <i>Cell</i> , 2016, 164, 644-655.	28.9	225
14	Rapid generation of novel models of RAG1 deficiency by CRISPR/Cas9-induced mutagenesis in murine zygotes. <i>Oncotarget</i> , 2016, 7, 12962-12974.	1.8	11
15	Chromosomal Loop Domains Direct the Recombination of Antigen Receptor Genes. <i>Cell</i> , 2015, 163, 947-959.	28.9	140
16	Orientation-specific joining of AID-initiated DNA breaks promotes antibody class switching. <i>Nature</i> , 2015, 525, 134-139.	27.8	93
17	Sequence-Intrinsic Mechanisms that Target AID Mutational Outcomes on Antibody Genes. <i>Cell</i> , 2015, 163, 1124-1137.	28.9	136
18	Genome-wide detection of DNA double-stranded breaks induced by engineered nucleases. <i>Nature Biotechnology</i> , 2015, 33, 179-186.	17.5	590

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19	Developmental propagation of V(D)J recombination-associated DNA breaks and translocations in mature B cells via dicentric chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10269-10274.	7.1	32
20	Convergent Transcription at Intragenic Super-Enhancers Targets AID-Initiated Genomic Instability. <i>Cell</i> , 2014, 159, 1538-1548.	28.9	221
21	<i>IgH</i> class switching exploits a general property of two DNA breaks to be joined <i>in cis</i> over long chromosomal distances. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2644-2649.	7.1	33