

Mamie Z Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5835689/publications.pdf>

Version: 2024-02-01

25
papers

4,853
citations

331670

21
h-index

580821

25
g-index

26
all docs

26
docs citations

26
times ranked

10390
citing authors

#	ARTICLE	IF	CITATIONS
1	Harnessing homologous recombination in vitro to generate recombinant DNA via SLIC. <i>Nature Methods</i> , 2007, 4, 251-256.	19.0	845
2	The DNA damage response induces inflammation and senescence by inhibiting autophagy of GATA4. <i>Science</i> , 2015, 349, aaa5612.	12.6	693
3	Viral epitope profiling of COVID-19 patients reveals cross-reactivity and correlates of severity. <i>Science</i> , 2020, 370, .	12.6	511
4	Cancer Proliferation Gene Discovery Through Functional Genomics. <i>Science</i> , 2008, 319, 620-624.	12.6	365
5	Comprehensive serological profiling of human populations using a synthetic human virome. <i>Science</i> , 2015, 348, aaa0698.	12.6	364
6	Measles virus infection diminishes preexisting antibodies that offer protection from other pathogens. <i>Science</i> , 2019, 366, 599-606.	12.6	294
7	Autoantigen discovery with a synthetic human peptidome. <i>Nature Biotechnology</i> , 2011, 29, 535-541.	17.5	267
8	SLIC: A Method for Sequence- and Ligation-Independent Cloning. <i>Methods in Molecular Biology</i> , 2012, 852, 51-59.	0.9	220
9	The Eukaryotic Proteome Is Shaped by E3 Ubiquitin Ligases Targeting C-Terminal Degrons. <i>Cell</i> , 2018, 173, 1622-1635.e14.	28.9	198
10	Recurrent Hemizygous Deletions in Cancers May Optimize Proliferative Potential. <i>Science</i> , 2012, 337, 104-109.	12.6	172
11	Profound Tissue Specificity in Proliferation Control Underlies Cancer Drivers and Aneuploidy Patterns. <i>Cell</i> , 2018, 173, 499-514.e23.	28.9	147
12	MAGIC, an in vivo genetic method for the rapid construction of recombinant DNA molecules. <i>Nature Genetics</i> , 2005, 37, 311-319.	21.4	124
13	The adaptive immune system is a major driver of selection for tumor suppressor gene inactivation. <i>Science</i> , 2021, 373, 1327-1335.	12.6	83
14	Systematic autoantigen analysis identifies a distinct subtype of scleroderma with coincident cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7526-E7534.	7.1	75
15	A Role for Mitochondrial Translation in Promotion of Viability in K-Ras Mutant Cells. <i>Cell Reports</i> , 2017, 20, 427-438.	6.4	73
16	Sources of Error in Mammalian Genetic Screens. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2781-2790.	1.8	64
17	A genetic interaction analysis identifies cancer drivers that modify EGFR dependency. <i>Genes and Development</i> , 2017, 31, 184-196.	5.9	58
18	Antibody responses to endemic coronaviruses modulate COVID-19 convalescent plasma functionality. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	58

#	ARTICLE	IF	CITATIONS
19	Integrated proteogenetic analysis reveals the landscape of a mitochondrial-autophagosome synapse during PARK2-dependent mitophagy. <i>Science Advances</i> , 2019, 5, eaay4624.	10.3	55
20	A Druggable Genome Screen Identifies Modifiers of α -Synuclein Levels via a Tiered Cross-Species Validation Approach. <i>Journal of Neuroscience</i> , 2018, 38, 9286-9301.	3.6	49
21	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	9.4	43
22	High-resolution epitope mapping by AllerScan reveals relationships between IgE and IgG repertoires during peanut oral immunotherapy. <i>Cell Reports Medicine</i> , 2021, 2, 100410.	6.5	25
23	Gain-of-function genetic screening identifies the antiviral function of TMEM120A via STING activation. <i>Nature Communications</i> , 2022, 13, 105.	12.8	17
24	Functional genomics reveals that tumors with activating phosphoinositide 3-kinase mutations are dependent on accelerated protein turnover. <i>Genes and Development</i> , 2016, 30, 2684-2695.	5.9	11
25	Diversified Application of Barcoded PLATO (PLATO-BC) Platform for Identification of Protein Interactions. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 319-331.	6.9	5