

Glenn S Cowley

List of Publications by Year in descending order

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Version: 2024-02-01

12
papers

3,228
citations

840776

11
h-index

1199594

12
g-index

13
all docs

13
docs citations

13
times ranked

7393
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016, 6, 914-929.	9.4	485
3	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E5564-73.	7.1	355
4	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , 2014, 1, 140035.	5.3	328
5	SQSTM1 Is a Pathogenic Target of 5q Copy Number Gains in Kidney Cancer. <i>Cancer Cell</i> , 2013, 24, 738-750.	16.8	135
6	Small-molecule targeting of brachyury transcription factor addiction in chordoma. <i>Nature Medicine</i> , 2019, 25, 292-300.	30.7	120
7	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2017, 128, 446-462.	8.2	117
8	Genome-wide screen identifies cullin-RING ligase machinery required for lenalidomide-dependent CRL4CRBN activity. <i>Blood</i> , 2018, 132, 1293-1303.	1.4	97
9	Functional, chemical genomic, and super-enhancer screening identify sensitivity to cyclin D1/CDK4 pathway inhibition in Ewing sarcoma. <i>Oncotarget</i> , 2015, 6, 30178-30193.	1.8	68
10	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. <i>Nature Communications</i> , 2019, 10, 2400.	12.8	37
11	HIF activation causes synthetic lethality between the <i>VHL</i> tumor suppressor and the <i>EZH1</i> histone methyltransferase. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	36
12	A genome-wide gain-of-function screen identifies CDKN2C as a HBV host factor. <i>Nature Communications</i> , 2020, 11, 2707.	12.8	11