

Computational correction of copy number effect improves essentiality screens in cancer cells

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Citation Report

#	ARTICLE	IF	CITATIONS
2	High-Throughput Approaches to Pinpoint Function within the Noncoding Genome. <i>Molecular Cell</i> , 2017, 68, 44-59.	4.5	54
3	Dual direction CRISPR transcriptional regulation screening uncovers gene networks driving drug resistance. <i>Scientific Reports</i> , 2017, 7, 17693.	1.6	43
4	Impact of Genetic Variation on CRISPR-Cas Targeting. <i>CRISPR Journal</i> , 2018, 1, 159-170.	1.4	24
5	Review of CRISPR/Cas9 sgRNA Design Tools. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2018, 10, 455-465.	2.2	180
6	EWS/FLI Confers Tumor Cell Synthetic Lethality to CDK12 Inhibition in Ewing Sarcoma. <i>Cancer Cell</i> , 2018, 33, 202-216.e6.	7.7	116
7	Disruption of mammalian SWI/SNF and polycomb complexes in human sarcomas: mechanisms and therapeutic opportunities. <i>Journal of Pathology</i> , 2018, 244, 638-649.	2.1	30
8	Targeting MYC dependency in ovarian cancer through inhibition of CDK7 and CDK12/13. <i>ELife</i> , 2018, 7, .	2.8	109
9	Early developmental arrest and impaired gastrointestinal homeostasis in U12-dependent splicing-defective <i>Rnpc3</i> -deficient mice. <i>Rna</i> , 2018, 24, 1856-1870.	1.6	24
10	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. <i>Nature Communications</i> , 2018, 9, 4610.	5.8	290
11	Optimized libraries for CRISPR-Cas9 genetic screens with multiple modalities. <i>Nature Communications</i> , 2018, 9, 5416.	5.8	535
12	High-resolution mapping of cancer cell networks using co-functional interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8594.	3.2	61
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16	Protein interaction and functional data indicate MTHFD2 involvement in RNA processing and translation. <i>Cancer & Metabolism</i> , 2018, 6, 12.	2.4	32
17	Precision Targeting of BFL-1/A1 and an ATM Co-dependency in Human Cancer. <i>Cell Reports</i> , 2018, 24, 3393-3403.e5.	2.9	15
18	CRISPhieRmix: a hierarchical mixture model for CRISPR pooled screens. <i>Genome Biology</i> , 2018, 19, 159.	3.8	36
19	A non-canonical SWI/SNF complex is a synthetic lethal target in cancers driven by BAF complex perturbation. <i>Nature Cell Biology</i> , 2018, 20, 1410-1420.	4.6	265

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20	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387.	9.4	334
21	Recent advances in combinatorial drug screening and synergy scoring. <i>Current Opinion in Pharmacology</i> , 2018, 42, 102-110.	1.7	80
22	ESS: A Tool for Genome-Scale Quantification of Essentiality Score for Reaction/Genes in Constraint-Based Modeling. <i>Frontiers in Physiology</i> , 2018, 9, 1355.	1.3	8
23	Contribution of allelic imbalance to colorectal cancer. <i>Nature Communications</i> , 2018, 9, 3664.	5.8	25
24	Interrogation of Mammalian Protein Complex Structure, Function, and Membership Using Genome-Scale Fitness Screens. <i>Cell Systems</i> , 2018, 6, 555-568.e7.	2.9	126
25	Targetable vulnerabilities in T- and NK-cell lymphomas identified through preclinical models. <i>Nature Communications</i> , 2018, 9, 2024.	5.8	80
26	Improved design and analysis of CRISPR knockout screens. <i>Bioinformatics</i> , 2018, 34, 4095-4101.	1.8	44
27	Synthetic lethal therapies for cancer: what's next after PARP inhibitors?. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 564-576.	12.5	303
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29	Synthetic Lethal Networks for Precision Oncology: Promises and Pitfalls. <i>Journal of Molecular Biology</i> , 2018, 430, 2900-2912.	2.0	21
30	Correction of copy number induced false positives in CRISPR screens. <i>PLoS Computational Biology</i> , 2018, 14, e1006279.	1.5	14
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39	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018, 560, 325-330.	13.7	662
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44	PAX8 activates metabolic genes via enhancer elements in Renal Cell Carcinoma. <i>Nature Communications</i> , 2019, 10, 3739.	5.8	49
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54	Chemical genomics reveals histone deacetylases are required for core regulatory transcription. <i>Nature Communications</i> , 2019, 10, 3004.	5.8	107
55	Essential genes shape cancer genomes through linear limitation of homozygous deletions. <i>Communications Biology</i> , 2019, 2, 262.	2.0	13

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57	Large-scale datasets uncovering cell signalling networks in cancer: context matters. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 118-124.	1.5	9
58	A ZDHHC5-GOLGA7 Protein Acyltransferase Complex Promotes Nonapoptotic Cell Death. <i>Cell Chemical Biology</i> , 2019, 26, 1716-1724.e9.	2.5	40
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90	Guide RNAs with embedded barcodes boost CRISPR-pooled screens. <i>Genome Biology</i> , 2019, 20, 20.	3.8	50
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161	Translational genomics and recent advances in oral squamous cell carcinoma. <i>Seminars in Cancer Biology</i> , 2020, 61, 71-83.	4.3	150
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