David E Root

List of Publications by Year
in descending order

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51 papers	23,392 citations	101543 36 h-index	182427 51 g-index
55 all docs	55 docs citations	55 times ranked	36837 citing authors

#	Article	IF	Citations
1	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. Science, 2014, 343, 84-87.	12.6	4,210
2	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. Nature Biotechnology, 2016, 34, 184-191.	17.5	3,168
3	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. Cell, 2017, 171, 1437-1452.e17.	28.9	2,281
4	Defining a Cancer Dependency Map. Cell, 2017, 170, 564-576.e16.	28.9	1,794
5	Computational correction of copy number effect improves specificity of CRISPRâ€“Cas9 essentiality screens in cancer cells. Nature Genetics, 2017, 49, 1779-1784.	21.4	1,436
6	Rational design of highly active sgRNAs for CRISPR-Cas9â€“mediated gene inactivation. Nature Biotechnology, 2014, 32, 1262-1267.	17.5	1,351
7	COT drives resistance to RAF inhibition through MAP kinase pathway reactivation. Nature, 2010, 468, 968-972.	27.8	1,325
8	Identification of RPS14 as a 5q- syndrome gene by RNA interference screen. Nature, 2008, 451, 335-339.	27.8	850
9	KRAS and YAP1 Converge to Regulate EMT and Tumor Survival. Cell, 2014, 158, 171-184.	28.9	608
10	A public genome-scale lentiviral expression library of human ORFs. Nature Methods, 2011, 8, 659-661.	19.0	477
11	A melanocyte lineage program confers resistance to MAP kinase pathway inhibition. Nature, 2013, 504, 138-142.	27.8	401
12	MTAP deletion confers enhanced dependency on the PRMT5 arginine methyltransferase in cancer cells. Science, 2016, 351, 1214-1218.	12.6	396
13	Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12372-12377.	7.1	383
14	The landscape of cancer cell line metabolism. Nature Medicine, 2019, 25, 850-860.	30.7	350
15	Mutational processes shape the landscape of TP53 mutations in human cancer. Nature Genetics, 2018, 50, 1381-1387.	21.4	334
16	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. Scientific Data, 2014, 1, 140035.	5.3	328
17	A Genome-Scale RNA Interference Screen Implicates NF1 Loss in Resistance to RAF Inhibition. Cancer Discovery, 2013, 3, 350-362.	9.4	299
18	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. Nature Communications, 2018, 9, 4610.	12.8	290

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19	A dominant-negative effect drives selection of TP53 missense mutations in myeloid malignancies. Science, 2019, 365, 599-604.	12.6	265
20	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. Nature, 2019, 568, 551-556.	27.8	253
21	A Genome-wide CRISPR Death Screen Identifies Genes Essential for Oxidative Phosphorylation. Cell Metabolism, 2016, 24, 875-885.	16.2	244
22	Orthologous CRISPRâ€“Cas9 enzymes for combinatorial genetic screens. Nature Biotechnology, 2018, 36, 179-189.	17.5	216
23	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. Nature Genetics, 2018, 50, 1240-1246.	21.4	199
24	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	16.8	171
25	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
26	A Functional Landscape of Resistance to ALK Inhibition in Lung Cancer. Cancer Cell, 2015, 27, 397-408.	16.8	150
27	Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. Cell Reports, 2016, 17, 1171-1183.	6.4	119
28	Cells Lacking the RB1 Tumor Suppressor Gene Are Hyperdependent on Aurora B Kinase for Survival. Cancer Discovery, 2019, 9, 230-247.	9.4	119
29	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. Journal of Clinical Investigation, 2017, 128, 446-462.	8.2	117
30	Complementary information derived from CRISPR Cas9 mediated gene deletion and suppression. Nature Communications, 2017, 8, 15403.	12.8	93
31	Acquired FGFR and FGF Alterations Confer Resistance to Estrogen Receptor (ER) Targeted Therapy in ER+ Metastatic Breast Cancer. Clinical Cancer Research, 2020, 26, 5974-5989.	7.0	87
32	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. Nature Biotechnology, 2021, 39, 697-704.	17.5	85
33	Csnk1a1 inhibition has p53-dependent therapeutic efficacy in acute myeloid leukemia. Journal of Experimental Medicine, 2014, 211, 605-612.	8.5	79
34	The Canonical Wnt Pathway Drives Macropinocytosis in Cancer. Cancer Research, 2018, 78, 4658-4670.	0.9	75
35	Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. Nature Genetics, 2021, 53, 1664-1672.	21.4	61
36	Genetic modifiers of EGFR dependence in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18661-18666.	7.1	46

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37	Neuronal differentiation and cell-cycle programs mediate response to BET-bromodomain inhibition in MYC-driven medulloblastoma. Nature Communications, 2019, 10, 2400.	12.8	37
38	A Functional Landscape of Resistance to MEK1/2 and CDK4/6 Inhibition in NRAS-Mutant Melanoma. Cancer Research, 2019, 79, 2352-2366.	0.9	34
39	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. Nature Structural and Molecular Biology, 2020, 27, 92-104.	8.2	30
40	LKB1/STK11 Is a Tumor Suppressor in the Progression of Myeloproliferative Neoplasms. Cancer Discovery, 2021, 11, 1398-1410.	9.4	29
41	Structureâ€“function analysis of the SHOC2â€“MRASâ€“PP1C holophosphatase complex. Nature, 2022, 609, 408-415.	27.8	28
42	Progression signature underlies clonal evolution and dissemination of multiple myeloma. Blood, 2021, 137, 2360-2372.	1.4	26
43	PPM1D mutations are oncogenic drivers of de novo diffuse midline glioma formation. Nature Communications, 2022, 13, 604.	12.8	22
44	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. Cancer Discovery, 2021, 11, 2282-2299.	9.4	21
45	Phosphate dysregulation via the XPR1â€“KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. Nature Cancer, 2022, 3, 681-695.	13.2	21
46	Pooled Lentiviralâ€Delivery Genetic Screens. Current Protocols in Molecular Biology, 2018, 121, 32.1.1-32.1.21.	2.9	20
47	Allosteric inhibition of PPM1D serine/threonine phosphatase via an altered conformational state. Nature Communications, 2022, 13, .	12.8	15
48	A Genome-scale CRISPR Screen Identifies the ERBB and mTOR Signaling Networks as Key Determinants of Response to PI3K Inhibition in Pancreatic Cancer. Molecular Cancer Therapeutics, 2020, 19, 1423-1435.	4.1	14
49	Systematic identification of biomarker-driven drug combinations to overcome resistance. Nature Chemical Biology, 2022, 18, 615-624.	8.0	14
50	A genome-wide gain-of-function screen identifies CDKN2C as a HBV host factor. Nature Communications, 2020, 11, 2707.	12.8	11
51	Genetic barcoding systematically compares genes in del(5q) MDS and reveals a central role for CSNK1A1 in clonal expansion. Blood Advances, 2022, 6, 1780-1796.	5.2	7