Kevin R Brown

List of Publications by Year
in descending order

56 papers	6,920 citations	172457 29 h-index	168389 53 g-index
66 all docs	66 docs citations	66 times ranked	12078 citing authors

#	Article	IF	Citations
1	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. Cell, 2015, 163, 1515-1526.	28.9	1,339
2	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. Science, 2005, 307, 1621-1625.	12.6	651
3	Online Predicted Human Interaction Database. Bioinformatics, 2005, 21, 2076-2082.	4.1	557
4	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. G3: Genes, Genomes, Genetics, 2017, 7, 2719-2727.	1.8	417
5	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. Cell, 2016, 164, 293-309.	28.9	399
6	Measuring error rates in genomic perturbation screens: gold standards for human functional genomics. Molecular Systems Biology, 2014, 10, 733.	7.2	322
7	Unequal evolutionary conservation of human protein interactions in interologous networks. Genome Biology, 2007, 8, R95.	9.6	308
8	Essential Gene Profiles in Breast, Pancreatic, and Ovarian Cancer Cells. Cancer Discovery, 2012, 2, 172-189.	9.4	276
9	Genome-wide CRISPR screens reveal a Wnt–FZD5 signaling circuit as a druggable vulnerability of RNF43-mutant pancreatic tumors. Nature Medicine, 2017, 23, 60-68.	30.7	261
10	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. Cell, 2021, 184, 226-242.e21.	28.9	258
11	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. Nature, 2020, 586, 120-126.	27.8	249
12	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. Bioinformatics, 2009, 25, 3327-3329.	4.1	234
13	Connective Tissue Disease-associated Interstitial Lung Diseases (CTD-ILD) â€" Report from OMERACT CTD-ILD Working Group. Journal of Rheumatology, 2015, 42, 2168-2171.	2.0	142
14	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. Molecular Cell, 2016, 62, 121-136.	9.7	142
15	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. Science Signaling, 2009, 2, ra84.	3.6	140
16	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. Molecular Systems Biology, 2013, 9, 696.	7.2	90
17	Essential Gene Profiles for Human Pluripotent Stem Cells Identify Uncharacterized Genes and Substrate Dependencies. Cell Reports, 2019, 27, 599-615.e12.	6.4	85
18	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9–Cas12a platform. Nature Biotechnology, 2020, 38, 638-648.	17.5	85

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19	Systematic identification of SH3 domain-mediated human protein–protein interactions by peptide array target screening. Proteomics, 2007, 7, 1775-1785.	2.2	74
20	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. Nature Metabolism, 2020, 2, 499-513.	11.9	72
21	Identification of novel ATP13A2 interactors and their role in α-synuclein misfolding and toxicity. Human Molecular Genetics, 2012, 21, 3785-3794.	2.9	66
22	Identification of P450 Oxidoreductase as a Major Determinant of Sensitivity to Hypoxia-Activated Prodrugs. Cancer Research, 2015, 75, 4211-4223.	0.9	65
23	Integrated proteomic and transcriptomic profiling of mouse lung development and Nmyc target genes. Molecular Systems Biology, 2007, 3, 109.	7.2	64
24	Genome-wide RNAi analysis reveals that simultaneous inhibition of specific mevalonate pathway genes potentiates tumor cell death. Oncotarget, 2015, 6, 26909-26921.	1.8	52
25	COLT-Cancer: functional genetic screening resource for essential genes in human cancer cell lines. Nucleic Acids Research, 2012, 40, D957-D963.	14.5	46
26	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. Cancer Discovery, 2022, 12, 1022-1045.	9.4	43
27	Interrogation of Functional Cell-Surface Markers Identifies CD151 Dependency in High-Grade Serous Ovarian Cancer. Cell Reports, 2017, 18, 2343-2358.	6.4	38
28	Cotargeting Ephrin Receptor Tyrosine Kinases A2 and A3 in Cancer Stem Cells Reduces Growth of Recurrent Glioblastoma. Cancer Research, 2018, 78, 5023-5037.	0.9	36
29	CRISPR screens are feasible in *TP* 53 wild–type cells. Molecular Systems Biology, 2019, 15, e8679.	7.2	32
30	A comprehensive platform for highly multiplexed mammalian functional genetic screens. BMC Genomics, 2011, 12, 213.	2.8	31
31	CD70 as an actionable immunotherapeutic target in recurrent glioblastoma and its microenvironment. , 2022, 10, e003289.		31
32	Substrate specificity of the p53-associated 3′-5′ exonuclease. Oncogene, 2000, 19, 3321-3329.	5.9	30
33	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. Acta Neuropathologica, 2017, 134, 923-940.	7.7	26
34	Functional genomics identifies new synergistic therapies for retinoblastoma. Oncogene, 2020, 39, 5338-5357.	5.9	26
35	Efficient generation of patient-matched malignant and normal primary cell cultures from clear cell renal cell carcinoma patients: clinically relevant models for research and personalized medicine. BMC Cancer, 2016, 16, 485.	2.6	23
36	A Novel Role for NUAK1 in Promoting Ovarian Cancer Metastasis through Regulation of Fibronectin Production in Spheroids. Cancers, 2020, 12, 1250.	3.7	20

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37	Haploinsufficiency of RREB1 causes a Noonan-like RASopathy via epigenetic reprogramming of RAS-MAPK pathway genes. Nature Communications, 2020, 11, 4673.	12.8	19
38	An oncogenic KRAS transcription program activates the RHOGEF ARHGEF2 to mediate transformed phenotypes in pancreatic cancer. Oncotarget, 2017, 8, 4484-4500.	1.8	18
39	NOX4 links metabolic regulation in pancreatic cancer to endoplasmic reticulum redox vulnerability and dependence on PRDX4. Science Advances, 2021, 7, .	10.3	15
40	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. Journal of Neuro-Oncology, 2019, 143, 417-428.	2.9	13
41	Targeting the centriolar replication factor STIL synergizes with DNA damaging agents for treatment of ovarian cancer. Oncotarget, 2017, 8, 27380-27392.	1.8	13
42	Inhibition of relaxin autocrine signaling confers therapeutic vulnerability in ovarian cancer. Journal of Clinical Investigation, 2021, 131, .	8.2	12
43	A nuclear 3â€²â€"5â€² exonuclease proofreads for the exonuclease-deficient DNA polymerase Î±. DNA Repair, 2002, 1, 795-810.	2.8	11
44	A rapid in vitro methodology for simultaneous target discovery and antibody generation against functional cell subpopulations. Scientific Reports, 2019, 9, 842.	3.3	10
45	RAD51-Mediated DNA Homologous Recombination Is Independent of PTEN Mutational Status. Cancers, 2020, 12, 3178.	3.7	10
46	Pooled CRISPR-Based Genetic Screens in Mammalian Cells. Journal of Visualized Experiments, 2019, , .	0.3	9
47	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. Molecular Systems Biology, 2021, 17, e10013.	7.2	8
48	A 3â€²-5â€² Exonuclease in Human Leukemia Cells. Journal of Biological Chemistry, 2000, 275, 25814-25819.	3.4	7
49	Analysis of combinatorial CRISPR screens with the Orthrus scoring pipeline. Nature Protocols, 2021, 16, 4766-4798.	12.0	7
50	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. G3: Genes, Genomes, Genetics, 2013, 3, 1375-1387.	1.8	5
51	Forward genetic screen in human podocytes identifies diphthamide biosynthesis genes as regulators of adhesion. American Journal of Physiology - Renal Physiology, 2019, 317, F1593-F1604.	2.7	4
52	Integrated Genomic, Transcriptomic, and RNA-Interference Analysis of Genes in Somatic Copy Number Gains in Pancreatic Ductal Adenocarcinoma. Pancreas, 2013, 42, 1016-1026.	1.1	3
53	Functional genomic characterization of a synthetic anti-HER3 antibody reveals a role for ubiquitination by RNF41 in the anti-proliferative response. Journal of Biological Chemistry, 2019, 294, 1396-1409.	3.4	3
54	MEDU-44. MUSASHI-1 IS A MASTER REGULATOR OF ABERRANT TRANSLATION IN GROUP 3 MEDULLOBLASTOMA. Neuro-Oncology, 2019, 21, ii112-ii113.	1.2	0

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55	Systematic Genome-Scale Identification of Host Factors for SARS-CoV-2 Infection Across Models Yields a Core Single Gene Dependency; <i>Ace2</i>. SSRN Electronic Journal, 0, , .	0.4	0
56	High-Throughput Screening of Protein Interaction Networks in the TGFÎ² Interactome: Understanding the Signaling Mechanisms Driving Tumor Progression. , 2008, , 265-284.		0