

# Kevin R Brown

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

6,920  
citations

172207  
29  
h-index

168136  
53  
g-index

66  
all docs

66  
docs citations

66  
times ranked

12078  
citing authors

#	ARTICLE	IF	CITATIONS
1	CD70 as an actionable immunotherapeutic target in recurrent glioblastoma and its microenvironment. , 2022, 10, e003289.		31
2	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. Cancer Discovery, 2022, 12, 1022-1045.	7.7	43
3	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. Cell, 2021, 184, 226-242.e21.	13.5	258
4	Inhibition of relaxin autocrine signaling confers therapeutic vulnerability in ovarian cancer. Journal of Clinical Investigation, 2021, 131, .	3.9	12
5	NOX4 links metabolic regulation in pancreatic cancer to endoplasmic reticulum redox vulnerability and dependence on PRDX4. Science Advances, 2021, 7, .	4.7	15
6	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. Molecular Systems Biology, 2021, 17, e10013.	3.2	8
7	Analysis of combinatorial CRISPR screens with the Orthrus scoring pipeline. Nature Protocols, 2021, 16, 4766-4798.	5.5	7
8	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. Nature, 2020, 586, 120-126.	13.7	249
9	Haploinsufficiency of RREB1 causes a Noonan-like RASopathy via epigenetic reprogramming of RAS-MAPK pathway genes. Nature Communications, 2020, 11, 4673.	5.8	19
10	RAD51-Mediated DNA Homologous Recombination Is Independent of PTEN Mutational Status. Cancers, 2020, 12, 3178.	1.7	10
11	A Novel Role for NUA1 in Promoting Ovarian Cancer Metastasis through Regulation of Fibronectin Production in Spheroids. Cancers, 2020, 12, 1250.	1.7	20
12	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.	5.1	72
13	Functional genomics identifies new synergistic therapies for retinoblastoma. Oncogene, 2020, 39, 5338-5357.	2.6	26
14	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9â€“Cas12a platform. Nature Biotechnology, 2020, 38, 638-648.	9.4	85
15	MEDU-44. MUSASHI-1 IS A MASTER REGULATOR OF ABERRANT TRANSLATION IN GROUP 3 MEDULLOBLASTOMA. Neuro-Oncology, 2019, 21, ii112-ii113.	0.6	0
16	Pooled CRISPR-Based Genetic Screens in Mammalian Cells. Journal of Visualized Experiments, 2019, , .	0.2	9
17	Forward genetic screen in human podocytes identifies diphthamide biosynthesis genes as regulators of adhesion. American Journal of Physiology - Renal Physiology, 2019, 317, F1593-F1604.	1.3	4
18	A rapid in vitro methodology for simultaneous target discovery and antibody generation against functional cell subpopulations. Scientific Reports, 2019, 9, 842.	1.6	10

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19	Bmi1 regulates human glioblastoma stem cells through activation of differential gene networks in CD133+ brain tumor initiating cells. <i>Journal of Neuro-Oncology</i> , 2019, 143, 417-428.	1.4	13
20	Essential Gene Profiles for Human Pluripotent Stem Cells Identify Uncharacterized Genes and Substrate Dependencies. <i>Cell Reports</i> , 2019, 27, 599-615.e12.	2.9	85
21	<sc>CRISPR</sc> screens are feasible in <i> <sc>TP</sc> 53 </i> wild-type cells. <i>Molecular Systems Biology</i> , 2019, 15, e8679.	3.2	32
22	Functional genomic characterization of a synthetic anti-HER3 antibody reveals a role for ubiquitination by RNF41 in the anti-proliferative response. <i>Journal of Biological Chemistry</i> , 2019, 294, 1396-1409.	1.6	3
23	Cotargeting Ephrin Receptor Tyrosine Kinases A2 and A3 in Cancer Stem Cells Reduces Growth of Recurrent Glioblastoma. <i>Cancer Research</i> , 2018, 78, 5023-5037.	0.4	36
24	Interrogation of Functional Cell-Surface Markers Identifies CD151 Dependency in High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2017, 18, 2343-2358.	2.9	38
25	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. <i>Acta Neuropathologica</i> , 2017, 134, 923-940.	3.9	26
26	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2719-2727.	0.8	417
27	Genome-wide CRISPR screens reveal a Wnt-FZD5 signaling circuit as a druggable vulnerability of RNF43-mutant pancreatic tumors. <i>Nature Medicine</i> , 2017, 23, 60-68.	15.2	261
28	An oncogenic KRAS transcription program activates the RHOGEF ARHGEF2 to mediate transformed phenotypes in pancreatic cancer. <i>Oncotarget</i> , 2017, 8, 4484-4500.	0.8	18
29	Targeting the centriolar replication factor STIL synergizes with DNA damaging agents for treatment of ovarian cancer. <i>Oncotarget</i> , 2017, 8, 27380-27392.	0.8	13
30	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. <i>BMC Cancer</i> , 2016, 16, 485.	1.1	23
31	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016, 164, 293-309.	13.5	399
32	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. <i>Molecular Cell</i> , 2016, 62, 121-136.	4.5	142
33	Connective Tissue Disease-associated Interstitial Lung Diseases (CTD-ILD) Report from OMERACT CTD-ILD Working Group. <i>Journal of Rheumatology</i> , 2015, 42, 2168-2171.	1.0	142
34	Identification of P450 Oxidoreductase as a Major Determinant of Sensitivity to Hypoxia-Activated Prodrugs. <i>Cancer Research</i> , 2015, 75, 4211-4223.	0.4	65
35	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015, 163, 1515-1526.	13.5	1,339
36	Genome-wide RNAi analysis reveals that simultaneous inhibition of specific mevalonate pathway genes potentiates tumor cell death. <i>Oncotarget</i> , 2015, 6, 26909-26921.	0.8	52

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37	Measuring error rates in genomic perturbation screens: gold standards for human functional genomics. <i>Molecular Systems Biology</i> , 2014, 10, 733.	3.2	322
38	Integrated Genomic, Transcriptomic, and RNA-Interference Analysis of Genes in Somatic Copy Number Gains in Pancreatic Ductal Adenocarcinoma. <i>Pancreas</i> , 2013, 42, 1016-1026.	0.5	3
39	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1375-1387.	0.8	5
40	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	3.2	90
41	COLT-Cancer: functional genetic screening resource for essential genes in human cancer cell lines. <i>Nucleic Acids Research</i> , 2012, 40, D957-D963.	6.5	46
42	Essential Gene Profiles in Breast, Pancreatic, and Ovarian Cancer Cells. <i>Cancer Discovery</i> , 2012, 2, 172-189.	7.7	276
43	Identification of novel ATP13A2 interactors and their role in $\alpha$ -synuclein misfolding and toxicity. <i>Human Molecular Genetics</i> , 2012, 21, 3785-3794.	1.4	66
44	A comprehensive platform for highly multiplexed mammalian functional genetic screens. <i>BMC Genomics</i> , 2011, 12, 213.	1.2	31
45	NAViGaTOR: Network Analysis, Visualization and Graphing Toronto. <i>Bioinformatics</i> , 2009, 25, 3327-3329.	1.8	234
46	Regulation of Epidermal Growth Factor Receptor Trafficking by Lysine Deacetylase HDAC6. <i>Science Signaling</i> , 2009, 2, ra84.	1.6	140
47	High-Throughput Screening of Protein Interaction Networks in the TGF $\beta$ Interactome: Understanding the Signaling Mechanisms Driving Tumor Progression. , 2008, , 265-284.		0
48	Integrated proteomic and transcriptomic profiling of mouse lung development and Nmyc target genes. <i>Molecular Systems Biology</i> , 2007, 3, 109.	3.2	64
49	Unequal evolutionary conservation of human protein interactions in interologous networks. <i>Genome Biology</i> , 2007, 8, R95.	13.9	308
50	Systematic identification of SH3 domain-mediated human protein-protein interactions by peptide array target screening. <i>Proteomics</i> , 2007, 7, 1775-1785.	1.3	74
51	Online Predicted Human Interaction Database. <i>Bioinformatics</i> , 2005, 21, 2076-2082.	1.8	557
52	High-Throughput Mapping of a Dynamic Signaling Network in Mammalian Cells. <i>Science</i> , 2005, 307, 1621-1625.	6.0	651
53	A nuclear 3' to 5' exonuclease proofreads for the exonuclease-deficient DNA polymerase $\delta$ . <i>DNA Repair</i> , 2002, 1, 795-810.	1.3	11
54	Substrate specificity of the p53-associated 3' to 5' exonuclease. <i>Oncogene</i> , 2000, 19, 3321-3329.	2.6	30

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55	A 3â€²-5â€² Exonuclease in Human Leukemia Cells. <i>Journal of Biological Chemistry</i> , 2000, 275, 25814-25819.	1.6	7
56	Systematic Genome-Scale Identification of Host Factors for SARS-CoV-2 Infection Across Models Yields a Core Single Gene Dependency; <i>Ace2</i>. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0