

# John G Doench

## List of Publications by Year in descending order

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Version: 2024-02-01

153  
papers

28,203  
citations

25423

59  
h-index

16791

127  
g-index

198  
all docs

198  
docs citations

198  
times ranked

45649  
citing authors

#	ARTICLE	IF	CITATIONS
1	YAP1 and PRDM14 converge to promote cell survival and tumorigenesis. <i>Developmental Cell</i> , 2022, 57, 212-227.e8.	3.1	9
2	A genome-scale CRISPR screen reveals PRMT1 as a critical regulator of androgen receptor signaling in prostate cancer. <i>Cell Reports</i> , 2022, 38, 110417.	2.9	17
3	Systematic identification of biomarker-driven drug combinations to overcome resistance. <i>Nature Chemical Biology</i> , 2022, 18, 615-624.	3.9	14
4	Benchmarking of SpCas9 variants enables deeper base editor screens of BRCA1 and BCL2. <i>Nature Communications</i> , 2022, 13, 1318.	5.8	25
5	PI3K activation allows immune evasion by promoting an inhibitory myeloid tumor microenvironment. , 2022, 10, e003402.		21
6	Phosphate dysregulation via the XPR1â€“KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 681-695.	5.7	21
7	Combinatorial GxGxE CRISPR screen identifies SLC25A39 in mitochondrial glutathione transport linking iron homeostasis to OXPHOS. <i>Nature Communications</i> , 2022, 13, 2483.	5.8	31
8	A genetic screen identifies a protective type III interferon response to <i>Cryptosporidium</i> that requires TLR3 dependent recognition. <i>PLoS Pathogens</i> , 2022, 18, e1010003.	2.1	16
9	Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	10
10	Progression signature underlies clonal evolution and dissemination of multiple myeloma. <i>Blood</i> , 2021, 137, 2360-2372.	0.6	26
11	Optimization of AsCas12a for combinatorial genetic screens in human cells. <i>Nature Biotechnology</i> , 2021, 39, 94-104.	9.4	96
12	Genome-wide CRISPR Screens Reveal Host Factors Critical for SARS-CoV-2 Infection. <i>Cell</i> , 2021, 184, 76-91.e13.	13.5	418
13	Intercellular Mitochondria Transfer to Macrophages Regulates White Adipose Tissue Homeostasis and Is Impaired in Obesity. <i>Cell Metabolism</i> , 2021, 33, 270-282.e8.	7.2	160
14	Tumor-suppressor function of Beclin 1 in breast cancer cells requires E-cadherin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
15	Massively parallel assessment of human variants with base editor screens. <i>Cell</i> , 2021, 184, 1064-1080.e20.	13.5	175
16	Targeting oncoproteins with a positive selection assay for protein degraders. <i>Science Advances</i> , 2021, 7, .	4.7	26
17	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	7.7	43
18	InÂvivo screens using a selective CRISPR antigen removal lentiviral vector system reveal immune dependencies in renal cell carcinoma. <i>Immunity</i> , 2021, 54, 571-585.e6.	6.6	50

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19	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	13.7	181
20	Control of gasdermin D oligomerization and pyroptosis by the Ragulator-Rag-mTORC1 pathway. <i>Cell</i> , 2021, 184, 4495-4511.e19.	13.5	201
21	Lrp1 is a host entry factor for Rift Valley fever virus. <i>Cell</i> , 2021, 184, 5163-5178.e24.	13.5	46
22	UFMylation inhibits the proinflammatory capacity of interferon- $\gamma$ -activated macrophages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
23	Discovery of putative tumor suppressors from CRISPR screens reveals rewired lipid metabolism in acute myeloid leukemia cells. <i>Nature Communications</i> , 2021, 12, 6506.	5.8	13
24	Whole-Genome CRISPR Screening Identifies N-Glycosylation As an Essential Pathway and a Potential Novel Therapeutic Target in CALR-Mutant MPN. <i>Blood</i> , 2021, 138, 58-58.	0.6	1
25	Paralog knockout profiling identifies DUSP4 and DUSP6 as a digenic dependence in MAPK pathway-driven cancers. <i>Nature Genetics</i> , 2021, 53, 1664-1672.	9.4	61
26	High-Throughput CRISPR Screens To Dissect Macrophage- <i>Shigella</i> Interactions. <i>MBio</i> , 2021, 12, e0215821.	1.8	4
27	Genome-wide CRISPR screen identifies host dependency factors for influenza A virus infection. <i>Nature Communications</i> , 2020, 11, 164.	5.8	136
28	CRISPR-Cas9 Genome-Wide Knockout Screen Identifies Mechanism of Selective Activity of Dehydrofalcariol in Mesenchymal Stem-like Triple-Negative Breast Cancer Cells. <i>Journal of Natural Products</i> , 2020, 83, 3080-3092.	1.5	13
29	Illuminating Host-Mycobacterial Interactions with Genome-wide CRISPR Knockout and CRISPRi Screens. <i>Cell Systems</i> , 2020, 11, 239-251.e7.	2.9	23
30	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , 2020, 52, 662-668.	9.4	168
31	DNA methylation enzymes and PRC1 restrict B-cell Epstein-Barr virus oncoprotein expression. <i>Nature Microbiology</i> , 2020, 5, 1051-1063.	5.9	32
32	Defective NADPH production in mitochondrial disease complex I causes inflammation and cell death. <i>Nature Communications</i> , 2020, 11, 2714.	5.8	69
33	Aldehyde dehydrogenase 3a2 protects AML cells from oxidative death and the synthetic lethality of ferroptosis inducers. <i>Blood</i> , 2020, 136, 1303-1316.	0.6	68
34	Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12. <i>Journal of Biological Chemistry</i> , 2020, 295, 3431-3446.	1.6	12
35	Genetic screens in isogenic mammalian cell lines without single cell cloning. <i>Nature Communications</i> , 2020, 11, 752.	5.8	83
36	Cytochrome P450 oxidoreductase contributes to phospholipid peroxidation in ferroptosis. <i>Nature Chemical Biology</i> , 2020, 16, 302-309.	3.9	396

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37	Genome-wide In Vivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. <i>Neuron</i> , 2020, 106, 76-89.e8.	3.8	62
38	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020, 1, 235-248.	5.7	430
39	Design and analysis of CRISPR-Cas experiments. <i>Nature Biotechnology</i> , 2020, 38, 813-823.	9.4	127
40	MYC Controls the Epstein-Barr Virus Lytic Switch. <i>Molecular Cell</i> , 2020, 78, 653-669.e8.	4.5	67
41	Correction: Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12.. <i>Journal of Biological Chemistry</i> , 2020, 295, 16464-16467.	1.6	0
42	6-Phosphogluconate Dehydrogenase Links Cytosolic Carbohydrate Metabolism to Protein Secretion via Modulation of Glutathione Levels. <i>Cell Chemical Biology</i> , 2019, 26, 1306-1314.e5.	2.5	22
43	Autophagy genes in myeloid cells counteract IFN $\gamma$ -induced TNF-mediated cell death and fatal TNF-induced shock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16497-16506.	3.3	35
44	CRISPR/Cas9 Screens Reveal Multiple Layers of B cell CD40 Regulation. <i>Cell Reports</i> , 2019, 28, 1307-1322.e8.	2.9	18
45	A Compendium of Genetic Modifiers of Mitochondrial Dysfunction Reveals Intra-organelle Buffering. <i>Cell</i> , 2019, 179, 1222-1238.e17.	13.5	109
46	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	7.7	224
47	CRISPR-suppressor scanning reveals a nonenzymatic role of LSD1 in AML. <i>Nature Chemical Biology</i> , 2019, 15, 529-539.	3.9	71
48	Discovering metabolic disease gene interactions by correlated effects on cellular morphology. <i>Molecular Metabolism</i> , 2019, 24, 108-119.	3.0	13
49	A GPX4-dependent cancer cell state underlies the clear-cell morphology and confers sensitivity to ferroptosis. <i>Nature Communications</i> , 2019, 10, 1617.	5.8	499
50	A CRISPR-Cas9 delivery system for in vivo screening of genes in the immune system. <i>Nature Communications</i> , 2019, 10, 1668.	5.8	78
51	Deubiquitinases Maintain Protein Homeostasis and Survival of Cancer Cells upon Glutathione Depletion. <i>Cell Metabolism</i> , 2019, 29, 1166-1181.e6.	7.2	121
52	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	5.8	160
53	Combinatorial CRISPR-knockout identifies interactions between key genes and regulatory pathways in myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e14-e15.	0.2	0
54	Progression signature underlies clonal evolution and dissemination of Multiple Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e19-e20.	0.2	0

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55	Gain-of-function studies with CRISPR-based transcriptional activation at endogenous genomic loci reveals genes with critical roles for myeloma cells. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e49.	0.2	0
56	CRISPR-Switch regulates sgRNA activity by Cre recombination for sequential editing of two loci. <i>Nature Communications</i> , 2019, 10, 5454.	5.8	31
57	Targeting REGNASE-1 programs long-lived effector T cells for cancer therapy. <i>Nature</i> , 2019, 576, 471-476.	13.7	251
58	A FACS-Based Genome-wide CRISPR Screen Reveals a Requirement for COPI in Chlamydia trachomatis Invasion. <i>IScience</i> , 2019, 11, 71-84.	1.9	21
59	Loss of ADAR1 in tumours overcomes resistance to immune checkpoint blockade. <i>Nature</i> , 2019, 565, 43-48.	13.7	449
60	Identification of Antinorovirus Genes in Human Cells Using Genome-Wide CRISPR Activation Screening. <i>Journal of Virology</i> , 2019, 93, .	1.5	40
61	Systematic Characterization of Genes Representing Preferential Molecular Vulnerabilities for Myeloma Cells Compared to Other Neoplasias - Implications for the Biology and Therapeutic Targeting of Myeloma. <i>Blood</i> , 2019, 134, 4407-4407.	0.6	4
62	Natural variation in <i>C. elegans</i> arsenic toxicity is explained by differences in branched chain amino acid metabolism. <i>ELife</i> , 2019, 8, .	2.8	66
63	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. <i>ELife</i> , 2019, 8, .	2.8	14
64	Abstract A146: Systematic discovery of immune regulatory mechanisms in tumor cells. , 2019, , .		0
65	Abstract 2690: Massively parallel multiplexed methods to screen hundreds of barcoded cancer cell line models with small molecules or genetic perturbations using next-generation sequencing. , 2019, , .		0
66	Functional Interactions between Transcription Factors Involved in Myeloma Pathogenesis - Biological and Therapeutic Implications. <i>Blood</i> , 2019, 134, 315-315.	0.6	0
67	Functional Characterization of Genes Driving Enhanced Biological Aggressiveness of Myeloma Cells: Identification of Novel and Understudied "Drivers" of Myeloma. <i>Blood</i> , 2019, 134, 313-313.	0.6	0
68	Abstract 2948: Novel cell line barcoding method reveals tepoxalin as a selective drug against MDR1-high tumor cells. , 2019, , .		0
69	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	9.4	216
70	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. <i>Nature Biomedical Engineering</i> , 2018, 2, 38-47.	11.6	230
71	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	6.0	641
72	Optimized libraries for CRISPR-Cas9 genetic screens with multiple modalities. <i>Nature Communications</i> , 2018, 9, 5416.	5.8	535

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73	DYNLL1 binds to MRE11 to limit DNA end resection in BRCA1-deficient cells. <i>Nature</i> , 2018, 563, 522-526.	13.7	156
74	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387.	9.4	334
75	A case of mistaken identity. <i>Nature Biotechnology</i> , 2018, 36, 802-804.	9.4	17
76	In Vivo Profiling of Leukemic Stem Cell Fitness Identifies Therapeutically Actionable Determinants of Growth. <i>Experimental Hematology</i> , 2018, 64, S86.	0.2	0
77	PPM1D-truncating mutations confer resistance to chemotherapy and sensitivity to PPM1D inhibition in hematopoietic cells. <i>Blood</i> , 2018, 132, 1095-1105.	0.6	160
78	Nitric Oxide Engages an Anti-inflammatory Feedback Loop Mediated by Peroxiredoxin 5 in Phagocytes. <i>Cell Reports</i> , 2018, 24, 838-850.	2.9	31
79	Uncoupling of sgRNAs from their associated barcodes during PCR amplification of combinatorial CRISPR screens. <i>PLoS ONE</i> , 2018, 13, e0197547.	1.1	37
80	miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. <i>Journal of Experimental Medicine</i> , 2018, 215, 2115-2136.	4.2	20
81	The Canonical Wnt Pathway Drives Macropinocytosis in Cancer. <i>Cancer Research</i> , 2018, 78, 4658-4670.	0.4	75
82	Am I ready for CRISPR? A user's guide to genetic screens. <i>Nature Reviews Genetics</i> , 2018, 19, 67-80.	7.7	325
83	CRISPR Screen Reveals that EHEC's T3SS and Shiga Toxin Rely on Shared Host Factors for Infection. <i>MBio</i> , 2018, 9, .	1.8	62
84	Genetic Determinants of Venetoclax Resistance in Lymphoid Malignancies. <i>Blood</i> , 2018, 132, 893-893.	0.6	4
85	An alternative splicing switch in FLNB promotes the mesenchymal cell state in human breast cancer. <i>ELife</i> , 2018, 7, .	2.8	91
86	Abstract 706: In vivo tumor-associated mutation screen identifies PI3K activation as a mechanism of resistance to PD-1 blockade. , 2018, , .		0
87	CRISPR Activation Screen for Drivers of MM Cell Proliferation. <i>Blood</i> , 2018, 132, 3197-3197.	0.6	0
88	Deciphering Clonal Evolution and Dissemination of Multiple Myeloma Cells In Vivo. <i>Blood</i> , 2018, 132, 55-55.	0.6	0
89	CRISPR Activation Screen for HDAC Inhibitor Resistance. <i>Blood</i> , 2018, 132, 3958-3958.	0.6	1
90	CRISPR-Based Dual-Knockout Screens Reveals Network of Interactions between Key Dependencies for Myeloma Cells and Highlights IRF4 As a Central Regulator of Myeloma Cell Behavior. <i>Blood</i> , 2018, 132, 1915-1915.	0.6	0

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91	Functional screen of MSI2 interactors identifies an essential role for SYNCRIP in myeloid leukemia stem cells. <i>Nature Genetics</i> , 2017, 49, 866-875.	9.4	75
92	CRISPR/Cas9 Screens Reveal Epstein-Barr Virus-Transformed B Cell Host Dependency Factors. <i>Cell Host and Microbe</i> , 2017, 21, 580-591.e7.	5.1	113
93	PARP3 is a promoter of chromosomal rearrangements and limits G4 DNA. <i>Nature Communications</i> , 2017, 8, 15110.	5.8	32
94	A genome-wide, in vivo dropout CRISPR screen in acute myeloid leukemia. <i>Experimental Hematology</i> , 2017, 53, S78-S79.	0.2	0
95	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. <i>Cell Systems</i> , 2017, 5, 105-118.e9.	2.9	40
96	In vivo CRISPR screening identifies Ptpn2 as a cancer immunotherapy target. <i>Nature</i> , 2017, 547, 413-418.	13.7	792
97	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17.	13.5	2,281
98	Dependency of a therapy-resistant state of cancer cells on a lipid peroxidase pathway. <i>Nature</i> , 2017, 547, 453-457.	13.7	1,194
99	KEAP1 loss modulates sensitivity to kinase targeted therapy in lung cancer. <i>ELife</i> , 2017, 6, .	2.8	92
100	Synergistic interactions with PI3K inhibition that induce apoptosis. <i>ELife</i> , 2017, 6, .	2.8	25
101	Natural variation in a single amino acid substitution underlies physiological responses to topoisomerase II poisons. <i>PLoS Genetics</i> , 2017, 13, e1006891.	1.5	75
102	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. <i>PLoS Biology</i> , 2017, 15, e2003213.	2.6	136
103	Creation of Novel Protein Variants with CRISPR/Cas9-Mediated Mutagenesis: Turning a Screening By-Product into a Discovery Tool. <i>PLoS ONE</i> , 2017, 12, e0170445.	1.1	50
104	Abstract 5020: A genome-scale ORF screen reveals an alternative splicing program that regulates mesenchymal and stem-like cell states in breast cancer. , 2017, , .		0
105	Abstract 1019: In vivo CRISPR screening identifies Ptpn2 as a target for cancer immunotherapy. , 2017, , .		1
106	Abstract 417: Defining molecular mechanisms of resistance to glioblastoma immunity using a novel CRISPR/Cas9 in vivo loss-of-function screening platform. , 2017, , .		0
107	Abstract 3182: Cytoskeletal modulation results in increased tumor survival and drug resistance through attenuation of p53 dependent apoptosis. , 2017, , .		0
108	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016, 6, 714-726.	7.7	139

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109	<scp>CRISPR</scp>/Cas9 gene editing special issue. FEBS Journal, 2016, 283, 3160-3161.	2.2	5
110	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in $\beta$ -Catenin-Active Cancers. Cell Systems, 2016, 3, 302-316.e4.	2.9	55
111	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	7.7	171
112	Discovery of a proteinaceous cellular receptor for a norovirus. Science, 2016, 353, 933-936.	6.0	241
113	A Genome-wide CRISPR Death Screen Identifies Genes Essential for Oxidative Phosphorylation. Cell Metabolism, 2016, 24, 875-885.	7.2	244
114	Bromodomain Inhibitors Correct Bioenergetic Deficiency Caused by Mitochondrial Disease Complex I Mutations. Molecular Cell, 2016, 64, 163-175.	4.5	50
115	CRISPR/Cas9 Screens Reveal Requirements for Host Cell Sulfation and Fucosylation in Bacterial Type III Secretion System-Mediated Cytotoxicity. Cell Host and Microbe, 2016, 20, 226-237.	5.1	64
116	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. Nature Biotechnology, 2016, 34, 184-191.	9.4	3,168
117	In Vivo Genome-Wide Crispr Library Screen in a Xenograft Mouse Model of Tumor Growth and Metastasis of Multiple Myeloma. Blood, 2016, 128, 1137-1137.	0.6	2
118	Genome-Scale Screen Reveals Genes Required for Lenalidomide-Mediated Degradation of Aiolos By CRL4-CRBN. Blood, 2016, 128, 5139-5139.	0.6	2
119	Abstract 4368: High-throughput phenotyping of lung cancer somatic mutations. , 2016, , .		1
120	RNA Binding Protein Syncrip Regulates the Leukemia Stem Cell Program. Blood, 2016, 128, 739-739.	0.6	0
121	Genetic screens and functional genomics using <scp>CRISPR</scp>/Cas9 technology. FEBS Journal, 2015, 282, 1383-1393.	2.2	82
122	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. Cell, 2015, 162, 412-424.	13.5	206
123	Alternative to the soft-agar assay that permits high-throughput drug and genetic screens for cellular transformation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5708-5713.	3.3	105
124	A forward genetic screen identifies erythrocyte CD55 as essential for <i>Plasmodium falciparum</i> invasion. Science, 2015, 348, 711-714.	6.0	107
125	DOT1L inhibits SIRT1-mediated epigenetic silencing to maintain leukemic gene expression in MLL-rearranged leukemia. Nature Medicine, 2015, 21, 335-343.	15.2	200
126	Functional genomics identifies negative regulatory nodes controlling phagocyte oxidative burst. Nature Communications, 2015, 6, 7838.	5.8	26



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127	HDAC5 Controls MEF2C-Driven Sclerostin Expression in Osteocytes. <i>Journal of Bone and Mineral Research</i> , 2015, 30, 400-411.	3.1	132
128	Morphological Profiles of RNAi-Induced Gene Knockdown Are Highly Reproducible but Dominated by Seed Effects. <i>PLoS ONE</i> , 2015, 10, e0131370.	1.1	31
129	Abstract 957: Towards precision functional genomics via next-generation functional mapping of cancer variants. , 2015, , .		0
130	Abstract PR07: Towards precision functional genomics via next-generation functional mapping of cancer variants. , 2015, , .		0
131	Balancing Proliferation, Differentiation, and Survival: Powerful Genetic and RNAi Technologies Reveal Essential microRNA Signaling for Leukemic Progenitor Cell Fitness. <i>Blood</i> , 2015, 126, 441-441.	0.6	0
132	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. <i>Science</i> , 2014, 343, 84-87.	6.0	4,210
133	Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inactivation. <i>Nature Biotechnology</i> , 2014, 32, 1262-1267.	9.4	1,351
134	Targeted shRNA screening identified critical roles of pleckstrin-2 in erythropoiesis. <i>Haematologica</i> , 2014, 99, 1157-1167.	1.7	28
135	Abstract 3316: Characterizing mechanisms of resistance to androgen deprivation in prostate cancer. , 2014, , .		0
136	Discovery and Characterization of Super-Enhancer-Associated Dependencies in Diffuse Large B Cell Lymphoma. <i>Cancer Cell</i> , 2013, 24, 777-790.	7.7	635
137	Identification of regulators of the innate immune response to cytosolic DNA and retroviral infection by an integrative approach. <i>Nature Immunology</i> , 2013, 14, 179-185.	7.0	104
138	SYK Inhibition Modulates Distinct PI3K/AKT-Dependent Survival Pathways and Cholesterol Biosynthesis in Diffuse Large B Cell Lymphomas. <i>Cancer Cell</i> , 2013, 23, 826-838.	7.7	152
139	Abstract B230: Targeting mitochondria for metastatic lung adenocarcinoma specific lethality.. , 2013, , .		0
140	Reduced Expression of Ribosomal Proteins Relieves MicroRNA-Mediated Repression. <i>Molecular Cell</i> , 2012, 46, 171-186.	4.5	26
141	Abstract 2957: Uncovering tumor-specific components of the p53 pathway using mouse models and RNAi. <i>Cancer Research</i> , 2012, 72, 2957-2957.	0.4	3
142	Targeted ShRNA Screening Identified Critical Role of Pleckstrin-2 in Erythropoiesis. <i>Blood</i> , 2012, 120, 3199-3199.	0.6	0
143	Aldehyde Dehydrogenase 3a2 (Aldh3a2) Represents a Distinct Metabolic Vulnerability in MLL-AF9 AML Leukemia Initiating Cells. <i>Blood</i> , 2012, 120, 208-208.	0.6	0
144	Distinct Metabolic Dependency of Normal and Leukemic Cells in a Mouse Model. <i>Blood</i> , 2011, 118, 759-759.	0.6	0

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145	Kinase requirements in human cells: I. Comparing kinase requirements across various cell types. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 16472-16477.	3.3	78
146	Comparison of siRNA-induced off-target RNA and protein effects. Rna, 2007, 13, 385-395.	1.6	127
147	Analysis of microRNA effector functions in vitro. Methods, 2007, 43, 91-104.	1.9	20
148	Recapitulation of Short RNA-Directed Translational Gene Silencing In Vitro. Molecular Cell, 2006, 22, 553-560.	4.5	166
149	RNA interference of Xenopus NMDAR NR1 in vitro and in vivo. Journal of Neuroscience Methods, 2006, 152, 65-73.	1.3	11
150	Screens Using RNAi and cDNA Expression as Surrogates for Genetics in Mammalian Tissue Culture Cells. Cold Spring Harbor Symposia on Quantitative Biology, 2005, 70, 449-459.	2.0	22
151	Specificity of microRNA target selection in translational repression. Genes and Development, 2004, 18, 504-511.	2.7	1,396
152	siRNAs can function as miRNAs. Genes and Development, 2003, 17, 438-442.	2.7	1,062
153	CRISPR/Cas9 Screens Reveal Multiple Layers of B Cell CD40 Regulation. SSRN Electronic Journal, 0, , .	0.4	0