

# John G Doench

## List of Publications by Year in descending order

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Version: 2024-02-01

153  
papers

28,203  
citations

22153

59  
h-index

14759

127  
g-index

198  
all docs

198  
docs citations

198  
times ranked

41629  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. <i>Science</i> , 2014, 343, 84-87.	12.6	4,210
2	Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. <i>Nature Biotechnology</i> , 2016, 34, 184-191.	17.5	3,168
3	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17.	28.9	2,281
4	Specificity of microRNA target selection in translational repression. <i>Genes and Development</i> , 2004, 18, 504-511.	5.9	1,396
5	Rational design of highly active sgRNAs for CRISPR-Cas9-mediated gene inactivation. <i>Nature Biotechnology</i> , 2014, 32, 1262-1267.	17.5	1,351
6	Dependency of a therapy-resistant state of cancer cells on a lipid peroxidase pathway. <i>Nature</i> , 2017, 547, 453-457.	27.8	1,194
7	siRNAs can function as miRNAs. <i>Genes and Development</i> , 2003, 17, 438-442.	5.9	1,062
8	In vivo CRISPR screening identifies Ptpn2 as a cancer immunotherapy target. <i>Nature</i> , 2017, 547, 413-418.	27.8	792
9	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	12.6	641
10	Discovery and Characterization of Super-Enhancer-Associated Dependencies in Diffuse Large B Cell Lymphoma. <i>Cancer Cell</i> , 2013, 24, 777-790.	16.8	635
11	Optimized libraries for CRISPR-Cas9 genetic screens with multiple modalities. <i>Nature Communications</i> , 2018, 9, 5416.	12.8	535
12	A GPX4-dependent cancer cell state underlies the clear-cell morphology and confers sensitivity to ferroptosis. <i>Nature Communications</i> , 2019, 10, 1617.	12.8	499
13	Loss of ADAR1 in tumours overcomes resistance to immune checkpoint blockade. <i>Nature</i> , 2019, 565, 43-48.	27.8	449
14	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020, 1, 235-248.	13.2	430
15	Genome-wide CRISPR Screens Reveal Host Factors Critical for SARS-CoV-2 Infection. <i>Cell</i> , 2021, 184, 76-91.e13.	28.9	418
16	Cytochrome P450 oxidoreductase contributes to phospholipid peroxidation in ferroptosis. <i>Nature Chemical Biology</i> , 2020, 16, 302-309.	8.0	396
17	Mutational processes shape the landscape of TP53 mutations in human cancer. <i>Nature Genetics</i> , 2018, 50, 1381-1387.	21.4	334
18	Am I ready for CRISPR? A user's guide to genetic screens. <i>Nature Reviews Genetics</i> , 2018, 19, 67-80.	16.3	325

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19	Targeting REGNASE-1 programs long-lived effector T cells for cancer therapy. <i>Nature</i> , 2019, 576, 471-476.	27.8	251
20	A Genome-wide CRISPR Death Screen Identifies Genes Essential for Oxidative Phosphorylation. <i>Cell Metabolism</i> , 2016, 24, 875-885.	16.2	244
21	Discovery of a proteinaceous cellular receptor for a norovirus. <i>Science</i> , 2016, 353, 933-936.	12.6	241
22	Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. <i>Nature Biomedical Engineering</i> , 2018, 2, 38-47.	22.5	230
23	Mitochondrial Reprogramming Underlies Resistance to BCL-2 Inhibition in Lymphoid Malignancies. <i>Cancer Cell</i> , 2019, 36, 369-384.e13.	16.8	224
24	Orthologous CRISPR-Cas9 enzymes for combinatorial genetic screens. <i>Nature Biotechnology</i> , 2018, 36, 179-189.	17.5	216
25	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015, 162, 412-424.	28.9	206
26	Control of gasdermin D oligomerization and pyroptosis by the Ragulator-Rag-mTORC1 pathway. <i>Cell</i> , 2021, 184, 4495-4511.e19.	28.9	201
27	DOT1L inhibits SIRT1-mediated epigenetic silencing to maintain leukemic gene expression in MLL-rearranged leukemia. <i>Nature Medicine</i> , 2015, 21, 335-343.	30.7	200
28	Epigenetic silencing by SETDB1 suppresses tumour intrinsic immunogenicity. <i>Nature</i> , 2021, 595, 309-314.	27.8	181
29	Massively parallel assessment of human variants with base editor screens. <i>Cell</i> , 2021, 184, 1064-1080.e20.	28.9	175
30	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	16.8	171
31	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , 2020, 52, 662-668.	21.4	168
32	Recapitulation of Short RNA-Directed Translational Gene Silencing In Vitro. <i>Molecular Cell</i> , 2006, 22, 553-560.	9.7	166
33	PPM1D-truncating mutations confer resistance to chemotherapy and sensitivity to PPM1D inhibition in hematopoietic cells. <i>Blood</i> , 2018, 132, 1095-1105.	1.4	160
34	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	12.8	160
35	Intercellular Mitochondria Transfer to Macrophages Regulates White Adipose Tissue Homeostasis and Is Impaired in Obesity. <i>Cell Metabolism</i> , 2021, 33, 270-282.e8.	16.2	160
36	DYNLL1 binds to MRE11 to limit DNA end resection in BRCA1-deficient cells. <i>Nature</i> , 2018, 563, 522-526.	27.8	156

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37	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.	16.8	152
38	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016, 6, 714-726.	9.4	139
39	Genome-wide CRISPR screen identifies host dependency factors for influenza A virus infection. <i>Nature Communications</i> , 2020, 11, 164.	12.8	136
40	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. <i>PLoS Biology</i> , 2017, 15, e2003213.	5.6	136
41	HDAC5 Controls MEF2C-Driven Sclerostin Expression in Osteocytes. <i>Journal of Bone and Mineral Research</i> , 2015, 30, 400-411.	2.8	132
42	Comparison of siRNA-induced off-target RNA and protein effects. <i>Rna</i> , 2007, 13, 385-395.	3.5	127
43	Design and analysis of CRISPR-Cas experiments. <i>Nature Biotechnology</i> , 2020, 38, 813-823.	17.5	127
44	Deubiquitinases Maintain Protein Homeostasis and Survival of Cancer Cells upon Glutathione Depletion. <i>Cell Metabolism</i> , 2019, 29, 1166-1181.e6.	16.2	121
45	CRISPR/Cas9 Screens Reveal Epstein-Barr Virus-Transformed B Cell Host Dependency Factors. <i>Cell Host and Microbe</i> , 2017, 21, 580-591.e7.	11.0	113
46	A Compendium of Genetic Modifiers of Mitochondrial Dysfunction Reveals Intra-organelle Buffering. <i>Cell</i> , 2019, 179, 1222-1238.e17.	28.9	109
47	A forward genetic screen identifies erythrocyte CD55 as essential for <i>Plasmodium falciparum</i> invasion. <i>Science</i> , 2015, 348, 711-714.	12.6	107
48	Alternative to the soft-agar assay that permits high-throughput drug and genetic screens for cellular transformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5708-5713.	7.1	105
49	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.	14.5	104
50	Optimization of AsCas12a for combinatorial genetic screens in human cells. <i>Nature Biotechnology</i> , 2021, 39, 94-104.	17.5	96
51	KEAP1 loss modulates sensitivity to kinase targeted therapy in lung cancer. <i>ELife</i> , 2017, 6, .	6.0	92
52	An alternative splicing switch in FLNB promotes the mesenchymal cell state in human breast cancer. <i>ELife</i> , 2018, 7, .	6.0	91
53	Genetic screens in isogenic mammalian cell lines without single cell cloning. <i>Nature Communications</i> , 2020, 11, 752.	12.8	83
54	Genetic screens and functional genomics using CRISPR/Cas9 technology. <i>FEBS Journal</i> , 2015, 282, 1383-1393.	4.7	82

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55	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.	7.1	78
56	A CRISPR-Cas9 delivery system for in vivo screening of genes in the immune system. Nature Communications, 2019, 10, 1668.	12.8	78
57	Functional screen of MSI2 interactors identifies an essential role for SYNCRIP in myeloid leukemia stem cells. Nature Genetics, 2017, 49, 866-875.	21.4	75
58	Natural variation in a single amino acid substitution underlies physiological responses to topoisomerase II poisons. PLoS Genetics, 2017, 13, e1006891.	3.5	75
59	The Canonical Wnt Pathway Drives Macropinocytosis in Cancer. Cancer Research, 2018, 78, 4658-4670.	0.9	75
60	CRISPR-suppressor scanning reveals a nonenzymatic role of LSD1 in AML. Nature Chemical Biology, 2019, 15, 529-539.	8.0	71
61	Defective NADPH production in mitochondrial disease complex I causes inflammation and cell death. Nature Communications, 2020, 11, 2714.	12.8	69
62	Aldehyde dehydrogenase 3a2 protects AML cells from oxidative death and the synthetic lethality of ferroptosis inducers. Blood, 2020, 136, 1303-1316.	1.4	68
63	MYC Controls the Epstein-Barr Virus Lytic Switch. Molecular Cell, 2020, 78, 653-669.e8.	9.7	67
64	Natural variation in C. elegans arsenic toxicity is explained by differences in branched chain amino acid metabolism. ELife, 2019, 8, .	6.0	66
65	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.	11.0	64
66	Genome-wide In Vivo CNS Screening Identifies Genes that Modify CNS Neuronal Survival and mHTT Toxicity. Neuron, 2020, 106, 76-89.e8.	8.1	62
67	CRISPR Screen Reveals that EHEC's T3SS and Shiga Toxin Rely on Shared Host Factors for Infection. MBio, 2018, 9, .	4.1	62
68	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
69	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in $\beta$ -Catenin-Active Cancers. Cell Systems, 2016, 3, 302-316.e4.	6.2	55
70	Bromodomain Inhibitors Correct Bioenergetic Deficiency Caused by Mitochondrial Disease Complex I Mutations. Molecular Cell, 2016, 64, 163-175.	9.7	50
71	Tumor-suppressor function of Beclin 1 in breast cancer cells requires E-cadherin. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	50
72	In Vivo screens using a selective CRISPR antigen removal lentiviral vector system reveal immune dependencies in renal cell carcinoma. Immunity, 2021, 54, 571-585.e6.	14.3	50

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73	Creation of Novel Protein Variants with CRISPR/Cas9-Mediated Mutagenesis: Turning a Screening By-Product into a Discovery Tool. PLoS ONE, 2017, 12, e0170445.	2.5	50
74	Lrp1 is a host entry factor for Rift Valley fever virus. Cell, 2021, 184, 5163-5178.e24.	28.9	46
75	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. Cancer Discovery, 2021, 11, 2050-2071.	9.4	43
76	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. Cell Systems, 2017, 5, 105-118.e9.	6.2	40
77	Identification of Antinorovirus Genes in Human Cells Using Genome-Wide CRISPR Activation Screening. Journal of Virology, 2019, 93, .	3.4	40
78	Uncoupling of sgRNAs from their associated barcodes during PCR amplification of combinatorial CRISPR screens. PLoS ONE, 2018, 13, e0197547.	2.5	37
79	Autophagy genes in myeloid cells counteract IFN $\beta$ -induced TNF-mediated cell death and fatal TNF-induced shock. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 16497-16506.	7.1	35
80	PARP3 is a promoter of chromosomal rearrangements and limits G4 DNA. Nature Communications, 2017, 8, 15110.	12.8	32
81	DNA methylation enzymes and PRC1 restrict B-cell Epstein-Barr virus oncoprotein expression. Nature Microbiology, 2020, 5, 1051-1063.	13.3	32
82	Nitric Oxide Engages an Anti-inflammatory Feedback Loop Mediated by Peroxiredoxin 5 in Phagocytes. Cell Reports, 2018, 24, 838-850.	6.4	31
83	CRISPR-Switch regulates sgRNA activity by Cre recombination for sequential editing of two loci. Nature Communications, 2019, 10, 5454.	12.8	31
84	Morphological Profiles of RNAi-Induced Gene Knockdown Are Highly Reproducible but Dominated by Seed Effects. PLoS ONE, 2015, 10, e0131370.	2.5	31
85	Combinatorial GxGxE CRISPR screen identifies SLC25A39 in mitochondrial glutathione transport linking iron homeostasis to OXPHOS. Nature Communications, 2022, 13, 2483.	12.8	31
86	Targeted shRNA screening identified critical roles of pleckstrin-2 in erythropoiesis. Haematologica, 2014, 99, 1157-1167.	3.5	28
87	Reduced Expression of Ribosomal Proteins Relieves MicroRNA-Mediated Repression. Molecular Cell, 2012, 46, 171-186.	9.7	26
88	Functional genomics identifies negative regulatory nodes controlling phagocyte oxidative burst. Nature Communications, 2015, 6, 7838.	12.8	26
89	Progression signature underlies clonal evolution and dissemination of multiple myeloma. Blood, 2021, 137, 2360-2372.	1.4	26
90	Targeting oncoproteins with a positive selection assay for protein degraders. Science Advances, 2021, 7, .	10.3	26

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91	Synergistic interactions with PI3K inhibition that induce apoptosis. <i>ELife</i> , 2017, 6, .	6.0	25
92	Benchmarking of SpCas9 variants enables deeper base editor screens of BRCA1 and BCL2. <i>Nature Communications</i> , 2022, 13, 1318.	12.8	25
93	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, .	7.1	24
94	Illuminating Host-Mycobacterial Interactions with Genome-wide CRISPR Knockout and CRISPRi Screens. <i>Cell Systems</i> , 2020, 11, 239-251.e7.	6.2	23
95	Screens Using RNAi and cDNA Expression as Surrogates for Genetics in Mammalian Tissue Culture Cells. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2005, 70, 449-459.	1.1	22
96	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.	5.2	22
97	A FACS-Based Genome-wide CRISPR Screen Reveals a Requirement for COPI in <i>Chlamydia trachomatis</i> Invasion. <i>IScience</i> , 2019, 11, 71-84.	4.1	21
98	PI3K activation allows immune evasion by promoting an inhibitory myeloid tumor microenvironment. , 2022, 10, e003402.		21
99	Phosphate dysregulation via the XPR1-KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 681-695.	13.2	21
100	Analysis of microRNA effector functions in vitro. <i>Methods</i> , 2007, 43, 91-104.	3.8	20
101	miR-196b target screen reveals mechanisms maintaining leukemia stemness with therapeutic potential. <i>Journal of Experimental Medicine</i> , 2018, 215, 2115-2136.	8.5	20
102	CRISPR/Cas9 Screens Reveal Multiple Layers of B cell CD40 Regulation. <i>Cell Reports</i> , 2019, 28, 1307-1322.e8.	6.4	18
103	A case of mistaken identity. <i>Nature Biotechnology</i> , 2018, 36, 802-804.	17.5	17
104	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.	6.4	17
105	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.	4.7	16
106	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. <i>ELife</i> , 2019, 8, .	6.0	14
107	Systematic identification of biomarker-driven drug combinations to overcome resistance. <i>Nature Chemical Biology</i> , 2022, 18, 615-624.	8.0	14
108	Discovering metabolic disease gene interactions by correlated effects on cellular morphology. <i>Molecular Metabolism</i> , 2019, 24, 108-119.	6.5	13

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109	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.	3.0	13
110	Discovery of putative tumor suppressors from CRISPR screens reveals rewired lipid metabolism in acute myeloid leukemia cells. <i>Nature Communications</i> , 2021, 12, 6506.	12.8	13
111	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.	3.4	12
112	RNA interference of <i>Xenopus</i> NMDAR NR1 in vitro and in vivo. <i>Journal of Neuroscience Methods</i> , 2006, 152, 65-73.	2.5	11
113	Reversal of viral and epigenetic HLA class I repression in Merkel cell carcinoma. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	10
114	YAP1 and PRDM14 converge to promote cell survival and tumorigenesis. <i>Developmental Cell</i> , 2022, 57, 212-227.e8.	7.0	9
115	<scp>CRISPR</scp>/Cas9 gene editing special issue. <i>FEBS Journal</i> , 2016, 283, 3160-3161.	4.7	5
116	Genetic Determinants of Venetoclax Resistance in Lymphoid Malignancies. <i>Blood</i> , 2018, 132, 893-893.	1.4	4
117	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.	1.4	4
118	High-Throughput CRISPR Screens To Dissect Macrophage- <i>Shigella</i> Interactions. <i>MBio</i> , 2021, 12, e0215821.	4.1	4
119	Abstract 2957: Uncovering tumor-specific components of the p53 pathway using mouse models and RNAi. <i>Cancer Research</i> , 2012, 72, 2957-2957.	0.9	3
120	In Vivo Genome-Wide Crispr Library Screen in a Xenograft Mouse Model of Tumor Growth and Metastasis of Multiple Myeloma. <i>Blood</i> , 2016, 128, 1137-1137.	1.4	2
121	Genome-Scale Screen Reveals Genes Required for Lenalidomide-Mediated Degradation of Aiolos By CRL4-CRBN. <i>Blood</i> , 2016, 128, 5139-5139.	1.4	2
122	Abstract 4368: High-throughput phenotyping of lung cancer somatic mutations. , 2016, , .		1
123	Abstract 1019:In vivoCRISPR screening identifies Ptpn2 as a target for cancer immunotherapy. , 2017, , .		1
124	CRISPR Activation Screen for HDAC Inhibitor Resistance. <i>Blood</i> , 2018, 132, 3958-3958.	1.4	1
125	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.	1.4	1
126	A genome-wide, in vivo dropout CRISPR screen in acute myeloid leukemia. <i>Experimental Hematology</i> , 2017, 53, S78-S79.	0.4	0



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127	In Vivo Profiling of Leukemic Stem Cell Fitness Identifies Therapeutically Actionable Determinants of Growth. <i>Experimental Hematology</i> , 2018, 64, S86.	0.4	0
128	Combinatorial CRISPR-knockout identifies interactions between key genes and regulatory pathways in myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e14-e15.	0.4	0
129	Progression signature underlies clonal evolution and dissemination of Multiple Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e19-e20.	0.4	0
130	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.	0.4	0
131	Distinct Metabolic Dependency of Normal and Leukemic Cells in a Mouse Model. <i>Blood</i> , 2011, 118, 759-759.	1.4	0
132	Targeted ShRNA Screening Identified Critical Role of Pleckstrin-2 in Erythropoiesis. <i>Blood</i> , 2012, 120, 3199-3199.	1.4	0
133	Aldehyde Dehydrogenase 3a2 (Aldh3a2) Represents a Distinct Metabolic Vulnerability in MLL-AF9 AML Leukemia Initiating Cells. <i>Blood</i> , 2012, 120, 208-208.	1.4	0
134	Abstract B230: Targeting mitochondria for metastatic lung adenocarcinoma specific lethality.. , 2013, , .		0
135	Abstract 3316: Characterizing mechanisms of resistance to androgen deprivation in prostate cancer. , 2014, , .		0
136	Abstract 957: Towards precision functional genomics via next-generation functional mapping of cancer variants. , 2015, , .		0
137	Abstract PR07: Towards precision functional genomics via next-generation functional mapping of cancer variants. , 2015, , .		0
138	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.	1.4	0
139	RNA Binding Protein Syncrip Regulates the Leukemia Stem Cell Program. <i>Blood</i> , 2016, 128, 739-739.	1.4	0
140	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
141	Abstract 417: Defining molecular mechanisms of resistance to glioblastoma immunity using a novel CRISPR/Cas9in vivoloss-of-function screening platform. , 2017, , .		0
142	Abstract 3182: Cytoskeletal modulation results in increased tumor survival and drug resistance through attenuation of p53 dependent apoptosis. , 2017, , .		0
143	Abstract 706: In vivo tumor-associated mutation screen identifies PI3K activation as a mechanism of resistance to PD-1 blockade. , 2018, , .		0
144	CRISPR Activation Screen for Drivers of MM Cell Proliferation. <i>Blood</i> , 2018, 132, 3197-3197.	1.4	0

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145	Deciphering Clonal Evolution and Dissemination of Multiple Myeloma Cells In Vivo. Blood, 2018, 132, 55-55.	1.4	0
146	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. Blood, 2018, 132, 1915-1915.	1.4	0
147	CRISPR/Cas9 Screens Reveal Multiple Layers of B Cell CD40 Regulation. SSRN Electronic Journal, 0, , .	0.4	0
148	Abstract A146: Systematic discovery of immune regulatory mechanisms in tumor cells. , 2019, , .		0
149	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
150	Functional Interactions between Transcription Factors Involved in Myeloma Pathogenesis - Biological and Therapeutic Implications. Blood, 2019, 134, 315-315.	1.4	0
151	Functional Characterization of Genes Driving Enhanced Biological Aggressiveness of Myeloma Cells: Identification of Novel and Understudied "Drivers" of Myeloma. Blood, 2019, 134, 313-313.	1.4	0
152	Correction: Mechanistic insights into cancer cell killing through interaction of phosphodiesterase 3A and schlafen family member 12.. Journal of Biological Chemistry, 2020, 295, 16464-16467.	3.4	0
153	Abstract 2948: Novel cell line barcoding method reveals tepoxalin as a selective drug against MDR1-high tumor cells. , 2019, , .		0