

# Jason Moffat

## List of Publications by Year in descending order

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Version: 2024-02-01

155  
papers

22,846  
citations

19608

61  
h-index

10127

140  
g-index

181  
all docs

181  
docs citations

181  
times ranked

39775  
citing authors

#	ARTICLE	IF	CITATIONS
1	CellProfiler: image analysis software for identifying and quantifying cell phenotypes. <i>Genome Biology</i> , 2006, 7, R100.	13.9	4,287
2	A Lentiviral RNAi Library for Human and Mouse Genes Applied to an Arrayed Viral High-Content Screen. <i>Cell</i> , 2006, 124, 1283-1298.	13.5	1,603
3	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015, 163, 1515-1526.	13.5	1,339
4	Ablation in Mice of the mTORC Components raptor, rictor, or mLST8 Reveals that mTORC2 Is Required for Signaling to Akt-FOXO and PKC $\zeta$ , but Not S6K1. <i>Developmental Cell</i> , 2006, 11, 859-871.	3.1	1,271
5	Mechanism of Inhibition of Protein-tyrosine Phosphatases by Vanadate and Pervanadate. <i>Journal of Biological Chemistry</i> , 1997, 272, 843-851.	1.6	749
6	Inhibition of Mitochondrial Translation as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2011, 20, 674-688.	7.7	546
7	Exploration of Essential Gene Functions via Titratable Promoter Alleles. <i>Cell</i> , 2004, 118, 31-44.	13.5	538
8	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. <i>Cell</i> , 2015, 163, 1484-1499.	13.5	446
9	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018, 560, 117-121.	13.7	445
10	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012, 14, 966-976.	4.6	431
11	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2719-2727.	0.8	417
12	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016, 164, 293-309.	13.5	399
13	Scoring diverse cellular morphologies in image-based screens with iterative feedback and machine learning. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1826-1831.	3.3	345
14	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013, 498, 241-245.	13.7	326
15	Measuring error rates in genomic perturbation screens: gold standards for human functional genomics. <i>Molecular Systems Biology</i> , 2014, 10, 733.	3.2	322
16	CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. <i>Nature</i> , 2018, 559, 285-289.	13.7	297
17	Intratumoral heterogeneity: pathways to treatment resistance and relapse in human glioblastoma. <i>Annals of Oncology</i> , 2017, 28, 1448-1456.	0.6	283
18	Essential Gene Profiles in Breast, Pancreatic, and Ovarian Cancer Cells. <i>Cancer Discovery</i> , 2012, 2, 172-189.	7.7	276

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19	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015, 27, 864-876.	7.7	265
20	Genome-wide CRISPR screens reveal a Wnt- $\beta$ -catenin signaling circuit as a druggable vulnerability of RNF43-mutant pancreatic tumors. <i>Nature Medicine</i> , 2017, 23, 60-68.	15.2	261
21	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , 2021, 184, 226-242.e21.	13.5	258
22	A Strategy for Modulation of Enzymes in the Ubiquitin System. <i>Science</i> , 2013, 339, 590-595.	6.0	257
23	Yeast Proteome Dynamics from Single Cell Imaging and Automated Analysis. <i>Cell</i> , 2015, 161, 1413-1424.	13.5	254
24	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020, 586, 120-126.	13.7	249
25	Emerging and evolving concepts in gene essentiality. <i>Nature Reviews Genetics</i> , 2018, 19, 34-49.	7.7	230
26	BAGEL: a computational framework for identifying essential genes from pooled library screens. <i>BMC Bioinformatics</i> , 2016, 17, 164.	1.2	216
27	Building mammalian signalling pathways with RNAi screens. <i>Nature Reviews Molecular Cell Biology</i> , 2006, 7, 177-187.	16.1	197
28	SMN and symmetric arginine dimethylation of RNA polymerase II C-terminal domain control termination. <i>Nature</i> , 2016, 529, 48-53.	13.7	185
29	Global Genetic Networks and the Genotype-to-Phenotype Relationship. <i>Cell</i> , 2019, 177, 85-100.	13.5	170
30	Regulation of CD133 by HDAC6 Promotes $\beta$ -Catenin Signaling to Suppress Cancer Cell Differentiation. <i>Cell Reports</i> , 2012, 2, 951-963.	2.9	161
31	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	11.8	155
32	The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. <i>Nature Methods</i> , 2014, 11, 585-592.	9.0	149
33	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. <i>Cell Reports</i> , 2015, 13, 2425-2439.	2.9	146
34	Multilayered Control of Alternative Splicing Regulatory Networks by Transcription Factors. <i>Molecular Cell</i> , 2017, 65, 539-553.e7.	4.5	143
35	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. <i>Molecular Cell</i> , 2016, 62, 121-136.	4.5	142
36	The ubiquitin-activating enzyme E1 as a therapeutic target for the treatment of leukemia and multiple myeloma. <i>Blood</i> , 2010, 115, 2251-2259.	0.6	139

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37	Cytosolic detection of the bacterial metabolite HBP activates TIFA-dependent innate immunity. <i>Science</i> , 2015, 348, 1251-1255.	6.0	134
38	Natural Variation in Gene Expression Modulates the Severity of Mutant Phenotypes. <i>Cell</i> , 2015, 162, 391-402.	13.5	129
39	Identifying chemogenetic interactions from CRISPR screens with drugZ. <i>Genome Medicine</i> , 2019, 11, 52.	3.6	127
40	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2542-2547.	3.3	124
41	Cyclin Partners Determine Pho85 Protein Kinase Substrate Specificity In Vitro and In Vivo: Control of Glycogen Biosynthesis by Pcl8 and Pcl10. <i>Molecular and Cellular Biology</i> , 1998, 18, 3289-3299.	1.1	119
42	A role for the TGF $\beta$ -Par6 polarity pathway in breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14028-14033.	3.3	115
43	The Rational Development of CD133-Targeting Immunotherapies for Glioblastoma. <i>Cell Stem Cell</i> , 2020, 26, 832-844.e6.	5.2	114
44	Transcriptional Coregulation by the Cell Integrity Mitogen-Activated Protein Kinase Slt2 and the Cell Cycle Regulator Swi4. <i>Molecular and Cellular Biology</i> , 2001, 21, 6515-6528.	1.1	109
45	A systematic approach to identify novel cancer drug targets using machine learning, inhibitor design and high-throughput screening. <i>Genome Medicine</i> , 2014, 6, 57.	3.6	101
46	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2833-2847.	2.5	100
47	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
48	Genome-wide CRISPR-Cas9 Interrogation of Splicing Networks Reveals a Mechanism for Recognition of Autism-Misregulated Neuronal Microexons. <i>Molecular Cell</i> , 2018, 72, 510-524.e12.	4.5	86
49	Dissection of a Complex Phenotype by Functional Genomics Reveals Roles for the Yeast Cyclin-Dependent Protein Kinase Pho85 in Stress Adaptation and Cell Integrity. <i>Molecular and Cellular Biology</i> , 2002, 22, 5076-5088.	1.1	85
50	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
51	Digital microfluidic isolation of single cells for -Omics. <i>Nature Communications</i> , 2020, 11, 5632.	5.8	85
52	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9-Cas12a platform. <i>Nature Biotechnology</i> , 2020, 38, 638-648.	9.4	85
53	Protocadherin-1 is essential for cell entry by New World hantaviruses. <i>Nature</i> , 2018, 563, 559-563.	13.7	84
54	A Lentiviral Functional Proteomics Approach Identifies Chromatin Remodeling Complexes Important for the Induction of Pluripotency. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 811-823.	2.5	83

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55	Late-G1 cyclin-CDK activity is essential for control of cell morphogenesis in budding yeast. <i>Nature Cell Biology</i> , 2004, 6, 59-66.	4.6	81
56	The SAGA Deubiquitination Module Promotes DNA Repair and Class Switch Recombination through ATM and DNAPK-Mediated $\gamma$ H2AX Formation. <i>Cell Reports</i> , 2016, 15, 1554-1565.	2.9	81
57	CD133 Protein N-Glycosylation Processing Contributes to Cell Surface Recognition of the Primitive Cell Marker AC133 Epitope. <i>Journal of Biological Chemistry</i> , 2011, 286, 41046-41056.	1.6	78
58	The RhoGEF GEF-H1 Is Required for Oncogenic RAS Signaling via KSR-1. <i>Cancer Cell</i> , 2014, 25, 181-195.	7.7	76
59	Developmentally Programmed Nuclear Destruction during Yeast Gametogenesis. <i>Developmental Cell</i> , 2012, 23, 35-44.	3.1	72
60	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. <i>Nature Metabolism</i> , 2020, 2, 499-513.	5.1	72
61	Affinity Selection from Peptide Libraries to Determine Substrate Specificity of Protein Tyrosine Phosphatases. <i>Analytical Biochemistry</i> , 1998, 258, 19-30.	1.1	70
62	CYCLoPs: A Comprehensive Database Constructed from Automated Analysis of Protein Abundance and Subcellular Localization Patterns in <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1223-1232.	0.8	69
63	Mammalian Cdk5 is a functional homologue of the budding yeast Pho85 cyclin-dependent protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 14445-14450.	3.3	67
64	Tailored tetravalent antibodies potently and specifically activate Wnt/Frizzled pathways in cells, organoids and mice. <i>ELife</i> , 2019, 8, .	2.8	67
65	Overexpression of the nonpancreatic secretory group II PLA2 messenger RNA and protein in colorectal adenomas from familial adenomatous polyposis patients. <i>Cancer Research</i> , 1998, 58, 500-3.	0.4	66
66	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
67	Selective targeting of neuroblastoma tumour-initiating cells by compounds identified in stem cell-based small molecule screens. <i>EMBO Molecular Medicine</i> , 2010, 2, 371-384.	3.3	62
68	Inhibition of SCF ubiquitin ligases by engineered ubiquitin variants that target the Cul1 binding site on the Skp1-F-box interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3527-3532.	3.3	61
69	Control of the RNA polymerase II phosphorylation state in promoter regions by CTD interaction domain-containing proteins RPRD1A and RPRD1B. <i>Transcription</i> , 2011, 2, 237-242.	1.7	59
70	Selective Inhibition of Histone Deacetylases Sensitizes Malignant Cells to Death Receptor Ligands. <i>Molecular Cancer Therapeutics</i> , 2010, 9, 246-256.	1.9	57
71	Functions of Pho85 cyclin-dependent kinases in budding yeast. , 2000, 4, 97-106.		55
72	Interaction Domains of Sos1/Grb2 Are Finely Tuned for Cooperative Control of Embryonic Stem Cell Fate. <i>Cell</i> , 2013, 152, 1008-1020.	13.5	53

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73	High-throughput genome-wide phenotypic screening via immunomagnetic cell sorting. <i>Nature Biomedical Engineering</i> , 2019, 3, 796-805.	11.6	53
74	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
75	Off-target effects associated with long dsRNAs in <i>Drosophila</i> RNAi screens. <i>Trends in Pharmacological Sciences</i> , 2007, 28, 149-151.	4.0	51
76	SATB2 augments $\hat{N}p63\hat{\pm}$ in head and neck squamous cell carcinoma. <i>EMBO Reports</i> , 2010, 11, 777-783.	2.0	50
77	Suppression of Cancer Progression by MGAT1 shRNA Knockdown. <i>PLoS ONE</i> , 2012, 7, e43721.	1.1	47
78	Targeting HER2 + breast cancer cells: Lysosomal accumulation of anti-HER2 antibodies is influenced by antibody binding site and conjugation to polymeric nanoparticles. <i>Journal of Controlled Release</i> , 2013, 172, 395-404.	4.8	47
79	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. <i>Structure</i> , 2019, 27, 590-605.e5.	1.6	47
80	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
81	Generation and Validation of Intracellular Ubiquitin Variant Inhibitors for USP7 and USP10. <i>Journal of Molecular Biology</i> , 2017, 429, 3546-3560.	2.0	44
82	Highly multiplexed and quantitative cell-surface protein profiling using genetically barcoded antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2836-2841.	3.3	44
83	System-Level Analysis of Neuroblastoma Tumor-Initiating Cells Implicates AURKB as a Novel Drug Target for Neuroblastoma. <i>Clinical Cancer Research</i> , 2010, 16, 4572-4582.	3.2	43
84	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. <i>Cancer Discovery</i> , 2022, 12, 1022-1045.	7.7	43
85	Dual Regulation by Pairs of Cyclin-Dependent Protein Kinases and Histone Deacetylases Controls G1 Transcription in Budding Yeast. <i>PLoS Biology</i> , 2009, 7, e1000188.	2.6	42
86	Context-dependent regulation of ferroptosis sensitivity. <i>Cell Chemical Biology</i> , 2022, 29, 1409-1418.e6.	2.5	42
87	The Mixed Lineage Leukemia (MLL) Fusion-Associated Gene <i>AF4</i> Promotes CD133 Transcription. <i>Cancer Research</i> , 2012, 72, 1929-1934.	0.4	40
88	A synthetic anti-Frizzled antibody engineered for broadened specificity exhibits enhanced anti-tumor properties. <i>MAbs</i> , 2018, 10, 1157-1167.	2.6	39
89	Pooled screening for antiproliferative inhibitors of protein-protein interactions. <i>Nature Chemical Biology</i> , 2016, 12, 275-281.	3.9	37
90	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

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91	Post-Translational Regulation of CD133 by ATase1/ATase2-Mediated Lysine Acetylation. <i>Journal of Molecular Biology</i> , 2014, 426, 2175-2182.	2.0	34
92	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , 2018, 9, 2280.	5.8	34
93	Analysis of early C2C12 myogenesis identifies stably and differentially expressed transcriptional regulators whose knock-down inhibits myoblast differentiation. <i>Physiological Genomics</i> , 2012, 44, 183-197.	1.0	33
94	shRNA Kinome Screen Identifies TBK1 as a Therapeutic Target for HER2+ Breast Cancer. <i>Cancer Research</i> , 2014, 74, 2119-2130.	0.4	32
95	<scp>CRISPR</scp> screens are feasible in <i> <scp>TP</scp> 53 </i> wildâ€type cells. <i>Molecular Systems Biology</i> , 2019, 15, e8679.	3.2	32
96	A comprehensive platform for highly multiplexed mammalian functional genetic screens. <i>BMC Genomics</i> , 2011, 12, 213.	1.2	31
97	A CD133-AKT-Wnt signaling axis drives glioblastoma brain tumor-initiating cells. <i>Oncogene</i> , 2020, 39, 1590-1599.	2.6	31
98	CD70 as an actionable immunotherapeutic target in recurrent glioblastoma and its microenvironment. , 2022, 10, e003289.		31
99	Efficient recovery of potent tumour-infiltrating lymphocytes through quantitative immunomagnetic cell sorting. <i>Nature Biomedical Engineering</i> , 2022, 6, 108-117.	11.6	31
100	A genome scale overexpression screen to reveal drug activity in human cells. <i>Genome Medicine</i> , 2014, 6, 32.	3.6	29
101	FAM72A antagonizes UNG2 to promote mutagenic repair during antibody maturation. <i>Nature</i> , 2021, 600, 324-328.	13.7	29
102	Genetic interaction networks in cancer cells. <i>Current Opinion in Genetics and Development</i> , 2019, 54, 64-72.	1.5	28
103	IPO11 mediates $\beta$ 2catenin nuclear import in a subset of colorectal cancers. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	27
104	Pooled Lentiviral shRNA Screening for Functional Genomics in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2011, 781, 161-182.	0.4	26
105	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. <i>Acta Neuropathologica</i> , 2017, 134, 923-940.	3.9	26
106	Functional genomics identifies new synergistic therapies for retinoblastoma. <i>Oncogene</i> , 2020, 39, 5338-5357.	2.6	26
107	Pooled Lentiviral CRISPR-Cas9 Screens for Functional Genomics in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2019, 1869, 169-188.	0.4	25
108	Inhibition of SREBP1 sensitizes cells to death ligands. <i>Oncotarget</i> , 2011, 2, 186-196.	0.8	25

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109	Interactions between Pho85 cyclin-dependent kinase complexes and the Swi5 transcription factor in budding yeast. <i>Molecular Microbiology</i> , 2000, 35, 825-834.	1.2	24
110	A genome wide shRNA screen identifies $\hat{1}\pm/\hat{1}^2$ hydrolase domain containing 4 (ABHD4) as a novel regulator of anoikis resistance. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2012, 17, 666-678.	2.2	24
111	RNA Interference Screen to Identify Kinases That Suppress Rescue of $\hat{1}^m$ F508-CFTR*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1569-1583.	2.5	24
112	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
113	Structure-guided design fine-tunes pharmacokinetics, tolerability, and antitumor profile of multispecific frizzled antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6812-6817.	3.3	23
114	LRRC8A-containing chloride channel is crucial for cell volume recovery and survival under hypertonic conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	23
115	The protein kinase Pho85 is required for asymmetric accumulation of the Ash1 protein in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2001, 42, 345-353.	1.2	21
116	Resveratrol has anti-leukemic activity associated with decreased O-GlcNAcylated proteins. <i>Experimental Hematology</i> , 2013, 41, 675-686.	0.2	19
117	SMYD2 lysine methyltransferase regulates leukemia cell growth and regeneration after genotoxic stress. <i>Oncotarget</i> , 2017, 8, 16712-16727.	0.8	18
118	Dependence of Human Colorectal Cells Lacking the FBW7 Tumor Suppressor on the Spindle Assembly Checkpoint. <i>Genetics</i> , 2015, 201, 885-895.	1.2	17
119	The Global Transcriptional Activator of <i>Saccharomyces cerevisiae</i> , Gcr1p, Mediates the Response to Glucose by Stimulating Protein Synthesis and CLN-Dependent Cell Cycle Progression. <i>Genetics</i> , 2003, 165, 1017-1029.	1.2	17
120	Ac`septin' a Signal. <i>Developmental Cell</i> , 2003, 5, 528-530.	3.1	15
121	CD133-Targeted Niche-Dependent Therapy in Cancer. <i>American Journal of Pathology</i> , 2014, 184, 1256-1262.	1.9	15
122	Selection of recombinant antiâ€‹scp>SH</scp>3 domain antibodies by highâ€‹throughput phage display. <i>Protein Science</i> , 2015, 24, 1890-1900.	3.1	15
123	NOX4 links metabolic regulation in pancreatic cancer to endoplasmic reticulum redox vulnerability and dependence on PRDX4. <i>Science Advances</i> , 2021, 7, .	4.7	15
124	SnapShot: High-Throughput Sequencing Applications. <i>Cell</i> , 2011, 146, 1044-1044.e2.	13.5	14
125	Identification of RNF168 as a PML nuclear body regulator. <i>Journal of Cell Science</i> , 2015, 129, 580-91.	1.2	14
126	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



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127	Kin17 facilitates multiple double-strand break repair pathways that govern B cell class switching. <i>Scientific Reports</i> , 2016, 6, 37215.	1.6	11
128	Differential regulation of FGFR3 by PTPN1 and PTPN2. <i>Proteomics</i> , 2015, 15, 419-433.	1.3	10
129	Cytokinetic effects of Wee1 disruption in pancreatic cancer. <i>Cell Cycle</i> , 2016, 15, 593-604.	1.3	10
130	A rapid in vitro methodology for simultaneous target discovery and antibody generation against functional cell subpopulations. <i>Scientific Reports</i> , 2019, 9, 842.	1.6	10
131	Paralogous synthetic lethality underlies genetic dependencies of the cancer-mutated gene <i>STAG2</i> . <i>Life Science Alliance</i> , 2021, 4, e202101083.	1.3	10
132	The Inhibitory NKR-P1B:Clr-b Recognition Axis Facilitates Detection of Oncogenic Transformation and Cancer Immunosurveillance. <i>Cancer Research</i> , 2018, 78, 3589-3603.	0.4	9
133	Pooled CRISPR-Based Genetic Screens in Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2019, , .	0.2	9
134	Direct interaction between CEP85 and STIL mediates PLk4-driven directed cell migration. <i>Journal of Cell Science</i> , 2020, 133, .	1.2	9
135	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. <i>Molecular Systems Biology</i> , 2021, 17, e10013.	3.2	8
136	A versatile lentiviral expression system to identify mammalian protein-protein interactions. <i>Methods</i> , 2012, 57, 409-416.	1.9	7
137	EPH Profiling of BTIC Populations in Glioblastoma Multiforme Using CyTOF. <i>Methods in Molecular Biology</i> , 2019, 1869, 155-168.	0.4	7
138	Analysis of combinatorial CRISPR screens with the Orthrus scoring pipeline. <i>Nature Protocols</i> , 2021, 16, 4766-4798.	5.5	7
139	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. <i>Journal of Molecular Biology</i> , 2019, 431, 1160-1171.	2.0	6
140	Miniature Short Hairpin RNA Screens to Characterize Antiproliferative Drugs. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1375-1387.	0.8	5
141	Dual Antigen T Cell Engagers Targeting CA9 as an Effective Immunotherapeutic Modality for Targeting CA9 in Solid Tumors. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	5
142	Scaling up the systematic hunt for mammalian genetic interactions. <i>Nature Methods</i> , 2013, 10, 397-399.	9.0	4
143	Automated inference procedure for the determination of cell growth parameters. <i>Physical Review E</i> , 2016, 93, 012402.	0.8	4
144	Forward genetic screen in human podocytes identifies diphthamide biosynthesis genes as regulators of adhesion. <i>American Journal of Physiology - Renal Physiology</i> , 2019, 317, F1593-F1604.	1.3	4

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145	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
146	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
147	Extensive mapping of an innate immune network with <scp>CRISPR</scp>. <i>Molecular Systems Biology</i> , 2015, 11, 821.	3.2	2
148	Design and Experimental Validation of Small Activating RNAs Targeting an Exogenous Promoter in Human Cells. <i>ACS Synthetic Biology</i> , 2017, 6, 628-637.	1.9	2
149	A Phosphoproteomics Approach to Identify Candidate Kinase Inhibitor Pathway Targets in Lymphoma-Like Primary Cell Lines. <i>Current Drug Discovery Technologies</i> , 2013, 10, 283-304.	0.6	2
150	RNA interference screens to uncover membrane protein biology. <i>Briefings in Functional Genomics</i> , 2013, 12, 422-429.	1.3	0
151	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
152	Genome-Wide shRNA Screen for DNA Damage Response Regulators in Human Hematopoietic Stem and Progenitor Cells. <i>Blood</i> , 2011, 118, 1289-1289.	0.6	0
153	Inhibition of Mitochondrial Translation As a Therapeutic Strategy for Acute Myeloid Leukemia (AML). <i>Blood</i> , 2011, 118, 233-233.	0.6	0
154	Identification of Acquired Notch3 Dependency in Metastatic Head and Neck Cancer. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
155	A Method to Map Gene Essentiality of Human Pluripotent Stem Cells by Genome-Scale CRISPR Screens with Inducible Cas9. <i>Methods in Molecular Biology</i> , 2022, 2377, 1-27.	0.4	0