

Jason Moffat

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

158
papers

16,386
citations

55
h-index

127
g-index

181
ext. papers

20,348
ext. citations

15.4
avg, IF

6.08
L-index

#	Paper	IF	Citations
158	CD70 as an actionable immunotherapeutic target in recurrent glioblastoma and its microenvironment. 2022 , 10,		4
157	Efficient recovery of potent tumour-infiltrating lymphocytes through quantitative immunomagnetic cell sorting.. <i>Nature Biomedical Engineering</i> , 2022 ,	19	2
156	High-content CRISPR screening. <i>Nature Reviews Methods Primers</i> , 2022 , 2,		10
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	1.4	
154	FAM72A antagonizes UNG2 to promote mutagenic repair during antibody maturation. <i>Nature</i> , 2021 , 600, 324-328	50.4	6
153	NOX4 links metabolic regulation in pancreatic cancer to endoplasmic reticulum redox vulnerability and dependence on PRDX4. <i>Science Advances</i> , 2021 , 7,	14.3	3
152	A method for benchmarking genetic screens reveals a predominant mitochondrial bias. <i>Molecular Systems Biology</i> , 2021 , 17, e10013	12.2	0
151	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,	11.5	3
150	Colorectal Cancer Cells Enter a Diapause-like DTP State to Survive Chemotherapy. <i>Cell</i> , 2021 , 184, 226-243.e2168	11.2	16
149	Paralogous synthetic lethality underlies genetic dependencies of the cancer-mutated gene. <i>Life Science Alliance</i> , 2021 , 4,	5.8	1
148	Analysis of combinatorial CRISPR screens with the Orthrus scoring pipeline. <i>Nature Protocols</i> , 2021 , 16, 4766-4798	18.8	3
147	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer.. <i>Cancer Discovery</i> , 2021 ,	24.4	4
146	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	14.6	22
145	The Rational Development of CD133-Targeting Immunotherapies for Glioblastoma. <i>Cell Stem Cell</i> , 2020 , 26, 832-844.e6	18	41
144	Functional genomics identifies new synergistic therapies for retinoblastoma. <i>Oncogene</i> , 2020 , 39, 5338-5357	10	10
143	Genetic interaction mapping and exon-resolution functional genomics with a hybrid Cas9-Cas12a platform. <i>Nature Biotechnology</i> , 2020 , 38, 638-648	44.5	54
142	IPO11 mediates Eatenin nuclear import in a subset of colorectal cancers. <i>Journal of Cell Biology</i> , 2020 , 219,	7.3	16

141	A CD133-AKT-Wnt signaling axis drives glioblastoma brain tumor-initiating cells. <i>Oncogene</i> , 2020 , 39, 1590-1599	9.2	17
140	Digital microfluidic isolation of single cells for -Omics. <i>Nature Communications</i> , 2020 , 11, 5632	17.4	29
139	Functional genomic landscape of cancer-intrinsic evasion of killing by T cells. <i>Nature</i> , 2020 , 586, 120-126	50.4	82
138	Direct interaction between CEP85 and STIL mediates PLK4-driven directed cell migration. <i>Journal of Cell Science</i> , 2020 , 133,	5.3	5
137	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	4.3	1
136	High-throughput genome-wide phenotypic screening via immunomagnetic cell sorting. <i>Nature Biomedical Engineering</i> , 2019 , 3, 796-805	19	32
135	A rapid in vitro methodology for simultaneous target discovery and antibody generation against functional cell subpopulations. <i>Scientific Reports</i> , 2019 , 9, 842	4.9	7
134	Structural and Functional Characterization of Ubiquitin Variant Inhibitors of USP15. <i>Structure</i> , 2019 , 27, 590-605.e5	5.2	32
133	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	4.8	9
132	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	11.5	13
131	Global Genetic Networks and the Genotype-to-Phenotype Relationship. <i>Cell</i> , 2019 , 177, 85-100	56.2	87
130	Genetic interaction networks in cancer cells. <i>Current Opinion in Genetics and Development</i> , 2019 , 54, 64-72	7.9	16
129	Essential Gene Profiles for Human Pluripotent Stem Cells Identify Uncharacterized Genes and Substrate Dependencies. <i>Cell Reports</i> , 2019 , 27, 599-615.e12	10.6	42
128	Yeast Two-Hybrid Analysis for Ubiquitin Variant Inhibitors of Human Deubiquitinases. <i>Journal of Molecular Biology</i> , 2019 , 431, 1160-1171	6.5	2
127	Identifying chemogenetic interactions from CRISPR screens with drugZ. <i>Genome Medicine</i> , 2019 , 11, 52	14.4	45
126	Pooled CRISPR-Based Genetic Screens in Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	5
125	Tailored tetravalent antibodies potently and specifically activate Wnt/Frizzled pathways in cells, organoids and mice. <i>ELife</i> , 2019 , 8,	8.9	24
124	CRISPR screens are feasible in TP53 wild-type cells. <i>Molecular Systems Biology</i> , 2019 , 15, e8679	12.2	21

123	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	5.4	0
122	Pooled Lentiviral CRISPR-Cas9 Screens for Functional Genomics in Mammalian Cells. <i>Methods in Molecular Biology</i> , 2019 , 1869, 169-188	1.4	21
121	EPH Profiling of BTIC Populations in Glioblastoma Multiforme Using CyTOF. <i>Methods in Molecular Biology</i> , 2019 , 1869, 155-168	1.4	3
120	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	11.5	30
119	The Inhibitory NKR-P1B:Clr-b Recognition Axis Facilitates Detection of Oncogenic Transformation and Cancer Immunosurveillance. <i>Cancer Research</i> , 2018 , 78, 3589-3603	10.1	6
118	Emerging and evolving concepts in gene essentiality. <i>Nature Reviews Genetics</i> , 2018 , 19, 34-49	30.1	131
117	The shieldin complex mediates 53BP1-dependent DNA repair. <i>Nature</i> , 2018 , 560, 117-121	50.4	277
116	Map of synthetic rescue interactions for the Fanconi anemia DNA repair pathway identifies USP48. <i>Nature Communications</i> , 2018 , 9, 2280	17.4	19
115	Protocadherin-1 is essential for cell entry by New World hantaviruses. <i>Nature</i> , 2018 , 563, 559-563	50.4	49
114	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	17.6	51
113	A synthetic anti-Frizzled antibody engineered for broadened specificity exhibits enhanced anti-tumor properties. <i>MAbs</i> , 2018 , 10, 1157-1167	6.6	22
112	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	10.1	30
111	CRISPR screens identify genomic ribonucleotides as a source of PARP-trapping lesions. <i>Nature</i> , 2018 , 559, 285-289	50.4	178
110	Multilayered Control of Alternative Splicing Regulatory Networks by Transcription Factors. <i>Molecular Cell</i> , 2017 , 65, 539-553.e7	17.6	65
109	Intratumoral heterogeneity: pathways to treatment resistance and relapse in human glioblastoma. <i>Annals of Oncology</i> , 2017 , 28, 1448-1456	10.3	174
108	Generation and Validation of Intracellular Ubiquitin Variant Inhibitors for USP7 and USP10. <i>Journal of Molecular Biology</i> , 2017 , 429, 3546-3560	6.5	31
107	Design and Experimental Validation of Small Activating RNAs Targeting an Exogenous Promoter in Human Cells. <i>ACS Synthetic Biology</i> , 2017 , 6, 628-637	5.7	2
106	RNAi screen identifies essential regulators of human brain metastasis-initiating cells. <i>Acta Neuropathologica</i> , 2017 , 134, 923-940	14.3	19

105	Evaluation and Design of Genome-Wide CRISPR/SpCas9 Knockout Screens. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 2719-2727	3.2	211
104	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	50.5	178
103	SMYD2 lysine methyltransferase regulates leukemia cell growth and regeneration after genotoxic stress. <i>Oncotarget</i> , 2017 , 8, 16712-16727	3.3	13
102	Kin17 facilitates multiple double-strand break repair pathways that govern B cell class switching. <i>Scientific Reports</i> , 2016 , 6, 37215	4.9	8
101	Automated inference procedure for the determination of cell growth parameters. <i>Physical Review E</i> , 2016 , 93, 012402	2.4	3
100	The SAGA Deubiquitination Module Promotes DNA Repair and Class Switch Recombination through ATM and DNAPK-Mediated H2AX Formation. <i>Cell Reports</i> , 2016 , 15, 1554-1565	10.6	65
99	BAGEL: a computational framework for identifying essential genes from pooled library screens. <i>BMC Bioinformatics</i> , 2016 , 17, 164	3.6	124
98	Functional Genomic Landscape of Human Breast Cancer Drivers, Vulnerabilities, and Resistance. <i>Cell</i> , 2016 , 164, 293-309	56.2	259
97	Cytokinetic effects of Wee1 disruption in pancreatic cancer. <i>Cell Cycle</i> , 2016 , 15, 593-604	4.7	8
96	Pooled screening for antiproliferative inhibitors of protein-protein interactions. <i>Nature Chemical Biology</i> , 2016 , 12, 275-81	11.7	26
95	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. <i>Molecular Cell</i> , 2016 , 62, 121-36	17.6	110
94	SMN and symmetric arginine dimethylation of RNA polymerase II C-terminal domain control termination. <i>Nature</i> , 2016 , 529, 48-53	50.4	130
93	Identification of RNF168 as a PML nuclear body regulator. <i>Journal of Cell Science</i> , 2016 , 129, 580-91	5.3	12
92	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	4.8	15
91	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, 3527-32	11.5	47
90	Natural Variation in Gene Expression Modulates the Severity of Mutant Phenotypes. <i>Cell</i> , 2015 , 162, 391-402	56.2	87
89	RNA Interference Screen to Identify Kinases That Suppress Rescue of B508-CFTR. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 1569-83	7.6	20
88	A High Through-put Platform for Recombinant Antibodies to Folded Proteins. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2833-47	7.6	75

87	Identification of P450 Oxidoreductase as a Major Determinant of Sensitivity to Hypoxia-Activated Prodrugs. <i>Cancer Research</i> , 2015 , 75, 4211-23	10.1	56
86	Dependence of Human Colorectal Cells Lacking the FBW7 Tumor Suppressor on the Spindle Assembly Checkpoint. <i>Genetics</i> , 2015 , 201, 885-95	4	12
85	High-Resolution CRISPR Screens Reveal Fitness Genes and Genotype-Specific Cancer Liabilities. <i>Cell</i> , 2015 , 163, 1515-26	56.2	863
84	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, 1223-32	3.2	54
83	Extensive mapping of an innate immune network with CRISPR. <i>Molecular Systems Biology</i> , 2015 , 11, 821	12.2	1
82	Selection of recombinant anti-SH3 domain antibodies by high-throughput phage display. <i>Protein Science</i> , 2015 , 24, 1890-900	6.3	12
81	Inhibition of the Mitochondrial Protease ClpP as a Therapeutic Strategy for Human Acute Myeloid Leukemia. <i>Cancer Cell</i> , 2015 , 27, 864-76	24.3	191
80	Yeast Proteome Dynamics from Single Cell Imaging and Automated Analysis. <i>Cell</i> , 2015 , 161, 1413-24	56.2	187
79	INNATE IMMUNITY. Cytosolic detection of the bacterial metabolite HBP activates TIFA-dependent innate immunity. <i>Science</i> , 2015 , 348, 1251-5	33.3	99
78	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. <i>Cell</i> , 2015 , 163, 1484-99	56.2	316
77	Yeast Proteome Dynamics from Single Cell Imaging and Automated Analysis. <i>Cell</i> , 2015 , 162, 221	56.2	4
76	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	10.6	97
75	Differential regulation of FGFR3 by PTPN1 and PTPN2. <i>Proteomics</i> , 2015 , 15, 419-33	4.8	9
74	Genome-wide RNAi analysis reveals that simultaneous inhibition of specific mevalonate pathway genes potentiates tumor cell death. <i>Oncotarget</i> , 2015 , 6, 26909-21	3.3	34
73	The mammalian-membrane two-hybrid assay (MaMTH) for probing membrane-protein interactions in human cells. <i>Nature Methods</i> , 2014 , 11, 585-92	21.6	105
72	shRNA kinome screen identifies TBK1 as a therapeutic target for HER2+ breast cancer. <i>Cancer Research</i> , 2014 , 74, 2119-30	10.1	26
71	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	14.4	67
70	A genome scale overexpression screen to reveal drug activity in human cells. <i>Genome Medicine</i> , 2014 , 6, 32	14.4	21

69	The RhoGEF GEF-H1 is required for oncogenic RAS signaling via KSR-1. <i>Cancer Cell</i> , 2014 , 25, 181-95	24.3	64
68	CD133-targeted niche-dependent therapy in cancer: a multipronged approach. <i>American Journal of Pathology</i> , 2014 , 184, 1256-62	5.8	13
67	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, 2542-7	11.5	82
66	Measuring error rates in genomic perturbation screens: gold standards for human functional genomics. <i>Molecular Systems Biology</i> , 2014 , 10, 733	12.2	203
65	Post-translational regulation of CD133 by ATase1/ATase2-mediated lysine acetylation. <i>Journal of Molecular Biology</i> , 2014 , 426, 2175-82	6.5	24
64	Evaluating Chromatin Regulators in Cancer Cell Lines Through RNAi-Glasses 2014 , 297-308		
63	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	11.7	41
62	RNA interference screens to uncover membrane protein biology. <i>Briefings in Functional Genomics</i> , 2013 , 12, 422-9	4.9	
61	A strategy for modulation of enzymes in the ubiquitin system. <i>Science</i> , 2013 , 339, 590-5	33.3	199
60	Resveratrol has anti-leukemic activity associated with decreased O-GlcNAcylated proteins. <i>Experimental Hematology</i> , 2013 , 41, 675-86	3.1	16
59	Interaction domains of Sos1/Grb2 are finely tuned for cooperative control of embryonic stem cell fate. <i>Cell</i> , 2013 , 152, 1008-20	56.2	45
58	MBNL proteins repress ES-cell-specific alternative splicing and reprogramming. <i>Nature</i> , 2013 , 498, 241-550.4	222	
57	Integrated genomic, transcriptomic, and RNA-interference analysis of genes in somatic copy number gains in pancreatic ductal adenocarcinoma. <i>Pancreas</i> , 2013 , 42, 1016-26	2.6	3
56	Miniature short hairpin RNA screens to characterize antiproliferative drugs. <i>G3: Genes, Genomes, Genetics</i> , 2013 , 3, 1375-87	3.2	4
55	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013 , 9, 696	12.2	69
54	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	1.5	2
53	Regulation of CD133 by HDAC6 promotes E-catenin signaling to suppress cancer cell differentiation. <i>Cell Reports</i> , 2012 , 2, 951-63	10.6	131
52	A versatile lentiviral expression system to identify mammalian protein-protein interactions. <i>Methods</i> , 2012 , 57, 409-16	4.6	6

51	Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. <i>Nature Cell Biology</i> , 2012 , 14, 966-76	23.4	322
50	Essential gene profiles in breast, pancreatic, and ovarian cancer cells. <i>Cancer Discovery</i> , 2012 , 2, 172-189	24.4	221
49	Developmentally programmed nuclear destruction during yeast gametogenesis. <i>Developmental Cell</i> , 2012 , 23, 35-44	10.2	51
48	Suppression of cancer progression by MGAT1 shRNA knockdown. <i>PLoS ONE</i> , 2012 , 7, e43721	3.7	31
47	The mixed lineage leukemia (MLL) fusion-associated gene AF4 promotes CD133 transcription. <i>Cancer Research</i> , 2012 , 72, 1929-34	10.1	34
46	A genome wide shRNA screen identifies a hydrolase domain containing 4 (ABHD4) as a novel regulator of anoikis resistance. <i>Apoptosis: an International Journal on Programmed Cell Death</i> , 2012 , 17, 666-78	5.4	20
45	Analysis of early C2C12 myogenesis identifies stably and differentially expressed transcriptional regulators whose knock-down inhibits myoblast differentiation. <i>Physiological Genomics</i> , 2012 , 44, 183-97	3.6	25
44	COLT-Cancer: functional genetic screening resource for essential genes in human cancer cell lines. <i>Nucleic Acids Research</i> , 2012 , 40, D957-63	20.1	44
43	SnapShot: High-throughput sequencing applications. <i>Cell</i> , 2011 , 146, 1044, 1044.e1-2	56.2	12
42	Pooled lentiviral shRNA screening for functional genomics in mammalian cells. <i>Methods in Molecular Biology</i> , 2011 , 781, 161-82	1.4	23
41	Inhibition of mitochondrial translation as a therapeutic strategy for human acute myeloid leukemia. <i>Cancer Cell</i> , 2011 , 20, 674-88	24.3	425
40	A comprehensive platform for highly multiplexed mammalian functional genetic screens. <i>BMC Genomics</i> , 2011 , 12, 213	4.5	28
39	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, 237-42	4.8	51
38	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, 41046-56	5.4	66
37	Inhibition of SREBP1 sensitizes cells to death ligands. <i>Oncotarget</i> , 2011 , 2, 186-96	3.3	23
36	Genome-Wide shRNA Screen for DNA Damage Response Regulators in Human Hematopoietic Stem and Progenitor Cells. <i>Blood</i> , 2011 , 118, 1289-1289	2.2	
35	Inhibition of Mitochondrial Translation As a Therapeutic Strategy for Acute Myeloid Leukemia (AML). <i>Blood</i> , 2011 , 118, 233-233	2.2	
34	SATB2 augments p63 in head and neck squamous cell carcinoma. <i>EMBO Reports</i> , 2010 , 11, 777-83	6.5	41

33	A lentiviral functional proteomics approach identifies chromatin remodeling complexes important for the induction of pluripotency. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 811-23	7.6	77
32	Selective inhibition of histone deacetylases sensitizes malignant cells to death receptor ligands. <i>Molecular Cancer Therapeutics</i> , 2010 , 9, 246-56	6.1	47
31	System-level analysis of neuroblastoma tumor-initiating cells implicates AURKB as a novel drug target for neuroblastoma. <i>Clinical Cancer Research</i> , 2010 , 16, 4572-82	12.9	36
30	The ubiquitin-activating enzyme E1 as a therapeutic target for the treatment of leukemia and multiple myeloma. <i>Blood</i> , 2010 , 115, 2251-9	2.2	122
29	Selective targeting of neuroblastoma tumour-initiating cells by compounds identified in stem cell-based small molecule screens. <i>EMBO Molecular Medicine</i> , 2010 , 2, 371-84	12	59
28	A role for the TGFbeta-Par6 polarity pathway in breast cancer progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 14028-33	11.5	103
27	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	9.7	34
26	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, 1826-31	11.5	290
25	Off-target effects associated with long dsRNAs in Drosophila RNAi screens. <i>Trends in Pharmacological Sciences</i> , 2007 , 28, 149-51	13.2	44
24	CellProfiler: image analysis software for identifying and quantifying cell phenotypes. <i>Genome Biology</i> , 2006 , 7, R100	18.3	3203
23	A lentiviral RNAi library for human and mouse genes applied to an arrayed viral high-content screen. <i>Cell</i> , 2006 , 124, 1283-98	56.2	1340
22	Ablation in mice of the mTORC components raptor, rictor, or mLST8 reveals that mTORC2 is required for signaling to Akt-FOXO and PKCalpha, but not S6K1. <i>Developmental Cell</i> , 2006 , 11, 859-71	10.2	1122
21	Building mammalian signalling pathways with RNAi screens. <i>Nature Reviews Molecular Cell Biology</i> , 2006 , 7, 177-87	48.7	179
20	Late-G1 cyclin-CDK activity is essential for control of cell morphogenesis in budding yeast. <i>Nature Cell Biology</i> , 2004 , 6, 59-66	23.4	76
19	Exploration of essential gene functions via titratable promoter alleles. <i>Cell</i> , 2004 , 118, 31-44	56.2	475
18	AcldeptinUa signal: kinase regulation by septins. <i>Developmental Cell</i> , 2003 , 5, 528-30	10.2	11
17	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, 1017-29	4	13
16	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, 5076-88	4.8	76

15	The protein kinase Pho85 is required for asymmetric accumulation of the Ash1 protein in <i>Saccharomyces cerevisiae</i> . <i>Molecular Microbiology</i> , 2001 , 42, 345-53	4.1	18
14	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, 6515-28	4.8	102
13	Interactions between Pho85 cyclin-dependent kinase complexes and the Swi5 transcription factor in budding yeast. <i>Molecular Microbiology</i> , 2000 , 35, 825-34	4.1	24
12	Functions of Pho85 cyclin-dependent kinases in budding yeast. <i>Progress in Cell Cycle Research</i> , 2000 , 4, 97-106		50
11	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, 14445-50	11.5	62
10	Affinity selection from peptide libraries to determine substrate specificity of protein tyrosine phosphatases. <i>Analytical Biochemistry</i> , 1998 , 258, 19-30	3.1	68
9	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, 3289-99	4.8	108
8	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	10.1	55
7	Mechanism of inhibition of protein-tyrosine phosphatases by vanadate and pervanadate. <i>Journal of Biological Chemistry</i> , 1997 , 272, 843-51	5.4	657
6	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer		1
5	Coessentiality and cofunctionality: a network approach to learning genetic vulnerabilities from cancer cell line fitness screens		2
4	FAM72A antagonizes UNG2 to promote mutagenic uracil repair during antibody maturation		1
3	Identifying chemogenetic interactions from CRISPR knockout screens with drugZ		1
2	Cell cycle regulation of mitochondrial protein import revealed by genome-scale pooled bimolecular fluorescence complementation screening		1
1	A cohesin traffic pattern genetically linked to gene regulation		3