

Pablo Tamayo

List of Publications by Citations

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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.

63
papers

38,811
citations

34
h-index

65
g-index

65
ext. papers

53,893
ext. citations

15.4
avg, IF

6.75
L-index

#	Paper	IF	Citations
63	Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15545-50	11.5	24578
62	The Molecular Signatures Database (MSigDB) hallmark gene set collection. <i>Cell Systems</i> , 2015 , 1, 417-425	10.6	3213
61	Molecular signatures database (MSigDB) 3.0. <i>Bioinformatics</i> , 2011 , 27, 1739-40	7.2	2487
60	Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. <i>Nature</i> , 2009 , 462, 108-12	50.4	1614
59	Metagenes and molecular pattern discovery using matrix factorization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 4164-9	11.5	1178
58	Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene Expression Microarray Data. <i>Machine Learning</i> , 2003 , 52, 91-118	4	1108
57	CDK8 is a colorectal cancer oncogene that regulates beta-catenin activity. <i>Nature</i> , 2008 , 455, 547-51	50.4	519
56	Integrative genomic analysis of medulloblastoma identifies a molecular subgroup that drives poor clinical outcome. <i>Journal of Clinical Oncology</i> , 2011 , 29, 1424-30	2.2	513
55	Synthetic lethal interaction between oncogenic KRAS dependency and STK33 suppression in human cancer cells. <i>Cell</i> , 2009 , 137, 821-34	56.2	454
54	A melanoma cell state distinction influences sensitivity to MAPK pathway inhibitors. <i>Cancer Discovery</i> , 2014 , 4, 816-27	24.4	338
53	Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12372-7	11.5	321
52	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , 2014 , 1, 140035	8.2	251
51	Inhibition of KRAS-driven tumorigenicity by interruption of an autocrine cytokine circuit. <i>Cancer Discovery</i> , 2014 , 4, 452-65	24.4	137
50	Targeted tumor-penetrating siRNA nanocomplexes for credentialing the ovarian cancer oncogene ID4. <i>Science Translational Medicine</i> , 2012 , 4, 147ra112	17.5	135
49	Tumor innate immunity primed by specific interferon-stimulated endogenous retroviruses. <i>Nature Medicine</i> , 2018 , 24, 1143-1150	50.5	131
48	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. <i>Nature Biotechnology</i> , 2016 , 34, 419-23	44.5	127
47	Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. <i>Cell Systems</i> , 2018 , 6, 484-495	15.24	5124

46	Targeting an IKBKE cytokine network impairs triple-negative breast cancer growth. <i>Journal of Clinical Investigation</i> , 2014 , 124, 5411-23	15.9	111
45	Metagene projection for cross-platform, cross-species characterization of global transcriptional states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5959-64	11.5	100
44	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016 , 6, 714-26	24.4	100
43	A genetic basis for the variation in the vulnerability of cancer to DNA damage. <i>Nature Communications</i> , 2016 , 7, 11428	17.4	95
42	ATARiS: computational quantification of gene suppression phenotypes from multisample RNAi screens. <i>Genome Research</i> , 2013 , 23, 665-78	9.7	93
41	A Platform of Synthetic Lethal Gene Interaction Networks Reveals that the GNAQ Uveal Melanoma Oncogene Controls the Hippo Pathway through FAK. <i>Cancer Cell</i> , 2019 , 35, 457-472.e5	24.3	93
40	Integrative radiogenomic profiling of squamous cell lung cancer. <i>Cancer Research</i> , 2013 , 73, 6289-98	10.1	83
39	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018 , 34, 396-410.e8	24.3	74
38	Illuminating the Onco-GPCRome: Novel G protein-coupled receptor-driven oncoendocrine networks and targets for cancer immunotherapy. <i>Journal of Biological Chemistry</i> , 2019 , 294, 11062-11086	5.4	73
37	Assembly and activation of the Hippo signalome by FAT1 tumor suppressor. <i>Nature Communications</i> , 2018 , 9, 2372	17.4	62
36	Predicting relapse in patients with medulloblastoma by integrating evidence from clinical and genomic features. <i>Journal of Clinical Oncology</i> , 2011 , 29, 1415-23	2.2	58
35	Characterizing genomic alterations in cancer by complementary functional associations. <i>Nature Biotechnology</i> , 2016 , 34, 539-46	44.5	57
34	Integrated genomic analysis of the 8q24 amplification in endometrial cancers identifies ATAD2 as essential to MYC-dependent cancers. <i>PLoS ONE</i> , 2013 , 8, e54873	3.7	56
33	DiSCoVERing Innovative Therapies for Rare Tumors: Combining Genetically Accurate Disease Models with In Silico Analysis to Identify Novel Therapeutic Targets. <i>Clinical Cancer Research</i> , 2016 , 22, 3903-14	12.9	43
32	An expanded universe of cancer targets. <i>Cell</i> , 2021 , 184, 1142-1155	56.2	38
31	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in E-Catenin-Active Cancers. <i>Cell Systems</i> , 2016 , 3, 302-316.e4	10.6	36
30	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018 , 50, 937-943	36.3	35
29	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. <i>Nature Communications</i> , 2019 , 10, 2188	17.4	34

28	MicroSCALE screening reveals genetic modifiers of therapeutic response in melanoma. <i>Science Signaling</i> , 2012 , 5, rs4	8.8	31
27	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. <i>Cell Systems</i> , 2018 , 7, 656-666.e4	10.6	30
26	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. <i>Cell Systems</i> , 2017 , 5, 105-118.e9	10.6	27
25	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. <i>Onc Immunology</i> , 2019 , 8, 1550341	7.2	26
24	Overcoming Resistance to Dual Innate Immune and MEK Inhibition Downstream of KRAS. <i>Cancer Cell</i> , 2018 , 34, 439-452.e6	24.3	24
23	Cannabinoids Promote Progression of HPV-Positive Head and Neck Squamous Cell Carcinoma via p38 MAPK Activation. <i>Clinical Cancer Research</i> , 2020 , 26, 2693-2703	12.9	22
22	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. <i>Blood Advances</i> , 2019 , 3, 2845-2858	7.8	21
21	The GenePattern Notebook Environment. <i>Cell Systems</i> , 2017 , 5, 149-151.e1	10.6	20
20	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. <i>ELife</i> , 2020 , 9,	8.9	19
19	Kataegis Expression Signature in Breast Cancer Is Associated with Late Onset, Better Prognosis, and Higher HER2 Levels. <i>Cell Reports</i> , 2016 , 16, 672-83	10.6	19
18	Role of ultraviolet mutational signature versus tumor mutation burden in predicting response to immunotherapy. <i>Molecular Oncology</i> , 2020 , 14, 1680-1694	7.9	16
17	Comprehensive Genomic Profiling Reveals Diverse but Actionable Molecular Portfolios across Hematologic Malignancies: Implications for Next Generation Clinical Trials. <i>Cancers</i> , 2018 , 11,	6.6	16
16	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020 , 39, 6327-6339	9.13	13
15	Mesenchymal and MAPK Expression Signatures Associate with Telomerase Promoter Mutations in Multiple Cancers. <i>Molecular Cancer Research</i> , 2020 , 18, 1050-1062	6.6	9
14	Functional Precision Medicine Identifies New Therapeutic Candidates for Medulloblastoma. <i>Cancer Research</i> , 2020 , 80, 5393-5407	10.1	9
13	Modelling bistable tumour population dynamics to design effective treatment strategies. <i>Journal of Theoretical Biology</i> , 2019 , 474, 88-102	2.3	6
12	TEAD1 and TEAD3 Play Redundant Roles in the Regulation of Human Epidermal Proliferation. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 2081-2084.e4	4.3	6
11	Human induced pluripotent stem cell-derived macrophages ameliorate liver fibrosis. <i>Stem Cells</i> , 2021 , 39, 1701-1717	5.8	4

10	SPT6 promotes epidermal differentiation and blockade of an intestinal-like phenotype through control of transcriptional elongation. <i>Nature Communications</i> , 2021 , 12, 784	17.4	4
9	The multikinase inhibitor RXDX-105 is effective against neuroblastoma and. <i>Oncotarget</i> , 2019 , 10, 6323-6333	6.3	3
8	Cyclin E Overexpression in Human Mammary Epithelial Cells Promotes Epithelial Cancer-Specific Copy Number Alterations. <i>iScience</i> , 2019 , 19, 850-859	6.1	2
7	Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. <i>Nucleic Acids Research</i> , 2020 , 48, 7079-7098	20.1	2
6	WNT Signaling Driven by R-spondin 1 and LGR6 in High-grade Serous Ovarian Cancer. <i>Anticancer Research</i> , 2020 , 40, 6017-6028	2.3	2
5	KIT Cells Mediate Imatinib Resistance in Gastrointestinal Stromal Tumor. <i>Molecular Cancer Therapeutics</i> , 2021 , 20, 2035-2048	6.1	2
4	Visualizing and interpreting single-cell gene expression datasets with Similarity Weighted Nonnegative Embedding		1
3	TORC1/2 kinase inhibition depletes glutathione and synergizes with carboplatin to suppress the growth of MYC-driven medulloblastoma. <i>Cancer Letters</i> , 2021 , 504, 137-145	9.9	1
2	Analysis of CDK12 alterations in a pan-cancer database.. <i>Cancer Medicine</i> , 2021 ,	4.8	1
1	CHMP2A regulates tumor sensitivity to natural killer cell-mediated cytotoxicity.. <i>Nature Communications</i> , 2022 , 13, 1899	17.4	0