

# Pablo Tamayo

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

63,910  
citations

76196

40  
h-index

114278

63  
g-index

65  
all docs

65  
docs citations

65  
times ranked

95188  
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15545-15550.	3.3	38,922
2	The Molecular Signatures Database Hallmark Gene Set Collection. Cell Systems, 2015, 1, 417-425.	2.9	7,719
3	Molecular signatures database (MSigDB) 3.0. Bioinformatics, 2011, 27, 1739-1740.	1.8	4,752
4	Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. Nature, 2009, 462, 108-112.	13.7	2,707
5	Metagenes and molecular pattern discovery using matrix factorization. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4164-4169.	3.3	1,649
6	Title is missing!. Machine Learning, 2003, 52, 91-118.	3.4	1,613
7	Integrative Genomic Analysis of Medulloblastoma Identifies a Molecular Subgroup That Drives Poor Clinical Outcome. Journal of Clinical Oncology, 2011, 29, 1424-1430.	0.8	609
8	CDK8 is a colorectal cancer oncogene that regulates $\beta$ -catenin activity. Nature, 2008, 455, 547-551.	13.7	594
9	Synthetic Lethal Interaction between Oncogenic KRAS Dependency and STK33 Suppression in Human Cancer Cells. Cell, 2009, 137, 821-834.	13.5	510
10	A Melanoma Cell State Distinction Influences Sensitivity to MAPK Pathway Inhibitors. Cancer Discovery, 2014, 4, 816-827.	7.7	448
11	Systematic investigation of genetic vulnerabilities across cancer cell lines reveals lineage-specific dependencies in ovarian cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12372-12377.	3.3	383
12	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. Scientific Data, 2014, 1, 140035.	2.4	328
13	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. Nature Biotechnology, 2016, 34, 419-423.	9.4	245
14	Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. Cell Systems, 2018, 6, 484-495.e5.	2.9	215
15	Tumor innate immunity primed by specific interferon-stimulated endogenous retroviruses. Nature Medicine, 2018, 24, 1143-1150.	15.2	212
16	Inhibition of KRAS-Driven Tumorigenicity by Interruption of an Autocrine Cytokine Circuit. Cancer Discovery, 2014, 4, 452-465.	7.7	169
17	A Platform of Synthetic Lethal Gene Interaction Networks Reveals that the GNAQ Uveal Melanoma Oncogene Controls the Hippo Pathway through FAK. Cancer Cell, 2019, 35, 457-472.e5.	7.7	169
18	Targeted Tumor-Penetrating siRNA Nanocomplexes for Credentialing the Ovarian Cancer Oncogene ID4. Science Translational Medicine, 2012, 4, 147ra112.	5.8	157

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19	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. <i>Cancer Cell</i> , 2018, 34, 396-410.e8.	7.7	146
20	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016, 6, 714-726.	7.7	139
21	A genetic basis for the variation in the vulnerability of cancer to DNA damage. <i>Nature Communications</i> , 2016, 7, 11428.	5.8	136
22	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	13.5	135
23	Illuminating the Onco-GPCRome: Novel G protein-coupled receptor-driven oncocrine networks and targets for cancer immunotherapy. <i>Journal of Biological Chemistry</i> , 2019, 294, 11062-11086.	1.6	129
24	Targeting an IKBKE cytokine network impairs triple-negative breast cancer growth. <i>Journal of Clinical Investigation</i> , 2014, 124, 5411-5423.	3.9	128
25	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, 5959-5964.	3.3	126
26	Assembly and activation of the Hippo signalome by FAT1 tumor suppressor. <i>Nature Communications</i> , 2018, 9, 2372.	5.8	119
27	ATARIS: Computational quantification of gene suppression phenotypes from multisample RNAi screens. <i>Genome Research</i> , 2013, 23, 665-678.	2.4	110
28	Integrative Radiogenomic Profiling of Squamous Cell Lung Cancer. <i>Cancer Research</i> , 2013, 73, 6289-6298.	0.4	108
29	Characterizing genomic alterations in cancer by complementary functional associations. <i>Nature Biotechnology</i> , 2016, 34, 539-546.	9.4	78
30	Predicting Relapse in Patients With Medulloblastoma by Integrating Evidence From Clinical and Genomic Features. <i>Journal of Clinical Oncology</i> , 2011, 29, 1415-1423.	0.8	76
31	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.	1.1	70
32	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. <i>Cell Systems</i> , 2018, 7, 656-666.e4.	2.9	63
33	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. <i>Nature Communications</i> , 2019, 10, 2188.	5.8	61
34	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. <i>Oncotmmunology</i> , 2019, 8, 1550341.	2.1	60
35	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in $\beta$ -Catenin-Active Cancers. <i>Cell Systems</i> , 2016, 3, 302-316.e4.	2.9	55
36	Overcoming Resistance to Dual Innate Immune and MEK Inhibition Downstream of KRAS. <i>Cancer Cell</i> , 2018, 34, 439-452.e6.	7.7	55

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37	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. <i>Nature Genetics</i> , 2018, 50, 937-943.	9.4	55
38	DiSCoVERing Innovative Therapies for Rare Tumors: Combining Genetically Accurate Disease Models with <i>In Silico</i> Analysis to Identify Novel Therapeutic Targets. <i>Clinical Cancer Research</i> , 2016, 22, 3903-3914.	3.2	54
39	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.	3.2	52
40	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. <i>Oncogene</i> , 2020, 39, 6327-6339.	2.6	48
41	Comprehensive Genomic Profiling Reveals Diverse but Actionable Molecular Portfolios across Hematologic Malignancies: Implications for Next Generation Clinical Trials. <i>Cancers</i> , 2019, 11, 11.	1.7	46
42	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. <i>ELife</i> , 2020, 9, .	2.8	46
43	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. <i>Cell Systems</i> , 2017, 5, 105-118.e9.	2.9	40
44	Functional Precision Medicine Identifies New Therapeutic Candidates for Medulloblastoma. <i>Cancer Research</i> , 2020, 80, 5393-5407.	0.4	38
45	The GenePattern Notebook Environment. <i>Cell Systems</i> , 2017, 5, 149-151.e1.	2.9	34
46	MicroSCALE Screening Reveals Genetic Modifiers of Therapeutic Response in Melanoma. <i>Science Signaling</i> , 2012, 5, rs4.	1.6	33
47	Kataegis Expression Signature in Breast Cancer Is Associated with Late Onset, Better Prognosis, and Higher HER2 Levels. <i>Cell Reports</i> , 2016, 16, 672-683.	2.9	33
48	Role of ultraviolet mutational signature versus tumor mutation burden in predicting response to immunotherapy. <i>Molecular Oncology</i> , 2020, 14, 1680-1694.	2.1	33
49	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. <i>Blood Advances</i> , 2019, 3, 2845-2858.	2.5	32
50	Mesenchymal and MAPK Expression Signatures Associate with Telomerase Promoter Mutations in Multiple Cancers. <i>Molecular Cancer Research</i> , 2020, 18, 1050-1062.	1.5	21
51	Human Induced Pluripotent Stem Cell-Derived Macrophages Ameliorate Liver Fibrosis. <i>Stem Cells</i> , 2021, 39, 1701-1717.	1.4	21
52	Modelling bistable tumour population dynamics to design effective treatment strategies. <i>Journal of Theoretical Biology</i> , 2019, 474, 88-102.	0.8	19
53	TEAD1 and TEAD3 Play Redundant Roles in the Regulation of Human Epidermal Proliferation. <i>Journal of Investigative Dermatology</i> , 2020, 140, 2081-2084.e4.	0.3	16
54	CHMP2A regulates tumor sensitivity to natural killer cell-mediated cytotoxicity. <i>Nature Communications</i> , 2022, 13, 1899.	5.8	16

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55	SPT6 promotes epidermal differentiation and blockade of an intestinal-like phenotype through control of transcriptional elongation. <i>Nature Communications</i> , 2021, 12, 784.	5.8	13
56	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.	6.5	12
57	KITlow Cells Mediate Imatinib Resistance in Gastrointestinal Stromal Tumor. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 2035-2048.	1.9	10
58	The multikinase inhibitor RXDX-105 is effective against neuroblastoma in vitro and in vivo. <i>Oncotarget</i> , 2019, 10, 6323-6333.	0.8	9
59	WNT Signaling Driven by R-spondin 1 and LGR6 in High-grade Serous Ovarian Cancer. <i>Anticancer Research</i> , 2020, 40, 6017-6028.	0.5	7
60	Analysis of <i>CDK12</i> alterations in a pan-cancer database. <i>Cancer Medicine</i> , 2022, 11, 753-763.	1.3	6
61	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.	3.2	5
62	Cyclin E Overexpression in Human Mammary Epithelial Cells Promotes Epithelial Cancer-Specific Copy Number Alterations. <i>IScience</i> , 2019, 19, 850-859.	1.9	3