Pablo Tamayo

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.

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	CHMP2A regulates tumor sensitivity to natural killer cell-mediated cytotoxicity.. *Nature Communications*, **2022**, 13, 1899	17.4	0
62	Human induced pluripotent stem cell-derived macrophages ameliorate liver fibrosis. *Stem Cells*, **2021**, 39, 1701-1717	5.8	4
61	An expanded universe of cancer targets. *Cell*, **2021**, 184, 1142-1155	56.2	38
60	TORC1/2 kinase inhibition depletes glutathione and synergizes with carboplatin to suppress the growth of MYC-driven medulloblastoma. *Cancer Letters*, **2021**, 504, 137-145	9.9	1
59	SPT6 promotes epidermal differentiation and blockade of an intestinal-like phenotype through control of transcriptional elongation. *Nature Communications*, **2021**, 12, 784	17.4	4
58	KIT Cells Mediate Imatinib Resistance in Gastrointestinal Stromal Tumor. *Molecular Cancer Therapeutics*, **2021**, 20, 2035-2048	6.1	2
57	Analysis of CDK12 alterations in a pan-cancer database.. *Cancer Medicine*, **2021**,	4.8	1
56	Tissue- and development-stage-specific mRNA and heterogeneous CNV signatures of human ribosomal proteins in normal and cancer samples. *Nucleic Acids Research*, **2020**, 48, 7079-7098	20.1	2
55	Role of ultraviolet mutational signature versus tumor mutation burden in predicting response to immunotherapy. *Molecular Oncology*, **2020**, 14, 1680-1694	7.9	16
54	TEAD1 and TEAD3 Play Redundant Roles in the Regulation of Human Epidermal Proliferation. *Journal of Investigative Dermatology*, **2020**, 140, 2081-2084.e4	4.3	6
53	Cannabinoids Promote Progression of HPV-Positive Head and Neck Squamous Cell Carcinoma via p38 MAPK Activation. *Clinical Cancer Research*, **2020**, 26, 2693-2703	12.9	22
52	Mesenchymal and MAPK Expression Signatures Associate with Telomerase Promoter Mutations in Multiple Cancers. *Molecular Cancer Research*, **2020**, 18, 1050-1062	6.6	9
51	STRIPAK directs PP2A activity toward MAP4K4 to promote oncogenic transformation of human cells. *ELife*, **2020**, 9,	8.9	19
50	Functional Precision Medicine Identifies New Therapeutic Candidates for Medulloblastoma. *Cancer Research*, **2020**, 80, 5393-5407	10.1	9
49	WNT Signaling Driven by R-spondin 1 and LGR6 in High-grade Serous Ovarian Cancer. *Anticancer Research*, **2020**, 40, 6017-6028	2.3	2
48	HPV E2, E4, E5 drive alternative carcinogenic pathways in HPV positive cancers. *Oncogene*, **2020**, 39, 6327-6339	9.2	13
47	Cyclin E Overexpression in Human Mammary Epithelial Cells Promotes Epithelial Cancer-Specific Copy Number Alterations. *IScience*, **2019**, 19, 850-859	6.1	2

46	Illuminating the Onco-GPCRome: Novel G protein-coupled receptor-driven oncocrine networks and targets for cancer immunotherapy. *Journal of Biological Chemistry*, **2019**, 294, 11062-11086	5.4	73
45	Modelling bistable tumour population dynamics to design effective treatment strategies. *Journal of Theoretical Biology*, **2019**, 474, 88-102	2.3	6
44	Chromatin dysregulation and DNA methylation at transcription start sites associated with transcriptional repression in cancers. *Nature Communications*, **2019**, 10, 2188	17.4	34
43	The multikinase inhibitor RXDX-105 is effective against neuroblastoma and. *Oncotarget*, **2019**, 10, 6323-6333	3.3	3
42	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	24.3	93
41	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. *Blood Advances*, **2019**, 3, 2845-2858	7.8	21
40	APOBEC-related mutagenesis and neo-peptide hydrophobicity: implications for response to immunotherapy. *OncoImmunology*, **2019**, 8, 1550341	7.2	26
39	Systematic Evaluation of Molecular Networks for Discovery of Disease Genes. *Cell Systems*, **2018**, 6, 484-495.e5	10.6	124
38	Tumor innate immunity primed by specific interferon-stimulated endogenous retroviruses. *Nature Medicine*, **2018**, 24, 1143-1150	50.5	131
37	Assembly and activation of the Hippo signalome by FAT1 tumor suppressor. *Nature Communications*, **2018**, 9, 2372	17.4	62
36	Comprehensive Genomic Profiling Reveals Diverse but Actionable Molecular Portfolios across Hematologic Malignancies: Implications for Next Generation Clinical Trials. *Cancers*, **2018**, 11,	6.6	16
35	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. *Cell Systems*, **2018**, 7, 656-666.e4	10.6	30
34	Proteomics, Post-translational Modifications, and Integrative Analyses Reveal Molecular Heterogeneity within Medulloblastoma Subgroups. *Cancer Cell*, **2018**, 34, 396-410.e8	24.3	74
33	Overcoming Resistance to Dual Innate Immune and MEK Inhibition Downstream of KRAS. *Cancer Cell*, **2018**, 34, 439-452.e6	24.3	24
32	Genome-scale analysis identifies paralog lethality as a vulnerability of chromosome 1p loss in cancer. *Nature Genetics*, **2018**, 50, 937-943	36.3	35
31	The GenePattern Notebook Environment. *Cell Systems*, **2017**, 5, 149-151.e1	10.6	20
30	Decomposing Oncogenic Transcriptional Signatures to Generate Maps of Divergent Cellular States. *Cell Systems*, **2017**, 5, 105-118.e9	10.6	27
29	A genetic basis for the variation in the vulnerability of cancer to DNA damage. *Nature Communications*, **2016**, 7, 11428	17.4	95

28	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. *Nature Biotechnology*, **2016**, 34, 419-23	44.5	127
27	Kataegis Expression Signature in Breast Cancer Is Associated with Late Onset, Better Prognosis, and Higher HER2 Levels. *Cell Reports*, **2016**, 16, 672-83	10.6	19
26	Characterizing genomic alterations in cancer by complementary functional associations. *Nature Biotechnology*, **2016**, 34, 539-46	44.5	57
25	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. *Cancer Discovery*, **2016**, 6, 714-26	24.4	100
24	DiSCoVERing Innovative Therapies for Rare Tumors: Combining Genetically Accurate Disease Models with In Silico Analysis to Identify Novel Therapeutic Targets. *Clinical Cancer Research*, **2016**, 22, 3903-14	12.9	43
23	Genetic and Proteomic Interrogation of Lower Confidence Candidate Genes Reveals Signaling Networks in βCatenin-Active Cancers. *Cell Systems*, **2016**, 3, 302-316.e4	10.6	36
22	The Molecular Signatures Database (MSigDB) hallmark gene set collection. *Cell Systems*, **2015**, 1, 417-425	10.6	3213
21	Inhibition of KRAS-driven tumorigenicity by interruption of an autocrine cytokine circuit. *Cancer Discovery*, **2014**, 4, 452-65	24.4	137
20	A melanoma cell state distinction influences sensitivity to MAPK pathway inhibitors. *Cancer Discovery*, **2014**, 4, 816-27	24.4	338
19	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	8.2	251
18	Targeting an IKBKE cytokine network impairs triple-negative breast cancer growth. *Journal of Clinical Investigation*, **2014**, 124, 5411-23	15.9	111
17	ATARiS: computational quantification of gene suppression phenotypes from multisample RNAi screens. *Genome Research*, **2013**, 23, 665-78	9.7	93
16	Integrative radiogenomic profiling of squamous cell lung cancer. *Cancer Research*, **2013**, 73, 6289-98	10.1	83
15	Integrated genomic analysis of the 8q24 amplification in endometrial cancers identifies ATAD2 as essential to MYC-dependent cancers. *PLoS ONE*, **2013**, 8, e54873	3.7	56
14	Targeted tumor-penetrating siRNA nanocomplexes for credentialing the ovarian cancer oncogene ID4. *Science Translational Medicine*, **2012**, 4, 147ra112	17.5	135
13	MicroSCALE screening reveals genetic modifiers of therapeutic response in melanoma. *Science Signaling*, **2012**, 5, rs4	8.8	31
12	Molecular signatures database (MSigDB) 3.0. *Bioinformatics*, **2011**, 27, 1739-40	7.2	2487
11	Integrative genomic analysis of medulloblastoma identifies a molecular subgroup that drives poor clinical outcome. *Journal of Clinical Oncology*, **2011**, 29, 1424-30	2.2	513

10	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, 12372-7	11.5	321
9	Predicting relapse in patients with medulloblastoma by integrating evidence from clinical and genomic features. *Journal of Clinical Oncology*, **2011**, 29, 1415-23	2.2	58
8	Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. *Nature*, **2009**, 462, 108-12	50.4	1614
7	Synthetic lethal interaction between oncogenic KRAS dependency and STK33 suppression in human cancer cells. *Cell*, **2009**, 137, 821-34	56.2	454
6	CDK8 is a colorectal cancer oncogene that regulates beta-catenin activity. *Nature*, **2008**, 455, 547-51	50.4	519
5	Metagene projection for cross-platform, cross-species characterization of global transcriptional states. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 5959-64	11.5	100
4	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, 15545-50	11.5	24578
3	Metagenes and molecular pattern discovery using matrix factorization. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 4164-9	11.5	1178
2	Consensus Clustering: A Resampling-Based Method for Class Discovery and Visualization of Gene Expression Microarray Data. *Machine Learning*, **2003**, 52, 91-118	4	1108
1	Visualizing and interpreting single-cell gene expression datasets with Similarity Weighted Nonnegative Embedding		1