

# Patrick J Paddison

## List of Publications by Year in descending order

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Version: 2024-02-01

29  
papers

1,356  
citations

430874

18  
h-index

477307

29  
g-index

38  
all docs

38  
docs citations

38  
times ranked

3190  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription elongation factors represent in vivo cancer dependencies in glioblastoma. <i>Nature</i> , 2017, 547, 355-359.	27.8	156
2	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.	6.4	146
3	Comparison of glioblastoma (GBM) molecular classification methods. <i>Seminars in Cancer Biology</i> , 2018, 53, 201-211.	9.6	125
4	Genome-wide RNAi screens in human brain tumor isolates reveal a novel viability requirement for PHF5A. <i>Genes and Development</i> , 2013, 27, 1032-1045.	5.9	114
5	Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. <i>Cell Systems</i> , 2016, 3, 172-186.	6.2	97
6	Cancer-Specific Requirement for BUB1B/BUBR1 in Human Brain Tumor Isolates and Genetically Transformed Cells. <i>Cancer Discovery</i> , 2013, 3, 198-211.	9.4	78
7	BuGZ Is Required for Bub3 Stability, Bub1 Kinetochore Function, and Chromosome Alignment. <i>Developmental Cell</i> , 2014, 28, 282-294.	7.0	64
8	A High-Content Small Molecule Screen Identifies Sensitivity of Glioblastoma Stem Cells to Inhibition of Polo-Like Kinase 1. <i>PLoS ONE</i> , 2013, 8, e77053.	2.5	53
9	Screen for reactivation of MeCP2 on the inactive X chromosome identifies the BMP/TGF- $\beta$ superfamily as a regulator of XIST expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1619-1624.	7.1	51
10	Comparison of tumor-associated YAP1 fusions identifies a recurrent set of functions critical for oncogenesis. <i>Genes and Development</i> , 2020, 34, 1051-1064.	5.9	48
11	N6-methyladenosine mRNA marking promotes selective translation of regulons required for human erythropoiesis. <i>Nature Communications</i> , 2019, 10, 4596.	12.8	42
12	Histone deposition pathways determine the chromatin landscapes of H3.1 and H3.3 K27M oncohistones. <i>ELife</i> , 2020, 9, .	6.0	42
13	Sensitivity to <i>BUB1B</i> Inhibition Defines an Alternative Classification of Glioblastoma. <i>Cancer Research</i> , 2017, 77, 5518-5529.	0.9	38
14	Ion channel expression patterns in glioblastoma stem cells with functional and therapeutic implications for malignancy. <i>PLoS ONE</i> , 2017, 12, e0172884.	2.5	37
15	Pan-cancer transcriptional signatures predictive of oncogenic mutations reveal that Fbw7 regulates cancer cell oxidative metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5462-5467.	7.1	31
16	PIP4K2A as a negative regulator of PI3K in PTEN-deficient glioblastoma. <i>Journal of Experimental Medicine</i> , 2019, 216, 1120-1134.	8.5	27
17	A kinase-deficient NTRK2 splice variant predominates in glioma and amplifies several oncogenic signaling pathways. <i>Nature Communications</i> , 2020, 11, 2977.	12.8	26
18	Neural GO: a quiescent-like state found in neuroepithelial-derived cells and glioma. <i>Molecular Systems Biology</i> , 2021, 17, e9522.	7.2	24

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19	Molecular Pathways: Regulation and Targeting of Kinetochore-Microtubule Attachment in Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 233-239.	7.0	23
20	<i>In vivo</i> RNAi screen identifies NLK as a negative regulator of mesenchymal activity in glioblastoma. <i>Oncotarget</i> , 2015, 6, 20145-20159.	1.8	23
21	Spontaneous Tumor Regression in Tasmanian Devils Associated with <i>RASL11A</i> Activation. <i>Genetics</i> , 2020, 215, 1143-1152.	2.9	22
22	ZNF131 suppresses centrosome fragmentation in glioblastoma stem-like cells through regulation of HAUS5. <i>Oncotarget</i> , 2017, 8, 48545-48562.	1.8	19
23	C9a/GLP-dependent H3K9me2 patterning alters chromatin structure at CpG islands in hematopoietic progenitors. <i>Epigenetics and Chromatin</i> , 2014, 7, 23.	3.9	18
24	A simple and highly efficient method for multi-allelic CRISPR-Cas9 editing in primary cell cultures. <i>Cancer Reports</i> , 2020, 3, e1269.	1.4	12
25	Involvement of DDX6 gene in radio- and chemoresistance in glioblastoma. <i>International Journal of Oncology</i> , 2016, 48, 1053-1062.	3.3	9
26	Efficient Multi-allelic Genome Editing of Primary Cell Cultures via CRISPR-Cas9 Ribonucleoprotein Nucleofection. <i>Current Protocols in Stem Cell Biology</i> , 2020, 54, e126.	3.0	9
27	BuGZ facilitates loading of spindle assembly checkpoint proteins to kinetochores in early mitosis. <i>Journal of Biological Chemistry</i> , 2020, 295, 14666-14677.	3.4	6
28	Global and context-specific transcriptional consequences of oncogenic Fbw7 mutations. <i>ELife</i> , 2022, 11, .	6.0	6
29	Functional dissection of human mitotic genes using CRISPR-Cas9 tiling screens. <i>Genes and Development</i> , 2022, 36, 495-510.	5.9	2