

# Matteo Pallocca

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6107200/publications.pdf>

Version: 2024-02-01

40  
papers

1,223  
citations

393982

19  
h-index

377514

34  
g-index

41  
all docs

41  
docs citations

41  
times ranked

2928  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deconvolution of malignant pleural effusions immune landscape unravels a novel macrophage signature associated with worse clinical outcome in lung adenocarcinoma patients. , 2022, 10, e004239.		6
2	Optimizing the Illumina COVIDSeq laboratorial and bioinformatics pipeline on thousands of samples for SARS-CoV-2 Variants of Concern tracking. Computational and Structural Biotechnology Journal, 2022, 20, 2558-2563.	1.9	2
3	Molecular dissection of a hyper-aggressive CFBF-MYH11/FLT3-ITDâ€“positive acute myeloid leukemia. Journal of Translational Medicine, 2022, 20, .	1.8	1
4	Control of replication stress and mitosis in colorectal cancer stem cells through the interplay of PARP1, MRE11 and RAD51. Cell Death and Differentiation, 2021, 28, 2060-2082.	5.0	19
5	Efficacy of immunotherapy in lung cancer with co-occurring mutations in NOTCH and homologous repair genes. , 2020, 8, e000946.		13
6	Che-1/AATF-induced transcriptionally active chromatin promotes cell proliferation in multiple myeloma. Blood Advances, 2020, 4, 5616-5630.	2.5	10
7	Next-Generation Sequencing Approaches for the Identification of Pathognomonic Fusion Transcripts in Sarcomas: The Experience of the Italian ACC Sarcoma Working Group. Frontiers in Oncology, 2020, 10, 489.	1.3	38
8	Hepatitis B protein HBx binds the DLEU2 lncRNA to sustain cccDNA and host cancer-related gene transcription. Gut, 2020, 69, 2016-2024.	6.1	92
9	Design of a companion bioinformatic tool to detect the emergence and geographical distribution of SARS-CoV-2 Spike protein genetic variants. Journal of Translational Medicine, 2020, 18, 494.	1.8	15
10	Multicohort and crossâ€“platform validation of a prognostic Wnt signature in colorectal cancer. Clinical and Translational Medicine, 2020, 10, e199.	1.7	1
11	Mutations in the KEAP1-NFE2L2 Pathway Define a Molecular Subset of Rapidly Progressing Lung Adenocarcinoma. Journal of Thoracic Oncology, 2019, 14, 1924-1934.	0.5	60
12	B4GALT1 Is a New Candidate to Maintain the Stemness of Lung Cancer Stem Cells. Journal of Clinical Medicine, 2019, 8, 1928.	1.0	13
13	Combinations of immuno-checkpoint inhibitors predictive biomarkers only marginally improve their individual accuracy. Journal of Translational Medicine, 2019, 17, 131.	1.8	17
14	Reverse Engineering Cancer: Inferring Transcriptional Gene Signatures from Copy Number Aberrations with ICARo. Cancers, 2019, 11, 256.	1.7	1
15	PTEN as a Prognostic/Predictive Biomarker in Cancer: An Unfulfilled Promise?. Cancers, 2019, 11, 435.	1.7	86
16	Poly-specific neoantigen-targeted cancer vaccines delay patient derived tumor growth. Journal of Experimental and Clinical Cancer Research, 2019, 38, 78.	3.5	32
17	Organoids as a new model for improving regenerative medicine and cancer personalized therapy in renal diseases. Cell Death and Disease, 2019, 10, 201.	2.7	105
18	The clinical significance of PD-L1 in advanced gastric cancer is dependent on <i>ARID1A</i> mutations and ATM expression. OncoImmunology, 2018, 7, e1457602.	2.1	11

#	ARTICLE	IF	CITATIONS
19	Che-1 is targeted by c-Myc to sustain proliferation in pre-B cell acute lymphoblastic leukemia. <i>EMBO Reports</i> , 2018, 19, .	2.0	23
20	Conditionally reprogrammed cells (CRC) methodology does not allow the <i>in vitro</i> expansion of patient-derived primary and metastatic lung cancer cells. <i>International Journal of Cancer</i> , 2018, 143, 88-99.	2.3	22
21	The perfect personalized cancer therapy: cancer vaccines against neoantigens. <i>Journal of Experimental and Clinical Cancer Research</i> , 2018, 37, 86.	3.5	82
22	CHK1-targeted therapy to deplete DNA replication-stressed, p53-deficient, hyperdiploid colorectal cancer stem cells. <i>Gut</i> , 2018, 67, 903-917.	6.1	64
23	Coexisting YAP expression and TP53 missense mutations delineates a molecular scenario unexpectedly associated with better survival outcomes in advanced gastric cancer. <i>Journal of Translational Medicine</i> , 2018, 16, 247.	1.8	6
24	Targeting a phospho-STAT3-miRNAs pathway improves vesicular hepatic steatosis in an <i>in vitro</i> and <i>in vivo</i> model. <i>Scientific Reports</i> , 2018, 8, 13638.	1.6	14
25	Long Non-coding MIR205HG Depletes Hsa-miR-590-3p Leading to Unrestrained Proliferation in Head and Neck Squamous Cell Carcinoma. <i>Theranostics</i> , 2018, 8, 1850-1868.	4.6	65
26	Deep sequencing and pathway-focused analysis revealed multigene oncodriver signatures predicting survival outcomes in advanced colorectal cancer. <i>Oncogenesis</i> , 2018, 7, 55.	2.1	12
27	Expression of the Hippo transducer TAZ in association with WNT pathway mutations impacts survival outcomes in advanced gastric cancer patients treated with first-line chemotherapy. <i>Journal of Translational Medicine</i> , 2018, 16, 22.	1.8	13
28	Abstract 350: Che-1/aatf-induced transcriptionally active chromatin promotes cell growth in multiple myeloma. , 2018, , .		1
29	DNA damage repair and survival outcomes in advanced gastric cancer patients treated with first-line chemotherapy. <i>International Journal of Cancer</i> , 2017, 140, 2587-2595.	2.3	30
30	Che-1 sustains hypoxic response of colorectal cancer cells by affecting Hif-1 $\alpha$ stabilization. <i>Journal of Experimental and Clinical Cancer Research</i> , 2017, 36, 32.	3.5	23
31	BCL-XL overexpression promotes tumor progression-associated properties. <i>Cell Death and Disease</i> , 2017, 8, 3216.	2.7	76
32	Deptor transcriptionally regulates endoplasmic reticulum homeostasis in multiple myeloma cells. <i>Oncotarget</i> , 2016, 7, 70546-70558.	0.8	19
33	Multitargeting activity of miR-24 inhibits long-term melatonin anticancer effects. <i>Oncotarget</i> , 2016, 7, 20532-20548.	0.8	49
34	A New Insight into Pediatric Leukemia: Che-1 Involvement in Oncogenic c-Myc Signaling. <i>Blood</i> , 2016, 128, 5267-5267.	0.6	0
35	RAP: RNA-Seq Analysis Pipeline, a new cloud-based NGS web application. <i>BMC Genomics</i> , 2015, 16, S3.	1.2	79
36	Che-1 modulates the decision between cell cycle arrest and apoptosis by its binding to p53. <i>Cell Death and Disease</i> , 2015, 6, e1764-e1764.	2.7	35

#	ARTICLE	IF	CITATIONS
37	ASPicDB: A Database Web Tool for Alternative Splicing Analysis. <i>Methods in Molecular Biology</i> , 2015, 1269, 365-378.	0.4	5
38	ODESSA: A high performance analysis pipeline for Ultra Deep targeted Exome Sequencing data. , 2014, , .		1
39	VDR primary targets by genome-wide transcriptional profiling. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 143, 348-356.	1.2	36
40	WEP: a high-performance analysis pipeline for whole-exome data. <i>BMC Bioinformatics</i> , 2013, 14, S11.	1.2	43