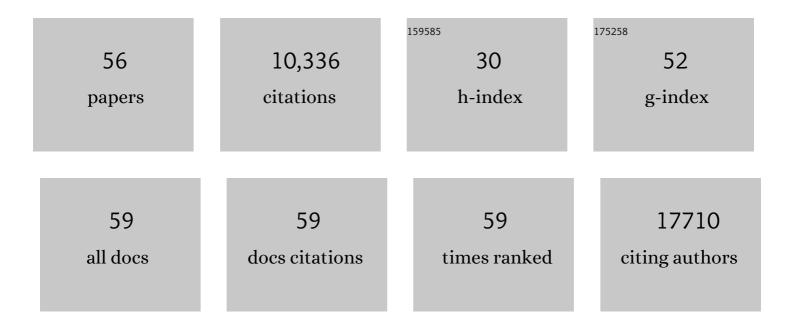
## Mattia Forcato

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5928917/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Role of YAP/TAZ in mechanotransduction. Nature, 2011, 474, 179-183.	27.8	4,288
2	The Hippo Transducer TAZ Confers Cancer Stem Cell-Related Traits on Breast Cancer Cells. Cell, 2011, 147, 759-772.	28.9	1,115
3	Genome-wide association between YAP/TAZ/TEAD andÂAP-1 at enhancers drives oncogenic growth. Nature Cell Biology, 2015, 17, 1218-1227.	10.3	865
4	IL-7 and IL-15 instruct the generation of human memory stem T cells from naive precursors. Blood, 2013, 121, 573-584.	1.4	455
5	Role of TAZ as Mediator of Wnt Signaling. Cell, 2012, 151, 1443-1456.	28.9	419
6	Muscle insulin sensitivity and glucose metabolism are controlled by the intrinsic muscle clock. Molecular Metabolism, 2014, 3, 29-41.	6.5	324
7	Aerobic glycolysis tunes <scp>YAP</scp> / <scp>TAZ</scp> transcriptional activity. EMBO Journal, 2015, 34, 1349-1370.	7.8	306
8	Comparison of computational methods for Hi-C data analysis. Nature Methods, 2017, 14, 679-685.	19.0	301
9	Transcriptional addiction in cancer cells is mediated by YAP/TAZ through BRD4. Nature Medicine, 2018, 24, 1599-1610.	30.7	228
10	SHARP1 suppresses breast cancer metastasis by promoting degradation of hypoxia-inducible factors. Nature, 2012, 487, 380-384.	27.8	213
11	Reprogramming normal cells into tumour precursors requires ECM stiffness and oncogene-mediated changes of cell mechanical properties. Nature Materials, 2020, 19, 797-806.	27.5	140
12	Extracellular matrix mechanical cues regulate lipid metabolism through Lipin-1 and SREBP. Nature Cell Biology, 2019, 21, 338-347.	10.3	135
13	Glucocorticoid receptor signalling activates YAP in breast cancer. Nature Communications, 2017, 8, 14073.	12.8	129
14	Generation of human memory stem T cells after haploidentical T-replete hematopoietic stem cell transplantation. Blood, 2015, 125, 2865-2874.	1.4	119
15	YAP/TAZ activity in stromal cells prevents ageing by controlling cGAS–STING. Nature, 2022, 607, 790-798.	27.8	89
16	MRF4 negatively regulates adult skeletal muscle growth by repressing MEF2 activity. Nature Communications, 2016, 7, 12397.	12.8	88
17	The mutant p53â€ <b>i</b> D4 complex controls VEGFA isoforms by recruiting lncRNA MALAT1. EMBO Reports, 2017, 18, 1331-1351.	4.5	78
18	Notch is a direct negative regulator of the DNA-damage response. Nature Structural and Molecular Biology, 2015, 22, 417-424.	8.2	68

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19	Hi-C analysis: from data generation to integration. Biophysical Reviews, 2019, 11, 67-78.	3.2	68
20	Transcription Factor-Directed Re-wiring of Chromatin Architecture for Somatic Cell Nuclear Reprogramming toward trans-Differentiation. Molecular Cell, 2019, 76, 453-472.e8.	9.7	67
21	The Reconstruction of Transcriptional Networks Reveals Critical Genes with Implications for Clinical Outcome of Multiple Myeloma. Clinical Cancer Research, 2011, 17, 7402-7412.	7.0	65
22	The calcineurin-NFAT pathway controls activity-dependent circadian gene expression in slow skeletal muscle. Molecular Metabolism, 2015, 4, 823-833.	6.5	58
23	F-actin dynamics regulates mammalian organ growth and cell fate maintenance. Journal of Hepatology, 2019, 71, 130-142.	3.7	56
24	<i>MCM7</i> and its hosted miR-25, 93 and 106b cluster elicit YAP/TAZ oncogenic activity in lung cancer. Carcinogenesis, 2017, 38, 64-75.	2.8	52
25	Circulating mucosal-associated invariant T cells identify patients responding to anti-PD-1 therapy. Nature Communications, 2021, 12, 1669.	12.8	48
26	Transcriptional profiling of human bronchial epithelial cell BEAS-2B exposed to diesel and biomass ultrafine particles. BMC Genomics, 2018, 19, 302.	2.8	43
27	Computational methods for the integrative analysis of single-cell data. Briefings in Bioinformatics, 2021, 22, 20-29.	6.5	43
28	Epigenomic landscape of human colorectal cancer unveils an aberrant core of pan-cancer enhancers orchestrated by YAP/TAZ. Nature Communications, 2021, 12, 2340.	12.8	43
29	Dynamic Effects of Topoisomerase I Inhibition on R-Loops and Short Transcripts at Active Promoters. PLoS ONE, 2016, 11, e0147053.	2.5	41
30	Alterations of redox and iron metabolism accompany the development of <scp>HIV</scp> latency. EMBO Journal, 2020, 39, e102209.	7.8	37
31	Hmgb3 Is Regulated by MicroRNA-206 during Muscle Regeneration. PLoS ONE, 2012, 7, e43464.	2.5	35
32	FGFR2 fusion proteins drive oncogenic transformation of mouse liver organoids towards cholangiocarcinoma. Journal of Hepatology, 2021, 75, 351-362.	3.7	35
33	Single-keratinocyte transcriptomic analyses identify different clonal types and proliferative potential mediated by FOXM1 in human epidermal stem cells. Nature Communications, 2021, 12, 2505.	12.8	31
34	Glycolysis downregulation is a hallmark of HIVâ€1 latency and sensitizes infected cells to oxidative stress. EMBO Molecular Medicine, 2021, 13, e13901.	6.9	30
35	Comparative genomics revealed key molecular targets to rapidly convert a reference rifamycin-producing bacterial strain into an overproducer by genetic engineering. Metabolic Engineering, 2014, 26, 1-16.	7.0	29
36	Global chromatin conformation differences in the Drosophila dosage compensated chromosome X. Nature Communications, 2019, 10, 5355.	12.8	28

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37	The transcriptional regulator ZNF398 mediates pluripotency and epithelial character downstream of TGF-beta in human PSCs. Nature Communications, 2020, 11, 2364.	12.8	20
38	APTANI2: update of aptamer selection through sequence-structure analysis. Bioinformatics, 2020, 36, 2266-2268.	4.1	19
39	ETV7 regulates breast cancer stem-like cell features by repressing IFN-response genes. Cell Death and Disease, 2021, 12, 742.	6.3	16
40	Microgravity and space radiation inhibit autophagy in human capillary endothelial cells, through either opposite or synergistic effects on specific molecular pathways. Cellular and Molecular Life Sciences, 2022, 79, 1.	5.4	16
41	EphB6 Regulates TFEB-Lysosomal Pathway and Survival of Disseminated Indolent Breast Cancer Cells. Cancers, 2021, 13, 1079.	3.7	14
42	Unravelling Heterogeneity of Amplified Human Amniotic Fluid Stem Cells Sub-Populations. Cells, 2021, 10, 158.	4.1	14
43	Computational methods for analyzing genome-wide chromosome conformation capture data. Current Opinion in Biotechnology, 2018, 54, 98-105.	6.6	12
44	GDA, a web-based tool for Genomics and Drugs integrated analysis. Nucleic Acids Research, 2018, 46, W148-W156.	14.5	9
45	MALAT1-dependent hsa_circ_0076611 regulates translation rate in triple-negative breast cancer. Communications Biology, 2022, 5, .	4.4	8
46	ASB2 is a direct target of FLI1 that sustains NF-κB pathway activation in germinal center-derived diffuse large B-cell lymphoma. Journal of Experimental and Clinical Cancer Research, 2021, 40, 357.	8.6	7
47	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
48	A multifactorial â€~Consensus Signature' by in silico analysis to predict response to neoadjuvant anthracycline-based chemotherapy in triple-negative breast cancer. Npj Breast Cancer, 2015, 1, 15003.	5.2	3
49	Characterization of GECPAR, a noncoding RNA that regulates the transcriptional program of diffuse large B cell lymphoma. Haematologica, 2021, , .	3.5	3
50	Computational Analysis of Hi-C Data. Methods in Molecular Biology, 2021, 2157, 103-125.	0.9	3
51	Differential proteomic profile of leukemic CD34+ progenitor cells from chronic myeloid leukemia patients. Oncotarget, 2018, 9, 21758-21769.	1.8	3
52	A comprehensive molecular and morphological study of the effects of space flight on human capillary endothelial cells: sample quality assessment and preliminary results Frontiers in Physiology, 0, 9, .	2.8	3
53	Gene Expression Analysis of T-Cells by Single-Cell RNA-Seq. Methods in Molecular Biology, 2021, 2285, 277-296.	0.9	1
54	Analysis of HiChIP Data. Methods in Molecular Biology, 2022, 2301, 209-234.	0.9	0

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55	Proteomic Profile Of CD34+ Cells From Chronic Myeloid Leukemia Patients and From Normal Donors. Blood, 2013, 122, 2712-2712.	1.4	ο
56	Revealing the Generation of Human Memory Stem T Cells in Haploidentical T-Replete Hematopoietic Stem Cell Transplantation. Blood, 2014, 124, 192-192.	1.4	0