

# Magali Michaut

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

2,070  
citations

331259

21  
h-index

243296

44  
g-index

69  
all docs

69  
docs citations

69  
times ranked

4748  
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional Genomic Identification of Predictors of Sensitivity and Mechanisms of Resistance to Multivalent Second-Generation TRAIL-R2 Agonists. <i>Molecular Cancer Therapeutics</i> , 2022, 21, 594-606.	1.9	1
2	Long-term feeder-free culture of human pancreatic progenitors on fibronectin or matrix-free polymer potentiates $\text{I}^2$ cell differentiation. <i>Stem Cell Reports</i> , 2022, 17, 1215-1228.	2.3	11
3	PTBP1 promotes hematopoietic stem cell maintenance and red blood cell development by ensuring sufficient availability of ribosomal constituents. <i>Cell Reports</i> , 2022, 39, 110793.	2.9	3
4	Kinome capture sequencing of high-grade serous ovarian carcinoma reveals novel mutations in the JAK3 gene. <i>PLoS ONE</i> , 2020, 15, e0235766.	1.1	2
5	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. <i>Cell Reports</i> , 2019, 29, 2756-2769.e6.	2.9	7
6	Principal component analysis of binary genomics data. <i>Briefings in Bioinformatics</i> , 2019, 20, 317-329.	3.2	21
7	iTOP: inferring the topology of omics data. <i>Bioinformatics</i> , 2018, 34, i988-i996.	1.8	19
8	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, <i>BRCA1</i> -like status, tumor-infiltrating immune cells and survival. <i>Oncolmmunology</i> , 2018, 7, e1509820.	2.1	80
9	Loss of functional BAP1 augments sensitivity to TRAIL in cancer cells. <i>ELife</i> , 2018, 7, .	2.8	20
10	The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. <i>PLoS Computational Biology</i> , 2018, 14, e1005802.	1.5	4
11	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	2.9	95
12	The <i>BRCA1</i> ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. <i>Breast Cancer Research</i> , 2017, 19, 99.	2.2	58
13	Abstract 575: PD-L1 positive tumor-infiltrating lymphocytes and mutational load in breast cancer. , 2017, , .		0
14	Abstract 3717: New therapies for the treatment of <i>BRAF</i> / <i>NRAS</i> wild type melanoma. , 2017, , .		0
15	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. <i>Scientific Reports</i> , 2016, 6, 18517.	1.6	143
16	OncoScape: Exploring the cancer aberration landscape by genomic data fusion. <i>Scientific Reports</i> , 2016, 6, 28103.	1.6	10
17	TANDEM: a two-stage approach to maximize interpretability of drug response models based on multiple molecular data types. <i>Bioinformatics</i> , 2016, 32, i413-i420.	1.8	64
18	ERBB2 Mutations Characterize a Subgroup of Muscle-invasive Bladder Cancers with Excellent Response to Neoadjuvant Chemotherapy. <i>European Urology</i> , 2016, 69, 384-388.	0.9	177

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19	Abstract 4783: Identification of new therapies for the treatment of BRAF/NRAS wild-type melanomas by functional screening approaches. , 2016, , .		0
20	BRCA1-like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. <i>Molecular Oncology</i> , 2015, 9, 1528-1538.	2.1	54
21	Next generation sequencing of triple negative breast cancer to find predictors for chemotherapy response. <i>Breast Cancer Research</i> , 2015, 17, 134.	2.2	58
22	A Quick Guide for Building a Successful Bioinformatics Community. <i>PLoS Computational Biology</i> , 2015, 11, e1003972.	1.5	23
23	Abstract P3-06-21: Next generation sequencing to find predictors for chemotherapy response in triple negative breast cancer. , 2015, , .		0
24	Learn from the Best. <i>PLoS Computational Biology</i> , 2014, 10, e1003645.	1.5	1
25	Building the Future of Bioinformatics through Student-Facilitated Conferencing. <i>PLoS Computational Biology</i> , 2014, 10, e1003458.	1.5	4
26	Crossing Borders for Science. <i>PLoS Computational Biology</i> , 2014, 10, e1003519.	1.5	0
27	Parallel In Vivo and In Vitro Melanoma RNAi Dropout Screens Reveal Synthetic Lethality between Hypoxia and DNA Damage Response Inhibition. <i>Cell Reports</i> , 2014, 9, 1375-1386.	2.9	34
28	Don't Wear Your New Shoes (Yet): Taking the Right Steps to Become a Successful Principal Investigator. <i>PLoS Computational Biology</i> , 2013, 9, e1002834.	1.5	3
29	The Regional Student Group Program of the ISCB Student Council: Stories from the Road. <i>PLoS Computational Biology</i> , 2013, 9, e1003241.	1.5	13
30	Explain Bioinformatics to Your Grandmother!. <i>PLoS Computational Biology</i> , 2013, 9, e1003305.	1.5	5
31	Ten Simple Rules for Starting a Regional Student Group. <i>PLoS Computational Biology</i> , 2013, 9, e1003340.	1.5	10
32	The Young PI Buzz: Learning from the Organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. <i>PLoS Computational Biology</i> , 2013, 9, e1003350.	1.5	2
33	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. <i>PLoS Computational Biology</i> , 2013, 9, e1003030.	1.5	62
34	Mapping the Hsp90 Genetic Interaction Network in <i>Candida albicans</i> Reveals Environmental Contingency and Rewired Circuitry. <i>PLoS Genetics</i> , 2012, 8, e1002562.	1.5	98
35	Multiple Genetic Interaction Experiments Provide Complementary Information Useful for Gene Function Prediction. <i>PLoS Computational Biology</i> , 2012, 8, e1002559.	1.5	17
36	A robust genomic signature for the detection of colorectal cancer patients with microsatellite instability phenotype and high mutation frequency. <i>Journal of Pathology</i> , 2012, 228, 586-595.	2.1	55

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37	An omics perspective of protein disorder. <i>Molecular BioSystems</i> , 2012, 8, 185-193.	2.9	12
38	Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.	1.5	95
39	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274
40	Bringing order to protein disorder through comparative genomics and genetic interactions. <i>Genome Biology</i> , 2011, 12, R14.	13.9	129
41	Putting genetic interactions in context through a global modular decomposition. <i>Genome Research</i> , 2011, 21, 1375-1387.	2.4	61
42	Ten Simple Rules for Getting Involved in Your Scientific Community. <i>PLoS Computational Biology</i> , 2011, 7, e1002232.	1.5	15
43	A Systems Biology Approach Reveals the Role of a Novel Methyltransferase in Response to Chemical Stress and Lipid Homeostasis. <i>PLoS Genetics</i> , 2011, 7, e1002332.	1.5	21
44	Protein Complexes are Central in the Yeast Genetic Landscape. <i>PLoS Computational Biology</i> , 2011, 7, e1001092.	1.5	57
45	Highlights from the 6th International Society for Computational Biology Student Council Symposium at the 18th Annual International Conference on Intelligent Systems for Molecular Biology. <i>BMC Bioinformatics</i> , 2010, 11, .	1.2	9
46	Genome-wide location analysis reveals a role for Sub1 in RNA polymerase III transcription. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 14265-14270.	3.3	47
47	InteroPORC: an automated tool to predict highly conserved protein interaction networks. <i>BMC Bioinformatics</i> , 2008, 9, .	1.2	3
48	InteroPORC: automated inference of highly conserved protein interaction networks. <i>Bioinformatics</i> , 2008, 24, 1625-1631.	1.8	39
49	Genome-wide location analysis reveals a role of TFIIIS in RNA polymerase III transcription. <i>Genes and Development</i> , 2008, 22, 1934-1947.	2.7	59
50	Cadmium triggers an integrated reprogramming of the metabolism of <i>Synechocystis</i> PCC6803, under the control of the Slr1738 regulator. <i>BMC Genomics</i> , 2007, 8, 350.	1.2	92
51	Mining Biological Data Using Pyramids. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , 2007, , 397-408.	0.1	1