Magali Michaut

List of Publications by Year
in descending order

51 papers	2,070 citations	331538 21 h-index	243529 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. Molecular Cancer Therapeutics, 2022, 21, 594-606.	1.9	1
2	Long-term feeder-free culture of human pancreatic progenitors on fibronectin or matrix-free polymer potentiates β cell differentiation. Stem Cell Reports, 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. Cell Reports, 2022, 39, 110793.	2.9	3
4	Kinome capture sequencing of high-grade serous ovarian carcinoma reveals novel mutations in the JAK3 gene. PLoS ONE, 2020, 15, e0235766.	1.1	2
5	ERG Controls B Cell Development by Promoting Igh V-to-DJ Recombination. Cell Reports, 2019, 29, 2756-2769.e6.	2.9	7
6	Principal component analysis of binary genomics data. Briefings in Bioinformatics, 2019, 20, 317-329.	3.2	21
7	iTOP: inferring the topology of omics data. Bioinformatics, 2018, 34, i988-i996.	1.8	19
8	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, *BRCA1*-like status, tumor-infiltrating immune cells and survival. OncoImmunology, 2018, 7, e1509820.	2.1	80
9	Loss of functional BAP1 augments sensitivity to TRAIL in cancer cells. ELife, 2018, 7, .	2.8	20
10	The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide. PLoS Computational Biology, 2018, 14, e1005802.	1.5	4
11	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	2.9	95
12	The BRCA1ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. Breast Cancer Research, 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 ofBRAF/NRASwild type melanoma. , 2017, , .		0
15	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. Scientific Reports, 2016, 6, 18517.	1.6	143
16	OncoScape: Exploring the cancer aberration landscape by genomic data fusion. Scientific Reports, 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. Bioinformatics, 2016, 32, i413-i420.	1.8	64
18	ERBB2 Mutations Characterize a Subgroup of Muscle-invasive Bladder Cancers with Excellent Response to Neoadjuvant Chemotherapy. European Urology, 2016, 69, 384-388.	0.9	177

#	Article	IF	Citations
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. Molecular Oncology, 2015, 9, 1528-1538.	2.1	54
21	Next generation sequencing of triple negative breast cancer to find predictors for chemotherapy response. Breast Cancer Research, 2015, 17, 134.	2.2	58
22	A Quick Guide for Building a Successful Bioinformatics Community. PLoS Computational Biology, 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. PLoS Computational Biology, 2014, 10, e1003645.	1.5	1
25	Building the Future of Bioinformatics through Student-Facilitated Conferencing. PLoS Computational Biology, 2014, 10, e1003458.	1.5	4
26	Crossing Borders for Science. PLoS Computational Biology, 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. Cell Reports, 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. PLoS Computational Biology, 2013, 9, e1002834.	1.5	3
29	The Regional Student Group Program of the ISCB Student Council: Stories from the Road. PLoS Computational Biology, 2013, 9, e1003241.	1.5	13
30	Explain Bioinformatics to Your Grandmother!. PLoS Computational Biology, 2013, 9, e1003305.	1.5	5
31	Ten Simple Rules for Starting a Regional Student Group. PLoS Computational Biology, 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. PLoS Computational Biology, 2013, 9, e1003350.	1.5	2
33	Distinct Types of Disorder in the Human Proteome: Functional Implications for Alternative Splicing. PLoS Computational Biology, 2013, 9, e1003030.	1.5	62
34	Mapping the Hsp90 Genetic Interaction Network in Candida albicans Reveals Environmental Contingency and Rewired Circuitry. PLoS Genetics, 2012, 8, e1002562.	1.5	98
35	Multiple Genetic Interaction Experiments Provide Complementary Information Useful for Gene Function Prediction. PLoS Computational Biology, 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. Journal of Pathology, 2012, 228, 586-595.	2.1	55

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