Philippe Marc

List of Publications by Year
in descending order

22 papers	1,099 citations	623734 14 h-index	713466 21 g-index
25 all docs	25 docs citations	25 times ranked	1513 citing authors

#	Article	IF	Citations
1	Coronary Artery Disease Polygenic Risk Score Identifies Patients at Higher Risk for Recurrent Cardiovascular Events in the CANTOS Trial. Circulation Genomic and Precision Medicine, 2021, , CIRCGEN121003440.	3.6	0
2	Ten simple rules to power drug discovery with data science. PLoS Computational Biology, 2020, 16, e1008126.	3.2	14
3	Generating Modeling Data From Repeat-Dose Toxicity Reports. Toxicological Sciences, 2018, 162, 287-300.	3.1	4
4	Legacy data sharing to improve drug safety assessment: the eTOX project. Nature Reviews Drug Discovery, 2017, 16, 811-812.	46.4	56
5	OntoBrowser: a collaborative tool for curation of ontologies by subject matter experts. Bioinformatics, 2017, 33, 148-149.	4.1	14
6	Value of shared preclinical safety studies â€" The eTOX database. Toxicology Reports, 2015, 2, 210-221.	3.3	21
7	The eTOX Data-Sharing Project to Advance in Silico Drug-Induced Toxicity Prediction. International Journal of Molecular Sciences, 2014, 15, 21136-21154.	4.1	56
8	Robust and tissue-independent gender-specific transcript biomarkers. Biomarkers, 2013, 18, 436-445.	1.9	32
9	Computational methods for early predictive safety assessment from biological and chemical data. Expert Opinion on Drug Metabolism and Toxicology, 2011, 7, 1497-1511.	3.3	28
10	yMGV: a cross-species expression data mining tool. Nucleic Acids Research, 2004, 32, 323D-325.	14.5	6
11	MiCoViTo: a tool for gene-centric comparison and visualization of yeast transcriptome states. BMC Bioinformatics, 2004, 5, 20.	2.6	4
12	A General Strategy to Uncover Transcription Factor Properties Identifies a New Regulator of Drug Resistance in Yeast. Journal of Biological Chemistry, 2003, 278, 11427-11432.	3.4	56
13	yMGV: helping biologists with yeast microarray data mining. Nucleic Acids Research, 2002, 30, 76-79.	14.5	27
14	Arrayplot for visualization and normalization of cDNA microarray data. Bioinformatics, 2002, 18, 888-889.	4.1	8
15	New Insights into the Pleiotropic Drug Resistance Network from Genome-Wide Characterization of the YRR1 Transcription Factor Regulation System. Molecular and Cellular Biology, 2002, 22, 2642-2649.	2.3	95
16	Genomeâ€wide analysis of mRNAs targeted to yeast mitochondria. EMBO Reports, 2002, 3, 159-164.	4.5	285
17	Transcriptional induction of repair genes during slowing of replication in irradiated Saccharomyces cerevisiae. Mutation Research DNA Repair, 2001, 487, 157-172.	3.7	24
18	Transcriptomes, transcription activators and microarrays. FEBS Letters, 2001, 498, 140-144.	2.8	30

#	Article	IF	Citations
19	An artificial transcription activator mimics the genome‑wide properties of the yeast Pdr1 transcription factor. EMBO Reports, 2001, 2, 493-498.	4.5	59
20	yMGV: a database for visualization and data mining of published genome-wide yeast expression data. Nucleic Acids Research, 2001, 29, 63e-63.	14.5	28
21	Genome microarray analysis of transcriptional activation in multidrug resistance yeast mutants. FEBS Letters, 2000, 470, 156-160.	2.8	243
22	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0