

Marine Jeanmougin

List of Publications by Year in descending order

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14
papers

1,448
citations

933447

10
h-index

1125743

13
g-index

14
all docs

14
docs citations

14
times ranked

3372
citing authors

#	ARTICLE	IF	CITATIONS
1	Early and accurate detection of cholangiocarcinoma in patients with primary sclerosing cholangitis by methylation markers in bile. <i>Hepatology</i> , 2022, 75, 59-73.	7.3	15
2	Spatial analysis and CD25-expression identify regulatory T cells as predictors of a poor prognosis in colorectal cancer. <i>Modern Pathology</i> , 2022, 35, 1236-1246.	5.5	8
3	Multiregional assessment of CIMP in primary colorectal cancers: Phenotype concordance but marker variability. <i>International Journal of Cancer</i> , 2021, 148, 1652-1657.	5.1	4
4	Improved prognostication of glioblastoma beyond molecular subtyping by transcriptional profiling of the tumor microenvironment. <i>Molecular Oncology</i> , 2020, 14, 1016-1027.	4.6	15
5	A robust internal control for high-precision DNA methylation analyses by droplet digital PCR. <i>Clinical Epigenetics</i> , 2018, 10, 24.	4.1	26
6	CpG island methylator phenotype identifies high risk patients among microsatellite stable <i>BRAF</i> mutated colorectal cancers. <i>International Journal of Cancer</i> , 2017, 141, 967-976.	5.1	40
7	Prognostic relevance of an epigenetic biomarker panel in sentinel lymph nodes from colon cancer patients. <i>Clinical Epigenetics</i> , 2017, 9, 97.	4.1	4
8	Experimental factors affecting the robustness of DNA methylation analysis. <i>Scientific Reports</i> , 2016, 6, 33936.	3.3	15
9	Breast Cancer Cell-Derived GM-CSF Licenses Regulatory Th2 Induction by Plasmacytoid Dendritic Cells in Aggressive Disease Subtypes. <i>Cancer Research</i> , 2015, 75, 2775-2787.	0.9	49
10	Human blood BDCA-1 dendritic cells differentiate into Langerhans-like cells with thymic stromal lymphopoietin and TGF- β 2. <i>Blood</i> , 2014, 124, 2411-2420.	1.4	72
11	Network Inference in Breast Cancer with Gaussian Graphical Models and Extensions. , 2014, , 121-146.		0
12	A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. <i>Briefings in Bioinformatics</i> , 2013, 14, 671-683.	6.5	1,064
13	Multiple Testing in Large-Scale Genetic Studies. <i>Methods in Molecular Biology</i> , 2012, 888, 213-233.	0.9	16
14	Should We Abandon the t-Test in the Analysis of Gene Expression Microarray Data: A Comparison of Variance Modeling Strategies. <i>PLoS ONE</i> , 2010, 5, e12336.	2.5	120