

Nathalie Pochet

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

12,370
citations

147801

31
h-index

161849

54
g-index

64
all docs

64
docs citations

64
times ranked

25393
citing authors

#	ARTICLE	IF	CITATIONS
1	Hepatocellular carcinoma chemoprevention by targeting the angiotensin-converting enzyme and EGFR transactivation. <i>JCI Insight</i> , 2022, 7, .	5.0	4
2	Hepatitis B virus compartmentalization and single-cell differentiation in hepatocellular carcinoma. <i>Life Science Alliance</i> , 2021, 4, e202101036.	2.8	4
3	A human liver cell-based system modeling a clinical prognostic liver signature for therapeutic discovery. <i>Nature Communications</i> , 2021, 12, 5525.	12.8	21
4	Aberrant expression of USF2 in refractory rheumatoid arthritis and its regulation of proinflammatory cytokines in Th17 cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30639-30648.	7.1	25
5	Imaging-AMARETTO: An Imaging Genomics Software Tool to Interrogate Multiomics Networks for Relevance to Radiography and Histopathology Imaging Biomarkers of Clinical Outcomes. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 421-435.	2.1	10
6	Combined Analysis of Metabolomes, Proteomes, and Transcriptomes of Hepatitis C Virus-Infected Cells and Liver to Identify Pathways Associated With Disease Development. <i>Gastroenterology</i> , 2019, 157, 537-551.e9.	1.3	71
7	Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. <i>Genome Biology</i> , 2019, 20, 213.	8.8	379
8	Complex Neurological Phenotype in Female Carriers of <i>NHE6</i> Mutations. <i>Molecular Neuropsychiatry</i> , 2019, 5, 98-108.	2.9	10
9	TFutils: Data structures for transcription factor bioinformatics. <i>F1000Research</i> , 2019, 8, 152.	1.6	1
10	TFutils: Data structures for transcription factor bioinformatics. <i>F1000Research</i> , 2019, 8, 152.	1.6	3
11	Hepatitis B Virus Evasion From Cyclic Guanosine Monophosphate-Adenosine Monophosphate Synthase Sensing in Human Hepatocytes. <i>Hepatology</i> , 2018, 68, 1695-1709.	7.3	66
12	Module Analysis Captures Pancancer Genetically and Epigenetically Deregulated Cancer Driver Genes for Smoking and Antiviral Response. <i>EBioMedicine</i> , 2018, 27, 156-166.	6.1	40
13	miR-135a-5p-mediated downregulation of protein tyrosine phosphatase receptor delta is a candidate driver of HCV-associated hepatocarcinogenesis. <i>Gut</i> , 2018, 67, 953-962.	12.1	59
14	Dissecting clinical outcome of porcine circovirus type 2 with in vivo derived transcriptomic signatures of host tissue responses. <i>BMC Genomics</i> , 2018, 19, 831.	2.8	4
15	Unraveling the host responses to hepatitis B virus infection using single cell RNAseq. <i>Journal of Hepatology</i> , 2017, 66, S28.	3.7	0
16	Spatiotemporal functional genomics uncovers cell circuits triggering liver disease biology of hepatitis C virus infection. <i>Journal of Hepatology</i> , 2017, 66, S320.	3.7	0
17	Transcriptional signature of human pro-inflammatory TH17 cells identifies reduced IL10 gene expression in multiple sclerosis. <i>Nature Communications</i> , 2017, 8, 1600.	12.8	93
18	Dissecting the role of non-coding RNAs in the accumulation of amyloid and tau neuropathologies in Alzheimer's disease. <i>Molecular Neurodegeneration</i> , 2017, 12, 51.	10.8	70

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19	Type I interferons and microbial metabolites of tryptophan modulate astrocyte activity and central nervous system inflammation via the aryl hydrocarbon receptor. <i>Nature Medicine</i> , 2016, 22, 586-597.	30.7	987
20	The CGAS-Sting Pathway Exhibits Antiviral Activity against Hepatitis B Virus Infection. <i>Journal of Hepatology</i> , 2016, 64, S396.	3.7	0
21	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	19.0	44
22	A targeted functional RNA interference screen uncovers glypican 5 as an entry factor for hepatitis B and D viruses. <i>Hepatology</i> , 2016, 63, 35-48.	7.3	131
23	High-throughput approaches to unravel hepatitis C virus-host interactions. <i>Virus Research</i> , 2016, 218, 18-24.	2.2	9
24	Abstract 5266: Fast and accurate fusion transcript detection using the Trinity Cancer Transcriptome Analysis Toolkit. , 2016, , .		0
25	Identification and characterization of latency-associated peptide-expressing $\hat{1}^3\hat{1}$ T cells. <i>Nature Communications</i> , 2015, 6, 8726.	12.8	45
26	Association of Brain DNA Methylation in <i>SORL1</i> , <i>ABCA7</i> , <i>HLA-DRB5</i> , <i>SLC24A4</i> , and <i>BIN1</i> With Pathological Diagnosis of Alzheimer Disease. <i>JAMA Neurology</i> , 2015, 72, 15.	9.0	239
27	ISDN2014_0028: REMOVED: Targeting miRâ€155 restores dysfunctional microglia and ameliorates disease in the SOD1 model of ALS. <i>International Journal of Developmental Neuroscience</i> , 2015, 47, 5-5.	1.6	1
28	Targeting mi<sc>R</sc>â€155 restores abnormal microglia and attenuates disease in <sc>SOD</sc>1 mice. <i>Annals of Neurology</i> , 2015, 77, 75-99.	5.3	295
29	Abstract 4859: Development of a cancer transcriptome analysis toolkit: identification of gene fusions in chronic lymphocytic leukemia. , 2015, , .		1
30	Somatic mutation as a mechanism of Wnt/ $\hat{1}^2$ -catenin pathway activation in CLL. <i>Blood</i> , 2014, 124, 1089-1098.	1.4	65
31	De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. <i>Nature Protocols</i> , 2013, 8, 1494-1512.	12.0	7,054
32	Mutations causing medullary cystic kidney disease type 1 lie in a large VNTR in MUC1 missed by massively parallel sequencing. <i>Nature Genetics</i> , 2013, 45, 299-303.	21.4	237
33	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013, 10, 623-629.	19.0	419
34	Integrative Genomic Analysis Implicates Gain of <i>PIK3CA</i> at 3q26 and <i>MYC</i> at 8q24 in Chronic Lymphocytic Leukemia. <i>Clinical Cancer Research</i> , 2012, 18, 3791-3802.	7.0	76
35	Germline copy number variation associated with Mendelian inheritance of CLL in two families. <i>Leukemia</i> , 2012, 26, 1710-1713.	7.2	10
36	A Transgenic Mouse Marking Live Replicating Cells Reveals InÂVivo Transcriptional Program of Proliferation. <i>Developmental Cell</i> , 2012, 23, 681-690.	7.0	54

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37	Nanowire-Mediated Delivery Enables Functional Interrogation of Primary Immune Cells: Application to the Analysis of Chronic Lymphocytic Leukemia. Nano Letters, 2012, 12, 6498-6504.	9.1	154
38	Transcriptional Profiling of Plasmodium falciparum Parasites from Patients with Severe Malaria Identifies Distinct Low vs. High Parasitemic Clusters. PLoS ONE, 2012, 7, e40739.	2.5	19
39	Risk Alleles Identified in Genome-Wide Association Studies Are Associated with Expression Quantitative Trait Loci in Chronic Lymphocytic Leukemia.. Blood, 2012, 120, 2875-2875.	1.4	1
40	RNA-Seq methods for imperfect samples: development, evaluation and applications. Genome Biology, 2011, 12, .	8.8	63
41	Novel Germline Genetic Variants Associated with Familial Chronic Lymphocytic Leukemia (CLL). Blood, 2011, 118, 465-465.	1.4	0
42	Non-invasive diagnosis of endometriosis based on a combined analysis of six plasma biomarkers. Human Reproduction, 2010, 25, 654-664.	0.9	124
43	Whole Genome Sequencing Identifies Functional Mutations In the Wnt Pathway In CLL. Blood, 2010, 116, 693-693.	1.4	5
44	Axillary lymph node status of operable breast cancers by combined steroid receptor and HER-2 status: triple positive tumours are more likely lymph node positive. Breast Cancer Research and Treatment, 2009, 113, 181-187.	2.5	76
45	Expression profiling to predict the clinical behaviour of ovarian cancer fails independent evaluation. BMC Cancer, 2008, 8, 18.	2.6	13
46	FLO1 Is a Variable Green Beard Gene that Drives Biofilm-like Cooperation in Budding Yeast. Cell, 2008, 135, 726-737.	28.9	398
47	Does Estrogen Receptorâ€“Negative/Progesterone Receptorâ€“Positive Breast Carcinoma Exist?. Journal of Clinical Oncology, 2008, 26, 335-336.	1.6	91
48	Occurrence and Outcome of Residual Trophoblastic Tissue. Journal of Ultrasound in Medicine, 2008, 27, 357-361.	1.7	100
49	Sequence-based estimation of minisatellite and microsatellite repeat variability. Genome Research, 2007, 17, 1787-1796.	5.5	180
50	Distinct physiological states of Plasmodium falciparum in malaria-infected patients. Nature, 2007, 450, 1091-1095.	27.8	220
51	P52 The axillary lymph node status (ALNS) of breast cancers by combined ER, PR and HER-2 expression: Triple positive tumours are more likely lymph node positive. Breast, 2007, 16, S27.	2.2	0
52	Body mass index and HER-2 overexpression in breast cancer patients over 50 years of age. Breast Cancer Research and Treatment, 2007, 106, 127-133.	2.5	19
53	Predicting the clinical behavior of ovarian cancer from gene expression profiles. International Journal of Gynecological Cancer, 2006, 16, 147-151.	2.5	23
54	Methodology in plasma proteomic pattern experiments. International Journal of Gynecological Cancer, 2006, 16, 1951-1952.	2.5	0

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55	Support vector machines versus logistic regression: improving prospective performance in clinical decision-making. <i>Ultrasound in Obstetrics and Gynecology</i> , 2006, 27, 607-608.	1.7	46
56	New models to predict depth of infiltration in endometrial carcinoma based on transvaginal sonography. <i>Ultrasound in Obstetrics and Gynecology</i> , 2006, 27, 664-671.	1.7	42
57	Molecular profiling of platinum resistant ovarian cancer: Use of the model in clinical practice. <i>International Journal of Cancer</i> , 2006, 119, 1511-1511.	5.1	1
58	Progesterone Receptor in Estrogen Receptorâ€“Positive Breast Cancer: The Association Between HER-2 and Lymph Node Involvement Is Age Related. <i>Journal of Clinical Oncology</i> , 2006, 24, 2595-2595.	1.6	6
59	Independent Test Set Performance in the Prediction of Early Relapse in Ovarian Cancer with Gene Expression Profiles. <i>Clinical Cancer Research</i> , 2005, 11, 7958-7959.	7.0	2
60	M@CBETH: a microarray classification benchmarking tool. <i>Bioinformatics</i> , 2005, 21, 3185-3186.	4.1	14
61	Systematic benchmarking of microarray data classification: assessing the role of non-linearity and dimensionality reduction. <i>Bioinformatics</i> , 2004, 20, 3185-3195.	4.1	243