

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	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
2	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
3	Comparative analysis of RNA sequencing methods for degraded or low-input samples. <i>Nature Methods</i> , 2013, 10, 623-629.	19.0	419
4	FLO1 Is a Variable Green Beard Gene that Drives Biofilm-like Cooperation in Budding Yeast. <i>Cell</i> , 2008, 135, 726-737.	28.9	398
5	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
6	Targeting miR-155 restores abnormal microglia and attenuates disease in SOD1 mice. <i>Annals of Neurology</i> , 2015, 77, 75-99.	5.3	295
7	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
8	Association of Brain DNA Methylation in SORL1, ABCA7, HLA-DRB5, SLC24A4, and BIN1 With Pathological Diagnosis of Alzheimer Disease. <i>JAMA Neurology</i> , 2015, 72, 15.	9.0	239
9	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
10	Distinct physiological states of Plasmodium falciparum in malaria-infected patients. <i>Nature</i> , 2007, 450, 1091-1095.	27.8	220
11	Sequence-based estimation of minisatellite and microsatellite repeat variability. <i>Genome Research</i> , 2007, 17, 1787-1796.	5.5	180
12	Nanowire-Mediated Delivery Enables Functional Interrogation of Primary Immune Cells: Application to the Analysis of Chronic Lymphocytic Leukemia. <i>Nano Letters</i> , 2012, 12, 6498-6504.	9.1	154
13	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
14	Non-invasive diagnosis of endometriosis based on a combined analysis of six plasma biomarkers. <i>Human Reproduction</i> , 2010, 25, 654-664.	0.9	124
15	Occurrence and Outcome of Residual Trophoblastic Tissue. <i>Journal of Ultrasound in Medicine</i> , 2008, 27, 357-361.	1.7	100
16	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
17	Does Estrogen Receptor-Negative/Progesterone Receptor-Positive Breast Carcinoma Exist?. <i>Journal of Clinical Oncology</i> , 2008, 26, 335-336.	1.6	91
18	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. <i>Breast Cancer Research and Treatment</i> , 2009, 113, 181-187.	2.5	76

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19	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
20	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
21	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
22	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
23	Somatic mutation as a mechanism of Wnt/ β -catenin pathway activation in CLL. <i>Blood</i> , 2014, 124, 1089-1098.	1.4	65
24	RNA-Seq methods for imperfect samples: development, evaluation and applications. <i>Genome Biology</i> , 2011, 12, .	8.8	63
25	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
26	A Transgenic Mouse Marking Live Replicating Cells Reveals In Vivo Transcriptional Program of Proliferation. <i>Developmental Cell</i> , 2012, 23, 681-690.	7.0	54
27	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
28	Identification and characterization of latency-associated peptide-expressing β T cells. <i>Nature Communications</i> , 2015, 6, 8726.	12.8	45
29	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	19.0	44
30	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
31	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
32	Aberrant expression of <i>USF2</i> 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
33	Predicting the clinical behavior of ovarian cancer from gene expression profiles. <i>International Journal of Gynecological Cancer</i> , 2006, 16, 147-151.	2.5	23
34	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
35	Body mass index and HER-2 overexpression in breast cancer patients over 50 years of age. <i>Breast Cancer Research and Treatment</i> , 2007, 106, 127-133.	2.5	19
36	Transcriptional Profiling of <i>Plasmodium falciparum</i> Parasites from Patients with Severe Malaria Identifies Distinct Low vs. High Parasitemic Clusters. <i>PLoS ONE</i> , 2012, 7, e40739.	2.5	19

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37	M@CBETH: a microarray classification benchmarking tool. <i>Bioinformatics</i> , 2005, 21, 3185-3186.	4.1	14
38	Expression profiling to predict the clinical behaviour of ovarian cancer fails independent evaluation. <i>BMC Cancer</i> , 2008, 8, 18.	2.6	13
39	Germline copy number variation associated with Mendelian inheritance of CLL in two families. <i>Leukemia</i> , 2012, 26, 1710-1713.	7.2	10
40	Complex Neurological Phenotype in Female Carriers of ϵ -Microseminoprotein Receptor Mutations. <i>Molecular Neuropsychiatry</i> , 2019, 5, 98-108.	2.9	10
41	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
42	High-throughput approaches to unravel hepatitis C virus-host interactions. <i>Virus Research</i> , 2016, 218, 18-24.	2.2	9
43	Progesterone Receptor in Estrogen Receptor-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
44	Whole Genome Sequencing Identifies Functional Mutations In the Wnt Pathway In CLL. <i>Blood</i> , 2010, 116, 693-693.	1.4	5
45	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
46	Hepatitis B virus compartmentalization and single-cell differentiation in hepatocellular carcinoma. <i>Life Science Alliance</i> , 2021, 4, e202101036.	2.8	4
47	Hepatocellular carcinoma chemoprevention by targeting the angiotensin-converting enzyme and EGFR transactivation. <i>JCI Insight</i> , 2022, 7, .	5.0	4
48	TFutils: Data structures for transcription factor bioinformatics. <i>F1000Research</i> , 2019, 8, 152.	1.6	3
49	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
50	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
51	ISDN2014_0028: REMOVED: Targeting miR-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
52	Risk Alleles Identified in Genome-Wide Association Studies Are Associated with Expression Quantitative Trait Loci in Chronic Lymphocytic Leukemia.. <i>Blood</i> , 2012, 120, 2875-2875.	1.4	1
53	Abstract 4859: Development of a cancer transcriptome analysis toolkit: identification of gene fusions in chronic lymphocytic leukemia. , 2015, , .		1
54	TFutils: Data structures for transcription factor bioinformatics. <i>F1000Research</i> , 2019, 8, 152.	1.6	1

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55	Methodology in plasma proteomic pattern experiments. International Journal of Gynecological Cancer, 2006, 16, 1951-1952.	2.5	0
56	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
57	The CGAS-Sting Pathway Exhibits Antiviral Activity against Hepatitis B Virus Infection. Journal of Hepatology, 2016, 64, S396.	3.7	0
58	Unraveling the host responses to hepatitis B virus infection using single cell RNAseq. Journal of Hepatology, 2017, 66, S28.	3.7	0
59	Spatiotemporal functional genomics uncovers cell circuits triggering liver disease biology of hepatitis C virus infection. Journal of Hepatology, 2017, 66, S320.	3.7	0
60	Novel Germline Genetic Variants Associated with Familial Chronic Lymphocytic Leukemia (CLL). Blood, 2011, 118, 465-465.	1.4	0
61	Abstract 5266: Fast and accurate fusion transcript detection using the Trinity Cancer Transcriptome Analysis Toolkit. , 2016, , .		0