Alejandra Cervera

List of Publications by Year
in descending order

24 papers	2,516 citations	840776 11 h-index	677142 22 g-index
29 all docs	29 docs citations	29 times ranked	6038 citing authors

#	Article	IF	Citations
1	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
2	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
3	Gene expression profiling of pre-eclamptic placentae by RNA sequencing. Scientific Reports, 2015, 5, 14107.	3.3	89
4	Anduril 2: upgraded large-scale data integration framework. Bioinformatics, 2019, 35, 3815-3817.	4.1	31
5	MicroRNAs regulate key cell survival pathways and mediate chemosensitivity during progression of diffuse large B-cell lymphoma. Blood Cancer Journal, 2017, 7, 654.	6.2	26
6	SePIA: RNA and small RNA sequence processing, integration, and analysis. BioData Mining, 2016, 9, 20.	4.0	25
7	Distinct subtypes of diffuse large B-cell lymphoma defined by hypermutated genes. Leukemia, 2019, 33, 2662-2672.	7.2	24
8	Deltex-1 mutations predict poor survival in diffuse large B-cell lymphoma. Haematologica, 2017, 102, e195-e198.	3.5	23
9	Alternative splicing discriminates molecular subtypes and has prognostic impact in diffuse large B-cell lymphoma. Blood Cancer Journal, 2017, 7, e596-e596.	6.2	14
10	Anagrelide for Gastrointestinal Stromal Tumor. Clinical Cancer Research, 2019, 25, 1676-1687.	7.0	14
11	Functional Profiling of FSH and Estradiol in Ovarian Granulosa Cell Tumors. Journal of the Endocrine Society, 2020, 4, bvaa034.	0.2	13
12	Human cell transformation by combined lineage conversion and oncogene expression. Oncogene, 2021, 40, 5533-5547.	5.9	12
13	Integrative Analysis of Deep Sequencing Data Identifies Estrogen Receptor Early Response Genes and Links ATAD3B to Poor Survival in Breast Cancer. PLoS Computational Biology, 2013, 9, e1003100.	3.2	11
14	Authorship attribution as a case of anomaly detection: A neural network model. International Journal of Hybrid Intelligent Systems, 2011, 8, 225-235.	1.2	7
15	Genomic Profile in a Non-Seminoma Testicular Germ-Cell Tumor Cohort Reveals a Potential Biomarker of Sensitivity to Platinum-Based Therapy. Cancers, 2022, 14, 2065.	3.7	5
16	Low Expression and Somatic Mutations of the KLHL6 Gene Predict Poor Survival in Patients with Activated B-Cell like Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2926-2926.	1.4	3
17	Low Expression of the CIITA Gene Predicts Poor Outcome in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2948-2948.	1.4	2
18	Detection of Different Authorship of Text Sequences through Self-organizing Maps and Mutual Information Function. Lecture Notes in Computer Science, 2010, , 186-195.	1.3	2

#	Article	IF	Citations
19	FUNGI: FUsioN Gene Integration toolset. Bioinformatics, 2021, 37, 3353-3355.	4.1	1
20	Decreasing Neighborhood Revisited in Self-Organizing Maps. Lecture Notes in Computer Science, 2008, , 671-679.	1.3	1
21	Alternative Splicing and Expression of Class II Tubulin Beta (TUBB2B) Are Associated with Outcome in Diffuse Large B-Cell Lymphoma. Blood, 2012, 120, 1557-1557.	1.4	1
22	A Neural Network May Show the Best Way to Learn How to Count for Students in Elementary Math Courses. , 2008, , .		0
23	Global Profiling Of Outcome Associated Alternative Splicing Events and Gene Expression In Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 75-75.	1.4	0
24	Somatic Mutations in E3 Ubiquitin Ligase Deltex 1 Are Associated with Survival in Diffuse Large B-Cell Lymphoma. Blood, 2014, 124, 1688-1688.	1.4	0