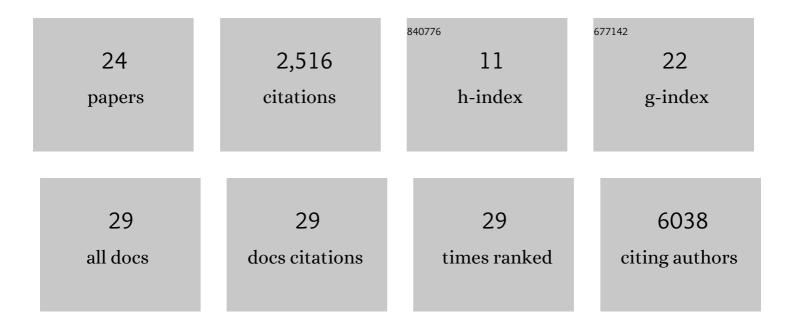
Alejandra Cervera

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5398502/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	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
2	FUNGI: FUsioN Gene Integration toolset. Bioinformatics, 2021, 37, 3353-3355.	4.1	1
3	Human cell transformation by combined lineage conversion and oncogene expression. Oncogene, 2021, 40, 5533-5547.	5.9	12
4	Functional Profiling of FSH and Estradiol in Ovarian Granulosa Cell Tumors. Journal of the Endocrine Society, 2020, 4, bvaa034.	0.2	13
5	Distinct subtypes of diffuse large B-cell lymphoma defined by hypermutated genes. Leukemia, 2019, 33, 2662-2672.	7.2	24
6	Anduril 2: upgraded large-scale data integration framework. Bioinformatics, 2019, 35, 3815-3817.	4.1	31
7	Anagrelide for Gastrointestinal Stromal Tumor. Clinical Cancer Research, 2019, 25, 1676-1687.	7.0	14
8	Modified penetrance of coding variants by cis-regulatory variation contributes to disease risk. Nature Genetics, 2018, 50, 1327-1334.	21.4	167
9	Deltex-1 mutations predict poor survival in diffuse large B-cell lymphoma. Haematologica, 2017, 102, e195-e198.	3.5	23
10	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
11	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
12	SePIA: RNA and small RNA sequence processing, integration, and analysis. BioData Mining, 2016, 9, 20.	4.0	25
13	A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13.	8.8	1,898
14	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
15	Low Expression of the CIITA Gene Predicts Poor Outcome in Diffuse Large B-Cell Lymphoma. Blood, 2016, 128, 2948-2948.	1.4	2
16	Gene expression profiling of pre-eclamptic placentae by RNA sequencing. Scientific Reports, 2015, 5, 14107.	3.3	89
17	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
18	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

ALEJANDRA CERVERA

#	Article	IF	CITATIONS
19	Global Profiling Of Outcome Associated Alternative Splicing Events and Gene Expression In Diffuse Large B-Cell Lymphoma. Blood, 2013, 122, 75-75.	1.4	Ο
20	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
21	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
22	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
23	A Neural Network May Show the Best Way to Learn How to Count for Students in Elementary Math Courses. , 2008, , .		0
24	Decreasing Neighborhood Revisited in Self-Organizing Maps. Lecture Notes in Computer Science, 2008, , 671-679.	1.3	1