## Joan Climent

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6667557/publications.pdf

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32	2,376	279798	477307
papers	citations	h-index	g-index
34	34	34	4528
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	FBXW7 Targets mTOR for Degradation and Cooperates with PTEN in Tumor Suppression. Science, 2008, 321, 1499-1502.	12.6	375
2	Homozygous deletions localize novel tumor suppressor genes in B-cell lymphomas. Blood, 2007, 109, 271-280.	1.4	227
3	Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana. Nature, 2000, 408, 820-823.	27.8	188
4	MALT1 is deregulated by both chromosomal translocation and amplification in B-cell non-Hodgkin lymphoma. Blood, 2003, 101, 4539-4546.	1.4	188
5	Mantle-cell lymphoma genotypes identified with CGH to BAC microarrays define a leukemic subgroup of disease and predict patient outcome. Blood, 2005, 105, 4445-4454.	1.4	180
6	Inverse and Direct Cancer Comorbidity in People with Central Nervous System Disorders: A Meta-Analysis of Cancer Incidence in 577,013 Participants of 50 Observational Studies. Psychotherapy and Psychosomatics, 2014, 83, 89-105.	8.8	164
7	Characterization of 8p21.3 chromosomal deletions in B-cell lymphoma: TRAIL-R1 and TRAIL-R2 as candidate dosage-dependent tumor suppressor genes. Blood, 2005, 106, 3214-3222.	1.4	137
8	No paradox, no progress: inverse cancer comorbidity in people with other complex diseases. Lancet Oncology, The, 2011, 12, 604-608.	10.7	122
9	Co-amplified genes at 8p12 and 11q13 in breast tumors cooperate with two major pathways in oncogenesis. Oncogene, 2009, 28, 1892-1903.	5.9	94
10	Loss of a novel tumor suppressor gene locus at chromosome 8p is associated with leukemic mantle cell lymphoma. Blood, 2001, 98, 3479-3482.	1.4	86
11	Deletion of Chromosome 11q Predicts Response to Anthracycline-Based Chemotherapy in Early Breast Cancer. Cancer Research, 2007, 67, 818-826.	0.9	75
12	Deletion of the <i>PER3 </i> Gene on Chromosome 1p36 in Recurrent ER-Positive Breast Cancer. Journal of Clinical Oncology, 2010, 28, 3770-3778.	1.6	57
13	MicroRNA profile in very young women with breast cancer. BMC Cancer, 2014, 14, 529.	2.6	56
14	Homeobox NKX2-3 promotes marginal-zone lymphomagenesis by activating B-cell receptor signalling and shaping lymphocyte dynamics. Nature Communications, 2016, 7, 11889.	12.8	42
15	Pleckstrin homology domain-interacting protein (PHIP) as a marker and mediator of melanoma metastasis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7067-7072.	7.1	39
16	Characterization of breast cancer by array comparative genomic hybridizationThis paper is one of a selection of papers published in this Special Issue, entitled 28th International West Coast Chromatin and Chromosome Conference, and has undergone the Journal's usual peer review process  Biochemistry and Cell Biology, 2007, 85, 497-508.	2.0	38
17	Hipk2 cooperates with p53 to suppress $\hat{l}^3$ -ray radiation-induced mouse thymic lymphoma. Oncogene, 2012, 31, 1176-1180.	5.9	36
18	Homozygous deletion of SOCS1 in primary mediastinal B-cell lymphoma detected by CGH to BAC microarrays. Leukemia, 2005, 19, 1082-1084.	7.2	35

#	Article	IF	CITATIONS
19	MicroRNA Profile in Response to Doxorubicin Treatment in Breast Cancer. Journal of Cellular Biochemistry, 2015, 116, 2061-2073.	2.6	31
20	Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. Molecular Autism, 2019, 10, 17.	4.9	30
21	Genomic loss of 18p predicts an adverse clinical outcome in patients with high-risk breast cancer. Clinical Cancer Research, 2002, 8, 3863-9.	7.0	29
22	Selective concomitant inhibition of mTORC1 and mTORC2 activity in estrogen receptor negative breast cancer cells by BN107 and oleanolic acid. International Journal of Cancer, 2010, 127, 1209-1219.	5.1	28
23	Transcriptomic and Genetic Associations between Alzheimer's Disease, Parkinson's Disease, and Cancer. Cancers, 2021, 13, 2990.	3.7	26
24	Genomic Abnormalities Acquired in the Blastic Transformation of Splenic Marginal Zone B-cell Lymphoma. Leukemia and Lymphoma, 2003, 44, 459-464.	1.3	24
25	Applications of computational homology to the analysis of treatment response in breast cancer patients. Topology and Its Applications, 2010, 157, 157-164.	0.4	24
26	A genomic approach to study down syndrome and cancer inverse comorbidity: untangling the chromosome 21. Frontiers in Physiology, 2015, 6, 10.	2.8	17
27	A COVID-19 Drug Repurposing Strategy through Quantitative Homological Similarities Using a Topological Data Analysis-Based Framework. Pharmaceutics, 2021, 13, 488.	4.5	13
28	Analysis of the CDKN2A and CDK4 Genes and HLA-DR and HLA-DQ Alleles in Two Spanish Familial Melanoma Kindreds. Acta Dermato-Venereologica, 2000, 80, 440-442.	1.3	10
29	Circadian PERformance in breast cancer: a germline and somatic genetic study of PER3VNTR polymorphisms and gene co-expression. Npj Breast Cancer, 2021, 7, 118.	5.2	3
30	DNA Methylation in Breast Cancer. , 2016, , 297-312.		1
31	miRNA Expression Analysis: Cell Lines HCC1500 and HCC1937 as Models for Breast Cancer in Young Women and the miR-23a as a Poor Prognostic Biomarker. Breast Cancer: Basic and Clinical Research, 2020, 14, 117822342097784.	1.1	0
32	Mantle Cell Lymphoma Genotypes Identified with CGH to BAC Microarrays Define Clinical Subgroups of Disease and Strongly Predict Patient Outcome Blood, 2004, 104, 695-695.	1.4	O