Antonio C Picornell

List of Publications by Year
in descending order

15 papers	478 citations	1039880 9 h-index	996849 15 g-index
16 all docs	16 docs citations	16 times ranked	1125 citing authors

#	Article	IF	Citations
1	Iterative Variable Selection for High-Dimensional Data: Prediction of Pathological Response in Triple-Negative Breast Cancer. Mathematics, 2021, 9, 222.	1.1	2
2	Concordance of Genomic Variants in Matched Primary Breast Cancer, Metastatic Tumor, and Circulating Tumor DNA: The MIRROR Study. JCO Precision Oncology, 2019, 3, 1-16.	1.5	7
3	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. Clinical Cancer Research, 2018, 24, 1845-1852.	3.2	84
4	A novel predictive approach for GVHD after allogeneic SCT based on clinical variables and cytokine gene polymorphisms. Blood Advances, 2018, 2, 1719-1737.	2.5	25
5	Pathological Response and Survival in Triple-Negative Breast Cancer Following Neoadjuvant Carboplatin plus Docetaxel. Clinical Cancer Research, 2018, 24, 5820-5829.	3.2	82
6	Efficacy of Neoadjuvant Carboplatin plus Docetaxel in Triple-Negative Breast Cancer: Combined Analysis of Two Cohorts. Clinical Cancer Research, 2017, 23, 649-657.	3.2	108
7	Prediction of non-muscle invasive bladder cancer outcomes assessed by innovative multimarker prognostic models. BMC Cancer, 2016, 16, 351.	1.1	8
8	Inflammatory-Related Genetic Variants in Non–Muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1144-1150.	1.1	8
9	Frequency of germline DNA genetic findings in an unselected prospective cohort of triple-negative breast cancer patients participating in a platinum-based neoadjuvant chemotherapy trial. Breast Cancer Research and Treatment, 2016, 156, 507-515.	1.1	27
10	A Cross-Sectional Comparison of Druggable Mutations in Primary Tumors, Metastatic Tissue, Circulating Tumor Cells, and Cell-Free Circulating DNA in Patients with Metastatic Breast Cancer: The MIRROR Study Protocol. JMIR Research Protocols, 2016, 5, e167.	0.5	6
11	Framework for the Integration of Genomics, Epigenomics and Transcriptomics in Complex Diseases. Human Heredity, 2015, 79, 124-136.	0.4	25
12	A New Multiple Single-Nucleotide Polymorphisms Based Predictive Model for Grades III to IV and Extensive Graft Versus Host Disease after Identical HLA-Allogeneic Stem-Cell. Blood, 2015, 126, 921-921.	0.6	4
13	Whole Genome Prediction of Bladder Cancer Risk With the Bayesian LASSO. Genetic Epidemiology, 2014, 38, 467-476.	0.6	11
14	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. PLoS ONE, 2012, 7, e29396.	1.1	36
15	Genetic Variations in the Sonic Hedgehog Pathway Affect Clinical Outcomes in Non–Muscle-Invasive Bladder Cancer. Cancer Prevention Research, 2010, 3, 1235-1245.	0.7	45