

Antonio C Picornell

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8942856/publications.pdf>

Version: 2024-02-01

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	Efficacy of Neoadjuvant Carboplatin plus Docetaxel in Triple-Negative Breast Cancer: Combined Analysis of Two Cohorts. <i>Clinical Cancer Research</i> , 2017, 23, 649-657.	3.2	108
2	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. <i>Clinical Cancer Research</i> , 2018, 24, 1845-1852.	3.2	84
3	Pathological Response and Survival in Triple-Negative Breast Cancer Following Neoadjuvant Carboplatin plus Docetaxel. <i>Clinical Cancer Research</i> , 2018, 24, 5820-5829.	3.2	82
4	Genetic Variations in the Sonic Hedgehog Pathway Affect Clinical Outcomes in Non-muscle-Invasive Bladder Cancer. <i>Cancer Prevention Research</i> , 2010, 3, 1235-1245.	0.7	45
5	Large-Scale Pathway-Based Analysis of Bladder Cancer Genome-Wide Association Data from Five Studies of European Background. <i>PLoS ONE</i> , 2012, 7, e29396.	1.1	36
6	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. <i>Breast Cancer Research and Treatment</i> , 2016, 156, 507-515.	1.1	27
7	Framework for the Integration of Genomics, Epigenomics and Transcriptomics in Complex Diseases. <i>Human Heredity</i> , 2015, 79, 124-136.	0.4	25
8	A novel predictive approach for GVHD after allogeneic SCT based on clinical variables and cytokine gene polymorphisms. <i>Blood Advances</i> , 2018, 2, 1719-1737.	2.5	25
9	Whole Genome Prediction of Bladder Cancer Risk With the Bayesian LASSO. <i>Genetic Epidemiology</i> , 2014, 38, 467-476.	0.6	11
10	Prediction of non-muscle invasive bladder cancer outcomes assessed by innovative multimarker prognostic models. <i>BMC Cancer</i> , 2016, 16, 351.	1.1	8
11	Inflammatory-Related Genetic Variants in Non-muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1144-1150.	1.1	8
12	Concordance of Genomic Variants in Matched Primary Breast Cancer, Metastatic Tumor, and Circulating Tumor DNA: The MIRROR Study. <i>JCO Precision Oncology</i> , 2019, 3, 1-16.	1.5	7
13	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. <i>JMIR Research Protocols</i> , 2016, 5, e167.	0.5	6
14	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. <i>Blood</i> , 2015, 126, 921-921.	0.6	4
15	Iterative Variable Selection for High-Dimensional Data: Prediction of Pathological Response in Triple-Negative Breast Cancer. <i>Mathematics</i> , 2021, 9, 222.	1.1	2