Hatice U Osmanbeyoglu

List of Publications by Year
in descending order

20 papers	1,464 citations	623734 14 h-index	713466 21 g-index
27 all docs	27 docs citations	27 times ranked	3366 citing authors

#	Article	IF	Citations
1	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
2	PI3K pathway regulates ER-dependent transcription in breast cancer through the epigenetic regulator KMT2D. Science, 2017, 355, 1324-1330.	12.6	217
3	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
4	A mechanism for expansion of regulatory T-cell repertoire and its role in self-tolerance. Nature, 2015, 528, 132-136.	27.8	123
5	An ATR and CHK1 kinase signaling mechanism that limits origin firing during unperturbed DNA replication. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13374-13383.	7.1	107
6	Thin alumina nanoporous membranes for similar size biomolecule separation. Journal of Membrane Science, 2009, 343, 1-6.	8.2	104
7	Linking signaling pathways to transcriptional programs in breast cancer. Genome Research, 2014, 24, 1869-1880.	5.5	57
8	WEE1 kinase inhibitor AZD1775 induces CDK1 kinase-dependent origin firing in unperturbed G1- and S-phase cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23891-23893.	7.1	57
9	Pancancer modelling predicts the context-specific impact of somatic mutations on transcriptional programs. Nature Communications, 2017, 8, 14249.	12.8	52
10	N-gram analysis of 970 microbial organisms reveals presence of biological language models. BMC Bioinformatics, 2011, 12, 12.	2.6	30
11	Evaluating the Barriers to Point-of-Care Documentation for Nursing Staff. CIN - Computers Informatics Nursing, 2012, 30, 126-133.	0.5	29
12	Ets transcription factor GABP controls T cell homeostasis and immunity. Nature Communications, 2017, 8, 1062.	12.8	22
13	Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancers. Nature Communications, 2019, 10, 4369.	12.8	18
14	Active machine learning for transmembrane helix prediction. BMC Bioinformatics, 2010, 11, S58.	2.6	17
15	Estrogen represses gene expression through reconfiguring chromatin structures. Nucleic Acids Research, 2013, 41, 8061-8071.	14.5	17
16	Recurrent Human Papillomavirusâ€"Related Head and Neck Cancer Undergoes Metabolic Reprogramming and Is Driven by Oxidative Phosphorylation. Clinical Cancer Research, 2021, 27, 6250-6264.	7.0	17
17	SWI/SNF tumor suppressor gene PBRM1/BAF180 in human clear cell kidney cancer. Molecular and Cellular Oncology, 2017, 4, e1342747.	0.7	10
18	SPaRTAN, a computational framework for linking cell-surface receptors to transcriptional regulators. Nucleic Acids Research, 2021, 49, 9633-9647.	14.5	9

#	Article	IF	Citations
19	Computational methods to dissect gene regulatory networks in cancer. Current Opinion in Systems Biology, 2017, 2, 115-122.	2.6	8
20	Improving ChIP-seq peak-calling for functional co-regulator binding by integrating multiple sources of biological information. BMC Genomics, 2012, 13, S1.	2.8	4