

Sajid A Marhon

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

644
citations

1170033

9
h-index

1051228

16
g-index

23
all docs

23
docs citations

23
times ranked

1102
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of the global miR-130a targetome reveals a role for TBL1XR1 in hematopoietic stem cell self-renewal and t(8;21) AML. <i>Cell Reports</i> , 2022, 38, 110481.	2.9	4
2	PRMT inhibition induces a viral mimicry response in triple-negative breast cancer. <i>Nature Chemical Biology</i> , 2022, 18, 821-830.	3.9	43
3	PLAG1 dampens protein synthesis to promote human hematopoietic stem cell self-renewal. <i>Blood</i> , 2022, 140, 992-1008.	0.6	11
4	DNA hypomethylating agents increase activation and cytolytic activity of CD8+ T cells. <i>Molecular Cell</i> , 2021, 81, 1469-1483.e8.	4.5	52
5	Mapping the cellular origin and early evolution of leukemia in Down syndrome. <i>Science</i> , 2021, 373, .	6.0	42
6	SAVMD: An adaptive signal processing method for identifying protein coding regions. <i>Biomedical Signal Processing and Control</i> , 2021, 70, 102998.	3.5	2
7	Epigenetic therapy induces transcription of inverted SINEs and ADAR1 dependency. <i>Nature</i> , 2020, 588, 169-173.	13.7	149
8	Mitochondrial carrier homolog 2 is necessary for AML survival. <i>Blood</i> , 2020, 136, 81-92.	0.6	19
9	Rev-erba dynamically modulates chromatin looping to control circadian gene transcription. <i>Science</i> , 2018, 359, 1274-1277.	6.0	171
10	Evaluation of Selected DNA Spectral Analysis-Based Gene Prediction Techniques. <i>Current Bioinformatics</i> , 2017, 12, 87-100.	0.7	3
11	Prediction of Protein Coding Regions Using a Wide-Range Wavelet Window Method. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 742-753.	1.9	30
12	Nucleotide distribution variance-based dynamic representation scheme for novel gene prediction. <i>Network Modeling Analysis in Health Informatics and Bioinformatics</i> , 2015, 4, 1.	1.2	1
13	A dynamic representation-based, de novo method for protein-coding region prediction and biological information detection. , 2015, 46, 10-18.		9
14	A New, Dynamic-Representation-Based Gene Finding Method with an Analysis of False Positive Peaks. , 2014, , .		0
15	Recurrent Neural Networks. <i>Intelligent Systems Reference Library</i> , 2013, , 29-65.	1.0	16
16	A brief comparison of DSP and HMM methods for gene finding. , 2012, , .		1
17	Gene Prediction Based on DNA Spectral Analysis: A Literature Review. <i>Journal of Computational Biology</i> , 2011, 18, 639-676.	0.8	65
18	Protein coding region prediction based on the adaptive representation method. , 2011, , .		7

#	ARTICLE	IF	CITATIONS
19	Theoretical justification of computing the 3-base periodicity using nucleotide distribution variance. BioSystems, 2010, 101, 185-186.	0.9	8