

Taejeong Bae

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

3,487
citations

623734

14
h-index

580821

25
g-index

32
all docs

32
docs citations

32
times ranked

8688
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic mosaicism reveals clonal distributions of neocortical development. <i>Nature</i> , 2022, 604, 689-696.	27.8	26
2	All2: A tool for selecting mosaic mutations from comprehensive multi-cell comparisons. <i>PLoS Computational Biology</i> , 2022, 18, e1009487.	3.2	2
3	The landscape of somatic mutation in cerebral cortex of autistic and neurotypical individuals revealed by ultra-deep whole-genome sequencing. <i>Nature Neuroscience</i> , 2021, 24, 176-185.	14.8	73
4	Landmarks of human embryonic development inscribed in somatic mutations. <i>Science</i> , 2021, 371, 1249-1253.	12.6	65
5	Comprehensive identification of somatic nucleotide variants in human brain tissue. <i>Genome Biology</i> , 2021, 22, 92.	8.8	26
6	Early developmental asymmetries in cell lineage trees in living individuals. <i>Science</i> , 2021, 371, 1245-1248.	12.6	39
7	Machine learning reveals bilateral distribution of somatic L1 insertions in human neurons and glia. <i>Nature Neuroscience</i> , 2021, 24, 186-196.	14.8	22
8	SCELLECTOR: ranking amplification bias in single cells using shallow sequencing. <i>BMC Bioinformatics</i> , 2020, 21, 521.	2.6	3
9	Complex mosaic structural variations in human fetal brains. <i>Genome Research</i> , 2020, 30, 1695-1704.	5.5	21
10	Molecular characterization of colorectal adenomas with and without malignancy reveals distinguishing genome, transcriptome and methylome alterations. <i>Scientific Reports</i> , 2018, 8, 3161.	3.3	35
11	Different mutational rates and mechanisms in human cells at pregastrulation and neurogenesis. <i>Science</i> , 2018, 359, 550-555.	12.6	216
12	Inferring modes of evolution from colorectal cancer with residual polyp of origin. <i>Oncotarget</i> , 2018, 9, 6780-6792.	1.8	3
13	Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. <i>Science</i> , 2017, 356, .	12.6	206
14	Colorectal Cancer with Residual Polyp of Origin: A Model of Malignant Transformation. <i>Translational Oncology</i> , 2016, 9, 280-286.	3.7	9
15	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	27.8	1,994
16	Restoration of paclitaxel resistance by CDK1 intervention in drug-resistant ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, bgv140.	2.8	27
17	The PsychENCODE project. <i>Nature Neuroscience</i> , 2015, 18, 1707-1712.	14.8	371
18	Transcriptome analysis indicates TFEB1 and YEATS4 as regulatory transcription factors for drug resistance of ovarian cancer. <i>Oncotarget</i> , 2015, 6, 31030-31038.	1.8	13

#	ARTICLE	IF	CITATIONS
19	Identification of upstream regulators for prognostic expression signature genes in colorectal cancer. <i>BMC Systems Biology</i> , 2013, 7, 86.	3.0	11
20	Identification of master regulator candidates in conjunction with network screening and inference. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 8, 366.	0.1	6
21	Selecting SNPs for pharmacogenomic association study. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 521.	0.1	6
22	Rational drug repositioning guided by an integrated pharmacological network of protein, disease and drug. <i>BMC Systems Biology</i> , 2012, 6, 80.	3.0	75
23	CDA: Combinatorial Drug Discovery Using Transcriptional Response Modules. <i>PLoS ONE</i> , 2012, 7, e42573.	2.5	57
24	GARNET “ gene set analysis with exploration of annotation relations. <i>BMC Bioinformatics</i> , 2011, 12, S25.	2.6	11
25	A procedure for identifying master regulators in conjunction with network screening and inference. , 2010, , .		1
26	Selecting SNPs for pharmacogenomic association study. , 2010, , .		0
27	Lipid raft proteome reveals ATP synthase complex in the cell surface. <i>Proteomics</i> , 2004, 4, 3536-3548.	2.2	160