Abhinav Nellore

List of Publications by Year
in descending order

36	3,796	279798	330143
papers	citations	23	37
		h-index	g-index

49	49	49	8058
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Oncogenic BRAF Regulates Oxidative Metabolism via PGC1Î± and MITF. Cancer Cell, 2013, 23, 302-315.	16.8	689
2	Human Leukocyte Antigen Susceptibility Map for Severe Acute Respiratory Syndrome Coronavirus 2. Journal of Virology, 2020, 94, .	3.4	434
3	Reproducible RNA-seq analysis using recount2. Nature Biotechnology, 2017, 35, 319-321.	17.5	395
4	The Growth Kinetics of TiO2Nanoparticles from Titanium(IV) Alkoxide at High Water/Titanium Ratio. Journal of Physical Chemistry B, 2003, 107, 1734-1738.	2.6	308
5	Integration of Genome-wide Approaches Identifies lncRNAs of Adult Neural Stem Cells and Their Progeny InÂVivo. Cell Stem Cell, 2013, 12, 616-628.	11.1	224
6	Thermodynamics and Bulk Viscosity of Approximate Black Hole Duals to Finite Temperature Quantum Chromodynamics. Physical Review Letters, 2008, 101, 131601.	7.8	205
7	Cloud computing for genomic data analysis and collaboration. Nature Reviews Genetics, 2018, 19, 208-219.	16.3	205
8	Mimicking the QCD equation of state with a dual black hole. Physical Review D, 2008, 78, .	4.7	175
9	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	8.8	103
10	qSVA framework for RNA quality correction in differential expression analysis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7130-7135.	7.1	95
11	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. Genome Biology, 2016, 17, 266.	8.8	94
12	Ground states of holographic superconductors. Physical Review D, 2009, 80, .	4.7	86
13	Burden of tumor mutations, neoepitopes, and other variants are weak predictors of cancer immunotherapy response and overall survival. Genome Medicine, 2020, 12, 33.	8.2	67
14	Bound on the speed of sound from holography. Physical Review D, 2009, 80, .	4.7	63
15	CHANCE: comprehensive software for quality control and validation of ChIP-seq data. Genome Biology, 2012, 13, R98.	9.6	60
16	Low-temperature behavior of the Abelian Higgs model in Anti-de Sitter space. Journal of High Energy Physics, 2009, 2009, 008-008.	4.7	57
17	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. Bioinformatics, 2017, 33, 4033-4040.	4.1	57
18	Flexible expressed region analysis for RNA-seq with<tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	14.5	54

#	Article	IF	Citations
19	ASCOT identifies key regulators of neuronal subtype-specific splicing. Nature Communications, 2020, 11, 137.	12.8	50
20	recount workflow: Accessing over 70,000 human RNA-seq samples with Bioconductor. F1000Research, 2017, 6, 1558.	1.6	50
21	Snaptron: querying splicing patterns across tens of thousands of RNA-seq samples. Bioinformatics, 2018, 34, 114-116.	4.1	39
22	Excited baryon decay widths in largeNcQCD. Physical Review D, 2004, 69, .	4.7	34
23	Population-level distribution and putative immunogenicity of cancer neoepitopes. BMC Cancer, 2018, 18, 414.	2.6	32
24	<tt>neoepiscope</tt> improves neoepitope prediction with multivariant phasing. Bioinformatics, 2020, 36, 713-720.	4.1	23
25	Recovery guarantees for exemplar-based clustering. Information and Computation, 2015, 245, 165-180.	0.7	18
26	Pion-nucleon scattering relations at next-to-leading order in$1/N_c$. Physical Review D, 2004, 70, .	4.7	16
27	NSeq: a multithreaded Java application for finding positioned nucleosomes from sequencing data. Frontiers in Genetics, 2013, 3, 320.	2.3	12
28	Putatively cancer-specific exon–exon junctions are shared across patients and present in developmental and other non-cancer cells. NAR Cancer, 2020, 2, zcaa001.	3.1	12
29	Human methylome variation across Infinium 450K data on the Gene Expression Omnibus. NAR Genomics and Bioinformatics, 2021, 3, lqab025.	3.2	12
30	Universal relations of transport coefficients from holography. Physical Review D, 2009, 80, .	4.7	10
31	Alternative splicing of MR1 regulates antigen presentation to MAIT cells. Scientific Reports, 2020, 10, 15429.	3.3	9
32	pepsickle rapidly and accurately predicts proteasomal cleavage sites for improved neoantigen identification. Bioinformatics, 2021, 37, 3723-3733.	4.1	6
33	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. Bioinformatics, 2016, 32, 2551-2553.	4.1	5
34	Quantization of exotic states in SU(3) soliton models: A solvable quantum mechanical analog. Physical Review D, 2004, 70, .	4.7	4
35	Tumor Mutation Burden—From Doubts to Concerns. JAMA Oncology, 2019, 5, 1808.	7.1	4
36	Minimal observed impact of <scp>HLA</scp> genotype on hospitalization and severity of <scp>SARS‐CoV</scp>‐2 infection. Hla, 2022, 99, 607-613.	0.6	4