

Benjamin C Hitz

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17
papers

1,881
citations

11
h-index

22
g-index

22
ext. papers

3,110
ext. citations

21
avg, IF

4.01
L-index

#	Paper	IF	Citations
17	The Encyclopedia of DNA elements (ENCODE): data portal update. <i>Nucleic Acids Research</i> , 2018 , 46, D794-D801	10.1	1778
16	ENCODE data at the ENCODE portal. <i>Nucleic Acids Research</i> , 2016 , 44, D726-32	20.1	292
15	H3K4me3 breadth is linked to cell identity and transcriptional consistency. <i>Cell</i> , 2014 , 158, 673-88	56.2	278
14	The reference genome sequence of <i>Saccharomyces cerevisiae</i> : then and now. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 389-98	3.2	213
13	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020 , 583, 744-751	50.4	76
12	Perspectives on ENCODE. <i>Nature</i> , 2020 , 583, 693-698	50.4	61
11	Ontology application and use at the ENCODE DCC. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	36
10	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020 , 48, D882-D889	20.1	29
9	Principles of metadata organization at the ENCODE data coordination center. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	29
8	The <i>Saccharomyces</i> Genome Database Variant Viewer. <i>Nucleic Acids Research</i> , 2016 , 44, D698-702	20.1	21
7	Systematic mapping of chromatin state landscapes during mouse development		15
6	Data Sanitization to Reduce Private Information Leakage from Functional Genomics. <i>Cell</i> , 2020 , 183, 905-917.e16	56.2	10
5	The ENCODE Portal as an Epigenomics Resource. <i>Current Protocols in Bioinformatics</i> , 2019 , 68, e89	24.2	10
4	SnoVault and encoded: A novel object-based storage system and applications to ENCODE metadata. <i>PLoS ONE</i> , 2017 , 12, e0175310	3.7	9
3	Prevention of data duplication for high throughput sequencing repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	9
2	Integration of new alternative reference strain genome sequences into the <i>Saccharomyces</i> genome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	8
1	CNN-Peaks: CHIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection. <i>Scientific Reports</i> , 2020 , 10, 7933	4.9	5

