

# Benjamin C Hitz

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/45180/publications.pdf>

Version: 2024-02-01

16  
papers

3,839  
citations

687220

13  
h-index

839398

18  
g-index

22  
all docs

22  
docs citations

22  
times ranked

9029  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Encyclopedia of DNA elements (ENCODE): data portal update. <i>Nucleic Acids Research</i> , 2018, 46, D794-D801.	6.5	1,559
2	ENCODE data at the ENCODE portal. <i>Nucleic Acids Research</i> , 2016, 44, D726-D732.	6.5	500
3	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. <i>Cell</i> , 2014, 158, 673-688.	13.5	404
4	New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. <i>Nucleic Acids Research</i> , 2020, 48, D882-D889.	6.5	381
5	The Reference Genome Sequence of <i>Saccharomyces cerevisiae</i> : Then and Now. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 389-398.	0.8	369
6	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	13.7	257
7	Perspectives on ENCODE. <i>Nature</i> , 2020, 583, 693-698.	13.7	123
8	Ontology application and use at the ENCODE DCC. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, .	1.4	42
9	Principles of metadata organization at the ENCODE data coordination center. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw001.	1.4	40
10	Data Sanitization to Reduce Private Information Leakage from Functional Genomics. <i>Cell</i> , 2020, 183, 905-917.e16.	13.5	28
11	The <i>Saccharomyces</i> Genome Database Variant Viewer. <i>Nucleic Acids Research</i> , 2016, 44, D698-D702.	6.5	23
12	The ENCODE Portal as an Epigenomics Resource. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e89.	25.8	23
13	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, baw074.	1.4	15
14	CNN-Peaks: ChIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection. <i>Scientific Reports</i> , 2020, 10, 7933.	1.6	14
15	SnoVault and encodeD: A novel object-based storage system and applications to ENCODE metadata. <i>PLoS ONE</i> , 2017, 12, e0175310.	1.1	14
16	Prevention of data duplication for high throughput sequencing repositories. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	1.4	9