

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

687363

13
h-index

839539

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. Nucleic Acids Research, 2018, 46, D794-D801. | 14.5 | 1,559 |
| 2 | ENCODE data at the ENCODE portal. Nucleic Acids Research, 2016, 44, D726-D732. | 14.5 | 500 |
| 3 | H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. Cell, 2014, 158, 673-688. | 28.9 | 404 |
| 4 | New developments on the Encyclopedia of DNA Elements (ENCODE) data portal. Nucleic Acids Research, 2020, 48, D882-D889. | 14.5 | 381 |
| 5 | The Reference Genome Sequence of <i>Saccharomyces cerevisiae</i> : Then and Now. G3: Genes, Genomes, Genetics, 2014, 4, 389-398. | 1.8 | 369 |
| 6 | An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751. | 27.8 | 257 |
| 7 | Perspectives on ENCODE. Nature, 2020, 583, 693-698. | 27.8 | 123 |
| 8 | Ontology application and use at the ENCODE DCC. Database: the Journal of Biological Databases and Curation, 2015, 2015, . | 3.0 | 42 |
| 9 | Principles of metadata organization at the ENCODE data coordination center. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw001. | 3.0 | 40 |
| 10 | Data Sanitization to Reduce Private Information Leakage from Functional Genomics. Cell, 2020, 183, 905-917.e16. | 28.9 | 28 |
| 11 | TheSaccharomycesGenome Database Variant Viewer. Nucleic Acids Research, 2016, 44, D698-D702. | 14.5 | 23 |
| 12 | The ENCODE Portal as an Epigenomics Resource. Current Protocols in Bioinformatics, 2019, 68, e89. | 25.8 | 23 |
| 13 | Integration of new alternative reference strain genome sequences into theSaccharomycesgenome database. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw074. | 3.0 | 15 |
| 14 | CNN-Peaks: ChIP-Seq peak detection pipeline using convolutional neural networks that imitate human visual inspection. Scientific Reports, 2020, 10, 7933. | 3.3 | 14 |
| 15 | SnoVault and encodedD: A novel object-based storage system and applications to ENCODE metadata. PLoS ONE, 2017, 12, e0175310. | 2.5 | 14 |
| 16 | Prevention of data duplication for high throughput sequencing repositories. Database: the Journal of Biological Databases and Curation, 2018, 2018, . | 3.0 | 9 |