

Chun-Nan Hsu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4904469/publications.pdf>

Version: 2024-02-01

15
papers

1,493
citations

840776

11
h-index

940533

16
g-index

23
all docs

23
docs citations

23
times ranked

2366
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Evaluation and accurate diagnoses of pediatric diseases using artificial intelligence. <i>Nature Medicine</i> , 2019, 25, 433-438. | 30.7 | 386 |
| 2 | Weakly supervised learning of biomedical information extraction from curated data. <i>BMC Bioinformatics</i> , 2016, 17, 1. | 2.6 | 342 |
| 3 | Federated learning for predicting clinical outcomes in patients with COVID-19. <i>Nature Medicine</i> , 2021, 27, 1735-1743. | 30.7 | 300 |
| 4 | Overview of BioCreative II gene normalization. <i>Genome Biology</i> , 2008, 9, S3. | 9.6 | 237 |
| 5 | Challenges in the construction of knowledge bases for human microbiome-disease associations. <i>Microbiome</i> , 2019, 7, 129. | 11.1 | 36 |
| 6 | RadBERT: Adapting Transformer-based Language Models to Radiology. <i>Radiology: Artificial Intelligence</i> , 2022, 4, . | 5.8 | 35 |
| 7 | BIOADI: a machine learning approach to identifying abbreviations and definitions in biological literature. <i>BMC Bioinformatics</i> , 2009, 10, S7. | 2.6 | 34 |
| 8 | Citing a Data Repository: A Case Study of the Protein Data Bank. <i>PLoS ONE</i> , 2015, 10, e0136631. | 2.5 | 26 |
| 9 | Identifying and characterizing highly similar notes in big clinical note datasets. <i>Journal of Biomedical Informatics</i> , 2018, 82, 63-69. | 4.3 | 20 |
| 10 | PombeX: Robust Cell Segmentation for Fission Yeast Transillumination Images. <i>PLoS ONE</i> , 2013, 8, e81434. | 2.5 | 17 |
| 11 | A phenome-wide association study (PheWAS) in the Population Architecture using Genomics and Epidemiology (PAGE) study reveals potential pleiotropy in African Americans. <i>PLoS ONE</i> , 2019, 14, e0226771. | 2.5 | 15 |
| 12 | Increasing metadata coverage of SRA BioSample entries using deep learning-based named entity recognition. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, . | 3.0 | 13 |
| 13 | Comparing the Use of Research Resource Identifiers and Natural Language Processing for Citation of Databases, Software, and Other Digital Artifacts. <i>Computing in Science and Engineering</i> , 2020, 22, 22-32. | 1.2 | 4 |
| 14 | Soft tagging of overlapping high confidence gene mention variants for cross-species full-text gene normalization. <i>BMC Bioinformatics</i> , 2011, 12, S6. | 2.6 | 3 |
| 15 | Antibody Watch: Text mining antibody specificity from the literature. <i>PLoS Computational Biology</i> , 2021, 17, e1008967. | 3.2 | 2 |