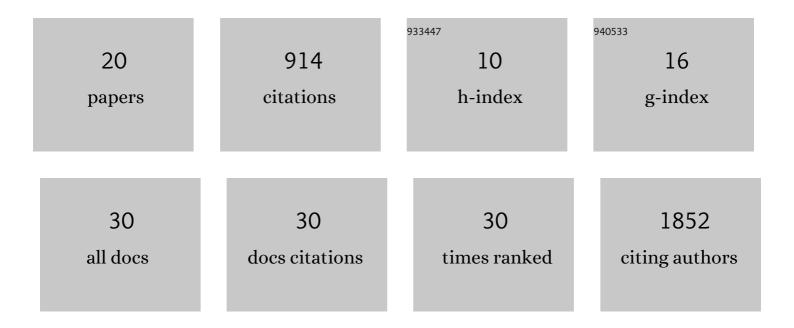
## Ling-Hong Hung

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4889597/publications.pdf Version: 2024-02-01



| #  | Article  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Data access for the 1,000 Plants (1KP) project. GigaScience, 2014, 3, 17.  | 6.4  | 582       |
| 2  | PROTINFO: new algorithms for enhanced protein structure predictions. Nucleic Acids Research, 2005, 33, W77-W80.  | 14.5 | 60        |
| 3  | Accurate and automated classification of protein secondary structure with PsiCSI. Protein Science, 2003, 12, 288-295.  | 7.6  | 44        |
| 4  | GUIdock: Using Docker Containers with a Common Graphics User Interface to Address the Reproducibility of Research. PLoS ONE, 2016, 11, e0152686.                                 | 2.5  | 40        |
| 5  | PROTINFO: secondary and tertiary protein structure prediction. Nucleic Acids Research, 2003, 31, 3296-3299.  | 14.5 | 38        |
| 6  | Reproducible Bioconductor workflows using browser-based interactive notebooks and containers.<br>Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 4-12. | 4.4  | 23        |
| 7  | Building Containerized Workflows Using the BioDepot-Workflow-Builder. Cell Systems, 2019, 9, 508-514.e3.   | 6.2  | 18        |
| 8  | fast_protein_cluster: parallel and optimized clustering of large-scale protein modeling data.<br>Bioinformatics, 2014, 30, 1774-1776.  | 4.1  | 16        |
| 9  | Accelerated protein structure comparison using TM-score-GPU. Bioinformatics, 2012, 28, 2191-2192.  | 4.1  | 15        |
| 10 | An automated assignment-free Bayesian approach for accurately identifying proton contacts from NOESY data. Journal of Biomolecular NMR, 2006, 36, 189-198.                       | 2.8  | 14        |
| 11 | GPU-Q-J, a fast method for calculating root mean square deviation (RMSD) after optimal superposition. BMC Research Notes, 2011, 4, 97.   | 1.4  | 11        |
| 12 | Hot-starting software containers for STAR aligner. GigaScience, 2018, 7, .   | 6.4  | 9         |
| 13 | Integration of Multiple Data Sources for Gene Network Inference Using Genetic Perturbation Data.<br>Journal of Computational Biology, 2019, 26, 1113-1129.                       | 1.6  | 7         |
| 14 | A graphical, interactive and GPU-enabled workflow to process long-read sequencing data. BMC<br>Genomics, 2021, 22, 626.  | 2.8  | 7         |
| 15 | De Novo Protein Structure Prediction. Biological and Medical Physics Series, 2007, , 43-63.  | 0.4  | 7         |
| 16 | Holistic optimization of an RNA-seq workflow for multi-threaded environments. Bioinformatics, 2019, 35, 4173-4175.   | 4.1  | 4         |
| 17 | An Investigation on Public Cloud Performance Variation for an RNA Sequencing Workflow. , 2020, , .   |      | 2         |
| 18 | Characterizing Performance Variation of Genomic Data Analysis Workflows on the Public Cloud. ,<br>2020, , .  |      | 1         |

| #  | Article   | IF | CITATIONS |
|----|---|----|-----------|
| 19 | Using BioDepot-workflow-Builder to Create and Execute Reproducible Bioinformatics Workflows. ,<br>2018, , . |    | 0         |
| 20 | Using BioDepot-workflow-builder to Access Public Databases in a Containerized Environment. , 2019, , .      |    | 0         |