

pridepy: A Python package to download and search data from PRIDE database

Selvakumar Kamatchinathan¹, Suresh Hewapathirana¹, Chakradhar Bandla¹, and Yasset Perez-Riverol¹

¹ European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

DOI: [N/A](#)

Software

- [Review](#) ↗
- [Repository](#) ↗
- [Archive](#) ↗

Editor: [Open Journals](#) ↗

Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: 01 January 1970

License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC BY 4.0](#)).

Summary

The Proteomics Identification Database (PRIDE) ([Perez-Riverol et al., 2022](#)) is the world's largest repository for proteomics data and a founding member of ProteomeXchange ([Deutsch et al., 2023](#)). We introduce pridepy, a Python client designed to access PRIDE Archive data, including project metadata and file downloads. pridepy offers a flexible programmatic interface for searching, retrieving, and downloading data via the PRIDE REST API. This tool simplifies the integration of PRIDE datasets into bioinformatics pipelines, making it easier for researchers to handle large datasets programmatically.

Statement of Need

The PRIDE Archive stores an extensive collection of proteomics data ([Perez-Riverol et al., 2022](#)), but manually accessing this data can be inefficient and time-consuming. With the growing need for cloud-based ([Dai et al., 2024](#)) and HPC bioinformatics tools ([Mehta et al., 2023](#)), command-line utilities that seamlessly interact with the PRIDE API are increasingly important. pridepy addresses this by enabling researchers to programmatically access PRIDE using Python, a widely adopted language. It allows efficient dataset integration into automated workflows, with support for large-scale data transfers via [Aspera](#), [Globus](#), FTP, and HTTPS, making it ideal for scalable, reproducible pipelines.

Methods

pridepy is built in Python and interacts with the [PRIDE Archive REST API](#). The library and package not only provide data models for each data structure of the API but also a set of commandline to facilitate their use by users. The main features of pridepy is dataset search and file download.

The client is available on [PyPI](#) and can be installed using pip. The source code is hosted on [GitHub](#) and is open-source under the Apache 2.0 license. In addition, a conda recipe is available for easy installation in conda environments. The package is continuously tested using GitHub Actions and has been successfully deployed on the EMBL-EBI HPC cluster.

Downloading files from PRIDE Archive

By 2024, PRIDE Archive stores the data in two different storage systems (**Figure 1**), one for public data and another for private data. The public data is stored in a S3-like storage system, called FIRE ([Thakur et al., 2024](#)), which also includes other major EMBL-EBI archives such as ENA (European Nucleotide Archive) and EGA (European Genome-phenome Archive). FIRE

has limited capabilities for data updates and deletions, making it ideal for long-term data storage. FIRE data is accessible via multiple protocols including FTP, Aspera and Globus. In contrast, private datasets are stored in a different file-system based on NFS, which is more flexible for data updates and deletion; but it is only accessible via PRIDE streaming protocol.

The `pridepy` client provides a simple command line interface to download files from PRIDE Archive using the following protocols. Each protocol offers different advantages: - **FTP**: Widely supported and easy to use - **Aspera**: High-speed file transfers, especially for large files or over long distances - **Globus**: Reliable transfers for very large datasets

These are currently the only supported protocols for file downloads.

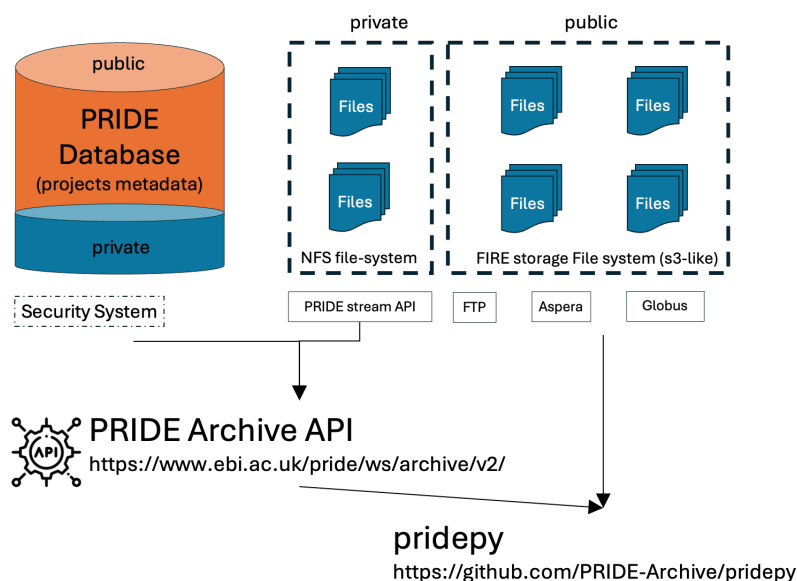


Figure 1: Figure 1: Architecture of transfer protocols supported by PRIDE Archive

Users can download files from PRIDE Archive using the following command options: - `download-all-public-raw-files`: command downloads all raw files from a dataset, it is useful for large-scale data retrieval and public datasets. - `download-file-by-name`: command downloads a single file by name. Users can specify the output directory, protocol (FTP, Aspera or Globus), and other options to customize the download process. For private datasets, the user and password are required to access the data.

One example of downloading all raw files using Aspera from a dataset is shown below:

```
$ pridepy download-all-raw-files \
-a PXD012353 \
-o /Users/yourname/Downloads/foldername/ \
-p aspera
```

This makes the client suitable for handling large-scale proteomics data in automated workflows, particularly in environments requiring bulk downloads of proteomics datasets.

Discussion and Future Directions

`pridepy` successfully simplifies access to the PRIDE Archive data, but future development could focus on improving the handling of large downloads by implementing parallel downloads. Additionally, we will expand the user documentation and examples could help broaden its use

within the scientific community; and at the same time produce a group of benchmarks to evaluate the performance of the client in different scenarios. We plan to continue extending the library to support more features of the PRIDE Archive API, such as dataset metadata streaming, and submission of new datasets to the PRIDE Archive.

Acknowledgments

We would like to thank the PRIDE Archive team and contributors to this project for their invaluable input and feedback. The work is supported by core funding from the European Molecular Biology Laboratory (EMBL) and the Wellcome Trust [grant numbers 208391/Z/17/Z and 223745/Z/21/Z], and the BBSRC grant 'DIA-Exchange' [BB/X001911/1].

References

- Dai, C., Pfeuffer, J., Wang, H., Zheng, P., Käll, L., Sachsenberg, T., Demichev, V., Bai, M., Kohlbacher, O., & Perez-Riverol, Y. (2024). Quantms: A cloud-based pipeline for quantitative proteomics enables the reanalysis of public proteomics data. *Nat. Methods*, 21(9), 1603–1607.
- Deutsch, E. W., Bandeira, N., Perez-Riverol, Y., Sharma, V., Carver, J. J., Mendoza, L., Kundu, D. J., Wang, S., Bandla, C., Kamatchinathan, S., Hewapathirana, S., Pullman, B. S., Wertz, J., Sun, Z., Kawano, S., Okuda, S., Watanabe, Y., MacLean, B., MacCoss, M. J., ... Vizcaíno, J. A. (2023). The ProteomeXchange consortium at 10 years: 2023 update. *Nucleic Acids Res.*, 51(D1), D1539–D1548.
- Mehta, S., Bernt, M., Chambers, M., Fahrner, M., Föll, M. C., Gruening, B., Horro, C., Johnson, J. E., Loux, V., Rajczewski, A. T., Schilling, O., Vandenbrouck, Y., Gustafsson, O. J. R., Thang, W. C. M., Hyde, C., Price, G., Jagtap, P. D., & Griffin, T. J. (2023). A galaxy of informatics resources for MS-based proteomics. *Expert Rev. Proteomics*, 20(11), 251–266.
- Perez-Riverol, Y., Bai, J., Bandla, C., García-Seisdedos, D., Hewapathirana, S., Kamatchinathan, S., Kundu, D. J., Prakash, A., Frericks-Zipper, A., Eisenacher, M., Walzer, M., Wang, S., Brazma, A., & Vizcaíno, J. A. (2022). The PRIDE database resources in 2022: A hub for mass spectrometry-based proteomics evidences. *Nucleic Acids Res.*, 50(D1), D543–D552.
- Thakur, M., Buniello, A., Brooksbank, C., Gurwitz, K. T., Hall, M., Hartley, M., Hulcoop, D. G., Leach, A. R., Marques, D., Martin, M., Mithani, A., McDonagh, E. M., Mutasa-Gottgens, E., Ochoa, D., Perez-Riverol, Y., Stephenson, J., Varadi, M., Velankar, S., Vizcaino, J. A., ... McEntyre, J. (2024). EMBL's european bioinformatics institute (EMBL-EBI) in 2023. *Nucleic Acids Res.*, 52(D1), D10–D17.