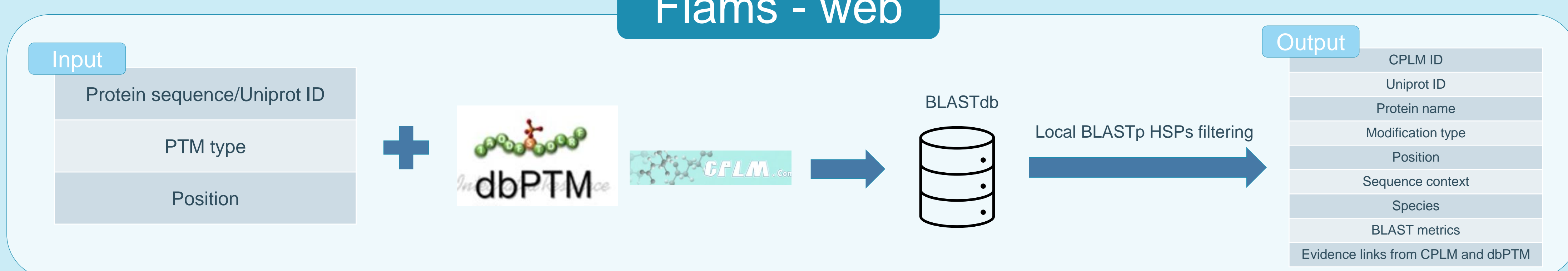


## FLAMS: An Update

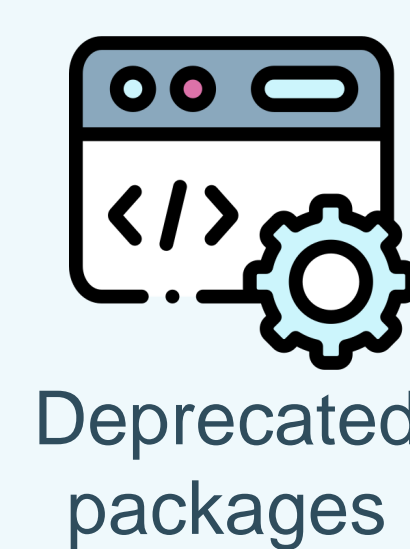
### Abstract

Find Lysine Acylations and other Modification Sites (FLAMS) is a Python3-based command line and web-tool that is used to compare input PTM sites with the CPLM, compendium of protein lysine modifications, and dbPTM, a database for exploring regulatory networks and functional associations of protein post—translational modifications. This tool helps researchers to quickly identify new and conserved PTM sites in their datasets. [1] The tool currently provides a tabular output with information about the PTM, but it can be further improved by incorporating links to external databases and integrating advanced protein visualization features. It is also valuable to log user query information, such as the specific modifications searched, the aligned amino acids, and the species associated with the sequence. This information can be used as feedback to further improve the tool and the information it provides.

### Flams - web



### Flams



### Protein visualization

#### Resources:

- Ngl viewer JavaScript library
- AlphaFold
- Uniprot API

#### Minimal

- Visualize protein structure
- Visualize PTMs on structure

#### Basic

- Visualize all other PTMs on same protein

#### Advanced

- Visualize functional sites:
  - Active sites
  - Binding sites

### Cross-linking

#### Resources:

- NCBI e-util
- Javascript

#### Minimal

- Uniprot ID
- CPLM ID

#### Basic

- Combine all evidence links
- Check formatting (regex)
- Fetch API (client side)
- Distribute links based on API response

### Usage statistics

#### Resources:

- SQLite3 database

#### Minimal

- Table = ip\_queries
- IP address | # queries

#### Basic

- Insights into what the most used PTMs are
- Table = modifications\_amino\_acids
- IP address | modification | amino acid | # repetitions

#### Advanced

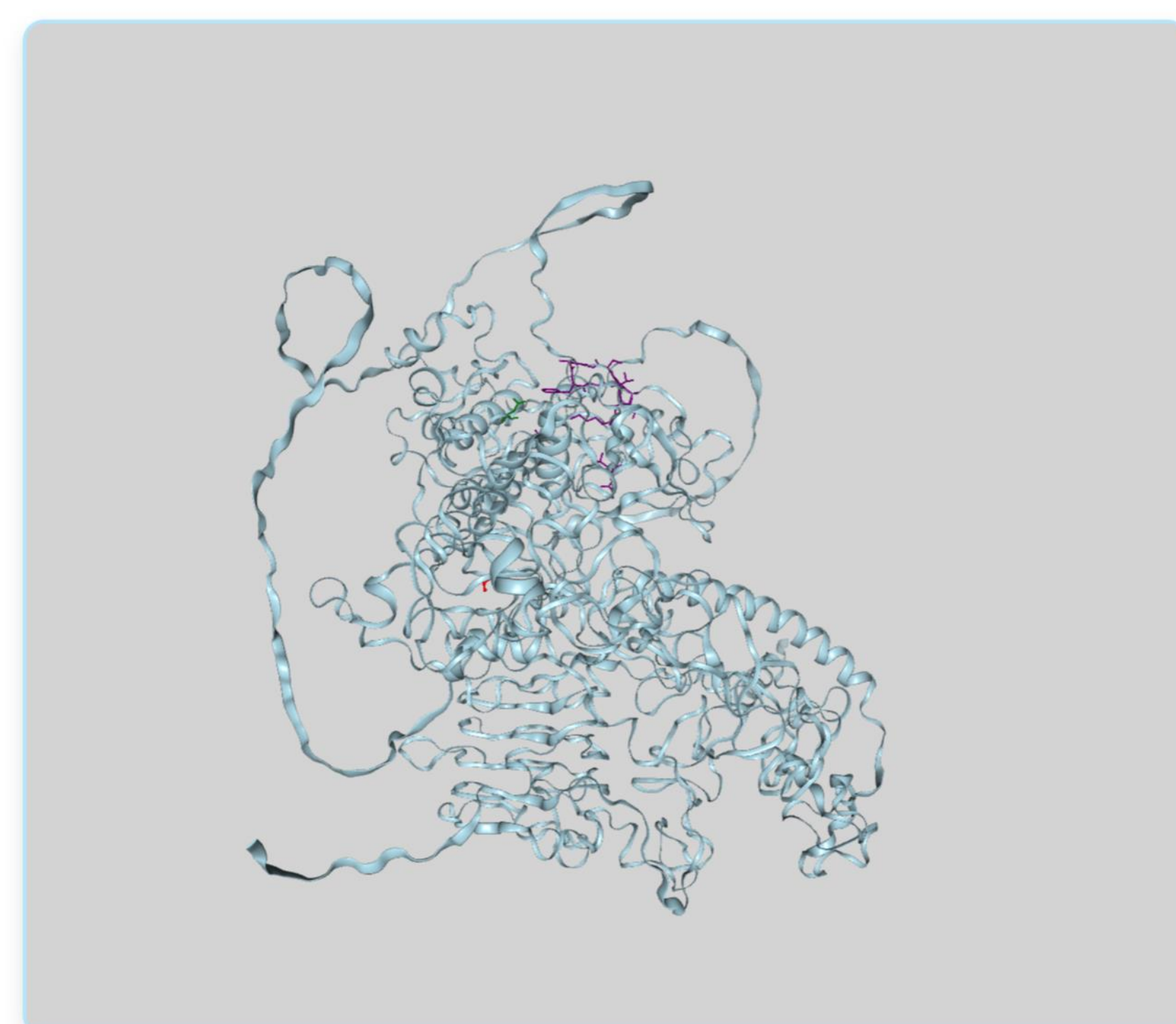
- Insights into what the most used species are
- Table = species\_modifications
- IP address | species | # repetitions

### Updating

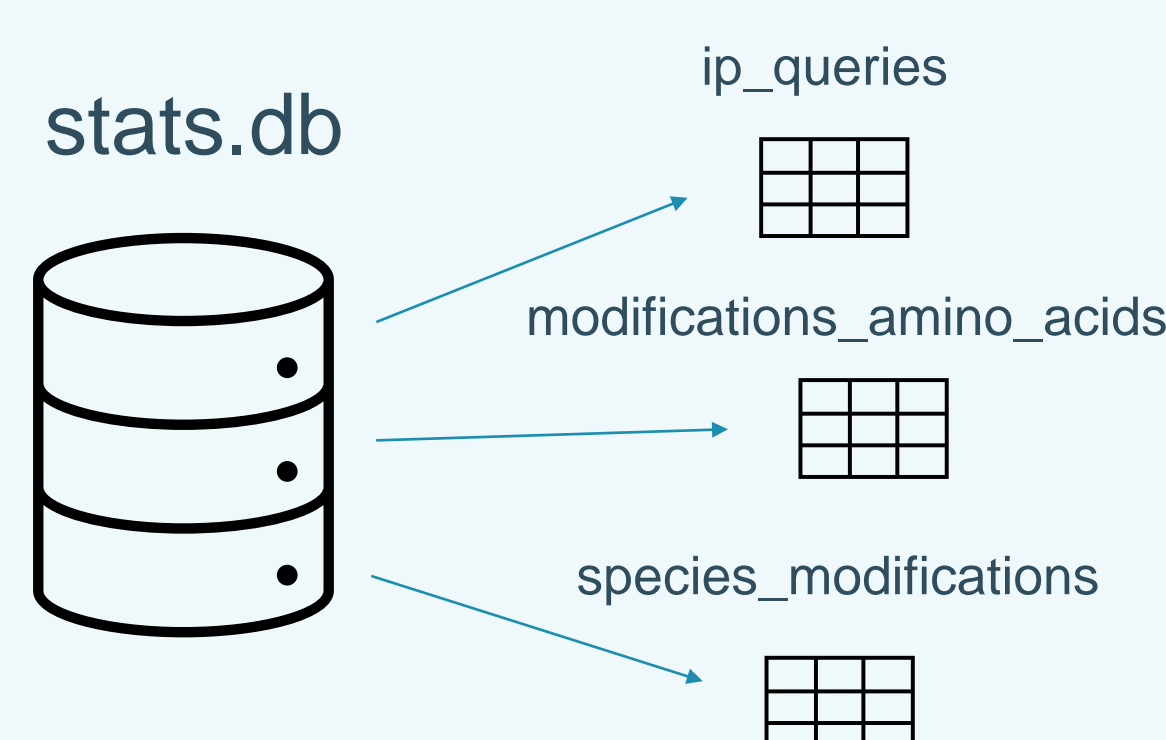
- Updating dependencies to latest versions: 12/2024
  - appdirs, biopython, certifi, charset-normalizer, idna, numpy, pandas, python-dateutil, pytz, requests, six, tzdata, urllib3
- Python update
- Refactored existing code to work with updated packages
- Unit testing
  - Coverage
- Updating CI to include unit test

### Result

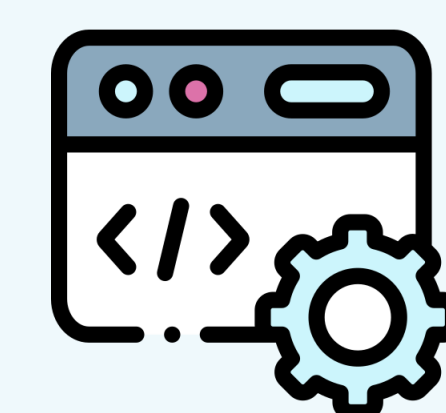
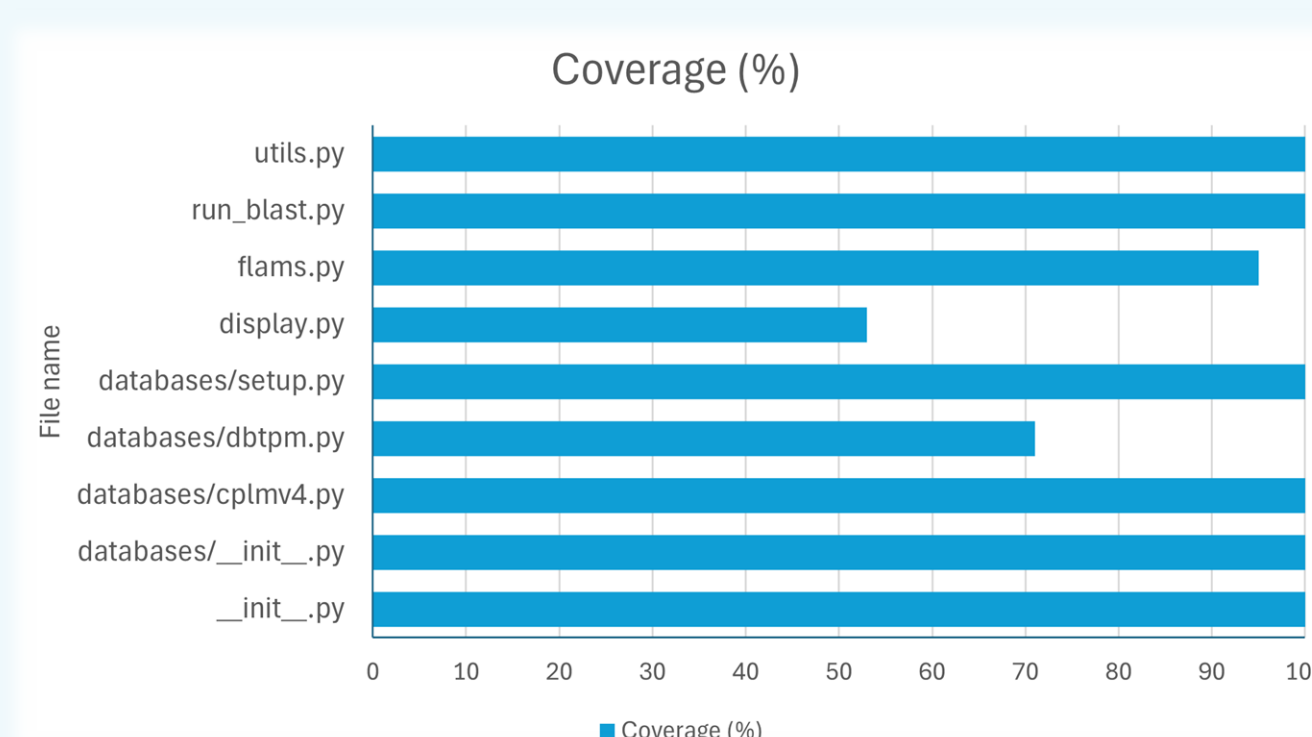
#### Visualize your PTM



- Legend
- PTMs (Post-translational Modifications)
  - Active Sites
  - Binding Sites



CPLM ID
Uniprot ID
Protein name
Modification type
Position
Sequence context
Species
BLAST metrics
Evidence links from CPLM and dbPTM



Updated packages

### Reference

[1] Longin, H.; Broeckart, N.; Langen, M.; Hari, R.; Kramarska, A.; Oikarinen, K.; Hendrix, H.; Lavigne, R.; Van Noort, V. FLAMS: Find Lysine Acylations and Other Modification Sites. *Bioinformatics* **2024**, *40* (1), btae005. <https://doi.org/10.1093/bioinformatics/btae005>.