JOHANNES GUTENBERG UNIVERSITÄT MAINZ

Examining repeats with databases

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RepeatsDB

RepeatsDB About Browse Search Stats Help IDs or free text Search

News

RepeatsDB **v3.0**
Release: **2020-09-15**
More info

Start

For a fast search use the top-right search box. Alternatively, visit the browse and search pages.

Contact

For questions and/or comments, please write to us at BioComputing UP.

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Citing RepeatsDB

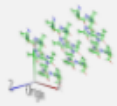
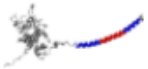
RepeatsDB in 2021: improved data and extended

RepeatsDB

RepeatsDB is a database of annotated tandem repeat protein structures. The database provides unit position, classification and reference to other databases. To start using RepeatsDB, please try the search box (top-right corner), the advanced search or the browse page.

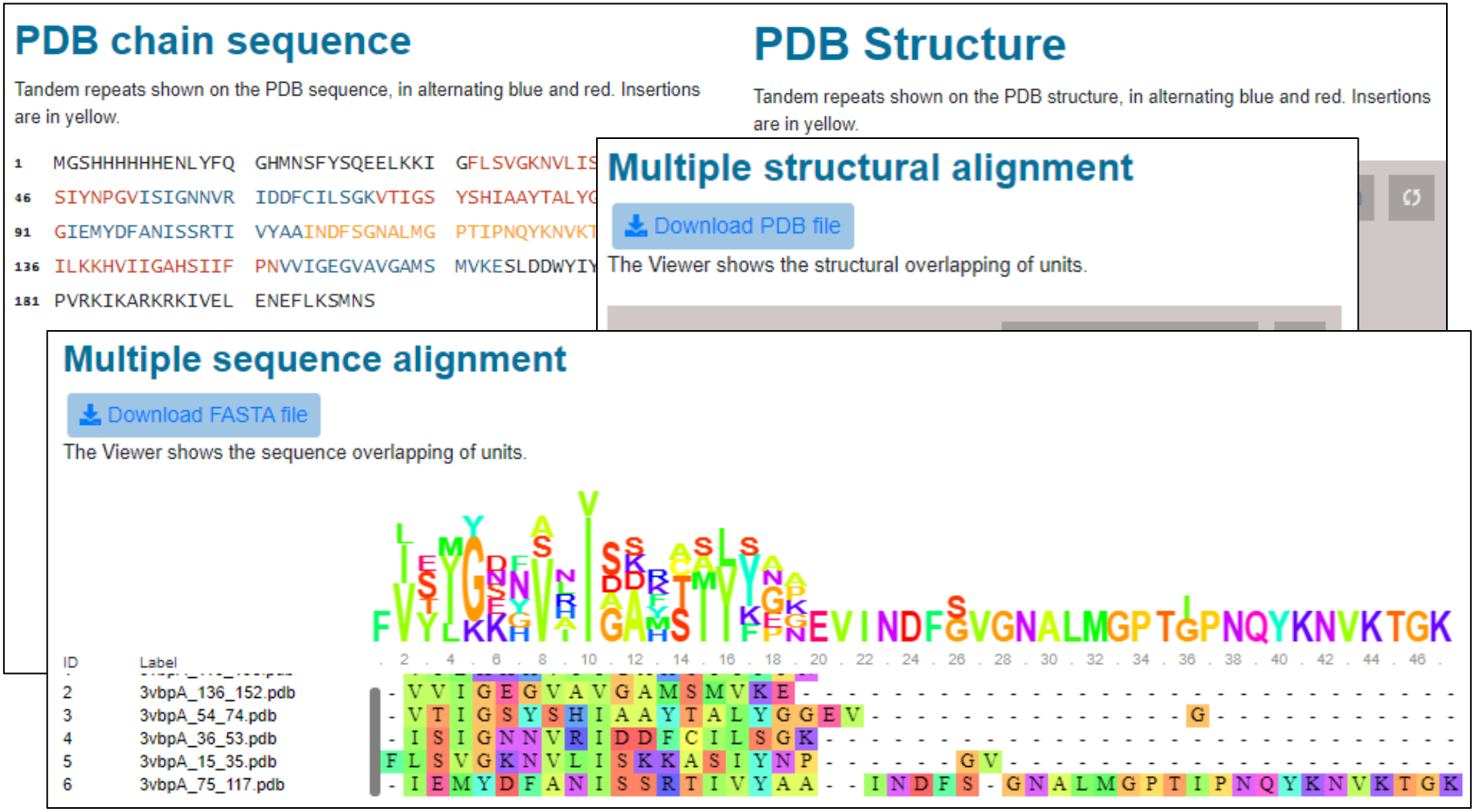
Check our web server RepeatsDB-lite for interactive prediction of repeat units in protein structures.

RepeatsDB contains the following **repeat classes**:

Class	Description	UniProt	PDBs	PDB chains	Regions	Units	Example
1 	Crystalline aggregates	0	3	3	3	0	-
2 	Fibrous repeat	21	39	86	86	393	P04115

RepeatsDB

https://repeatsdb.bio.unipd.it/structure/3vbpA



Exercise 1. Examining repeat structures in repeatsDB

- Go to RepeatsDB: http://repeatsdb.bio.unipd.it/

- Click the "Search" tab, then search "Repeat unit number"

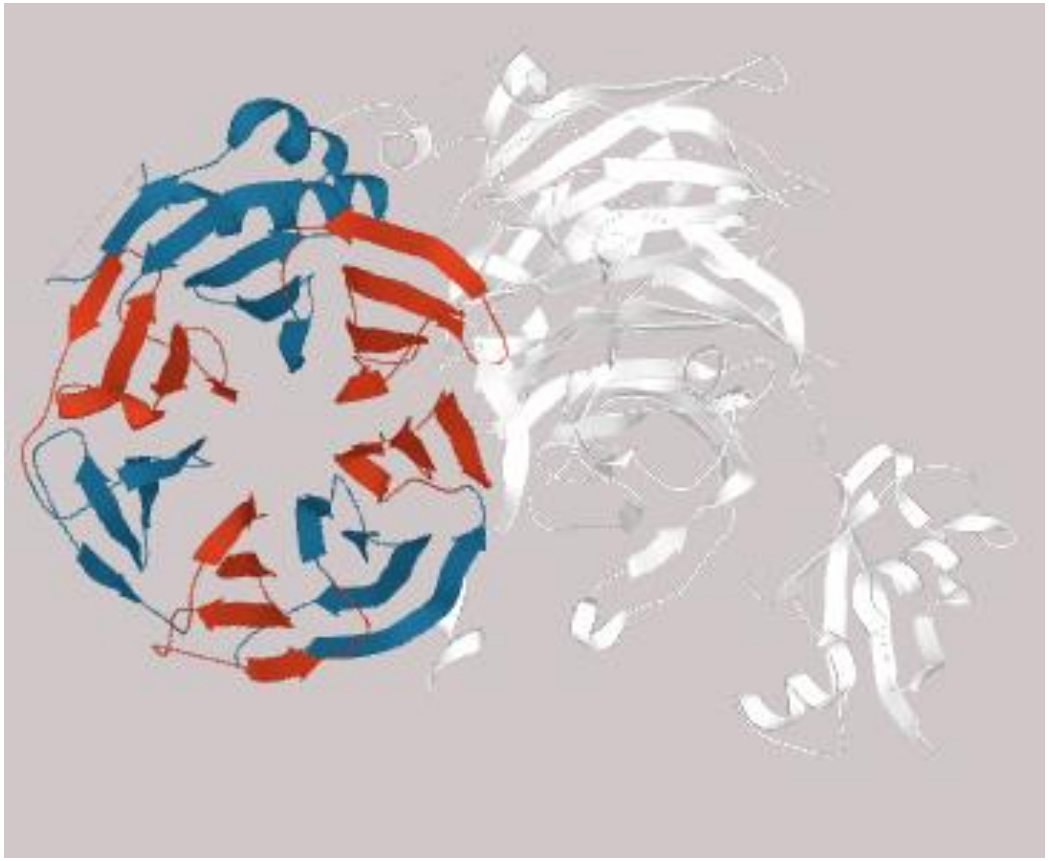
- Choose one example and write down the PDB name (e.g. 6yc3B).

- Check the assignment of the units. Is it correct? What about insertions? Are there mistakes? Write an evaluation: Looks good / one repeat wrong / many mistakes / total mess

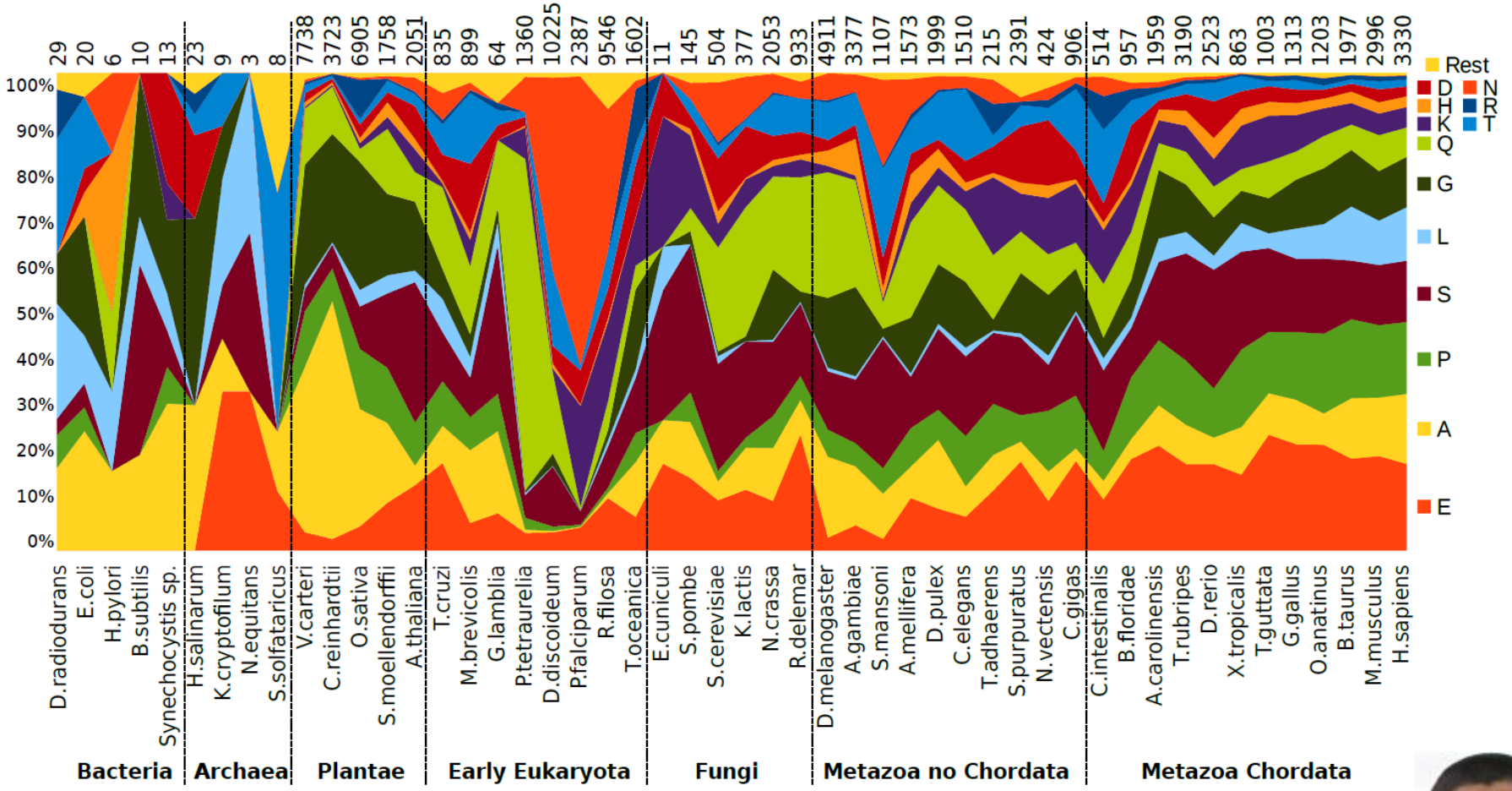
Example

https://repeatsdb.bio.unipd.it/structure/5cxbB

1. looks good
2. one repeat wrong
3. **many mistakes**
4. total mess

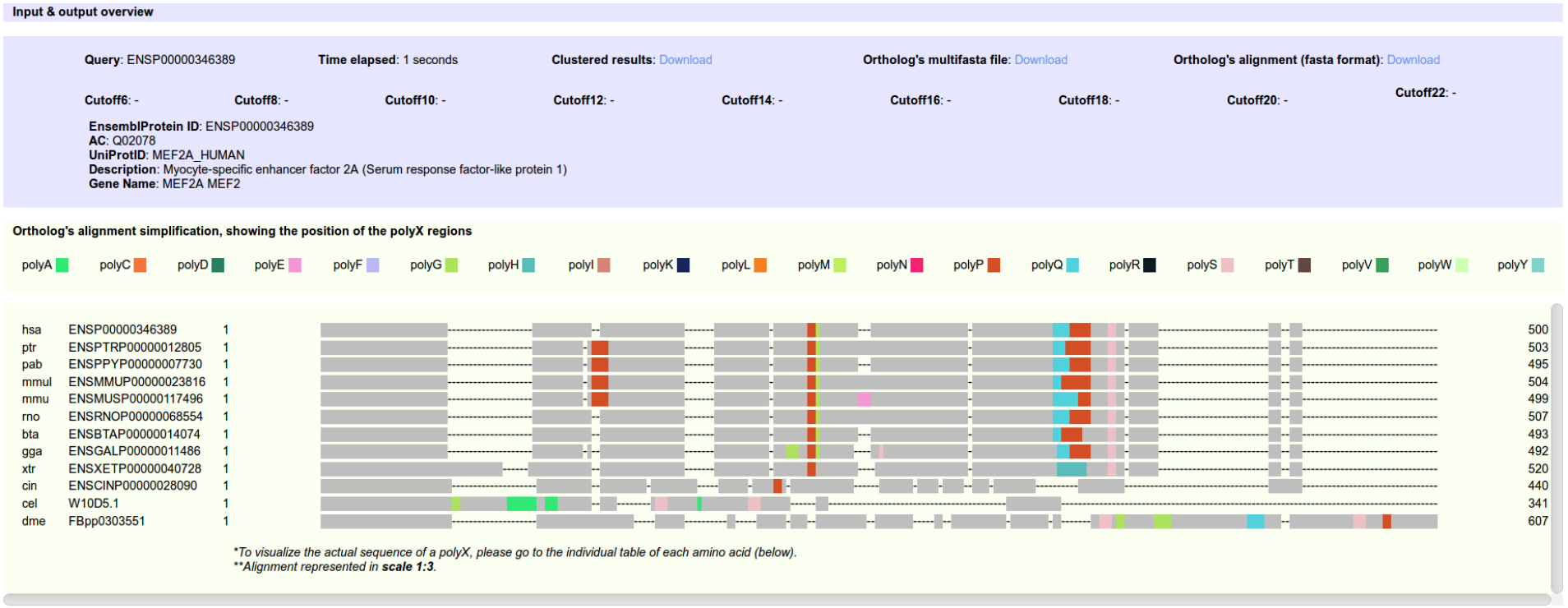


Evolution of homorepeats in 50 species



Pablo Mier

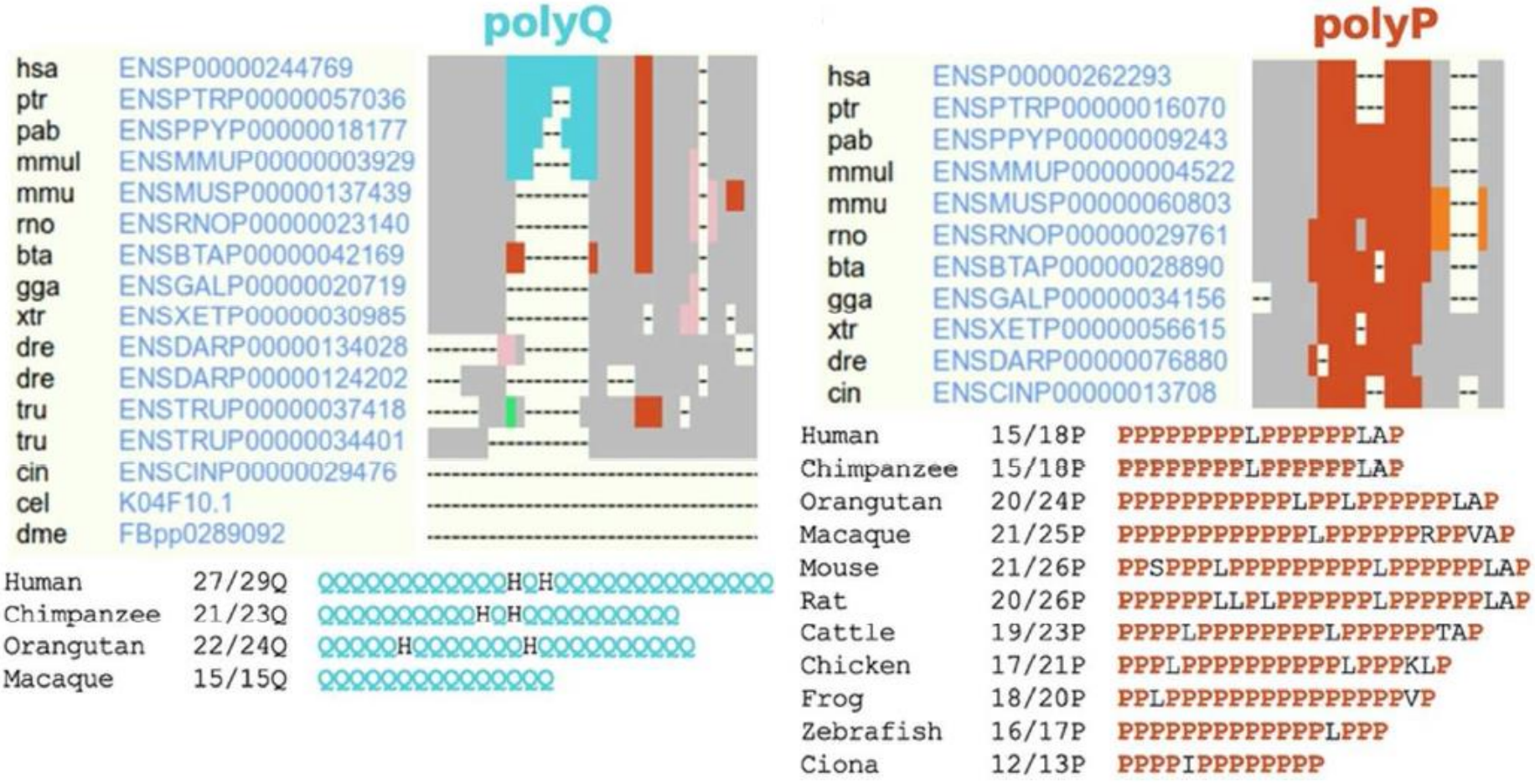
Context and evolution of homorepeats



dAtabase of **P**olyX **E**volution

Mier *et al.* (2016) Bioinformatics

Context and evolution of homorepeats

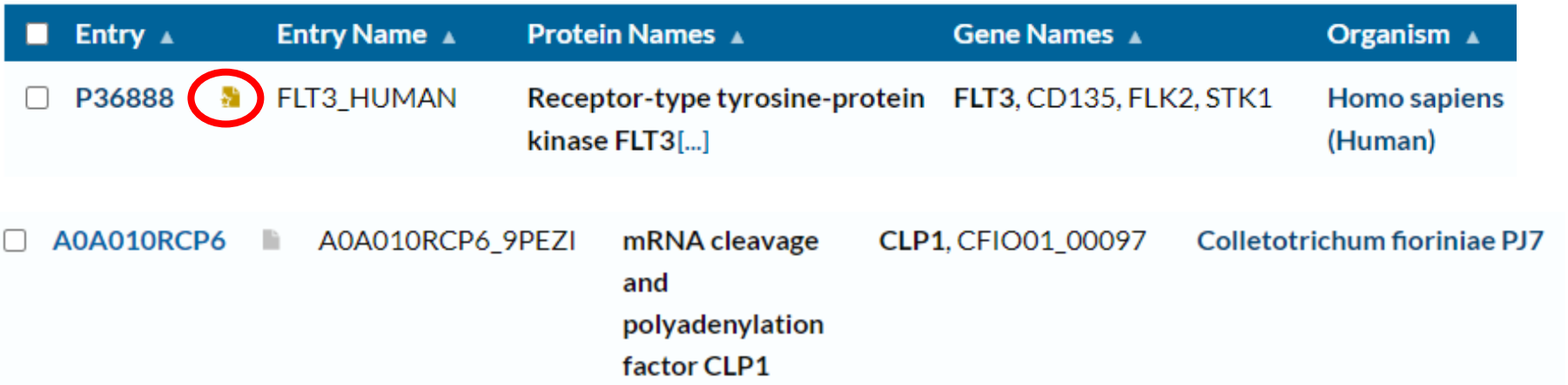


dAtabase of **P**olyX **E**volution

Mier *et al.* (2016) Bioinformatics

Exercise 2. Viewing homorepeats in an alignment with dAPE

•Find a random human protein in **UniProt**. Make sure that it is a reviewed entry.
Write the Entry Name.



Exercise 2. Viewing homorepeats in an alignment with dAPE

- Find a random human protein in **UniProt**. Make sure that it is a reviewed entry.
  Write the Entry Name.

- Copy the Entry ID (e.g. P10275).

- Go to the dAPE web page:
  http://cbdm-01.zdv.uni-mainz.de/~munoz/polyx/

- Use the Entry ID in option A

- Hit the "Report the evolution of its polyX" button

- Write down: (1) Which type of polyX has the human protein? (2) Which **additional** polyX not in the human protein were found in the orthologs?

Exercise 3. Find structures of short repeats

- Go to the PDB web page: https://www.rcsb.org/

- Go to Search > Advanced Search

- Type a short repeat in the Sequence Motif: as many repeats as possible; Use Mode PROSITE and RegExp (example: QQQQ / another example: [SP]SA[SP]SA[SP]SA)

- Click "count" to see if there are any cases

- Check the structure (3D View) to see if the repeat is in the structure (it could be disordered = absent)

- Write down the PDB name, RegExp and structure

Example 3NB9 QQQQ alpha-helix
Example 3FRC NNNN absent