

EMBL-EBI

UniProt Tools Hands-on

Exploring protein function using UniProt resources



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Introduction

Scope: The tutorial exercises provide examples of how to use UniProt resources and are intended to be completed as part of a workshop where UniProt resources and tools will be introduced beforehand. Despite using specific proteins for searches etc., the exercises are generic in terms of the workflows demonstrated.

Target audience: New to intermediate users of the UniProt resources. In terms of understanding the subject matter there are no prerequisites for these exercises apart from basic knowledge in biology.

Technical requirements: Access to an internet browser. The URL for UniProt is <http://www.uniprot.org>

Note: Where exercises ask for numbers of hits as part of the tasks, these are deliberately not given as they might change in time due to new proteins being annotated, evolving knowledge etc.

Help: Outside courses or workshops please use help@uniprot.org to contact us with any questions you might have.

Part I BLAST Service



To run a BLAST from the UniProt website, click on the BLAST link found in the upper left corner of the website.

[a] Enter either a protein or nucleotide sequence or a UniProt identifier into the form field. For this exercise use Q00987.

[b] Optionally, change the program parameters with the dropdown menus under the form.

[c] Click the  button.

Q1: How many results have a 3d structure attached to them? (hint: notice the filters on the left)

Q2: How would you download all 'reviewed' results? What download formats exist?

Part 2. Align

The Align tool allows you to align two or more protein sequences alongside each other, giving you the ability to highlight areas of similarity which may be associated with specific features or characteristics.



Click on the Align link found in the upper left corner of the website.

[a] Enter MDM2_HUMAN and MDM2_MOUSE.

[b] Click the  button.

Q3: How many identical positions exist between the two sequences?

(Hint: Check the results information at the bottom of the Alignment)



Try highlighting the Zinc finger regions of the sequences.

Q4: What colour is displayed?

Q5: How many zinc fingers are in the sequences?

Part III Retrieve/ ID Mapping



To run an ID Mapping, click on the Retrieve/ ID Mapping link in the upper left corner of the webpage.

[a] Enter identifiers, separated by a space or a new line, into the form field. For this example use the values: MDM2_HUMAN MDM2_MOUSE

[b] You would like to convert these from UniProtKB IDs to 'PDB' IDs.

Q6: How many PDB results are found and for which UniProt ID?



For batch retrieval of UniProt entries, click on the Retrieve/ ID Mapping link in the upper left corner of the webpage.

You find this batch of UniProtKB identifiers in a paper and you would like to find the latest UniProtKB entries for these.

Q9UQB8

P63244

P14672

P08833

P18065

Q7: How would you find results for all corresponding UniProtKB entries?

Q8: How would you download the results in the tab-delimited format?