**Exercise 2 – Domain Analysis using ‘Interpro’ online**

**Objectives:**

- to roughly understand what a ‘protein domain’ is

- to learn to discover and browse domain information using InterPro.

- to learn how to download the ‘seed’ alignment sequences for a given domain.

**Our test protein:**

same protein as in exercise 1, from the 1000-year old skeleton:

GFFGDRVGRKFIIWFSILGTAPFALWLPYADADTTAILVILIGFIISSAFASILVYSQELLPKKIGMISGVFYGFAFGMGGLASALLGKLIDLTDITFVYKVCSFLPLMGLIAYFLPNLRKVKMKE

**1) What is a ‘protein domain’:**

in short, a *protein domain* is a short stretch of multiple sequence alignment that somehow seems ‘important’ enough to be given its own name and annotation. Most proteins typically consist of one or more than one protein domain, but also of non-domain sections that align less well and may perhaps be less important or at least less diagnostic of function.

In practice, protein domains are discovered by experts staring at alignments all day. As part of describing and naming a new domain, these experts will usually provide a summary on where the domain can be found, and what function it might have. Within the actual proteins, domains often represent autonomously folding structural subunits. Many proteins are consisting of multiple different domains, which can be rearranged and exchanged over evolutionary timescales (‘domain shuffling’). As of today, most domains in existence have probably been discovered and described already.

**2) submit the test protein for a domain search**

after exploring an unknown protein against sequence databases (exercise 1), the next typical strategy is to search it for previously described domains. This may provide a broader idea of its function, and often also some three-dimensional structure information.

- open your browser (Chrome/Firefox), and take it to the EBI website:  
https://www.ebi.ac.uk/

- Click on “Services” (on the very top of the page), and then on to “InterPro” (you can use the searchbox to find it).

- Use copy-and-paste to enter our test protein into the box ‘Search by sequence’, and click ‘Search’.

- after a while, a graphical summary will show up, indicating domains and features that have been found for our test protein. First choose “Options” and then “Color by” (drop-down box just above graph) “Domain Relationship”.

Towards the bottom of the page, you can see the “other features” section. Hover your mouse over grey lines in this section, you will find at least four of them are likely transmembrane regions, so the protein may be sitting in a membrane. The colored lines above are the actual domains. They refer to the very same domain several times, but some of the classifications are more generic (‘superfamily’), whereas other ones are more specific (‘domain’).

- now, click on domain accession ‘IPR020846’ on the right of first line under “Domains”. This brings up the so-called ‘Interpro-abstract’, which provides an excellent summary of the general function of this protein family. As you will see, it is a transporter, which the cell uses to transport a variety of ‘small molecules’ across the membrane. Now we know a lot more already, but of course the annotation is too generic to let us know which is the preferred ‘small molecule’ that our protein wants to transport.

- now, notice that in the annotation, it said that these proteins typically have 12 trans-membrane regions, but we only found four … this is another indication that our test protein from the skeleton is indeed incomplete. Hence, let’s repeat the analysis with the closest relative it has in the sequence databases (this is the ‘best hit’ we found in exercise 1)

- Copy-and-paste the first best hit found in the file “input\_proteins\_1.fa” (the file generated from exercise 1). It should be the second entry in that file. Submit this protein to InterPro, as before. How many transmembrane sections do you find now? (take care to remove the gap characters [“-“] before submitting)

- Next, let’s find out a bit more about this domain. Proceed to the Interpro abstract again, like before (‘IPR020846’).

- Towards the top of the abstract, click on ‘Taxonomy’ … this will tell us in which organisms the domain is found. If you scroll down a bit, (to the circular illustration) you will find that it occurs virtually everywhere (Bacteria, Eukaryotes, Archaea, even in viruses).

- finally, click on the ‘Structures’ section. This will provide examples of known three-dimensional structures. Select one entry, and look at the protein structure. Now we know how our protein generally looks like … but again no useful information about the substrate (in this case, the proteins with the solved structure transport mainly sugars).

**2) download a ‘seed’ alignment from Pfam**

the Pfam database (= “Protein families”) is similar to InterPro, but is actually one of the original databases for protein domains (in contrast, InterPro is a ‘meta-resource’ bundling several original databases such as Pfam).

For many of its domains, Pfam maintains a ‘seed’ alignment, which is the original alignment that was made by the discoverer of the domain (or an updated version thereof). It is made up of non-redundant, representative sequences, and often has been quality-checked manually. For further work on alignments and trees, we’ll get one such seed alignment from Pfam now.

- open your browser (Chrome/Firefox\_, and take it to the Pfam website:  
http://pfam-legacy.xfam.org

- under “JUMP TO”, enter the Pfam name of our domain, it is called ‘MFS\_1’.

- click on MFS\_1 to bring up the annotation page. After having a look around, click on the Alignment tab located on the left. Now, under the section “Format an alignment”, choose the format “FASTA”, and set Gaps as “Gaps as ‘-‘ (dashes). Under Download/View choose ‘Download’, and then click on “Generate”.

- when offered the file for download, save it onto your laptop, and give it the name “input\_proteins\_2.fa”.

- please upload this to the “Documents/Bio334\_Data” data folder as before.

- If the Pfam website happens to be down, please feel free to proceed directly to Exercise 3 and use file “input\_proteins\_2.fa” we have provided through OLAT.