

# CFG - Practical session 2

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## Alignment questions

Which is/are the most likely mutational process/es explaining the pattern observed between the positions 1,417 and 1,438 (numbers according to the top bar of JalView).

- ☐ Inversion
- ☐ Duplication and loss
- ☐ Point mutation
- ☒ Insertion and deletion

Clear selection

Calculate and report the % of sites in the alignment that are gaps

26.13%

By looking at the results of the protein domain analyses, which molecular function would you assign to this set of sequences?

- ☐ Electron transport
- ☐ Catalytic activity
- ☒ Extracellular matrix
- ☐ Protein binding

Clear selection



Look at the 'Domain' and 'Repeat' rows at Interpro results. List all the differences that you find, if any, between the three queried sequences.

Annotate the **ungaped** positions that you want to talk about. *Max.: 500 characters*

Von Willebrand factor type C domain, is different in the Micropterus and not present in the other 2 species. The repeat regions are the same although being in different positions for example the Collagen Triple Helix repeat (32-75) for the Homo Sapiens but it is not present in that position for the Bos Mutus

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