

Today is the day you've been waiting for, using the hottest tool in town, AlphaFold2.

>protein_pulled_from_a_magicians_hat

TYSADVAVSLLKHAKEQGKCFNLQLQKLTIVCHGLSLAHFQRPLVVDDVFAWKFGPVVPSV
YFRFKSYGSSVIPEQCDVALDQESIVKDVVSKLGHLTGSQLVDLTHREGSPWHQVWDGTHQ
KVIPDHLIAHYTQIKQSGRTASL

Q1. Wait, do we actually need to use AlphaFold2 for this? Is there a homologue in the PDB that you could use for homology modeling?

Q2. What organism is it from?

Q3. What about known domains?

Q4. (Googling question) What are DUF domains and where do they come from?

Q5. Go ahead and predict the structure with AlphaFold2 via ColabFold. Save the structure.

Q7. See if you can use Consurf to colour the AF2 structure by conservation.

Q8. Are there any structurally similar proteins in the PDB?

Q9. Search Pubmed with this particular DUF domain name. What does this protein have in common with yesterday's protein?

Continue analysing your pet protein using the tools you've come across in the course