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🌐 Homology Modelling of Pacer RH domain in SWISS-MODEL

🦾 In 1 collection

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ABSTRACT

Using the Rubicon RH - Rab7 crystal structure as a template (6wcw)

PROTOCOL integer ID: 90724

Swiss-M

1   In Swiss Model,

> start new modelling project
> upload target sequence. Here, used the human Pacer (RUBCNL) sequence acquired from uniprot:

>sp|Q9H714|PACER_HUMAN Protein associated with UVRAG as autophagy enhancer OS=Homo sapiens OX=9606 GN=RUBCNL PE=1 SV=3
MVSQSTVRQDSPVEPWEGISDHSGIIDGSPRLLNTDHPPCQLDIRLMRHKAVWINPQDVQ
QQPQDLQSQVPAAGNSGTHFVTDAASPSGPSPSCLGDSLAETTLSEDTTDSVGSASPHGS
SEKSSSFSLSSTEVHMVRPGYSHRVSLPTSPGILATSPYPETDSAFFEPSHLTSAADEGA
VQVSRRTISSNSFSPEVFVLPVDVEKENAHFYVADMIISAMEKMKCNILSQQQTESWSKE
VSGLLGSDQPDSEMTFDTNIKQESGSSTSSYSGYEGCAVLQVSPVTETRTYHDVKEICKC
DVDEFVILELGDFNDITETCSCSCSSSKSVTYEPDFNSAELLAKELYRVFQKCWILSVVN
SQLAGSLSAAGSIVVNEECVRKDFESSMNVVQEIKFKSRIRGTEDWAPPRFQIIFNIHPP
LKRDLVVAAQNFFCAGCGTPVEPKFVKRLRYCEYLGKYFCDCCHSYAESCIPARILMMWD
FKKYYVSNFSKQLLDSIWHQPIFNLLSIGQSLYAKAKELDRVKEIQEQLFHIKKLLKTCR
FANSALKEFEQVPGHLTDELHLFSLEDLVRIKKGLLAPLLKDILKASLAHVAGCELCQGK
GFICEFCQNTTVIFPFQTATCRRCSACRACFHKQCFQSSECPRCARITARRKLLESVASA
AT

2   > Search for template

3   Search should yield a top hit corresponding to the Alphafold model of Pacer, and subsequent hits represent using the Rubicon RH domain as a template (6wcw).

Select the hit that aligns Pacer to the Rubicon structure (6wcw), and > build model. From here, the file can be downloaded as a PDB and used in downstream modelling steps.

Build Rab7 complex model

4   >Open Pymol
>open downloaded Pacer homology model

>fetch rubicon-rab7 dimer crystal structure by typing "fetch 6wcw" in the command line

5   >Align Rubicon crystal structure and Pacer homology model using the "align" command.

6   >Delete rubicon monomer, and expansion binding site between the pacer homology model and rab7. Focus on S72 of Rab7