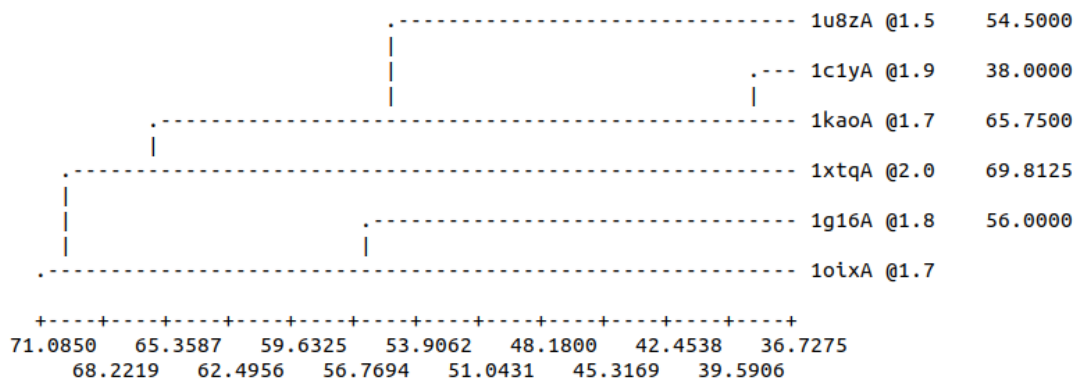


GTPase KRas isoform 1 [Mus musculus]: NP_001390169.1

- Best templates from build_profile.py:
 - a) 1c1yA (58.08% identical)
 - b) 1u8zA (55.35% identical)
 - c) 1kaoA (51.22% identical)
 - d) 1xtqA (37.04% identical)
 - e) 1oixA (36.65% identical)
 - f) 1g16A (35.71% identical)
- Weighted pair-group average clustering based on a distance matrix (from compare.py):



Based on identity and template quality, 1kaoA seems to be a good template for our model NP_001390169.1.

- Pairwise dynamic programming alignment between the model and template (from align2d.py)

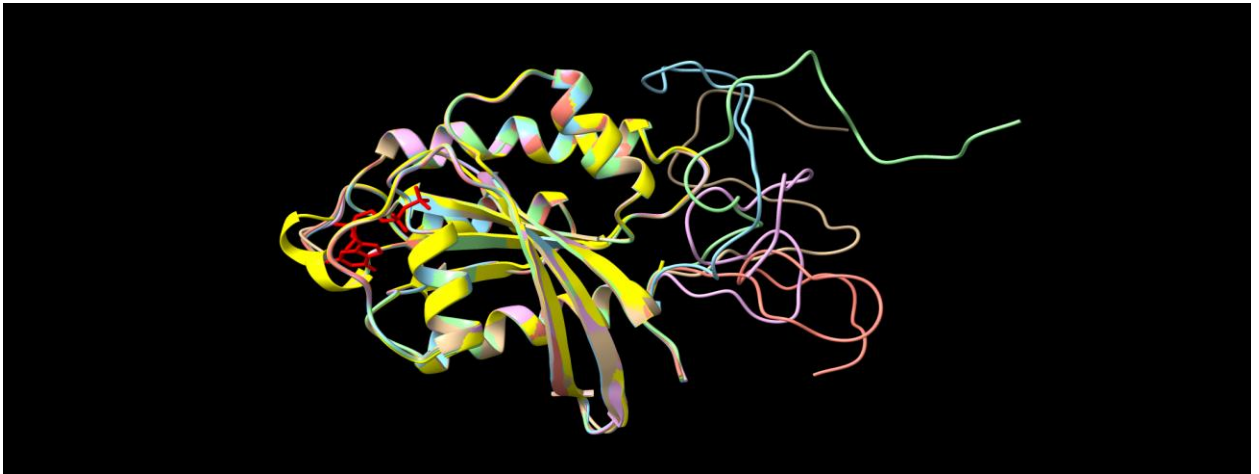
```

Residue-residue metric : $(LIB)/as1.sim.mat
Diagonal               : 100
Overhang               : 0
Maximal gap length    : 50
Local alignment        : F
MATRIX_OFFSET (local aln): 0.0000
FIX_OFFSETS           : 0.0 -1.0 -2.0 -3.0 -4.0
N_SUBOPT               : 0
SUBOPT_OFFSET          : 0.0000
Alignment block        : 1
Gap introduction penalty : -100.0000
Gap extension penalty  : 0.0000
Gap diagonal penalty   : 0.0000
Structure gap penalties : 3.500 3.500 3.500 0.200 4.000 6.500 2.000 0.000
Break-break bonus      : 10000.0000
Length of alignment    : 189
Score                  : 115289.7109
  
```

- Successfully produced pdb model files from model-single.py:

```
>> Summary of successfully produced models:
Filename                               molpdf      DOPE score      GA341 score
-----
NP001390169.B99990001.pdb             955.23035    -18822.27539    1.00000
NP001390169.B99990002.pdb             883.28284    -18804.12891    1.00000
NP001390169.B99990003.pdb             888.41479    -18650.82812    1.00000
NP001390169.B99990004.pdb             986.68323    -18793.35547    1.00000
NP001390169.B99990005.pdb             829.80103    -18838.54297    1.00000
```

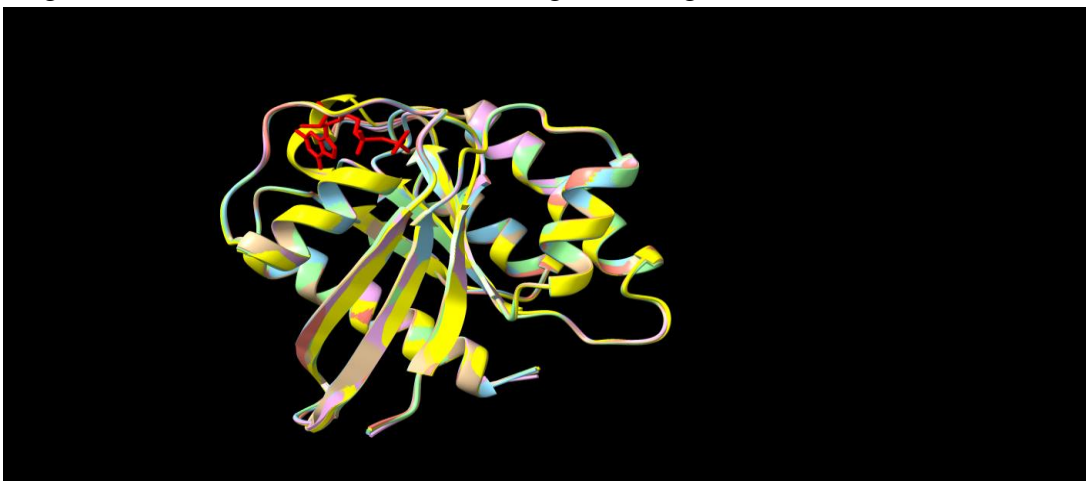
- Alignment of 1kao and our model from ChimeraX:



Template(1kao): yellow

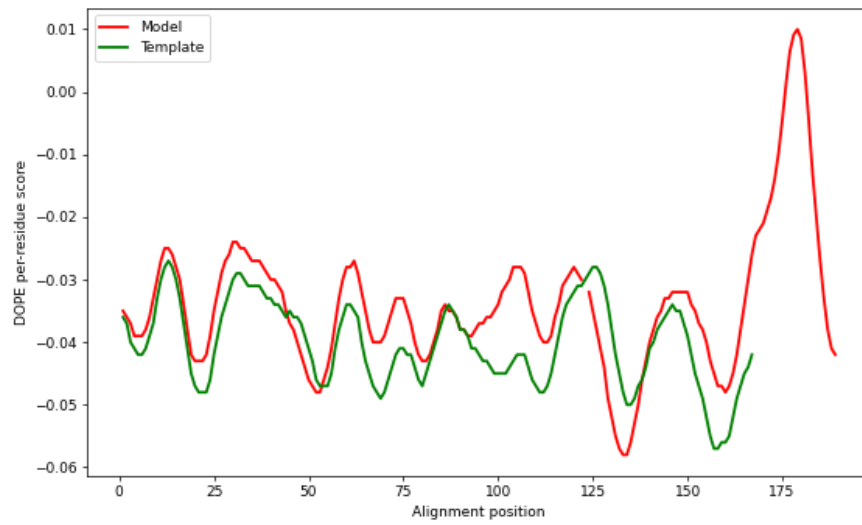
There is gap towards the C-terminus end of the template. As a result, the structure of that region of the model is unknown.

- Alignment of 1kao and model after deleting the unaligned C-terminus end of the model



Template(1kao): yellow

- DOPE Score for Model and Template



High DOPE pre-residue score for model after position ~175 because the structure is unknown given its absence in the template 1kaoA.