The following Modeller script were used

```python
from modeller import *         # Load standard Modeller classes
from modeller.automodel import * # Load the automodel class

log.verbose()                           # request verbose output
env = environ()                   # create a new MODELLER environment to build
                                 #this model in directories for input atom files
env.io.atom_files_directory = './:../atom_files' # PDB files position

a = automodel(env,
              alnfile  = 'filename.ali',  # alignment filename (PIR format)
              knowns   = ('1uul', '1e2y'), # codes of the templates in alignment filename
              sequence = '1tryp')          # code of the target

a.starting_model= 1             # index of the first model
a.ending_model  = 5            # index of the last model
                                 # (determines how many models to calculate)

a.make()                        # do the actual homology modeling
```