



## Analyse d'articles scientifiques récents

```
align2d.py
from modeller import *
log.verbose()

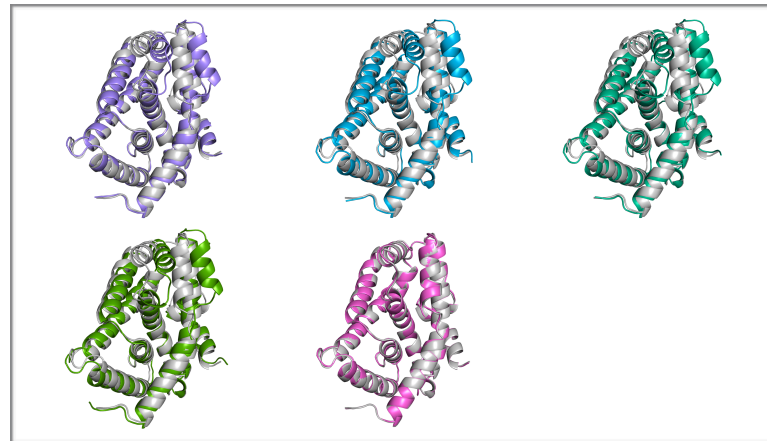
env = environ()
env.libs.topology.read('$LIB/top_heav.lib')

# Read target sequence:
aln = alignment(env)
aln.append(file='PDGFR_beta.ali', align_codes='PDGFR_beta')

# Extract sequence(s) to align from pdb files:
mdl = model(env, file='XXXX', model_segment=('FIRST:A', 'LAST:A'))
aln.append_model(mdl, align_codes='XXXX', atom_files='XXXX.pdb')
mdl = model(env, file='YYYY', model_segment=('FIRST:A', 'LAST:A'))
aln.append_model(mdl, align_codes='YYYY', atom_files='YYYY.pdb')

# Structure sensitive variable gap penalty sequence-sequence alignment:
aln.salign(rr_file='$LIB/blosum62.sim.mat', # Substitution matrix used
max_gap_length=30,
gap_function=True,
feature_weights=(1., 0., 0., 0., 0., 0.),
gap_penalties=(-10, -10),
similarity_flag=True) # Ensuring that the dynamic programming
# matrix is not scaled to a difference matrix

aln.write(file='align2d.ali', alignment_format='PIR')
```



## Un enseignement didactique fondé sur la pédagogie et l'interaction

15 séances de cours, 15 séances de TP 18 h 15-20 h 15

