### Tools for 3D molecule interactive visualization

**PART 1:**

Comparing the protein complexes PAR1-westernCagA and AMPK-PKI

1. Download and open 3IEC.
2. Hide everything.
3. Show the cartoon representation of the complex
4. Show the sequence: ‘Display->Sequence On’
5. Select chain A and E and rename them.
6. Show only PAR1 and westernCagA
7. Change colours (CagA: yellow, PAR1: gray)
8. Open 4WB5
9. Rename the chains A and I from 4WB5 and show their cartoon representations
10. Change colours (AMPK: gray, PKI: green)
11. Align 4WB5 to PAR1 and see the RMS (1.430)
12. Hide AMPK
13. Show the surface of PAR1: PAR1->S->surface
14. Save Molecule: PAR1 as ‘PAR1\_only’.
15. Open PAR1\_only.pdb
16. Align PAR1\_only to PAR1. See the RMS.
17. Change the color of PAR1\_only to gray
18. Hide PAR1
19. Show the surface of PAR1\_only
20. Change the background color: Display->Backgorund->white
21. Increase the quality of the graphics: Display->Quality->Maximum Quality
22. Save a PNG: File->Save Image As->PNG

**PART 2:**

Running a Pymol script.

Download the .pml script from: <https://git.embl.de/hsanchez/BTM2016_PDBs/tree/master>

Try to load it to Pymol.

Open a new session and go to File->Run and choose Script\_CagA.pml

! If it does not work, try again

! If it did not work again, copy paste the code to the ‘PyMOL>’ prompt.

Compare with the publication from Nesic et al. (2010) in the same link.

**PART 3:**

Lets check how close are the two molecules

1. Hide the surface from PAR1\_only. Show the cartoon representation.
2. Show the non-alpha carbons of the anchoring residues as published by Nesic D., et al., 2010 (Leu950, Arg952, Val956 and Leu959 in westernCagA; Glu136, Asp139, Asp193, Asp251).
   1. Try typing a command: ‘show sticks, Par1\_only and resi 136’
   2. Or: ‘show sticks, 3IEC and chain E and resi 950’
3. Calculate the distance between the Asp139 from PAR1 and Arg952 from westernCagA, use the closest hydrogens.
   1. Wizard->Measurment. Then click on the atoms (you should see that the distance is 3.1 A).
   2. Draw the hydrogen bonds: Select the anchoring residues from CagA. Go to westernCagA->A->Find->Polar contacts->to other atoms in object.
4. Explore more options in: <https://pymolwiki.org/index.php/Main_Page>
5. For example, Got to ‘Table of Contents->Settings (Documented)->Cartoon highlight color’, and Copy/Paste the setting.

**PART 4:**

A second strain of *Helicobacter pylori* exists and has some mutations in the amino acids that correspond to the anchoring region of Western CagA to Par1.

Lets generate a model of the East Asian CagA based on 3IEC:

1. Install Modeller: <https://salilab.org/modeller/download_installation.html>
2. Register or temporally use the license key: MODELIRANJE
   1. Issue on Windows: Copy/Paste the application mod9.17 from C:\Program Files\Modeller9.17\lib\x86\_64-w64 to your working directory. Then use the cmd as if it was a terminal.
3. Download the sequence file Western\_EastAsian.ali from git.
4. Modify align2d.py
5. Open a Teminal and go to your working directory.
6. Align the two sequences. Run: mod9.17 align2d.py
7. Check the alignments: CagAs.ali and CagAs.pap
8. Modify the model-single.py script.
9. Generate the models. Run: mod9.17 model-single.py
10. Check the file model-single.log
11. Find the model with the lowest Discrete optimized protein energy (DOPE) or the one with the highest GA341 score. These values are at the end of the log file.
12. Load the corresponding model to your Pymol session
13. Align it to CagA
14. See the RMS.
15. Align it now to PKI and compare the RMS.