Targets:

1. Easy: Symmetric structure (T0893, dimer, PDB: 5idj)
2. More complex: (T0860, trimer, PDB: 5fjl)

Preprocess targets:

1. Split PDB files to monomers (or use Chimera)

Tools:

1. Understand input parameters to RosettaDock, ZDOCK, ClusPRO (allows choose the chain)

<http://rosie.rosettacommons.org>

[zdock.umassmed.edu](http://zdock.umassmed.edu/)

<https://cluspro.bu.edu/home.php>

Evaluation:

1. RMSD, IRMSD, pairwise-contacts (custom code)
2. PROFIT (<http://www.bioinf.org.uk/profit/>)

Visualization of results (Chimera)

Timeline:

* Discussion of plan (April 10th) DONE!
* Presentation of plan (April 15th)
* Discussion of results (April 22nd)

Task assignment:

1. Select the targets (Farhan and Olha) DONE!
2. Preprocessing of targets (Farhan)
3. Running tools (RosettaDock: Olha; ZDOCK: Carlos, ClusPRO: Zaman and Sriganesh)
4. Evaluation (everybody)
5. Visualization (everybody)
6. Writing report (everybody)

Distribution of the project: GitHub repository