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| **Date** | **Task** | **Remark** |
|  June 7th  | Sirt3/AADAPr ( open loop simulation) job submittedInstallation of Schrodinger software done. | This job will be completed by Friday evening.I will be doing the MM/PBSA scoring on June 11th (Saturday ) |
|  June 9th -10th  | Modelling the Sirt3/AADPr product complex with an open loop conformation in Prime. This task includes side chain prediction, model refinement using Prime and model validation. The protocol employed by Ping would be followed for consistency purpose. | Once the modelling job is done the preliminary data form the modelling will be send out to Dr. Raj for his evaluation and approval before subjecting the model for MD simulation |
| June 12th**(WEEKEND)** | Compute the MM/PBSA energies for Sirt3/AADPR (closed loop conformation) | Send out the report to Dr.Raj for his analysis **TASK COMPLETE** |
| June 13th | Modelling Sirt3/AADPr from 4FVT.No side chain modelling, only prime energy refinement | **TASK COMPLETE**  |
| June 14th  | Modelling Sirt3/AADPr from 4FVT and grating the 4BVG loop.Includes side chain modelling, prime energy refinement of the modelled sidechain followed by entire protein minimization | The reaming time will be used for setting up the system for short **equilibration MD simulation**.1. Sitr3/AADPr (4BVH with 3GLS loop)
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|  June 15th  | Setting up short Equilibration MD simulation for a)Sirt3/AADPR/peptide (4FVT )b)Sirt3/AADPr/peptide (4FVT with 4BVGloop) | Analyzing the equilibration results using MM/PBSA scripts. |
| June 16th | Send out the MM/GBSA score form the short equilibration MD to Dr.Raj to decide on the pair for MD simulationThe rest of the day will be used for carrying out the Miscellaneous task listed at the end | Launching a 15 ns MD simulation of the systems decided by Dr.Raj |
| June 16th | Miscellaneous task items 1,2 ( needs to write a Perl script ) | MD simulation will be running  |
| June 17th | Miscellaneous task items3,8 and 10Mostly methodology write-up work  | MD simulation will be running |
| June 19th**(WEEKEND)** | Compute MM-PBSA and MM/GBSA binding energies from MD trajectories  | MD simulations will be completed on Saturday. |
| June 20th | Miscellaneous task items4 -9  |  |
| June 21st | Miscellaneous task items4-9Continued .. |  |
| June 22nd | Reserve day to complete and pending task |  |
| June 23-24 rd | Work on side chain validation dataPresenting the dataMiscellaneous task 12 |  |

**The following are the tasks for the paper based on the priority and the time of availability of the data.**

1. Creating probability density distribution plots based on the energies of each frame in the MD simulation. (Perl script needs to be written). Sirt3/INT/NAM complex data available. Sirt3/AADPr product complex data will be computed upon completion of the MD simulation.
2. Ligand interaction diagrams for Sirt3/INT/NAM complex (data available) the other system (Sirt3/AADPr closed and open product complex data not available).
3. Incorporating the references for the computational section and a draft of the methodology has to be written (Will be adapted from the previous PLOS one paper).
4. Fig ------Simulated B factor values for Sirt3/OADPr product complex modeled based on native and closed conformation (4BVH). Note Sirt3/INT/NAM Bfac data already completed.
5. Fig ------ Per-residue RMSD values for the cofactor binding loop region calculated with respect to MD averaged structure of Sirt3/OADPr complex based on open/closed loop conformation. Note Sirt3/INT/NAM rmsd plot already completed.
6. Revise the Table …..MM/GBSA and MM/PBSA conformational energies and binding affinity calculation based on the new simulation results (Sirt3/OADPr closed loop). Also revise the earlier MM/GBSA and MM/PBSA table prepared for Sirt3/INT/NAM as suggested by Dr.Raj because NAM data shows insufficient sampling leading to convergence issue.
7. Time series plot of MM/GBSA and MM/PBSA energies for Sirt3/OAADPr closed/open loop conformation. Also revise the old plot (Sirt3/INT/NAM) with 2 or 3 traces as suggested by Dr.Raj (I guess we can show only 2 traces and not 3 traces).
8. Receptor with INT
9. Receptor with NAM
10. NOT SURE if INT/NAM with receptor can be calculated anyways will give it a try).
11. Also consider showing a plot form t=0
12. Method for Ligand/NAM placement needs to identified and written for the completeness of supplementary section
13. Identify B factors for any Sir2 simulations available from PL’s data if any to make the plot analogous to that for SIRT3.
14. MD simulation method protocol and particular treatment of non-standard residues has to be written. ( This will be linked to the MD methodology section)
15. Starting structures for simulations (for SI)
16. Identifying all data on side chain validation carried out by Ping and present the data in a format so as to distinguish sampling/energy errors.