The technical specifications for Proteomics:-

Samples: Co-IP samples/Whole cell lysates

Number of samples: 14-16

- 1. The vendor must have in-house Mass Spec facility.
- 2. The Vendor must share proofs for In-house Mass spec facility with instrument installation reports.
- 3. The vendor should have demonstrated scientific capability for the successful completion of undertaken proteomics project, as documented by the vendor/Service provider having research publications in peer reviewed journals. Appropriate web link to support this claim should accompany the tender proposal.
- 4. Label Free analysis of CO-IP samples for Interactome and PTM identification including protease digestion and proteome analysis on nano-UHPLC MS/MS chromatography on Orbitrap Exploris.
- 5. MS Data resolution: Minimum MS1 resolution of 60000 and MS2 resolution of 15000.
- 6. Machine sensitivity data with complex standards must be provided along with results.
- 7. Data analysis: Raw data must be searched with Sequest and Amanda search engines
- 8. The False discovery rate for identifying the proteins should be maximum 1%.
- 9. Identification of Post translational modifications (Phosphorylation, Acetylation, Ubiquitination etc) in the interactome proteins
- 10. Complete data analysis support along with raw files submission to database repository.
- 11. RESULT DELIVERY TIME: Within 3-4 weeks after QC qualified sample submission.
- 12. Compiled material and methods for publication support as per international standards according to satisfaction of the PI.