

Interactome Analysis of Lin28a by Proteomics approach

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Protein-protein interactions are important in cell biology, many protein complexes participating in numerous biological processes such as transcription, translation and cell cycle. MS-based proteomics techniques are applied for characterising the interactome, such as affinity purification coupled to mass spectrometry which is used to selectively enrich and identify interacting partners of a bait protein. Lin28a is an RNA binding protein which plays a crucial role in embryonic stem cell differentiation, developmental timing, cellular proliferation and metabolism. To identify Lin28a-interacting proteins in Epiblast-like stem cells (EpiLCs) was performed immunoprecipitation using an antibody specific to exogenous Lin28a. Thus, the protein complex was analyzed by liquid chromatography-coupled mass spectrometry. In particular, the interactome of the wild type form and of two mutants, $\Delta 18$ and $\Delta 28$ respectively, was characterized. The results of proteomic analysis showed that 309 proteins were co-purified with Lin28a and 217 of these 309 proteins were statistically significant both in wild type and in mutants when compared to the mock sample. Therefore, the identification of the exogenous Lin28a protein interactome in EpiLCs, provided a molecular basis of the involvement of Lin28a in a wide range of molecular processes, from chromatin organization to translation, differentiation, and development.