English Abstract

The incoming paradigm of the network (or systems) biology calls for a new high throughput tool for a wide scale study of protein-protein interactions. Mass spectrometry-based proteomics have experienced a great progress in recent years and have become an indispensable technology of elementary as well as clinical research.

Glutamate carboxypeptidase II (GCPII; EC 3.5.17.21) is a transmembrane protein with two known enzymatic activities. Its expression is highly upregulated in some solid tumors and also in tumor-associated neovasculature in general. Nevertheless, none of the two enzymatic activities were shown to be physiologically relevant to these cells. Some facts point at a possible receptor function of GCPII, however, no specific binding partner has been found yet.

In the search for potential binding partners and/or ligands of GCPII, a series of methods have been employed, including pull-down experiment, immunoprecipitation and mass spectrometry. Sample preparation and mass spectrometry data processing methodology was specifically developed in order to identify potential binding partners. As one of the outcome of that methodology, the interaction of β-subunit of F1 ATP synthase was selected for further detailed analysis as a putative ligand of GCPII.