Researchers have used lab technology called mass spectrometry to study the proteins expressed by human cancer cells. The advance, which is described in a new Molecular Oncology article, allows for the quantitation of thousands of tumour proteins over the course of several hours.

The strategy was used to identify several proteins that were over-expressed in a rare form of bladder cancer that did not respond to chemotherapy.

The findings reveal that proteomics—the large scale study of all proteins in a given system—has the potential to quickly provide robust personalised therapeutic options for cancer patients in which standard clinical options have been exhausted.