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.

**Additional Information**


**About Journal**

*Molecular Oncology* is an Open Access international journal that highlights new discoveries, approaches, as well as technical developments, in basic, clinical and discovery-driven translational cancer research.

The emphasis is on work that significantly advances our understanding of disease processes leading to human tumour development and/or establishes novel concepts of clear clinical significance in diagnosis, prognosis and prevention strategies for cancer patients.

**Language:**

English