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.


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.