Protein Analysis May Reveal New Cancer Treatment Targets

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**Contacts:**
Penny Smith Tel: +44 (0)1243 770448 sciencenewsroom@wiley.com

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**

**Link to Study:** https://febs.onlinelibrary.wiley.com/doi/10.1002/1878-0261.12326

**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:**
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