

## **DBT-InSTEM scientists pave way for developing new biomarkers for diseases**

New Delhi, Aug 27: The ability to test proteomic changes in the blood dynamically has critical implications to the discovery and tracking of biomarkers for a variety of metabolic, myeloid and infectious diseases. The biomarkers can range from detection of viral/bacterial peptides to validating whether a specific biochemical pathway has been engaged by a given drug as a part of treatment efficacy monitoring. However, to date it has been cumbersome to identify newly synthesized proteins from whole blood derived from usual blood collection methods.



In a collaborative project with scientists from New York University, faculty from the Centre for Neuro developmental Synaptopathies, along with faculty from Mass Spectrometry Facility at the Bangalore Life Science Cluster, have developed a method to incubate, label and then detect newly synthesized proteins in freshly collected blood via mass spectrometry.

Testing the proof of concept in mice and rat blood, the group was able to identify proteins from erythrocytes, lymphocytes and platelets in samples. The proteomic work done in this project has adopted cutting edge peptide identification algorithms to enhance peptide detection.

This research work provides proof of principle evidence for a what may be rapidly deployable method to label newly synthesized proteins in the freshly collected blood samples to detect dynamic protein shifts and develop novel biomarkers for a variety of disease conditions. The work has been published recently in American Chemical Society's Journal of

Proteome Research (Aug 2020) titled ‘Optimization of protocols for detection of de novo protein synthesis in whole blood samples via azide-alkyne cycloaddition.’

**Reference:**

Bowling H.L., Kasper A., Patole C., Venkatasubramani J.P., Leventer S. P., Carmody E., Sharp K., Berry-Kravis E., Kirshenbaum K., Klann E., and Bhattacharya A. (2020) Optimization of protocols for detection of de novo protein synthesis in whole blood samples via azide-alkyne cycloaddition. *Journal of Proteome Research* (Published on Aug 04, 2020)

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