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**Citation (summary) on the outstanding research work on which the award is claimed  
(250 words)**

Dr. Debarka Sengupta's interdisciplinary research at the crossroads of cancer biology and artificial intelligence has unveiled fresh opportunities for harnessing transcriptomics and AI in the realm of blood-based cancer detection and therapeutic decision-making. Recent endeavors by his team have showcased the potential of employing single-cell transcriptomics and AI to detect and characterize individual circulating tumor cells present in patients' blood samples. Notably, this method enabled blood-based identification of single circulating triple-negative breast cancer cells, which lack specific surface markers. Further, Dr. Sengupta's group recently reported a groundbreaking advancement in AI-driven drug response inference using cancer transcriptomes. Their novel framework, named Precily, utilizes cancer gene expression data and drug descriptors to construct a specialized deep learning architecture for forecasting drug responses. This framework intelligently projects raw gene expressions into a meta-space that encompasses pathways implicated in cancer, effectively mitigating the inherent noise within transcriptomic data. Precily exhibited remarkable performance when evaluated on transcriptomic datasets from prostate cancer cell lines and mouse xenografts subjected to varying treatment conditions. Additionally, the team showcased the clinical utility of their approach by applying it to patient drug response data derived from publicly accessible human cancer datasets. These advancements stand as a remarkable contribution by Dr. Sengupta's team, broadening the scope of next-generation cancer care by leveraging AI-detectable molecular patterns, in contrast to traditional approaches based solely on singled-out biomarkers.

  
(Anurag Agrawal)