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Karkinos Healthcare & IIT Bombay to fight cancer using next generation omics technologies

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Advocating for collaboration between academia and health industry to fight against cancer

Karkinos Healthcare and the Indian Institute of Technology (IIT) Bombay have joined hands to share the expertise of 100+ doctors from Karkinos Healthcare and academia to bring in synergy for cancer care.

Dr Prashant Kumar, Chief Scientific Officer, Karkinos Healthcare, and Prof. Sanjeeva Srivastava, IIT Bombay (currently a Visiting Professor at the University of California San Francisco) have collaborated to bring the academia and industry experiences together to fight against cancer by utilising next generation omics technologies.

The advancements in genomics and proteomics in recent years has given a remarkable boost to our understanding about the disease pathology. Proteogenomics are adding new capabilities of providing novel insights at an unprecedented scale, which was not possible earlier.

Teams from Karkinos and IIT Bombay have initiated a project on brain tumours, which are still one of the most deadly cancers. The team is planning to expand this work to other commonly occurring cancers in India. Genes or proteins alone only represent limited information. Therefore, recent efforts have been made by the researchers to combine mass spectrometry-based proteomics data with genomics to advance Proteogenomics investigations in cancers.

Commenting on this collaboration, Dr Sanjeeva Srivastava said, “At IIT Bombay, we have setup large infrastructure of proteomics based technologies using mass spectrometry and protein microarrays to identify protein based biomarkers.”

On the other hand, the team at Karkinos has set up state-of-the-art genomics technologies, and data analysis to accelerate biological and biomedical research. Dr Prashant Kumar said, “In a short time we have enabled the latest next generation sequencing platforms and multi-omics data analysis workflow to sequence alterations in cancer genomes. We have streamlined the whole genome sequencing process which will offer rapid, accurate variant analysis.”