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Akrivia Biosciences decodes breast cancer genomic heterogeneity

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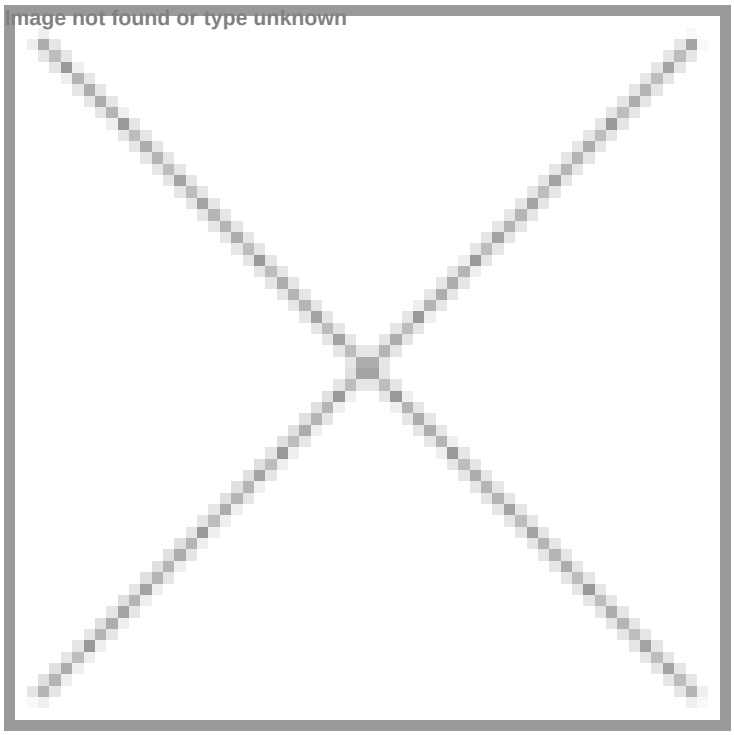
To build a new generation of precision oncology tools that understand cancer not as isolated lesions



Akrivia Biosciences, a cancer genomics startup based in London and Mumbai, has announced a foundational scientific breakthrough that uncovers hidden organisation of cancer genomes, successfully decoding breast cancer genomic heterogeneity—a major bottleneck that has historically hindered the comprehensive understanding of tumour biology in patients.

The research reveals that tumour mutations are not chaotic, isolated events, but are highly organised into distinct functional programmes that dictate tumour behaviour, survival, and therapeutic resistance.

For years, the sheer complexity and chaotic nature of genomic alterations in cancer have forced precision oncology into a rigid, binary approach of treating isolated mutations.

Leveraging this groundbreaking new discovery, Akrivia has developed T-OMICS™, an extraordinary multi-omics-based framework that solves the ER+/HER2- disease puzzle to a major extent. Akrivia is currently preparing to deploy T-OMICS™ as a targeted decision-support tool specifically designed to address the unmet needs of the advanced breast cancer patient population.

Akrivia is initially deploying the T-OMICS™ platform to tackle the specific unmet need in metastatic ER+/HER2– breast cancer, with the clear potential to apply the foundational organisational principles across multiple other malignancies in the future.