

MedGenome to discuss novel algorithm for neo-epitope prediction at the AACR Annual Meeting 2017 in Washington D.C.

Poster titled "A novel algorithm to identify TCR-binding somatic mutations from human cancers" will be presented at AACR 2017



FOSTER CITY, CA, UNITED STATES,
March 13, 2017 /EINPresswire.com/ --

MedGenome will be presenting a poster titled "A novel algorithm to identify TCR-binding somatic mutations from human cancers" at the AACR Annual Meeting 2017, April 1-5, 2017, Washington DC, USA.

Preclinical and clinical studies have demonstrated superior response when treated with a combination of cancer-derived neoantigen vaccines with checkpoint control inhibitors. This increased response is predicted to be due to enhanced priming and expansion of tumor-specific naïve and memory T-cells. Current approaches to identify T-cell neoepitopes lack the ability to predict whether the HLA-bound peptide will engage T-cells by binding to the T-cell receptors (TCRs). A team of bioinformatics scientists from MedGenome has developed a novel approach to predict the binding of HLA-peptide complexes to TCRs by analyzing the physicochemical properties of amino acids and their positional biases in the HLA-peptide-TCR complex. Using machine learning approaches the team has built a classification model to predict whether a given 9-mer peptide can engage TCR or not. The inclusion of the TCR binding step to the standard neoepitope prediction has increased the accuracy of prediction by reducing false positives and false negatives significantly.

About MedGenome

MedGenome (<http://www.medgenome.com>) is a genomics-driven research and diagnostics company with a mission to improve global health by decoding the genetic information contained in an individual's genome. Its unique access to genomics data with clinical and phenotypic data provides insights into complex diseases at the genetic and molecular level to facilitate research in personalized health care. MedGenome is a market leader for genomic diagnostics in South Asia and a leading provider of genomics research services globally. It is also a founding member of GenomeAsia 100K initiative to sequence 100,000 genomes in South, North and East Asia.

Our NGS lab in Foster City, California is ISO 15189 compliant, CLIA certified and CAP accredited.

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