Dr. Preethi Gunaratne is a Moores Professor and Director, Sequencing Core at the University of Houston. As the Director, cDNA sequencing team at the Baylor Human Genome Sequencing Center, she directly contribute do the sequencing & annotation of Human Chromosomes 3, 12 and X and led her team to make the largest single contribution to the Mammalian Gene Collection (MGC) in Phase I. She led the microRNA and LncRNA analysis working groups for multiple cancers in NCI-The Cancer Genome Atlas (TCGA) project. At UH she established a platform for extracting new druggable targets and biomarkers from the non-coding RNA driven transcriptomes. More recently, her group has extended this platform to rescue reads discarded through the discordant paired end read filter to discover immunogenic neoantigens from chimeric RNAs. Sequencing 500PDX models representing 28 cancer types, her group has discovered18,000 fusions. Integrating multiple bioinformatics pipelines including Star Fusion, Ariba for fusion discovery with MHC-Nuggets and Mixed MHCpred for HLA Class I and Class II matching and single cell RNA-seq with TCR/BCR-seq she has established a robust platform for designing personalized peptide and mRNA vaccines for cancer treatment and prediction.

KEYNOTE SESSSION 3, Friday June 14th, Parthenon A/B