令和6年度横浜市立大学医学会講演会 共同利用・共同研究拠点/BIOINFORMATICS LAB主催

## HOW CAN WE USE GENOMICS TO PREVENT COMPLEX DISORDERS?

VARIANTS



**CIRCULATING DNA** 

PREVENTION

**JUHA KERE, MD, PHD** PROFESSOR OF MOLECULAR GENETICS, KAROLINSKA INSTITUTET STOCKHOLM, SWEDEN

## № 11月12日(火) 14:00-15:00 FUKUURA看護棟M201 ON-SITE・ZOOM

NON-CODING RNAS

Starting from 2007, we have witnessed the burst of genome-wide association studies (GWAS); the rapid development of DNA sequencing technologies; and the progress in transcriptome and epigenetic studies. This knowledge might benefit early diagnostics and disease prevention. We have learned of the importance of enhancers and non-coding RNAs; population differences in genetic architecture; and the role of extremely rare variants in pinpointing new targets for drug development. But despite over 6,000 published GWAS results, the sensitivity and specificity of polygenic risk scores (PRS) remain too low to predict most complex disorders. Monitoring pathogenic processes by looking for signs of tissue damage based on free circulating DNA (cell-free DNA, cfDNA) offers sensitive, specific, and low-cost analyses that might help to detect early signs of diseases.

## ※当日のAM9:30まで受付 REGISTER・申し込み ※Zoomの招待メールは当日のAM10:00以降にお送りします。 ロビュミロ

● 問い合わせ先 ● 横浜市立大学 研究推進部 研究・産学連携推進課 研究企画担当 石塚・竹内 kyoudou@yokohama-cu.ac.jp



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