

Methylation marker to estimate the risk for afflictedness with an addiction (P-1233)

Key facts

- Estimates the risk of a subject for afflictedness with an addiction
- Based on methylation analysis / bisulfite sequencing

Abstract

Addiction to nicotine, alcohol or other substances is the cause of a multitude of severe diseases and is therefore considered to be a major threat to individuals and public health systems. Hence, methods for estimating the risk for afflictedness with an addiction in an individual could be very valuable in terms of enrolling people in preventive programs or providing information for insurance purposes.

Development Stage

In silico analysis has been conducted.

The Technology

Methylation data from umbilical cord blood has been used for determining regions in the genome which are affected by the smoking behavior of the child's mother. Methylation patterns were found pointing towards an increased risk of afflictedness with an addiction in new-borns. In addition, genetic variants play a role in reinforcing this risk.

Applications and Commercial Opportunity

DKFZ is looking for a commercial partner to further validate and develop a commercial test kit based on bisulfite sequencing.

Inventors

The investigators are: Roland Eils, Tobias Bauer, Matthias Bieg, Carl Herrmann, Saskia Trump, Irina Lehmann, Mario Bauer, Loreen Thürmann from the German Cancer Research Center, the University of Heidelberg and the Helmholtz Centre for Environmental Research Leipzig

Intellectual Property

A European patent application EP 1519809.2 "Methylation and/or SNP genotype of a commuter enhancer as a risk marker" has been filed with priority date 4.12.2015

Further Information

No other public information is currently available, but further information (speaking with the inventor) is available under a signed Confidential Disclosure Agreement (CDA).

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