

Ústav molekulární genetiky AV ČR, v.v.i.  
a  
Centrum aplikované genomiky

si Vás dovolují pozvat na přednášku

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## **Genomic landscape of autism spectrum disorders**

Recent studies have suggested that copy number variations (CNVs) may predispose to autism. To address the relative contributions of rare and common variations in autism spectrum disorders (ASD), we performed CNV and SNP-based analyses in 943 autism families (4,454 individuals) and 1,612 control subjects

**Přednáška se koná 18. července 2008 ve 14.00 hod  
v Ústavu molekulární genetiky AV ČR  
(posluchárna v přízemí budovy F, Videňská 1083, Praha 4 –  
Krč)**

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