

## **Prefrontal cortex proteomics analysis in Schizophrenia**

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Schizophrenia genomics has achieved unprecedented advances. A decade ago, there was perhaps one solid finding for schizophrenia, and there are now 130+ loci that meet consensus criteria for significance and replication. Considerably larger genomic studies are in progress, and will increase knowledge. These results provide multiple entrées into the fundamental biology of schizophrenia, and are consistent with molecules that interact in a “network medicine” paradigm. Recent schizophrenia findings implicate proteins involved in developmental processes and molecular machines (e.g., Ca<sub>v</sub>1 channels and synaptic subsets). An integrated approach to deciphering protein networks in schizophrenia is timely and feasible.

Aim: Use existing postmortem prefrontal cortical samples (BA9) from schizophrenia cases and controls (matched for age, sex, & postmortem interval, from NBB) and extract proteins. Request samples to enable analysis of cases vs. controls passing rigorous quality control. Most samples will have RNAseq & CHIPseq via CommonMind. (b) Perform global proteomics. Identify and quantify proteins in schizophrenia cases and controls using mass spectrometry at unprecedented scale. Identify differentially expressed proteins (accounting for subject covariates and multiple comparisons). Validate top findings.

No results are available at the moment because we are still expecting additional NBB samples to be able to execute the study.