

alpha-Synuclein OMICS to identify Drug-targets (SynOD)

Aggregation of the protein **alpha-synuclein** in neurons and oligodendrocytes in the brain causes a group of neurodegenerative diseases collectively referred to as **synucleinopathies**. These include among others **Parkinson's disease (PD)**, dementia with **Lewy bodies (DLB)**, and **Multiple System Atrophy (MSA)**. All randomized, controlled clinical trials with investigational drugs failed to show significant slowing of disease progression in synucleinopathies compared to placebo, so far. It is therefore essential to increase the knowledge about the molecular causes and consequences of alpha-synuclein pathology to identify **novel therapeutic targets** and to develop **more powerful therapeutic interventions**. In preparatory projects, the group of applicants has already generated **large datasets in patients-derived materials** (genome-wide association study, epigenome-wide DNA methylation study, miRNA sequencing in MSA and PD) and **corresponding cell models** (DNA methylome, miRnome, transcriptome, proteome, siRNA modifier screen, functional compound screens). In this proposed SynOD project, the consortium will assemble the unique large OMICS datasets described above and explore them by powerful computational methods to generate an integrated map of molecular pathways involved in synucleinopathies, with a particular focus to identify drug-targets therein.

Project Data:

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