



Identifying causal genes to be used as drug targets

A top 10 global pharmaceutical company wanted to build its pipeline for identification of causal genes within genomewide association study (GWAS) loci using Parkinson's disease as a test case and extending to other indications later.

Linking GWAS hits and causal genes in complex disease is typically a multi-step process that starts with the identification of the true causal variant, followed by linking to the target gene.

Power of extensive data sources and advanced analytics

The Clarivate[™] Discovery and
Translational Sciences consulting team
proposed a complementary systems
biology approach, leveraging functional
gene annotations to directly infer the
most likely causal gene in the associated
locus. The team used a proprietary
Clarivate analytic workflow that was
developed to discover drug targets.
Data sources for the workflow include
Cortellis Drug Discovery Intelligence[™],
which has biomarker data for ~3K
diseases; MetaBase[™], which has ~1.5M
molecular interactions; and the Clarivate
Computational Biology Methods for

Drug Discovery (CBBD) program, which focuses on the implementation of advanced state-of-the-art approaches for network and pathway analysis of OMICs data. Data integration was accomplished using machine learning analysis to build a predictive model and prioritize the targets.

Based on the output, the company benefitted from the following:



an integrated workflow for annotation and prioritization of candidate genes from GWAS loci,



the ability to highlight the most likely causal gene in each GWAS locus and



promising causal genes for Parkinson's disease risk, with detailed supportive external evidence.

For more information on how the Discovery and Translational Sciences consulting team can help accelerate your research with advanced analytics and actionable insights, visit our website at:

clarivate.com/products/clarivate-consulting-services/

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