

Computational prediction of the molecular mechanisms involved in migration

Jiao Wang

Abstract

Citation: Jiao Wang Computational prediction of the molecular mechanisms involved in migration. **protocols.io**
dx.doi.org/10.17504/protocols.io.iapcadn

Published: 05 Jun 2017

Protocol

Step 1.

Obtain the protein-protein interaction network (PPIN) for *Mus musculus* from the STRING 10.0 database containing all known and predicted protein-protein interactions.

Step 2.

Superimpose our previous mass spectrometry results of the TMEM30A complex in mouse tissue and the known migration-related genes from the literature onto the PPIN from the STRING database.

Step 3.

Extract the sub-network of these selected proteins from the whole PPIN in STRING.

Step 4.

Use DAVID to conduct the function and pathway enrichment analysis.

Step 5.

Visualize the signaling network with Cytoscape.