Table S1. Twelve of the most and least successfully predicted target biological process annotations

Successful	**Unsuccessful**
mRNA metabolic process	Secondary metabolic process
Transcription from RNA polymerase III promoter	Response to inorganic substance
rRNA metabolic process	Regulation of translation
Regulation of progression through cell cycle	Fermentation
Hydrogen transport	Second-messenger-mediated signaling
Nucleocytoplasmic transport	Cellular respiration
DNA replication	Oxygen and reactive oxygen species metabolic process
Cytoskeleton organization and biogenesis	Lipid metabolic process
Proteolysis	Vitamin metabolic process
Ribosome biogenesis and assembly	Cell wall organization and biogenesis
Small GTPase mediated signal transduction	Protein processing
Vesicle-mediated transport	Lipid transport

The biological process annotations (BP) of the most and least likely target proteins to be annotated correctly with zorch integrated by Generalized Functional Linkages (GFL) are shown. Predictions were made with uniform priors and evaluated at 206 general BP. In general, those proteins involved in stable complexes were among the most accurately predicted.