Electronic Supplementary Material_7; Data file S3

Sequential lipidomic, metabolomic and proteomic analyses of serum, liver and heart tissue specimens from peroxisomal biogenesis factor 11α knockout mice

Vannuruswamy Garikapati[1,2], Claudia Colasante[2], Eveline Baumgart-Vogt[2*], Bernhard Spengler[1*]

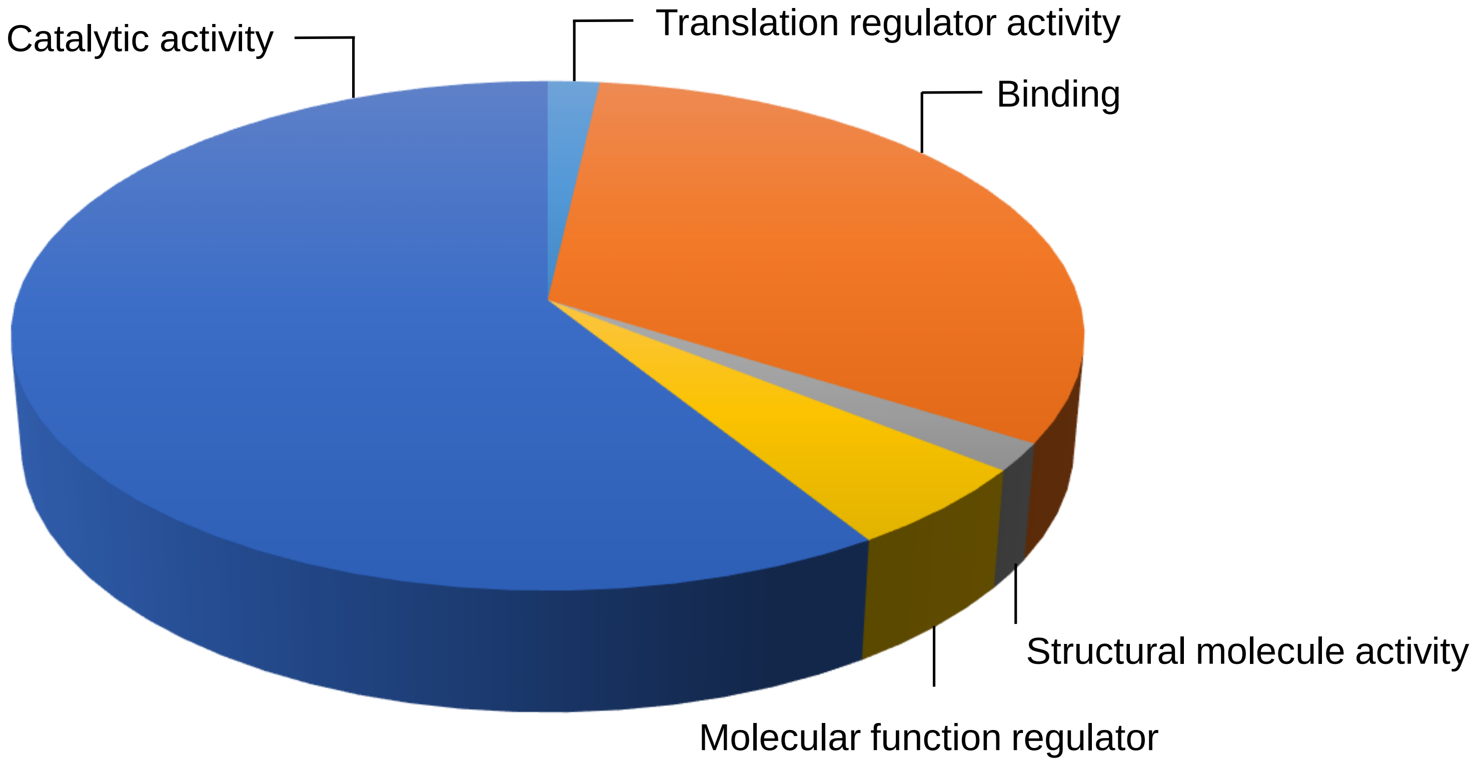
[1]Institute of Inorganic and Analytical Chemistry, Justus Liebig University Giessen, 35392 Giessen, Germany

[2]Institute for Anatomy and Cell Biology II, Division of Medical Cell Biology, Justus Liebig University Giessen, 35392 Giessen, Germany

Bioinformatics analysis using PANTHER (v14.1) classification system

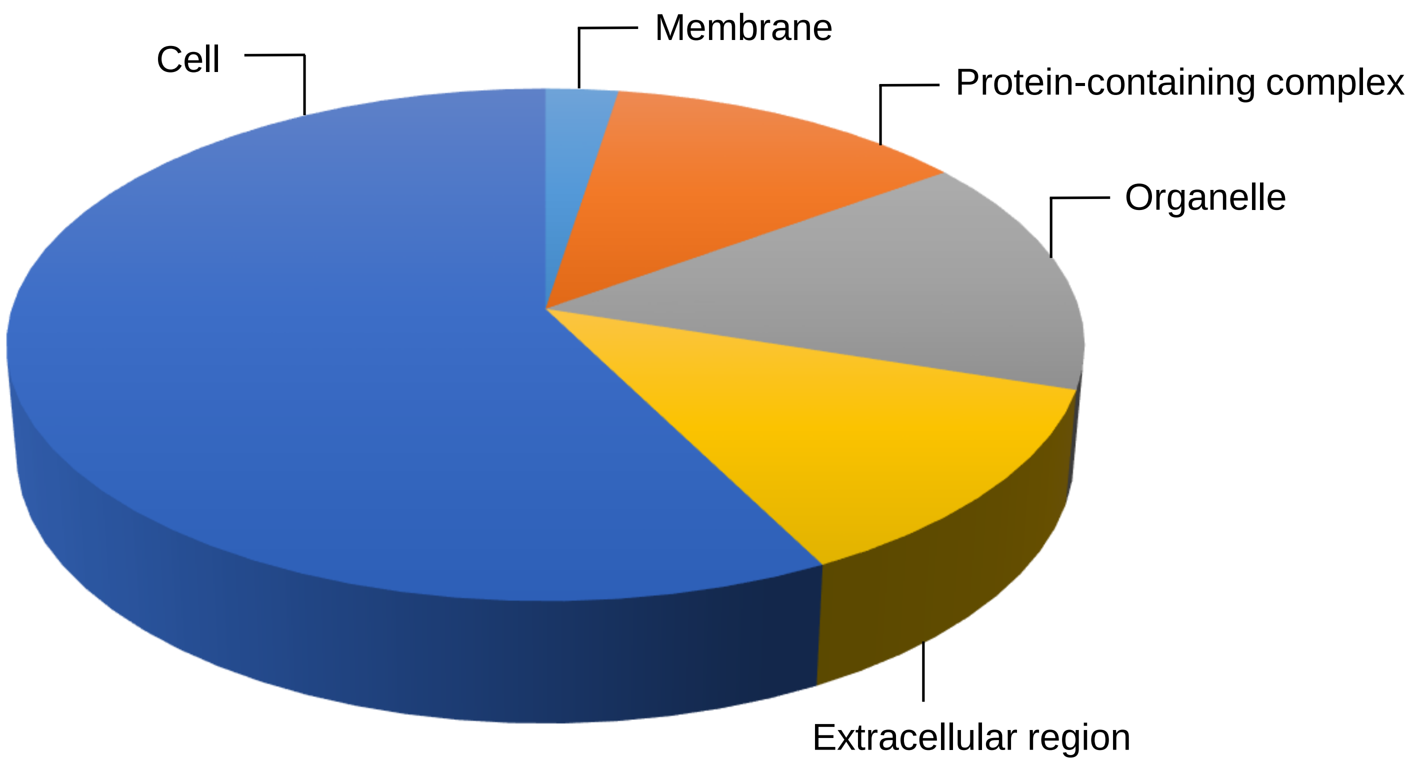
Wild type control and peroxisomal biogenesis factor 11α knockout mouse liver proteome

Molecular functions



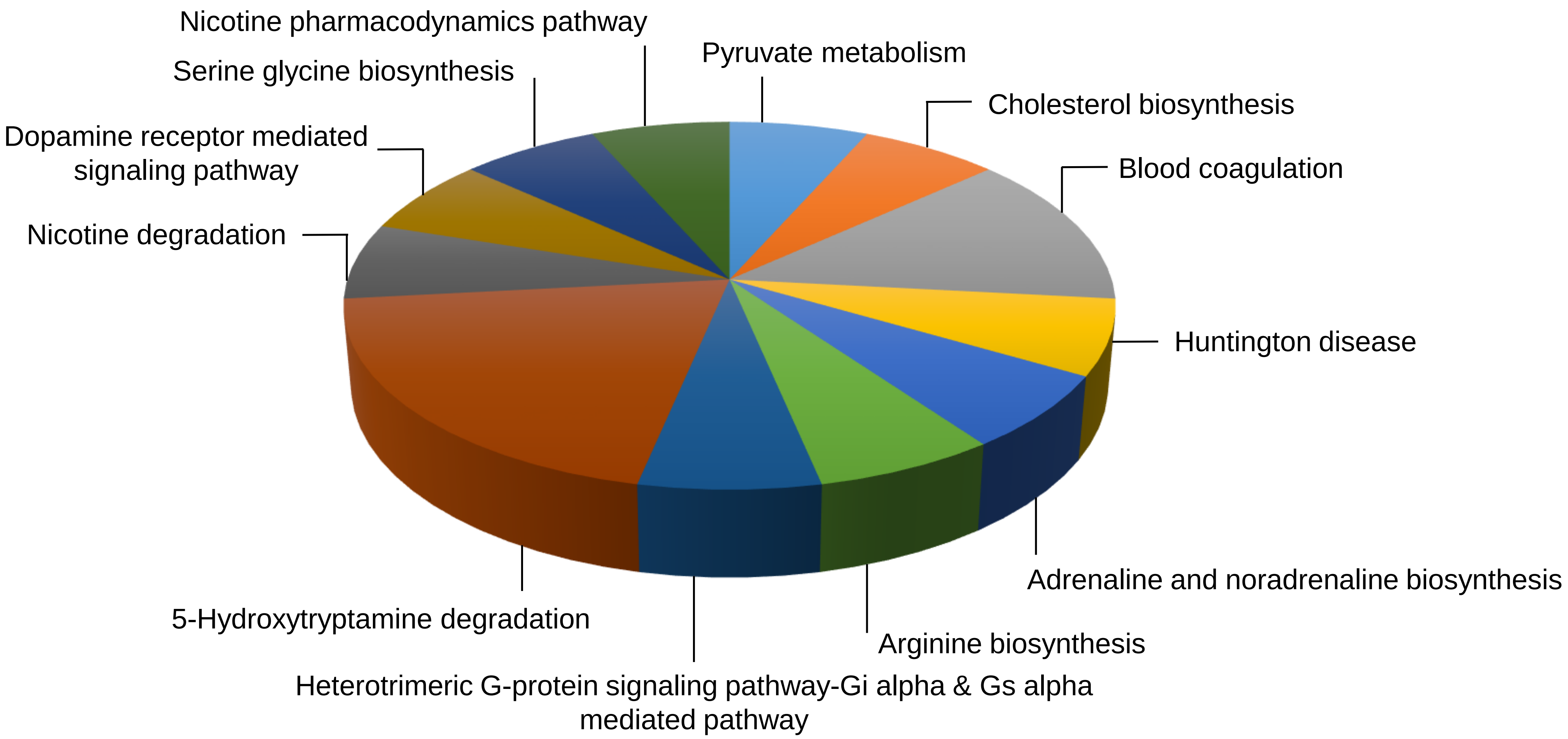
Bioinformatics analysis of the differentially abundant protein dataset (liver) depicting the molecular functions of the proteins

Cellular components



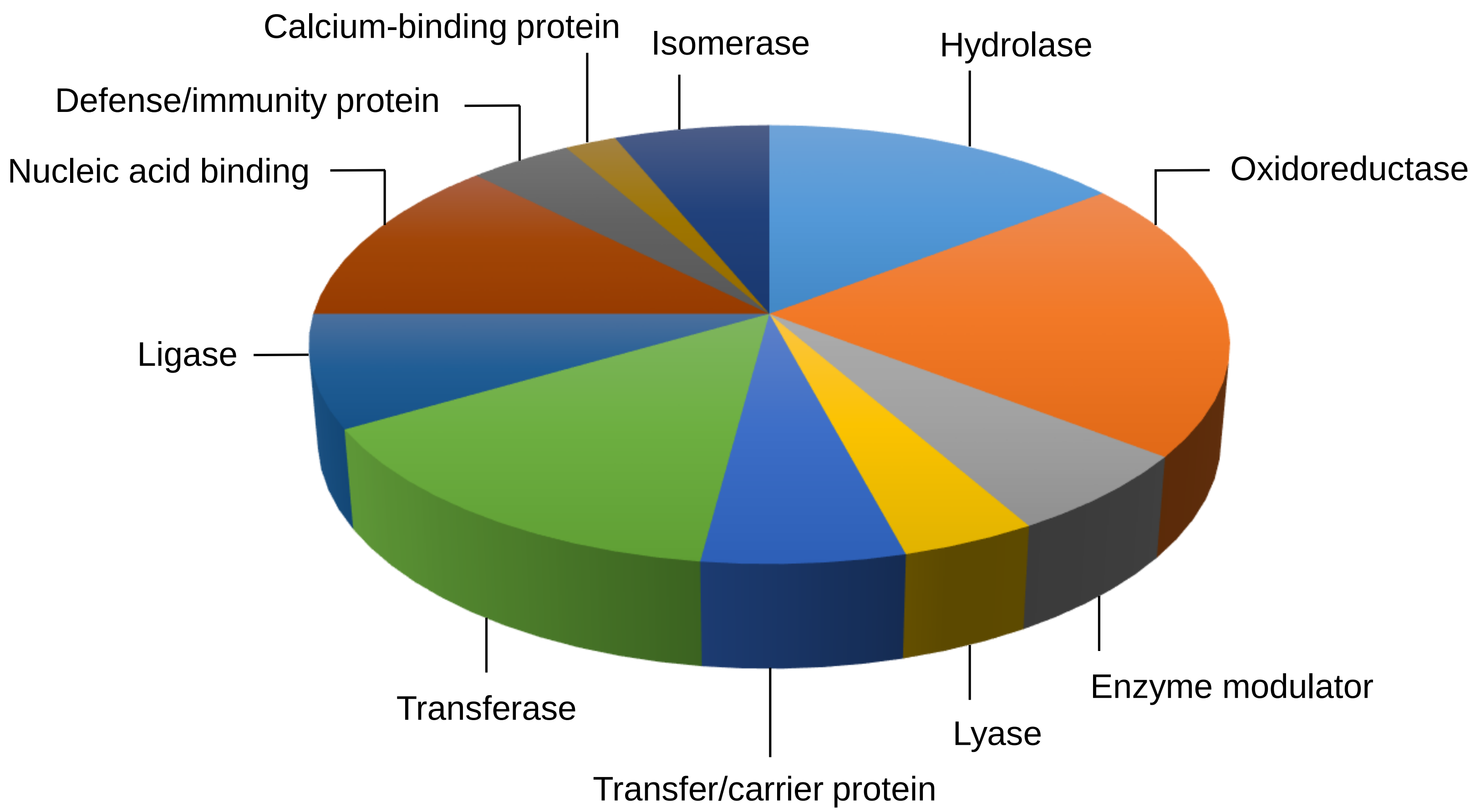
Bioinformatics analysis of the differentially abundant protein dataset (liver) depicting the cellular components of the proteins

Pathways



Bioinformatics analysis of the differentially abundant protein dataset (liver) depicting the pathways altered

Protein classes

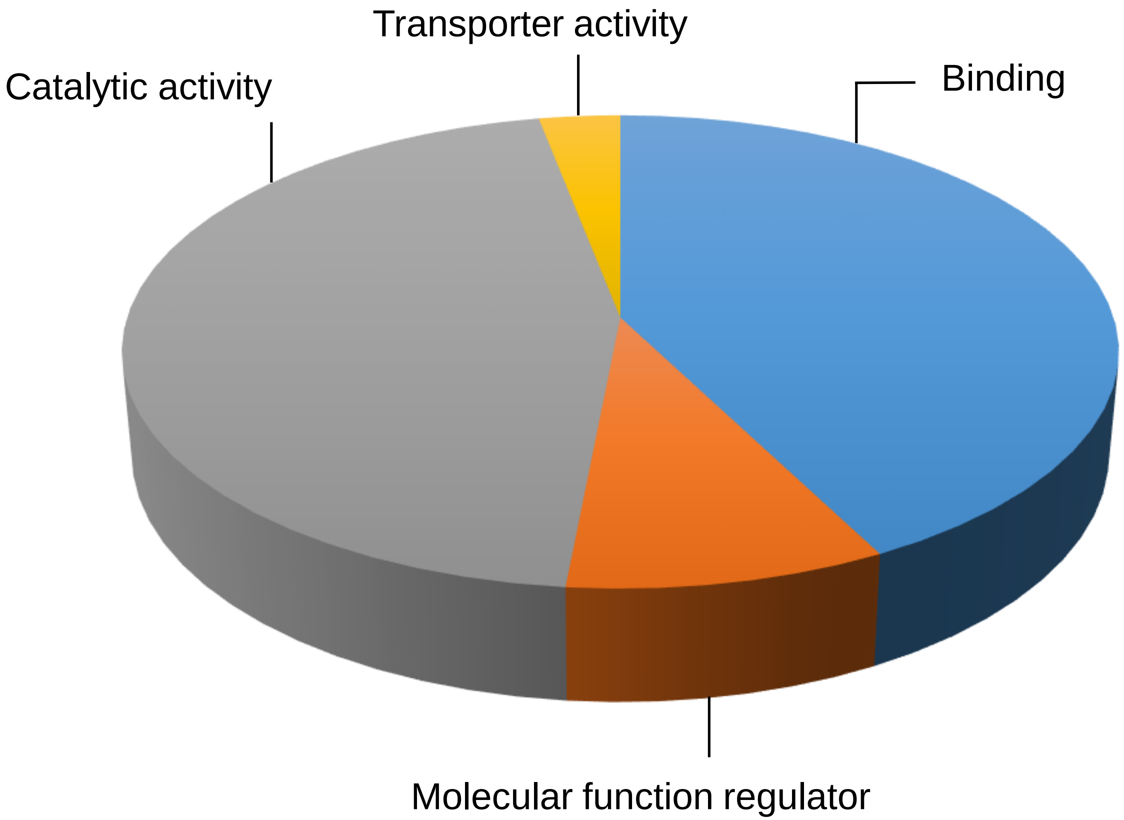


Bioinformatics analysis of the differentially abundant protein dataset (liver) depicting the protein classes

Bioinformatics analysis using PANTHER (v14.1) classification system

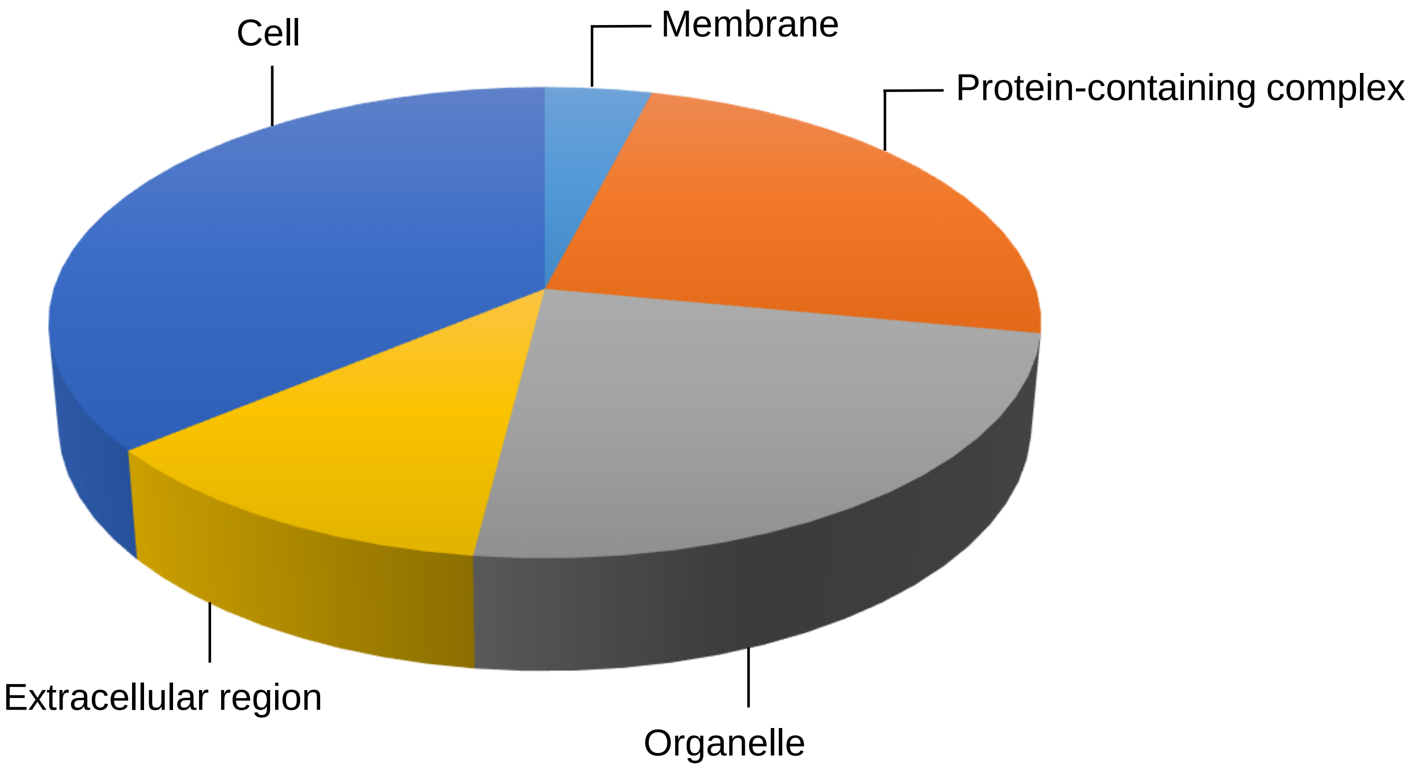
Wild type control and peroxisomal biogenesis factor 11α knockout mouse heart proteome

Molecular functions



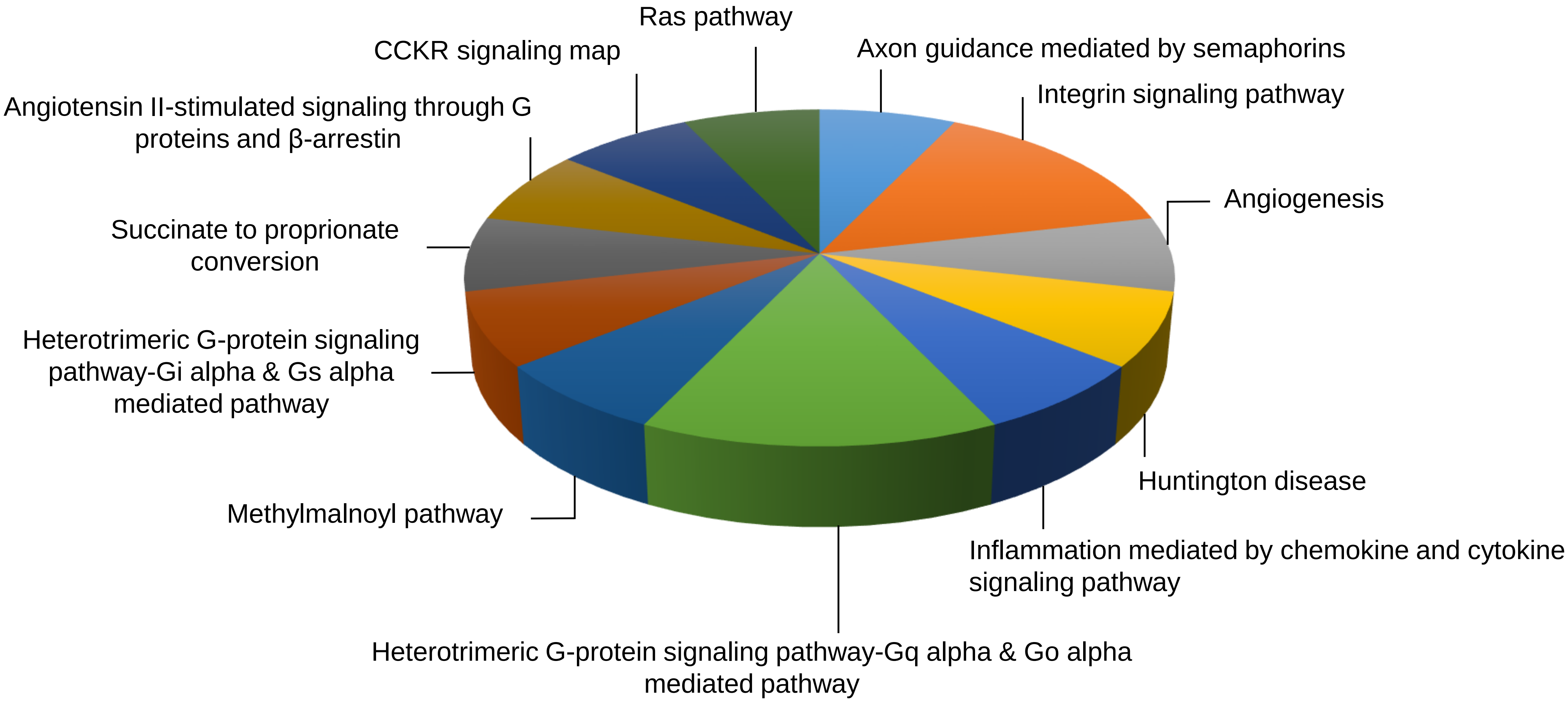
Bioinformatics analysis of the differentially abundant protein (heart) dataset depicting the molecular functions of the proteins

Cellular components



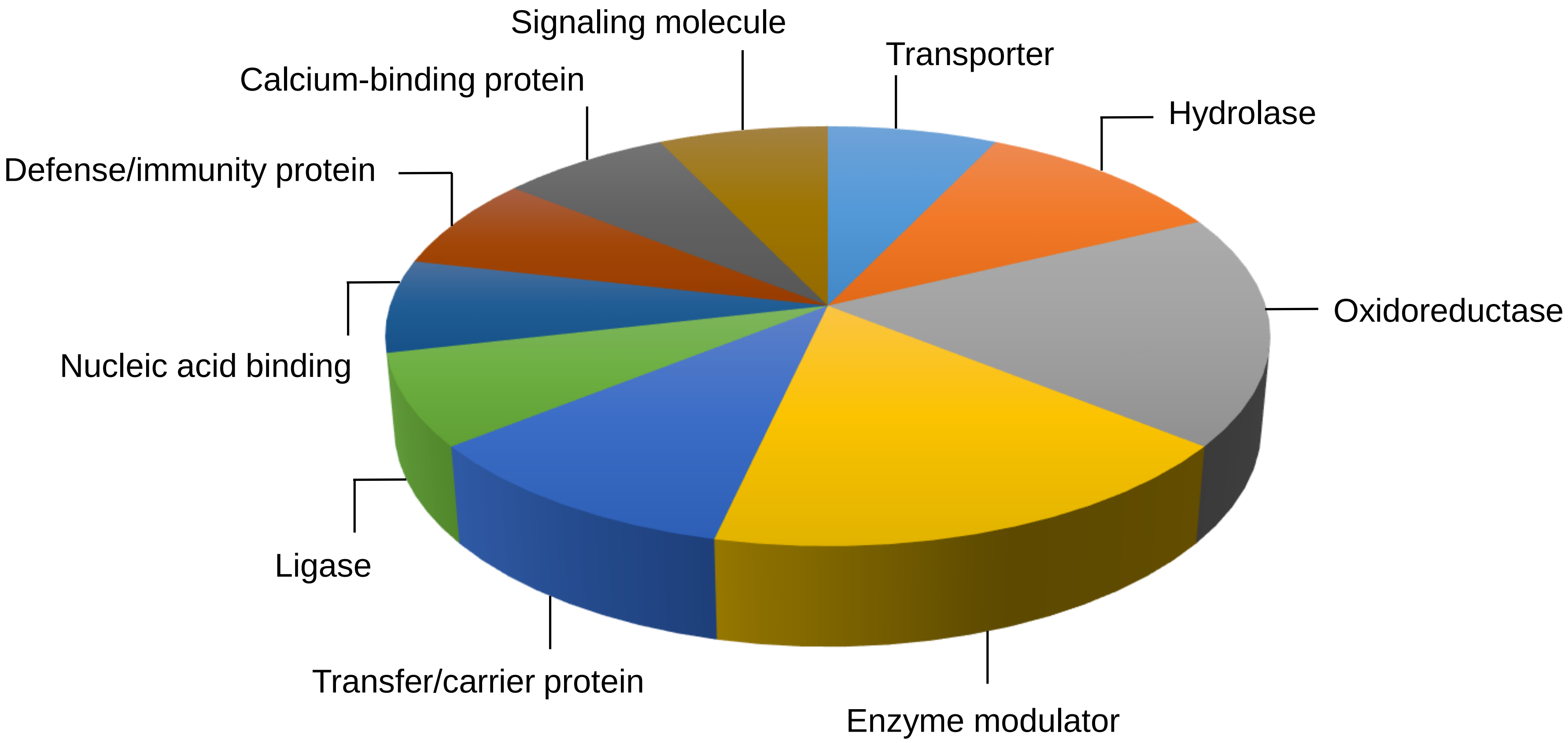
Bioinformatics analysis of the differentially abundant protein dataset (heart) depicting the cellular components of the proteins

Pathways



Bioinformatics analysis of the differentially abundant protein dataset (heart) depicting the pathways altered

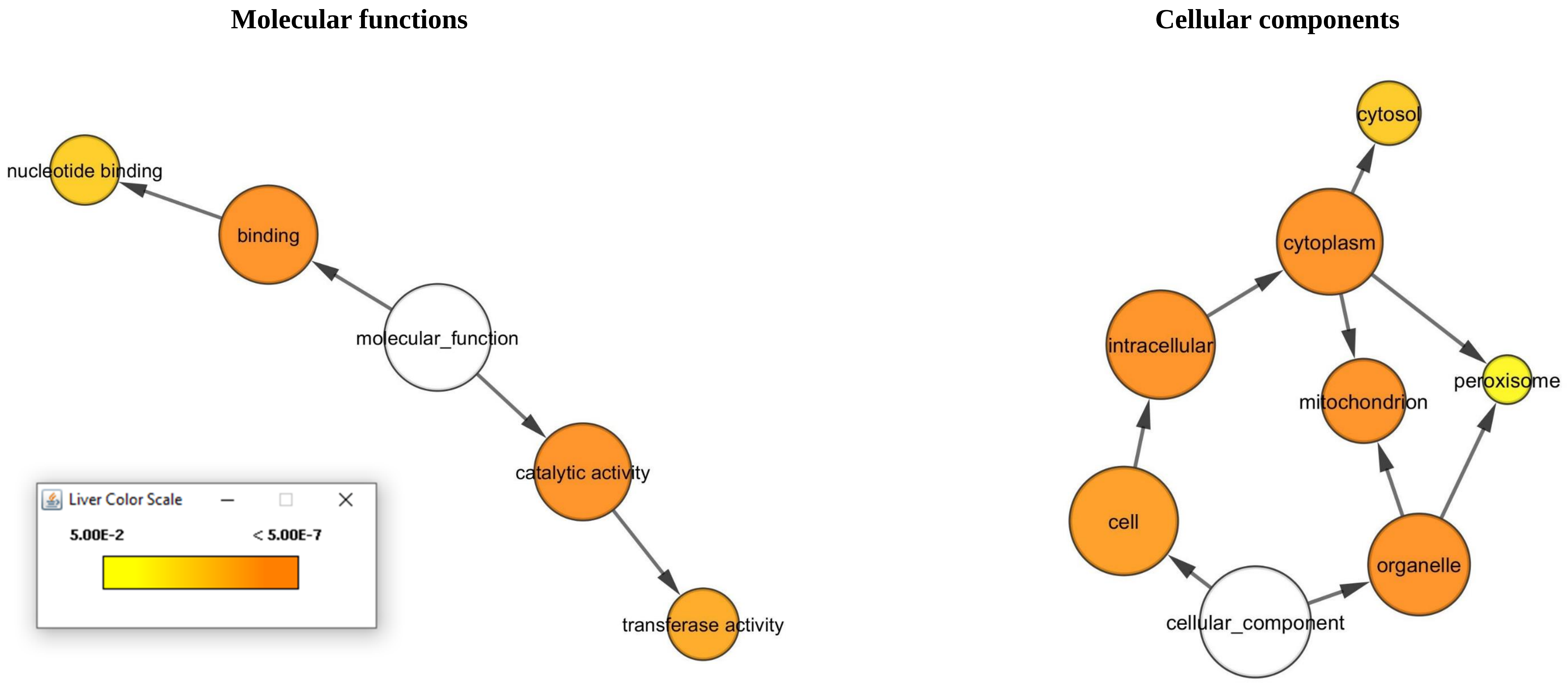
Protein classes



Bioinformatics analysis of the differentially abundant protein dataset (heart) depicting the protein classes

Bioinformatics analysis using Cytoscape (v3.7.2) and BiNGO (v3.0.3)

Wild type control and peroxisomal biogenesis factor 11α knockout mouse liver proteome



Molecular functions

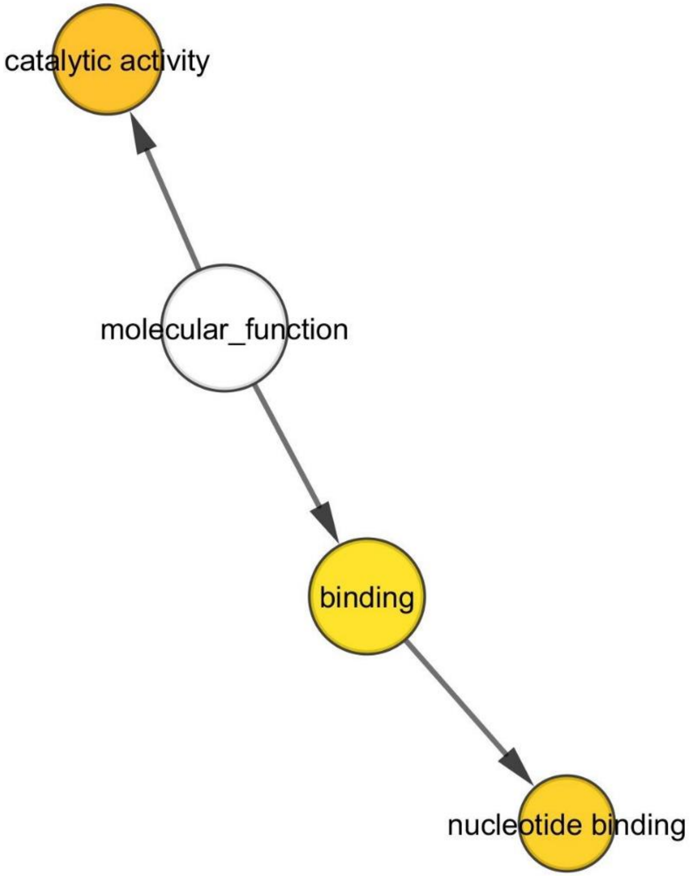
Cellular components

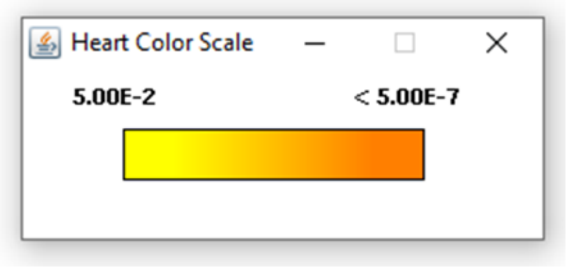
Bioinformatics analysis of the differentially abundant protein (liver) dataset depicting the molecular functions and cellular components of the proteins

Bioinformatics analysis using Cytoscape (v3.7.2) and BiNGO (v3.0.3)

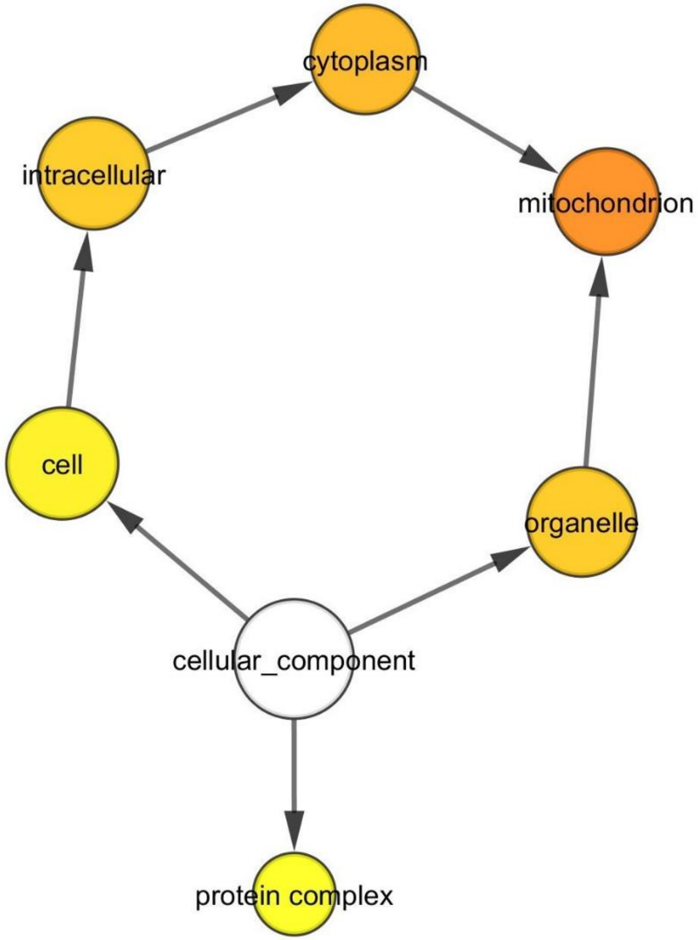
Wild type control and peroxisomal biogenesis factor 11α knockout mouse heart proteome

Molecular functions





Cellular components



Bioinformatics analysis of the differentially abundant protein (heart) dataset depicting the molecular functions and cellular components of the proteins