

1. 基于 DAVID 提供的对基因中属于人的并且能够匹配蛋白的部分筛选出来

Annotation Summary Results

[Help and Tool Manual](#)

Current Gene List: List_1 **2666 DAVID IDs**

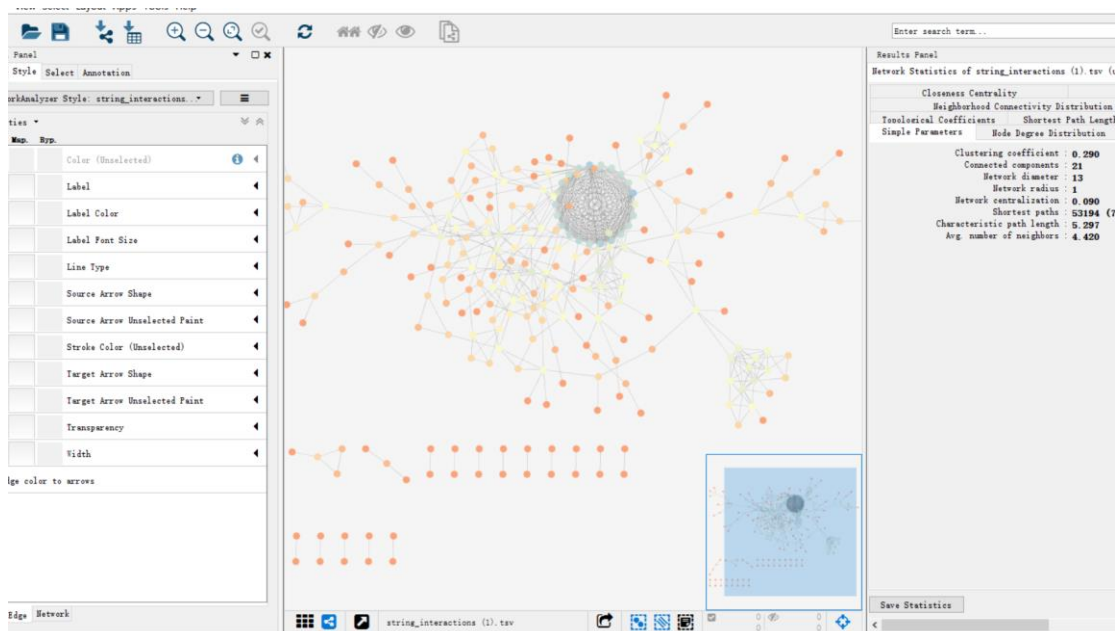
Current Background: Homo sapiens **Check Defaults** ☒ **Clear All**

- ☒ **Disease** (1 selected)
- ☒ **Functional_Categories** (3 selected)
- ☒ **Gene_Ontology** (3 selected)
- ☒ **General_Annotations** (0 selected)
- ☒ **Literature** (0 selected)
- ☒ **Main_Accessions** (0 selected)
- ☒ **Pathways** (3 selected)
- ☒ **Protein_Domains** (3 selected)
- ☒ **Protein_Interactions** (0 selected)
- ☒ **Tissue_Expression** (0 selected)

Red annotation categories denote DAVID defined defaults

Combined View for Selected Annotation

2. 在通过 String 和 Cytoscape 做出网络图



3. 请注意 pdf 文件夹中有部分为颜色标记说明, 可方便分析