**Database files required by PathOlogist software**

======================================================================

All files are tab-delimited text file without column header

1. **patholigist.pathways.txt**

Column 1: Pathway number (ID)

Column 2: Pathway names

Note: current version has 621 pathways (2010)

1. **pathologist.db.txt**

Column 1: Pathway names (total 618)

Column 2: Pathway number (ID) (total 621)

Column 3: Molecular type (protein, compound, complex, RNA)

Column 4: Molecular name (gene symbol, total 10058)

Column 5: Molecular number (ID) (total 12855)

Column 6: Molecular link (LL or UP) (total 5310)

Column 7: Status (inactive, or active1~4)

Column 8: Unclear (total 9)

Column 9: Cellular location (total 80)

Column 10: Molecular role (agent, input, or output, inhibitor)

Column 11: interaction number (ID) (total 14458)

Column 12 Interaction type (total 417)

Note: when read this table with R, the quote=”” has to be defined with read.table.

1. **pathologist.complexes.txt**

Column 1: Complex ID (total 3288)

Column 2: Molecular type (protein, compound, complex, RNA)

Column 3: Molecular name (total 2411)

Column 4: Molecular number (ID) (total 2706)

Column 5: Molecular link (LL or UP) (total 2318)

Column 6: Status (inactive, or active1~3)

Column 7: Unclear (total 420)

Column 8: Cellular location (total 14)

Column 9: components

Column 10: Same as column 1.

UP2LL.txt

Column 1: Protein ID (total 126461)

Column 2: Gene ID (total 21373)

1. **Affymetrix expression array annotation files**

Generated from Affymetrix expression array annotation files

Column 1: probe set ID

Column 2: Entrez gene ID