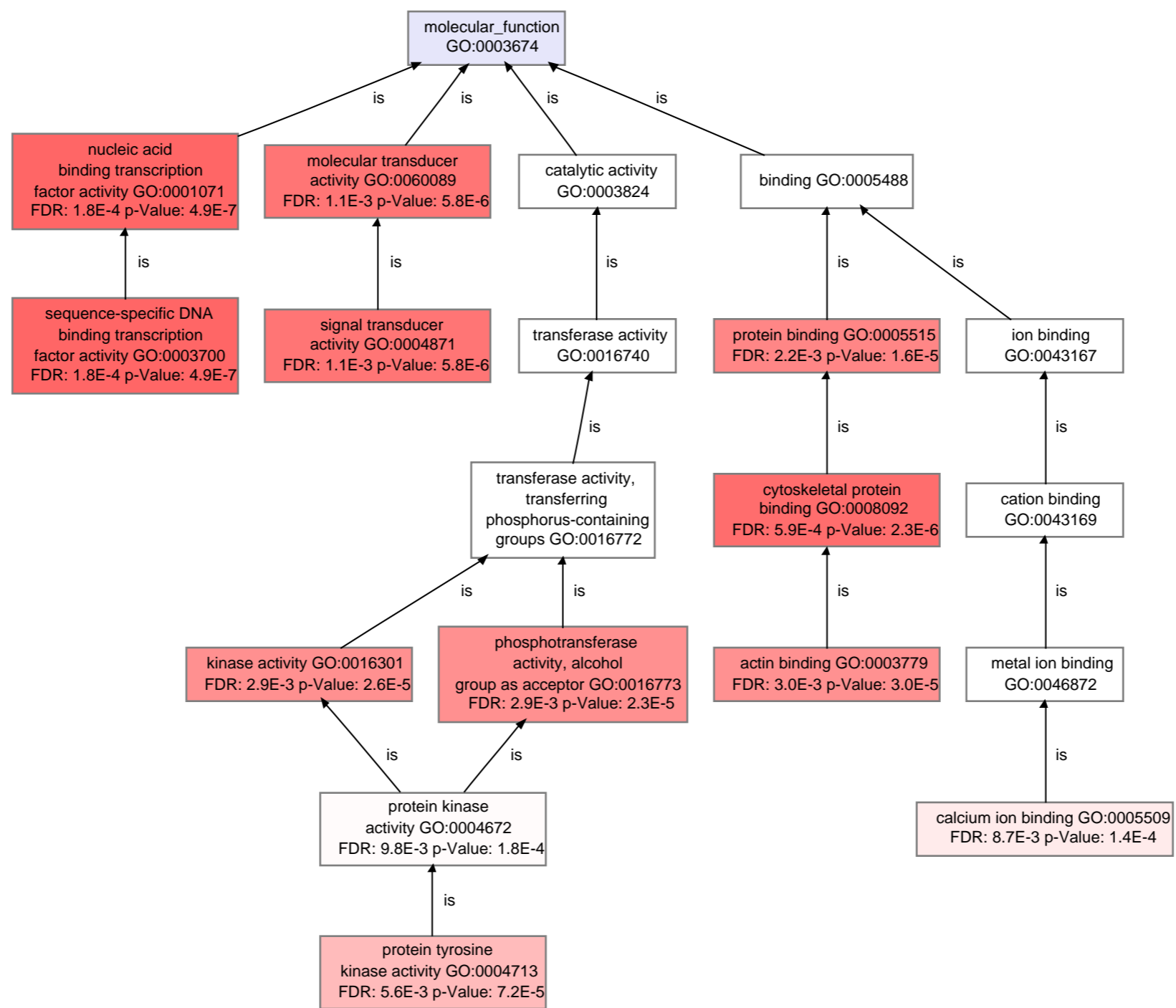
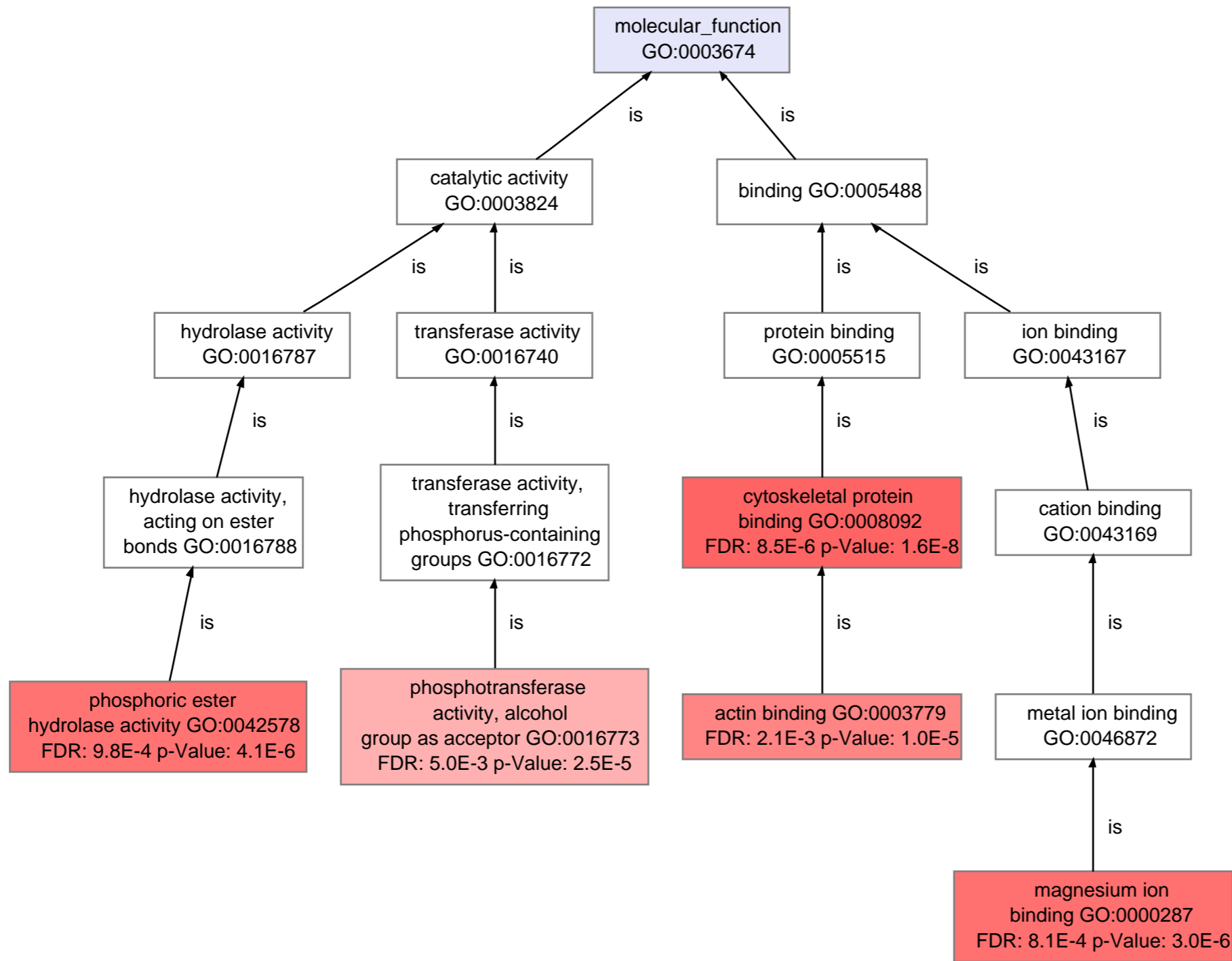


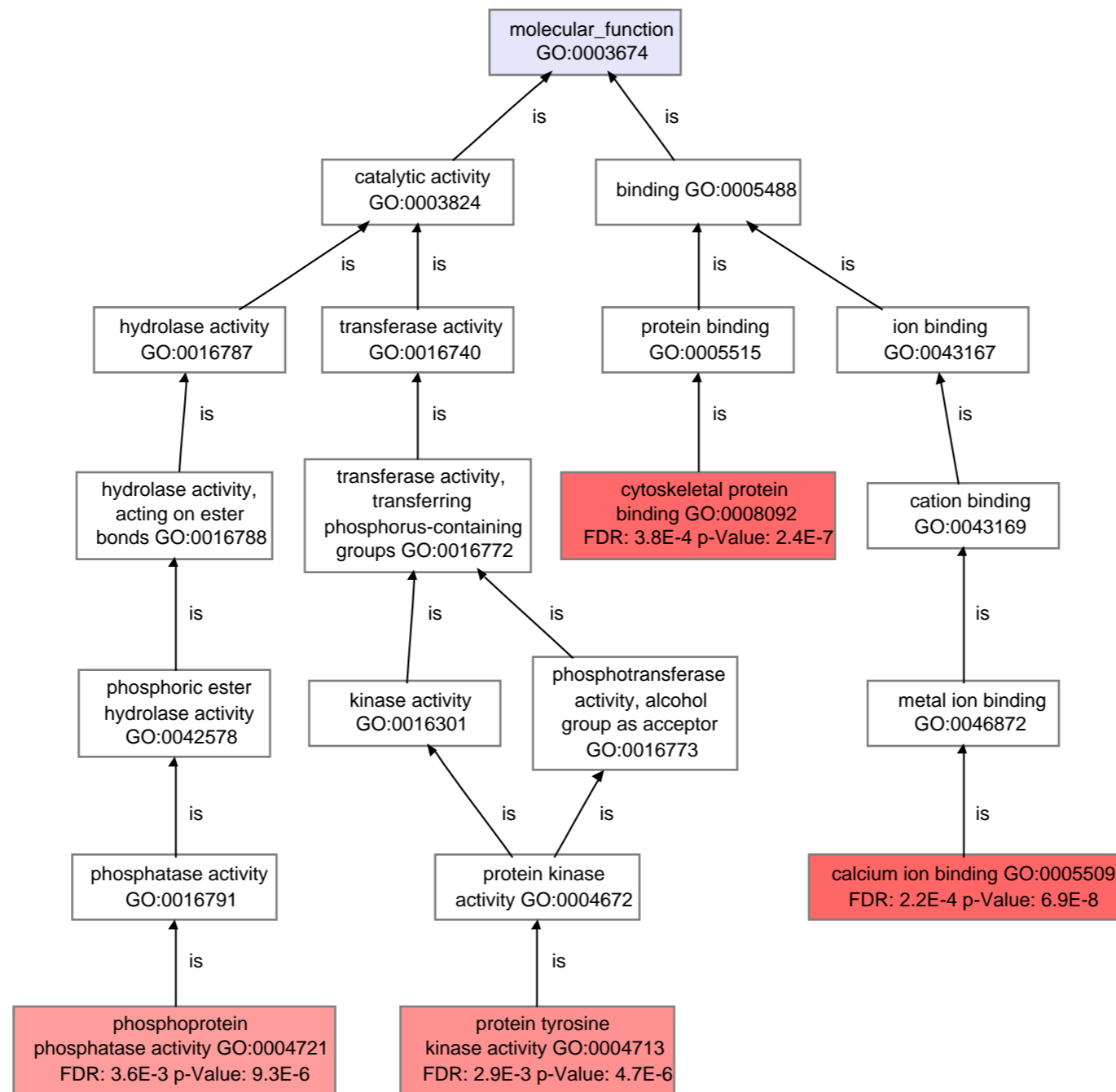
Figure S2. Color-coded gene ontology (GO) graph showing significantly enriched GO terms describing molecular functions. Predicted targets of miRNAs within each cluster (Figure 4) were analyzed separately. A false discovery rate (FDR) of 0.01 was used as the threshold. For each GO term, a brief description, GO number, FDR and P value were shown. No GO term was significantly enriched for targets of miRNAs in cluster 3 at a FDR of 0.01.



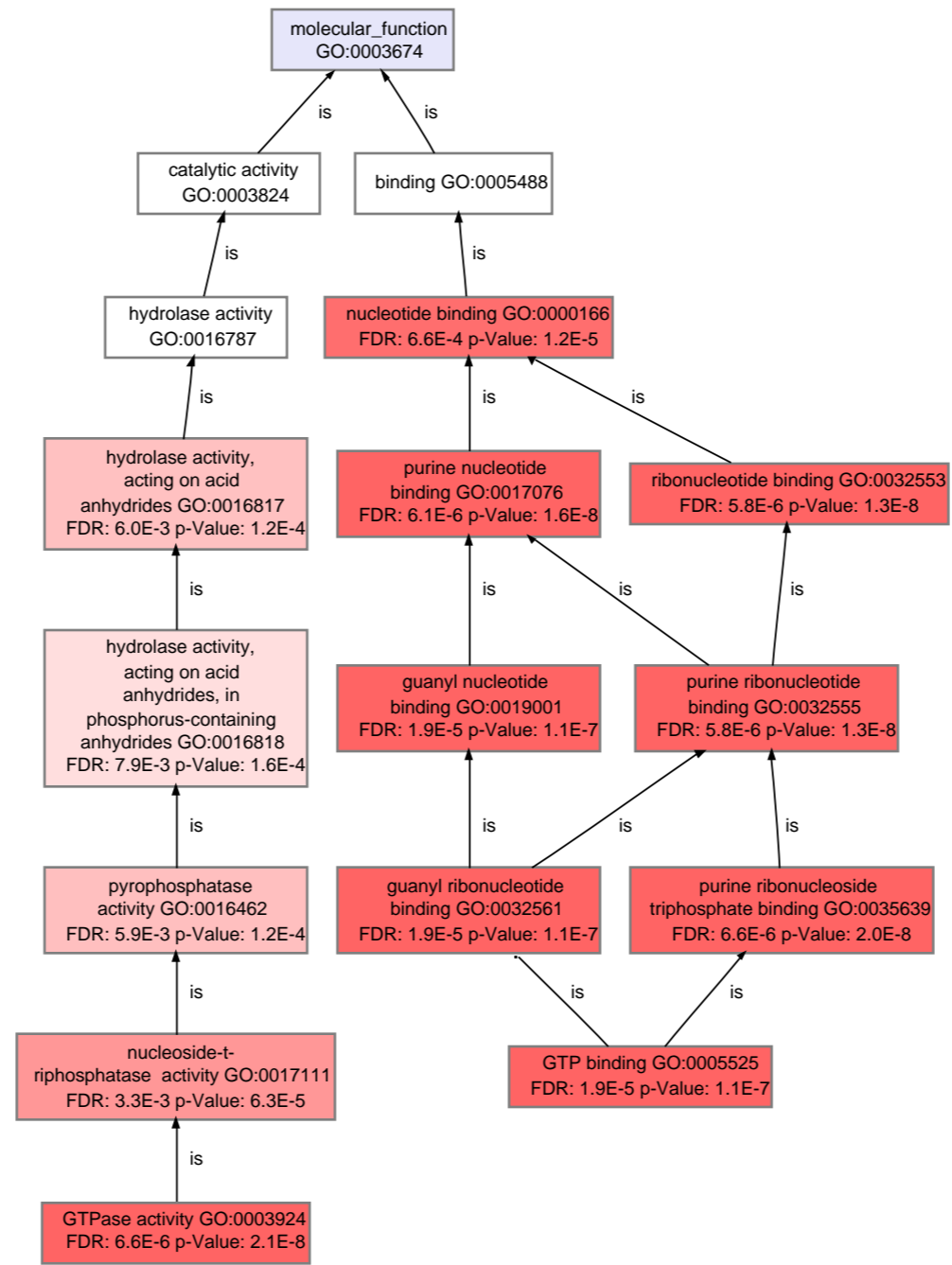
Enriched Graph



Enriched Graph



Enriched Graph



Enriched Graph