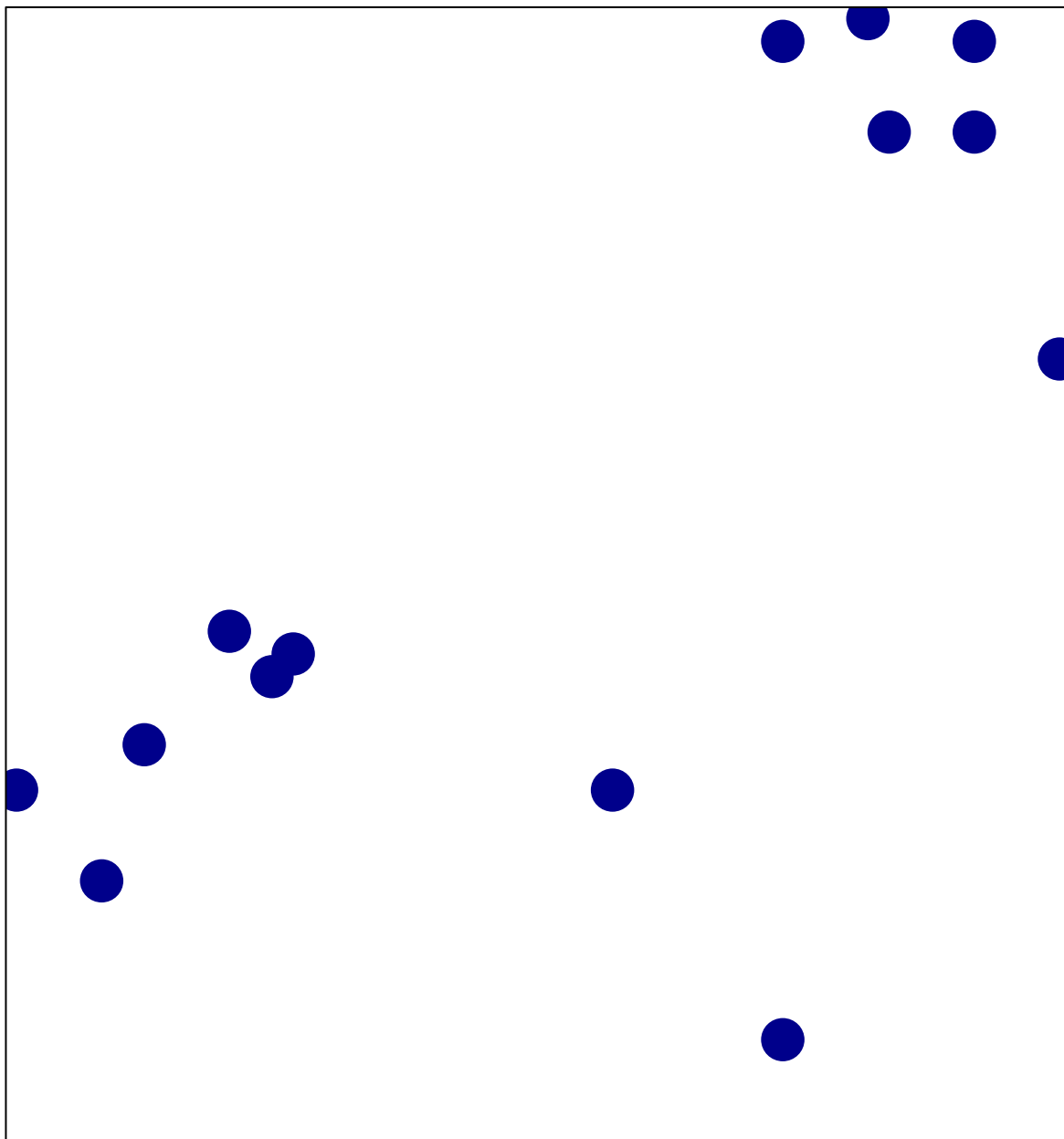


# REACTOME\_PROCESSING\_OF\_CAPPED\_INTRON\_CONTAINING\_PRE\_MRNA



# features = 14  
chi-square p = 0.84

# \_PROCESSING\_OF\_CAPPED\_INTRON\_CONTAINING



# features = 14 , max = 1