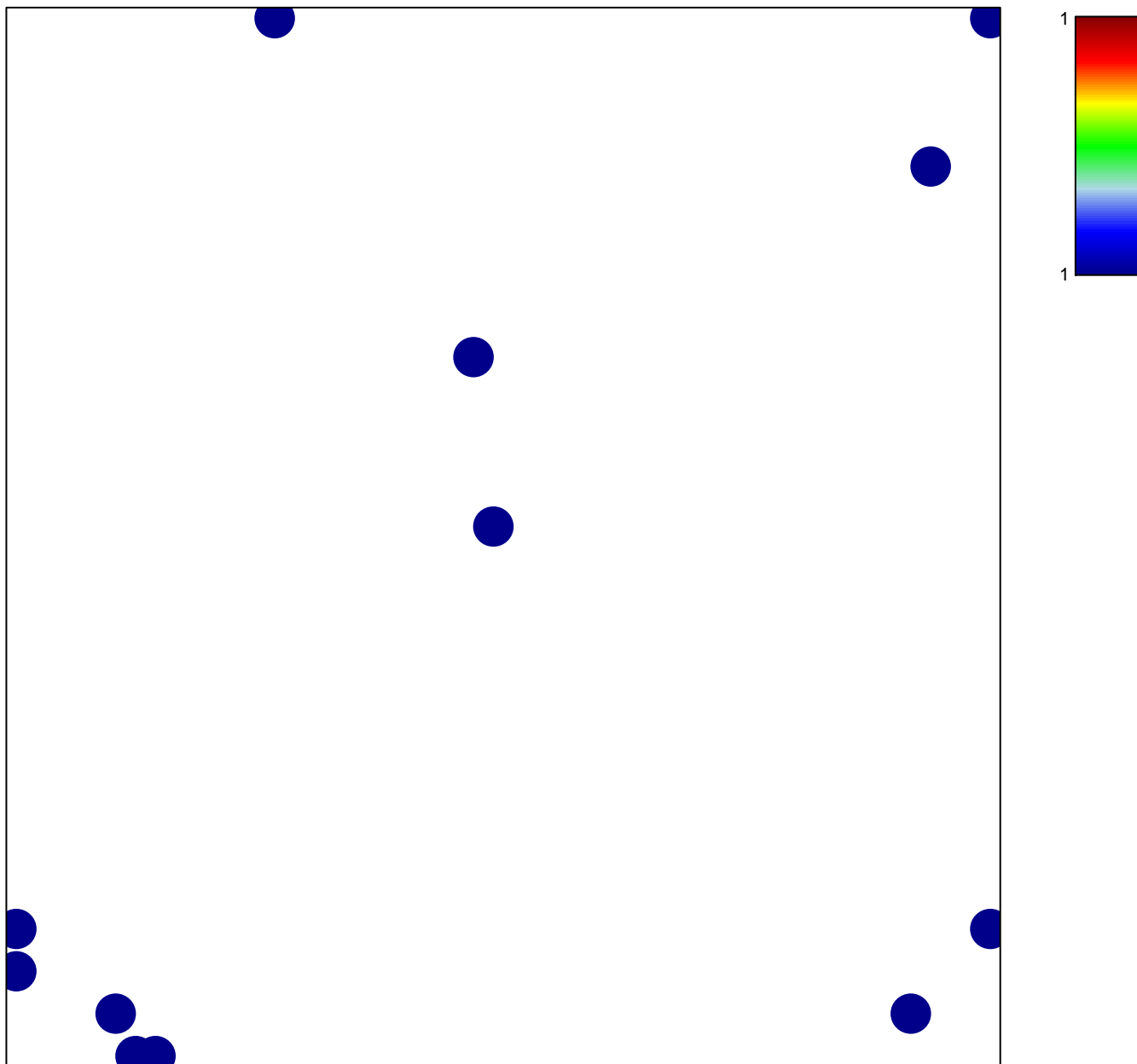
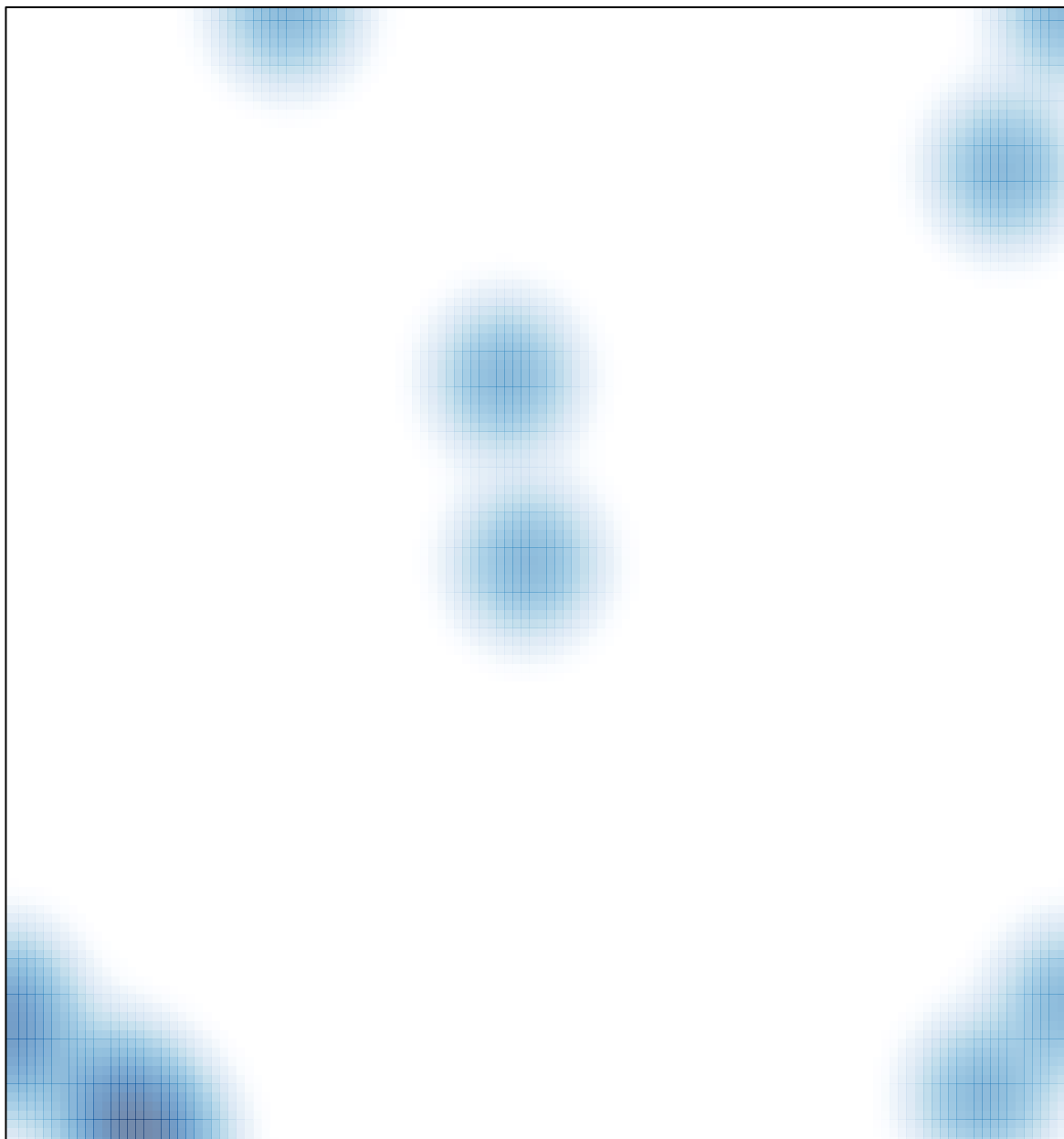


# heparan sulfate proteoglycan binding



# features = 12  
chi-square p = 0.82

# heparan sulfate proteoglycan binding



# features = 12 , max = 1