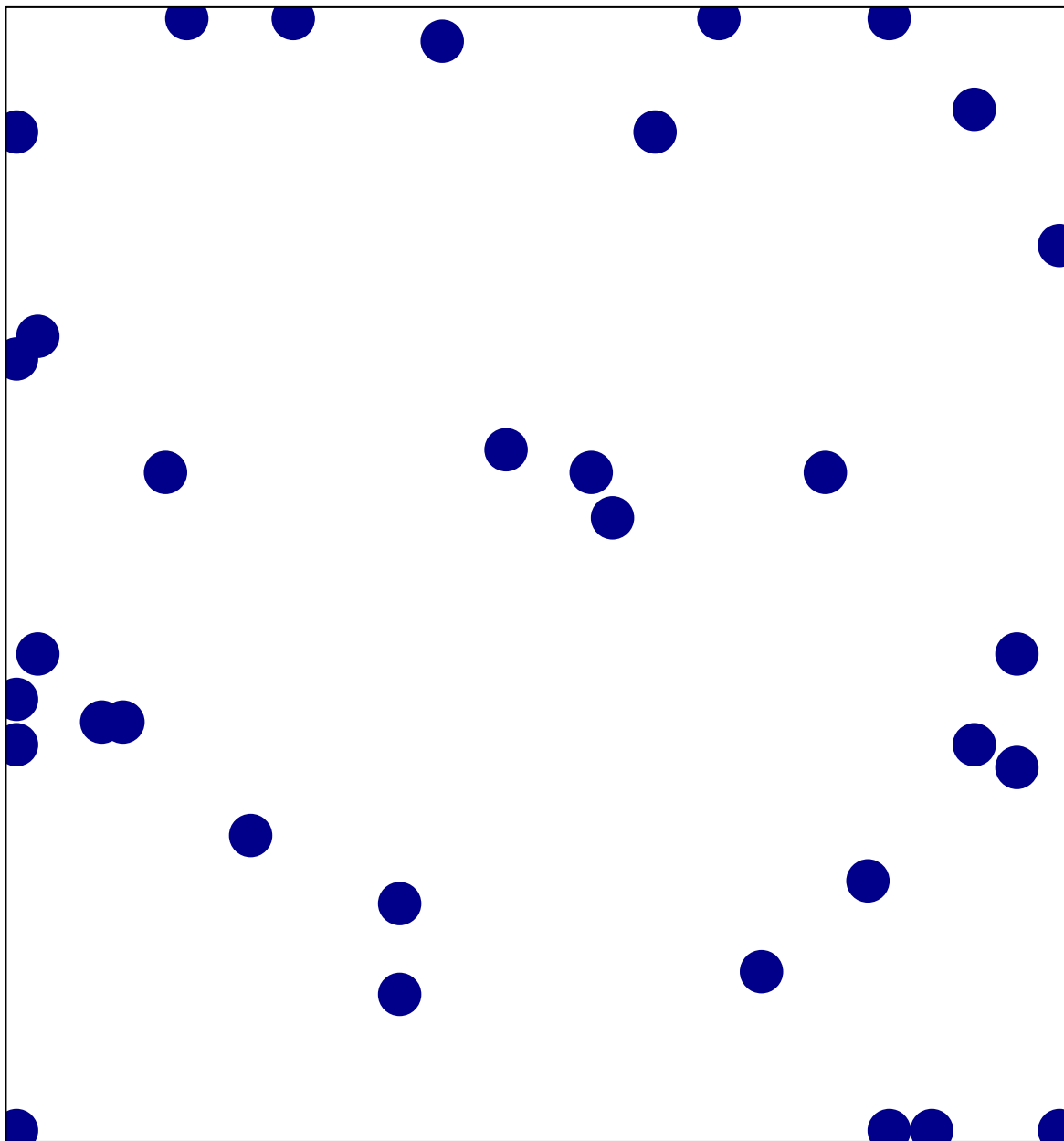
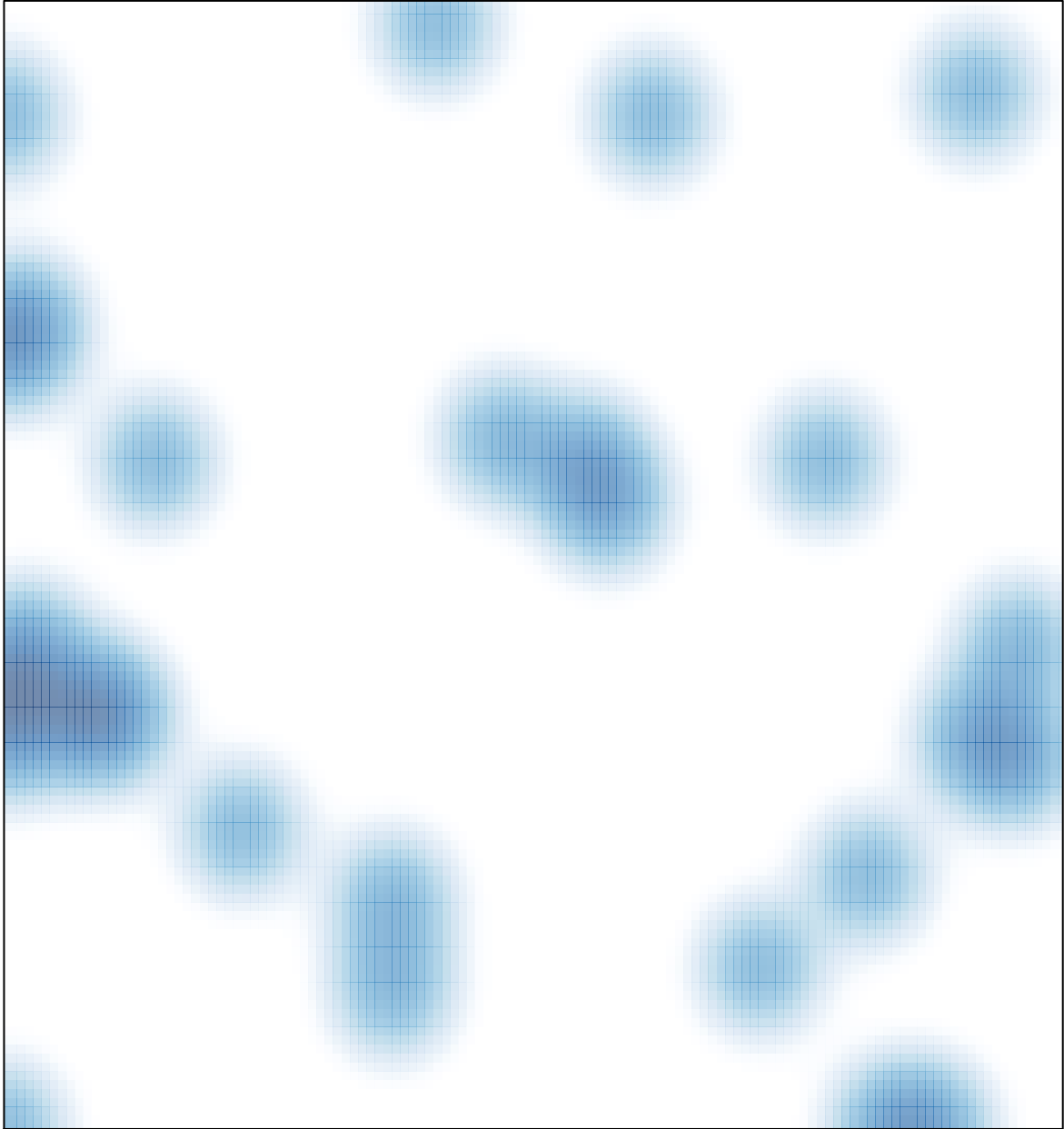


# peptide binding



# features = 33  
chi-square p = 0.81

# peptide binding



# features = 33 , max = 1