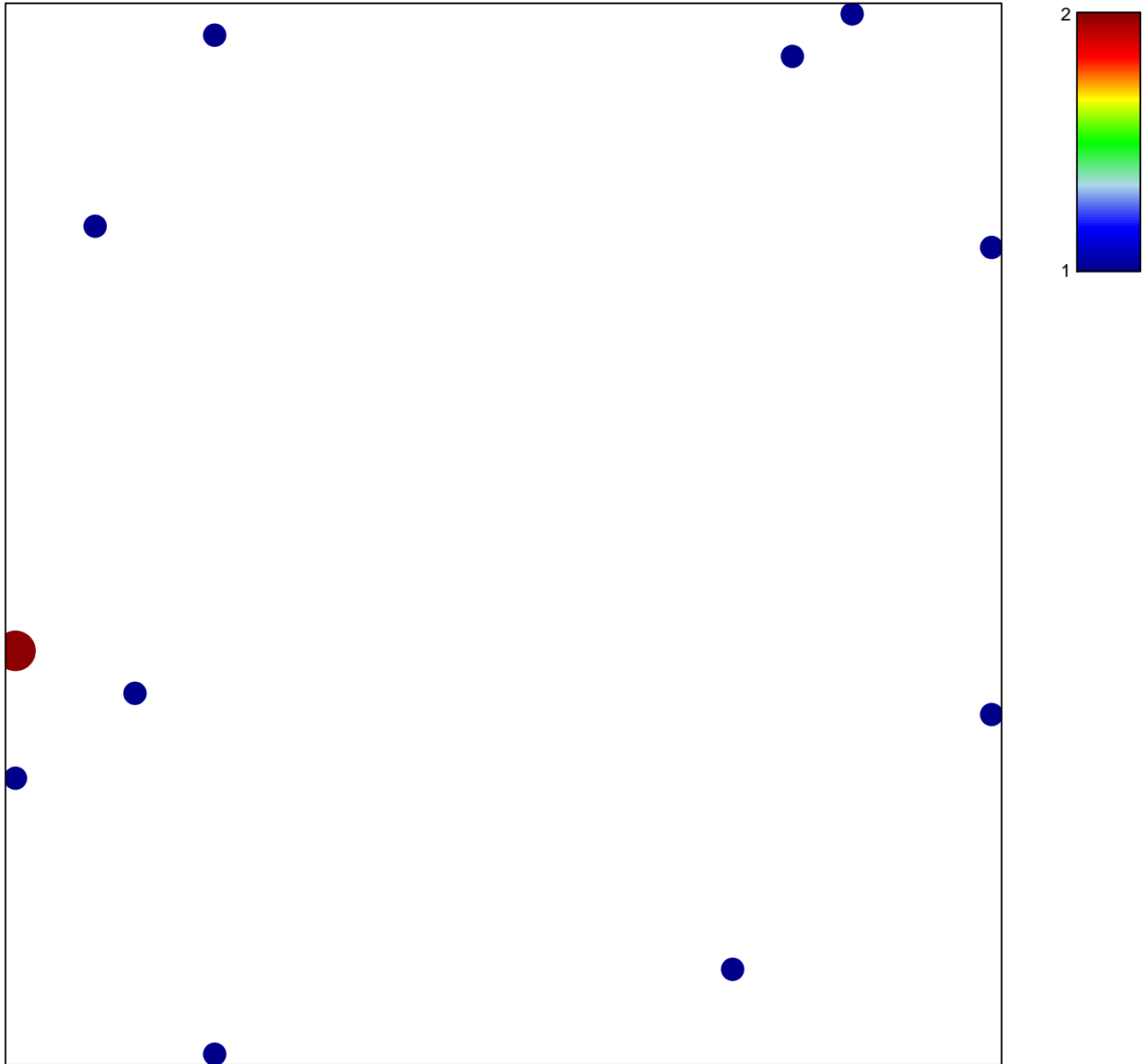
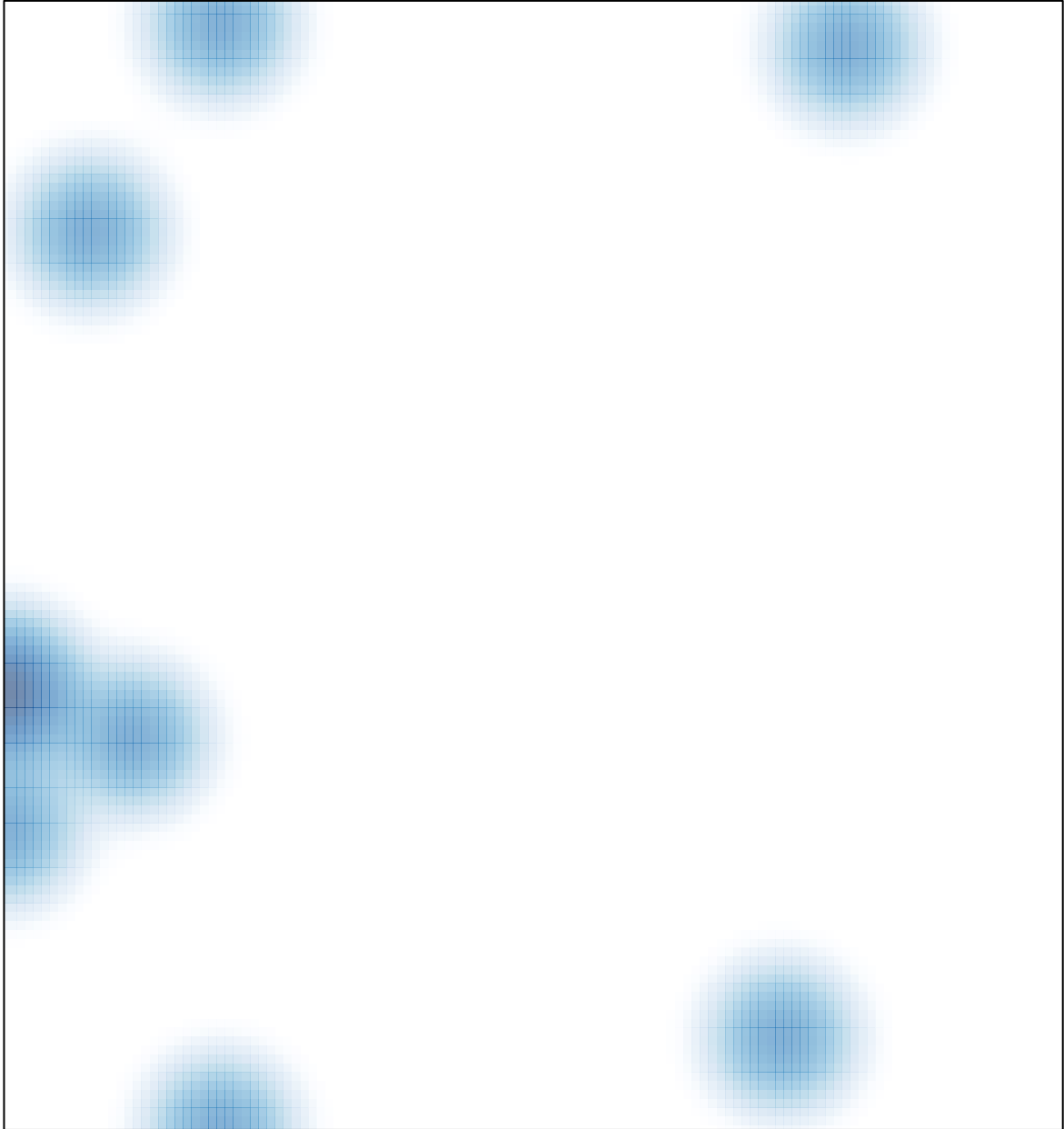


misfolded protein binding



features = 12
chi-square p = 0.82

misfolded protein binding



features = 12 , max = 2