methylated histone residue binding
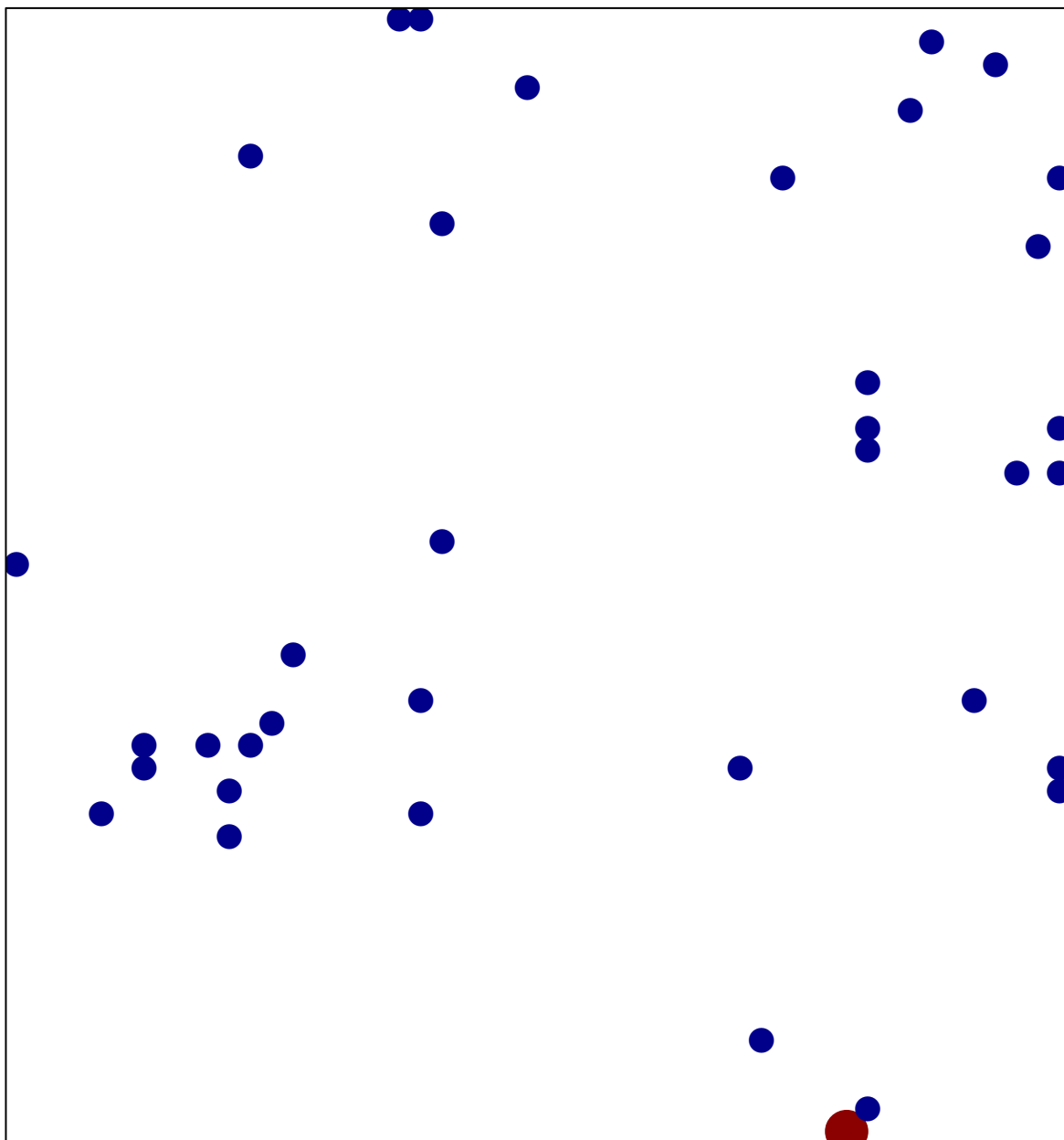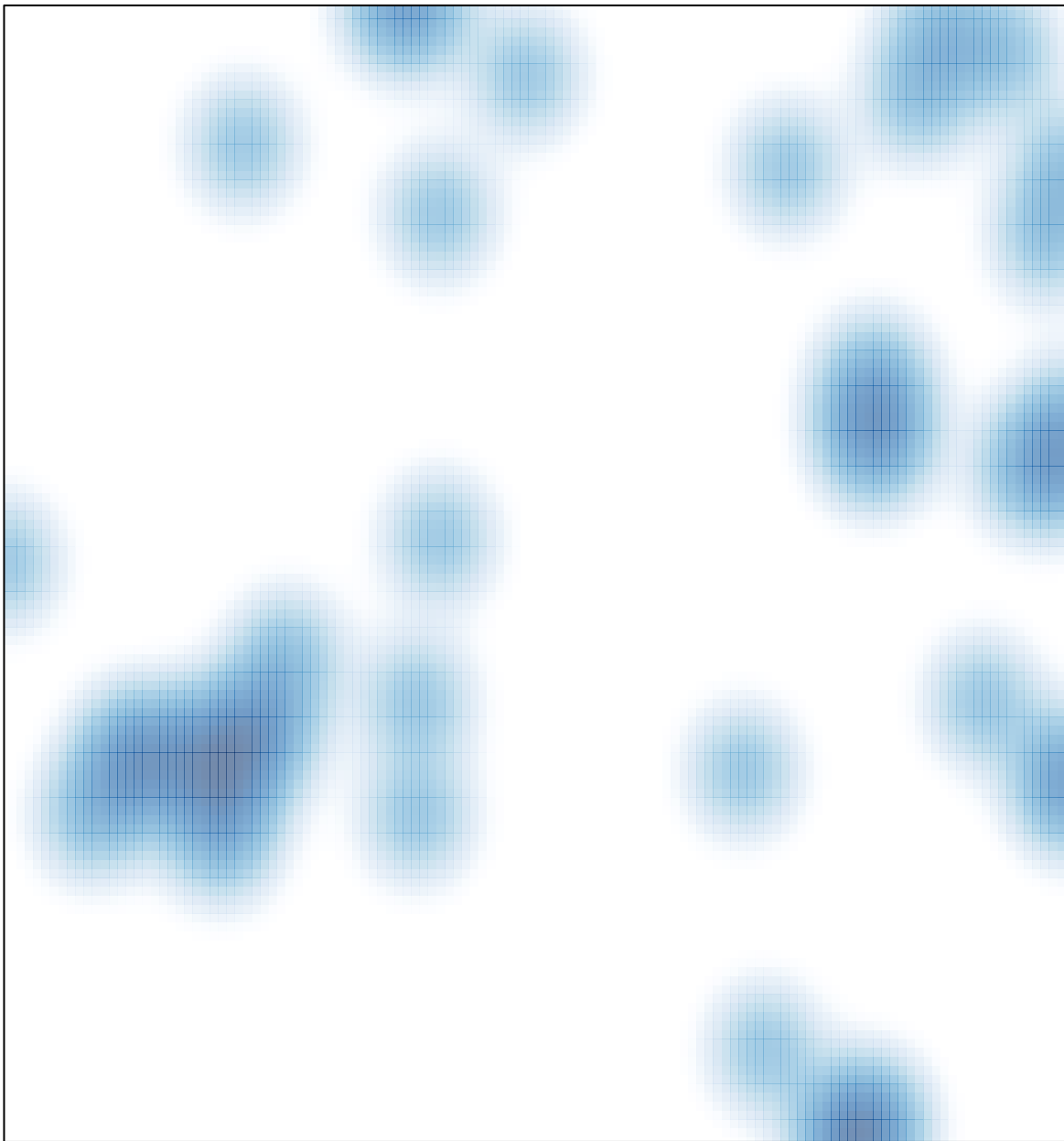

features = 38
chi−square p = 0.82

methylated histone residue binding

features = 38 , max = 2