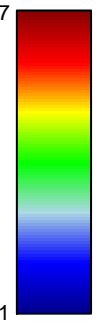
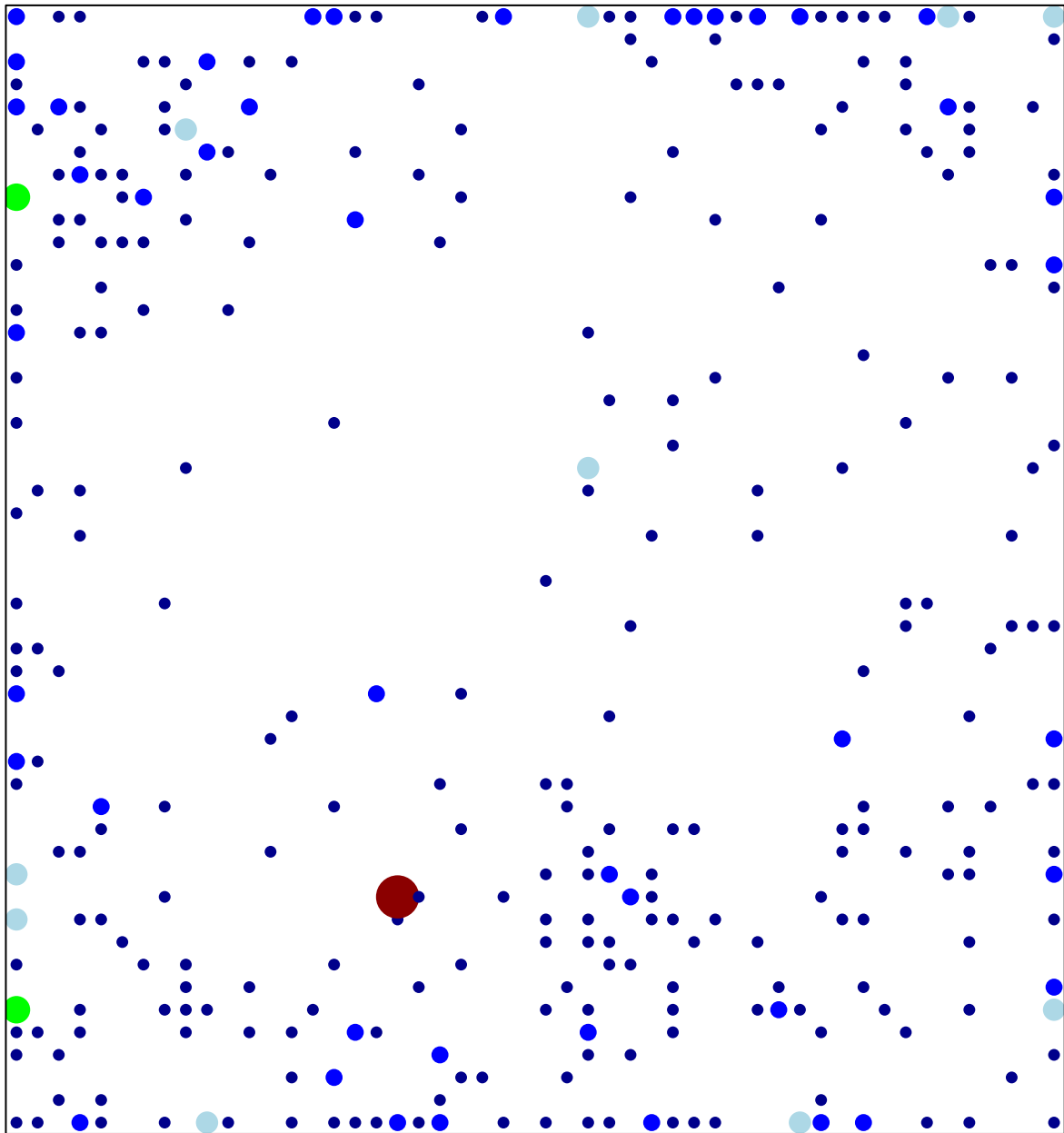
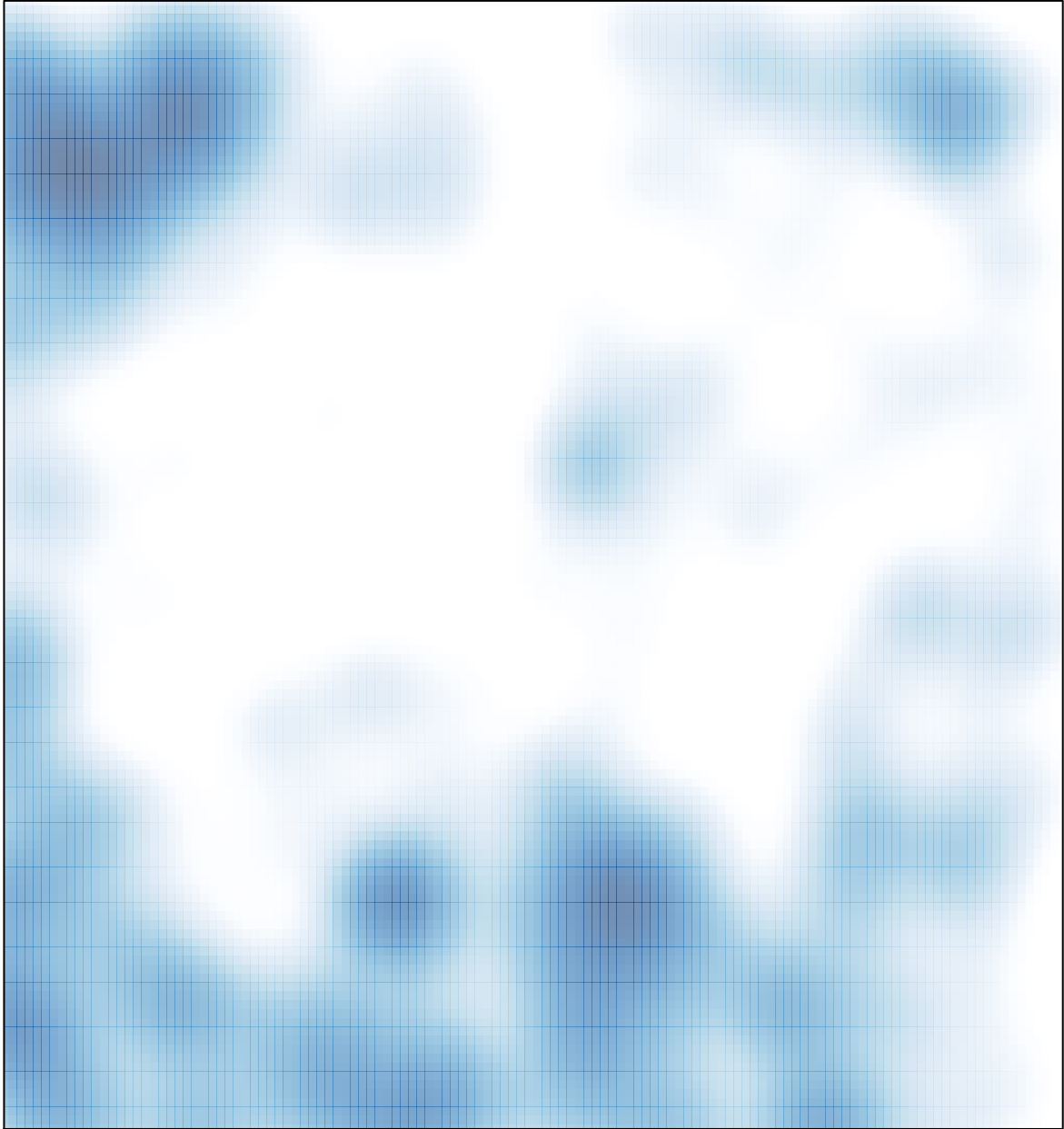


nucleotide binding



features = 386
chi-square p = 0.61

nucleotide binding



features = 386 , max = 7