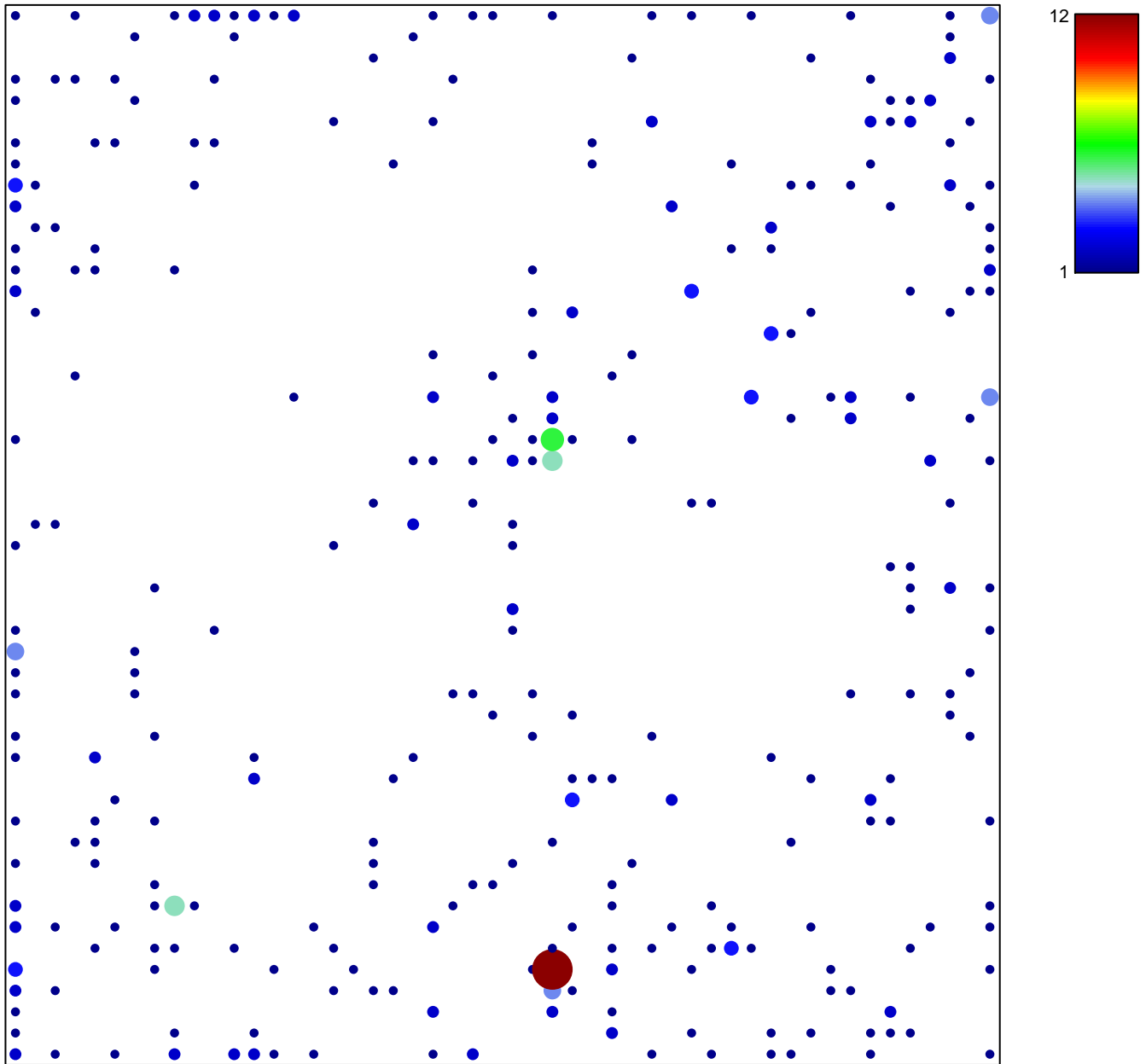
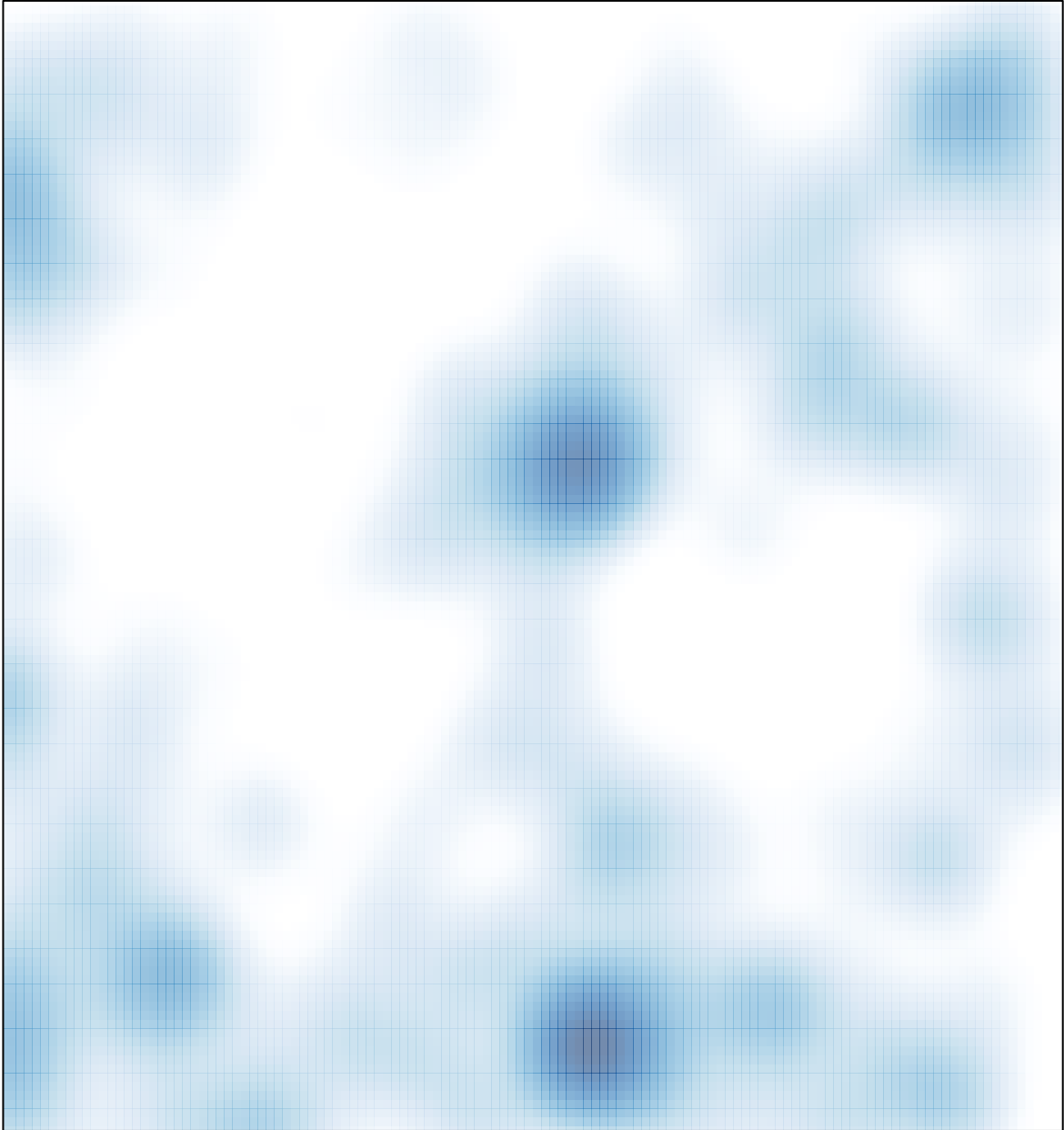


# proteolysis



# features = 388  
chi-square p = 0.65

# proteolysis



# features = 388 , max = 12