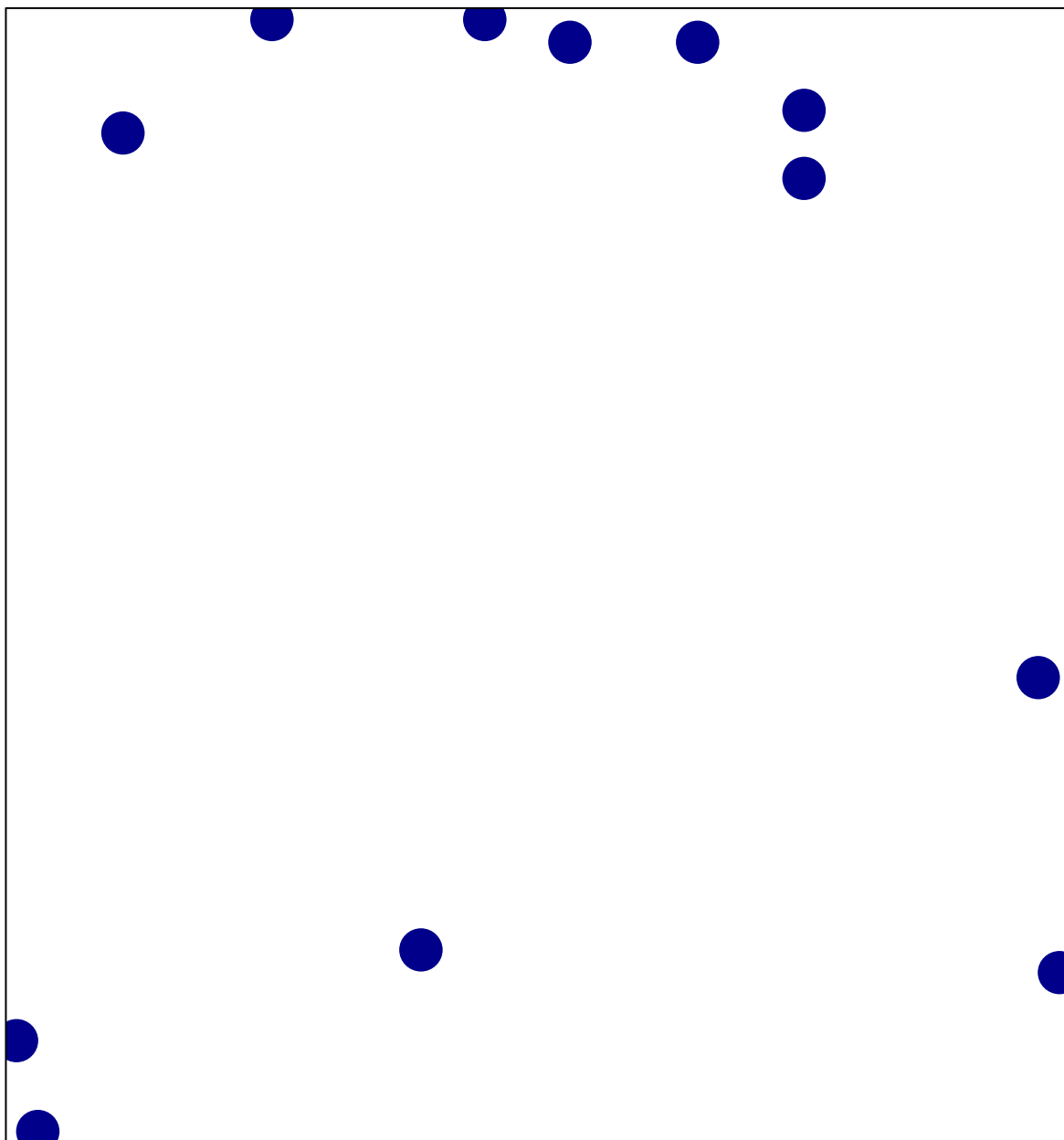
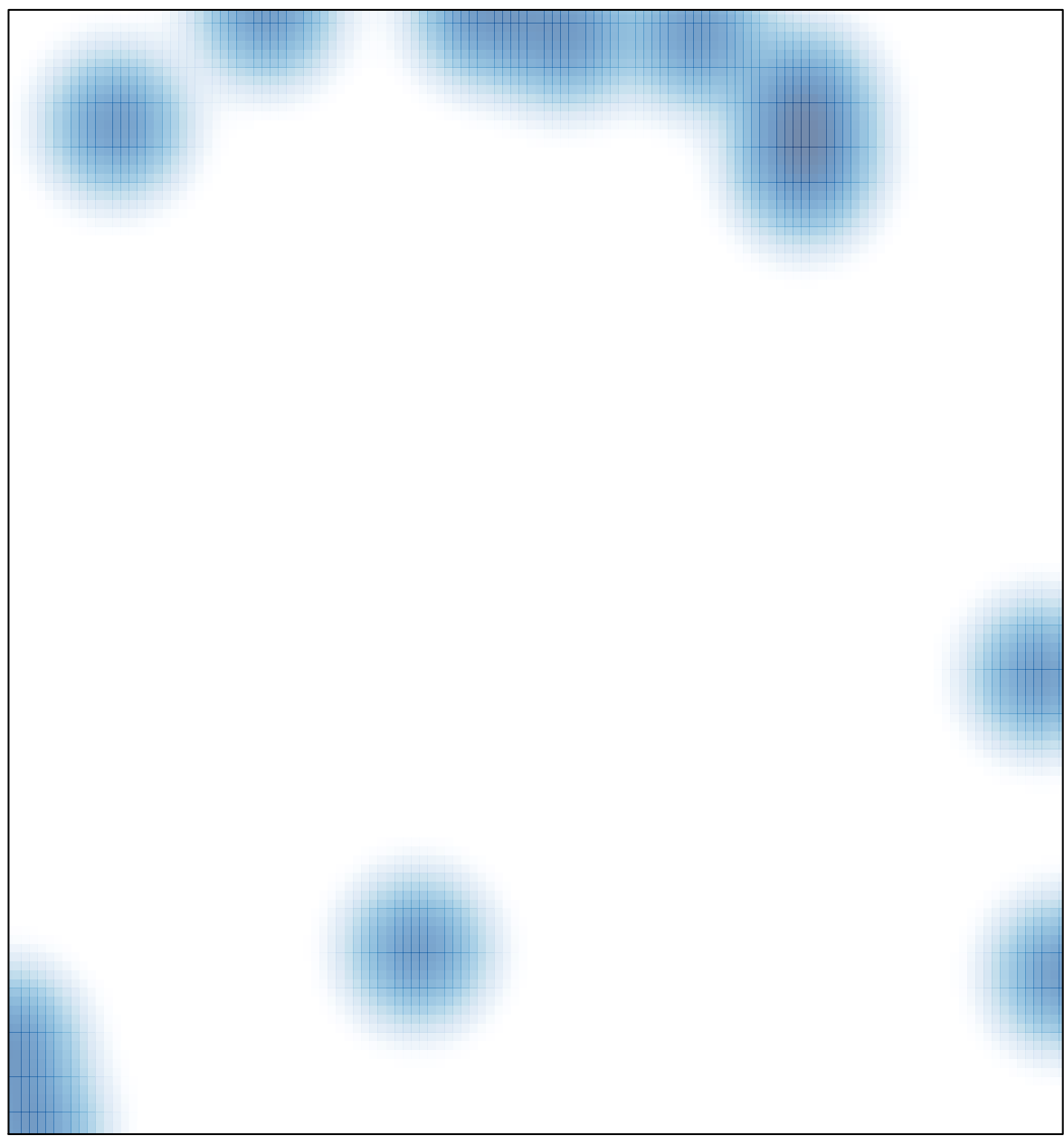


willscher_GBM_LTSwt_proteomics-C_UP



features = 12
chi-square p = 0.84

willscher_GBM_LTSwt_proteomics-C_UP



features = 12 , max = 1