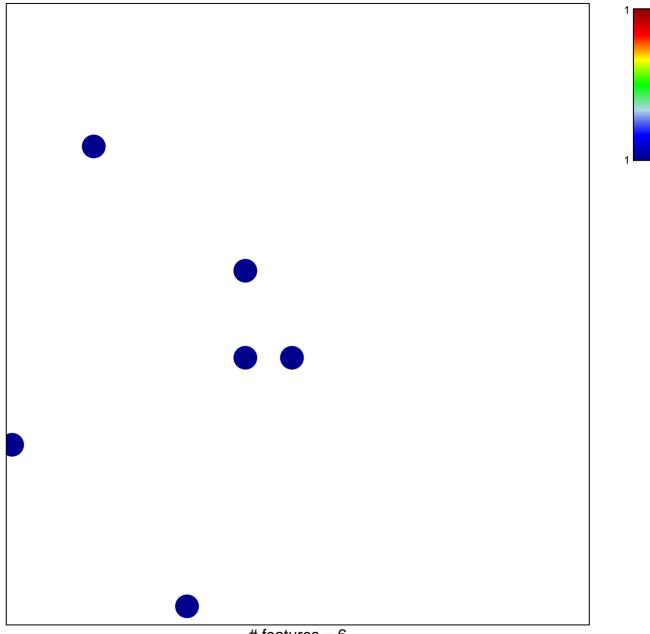
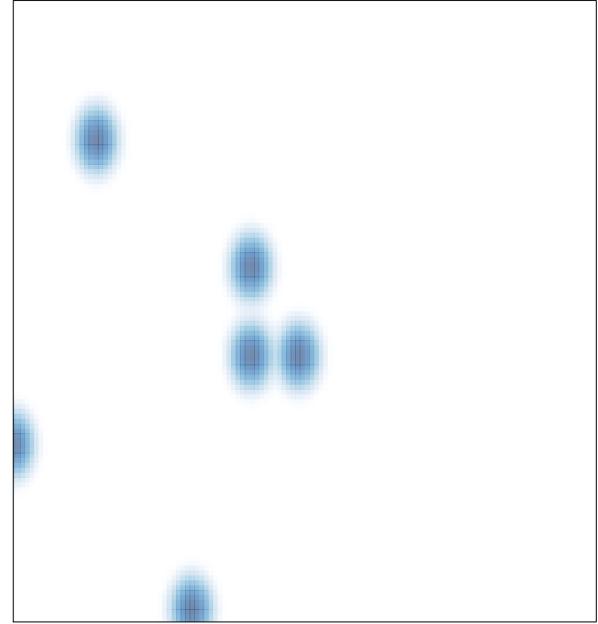
## **REACTOME\_CLASS\_A1\_RHODOPSIN\_LIKE\_RECEPTORS**



# features = 6 chi-square p = 0.83

## EACTOME\_CLASS\_A1\_RHODOPSIN\_LIKE\_RECEPTO



# features = 6, max = 1