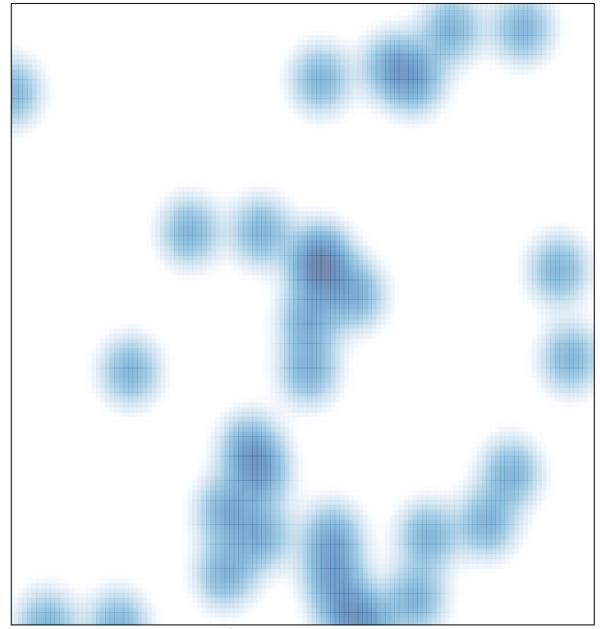


## Christensen\_hypomethylated\_in\_secondary\_glioblastoma

## ristensen\_hypomethylated\_in\_secondary\_glioblasto



# features = 37, max = 2