

ot_detected-with_ChIP_rna_cutoff_proximal.inactive.accUp.H3K27me3_GO_BP



differentiation cell involved process tubule metanephric formation
development morphogenesis regulation

Similarity
0.8
0.6
0.4
0.2
0

compound positive cellular macromolecule transcription rna
process regulation biosynthetic metabolic

cohesion division segregation chromosome maintenance
regulation positive sister chromatid mitotic

glucose peroxide hydrogen
response cellular acid stimulus retinoic hexose monosaccharide