

```
ego_cc <- enrichGO(gene = gene, OrgDb = org.Hs.eg.db, ont = "CC", pAdjustMethods = "BH", minGSSize  
= 1, pvalueCutoff = 0.01, qvalueCutoff = 0.01, readable = TRUE) write.table(as.data.frame(ego_CC@result),  
file = "test_CC.txt") barplot(ego_CC, showCategory = 15, title="EnrichmentGO_CC") dotplot(ego_Bp,  
title = "EnrichmentGO_CC_dot")
```