**OrgDb**

|  |
| --- |
| **idmap** |
| Entrez  genename  map  ensembl  symbol  alias |

|  |
| --- |
| **accesion** |
| entrez  accnum  refseq |

|  |
| --- |
| **ensenbltrans** |
| Entrez  unigene  ensenbltrans |

|  |
| --- |
| ***pmid*** |
| *Entrez*  *omim*  *pmid* |

|  |
| --- |
| ***protein*** |
| *entrez*  *enzyme*  *ensemblprot*  *uniprot* |

|  |
| --- |
| **ipi** |
| entrez  ipi  pfam  prosite |

|  |
| --- |
| **view\_go** |
| entrez  go  evidence  ontology |

|  |
| --- |
| **view\_goall** |
| entrez  goall  evidenceall  ontologyall |

**TxDb**

|  |
| --- |
| **txdb** |
| entrez  txid  txname  txtype  txchrom  txstrand  txstart  txend  exonid  exonname  exonchrom  exonstrand  exonstart  exonend  exonrank  cdsid  cdsname  cdschrom  cdsstrand  cdsstart  cdsend |

org = "org.Hs.eg.db"

txdb = "TxDb.Hsapiens.UCSC.hg38.knownGene"

idmap = tbl\_org\_idmap(org)

transcript = tbl\_txdb(txdb)

system.time(inner\_join(idmap, transcript, copy = TRUE) %>%

filter(symbol == "PTEN") %>%

dplyr::select(entrez, symbol, txid, txname, txstart, txend))

system.time(inner\_join(transcript, idmap, copy = TRUE) %>%

filter(symbol == "PTEN") %>%

dplyr::select(entrez, symbol, txid, txname, txstart, txend))

entrez <- idmap %>% filter(symbol == "PTEN") %>% dplyr::select(entrez, symbol)

system.time(inner\_join(transcript, entrez, copy = TRUE) %>%

filter(symbol == "PTEN") %>%

dplyr::select(entrez, symbol, txid, txname, txstart, txend))