

```

data<-read_excel(pgfile1,sheet=pgsheet1)
c1<-which(colnames(data)== "CAS_Number")
c2<-which(colnames(data)== "Carcinogen?")
c3<-which(colnames(data)== "NIOSH Skin notation?")
c4<-which(colnames(data)== "OSHA Skin notation?")
c5<-which(colnames(data)== "TWA REL Units")
c6<-which(colnames(data)== "TWA PEL Units")
c7<-which(colnames(data)== "REL Ceiling Value")
c8<-which(colnames(data)== "PEL Ceiling value")
c9<-which(colnames(data)== "REL Short term exposure Limit Value")
c10<-which(colnames(data)== "PEL Excursion limit Value")
c11<-which(colnames(data)== "PEL Short term exposure limit Value")
data1<-cbind(data[,c(c1,c2,c3,c4,c5,c6,c7,c8,c9,c10,c11)])
colnames(data1)=c("CAS","Carc","Nnot","Onot","Runits","Punits","Rceil","P
ceil","Rexp","Pexc","Pexp")

```

```

all1<-left_join(filter(tlist,!is.na(tlist$CAS)),data1,by="CAS")

```

```

all2<-filter(tlist,is.na(tlist$CAS))

```

```

all<-bind_rows(all1,all2)

```

```

for(i in 1:nrow(all)){

```

```

  if(!is.na(all$Carc[i])){

```

```

    if(all$Carc[i]=="Ca"){

```

```

      all$human[i]<-all$human[i]+1

```

```

      all$qual[i]<-all$qual[i]+1

```

```

      all$h_carc[i]<-all$h_carc[i]+1

```

```

      all$ql_carc[i]<-all$ql_carc[i]+1}

```

```

    if(all$Nn[i]=="[skin]") {

```

```

      all$tox[i]<-all$tox[i]+1

```

```

      all$t_habs[i]<-all$t_habs[i]+1}

```

```

    if(all$Onot[i]=="[skin]") {

```

```

      all$tox[i]<-all$tox[i]+1

```

```

      all$t_habs[i]<-all$t_habs[i]+1}

```

```

    if(all$Runits[i] != 'NA'){

```

```

      all$human[i]<-all$human[i]+1

```

```

      all$h_syst[i]<-all$h_syst[i]+1

```

```

      all$quan[i]<-all$quan[i]+1

```

```

      all$qn_syst[i]<-all$qn_syst[i]+1}

```

```

    if(all$Punits[i] != 'NA'){

```

```

      all$human[i]<-all$human[i]+1

```

```

      all$h_syst[i]<-all$h_syst[i]+1

```

```

      all$quan[i]<-all$quan[i]+1

```

```

      all$qn_syst[i]<-all$qn_syst[i]+1}

```

```

    if(all$Rceil[i] != 'NA'){

```

```

      all$human[i]<-all$human[i]+1

```

```

      all$h_acute[i]<-all$h_acute[i]+1

```

```

      all$quan[i]<-all$quan[i]+1

```

```

      all$qn_acute[i]<-all$qn_acute[i]+1}

```

```

    if(all$Pceil[i] != 'NA'){

```

```

      all$human[i]<-all$human[i]+1

```

```

      all$h_acute[i]<-all$h_acute[i]+1

```

```

      all$quan[i]<-all$quan[i]+1

```

```

      all$qn_acute[i]<-all$qn_acute[i]+1}

```

```

    if(all$Rexp[i] != 'NA'){

```

```

      all$human[i]<-all$human[i]+1

```

```

    all$h_acute[i]<-all$h_acute[i]+1
    all$quan[i]<-all$quan[i]+1
    all$qn_acute[i]<-all$qn_acute[i]+1}
if(all$Pexc[i] != 'NA'){
    all$human[i]<-all$human[i]+1
    all$h_acute[i]<-all$h_acute[i]+1
    all$quan[i]<-all$quan[i]+1
    all$qn_acute[i]<-all$qn_acute[i]+1}
if(all$Pexp[i] != 'NA'){
    all$human[i]<-all$human[i]+1
    all$h_acute[i]<-all$h_acute[i]+1
    all$quan[i]<-all$quan[i]+1
    all$qn_acute[i]<-all$qn_acute[i]+1}}}

all<-all[order(all$CID,all$CAS,na.last=FALSE),]

wb <- loadWorkbook(outfile)
writeData(wb, sheet = "PG", all[1:ncolt], colNames = F,startRow=3)
saveWorkbook(wb,outfile,overwrite = T)

```