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data<-read_excel(wdfile1,sheet=wdsheet1)
data[, 'an']<-ifelse(!is.na (data$Assay),1,0)
data[, 'a_r']<-ifelse(!is.na (data$Assay),1,0)
data[, 'a_n']<-ifelse(data$Assay %in% c("Cholinesterase", "DART,
Cholinesterase"),1,0)
data[, 'qn']<-ifelse(data$Endpoint=="LOEL",1,0)
data[, 'q_r']<-ifelse(!is.na (data$Assay) & data$Endpoint=="LOEL",1,0)
data[, 'q_n']<-ifelse(data$Assay %in% c("Cholinesterase", "DART,
Cholinesterase") & data$Endpoint=="LOEL",1,0)

na<- data %>% group_by(data$CASRN,data$reference) %>%

summarize(an=max(an),a_r=max(a_r),a_n=max(a_n),qn=max(qn),q_r=max(q_r),q_
n=max(q_n))
n2a<- na %>% group_by(na[,1]) %>%

summarize(an=sum(an),a_r=sum(a_r),a_n=sum(a_n),qn=sum(qn),q_r=sum(q_r),q_
n=sum(q_n))
colnames(n2a)<-c('CAS','an','a_r','a_n','qn','q_r','q_n')

nb<- data %>% group_by(data$'QSAR Ready ID',data$reference) %>%

summarize(an=max(an),a_r=max(a_r),a_n=max(a_n),qn=max(qn),q_r=max(q_r),q_
n=max(q_n))
n2b<- nb %>% group_by(nb[,1]) %>%

summarize(an=sum(an),a_r=sum(a_r),a_n=sum(a_n),qn=sum(qn),q_r=sum(q_r),q_
n=sum(q_n))
colnames(n2b)<-c('Inchikey','an','a_r','a_n','qn','q_r','q_n')

all1<-left_join(filter(tlist,!is.na(tlist$CAS)),n2a,by='CAS')
all2<-left_join(filter(tlist,is.na(tlist$CAS)),n2b,by='Inchikey')
all<-rbind(all1,all2)

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

for (i in 1:dim(all)[1]) {
  all$animal[i]<-all$an[i]
  all$a_neuro[i]<-all$a_n[i]
  all$a_repro[i]<-all$a_r[i]
  all$quan[i]<-all$qn[i]
  all$qn_neuro[i]<-all$q_n[i]
  all$qn_repro[i]<-all$q_r[i]}
all[,5:ncol][is.na(all[,5:ncol])] <- 0

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

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