```
plot.Chem.PK <-
function(this.CAS=NULL,this.name=NULL,predict=T,compartment="Cven",xlim=NULL,ylim=NULL,cex.lab
=1.5,cex=2,log="y",col.vec=c("blue","red","green","blueviolet","springgreen","navyblue","pink","teal"),pch.v
ec=c(19,15,17,21,22,24,25,23))
{
  if (is.null(this.CAS) & is.null(this.name))
  {
    cat("Must specifiy compound name or CAS.\n")
  } else if ((!is.null(this.CAS) & !any(chem.invivo.PK.data$CAS==this.CAS)) & (!is.null(this.name) &
!any(chem.invivo.PK.data$Compound==this.name)))
  {
    cat("Compound not found.\n")
  } else {
    if (!is.null(this.CAS))
    {
      this.chem.data <- subset(chem.invivo.PK.data,CAS==this.CAS)
      this.name <- this.chem.data[1,"Compound"]
    } else {
      this.chem.data <- subset(chem.invivo.PK.data,Compound==this.name)
      this.CAS <- this.chem.data[1,"CAS"]
    }
    chem.physical_and_invitro.data.index <- which(chem.physical_and_invitro.data$CAS==this.CAS)

    if (regexpr("x",log)!=-1) this.chem.data <- this.chem.data[this.chem.data[,"Time"]!=0,]
    if (regexpr("y",log)!=-1)  this.chem.data <- this.chem.data[this.chem.data[,"Value"]>0,]
    if (is.null(xlim)) xlim <- c(0,max(this.chem.data$Time))
    if (is.null(ylim)) ylim <- c(min(this.chem.data$Value)/30,max(this.chem.data$Value)*5)
    if (length(unique(this.chem.data[,"Time Units"]))>1) browser()
    time.units <- this.chem.data[1,"Time Units"]
    if (length(unique(this.chem.data[,"Media"]))>1) browser()
    media <- this.chem.data[1,"Media"]
    if (length(unique(this.chem.data[,"Media Units"]))>1) browser()
    media.units <- this.chem.data[1,"Media Units"]
    dose.units <- unique(this.chem.data[,"Dose Units and Type"])
    plot(-1,-
1,xlim=xlim,ylim=ylim,cex.lab=cex.lab,xlab=paste("Time",time.units),ylab=paste(media,media.units),main
=paste(this.name," (",this.CAS,")",sep=""),log=log)
    if (regexpr("x",log)!=-1)
    {
      legend.x1 <- exp(log(xlim[1])+(log(xlim[2])-log(xlim[1]))*0.7)
      legend.x2 <- exp(log(xlim[1])+(log(xlim[2])-log(xlim[1]))*0.72)
    } else {
      legend.x1 <- xlim[1]+(xlim[2]-xlim[1])*0.3
      legend.x2 <- xlim[1]+(xlim[2]-xlim[1])*0.32
    }
    if (regexpr("y",log)!=-1)  this.chem.data <- this.chem.data[this.chem.data[,"Value"]>0,]
    this.index <- 0
    AUCs <- list()
    Cmaxs <- list()
    AUCs.pred <- list()
    Cmaxs.pred <- list()
    for (this.study in unique(this.chem.data[,"Reference"]))
    {
      this.chem.species <- this.chem.data[this.chem.data[,"Reference"]==this.study,"Species"][1]
      this.chem.species <- gsub("^ .", "", this.chem.species)
      this.chem.species <- gsub(" $", "", this.chem.species)
```

```
    this.phys.species <- this.chem.species
    if (predict)
    {
      if (!(this.chem.species %in% colnames(chem.physical_and_invitro.data)))
      {
        if (toupper(this.chem.species) %in% toupper(colnames(chem.physical_and_invitro.data)))
        {
          new.species <-
colnames(chem.physical_and_invitro.data)[toupper(colnames(chem.physical_and_invitro.data))==toupper
(this.chem.species)]
          warning(paste(this.chem.species,"coerced to",new.species))
          this.chem.species <- new.species
        } else {
          warning(paste("Chemical specific data for",this.chem.species,"not found, using Human"))
          this.chem.species <- "Human"
        }
      }
      if (chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,this.chem.species]!="Y")
      {
        if (chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,"Human"]=="Y")
        {
          warning(paste("Chemical specific data for",this.chem.species,"incomplete, using Human"))
          this.chem.species <- "Human"
        } else {
          warning("Incomplete chemical specific data, predict=FALSE")
          predict <- FALSE
        }
      }
    }

    this.study.subset <- this.chem.data[this.chem.data[,"Reference"]==this.study,]
    for (this.dose.type in unique(this.study.subset[,"Dose Units and Type"]))
    {
      this.dose.subset <- this.study.subset[this.study.subset[,"Dose Units and Type"]==this.dose.type,]
      for (this.dose in unique(this.dose.subset[,"Dose"]))
      {
        this.index <- this.index + 1

matplot(this.dose.subset[this.dose.subset[,"Dose"]==this.dose,"Time"],this.dose.subset[this.dose.subset[,
"Dose"]==this.dose,"Value"],pch=pch.vec[this.index],col=col.vec[this.index],cex=cex,add=T)

        if (regexpr("y",log)!=-1) legend.y <- exp(log(ylim[1])+(log(ylim[2])-log(ylim[1]))*0.06*this.index)
        else legend.y <- ylim[1]+(ylim[2]-ylim[1])*0.06*this.index
        matplot(legend.x1,legend.y,pch=pch.vec[this.index],col=col.vec[this.index],cex=1.25*cex,add=T)
        text(legend.x2,legend.y,paste(this.dose," ",this.dose.type," ",this.phys.species,"
(",this.study,")",sep=""),cex=cex/1.5,pos=4)

        AUCs[[paste(this.dose," ",this.dose.type," ",this.phys.species," (",this.study,")",sep="")]] <-
calc.AUC(this.dose.subset[this.dose.subset[,"Dose"]==this.dose,c("Time","Value")])
        Cmaxs[[paste(this.dose," ",this.dose.type," ",this.phys.species," (",this.study,")",sep="")]] <-
max(this.dose.subset[this.dose.subset[,"Dose"]==this.dose,"Value"])

        if (predict)
        {
          this.weight <- this.chem.data[this.chem.data[,"Reference"]==this.study,"Species Weight"][1]
          PBPK.params <-
```

```
Parameterize_vLiverPBPK(chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,"MW"],

chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,paste(this.chem.species,"Clint",se
p=".")],

chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,paste(this.chem.species,"Fub",sep
=".")],
                        chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,"pKa"],
                        chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,"logP"],
                        species=this.phys.species,
                        BW=this.weight)

        if (regexpr("mg/kg",this.dose.type)!=-1)
dose.units.convert=1/chem.physical_and_invitro.data[chem.physical_and_invitro.data.index,"MW"]/1000
        else browser()
        if (regexpr("iv",this.dose.type)!=-1 | regexpr("sc",this.dose.type)!=-1)
        {
          dose.times <- 0
          params <-
c(PBPK.params,list(ivdose=this.dose*dose.units.convert,DietInput=matrix(c(0,0),ncol=2)))
        } else {
          dose.times <- 0
          params <-
c(PBPK.params,list(DietInput=matrix(c(0,24,48,this.dose*dose.units.convert,0,0),ncol=2)))

        }
        out <- vliver_pbpk(seq(xlim[1],xlim[2],0.1),params)$result
        matplot(out[,"time"],out[,compartment]/dose.units.convert,type="l",col=col.vec[this.index],add=T)
        AUCs.pred[[paste(this.dose," ",this.dose.type," ",this.phys.species," (",this.study,")",sep="")]] <-
calc.AUC(out[,c("time",compartment)])/dose.units.convert
        Cmaxs.pred[[paste(this.dose," ",this.dose.type," ",this.phys.species," (",this.study,")",sep="")]] <-
max(out[,compartment])/dose.units.convert
      }
    }
  }
}

return(list(chem.data=this.chem.data,AUCs=AUCs,Cmaxs=Cmaxs,AUCs.pred=AUCs.pred,Cmaxs.pred=
Cmaxs.pred))
 }
}
```