```
calc_vLiver_Css <- function(chem.name=NULL,
                            chem.CAS=NULL,
                            daily.dose=1,
                            which.quantile=0.95,
                            species="Human",
                            clearance.assay.conc=NULL,
                            units="mgperL",
                            censored.params=list(fub=list(sd=0.2,lod=0.01)),

vary.params=list(BW=0.2,liver.volume.per.kgBW=0.2,QGFRc=0.2,Qhc=0.2,million.cells.per.gliver=0.2,CLi
nt=0.2),
                            doses.per.day=NULL,days=100,timepoints=1000)
{
  if (is.null(chem.CAS) & is.null(chem.name))
  {
    stop("Must specifiy compound name or CAS.\n")
  } else if ((!is.null(chem.CAS) & !any(chem.physical_and_invitro.data[,"CAS"]==chem.CAS)) &
(!is.null(chem.name) & !any(chem.physical_and_invitro.data[,"Compound"]==chem.name)))
  {
    stop("Compound not found.\n")
  } else {
    if (!is.null(chem.CAS)) chem.name <-
chem.physical_and_invitro.data[chem.physical_and_invitro.data[,"CAS"]==chem.CAS,"Compound"][1]
    else chem.CAS <-
chem.physical_and_invitro.data[chem.physical_and_invitro.data[,"Compound"]==chem.name,"CAS"][1]
    these.params <- parameterize_SteadyState(chem.CAS,species=species)
    MW <- get_param("MW",these.params,"calc_vLiver_Css")
    if (units == "mgperL") out.units.convert <- MW/1000
    else browser()

return(out.units.convert*UVPKM("calc_Css",these.params,censored.params=censored.params,which.qua
ntile=which.quantile,doses.per.day=doses.per.day,days=days,timepoints=timepoints))
  }
}
```