

# Physiologically based pharmacokinetic model

## ODE system : Time varying state

```
// Concentrations in the tissues and in the capillary blood of the tissues
double CA_free = APlas_free/VPlas; // mg/L, Free PFOSC concentration in the plasma
double CA = CA_free/Free; // mg/L, Concentration of total PFOS in plasma

double CL = AL/VL; // mg/L, Concentration of parent drug in the tissue of liver
double CVL = CL/PL; // mg/L, Concentration of parent drug in the capillary blood of liver

double CKb = AKb/VKb; // mg/L, Concentration of PFOS in Kidney blood
double CVK = CKb/PK; // mg/L, Concentration of PFOS in Kidney compartment
double CK = CVK*PK;

double CRest = ARest/VRest; // mg/L, Crest drug concentration in the rest of the body (mg/L)
double CVRest = CRest/PRest; // mg/L, Concentration of parent drug in the capillary blood of the rest of body

// Kidney compartment plus 2 subcompartment (Proximal Tubule cells: PTC, Filtrate: Fil)
// Concentration in kidney, PTC and fil

double CPTC = APTC/VPTC; // mg/L, Concentration of PFOS in PTC blood
double Cfil = AFil/Vfil; // mg/L, Concentration of PFOS in FIL blood

// Virtual compartment:
// Basolateral transport : (baso)
// Diffusion : (dif)
// Apical transport : (apical)
// efflux clearance : (efflux)
// Clearance via glomerular filtration (CL)

double RA_baso = (Vmax_baso*CKb)/(Km_baso+CKb); // mg/h, Rate of basolateral transporters
dxdt_A_baso = RA_baso; // mg, Amount of basolateral transporters
double RA_apical = (Vmax_apical*Cfil)/(Km_apical + Cfil); // mg/h, Rate of apical transporter
dxdt_A_apical = RA_apical; // mg, Amount of apical transporter
double Rdif = Kdif*(CKb - CPTC); // mg/h, Rate of diffusion from into the PTC
dxdt_Adif = Rdif; // mg, Amount moved via glomarular filtration
double RAefflux = Kefflux*APTC; // mg/h, Rate of efflux clearance rate from PTC to blood
dxdt_Aefflux = RAefflux; // mg, Amount of efflux clearance rate from PTC to blood
double RCI = CA*GFR*Free; // mg/h, Rate of clearance (CL) to via glomerular filtration (GFR)
dxdt_ACI = RCI; // mg, Amount of clearance via GFR
```

```
// PFOS in plasma
double RPlas_free = (QRest*CVRest*Free)+(QK*CVK*Free)+(QL*CVL*Free)-(QC*CA*Free)+RAefflux; // mg/h, Rate of change in the plasma
double RPlas = (QRest*CVRest)+(QK*CVK)+(QL*CVL)-(QC*CA);
dxdt_APlas_free = RPlas_free; // mg, Amount in the plasma
dxdt_APlas = RPlas; // mg, Amount in the plasma
dxdt_AUCCA_free = CA_free; // mg*h/L, Area under curve of PFOS in liver compartment

// Proximal Tubule Cells (PTC)
double RPTC = Rdif + RA_apical + RA_baso - RAefflux; // mg/h, Rate of change in PTC
dxdt_APTC = RPTC; // mg, Amount moved in PTC
dxdt_AUCCPTC = CPTC; // mg*h/L, Area under curve of PFOS in the compartment of PTC

// Proximal Tubule Lumen/ Filtrate (Fil)
double Rfil = CA*GFR*Free - RA_apical - AFil*Kurine; // mg/h, Rate of change in Fil
dxdt_AFil = Rfil; // mg, Amount moved in Fil
dxdt_AUCfil = Cfil; // mg*h/L, Area under curve of PFOS in the compartment of Fil

// Urine elimination
double Rurine = Kurine*AFil; // mg/h, Rate of change in urine
dxdt_Aurine = Rurine; // mg, Amount in urine
double Curine = Rurine/Kvoid; //

// Kidney compartment
double RKb = QK*(CA-CVK)*Free - CA*GFR*Free - Rdif - RA_baso; // mg/h, Rate of change in Kidney compartment
dxdt_AKb = RKb; // mg, Amount in kidney compartment
dxdt_AUCKb = CK; // mg*h/L, Area under curve of PFOS in the Kidney compartment
```

```
// PFOS in the compartment of rest of body, flow-limited model
double RRest = QRest*(CA-CVRest)*Free; // mg/h, Rate of change in rest of body
dxdt_ARest = RRest; // mg, Amount in rest of body
dxdt_AUCCRest = CRest; // mg*h/L, Area under curve of PFOS in the compartment of rest of body
```

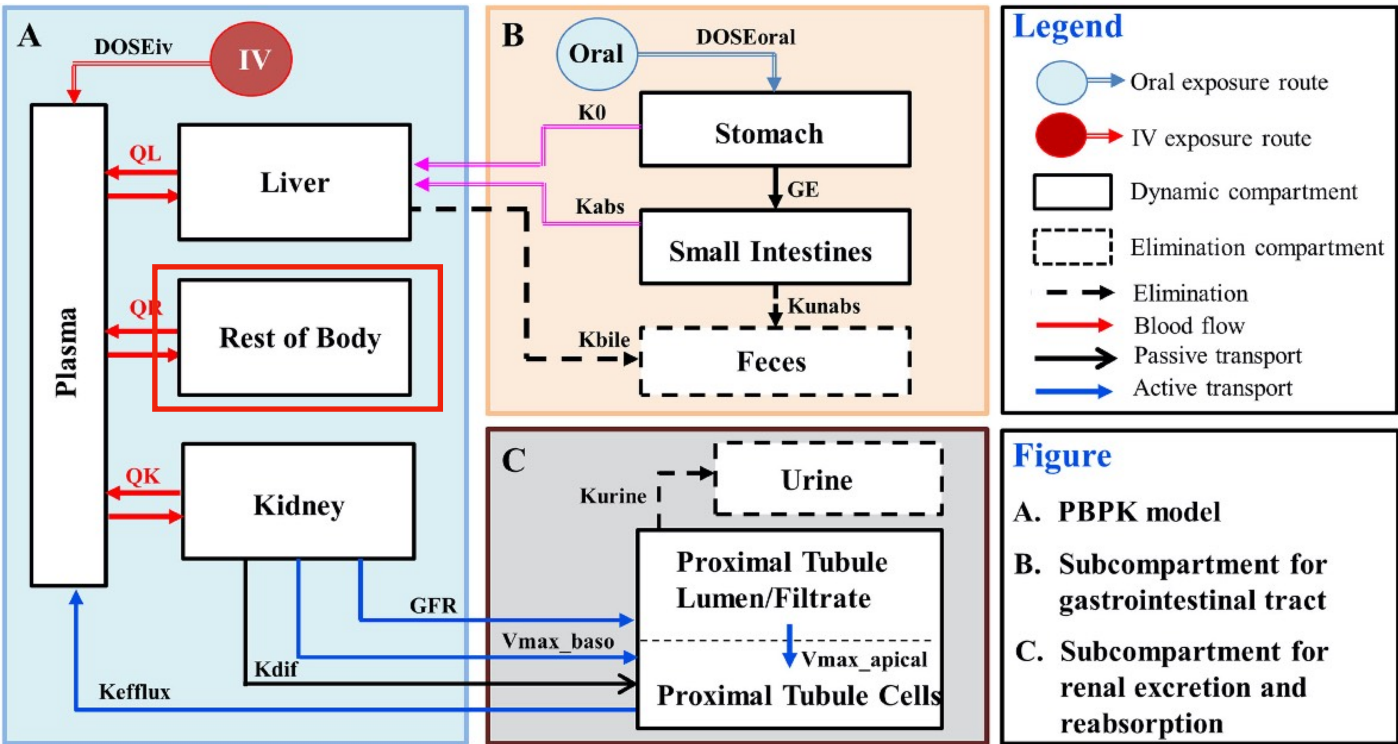
```
// Gastrointestinal (GI) tract
// Stomach compartment
double RST = - K0*AST - GE*AST; // mg/h, Rate of chagne in Stomach compartment
dxdt_AST = RST; // mg, Amount in Stomach
double RabstST = K0*AST; // mg/h, Rate of absorption in the stomach
dxdt_AabsST = RabstST; // mg, Amount absorbed in the stomach
```

```
// Small intestine compartment
double RSI = GE*AST - Kabs*ASI - Kunabs*ASI; // mg/h, Rate of chagne in Small intestine compartment
dxdt_ASI = RSI; // mg, Amount in Small intestine
double RabstSI = Kabs*ASI; // mg/h, Rate of absorption in the Small intestine
dxdt_AabsSI = RabstSI; // mg, Amount absorbed in the Small intestine
double Total_oral_uptake = AabsSI + AabsST; // mg, Total oral uptake in the GI
```

```
// Biliary excretion
double Abile = Kbile*AL; // mg, Amount of PFOS in bile excretion
double amount_per_gram_liver = (AL/ML)*1000; // ug/g, Amount of PFOS in liver per gram liver

// Feces compartment
double Rfeces = Kbile*AL+ Kunabs*ASI; // mg/h, Rate of change in feces compartment
dxdt_Afeces = Rfeces; // mg, Amount of the feces compartment
```

```
// PFOS in liver compartment, flow-limited model
double RL = QL*(CA-CVL)*Free - Kbile*AL + Kabs*ASI + K0*AST; // mg/h, Rate of chagne in liver compartment
dxdt_AL = RL; // mg, Amount in liver compartment
dxdt_AUCCCL = CL; // mg*h/L, Area under curve of PFOS in liver compartment
```



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double CKb = AKb/VKb; // mg/L, Concentration of PFOS in Kidney blood
double CVK = CKb/PK; // mg/L, Concentration of PFOS in Kidney compartment
double CK = CVK*PK;

double CRest = ARest/VRest; // mg/L, Crest drug concentration in the rest of the body (mg/L)
double CVRest = CRest/PRest; // mg/L, Concentration of parent drug in the capillary blood of the rest of body

// Kidney compartment plus 2 subcompartment (Proximal Tubule cells: PTC, Filtrate: Fil)
// Concentration in kidney, PTC and fil

double CPTC = APTC/VPTC; // mg/L, Concentration of PFOS in PTC blood
double Cfil = AFil/Vfil; // mg/L, Concentration of PFOS in FIL blood

// Virtual compartment:
// Basolateral transport : (baso)
// Diffusion : (dif)
// Apical transport : (apical)
// efflux clearance : (efflux)
// Clearance via glomerular filtration (CL)

double RA_baso = (Vmax_baso*CKb)/(Km_baso+CKb); // mg/h, Rate of basolateral transporters
dxdt_A_baso = RA_baso; // mg, Amount of basolateral transporters
double RA_apical = (Vmax_apical*Cfil)/(Km_apical + Cfil); // mg/h, Rate of apical transporter
dxdt_A_apical = RA_apical; // mg, Amount of apical transporter
double Rdif = Kdif*(CKb - CPTC); // mg/h, Rate of diffusion from into the PTC
dxdt_Adif = Rdif; // mg, Amount moved via glomarular filtration
double RAefflux = Kefflux*APTC; // mg/h, Rate of efflux clearance rate from PTC to blood
dxdt_Aefflux = RAefflux; // mg, Amount of efflux clearance rate from PTC to blood
double RCI = CA*GFR*Free; // mg/h, Rate of clearance (CL) to via glomerular filtration (GFR)
dxdt_ACI = RCI; // mg, Amount of clearance via GFR
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// PFOS in plasma
double RPlas_free = (QRest*CVRest*Free)+(QK*CVK*Free)+(QL*CVL*Free)-(QC*CA*Free)+RAefflux; // mg/h, Rate of change in the plasma
double RPlas = (QRest*CVRest)+(QK*CVK)+(QL*CVL)-(QC*CA);
dxdt_APlas_free = RPlas_free; // mg, Amount in the plasma
dxdt_APlas = RPlas; // mg, Amount in the plasma
dxdt_AUCCA_free = CA_free; // mg*h/L, Area under curve of PFOS in liver compartment

// Proximal Tubule Cells (PTC)
double RPTC = Rdif + RA_apical + RA_baso - RAefflux; // mg/h, Rate of change in PTC
dxdt_APTC = RPTC; // mg, Amount moved in PTC
dxdt_AUCCPTC = CPTC; // mg*h/L, Area under curve of PFOS in the compartment of PTC

// Proximal Tubule Lumen/ Filtrate (Fil)
double Rfil = CA*GFR*Free - RA_apical - AFil*Kurine; // mg/h, Rate of change in Fil
dxdt_AFil = Rfil; // mg, Amount moved in Fil
dxdt_AUCfil = Cfil; // mg*h/L, Area under curve of PFOS in the compartment of Fil

// Urine elimination
double Rurine = Kurine*AFil; // mg/h, Rate of change in urine
dxdt_Aurine = Rurine; // mg, Amount in urine
double Curine = Rurine/Kvoid; //

// Kidney compartment
double RKb = QK*(CA-CVK)*Free - CA*GFR*Free - Rdif - RA_baso; // mg/h, Rate of change in Kidney compartment
dxdt_AKb = RKb; // mg, Amount in kidney compartment
dxdt_AUCKb = CK; // mg*h/L, Area under curve of PFOS in the Kidney compartment

// PFOS in the compartment of rest of body, flow-limited model
double RRest = QRest*(CA-CVRest)*Free; // mg/h, Rate of change in rest of body
dxdt_ARest = RRest; // mg, Amount in rest of body
dxdt_AUCCRest = CRest; // mg*h/L, Area under curve of PFOS in the compartment of rest of body
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```
// Gastrointestinal (GI) tract
// Stomach compartment
double RST = - K0*AST - GE*AST; // mg/h, Rate of chagne in Stomach compartment
dxdt_AST = RST; // mg, Amount in Stomach
double RabsST = K0*AST; // mg/h, Rate of absorption in the stomach
dxdt_AabsST = RabsST; // mg, Amount absorbed in the stomach
```

```
// Small intestine compartment
double RSI = GE*AST - Kabs*ASI - Kunabs*ASI; // mg/h, Rate of chagne in Small intestine compartment
dxdt_ASI = RSI; // mg, Amount in Small intestine
double RabsSI = Kabs*ASI; // mg/h, Rate of absorption in the Small intestine
dxdt_AabsSI = RabsSI; // mg, Amount absorbed in the Small intestine
double Total_oral_uptake = AabsSI + AabsST; // mg, Total oral uptake in the GI

// Biliary excretion
double Abile = Kbile*AL; // mg, Amount of PFOS in bile excretion
double amount_per_gram_liver = (AL/ML)*1000; // ug/g, Amount of PFOS in liver per gram liver

// Feces compartment
double Rfeces = Kbile*AL+ Kunabs*ASI; // mg/h, Rate of change in feces compartment
dxdt_Afeces = Rfeces; // mg, Amount of the feces compartment
```

```
// PFOS in liver compartment, flow-limited model
double RL = QL*(CA-CVL)*Free - Kbile*AL + Kabs*ASI + K0*AST; // mg/h, Rate of chagne in liver compartment
dxdt_AL = RL; // mg, Amount in liver compartment
dxdt_AUCCL = CL; // mg*h/L, Area under curve of PFOS in liver compartment
```

