

PBPK Model equations

The following equations describe the transport of labeled (indexed with *) and unlabeled peptide via blood flow, extravasation, binding, internalization, degradation and release, excretion and radioactive decay. The peptide was injected as a 51 ± 8 min infusion for pre-therapeutic measurements.

Compared to the recently published model (1), more organs (including the red marrow) are explicitly, i.e. closer to physiological reality, modelled. A less empirical and more physiological model usually allows more accurate extrapolation from different condition (here different peptide amounts) and can be easier adapted for other peptides. The variables are defined in Table A.

Bound and internalized peptide:

Liver, spleen, tumor, kidney, red marrow (RM), GI, muscle, prostate/uterus, adrenals and rest.

Constraint for total sst2 receptors $R_{0,i}$

$$R_{0,i} = R_i + RP_i + RP_i^* \quad (1)$$

Internalized peptide

$$\begin{aligned} \frac{d}{dt} P_{\text{intern } i} &= \lambda_{\text{int},i} \cdot RP_i - \lambda_{\text{release},i} \cdot P_{\text{intern } i} + \lambda_{\text{phy}} \cdot P_{\text{intern } i}^* \\ \frac{d}{dt} P_{\text{intern } i}^* &= \lambda_{\text{int},i} \cdot RP_i^* - \lambda_{\text{release},i} \cdot P_{\text{intern } i}^* - \lambda_{\text{phy}} \cdot P_{\text{intern } i}^* \end{aligned} \quad (2)$$

Bound peptide on cell surface

$$\begin{aligned}
\frac{d}{dt} RP_i &= k_{on} \cdot P_{i,int} \cdot \frac{R_i}{V_{i,int}} - (k_{off} + \lambda_{int,i}) \cdot RP_i + \lambda_{phy} \cdot RP_i^* \\
\frac{d}{dt} RP_i^* &= k_{on} \cdot P_{i,int}^* \cdot \frac{R_i}{V_{i,int}} - (k_{off} + \lambda_{int,i}) \cdot RP_i^* - \lambda_{phy} \cdot RP_i^*
\end{aligned}
\tag{3}$$

Free peptide, vascular:

Transcapillary extravasation is described by the permeability surface area product (PS_i) and the vascular ($V_{i,v}$) and interstitial volumes ($V_{i,int}$) of the pertaining tissue. Convection from the vascular to the interstitial space is neglected as ^{90}Y -DOTATATE represents a rather small molecule (2).

All tissues except kidneys and lungs

$$\begin{aligned}
\frac{d}{dt} P_{i,v} &= PS_i \left(\frac{P_{i,int}}{V_{i,int}} - \frac{P_{i,v}}{V_{i,v}} \right) + F_i \left(\frac{P_{ART}}{V_{ART}} - \frac{P_{i,v}}{V_{i,v}} \right) + \lambda_{phy} \cdot P_{i,v}^* \\
\frac{d}{dt} P_{i,v}^* &= PS_i \left(\frac{P_{i,int}^*}{V_{i,int}} - \frac{P_{i,v}^*}{V_{i,v}} \right) + F_i \left(\frac{P_{ART}^*}{V_{ART}} - \frac{P_{i,v}^*}{V_{i,v}} \right) - \lambda_{phy} \cdot P_{i,v}^*
\end{aligned}
\tag{4}$$

For brain $PS = 0$

Lungs

$$\begin{aligned}
\frac{d}{dt} P_{LU,v} &= PS_{LU} \left(\frac{P_{LU,int}}{V_{LU,int}} - \frac{P_{LU,v}}{V_{LU,v}} \right) + F \left(\frac{P_{VEN}}{V_{VEN}} - \frac{P_{LU,v}}{V_{LU,v}} \right) + \lambda_{phy} \cdot P_{LU,v}^* \\
\frac{d}{dt} P_{LU,v}^* &= PS_{LU} \left(\frac{P_{LU,int}^*}{V_{LU,int}} - \frac{P_{LU,v}^*}{V_{LU,v}} \right) + F \left(\frac{P_{VEN}}{V_{VEN}} - \frac{P_{LU,v}^*}{V_{LU,v}} \right) - \lambda_{phy} \cdot P_{LU,v}^*
\end{aligned}
\tag{5}$$

Kidneys

$$\begin{aligned}
\frac{d}{dt} P_{K,v} &= -\frac{P_{K,v}}{V_{K,v}} \cdot (F_{fil} + F_K) + \frac{F_K}{V_{ART}} \cdot P_{ART} + \frac{P_{intra,K}}{V_{intra,K}} \cdot (F_{fil} - F_{ex}) + \lambda_{phy} \cdot P_{K,v} \\
\frac{d}{dt} P_{K,v}^* &= -\frac{P_{K,v}^*}{V_{K,v}} \cdot (F_{fil} + F_K) + \frac{F_K}{V_{ART}} \cdot P_{ART}^* + \frac{P_{intra,K}^*}{V_{intra,K}} \cdot (F_{fil} - F_{ex}) - \lambda_{phy} \cdot P_{K,v}^*
\end{aligned} \tag{6}$$

Veins

$$\begin{aligned}
\frac{d}{dt} P_{VEN} &= -k_{Pr} \cdot P_{VEN} + \sum \frac{F_i}{V_i} P_{i,v} - \frac{F_M}{V_M} P_{M,v} - \frac{F_{GL}}{V_{GL}} P_{GL,v} + \frac{F_M + F_{GL}}{V_L} P_{L,v} + \lambda_{phy} \cdot P_{VEN} \\
\frac{d}{dt} P_{VEN}^* &= -k_{Pr} \cdot P_{VEN}^* + \sum \frac{F_i}{V_i} P_{i,v}^* - \frac{F_M}{V_M} P_{M,v}^* - \frac{F_{GL}}{V_{GL}} P_{GL,v}^* + \frac{F_M + F_{GL}}{V_L} P_{L,v}^* - \lambda_{phy} \cdot P_{VEN}^*
\end{aligned} \tag{7}$$

Arteries

$$\begin{aligned}
\frac{d}{dt} P_{ART} &= -\sum \frac{F_i}{V_{ART}} \cdot P_{i,v} + \frac{F}{V_{LU,v}} \cdot P_{LU,v} + \lambda_{phy} \cdot P_{ART} \\
\frac{d}{dt} P_{ART}^* &= -\sum \frac{F_i}{V_{ART}} \cdot P_{i,v}^* + \frac{F}{V_{LU,v}} \cdot P_{LU,v} - \lambda_{phy} \cdot P_{ART}^*
\end{aligned} \tag{8}$$

Free peptide, interstitial spaces:

Kidneys:

$$\begin{aligned}
\frac{d}{dt} P_{K,int} &= -k_{on} \cdot P_{K,int} \cdot \frac{R_K}{V_{K,int}} + k_{off} \cdot RP_K + F_{fil} \left(\frac{P_{K,v}}{V_{K,v}} - \frac{P_{K,int}}{V_{K,int}} \right) + \lambda_{phy} \cdot P_{K,int} \\
\frac{d}{dt} P_{K,int}^* &= -k_{on} \cdot P_{K,int}^* \cdot \frac{R_K}{V_{K,int}} + k_{off} \cdot RP_K^* + F_{fil} \left(\frac{P_{K,v}^*}{V_{K,v}} - \frac{P_{K,int}^*}{V_{K,int}} \right) - \lambda_{phy} \cdot P_{K,int}^*
\end{aligned} \tag{9}$$

Skin, adipose tissue, heart, bone, lungs and brain (PS = 0):

$$\begin{aligned}\frac{d}{dt} P_{i,int} &= PS_i \left(\frac{P_{i,v}}{V_{i,v}} - \frac{P_{i,int}}{V_{i,int}} \right) + \lambda_{phy} \cdot P_{i,int}^* \\ \frac{d}{dt} P_{i,int}^* &= PS_i \left(\frac{P_{i,v}^*}{V_{i,v}} - \frac{P_{i,int}^*}{V_{i,int}} \right) - \lambda_{phy} \cdot P_{i,int}^*\end{aligned}\tag{10}$$

Liver, spleen, tumor, RM, GI, muscle, prostate/uterus, adrenals, rest:

$$\begin{aligned}\frac{d}{dt} P_{i,int} &= -k_{on} \cdot P_{i,int} \cdot \frac{R_i}{V_{i,int}} + k_{off} \cdot RP_i + PS_i \left(\frac{P_{i,v}}{V_{i,v}} - \frac{P_{i,int}}{V_{i,int}} \right) + \lambda_{phy} \cdot P_{i,int}^* \\ \frac{d}{dt} P_{i,int}^* &= -k_{on} \cdot P_{i,int}^* \cdot \frac{R_i}{V_{i,int}} + k_{off} \cdot RP_i^* + PS_i \left(\frac{P_{i,v}^*}{V_{i,v}} - \frac{P_{i,int}^*}{V_{i,int}} \right) - \lambda_{phy} \cdot P_{i,int}^*\end{aligned}\tag{11}$$

Further equations:

Peptide in kidney cells (unspecific)

$$\begin{aligned}\frac{d}{dt} P_{intra,K} &= \frac{P_{int,K}}{V_{int,K}} \cdot (F_{fil} - F_{ex}) - \frac{P_{intra,K}}{V_{intra,K}} \cdot (F_{fil} - F_{ex}) + \lambda_{phy} \cdot P_{intra,K}^* \\ \frac{d}{dt} P_{intra,K}^* &= \frac{P_{int,K}^*}{V_{int,K}} \cdot (F_{fil} - F_{ex}) - \frac{P_{intra,K}^*}{V_{intra,K}} \cdot (F_{fil} - F_{ex}) - \lambda_{phy} \cdot P_{intra,K}^*\end{aligned}\tag{12}$$

Bound to protein

$$\begin{aligned}\frac{d}{dt} PPR &= k_{PR} \cdot P_{VEN} + \lambda_{phy} \cdot PPR^* \\ \frac{d}{dt} PPR^* &= k_{PR} \cdot P_{VEN}^* - \lambda_{phy} \cdot PPR^*\end{aligned}\tag{13}$$

SUPPLEMENTAL TABLE 1 Parameter definition

Variable		Value	Unit	Source
K_{on}	association rate	k_{off} / K_D	$l \cdot nmol^{-1} \cdot min^{-1}$	
k_{off}	dissociation rate	0.04	min^{-1}	(3) ^a
K_D	dissociation constant	0.4	$nmol \cdot l^{-1}$	(1)
λ_{phy}	physical decay ^{111}In ^{90}Y	$1.72 \cdot 10^{-4}$ and $1.80 \cdot 10^{-4}$	min^{-1}	
BW	body weight	individually measured	kg	
H	hematocrit	individually measured	unity	
F	flow total serum	$V_P \cdot 1.23/min^b$	$l \cdot min^{-1}$	(4)
V_P	volume of total body serum	male $2.8 \cdot (1-H) \cdot BSA$ female $2.4 \cdot (1-H) \cdot BSA$	l	(5)
Tumor				
$V_{TU,total}$	total volume of tumor 1 and 2	measured	l	
$V_{TU,int}$	interstitial space of tumor	$V_{tu,int} \cdot V_{TU,total}$	l	
$V_{TU,v}$	interstitial space of tumor	$V_{tu,v} \cdot V_{TU,total}$	l	
$v_{TU,int}$	interstitial space fraction of total tumor	0.3 for NET 0.23 for meningioma	unity	derived from (6) menin. (7)
$v_{TU,v}$	vascular fraction of total tumor	0.1 for NET 0.11 for meningioma	unity	NET (8) menin. (7)
F_{TU}	serum flow tumor	$f_{tu} \cdot (1-H) \cdot V_{total,Tu}$	$l \cdot min^{-1}$	
f_{TU}	serum flow density tumor	1.0·(1-H) for NET metastasis 0.9·(1-H) for meningioma	$ml \cdot min^{-1} \cdot g^{-1}$	NET (8) menin. (9)
PS_{TU}	permeability surface area product	$k_{TU} \cdot V_{TU,total}$	$ml \cdot min^{-1}$	
k_{TU}	permeability surface area product per unit mass (scaled for molecule size of DOTATATE)	0.2 NET metastasis 0.31 meningioma	$ml \cdot min^{-1} \cdot g^{-1}$	NET (8) menin. (7)
$[R_{TU,0}]$	sst2 receptor density tumour	fitted	$nmol \cdot l^{-1}$	
$R_{TU,0}$	sst2 receptor number tumour	$[R_{TU,0}] \cdot V_{TU,total}$	nmol	
$\lambda_{TU,int}$		0.001 (preliminary fits, Sup. D)	min^{-1}	
$\lambda_{TU,release}$		fitted	min^{-1}	
Measured organs				
$V_{L,total}$	volume total liver	individually measured	l	
$V_{S,total}$	volume total spleen	individually measured	l	
$V_{K,total}$	volume total kidney	individually measured	l	
$V_{i,v}$	Vascular (serum) volume organ liver, spleen, kidney	$V_{i,total} \cdot V_{i,v}$	l	
$V_{i,int}$	interstitial volume liver, spleen, kidneys	$V_{i,total} \cdot V_{i,int}$	l	
$V_{K,intra}$	volume intracellular kidney	$(V_{K,total} - V_{K,int} - V_{K,v}) \cdot 2/3^c$	l	
$v_{L,v}$	vascular (serum) fraction liver	0.085	unity	(10)
$v_{S,v}$	vascular (serum) fraction spleen	0.12	unity	(10)
$v_{K,v}$	vascular (serum) fraction kidneys	0.055	unity	(10)
$v_{L,int}$	interstitial fraction liver	0.2	unity	(10)
$v_{S,int}$	interstitial fraction spleen	0.2	unity	(10)
$v_{K,int}$	interstitial fraction kidney	0.15	unity	(10)
F_L	serum flow liver arterial	$0.065 \cdot F$	$l \cdot min^{-1}$	(4)
F_S	serum flow spleen	$0.03 \cdot F$	$l \cdot min^{-1}$	(4)
F_K	serum flow kidneys	$0.19 \cdot F$	$l \cdot min^{-1}$	(4)
ϕ	ratio of sieving coefficients	$\Theta_{DOTATATE} / \Theta_{Cr-51-EDTA} = 0.66$	unity	(11)
F_{fil}	filtration	$GFR_{measured} \cdot \phi^d$	$l \cdot min^{-1}$	
F_{ex}	excretion	$F_{fil} \cdot f_{ex}$	$l \cdot min^{-1}$	
f_{ex}	excretion/filtration	0.98	unity	(1)
k_L	permeability surface area product per unit mass for liver	$k_{MUS} \cdot 100$	$ml \cdot min^{-1} \cdot g^{-1}$	(12)
k_S	permeability surface area product per unit mass for spleen	k_L (due to similar capillary structure)	$ml \cdot min^{-1} \cdot g^{-1}$	
$[R_{L,0}]$	receptor density liver	fitted	$nmol \cdot l^{-1}$	
$[R_{S,0}]$	receptor density spleen	fitted	$nmol \cdot l^{-1}$	
$[R_{K,0}]$	receptor density kidneys	fitted	$nmol \cdot l^{-1}$	
$\lambda_{L,int}$	internalization rate sst2 liver	$\lambda_{K,int}$	min^{-1}	(13)

$\lambda_{S,int}$	internalization rate sst2 spleen	$\lambda_{K,int}$	min^{-1}	(13)
$\lambda_{K,int}$	internalization rate sst2 kidneys	$\lambda_{TU,int} \cdot 1.7^e$	min^{-1}	(13)
$\lambda_{L,release}$	release rate liver	$\lambda_{NT,release}$	min^{-1}	(1, 14)
$\lambda_{S,release}$	release rate spleen	$\lambda_{NT,release}$	min^{-1}	(1)
$\lambda_{K,release}$	release rate kidneys	$\lambda_{NT,release}$	min^{-1}	(1)
Other organs				
$V_{PRO,total}$	volume total prostate	$0.016 \cdot \text{BW}/71$		(15)
$V_{UT,total}$	volume total uterus	$0.080 \cdot \text{BW}/71$		(15)
$V_{LU,total}$	volume total lungs	$1 \cdot \text{BW}/71$		(15)
$V_{AD,total}$	volume total adrenals	$0.014 \cdot \text{BW}/71$		(15)
$V_{MUS,total}$	volume total muscles	$30.078 \cdot \text{BW}/71$		(15)
$V_{GI,total}$	volume total GI + pancreas	$(0.385+0.548+0.104+0.15) \cdot \text{BW}/71$		(15)
$V_{SKIN,total}$	volume total skin	$3.408 \cdot \text{BW}/71$		(15)
$V_{ADI,total}$	volume total adipose tissue	$13.465 \cdot \text{BW}/71$		
$V_{RM,total}$	volume total red marrow	$1.1 \cdot \text{BW}/71$		(15)
$V_{BONE,total}$	volume total bone without red marrow	$10.165 \cdot \text{BW}/71 - V_{RM,total}$		(15)
$V_{HRT,total}$	volume total heart	$0.341 \cdot \text{BW}/71$		(15)
$V_{BR,total}$	volume total brain	$1.45 \cdot \text{BW}/71$		(15)
V_{BW}	volume of total body based on BW	$1 \text{ ml} \triangleq 1 \text{ g}$		
$V_{REST,total}$	volume of rest body i = all organs except tumor	$V_{BW} - \sum_i V_{i,total}$		
$V_{PRO,v}$	vascular fraction prostate/uterus	$0.04 \cdot (1-H) \cdot V_{PRO,total}$		(16)
$V_{UT,v}$	vascular fraction prostate/uterus	$0.07 \cdot (1-H) \cdot V_{UT,total}$		(17)
$V_{LU,v}$	vascular (serum) volume lungs	$0.105 \cdot V_P$		(4)
$V_{AD,v}$	vascular (serum) volume adrenals	$0.03 \cdot (1-H) \cdot V_{AD,total}$		(15)
$V_{MUS,v}$	vascular (serum) volume muscles	$0.14 \cdot V_P$		(4)
$V_{GI,v}$	vascular (serum) volume GI+ pancreas	$0.076 \cdot V_P$		(4)
$V_{SKIN,v}$	vascular(serum) volume skin	$0.03 \cdot V_P$		(4)
$V_{ADI,v}$	vascular(serum) volume adipose tissue	$0.05 \cdot V_P$		(4)
$V_{RM,v}$	vascular(serum) volume red marrow	$0.04 \cdot V_P$		(4)
$V_{BONE,v}$	vascular volume bone without red marrow	$0.07 \cdot V_P - V_{RM}$		(4)
$V_{HRT,v}$	vascular (serum) volume heart	$0.01 \cdot V_P$		(4)
$V_{BR,v}$	vascular(serum) volume brain	$0.012 \cdot V_P$		(4)
$V_{REST,v}$	serum volume rest i = all organs except tumor	$V_P - \sum_i V_{i,v}$		
V_{ART}	arterial serum plus ½ serum content of heart	$0.06 \cdot V_P + 0.045 \cdot V_P$		(4)
V_{VENES}	venous serum plus ½ serum content of heart	$0.18 \cdot V_P + 0.045 \cdot V_P$		(4)
$V_{PRO,int}$	interstitial volume prostate/uterus	$0.25 \cdot V_{PRO,total}$		(16)
$V_{UT,int}$	interstitial volume prostate/uterus	$0.5 \cdot V_{UT,total}$		(18)
$V_{LU,int}$	interstitial volume lungs	$V_{LU,v} \cdot \alpha_{LU}$		
$V_{AD,int}$	interstitial volume adrenals (the value for salivary gland is used)	$0.24 \cdot V_{AD,total}$		(19)
$V_{MUS,int}$	interstitial volume muscles	$V_{MUS,v} \cdot \alpha_{MUS}$		
$V_{GI,int}$	interstitial volume GI+ pancreas	$V_{GI,v} \cdot \alpha_{GI}$		
$V_{SKIN,int}$	interstitial volume skin	$V_{SKIN,v} \cdot \alpha_{SKIN}$		
$V_{ADI,int}$	interstitial volume adipose tissue	$V_{ADI,v} \cdot \alpha_{ADI}$		
$V_{RM,int}$	interstitial volume red marrow	$V_{RM,v} \cdot \alpha_{RM}$		
$V_{BONE,int}$	interstitial volume bone without red marrow	$V_{BONE,v} \cdot \alpha_{BONE}$		
$V_{HRT,int}$	interstitial volume heart	$V_{HRT,v} \cdot \alpha_{HRT}$		
$V_{REST,int}$	volume of rest body	$V_{REST,v} \cdot \alpha_{REST}$		
α_{MUS}	ratio of interstitial to vascular volume average man	$V_{MUS,int}/V_{MUS,v} = 5.9$	unity	(10)
α_{GI}	ratio of interstitial to vascular volume	$V_{GI,int}/V_{GI,v} = 8.8$	unity	(10)

	average man			
α_{SKIN}	ratio of interstitial to vascular volume average man	$V_{SKIN,int}/V_{SKIN,v} = 8.9$	unity	(10)
α_{ADI}	ratio of interstitial to vascular volume average man	$V_{ADI,int}/V_{ADI,v} = 15.5$	unity	(10)
α_{RM}	ratio of interstitial to vascular volume average man	$V_{RM,int}/V_{RM,v} = 3.7$	unity	(10)
α_{HRT}	ratio of interstitial to vascular volume average man	$V_{HRT,int}/V_{HRT,v} = 3.7$	unity	(10)
α_{LU}	ratio of interstitial to vascular volume average man	$V_{LU,int}/V_{LU,v} = 5.5$	unity	(10)
α_{BONE}	ratio of interstitial to vascular volume average man	$V_{BONE,int}/V_{BONE,v} = 9.3$	unity	(10)
α_{REST}	ratio of interstitial to vascular volume average man	$V_{REST,int}/V_{REST,v} = 3.7$	unity	(10)
f_{PRO}		0.18	$ml \cdot min^{-1} \cdot g^{-1}$	(16)
f_{UT}		1	$ml \cdot min^{-1} \cdot g^{-1}$	(18)
f_{AD}		6	$ml \cdot min^{-1} \cdot g^{-1}$	(15)
F_{PRO} F_{UT}	Total serum flow to prostate/uterus	$f_{PRO} \cdot (1-H) \cdot V_{PRO,total}$ $f_{UT} \cdot (1-H) \cdot V_{UT,total}$	$ml \cdot min^{-1}$	
F_{LU}	Total serum flow lungs	F	$ml \cdot min^{-1}$	(4)
F_{AD}	Total serum flow to adrenals	$f_{AD} \cdot (1-H) \cdot V_{AD,total}$	$ml \cdot min^{-1}$	
F_{MUS}	Total serum flow to muscle	$0.17 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{GI}	Total serum flow to GI+ pancreas	$0.16 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{SKIN}	Total serum flow to skin	$0.05 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{ADI}	Total serum flow to adipose	$0.05 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{RM}	Total serum flow to red marrow (RM)	$0.03 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{BONE}	Total serum flow to bone (without RM)	$0.05 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{HRT}	Total serum flow to heart	$0.04 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{BR}	Total serum flow to brain	$0.12 \cdot F$	$ml \cdot min^{-1}$	(4)
F_{REST}	$i =$ all organs except tumor	$F - \sum_i F_i$	$ml \cdot min^{-1}$	
F_{TOTAL}		$F + F_{TU,1} + F_{TU,2} + F_{TU,REST}$	$ml \cdot min^{-1}$	
PS_i	permeability surface area product	$k_i \cdot V_{i\ total}$	$ml \cdot min^{-1}$	
k_{PRO} k_{UT}	permeability surface area product per unit mass (scaled for molecule size of DOTATATE) for prostate/uterus	0.1 0.2	$ml \cdot min^{-1} \cdot g^{-1}$	(16) (18)
k_{LU}	permeability surface area product per unit mass for lungs	$k_{MUS} \cdot 100$	$ml \cdot min^{-1} \cdot g^{-1}$	(12)
k_{AD}	permeability surface area product per unit mass for adrenals	$k_{MUS} \cdot 100$ (assumed to be very high as for salivary glands)	$ml \cdot min^{-1} \cdot g^{-1}$	(20)
k_{MUS}	permeability surface area product per unit mass for muscle	0.02	$ml \cdot min^{-1} \cdot g^{-1}$	(12)
k_{GI}	permeability surface area product per unit mass for GI and pancreas	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	
k_{SKIN}	permeability surface area product per unit mass for skin	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	
k_{ADI}	permeability surface area product per unit mass for adipose	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	
k_{RM}	permeability surface area product per unit mass for red marrow	k_L (assumed to similar to liver)	$ml \cdot min^{-1} \cdot g^{-1}$	
k_{HRT}	permeability surface area product per unit mass for heart	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	
k_{BONE}	permeability surface area product per unit mass for bone	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	

k_{REST}	permeability surface area product per unit mass for rest	0.02 (assumed to similar to muscle)	$ml \cdot min^{-1} \cdot g^{-1}$	
$[R_{PRO,0}]$ $[R_{UT,0}]$	receptor density prostate based on sst2 density ratios calculated from (21)	$[R_{K,0}] \cdot 0.26$ $[R_{K,0}] \cdot 0.092$	$nmol \cdot l^{-1}$	(21)
$[R_{AD,0}]$	receptor density adrenals based on sst2 density ratios calculated from (21)	$[R_{K,0}] \cdot 1.65$	$nmol \cdot l^{-1}$	(21)
$[R_{MUS,0}]$	receptor density muscle based on sst2 density ratios calculated from (21)	$[R_{K,0}] \cdot 0.0056$	$nmol \cdot l^{-1}$	(21)
$[R_{GI,0}]$	receptor density GI + pancreas based on sst2 density ratios calculated from (21)	$[R_{K,0}] \cdot 0.16$	$nmol \cdot l^{-1}$	(21)
$[R_{RM,0}]$	receptor density RM based on sst2 density ratios calculated from (21)	$[R_{K,0}] \cdot 0.028$	$nmol \cdot l^{-1}$	(21)
$[R_{REST,0}]$	receptor density rest based on sst2 density ratios calculated from (21)	fitted	$nmol \cdot l^{-1}$	
$\lambda_{NT,int}$	internalization rate for sst2 normal tissue	$\lambda_{K,int}$	min^{-1}	(22)
$\lambda_{NT,release}$	degradation and release from sst2 cells normal tissue	fitted	min^{-1}	(1)
R	receptors free		nmol	
$R_{i,0}$	receptors total number of organ i	$[R_{i,0}] \cdot V_{i,total}$	nmol	
$[R_{i,0}]$	receptor density of organ i		$nmol \cdot l^{-1}$	
RP_i	peptide bound		nmol	
PPR	peptide bound to serum protein		nmol	
k_{PR}	binding rate peptide to serum	fitted	min^{-1}	
P_{intern}	peptide internalized		nmol	
$P_{i,v}$	peptide free vascular		nmol	
$P_{i,int}$	peptide free interstitial		nmol	
$P_{K,intra}$	peptide interacellular kidneys		nmol	

^aIn house Biacore measurements (23) of PSMA specific peptides yielded typical values of 0.04 1/min. Ferl et al report similar values [1].

^bFor the average normal adult (blood) $F = 6500 \text{ ml/min}$ and $V = 5300 \text{ ml}$. Therefore, a factor of 1.23 was assigned to account for the changes in total serum flow due to volume changes.

^cIt is assumed that 2/3 of the total intracellular volume of the kidney is represented by the proximal tubular cells

^d Scaling of GFR due to different molecular sizes

^eThe internalization of $^{111}\text{In-DOTATATE}$ was not directly measured for kidney cells (13). However, in reference (13) the kidney and tumor cell values for other ^{111}In -labeled ligands are reported. The mean value of the kidney to tumor ratio for these actually measured internalization rates was calculated. This average value of 1.7 was used as the ratio of kidney to the tumor $^{111}\text{In-DOTATATE}$ internalization rate.

2D imaging corrections:

Background correction, self-attenuation and scatter corrections were performed according to MIRD pamphlet 16 (24) for conjugative view counting. For organ activity estimation, a ROI was placed in an area with no overlapping activity of other organs and then scaled according to the total organ size. The background ROI was placed in the abdomen. For liver metastasis, the liver or abdomen were considered background depending on the size of the lesion.

For red marrow, time activity data could not be directly delineated. The herein used PBPK model allowed including information such as receptor density (according to Boy et al.) in the red marrow. It further allowed simultaneously fitting all parameters to all data (serum, whole body and all organs plus tumor). The time-integrated activity coefficient was estimated by integrating all compartments describing the red marrow including red marrow serum, interstitial space, bound and internalized peptide. For red marrow absorbed dose estimation, see equation 21, below.

Absorbed dose (D) and biologically effective dose (BED):

To calculate the absorbed dose and the BED of the kidneys, tumor, spleen and liver, the following equations and parameter values (Table B) were used:

$$\dot{D}_i(t) = A_i(t) \cdot S_{i \leftarrow i} = A_{inj} \cdot a_i(t) \cdot S_{i \leftarrow i} \quad (14)$$

$$D_i(T) = \int_0^T \dot{D}_i(t) dt = A_{inj} \cdot \tilde{a}_i(T) \cdot S_{i \leftarrow i} \quad (15)$$

The BED (25) is defined as

$$BED_i = D_i \cdot \left(1 + \frac{G_i}{\alpha_i / \beta_i} \cdot D_i\right) \quad (16)$$

The factor G_i (Lea–Catcheside factor) (25) is defined as

$$G_i(T) = \frac{2}{D_i^2} \cdot \int_0^T \dot{D}_i(t) dt \cdot \int_0^t \dot{D}_i(\omega) \cdot e^{-\mu_i(t-\omega)} d\omega \quad (17)$$

Thus, after inserting Eq. (17) in (16) one obtains

$$BED_i = D_i + \frac{2 \cdot \int_0^T \dot{D}_i(t) dt \cdot \int_0^t \dot{D}_i(\omega) \cdot e^{-\mu_i(t-\omega)} d\omega}{\alpha_i / \beta_i} \quad (18)$$

The activity to administer yielding a fixed kidney $BED_{K, fixed}$ is calculated according to

$$BED_{K, fixed} = A_{inj, BED_{K, fixed}} \cdot \tilde{a}_K(T) \cdot S_{K \leftarrow K} + \frac{2 \cdot A_{inj, BED_{K, fixed}} \int_0^T a_K(t) \cdot S_{K \leftarrow K} dt \cdot \int_0^t a_K(\omega) \cdot S_{K \leftarrow K} \cdot e^{-\mu_K(t-\omega)} d\omega}{\alpha_K / \beta_K} \quad (19)$$

Solving Eq (19) for the administered activity yields

$$\begin{aligned}
A_{inj, BED_{K, fixed}} &= \frac{-\tilde{a}_K(T) \cdot S_{K \leftarrow K} \pm \sqrt{(\tilde{a}_K(T) \cdot S_{K \leftarrow K})^2 + \frac{8 \cdot \int_0^T a_K(t) \cdot S_{K \leftarrow K} dt \cdot \int_0^t a_K(\omega) \cdot S_{K \leftarrow K} \cdot e^{-\mu_K(t-\omega)} d\omega \cdot BED_{K, fixed}}{\alpha_K / \beta_K}}}{4 \cdot \int_0^T a_K(t) \cdot S_{K \leftarrow K} dt \cdot \int_0^t a_K(\omega) \cdot S_{K \leftarrow K} \cdot e^{-\mu_K(t-\omega)} d\omega} \\
&\quad \alpha_K / \beta_K \\
A_{inj, BED_{K, fixed}} &= \frac{-\tilde{a}_K(T) \pm \sqrt{\tilde{a}_K(T)^2 + \frac{8 \cdot \int_0^T a_K(t) \cdot dt \cdot \int_0^t a_K(\omega) \cdot e^{-\mu_K(t-\omega)} d\omega \cdot BED_{K, fixed}}{\alpha_K / \beta_K}}}{4 \cdot S_{K \leftarrow K} \cdot \int_0^T a_K(t) \cdot dt \cdot \int_0^t a_K(\omega) \cdot e^{-\mu_K(t-\omega)} d\omega} \\
&\quad \alpha_K / \beta_K
\end{aligned} \tag{20}$$

To calculate the BED of the red marrow, equation (21) was used instead of Eq. (14):

$$\dot{D}_{RM} = A_{RM}(t) \cdot S_{RM \leftarrow RM} + A_{REM}(t) \cdot S_{RM \leftarrow REM} \tag{21}$$

SUPPLEMENTAL TABLE 2

Variable		Value	Unit	Source
$S_{K \leftarrow K}$	dose factor kidney to kidney phantom (are scaled using the actual organ mass)	$2.93 \cdot 10^{-5}$ male $3.18 \cdot 10^{-5}$ female	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(26)
$S_{S \leftarrow S}$	dose factor kidney to kidney phantom (are scaled using the actual organ mass)	$4.76 \cdot 10^{-5}$ male $5.80 \cdot 10^{-5}$ female	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(26)
$S_{L \leftarrow L}$	dose factor kidney to kidney phantom (are scaled using the actual organ mass)	$4.70 \cdot 10^{-6}$ male $6.42 \cdot 10^{-6}$ female	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(26)
$S_{TU \leftarrow TU}$	dose factor tumor to tumor phantom	Table C	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(27)
$S_{RM \leftarrow RM}$	dose factor red marrow to red marrow phantom (are scaled using BW)	$3.52 \cdot 10^{-6}$ male $3.14 \cdot 10^{-6}$ female	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(26)
$S_{RM \leftarrow REM}$	dose factor remainder to red marrow corrected according to Hindorf et al.	$8.46 \cdot 10^{-8}$ male $1.03 \cdot 10^{-7}$ female	$\text{Gy} \cdot \text{min}^{-1} \cdot \text{MBq}^{-1}$	(26) (28)
α/β_K	radiobiological parameters kidneys	2.5	Gy	(29)
μ_K	repair rate kidney	$\ln(2)/60/2.8$	min^{-1}	(29)
α/β_S	radiobiological parameters spleen	α/β_K	Gy	
μ_S	repair rate spleen	μ_K	min^{-1}	(29)
α/β_L	radiobiological parameters liver	α/β_K	Gy	
μ_L	repair rate liver	μ_K	min^{-1}	
α/β_{TU}	radiobiological parameters tumor	10	Gy	(30)
μ_{TU}	repair rate tumor	$\ln(2)/60/1$	min^{-1}	(30)
α/β_{RM}	radiobiological parameters red marrow	15	Gy	(31)
μ_{RM}	repair rate red marrow	$\ln(2)/60/1.5$	min^{-1}	(31)
A_i	activity of organ i		MBq	
A_{REM}	activity of remainder	$A_{\text{Total}} - A_{TU} - A_L$ $- A_S - A_K - A_{RM}$	MBq	
A_{inj}	injected activity		MBq	
$A_{inj, BED K, fixed}$	activity to inject for $BED_K = 20 \text{ Gy}$		MBq	
\tilde{a}_i	time-integrated activity coefficient of organ i		h	
a_i	fraction of administered activity of organ i		unity	
D_i	absorbed dose to organ i		Gy	
\dot{D}_i	absorbed dose rate to organ i		$\text{Gy} \cdot \text{min}^{-1}$	
T	Integration time	30000	min	
G_i	Lea–Catcheside factor of organ i		unity	(30)
BED_i	biologically effective dose to organ i		Gy	(30)

SUPPLEMENTAL TABLE 3

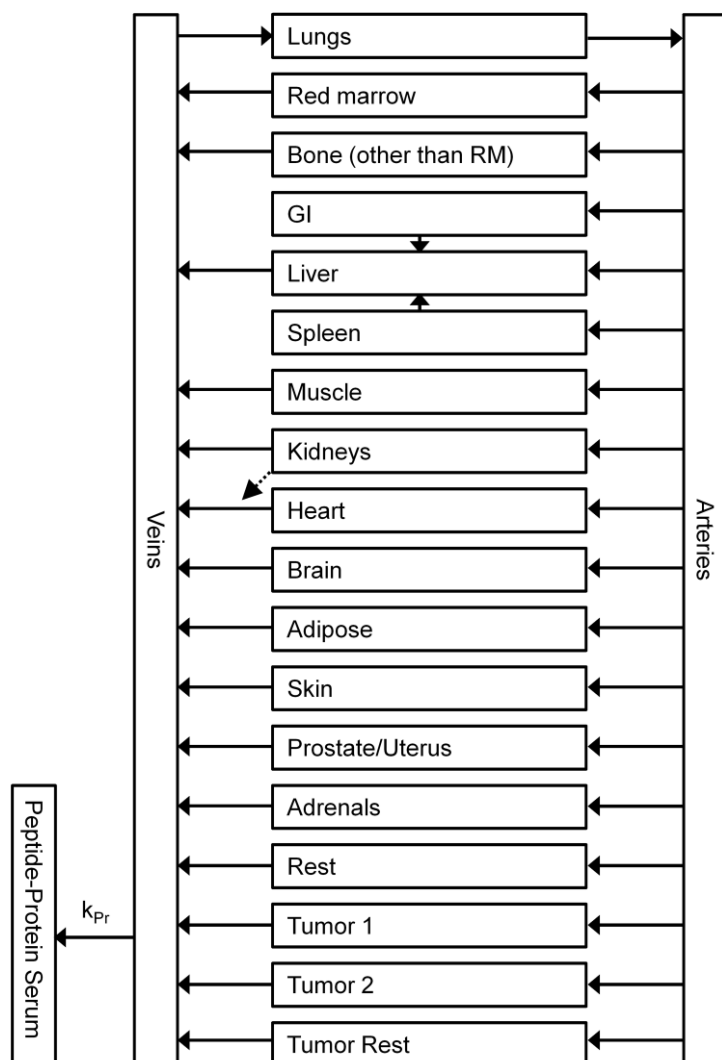
Volume [ml]	Tumor dose factors [Gy·min ⁻¹ ·MBq ⁻¹]
0.5	1.27·10 ⁻²
2	3.64·10 ⁻³
2.8	2.50·10 ⁻³
3	2.40·10 ⁻³
4	1.90·10 ⁻³
20	4.08·10 ⁻⁴
23	3.50·10 ⁻⁴
30	2.80·10 ⁻⁴
87	9.00·10 ⁻⁵
111	8.00·10 ⁻⁵
116	7.80·10 ⁻⁵
2522	3.50·10 ⁻⁶

References

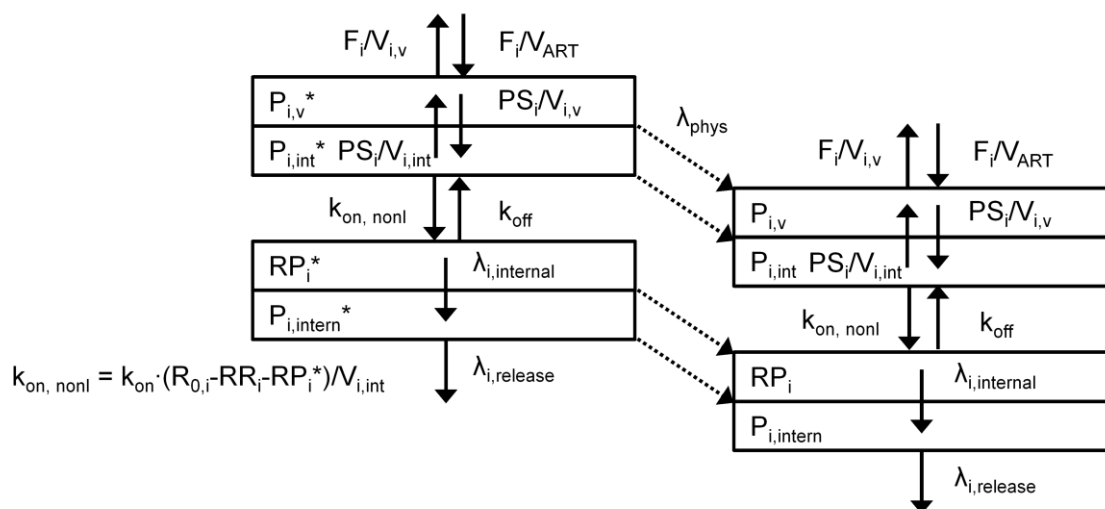
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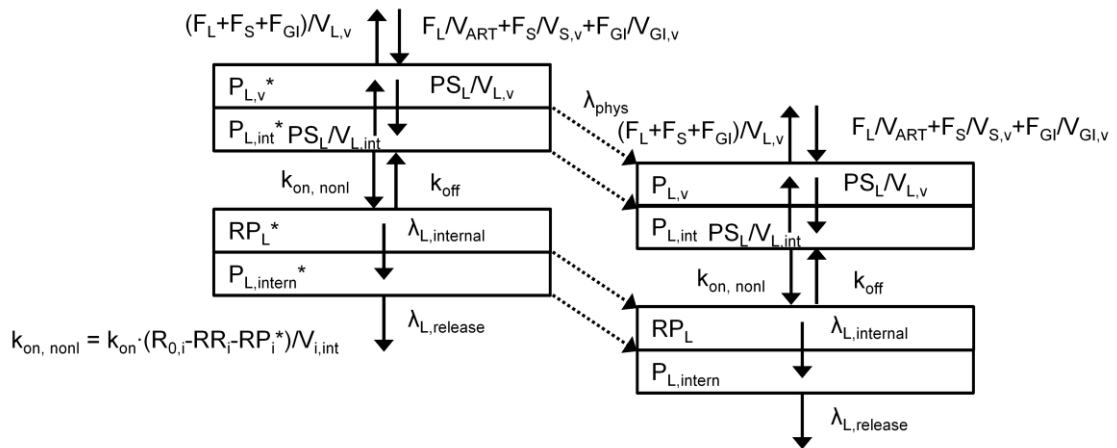
PBPK Model compartments



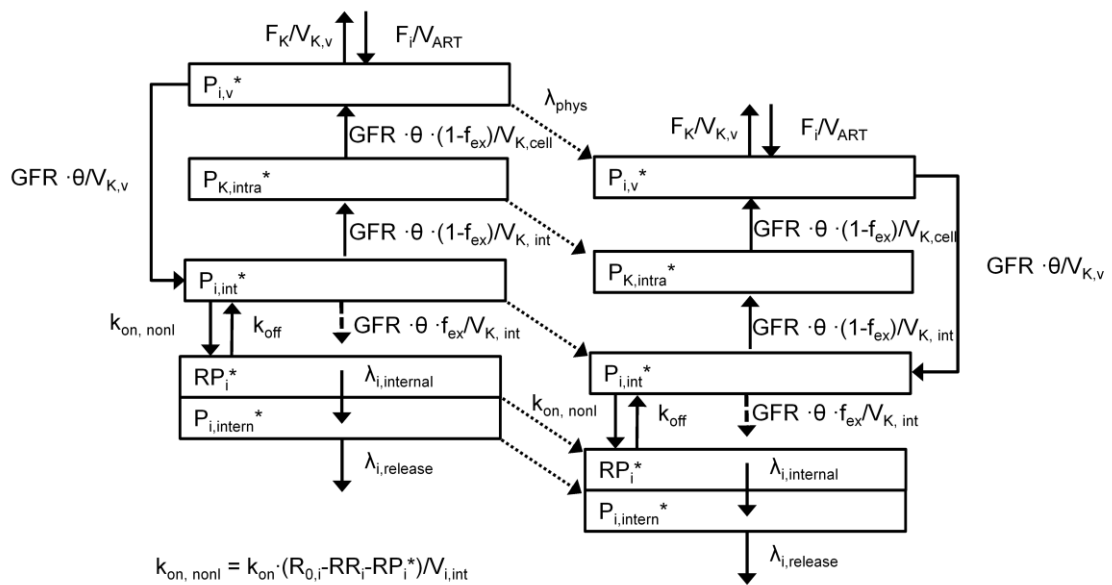
SUPPLEMENTAL FIGURE 1: Main model structure: All organs are represented by a rectangular compartment and are connected via blood flow. Each organ within this model, except arteries, veins, brain and protein serum, is divided into sub-compartments. The substance is cleared via kidneys. The compartment “Peptide-Protein serum” contains peptide bound to serum protein. As the fraction of bound peptide to proteins compared to the total amount is small and to reduce the complexity, only the „veins“ were connected to this compartment. The corresponding fraction for each specific organ was considered in the fitting process by assigning the data to the specific compartments.



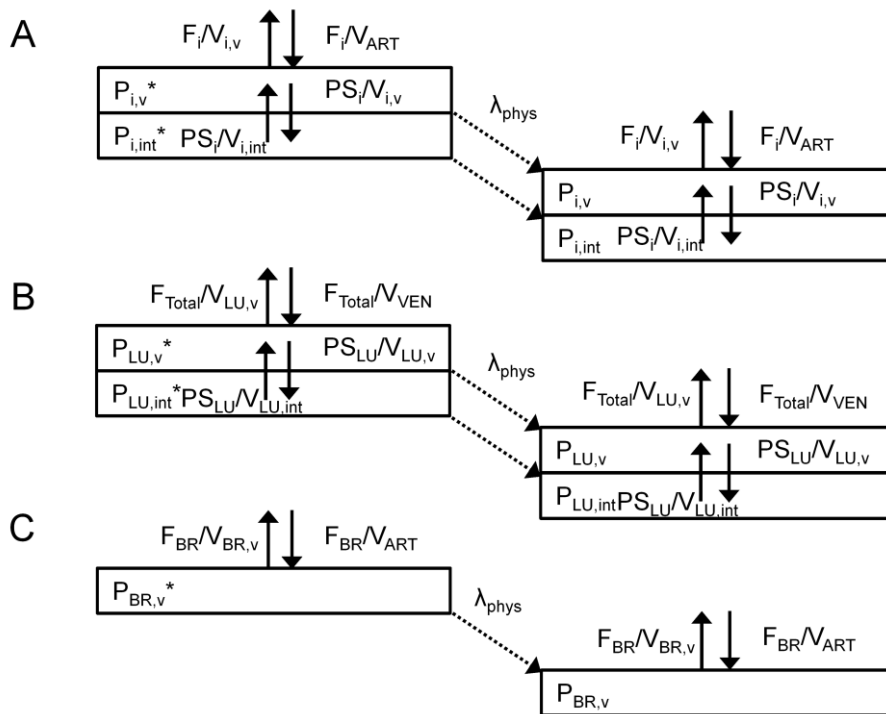
SUPPLEMENTAL FIGURE 2a: Red marrow, GI, spleen, muscle, prostate (uterus), adrenals, rest and tumor: The entire model consists of two systems, one for labeled (with *) and one for unlabeled peptide. The systems are connected by the competition for free receptors ($k_{on, nonl} = k_{on} \cdot (R_{0,i} - RR_i - RP_i^*) / V_{i,int}$) and by the physical decay (λ_{phys}). All physiological parameters are assumed equal for the labeled and unlabeled substance. k_{off} is the dissociation rate, the transport of peptide via serum flow to organ is described by F_i/V_{ART} (where F_i is serum flow and V_{ART} is serum volume of the arteries). $F_i/V_{i,v}$ describes the transport of peptide via serum flow out of organ. $V_{i,v}$ is the serum volume of the respective organ. RP_i is sst2 specific bound peptide to the cell surface. $P_{i,v}$ and $P_{i,int}$ are free peptide of the vascular ($V_{i,v}$) and interstitial space ($V_{i,int}$), respectively. PS_i is the permeability surface area product. $\lambda_{i,internal}$ is the internalisation rate of bound peptide and $\lambda_{i,release}$ the release rate of ^{111}In (and degraded peptide) from the cell.



SUPPLEMENTAL FIGURE 2b: Liver: For the liver, the model description of Figure 2a applies but the plasma flow is composed of liver arterial, GI and spleen flow.



SUPPLEMENTAL FIGURE 2c: Kidneys: The peptide is transported via serum flow to the vascular compartment and then filtrated into the interstitial part. Due to the administration of amino acids the largest fraction ($f_{ex} = 0.98$, Table A) of peptide is excreted. All unspecific uptake mechanisms are modelled with flow $GFR \cdot \theta \cdot (1-f_{ex})$ in and out of kidney cells.



SUPPLEMENTAL FIGURE 3: sst2 negative tissue and brain: For adipose, bone (other than red marrow), skin, heart (A) and lung (B), the model on the organ level simplifies to the transport of peptide via serum flow and transcapillary extravasation. For brain (C) the model reduces to serum flow.

Supplemental Data. Fitted curves and estimated parameters

Patient	Measurements and Modell	Number of data points	Akaike weight	$[R_{K,0}]$	$[R_{S,0}]$	$[R_{L,0}]$	$[R_{REST,0}]$	$[R_{TU1,0}]$	$[R_{TU2,0}]$	$\lambda_{NT,release}$	$\lambda_{TU1,release}$	$\lambda_{TU2,release}$	$V_{TUMOR,total}$	f_{TU1}	f_{TU2}	k_{PR}
			[unity]	[nmol/L]						[min ⁻¹ ·10 ⁻⁴]			[L]	[ml min ⁻¹ g ⁻¹]		[min ⁻¹ ·10 ⁻⁴]
P1	N1 M3	39	1	6.5	8.7	1.4	0.5	15	9.2	0.7	1.1	1.8	-	0.10	0.20	4.7
	N2 M3	39	1	8.8	11	2.5	0.5	18	11	0.7	1.1	1.8	-	0.10	0.20	5.6
	N3 M3	39	1	7.3	9.2	2.0	0.5	17	12	0.7	1.1	1.8	-	0.1	0.2	3.8
P2	N4 M3	34	1	5.7	7.8	1.0	0.4	24	-	1.1	1.7	-	-	0.10	-	4.3
	N5 M3	34	1	5.7	7.8	1.0	0.4	24	-	0.5	1.7	-	-	0.10	-	4.3
P3	N6 M1	38	1	6.2	17	0.9	0.4	5.0	34	0.5	3.0	1.7	-	0.90	0.90	4.0
P4	N7 M1	34	1	8.8	12	1.1	0.9	30	-	1.7	2.1	2.1	-	1.00	1.00	2.1
P5	N8 M2	29	0.8	7.1	13	1.2	0.5 fixed	29	-	2.1	0.0	0.0	0 fixed	0.10	-	24
	N8 M3	29	0.2	7.1	13	1.2	0.5 fixed	27	-	2.3	0.0	0.0	0 fixed	0.11	-	23
P6	N9 M1	32	1	7.5	-	1.5	0.5 fixed	19	35	1.2	2.0	1.1	0.1	1.0	1.0	17
P7	N10 M3	39	1	2.8	3.9	1.1	0.5 fixed	11	7	1.2	0.0	0.0	0.0	0.03	0.02	10
P8	N11 M3	39	1	2.3	4.7	0.6	0.5 fixed	16	25	0.6	0.0	0.0	0.2	0.02	1.00	10
P9	N12 M3	39	1	8.7	18	2.1	0.5 fixed	14	7	1.4	2.1	0.8	1.2	0.06	0.03	17

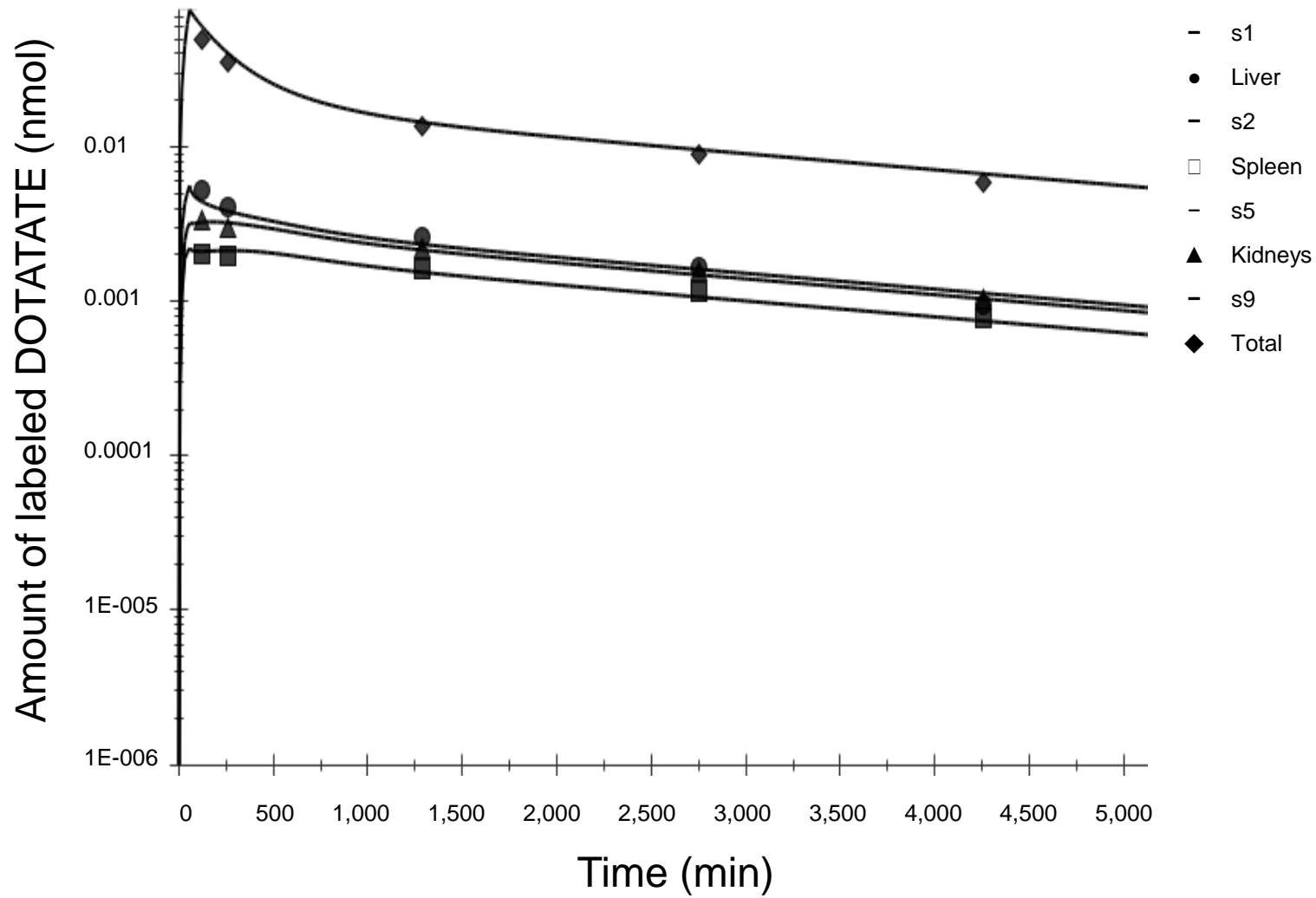
The relative SD of all parameters were < 50%. All elements of the correlation matrix were < 0.8.

For patient 1 (N1-3) and 2 (N4-5) an iterative two-stage parametric population fit using all pre-therapeutic measurements for parameter estimation was conducted. The total tumor volume could be delineated for meningioma but not for patients with metastasizing NETs. Therefore, the models were first fitted to time activity data of meningioma patients. The estimated value for the receptor concentration of the remaining tissue, $[R_{REST,0}]$ was then used as a fixed value for the individual fitting of the NET patients. Thus, the additional tumor volume (other than the explicitly delineated lesions) was estimated. For patient 5 also the average liver receptor concentration was fixed, because the high tumor load did not allow to distinguish between normal and tumor tissue in liver.

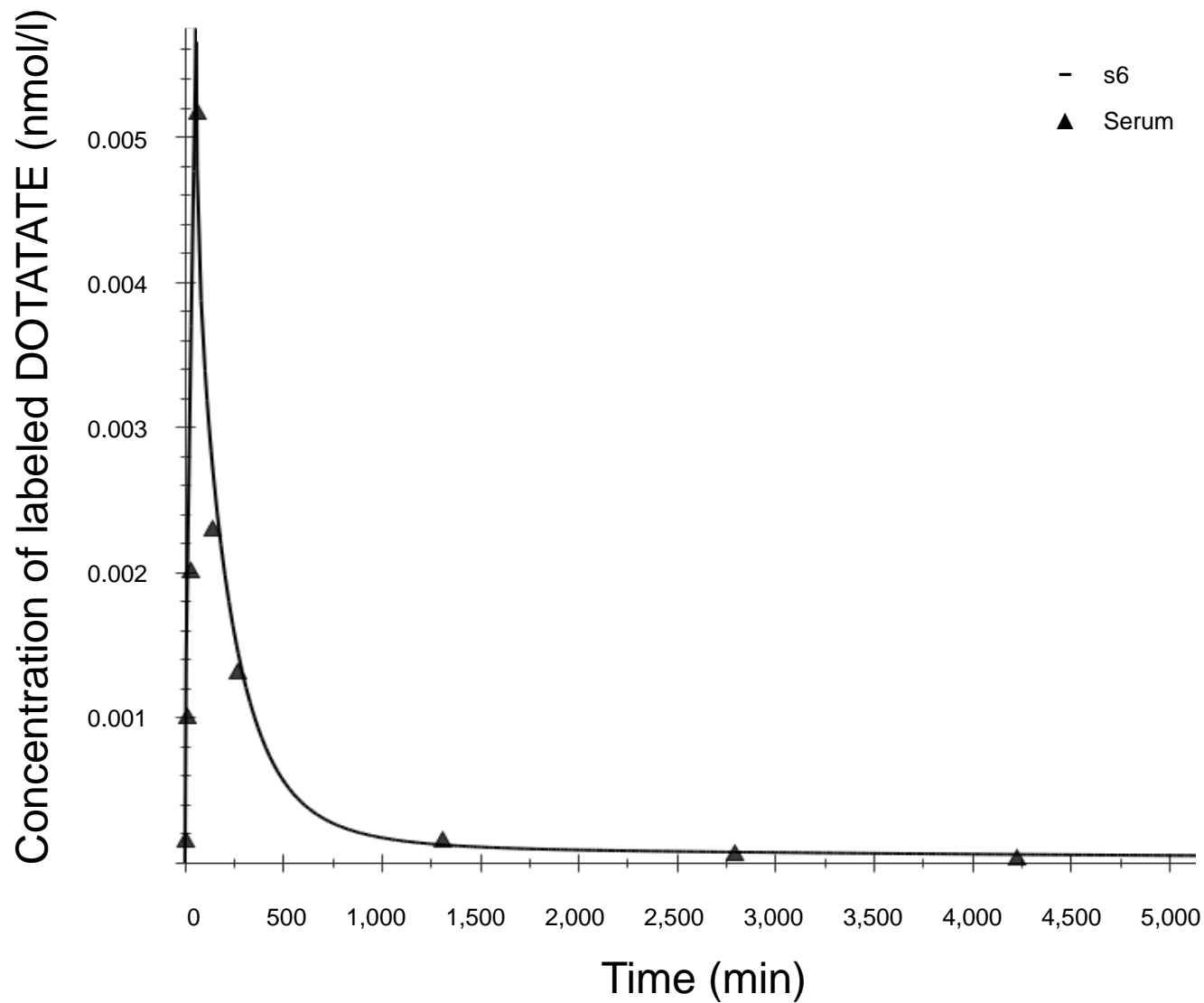
Preliminary fits showed that the internalization rates of kidney, liver and spleen were similar and in the order of 10^{-3} . To reduce parameter correlation, the kidney and tumor internalization rate were fixed to $\lambda_{K,int} = 0.0017 \text{ min}^{-1}$ and $\lambda_{TU,int} = 0.001 \text{ min}^{-1}$, respectively. A sensitivity analysis (Supplement D) showed little influence of these assumptions on the results.

The overall error (bias and uncertainty) of the data could not be determined. However, the estimated relative standard error within the data was < 10 % for all curves except for the serum measurements of data set N1 and N5.

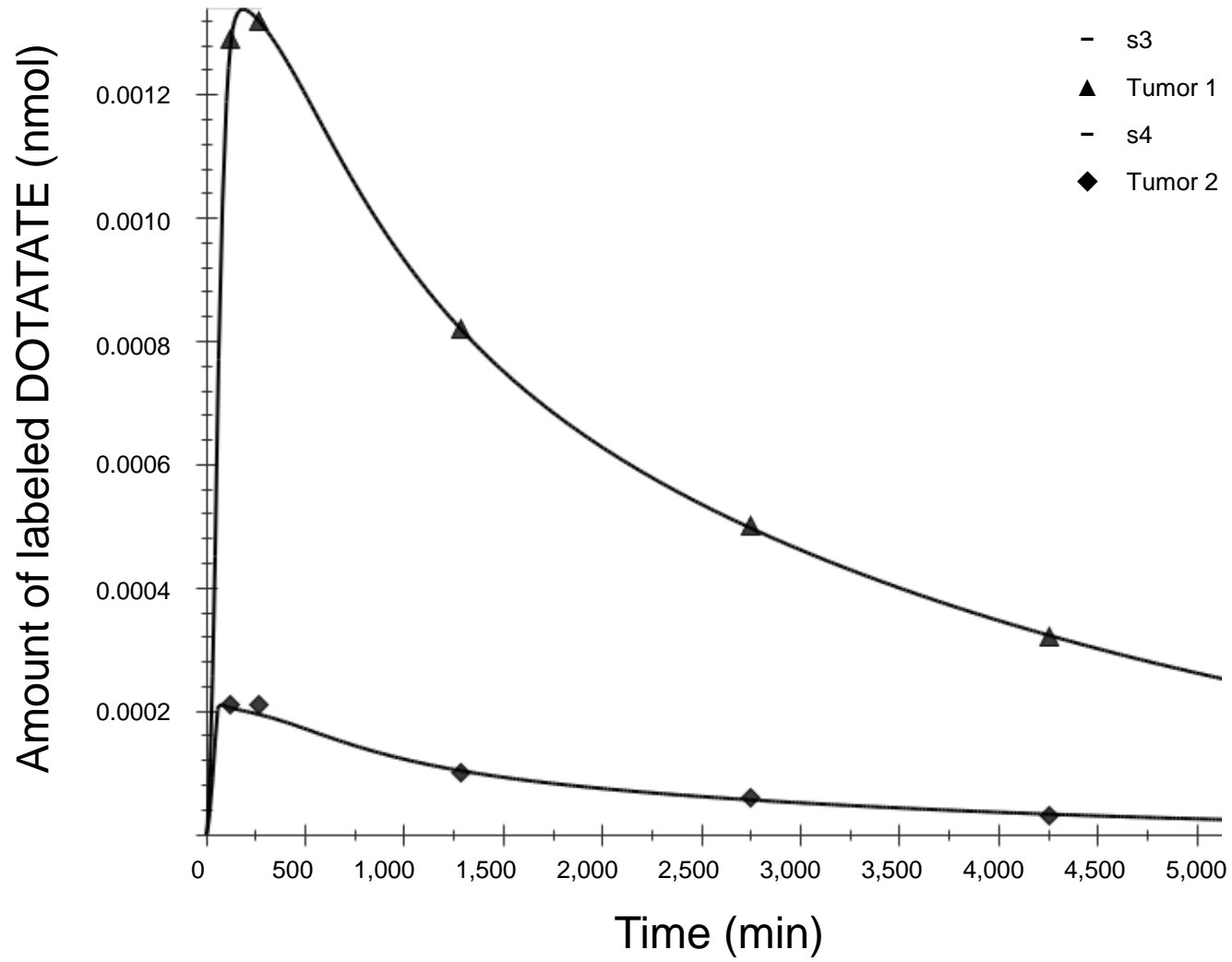
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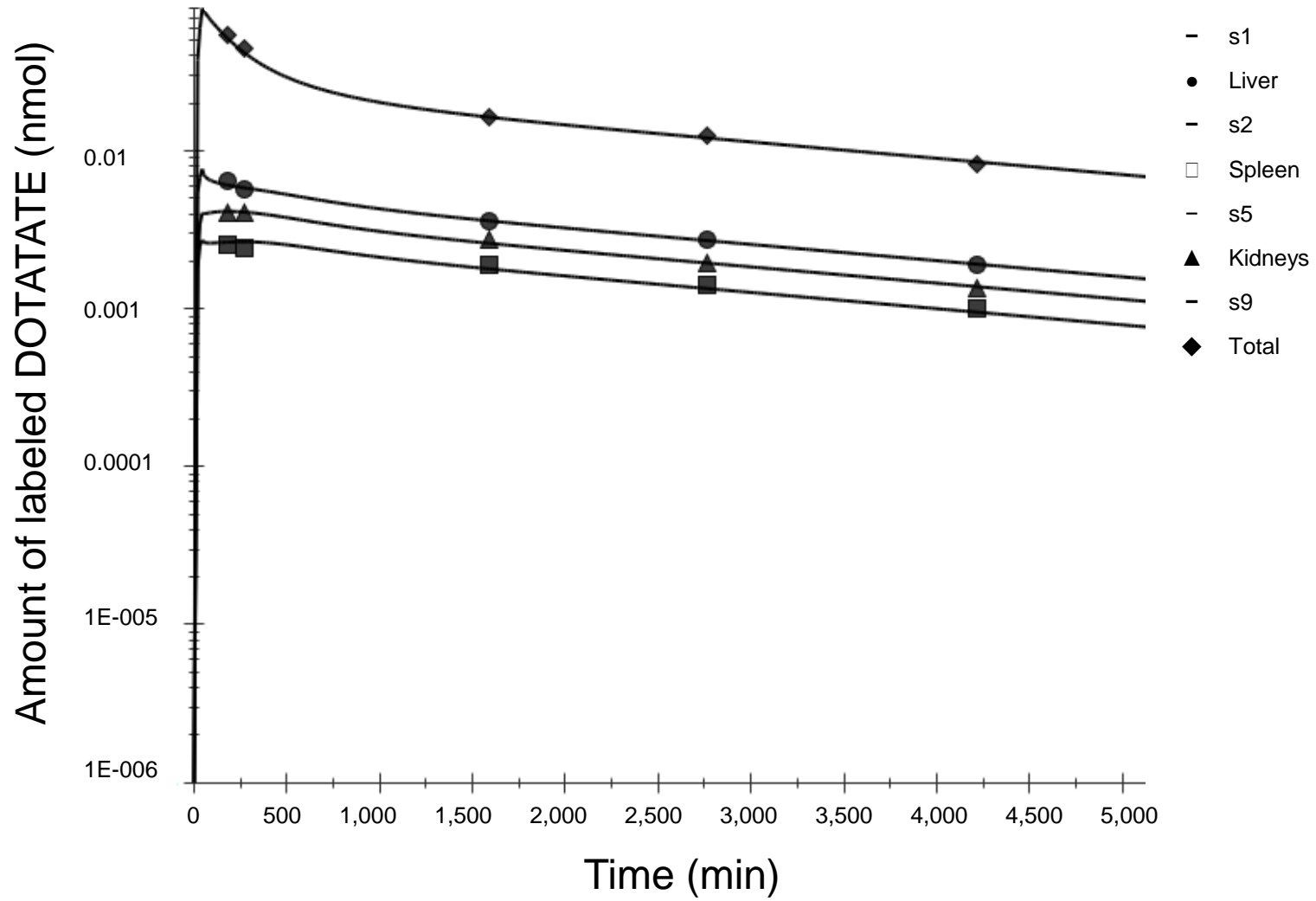
1B



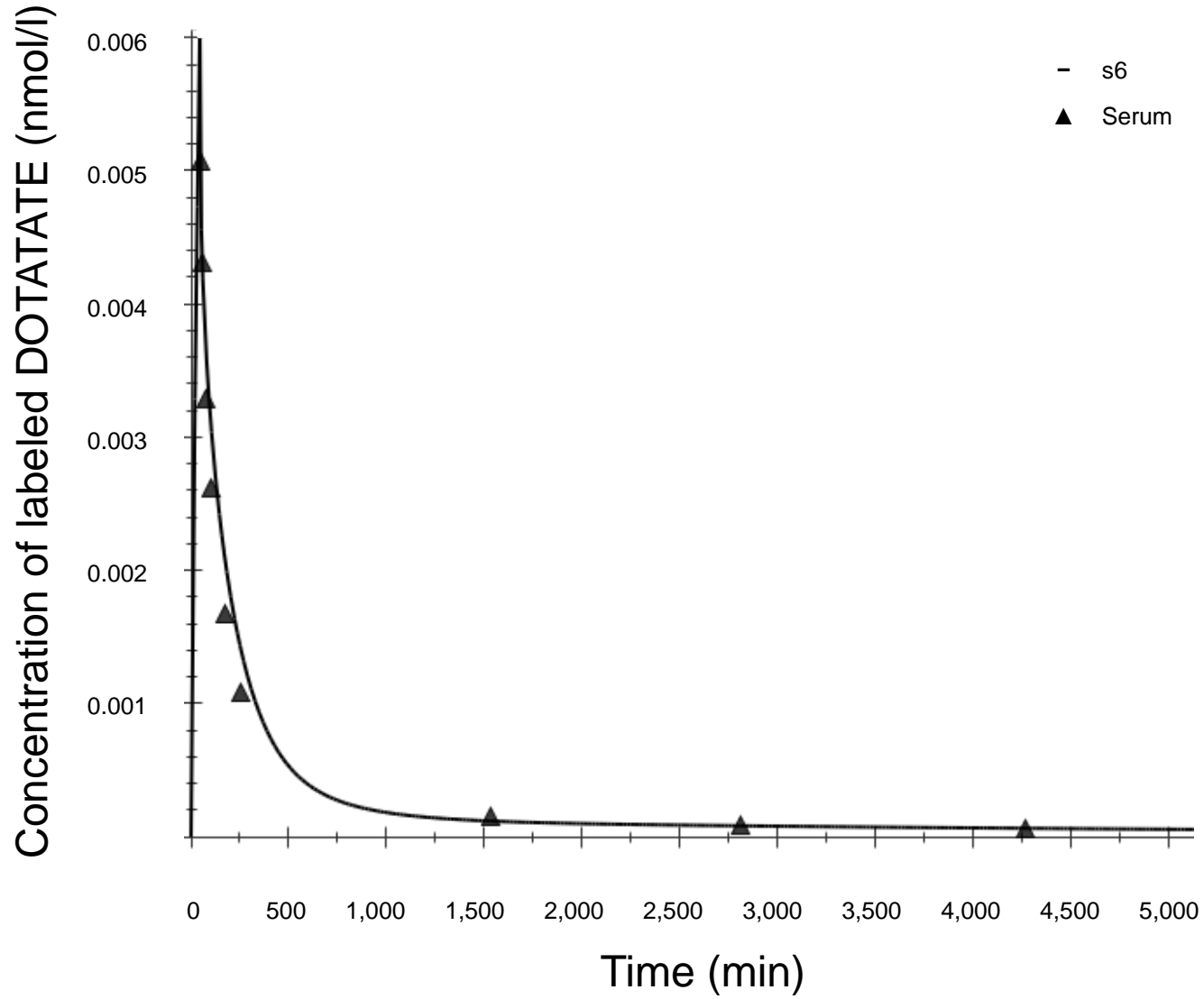
1C



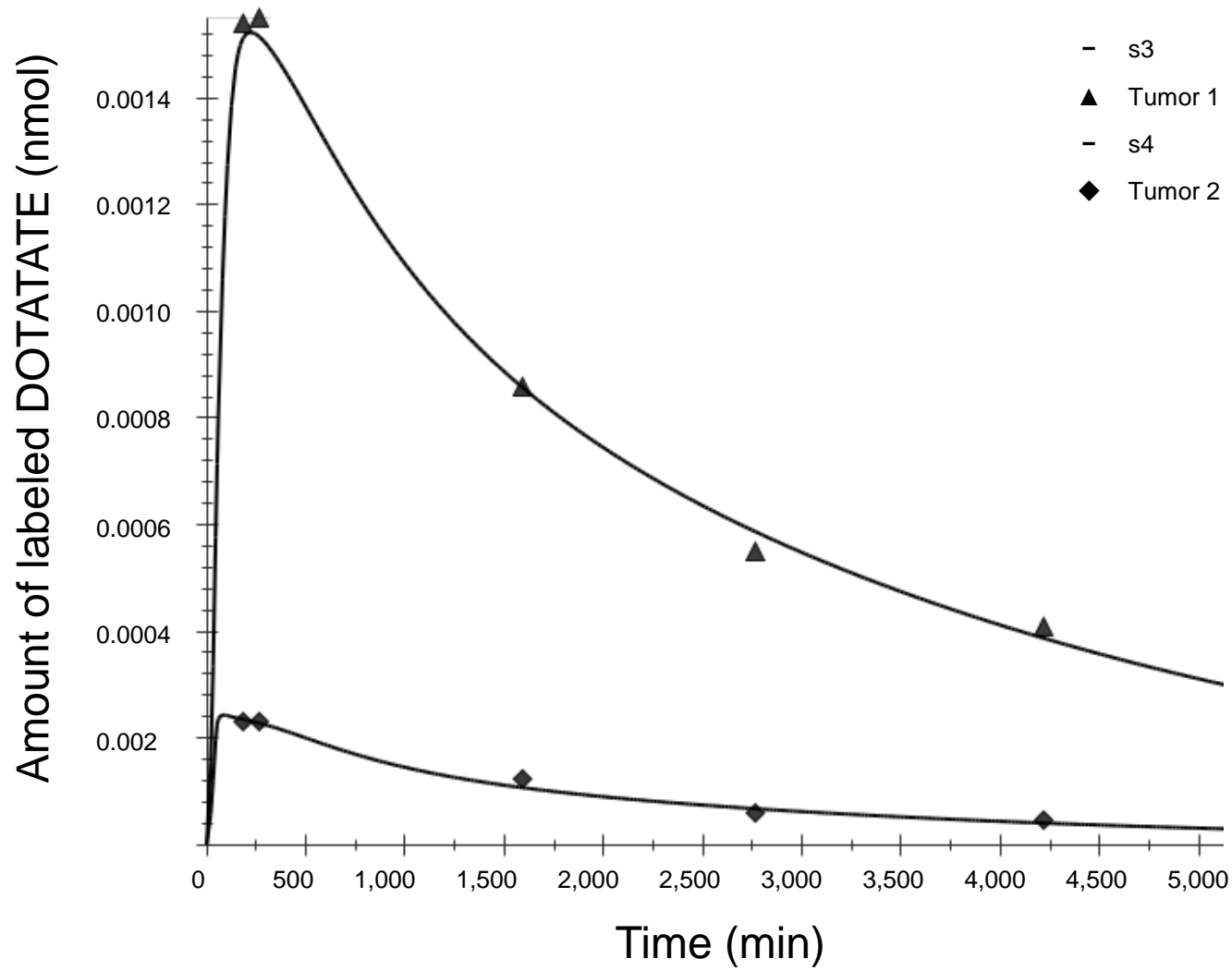
2A



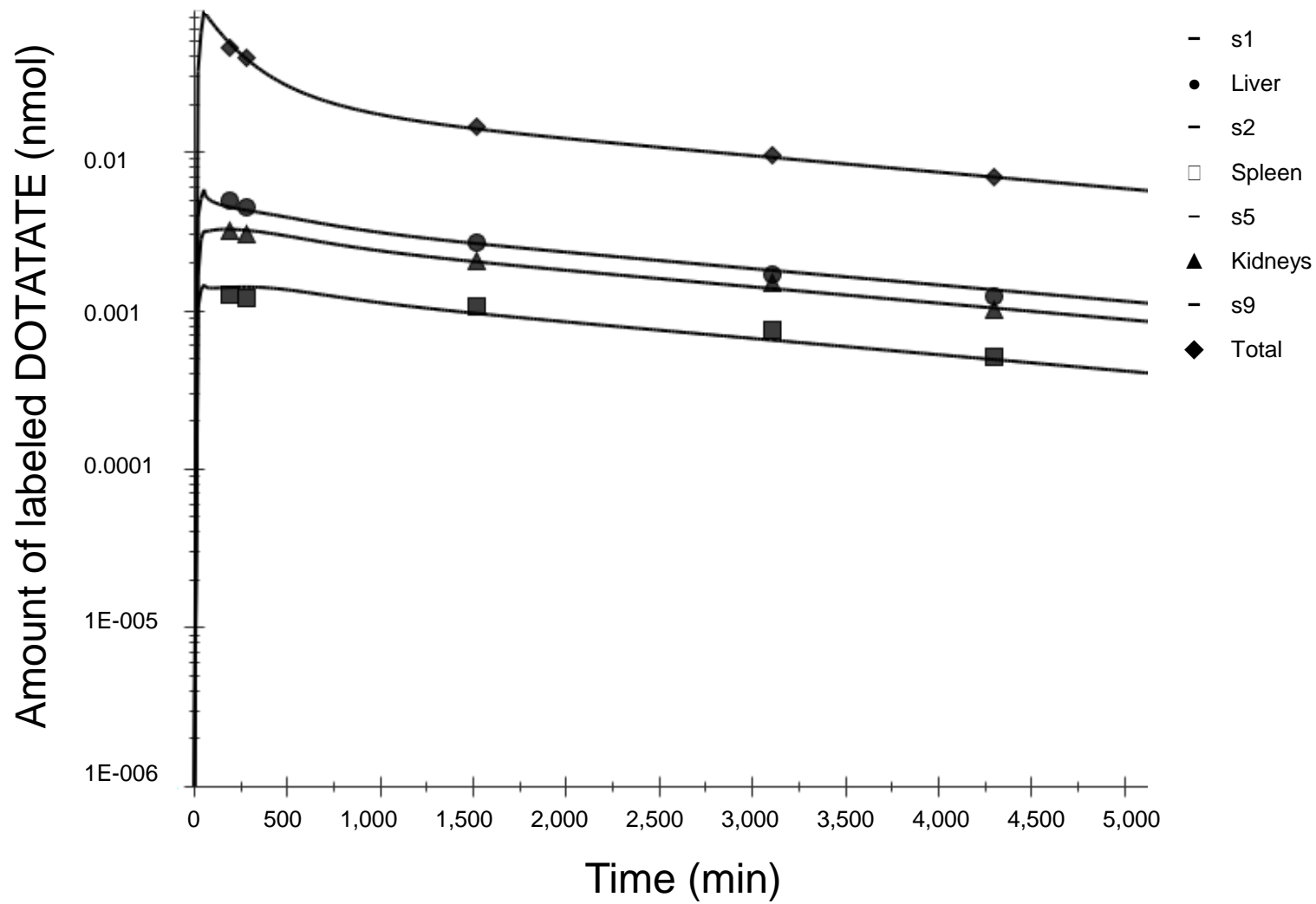
2B



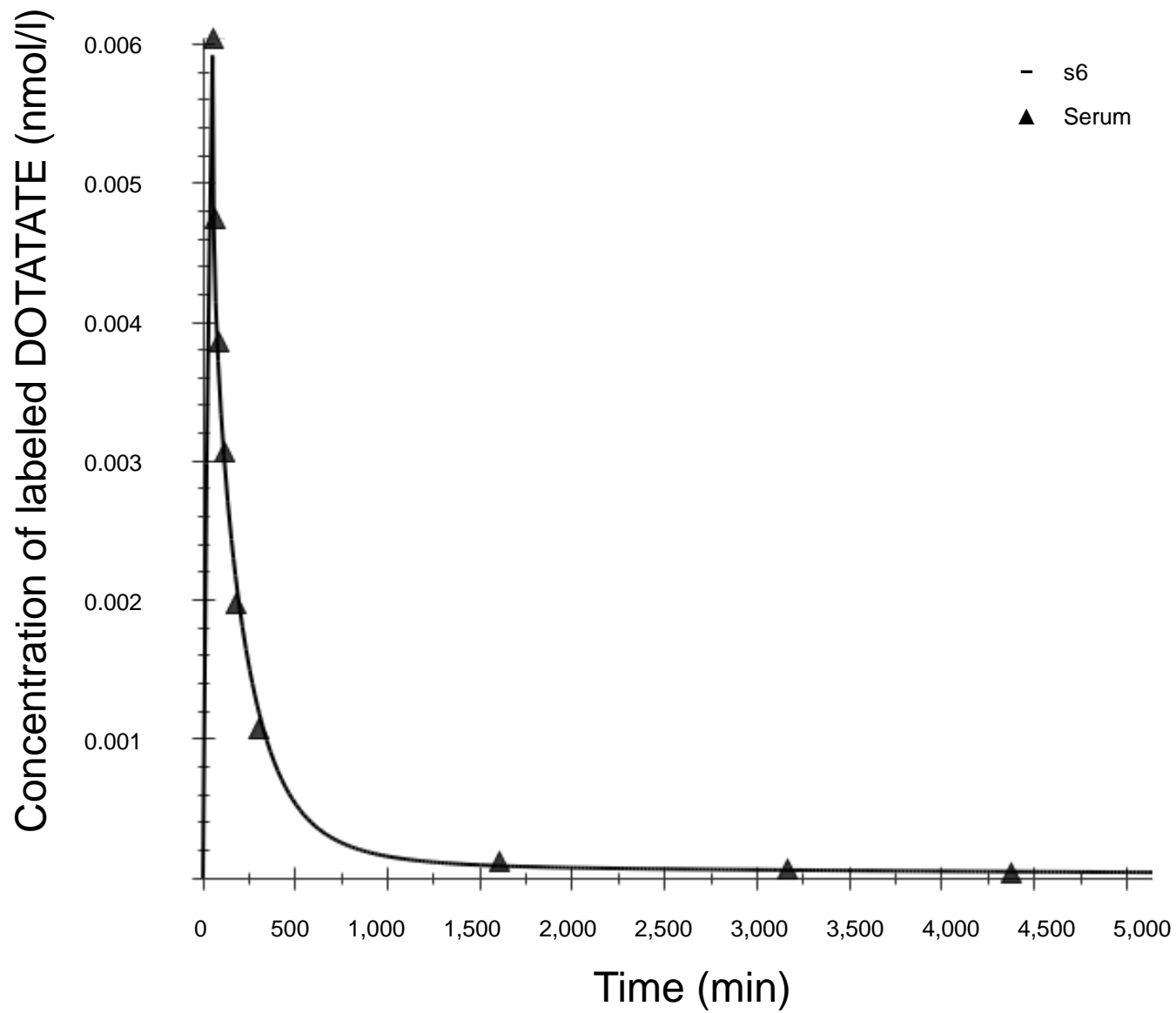
2C



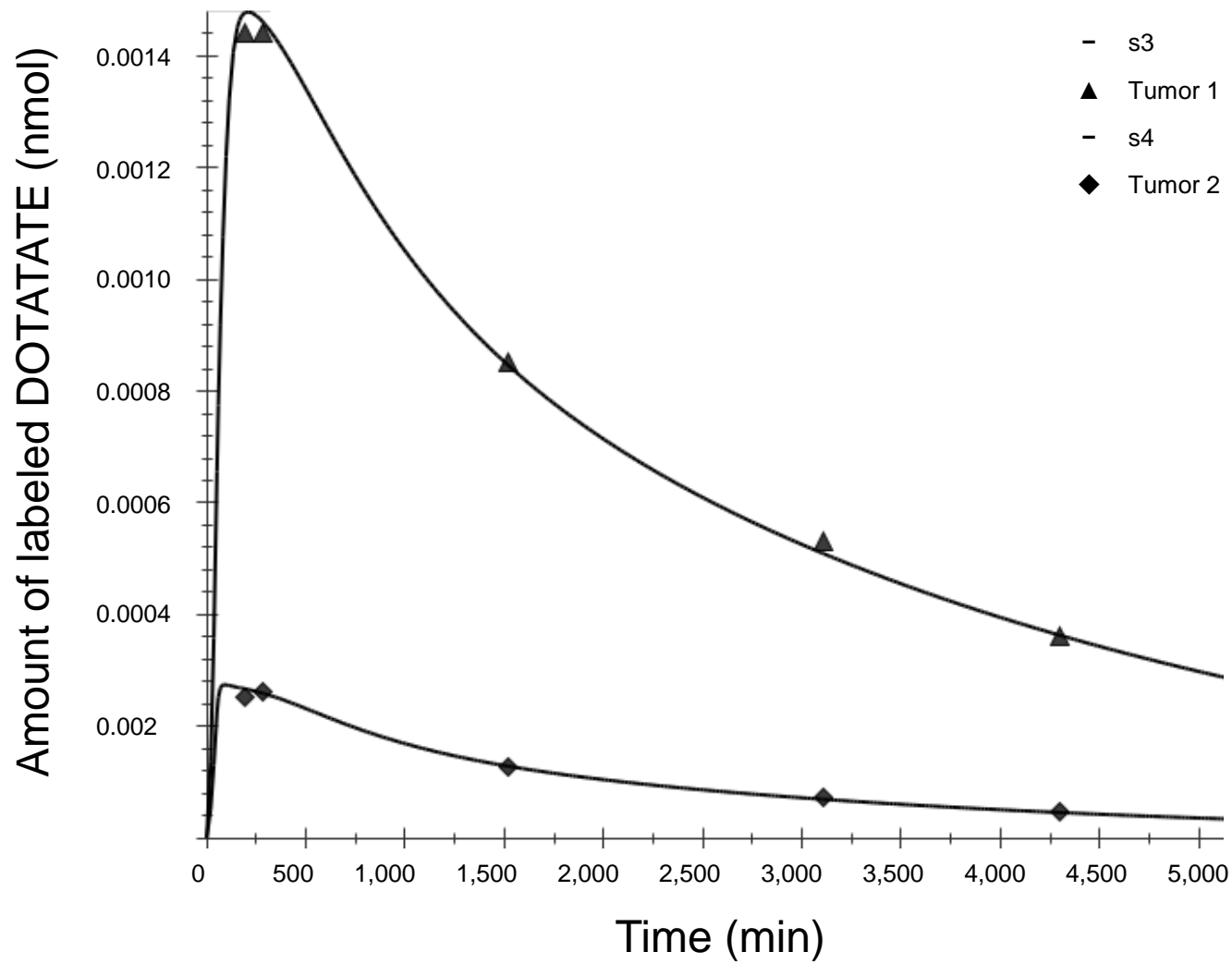
3A



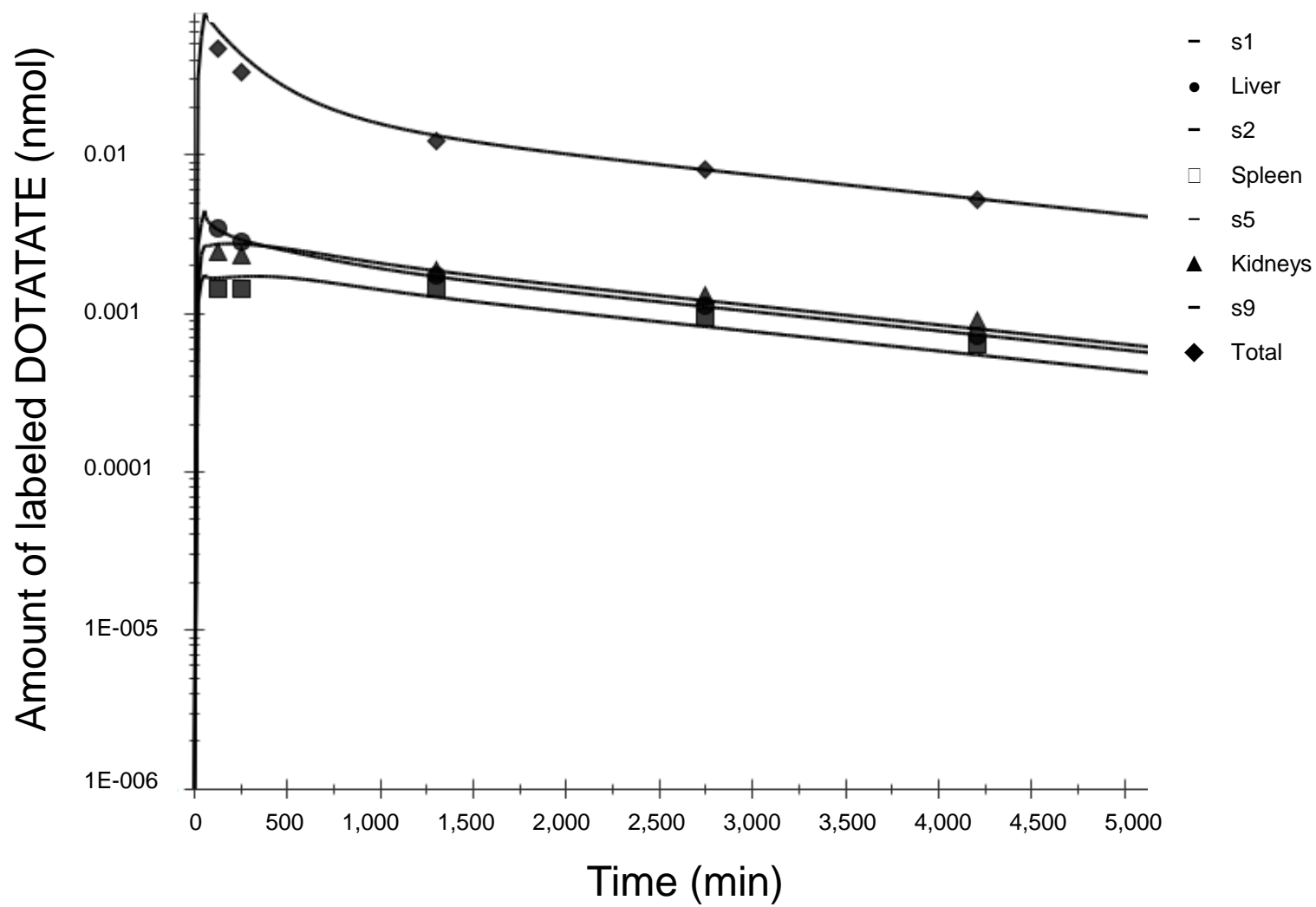
3B



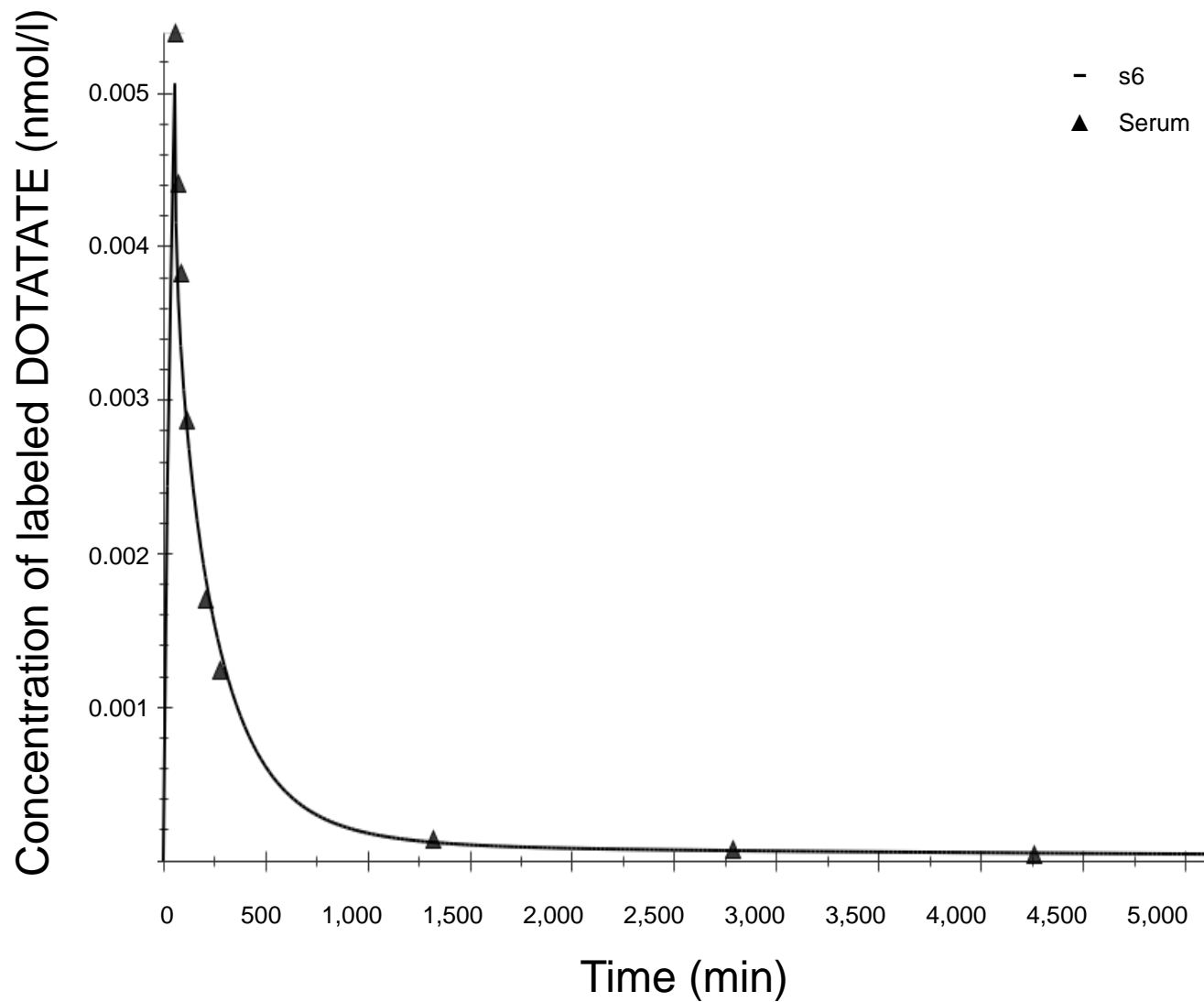
3C



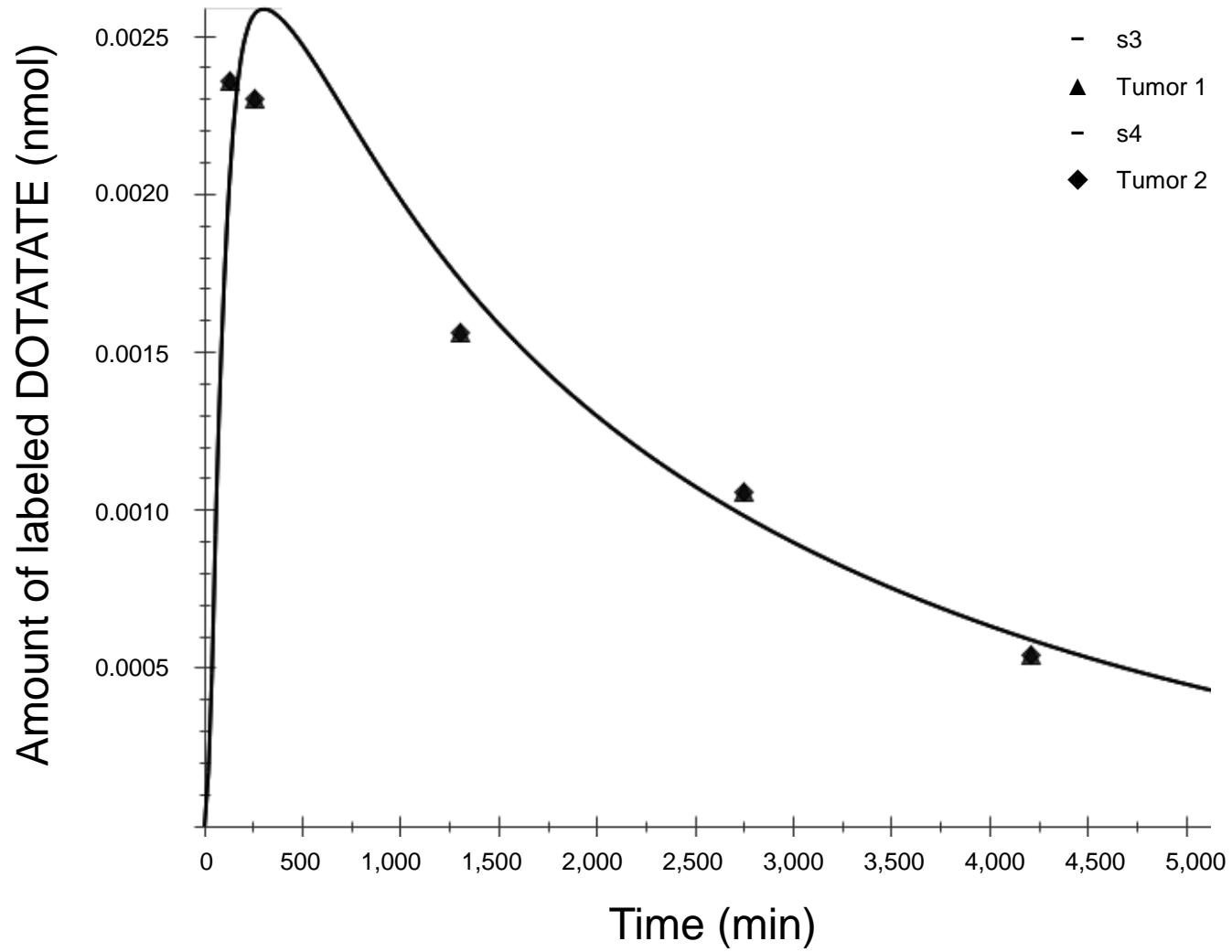
4A



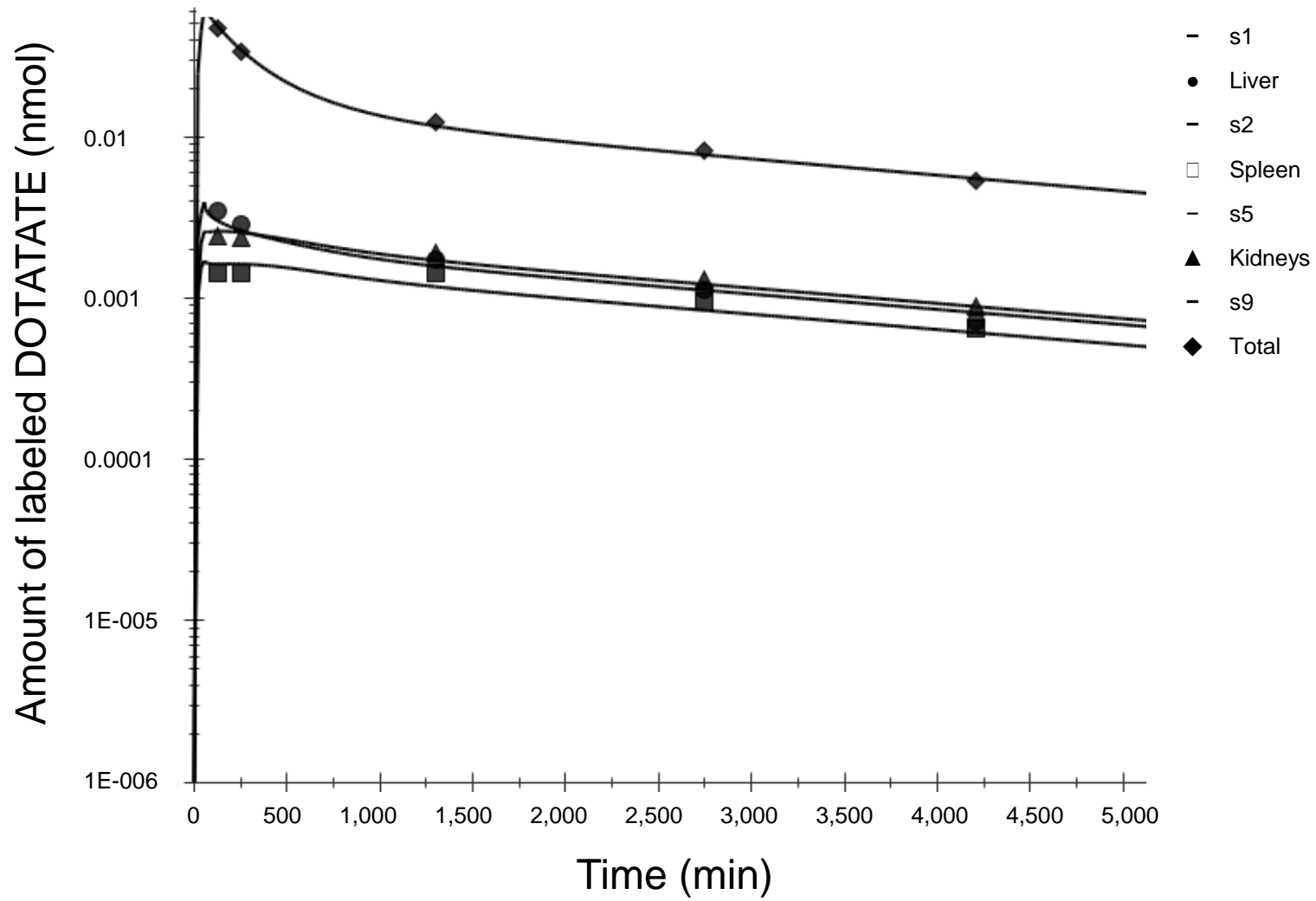
4B



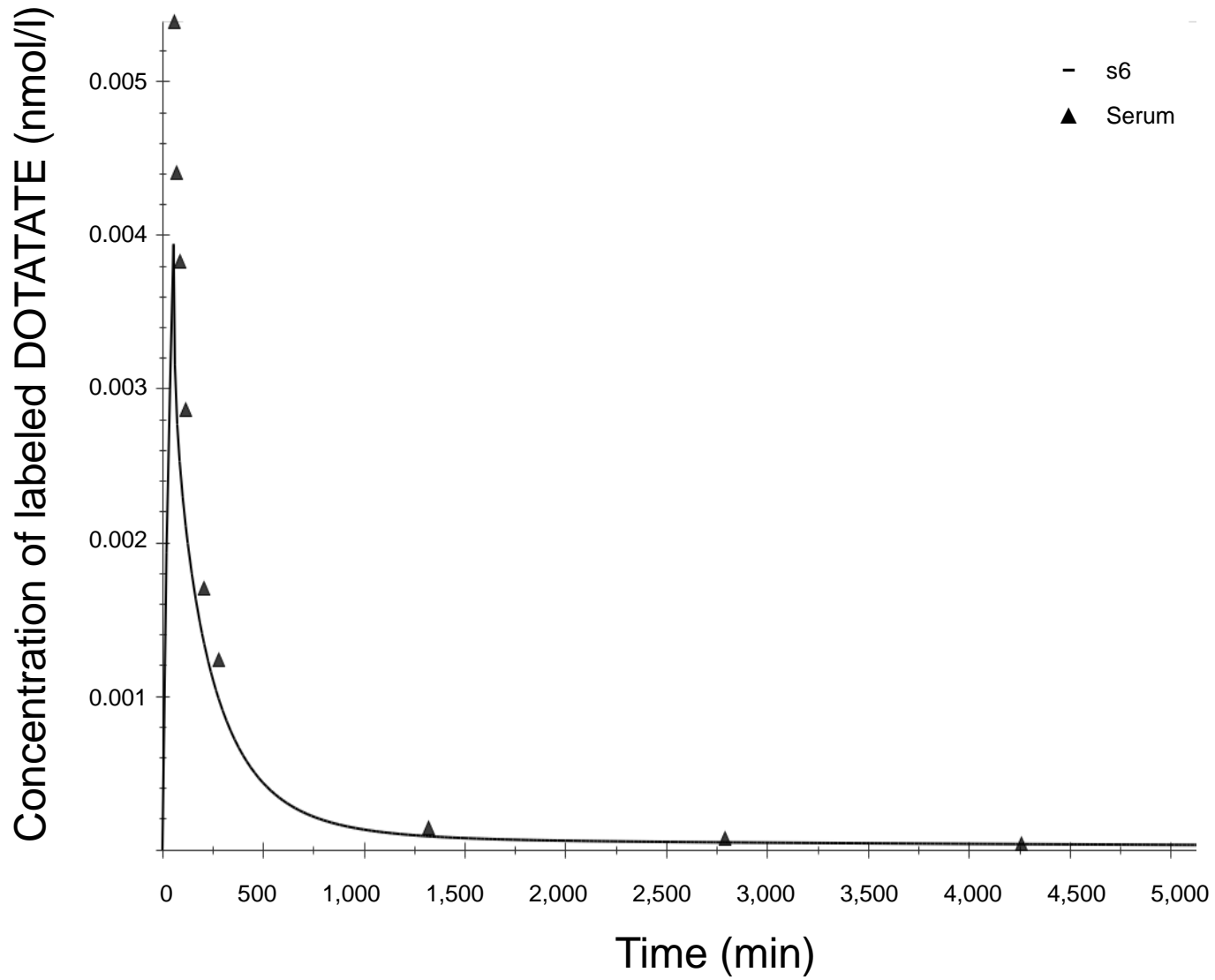
4C



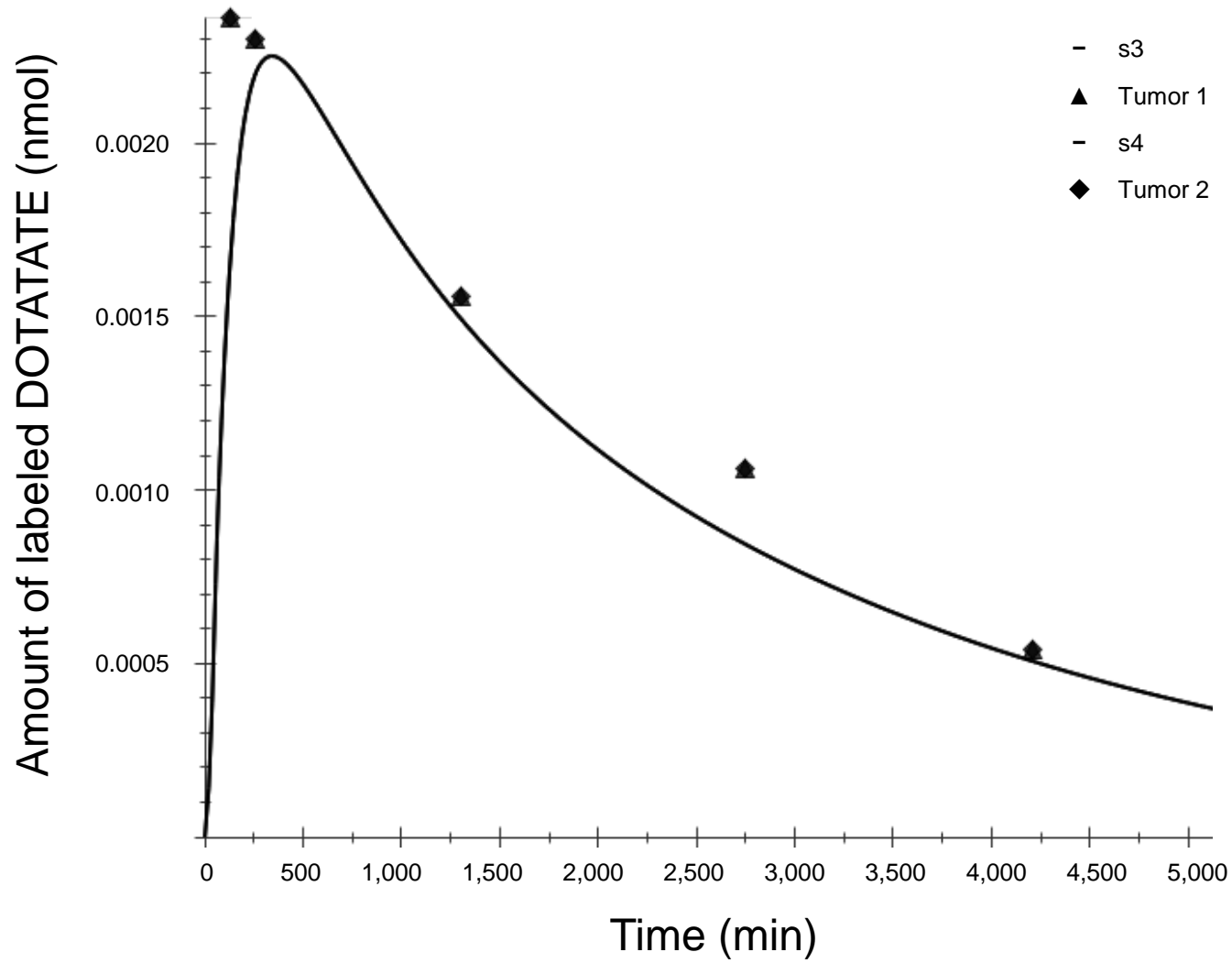
5A



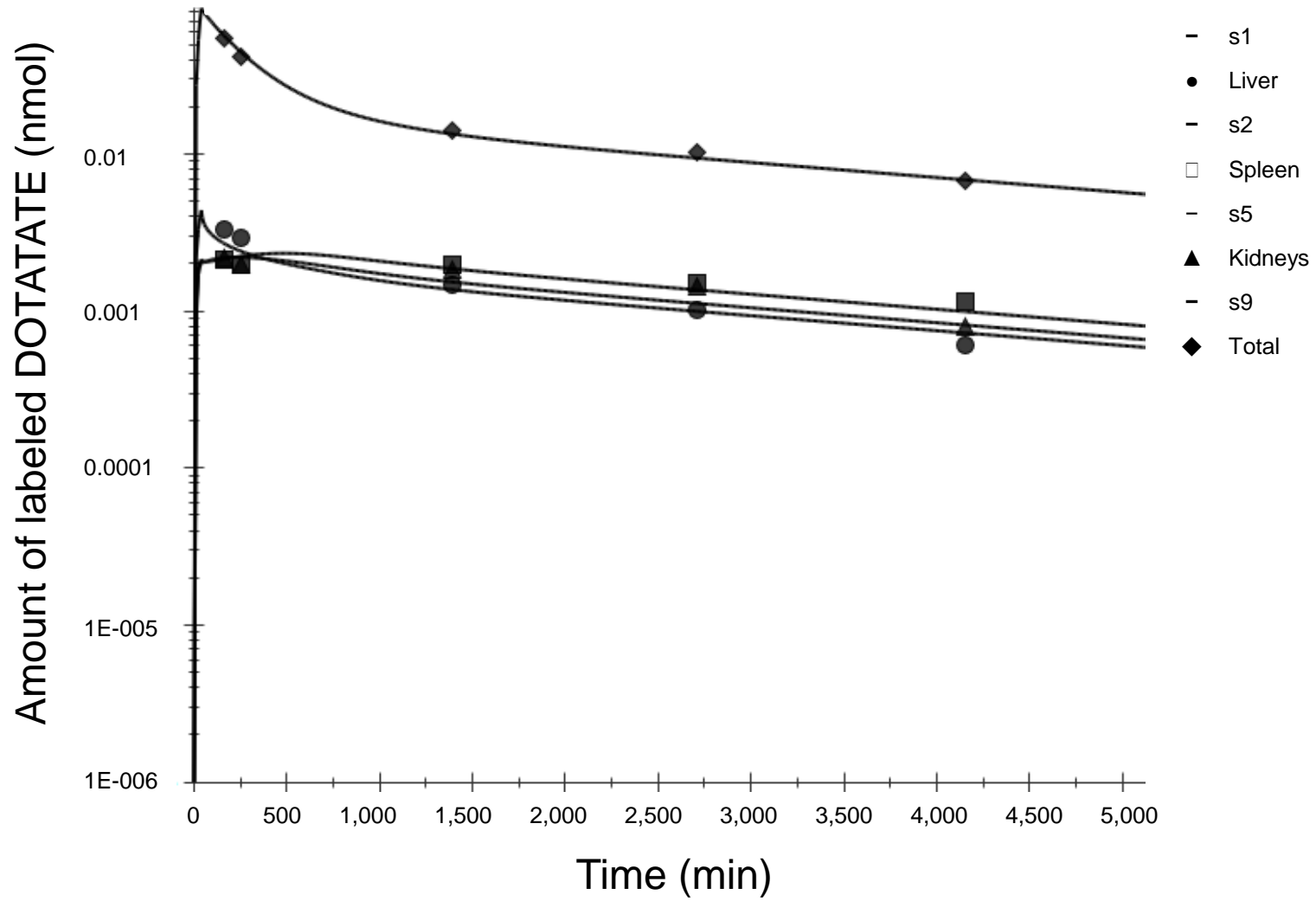
5B



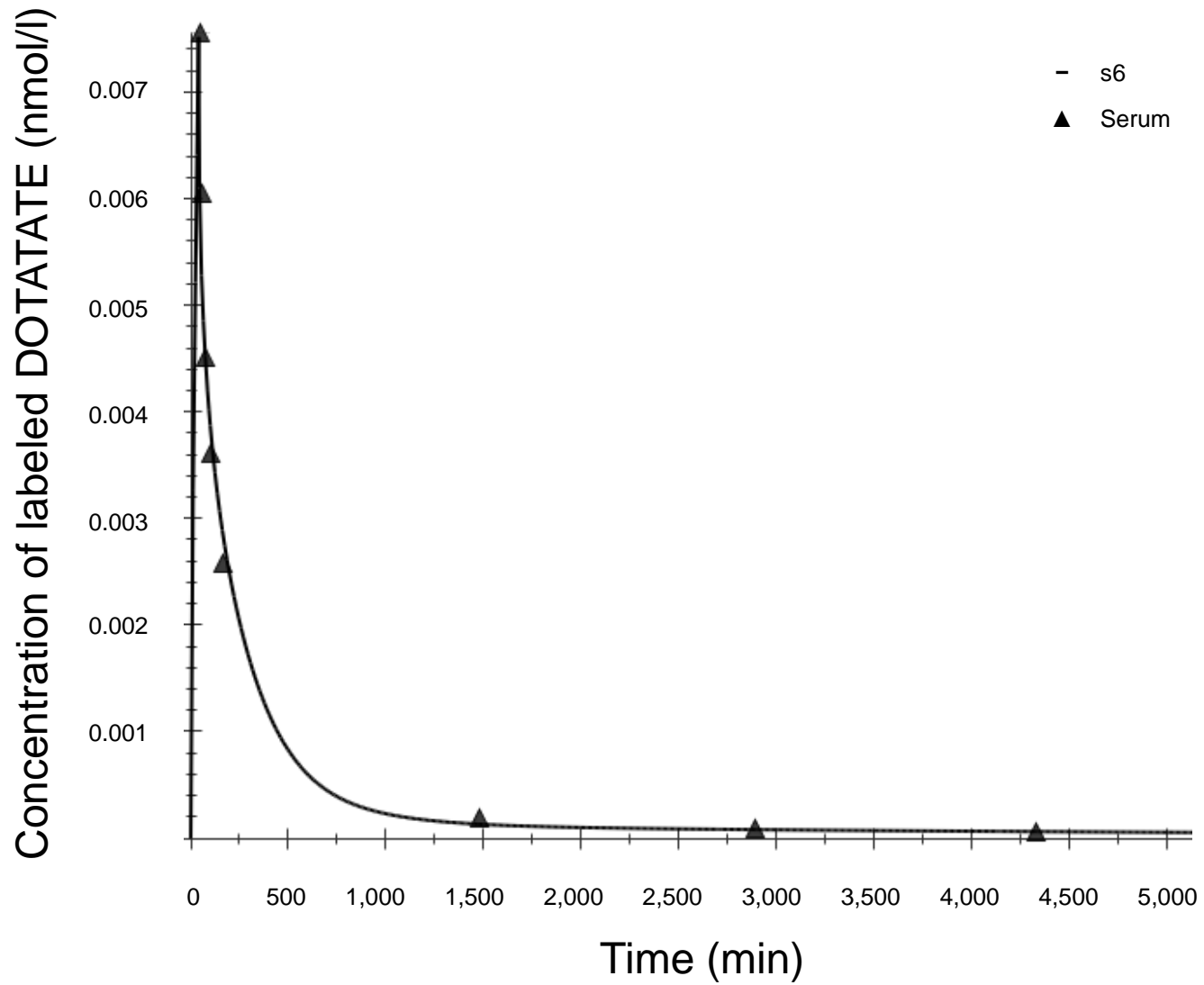
5C



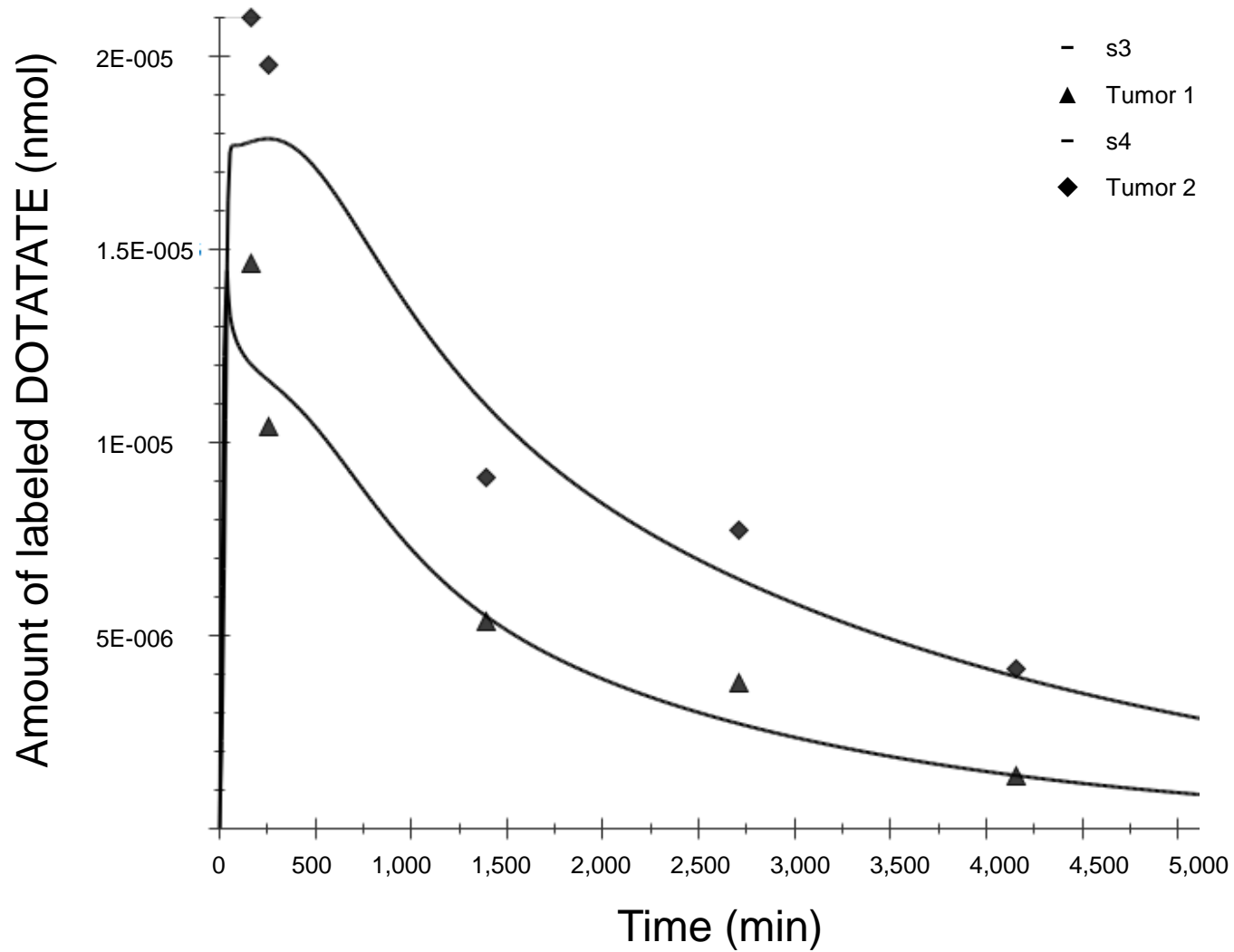
6A



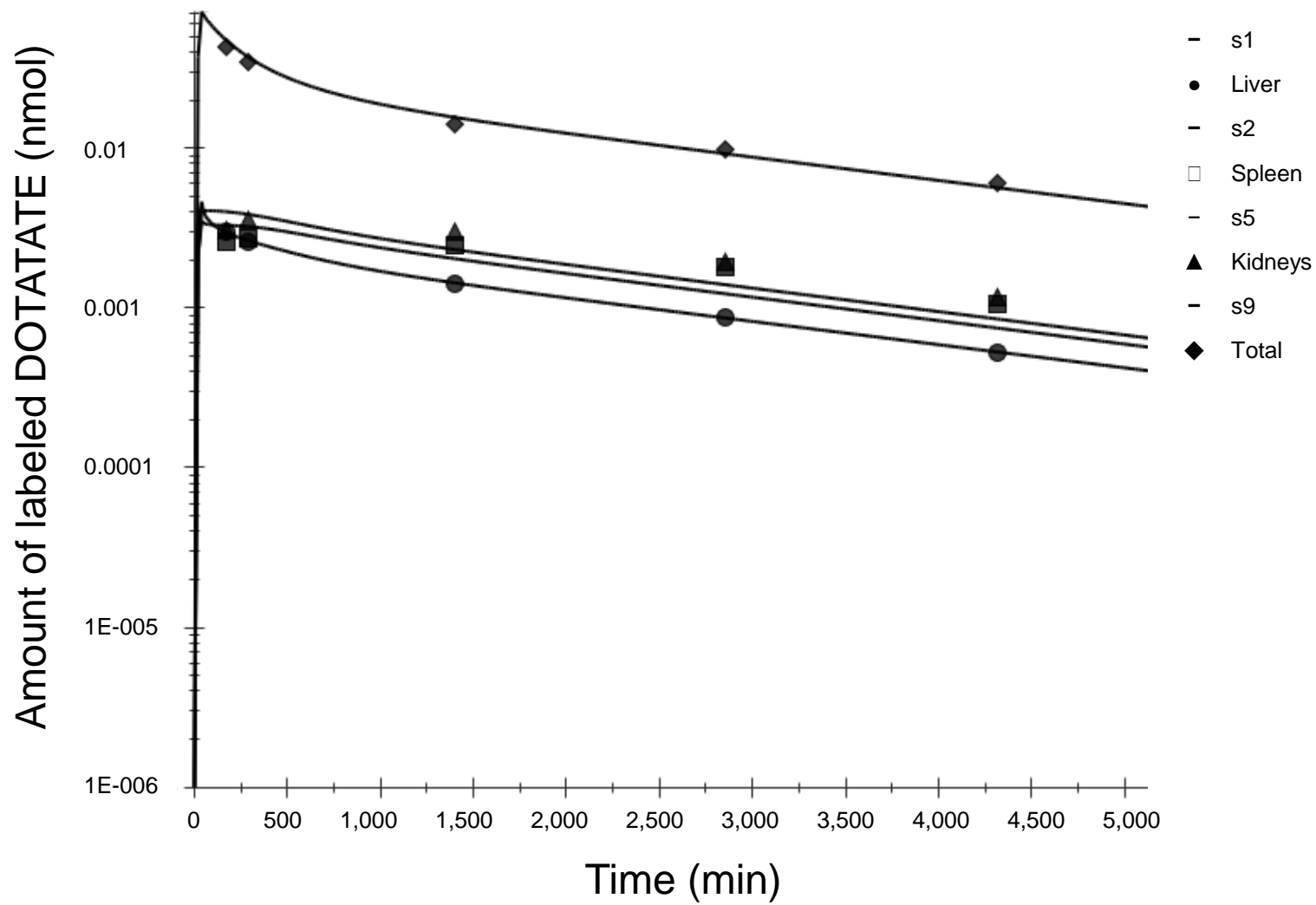
6B



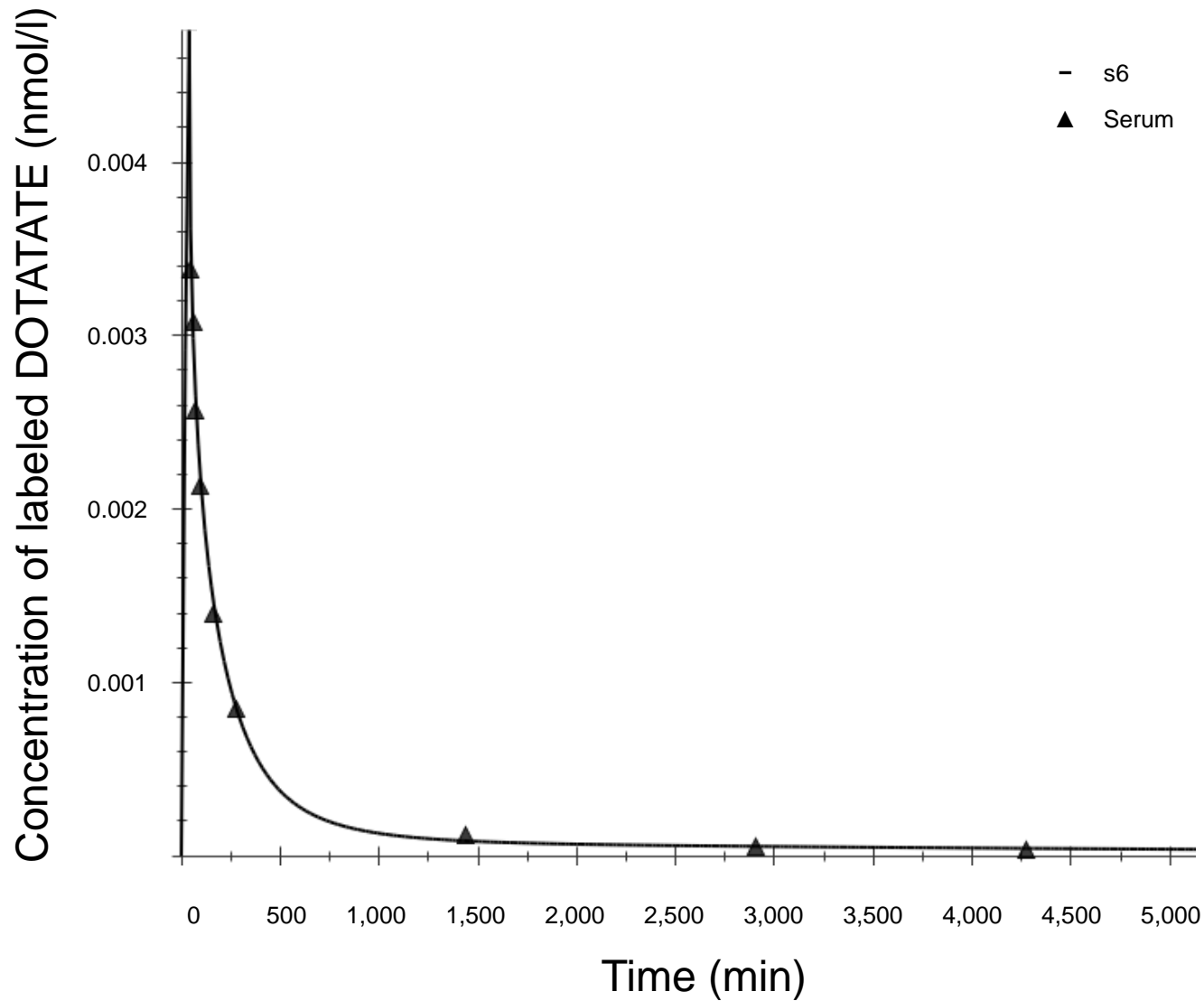
6C



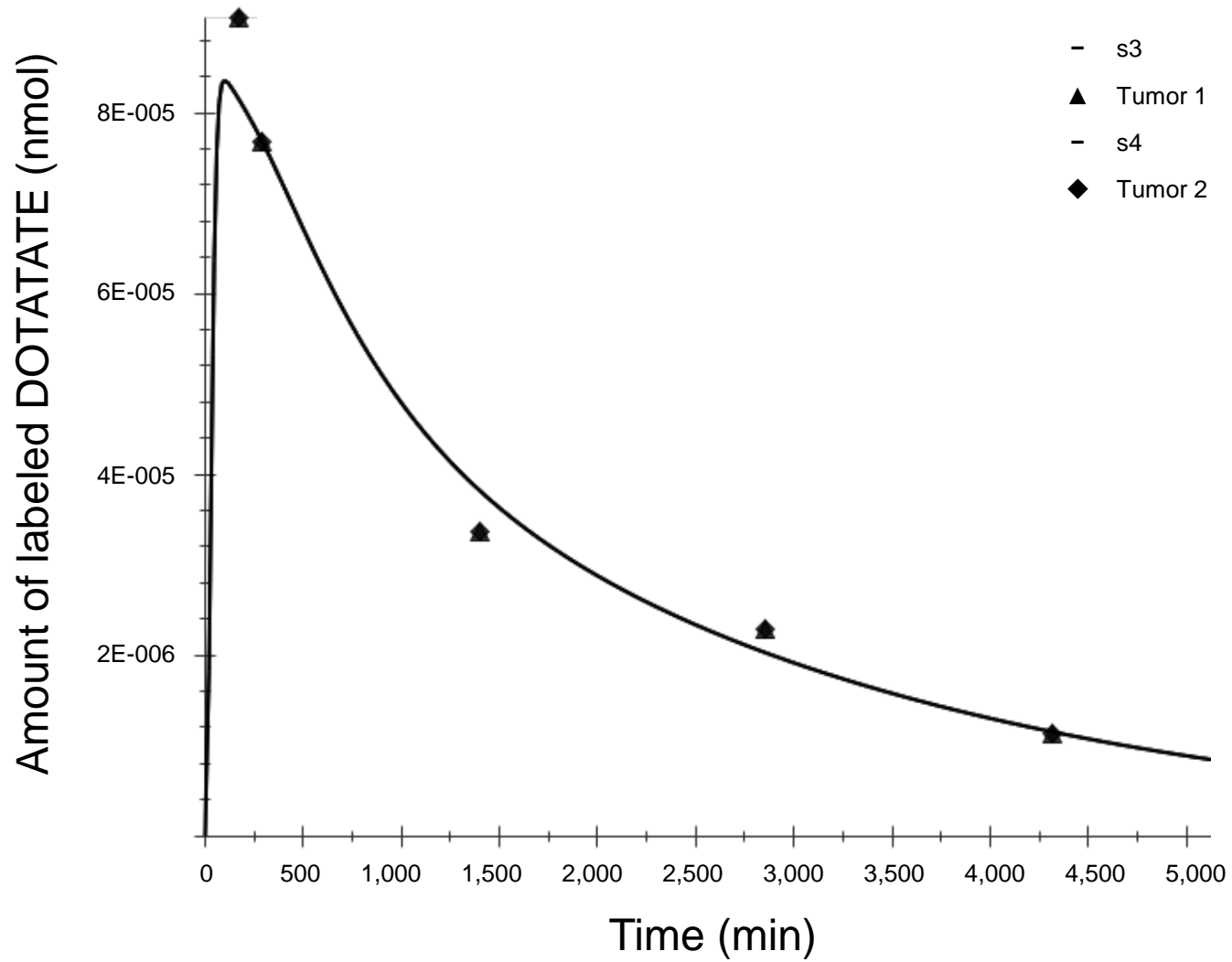
7A



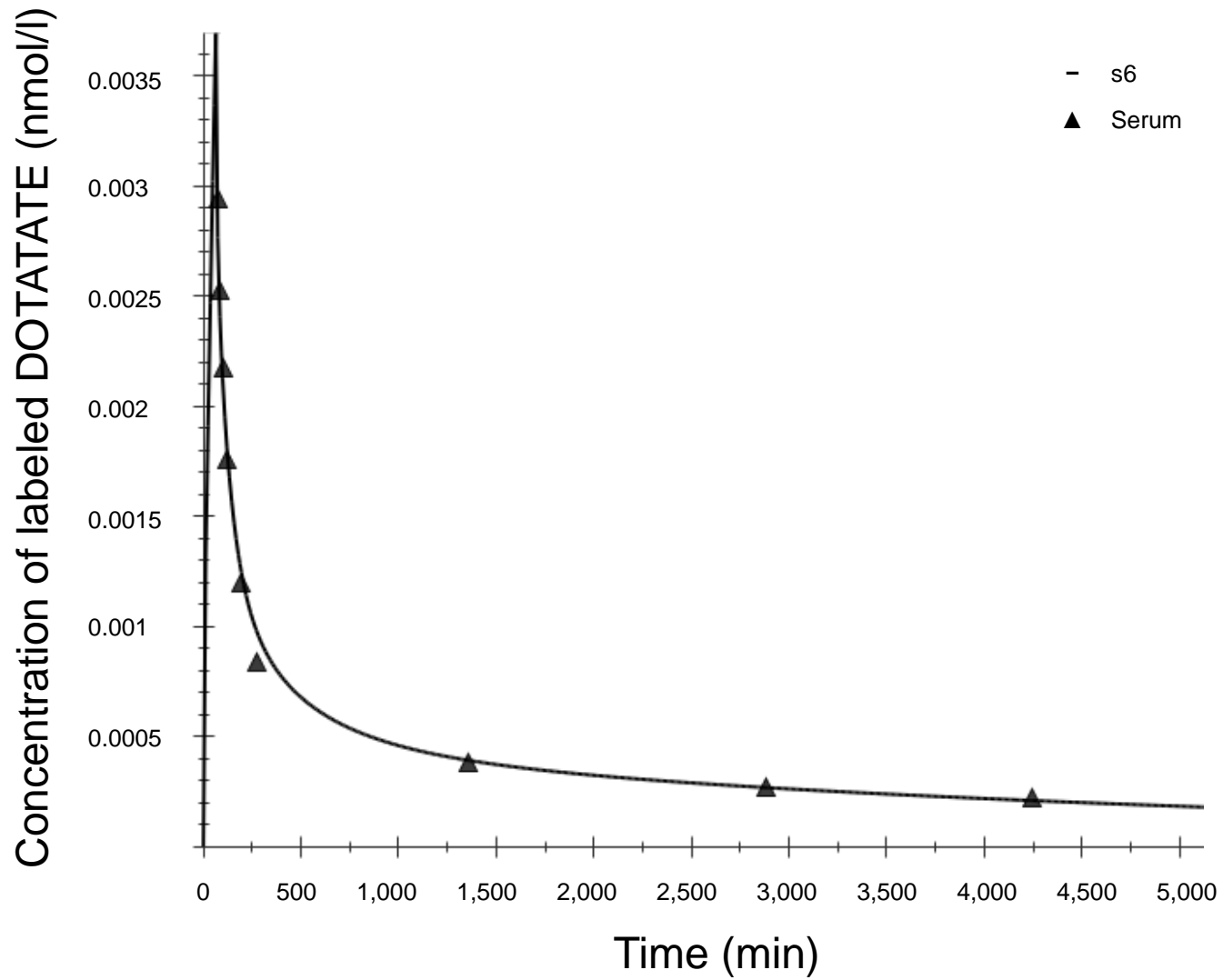
7B



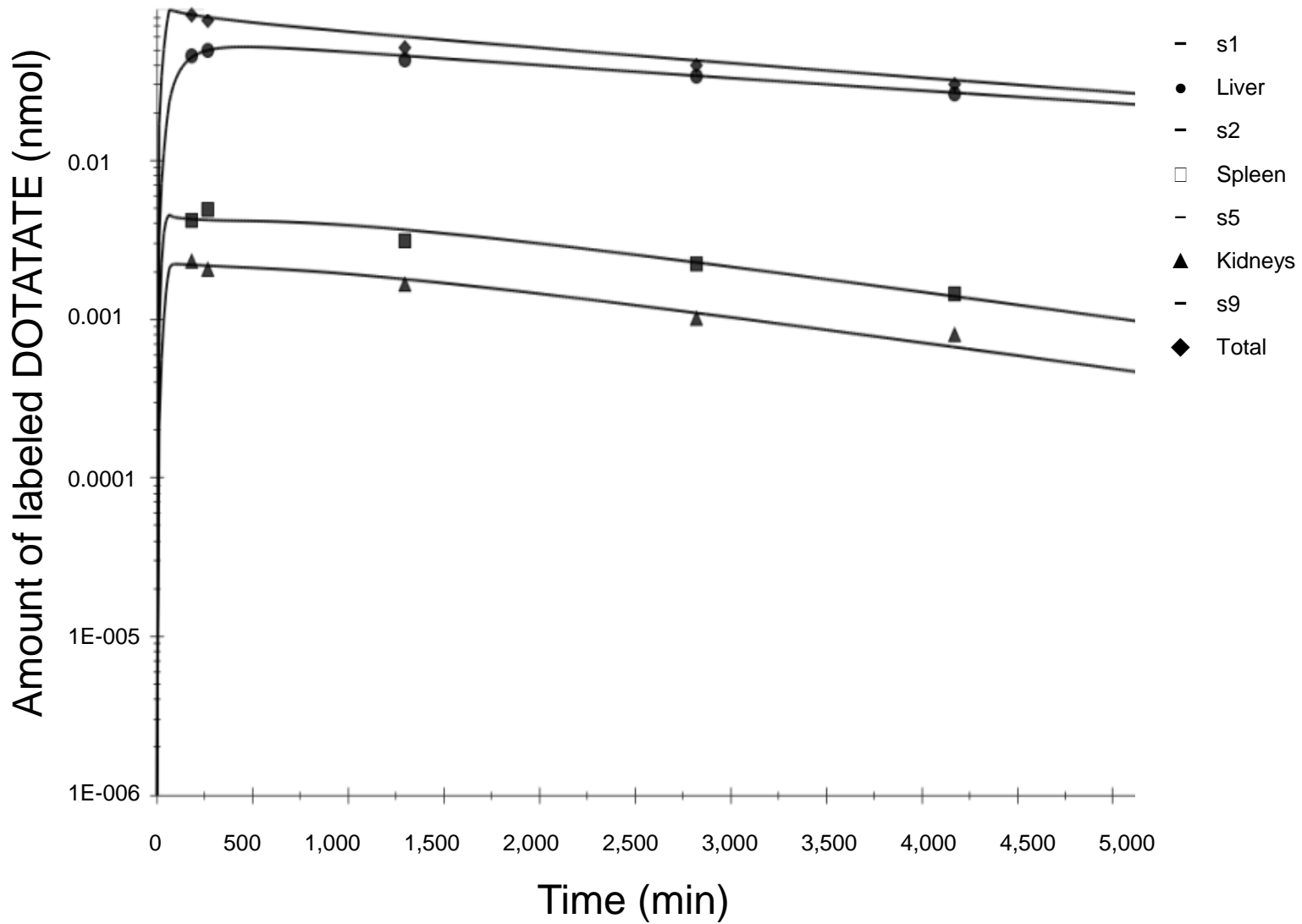
7C



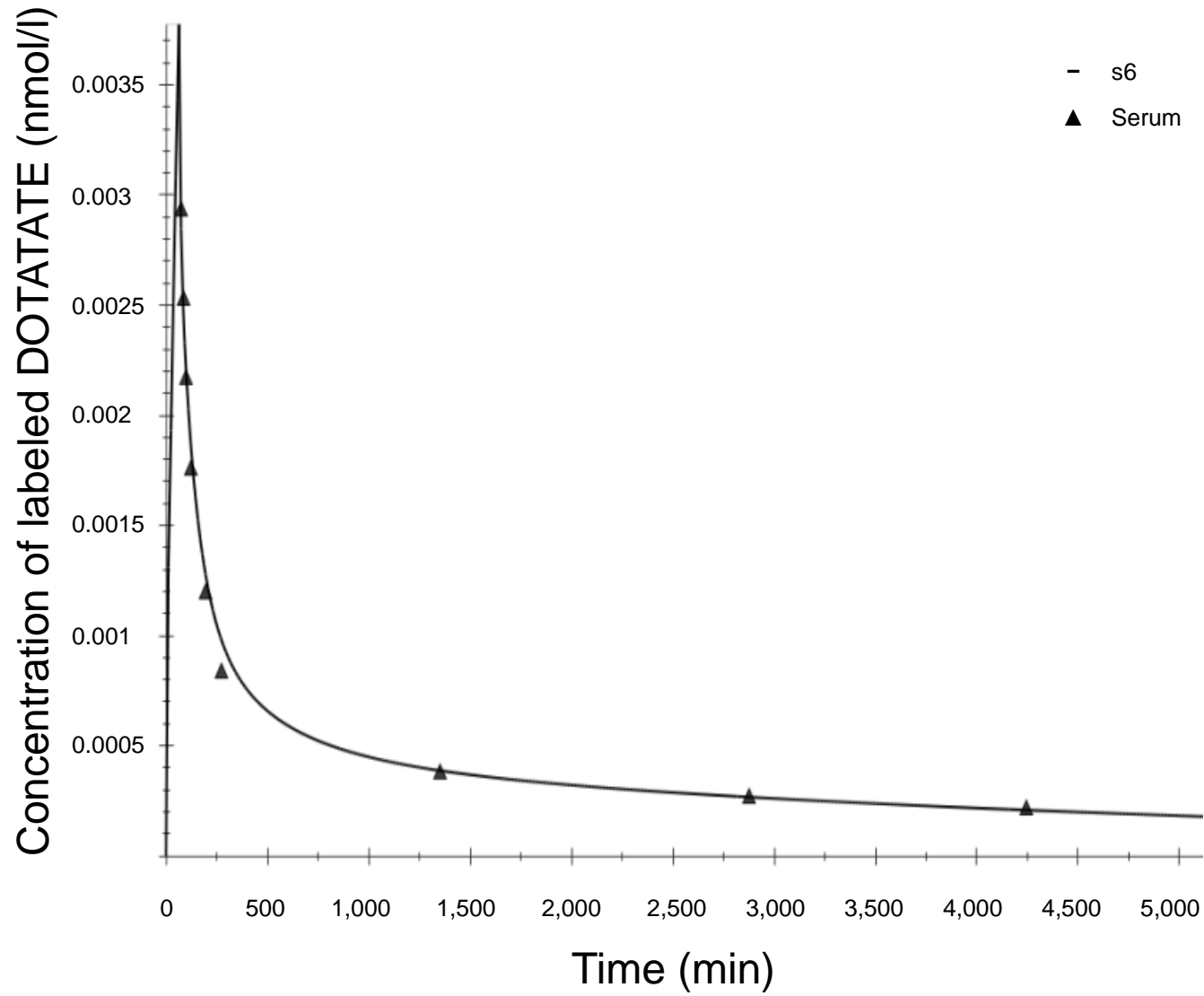
8B



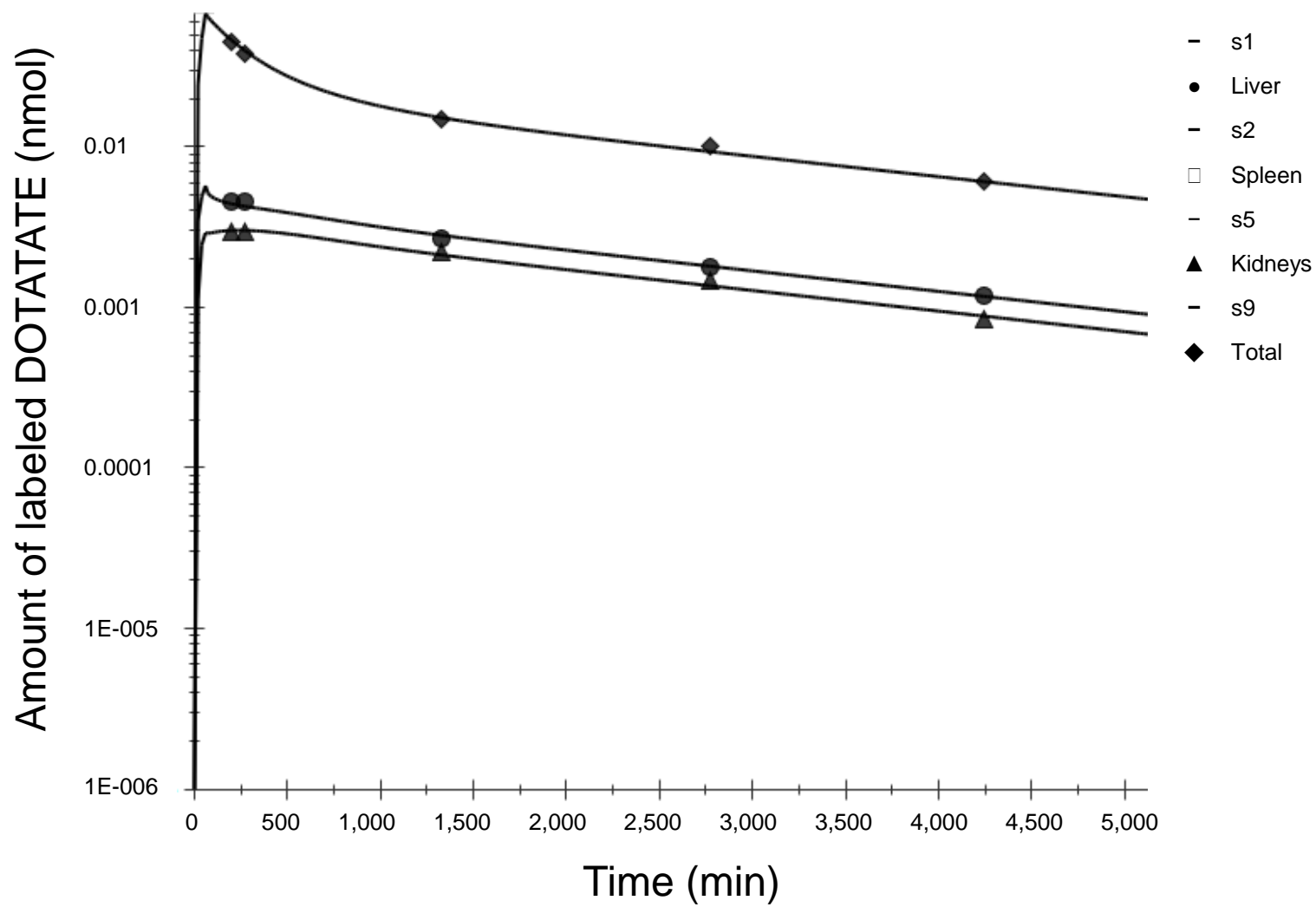
8C



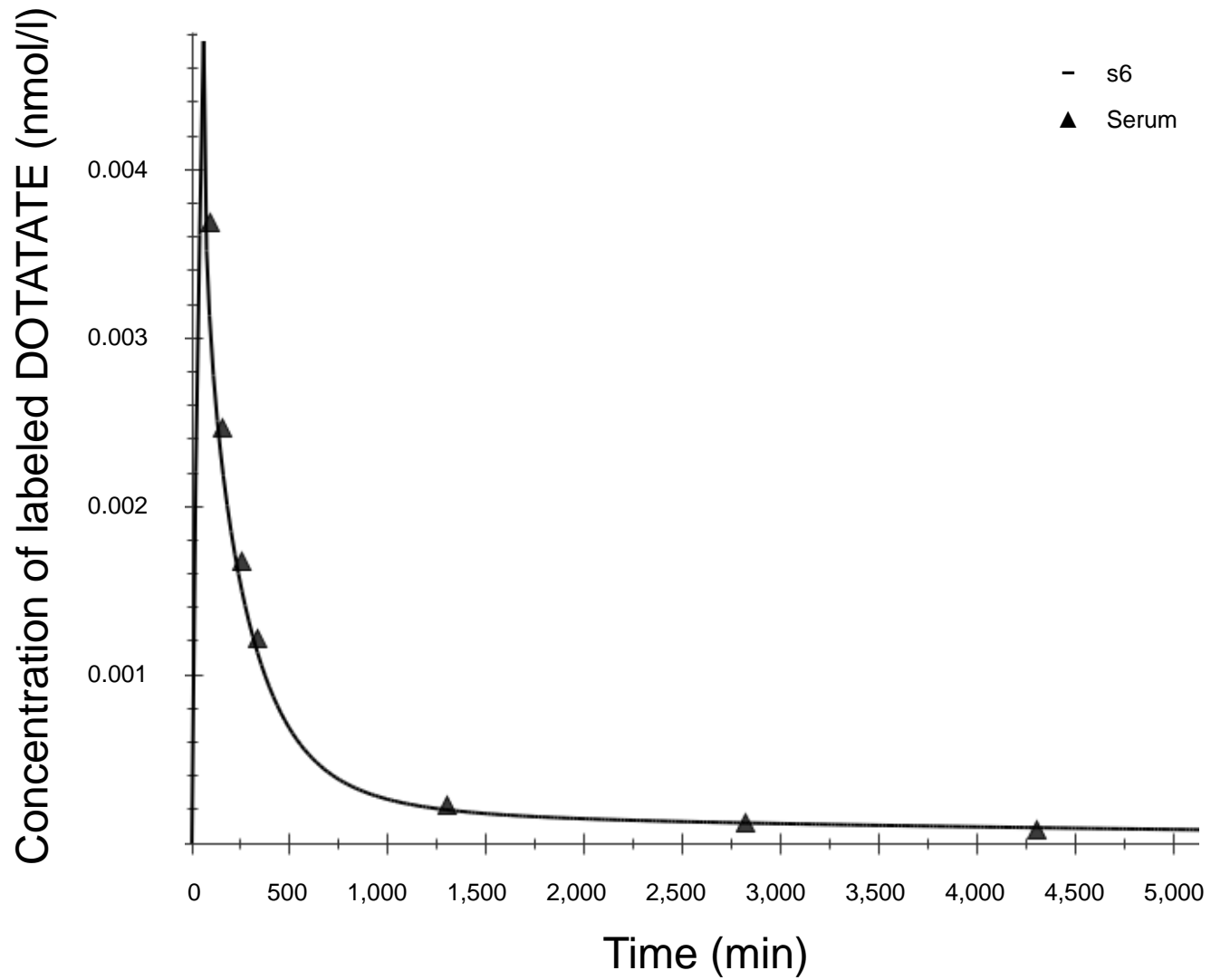
88 D



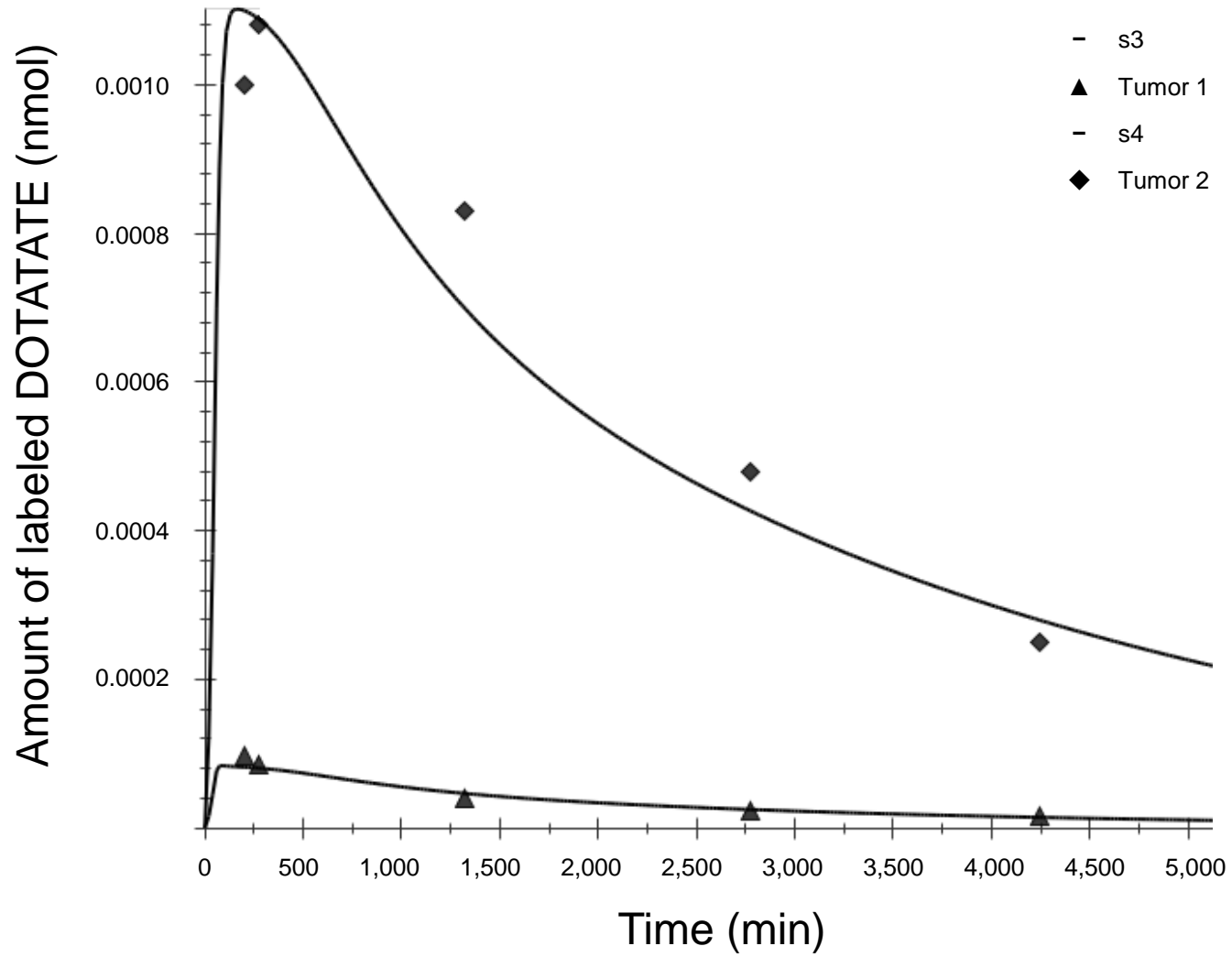
9A



9B

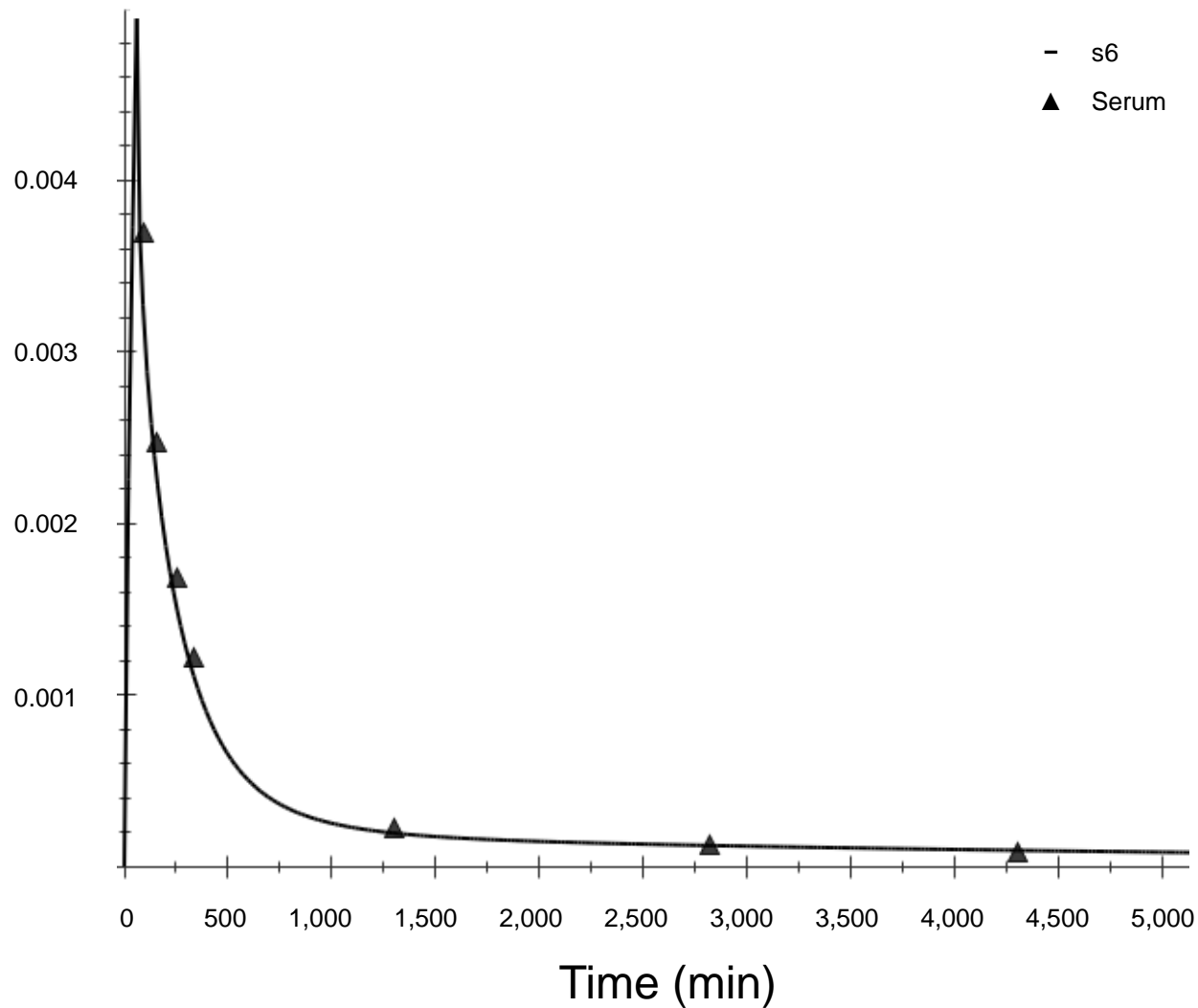


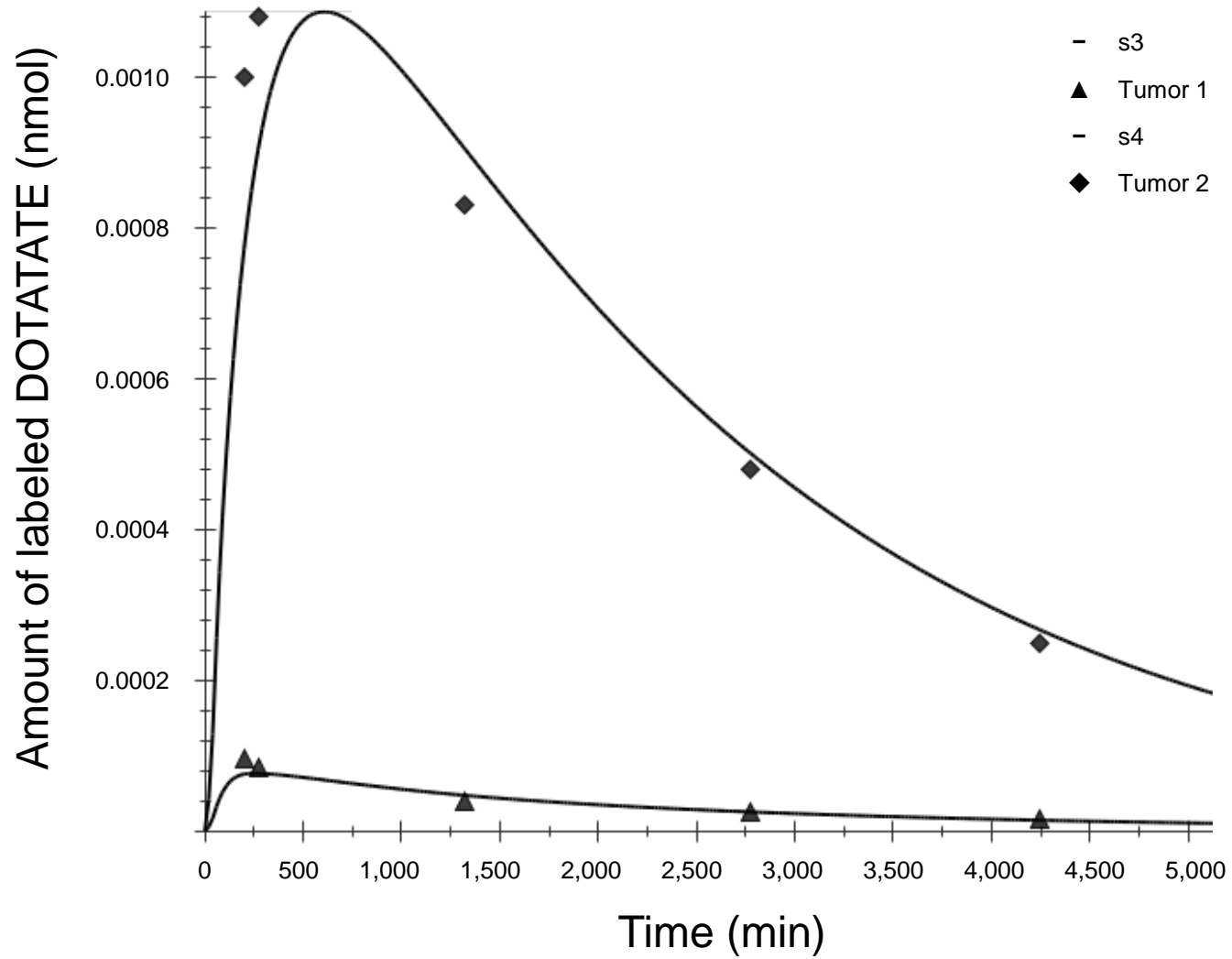
90



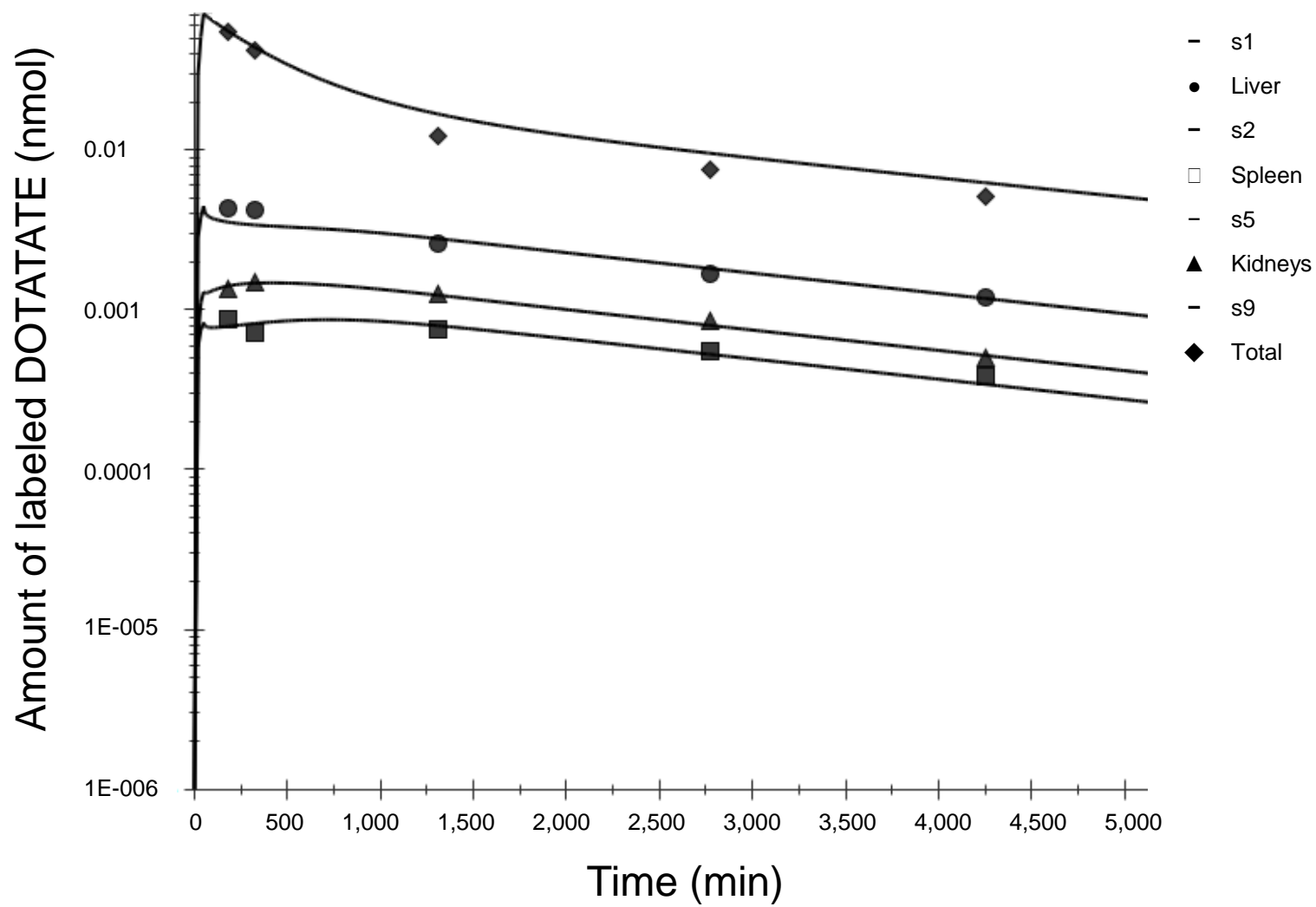
9E

Concentration of labeled DOTATATE (nmol/l)



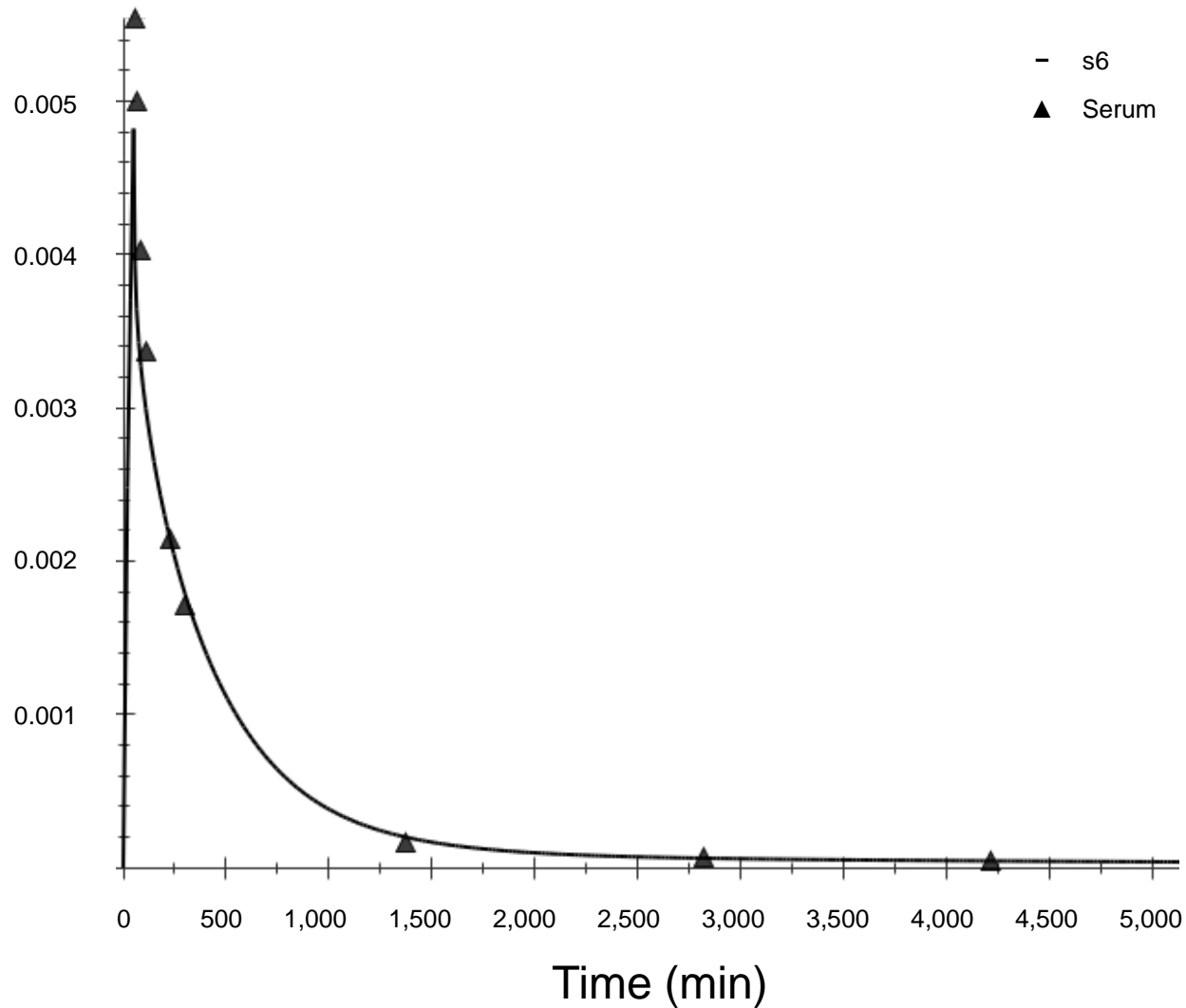


10A

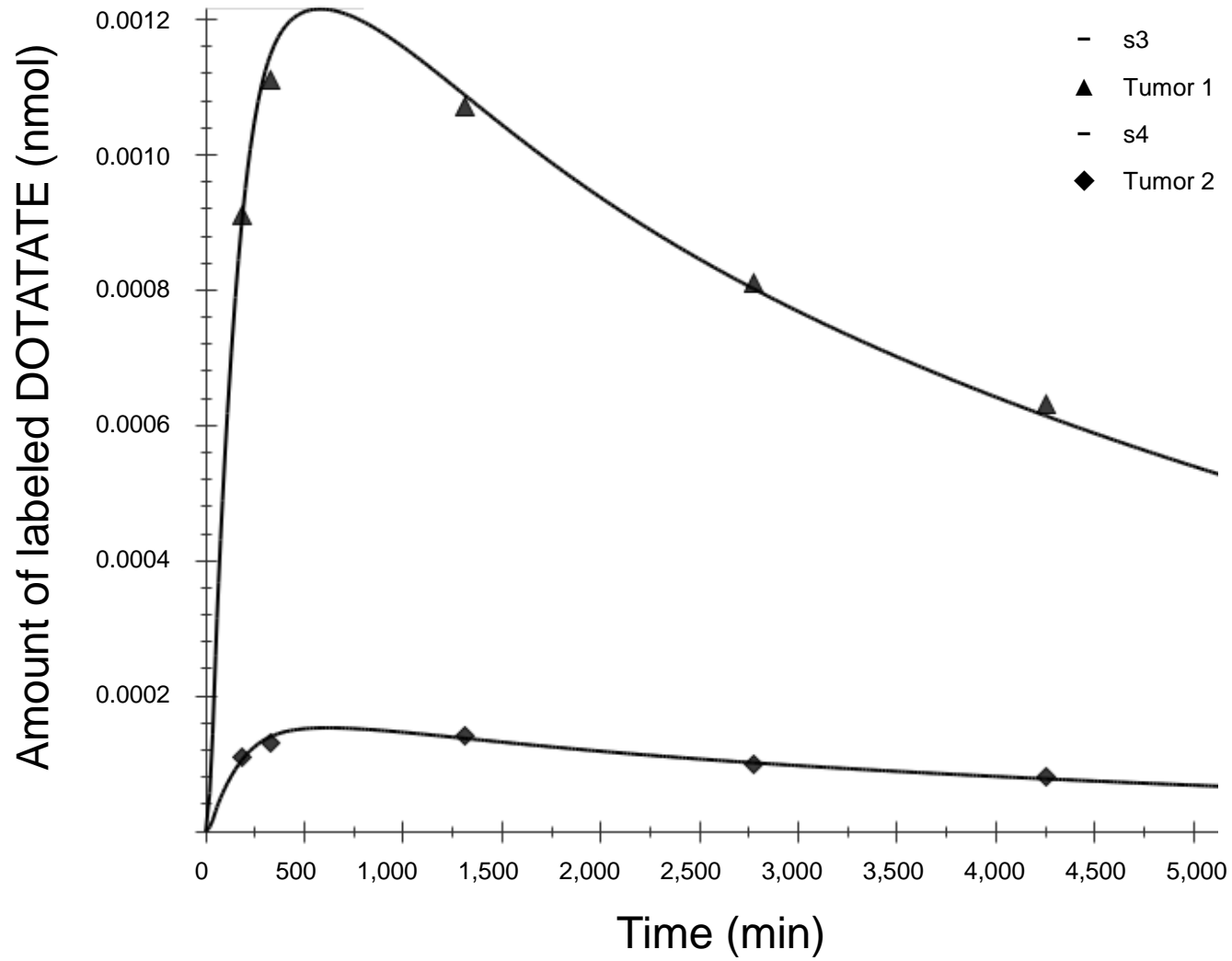


10B

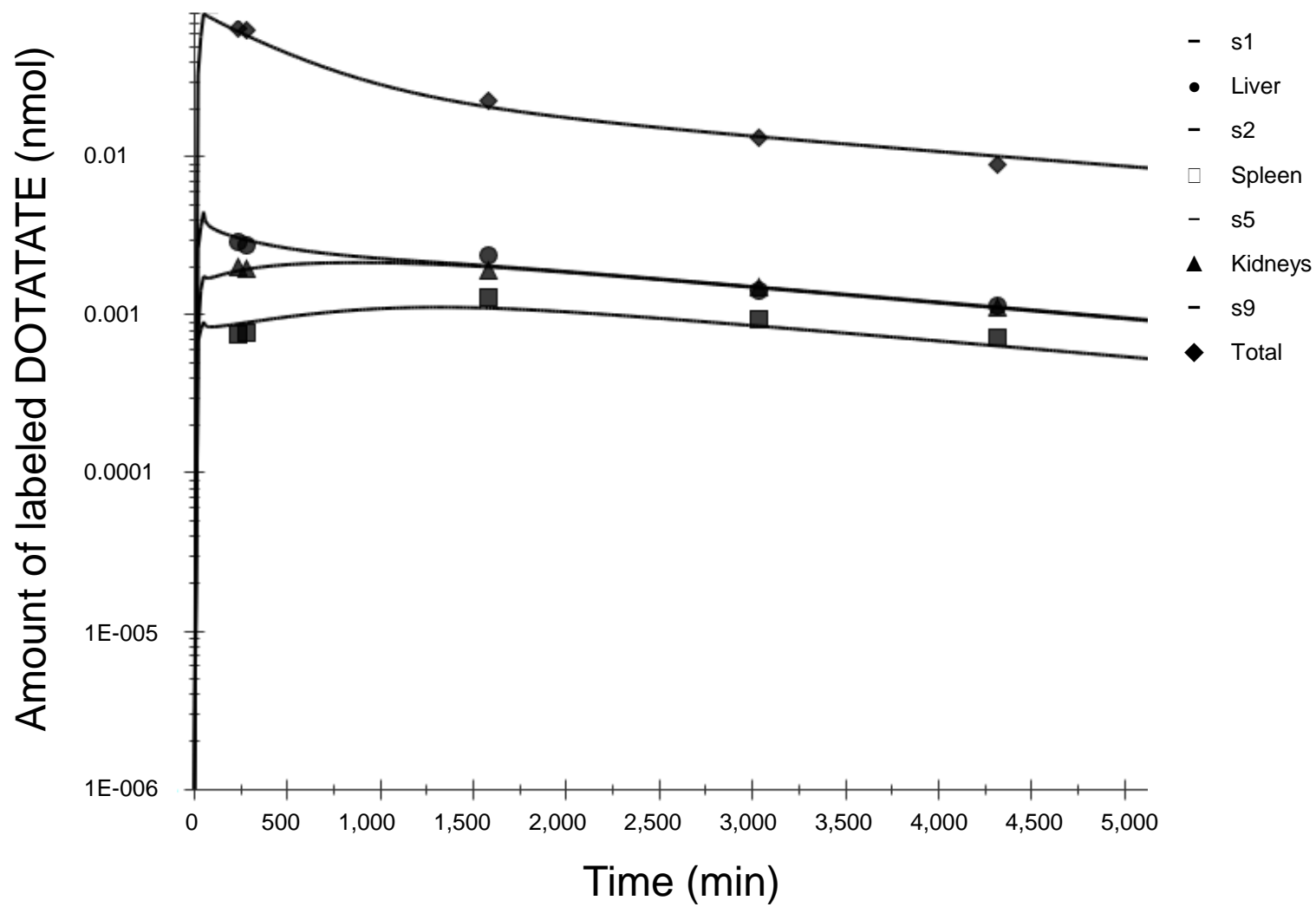
Concentration of labeled DOTATATE (nmol/l)



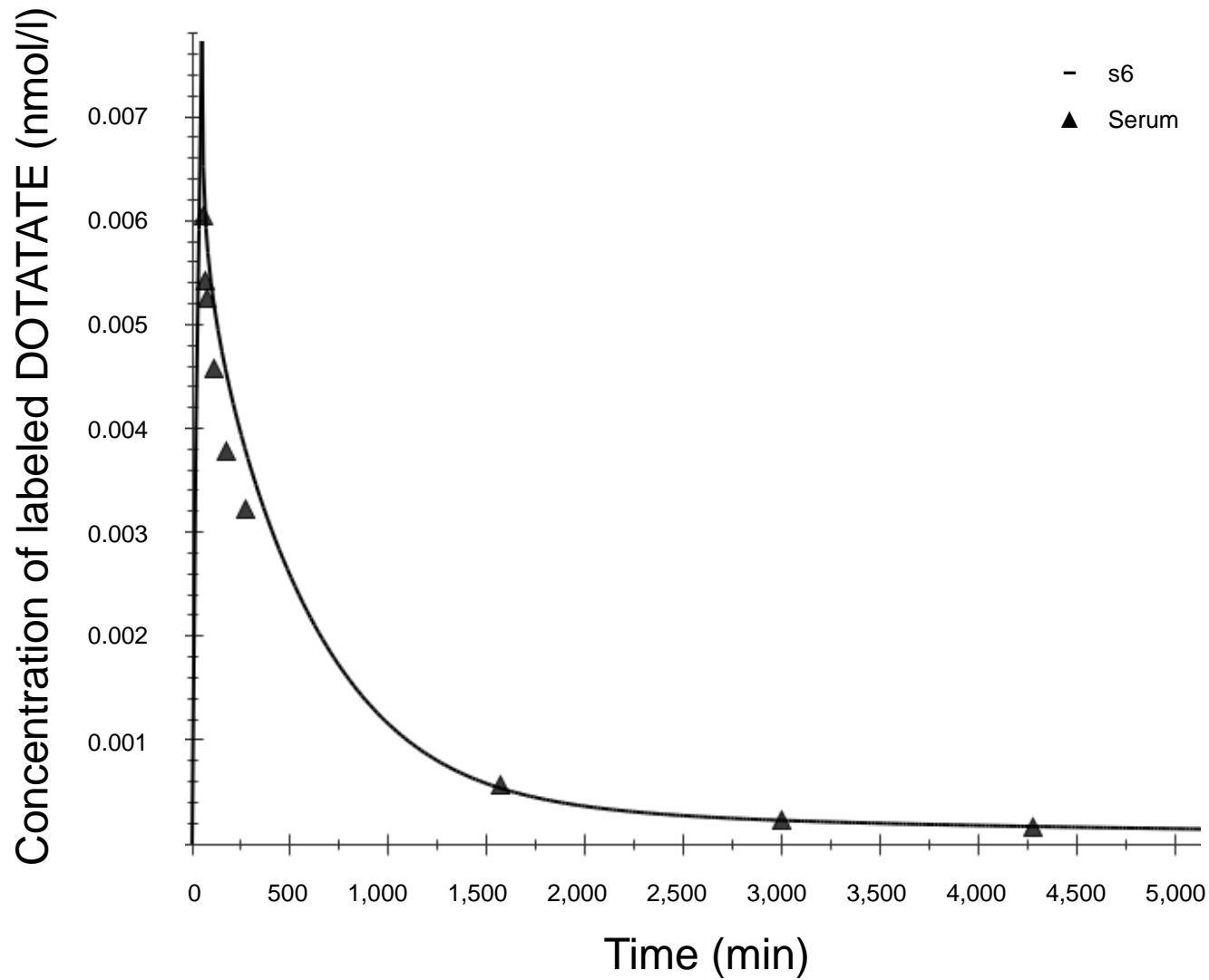
10C



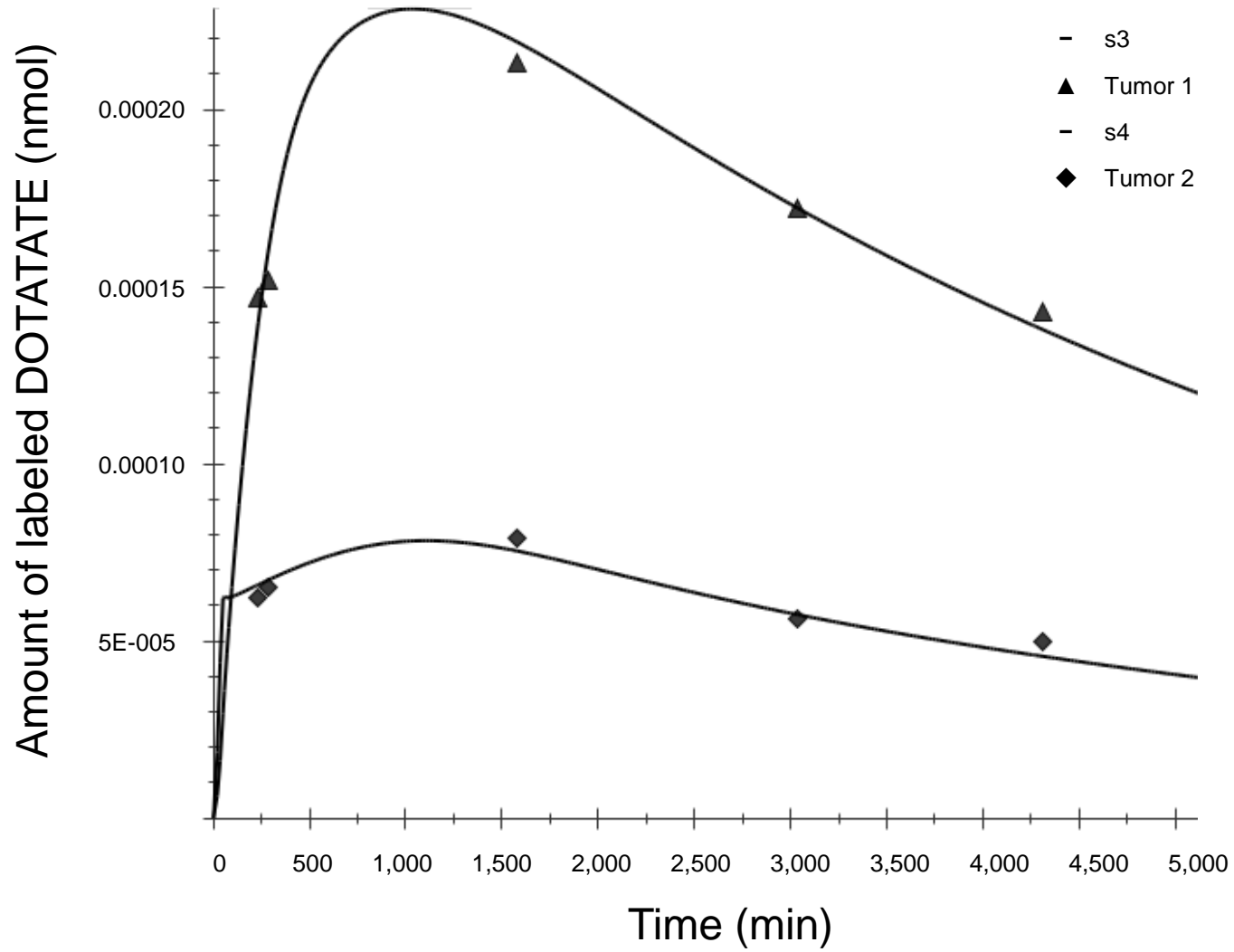
11A



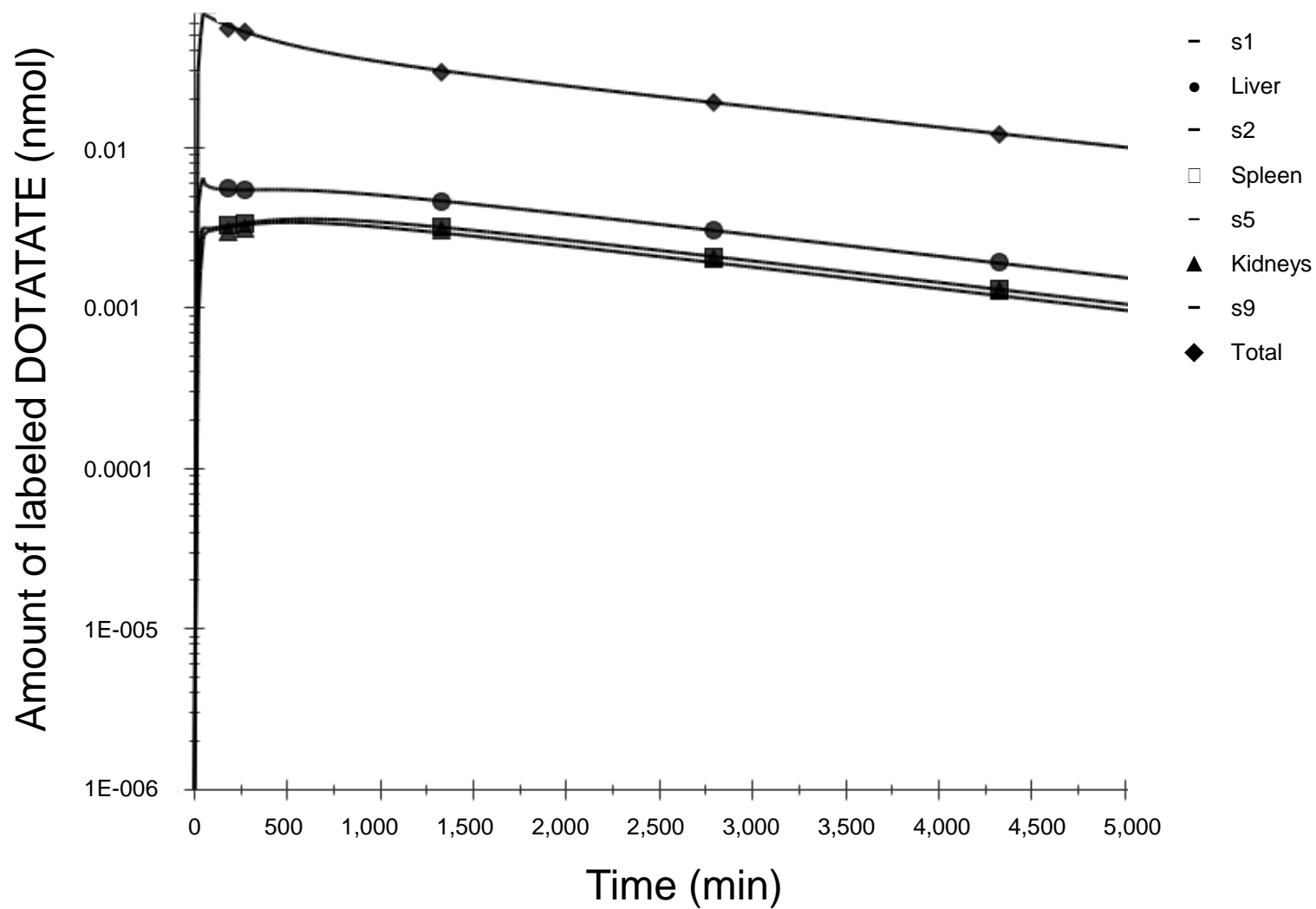
11B



11C

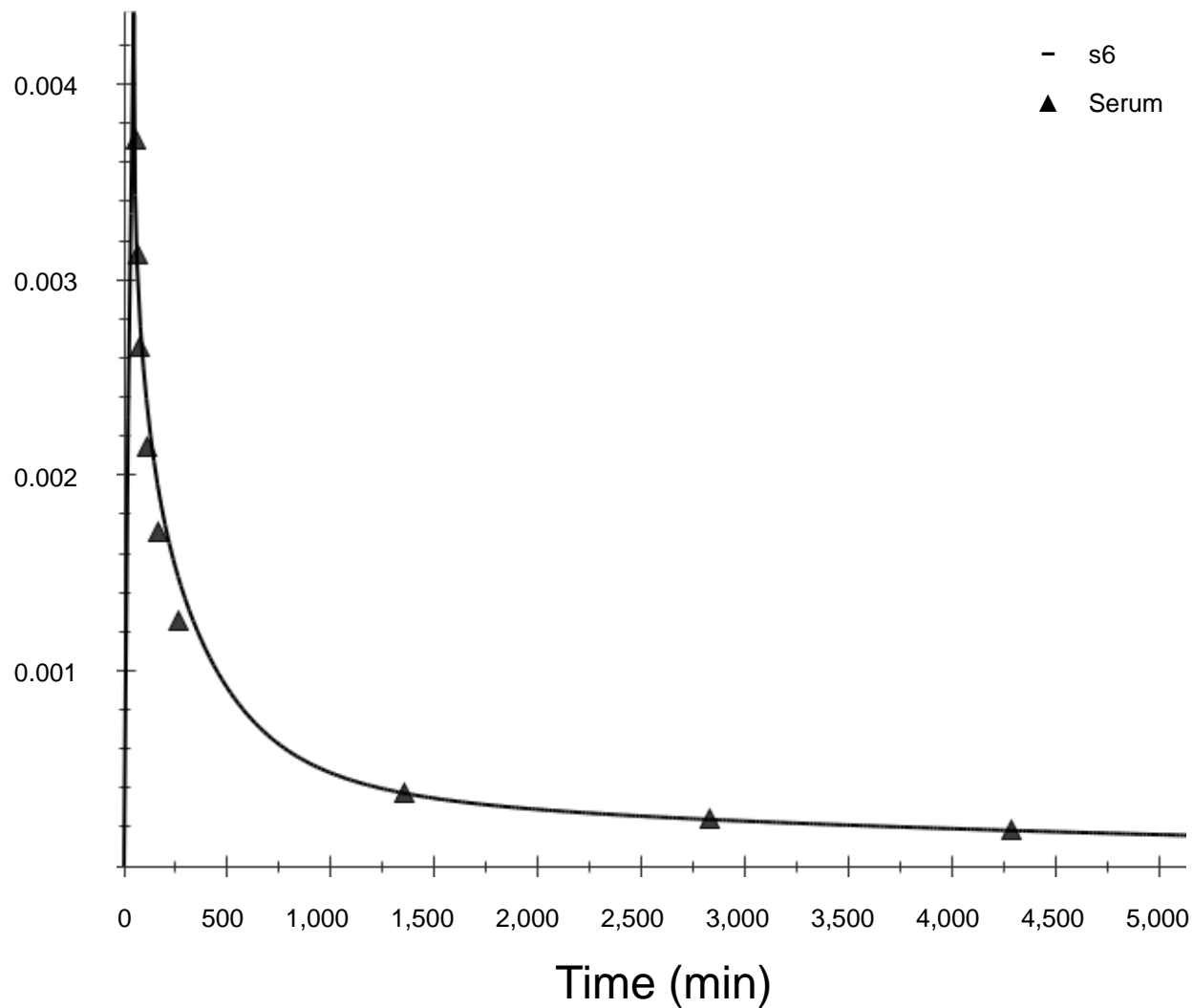


12A

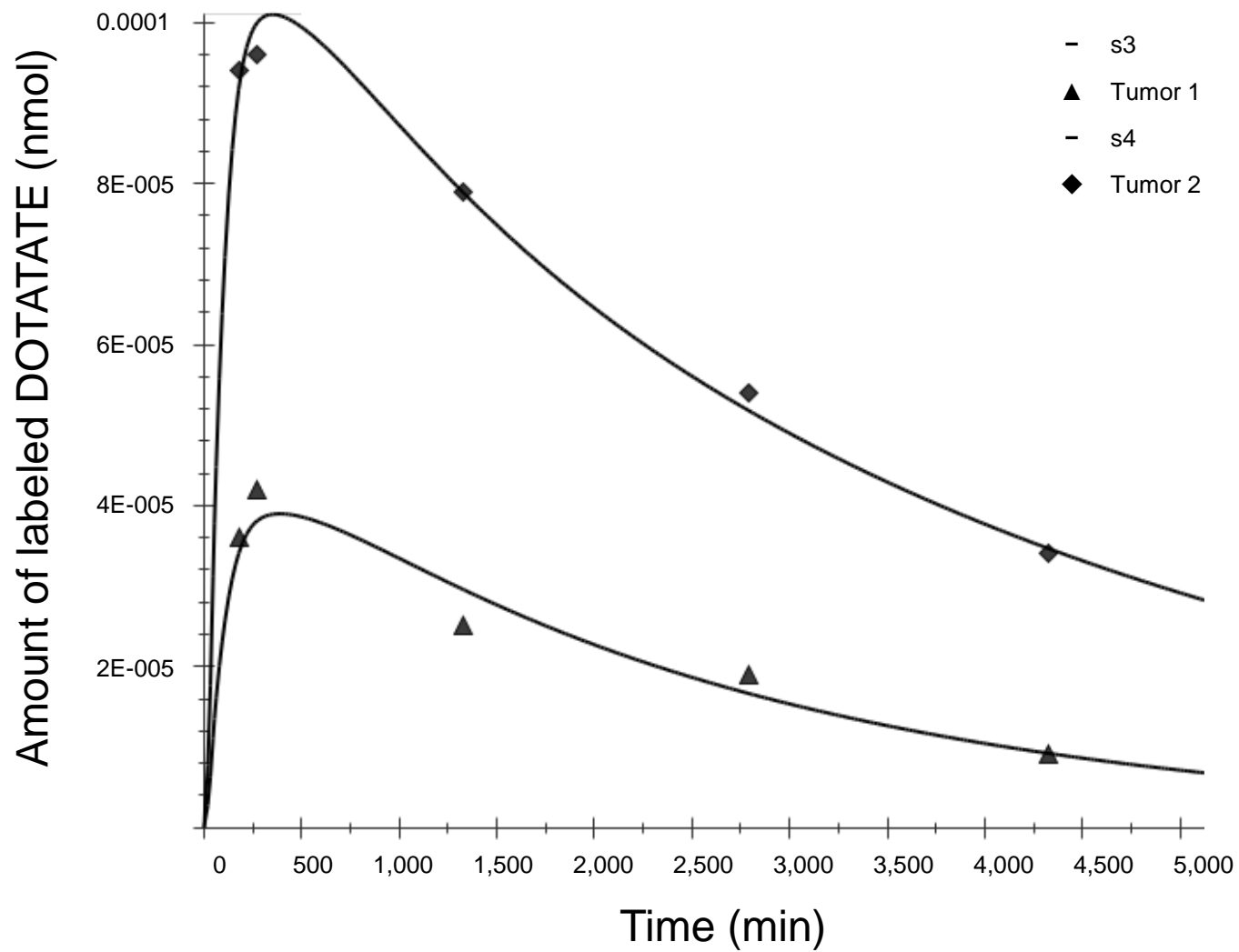


12B

Concentration of labeled DOTATATE (nmol/l)



12C



Supplemental Data

Optimal BED ratio simulations for N1-N12 (Figures 1-12)

Figure 1

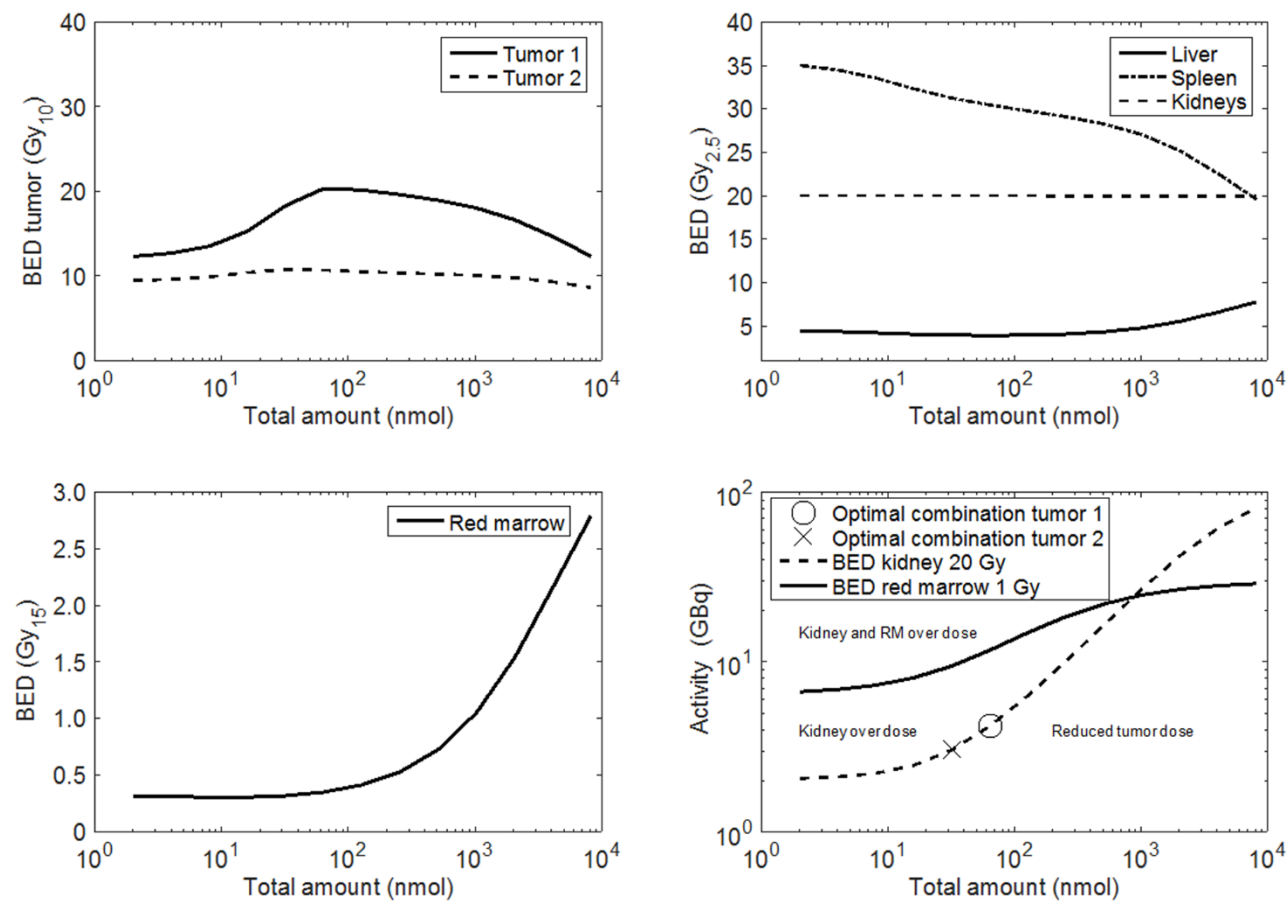


Figure 2

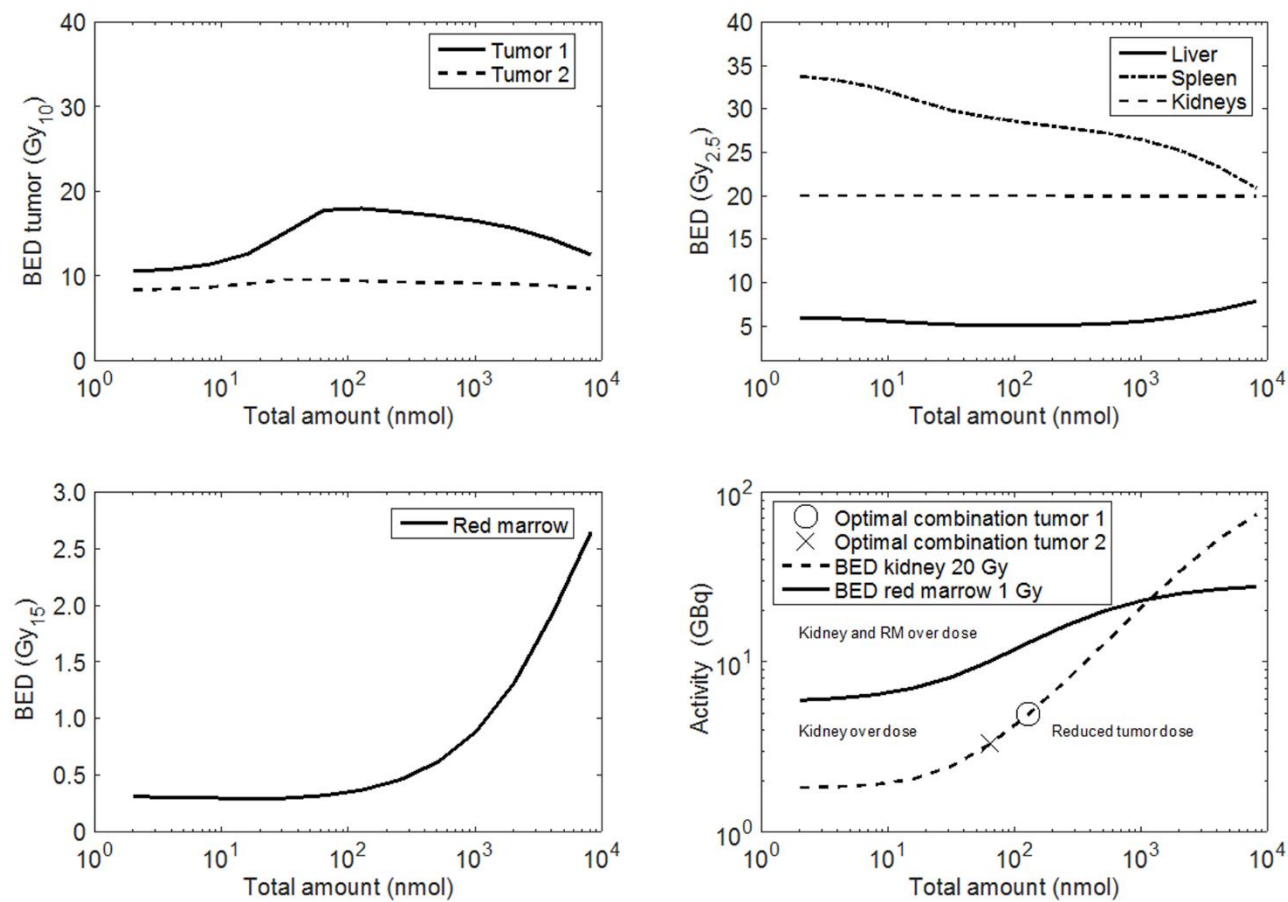


Figure 3

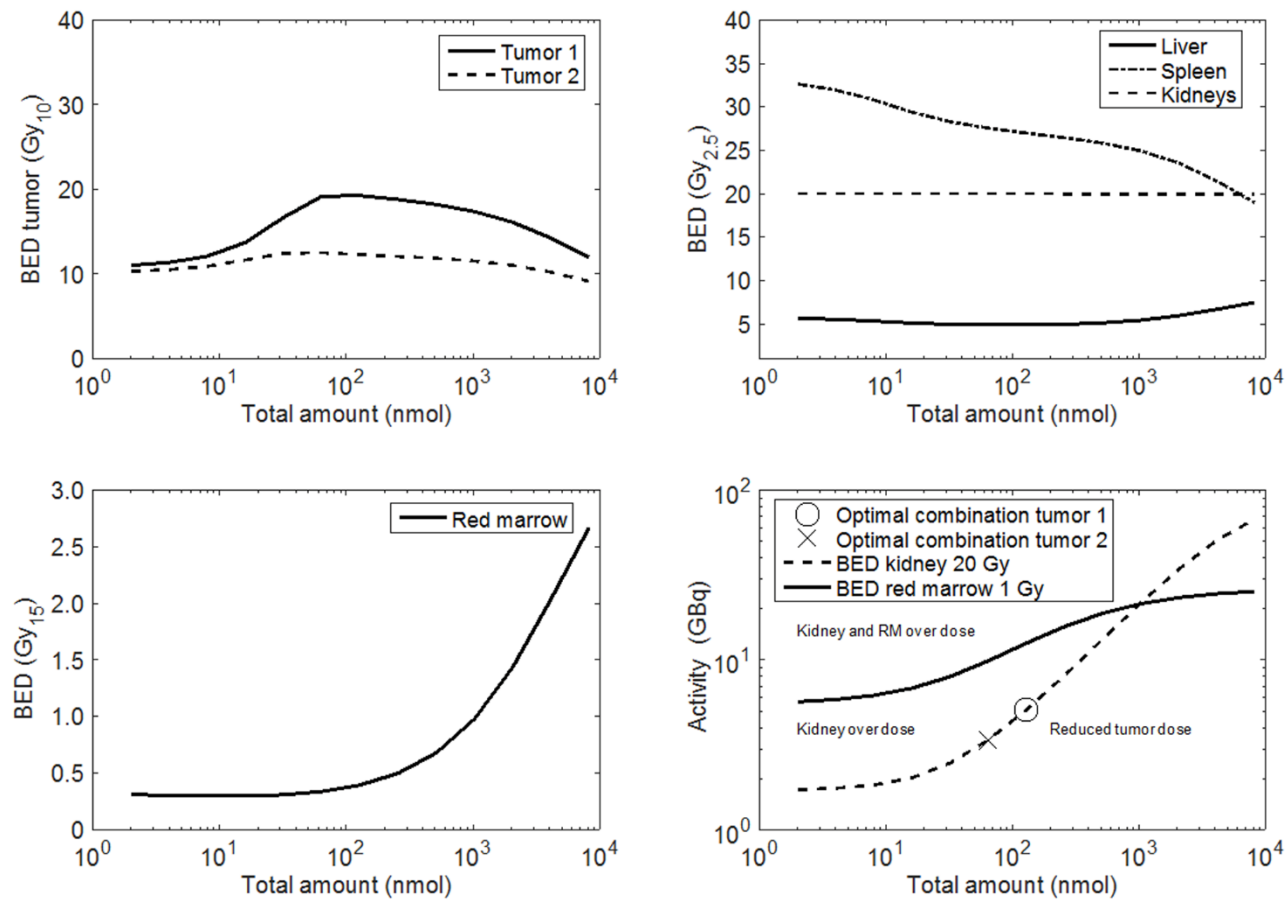


Figure 4

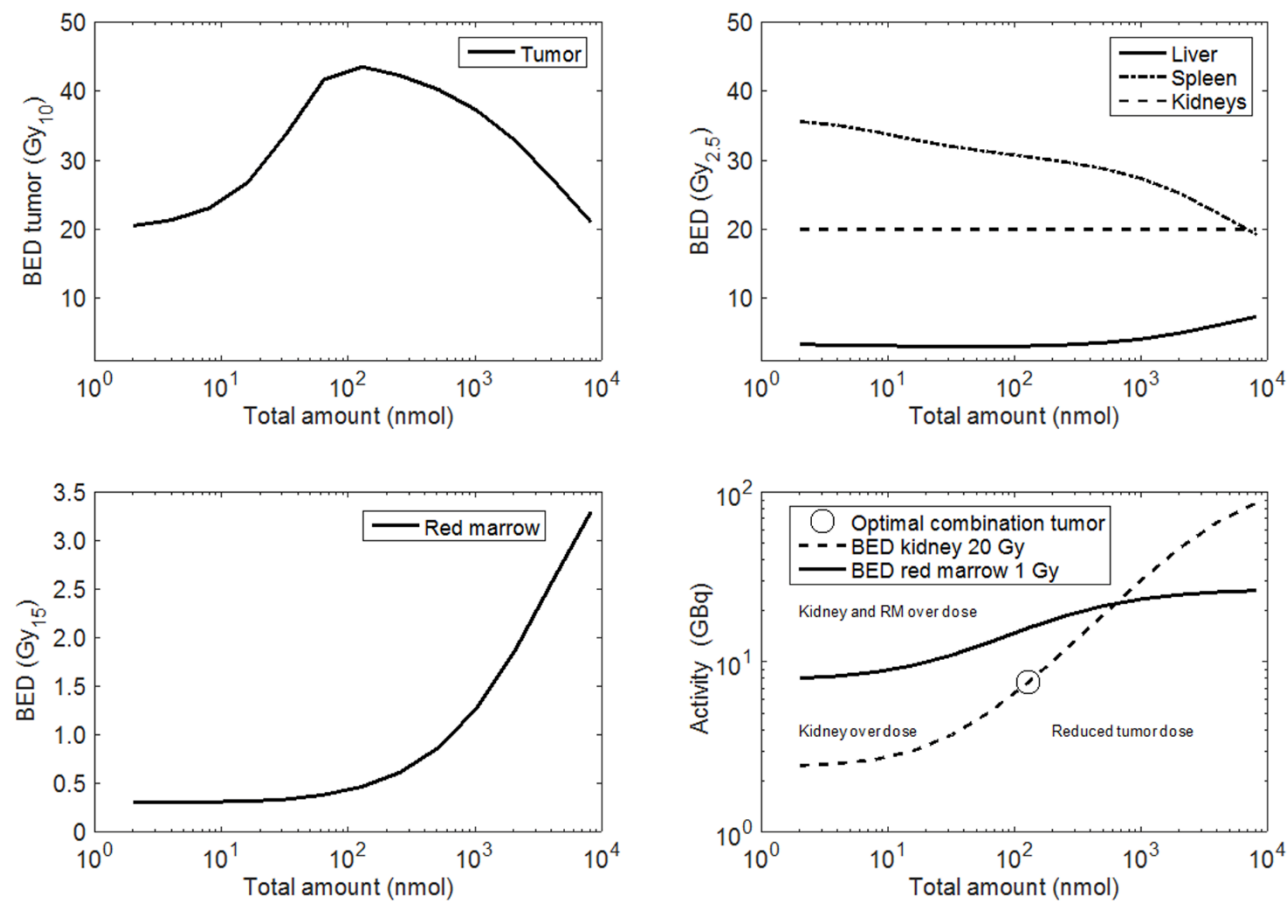


Figure 5

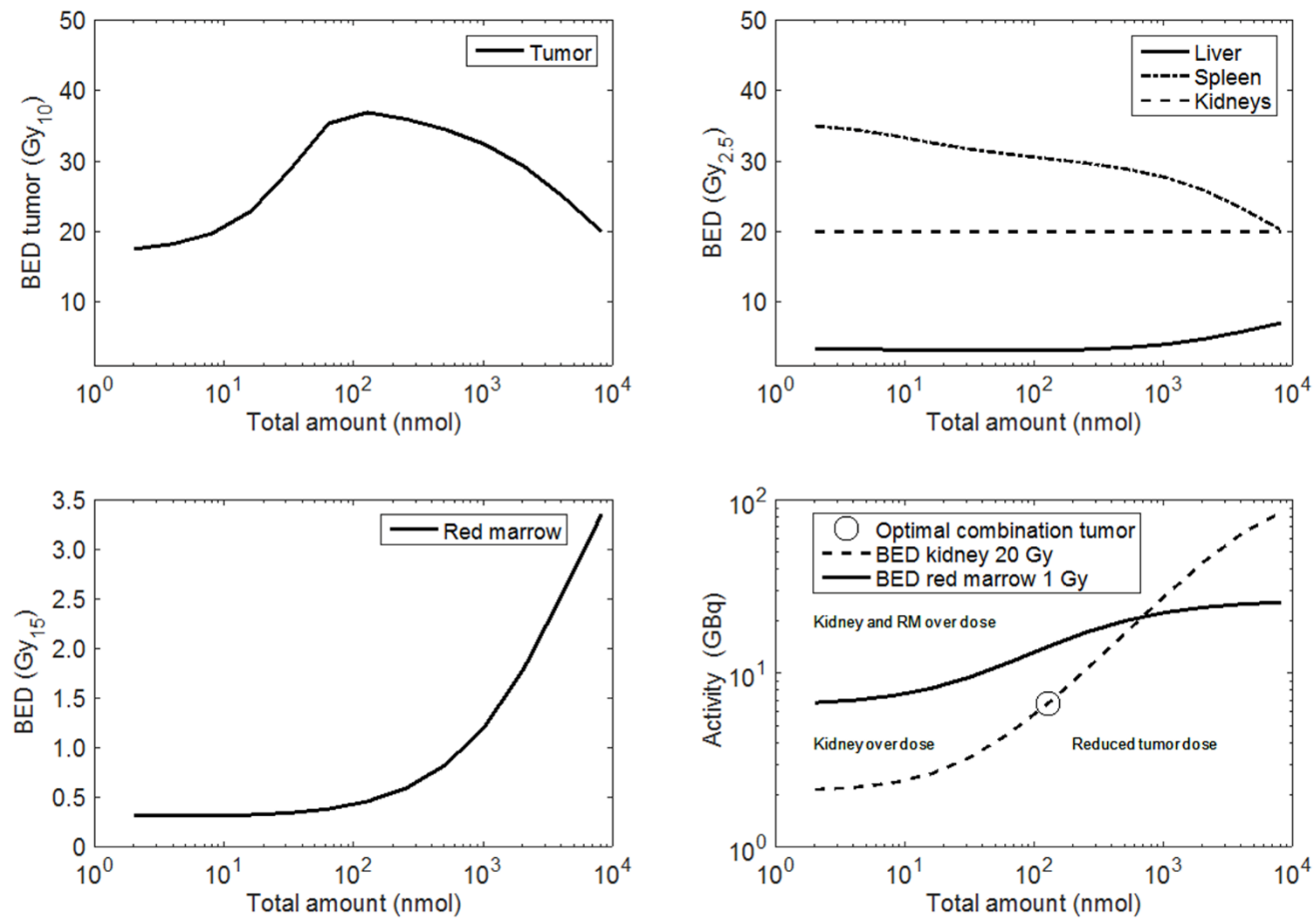


Figure 6

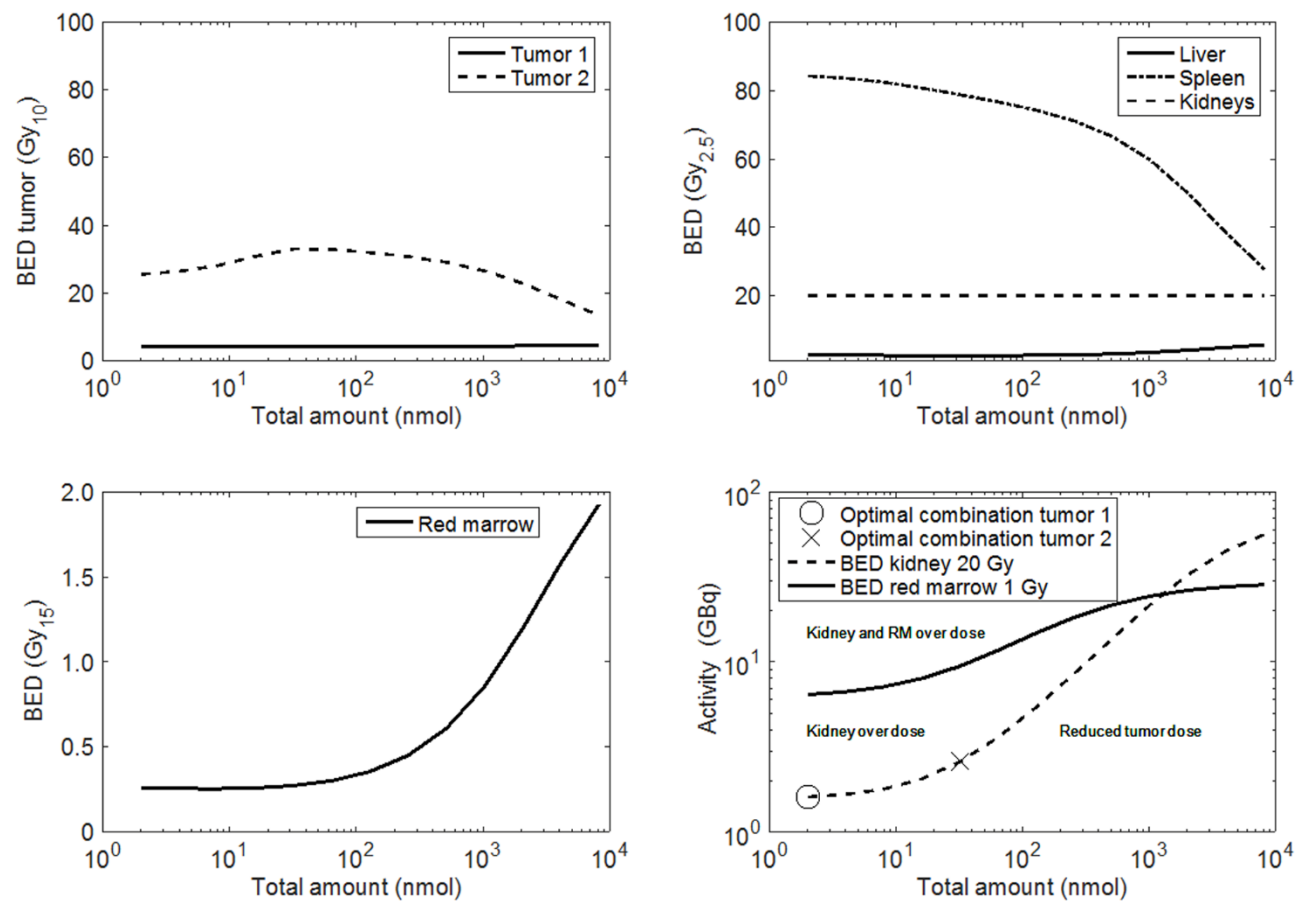


Figure 7

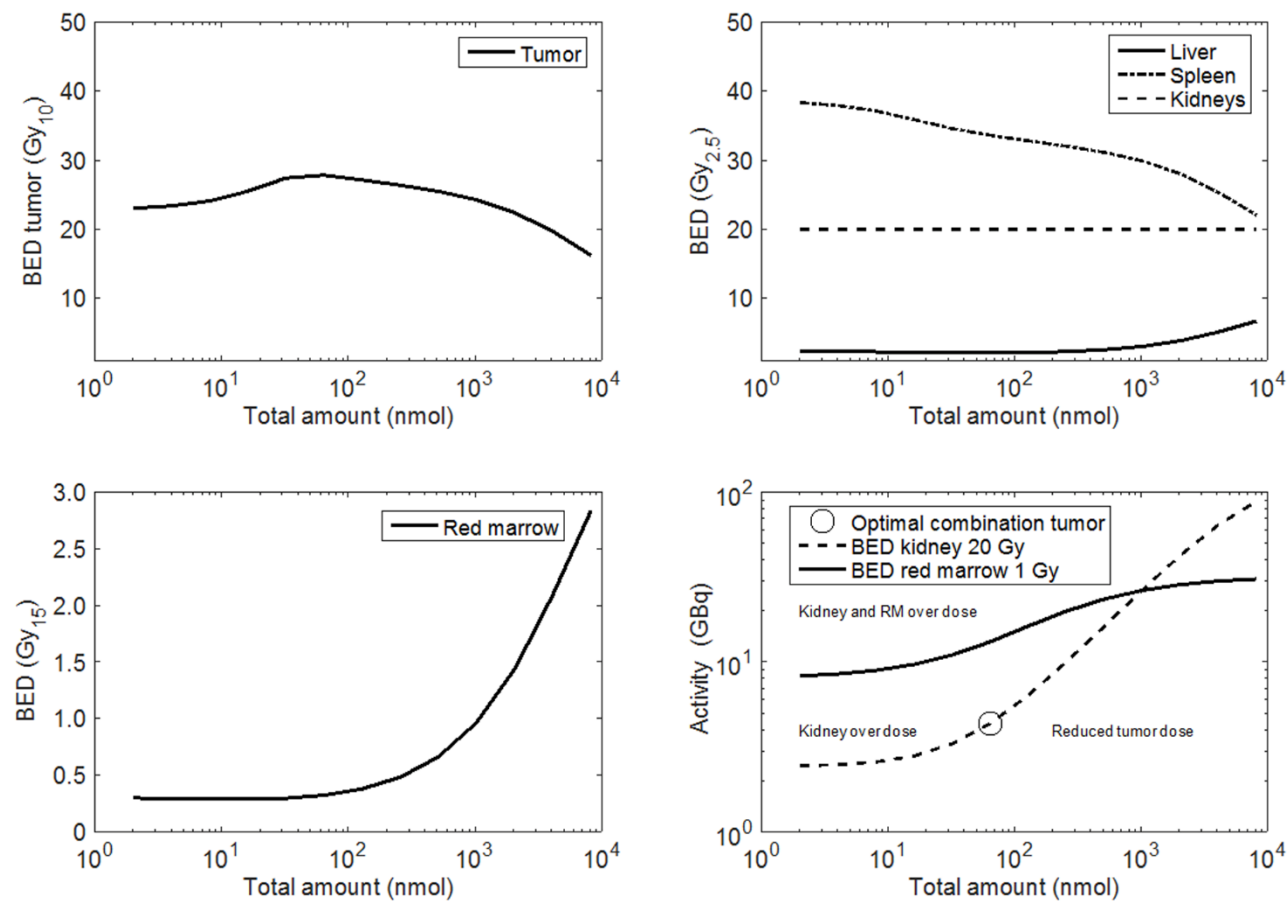


Figure 8

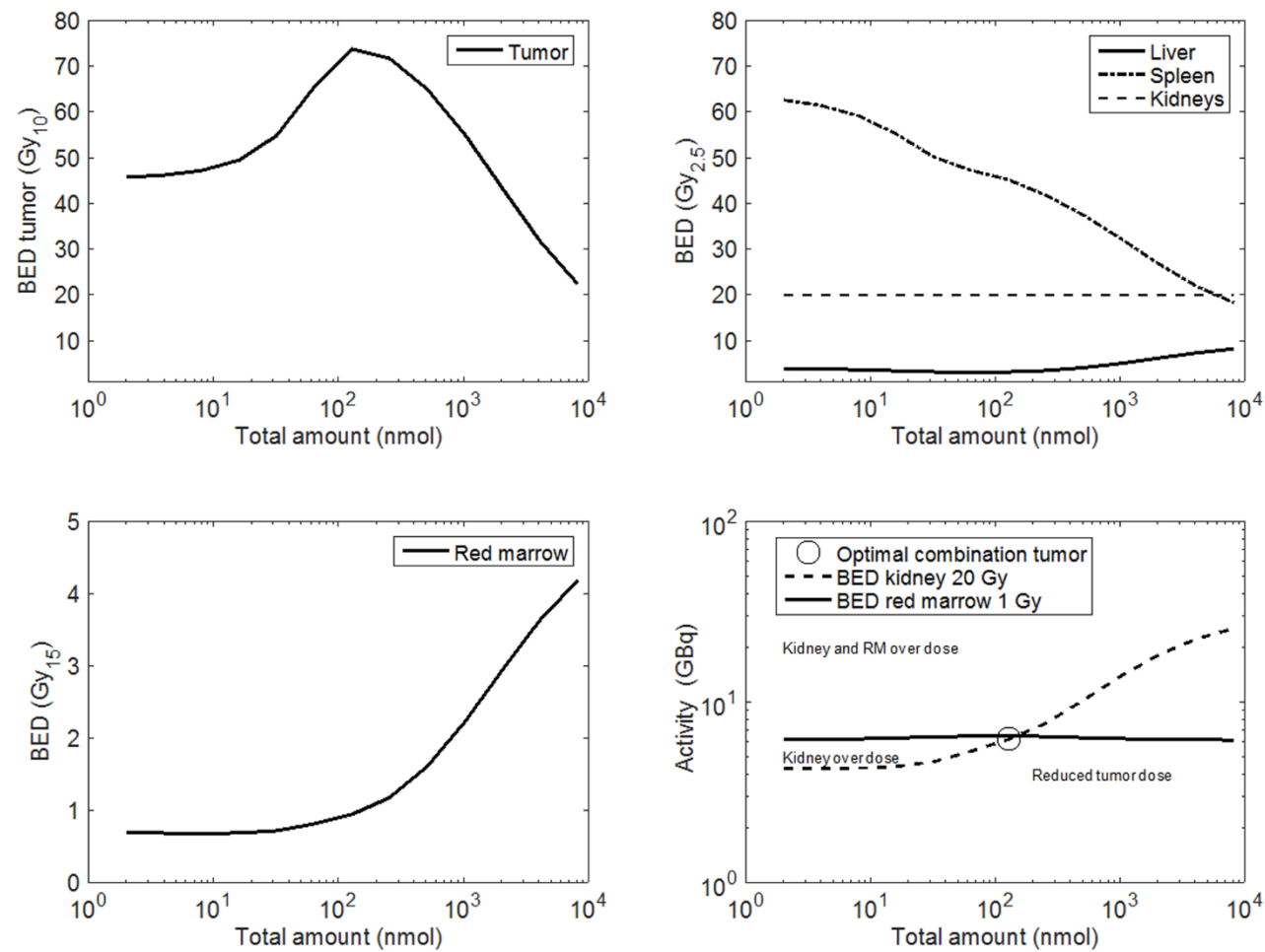


Figure 9

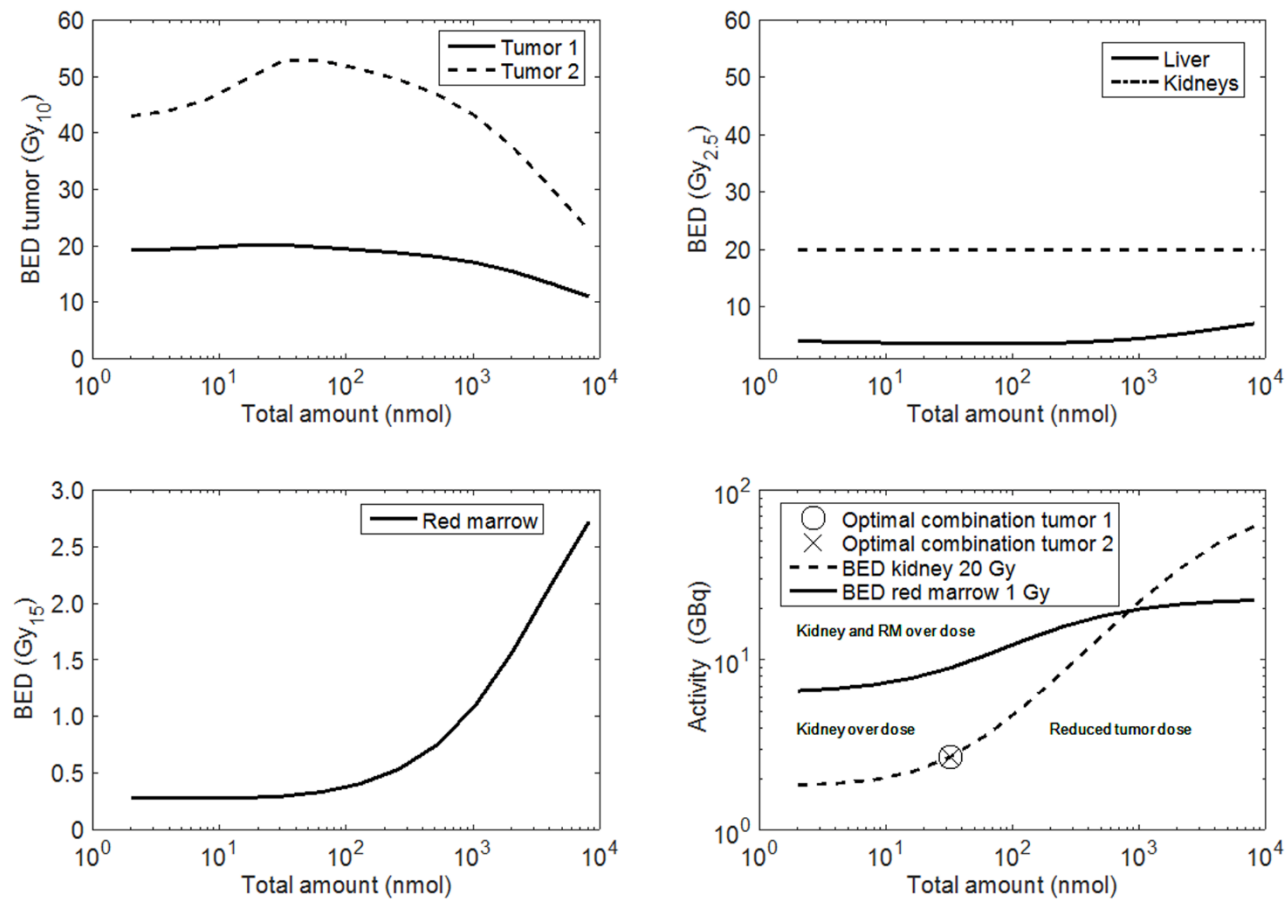


Figure 10

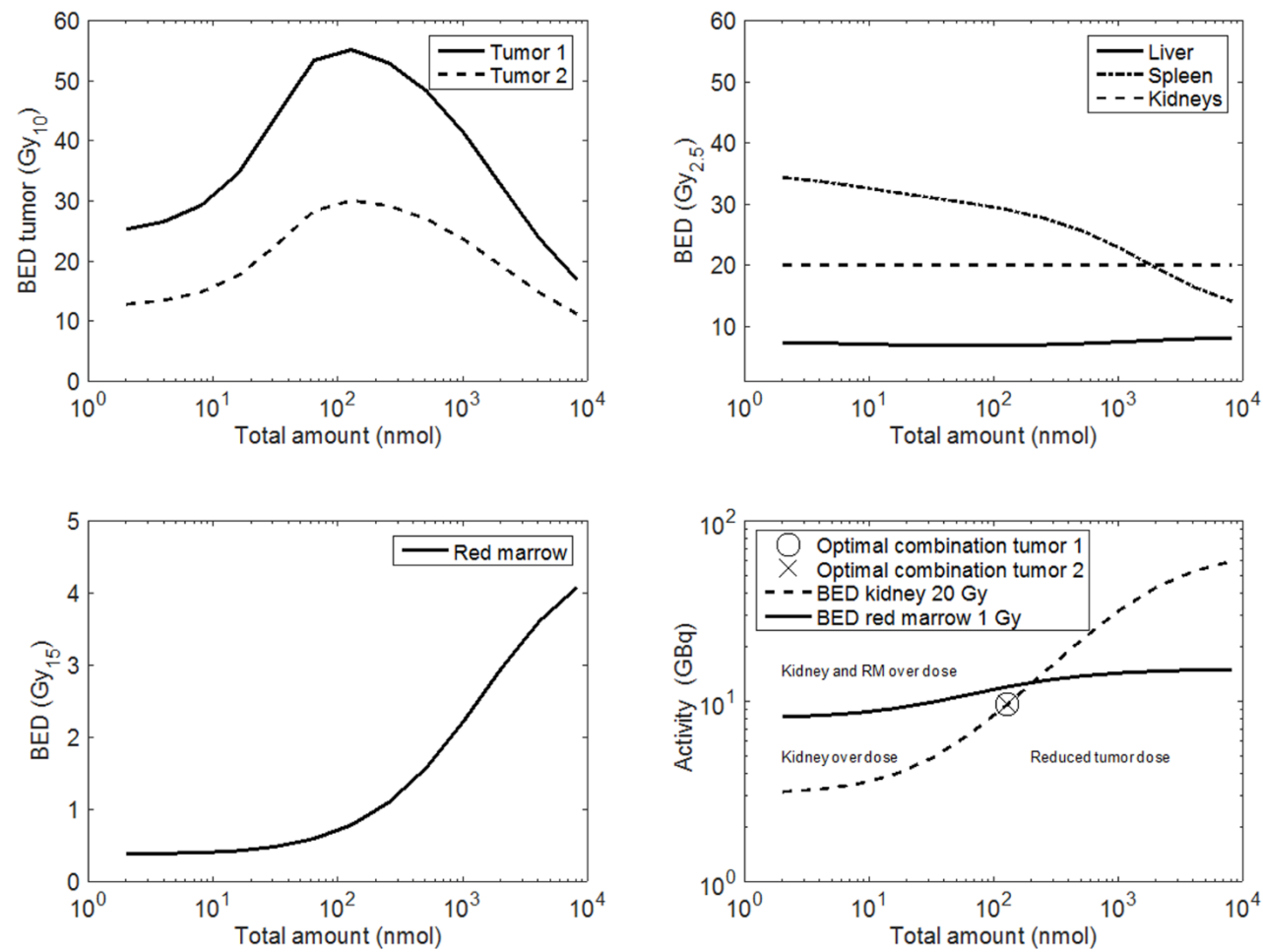


Figure 11

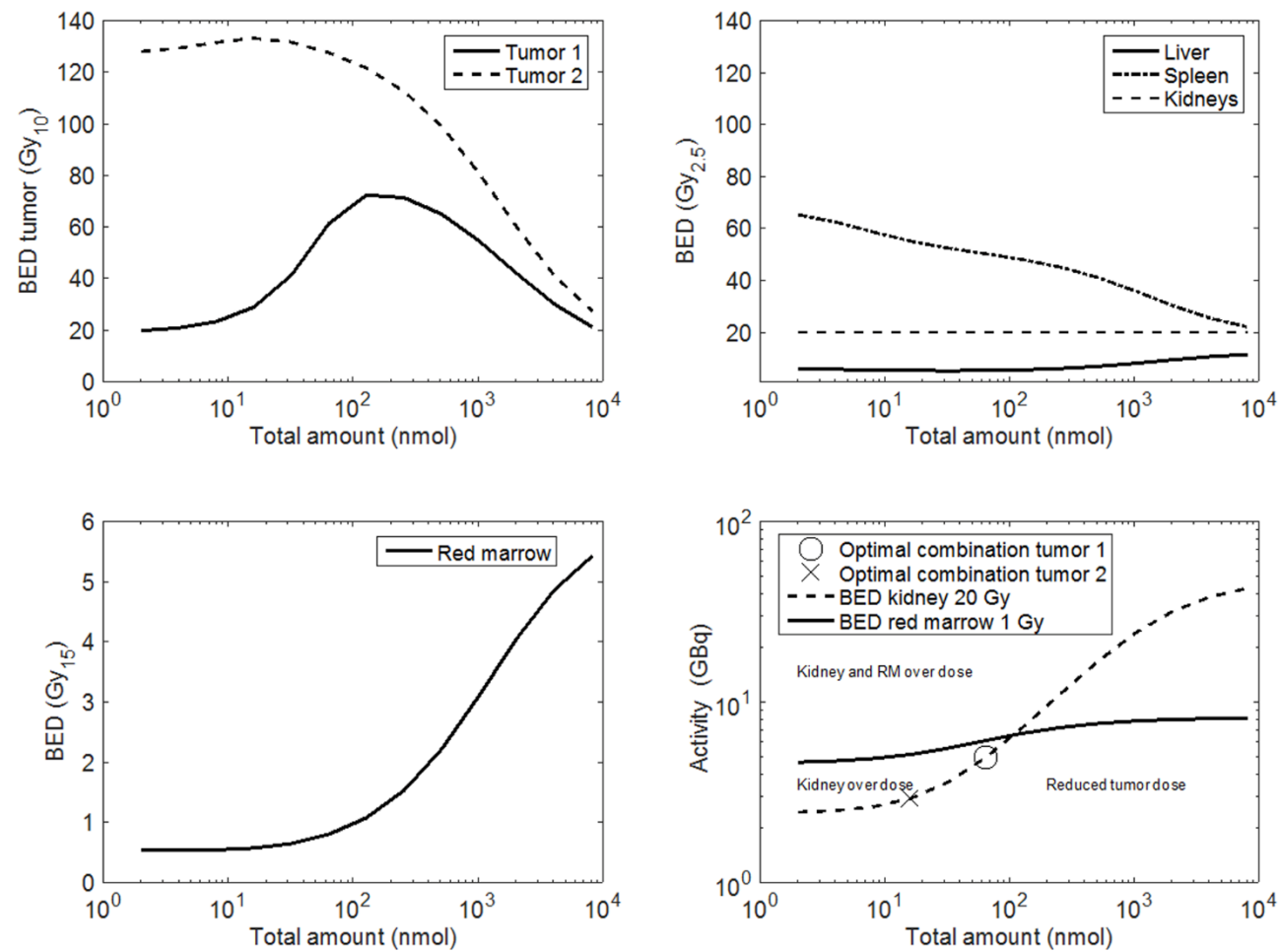
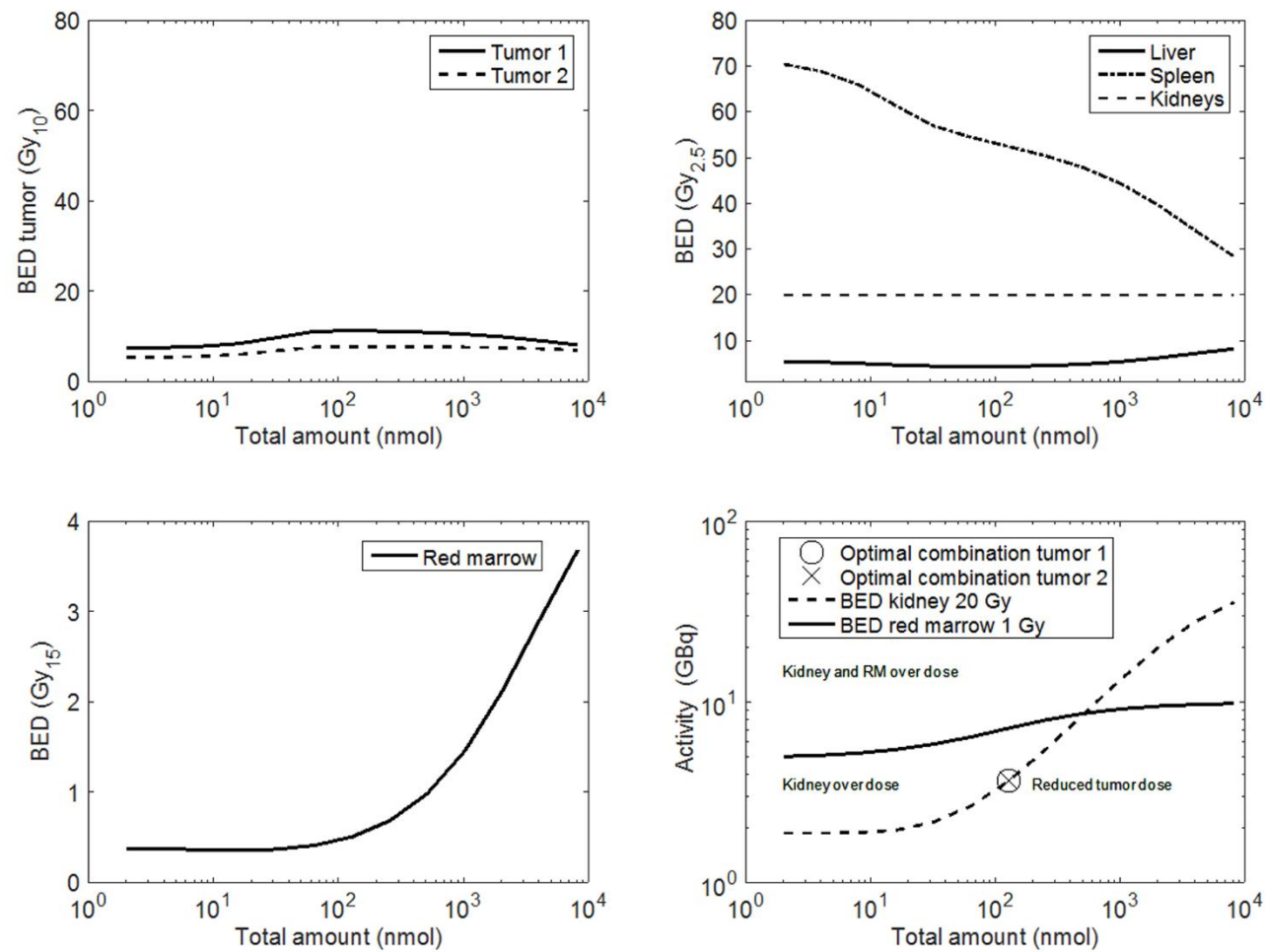


Figure 12

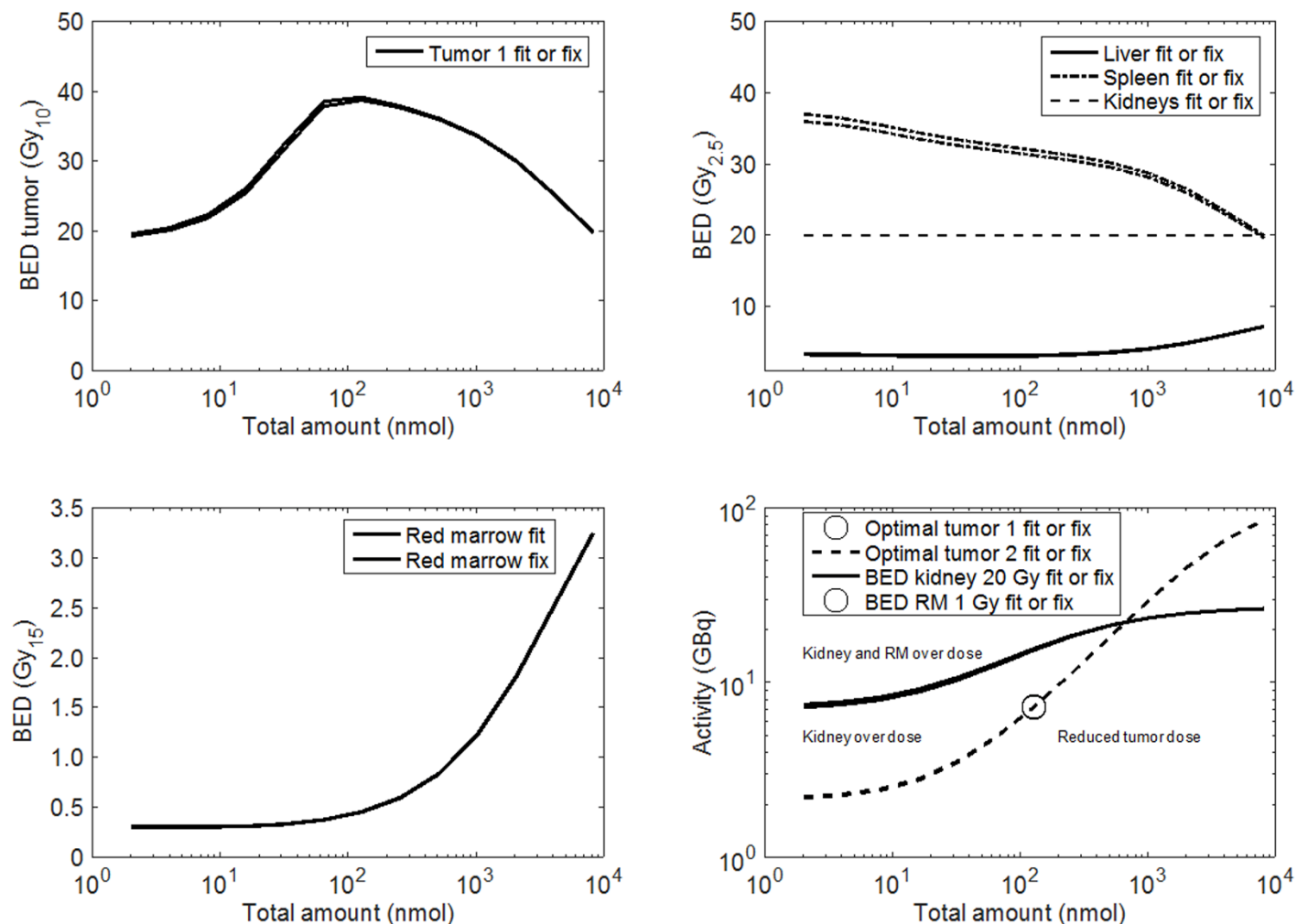


Supplemental Data

internalization rate sensitivity analysis

Figure 1

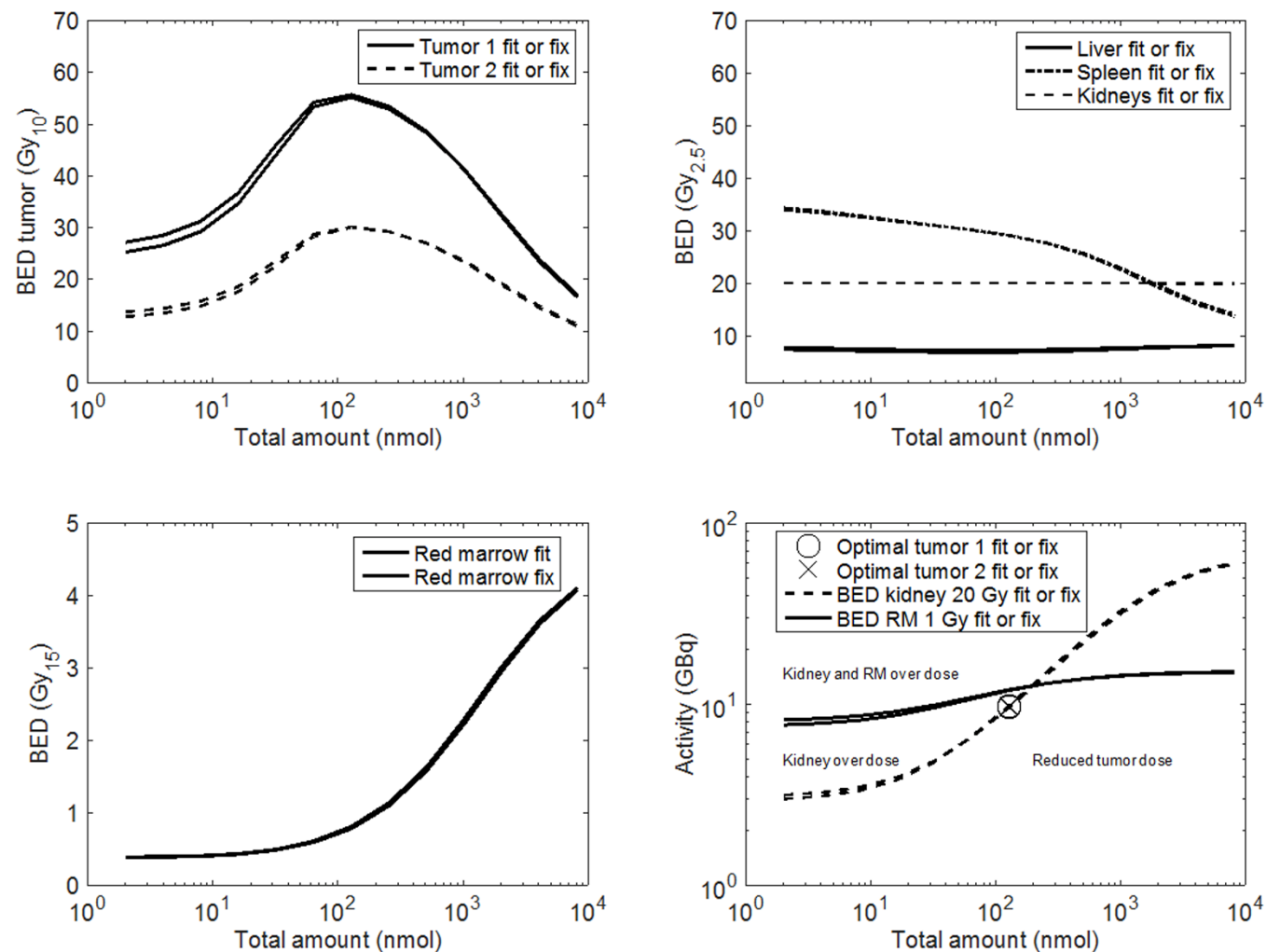
Patient 2, N4



The internalisation rate was fixed due to high correlation. However, for the sensitivity analysis the internalisation rate was also fitted to the data. The fitted parameters of both cases were used for the simulations. The curves are very similar, as the assumed internalisation rate (0.0017 min^{-1}), is similar to the fitted (0.0023 min^{-1}) and small changes are compensated by changes in the receptor densities during the fitting process. If considerably larger or smaller internalisation rates are assumed and fixed, the model can not be adequately fitted (bad fits). Therefore, the assumption is reasonable and can be used for modelling and simulation.

Figure 2

Patient 7, N10



The internalisation rate was fixed due to high correlation. However, for the sensitivity analysis the internalisation rate was also fitted to the data. The fitted parameters of both cases were used for the simulations. The curves are very similar, as the assumed internalisation rate (0.0017 min^{-1}), is similar to the fitted (0.001 min^{-1}) and small changes are compensated by changes in the receptor densities during the fitting process. If considerably larger or smaller internalisation rates are assumed and fixed, the model can not be adequately fitted (bad fits). Therefore, the assumption is reasonable and can be used for modelling and simulation.