

Model code

Model S1: Gunn Rat KroneckerBio Model File

```
## UGTA1A Model ##

#####
% Compartments UGTA1A Model
Plasma 3 0.0078 # (L) Volume of the central compartment

#####
% States Plasma
#Name      SeedName (=Multiplayer)
LNP        LNP_0=0.0078
LNPr       LNPr_0=0.0078
LNPa       LNPa_0=0.0078
LNPe       LNPe_0=0.0078
mRNAC      mRNAC_0=0.0078
UGTc       UGTc_0=0.0078
Bil        Bil_0=0.0078
MGT        MGT_0=0.0078
DGT        DGT_0=0.0078
sBil       sBil_0=0.0078
Bil:UGTc   Bil:UGTc_0=0.0078

% Outputs
#PlasmaDrug          LNP
#ConjugatedBilirubin MGT DGT
#UnconjugatedBilirubin Bil
#mRNA                mRNAC
#UGTc                UGTc
TotalBilirubin      Bil MGT DGT
```

```

PlasmaDrug          LNP
mRNA               mRNAC  LNPa  LNPe
Enzyme              UGTC   Bil:UGTC
cytomRNA           mRNAC

% Inputs Plasma
running            0

#####
% Parameters
kw                 1e-5
k12                1e-5
k21                1e-5
ka                 1e-5
ke                 1e-5
de                 1e-5
kl                 1e-5
dmRNA              1e-5
kt                 1e-5
ktbg               1e-5
dUGTC              1e-5
kcat               1e-5
kclearBil          1e-5
kclearMGT          1e-5
kclearDGT          1e-5
kelSbil             1e-5
ksyn               1e-5
ksynhigh            1e-5
kon                1e-5
koff                1e-5

#####
% Seeds
#Name      Value

```

LNP_0	0
LNPP_0	0
LNPA_0	0
LNPE_0	0
mRNAC_0	0
UGTc_0	0
Bil_0	0
MGT_0	0
DGT_0	0
sBil_0	1
Bil:UGTc_0	0
 #####	
% Reactions Plasma	
LNP	0 0 0 kw 0 "(1) 1st order elimination"
LNPP	0 0 0 kw 0 "(1) distribution"
LNPA	0 0 0 ka 0 "(2) Attachment"
LNPE	0 0 0 ke 0 "(3) endocytosis"
LNPE	0 0 0 de 0 "(4) fails to escape from endosome"
mRNAC	0 0 0 kl 0 "(5) escape from endosome"
mRNAC	0 0 0 dmRNA 0 "(7) mRNA degrades"
0	0 0 UGTc ktbg 0 "(8) endogenous translation"
mRNAC	0 mRNAC UGTc kt 0 "(9) translation"
UGTc	0 0 0 dUGTc 0 "(10) Cytoplasmic protein degrades"
Bil:UGTc	0 Bil dUGTc 0 "(10) Cytoplasmic protein degrades"
UGTc	Bil Bil:UGTc 0 kon koff "(11) Glucuronidation"
Bil:UGTc	0 UGTc MGT kcat 0 "(12) Gluronidation"
UGTc	MGT UGTc DGT kcat 0 "(13) Gluronidation"
0	0 Bil 0 ksyn 0 "(14) Production of Bilirubin"
sBil	0 Bil sBil ksynhigh 0 "(15) High Production of Bilirubin"
sBil	running 0 0 kelSbil 0 "(16) Production of Bilirubin"
Bil	0 0 0 kclearBil 0 "(17) Elimination of Bilirubin"
MGT	0 0 0 kclearMGT 0 "(18) Elimination of Monglucouronide"
DGT	0 0 0 kclearDGT 0 "(19) Elimination of Diglucouronide"

Supplemental Model 2 CN1 Human KroneckerBio Model File

```
## UGTA1A Model ##

#####
% Compartments UGTA1A Model
Plasma 3 3.0 # (L) Volume of the central compartment

#####
% States Plasma
#Name      SeedName (=Multiplier)
LNP        LNP_0=3.0
LNPP       LNPP_0=3.0
LNPa       LNPa_0=3.0
LNPe       LNPe_0=3.0
mRNAC      mRNAC_0=3.0
UGTc       UGTc_0=3.0
Bil        Bil_0=3.0
MGT        MGT_0=3.0
DGT        DGT_0=3.0
sBil       sBil_0=3.0
Bil:UGTc   Bil:UGTc_0=3.0
ADA        ADA_0=3.0

%
% Outputs
#PlasmaDrug          LNP
#ConjugatedBilirubin MGT DGT
#UnconjugatedBilirubin Bil
#mRNA                 mRNAC
#UGTc                 UGTc
TotalBilirubin       Bil MGT DGT
PlasmaDrug            LNP
mRNA                 mRNAC LNPa LNPe
```

```

Enzyme           UGTC Bil:UGTC
cytomRNA        mRNAc
LNPa            LNPa

% Inputs Plasma

ksynhigh        1e-5
ksyn            1e-5
kada            0

#####
# Parameters

kw              1e-5
k12             1e-5
k21             1e-5
ka              1e-5
ke              1e-5
de              1e-5
kl              1e-5
dmRNA          1e-5
kt              1e-5
ktbg            1e-5
dUGTC          1e-5
kcat            1e-5
kclearBil      1e-5
kclearMGT      1e-5
kclearDGT      1e-5
kelSbil        1e-5
kon             1e-5
koff            1e-5
ktemp           1
ktemp2          1
ktemp3          1
kada_deg       1e-5
#####

```

```
% Seeds
#Name      Value
LNP_0      0
LNPP_0     0
LNPA_0     0
LNPE_0     0
mRNAC_0    0
UGTc_0     0
Bil_0      0
MGT_0      0
DGT_0      0
sBil_0     0
Bil:UGTc_0 0
ADA_0      0
#####
% Reactions Plasma
LNP      0      0      0      kw      0      "(1) 1st order elimination"
LNP      0      LNPP   0      k12     k21    "(1) distribution"
LNPP     0      0      0      kw      0      "(1) 1st order elimination"
LNP      0      LNPA   0      ka      0      "(2) Attachment"
LNPA     0      LNPE   0      ke      0      "(3) endocytosis"
LNPE     0      0      0      de      0      "(4) fails to escape from endosome"
LNPE     0      mRNAC  0      kl      0      "(5) escape from endosome"
mRNAC   0      0      0      dmRNA  0      "(7) mRNA degrades"
0        0      0      UGTc   ktbg   0      "(8) endogenous translation"
mRNAC   0      mRNAC  UGTc   kt     0      "(9) translation"
UGTc    0        0      dUGTc  0      "(10) Cytoplasmic protein degrades"
Bil:UGTc 0      Bil    dUGTc  0      "(10) Cytoplasmic protein degrades"
UGTc    Bil    Bil:UGTc 0      kon     koff  "(11) Glucuronididation"
Bil:UGTc 0      UGTc   MGT    kcat   0      "(12) Gluronididation"

UGTc    MGT    UGTc:MGT 0      kon     koff  "(13) Gluronididation"
UGTc:MGT 0      UGTc   DGT    kcat   0      "(13) Gluronididation"

ksyn    0      Bil    0      ktemp  0      "(14) Production of Bilirubin"
sBil    0      Bil    0      kelsbil 0      "(15) High Production of Bilirubin"
```

0	ksynhigh	sBil	0	ktemp2	0	"(15) High Production of Bilirubin"
Bil	0	0	0	kclearBil	0	"(17) Elimination of Bilirubin"
MGT	0	0	0	kclearMGT	0	"(18) Elimination of Monglucouronide"
DGT	0	0	0	kclearDGT	0	"(19) Elimination of Diglucouronide"
kada	0	ADA	0	ktemp3	0	"(20) ramping up of accelerated ...
clearance (called ADA here but could be something else"						
ADA	LNP	0	0	kada_deg	0	"(21) ADA binding to LNP and immediately degrading complex"