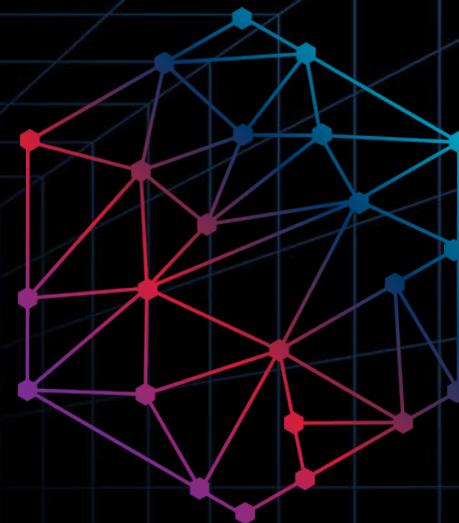


Model-Informed Drug Development

**MIDD+**

2021 Virtual Conference



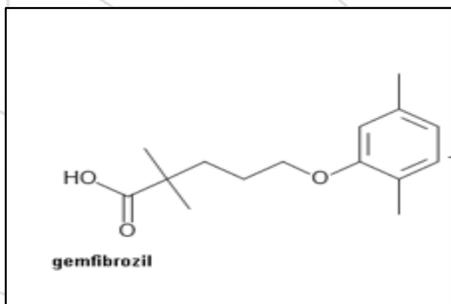
# GastroPlus® DDI Standards Update Project

Simulations Plus, DDI Task Force

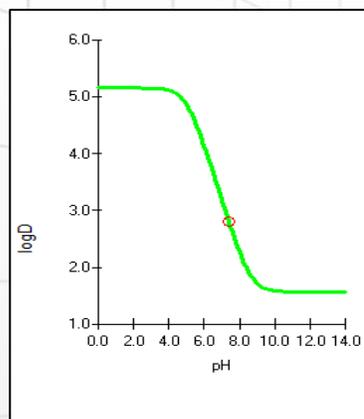
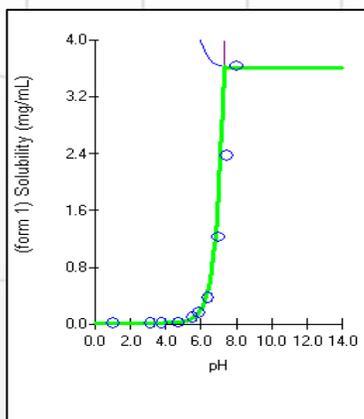
# Outline of Process for Model Development and Documentation

- Creation of GP a project starts with structure import using ADMET Predictor Module for both substrates and perpetrators.
  - Physicochemical, biopharmaceutical, and biochemical properties
  - Initial evaluation via “Chemistry Classification” with all aspects of ADMET
  - Extensive literature collection and spreadsheet documentation.
    - Workbook with multiple sheets for Compound Properties
    - DDI study data for multiple perpetration mechanisms.
  - First simulations for “Measured Properties” with parameter sensitivity analysis.
  - Model building for individual substrate and/or perpetrator simulations compared to observed data
    - Single escalating doses (for nonlinear dose dependence)
    - Multiple dosing (for autoinhibition / autoinduction).
  - DDI simulations for all appropriate mechanisms on both substrate and perpetrator.
  - Analysis of results using the “Guest”<sup>\*</sup> criterion for accuracy of AUC Ratios
  - Preparation of slides and written reports suitable for regulatory submission.

# Gemfibrozil BCS II Physicochemical Properties



**MW = 250.34**



Estimated Solubility Factor after fitting pH  
Vs solubility profile = 156.9  
Adjusted Sol factor = 180

AP 10.0 = ADMET Predictor v. 10.0  
S+ = properties predicted with Simulations Plus models  
S+Sw = native solubility in pure water  
S+Peff = human jejunal permeability estimate  
N.A = Not Available

S+LogP = 4 (AP 10.0)

Exp LogD (Octanol/H<sub>2</sub>O) @ pH7.4 = 2.8 (Luner et. al., Pharm. Res.11(12):1755 (1994))

NOTE: Changed LogD (7.4) = 0.8 to calculate Kps then changed back to 2.8 to run simulations.

S+pKa = 4.92 (Acid) (AP 10.0)

Exp pKa = 5 (Luner et. al., Pharm. Res.11(12):1755 (1994))

S+Sw = 0.0826 mg/ml @ pH 4.24 (AP 10.0)

Exp Sw = 0.02 mg/ml @ pH 1 37 deg C (LOW) (Luner et. al., Pharm. Res.11(12):1755 (1994))

S+Solubility Factor = 276.89

S+FaSSIF = 0.42 mg/ml, S+ FeSSIF = 0.62 mg/ml (AP 10.0)

Exp FaSSIF = N.A

S+Peff =  $7.33 \times 10^{-4}$  (cm/s) (AP 10.0) (HIGH)

Caco-2 Papp A->B =  $5.89 \times 10^{-5}$  (Absorptions Systems Lighthouse Database)

Caco-2 Papp B->A =  $4.73 \times 10^{-5}$  (Absorptions Systems Lighthouse Database)

Caco-2 Converted to Hum Peff =  $5.60 \times 10^{-4}$  cm/s (From GeoMean =  $5.28 \times 10^{-5}$  cm/s from Abs Sys Caco-2)

S+hum\_fup% = 5.18 % (AP 10.0)

Exp. Fup = 3.5% (Oprea and Benet Wombat database)

S+RBP = 0.67 (AP 10.0)

Exp Rbp = 0.75 (Deguchi et. al., Drug.Metab.Dispos.39(5):820 (2011))

S+Enzyme Substrate: CYP2C9(48%), CYP2C19(71%), UGT1A1(68%), UGT1A3(97%), UGT1A9(76%), UGT2B7(93%)

S+Transporter Substrate: P-gp(75%), OATP1B1(99%), OAT1(87%),

Exp Enzyme Substrate: 2C9, 2C19, UGT1A3, UGT2B7

Exp Transporter Substrate: OATP1B1 (liver influx)

S+Enzyme Inhibitor: CYP2C9(77%)

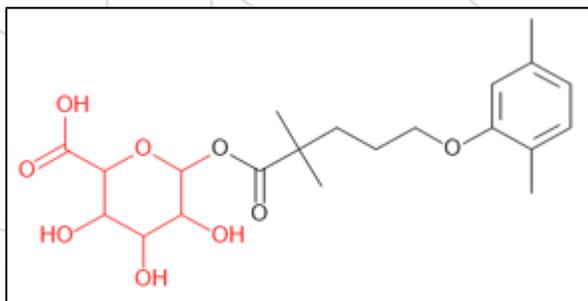
S+Transporter Inhibitor: OAT1(95%), OAT3(76%),

Exp Enzyme Inhibitor: 2C8, 2C9

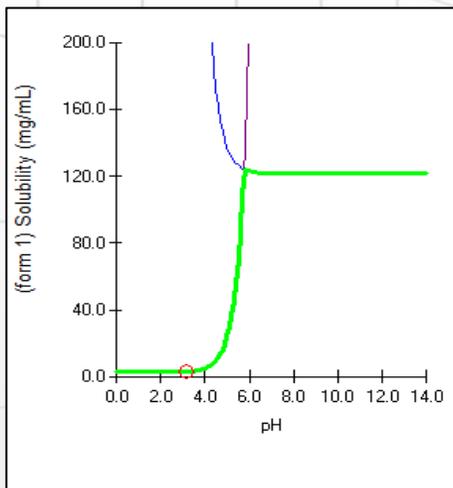
Exp Transporter Inhibitor: NTCP, OAT3, OATP1B1, OATP1B3



# Gemfibrozil Glucuronide Physicochemical Properties



**MW = 426.47**



AP 10.0 = ADMET Predictor v. 10.0

S+ = properties predicted with Simulations Plus models

S+Sw = native solubility in pure water

S+Peff = human jejunal permeability estimate

N.A = Not Available

**S+LogP = 1.67 (AP 10.0)**

**Exp LogD (Octanol/H<sub>2</sub>O) @ pH7.4**

**Exp log P extrapolated from Log D**

**S+pKa = 4.12 (Acid)**

**Exp pKa = N.A**

**S+Sw = 3.0900 mg/ml @ pH 3.15 (AP 9.5)**

**Exp Sw = N.A**

**S+Solubility Factor = 43.48**

**S+FaSSIF = 1.13 mg/ml, S+ FeSSIF = 2.71 mg/ml**

**Exp FaSSIF = N.A**

**S+Peff = 4.0E-5 (cm/s) (AP 10.0)**

**S+hum\_fup% = 11.2% (AP 10.0)**

**Exp. Fup% = 11.5% (Shitara et al., J.Pharmacol. Exp.Ther. 311(1):228(2004))**

**NOTE: For all simulations Fup% = 5.0 to correct the Vdss for glucuronide**

**S+RBP = 0.65 (AP 10.0)**

**Exp Rbp = N.A**

**S+Enzyme Substrate:**

**Exp Enzyme Substrate: Hydrolase**

**S+Transporter Substrate: P-gp(99%), OATP1B1(99%), OATP1B3(93%), OAT1(65%), OAT3(97%), OCT1(76%)**

**Exp Transporter Substrate: OATP1B1 (liver influx), OAT3 (kidney influx), MRP2 (liver-bile efflux), MRP3 (liver-systemic efflux), MRP4 (kidney-tubule efflux)**

**S+Enzyme Inhibitor: CYP2C9(35%), CYP3A4(42%)**

**S+Transporter Inhibitor:**

**Exp Enzyme Inhibitor: 2C8, 2C9**

**Exp Transporter Inhibitor: NTCP, OAT3, OATP1B1, OATP1B3**



# Extended Clearance CS (ECCS)

Gemfibrozil S+CL\_Mech = Metabolism

Compound are assigned to one of six classes based on:

- 1) High or low permeability
- 2) High or low MW (400 g/mol)
- 3) Ionization class: Acids/Zwitterions versus Bases/Neutrals

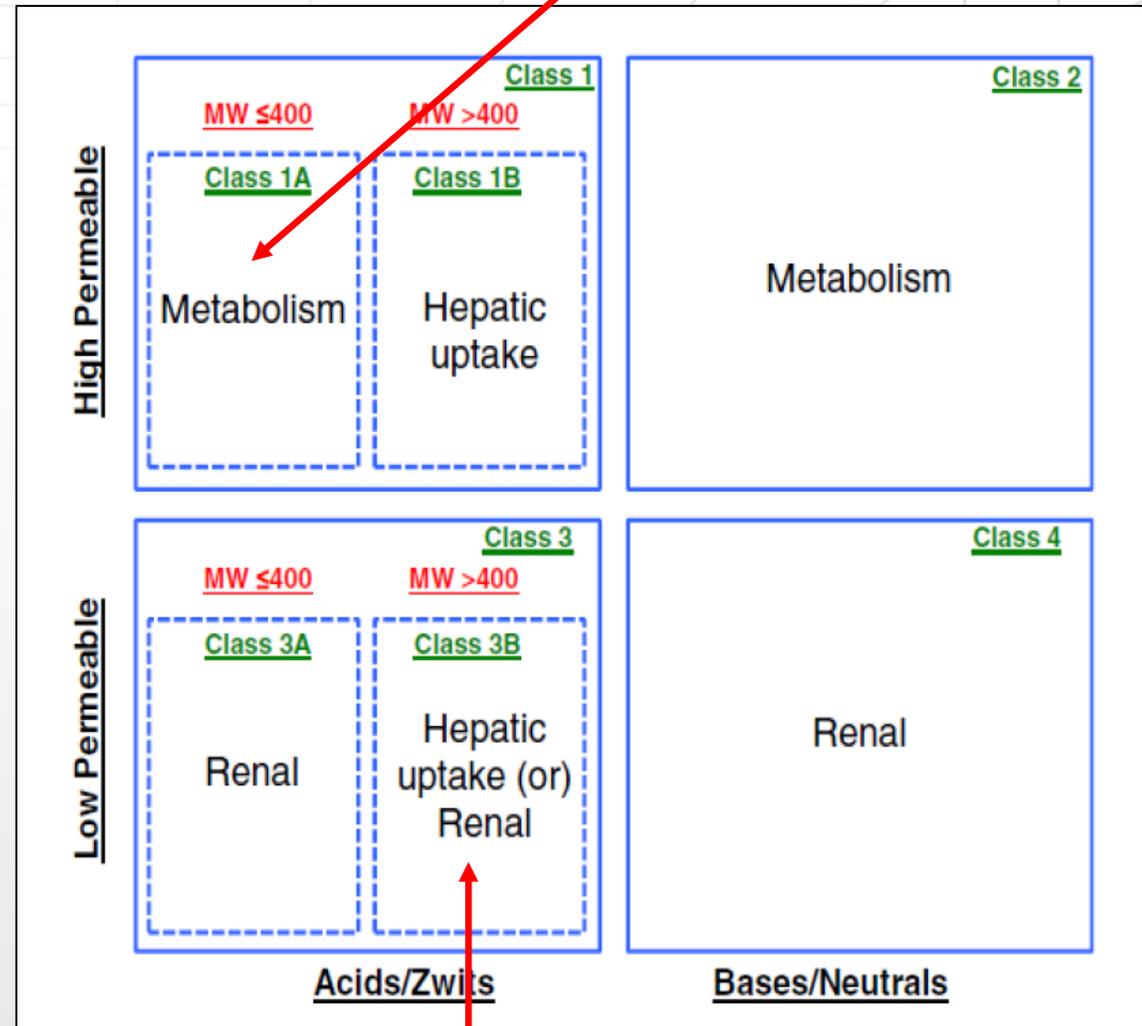
Class 1A and 2 are metabolism

Classes 3A and 4 are renal

Class 1B is hepatic uptake

Class 3B is hepatic uptake or renal

Varma M., et. al. Pharm. Res. 2015, 32, 3785.



GEM-glucuronide S+CL\_Mech = Hepatic Uptake

# Varma and ADMET Predictor ECCS models

Varma ECCS

Observed	Renal	2	11	45
	Metabolism	0	188	9
	Hep.uptake	12	0	1
		Hep.uptake	Metabolism	Renal
		Predicted		

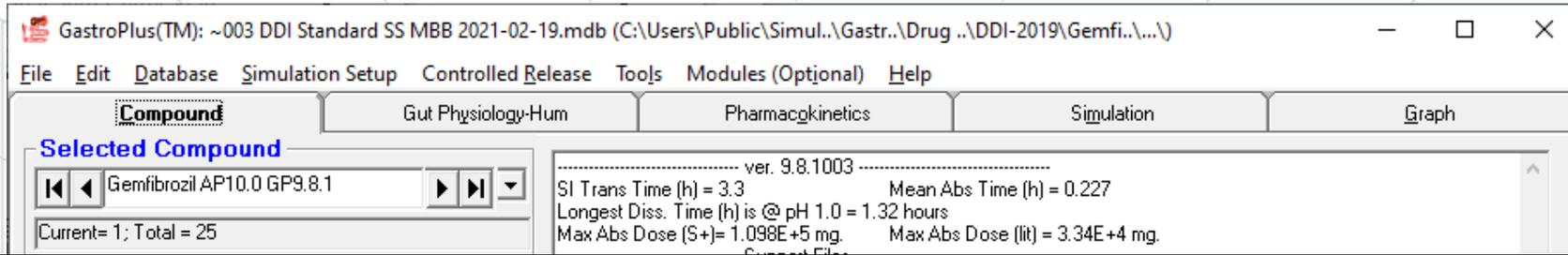
S+Hum CL Mech.

Observed	Renal	0	2	70
	Metabolism	0	183	7
	Hep.uptake	18	0	1
		Hep.uptake	Metabolism	Renal
		Predicted		

Statistic	ECCS	Hum CL Mech Bin
Concordance	91%	96%
Youden	0.78	0.94
Coverage	88%	92%



# Purely *in silico* model

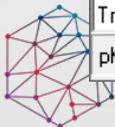
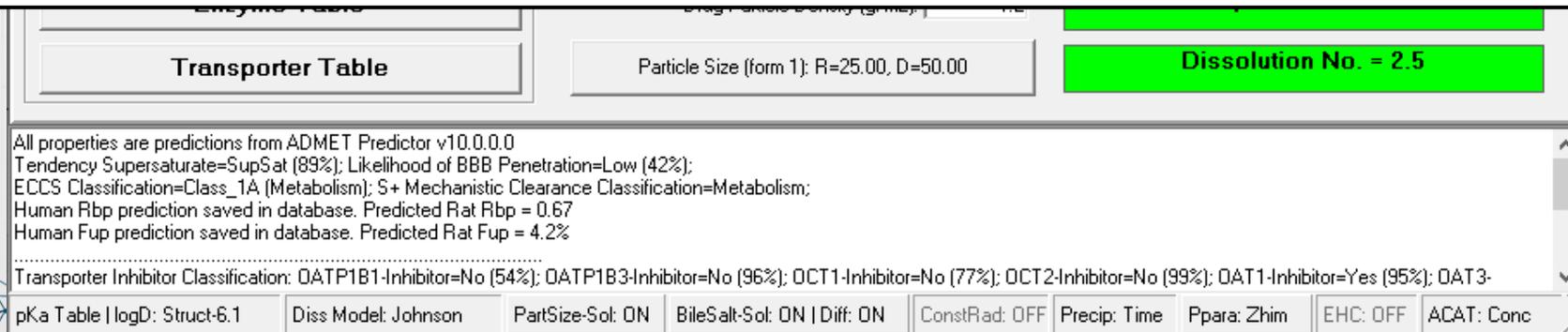


All properties are predictions from ADMET Predictor v10.0.0.0  
Tendency Supersaturate=SupSat (89%); Likelihood of BBB Penetration=Low (42%);  
ECCS Classification=Class\_1A (Metabolism); S+ Mechanistic Clearance Classification=Metabolism;  
Human Rbp prediction saved in database. Predicted Rat Rbp = 0.67  
Human Fup prediction saved in database. Predicted Rat Fup = 4.2%

.....

Transporter Inhibitor Classification: OATP1B1-Inhibitor=No (54%); OATP1B3-Inhibitor=No (96%); OCT1-Inhibitor=No (77%); OCT2-Inhibitor=No (99%); OAT1-Inhibitor=Yes (95%); OAT3-Inhibitor=Yes (76%); Pgp-Inhibitor=No (96%); BSEP-Inhibitor=No (66%); BCRP-Inhibitor=No (97%);  
Transporter Substrate Classification: OATP1B1-Substrate=Yes (99%); OATP1B3-Substrate=No (60%); OCT1-Substrate=Yes (96%); OCT2-Substrate=Yes (74%); OAT1-Substrate=Yes (87%); OAT3-Substrate=Yes (75%); Pgp-Substrate=Yes (75%); BCRP-Substrate=No (95%);  
Transporter Km Values: OATP1B1-Km=24.62uM; OATP1B3-Km=66.47uM; OCT1-Km=8.66uM; OCT2-Km=18.12uM; OAT1-Km=25.48uM; OAT3-Km=122.11uM;  
Transporter IC50 Values: BSEP-IC50=48.26uM;

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# Documentation directly in comment field of database

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MBB, 4/5/2020, Updated 12/27/2020

Clinical data from

Changed log P to log D(7.4) = 1.3 Ref. Measured in Roche discovery assays: Baneyx-EurJPharmSci-56-1-2014-PBPK modeling of CYP3A4 induction by rifampicin

Used log P = 1.5 to calculate Kps and changed back log p = 1.3

Changed Solubility to 0.64 at pH 5.5 Ref. Becker-J Pharm Sci-98-7-2252-2009-Rifampicin Biowaiver monograph- pH Vs Solubility profile

Roche PAMPA based conversion to Peff = 0.4E-4 cm/s (a value determined from PAMPA. Ref. Measured in Roche discovery assays: Baneyx-EurJPharmSci-56-1-2014) was increased by 6.2-Fold to 2.48E-4 cm/s per Baneyx for all records.

Changed fup% = 7% Ref. Yoshikado-ClinPharmTherap-100-5-513-2016-Supplement

Changed Rbp = 0.8 to calculate Kps that match the Noncompartmental Vdss for healthy subjects.

etc.

-----

Induction Added: NOTE: EC50.u = 64 nM Unbound 3A4 induction from Asami R, CPT Pharmacometrics Syst. Pharmacol. 7: 186 (2018). Applied to all PXR related genes.

P-gp EC50,t,HLM = 26 uM and Emax = 4.4 Ref: Anuzanit-J pharm Pharm Sci-14-2-236-2011- Induction of P-gp by rifampin

P-gp EC50,t,Hep = 0.064 uM and Emax = 2.2 Ref. Lutz-CPT-104-6-1182-2018 concludes that EC50 for PXR induced genes should be the same.

etc.

UGT1A1 EC50,t,Hep = 0.064 uM and Emax = 4.4 Emax is the average of 3 values from Moscovitz (Note: Same Emax as UGT2B7 which are in both Gut and Liver Ref. Moscovitz, 2018

etc.

-----

Inhibition Added:

P-gp inhibition Ki,t,HLM = 13.7 uM Substrate E17G and NMQ Ref. for HEK293 inverted memb. vesicles Ave. Pedersen-EurJPharmSci-103-70-2017

OATP1B1 inhibition Ki = 0.62 uM Substrate = 3H-TIC Ref. Takashima T. J. Nucl. Med. 53:741 (2012)

3A4 inhibition Ki,u = 18.5 uM Ref. Kajosaari-BasicClinicalPharmacolToxicol-97-249-2005

etc.

All properties are predictions from ADMET Predictor v9.5.0.0  
 Tendency Supersaturate=SupSat; Likelihood of BBB Penetration=Low (92%); Pgp-Inhibitor=Yes (97%); Pgp-Substrate=Yes (94%); OATP1B1-Inhibitor=Yes (91%); OCT2-Inhibitor=No (95%); BSEP-Inhibitor=Yes (83%); BCRP-Substrate=Yes (54%); ECCS Classification=Class\_4; High\_MWt; S+ Mechanistic Clearance Classification=HepUptake;  
 Human Rbp prediction saved in database. Predicted Rat Rbp = 1.25  
 Human Fup prediction saved in database. Predicted Rat Fup = 11.27%

-----

MBB, 4/5/2020, Updated 12/27/2020

Clinical data from

Changed log P to log D(7.4) = 1.3 Ref. Measured in Roche discovery assays: Baneyx-EurJPharmSci-56-1-2014-PBPK modeling of CYP3A4 induction by rifampicin

Used log P = 1.5 to calculate Kps and changed back log p = 1.3

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etc.

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etc.

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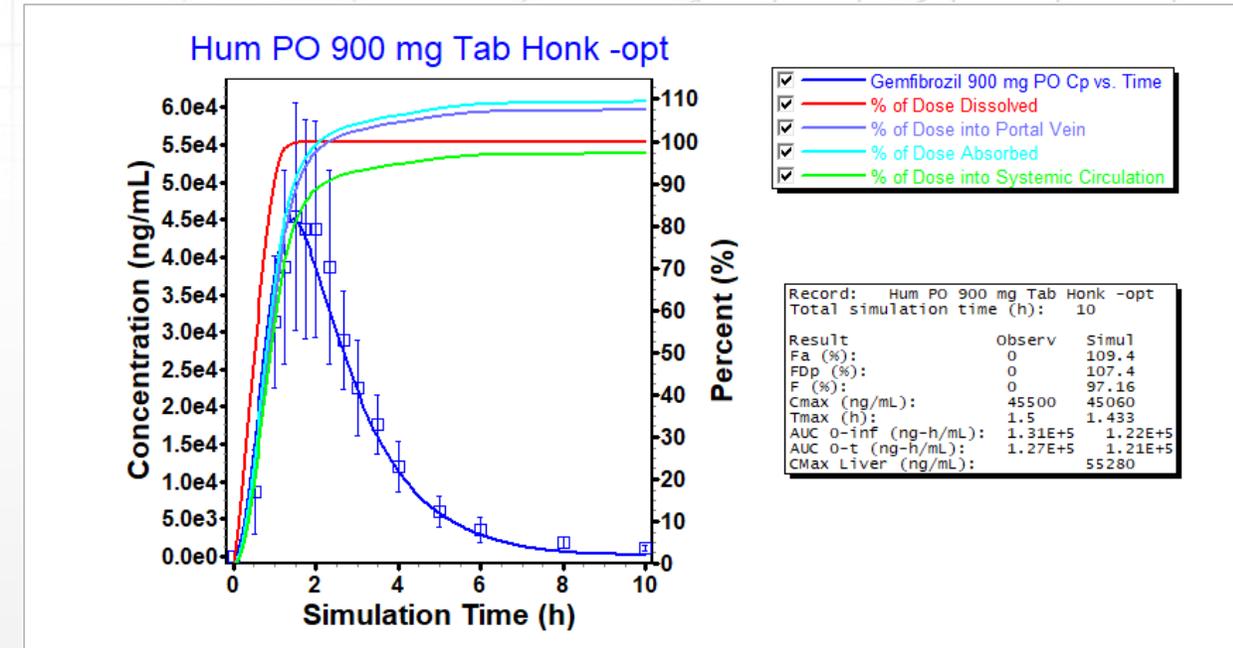
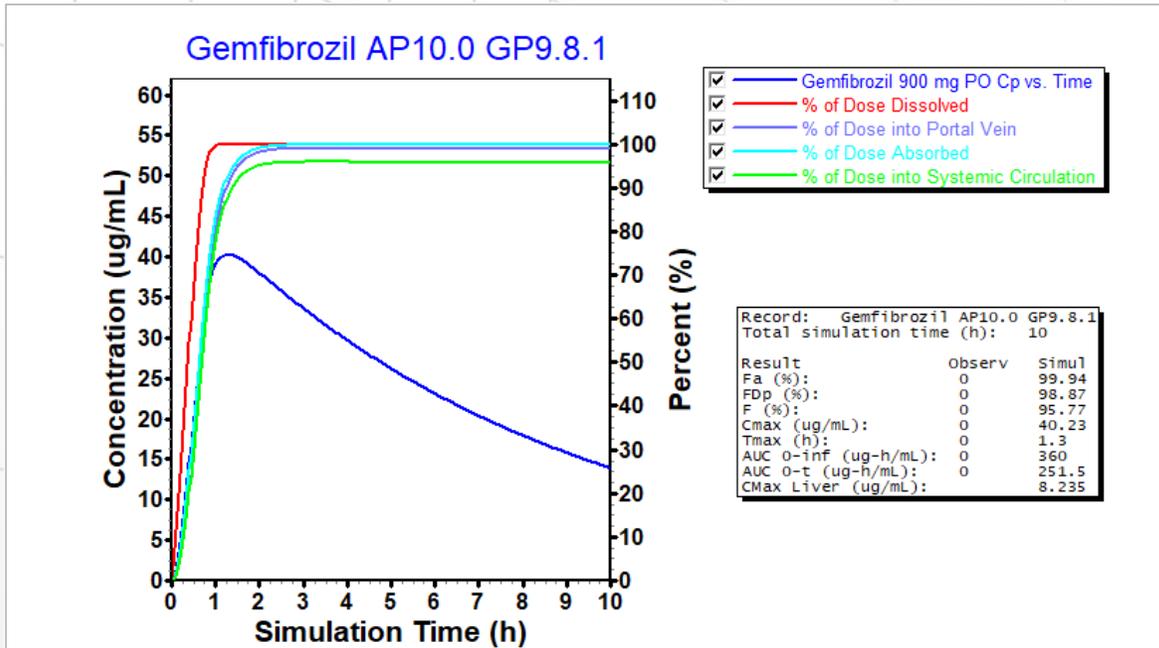
3A4 inhibition Ki,u = 18.5 uM Ref. Kajosaari-BasicClinicalPharmacolToxicol-97-249-2005

etc.

# Hum PO 900 mg Tab *in silico* vs. Honkalammi

Purely *in silico*

All mechanisms *in silico*, *in vitro*, & fitted



Physiology used: Healthy Male 23 years 73 Kg 23 BMI

All mechanisms PBPK Model: Liver and Kidney were assumed Permeability limited organs; the rest were assumed perfusion limited Kps for the Glucuronide record were calculated using the Poulin-extracellular method was used for both Perfusion Limited and for Permeability limited tissues.

# Conclusions and Recommended Testing Based on *in silico* properties

- Low solubility in stomach probably won't reduce bioavailability but may result in slow dissolution and longer  $T_{\max}$ .
- Low MWt, high permeability, and acidic pKa of parent GEM suggest mainly metabolic clearance by Phase I (2C9 and 2C19) and Phase II (UGT1A3 and UGT2B7) enzymes.
- AP10.0 transporter module suggests possible liver and kidney influx.
- High MWt, low permability, and acidic pKa of GEM-glucuronide suggests systemic clearance by hepatic and renal influx.
- Both parent and glucuronide metabolite may be involved in DDI inhibition of enzymes.



# Outline of Process for Model Development and Documentation

- Creation of GP a project starts with structure import using ADMET Predictor Module for both substrates and perpetrators.
  - Physicochemical, biopharmaceutical, and biochemical properties
  - Initial evaluation via “Chemistry Classification” with all aspects of ADMET
    - Solubility vs. pH, dissolution, absorption (w/ influx and efflux transporters), clearance (metabolic, biliary, and renal), distribution, excretion, and toxicity.
  - Extensive literature collection and spreadsheet documentation.
    - Workbook with multiple sheets for Physicochemical, Metabolic, Transporter, Preclinical, and Clinical single compound and DDI study data for multiple perpetration mechanisms.
  - First simulations for “Measured Properties” with parameter sensitivity analysis.
  - Model building for individual substrate and/or perpetrator simulations compared to observed data for single escalating doses (for nonlinear dose dependence), multiple dosing (for autoinhibition / autoinduction).
  - DDI simulations for all appropriate mechanisms on both substrate and perpetrator.
  - Analysis of results using the “Guest”\* criterion for different levels of accuracy cutoff for increasing AUC (inhibition) and decreasing AUC (induction).
  - Preparation of slides and written reports suitable for regulatory submission.



# Human Cp vs. time profiles before and after GEM and GEM-glucuronide DDIs

## Subset of 13 references from a total of 83:

1. Hermening-JChromatogrB BiomedSci-741-2-129-2000-PK profiles-of-gemfibrozil-and-glucuronide-and-covalent-adducts-PO-900-mg
2. Hirano-DrugMetabDisp-34-7-1229-2006-DDI-Pitavastatin-Verapamil-Ki-hepatic-uptake-OAT1B1
3. Ho-Gastroenterology-130-6-1793-2006-Rosuvastatin-hepatic-uptake-OATP and NTCP-Vmax-Km transporters
4. Honkalammi-DrugMetabDispos-39-10-1977-2011-Human data-Repaglinide-Gemfibrozile DDI-2C8 activity
5. Kajosaari-Backmann-BasicClinPharmacolToxicol-97-249-2005-Metabolism-Repaglinide-Gemfibrozil-CYP2C8-Ki-CYP3A4
6. Nakagomi-Xenobiotica-37-4-416-2007\_Inhibition of hOAT3 pravastatin transport by gemfibrozil and glucuronide human
7. Nakagomi-Hagihara-Xenobiotica-37-5-474-2007-Gemfibrozil-and-its-glucuronide-inhibit-OATP1B1
8. Ogilvie-DrugMetabDispos-34-1-191-2006-Gemfibrozil Glucuronide-HLM study-NADPH dependent inactivation-2C8
9. Schneck-ClinPharmacolTher-75-5-455-2004-Rosuvastatin and Gemfibrozil DDI
10. Wang-CPT- PharmacometSysPharmacol-6-4-228-2017-Transporter Based DDI Rosuvastatin PBPK model SimCyp
11. Wen-Neuvoven-DrugMetabDisposition-29-11-1359-2001-invitro-2C9 inhibition-Gemfibrozil
12. Yamazaki-Lin-Xenobiotica-35-7-737-2005-OATP1B1-MRP2-P-gp-mediated transport-Gemfibrozil-DDI-Fibric acid derivatives
13. Yoshida-ClinPharmTherap-91-6-1053-2012-Transporter-DDI-of-OATP-Substrates-from-in-vitro-studies-w-Supplements

# Extensive Workbook for all DDI Standards

Property	Value	Units	Ref.
<b>Physicochemical Properties</b>			
MWt			
SS, 05\18\2020 Updated 09\22\2020		250.34	
<b>S+logP</b>	4		ADMET Predictor ver. 10.0
Exp log D (Oct/H2O)@pH 7.4	2.8		Luner-Radebaugh-PharmRes-11-12-1755-1994-Gemfibrozil-pH sol
Exp log P extrapolated from Log D	5.2		GP 9.7
<b>pKas</b>			
S+Acid pKa	4.92		ADMET Predictor ver. 10.0
Exp Acid pKa	5		Luner-Radebaugh-PharmRes-11-12-1755-1994-Gemfibrozil-pH sol
<b>Solubility</b>			
S+Sw	0.0826	mg/mL	ADMET Predictor ver. 10.0
S+pH	4.24		ADMET Predictor ver. 10.0
S+Solubility Factor	276.89		ADMET Predictor ver. 10.0
Aq. Sol from GSE	0.00213	mg/mL	Yalkowsky GSE
Exp. Solubility @ pH 1 @37 deg C	0.02000	mg/mL	Luner-Radebaugh-PharmRes-11-12-1755-1994-Gemfibrozil-pH sol
S+FaSSIF @ pH 6.5	0.4200	mg/mL	ADMET Predictor ver. 10.0
S+FeSSIF @ pH 5.0	0.6200	mg/mL	ADMET Predictor ver. 10.0
<b>Permeability</b>			
S+Peff	7.33E+04	cm/s	ADMET Predictor ver. 10.0
Caco-2 Papp A->B	5.89E-05		Absorptions Systems Lighthouse Database
Caco-2 Papp B->A	4.73E-05		Absorptions Systems Lighthouse Database
Ratio B->A / A->B	0.80		
GeoMean B->A and A->B	5.28E-05		Absorptions Systems Lighthouse Database
P-gp Substrate	No	Yes/No	
Caco-2 Converted to Hum Peff	5.60E-04	cm/s	Converted from GeoMean of Absorption Systems Caco-2
<b>Blood to Plasma Conc. Ratio</b>			
S+Rbp	0.67		ADMET Predictor ver. 10.0
Ex Rbp			
Fitted for PBPK			
<b>Fraction Unbound in Plasma</b>			
S+PrUnbnd	5.18 %		ADMET Predictor ver. 10.0
Ex fup	3.5 %		Oprea and Benet Wombat database
Ex fup	2 %		Miller-ClinPharmacokinet-34-2-155-1998-Clinical PK of Fibric Acid
<b>Melting Point</b>			

Estimated free base solubility using GSE Ref. Sanghvi-Yalkowsky-QSARCombSci-22-2-258-2003-Estim

$$\log S = 0.5 - 0.01(m.p. \text{ } ^\circ\text{C} - 25) - \log P$$

log S = 0.5 - 0.01(122-25) - 3.97 = -4.45

Aq. Sol

-5.07E+00 Log Sol (M)

8.51E-06 M

0.002 g/L

ISIS/Base

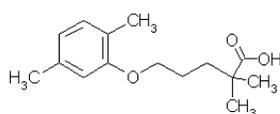
BIOPYTEMASTER-2008.DB/Main

ISIS/Base

ABS-SYSTEMS-LIGHTHOUSE-DATABASE-MBB-3-15-05.DB/Main

Forms Query Browse Update

Search Domain: All 1 of 1

Structure	ID	LDS_PN
	186	L0186
Compound_Name	CAS_RegistryNumber	
Gemfibrozil	25812-30-0	
*fm1a_Structure	*mol_weight_Structure	
C <sub>15</sub> H <sub>22</sub> O <sub>3</sub>	250.3408	
Selected	Therapeutic_Category	
	Antihyperlipoproteinemic	

PctBound_HumanPlasmaProt_Log	PctBound_RatPlasmaProt_Log	OralBioavailability_LitValue	MolWeight_LDS_File
		98.0000	250.3000
PctRemaining_HumanLiverMsomes	PctRemaining_RatLiverMsomes	Papp_Caco2_AB_Log (Papp x 10E6)	Papp_Caco2_BA_Log
35.3000	67.5000	1.7699	1.6746
BrainPlasmaRatioRat_Log	Clearance_LitValue (L/h)	Papp_MDR_MDCK_AB_Log	Papp_MDR_MDCK_BA_Log
	1.7000		
DoseNumber_LitValue	EffluxRatio_Caco2_Log	pKa1	pKa2
240.0000	-0.0953	4.8900	
EffluxRatio_MDR_MDCK_Log	HIA_LitValue	pKa3	HIA_LitValue
InVitroHalfLife_HumanLvrMsomes (min)	InVitroHalfLife_RatLiverMsomes (min)	Solubility_LitValue (ng/mL)	Solubility_pH20 (ng/mL)
63.3000	37.9000	0.0100	
LogP_Predicted	LogP	Solubility_pH74	Uptake_RatBrainPerfusion_Log
4.8000	4.6370		
MaximumDoseStrength_LitValue	VolumeOfDistribution_LitValue (L/Kg)	CLint_uL_min_milCells	CLint_mL_min_mg
0.0100	0.1400		
Papp_Caco2_AB_BCS_pH65	Recov_Caco2_AB_BCS_pH65	Papp_Caco2_AB_BCS_pH74	Recov_Caco2_AB_BCS_pH74

# Extensive Workbook for all DDI Standards

X77

All subjects received 3 mg oral MDZ, followed by the indicated dose of oral ALF. Results are given as mean  $\pm$  SD (N = 10).  
 ND, Not determined (the calculated  $F_{12}$  for MDZ after rifampin was either zero or indefinite because  $F_{11}$  was zero); CL/F, oral clearance; V<sub>c</sub>/F, volume of central compartment; F<sub>abs</sub>, oral bioavailability; F<sub>int</sub>, intestinal bioavailability; CL<sub>int,eff</sub>, effect clearance.  
 \*Significantly different from same-dose control (P < .05).

GastroPlus(TM) 9.8.0008		12/23/2020 9:24:33 AM					
Compound 1:		Victim					
Database:		Midazolam-GP-9.7-DDI-Standard-VL-2020-09-07-MBB-2020-12-22.mdb					
Record:		Midaz PO 3.0mg vs RIF 600mg 5d Kharasch					
Compound 2:		Perpetrator: 3A4 ind. & inh., UGT1A3 ind., MRP2 inh., and OATP1B1 inh.					
Database:		Rifampicin-GP9.8-DDI-Standard-KS-MBB-SA-RC-2020-12-22.mdb					
Record:		Rifamp 600mg PO DDI PO 3mg MDZ Kharasch					
[NewTable]		Dynamic Simulation Results					
Compound	Fa [%]	FDp [%]	F [%]	Cmax [ug/mL]	Tmax [h]	AUC[0-t] [ng-h/mL]	AUC[0-inf] [ng-h/mL]
95 Midaz PO 3.0mg vs RIF 600mg 5d Kharasch-baseline	99.99	27.94	15.15	0.00688	132.7	18.26	20.13
96 Rifamp 600mg PO DDI PO 3mg MDZ Kharasch-baseline	99.95	97.86	90.54	12.76	121.6	473000	474000
97 RIF-Gluc Metabolite-baseline	0	0	0	1.907	99.64	99900	100000
98 Midaz PO 3.0mg vs RIF 600mg 5d Kharasch-DDI	99.99	5.487	0.756	0.00034	132.4	0.524	0.54
99 Rifamp 600mg PO DDI PO 3mg MDZ Kharasch-DDI	99.97	86.52	75.92	12.18	1.5	251000	251000
100 RIF-Gluc Metabolite-DDI	0	0	0	2.419	3.76	92500	92600
101 Midaz PO 3.0mg vs RIF 600mg 5d Kharasch-ratio	1	0.196	0.05	0.05	0.998	0.029	0.027
102 Rifamp 600mg PO DDI PO 3mg MDZ Kharasch-ratio	1	0.884	0.839	0.955	0.012	0.531	0.53
103 RIF-Gluc Metabolite-ratio	0	0	0	1.268	0.038	0.926	0.926

Midaz. 3 mg PO 12 hr after RIF 600 mg QD for 6 days Baseline

Midaz 3 mg PO 12 hr after RIF 600 mg QD for 6 days Full DDI

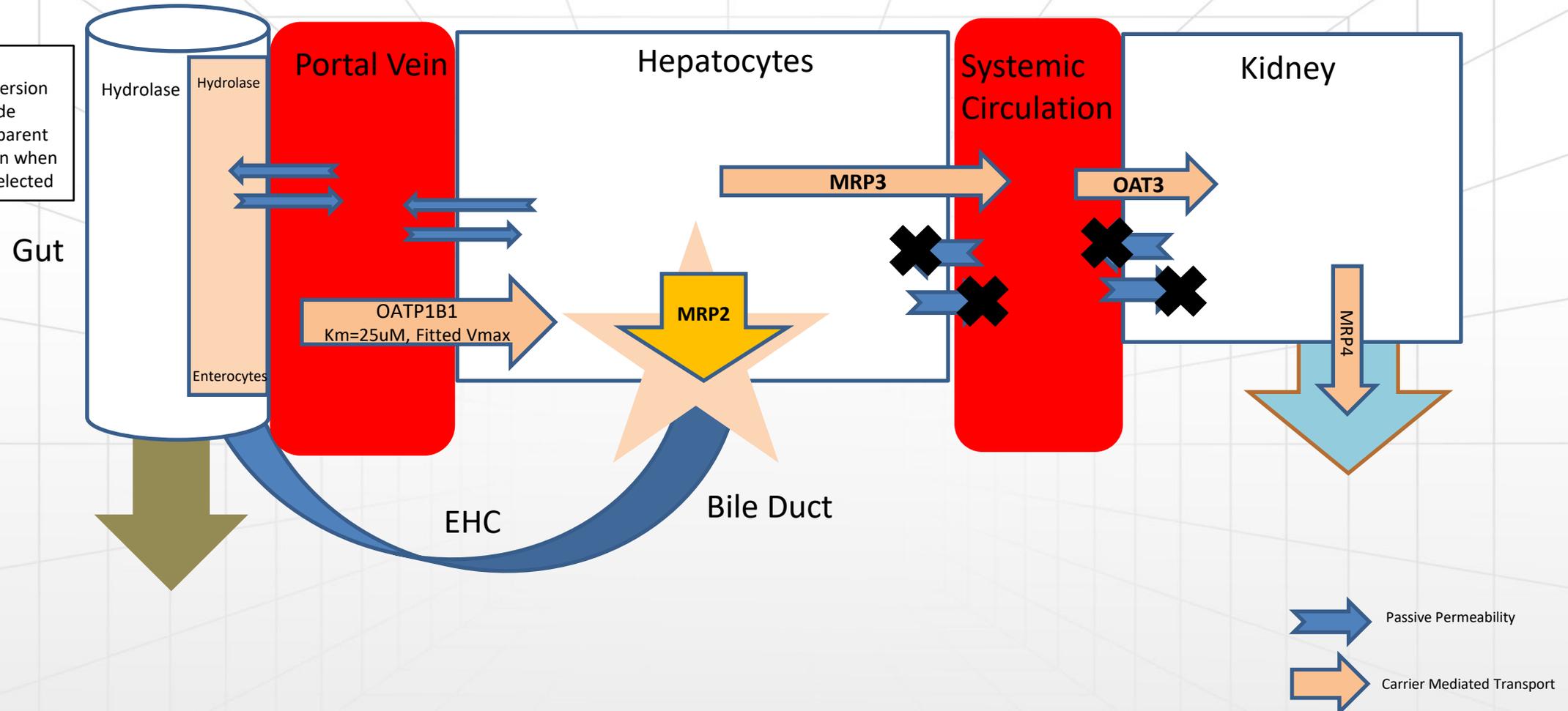
Peloquin 600mg PO Results | Acocella 600mg 900mg PO QD | Acocella 600mg 900mg Results | Kharasch 2011 600mg DDI Alf IV | Khar. 2004 600mg vs Midaz IV | **Khar. 2004 600mg vs Midaz PO**

# Inclusion of a spreadsheet for fast editing of Perpetrator Table with new "Validated" Field

Ogilvie-Parkinson-DrugMetabDispos-34-1-191-2006-Reversible Inhibition (IC50,t,HLM) of paclitaxel metabolism by gemfibrozil glucuronide in HLM.														
A	B	C	D	E	F	G	H	I	J	K	L	M		
1	Perpetrators Table													
2	OrigOr	Generic	Enzyme	InhibitionConstant	InhibitionConstantUnits	InhibitionConstantType	Substrate	Reference	InVitroFu	InVitroFuType	InVitroProtConc	Kinact	Validated	
84	82	Gem Gluc Tornio EC Kps	2C8	20	uM	IC50-irr-in vitro, T	Paclitaxel	Ogilvie-Parkinson-DrugMetabDispos-34	0.992	Calc(Hallifax)-HLM	0.1	0.21	TRUE	
85	83	Gem Gluc Tornio EC Kps	2C8	24	uM	IC50-rev-in vitro, T	Paclitaxel	Ogilvie-Parkinson-DrugMetabDispos-34	0.826	Calc(Hallifax)-HLM	0.5	0	FALSE	
86	84	Gem Gluc Tornio EC Kps	OAT3	9.9	uM	Ki-rev-in vitro, U	14C-Pravastatin	Nakagomi-Hagihara-Xenobiotica-37-4-4	-1	Unknown	0.5	0	TRUE	
87	85	Gem Gluc Tornio EC Kps	OAT3	13	uM	IC50-rev-in vitro, U	Unknown	Yoshida-ClinPharmTherap-91-6-1053-20	-1	Unknown	0.5	0	FALSE	
88	86	Gem Gluc Tornio EC Kps	OATP1B1	22.6	uM	Ki-rev-in vitro, U	3H-Pitavastatin	Hirano-Sugiyama-DrugMetabDisposition	-1	Unknown	0.5	0	FALSE	
89	87	Gem Gluc Tornio EC Kps	OATP1B1	15.7	uM	Ki-rev-in vitro, T	14C-Pravastatin	Nakagomi-hagihara-Xenobiotica-37-5-4	0.987	Calc(Austin)-Hep	0.5	0	FALSE	
90	88	Gem Gluc Tornio EC Kps	OATP1B1	7.6	uM	Ki-rev-in vitro, U	14C-Pravastatin	Nakagomi-hagihara-Xenobiotica-37-5-4	-1	Unknown	0.5	0	TRUE	
91	89	Gem Gluc Tornio EC Kps	OATP1B1	14	uM	IC50-rev-in vitro, U	Unknown	Yoshida-ClinPharmTherap-91-6-1053-20	-1	Unknown	0.5	0	FALSE	
92	90	Gem Gluc Tornio EC Kps	OATP1B3	74	uM	IC50-rev-in vitro, U	Unknown	Yoshida-ClinPharmTherap-91-6-1053-20	-1	Unknown	0.5	0	FALSE	
93	91	GEM PO 600 mg DDI Repag Tornio	2C8	30.4	uM	Ki-rev-in vitro, T	Paclitaxel	Kajosaari-Backmann-BasicClinPharmacol	0.826	Calc(Hallifax)-HLM	0.5	0	TRUE	
94	92	GEM PO 600 mg DDI Repag Tornio	2C8	120	uM	IC50-rev-in vitro, T	Paclitaxel	Ogilvie-Parkinson-DrugMetabDispos-34	0.826	Calc(Hallifax)-HLM	0.5	0	FALSE	
95	93	GEM PO 600 mg DDI Repag Tornio	2C9	30	uM	IC50-rev-in vitro, T	Diclofenac	Ogilvie-Parkinson-DrugMetabDispos-34	0.826	Calc(Hallifax)-HLM	0.5	0	FALSE	
96	94	GEM PO 600 mg DDI Repag Tornio	2C9	4	uM	Ki-rev-in vitro, U	Tolbutamide	Wang-JPET-302-1-43-2002-Unbound inhi	-1	Unknown	0.5	0	FALSE	
97	95	GEM PO 600 mg DDI Repag Tornio	2C9	5.8	uM	Ki-rev-in vitro, T	Tolbutamide	Wen-Neuvoven-DrugMetabDisposition	0.826	Calc(Hallifax)-HLM	0.5	0	TRUE	
98	96	GEM PO 600 mg DDI Repag Tornio	NTCP	23	uM	IC50-rev-in vitro, U	Rosuvastatin	Ho et al-Gastroenterology. 2006-130(6)1	-1	Unknown	0.5	0	FALSE	
99	97	GEM PO 600 mg DDI Repag Tornio	OAT3	3.4	uM	Ki-rev-in vitro, U	14C-Pravastatin	Nakagomi-Hagihara-Xenobiotica-37-4-4	-1	Unknown	0.5	0	FALSE	
100	98	GEM PO 600 mg DDI Repag Tornio	OAT3	3.2	uM	IC50-rev-in vitro, U	Unknown	Yoshida-ClinPharmTherap-91-6-1053-20	-1	Unknown	0.5	0	FALSE	
101	99	GEM PO 600 mg DDI Repag Tornio	OATP1B1	25.2	uM	Ki-rev-in vitro, U	3H-Pitavastatin	Hirano-Sugiyama-DrugMetabDisposition	-1	Unknown	0.5	0	FALSE	
102	100	GEM PO 600 mg DDI Repag Tornio	OATP1B1	31.7	uM	Ki-rev-in vitro, T	14C-Pravastatin	Nakagomi-hagihara-Xenobiotica-37-5-4	0.645	Calc(Austin)-Hep	0.5	0	FALSE	
103	101	GEM PO 600 mg DDI Repag Tornio	OATP1B1	15.1	uM	Ki-rev-in vitro, U	14C-Pravastatin	Nakagomi-hagihara-Xenobiotica-37-5-4	-1	Unknown	0.5	0	FALSE	
104	102	GEM PO 600 mg DDI Repag Tornio	OATP1B1	4	uM	IC50-rev-in vitro, U	3H-Rosuvastatin	Schneck-ClinPharmacolTher-75-5-455-20	-1	Unknown	0.5	0	FALSE	
105	103	GEM PO 600 mg DDI Repag Tornio	OATP1B1	12.5	uM	Ki-rev-in vitro, U	3H-E217BETAG	Yamazaki-Lin-Xenobiotica-35-7-737-200	-1	Unknown	0.5	0	TRUE	
106	104	GEM PO 600 mg DDI Repag Tornio	OATP1B1	20	uM	IC50-rev-in vitro, U	Unknown	Yoshida-ClinPharmTherap-91-6-1053-20	-1	Unknown	0.5	0	FALSE	

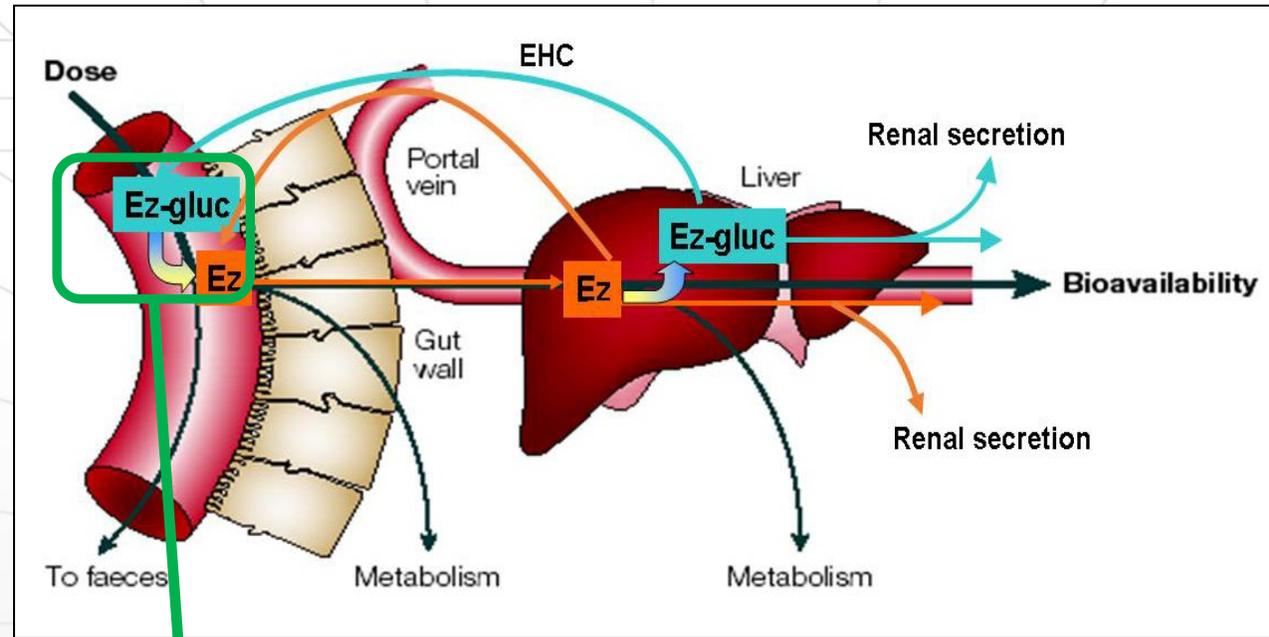
For example: the rifampicin perpetrator table has > 400 rows

✓ GP 9.8.1  
Allows for conversion of all glucuronide metabolite to parent in the gut lumen when EHC option is selected



# Metabolite- Gemfibrozil Glucuronide

# Acyl-glucuronide Conversion to Parent in Gut Lumen



Enterohaepatic Circulation Parameters

Biliary Excretion Model

Biliary Clearance Fraction: 0.5

Allow to Re-Absorb

Convert to Parent in Lumen

Physiological EHC Parameters

Gallbladder Emptying Time: (min) 30

Gallbladder Diversion Fraction: 0.75

OK

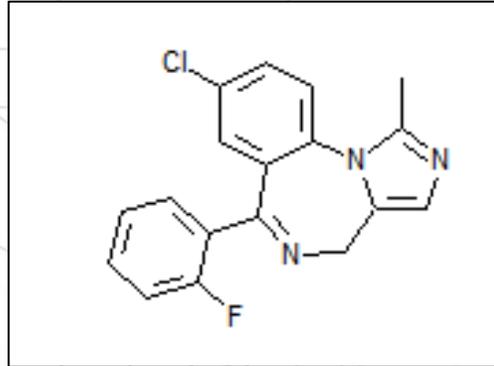
Cancel

- This is not a general solution for compound metabolism in gut lumen (that is coming in GPX)
- It is applicable primarily for acyl-glucuronide metabolites
- It produces parent compound in the lumen for re-absorption
- Assumes breakdown of glucuronides so molecular ratio = 1

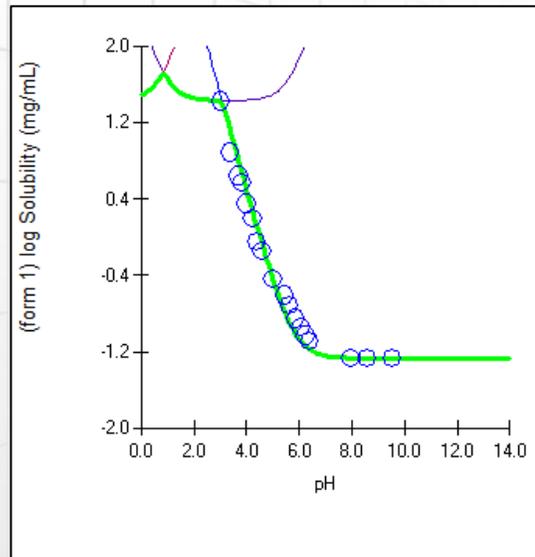
# Outline of Process for Model Development and Documentation

- Creation of GP a project starts with structure import using ADMET Predictor Module for both substrates and perpetrators.
  - Physicochemical, biopharmaceutical, and biochemical properties
  - Initial evaluation via “Chemistry Classification” with all aspects of ADMET
    - Solubility vs. pH, dissolution, absorption (w/ influx and efflux transporters), clearance (metabolic, biliary, and renal), distribution, excretion, and toxicity.
  - Extensive literature collection and spreadsheet documentation.
    - Workbook with multiple sheets for Physicochemical, Metabolic, Transporter, Preclinical, and Clinical single compound and DDI study data for multiple perpetration mechanisms.
  - First simulations for “Measured Properties” with parameter sensitivity analysis.
  - Model building for individual substrate and/or perpetrator simulations compared to observed data for single escalating doses (for nonlinear dose dependence), multiple dosing (for autoinhibition / autoinduction).
  - DDI simulations for all appropriate mechanisms on both substrate and perpetrator.
  - Analysis of results using the “Guest”<sup>\*</sup> criterion for different levels of accuracy cutoff for increasing AUC (inhibition) and decreasing AUC (induction).
  - Preparation of slides and written reports suitable for regulatory submission.

# Midazolam BCS/BDDCS II Physicochemical Properties



**MW = 325.77**



AP 9.5 = ADMET Predictor v. 9.5  
S+ = properties predicted with Simulations Plus models  
S+Sw = native solubility in pure water  
S+Peff = human jejunal permeability estimate

**S+LogP = 3.56 (AP 9.5)**

**Exp LogP = 2.7 (Hoffmann-La Roche)**

**S+pKa = 4.57 (Base) and 0.84 (Base)**

**Exp pKa = 6.04 (Andersin-JPharmaceutBioMedAnal-9-6-451-1991)**

**S+Sw = 2.1 µg/mL @ pH = 7.05 (AP 9.5)**

**Exp Sw = 54 µg/mL @ pH 9.5 Andersin, 1991) LOW**

**S+FaSSIF = 33 µg/mL, S+ FeSSIF = 210 µg/mL**

**Exp FaSSIF = 11 µg/mL, (personal communication ??)**

**S+Peff =  $7.55 \times 10^{-4}$  (cm/s) (AP 9.5) HIGH**

**Exp Ussing Papp =  $3.8E-5$  cm/s (Sjoberg-Ungel, 2013)**

**Conversion to Hum. Jej. Peff =  $3.82E-4$  cm/s**

**S+HLM-3A4 Km = 21 µM Vmax = 3.5 nmol/min/mg Prot. (AP 9.5)**

**Exp CYP3A4 Km = 3.7 µM (Paine, 1997)**

**Exp CYP3A4 Vmax = 0.85 nmol/min/mg Prot.**

**Exp CYP3A4 Km = 2.27 mM (Walsky, 2004)**

**Exp CYP3A4 Vmax = 1.22 nmol/min/mg Prot.**

**S+hum\_fup% = 6.61 (AP 9.5)**

**Exp. Fup = 4.4% Ave. (de Vries, 199) and (Fisher, 1999)**

**S+RBP = 0.78 (AP 9.5)**

**Exp Rbp = 0.55 (Gertz, 2011)**



# PBPK Model for Midazolam 7.5 mg PO Solution Bornemann

- Assumptions:

- Perfusion-limited midazolam
- Permeability-limited liver and kidney for 1-OH-midazolam
- Added MRP3 liver basolateral to efflux metabolite to systemic circulation for PO records only.

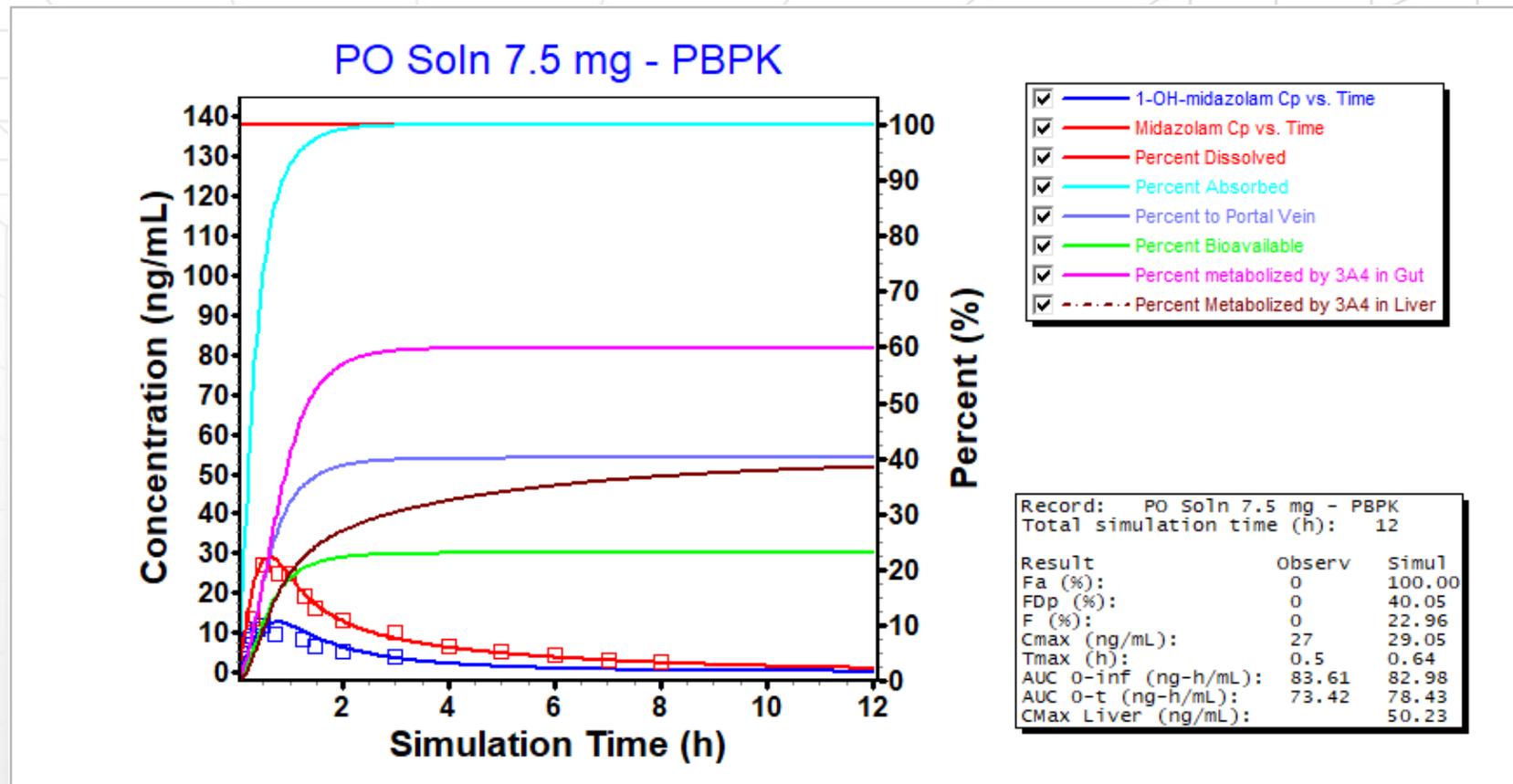
-  $f_{u_{ent}} = 4.4\%$

- Clearance:

- Paine-J. Pharmacol. Exp. Ther., 283:1552 (1997) unbound  $K_m = 3.7 \mu\text{M}$  and  $V_{max} = 0.85 \text{ nmol/min/mg}$  micro. Prot.

- Distribution:

- Midazolam Lukacova default  $K_p$  calculation
- 1-OH-midazolam reduced  $\log P = 2.2$  to calc.  $K_p$ s and then ran simulation with  $\log P = 2.57$



Clinical data from:

Bornemann-EurJ Clin Pharmacol-29-1-91-1985

# PBPK Model for Midazolam 30 mg PO Solution Bornemann

- **Assumptions:**

- Perfusion-limited midazolam
- Permeability-limited liver and kidney for 1-OH-midazolam
- Added MRP3 liver basolateral to efflux metabolite to systemic circulation for PO records only.

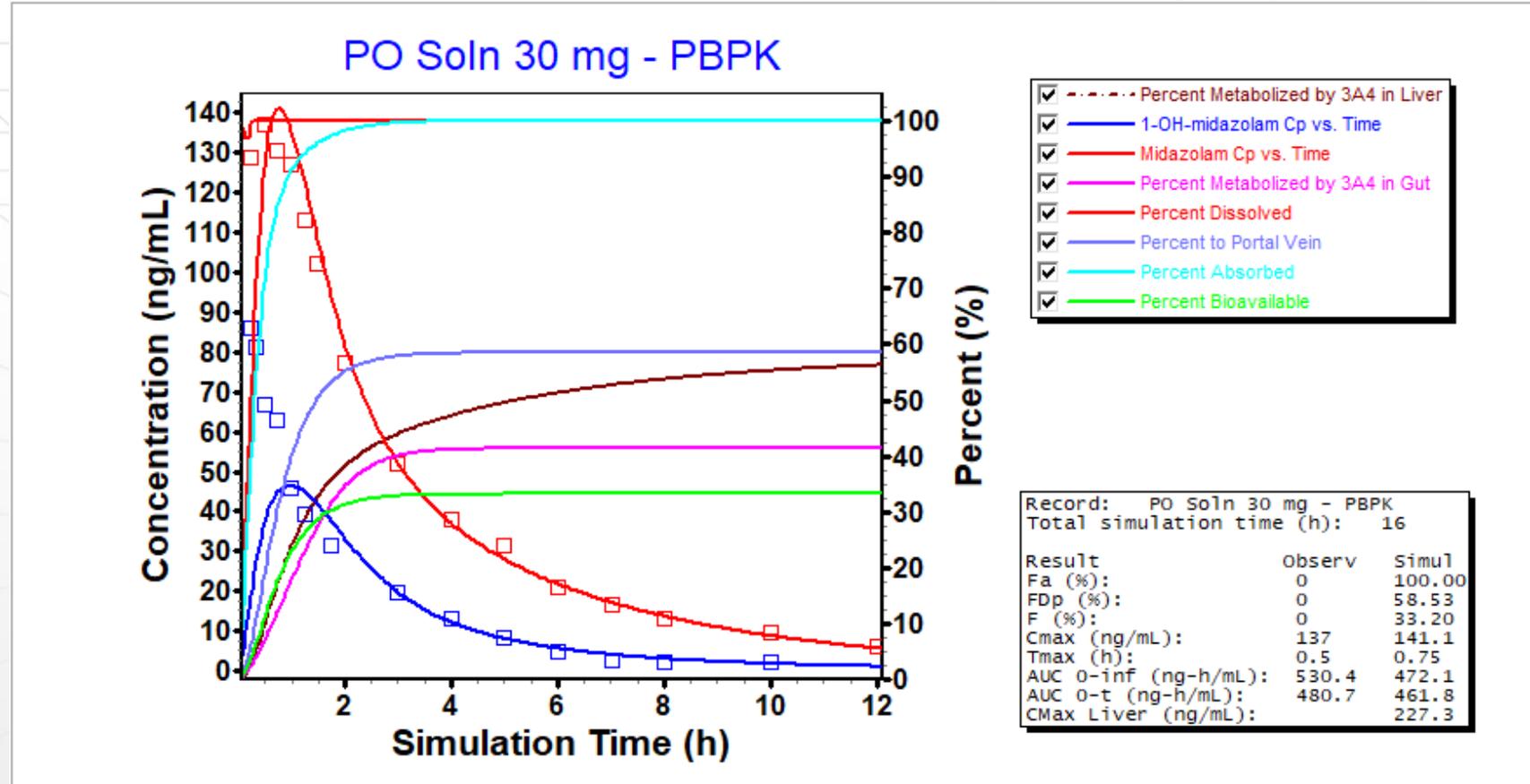
–  $f_{u_{ent}} = 4.4\%$

- **Clearance:**

- Paine-J. Pharmacol. Exp. Ther., 283:1552 (1997) unbound  $K_m = 3.7 \mu\text{M}$  and  $V_{max} = 0.85 \text{ nmol/min/mg}$  micro. Prot.

- **Distribution:**

- Midazolam Lukacova default Kp calculation
- 1-OH-midazolam reduced log P = 2.2 to calc. Kps and then ran simulation with log P = 2.57



Clinical data from:

Bornemann-EurJ Clin Pharmacol-29-1-91-1985

# Midaz. 7.5 mg PO Tab DDI vs. Keto. 400 mg QD for 4 days: Olkkola

## Baseline Simulation without DDI interactions

- Assumptions:

- Perfusion-limited midazolam
- Permeability-limited liver and kidney for 1-OH-midazolam
- Ketoconazole: 3A4 total Rev.  $IC_{50} = 26 \text{ nM}$ , 3A4 total Irrev.  $IC_{50} = 15 \text{ nM}$ ,  $K_{inact} = 0.001 \text{ min}^{-1}$  and P-gp total  $IC_{50} = 5.6 \text{ }\mu\text{M}$
- Reduced  $f_{u_{ent}} = 4.4\%$  (Ref. Trevaskis-PharmRes-28-9-2176-2011)

- Clearance:

- Paine-J. Pharmacol. Exp. Ther., 283:1552 (1997) unbound  $K_{m,u} = 3.7 \text{ }\mu\text{M}$  and  $V_{max} = 0.977 \text{ nmol/min/mg micro. Prot.}$  The 1.15-fold higher clearance was used due to the Olkkola population of 7 females and 2 male subjects.

- Distribution:

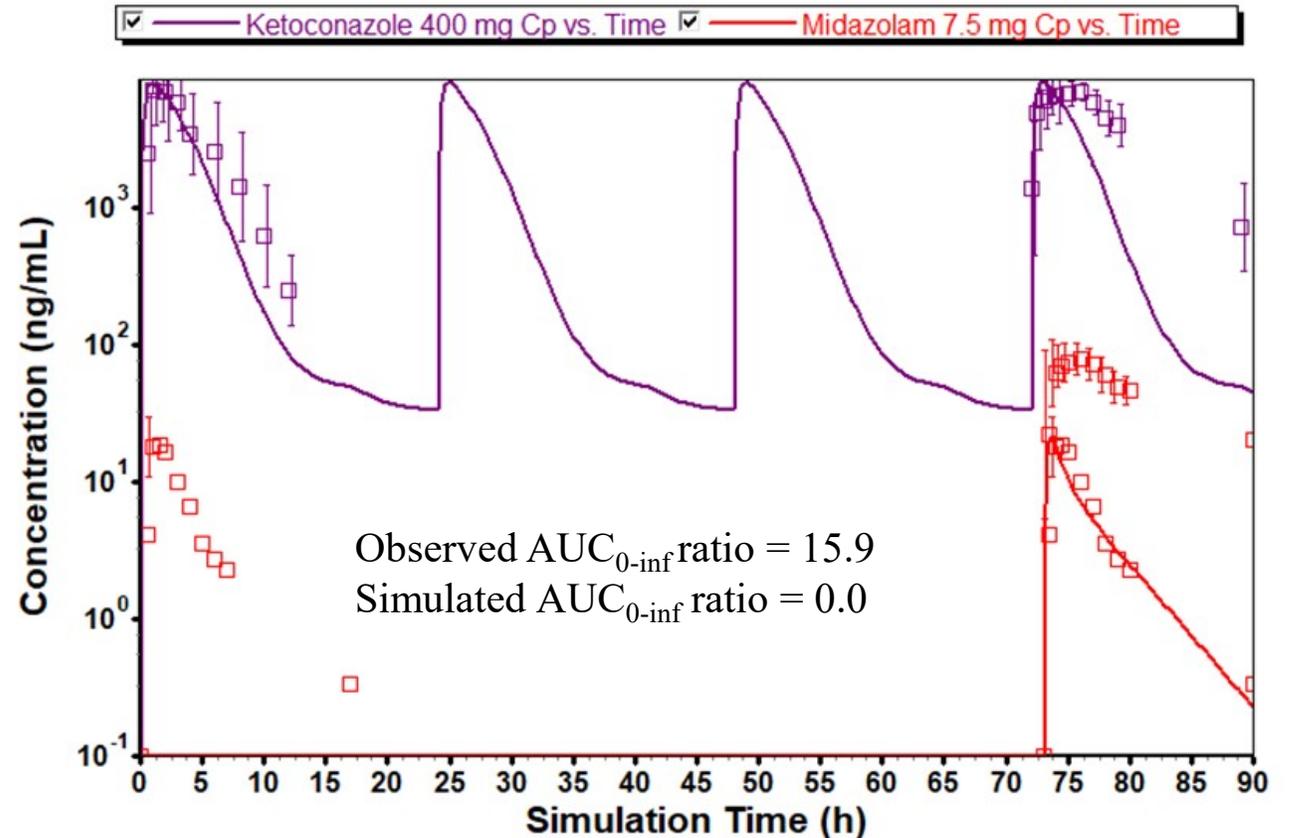
- Midazolam Lukacova default Kp calculation
- 1-OH-midazolam reduced log P = 2.2 to calc. Kps and then ran simulation with log P = 2.57

Midazolam clinical data from: Olkkola-ClinPharmacolTherap-55-5-481-1994

Ketoconazole clinical data from: Daneshmend-Antimicrobial agents and Chemotherapy-25-1-1-1984 and Olkkola-ClinPharmacolTherap-55-5-481-1994

Ketoconazole TDI parameters from: Haarhoff-Xenobiotica-47-6-470-2017

Midaz. PO 7.5 mg 1 hr. after Keto. PO 400 mg for 4 days. Baseline



Model-Informed Drug Development



# In vitro CYP3A Inhibition Parameters ( $IC_{50,t,HLM}$ ) for Ketoconazole

474 Z. E. Haarhoff et al.

Xenobiotica, 2017; 47(6): 470–478

Table 2. Evaluation of CYP3A inhibition with HLM and CLM.

Inhibitor	HLM			CLM		
	$IC_{50}$ ( $\mu$ M)			$IC_{50}$ ( $\mu$ M)		
	Non-preincubation (0 min)	Preincubation (30 min)	Ratio	Non-preincubation (0 min)	Preincubation (30 min)	Ratio
Amprenavir	0.55 ± 0.08	0.084 ± 0.025	6.5	0.3 ± 0.04	0.2 ± 0.03	1.7
Azithromycin	>100	>100	1.0	>100	>100	1.0
Bergamottin	>50	0.17 ± 0.04	>294.1	>50	1.3 ± 0.4	>38.5
Buspirone	>50	15.8 ± 2.9	>3.2	>50	>50	1.0
Cimetidine	>100	>100	1.0	>100	>100	1.0
Clarithromycin	>50	8.2 ± 0.3	>6.1	>50	15.1 ± 0.4	>3.3
Clozapine	>50	21.2 ± 3.7	>2.4	>50	27.2 ± 6.2	>1.8
Cyclosporin A	24.4 ± 5.8	5.8 ± 1.0	4.2	12.0 ± 2.6	7.0 ± 1.5	1.7
Dextromethorphan	>50	>50	1.0	>50	>50	1.0
Diltiazem	43.5 ± 8.6	7.7 ± 1.7	5.6	30.7 ± 4.8	1.4 ± 0.4	21.9
Erythromycin	>100	12.1 ± 3.3	>8.3	>100	54.2 ± 10.2	>1.8
Ethinylestradiol	41.7 ± 1.7	5.2 ± 0.5	8.0	31.4 ± 1.6	4.5 ± 0.8	7.0
Felodipine	4.1 ± 1.3	4.0 ± 0.4	1.0	4.5 ± 1.1	7.4 ± 2.2	0.6
Fluconazole	3.2 ± 0.6	3.7 ± 0.7	0.86	6.8 ± 0.9	6.9 ± 0.6	1.0
Fluoxetine	>50	>50	1.0	>50	>50	1.0
Fluvoxamine	>50	>50	1.0	>50	>50	1.0
Furafylline	>50	>50	1.0	>50	>50	1.0
Irinotecan	>100	>100	1.0	>100	>100	1.0
Isoniazid	>100	>100	1.0	>100	>100	1.0
Itraconazole	0.068 ± 0.017	0.017 ± 0.006	4.0	0.12 ± 0.02	0.054 ± 0.009	2.2
Ketoconazole	0.026 ± 0.010	0.015 ± 0.003	1.7	0.04 ± 0.006	0.056 ± 0.009	0.7
Mibefradil	0.67 ± 0.14	0.017 ± 0.004	39.4	1.0 ± 0.2	0.17 ± 0.04	5.9

- Optimized  $K_{inact} = 0.001 \text{ min}^{-1}$  was used for irreversible inhibition

Publication supporting competitive and time-dependent inhibition by ketoconazole

Haarhoff-Xenobiotica-47-6-470-2017



# Midaz. 7.5 mg PO Tab DDI vs. Keto. 400 mg QD for 4 days: Olkkola

## Simulated AUC Ratio w/autoinhibition is accurate by adding: Irreversible IC<sub>50</sub> for 3A4

### Assumptions:

- Perfusion-limited midazolam
- Permeability-limited liver and kidney for 1-OH-midazolam
- Ketoconazole: 3A4 total Rev. IC<sub>50</sub> = 26 nM, 3A4 total Irrev. IC<sub>50</sub> = 15 nM, Kinact = 0.001 min<sup>-1</sup> and P-gp total IC<sub>50</sub> = 5.6 μM
- Reduced fu<sub>ent</sub> = 4.4% (Ref. Trevaskis-PharmRes-28-9-2176-2011)

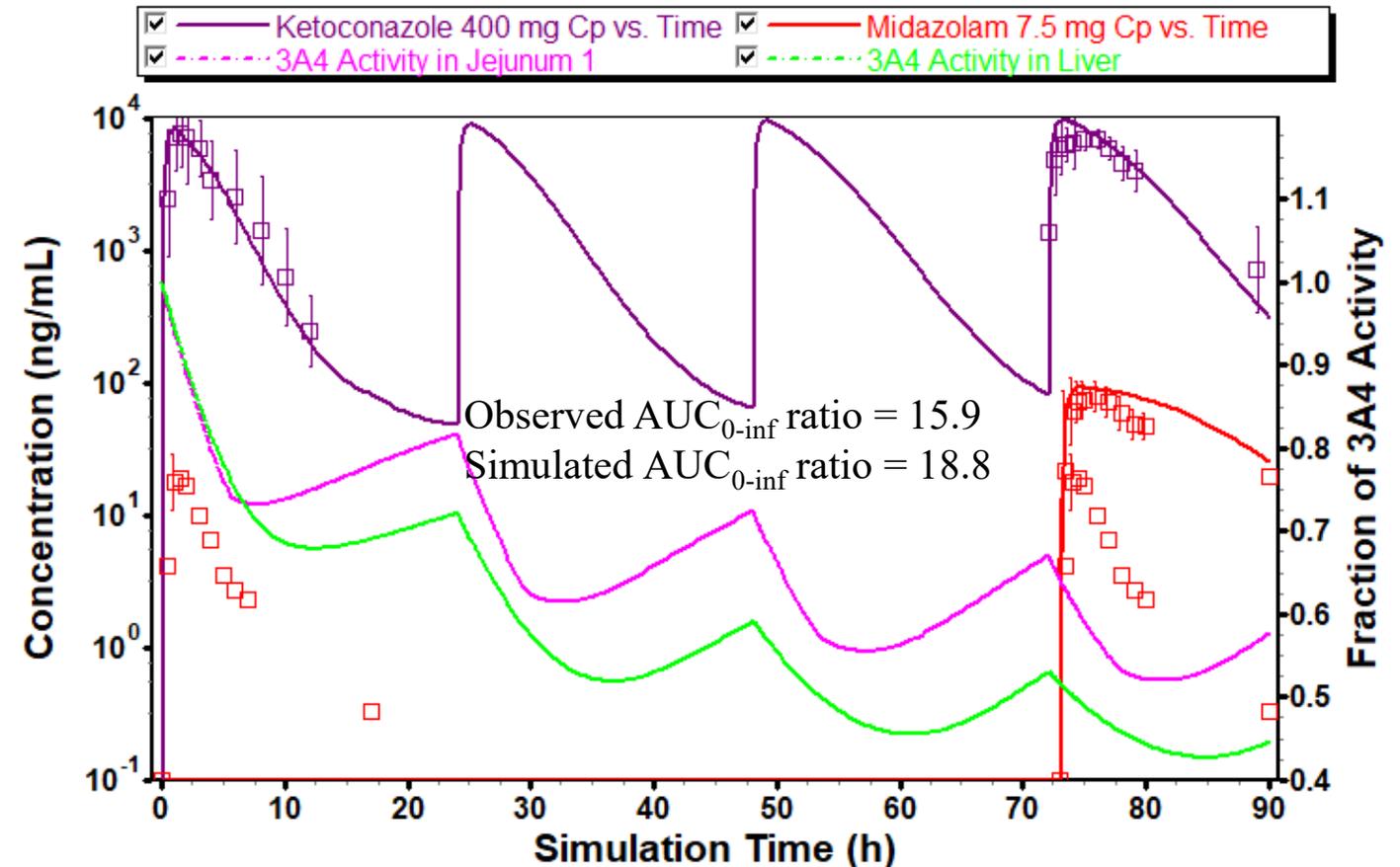
### Clearance:

- Paine-J. Pharmacol. Exp. Ther., 283:1552 (1997) unbound K<sub>m</sub> = 3.7 μM and V<sub>max</sub> = 0.977 nmol/min/mg micro. Prot. The 1.15-fold higher clearance was used due to the Olkkola population of 7 females and 2 male subjects.

### Distribution:

- Midazolam Lukacova default Kp calculation
- 1-OH-midazolam reduced log P = 2.2 to calc. Kps and then ran simulation with log P = 2.57

### Midaz. PO Tab 7.5 mg 1 hr after Keto. PO 400 mg for 4 days Full DDI



Midazolam clinical data from: Olkkola-ClinPharmacolTherap-55-5-481-1994

Ketoconazole clinical data from: Daneshmend-Antimicrobial agents and Chemotherapy-25-1-1-1984 and Olkkola-ClinPharmacolTherap-55-5-481-1994

Ketoconazole TDI parameters from: Haarhoff-Xenobiotica-47-6-470-2017



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  - First simulations for “Measured Properties” with parameter sensitivity analysis.
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  - Analysis of results using the “Guest”\* criterion for different levels of accuracy cutoff for increasing AUC (inhibition) and decreasing AUC (induction).
  - Preparation of slides and written reports suitable for regulatory submission.

# Newer DDI Module with "Validated" Field

Drug-Drug Interaction Predictions  
 File Current Compound Interacting Compounds Options Help

Prediction Type:  Steady-State Prediction  Dynamic Simulation  Single Sim  Pop Sim  DILIsym

Simulation Mode: Run Baseline Simulation Run Full Simulation Close

Interacting Compound(s): ~Standard SS MBB 2021-02-19.mdb

Perpetrator: GEM PO 600 mg DDI Repag Tornio Show Notes for Interacting Compound

Perpetrator Parameters

Perpetrator	Enz / Trans	Inh/Ind Const Type	Inh/Ind Const Value	Inh/Ind Const Units	kinact [min-1] /Emax	Select	Validated	In Vitro Fu	In Vitro Fu Type	In vitro F [mg/mL]
Gem Gluc EC Kps Tornio	OATP1B1	Ki-rev-in vitro. U	7.6	uM	0	<input checked="" type="checkbox"/>	True	-1	Unknown	0.5
Gem Gluc EC Kps Tornio	OATP1B1	IC50-rev-in vitro. U	14	uM	0	<input type="checkbox"/>	False	-1	Unknown	0.5
Gem Gluc EC Kps Tornio	OATP1B3	IC50-rev-in vitro. U	74	uM	0	<input type="checkbox"/>	False	-1	Unknown	0.5
GEM PO 600 mg DDI Repag Tornio	2C8	Ki-rev-in vitro. T	30.4	uM	0	<input checked="" type="checkbox"/>	True	0.826	Calc(Hallifax)-HLM	0.5
GEM PO 600 mg DDI Repag Tornio	2C8	IC50-rev-in vitro. T	120	uM	0	<input type="checkbox"/>	False	0.826	Calc(Hallifax)-HLM	0.5
GEM PO 600 mg DDI Repag Tornio	2C9	IC50-rev-in vitro. T	30	uM	0	<input type="checkbox"/>	False	0.826	Calc(Hallifax)-HLM	0.5
GEM PO 600 mg DDI Repag Tornio	2C9	Ki-rev-in vitro. U	4	uM	0	<input type="checkbox"/>	False	-1	Unknown	0.5
GEM PO 600 mg DDI Repag Tornio	2C9	Ki-rev-in vitro. T	5.8	uM	0	<input checked="" type="checkbox"/>	True	0.826	Calc(Hallifax)-HLM	0.5

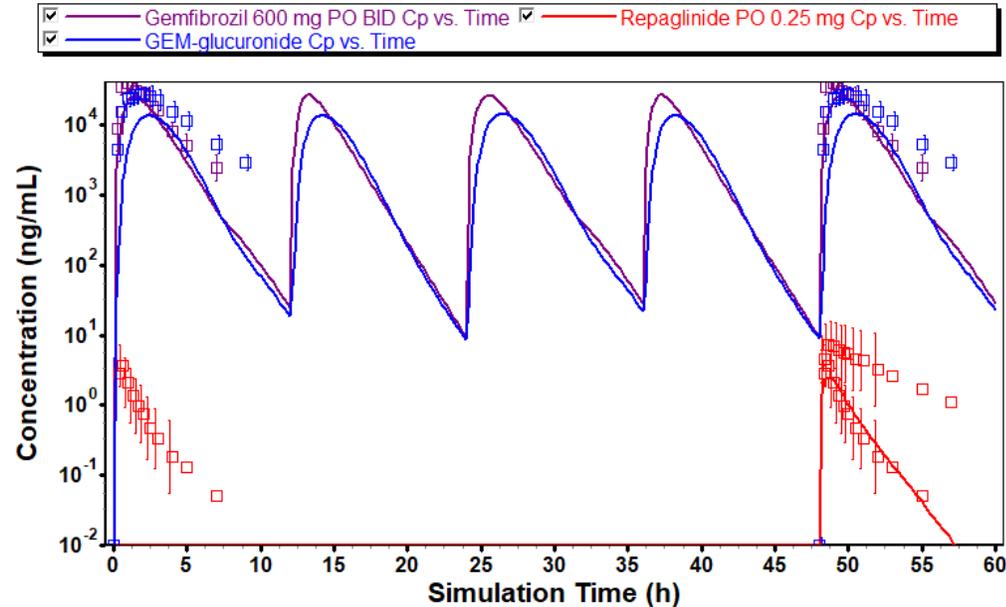
3 Add Enz/Trans  
4 Delete Enz/Trans  
?

Dosing Information: Dose [mg]: 600 Int [h]: 12 CL [L/h]: 11.228

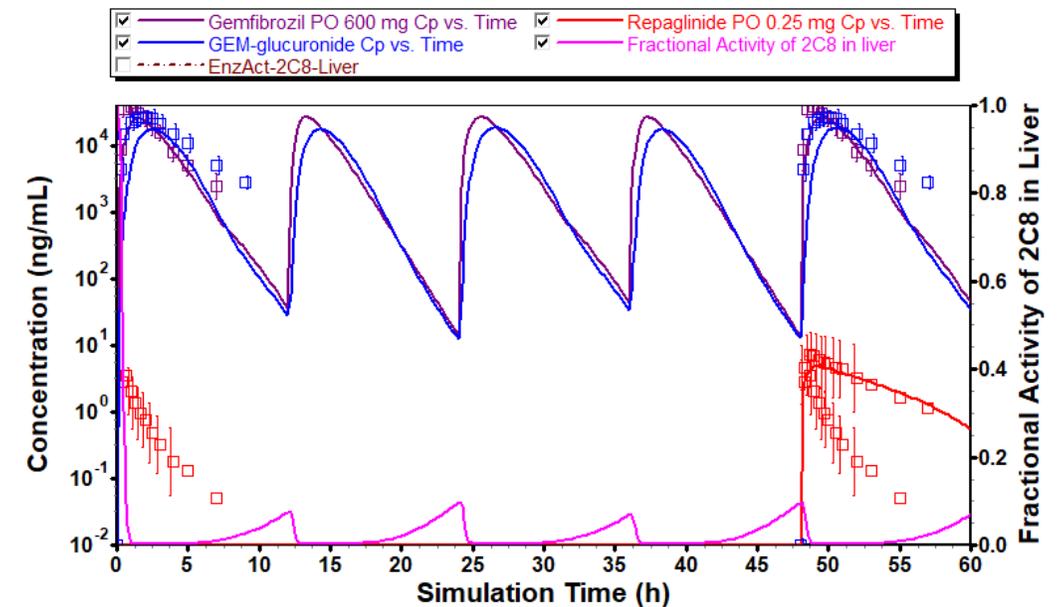
Rate Constants [1/h]: ka: 0 kel: 0.98989

# Repaglinide PO 2.5 mg on Day 3 after 5 doses of GEM 600 mg PO

Repag. PO 0.25 mg on Day 3 after 5 doses of Gemfibrozil PO 600 mg BID Baseline



Results: Dynamic Simulation - Compet - TDI



Ki values selected are:

- 1.) 12.5  $\mu\text{M}$  for OATP1B1 ( Gemfibrozil parent)
- 2.) 7.6  $\mu\text{M}$  for OATP1B1 ( Glucuronide )
- 3.) 30.4  $\mu\text{M}$  for the CYP2C8 ( Reversible) for the parent and
- 4.) 20  $\mu\text{M}$  for Irrev inhibition and  $K_{\text{inact}} = 0.21 \text{ min}^{-1}$  of CYP2C8 for the Glucuronide
- 5.) 3.4  $\mu\text{M}$  for the OAT3 ( Rev inhibition) for the parent and
- 6.) 9.9  $\mu\text{M}$  for the OAT3 (Rev inhibition) Glucuronide
- 7.) 5.8  $\mu\text{M}$  for the CYP2C9 (Rev Inhibition) by Parent

Repaglinide record: Repaglinide\_PO\_0.25mg\_Gem 600 mg

GEM Record:GEM PO 600 mg DDI Repag Tornio

GEM-Gluc record: Gem-Gluc EC Kps Tornio

Gemfibrozil was dosed with DDI module ( 600 mg, BID dosing interval)

Observed data for GEM and GEM gluc and Repaglinide before and after DDI in the plot is from Tornio et. al., 2008

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# Eleanor J. Guest et al. DMD, 39(2):170 (2011)

## Materials and Methods

The traditional two-fold predictive measure is bounded two-fold above and below the observed value: any prediction within these boundaries is classed as a successful prediction (see Fig. 1). Therefore, if the observed ratio,  $AUC_{+inhibitor}/AUC_{control}$  is 1, the boundaries would be from 0.5 to 2.0. As noted in the *Introduction*, this range is too wide for an interaction, which is in fact not present. As a result, we propose new limits, as shown in eqs. 1 to 3 below. The limits coalesce when the observed ratio is 1 and approach the traditional two-fold limits as the ratio becomes larger (Fig. 1).

$$\text{Upper limit: } R_{obs} * \text{Limit} \quad (1)$$

$$\text{Lower limit: } R_{obs} / \text{Limit}$$

$$\text{Limit} = \frac{1 + 2(R_{obs} - 1)}{R_{obs}}$$

where  $R_{obs}$  represents  $AUC_{+inhibitor}/AUC_{control}$  inhibition DDIs. The new predictive measure

fold. The trend of lower prediction accuracy at higher potency of DDIs reported in previous studies is no longer apparent when predictions are assessed via the new predictive measure. Thus, the study proposes a more logical method for the assessment of prediction success and its application for induction and inhibition DDIs.

To allow for uncertainty in the observed ratio, the new predictive measure is assessed by considering DDIs involving midazolam; a commonly used CYP3A4 victim drug (Bjornsson et al., 2003; Galetin et al., 2005). In this case, upper and lower limits are as defined in eqs. 1 and 2, respectively, but the variability is now introduced into the limit as shown in eq. 4.

$$\text{Limit} = \frac{\delta + 2(R_{obs} - 1)}{R_{obs}} \quad (4)$$

where  $\delta$  is a parameter that accounts for variability. If  $\delta = 1$ , there is no variability and limits revert to those defined by eq. 3. If  $\delta = 1.25$  and  $R_{obs} = 1$ , then the limits on  $R$  are between 0.80 and 1.25, corresponding to the conventional 20% limits used in bioequivalence testing (United States Food and Drug Administration, 2003). Note that these limits are symmetrical on the

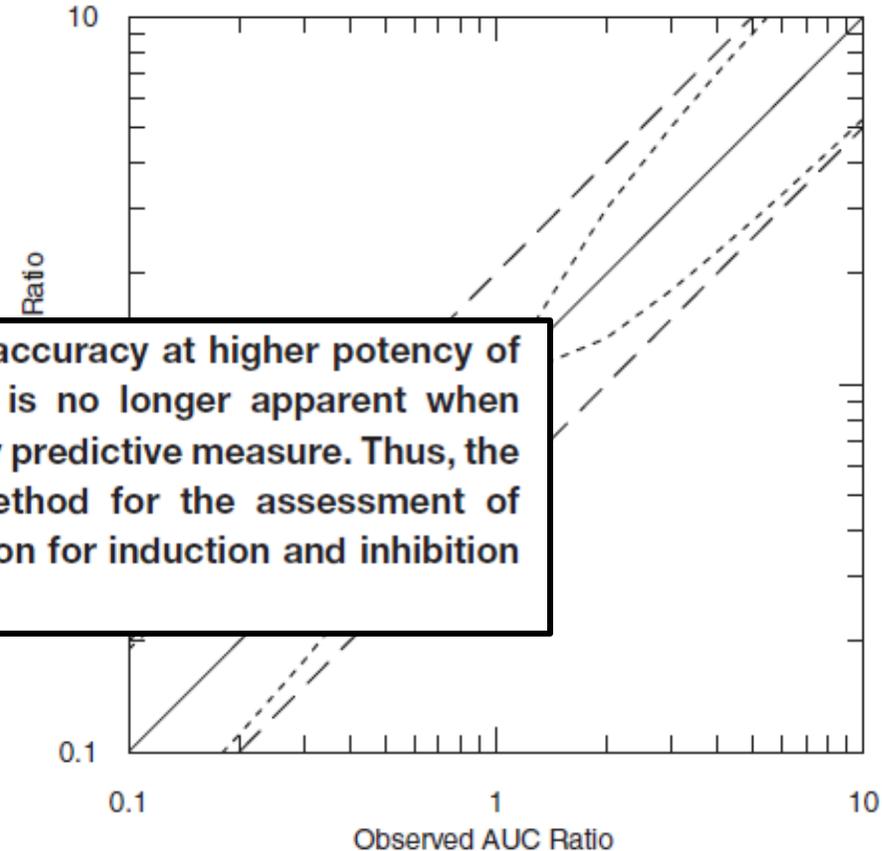


FIG. 1. Schematic graph displaying the limits of the different predictive measures; the traditional two-fold predictive measure (dashed lines) and the proposed new predictive measure (dotted lines). Observed AUC ratios include both induction and inhibition DDIs.

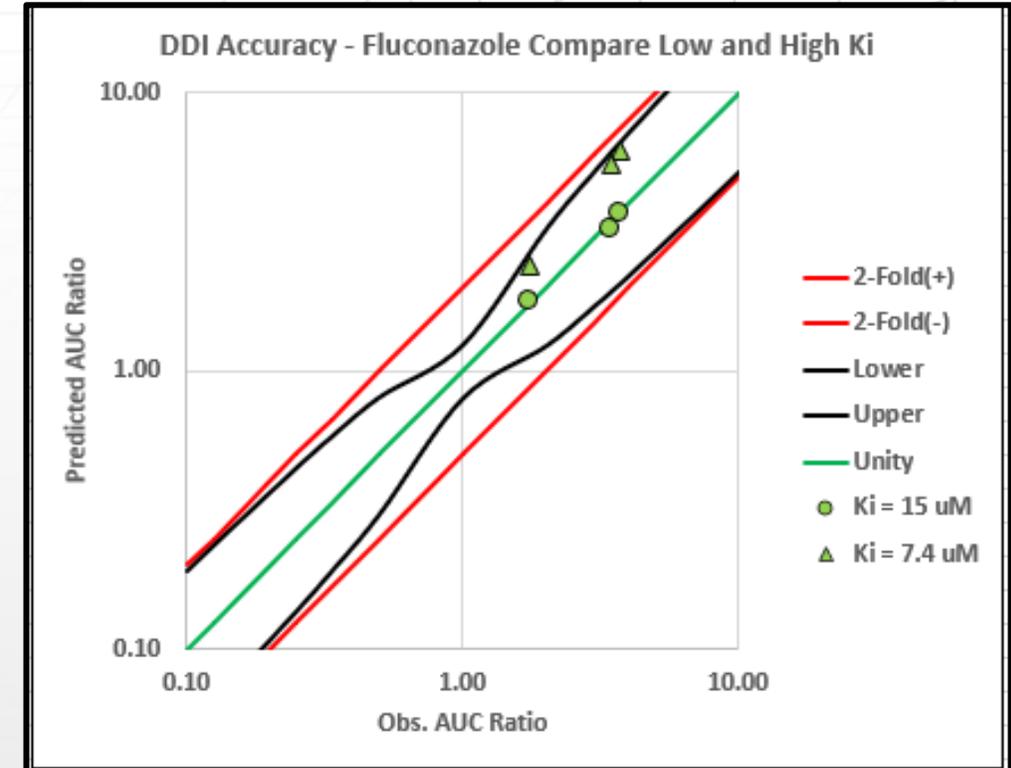
# Midazolam DDI vs. Fluconazole

	Variability		1.25	Guest Limits			log Limits				
	Obs Ratio	Variability (CV)	Limit	Upper	Lower	Unity	2-fold(+)	2-fold(-)	UL	LL	Center
Reciprocal of ratio 2 -10	0.10	1.25	1.93	0.19	0.05	0.10	0.20	0.05	-0.28	0.28	0
	0.13	1.25	1.91	0.24	0.07	0.13	0.25	0.06	-0.28	0.28	0
	0.25	1.25	1.81	0.45	0.14	0.25	0.50	0.13	-0.26	0.26	0
	0.33	1.25	1.75	0.58	0.19	0.33	0.67	0.17	-0.24	0.24	0
	0.50	1.25	1.63	0.81	0.31	0.50	1.00	0.25	-0.21	0.21	0.00
1.00	1.25	1.25	1.25	1.25	0.80	1	2.00	0.50	0.10	-0.10	0
2.00	1.25	1.63	3.25	1.23	2	4.00	1.00	0.21	-0.21	0	
3.00	1.25	1.75	5.25	1.71	3	6.00	1.50	0.24	-0.24	0	
4.00	1.25	1.81	7.25	2.21	4	8.00	2.00	0.26	-0.26	0	
8.00	1.25	1.91	15.25	4.20	8	16.00	4.00	0.28	-0.28	0	
10.00	1.25	1.93	19.25	5.19	10	20.00	5.00	0.28	-0.28	0	

Guest Criteria for Ki = 15 uM					Guest Criteria for Ki = 15 uM				
CV	Limit	Up Lim	Low Lim	Predicted	CV	Limit	Up Lim	Low Lim	Predicted
Cmax					AUC0-t				
1.25	1.67	3.84	1.37	2.07	1.25	1.80	6.70	2.07	3.69
1.25	1.58	2.82	1.13	1.86	1.25	1.78	6.13	1.93	3.23
1.25	-	-	-	-	1.25	1.57	2.73	1.11	1.79

Guest Criteria for Ki = 7.4 uM					Guest Criteria for Ki = 7.4 uM				
CV	Limit	Up Lim	Low Lim	Predicted	CV	Limit	Up Lim	Low Lim	Predicted
Cmax					AUC0-t				
1.25	1.67	3.84	1.37	2.57	1.25	1.80	6.70	2.07	6.19
1.25	1.58	2.82	1.13	2.32	1.25	1.78	6.13	1.93	5.50
1.25	-	-	-	-	1.25	1.57	2.73	1.11	2.37



# Outline of Process for Model Development and Documentation

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# Written Report of Model Development and Validations

**Table 6** Baseline Simulations of Sensitive CYP3A4 Substrates: Simulated Versus Observed PK Parameters of Triazolam and Midazolam.

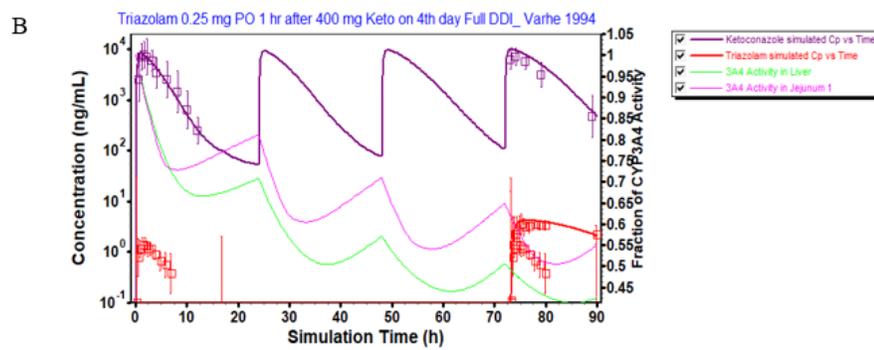
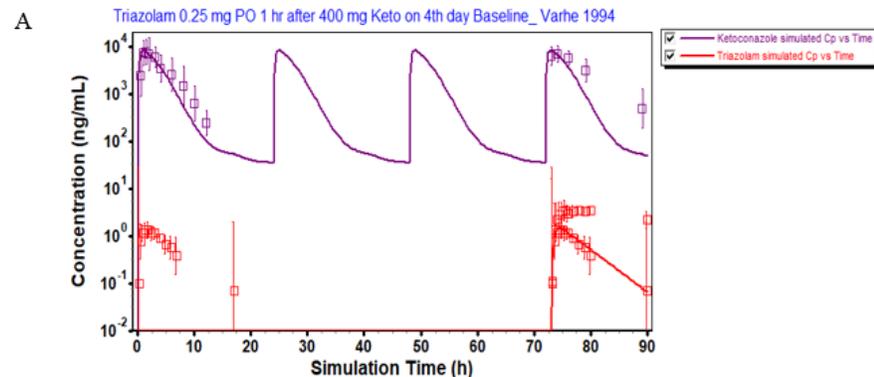
Reference	Substrate Dose and Regimen	Observed <sup>#</sup>		Simulated	
		C <sub>max</sub> (ng/mL)	AUC <sub>0-t</sub> (ng*hr/mL)	C <sub>max</sub> (ng/mL)	AUC <sub>0-t</sub> (ng*hr/mL)
(Varhe, Olkkola et al. 1994)	0.25 mg single dose triazolam tablet	1.5 ± 0.2	5.9 ± 0.7	1.49	8.86
(Greenblatt, Wright et al. 1998)	0.25 mg single dose triazolam tablet	2.6 ± 0.3	10.6 ± 1.6 <sup>§</sup>	1.82	11.06 <sup>§</sup>
(Olkkola, Backman et al. 1994)	7.5 mg PO midazolam	22 ± 6	65 ± 10 <sup>§</sup>	25	82.99 <sup>§</sup>

<sup>#</sup>Observed values are from the average of individual values, and represent mean ± standard error; <sup>§</sup>represent AUC<sub>0-inf</sub>

**Table 7** DDI Simulations of Sensitive CYP3A4 Substrates: Simulated Versus Observed PK Parameters of Triazolam and Midazolam With or Without Co-administration of Ketoconazole

Reference	Substrate		C <sub>max</sub> (ng/mL)	AUC <sub>0-t</sub> (ng*h/mL)
(Varhe, Olkkola et al. 1994)	Triazolam	Observed baseline <sup>#</sup>	1.5 ± 0.2	5.9 ± 0.7
		Simulated baseline	1.49	8.86
		Observed DDI <sup>#</sup>	4.6 ± 0.5	48.1 ± 5.3
		Simulated DDI	4.24	55.82
		Observed DDI ratio <sup>#</sup>	3.07	8.1
		Simulated DDI ratio	2.85	6.3
(Greenblatt, Wright et al. 1998)	Triazolam	Observed baseline <sup>#</sup>	2.6 ± 0.3	10.6 ± 1.6 <sup>§</sup>
		Simulated baseline	1.82	11.06 <sup>§</sup>
		Observed DDI <sup>#</sup>	5.4 ± 0.4	145.4 ± 39.1 <sup>§</sup>
		Simulated DDI	4.71	142.6 <sup>§</sup>
		Observed DDI ratio <sup>#</sup>	2.1	13.7 <sup>§</sup>
		Simulated DDI ratio	2.59	12.9 <sup>§</sup>
(Olkkola, Backman et al. 1994)	Midazolam	Observed baseline <sup>#</sup>	22 ± 6 <sup>§</sup>	65 ± 10 <sup>§</sup>
		Simulated baseline	25	82.99 <sup>§</sup>
		Observed DDI <sup>#</sup>	90 ± 7	1033.3 <sup>§</sup>
		Simulated DDI	96	1300.7 <sup>§</sup>
		Observed DDI ratio	4.09	15.9 <sup>§</sup>
		Simulated DDI ratio	3.84	15.7 <sup>§</sup>

<sup>#</sup>Parameters are from the average of observed individual values and represent mean ± standard error; <sup>§</sup>represent AUC<sub>0-inf</sub>, the simulated DDI ratios were highlighted in green while observed DDI ratios were highlighted in blue.



**Figure 6** Baseline Simulation Without a Drug-Drug Interaction (A, Top) and Full Dynamic Simulation With a Drug-Drug Interaction (B, Bottom) Between Ketoconazole and Triazolam

Ketoconazole (400 mg) was administered for four doses, and 0.25 mg triazolam was given at 3 PM after the fourth dose of KCZ (given at 2 PM) (Varhe, Olkkola et al. 1994).

The open squares and error bars represent the mean observed data and coefficient of variation, respectively, and the simulated (line) C<sub>p</sub>-time profiles for triazolam (red) and ketoconazole (purple). The simulated CYP3A4 activity in liver is highlighted in green, and the simulated

# Conclusions

- The GP DDI Standard Update Project Team have made significant advances in the ability to simulate complex mechanistic drug-drug interactions involving enzymes, transporters, and enterohepatic circulation.
- Now DDI simulations will be accomplished with a full database of validation study records for both substrates and perpetrators
- We provide extensive literature references, data compilation, slides, and written documentation and GastroPlus model files that can be used for regulatory submissions
- When documentation is in a complete draft form, all components are scientifically reviewed and formatted as a complete package for regulatory review of novel compound results.
- All complete models will be available for download by registered GP license holders.

# Acknowledgements

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Consulting Studies  
Cheminformatics

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