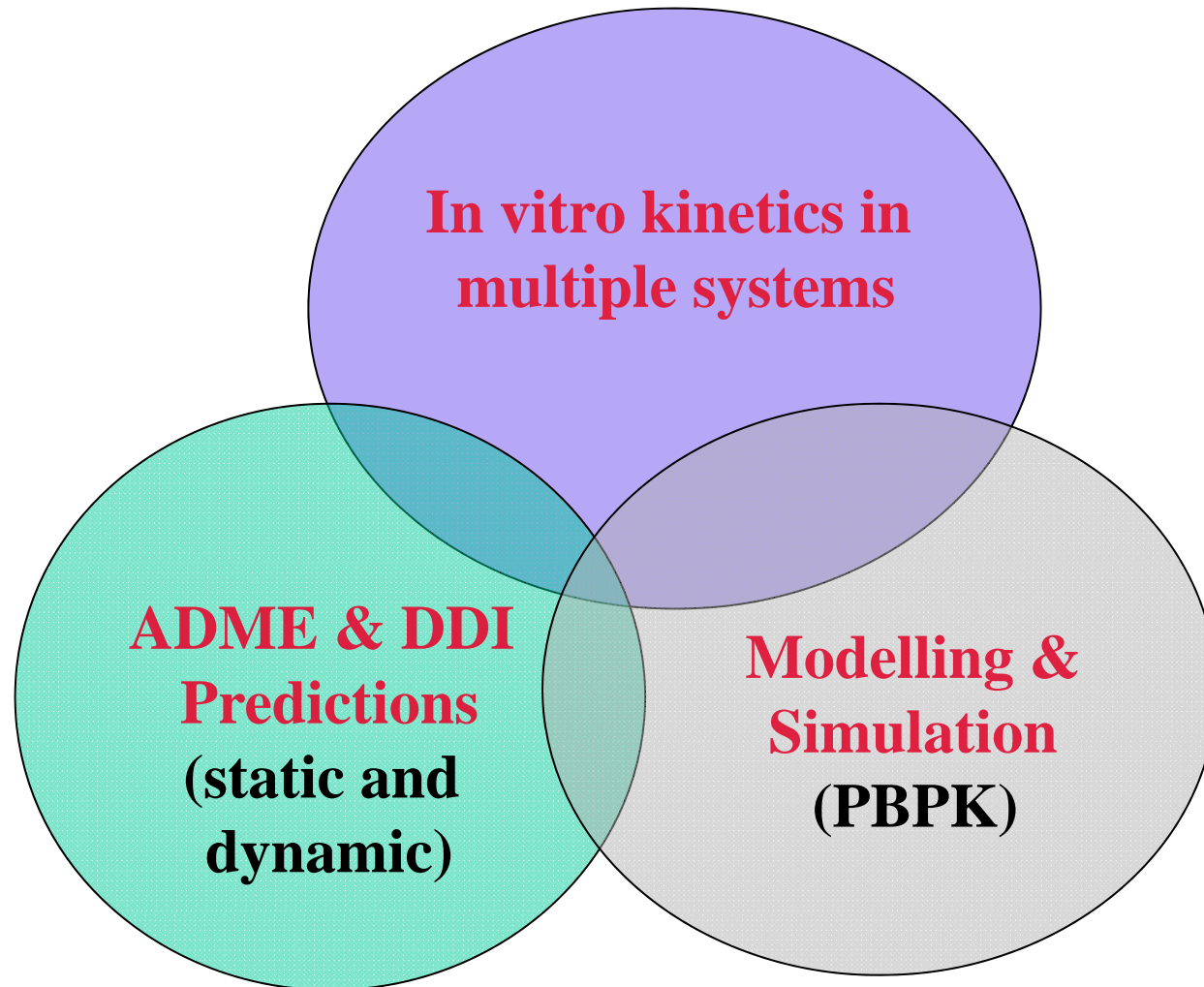


# **Interplay between enzymes and transporters in defining hepatic drug clearance and intracellular concentration of drugs**

**J Brian Houston**

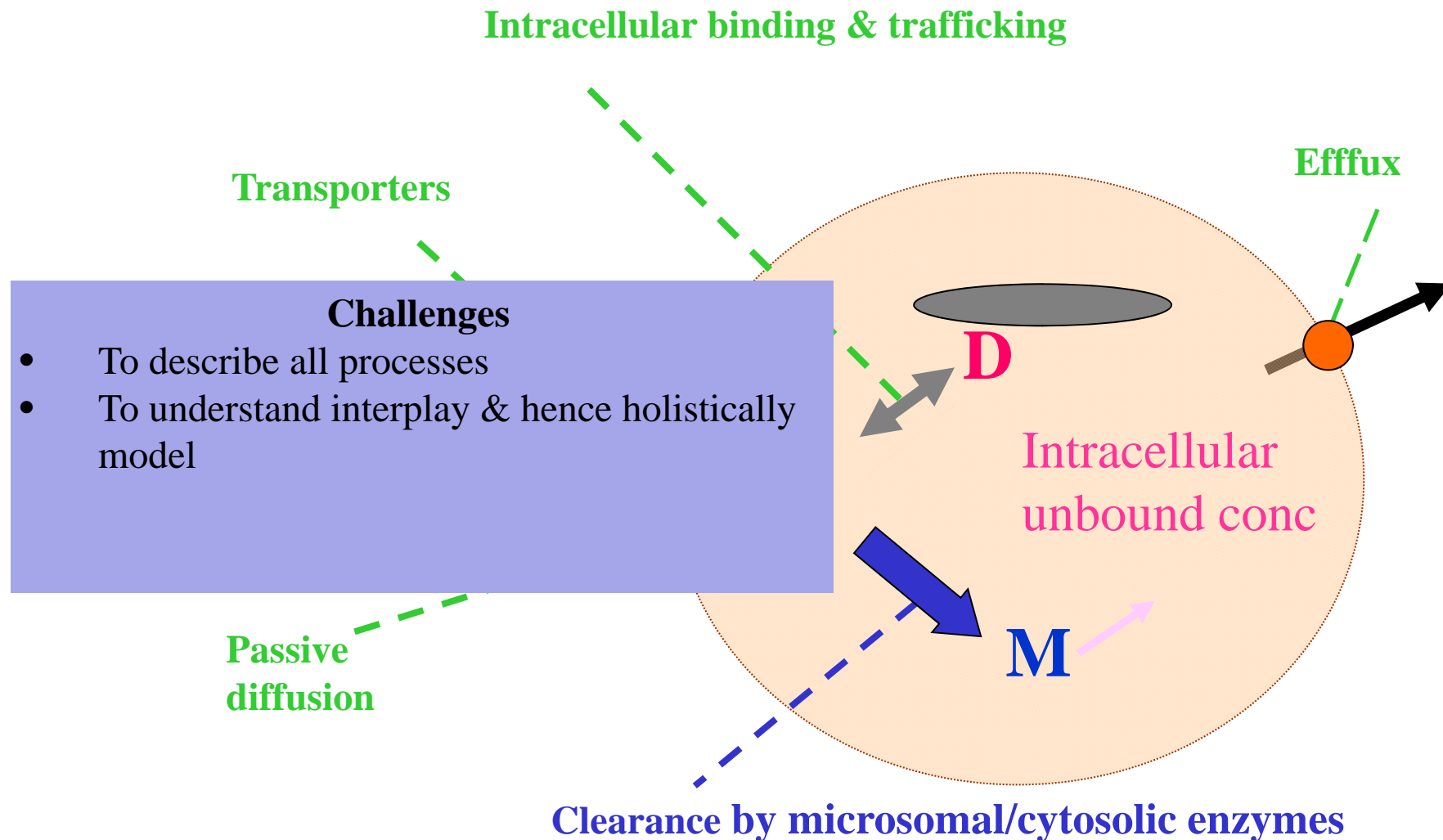
**Centre for Applied Pharmacokinetic Research  
(CAPkR)**

# Three elements of mechanism-based prediction of human PK



# Generic view of drug kinetics in hepatocytes:

Various processes defining drug intracellular concentration



# Extending Classic Hepatic Clearance Models:

Use of  $CL_{\text{int,app}}$  to delineate transporters & enzymes and their 'Interplay'

Prediction (static) equations well established:  
e.g. well-stirred liver model

$$CL = \frac{Q_h \cdot fu_b \cdot CL_{\text{int}}}{Q_h + fu_b \cdot CL_{\text{int}}}$$

Extended with use of  $CL_{\text{int,app}}$  to encompass hepatocellular sequential processes (Interplay model) based on Sugiyama and Pang.

$$CL_{\text{int,app}} = CL_{\text{int,met}} \frac{CL_{\text{int,active}} + CL_{\text{int,pass}}}{CL_{\text{int,met}} + CL_{\text{int,pass}} + CL_{\text{int,eff}}}$$

## $CL_{int,app}$ – Interplay of transporters and enzymes

$$CL_{int,app} = CL_{int,met} \frac{CL_{int,active} + CL_{int,pass}}{CL_{int,met} + CL_{int,pass} + CL_{int,eff}}$$

- High passive permeability
  - reduces to  $CL_{int,met}$
- Low passive permeability (with minimal efflux)
  - reduces to  $CL_{int,active}$
- Various intermediate cases. The second term collective –  $Kp_u$  (partition coefficient for unbound drug)

# In vitro tools for assessment of hepatic uptake

- Hepatocytes:
  - Suspension culture - direct cell uptake (oil separation)
  - Plated cells (also sandwich configuration)
  - Single time points or full time course of uptake & metabolism
- Comparative scaled activity in hepatocytes relative to microsomes (subcellular preparation)
- Sometimes rat better option than human
  - Higher activity and less confounding issues surrounding preparation and storage
  - Minimal inter-individual variation
  - Potential extrapolation to human
- $CL$  terms main metric, and for inhibition DDIs  $K_i$   
where  $CL_i = CL_{\text{control}} / 1 + K_i$

# Characterisation of extent of hepatic uptake

## What are we measuring with $Kp_u$ ?

- $Kp_u$  = Cell to medium (plasma) unbound concentration ratio

$$Kp_u = \frac{CL_{\text{int},\text{uptake}} + CL_{\text{int},\text{passive}}}{CL_{\text{int},\text{passive}}} \quad [\text{True } Kp_u - \text{at steady state when no metabolism or efflux}]$$

$$Kp_u = \frac{CL_{\text{int},\text{pass}} + CL_{\text{int},\text{uptake}}}{CL_{\text{int},\text{pass}} + CL_{\text{int},\text{efflux}} + CL_{\text{int},\text{met}}} \quad [\text{Apparent } Kp_u]$$

- Contrasts with  $Kp_{\text{total}}$  (ratio of total concentrations) which reflects both uptake and intracellular binding

$$Kp_u = fu_{\text{cell}} \cdot Kp_{\text{total}}$$

Used together estimates intracellular drug concentration

# Comparison of microsomes and hepatocytes

## Evidence for hepatic uptake affecting CL and DDI prediction

If active uptake process occurring, substrate or inhibitor may show higher 'affinity' in hepatocytes compared to microsomes –

i.e. lower  $K_m$  or  $K_i$  as

$$[S]_{u,plasma} \ll [S]_{u,liver} \text{ or } [I]_{u,plasma} \ll [I]_{u,liver}$$

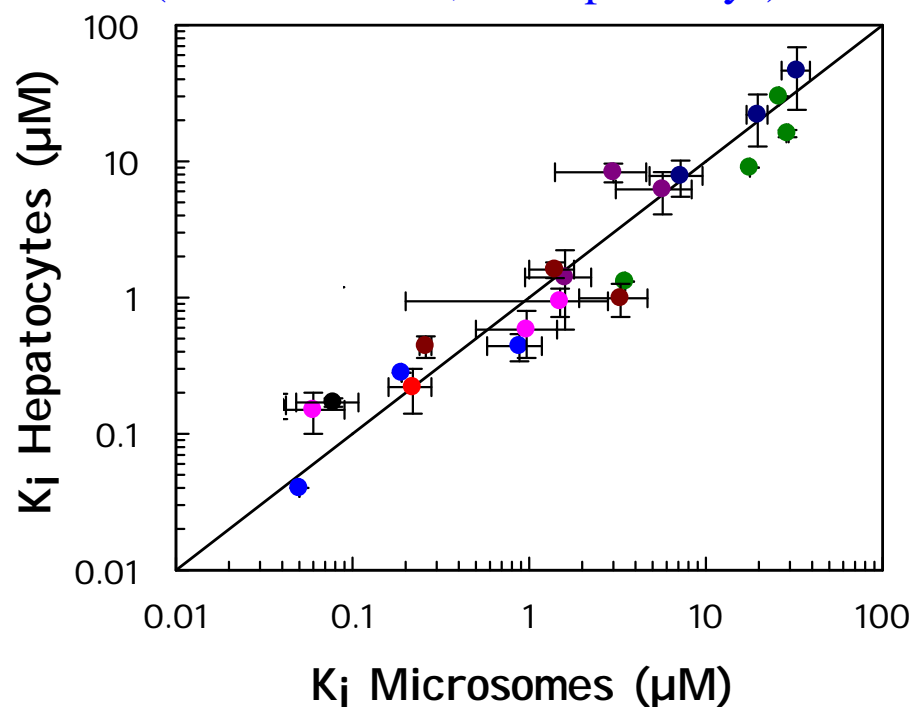
$$K_{p,u} = \frac{K_{i,microsome}}{K_{i,hepatocyte}}$$

$$= \frac{K_{m,microsome}}{K_{m,hepatocyte}} = \frac{CL_{int,hepatocyte}}{CL_{int,microsome}}$$



# Impact of hepatic intracellular binding?: $K_i$ Microsomes vs. Hepatocytes

(n= 7 inhibitors, n=21 pathways)



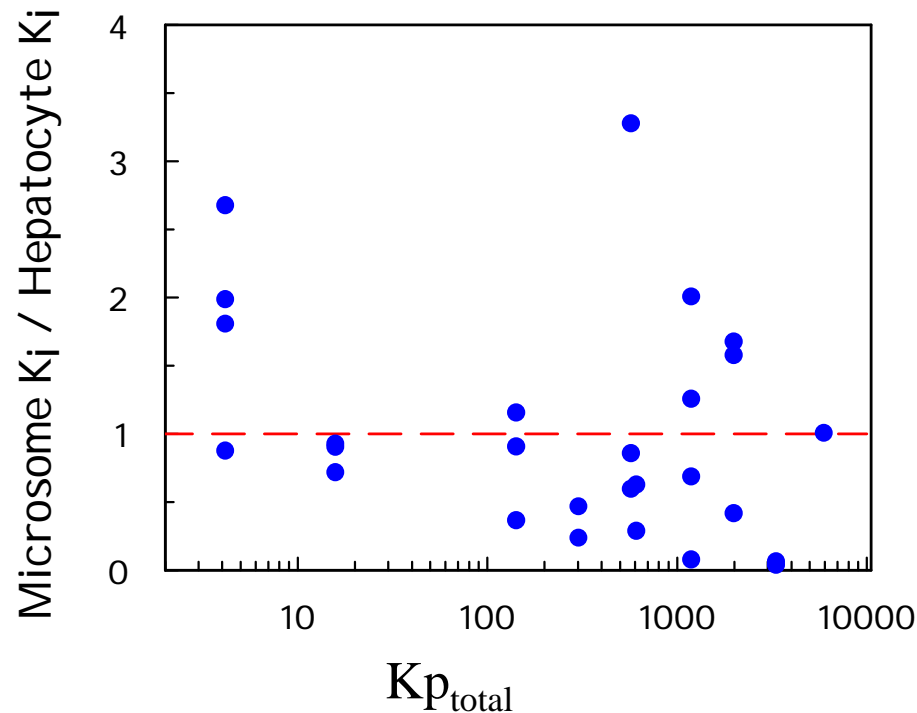
○ Miconazole      ○ Fluconazole  
○ Ketoconazole    ○ Quinine  
○ Fluoxetine       ○ Fluvoxamine  
○ Omeprazole

Inhibitor	Cell-to-Media Ratio ( $K_{p_{\text{total}}}$ )
MCZ	6000
FXT	2010
KCZ	1200
FVX	577
QUI	143
OMP	16
FCZ	4.2

- Good agreement between  $K_i$  values in both systems (both corrected for non specific binding)
- $K_{p_u}$  approximately 1

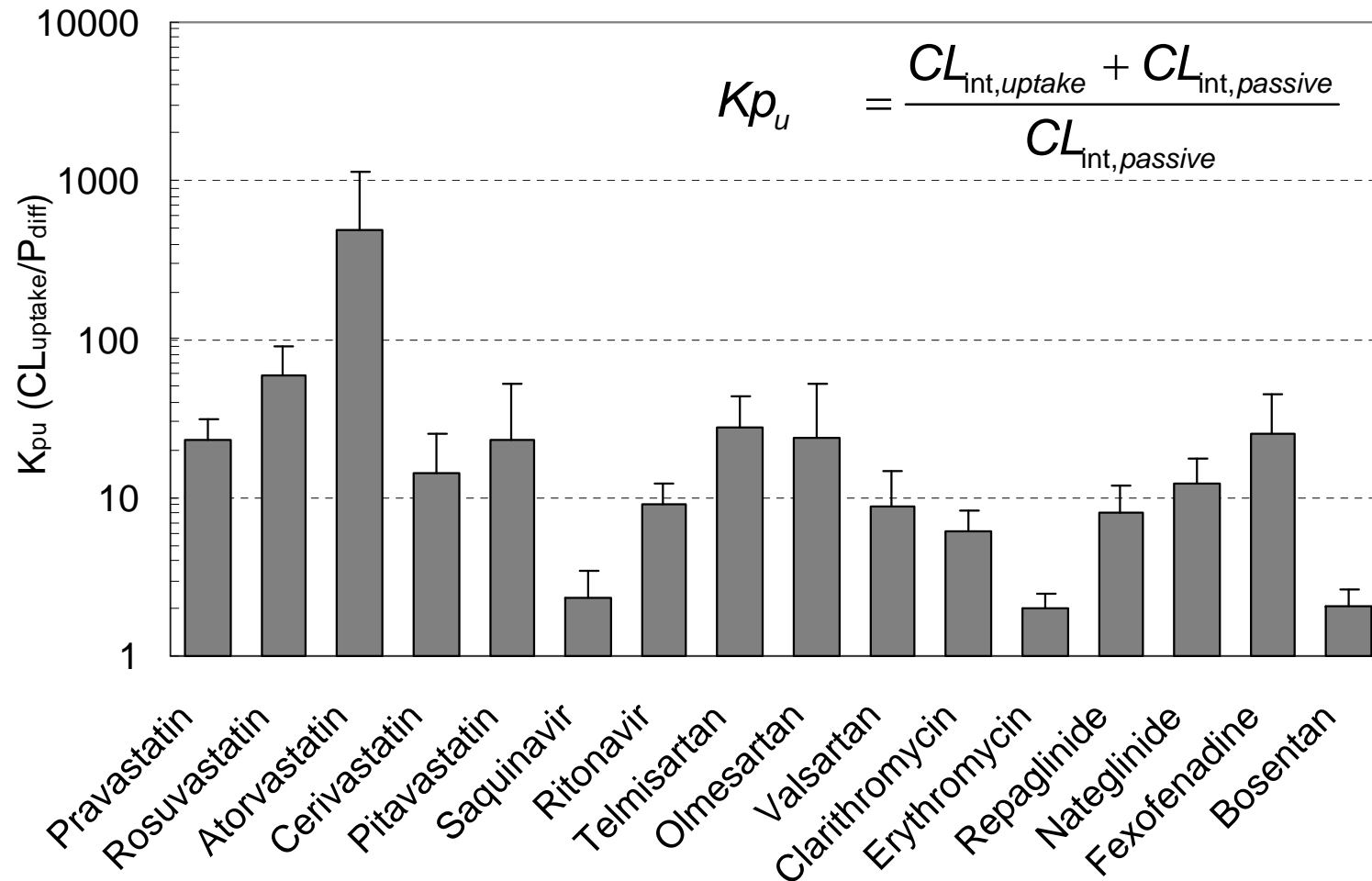
# Lack of impact of hepatic uptake:

## Microsomal & Hepatocyte $K_i$ ratio vs. $K_{p_{total}}$



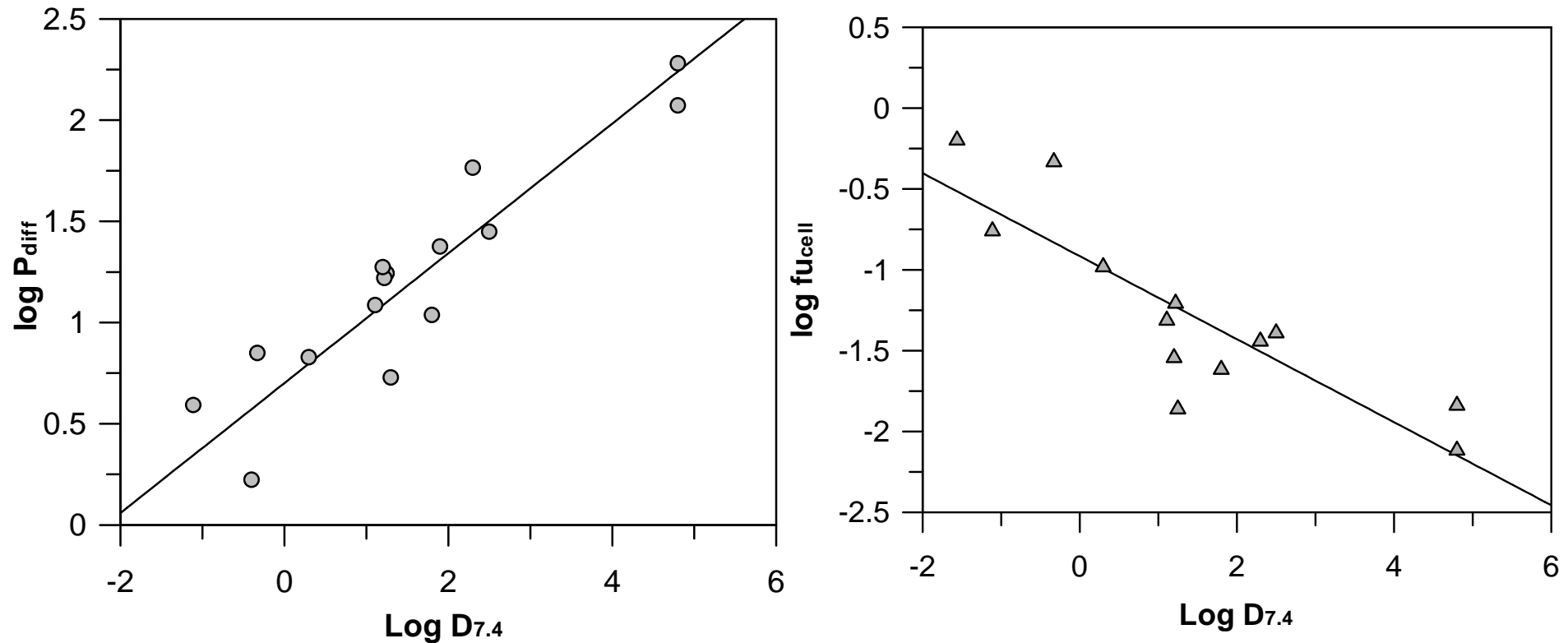
- $K_{p_{total}}$  differ over 3 orders of magnitude
- No correlation between  $K_i$  ratio and  $K_{p_{total}}$  ( $n = 27$ )

# $Kp_u \neq 1$ – importance of uptake transporters for 16 drugs in rat (*Yabe et al DMD 2011*)



- $Kp_u$  (CL<sub>uptake</sub>/P<sub>diff</sub>) 250-fold range (erythromycin and atorvastatin).

# Covariate analysis



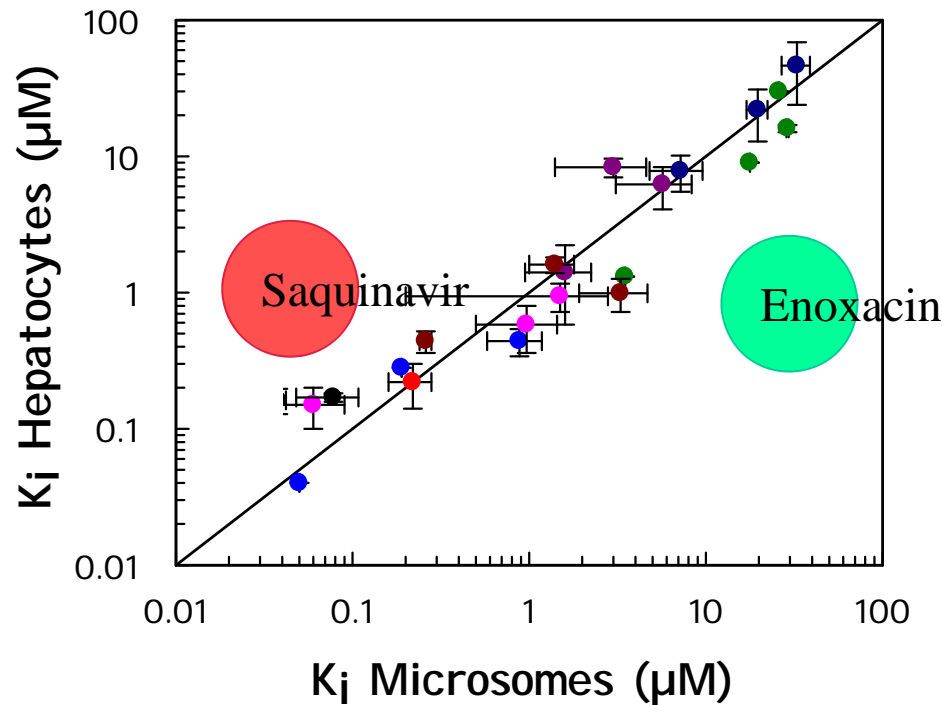
Useful for cross-species and cross-systems extrapolation

But no statistical relationship between:

$\log D$  and any active uptake parameters

# Interplay examples - $K_{pu} \neq 1$ : actively transported drugs

(n= 7 inhibitors, n=21 pathways)

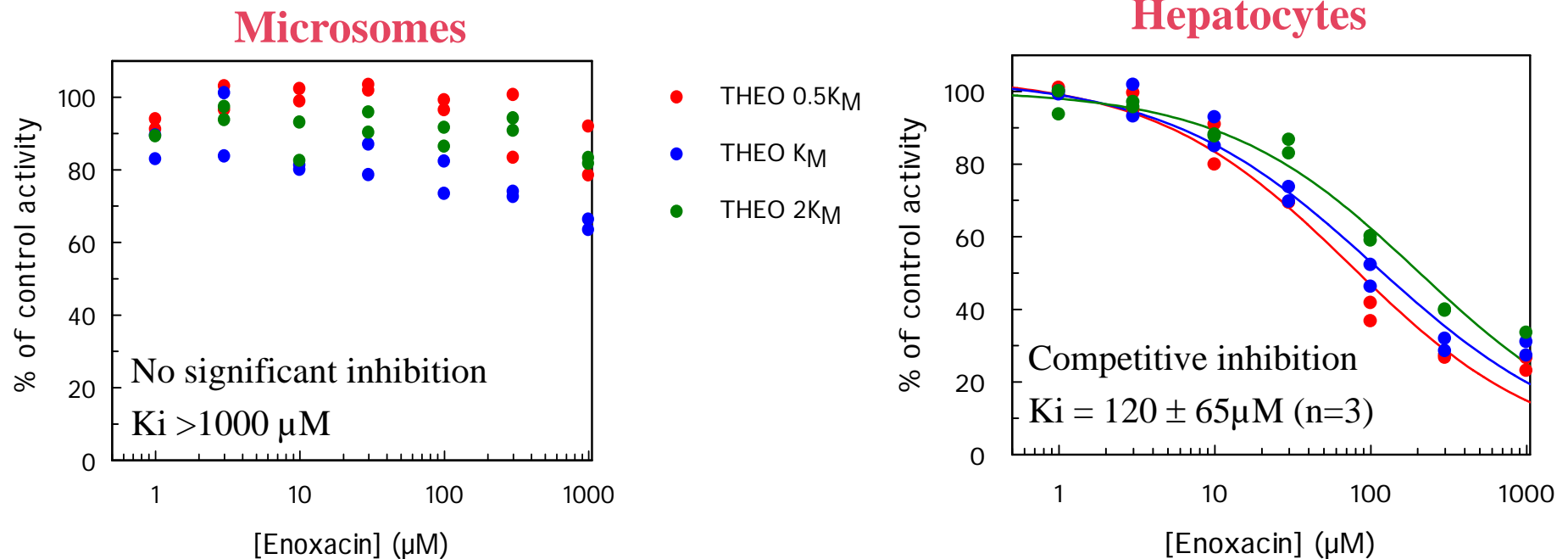


Inhibitor	Cell-to-Media Ratio (Kp)
MCZ	6000
FXT	2010
KCZ	1200
FVX	577
QUI	143
OMP	16
FCZ	4.2

- Good agreement between  $K_i$  values in both systems (except the higher affinity inhibitors)
- $K_{pu}$  approximately 1

# Example 1: Enoxacin inhibition of theophylline oxidation

Substantial DDI reported in humans and rats



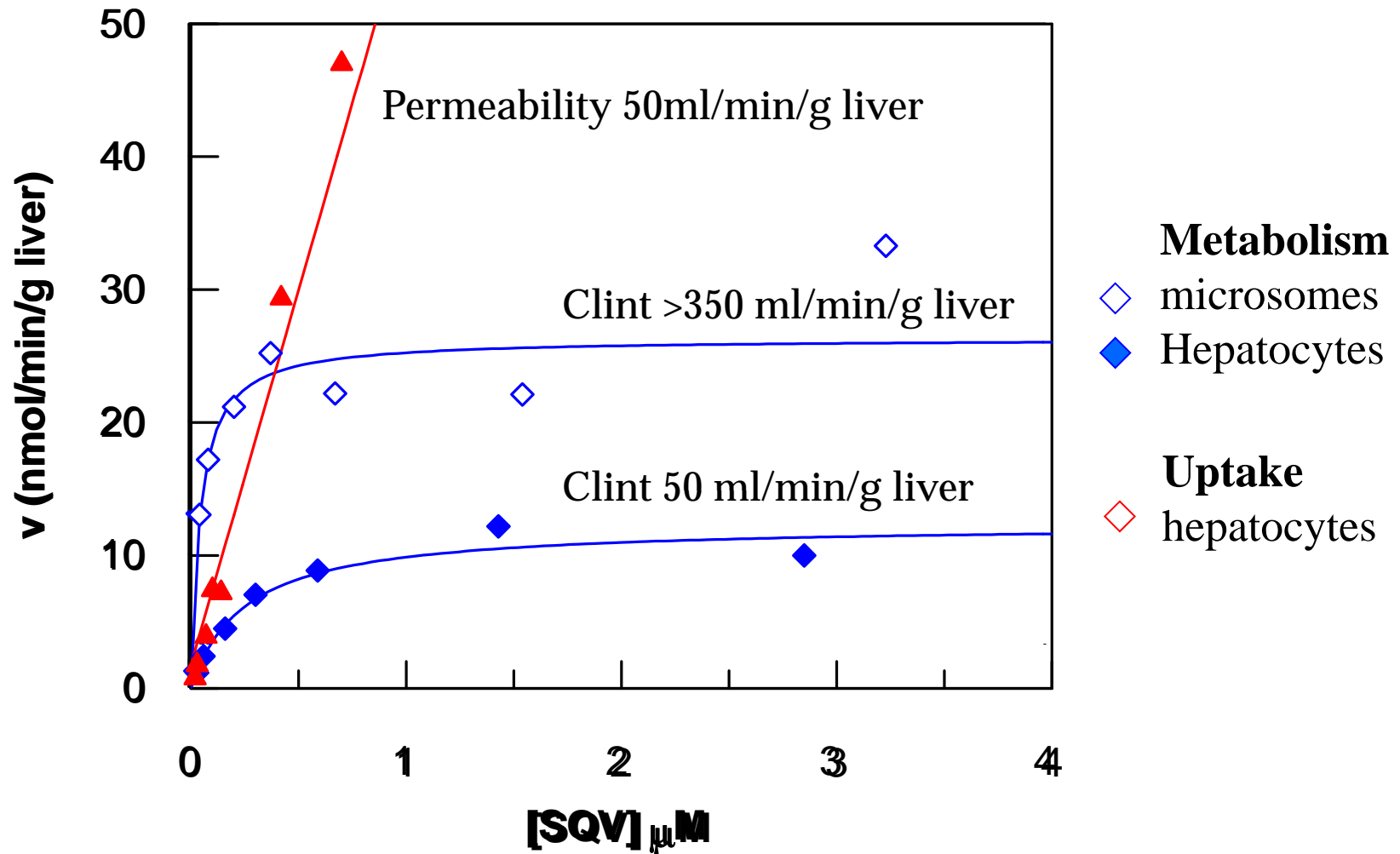
- Significantly more potent (>20) inhibition in cells vs. microsomes
- Active uptake of enoxacin
- Similar scenario observed with erythromycin

Brown et al, 2010

## Example 2: Inhibition of CYP3A by HIV protease inhibitors – nelfinavir and saquinavir

- Well documented examples of actively transported drugs with substantial DDIs
- Hepatocyte-microsomal difference in  $K_i$  to be expected
- Similar scenario to enoxacin and erythromycin?

# Saquinavir metabolism and uptake in rat



Uptake is rate limiting and defines CL



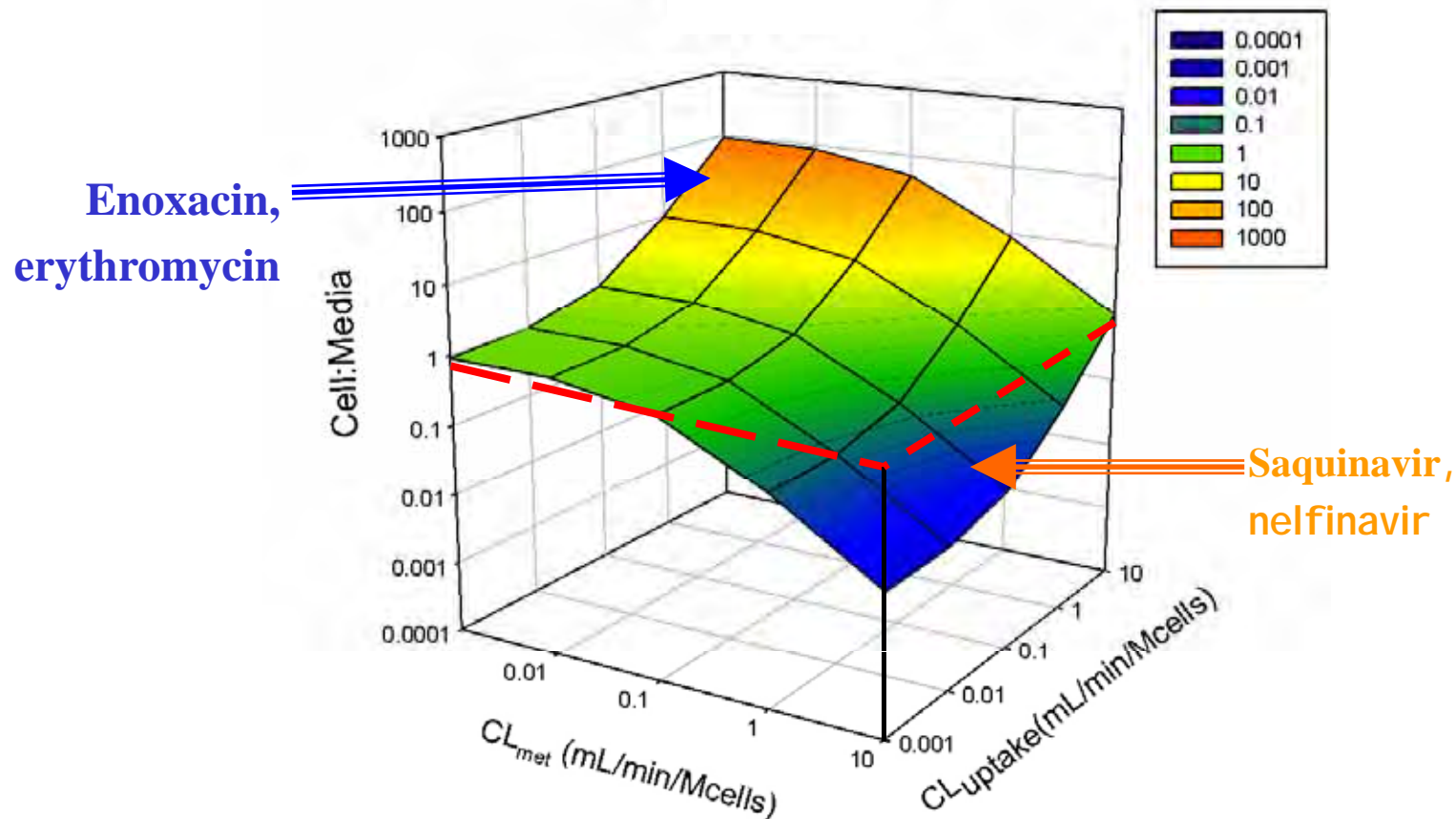
## Hepatic uptake and microsomal:hepatocyte $K_m$ & $K_i$ ratios for saquinavir and nelfinavir

	Microsomal:hepatocellular ratio		
Drug ( $K_{p_{total}}$ )	$K_m$	$K_i$	$K_{pu}$
Saquinavir (306)	0.16	0.34	6.8
Nelfinavir (3350)	0.03	0.04	5.7

Opposite effect to enoxacin & erythromycin cases

# Framework for interplay of metabolism & transporters on $Kp_u$

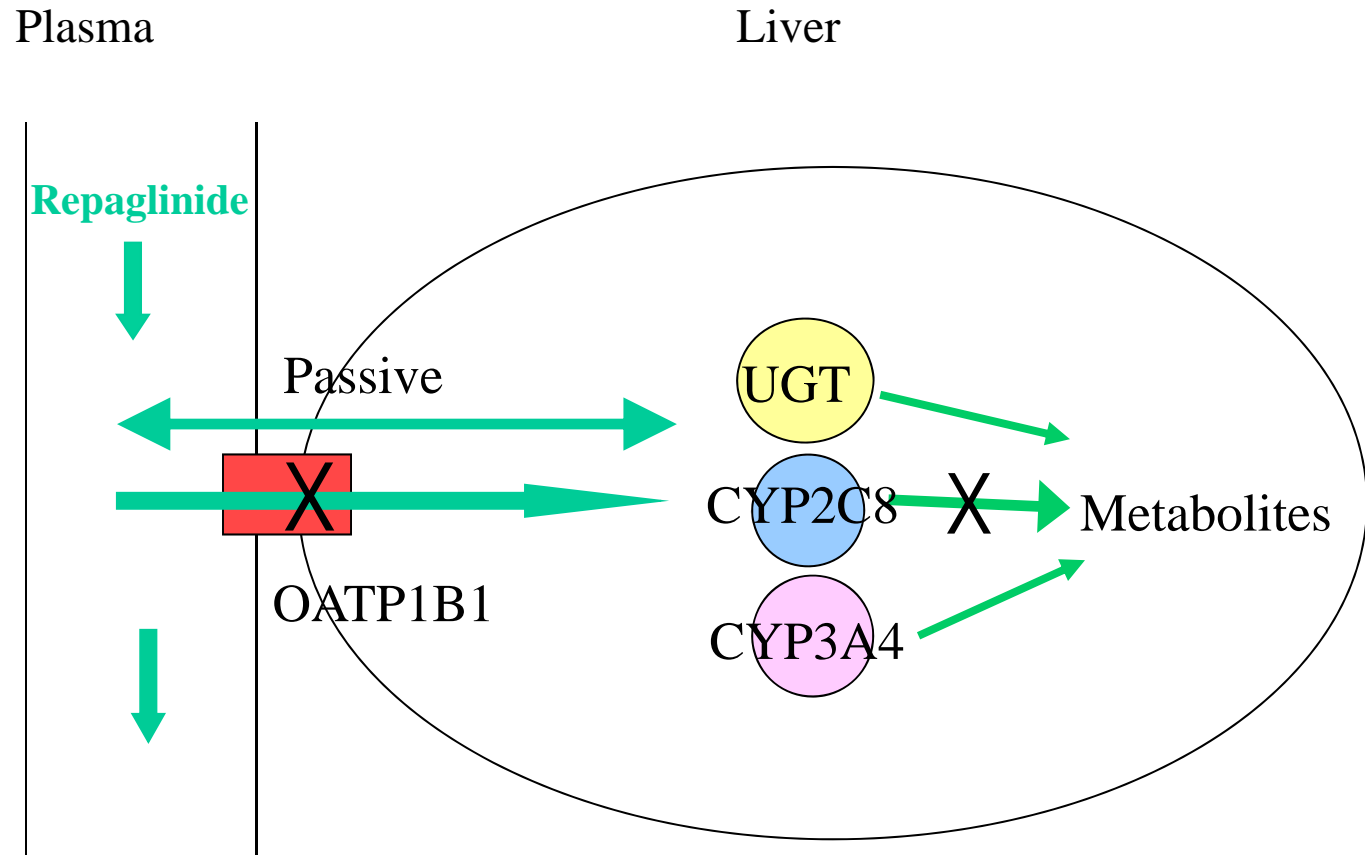
(Intermediate permeability 0.1 ml/min/M cells)



- No efflux or tissue binding

## Example 3: Repaglinide-Gemfibrozil DDI

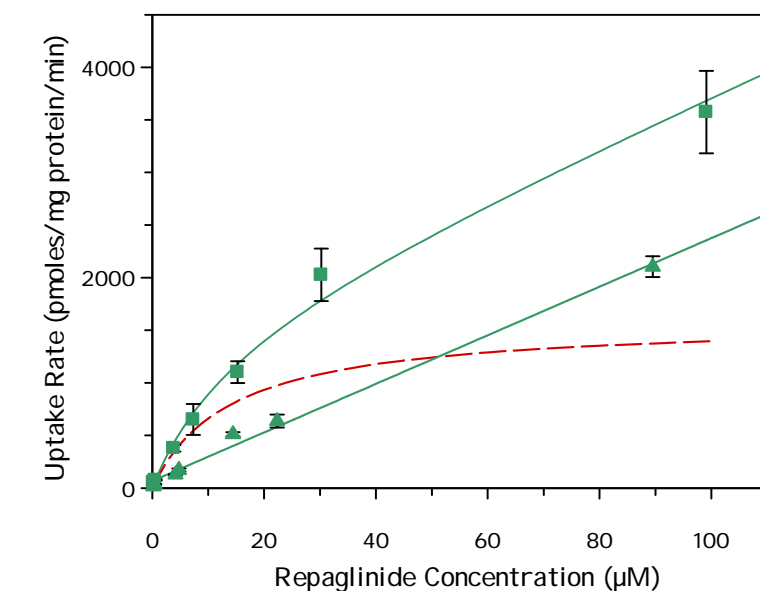
Inhibition of both hepatic uptake and metabolism



X - inhibition by GFZ and GFZ-glucuronide

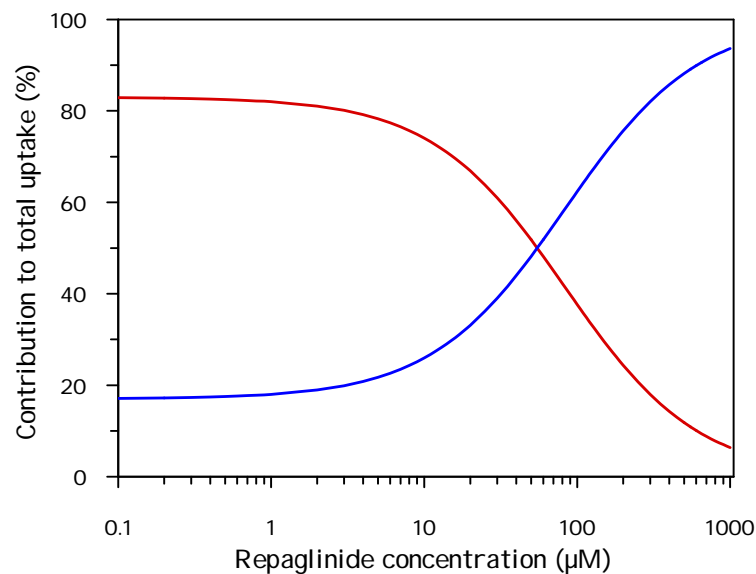
**DDI at both transporter and P450 level - sequential effect**

# Repaglinide uptake in human hepatocytes



■ Total uptake  
▲ Passive component (4°C)  
--- Active component (simulated data)

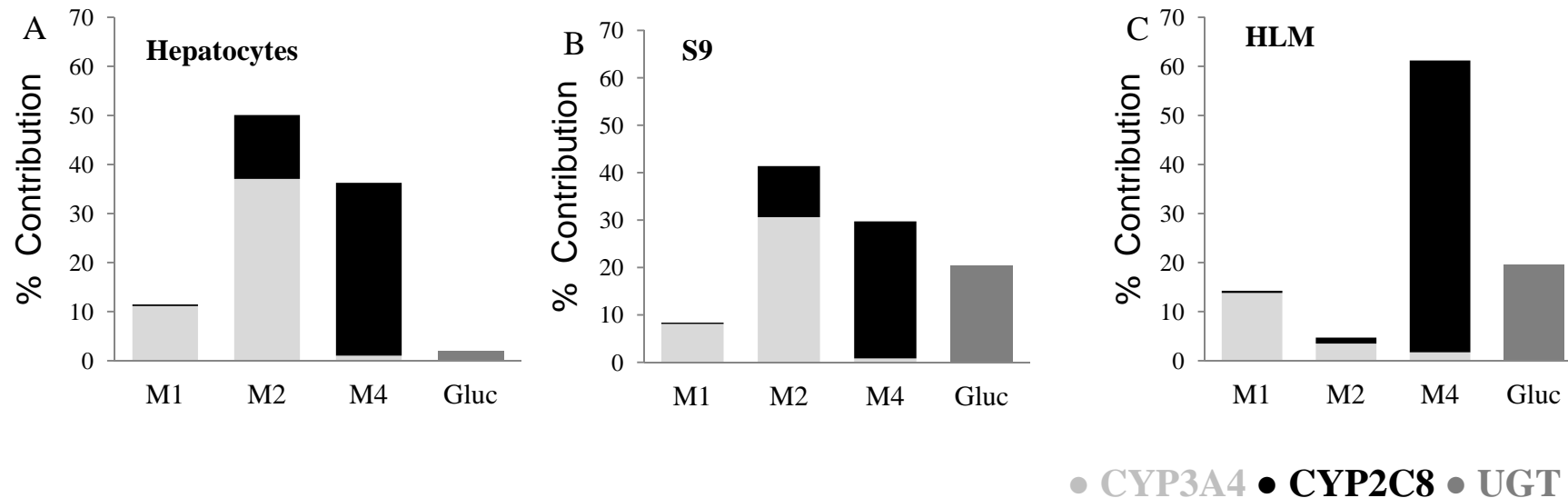
$K_m = 14.1 \mu\text{M}$



$CL_{\text{uptake}}$  5-fold greater  
than the passive component  
at therapeutic concentrations

IC<sub>50</sub> 4.3 and 7.4 μM for GFZ and GFZ-glucuronide, respectively

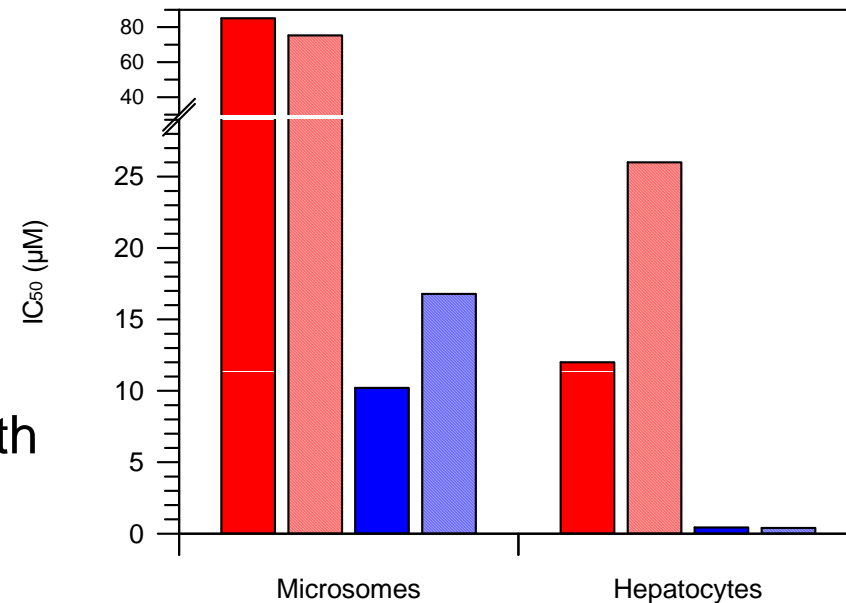
# Comparison of contribution (based on Clints) of pathways across *in vitro* systems



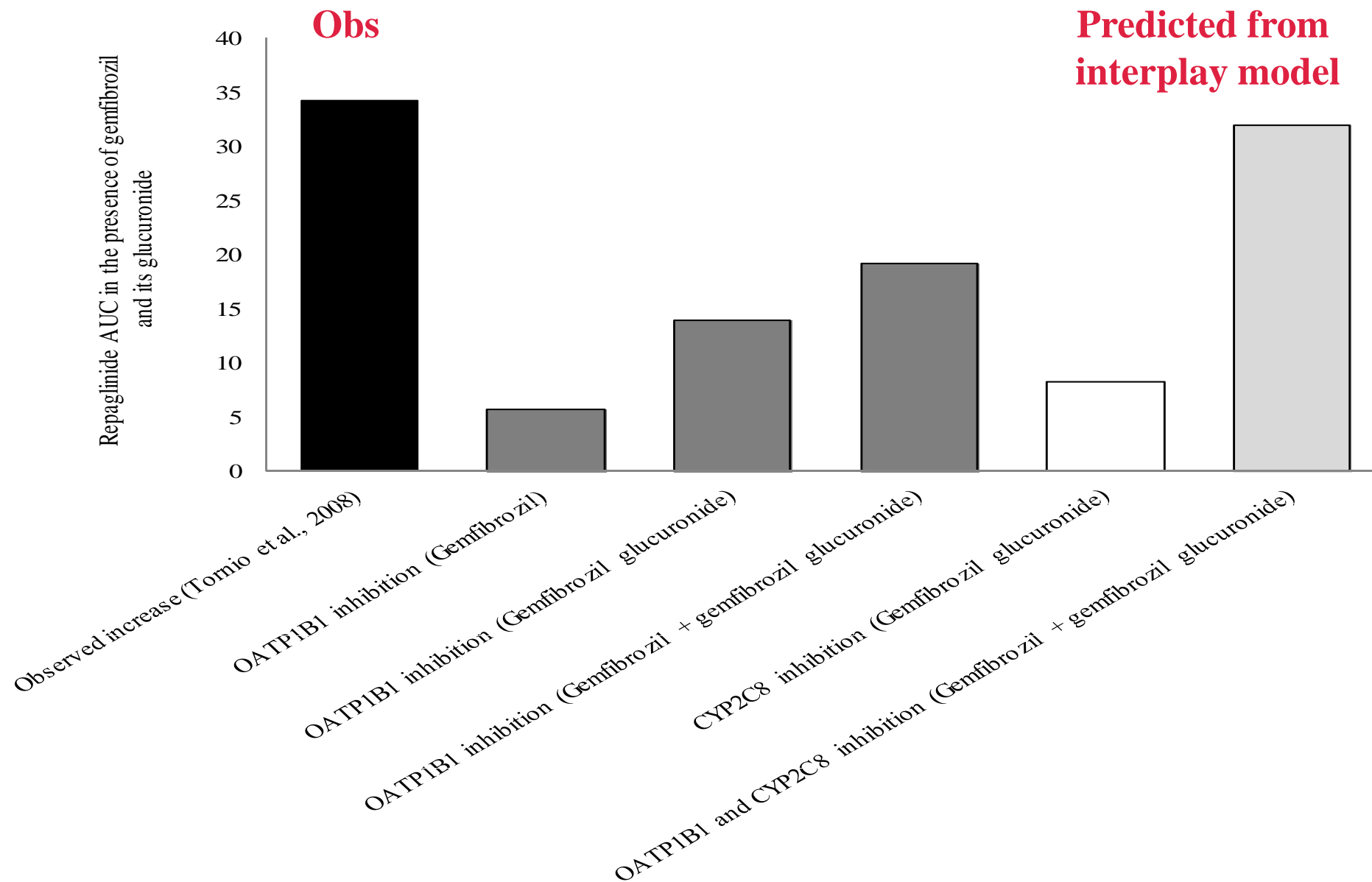
- M2 contributed similar % in S9 and hepatocytes (66% *in vivo*), needs aldehyde dehydrogenase to drive pathway.
- 5% contribution of M2 observed in HLM → increased importance of M1 and M4
- Similar contribution of CYP3A4 and CYP2C8 in S9 and hepatocytes

# Inhibition of CYP2C8 by Gemfibrozil *in vitro*

- Using repaglinide depletion and rosiglitazone para-hydroxylation
- Competitive inhibition (red bars) - Microsomal/hepatocyte ratios **7 and 3**
- Time dependant inhibition, with pre-incubation (blue bars) - Microsomal/hepatocyte ratio **24 and 44** [greater accumulation of glucuronide?]



# Prediction of Repaglinide-Gemfibrozil DDI



# Summary

- Use of rat hepatocytes provides a comprehensive package of clearance mechanisms for PBPK modelling to delineate intracellular events.
- *K<sub>p</sub>* parameters particularly useful. Allows resolution of cellular binding and active transport processes.
- Unbound intracellular drug concentration needed – consequences of transporters.
- Certain parameters are translatable to humans ( $P_{\text{diff}}$ ,  $f_{u_{\text{cell}}}$ )



# Acknowledgements

Aleksandra Galetin, David Hallifax

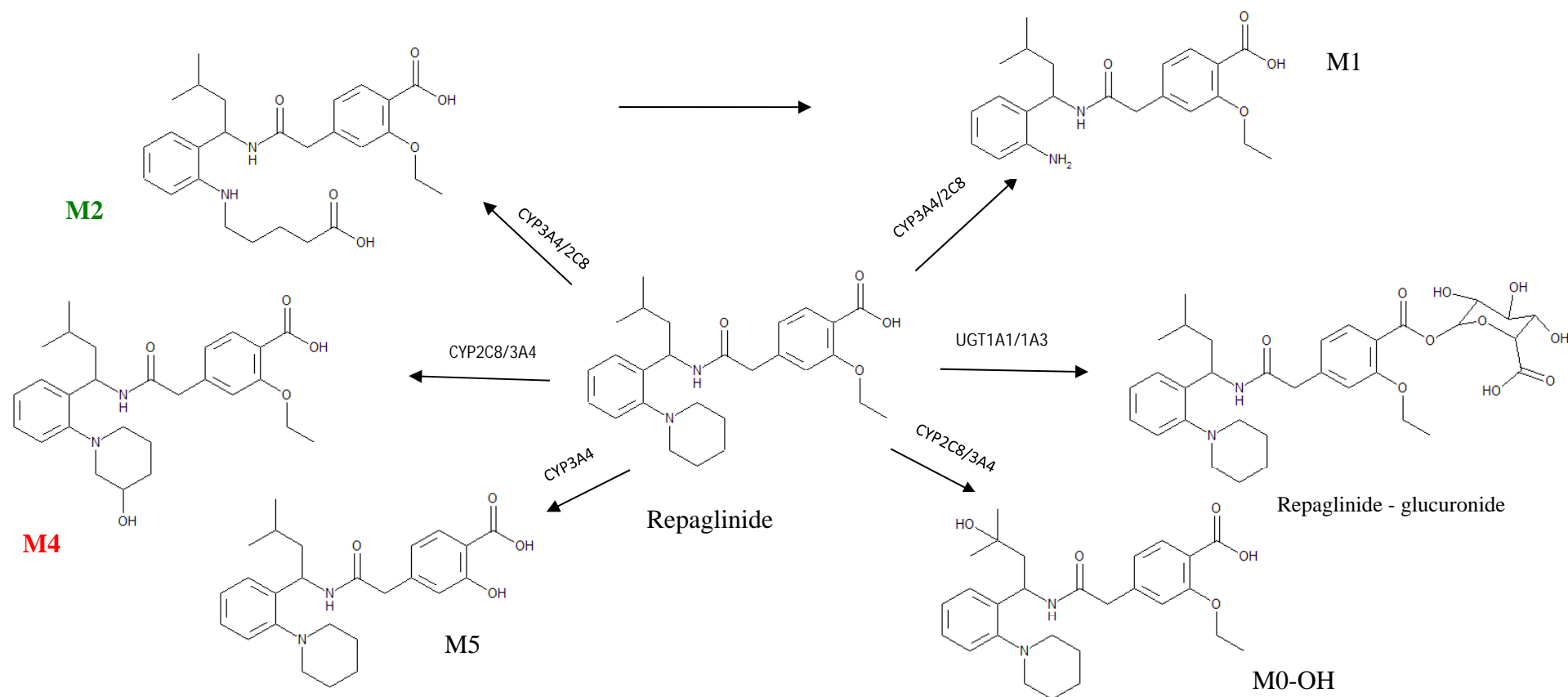
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<http://www.capkr.manchester.ac.uk>



# Repaglinide metabolism in human hepatocytes, S9 and microsomes



- Previous *in vitro* study identified **M1** and **M4** as major metabolites
- **M2** reported as major *in vivo* metabolite (66% of dose excreted in faeces and urine)
- No *in vitro* data available to confirm predominant role of CYP2C8 in repaglinide metabolism