

Table 1 Representative cytochrome P450 (CYP) basal activities in skin microsomes of various mammalian species

Activity (preferential for)	Human	Rat	Mouse	Guinea pig	Pig
AHH (CYP1 family)	0.24–1.35 ^a	1.25 ± 0.11 ^a	m ^b : 3.3–8 ^a ; f ^b : 17–21 ^a	2.51 ± 0.35 ^a	
EROD (CYP1 family)	bd–35 ^a	m: 3.6 ± 0.3; f: 1.5 ± 0.2 ^a	m: bd; f: 3–19 ^a		4.62 ± 0.54 ^b
ECOD (CYP1A, 2B)	bd–12 ^a	0.36–2.15 ^a	10.4–80 ^a	3.8 ± 2.7 ^a	(13.2 ± 2.5 ^b)
MROD (CYP1A2)	bd to +				
PROD (CYP2B)	bd to bq	m: 3.7 ± 1.3; f: 1.8 ± 0.1 ^a	m: bq; f: 0.1–1.7 ^a	bq	bd
BROD (CYP3A, 2B)		m: 4.4 ± 0.9; f: 2.1 ± 0.2 ^a			
Aminopyrine- <i>N</i> -demethylase (CYP2B, 3A)		1,000–4200 ^a	+		
Tolbutamide 4-hydroxylation (CYP2C9)	0.46 ± 0.05 ^b	0.47 ± 0.04 ^b	bd		1.66 ± 0.49 ^b
Bufuralol 1-hydroxylation (CYP2D6)	bd	1.33 ± 0.17 ^b	9.23 ± 0.67 ^b		0.26 ± 0.03 ^b
Chlorzoxazone 6-hydroxylation (CYP2E1)	2.83 ± 0.34 ^b	bd	20.8 ± 0.5 ^b		bd
Para-nitrophenol hydroxylation (CYP2E1)	bd/+	bd ^c	f: 40 ± 10 ^a		
Midazolam 1-hydroxylation (CYP3A)	2.35 ± 0.23 ^b	0.58 ± 0.09 ^b	8.70 ± 0.28 ^b		2.32 ± 0.21 ^b
Benzoquinoline <i>O</i> -dealkylation (CYP3A)	bd–76 ± 41 ^a				
Erythromycin <i>N</i> -demethylation (CYP3A)	+	bd–270 ^a	f: 540–1100 ^a		

More examples and references in the text

AHH aryl hydrocarbon hydroxylase, phenolic benzo[*a*]pyrene metabolites determined with 3-hydroxy-benzo[*a*]pyrene as standard, *bd* below detection, *BROD* 7-benzoyloxyresorufin *O*-debenzylase, *bq* below quantification, *ECOD* 7-ethoxycoumarin *O*-deethylase, *EROD* 7-ethoxyresorufin *O*-deethylase, *f* female, *m* male, *MROD* 7-methoxyresorufin *O*-demethylase, *PROD* pentoxyresorufin *O*-deethylase

^a pmol/mg protein/min

^b pmol/mg protein/h, numbers in brackets: in medium of short-term culture

^c In epidermal microsomes