Sulfotransferases (SULTs) are a family of phase II drug-metabolizing enzymes involved in detoxication of xenobiotics (e.g., acetaminophen), bioactivation of drugs like minoxidil (Falany and Kerl, 1990), and activation of certain carcinogens (Glatt et al., 1994; van De Poll et al., 1989). Additionally, SULTs metabolize endogenous compounds, such as steroid hormones and neurotransmitters. SULTs utilize the activated sulfate donor 3′-phosphoadenosine 5′-phosphosulfate to catalyze the transfer of a sulfuryl functional group from the activated sulfate donor to various substrates (Mulder and Jakoby, 1990), which leads to an enhanced solubility for these compounds to be excreted. In contrast, the addition of a sulfuryl moiety can create highly reactive, electrophilic compounds that form covalent adducts with macromolecules such as nucleic acids (Miller et al., 1994).

Historically, the SULTs were classified on the basis of substrate specificity. However, these enzymes exhibit broad and overlapping substrate specificity that precludes identifying each enzyme by the reaction substrate(s). The previous classification scheme has led to confusion owing to the lack of strict substrate specificity (Hernandez et al., 1992). Recently, there has been an effort to classify these enzymes based more precisely on their respective cDNA sequences (Weinshilboum et al., 1994; Yamazoe et al., 1994a). This nomenclature scheme should resolve some of the problems associated with identifying SULT isoforms based on the biochemistry of sulfation. Another benefit of identifying sulfotransferases at the level of cDNA is that molecular probes can now be designed that are specific for each sulfotransferase.

There are published reports describing the sex-specific distribution of particular SULT enzymes in rats. The male-predominant phenol-sulfotransferase family is designated SULT1. Of these, SULT1A1 exhibits male-predominant expression, whereas SULT1C1 is almost exclusively expressed in males (Liu and Klaassen, 1996a; Yamazoe et al., 1994b). However, low-level expression of SULT1C1 mRNA was detected in female rat liver at 45 days of age (Liu and Klaassen, 1996a). Little information is available on the SULT1B1 enzyme in terms of its sex-specific distribution, although a recent report has defined, in part, its developmental and tissue expression (Araké et al., 1997). Estrogen sulfotransferase (SULT1E2) is also classified as a phenol-type sulfotransferase exhibiting male predominance, yet this enzyme is a distinct member of this family based on its ability to sulfate estrogens (Demyan et al., 1992).

A second major family of sulfotransferase enzymes comprises the hydroxysteroid SULT (SULT2 family), which are distinct from the phenol SULTs. These enzymes are distinct not only in terms of substrate but also in that they are female predominant in rats. The...
hydroxysteroid SULTs catalyze the sulfation of compounds like dehydroepiandrosterone, epiandrosterone, and androsterone. Two very similar hydroxysteroid SULTs were cloned from rats (SULT20/21 and SULT40/41), which exhibited 94% homology at the level of nucleotide sequence (Ogura et al., 1989, 1990). Another hydroxysteroid SULT isoenzyme was later identified and designated as SULT60 (Watabe et al., 1994). Each of these hydroxysteroid SULTs (SULT20/21, SULT40/41, and SULT60) exhibits at least 80% identity in both nucleotide and amino acid sequence. The SULT20 and SULT21 cDNAs were identified as allelic variants at the nucleotide sequence level. The protein sequences are ~99% identical (Watabe et al., 1994) and cannot be distinguished by antibodies. The SULT40/41 cDNAs, like SULT20/21, are extremely similar and cannot readily be distinguished by Northern or Western blot analysis. The functional significance of such similar proteins is not yet known, although bacterially expressed SULT40 and SULT41 subunits combined as homodimers were indistinguishable from rat hydroxysteroid sulfotransferase in terms of chromatographic, electrophoretic, and functional characteristics (Watabe et al., 1994).

In the present study, we have analyzed the tissue-specific expression pattern of the three known male-dominant sulfotransferases from the SULT1 family: SULT1A1, SULT1C1, and SULT1E2. We also examined the tissue distribution of the three members of the SULT2 family, SULT20/21, SULT40/41, and SULT60, which exhibit female predominance. In addition, we have analyzed the tissue distribution of a recently reported sulfotransferase (Sakakibara et al., 1995). This novel SULT, referred to here as SULT1B1, reportedly has high activity toward numerous substrates including D- and L-dopa, 3,3′-triiodo-L-thyronine, 3,3′-5-triiodo-D-thyronine, and dopamine, as well as p-nitrophenol. This SULT is extremely similar to another SULT cDNA clone, designated SULT1B1 (Yamazoe et al., 1994a, Sakakibara et al., 1995). A recent report by Fujita et al. (1997) indicated that dopa/tyrosine SULT and SULT1B1 are identical proteins except for the substitution of Glu for Gly, respectively, at amino acid 68.

One of the major impediments in the study of the SULT enzymes arises from the previous lack of specific molecular probes to identify the SULT isoforms responsible for enzymatic activity. The fact that SULT enzymes have overlapping substrate specificity can lead to ambiguities as to which SULT is responsible for sulfating a particular substrate (e.g., SULT1C1 and SULT1B1 have activity toward thyroid hormones). Specific oligonucleotides that can distinguish between SULTs at the level of their respective mRNAs overcome these problems. Our previous work, utilizing specific oligonucleotides, has delineated hormonal responsiveness of six major SULTs in male and female rats (Liu and Klaassen, 1996a, 1996b).

The primary goal of this study was to examine the tissue distribution of seven SULT mRNAs in rats; in addition, we may identify other tissues, besides liver, that contribute quantitatively to the process of sulfation. This study utilized Northern blot analysis with oligonucleotide probes specific for each SULT mRNA. These probes allow detection of specific SULT isoforms and eliminate potential problems associated with broad substrate specificities and antibody cross-reactivity.

### Materials and Methods

**Reagents and Buffers.** All reagents were of molecular biology grade (Sigma) and were used as described previously (Liu and Klaassen, 1996a, 1996b). MOPS buffer was 0.2 M 3-[N-morpholino]propanesulfonic acid, 0.05 M sodium acetate, and 0.01 M EDTA (pH 7.2), which was diluted 10-fold with DEPC-treated dH2O prior to use. Prehybridization and hybridization solutions were obtained from Sigma. ZetaProbe GT blotting membranes were from Bio-Rad. Ultrapure agarose was purchased from Gibco-BRL (Gaithersburg, MD).

**Animals.** Male and female Sprague-Dawley rats (200–250 g; ~90 days of age; 12/group/sex) were used for this study. Rats were housed in an AAALAC-accredited facility with free access to food (Teklad 4% mouse and rat diet #7001) and tap water for at least 1 week prior to use. Rats were anesthetized with CO2, and the following tissues were isolated: brain, liver, lung, heart, intestine, kidney, adrenal gland, ovary, uterus, testes, prostate, and spleen. The tissues were flash frozen in liquid N2 and stored at −80°C until further use.

**Total and Messenger RNA Isolation.** Total RNA was isolated using RNAzol B reagent (Tel-Test Inc., Friendswood, TX) utilizing instructions provided by the manufacturer. Briefly, 0.2 g of each tissue was added to 2.0 ml of RNAzol B and placed in sterile polypropylene vials and subjected to homogenization with a Polytron (Brinkman, Westbury, NY). Chloroform (0.2 ml) was added to each homogenate, and the vials were vigorously shaken for 45 sec, followed by incubation at 4°C for 7–8 min. The vials were then subjected to centrifugation at 10,000g for 15 min. The aqueous (upper) phase was removed, and total RNA was precipitated for 30 min at −20°C in 3–4 ml of isopropanol. After precipitation, the vials were centrifuged at 12,000g for 15 min. The supernatant was removed, and each pellet was washed with 3.0 ml of 75% ethanol and centrifuged again at 7,500g for 10 min. After centrifugation, the supernatant was discarded, and the residual ethanol evaporated. Each pellet was resuspended in 0.2 ml of 0.25% SDS in 10 mM Tris (pH 7.5). RNA concentration and purity were assessed by ultraviolet absorbance at 260 nm and by A260/A280 ratio, respectively.

**Messenger RNA was isolated from total RNA by affinity purification utilizing oligo d(T)-cellulose (Pharmacia, Piscataway, NJ) in 0.5 M NaCl in 10 mM Tris (pH 7.5) for 30 min at 22°C. The RNA-oligo d(T) cellulose was transferred to 0.45-μm cellulose acetate microcentrifuge filters (Costar, Cambridge, MA) and centrifuged at 10,000g for 5 min. Non-polyadenylated RNA was removed by washing the oligo d(T) cellulose pellet twice with 0.25 ml of 0.25 M NaCl in 10 mM Tris (pH 7.5). Each wash step was followed by brief centrifugation at 10,000g. Messenger RNA was eluted from the oligo d(T) cellulose by three 0.1-ml washes with 10 mM Tris (pH 7.5). Messenger RNA was precipitated with sodium acetate and ethanol at −70°C for 3 hr, followed by centrifugation at 14,000g for 25 min. Quantification of mRNA was performed by analysis of ultraviolet absorbance at 260 nm.

**Oligonucleotide Probes.** Oligonucleotide probes were based on published sequences and synthesized by the Biotechnology Support Facility at the University of Kansas Medical Center. Each probe was assessed for uniqueness by BLAST searches of the GenBank nucleotide sequence database. Oligonucleotides were designed to be complementary to certain sequences of the respective cDNA and are within the open reading frames of each SULT. SULT1A1, SULT1C1, and SULT1E2 oligonucleotides complement nucleotides 82–101 of the cDNA sequence reported by Ozawa et al. (1993), nucleotides 1050–1069 of the cDNA sequence reported by Nagata et al. (1993), and nucleotides 364–383 of the cDNA sequence reported by Demyan et al. (1992), respectively. SULT20/21, SULT40/41, and SULT60 complement nucleotides 761–780 of the cDNA sequence reported by Ogura et al. (1989), nucleotides 547–566 of the cDNA sequence reported by Nagata et al. (1993), and nucleotides 436–455 of the cDNA sequence reported by Watabe et al. (1994), respectively. The SULT1B1-specific oligonucleotide was complementary to the SULT1B1 cDNA sequence.
nucleotides 814–834 of the cDNA sequence reported by Sakakibara et al. (1995) and complementary to nucleotides 882–903 of the sequence reported by Fujita et al. (1997). The oligonucleotide sequences and the GenBank accession numbers are provided in table 1.

Each oligonucleotide was labeled with [α-32P]dATP (6,000 Ci/mmol) (Amersham) by tailing with terminal deoxynucleotidyl transferase (Boehringer Mannheim). Oligonucleotide labeling reactions were terminated by addition of 5 μl (10% v/v) 0.5 M EDTA. Labeled oligonucleotides were chromatographically purified using G-25 (fine) Sephadex (Pharmacia) spin columns (Boehringer Mannheim).

**Northern Blot Analysis.** Messenger RNA was carefully quantitated by ultraviolet absorbance at 260 nm to ensure equivalent loading. Messenger RNA was denatured and separated on agarose-formaldehyde gels (1.2% agarose) for 5 hr at 70 volts in 1× MOPS buffer. Ethidium bromide fluorescence under ultraviolet light indicated that gel loading was equivalent for all samples (10 μg/lane, except where indicated). RNA was transferred onto nylon membranes by capillary action in 10× SSC [1× SSC = 0.15 M sodium chloride, 0.015 M sodium citrate (pH 7.0)]. Membranes were dried for 1 hr at 70°C and then cross-linked under ultraviolet light, followed by prehybridization (4 hr) and hybridization overnight (18 hr) with 32P-labeled oligonucleotide probes specific for each sulfotransferase. Hybridization was performed at 46°C in 20% formamide for each SULT except SULT1A1, which was hybridized at 52°C without formamide. The membranes were washed twice in 2× SSC in 20 min at 46°C and then washed once in 1× SSC in 2× SSC at 46°C, followed by a final wash in 1× SSC in 2× SSC at 50°C. Hybridization signals were detected and quantified following exposure to phosphor screens and analysis by phosphorautoradiography using Imagequant software (Molecular Dynamics, Sunnyvale, CA). RNA input vs. signal intensity was monitored by loading a range of concentrations of hepatic mRNA. This also allowed comparison of the hepatic expression levels with that observed in other tissues. In addition, hybridization to 28 S rRNA was utilized as a loading control for extrahepatic tissues.

Because of the small quantities of mRNA that can be obtained from small organs (e.g., adrenal gland, prostate, and ovaries), mRNA was pooled to obtain the necessary 40 μg of mRNA (i.e., 10 μg/tissue/lane × four separate gels). Data are reported as the mean ± SEM for four determinations and was calculated from the data of four separate Northern blots run in parallel with pooled rat mRNA.

**Results**

The tissue-specific expression of the mRNA for three male-pre-dominant phenol SULTs and three female-predominant hydroxysteroid SULTs was examined. We also analyzed the tissue distribution of SULT1B1, a novel SULT implicated in the sulfation of tyrosine and thyroid hormones (Sakakibara et al., 1995). Comprehensive data on the tissue distribution of each of the SULT isoforms has been lacking owing to the lack of specific molecular probes. Our approach of utilizing specific oligonucleotides has already yielded valuable information on the hormonal regulation of SULT mRNA in rats (Liu and Klaassen, 1996a, 1996b, 1996c).

Tissue-specific expression of the phenol SULT, SULT1A1, is shown in fig. 1. SULT1A1 mRNA was detected in numerous tissues by hybridization with an oligonucleotide specific for SULT1A1. The highest level of SULT1A1 expression was in liver. Additionally, SULT1A1 message was detected in brain, lung, heart, intestine, kidney, adrenal gland, testis, and spleen.

Messenger RNA for the recently cloned SULT, SULT1B1, was detected in male rats (fig. 2). As was observed for the SULT1A1 phenol SULT, SULT1B1 mRNA was detected in liver. In addition, however, both intestine and kidney contained SULT1B1 mRNA.

The tissue-specific expression of hydroxysteroidal SULT, SULT1C1, is shown in fig. 3. This particular SULT, similar to other SULT mRNAs, is primarily expressed in hepatic tissue. In contrast to SULT1A1, mRNA for SULT1C1 was not detected extensively in...
The hybridization detected from 10 heart was just detectable under the conditions of this experiment. Indeed, the hybridization signal observed in mRNA from heart was detected only in liver and heart (fig. 4). The hepatic expression of SULT1C1 mRNA.

Extrahepatic tissues; however, kidney and spleen did express SULT1C1 mRNA.

Male-predominant estrogen SULT, SULT1E2, mRNA expression was detected only in liver and heart (fig. 4). The hepatic expression of this SULT was about 3 orders of magnitude greater than that observed in heart. Indeed, the hybridization signal observed in mRNA from heart was just detectable under the conditions of this experiment.

The expression of the phenol-SULT mRNAs is summarized in table 2. The hybridization detected from 10 µg of male rat liver SULT mRNA was set at 100%. Values were derived by dividing the hybridization signal from each tissue by the hybridization signal obtained in liver. Extrahepatic expression is lower than that observed in liver without exception. Indeed, in certain cases, the tissue mRNA expression is less than 1% of that observed in liver (e.g., SULT1C1 mRNA in kidney and spleen) or is undetectable. Expression of SULT1A1 was relatively high in lung (10% of the hepatic level) and adrenal gland (5% of the hepatic level). SULT1B1 mRNA expression in intestine and kidney was 25 and 10%, respectively, of liver expression for this message.

The three female-predominant hydroxysteroid SULTs examined for messenger RNA expression in this study are depicted in figs. 5-7. The hydroxysteroid SULTs were predominantly expressed in liver, similar to the expression pattern observed in males for the phenol SULTs. In fact, adrenal gland was the only extrahepatic tissue in which the hydroxysteroid-SULT mRNAs were detected. The SULT20/21 isoform was detected in adrenal gland at ≤1% of the level observed in liver, as depicted in fig. 5. The SULT40/41 hydroxysteroid-SULT isoform was detected only in liver (fig. 6). The SULT60 isoform, like SULT20/21, was also detected in adrenal gland (fig. 7), also at less than 1% of the hepatic level, as shown in table 3. The tissue expression of a recently cloned member of the SULT family of enzymes, SULT1B1 (Fujita et al., 1997; Sakakibara et al., 1995), was examined. This SULT was detected in female rat liver (fig. 8). Additionally, mRNA for this particular SULT was present in both intestine and kidney of female rats.

Hydroxysteroid-SULT and female SULT1B1 expression is summarized in table 3. Similar to that described above for male-dominant SULTs, the hybridization observed from 10 µg of liver mRNA was set at 100% for each SULT. Values for extrahepatic expression were derived by dividing the hybridization signal of each tissue by that observed in 10 µg of liver for each SULT isoform. Adrenal expression of SULT20/21 was 0.001% of the expression observed in liver, whereas expression of SULT60 in adrenal gland was 0.2% of the hepatic level. Expression of the SULT1B1 mRNA was 15 and 5% in intestine and kidney, respectively, of the level observed in liver.

TABLE 2

Expression of phenol sulfotransferase mRNAs in male rats

<table>
<thead>
<tr>
<th>SULTa1</th>
<th>SULTB1</th>
<th>SULTC1</th>
<th>SULTE2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liverb</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Brain</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lung</td>
<td>10</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Heart</td>
<td>2.5</td>
<td>0.06</td>
<td>0.2</td>
</tr>
<tr>
<td>Intestine</td>
<td>0.4</td>
<td>25</td>
<td></td>
</tr>
<tr>
<td>Kidney</td>
<td>2.5</td>
<td>10</td>
<td>0.2</td>
</tr>
<tr>
<td>Adrenal</td>
<td>5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Prostate</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Testes</td>
<td>1.5</td>
<td>0.4</td>
<td></td>
</tr>
</tbody>
</table>

*b Liver expression was set at 100%. Extrahepatic expression is percent of hepatic expression for each sulfotransferase isoform.
The objective of the present study was to examine the tissue distribution of SULT mRNA expression in male and female rats and to compare expression levels of each SULT isoform relative to hepatic expression. This is a comprehensive study that examined all seven known major SULT isoforms in a wide variety of tissues including brain, liver, lung, heart, intestine, kidney, adrenal gland, ovary, uterus, prostate, testis, and spleen. Specific oligonucleotide probes were utilized that had been designed from published cDNA sequences, which allowed identification of each SULT without the problems inherent in enzyme assays involving overlapping substrate specificities. In addition, these probes allow detection of mRNA at low levels of expression. The specificity of the oligonucleotides has been demonstrated in our previous studies that analyzed ontogeny and hormonal regulation of SULT mRNA (Liu and Klaassen, 1996a, 1996b, 1996c). The SULT enzyme mRNAs from both male and female rats were found at the highest concentrations in liver. This hepatic expression is consistent with liver being the major site of drug-metabolizing enzymes, including both phase I monooxygenase (e.g., P450) and phase II conjugating enzyme systems (e.g., sulfation, glucuronidation, acetylation, methylation, and amino acid conjugation). The extrahaepatic expression of the female-predominant hydroxysteroid SULTs (SULT20/21, SULT40/41, and SULT60) was extremely limited. Indeed, only SULT20/21 and SULT60 were expressed at very low levels in nonhepatic tissues. There was a recent report that described the cloning and identification of a new isoform of estrogen SULT designated as r-EST6 (Falany et al., 1995). Our oligonucleotide for SULT1E2 was

---

**Fig. 5.** Northern blot analysis and quantification of female rat poly(A⁺) mRNA for SULT20/21 in hepatic and extrahepatic tissues. (Upper panel) Phosphorautoradiogram of the SULT20/21-probed blot. Lanes 1–4 are female rat liver at 10, 3, 1, and 0.3 μg of poly(A⁺) mRNA. Lanes 5–12 are 10 μg of poly(A⁺) mRNA from the tissues listed. (Lower panel) Quantification of SULT20/21 hybridization signal in liver and extrahepatic tissues. Extrahepatic hybridization signals were expressed relative to 28 S rRNA to correct for differences in loading. Each blot was quantified by PhosphorImager analysis using Imagequant software by measuring pixel density units for each hybridization signal corrected for background.

**Fig. 6.** Northern blot analysis and quantification of female rat poly(A⁺) mRNA for SULT40/41 in hepatic and extrahepatic tissues. (Upper panel) Phosphorautoradiogram of the SULT40/41-probed blot. Lanes 1–4 are female rat liver at 10, 3, 1, and 0.3 μg of poly(A⁺) mRNA. Lanes 5–12 are 10 μg of poly(A⁺) mRNA from the tissues listed. (Lower panel) Quantification of SULT40/41 hybridization signal in liver and extrahepatic tissues. Extrahepatic hybridization signals were expressed relative to 28 S rRNA to correct for differences in loading. Each blot was quantified by PhosphorImager analysis using Imagequant software by measuring pixel density units for each hybridization signal corrected for background.

**Fig. 7.** Northern blot analysis and quantification of female rat poly(A⁺) mRNA for SULT60 in hepatic and extrahepatic tissues. (Upper panel) Phosphorautoradiogram of the SULT60-probed blot. Lanes 1–4 are female rat liver at 10, 3, 1, and 0.3 μg of poly(A⁺) mRNA. Lanes 5–12 are 10 μg of poly(A⁺) mRNA from the tissues listed. (Lower panel) Quantification of SULT60 hybridization signal in liver and extrahepatic tissues. Extrahepatic hybridization signals were expressed relative to 28 S rRNA to correct for differences in loading. Each blot was quantified by PhosphorImager analysis using Imagequant software by measuring pixel density units for each hybridization signal corrected for background.
designed to detect the sequence reported by Demyan et al. (1992), which differs by one base (G vs. T) at nucleotide 271 of the r-EST-6 sequence. Thus, our SULT1E2 oligonucleotide would be expected to detect the r-EST6 isoform. Of interest, however, was the widespread sequence. Thus, our SULT1E2 oligonucleotide would be expected to vs. philes, which have the potential to alter endogenous molecules in- tion from the body. Alternatively, SULT activity in lung could result these chemicals with sulfate, which would facilitate their rapid excre- primary defense against harmful airborne chemicals by conjugation of SULT in lung is interesting, as the lung is a primary sight of uptake; adrenal gland (1992), which have the potential to alter endogenous molecules including thyroid hormones (Sakakibara et al., 1995). This study also elucidated an expression pattern of female-domi- nant hydroxysteroid SULTs. The hydroxysteroid SULTs are primarily expressed in female rat liver. The extrahepatic expression of the hydroxysteroid SULTs was limited to the adrenal gland. The adrenal expression of the hydroxysteroid-SULT mRNAs was limited to less than 1% of the expression observed in liver. The detection of HST-a (SULT-20/21) expression has been reported in extrahepatic tissues, including lung and kidney of female rats (Runge-Morris, 1994). HST-a mRNA was amplified by reverse-transcriptase polymerase chain reaction, and the resultant cDNA specific for HST-a was detected by Southern blot. The use of reverse transcriptase-poly- merase chain reaction to amplify mRNAs has resulted in detection of extremely low-level transcripts. However, the level of functional protein that results from such low-level mRNA expression, as well as the low-level expression observed in the present study, is not yet clear. Additionally, intra-tissue differences in SULT mRNA expression cannot be evaluated in whole tissue homogenates. Yet, it is clear that liver, which exhibits high-level expression of SULTs, is a major site of sulfation. Thus, the relative contribution to sulfation of the tissues with low-level SULT expression is uncertain. The significance of extrahepatic sulfation, although still largely unknown, might lie in the ability of these enzymes to modulate levels of hormones and neuro- transmitters at the autocrine or paracrine level. It has also been suggested that steroid sulfates might serve as transport forms for these hormones and are converted into the active form at the target tissue by steroid sulfatase (Hobkirk, 1985; Tseng et al., 1983). Additionally, tissue-specific localization of SULTs might be important in the sus- ceptibility of certain organs to toxic and carcinogenic effects of xenobiotics.

This study establishes a baseline of expression for extrahepatic tissue distribution of SULT mRNAs in rats. This is potentially im-
portant in regard to recent studies that have reported inducibility of SULTs in response to certain agents or treatments (Coughtrie et al., 1990; Labrie et al., 1994; Liu and Klaassen, 1996a, 1996b, 1996c; Meyers et al., 1983). Alterations in SULT levels in response to treatment paradigms are frequently studied in liver because this tissue expresses substantial enzyme message and enzyme protein. The demonstration here of significant extrahepatic expression of certain SULT isoforms, especially SULT1A1 and SULT1B1, indicates that extrahepatic modulation of SULT expression should be examined more closely.

Acknowledgment. The authors thank the Center for Environmental and Occupational Health at the University of Kansas Medical Center for the use of their instruments and equipment.

References


