Supplementary information

A database of optimized proteomic quantitative methods for 284 human drug disposition related proteins for applications in PBPK modeling

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Running title: Proteomic quantification methods for ADME proteins

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Supplementary Table 1: Optimized LC methods for peptide separation using two different UPLC columns

Supplementary Table 2: List of investigated ADME gene products, optimized surrogate peptides and LC-MRM parameters

Supplementary Table 3: Number of donors in subcellular fractions obtained from Xenotech, LLC and UW. Number in parenthesis indicates lot number.

Supplementary Fig. 1. Correlation of predicted retention time (RT) and predicted hydropathy (SSRT) in two different columns, A. ACQUITY UPLC BEH C18 Column, 1.7 µm, 3 mm X 150 mm, and B. ACQUITY UPLC® HSS T3 1.8 µm, 2.1 x 100 mm, Waters (Methods 1 and 2 in supplementary Table 1, respectively)

Supplementary Fig. 2. Differential expression of representative DMEs in microsomal vs. cytosolic fraction. Values are expressed as % of cytosolic expression level to microsome expression level (i.e., cytosol value/microsome value). The values in the y-axis are in logarithmic scale.

Supplementary Fig. 3. Relative expression of selected ADME proteins in human liver, kidney, intestine and lung, standardized to liver. The % relative values in the y-axis are in logarithmic scale. Once area ratios for each peptide were established, the relative expression level for the liver was set as "100", and the values from other tissues for the same protein were compared. If no expression was seen in a tissue, it was determined to be "0". If the liver had no expression, the kidney was considered as "100", and other tissue expression was compared to the kidney. If neither liver nor kidney had expression, then the intestinal value was set to "100".

Supplementary Figs. 4 and 5. Screenshots of Qpromics database showing live online output and excel output for a representative method search.

Supplementary Table 1S: LC methods for quantification of surrogate peptides of DMEs, transporters and receptors

	LC Method 1		
Column	UPLC column (ACQUITY UPLC BEH C18 Column, 1.7 µm, 3 mm X 150 mm, Waters)		
Guard column	Security Guard column (C18, 4 mm × 2.0 mm, Phenomenex)		
Run Time:	48 min		
Injection volumne	5 µl		
Column oven temperature	25 °C		
Autosampler temperature	6 °C		
Gradient Table:			
Time	Flow Rate (ml/min)	%A	%B
0.0	0.3	97	3
3.0	0.3	97	3

10.0	0.3	90	10
40.0	0.3	10	90
40.9	0.3	10	90
41.0	0.3	97	3
48.0	0.3	97	3

LC Method 2

Column	UPLC column (ACQUITY UPLC HSS T3 1.8 µm, 2.1 x 100 mm, Waters)		
Guard column	Security Guard column (C18, 4 mm × 2.0 mm, Phenomenex)		
Run Time:	27 min		
Injection volumne	5 µl		
Column oven temperature	25 °C		
Autosampler temperature	6 °C		
Gradient Table:			
Time	Flow Rate (ml/min)	%A	%B
0.0	0.3	97	3
4.0	0.3	97	3
8.0	0.3	87	13
18.0	0.3	70	30
22.9	0.3	60	40
23.0	0.3	40	60
23.1	0.3	97	3
27.0	0.3	97	3

A = 0.1% formic acid water; B = 0.1% formic acid acetonitrile

Supplementary Table 2Sa: Unique surrogate peptides identified for ADME proteins

Uniprot ID and protein name	Peptide
P00352, ALDH1A1	ANNTFYGLSAGVFTK
P00352, ALDH1A1	IFVEESIYDEFVR
P00352, ALDH1A1	IFINNEWHDSVSGK
O94788, ALDH1A2	IFINNEWQNSESGR
O94788, ALDH1A2	ILELIQSGVAEGAK
O94788, ALDH1A2	ANNSDFGLVAAVFTNDINK
P04798, CYP1A1	IQEELDTVIGR
P04798, CYP1A1	YLPNPSLNAFK
P04798, CYP1A1	HSSFVPFTIPHSTTR
P05177, CYP1A2	FLTADGTAINKPLSEK
P05177, CYP1A2	IGSTPVLVLSR
P05177, CYP1A2	NTHEFVETASSGNPLDFFPILR
P11509, CYP2A6	GTGGANIDPTFFLSR
P11509, CYP2A6	DPSFFSNPQDFNPQHFLNEK

P20813, CYP2B6	TEAFIPFSLGK
P20813, CYP2B6	GYGVIFANGNR
P20813, CYP2B6	IQEEAQCLIEELR
P33260, CYP2C18	DIDITPIANAFGR
P33260, CYP2C18	GTTIITSLTSVLHNDK
P33260, CYP2C18	EALIDHGEEFSGR
P10632, CYP2C8	YSDLVPTGVPHAVTTDTK
P10632, CYP2C8	VQEEIDHVIGR
P11712, CYP2C9	YIDLLPTSLPHAVTCDIK
P11712, CYP2C9	GIFPLAER
P11712, CYP2C9	LPPGPTPLPVIGNILQIGIK
P10635, CYP2D6	GTTLITNLSSVLK
P10635, CYP2D6	VQQEIDDVIGQVR
P10635, CYP2D6	AVSNVIASLTCGR
P05181, CYP2E1	FITLVPSNLPHEATR
P05181, CYP2E1	FGPVFTLYVGSQR
P05181, CYP2E1	GTVVVPTLDSVLYDNQEFPDPEK
P51589, CYP2J2	VIGQGQQPSTAAR
P51589, CYP2J2	EVTVDTTLAGYHLPK
P51589, CYP2J2	LLDEVTYLEASK
P08684, CYP3A4	LSLGGLLQPEKPVVLK
P08684, CYP3A4	LGIPGPTPLPFLGNILSYHK
P08684, CYP3A4	EVTNFLR
Q9HB55, CYP3A43	LDNLPILQPEKPIVLK
Q9HB55, CYP3A43	TLLSPAFTSVK
Q9HB55, CYP3A43	DIEINGVFIPK
P20815, CYP3A5	LDTQGLLQPEKPIVLK
P20815, CYP3A5	DVEINGVFIPK
P20815, CYP3A5	DSIDPYIYTPFGTGPR
P24462, CYP3A7	FGGLLLTEKPIVLK
P24462, CYP3A7	FNPLDPFVLSIK
P24462, CYP3A7	LGIPGPTPLPFLGNALSFR
P30711, GSTT1	GQHLSDAFAQVNPLK
P30711, GSTT1	VDEYLAWQHTTLR
P30711, GSTT1	VEAAVGEDLFQEAHEVILK
P18440, NAT1	EQYIPNEEFLHSDLLEDSK
P18440, NAT1	NIFNISLQR
P18440, NAT1	TLSEEEIEK
P11245, NAT2	LDLETLTDILEHQIR
P11245, NAT2	TLTEEEVEEVLK
P50225, SULT1A1	VHPEPGTWDSFLEK
P50225, SULT1A1	SLPEETVDFVVQHTSFK
P22309, UGT1A1	GHEIVVLAPDASLYIR
P22309, UGT1A1	ESFVSLGHNVFENDSFLQR
Q9HAW8, UGT1A10	TYSTSYTLEDQNR
Q9HAW8, UGT1A10	YFSLPSVVFTR
P35503, UGT1A3	HLNATSFDVVLTDPVNLCAAVLAK
P22310, UGT1A4	FFTLTAYAVPWTQK
P22310, UGT1A4	GTQCPNPSSYIPK
P22310, UGT1A4	YLSIPAVFFWR

P35504, UGT1A5	YLSIPAVFFLR
P35504, UGT1A5	EVSVVDLVSHASVWLFR
P19224, UGT1A6	DVDIITLYQK
P19224, UGT1A6	SFLTAPQTEYR
P19224, UGT1A6	DIVEVLSDR
Q9HAW7, UGT1A7	TYSTSYTLEDQDR
Q9HAW7, UGT1A7	GIFCHYLEEGAQCPAPLSYVPR
Q9HAW9, UGT1A8	ESSFDAVFLDPFDACGLIVAK
Q9HAW9, UGT1A8	GIACHYLEEGAQCPAPLSYVPR
O60656, UGT1A9	ESSFDAVFLDPFDNCGLIVAK
O60656, UGT1A9	AFAHAQWK
P54855, UGT2B15	SVINDPVYK
P54855, UGT2B15	GHEVTVLTSSASTLVNASK
P54855, UGT2B15	NYLEDSLLK
O75795, UGT2B17	FSVGYTVEK
O75795, UGT2B17	SVINDPIYK
O75795, UGT2B17	LCEDAVLNK
P16662, UGT2B7	ANVIASALAQIPQK
P16662, UGT2B7	IEIYPTSLTK
P16662, UGT2B7	TILDELIQR
P09488, GSTM1	RPWFAGNK
P09488, GSTM1	FLPRPVFSK
P09211, GSTP1	FQDGDLTLYQSNTILR
P09211, GSTP1	ALPGQLKPFETLLSQNQGGK
P09211, GSTP1	EEVVTVETWQEGSLK
P33261, CYP2C19	GTTILTSLTSVLHDNK
P33261, CYP2C19	HFLDEGGNFK
P51580, TPMT	TAFHQEQGHQLLK
P51580, TPMT	NQVLTLEEWQDK
P51580, TPMT	SWGIDCLFEK
P08183, ABCB1	AGAVAEEVLAAIR
P08183, ABCB1	IATEAIENFR
Q92887, ABCC2	YLGGDDLDTSAIR
Q92887, ABCC2	NQSQSQDALVLEDVEK
Q92887, ABCC2	LTIIPQDPILFSGSLR
O15438, ABCC3	IDGLNVADIGLHDLR
O15438, ABCC3	GVVAEFDSPANLIAAR
O15438, ABCC3	NVDPNPYPETSAGFLSR
O15439, ABCC4	IQTFLLLDEISQR
O15439, ABCC4	AEAAALTETAK.heavy
O15439, ABCC4	DGALESQDTENVPVTLSEENR
Q9UNQ0, ABCG2	LFDSLTLLASGR
Q9UNQ0, ABCG2	SSLLDVLAAR
Q9UNQ0, ABCG2	TIIFSIHQPR
Q14973, SLC10A1	GIYDGDLK
Q16348, SLC15A2	YHNLSLYTEHSVQEK
Q16348, SLC15A2	IYNKPPPEGNIVAQVFK
O15245, SLC22A1	YEVDWNQSALSCVDPLASLATNR
O15245, SLC22A1	LSPSFADLFR
O15245, SLC22A1	ENTIYLK

O15244, SLC22A2	SPGVAELSLR
O15244, SLC22A2	CGWSPAEELNYTVPGPGPAGEASPR
O15244, SLC22A2	LNPSFLDLVR
O75751, SLC22A3	GIALPETVDDVEK
O75751, SLC22A3	FLQGVFGK
O75751, SLC22A3	GPSAAALAER
Q4U2R8, SLC22A6	NGGLEVWLPR
Q4U2R8, SLC22A6	EAGIYPR
O00337, SLC28A1	AGSSFVFGEALVK
O00337, SLC28A1	LAGAEEWVGDR
O00337, SLC28A1	LTYGDAQNLIEAASTGAAISVK
O43868, SLC28A2	TDAQGHSLGDGLGPSTYQR
O43868, SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK
O43868, SLC28A2	GAEADCVSFPNTSFTNR
Q9HAS3, SLC28A3	GPGEVIPGGNHSLYSLK
Q9HAS3, SLC28A3	FVNGVQQYISIR
Q9HAS3, SLC28A3	TFFNEFVAYEHLSK
P46721, SLCO1A2	EGLETNADIIK
P46721, SLCO1A2	CHLPGENASSGTELIETK
P46721, SLCO1A2	IYDSTTFR
Q9Y6L6, SLCO1B1	NVTGFFQSFK
Q9NPD5, SLCO1B3	IYNSVFFGR
Q9NPD5, SLCO1B3	NQTANLTNQGK
Q9NPD5, SLCO1B3	WSTNSCGAQGACR
O94956, SLCO2B1	SSPAVEQQLLVSGPGK
O94956, SLCO2B1	ASPDPQDVRPSVFHNIK
O94956, SLCO2B1	VLAVTDSPAR
Q6ZQN7, SLCO4C1	GIENLAFVPSSPDILR
Q6ZQN7, SLCO4C1	ENAVVTNVLAEQDLNK
Q6ZQN7, SLCO4C1	HLPGTAEIQAGK
P07327, ADH1A	NDVSNPQGTLQDGTSR
P07327, ADH1A	KPIHHFLGISTFSQYTVVDENAVAK
P07327, ADH1A	GAILGGFK
P00325, ADH1B	KPFSIEDVEVAPPK
P00325, ADH1B	AAVLWEVK
P00326, ADH1C	VCLIGCGFSTGYGSAVK
P00326, ADH1C	INEGFDLLR
P00326, ADH1C	GAIFGGFK
P47895, ALDH1A3	LLHQLADLVER
P47895, ALDH1A3	AVEAAQVAFQR
P47895, ALDH1A3	EQICEVEEGDKPDVDK
Q06278, AOX1	LILNEVSLLGSAPGGK
Q06278, AOX1	NHPEPTLDQLTDALGGNLCR
Q06278, AOX1	GLHGPLTLNSPLTPEK
P23141, CES1	AISESGVALTSVLVK
P23141, CES1	EGYLQIGANTQAAQK
P23141, CES1	AGQLLSELFTNR
O00748, CES2	FTEEEEQLSR
O00748, CES2	TTHTGQVLGSLVHVK
O00748, CES2	ADHGDELPFVFR

Q12882, DPYD	ADVVISAFGSVLSDPK
Q12882, DPYD	LTPNVTDIVSIAR
Q12882, DPYD	DSADIESILALNPR
P07099, EPHX1	GGHFAAFEEPELLAQDIR
P07099, EPHX1	VETSDEEIHDLHQR
P07099, EPHX1	YLEDGGLER
P34913, EPHX2	VCEAGGLFVNSPEEPSLSR
P34913, EPHX2	GLLNDAFQK
P34913, EPHX2	ASPSEVVFLDDIGANLKPAR
Q01740, FMO1	SDDLGGLWR
Q01740, FMO1	VEDGQASLYK
Q99518, FMO2	ASIYQSVVTNTSK
Q99518, FMO2	WFNHENYGLEPQNK
Q99518, FMO2	YIFPAHLDK
P31513, FMO3	NNLPTAISDWLYVK
P31513, FMO3	LVGPGQWPGAR
P31513, FMO3	VAIIGAGVSGLASIR
P08263, GSTA1	LHYFNAR
P09210, GSTA2	LHYSNIR
P09210, GSTA2	LALIQEK
Q16772, GSTA3	VLQSHGQDYLVGNK
Q16772, GSTA3	FIGSAEDLGK
Q16772, GSTA3	LHYFNGR
O15217, GSTA4	SILHYIADK
O15217, GSTA4	YFPVFEK
Q7RTV2, GSTA5	WLLAAAGVELEEK
Q7RTV2, GSTA5	FLESAEDLDK
Q7RTV2, GSTA5	FLQPGSQR
P28161, GSTM2	LGLDFPNLPYLIDGTHK
P28161, GSTM2	NQVFEPSCLDAFPNLK
P28161, GSTM2	ITFVDFIAYDVLER
P21266, GSTM3	IAAYLQSDQFCK
P21266, GSTM3	LKPQYLEELPGQLK
P21266, GSTM3	FSWFAGEK
Q03013, GSTM4	IFEPNCLDAFPNLK
Q03013, GSTM4	ITFVDFLAYDVLDLHR
Q03013, GSTM4	RPWFVGDK
P50226, SULT1A2	VYPHPGTWESFLEK
P50226, SULT1A2	FDADYAK
P50224, SULT1A3*	AHPEPGTWDSFLEK
P50224, SULT1A3*	DVAVSYYHFHR
O43704, SULT1B1	NYFTVAQNEK
O43704, SULT1B1	IEQFHSRPDDIVIATYPK
O43704, SULT1B1	THLPTDLLPK
O00338, SULT1C1/C2	IVQETSFEK
O00338, SULT1C1/C2	NHFTVAQNER
O00338, SULT1C1/C2	VVWGSWFDHVK
P49888, SULT1E1	NHFTVALNEK
P49888, SULT1E1	LIHFLER
Q06520, SULT2A1	NHFTVAQAEDFDK

Q06520, SULT2A1	TLEPEELNLILK
Q06520, SULT2A1	LFSSHLPIQLFPK
O00204, SULT2B1	GEVQFGSWFDHIK
O00204, SULT2B1	APWCETIVGAFSLPDQYSPR
O00204, SULT2B1	NHFTVAQSEAFDR
Q9BR01, SULT4A1	DLVVSYYQFHR
Q9BR01, SULT4A1	FLPSDLHNGDSK
Q9BR01, SULT4A1	YFEFHGVR
Q9Y4X1, UGT2A1	ANLIASALAQIPQK
Q9Y4X1, UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK
P36537, UGT2B10	GHEVTVLASSASILFDPNDSSTLK
O75310, UGT2B11	GHEVTVLASSASILFDPNDASTLK
O75310, UGT2B11	FTPGYTIER
Q9BY64, UGT2B28	WIPQNDLLGLPK
Q9BY64, UGT2B28	GHEVTVLASSASILFDPNDAFTLK
P06133, UGT2B4	ANVIASALAK
P06133, UGT2B4	FEVYPVSLTK
P06133, UGT2B4	TILDELVQR
O95342, ABCB11	AAATSIFETIDR
O95342, ABCB11	VGFFQLFR
O95342, ABCB11	AADTIIGFEHGTAVER
Q9NSA0, SLC22A11	GKPDQALQELR
Q9NSA0, SLC22A11	SVLDLFCVPVLR
Q9NSA0, SLC22A11	SVFTSTIVAK
Q96S37, SLC22A12	ATHGTLGNSVLK
Q96S37, SLC22A12	SIFTSTIVAK
Q96S37, SLC22A12	LDWGLQELWR
Q86VW1, SLC22A16	ENTSSLGYEYTGSK
Q86VW1, SLC22A16	LLLTTNNSGLEK
Q86VW1, SLC22A16	LSELLSLDLQGPVSNSPTEVQK
Q9H015, SLC22A4	WLISQR
Q9H015, SLC22A4	DYDEVIAFLGEWGPFQR
Q9H015, SLC22A4	AFILDLFR
O76082, SLC22A5	FEEAEVIIR
O76082, SLC22A5	QQSHNILDLLR
O76082, SLC22A5	ANGIVVPSTIFDPSELQDLSSK
Q9Y694, SLC22A7	FAYPQALPNTTLGEER
Q9Y694, SLC22A7	QAQLPETIQDVER
Q9Y694, SLC22A7	CALPGAPANFSHQDVWLEAHLPR
Q8TCC7, SLC22A8	FVHPPNASLPNDTQR
Q8TCC7, SLC22A8	YTASDLFR
Q8IVM8, SLC22A9	NKPLFDTIQDEK
Q8IVM8, SLC22A9	DTLTLEILK
Q6PCB7, SLC27A1	LLGQTDVAVYGVAVPGVEGK
Q6PCB7, SLC27A1	FCSGDLGPEGILPDTHLLDPLLK
Q6PCB7, SLC27A1	QGHYLPLNEAVYTR
Q99808, SLC29A1	EESGVSVSNSQPTNESHSIK
Q99808, SLC29A1	DAQASAAPAAPLPER
Q99808, SLC29A1	LEGPGEQETK
Q14542, SLC29A2	AELLQSDENGIPSSPQK

Q14542, SLC29A2	SLTSYFLWPDEDSR
Q14542, SLC29A2	SSQAQAQELETK
Q96FL8, SLC47A1	QEEPLPEHPQDGAK
Q96FL8, SLC47A1	ACQQAQVHANLK
Q96FL8, SLC47A1	GGPEATLEVR
Q86VL8, SLC47A2	TPEEAHALSAPTSR
Q86VL8, SLC47A2	AVLSSVATGSSPGITLTTYSR
Q86VL8, SLC47A2	SECHVDFFR

Supplementary Table 2Sb: List of ADME gene products, surrogate peptides and LC-MRM parameters for Xevo TQS triple quadrupole instrument

Protein	Peptide	RT	Parent	Product	CV	CE
ABCB1	AGAVAEEVLAAIR	35.1	635.4	971.6	35	21
ABCB1	AGAVAEEVLAAIR	35.1	635.4	900.5	35	21
ABCB1	AGAVAEEVLAAIR	35.1	635.4	430.3	35	21
ABCB1	AGAVAEEVLAAI**R**	35.1	640.4	981.6	35	21
ABCB1	AGAVAEEVLAAI**R**	35.1	640.4	440.3	35	21
ABCB1	IATEAIENFR	24.5	582.3	486.3	35	15
ABCB1	IATEAIENFR	24.5	582.3	979.5	35	15
ABCB1	IATEAIENFR	24.5	582.3	749.4	35	15
ABCB1	IATEAIENFR	24.5	582.3	678.4	35	15
ABCB1	IATEAIENFR	24.5	582.3	490.2	35	15
ABCB1	IATEAIENF**R**	24.5	587.3	688.4	35	15
ABCB1	IATEAIENF**R**	24.5	587.3	495.2	35	15
ABCB11	AAATSIFETIDR	31.0	647.8	980.5	35	21
ABCB11	AAATSIFETIDR	31.0	647.8	780.4	35	21
ABCB11	AAATSIFETIDR	31.0	647.8	633.3	35	21
ABCB11	AAATSIFETID**R**	31.0	652.8	903.5	35	21
ABCB11	AAATSIFETID**R**	31.0	652.8	790.4	35	21
ABCB11	AADTIIGFEHGTAVER	24.9	563.0	472.2	35	16
ABCB11	AADTIIGFEHGTAVER	24.9	563.0	608.3	35	16
ABCB11	AADTIIGFEHGTAVER	24.9	563.0	551.8	35	16
ABCB11	AADTIIGFEHGTAVE**R**	24.9	566.3	613.3	35	16
ABCB11	AADTIIGFEHGTAVE**R**	24.9	566.3	556.8	35	16
ABCB11	VGFFQLFR	40.9	507.3	914.5	35	17
ABCB11	VGFFQLFR	40.9	507.3	710.4	35	17
ABCB11	VGFFQLFR	40.9	507.3	563.3	35	17
ABCB11	VGFFQLF**R**	40.9	512.3	720.4	35	17
ABCB11	VGFFQLF**R**	40.9	512.3	573.3	35	17
ABCC2	LTIIPQDPILFSGSLR	39.1	885.5	1329.7	35	25
ABCC2	LTIIPQDPILFSGSLR	39.1	885.5	721.9	35	25
ABCC2	LTIIPQDPILFSGSLR	39.1	885.5	665.4	35	25
ABCC2	LTIIPQDPILFSGSL**R**	39.1	890.5	1339.7	35	25
ABCC2	LTIIPQDPILFSGSL**R**	39.1	890.5	670.4	35	25
ABCC2	NQSQSQDALVLEDVEK	28.7	901.9	831.4	35	33
ABCC2	NQSQSQDALVLEDVEK	28.7	901.9	732.4	35	33
ABCC2	NQSQSQDALVLEDVEK	28.7	901.9	619.3	35	33
ABCC2	NQSQSQDALVLEDVEK	28.7	901.9	490.3	35	33
ABCC2	NQSQSQDALVLEDVE**K**	28.7	905.9	839.5	35	33
ABCC2	NQSQSQDALVLEDVE**K**	28.7	905.9	740.4	35	33
ABCC2	NQSQSQDALVLEDVE**K**	28.7	905.9	627.3	35	33
ABCC2	NQSQSQDALVLEDVE**K**	28.7	905.9	498.3	35	33
ABCC2	YLGGDDLDTSAIR	24.6	698.3	1119.5	35	27
ABCC2	YLGGDDLDTSAIR	24.6	698.3	775.4	35	27
ABCC2	YLGGDDLDTSAIR	24.6	698.3	662.3	35	27
ABCC2	YLGGDDLDTSAIR	24.6	698.3	547.3	35	27
ABCC2	YLGGDDLDTSAI**R**	24.6	703.3	1129.5	35	27
ABCC2	YLGGDDLDTSAI**R**	24.6	703.3	557.3	35	27

ABCC3	GVVAEFDSPANLIAAR	32.9	815.4	1174.6	35	21
ABCC3	GVVAEFDSPANLIAAR	32.9	815.4	1027.6	35	21
ABCC3	GVVAEFDSPANLIAAR	32.9	815.4	825.5	35	21
ABCC3	GVVAEFDSPANLIAAR	32.9	815.4	317.2	35	21
ABCC3	GVVAEFDSPANLIAA**R**	32.9	820.4	835.5	35	21
ABCC3	GVVAEFDSPANLIAA**R**	32.9	820.4	327.2	35	21
ABCC3	IDGLNVADIGLHDLR	32.7	541.0	288.2	35	20
ABCC3	IDGLNVADIGLHDLR	32.7	541.0	754.4	35	20
ABCC3	IDGLNVADIGLHDLR	32.7	541.0	696.9	35	20
ABCC3	IDGLNVADIGLHDLR	32.7	541.0	611.8	35	20
ABCC3	IDGLNVADIGLHDLR	32.7	541.0	505.3	35	20
ABCC3	IDGLNVADIGLHDL**R**	32.7	544.3	298.2	35	20
ABCC3	IDGLNVADIGLHDL**R**	32.7	544.3	510.3	35	20
ABCC3	NVDPNPYPETSAGFLSR	27.2	932.4	1324.7	35	25
ABCC3	NVDPNPYPETSAGFLSR	27.2	932.4	1064.5	35	25
ABCC3	NVDPNPYPETSAGFLSR	27.2	932.4	825.9	35	25
ABCC3	NVDPNPYPETSAGFLSR	27.2	932.4	768.4	35	25
ABCC3	NVDPNPYPETSAGFLS**R**	27.2	937.5	830.9	35	25
ABCC3	NVDPNPYPETSAGFLS**R**	27.2	937.5	773.4	35	25
ABCC4	AEAAALTETAK	27.2	542.3	883.5	35	22
ABCC4	AEAAALTETAK	27.2	542.3	812.5	35	22
ABCC4	AEAAALTETAK	27.2	542.3	741.4	35	22
ABCC4	AEAAALTETAK	27.2	542.3	670.4	35	22
ABCC4	AEAAALTETAK	27.2	542.3	557.3	35	22
ABCC4	AEAAALTETA**K**	27.2	538.3	875.5	35	22
ABCC4	AEAAALTETA**K**	27.2	538.3	804.4	35	22
ABCC4	AEAAALTETA**K**	27.2	538.3	733.4	35	22
ABCC4	AEAAALTETA**K**	27.2	538.3	662.4	35	22
ABCC4	AEAAALTETA**K**	27.2	538.3	549.3	35	22
ABCC4	DGALESQDTENVPVTLSEENR	24.1	1152.0	1044.5	35	37
ABCC4	DGALESQDTENVPVTLSEENR	24.1	1152.0	848.4	35	37
ABCC4	DGALESQDTENVPVTLSEENR	24.1	1152.0	634.3	35	37
ABCC4	DGALESQDTENVPVTLSEEN**R**	24.1	1157.0	1054.5	35	37
ABCC4	DGALESQDTENVPVTLSEEN**R**	24.1	1157.0	644.3	35	37
ABCC4	IQTFLLLDEISQR	27.2	788.4	973.5	35	25
ABCC4	IQTFLLLDEISQR	27.2	788.4	860.4	35	25
ABCC4	IQTFLLLDEISQR	27.2	788.4	747.4	35	25
ABCC4	IQTFLLLDEISQ**R**	27.2	793.4	983.5	35	25
ABCC4	IQTFLLLDEISQ**R**	27.2	793.4	870.5	35	25
ABCC4	IQTFLLLDEISQ**R**	27.2	793.4	757.4	35	25
ABCG2	LFDSLTLLASGR	36.3	646.9	1032.6	35	17
ABCG2	LFDSLTLLASGR	36.3	646.9	717.4	35	17
ABCG2	LFDSLTLLASGR	36.3	646.9	503.3	35	17
ABCG2	LFDSLTLLASGR	36.3	646.9	390.2	35	17
ABCG2	LFDSLTLLASGR	36.3	646.9	319.2	35	17
ABCG2	LFDSLTLLASG**R**	36.3	651.9	400.2	35	17
ABCG2	LFDSLTLLASG**R**	36.3	651.9	329.2	35	17
ABCG2	SSLLDVLAAR	35.3	522.8	757.5	35	17
ABCG2	SSLLDVLAAR	35.3	522.8	644.4	35	17
ABCG2	SSLLDVLAAR	35.3	522.8	430.3	35	17

ABCG2	SSLLDVLAA**R**	35.3	527.8	654.4	35	17
ABCG2	SSLLDVLAA**R**	35.3	527.8	440.3	35	17
ADH1A	GAILGGFK	25.3	762.5	408.2	35	25
ADH1A	GAILGGFK	25.3	381.7	521.3	35	13
ADH1A	GAILGGFK	25.3	381.7	408.2	35	13
ADH1A	GAILGGF**K**	25.3	385.7	529.3	35	13
ADH1A	GAILGGF**K**	25.3	385.7	416.2	35	13
ADH1A	NDVSNPQGTLQDGTSR	15.9	844.9	1159.6	35	31
ADH1A	NDVSNPQGTLQDGTSR	15.9	844.9	535.2	35	31
ADH1A	NDVSNPQGTLQDGTSR	15.9	844.9	420.2	35	31
ADH1A	NDVSNPQGTLQDGTS**R**	15.9	849.9	1169.6	35	31
ADH1A	NDVSNPQGTLQDGTS**R**	15.9	849.9	430.2	35	31
ADH1B	AAVLWEVK	28.3	458.3	242.1	35	11
ADH1B	AAVLWEVK	28.3	458.3	674.4	35	11
ADH1B	AAVLWEVK	28.3	458.3	561.3	35	11
ADH1B	AAVLWEV**K**	28.3	462.3	242.1	35	11
ADH1B	AAVLWEV**K**	28.3	462.3	569.3	35	11
ADH1B	KPFSIEDVEVAPPK	24.6	519.3	511.3	35	19
ADH1B	KPFSIEDVEVAPPK	24.6	519.3	412.3	35	19
ADH1B	KPFSIEDVEVAPPK	24.6	519.3	341.2	35	19
ADH1B	KPFSIEDVEVAPP**K**	24.6	522.0	420.3	35	19
ADH1B	KPFSIEDVEVAPP**K**	24.6	522.0	349.2	35	19
ADH1C	GAIFGGFK	27.9	398.7	668.4	35	13
ADH1C	GAIFGGFK	27.9	398.7	555.3	35	13
ADH1C	GAIFGGFK	27.9	398.7	408.2	35	13
ADH1C	GAIFGGF**K**	27.9	402.7	563.3	35	13
ADH1C	GAIFGGF**K**	27.9	402.7	416.2	35	13
ADH1C	INEGFDLLR	31.2	538.8	228.1	35	14
ADH1C	INEGFDLLR	31.2	538.8	849.4	35	14
ADH1C	INEGFDLLR	31.2	538.8	720.4	35	14
ADH1C	INEGFDLL**R**	31.2	543.8	228.1	35	14
ADH1C	INEGFDLL**R**	31.2	543.8	859.5	35	14
ADH1C	INEGFDLL**R**	31.2	543.8	730.4	35	14
ADH1C	V**C**LIG**C**GFSTGYGSAVK	29.7	888.4	1290.6	35	29
ADH1C	V**C**LIG**C**GFSTGYGSAVK	29.7	888.4	869.4	35	29
ADH1C	V**C**LIG**C**GFSTGYGSAVK	29.7	888.4	758.9	35	29
ADH1C	V**C**LIG**C**GFSTGYGSAV**K**	29.7	892.4	1298.6	35	29
ADH1C	V**C**LIG**C**GFSTGYGSAV**K**	29.7	892.4	877.5	35	29
ALDH1A1	ANNTFYGLSAGVFTK	33.3	795.4	1042.6	35	24
ALDH1A1	ANNTFYGLSAGVFTK	33.3	795.4	879.5	35	24
ALDH1A1	ANNTFYGLSAGVFTK	33.3	795.4	395.2	35	24
ALDH1A1	ANNTFYGLSAGVFT**K**	33.3	799.4	887.5	35	24
ALDH1A1	ANNTFYGLSAGVFT**K**	33.3	799.4	403.2	35	24
ALDH1A1	IFINNEWHDSVSGK	24.9	549.3	291.2	35	15
ALDH1A1	IFINNEWHDSVSGK	24.9	549.3	693.3	35	15
ALDH1A1	IFINNEWHDSVSGK	24.9	549.3	636.8	35	15
ALDH1A1	IFINNEWHDSVSG**K**	24.9	551.9	697.3	35	15
ALDH1A1	IFINNEWHDSVSG**K**	24.9	551.9	640.8	35	15
ALDH1A1	IFVEESIYDEFVR	37.6	823.4	261.2	35	27
ALDH1A1	IFVEESIYDEFVR	37.6	823.4	360.2	35	27

ALDH1A1	IFVEESIYDEFVR	37.6	823.4	665.3	35	27
ALDH1A1	IFVEESIYDEFV**R**	37.6	828.4	261.2	35	27
ALDH1A1	IFVEESIYDEFV**R**	37.6	828.4	360.2	35	27
ALDH1A2	ANNSDFGLVAAVFTNDINK	39.9	1005.5	1191.6	35	27
ALDH1A2	ANNSDFGLVAAVFTNDINK	39.9	1005.5	1092.6	35	27
ALDH1A2	ANNSDFGLVAAVFTNDINK	39.9	1005.5	1021.5	35	27
ALDH1A2	ANNSDFGLVAAVFTNDINK	39.9	1005.5	950.5	35	27
ALDH1A2	ANNSDFGLVAAVFTNDINK	39.9	1005.5	851.4	35	27
ALDH1A2	ANNSDFGLVAAVFTNDIN**K**	39.9	1009.5	1100.6	35	27
ALDH1A2	ANNSDFGLVAAVFTNDIN**K**	39.9	1009.5	859.4	35	27
ALDH1A2	IFINNEWQNSESGR	25.9	847.4	963.4	35	27
ALDH1A2	IFINNEWQNSESGR	25.9	847.4	777.3	35	27
ALDH1A2	IFINNEWQNSESGR	25.9	847.4	535.2	35	27
ALDH1A2	IFINNEWQNSESGR	25.9	847.4	319.2	35	27
ALDH1A2	IFINNEWQNSESGR	25.9	847.4	717.3	35	27
ALDH1A2	IFINNEWQNSESG**R**	25.9	852.4	787.4	35	27
ALDH1A2	IFINNEWQNSESG**R**	25.9	852.4	329.2	35	27
ALDH1A2	ILELIQSGVAEGAK	28.9	714.4	846.4	35	18
ALDH1A2	ILELIQSGVAEGAK	28.9	714.4	631.3	35	18
ALDH1A2	ILELIQSGVAEGAK	28.9	714.4	475.3	35	18
ALDH1A2	ILELIQSGVAEGA**K**	28.9	718.4	854.4	35	18
ALDH1A2	ILELIQSGVAEGA**K**	28.9	718.4	639.4	35	18
ALDH1A3	AVEAAQVAFQR	20.9	595.3	819.4	35	15
ALDH1A3	AVEAAQVAFQR	20.9	595.3	748.4	35	15
ALDH1A3	AVEAAQVAFQR	20.9	595.3	450.2	35	15
ALDH1A3	AVEAAQVAFQ**R**	20.9	600.3	531.3	35	15
ALDH1A3	AVEAAQVAFQ**R**	20.9	600.3	460.3	35	15
ALDH1A3	LLHQLADLVER	29.0	436.3	631.3	35	11
ALDH1A3	LLHQLADLVER	29.0	436.3	403.2	35	11
ALDH1A3	LLHQLADLVER	29.0	436.3	304.2	35	11
ALDH1A3	LLHQLADLVE**R**	29.0	439.6	413.2	35	11
ALDH1A3	LLHQLADLVE**R**	29.0	439.6	314.2	35	11
AOX1	GLHGPLTLNSPLTPEK	27.9	837.5	1301.7	35	31
AOX1	GLHGPLTLNSPLTPEK	27.9	837.5	1366.8	35	31
AOX1	GLHGPLTLNSPLTPEK	27.9	837.5	1309.7	35	31
AOX1	GLHGPLTLNSPLTPEK	27.9	837.5	373.2	35	31
AOX1	GLHGPLTLNSPLTPE**K**	27.9	841.5	1301.7	35	31
AOX1	GLHGPLTLNSPLTPE**K**	27.9	841.5	1374.8	35	31
AOX1	GLHGPLTLNSPLTPE**K**	27.9	841.5	1317.8	35	31
AOX1	GLHGPLTLNSPLTPE**K**	27.9	841.5	381.2	35	31
AOX1	LILNEVSLLGSAPGGK	34.2	784.5	886.5	35	30
AOX1	LILNEVSLLGSAPGGK	34.2	784.5	573.3	35	30
AOX1	LILNEVSLLGSAPGGK	34.2	784.5	358.2	35	30
AOX1	LILNEVSLLGSAPGG**K**	34.2	788.5	581.3	35	30
AOX1	LILNEVSLLGSAPGG**K**	34.2	788.5	366.2	35	30
CES1	AGQLLSELFTNR	35.9	674.9	257.1	35	26
CES1	AGQLLSELFTNR	35.9	674.9	370.2	35	26
CES1	AGQLLSELFTNR	35.9	674.9	866.4	35	26
CES1	AGQLLSELFTN**R**	35.9	679.9	257.1	35	26
CES1	AGQLLSELFTN**R**	35.9	679.9	370.2	35	26

CES1	AISESGVALTSVLVK	31.2	737.4	830.5	35	20
CES1	AISESGVALTSVLVK	31.2	737.4	759.5	35	20
CES1	AISESGVALTSVLVK	31.2	737.4	646.4	35	20
CES1	AISESGVALTSVLV**K**	31.2	741.4	838.5	35	20
CES1	AISESGVALTSVLV**K**	31.2	741.4	767.5	35	20
CES1	EGYLQIGANTQAAQK	22.5	796.4	350.1	35	30
CES1	EGYLQIGANTQAAQK	22.5	796.4	888.5	35	30
CES1	EGYLQIGANTQAAQK	22.5	796.4	417.2	35	30
CES1	EGYLQIGANTQAAQ**K**	22.5	800.4	350.1	35	30
CES1	EGYLQIGANTQAAQ**K**	22.5	800.4	896.5	35	30
CES2	ADHGDELPFVFR	32.4	701.8	1079.6	35	27
CES2	ADHGDELPFVFR	32.4	701.8	665.4	35	27
CES2	ADHGDELPFVFR	32.4	701.8	322.2	35	27
CES2	ADHGDELPFVF**R**	32.4	706.8	675.4	35	27
CES2	ADHGDELPFVF**R**	32.4	706.8	332.2	35	27
CES2	FTEEEEQLSR	17.4	634.3	761.4	35	21
CES2	FTEEEEQLSR	17.4	634.3	375.2	35	21
CES2	FTEEEEQLSR	17.4	634.3	262.2	35	21
CES2	FTEEEEQLS**R**	17.4	639.3	771.4	35	21
CES2	FTEEEEQLS**R**	17.4	639.3	272.2	35	21
CES2	TTHTGQVLGSLVHVK	23.0	788.9	739.4	35	30
CES2	TTHTGQVLGSLVHVK	23.0	788.9	383.2	35	30
CES2	TTHTGQVLGSLVHVK	23.0	788.9	687.9	35	30
CES2	TTHTGQVLGSLVHV**K**	23.0	793.0	391.3	35	30
CES2	TTHTGQVLGSLVHV**K**	23.0	793.0	691.9	35	30
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	225.1	35	8
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	558.3	35	8
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	698.4	35	8
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	578.8	35	8
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	349.7	35	8
CYP1A1	HSSFVPFTIPHSTTR	26.6	429.2	386.2	35	8
CYP1A1	HSSFVPFTIPHSTT**R**	26.6	431.7	583.8	35	8
CYP1A1	HSSFVPFTIPHSTT**R**	26.6	431.7	389.5	35	8
CYP1A1	IQEELDTVIGR	25.6	636.8	371.2	35	21
CYP1A1	IQEELDTVIGR	25.6	636.8	660.4	35	21
CYP1A1	IQEELDTVIGR	25.6	636.8	345.2	35	21
CYP1A1	IQEELDTVIG**R**	25.6	641.8	1041.5	35	21
CYP1A1	IQEELDTVIG**R**	25.6	641.8	355.2	35	21
CYP1A2	FLTADGTAINKPLSEK	22.7	853.0	815.5	35	31
CYP1A2	FLTADGTAINKPLSEK	22.7	853.0	573.3	35	31
CYP1A2	FLTADGTAINKPLSEK	22.7	853.0	579.3	35	31
CYP1A2	FLTADGTAINKPLSE**K**	22.7	857.0	581.3	35	31
CYP1A2	FLTADGTAINKPLSE**K**	22.7	857.0	583.3	35	31
CYP1A2	IGSTPVLVLSR	27.3	571.4	783.5	35	19
CYP1A2	IGSTPVLVLSR	27.3	571.4	375.2	35	19
CYP1A2	IGSTPVLVLSR	27.3	571.4	392.3	35	19
CYP1A2	IGSTPVLVLS**R**	27.3	576.4	793.5	35	19
CYP1A2	IGSTPVLVLS**R**	27.3	576.4	397.3	35	19
CYP1A2	NTHEFVETASSGNPLDFFPILR	42.6	831.1	1117.6	35	21
CYP1A2	NTHEFVETASSGNPLDFFPILR	42.6	831.1	645.4	35	21

CYP1A2	NTHEFVETASSGNPLDFFPILR	42.6	831.1	498.3	35	21
CYP1A2	NTHEFVETASSGNPLDFFPIL**R**	42.6	834.4	655.4	35	21
CYP1A2	NTHEFVETASSGNPLDFFPIL**R**	42.6	834.4	508.3	35	21
CYP2A6	DPSFFSNPQDFNPQHFLNEK	36.7	1204.6	1012.5	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNEK	36.7	1204.6	787.4	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNEK	36.7	1204.6	650.4	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNEK	36.7	1204.6	1147.0	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	36.7	1208.6	1020.5	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	36.7	1208.6	795.4	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	36.7	1208.6	658.4	35	33
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	36.7	1208.6	1151.0	35	33
CYP2A6	GTGGANIDPTFFLSR	33.8	776.9	982.5	35	29
CYP2A6	GTGGANIDPTFFLSR	33.8	776.9	867.5	35	29
CYP2A6	GTGGANIDPTFFLSR	33.8	776.9	522.3	35	29
CYP2A6	GTGGANIDPTFFLS**R**	33.8	781.9	992.5	35	29
CYP2A6	GTGGANIDPTFFLS**R**	33.8	781.9	877.5	35	29
CYP2B6	GYGVIFANGNR	25.5	584.3	221.1	35	23
CYP2B6	GYGVIFANGNR	25.5	584.3	278.1	35	23
CYP2B6	GYGVIFANGNR	25.5	584.3	678.3	35	23
CYP2B6	GYGVIFANGN**R**	25.5	589.3	221.1	35	23
CYP2B6	GYGVIFANGN**R**	25.5	589.3	278.1	35	23
CYP2B6	IQEEAQ**C**LIEELR	32.8	815.9	242.1	35	26
CYP2B6	IQEEAQ**C**LIEELR	32.8	815.9	932.5	35	26
CYP2B6	IQEEAQ**C**LIEELR	32.8	815.9	288.2	35	26
CYP2B6	IQEEAQ**C**LIEEL**R**	32.8	820.9	242.1	35	26
CYP2B6	IQEEAQ**C**LIEEL**R**	32.8	820.9	556.3	35	26
CYP2B6	TEAFIPFSLGK	35.1	605.3	302.1	35	20
CYP2B6	TEAFIPFSLGK	35.1	605.3	979.6	35	20
CYP2B6	TEAFIPFSLGK	35.1	605.3	648.4	35	20
CYP2B6	TEAFIPFSLG**K**	35.1	609.3	302.1	35	20
CYP2B6	TEAFIPFSLG**K**	35.1	609.3	656.4	35	20
CYP2C18	EALIDHGEEFSGR	20.4	487.2	319.2	35	10
CYP2C18	EALIDHGEEFSGR	20.4	487.2	630.3	35	10
CYP2C18	EALIDHGEEFSGR	20.4	487.2	573.8	35	10
CYP2C18	EALIDHGEEFSG**R**	20.4	490.6	578.8	35	10
CYP2C18	EALIDHGEEFSG**R**	20.4	490.6	522.2	35	10
CYP2C18	GTTIITSLTSVLHNDK	35.0	567.3	626.3	35	16
CYP2C18	GTTIITSLTSVLHNDK	35.0	567.3	513.2	35	16
CYP2C18	GTTIITSLTSVLHNDK	35.0	567.3	771.4	35	16
CYP2C18	GTTIITSLTSVLHNDK	35.0	567.3	607.8	35	16
CYP2C18	GTTIITSLTSVLHND**K**	35.0	570.0	521.3	35	16
CYP2C18	GTTIITSLTSVLHND**K**	35.0	570.0	611.8	35	16
CYP2C19	GTTILTSLTSVLHDNK	35.0	567.3	513.2	35	20
CYP2C19	GTTILTSLTSVLHDNK	35.0	567.3	664.4	35	20
CYP2C19	GTTILTSLTSVLHDNK	35.0	567.3	607.8	35	20
CYP2C19	GTTILTSLTSVLHDN**K**	35.0	570.0	521.3	35	20
CYP2C19	GTTILTSLTSVLHDN**K**	35.0	570.0	668.4	35	20
CYP2C19	HFLDEGGNFK	21.1	388.5	522.3	35	7
CYP2C19	HFLDEGGNFK	21.1	388.5	465.2	35	7
CYP2C19	HFLDEGGNFK	21.1	388.5	261.6	35	7

CYP2C19	HFLDEGGNF**K**	21.1	391.2	530.3	35	7
CYP2C19	HFLDEGGNF**K**	21.1	391.2	265.6	35	7
CYP2C8	VQEEIDHVIGR	20.5	647.8	1067.5	35	26
CYP2C8	VQEEIDHVIGR	20.5	647.8	581.4	35	26
CYP2C8	VQEEIDHVIGR	20.5	647.8	232.1	35	26
CYP2C8	VQEEIDHVIG**R**	20.5	652.8	591.4	35	26
CYP2C8	VQEEIDHVIG**R**	20.5	652.8	242.1	35	26
CYP2C8	YSDLVPTGVPHAVTTDTK	24.1	634.3	578.3	35	14
CYP2C8	YSDLVPTGVPHAVTTDTK	24.1	634.3	711.9	35	14
CYP2C8	YSDLVPTGVPHAVTTDTK	24.1	634.3	662.3	35	14
CYP2C8	YSDLVPTGVPHAVTTDT**K**	24.1	637.0	578.3	35	14
CYP2C8	YSDLVPTGVPHAVTTDT**K**	24.1	637.0	666.4	35	14
CYP2C9	GIFPLAER	29.7	451.8	585.3	35	10
CYP2C9	GIFPLAER	29.7	451.8	366.7	35	10
CYP2C9	GIFPLAER	29.7	451.8	293.2	35	10
CYP2C9	GIFPLAE**R**	29.7	456.8	595.3	35	10
CYP2C9	GIFPLAE**R**	29.7	456.8	371.7	35	10
CYP2C9	YIDLLPTSLPHAVT**C**DIK	34.8	1028.5	1040.5	35	33
CYP2C9	YIDLLPTSLPHAVT**C**DIK	34.8	1028.5	636.3	35	33
CYP2C9	YIDLLPTSLPHAVT**C**DIK	34.8	1028.5	719.9	35	33
CYP2C9	YIDLLPTSLPHAVT**C**DI**K**	34.8	1032.5	1048.5	35	33
CYP2C9	YIDLLPTSLPHAVT**C**DI**K**	34.8	1032.5	723.9	35	33
CYP2D6	GTTLITNLSSVLK	33.0	673.9	974.6	35	22
CYP2D6	GTTLITNLSSVLK	29.7	673.9	861.5	35	22
CYP2D6	GTTLITNLSSVLK	29.7	673.9	760.5	35	22
CYP2D6	GTTLITNLSSVLK	29.7	673.9	646.4	35	22
CYP2D6	GTTLITNLSSVLK	29.7	673.9	533.3	35	22
CYP2D6	GTTLITNLSSVL**K**	29.7	677.9	982.6	35	22
CYP2D6	GTTLITNLSSVL**K**	29.7	677.9	869.5	35	22
CYP2D6	GTTLITNLSSVL**K**	29.7	677.9	768.5	35	22
CYP2D6	GTTLITNLSSVL**K**	29.7	677.9	654.4	35	22
CYP2D6	GTTLITNLSSVL**K**	29.7	677.9	541.3	35	22
CYP2D6	VQQEIDDVIGQVR	27.1	749.9	1271.7	35	19
CYP2D6	VQQEIDDVIGQVR	27.1	749.9	572.4	35	19
CYP2D6	VQQEIDDVIGQVR	27.1	749.9	459.3	35	19
CYP2D6	VQQEIDDVIGQV**R**	27.1	754.9	582.4	35	19
CYP2D6	VQQEIDDVIGQV**R**	27.1	754.9	469.3	35	19
CYP2E1	FGPVFTLYVGSQR	35.8	735.9	709.4	35	20
CYP2E1	FGPVFTLYVGSQR	35.8	735.9	447.2	35	20
CYP2E1	FGPVFTLYVGSQR	35.8	735.9	633.8	35	20
CYP2E1	FGPVFTLYVGSQ**R**	35.8	740.9	457.2	35	20
CYP2E1	FGPVFTLYVGSQ**R**	35.8	740.9	638.8	35	20
CYP2E1	FITLVPSNLPHEATR	29.2	848.0	574.4	35	27
CYP2E1	FITLVPSNLPHEATR	29.2	848.0	1121.6	35	27
CYP2E1	FITLVPSNLPHEATR	29.2	848.0	561.3	35	27
CYP2E1	FITLVPSNLPHEAT**R**	29.2	853.0	1131.6	35	27
CYP2E1	FITLVPSNLPHEAT**R**	29.2	853.0	566.3	35	27
CYP2J2	LLDEVTYLEASK	29.0	690.9	1154.6	35	22
CYP2J2	LLDEVTYLEASK	29.0	690.9	910.5	35	22
CYP2J2	LLDEVTYLEASK	29.0	690.9	811.4	35	22

CYP2J2	LLDEVTYLEASK	29.0	690.9	710.4	35	22
CYP2J2	LLDEVTYLEASK	29.0	690.9	434.2	35	22
CYP2J2	LLDEVTYLEAS**K**	29.0	694.9	1162.6	35	22
CYP2J2	LLDEVTYLEAS**K**	29.0	694.9	819.4	35	22
CYP2J2	VIGQGQQPSTAAR	12.5	656.9	915.5	35	25
CYP2J2	VIGQGQQPSTAAR	12.5	656.9	602.3	35	25
CYP2J2	VIGQGQQPSTAAR	12.5	656.9	550.8	35	25
CYP2J2	VIGQGQQPSTAA**R**	12.5	661.9	612.3	35	25
CYP2J2	VIGQGQQPSTAA**R**	12.5	661.9	612.3	35	25
CYP3A4	EVTNFLR	23.8	439.7	229.1	35	15
CYP3A4	EVTNFLR	23.8	439.7	330.2	35	15
CYP3A4	EVTNFLR	23.8	439.7	650.4	35	15
CYP3A4	EVTNFL**R**	23.8	444.7	229.1	35	15
CYP3A4	EVTNFL**R**	23.8	444.7	660.4	35	15
CYP3A4	LGIPGPTPLPFLGNILSYHK	36.0	712.1	284.2	35	17
CYP3A4	LGIPGPTPLPFLGNILSYHK	36.0	712.1	846.5	35	17
CYP3A4	LGIPGPTPLPFLGNILSYHK	36.0	712.1	1044.6	35	17
CYP3A4	LGIPGPTPLPFLGNILSYHK	36.0	712.1	931.5	35	17
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	36.0	714.7	284.2	35	17
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	36.0	714.7	846.5	35	17
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	36.0	714.7	1052.6	35	17
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	36.0	714.7	939.5	35	17
CYP3A4	LSLGGLLQPEKPVVLK	36.0	846.0	909.6	35	24
CYP3A4	LSLGGLLQPEKPVVLK	36.0	846.0	689.4	35	24
CYP3A4	LSLGGLLQPEKPVVLK	36.0	564.4	746.0	35	13
CYP3A4	LSLGGLLQPEKPVVL**K**	36.0	850.0	917.6	35	24
CYP3A4	LSLGGLLQPEKPVVL**K**	36.0	850.0	750.0	35	24
CYP3A4	LSLGGLLQPEKPVVL**K**	36.0	850.0	693.4	35	24
CYP3A4	LSLGGLLQPEKPVVL**K**	36.0	567.0	750.0	35	13
CYP3A43	DIEINGVFIPK	31.8	622.8	229.1	35	20
CYP3A43	DIEINGVFIPK	31.8	622.8	358.2	35	20
CYP3A43	DIEINGVFIPK	31.8	622.8	1016.6	35	20
CYP3A43	DIEINGVFIPK	31.8	622.8	887.5	35	20
CYP3A43	DIEINGVFIPK	31.8	622.8	774.5	35	20
CYP3A43	DIEINGVFIPK	31.8	622.8	244.2	35	20
CYP3A43	DIEINGVFIP**K**	31.8	626.9	229.1	35	20
CYP3A43	DIEINGVFIP**K**	31.8	626.9	252.2	35	20
CYP3A43	LDNLPILQPEKPIVLK	32.4	610.7	229.1	35	17
CYP3A43	LDNLPILQPEKPIVLK	32.4	610.7	687.9	35	17
CYP3A43	LDNLPILQPEKPIVLK	32.4	610.7	462.3	35	17
CYP3A43	LDNLPILQPEKPIVL**K**	32.4	613.4	229.1	35	17
CYP3A43	LDNLPILQPEKPIVL**K**	32.4	613.4	691.9	35	17
CYP3A43	TLLSPAFTSVK	29.1	582.3	215.1	35	14
CYP3A43	TLLSPAFTSVK	29.1	582.3	328.2	35	14
CYP3A43	TLLSPAFTSVK	29.1	582.3	949.5	35	14
CYP3A43	TLLSPAFTSVK	29.1	582.3	836.5	35	14
CYP3A43	TLLSPAFTSVK	29.1	582.3	749.4	35	14
CYP3A43	TLLSPAFTSV**K**	29.1	586.3	215.1	35	14
CYP3A43	TLLSPAFTSV**K**	29.1	586.3	328.2	35	14
CYP3A5	DSIDPYIYTPFGTGPR	34.7	899.9	1368.7	35	29

CYP3A5	DSIDPYIYTPFGTGPR	34.7	899.9	995.5	35	29
CYP3A5	DSIDPYIYTPFGTGPR	34.7	899.9	832.4	35	29
CYP3A5	DSIDPYIYTPFGTGPR	34.7	899.9	731.4	35	29
CYP3A5	DSIDPYIYTPFGTGP**R**	34.7	904.9	1378.7	35	29
CYP3A5	DSIDPYIYTPFGTGP**R**	34.7	904.9	1005.5	35	29
CYP3A5	DSIDPYIYTPFGTGP**R**	34.7	904.9	842.4	35	29
CYP3A5	DSIDPYIYTPFGTGP**R**	34.7	904.9	741.4	35	29
CYP3A5	DVEINGVFIPK	29.9	615.8	1016.6	35	16
CYP3A5	DVEINGVFIPK	29.9	615.8	887.5	35	16
CYP3A5	DVEINGVFIPK	29.9	615.8	774.5	35	16
CYP3A5	DVEINGVFIPK	29.9	615.8	504.3	35	16
CYP3A5	DVEINGVFIPK	29.9	615.8	244.2	35	16
CYP3A5	DVEINGVFIP**K**	29.9	619.8	782.5	35	16
CYP3A5	DVEINGVFIP**K**	29.9	619.8	252.2	35	16
CYP3A5	LDTQGLLQPEKPIVLK	28.9	896.5	741.4	35	33
CYP3A5	LDTQGLLQPEKPIVLK	28.9	896.5	869.5	35	33
CYP3A5	LDTQGLLQPEKPIVLK	28.9	896.5	1334.8	35	33
CYP3A5	LDTQGLLQPEKPIVLK	28.9	896.5	923.6	35	33
CYP3A5	LDTQGLLQPEKPIVLK	28.9	896.5	569.4	35	33
CYP3A5	LDTQGLLQPEKPIVL**K**	28.9	900.5	931.6	35	33
CYP3A5	LDTQGLLQPEKPIVL**K**	28.9	900.5	577.4	35	33
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	375.2	35	30
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	488.3	35	30
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	1040.7	35	30
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	927.6	35	30
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	569.4	35	30
CYP3A7	FGGLLLTEKPIVLK	33.2	764.5	260.2	35	30
CYP3A7	FGGLLLTEKPIVL**K**	33.2	768.5	375.2	35	30
CYP3A7	FGGLLLTEKPIVL**K**	33.2	768.5	268.2	35	30
CYP3A7	FNPLDPFVLSIK	42.2	695.4	262.1	35	23
CYP3A7	FNPLDPFVLSIK	42.2	695.4	803.5	35	23
CYP3A7	FNPLDPFVLSIK	42.2	695.4	347.2	35	23
CYP3A7	FNPLDPFVLSI**K**	42.2	699.4	262.1	35	23
CYP3A7	FNPLDPFVLSI**K**	42.2	699.4	568.8	35	23
CYP3A7	LGIPGPTPLPFLGNALSFR	42.6	984.1	1331.7	35	27
CYP3A7	LGIPGPTPLPFLGNALSFR	42.6	984.1	1121.6	35	27
CYP3A7	LGIPGPTPLPFLGNALSFR	42.6	984.1	764.4	35	27
CYP3A7	LGIPGPTPLPFLGNALSFR	42.6	984.1	409.2	35	27
CYP3A7	LGIPGPTPLPFLGNALSF**R**	42.6	989.1	1131.6	35	27
CYP3A7	LGIPGPTPLPFLGNALSF**R**	42.6	989.1	419.2	35	27
DPYD	LTPNVTDIVSIAR	32.0	699.9	874.5	35	19
DPYD	LTPNVTDIVSIAR	32.0	699.9	446.3	35	19
DPYD	LTPNVTDIVSIAR	32.0	699.9	592.8	35	19
DPYD	LTPNVTDIVSIA**R**	32.0	704.9	884.5	35	19
DPYD	LTPNVTDIVSIA**R**	32.0	704.9	597.8	35	19
EPHX1	GGHFAAFEEPELLAQDIR	34.3	1000.5	252.1	35	35
EPHX1	GGHFAAFEEPELLAQDIR	34.3	667.3	602.3	35	22
EPHX1	GGHFAAFEEPELLAQDIR	34.3	667.3	288.2	35	22
EPHX1	GGHFAAFEEPELLAQDI**R**	34.3	670.7	612.3	35	22
EPHX1	GGHFAAFEEPELLAQDI**R**	34.3	670.7	298.2	35	22

EPHX1	VETSDEEIHDLHQR	15.1	427.7	689.8	35	15
EPHX1	VETSDEEIHDLHQR	15.1	427.7	459.7	35	15
EPHX1	VETSDEEIHDLHQR	15.1	427.7	403.2	35	15
EPHX1	VETSDEEIHDLHQ**R**	15.1	430.2	651.3	35	15
EPHX1	VETSDEEIHDLHQ**R**	15.1	430.2	408.2	35	15
EPHX1	YLEDGGLER	18.9	526.3	277.2	35	13
EPHX1	YLEDGGLER	18.9	526.3	775.4	35	13
EPHX1	YLEDGGLER	18.9	526.3	646.3	35	13
EPHX1	YLEDGGLE**R**	18.9	531.3	277.2	35	13
EPHX1	YLEDGGLE**R**	18.9	531.3	785.4	35	13
EPHX2	ASPSEVVFLDDIGANLKPAR	35.4	700.4	764.9	35	20
EPHX2	ASPSEVVFLDDIGANLKPAR	35.4	700.4	715.4	35	20
EPHX2	ASPSEVVFLDDIGANLKPAR	35.4	700.4	641.9	35	20
EPHX2	ASPSEVVFLDDIGANLKPA**R**	35.4	703.7	769.9	35	20
EPHX2	ASPSEVVFLDDIGANLKPA**R**	35.4	703.7	720.4	35	20
EPHX2	GLLNDAFQK	27.5	503.3	835.4	35	13
EPHX2	GLLNDAFQK	27.5	503.3	722.3	35	13
EPHX2	GLLNDAFQK	27.5	503.3	418.2	35	13
EPHX2	GLLNDAFQ**K**	27.5	507.3	730.4	35	13
EPHX2	GLLNDAFQ**K**	27.5	507.3	422.2	35	13
EPHX2	V**C**EAGGLFVNSPEEPSLSR	28.6	1024.5	1115.5	35	33
EPHX2	V**C**EAGGLFVNSPEEPSLSR	28.6	1024.5	914.5	35	33
EPHX2	V**C**EAGGLFVNSPEEPSLSR	28.6	1024.5	559.3	35	33
EPHX2	V**C**EAGGLFVNSPEEPSLS**R**	28.6	1029.5	924.5	35	33
EPHX2	V**C**EAGGLFVNSPEEPSLS**R**	28.6	1029.5	569.3	35	33
FMO1	SDDLGGLWR	29.6	509.8	203.1	35	17
FMO1	SDDLGGLWR	29.6	509.8	318.1	35	17
FMO1	SDDLGGLWR	29.6	509.8	588.3	35	17
FMO1	SDDLGGLW**R**	29.6	514.8	318.1	35	17
FMO1	SDDLGGLW**R**	29.6	514.8	598.3	35	17
FMO1	VEDGQASLYK	15.8	555.3	229.1	35	18
FMO1	VEDGQASLYK	15.8	555.3	881.4	35	18
FMO1	VEDGQASLYK	15.8	555.3	310.2	35	18
FMO1	VEDGQASLY**K**	15.8	559.3	229.1	35	18
FMO1	VEDGQASLY**K**	15.8	559.3	889.5	35	18
FMO2	ASIYQSVVTNTSK	23.2	699.4	272.2	35	19
FMO2	ASIYQSVVTNTSK	23.2	699.4	1126.6	35	19
FMO2	ASIYQSVVTNTSK	23.2	699.4	835.5	35	19
FMO2	ASIYQSVVTNTSK	23.2	699.4	649.4	35	19
FMO2	ASIYQSVVTNTSK	23.2	699.4	550.3	35	19
FMO2	ASIYQSVVTNTS**K**	23.2	703.4	843.5	35	19
FMO2	ASIYQSVVTNTS**K**	23.2	703.4	657.4	35	19
FMO2	WFNHENYGLEPQNK	24.1	592.6	645.8	35	17
FMO2	WFNHENYGLEPQNK	24.1	592.6	785.4	35	17
FMO2	WFNHENYGLEPQNK	24.1	592.6	615.3	35	17
FMO2	WFNHENYGLEPQNK	24.1	592.6	486.3	35	17
FMO2	WFNHENYGLEPQNK	24.1	592.6	261.2	35	17
FMO2	WFNHENYGLEPQN**K**	24.1	595.3	494.3	35	17
FMO2	WFNHENYGLEPQN**K**	24.1	595.3	269.2	35	17
FMO2	YIFPAHLDK	24.4	368.5	277.2	35	9

FMO2	YIFPAHLDK	24.4	368.5	414.2	35	9
FMO2	YIFPAHLDK	24.4	368.5	340.7	35	9
FMO2	YIFPAHLD**K**	24.4	371.2	418.2	35	9
FMO2	YIFPAHLD**K**	24.4	371.2	344.7	35	9
FMO3	LVGPGQWPGAR	24.5	569.3	400.2	35	15
FMO3	LVGPGQWPGAR	24.5	569.3	463.2	35	15
FMO3	LVGPGQWPGAR	24.5	569.3	434.7	35	15
FMO3	LVGPGQWPGA**R**	24.5	574.3	410.2	35	15
FMO3	LVGPGQWPGA**R**	24.5	574.3	468.2	35	15
FMO3	NNLPTAISDWLYVK	39.8	817.4	342.2	35	22
FMO3	NNLPTAISDWLYVK	39.8	817.4	1292.7	35	22
FMO3	NNLPTAISDWLYVK	39.8	817.4	646.8	35	22
FMO3	NNLPTAISDWLYV**K**	39.8	821.4	342.2	35	22
FMO3	NNLPTAISDWLYV**K**	39.8	821.4	1300.7	35	22
FMO3	VAIIGAGVSGLASIR	32.1	692.4	987.6	35	19
FMO3	VAIIGAGVSGLASIR	32.1	692.4	703.4	35	19
FMO3	VAIIGAGVSGLASIR	32.1	692.4	550.8	35	19
FMO3	VAIIGAGVSGLASI**R**	32.1	697.4	997.6	35	19
FMO3	VAIIGAGVSGLASI**R**	32.1	697.4	713.4	35	19
GSTA1	LHYFNAR	17.7	460.7	251.2	35	15
GSTA1	LHYFNAR	17.7	460.7	670.3	35	15
GSTA1	LHYFNAR	17.7	460.7	404.2	35	15
GSTA1	LHYFNA**R**	17.7	465.7	251.2	35	15
GSTA1	LHYFNA**R**	17.7	465.7	680.3	35	15
GSTA2	LALIQEK	21.4	407.8	701.4	35	14
GSTA2	LALIQEK	21.4	407.8	630.4	35	14
GSTA2	LALIQEK	21.4	407.8	517.3	35	14
GSTA2	LALIQE**K**	21.4	411.8	709.4	35	14
GSTA2	LALIQE**K**	21.4	411.8	638.4	35	14
GSTA2	LHYSNIR	13.7	451.7	652.3	35	15
GSTA2	LHYSNIR	13.7	451.7	489.3	35	15
GSTA2	LHYSNIR	13.7	451.7	395.2	35	15
GSTA2	LHYSNI**R**	13.7	456.7	499.3	35	15
GSTA2	LHYSNI**R**	13.7	456.7	400.2	35	15
GSTA3	FIGSAEDLGK	21.1	518.8	632.3	35	12
GSTA3	FIGSAEDLGK	21.1	518.8	432.2	35	12
GSTA3	FIGSAEDLGK	21.1	518.8	204.1	35	12
GSTA3	FIGSAEDLG**K**	21.1	522.8	261.2	35	12
GSTA3	FIGSAEDLG**K**	21.1	522.8	784.4	35	12
GSTA3	LHYFNGR	16.7	302.8	338.2	35	6
GSTA3	LHYFNGR	16.7	302.8	346.2	35	6
GSTA3	LHYFNGR	16.7	302.8	232.1	35	6
GSTA3	LHYFNG**R**	16.7	306.2	356.2	35	6
GSTA3	LHYFNG**R**	16.7	306.2	242.1	35	6
GSTA3	VLQSHGQDYLVGNK	18.1	779.4	993.5	35	30
GSTA3	VLQSHGQDYLVGNK	18.1	779.4	417.2	35	30
GSTA3	VLQSHGQDYLVGNK	18.1	779.4	318.2	35	30
GSTA3	VLQSHGQDYLVGNK	18.1	779.4	673.3	35	30
GSTA3	VLQSHGQDYLVGN**K**	18.1	783.4	425.3	35	30
GSTA3	VLQSHGQDYLVGN**K**	18.1	783.4	326.2	35	30

GSTA4	SILHYIADK	23.5	353.9	201.1	35	8
GSTA4	SILHYIADK	23.5	353.9	430.2	35	8
GSTA4	SILHYIADK	23.5	353.9	373.7	35	8
GSTA4	SILHYIAD**K**	23.5	356.5	434.2	35	8
GSTA4	SILHYIAD**K**	23.5	356.5	377.7	35	8
GSTA4	YFPVFEK	29.1	465.2	311.1	35	11
GSTA4	YFPVFEK	29.1	465.2	619.3	35	11
GSTA4	YFPVFEK	29.1	465.2	423.2	35	11
GSTA4	YFPVFEK	29.1	465.2	276.2	35	11
GSTA4	YFPVFEK	29.1	465.2	310.2	35	11
GSTA4	YFPVFE**K**	29.1	469.2	311.1	35	11
GSTA4	YFPVFE**K**	29.1	469.2	627.4	35	11
GSTA5	FLESAEDLDK	27.5	583.8	261.2	35	23
GSTA5	FLESAEDLDK	27.5	583.8	390.2	35	23
GSTA5	FLESAEDLDK	27.5	583.8	906.4	35	23
GSTA5	FLESAEDLD**K**	27.5	587.8	261.2	35	23
GSTA5	FLESAEDLD**K**	27.5	587.8	390.2	35	23
GSTA5	FLQPGSQR	15.7	466.8	261.2	35	16
GSTA5	FLQPGSQR	15.7	466.8	672.3	35	16
GSTA5	FLQPGSQR	15.7	466.8	544.3	35	16
GSTA5	FLQPGSQ**R**	15.7	471.8	261.2	35	16
GSTA5	FLQPGSQ**R**	15.7	471.8	554.3	35	16
GSTA5	WLLAAAGVELEEK	35.4	714.9	300.2	35	23
GSTA5	WLLAAAGVELEEK	35.4	714.9	413.3	35	23
GSTA5	WLLAAAGVELEEK	35.4	714.9	1016.5	35	23
GSTA5	WLLAAAGVELEEK	35.4	714.9	803.4	35	23
GSTA5	WLLAAAGVELEEK	35.4	714.9	405.2	35	23
GSTA5	WLLAAAGVELEE**K**	35.4	718.9	300.2	35	23
GSTA5	WLLAAAGVELEE**K**	35.4	718.9	413.2	35	23
GSTM1	FLPRPVFSK	24.2	545.8	830.5	35	18
GSTM1	FLPRPVFSK	24.2	545.8	234.1	35	18
GSTM1	FLPRPVFSK	24.2	545.8	415.7	35	18
GSTM1	FLPRPVFS**K**	24.2	549.8	857.5	35	18
GSTM1	FLPRPVFS**K**	24.2	549.8	419.8	35	18
GSTM1	RPWFAGNK	19.7	488.3	587.3	35	20
GSTM1	RPWFAGNK	19.7	488.3	658.3	35	20
GSTM1	RPWFAGNK	19.7	488.3	318.2	35	20
GSTM1	RPWFAGN**K**	19.7	492.3	587.3	35	20
GSTM1	RPWFAGN**K**	19.7	492.3	269.2	35	20
GSTM2	ITFVDFIAYDVLER	38.6	850.9	865.4	35	27
GSTM2	ITFVDFIAYDVLER	38.6	850.9	794.4	35	27
GSTM2	ITFVDFIAYDVLER	38.6	850.9	631.3	35	27
GSTM2	ITFVDFIAYDVLER	38.6	850.9	516.3	35	27
GSTM2	ITFVDFIAYDVLER	38.6	850.9	304.2	35	27
GSTM2	ITFVDFIAYDVLE**R**	38.6	856.0	875.4	35	27
GSTM2	ITFVDFIAYDVLE**R**	38.6	856.0	804.4	35	27
GSTM2	ITFVDFIAYDVLE**R**	38.6	856.0	641.3	35	27
GSTM2	ITFVDFIAYDVLE**R**	38.6	856.0	526.3	35	27
GSTM2	ITFVDFIAYDVLE**R**	38.6	856.0	314.2	35	27
GSTM2	LGLDFPNLPYLIDGTHK	40.1	638.3	757.9	35	18

GSTM2	LGLDFPNLPYLIDGTHK	40.1	638.3	684.4	35	18
GSTM2	LGLDFPNLPYLIDGTHK	40.1	638.3	522.3	35	18
GSTM2	LGLDFPNLPYLIDGTH**K**	40.1	641.0	688.4	35	18
GSTM2	LGLDFPNLPYLIDGTH**K**	40.1	641.0	526.3	35	18
GSTM2	NQVFEPS**C**LDAFPNLK	34.1	940.0	689.4	35	31
GSTM2	NQVFEPS**C**LDAFPNLK	34.1	940.0	618.4	35	31
GSTM2	NQVFEPS**C**LDAFPNLK	34.1	940.0	471.3	35	31
GSTM2	NQVFEPS**C**LDAFPNL**K**	34.1	944.0	1269.6	35	31
GSTM2	NQVFEPS**C**LDAFPNL**K**	34.1	944.0	479.3	35	31
GSTM3	FSWFAGEK	30.8	486.2	235.1	35	16
GSTM3	FSWFAGEK	30.8	486.2	737.4	35	16
GSTM3	FSWFAGEK	30.8	486.2	404.2	35	16
GSTM3	FSWFAGE**K**	30.8	490.2	235.1	35	16
GSTM3	FSWFAGE**K**	30.8	490.2	745.4	35	16
GSTM3	IAAYLQSDQF**C**K	24.2	722.4	256.2	35	27
GSTM3	IAAYLQSDQF**C**K	24.2	722.4	912.4	35	27
GSTM3	IAAYLQSDQF**C**K	24.2	722.4	307.1	35	27
GSTM3	IAAYLQSDQF**CK**	24.2	726.4	256.2	35	27
GSTM3	IAAYLQSDQF**CK**	24.2	726.4	315.2	35	27
GSTM3	LKPQYLEELPGQLK	27.9	828.5	655.4	35	27
GSTM3	LKPQYLEELPGQLK	27.9	828.5	542.3	35	27
GSTM3	LKPQYLEELPGQLK	27.9	828.5	707.9	35	27
GSTM3	LKPQYLEELPGQL**K**	27.9	832.5	550.3	35	27
GSTM3	LKPQYLEELPGQL**K**	27.9	832.5	711.9	35	27
GSTM4	IFEPN**C**LDAFPNLK	34.3	839.4	1288.6	35	31
GSTM4	IFEPN**C**LDAFPNLK	34.3	839.4	804.4	35	31
GSTM4	IFEPN**C**LDAFPNLK	34.3	839.4	618.4	35	31
GSTM4	IFEPN**C**LDAFPNLK	34.3	839.4	471.3	35	31
GSTM4	IFEPN**C**LDAFPNLK	34.3	839.4	709.3	35	31
GSTM4	IFEPN**C**LDAFPNL**K**	34.3	843.4	626.4	35	31
GSTM4	IFEPN**C**LDAFPNL**K**	34.3	843.4	479.3	35	31
GSTM4	RPWFVGDK	23.2	502.8	587.3	35	22
GSTM4	RPWFVGDK	23.2	502.8	686.4	35	22
GSTM4	RPWFVGDK	23.2	502.8	858.4	35	22
GSTM4	RPWFVGDK	23.2	502.8	319.2	35	22
GSTM4	RPWFVGD**K**	23.2	506.8	587.3	35	22
GSTM4	RPWFVGD**K**	23.2	506.8	327.2	35	22
GSTP1	ALPGQLKPFETLLSQNQGGK	33.4	709.4	831.4	35	21
GSTP1	ALPGQLKPFETLLSQNQGGK	33.4	709.4	718.3	35	21
GSTP1	ALPGQLKPFETLLSQNQGGK	33.4	709.4	971.5	35	21
GSTP1	ALPGQLKPFETLLSQNQGG**K**	33.4	712.1	839.4	35	21
GSTP1	ALPGQLKPFETLLSQNQGG**K**	33.4	712.1	726.4	35	21
GSTP1	EEVVTVETWQEGSLK	35.1	867.4	948.5	35	28
GSTP1	EEVVTVETWQEGSLK	35.1	867.4	847.4	35	28
GSTP1	EEVVTVETWQEGSLK	35.1	867.4	260.2	35	28
GSTP1	EEVVTVETWQEGSL**K**	35.1	871.4	855.4	35	28
GSTP1	EEVVTVETWQEGSL**K**	35.1	871.4	268.2	35	28
GSTP1	FQDGDLTLYQSNTILR	31.2	942.5	1208.7	35	30
GSTP1	FQDGDLTLYQSNTILR	31.2	942.5	994.5	35	30
GSTP1	FQDGDLTLYQSNTILR	31.2	942.5	831.5	35	30

GSTP1	FQDGDLTLYQSNTILR	31.2	942.5	703.4	35	30
GSTP1	FQDGDLTLYQSNTILR	31.2	942.5	288.2	35	30
GSTP1	FQDGDLTLYQSNTIL**R**	31.2	947.5	1218.7	35	30
GSTP1	FQDGDLTLYQSNTIL**R**	31.2	947.5	1004.5	35	30
GSTP1	FQDGDLTLYQSNTIL**R**	31.2	947.5	841.5	35	30
GSTP1	FQDGDLTLYQSNTIL**R**	31.2	947.5	713.4	35	30
GSTP1	FQDGDLTLYQSNTIL**R**	31.2	947.5	298.2	35	30
GSTT1	GQHLSDAFAQVNPLK	28.2	812.9	1189.6	35	26
GSTT1	GQHLSDAFAQVNPLK	28.2	812.9	769.5	35	26
GSTT1	GQHLSDAFAQVNPLK	28.2	812.9	471.3	35	26
GSTT1	GQHLSDAFAQVNPLK	28.2	812.9	720.4	35	26
GSTT1	GQHLSDAFAQVNPL**K**	28.2	816.9	1197.6	35	26
GSTT1	GQHLSDAFAQVNPL**K**	28.2	816.9	724.4	35	26
GSTT1	VDEYLAWQHTTLR	27.2	544.6	563.3	35	15
GSTT1	VDEYLAWQHTTLR	27.2	544.6	506.8	35	15
GSTT1	VDEYLAWQHTTL**R**	27.2	547.9	771.9	35	15
GSTT1	VDEYLAWQHTTL**R**	27.2	547.9	714.4	35	15
GSTT1	VEAAVGEDLFQEAHEVILK	36.2	699.7	935.0	35	20
GSTT1	VEAAVGEDLFQEAHEVILK	36.2	699.7	864.0	35	20
GSTT1	VEAAVGEDLFQEAHEVILK	36.2	699.7	814.4	35	20
GSTT1	VEAAVGEDLFQEAHEVIL**K**	36.2	702.4	939.0	35	20
GSTT1	VEAAVGEDLFQEAHEVIL**K**	36.2	702.4	818.4	35	20
NAT1	NIFNISLQR	32.3	552.8	877.5	35	14
NAT1	NIFNISLQR	32.3	552.8	730.4	35	14
NAT1	NIFNISLQR	32.3	552.8	503.3	35	14
NAT1	NIFNISLQ**R**	32.3	557.8	887.5	35	14
NAT1	NIFNISLQ**R**	32.3	557.8	513.3	35	14
NAT1	TLSEEEIEK	16.6	539.3	215.1	35	14
NAT1	TLSEEEIEK	16.6	539.3	863.4	35	14
NAT1	TLSEEEIEK	16.6	539.3	776.4	35	14
NAT1	TLSEEEIEK	16.6	539.3	647.3	35	14
NAT1	TLSEEEIE**K**	16.6	543.3	215.1	35	14
NAT1	TLSEEEIE**K**	16.6	543.3	871.4	35	14
NAT2	TLTEEEVEEVLK	30.8	709.9	215.1	35	23
NAT2	TLTEEEVEEVLK	30.8	709.9	316.2	35	23
NAT2	TLTEEEVEEVLK	30.8	709.9	1204.6	35	23
NAT2	TLTEEEVEEVLK	30.8	709.9	974.5	35	23
NAT2	TLTEEEVEEVLK	30.8	709.9	617.4	35	23
NAT2	TLTEEEVEEVLK	30.8	709.9	260.2	35	23
NAT2	TLTEEEVEEVL**K**	30.8	713.9	215.1	35	23
NAT2	TLTEEEVEEVL**K**	30.8	713.9	268.2	35	23
SLC10A1	GIYDGDLK	20.0	440.7	710.3	35	15
SLC10A1	GIYDGDLK	20.0	440.7	547.3	35	15
SLC10A1	GIYDGDLK	20.0	440.7	432.2	35	15
SLC10A1	GIYDGDLK	20.0	440.7	260.2	35	15
SLC10A1	GIYDGDLK	20.0	440.7	355.7	35	15
SLC10A1	GIYDGDL**K**	20.0	444.7	718.3	35	15
SLC10A1	GIYDGDL**K**	20.0	444.7	359.7	35	15
SLC15A2	IYNKPPPEGNIVAQVFK	30.5	638.7	691.4	35	18
SLC15A2	IYNKPPPEGNIVAQVFK	30.5	638.7	592.3	35	18

SLC15A2	IYNKPPPEGNIVAQVFK	30.5	638.7	698.4	35	18
SLC15A2	IYNKPPPEGNIVAQVF**K**	30.5	641.4	277.2	35	18
SLC15A2	IYNKPPPEGNIVAQVF**K**	30.5	641.4	702.4	35	18
SLC15A2	YHNLSLYTEHSVQEK	19.3	462.7	301.1	35	12
SLC15A2	YHNLSLYTEHSVQEK	19.3	462.7	590.3	35	12
SLC15A2	YHNLSLYTEHSVQEK	19.3	462.7	560.8	35	12
SLC15A2	YHNLSLYTEHSVQE**K**	19.3	464.7	564.8	35	12
SLC15A2	YHNLSLYTEHSVQE**K**	19.3	464.7	483.2	35	12
SLC22A1	ENTIYLK	16.4	440.7	244.1	35	10
SLC22A1	ENTIYLK	16.4	440.7	536.3	35	10
SLC22A1	ENTIYLK	16.4	440.7	423.3	35	10
SLC22A1	ENTIYLK	16.4	440.7	260.2	35	10
SLC22A1	ENTIYL**K**	16.4	444.7	244.1	35	10
SLC22A1	ENTIYL**K**	16.4	444.7	544.4	35	10
SLC22A1	ENTIYL**K**	16.4	444.7	431.3	35	10
SLC22A1	ENTIYL**K**	16.4	444.7	268.2	35	10
SLC22A1	LSPSFADLFR	34.9	576.8	603.3	35	19
SLC22A1	LSPSFADLFR	34.9	576.8	621.3	35	19
SLC22A1	LSPSFADLFR	34.9	576.8	435.3	35	19
SLC22A1	LSPSFADLFR	34.9	576.8	322.2	35	19
SLC22A1	LSPSFADLF**R**	34.9	581.8	603.3	35	19
SLC22A1	LSPSFADLF**R**	34.9	581.8	332.2	35	19
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	1057.6	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	942.5	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	732.4	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	574.3	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	461.2	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATNR	38.7	1305.1	289.2	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATN**R**	38.7	1310.1	952.5	35	42
SLC22A1	YEVDWNQSALS**C**VDPLASLATN**R**	38.7	1310.1	471.3	35	42
SLC22A11	GKPDQALQELR	19.4	627.8	1069.6	35	21
SLC22A11	GKPDQALQELR	19.4	627.8	417.2	35	21
SLC22A11	GKPDQALQELR	19.4	627.8	288.2	35	21
SLC22A11	GKPDQALQELR	19.4	627.8	535.3	35	21
SLC22A11	GKPDQALQEL**R**	19.4	632.8	1079.6	35	21
SLC22A11	GKPDQALQEL**R**	19.4	632.8	427.3	35	21
SLC22A11	GKPDQALQEL**R**	19.4	632.8	298.2	35	21
SLC22A11	GKPDQALQEL**R**	19.4	632.8	540.3	35	21
SLC22A11	SVFTSTIVAK	24.7	526.8	866.5	35	13
SLC22A11	SVFTSTIVAK	24.7	526.8	719.4	35	13
SLC22A11	SVFTSTIVAK	24.7	526.8	433.8	35	13
SLC22A11	SVFTSTIVA**K**	24.7	530.8	874.5	35	13
SLC22A11	SVFTSTIVA**K**	24.7	530.8	437.8	35	13
SLC22A11	SVLDLF**C**VPVLR	42.5	709.4	890.5	35	19
SLC22A11	SVLDLF**C**VPVLR	42.5	709.4	743.4	35	19
SLC22A11	SVLDLF**C**VPVLR	42.5	709.4	583.4	35	19
SLC22A11	SVLDLF**C**VPVLR	42.5	709.4	484.3	35	19
SLC22A11	SVLDLF**C**VPVL**R**	42.5	714.4	593.4	35	19
SLC22A11	SVLDLF**C**VPVL**R**	42.5	714.4	494.3	35	19
SLC22A12	ATHGTLGNSVLK	16.9	399.9	617.4	35	14

SLC22A12	ATHGTLGNSVLK	16.9	399.9	560.3	35	14
SLC22A12	ATHGTLGNSVLK	16.9	399.9	446.3	35	14
SLC22A12	ATHGTLGNSVLK	16.9	399.9	260.2	35	14
SLC22A12	ATHGTLGNSVLK	16.9	399.9	309.2	35	14
SLC22A12	ATHGTLGNSVL**K**	16.9	402.6	625.4	35	14
SLC22A12	ATHGTLGNSVL**K**	16.9	402.6	454.3	35	14
SLC22A12	ATHGTLGNSVL**K**	16.9	402.6	268.2	35	14
SLC22A12	LDWGLQELWR	40.6	658.3	472.2	35	21
SLC22A12	LDWGLQELWR	40.6	658.3	901.5	35	21
SLC22A12	LDWGLQELWR	40.6	658.3	361.2	35	21
SLC22A12	LDWGLQELW**R**	40.6	663.3	741.4	35	21
SLC22A12	LDWGLQELW**R**	40.6	663.3	371.2	35	21
SLC22A12	SIFTSTIVAK	27.4	533.8	201.1	35	14
SLC22A12	SIFTSTIVAK	27.4	533.8	866.5	35	14
SLC22A12	SIFTSTIVAK	27.4	533.8	719.4	35	14
SLC22A12	SIFTSTIVA**K**	27.4	537.8	201.1	35	14
SLC22A12	SIFTSTIVA**K**	27.4	537.8	874.5	35	14
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	244.1	35	29
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	904.4	35	29
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	847.4	35	29
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	684.3	35	29
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	392.2	35	29
SLC22A16	ENTSSLGYEYTGSK	19.0	768.3	291.2	35	29
SLC22A16	ENTSSLGYEYTGS**K**	19.0	772.4	400.2	35	29
SLC22A16	ENTSSLGYEYTGS**K**	19.0	772.4	299.2	35	29
SLC22A16	LLLTTNNSGLEK	23.7	651.9	227.2	35	21
SLC22A16	LLLTTNNSGLEK	23.7	651.9	340.3	35	21
SLC22A16	LLLTTNNSGLEK	23.7	651.9	1076.6	35	21
SLC22A16	LLLTTNNSGLEK	23.7	651.9	963.5	35	21
SLC22A16	LLLTTNNSGLEK	23.7	651.9	862.4	35	21
SLC22A16	LLLTTNNSGLE**K**	23.7	655.9	227.2	35	21
SLC22A16	LLLTTNNSGLE**K**	23.7	655.9	971.5	35	21
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASPR	31.0	1300.1	1092.5	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASPR	31.0	1300.1	784.4	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASPR	31.0	1300.1	616.3	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASPR	31.0	1300.1	359.2	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASPR	31.0	1300.1	272.2	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASP**R**	31.0	1305.1	1102.6	35	45
SLC22A2	**C**GWSPAEELNYTVPGPGPAGEASP**R**	31.0	1305.1	282.2	35	45
SLC22A2	LNPSFLDLVR	36.0	587.3	228.1	35	14
SLC22A2	LNPSFLDLVR	36.0	587.3	946.5	35	14
SLC22A2	LNPSFLDLVR	36.0	587.3	473.8	35	14
SLC22A2	LNPSFLDLV**R**	36.0	592.3	228.1	35	14
SLC22A2	LNPSFLDLV**R**	36.0	592.3	478.8	35	14
SLC22A2	SPGVAELSLR	24.4	514.8	341.2	35	17
SLC22A2	SPGVAELSLR	24.4	514.8	844.5	35	17
SLC22A2	SPGVAELSLR	24.4	514.8	688.4	35	17
SLC22A2	SPGVAELSL**R**	24.4	519.8	341.2	35	17
SLC22A2	SPGVAELSL**R**	24.4	519.8	698.4	35	17
SLC22A3	FLQGVFGK	28.8	448.3	261.2	35	15

SLC22A3	FLQGVFGK	28.8	448.3	635.4	35	15
SLC22A3	FLQGVFGK	28.8	448.3	507.3	35	15
SLC22A3	FLQGVFG**K**	28.8	452.3	261.2	35	15
SLC22A3	FLQGVFG**K**	28.8	452.3	643.4	35	15
SLC22A3	GIALPETVDDVEK	26.2	693.4	242.1	35	23
SLC22A3	GIALPETVDDVEK	26.2	693.4	355.2	35	23
SLC22A3	GIALPETVDDVEK	26.2	693.4	1031.5	35	23
SLC22A3	GIALPETVDDVEK	26.2	693.4	805.4	35	23
SLC22A3	GIALPETVDDVEK	26.2	693.4	516.2	35	23
SLC22A3	GIALPETVDDVE**K**	26.2	697.4	242.1	35	23
SLC22A3	GIALPETVDDVE**K**	26.2	697.4	520.3	35	23
SLC22A3	GPSAAALAER	16.0	471.8	630.4	35	16
SLC22A3	GPSAAALAER	16.0	471.8	559.3	35	16
SLC22A3	GPSAAALAER	16.0	471.8	375.2	35	16
SLC22A3	GPSAAALAE**R**	16.0	476.8	640.4	35	16
SLC22A3	GPSAAALAE**R**	16.0	476.8	569.3	35	16
SLC22A4	DYDEVIAFLGEWGPFQR	42.8	1021.5	394.1	35	33
SLC22A4	DYDEVIAFLGEWGPFQR	42.8	1021.5	523.2	35	33
SLC22A4	DYDEVIAFLGEWGPFQR	42.8	1021.5	622.2	35	33
SLC22A4	DYDEVIAFLGEWGPFQ**R**	42.8	1026.5	394.1	35	33
SLC22A4	DYDEVIAFLGEWGPFQ**R**	42.8	1026.5	523.2	35	33
SLC22A5	ANGIVVPSTIFDPSELQDLSSK	37.8	1159.1	243.1	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSSK	37.8	1159.1	356.2	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSSK	37.8	1159.1	455.3	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSSK	37.8	1159.1	554.3	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSSK	37.8	1159.1	1103.6	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSS**K**	37.8	1163.1	243.1	35	42
SLC22A5	ANGIVVPSTIFDPSELQDLSS**K**	37.8	1163.1	356.2	35	42
SLC22A5	FEEAEVIIR	25.6	553.3	829.5	35	18
SLC22A5	FEEAEVIIR	25.6	553.3	500.4	35	18
SLC22A5	FEEAEVIIR	25.6	553.3	288.2	35	18
SLC22A5	FEEAEVII**R**	25.6	558.3	839.5	35	18
SLC22A5	FEEAEVII**R**	25.6	558.3	510.4	35	18
SLC22A5	QQSHNILDLLR	30.0	446.2	629.4	35	11
SLC22A5	QQSHNILDLLR	30.0	446.2	516.3	35	11
SLC22A5	QQSHNILDLLR	30.0	446.2	288.2	35	11
SLC22A5	QQSHNILDLLR	30.0	446.2	315.2	35	11
SLC22A5	QQSHNILDLL**R**	30.0	449.6	639.4	35	11
SLC22A5	QQSHNILDLL**R**	30.0	449.6	526.3	35	11
SLC22A6	EAGIYPR	16.0	403.2	201.1	35	18
SLC22A6	EAGIYPR	16.0	403.2	605.3	35	18
SLC22A6	EAGIYPR	16.0	403.2	548.3	35	18
SLC22A6	EAGIYPR	16.0	403.2	435.2	35	18
SLC22A6	EAGIYPR	16.0	403.2	272.2	35	18
SLC22A6	EAGIYP**R**	16.0	408.2	445.2	35	18
SLC22A6	EAGIYP**R**	16.0	408.2	282.2	35	18
SLC22A6	NGGLEVWLPR	33.7	570.8	229.1	35	19
SLC22A6	NGGLEVWLPR	33.7	570.8	799.4	35	19
SLC22A6	NGGLEVWLPR	33.7	570.8	670.4	35	19
SLC22A6	NGGLEVWLPR	33.7	570.8	571.3	35	19

SLC22A6	NGGLEVWLPR	33.7	570.8	272.2	35	19
SLC22A6	NGGLEVWLP**R**	33.7	575.8	229.1	35	19
SLC22A6	NGGLEVWLP**R**	33.7	575.8	282.2	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLPR	32.2	647.3	232.1	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLPR	32.2	647.3	835.5	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLPR	32.2	647.3	722.4	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLPR	32.2	647.3	385.3	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLPR	32.2	647.3	272.2	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLP**R**	32.2	649.8	232.1	35	19
SLC22A7	**C**ALPGAPANFSHQDVWLEAHLP**R**	32.2	649.8	282.2	35	19
SLC22A7	FAYPQALPNTTLGEER	28.3	904.0	219.1	35	25
SLC22A7	FAYPQALPNTTLGEER	28.3	904.0	382.2	35	25
SLC22A7	FAYPQALPNTTLGEER	28.3	904.0	1425.7	35	25
SLC22A7	FAYPQALPNTTLGEER	28.3	904.0	1016.5	35	25
SLC22A7	FAYPQALPNTTLGEER	28.3	904.0	713.4	35	25
SLC22A7	FAYPQALPNTTLGEE**R**	28.3	909.0	1026.5	35	25
SLC22A7	FAYPQALPNTTLGEE**R**	28.3	909.0	718.4	35	25
SLC22A7	QAQLPETIQDVER	24.4	763.9	328.2	35	30
SLC22A7	QAQLPETIQDVER	24.4	763.9	441.2	35	30
SLC22A7	QAQLPETIQDVER	24.4	763.9	1086.5	35	30
SLC22A7	QAQLPETIQDVER	24.4	763.9	543.8	35	30
SLC22A7	QAQLPETIQDVE**R**	24.4	768.9	328.2	35	30
SLC22A7	QAQLPETIQDVE**R**	24.4	768.9	1096.6	35	30
SLC22A8	FVHPPNASLPNDTQR	19.7	565.0	482.3	35	12
SLC22A8	FVHPPNASLPNDTQR	19.7	565.0	730.3	35	12
SLC22A8	FVHPPNASLPNDTQR	19.7	565.0	633.3	35	12
SLC22A8	FVHPPNASLPNDTQR	19.7	565.0	365.7	35	12
SLC22A8	FVHPPNASLPNDTQ**R**	19.7	568.3	740.4	35	12
SLC22A8	FVHPPNASLPNDTQ**R**	19.7	568.3	370.7	35	12
SLC22A8	YTASDLFR	26.8	486.7	265.1	35	12
SLC22A8	YTASDLFR	26.8	486.7	708.4	35	12
SLC22A8	YTASDLFR	26.8	486.7	637.3	35	12
SLC22A8	YTASDLF**R**	26.8	491.7	265.1	35	12
SLC22A8	YTASDLF**R**	26.8	491.7	718.4	35	12
SLC22A9	DTLTLEILK	33.0	523.3	217.1	35	13
SLC22A9	DTLTLEILK	33.0	523.3	829.5	35	13
SLC22A9	DTLTLEILK	33.0	523.3	716.5	35	13
SLC22A9	DTLTLEIL**K**	33.0	527.3	217.1	35	13
SLC22A9	DTLTLEIL**K**	33.0	527.3	724.5	35	13
SLC22A9	NKPLFDTIQDEK	23.4	483.3	453.3	35	13
SLC22A9	NKPLFDTIQDEK	23.4	483.3	632.3	35	13
SLC22A9	NKPLFDTIQDEK	23.4	483.3	519.2	35	13
SLC22A9	NKPLFDTIQDEK	23.4	483.3	391.2	35	13
SLC22A9	NKPLFDTIQDEK	23.4	483.3	276.2	35	13
SLC22A9	NKPLFDTIQDE**K**	23.4	485.9	527.3	35	13
SLC22A9	NKPLFDTIQDE**K**	23.4	485.9	284.2	35	13
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLLK	40.7	836.4	470.3	35	25
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLLK	40.7	836.4	1100.6	35	25
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLLK	40.7	836.4	914.5	35	25
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLLK	40.7	836.4	886.0	35	25

SLC27A1	F**C**SGDLGPEGILPDTHLLDPLLK	40.7	836.4	631.4	35	25
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLL**K**	40.7	839.1	478.3	35	25
SLC27A1	F**C**SGDLGPEGILPDTHLLDPLL**K**	40.7	839.1	918.5	35	25
SLC27A1	LLGQTDVAVYGVAVPGVEGK	31.6	986.5	912.5	35	37
SLC27A1	LLGQTDVAVYGVAVPGVEGK	31.6	986.5	756.4	35	37
SLC27A1	LLGQTDVAVYGVAVPGVEGK	31.6	986.5	586.3	35	37
SLC27A1	LLGQTDVAVYGVAVPGVEG**K**	31.6	990.5	1083.6	35	37
SLC27A1	LLGQTDVAVYGVAVPGVEG**K**	31.6	990.5	594.3	35	37
SLC27A1	QGHYLPLNEAVYTR	24.9	830.9	599.3	35	27
SLC27A1	QGHYLPLNEAVYTR	24.9	830.9	1175.6	35	27
SLC27A1	QGHYLPLNEAVYTR	24.9	830.9	1062.6	35	27
SLC27A1	QGHYLPLNEAVYTR	24.9	830.9	439.2	35	27
SLC27A1	QGHYLPLNEAVYT**R**	24.9	835.9	599.3	35	27
SLC27A1	QGHYLPLNEAVYT**R**	24.9	835.9	1072.6	35	27
SLC28A1	AGSSFVFGEALVK	32.9	656.4	862.5	35	21
SLC28A1	AGSSFVFGEALVK	32.9	656.4	763.4	35	21
SLC28A1	AGSSFVFGEALVK	32.9	656.4	616.4	35	21
SLC28A1	AGSSFVFGEALVK	32.9	656.4	430.3	35	21
SLC28A1	AGSSFVFGEALVK	32.9	656.4	246.2	35	21
SLC28A1	AGSSFVFGEALV**K**	32.9	660.4	771.4	35	21
SLC28A1	AGSSFVFGEALV**K**	32.9	660.4	624.4	35	21
SLC28A1	LAGAEEWVGDR	23.6	601.8	1018.5	35	20
SLC28A1	LAGAEEWVGDR	23.6	601.8	890.4	35	20
SLC28A1	LAGAEEWVGDR	23.6	601.8	761.4	35	20
SLC28A1	LAGAEEWVGDR	23.6	601.8	632.3	35	20
SLC28A1	LAGAEEWVGDR	23.6	601.8	347.2	35	20
SLC28A1	LAGAEEWVGD**R**	23.6	606.8	1028.5	35	20
SLC28A1	LAGAEEWVGD**R**	23.6	606.8	357.2	35	20
SLC28A1	LTYGDAQNLIEAASTGAAISVK	35.9	1097.1	975.5	35	35
SLC28A1	LTYGDAQNLIEAASTGAAISVK	35.9	1097.1	517.3	35	35
SLC28A1	LTYGDAQNLIEAASTGAAISVK	35.9	1097.1	333.2	35	35
SLC28A1	LTYGDAQNLIEAASTGAAISVK	35.9	1097.1	990.0	35	35
SLC28A1	LTYGDAQNLIEAASTGAAISV**K**	35.9	1101.1	525.3	35	35
SLC28A1	LTYGDAQNLIEAASTGAAISV**K**	35.9	1101.1	341.2	35	35
SLC28A2	GAEAD**C**VSFPNTSFTNR	26.6	936.9	444.2	35	25
SLC28A2	GAEAD**C**VSFPNTSFTNR	26.6	936.9	1170.6	35	25
SLC28A2	GAEAD**C**VSFPNTSFTNR	26.6	936.9	390.2	35	25
SLC28A2	GAEAD**C**VSFPNTSFTNR	26.6	936.9	289.2	35	25
SLC28A2	GAEAD**C**VSFPNTSFTN**R**	26.6	941.9	946.5	35	25
SLC28A2	GAEAD**C**VSFPNTSFTN**R**	26.6	941.9	400.2	35	25
SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK	34.6	1233.6	1360.6	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK	34.6	1233.6	1246.6	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK	34.6	1233.6	818.4	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK	34.6	1233.6	674.3	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWEDK	34.6	1233.6	262.1	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWED**K**	34.6	1237.6	1254.6	35	39
SLC28A2	GLFQSTSLNGTNPPSFSGPWED**K**	34.6	1237.6	270.2	35	39
SLC28A2	TDAQGHSLGDGLGPSTYQR	19.8	654.0	217.1	35	19
SLC28A2	TDAQGHSLGDGLGPSTYQR	19.8	654.0	808.4	35	19
SLC28A2	TDAQGHSLGDGLGPSTYQR	19.8	654.0	751.4	35	19

SLC28A2	TDAQGHSLGDGLGPSTYQR	19.8	654.0	466.2	35	19
SLC28A2	TDAQGHSLGDGLGPSTYQR	19.8	654.0	489.8	35	19
SLC28A2	TDAQGHSLGDGLGPSTYQ**R**	19.8	657.3	818.4	35	19
SLC28A2	TDAQGHSLGDGLGPSTYQ**R**	19.8	657.3	761.4	35	19
SLC28A3	FVNGVQQYISIR	29.6	712.4	247.1	35	23
SLC28A3	FVNGVQQYISIR	29.6	712.4	1177.6	35	23
SLC28A3	FVNGVQQYISIR	29.6	712.4	907.5	35	23
SLC28A3	FVNGVQQYISIR	29.6	712.4	375.2	35	23
SLC28A3	FVNGVQQYISI**R**	29.6	717.4	247.1	35	23
SLC28A3	FVNGVQQYISI**R**	29.6	717.4	385.2	35	23
SLC28A3	GPGEVIPGGNHSLYSLK	25.1	575.6	440.2	35	16
SLC28A3	GPGEVIPGGNHSLYSLK	25.1	575.6	553.3	35	16
SLC28A3	GPGEVIPGGNHSLYSLK	25.1	575.6	692.9	35	16
SLC28A3	GPGEVIPGGNHSLYSLK	25.1	575.6	586.8	35	16
SLC28A3	GPGEVIPGGNHSLYSL**K**	25.1	578.3	696.9	35	16
SLC28A3	GPGEVIPGGNHSLYSL**K**	25.1	578.3	590.8	35	16
SLC28A3	TFFNEFVAYEHLSK	34.9	578.0	249.1	35	16
SLC28A3	TFFNEFVAYEHLSK	34.9	578.0	847.4	35	16
SLC28A3	TFFNEFVAYEHLSK	34.9	578.0	742.4	35	16
SLC28A3	TFFNEFVAYEHLS**K**	34.9	580.6	249.1	35	16
SLC28A3	TFFNEFVAYEHLS**K**	34.9	580.6	746.4	35	16
SLC29A1	DAQASAAPAAPLPER	17.8	732.9	921.5	35	20
SLC29A1	DAQASAAPAAPLPER	17.8	732.9	850.5	35	20
SLC29A1	DAQASAAPAAPLPER	17.8	732.9	611.4	35	20
SLC29A1	DAQASAAPAAPLPER	17.8	732.9	401.2	35	20
SLC29A1	DAQASAAPAAPLPE**R**	17.8	737.9	860.5	35	20
SLC29A1	DAQASAAPAAPLPE**R**	17.8	737.9	411.2	35	20
SLC29A1	EESGVSVSNSQPTNESHSIK	14.4	1058.5	1012.5	35	39
SLC29A1	EESGVSVSNSQPTNESHSIK	14.4	1058.5	571.3	35	39
SLC29A1	EESGVSVSNSQPTNESHSIK	14.4	1058.5	807.9	35	39
SLC29A1	EESGVSVSNSQPTNESHSI**K**	14.4	1062.5	1020.5	35	39
SLC29A1	EESGVSVSNSQPTNESHSI**K**	14.4	1062.5	579.3	35	39
SLC29A1	LEGPGEQETK	12.3	544.3	300.2	35	18
SLC29A1	LEGPGEQETK	12.3	544.3	248.2	35	18
SLC29A1	LEGPGEQETK	12.3	544.3	394.7	35	18
SLC29A1	LEGPGEQET**K**	12.3	548.3	853.4	35	18
SLC29A1	LEGPGEQET**K**	12.3	548.3	427.2	35	18
SLC29A2	AELLQSDENGIPSSPQK	21.8	907.0	314.2	35	25
SLC29A2	AELLQSDENGIPSSPQK	21.8	907.0	643.3	35	25
SLC29A2	AELLQSDENGIPSSPQK	21.8	907.0	372.2	35	25
SLC29A2	AELLQSDENGIPSSPQ**K**	21.8	911.0	314.2	35	25
SLC29A2	AELLQSDENGIPSSPQ**K**	21.8	911.0	651.4	35	25
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	1164.5	35	28
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	1017.5	35	28
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	904.4	35	28
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	718.3	35	28
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	506.2	35	28
SLC29A2	SLTSYFLWPDEDSR	38.2	858.4	262.2	35	28
SLC29A2	SLTSYFLWPDEDS**R**	38.2	863.4	728.3	35	28
SLC29A2	SLTSYFLWPDEDS**R**	38.2	863.4	272.2	35	28

SLC29A2	SSQAQAQELETK	13.1	660.3	374.2	35	22
SLC29A2	SSQAQAQELETK	13.1	660.3	946.5	35	22
SLC29A2	SSQAQAQELETK	13.1	660.3	818.4	35	22
SLC29A2	SSQAQAQELETK	13.1	660.3	377.2	35	22
SLC29A2	SSQAQAQELETK	13.1	660.3	248.2	35	22
SLC29A2	SSQAQAQELET**K**	13.1	664.3	374.2	35	22
SLC29A2	SSQAQAQELET**K**	13.1	664.3	256.2	35	22
SLC47A1	A**C**QQAQVHANLK	12.5	456.6	232.1	35	17
SLC47A1	A**C**QQAQVHANLK	12.5	456.6	445.3	35	17
SLC47A1	A**C**QQAQVHANLK	12.5	456.6	648.8	35	17
SLC47A1	A**C**QQAQVHANL**K**	12.5	459.2	232.1	35	17
SLC47A1	A**C**QQAQVHANL**K**	12.5	459.2	453.3	35	17
SLC47A1	GGPEATLEVR	19.3	514.8	688.4	35	17
SLC47A1	GGPEATLEVR	19.3	514.8	617.4	35	17
SLC47A1	GGPEATLEVR	19.3	514.8	516.3	35	17
SLC47A1	GGPEATLEV**R**	19.3	519.8	698.4	35	17
SLC47A1	GGPEATLEV**R**	19.3	519.8	627.4	35	17
SLC47A1	QEEPLPEHPQDGAK	14.1	525.6	258.1	35	19
SLC47A1	QEEPLPEHPQDGAK	14.1	525.6	615.3	35	19
SLC47A1	QEEPLPEHPQDGAK	14.1	525.6	659.3	35	19
SLC47A1	QEEPLPEHPQDGAK	14.1	525.6	594.8	35	19
SLC47A1	QEEPLPEHPQDGAK	14.1	525.6	489.7	35	19
SLC47A1	QEEPLPEHPQDGA**K**	14.1	528.3	623.3	35	19
SLC47A1	QEEPLPEHPQDGA**K**	14.1	528.3	493.7	35	19
SLC47A2	SE**C**HVDFFR	24.1	399.5	217.1	35	10
SLC47A2	SE**C**HVDFFR	24.1	399.5	469.3	35	10
SLC47A2	SE**C**HVDFFR	24.1	399.5	490.7	35	10
SLC47A2	SE**C**HVDFF**R**	24.1	402.8	217.1	35	10
SLC47A2	SE**C**HVDFF**R**	24.1	402.8	495.7	35	10
SLC47A2	TPEEAHALSAPTSR	14.9	489.6	618.3	35	18
SLC47A2	TPEEAHALSAPTSR	14.9	489.6	531.3	35	18
SLC47A2	TPEEAHALSAPTSR	14.9	489.6	460.3	35	18
SLC47A2	TPEEAHALSAPTS**R**	14.9	492.9	628.3	35	18
SLC47A2	TPEEAHALSAPTS**R**	14.9	492.9	470.3	35	18
SLCO1A2	**C**HLPGENASSGTELIETK	21.4	648.3	411.2	35	24
SLCO1A2	**C**HLPGENASSGTELIETK	21.4	648.3	603.4	35	24
SLCO1A2	**C**HLPGENASSGTELIETK	21.4	648.3	490.3	35	24
SLCO1A2	**C**HLPGENASSGTELIETK	21.4	648.3	377.2	35	24
SLCO1A2	**C**HLPGENASSGTELIETK	21.4	648.3	248.2	35	24
SLCO1A2	**C**HLPGENASSGTELIET**K**	21.4	651.0	385.2	35	24
SLCO1A2	**C**HLPGENASSGTELIET**K**	21.4	651.0	256.2	35	24
SLCO1A2	EGLETNADIIK	22.8	601.8	903.5	35	16
SLCO1A2	EGLETNADIIK	22.8	601.8	774.4	35	16
SLCO1A2	EGLETNADIIK	22.8	601.8	673.4	35	16
SLCO1A2	EGLETNADIIK	22.8	601.8	559.3	35	16
SLCO1A2	EGLETNADIIK	22.8	601.8	488.3	35	16
SLCO1A2	EGLETNADIIK	22.8	601.8	260.2	35	16
SLCO1A2	EGLETNADII**K**	22.8	605.8	782.4	35	16
SLCO1A2	EGLETNADII**K**	22.8	605.8	268.2	35	16
SLCO1B1	NVTGFFQSFK	33.7	587.8	214.1	35	14

SLCO1B1	NVTGFFQSFK	33.7	587.8	315.2	35	14
SLCO1B1	NVTGFFQSFK	33.7	587.8	961.5	35	14
SLCO1B1	NVTGFFQSF**K**	33.7	591.8	214.1	35	14
SLCO1B1	NVTGFFQSF**K**	33.7	591.8	969.5	35	14
SLCO1B3	IYNSVFFGR	24.5	551.8	277.2	35	18
SLCO1B3	IYNSVFFGR	24.5	551.8	826.4	35	18
SLCO1B3	IYNSVFFGR	24.5	551.8	413.7	35	18
SLCO1B3	IYNSVFFG**R**	24.5	556.8	277.2	35	18
SLCO1B3	IYNSVFFG**R**	24.5	556.8	418.7	35	18
SLCO1B3	NQTANLTNQGK	11.7	594.8	243.1	35	19
SLCO1B3	NQTANLTNQGK	11.7	594.8	344.2	35	19
SLCO1B3	NQTANLTNQGK	11.7	594.8	946.5	35	19
SLCO1B3	NQTANLTNQGK	11.7	594.8	845.4	35	19
SLCO1B3	NQTANLTNQGK	11.7	594.8	774.4	35	19
SLCO1B3	NQTANLTNQG**K**	11.7	598.8	243.1	35	19
SLCO1B3	NQTANLTNQG**K**	11.7	598.8	954.5	35	19
SLCO1B3	WSTNS**C**GAQGA**C**R	13.7	727.8	274.1	35	24
SLCO1B3	WSTNS**C**GAQGA**C**R	13.7	727.8	1181.5	35	24
SLCO1B3	WSTNS**C**GAQGA**C**R	13.7	727.8	1080.4	35	24
SLCO1B3	WSTNS**C**GAQGA**C**R	13.7	727.8	966.4	35	24
SLCO1B3	WSTNS**C**GAQGA**CR**	13.7	732.8	274.1	35	24
SLCO1B3	WSTNS**C**GAQGA**CR**	13.7	732.8	1090.4	35	24
SLCO2B1	ASPDPQDVRPSVFHNIK	21.7	477.5	549.3	35	12
SLCO2B1	ASPDPQDVRPSVFHNIK	21.7	477.5	471.3	35	12
SLCO2B1	ASPDPQDVRPSVFHNIK	21.7	477.5	512.9	35	12
SLCO2B1	ASPDPQDVRPSVFHNIK	21.7	477.5	437.9	35	12
SLCO2B1	ASPDPQDVRPSVFHNI**K**	21.7	479.5	515.6	35	12
SLCO2B1	ASPDPQDVRPSVFHNI**K**	21.7	479.5	440.6	35	12
SLCO2B1	SSPAVEQQLLVSGPGK	24.1	798.9	445.2	35	22
SLCO2B1	SSPAVEQQLLVSGPGK	24.1	798.9	358.2	35	22
SLCO2B1	SSPAVEQQLLVSGPGK	24.1	798.9	711.9	35	22
SLCO2B1	SSPAVEQQLLVSGPG**K**	24.1	802.9	366.2	35	22
SLCO2B1	SSPAVEQQLLVSGPG**K**	24.1	802.9	715.9	35	22
SLCO2B1	VLAVTDSPAR	17.2	514.8	284.2	35	13
SLCO2B1	VLAVTDSPAR	17.2	514.8	816.4	35	13
SLCO2B1	VLAVTDSPAR	17.2	514.8	646.3	35	13
SLCO2B1	VLAVTDSPA**R**	17.2	519.8	213.2	35	13
SLCO2B1	VLAVTDSPA**R**	17.2	519.8	284.2	35	13
SLCO4C1	ENAVVTNVLAEQDLNK	27.0	879.0	315.1	35	32
SLCO4C1	ENAVVTNVLAEQDLNK	27.0	879.0	414.2	35	32
SLCO4C1	ENAVVTNVLAEQDLNK	27.0	879.0	930.5	35	32
SLCO4C1	ENAVVTNVLAEQDLNK	27.0	879.0	817.4	35	32
SLCO4C1	ENAVVTNVLAEQDLNK	27.0	879.0	261.2	35	32
SLCO4C1	ENAVVTNVLAEQDLN**K**	27.0	883.0	315.1	35	32
SLCO4C1	ENAVVTNVLAEQDLN**K**	27.0	883.0	269.2	35	32
SLCO4C1	GIENLAFVPSSPDILR	35.7	864.5	844.5	35	28
SLCO4C1	GIENLAFVPSSPDILR	35.7	864.5	1201.7	35	28
SLCO4C1	GIENLAFVPSSPDILR	35.7	864.5	983.6	35	28
SLCO4C1	GIENLAFVPSSPDILR	35.7	864.5	884.5	35	28
SLCO4C1	GIENLAFVPSSPDIL**R**	35.7	869.5	993.6	35	28

SLCO4C1	GIENLAFVPSSPDIL**R**	35.7	869.5	894.5	35	28
SLCO4C1	HLPGTAEIQAGK	16.4	407.9	577.3	35	14
SLCO4C1	HLPGTAEIQAGK	16.4	407.9	353.7	35	14
SLCO4C1	HLPGTAEIQAGK	16.4	407.9	516.3	35	14
SLCO4C1	HLPGTAEIQAGK	16.4	407.9	275.2	35	14
SLCO4C1	HLPGTAEIQAG**K**	16.4	410.6	524.3	35	14
SLCO4C1	HLPGTAEIQAG**K**	16.4	410.6	283.2	35	14
SULT1A1	SLPEETVDFVVQHTSFK	37.1	655.0	201.1	35	15
SULT1A1	SLPEETVDFVVQHTSFK	37.1	655.0	427.2	35	15
SULT1A1	SLPEETVDFVVQHTSFK	37.1	655.0	945.5	35	15
SULT1A1	SLPEETVDFVVQHTSF**K**	37.1	657.7	201.1	35	15
SULT1A1	SLPEETVDFVVQHTSF**K**	37.1	657.7	854.5	35	15
SULT1A1	VHPEPGTWDSFLEK	30.1	821.4	237.1	35	30
SULT1A1	VHPEPGTWDSFLEK	30.1	821.4	703.3	35	30
SULT1A1	VHPEPGTWDSFLEK	30.1	547.9	237.1	35	20
SULT1A1	VHPEPGTWDSFLE**K**	30.1	825.4	237.1	35	30
SULT1A1	VHPEPGTWDSFLE**K**	30.1	550.6	237.1	35	20
SULT1A2	FDADYAK	15.5	415.2	263.1	35	10
SULT1A2	FDADYAK	15.5	415.2	334.1	35	10
SULT1A2	FDADYAK	15.5	415.2	449.2	35	10
SULT1A2	FDADYAK	15.5	415.2	682.3	35	10
SULT1A2	FDADYAK	15.5	415.2	567.3	35	10
SULT1A2	FDADYA**K**	15.5	419.2	263.1	35	10
SULT1A2	FDADYA**K**	15.5	419.2	575.3	35	10
SULT1A2	VYPHPGTWESFLEK	31.8	563.9	623.3	35	12
SULT1A2	VYPHPGTWESFLEK	31.8	563.9	795.9	35	12
SULT1A2	VYPHPGTWESFLEK	31.8	563.9	714.4	35	12
SULT1A2	VYPHPGTWESFLEK	31.8	563.9	597.3	35	12
SULT1A2	VYPHPGTWESFLE**K**	31.8	566.6	718.4	35	12
SULT1A2	VYPHPGTWESFLE**K**	31.8	566.6	601.3	35	12
SULT1A3	AHPEPGTWDSFLEK	29.7	538.6	209.1	35	20
SULT1A3	AHPEPGTWDSFLEK	29.7	538.6	690.3	35	20
SULT1A3	AHPEPGTWDSFLEK	29.7	538.6	345.7	35	20
SULT1A3	AHPEPGTWDSFLEK	29.7	538.6	924.4	35	20
SULT1A3	AHPEPGTWDSFLEK	29.7	538.6	738.4	35	20
SULT1A3	AHPEPGTWDSFLE**K**	29.7	541.3	209.1	35	20
SULT1A3	AHPEPGTWDSFLE**K**	29.7	541.3	746.4	35	20
SULT1A3	DVAVSYYHFHR	21.1	349.2	215.1	35	8
SULT1A3	DVAVSYYHFHR	21.1	349.2	286.1	35	8
SULT1A3	DVAVSYYHFHR	21.1	349.2	385.2	35	8
SULT1A3	DVAVSYYHFHR	21.1	349.2	236.6	35	8
SULT1A3	DVAVSYYHFHR	21.1	349.2	596.3	35	8
SULT1A3	DVAVSYYHFHR	21.1	349.2	459.2	35	8
SULT1A3	DVAVSYYHFH**R**	21.1	351.7	215.1	35	8
SULT1A3	DVAVSYYHFH**R**	21.1	351.7	385.2	35	8
SULT1B1	IEQFHSRPDDIVIATYPK	24.7	533.0	613.3	35	14
SULT1B1	IEQFHSRPDDIVIATYPK	24.7	533.0	669.8	35	14
SULT1B1	IEQFHSRPDDIVIATYPK	24.7	533.0	719.4	35	14
SULT1B1	IEQFHSRPDDIVIATYP**K**	24.7	535.0	669.8	35	14
SULT1B1	IEQFHSRPDDIVIATYP**K**	24.7	535.0	719.4	35	14

SULT1B1	NYFTVAQNEK	21.7	607.3	278.1	35	15
SULT1B1	NYFTVAQNEK	21.7	607.3	425.2	35	15
SULT1B1	NYFTVAQNEK	21.7	607.3	789.4	35	15
SULT1B1	NYFTVAQNE**K**	21.7	611.3	278.1	35	15
SULT1B1	NYFTVAQNE**K**	21.7	611.3	425.2	35	15
SULT1B1	THLPTDLLPK	26.6	567.8	239.1	35	19
SULT1B1	THLPTDLLPK	26.6	567.8	352.2	35	19
SULT1B1	THLPTDLLPK	26.6	567.8	244.2	35	19
SULT1B1	THLPTDLLP**K**	26.6	571.8	239.1	35	19
SULT1B1	THLPTDLLP**K**	26.6	571.8	352.2	35	19
SULT1C1/C2	IVQETSFEK	17.0	540.8	341.2	35	14
SULT1C1/C2	IVQETSFEK	17.0	540.8	868.4	35	14
SULT1C1/C2	IVQETSFEK	17.0	540.8	484.2	35	14
SULT1C1/C2	IVQETSFE**K**	17.0	544.8	341.2	35	14
SULT1C1/C2	IVQETSFE**K**	17.0	544.8	876.4	35	14
SULT1C1/C2	NHFTVAQNER	13.3	405.9	546.3	35	7
SULT1C1/C2	NHFTVAQNER	13.3	405.9	418.2	35	7
SULT1C1/C2	NHFTVAQNER	13.3	405.9	309.2	35	7
SULT1C1/C2	NHFTVAQNE**R**	13.3	409.2	314.2	35	7
SULT1C1/C2	NHFTVAQNE**R**	13.3	409.2	314.2	35	7
SULT1C1/C2	VVWGSWFDHVK	34.1	453.9	630.8	35	12
SULT1C1/C2	VVWGSWFDHVK	34.1	453.9	581.3	35	12
SULT1C1/C2	VVWGSWFDHVK	34.1	453.9	488.2	35	12
SULT1C1/C2	VVWGSWFDHV**K**	34.1	456.6	585.3	35	12
SULT1C1/C2	VVWGSWFDHV**K**	34.1	456.6	492.2	35	12
SULT1E1	LIHFLER	25.0	464.3	364.2	35	15
SULT1E1	LIHFLER	25.0	464.3	701.4	35	15
SULT1E1	LIHFLER	25.0	464.3	351.2	35	15
SULT1E1	LIHFLE**R**	25.0	469.3	574.3	35	15
SULT1E1	LIHFLE**R**	25.0	469.3	356.2	35	15
SULT1E1	NHFTVALNEK	19.7	586.8	399.2	35	15
SULT1E1	NHFTVALNEK	19.7	586.8	921.5	35	15
SULT1E1	NHFTVALNEK	19.7	586.8	774.4	35	15
SULT1E1	NHFTVALNEK	19.7	586.8	574.3	35	15
SULT1E1	NHFTVALNE**K**	19.7	590.8	399.2	35	15
SULT1E1	NHFTVALNE**K**	19.7	590.8	582.3	35	15
SULT2A1	LFSSHLPIQLFPK	35.1	763.9	842.5	35	25
SULT2A1	LFSSHLPIQLFPK	35.1	763.9	391.2	35	25
SULT2A1	LFSSHLPIQLFPK	35.1	763.9	244.2	35	25
SULT2A1	LFSSHLPIQLFP**K**	35.1	767.9	399.2	35	25
SULT2A1	LFSSHLPIQLFP**K**	35.1	767.9	252.2	35	25
SULT2A1	NHFTVAQAEDFDK	21.9	761.4	399.2	35	25
SULT2A1	NHFTVAQAEDFDK	21.9	761.4	1270.6	35	25
SULT2A1	NHFTVAQAEDFDK	21.9	761.4	1123.5	35	25
SULT2A1	NHFTVAQAEDFD**K**	21.9	765.4	399.2	35	25
SULT2A1	NHFTVAQAEDFD**K**	21.9	765.4	1131.5	35	25
SULT2A1	TLEPEELNLILK	35.2	706.4	344.2	35	18
SULT2A1	TLEPEELNLILK	35.2	706.4	1068.6	35	18
SULT2A1	TLEPEELNLILK	35.2	706.4	260.2	35	18
SULT2A1	TLEPEELNLIL**K**	35.2	710.4	344.2	35	18

SULT2A1	TLEPEELNLIL**K**	35.2	710.4	1076.6	35	18
SULT2B1	APW**C**ETIVGAFSLPDQYSPR	40.0	1147.5	1337.6	35	34
SULT2B1	APW**C**ETIVGAFSLPDQYSPR	40.0	1147.5	862.4	35	34
SULT2B1	APW**C**ETIVGAFSLPDQYSPR	40.0	765.4	862.4	35	20
SULT2B1	APW**C**ETIVGAFSLPDQYSPR	40.0	765.4	431.7	35	20
SULT2B1	APW**C**ETIVGAFSLPDQYSP**R**	40.0	1152.6	872.4	35	34
SULT2B1	APW**C**ETIVGAFSLPDQYSP**R**	40.0	768.7	872.4	35	20
SULT2B1	APW**C**ETIVGAFSLPDQYSP**R**	40.0	768.7	436.7	35	20
SULT2B1	GEVQFGSWFDHIK	34.3	775.4	1136.6	35	25
SULT2B1	GEVQFGSWFDHIK	34.3	775.4	989.5	35	25
SULT2B1	GEVQFGSWFDHIK	34.3	775.4	397.3	35	25
SULT2B1	GEVQFGSWFDHIK	34.3	775.4	682.3	35	25
SULT2B1	GEVQFGSWFDHIK	34.3	775.4	632.8	35	25
SULT2B1	GEVQFGSWFDHI**K**	34.3	779.4	997.5	35	25
SULT2B1	GEVQFGSWFDHI**K**	34.3	779.4	405.3	35	25
SULT2B1	NHFTVAQSEAFDR	20.7	507.9	670.3	35	14
SULT2B1	NHFTVAQSEAFDR	20.7	507.9	335.7	35	14
SULT2B1	NHFTVAQSEAFDR	20.7	507.9	437.2	35	14
SULT2B1	NHFTVAQSEAFD**R**	20.7	511.2	734.3	35	14
SULT2B1	NHFTVAQSEAFD**R**	20.7	511.2	518.3	35	14
SULT4A1	DLVVSYYQFHR	27.6	713.9	1099.5	35	23
SULT4A1	DLVVSYYQFHR	27.6	713.9	1000.5	35	23
SULT4A1	DLVVSYYQFHR	27.6	713.9	550.3	35	23
SULT4A1	DLVVSYYQFH**R**	27.6	718.9	1010.5	35	23
SULT4A1	DLVVSYYQFH**R**	27.6	718.9	555.3	35	23
SULT4A1	FLPSDLHNGDSK	18.5	443.9	261.2	35	11
SULT4A1	FLPSDLHNGDSK	18.5	443.9	560.3	35	11
SULT4A1	FLPSDLHNGDSK	18.5	443.9	657.3	35	11
SULT4A1	FLPSDLHNGDSK	18.5	443.9	234.1	35	11
SULT4A1	FLPSDLHNGDSK	18.5	443.9	591.8	35	11
SULT4A1	FLPSDLHNGDSK	18.5	443.9	535.2	35	11
SULT4A1	FLPSDLHNGDS**K**	18.5	446.6	242.2	35	11
SULT4A1	FLPSDLHNGDS**K**	18.5	446.6	539.3	35	11
SULT4A1	YFEFHGVR	23.8	352.2	311.1	35	13
SULT4A1	YFEFHGVR	23.8	352.2	331.2	35	13
SULT4A1	YFEFHGVR	23.8	352.2	446.2	35	13
SULT4A1	YFEFHGVR	23.8	352.2	372.7	35	13
SULT4A1	YFEFHGVR	23.8	352.2	308.2	35	13
SULT4A1	YFEFHGV**R**	23.8	355.5	341.2	35	13
SULT4A1	YFEFHGV**R**	23.8	355.5	451.2	35	13
TPMT	NQVLTLEEWQDK	33.7	751.9	1048.5	35	24
TPMT	NQVLTLEEWQDK	33.7	751.9	947.4	35	24
TPMT	NQVLTLEEWQDK	33.7	751.9	834.4	35	24
TPMT	NQVLTLEEWQDK	33.7	751.9	705.3	35	24
TPMT	NQVLTLEEWQDK	33.7	751.9	576.3	35	24
TPMT	NQVLTLEEWQD**K**	33.7	755.9	1056.5	35	24
TPMT	NQVLTLEEWQD**K**	33.7	755.9	955.5	35	24
TPMT	NQVLTLEEWQD**K**	33.7	755.9	842.4	35	24
TPMT	NQVLTLEEWQD**K**	33.7	755.9	713.3	35	24
TPMT	NQVLTLEEWQD**K**	33.7	755.9	584.3	35	24

TPMT	SWGID**C**LFEK	33.6	627.8	331.1	35	17
TPMT	SWGID**C**LFEK	33.6	627.8	444.2	35	17
TPMT	SWGID**C**LFEK	33.6	627.8	811.4	35	17
TPMT	SWGID**C**LFEK	33.6	627.8	536.3	35	17
TPMT	SWGID**C**LFEK	33.6	627.8	584.3	35	17
TPMT	SWGID**C**LFE**K**	33.6	631.8	331.1	35	17
TPMT	SWGID**C**LFE**K**	33.6	631.8	819.4	35	17
TPMT	TAFHQEQGHQLLK	15.7	768.9	582.8	35	30
TPMT	TAFHQEQGHQLLK	15.7	768.9	682.9	35	30
TPMT	TAFHQEQGHQLLK	15.7	768.9	609.3	35	30
TPMT	TAFHQEQGHQLL**K**	15.7	772.9	582.8	35	30
TPMT	TAFHQEQGHQLL**K**	15.7	772.9	613.3	35	30
UGT1A1	ESFVSLGHNVFENDSFLQR	34.9	742.4	650.4	35	22
UGT1A1	ESFVSLGHNVFENDSFLQR	34.9	742.4	303.2	35	22
UGT1A1	ESFVSLGHNVFENDSFLQR	34.9	742.4	881.9	35	22
UGT1A1	ESFVSLGHNVFENDSFLQ**R**	34.9	745.7	660.4	35	22
UGT1A1	ESFVSLGHNVFENDSFLQ**R**	34.9	745.7	886.9	35	22
UGT1A1	GHEIVVLAPDASLYIR	32.1	585.0	819.5	35	12
UGT1A1	GHEIVVLAPDASLYIR	32.1	585.0	410.2	35	12
UGT1A1	GHEIVVLAPDASLYIR	32.1	585.0	467.8	35	12
UGT1A1	GHEIVVLAPDASLYI**R**	32.1	588.3	410.2	35	12
UGT1A1	GHEIVVLAPDASLYI**R**	32.1	588.3	472.8	35	12
UGT1A10	TYSTSYTLEDQNR	19.1	789.4	1313.6	35	22
UGT1A10	TYSTSYTLEDQNR	19.1	789.4	1038.5	35	22
UGT1A10	TYSTSYTLEDQNR	19.1	789.4	875.4	35	22
UGT1A10	TYSTSYTLEDQNR	19.1	789.4	661.3	35	22
UGT1A10	TYSTSYTLEDQNR	19.1	789.4	532.2	35	22
UGT1A10	TYSTSYTLEDQN**R**	19.1	794.4	885.4	35	22
UGT1A10	TYSTSYTLEDQN**R**	19.1	794.4	671.3	35	22
UGT1A10	YFSLPSVVFTR	37.1	658.4	398.2	35	21
UGT1A10	YFSLPSVVFTR	37.1	658.4	1005.6	35	21
UGT1A10	YFSLPSVVFTR	37.1	658.4	805.5	35	21
UGT1A10	YFSLPSVVFTR	37.1	658.4	522.3	35	21
UGT1A10	YFSLPSVVFT**R**	37.1	663.4	398.2	35	21
UGT1A10	YFSLPSVVFT**R**	37.1	663.4	815.5	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	38.6	856.8	886.4	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	38.6	856.8	1084.5	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	38.6	856.8	1155.7	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	38.6	856.8	959.5	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLA**K**	38.6	859.5	1084.5	35	21
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLA**K**	38.6	859.5	1163.7	35	21
UGT1A4	FFTLTAYAVPWTQK	39.1	836.9	992.5	35	27
UGT1A4	FFTLTAYAVPWTQK	39.1	836.9	758.4	35	27
UGT1A4	FFTLTAYAVPWTQK	39.1	836.9	659.4	35	27
UGT1A4	FFTLTAYAVPWTQ**K**	39.1	840.9	1000.5	35	27
UGT1A4	FFTLTAYAVPWTQ**K**	39.1	840.9	667.4	35	27
UGT1A4	YLSIPAVFFWR	41.1	699.9	277.2	35	23
UGT1A4	YLSIPAVFFWR	41.1	699.9	364.2	35	23
UGT1A4	YLSIPAVFFWR	41.1	699.9	922.5	35	23
UGT1A4	YLSIPAVFFW**R**	41.1	704.9	277.2	35	23

UGT1A4	YLSIPAVFFW**R**	41.1	704.9	932.5	35	23
UGT1A5	EVSVVDLVSHASVWLFR	33.0	648.4	841.5	35	19
UGT1A5	EVSVVDLVSHASVWLFR	33.0	648.4	720.4	35	19
UGT1A5	EVSVVDLVSHASVWLFR	33.0	648.4	621.4	35	19
UGT1A5	EVSVVDLVSHASVWLF**R**	33.0	651.7	730.4	35	19
UGT1A5	EVSVVDLVSHASVWLF**R**	33.0	651.7	631.4	35	19
UGT1A5	YLSIPAVFFLR	42.2	663.4	277.2	35	18
UGT1A5	YLSIPAVFFLR	42.2	663.4	364.2	35	18
UGT1A5	YLSIPAVFFLR	42.2	663.4	239.1	35	18
UGT1A5	YLSIPAVFFLR	42.2	663.4	1049.6	35	18
UGT1A5	YLSIPAVFFLR	42.2	663.4	962.6	35	18
UGT1A5	YLSIPAVFFL**R**	42.2	668.4	277.2	35	18
UGT1A5	YLSIPAVFFL**R**	42.2	668.4	364.2	35	18
UGT1A6	DIVEVLSDR	28.8	523.3	718.4	35	17
UGT1A6	DIVEVLSDR	28.8	523.3	589.3	35	17
UGT1A6	DIVEVLSDR	28.8	523.3	490.3	35	17
UGT1A6	DIVEVLSD**R**	28.8	528.3	728.4	35	17
UGT1A6	DIVEVLSD**R**	28.8	528.3	500.3	35	17
UGT1A6	DVDIITLYQK	30.5	604.3	443.2	35	20
UGT1A6	DVDIITLYQK	30.5	604.3	765.5	35	20
UGT1A6	DVDIITLYQK	30.5	604.3	652.4	35	20
UGT1A6	DVDIITLYQ**K**	30.5	608.3	443.2	35	20
UGT1A6	DVDIITLYQ**K**	30.5	608.3	773.5	35	20
UGT1A6	SFLTAPQTEYR	25.0	656.8	965.5	35	17
UGT1A6	SFLTAPQTEYR	25.0	656.8	864.4	35	17
UGT1A6	SFLTAPQTEYR	25.0	656.8	793.4	35	17
UGT1A6	SFLTAPQTEY**R**	25.0	661.8	803.4	35	17
UGT1A6	SFLTAPQTEY**R**	25.0	661.8	348.2	35	17
UGT1A7	GIF**C**HYLEEGAQ**C**PAPLSYVPR	33.3	855.4	703.3	35	26
UGT1A7	GIF**C**HYLEEGAQ**C**PAPLSYVPR	33.3	855.4	999.6	35	26
UGT1A7	GIF**C**HYLEEGAQ**C**PAPLSYVPR	33.3	855.4	831.5	35	26
UGT1A7	GIF**C**HYLEEGAQ**C**PAPLSYVP**R**	33.3	858.7	1009.6	35	26
UGT1A7	GIF**C**HYLEEGAQ**C**PAPLSYVP**R**	33.3	858.7	841.5	35	26
UGT1A7	TYSTSYTLEDQDR	19.4	789.8	1314.6	35	22
UGT1A7	TYSTSYTLEDQDR	19.4	789.8	876.4	35	22
UGT1A7	TYSTSYTLEDQDR	19.4	789.8	775.4	35	22
UGT1A7	TYSTSYTLEDQDR	19.4	789.8	662.3	35	22
UGT1A7	TYSTSYTLEDQD**R**	19.4	794.9	886.4	35	22
UGT1A7	TYSTSYTLEDQD**R**	19.4	794.9	785.4	35	22
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVPR	29.2	830.1	601.3	35	21
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVPR	29.2	830.1	665.3	35	21
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVPR	29.2	830.1	999.6	35	21
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVPR	29.2	830.1	831.5	35	21
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVP**R**	29.2	833.4	1009.6	35	21
UGT1A8	GIA**C**HYLEEGAQ**C**PAPLSYVP**R**	29.2	833.4	841.5	35	21
UGT1A9	AFAHAQWK	17.0	320.2	444.2	35	7
UGT1A9	AFAHAQWK	17.0	320.2	370.7	35	7
UGT1A9	AFAHAQWK	17.0	320.2	335.2	35	7
UGT1A9	AFAHAQW**K**	17.0	322.8	448.2	35	7
UGT1A9	AFAHAQW**K**	17.0	322.8	374.7	35	7

UGT2A1	ANLIASALAQIPQK	31.4	719.4	1026.6	35	19
UGT2A1	ANLIASALAQIPQK	31.4	719.4	955.6	35	19
UGT2A1	ANLIASALAQIPQK	31.4	719.4	797.5	35	19
UGT2A1	ANLIASALAQIPQK	31.4	719.4	684.4	35	19
UGT2A1	ANLIASALAQIPQK	31.4	719.4	372.2	35	19
UGT2A1	ANLIASALAQIPQ**K**	31.4	723.4	805.5	35	19
UGT2A1	ANLIASALAQIPQ**K**	31.4	723.4	380.2	35	19
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK	36.5	705.1	226.2	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK	36.5	705.1	551.3	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK	36.5	705.1	438.2	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK	36.5	705.1	244.2	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHPK	36.5	705.1	559.8	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHP**K**	36.5	707.1	226.2	35	21
UGT2A1	KPATLGNNTQLFDWIPQNDLLGHP**K**	36.5	707.1	563.8	35	21
UGT2B10	GHEVTVLASSASILFDPNDSSTLK	35.2	830.1	1123.5	35	25
UGT2B10	GHEVTVLASSASILFDPNDSSTLK	35.2	830.1	976.5	35	25
UGT2B10	GHEVTVLASSASILFDPNDSSTLK	35.2	830.1	861.4	35	25
UGT2B10	GHEVTVLASSASILFDPNDSSTL**K**	35.2	832.8	984.5	35	25
UGT2B10	GHEVTVLASSASILFDPNDSSTL**K**	35.2	832.8	869.4	35	25
UGT2B11	FTPGYTIER	21.5	542.3	249.1	35	14
UGT2B11	FTPGYTIER	21.5	542.3	835.4	35	14
UGT2B11	FTPGYTIER	21.5	542.3	738.4	35	14
UGT2B11	FTPGYTIER	21.5	542.3	518.3	35	14
UGT2B11	FTPGYTIER	21.5	542.3	418.2	35	14
UGT2B11	FTPGYTIE**R**	21.5	547.3	249.1	35	14
UGT2B11	FTPGYTIE**R**	21.5	547.3	423.2	35	14
UGT2B11	GHEVTVLASSASILFDPNDASTLK	35.6	824.8	1107.5	35	25
UGT2B11	GHEVTVLASSASILFDPNDASTLK	35.6	824.8	960.5	35	25
UGT2B11	GHEVTVLASSASILFDPNDASTLK	35.6	824.8	845.4	35	25
UGT2B11	GHEVTVLASSASILFDPNDASTL**K**	35.6	827.4	1115.5	35	25
UGT2B11	GHEVTVLASSASILFDPNDASTL**K**	35.6	827.4	853.5	35	25
UGT2B15	GHEVTVLTSSASTLVNASK	26.5	634.3	419.2	35	14
UGT2B15	GHEVTVLTSSASTLVNASK	26.5	634.3	819.5	35	14
UGT2B15	GHEVTVLTSSASTLVNASK	26.5	634.3	631.4	35	14
UGT2B15	GHEVTVLTSSASTLVNASK	26.5	634.3	518.3	35	14
UGT2B15	GHEVTVLTSSASTLVNASK	26.5	634.3	234.1	35	14
UGT2B15	GHEVTVLTSSASTLVNAS**K**	26.5	637.0	827.5	35	14
UGT2B15	GHEVTVLTSSASTLVNAS**K**	26.5	637.0	526.3	35	14
UGT2B15	NYLEDSLLK	29.2	547.8	278.1	35	14
UGT2B15	NYLEDSLLK	29.2	547.8	817.5	35	14
UGT2B15	NYLEDSLLK	29.2	547.8	704.4	35	14
UGT2B15	NYLEDSLL**K**	29.2	551.8	278.1	35	14
UGT2B15	NYLEDSLL**K**	29.2	551.8	825.5	35	14
UGT2B15	SVINDPVYK	20.2	517.8	848.5	35	13
UGT2B15	SVINDPVYK	20.2	517.8	735.4	35	13
UGT2B15	SVINDPVYK	20.2	517.8	424.7	35	13
UGT2B15	SVINDPVY**K**	20.2	521.8	856.5	35	13
UGT2B15	SVINDPVY**K**	20.2	521.8	428.7	35	13
UGT2B17	FSVGYTVEK	19.5	515.3	235.1	35	17
UGT2B17	FSVGYTVEK	19.5	515.3	882.5	35	17

UGT2B17	FSVGYTVEK	19.5	515.3	795.4	35	17
UGT2B17	FSVGYTVEK	19.5	515.3	696.4	35	17
UGT2B17	FSVGYTVEK	19.5	515.3	639.3	35	17
UGT2B17	FSVGYTVE**K**	19.5	519.3	235.1	35	17
UGT2B17	FSVGYTVE**K**	19.5	519.3	704.4	35	17
UGT2B17	L**C**EDAVLNK	18.0	531.3	788.4	35	22
UGT2B17	L**C**EDAVLNK	18.0	531.3	659.4	35	22
UGT2B17	L**C**EDAVLNK	18.0	531.3	374.2	35	22
UGT2B17	L**C**EDAVLNK	18.0	531.3	261.2	35	22
UGT2B17	L**C**EDAVLN**K**	18.0	535.3	382.3	35	22
UGT2B17	L**C**EDAVLN**K**	18.0	535.3	269.2	35	22
UGT2B17	SVINDPIYK	22.6	524.8	862.5	35	13
UGT2B17	SVINDPIYK	22.6	524.8	749.4	35	13
UGT2B17	SVINDPIYK	22.6	524.8	431.7	35	13
UGT2B17	SVINDPIY**K**	22.6	528.8	870.5	35	13
UGT2B17	SVINDPIY**K**	22.6	528.8	435.7	35	13
UGT2B28	GHEVTVLASSASILFDPNDAFTLK	40.3	844.8	1167.6	35	22
UGT2B28	GHEVTVLASSASILFDPNDAFTLK	40.3	844.8	1020.5	35	22
UGT2B28	GHEVTVLASSASILFDPNDAFTLK	40.3	844.8	905.5	35	22
UGT2B28	GHEVTVLASSASILFDPNDAFTL**K**	40.3	847.4	1175.6	35	22
UGT2B28	GHEVTVLASSASILFDPNDAFTL**K**	40.3	847.4	913.5	35	22
UGT2B28	WIPQNDLLGLPK	33.8	697.4	300.2	35	18
UGT2B28	WIPQNDLLGLPK	33.8	697.4	1094.6	35	18
UGT2B28	WIPQNDLLGLPK	33.8	697.4	869.5	35	18
UGT2B28	WIPQNDLLGLPK	33.8	697.4	414.3	35	18
UGT2B28	WIPQNDLLGLPK	33.8	697.4	244.2	35	18
UGT2B28	WIPQNDLLGLPK	33.8	697.4	547.8	35	18
UGT2B28	WIPQNDLLGLP**K**	33.8	701.4	300.2	35	18
UGT2B28	WIPQNDLLGLP**K**	33.8	701.4	551.8	35	18
UGT2B4	ANVIASALAK	24.2	479.3	285.2	35	13
UGT2B4	ANVIASALAK	24.2	479.3	673.4	35	13
UGT2B4	ANVIASALAK	24.2	479.3	560.3	35	13
UGT2B4	ANVIASALA**K**	24.2	483.3	285.2	35	13
UGT2B4	ANVIASALA**K**	24.2	483.3	568.4	35	13
UGT2B4	FEVYPVSLTK	29.4	1182.6	644.4	35	19
UGT2B4	FEVYPVSLTK	29.4	591.8	906.5	35	19
UGT2B4	FEVYPVSLTK	29.4	591.8	807.5	35	19
UGT2B4	FEVYPVSLT**K**	29.4	595.8	914.5	35	19
UGT2B4	FEVYPVSLT**K**	29.4	595.8	815.5	35	19
UGT2B4	TILDELVQR	32.3	543.8	872.5	35	18
UGT2B4	TILDELVQR	32.3	543.8	759.4	35	18
UGT2B4	TILDELVQR	32.3	543.8	644.4	35	18
UGT2B4	TILDELVQ**R**	32.3	548.8	882.5	35	18
UGT2B4	TILDELVQ**R**	32.3	548.8	769.4	35	18
UGT2B7	ANVIASALAQIPQK	32.8	712.4	797.5	35	19
UGT2B7	ANVIASALAQIPQK	32.8	712.4	684.4	35	19
UGT2B7	ANVIASALAQIPQK	32.8	712.4	372.2	35	19
UGT2B7	ANVIASALAQIPQ**K**	32.8	716.4	692.4	35	19
UGT2B7	ANVIASALAQIPQ**K**	32.8	716.4	380.2	35	19
UGT2B7	IEIYPTSLTK	26.4	582.8	922.5	35	19

UGT2B7	IEIYPTSLTK	26.4	582.8	809.4	35	19
UGT2B7	IEIYPTSLTK	26.4	582.8	646.4	35	19
UGT2B7	IEIYPTSLT**K**	26.4	586.8	817.5	35	19
UGT2B7	IEIYPTSLT**K**	26.4	586.8	654.4	35	19
UGT2B7	TILDELIQR	29.0	550.8	886.5	35	17
UGT2B7	TILDELIQR	29.0	550.8	773.4	35	17
UGT2B7	TILDELIQR	29.0	550.8	658.4	35	17
UGT2B7	TILDELIQR	29.0	550.8	416.3	35	17
UGT2B7	TILDELIQ**R**	29.0	555.8	896.5	35	17
UGT2B7	TILDELIQ**R**	29.0	555.8	783.4	35	17
UGT2B7	TILDELIQ**R**	29.0	555.8	668.4	35	17
UGT2B7	TILDELIQ**R**	29.0	555.8	426.3	35	17

R, **K** and **C** correspond to heavy arginine (R[13C6, 15N4]), heavy lysine (K[13C6, 15N2]) and carbamidomethylated cysteine (+57 Da).

Supplementary Table 2Sc: List of ADME gene products, surrogate peptides and LC-MRM parameters for AB Sciex 6500 triple quadrupole instrument

Protein	Peptide	RT	Parent	Product	DP	CE
ADH1A	GAILGGFK	12.4	381.7	521.3	59	20
ADH1A	GAILGGFK	12.4	381.7	408.2	59	20
ADH1A	GAILGGFK	12.4	762.5	408.2	87	20
ADH1A	GAILGGF**K**	12.4	385.7	529.3	59	20
ADH1A	GAILGGF**K**	12.4	385.7	416.2	59	20
ADH1A	KPIHHFLGISTFSQYTVVDENAVAK	14.0	934.5	797.4	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVAK	14.0	934.5	1045.6	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVAK	14.0	934.5	845.4	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVAK	14.0	934.5	746.4	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVA**K**	14.0	937.2	797.4	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVA**K**	14.0	937.2	1053.6	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVA**K**	14.0	937.2	853.5	99	41
ADH1A	KPIHHFLGISTFSQYTVVDENAVA**K**	14.0	937.2	754.4	99	41
ADH1A	NDVSNPQGTLQDGTSR	9.0	844.9	1159.6	93	39
ADH1A	NDVSNPQGTLQDGTSR	9.0	844.9	535.2	93	39
ADH1A	NDVSNPQGTLQDGTSR	9.0	844.9	420.2	93	39
ADH1A	NDVSNPQGTLQDGTS**R**	9.0	849.9	1169.6	93	39
ADH1A	NDVSNPQGTLQDGTS**R**	9.0	849.9	430.2	93	39
ADH1B	AAVLWEVK	13.7	458.3	242.2	65	18
ADH1B	AAVLWEVK	13.7	458.3	674.4	65	18
ADH1B	AAVLWEVK	13.7	458.3	561.3	65	18
ADH1B	AAVLWEV**K**	13.7	462.3	242.2	65	18
ADH1B	AAVLWEV**K**	13.7	462.3	569.3	65	18
ADH1C	GAIFGGFK	13.5	398.7	668.4	60	20
ADH1C	GAIFGGFK	13.5	398.7	555.3	60	20
ADH1C	GAIFGGFK	13.5	398.7	408.2	60	20
ADH1C	GAIFGGF**K**	13.5	402.7	563.3	60	20
ADH1C	GAIFGGF**K**	13.5	402.7	416.2	60	20
ADH1C	INEGFDLLR	14.8	538.8	228.1	70	21
ADH1C	INEGFDLLR	14.8	538.8	849.4	70	21
ADH1C	INEGFDLLR	14.8	538.8	720.4	70	21
ADH1C	INEGFDLL**R**	14.8	543.8	228.1	70	21
ADH1C	INEGFDLL**R**	14.8	543.8	859.5	70	21
ADH1C	INEGFDLL**R**	14.8	543.8	730.4	70	21
ADH1C	V**C**LIG**C**GFSTGYGSAVK	14.5	888.4	1290.6	96	39
ADH1C	V**C**LIG**C**GFSTGYGSAVK	14.5	888.4	869.4	96	39
ADH1C	V**C**LIG**C**GFSTGYGSAVK	14.5	888.4	758.9	96	39
ADH1C	V**C**LIG**C**GFSTGYGSAV**K**	14.5	892.4	1298.6	96	39
ADH1C	V**C**LIG**C**GFSTGYGSAV**K**	14.5	892.4	877.5	96	39
ALDH1A1	ANNTFYGLSAGVFTK	15.9	795.4	1042.6	89	37
ALDH1A1	ANNTFYGLSAGVFTK	15.9	795.4	879.5	89	37
ALDH1A1	ANNTFYGLSAGVFTK	15.9	795.4	395.2	89	37
ALDH1A1	ANNTFYGLSAGVFT**K**	15.9	799.4	887.5	89	37
ALDH1A1	ANNTFYGLSAGVFT**K**	15.9	799.4	403.2	89	37
ALDH1A1	IFINNEWHDSVSGK	12.4	549.3	291.2	71	23
ALDH1A1	IFINNEWHDSVSGK	12.4	549.3	693.3	71	23
ALDH1A1	IFINNEWHDSVSGK	12.4	549.3	636.8	71	23

ALDH1A1	IFINNEWHDSVSG**K**	12.4	551.9	697.3	71	23
ALDH1A1	IFINNEWHDSVSG**K**	12.4	551.9	640.8	71	23
ALDH1A1	IFVEESIYDEFVR	17.9	823.4	261.2	91	38
ALDH1A1	IFVEESIYDEFVR	17.9	823.4	360.2	91	38
ALDH1A1	IFVEESIYDEFVR	17.9	823.4	665.3	91	38
ALDH1A1	IFVEESIYDEFV**R**	17.9	828.4	261.2	91	38
ALDH1A1	IFVEESIYDEFV**R**	17.9	828.4	360.2	91	38
ALDH1A3	EQI**C**EVEEGDKPDVDK	11.0	630.6	566.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVDK	11.0	630.6	680.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVDK	11.0	630.6	760.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVDK	11.0	630.6	501.7	77	32
ALDH1A3	EQI**C**EVEEGDKPDVD**K**	11.0	633.3	570.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVD**K**	11.0	633.3	684.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVD**K**	11.0	633.3	764.3	77	32
ALDH1A3	EQI**C**EVEEGDKPDVD**K**	11.0	633.3	505.7	77	32
ALDH1A3	LLHQLADLVER	16.0	436.3	304.2	63	21
ALDH1A3	LLHQLADLVER	16.0	436.3	403.2	63	21
ALDH1A3	LLHQLADLVER	16.0	436.3	631.3	63	21
ALDH1A3	LLHQLADLVER	16.0	436.3	304.2	63	21
ALDH1A3	LLHQLADLVER	16.0	436.3	403.2	63	21
ALDH1A3	LLHQLADLVER	16.0	436.3	631.3	63	21
ALDH1A3	LLHQLADLVE**R**	16.0	439.6	314.2	63	21
ALDH1A3	LLHQLADLVE**R**	16.0	439.6	413.2	63	21
ALDH1A3	LLHQLADLVE**R**	16.0	439.6	314.2	63	21
ALDH1A3	LLHQLADLVE**R**	16.0	439.6	413.2	63	21
AOX1	GLHGPLTLNSPLTPEK	13.6	837.5	1301.7	92	42
AOX1	GLHGPLTLNSPLTPEK	13.6	837.5	1366.8	92	42
AOX1	GLHGPLTLNSPLTPEK	13.6	837.5	1309.7	92	42
AOX1	GLHGPLTLNSPLTPEK	13.6	837.5	373.2	92	42
AOX1	GLHGPLTLNSPLTPE**K**	13.6	841.5	1301.7	92	42
AOX1	GLHGPLTLNSPLTPE**K**	13.6	841.5	1374.8	92	42
AOX1	GLHGPLTLNSPLTPE**K**	13.6	841.5	1317.8	92	42
AOX1	GLHGPLTLNSPLTPE**K**	13.6	841.5	381.2	92	42
AOX1	LILNEVSLLGSAPGGK	16.4	784.5	886.5	88	42
AOX1	LILNEVSLLGSAPGGK	16.4	784.5	573.3	88	42
AOX1	LILNEVSLLGSAPGGK	16.4	784.5	358.2	88	42
AOX1	LILNEVSLLGSAPGG**K**	16.4	788.5	581.3	88	42
AOX1	LILNEVSLLGSAPGG**K**	16.4	788.5	366.2	88	42
CES1	AGQLLSELFTNR	16.8	674.9	257.1	80	33
CES1	AGQLLSELFTNR	16.8	674.9	370.2	80	33
CES1	AGQLLSELFTNR	16.8	674.9	866.4	80	33
CES1	AGQLLSELFTN**R**	16.8	679.9	257.1	80	33
CES1	AGQLLSELFTN**R**	16.8	679.9	370.2	80	33
CES1	AISESGVALTSVLVK	15.3	737.4	830.5	85	28
CES1	AISESGVALTSVLVK	15.3	737.4	759.5	85	28
CES1	AISESGVALTSVLVK	15.3	737.4	646.4	85	28
CES1	AISESGVALTSVLV**K**	15.3	741.4	838.5	85	28
CES1	AISESGVALTSVLV**K**	15.3	741.4	767.5	85	28
CES1	EGYLQIGANTQAAQK	11.4	796.4	350.1	89	31
CES1	EGYLQIGANTQAAQK	11.4	796.4	888.5	89	31

CES1	EGYLQIGANTQAAQK	11.4	796.4	417.2	89	31
CES1	EGYLQIGANTQAAQ**K**	11.4	800.4	350.1	89	31
CES1	EGYLQIGANTQAAQ**K**	11.4	800.4	896.5	89	31
CES2	ADHGDELPFVFR	15.0	701.8	1079.6	82	39
CES2	ADHGDELPFVFR	15.0	701.8	665.4	82	39
CES2	ADHGDELPFVFR	15.0	701.8	322.2	82	39
CES2	ADHGDELPFVF**R**	15.0	706.8	675.4	82	39
CES2	ADHGDELPFVF**R**	15.0	706.8	332.2	82	39
CES2	TTHTGQVLGSLVHVK	11.5	788.9	739.4	89	37
CES2	TTHTGQVLGSLVHVK	11.5	788.9	383.2	89	37
CES2	TTHTGQVLGSLVHVK	11.5	788.9	687.9	89	37
CES2	TTHTGQVLGSLVHV**K**	11.5	793.0	391.3	89	37
CES2	TTHTGQVLGSLVHV**K**	11.5	793.0	691.9	89	37
CP2C8	GLGIISSNGK	10.7	473.3	492.2	80	22
CP2C8	GLGIISSNGK	10.7	473.3	605.3	80	22
CP2C8	GLGIISSNGK	10.7	473.3	628.4	80	22
CP2C8	GLGIISSNGK	10.7	473.3	775.4	80	22
CP2C8	GLGIISSNG**K**	10.7	477.3	500.3	80	22
CP2C8	GLGIISSNG**K**	10.7	477.3	613.3	80	22
CYP19A1	GIIFNNNPELWK	10.0	722.9	333.2	80	30
CYP19A1	GIIFNNNPELWK	10.0	722.9	672.4	80	30
CYP19A1	GIIFNNNPELWK	10.0	722.9	1014.5	80	30
CYP19A1	GIIFNNNPELW**K**	10.0	726.9	680.4	80	30
CYP19A1	GIIFNNNPELW**K**	10.0	726.9	1169.6	80	30
CYP1A1	FLTPDGAIDK	11.7	538.8	261.2	80	22
CYP1A1	FLTPDGAIDK	11.7	538.8	715.4	80	22
CYP1A1	FLTPDGAIDK	11.7	538.8	816.4	80	22
CYP1A1	FLTPDGAID**K**	11.7	542.8	261.2	80	22
CYP1A1	FLTPDGAID**K**	11.7	542.8	723.4	80	22
CYP1A2	IGSTPVLVLSR	13.5	571.4	783.5	73	29
CYP1A2	IGSTPVLVLSR	13.5	571.4	375.2	73	29
CYP1A2	IGSTPVLVLSR	13.5	571.4	392.3	73	29
CYP1A2	IGSTPVLVLS**R**	13.5	576.4	793.5	73	29
CYP1A2	IGSTPVLVLS**R**	13.5	576.4	397.3	73	29
CYP1A2	NTHEFVETASSGNPLDFFPILR	19.2	831.1	1117.6	80	30
CYP1A2	NTHEFVETASSGNPLDFFPILR	19.2	831.1	645.4	80	30
CYP1A2	NTHEFVETASSGNPLDFFPILR	19.2	831.1	498.3	80	30
CYP1A2	NTHEFVETASSGNPLDFFPIL**R**	19.2	834.4	655.4	80	30
CYP1A2	NTHEFVETASSGNPLDFFPIL**R**	19.2	834.4	508.3	80	30
CYP1A2	YLPNPALQ**R**	10.8	541.3	594.4	80	24
CYP1A2	YLPNPALQ**R**	10.8	541.3	805.5	80	24
CYP1A2	YLPNPALQR	10.8	536.3	277.2	80	19
CYP1A2	YLPNPALQR	10.8	536.3	303.2	80	19
CYP1A2	YLPNPALQR	10.8	536.3	584.4	80	19
CYP1A2	YLPNPALQR	10.8	536.3	795.5	80	19
CYP2A6	DPSFFSNPQDFNPQHFLNEK	14.5	1204.6	1012.5	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNEK	14.5	1204.6	787.4	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNEK	14.5	1204.6	650.4	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNEK	14.5	1204.6	1147.0	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	14.5	1208.6	1020.5	119	45

CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	14.5	1208.6	795.4	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	14.5	1208.6	658.4	119	45
CYP2A6	DPSFFSNPQDFNPQHFLNE**K**	14.5	1208.6	1151.0	119	45
CYP2A6	GTGGANIDPTFFLS	16.2	776.9	982.5	88	30
CYP2A6	GTGGANIDPTFFLS	16.2	776.9	867.5	88	30
CYP2A6	GTGGANIDPTFFLS	16.2	776.9	522.3	88	30
CYP2A6	GTGGANIDPTFFLS**K**	16.2	781.9	992.5	88	30
CYP2A6	GTGGANIDPTFFLS**K**	16.2	781.9	877.5	88	30
CYP2A6	GTGGANIDPTFFLSR	16.1	776.9	982.5	75	32
CYP2A6	GTGGANIDPTFFLSR	16.1	776.9	867.5	75	32
CYP2A6	GTGGANIDPTFFLSR	16.1	776.9	522.3	75	32
CYP2A6	GTGGANIDPTFFLS**R**	16.1	781.9	992.5	75	32
CYP2A6	GTGGANIDPTFFLS**R**	16.1	781.9	877.5	75	32
CYP2B6	TEAFIPFSLGK	16.6	605.3	648.4	80	22
CYP2B6	TEAFIPFSLGK	16.6	605.3	908.5	80	22
CYP2B6	TEAFIPFSLGK	16.6	605.3	979.6	80	22
CYP2B6	TEAFIPFSLG**K**	16.6	609.3	656.4	80	22
CYP2B6	TEAFIPFSLG**K**	16.6	609.3	987.6	80	22
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVPR	14.8	830.1	665.3	80	30
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVPR	14.8	830.1	999.6	80	30
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVPR	14.8	830.1	831.5	80	30
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVPR	14.8	830.1	601.3	80	30
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVP**R**	14.8	833.4	1009.6	80	30
CYP2B6	GIA**C**HYLEEGAQ**C**PAPLSYVP**R**	14.8	833.4	841.5	80	30
CYP2C18	DIDITPIANAFGR	16.6	701.9	1174.6	82	34
CYP2C18	DIDITPIANAFGR	16.6	701.9	946.5	82	34
CYP2C18	DIDITPIANAFGR	16.6	701.9	845.5	82	34
CYP2C18	DIDITPIANAFGR	16.6	701.9	635.3	82	34
CYP2C18	DIDITPIANAFG**R**	16.6	706.9	1184.6	82	34
CYP2C18	DIDITPIANAFG**R**	16.6	706.9	956.5	82	34
CYP2C18	DIDITPIANAFG**R**	16.6	706.9	855.5	82	34
CYP2C18	DIDITPIANAFG**R**	16.6	706.9	645.3	82	34
CYP2C19	GTTILTSLTSVLHDNK	17.0	567.3	513.2	73	22
CYP2C19	GTTILTSLTSVLHDNK	17.0	567.3	664.4	73	22
CYP2C19	GTTILTSLTSVLHDNK	17.0	567.3	607.8	73	22
CYP2C19	GTTILTSLTSVLHDN**K**	17.0	570.0	521.3	73	22
CYP2C19	GTTILTSLTSVLHDN**K**	17.0	570.0	668.4	73	22
CYP2C19	HFLDEGGNFK	11.0	388.5	522.3	59	12
CYP2C19	HFLDEGGNFK	11.0	388.5	465.2	59	12
CYP2C19	HFLDEGGNFK	11.0	388.5	261.6	59	12
CYP2C19	HFLDEGGNF**K**	11.0	391.2	530.3	59	12
CYP2C19	HFLDEGGNF**K**	11.0	391.2	265.6	59	12
CYP2C8	YSDLVPTGVPHAVTTDTK	12.2	634.3	578.3	77	27
CYP2C8	YSDLVPTGVPHAVTTDTK	12.2	634.3	711.9	77	27
CYP2C8	YSDLVPTGVPHAVTTDTK	12.2	634.3	662.3	77	27
CYP2C8	YSDLVPTGVPHAVTTDT**K**	12.2	637.0	578.3	77	27
CYP2C8	YSDLVPTGVPHAVTTDT**K**	12.2	637.0	666.4	77	27
CYP2C9	GIFPLAER	14.3	451.8	585.3	64	17
CYP2C9	GIFPLAER	14.3	451.8	366.7	64	17
CYP2C9	GIFPLAER	14.3	451.8	293.2	64	17

CYP2C9	GIFPLAE**R**	14.3	456.8	595.3	64	17
CYP2C9	GIFPLAE**R**	14.3	456.8	371.7	64	17
CYP2C9	LPPGPTPLPVIGNILQIGIK	21.0	1019.1	773.5	105	46
CYP2C9	LPPGPTPLPVIGNILQIGIK	21.0	1019.1	1068.7	105	46
CYP2C9	LPPGPTPLPVIGNILQIGIK	21.0	1019.1	962.6	105	46
CYP2C9	LPPGPTPLPVIGNILQIGIK	21.0	1019.1	914.1	105	46
CYP2C9	LPPGPTPLPVIGNILQIGI**K**	21.0	1023.1	1076.7	105	46
CYP2C9	LPPGPTPLPVIGNILQIGI**K**	21.0	1023.1	918.1	105	46
CYP2C9	LPPGPTPLPVIGNILQIGI**K**	21.0	1023.1	773.5	105	46
CYP2C9	LPPGPTPLPVIGNILQIGI**K**	21.0	1023.1	966.6	105	46
CYP2D6	AVSNVIASLT**C**GR	15.0	674.4	471.3	80	26
CYP2D6	AVSNVIASLT**C**GR	15.0	674.4	877.5	80	26
CYP2D6	AVSNVIASLT**C**GR	15.0	674.4	764.4	80	26
CYP2D6	AVSNVIASLT**C**GR	15.0	674.4	693.3	80	26
CYP2D6	AVSNVIASLT**C**G**R**	15.0	679.4	471.3	80	26
CYP2D6	AVSNVIASLT**C**G**R**	15.0	679.4	887.5	80	26
CYP2D6	AVSNVIASLT**C**G**R**	15.0	679.4	774.4	80	26
CYP2D6	AVSNVIASLT**C**G**R**	15.0	679.4	703.3	80	26
CYP2D6	VQQEIDDVIGQVR	13.3	749.9	1271.7	86	30
CYP2D6	VQQEIDDVIGQVR	13.3	749.9	572.4	86	30
CYP2D6	VQQEIDDVIGQVR	13.3	749.9	459.3	86	30
CYP2D6	VQQEIDDVIGQV**R**	13.3	754.9	582.4	86	30
CYP2D6	VQQEIDDVIGQV**R**	13.3	754.9	469.3	86	30
CYP2E1	FGPVFTLYVGSQR	17.0	735.9	709.4	85	35
CYP2E1	FGPVFTLYVGSQR	17.0	735.9	447.2	85	35
CYP2E1	FGPVFTLYVGSQR	17.0	735.9	633.8	85	35
CYP2E1	FGPVFTLYVGSQ**R**	17.0	740.9	457.2	85	35
CYP2E1	FGPVFTLYVGSQ**R**	17.0	740.9	638.8	85	35
CYP2E1	FITLVPSNLPHEATR	14.1	848.0	574.4	94	40
CYP2E1	FITLVPSNLPHEATR	14.1	848.0	1121.6	94	40
CYP2E1	FITLVPSNLPHEATR	14.1	848.0	561.3	94	40
CYP2E1	FITLVPSNLPHEAT**R**	14.1	853.0	1131.6	94	40
CYP2E1	FITLVPSNLPHEAT**R**	14.1	853.0	566.3	94	40
CYP2J2	LLDEVTYLEASK	14.2	690.9	1154.6	82	34
CYP2J2	LLDEVTYLEASK	14.2	690.9	910.5	82	34
CYP2J2	LLDEVTYLEASK	14.2	690.9	811.4	82	34
CYP2J2	LLDEVTYLEASK	14.2	690.9	710.4	82	34
CYP2J2	LLDEVTYLEASK	14.2	690.9	434.2	82	34
CYP2J2	LLDEVTYLEAS**K**	14.2	694.9	1162.6	82	34
CYP2J2	LLDEVTYLEAS**K**	14.2	694.9	819.4	82	34
CYP2J2	VIGQGQQPSTAAR	8.0	656.9	915.5	79	33
CYP2J2	VIGQGQQPSTAAR	8.0	656.9	602.3	79	33
CYP2J2	VIGQGQQPSTAAR	8.0	656.9	550.8	79	33
CYP2J2	VIGQGQQPSTAA**R**	8.0	661.9	612.3	79	33
CYP2J2	VIGQGQQPSTAA**R**	8.0	661.9	612.3	79	33
CYP3A4	EVTNFLR	12.0	439.7	229.1	63	25
CYP3A4	EVTNFLR	12.0	439.7	330.2	63	25
CYP3A4	EVTNFLR	12.0	439.7	650.4	63	25
CYP3A4	EVTNFL**R**	12.0	444.7	229.1	63	25
CYP3A4	EVTNFL**R**	12.0	444.7	660.4	63	25

CYP3A4	LGIPGPTPLPFLGNILSYHK	20.4	712.1	284.2	83	34
CYP3A4	LGIPGPTPLPFLGNILSYHK	20.4	712.1	846.5	83	34
CYP3A4	LGIPGPTPLPFLGNILSYHK	20.4	712.1	1044.6	83	34
CYP3A4	LGIPGPTPLPFLGNILSYHK	20.4	712.1	931.5	83	34
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	20.4	714.7	284.2	83	34
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	20.4	714.7	846.5	83	34
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	20.4	714.7	1052.6	83	34
CYP3A4	LGIPGPTPLPFLGNILSYH**K**	20.4	714.7	939.5	83	34
CYP3A43	TLLSPAFTSVK	19.0	582.3	215.1	74	30
CYP3A43	TLLSPAFTSVK	19.0	582.3	328.2	74	30
CYP3A43	TLLSPAFTSVK	19.0	582.3	949.5	74	30
CYP3A43	TLLSPAFTSVK	19.0	582.3	836.5	74	30
CYP3A43	TLLSPAFTSVK	19.0	582.3	749.4	73	30
CYP3A5	DSIDPYIYTPFGTGPR	15.3	899.9	1368.7	97	34
CYP3A5	DSIDPYIYTPFGTGPR	15.3	899.9	995.5	97	34
CYP3A5	DSIDPYIYTPFGTGPR	15.3	899.9	832.4	97	34
CYP3A5	DSIDPYIYTPFGTGPR	15.3	899.9	731.4	97	34
CYP3A5	DSIDPYIYTPFGTGP**R**	15.3	904.9	1378.7	97	34
CYP3A5	DSIDPYIYTPFGTGP**R**	15.3	904.9	1005.5	97	34
CYP3A5	DSIDPYIYTPFGTGP**R**	15.3	904.9	842.4	97	34
CYP3A5	DSIDPYIYTPFGTGP**R**	15.3	904.9	741.4	97	34
CYP3A5	DTINFLSK	13.1	469.3	217.1	80	17
CYP3A5	DTINFLSK	13.1	469.3	234.2	80	17
CYP3A5	DTINFLSK	13.1	469.3	347.2	80	17
CYP3A5	DTINFLS**K**	13.1	473.3	616.4	80	17
CYP3A5	DTINFLS**K**	13.1	473.3	729.4	80	17
CYP3A5	DVEINGVFIPK	14.8	615.8	1016.6	76	24
CYP3A5	DVEINGVFIPK	14.8	615.8	887.5	76	24
CYP3A5	DVEINGVFIPK	14.8	615.8	774.5	76	24
CYP3A5	DVEINGVFIPK	14.8	615.8	504.3	76	24
CYP3A5	DVEINGVFIPK	14.8	615.8	244.2	76	24
CYP3A5	DVEINGVFIP**K**	14.8	619.8	782.5	76	24
CYP3A5	DVEINGVFIP**K**	14.8	619.8	252.2	76	24
CYP3A5	LDTQGLLQPEKPIVLK	16.5	896.5	741.4	97	34
CYP3A5	LDTQGLLQPEKPIVLK	16.5	896.5	869.5	97	34
CYP3A5	LDTQGLLQPEKPIVLK	16.5	896.5	1334.8	97	34
CYP3A5	LDTQGLLQPEKPIVLK	16.5	896.5	923.6	97	34
CYP3A5	LDTQGLLQPEKPIVLK	16.5	896.5	569.4	97	34
CYP3A5	LDTQGLLQPEKPIVL**K**	15.7	900.5	931.6	97	34
CYP3A5	LDTQGLLQPEKPIVL**K**	15.7	900.5	577.4	97	34
CYP3A7	FNPLDPFVLSIK	19.4	695.4	262.1	82	30
CYP3A7	FNPLDPFVLSIK	19.4	695.4	803.5	82	30
CYP3A7	FNPLDPFVLSIK	19.4	695.4	347.2	82	30
CYP3A7	FNPLDPFVLSI**K**	19.4	699.4	262.1	82	30
CYP3A7	FNPLDPFVLSI**K**	19.4	699.4	568.8	82	30
CYP3A7	LGIPGPTPLPFLGNALSFR	20.6	984.1	1331.7	103	44
CYP3A7	LGIPGPTPLPFLGNALSFR	20.6	984.1	1121.6	103	44
CYP3A7	LGIPGPTPLPFLGNALSFR	20.6	984.1	764.4	103	44
CYP3A7	LGIPGPTPLPFLGNALSFR	20.6	984.1	409.2	103	44
CYP3A7	LGIPGPTPLPFLGNALSF**R**	20.6	989.1	1131.6	103	44

CYP3A7	LGIPGPTPLPFLGNALSF**R**	20.6	989.1	419.2	103	44
DPYD	ADVVISAFGSVLSDPK	16.8	802.9	1220.7	90	38
DPYD	ADVVISAFGSVLSDPK	16.8	802.9	1107.6	90	38
DPYD	ADVVISAFGSVLSDPK	16.8	802.9	1020.5	90	38
DPYD	ADVVISAFGSVLSDPK	16.8	802.9	949.5	90	38
DPYD	ADVVISAFGSVLSDPK	16.8	802.9	244.2	90	38
DPYD	ADVVISAFGSVLSDP**K**	16.8	806.9	1228.7	90	38
DPYD	ADVVISAFGSVLSDP**K**	16.8	806.9	1115.6	90	38
DPYD	ADVVISAFGSVLSDP**K**	16.8	806.9	1028.6	90	38
DPYD	ADVVISAFGSVLSDP**K**	16.8	806.9	957.5	90	38
DPYD	ADVVISAFGSVLSDP**K**	16.8	806.9	252.2	90	38
DPYD	DSADIESILALNPR	16.3	757.4	1012.6	86	36
DPYD	DSADIESILALNPR	16.3	757.4	683.4	86	36
DPYD	DSADIESILALNPR	16.3	757.4	570.3	86	36
DPYD	DSADIESILALNPR	16.3	757.4	386.2	86	36
DPYD	DSADIESILALNPR	16.3	757.4	272.2	86	36
DPYD	DSADIESILALNP**R**	16.3	762.4	1022.6	86	36
DPYD	DSADIESILALNP**R**	16.3	762.4	693.4	86	36
DPYD	DSADIESILALNP**R**	16.3	762.4	580.3	86	36
DPYD	DSADIESILALNP**R**	16.3	762.4	396.2	86	36
DPYD	DSADIESILALNP**R**	16.3	762.4	282.2	86	36
DPYD	LTPNVTDIVSIAR	16.0	699.9	874.5	82	28
DPYD	LTPNVTDIVSIAR	16.0	699.9	446.3	82	28
DPYD	LTPNVTDIVSIAR	16.0	699.9	592.8	82	28
DPYD	LTPNVTDIVSIA**R**	16.0	704.9	884.5	82	28
DPYD	LTPNVTDIVSIA**R**	16.0	704.9	597.8	82	28
EPHX1	VETSDEEIHDLHQR	8.7	427.7	689.8	62	25
EPHX1	VETSDEEIHDLHQR	8.7	427.7	459.7	62	25
EPHX1	VETSDEEIHDLHQR	8.7	427.7	403.2	62	25
EPHX1	VETSDEEIHDLHQ**R**	8.7	430.2	651.3	62	25
EPHX1	VETSDEEIHDLHQ**R**	8.7	430.2	408.2	62	25
EPHX1	YLEDGGLER	10.0	526.3	277.2	70	28
EPHX1	YLEDGGLER	10.0	526.3	775.4	70	28
EPHX1	YLEDGGLER	10.0	526.3	646.3	70	28
EPHX1	YLEDGGLE**R**	10.0	531.3	277.2	70	28
EPHX1	YLEDGGLE**R**	10.0	531.3	785.4	70	28
EPHX2	ASPSEVVFLDDIGANLKPAR	18.0	700.4	764.9	82	31
EPHX2	ASPSEVVFLDDIGANLKPAR	18.0	700.4	715.4	82	31
EPHX2	ASPSEVVFLDDIGANLKPAR	18.0	700.4	641.9	82	31
EPHX2	ASPSEVVFLDDIGANLKPA**R**	18.0	703.7	769.9	82	31
EPHX2	ASPSEVVFLDDIGANLKPA**R**	18.0	703.7	720.4	82	31
EPHX2	GLLNDAFQK	13.2	503.3	835.4	68	23
EPHX2	GLLNDAFQK	13.2	503.3	722.3	68	23
EPHX2	GLLNDAFQK	13.2	503.3	418.2	68	23
EPHX2	GLLNDAFQ**K**	13.2	507.3	730.4	68	23
EPHX2	GLLNDAFQ**K**	13.2	507.3	422.2	68	23
EPHX2	V**C**EAGGLFVNSPEEPSLSR	17.5	1024.5	1115.5	106	50
EPHX2	V**C**EAGGLFVNSPEEPSLSR	17.5	1024.5	914.5	106	50
EPHX2	V**C**EAGGLFVNSPEEPSLSR	17.5	1024.5	559.3	106	50
EPHX2	V**C**EAGGLFVNSPEEPSLS**R**	17.5	1029.5	924.5	106	50

EPHX2	V**C**EAGGLFVNSPEEPSLS**R**	17.5	1029.5	569.3	106	50
FMO1	SDDLGGLWR	14.2	509.8	203.1	68	27
FMO1	SDDLGGLWR	14.2	509.8	318.1	68	27
FMO1	SDDLGGLWR	14.2	509.8	588.3	68	27
FMO1	SDDLGGLW**R**	14.2	514.8	318.1	68	27
FMO1	SDDLGGLW**R**	14.2	514.8	598.3	68	27
FMO1	VEDGQASLYK	9.1	555.3	229.1	72	24
FMO1	VEDGQASLYK	9.1	555.3	881.4	72	24
FMO1	VEDGQASLYK	9.1	555.3	310.2	72	24
FMO1	VEDGQASLY**K**	9.1	559.3	229.1	72	24
FMO1	VEDGQASLY**K**	9.1	559.3	889.5	72	24
FMO3	LVGPGQWPGAR	12.3	569.3	400.2	73	25
FMO3	LVGPGQWPGAR	12.3	569.3	463.2	73	25
FMO3	LVGPGQWPGAR	12.3	569.3	434.7	73	25
FMO3	LVGPGQWPGA**R**	12.3	574.3	410.2	73	25
FMO3	LVGPGQWPGA**R**	12.3	574.3	468.2	73	25
FMO3	NNLPTAISDWLYVK	18.7	817.4	342.2	91	31
FMO3	NNLPTAISDWLYVK	18.7	817.4	1292.7	91	31
FMO3	NNLPTAISDWLYVK	18.7	817.4	646.8	91	31
FMO3	NNLPTAISDWLYV**K**	18.7	821.4	342.2	91	31
FMO3	NNLPTAISDWLYV**K**	18.7	821.4	1300.7	91	31
FMO3	VAIIGAGVSGLASIR	15.6	692.4	987.6	82	34
FMO3	VAIIGAGVSGLASIR	15.6	692.4	703.4	82	34
FMO3	VAIIGAGVSGLASIR	15.6	692.4	550.8	82	34
FMO3	VAIIGAGVSGLASI**R**	15.6	697.4	997.6	82	34
FMO3	VAIIGAGVSGLASI**R**	15.6	697.4	713.4	82	34
GSTA1	LHYFNAR	9.4	460.7	251.2	65	22
GSTA1	LHYFNAR	9.4	460.7	670.3	65	22
GSTA1	LHYFNAR	9.4	460.7	404.2	65	22
GSTA1	LHYFNA**R**	9.4	465.7	251.2	65	22
GSTA1	LHYFNA**R**	9.4	465.7	680.3	65	22
GSTA2	LALIQEK	10.9	407.8	701.4	61	19
GSTA2	LALIQEK	10.9	407.8	630.4	61	19
GSTA2	LALIQEK	10.9	407.8	517.3	61	19
GSTA2	LALIQE**K**	10.9	411.8	709.4	61	19
GSTA2	LALIQE**K**	10.9	411.8	638.4	61	19
GSTA2	LHYSNIR	8.4	451.7	652.3	64	22
GSTA2	LHYSNIR	8.4	451.7	489.3	64	22
GSTA2	LHYSNIR	8.4	451.7	395.2	64	22
GSTA2	LHYSNI**R**	8.4	456.8	499.3	64	22
GSTA2	LHYSNI**R**	8.4	456.8	400.2	64	22
GSTA3	FIGSAEDLGK	10.9	518.8	632.3	69	23
GSTA3	FIGSAEDLGK	10.9	518.8	432.2	69	23
GSTA3	FIGSAEDLGK	10.9	518.8	204.1	69	23
GSTA3	FIGSAEDLGK	13.2	522.8	261.2	69	28
GSTA3	FIGSAEDLGK	13.2	522.8	784.4	69	28
GSTA3	FIGSAEDLGK	13.2	522.8	261.2	69	28
GSTA3	FIGSAEDLGK	13.2	522.8	784.4	69	28
GSTA3	FIGSAEDLG**K**	10.9	522.8	261.2	69	23
GSTA3	FIGSAEDLG**K**	10.9	522.8	784.4	69	23

GSTA3	LHYFNGR	13.3	302.8	338.2	53	14
GSTA3	LHYFNGR	13.3	302.8	232.1	53	14
GSTA3	LHYFNGR	13.3	302.8	346.2	53	14
GSTA3	LHYFNGR	13.3	302.8	338.2	53	14
GSTA3	LHYFNGR	13.3	302.8	232.1	53	14
GSTA3	LHYFNGR	13.3	302.8	346.2	53	14
GSTA3	LHYFNG**R**	13.3	306.2	242.1	53	14
GSTA3	LHYFNG**R**	13.3	306.2	356.2	53	14
GSTA3	LHYFNG**R**	13.3	306.2	242.1	53	14
GSTA3	LHYFNG**R**	13.3	306.2	356.2	53	14
GSTA4	YFPVFEK	14.0	465.2	311.1	65	21
GSTA4	YFPVFEK	14.0	465.2	619.3	65	21
GSTA4	YFPVFEK	14.0	465.2	423.2	65	21
GSTA4	YFPVFEK	14.0	465.2	276.2	65	21
GSTA4	YFPVFEK	14.0	465.2	310.2	65	21
GSTA4	YFPVFE**K**	14.0	469.2	311.1	65	21
GSTA4	YFPVFE**K**	14.0	469.2	627.4	65	21
GSTA5	FLESAEDLDK	11.6	583.8	261.2	74	30
GSTA5	FLESAEDLDK	11.6	583.8	390.2	74	30
GSTA5	FLESAEDLDK	11.6	583.8	906.4	74	30
GSTA5	FLESAEDLDK	11.6	583.8	261.2	74	30
GSTA5	FLESAEDLDK	11.6	583.8	390.2	74	30
GSTA5	FLESAEDLDK	11.6	583.8	906.4	74	30
GSTA5	FLESAEDLD**K**	11.6	587.8	261.2	74	30
GSTA5	FLESAEDLD**K**	11.6	587.8	390.2	74	30
GSTA5	FLESAEDLD**K**	11.6	587.8	261.2	74	30
GSTA5	FLESAEDLD**K**	11.6	587.8	390.2	74	30
GSTA5	FLQPGSQR	8.2	466.8	261.2	65	26
GSTA5	FLQPGSQR	8.2	466.8	544.3	65	26
GSTA5	FLQPGSQR	8.2	466.8	672.3	65	26
GSTA5	FLQPGSQR	8.2	466.8	261.2	65	26
GSTA5	FLQPGSQR	8.2	466.8	544.3	65	26
GSTA5	FLQPGSQR	8.2	466.8	672.3	65	26
GSTA5	FLQPGSQ**R**	8.2	471.8	261.2	65	26
GSTA5	FLQPGSQ**R**	8.2	471.8	554.3	65	26
GSTA5	FLQPGSQ**R**	8.2	471.8	261.2	65	26
GSTA5	FLQPGSQ**R**	8.2	471.8	554.3	65	26
GSTM2	NQVFEPS**C**LDAFPNLK	16.4	940.0	689.4	100	48
GSTM2	NQVFEPS**C**LDAFPNLK	16.4	940.0	618.4	100	48
GSTM2	NQVFEPS**C**LDAFPNLK	16.4	940.0	471.3	100	48
GSTM2	NQVFEPS**C**LDAFPNL**K**	16.4	944.0	1269.6	100	48
GSTM2	NQVFEPS**C**LDAFPNL**K**	16.4	944.0	479.3	100	48
GSTM3	FSWFAGEK	14.6	486.2	235.1	67	21
GSTM3	FSWFAGEK	14.6	486.2	737.4	67	21
GSTM3	FSWFAGEK	14.6	486.2	404.2	67	21
GSTM3	FSWFAGE**K**	14.6	490.2	235.1	67	21
GSTM3	FSWFAGE**K**	14.6	490.2	745.4	67	21
GSTM4	IFEPN**C**LDAFPNLK	16.4	839.4	1288.6	92	44
GSTM4	IFEPN**C**LDAFPNLK	16.4	839.4	804.4	92	44
GSTM4	IFEPN**C**LDAFPNLK	16.4	839.4	618.4	92	44

GSTM4	IFEPN**C**LDAFPNLK	16.4	839.4	471.3	92	44
GSTM4	IFEPN**C**LDAFPNLK	16.4	839.4	709.3	92	44
GSTM4	IFEPN**C**LDAFPNL**K**	16.4	843.4	626.4	92	44
GSTM4	IFEPN**C**LDAFPNL**K**	16.4	843.4	479.3	92	44
GSTM4	ITFVDFLAYDVLDLHR	23.7	646.3	861.9	78	33
GSTM4	ITFVDFLAYDVLDLHR	23.7	646.3	861.9	78	33
GSTM4	ITFVDFLAYDVLDLH**R**	23.7	649.7	867.0	78	33
GSTM4	ITFVDFLAYDVLDLH**R**	23.7	649.7	867.0	78	33
GSTM4	RPWFVGDK	10.9	502.8	587.3	68	27
GSTM4	RPWFVGDK	10.9	502.8	686.4	68	27
GSTM4	RPWFVGDK	10.9	502.8	858.4	68	27
GSTM4	RPWFVGDK	10.9	502.8	319.2	68	27
GSTM4	RPWFVGDK	10.9	502.8	587.3	68	27
GSTM4	RPWFVGDK	10.9	502.8	686.4	68	27
GSTM4	RPWFVGDK	10.9	502.8	858.4	68	27
GSTM4	RPWFVGDK	10.9	502.8	319.2	68	27
GSTM4	RPWFVGD**K**	10.9	506.8	587.3	68	27
GSTM4	RPWFVGD**K**	10.9	506.8	327.2	68	27
GSTM4	RPWFVGD**K**	10.9	506.8	587.3	68	27
GSTM4	RPWFVGD**K**	10.9	506.8	327.2	68	27
GSTP1	EEVVTVETWQEGSLK	13.8	867.4	948.5	94	35
GSTP1	EEVVTVETWQEGSLK	13.8	867.4	847.4	94	35
GSTP1	EEVVTVETWQEGSLK	13.8	867.4	260.2	94	35
GSTP1	EEVVTVETWQEGSL**K**	13.8	871.4	855.4	94	35
GSTP1	EEVVTVETWQEGSL**K**	13.8	871.4	268.2	94	35
GSTT1	VDEYLAWQHTTLR	13.3	544.6	563.3	71	22
GSTT1	VDEYLAWQHTTLR	13.3	544.6	506.8	71	22
GSTT1	VDEYLAWQHTTL**R**	13.3	547.9	771.9	71	22
GSTT1	VDEYLAWQHTTL**R**	13.3	547.9	714.4	71	22
GSTT1	VEAAVGEDLFQEAHEVILK	16.5	699.7	935.0	82	31
GSTT1	VEAAVGEDLFQEAHEVILK	16.5	699.7	864.0	82	31
GSTT1	VEAAVGEDLFQEAHEVILK	16.5	699.7	814.4	82	31
GSTT1	VEAAVGEDLFQEAHEVIL**K**	16.5	702.4	939.0	82	31
GSTT1	VEAAVGEDLFQEAHEVIL**K**	16.5	702.4	818.4	82	31
SULT1A1	ILEFVGR	13.2	417.3	607.3	80	24
SULT1A1	ILEFVGR	13.2	417.3	478.3	80	24
SULT1A1	ILEFVGR	13.2	417.3	356.2	80	24
SULT1A1	ILEFVGR	13.2	417.3	331.2	80	24
SULT1A1	SLPEETVDFVVQHTSFK	17.5	655.0	201.1	79	26
SULT1A1	SLPEETVDFVVQHTSFK	17.5	655.0	427.2	79	26
SULT1A1	SLPEETVDFVVQHTSFK	17.5	655.0	945.5	79	26
SULT1A1	SLPEETVDFVVQHTSF**K**	17.5	657.7	201.1	79	26
SULT1A1	SLPEETVDFVVQHTSF**K**	17.5	657.7	854.5	79	26
SULT1A1	TTFTVAQNER	17.1	583.8	617.3	80	31
SULT1A1	TTFTVAQNER	17.1	583.8	482.8	80	31
SULT1A1	TTFTVAQNER	17.1	583.8	546.3	80	31
SULT1A1	TTFTVAQNER	17.1	583.8	550.3	80	31
SULT1A1	VHPEPGTWDSFLEK	14.4	547.9	237.1	71	27
SULT1A1	VHPEPGTWDSFLEK	14.4	821.4	237.1	91	37
SULT1A1	VHPEPGTWDSFLEK	14.4	821.4	703.3	91	37

SULT1A1	VHPEPGTWDSFLE**K**	14.4	550.6	237.1	71	27
SULT1A1	VHPEPGTWDSFLE**K**	14.4	825.4	237.1	91	37
SULT1A2	FDADYAK	12.1	415.2	263.1	61	24
SULT1A2	FDADYAK	12.1	415.2	334.1	61	24
SULT1A2	FDADYAK	12.1	415.2	449.2	61	24
SULT1A2	FDADYAK	12.1	415.2	567.3	61	24
SULT1A2	FDADYAK	12.1	415.2	682.3	61	24
SULT1A2	FDADYAK	12.1	415.2	263.1	61	24
SULT1A2	FDADYAK	12.1	415.2	334.1	61	24
SULT1A2	FDADYAK	12.1	415.2	449.2	61	24
SULT1A2	FDADYAK	12.1	415.2	567.3	61	24
SULT1A2	FDADYAK	12.1	415.2	682.3	61	24
SULT1A2	FDADYA**K**	12.1	419.2	263.1	61	24
SULT1A2	FDADYA**K**	12.1	419.2	575.3	61	24
SULT1A2	FDADYA**K**	12.1	419.2	263.1	61	24
SULT1A2	FDADYA**K**	12.1	419.2	575.3	61	24
SULT1A2	VYPHPGTWESFLEK	15.2	563.9	623.3	72	27
SULT1A2	VYPHPGTWESFLEK	15.2	563.9	795.9	72	27
SULT1A2	VYPHPGTWESFLEK	15.2	563.9	714.4	72	27
SULT1A2	VYPHPGTWESFLEK	15.2	563.9	597.3	72	27
SULT1A2	VYPHPGTWESFLE**K**	15.2	566.6	718.4	72	27
SULT1A2	VYPHPGTWESFLE**K**	15.2	566.6	601.3	72	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	209.1	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	690.3	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	345.7	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	738.4	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	924.4	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	209.1	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	690.3	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	345.7	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	738.4	70	27
SULT1A3	AHPEPGTWDSFLEK	14.9	538.6	924.4	70	27
SULT1A3	AHPEPGTWDSFLE**K**	14.9	541.3	209.1	70	27
SULT1A3	AHPEPGTWDSFLE**K**	14.9	541.3	746.4	70	27
SULT1A3	AHPEPGTWDSFLE**K**	14.9	541.3	209.1	70	27
SULT1A3	AHPEPGTWDSFLE**K**	14.9	541.3	746.4	70	27
SULT1A3	DVAVSYYHFHR	17.1	349.2	215.1	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	286.1	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	385.2	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	236.6	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	459.2	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	596.3	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	215.1	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	286.1	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	385.2	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	236.6	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	459.2	57	17
SULT1A3	DVAVSYYHFHR	17.1	349.2	596.3	57	17
SULT1A3	DVAVSYYHFH**R**	17.1	351.7	215.1	57	17
SULT1A3	DVAVSYYHFH**R**	17.1	351.7	385.2	57	17

SULT1A3	DVAVSYYHFH**R**	17.1	351.7	215.1	57	17
SULT1A3	DVAVSYYHFH**R**	17.1	351.7	385.2	57	17
SULT1B1	NYFTVAQNEK	11.0	607.3	278.1	75	28
SULT1B1	NYFTVAQNEK	11.0	607.3	425.2	75	28
SULT1B1	NYFTVAQNEK	11.0	607.3	789.4	75	28
SULT1B1	NYFTVAQNE**K**	11.0	611.3	278.1	75	28
SULT1B1	NYFTVAQNE**K**	11.0	611.3	425.2	75	28
SULT1E1	LIHFLER	13.8	464.3	364.2	65	26
SULT1E1	LIHFLER	13.8	464.3	701.4	65	26
SULT1E1	LIHFLER	13.8	464.3	351.2	65	26
SULT1E1	LIHFLER	13.8	464.3	364.2	65	26
SULT1E1	LIHFLER	13.8	464.3	701.4	65	26
SULT1E1	LIHFLER	13.8	464.3	351.2	65	26
SULT1E1	LIHFLE**R**	13.8	469.3	574.3	65	26
SULT1E1	LIHFLE**R**	13.8	469.3	356.2	65	26
SULT1E1	LIHFLE**R**	13.8	469.3	574.3	65	26
SULT1E1	LIHFLE**R**	13.8	469.3	356.2	65	26
SULT1E1	NHFTVALNEK	11.2	586.8	399.2	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	574.3	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	774.4	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	921.5	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	399.2	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	574.3	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	774.4	74	30
SULT1E1	NHFTVALNEK	11.2	586.8	921.5	74	30
SULT1E1	NHFTVALNE**K**	11.2	590.8	399.2	74	30
SULT1E1	NHFTVALNE**K**	11.2	590.8	582.3	74	30
SULT1E1	NHFTVALNE**K**	11.2	590.8	399.2	74	30
SULT1E1	NHFTVALNE**K**	11.2	590.8	582.3	74	30
SULT2A1	LFSSHLPIQLFPK	18.1	763.9	842.5	80	39
SULT2A1	LFSSHLPIQLFPK	18.1	763.9	955.6	80	39
SULT2A1	LFSSHLPIQLFPK	18.1	763.9	633.9	80	39
SULT2A1	LFSSHLPIQLFPK	18.1	763.9	1092.7	80	39
SULT2A1	NFLLLSYEELK	17.9	684.9	881.5	80	36
SULT2A1	NFLLLSYEELK	17.9	684.9	768.4	80	36
SULT2A1	NFLLLSYEELK	17.9	684.9	375.2	80	36
SULT2A1	NFLLLSYEELK	17.9	684.9	994.6	80	36
SULT2A1	NHFTVAQAEDFDK	11.2	761.4	399.2	87	33
SULT2A1	NHFTVAQAEDFDK	11.2	761.4	1270.6	87	33
SULT2A1	NHFTVAQAEDFDK	11.2	761.4	1123.5	87	33
SULT2A1	NHFTVAQAEDFD**K**	11.2	765.4	399.2	87	33
SULT2A1	NHFTVAQAEDFD**K**	11.2	765.4	1131.5	87	33
SULT2A1	TLEPEELNLILK	16.9	706.4	344.2	83	33
SULT2A1	TLEPEELNLILK	16.9	706.4	1068.6	83	33
SULT2A1	TLEPEELNLILK	16.9	706.4	260.2	83	33
SULT2A1	TLEPEELNLILK	17.3	706.4	1068.6	80	37
SULT2A1	TLEPEELNLILK	17.3	706.4	599.3	80	37
SULT2A1	TLEPEELNLILK	17.3	706.4	1197.7	80	37
SULT2A1	TLEPEELNLILK	17.3	706.4	344.2	80	37
SULT2A1	TLEPEELNLILK	13.9	710.4	344.2	83	34

SULT2A1	TLEPEELNLILK	13.9	710.4	1076.6	83	34
SULT2A1	TLEPEELNLILK	13.9	710.4	344.2	83	34
SULT2A1	TLEPEELNLILK	13.9	710.4	1076.6	83	34
SULT2A1	TLEPEELNLIL**K**	16.9	710.4	344.2	83	33
SULT2A1	TLEPEELNLIL**K**	16.9	710.4	1076.6	83	33
SULT4A1	DLVVSYYQFHR	13.6	713.9	1099.5	83	32
SULT4A1	DLVVSYYQFHR	13.6	713.9	1000.5	83	32
SULT4A1	DLVVSYYQFHR	13.6	713.9	550.3	83	32
SULT4A1	DLVVSYYQFH**R**	13.6	718.9	1010.5	83	32
SULT4A1	DLVVSYYQFH**R**	13.6	718.9	555.3	83	32
SULT4A1	FLPSDLHNGDSK	15.8	443.9	261.2	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	560.3	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	535.2	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	591.8	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	234.1	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	657.3	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	261.2	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	560.3	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	535.2	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	591.8	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	234.1	64	22
SULT4A1	FLPSDLHNGDSK	15.8	443.9	657.3	64	22
SULT4A1	FLPSDLHNGDS**K**	15.8	446.6	539.3	64	22
SULT4A1	FLPSDLHNGDS**K**	15.8	446.6	242.2	64	22
SULT4A1	FLPSDLHNGDS**K**	15.8	446.6	539.3	64	22
SULT4A1	FLPSDLHNGDS**K**	15.8	446.6	242.2	64	22
SULT4A1	YFEFHGVR	20.5	352.2	311.1	57	17
SULT4A1	YFEFHGVR	20.5	352.2	331.2	57	17
SULT4A1	YFEFHGVR	20.5	352.2	308.2	57	17
SULT4A1	YFEFHGVR	20.5	352.2	372.7	57	17
SULT4A1	YFEFHGVR	20.5	352.2	446.2	57	17
SULT4A1	YFEFHGVR	20.5	352.2	311.1	57	17
SULT4A1	YFEFHGVR	20.5	352.2	331.2	57	17
SULT4A1	YFEFHGVR	20.5	352.2	308.2	57	17
SULT4A1	YFEFHGVR	20.5	352.2	372.7	57	17
SULT4A1	YFEFHGVR	20.5	352.2	446.2	57	17
SULT4A1	YFEFHGV**R**	20.5	355.5	341.2	57	17
SULT4A1	YFEFHGV**R**	20.5	355.5	451.2	57	17
SULT4A1	YFEFHGV**R**	20.5	355.5	341.2	57	17
SULT4A1	YFEFHGV**R**	20.5	355.5	451.2	57	17
TPMT	NQVLTLEEWQDK	14.1	751.9	1048.5	86	35
TPMT	NQVLTLEEWQDK	14.1	751.9	947.4	86	35
TPMT	NQVLTLEEWQDK	14.1	751.9	834.4	86	35
TPMT	NQVLTLEEWQDK	14.1	751.9	705.3	86	35
TPMT	NQVLTLEEWQDK	14.1	751.9	576.3	86	35
TPMT	NQVLTLEEWQD**K**	14.1	755.9	1056.5	86	35
TPMT	NQVLTLEEWQD**K**	14.1	755.9	955.5	86	35
TPMT	NQVLTLEEWQD**K**	14.1	755.9	842.4	86	35
TPMT	NQVLTLEEWQD**K**	14.1	755.9	713.3	86	35
TPMT	NQVLTLEEWQD**K**	14.1	755.9	584.3	86	35

TPMT	SWGID**C**LFEK	17.6	627.8	536.3	77	30
TPMT	SWGID**C**LFEK	17.6	627.8	584.3	77	30
TPMT	SWGID**C**LFE**K**	17.6	631.8	331.1	77	30
TPMT	SWGID**C**LFE**K**	17.6	631.8	819.4	77	30
UGT1A1	DGAFYTLK	12.4	457.7	244.1	80	16
UGT1A1	DGAFYTLK	12.4	457.7	260.2	80	16
UGT1A1	DGAFYTL**K**	12.4	461.8	244.2	80	16
UGT1A1	DGAFYTL**K**	12.4	461.8	369.3	80	16
UGT1A1	DGAFYTL**K**	12.4	461.8	679.4	80	16
UGT1A1	ESFVSLGHNVFENDSFLQR	16.5	742.4	650.4	85	31
UGT1A1	ESFVSLGHNVFENDSFLQR	16.5	742.4	303.2	85	31
UGT1A1	ESFVSLGHNVFENDSFLQR	16.5	742.4	881.9	85	31
UGT1A1	ESFVSLGHNVFENDSFLQ**R**	16.5	745.7	660.4	85	31
UGT1A1	ESFVSLGHNVFENDSFLQ**R**	16.5	745.7	886.9	85	31
UGT1A1	GHEIVVLAPDASLYIR	14.5	585.0	819.5	74	22
UGT1A1	GHEIVVLAPDASLYIR	14.5	585.0	410.2	74	22
UGT1A1	GHEIVVLAPDASLYIR	14.5	585.0	467.8	74	22
UGT1A1	GHEIVVLAPDASLYI**R**	14.5	588.3	410.2	74	22
UGT1A1	GHEIVVLAPDASLYI**R**	14.5	588.3	472.8	74	22
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	20.0	856.8	886.4	94	37
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	20.0	856.8	1084.5	94	37
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	20.0	856.8	1155.7	94	37
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLAK	20.0	856.8	959.5	94	37
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLA**K**	20.0	859.5	1084.5	94	37
UGT1A3	HLNATSFDVVLTDPVNL**C**AAVLA**K**	20.0	859.5	1163.7	94	37
UGT1A3	YLSIPTVFFLR	20.3	678.4	277.2	80	27
UGT1A3	YLSIPTVFFLR	20.3	678.4	879.5	80	27
UGT1A3	YLSIPTVFFLR	20.3	678.4	1079.6	80	27
UGT1A3	YLSIPTVFFL**R**	20.3	683.4	277.2	80	27
UGT1A3	YLSIPTVFFL**R**	20.3	683.4	889.5	80	27
UGT1A4	FFTLTAYAVPWTQK	18.6	836.9	992.5	92	32
UGT1A4	FFTLTAYAVPWTQK	18.6	836.9	758.4	92	32
UGT1A4	FFTLTAYAVPWTQK	18.6	836.9	659.4	92	32
UGT1A4	FFTLTAYAVPWTQ**K**	18.6	840.9	1000.5	92	32
UGT1A4	FFTLTAYAVPWTQ**K**	18.6	840.9	667.4	92	32
UGT1A4	GTQ**C**PNPSSYIPK	11.6	724.8	1002.5	84	28
UGT1A4	GTQ**C**PNPSSYIPK	11.6	724.8	791.4	84	28
UGT1A4	GTQ**C**PNPSSYIPK	11.6	724.8	244.2	84	28
UGT1A4	GTQ**C**PNPSSYIPK	11.6	724.8	581.8	84	28
UGT1A4	GTQ**C**PNPSSYIP**K**	11.6	728.9	1010.5	84	28
UGT1A4	GTQ**C**PNPSSYIP**K**	11.6	728.9	799.4	84	28
UGT1A4	GTQ**C**PNPSSYIP**K**	11.6	728.9	252.2	84	28
UGT1A4	GTQ**C**PNPSSYIP**K**	11.6	728.9	585.8	84	28
UGT1A4	YLSIPAVFFWR	21.3	699.9	277.2	82	27
UGT1A4	YLSIPAVFFWR	21.3	699.9	364.2	82	27
UGT1A4	YLSIPAVFFWR	21.3	699.9	922.5	82	27
UGT1A4	YLSIPAVFFWR	21.4	699.9	277.2	82	30
UGT1A4	YLSIPAVFFWR	21.4	699.9	364.2	82	30
UGT1A4	YLSIPAVFFWR	21.4	699.9	922.5	82	30
UGT1A4	YLSIPAVFFW**R**	21.3	704.9	277.2	82	27

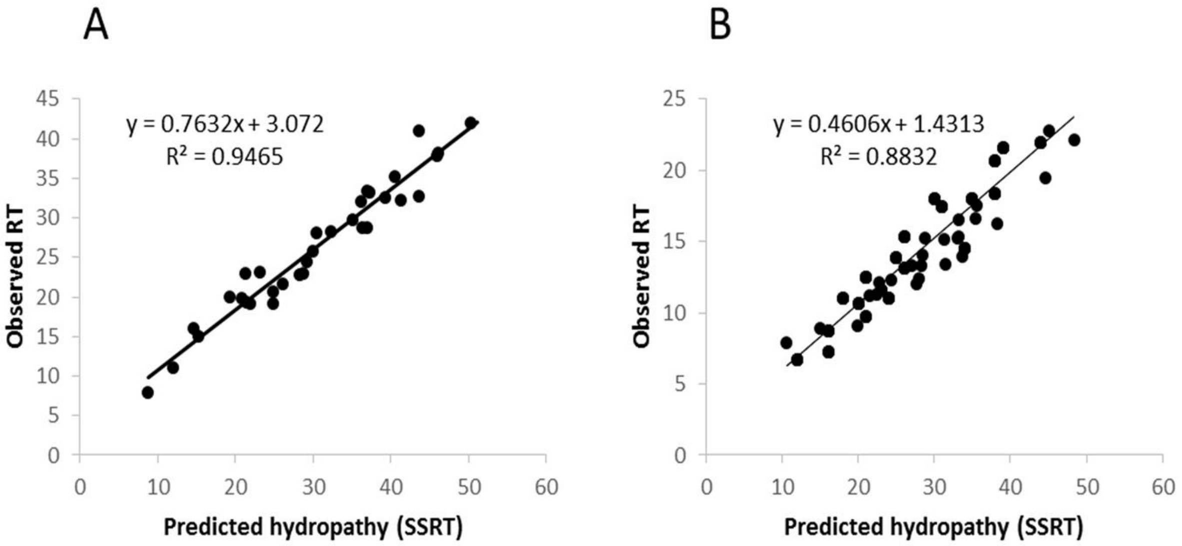
UGT1A4	YLSIPAVFFW**R**	21.3	704.9	932.5	82	27
UGT1A4	YLSIPAVFFW**R**	21.4	704.9	277.2	82	30
UGT1A4	YLSIPAVFFW**R**	21.4	704.9	932.5	82	30
UGT1A6	DIVEVLSDR	14.0	523.3	718.4	69	28
UGT1A6	DIVEVLSDR	14.0	523.3	589.3	69	28
UGT1A6	DIVEVLSDR	14.0	523.3	490.3	69	28
UGT1A6	DIVEVLSD**R**	14.0	528.3	728.4	69	28
UGT1A6	DIVEVLSD**R**	14.0	528.3	500.3	69	28
UGT1A6	SFLTAPQTEYR	12.5	656.8	965.5	79	28
UGT1A6	SFLTAPQTEYR	12.5	656.8	864.4	79	28
UGT1A6	SFLTAPQTEYR	12.5	656.8	793.4	79	28
UGT1A6	SFLTAPQTEY**R**	12.5	661.8	803.4	79	28
UGT1A6	SFLTAPQTEY**R**	12.5	661.8	348.2	79	28
UGT1A9	AFAHAQWK	9.3	320.2	444.2	55	15
UGT1A9	AFAHAQWK	9.3	320.2	370.7	55	15
UGT1A9	AFAHAQWK	9.3	320.2	335.2	55	15
UGT1A9	AFAHAQW**K**	9.3	322.8	448.2	55	15
UGT1A9	AFAHAQW**K**	9.3	322.8	374.7	55	15
UGT1A9	ESSFDAVFLDPFDN**C**GLIVAK	20.4	1172.6	736.3	117	44
UGT1A9	ESSFDAVFLDPFDN**C**GLIVAK	20.4	1172.6	1348.7	117	44
UGT1A9	ESSFDAVFLDPFDN**C**GLIVAK	20.4	1172.6	1233.6	117	44
UGT1A9	ESSFDAVFLDPFDN**C**GLIVA**K**	20.4	1176.6	736.3	117	44
UGT1A9	ESSFDAVFLDPFDN**C**GLIVA**K**	20.4	1176.6	1356.7	117	44
UGT1A9	ESSFDAVFLDPFDN**C**GLIVA**K**	20.4	1176.6	1241.6	117	44
UGT2B10	GHEVTVLASSASILFDPNDSSTLK	16.6	830.1	861.4	80	35
UGT2B10	GHEVTVLASSASILFDPNDSSTLK	16.6	830.1	1123.5	80	35
UGT2B10	GHEVTVLASSASILFDPNDSSTL**K**	16.6	832.8	869.4	80	35
UGT2B10	GHEVTVLASSASILFDPNDSSTL**K**	16.6	832.8	1131.5	80	35
UGT2B11	FTPGYTIER	11.1	542.3	418.2	80	18
UGT2B11	FTPGYTIER	11.1	542.3	738.4	80	18
UGT2B11	FTPGYTIER	11.1	542.3	835.4	80	18
UGT2B11	FTPGYTIE**R**	11.1	547.3	423.2	80	18
UGT2B11	FTPGYTIE**R**	11.1	547.3	845.4	80	18
UGT2B15	NYLEDSLLK	14.1	547.8	278.1	71	29
UGT2B15	NYLEDSLLK	14.1	547.8	817.5	71	29
UGT2B15	NYLEDSLLK	14.1	547.8	704.4	71	29
UGT2B15	NYLEDSLL**K**	14.1	551.8	278.1	71	29
UGT2B15	NYLEDSLL**K**	14.1	551.8	825.5	71	29
UGT2B15	SVINDPVYK	10.6	517.8	848.5	69	23
UGT2B15	SVINDPVYK	10.6	517.8	735.4	69	23
UGT2B15	SVINDPVYK	10.6	517.8	424.7	69	23
UGT2B15	SVINDPVY**K**	10.6	521.8	856.5	69	23
UGT2B15	SVINDPVY**K**	10.6	521.8	428.7	69	23
UGT2B17	FSVGYTVEK	11.4	515.3	235.1	69	27
UGT2B17	FSVGYTVEK	11.4	515.3	882.5	69	27
UGT2B17	FSVGYTVEK	11.4	515.3	795.4	69	27
UGT2B17	FSVGYTVEK	11.4	515.3	696.4	69	27
UGT2B17	FSVGYTVEK	11.4	515.3	639.3	69	27
UGT2B17	FSVGYTVE**K**	11.4	519.3	235.1	69	27
UGT2B17	FSVGYTVE**K**	11.4	519.3	704.4	69	27

UGT2B17	SVINDPIYK	11.5	524.8	862.5	69	23
UGT2B17	SVINDPIYK	11.5	524.8	749.4	69	23
UGT2B17	SVINDPIYK	11.5	524.8	431.7	69	23
UGT2B17	SVINDPIY**K**	11.5	528.8	870.5	69	23
UGT2B17	SVINDPIY**K**	11.5	528.8	435.7	69	23
UGT2B4	FSPGYAIEK	10.0	1011.5	389.2	80	30
UGT2B4	FSPGYAIEK	10.0	1011.5	777.4	80	30
UGT2B4	FSPGYAIEK	10.0	1011.5	864.5	80	30
UGT2B4	FSPGYAIE**K**	10.0	1019.5	397.3	80	30
UGT2B4	TILDELVQR	15.3	543.8	872.5	71	28
UGT2B4	TILDELVQR	15.3	543.8	759.4	71	28
UGT2B4	TILDELVQR	15.3	543.8	644.4	71	28
UGT2B4	TILDELVQ**R**	15.3	548.8	882.5	71	28
UGT2B4	TILDELVQ**R**	15.3	548.8	769.4	71	28
UGT2B7	IEIYPTSLTK	13.1	582.8	922.5	74	25
UGT2B7	IEIYPTSLTK	13.1	582.8	809.4	74	25
UGT2B7	IEIYPTSLTK	13.1	582.8	646.4	74	25
UGT2B7	IEIYPTSLT**K**	13.1	586.8	817.5	74	25
UGT2B7	IEIYPTSLT**K**	13.1	586.8	654.4	74	25
UGT2B7	TILDELIQR	16.4	550.8	886.5	71	29
UGT2B7	TILDELIQR	16.4	550.8	773.4	71	29
UGT2B7	TILDELIQR	16.4	550.8	658.4	71	29
UGT2B7	TILDELIQR	16.4	550.8	416.3	71	29
UGT2B7	TILDELIQ**R**	16.4	555.8	896.5	71	29
UGT2B7	TILDELIQ**R**	16.4	555.8	783.4	71	29
UGT2B7	TILDELIQ**R**	16.4	555.8	668.4	71	29
UGT2B7	TILDELIQ**R**	16.4	555.8	426.3	71	29

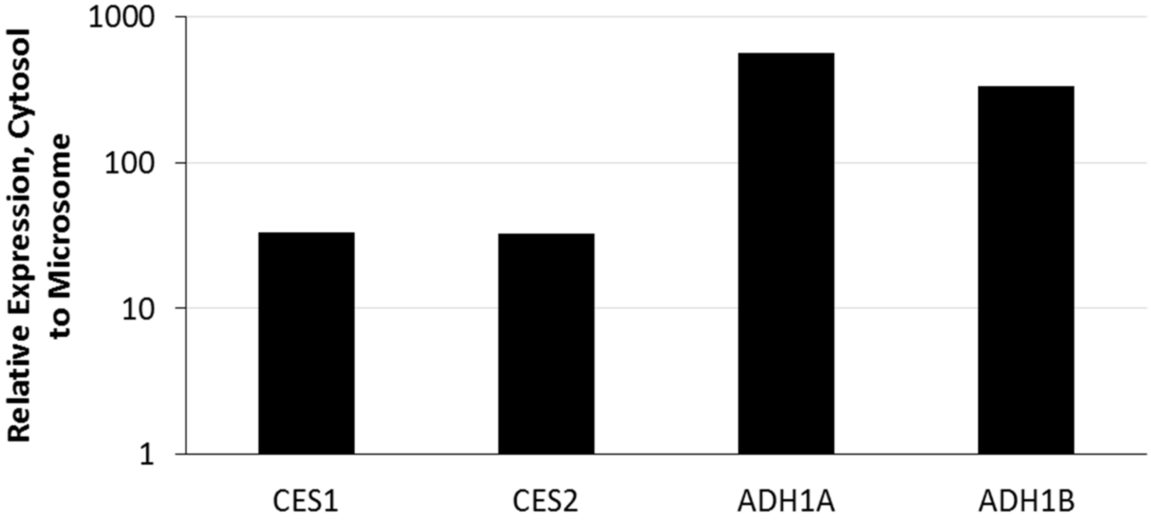
R, **K** and **C** correspond to heavy arginine (R[13C6, 15N4]), heavy lysine (K[13C6, 15N2]) and carbamidomethylated cysteine (+57 Da).

Supplementary Table 3S: Number of donors in subcellular fractions obtained from Xenotech, LLC and UW. Number in parenthesis indicates lot number.

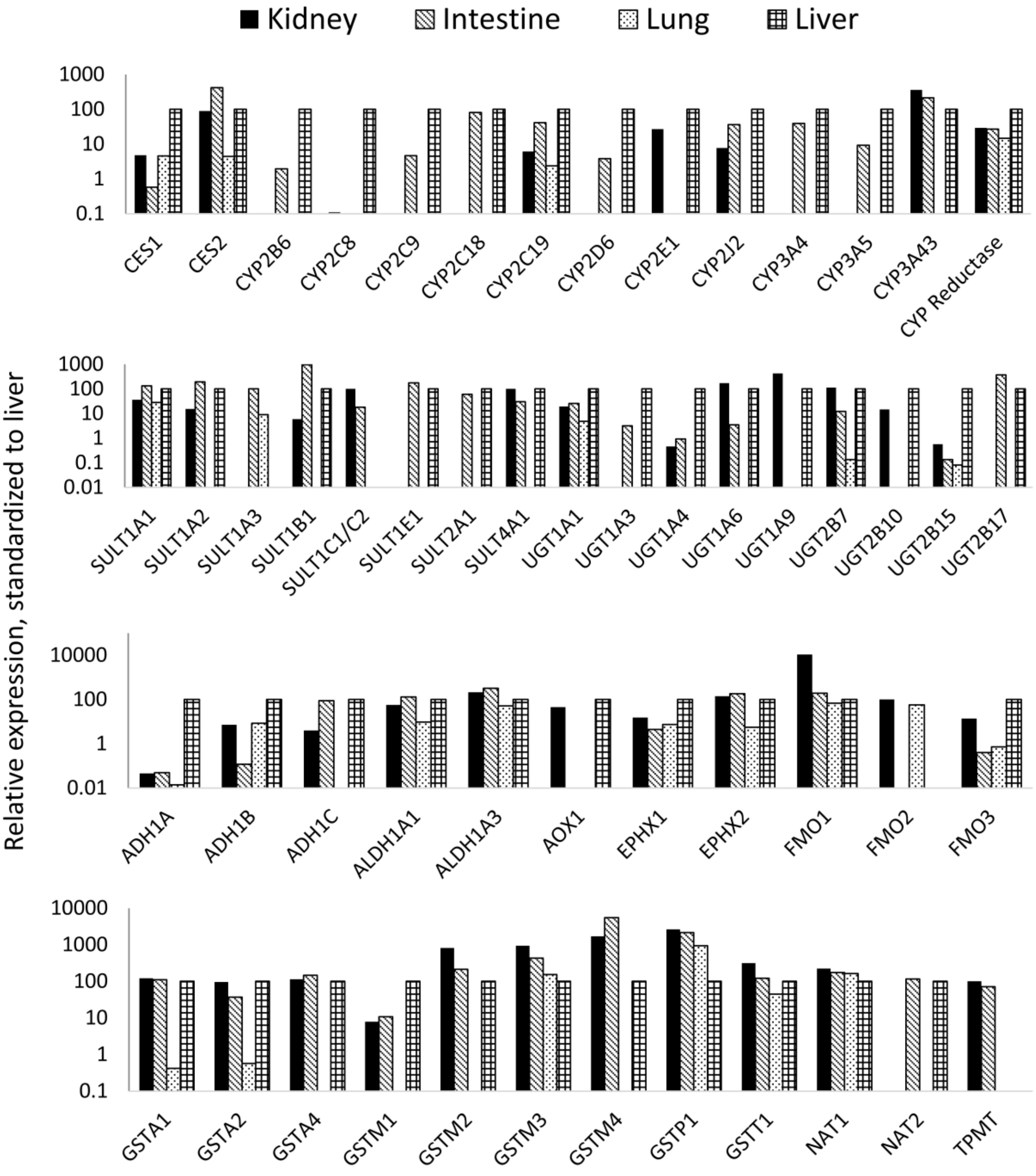
Organ	Number of donors			
	Microsome	S9	Cytosol	Total Membrane
Liver	200 (1410230)	50 (1210091)	50 (1410012)	6
Kidney	13 (1410120)	13 (1410118)		6
Intestine	10 (1410074)	10 (1410073)		
Lung	4 (1310116)			



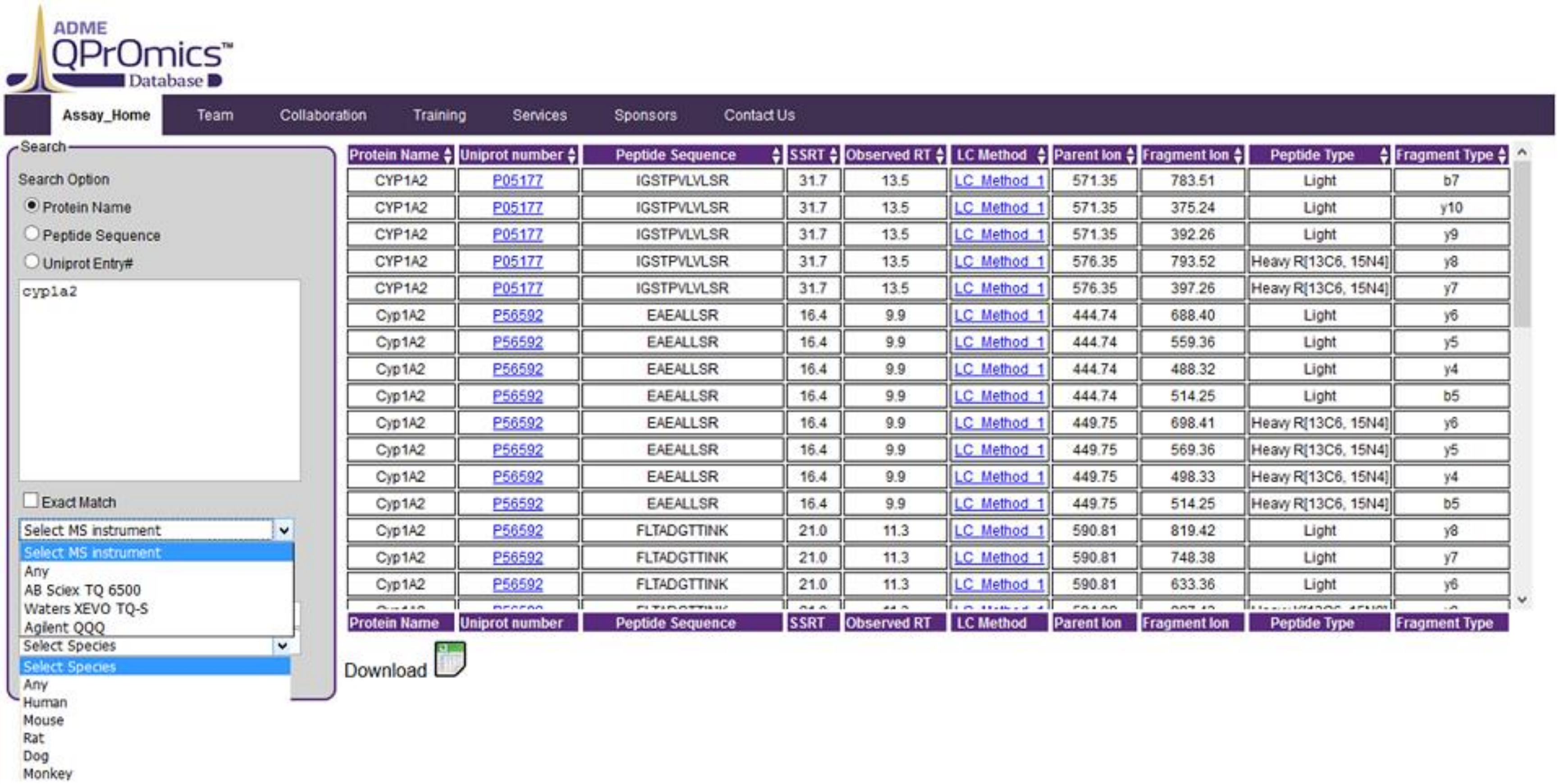
Supplementary Fig. 1S



Supplementary Fig. 2S



Supplementary Fig. 3S



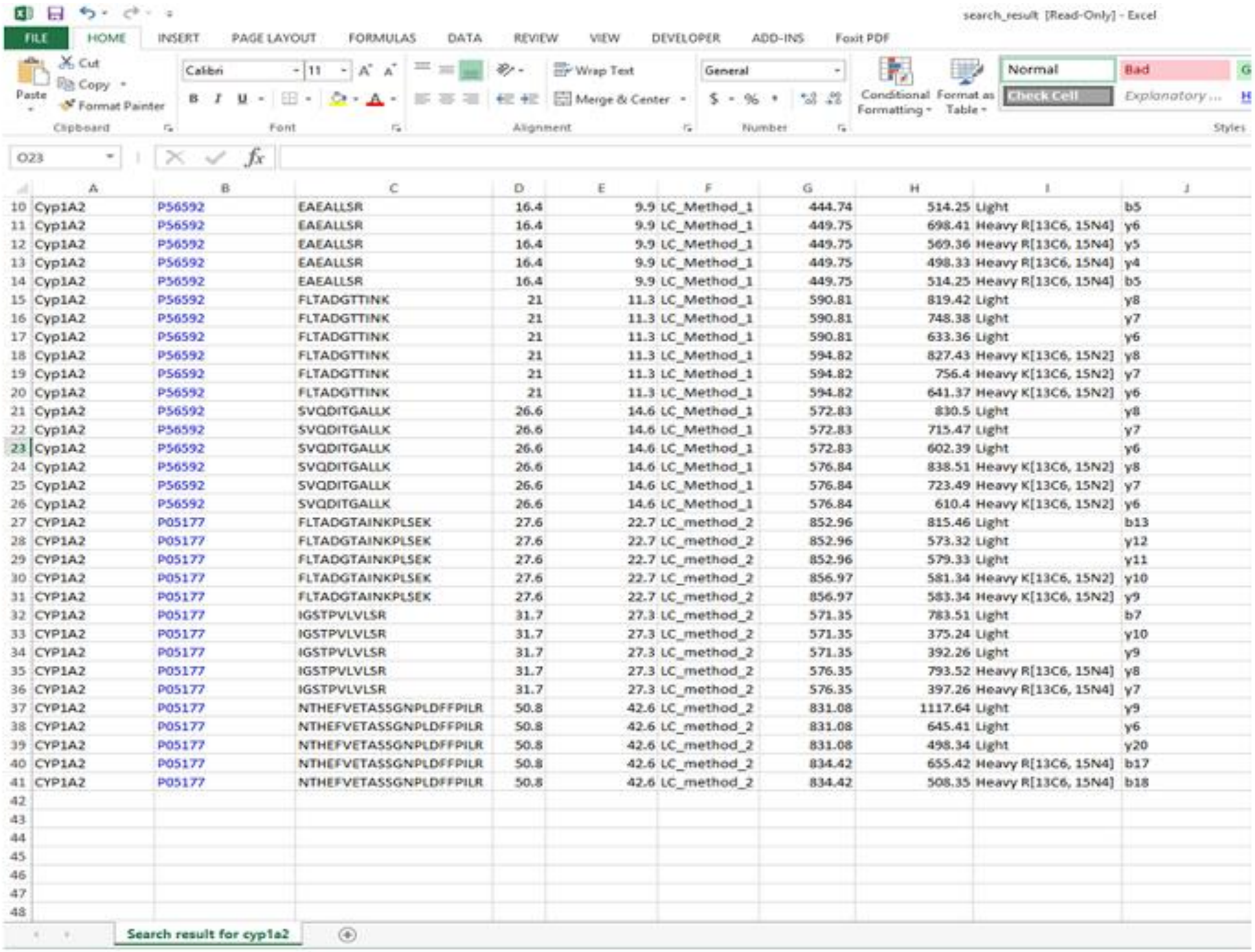
● Protein Name
○ Peptide Sequence
○ Uniprot Entry#

cyp1a2

☐ Exact Match

Protein Name	Uniprot number	Peptide Sequence	SSRT	Observed RT	LC Method	Parent Ion	Fragment Ion	Peptide Type	Fragment Type
CYP1A2	P05177	IGSTPVLVLSR	31.7	13.5	LC Method 1	571.35	783.51	Light	b7
CYP1A2	P05177	IGSTPVLVLSR	31.7	13.5	LC Method 1	571.35	375.24	Light	y10
CYP1A2	P05177	IGSTPVLVLSR	31.7	13.5	LC Method 1	571.35	392.26	Light	y9
CYP1A2	P05177	IGSTPVLVLSR	31.7	13.5	LC Method 1	576.35	793.52	Heavy R[13C6, 15N4]	y8
CYP1A2	P05177	IGSTPVLVLSR	31.7	13.5	LC Method 1	576.35	397.26	Heavy R[13C6, 15N4]	y7
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	444.74	688.40	Light	y6
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	444.74	559.36	Light	y5
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	444.74	488.32	Light	y4
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	444.74	514.25	Light	b5
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	449.75	698.41	Heavy R[13C6, 15N4]	y6
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	449.75	569.36	Heavy R[13C6, 15N4]	y5
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	449.75	498.33	Heavy R[13C6, 15N4]	y4
Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC Method 1	449.75	514.25	Heavy R[13C6, 15N4]	b5
Cyp1A2	P56592	FLTADGTTINK	21.0	11.3	LC Method 1	590.81	819.42	Light	y8
Cyp1A2	P56592	FLTADGTTINK	21.0	11.3	LC Method 1	590.81	748.38	Light	y7
Cyp1A2	P56592	FLTADGTTINK	21.0	11.3	LC Method 1	590.81	633.36	Light	y6

Supplementary Fig. 4S



	A	B	C	D	E	F	G	H	I	J
10	Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC_Method_1	444.74	514.25	Light	b5
11	Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC_Method_1	449.75	698.41	Heavy R[13C6, 15N4]	y6
12	Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC_Method_1	449.75	569.36	Heavy R[13C6, 15N4]	y5
13	Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC_Method_1	449.75	498.33	Heavy R[13C6, 15N4]	y4
14	Cyp1A2	P56592	EAEALLSR	16.4	9.9	LC_Method_1	449.75	514.25	Heavy R[13C6, 15N4]	b5
15	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	590.81	819.42	Light	y8
16	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	590.81	748.38	Light	y7
17	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	590.81	633.36	Light	y6
18	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	594.82	827.43	Heavy K[13C6, 15N2]	y8
19	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	594.82	756.4	Heavy K[13C6, 15N2]	y7
20	Cyp1A2	P56592	FLTADGTTINK	21	11.3	LC_Method_1	594.82	641.37	Heavy K[13C6, 15N2]	y6
21	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	572.83	830.5	Light	y8
22	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	572.83	715.47	Light	y7
23	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	572.83	602.39	Light	y6
24	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	576.84	838.51	Heavy K[13C6, 15N2]	y8
25	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	576.84	723.49	Heavy K[13C6, 15N2]	y7
26	Cyp1A2	P56592	SVQDITGALLK	26.6	14.6	LC_Method_1	576.84	610.4	Heavy K[13C6, 15N2]	y6
27	CYP1A2	P05177	FLTADGTAINKPLSEK	27.6	22.7	LC_method_2	852.96	815.46	Light	b13
28	CYP1A2	P05177	FLTADGTAINKPLSEK	27.6	22.7	LC_method_2	852.96	573.32	Light	y12
29	CYP1A2	P05177	FLTADGTAINKPLSEK	27.6	22.7	LC_method_2	852.96	579.33	Light	y11
30	CYP1A2	P05177	FLTADGTAINKPLSEK	27.6	22.7	LC_method_2	856.97	581.34	Heavy K[13C6, 15N2]	y10
31	CYP1A2	P05177	FLTADGTAINKPLSEK	27.6	22.7	LC_method_2	856.97	583.34	Heavy K[13C6, 15N2]	y9
32	CYP1A2	P05177	IGSTPVLVLSR	31.7	27.3	LC_method_2	571.35	783.51	Light	b7
33	CYP1A2	P05177	IGSTPVLVLSR	31.7	27.3	LC_method_2	571.35	375.24	Light	y10
34	CYP1A2	P05177	IGSTPVLVLSR	31.7	27.3	LC_method_2	571.35	392.26	Light	y9
35	CYP1A2	P05177	IGSTPVLVLSR	31.7	27.3	LC_method_2	576.35	793.52	Heavy R[13C6, 15N4]	y8
36	CYP1A2	P05177	IGSTPVLVLSR	31.7	27.3	LC_method_2	576.35	397.26	Heavy R[13C6, 15N4]	y7
37	CYP1A2	P05177	NTHEFVETASSGNPLDFFPILR	50.8	42.6	LC_method_2	831.08	1117.64	Light	y9
38	CYP1A2	P05177	NTHEFVETASSGNPLDFFPILR	50.8	42.6	LC_method_2	831.08	645.41	Light	y6
39	CYP1A2	P05177	NTHEFVETASSGNPLDFFPILR	50.8	42.6	LC_method_2	831.08	498.34	Light	y20
40	CYP1A2	P05177	NTHEFVETASSGNPLDFFPILR	50.8	42.6	LC_method_2	834.42	655.42	Heavy R[13C6, 15N4]	b17
41	CYP1A2	P05177	NTHEFVETASSGNPLDFFPILR	50.8	42.6	LC_method_2	834.42	508.35	Heavy R[13C6, 15N4]	b18
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Supplementary Fig. 5S