Electronic Supplementary Material (ESI) for Natural Product Reports.

Natural product *C*-glycosyltransferases – a scarcely characterized enzymatic activity with biotechnological potential

Supplementary Information

Supplementary Table 1. Catalytic rates, glycosylation sites and selectivity of recombinant *C*-GTs

C-GT[Reference] Sugar acceptor/donor*	Specific activity (nkat mg protein^{-1})	k_{cat} (s^{-1})	K_m (μM)	Catalytic efficiency k_{cat}/K_m ($M^{-1} s^{-1}$)	*C*-glycosylation site	*O*-GT/ di-*C*-GT Activity
UGT73B4[1]						yes/n.p.
2-HADNT	1.10 ± 0.18	–	–	0.35×10^3	–	
4-HADNT	1.15 ± 0.09	–	–	0.22×10^3	–	
UGT73C1[1]						yes/n.p.
2-HADNT	0.82 ± 0.01	–	–	–	–	
4-HADNT	2.13 ± 0.16	–	–	–	–	
OsCGT[2,3]						yes/n.p.
2-hydroxynaringenin	1.119 ± 0.036	3.13	2.5	1.25×10^6	6-*C*-	
2-hydroxyeriodictyol	0.466 ± 0.003	–	–	–	–	
phloretin	0.587 ± 0.019	10.84	4.78	2.27×10^6	–	
2,5,7-trihydroxyflavanone	0.382 ± 0.027	0.76	16.5	0.46×10^5	6-*C*-, 8-*C*-	
2',4',6'-trihydroxydihydrochalcone	0.35 ± 0.045	0.75	8.3	0.91×10^5	–	
2,4,6-trihydroxybenzophenone	0.048 ± 0.002	0.11	8	0.14×10^5	–	
ZmUGT/UGT708A6[4]						n.p./n.p.
2-hydroxynaringenin	–	–	–	–	6-*C*-, 8-*C*-	
FeCGTa/UGT708C1[5]						n.p./n.p.
2-hydroxynaringenin	35.7 ± 1.9	3.2	4.4 ± 0.9	7.2×10^5	–	
2-hydroxyeriodictyol	28.1 ± 1.7	–	–	–	–	
2-hydroxypinocembrin	34.2 ± 2.7	10.2	40.0 ± 3.3	2.5×10^5	–	
phloretin	5.2 ± 0.3	–	–	–	–	
2-phenyl-2',4',6'-trihydroxyactophenone	12.7 ± 1.1	1.9	36.5 ± 4.4	5.3×10^4	–	
2',4',6'-trihydroxyacetophenone	10.1 ± 0.8	–	–	–	–	
2,4,6-trihydroxybenzaldehyde	2.2 ± 0.4	–	–	–	–	
UDP-Glc (2-hydroxypinocembrin)	35.5 ± 1.2	4.5	58.1 ± 5.1	7.8×10^4	–	
UDP-Xyl (2-hydroxypinocembrin)	1.8 ± 0.2	–	–	–	–	
FeCGTb/UGT708C2[5]						n.p./n.p.
2-hydroxynaringenin	34.5 ± 1.3	3.1	3.7 ± 1.8	8.3×10^5	–	
2-hydroxyeriodictyol	23.9 ± 1.0	–	–	–	–	
2-hydroxypinocembrin	55.1 ± 2.5	2.3	6.5 ± 1.2	3.6×10^5	–	
phloretin	8.4 ± 0.2	–	–	–	–	
2-phenyl-2',4',6'-trihydroxyactophenone	45.0 ± 0.4	4.0	38.5 ± 4.8	1.0×10^5	–	
2',4',6'-trihydroxyacetophenone	12.5 ± 0.7	–	–	–	–	
2,4,6-trihydroxybenzaldehyde	2.5 ± 0.1	–	–	–	–	
UDP-Glc (2-hydroxypinocembrin)	25.6 ± 0.1	2.3	36.0 ± 3.7	6.4×10^4	–	

UDP-Xyl (2-hydroxypinocembrin)	0.7	–	–	–	–	
GmCGT/UGT708D1[6]						n.p./n.p.
2-hydroxynaringenin	–	–	–	–	6-*C*-, 8-*C*-	
GtUF6CGT1[7]						n.p./n.p.
apigenin	0.1157 ± 0.0029	–	–	–	6-*C*-	
luteolin	0.2488 ± 0.0101	–	–	–	6-*C*-	
MiCGT[8]						yes/n.p.
maclurin	–	1.6	47.0	5.2×10^3	3-*C*-	
norathyriol	–	0.8	159.2	3.4×10^4	–	
MiCGTb[9]						yes/n.p.
phloretin	–	0.79	166.0	0.047×10^5	3-*C*-	
FcCGT/UGT708G1[10]						n.p./yes
2-hydroxynaringenin	63.4 ± 3.6	7.6 ± 0.5	0.85 ± 0.1	8.9×10^6	6-*C*-, 8-*C*-	
2-hydroxypinocembrin	67.6 ± 4.3	–	–	–	–	
phloretin	34.2 ± 4.2	12.0 ± 0.9	<0.5	$>2.4 \times 10^7$	3′-*C*-	
2-phenyl-2′,4′,6′-trihydroxyactophenone	37.9 ± 0.8	–	–	–	–	
maclurin	0.8 ± 0.0	–	–	–	–	
2′,4′,6′-trihydroxyacetophenone	5.6 ± 0.2	–	–	–	–	
2,4,6-trihydroxybenzaldehyde	1.9 ± 0.0	–	–	–	–	
6-*C*-glucosyl-2-hydroxynaringenin	24.4 ± 0.3	5.7 ± 1.1	112.5 ± 22.0	5.1×10^4	8-*C*-	
nothofagin (3′-*C*-glucosyl-phloretin)	59.6 ± 0.7	5.3 ± 0.4	14.4 ± 1.8	3.7×10^5	5′-*C*-	
3′-*C*-glucosyl-2-phenyl-2′,4′,6′-trihydroxyacetophenone	9.8 ± 0.2	–	–	–	–	
phloridzin	0.062	–	–	–	–	
UDP-Glc (nothofagin)	–	0.8 ± 0.1	71.5 ± 13.4	1.1×10^4	–	
UDP-Glc (2-hydroxynaringenin)	40.6 ± 5.1	–	–	–	–	
UDP-Xyl (2-hydroxynaringenin)	10.7 ± 0.8	–	–	–	–	
UDP-Gal (2-hydroxynaringenin)	0.94 ± 0.07	–	–	–	–	
CuCGT/UGT708G2[10]						n.p./yes
2-hydroxynaringenin	21.2 ± 2.1	–	–	–	–	
2-hydroxypinocembrin	26.0 ± 0.4	–	–	–	–	
phloretin	6.6 ± 0.1	–	–	–	–	
2-phenyl-2′,4′,6′-trihydroxyactophenone	18.9 ± 1.9	–	–	–	–	
maclurin	1.3 ± 0.1	–	–	–	–	
2′,4′,6′-trihydroxyacetophenone	2.9 ± 0.2	–	–	–	–	
2,4,6-trihydroxybenzaldehyde	0.9 ± 0.0	–	–	–	–	
6-*C*-glucosyl-2-hydroxynaringenin	12.4 ± 0.2	–	–	–	–	
nothofagin (3′-*C*-glucosyl-phloretin)	22.2 ± 1.0	–	–	–	–	
3′-*C*-glucosyl-2-phenyl-2′,4′,6′-trihydroxyacetophenone	21.2 ± 0.4	–	–	–	–	
phloridzin	0.021	–	–	–	–	
UDP-Glc (2-hydroxynaringenin)	15.3 ± 0.6	–	–	–	–	
UDP-Xyl (2-hydroxynaringenin)	5.7 ± 0.3	–	–	–	–	
UDP-Gal (2-hydroxynaringenin)	0.24 ± 0.04	–	–	–	–	
PlUGT43[11]						n.p./n.p.
daidzein	–	0.35 ± 0.01	32.8 ± 2.69	1.1×10^4	8-*C*-	

genistein	–	0.45 ± 0.01	12.16 ± 1.58	3.7×10^4	8-*C*-	
TcCGT1[12]						yes/yes
apigenin	–	1.1	9.0	1.2×10^5	6-*C*-	
luteolin	–	1.2	11.8	1.0×10^5	6-*C*-	
UDP-Glc (apigenin)	–	0.4	42.3	9.7×10^3	–	
UDP-Glc (luteolin)	–	0.1	43.1	2.3×10^3	–	
WjGT1/UGT84A57[13]						n.p./n.p.
apigenin	1.41 ± 0.02	0.55 ± 0.09	1.28 ± 0.41	4.4×10^5	6-*C*-	
luteolin	1.18 ± 0.09	–	–	–	–	
phloretin	0.52 ± 0.15	–	–	–	–	
kaempferol	0.33 ± 0.01	–	–	–	–	
quercetin	0.50 ± 0.04	–	–	–	–	
naringenin	1.22 ± 0.08	–	–	–	–	
UDP-Glc (apigenin)	1.41 ± 0.02	0.15 ± 0.02	168 ± 38	8.9×10^2	–	
GgCGT/UGT708B4[14]						yes/yes
nothofagin	–	–	4.5	–	5′-*C*-	
OsCGT2/UGT708A4[15]						n.p./n.p.
phloretin	–	–	3.47 ± 1.73	–	3′-*C*-	
2-hydroxynaringenin	–	–	–	–		
OsCGT3/UGT708A2[15]						n.p./n.p.
phloretin	–	–	51.06 ± 30.64	–	3′-*C*-	
OsCGT6/UGT708A40[15]						n.p./n.p.
phloretin	–	–	116.8 ± 33.7	–	3′-*C*-	
TaCGT1-A/UGT708A14[15]						n.p./n.p.
phloretin	–	–	4.57 ± 2.19	–	3′-*C*-	
2-hydroxynaringenin	–	–	25.82 ± 6.62	–	6-*C*-	
TaCGT1-B/UGT708A52[15]						n.p./n.p.
phloretin	–	–	7.71 ± 3.42	–	3′-*C*-	
TaCGT1-D/UGT708A53[15]						n.p./n.p.
phloretin	–	–	19.01 ± 4.07	–	3′-*C*-	
2-hydroxynaringenin	–	–	19.40 ± 7.55	–	6-*C*-	
TaCGT2-A/UGT708A15[15]						n.p./n.p.
phloretin	–	–	26.54 ± 3.33	–	3′-*C*-	
TaCGT2-B/UGT708A54[15]						n.p./n.p.
phloretin	–	–	44.12 ± 8.37	–	3′-*C*-	
SbCGT1/UGT708A36[15]						n.p./n.p.
phloretin	–	–	4.22 ± 2.48	–	3′-*C*-	
2-hydroxynaringenin	–	–	28.01 ± 7.85	–	6-*C*-	
SbCGT2/UGT708A35[15]						n.p./n.p.
phloretin	–	–	27.05 ± 11.59	–	3′-*C*-	
SbCGT3/UGT708A34[15]						n.p./n.p.
phloretin	–	–	19.15 ± 4.92	–	3′-*C*-	

ZmCGT2/UGT708A5[15]						n.p./n.p.
phloretin	–	–	36.92 ± 7.87	–	3′-*C*-	
ZmCGT3/UGT708A11[15]						n.p./n.p.
phloretin	–	–	35.66 ± 8.29	–	3′-*C*-	
ZmCGT4/UGT708A41[15]						n.p./n.p.
phloretin	–	–	39.13 ± 12.29	–	3′-*C*-	
ZmCGT5/UGT708A42[15]						n.p./n.p.
phloretin	–	–	15.73 ± 6.71	–	3′-*C*-	
SiCGT1/UGT708A31[15]						n.p./n.p.
phloretin	–	–	5.32 ± 0.80	–	3′-*C*-	
2-hydroxynaringenin	–	–	19.29 ± 5.42	–	6-*C*-	
SiCGT2/UGT708A32[15]						n.p./n.p.
phloretin	–	–	22.00 ± 9.24	–	3′-*C*-	
SiCGT3/UGT708A33[15]						n.p./n.p.
phloretin	–	–	21.06 ± 8.50	–	3′-*C*-	
BdCGT1/UGT708A7[15]						n.p./n.p.
phloretin	–	–	2.72 ± 1.39	–	3′-*C*-	
2-hydroxynaringenin	–	–	24.27 ± 10.37	–	6-*C*-	
BdCGT2/UGT708A8[15]						n.p./n.p.
phloretin	–	–	17.97 ± 3.94	–	3′-*C*-	
PhCGT1/UGT708A43[15]						n.p./n.p.
phloretin	–	–	15.83 ± 6.98	–	3′-*C*-	
2-hydroxynaringenin	–	–	1.75 ± 0.66	4.28×10^4	6-*C*-	
PhCGT2/UGT708A46[15]						n.p./n.p.
phloretin	–	–	76.35 ± 41.16	–	3′-*C*-	
PgCGT1/UGT708A44[15]						n.p./n.p.
phloretin	–	–	12.87 ± 4.46	–	3′-*C*-	
2-hydroxynaringenin	–	–	2.75 ± 0.75	–	6-*C*-	
PpCGT1/UGT708A45[15]						n.p./n.p.
phloretin	–	–	12.73 ± 4.69	–	3′-*C*-	
IroB[16]						n.p./yes
enterobactin	–	0.187 ± 0.032	5.2 ± 1.6	0.36×10^5	5-*C*-	
MGE	–	–	–	–	5-*C*-	
salmochelin S4	–	–	–	–	5-*C*-	
UDP-Glc (enterobactin)	–	0.162 ± 0.027	13.3 ± 2.1	0.12×10^5	–	
UrdGT2[17,18]						n.p./n.p.
UWM6	–	–	–	–	9-*C*-	
SsfS6[19]						n.p./n.p.
tetracycline-like	–	–	–	–	9-*C*-	
DcUGT2[20]						n.p./n.p.

flavokermesic acid	–	–	–	–	7-*C*-
kermesic acid	–	–	–	–	7-*C*-

*UDP-Glc unless specified otherwise, – - not determined, n.p. - not provided

Supplementary Table 2. Amino acid sequences of *C*-GTs

C-GT name(s)	Uniprot /Genbank	AA	Protein sequence
UGT73B2	Q94C57	483	MGSDHHHRKLHVMFFPFMAYGHMIPTLDMAKLFSSRGAKSTILTTSLNSKILQKPIDTFKNLNPGLE IDIQIFNFPCVELGLPEGCENVDFFTSNNNDDKNEMIVKFFFSTRFFKDQLEKLLGTTRPDCLIADMF FPWATEAAGKFNVPRLVFHGTGYFSLCAGYCIGVHKPQKRVASSSEPFVIPELPGNIVITEEQIIDGD GESDMGKFMTEVRESEVKSSGVVLNSFYELEHDYADFYKSCVQKRAWHIGPLSVYNRGFEEKAERG KKANIDEAECLKWLDSKKPNSVIYVSFGSVAFFKNEQLFEIAAGLEASGTSFIWVVRKTKDDREEWLP EGFEERVKGKGMIIRGWAPQVLILDHQATGGFVTHCGWNSLLEGVAAGLPMVTWPVGAEQFYN EKLVTQVLRTGVSVGASKHMKVMMGDFISREKVDKAVREVLAGEAAEERRRRAKKLAAMAKAAV EEGGSSFNDLNSFMEEFSS
UGT73B4	Q7Y232	484	MNREQIHILFFPFMAHGHMIPLLDMAKLFARRGAKSTLLTTPINAKILEKPIEAFKVQNPDLEIGIKIL NFPCVELGLPEGCENRDFINSYQKSDSFDLFLKFLFSTKYMKQQLESFIETTKPSALVADMFFPWATE SAEKIGVPRLVFHGTSSFALCCSYNMRIHKPHKKVASSSTPFVIPGLPGDIVITEDQANVTNEETPFGK FWKEVRESETSSFGVLVNSFYELESSYADFYRSFVAKKAWHIGPLSLSNRGIAEKAGRGKKANIDEQE CLKWLDSKTPGSVVYLSFGSGTGLPNEQLLEIAFGLEGSGQNFIWVVSKNENQVGTGENEDWLPK GFEERNKGKGLIIRGWAPQVLILDHKAIGGFVTHCGWNSTLEGIAAGLPMVTWPMGAEQFYNEKL LTKVLRIGVNVGATELVKKGKLISRAQVEKAVREVIGGEKAEERRLRAKELGEMAKAAVEEGGSSYN DVNKFMEELNGRK
UGT73B5	Q9ZQG4	484	MNREVSERIHILFFPFMAQGHMIPILDMAKLFSRRGAKSTLLTTPINAKIFEKPIEAFKNQNPDLEIGI KIFNFPCVELGLPEGCENADFINSYQKSDSGDLFLKFLFSTKYMKQQLESFIETTKPSALVADMFFPW ATESAEKLGVPRLVFHGTSFFSLCCSYNMRIHKPHKKVATSSTPFVIPGLPGDIVITEDQANVAKEETP MGKFMKEVRESETNSFGVLVNSFYELESAYADFYRSFVAKRAWHIGPLSLSNRELGEKARRGKKANI DEQECLKWLDSKTPGSVVYLSFGSGTNFTNDQLLEIAFGLEGSGQSFIWVVRKNENQGDNEEWLP EGFKERTTGKGLIIPGWAPQVLILDHKAIGGFVTHCGWNSAIEGIAAGLPMVTWPMGAEQFYNEK LLTKVLRIGVNVGATELVKKGKLISRAQVEKAVREVIGGEKAEERRLWAKKLGEMAKAAVEEGGSSY NDVNKFMEELNGRK
UGT73C1	Q9ZQ99	491	MASEFRPPLHFVLFPFMAQGHMIPMVDIARLLAQRGVTITIVTTPQNAGRFKNVLSRAIQSGLPINL VQVKFPSQESGSPEGQENLDLLDSLGASLTFFKAFSLLEEPVEKLLKEIQPRPNCIIADMCLPYTNRIAK NLGIPKIIFHGMCCFNLLCTHIMHQNHEFLETIESDKEYFPIPNFPDRVEFTKSQLPMVLVAGDWKD FLDGMTEGDNTSYGVIVNTFEELEPAYVRDYKKVKAGKIWSIGPVSLCNKLGEDQAERGNKADIDQ DECIKWLDSKEEGSVLYVCLGSICNLPLSQLKELGLGLEESQRPFIWVIRGWEKYNELLEWISESGYKE RIKERGLLITGWSPQMLILTHPAVGGFLTHCGWNSTLEGITSGVPLLTWPLFGDQFCNEKLAVQILK AGVRAGVEESMRWGEEEKIGVLVDKEGVKKAVEELMGDSNDAKERRKRVKELGELAHKAVEEGG SSHSNITFLLQDIMQLEQPKK
UGT73C6	Q9ZQ95	495	MAFEKNNEPFPLHFVLFPFMAQGHMIPMVDIARLLAQRGVLITIVTTPHNAARFKNVLNRAIESGL PINLVQVKFPYQEAGLQEGQENMDLLTTMEQITSFFKAVNLLKEPVQNLIEEMSPRPSCLISDMCLS YTSEIAKKFKIPKILFHGMGCFCLLCVNVLRKNREILDNLKSDKEYFIVPYFPDRVEFTRPQVPVETYVP AGWKEILEDMVEADKTSYGVIVNSFQELEPAYAKDFKEARSGKAWTIGPVSLCNKVGVDKAERGN KSDIDQDECLEWLDSKEPGSVLYVCLGSICNLPLSQLLELGLGLEESQRPFIWVIRGWEKYKELVEWF SESGFEDRIQDRGLLIKGWSPQMLILSHPSVGGFLTHCGWNSTLEGITAGLPMLTWPLFADQFCNE KLVVQILKVGVSAEVKEVMKWGEEEKIGVLVDKEGVKKAVEELMGESDDAKERRRRAKELGESAHK AVEEGGSSHSNITFLLQDIMQLAQSNN
UGT74E2	Q9SYK9	453	MREGSHLIVLPFPGQGHITPMSQFCKRLASKGLKLTLVLVSDKPSPPYKTEHDSITVFPISNGFQEGEE PLQDLDDYMERVETSIKNTLPKLVEDMKLSGNPPRAIVYDSTMPWLLDVAHSYGLSGAVFFTQPW LVTAIYYHVFKGSFSVPSTKYGHSTLASFPSFPMLTANDLPSFLCESSSYPNILRIVVDQLSNIDRVDIVL CNTFDKLEEKLLKWVQSLWPVLNIGPTVPSMYLDKRLSEDKNYGFSLFNAKVAECMEWLNSKEPNS VVYLSFGSLVILKEDQMLELAAGLKQSGRFFLWVVRETETHKLPRNYVEEIGEKGLIVSWSPQLDVLA

			HKSIGCFLTHCGWNSTLEGLSLGVPMIGMPHWTDQPTNAKFMQDVWKVGVRVKAEGDGFVRR EEIMRSVEEVMEGEKGKEIRKNAEKWKVLAQEAVSEGGSSDKSINEFVSMFC
OsCGT	**C3W7B0**	471	MPSSGDAAGRRPHVVLIPSAGMGHLVPFGRLAVALSSGHGCDVSLVTVLPTVSTAESKHLDALFDA FPAVRRLDFELAPFDASEFPGADPFFLRFEAMRRSAPLLGPLLTGAGASALATDIALTSVVIPVAKEQ GLPCHILFTASAAMLSLCAYFPTYLDANAGGGGGVGDVDIPGVYRIPKASIPQALHDPNHLFTRQFV ANGRSLTSAAGILVNTFDALEPEAVAALQQGKVASGFPPVFAVGPLLPASNQAKDPQANYMEWLD AQPARSVVYVSFGSRKAISREQLRELAAGLEGSGHRFLWVVKSTVVDRDDAAELGELLDEGFLERVE KRGLVTKAWVDQEEVLKHESVALFVSHCGWNSVTEAAASGVPVLALPRFGDQRVNSGVVARAGL GVWADTWSWEGEAGVIGAEEISEKVKAAMADEALRMKAASLAEAAAKAVAGGGSSHRCLAEFA RLCQGGTCRTN
ZmUGT /UGT708A6	**A0A096SRM5**	475	MAANGGDHTSARPHVVLLPSAGMGHLVPFARLAVALSEGHGCNVSVAAVQPTVSSAESRLLDALF VAAAPAVRRLDFRLAPFDESEFPGADPFFLRFEATRRSAPLLGPLLDAAEASALVTDIVLASVALPVAR ERGVPCYVLFTSSAAMLSLCAYFPAYLDAHAAAGSVGVGVGNVDIPGVFRIPKSSVPQALHDPDHL FTQQFVANGRCLVACDGILVNTFDAFEPDAVTALRQGSITVSGGFPPVFTVGPMLPVRFQAEETAD YMRWLSAQPPRSVVYVSFGSRKAIPRDQLRELAAGLEASGKRFLWVVKSTIVDRDDTADLGGLLGD GFLERVQGRAFVTMGWVEQEEILQHGSVGLFISHCGWNSLTEAAAFGVPVLAWPRFGDQRVNA ALVARSGLGAWEEGWTWDGEEGLTTRKEVAKKIKGMMGYDAVAEKAAKVGDAAAAAIAKCGTS YQSLEEFVQRCRDAERK
FeCGTa /UGT708C1	**A0A0A1HA03**	457	MMGDLTTSFPATTLTTNDQPHVVVCSGAGMGHLTPFLNLASALSSAPYNCKVTLLIVIPLITDAESH HISSFFSSHPTIHRLDFHVNLPAPKPNVDPFFLRYKSISDSAHRLPVHLSALSPPISAVFSDFLFTQGLN TTLPHLPNYTFTTTSARFFTLMSYVPHLAKSSSSSPVEIPGLEPFPTDNIPPPFFNPEHIFTSFTISNAKY FSLSKGILVNTFDSFEPETLSALNSGDTLSDLPPVIPIGPLNELEHNKQEELLPWLDQQPEKSVLYVSFG NRTAMSSDQILELGMGLERSDCRFIWVVKTSKIDKDDKSELRKLFGEELYLKLSEKGKLVKWVNQTEI LGHTAVGGFLSHCGWNSVMEAARRGVPILAWPQHGDQRENAWVVEKAGLGVWEREWASGIQ AAIVEKVKMIMGNNDLRKSAMKVGEEAKRACDVGGSSATALMNIIGSLKR
FeCGTb /UGT708C2	**A0A0A1H7N4**	457	MMGDLTTSFPATTLTTNEQPHVVVCSGAGMGHLIPFLNLASTLSSAPYRCKVTLLIVIPLITDAESHHI SSFFSSHPTIHRLDFHVNLPAPKPNVDPFFLRYKSISDSAHRLPVHLSTLAPPISAVFSDFLFTQGLNTT LPHLPNYTFTTTSARFFTLMSYVPHLAKSSSSSPVEIPGLEPFPTDNIPPPFFNPDHIFTSFTISNANYLS LSKGIIVNTFDSFEPETLSALNSGDSLPDLPPVIPIGPLNELEHNKQEELLPWLDQQPEKSVLYVSFGN RTAMSSDQILELGMGLERSDCRFIWVVKTSKIDKDDKSELRKLFGEELYVKLSEKGKLVKWVNQTEIL GHTAVGGFLSHCGWNSVMEAARRGVPILAWPQHGDQRENAWVVEKAGLGVWEREWSSGIQV AIVEKVKMIMGNNDLRNSAVRVGEEAKRACDVGGSSATALMNIIGSLKR
GmCGT /UGT708D1	**I1L3T1**	480	MSSSEGVVHVAFLPSAGMGHLNPFLRLAATFIRYGCKVTLITPKPTVSLAESNLISRFCSSFPHQVTQL DLNLVSVDPTTVDTIDPFFLQFETIRRSLHLLPPILSLLSTPLSAFIYDITLITPLLSVIEKLSCPSYLYFTSSA RMFSFFARVSVLSASNPGQTPSSFIGDDGVKIPGFTSPIPRSSVPPAILQASSNLFQRIMLEDSANVTK LNNGVFINSFEELEGEALAALNGGKVLEGLPPVYGVGPLMACEYEKGDEEGQKGCMSSIVKWLDE QSKGSVVYVSLGNRTETRREQIKDMALGLIECGYGFLWVVKLKRVDKEDEEGLEEVLGSELSSKVKE KGVVVKEFVDQVEILGHPSVGGFLSHGGWNSVTETVWKGVPCLSWPQHSDQKMSAEVIRMSG MGIWPEEWGWGTQDVVKGDEIAKRIKEMMSNESLRVKAGELKEAALKAAGVGGSCEVTIKRQIE EWKRNAQAN
GtUF6CGT1	**A0A0B6VIJ5**	477	MGSLTNNDNLHIFLVCFIGQGVVNPMLRLGKAFASKGLLVTLSAPEIVGTEIRKANNLNDDQPIKVG SGMIRFEFFDDGWESVNGSKPFDVWVYINHLDQTGRQKLPIMLKKHEETGTPVSCLILNPLVPWV ADVADSLQIPCATLWVQSCASFSAYYHYHHGLVPFPTESEPEIDVQLPGMPLLKYDEVPDYLHPRTP YPFFGTNILGQFKNLSKNFCILMDTFYELEHEIIDNMCKLCPIKPIGPLFKIPKDPSSNGITGNFMKVD DCKEWLDSRPTSTVVYVSVGSVVYLKQEQVTEMAYGILNSEVSFLWVLRPPSKRIGTEPHVLPEEFW EKAGDRGKVVQWSPQEQVLAHPATVGFLTHCGWNSTQEAISSGVPVITFPQFGDQVTNAKFLVEE FKVGVRLGRGELENRIITRDEVERALREITSGPKAEEVKENALKWKKKAEETVAKGGYSERNLVGFIE EVARKTGTK
MiCGT	**A0A0M4KE44**	470	MSASDALNSCPHVALLLSSGMGHLTPCLRFAATLVQHHCRVTIITNYPTVSVAESRAISLLLSDFPQIT EKQFHLLPFDPSTANTTDPFFLRWEAIRRSAHLLNPLLSSISPPLSALVIDSSLVSSFVPVAANLDLPSY VLFTSSTRMCSLEETFPAFVASKTNFDSIQLDDVIEIPGFSPVPVSSVPPVFLNLNHLFTTMLIQNGQS FRKANGILINTFEALEGGILPGINDKRAADGLPPYCSVGPLLPCKFEKTECSAPVKWLDDQPEGSVVY VSFGSRFALSSEQIKELGDGLIRSGCRFLWVVKCKKVDQEDEESLDELLGRDVLEKIKKYGFVIKNWV NQQEILDHRAVGGFVTHGGWNSSMEAVWHGVPMLVWPQFGDQKINAEVIERSGLGMWVKR WGWGTQQLVKGEEIGERIKDLMGNNPLRVRAKTLREEARKAIEVGGSSEKTLKELIENWKKTSRKT
MiCGTb	**A0A140GC03**	470	MSASDALNSYPHVALLPSSGMGHLMPFLRLAATLVQHHCRVTVITIYPTVSVAESRAISSLFSAFPQI TEKQFHLLPFDPSSANSTDPFFLRWEAIRRSVHLLTPLLSSISPSLSAIVTDTSLISSVVPVTANLDLPNYI LFTSSTRMCSLIEAFPAFVASKTNFDSIQLDDVIEIQSFSPIPVSSIPPVLLNLNNLFTTTLIQNGQSFRK

			ANGILINTFEALEADIPLGINDKRSLDGLPPFCSVGPLLPCEFEKIECSAPVKWLDDQPEGSVVYVSFG SRFALSSEQIKELGDGLIRSGCRFLWVVKCKKVDQEDEESLDELLGRDLLEKIKKYGFVIKNWVNQQE ILDHRAVGGFVTHGGWNSLMEAVWHGVPMLVWPQFGDQKINAEVIERSGLGMWVKRWGWG TQQLVKGEEIGERIKDLMGNNPLRVRAKTLREEARKAIEVGGSSEKTLKELIENWKKTSRKT
FcCGT /UGT708G1	A0A224AM54	472	MSDSGGFDSHPHVALIPSAGMGHLTPFLRLAASLVQHHCRVTLITTYPTVSLAETQHVSHFLSAYPQ VTEKRFHLLPFDPNSANATDPFFLRWEAIRRSAHLLAPLLSPPLSALITDVTLISAVLPVTINLHLPNYVL FTASARMFSLTASFPAIVASKSTSSGSVEFDDDFIEIPGLPPIPLSSVPPAVMDSKSLFATSFLENGNSF VKSNGVLINSFDALEADTLVALNGRRVVAGLPPVYAVGPLLPCEFEKRDDPSTSLILKWLDDQPEGS VVYVSFGSRLALSMEQTKELGNGLLSSGCRFLWVVKGKTVDKEDEESLKNVLGHELMEKIKDQGLV VKNWVDQDKVLSHRAVGGFVSHGGWNSLVEAARHGVPVLVWPQFGDQKINAEAVESAGLGM WVRSWGWGTELRAKGDEIGLKIKDLMANDFLREQAKRIEEEARKAIGVGGSSERTFKELIDKWKCN NNTH
CuCGT /UGT708G2	A0A224AKZ9	472	MSDSGGFDSHPHVALIPSAGMGHLTPFLRLAASLVQHHCRVTLITTYPTVSLAETQHVSHFLSAYPQ VTEKRFHLLPFDPNSANATDPFLLRWEAIRRSAHLLAPLLSPPLSALITDVTLISAVLPVTINLHLPNYVL FTASAKMFSLTASFPAIVASKSTSSGSVEFDDDFIEIPGLPPIPLSSVPPAVMDSKSLFATSFLENGNSF VKSNGVLINSFDALEADTLVALNGRRVVAGLPPVYAVGPLLPCEFEKRDDPSTSLILKWLDDQPEGS VVYVSFGSRLALSMEQTKELGDGLLSSGCRFLWVVKGKIVDKEDEESLKNVLGHELTEKIKDQGLVV KNWVDQDKVLSHRAVGGFVSHGGWNSLVEAARHGVPLLVWPHFGDQKINAEAVERAGLGMW VRSWGWGTELRAKGDEIGLKIKDLMANDFLREQAKRIEEEARKAIGVGGSSERTFKELIDKWKCNN NTH
ChCGT /UGT708G3	A0A224AMA5	472	MSDSGGFDSHPHVALIPSAGMGHLTPFLRLAASLVQHHCRVTLITTYPTVSLAETQHVSHFLSAYPQ VTENRFHLLPFDPNSANATDPFLLRWEAIRRSAHLLAPLLSPPLSALITDVTLISAVLPVTINLHLPNYV LFTASAKMFSLTASFPAIVASKSTSSGSVEFDDDFIEIPGLPPIPLSSVPPAVMDSKSLFATSFLENGNS FVKSNGVLINSFDALEADTLVALNGRRVVAGLPPVYAVGPLLPCEFEKRDDPSTSLILKWLDDQPEG SVVYVSFGSRLALSMEQTKELGDGLLSSGCRFLWVVKGKNVDKEDEESLKNVLGHELTEKIKDQGLV VKNWVDQDKVLSHRAVGGFVSHGGWNSLVEAARHGVPVLVWPHFGDQKINAEAVERAGLGM WVRSWGWGTELRAKGDEIGLKIKDLMANDFLREQAKRSEEEARKAIGVGGSSERTFKELIDKWKC NNNTH
PlUGT43	A0A172J2G3	469	MTRYEVVFIAIPTLGNLVPQVEFANLLTKHDPRFSATILTVSMPQRPLMNTYVQARASSAANIKLLQ LPIVDPPAPEQYQTLVGFLSLHMQNHKHHVKHALLNLMKTTESNSSNSVRLAAIFVDMFSTTLIDVA AELAVPCYLFFASPASCLGFTLDLPRFDLAESKSEFTVPCFKNLLPRSVFPNLVLDAKDGTFWLSYHAR RYKETKGIVINTLQELETHALQSLHNDSQLQRVYPIGPILDLVGSAQWDPNPAQYKRIMEWLDQQP LSSVVLLCFGSMGSLEANQVEEIAIGLERAGVRFLWALRESPKAQLEYPRDYENHKDVLPDGFLERT NNIGLVCGWVPQAVVLAHKAVGGFVSHCGWNSILESLWHGVPVATWPLYSEQQMNAFQMVRD LGLAVEISVDYRVGADLVRAEEVENGLRSLMKGGDEIRRKVKEMSDTCRGALLENGSSYSNLVSLIQ ELTS
TcCGT1	A0A4Y5RXX8	483	MEKSNPNSTSKPHVFLLASPGMGHLIPFLELSKRLVTLNTLQVTLFIVSNEATKARSHLMESSNNFHP DLELVDLTPANLSELLSTDATVFKRIFLITQAAIKDLESRISSMSTPPAALIVDVFSMDAFPVADRFGIK KYVFVTLNAWFLALTTYVRTLDREIEGEYVDLPEPIAIPGCKPLRPEDVFDPMLSRSSDGYRPYLGMS ERLTKADGLLLNTWEALEPVSLKALRENEKLNQIMTPPLYPVGPVARTTVQEVVGNECLDWLSKQP TESVLYVALGSGGIISYKQMTELAWGLEMSRQRFIWVVRLPTMEKDGACRFFSDVNVKGPLEYLPE GFLDRNKELGMVLPNWGPQDAILAHPSTGGFLSHCGWNSSLESIVNGVPVIAWPLYAEQKMNAT LLTEELGVAVRPEVLPTKAVVSRDEIEKMVRRVIESKEGKMKRNRARSVQSDALKAIEKGGSSYNTLI EVAKEFEKNHKVL
WjGT1 /UGT84A57	BBI55602.1	480	MELETSSSPNPIHVMLVSFQGQGSVSPLLRLGKLIASKGPVVTFVTTEFWGKKMRQANKIVDGELK PVGSGYIRFEFFDDGWAEDDARRGDFDLYLSQLEQAGKRQVSKIVRRYEEKNDPVSCLINNPFIPW VGHVAEEFNILYAVLWIQSCACFSTYYHYQNGSVSFPTETEPKLDVKLPCAPVLKHDEIPTFLHPSSSH FTAMRQAALGIFENLSKPFCVLISSFDALEQEVIDYMSKLCPIKTVGPLFKVAKTVISDVSGDFCKPSD QCLEWLDSRPRSSVVYISFGTVAYLKQEQMEEIARGVLQSGLSFLWVIRPPLEDLRLEAHVVPRELKE ASDKGIGKIVDWCPQDQVLAHPSLACFVTHCGWNSTTEALSSGVPVVCFPQWGDQVTNAVYMV DVFKTAVRLGRGAAEGRVVPGEEVAEKLLEATVGEKAEELRKNALKWKAESEAAVAPGGSSEKNFR EFMEKLGVKENGH
GgCGT /UGT708B4	QGL05036.1	472	MGENNMSSIAPHPVVHVALLPSAGMGHLTPFLRLASLLLHQHCHVTLITPQPTVSKAEEDLLSRFLS AFPQVNQLHFHLPPSDSTISTDPFFLQFASIRSSSHLLTPLLSSLTPPLSSFIYDMTLISPLLPIAESLGVP HYILFTSSATMFSFFSYFPTLAKSESFPGKLDFVEIPGVSVSSIPRSSIPPPLLVPNSLFGKLFMEDSPKLK KLHGVLVNTFEGIEKLSLEALNGGKVVKGLPPVYGVGPFVPCEFEKVVKRGETISEWLDEQPSGSVV YVSFGSRTAMGREQLREVGDGLVKSGWRFLWVVKDKIVDRAEEEGLDGVLGFELVERMVKEKKGL VVKEWVDQSEILGHKAVGGFVSHCGWNSVVEAAWFGVKILGWPLHGDQKINAEVVAKGGWGV

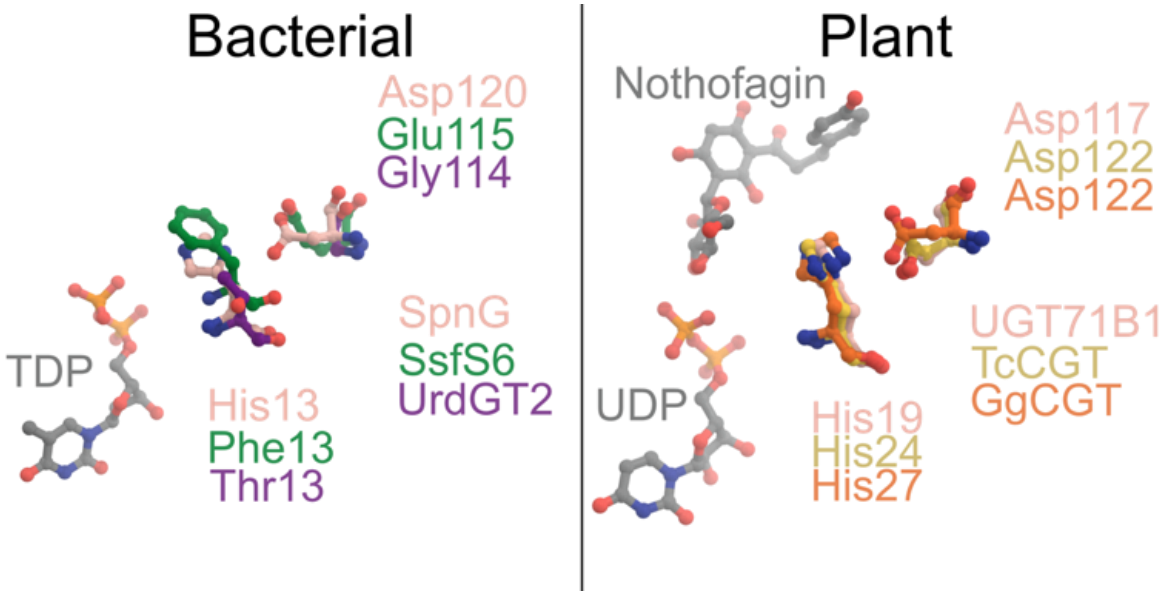
			WKEGWDWEGERLVKGEEIGEAIREVMNDESLVMKATQVKKDARKAISVGGGCEVALQKLMEVW KKNV
OsCGT2 /UGT708A4	**Q5VMG8**	485	MCSAATPNSGDVRATPGSSRPHVVLLPSAGMGHLVPFTRLAAALCSGHGCDVSLVAAVPTVSSAE ARHLAAHFTAFPAVRRLELDLASLDVSEFAGADPFYVRYEAIRRSASLLAPLLAGGASAAASALVADI ALASVVIPVAKDLRLPCYVFFTASATMFSFLAYLPTYLDANAGGGHAIGDVDVPGVCRVPTSSVPQA LHDPDDIFTRQFIANARSLANADGLVVNAFDALEPEAVAALRQGTVAAGLPPVFAVGPLSPAPIPAK DSGSYLPWLDAQPARSVVYVSFGSRKALPRDQLSELAAGLEASGHRFLWVVKGAVVDRDDAGELT DLLGEAFLQRIHGRGLVTMAWVRQEEVLNHPSVGLFISHCGWNSVTEAAASGVPVVAWPRFADQ RVNAGVVARAGIGVWVDTWSWEGEDDGVVSAEDIAGKVRSAMADEGVRKAAASVREAAARAV AAGGSSYRSLAELVRRCRDGLVITNGM
OsCGT3 /UGT708A2	**Q5VME5**	481	MAPPPAVLSSGELGARGHTRPHVVFVPSAGMGHLLQFFRFIGALSAHDVDISVVTVFPTVSAAEAD HFAALFRDYPSVRRLDFDLLPFDASEFPGGDPFLLRWEALRRSLHLLGPVIAGVTPRVTATVTDVTLV SHVNPIAKDLGVQCHVLYVSSAAMMSLCSYFPIYLDNKDAGADVGDVDIPGVRRLKRSWLPQPLLD LNKLFTKQFIENGREMVKTDGVLINTFDALEPVALAALRDGKVVRGFPPVFAVGPHSSLASEATKGA AADAEGSPMAWLRQQPARSVVYVAFGSRCAVSHEQIREIAAGLEASGSRFLWILKTTVVDRDDDA GIRDVLGDGFLERVRGRGVVTKAWVDQDAVLRDPAVGLFLSHSGWNSVIEAATAGVPLLAWPRG GDHRVAATVVASSGVGVWMEQWSWDGEEWVVSGEEIGGKVKEMMADAGVREKAAKVGEEV AKAVAVGGTSHTGILDFVAKLKAAT
OsCGT4 /UGT708A1	**A2YBW7**	476	MAPPTVLNSGEPDSRRRARPHVVFVPSAGMGHLLPFFRFIGALSAHDVDISVVTVLPTVSAAENDH FARLFQDFPSIRRVDFNLLPLDASEFPGADPFLLRWEALRRSMHLLAPAIAGVSPRATAVVTDVTLVS HVNAIAKDLQLQCHVLFISSATMMSFLSYFPIYLDNKDAQADVGDVDIPGVRRLKRSWLPQPLLDL DKLFTKQFIDNGREVVKTDGVLINTFDALEPVALAALRDGKVIRGFPSVFAVGPYSSLASETKAADAE SSALAWLNQQPARSVVYVAFGNRYHVSNDQLREIAAGLEASGCRFLWIVKTTAVDRDEAAGVRDV LGDGFVDRVRGRGMVTKAWVDQEAVLGHPAVGLFLSHSGWNSVTEAAAAGVPLLAWPRAGDH RVAGTVVASSGVGVWMEQWSWDGEEWLVSGQEIGGKVKEMMADAGVRERAAKVGELAAKAV AEGGTSRTSMLEFVAKLKAT
OsCGT5 /UGT708A39	**A2YBW8**	476	MPPPTVLNSGEPDSRRRARPHVVFVPSAGMGHLLPFFRFIGALSAHDVDISVVTVLPTVSAAEADH FARLFQDFPSIRRVDFNLLPLDASEFPGADPFLLRWEALRRSMHLLAPAIAGVRPRATAVVTDVTLVS HVNPIAKDLRLQCHVLFISSATMMSLCSYFPIYLDNKDAEADVGDIDIPGVRRLKRSWLPQPLLDLDK LFTKQFIDNGREVVKTDGVLINTFDALEPVALAALRDGKVIRGFPSVFAVGPYSSLASEKKAADAESS ALAWLNQQPARSVVYVAFGNRYHVSNDQLREIAAGLEASGCRFLWIVKTTAVDRDEAAGVRDVL GDGFVDRVRGRGMVTKAWVDQEAVLGHPAVGLFLSHSGWNSVTEAAAAGVPLLAWPRAGDHR VAGTVVASSGVGVWMEQWSWDGEEWLVSGQEIGGKVKEMMADAGVRERAAKVGEQAAKAV AEGGTSRTSMLEFVAKLKAA
OsCGT6 /UGT708A40	**A2YBX1**	479	MAPPTVLNSGEPDSRRRARPHVVFVPSAGMGHLLPFFRFIGALSAHDVDISVVTVLPTVSAAEADH FARLFQDFPSIRRVDFNLLPLDASEFPGADPFLLRWEALRRSMHLLAPAIAGVSPRATAVVTDVTLVS HVNPIAKDLRLQCHVLFISSATMMSLCSYFPIYLDNKDAEADVGDIDIPGVRRLKRSWLPQPLLDLDK LFTKQFIDNGREVVKTDGVLINTFDALEPVALAALRDGKVIRGFPPVFAVGPYSSLASEKKAADADQS SALAWLDQQPARSVVYVAFGNRCTVSNDQLREIAAGLEASGCRFLWILKTTVVDRDEAAAGGVRD VLGDGFMERVKGRGMVTKEWVDQEAVLGHPAVGLFLSHSGWNSVTEAAAAGVPLLAWPRGGD HRVAATVVASSGVGVWMEQWSWDGEEWLVSGEEIGGKVKEMMADDAVRERAAKVGEEAAKA VAEGGTSRTSMLEFVAKLKAA
TaCGT1-A /UGT708A14	**A0A3B6RGT4**	484	MPTSGDASGALPHPHVVLLPSAGMGHLVPFSRLAVSLSSSDHGCGVSVATVLPTVSSAESAHLEAL FSACPAVRRLDFHLARFDASEFPGADPFFLRFEAMRRSAPLLGPLLAGAGASALVTDIALASVVIPVA KELGLPCYVLFTASTAMLSLCVHFPAYLDANAGGPVGDVDVPGVYRISKASIPQALHHPEHLFTRQF VANGRELAKADGLLVNSFDEFEPEAIAALRDGSVVAGFPNVFSVGPLAPVSFSASEPAENQADYMQ WLAAQPARSVVYVSFGSRKAISKDQLRELAVGLEASGHRFLWVVKSTVVDRDDEAELSELLGEGFLE RVQGRGMVTKGWVEQEEVLKQESIGLFISHCGWNSVTEAAANGLPVLAWPRFGDQRVNAGVVA RSGLGVWEERWSWEGEEGMVSGESIAEKVKAVMADETVRNKAVSVQDAAAKAVADGGTSYRSL AQFVQRCRDLSVSKATFRRSVNTE
TaCGT1-B /UGT708A52	**A0A3B6SEV6**	472	MPTSGDGSGALPHVVLLPSAGMGHLVPFSRLAVSFSSSDHGCGVSVVTVLPTVSSAESAHLDALFG ACPAVRRLDFHLARFDASEFPGADPFFLRFEAMRRSAPLLGPLLAGAGASALVTDIALASVVIPVARE LRLPCYVLFTASAAMLSLCVHFPAYLDANAGGPVGDVDIPGVYRVPKASIPQALHHPEHLFTRQFVA NGRELAKSDGLLVNSFDEFEPEAISALRDGSVAAGFPPVFSVGPLAPVSFSAGEPPENQADYMRWL EAQPTRSVVYVSFGSRKAISKDQLKELAVGLEASGHRFLWVVKSTVVDREDEAELSELLGEGFLERV HGRGMVTKGWVEQEEVLKQESIGLFISHCGWNSVTEAAANGLPVLAWPRFGDQRVNAGVVARS GLGVWEERWSWEGEEGVVSGENIAEKVKAVMADETVRNKAVSVQDAAAKAVADGGTSYRSLAQ FVQRCRDLSVSK

TaCGT1-D /UGT708A53	A0A3B6TPG6	474	MPTSGDASGALPHPHVVLLPSAGMGHLVPFSRLAVSLSSPGHGCGVSVATVLPTVSSAESAHLDAL FGACPAVRRLDFHLAPFDASEFPGADPFFLRFEAMRRSAPLLGPLLAGAGASALVTDIALASVVIPVA RDLRLPCYVLFTASAAMLSLCVHFPAYLDANAGGPVGDVGIPGVYRVPKASIPQALHHPEHLFTQQ FVANGRELAKADGLLVNSFDAFEPEAIAALRNGSVAAGFPPVFSVGPLAPVSFSASEPPENQADYM RWLEAQPARSVVYVSFGSRKAISKDQLRELAVGLEASGHRFLWVVKSTVVDRDDEAELSELLGEGFL ERVQGRGMVTKGWVEQEEVLKQESIGLFISHCGWNSVTEAAANGLPVLAWPRFGDQRVNAGVV ARSGLGVWEERWSWEGEEGTVSGHNIAEKVKTVMADKTVRNKAVSVQDAAAEAVADGGTSYRS LAQFVQRCRDLSVSK
TaCGT2-A /UGT708A15	A0A3B6RGR9	469	MASSSRDDRAGAAAPRPRIVLLPSAGMGHLAPFSRLAAALSSGHACDVSLVTVLPTVSSAESGQLD ALFAAFPAVRRLDFHLPPLDAPELSGADPFYVHYEATRRSARLLAPLLAAADASALIADISLASVLIPVA SELRLPCYVFFTASATMFSFYAYYPTYLDATGAGDADVPGVYRIPKSSFPQALHDRNNLFTQQFVAN GRSLSKADGLLINTFDDLEPEAVTALRQGSVVPGFPPVFTVGPLSPVSFPARASSDYSAWLDAQPER SVVYVSFGSRKALARDQLSELADGLEASGCRFLWVVKGAVVDKDDGAELSELLGEGFLQRVSGRAL VTKAWVEQGEVLKHPAIGMFVSHCGWNSLTEAFATGVPVLAWPRFADQRVNAGIVARCGAGV WVERWSWEGDDGVVKGEEIAEKVKSVMADEMLRRSSTVVREAATTAVAGGGTSYRSLAELVARC CHGSALQ
TaCGT2-B /UGT708A54	A0A3B6SB95	469	MASSPRDDRAGAAAPRPRIVLLPSASMGHLAPFSRLAAALSSGHACDVSLVTVLPTVSSAESGQLD ALFAAFPAVRRLDFQLPPLDAPELSGADPFYVHYEATRRSARLLAPLLAAADASVLVADISLASVLIPV ASELRLPCYVFFTASATMFSFYAYYPTYLDAAGAGDADVPGVYRIPKSSFPQALHDRNNLFTQQFVA NGRSLSKADGLLINTFDALEPEAVTALRQGSVVPGCPPVFTVGPLSPVSFPARASADYSACLDAQPE RSVVYVSFGSRKALARDQLSELADGLEASGCRFLWVVKGAVVDKDDGAELSELLGEGFLQRVSGRA LVTKAWVEQGEVLKHPAIGMFVSHCGWDSLTEAFATGVPVLAWPRFADQRVNAGIVARCGAGV WVERWSWEGDEGVVKGEEIAEKVKSVMANEMLRRSSTMVREAAMTAVAGGGTSYRSLAELVAR CCDGSASQ
TaCGT2-D /UGT708A55	A0A3B6TNL8	474	MASSSRDDRAGAAAPRPRIVLIPSAGMGHLAPFSRLAAALSSGHTCNVSLVTVLPTVSSAESGHLDA LFAAFPAVRRLDFQLPPLDAPELSGADPFYVHYEATRRSARLLAPLLAAADASALVADISLASVLIPVA SELRLPCYVFFTASATMFSFYAYYPTYLDAAGAGDADVPGVYRIPKSSFPQALHDRNNLFTQQFVAN GQSLSKADGLLINTFDALEPEAVTALRQGSVVPGFPPVFNVGPLSPVSFPARASSDYSAWLDAQPER SVVYVSFGSRKALARDQLSELADGLEASGCRFLWVVKGTVVDKDDGAELSELLGEGFLQRVSGRAL VTKAWVEQGEVLKHPAIGMFVSHCGWNSLTEAFASGVPVLAWPRFADQRVNAGIVARRGAGV WVERWSWEGDDGVVKGEEIAEKVKSVMADEMLRRSSTVVREAAMTAVAGGGTSYRSLAELVAR CCDGSASNAPSEA
SbCGT1 /UGT708A36	C5Z8Y8	476	MAPSAMPASGDHTGATPHVVLLPSAGMGHLVPFARLAVALSEGHGCDVSFAAVLPTVSSAESRHL RALFAAAPAVRRLDFRLAPFDESQFPGADPFFLRFEALRRSAPLLGPLLDAAQASALVTDIVLASVVL PVAKARGVPCYVLFTSSAAMLSLCAYFPAHLDANAAAGGGRLGVGDVDIPGVYRIPKSSVPQALHD PKHLFTQQFVANGRGLVAADGILVNTFDAFEPDAITALRQGSVVSDFPPVFAVGPLQPVRFQVAEK PAHYMRWLSAQPARSVVYVSFGSRKAISTDQLRELAAGLEASGQRFLWVVKSTVVDRDDAADLAD LLGDGFLERVQGRAFVTKGWVEQEEILQHGSVGLFISHCGWNSVTEAAAFGVPVLAWPRFGDQR VNAAVVARGGLGAWEERWTWDGEKGLVTGEEVAEKINAVVGNDVVARKAARVGDAAAAAAGK GGTSYQSLADFVGRCRDAGW
SbCGT2 /UGT708A35	C5Z8Y5	482	MSSPALSTTSSHVPRGAPHVVLFPSAGMGHLVPFTRLAVALSAGHGCDISLVTAMPTVSSAESRHIA ALCAAFPAIRQLDLDLRLAPFDASSEFPGADPFYVRYEALRRAAPVLLGPLLAGAGASALVADIALAS VAIPVARELHVPCFVFFTASATMFSLKAYFPTYLDAVGAGHGVGDVDVPGVYRIPSSSVPQALHDP DNIFTRQFVANGRALVTADGLLVNAFHAMEPEAVEALRGGSVVPGLPPVFAVGPLMPVSELRETG EAEQEQGNCYREWLDEQPPRSVVYVSFGSRKALPKDQMNELAAGLEACGHRFLWVVKGAVVDR DDAGELSDLLGEGFLRRVQGQGRGLVTKSWVEQEEVLRHPAVALFVSHCGWNSVTEAASGGVPV LAWPRFADQRVNARVVARAGLGVWAEQWSWEGEEAVVRAEEIAELVMEAMGDDAMAEKAAN VREAASRAVADGGTSYQSLAAFVRRCTA
SbCGT3 /UGT708A34	C5Z8Y2	487	MAPPATKSLGELDGGARPHVMFIPSAGMGHLLPFFRVIAALAAHDVVDISVVTVLPTVSAAEADHF ASLFAALPRVSRVDFHLLPFDASSEFPGHDPFLLRWEALRRSAHLFRPLIAGAAGPRVSAVVTDVTLT SHVIPIAKELGVQCHVLFVSCATMLSLAAYTPVHLDKKNKGEHGPGVGVGVGVGDVDIPGVRRIPQ SYLPQPLLDLNKLFTKQFIDNGREIINADGFLVNTFDALEPVALAALRDGKVVAGFPPVYAIGPLRSKE EEATTGSPPVAWLDEQPARSVVYVAFGNRNAVSLEQIREIAAGLEASGCRFLWVLKTTTVDRDDTA ELTDDVLGEGFLERVQGRGLVTKAWVDQEAVLKHASVGLFLSHSGWNSVTEAAAAGVPLLAWPR GGDHRVNATVVVSGGVGVWMEQWSWDGEDWLVTGEEIGKKVKEVMSDAAVRARATRTGEEA AKAVAEGGTSYRSMQKFISSLKAHCSP
SbCGT4 /UGT708A38	A0A194YGR9	459	MATPPATKSLLGELNGGGASRPHVMFIPSAGMGHLLPFFRFIASLARHDDDVDISVVTVLPTVSAAE ADHFSGLFAAFPRVRRVDFPSHDRDPFIVRWEALRRSAHLIGPLIAGAAPRVSAVITDVTLTSHVIPIA

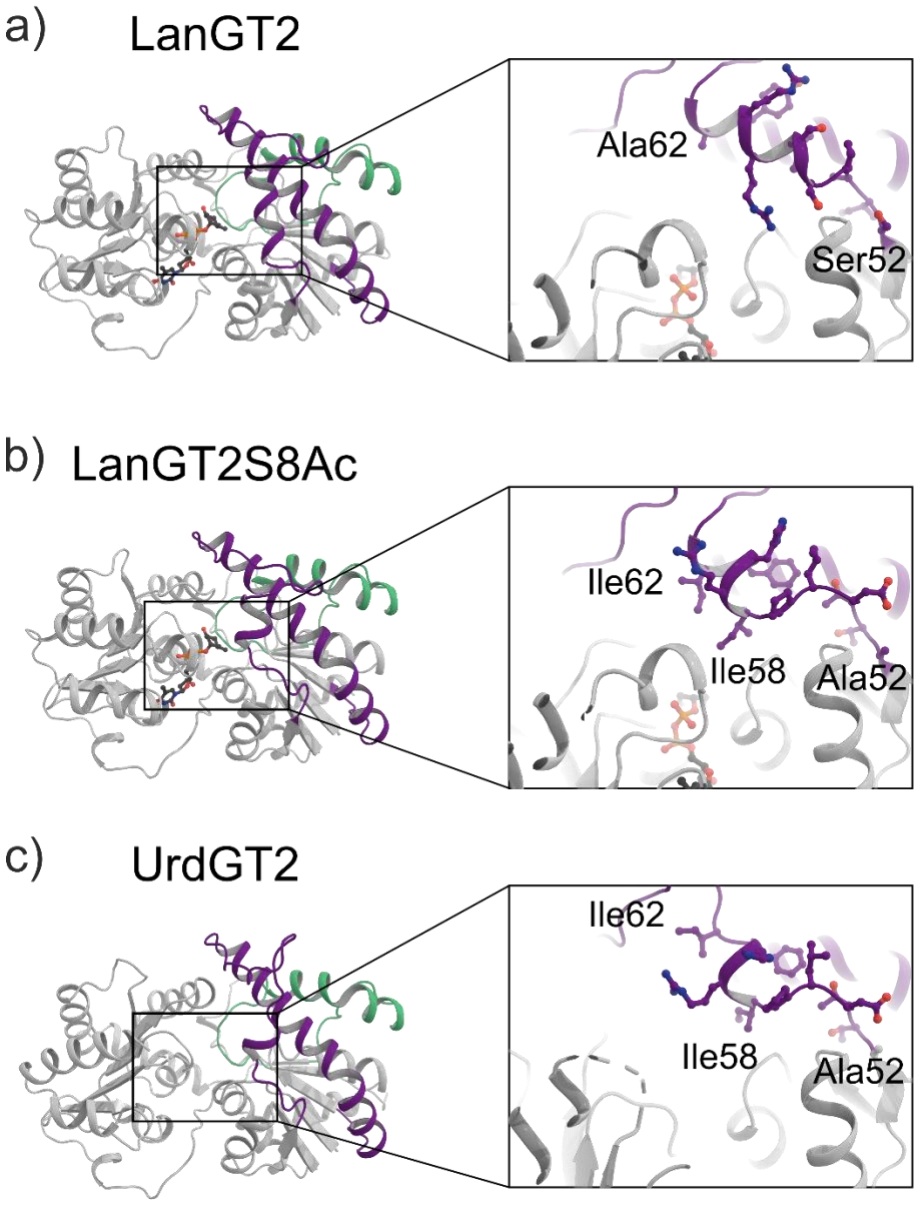
			KKLGVQCHVLFISCATIKKAEQGPGAGVGAVDIPGVRRIPESCLPQPLLDLNKQFTKQFIDNGRENIN ADGILVNTFDALEPAALAALRDGKVVPGFPFPPVYAIGPLRSVVDKEDSSSSSPVVAWLDKQPARSV VYVAFGNRSAVSHAHIREIAAGLEASGCRFLWVLKTTKVDRDDTAELTDVLGEGFLERLHQQQGQG QGQHGMVTKEWVDQEALLKHASVGLYLSHSGWNSVTEAAAAGVPLLAWPRGGDHRVNHWSW DGEDWLVTGEEIAEKVKEVMSDAAVRARATRTGEEAAMAVAEGGTSYRSMQQFVSSLKKAT
ZmCGT2 /UGT708A5	**B6SWX3**	482	MAPPPAMQSPGELNDGAYDAPHILFIPSAGIGHLTPVFRVIAGFSSRGIDVSVVTVLPTVSAAETDYF NGLFADYPAVRRVDMHLLPLDASEFTREDPFFLRWEALRRSVHLLRPIITNAAPRITAIITDITLTSCVI PIAKELDVPCHVLFPTAATMLSLNAYYPVYLEKLKGGPEPGVIGDAVDIPGVFRVPRSALPPALLDVN KLFTKQFIDNGRAIVKADGVLVNTFDAVEPAPLAALRGGKIVPGYPPVYTIGPLKSHATKAGDKPGD ALLDEWLGKQRARSVVYVAFGNRSAARLDQIREIAAGLEDSGYPFLWVLKTTKVDREDDAELAEVL GDGYLERVKGRGIVTKGWVEQEELLKHPAVGMFVSHGGWNSALEASSAGVPLLVWPQLGDHRV NAMAAVRAGIGAWAEHWSWDGEDTLVTRQEIADKVKEVMADGKLRASVAVAREEAAKAVAEG GTSYRNMHDFIAKLKGGA
ZmCGT3 /UGT708A11	**A0A1D6LXE6**	483	MAPPATNSPGEVDSGGRPHVMFIPSAGMGHLIPFFRFIAALAGQSVDISVVTVLPTVSAAEEDYFTS LFAALPRVRRVDLHLLPFDASKLPSNDRDPFVLRWEALRRSAHLLGPLIAGAAPRVSAVITDVTLTSH VIPIAKELGVQCHVLFPSSATMLSLLAYTPVHIDKKAEQGSDIGDVDIPGVCRIPQSCLPQVLLHLDKL FTKQFIANGREIINADGFLVNTFDALEPVALAALRDGKVVPGFPPVYAIGPLMSQQNSVDEGGKEE GSGSPVAWLDEQPARSVVYVAFGNRCAVSHDQIREIAAGLEASNCRFLWVLKTTTVDRDDSAVLTE LLGEEFLERVQGRGLVTKAWVDQEALLKHPAMGLFLSHSGWNSVTEAAAASVPLLAWPRGGDHR VNAMVTVSGGVGMWMEHWSWDGEDWLVTGVEIAKKVKEVMSDEAVRARTTRTAEEAAKAVA EGGTSYRSMEEFISSVKATVAS
ZmCGT4 /UGT708A41	**B4FAN3**	479	MSSPAPSSASRSSHGSRGSPRIVLFPSAGMGHLVPFTRLAVALSAGHGCEISLLTALPTVSSAESRHIA ALYAAFPAIRQLDLRFAPFDASSEFPGADPFYLRYEALRRCAPSLLGPLLAGAGASALVVDMALASVA IPVARELHVPCFVFFTASATMLSFKAYFPTYLDDVGAGHGVGDVDVPGVYRIPSSSVPQALHDPDNI FTRQFVANGRALATADGLLVNAFHAMEPEAVEALQGRFVLSVLPPVFAVGPLMPVNDLRETGEAA QKQGNYRAWLDEQPPRSVVYVSFGSRKALPKDQIKELAAGLEACGHRFLWVVKGAVVDRDDAGE LSELLGEAFLRRVHGRGLVTKSWVEQEEVLRHPAVALFVSHCGWNSVTEAVSSGVPVLAWPRFAD QRVNARVVVRCGLGVWADQWSWEGEEALVRAEEITALVMEAMEDDAMAVKAANVREAASRA VVDGGTSYRSLAAFVRRCTA
ZmCGT5 /UGT708A42	**B4FM13**	484	MSSPAPSSPSRSSHGSRSSPRIVLFPSAGMGHLVPFTRLAVALSAGHGCDISLVTALPTVSSAESRHIA ALYAAFPAIRQLDLRFAPFDASSEFPGADPFYLRYEALRRCAPSLLGPLLAGAGASALVVDMALASVA IPVARELHVPCFVFFTASATMLSFKAYFPTYLDDVGAGHGVGDVDVPGVYRIPSSSVPQALHDPDNI FTRQFVANGRALATADGLLVNAFHAMEPEAVEALQGRFVLSVLPPVFAVGPLMPVNDLRETGEAA QKQGNYRAWLDEQPPRPVVYVSFGSRKALPKDQIKELAAGLEACGHRFLWVVKGAVVDRDDAGE LSELLGEAFLRRVQGRGLVTKSWVEQEEVLRHPAVALFVSHCGWNSVTEAVSSGVPVLAWPRFAD QRVNASVVVRCGLGVWAEQWSWEGEEALVRAEEIAALVMEAMGDDAMAVKTANVREAASRA VVDGGTSYLCLAAFVHRCIAPREVI
SiCGT1 /UGT708A31	**K3XWN4**	475	MPTSGDHSGARPHVVLLPSAGMGHLVPFGRLAVALSAGHGCDVSVAAVLPTVSSAEARHLEALFA AADPAVRRLDFRLAPFDASEFPGADPFFLRFEAMRRSAPLLGPLLATAGASAVVTDIVLASVVLPVA RECGVPCYVLFTASAAMLAFCAHFPGYLDANSAAGRAGVVGDVDIPGVYRIPKSSVPQALHDPKHL FTQQFVANGRGLVDADGILVNTFDALEPEAVTALRKGKVVSSFPLVFAVGPLLPVMFPAKDPAGY MQWLDAQPARSVVYVSFGSRTAISPDQLLELAAGLEASGHRFLWVVKSTVVDRDDAGELGDLLGH GFLERVRGRALVTKGWVEQEEILQHGSVGLFVSHCGWNSVTEAAAFGVPVLAWPRFGDQRINAA VVTRGGLGAWEERWSWDGEEGLVSGEEVGEKIKAVMADETVAKKAAAVGDAAAAAATSKGGTS YRSLAEFVGRCRDAGSRQDR
SiCGT2 /UGT708A32	**K3XWJ1**	494	MSSPPPPNSTSDDCQGTAATPHIVLFPSAGMGHLVPFTRLAVALSAGHCCDVSLVTALPTVSSAESC HIAALFAAFPAVRRLDLRLAPLDASSEFPGADPFYVRYEALRRSTPLLLGPLLAGASASALVADIALAS VAIPVARELRVPCYVFFTASATMLSFKAYFPTYLDANGGAGHSVGDVDVPGVCRVPRSSIPQALHD PDDIFTRQFVANGRALVAADGLLVNAFEAMEPEAVAALLGGSVVASLPPVFAVGPLMPLNLREAA EEQGNYRAWLDAQPPRSVVYVSFGSRKALARDQIRELAAWLEACGHRFLWVVKGAVVDRDDACE LSDLLGEGFQRRVEGRGLVTKSWVEQDEVLRHPAVGLFVSHCGWNSVTEAAANGVPVLAWPRFA DQRVNARVVARAGFGVWVERWSWEGEEAVVGAEEIAEQVVAAMGDQAVAEKAASVRDEAAR AVADGGTSQQSLAEFVRRCRGGLAGPGTDLGRTWTARG
SiCGT3 /UGT708A33	**K3Y181**	467	MKSPGELGSGARPHVMFIPSAGMGHLLPFLRVIAALARHDDVDVSVVTVLPTVSAAEADHLAGLF AAFPRVRRADLHLLPFDASEFPGHDPFLLRWEALRRSAHLLRPLIACGAAPRVSAIVTDVTLASHVIPI SKELNVQCHVHFISCATMLSLLAKAELGPGVGDVDIPGVRRIPESYLPQPLRDLNNVFTKQFIDNGR EIINADGILVNTFDALEPAALAALRDGKVVPGFPPVNAIGPLDSHTASTANAKQSEPAGSPVAWLGE QPARSVVYVAFGNRSAVSRDQLRQIAAGLEASGCRFLWVLKTTTVDKDDNTEVEDVLGCGFLERVR

			GRGLVTKAWVDQEALLKHPAVGLFLSHSGWNSVVEAAAAGMPLLAWPRGGDQRVNAMVVASG GFGVWMEHWSWDGEDRLVTGEEIREKVKEVMSDAAVRVRAMKTGEEAAKAVAEGGTSYRSMQ EFIGKLRAT
BdCGT1 /UGT708A7	I1GYZ6	472	MPTSGDGPTSQPHVVLLPSAGMGHLVPFSRLAVALSSAHGCDVSLVTVLPTVSSAESSHLEALFGAF PAVRRLEFHLADFDASEFPNADPFFLRFEAMRRSAPLLLGPLLARASATALVTDIALSSVVIPVAKQLR LPCYVLFTASAAMLSLCVHFPAYLDANGNGLVGDVDIPGVYQIPKASVPQALHDPKHLFTRQFVAN GRELAKSDGVLVNSFDAFEPEAIAALREGAVSAAGFFPPVFSVGPLAPVSFPAGNNNRADYIQWLE AQPARSVVYVSFGSRKAVARDQLRELAAGLEASGHRFLWVVKSTVVDRDDDADLGELLGEGFLER VQGRGMVTKGWVEQEDVLKQESVGLFISHCGWNSVTEAAAGGLPVLAWPRFGDQRVNAGVVA RSGLGVWVDSWSWEGEEGVVSGESIAEKVKAVMGDEIARNKAVSVRDAAAKAVADGGTSYRNL ARFAQRCRDGRVRE
BdCGT2 /UGT708A8	I1GZD7	487	MADLAAMPNSGEQQGRDAPAPPHLVFVPSAGMGHLLPFTRFIADLANENVEISVVTALPTVSAAE AAHFADLFAAFPRIRRIDFNLLPFDESAFPGADPFLLRWESLRRSAQLLGPLIAAAVPRASAVVTDVTL ASQVIPIAKDELNLPCHILFISCATMLSLVAYFPVYLDGAKADHLVGDVDIPGVLRLPVSSPPQVLRNP DSLFTKQFIANGRTIAKSDGILVNTFRALEPEALSALNSGKVVPGFPPVYAVGPLKSSITMTTSTGSSD KDEGAAAGGSPMAWLGEQPAGSVVYVAFGNRHGVSLEQIREIAAGLEASGCGFLWVLKTTVVDR EDTAELEDVLGRGFLGRVTGRGLVTKEWVDQEAVLQHPAVGLYLSHAGWNSVTESAAYGVPMLV WPTAGDQRVIATVVASAGFGLWMEHWDWESLVSGAEIGEKVKEVMGNEGIKARAAKVSEEAAK AVAEGGSSHRSMQEFLAKLKPSTT
PhCGT1 /UGT708A43	MK616588	472	MPTSGGRTGDRPHVILLPSAGMGHLVPFSRLAVALSSGHGCDVSVVAVLPTVSAAESRHLQGLLDA SPAVRRLDLHLAPFDESEFPGADPFFLRFEAMRRSAPLLGPLLADTGASALVTDIALASVVIPVAKEIH LPCYVLFTASAAMLSFCAYFPTYLDTNAGRVVGDVDIPGVYRIPKASIPQALHDPNHLFTRQFVANG QDLAKADGVLVNTFDALELEAVTALRQGSVAAGFPPVFSVGPLVTVNLPAGEAAKESGNDYMYWL DAQPAQSVVYVSFGSRKAISRDQVRELAIGLEASGQPFLWVVKSTVVDRDDSAELSELLGEGFLERV QGQGFVTKAWVEQEEVLKHESIGLFISHCGWNSVTEAAASGVPVLAWPRFGDQRVNAGVVARG GLGVWVERWSWEGEEDVVSGEEIAEKVKAVMADETVRKKAASVGEAAVKEFADGGTSYRSLTEF VRRCRDLAVLD
PhCGT2 /UGT708A46	MK616589	471	MASRAMPSSSDRTGGAPRVVLLPSAGMGHLVPFGRLAVALSSGHACDVSVVTVLPTVSSAESKHL QGLFDAFPAVRRLDLHLAPFDASEFSDADPFYVRYEAVRRSAPLLGPLLADADASALVADIALASVVI PVAKELLIPCYIFFTASATMFSLLAYFPTYLHSNAGHSIGDVDVPGVYRIPMSSIPQALHDPNNLFTQ QFVANGRSLAEADGLLVNTFDAFEPEAVTALRHGTVAPGFPPVFALGPLSPVGFPAGEAARESGNY TTWLDAQPARSVVYVSFGSRKALLRDQLSELAAGLEASGCRFLWVVKGTVVDRDDDRELRELLGEV FLQRVNGRALVTKAWVEQEEVLKHPAVGLFISHCGWNSVTEATVSGVPVLAWPRFADQRVSAGV VARRGLGVWVERWSWEGEERVVTGDEIAEKVKSVLADETLRKNSTMVREAAAAAVATGGTSYRS LAKFVRRCST
PhCGT3 /UGT708A48	MK616590	473	MAPPATLRSGEPDRDTPHVIFIPSAGMGHLYPFFRFIAALSSYGVDISVVTILPTVSAAEADHFAGLF AAFPSIRRIDFHLLPLDTNEFPGADPFFLRWEELRRSAHLLGPLIASATPRVSTIVSDVTLASHVIPIAKE LHIPCHVLFISCATMLSLNAYFPVYLDTKAGMDGIGDVDIPGVCRIPKSSLPQALLDLNKLFTKQFIEN GREITKADGILVNTFDALEPKALATLRDGTVVTRFPPVFAIGPLTSHSPAAGERVDAGFPLAWLAEQ PTRSVVYVAFGNRNAVTLDQIREIAVGLEASGFRFLWVLKTTVVDHEDTAELKDVLGDGFLERVKGR SLVTKAWVDQEAILKHPAVGLYLSHSGWNSVAEAAAYGVPMLAWPRGGDHRVNATVVVSGGVG VWMEHWSWDGEDRLVSGKEIGDKVKEVMLDAAVRARAAKVGEEADKALTEGGSSYRSMQQFV AKLKNN
PhCGT4 /UGT708A50	MK616591	474	MAPPEMLSSGEQDRGAPHVVFIPSAGMGHLLPFFRFITALSSHDVDISVVTVLPTVTTAEADHFAAL FTALPRIRRINFNLLPLDASAFPGADPFFLRWESLRRSAHLLGPLLAGATPSMSAVITDVTLASQVIPIV KDELHLSCHILFPSSTTMLSLCAYFPTYLDGANADHVVSDVDVPGVRRFTKATLPQALHDPNNLFTK QFVANGRGFTKADGFLLNTFEALEPEAIAALRGGKVIPCFPPVFTVAPLKSMIPADSEKVGAGSPMA WLDEQPARSVVYVAFGNRCAVTLDQIREIAAGLETSSFRFLWVLKTTVVDREDTVELKDVLGDGFLE RMQGRGLVTKAWVDQEAVLNHPAVGLFLSHSGWNSVVEAAVGGVPLLAWPRFGDHRVNATA MVSGGVGVWMEHWSWDGEDRLVSGEEIGEKVKEVMADETVRARVAKVREEAAKAVAEGGSSY RSMQEFVAKLKAN
PgCGT1 /UGT708A44	MK616592	472	MPTSGGRTGGRPHVILLPSAGMGHLVPFSRLAVGLSSGHGCDVSVVAVLPTVSAAESRHLQGLLD ASPAVRRLDLHLAPFDESEFPGADPFFLRFEAMRRSAPLLGPLLADTGASALVTDIALASVVIPVAKEI HLPCYVLFTASAAMLSFCAYFPTYLDTNAGRVVGDVDIPGVYRIPKASIPQALHDPNHLFTRQFVAN GQDLAKADGVLVNTFDALELEAVTALRQGSVAAGFPPVFSVGPLVTVNLPAGEAAKESGNDYMY WLDAQPAQSVVYVSFGSRKAISRDQVRELAVGLEASGQRFLWVVKSTVVDRDDSAELSELLGEGFL ERVQGQGFVTKAWVEQEEVLKHESIGLFISHCGWNSVTEAAASGVPVLAWPRFGDQRVNAGVVA

			RGGLGVWVERWSWEGEEGVVSGEEIAEKVKAVMADETVRKKAASVGEAAVKEFADGGTSYRSLT EFVRRCRDLAVLD
PpCGT1 /UGT708A45	MK616593	472	MPTSGSRTGGRPHVILLPSAGMGHLVPFSRLAVALSSGHGCDVSVVAVLPTVSAAESRHLQGLLDA SPAVRRLDLHLAPFDESEFPGADPFFLRFEAMRRSAPLLGPLLADTGESALVTDIALASVVIPVAKEIH LPCYVLFTASAAMLSFCAYFPTYLDTNAGRVVGDVDIPGVYRIPKASIPQALHDRNHLFTRQFVANG QDLAKADGVLVNTFDALELEAVTALRQGSVAAGFPPVFSVGPLVTVNLPAGEAAKESGNDYMYWL DAQPARSVVYVSFGSRKAISRNQVRELAVGLEASGQRFLWVVKSTVVDRDDSAELSELLDEGFLERV QGRGLVTKAWVEQEEVLKHESIGLFISHCGWNSVTEAAASGVPVLAWPRFGDQRVNAGVVARGG LGVWVERWSWEGEEGVVSGEEIAEKVKAVMADETVRKKAASVGEAAVKEFADGGTSYRSLTEFV RRCRDLAVLD
UrdGT2	Q9RPA7	365	MFALAPLATAARNAGHQVVMAANQDMGPVVTGVGLPAVATTDLPIRHFITTDREGRPEAIPSDP VAQARFTGRWFARMAASSLPRMLDFSRAWRPDLIVGGTMSYVAPLLALHLGVPHARQTWDAVD ADGIHPGADAELRPELSELGLERLPAPDLFIDICPPSLRPANAAPARMMRHVATSRQCPLEPWMYT RDTRQRVLVTSGSRVAKESYDRNFDFLRGLAKDLVRWDVELIVAAPDTVAEALRAEVPQARVGWT PLDVVAPTCDLLVHHAGGVSTLTGLSAGEPQLLIPKGSVLEAPARRVADYGAAIALLPGEDSTEAIAD SCQELHAKDTYARRAQDLSREISGMPLPATVVTALEQLA
gilGT	Q7X2H0	379	MKALFYAAGTSPASAFAIGPLASALRLSGHDVLVASFEEMSGAVTGIGLPSLPVARGHTTESIKAAA GGKPAIEYPHRPEQEMPYLGHWFGRQGSHVFDDLVDVARTWGADVLIAGSQGHGAEIAARFLGI PFVRQSWDLFDVGGYEEYLLEEMADELARIGSDALPDPSLKIDICPPGLVGATGTFMRWTPHNMQ RAIEPWMLTAPDAGRVCLTMGSFRYAFPGAMDRISAIVEGLLELEVEVVVAIGEAEGQRLQEKYPR VRAGWIPLEAILPTCEVIIHPAGGLTAINAINTATPQLILNPFEAFVPRLKHLTDYGCARTLYREEGTPE AITQVVKEMLGDPSYSSRARRLAEQGATAPTAVGMVPLIEDLLARKG
saqGT5	C4NYL6	383	MKVLFVAGGSPATVFALAPLATAVRNAGHQAFMAATDDMMPVVAGAGLPGVPVTPLPIRHFITT DRAGRPLTIPADPAEEARFTGRWFARMAVASMPPLHELAAGWRPDVVVGGTMSYAAPLLAARL GVPFVRQAWDAVEATGVHPGADEELQPELRELGLDRLPEPDLFVDICPPSLRPADAGPAQQMRFV PANAQRSLAPWMYRRGERPRVCVTSGSRVTRGRTYDRNYQFLLDMVGKLTELDVELLVAAPEEVA DGLRAEHGGLRAGWIPLDVVAPTCDVLVHHAGGVSSLTALNAALPQLLMPKGAVLVEPARRIARR GAAIALTPEEETTEAIITACQQLLTEPSYRAAAETLSREIAAMPLPADVVGALEKLVQSPA
SsfS6	D6MSX4	383	MRILVIAGCSEGFVMPLVPLSWALRAAGHEVLVAASENMGPTVTGAGLPFAPTCPSLDMPEVLSW DREGNRTTMPREEKPLLEHIGRGYGRLVLRMRDEALALAERWKPDLVLTETYSLTGPLVAATLGIP WIEQSIRLASPELIKSAGVGELAPELAELGLTDFPDPLLSIDVCPPSMEAQPKPGTTKMRYVPYNGRN DQVPSWVFEERKQPRLCLTFGTRVPLPNTNTIPGGLSLLQALSQELPKLGFEVVVAVSDKLAQTLQP LPEGVLAAGQFPLSAIMPACDVVVHHGGHGTTLTCLSEGVPQVSVPVIAEVWDSARLLHAAGAGV EVPWEQAGVESVLAACARIRDDSSYVGNARRLAAEMATLPTPADIVRLIEQA
IroB	A0A0H2V630	387	MRRLPDLDRQAERDFLMRILFVGPPLYGLLYPVLSLAQAFRVNGHEVLIASGGQFAQKAAEAGLVV FDAAPGLDSEAGYRHHEAQRKKSNIGTQMGNFSFFSEEMADHLVEFAGHWRPDLIIYPPLGVIGPL IAAKYDIPVVMQTVGFGHTPWHIRGVTRSLTDAYRRHNVGATPRDMAWIDVTPPSMSILENDGE PIIPMQYVPYNGGAVWEPWWERRPDRKRLLVSLGTVKPMVDGLDLIAWVMDSASEVDAEIILHIS ANARSDLRSLPSNVRLVDWIPMGVFLNGADGFIHHGGAGNTLTALHAGIPQIVFGQGADRPVNA RVVAERGCGIIPGDVGLSSNMINAFLNNRSLRKASEEVAAEMAAQPCPGEVAKSLITMVQKG
DcUGT2	A0A291PQH4	515	MEFRLLILALFSVLMSTSNGAEILALFPIHGISNYNVAEALLKTLANRGHNVTVVTSFPQKKPVPNLYE IDVSGAKGLATNSIHFERLQTIIQDVKSNFKNMVRLSRTYCEIMFSDPRVLNIRDKKFDLVINAVFGS DCDAGFAWKSQAPLISILNARHTPWALHRMGNPSNPAYMPVIHSRFPVKMNFFQRMINTGWHL YFLYMYFYYGNGEDANKMARKFFGNDMPDINEMVFNTSLLFVNTHFSVDMPYPLVPNCIEIGGIH VKEPQPLPLEIQKFMDEAEHGVIFFTLGSMVRTSTFPNQTIQAFKEAFAELPQRVLWKFENENEDM PSNVLIRKWFPQNDIFGHKNIKAFISHGGNSGALEAVHFGVPIIGIPLFYDQYRNILSFVKEGVAVLLD VNDLTKDNILSSVRTVVNDKSYSERMKALSQLFRDRPMSPLDTAVYWTEYVIRHRGAHHLKTAGAF LHWYQYLLLDVITFLLVTFCAFCFIVKYICKALIHHYWSSSKSEKLKKN



Supplementary Fig. 1 Residues corresponding to position of catalytic dyad. Comparison to SpnG from *Saccharopolyspora spinosa*[21] (PDB ID: 3UYK) for bacterial and UGT72B1 from *A. thaliana*[22] (PDB ID:2VCE) for plant *C*-GTs.



Supplementary Fig. 2 The grafted loop in LanGT2 engineering. a) The native LanGT2 b) LanGT2S8Ac with the grafted loop from UrdGT2 c) native UrdGT2. Ile58 positions the substrate in favor of *C*-glycosylation in the engineered LanGT2S8Ac instead of the *O*-glycosylation of native LanGT2.[23,24]

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