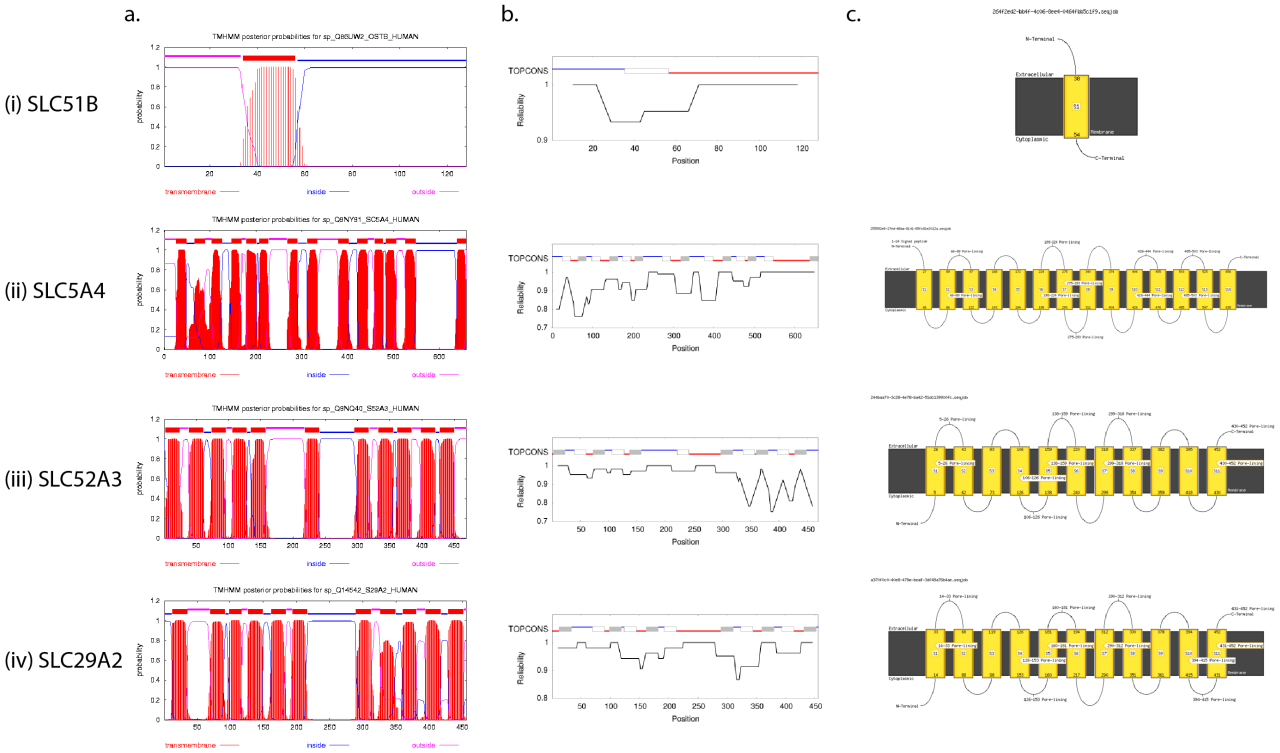
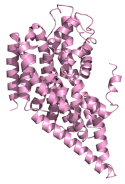
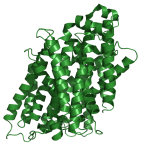
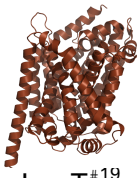
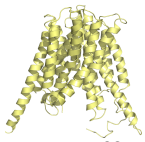
Supplementary Figures



Supplementary Figure 1. Transmembrane helix prediction for selected SLC members. Transmembrane helices were predicted using (**a**) TMHMM (v. 2.0)[13], (**b**) MEMSAT-SVM[14], and (**c**) TOPCONS[15] for the (**i**) organic solute transporter subunit β (SLC51B), (**ii**) low affinity Na^+-glucose co-transporter SLC5A4, (**iii**) riboflavin transporter 2 (SLC52A3), and (**iv**) equilibrative nucleoside transporter 2 (SLC29A2). The predicted transmembrane helices are indicated by red bars (TMHMM), white/gray rectangles (MEMSAT-SVM), and yellow bars (TOPCONS). SLC51B, SLC5A4, SLC52A3, and SLC29A2 are predicted to have 1, 14, 11, and 11 transmembrane helices, respectively, by the three predictors.

Supplementary Tables

Family[a]	Function[b]	Template Structure[c]	Percent Sequence Identity[d]	Representative Ligands[e]
SLC1 (7)	High-affinity glutamate and neutral amino acid transporter family	 Glt(Ph)[16]	34 (3.6×10^{-90})	Glutamate[3], glutamine[3]
SLC2 (14)	Facilitative glucose transporters	 XylE*[17]	31 (2.8×10^{-54})	Glucose[3], uric acid[3]
SLC5 (12)	Na^+- glucose co-transporters	 vSGLT#[18]	32 (1.1×10^{-69})	Dapagliflozin[2], canagliflozin[2], ipragliflozin[2]
SLC6 (21)	Na^+- and Cl^--dependent neurotransmitter transporters	 LeuT#[19]	26 (6×10^{-109})	Fluoxetine[1], fluvoxamine[1], citalopram[1], venlafaxine[1], paroxetine[1], radioiodinated metaiodobenzylguanidine[2] (^{131}I-MIBG), serotonin[3], norepinephrine[3], dopamine[3], GABA[3], amino acids[3]
SLC13 (5)	Na^+-sulfate/carboxylate co-transporters	 VcINDY[20]	32 (1.7×10^{-47})	Succinate[3], citrate[3], alpha-ketoglutarate[3]
SLC25 (46)	Mitochondrial carriers	 UCP2[21]	96 (1.4×10^{-62})	Citrate[3], ornithine[3], adenosine triphosphate[3], aspartate[3], thiamine pyrophosphate[3]

SLC37 (4)	Sugar-phosphate/phosphate exchangers	 GlpT*[22]	25 (6.2×10^{-45})	Glucose-6-phosphate[3]

Supplementary Table 1: Selected SLC families (which contain drug targets) that can be modeled based on a template structures.

a *Family* marks the human SLC family, as annotated by the Bioparadigms database[23]. The number of human protein sequences in the family is provided in parenthesis.

b *Function* gives the function of the human family, as described in the Bioparadigms database

c *Template Structure* describes the most related atomic structure to the family. Structures with the MFS and NSS folds are marked with '*' and '#', respectively.

d *Percent Sequence Identity* provides the percent sequence identity of the best scoring hit from each family; E-value is given in parenthesis.

e *Representative Ligands* gives examples of small molecules that interacts with the transporter. A small molecule ligand can be one of the following:

[1]Clinical drug that is an inhibitor of the transporter.

[2]Clinical drug that is a substrate of the transporter.

[3]Endogenous compound that is substrate of the transporter.