

Figure S1

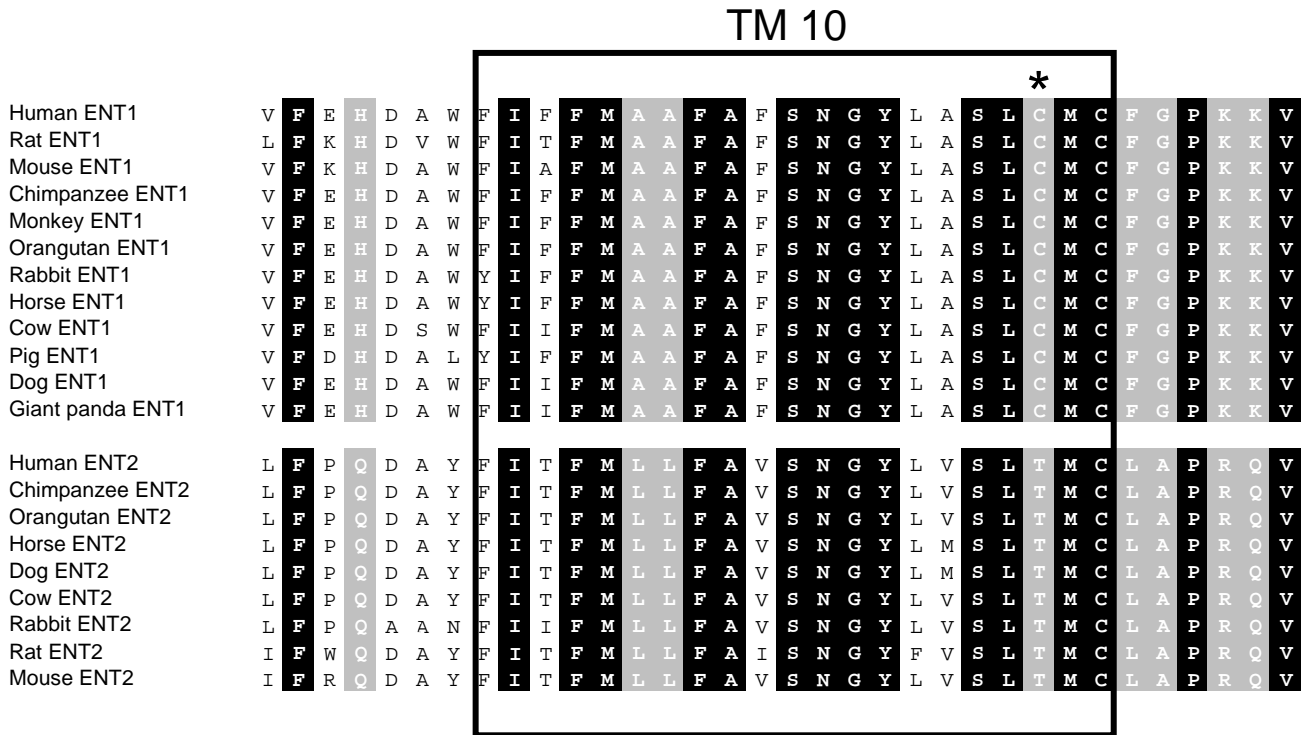


FIGURE S1. **Helix 10 amino acid residues of human and other mammalian ENT1 and ENT2 proteins.** Alignment of predicted amino acid sequences in TM 10 of hENT1 (AAC51103), rENT1 (NP_113872), mENT1 (AAF78452), chimpanzee ENT1 (XP_518505), monkey ENT1 (XP_001091338), orangutan ENT1 (NP_001153270), rabbit ENT1 (XP_002714490), horse ENT1 (XP_001502385), cow ENT1 (NP_001029570), pig ENT1 (XP_003128473), dog ENT1 (NP_001003367), giant panda ENT1 (XP_002914503), hENT2 (NP_001523), rENT2 (NP_113926), mENT2 (AAF78477), chimpanzee ENT2 (XP_001171483), orangutan ENT2 (NP_001153269), horse ENT2 (XP_001496036), dog ENT2 (XP_854729), cow ENT2 (NP_001096739) and rabbit ENT2 (AAK11605). Residues identical in all sequences are indicated by black boxes. Residues highly conserved in either the ENT1 or ENT2 subfamilies are indicated by grey boxes. The position of hENT1 C414 is indicated by an asterisk.

Figure S2

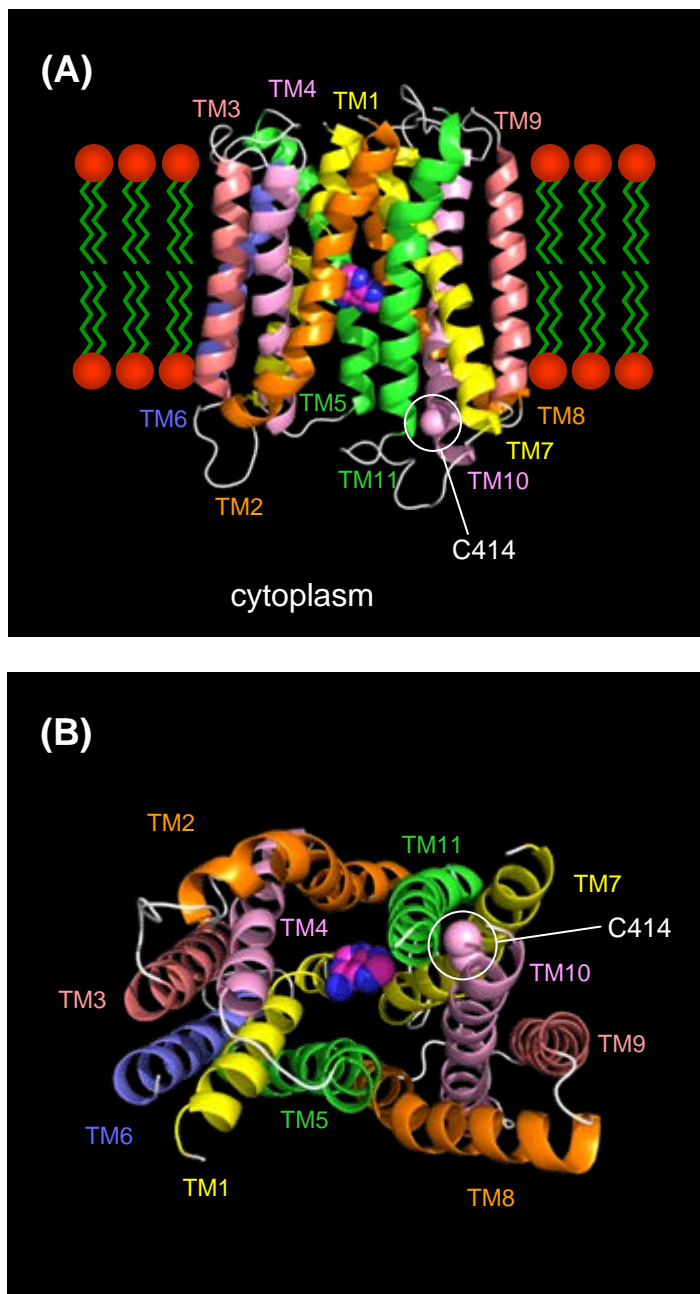


FIGURE S2. **Homology model of hENT1.** Shown is the 3-D model of hENT1 based on the crystal structure of the *E. coli* glycerol 3-phosphate transporter GltT, viewed from within the plane of the lipid bilayer (A) and from the cytoplasmic side of the membrane (B). The side chain of C414 in TM 10 is shown in space-filling form and some loops have been removed for clarity. An adenine molecule has been included in the putative nucleoside/nucleobase permeant binding site to indicate scale, but the precise location and orientation have been arbitrarily chosen (adapted from *ref 10*).