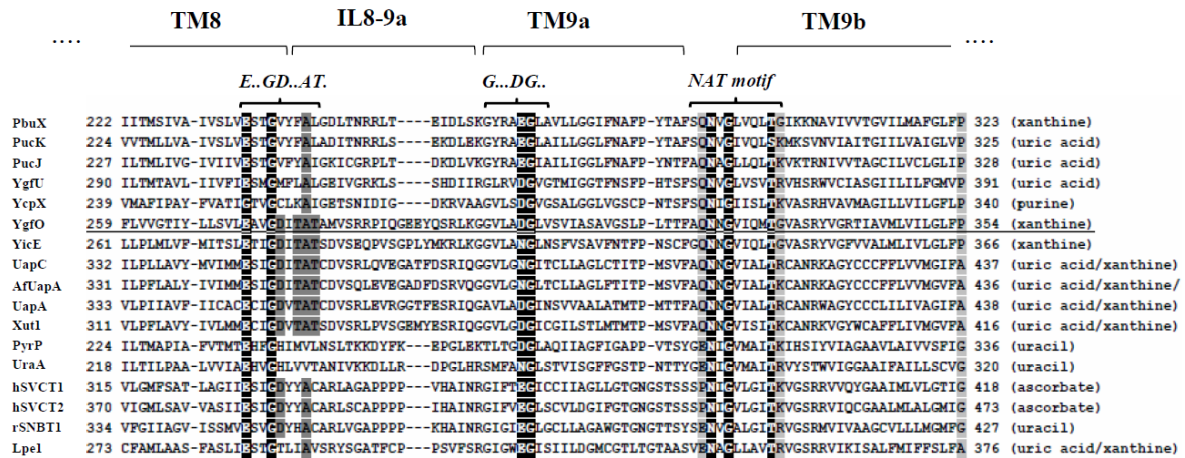


## Supplemental Data

### Figure S1



**Alignment of functionally characterized members of the NAT/NCS2 family in sequences of amphipathic helices TM8, TM9a and TM9b, and intervening loops.** Shown is a consensus of the 17 characterized NAT/NCS2 transporters, including *Escherichia coli* YgfO (XanQ) (P67444), YicE (XanP) (P0AGM9), YgfU (Q46821) (Papakostas and Frillingos, unpublished results), and UraA (P0AGM7), *Bacillus subtilis* PbuX (P42086), PucK (O32140), and PucJ (O32139), *Clostridium perfringens* YcpX (BAB80103), *Lactococcus lactis* PyrP (AAK05701), *Aspergillus nidulans* UapA (Q07307) and UapC (P487777), *A. fumigatus* AfUapA (XP748919), *Candida albicans* Xut1 (AAX2221), *Zea mays* Lpe1 (AAB17501), *Homo sapiens* SVCT1 (SLC23A1) (AAH50261) and SVCT2 (SLC23A2) (Q9UGH3) and *Rattus norvegicus* SNBT1 (AB511909) (Yamamoto et al., 2010). The full-length sequences were aligned using ClustalW and part of this alignment including the residues of interest is presented. Major substrates of each transporter are shown on the right. Positions of high sequence conservation are shown in dark background and conserved sequence motifs, including the NAT-signature motif AQNxGxxxxTG (loop between TM9a and TM9b) (Georgopoulou et al., 2010), ExxGDxxAT (TM8 and IL8-9a), and GxxxDG (TM9a) are indicated above.

### References used in Figure S1

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