ESM_1: Membrane-traversing mechanism of thyroid hormone transport by monocarboxylate transporter 8

Cellular and Molecular Life Sciences

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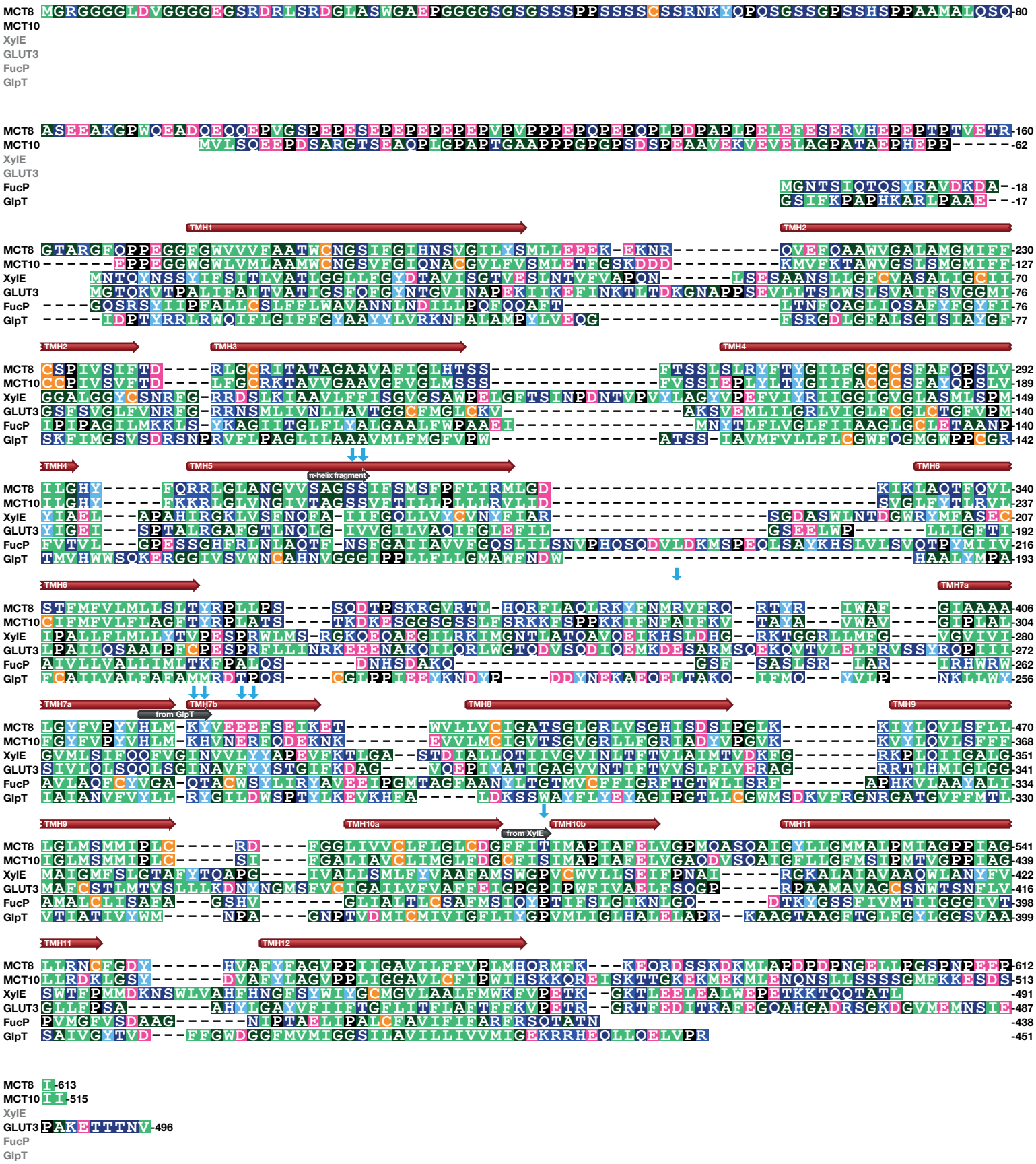

ESM_1: Full sequence alignment of human monocarboxylate transporters 8 (MCT8), 10 (MCT10), the bacterial xylose transporter (XylE, PDB ID: 4aj4 [23] and 4gby [24]) and it's human homologue the glucose transporter 3 (GLUT3, PDB ID: 4zwc [26]), the bacterial fucose transporter (FucP, PDB ID: 3o7q [27]) as well as the bacterial glycerol-3-phosphate transporter (GlpT, PDB ID: 1pw4 [14]). Numbers on the right indicate the respective amino acid number of the last residue in each row. Transmembrane helices (TMH) are annotated as red arrows. Fragments used for manual adjustments of prominent helix distortions in TMH5 (π-helix fragment from PDB ID 2qd3 [25] residues 351-355) and TMH7 (fragment from GlpT, PDB ID: 1pw4 [14] according to the alignment) are indicated as black arrows. Green, hydrophobic residues; blue, basic; magenta, acidic; dark blue, hydrophilic; yellow, cysteines; cyan, tyrosines; black, proline. Positions of at which substituions were introduced are indicated by cyan arrows.