Three synthetic peptides corresponding to transmembrane segments TMS1, TMS3 and TMS6 of secondary-active transporter MntH from Escherichia coli were used as a suitable alternative model enabling to study TMS structure, TMS interaction with membranes, TMS mutual interaction and also function of MntH. The secondary structure of the peptides was estimated in different environments using circular dichroism spectroscopy. These peptides interacted with and adopted helical conformation in lipid membranes. Electrophysiological experiments demonstrated that individual TMS were able under certain conditions to form ion channels in model biological membranes. Electrophysiological properties of these weakly cation-selective ion channels were strongly dependent on surrounding pH. Manganese ion, as a physiological substrate of MntH, enhanced the conductivity of TMS1 and TMS6 channels, influenced the transition between closed and open states and affected the conformation of all studied peptides. For TMS3 Mn^{2+} was crucial for formation of ion channels. It was shown that a single functionally important TMS can retain some of the functional properties of the full-length protein. These findings can contribute to understanding of structure-function relationship at the molecular level. However, it remains unclear to what extent the peptide-specific channel activity represents a functional aspect of the full-length membrane carrier protein.