

Prediction summary of each unique method. An asterisk above the corresponding alignment position indicates each functional site (red = leucine/Na⁺ binding site, green = predicted cytoplasmic gate residue, and purple = predicted extracellular/periplasmic gate residue). Shading of the LeuT_{Aa} sequence indicates sites that are predicted by one (cyan), two (green), three (yellow), four (red), or five (magenta) prediction techniques. As discussed in the text, SDPpred is not considered in the intersect results due to poor overall performance, nor is it considered in the color-coding here. The technique that predicts each site is noted below each alignment position (P = Phylogenetic Motif, F = False Positive Expectation, E = Evolutionary Trace, S = Site Conservation, R = Rate4Site, and D = SDPpred). Transmembrane and other helices are indicated as well. Numbering is based on the LeuT_{Aa} structure.



