



Figure S4. Sequence alignment of human TRPC6 (hTRPC6), hTRPC3, hTRPC7 and Drosophila TRP (dmTRP).

Secondary structure elements are depicted above sequences (cylinders for a helices, lines for loops and dashed lines for unmodeled residues). Conserved residues are highlighted in purple and highly conserved residues are in blue. The residues that are involved in BTDM binding are labeled with asterisks. The non-conserved extended C-terminus of Drosophila TRP channel is not shown due to limited space.