



S4 Fig. Multiple sequence alignment of RsBcsA, AtumCrdS and SmBgsA. Identical residues are shaded black while those with similarity shaded grey. Insertions/deletions are highlighted yellow. Secondary structure and key motifs are also noted. TM helices are numbered starting from TM minus 2 (TM-2) and TM minus 1 (TM-1) for BcsA and CrdS, respectively, so that the numbering aligns with the first TM helix of BgsA, and for the plant CesA/CSLs.