



Supplementary Figure 6. Alignment of the thalassorhodopsins with the rhodopsin of *D. donghaensis* MED134 and other cloned rhodopsins sequences. Predicted transmembrane helices are marked by boxes. Identical residues are indicated in red. Residues in blue are conserved in more than 70% of the sequences. Key amino acids for rhodopsins functionality (listed herein with EBAC31A08 numbering) are marked by colors: Lys131 (K) binds retinal, and Asp97 (D) and Glu108 (E) function as Schiff base proton acceptor and donor, respectively. Metionin (M) in position 105 (*) in the thalassorhodopsins sequences indicate an absorption maxima at the green spectrum range. Letters (G) and (B) in the name of the sequences indicate the range of the spectrum. (The GenBank accession numbers of the sequences used for the alignment are as follows: *Dokdonia donghaensis* MED134, ZP_01049273; Pop-2 HF10_3D09, 82548293; Pop-3 HF70_19B12, 82548286; Pop-4 HF70_59C08, 77024964; *G. pallidula*, WP_006008821; C. Pelagibacter ubique HTCC1062 (SAR11), YP_266049; Pelagibacter sp. HTCC7211, WP_008544914; eBAC20E09, AAS73014; gammaproteobacteria HTCC2207 (SAR192), EAS48197; eBAC31A08 (SAR86), WP008490645; HOT75m4, AAK30179; REDr6a5a6, AAO21455).