

Supporting Information:

Anion binding to mutants of the Schiff base counterion in heliorhodopsin 48C12

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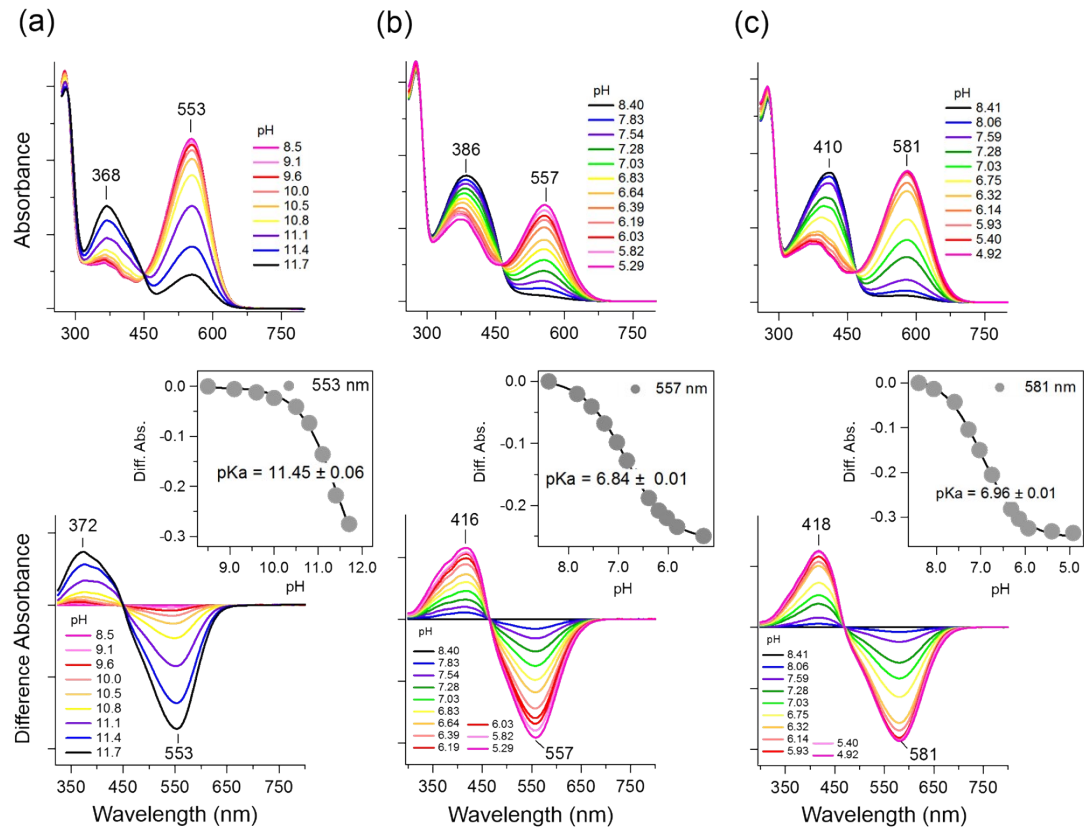


Figure S1. pH titration results of WT (a), E107A (b), and E107Q (c) of heliorhodopsin 48C12, measured in a six-mix buffer (citrate, MES, HEPES, MOPS, CHES, CAPS; conc. of each buffer was 20 mM), 100 mM NaCl, 0.05% DDM. Fig. S1(a) is reproduced from Ref. 21. The 4-nm differences in λ_{max} of visible absorption in (b) and (c) presumably originate from those in pH and salt concentration.

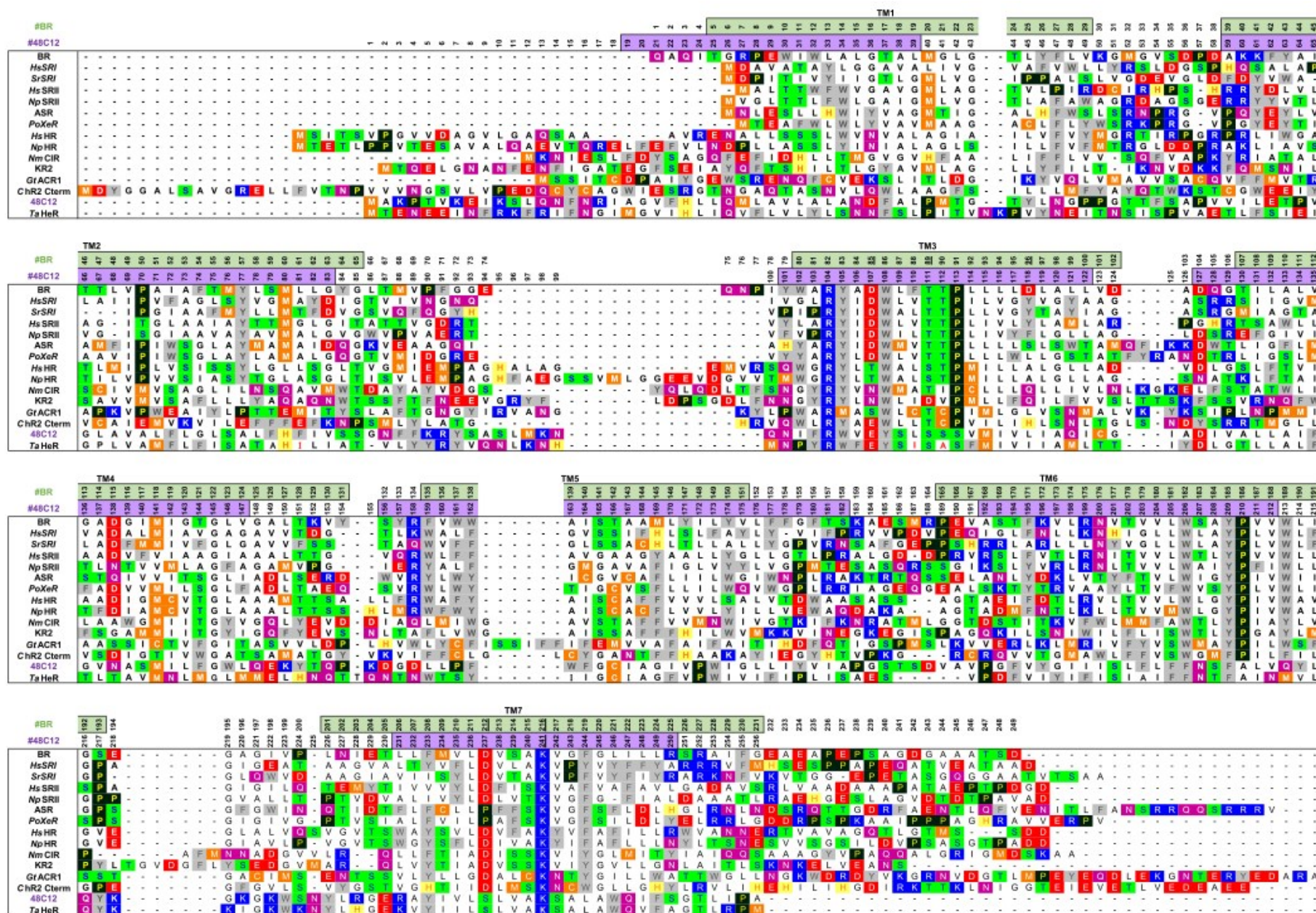


Figure S2. Sequential comparison of heliorhodopsins (48C12 and *TaHeR*) with type-1 rhodopsins. The helical regions of BR based on the crystal structure (PDB ID: 1MOL) are represented by light green color rectangle.