

Figure S1. (A) A 3D structure and (B) ADM for the circadian clock protein KaiA (PDB code: 1R8J). The G and H helix part is purple in color. The flavodoxin domain is enclosed by a red circle. A Rossmann fold is blue in color in (A). The ADM predicted regions are enclosed by blue triangles in (B). The segment of a predicted region is labeled near the diagonal of the map. The location of an α -helix is denoted by a red bar on the diagonal. (A β -strand is denoted by a purple arrow in (B)).

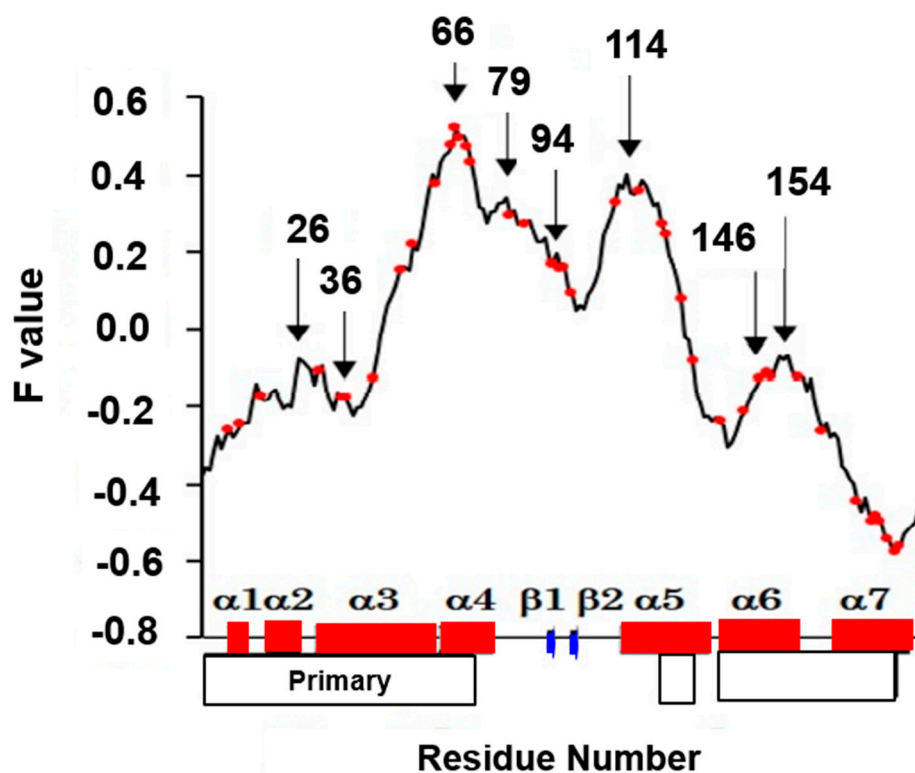
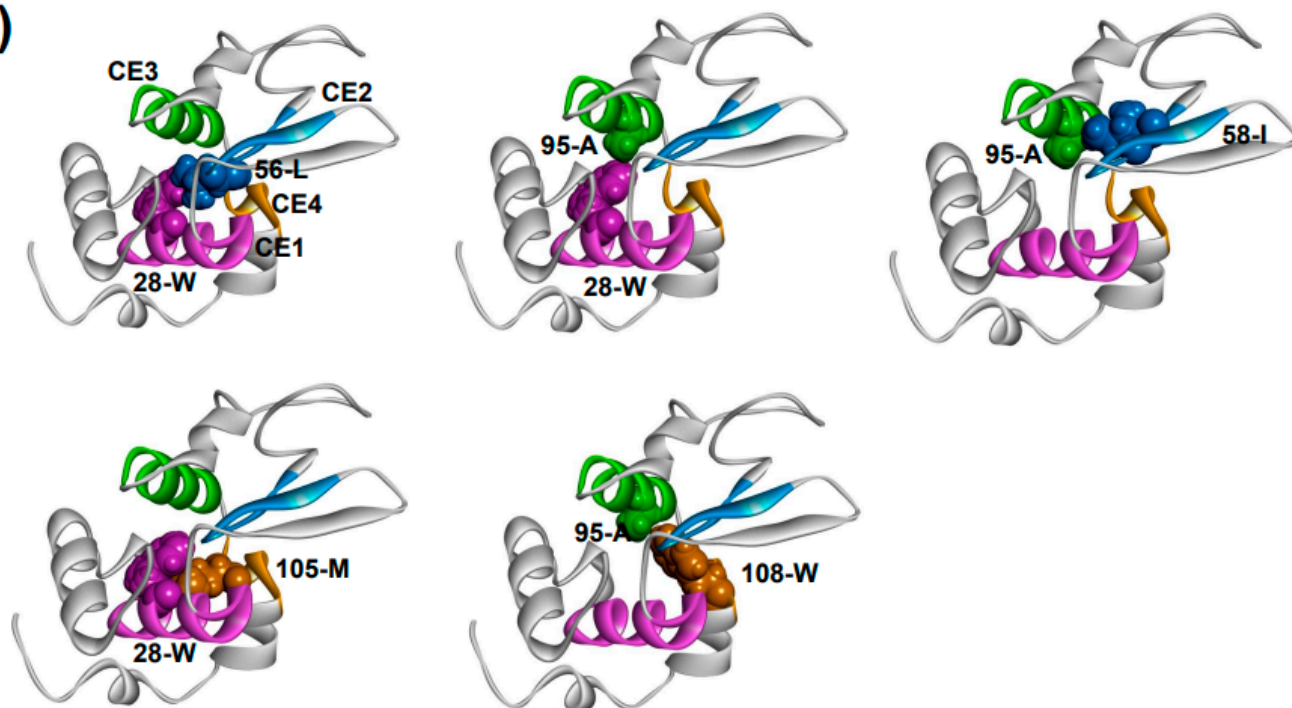
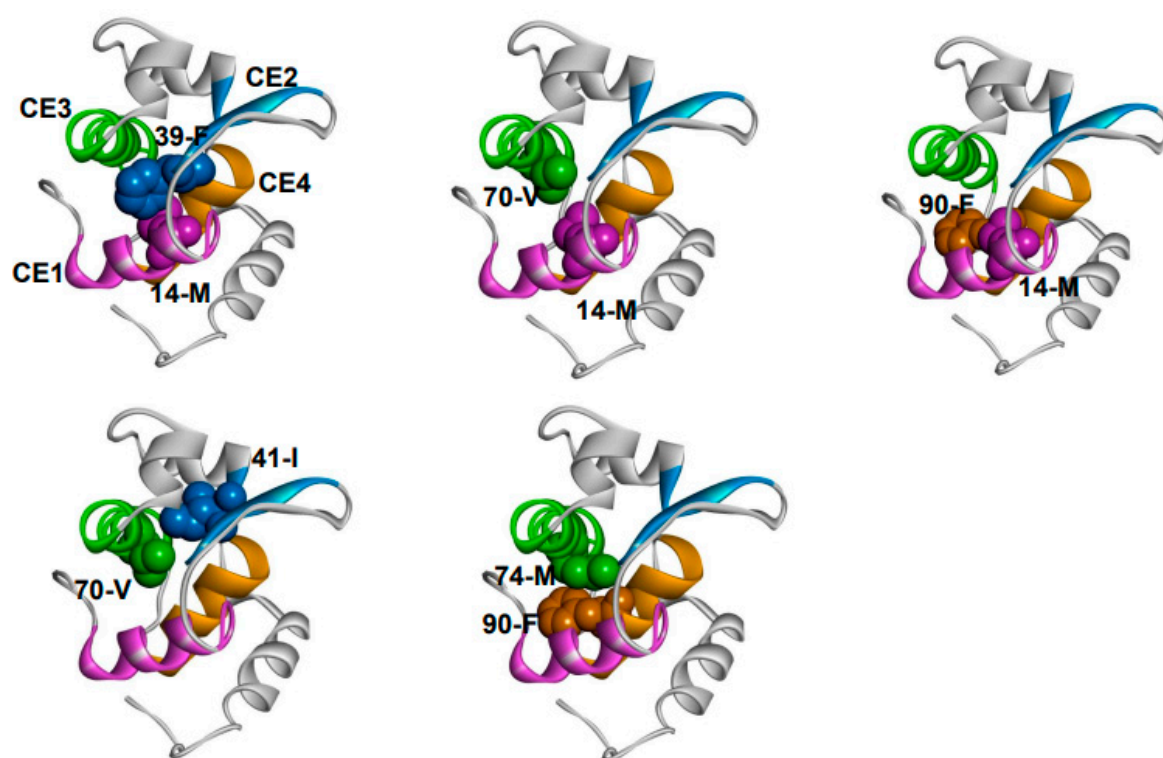


Figure S2 The F-value plot for 153L. A red bar and a blue arrow along the abscissa of a plot indicate the α -helix and β -strand, respectively. An open bar in the bottom of a figure represents a predicted region by ADM. "Primary" means the region with the highest η -value. A red dot indicates a CHR.

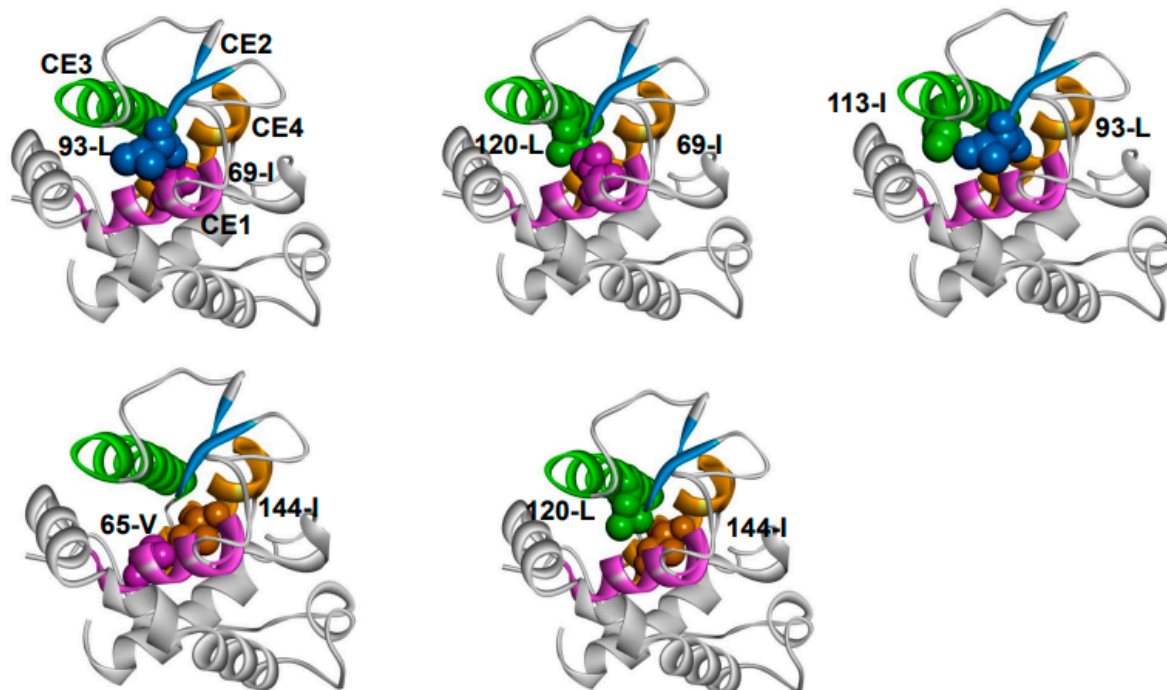
(A)



(B)



(C)



(D)

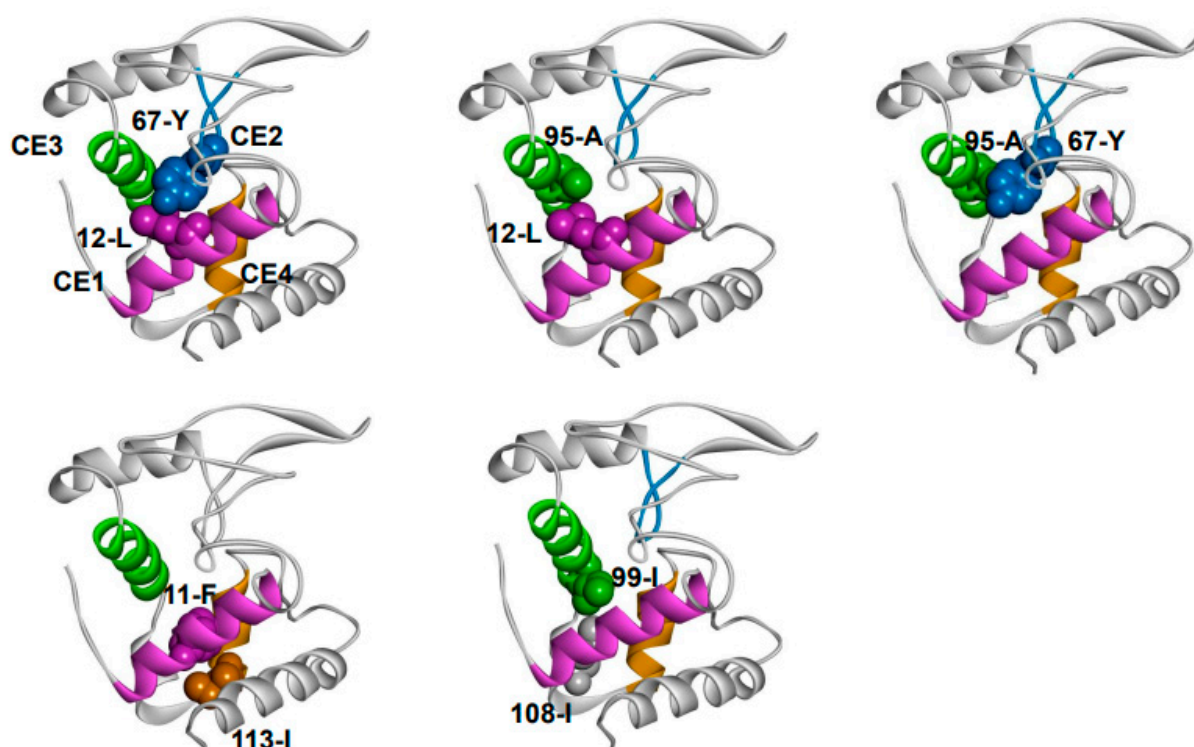


Figure S3: The hydrophobic contacts formed by CHRs in two common secondary structures observed in 2VB1 (A), 2DQA (B), 153L (C) and 1AM7 (D). A secondary structure with the same color denotes a structurally common element (labeled by CE1 (magenta), CE2(blue), CE3(green) and CE4(orange)) in all lysozymes.