Supplemental Figures

Fig. S1. Stereo view of the electron density map of the full-length CusC channel at a resolution of 2.09 Å. This is a $2F_o - F_c$ electron density map (white mesh) contoured at 1.2 σ. The Cα traces of CusC are colored red.

Fig. S2. Secondary structural topology of the CusC monomer. The topology was constructed based on the crystal structure of CusC. The α-helices and β-strands are colored blue and red, respectively.

Fig. S3. Stereo view of the experimental electron density map of the ΔC1 mutant at a resolution of 2.53 Å. Anomalous maps of the 10 selenium sites (contoured at 3 σ), corresponding to the five methionines from each protomer, are colored green. The electron density (colored white) is contoured at the 1.2 σ level and superimposed with the Cα traces of the two ΔC1 protomers (red and blue) in the asymmetric unit.

Fig. S4. Crystal packing of ΔC1. Packing diagram of ΔC1viewed along the (a) *a* axis. (b) Packing diagram of ΔC1viewed orthogonal to (a). The ΔC1 molecules are colored red and green.

Fig. S5. Stereo view of the electron density map of the C1S CusC mutant at a resolution of 2.69 Å. The electron density (colored white) is contoured at the 1.2 σ level and superimposed with the Cα traces of two C1S protomers (blue and green) in the asymmetric unit.

Fig. S6. Representative gel filtration experiment. The experiment demonstrated that the C1S mutant is monomeric. The *y* axis values were defined as: $K_{av} = (V_e - V_0)/(V_T - V_0)$, where V_T,V_e, and V_0 are the total column volume, elution volume, and void volume of the column, respectively. Standards used were: A, cytochrome C (M_r 12,400); B, carbonic anhydrase (M_r 29,000); C, albumin bovine serum (M_r 66,000); D, alcohol dehydrogenase (M_r 150,000); and E, β-Amylase (M_r 200,000). The void volume was measured using blue dextran (M_r 2,000,000). The experiment suggested an average molecular weight of 48.1 ± 4.0 kDa for the C1S mutant. This value is in good agreement with the theoretical value of 48.4 kDa for one C1S molecule, indicating that the C1S mutant is monomeric in form.

Figure S1

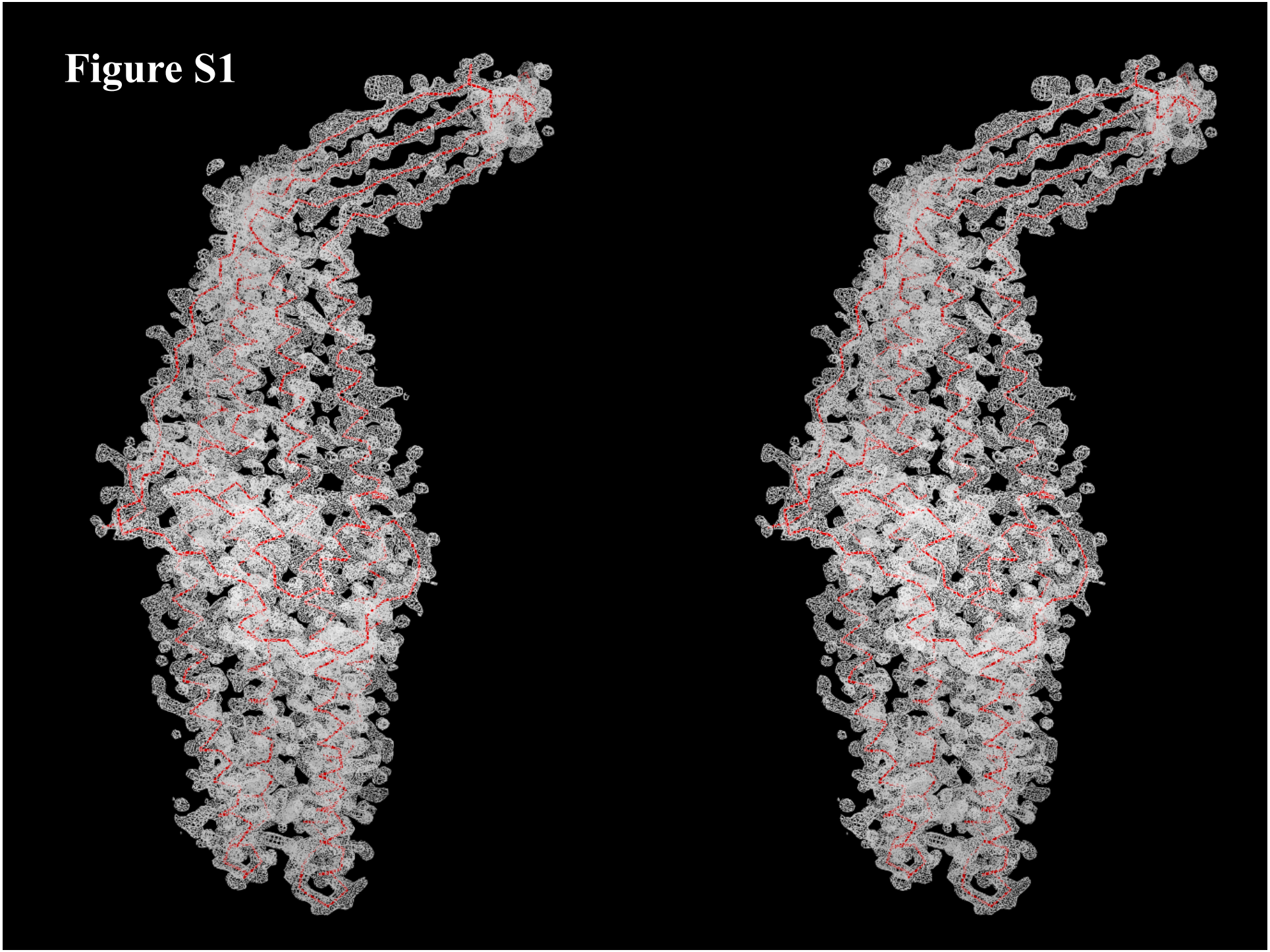
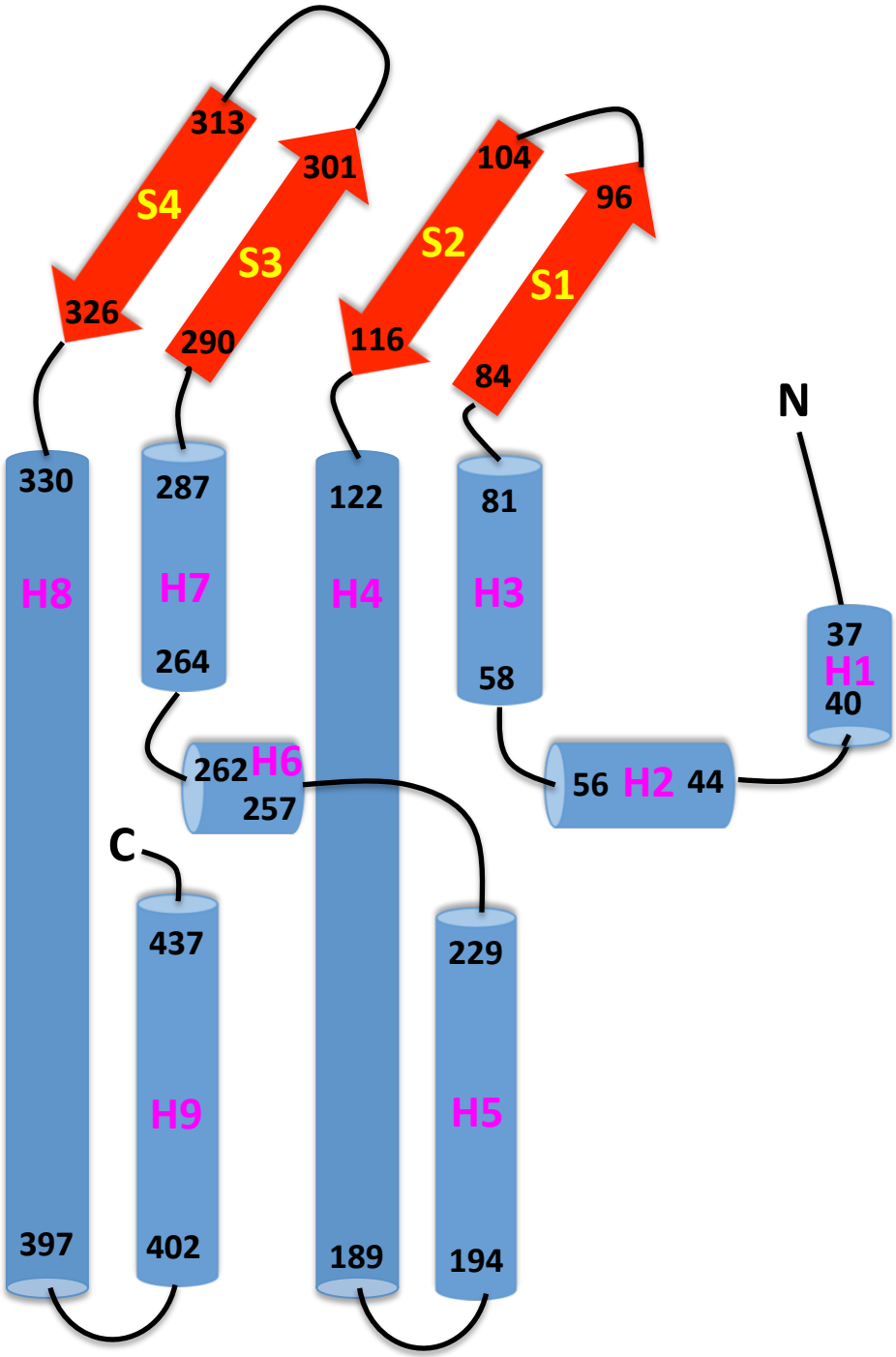


Figure S2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H8
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H4
189
81
H3
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C
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H9
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229
H5
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Figure S3

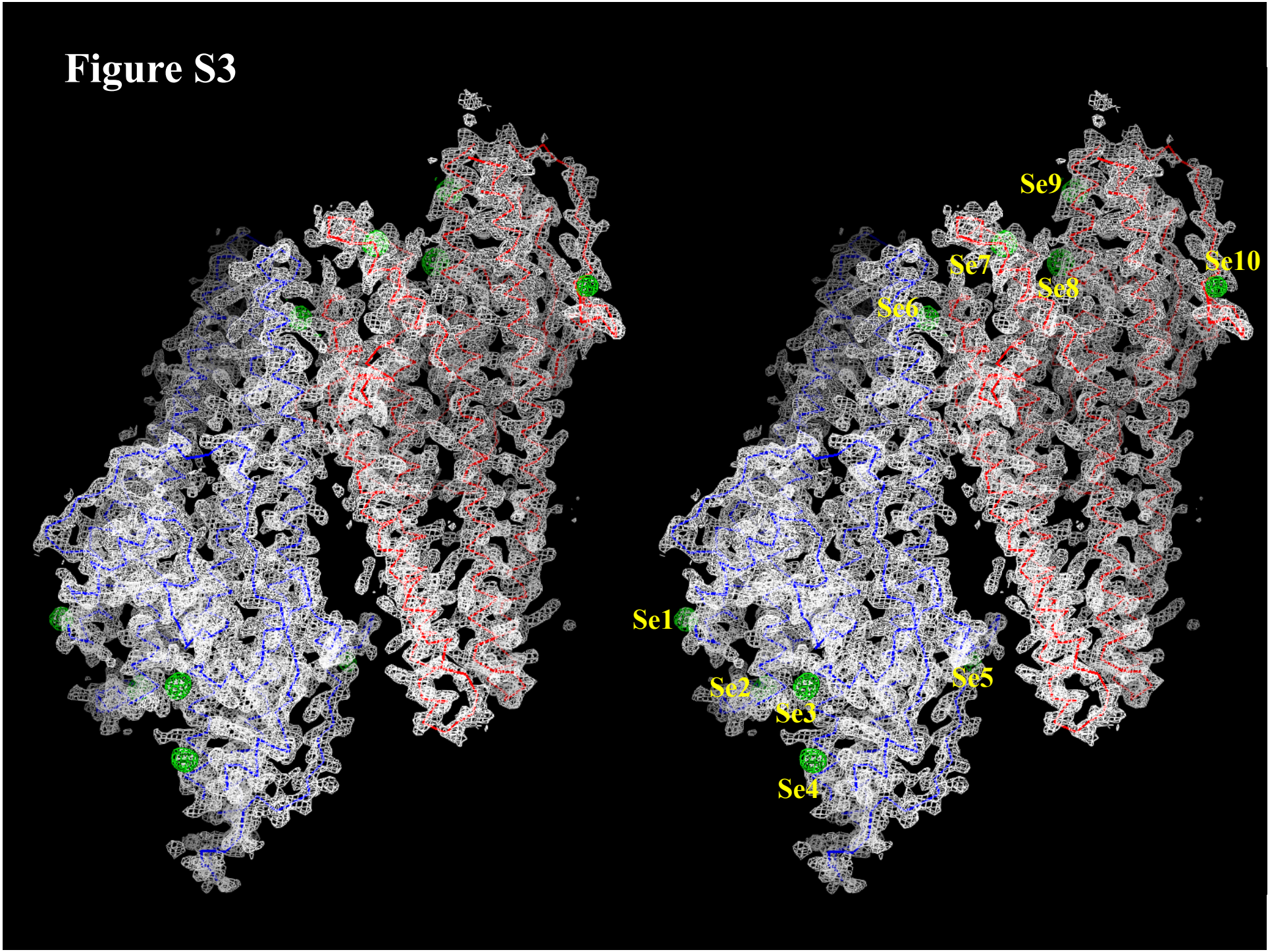


Figure S4a

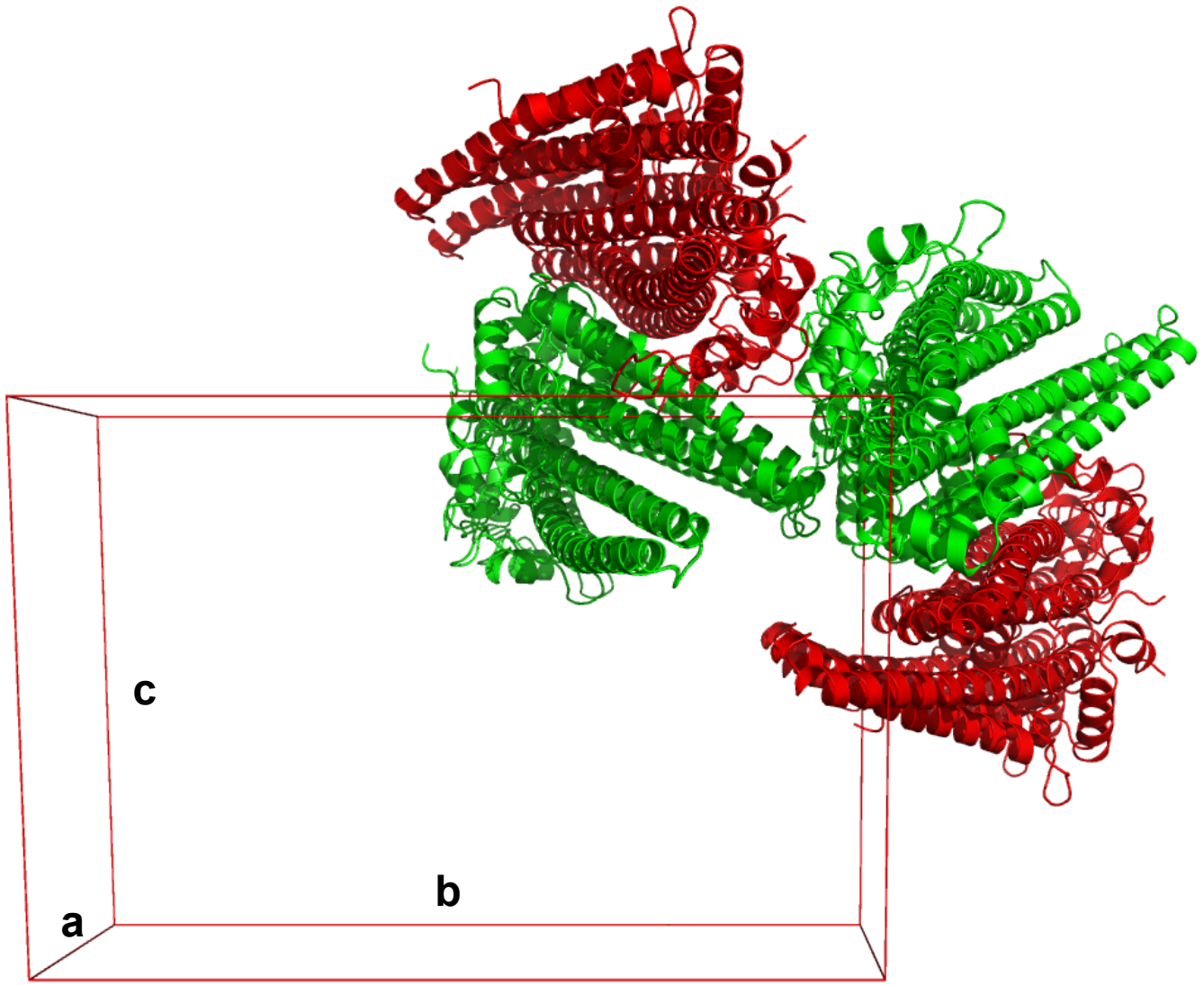


Figure S4b

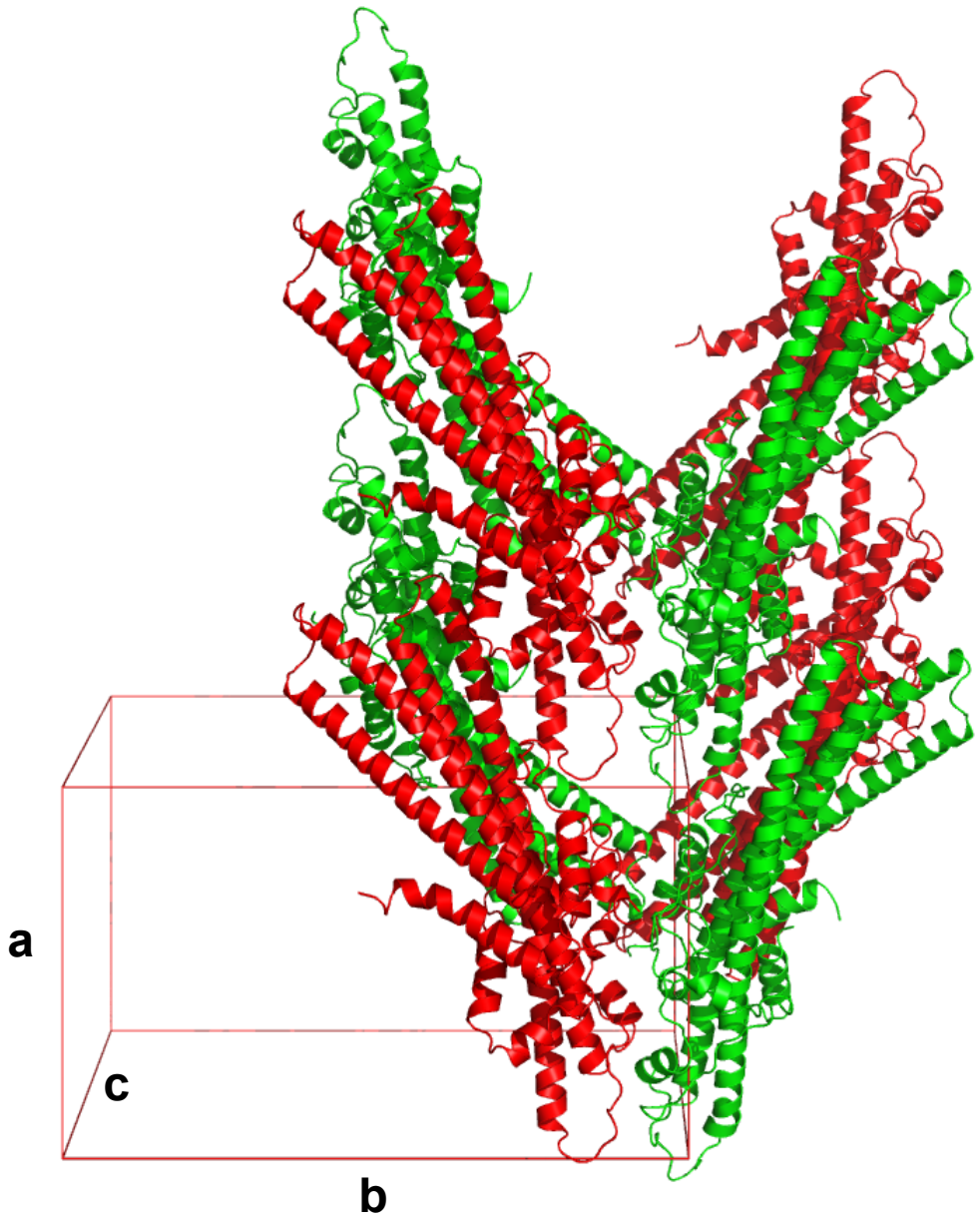


Figure S5

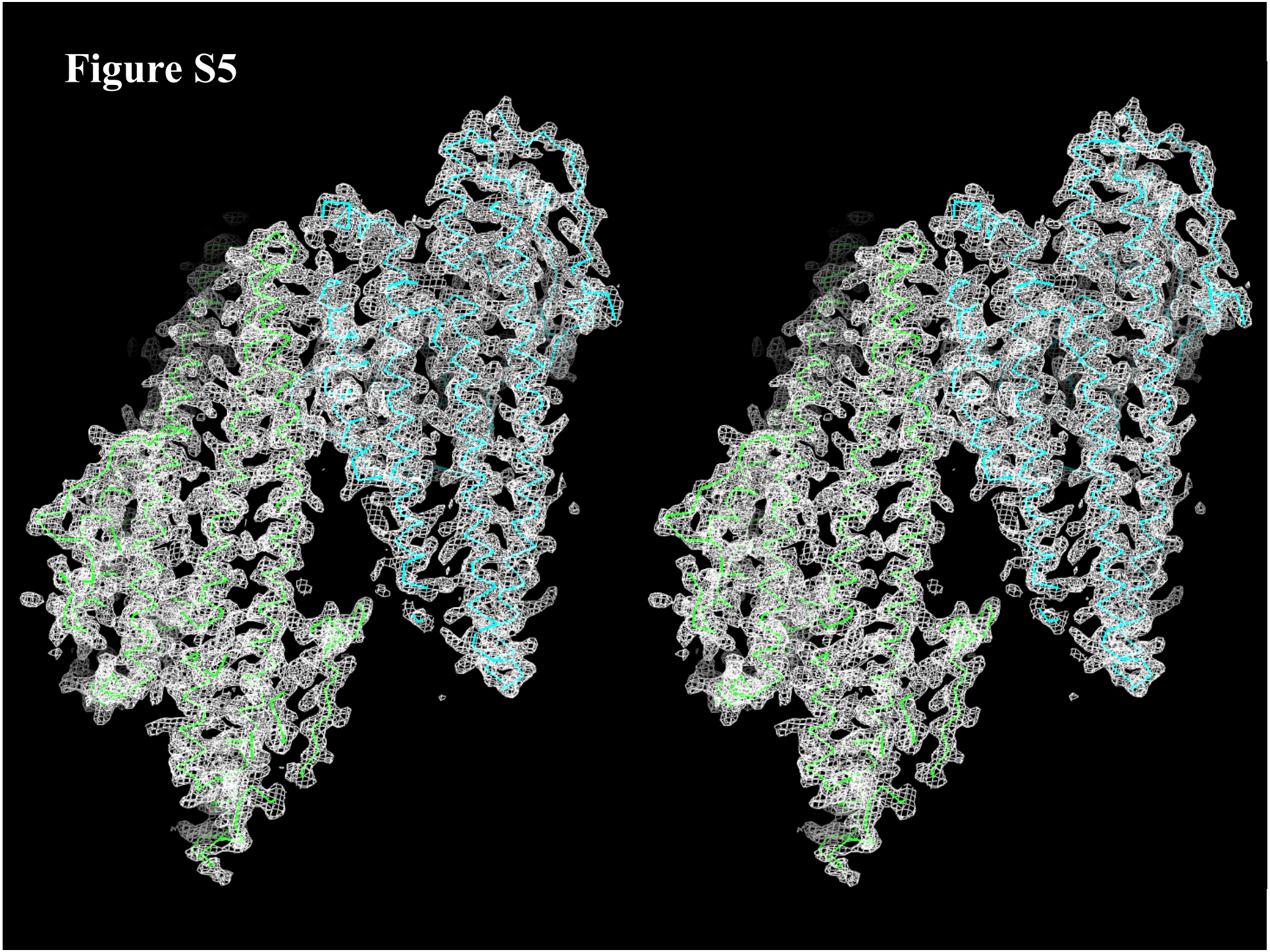
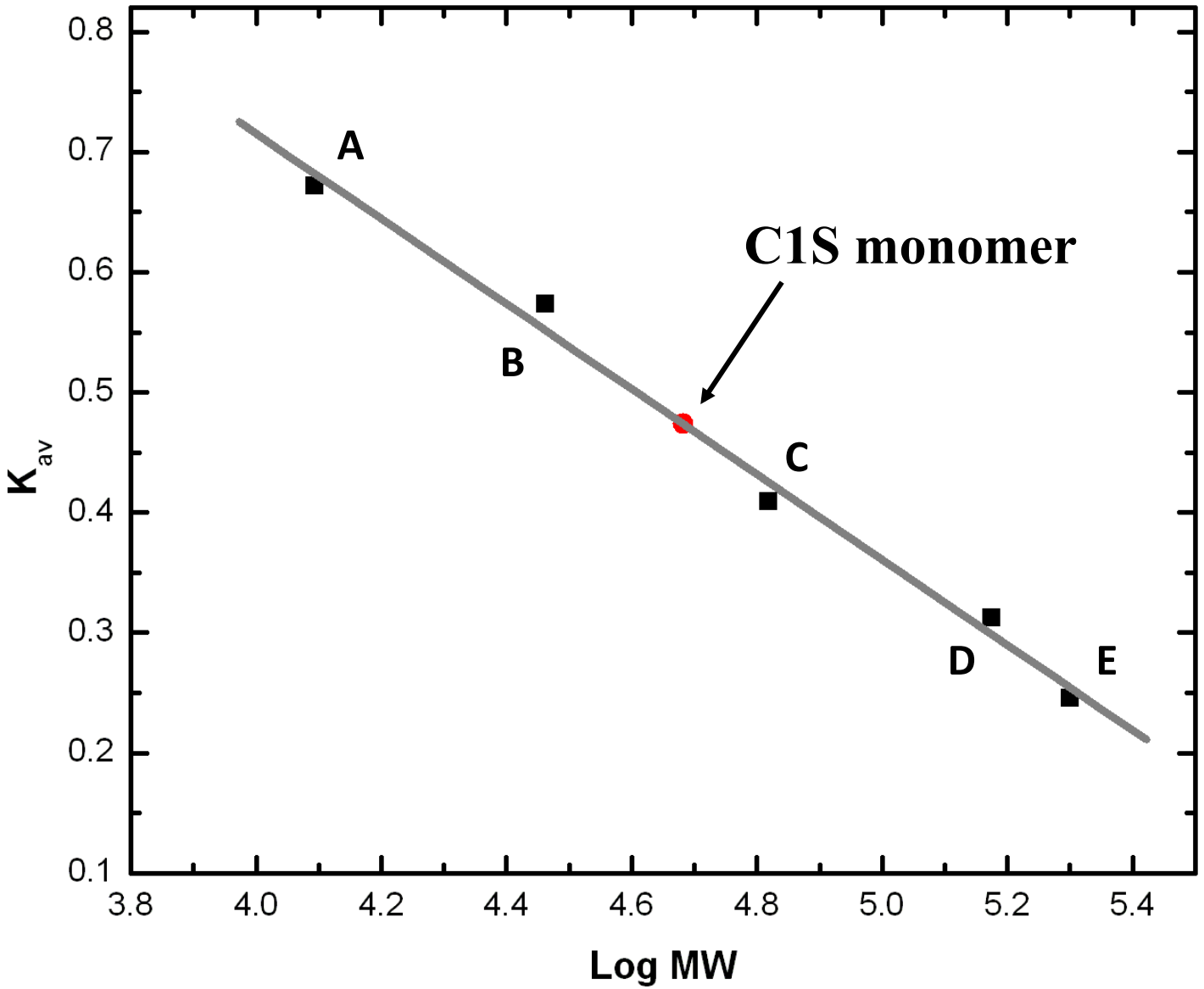


Figure S6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4.6
4.8
5.0
5.2
5.4
Log MW
A
B
C
D
E
C1S monomer