Supporting Information

Structural analysis of diheme cytochrome *c* by hydrogen deuterium exchange mass spectrometry and homology modeling

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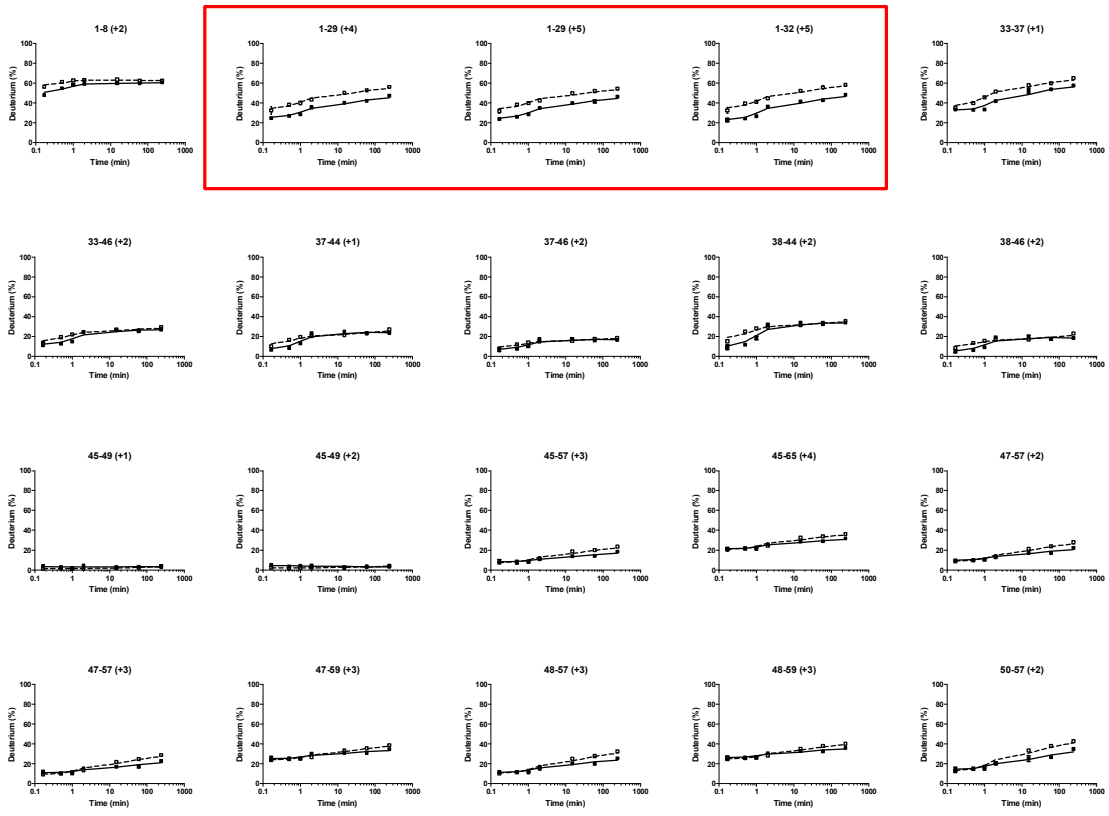
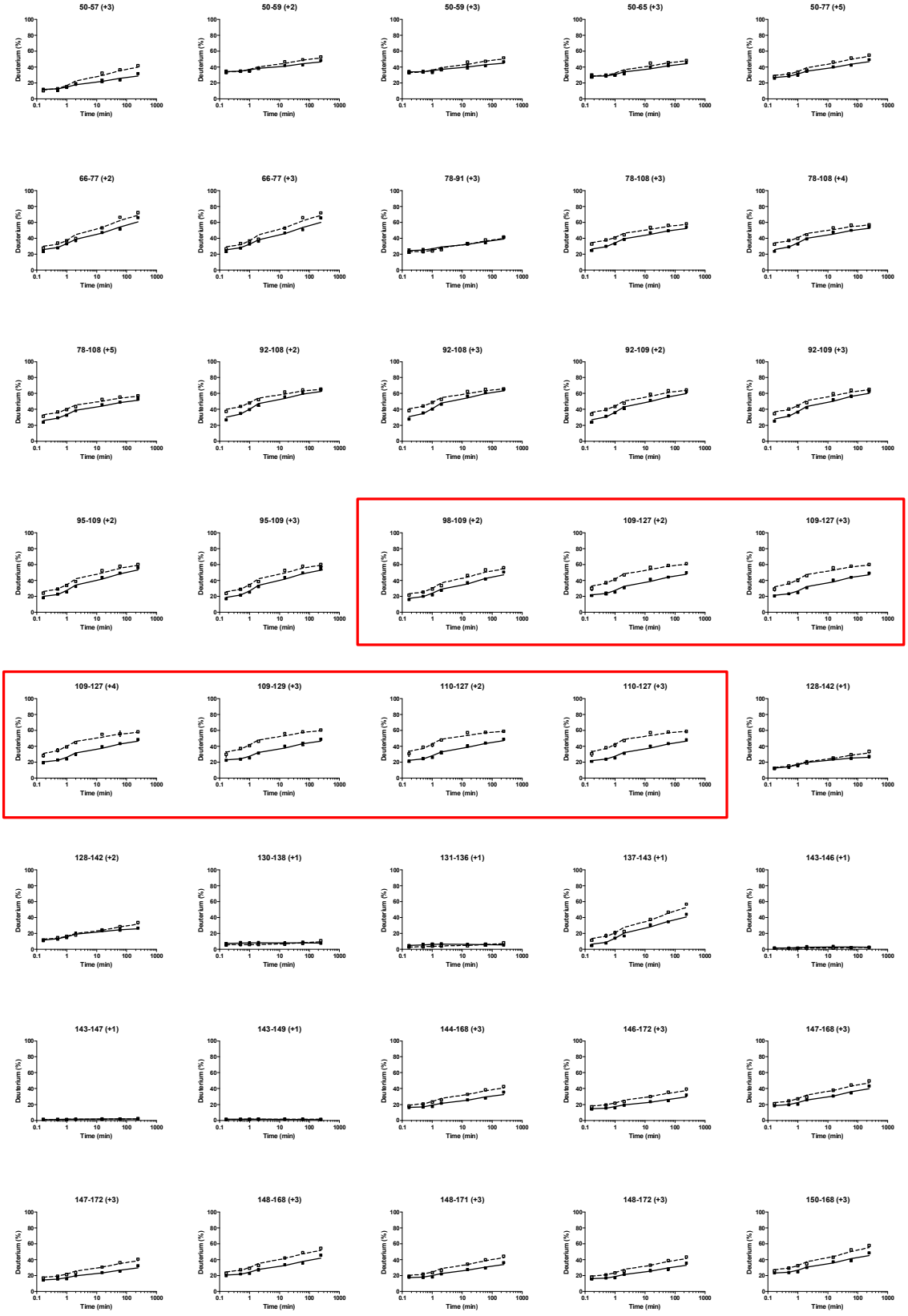
HDX kinetic curves




50-57 (+3)
50-59 (+2)
50-59 (+3)
50-65 (+3)
50-77 (+5)
66-77 (+2)
66-77 (+3)
78-91 (+3)
78-108 (+3)
78-108 (+4)
78-108 (+5)
92-108 (+2)
92-108 (+3)
92-109 (+2)
92-109 (+3)
95-109 (+2)
95-109 (+3)
98-109 (+2)
109-127 (+2)
109-127 (+3)
109-127 (+4)
109-129 (+3)
110-127 (+2)
110-127 (+3)
128-142 (+1)
128-142 (+2)
130-138 (+1)
131-136 (+1)
137-143 (+1)
143-146 (+1)
143-147 (+1)
143-149 (+1)
144-168 (+3)
146-172 (+3)
147-168 (+3)
147-172 (+3)
148-168 (+3)
148-171 (+3)
148-172 (+3)
150-168 (+3)
Deuterium (%)
Time (min)

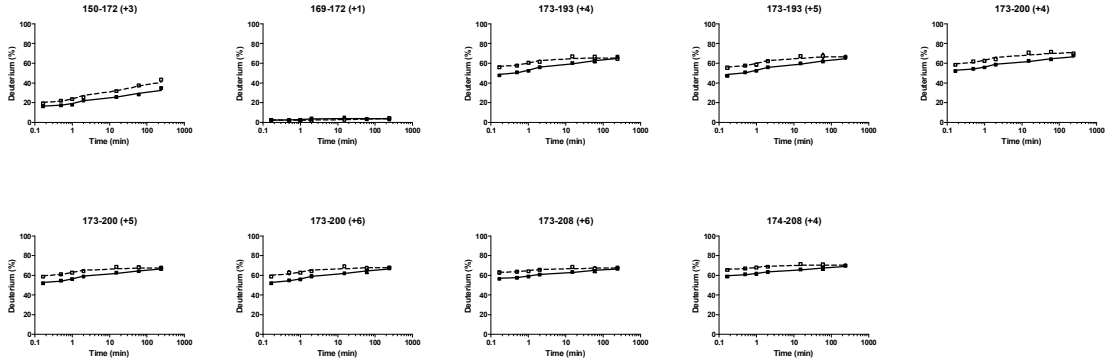


Figure S1. Kinetic curves of all the peptides used for HDX mapping for reduced (solid line) and oxidized (dash line) states of the DHCC. The peptides involved in heme *c* binding pockets are highlighted in red frames. Numbers in parentheses with "+" sign are the charge states of the peptides.

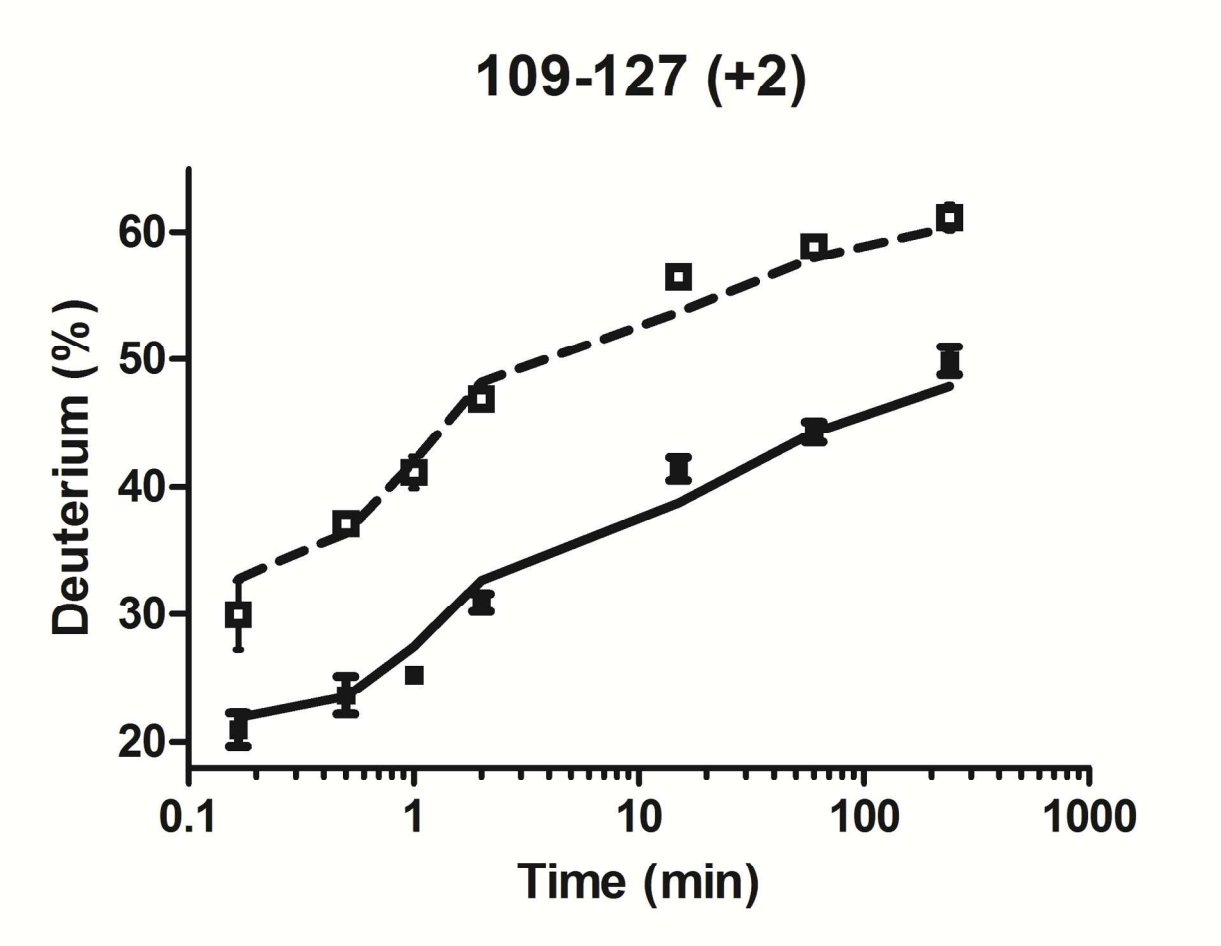


Figure S2. Selected HDX kinetic curves for demonstration of the precision for each experiment. The curves are typical through the sequence.

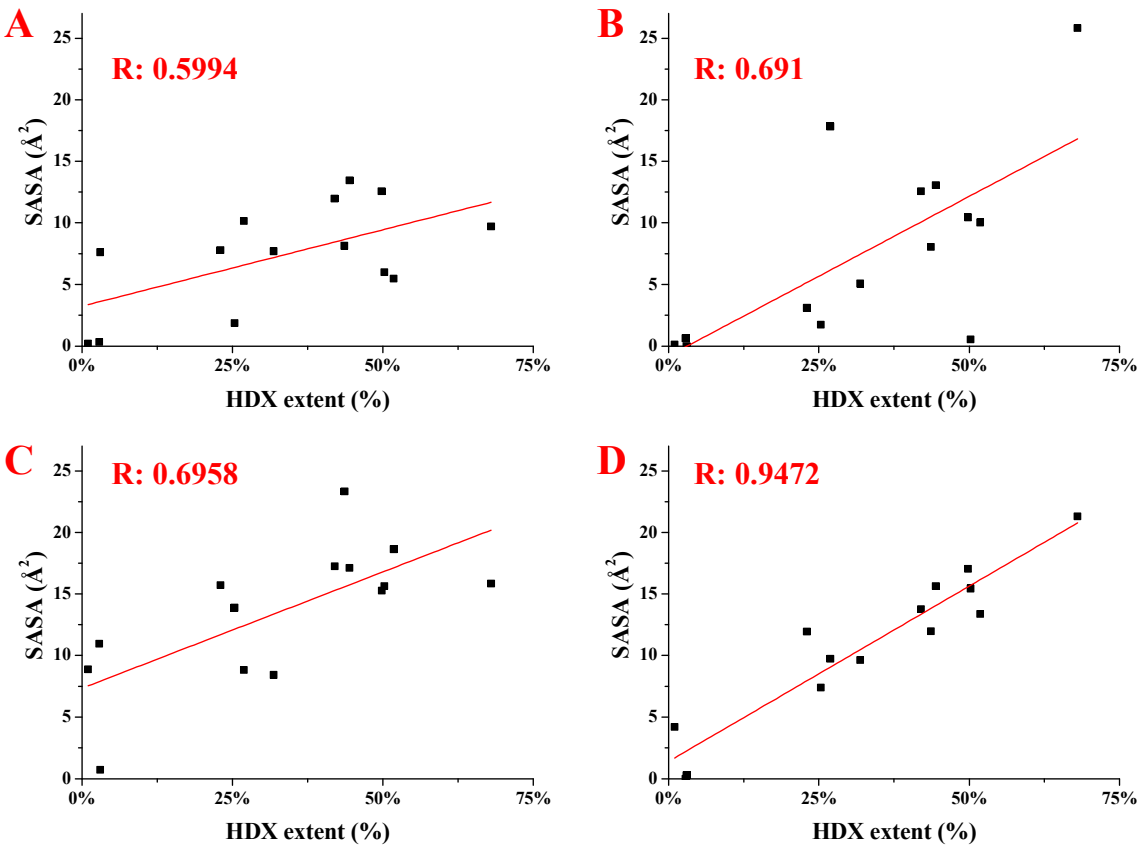


Figure S3. Correlation of HDX and SASA data for all models A (A), B (B), C (C) and D (D). The Pearson correlation coefficients R's are shown in red.