

Supplementary material

Human Vitamin K Epoxide Reductase as a Target of its Redox Protein

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Table S1. Hydrogen bonds involving L-loop residues in crystallographic structures 6wvi (apo-c) and 6wv3 (holo-c) of VKOR in the oxidized state. Distances (D...A and H...A, Å) between donor (D) and acceptor (A) atoms, and hydrogen (H) and acceptor (A) atoms, and the pseudo-valent angle at H (°). Amino acids forming H-bond by backbone and side chains are denoted in black and blue respectively. H-bonds observed in both forms are highlighted in blue.

H-bond	Distance D...A/H...A/ ∠A-H-D	H-bond	Distance D...A/H...A/ ∠A-H-D
apo-c		holo-c	
D36(N)...H33(O)	3.09/2.16/157.8	D36(N)...A32(O)	2.83/1.87/157.6
Y39(O)...S50(O)	2.47 /1.54/167.4	R33(N)...R37(O)	2.84/1.88/158.8
S50(N)...S48(O)	3.12/2.24/163.3	R40(N)...G46(O)	2.93/1.97/156.3
S52(N)...Y39(O)	3.12/2.23/149.9	L42(N)...Y25(O;TM1)	2.90/1.96/153.7
R61(N)...N77(O)	3.06/2.14/154.4	D44(N)...A41(O)	3.01/2.08/153.2
		I49 (O2)... V45(N)	3.05/2.20/140.5
G62(N)...Q78(O)	2.65/1.72/156.0	G62(N)...Q78(O2)	2.72/1.84/143.4
F63(N)...N80(O;TM2)	2.85/2.02/139.8	F63(N)...N80(O;TM2)	2.87/1.91/156.7
S68(N)...F70(O)	2.77/2.07/126.4	L76(N)...S74(O)	2.97/2.06/148.3
D73(N)...G71(O)	3.00/2.25/131.5		
Q78(N)...A75(O)	2.57/1.62/158.4	Q78(N)...I75(O)	3.05/2.13/150.5
N80(N;TM2)...W59(O)	2.58/1.69/148.0	N80(N;TM2)...W59(O)	2.79/1.81/164.4
N80(N;TM2)...G60(O)	2.96/2.06/150.0	N80(N;TM2)...G60(O)	3.18/2.19/166.8

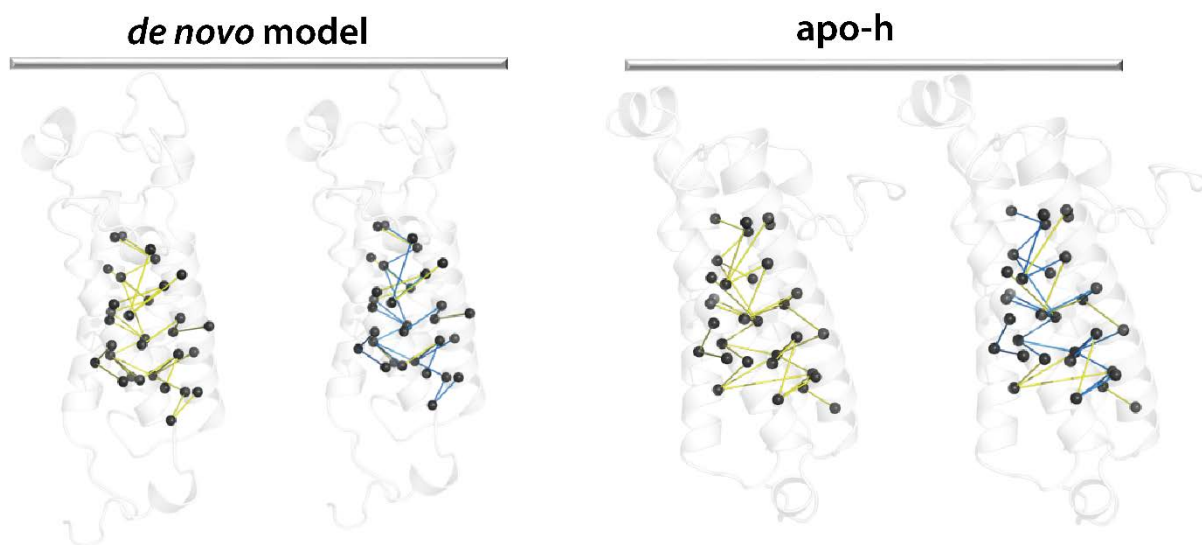


Figure S1. Non-covalent interactions stabilising hVKORC1 TMD helices in *de novo* model embedded in phospholipid bilayers mimicking the ER membrane in aqueous solution, and apo-h form simulated in aqueous solution. Non-covalent interactions, denoted as an undirected graph whose vertices represent a residue and a link between two residues reflects the presence of at least one type of non-covalent interaction. Van-der-Waals contacts (≤ 4.0 Å, events with frequency ≥ 0.8) were calculated for all heavy atoms (O, N, C and S). All observed contacts in each model (left) and blue links discriminated contacts common between two models (right).

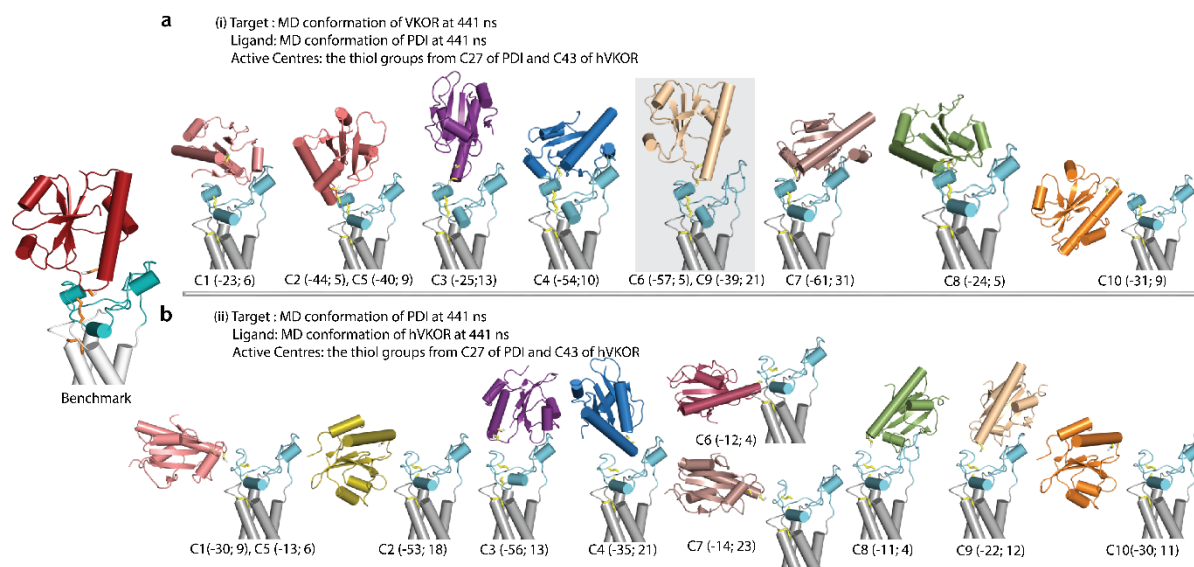


Figure S2. Protein-protein computational docking using an information-driven method on benchmark complex PDI-hVKORC1. Top 10 models produced by HADDOCK for the reference structure (benchmark) using two scenarios for a ligand-target pair, (i) (a) and (ii) (b). For each cluster, the representative conformations with the HADDOCK score (a.u.) and a cluster population (number of observation) are shown. Protein is shown as a cartoon with helices as cylinders and disulfide bridges in yellow sticks.