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**Supporting information for article:**

# Structural insights into the mechanism of the drastic changes in enzymatic activity of the cytochrome P450 vitamin $D_3$ hydroxylase (CYP107BR1) caused by a mutation distant from the active site

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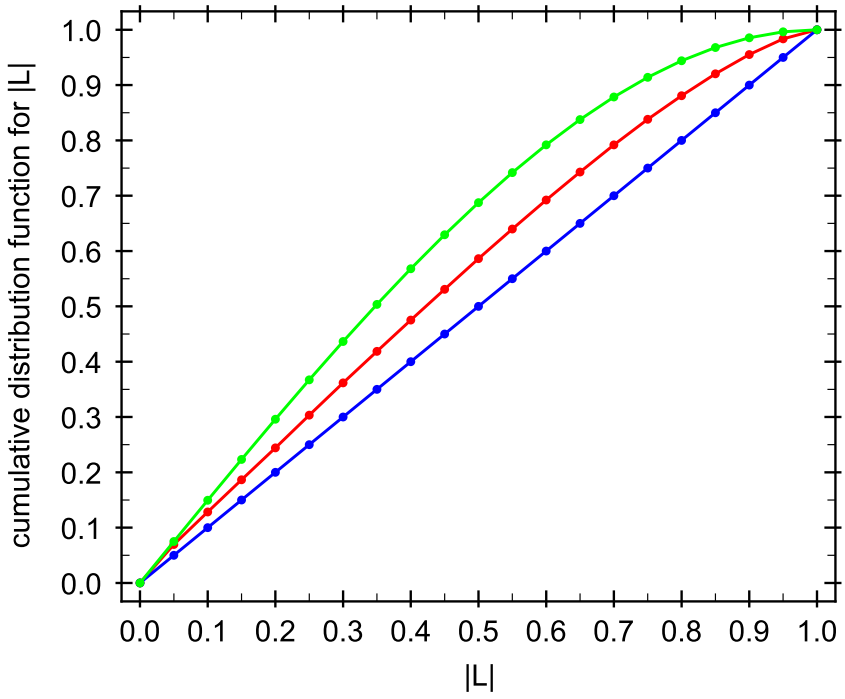


**Figure S1.** The L-test analysis (Padilla & Yeates, 2003) using the data of Vdh-L348M processed in space group $P22_12_1$. $L = I_1 - I_2 /(I_1 + I_2)$, where $I_1$ and $I_2$ represent the intensities of independent reflections. The blue and green lines represent the theoretical distribution of $L$ for untwinned and twinned data, respectively. The red line represents the observed distribution of $L$ for Vdh-L348M.

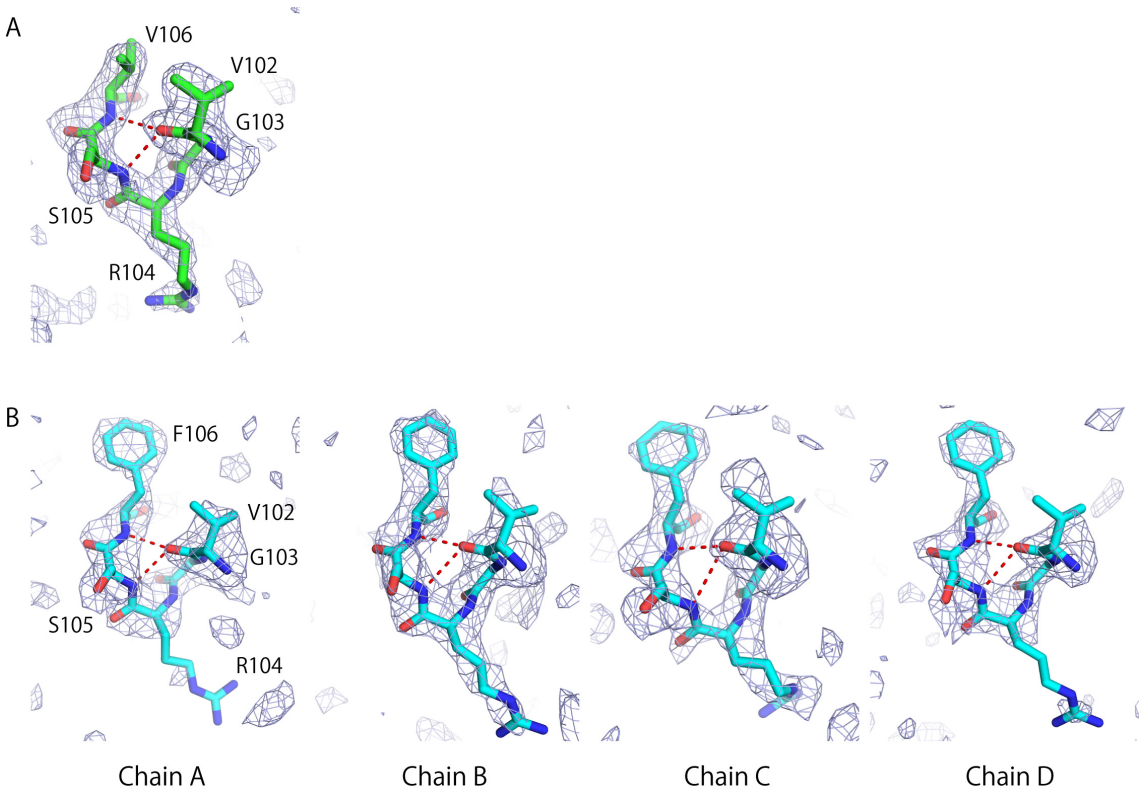


**Figure S2.** The *mF*o − *DF*c omit map for the residues 102-106 of Vdh-F106V contoured at 2.5σ level (A) and of Vdh-L348M at 2.2σ level (B). The maps were calculated at early stage of model refinement using the model without the residues 102-106. The final refined models are also shown. Red dashed lines represent hydrogen bonds between main-chain O of V102 and main-chain N of F106/V106/S105.