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Supporting information for article:

Influence of the presence of the heme cofactor on the JK-loop structure in indoleamine 2,3-dioxygenase 1

Manon Mirgaux, Laurence Leherte and Johan Wouters

1. Type of conformation for JK-loop in the C-terminal part from literature

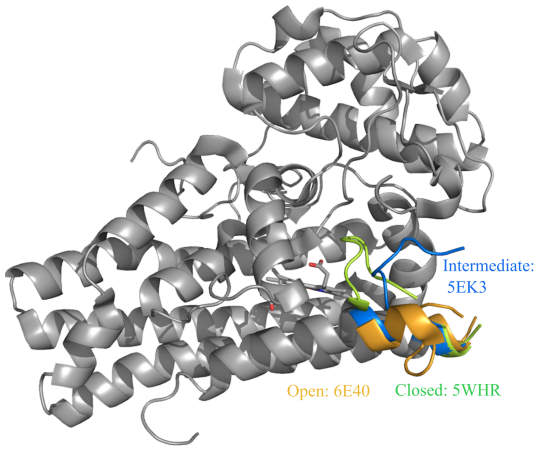

Fig. S1. Conformation of the C-terminal part for the JK-loop in the literature. (a) Closed conformation from 5WHR (green) (b) Intermediate conformation from 5EK3 (blue) (c) Open conformation from 6E40 (orange).

2. Solvatation in Molecular Dynamic simulation

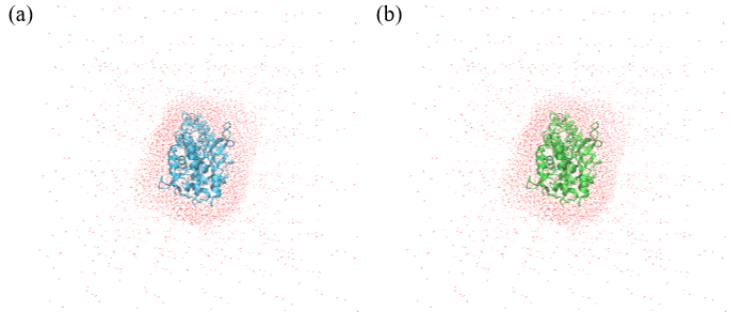

Fig. S2. All-atom water solvent in each simulation. (a) Simulation with the heme cofactor. (b) Simulation without the heme cofactor.

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3. Dimerization interface

Table S1. *Distances involved in dimeric interaction in the small unit from Fig. 4.*

Dimerisation interface	Monomer	Amino acids (atoms)	Monomer	Amino acids (atoms)	Distances (Å)
P104-E119	A	D68 (OD2)	D	M64 (SD)	3.9
	A	M64 (SD)	D	D68 (OD1)	3.8
	A	M64 (SD)	D	D68 (OD2)	3.6
	A	D68 (OD2)	D	R105 (NH2)	3.9
	A	Q113 (NE2)	D	Q113 (OE1)	3.8
	A	Q113 (OE1)	D	Q113 (NE2)	3.9
	A	K257 (NZ)	D	E119 (OE1)	3.6
	A	K257 (NZ)	D	E119 (OE2)	3.6
Y36-H45	A	N37 (OD1)	D	R58 (NH2)	2.6
and Q54-K61	A	D38 (OD1)	D	W609 (O)	2.7
	D	W609 (O)	D	R58 (NH2)	3.6
	D	W609 (O)	D	Q54 (OE1)	2.3
	D	W608 (O)	D	R58 (NH1)	2.3
	D	W608 (O)	D	E57 (OE2)	2.9
	D	R58 (NH1)	D	E57 (OE2)	4.2
	A	R58 (NH1)	D	E57 (OE1)	2.9
	A	R58 (NH1)	D	E57 (OE2)	3.4
	A	R58 (NH2)	D	E57 (OE1)	2.3
	A	R58 (NH2)	D	E57 (OE2)	3.5
	D	E57 (OE1)	D	K61 (NZ)	3.0

Table S2. *Distance involved in dimeric interaction in the large unit from Fig. 5.*

Dimerization interface	Monomer	Amino acids (atoms)	Monomer	Amino acids (atoms)	Distances (Å)
Helix D	A	D219 (OD1)	A	W613 (O)	2.4
	A	D219 (OD1)	A	W745 (O)	3.7
	A	D219 (OD2)	A	W745 (O)	3.8
	A	D219 (OD1)	A	W735 (O)	2.4
	A	W745 (O)	D	W735 (O)	3.4
	A	W745 (O)	D	W718 (O)	2.2
	D	W718 (O)	D	H220 (O)	3.6
	A	D219 (OD2)	D	W621 (O)	3.5
	D	W612 (O)	D	W718 (O)	3.6
	A	W612 (O)	D	H218 (O)	2.4
	A	W612 (O)	D	E146 (OE2)	3.2
	A	W612 (O)	D	H220 (NE2)	3.2
	D	W614 (O)	D	E146 (OE1)	2.4
	D	W614 (O)	D	E146 (OE2)	2.6
	D	W614 (O)	D	W732 (O)	2.4
	D	W614 (O)	D	W603 (O)	2.5
	D	W603 (O)	D	H220 (NE2)	3.8
	A	H218 (NE2)	D	D219 (OD1)	3.8
	A	H218 (ND1)	D	D219 (OD2)	4.0
	A	H218 (ND1)	D	D219 (OD1)	4.1
	A	H218 (NE2)	D	D219 (OD2)	4.9
BC-loop and HI-loop	A	R193 (NH1)	A	D325 (OD1)	2.8
	A	R193 (NH1)	A	D325 (OD2)	3.3
	A	R193 (NE)	A	D325 (OD2)	2.7
	A	D325 (OD2)	C	R193 (NE)	4.7
	A	Q191 (OE1)	C	K323 (NZ)	4.1
	A	K323 (NZ)	C	Q191 (OE1)	4.3
	C	K323 (NZ)	C	Q191 (OE1)	4.1
	C	D325 (OD2)	C	R193 (NH1)	3.4
	C	D325 (OD1)	C	R193 (NH1)	2.9
	C	D325 (OD2)	C	R193 (NE)	2.7

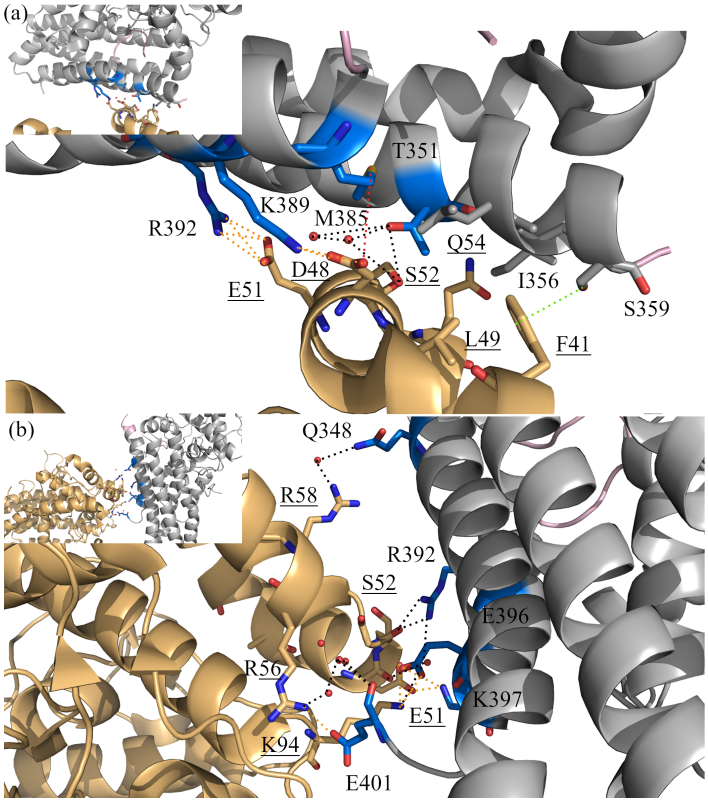

Fig. S3. Dimerization interfaces in 5WHR around the JK-loop. (a) Interface with the α-helix H45-S52 (b) Interface with the α-helix Q54-K61.

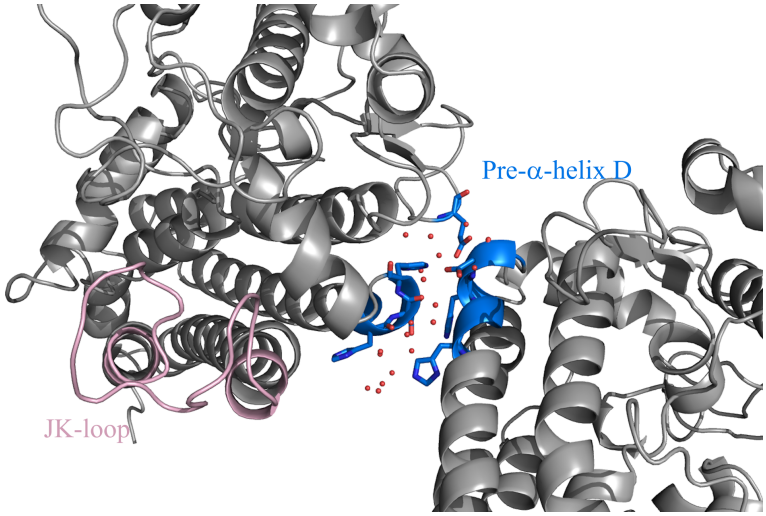

Fig. S4. Dimerization interface of the α-helix D (in blue) in relation to the JK-loop (in pink).

4. Conformation of JK-loop in 7A62

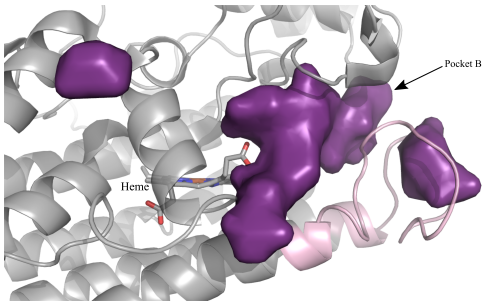

Fig. S5. Volume of the pocket B resulting of the JK-loop conformation. Cavity was generated by POCASA 1.1. server (Yu, J. *et al.*, 2010).

5. Link between JK-loop conformation and heme lability supported by Molecular Dynamics

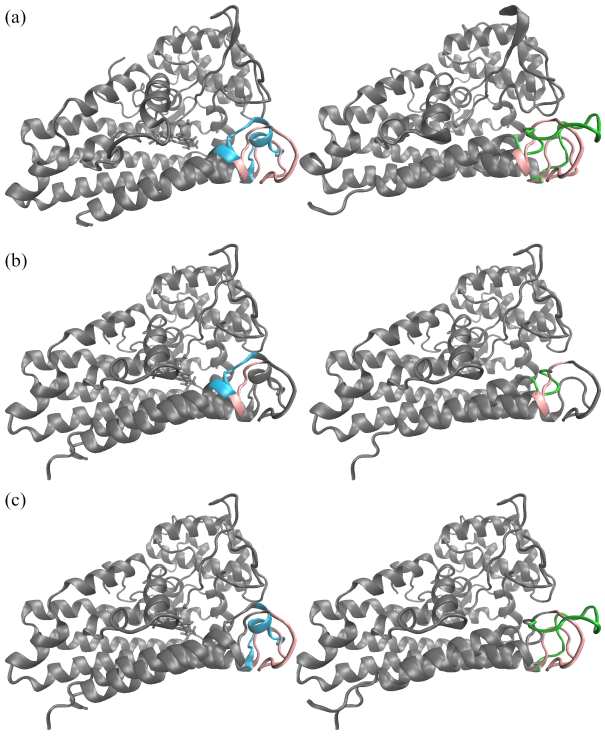

Fig. S6. Superimposition of the crystal (pink), MD simulation with the heme cofactor at t = 200 ns (cyan), and MD simulation structure without the heme cofactor at t = 200 ns (green) (a) Overall view (b) C-terminal part of the JK-loop (E375 to G380) (c) N-terminal part of the JK-loop (Q360 to E374).

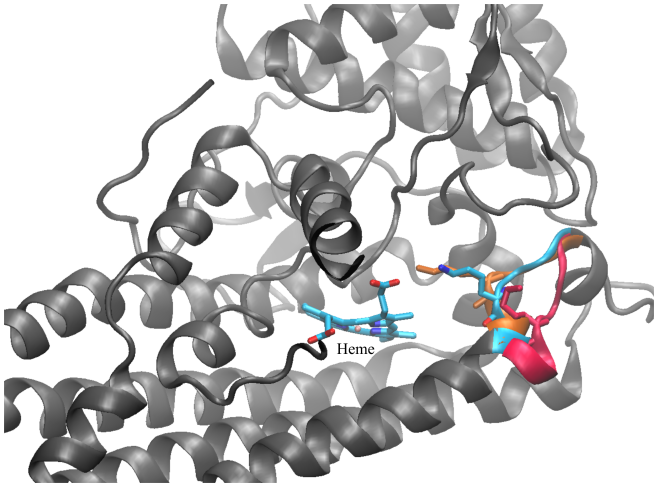

Fig. S7. Superimposition of different locations for K377 obtained from the MD simulation with the heme cofactor. Conformations are clustered in three groups: closed (in orange, the distance between K377 and A264 varies from 6 Å to 10 Å, 16.1% of the conformations), intermediate (in cyan, the distance between K377 and A264 varies from 10 Å to 16 Å, 79.3% of the conformations) and open (in red, the distance between K377 and A264 is larger than 16 Å, 4.6% of the conformations). Percentages were calculated over a 200 ns MD simulation at 300 K and 1 bar.

References

Yu, J., Zhou, Y., Tanaka, I., & Yao, M. (2010). *Bioinformatics*, **26**, 46-52.