Table S1. A comparison of distances and side-chain conformations in selected $P450_{BM3}$ crystal structures. SF WT data are the average of three substrate-free structures (PDB codes: 2HPD, 1BU7 and 2IJ2). SB WT data are the average of three substrate-bound structures (PDB codes: 1FAG, 1JPZ and 1ZO9). SB ex WT data are the average of two substrate-bound mutant structures (PDB codes: 2UWH and 3CBD). The data for each individual PDB structure were calculated by averaging all the molecules in the asymmetric cell.

(Å)	SF WT	SB WT	SB ex WT	KT2	I401P
Axial water ligand distances					
Fe–OH_2	2.4	**3.5**	**3.3**	2.6	**3.6**
Ala264CO–OH_2	2.7	2.8	3.0	**3.7**	3.0
Inter-I-helix distances					
Thr260CO–Ala264NH	2.9	2.8	2.8	2.8	2.8
Phe261CO–Gly265NH	3.0	2.9	2.9	2.6	2.8
Leu262CO–His266NH	3.1	**3.8**	**3.9**	**3.8**	**3.9**
Ile263CO–Glu267NH	**4.8**	3.2	3.1	3.3	**5.2**
Ala264CO–Thr268NH	**4.6**	**4.8**	**5.0**	**4.9**	**4.6**
Gly265CO–Thr269NH	3.4	**6.0**	**6.0**	**5.9**	**5.7**
His266NH–Ser270NH	3.2	3.0	2.9	2.9	2.9
Glu267NH–Gly271NH	2.9	3.1	3.1	3.1	2.9
Thr268NH–Leu272NH	3.1	3.0	3.0	3.0	3.0
His266Nδ–Leu262CO	2.9	**4.8 (*)**	**4.8**	**4.9**	2.8
His266Nδ–Ile263CO	3.2	**5.1 (*)**	**4.9**	**4.9**	**5.4**
Gly265CO–Thr268OH	3.3	**6.3**	**6.5**	**6.2**	**5.4**
Gly265CO–Thr269OH	2.9	**4.5**	**4.5**	**4.4**	**4.3**
I-helix/G-helix distances					
Lys224NH_2–Asp251CO_2	3.1	**8.0**	**8.5**	**8.1**	(‡)
Asp217Cα–Arg255Cα	6.3	**8.5**	**8.4 (†)**	**8.2**	6.3
Side-chain rotations					
Phe87 ring (ca. 90°)	No	**Yes**	**Yes**	**Mol. B**	No
Phe158 at Cβ (ca. 90°)	No	**Yes**	**Yes**	**Yes**	No
Phe261 ring (ca. 90°)	No	**Yes**	**Yes**	**Yes**	No
His 266 ring (ca. 180°)	No	**Yes**	**Yes**	**Yes**	No
Glu267 carboxylate (ca. 90°)	No	**Yes**	**Yes**	**Yes**	**Yes**
Side-chain displacements					
His266 (towards the E-helix)	No	**Yes**	**Yes**	**Yes**	**Yes**
Leu437 (away from Phe87Cζ)	No	**Yes**	**Yes**	**Mol. B**	No

(*) Based on the supposition that the imidazole ring of His266 in the *N*-palmitoyl methionine structure (1ZO9) is rotated through 180° relative to SF structures, as in the *N*-palmitoyl glycine-bound and other SB crystal structures rather than as depicted in the current PDB file.
(†) Residue 255 is serine in 139-3 (‡) Lys224 is unresolved in both I401P molecules