Influence of the LOV domain on low-lying excited states of flavin: A combined quantum-mechanics / molecular-mechanics investigation Supporting Information

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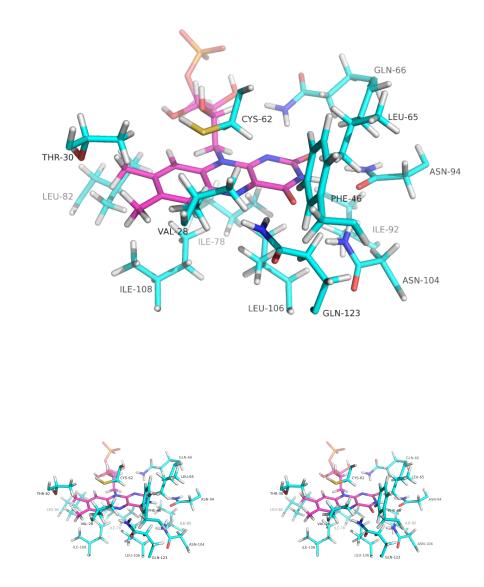


Figure 1: Graphical representation of the flavin binding pocket (top). For a better 3D impression of the binding pocket the scene is shown in stereo representation (bottom). (Figures of protein molecules were created using PyMol (www.pymol.org).)

Preparation of the system The initial geometry was based on an X-ray structure (PDB code 2PR5).¹ For this investigation, only the core LOV domain (residue 25-126) was considered in our calculations. One monomer from the crystallographic dimer was used with its FMN cofactor, which corresponds to the A chain of the PDB structure. 240 associated crystal water molecules (chain A) were included in the model. Apart from CYS62 there are four different residues with alternate atom positions, namely THR54, LYS60, THR100 and ASN107, all located outside the FMN binding pocket. Upon visible inspection of their environment, conformation B was chosen for LYS60 due to favorable hydrogen bonds with crystal water w874 and w908, and conformation A was taken for the remaining residues. Protein hydrogen positions were built with CHARMM.² The assignments of the protonation state of ionizable groups were cross-checked with the empirical pK_a prediction program propKa.³ On the basis of this evaluation, the only histidine residue (HIS69) was protonated due to favorable hydrogen bonding with w851 and w852. Note that this residue is found to be outside the binding pocket. The system was neutralized with 9 sodium ions and solvated in a 35 Å water sphere. The force-field parameters for the FMN cofactor were adapted from published FAD parameters.⁴ The charges of the phosphate atoms (PB, O3A, O3B) in the ribityl chain were manually adjusted with the constraint that the total charge of the FMN cofactor remains -2. The resulting values given in Figure 2 are comparable to MM charges adopted in other recent studies.^{5,6} Minor variations in the chosen force-field parameters for FMN are not expected to be critical for our purposes, since a full MM description of the cofactor is used only during the setup phase; in the OM/MM calculations, the crucial chromophore part of the cofactor is always included in the QM region. During system setup, all (non-hydrogen) atoms of protein and cofactor were frozen to preserve the X-ray structure, and only hydrogen atoms and water molecules were allowed to move during the various minimization steps (1000 steps of steepest descent (SD) minimization followed by 1000 steps of adopted basis Newton-Raphson (abNR) minimization). In order to retain the two CYS62 conformations, we refrained from performing MM molecular dynamics simulations.

RESI FMN -2.000	!	
GROUP	!	GROUP
ATOM O3A O2L -0.90	! 01B	ATOM NX1 NX1 -0.89
ATOM PB P 1.10	!	ATOM HX1 HX1 0.43
ATOM 01B 02L -0.90	! O3B-PB-O3A	ATOM CX1 CX1 0.82
ATOM 02B 02L -0.90	!	ATOM OX1 OX1 -0.61
ATOM O3B OSL -0.40	! 02B	ATOM CX2 CX2 0.24
GROUP	! HS51-CS5-HS52	ATOM CX3 CX3 0.37
ATOM CS1 CT2 0.21	!	ATOM NX2 NX2 -0.81
ATOM HS11 HA 0.09	! HS41-CS4-OS4-HS42	ATOM CX4 CX4 1.09
ATOM HS12 HA 0.09	!	ATOM OX2 OX2 -0.66
ATOM CS2 CT1 0.17	! HS31-CS3-OS3-HS32	ATOM NY1 NY1 -0.60
ATOM HS21 HA 0.09	!	ATOM CY1 CY1 0.60
ATOM OS2 OH1 -0.66	! HS21-CS2-OS2-HS22	ATOM CY2 CY2 -0.30
ATOM HS22 H 0.43	!	ATOM NY2 NY2 0.20
ATOM CS3 CT1 0.17	! HS11-CS1-HS12	ATOM CZ1 CZ1 -0.46
ATOM HS31 HA 0.09	! \	ATOM HZ1 HZ1 0.24
ATOM OS3 OH1 -0.66	! \	ATOM CZ2 CZ2 0.19
ATOM HS32 H 0.43	! \	ATOM CZ5 CT3 -0.44
ATOM CS4 CT1 0.17	! \	ATOM HZ51 HA 0.09
ATOM HS41 HA 0.09	! \	ATOM HZ52 HA 0.09
ATOM OS4 OH1 -0.66	! \	ATOM HZ53 HA 0.09
ATOM HS42 H 0.43	! \ HZ4 HZ61 HZ62	ATOM CZ3 CZ3 0.18
ATOM CS5 CT2 0.22	! \ /	ATOM CZ6 CT3 -0.48
ATOM HS51 HA 0.09	! OX2 NX2 NY2 CZ4 CZ6HZ63	ATOM HZ61 HA 0.09
ATOM HS52 HA 0.09	! \\ / \ / \\ /	ATOM HZ62 HA 0.09
	! CX4 CX3 CY2 CZ3 HZ53	ATOM HZ63 HA 0.09
	!	ATOM CZ4 CZ4 -0.28
	! NX1 CX2 CY1 CZ2CZ5HZ52	ATOM HZ4 HZ4 0.19
	$! / \backslash / / / / / $	
	! HX1 CX1 NY1 CZ1 HZ51	
	!	
	! OX1 HZ1	

Figure 2: CHARMM charges for flavin mononucleotide (FMN) adapted from FAD parameters by Luo et al.⁴

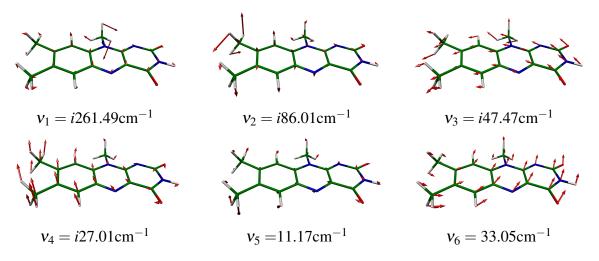


Figure 3: Distortions along low-energy vibrational normal modes at the S_1 geometry. For the nuclear arrangements of the other states a qualitatively similar picture is found.

Table 1: Selected ground-state bond lengths [pm] of LF for the four QM regions in confA and confB, respectively. Atomic labels are displayed in Figure 2 of the main paper.

	LOV (Konf. A)					LOV (Konf. B)			
	QM-1	QM-2	QM-3	QM-4	QM-1	QM-2	QM-3	QM-4	
N_1-C_2	136.4	136.0	136.3	136.1	136.2	135.9	136.2	135.9	
C_2-N_3	140.9	140.4	141.1	140.4	141.0	140.3	140.9	140.2	
N_3-C_4	137.0	136.9	136.8	136.9	136.9	136.9	137.0	137.0	
C_4 - C_{4a}	148.3	148.1	148.0	148.1	148.2	148.3	148.2	148.3	
C_{4a} -N ₅	130.1	130.2	130.1	130.2	130.1	130.2	130.0	130.1	
N_5-C_{5a}	135.1	135.0	134.9	134.9	135.2	135.2	135.2	135.2	
C_{5a} - C_6	140.8	140.9	140.9	140.9	140.9	140.9	141.0	141.0	
C_6-C_7	137.1	137.0	137.0	137.0	137.2	137.2	137.2	137.2	
C_7-C_8	142.7	142.8	142.7	142.7	142.8	142.8	142.8	142.8	
C_8-C_9	138.7	138.6	138.7	138.7	138.4	138.5	138.5	138.5	
C_9-C_{9a}	139.9	139.8	139.9	139.8	139.9	139.9	139.9	139.9	
C _{9a} -N ₁₀	139.5	139.2	139.3	139.3	138.9	138.9	139.0	138.9	
N ₁₀ -C _{10a}	137.4	137.1	137.3	137.1	137.2	137.0	137.3	137.0	
C_{10a} -N ₁	131.6	131.8	131.7	131.8	131.5	131.7	131.6	131.7	
C_{5a} - C_{9a}	142.2	142.3	142.2	142.2	142.1	142.1	142.1	142.1	
C_{4a} - C_{10a}	145.0	144.6	144.8	144.5	144.8	144.5	144.9	144.6	
C ₂ -O	122.7	123.5	122.6	123.4	122.7	123.4	122.7	123.4	
C ₄ -O	122.1	122.5	122.4	122.5	122.3	122.4	122.2	122.3	

Table 2: Selected excited-state bond lengths [pm] of LF for region QM-1 in confA and confB, respectively. The data of LF in vacuum is taken from.⁷ Atomic labels are displayed in Figure 2 of the main paper.

	$^{1}(\pi\pi^{*})$ S ₁			3	$^{3}(\pi\pi^{*}) \mathbf{T}_{1}$			$^{3}(\pi\pi^{*}) \mathbf{T}_{2}$		
	LF	confA	confB	LF	confA	confB	LF	confA	confB	
N ₁ -C ₂	139.9	138.5	138.7	139.1	138.1	138.1	137.9	136.2	136.1	
C_2-N_3	137.8	137.8	137.6	138.4	138.2	138.0	140.8	140.3	140.4	
N_3-C_4	141.4	139.7	139.9	139.8	138.9	139.1	138.9	137.6	137.7	
C_4 - C_{4a}	145.5	144.6	144.5	147.0	145.7	145.6	147.1	145.7	145.7	
C_{4a} -N ₅	135.5	134.0	134.1	136.5	133.9	134.0	136.3	136.9	136.9	
N_5-C_{5a}	134.3	136.7	136.5	133.8	136.2	136.2	133.2	132.8	132.8	
C_{5a} - C_6	140.6	138.8	138.9	141.7	138.4	138.6	143.2	144.0	144.1	
C_6-C_7	139.0	141.8	141.6	137.7	140.5	140.3	143.6	140.0	140.4	
C7-C8	142.4	140.5	140.6	143.2	142.3	142.4	137.3	138.6	138.5	
C_8-C_9	138.9	139.3	139.1	138.8	138.0	137.9	144.7	145.4	145.2	
C_9-C_{9a}	140.3	142.3	142.0	139.7	141.5	141.3	140.0	138.9	139.0	
$C_{9a}-N_{10}$	138.7	138.9	138.7	138.7	137.7	137.6	137.7	140.1	139.6	
N_{10} - C_{10a}	137.6	139.4	139.0	140.0	142.4	141.9	141.6	139.1	139.0	
C_{10a} - N_1	133.3	131.6	131.7	132.4	131.4	131.4	130.5	131.8	131.8	
C_{5a} - C_{9a}	144.1	141.5	141.8	144.9	144.6	144.6	142.1	141.9	142.0	
C_{4a} - C_{10a}	142.5	143.7	143.5	141.3	141.9	141.7	142.5	142.8	142.6	
C ₂ -O	121.9	122.9	123.0	121.9	123.1	123.1	121.5	123.1	123.1	
C ₄ -O	121.7	122.9	123.1	121.5	122.9	122.8	121.9	123.2	123.1	

	electronic	nic $\Delta \mathbf{E}(f(r))$					
	structure	QM-1	QM-2	QM-3	QM-4		
S ₀	ground state	0.00	0.00	0.00	0.00		
S_1	$\pi_H o \pi_L^*$	2.84	2.79	2.82	2.77		
		(0.2804)	(0.2974)	(0.2321)	(0.2438)		
S_2	$\pi_{H-1} ightarrow \pi_L^*$	3.40	3.31	3.21	3.14		
	-	(0.2926)	(0.2500)	(0.2367)	(0.2470)		
S ₃	$n_N o \pi_L^*$	3.46	3.35	3.45	3.34		
CT	$p_S ightarrow \pi_L^{ar *}$			3.65	3.57		
S_4	$n_O o \pi_L^{*}$	3.87	3.71	3.89	3.71		

Table 3: confA:Vertical singlet excitation energies ΔE [eV] for different QM regions. In addition to the dominant excitations, oscillator strengths f(r) of optically bright states are given.

Table 4: confB:Vertical singlet excitation energies ΔE [eV] for different QM regions. In addition to the dominant excitations, oscillator strengths f(r) of optically bright states are given.

	electronic		f(r))			
	structure	QM-1	QM-2	QM-3	QM-4	
S ₀	ground state	0.00	0.00	0.00	0.00	
S_1	$\pi_{\!H} ightarrow \pi_L^*$	2.86	2.82	2.85	2.83	
		(0.2935)	(0.3089)	(0.2718)	(0.2880)	
S_2	$\pi_{H-1} o \pi_L^*$	3.46	3.38	3.39 ^{<i>a</i>}	3.37 ^{<i>a</i>}	
	2	(0.2701)	(0.2892)	(0.2253)	(0.1928)	
S_3	$n_N o \pi_L^*$	3.47	3.34	3.45 ^{<i>a</i>}	3.31 ^{<i>a</i>}	
	L			(0.0422)	(0.0833)	
S_4	$n_O o \pi_L^*$	3.87	3.69	3.88	3.70	
CT	$p_S o \pi_L^*$			3.92	3.83	
$a \operatorname{The} \pi_{H-1} \to \pi_I^* \text{ and } n_N \to \pi_I^* \text{ excitations mix.}$						

The $\pi_{H-1} \to \pi_L^*$ and $n_N \to \pi_L^*$ excitations mix.

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