Supplemental Information

Variation in LOV Photoreceptor Activation Dynamics Probed by Time Resolved Infrared Spectroscopy

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Table S1: Assignment of LOV Spectra				
EAS1	AsLOV2	YtvA	LovK	EL222
1FMN*	1375	1379	1382	1378
1FMN*	1413	1418	1424	1419
GS Bleach	1550	1548	1552	1544
GS Bleach	1583	1580	1586	1580
Protein		1615	1612	1615
C2=O	1622	1629	1632	1631
Asn (-)	1669	1663	1662	1652
Gln513	1690	1702	1700	1700
EAS2				
3FMN*	1438	1440	1443	1428
3FMN*	1491	1491	1488	1488
GS Bleach	1550	1548	1552	1544
GS Bleach	1583	1580	1586	1580
Protein		1615	1612	1615
C2=O	1622	1629	1632	1631
Asn (-)	1669	1663	1662	1652
Gln513	1690	1702	1700	1700
EAS3				
Protein (-)	1404	1406	1411	1406
Protein (+)	1417	1417	1424	1418
Protein (-)	1426	1430	1433	1430
Protein (+)	1435	1443	1453	1450
β-sheet N-H		1526		
C4C10a (+)	1541	1541	1547	1553
C4C10a (-)	1553	1550	1553	1541
β-sheet C=O	1625	1619	1633	1631
Jα helix	1634			
β-sheet C=O			1650	1645
FMN/Protein	1665	1667	1669	1665
Gln513	1690	1695	1695	1700
C4=O	1722	1720	1718	

Table S1: Band assignments were based on the effect of ^{13}C labelling on the spectrum of AsLOV2.

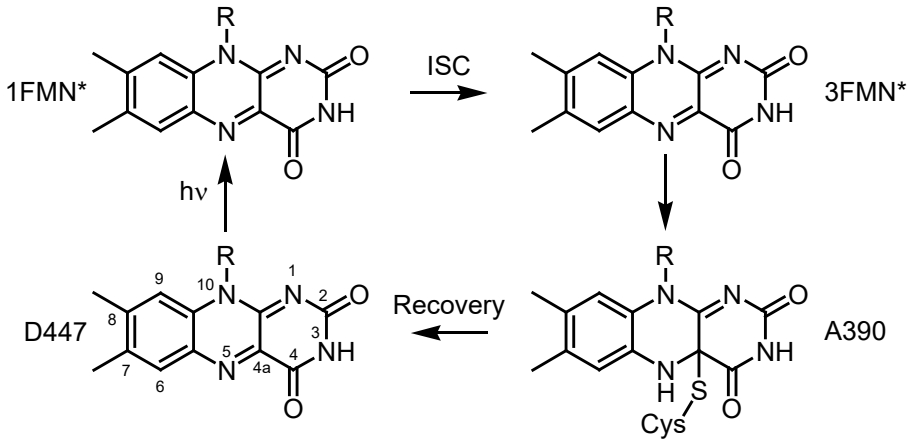

Figure S1: The LOV Photocycle

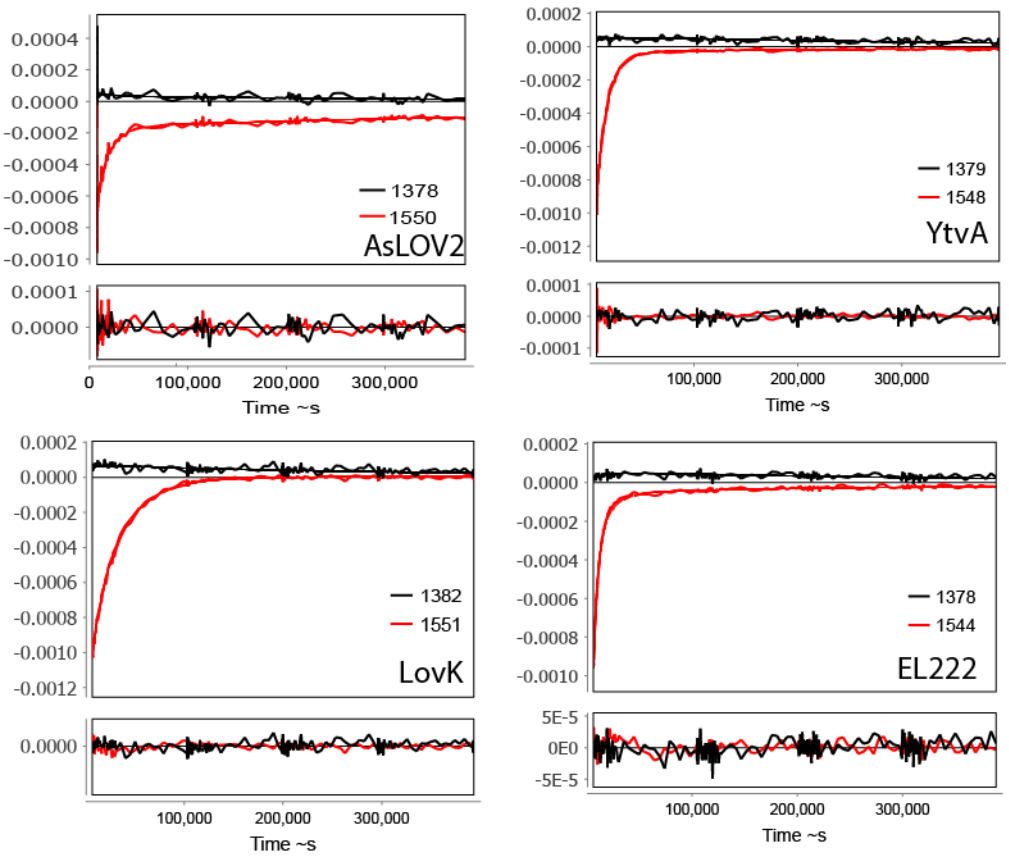

Figure S2: Kinetic traces and residuals showing quality of fit. Excited state decay is shown in black and ground state recovery is shown in red.

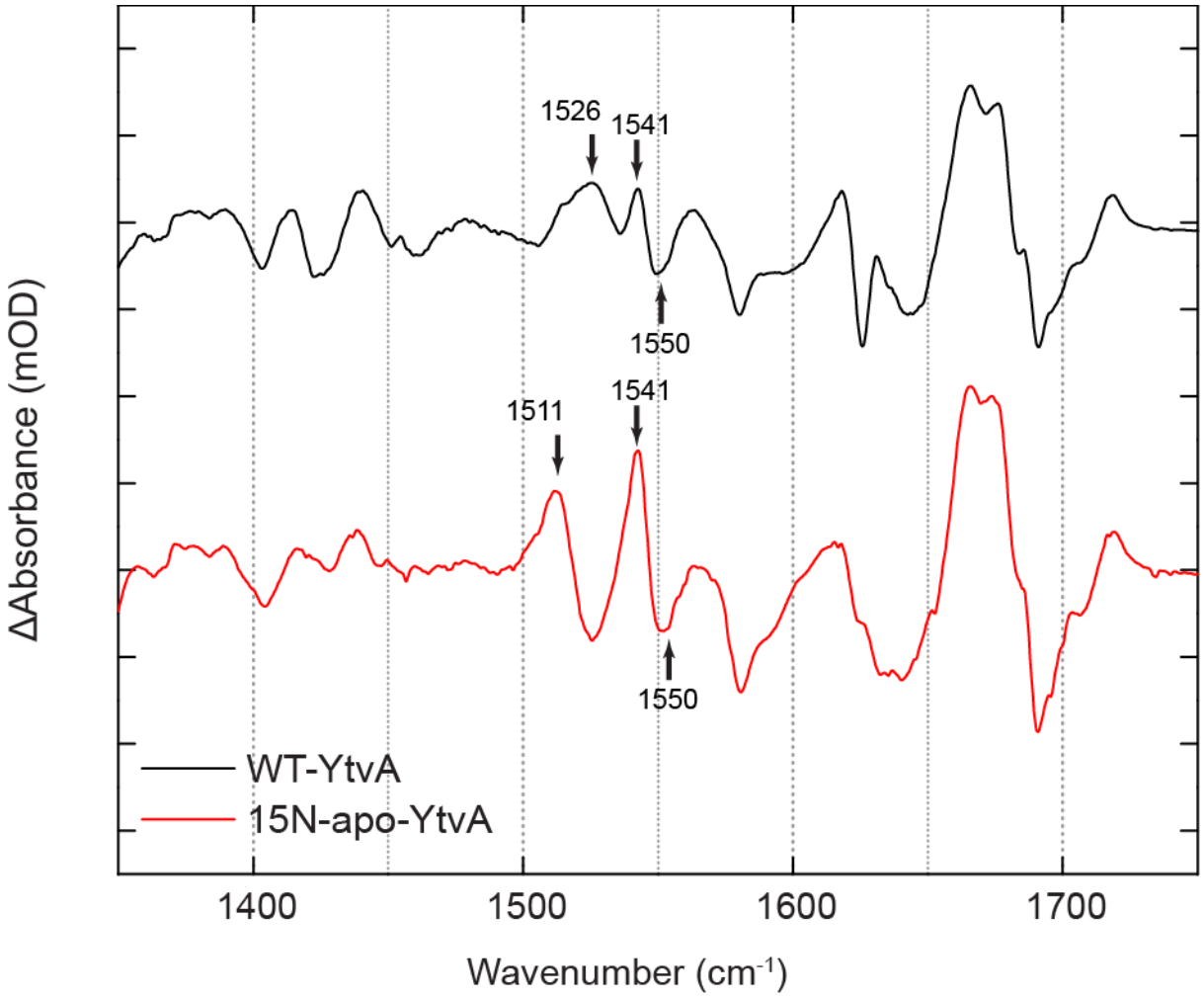

Figure S3: L-D FTIR of [^{15}N-apoprotein]-YtvA

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AsLOV2      ---------------------------------LATTLERIEKNFVITDPRLPDNPIIFA
YtvA        MASFQS--------FGIPGQLE----------VIKKALDHVRVGVVITDPALEDNPIVYV
LovK        MEDYSESRRAGERLAAGHGVDD----------PFAAAISATRMAMIVADATQPDIPIIFA
EL222       MGQDRP-----IDGSGAPGADDTRVEVQPPAQWVLDLIEASPIASVVSDPRLADNPLIAI
                                             .   :.      :::*    * *::

AsLOV2      SDSFLQLTEYSREEILGRNCRFLQGPETDRATVRKIRDAIDNQTEVTVQLINYTKSGKKF
YtvA        NQGFVQMTGYETEEILGKNCRFLQGKHTDPAEVDNIRTALQNKEPVTVQIQNYKKDGTMF
LovK        NDAFLRLTGYARDEVIGRNCRFLQGPDTDPKAIQAVRDALAAGEDVAVDLLNYRKDGSPF
EL222       NQAFTDLTGYSEEECVGRNCRFLAGSGTEPWLTDKIRQGVREHKPVLVEILNYKKDGTPF
            .:.*  :* *  :* :*:***** *  *:      :* .:     * *:: ** *.*. *

AsLOV2      WNLFHLQPMRDQKGDVQYFIGVQLDGTEHVRDAAER----EGV--MLIKKTAENIDEAAK
YtvA        WNELNIDPMEIE--DKTYFVGIQNDITKQKEYEKL------------LEDSLTEITALS-
LovK        WNALNMSPVRNDAGQLVYFFGSQVDVTDKKVVELRARDHSDGLQQMVEERTRE-------
EL222       RNAVLVAPIYDDDDELLYFLGSQVEVDDDQPNMGMARRERAA--EM--------------
             * . : *:  :  :  **.* * :  ..

AsLOV2      EL
YtvA        --
LovK        --
EL222       --
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Figure S4: Sequence alignment of the AsLOV2, YtvA, LovK, and EL222 LOV domains. Conserved LOV core motif is highlighted in yellow and shows the Gln to Ala replacement in EL222 and the prediction of Gln for LovK. F494 in AsLOV2 and corresponding residues in YtvA, LovK, and EL222 are highlighted in green.

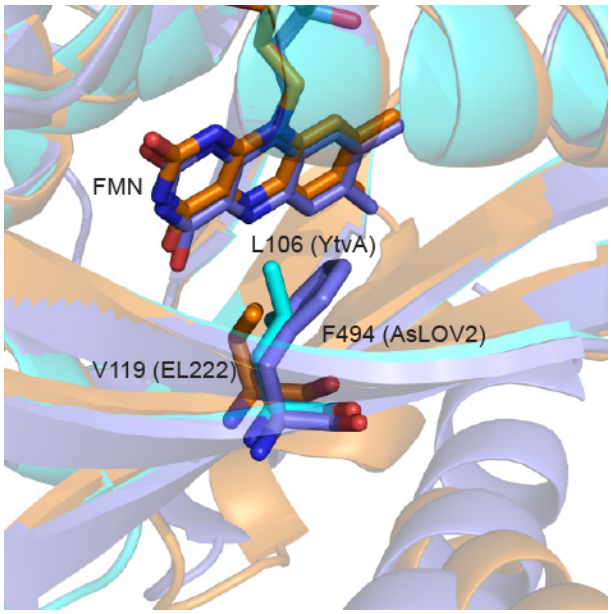

Figure S5: F494 forms a π-stacking interaction with the isoalloxazine ring of FMN.

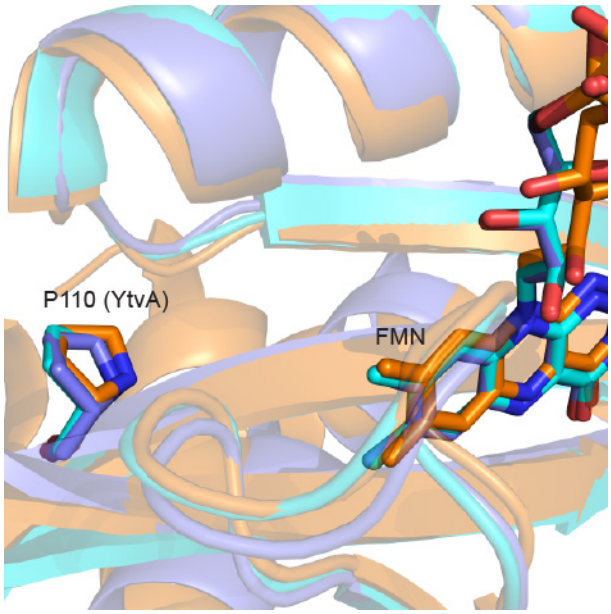

Figure S6: Proline residues on the LOV β-sheet.