



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:21 PM UTC

PDB ID : 6FPH / pdb\_00006fph  
Title : The crystal structure of *P.fluorescens* Kynurenine 3-monooxygenase (KMO) in complex with competitive inhibitor No. 1h  
Authors : Levy, C.W.; Leys, D.  
Deposited on : 2018-02-09  
Resolution : 2.00 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

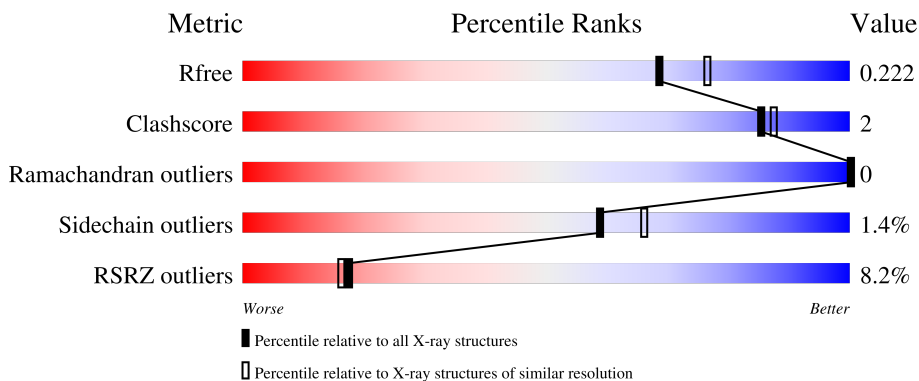
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

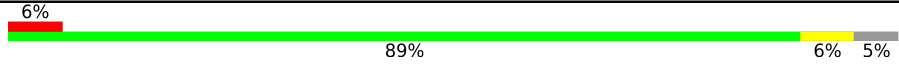
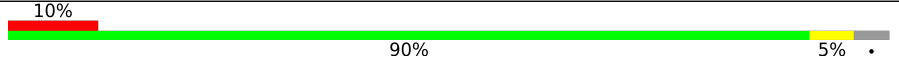
The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	460	 6% 89% 6% 5%
1	B	460	 10% 90% 5% 5%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 14495 atoms, of which 6950 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Kynurenine 3-monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	439	6878	2163	3421	641	634	19	0	10	0
1	B	441	6918	2174	3445	646	635	18	0	12	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	251	SER	CYS	engineered mutation	UNP Q84HF5
A	460	SER	CYS	engineered mutation	UNP Q84HF5
B	251	SER	CYS	engineered mutation	UNP Q84HF5
B	460	SER	CYS	engineered mutation	UNP Q84HF5

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).

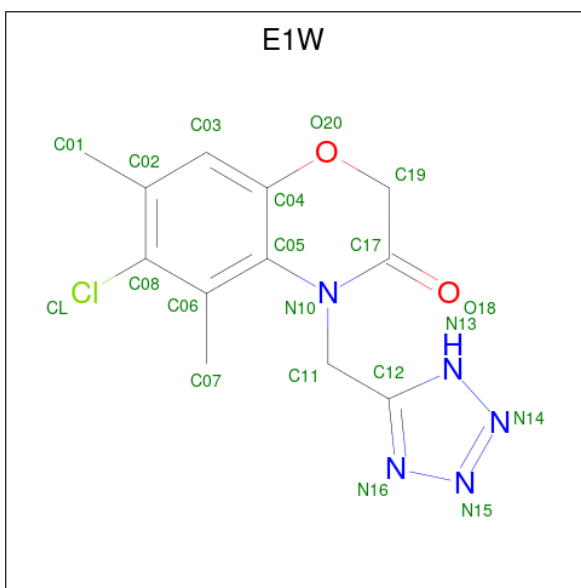


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	A	1	Total	C	H	N	O	P	0	0
			84	27	31	9	15	2		
2	B	1	Total	C	H	N	O	P	0	0
			84	27	31	9	15	2		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is 6-chloranyl-5,7-dimethyl-4-(1 {H}-1,2,3,4-tetrazol-5-ylmethyl)-1,4-benzoxazin-3-one (CCD ID: E1W) (formula: C<sub>12</sub>H<sub>12</sub>ClN<sub>5</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	Cl	H	N	O	0	0
			31	12	1	11	5	2		
4	B	1	Total	C	Cl	H	N	O	0	0
			31	12	1	11	5	2		

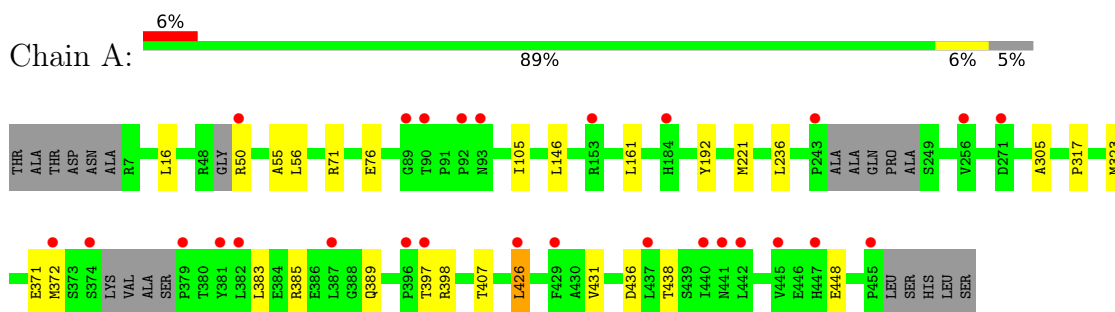
- Molecule 5 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	A	257	Total 257	O 257	0	0
5	B	210	Total 210	O 210	0	0

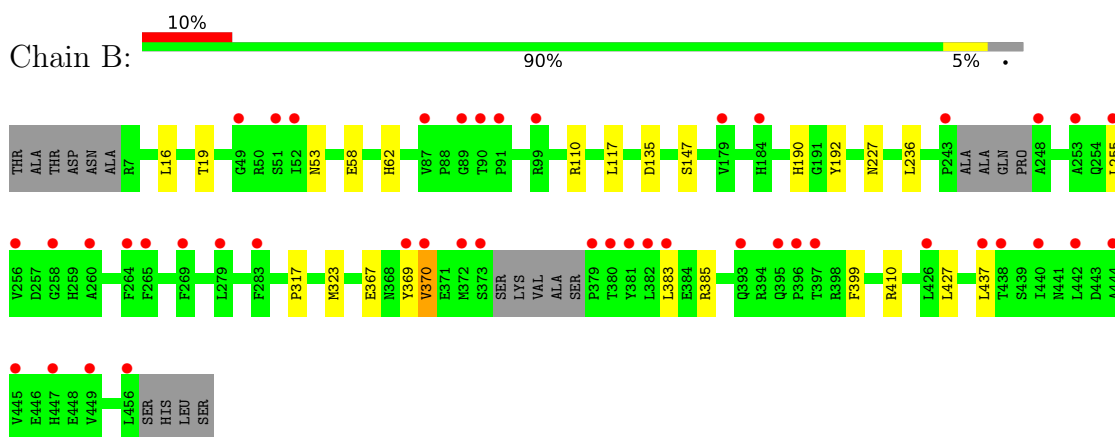
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Kynurenine 3-monooxygenase



- Molecule 1: Kynurenine 3-monooxygenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.35Å 53.25Å 135.84Å 90.00° 103.81° 90.00°	Depositor
Resolution (Å)	29.35 – 2.00 29.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.35-2.00) 99.7 (29.35-2.00)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.52 (at 2.00Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, $R_{free}$	0.192 , 0.218 (Not available) , 0.222	Depositor DCC
$R_{free}$ test set	3248 reflections (4.20%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.8	Xtrriage
Anisotropy	0.012	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 36.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	14495	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.73 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.0382e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, E1W, FAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.12	0/3561	0.30	0/4830
1	B	0.11	0/3591	0.29	0/4872
All	All	0.11	0/7152	0.30	0/9702

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3457	3421	3383	17	0
1	B	3473	3445	3400	14	0
2	A	53	31	31	0	0
2	B	53	31	31	1	0
3	A	1	0	0	1	0
3	B	1	0	0	1	0
4	A	20	11	0	0	0
4	B	20	11	0	0	0
5	A	257	0	0	1	0
5	B	210	0	0	0	0
All	All	7545	6950	6845	31	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (31) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ILE:HD11	1:A:407:THR:CG2	2.22	0.70
1:A:16:LEU:HD13	1:A:323[B]:MET:HG3	1.73	0.69
1:A:221:MET:HE1	1:A:372:MET:CE	2.29	0.63
1:B:317:PRO:HA	3:B:502:CL:CL	2.41	0.58
1:A:397:THR:HG23	1:A:398:ARG:HG3	1.84	0.58
1:A:221:MET:HE1	1:A:372:MET:HE1	1.85	0.57
1:A:56:LEU:HD13	1:A:323[B]:MET:HE1	1.87	0.56
1:B:110[B]:ARG:NH1	2:B:501:FAD:O4'	2.38	0.54
1:A:436:ASP:OD1	1:A:438:THR:OG1	2.25	0.53
1:B:58:GLU:OE2	1:B:410[A]:ARG:NH1	2.42	0.51
1:A:56:LEU:CD1	1:A:323[B]:MET:HE1	2.41	0.50
1:A:105:ILE:HD11	1:A:407:THR:HG21	1.91	0.50
1:B:135:ASP:OD1	1:B:147:SER:OG	2.28	0.50
1:A:317:PRO:HA	3:A:502:CL:CL	2.50	0.49
1:B:19[B]:THR:CG2	1:B:117:LEU:HB3	2.46	0.45
1:B:190:HIS:NE2	1:B:369:TYR:OH	2.50	0.45
1:A:383:LEU:HD23	1:A:431:VAL:HG13	1.99	0.45
1:A:426:LEU:HD21	1:A:448:GLU:CG	2.47	0.45
1:B:383:LEU:HD11	1:B:437:LEU:HG	1.98	0.45
1:A:55:ALA:HB1	1:A:105:ILE:HG21	1.98	0.44
1:B:53:ASN:ND2	1:B:227:ASN:OD1	2.44	0.44
1:B:192:TYR:HA	1:B:236:LEU:O	2.17	0.44
1:A:161:LEU:O	1:A:305:ALA:HA	2.18	0.43
1:B:190:HIS:HE2	1:B:369:TYR:HH	1.64	0.43
1:B:367:GLU:O	1:B:370:VAL:HG22	2.18	0.43
1:B:62:HIS:CG	1:B:410[B]:ARG:HD3	2.54	0.43
1:A:50:ARG:NH2	5:A:616:HOH:O	2.52	0.43
1:A:105:ILE:HD11	1:A:407:THR:HG22	2.01	0.42
1:B:399:PHE:HZ	1:B:427:LEU:HD11	1.85	0.41
1:B:16:LEU:HD13	1:B:323[A]:MET:HG3	2.02	0.41
1:A:192:TYR:HA	1:A:236:LEU:O	2.20	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	441/460 (96%)	435 (99%)	6 (1%)	0	100	100
1	B	447/460 (97%)	435 (97%)	12 (3%)	0	100	100
All	All	888/920 (96%)	870 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	366/371 (99%)	359 (98%)	7 (2%)	50	56
1	B	367/371 (99%)	364 (99%)	3 (1%)	73	80
All	All	733/742 (99%)	723 (99%)	10 (1%)	59	66

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	ARG
1	A	76	GLU
1	A	146	LEU
1	A	371	GLU
1	A	385	ARG
1	A	389	GLN
1	A	426	LEU
1	B	255	LEU

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Mol	Chain	Res	Type
1	B	370	VAL
1	B	385	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	131	ASN
1	A	184	HIS
1	A	196	GLN
1	A	204	GLN
1	A	210	ASN
1	B	31	GLN
1	B	33	ASN
1	B	188	GLN
1	B	441	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	E1W	A	503	-	22,22,22	2.33	6 (27%)	25,32,32	1.60	7 (28%)
4	E1W	B	503	-	22,22,22	2.30	7 (31%)	25,32,32	1.52	5 (20%)
2	FAD	B	501	-	58,58,58	0.30	0	85,89,89	0.34	0
2	FAD	A	501	-	58,58,58	0.32	0	85,89,89	0.34	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	E1W	A	503	-	-	0/4/17/17	0/3/3/3
4	E1W	B	503	-	-	2/4/17/17	0/3/3/3
2	FAD	B	501	-	-	1/34/50/50	0/6/6/6
2	FAD	A	501	-	-	1/34/50/50	0/6/6/6

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	E1W	O20-C04	7.46	1.46	1.37
4	A	503	E1W	O20-C04	7.43	1.46	1.37
4	B	503	E1W	N14-N15	3.47	1.36	1.30
4	A	503	E1W	N14-N15	3.46	1.36	1.30
4	A	503	E1W	C08-CL	3.16	1.79	1.72
4	A	503	E1W	C11-C12	3.04	1.53	1.49
4	A	503	E1W	C17-N10	2.96	1.41	1.36
4	B	503	E1W	C17-N10	2.95	1.41	1.36
4	B	503	E1W	C08-CL	2.91	1.79	1.72
4	A	503	E1W	C05-N10	2.79	1.47	1.42
4	B	503	E1W	C05-N10	2.69	1.47	1.42
4	B	503	E1W	C11-C12	2.62	1.52	1.49
4	B	503	E1W	C05-C06	2.08	1.44	1.40

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	E1W	C11-N10-C05	3.04	124.64	120.51
4	A	503	E1W	N16-N15-N14	-3.02	106.90	110.50
4	B	503	E1W	N16-N15-N14	-2.92	107.01	110.50
4	B	503	E1W	C11-N10-C05	2.83	124.35	120.51
4	A	503	E1W	C06-C05-N10	2.25	125.64	121.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	E1W	C19-O20-C04	-2.24	109.01	115.65
4	B	503	E1W	C06-C05-N10	2.24	125.62	121.42
4	B	503	E1W	C19-C17-N10	-2.24	113.58	116.80
4	A	503	E1W	C07-C06-C08	-2.22	117.20	121.23
4	A	503	E1W	C19-C17-N10	-2.21	113.62	116.80
4	A	503	E1W	C19-O20-C04	-2.20	109.15	115.65
4	A	503	E1W	C12-N16-N15	2.05	108.41	105.96

There are no chirality outliers.

All (4) torsion outliers are listed below:

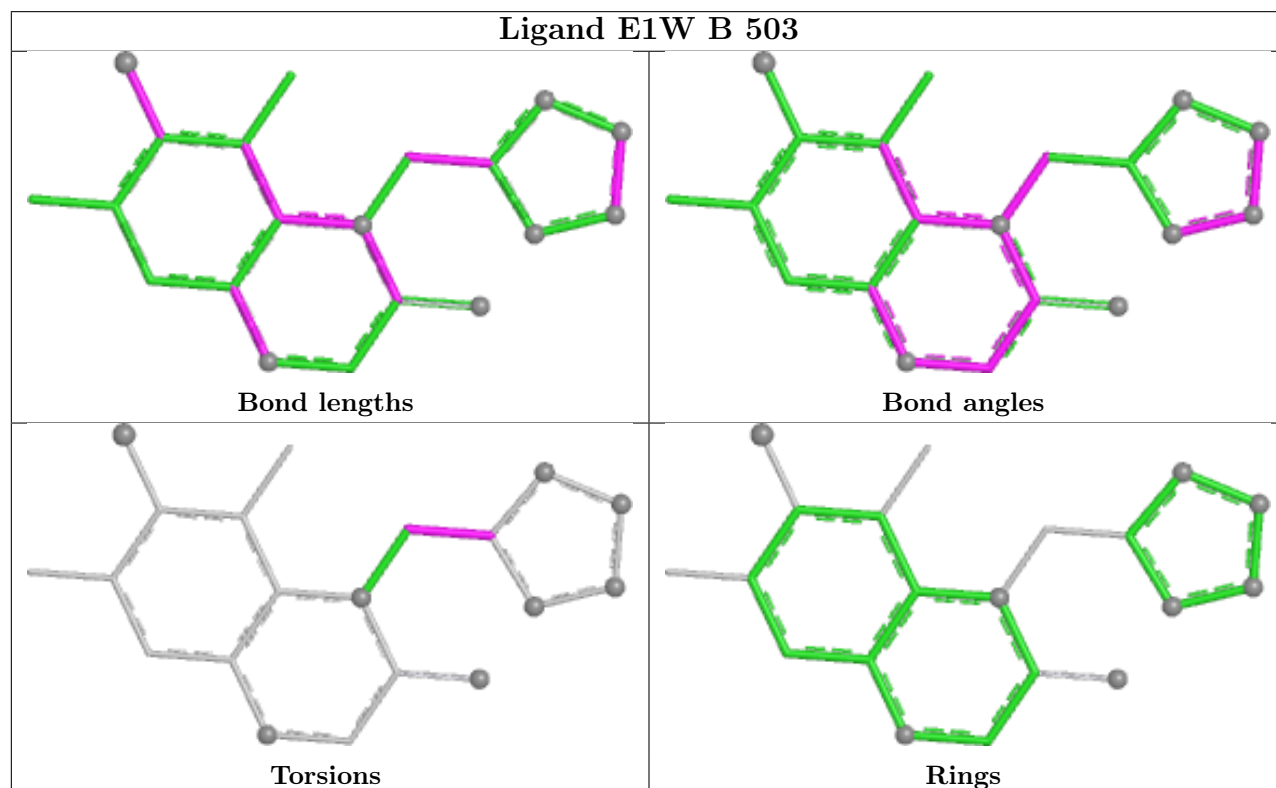
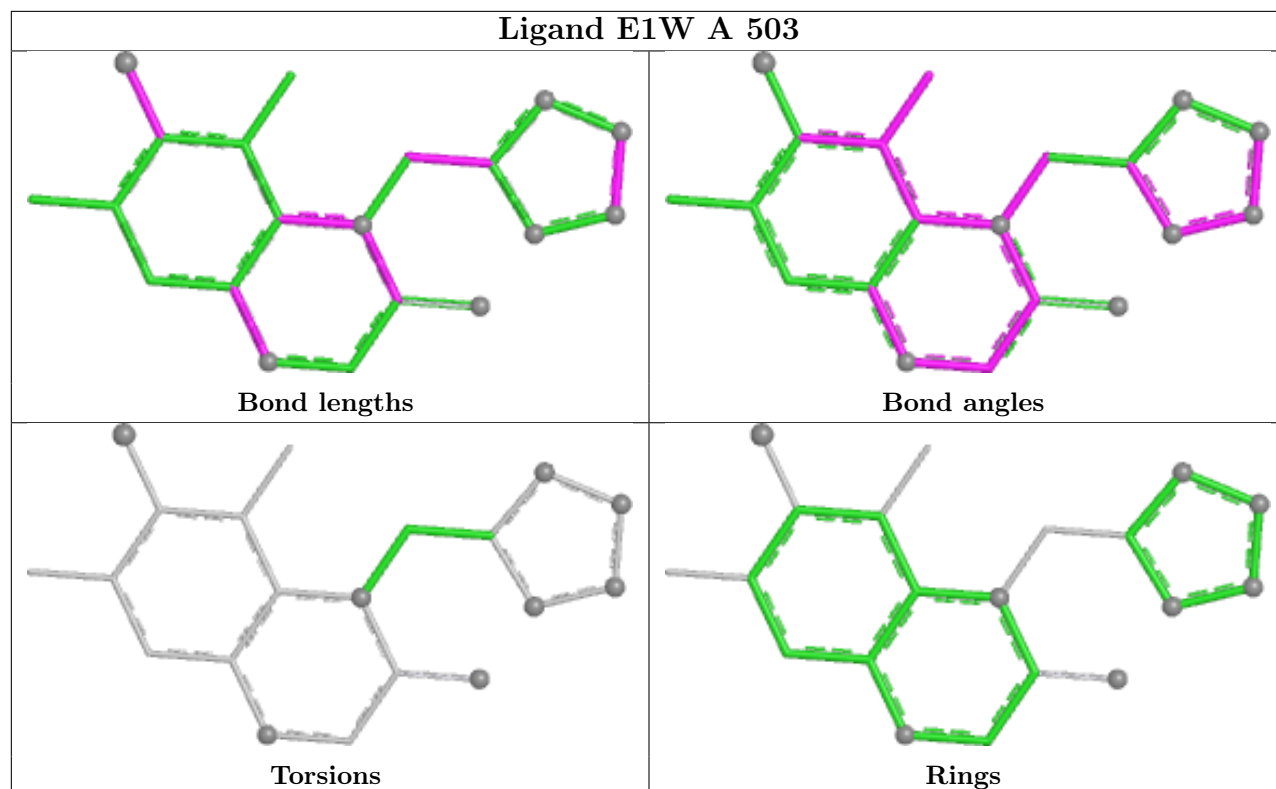
Mol	Chain	Res	Type	Atoms
4	B	503	E1W	N10-C11-C12-N16
4	B	503	E1W	N10-C11-C12-N13
2	A	501	FAD	O4B-C4B-C5B-O5B
2	B	501	FAD	O4B-C4B-C5B-O5B

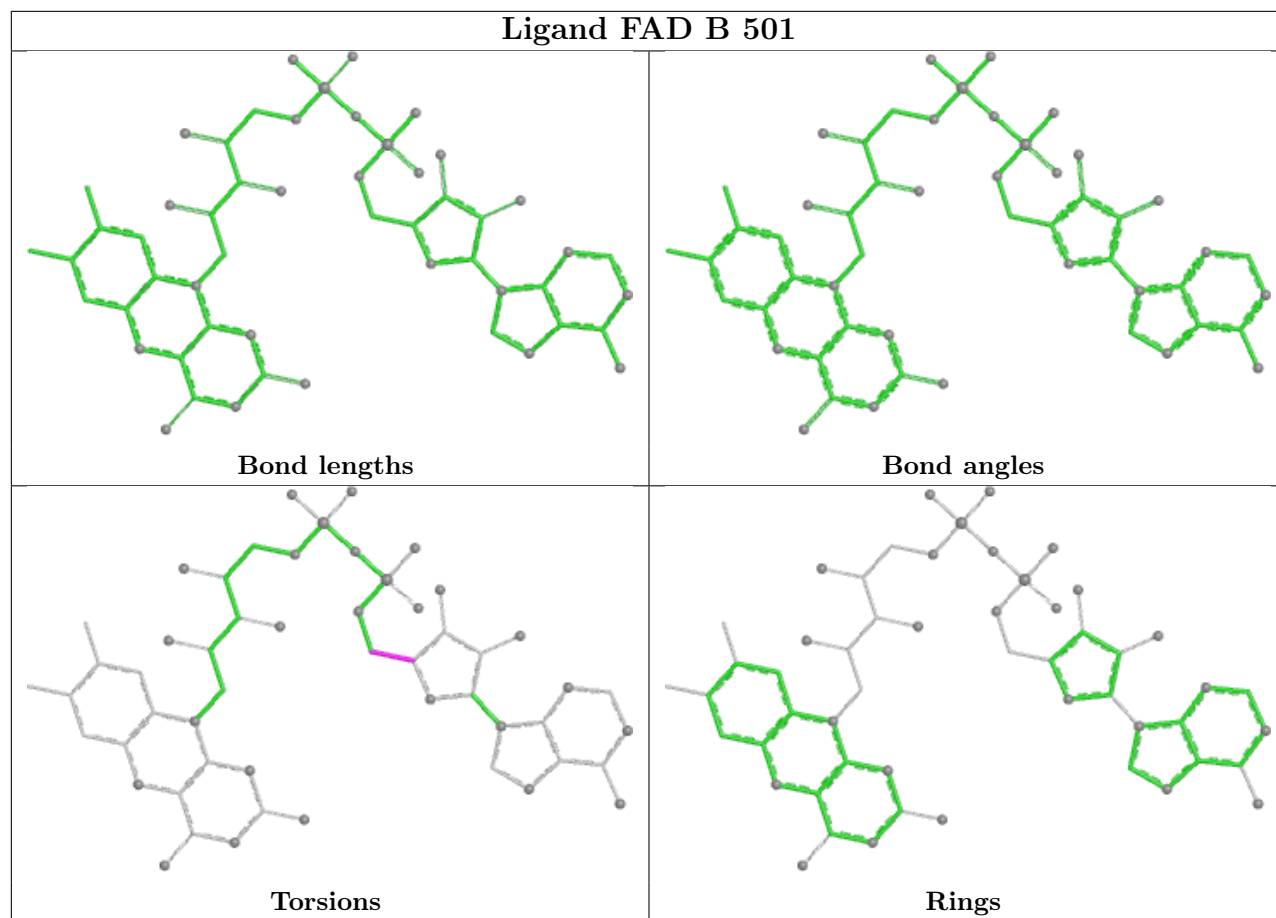
There are no ring outliers.

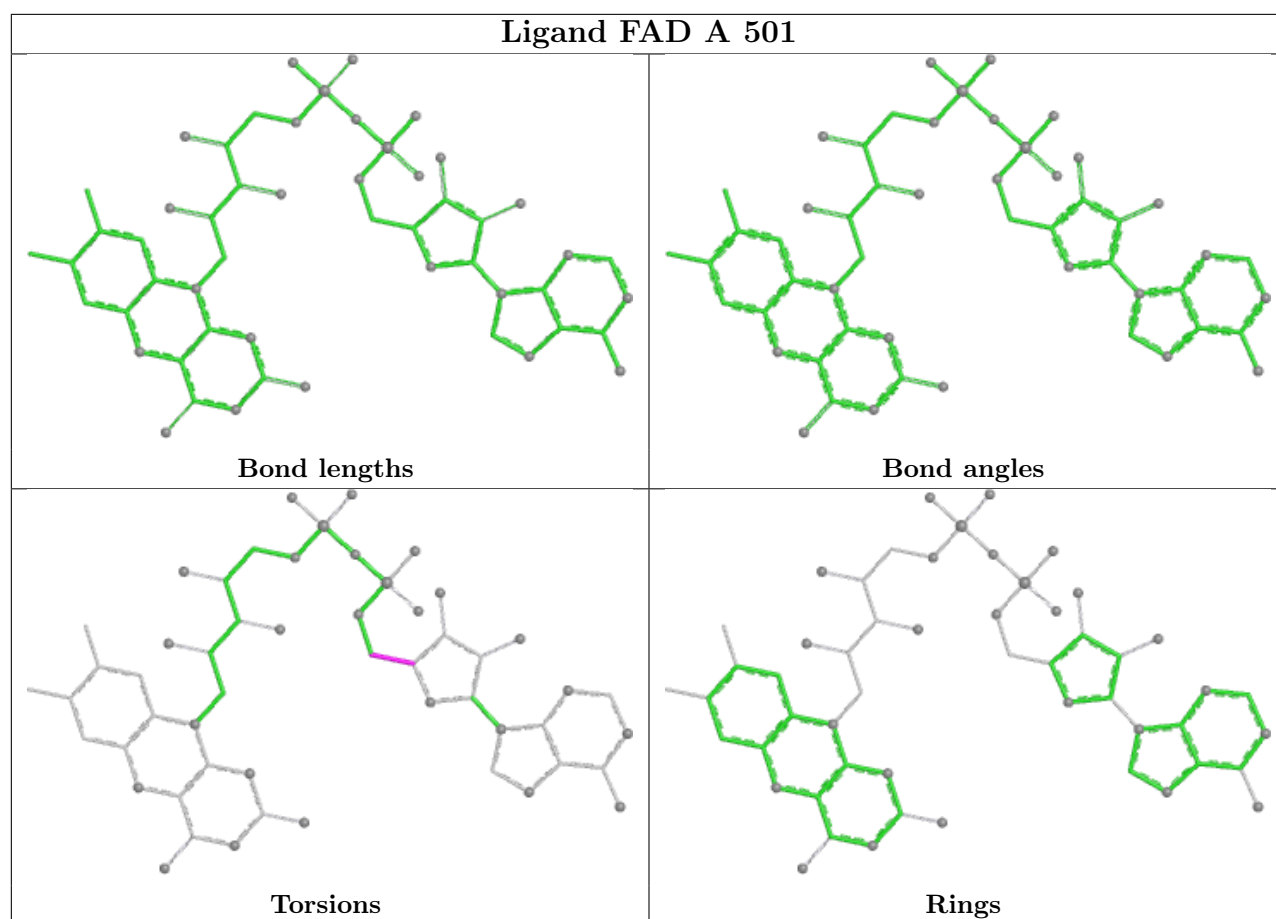
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	FAD	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	439/460 (95%)	0.09	27 (6%) 26 25	11, 34, 80, 106	6 (1%)
1	B	441/460 (95%)	0.39	45 (10%) 12 11	12, 39, 84, 113	6 (1%)
All	All	880/920 (95%)	0.24	72 (8%) 17 16	11, 36, 84, 113	12 (1%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	ALA	4.8
1	B	445	VAL	4.3
1	B	442	LEU	4.3
1	B	379	PRO	4.2
1	A	381	TYR	3.7
1	A	379	PRO	3.6
1	A	372	MET	3.6
1	B	437	LEU	3.5
1	B	373	SER	3.4
1	B	447	HIS	3.3
1	B	372	MET	3.3
1	B	444	ALA	3.2
1	B	382	LEU	3.2
1	B	449	VAL	3.1
1	B	243	PRO	3.1
1	B	283	PHE	3.1
1	A	447	HIS	3.1
1	B	279	LEU	3.1
1	A	89	GLY	3.0
1	B	184	HIS	2.9
1	B	397	THR	2.9
1	A	271	ASP	2.8
1	A	50	ARG	2.8
1	B	438	THR	2.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	51	SER	2.8
1	B	381	TYR	2.8
1	A	437	LEU	2.7
1	B	255	LEU	2.7
1	B	256	VAL	2.7
1	A	93	ASN	2.6
1	B	370	VAL	2.6
1	B	52	ILE	2.5
1	A	455	PRO	2.5
1	B	253	ALA	2.5
1	A	397	THR	2.5
1	A	374	SER	2.5
1	B	380	THR	2.5
1	A	429	PHE	2.5
1	A	256	VAL	2.4
1	B	87	VAL	2.4
1	B	369	TYR	2.4
1	B	383	LEU	2.4
1	A	440	ILE	2.4
1	A	445	VAL	2.4
1	A	90	THR	2.4
1	A	243	PRO	2.4
1	A	426	LEU	2.4
1	B	89	GLY	2.4
1	B	264	PHE	2.4
1	A	387	LEU	2.3
1	A	153	ARG	2.3
1	A	396	PRO	2.3
1	B	90	THR	2.3
1	B	395	GLN	2.2
1	B	269	PHE	2.2
1	B	396	PRO	2.2
1	B	258	GLY	2.2
1	B	456	LEU	2.2
1	A	441	ASN	2.2
1	B	49	GLY	2.2
1	A	442	LEU	2.2
1	B	426	LEU	2.2
1	B	91	PRO	2.1
1	B	393	GLN	2.1
1	B	99	ARG	2.1
1	B	260	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	382	LEU	2.1
1	A	184	HIS	2.1
1	B	440	ILE	2.1
1	B	265	PHE	2.1
1	A	92	PRO	2.0
1	B	179	VAL	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

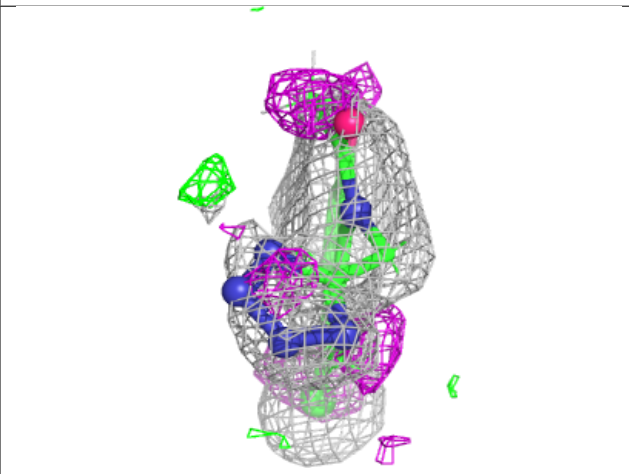
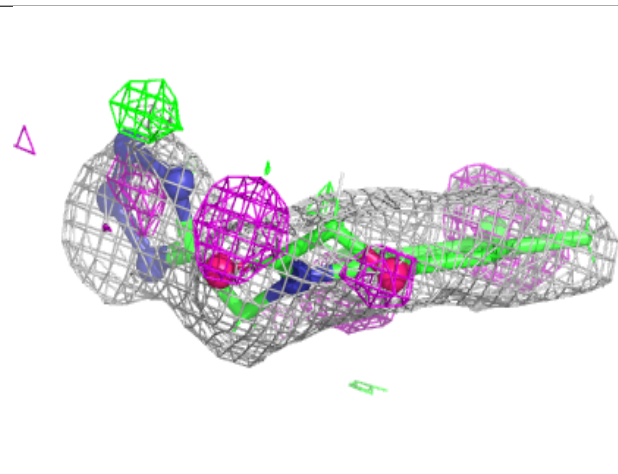
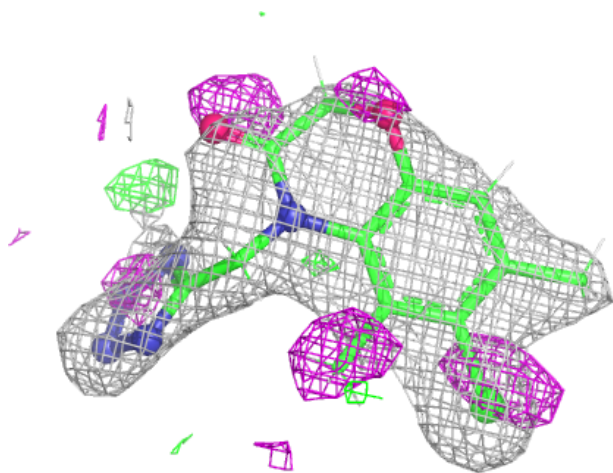
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	E1W	A	503	20/20	0.84	0.14	34,49,63,63	0
4	E1W	B	503	20/20	0.86	0.14	40,49,60,69	0
3	CL	A	502	1/1	0.97	0.06	26,26,26,26	0
3	CL	B	502	1/1	0.97	0.06	25,25,25,25	0
2	FAD	A	501	53/53	0.98	0.05	16,22,32,35	0
2	FAD	B	501	53/53	0.98	0.05	16,24,36,40	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

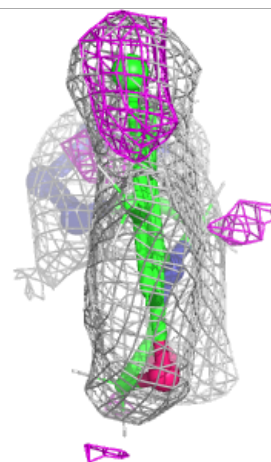
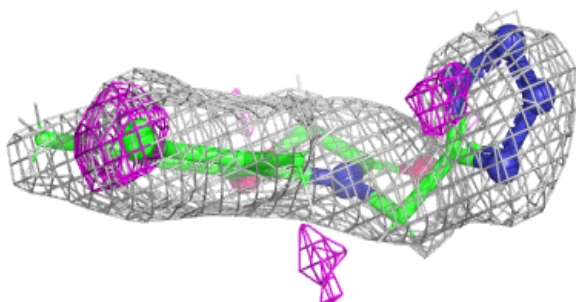
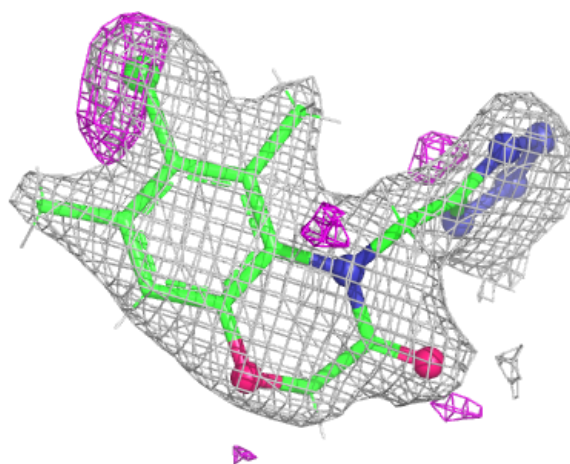
**Electron density around E1W A 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



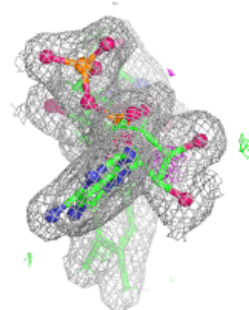
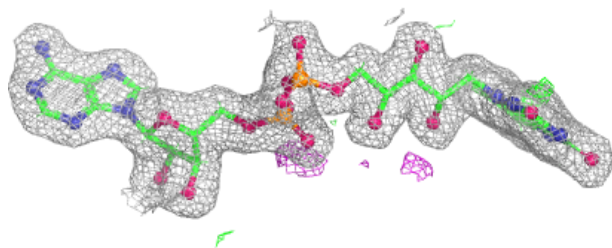
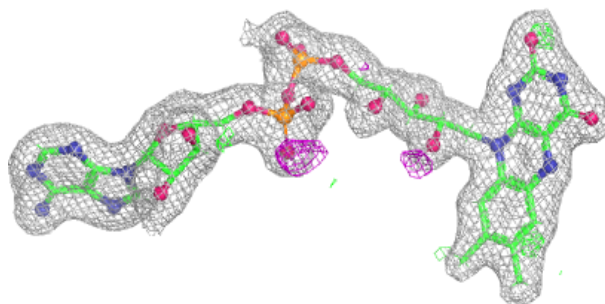
**Electron density around E1W B 503:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

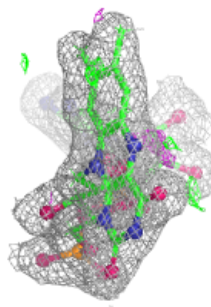
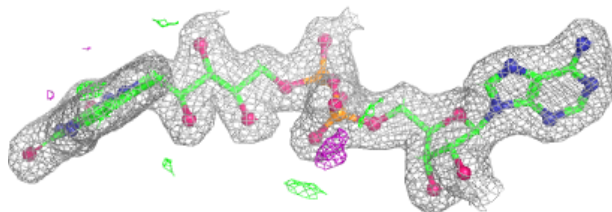
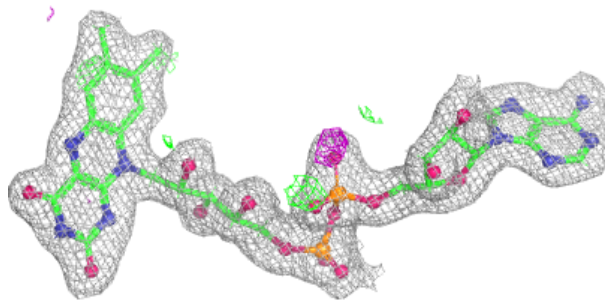


**Electron density around FAD A 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD B 501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.