

wwPDB X-ray Structure Validation Summary Report (i)

May 23, 2020 – 06:31 pm BST

PDB ID : 2IVD

Title: Structure of protoporphyrinogen oxidase from Myxococcus xanthus with aci-

fluorfen

Authors: Corradi, H.R.; Corrigall, A.V.; Boix, E.; Mohan, C.G.; Sturrock, E.D.; Meiss-

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Deposited on : 2006-06-12

Resolution : 2.30 Å(reported)

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

We welcome your comments at 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.11

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

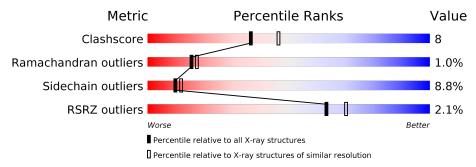
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.30 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{resolution range}(ext{Å}))$
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	478	75%	15%	•	6%
1	В	478	79%	12%	·	6%



2 Entry composition (i)

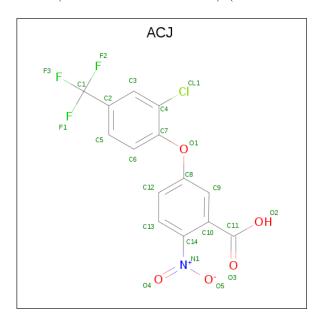
There are 6 unique types of molecules in this entry. The entry contains 7129 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTOPORPHYRINOGEN OXIDASE.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	Δ	449	Total	С	Ν	О	S	20	0	0	
1	11	110	3313	2085	627	595	6	20	U	0	
1	D	449	Total	С	N	Ο	S	28	0	0	
1	Б	449	3319	2087	627	599	6	20	28 0		

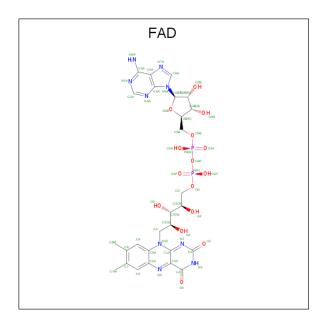
• Molecule 2 is 5-[2-CHLORO-4-(TRIFLUOROMETHYL)PHENOXY]-2-NITROBENZOIC ACID (three-letter code: ACJ) (formula: C₁₄H₇ClF₃NO₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
9	Λ	1	Total	С	Cl	F	N	О	0	0
	A	1	24	14	1	3	1	5	0	U
9	D	1	Total	С	Cl	F	N	О	0	0
2	D	1	24	14	1	3	1	5	U	U

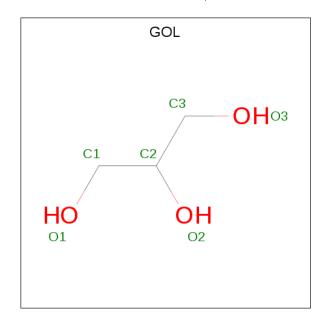
• Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
2	Λ.	1	Total	С	N	О	Р	0	0	
3	A	1	53	27	9	15	2	U		
9	D	1	Total	С	N	О	Р	0	0	
3	Б	1	53	27	9	15	2	U	0	

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0
4	A	1	Total C O 6 3 3	0	0

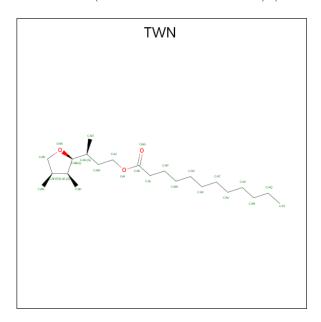
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0
4	В	1	Total C O 6 3 3	0	0

• Molecule 5 is (3S)-3-[(2S,3S,4R)-3,4-DIMETHYLTETRAHYDROFURAN-2-YL]BUTYL LAURATE (three-letter code: TWN) (formula: $C_{22}H_{42}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total C O 25 22 3	0	0

• Molecule 6 is water.

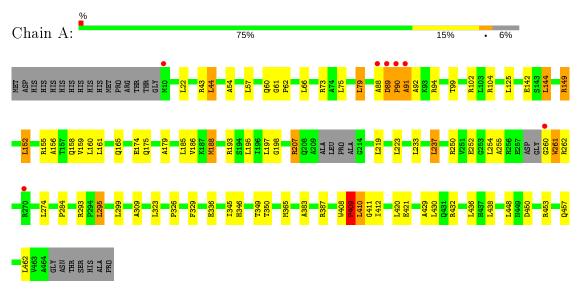
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	146	Total O 146 146	0	0
6	В	142	Total O 142 142	0	0



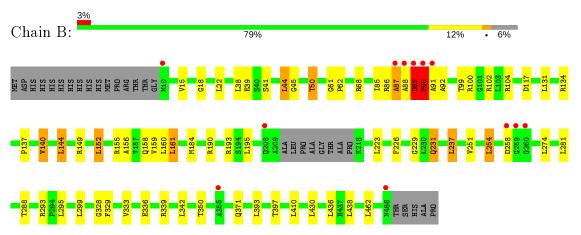
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: PROTOPORPHYRINOGEN OXIDASE



• Molecule 1: PROTOPORPHYRINOGEN OXIDASE





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants	148.92Å 148.92Å 131.92Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.39 - 2.30	Depositor
Resolution (A)	49.37 - 2.30	EDS
% Data completeness	86.3 (49.39-2.30)	Depositor
(in resolution range)	86.3 (49.37-2.30)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.10 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D	0.234 , 0.283	Depositor
R, R_{free}	0.238 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	36.3	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 35.3	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7129	wwPDB-VP
Average B, all atoms $(Å^2)$	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.22% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: GOL, TWN, FAD, ACJ

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.47	0/3370	0.69	1/4574 (0.0%)	
1	В	0.46	0/3376	0.67	4/4580 (0.1%)	
All	All	0.46	0/6746	0.68	5/9154 (0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	В	0	4
All	All	0	7

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Type Atoms		$Observed(^o)$	$\mathbf{Ideal}(^o)$
1	A	149	ARG	NE-CZ-NH2	-6.38	117.11	120.30
1	В	149	ARG	NE-CZ-NH1	5.78	123.19	120.30
1	В	89	ASP	C-N-CD	-5.75	107.95	120.60
1	В	89	ASP	CB-CG-OD2	5.25	123.02	118.30
1	В	149	ARG	NE-CZ-NH2	-5.05	117.78	120.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	345	ILE	Peptide

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Mol	Chain	Res	Type	Group
1	A	409	PRO	Peptide
1	A	410	LEU	Peptide
1	В	87	ALA	Peptide
1	В	89	ASP	Peptide

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	3313	0	3367	53	0
1	В	3319	0	3375	48	0
2	A	24	0	6	1	0
2	В	24	0	6	1	0
3	A	53	0	31	4	0
3	В	53	0	31	2	0
4	A	12	0	16	2	0
4	В	18	0	24	1	0
5	В	25	0	42	12	0
6	A	146	0	0	3	0
6	В	142	0	0	1	0
All	All	7129	0	6898	107	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 8.

The worst 5 of 107 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{array}{ll} ext{Interatomic} \ ext{distance} & (ext{Å}) \end{array}$	Clash overlap (Å)
1:B:134:ARG:HE	5:B:1472:TWN:HAF	0.98	1.10
1:B:18:GLY:HA2	1:B:45:GLY:O	1.51	1.09
1:B:134:ARG:NE	5:B:1472:TWN:HAF	1.69	1.05
1:A:309:ALA:O	1:A:411:GLY:HA3	1.58	1.04
1:B:134:ARG:HH11	5:B:1472:TWN:HAN1	1.20	1.02

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	nain Analysed Favoured Allowed		Outliers	Percentiles	
1	A	443/478 (93%)	423 (96%)	15 (3%)	5 (1%)	14 15
1	В	445/478~(93%)	431 (97%)	10 (2%)	4 (1%)	17 20
All	All	888/956 (93%)	854 (96%)	25 (3%)	9 (1%)	15 17

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	90	PRO
1	В	258	ASP
1	A	90	PRO
1	A	91	ALA
1	A	261	TRP

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	Analysed Rotameric Outliers		Percentiles		
1	A	317/344 (92%)	285 (90%)	32 (10%)	7	9	
1	В	319/344 (93%)	295 (92%)	24 (8%)	13	17	
All	All	$636/688 \; (92\%)$	580 (91%)	56 (9%)	10	12	

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	420	LEU

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Mol	Chain	Res	Type
1	A	462	LEU
1	В	371	GLN
1	A	421	GLU
1	A	436	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	${f Res}$	\mathbf{Type}
1	A	346	HIS
1	В	431	GLN
1	A	416	ASN
1	A	315	HIS
1	В	158	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

10 ligands are modelled in this entry.

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).



Mal	Mol Type Chain Res		Res	Link	Во	Bond lengths			Bond angles							
MIOI	Type	Chain	nes	nes	ries	nes	nes	nes	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	FAD	В	1469	-	51,58,58	1.35	6 (11%)	60,89,89	1.73	6 (10%)						
2	ACJ	A	1465	-	22,25,25	3.38	6 (27%)	29,37,37	1.06	2 (6%)						
4	GOL	A	1468	-	5,5,5	0.49	0	5,5,5	0.81	0						
4	GOL	В	1471	-	5,5,5	0.34	0	5,5,5	0.45	0						
3	FAD	A	1466	-	51,58,58	1.41	6 (11%)	60,89,89	1.74	6 (10%)						
4	GOL	В	1467	-	5,5,5	0.44	0	5,5,5	0.53	0						
2	ACJ	В	1468	-	22,25,25	3.48	6 (27%)	29,37,37	2.68	8 (27%)						
4	GOL	В	1470	-	5,5,5	0.28	0	5,5,5	0.65	0						
4	GOL	A	1467	-	5,5,5	0.36	0	5,5,5	0.55	0						
5	TWN	В	1472	-	25,25,25	0.53	0	25,30,30	1.30	4 (16%)						

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
3	FAD	В	1469	-	-	5/30/50/50	0/6/6/6
2	ACJ	A	1465	-	-	0/12/18/18	0/2/2/2
4	GOL	A	1468	-	-	2/4/4/4	1
4	GOL	В	1471	-	-	2/4/4/4	-
3	FAD	A	1466	-	-	2/30/50/50	0/6/6/6
4	GOL	В	1467	-	-	1/4/4/4	-
2	ACJ	В	1468	-	-	0/12/18/18	0/2/2/2
4	GOL	В	1470	-	-	2/4/4/4	-
4	GOL	A	1467	-	-	4/4/4/4	-
5	TWN	В	1472	_	-	12/21/34/34	0/1/1/1

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	В	1468	ACJ	O4-N1	10.30	1.40	1.22
2	A	1465	ACJ	O4-N1	9.89	1.39	1.22
2	В	1468	ACJ	C10-C14	8.84	1.50	1.40
2	A	1465	ACJ	C10-C14	8.51	1.50	1.40
2	A	1465	ACJ	C7-C4	5.53	1.49	1.39

The worst 5 of 26 bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1468	ACJ	F3-C1-C2	-7.64	96.16	112.93
3	В	1469	FAD	C4-N3-C2	7.44	121.43	115.14
3	A	1466	FAD	C4-N3-C2	7.06	121.10	115.14
2	В	1468	ACJ	F2-C1-C2	-6.58	98.48	112.93
2	В	1468	ACJ	F1-C1-C2	-6.41	98.85	112.93

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	1469	FAD	C2'-C1'-N10-C9A
3	В	1469	FAD	N10-C1'-C2'-O2'
3	В	1469	FAD	N10-C1'-C2'-C3'
3	В	1469	FAD	C5'-O5'-P-O3P
4	A	1468	GOL	C1-C2-C3-O3

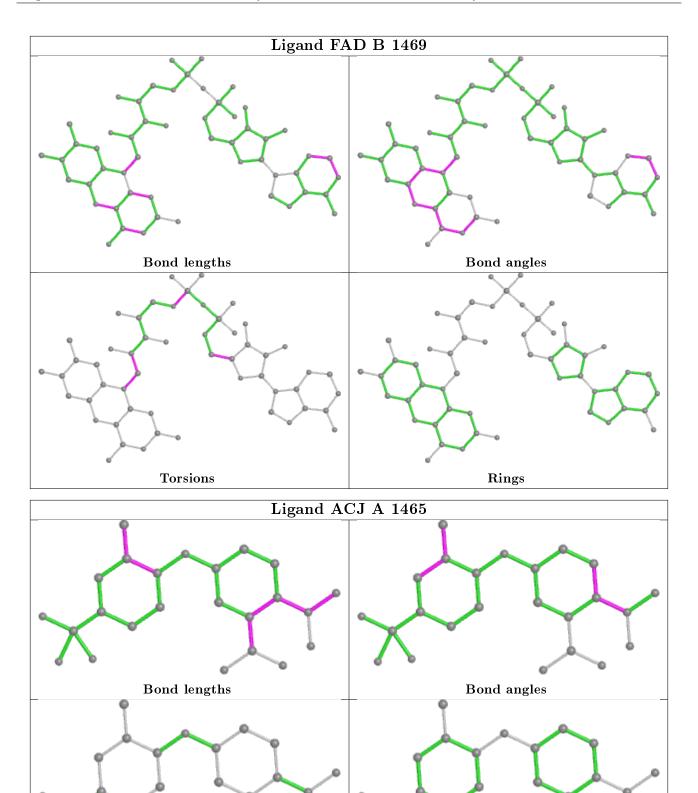
There are no ring outliers.

7 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	1469	FAD	2	0
2	A	1465	ACJ	1	0
4	A	1468	GOL	2	0
3	A	1466	FAD	4	0
4	В	1467	GOL	1	0
2	В	1468	ACJ	1	0
5	В	1472	TWN	12	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 then 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.

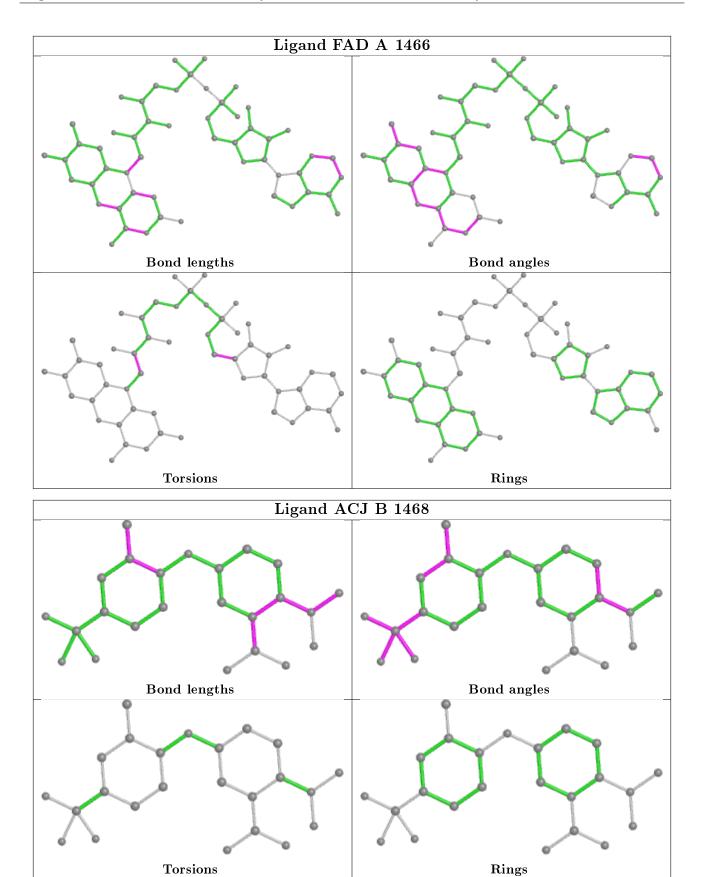




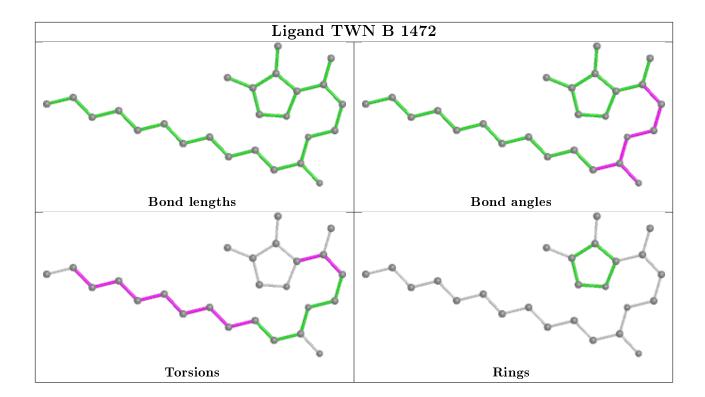


Rings

Torsions







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 (i)

6.1 Protein, DNA and RNA chains (i)

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^{th} 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			$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	449/478 (93%)	-0.03	7 (1%) 72 77	17, 34, 50, 62	6 (1%)
1	В	449/478 (93%)	-0.08	12 (2%) 54 62	16, 34, 50, 62	8 (1%)
All	All	898/956 (93%)	-0.06	19 (2%) 63 70	16, 34, 50, 62	14 (1%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	${f Res}$	Type	RSRZ
1	В	259	GLY	4.6
1	A	10	MET	4.4
1	A	91	ALA	4.2
1	A	260	GLY	3.8
1	В	466	ASN	3.7

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 carbohydrates in this entry.

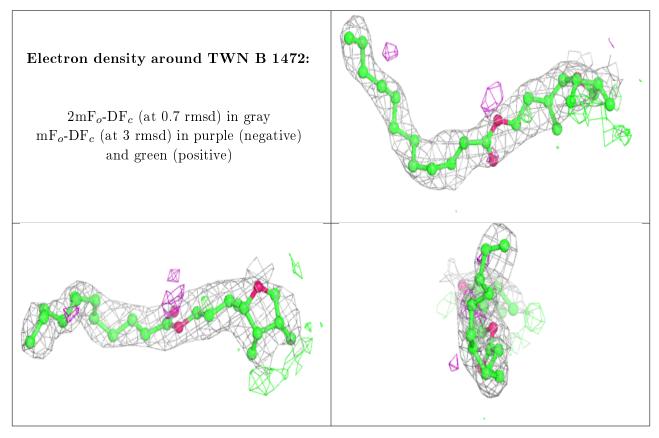
6.4 Ligands (i)

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^{th} 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	${f B-factors}({f \AA}^2)$	Q < 0.9
5	TWN	В	1472	25/25	0.79	0.22	63,65,66,67	0
4	GOL	В	1467	6/6	0.82	0.15	42,42,43,43	0
2	ACJ	В	1468	24/24	0.84	0.22	52,53,54,56	0
4	GOL	A	1467	6/6	0.90	0.17	32,34,36,37	0
4	GOL	A	1468	6/6	0.90	0.14	23,29,31,33	0
2	ACJ	A	1465	24/24	0.91	0.20	49,50,51,52	0
4	GOL	В	1471	6/6	0.91	0.15	32,35,37,39	0
4	GOL	В	1470	6/6	0.95	0.13	28,29,29,29	0
3	FAD	A	1466	53/53	0.96	0.12	23,26,29,29	0
3	FAD	В	1469	53/53	0.96	0.12	25,28,32,32	0

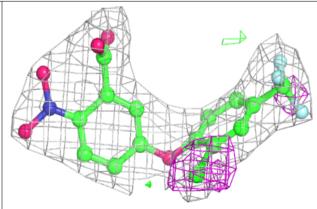
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

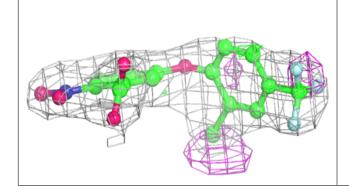


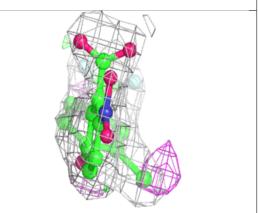


Electron density around ACJ B 1468:

 $2 \mathrm{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

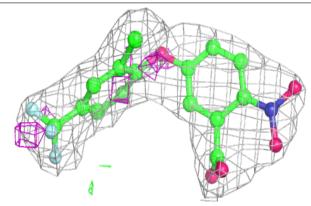


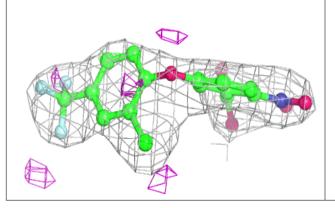


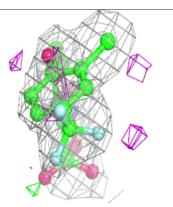


Electron density around ACJ A 1465:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



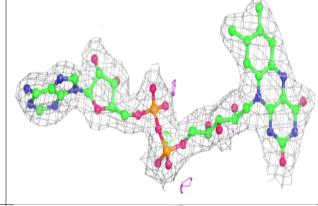


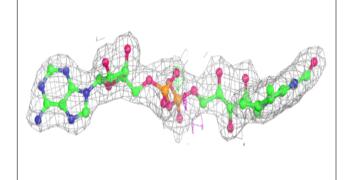


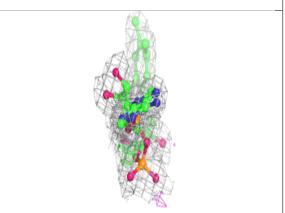


Electron density around FAD A 1466:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

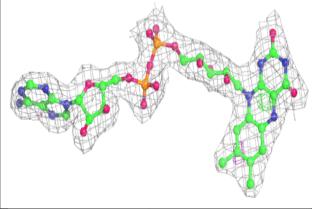


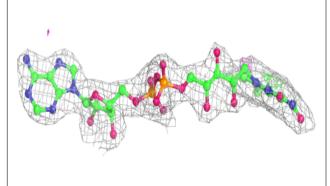


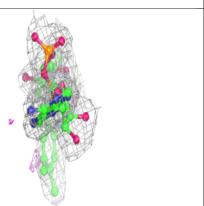


Electron density around FAD B 1469:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

