



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:37 AM BST

PDB ID : 4IVO
Title : Structure of human protoporphyrinogen IX oxidase(R59Q)
Authors : Xiaohong, Q.; Baifan, W.
Deposited on : 2013-01-23
Resolution : 2.60 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

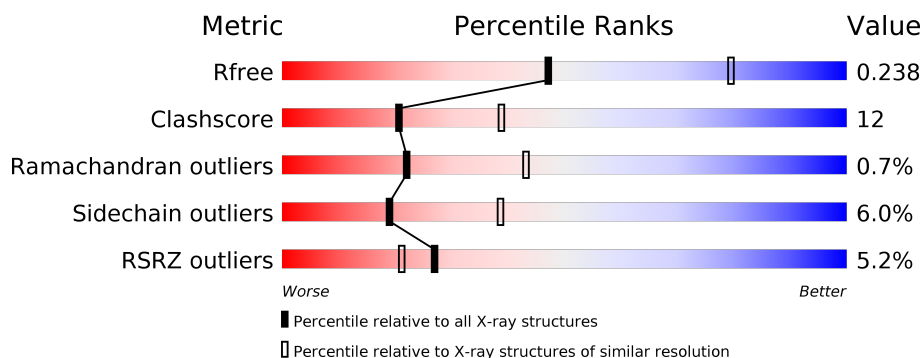
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 $\leq 5\%$. 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	B	483	<div> <div>5%</div> <div>72%</div> <div>22%</div> <div>• •</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	B	503	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3626 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.

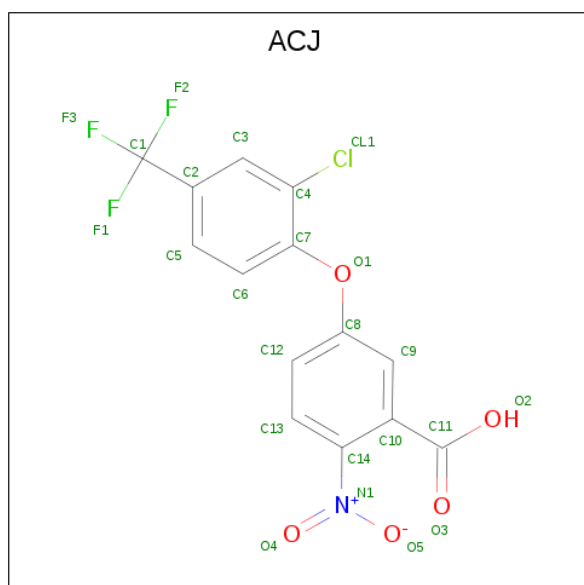
- Molecule 1 is a protein called Protoporphyrinogen oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	464	3461	2188	625	636	12	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

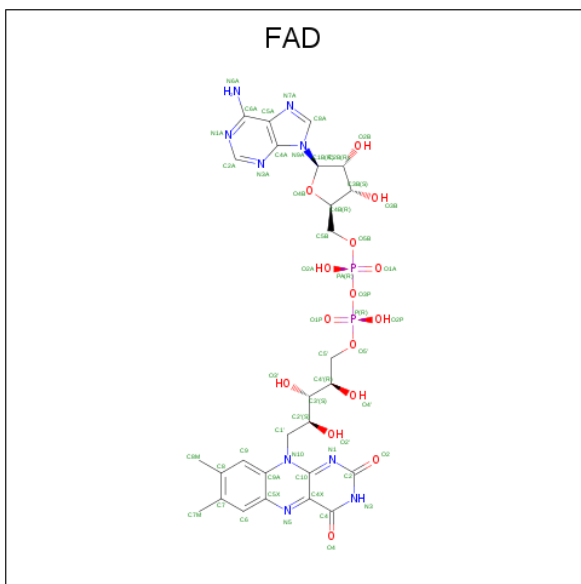
Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	EXPRESSION TAG	UNP P50336
B	-4	HIS	-	EXPRESSION TAG	UNP P50336
B	-3	HIS	-	EXPRESSION TAG	UNP P50336
B	-2	HIS	-	EXPRESSION TAG	UNP P50336
B	-1	HIS	-	EXPRESSION TAG	UNP P50336
B	0	HIS	-	EXPRESSION TAG	UNP P50336
B	59	GLN	ARG	ENGINEERED MUTATION	UNP P50336

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



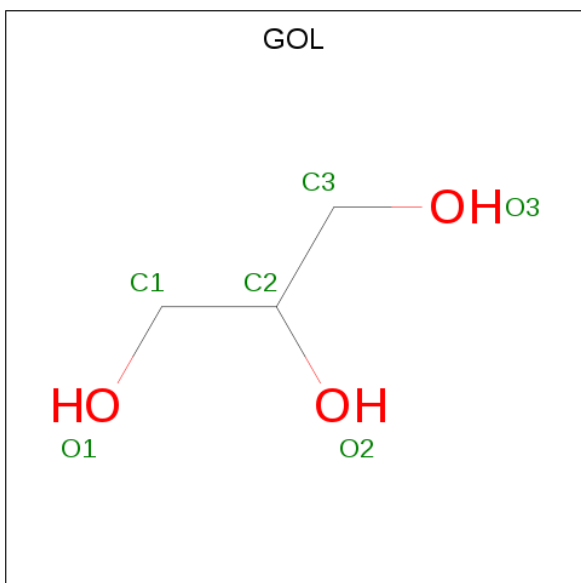
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	Cl	F	N	O	0	0
			24	14	1	3	1	5		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	76	Total	O	0	0
			76	76		

4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	135.81Å 135.81Å 158.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.58 – 2.60 30.58 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.5 (30.58-2.60) 98.8 (30.58-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.18 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4 _486)	Depositor
R, R_{free}	0.177 , 0.238 0.176 , 0.238	Depositor DCC
R_{free} test set	880 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.024 for -2/3*h-1/3*k+2/3*l,-1/3*h-2/3*k-2/3*l,2/3*h-2/3*k+1/3*l 0.019 for -h,1/3*h-1/3*k+2/3*l,2/3*h+4/3*k+1/3*l 0.006 for -1/3*h+1/3*k-2/3*l,-k,-4/3*h-2/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3626	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, 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	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	0.42	0/3536	0.55	0/4812

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	B	3461	0	3485	86	0
2	B	24	0	6	1	0
3	B	53	0	31	5	0
4	B	12	0	16	4	0
5	B	76	0	0	2	0
All	All	3626	0	3538	87	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 12.

All (87) 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:B:235:MET:HG2	5:B:621:HOH:O	1.64	0.95
1:B:93:ALA:HB2	1:B:351:VAL:HG12	1.49	0.93
1:B:62:ARG:CZ	1:B:97:ARG:HH22	1.87	0.88
1:B:62:ARG:NH1	1:B:97:ARG:HH22	1.78	0.80
1:B:198:LEU:O	1:B:202:LEU:HG	1.83	0.79
1:B:181:ARG:HH21	4:B:504:GOL:H11	1.47	0.78
1:B:264:ALA:O	1:B:265:GLU:HB2	1.85	0.75
2:B:501:ACJ:O3	2:B:501:ACJ:O4	2.05	0.74
1:B:62:ARG:NH2	1:B:97:ARG:HH22	1.85	0.74
1:B:19:TYR:CZ	1:B:23:ARG:HD3	2.26	0.70
1:B:10:GLY:HA3	1:B:39:LEU:HD22	1.74	0.70
1:B:359:SER:HA	1:B:360:PRO:C	2.15	0.66
1:B:6:VAL:HG23	1:B:279:ALA:HB2	1.77	0.66
1:B:58:PRO:HA	3:B:502:FAD:N5	2.12	0.65
1:B:429:LYS:HG2	4:B:503:GOL:H11	1.78	0.64
1:B:44:ARG:HG2	1:B:56:LEU:HD12	1.81	0.62
1:B:50:ASN:HD22	1:B:50:ASN:H	1.45	0.62
1:B:58:PRO:HB3	3:B:502:FAD:C4X	2.29	0.62
1:B:12:ILE:HG13	1:B:460:ILE:HD13	1.82	0.61
1:B:138:ARG:HH21	1:B:195:ARG:HG2	1.66	0.60
1:B:413:HIS:HD2	5:B:641:HOH:O	1.83	0.60
1:B:62:ARG:NH2	1:B:97:ARG:NH2	2.48	0.60
1:B:63:PRO:HD3	1:B:226:GLN:HA	1.83	0.60
1:B:95:GLN:O	1:B:96:ASN:ND2	2.34	0.60
1:B:236:LEU:HB3	1:B:237:PRO:HD3	1.84	0.60
1:B:173:GLY:HA3	1:B:421:GLN:HE22	1.68	0.59
1:B:391:GLN:O	1:B:395:GLU:HG3	2.03	0.58
1:B:132:ARG:O	1:B:136:LYS:HD3	2.04	0.58
1:B:125:PRO:HG2	1:B:128:TRP:HD1	1.69	0.57
1:B:192:GLN:OE1	1:B:192:GLN:HA	2.04	0.57
1:B:8:LEU:HD22	1:B:257:VAL:HG21	1.88	0.56
1:B:255:GLN:HE21	1:B:255:GLN:HA	1.71	0.56
1:B:128:TRP:O	1:B:132:ARG:HG3	2.06	0.55
1:B:96:ASN:HB2	1:B:330:GLY:HA2	1.88	0.55
1:B:62:ARG:CZ	1:B:97:ARG:NH2	2.66	0.54
1:B:6:VAL:CG2	1:B:279:ALA:HB2	2.37	0.54
1:B:456:VAL:O	1:B:460:ILE:HG12	2.08	0.53
1:B:34:GLU:HG2	1:B:39:LEU:HD23	1.89	0.53
1:B:146:VAL:HG11	1:B:167:CYS:SG	2.48	0.53
1:B:133:GLU:OE2	1:B:197:ILE:N	2.44	0.51
1:B:264:ALA:O	1:B:265:GLU:CB	2.58	0.51
1:B:377:LEU:HB3	1:B:384:LEU:HD21	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:363:LEU:HD12	1:B:364:ARG:N	2.26	0.50
1:B:112:LEU:N	1:B:112:LEU:HD22	2.26	0.50
1:B:316:VAL:HG22	1:B:368:MET:SD	2.52	0.50
1:B:35:SER:HB3	1:B:256:PRO:HA	1.94	0.49
1:B:154:LEU:HB3	1:B:158:VAL:HG11	1.95	0.48
1:B:58:PRO:HB3	3:B:502:FAD:C4	2.44	0.48
1:B:63:PRO:CD	1:B:226:GLN:HA	2.43	0.48
1:B:19:TYR:O	1:B:23:ARG:HG3	2.14	0.48
1:B:240:LEU:O	1:B:244:LEU:HG	2.14	0.48
1:B:62:ARG:HH12	1:B:97:ARG:HH22	1.58	0.48
1:B:428:GLN:HG3	4:B:503:GOL:H2	1.95	0.48
1:B:125:PRO:HG2	1:B:128:TRP:CD1	2.49	0.47
1:B:71:THR:O	1:B:75:VAL:HG23	2.14	0.47
1:B:426:HIS:HA	1:B:429:LYS:HE3	1.96	0.47
1:B:98:PHE:HB2	1:B:333:HIS:HB3	1.97	0.47
1:B:145:THR:HA	1:B:178:LEU:O	2.15	0.47
1:B:363:LEU:C	1:B:363:LEU:HD12	2.35	0.47
1:B:152:ARG:HH11	1:B:152:ARG:HG2	1.80	0.46
1:B:213:SER:O	1:B:217:ARG:HG3	2.15	0.46
1:B:144:GLU:C	1:B:424:LEU:HD21	2.36	0.46
1:B:41:GLY:HA3	3:B:502:FAD:O1A	2.15	0.46
1:B:149:PHE:O	1:B:153:ARG:HG3	2.16	0.46
1:B:12:ILE:HG13	1:B:460:ILE:CD1	2.47	0.45
1:B:134:LEU:HA	1:B:196:SER:HB2	1.98	0.45
1:B:191:GLU:O	1:B:194:HIS:O	2.35	0.45
1:B:286:ILE:HD12	1:B:290:VAL:HG12	1.98	0.44
1:B:100:TYR:OH	1:B:103:GLY:HA2	2.17	0.44
1:B:137:PRO:HB2	1:B:138:ARG:H	1.56	0.44
1:B:62:ARG:NH1	1:B:97:ARG:NH2	2.56	0.44
1:B:133:GLU:OE1	1:B:134:LEU:HD23	2.18	0.43
1:B:138:ARG:HH21	1:B:195:ARG:CD	2.31	0.43
1:B:267:ARG:NH2	1:B:278:GLU:HB3	2.33	0.42
1:B:138:ARG:HH21	1:B:195:ARG:CG	2.29	0.42
1:B:24:ALA:O	1:B:27:PRO:HD3	2.19	0.42
1:B:130:GLY:O	1:B:133:GLU:HB3	2.20	0.41
1:B:150:ALA:HB2	1:B:163:MET:HG3	2.03	0.41
1:B:19:TYR:CE1	1:B:23:ARG:HD3	2.55	0.41
1:B:111:GLY:O	1:B:112:LEU:C	2.59	0.41
1:B:428:GLN:CG	4:B:503:GOL:H2	2.51	0.41
1:B:15:LEU:HB3	1:B:240:LEU:HD13	2.03	0.41
1:B:257:VAL:H	3:B:502:FAD:H62A	1.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:ARG:HH12	1:B:97:ARG:HH12	1.68	0.41
1:B:61:ILE:O	1:B:226:GLN:HB2	2.21	0.41
1:B:133:GLU:OE2	1:B:153:ARG:NH1	2.54	0.40
1:B:360:PRO:HA	1:B:361:PRO:HD3	1.91	0.40

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	B	458/483 (95%)	439 (96%)	16 (4%)	3 (1%)	22	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	137	PRO
1	B	89	GLY
1	B	265	GLU

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	B	366/386 (95%)	344 (94%)	22 (6%)	19	39

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	47	ARG
1	B	50	ASN
1	B	76	SER
1	B	112	LEU
1	B	119	SER
1	B	127	PHE
1	B	136	LYS
1	B	189	GLN
1	B	196	SER
1	B	210	GLN
1	B	215	LEU
1	B	238	GLN
1	B	255	GLN
1	B	263	GLN
1	B	265	GLU
1	B	294	LEU
1	B	363	LEU
1	B	377	LEU
1	B	391	GLN
1	B	404	LYS
1	B	424	LEU
1	B	469	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	50	ASN
1	B	59	GLN
1	B	96	ASN
1	B	189	GLN
1	B	194	HIS
1	B	210	GLN
1	B	226	GLN
1	B	238	GLN
1	B	255	GLN
1	B	318	ASN
1	B	322	GLN
1	B	391	GLN
1	B	413	HIS
1	B	421	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	GOL	B	503	-	5,5,5	0.66	0	5,5,5	1.35	0
2	ACJ	B	501	-	22,25,25	1.23	2 (9%)	29,37,37	0.99	1 (3%)
4	GOL	B	504	-	5,5,5	0.55	0	5,5,5	1.72	1 (20%)
3	FAD	B	502	-	51,58,58	1.42	6 (11%)	60,89,89	1.73	6 (10%)

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	GOL	B	503	-	-	2/4/4/4	-
2	ACJ	B	501	-	-	0/12/18/18	0/2/2/2
4	GOL	B	504	-	-	1/4/4/4	-
3	FAD	B	502	-	-	2/30/50/50	0/6/6/6

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	FAD	C10-N1	5.02	1.39	1.33
3	B	502	FAD	C2A-N3A	4.20	1.38	1.32
2	B	501	ACJ	O4-N1	4.11	1.29	1.22
3	B	502	FAD	C4X-N5	3.67	1.38	1.33
2	B	501	ACJ	C10-C11	3.26	1.50	1.47
3	B	502	FAD	C1'-N10	2.90	1.51	1.48
3	B	502	FAD	C4-N3	2.82	1.38	1.33
3	B	502	FAD	C2A-N1A	2.55	1.38	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	FAD	C4-N3-C2	7.07	121.11	115.14
3	B	502	FAD	N3A-C2A-N1A	-6.00	119.30	128.68
3	B	502	FAD	C5X-C9A-N10	4.02	120.63	117.72
3	B	502	FAD	C4X-N5-C5X	3.89	120.66	116.77
3	B	502	FAD	C4X-C4-N3	-3.43	118.73	123.43
2	B	501	ACJ	F3-C1-C2	-2.51	107.41	112.93
3	B	502	FAD	C8M-C8-C9	-2.32	114.80	120.34
4	B	504	GOL	O3-C3-C2	2.25	120.98	110.20

There are no chirality outliers.

All (5) torsion outliers are listed below:

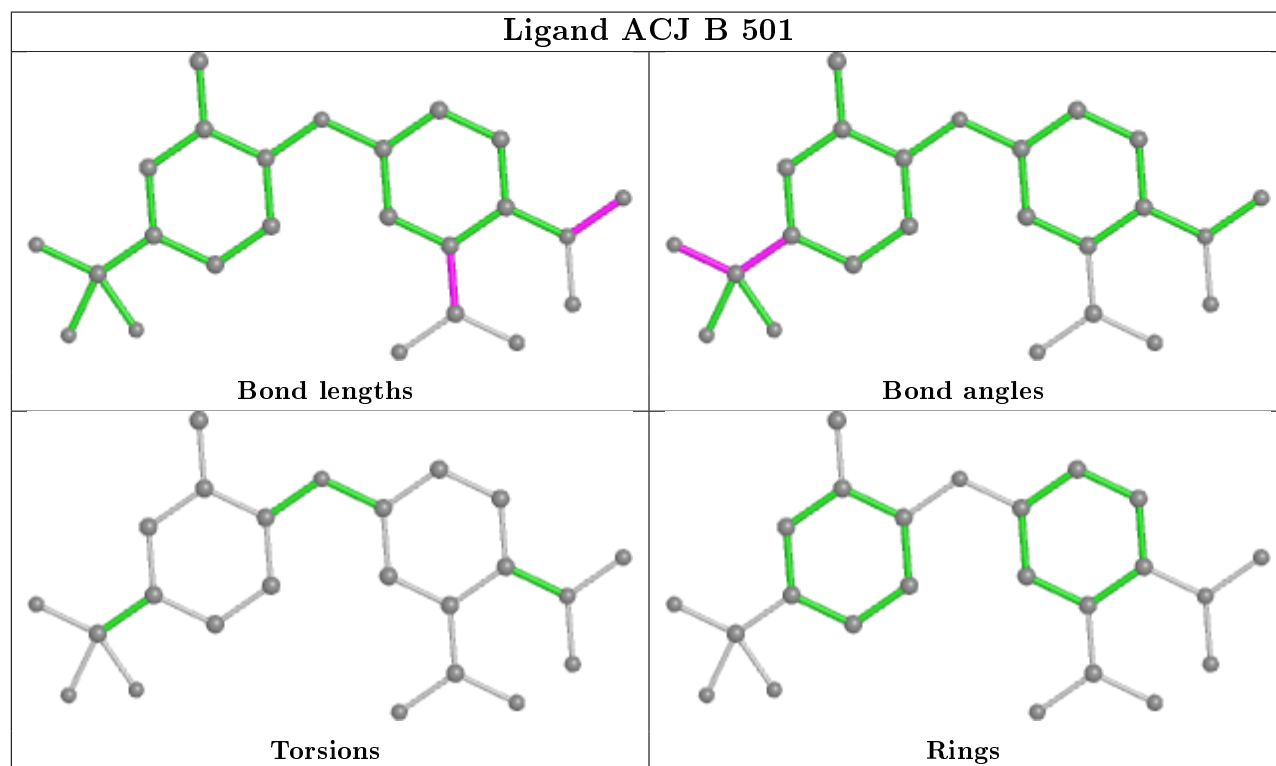
Mol	Chain	Res	Type	Atoms
4	B	503	GOL	O1-C1-C2-C3
3	B	502	FAD	N10-C1'-C2'-O2'
4	B	504	GOL	O2-C2-C3-O3
4	B	503	GOL	O2-C2-C3-O3
3	B	502	FAD	O4B-C4B-C5B-O5B

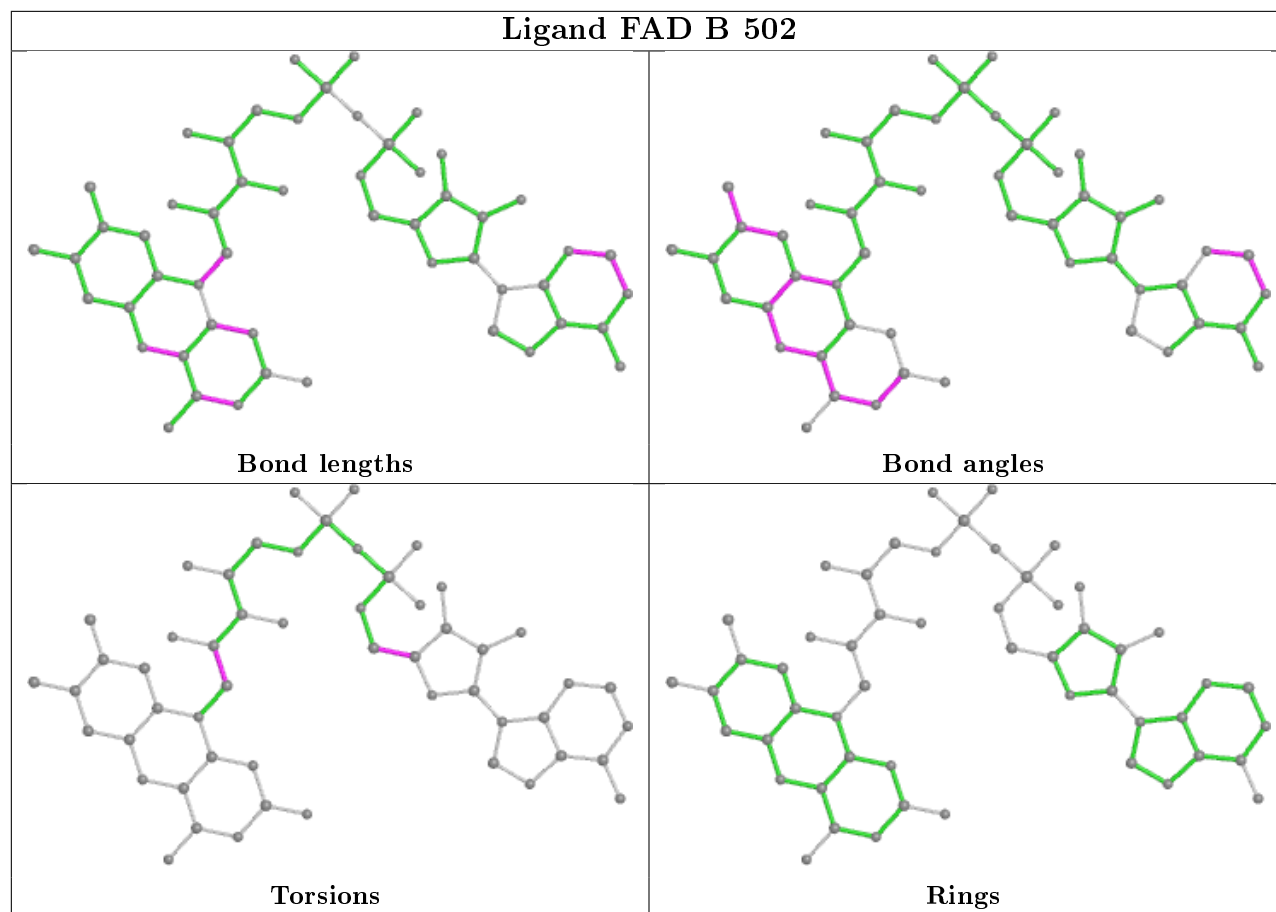
There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	GOL	3	0
2	B	501	ACJ	1	0
4	B	504	GOL	1	0
3	B	502	FAD	5	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, 95th 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 ²)	Q<0.9
1	B	464/483 (96%)	-0.10	24 (5%)	27 21	10, 24, 65, 92	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	202	LEU	6.4
1	B	204	GLY	5.6
1	B	2	GLY	5.5
1	B	201	LEU	5.2
1	B	128	TRP	5.1
1	B	112	LEU	4.6
1	B	95	GLN	4.1
1	B	127	PHE	3.7
1	B	110	THR	3.3
1	B	265	GLU	3.2
1	B	118	PRO	3.2
1	B	111	GLY	2.9
1	B	199	LEU	2.8
1	B	203	LEU	2.7
1	B	210	GLN	2.7
1	B	94	ALA	2.6
1	B	381	GLY	2.6
1	B	135	THR	2.5
1	B	264	ALA	2.5
1	B	91	HIS	2.5
1	B	297	ALA	2.2
1	B	117	ARG	2.1
1	B	211	PRO	2.1
1	B	132	ARG	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 monosaccharides in this entry.

6.4 Ligands [i](#)

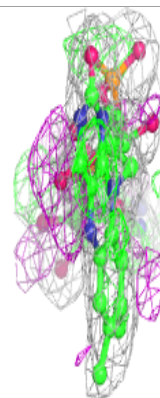
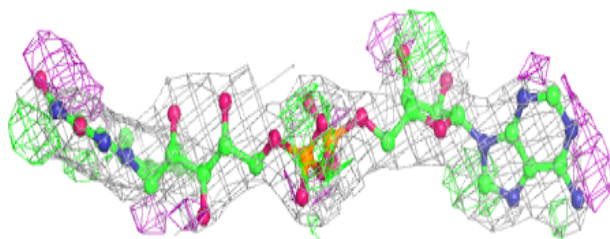
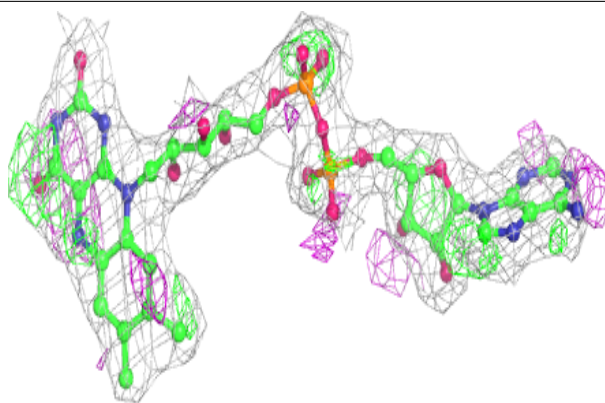
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	B	503	6/6	0.79	0.50	45,47,52,52	0
4	GOL	B	504	6/6	0.82	0.19	33,36,41,49	0
3	FAD	B	502	53/53	0.92	0.22	15,20,27,34	0
2	ACJ	B	501	24/24	0.97	0.14	14,20,39,40	0

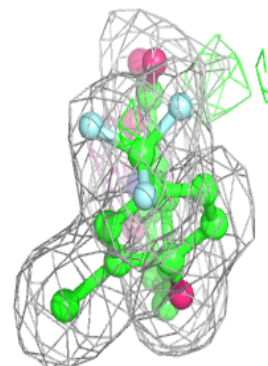
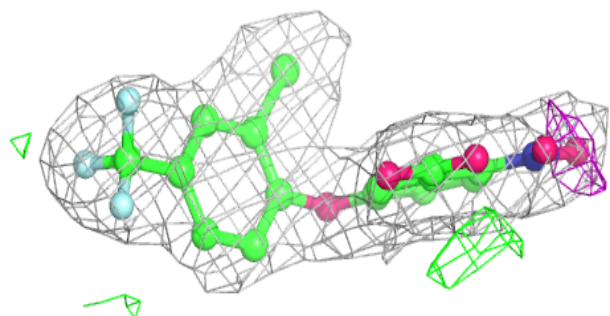
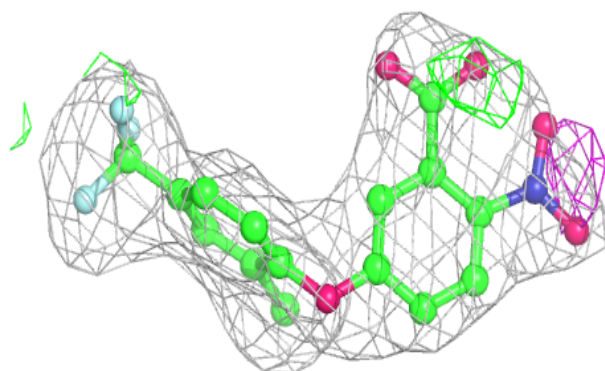
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FAD B 502:

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

**Electron density around ACJ 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.