

wwPDB X-ray Structure Validation Summary Report (i)

Nov 22, 2023 – 11:04 PM JST

PDB ID	:	7XRN
Title	:	Ethanolamine ammonia-lyase complexed with AdoMeCbl in the presence of
		substrate
Authors	:	Shibata, N.; Toraya, T.
Deposited on	:	2022-05-10
Resolution	:	2.07 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

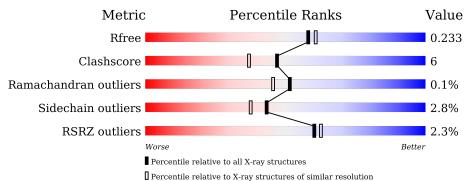
MolProbity Mogul Xtriage (Phenix) EDS	:	4.02b-467 1.8.5 (274361), CSD as541be (2020) 1.13 2.36
buster-report Percentile statistics Refmac	: : :	1.1.7 (2018) 20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

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 2.07 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	2684(2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 >=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	А	453	89%	11%
1	С	453	88%	12%
2	В	263	78%	17% •
2	D	263	6%	19% ••



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 11835 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 Ethanolamine ammonia-lyase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	453	Total 3475	C 2177	1,	O 681	S 22	0	2	0
1	С	453	Total 3467	C 2172	1,	O 680	S 22	0	1	0

• Molecule 2 is a protein called Ethanolamine ammonia-lyase small subunit.

Mol	Chain	Residues		At	oms		ZeroOcc	AltConf	Trace	
0	D	252	Total	С	Ν	0	S	0	2	0
	D		1930	1205	351	364	10	0		
0	р	252	Total	С	Ν	0	S	0	0	0
	2 D	252	1916	1197	347	362	10	0	U	

There are 22 discrepancies between the modelled and reference sequences:

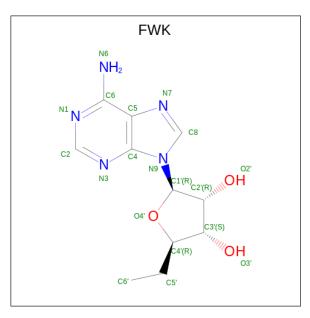
Chain	Residue	Modelled	Actual	Comment	Reference
В	33	MET	-	initiating methionine	UNP P19636
В	34	ASP	-	expression tag	UNP P19636
В	35	GLN	-	expression tag	UNP P19636
В	36	SER	-	expression tag	UNP P19636
В	37	SER	-	expression tag	UNP P19636
В	38	HIS	-	expression tag	UNP P19636
В	39	HIS	-	expression tag	UNP P19636
В	40	HIS	-	expression tag	UNP P19636
В	41	HIS	-	expression tag	UNP P19636
В	42	HIS	-	expression tag	UNP P19636
В	43	HIS	-	expression tag	UNP P19636
D	33	MET	-	initiating methionine	UNP P19636
D	34	ASP	-	expression tag	UNP P19636
D	35	GLN	-	expression tag	UNP P19636
D	36	SER	-	expression tag	UNP P19636
D	37	SER	-	expression tag	UNP P19636



Chain	Residue	Modelled	Actual	Comment	Reference
D	38	HIS	-	expression tag	UNP P19636
D	39	HIS	-	expression tag	UNP P19636
D	40	HIS	-	expression tag	UNP P19636
D	41	HIS	-	expression tag	UNP P19636
D	42	HIS	-	expression tag	UNP P19636
D	43	HIS	-	expression tag	UNP P19636

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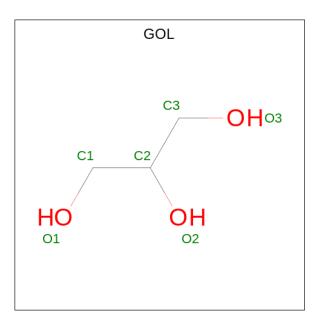
• Molecule 3 is (2 {R},3 {R},4 {S},5 {R})-2-(6-aminopurin-9-yl)-5-ethyl-oxolane-3,4-diol (three-letter code: FWK) (formula: $C_{11}H_{15}N_5O_3$).



M	ol	Chain	Residues	Atoms				ZeroOcc	AltConf
3		А	1	Total 36				0	1
3		С	1	Total 18	C	N	0	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

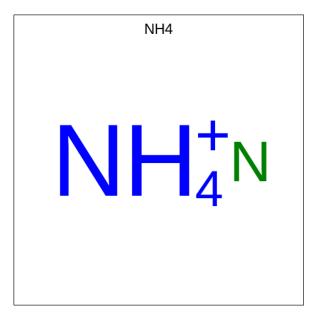




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
4	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

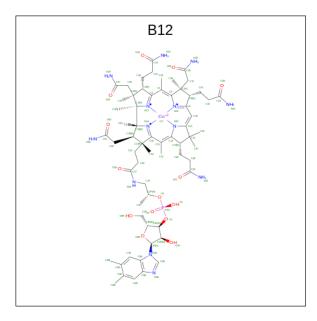
• Molecule 5 is AMMONIUM ION (three-letter code: NH4) (formula: H_4N).





Γ	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	5	А	1	Total N 1 1	0	0
	5	С	1	Total N 1 1	0	0

• Molecule 6 is COBALAMIN (three-letter code: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf		
6	В	Р	1	Total	С	Co	Ν	Ο	Р	0	1
0		L	95	64	1	14	15	1	0	1	
6	Л	1	Total	С	Co	Ν	Ο	Р	0	0	
		1	91	62	1	13	14	1	0	0	



• Molecule 7 is water.

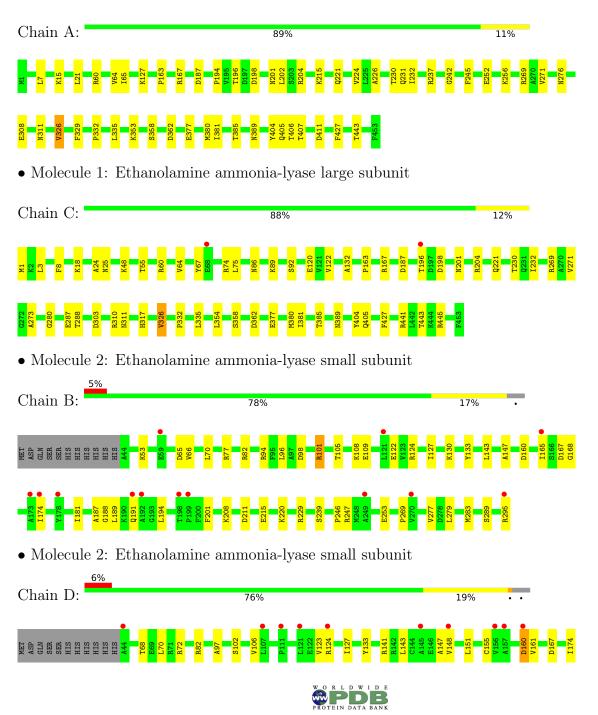
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	294	Total O 294 294	0	0
7	В	101	Total O 101 101	0	0
7	С	283	Total O 283 283	0	0
7	D	91	Total O 91 91	0	0



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: Ethanolamine ammonia-lyase large subunit







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants	242.38Å 242.38Å 76.59Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.16 - 2.07	Depositor
Resolution (A)	48.16 - 2.07	EDS
% Data completeness	99.9 (48.16-2.07)	Depositor
(in resolution range)	98.6(48.16-2.07)	EDS
R _{merge}	0.07	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.70 (at 2.07 Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
P. P.	0.214 , 0.241	Depositor
R, R_{free}	0.216 , 0.233	DCC
R_{free} test set	7806 reflections (5.00%)	wwPDB-VP
Wilson B-factor $(Å^2)$	27.4	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36 , 33.8	EDS
L-test for twinning ²	$< L > = 0.36, < L^2 > = 0.18$	Xtriage
Estimated twinning fraction	0.110 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11835	wwPDB-VP
Average B, all atoms $(Å^2)$	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.13% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: B12, FWK, GOL, NH4

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	Bond lengths		angles
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.24	0/3535	0.47	0/4787
1	С	0.24	0/3524	0.46	0/4772
2	В	0.24	0/1960	0.54	0/2655
2	D	0.24	0/1943	0.51	0/2633
All	All	0.24	0/10962	0.48	0/14847

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	А	3475	0	3433	31	0
1	С	3467	0	3424	29	0
2	В	1930	0	1990	27	0
2	D	1916	0	1973	36	0
3	А	36	0	0	2	0
3	С	18	0	0	1	0
4	А	12	0	16	0	0
4	В	6	0	8	0	0
4	С	18	0	24	2	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	А	1	0	0	0	0
5	С	1	0	0	0	0
6	В	95	0	8	3	0
6	D	91	0	88	9	0
7	А	294	0	0	3	0
7	В	101	0	0	2	0
7	С	283	0	0	6	0
7	D	91	0	0	1	0
All	All	11835	0	10964	131	0

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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 6.

The worst 5 of 131 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)
2:B:160:ASP:HB2	2:B:194:LEU:HD13	1.58	0.85
2:D:180:GLU:HG2	2:D:270:VAL:HG23	1.73	0.69
1:A:237:ARG:NH1	7:A:601:HOH:O	2.26	0.68
1:A:201:ASN:OD1	1:A:204:ARG:NH2	2.27	0.66
2:D:160:ASP:HB2	2:D:194:LEU:HD12	1.80	0.63

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	Perce	ntiles
1	А	453/453~(100%)	432~(95%)	20~(4%)	1 (0%)	47	39
1	С	452/453~(100%)	428 (95%)	23~(5%)	1 (0%)	47	39
2	В	252/263~(96%)	243~(96%)	9~(4%)	0	100	100



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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
2	D	250/263~(95%)	245~(98%)	5(2%)	0	100	100
All	All	1407/1432~(98%)	1348 (96%)	57~(4%)	2~(0%)	51	45

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	163	PRO
1	С	163	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	372/370~(100%)	364~(98%)	8 (2%)	52 46
1	С	371/370~(100%)	363~(98%)	8 (2%)	52 46
2	В	208/217~(96%)	202~(97%)	6 (3%)	42 36
2	D	206/217~(95%)	196~(95%)	10 (5%)	25 17
All	All	1157/1174~(99%)	1125 (97%)	32 (3%)	43 37

 $5~{\rm of}~32$ residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
2	D	194	LEU
2	D	229	ARG
2	В	239	SER
2	В	229	ARG
2	D	236	GLU

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such side chains are listed below:

Mol	Chain	Res	Type
1	С	217	ASN
2	D	60	ASN



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Mol	Chain	Res	Type
2	D	261	ASN
2	D	158	ASN
2	D	191	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 2 are modelled with single atom - leaving 12 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	Bo	nd lengt	ths	Bond angles		
MOI	Type	Ullalli	nes	LIIIK	Counts	ounts $ RMSZ \# Z > 2$		Counts	RMSZ	# Z > 2
6	B12	В	601[A]	-	90,101,101	1.32	8 (8%)	137,166,166	1.21	18 (13%)
3	FWK	А	501[A]	-	17,20,21	1.13	1 (5%)	15,30,31	1.99	4 (26%)
3	FWK	С	501	-	17,20,21	1.12	1 (5%)	15,30,31	1.93	4 (26%)
4	GOL	А	503	-	$5,\!5,\!5$	0.89	0	5,5,5	0.98	0
6	B12	В	601[B]	-	90,101,101	1.31	8 (8%)	137,166,166	1.21	18 (13%)
3	FWK	А	501[B]	-	17,20,21	1.07	1 (5%)	15,30,31	1.70	4 (26%)
4	GOL	С	502	-	$5,\!5,\!5$	0.91	0	5,5,5	1.01	0
4	GOL	С	504	-	$5,\!5,\!5$	0.93	0	5,5,5	0.99	0



Mol	Mol Type Chain Res		Res	Link	Bond lengths			Bond angles		
INIOI	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	B12	D	601	-	90,101,101	1.32	10 (11%)	137,166,166	1.19	<mark>16 (11%)</mark>
4	GOL	А	502	-	5,5,5	0.91	0	$5,\!5,\!5$	0.98	0
4	GOL	В	602	-	$5,\!5,\!5$	0.90	0	$5,\!5,\!5$	1.01	0
4	GOL	С	503	-	$5,\!5,\!5$	0.96	0	$5,\!5,\!5$	1.00	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
6	B12	В	601[A]	-	-	14/52/223/223	0/3/11/11
3	FWK	А	501[A]	-	-	0/0/20/22	0/3/3/3
3	FWK	С	501	-	-	0/0/20/22	0/3/3/3
4	GOL	А	503	-	-	2/4/4/4	-
6	B12	В	601[B]	-	-	14/52/223/223	0/3/11/11
3	FWK	А	501[B]	-	-	0/0/20/22	0/3/3/3
4	GOL	С	502	-	-	2/4/4/4	-
4	GOL	С	504	-	-	2/4/4/4	-
6	B12	D	601	-	-	14/52/223/223	0/3/11/11
4	GOL	А	502	-	-	2/4/4/4	-
4	GOL	В	602	-	-	0/4/4/4	-
4	GOL	С	503	_	_	4/4/4/4	_

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
6	В	601[A]	B12	C14-N23	-5.23	1.28	1.35
6	В	601[B]	B12	C14-N23	-5.23	1.28	1.35
6	D	601	B12	C14-N23	-5.15	1.28	1.35
6	В	601[A]	B12	C8B-C9B	4.18	1.49	1.40
6	В	601[B]	B12	C8B-C9B	4.18	1.49	1.40

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	501[A]	FWK	C5'-C4'-C3'	-5.06	110.39	115.70
3	С	501	FWK	C5'-C4'-C3'	-4.47	111.00	115.70
6	В	601[A]	B12	C17-C16-C15	3.53	131.82	126.26
6	В	601[B]	B12	C17-C16-C15	3.53	131.82	126.26



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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
6	D	601	B12	C17-C16-C15	3.52	131.80	126.26

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	503	GOL	C1-C2-C3-O3
4	А	503	GOL	O2-C2-C3-O3
4	С	502	GOL	O1-C1-C2-C3
4	С	504	GOL	C1-C2-C3-O3
4	С	504	GOL	O2-C2-C3-O3

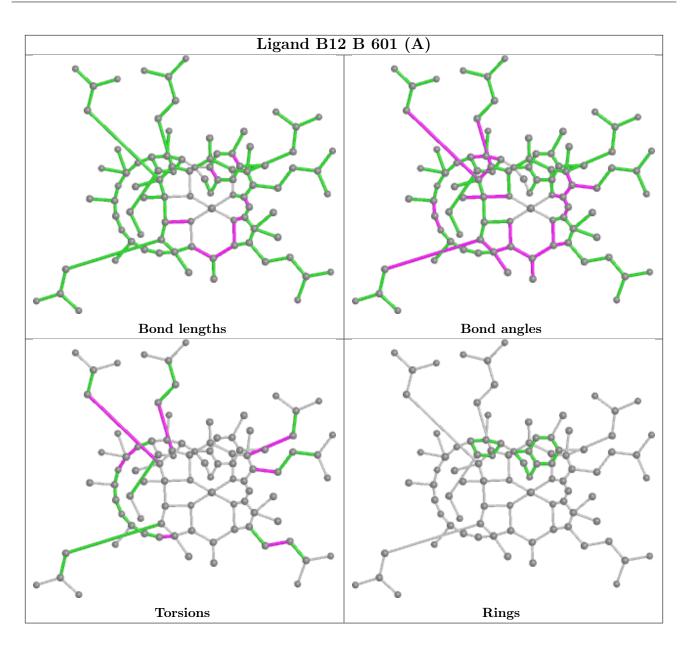
There are no ring outliers.

7 monomers are involved in 17 short contacts:

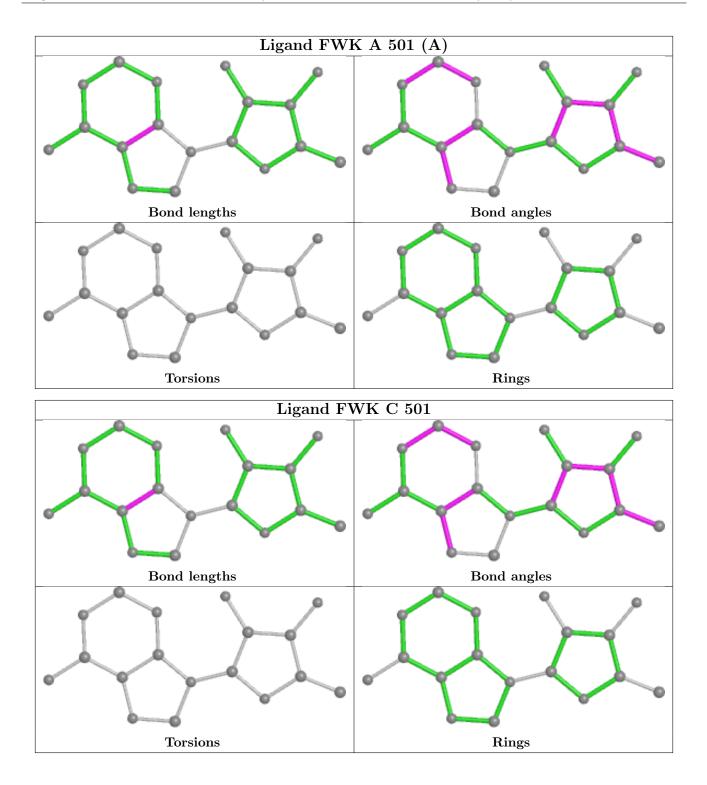
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	В	601[A]	B12	1	0
3	А	501[A]	FWK	1	0
3	С	501	FWK	1	0
6	В	601[B]	B12	2	0
3	А	501[B]	FWK	1	0
6	D	601	B12	9	0
4	С	503	GOL	2	0

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.

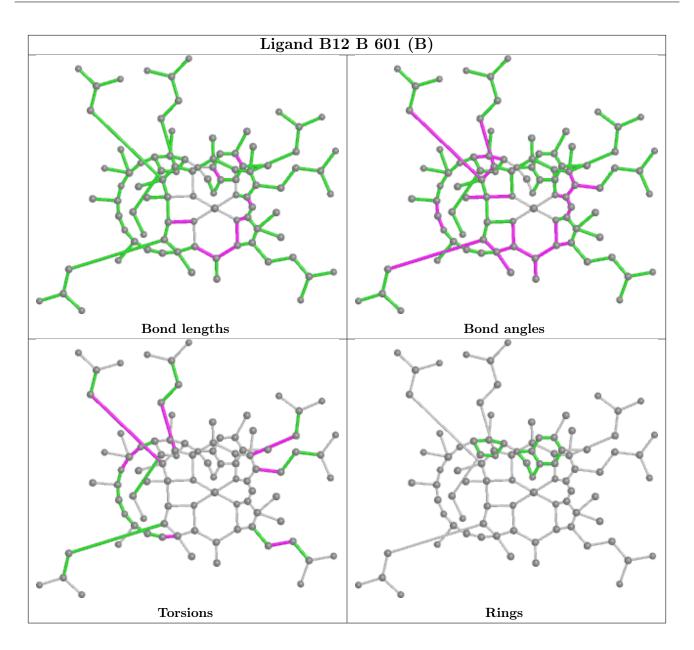






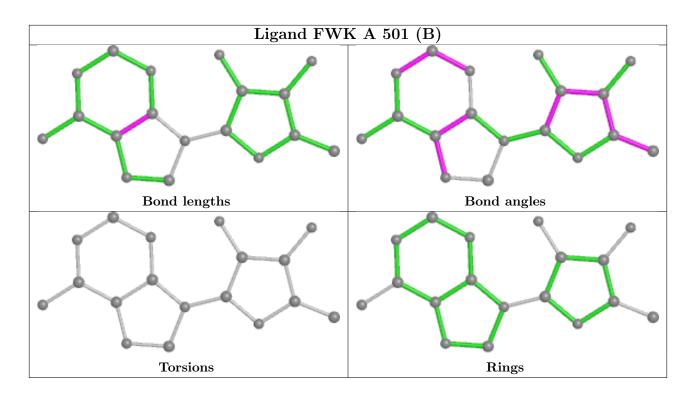






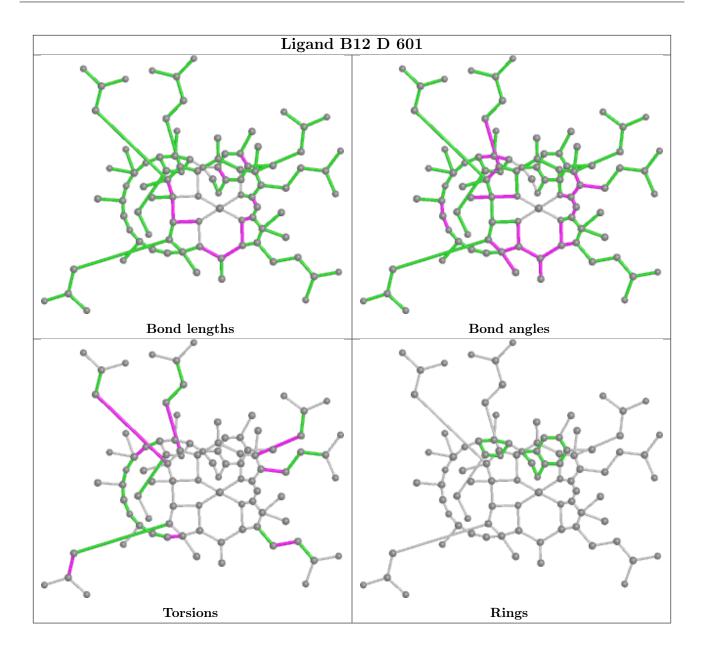












5.7 Other polymers (i)

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	Analysed	$\langle RSRZ \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	А	453/453~(100%)	-0.06	0 100 100	17, 27, 39, 51	0
1	С	453/453~(100%)	-0.07	2 (0%) 92 93	16, 28, 44, 67	0
2	В	252/263~(95%)	0.42	13 (5%) 27 27	26, 45, 59, 81	0
2	D	252/263~(95%)	0.50	17 (6%) 17 18	20, 50, 72, 96	0
All	All	1410/1432~(98%)	0.12	32 (2%) 60 63	16, 33, 60, 96	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
2	В	199	PRO	4.5
2	D	157	ALA	4.4
2	D	111	PRO	4.1
2	D	192	ALA	4.0
2	D	295	ARG	4.0

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.

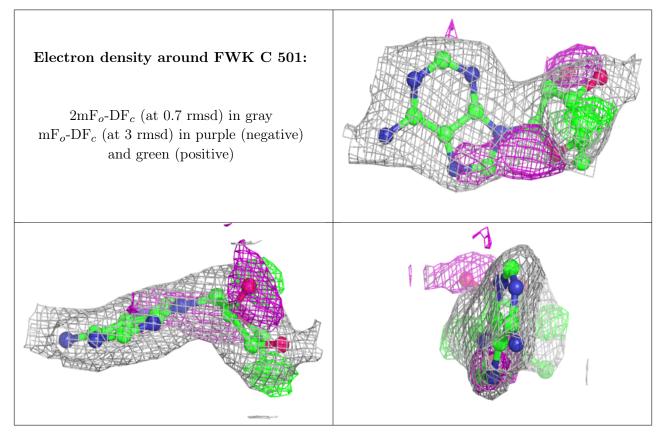
6.4 Ligands (i)

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, 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.

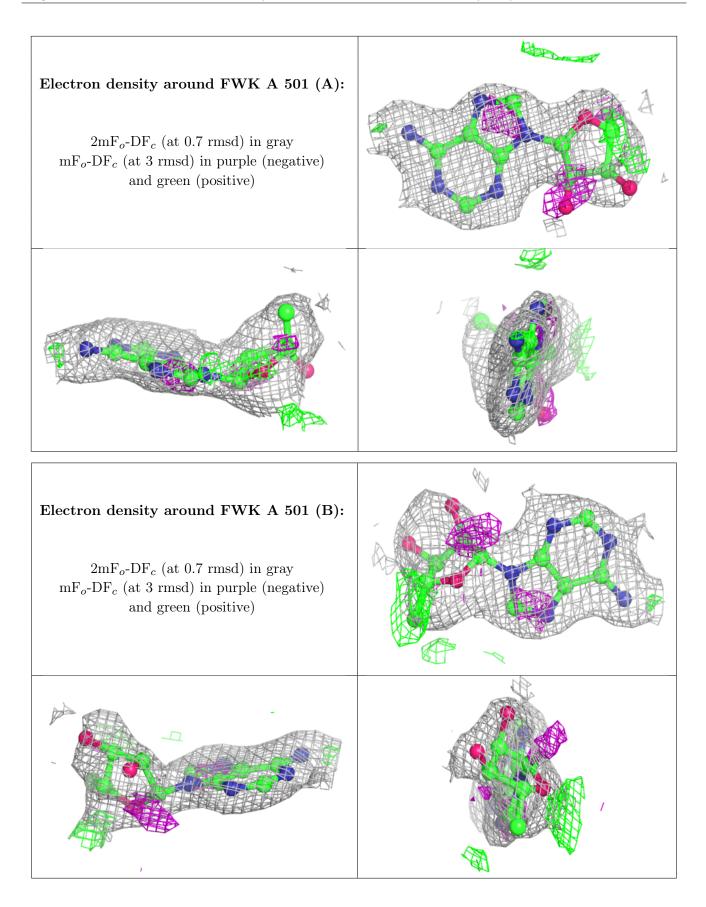


Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	А	502	6/6	0.70	0.22	38,45,48,56	0
3	FWK	С	501	18/19	0.79	0.22	34,35,42,49	0
4	GOL	А	503	6/6	0.79	0.24	33,34,41,49	0
4	GOL	В	602	6/6	0.86	0.17	35,40,44,45	0
3	FWK	А	501[A]	18/19	0.89	0.25	28,31,32,33	18
3	FWK	А	501[B]	18/19	0.89	0.25	28,31,32,34	18
4	GOL	С	502	6/6	0.89	0.17	30,33,37,38	0
4	GOL	С	503	6/6	0.93	0.13	23,29,38,40	0
4	GOL	С	504	6/6	0.93	0.16	23,29,31,31	0
5	NH4	С	505	1/1	0.95	0.21	26,26,26,26	0
6	B12	В	601[A]	91/91	0.95	0.14	$28,\!33,\!40,\!45$	4
6	B12	В	601[B]	91/91	0.95	0.14	28,33,40,45	4
6	B12	D	601	91/91	0.95	0.13	33,35,41,45	0
5	NH4	А	504	1/1	0.97	0.11	21,21,21,21	0

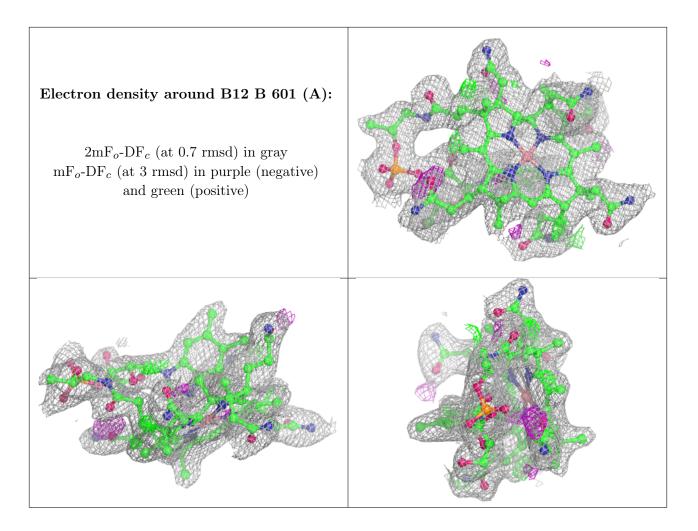
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



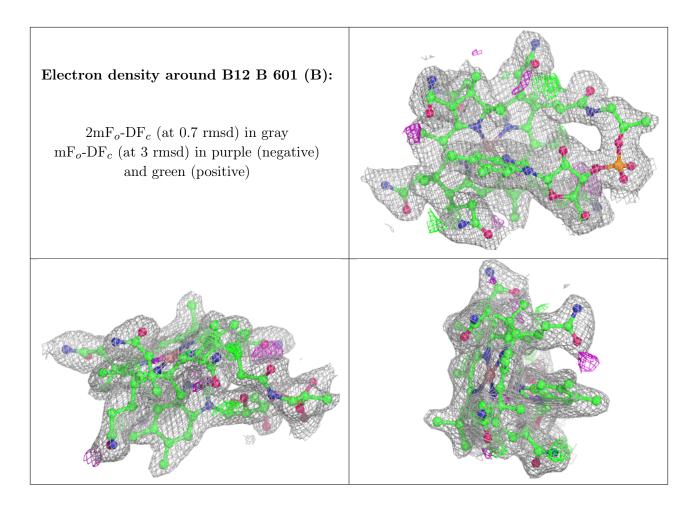




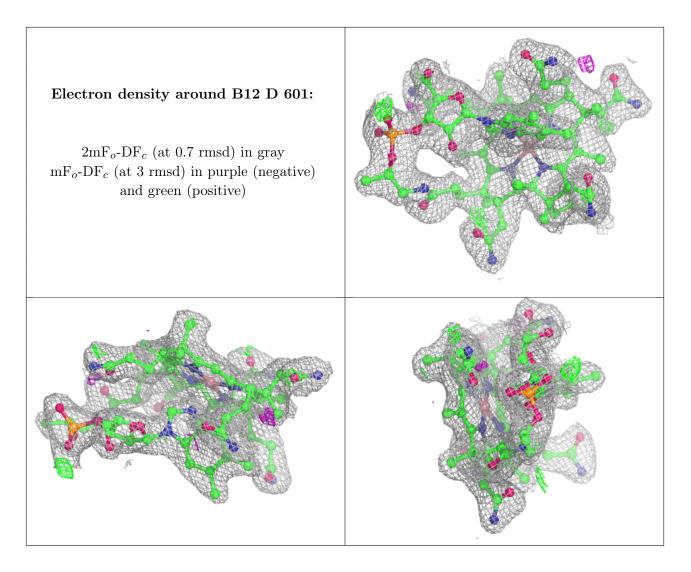












6.5 Other polymers (i)

There are no such residues in this entry.

