Full wwPDB X-ray Structure Validation Report (i)

Oct 27, 2026 – 09:12 pm GMT

PDB ID	:	30FO / pdb_000030fo
Title	:	Putative Polyurethane Degrading Amidase in PMS Bound State
Authors	:	Bicer, D.; Otzen, D.E.; Morth, J.P.; Thirup, S.S.
Deposited on	:	2026-04-23
Resolution	:	1.80 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 (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 (i)) were used in the production of this report:

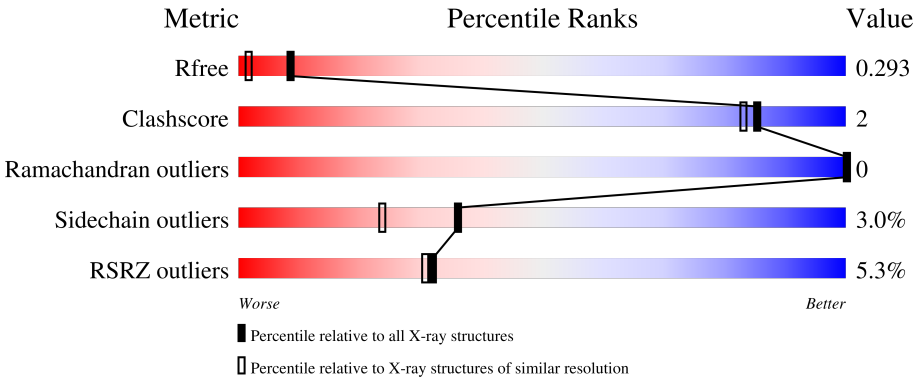
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	A	433	6% 93% 5% ••
1	B	433	5% 91% 6% ••

2 Entry composition

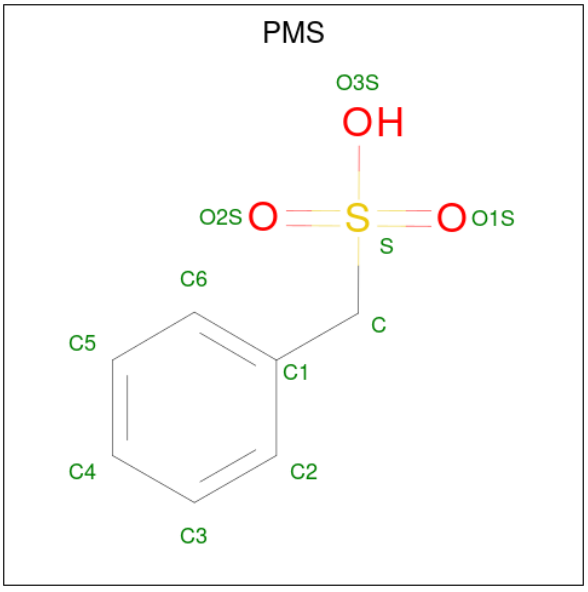
There are 3 unique types of molecules in this entry. The entry contains 6788 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Amidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3152	1974	578	589	11			
1	B	425	Total	C	N	O	S	0	0	0
			3140	1968	576	585	11			

- Molecule 2 is phenylmethanesulfonic acid (CCD ID: PMS) (formula: $C_7H_8O_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			10	7	2	1		
2	B	1	Total	C	O	S	0	0
			10	7	2	1		

- Molecule 3 is water.

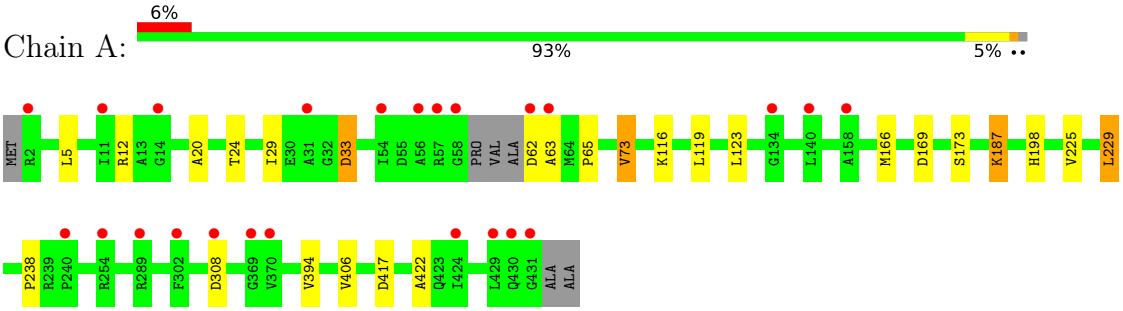
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	234	Total O 234 234	0	0
3	B	242	Total O 242 242	0	0

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.

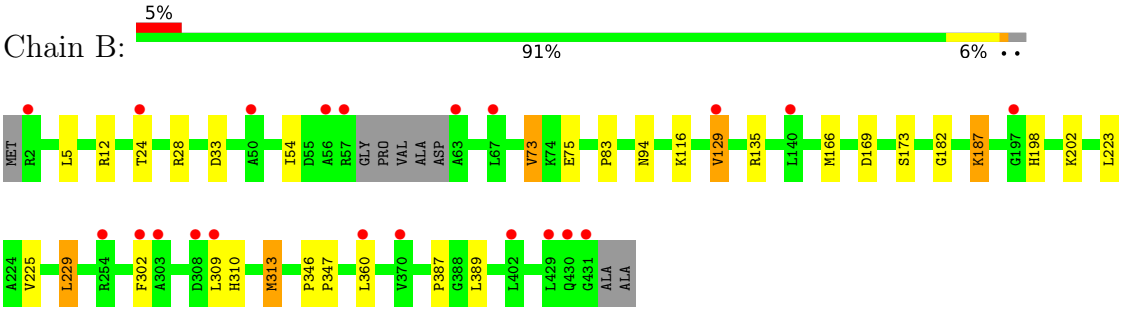
- Molecule 1: Amidase

Chain A:



- Molecule 1: Amidase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	111.52Å 111.52Å 436.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.94 – 1.80 20.94 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (20.94-1.80) 99.8 (20.94-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.13 (at 1.79Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.283 , 0.293 0.283 , 0.293	Depositor DCC
R_{free} test set	7323 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	28.4	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 33.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	6788	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PMS

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	0.29	0/3223	0.52	1/4406 (0.0%)
1	B	0.29	0/3211	0.52	1/4390 (0.0%)
All	All	0.29	0/6434	0.52	2/8796 (0.0%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	229	LEU	CA-CB-CG	6.07	137.55	116.30
1	B	229	LEU	CA-CB-CG	5.76	136.48	116.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	198	HIS	Peptide
1	B	198	HIS	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	3152	0	3124	11	0
1	B	3140	0	3117	16	0
2	A	10	0	7	0	0
2	B	10	0	7	1	0
3	A	234	0	0	0	0
3	B	242	0	0	2	0
All	All	6788	0	6255	27	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 (27) 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:129:VAL:HG22	1:B:135:ARG:HG3	1.75	0.68
1:B:169:ASP:HA	1:B:173:SER:HB2	1.88	0.54
1:A:169:ASP:HA	1:A:173:SER:HB2	1.89	0.54
1:B:73:VAL:O	1:B:116:LYS:HA	2.10	0.51
1:B:73:VAL:HG22	1:B:166:MET:HB3	1.92	0.51
1:A:63:ALA:O	1:A:65:PRO:HD3	2.10	0.51
1:B:94:ASN:OD1	1:B:202:LYS:HE3	2.11	0.50
1:B:310:HIS:O	1:B:313:MET:HG3	2.11	0.50
1:B:24:THR:HG22	1:B:28:ARG:NH1	2.26	0.50
1:B:187:LYS:O	1:B:187:LYS:HE3	2.11	0.50
1:B:387:PRO:HG2	1:B:389:LEU:HG	1.94	0.49
1:A:20:ALA:O	1:A:24:THR:HG23	2.13	0.48
1:B:75:GLU:HA	1:B:116:LYS:HB3	1.96	0.47
1:A:238:PRO:HA	1:A:417:ASP:OD1	2.15	0.47
1:B:302:PHE:CE2	2:B:501:PMS:H5	2.50	0.47
1:A:73:VAL:O	1:A:116:LYS:HA	2.15	0.46
1:A:73:VAL:HG22	1:A:166:MET:HB3	1.98	0.45
1:A:5:LEU:HD21	1:A:225:VAL:HG21	2.01	0.43
1:A:187:LYS:O	1:A:187:LYS:HE3	2.19	0.43
1:B:346:PRO:HA	1:B:347:PRO:HD3	1.92	0.42
1:A:119:LEU:HD22	1:A:123:LEU:HD11	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:83:PRO:HA	1:B:94:ASN:O	2.20	0.42
1:B:5:LEU:HD21	1:B:225:VAL:HG21	2.02	0.42
1:A:394:VAL:HB	1:A:422:ALA:HB1	2.03	0.41
1:B:129:VAL:HG21	3:B:803:HOH:O	2.20	0.41
1:A:29:ILE:O	1:A:33:ASP:HB2	2.21	0.41
1:B:182:GLY:HA2	3:B:689:HOH: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	423/433 (98%)	410 (97%)	13 (3%)	0	100	100
1	B	421/433 (97%)	412 (98%)	9 (2%)	0	100	100
All	All	844/866 (98%)	822 (97%)	22 (3%)	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	313/316 (99%)	305 (97%)	8 (3%)	40	28
1	B	312/316 (99%)	301 (96%)	11 (4%)	32	19

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	625/632 (99%)	606 (97%)	19 (3%)	36 24

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ARG
1	A	33	ASP
1	A	62	ASP
1	A	73	VAL
1	A	187	LYS
1	A	229	LEU
1	A	308	ASP
1	A	406	VAL
1	B	12	ARG
1	B	33	ASP
1	B	54	ILE
1	B	73	VAL
1	B	129	VAL
1	B	187	LYS
1	B	223	LEU
1	B	229	LEU
1	B	309	LEU
1	B	313	MET
1	B	360	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	HIS
1	A	191	ASN
1	A	299	ASN
1	B	91	HIS
1	B	310	HIS

5.3.3 RNA

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)

2 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	$\#\|Z\| > 2$
2	PMS	B	501	1	7,10,11	0.41	0	11,12,15	1.32	2 (18%)
2	PMS	A	501	1	7,10,11	0.37	0	11,12,15	1.31	1 (9%)

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
2	PMS	B	501	1	-	0/4/4/5	0/1/1/1
2	PMS	A	501	1	-	0/4/4/5	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	PMS	O2S-S-C	3.94	111.95	105.56
2	B	501	PMS	O2S-S-C	3.63	111.45	105.56
2	B	501	PMS	O1S-S-C	2.12	109.00	105.56

There are no chirality outliers.

There are no torsion outliers.

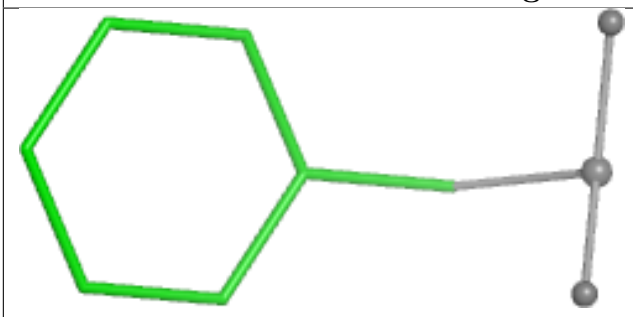
There are no ring outliers.

1 monomer is involved in 1 short contact:

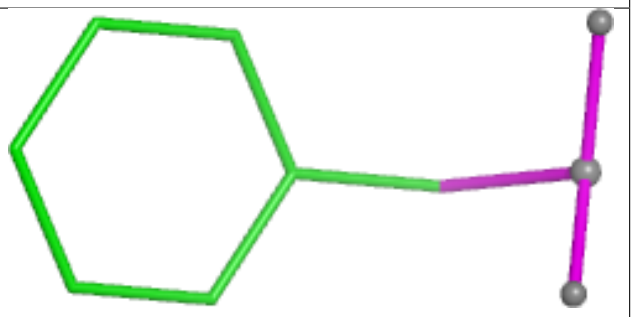
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	PMS	1	0

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 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.

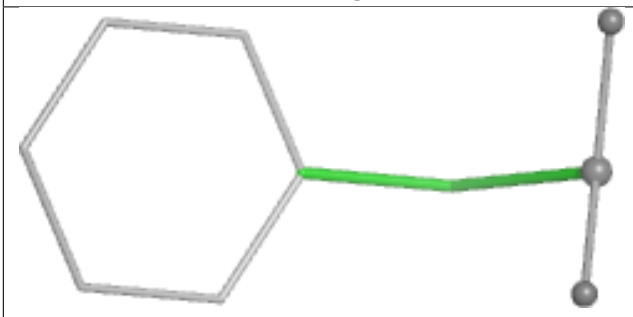
Ligand PMS B 501



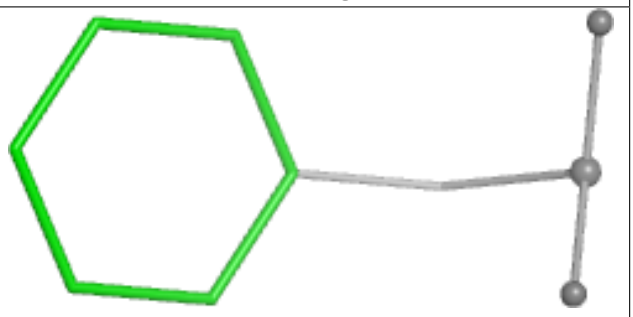
Bond lengths



Bond angles

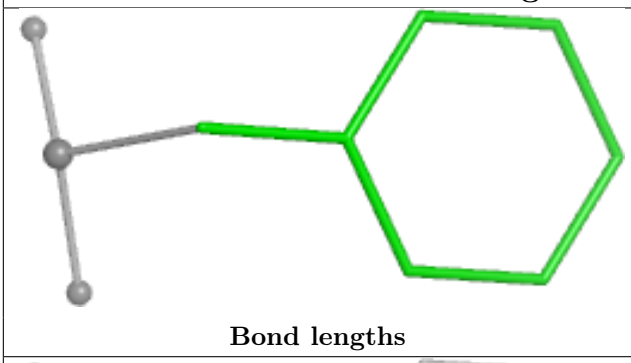


Torsions

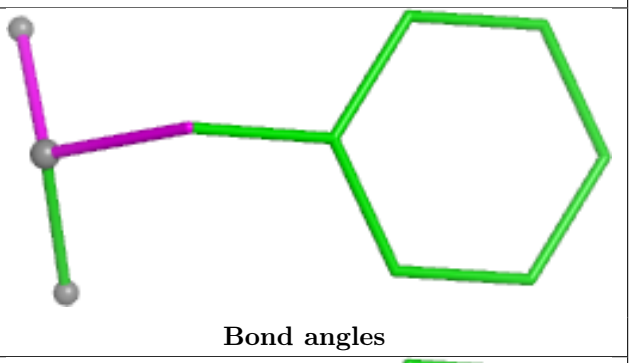


Rings

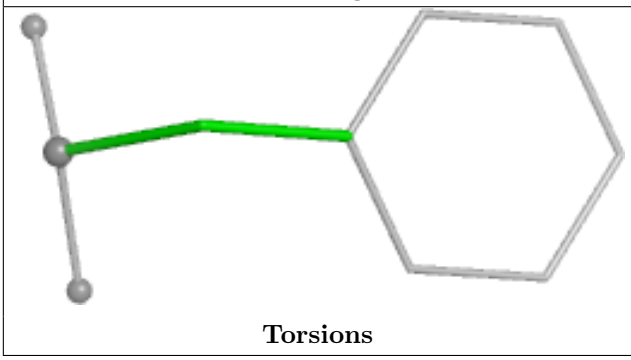
Ligand PMS A 501



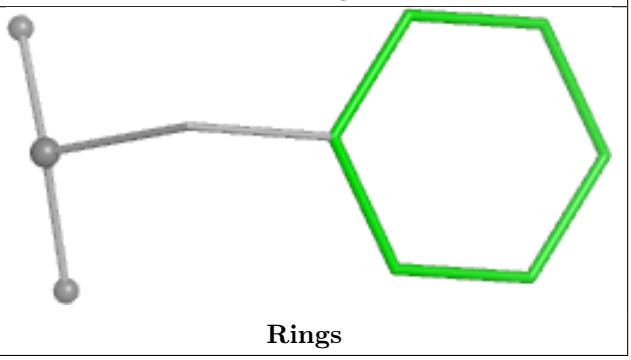
Bond lengths



Bond angles



Torsions



Rings

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^{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	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	427/433 (98%)	0.58	24 (5%)	30	29	19, 29, 45, 90	1 (0%)
1	B	425/433 (98%)	0.60	21 (4%)	35	33	20, 29, 46, 90	1 (0%)
All	All	852/866 (98%)	0.59	45 (5%)	32	31	19, 29, 46, 90	2 (0%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	431	GLY	7.8
1	B	431	GLY	6.7
1	A	62	ASP	5.5
1	A	58	GLY	5.1
1	B	430	GLN	4.3
1	A	430	GLN	4.3
1	B	56	ALA	4.1
1	A	63	ALA	4.1
1	B	63	ALA	4.0
1	A	56	ALA	3.8
1	A	240	PRO	3.7
1	B	429	LEU	3.5
1	A	429	LEU	3.3
1	A	57	ARG	3.0
1	B	67	LEU	2.9
1	A	302	PHE	2.8
1	A	369	GLY	2.8
1	B	57	ARG	2.7
1	B	24	THR	2.6
1	A	308	ASP	2.6
1	B	370	VAL	2.6
1	A	424	ILE	2.4
1	A	289	ARG	2.4
1	B	308	ASP	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	50	ALA	2.4
1	A	14	GLY	2.4
1	B	360	LEU	2.3
1	A	370	VAL	2.3
1	A	2	ARG	2.2
1	B	140	LEU	2.2
1	B	309	LEU	2.2
1	B	303	ALA	2.2
1	B	402	LEU	2.2
1	A	134	GLY	2.2
1	B	254	ARG	2.2
1	B	129	VAL	2.1
1	A	140	LEU	2.1
1	A	254	ARG	2.1
1	B	2	ARG	2.1
1	A	158	ALA	2.1
1	A	11	ILE	2.1
1	A	31	ALA	2.1
1	B	197	GLY	2.0
1	A	54	ILE	2.0
1	B	302	PHE	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)

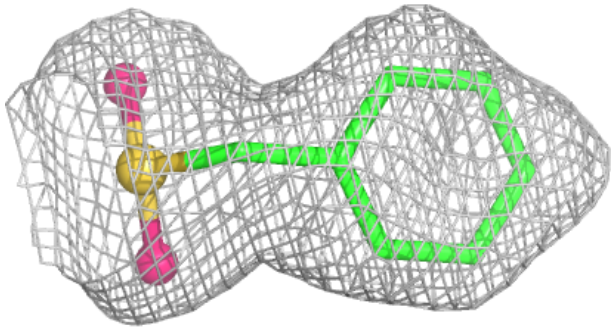
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

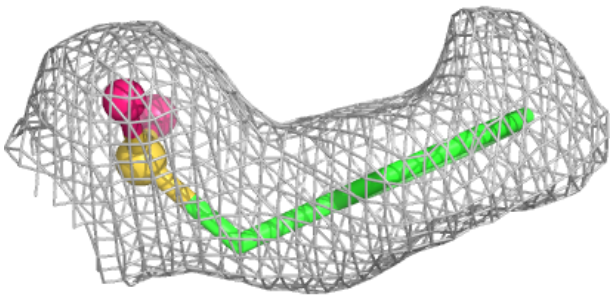
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PMS	A	501	10/11	0.95	0.12	30,41,44,49	10
2	PMS	B	501	10/11	0.97	0.10	29,37,43,45	10

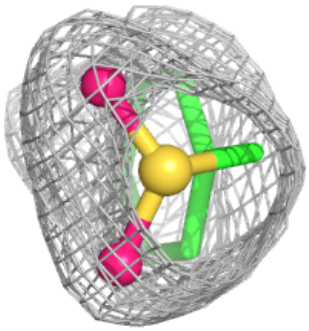
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PMS 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)

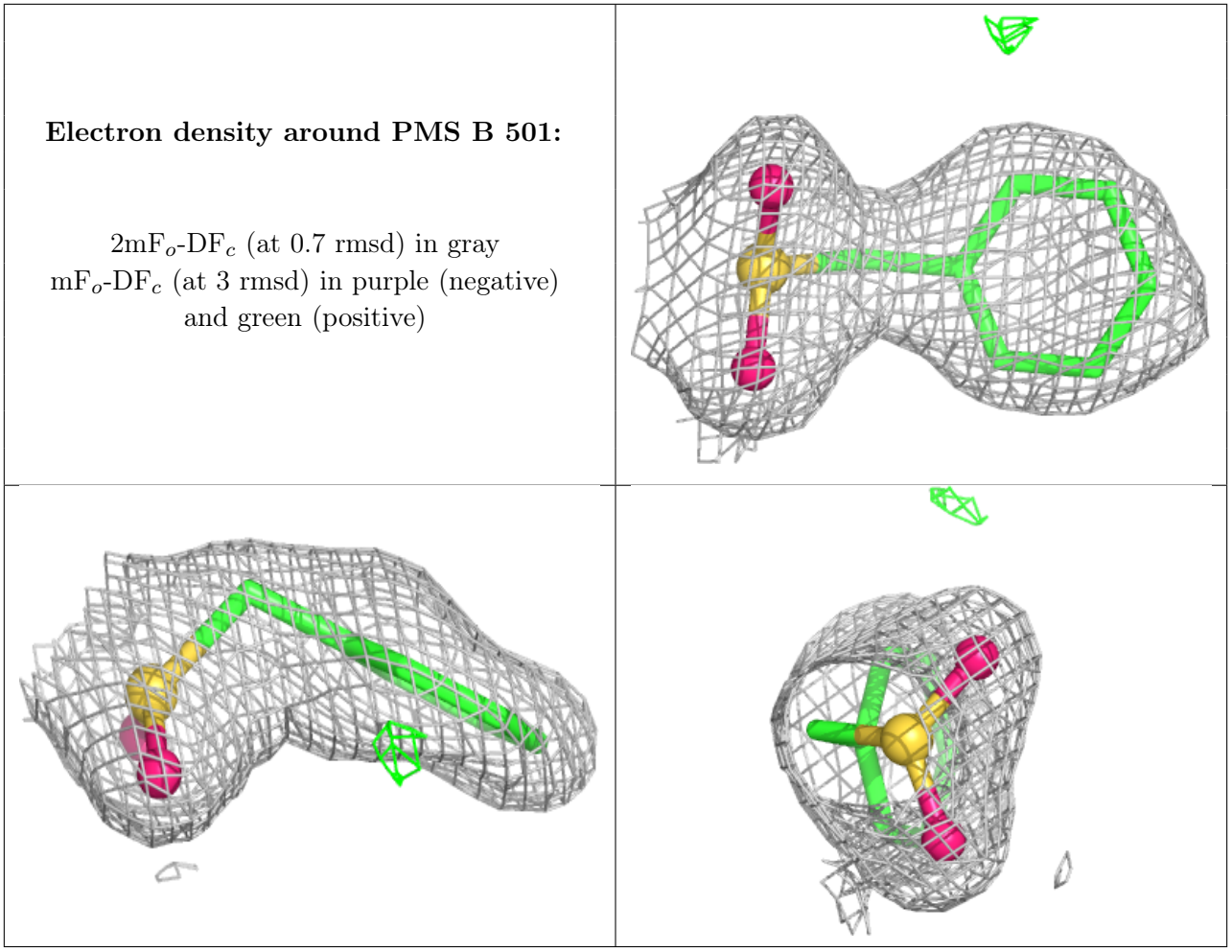






Electron density around PMS B 501:

$2mF_o$-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

There are no such residues in this entry.