

wwPDB X-ray Structure Validation Summary Report (i)

Jan 6, 2022 – 12:15 pm GMT

PDB ID	:	7B8Z
Title	:	Notum-Fragment 277
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Deposited on		
Resolution	:	1.73 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:

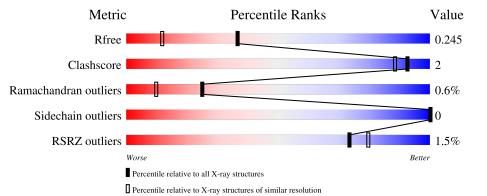
MolDrobity		4 021 467
MolProbity		
Mogul	:	1.8.4, CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.24
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

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 1.73 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	3764(1.76-1.72)
Clashscore	141614	3923 (1.76-1.72)
Ramachandran outliers	138981	3878 (1.76-1.72)
Sidechain outliers	138945	3878 (1.76-1.72)
RSRZ outliers	127900	3705 (1.76-1.72)

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	383	% 	•• 11%



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2826 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 Palmitoleoyl-protein carboxylesterase NOTUM.

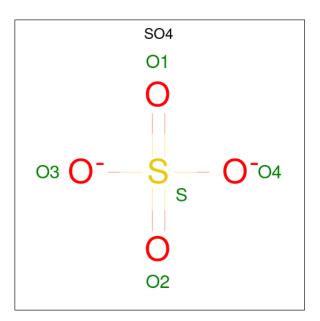
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	342	Total 2680	C 1709	N 466	0 489	S 16	0	4	0

Chain Residue Modelled Actual Comment Reference **UNP Q6P988** А 78 GLU _ cloning artifact THR А 79 cloning artifact UNP Q6P988 -Α GLY cloning artifact **UNP Q6P988** 80 _ А 330 SER CYS engineered mutation UNP Q6P988 А 452GLY UNP Q6P988 _ expression tag А 453THR expression tag UNP Q6P988 _ LYS А 454 expression tag **UNP Q6P988** -А 455HIS _ expression tag UNP Q6P988 HIS А 456expression tag **UNP Q6P988** _ Α HIS **UNP** Q6P988 457expression tag -А 458HIS expression tag UNP Q6P988 _ HIS А 459**UNP Q6P988** expression tag _ А 460 HIS UNP Q6P988 _ expression tag

There are 13 discrepancies between the modelled and reference sequences:

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

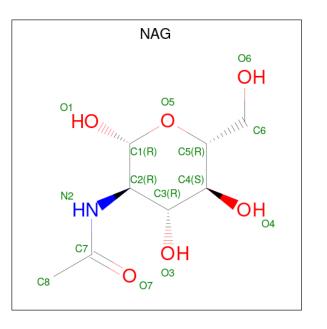




Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
2	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0

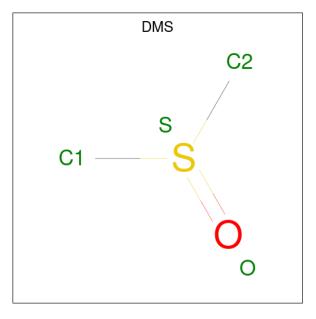
• Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





Mol	Chain	Residues	A	Atoms		ZeroOcc	AltConf	
3	А	1	Total 14	C 8	N 1	O 5	0	0

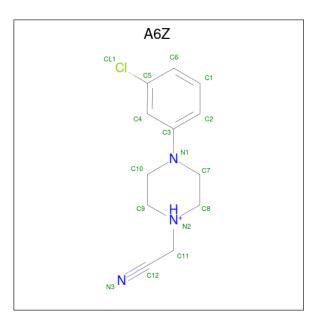
• Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	A	ton	ns		ZeroOcc	AltConf
4	А	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	0 1	${f S}$ 1	0	0

• Molecule 5 is 2-[4-(3-chlorophenyl)piperazin-1-ium-1-yl]ethanenitrile (three-letter code: A6Z) (formula: $C_{12}H_{15}ClN_3$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
E.	Δ	1	Total	С	Cl	Ν	0	0
0	A	1	16	12	1	3	0	0

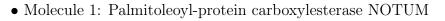
• Molecule 6 is water.

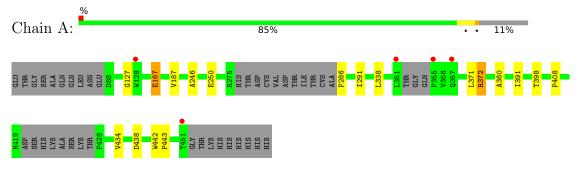
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	77	Total O 77 77	0	0



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.







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	59.46Å 73.60Å 78.76Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.77 - 1.73	Depositor
	53.77 - 1.73	EDS
% Data completeness	98.1 (53.77-1.73)	Depositor
(in resolution range)	98.7(53.77-1.73)	EDS
R _{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.36 (at 1.73 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.227 , 0.243	Depositor
It, Itfree	0.228 , 0.245	DCC
R_{free} test set	1783 reflections $(4.91%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	24.0	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2826	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 5.94% 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: SO4, DMS, A6Z, NAG

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).

Mal	Chain	Boi	nd lengths	Bond angles		
Mol Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.48	1/2756~(0.0%)	0.97	8/3758~(0.2%)	

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	А	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	А	372	ARG	CB-CG	-5.48	1.37	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	А	167	GLU	OE1-CD-OE2	-34.96	81.35	123.30
1	А	167	GLU	CG-CD-OE1	20.82	159.95	118.30
1	А	167	GLU	CG-CD-OE2	-15.38	87.54	118.30
1	А	372	ARG	NE-CZ-NH2	-9.22	115.69	120.30
1	А	372	ARG	CG-CD-NE	-8.00	94.99	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	167	GLU	Sidechain



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	2680	0	2516	8	0
2	А	35	0	0	0	0
3	А	14	0	13	0	0
4	А	4	0	6	1	0
5	А	16	0	0	0	0
6	А	77	0	0	0	0
All	All	2826	0	2535	8	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.

The worst 5 of 8 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:LEU:HA	1:A:371[A]:LEU:HD23	1.83	0.59
1:A:380:ALA:HA	1:A:434:VAL:HG12	1.86	0.58
1:A:187:VAL:O	1:A:187:VAL:HG12	2.13	0.49
1:A:246:ALA:O	1:A:250:GLU:HG3	2.13	0.49
1:A:398:THR:HG22	1:A:408:PRO:HG2	1.94	0.48

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	А	337/383~(88%)	324 (96%)	11 (3%)	2(1%)	25 10	



All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	391	ILE
1	А	127	GLY

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	282/333~(85%)	282 (100%)	0	100 100		

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

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



Mol	Turne	Chain	Res	Link	Bo	ond leng	ths	Bond angles		
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
2	SO4	А	505	-	4,4,4	0.12	0	6,6,6	0.26	0
2	SO4	А	509	-	4,4,4	0.15	0	6,6,6	0.09	0
4	DMS	А	503	-	3,3,3	0.71	0	3,3,3	0.31	0
2	SO4	А	506	-	4,4,4	0.20	0	6,6,6	0.28	0
2	SO4	А	508	-	4,4,4	0.14	0	6,6,6	0.16	0
2	SO4	А	507	-	4,4,4	0.15	0	6,6,6	0.13	0
2	SO4	А	501	-	4,4,4	0.16	0	6,6,6	0.27	0
2	SO4	А	504	-	4,4,4	0.11	0	6,6,6	0.17	0
3	NAG	А	502	1	14,14,15	0.27	0	17,19,21	0.62	0
5	A6Z	А	510	-	17,17,17	2.21	6 (35%)	22,22,22	1.07	1 (4%)

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).

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	NAG	А	502	1	-	0/6/23/26	0/1/1/1
5	A6Z	А	510	-	-	0/6/17/17	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	А	510	A6Z	C11-N2	5.53	1.52	1.46
5	А	510	A6Z	C11-C12	3.53	1.52	1.47
5	А	510	A6Z	C3-N1	3.50	1.48	1.38
5	А	510	A6Z	C10-N1	2.77	1.51	1.46
5	А	510	A6Z	C5-CL1	2.71	1.80	1.74

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	A	510	A6Z	C12-C11-N2	-2.01	111.56	113.98

There are no chirality outliers.

There are no torsion outliers.

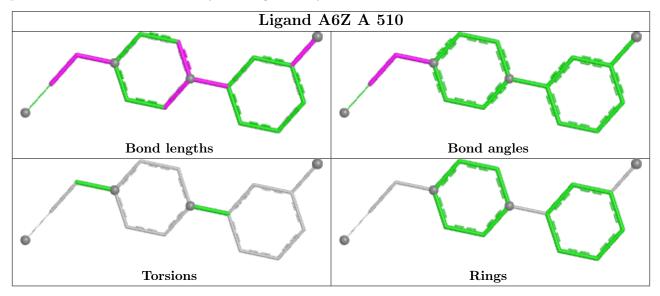
There are no ring outliers.



1	monomer	\mathbf{is}	involved	in	1	short contact:	
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	503	DMS	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.



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	А	1

All chain breaks are listed below:



Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	286:PRO	С	288:THR	N	3.45



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	<RSRZ $>$	#RSRZ>2		$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9
1	А	342/383~(89%)	-0.08	5 (1%) 73 8)	19, 28, 42, 55	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	128	TRP	3.7
1	А	355	PRO	3.5
1	А	451	THR	2.4
1	А	351	LEU	2.2
1	А	357	GLN	2.1

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	\mathbf{RSR}	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	NAG	А	502	14/15	0.62	0.27	$54,\!59,\!66,\!67$	0
2	SO4	А	508	5/5	0.75	0.24	56,59,62,63	0

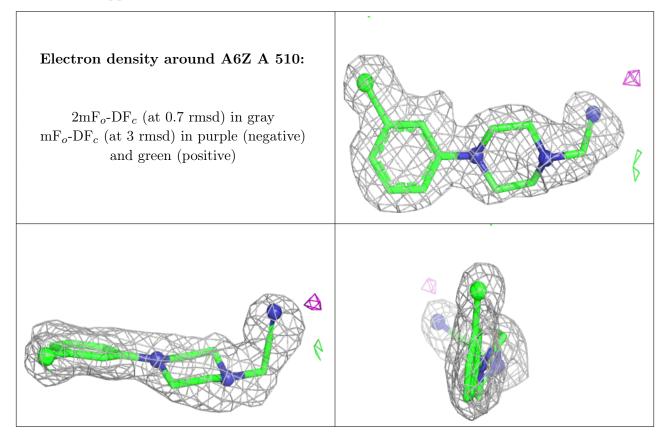
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
2	SO4	А	509	5/5	0.89	0.19	68,72,82,87	0
5	A6Z	А	510	16/16	0.90	0.16	$30,\!33,\!38,\!52$	0
2	SO4	А	507	5/5	0.93	0.31	48,55,60,60	0
2	SO4	А	504	5/5	0.94	0.16	48,54,58,61	0
2	SO4	А	506	5/5	0.95	0.19	33,38,44,46	0
4	DMS	А	503	4/4	0.96	0.08	33,33,42,46	0
2	SO4	А	505	5/5	0.98	0.06	33,36,40,43	0
2	SO4	А	501	5/5	0.99	0.07	28,29,30,32	0

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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.

