

# wwPDB X-ray Structure Validation Summary Report (i)

#### Mar 26, 2024 – 12:07 pm GMT

PDB ID	:	8RQP
Title	:	In meso structure of the alginate exporter, AlgE, from Pseudomonas aerugi-
		nosa in 7.10 monoacylglycerol
Authors	:	Smithers, L.; Boland, C.; Krawinski, P.; Caffrey, M.
Deposited on	:	2024-01-19
Resolution	:	1.45  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:

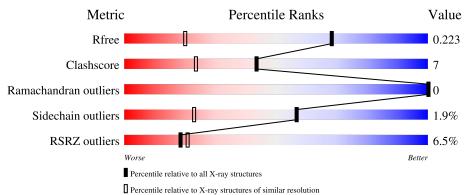
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

# 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 1.45 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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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		
			6%		
1	А	479	84%	12%	•



# 2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 4690 atoms, of which 455 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 Alginate production protein AlgE.

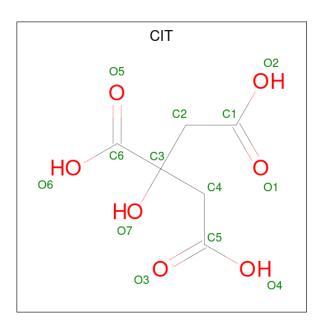
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	459	Total 3697	C 2305	N 667	0 721	$\frac{S}{4}$	13	14	0

Chain	Residue	Modelled	Actual	Comment	Reference
А	12	MET	-	initiating methionine	UNP P18895
А	13	GLY	-	expression tag	UNP P18895
A	14	SER	-	expression tag	UNP P18895
А	15	SER	-	expression tag	UNP P18895
А	16	HIS	-	expression tag	UNP P18895
А	17	HIS	-	expression tag	UNP P18895
А	18	HIS	-	expression tag	UNP P18895
А	19	HIS	-	expression tag	UNP P18895
А	20	HIS	-	expression tag	UNP P18895
А	21	HIS	-	expression tag	UNP P18895
А	22	SER	-	expression tag	UNP P18895
А	23	SER	-	expression tag	UNP P18895
А	24	GLY	-	expression tag	UNP P18895
A	25	LEU	-	expression tag	UNP P18895
А	26	VAL	-	expression tag	UNP P18895
А	27	PRO	-	expression tag	UNP P18895
А	28	ARG	-	expression tag	UNP P18895
А	29	GLY	-	expression tag	UNP P18895
А	30	SER	-	expression tag	UNP P18895
А	31	HIS	-	expression tag	UNP P18895
А	32	MET	-	expression tag	UNP P18895

There are 21 discrepancies between the modelled and reference sequences:

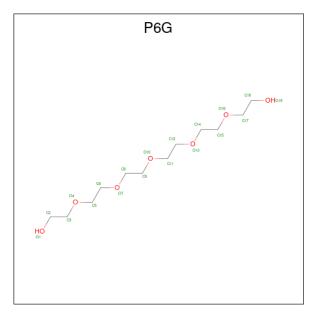
• Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula:  $C_6H_8O_7$ ).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	А	1	Total 18	С 6	H5	O 7	0	0

• Molecule 3 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula:  $C_{12}H_{26}O_7$ ).

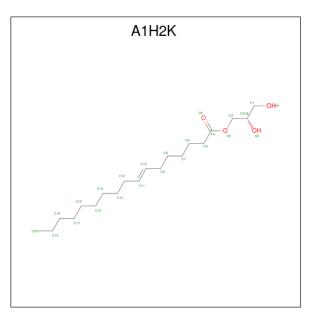


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	А	1	Total	-		-	0	0
			37	-		-		
3	А	1	Total				0	0
	11	Ĩ	23	6	13	4	Ŭ	0

• Molecule 4 is 7.10 monoacyl<br/>glycerol (S-form) (three-letter code: A1H2K) (formula:<br/>  $\rm C_{20}H_{38}O_4)$ 



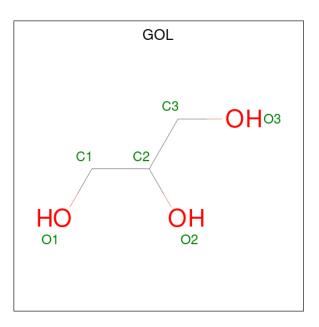
(labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	Total         C         H         O           62         20         38         4	0	0
4	А	1	Total         C         H         O           62         20         38         4	2	0
4	А	1	Total C H 44 15 29	0	0
4	А	1	Total         C         H         O           62         20         38         4	2	0
4	А	1	Total         C         H         O           62         20         38         4	2	0
4	А	1	Total         C         H         O           62         20         38         4	2	0
4	А	1	Total C H 44 15 29	0	0
4	А	1	Total         C         H         O           62         20         38         4	2	0
4	А	1	Total         C         H         O           62         20         38         4	2	0

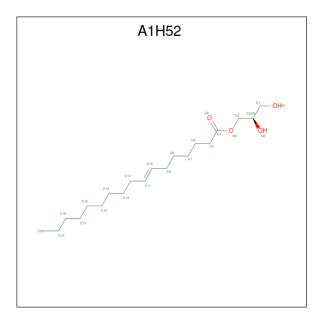
• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).





Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
5	А	1	Total C 14 3			0	0
5	А	1	Total C 14 3	С Н 8 8	O 3	0	0

• Molecule 6 is 7.10 monoacylglycerol (R-form) (three-letter code: A1H52) (formula:  $C_{20}H_{38}O_4$ ).



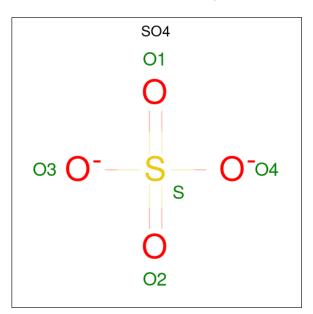
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	Λ	1	Total	С	Η	Ο	2	0
0	А	1	62	20	38	4		0
6	Λ	1	Total	С	Η	Ο	2	0
0	А	L	62	20	38	4		0



• Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	Total Na 1 1	0	0

• Molecule 8 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
8	А	1	Total 5	0 4	S 1	0	0

• Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	А	1	Total 1	Ca 1	0	0

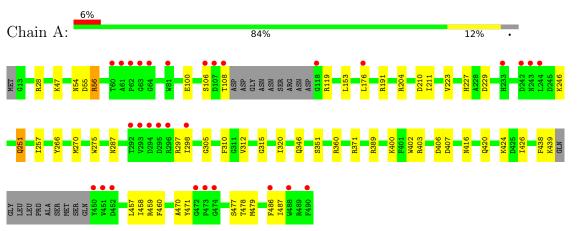
• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	А	234	Total         O           234         234	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: Alginate production protein AlgE



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	57.36Å 74.55Å 115.91Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $102.49^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	39.37 - 1.45	Depositor
Resolution (A)	39.37 - 1.45	EDS
% Data completeness	72.3 (39.37-1.45)	Depositor
(in resolution range)	72.4(39.37-1.45)	EDS
R <sub>merge</sub>	(Not available)	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.30 (at 1.45 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
P. P.	0.190 , $0.223$	Depositor
$R, R_{free}$	0.190 , $0.223$	DCC
$R_{free}$ test set	3105 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	15.4	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.34 , $49.2$	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4690	wwPDB-VP
Average B, all atoms $(Å^2)$	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.24% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: CIT, GOL, P6G, A1H52, NA, A1H2K, CA, SO4

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	Bo	ond angles
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	А	0.67	0/3795	0.79	2/5145~(0.0%)

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	А	479	MET	CG-SD-CE	-6.95	89.08	100.20
1	А	351	SER	CB-CA-C	-5.57	99.51	110.10

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	3697	0	3427	50	0
2	А	13	5	5	0	0
3	А	26	34	34	5	0
4	А	198	324	0	3	0
5	А	12	16	16	0	0
6	А	48	76	0	0	0
7	А	1	0	0	0	0
8	А	5	0	0	0	0
9	А	1	0	0	0	0

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Contr	naca from	i previous	pagc			
Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	А	234	0	0	6	1
All	All	4235	455	3482	50	1

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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 7.

The worst 5 of 50 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:458[A]:ILE:HD13	1:A:486:PHE:CD2	2.11	0.85
1:A:223:VAL:HG12	1:A:257[A]:ILE:HD12	1.64	0.77
1:A:420:GLN:HG2	1:A:470:ALA:O	1.95	0.66
1:A:420:GLN:HE21	1:A:471:TYR:C	2.00	0.65
1:A:153:LEU:HD23	10:A:608:HOH:O	1.98	0.62

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:803:HOH:O	10:A:803:HOH:O[2_655]	2.19	0.01

### 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	461/479~(96%)	446 (97%)	15 (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	А	379/388~(98%)	372~(98%)	7~(2%)	59 26

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
1	А	251	GLN
1	А	270	MET
1	А	477	SER
1	А	407	ASP
1	А	176	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	251	GLN
1	А	416	ASN
1	А	420	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 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
MOI	Type	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
6	A1H52	А	516	-	$23,\!23,\!23$	0.52	1 (4%)	$24,\!24,\!24$	0.94	2 (8%)
3	P6G	А	506	-	9,9,18	0.18	0	8,8,17	0.61	0
4	A1H2K	А	508	-	23,23,23	0.33	0	24,24,24	0.47	0
4	A1H2K	А	509	-	$23,\!23,\!23$	0.28	0	$24,\!24,\!24$	0.62	0
4	A1H2K	А	507	-	$23,\!23,\!23$	0.28	0	$24,\!24,\!24$	0.39	0
4	A1H2K	А	504	-	$23,\!23,\!23$	0.22	0	$24,\!24,\!24$	0.47	0
4	A1H2K	А	510	-	14,14,23	0.20	0	13,13,24	0.57	0
3	P6G	А	502	-	$15,\!15,\!18$	0.21	0	$14,\!14,\!17$	0.64	0
4	A1H2K	А	511	-	23,23,23	0.30	0	24,24,24	0.56	0
5	GOL	А	512	-	$5,\!5,\!5$	0.65	0	$5,\!5,\!5$	1.00	0
4	A1H2K	А	505	-	14,14,23	0.17	0	13,13,24	0.28	0
6	A1H52	А	513	-	23,23,23	0.37	0	24,24,24	0.91	0
4	A1H2K	А	515	-	23,23,23	0.30	0	24,24,24	0.53	0
2	CIT	А	501	-	12,12,12	1.14	0	17,17,17	1.42	3 (17%)
5	GOL	А	514	-	$5,\!5,\!5$	0.99	0	$5,\!5,\!5$	0.93	0
8	SO4	А	518	-	4,4,4	0.35	0	$6,\!6,\!6$	0.48	0
4	A1H2K	А	503	-	23,23,23	0.26	0	24,24,24	0.42	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	A1H52	А	516	-	-	8/23/23/23	-
3	P6G	А	506	-	-	3/7/7/16	-
4	A1H2K	А	508	-	-	7/23/23/23	-
4	A1H2K	А	509	-	-	10/23/23/23	-
4	A1H2K	А	507	-	-	8/23/23/23	-
4	A1H2K	А	504	-	-	7/23/23/23	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1H2K	А	510	-	-	2/12/12/23	-
3	P6G	А	502	-	-	7/13/13/16	-
4	A1H2K	А	511	-	-	6/23/23/23	-
5	GOL	А	512	-	-	0/4/4/4	-
4	A1H2K	А	505	-	-	3/12/12/23	-
6	A1H52	А	513	-	-	11/23/23/23	-
4	A1H2K	А	515	-	-	11/23/23/23	-
2	CIT	А	501	-	-	0/16/16/16	-
5	GOL	А	514	-	-	2/4/4/4	-
4	A1H2K	А	503	-	-	10/23/23/23	-

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All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
6	А	516	A1H52	O2-C2	-2.29	1.36	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
6	А	516	A1H52	O2-C2-C3	3.03	120.19	109.56
2	А	501	CIT	O6-C6-C3	3.02	118.29	113.05
6	А	516	A1H52	O2-C2-C1	2.38	119.59	109.12
2	А	501	CIT	O2-C1-O1	-2.30	117.56	123.30
2	А	501	CIT	O4-C5-O3	-2.06	118.17	123.30

There are no chirality outliers.

5 of 95 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	507		O1-C1-C2-C3
4	А	508	A1H2K	O2-C2-C3-O3
4	А	515	A1H2K	O1-C1-C2-O2
4	А	515	A1H2K	C1-C2-C3-O3
4	А	515	A1H2K	O2-C2-C3-O3

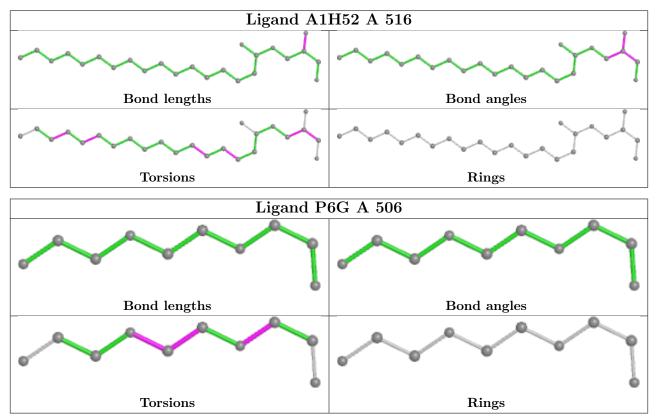
There are no ring outliers.

5 monomers are involved in 8 short contacts:

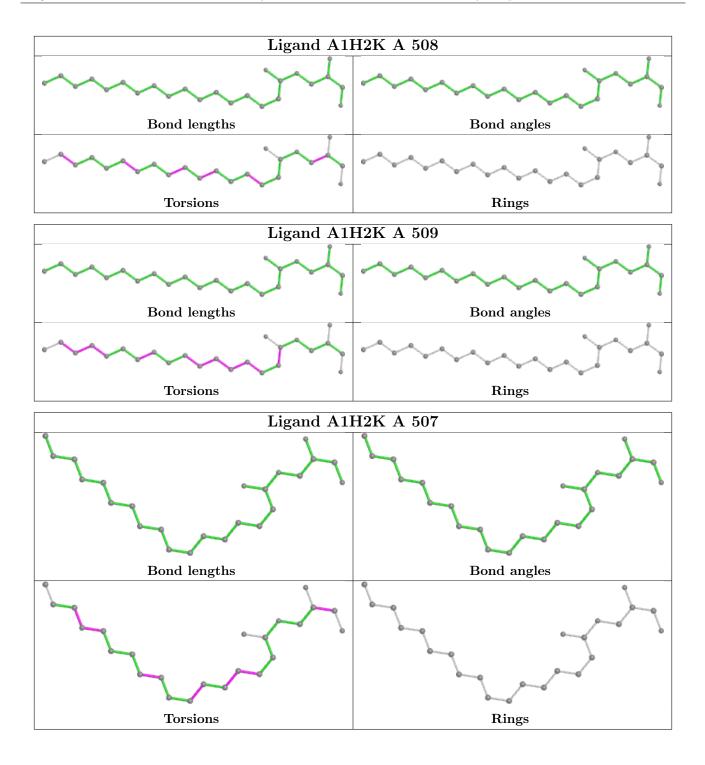


Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	506	P6G	1	0
4	А	508	A1H2K	1	0
4	А	507	A1H2K	1	0
3	А	502	P6G	4	0
4	А	511	A1H2K	1	0

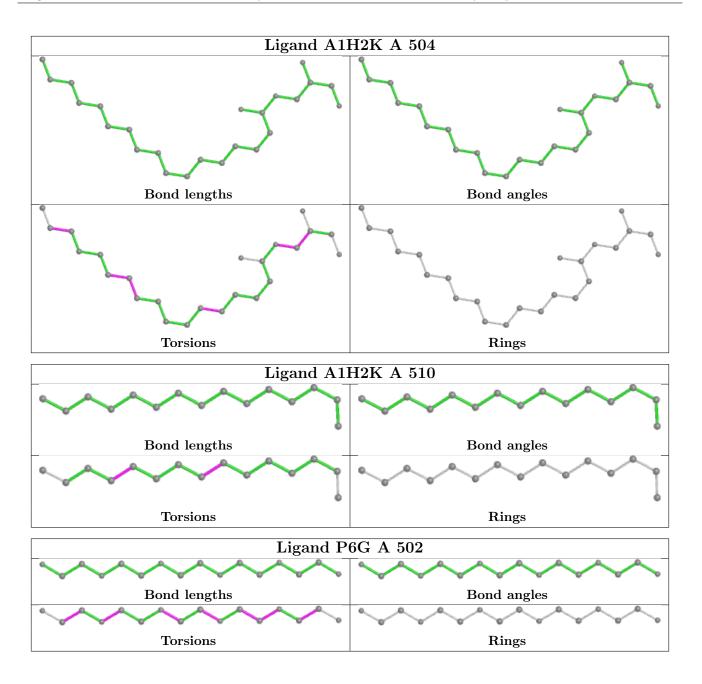
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



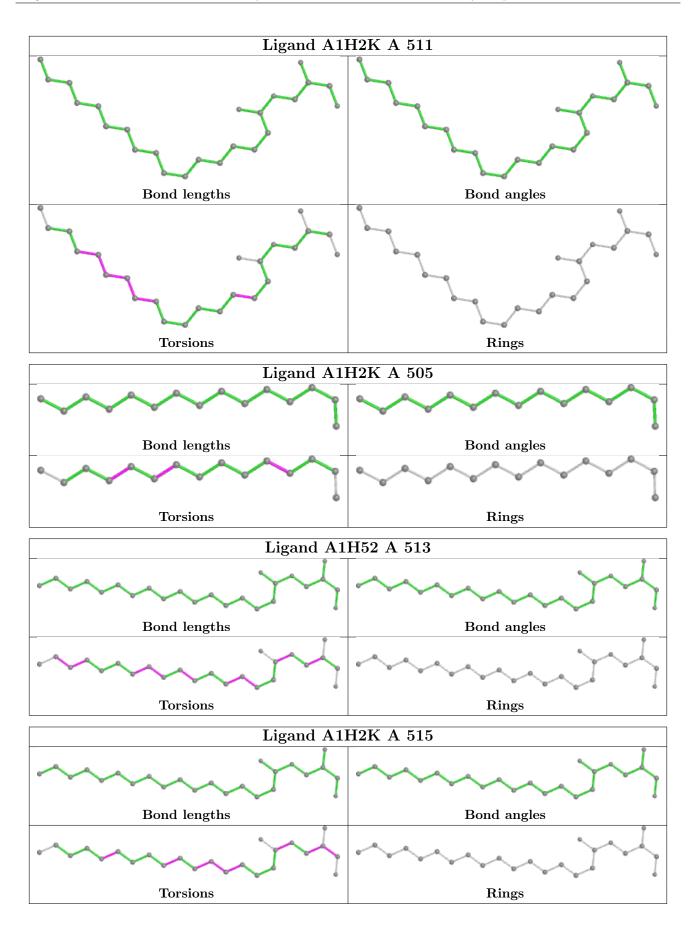




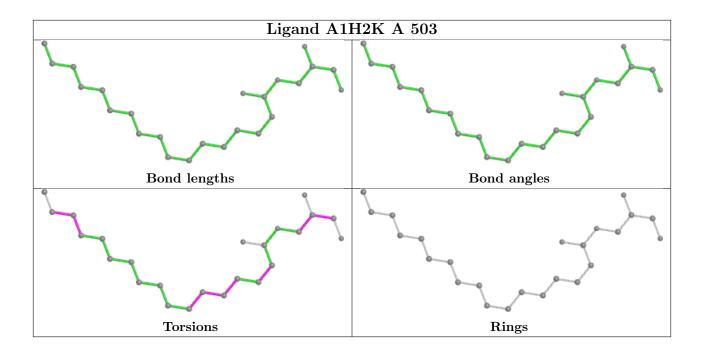












## 5.7 Other polymers (i)

There are no such residues in this entry.

## 5.8 Polymer linkage issues (i)

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	459/479~(95%)	0.21	30 (6%) 18 21	10, 18, 43, 86	35~(7%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	295	ASP	10.3
1	А	294	ASP	7.9
1	А	450	TYR	6.4
1	А	243	ASN	5.5
1	А	63	GLY	5.3

## 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.

4         A1H2K         A         508         24/24         0.73         0.26         38,57,77,86         2           4         A1H2K         A         504         24/24         0.75         0.25         20.46.67.83         2	Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
4 A1H2K A 504 24/24 0.75 0.25 20.46.67.83 2	4	A1H2K	А	508	24/24	0.73	0.26	38,57,77,86	2
	4	A1H2K	А	504	24/24	0.75	0.25	20,46,67,83	2

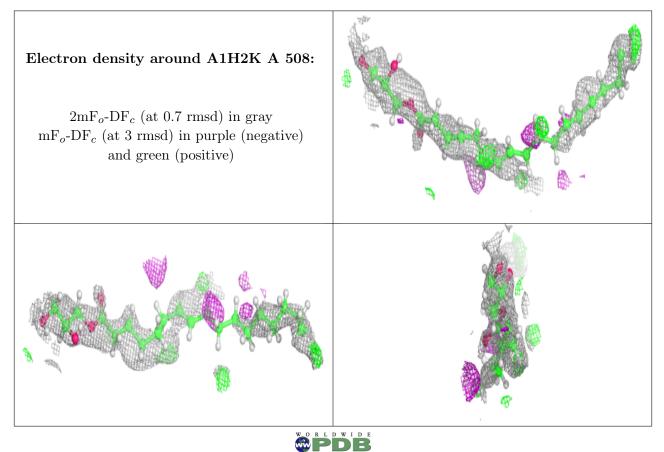
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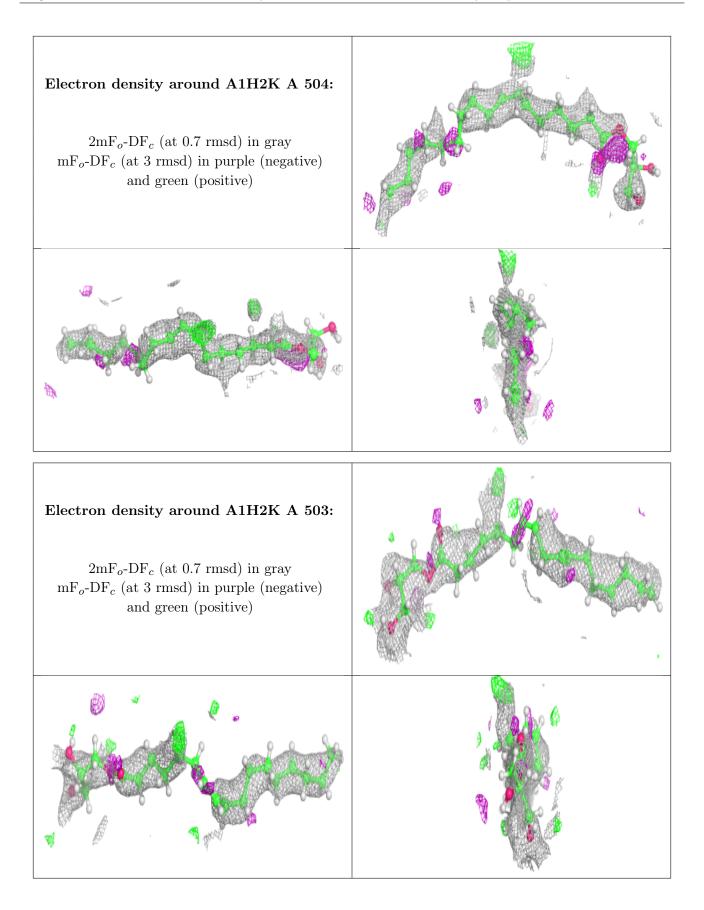


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B$ -factors $(Å^2)$	Q<0.9
4	A1H2K	А	503	24/24	0.75	0.27	27,50,67,83	0
4	A1H2K	А	507	24/24	0.76	0.25	40,56,80,84	2
6	A1H52	А	513	24/24	0.78	0.36	31,57,80,96	2
4	A1H2K	А	505	15/24	0.79	0.20	$24,\!39,\!59,\!59$	0
4	A1H2K	А	515	24/24	0.80	0.26	$24,\!47,\!59,\!64$	2
4	A1H2K	А	509	24/24	0.80	0.21	$25,\!41,\!61,\!63$	2
6	A1H52	А	516	24/24	0.80	0.33	32,56,83,93	2
5	GOL	A	514	6/6	0.81	0.34	$36,\!45,\!54,\!55$	0
5	GOL	A	512	6/6	0.83	0.15	$28,\!34,\!40,\!48$	14
4	A1H2K	А	510	15/24	0.83	0.22	$27,\!42,\!62,\!62$	0
4	A1H2K	A	511	24/24	0.84	0.23	$25,\!48,\!61,\!66$	2
3	P6G	А	506	10/19	0.92	0.23	$7,\!22,\!31,\!36$	23
3	P6G	A	502	16/19	0.92	0.13	$13,\!27,\!40,\!49$	37
2	CIT	А	501	13/13	0.93	0.11	17,22,27,33	6
9	CA	A	519	1/1	0.96	0.18	$68,\!68,\!68,\!68$	0
8	SO4	А	518	5/5	0.99	0.08	$13,\!14,\!16,\!16$	5
7	NA	А	517	1/1	1.00	0.05	18,18,18,18	0

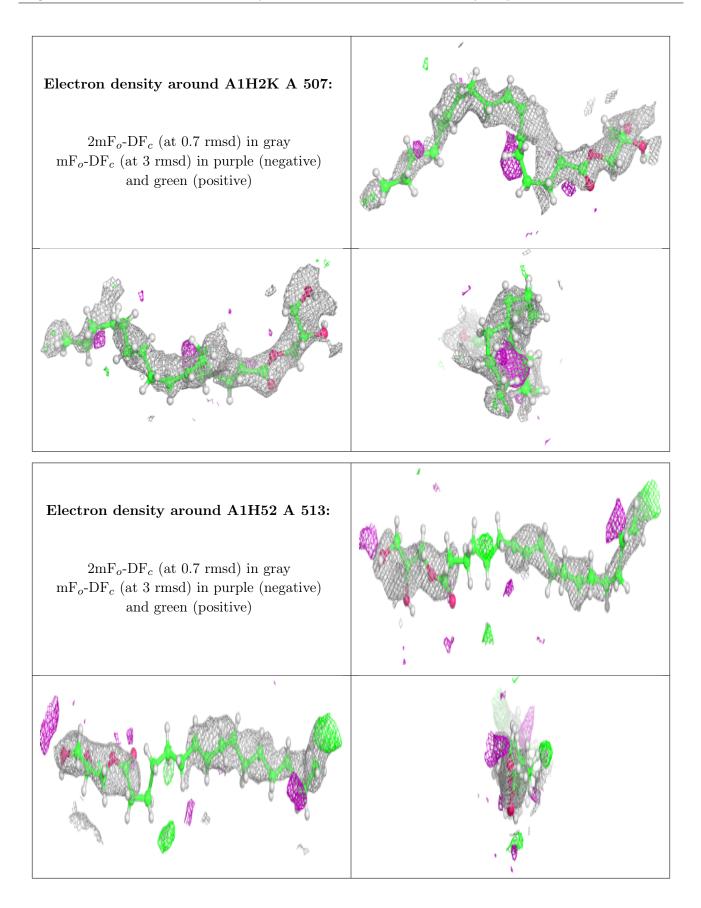
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The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also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

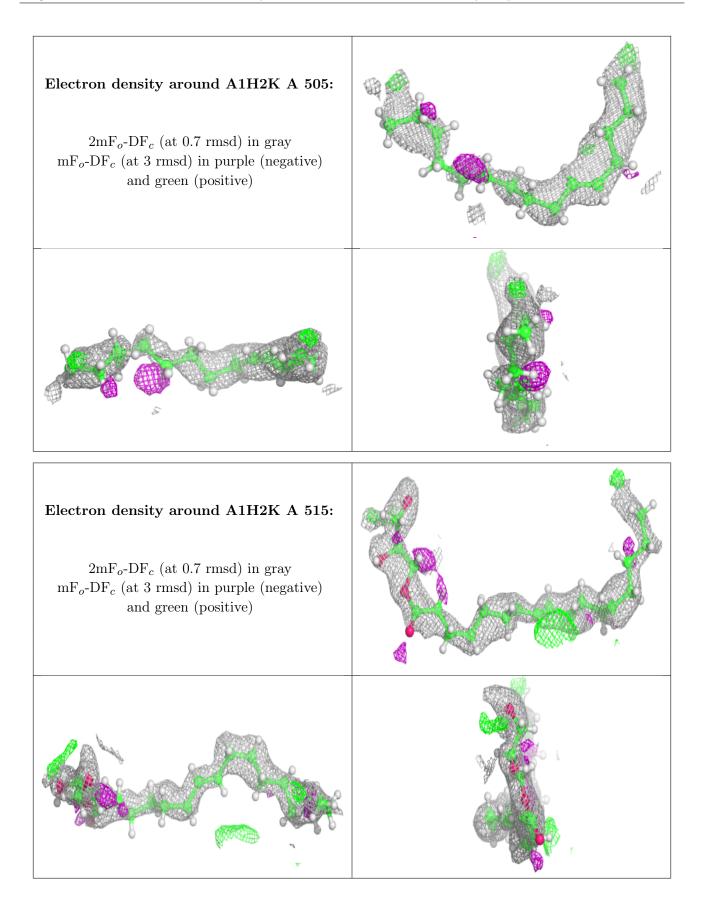




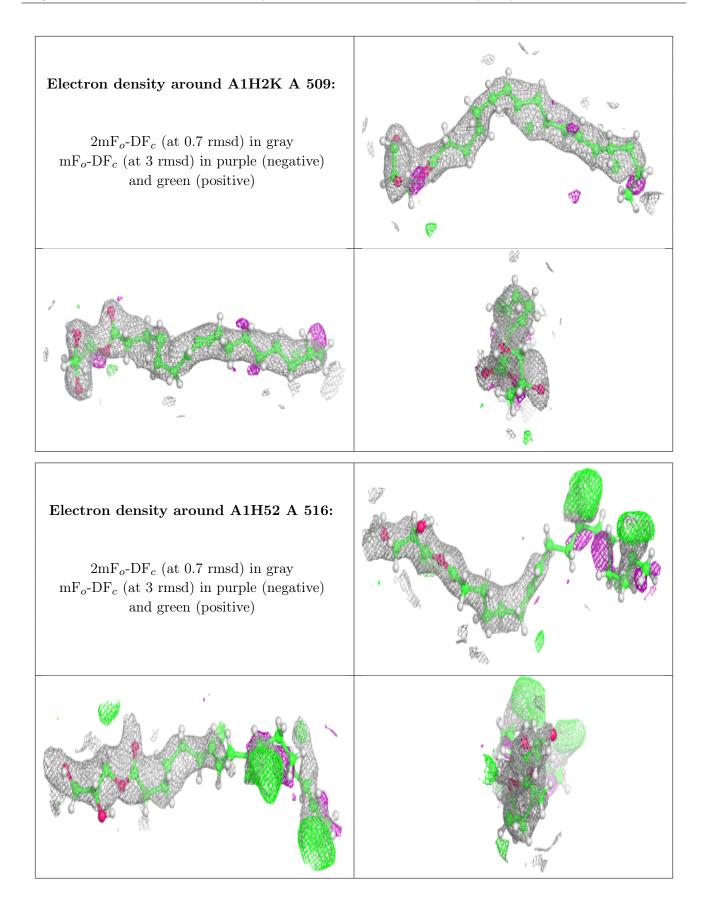




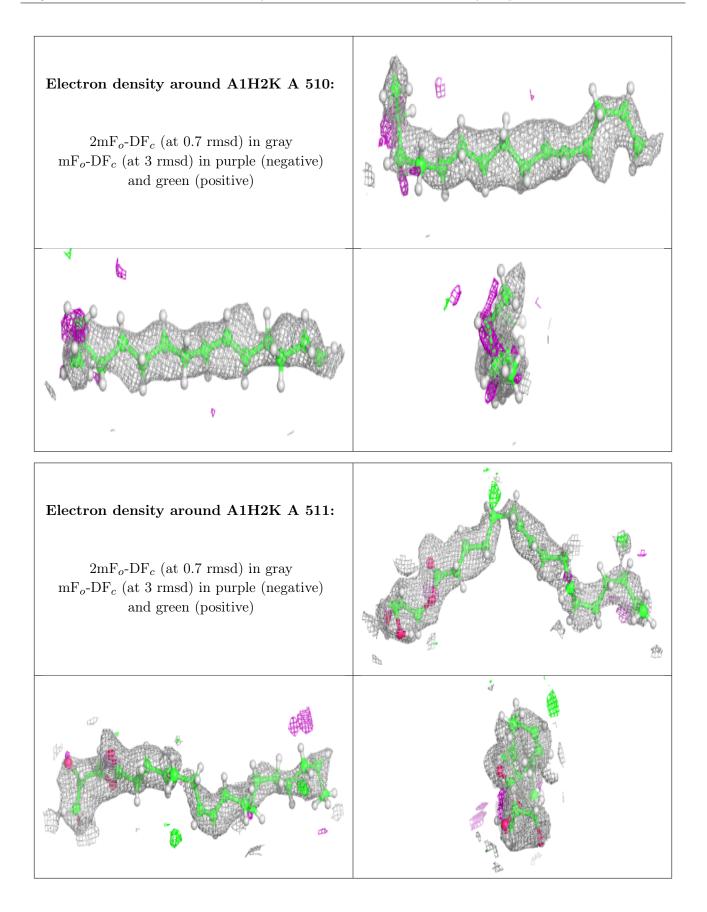




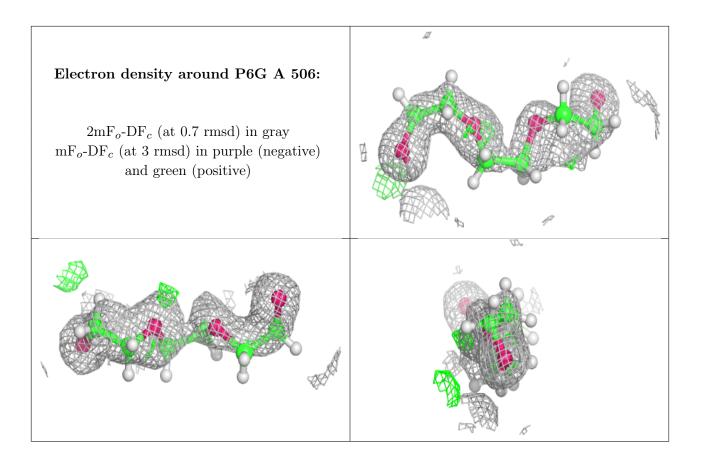




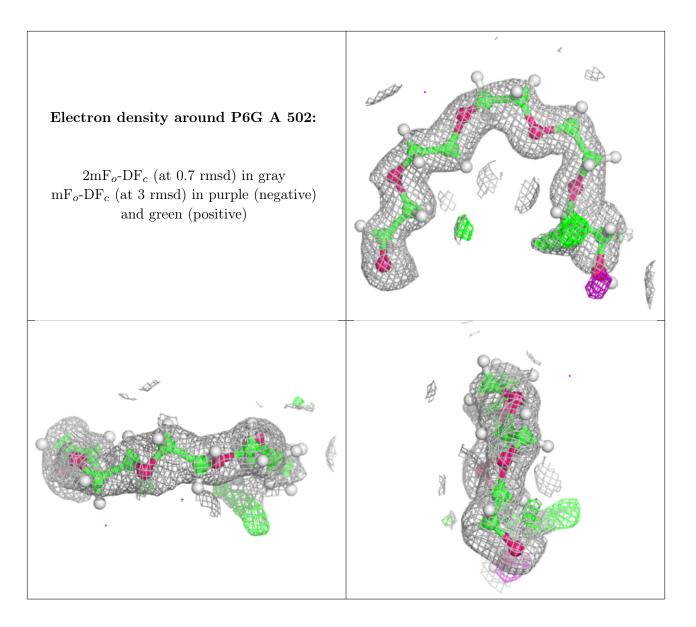












## 6.5 Other polymers (i)

There are no such residues in this entry.

