



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 4, 2024 – 09:11 pm GMT

PDB ID : 4XNL  
Title : X-ray structure of AlgE2  
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Deposited on : 2015-01-15  
Resolution : 2.90 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

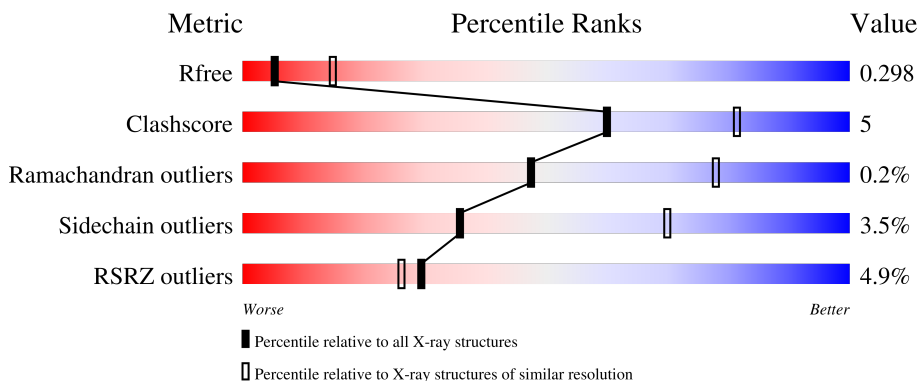
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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  $\geq 3$ , 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	A	490	

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
2	LDA	A	504	-	-	-	X

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
3	78M	A	508	-	-	-	X
3	78M	A	512	-	-	-	X

## 2 Entry composition [i](#)

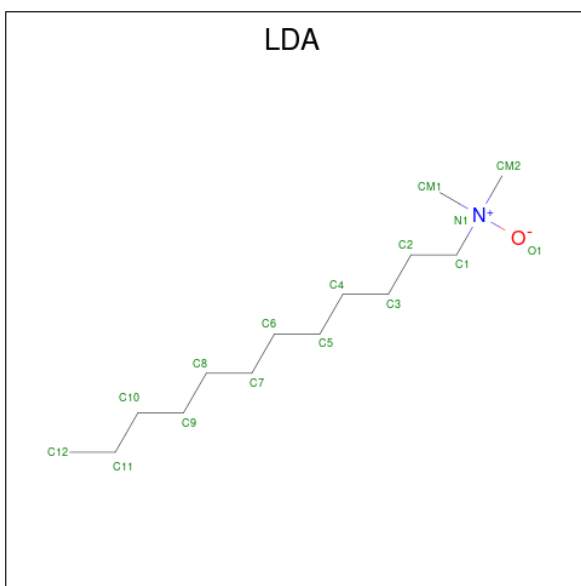
There are 7 unique types of molecules in this entry. The entry contains 3635 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alginate production protein AlgE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	425	3377	2111	602	661	3	0	0	0

- Molecule 2 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: C<sub>14</sub>H<sub>31</sub>NO).



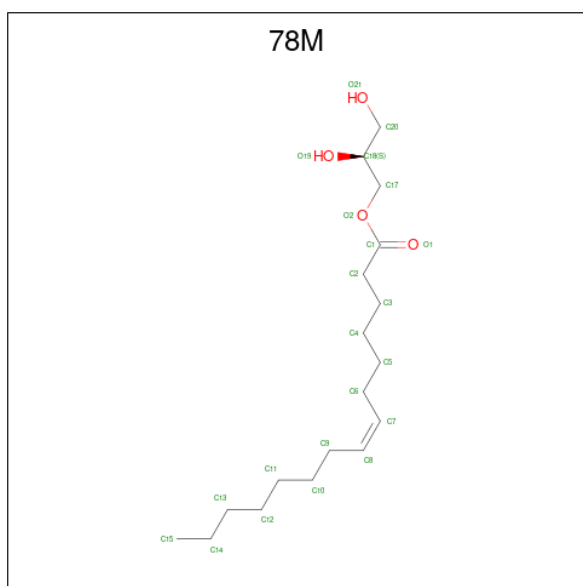
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	16	14	1	1	0	0
2	A	1	16	14	1	1	0	0
2	A	1	11	9	1	1	0	0
2	A	1	16	14	1	1	0	0
2	A	1	9	9			0	0

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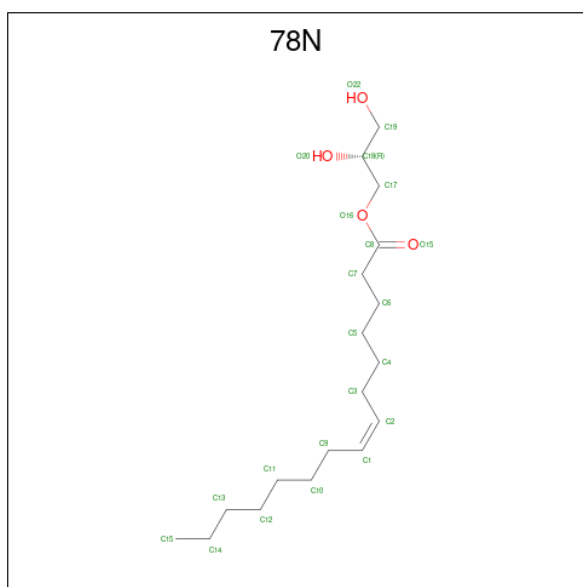
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 11 11	0	0
2	A	1	Total C N O 16 14 1 1	0	0
2	A	1	Total C N O 16 14 1 1	0	0

- Molecule 3 is (2S)-2,3-DIHYDROXYPROPYL(7Z)-PENTADEC-7-ENOATE (three-letter code: 78M) (formula: C<sub>18</sub>H<sub>34</sub>O<sub>4</sub>).



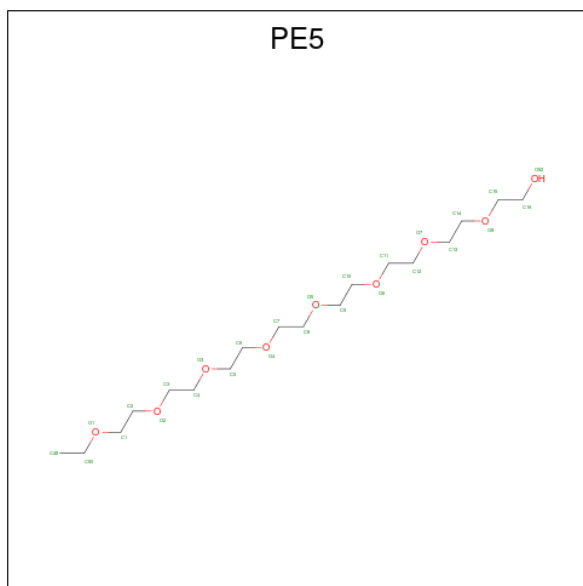
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 22 18 4	0	0
3	A	1	Total C O 22 18 4	0	0
3	A	1	Total C O 22 18 4	0	0
3	A	1	Total C O 22 18 4	0	0

- Molecule 4 is (2R)-2,3-DIHYDROXYPROPYL(7Z)-PENTADEC-7-ENOATE (three-letter code: 78N) (formula: C<sub>18</sub>H<sub>34</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			22	18	4		

- Molecule 5 is 3,6,9,12,15,18,21,24-OCTAOXAHEXACOSAN-1-OL (three-letter code: PE5) (formula:  $C_{18}H_{38}O_9$ ).



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

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		

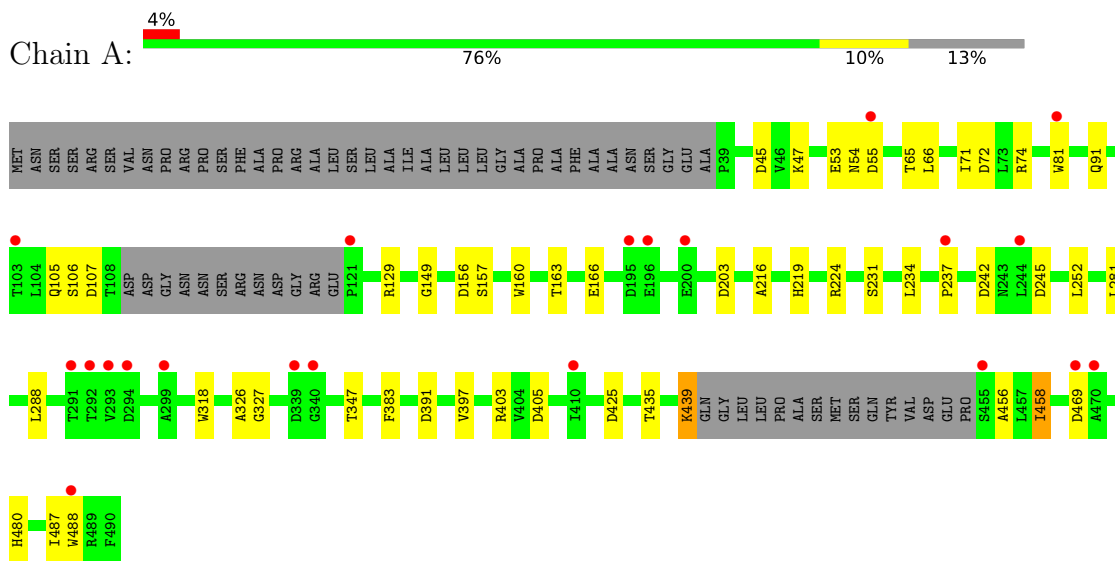
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	28	Total	O	0	0
			28	28		

### 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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.38Å 73.12Å 184.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.12 – 2.90 47.12 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (47.12-2.90) 96.5 (47.12-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 2.91Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, $R_{free}$	0.251 , 0.287 0.274 , 0.298	Depositor DCC
$R_{free}$ test set	720 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	52.0	Xtrriage
Anisotropy	0.534	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 41.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	3635	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<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.

## 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: 78N, PE5, CA, LDA, 78M

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	0.38	0/3462	0.69	1/4693 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	ASN	C-N-CA	5.41	135.21	121.70

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	A	3377	0	3142	31	0
2	A	111	0	205	5	0
3	A	88	0	136	3	0
4	A	22	0	34	1	0
5	A	8	0	8	1	0
6	A	1	0	0	0	0
7	A	28	0	0	0	0
All	All	3635	0	3525	33	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 5.

All (33) 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:456:ALA:HB2	1:A:488:TRP:HE3	1.60	0.66
1:A:456:ALA:HB1	1:A:487:ILE:O	1.97	0.65
1:A:439:LYS:HE3	1:A:439:LYS:H	1.63	0.64
1:A:480:HIS:HB2	3:A:510:78M:H7	1.80	0.64
1:A:456:ALA:HB2	1:A:488:TRP:CE3	2.37	0.59
1:A:105:GLN:HB3	1:A:163:THR:HB	1.85	0.58
1:A:166:GLU:HB3	2:A:506:LDA:H62	1.83	0.58
1:A:252:LEU:HB3	1:A:281:LEU:HD11	1.86	0.57
1:A:47:LYS:HG3	1:A:487:ILE:HG12	1.90	0.53
1:A:456:ALA:CB	1:A:488:TRP:HE3	2.23	0.52
1:A:425:ASP:HB3	1:A:469:ASP:HB2	1.95	0.48
1:A:45:ASP:HB2	1:A:74:ARG:HB2	1.96	0.47
1:A:160:TRP:CD2	1:A:224:ARG:HD2	2.51	0.45
1:A:234:LEU:HB3	1:A:288:LEU:HD13	1.99	0.45
1:A:318:TRP:CD1	1:A:327:GLY:HA2	2.52	0.45
1:A:318:TRP:CD1	1:A:318:TRP:N	2.84	0.44
1:A:234:LEU:HD22	1:A:288:LEU:HB2	1.98	0.44
1:A:347:THR:HG23	5:A:511:PE5:C5	2.47	0.44
1:A:203:ASP:HB3	1:A:231:SER:HB3	2.00	0.43
1:A:216:ALA:HB3	1:A:219:HIS:HB2	1.98	0.43
1:A:149:GLY:HA2	2:A:506:LDA:H61	2.00	0.43
1:A:456:ALA:CB	1:A:487:ILE:O	2.65	0.43
1:A:403:ARG:HG2	1:A:405:ASP:O	2.19	0.43
1:A:53:GLU:HG2	1:A:66:LEU:HB2	2.00	0.43
1:A:383:PHE:HB3	1:A:397:VAL:HG13	2.01	0.43
1:A:91:GLN:HB2	1:A:129:ARG:HG2	2.01	0.42
1:A:47:LYS:HB3	1:A:72:ASP:HB3	2.02	0.42
1:A:71:ILE:HG21	2:A:514:LDA:H91	2.01	0.42
1:A:458:ILE:HG23	4:A:509:78N:H111	2.02	0.41
2:A:504:LDA:HM21	2:A:504:LDA:H22	1.83	0.41
1:A:81:TRP:HZ2	3:A:507:78M:H18	1.85	0.41
3:A:507:78M:H92C	3:A:507:78M:H61C	1.80	0.41
1:A:326:ALA:HB3	2:A:501:LDA:H92	2.03	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	A	419/490 (86%)	395 (94%)	23 (6%)	1 (0%)	47 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	237	PRO

### 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	344/394 (87%)	332 (96%)	12 (4%)	36 70

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASP
1	A	65	THR
1	A	106	SER
1	A	107	ASP
1	A	156	ASP
1	A	157	SER
1	A	242	ASP
1	A	245	ASP
1	A	391	ASP
1	A	435	THR

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Mol	Chain	Res	Type
1	A	439	LYS
1	A	458	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	308	ASN

### 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 15 ligands modelled in this entry, 1 is monoatomic - leaving 14 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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	LDA	A	502	-	12,15,15	2.54	1 (8%)	14,17,17	0.75	0
2	LDA	A	513	-	12,15,15	2.51	1 (8%)	14,17,17	0.83	1 (7%)
3	78M	A	507	-	21,21,21	0.83	1 (4%)	22,22,22	0.68	1 (4%)
3	78M	A	508	-	21,21,21	0.84	1 (4%)	22,22,22	0.74	1 (4%)
3	78M	A	512	-	21,21,21	0.82	1 (4%)	22,22,22	0.71	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	LDA	A	504	-	12,15,15	2.55	1 (8%)	14,17,17	0.58	0
4	78N	A	509	-	21,21,21	1.27	1 (4%)	22,22,22	0.88	1 (4%)
2	LDA	A	514	-	12,15,15	2.61	1 (8%)	14,17,17	0.44	0
5	PE5	A	511	-	7,7,26	0.27	0	6,6,25	0.37	0
2	LDA	A	503	-	7,10,15	3.24	1 (14%)	9,12,17	0.40	0
2	LDA	A	505	-	8,8,15	0.66	0	7,7,17	0.25	0
2	LDA	A	506	-	10,10,15	0.68	0	9,9,17	0.24	0
2	LDA	A	501	-	12,15,15	2.55	1 (8%)	14,17,17	0.48	0
3	78M	A	510	-	21,21,21	0.83	1 (4%)	22,22,22	0.67	1 (4%)

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	LDA	A	502	-	-	7/13/13/13	-
2	LDA	A	513	-	-	9/13/13/13	-
3	78M	A	507	-	-	11/21/21/21	-
3	78M	A	508	-	-	12/21/21/21	-
3	78M	A	512	-	-	7/21/21/21	-
2	LDA	A	504	-	-	7/13/13/13	-
4	78N	A	509	-	-	17/21/21/21	-
2	LDA	A	514	-	-	6/13/13/13	-
5	PE5	A	511	-	-	2/5/5/24	-
2	LDA	A	503	-	-	6/8/8/13	-
2	LDA	A	505	-	-	5/6/6/13	-
2	LDA	A	506	-	-	7/8/8/13	-
2	LDA	A	501	-	-	8/13/13/13	-
3	78M	A	510	-	-	9/21/21/21	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	514	LDA	O1-N1	-8.72	1.21	1.42
2	A	501	LDA	O1-N1	-8.53	1.22	1.42
2	A	504	LDA	O1-N1	-8.52	1.22	1.42
2	A	502	LDA	O1-N1	-8.51	1.22	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	503	LDA	O1-N1	-8.35	1.22	1.42
2	A	513	LDA	O1-N1	-8.35	1.22	1.42
4	A	509	78N	O16-C8	4.52	1.46	1.33
3	A	510	78M	O2-C1	3.32	1.43	1.33
3	A	507	78M	O2-C1	3.30	1.43	1.33
3	A	508	78M	O2-C1	3.30	1.43	1.33
3	A	512	78M	O2-C1	3.25	1.42	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	509	78N	O16-C8-C7	3.03	121.40	111.91
3	A	508	78M	O2-C1-C2	2.62	120.12	111.91
3	A	512	78M	O2-C1-C2	2.47	119.65	111.91
3	A	510	78M	O2-C1-C2	2.41	119.47	111.91
3	A	507	78M	O2-C1-C2	2.32	119.20	111.91
2	A	513	LDA	O1-N1-C1	2.06	114.32	109.27

There are no chirality outliers.

All (113) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	LDA	N1-C1-C2-C3
2	A	502	LDA	N1-C1-C2-C3
2	A	504	LDA	C2-C1-N1-O1
2	A	504	LDA	C2-C1-N1-CM1
2	A	504	LDA	C2-C1-N1-CM2
2	A	504	LDA	N1-C1-C2-C3
2	A	513	LDA	C2-C1-N1-CM1
2	A	513	LDA	C2-C1-N1-CM2
2	A	514	LDA	N1-C1-C2-C3
3	A	507	78M	C17-C18-C20-O21
3	A	508	78M	C17-C18-C20-O21
3	A	510	78M	C17-C18-C20-O21
4	A	509	78N	O16-C17-C18-O20
4	A	509	78N	O15-C8-O16-C17
4	A	509	78N	C7-C8-O16-C17
3	A	508	78M	C2-C1-O2-C17
3	A	512	78M	C2-C1-O2-C17
3	A	512	78M	O1-C1-O2-C17
5	A	511	PE5	O2-C3-C4-O3
3	A	508	78M	O1-C1-O2-C17

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Mol	Chain	Res	Type	Atoms
3	A	508	78M	C1-C2-C3-C4
3	A	507	78M	C1-C2-C3-C4
2	A	502	LDA	C7-C8-C9-C10
2	A	506	LDA	C5-C6-C7-C8
3	A	507	78M	C9-C10-C11-C12
4	A	509	78N	O16-C17-C18-C19
2	A	501	LDA	C4-C5-C6-C7
2	A	501	LDA	C5-C6-C7-C8
2	A	504	LDA	C5-C6-C7-C8
3	A	507	78M	C10-C11-C12-C13
3	A	510	78M	C11-C12-C13-C14
2	A	514	LDA	C7-C8-C9-C10
2	A	514	LDA	C11-C10-C9-C8
2	A	514	LDA	C5-C6-C7-C8
4	A	509	78N	C9-C10-C11-C12
2	A	513	LDA	C3-C4-C5-C6
3	A	508	78M	C11-C12-C13-C14
2	A	501	LDA	C6-C7-C8-C9
2	A	501	LDA	C11-C10-C9-C8
2	A	502	LDA	C4-C5-C6-C7
2	A	513	LDA	C2-C3-C4-C5
4	A	509	78N	C10-C11-C12-C13
2	A	505	LDA	C2-C3-C4-C5
2	A	505	LDA	C5-C6-C7-C8
3	A	508	78M	C9-C10-C11-C12
4	A	509	78N	C3-C4-C5-C6
2	A	513	LDA	C6-C7-C8-C9
3	A	512	78M	C10-C11-C12-C13
2	A	513	LDA	C4-C5-C6-C7
4	A	509	78N	C11-C12-C13-C14
3	A	507	78M	C3-C4-C5-C6
2	A	502	LDA	C11-C10-C9-C8
3	A	508	78M	C2-C3-C4-C5
2	A	503	LDA	C1-C2-C3-C4
3	A	512	78M	C11-C12-C13-C14
2	A	506	LDA	C2-C3-C4-C5
3	A	510	78M	C2-C3-C4-C5
3	A	507	78M	O2-C17-C18-O19
3	A	507	78M	C11-C10-C9-C8
4	A	509	78N	C2-C3-C4-C5
2	A	513	LDA	C1-C2-C3-C4
3	A	510	78M	C3-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
3	A	508	78M	C4-C5-C6-C7
2	A	503	LDA	C2-C3-C4-C5
2	A	501	LDA	C3-C4-C5-C6
2	A	501	LDA	C1-C2-C3-C4
2	A	504	LDA	C2-C3-C4-C5
2	A	506	LDA	C11-C10-C9-C8
4	A	509	78N	C4-C5-C6-C7
2	A	514	LDA	C1-C2-C3-C4
4	A	509	78N	C12-C13-C14-C15
3	A	507	78M	O19-C18-C20-O21
3	A	508	78M	O19-C18-C20-O21
3	A	510	78M	O19-C18-C20-O21
3	A	508	78M	C12-C13-C14-C15
2	A	506	LDA	C6-C7-C8-C9
2	A	502	LDA	C9-C10-C11-C12
2	A	514	LDA	C9-C10-C11-C12
2	A	506	LDA	C1-C2-C3-C4
2	A	503	LDA	N1-C1-C2-C3
2	A	503	LDA	C4-C5-C6-C7
4	A	509	78N	C5-C6-C7-C8
2	A	505	LDA	C3-C4-C5-C6
2	A	501	LDA	C9-C10-C11-C12
3	A	508	78M	C3-C4-C5-C6
2	A	502	LDA	C2-C3-C4-C5
2	A	513	LDA	C9-C10-C11-C12
2	A	503	LDA	C2-C1-N1-CM1
4	A	509	78N	C11-C10-C9-C1
5	A	511	PE5	C1-C2-O2-C3
2	A	502	LDA	C1-C2-C3-C4
2	A	506	LDA	C7-C8-C9-C10
3	A	507	78M	O1-C1-O2-C17
3	A	507	78M	C2-C1-O2-C17
2	A	505	LDA	C6-C7-C8-C9
3	A	510	78M	C11-C10-C9-C8
3	A	507	78M	C4-C5-C6-C7
3	A	512	78M	C7-C8-C9-C10
3	A	512	78M	C3-C4-C5-C6
2	A	504	LDA	C3-C4-C5-C6
4	A	509	78N	C2-C1-C9-C10
3	A	510	78M	O2-C1-C2-C3
3	A	510	78M	C5-C6-C7-C8
2	A	505	LDA	C1-C2-C3-C4

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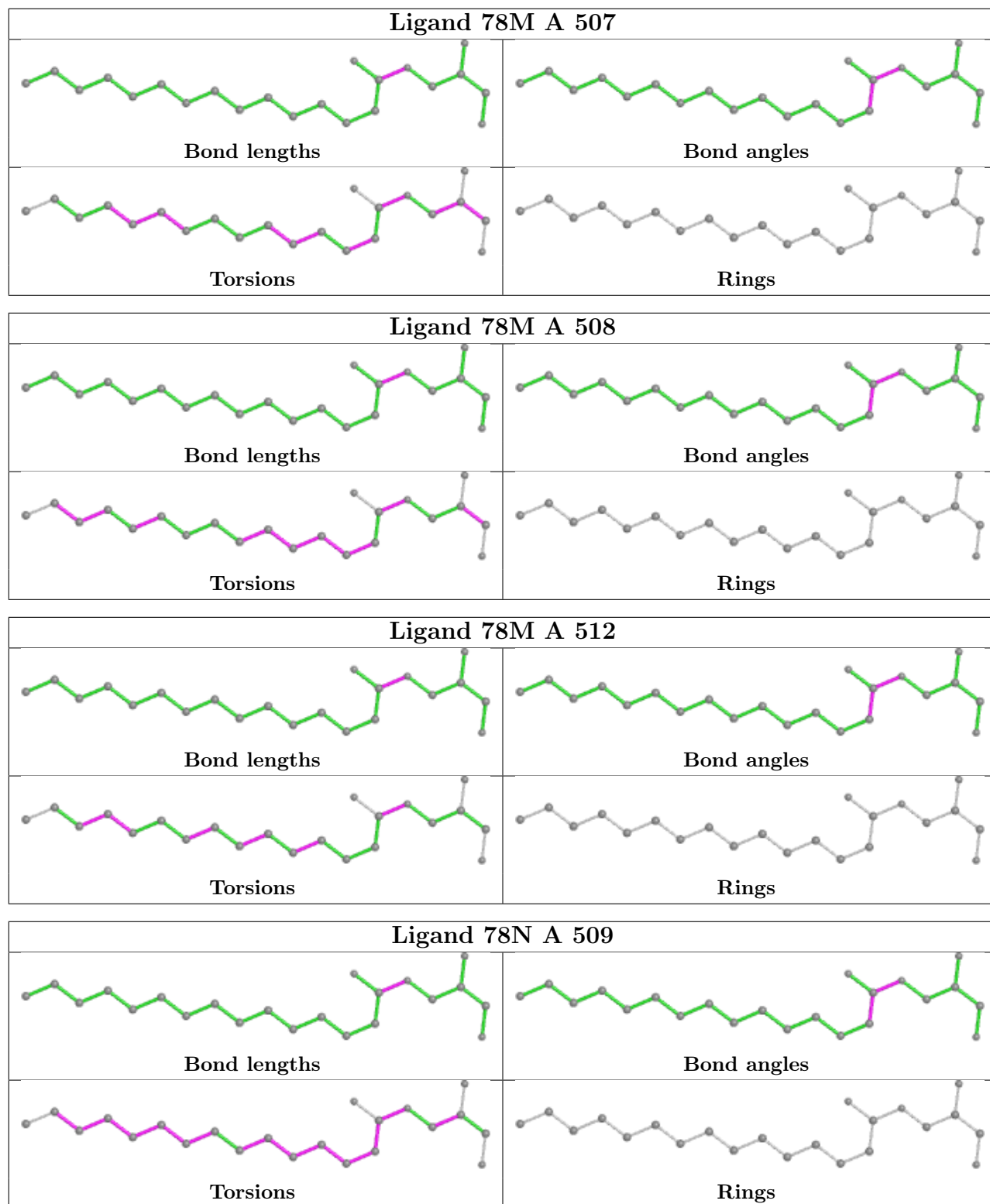
Mol	Chain	Res	Type	Atoms
3	A	512	78M	C5-C6-C7-C8
4	A	509	78N	C1-C2-C3-C4
4	A	509	78N	C6-C7-C8-O16
3	A	510	78M	O1-C1-C2-C3
2	A	506	LDA	C4-C5-C6-C7
2	A	503	LDA	C2-C1-N1-O1
2	A	513	LDA	C2-C1-N1-O1
4	A	509	78N	C6-C7-C8-O15
3	A	508	78M	C5-C6-C7-C8

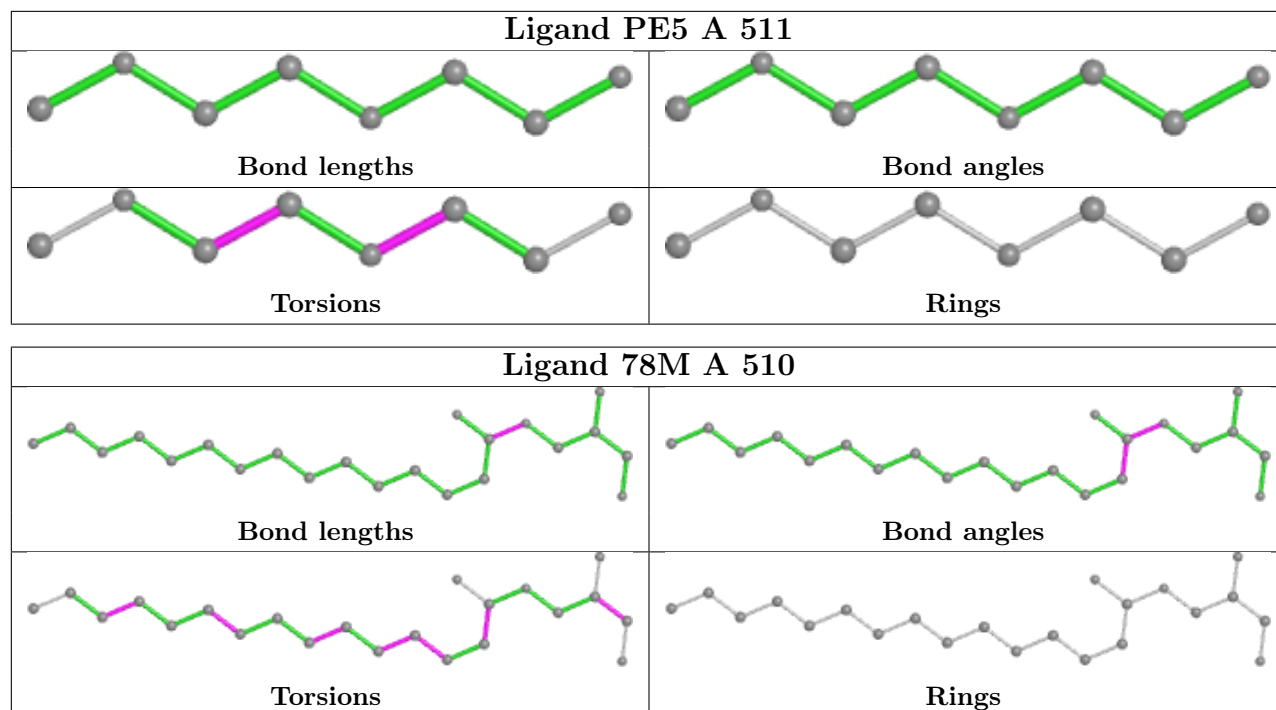
There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	507	78M	2	0
2	A	504	LDA	1	0
4	A	509	78N	1	0
2	A	514	LDA	1	0
5	A	511	PE5	1	0
2	A	506	LDA	2	0
2	A	501	LDA	1	0
3	A	510	78M	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 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 [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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	425/490 (86%)	0.32	21 (4%) 29 26	32, 51, 78, 99	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	VAL	4.5
1	A	195	ASP	3.9
1	A	121	PRO	3.8
1	A	292	THR	3.5
1	A	81	TRP	3.5
1	A	244	LEU	3.5
1	A	455	SER	3.1
1	A	291	THR	3.0
1	A	55	ASP	3.0
1	A	103	THR	2.8
1	A	470	ALA	2.8
1	A	339	ASP	2.6
1	A	237	PRO	2.4
1	A	410	ILE	2.3
1	A	196	GLU	2.3
1	A	469	ASP	2.2
1	A	340	GLY	2.1
1	A	294	ASP	2.1
1	A	488	TRP	2.1
1	A	200	GLU	2.1
1	A	299	ALA	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](#)

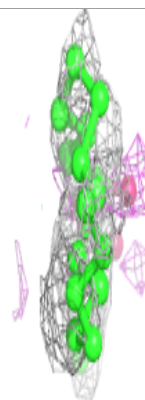
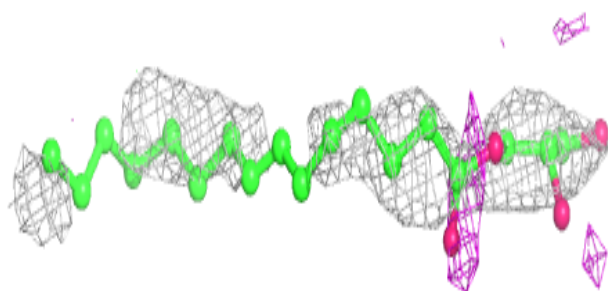
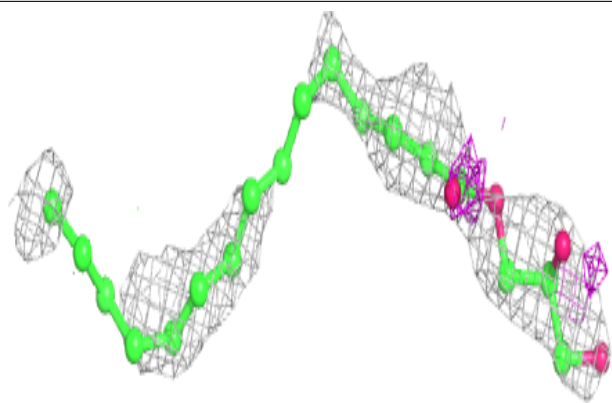
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	78M	A	512	22/22	0.69	0.56	65,67,69,70	0
2	LDA	A	513	16/16	0.72	0.34	60,71,82,82	0
3	78M	A	508	22/22	0.74	0.59	67,70,75,76	0
2	LDA	A	504	16/16	0.76	0.43	55,64,80,80	0
3	78M	A	510	22/22	0.81	0.45	65,71,78,79	0
4	78N	A	509	22/22	0.83	0.39	48,65,77,77	0
2	LDA	A	506	11/16	0.84	0.38	41,45,49,49	0
2	LDA	A	503	11/16	0.84	0.24	48,53,63,63	0
2	LDA	A	505	9/16	0.85	0.26	35,39,47,47	0
2	LDA	A	502	16/16	0.86	0.32	51,58,69,69	0
2	LDA	A	501	16/16	0.86	0.25	31,38,58,59	0
2	LDA	A	514	16/16	0.87	0.37	62,63,67,67	0
3	78M	A	507	22/22	0.89	0.36	32,43,53,54	0
5	PE5	A	511	8/27	0.89	0.34	44,45,45,45	0
6	CA	A	515	1/1	0.89	0.07	54,54,54,54	0

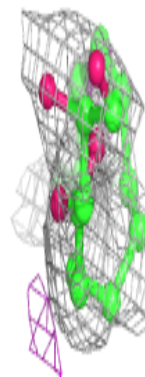
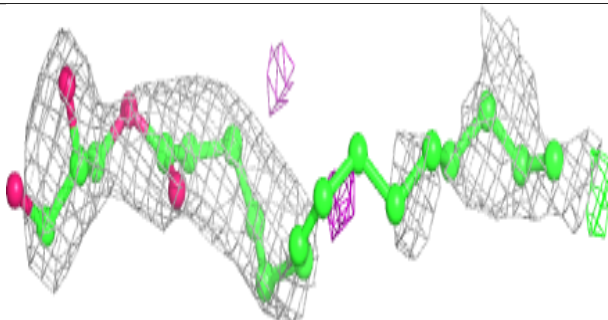
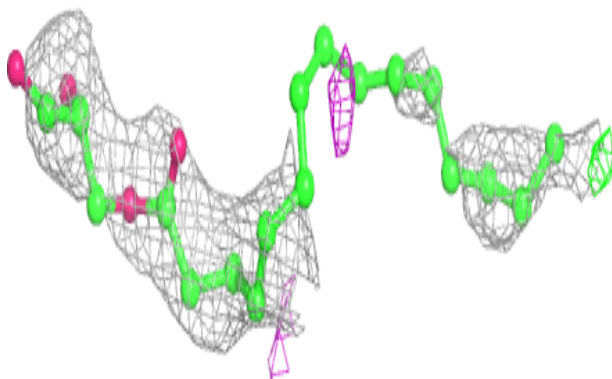
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around 78M A 512:**

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

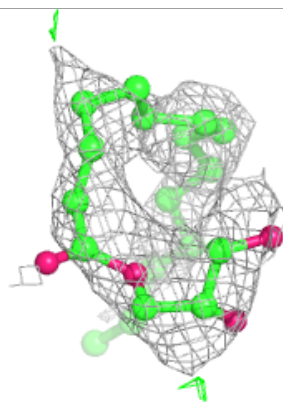
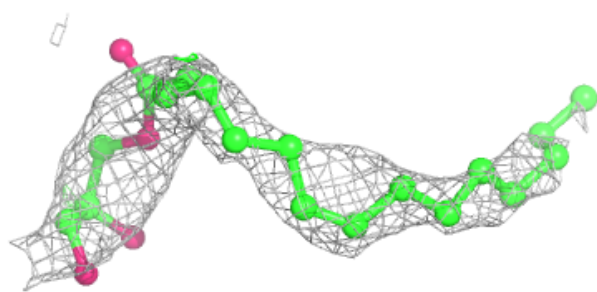
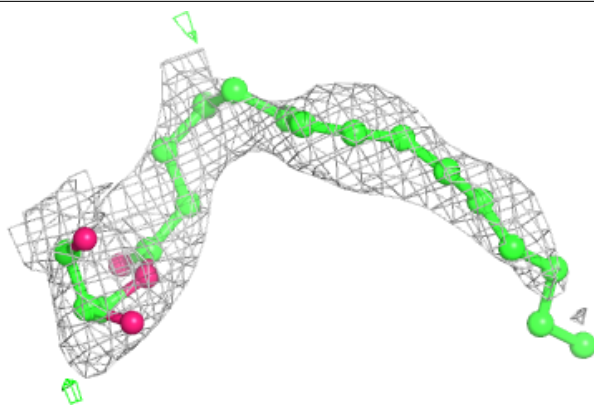
**Electron density around 78M A 508:**

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

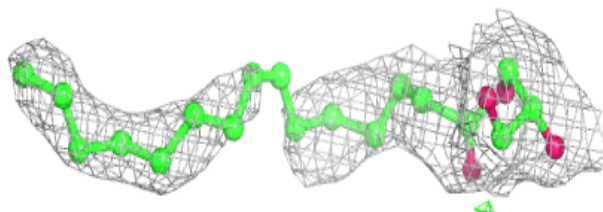
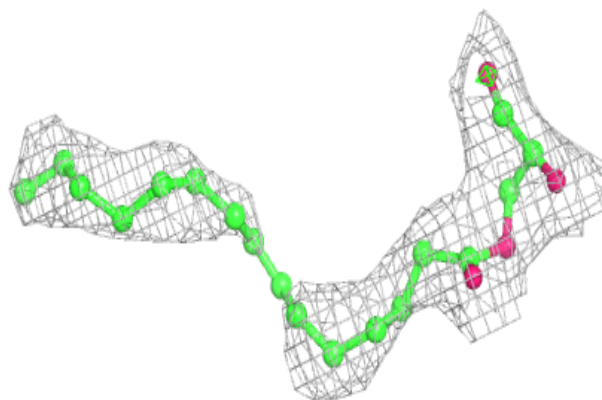


**Electron density around 78M A 510:**

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

**Electron density around 78N A 509:**

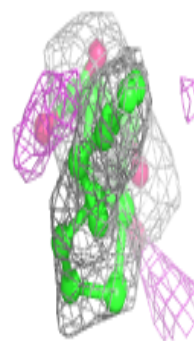
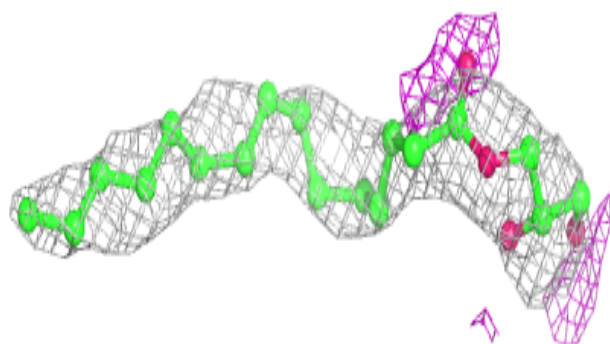
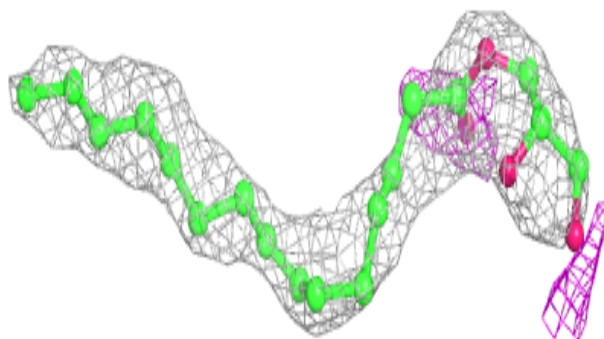
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



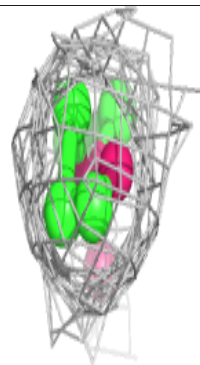
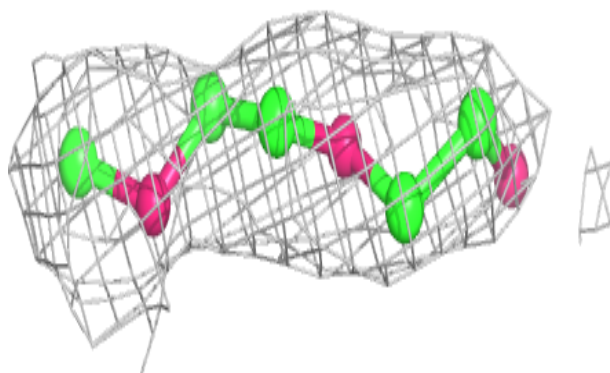
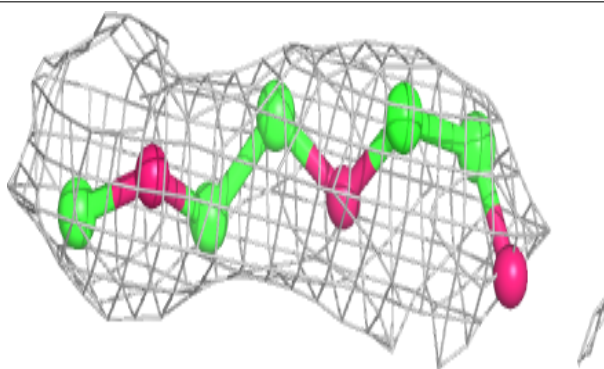


**Electron density around 78M A 507:**

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

**Electron density around PE5 A 511:**

$2mF_o-DF_c$  (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.