



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 07:42 AM EDT

PDB ID : 4XNL / pdb_00004xnl
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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

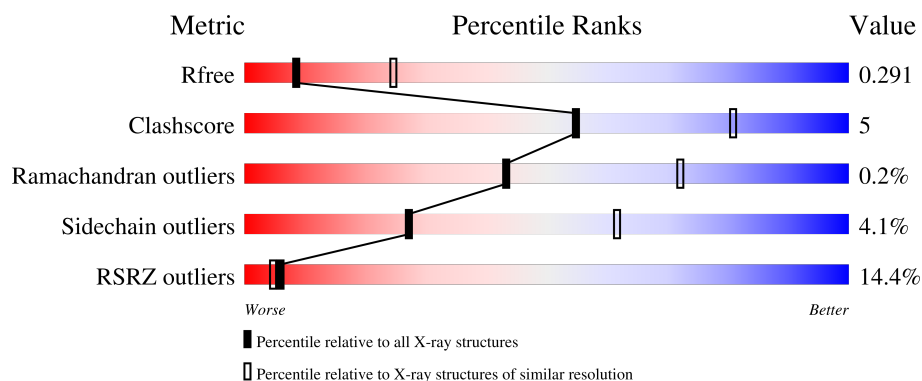
1 Overall quality at a glance

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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 ≥ 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	

2 Entry composition [i](#)

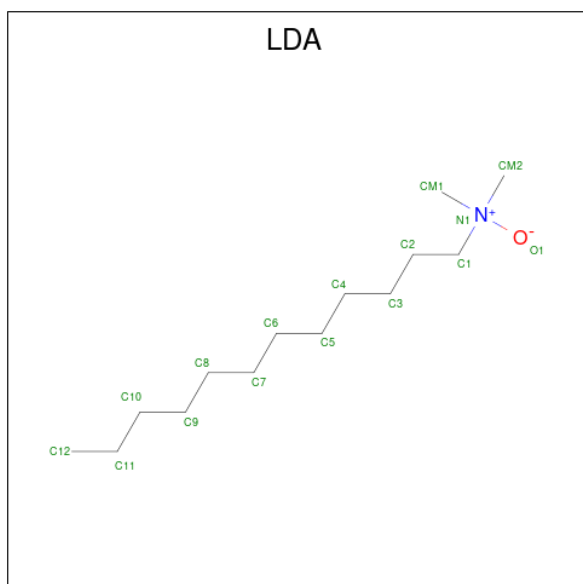
There are 7 unique types of molecules in this entry. The entry contains 3635 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	425	Total	C	N	O	S	0	0	0
			3377	2111	602	661	3			

- Molecule 2 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: $C_{14}H_{31}NO$).



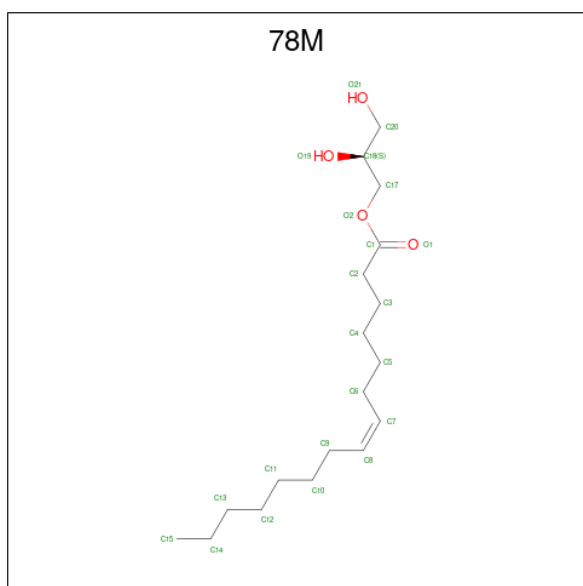
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	A	1	Total	C	N	O	0	0
			11	9	1	1		
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	A	1	Total	C			0	0
			9	9				

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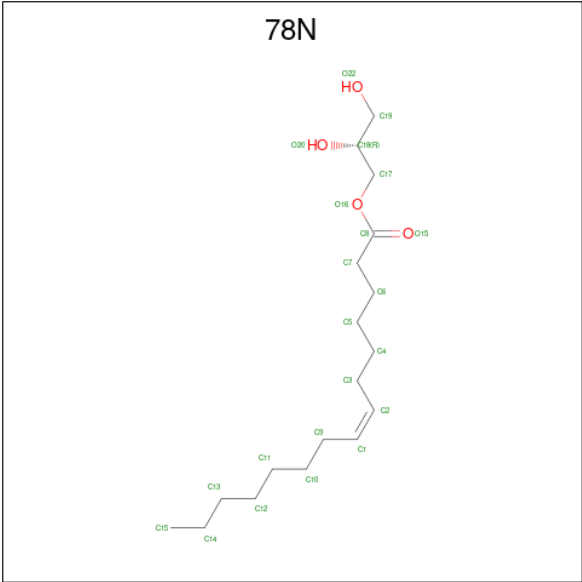
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C			0	0
			11	11				
2	A	1	Total	C	N	O	0	0
			16	14	1	1		
2	A	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 3 is (2S)-2,3-DIHYDROXYPROPYL(7Z)-PENTADEC-7-ENOATE (CCD ID: 78M) (formula: C₁₈H₃₄O₄).



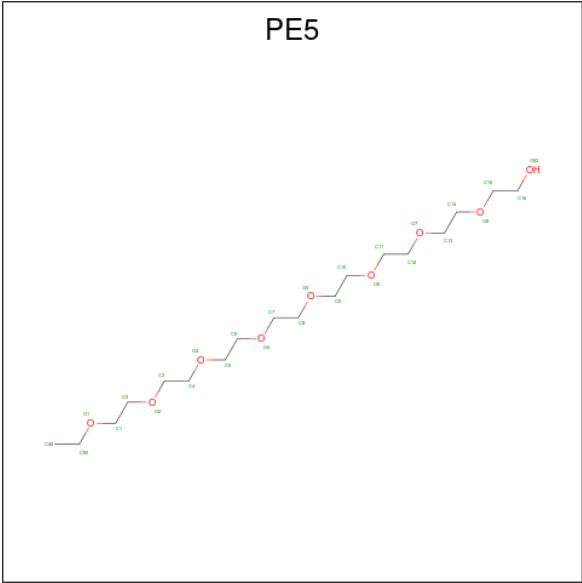
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O		0	0
			22	18	4			
3	A	1	Total	C	O		0	0
			22	18	4			
3	A	1	Total	C	O		0	0
			22	18	4			
3	A	1	Total	C	O		0	0
			22	18	4			

- Molecule 4 is (2R)-2,3-DIHYDROXYPROPYL(7Z)-PENTADEC-7-ENOATE (CCD ID: 78N) (formula: C₁₈H₃₄O₄).



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 (CCD ID: PE5) (formula: C₁₈H₃₈O₉).



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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

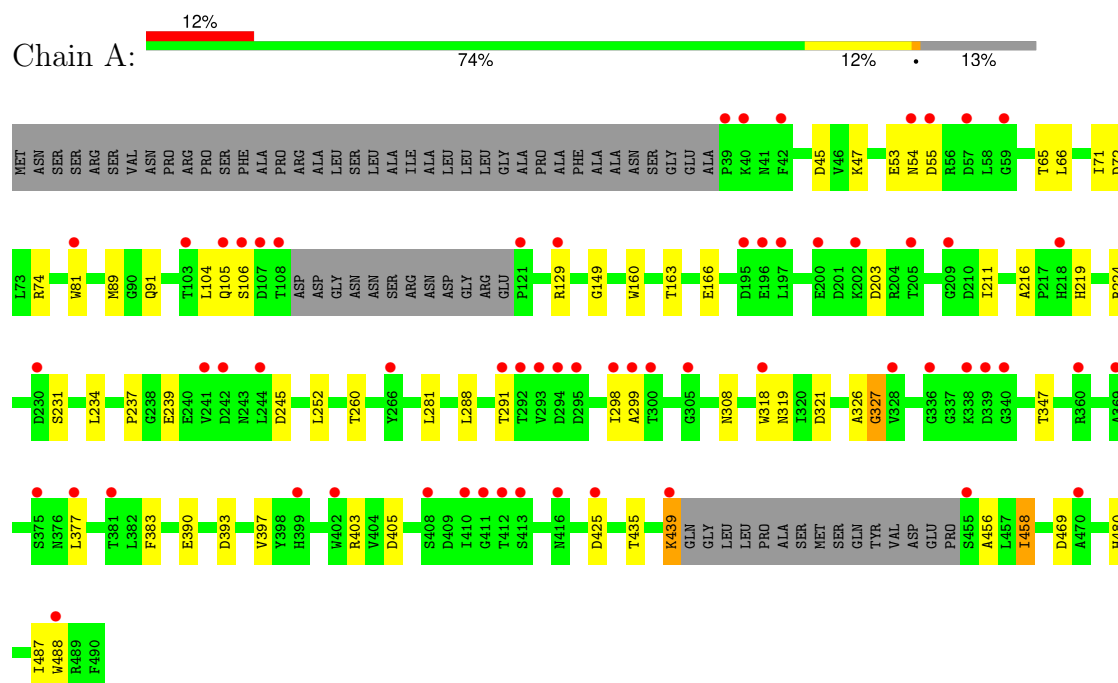
- Molecule 7 is water.

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.251 , 0.287 0.270 , 0.291	Depositor DCC
R_{free} test set	720 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtriage
Anisotropy	0.534	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3635	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

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.

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

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	0.68	0/3462	1.24	11/4693 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	54	ASN	CA-C-N	7.16	135.21	121.54
1	A	54	ASN	C-N-CA	7.16	135.21	121.54
1	A	390	GLU	N-CA-C	-7.15	103.12	112.41
1	A	319	ASN	CA-C-N	5.69	127.94	120.60
1	A	319	ASN	C-N-CA	5.69	127.94	120.60
1	A	393	ASP	CA-CB-CG	5.50	118.10	112.60
1	A	299	ALA	N-CA-C	5.39	117.16	111.28
1	A	291	THR	CA-C-N	5.39	128.25	120.38
1	A	291	THR	C-N-CA	5.39	128.25	120.38
1	A	327	GLY	N-CA-C	5.32	118.75	110.88
1	A	321	ASP	CA-CB-CG	5.04	117.64	112.60

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	32	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	34	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 (34) 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:74:ARG:HB3	1:A:89:MET:HE2	1.84	0.59
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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%)	43 72

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%)	330 (96%)	14 (4%)	27 61

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASP
1	A	65	THR
1	A	104	LEU
1	A	106	SER
1	A	211	ILE
1	A	239	GLU
1	A	245	ASP
1	A	260	THR
1	A	298	ILE
1	A	308	ASN
1	A	377	LEU
1	A	435	THR
1	A	439	LYS
1	A	458	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	105	GLN
1	A	161	GLN
1	A	164	ASN
1	A	185	GLN
1	A	265	ASN
1	A	308	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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	505	-	8,8,15	0.72	0	7,7,17	0.24	0
2	LDA	A	501	-	13,15,15	2.78	2 (15%)	14,17,17	0.48	0
2	LDA	A	506	-	10,10,15	0.74	0	9,9,17	0.24	0
2	LDA	A	504	-	13,15,15	2.82	2 (15%)	14,17,17	0.58	0
3	78M	A	507	-	21,21,21	0.83	1 (4%)	22,22,22	0.70	1 (4%)
2	LDA	A	514	-	13,15,15	2.89	2 (15%)	14,17,17	0.43	0
3	78M	A	510	-	21,21,21	0.84	1 (4%)	22,22,22	0.69	1 (4%)
3	78M	A	512	-	21,21,21	0.82	1 (4%)	22,22,22	0.73	1 (4%)
5	PE5	A	511	-	7,7,26	0.28	0	6,6,25	0.37	0
2	LDA	A	502	-	13,15,15	2.92	2 (15%)	14,17,17	0.74	0
3	78M	A	508	-	21,21,21	0.84	1 (4%)	22,22,22	0.76	1 (4%)
2	LDA	A	503	-	8,10,15	3.42	2 (25%)	9,12,17	0.39	0
4	78N	A	509	-	21,21,21	1.28	1 (4%)	22,22,22	0.90	1 (4%)
2	LDA	A	513	-	13,15,15	2.87	2 (15%)	14,17,17	0.82	1 (7%)

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	505	-	-	5/6/6/13	-
2	LDA	A	501	-	-	8/13/13/13	-
2	LDA	A	506	-	-	7/8/8/13	-
2	LDA	A	504	-	-	7/13/13/13	-
3	78M	A	507	-	-	11/21/21/21	-
2	LDA	A	514	-	-	6/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	78M	A	510	-	-	9/21/21/21	-
3	78M	A	512	-	-	7/21/21/21	-
5	PE5	A	511	-	-	2/5/5/24	-
2	LDA	A	502	-	-	7/13/13/13	-
3	78M	A	508	-	-	11/21/21/21	-
2	LDA	A	503	-	-	6/8/8/13	-
4	78N	A	509	-	-	16/21/21/21	-
2	LDA	A	513	-	-	9/13/13/13	-

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	514	LDA	O1-N1	-8.33	1.21	1.42
2	A	501	LDA	O1-N1	-8.14	1.22	1.42
2	A	504	LDA	O1-N1	-8.13	1.22	1.42
2	A	502	LDA	O1-N1	-8.12	1.22	1.42
2	A	503	LDA	O1-N1	-7.97	1.22	1.42
2	A	513	LDA	O1-N1	-7.97	1.22	1.42
2	A	502	LDA	C1-N1	-6.22	1.45	1.51
2	A	513	LDA	C1-N1	-6.07	1.45	1.51
2	A	514	LDA	C1-N1	-5.70	1.45	1.51
2	A	504	LDA	C1-N1	-5.54	1.45	1.51
2	A	501	LDA	C1-N1	-5.31	1.46	1.51
2	A	503	LDA	C1-N1	-5.04	1.46	1.51
4	A	509	78N	O16-C8	4.53	1.46	1.33
3	A	510	78M	O2-C1	3.33	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	3.14	121.40	111.83
3	A	508	78M	O2-C1-C2	2.72	120.12	111.83
3	A	512	78M	O2-C1-C2	2.56	119.65	111.83
3	A	510	78M	O2-C1-C2	2.51	119.47	111.83
3	A	507	78M	O2-C1-C2	2.42	119.20	111.83
2	A	513	LDA	O1-N1-C1	2.06	114.32	109.27

There are no chirality outliers.

All (111) 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
3	A	508	78M	O1-C1-O2-C17
5	A	511	PE5	O2-C3-C4-O3
3	A	508	78M	C1-C2-C3-C4
3	A	507	78M	C1-C2-C3-C4
4	A	509	78N	O16-C17-C18-C19
2	A	501	LDA	C5-C6-C7-C8
2	A	506	LDA	C5-C6-C7-C8
3	A	507	78M	C9-C10-C11-C12
2	A	502	LDA	C7-C8-C9-C10
3	A	510	78M	C11-C12-C13-C14
2	A	504	LDA	C5-C6-C7-C8
2	A	501	LDA	C4-C5-C6-C7
3	A	507	78M	C10-C11-C12-C13
2	A	514	LDA	C5-C6-C7-C8
4	A	509	78N	C9-C10-C11-C12
2	A	514	LDA	C7-C8-C9-C10
2	A	514	LDA	C11-C10-C9-C8
2	A	513	LDA	C3-C4-C5-C6
2	A	505	LDA	C5-C6-C7-C8
2	A	513	LDA	C2-C3-C4-C5
3	A	508	78M	C9-C10-C11-C12
4	A	509	78N	C3-C4-C5-C6

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

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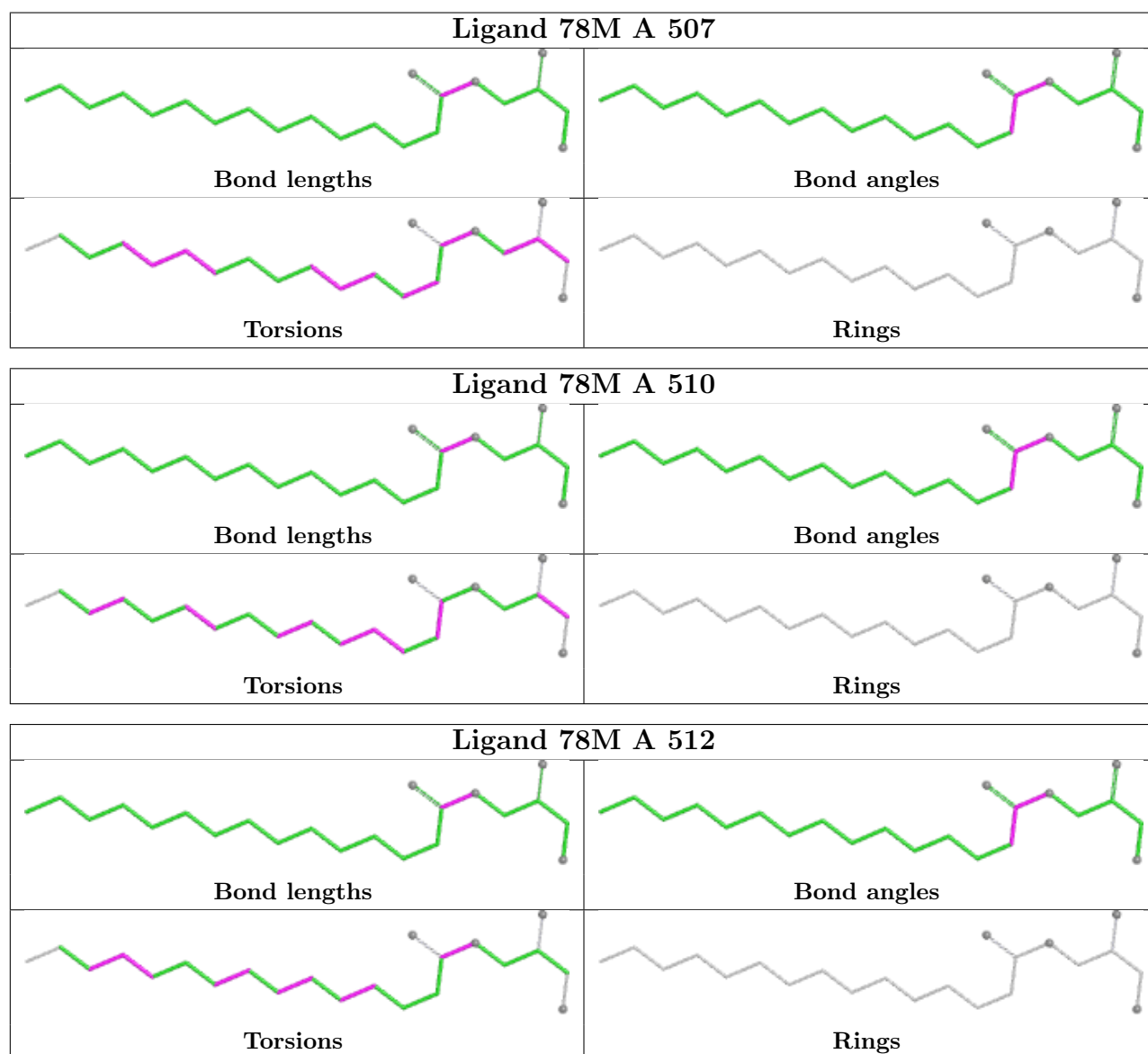
Mol	Chain	Res	Type	Atoms
2	A	505	LDA	C3-C4-C5-C6
3	A	508	78M	C3-C4-C5-C6
4	A	509	78N	C11-C10-C9-C1
2	A	502	LDA	C2-C3-C4-C5
2	A	503	LDA	C2-C1-N1-CM1
5	A	511	PE5	C1-C2-O2-C3
2	A	513	LDA	C9-C10-C11-C12
2	A	503	LDA	N1-C1-C2-C3
2	A	502	LDA	C1-C2-C3-C4
3	A	507	78M	O1-C1-O2-C17
2	A	506	LDA	C7-C8-C9-C10
3	A	507	78M	C2-C1-O2-C17
3	A	510	78M	C11-C10-C9-C8
3	A	512	78M	C7-C8-C9-C10
2	A	505	LDA	C6-C7-C8-C9
3	A	507	78M	C4-C5-C6-C7
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	C5-C6-C7-C8
3	A	512	78M	C5-C6-C7-C8
4	A	509	78N	C1-C2-C3-C4
3	A	510	78M	O2-C1-C2-C3
2	A	505	LDA	C1-C2-C3-C4
4	A	509	78N	C6-C7-C8-O16
2	A	506	LDA	C4-C5-C6-C7
2	A	503	LDA	C2-C1-N1-O1
2	A	513	LDA	C2-C1-N1-O1
3	A	510	78M	O1-C1-C2-C3

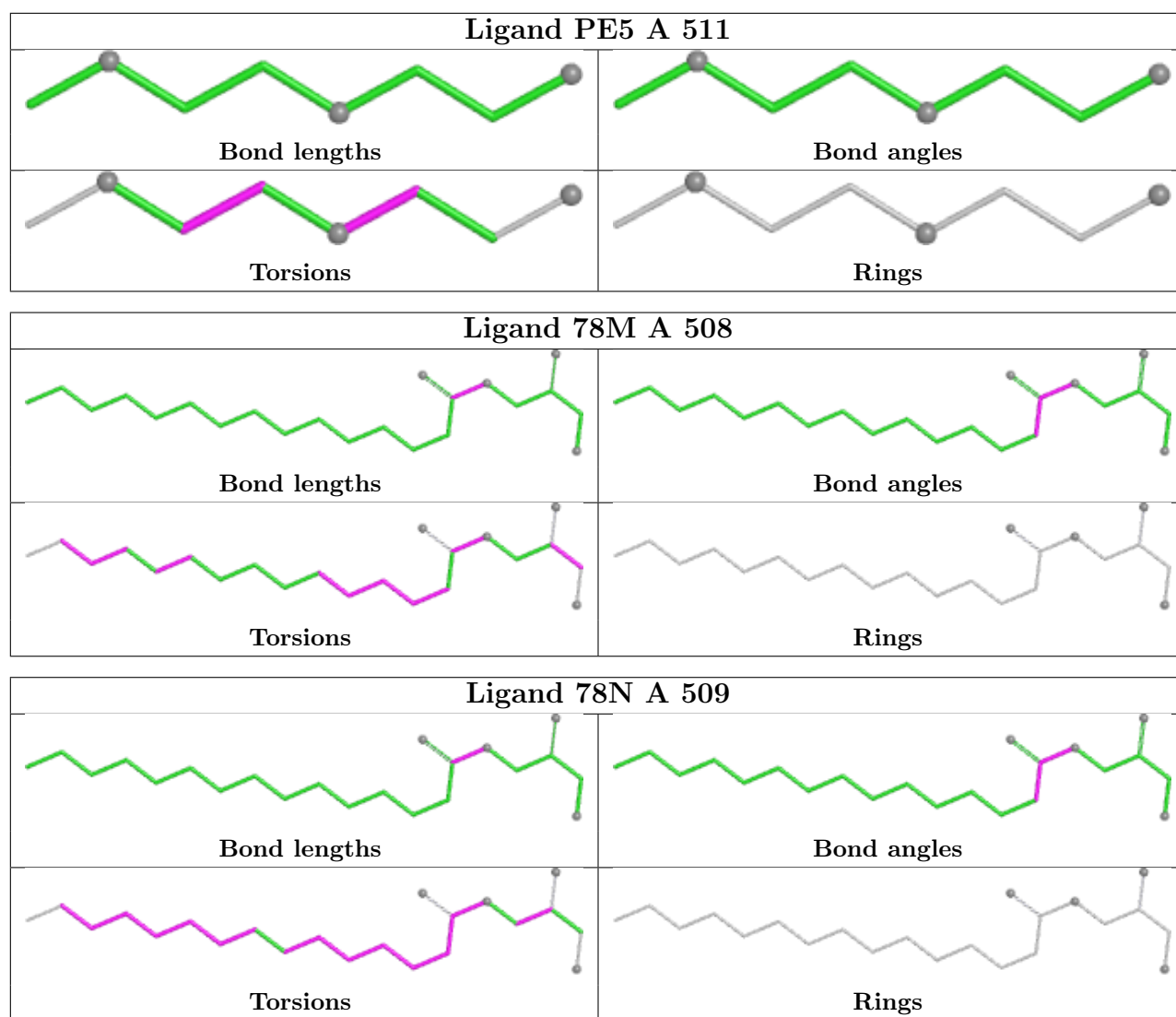
There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	LDA	1	0
2	A	506	LDA	2	0
2	A	504	LDA	1	0
3	A	507	78M	2	0
2	A	514	LDA	1	0
3	A	510	78M	1	0
5	A	511	PE5	1	0
4	A	509	78N	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 ⓘ

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, 95th 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	425/490 (86%)	1.07	61 (14%) 6 5	32, 51, 78, 99	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	VAL	6.1
1	A	81	TRP	5.9
1	A	121	PRO	4.4
1	A	55	ASP	4.2
1	A	108	THR	4.2
1	A	339	ASP	4.2
1	A	57	ASP	4.2
1	A	291	THR	4.1
1	A	292	THR	3.9
1	A	244	LEU	3.7
1	A	411	GLY	3.7
1	A	103	THR	3.6
1	A	59	GLY	3.5
1	A	338	LYS	3.4
1	A	241	VAL	3.4
1	A	54	ASN	3.2
1	A	425	ASP	3.2
1	A	266	TYR	3.1
1	A	294	ASP	3.1
1	A	106	SER	2.9
1	A	197	LEU	2.8
1	A	402	TRP	2.8
1	A	39	PRO	2.8
1	A	42	PHE	2.7
1	A	340	GLY	2.7
1	A	455	SER	2.7
1	A	381	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	439	LYS	2.6
1	A	298	ILE	2.6
1	A	195	ASP	2.6
1	A	230	ASP	2.6
1	A	299	ALA	2.6
1	A	375	SER	2.6
1	A	377	LEU	2.6
1	A	209	GLY	2.5
1	A	318	TRP	2.5
1	A	408	SER	2.5
1	A	129	ARG	2.5
1	A	416	ASN	2.4
1	A	107	ASP	2.3
1	A	196	GLU	2.3
1	A	200	GLU	2.3
1	A	369	ALA	2.3
1	A	410	ILE	2.3
1	A	205	THR	2.3
1	A	412	THR	2.3
1	A	305	GLY	2.3
1	A	488	TRP	2.2
1	A	470	ALA	2.2
1	A	300	THR	2.2
1	A	336	GLY	2.2
1	A	399	HIS	2.2
1	A	328	VAL	2.1
1	A	413	SER	2.1
1	A	360	ARG	2.1
1	A	242	ASP	2.1
1	A	218	HIS	2.1
1	A	40	LYS	2.1
1	A	105	GLN	2.0
1	A	202	LYS	2.0
1	A	295	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

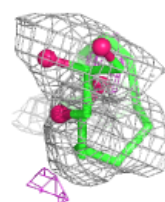
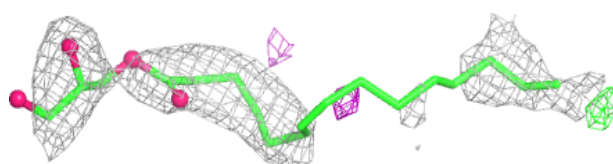
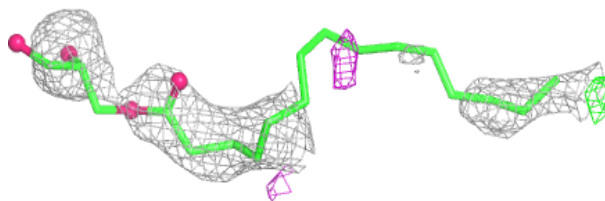
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	78M	A	508	22/22	0.64	0.25	67,70,75,76	0
3	78M	A	512	22/22	0.68	0.26	65,67,69,70	0
2	LDA	A	502	16/16	0.70	0.21	51,58,69,69	0
2	LDA	A	513	16/16	0.71	0.22	60,71,82,82	0
2	LDA	A	503	11/16	0.75	0.21	48,53,63,63	0
4	78N	A	509	22/22	0.78	0.18	48,65,77,77	0
2	LDA	A	501	16/16	0.80	0.18	31,38,58,59	0
2	LDA	A	506	11/16	0.80	0.17	41,45,49,49	0
3	78M	A	510	22/22	0.81	0.21	65,71,78,79	0
2	LDA	A	505	9/16	0.82	0.17	35,39,47,47	0
2	LDA	A	504	16/16	0.83	0.23	55,64,80,80	0
2	LDA	A	514	16/16	0.84	0.21	62,63,67,67	0
3	78M	A	507	22/22	0.84	0.17	32,43,53,54	0
5	PE5	A	511	8/27	0.91	0.15	44,45,45,45	0
6	CA	A	515	1/1	0.95	0.06	54,54,54,54	0

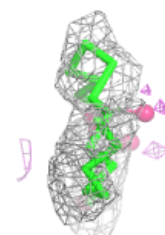
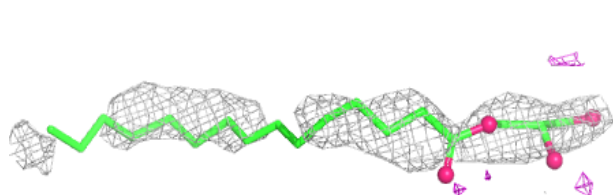
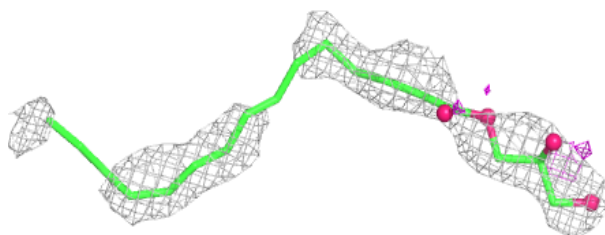
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 78M A 508:

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

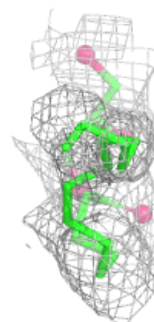
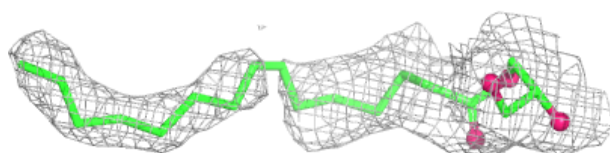
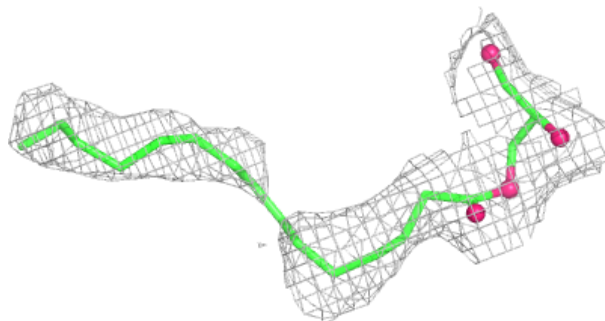
**Electron density around 78M A 512:**

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

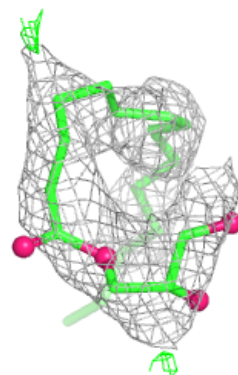
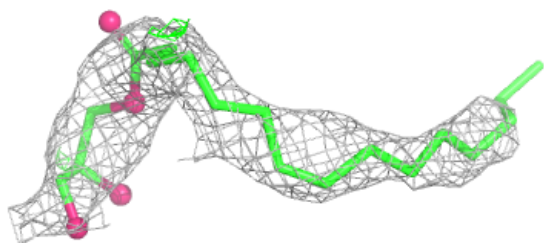
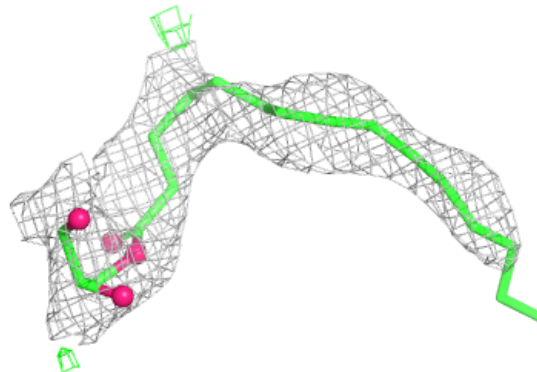


Electron density around 78N A 509:

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

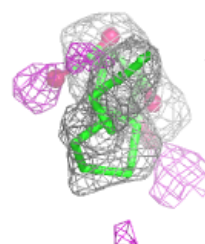
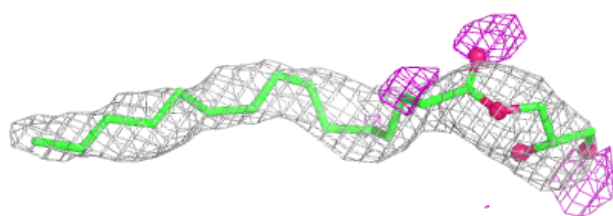
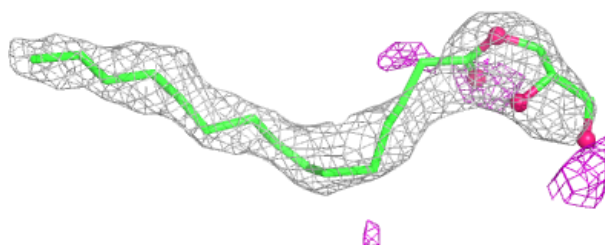
**Electron density around 78M A 510:**

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

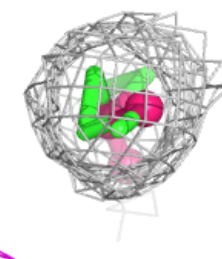
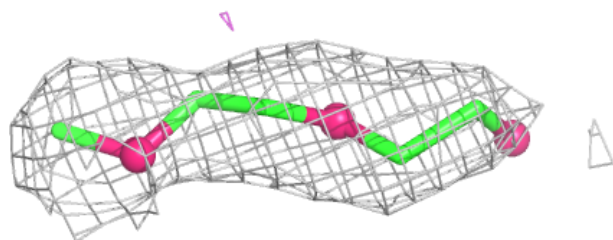
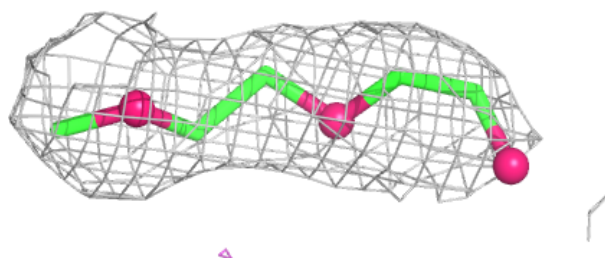


Electron density around 78M A 507:

$2mF_o-DF_c$ (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.