



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 02:47 PM BST

PDB ID : 5EGF
Title : The crystal structure of SeMet-CT
Authors : Zhang, J.R.; Tang, Y.; Zhou, J.H.
Deposited on : 2015-10-27
Resolution : 2.29 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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) : 2.13.1

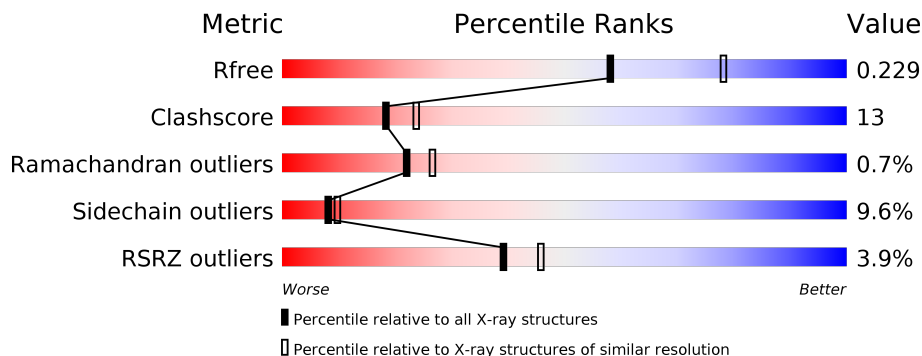
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 on 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	486	 3% 65% 23% 9%
1	B	486	 3% 68% 21% 9%
1	C	486	 4% 62% 25% 9%
1	D	486	 4% 63% 25% 9%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	EDO	A	504	-	-	X	-
2	EDO	B	502	-	-	X	-
2	EDO	B	506	-	-	X	-
2	EDO	B	508	-	-	X	-
2	EDO	C	501	-	-	X	-
2	EDO	C	504	-	-	X	-
2	EDO	C	508	-	-	-	X
2	EDO	D	505	-	-	-	X
3	C8E	A	508	-	-	X	-
3	C8E	B	512	-	-	X	-
3	C8E	C	509	-	-	X	-
3	C8E	D	511	-	-	X	-

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 14879 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 TqaA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	442	3529	2257	609	650	7	6	0	1	0
1	B	443	3527	2252	609	653	7	6	0	1	0
1	C	444	3544	2265	612	654	7	6	0	2	0
1	D	442	3529	2257	609	650	7	6	0	1	0

There are 32 discrepancies between the modelled and reference sequences:

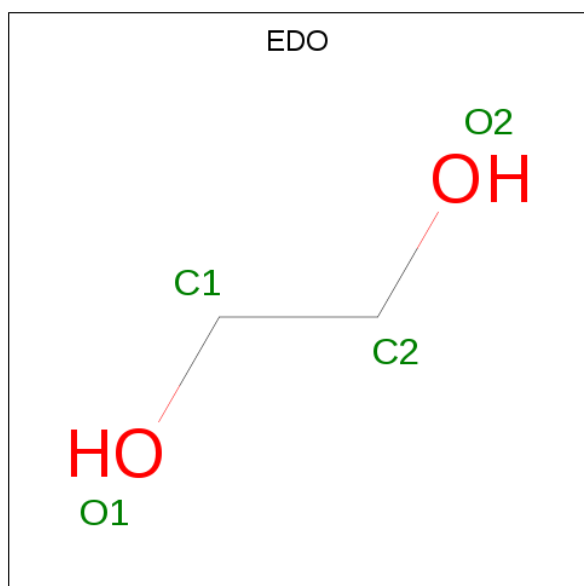
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	HIS	-	expression tag	UNP F1CWE4
A	3	HIS	-	expression tag	UNP F1CWE4
A	4	HIS	-	expression tag	UNP F1CWE4
A	5	HIS	-	expression tag	UNP F1CWE4
A	6	HIS	-	expression tag	UNP F1CWE4
A	7	HIS	-	expression tag	UNP F1CWE4
A	35	ALA	LYS	engineered mutation	UNP F1CWE4
A	36	ALA	GLU	engineered mutation	UNP F1CWE4
B	2	HIS	-	expression tag	UNP F1CWE4
B	3	HIS	-	expression tag	UNP F1CWE4
B	4	HIS	-	expression tag	UNP F1CWE4
B	5	HIS	-	expression tag	UNP F1CWE4
B	6	HIS	-	expression tag	UNP F1CWE4
B	7	HIS	-	expression tag	UNP F1CWE4
B	35	ALA	LYS	engineered mutation	UNP F1CWE4
B	36	ALA	GLU	engineered mutation	UNP F1CWE4
C	2	HIS	-	expression tag	UNP F1CWE4
C	3	HIS	-	expression tag	UNP F1CWE4
C	4	HIS	-	expression tag	UNP F1CWE4
C	5	HIS	-	expression tag	UNP F1CWE4
C	6	HIS	-	expression tag	UNP F1CWE4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	7	HIS	-	expression tag	UNP F1CWE4
C	35	ALA	LYS	engineered mutation	UNP F1CWE4
C	36	ALA	GLU	engineered mutation	UNP F1CWE4
D	2	HIS	-	expression tag	UNP F1CWE4
D	3	HIS	-	expression tag	UNP F1CWE4
D	4	HIS	-	expression tag	UNP F1CWE4
D	5	HIS	-	expression tag	UNP F1CWE4
D	6	HIS	-	expression tag	UNP F1CWE4
D	7	HIS	-	expression tag	UNP F1CWE4
D	35	ALA	LYS	engineered mutation	UNP F1CWE4
D	36	ALA	GLU	engineered mutation	UNP F1CWE4

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0

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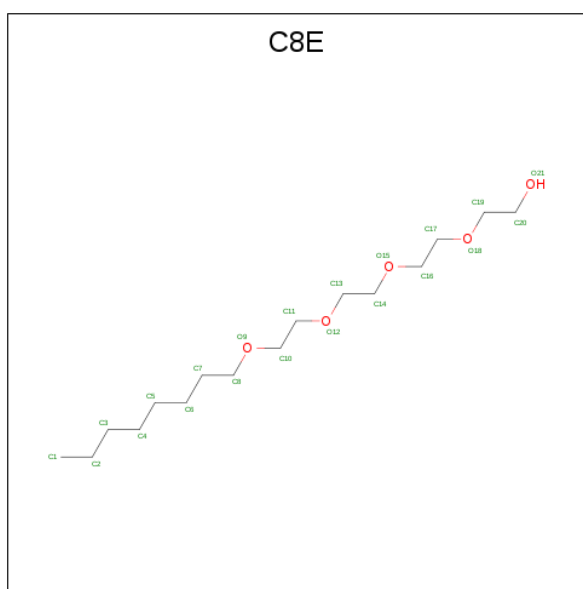
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	B	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	C	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0
2	D	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0

- Molecule 3 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: C₁₆H₃₄O₅).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 21 16 5	0	0
3	B	1	Total C O 21 16 5	0	0
3	C	1	Total C O 21 16 5	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			21	16	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	115	Total	O	0	0
			115	115		
4	B	179	Total	O	0	0
			179	179		
4	C	134	Total	O	0	0
			134	134		
4	D	98	Total	O	0	0
			98	98		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	216.60Å 100.28Å 128.23Å 90.00° 100.18° 90.00°	Depositor
Resolution (Å)	29.75 – 2.29 29.75 – 2.29	Depositor EDS
% Data completeness (in resolution range)	85.4 (29.75-2.29) 85.1 (29.75-2.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.94 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.7_650	Depositor
R, R_{free}	0.225 , 0.266 0.226 , 0.229	Depositor DCC
R_{free} test set	1880 reflections (1.66%)	wwPDB-VP
Wilson B-factor (Å ²)	42.5	Xtrriage
Anisotropy	0.411	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14879	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.42% 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: C8E, EDO

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	0.45	0/3626	0.61	0/4946
1	B	0.50	0/3623	0.63	1/4941 (0.0%)
1	C	0.44	0/3645	0.58	0/4970
1	D	0.41	0/3626	0.57	0/4946
All	All	0.45	0/14520	0.60	1/19803 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	247	ALA	N-CA-C	5.09	124.74	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	484	ASP	Peptide
1	B	247	ALA	Peptide

5.2 Too-close contacts

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	3529	0	3454	89	0
1	B	3527	0	3452	78	0
1	C	3544	0	3466	100	0
1	D	3529	0	3454	96	0
2	A	28	0	42	9	0
2	B	40	0	60	20	0
2	C	32	0	48	16	0
2	D	40	0	60	9	0
3	A	21	0	34	9	0
3	B	21	0	34	16	0
3	C	21	0	34	12	0
3	D	21	0	34	9	0
4	A	115	0	0	2	0
4	B	179	0	0	6	0
4	C	134	0	0	9	0
4	D	98	0	0	5	0
All	All	14879	0	14172	378	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 13.

The worst 5 of 378 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)
2:B:502:EDO:H11	3:B:512:C8E:H13	1.34	1.08
2:C:501:EDO:H21	3:C:509:C8E:H81	1.36	1.02
2:B:502:EDO:H22	3:B:512:C8E:H32	1.44	0.99
1:B:95:ARG:HH21	1:B:203:LEU:HB3	1.25	0.98
1:D:56:THR:HG22	1:D:59:GLN:H	1.30	0.97

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	437/486 (90%)	410 (94%)	24 (6%)	3 (1%)	22	26
1	B	438/486 (90%)	413 (94%)	21 (5%)	4 (1%)	17	20
1	C	440/486 (90%)	415 (94%)	22 (5%)	3 (1%)	22	26
1	D	437/486 (90%)	412 (94%)	22 (5%)	3 (1%)	22	26
All	All	1752/1944 (90%)	1650 (94%)	89 (5%)	13 (1%)	22	26

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	341	ASP
1	B	247	ALA
1	B	249	ARG
1	D	247	ALA
1	B	485	ILE

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	397/424 (94%)	357 (90%)	40 (10%)	7	9
1	B	398/424 (94%)	366 (92%)	32 (8%)	12	15
1	C	400/424 (94%)	357 (89%)	43 (11%)	6	7
1	D	397/424 (94%)	360 (91%)	37 (9%)	9	10
All	All	1592/1696 (94%)	1440 (90%)	152 (10%)	8	10

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	430	LEU
1	C	155	SER
1	D	374	GLN
1	B	482	LEU
1	C	83	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	390	GLN
1	C	168	ASN
1	D	390	GLN
1	C	31	GLN
1	C	170	HIS

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](#)

39 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	D	510	-	3,3,3	0.54	0	2,2,2	0.57	0
2	EDO	B	506	-	3,3,3	0.38	0	2,2,2	0.34	0
3	C8E	D	511	-	20,20,20	0.46	0	19,19,19	0.41	0
2	EDO	C	506	-	3,3,3	0.46	0	2,2,2	0.26	0
2	EDO	D	502	-	3,3,3	0.50	0	2,2,2	0.27	0
2	EDO	C	507	-	3,3,3	0.53	0	2,2,2	0.20	0
2	EDO	C	502	-	3,3,3	0.50	0	2,2,2	0.24	0
2	EDO	B	505	-	3,3,3	0.48	0	2,2,2	0.33	0
2	EDO	C	503	-	3,3,3	0.49	0	2,2,2	0.22	0
2	EDO	A	503	-	3,3,3	0.57	0	2,2,2	0.11	0
2	EDO	D	508	-	3,3,3	0.52	0	2,2,2	0.33	0
2	EDO	D	503	-	3,3,3	0.57	0	2,2,2	0.14	0
2	EDO	B	507	-	3,3,3	0.54	0	2,2,2	0.19	0
2	EDO	A	502	-	3,3,3	0.54	0	2,2,2	0.18	0
3	C8E	A	508	-	20,20,20	0.43	0	19,19,19	0.39	0
2	EDO	C	508	-	3,3,3	0.50	0	2,2,2	0.32	0
2	EDO	D	501	-	3,3,3	0.50	0	2,2,2	0.32	0
2	EDO	B	501	-	3,3,3	0.54	0	2,2,2	0.28	0
2	EDO	D	505	-	3,3,3	0.53	0	2,2,2	0.22	0
2	EDO	A	505	-	3,3,3	0.63	0	2,2,2	0.15	0
2	EDO	C	505	-	3,3,3	0.48	0	2,2,2	0.34	0
2	EDO	D	507	-	3,3,3	0.51	0	2,2,2	0.16	0
2	EDO	B	511	-	3,3,3	0.51	0	2,2,2	0.37	0
3	C8E	B	512	-	20,20,20	0.34	0	19,19,19	0.64	0
2	EDO	D	506	-	3,3,3	0.48	0	2,2,2	0.26	0
3	C8E	C	509	-	20,20,20	0.40	0	19,19,19	0.76	0
2	EDO	D	509	-	3,3,3	0.50	0	2,2,2	0.29	0
2	EDO	C	501	-	3,3,3	0.47	0	2,2,2	0.26	0
2	EDO	B	503	-	3,3,3	0.64	0	2,2,2	0.12	0
2	EDO	B	508	-	3,3,3	0.69	0	2,2,2	0.10	0
2	EDO	A	506	-	3,3,3	0.48	0	2,2,2	0.33	0
2	EDO	B	502	-	3,3,3	0.41	0	2,2,2	0.34	0
2	EDO	A	507	-	3,3,3	0.50	0	2,2,2	0.27	0
2	EDO	C	504	-	3,3,3	0.63	0	2,2,2	0.20	0
2	EDO	D	504	-	3,3,3	0.55	0	2,2,2	0.14	0
2	EDO	A	504	-	3,3,3	0.46	0	2,2,2	0.40	0
2	EDO	B	504	-	3,3,3	0.72	0	2,2,2	0.16	0
2	EDO	B	509	-	3,3,3	0.54	0	2,2,2	0.25	0
2	EDO	A	501	-	3,3,3	0.56	0	2,2,2	0.21	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
2	EDO	D	510	-	-	1/1/1/1	-
2	EDO	B	506	-	-	0/1/1/1	-
3	C8E	D	511	-	-	13/18/18/18	-
2	EDO	C	506	-	-	1/1/1/1	-
2	EDO	D	502	-	-	1/1/1/1	-
2	EDO	C	507	-	-	0/1/1/1	-
2	EDO	C	502	-	-	0/1/1/1	-
2	EDO	B	505	-	-	1/1/1/1	-
2	EDO	C	503	-	-	0/1/1/1	-
2	EDO	A	503	-	-	1/1/1/1	-
2	EDO	D	508	-	-	0/1/1/1	-
2	EDO	D	503	-	-	0/1/1/1	-
2	EDO	B	507	-	-	1/1/1/1	-
2	EDO	A	502	-	-	0/1/1/1	-
3	C8E	A	508	-	-	9/18/18/18	-
2	EDO	C	508	-	-	1/1/1/1	-
2	EDO	D	501	-	-	1/1/1/1	-
2	EDO	B	501	-	-	0/1/1/1	-
2	EDO	D	505	-	-	1/1/1/1	-
2	EDO	A	505	-	-	1/1/1/1	-
2	EDO	C	505	-	-	0/1/1/1	-
2	EDO	D	507	-	-	0/1/1/1	-
2	EDO	B	511	-	-	1/1/1/1	-
3	C8E	B	512	-	-	10/18/18/18	-
2	EDO	D	506	-	-	1/1/1/1	-
3	C8E	C	509	-	-	12/18/18/18	-
2	EDO	D	509	-	-	1/1/1/1	-
2	EDO	C	501	-	-	0/1/1/1	-
2	EDO	B	503	-	-	0/1/1/1	-
2	EDO	B	508	-	-	1/1/1/1	-
2	EDO	A	506	-	-	0/1/1/1	-
2	EDO	B	502	-	-	0/1/1/1	-
2	EDO	A	507	-	-	1/1/1/1	-
2	EDO	C	504	-	-	1/1/1/1	-
2	EDO	D	504	-	-	1/1/1/1	-
2	EDO	A	504	-	-	0/1/1/1	-
2	EDO	B	504	-	-	0/1/1/1	-
2	EDO	B	509	-	-	1/1/1/1	-
2	EDO	A	501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 62 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	509	C8E	O9-C10-C11-O12
3	D	511	C8E	O12-C13-C14-O15
3	A	508	C8E	C6-C7-C8-O9
3	D	511	C8E	C6-C7-C8-O9
3	D	511	C8E	O18-C19-C20-O21

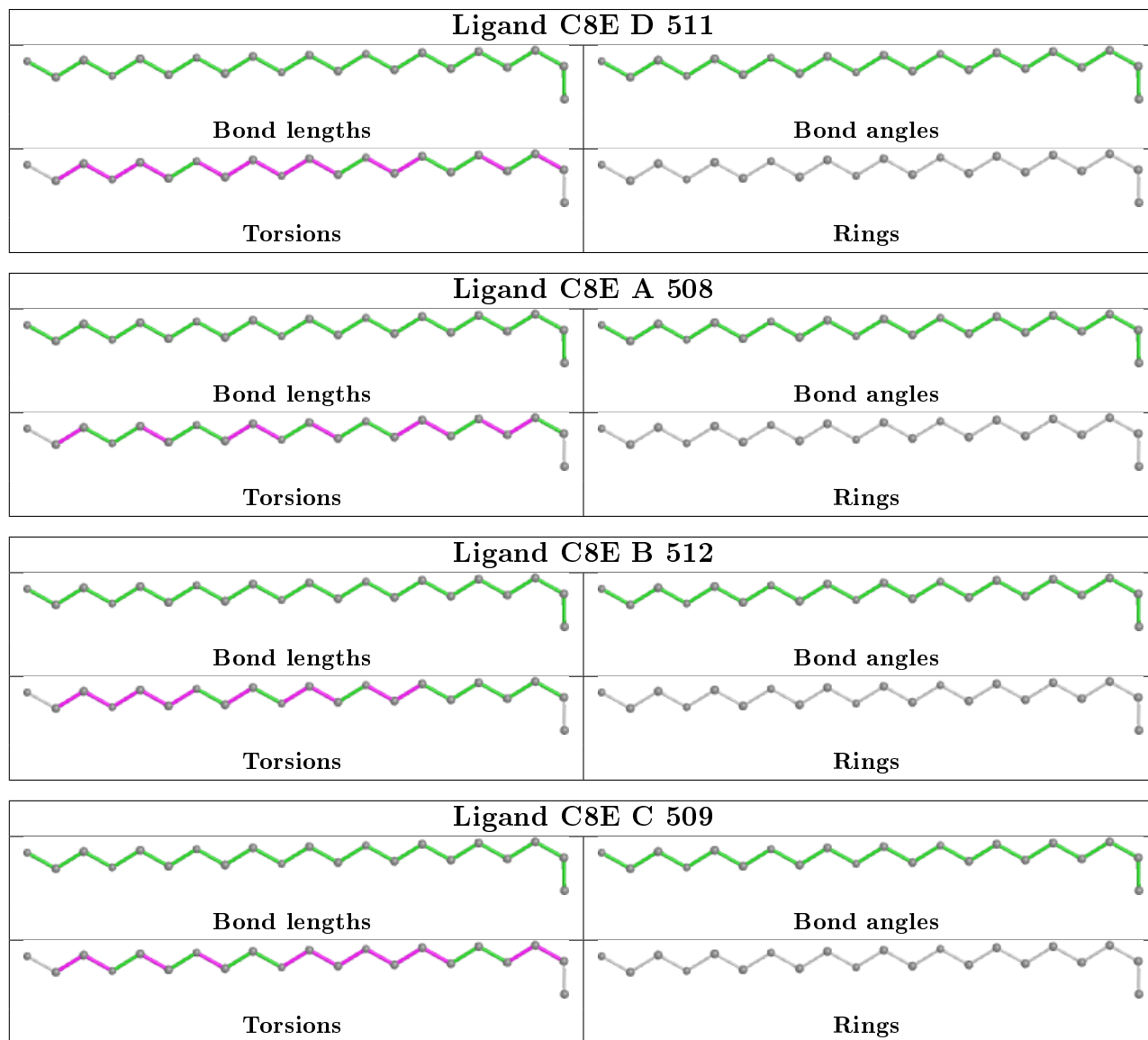
There are no ring outliers.

25 monomers are involved in 75 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	510	EDO	1	0
2	B	506	EDO	6	0
3	D	511	C8E	9	0
2	C	506	EDO	1	0
2	D	502	EDO	1	0
2	C	502	EDO	1	0
2	B	505	EDO	3	0
2	A	503	EDO	3	0
2	D	508	EDO	1	0
2	D	503	EDO	3	0
3	A	508	C8E	9	0
2	A	505	EDO	1	0
2	C	505	EDO	1	0
2	D	507	EDO	1	0
3	B	512	C8E	16	0
2	D	506	EDO	1	0
3	C	509	C8E	12	0
2	C	501	EDO	9	0
2	B	508	EDO	4	0
2	A	506	EDO	1	0
2	B	502	EDO	6	0
2	C	504	EDO	4	0
2	D	504	EDO	1	0
2	A	504	EDO	4	0
2	B	504	EDO	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

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, 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	436/486 (89%)	0.12	15 (3%) 45 52	31, 53, 85, 153	0
1	B	437/486 (89%)	0.06	17 (3%) 39 46	25, 44, 79, 139	0
1	C	438/486 (90%)	0.15	18 (4%) 37 44	27, 50, 92, 144	0
1	D	436/486 (89%)	0.17	19 (4%) 34 41	34, 56, 91, 133	0
All	All	1747/1944 (89%)	0.12	69 (3%) 39 46	25, 51, 88, 153	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	342	SER	5.0
1	C	485	ILE	4.5
1	D	486	THR	3.8
1	D	485	ILE	3.8
1	C	28	LYS	3.7

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](#)

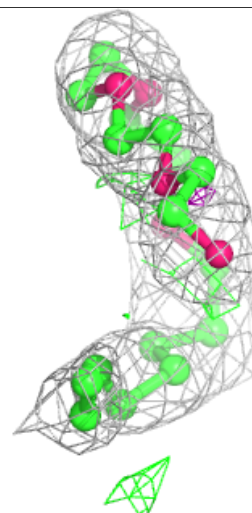
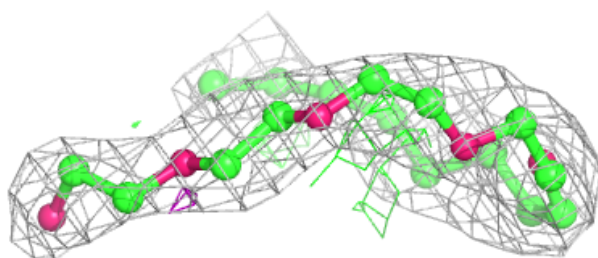
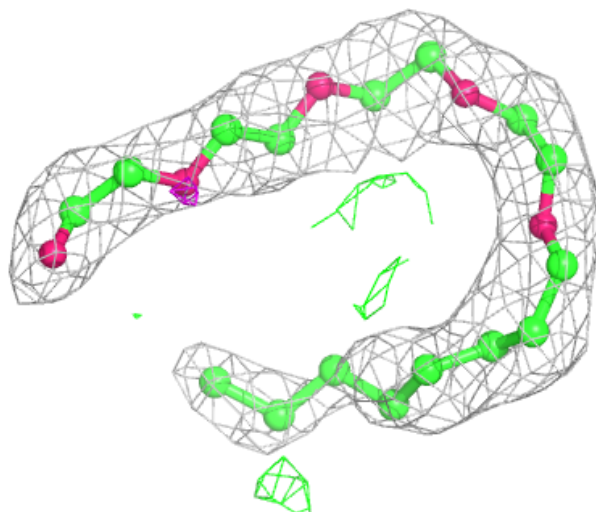
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	EDO	D	505	4/4	0.56	0.40	91,91,91,91	0
2	EDO	D	504	4/4	0.62	0.30	68,68,68,68	0
2	EDO	D	509	4/4	0.64	0.25	85,85,85,85	0
2	EDO	C	508	4/4	0.66	0.45	82,82,82,82	0
2	EDO	D	506	4/4	0.68	0.38	83,83,83,83	0
2	EDO	A	503	4/4	0.70	0.34	65,65,65,65	0
2	EDO	B	503	4/4	0.72	0.33	56,56,56,56	0
2	EDO	A	505	4/4	0.72	0.23	64,64,64,64	0
2	EDO	A	502	4/4	0.77	0.22	74,74,74,74	0
2	EDO	A	504	4/4	0.77	0.34	54,54,54,54	0
2	EDO	B	507	4/4	0.78	0.31	67,67,67,67	0
2	EDO	B	508	4/4	0.81	0.38	58,58,58,58	0
2	EDO	D	501	4/4	0.82	0.19	78,78,78,78	0
2	EDO	B	509	4/4	0.82	0.22	62,62,62,62	0
2	EDO	A	507	4/4	0.83	0.21	84,84,84,84	0
2	EDO	A	506	4/4	0.83	0.27	72,72,72,72	0
2	EDO	D	510	4/4	0.84	0.22	57,57,57,57	0
2	EDO	C	504	4/4	0.85	0.26	51,51,51,51	0
2	EDO	D	502	4/4	0.85	0.30	71,71,71,71	0
2	EDO	C	506	4/4	0.86	0.45	63,63,63,63	0
3	C8E	A	508	21/21	0.86	0.27	66,66,66,66	0
2	EDO	C	505	4/4	0.87	0.22	60,60,60,60	0
2	EDO	B	501	4/4	0.88	0.24	62,62,62,62	0
2	EDO	B	511	4/4	0.89	0.23	71,71,71,71	0
2	EDO	C	501	4/4	0.92	0.24	53,53,53,53	0
3	C8E	D	511	21/21	0.93	0.20	65,65,65,65	0
3	C8E	B	512	21/21	0.94	0.22	42,42,42,42	0
2	EDO	B	502	4/4	0.94	0.20	48,48,48,48	0
2	EDO	D	508	4/4	0.94	0.16	67,67,67,67	0
2	EDO	D	503	4/4	0.94	0.14	49,49,49,49	0
2	EDO	C	502	4/4	0.94	0.24	59,59,59,59	0
2	EDO	D	507	4/4	0.94	0.11	44,44,44,44	0
2	EDO	B	506	4/4	0.94	0.26	42,42,42,42	0
2	EDO	B	504	4/4	0.95	0.09	38,38,38,38	0
3	C8E	C	509	21/21	0.95	0.17	42,42,42,42	0
2	EDO	C	503	4/4	0.96	0.15	57,57,57,57	0
2	EDO	C	507	4/4	0.96	0.11	38,38,38,38	0
2	EDO	B	505	4/4	0.96	0.26	45,45,45,45	0
2	EDO	A	501	4/4	0.97	0.08	45,45,45,45	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.

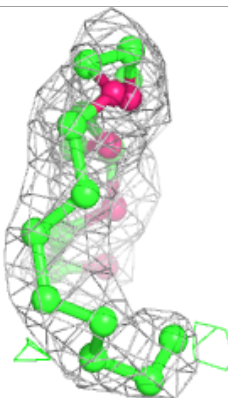
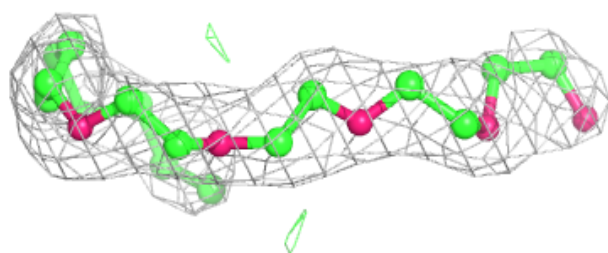
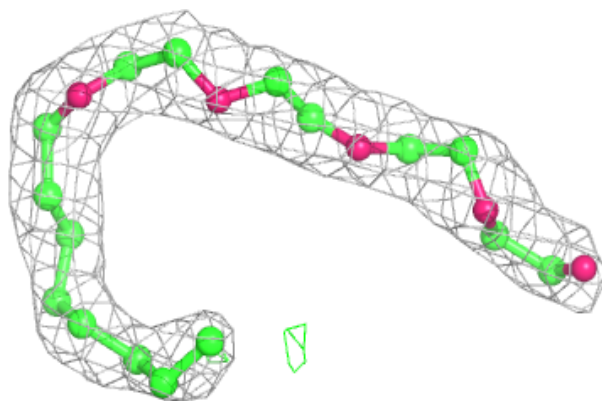
Electron density around C8E A 508:

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

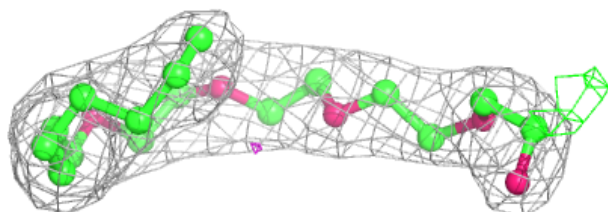
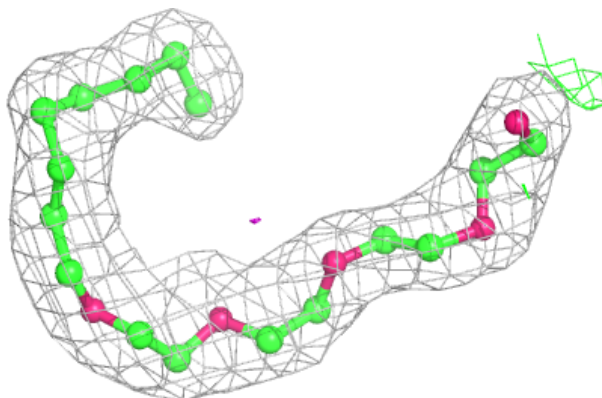


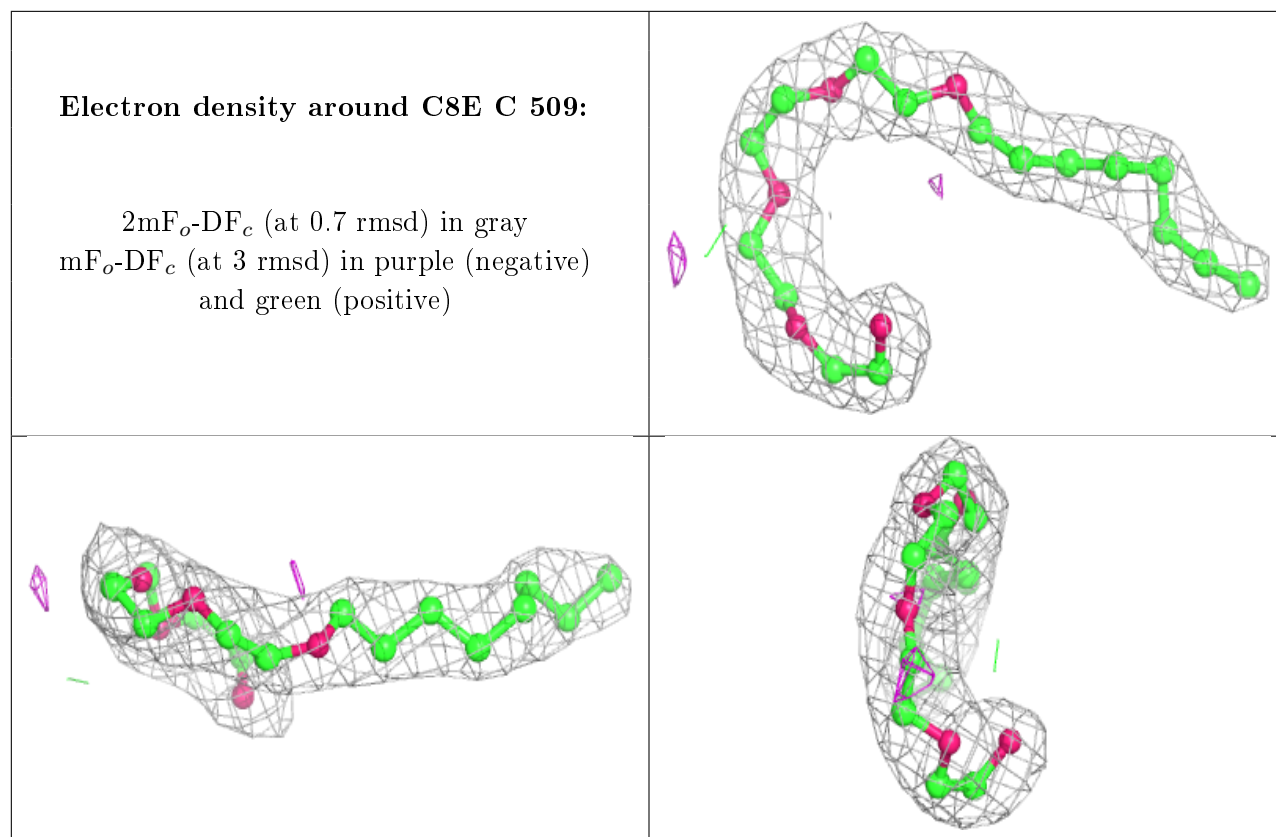
Electron density around C8E D 511:

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

**Electron density around C8E B 512:**

$2mF_o-DF_c$ (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.