Full wwPDB X-ray Structure Validation Report (i)

Nov 2, 2021 – 11:16 pm GMT

PDB ID	:	7Q4J
Title	:	A thermostable lipase from Thermoanaerobacter thermohydrosulfuricus in complex a monoacylglycerol intermediate
Deposited on	:	2021-10-31
Resolution	:	1.91 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

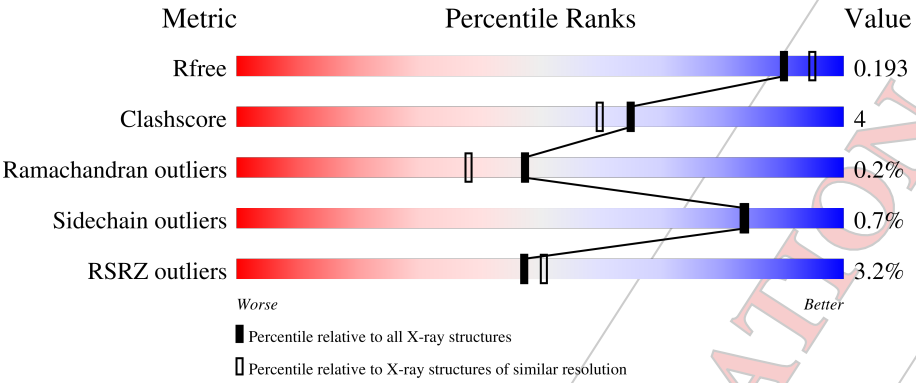
MolProbity	:	4.02b-467
Mogul	:	1.8.4 (270009), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 1.91 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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 <=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	259	3% 93% 6%
2	B	259	2% 90% 10%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 4608 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.

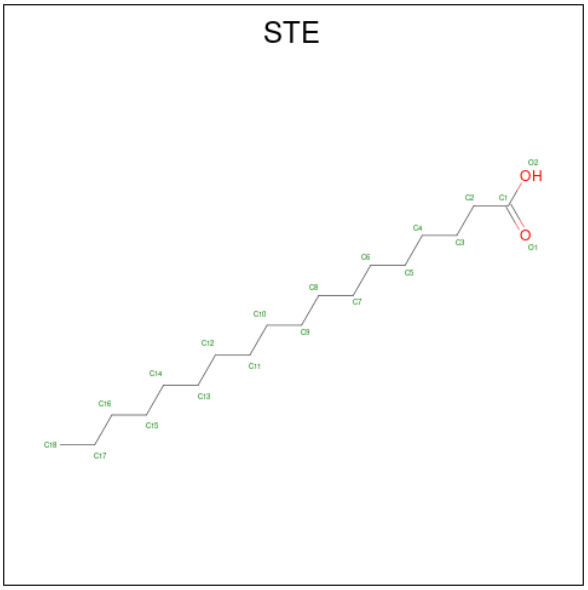
- Molecule 1 is a protein called Hydrolase_4 domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	259	2086	1342	338	395	11	0	3	0

- Molecule 2 is a protein called Hydrolase_4 domain-containing protein.

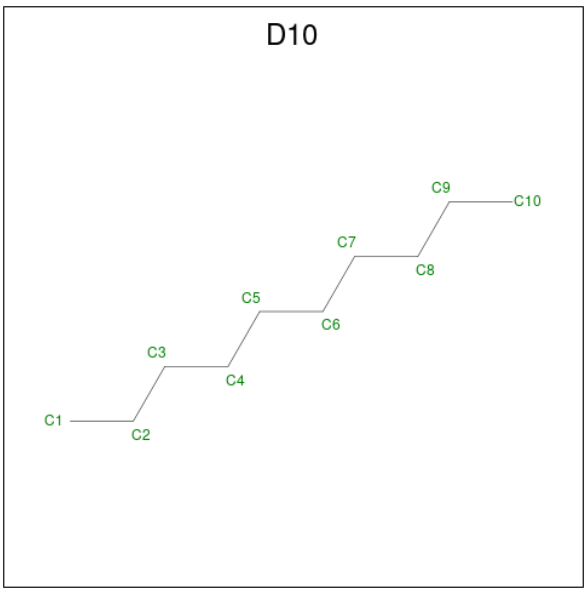
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
2	B	259	2099	1351	339	398	11	0	3	0

- Molecule 3 is STEARIC ACID (three-letter code: STE) (formula: $C_{18}H_{36}O_2$) (labeled as "Ligand of Interest" by depositor).



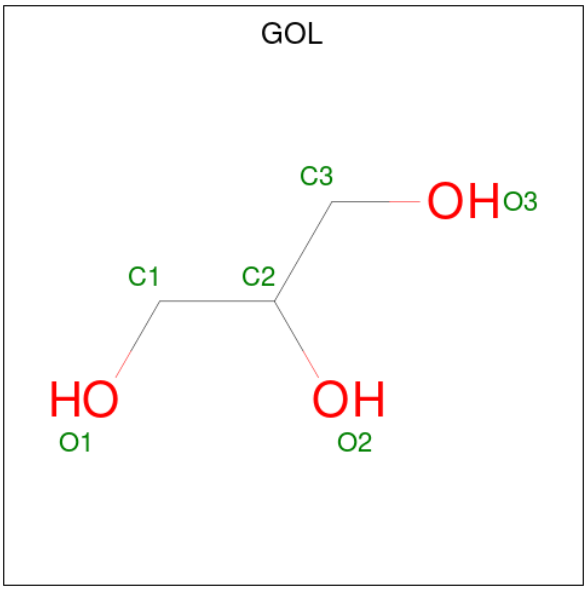
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
3	A	1	19	18	1		0	0
3	B	1	Total	C	O		0	0
			19	18	1			

- Molecule 4 is DECANE (three-letter code: D10) (formula: $C_{10}H_{22}$).



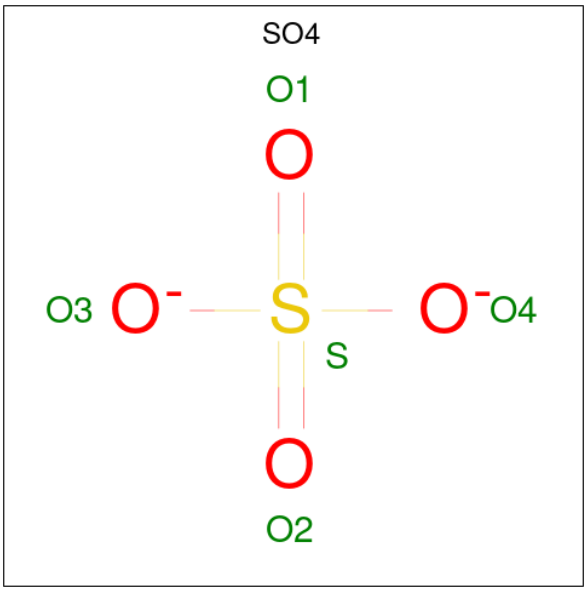
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 8 8	0	0
4	A	1	Total C 8 8	0	0
4	B	1	Total C 9 9	0	0
4	B	1	Total C 10 10	0	0

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0
5	B	1	Total C O 6 3 3	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Cl 1 1	0	0

- Molecule 8 is water.

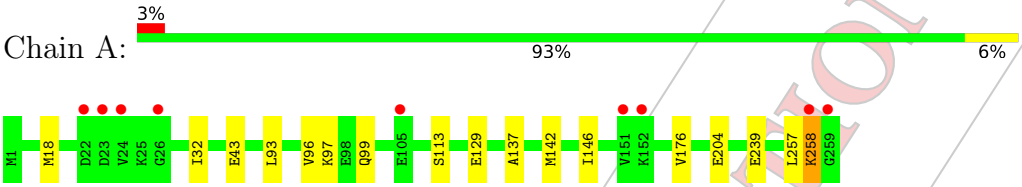
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	132	Total O 132 132	0	0
8	B	155	Total O 155 155	0	0

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.

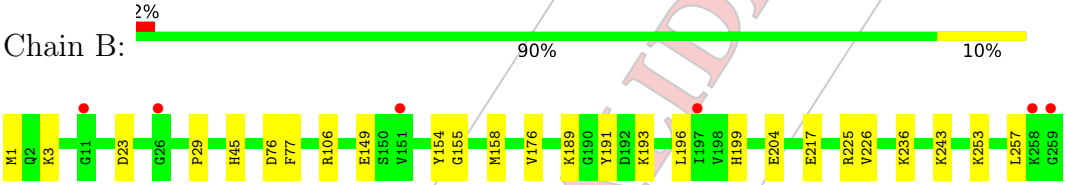
• Molecule 1: Hydrolase_4 domain-containing protein

Chain A:



• Molecule 2: Hydrolase_4 domain-containing protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	137.53Å 137.53Å 67.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.75 – 1.91 19.75 – 1.91	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.75-1.91) 96.8 (19.75-1.91)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.157 , 0.195 0.158 , 0.193	Depositor DCC
R_{free} test set	1532 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å^2)	36.2	Xtriage
Anisotropy	0.634	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4608	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, STE, D10, MLY, SO4, GOL, MLZ

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	0.57	0/1994	0.64	0/2666
2	B	0.62	0/1962	0.65	0/2621
All	All	0.59	0/3956	0.65	0/5287

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2086	0	2085	11	0
2	B	2099	0	2099	19	0
3	A	19	0	35	5	0
3	B	19	0	35	6	0
4	A	16	0	30	3	0
4	B	19	0	39	2	0
5	A	18	0	24	0	0
5	B	24	0	32	6	0
6	A	20	0	0	1	0
7	A	1	0	0	0	0
8	A	132	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	155	0	0	2	0
All	All	4608	0	4379	36	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 4.

All (36) 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)
3:A:301:STE:H31	4:A:303:D10:H13	1.43	1.01
2:B:45:HIS:H	5:B:307:GOL:H31	1.34	0.92
2:B:225:ARG:HE	5:B:306:GOL:H12	1.37	0.88
2:B:76:ASP:HB3	5:B:305:GOL:O1	1.85	0.77
1:A:18:MSE:HE1	1:A:99:GLN:HG3	1.72	0.70
2:B:149:GLU:HB2	3:B:301:STE:H141	1.74	0.69
1:A:239[B]:GLU:OE1	8:A:402:HOH:O	2.12	0.67
6:A:309:SO4:O2	8:A:401:HOH:O	2.08	0.66
2:B:253:MLZ:HG2	2:B:257:LEU:HD12	1.78	0.64
2:B:196:LEU:HD11	2:B:226:VAL:HG23	1.80	0.62
2:B:77:PHE:H	5:B:305:GOL:H2	1.64	0.60
8:A:453:HOH:O	5:B:307:GOL:H32	2.01	0.59
1:A:142:MSE:SE	3:A:301:STE:H21	2.54	0.58
3:A:301:STE:H91	4:A:303:D10:H71	1.90	0.52
2:B:191:TYR:CZ	2:B:193:MLY:HB3	2.48	0.49
1:A:204:GLU:HA	4:A:302:D10:H61	1.95	0.48
2:B:243:MLY:HH22	8:B:497:HOH:O	2.13	0.48
3:B:301:STE:H182	8:B:523:HOH:O	2.13	0.47
1:A:257:LEU:O	1:A:258:LYS:HE2	2.13	0.47
2:B:29:PRO:HG3	2:B:106:ARG:HD3	1.97	0.47
2:B:189:LYS:HD2	2:B:217:GLU:O	2.15	0.47
3:B:301:STE:H102	4:B:303:D10:H71	1.98	0.46
1:A:97:MLY:HE2	1:A:129:GLU:OE1	2.16	0.46
2:B:154:TYR:HB3	3:B:301:STE:H152	1.97	0.46
1:A:146:ILE:HD13	3:A:301:STE:H101	1.97	0.46
2:B:158:MSE:HE3	2:B:176:VAL:HG21	1.98	0.45
1:A:176:VAL:HG21	3:A:301:STE:H162	1.98	0.45
2:B:1:MSE:HE1	2:B:3:MLY:HD2	1.98	0.45
2:B:204:GLU:HA	4:B:302:D10:H32	2.00	0.43
1:A:93:LEU:HG	1:A:97:MLY:HD3	2.00	0.43
1:A:32:ILE:HG12	1:A:96:VAL:HG21	2.01	0.43
2:B:225:ARG:HH21	5:B:306:GOL:H31	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:155:GLY:HA2	3:B:301:STE:H161	2.02	0.42
2:B:45:HIS:CD2	2:B:236:MLY:HG2	2.56	0.41
2:B:149:GLU:HG3	3:B:301:STE:H121	2.03	0.40
1:A:113:SER:HA	1:A:137:ALA:O	2.21	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	249/259 (96%)	243 (98%)	5 (2%)	1 (0%)	34 24
2	B	245/259 (95%)	240 (98%)	5 (2%)	0	100 100
All	All	494/518 (95%)	483 (98%)	10 (2%)	1 (0%)	47 38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	GLU

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	212/200 (106%)	211 (100%)	1 (0%)	88 89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	210/196 (107%)	208 (99%)	2 (1%)	76 75
All	All	422/396 (107%)	419 (99%)	3 (1%)	84 83

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258	LYS
2	B	23	ASP
2	B	199	HIS

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

26 non-standard protein/DNA/RNA residues are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

Ligand STE A 301	
Bond lengths	Bond angles
Torsions	Rings

Ligand STE B 301	
Bond lengths	Bond angles
Torsions	Rings

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, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	237/259 (91%)	-0.02	9 (3%) 40 43	32, 42, 65, 97	2 (0%)
2	B	233/259 (89%)	-0.09	6 (2%) 56 59	30, 38, 56, 86	6 (2%)
All	All	470/518 (90%)	-0.05	15 (3%) 47 50	30, 40, 61, 97	8 (1%)

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	23	ASP	4.5
2	B	259	GLY	4.2
1	A	259	GLY	4.0
2	B	151	VAL	3.9
1	A	151	VAL	3.6
1	A	258	LYS	3.5
1	A	26	GLY	3.3
2	B	197	ILE	2.5
1	A	24	VAL	2.5
1	A	22	ASP	2.3
1	A	105	GLU	2.2
2	B	258	LYS	2.1
1	A	152	LYS	2.1
2	B	11	GLY	2.0
2	B	26	GLY	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MLY	B	209	11/12	0.88	0.16	33,37,70,71	0
2	MLZ	B	152	10/11	0.90	0.17	46,51,66,67	0
2	MLY	B	236	11/12	0.90	0.14	35,39,62,64	0
1	MLY	A	236	11/12	0.91	0.12	38,44,61,61	0
2	MLZ	B	254	10/11	0.91	0.19	43,48,73,75	0
2	MLY	B	25	11/12	0.92	0.17	48,55,68,70	0
1	MLZ	A	253	10/11	0.92	0.10	43,60,70,71	0
2	MLY	B	170	11/12	0.92	0.14	36,38,55,57	0
2	MLY	B	193	11/12	0.93	0.12	40,46,62,64	0
1	MLY	A	127	11/12	0.93	0.18	47,55,70,74	0
2	MLZ	B	194	10/11	0.94	0.11	34,38,62,62	0
2	MLZ	B	253	10/11	0.94	0.12	37,47,73,73	0
1	MLZ	A	209	10/11	0.94	0.13	38,41,72,72	0
1	MLY	A	97	11/12	0.95	0.08	41,48,55,57	0
1	MLY	A	94	11/12	0.95	0.11	39,44,62,65	0
1	MLZ	A	242	10/11	0.95	0.11	33,42,62,63	2
1	MLY	A	170	11/12	0.95	0.10	31,36,48,54	0
1	MLZ	A	194	10/11	0.95	0.11	43,50,68,71	0
2	MLZ	B	94	10/11	0.95	0.10	37,41,64,66	0
2	MLY	B	127	11/12	0.95	0.15	40,50,67,69	0
2	MLZ	B	131	10/11	0.95	0.08	39,41,60,64	0
2	MLY	B	57	11/12	0.96	0.11	36,47,70,74	0
1	MLY	A	243	11/12	0.96	0.09	40,42,50,52	0
1	MLY	A	12	11/12	0.97	0.08	36,46,61,63	0
2	MLY	B	3	11/12	0.98	0.08	31,34,52,52	0
2	MLY	B	243	11/12	0.98	0.06	32,35,48,49	0

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(Å^2)	Q<0.9
5	GOL	A	306	6/6	0.64	0.25	70,72,73,73	0
4	D10	B	303	10/10	0.79	0.28	58,65,68,69	0
3	STE	A	301	19/20	0.84	0.21	28,58,66,67	0

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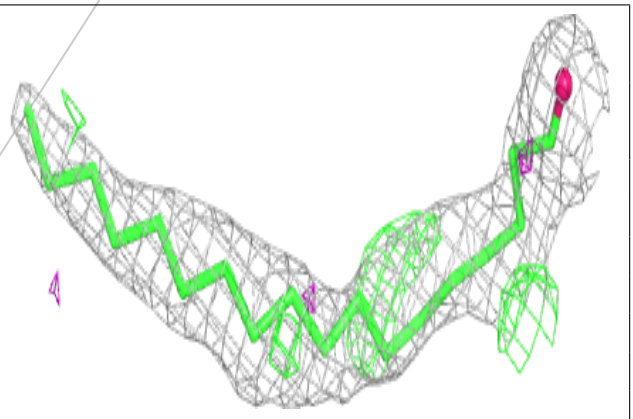
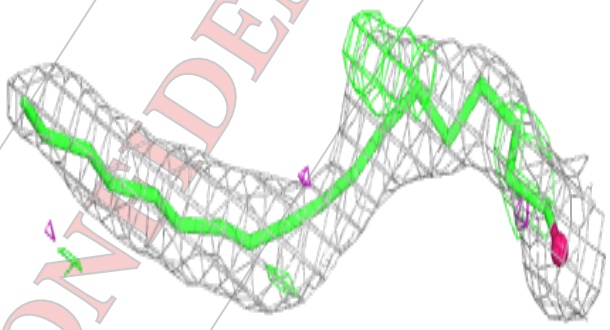
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	GOL	B	306	6/6	0.84	0.18	59,68,69,70	0
5	GOL	A	305	6/6	0.85	0.23	66,69,71,71	0
4	D10	A	302	8/10	0.86	0.20	48,51,58,59	0
5	GOL	B	307	6/6	0.87	0.24	59,61,68,68	0
5	GOL	B	304	6/6	0.89	0.13	47,55,57,57	0
3	STE	B	301	19/20	0.90	0.20	29,55,64,64	0
6	SO4	A	308	5/5	0.90	0.21	88,90,91,92	5
4	D10	B	302	9/10	0.91	0.13	50,52,58,59	0
4	D10	A	303	8/10	0.91	0.10	57,63,64,67	0
6	SO4	A	310	5/5	0.91	0.31	87,88,89,89	5
5	GOL	B	305	6/6	0.92	0.20	37,48,49,56	6
5	GOL	A	304	6/6	0.94	0.09	56,60,61,63	0
6	SO4	A	309	5/5	0.95	0.15	75,77,78,80	5
6	SO4	A	307	5/5	0.96	0.11	43,55,60,61	5
7	CL	A	311	1/1	0.99	0.05	37,37,37,37	0

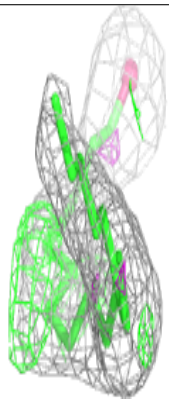
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around STE A 301:

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

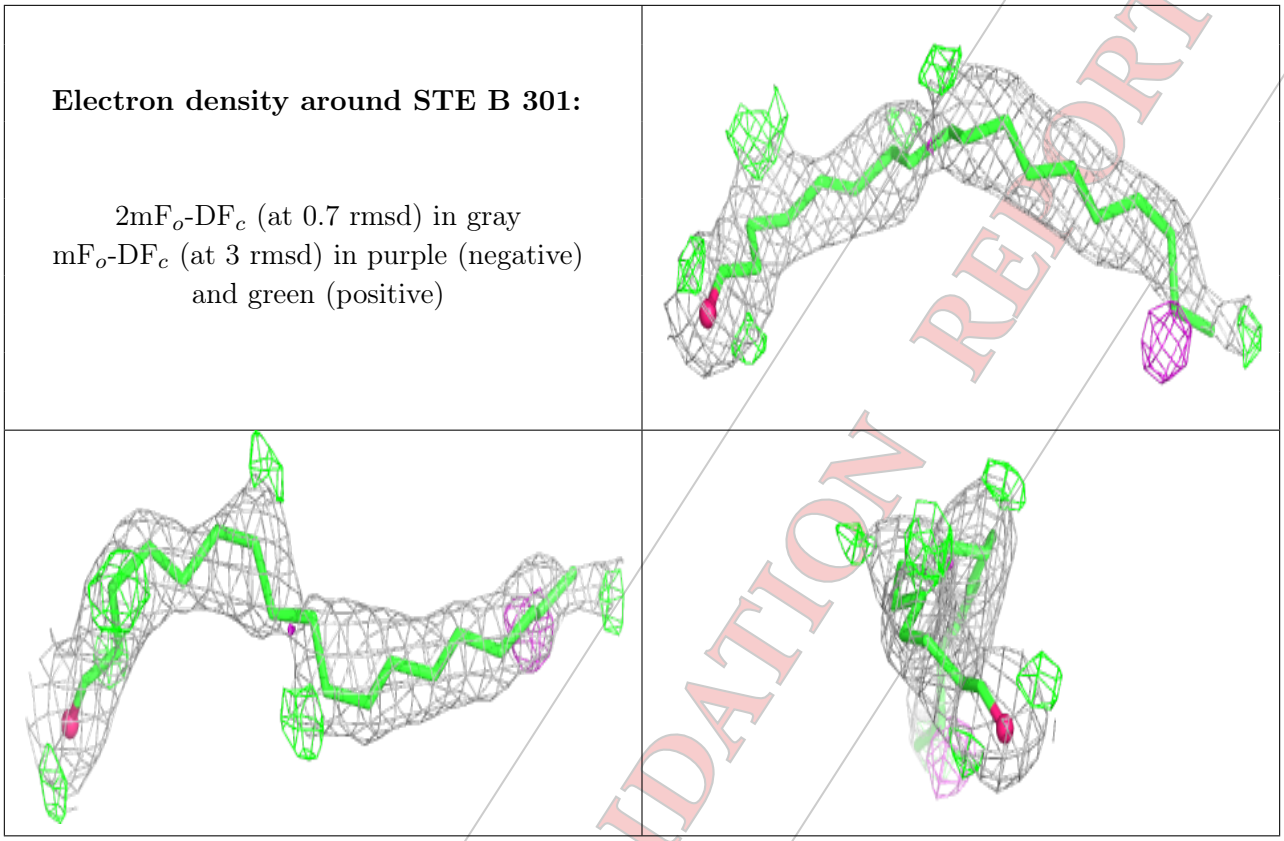






Electron density around STE B 301:

$2mF_o$-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.