



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 21, 2022 – 04:08 PM EST

PDB ID : 7SUC
Title : XFEL Serial Crystallography Reveals the Room Temperature Structure of Methyl-Coenzyme M Reductase
Authors : Ohmer, C.J.; Dasgupta, M.
Deposited on : 2021-11-16
Resolution : 1.90 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	:	2.26
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)	:	2.26

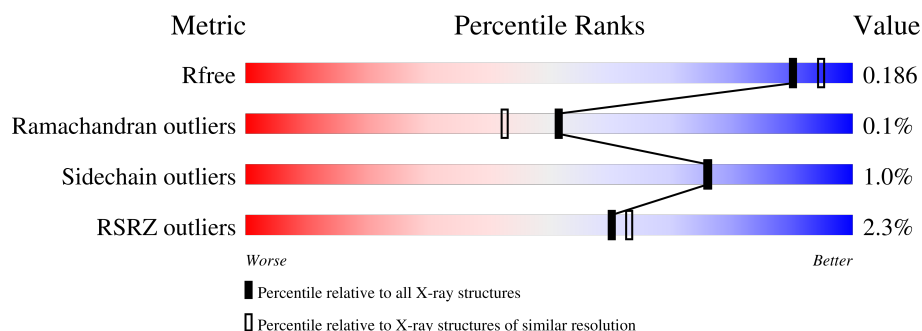
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 $\leq 5\%$. 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	548	<div> <div>%</div> <div>98%</div> <div>.</div> </div>
1	a	548	<div> <div>%</div> <div>98%</div> <div>.</div> </div>
2	B	442	<div> <div>%</div> <div>99%</div> <div>.</div> </div>
2	b	442	<div> <div>2%</div> <div>99%</div> <div>.</div> </div>
3	C	246	<div> <div>7%</div> <div>99%</div> <div>.</div> </div>
3	c	246	<div> <div>7%</div> <div>99%</div> <div>.</div> </div>

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
8	ACT	A	605[B]	-	-	-	X
9	EDO	a	605	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 39730 atoms, of which 19268 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 Methyl-coenzyme M reductase I subunit alpha.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	548	Total	C	H	N	O	S	6	16	0
			8447	2731	4133	720	843	20			
1	a	548	Total	C	H	N	O	S	13	21	0
			8547	2764	4192	720	851	20			

- Molecule 2 is a protein called Methyl-coenzyme M reductase I subunit beta.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	442	Total	C	H	N	O	S	0	13	0
			6768	2141	3393	555	661	18			
2	b	442	Total	C	H	N	O	S	0	22	0
			6848	2166	3434	556	671	21			

- Molecule 3 is a protein called Methyl-coenzyme M reductase I subunit gamma.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	246	Total	C	H	N	O	S	0	8	0
			3995	1259	1965	354	405	12			
3	c	246	Total	C	H	N	O	S	0	10	0
			4039	1270	1994	357	407	11			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

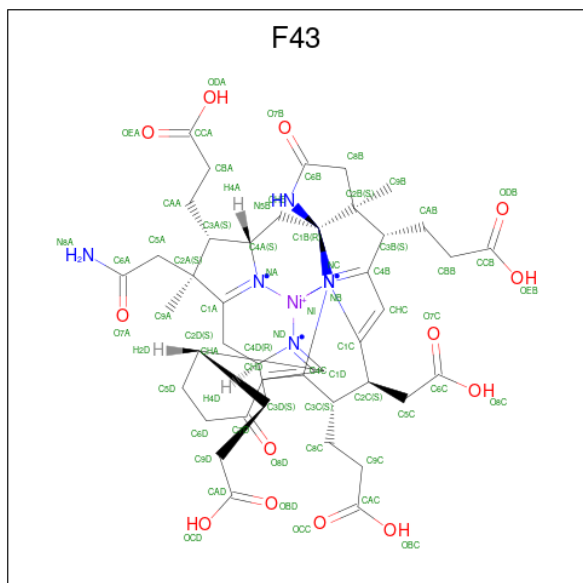
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	a	2	Total	Mg	0	0
			2	2		

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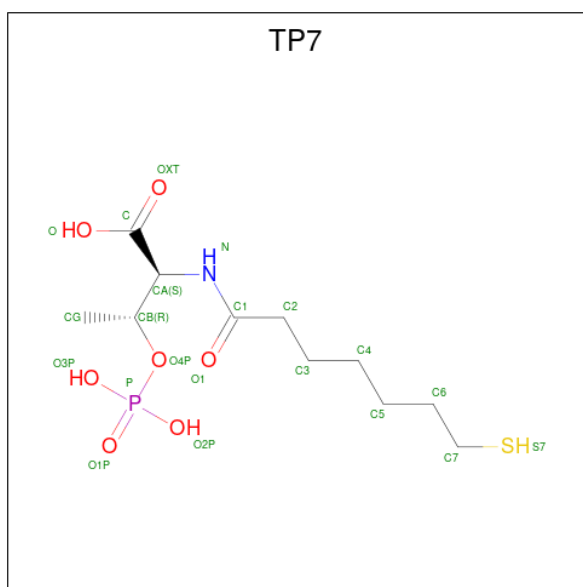
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	b	1	Total	Mg	0	0
			1	1		
4	c	1	Total	Mg	0	0
			1	1		

- Molecule 5 is FACTOR 430 (three-letter code: F43) (formula: $C_{42}H_{51}N_6NiO_{13}$) (labeled as "Ligand of Interest" by depositor).



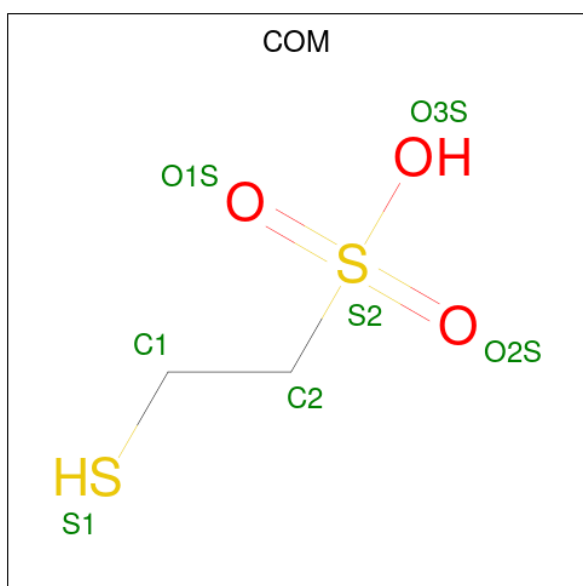
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	Ni	O	0	0
			113	42	51	6	1	13		
5	a	1	Total	C	H	N	Ni	O	0	0
			113	42	51	6	1	13		

- Molecule 6 is Coenzyme B (three-letter code: TP7) (formula: $C_{11}H_{22}NO_7PS$) (labeled as "Ligand of Interest" by depositor).



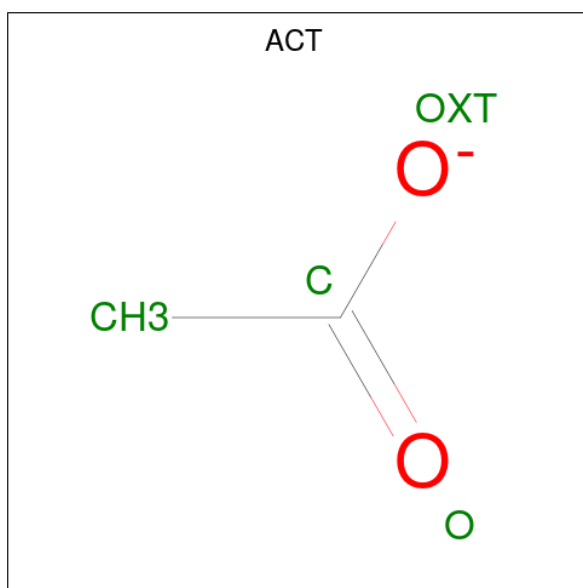
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	P	S	0	1
			40	11	19	1	7	1	1		
6	A	1	Total	C	H	N	O	P	S	0	1
			40	11	19	1	7	1	1		

- Molecule 7 is 1-THIOETHANESULFONIC ACID (three-letter code: COM) (formula: $C_2H_6O_3S_2$).



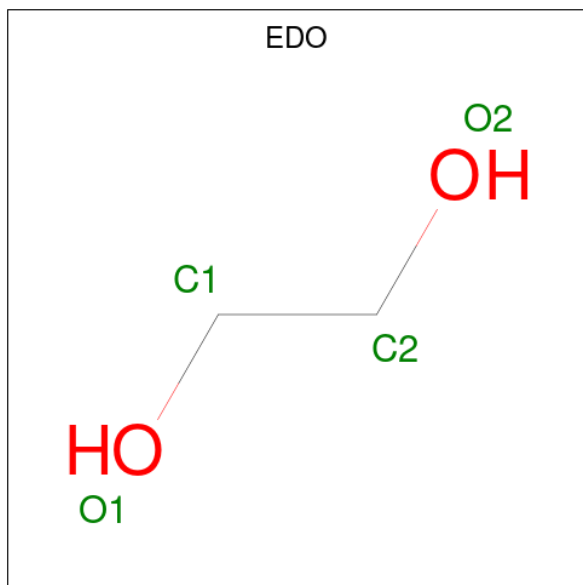
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	H	O	S	0	0
			11	2	4	3	2		
7	a	1	Total	C	H	O	S	0	0
			11	2	4	3	2		

- Molecule 8 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	0	1
			7	2	3	2		

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	a	1	Total	C	H	O	0	0
			10	2	6	2		

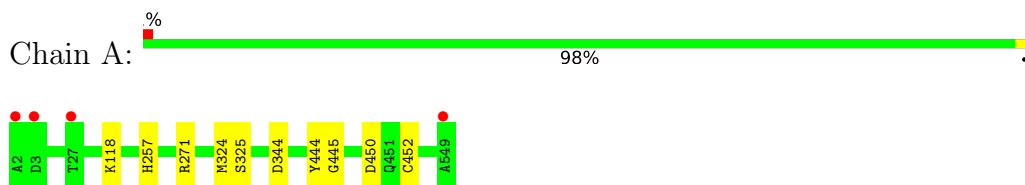
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	199	Total 199	O 199	0	0
10	B	117	Total 117	O 117	0	0
10	C	62	Total 62	O 62	0	0
10	a	178	Total 178	O 178	0	0
10	b	108	Total 108	O 108	0	0
10	c	70	Total 70	O 70	0	0

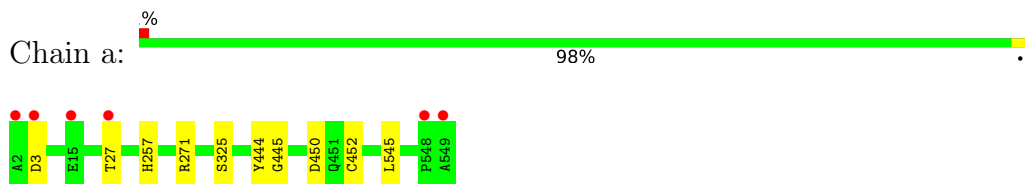
3 Residue-property plots [i](#)

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.

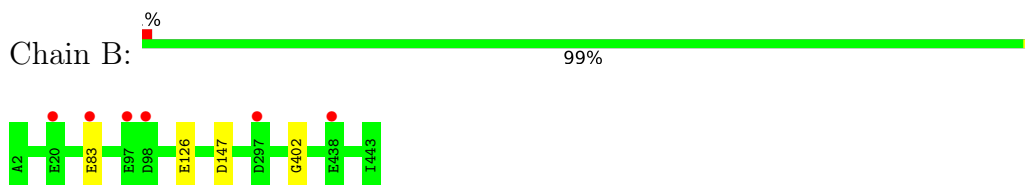
- Molecule 1: Methyl-coenzyme M reductase I subunit alpha



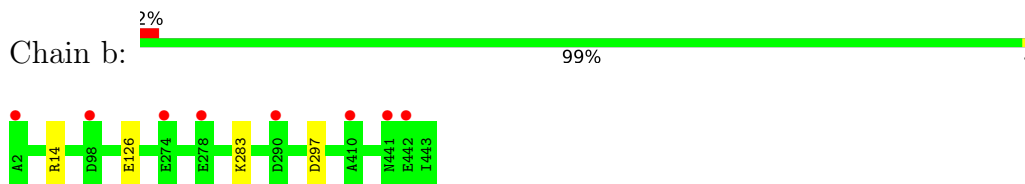
- Molecule 1: Methyl-coenzyme M reductase I subunit alpha



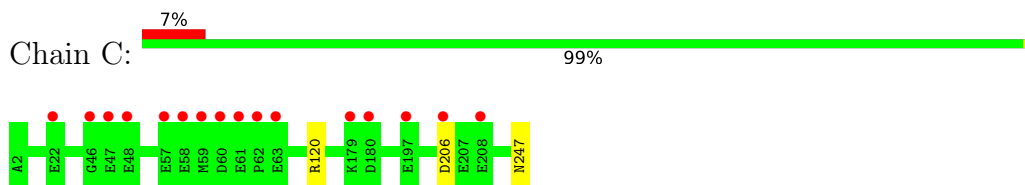
- Molecule 2: Methyl-coenzyme M reductase I subunit beta



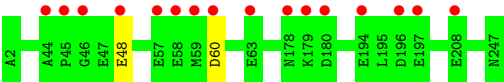
- Molecule 2: Methyl-coenzyme M reductase I subunit beta



- Molecule 3: Methyl-coenzyme M reductase I subunit gamma



- Molecule 3: Methyl-coenzyme M reductase I subunit gamma



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.08Å 119.78Å 123.21Å 90.00° 91.73° 90.00°	Depositor
Resolution (Å)	21.25 – 1.90 21.25 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (21.25-1.90) 91.2 (21.25-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.67 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.152 , 0.186 0.152 , 0.186	Depositor DCC
R_{free} test set	2010 reflections (1.06%)	wwPDB-VP
Wilson B-factor (Å ²)	21.7	Xtriage
Anisotropy	0.298	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k 0.022 for -h,-l,-k 0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	39730	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: TP7, MG, ACT, COM, SMC, EDO, AGM, DYA, MGN, F43, GL3, MHS

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	0.31	0/4417	0.57	1/5994 (0.0%)
1	a	0.30	0/4460	0.56	0/6052
2	B	0.30	0/3475	0.54	0/4706
2	b	0.30	0/3550	0.54	0/4805
3	C	0.30	0/2098	0.60	0/2826
3	c	0.30	0/2112	0.61	0/2844
All	All	0.30	0/20112	0.56	1/27227 (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	324	MET	CG-SD-CE	5.32	108.72	100.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	556/548 (102%)	536 (96%)	19 (3%)	1 (0%)	47	38
1	a	561/548 (102%)	540 (96%)	20 (4%)	1 (0%)	47	38
2	B	453/442 (102%)	443 (98%)	9 (2%)	1 (0%)	47	38
2	b	462/442 (104%)	455 (98%)	7 (2%)	0	100	100
3	C	252/246 (102%)	243 (96%)	9 (4%)	0	100	100
3	c	254/246 (103%)	247 (97%)	7 (3%)	0	100	100
All	All	2538/2472 (103%)	2464 (97%)	71 (3%)	3 (0%)	51	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	325	SER
1	a	325	SER
2	B	402	GLY

5.3.2 Protein sidechains ⓘ

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	447/432 (104%)	444 (99%)	3 (1%)	84	84
1	a	452/432 (105%)	447 (99%)	5 (1%)	73	73
2	B	354/341 (104%)	350 (99%)	4 (1%)	73	73
2	b	363/341 (106%)	358 (99%)	5 (1%)	67	65
3	C	222/214 (104%)	219 (99%)	3 (1%)	67	65
3	c	224/214 (105%)	222 (99%)	2 (1%)	78	79
All	All	2062/1974 (104%)	2040 (99%)	22 (1%)	76	73

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	545	LEU
2	b	283	LYS
2	b	126	GLU
2	b	297[A]	ASP
2	B	147	ASP

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

Mol	Chain	Res	Type
2	B	21	GLN
2	B	421	GLN
3	C	178	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues 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
1	DYA	a	450	1	4,7,8	3.48	3 (75%)	1,8,10	5.61	1 (100%)
1	SMC	A	452	1	5,6,7	1.25	1 (20%)	2,6,8	2.03	1 (50%)
1	DYA	A	450	1	4,7,8	3.49	3 (75%)	1,8,10	5.69	1 (100%)
1	GL3	a	445	1	2,3,4	1.71	1 (50%)	1,2,4	0.46	0
1	MHS	A	257	1	7,11,12	1.20	0	6,14,16	1.67	2 (33%)
1	SMC	a	452	1	5,6,7	1.16	1 (20%)	2,6,8	1.24	0
1	GL3	A	445	1	2,3,4	1.78	1 (50%)	1,2,4	0.16	0
1	AGM	A	271	1	10,11,12	1.25	1 (10%)	6,13,15	1.29	1 (16%)
1	AGM	a	271	1	10,11,12	1.15	1 (10%)	6,13,15	0.95	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MGN	a	400	1	6,9,10	0.76	0	5,12,14	0.72	0
1	MGN	A	400	1	6,9,10	0.75	0	5,12,14	0.83	0
1	MHS	a	257	1	7,11,12	1.19	1 (14%)	6,14,16	1.75	2 (33%)

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
1	DYA	a	450	1	-	2/2/6/8	-
1	SMC	A	452	1	-	1/3/5/7	-
1	DYA	A	450	1	-	2/2/6/8	-
1	GL3	a	445	1	-	1/1/1/2	-
1	MHS	A	257	1	-	0/5/6/8	0/1/1/1
1	SMC	a	452	1	-	1/3/5/7	-
1	GL3	A	445	1	-	0/1/1/2	-
1	AGM	A	271	1	-	2/10/11/13	-
1	AGM	a	271	1	-	1/10/11/13	-
1	MGN	a	400	1	-	2/7/9/12	-
1	MGN	A	400	1	-	2/7/9/12	-
1	MHS	a	257	1	-	0/5/6/8	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	450	DYA	C-CA	4.58	1.52	1.45
1	a	450	DYA	C-CA	4.42	1.52	1.45
1	A	450	DYA	CA-N	3.94	1.45	1.35
1	a	450	DYA	CA-N	3.69	1.44	1.35
1	a	450	DYA	CB-CA	-3.44	1.28	1.36

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	450	DYA	O-C-CA	-5.69	118.16	125.39
1	a	450	DYA	O-C-CA	-5.61	118.26	125.39
1	A	257	MHS	CB-CA-C	-3.07	105.71	111.47
1	a	257	MHS	CB-CA-C	-3.01	105.83	111.47
1	a	257	MHS	CM-ND1-CG	2.86	128.24	124.44

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	450	DYA	N-CA-CB-CG
1	A	450	DYA	O-C-CA-CB
1	A	452	SMC	CA-CB-SG-CS
1	a	450	DYA	N-CA-CB-CG
1	a	450	DYA	O-C-CA-CB

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 15 ligands modelled in this entry, 7 are monoatomic - leaving 8 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	$\# Z > 2$
5	F43	A	602	7,1	46,71,71	2.38	4 (8%)	48,118,118	1.37	8 (16%)
7	COM	a	604	5	6,6,6	1.42	0	7,8,8	1.96	2 (28%)
6	TP7	A	603[A]	-	16,20,20	1.16	1 (6%)	18,26,26	0.93	1 (5%)
9	EDO	a	605	-	3,3,3	0.50	0	2,2,2	0.29	0
5	F43	a	603	7,1	46,71,71	2.30	4 (8%)	48,118,118	1.41	9 (18%)
6	TP7	A	606[A]	-	16,20,20	1.14	1 (6%)	18,26,26	0.83	0
7	COM	A	604	5	6,6,6	1.59	2 (33%)	7,8,8	1.47	1 (14%)
8	ACT	A	605[B]	-	1,3,3	5.32	1 (100%)	0,3,3	-	-

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
5	F43	A	602	7,1	-	2/18/185/185	-
7	COM	a	604	5	-	0/4/4/4	-
6	TP7	A	603[A]	-	-	2/20/24/24	-
9	EDO	a	605	-	-	0/1/1/1	-
5	F43	a	603	7,1	-	2/18/185/185	-
6	TP7	A	606[A]	-	-	0/20/24/24	-
7	COM	A	604	5	-	0/4/4/4	-

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	602	F43	NI-NA	9.91	2.10	1.89
5	a	603	F43	NI-NA	9.63	2.10	1.89
5	A	602	F43	NI-NB	9.28	2.09	1.89
5	a	603	F43	NI-NB	9.00	2.08	1.89
5	A	602	F43	NI-ND	7.44	2.05	1.89

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	a	604	COM	O2S-S2-C2	3.91	111.62	106.92
5	A	602	F43	C2A-C3A-C4A	-3.71	96.71	102.36
5	a	603	F43	C5D-C2D-C1D	-3.66	105.52	110.45
5	a	603	F43	C2A-C3A-C4A	-3.52	96.99	102.36
5	a	603	F43	C9D-C3D-C4D	-2.93	106.92	114.67

There are no chirality outliers.

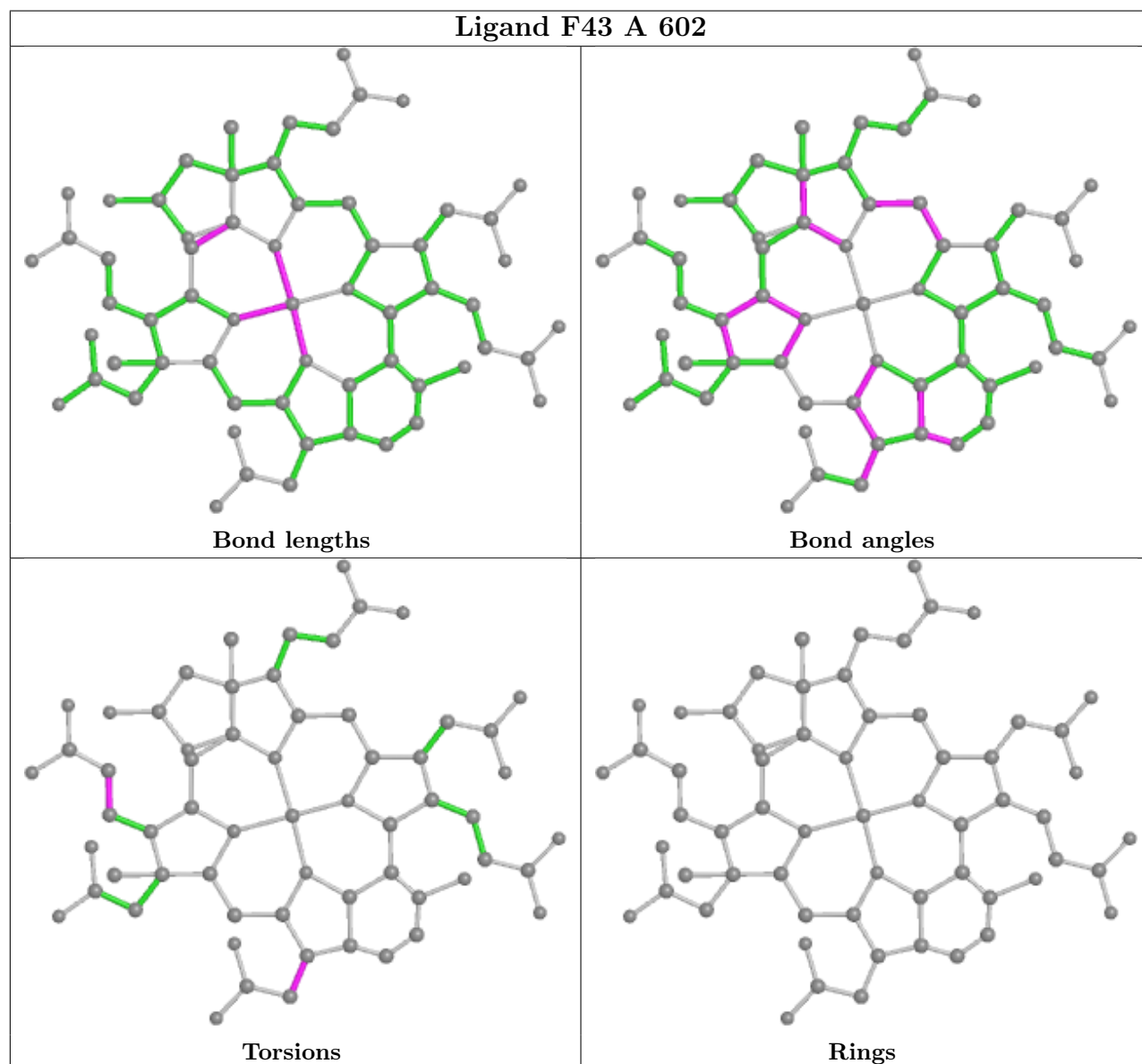
5 of 6 torsion outliers are listed below:

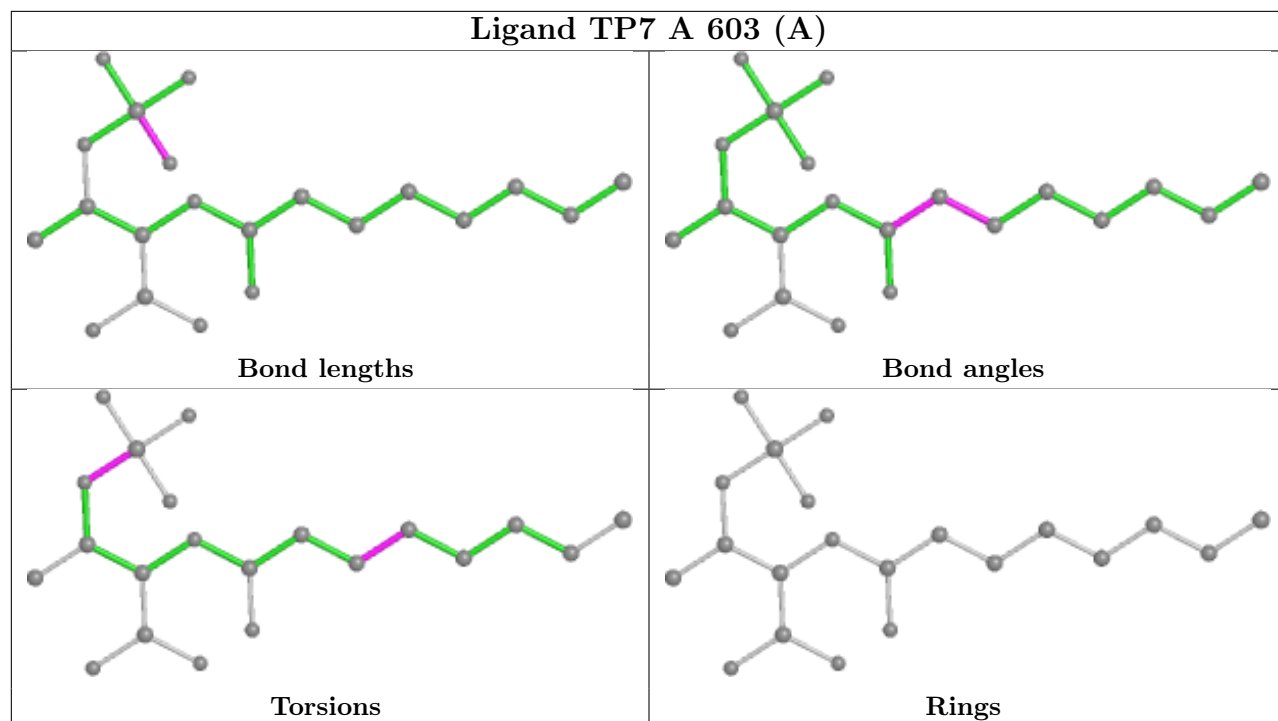
Mol	Chain	Res	Type	Atoms
5	A	602	F43	C2D-C3D-C9D-CAD
5	a	603	F43	C2D-C3D-C9D-CAD
5	A	602	F43	C3A-CAA-CBA-CCA
5	a	603	F43	C3A-CAA-CBA-CCA
6	A	603[A]	TP7	CB-O4P-P-O3P

There are no ring outliers.

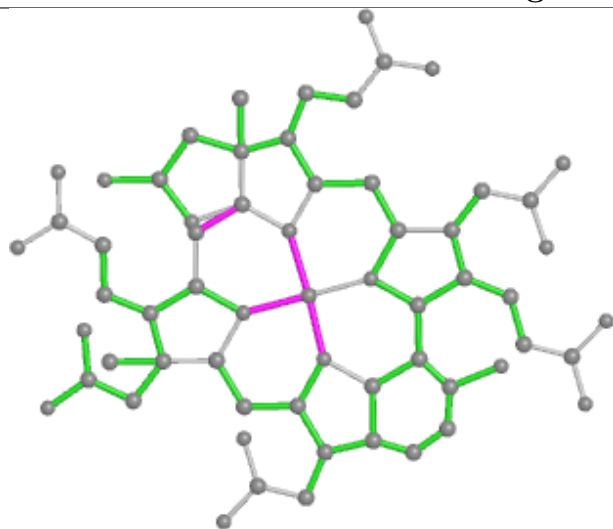
No monomer is involved in short contacts.

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 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.

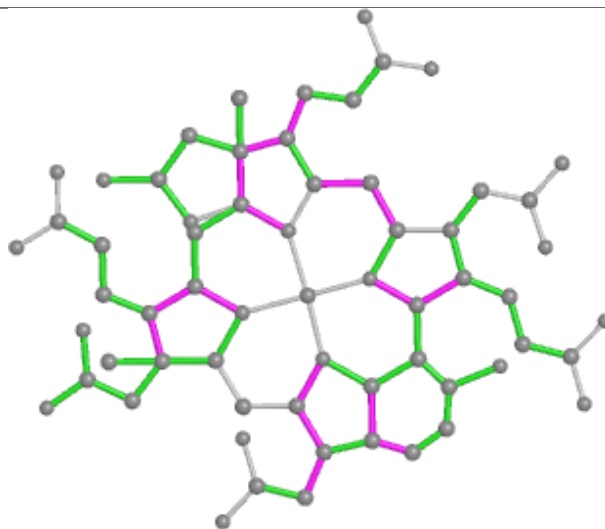




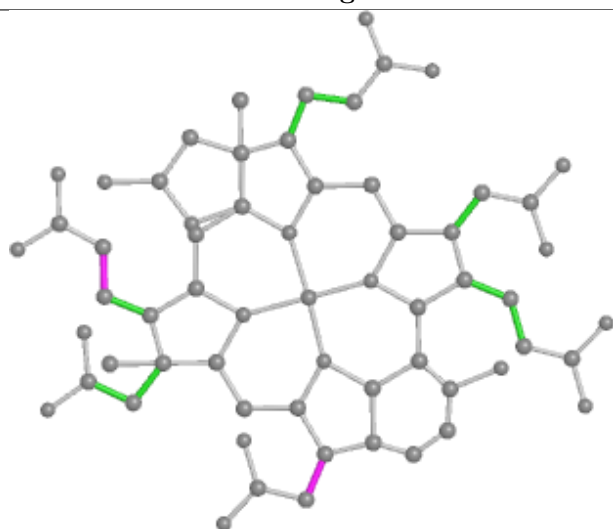
Ligand F43 a 603



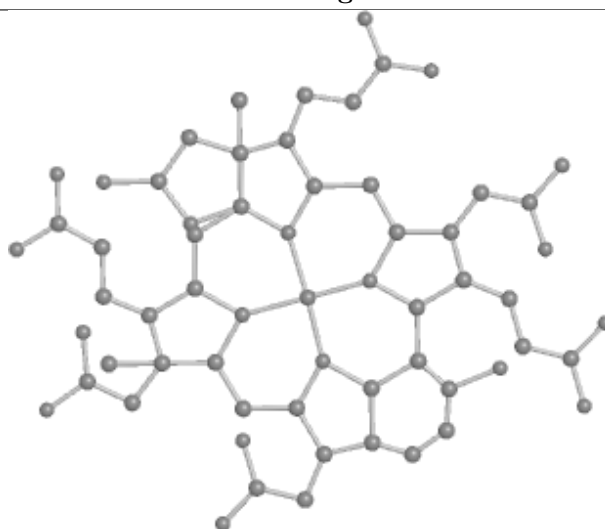
Bond lengths



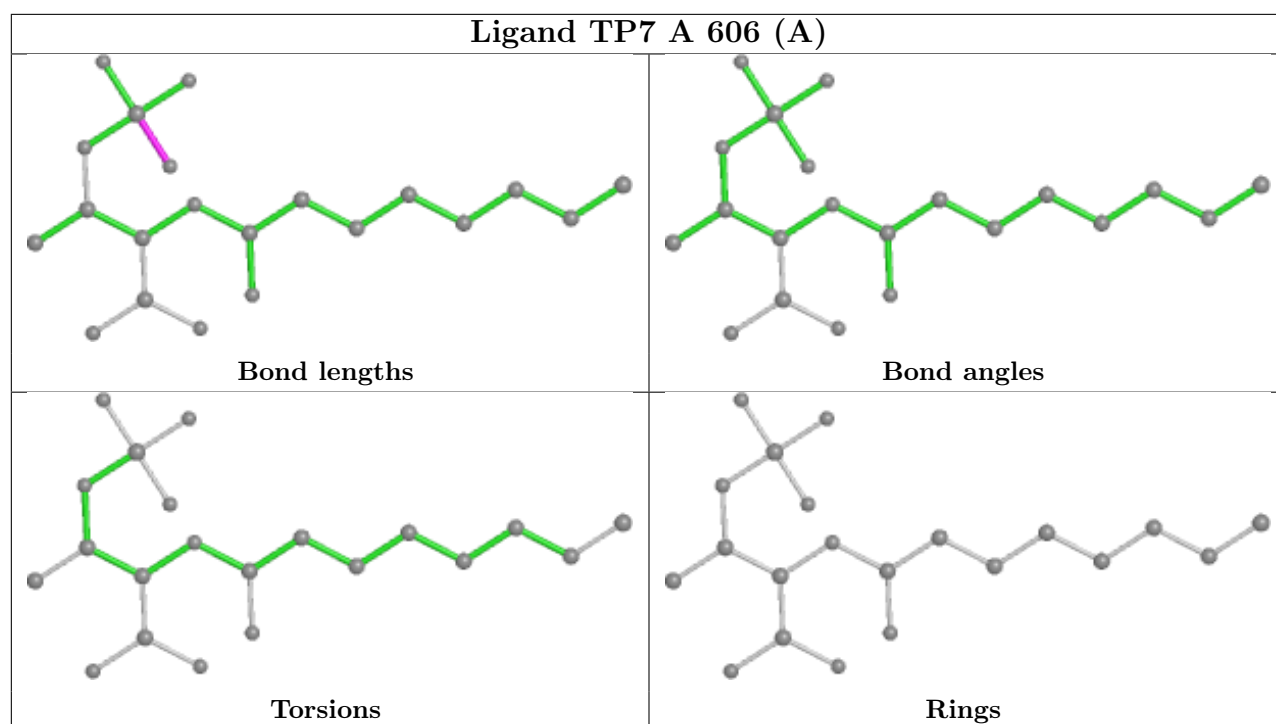
Bond angles



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 [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	542/548 (98%)	-0.33	4 (0%) 87 88	16, 24, 40, 76	1 (0%)
1	a	542/548 (98%)	-0.35	6 (1%) 80 82	16, 24, 39, 78	1 (0%)
2	B	442/442 (100%)	-0.18	6 (1%) 75 77	18, 30, 45, 77	0
2	b	442/442 (100%)	-0.11	8 (1%) 68 71	20, 31, 48, 66	0
3	C	246/246 (100%)	0.04	16 (6%) 18 21	22, 33, 58, 90	0
3	c	246/246 (100%)	0.08	16 (6%) 18 21	23, 35, 59, 85	0
All	All	2460/2472 (99%)	-0.19	56 (2%) 60 63	16, 28, 47, 90	2 (0%)

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	6.8
3	C	60	ASP	5.8
1	a	2	ALA	5.8
2	b	2	ALA	5.8
1	a	549	ALA	5.5

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	MHS	a	257	11/12	0.94	0.14	25,32,40,40	0
1	DYA	A	450	8/9	0.95	0.10	20,23,23,23	0
1	MHS	A	257	11/12	0.95	0.10	27,34,44,44	0
1	DYA	a	450	8/9	0.95	0.10	19,21,22,22	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MGN	A	400	10/11	0.96	0.08	19,22,25,25	0
1	AGM	a	271	12/13	0.97	0.09	18,21,25,26	0
1	MGN	a	400	10/11	0.97	0.08	17,22,24,25	0
1	AGM	A	271	12/13	0.97	0.08	18,22,26,26	0
1	GL3	A	445	4/5	0.98	0.09	19,22,23,28	0
1	SMC	A	452	7/8	0.98	0.07	19,23,27,27	0
1	GL3	a	445	4/5	0.99	0.09	19,20,27,27	0
1	SMC	a	452	7/8	0.99	0.06	20,23,27,27	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

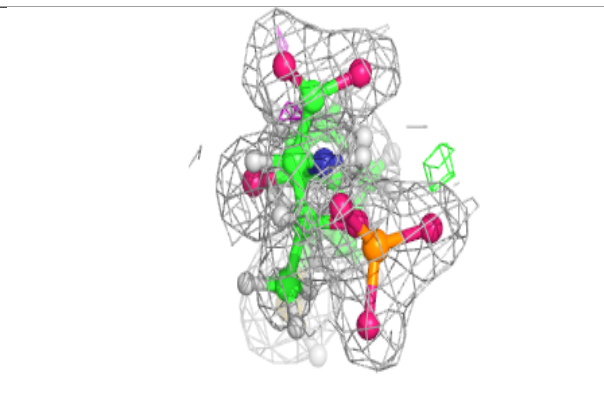
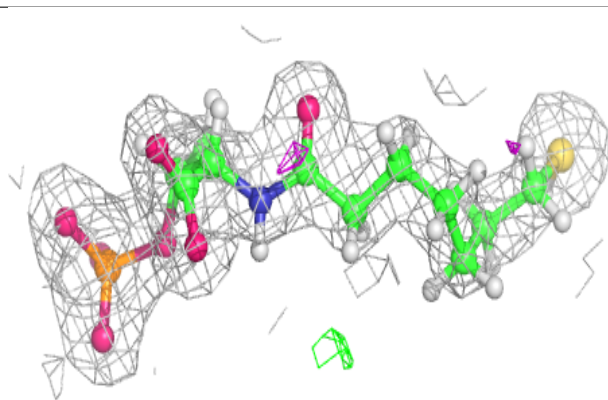
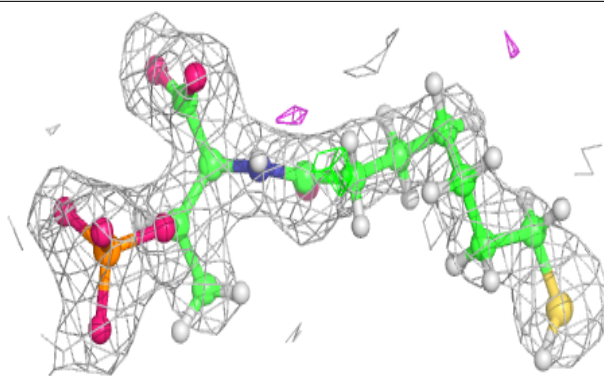
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	EDO	a	605	4/4	0.69	0.43	52,64,74,77	0
4	MG	a	602	1/1	0.70	0.28	61,61,61,61	0
8	ACT	A	605[B]	4/4	0.73	0.46	29,32,37,37	7
4	MG	A	601	1/1	0.73	0.30	59,59,59,59	0
4	MG	C	301	1/1	0.74	0.21	56,56,56,56	0
4	MG	a	601	1/1	0.75	0.18	55,55,55,55	0
4	MG	b	501	1/1	0.85	0.28	66,66,66,66	0
4	MG	B	501	1/1	0.87	0.25	63,63,63,63	0
4	MG	c	301	1/1	0.89	0.23	52,52,52,52	0
6	TP7	A	603[A]	21/21	0.98	0.08	20,25,29,29	40
6	TP7	A	606[A]	21/21	0.98	0.07	19,26,31,32	0
5	F43	A	602	62/62	0.98	0.07	17,23,27,33	0
5	F43	a	603	62/62	0.98	0.07	17,22,27,30	0
7	COM	A	604	7/7	0.99	0.05	22,23,28,28	0
7	COM	a	604	7/7	0.99	0.07	24,25,31,31	0

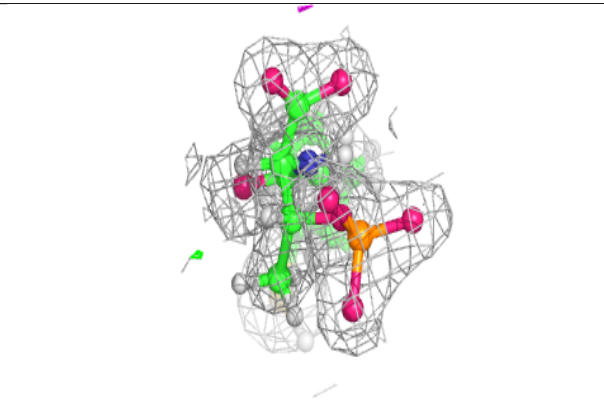
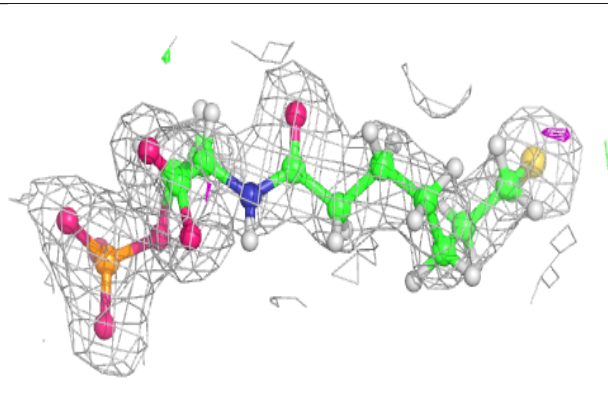
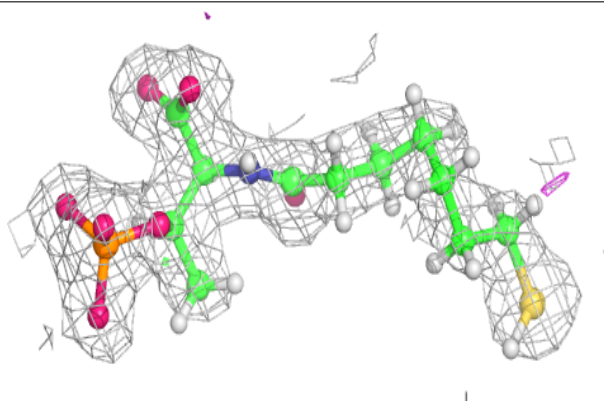
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TP7 A 603 (A):

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

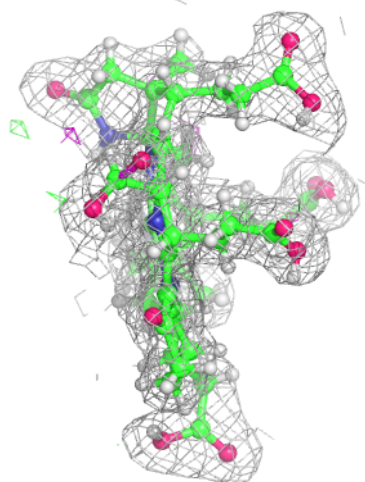
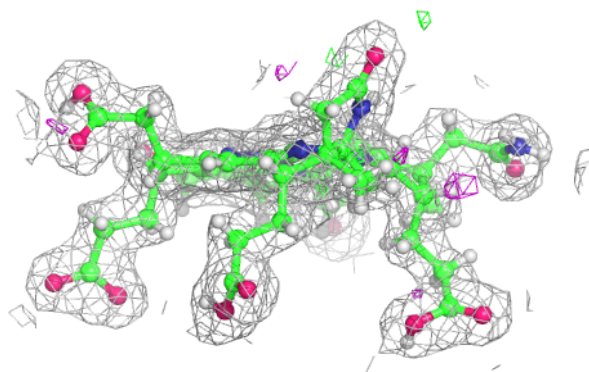
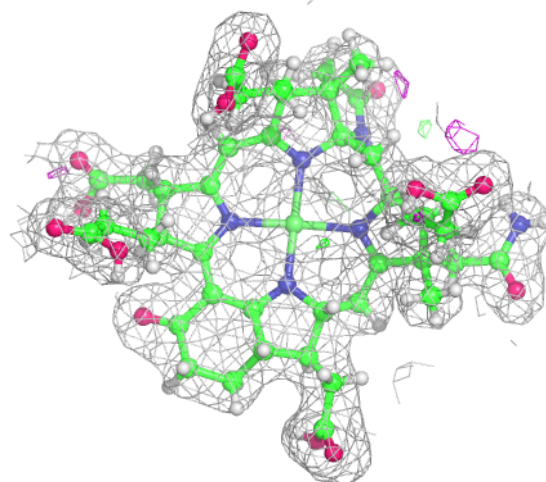
**Electron density around TP7 A 606 (A):**

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



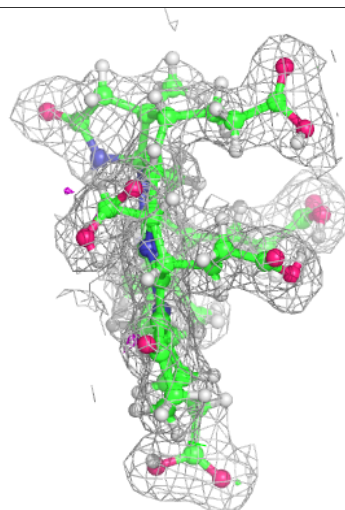
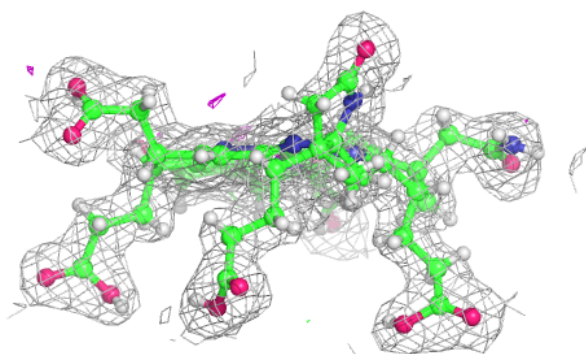
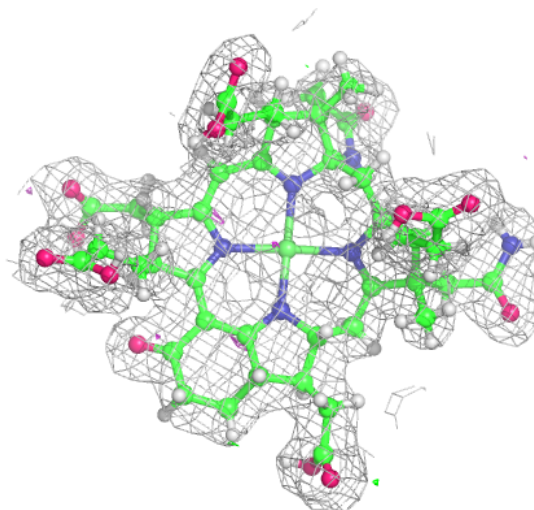
Electron density around F43 A 602:

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



Electron density around F43 a 603:

$2mF_o-DF_c$ (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.