wwPDB X-ray Structure Validation Summary Report (i)

Aug 4, 2026 – 05:44 PM EDT

PDB ID	:	3POT / pdb_00003pot
Title	:	Structural analysis of a Ni(III)-methyl species in methyl-coenzyme M reductase from Methanothermobacter marburgensis
Authors	:	Cedervall, P.E.; Wilmot, C.M.
Deposited on	:	2010-11-23
Resolution	:	1.20 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 (i) 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 (i)) were used in the production of this report:

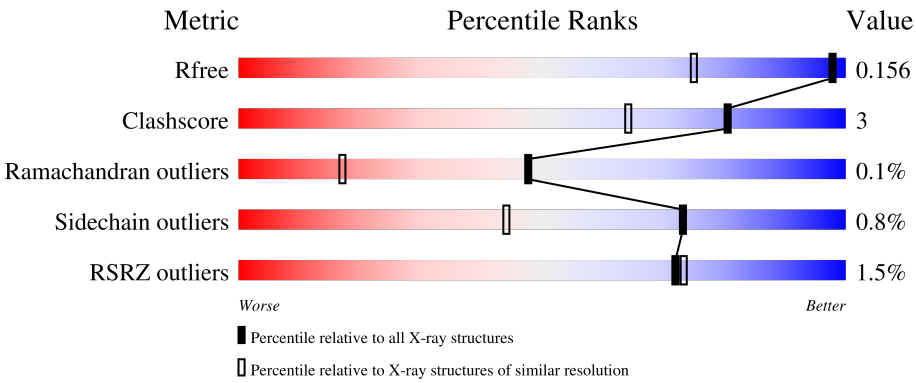
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

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 1.20 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	1216 (1.20-1.20)
Clashscore	190562	1265 (1.20-1.20)
Ramachandran outliers	187476	1226 (1.20-1.20)
Sidechain outliers	187428	1226 (1.20-1.20)
RSRZ outliers	180081	1214 (1.20-1.20)

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	550	% 95% 5%
1	D	550	% 93% 6%
2	B	443	95% 5%
2	E	443	% 95% 5%
3	C	249	4% 95% . .

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Mol	Chain	Length	Quality of chain
3	F	249	5% 94%

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
6	COM	A	556[A]	-	X	-	-
6	COM	D	555[A]	-	X	-	-
9	06C	A	559[B]	-	X	-	-
9	06C	D	556[B]	-	X	-	-

2 Entry composition (i)

There are 12 unique types of molecules in this entry. The entry contains 22289 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 Methyl-coenzyme M reductase I subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	548	4295	2719	717	839	20	0	8	0
1	D	548	4303	2731	716	836	20	0	10	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	442	3392	2156	559	656	21	0	12	0
2	E	442	3377	2149	552	654	22	0	11	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	246	2023	1252	358	401	12	0	6	0
3	F	246	2021	1253	358	398	12	0	5	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

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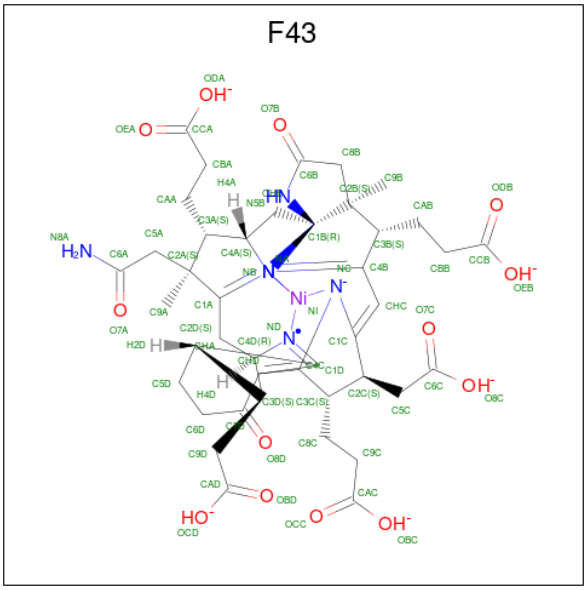
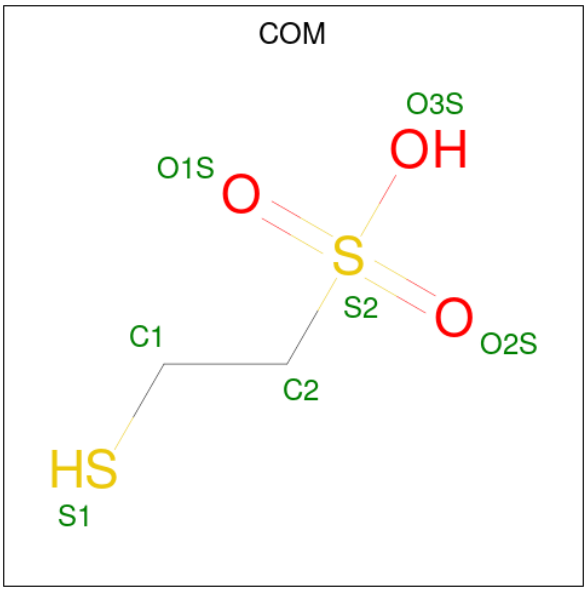
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	E	2	2	2	0	1
			Total	Mg		
4	F	1	1	1	0	0

- Molecule 5 is FACTOR 430 (CCD ID: F43) (formula: $C_{42}H_{51}N_6NiO_{13}$).



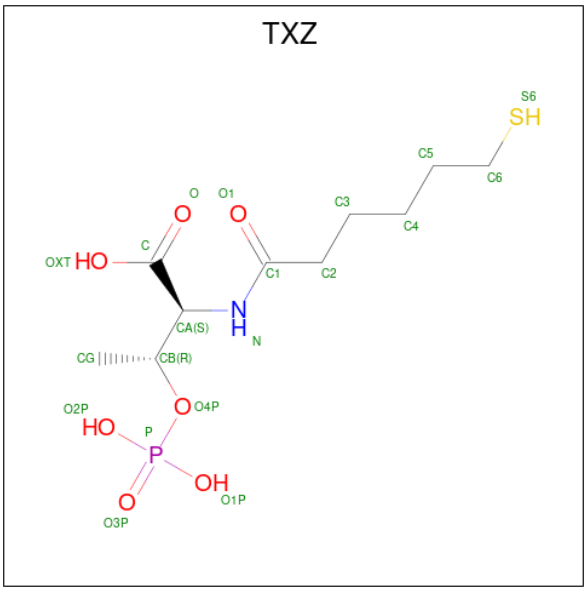
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	Ni	O		
5	A	1	62	42	6	1	13	0	0
			Total	C	N	Ni	O		
5	D	1	62	42	6	1	13	0	0

- Molecule 6 is 1-THIOETHANESULFONIC ACID (CCD ID: COM) (formula: $C_2H_6O_3S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
6	A	1	7	2	3	2	0	1
			Total	C	O	S		
6	D	1	7	2	3	2	0	1

- Molecule 7 is O-phosphono-N-(6-sulfanylhexanoyl)-L-threonine (CCD ID: TXZ) (formula: $C_{10}H_{20}NO_7PS$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
7	A	1	20	10	1	7	1	1	0	1

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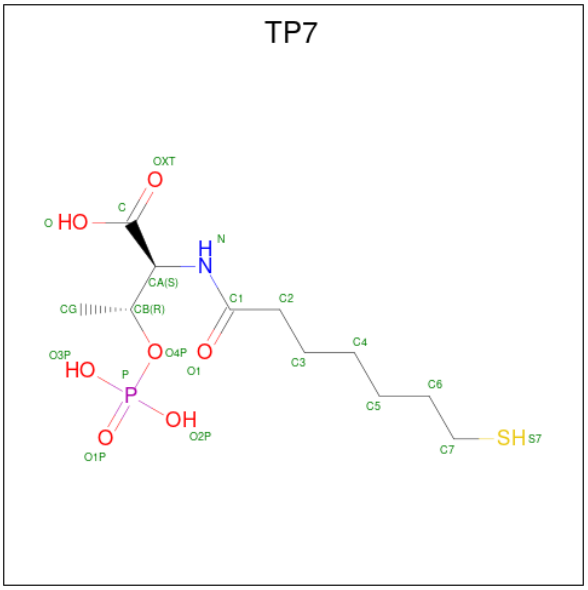
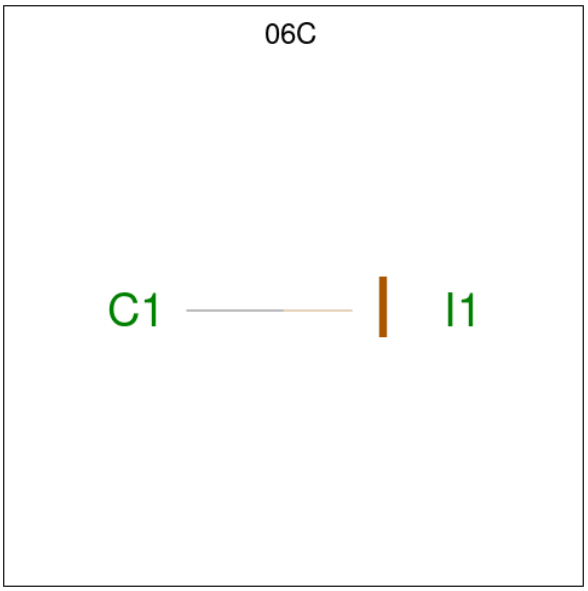
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
7	D	1	20	10	1	7	1	1	0	1

- Molecule 8 is Coenzyme B (CCD ID: TP7) (formula: $C_{11}H_{22}NO_7PS$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
8	A	1	21	11	1	7	1	1	0	1
8	D	1	21	11	1	7	1	1	0	1

- Molecule 9 is Iodomethane (CCD ID: 06C) (formula: CH_3I).

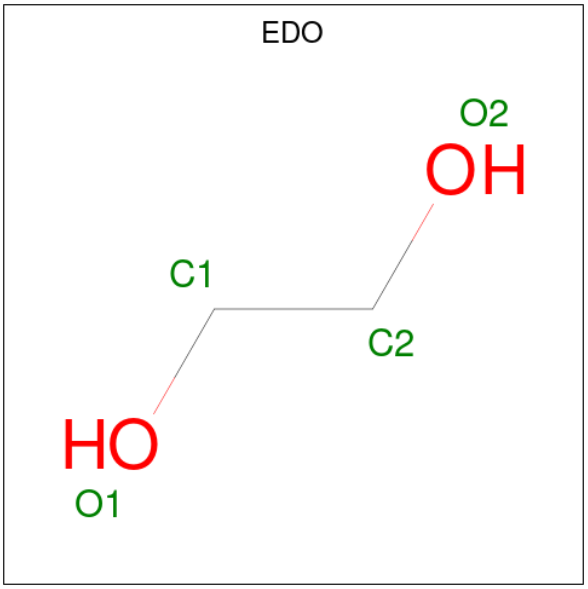


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C I 2 1 1	0	1
9	D	1	Total C I 2 1 1	0	1

- Molecule 10 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total K 1 1	0	0

- Molecule 11 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 12 is water.

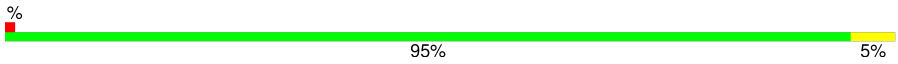
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
12	A	551	560	560	0	9
			Total	O		
12	B	462	465	465	0	5
			Total	O		
12	C	285	290	290	0	6
			Total	O		
12	D	586	594	594	0	11
			Total	O		
12	E	440	448	448	0	13
			Total	O		
12	F	278	280	280	0	2

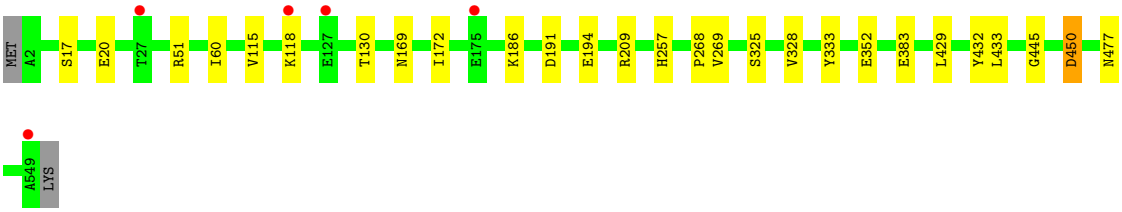
3 Residue-property plots (i)

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

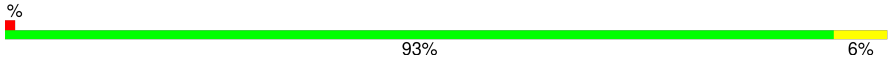
Chain A:

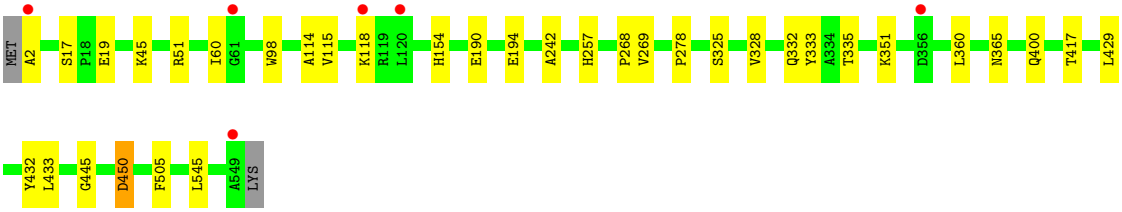




• Molecule 1: Methyl-coenzyme M reductase I subunit alpha

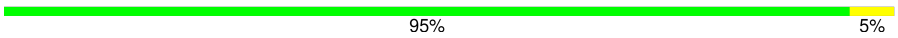
Chain D:





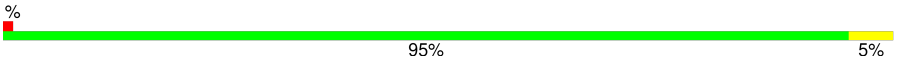
• Molecule 2: Methyl-coenzyme M reductase I subunit beta

Chain B:



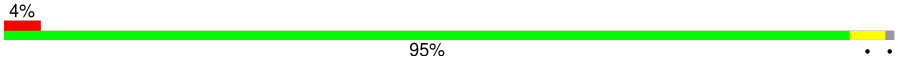
• Molecule 2: Methyl-coenzyme M reductase I subunit beta

Chain E:



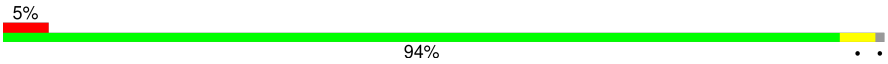
• Molecule 3: Methyl-coenzyme M reductase I subunit gamma

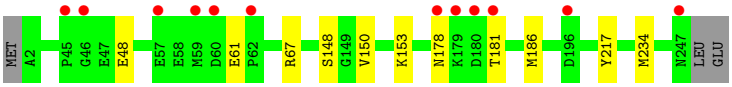
Chain C:



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

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.89Å 118.17Å 122.39Å 90.00° 91.94° 90.00°	Depositor
Resolution (Å)	50.00 – 1.20 50.00 – 1.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-1.20) 99.9 (50.00-1.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.59 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.132 , 0.156 0.132 , 0.156	Depositor DCC
R_{free} test set	36128 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	8.6	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 33.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.007 for -h,-l,-k 0.012 for h,-k,-l	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	22289	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: TXZ, TP7, 06C, MHS, MGN, EDO, K, MG, AGM, SMC, F43, COM, GL3

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	1.14	1/4366 (0.0%)	1.04	6/5926 (0.1%)
1	D	1.18	5/4379 (0.1%)	1.05	4/5946 (0.1%)
2	B	1.09	0/3473	0.99	1/4698 (0.0%)
2	E	1.09	0/3464	1.00	0/4687
3	C	1.22	0/2075	1.05	1/2794 (0.0%)
3	F	1.20	2/2069 (0.1%)	1.06	0/2786
All	All	1.15	8/19826 (0.0%)	1.03	12/26837 (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	1	1
1	D	1	1
2	B	0	1
2	E	0	2
All	All	2	5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	269	VAL	CA-CB	8.87	1.65	1.54
1	D	60	ILE	CA-CB	8.52	1.64	1.54
1	A	450	ASP	CA-CB	-6.94	1.42	1.53
1	D	450	ASP	CA-C	-5.67	1.45	1.52
3	F	153	LYS	CG-CD	5.50	1.69	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	450	ASP	N-CA-CB	7.91	121.74	110.12
1	A	269	VAL	N-CA-C	7.62	119.31	110.62
1	D	450	ASP	N-CA-CB	6.66	119.91	110.12
1	D	450	ASP	CB-CA-C	6.33	121.31	110.79
2	B	3	LYS	CD-CE-NZ	-6.25	91.89	111.90

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	450	ASP	CA
1	D	450	ASP	CA

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	51	ARG	Sidechain
2	B	333	TYR	Sidechain
1	D	51	ARG	Sidechain
2	E	333	TYR	Sidechain
2	E	72	ARG	Sidechain

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	4295	0	4103	26	0
1	D	4303	0	4134	26	0
2	B	3392	0	3411	20	0
2	E	3377	0	3398	23	0
3	C	2023	0	1958	20	0
3	F	2021	0	1964	13	0
4	A	4	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
4	F	1	0	0	0	0
5	A	62	0	43	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	62	0	43	1	0
6	A	7	0	4	0	0
6	D	7	0	5	0	0
7	A	20	0	17	0	0
7	D	20	0	17	0	0
8	A	21	0	19	0	0
8	D	21	0	19	0	0
9	A	2	0	0	1	0
9	D	2	0	0	1	0
10	A	1	0	0	0	0
11	D	4	0	6	0	0
12	A	560	0	0	8	0
12	B	465	0	0	3	0
12	C	290	0	0	4	0
12	D	594	0	0	6	0
12	E	448	0	0	4	0
12	F	280	0	0	2	0
All	All	22289	0	19141	100	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 3.

The worst 5 of 100 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:432:TYR:HB2	3:C:234[B]:MET:HE3	1.10	1.09
1:A:432:TYR:CB	3:C:234[B]:MET:HE3	1.83	1.09
1:A:429:LEU:HD12	3:C:234[B]:MET:HE1	1.08	1.06
1:A:429:LEU:CD1	3:C:234[B]:MET:HE1	1.91	1.00
1:A:432:TYR:HB2	3:C:234[B]:MET:CE	1.92	0.99

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	549/550 (100%)	534 (97%)	14 (3%)	1 (0%)	43	16
1	D	551/550 (100%)	536 (97%)	14 (2%)	1 (0%)	43	16
2	B	453/443 (102%)	445 (98%)	8 (2%)	0	100	100
2	E	452/443 (102%)	447 (99%)	5 (1%)	0	100	100
3	C	250/249 (100%)	245 (98%)	5 (2%)	0	100	100
3	F	249/249 (100%)	243 (98%)	6 (2%)	0	100	100
All	All	2504/2484 (101%)	2450 (98%)	52 (2%)	2 (0%)	48	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	325	SER
1	A	325	SER

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	441/435 (101%)	438 (99%)	3 (1%)	76	47
1	D	443/435 (102%)	441 (100%)	2 (0%)	81	59
2	B	354/342 (104%)	353 (100%)	1 (0%)	86	67
2	E	353/342 (103%)	349 (99%)	4 (1%)	65	31
3	C	220/217 (101%)	217 (99%)	3 (1%)	59	24
3	F	219/217 (101%)	214 (98%)	5 (2%)	44	9
All	All	2030/1988 (102%)	2012 (99%)	18 (1%)	73	40

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	148[A]	SER

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Mol	Chain	Res	Type
3	F	186	MET
3	F	150	VAL
1	D	450	ASP
3	F	61	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	296	ASN
1	D	317	GLN
3	F	121	GLN
2	E	102	ASN
2	E	115	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

10 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	AGM	A	271	1	10,11,12	0.83	0	7,13,15	1.11	0
1	MGN	A	400	1	6,9,10	0.92	0	7,12,14	0.83	0
1	MGN	D	400	1	6,9,10	1.71	2 (33%)	7,12,14	0.86	0
1	MHS	A	257	1	10,11,12	2.13	3 (30%)	5,14,16	10.36	3 (60%)
1	MHS	D	257	1	10,11,12	1.91	2 (20%)	5,14,16	10.11	3 (60%)
1	AGM	D	271	1	10,11,12	0.81	0	7,13,15	0.77	0
1	SMC	D	452	1	5,6,7	0.71	0	3,6,8	0.89	0
1	GL3	D	445	1	2,3,4	2.47	1 (50%)	1,2,4	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	SMC	A	452	1	5,6,7	0.86	0	3,6,8	1.03	0
1	GL3	A	445	1	2,3,4	2.58	1 (50%)	1,2,4	0.74	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
1	AGM	A	271	1	-	2/10/11/13	-
1	MGN	A	400	1	-	0/7/9/12	-
1	MGN	D	400	1	-	0/7/9/12	-
1	MHS	A	257	1	-	0/5/6/8	0/1/1/1
1	MHS	D	257	1	-	0/5/6/8	0/1/1/1
1	AGM	D	271	1	-	2/10/11/13	-
1	SMC	D	452	1	-	1/3/5/7	-
1	GL3	D	445	1	-	0/1/1/2	-
1	SMC	A	452	1	-	1/3/5/7	-
1	GL3	A	445	1	-	1/1/1/2	-

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	257	MHS	CE1-NE2	4.54	1.43	1.32
1	D	257	MHS	CE1-NE2	4.27	1.43	1.32
1	A	445	GL3	C-S	-3.65	1.65	1.80
1	D	445	GL3	C-S	-3.50	1.66	1.80
1	D	400	MGN	CB1-CA	-3.46	1.51	1.55

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	257	MHS	ND1-CE1-NE2	-22.38	99.61	112.94
1	D	257	MHS	ND1-CE1-NE2	-21.47	100.16	112.94
1	A	257	MHS	CM-ND1-CE1	-4.92	117.08	126.28
1	D	257	MHS	CD2-NE2-CE1	4.86	111.60	105.24
1	D	257	MHS	CM-ND1-CE1	-4.71	117.47	126.28

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	452	SMC	CA-CB-SG-CS
1	A	452	SMC	CA-CB-SG-CS
1	A	445	GL3	S-C-CA-N
1	A	271	AGM	CE2-CD-NE1-CZ
1	A	271	AGM	NE1-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 24 ligands modelled in this entry, 13 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
7	TXZ	A	557[B]	-	18,19,19	0.87	0	23,25,25	1.33	4 (17%)
5	F43	D	552	1,6	63,71,71	2.29	10 (15%)	73,118,118	1.46	12 (16%)
8	TP7	A	558[A]	-	19,20,20	0.77	0	24,26,26	1.24	2 (8%)
8	TP7	D	553[A]	-	19,20,20	0.78	1 (5%)	24,26,26	1.17	3 (12%)
6	COM	A	556[A]	5	6,6,6	4.56	2 (33%)	8,8,8	4.30	7 (87%)
9	06C	D	556[B]	-	1,1,1	19.71	1 (100%)	-		
6	COM	D	555[A]	5	6,6,6	4.57	2 (33%)	8,8,8	3.63	5 (62%)
7	TXZ	D	554[B]	-	18,19,19	0.93	1 (5%)	23,25,25	1.11	2 (8%)
5	F43	A	555	1,6	63,71,71	2.11	9 (14%)	73,118,118	1.40	13 (17%)
9	06C	A	559[B]	-	1,1,1	19.23	1 (100%)	-		
11	EDO	D	558	-	3,3,3	0.40	0	2,2,2	0.54	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
7	TXZ	A	557[B]	-	-	2/23/23/23	-
5	F43	D	552	1,6	-	11/28/185/185	-
8	TP7	A	558[A]	-	-	2/24/24/24	-
8	TP7	D	553[A]	-	-	2/24/24/24	-
6	COM	A	556[A]	5	-	1/4/4/4	-
6	COM	D	555[A]	5	-	1/4/4/4	-
7	TXZ	D	554[B]	-	-	2/23/23/23	-
5	F43	A	555	1,6	-	11/28/185/185	-
11	EDO	D	558	-	-	1/1/1/1	-

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	D	556[B]	06C	C1-I1	19.71	4.18	2.09
9	A	559[B]	06C	C1-I1	19.23	4.13	2.09
6	D	555[A]	COM	C2-S2	-10.86	1.62	1.77
6	A	556[A]	COM	C2-S2	-10.39	1.63	1.77
5	D	552	F43	NI-NB	9.54	2.12	1.89

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	556[A]	COM	O1S-S2-C2	8.66	119.81	106.73
6	D	555[A]	COM	O1S-S2-C2	7.40	117.91	106.73
6	A	556[A]	COM	O3S-S2-O2S	-5.42	97.85	111.40
6	D	555[A]	COM	O3S-S2-O2S	-4.32	100.59	111.40
6	D	555[A]	COM	O2S-S2-C2	4.21	113.09	106.73

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	555	F43	C3A-CAA-CBA-CCA
5	D	552	F43	C3A-CAA-CBA-CCA
8	A	558[A]	TP7	C2-C3-C4-C5
11	D	558	EDO	O1-C1-C2-O2
6	A	556[A]	COM	C1-C2-S2-O2S

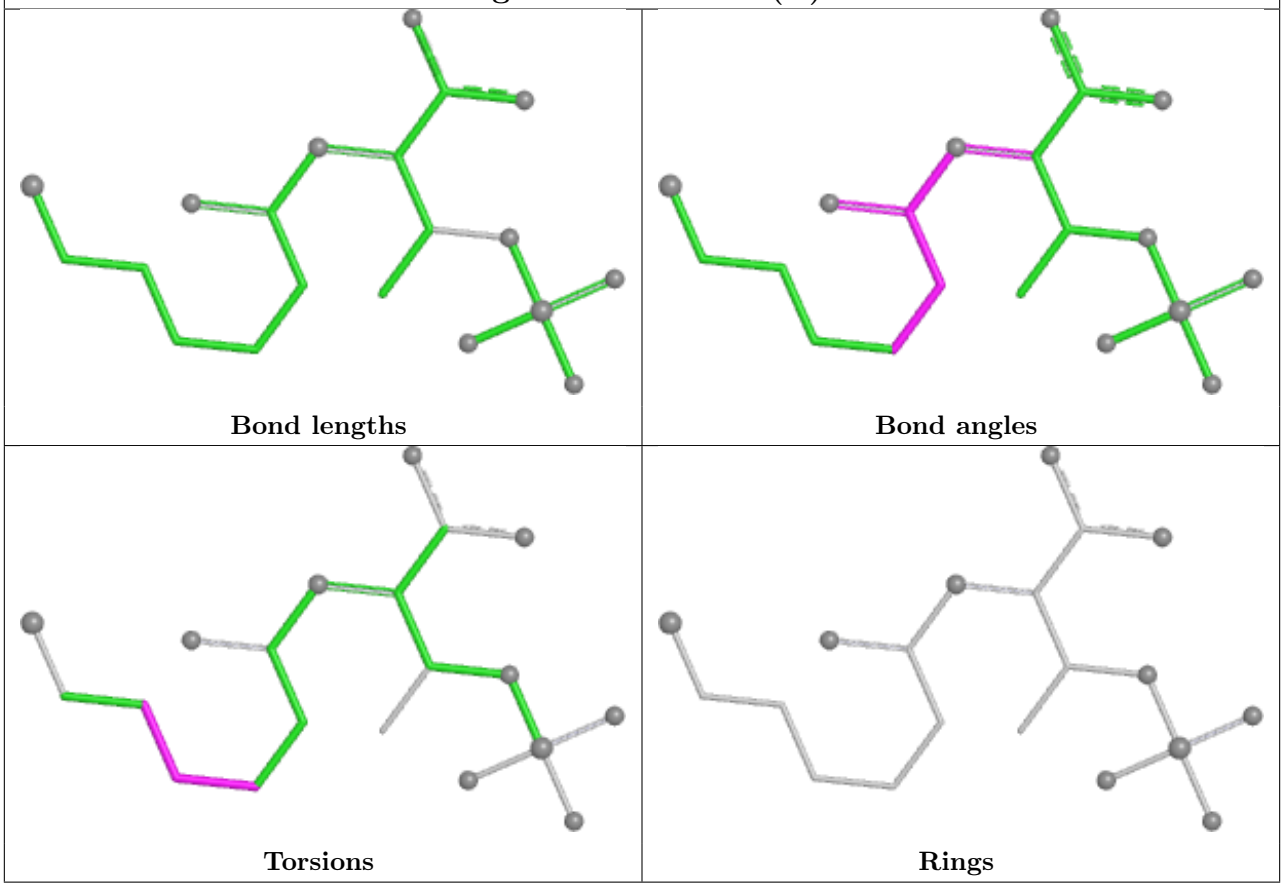
There are no ring outliers.

4 monomers are involved in 4 short contacts:

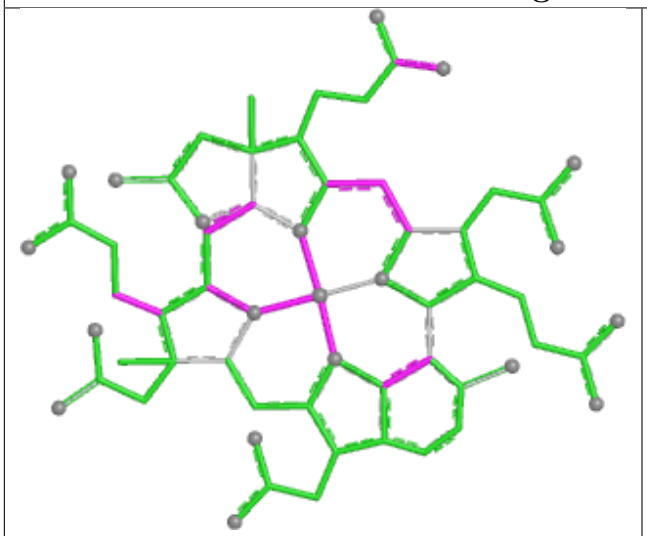
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	552	F43	1	0
9	D	556[B]	06C	1	0
5	A	555	F43	1	0
9	A	559[B]	06C	1	0

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 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.

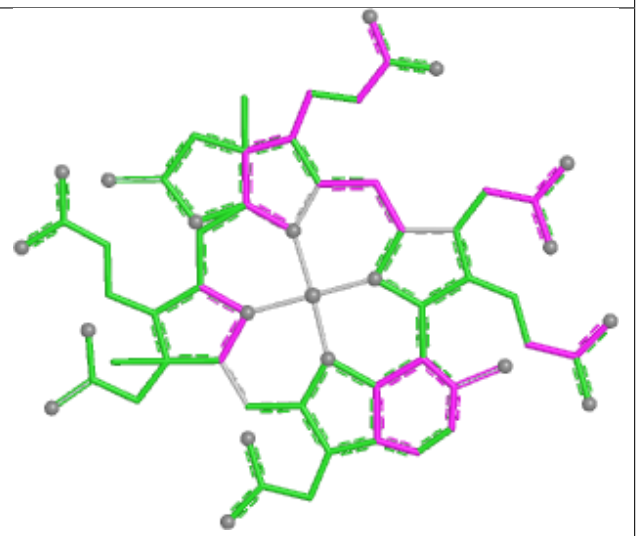
Ligand TXZ A 557 (B)



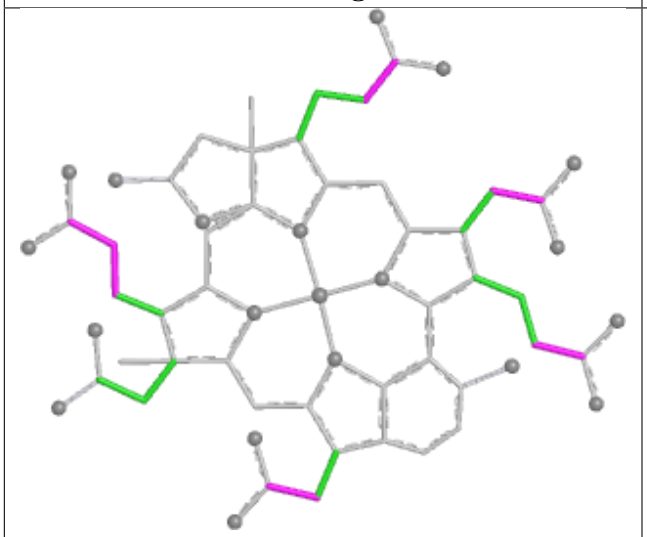
Ligand F43 D 552



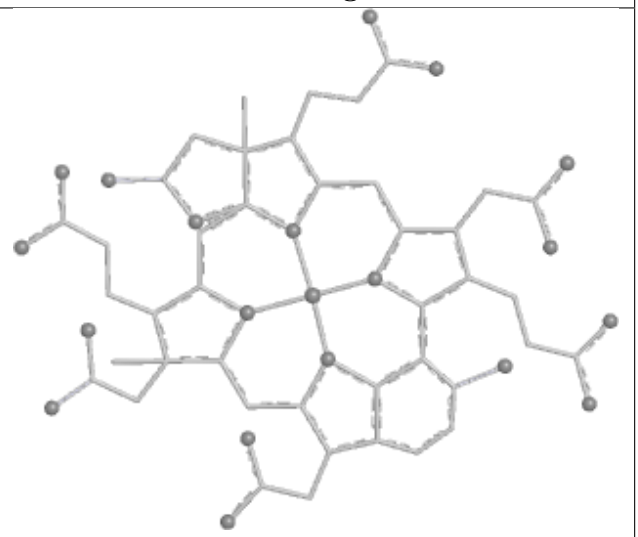
Bond lengths



Bond angles

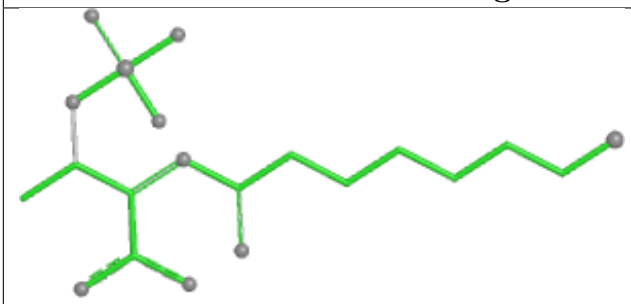


Torsions

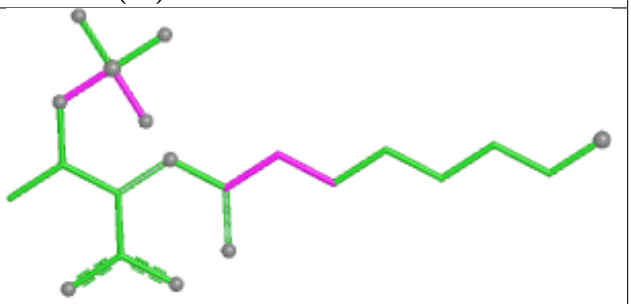


Rings

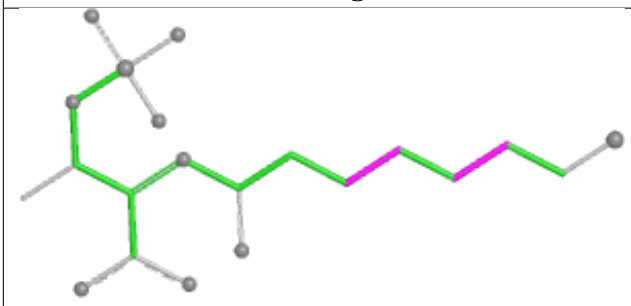
Ligand TP7 A 558 (A)



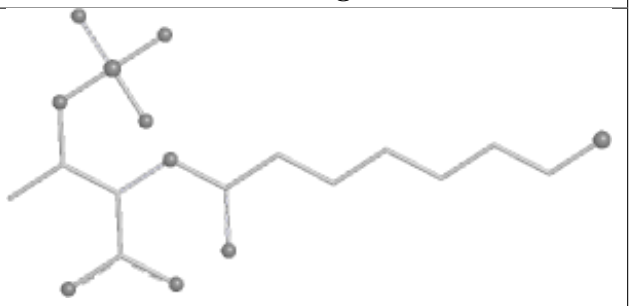
Bond lengths



Bond angles

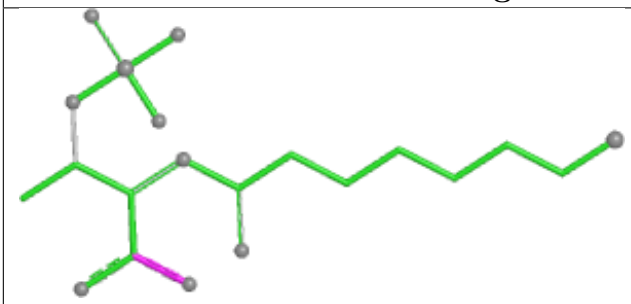


Torsions

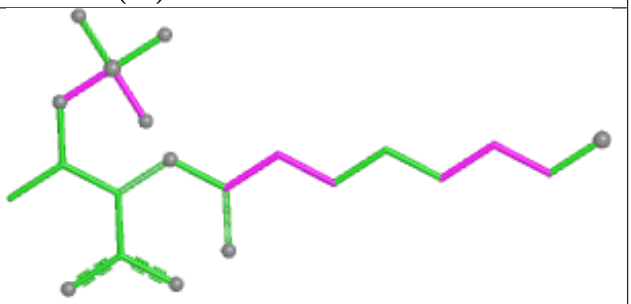


Rings

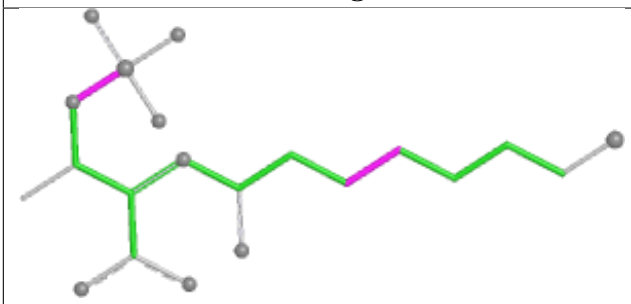
Ligand TP7 D 553 (A)



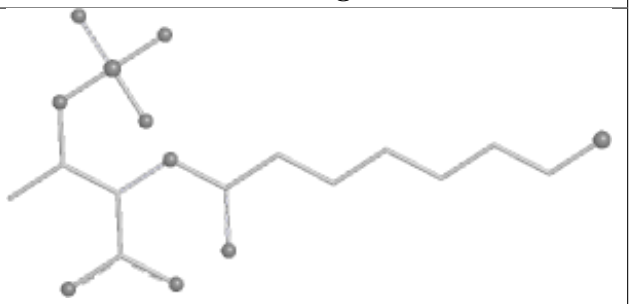
Bond lengths



Bond angles

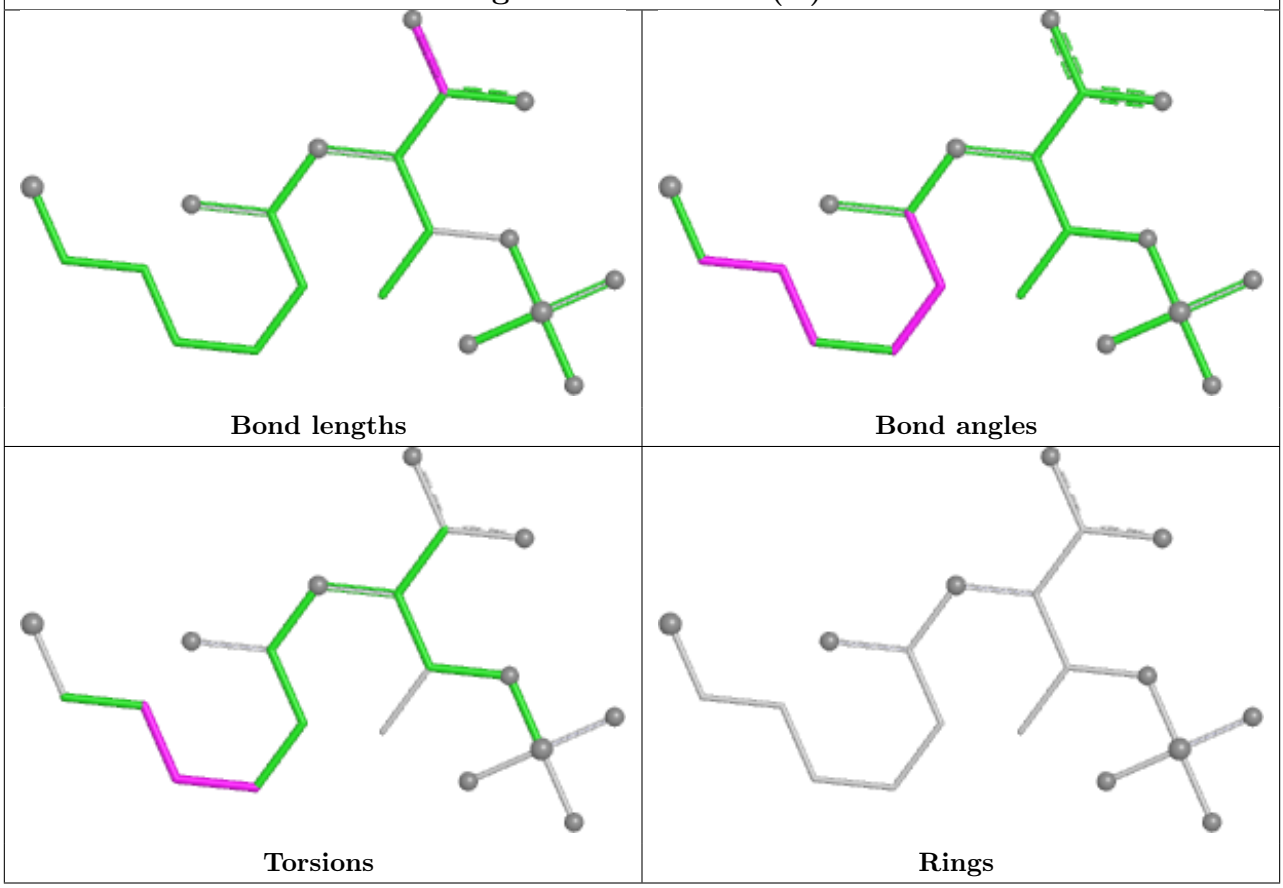


Torsions

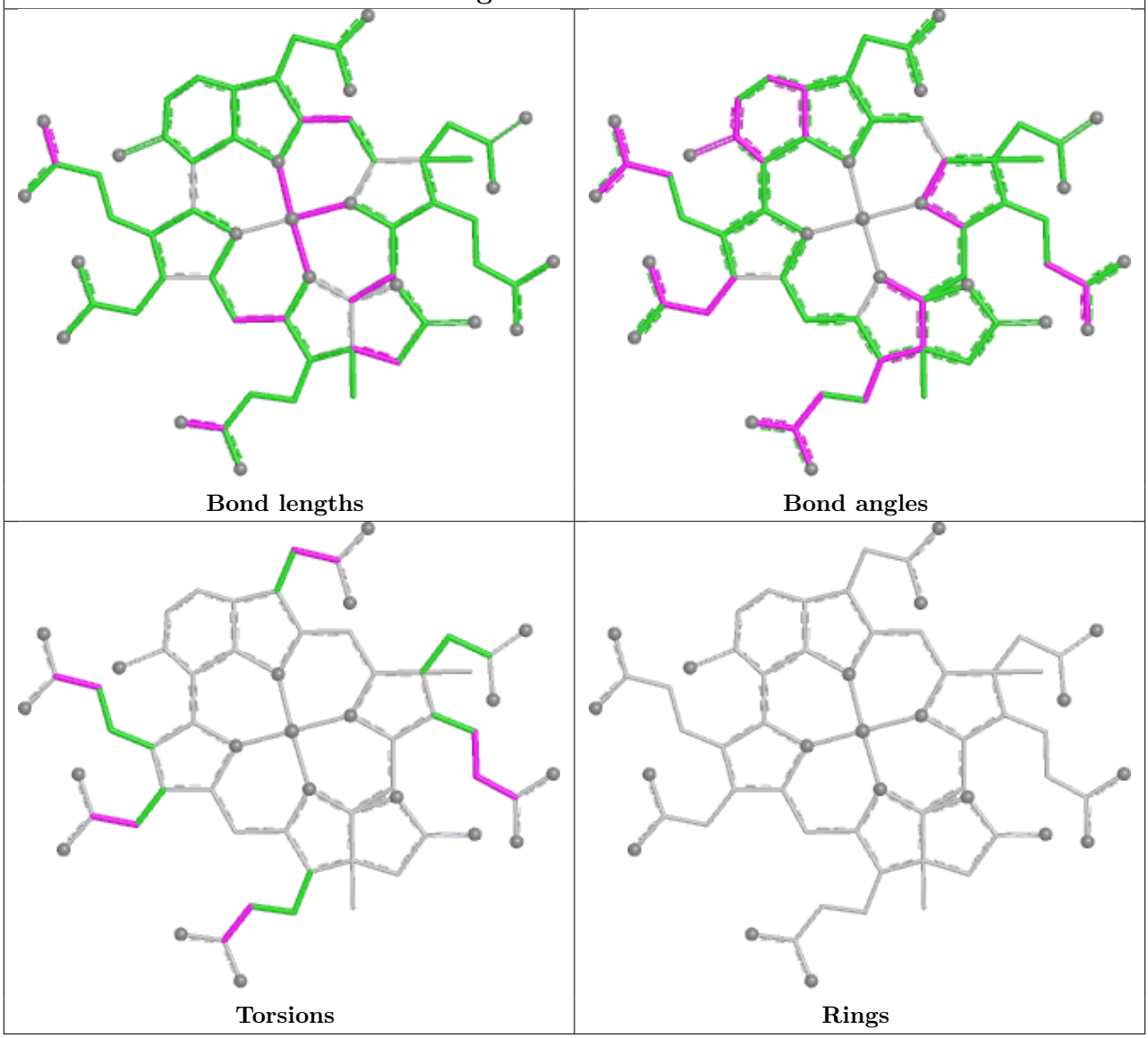


Rings

Ligand TXZ D 554 (B)



Ligand F43 A 555



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	543/550 (98%)	-0.51	5 (0%)	81	84	4, 8, 18, 31	8 (1%)
1	D	543/550 (98%)	-0.52	6 (1%)	78	79	4, 8, 16, 34	10 (1%)
2	B	442/443 (99%)	-0.41	0	100	100	4, 9, 18, 34	12 (2%)
2	E	442/443 (99%)	-0.33	5 (1%)	78	79	5, 10, 21, 39	11 (2%)
3	C	246/249 (98%)	-0.07	9 (3%)	45	45	5, 12, 29, 45	6 (2%)
3	F	246/249 (98%)	-0.06	12 (4%)	35	37	5, 11, 28, 49	5 (2%)
All	All	2462/2484 (99%)	-0.37	37 (1%)	72	73	4, 9, 20, 49	52 (2%)

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	ALA	4.3
3	C	62	PRO	3.6
1	D	356	ASP	3.5
2	E	2	ALA	3.3
3	F	60	ASP	3.3

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	0.98	0.05	7,8,11,15	0
1	MHS	D	257	11/12	0.98	0.04	7,8,10,13	0
1	AGM	D	271	12/13	0.98	0.04	4,5,6,6	0
1	SMC	A	452	7/8	0.99	0.04	5,6,7,8	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	AGM	A	271	12/13	0.99	0.04	5,5,6,7	0
1	MGN	A	400	10/11	0.99	0.03	5,6,7,7	0
1	MGN	D	400	10/11	0.99	0.03	4,5,6,6	0
1	SMC	D	452	7/8	0.99	0.04	6,6,8,8	0
1	GL3	D	445	4/5	1.00	0.02	5,5,5,5	0
1	GL3	A	445	4/5	1.00	0.04	4,5,5,5	0

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(Å^2)	Q<0.9
11	EDO	D	558	4/4	0.84	0.12	26,26,31,31	0
4	MG	E	445[A]	1/1	0.96	0.17	16,16,16,16	1
4	MG	B	445[B]	1/1	0.97	0.04	9,9,9,9	1
4	MG	A	554	1/1	0.97	0.21	16,16,16,16	0
4	MG	B	444	1/1	0.97	0.13	19,19,19,19	0
4	MG	A	553[A]	1/1	0.98	0.09	8,8,8,8	1
6	COM	A	556[A]	7/7	0.98	0.08	7,8,11,11	7
4	MG	C	251	1/1	0.98	0.09	11,11,11,11	1
4	MG	D	551	1/1	0.99	0.16	17,17,17,17	0
4	MG	E	444	1/1	0.99	0.18	18,18,18,18	0
4	MG	A	552[B]	1/1	0.99	0.03	8,8,8,8	1
4	MG	F	250	1/1	0.99	0.05	12,12,12,12	0
5	F43	A	555	62/62	0.99	0.03	4,5,7,9	0
5	F43	D	552	62/62	0.99	0.04	5,6,8,11	0
4	MG	C	250	1/1	0.99	0.04	13,13,13,13	0
6	COM	D	555[A]	7/7	0.99	0.05	6,7,9,9	7
7	TXZ	A	557[B]	20/20	0.99	0.04	7,7,8,9	20
7	TXZ	D	554[B]	20/20	0.99	0.04	6,7,8,8	20
8	TP7	A	558[A]	21/21	0.99	0.04	5,6,8,8	21
8	TP7	D	553[A]	21/21	0.99	0.04	4,5,7,7	21
4	MG	A	551	1/1	0.99	0.11	13,13,13,13	0
9	06C	D	556[B]	2/2	1.00	0.01	4,4,4,7	2

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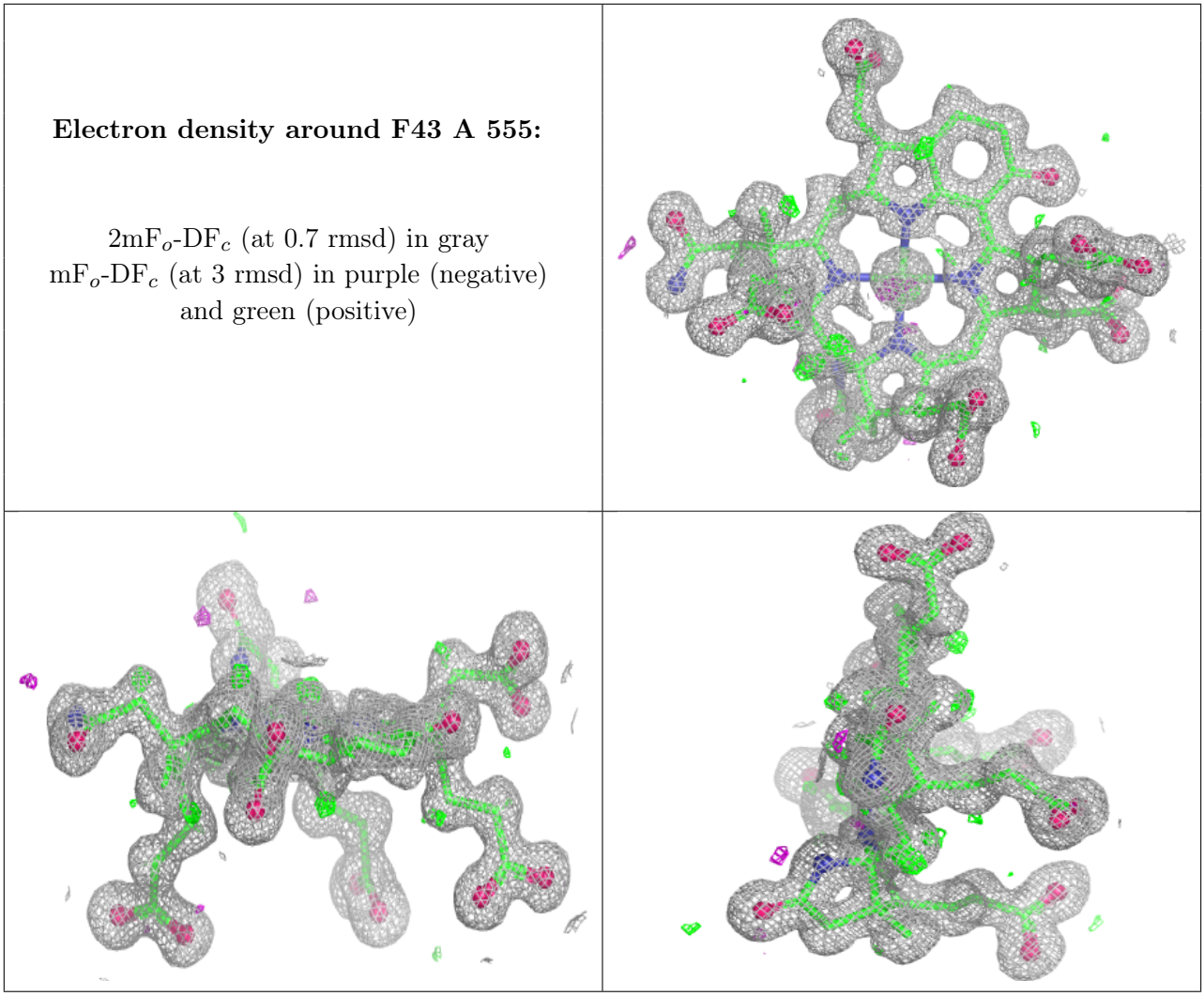
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
10	K	A	561	1/1	1.00	0.04	8,8,8,8	0
9	06C	A	559[B]	2/2	1.00	0.02	4,4,4,7	2

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.

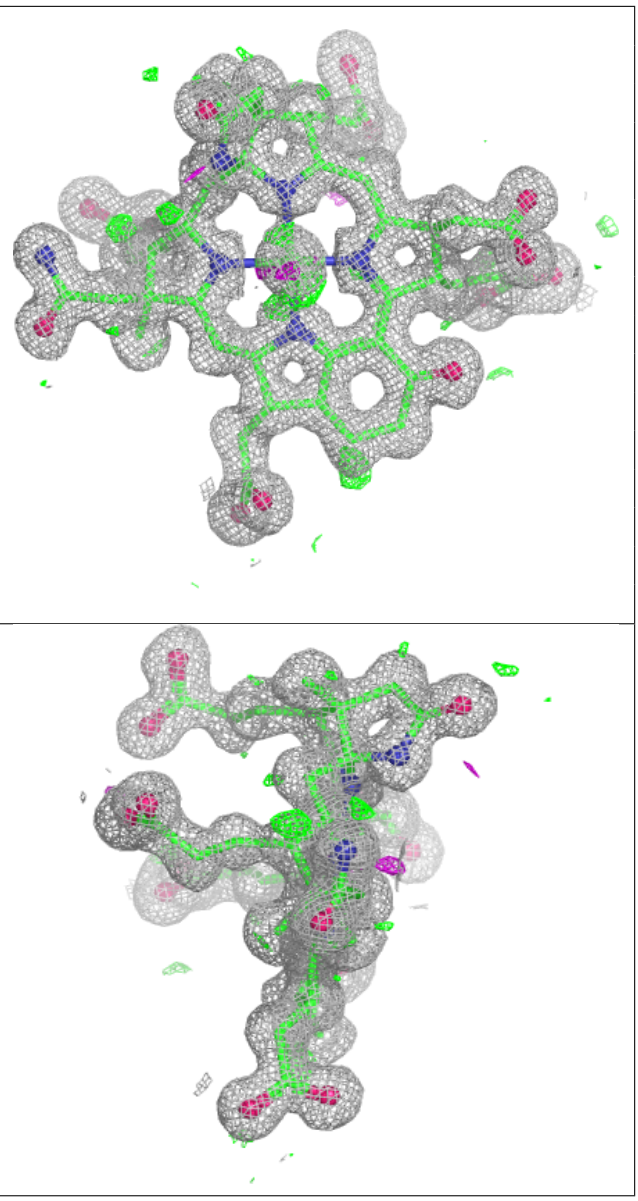
Electron density around F43 A 555:

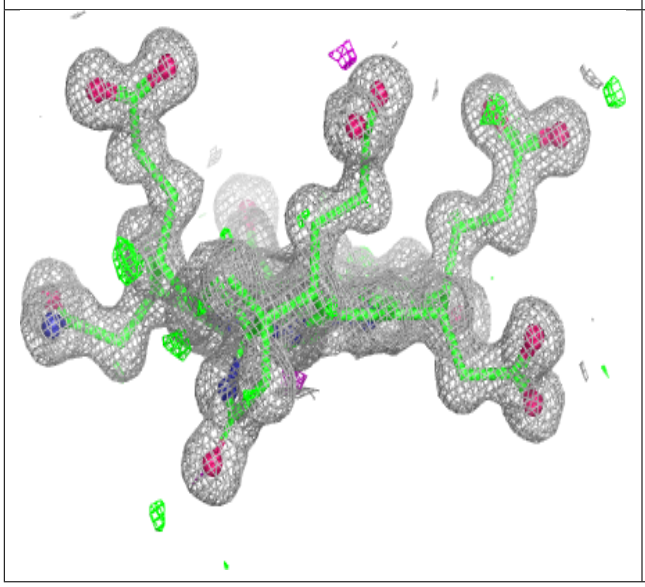
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)



Electron density around F43 D 552:

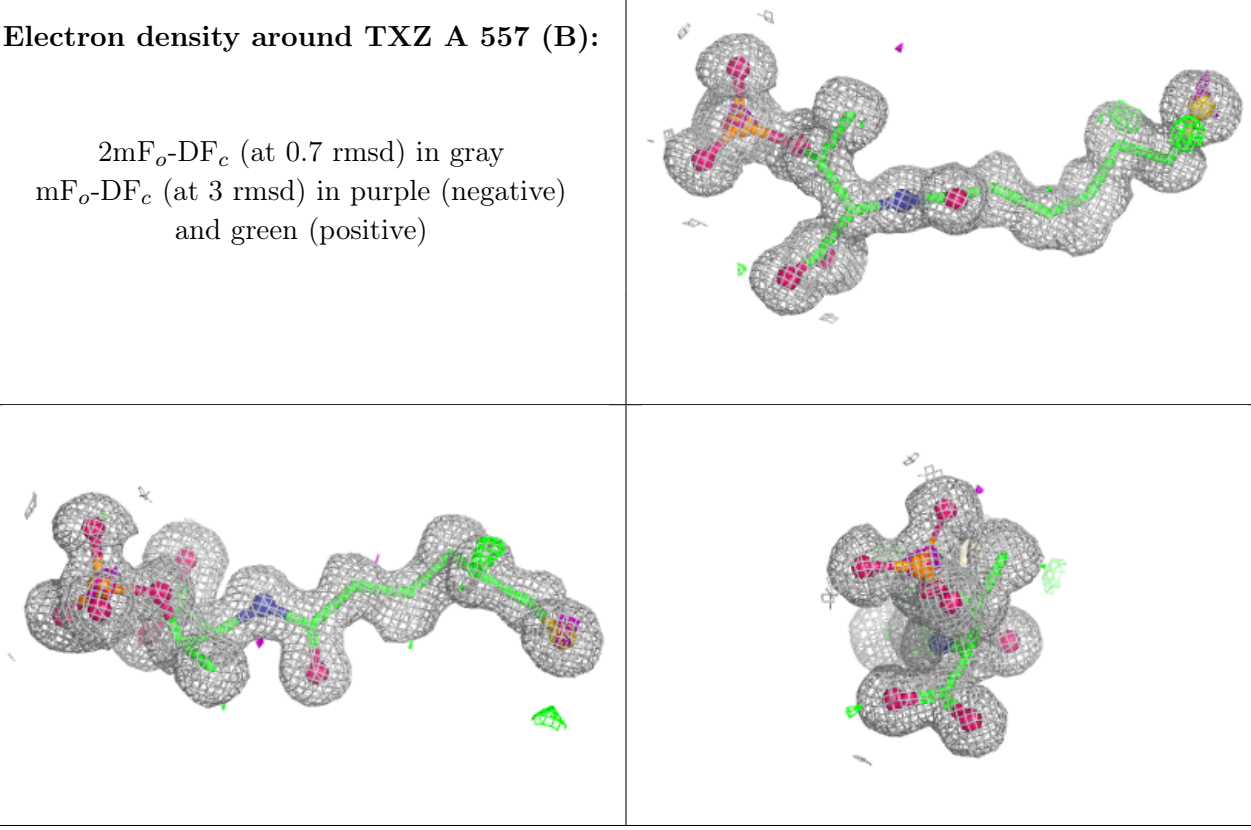
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





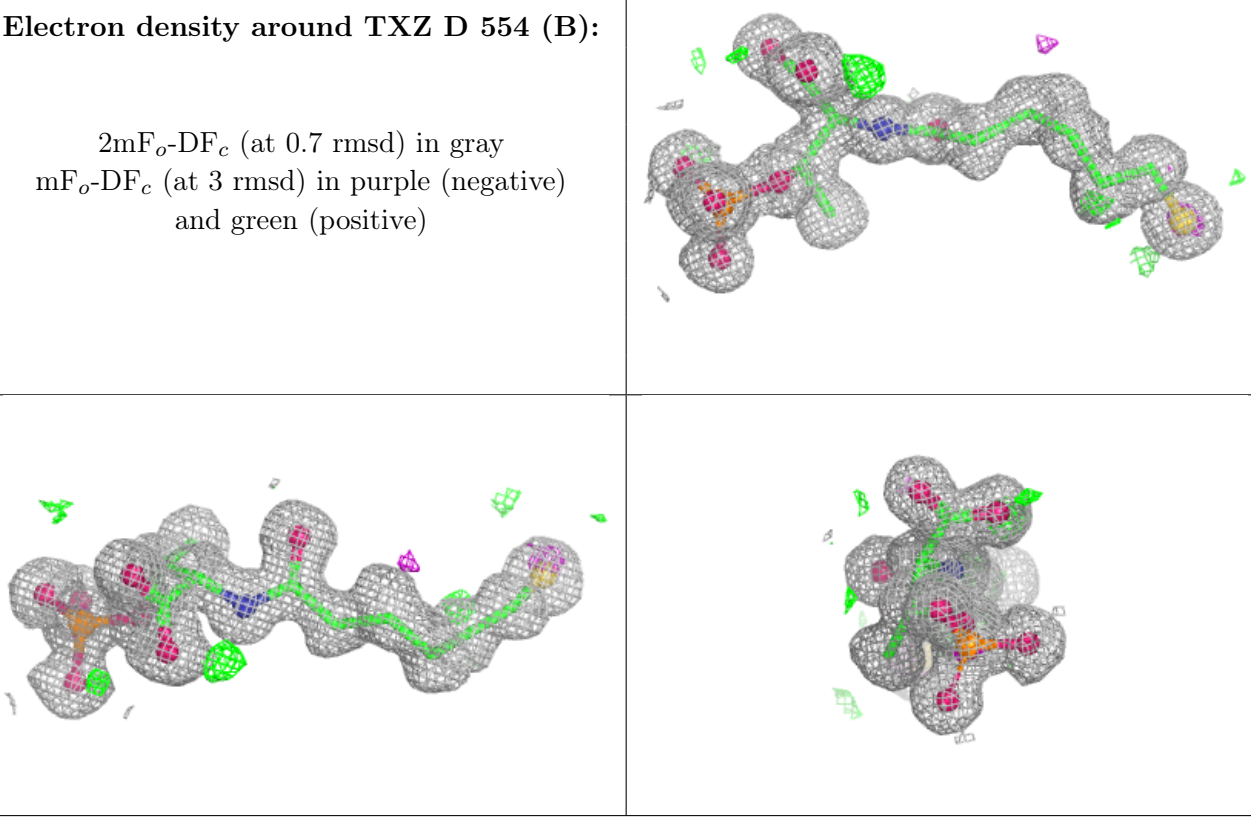
Electron density around TXZ A 557 (B):

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



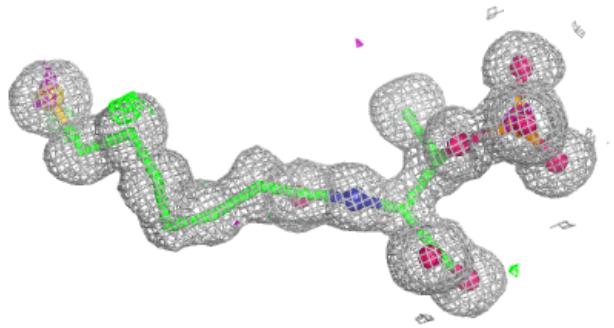
Electron density around TXZ D 554 (B):

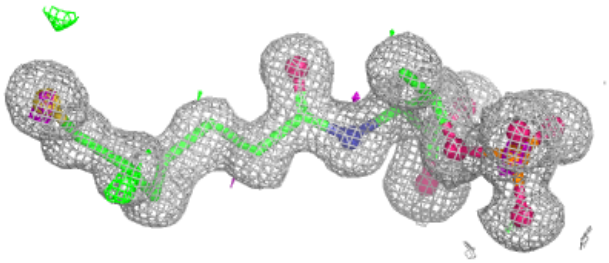
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

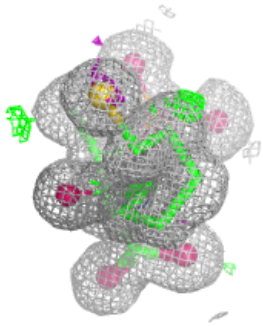


Electron density around TP7 A 558 (A):

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

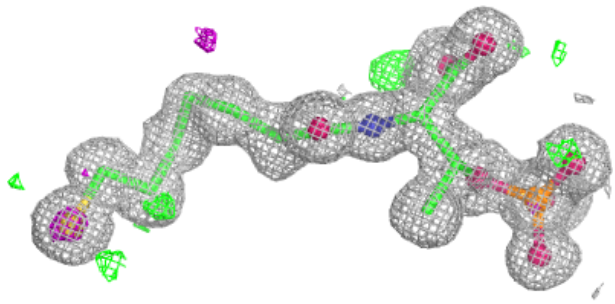


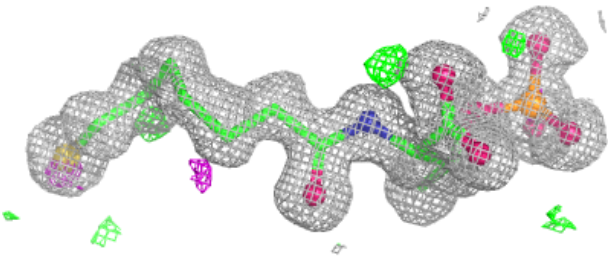


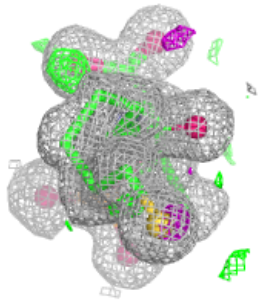


Electron density around TP7 D 553 (A):

$2mF_o$-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.