wwPDB X-ray Structure Validation Summary Report (i)

Aug 24, 2026 – 12:32 pm BST

PDB ID	:	5G0R / pdb_00005g0r
Title	:	METHYL-COENZYME M REDUCTASE I FROM METHANOTHERMOBACTER MARBURGENSIS EXPOSED TO 3-NITROOXYPROPANOL
Authors	:	Wagner, T.
Deposited on	:	2016-03-22
Resolution	:	1.25 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:

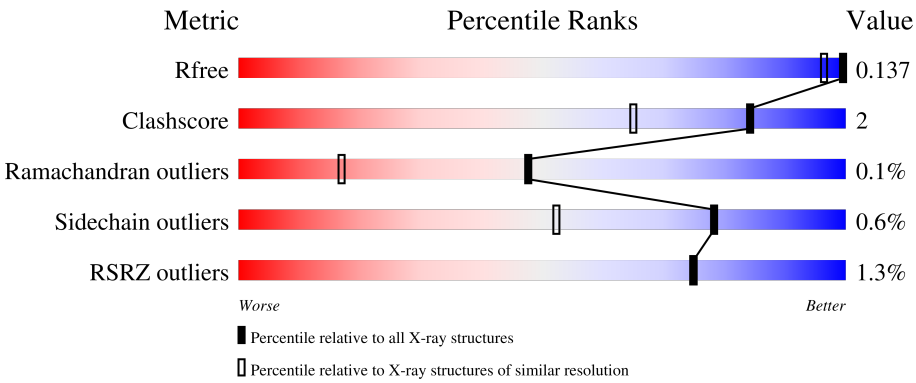
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 1.25 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	1693 (1.28-1.24)
Clashscore	190562	1730 (1.28-1.24)
Ramachandran outliers	187476	1695 (1.28-1.24)
Sidechain outliers	187428	1694 (1.28-1.24)
RSRZ outliers	180081	1693 (1.28-1.24)

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	.% 94% 6%
1	D	550	.% 94% 6%
2	B	443	97% .
2	E	443	.% 95% 5%
3	C	249	3% 95% .

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Mol	Chain	Length	Quality of chain
3	F	249	3% 94% 6%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 22540 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	549	4391	2790	724	857	20	0	25	1
1	D	548	4394	2793	722	859	20	0	24	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	3433	2185	563	664	21	0	19	0
2	E	442	3409	2177	557	653	22	0	17	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	248	2052	1271	360	410	11	0	8	0
3	F	248	2061	1278	367	405	11	0	8	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	6	6	6	0	1
4	B	2	2	2	0	1
4	C	2	2	2	0	0

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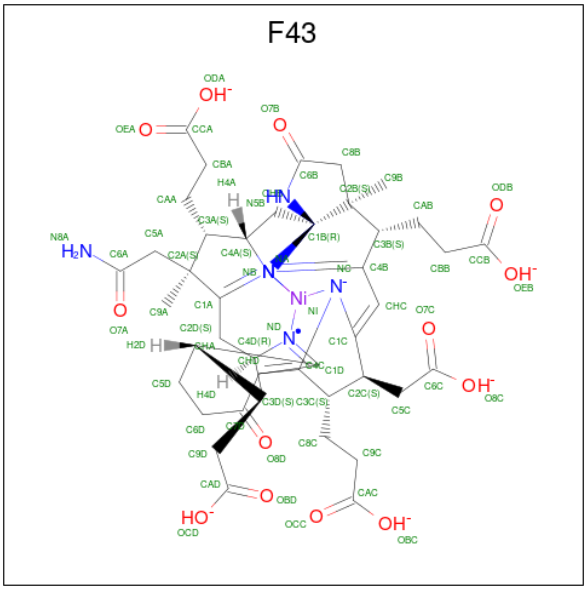
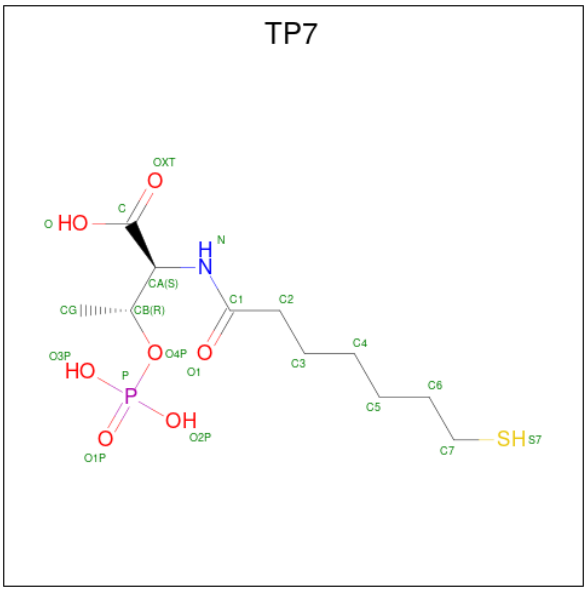
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	D	3	3	3	0	0
			Total	Mg		
4	E	4	4	4	0	1
			Total	Mg		
4	F	1	1	1	0	0

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



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

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
7	A	2	2	2	0	0
7	D	1	1	1	0	0

- Molecule 8 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 9 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
9	A	1	1	1	0	0
9	B	1	1	1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
9	E	1	1	1	0	0

- Molecule 10 is water.

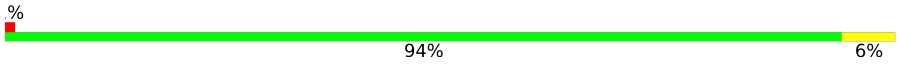
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
10	A	640	640	640	0	0
			Total	O		
10	B	511	511	511	0	0
			Total	O		
10	C	263	263	263	0	2
			Total	O		
10	D	542	542	542	0	1
			Total	O		
10	E	413	413	413	0	0
			Total	O		
10	F	240	240	240	0	0

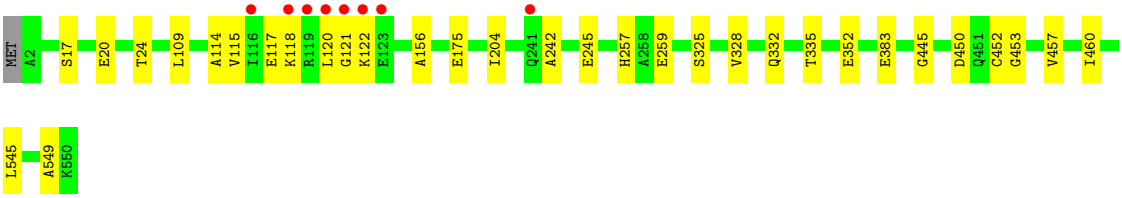
3 Residue-property plots (i)

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

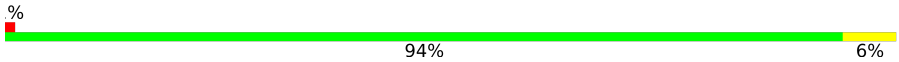
Chain A:

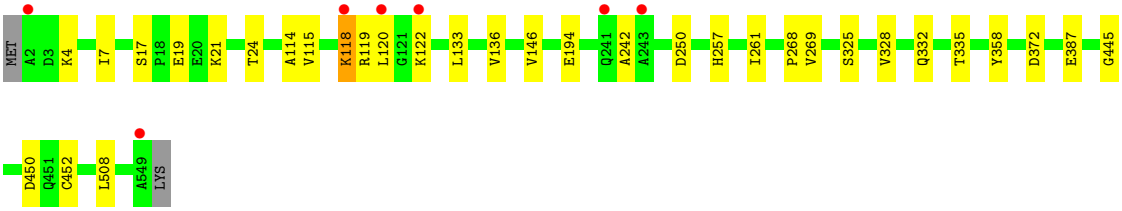




• Molecule 1: METHYL-COENZYME M REDUCTASE I SUBUNIT ALPHA

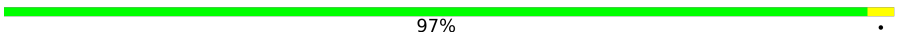
Chain D:





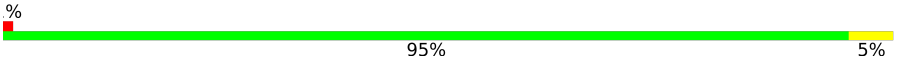
• Molecule 2: METHYL-COENZYME M REDUCTASE I SUBUNIT BETA

Chain B:



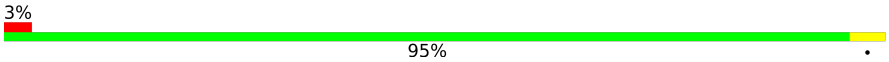
• Molecule 2: METHYL-COENZYME M REDUCTASE I SUBUNIT BETA

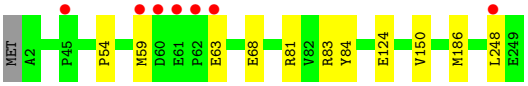
Chain E:



• Molecule 3: METHYL-COENZYME M REDUCTASE I SUBUNIT GAMMA

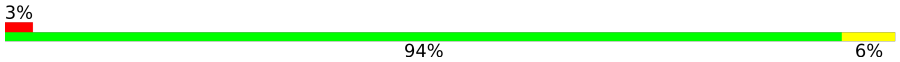
Chain C:

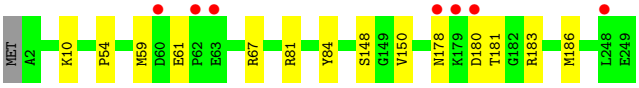




• Molecule 3: METHYL-COENZYME M REDUCTASE I SUBUNIT GAMMA

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	82.20Å 118.10Å 122.64Å 90.00° 92.03° 90.00°	Depositor
Resolution (Å)	38.80 – 1.25 38.80 – 1.25	Depositor EDS
% Data completeness (in resolution range)	98.4 (38.80-1.25) 98.5 (38.80-1.25)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.92 (at 1.25Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.105 , 0.124 0.121 , 0.137	Depositor DCC
R_{free} test set	31701 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	10.0	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 39.8	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 0.013 for h,-k,-l	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	22540	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: MG, AGM, TP7, MHS, DYA, CL, NA, MGN, K, GL3, SMC, F43

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	0.64	1/4498 (0.0%)	0.78	0/6106
1	D	0.65	1/4495 (0.0%)	0.79	1/6101 (0.0%)
2	B	0.62	0/3532	0.75	0/4777
2	E	0.61	0/3514	0.75	0/4752
3	C	0.63	0/2110	0.80	0/2841
3	F	0.62	0/2118	0.80	0/2849
All	All	0.63	2/20267 (0.0%)	0.78	1/27426 (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
2	B	0	1
2	E	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	269	VAL	CA-CB	8.90	1.65	1.54
1	A	549	ALA	C-N	-6.11	1.24	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	146	VAL	N-CA-C	5.76	116.17	111.62

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	333	TYR	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	4391	0	4235	25	0
1	D	4394	0	4228	26	0
2	B	3433	0	3466	21	0
2	E	3409	0	3469	21	0
3	C	2052	0	1987	9	0
3	F	2061	0	2015	10	0
4	A	6	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	3	0	0	0	0
4	E	4	0	0	0	0
4	F	1	0	0	0	0
5	A	62	0	43	1	0
5	D	62	0	43	1	0
6	A	21	0	19	0	0
6	D	21	0	19	0	0
7	A	2	0	0	0	0
7	D	1	0	0	0	0
8	A	1	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	E	1	0	0	0	0
10	A	640	0	0	11	1
10	B	511	0	0	4	0
10	C	263	0	0	1	0
10	D	542	0	0	5	1
10	E	413	0	0	2	0
10	F	240	0	0	1	0
All	All	22540	0	19524	92	1

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 2.

The worst 5 of 92 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:D:114:ALA:O	1:D:118:LYS:HG2	1.83	0.78
2:B:405[A]:MET:SD	1:D:115:VAL:HG22	2.25	0.76
2:E:322[B]:ARG:NH2	3:F:67[B]:ARG:HG3	2.05	0.71
2:B:14[A]:ARG:CZ	3:C:63:GLU:OE2	2.43	0.67
2:B:299:LEU:HD21	2:B:349[A]:PHE:CE1	2.30	0.66

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2630:HOH:O	10:D:2436:HOH:O[2_644]	2.15	0.05

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	566/550 (103%)	548 (97%)	17 (3%)	1 (0%)	43	16
1	D	564/550 (102%)	544 (96%)	19 (3%)	1 (0%)	43	16
2	B	460/443 (104%)	453 (98%)	7 (2%)	0	100	100
2	E	458/443 (103%)	451 (98%)	7 (2%)	0	100	100
3	C	254/249 (102%)	249 (98%)	5 (2%)	0	100	100
3	F	254/249 (102%)	248 (98%)	6 (2%)	0	100	100
All	All	2556/2484 (103%)	2493 (98%)	61 (2%)	2 (0%)	48	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	325	SER
1	D	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	457/434 (105%)	454 (99%)	3 (1%)	76	47
1	D	456/434 (105%)	454 (100%)	2 (0%)	84	63
2	B	361/342 (106%)	361 (100%)	0	100	100
2	E	359/342 (105%)	359 (100%)	0	100	100
3	C	224/217 (103%)	221 (99%)	3 (1%)	61	24
3	F	224/217 (103%)	219 (98%)	5 (2%)	45	10
All	All	2081/1986 (105%)	2068 (99%)	13 (1%)	78	52

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	120	LEU
3	F	61	GLU
3	F	186	MET
3	F	148[B]	SER
3	F	150	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	437	GLN
2	E	102	ASN
2	E	421	GLN
2	E	115	GLN
2	B	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)

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	MGN	D	400	1	6,9,10	0.78	0	5,12,14	0.34	0
1	MHS	A	257	1	10,11,12	1.23	1 (10%)	6,14,16	2.19	3 (50%)
1	DYA	D	450	1	7,7,8	1.60	2 (28%)	5,8,10	2.32	3 (60%)
1	SMC	A	452	1	5,6,7	0.72	0	2,6,8	1.69	1 (50%)
1	MHS	D	257	1	10,11,12	1.38	0	6,14,16	3.03	1 (16%)
1	AGM	D	271	1	10,11,12	0.84	0	6,13,15	0.64	0
1	GL3	A	445	1	2,3,4	3.53	1 (50%)	1,2,4	0.44	0
1	GL3	D	445	1	2,3,4	2.72	1 (50%)	1,2,4	0.37	0
1	DYA	A	450	1	7,7,8	1.39	1 (14%)	5,8,10	2.34	2 (40%)
1	MGN	A	400	1	6,9,10	0.63	0	5,12,14	0.67	0
1	AGM	A	271	1	10,11,12	0.73	0	6,13,15	1.16	0
1	SMC	D	452	1	5,6,7	0.83	0	2,6,8	2.06	1 (50%)

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	MGN	D	400	1	-	0/7/9/12	-
1	MHS	A	257	1	-	0/5/6/8	0/1/1/1
1	DYA	D	450	1	-	3/4/6/8	-
1	SMC	A	452	1	-	1/3/5/7	-
1	MHS	D	257	1	-	0/5/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	AGM	D	271	1	-	2/10/11/13	-
1	GL3	A	445	1	-	0/1/1/2	-
1	GL3	D	445	1	-	1/1/1/2	-
1	DYA	A	450	1	-	3/4/6/8	-
1	MGN	A	400	1	-	0/7/9/12	-
1	AGM	A	271	1	-	2/10/11/13	-
1	SMC	D	452	1	-	1/3/5/7	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	445	GL3	C-S	-4.99	1.63	1.80
1	D	445	GL3	C-S	-3.84	1.67	1.80
1	D	450	DYA	OD1-CG	-2.81	1.23	1.30
1	A	450	DYA	CA-N	2.60	1.41	1.35
1	D	450	DYA	CA-N	2.14	1.40	1.35

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	257	MHS	ND1-CE1-NE2	-6.93	108.88	112.93
1	A	257	MHS	ND1-CE1-NE2	-4.39	110.36	112.93
1	A	450	DYA	O-C-CA	-3.53	120.90	125.39
1	D	450	DYA	CA-CB-CG	-3.47	118.37	126.82
1	A	450	DYA	CA-CB-CG	-3.45	118.43	126.82

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	450	DYA	O-C-CA-CB
1	A	450	DYA	CA-CB-CG-OD1
1	A	452	SMC	CA-CB-SG-CS
1	D	450	DYA	O-C-CA-CB
1	D	450	DYA	CA-CB-CG-OD2

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 29 ligands modelled in this entry, 25 are monoatomic - leaving 4 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	554	10,1	61,71,71	2.25	7 (11%)	64,118,118	1.17	6 (9%)
6	TP7	A	557	-	19,20,20	0.61	0	24,26,26	0.84	0
6	TP7	D	556	-	19,20,20	0.76	0	24,26,26	0.74	0
5	F43	D	552	10,1	61,71,71	2.25	6 (9%)	64,118,118	1.22	8 (12%)

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	554	10,1	-	5/28/185/185	-
6	TP7	A	557	-	-	1/24/24/24	-
6	TP7	D	556	-	-	0/24/24/24	-
5	F43	D	552	10,1	-	5/28/185/185	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	552	F43	NI-NA	11.06	2.13	1.89
5	A	554	F43	NI-NB	9.64	2.10	1.89
5	A	554	F43	NI-NA	9.48	2.10	1.89
5	A	554	F43	NI-ND	8.32	2.07	1.89
5	D	552	F43	NI-NB	8.12	2.07	1.89

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	552	F43	O8D-C7D-C6D	-3.68	114.82	120.86
5	A	554	F43	O8D-C7D-C6D	-3.56	115.03	120.86
5	A	554	F43	O7B-C6B-C8B	-3.50	122.32	126.59
5	D	552	F43	C2B-C1B-NB	2.98	106.29	101.84
5	D	552	F43	C5D-C2D-C1D	2.56	113.89	110.45

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	554	F43	C3A-CAA-CBA-CCA
5	D	552	F43	C3A-CAA-CBA-CCA
5	D	552	F43	CAB-CBB-CCB-ODB
5	A	554	F43	CAB-CBB-CCB-ODB
5	D	552	F43	CAB-CBB-CCB-OEB

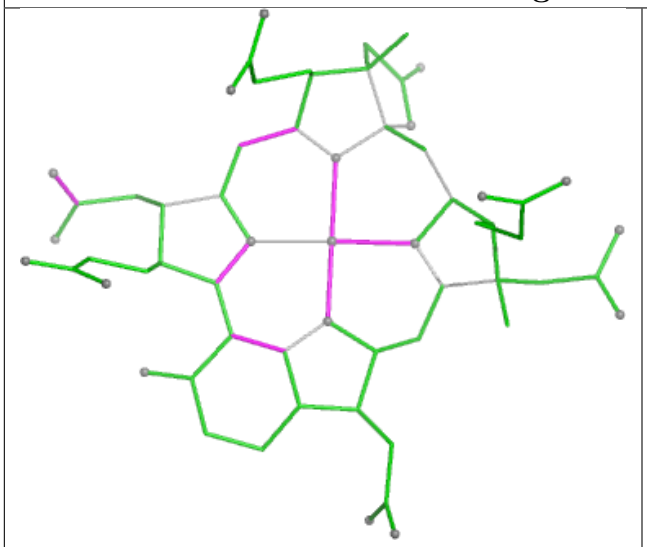
There are no ring outliers.

2 monomers are involved in 2 short contacts:

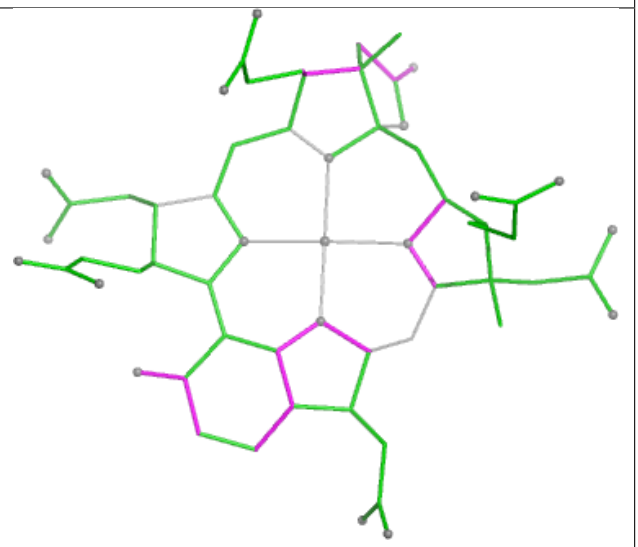
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	554	F43	1	0
5	D	552	F43	1	0

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.

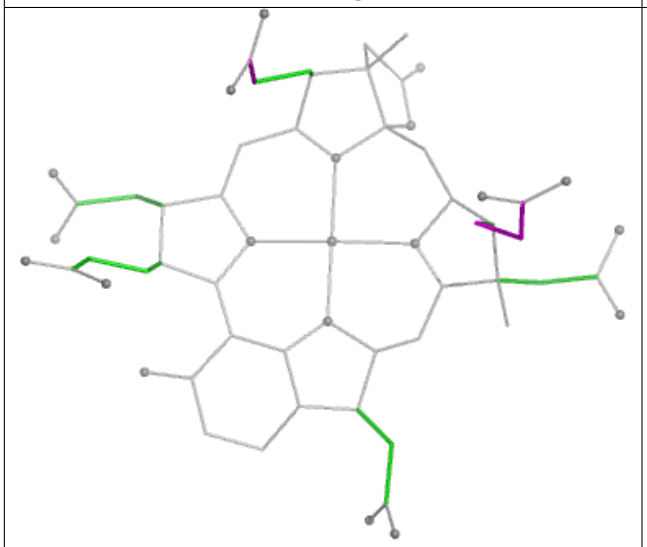
Ligand F43 A 554



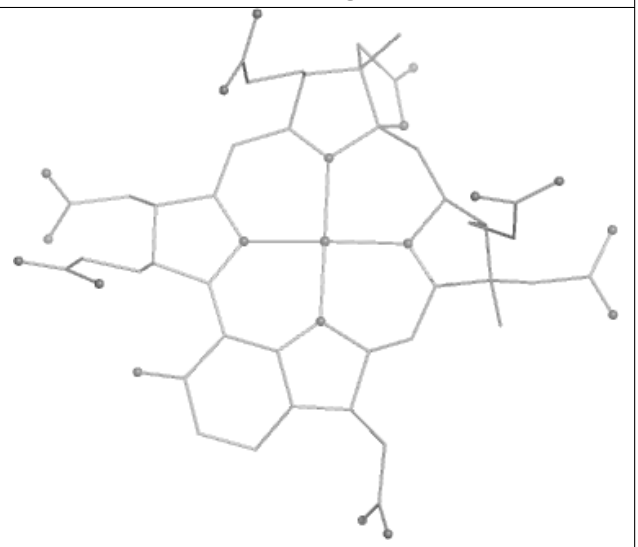
Bond lengths



Bond angles

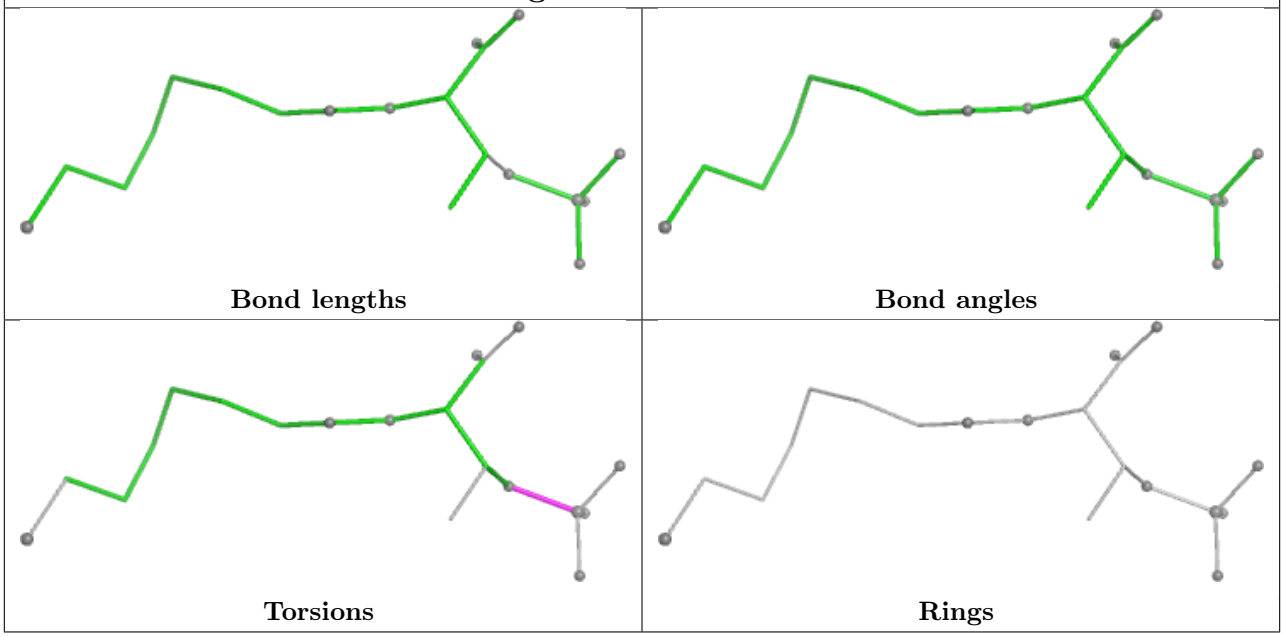


Torsions

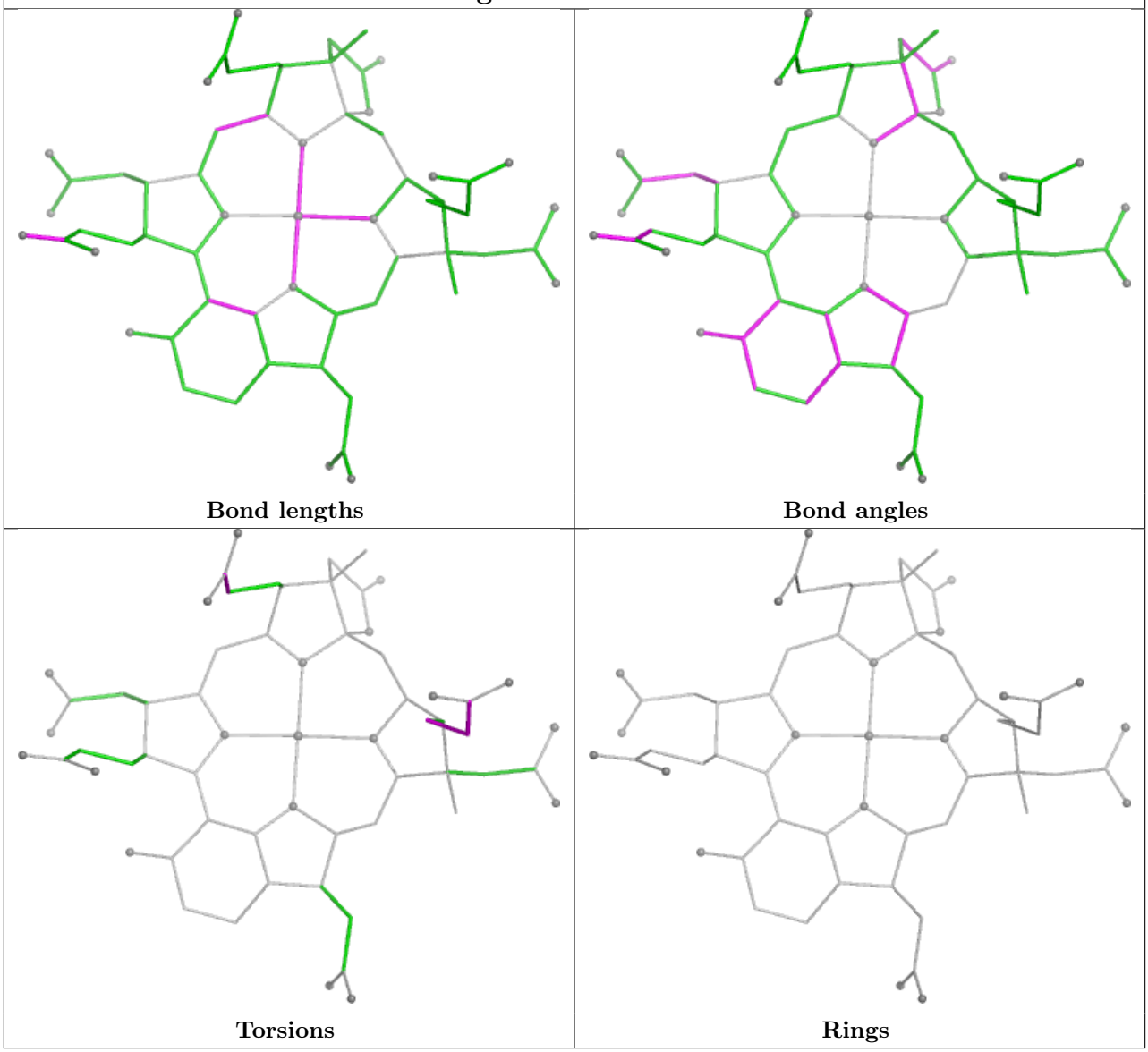


Rings

Ligand TP7 A 557



Ligand F43 D 552



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%)	-0.57	8 (1%)	72	72	4, 9, 22, 67	28 (5%)
1	D	542/550 (98%)	-0.58	7 (1%)	75	75	4, 9, 22, 69	24 (4%)
2	B	442/443 (99%)	-0.51	0	100	100	4, 12, 22, 51	19 (4%)
2	E	442/443 (99%)	-0.43	3 (0%)	84	85	5, 13, 26, 52	17 (3%)
3	C	248/249 (99%)	-0.16	7 (2%)	55	57	7, 16, 43, 73	8 (3%)
3	F	248/249 (99%)	-0.19	7 (2%)	55	57	6, 16, 43, 89	8 (3%)
All	All	2465/2484 (99%)	-0.45	32 (1%)	75	75	4, 12, 28, 89	104 (4%)

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	LEU	5.1
1	A	122	LYS	5.0
1	D	122	LYS	4.9
3	C	248	LEU	4.2
1	D	118	LYS	4.0

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	0.04	8,9,12,13	0
1	MGN	A	400	10/11	0.98	0.03	7,8,9,9	0
1	AGM	A	271	12/13	0.99	0.03	5,6,6,7	0
1	DYA	A	450	8/9	0.99	0.03	6,8,9,9	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	SMC	A	452	7/8	0.99	0.04	7,8,9,10	0
1	MHS	D	257	11/12	0.99	0.03	8,9,12,13	0
1	AGM	D	271	12/13	0.99	0.03	5,5,6,6	0
1	MGN	D	400	10/11	0.99	0.03	6,7,8,8	0
1	DYA	D	450	8/9	0.99	0.03	6,8,9,9	0
1	SMC	D	452	7/8	0.99	0.04	7,8,10,10	0
1	GL3	A	445	4/5	1.00	0.03	6,7,7,7	0
1	GL3	D	445	4/5	1.00	0.01	6,6,7,7	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
4	MG	A	551	1/1	0.91	0.23	33,33,33,33	0
4	MG	B	445[B]	1/1	0.93	0.16	20,20,20,20	1
4	MG	A	1500	1/1	0.95	0.05	23,23,23,23	1
4	MG	A	1501	1/1	0.96	0.19	24,24,24,24	1
4	MG	E	446	1/1	0.96	0.07	25,25,25,25	1
4	MG	D	1500	1/1	0.97	0.09	22,22,22,22	1
4	MG	B	444	1/1	0.97	0.16	31,31,31,31	0
4	MG	D	551	1/1	0.98	0.05	13,13,13,13	1
4	MG	A	553[A]	1/1	0.98	0.07	14,14,14,14	1
4	MG	E	444	1/1	0.98	0.04	18,18,18,18	1
4	MG	E	445[A]	1/1	0.98	0.04	16,16,16,16	1
4	MG	A	563	1/1	0.98	0.08	26,26,26,26	0
4	MG	E	1500	1/1	0.98	0.06	19,19,19,19	1
4	MG	C	251	1/1	0.99	0.04	11,11,11,11	1
4	MG	A	562	1/1	0.99	0.25	20,20,20,20	0
4	MG	D	557	1/1	0.99	0.06	22,22,22,22	0
4	MG	C	250	1/1	0.99	0.06	18,18,18,18	0
4	MG	F	250	1/1	0.99	0.08	18,18,18,18	0
5	F43	A	554	62/62	0.99	0.03	5,7,10,12	0
5	F43	D	552	62/62	0.99	0.03	6,8,10,14	0

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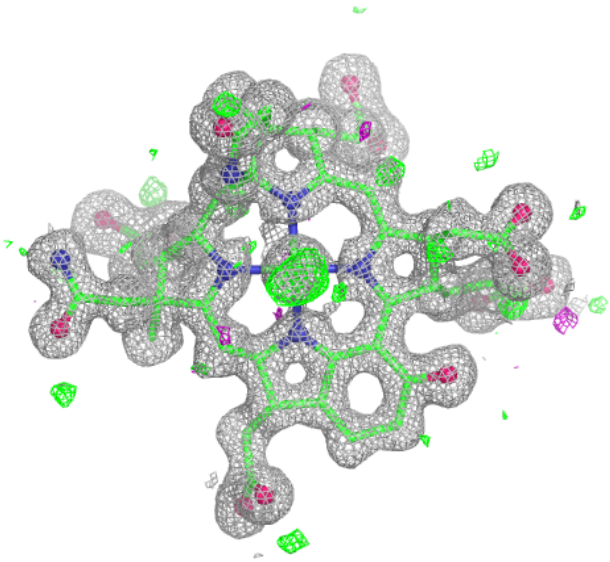
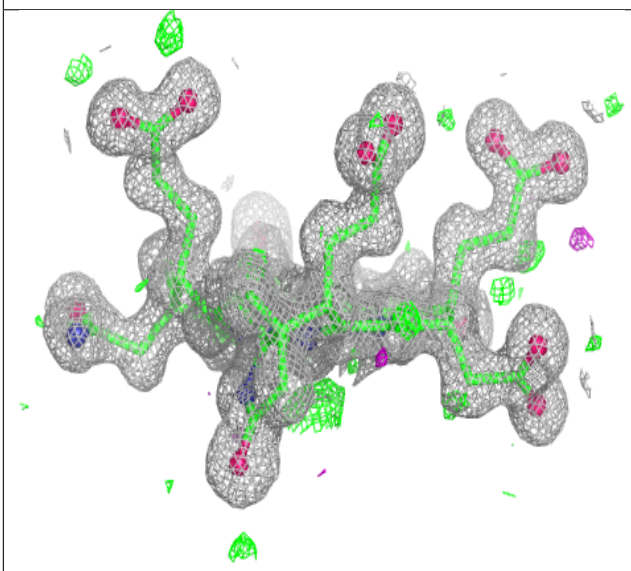
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	TP7	A	557	21/21	0.99	0.03	6,6,7,7	0
6	TP7	D	556	21/21	0.99	0.03	5,6,6,7	0
9	CL	A	1551	1/1	0.99	0.06	18,18,18,18	0
7	NA	A	1502	1/1	1.00	0.04	16,16,16,16	0
7	NA	D	558	1/1	1.00	0.10	13,13,13,13	0
8	K	A	1550	1/1	1.00	0.04	8,8,8,8	0
7	NA	A	564	1/1	1.00	0.05	14,14,14,14	0
9	CL	B	1444	1/1	1.00	0.06	16,16,16,16	0
9	CL	E	1444	1/1	1.00	0.06	20,20,20,20	0

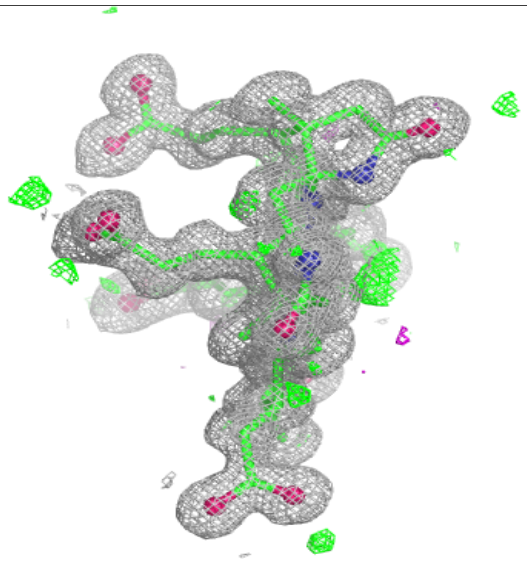
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around F43 A 554:

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

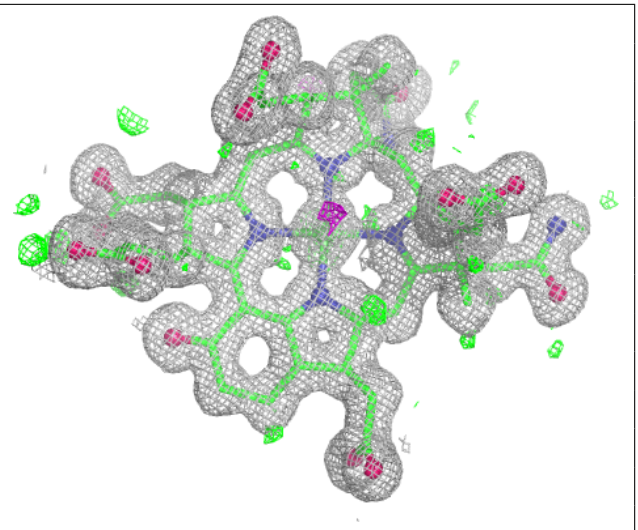


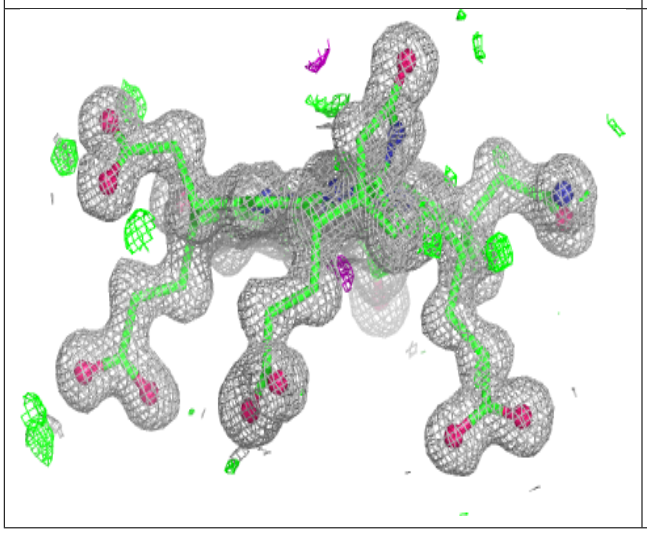


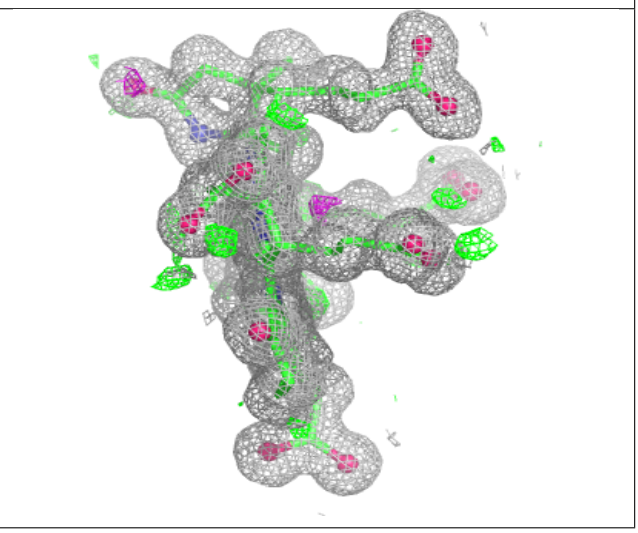


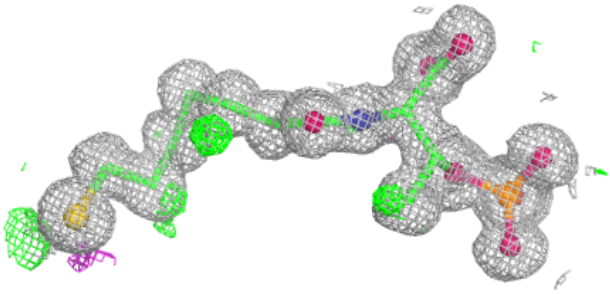
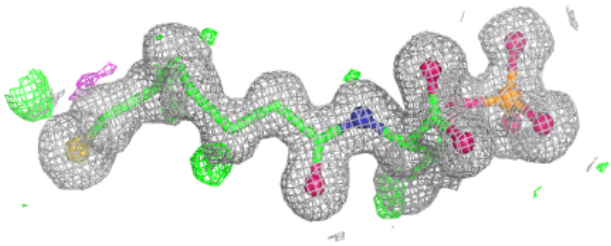
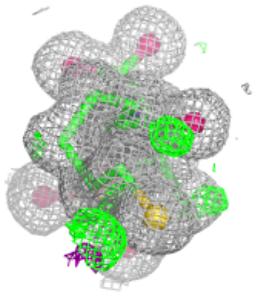
Electron density around F43 D 552:

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







Electron density around TP7 A 557: 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.