



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 27, 2026 – 04:51 pm BST

PDB ID : 6T7J / pdb_00006t7j
Title : As-isolated Ni-free crystal structure of carbon monoxide dehydrogenase from Thermococcus sp. AM4 produced without CooC maturase
Authors : Dobbek, H.; Jeoung, J.-H.
Deposited on : 2019-10-22
Resolution : 2.43 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) 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

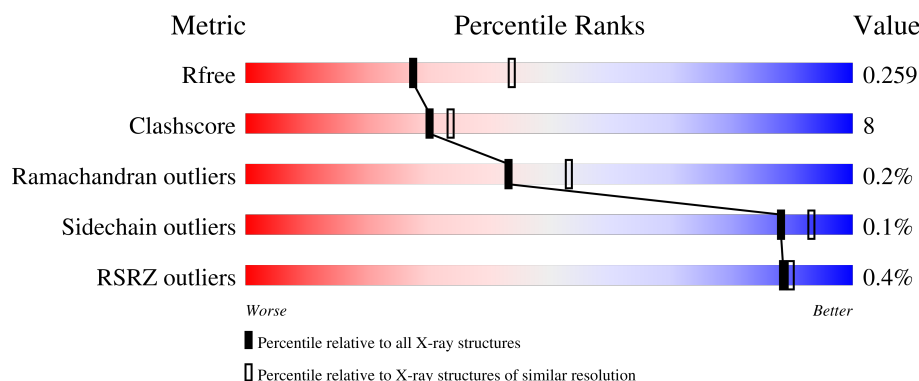
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.43 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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	632	 83% 16%
1	B	632	 81% 19%
1	D	632	 77% 22%

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
3	FES	A	702	-	-	X	-

2 Entry composition [i](#)

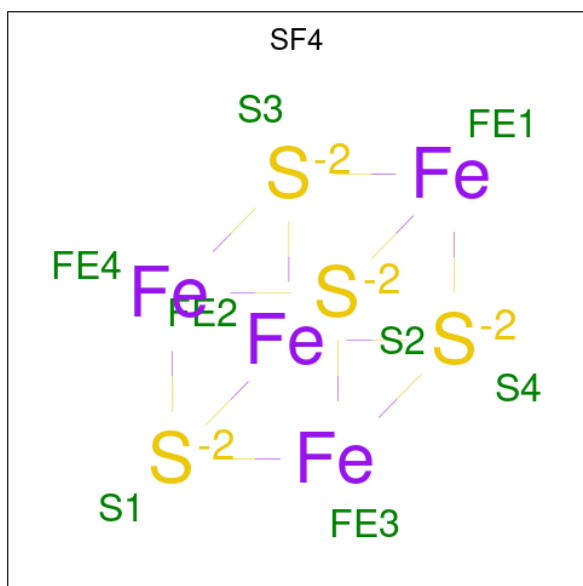
There are 9 unique types of molecules in this entry. The entry contains 14591 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Carbon monoxide dehydrogenase.

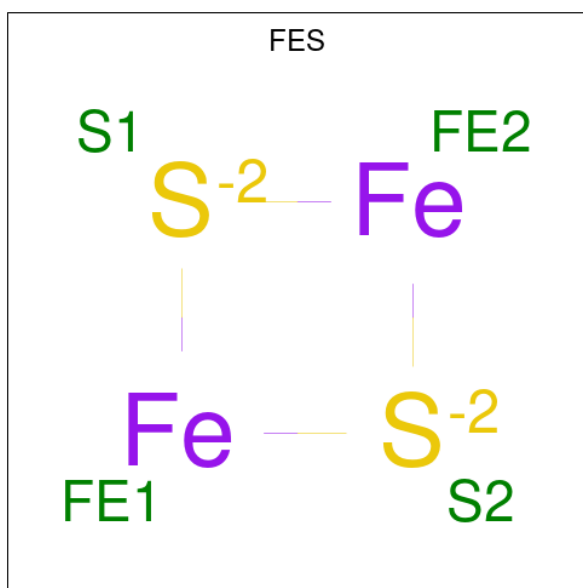
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	632	Total	C	N	O	S	0	0	0
			4768	3035	819	877	37			
1	A	631	Total	C	N	O	S	0	1	0
			4763	3032	818	876	37			
1	D	629	Total	C	N	O	S	0	1	0
			4749	3024	816	872	37			

- Molecule 2 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



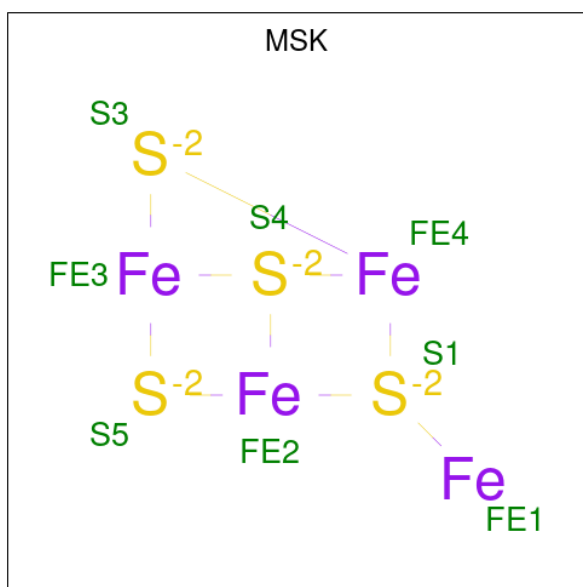
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	Fe	S	0	0
			8	4	4		
2	A	1	Total	Fe	S	0	0
			8	4	4		
2	D	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 3 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



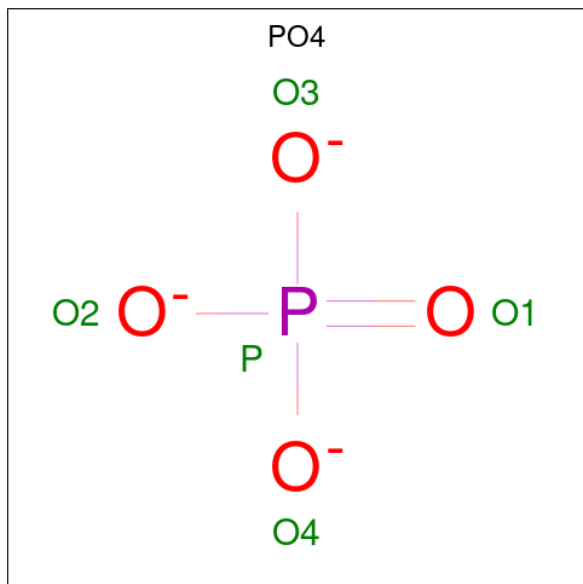
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	Fe	S	0	0
			4	2	2		
3	A	1	Total	Fe	S	0	0
			4	2	2		
3	D	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 4 is Broken Fe₄S₄ cluster (CCD ID: MSK) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



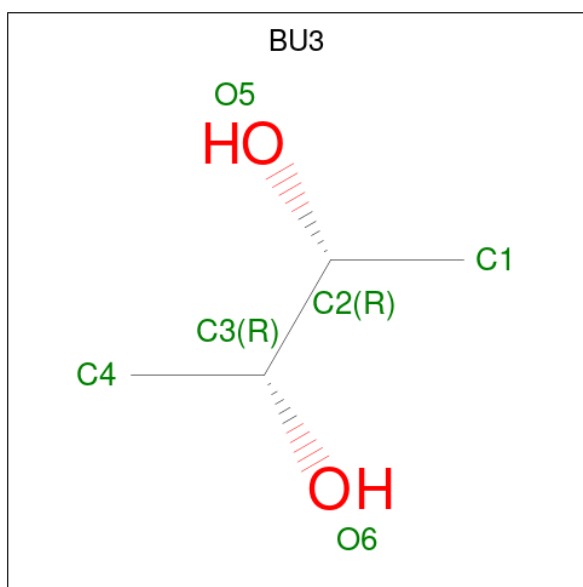
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



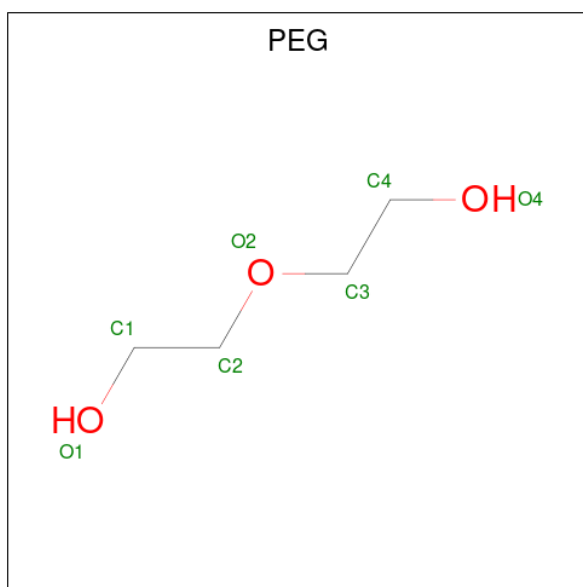
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is (R,R)-2,3-BUTANEDIOL (CCD ID: BU3) (formula: $C_4H_{10}O_2$).



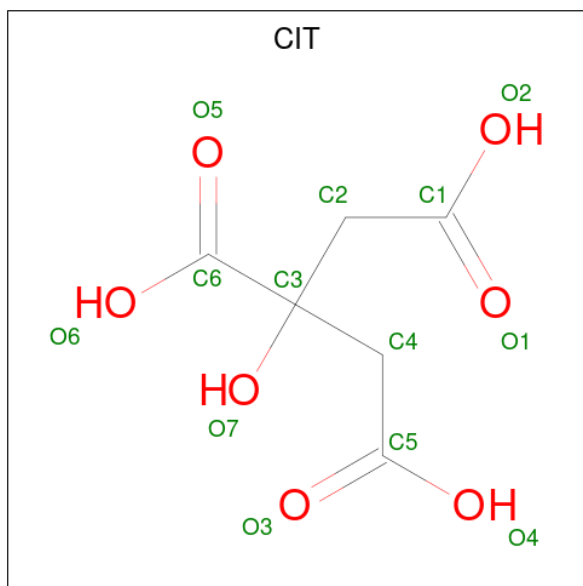
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	4	2		
6	B	1	Total	C	O	0	0
			6	4	2		
6	B	1	Total	C	O	0	0
			6	4	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			13	6	7		

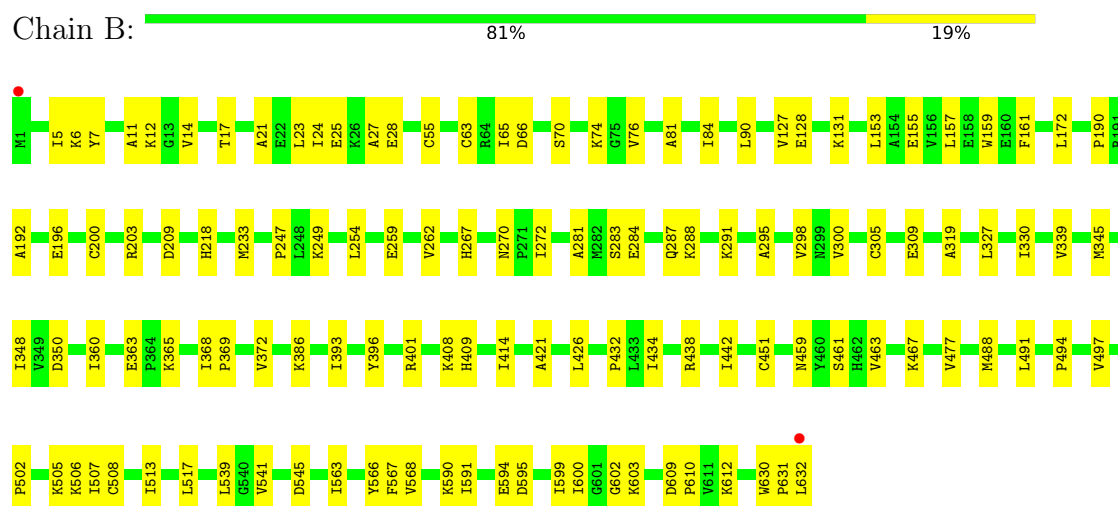
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	75	Total	O	0	0
			75	75		
9	A	63	Total	O	0	0
			63	63		
9	D	55	Total	O	0	0
			55	55		

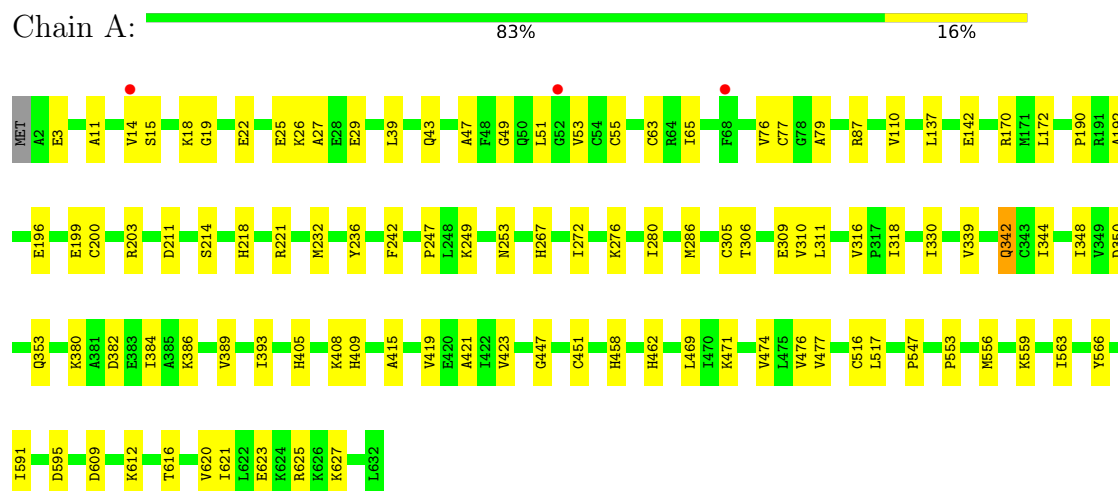
3 Residue-property plots

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.

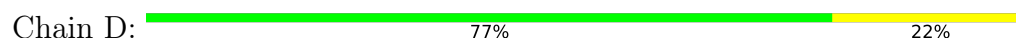
- Molecule 1: Carbon monoxide dehydrogenase



- Molecule 1: Carbon monoxide dehydrogenase



- Molecule 1: Carbon monoxide dehydrogenase



Y566	I434	V301	K163	MET
A569	G447	V310	D166	ALA
V579	I448	L311	L169	GLU
P580	P454	R312	L172	Y4
I591	K457	L314	A173	I5
D595	H458	V316	L174	K6
I600	N459	P317	R179	Y7
G602	Y460	A319	I180	R8
K626	V463	L323	K181	V9
L632	L464	E326	P190	S15
	L465	I330	R191	H37
	V477	A333	A192	R56
	S483	V339	E196	C63
	I484	Q342	C200	R64
	A485	C343	V208	I65
	A486	I344	H218	V76
	A487	M345	R221	A81
	N488	I348	S229	L90
	L489	H356	M233	R91
	G490	N377	D239	M92
	L491	I384	P247	S101
	N492	R390	L254	V110
	S493	I393	K258	G113
	V497	E394	E259	V114
	D498	P397	Y261	A115
	L499	R401	V262	E116
	A500	Y404	M263	G117
	L504	I406	I264	R118
	K505	P407	H267	F119
	C508	K408	G268	K123
	I513	H409	A278	L124
	H518	A415	M286	T125
	C522	L426	Y293	T136
	A536	P432	V298	I139
	L539	L433	V300	E142
	G540			G143
	V541			K144
	D542			D145
	I543			E146
	S544			I149
	D545			V156
	B558			W159
	I563			

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	268.14Å 64.06Å 100.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.32 – 2.43 47.32 – 2.43	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.32-2.43) 99.6 (47.32-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.16-3549	Depositor
R, R_{free}	(Not available) , (Not available) 0.205 , 0.259	Depositor DCC
R_{free} test set	2100 reflections (2.84%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14591	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: BU3, PO4, SF4, MSK, CIT, FES, PEG

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	0.15	0/4857	0.38	0/6577
1	B	0.23	0/4858	0.39	0/6576
1	D	0.46	1/4843 (0.0%)	0.40	1/6558 (0.0%)
All	All	0.31	1/14558 (0.0%)	0.39	1/19711 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	408	LYS	CE-NZ	28.73	2.35	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	408	LYS	CB-CG-CD	-5.43	98.81	111.30

There are no chirality outliers.

There are no planarity outliers.

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	4763	0	4875	68	1
1	B	4768	0	4881	85	2
1	D	4749	0	4864	93	5

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	8	0	0	0	0
2	B	8	0	0	0	0
2	D	8	0	0	0	0
3	A	4	0	0	0	2
3	B	4	0	0	0	0
3	D	4	0	0	0	0
4	A	8	0	0	1	0
4	B	8	0	0	1	0
4	D	8	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	1	0
5	D	10	0	0	1	0
6	B	18	0	30	2	0
7	B	7	0	10	1	0
8	A	13	0	5	2	0
9	A	63	0	0	3	0
9	B	75	0	0	2	0
9	D	55	0	0	2	0
All	All	14591	0	14665	244	7

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 8.

The worst 5 of 244 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:408:LYS:CE	1:D:408:LYS:NZ	2.35	0.90
1:B:259:GLU:OE2	1:A:408:LYS:HD2	1.72	0.89
1:D:408:LYS:O	1:D:408:LYS:HD3	1.76	0.84
1:B:284:GLU:OE2	1:B:288:LYS:HD2	1.79	0.83
1:A:63:CYS:SG	1:A:76:VAL:HG23	2.19	0.82

The worst 5 of 7 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)
1:D:408:LYS:NZ	1:D:408:LYS:NZ[2_555]	1.76	0.44
1:B:74:LYS:NZ	1:B:350:ASP:OD2[2_565]	1.78	0.42
1:D:56:ARG:NH1	3:A:702:FES:S2[3_546]	2.00	0.20
1:D:408:LYS:CE	1:D:408:LYS:CE[2_555]	2.07	0.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:GLU:OE2	1:D:6:LYS:O[1_554]	2.17	0.03

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	630/632 (100%)	604 (96%)	25 (4%)	1 (0%)	43	53
1	B	629/632 (100%)	605 (96%)	24 (4%)	0	100	100
1	D	628/632 (99%)	605 (96%)	21 (3%)	2 (0%)	36	44
All	All	1887/1896 (100%)	1814 (96%)	70 (4%)	3 (0%)	43	53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	GLN
1	D	342	GLN
1	D	208	VAL

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	505/505 (100%)	505 (100%)	0	100	100
1	B	505/505 (100%)	505 (100%)	0	100	100
1	D	504/505 (100%)	502 (100%)	2 (0%)	84	89

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1514/1515 (100%)	1512 (100%)	2 (0%)	88 93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	522[A]	CYS
1	D	522[B]	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	120	GLN
1	D	452	ASN
1	A	452	ASN
1	B	586	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](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

18 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	PO4	A	704	-	4,4,4	0.90	0	6,6,6	0.44	0
7	PEG	B	708	-	6,6,6	0.45	0	5,5,5	0.25	0
2	SF4	A	701	1	0,12,12	-	-	-		
2	SF4	D	701	1	0,12,12	-	-	-		
6	BU3	B	707	-	4,5,5	0.35	0	6,6,6	0.25	0
4	MSK	D	703	1	0,10,10	-	-	-		
3	FES	B	702	1	0,4,4	-	-	-		
5	PO4	D	705	-	4,4,4	0.90	0	6,6,6	0.43	0
4	MSK	B	703	1	0,10,10	-	-	-		
5	PO4	D	704	-	4,4,4	0.89	0	6,6,6	0.44	0
6	BU3	B	706	-	4,5,5	0.32	0	6,6,6	0.27	0
2	SF4	B	701	1	0,12,12	-	-	-		
3	FES	D	702	1,3	0,4,4	-	-	-		
3	FES	A	702	1,3	0,4,4	-	-	-		
5	PO4	B	704	-	4,4,4	0.87	0	6,6,6	0.47	0
6	BU3	B	705	-	4,5,5	0.28	0	6,6,6	0.28	0
8	CIT	A	705	-	12,12,12	1.07	0	17,17,17	1.82	5 (29%)
4	MSK	A	703	1	0,10,10	-	-	-		

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	PEG	B	708	-	-	3/4/4/4	-
6	BU3	B	707	-	-	4/4/4/4	-
2	SF4	A	701	1	-	-	0/6/5/5
2	SF4	D	701	1	-	-	0/6/5/5
4	MSK	D	703	1	-	-	0/3/3/3
3	FES	B	702	1	-	-	0/1/1/1
4	MSK	B	703	1	-	-	0/3/3/3
6	BU3	B	706	-	-	0/4/4/4	-
2	SF4	B	701	1	-	-	0/6/5/5
3	FES	D	702	1,3	-	-	0/1/1/1
3	FES	A	702	1,3	-	-	0/1/1/1
6	BU3	B	705	-	-	0/4/4/4	-
8	CIT	A	705	-	-	8/16/16/16	-
4	MSK	A	703	1	-	-	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	705	CIT	O6-C6-C3	3.95	119.91	113.05
8	A	705	CIT	O2-C1-C2	2.74	123.14	114.35
8	A	705	CIT	O4-C5-O3	-2.71	116.55	123.30
8	A	705	CIT	O2-C1-O1	-2.19	117.84	123.30
8	A	705	CIT	C4-C3-C2	2.04	114.49	109.16

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	707	BU3	O5-C2-C3-O6
6	B	707	BU3	C1-C2-C3-O6
6	B	707	BU3	O5-C2-C3-C4
6	B	707	BU3	C1-C2-C3-C4
8	A	705	CIT	C2-C3-C6-O5

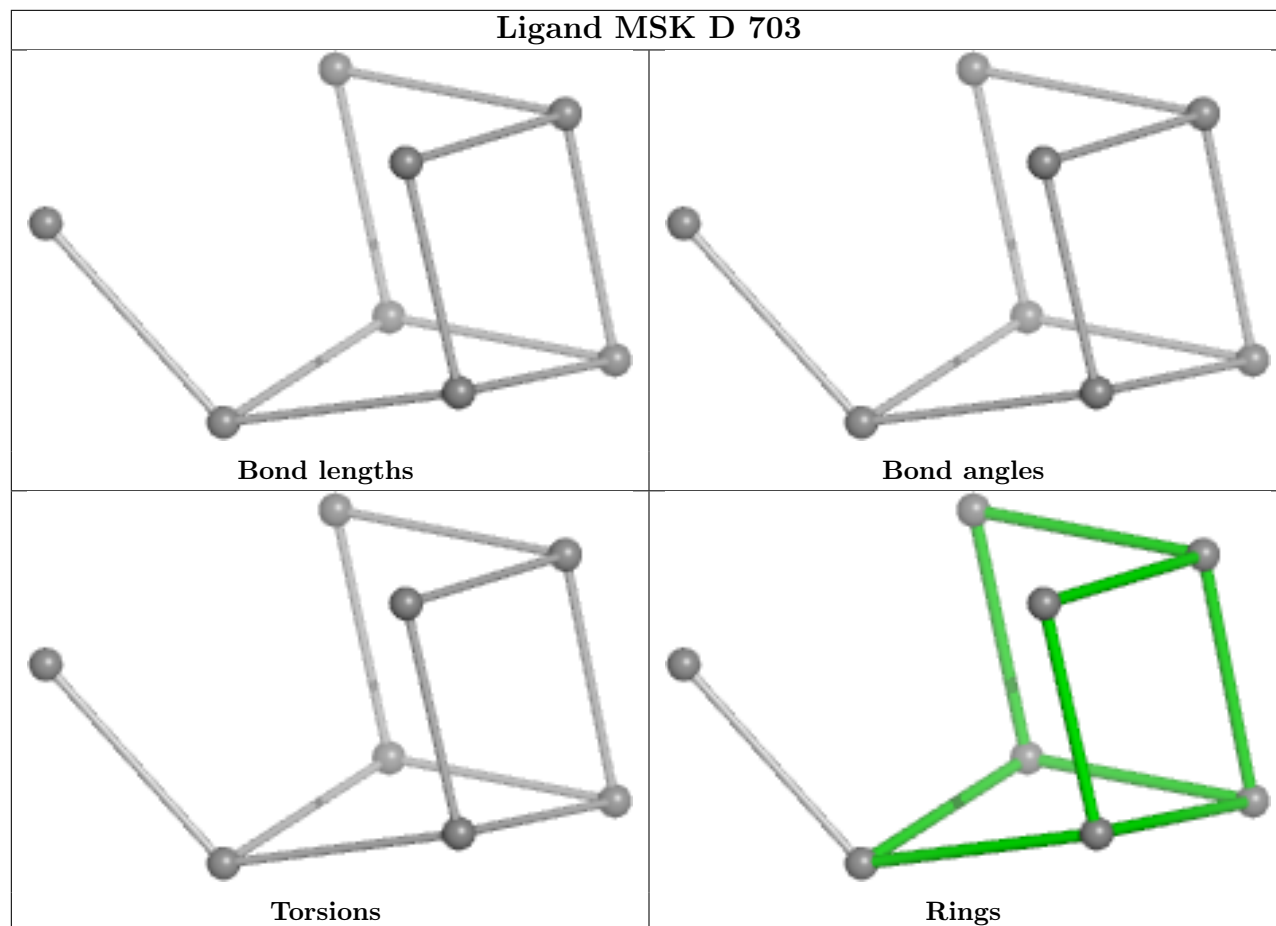
There are no ring outliers.

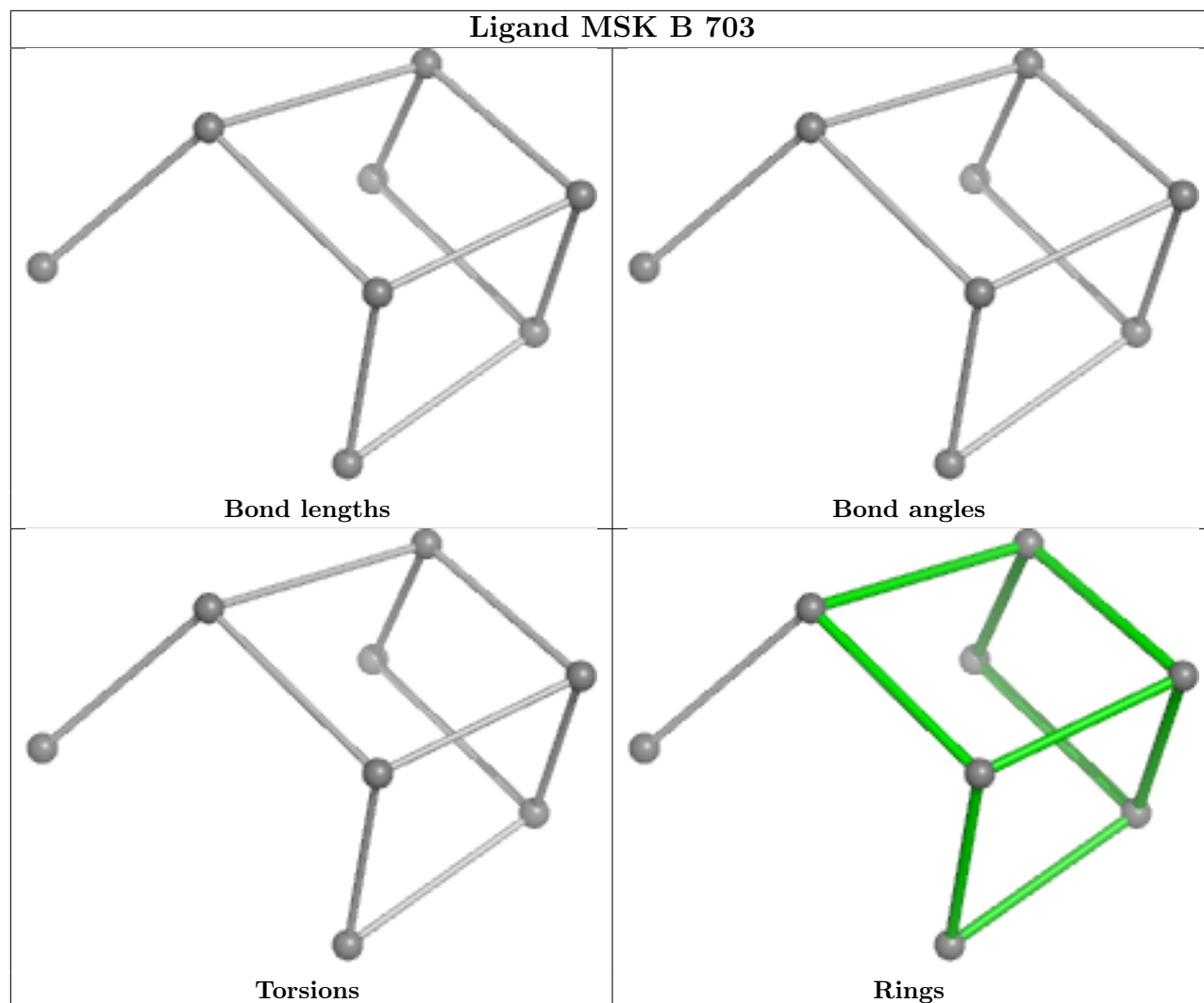
8 monomers are involved in 11 short contacts:

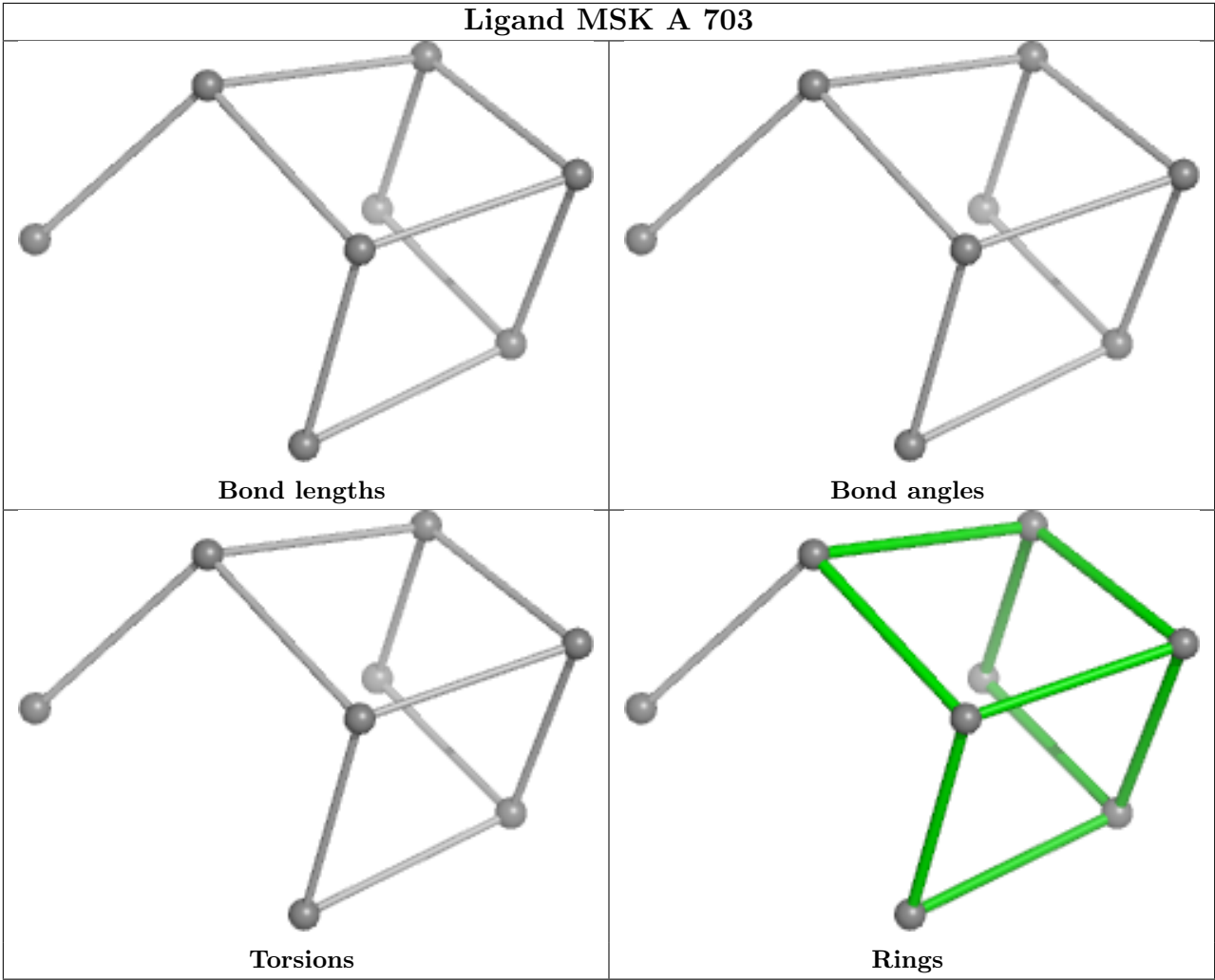
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	708	PEG	1	0
5	D	705	PO4	1	0
4	B	703	MSK	1	0
3	A	702	FES	0	2
5	B	704	PO4	1	0
6	B	705	BU3	2	0
8	A	705	CIT	2	0
4	A	703	MSK	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	631:PRO	C	632:LEU	N	3.94

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	631/632 (99%)	-0.21	3 (0%)	87 89	33, 52, 68, 104	1 (0%)
1	B	632/632 (100%)	-0.20	2 (0%)	90 91	39, 54, 68, 100	0
1	D	629/632 (99%)	-0.23	2 (0%)	90 91	31, 50, 69, 87	1 (0%)
All	All	1892/1896 (99%)	-0.22	7 (0%)	88 90	31, 52, 68, 104	2 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	PHE	2.6
1	B	1	MET	2.4
1	A	14	VAL	2.3
1	D	101	SER	2.2
1	A	52	GLY	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

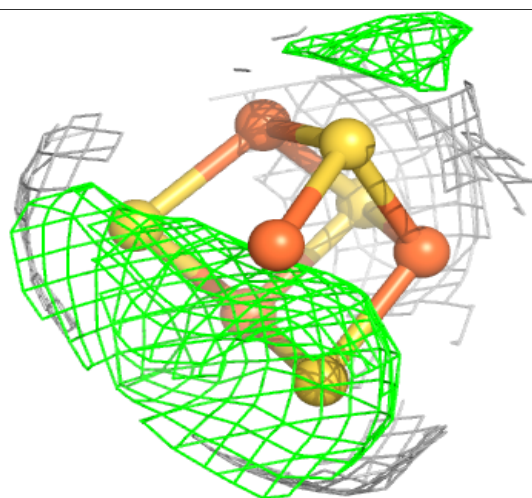
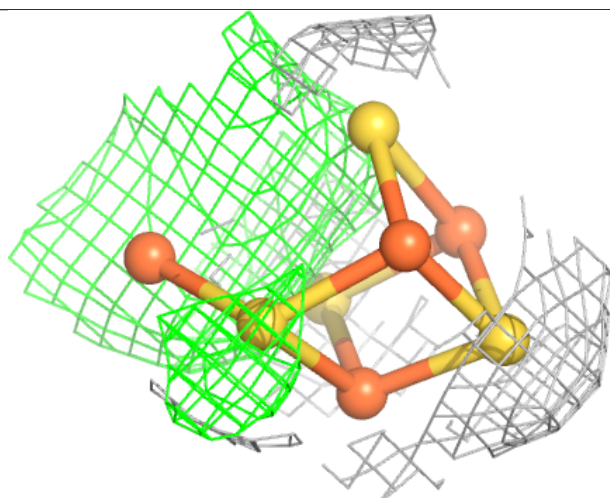
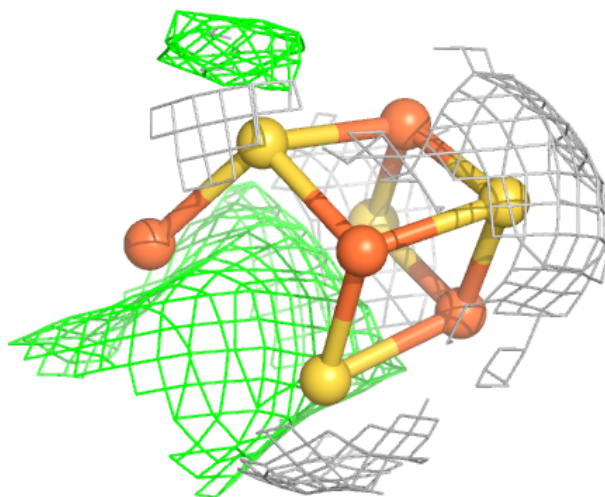
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	D	705	5/5	0.42	0.12	83,96,104,113	0
5	PO4	B	704	5/5	0.55	0.10	82,85,95,110	0
8	CIT	A	705	13/13	0.56	0.14	74,78,83,84	0
6	BU3	B	705	6/6	0.59	0.18	53,61,69,73	0
5	PO4	A	704	5/5	0.76	0.10	82,84,95,96	0
7	PEG	B	708	7/7	0.79	0.13	64,66,72,75	0
6	BU3	B	707	6/6	0.81	0.12	65,74,76,80	0
6	BU3	B	706	6/6	0.83	0.12	62,70,76,79	0
5	PO4	D	704	5/5	0.89	0.09	45,53,62,71	5
3	FES	A	702	4/4	0.91	0.09	71,73,77,80	4
3	FES	D	702	4/4	0.93	0.09	68,70,73,78	4
4	MSK	A	703	8/8	0.94	0.07	47,50,61,61	4
4	MSK	D	703	8/8	0.96	0.08	42,50,61,68	6
4	MSK	B	703	8/8	0.98	0.06	47,51,60,63	6
2	SF4	B	701	8/8	0.98	0.05	39,42,43,44	0
3	FES	B	702	4/4	0.98	0.06	57,60,63,68	4
2	SF4	D	701	8/8	0.99	0.04	40,43,46,49	0
2	SF4	A	701	8/8	0.99	0.05	41,43,47,51	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.

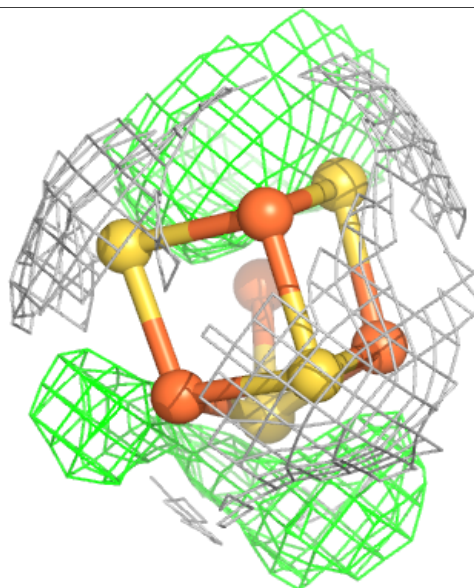
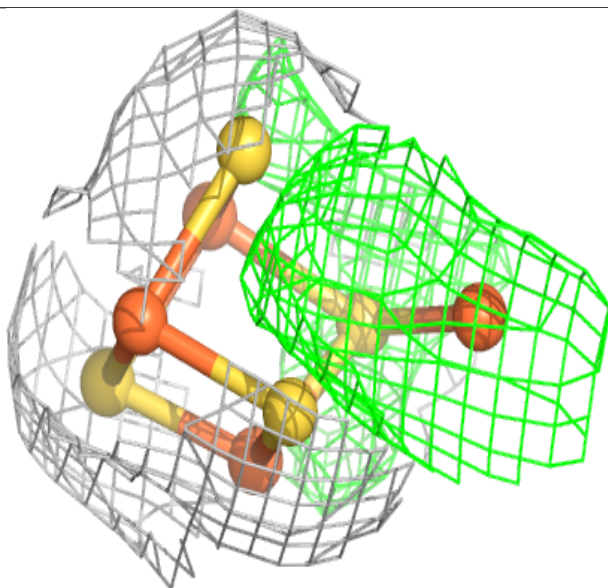
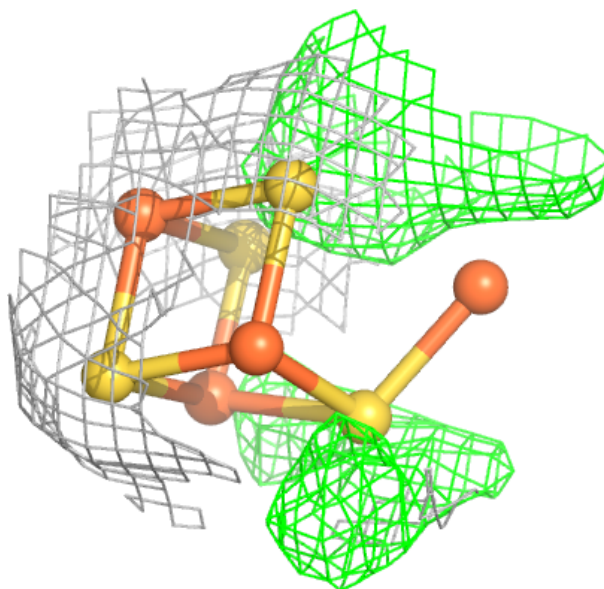
Electron density around MSK A 703:

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



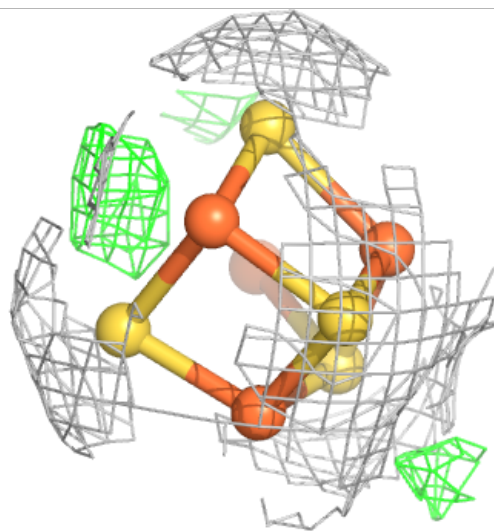
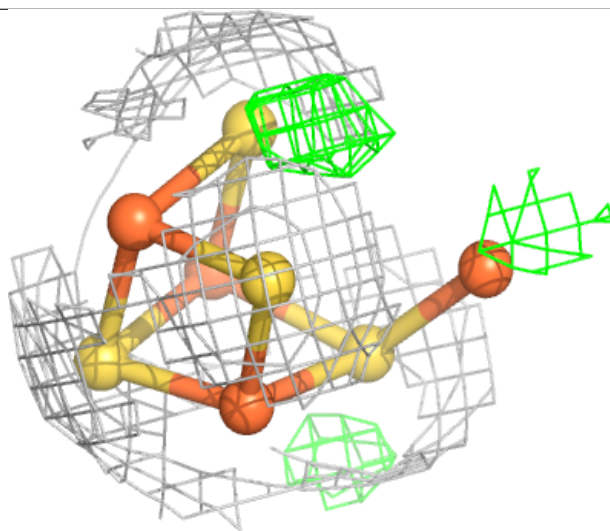
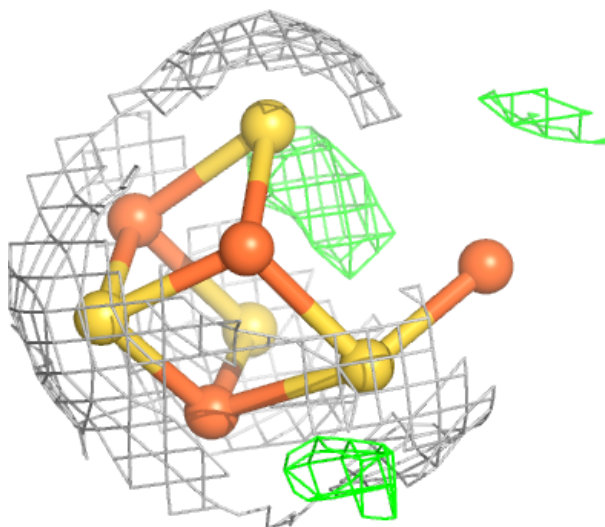
Electron density around MSK D 703:

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



Electron density around MSK B 703:

$2mF_o-DF_c$ (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.