



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2022 – 06:07 PM EDT

PDB ID : 7SXM
Title : Structure of Xenon-derivatized Methyl-Coenzyme M Reductase from Methanothermobacter marburgensis
Authors : Chen, P.Y.-T.; Drennan, C.L.
Deposited on : 2021-11-23
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.27
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.27

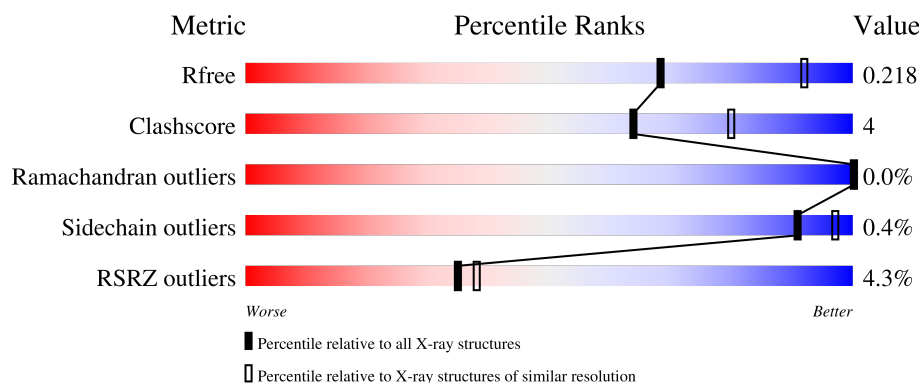
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	548	<div><div></div><div>89%</div><div>11%</div></div>
1	D	548	<div><div></div><div>87%</div><div>12%</div></div>
2	B	442	<div><div>3%</div><div></div><div>88%</div><div>12%</div></div>
2	E	442	<div><div>7%</div><div></div><div>89%</div><div>10%</div></div>
3	C	246	<div><div>9%</div><div></div><div>93%</div><div>6%</div></div>

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Mol	Chain	Length	Quality of chain
3	F	246	<div><div></div><div>16%</div><div>89%</div><div>10%</div></div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	XE	B	501[A]	-	-	X	-
10	XE	E	501[A]	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 20235 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
1	A	547	Total	C	N	O	S	0	2	0
			4263	2698	717	828	20			
1	D	547	Total	C	N	O	S	0	3	0
			4265	2699	717	829	20			

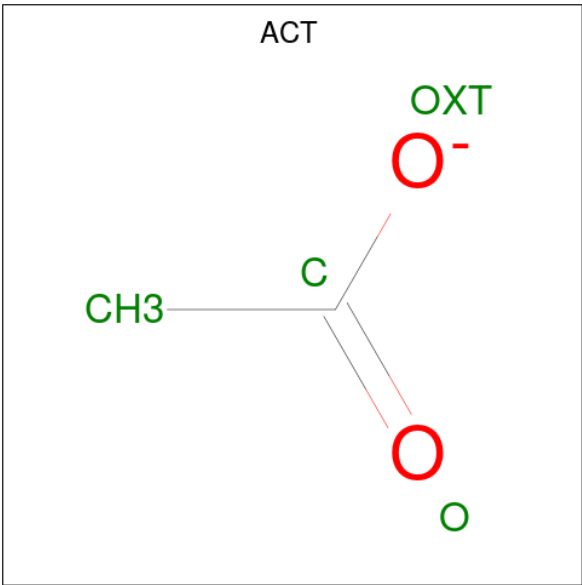
- Molecule 2 is a protein called Methyl-coenzyme M reductase I subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	442	Total	C	N	O	S	0	9	0
			3364	2131	557	658	18			
2	E	442	Total	C	N	O	S	0	9	0
			3364	2131	557	658	18			

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

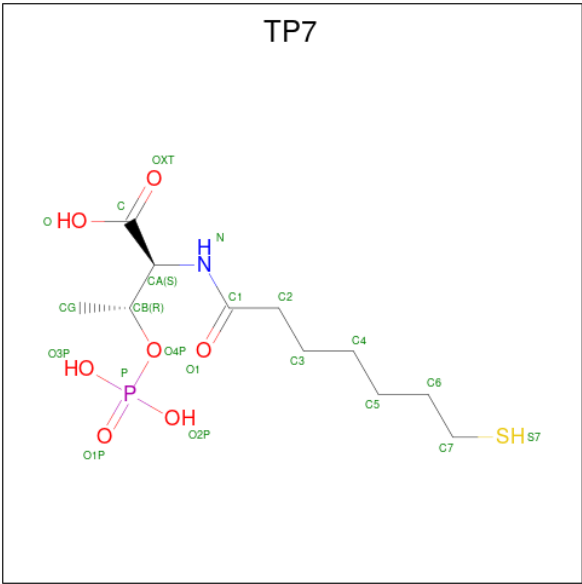
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	243	Total	C	N	O	S	0	1	0
			1968	1219	350	389	10			
3	F	243	Total	C	N	O	S	0	0	0
			1966	1218	350	388	10			

- Molecule 4 is FACTOR 430 (three-letter code: F43) (formula: C₄₂H₅₁N₆NiO₁₃).



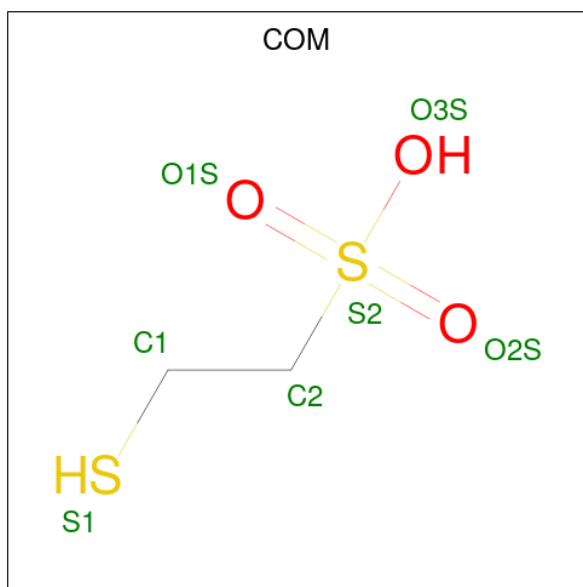
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	1
			4	2	2		
6	D	1	Total	C	O	0	1
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is Coenzyme B (three-letter code: TP7) (formula: $C_{11}H_{22}NO_7PS$).



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

- Molecule 8 is 1-THIOETHANESULFONIC ACID (three-letter code: COM) (formula: $C_2H_6O_3S_2$).



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

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Na		
			1	1	0	0

- Molecule 10 is XENON (three-letter code: XE) (formula: Xe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	Xe		
			1	1	0	0
10	B	3	Total	Xe		
			3	3	0	2

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	D	1	Total 1	Xe 1	0	0
10	E	3	Total 3	Xe 3	0	2

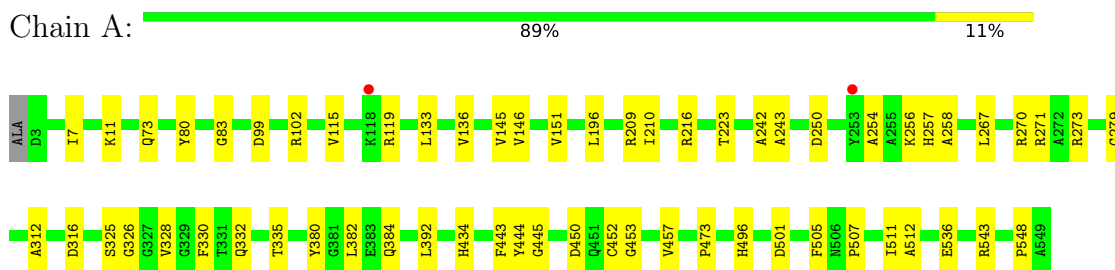
- Molecule 11 is water.

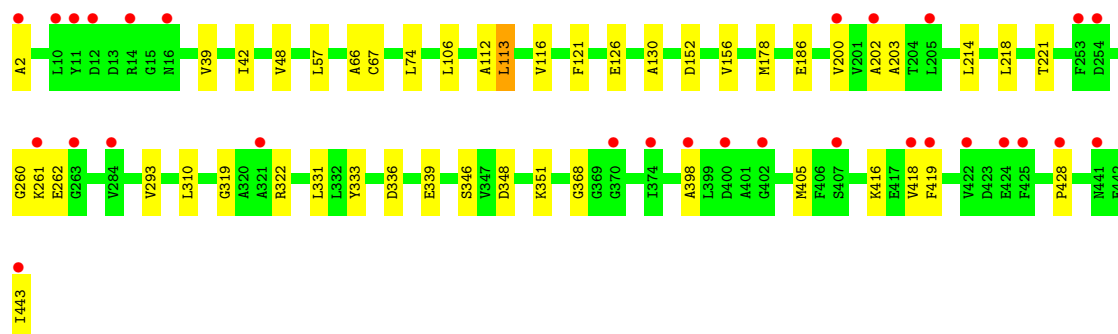
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	236	Total 236	O 236	0	8
11	B	129	Total 129	O 129	0	1
11	C	67	Total 67	O 67	0	0
11	D	210	Total 210	O 210	0	9
11	E	124	Total 124	O 124	0	1
11	F	72	Total 72	O 72	0	0

3 Residue-property plots

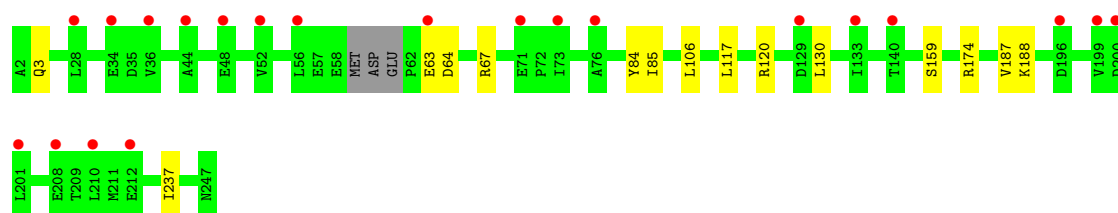
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Methyl-coenzyme M reductase I subunit alpha

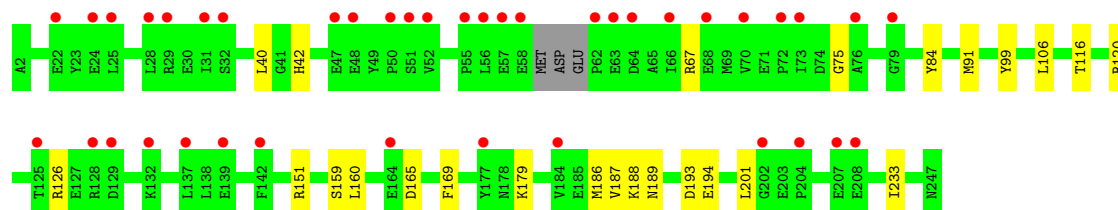
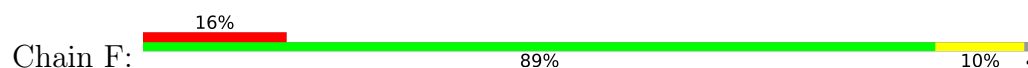




- Molecule 3: Methyl-coenzyme M reductase I subunit gamma



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.96Å 115.74Å 123.40Å 90.00° 92.53° 90.00°	Depositor
Resolution (Å)	69.63 – 2.50 69.63 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.0 (69.63-2.50) 91.8 (69.63-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.178 , 0.218 0.178 , 0.218	Depositor DCC
R_{free} test set	3840 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.376	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20235	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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: GL3, MG, XE, ACT, MHS, F43, TP7, AGM, COM, NA, SMC, DYA, MGN

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	0.25	0/4307	0.42	0/5842
1	D	0.25	0/4313	0.42	0/5850
2	B	0.25	0/3421	0.43	0/4635
2	E	0.25	0/3421	0.42	0/4635
3	C	0.24	0/2007	0.43	0/2702
3	F	0.24	0/2001	0.42	0/2694
All	All	0.25	0/19470	0.42	0/26358

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	4263	0	4070	38	0
1	D	4265	0	4071	46	0
2	B	3364	0	3347	39	0
2	E	3364	0	3347	32	0
3	C	1968	0	1901	12	0
3	F	1966	0	1900	20	0
4	A	124	0	86	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
5	D	1	0	0	0	0
6	A	8	0	6	1	0
6	D	8	0	4	1	0
7	A	42	0	36	7	0
8	A	7	0	4	2	0
8	D	7	0	4	2	0
9	A	1	0	0	0	0
10	A	1	0	0	0	0
10	B	3	0	0	3	0
10	D	1	0	0	0	0
10	E	3	0	0	2	0
11	A	236	0	0	4	0
11	B	129	0	0	3	0
11	C	67	0	0	0	0
11	D	210	0	0	3	0
11	E	124	0	0	3	0
11	F	72	0	0	2	0
All	All	20235	0	18776	162	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 162 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)
2:E:202:ALA:HB1	2:E:416:LYS:HB3	1.63	0.81
1:D:254:ALA:HA	1:D:258:ALA:HB3	1.67	0.75
1:A:254:ALA:HA	1:A:258:ALA:HB3	1.69	0.74
2:B:214:LEU:HB2	2:B:428:PRO:HG3	1.70	0.74
2:B:42:ILE:HG12	2:B:419[B]:PHE:HZ	1.54	0.72

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	541/548 (99%)	522 (96%)	19 (4%)	0	100	100
1	D	542/548 (99%)	522 (96%)	20 (4%)	0	100	100
2	B	449/442 (102%)	435 (97%)	14 (3%)	0	100	100
2	E	449/442 (102%)	434 (97%)	13 (3%)	2 (0%)	34	54
3	C	240/246 (98%)	236 (98%)	4 (2%)	0	100	100
3	F	239/246 (97%)	236 (99%)	3 (1%)	0	100	100
All	All	2460/2472 (100%)	2385 (97%)	73 (3%)	2 (0%)	100	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	368[A]	GLY
2	E	368[B]	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	434/432 (100%)	432 (100%)	2 (0%)	88	96
1	D	435/432 (101%)	433 (100%)	2 (0%)	88	96
2	B	346/341 (102%)	345 (100%)	1 (0%)	92	97
2	E	346/341 (102%)	344 (99%)	2 (1%)	86	95
3	C	212/214 (99%)	211 (100%)	1 (0%)	88	96
3	F	211/214 (99%)	211 (100%)	0	100	100
All	All	1984/1974 (100%)	1976 (100%)	8 (0%)	91	97

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	126	GLU

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Mol	Chain	Res	Type
2	E	113	LEU
1	D	444	TYR
3	C	3	GLN
1	D	543	ARG

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	AGM	D	271	1	10,11,12	1.27	1 (10%)	6,13,15	1.11	0
1	GL3	A	445	1	2,3,4	1.75	1 (50%)	1,2,4	0.37	0
1	AGM	A	271	1	10,11,12	1.33	1 (10%)	6,13,15	1.25	0
1	DYA	D	450	1	4,7,8	2.16	2 (50%)	1,8,10	3.70	1 (100%)
1	MHS	D	257	1	7,11,12	1.20	0	6,14,16	1.70	2 (33%)
1	MGN	A	400	1	6,9,10	0.85	0	5,12,14	0.73	0
1	GL3	D	445	1	2,3,4	1.77	1 (50%)	1,2,4	0.37	0
1	MGN	D	400	1	6,9,10	0.84	0	5,12,14	0.88	0
1	SMC	D	452	1	5,6,7	1.28	1 (20%)	2,6,8	1.23	0
1	DYA	A	450	1	4,7,8	2.14	2 (50%)	1,8,10	3.74	1 (100%)
1	SMC	A	452	1	5,6,7	1.36	1 (20%)	2,6,8	1.27	0
1	MHS	A	257	1	7,11,12	1.19	0	6,14,16	1.71	2 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	AGM	D	271	1	-	3/10/11/13	-
1	GL3	A	445	1	-	0/1/1/2	-
1	AGM	A	271	1	-	2/10/11/13	-
1	DYA	D	450	1	-	2/2/6/8	-
1	MHS	D	257	1	-	0/5/6/8	0/1/1/1
1	MGN	A	400	1	-	0/7/9/12	-
1	GL3	D	445	1	-	0/1/1/2	-
1	MGN	D	400	1	-	0/7/9/12	-
1	SMC	D	452	1	-	1/3/5/7	-
1	DYA	A	450	1	-	2/2/6/8	-
1	SMC	A	452	1	-	1/3/5/7	-
1	MHS	A	257	1	-	0/5/6/8	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	271	AGM	CZ-NE1	3.16	1.38	1.33
1	D	271	AGM	CZ-NE1	2.96	1.38	1.33
1	A	450	DYA	CA-N	2.79	1.42	1.35
1	D	450	DYA	CA-N	2.78	1.42	1.35
1	A	452	SMC	CB-SG	-2.67	1.77	1.80

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	450	DYA	O-C-CA	-3.74	120.64	125.39
1	D	450	DYA	O-C-CA	-3.70	120.68	125.39
1	A	257	MHS	CB-CA-C	-3.06	105.73	111.47
1	D	257	MHS	CB-CA-C	-3.03	105.79	111.47
1	D	257	MHS	CM-ND1-CG	2.68	128.00	124.44

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

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

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Mol	Chain	Res	Type	Atoms
1	D	450	DYA	N-CA-CB-CG
1	D	450	DYA	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 11 are monoatomic - leaving 10 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	$\# Z > 2$
8	COM	A	605	4	6,6,6	1.48	2 (33%)	7,8,8	0.55	0
6	ACT	D	605	5	1,3,3	6.26	1 (100%)	0,3,3	-	-
7	TP7	A	604[A]	-	16,20,20	0.85	1 (6%)	18,26,26	0.91	0
6	ACT	A	606[B]	-	1,3,3	6.24	1 (100%)	0,3,3	-	-
8	COM	D	602	4	6,6,6	1.57	2 (33%)	7,8,8	0.81	0
4	F43	A	601	1,8	46,71,71	3.03	10 (21%)	48,118,118	1.62	11 (22%)
6	ACT	D	601[B]	-	1,3,3	6.16	1 (100%)	0,3,3	-	-
7	TP7	A	609[A]	-	16,20,20	0.72	0	18,26,26	1.03	1 (5%)
6	ACT	A	603	5	1,3,3	6.57	1 (100%)	0,3,3	-	-
4	F43	A	608	1,8	46,71,71	3.00	11 (23%)	48,118,118	1.63	9 (18%)

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
8	COM	A	605	4	-	3/4/4/4	-
7	TP7	A	604[A]	-	-	1/20/24/24	-
8	COM	D	602	4	-	3/4/4/4	-
4	F43	A	601	1,8	-	2/18/185/185	-
7	TP7	A	609[A]	-	-	2/20/24/24	-
4	F43	A	608	1,8	-	3/18/185/185	-

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	F43	NI-NB	10.44	2.12	1.89
4	A	608	F43	NI-NA	10.35	2.11	1.89
4	A	608	F43	NI-NB	10.30	2.11	1.89
4	A	601	F43	NI-NA	10.18	2.11	1.89
4	A	601	F43	NI-ND	7.87	2.06	1.89

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	601	F43	O8D-C7D-C6D	-3.48	115.16	120.86
4	A	608	F43	O8D-C7D-C6D	-3.47	115.17	120.86
4	A	601	F43	C5D-C2D-C1D	3.39	115.01	110.45
4	A	608	F43	C5D-C2D-C1D	3.31	114.91	110.45
4	A	608	F43	C3D-C4D-ND	3.18	107.28	102.34

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	608	F43	C2D-C3D-C9D-CAD
8	A	605	COM	C1-C2-S2-O1S
8	A	605	COM	C1-C2-S2-O2S
8	D	602	COM	C1-C2-S2-O1S
8	D	602	COM	C1-C2-S2-O2S

There are no ring outliers.

8 monomers are involved in 17 short contacts:

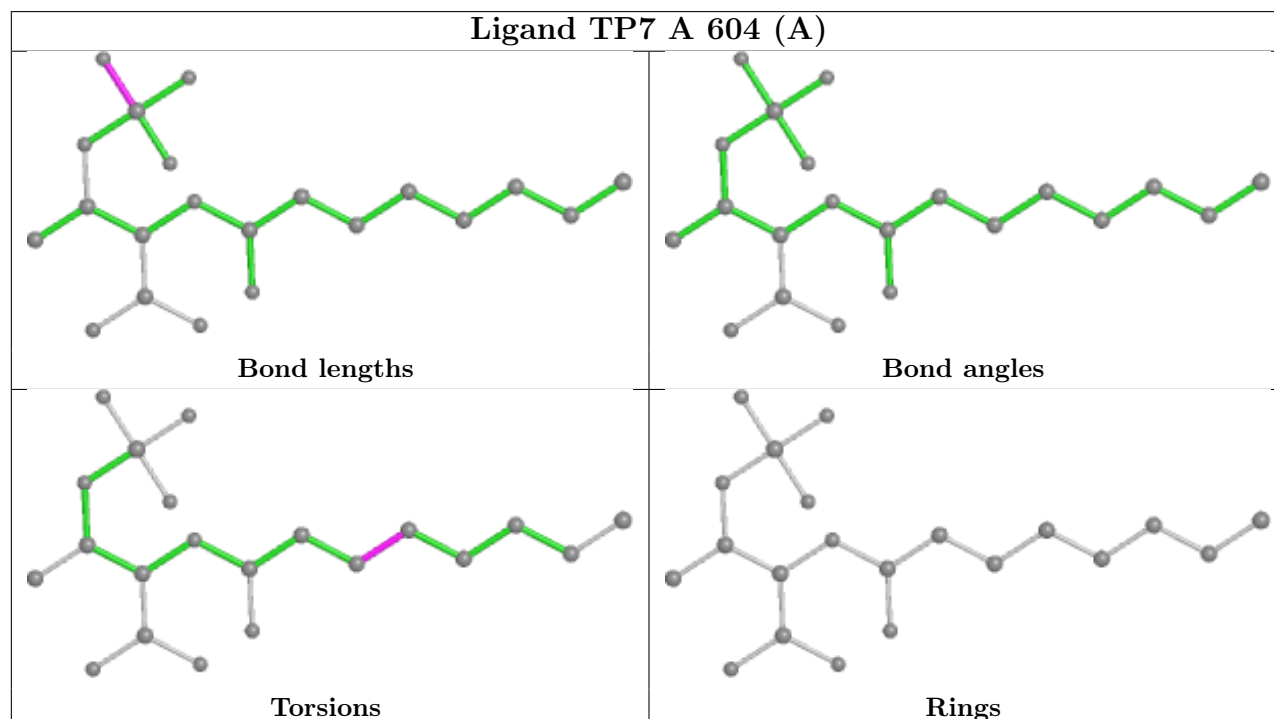
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	605	COM	2	0
7	A	604[A]	TP7	4	0

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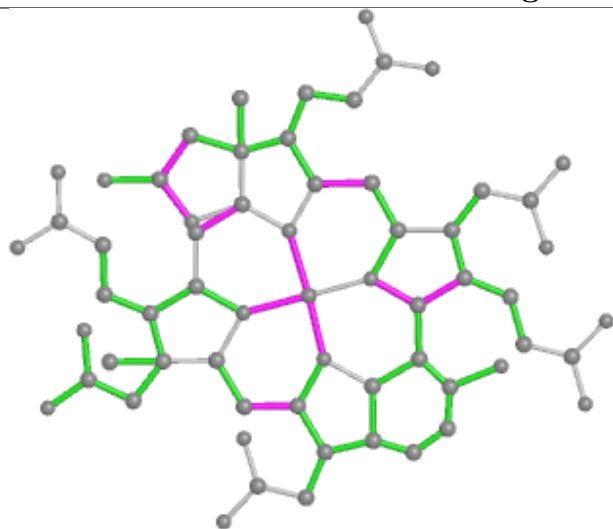
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	606[B]	ACT	1	0
8	D	602	COM	2	0
4	A	601	F43	3	0
6	D	601[B]	ACT	1	0
7	A	609[A]	TP7	3	0
4	A	608	F43	3	0

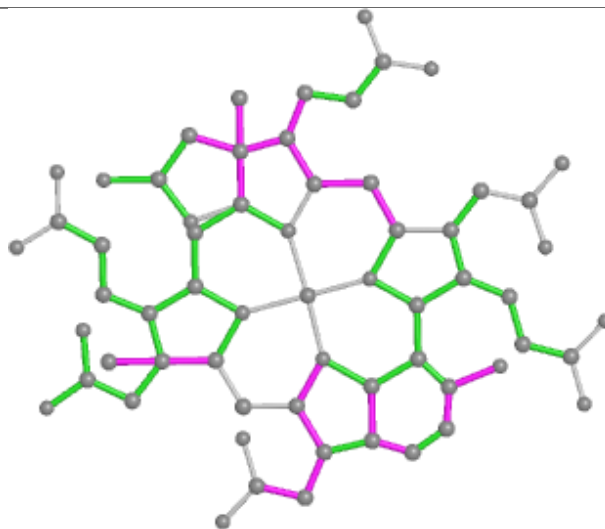
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



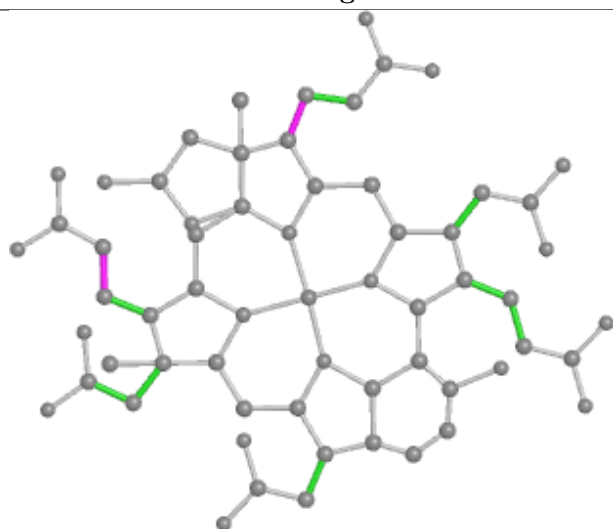
Ligand F43 A 601



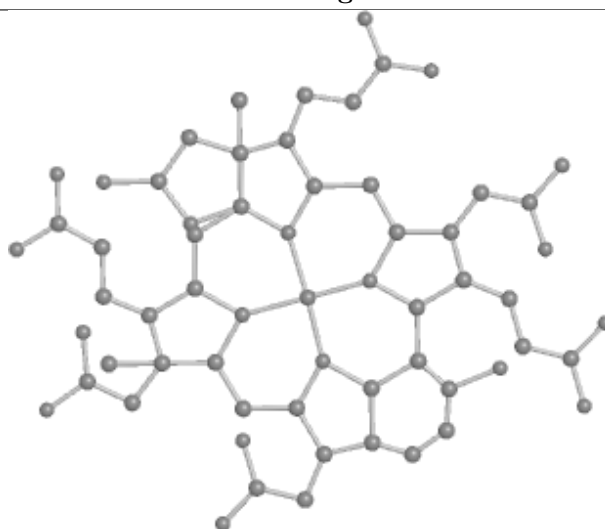
Bond lengths



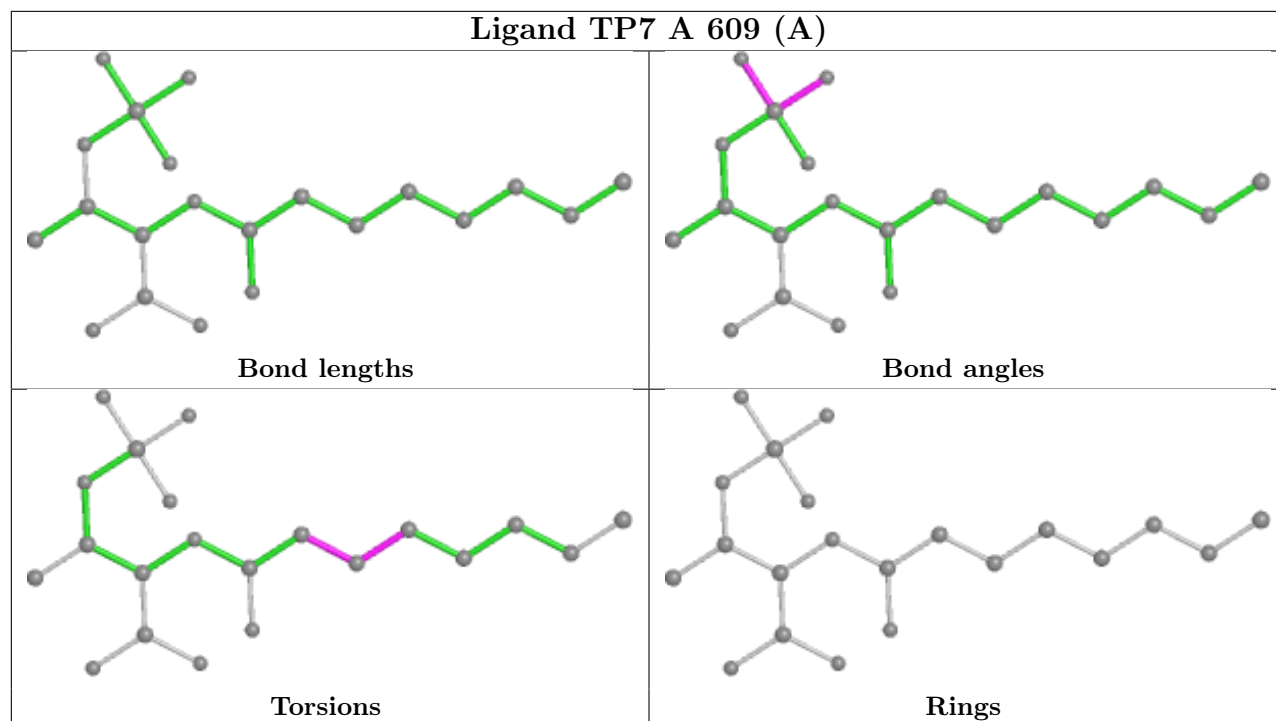
Bond angles

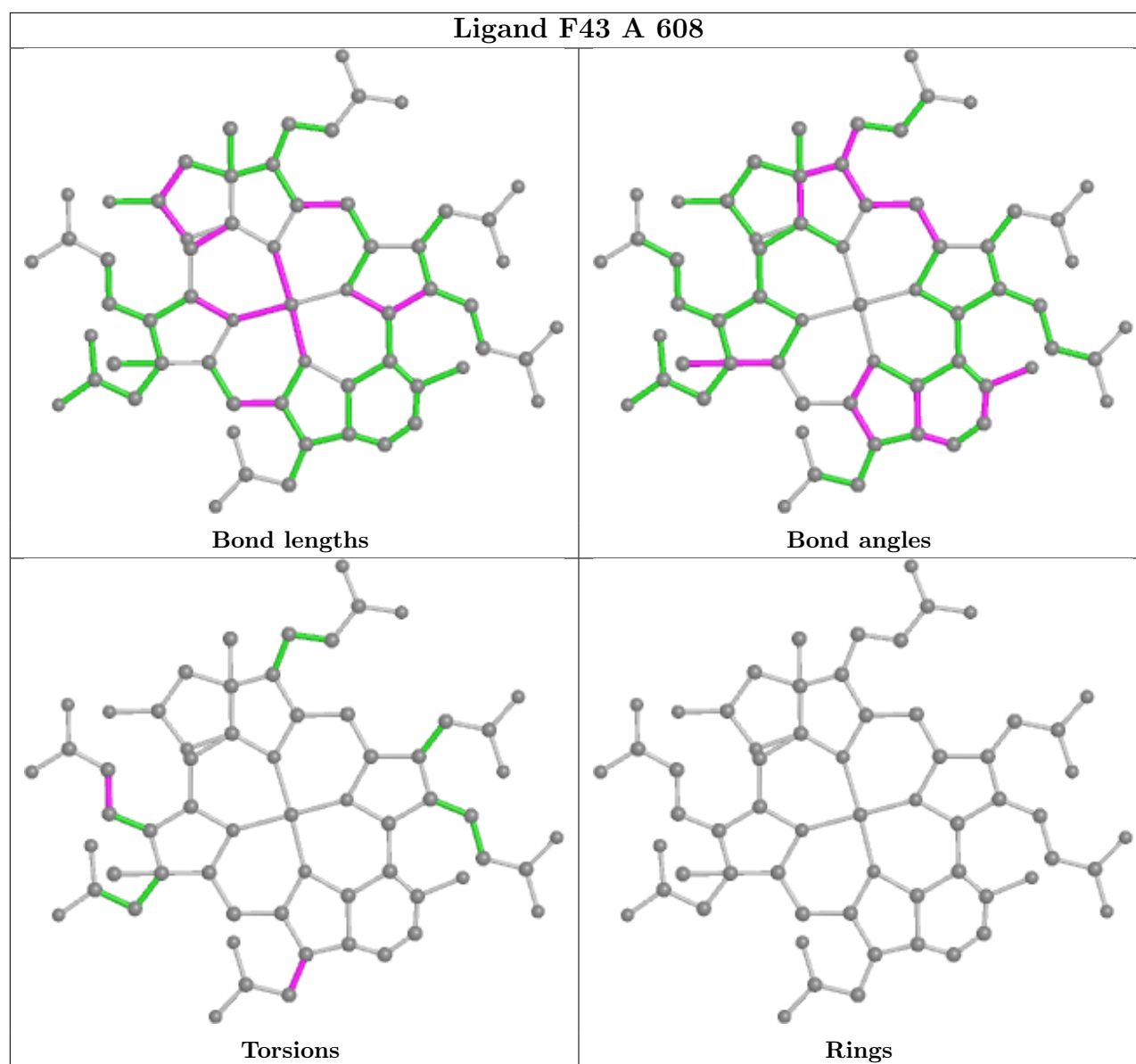


Torsions



Rings





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	541/548 (98%)	-0.26	2 (0%) 92 93	22, 31, 50, 69	0
1	D	541/548 (98%)	-0.25	2 (0%) 92 93	20, 31, 46, 66	0
2	B	442/442 (100%)	0.02	12 (2%) 54 58	24, 40, 57, 71	0
2	E	442/442 (100%)	0.31	29 (6%) 18 19	26, 45, 71, 82	0
3	C	243/246 (98%)	0.54	21 (8%) 10 10	27, 41, 64, 77	0
3	F	243/246 (98%)	0.91	40 (16%) 1 1	30, 49, 76, 88	0
All	All	2452/2472 (99%)	0.09	106 (4%) 35 38	20, 37, 65, 88	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	205	LEU	5.5
3	F	70	VAL	5.4
3	F	66	ILE	4.7
1	D	549	ALA	4.5
3	C	76	ALA	4.4

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	0.85	0.19	49,51,55,57	0
1	MHS	D	257	11/12	0.88	0.21	44,46,50,50	0
1	AGM	A	271	12/13	0.95	0.17	27,32,35,36	0
1	MGN	A	400	10/11	0.96	0.15	21,25,28,28	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	AGM	D	271	12/13	0.96	0.16	27,30,32,32	0
1	MGN	D	400	10/11	0.96	0.12	23,27,29,33	0
1	DYA	D	450	8/9	0.97	0.12	24,29,30,31	0
1	DYA	A	450	8/9	0.98	0.13	24,27,29,29	0
1	SMC	A	452	7/8	0.98	0.13	27,28,30,30	0
1	GL3	D	445	4/5	0.98	0.10	26,27,27,29	0
1	GL3	A	445	4/5	0.98	0.12	23,24,24,26	0
1	SMC	D	452	7/8	0.98	0.13	27,29,31,31	0

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
10	XE	B	503	1/1	0.91	0.57	40,40,40,40	1
10	XE	B	501[A]	1/1	0.92	0.09	51,51,51,51	1
6	ACT	A	606[B]	4/4	0.94	0.22	37,38,39,40	4
7	TP7	A	609[A]	21/21	0.94	0.18	28,34,42,43	21
10	XE	D	603	1/1	0.94	0.06	49,49,49,49	1
8	COM	D	602	7/7	0.95	0.20	35,37,44,45	0
8	COM	A	605	7/7	0.96	0.27	31,34,40,42	0
5	MG	A	602	1/1	0.97	0.05	37,37,37,37	0
5	MG	D	604	1/1	0.97	0.11	34,34,34,34	0
6	ACT	A	603	4/4	0.97	0.10	33,35,37,37	0
4	F43	A	601	62/62	0.97	0.12	26,30,35,39	0
6	ACT	D	601[B]	4/4	0.97	0.23	35,35,35,36	4
7	TP7	A	604[A]	21/21	0.97	0.18	25,33,38,39	21
10	XE	E	501[A]	1/1	0.97	0.12	45,45,45,45	1
4	F43	A	608	62/62	0.98	0.13	21,26,31,33	0
10	XE	B	502[B]	1/1	0.98	0.06	47,47,47,47	1
6	ACT	D	605	4/4	0.98	0.10	32,32,33,35	0
9	NA	A	607	1/1	0.98	0.17	20,20,20,20	0
10	XE	A	610	1/1	0.98	0.08	46,46,46,46	1
10	XE	E	502[B]	1/1	0.98	0.11	47,47,47,47	1

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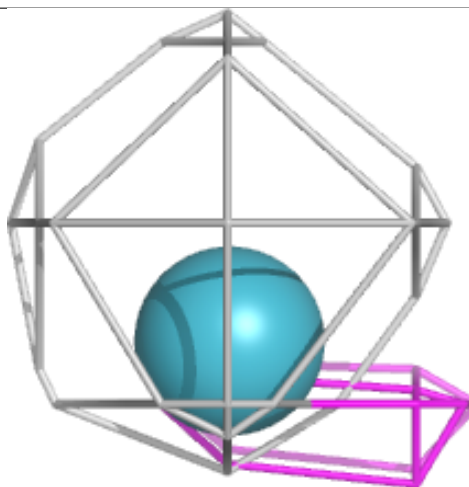
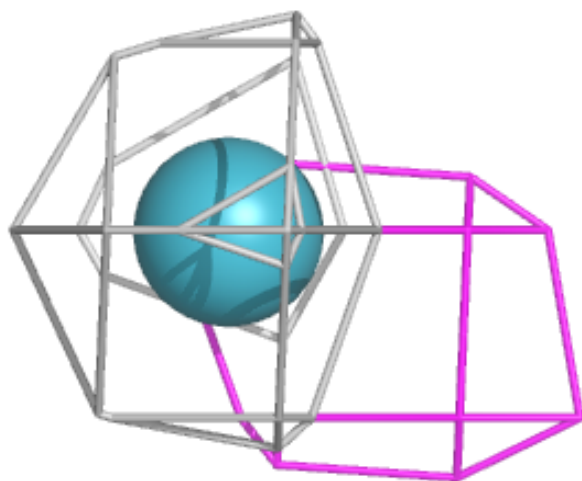
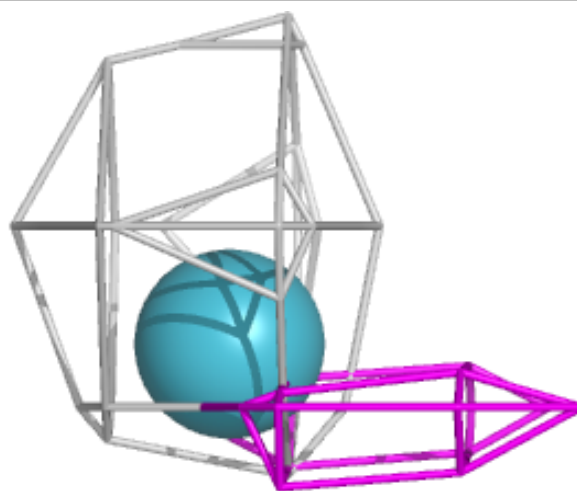
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
10	XE	E	503	1/1	0.98	0.43	40,40,40,40	1

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.

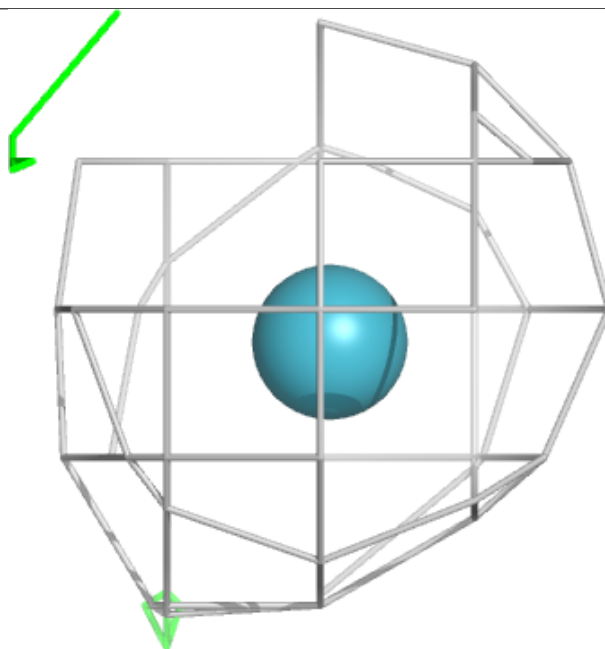
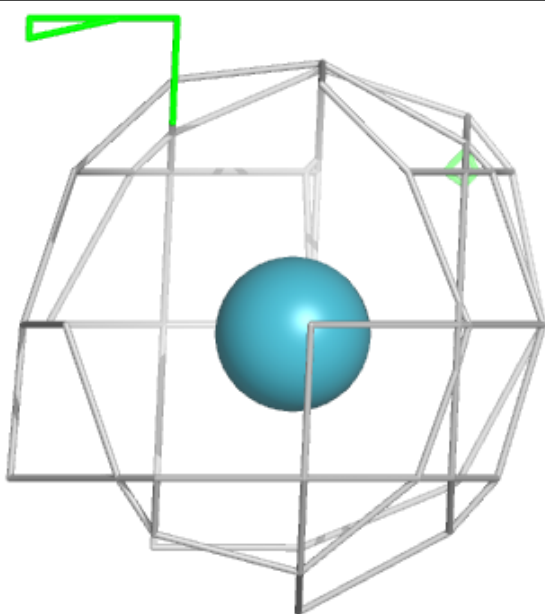
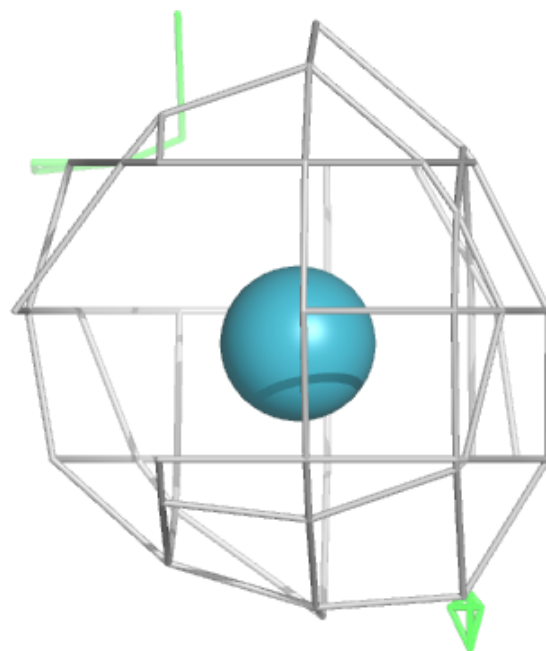
Electron density around XE B 503:

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



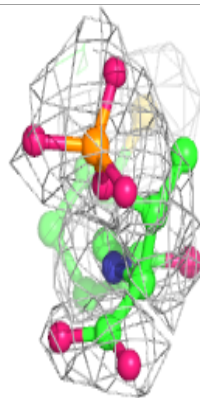
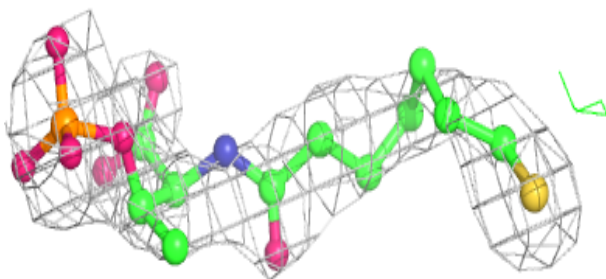
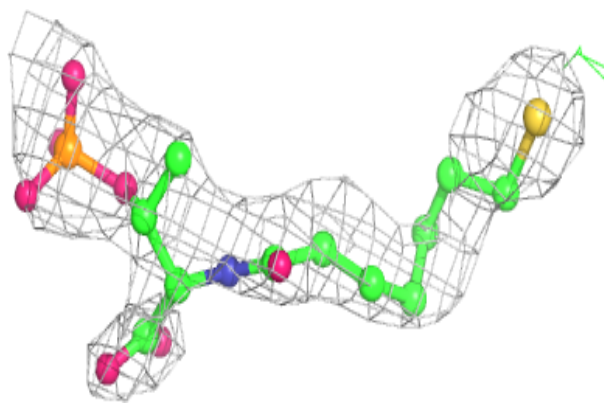
Electron density around XE B 501 (A):

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



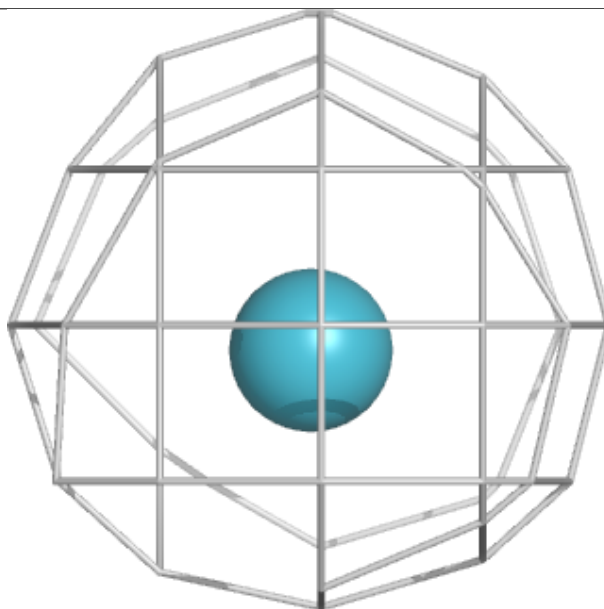
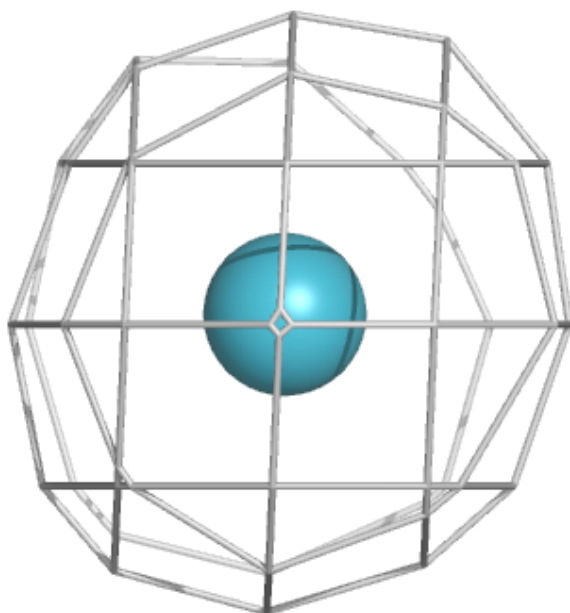
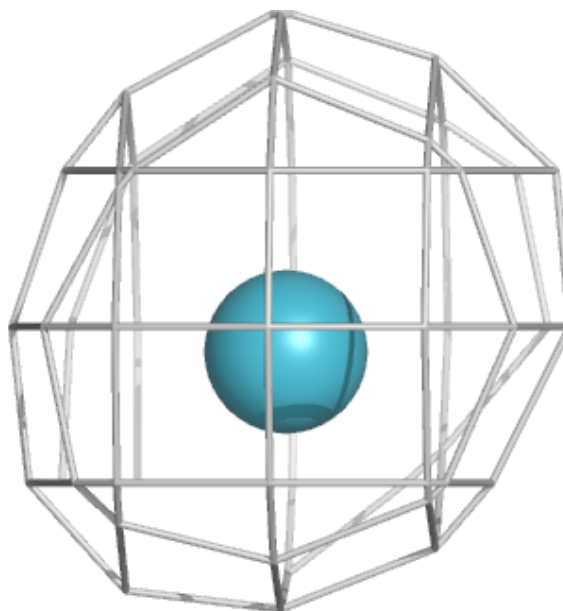
Electron density around TP7 A 609 (A):

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



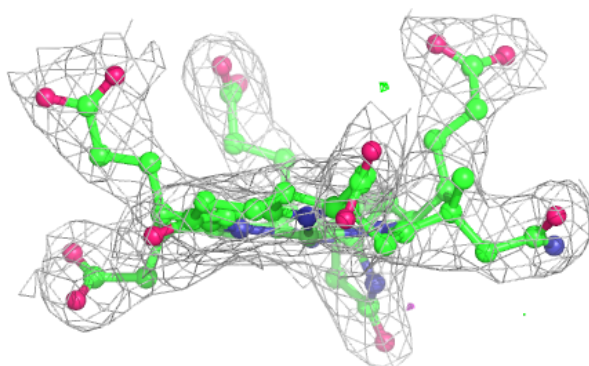
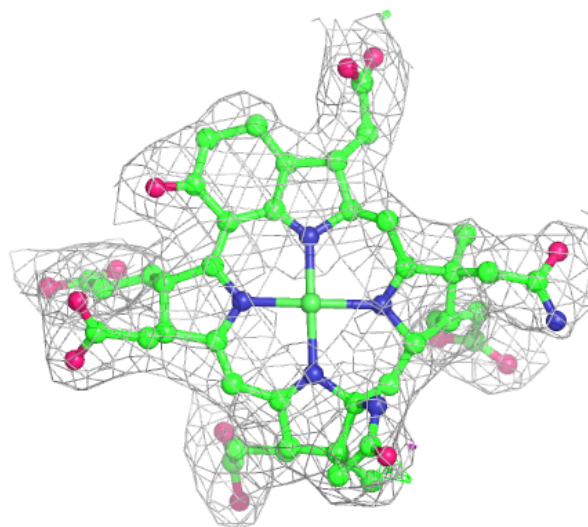
Electron density around XE D 603:

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



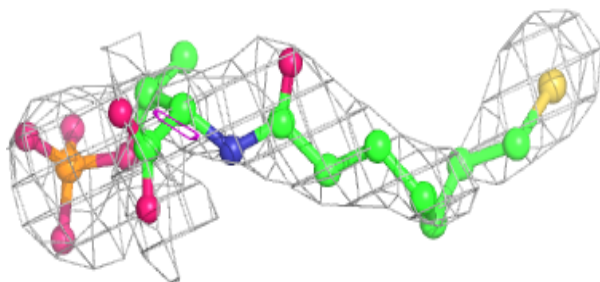
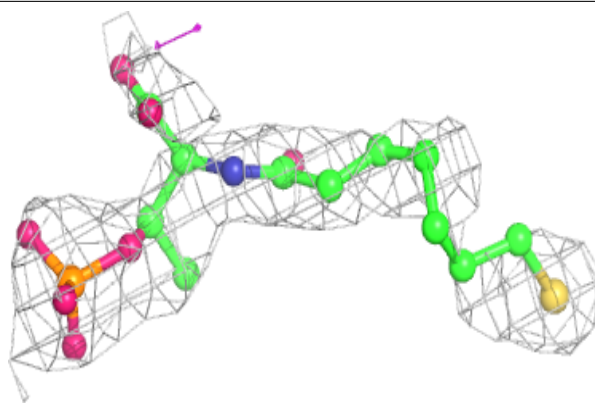
Electron density around F43 A 601:

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



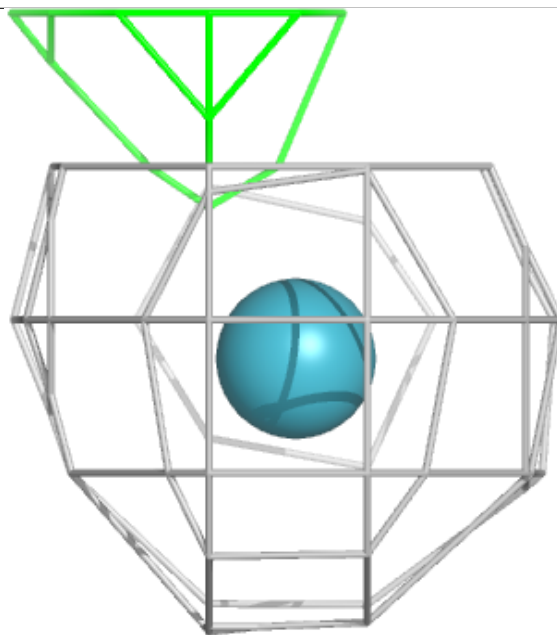
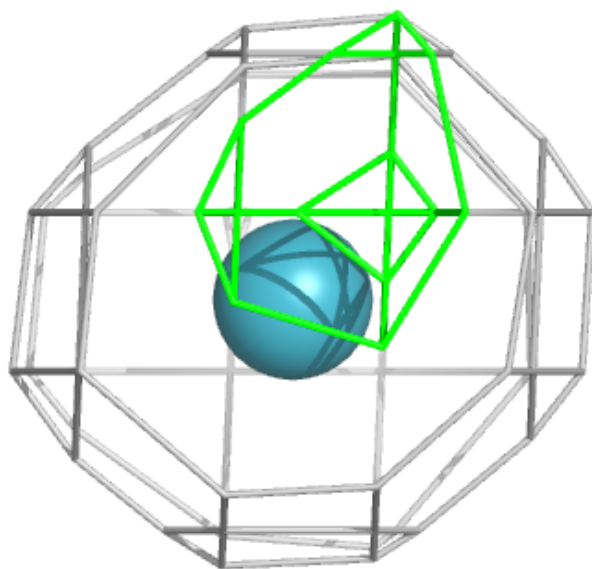
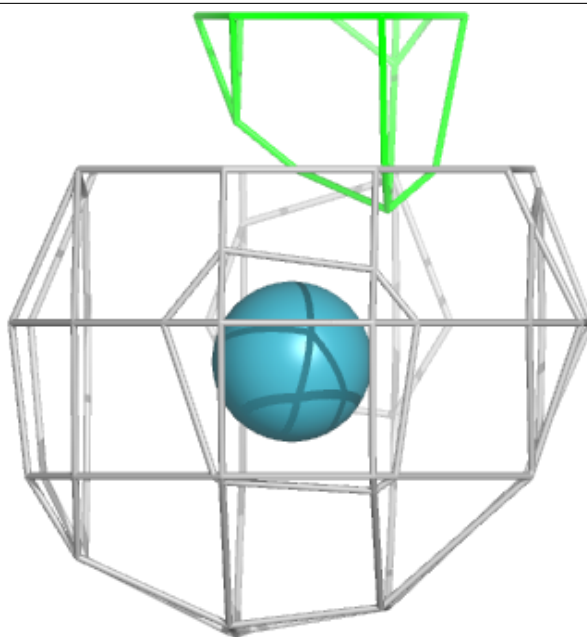
Electron density around TP7 A 604 (A):

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



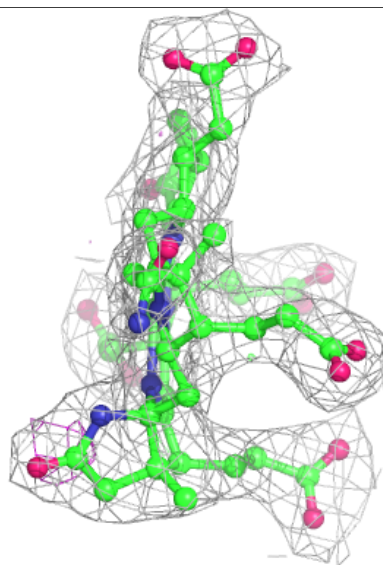
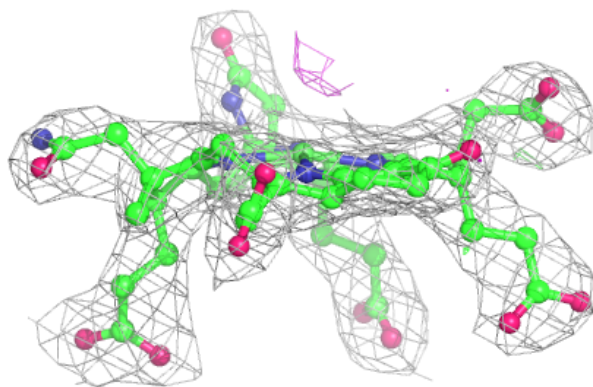
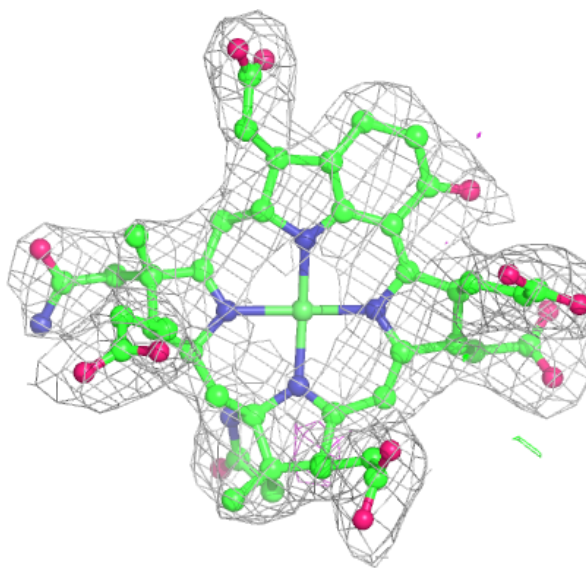
Electron density around XE E 501 (A):

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



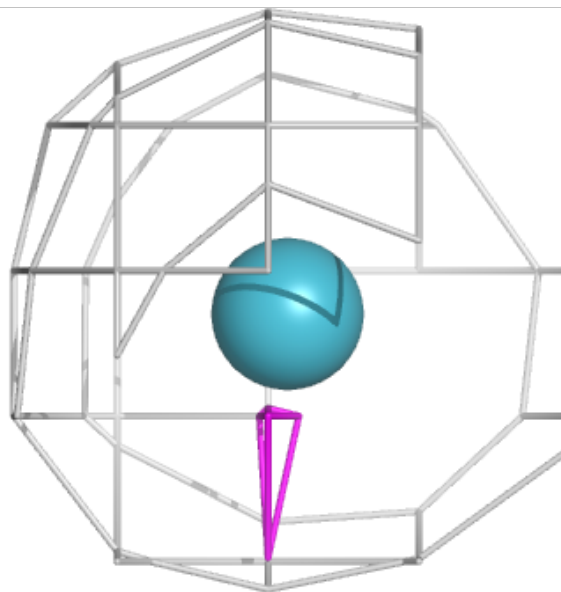
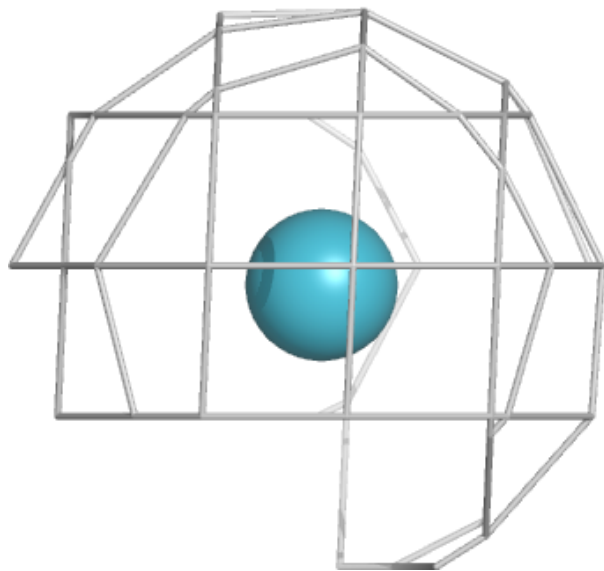
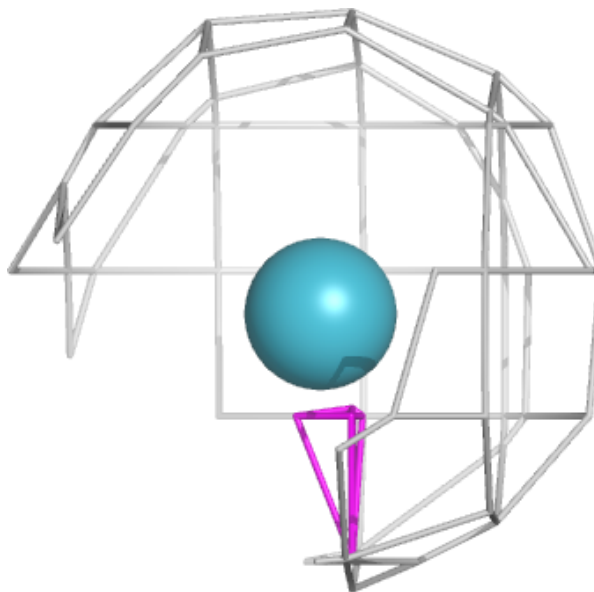
Electron density around F43 A 608:

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



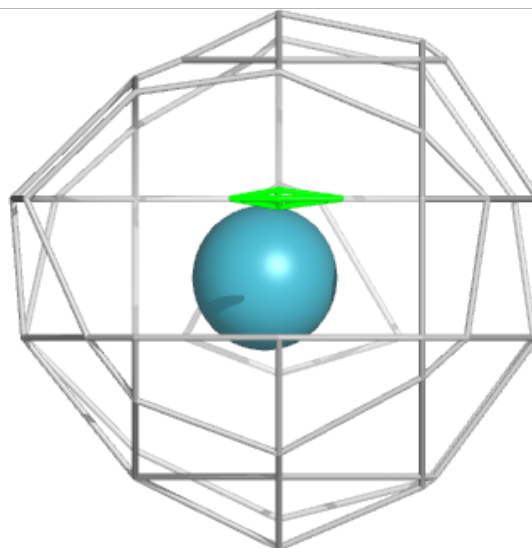
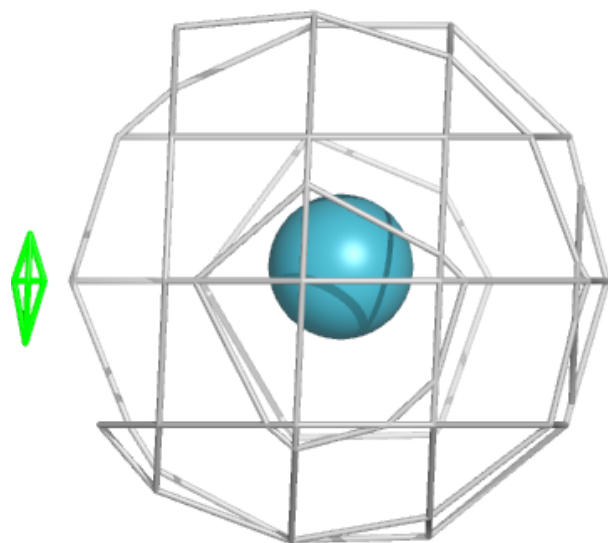
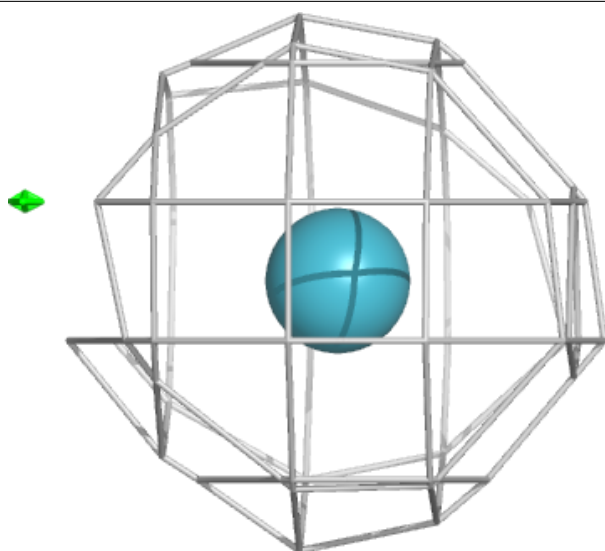
Electron density around XE B 502 (B):

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



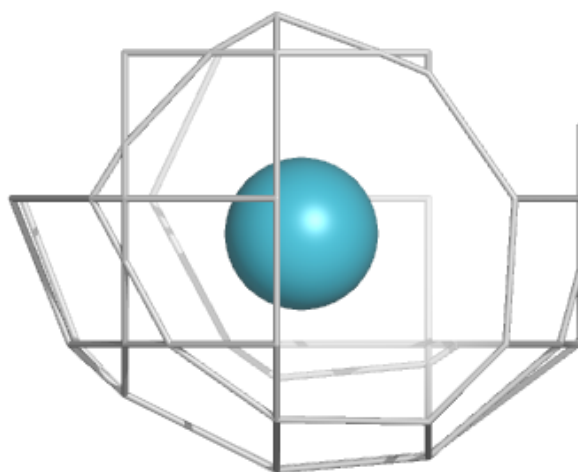
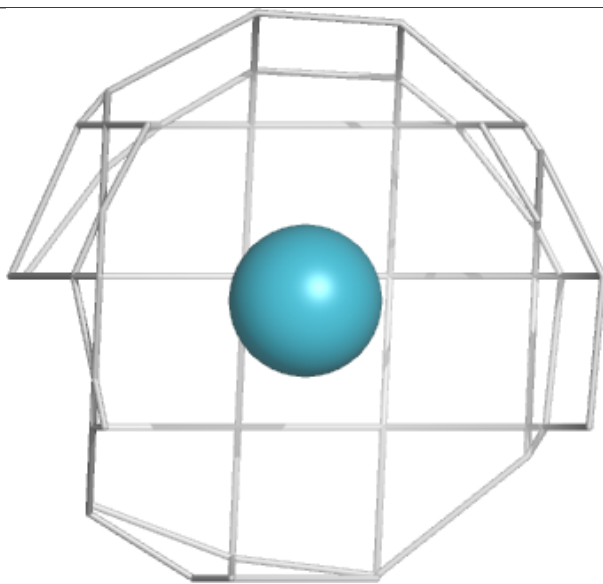
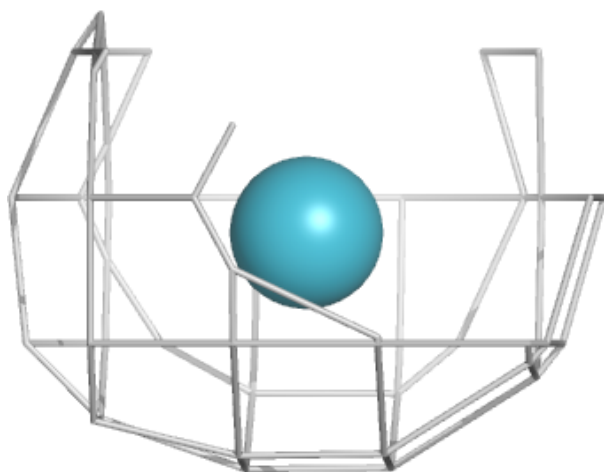
Electron density around XE A 610:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



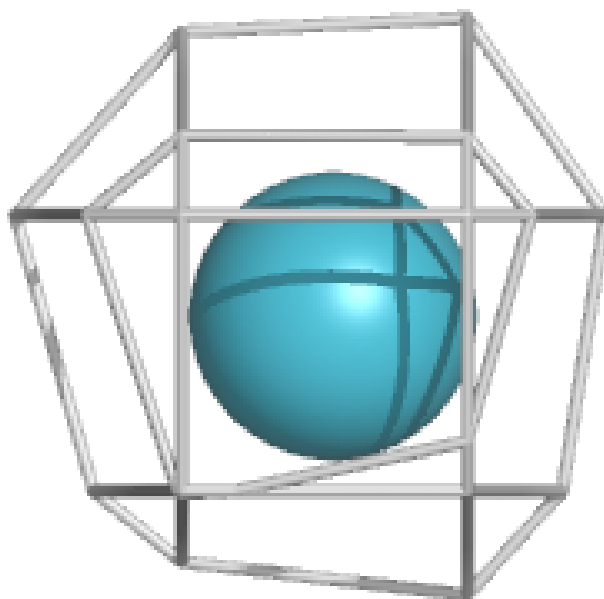
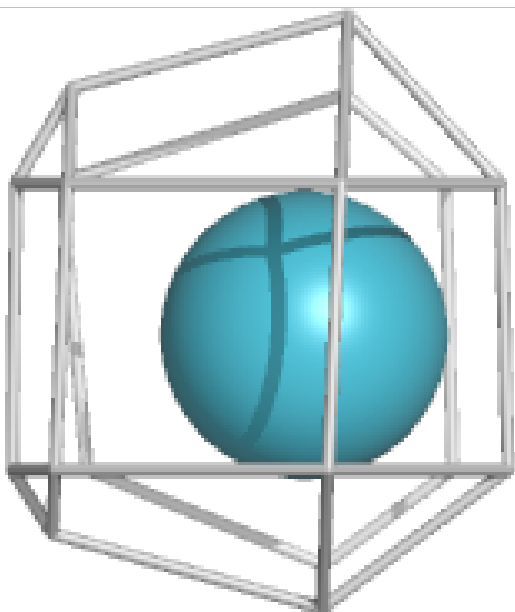
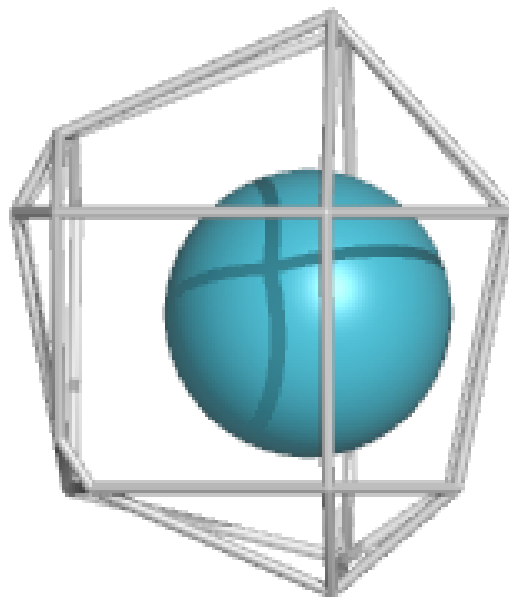
Electron density around XE E 502 (B):

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



Electron density around XE E 503:

$2mF_o-DF_c$ (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.