wwPDB X-ray Structure Validation Summary Report (i)

Nov 16, 2020 – 09:28 PM GMT

PDB ID	:	6ZUK
Title	:	Crystal structure of dimethylated RSL-N23H/G68H (RSL-B6) in complex with cucurbit[7]uril and zinc
Authors	:	Guagnini, F.; Engilberge, S.; Flood, R.J.; Ramberg, K.O.; Crowley, P.B.
Deposited on	:	2020-07-23
Resolution	:	2.03 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 following versions of software and data (see references (i)) were used in the production of this report:

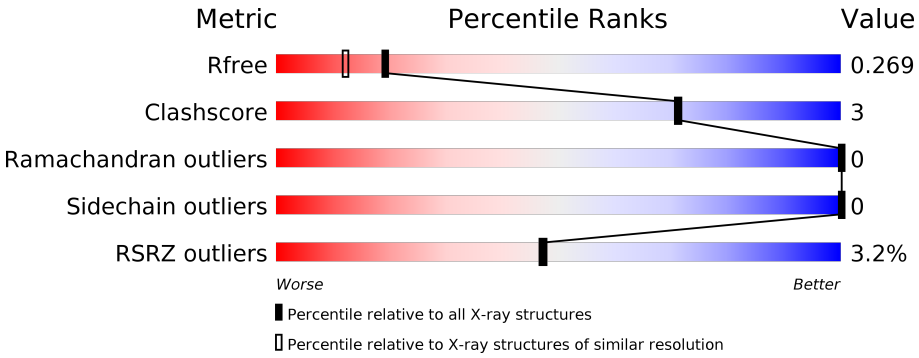
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

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 2.03 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 on 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	88	88% 13%
1	B	88	93% 7%
1	C	88	3% 88% 11%
1	D	88	88% 11%
1	E	88	3% 91% 8%
1	F	88	9% 90% 9%

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
2	QQ7	A	101	X	-	-	-
2	QQ7	B	101	X	-	-	-
2	QQ7	C	101	X	-	-	-
2	QQ7	D	101	X	-	-	-
2	QQ7	E	101	X	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5184 atoms, of which 290 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 Fucose-binding lectin protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	88	Total	C	N	O	S	0	0	0
			688	437	118	131	2			
1	B	88	Total	C	N	O	S	0	0	0
			688	437	118	131	2			
1	C	88	Total	C	N	O	S	0	0	0
			688	437	118	131	2			
1	D	87	Total	C	N	O	S	0	0	0
			680	432	117	129	2			
1	E	87	Total	C	N	O	S	0	0	0
			680	432	117	129	2			
1	F	87	Total	C	N	O	S	0	0	0
			680	432	117	129	2			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	SNM	-	expression tag	UNP A0A0S4TLR1
A	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
A	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1
A	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
A	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
A	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
A	70	MLY	THR	conflict	UNP A0A0S4TLR1
B	2	SNM	-	expression tag	UNP A0A0S4TLR1
B	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
B	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1
B	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
B	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
B	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
B	70	MLY	THR	conflict	UNP A0A0S4TLR1
C	2	SNM	-	expression tag	UNP A0A0S4TLR1
C	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
C	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1

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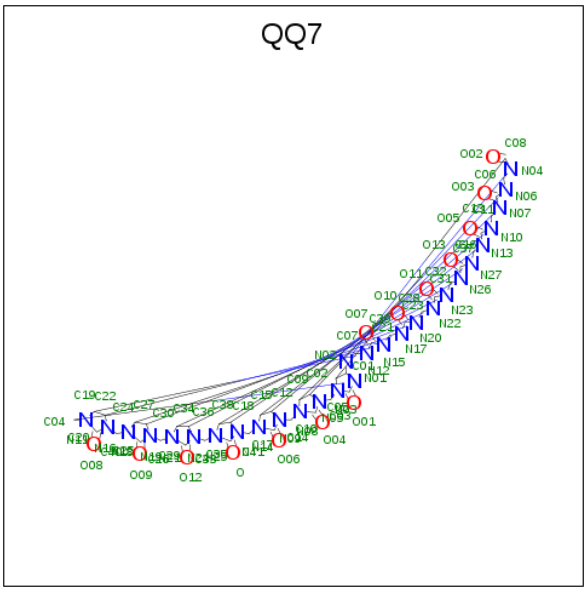
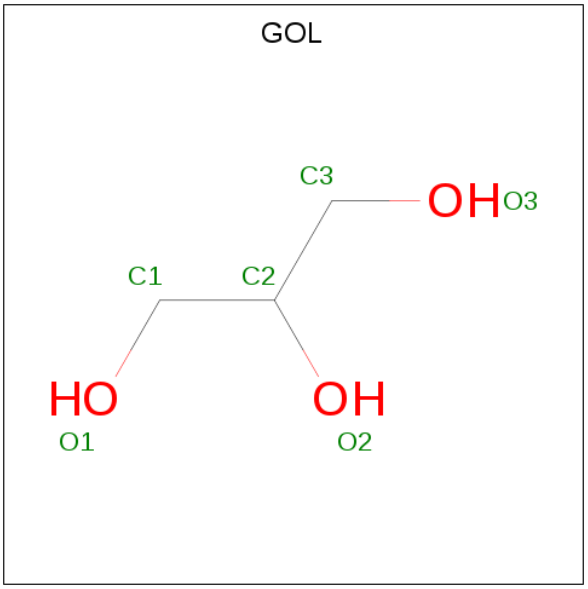
Chain	Residue	Modelled	Actual	Comment	Reference
C	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
C	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
C	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
C	70	MLY	THR	conflict	UNP A0A0S4TLR1
D	2	SNM	-	expression tag	UNP A0A0S4TLR1
D	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
D	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1
D	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
D	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
D	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
D	70	MLY	THR	conflict	UNP A0A0S4TLR1
E	2	SNM	-	expression tag	UNP A0A0S4TLR1
E	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
E	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1
E	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
E	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
E	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
E	70	MLY	THR	conflict	UNP A0A0S4TLR1
F	2	SNM	-	expression tag	UNP A0A0S4TLR1
F	23	HIS	ASN	engineered mutation	UNP A0A0S4TLR1
F	60	SER	HIS	engineered mutation	UNP A0A0S4TLR1
F	67	ASN	THR	engineered mutation	UNP A0A0S4TLR1
F	68	HIS	GLY	engineered mutation	UNP A0A0S4TLR1
F	69	GLY	THR	engineered mutation	UNP A0A0S4TLR1
F	70	MLY	THR	conflict	UNP A0A0S4TLR1

- Molecule 2 is cucurbit[7]uril (three-letter code: QQ7) (formula: $C_{42}H_{42}N_{28}O_{14}$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			126	42	42	28	14		
2	B	1	Total	C	H	N	O	0	0
			126	42	42	28	14		
2	C	1	Total	C	H	N	O	0	0
			126	42	42	28	14		
2	D	1	Total	C	H	N	O	0	0
			126	42	42	28	14		
2	E	1	Total	C	H	N	O	0	0
			126	42	42	28	14		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C H O 14 3 8 3	0	0
3	A	1	Total C H O 14 3 8 3	0	0
3	B	1	Total C H O 14 3 8 3	0	0
3	B	1	Total C H O 14 3 8 3	0	0
3	C	1	Total C H O 14 3 8 3	0	0
3	C	1	Total C H O 14 3 8 3	0	0
3	D	1	Total C H O 14 3 8 3	0	0
3	D	1	Total C H O 14 3 8 3	0	0
3	E	1	Total C H O 14 3 8 3	0	0
3	F	1	Total C H O 14 3 8 3	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Zn 2 2	0	0
4	A	1	Total Zn 1 1	0	0
4	C	2	Total Zn 2 2	0	0
4	E	1	Total Zn 1 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total Na 1 1	0	0

- Molecule 6 is water.

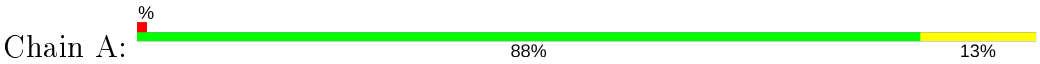
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	68	Total O 68 68	0	0
6	B	75	Total O 75 75	0	0
6	C	60	Total O 60 60	0	0
6	D	32	Total O 32 32	0	0
6	E	30	Total O 30 30	0	0
6	F	38	Total O 38 38	0	0

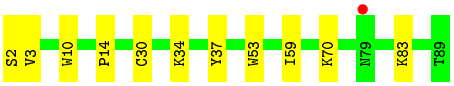
3 Residue-property plots (i)

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: Fucose-binding lectin protein

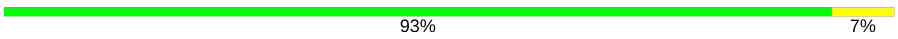
Chain A:

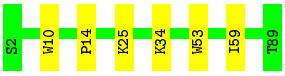




- Molecule 1: Fucose-binding lectin protein

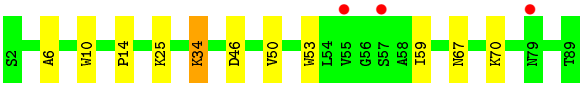
Chain B:





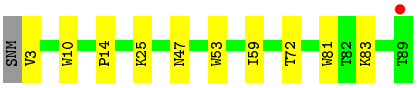
- Molecule 1: Fucose-binding lectin protein

Chain C:



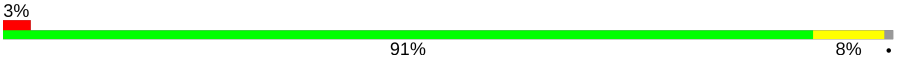
- Molecule 1: Fucose-binding lectin protein

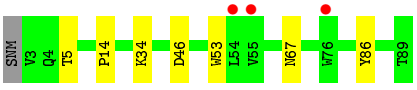
Chain D:



- Molecule 1: Fucose-binding lectin protein

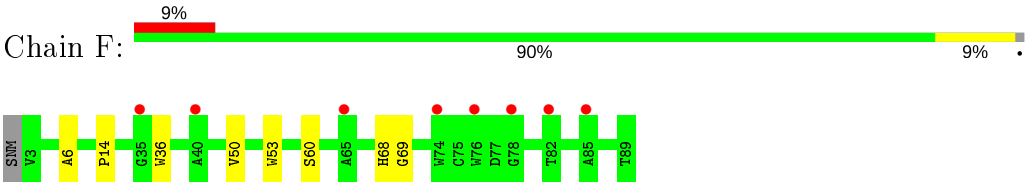
Chain E:





- Molecule 1: Fucose-binding lectin protein

Chain F:


9%
90%
9%
SNM
V3
A6
P14
G35
W36
A40
V50
W53
S60
A65
H68
G69
W74
C75
W76
D77
G78
T82
A85
T89

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	50.48Å 50.63Å 74.81Å 71.12° 83.15° 60.13°	Depositor
Resolution (Å)	43.72 – 2.03 43.72 – 2.03	Depositor EDS
% Data completeness (in resolution range)	97.1 (43.72-2.03) 97.1 (43.72-2.03)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.37 (at 2.03Å)	Xtriage
Refinement program	BUSTER 2.10.3 (29-NOV-2019)	Depositor
R, R_{free}	0.220 , 0.253 0.229 , 0.269	Depositor DCC
R_{free} test set	1741 reflections (4.56%)	wwPDB-VP
Wilson B-factor (Å^2)	30.2	Xtriage
Anisotropy	0.205	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 54.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.056 for -h+k,k,k-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5184	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, NA, SNM, QQ7, MLY

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	0.27	0/658	0.43	0/906
1	B	0.25	0/658	0.43	0/906
1	C	0.27	0/658	0.43	0/906
1	D	0.21	0/658	0.39	0/906
1	E	0.20	0/658	0.37	0/906
1	F	0.21	0/658	0.39	0/906
All	All	0.24	0/3948	0.41	0/5436

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

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	688	0	630	7	0
1	B	688	0	630	3	0
1	C	688	0	630	8	0
1	D	680	0	630	8	0
1	E	680	0	630	7	0
1	F	680	0	629	8	0
2	A	84	42	42	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	84	42	42	0	0
2	C	84	42	42	0	0
2	D	84	42	42	0	0
2	E	84	42	42	0	0
3	A	12	16	16	0	0
3	B	12	16	16	1	0
3	C	12	16	16	0	0
3	D	12	16	16	1	0
3	E	6	8	8	0	0
3	F	6	8	8	0	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	E	1	0	0	0	0
5	C	1	0	0	0	0
6	A	68	0	0	2	0
6	B	75	0	0	1	0
6	C	60	0	0	1	0
6	D	32	0	0	0	0
6	E	30	0	0	0	0
6	F	38	0	0	0	0
All	All	4894	290	4069	30	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 30 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)
3:B:103:GOL:H31	6:B:237:HOH:O	2.02	0.58
1:C:46:ASP:OD2	1:C:67:ASN:O	2.21	0.58
1:A:70:MLY:HE2	6:A:236:HOH:O	2.04	0.57
1:E:53:TRP:CE2	1:F:14:PRO:HG3	2.39	0.56
1:C:34:MLY:HH22	6:C:201:HOH:O	2.06	0.56

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	81/88 (92%)	78 (96%)	3 (4%)	0	100	100
1	B	81/88 (92%)	78 (96%)	3 (4%)	0	100	100
1	C	81/88 (92%)	77 (95%)	4 (5%)	0	100	100
1	D	81/88 (92%)	79 (98%)	2 (2%)	0	100	100
1	E	81/88 (92%)	76 (94%)	5 (6%)	0	100	100
1	F	81/88 (92%)	79 (98%)	2 (2%)	0	100	100
All	All	486/528 (92%)	467 (96%)	19 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	64/64 (100%)	64 (100%)	0	100	100
1	B	64/64 (100%)	64 (100%)	0	100	100
1	C	64/64 (100%)	64 (100%)	0	100	100
1	D	64/64 (100%)	64 (100%)	0	100	100
1	E	64/64 (100%)	64 (100%)	0	100	100
1	F	64/64 (100%)	64 (100%)	0	100	100
All	All	384/384 (100%)	384 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	47	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

27 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	MLY	F	25	1	9,10,11	0.62	0	6,11,13	1.15	0
1	MLY	D	83	1	9,10,11	0.54	0	6,11,13	0.98	0
1	MLY	D	34	1	9,10,11	0.58	0	6,11,13	0.90	0
1	MLY	E	70	1	9,10,11	0.56	0	6,11,13	0.94	0
1	MLY	E	34	1	9,10,11	0.70	0	6,11,13	1.33	1 (16%)
1	MLY	A	83	1	9,10,11	0.65	0	6,11,13	1.12	1 (16%)
1	SNM	C	2	-	5,7,8	0.70	0	4,8,10	0.28	0
1	MLY	F	83	1	9,10,11	0.56	0	6,11,13	1.14	0
1	MLY	B	34	1	9,10,11	0.44	0	6,11,13	1.77	3 (50%)
1	MLY	C	25	1	9,10,11	1.14	1 (11%)	6,11,13	0.89	0
1	MLY	A	70	1	9,10,11	0.69	0	6,11,13	1.09	0
1	MLY	C	70	1	9,10,11	0.62	0	6,11,13	0.90	0
1	MLY	D	70	1	9,10,11	0.49	0	6,11,13	1.14	0
1	MLY	E	83	1	9,10,11	0.57	0	6,11,13	1.02	0
1	SNM	B	2	-	5,7,8	0.70	0	4,8,10	0.34	0
1	MLY	F	70	1	9,10,11	0.86	0	6,11,13	1.03	0
1	MLY	B	70	1	9,10,11	0.72	0	6,11,13	1.21	0
1	MLY	E	25	1	9,10,11	0.63	0	6,11,13	1.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	MLY	B	25	1	9,10,11	0.68	0	6,11,13	1.21	1 (16%)
1	MLY	A	34	1	9,10,11	0.84	0	6,11,13	0.96	0
1	MLY	C	34	1	9,10,11	0.78	0	6,11,13	1.38	1 (16%)
1	MLY	B	83	1	9,10,11	0.55	0	6,11,13	1.02	0
1	MLY	A	25	1	9,10,11	0.64	0	6,11,13	1.11	0
1	MLY	D	25	1	9,10,11	0.53	0	6,11,13	1.33	1 (16%)
1	MLY	C	83	1	9,10,11	0.69	0	6,11,13	1.00	0
1	SNM	A	2	-	5,7,8	0.69	0	4,8,10	0.30	0
1	MLY	F	34	1	9,10,11	0.79	0	6,11,13	1.06	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	F	25	1	-	1/8/9/11	-
1	MLY	D	83	1	-	2/8/9/11	-
1	MLY	D	34	1	-	1/8/9/11	-
1	MLY	E	70	1	-	1/8/9/11	-
1	MLY	E	34	1	-	2/8/9/11	-
1	MLY	A	83	1	-	4/8/9/11	-
1	SNM	C	2	-	-	0/4/8/10	-
1	MLY	F	83	1	-	3/8/9/11	-
1	MLY	B	34	1	-	2/8/9/11	-
1	MLY	C	25	1	-	5/8/9/11	-
1	MLY	A	70	1	-	2/8/9/11	-
1	MLY	C	70	1	-	5/8/9/11	-
1	MLY	D	70	1	-	3/8/9/11	-
1	MLY	E	83	1	-	2/8/9/11	-
1	SNM	B	2	-	-	2/4/8/10	-
1	MLY	F	70	1	-	3/8/9/11	-
1	MLY	B	70	1	-	5/8/9/11	-
1	MLY	E	25	1	-	2/8/9/11	-
1	MLY	B	25	1	-	2/8/9/11	-
1	MLY	A	34	1	-	4/8/9/11	-
1	MLY	C	34	1	-	2/8/9/11	-
1	MLY	B	83	1	-	4/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	25	1	-	2/8/9/11	-
1	MLY	D	25	1	-	2/8/9/11	-
1	MLY	C	83	1	-	5/8/9/11	-
1	SNM	A	2	-	-	2/4/8/10	-
1	MLY	F	34	1	-	5/8/9/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	25	MLY	CB-CA	2.78	1.57	1.53

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	34	MLY	CD-CE-NZ	-2.56	106.85	113.79
1	C	34	MLY	CH2-NZ-CH1	-2.42	103.47	109.73
1	E	34	MLY	CH2-NZ-CH1	-2.30	103.78	109.73
1	D	25	MLY	CD-CE-NZ	-2.25	107.69	113.79
1	B	34	MLY	CG-CD-CE	-2.11	103.47	113.21

There are no chirality outliers.

5 of 73 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	34	MLY	C-CA-CB-CG
1	A	83	MLY	O-C-CA-CB
1	F	83	MLY	N-CA-CB-CG
1	F	83	MLY	C-CA-CB-CG
1	C	25	MLY	O-C-CA-CB

There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	83	MLY	1	0
1	A	70	MLY	1	0
1	C	70	MLY	1	0
1	A	34	MLY	1	0
1	C	34	MLY	2	0
1	A	2	SNM	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 22 ligands modelled in this entry, 7 are monoatomic - leaving 15 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	$\#\|Z\| > 2$
3	GOL	A	102	-	5,5,5	0.06	0	5,5,5	0.37	0
3	GOL	C	102	-	5,5,5	0.13	0	5,5,5	0.32	0
3	GOL	E	102	-	5,5,5	0.06	0	5,5,5	0.14	0
2	QQ7	D	101	-	105,105,105	0.13	0	182,182,182	0.23	0
3	GOL	F	101	-	5,5,5	0.06	0	5,5,5	0.14	0
2	QQ7	A	101	5	105,105,105	0.14	0	182,182,182	0.23	0
3	GOL	B	102	-	5,5,5	0.10	0	5,5,5	0.12	0
2	QQ7	C	101	5	105,105,105	0.15	0	182,182,182	0.24	0
3	GOL	D	102	-	5,5,5	0.10	0	5,5,5	0.12	0
2	QQ7	E	101	-	105,105,105	0.13	0	182,182,182	0.23	0
3	GOL	A	103	-	5,5,5	0.16	0	5,5,5	0.27	0
3	GOL	C	103	-	5,5,5	0.04	0	5,5,5	0.22	0
3	GOL	B	103	-	5,5,5	0.11	0	5,5,5	0.39	0
3	GOL	D	103	-	5,5,5	0.10	0	5,5,5	0.20	0
2	QQ7	B	101	5	105,105,105	0.15	0	182,182,182	0.23	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	102	-	-	2/4/4/4	-
3	GOL	C	102	-	-	2/4/4/4	-
3	GOL	E	102	-	-	0/4/4/4	-
2	QQ7	D	101	-	14/14/56/56	-	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	F	101	-	-	0/4/4/4	-
2	QQ7	A	101	5	14/14/56/56	-	-
3	GOL	B	102	-	-	0/4/4/4	-
2	QQ7	C	101	5	14/14/56/56	-	-
3	GOL	D	102	-	-	0/4/4/4	-
2	QQ7	E	101	-	14/14/56/56	-	-
3	GOL	A	103	-	-	0/4/4/4	-
3	GOL	C	103	-	-	2/4/4/4	-
3	GOL	B	103	-	-	4/4/4/4	-
3	GOL	D	103	-	-	2/4/4/4	-
2	QQ7	B	101	5	14/14/56/56	-	-

There are no bond length outliers.

There are no bond angle outliers.

5 of 70 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	101	QQ7	N14
2	A	101	QQ7	N01
2	A	101	QQ7	N24
2	A	101	QQ7	N08
2	A	101	QQ7	N03

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	102	GOL	O1-C1-C2-C3
3	C	103	GOL	C1-C2-C3-O3
3	C	103	GOL	O2-C2-C3-O3
3	B	103	GOL	O1-C1-C2-C3
3	D	103	GOL	C1-C2-C3-O3

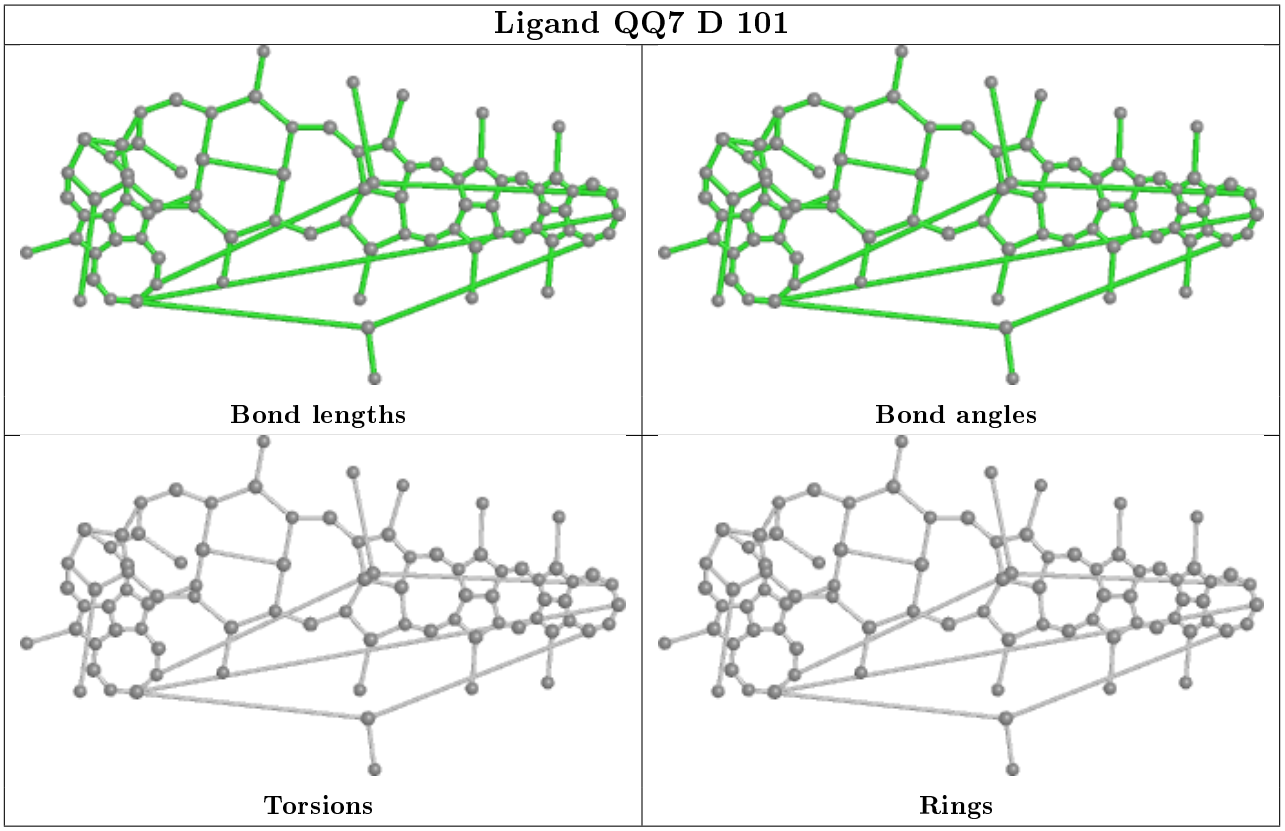
There are no ring outliers.

2 monomers are involved in 2 short contacts:

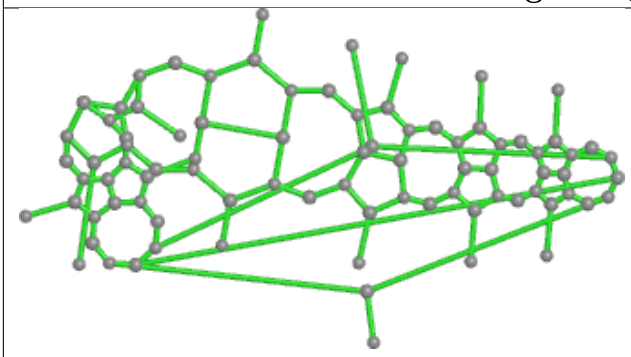
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	103	GOL	1	0
3	D	103	GOL	1	0

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.

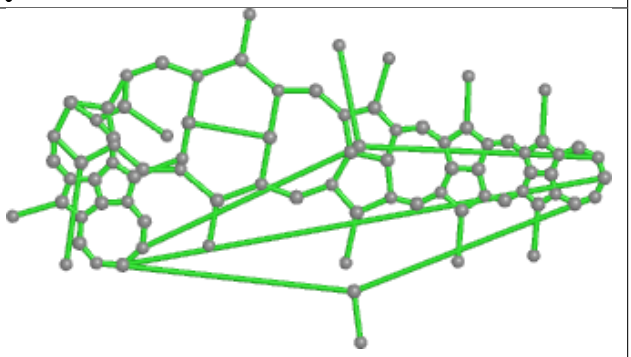
Ligand QQ7 D 101



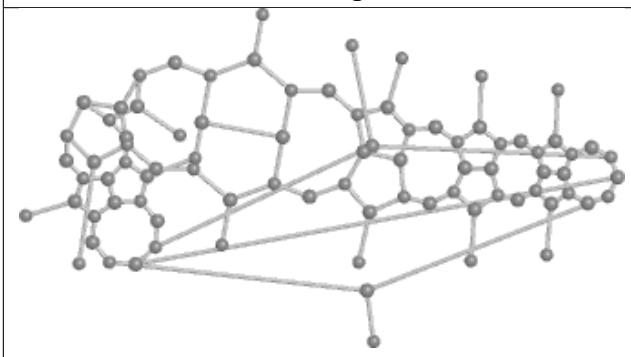
Ligand QQ7 A 101



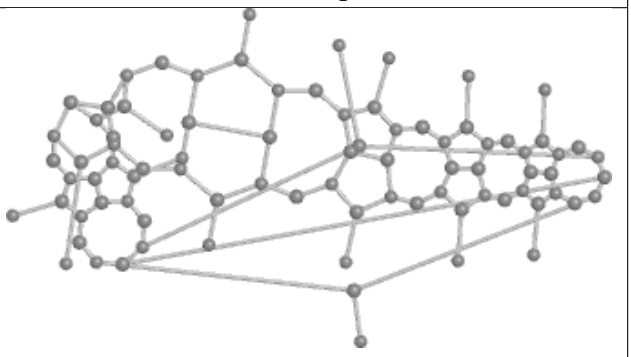
Bond lengths



Bond angles

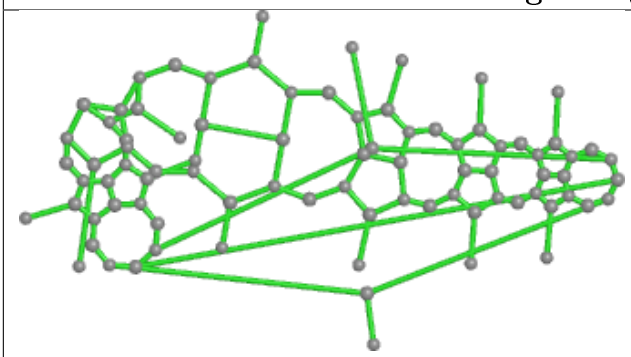


Torsions

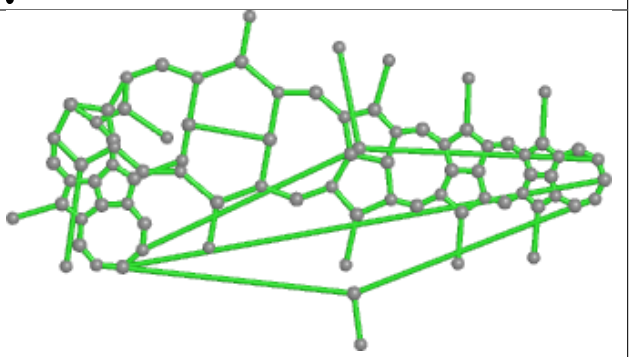


Rings

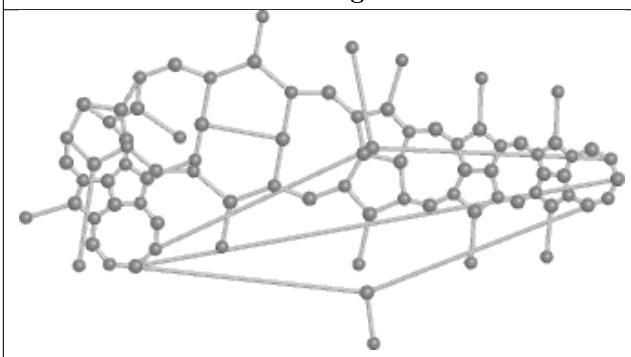
Ligand QQ7 C 101



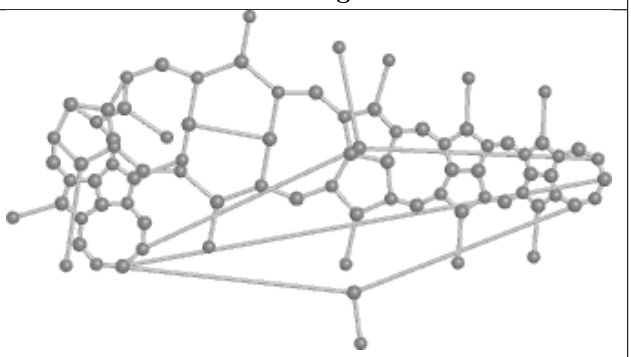
Bond lengths



Bond angles

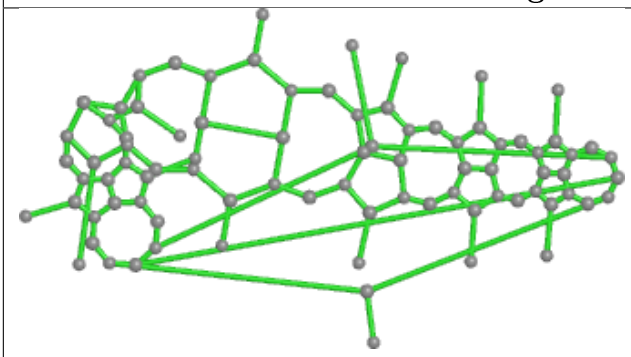


Torsions

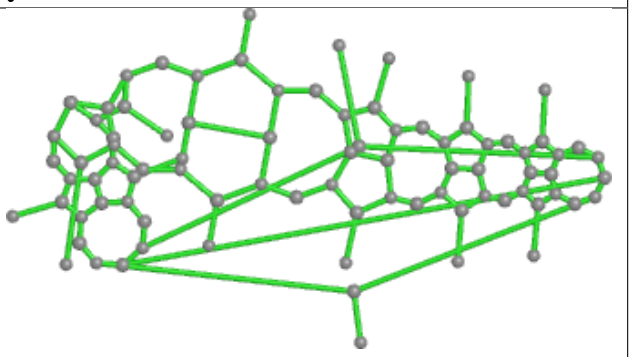


Rings

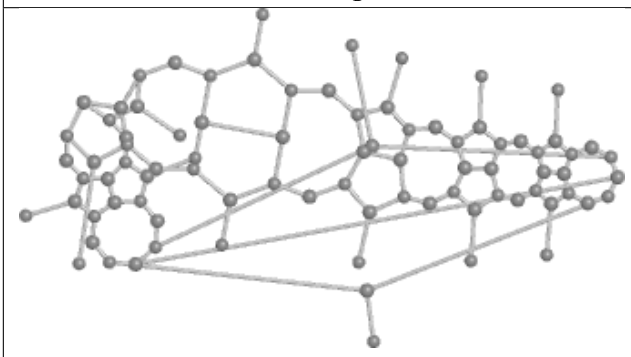
Ligand QQ7 E 101



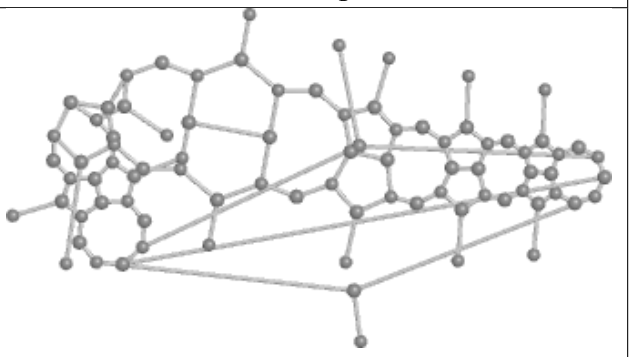
Bond lengths



Bond angles

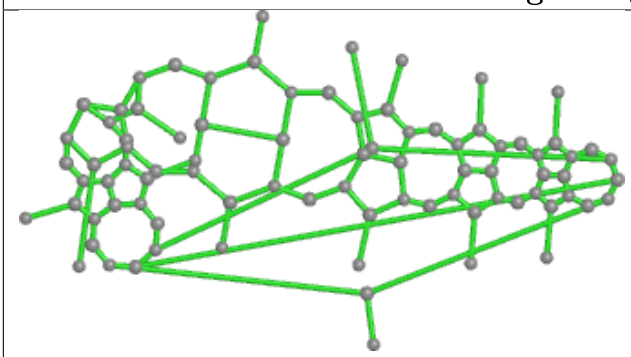


Torsions

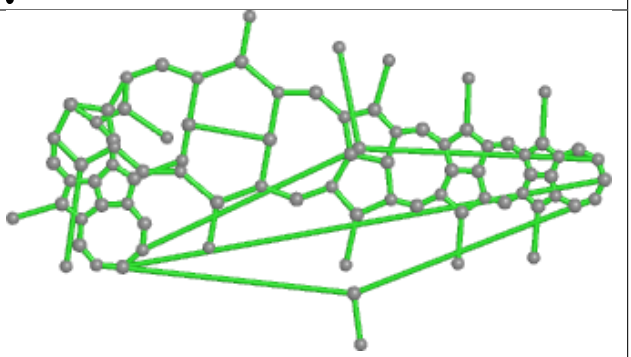


Rings

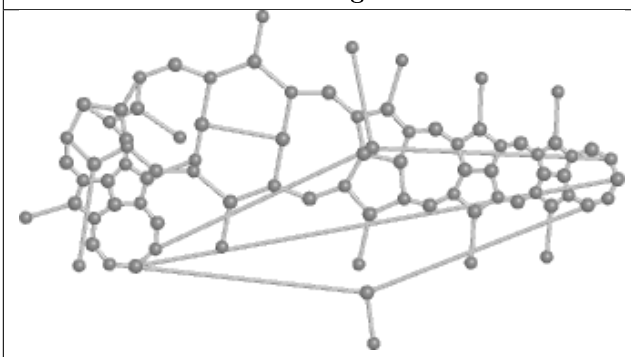
Ligand QQ7 B 101



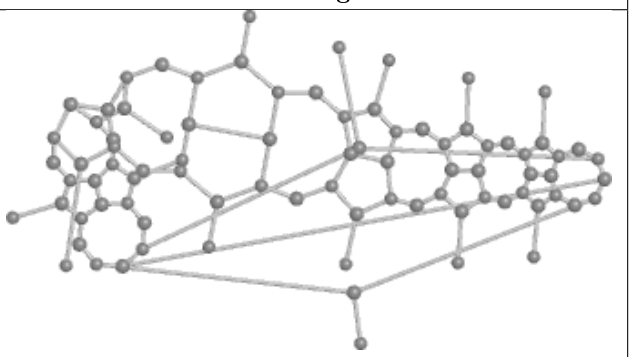
Bond lengths



Bond angles



Torsions



Rings

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
1	A	1
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	2:SNM	C	3:VAL	N	3.68
1	C	2:SNM	C	3:VAL	N	3.67
1	A	2:SNM	C	3:VAL	N	3.54

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, 95^{th} 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	83/88 (94%)	0.09	1 (1%) 79 78	15, 24, 39, 65	0
1	B	83/88 (94%)	0.20	0 100 100	15, 27, 47, 61	0
1	C	83/88 (94%)	0.42	3 (3%) 42 42	14, 27, 50, 67	0
1	D	83/88 (94%)	0.30	1 (1%) 79 78	24, 37, 53, 63	0
1	E	83/88 (94%)	0.49	3 (3%) 42 42	25, 38, 53, 69	0
1	F	83/88 (94%)	0.69	8 (9%) 8 7	28, 42, 57, 69	0
All	All	498/528 (94%)	0.37	16 (3%) 47 47	14, 34, 53, 69	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	55	VAL	5.9
1	C	57	SER	4.3
1	C	79	ASN	3.5
1	D	89	THR	3.3
1	E	54	LEU	2.8

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, 95^{th} 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	SNM	C	2	8/9	0.62	0.21	96,97,97,97	0
1	SNM	A	2	8/9	0.72	0.32	101,102,103,104	0
1	SNM	B	2	8/9	0.73	0.26	92,93,93,93	0
1	MLY	F	34	11/12	0.76	0.23	54,56,66,68	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	MLY	E	83	11/12	0.79	0.22	50,55,71,73	0
1	MLY	B	83	11/12	0.80	0.19	33,38,62,63	0
1	MLY	E	34	11/12	0.80	0.24	51,54,69,70	0
1	MLY	D	83	11/12	0.80	0.21	45,48,77,77	0
1	MLY	C	83	11/12	0.81	0.20	33,36,53,53	0
1	MLY	D	70	11/12	0.84	0.23	45,46,70,71	0
1	MLY	B	25	11/12	0.84	0.24	27,32,65,65	0
1	MLY	F	70	11/12	0.86	0.23	37,43,61,62	0
1	MLY	A	34	11/12	0.86	0.19	25,29,42,45	0
1	MLY	A	83	11/12	0.88	0.16	28,32,49,53	0
1	MLY	F	83	11/12	0.88	0.22	45,50,71,73	0
1	MLY	D	25	11/12	0.89	0.20	30,35,59,61	0
1	MLY	F	25	11/12	0.89	0.25	32,40,76,77	0
1	MLY	E	70	11/12	0.90	0.15	38,48,65,66	0
1	MLY	C	25	11/12	0.91	0.17	23,30,53,57	0
1	MLY	E	25	11/12	0.92	0.15	33,34,59,61	0
1	MLY	D	34	11/12	0.92	0.18	44,48,62,63	0
1	MLY	C	70	11/12	0.92	0.16	30,39,71,72	0
1	MLY	B	70	11/12	0.92	0.24	32,37,61,61	0
1	MLY	A	70	11/12	0.93	0.16	28,37,56,58	0
1	MLY	A	25	11/12	0.93	0.22	24,33,65,65	0
1	MLY	C	34	11/12	0.93	0.15	26,30,37,43	0
1	MLY	B	34	11/12	0.95	0.12	30,38,41,42	0

6.3 Carbohydrates (i)

There are no monosaccharides 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
2	QQ7	E	101	84/84	0.45	0.45	76,80,96,96	126
2	QQ7	D	101	84/84	0.69	0.26	50,63,78,79	126
3	GOL	D	102	6/6	0.71	0.17	35,42,46,47	0
3	GOL	B	103	6/6	0.78	0.22	29,35,41,41	0
3	GOL	F	101	6/6	0.81	0.21	41,49,57,57	0

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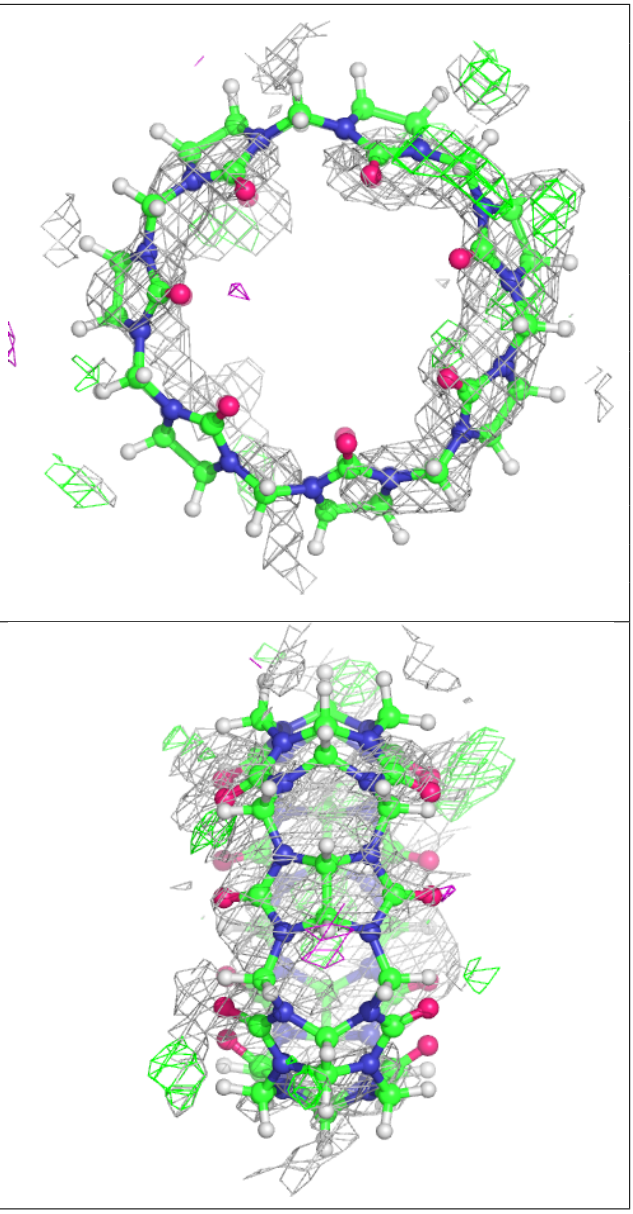
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	E	102	6/6	0.81	0.15	50,61,65,66	0
3	GOL	D	103	6/6	0.84	0.12	43,51,54,56	0
3	GOL	C	102	6/6	0.84	0.16	30,40,44,49	0
3	GOL	A	103	6/6	0.88	0.19	24,31,37,37	0
3	GOL	A	102	6/6	0.89	0.15	30,37,44,44	0
4	ZN	B	105	1/1	0.91	0.10	70,70,70,70	0
2	QQ7	C	101	84/84	0.92	0.12	16,29,37,40	0
5	NA	C	106	1/1	0.93	0.08	26,26,26,26	0
3	GOL	B	102	6/6	0.93	0.12	25,33,38,40	0
4	ZN	A	104	1/1	0.93	0.09	65,65,65,65	0
2	QQ7	A	101	84/84	0.94	0.12	19,27,35,38	0
4	ZN	E	103	1/1	0.94	0.11	63,63,63,63	0
2	QQ7	B	101	84/84	0.95	0.12	20,28,34,36	0
4	ZN	C	105	1/1	0.96	0.11	60,60,60,60	0
3	GOL	C	103	6/6	0.96	0.15	27,35,39,42	0
4	ZN	B	104	1/1	0.97	0.07	66,66,66,66	0
4	ZN	C	104	1/1	0.98	0.08	66,66,66,66	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.

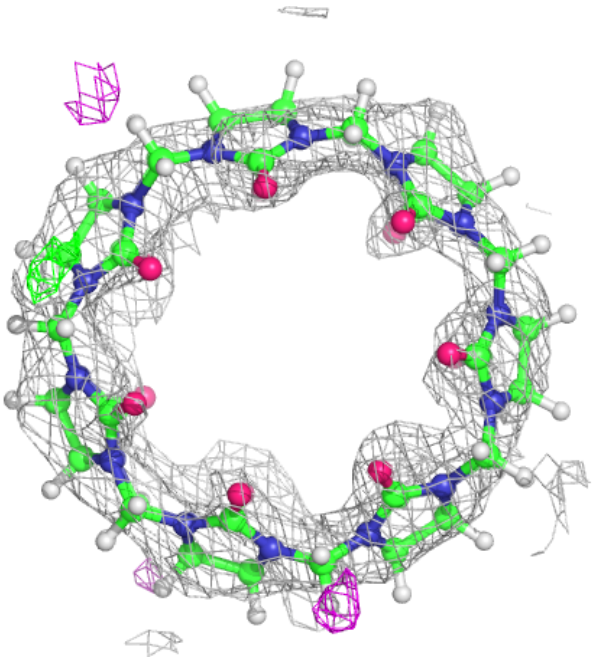
Electron density around QQ7 E 101:

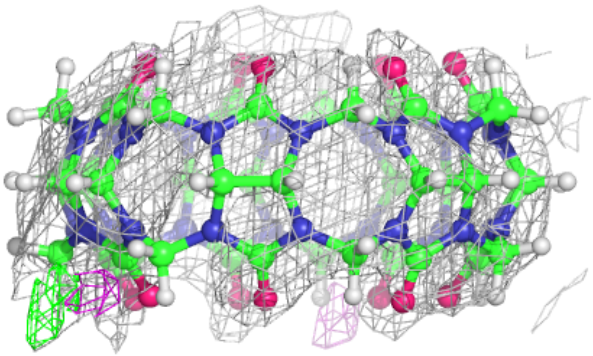
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

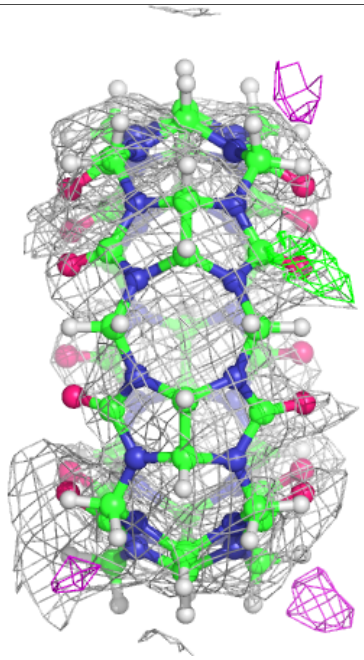


Electron density around QQ7 D 101:

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

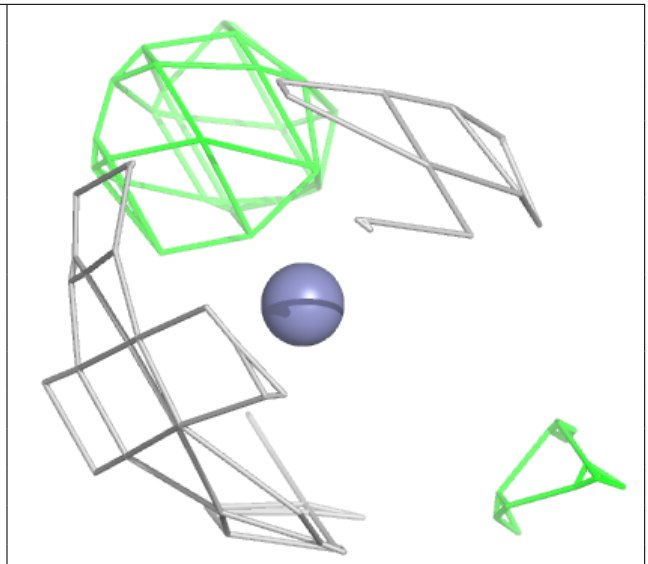


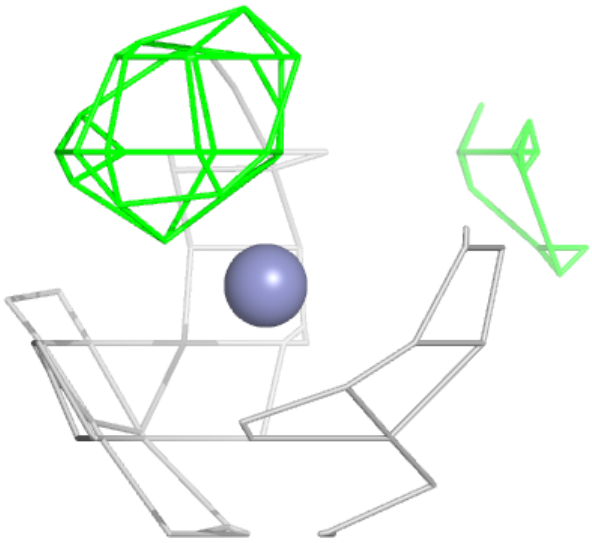


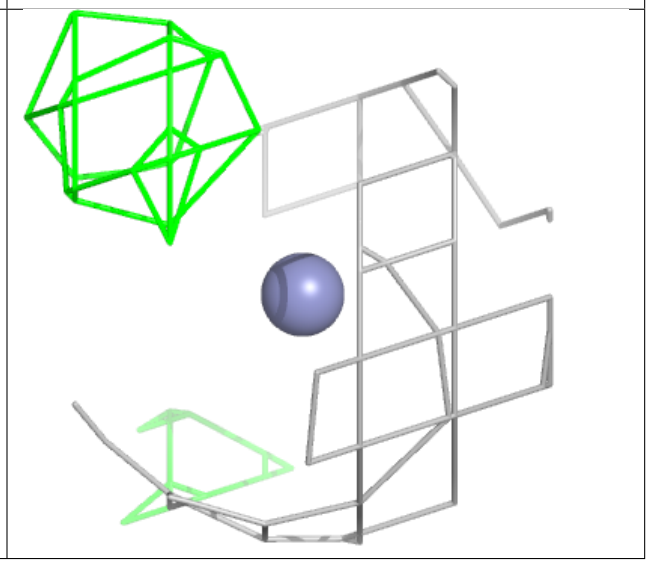


Electron density around ZN B 105:

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

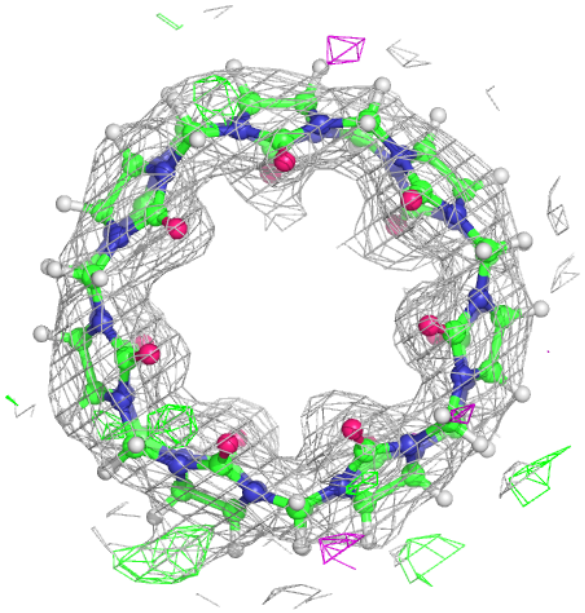


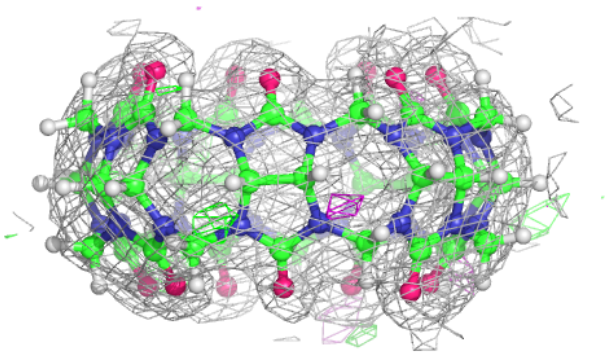


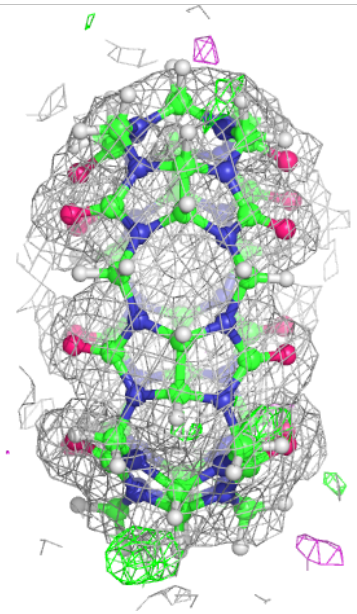


Electron density around QQ7 C 101:

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

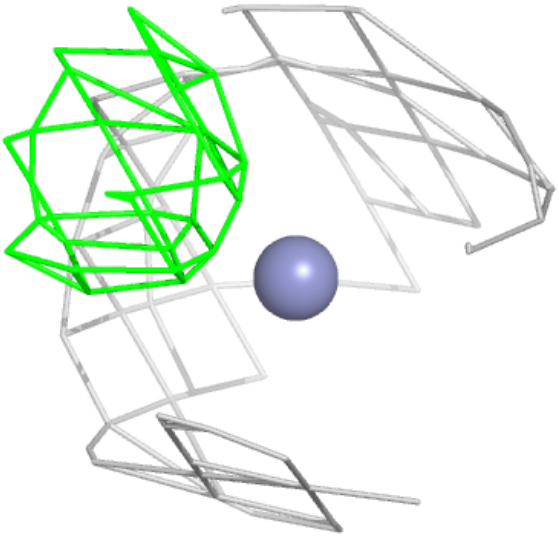


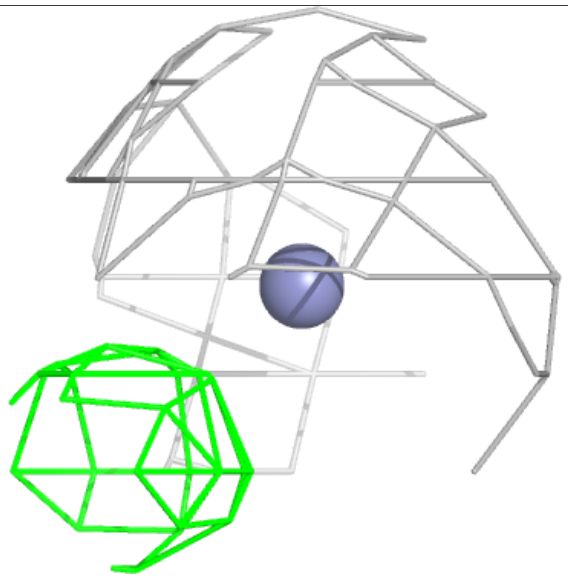


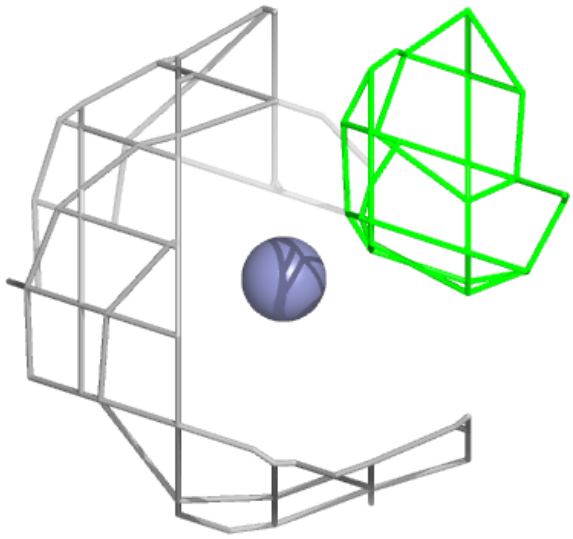


Electron density around ZN A 104:

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

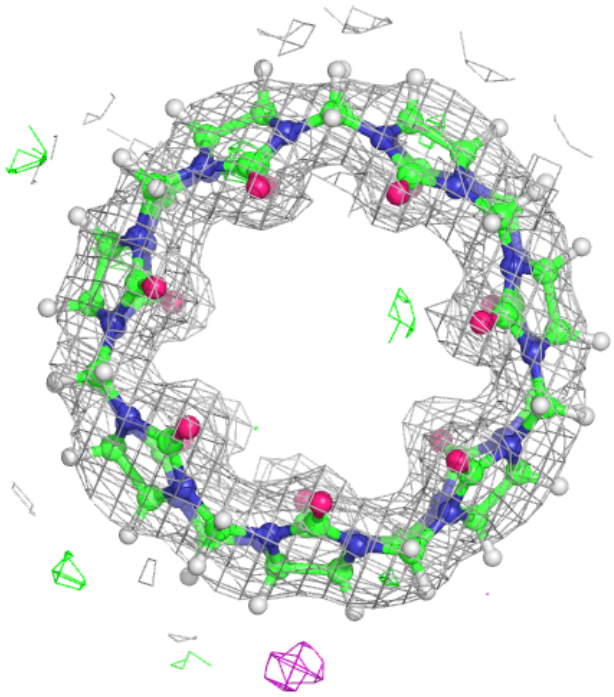


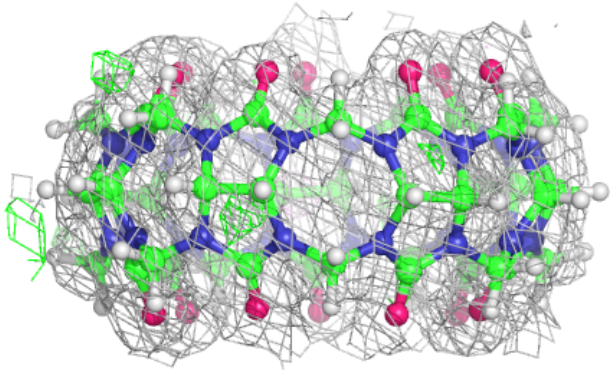


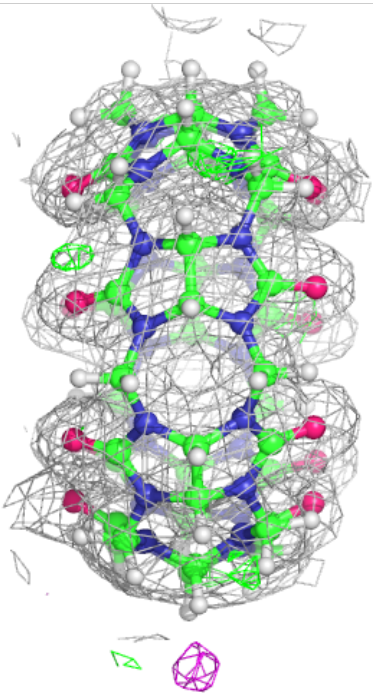


Electron density around QQ7 A 101:

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

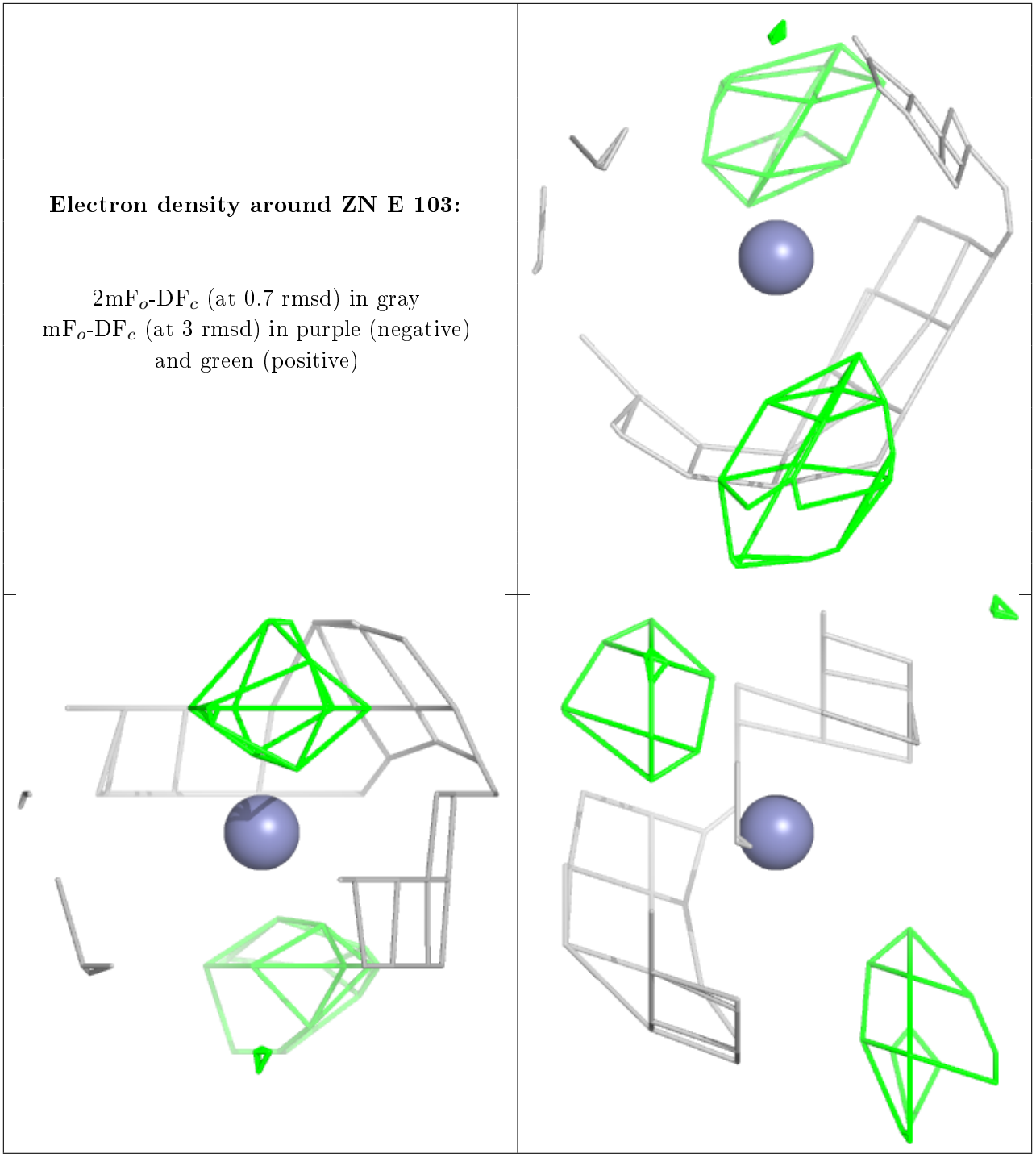






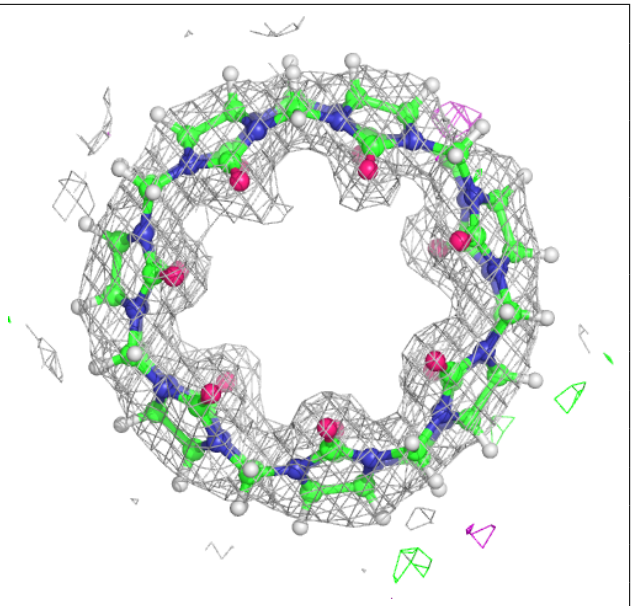
Electron density around ZN E 103:

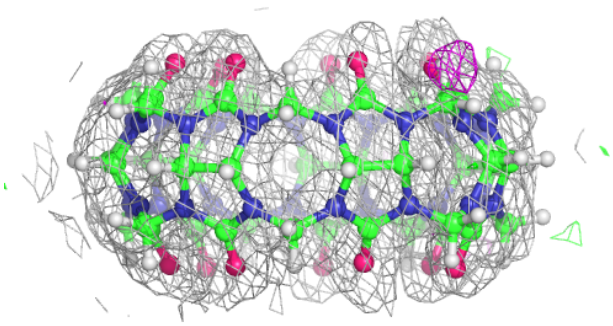
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

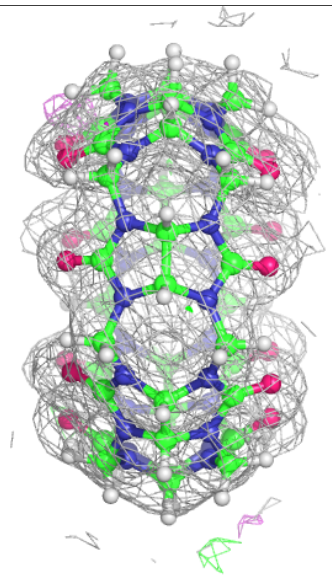


Electron density around QQ7 B 101:

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

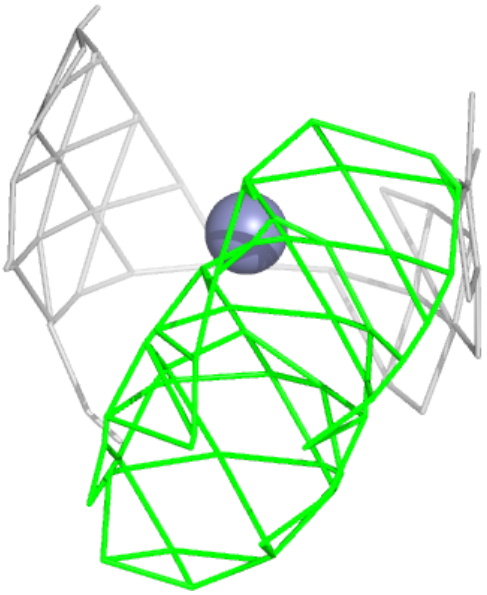


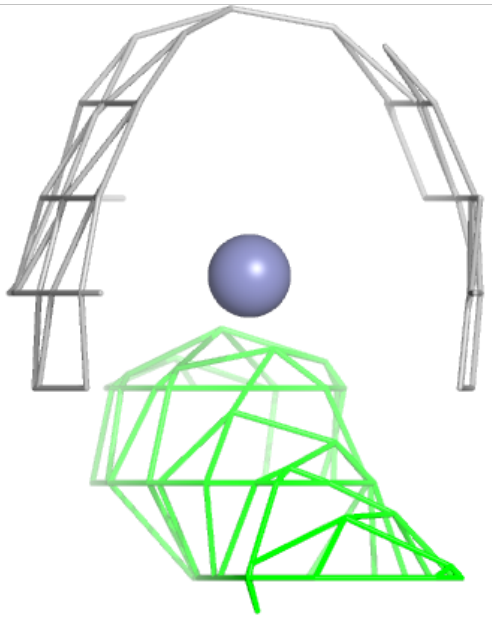


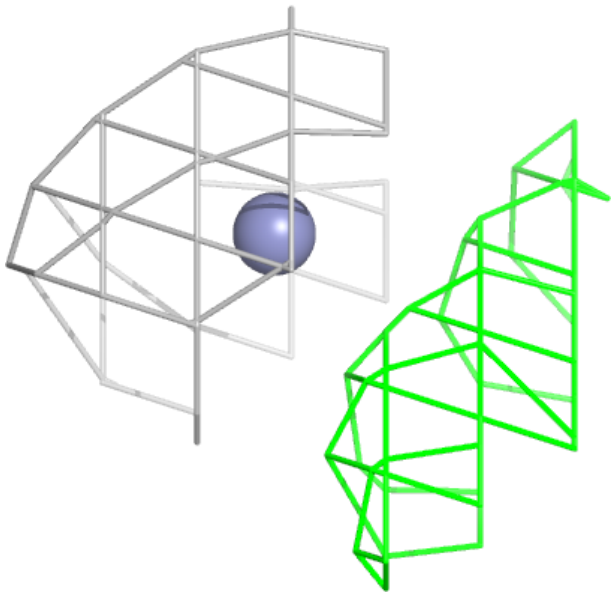


Electron density around ZN C 105:

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

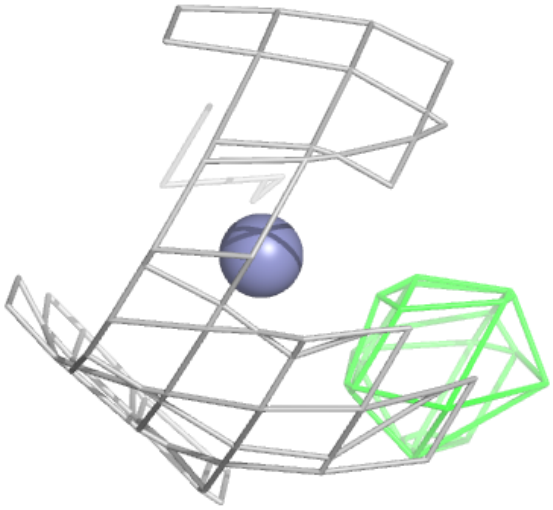


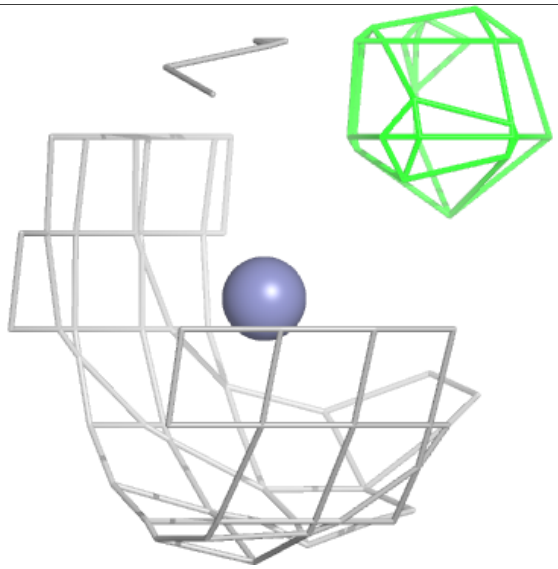


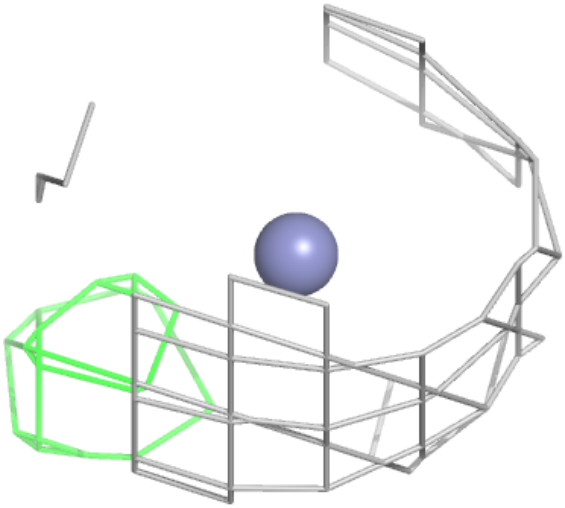


Electron density around ZN B 104:

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

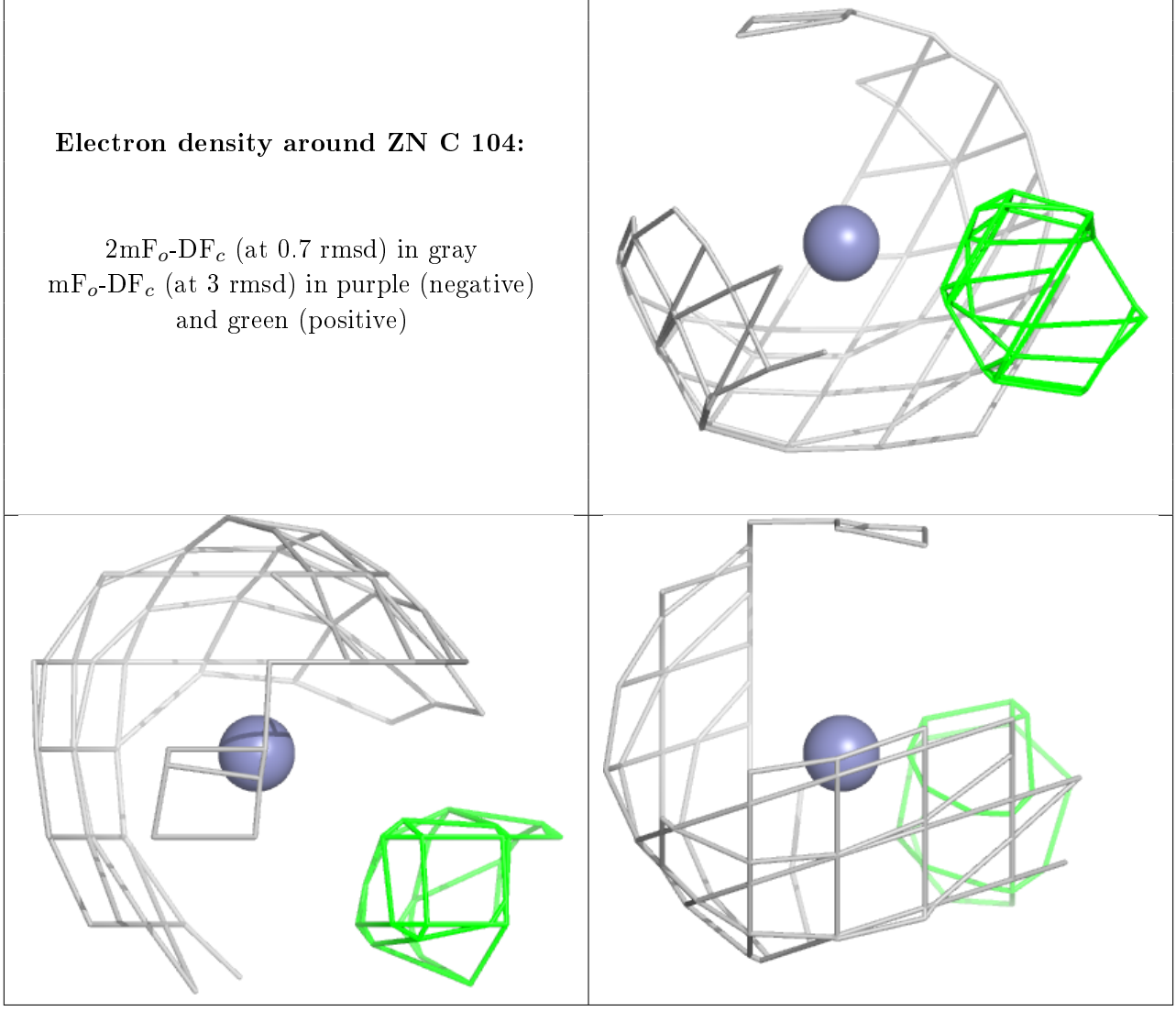






Electron density around ZN C 104:

$2mF_o$-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

There are no such residues in this entry.