



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:50 AM UTC

PDB ID : 6S99 / pdb_00006s99
Title : Dimethylated fusion protein of RSL and trimeric coiled coil in complex with cucurbit[7]uril
Authors : Ramberg, K.; Engilberge, S.; Crowley, P.B.
Deposited on : 2019-07-11
Resolution : 2.65 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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

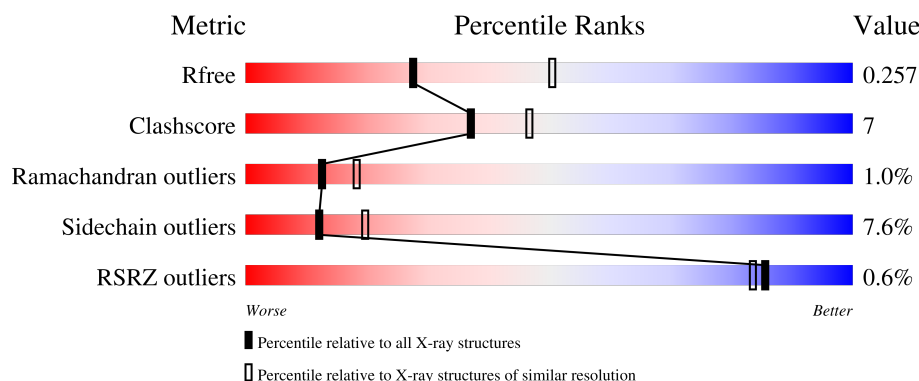
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	2053 (2.66-2.62)
Clashscore	190562	2097 (2.66-2.62)
Ramachandran outliers	187476	2066 (2.66-2.62)
Sidechain outliers	187428	2066 (2.66-2.62)
RSRZ outliers	180081	2052 (2.66-2.62)

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	114	% 83% 15% ..
1	B	114	% 79% 18% ...
1	C	114	81% 18% .
1	D	114	% 84% 13% ..
1	E	114	% 85% 14% .

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Mol	Chain	Length	Quality of chain
1	F	114	

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	QQ7	A	403	X	-	-	-
3	QQ7	B	403	X	-	-	-
3	QQ7	C	403	X	-	-	-
3	QQ7	D	403	X	-	-	-
3	QQ7	E	403	X	-	-	-
3	QQ7	F	403	X	-	-	-

2 Entry composition [i](#)

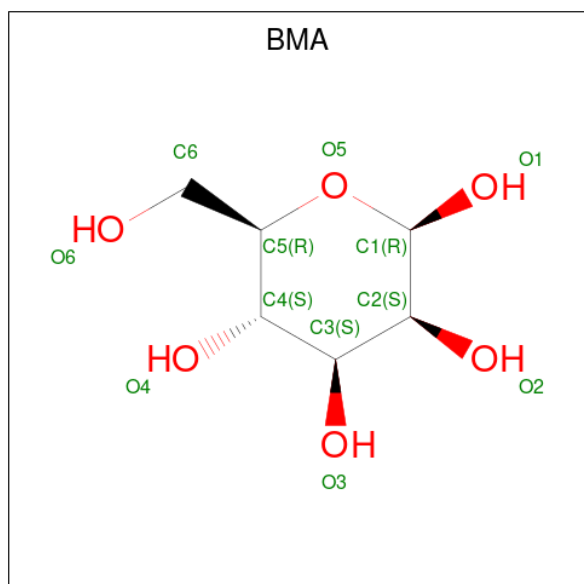
There are 4 unique types of molecules in this entry. The entry contains 5590 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein.

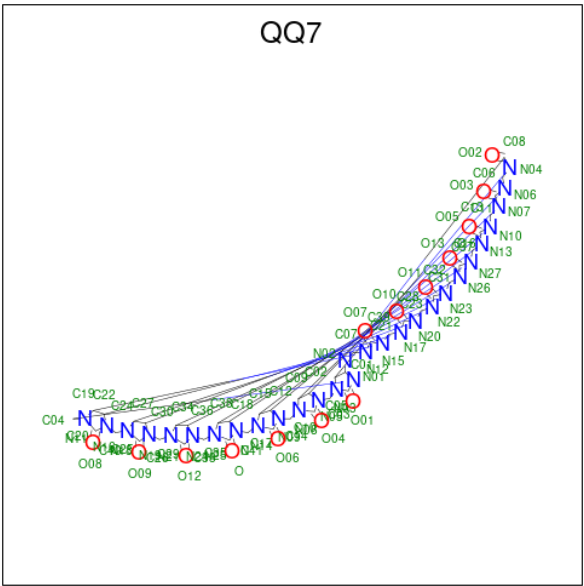
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			
1	B	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			
1	C	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			
1	D	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			
1	E	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			
1	F	113	Total	C	N	O	S	0	0	0
			805	506	140	157	2			

- Molecule 2 is beta-D-mannopyranose (CCD ID: BMA) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			12	6	6		
2	A	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	B	1	Total	C	O	0	0
			12	6	6		
2	C	1	Total	C	O	0	0
			12	6	6		
2	C	1	Total	C	O	0	0
			12	6	6		
2	D	1	Total	C	O	0	0
			12	6	6		
2	D	1	Total	C	O	0	0
			12	6	6		
2	E	1	Total	C	O	0	0
			12	6	6		
2	E	1	Total	C	O	0	0
			12	6	6		
2	F	1	Total	C	O	0	0
			12	6	6		
2	F	1	Total	C	O	0	0
			12	6	6		

- Molecule 3 is cucurbit[7]uril (CCD ID: QQ7) (formula: C₄₂H₄₂N₂₈O₁₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			84	42	28	14		
3	B	1	Total	C	N	O	0	0
			84	42	28	14		
3	C	1	Total	C	N	O	0	0
			84	42	28	14		
3	D	1	Total	C	N	O	0	0
			84	42	28	14		
3	E	1	Total	C	N	O	0	0
			84	42	28	14		
3	F	1	Total	C	N	O	0	0
			84	42	28	14		

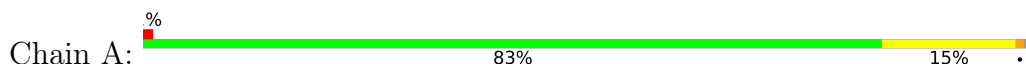
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	18	Total	O	0	0
			18	18		
4	B	21	Total	O	0	0
			21	21		
4	C	21	Total	O	0	0
			21	21		
4	D	12	Total	O	0	0
			12	12		
4	E	18	Total	O	0	0
			18	18		
4	F	22	Total	O	0	0
			22	22		

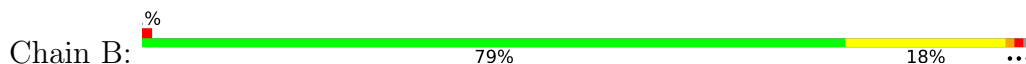
3 Residue-property plots

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.

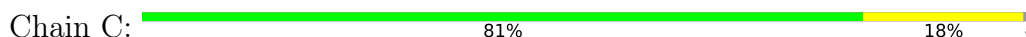
- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein



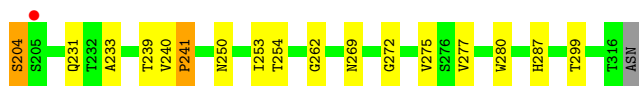
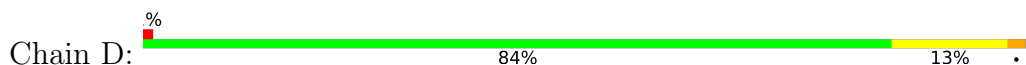
- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein



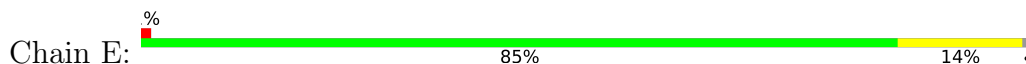
- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein



- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein



- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein



- Molecule 1: 4dzn-RSL,Fucose-binding lectin protein,Fucose-binding lectin protein

Chain F:

81%

18%

..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.22Å 51.24Å 111.28Å 76.80° 89.88° 60.05°	Depositor
Resolution (Å)	42.84 – 2.65 42.84 – 2.65	Depositor EDS
% Data completeness (in resolution range)	97.3 (42.84-2.65) 96.0 (42.84-2.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.225 , 0.257 0.227 , 0.257	Depositor DCC
R_{free} test set	1410 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.678	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.427 for -h+k,-h,-k+l 0.427 for -k,h-k,h-k+l 0.368 for h,h-k,-l 0.368 for -h+k,k,k-l 0.359 for -k,-h,-h+k-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	5590	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.70% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: QQ7, SNM, BMA, 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	1.02	0/766	0.99	0/1059
1	B	1.01	0/766	1.00	0/1059
1	C	1.02	0/766	0.99	0/1059
1	D	1.01	0/766	0.98	0/1059
1	E	1.02	0/766	1.00	0/1059
1	F	1.02	0/766	0.99	0/1059
All	All	1.02	0/4596	0.99	0/6354

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
1	F	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	204	SNM	Mainchain
1	D	204	SNM	Mainchain
1	F	204	SNM	Mainchain

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	805	0	704	12	0
1	B	805	0	702	16	0
1	C	805	0	703	12	0
1	D	805	0	702	10	0
1	E	805	0	703	11	0
1	F	805	0	702	13	0
2	A	24	0	24	0	0
2	B	24	0	24	0	0
2	C	24	0	24	0	0
2	D	24	0	24	0	0
2	E	24	0	24	0	0
2	F	24	0	24	0	0
3	A	84	0	42	0	0
3	B	84	0	42	2	0
3	C	84	0	42	2	0
3	D	84	0	42	1	0
3	E	84	0	42	0	0
3	F	84	0	42	0	0
4	A	18	0	0	0	0
4	B	21	0	0	0	0
4	C	21	0	0	0	0
4	D	12	0	0	0	0
4	E	18	0	0	0	0
4	F	22	0	0	0	0
All	All	5590	0	4612	72	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 7.

The worst 5 of 72 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:E:240:VAL:N	1:E:241:PRO:HA	2.05	0.72
1:B:240:VAL:N	1:B:241:PRO:HA	2.05	0.70
1:D:240:VAL:N	1:D:241:PRO:HA	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:VAL:N	1:C:241:PRO:HA	2.08	0.69
1:A:240:VAL:N	1:A:241:PRO:HA	2.08	0.68

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	104/114 (91%)	96 (92%)	7 (7%)	1 (1%)	12	18
1	B	104/114 (91%)	96 (92%)	7 (7%)	1 (1%)	12	18
1	C	104/114 (91%)	95 (91%)	7 (7%)	2 (2%)	6	8
1	D	104/114 (91%)	97 (93%)	6 (6%)	1 (1%)	12	18
1	E	104/114 (91%)	97 (93%)	7 (7%)	0	100	100
1	F	104/114 (91%)	93 (89%)	10 (10%)	1 (1%)	12	18
All	All	624/684 (91%)	574 (92%)	44 (7%)	6 (1%)	12	18

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	220	GLU
1	F	217	LEU
1	B	230	VAL
1	C	295	GLY
1	D	241	PRO

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	66/78 (85%)	61 (92%)	5 (8%)	12	20
1	B	66/78 (85%)	60 (91%)	6 (9%)	9	13
1	C	66/78 (85%)	62 (94%)	4 (6%)	17	29
1	D	66/78 (85%)	61 (92%)	5 (8%)	12	20
1	E	66/78 (85%)	61 (92%)	5 (8%)	12	20
1	F	66/78 (85%)	61 (92%)	5 (8%)	12	20
All	All	396/468 (85%)	366 (92%)	30 (8%)	12	20

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	299	THR
1	F	254	THR
1	D	254	THR
1	F	299	THR
1	E	299	THR

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	D	269	ASN
1	D	274	ASN
1	F	274	ASN
1	F	269	ASN
1	C	269	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

48 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	C	252	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	C	219	1	3,4,11	0.87	0	2,4,13	1.32	0
1	MLY	B	252	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	C	225	1	3,4,11	0.85	0	2,4,13	1.32	0
1	MLY	B	225	1	3,4,11	0.87	0	2,4,13	1.38	0
1	MLY	E	310	1	9,10,11	0.51	0	6,11,13	0.06	0
1	SNM	E	204	1	5,6,8	1.41	0	3,7,10	0.30	0
1	MLY	A	218	1	3,4,11	0.86	0	2,4,13	1.37	0
1	MLY	E	261	1	9,10,11	0.51	0	6,11,13	0.07	0
1	SNM	D	204	1	5,6,8	1.41	0	3,7,10	0.29	0
1	MLY	D	211	1	3,4,11	0.85	0	2,4,13	1.32	0
1	MLY	E	252	1	9,10,11	0.51	0	6,11,13	0.07	0
1	MLY	D	261	1	9,10,11	0.52	0	6,11,13	0.06	0
1	MLY	F	310	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	E	218	1	3,4,11	0.86	0	2,4,13	1.32	0
1	MLY	E	219	1	3,4,11	0.85	0	2,4,13	1.34	0
1	MLY	D	252	1	9,10,11	0.52	0	6,11,13	0.06	0
1	MLY	F	211	1	3,4,11	0.85	0	2,4,13	1.36	0
1	MLY	A	261	1	9,10,11	0.52	0	6,11,13	0.07	0
1	SNM	A	204	1	5,6,8	1.40	0	3,7,10	0.30	0
1	MLY	F	225	1	3,4,11	0.85	0	2,4,13	1.40	0
1	MLY	D	219	1	3,4,11	0.85	0	2,4,13	1.38	0
1	MLY	F	218	1	3,4,11	0.84	0	2,4,13	1.39	0
1	SNM	C	204	1	5,6,8	1.39	0	3,7,10	0.30	0
1	MLY	A	219	1	3,4,11	0.84	0	2,4,13	1.31	0
1	MLY	B	310	1	9,10,11	0.52	0	6,11,13	0.06	0
1	MLY	C	211	1	3,4,11	0.85	0	2,4,13	1.31	0
1	MLY	C	261	1	9,10,11	0.51	0	6,11,13	0.07	0
1	MLY	D	218	1	3,4,11	0.85	0	2,4,13	1.32	0
1	MLY	A	252	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	F	252	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	C	218	1	3,4,11	0.85	0	2,4,13	1.36	0
1	MLY	F	261	1	9,10,11	0.52	0	6,11,13	0.07	0
1	MLY	D	310	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	A	225	1	3,4,11	0.86	0	2,4,13	1.35	0
1	SNM	F	204	1	5,6,8	1.41	0	3,7,10	0.30	0
1	MLY	F	219	1	3,4,11	0.85	0	2,4,13	1.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	A	310	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	E	211	1	3,4,11	0.85	0	2,4,13	1.33	0
1	MLY	B	211	1	3,4,11	0.86	0	2,4,13	1.32	0
1	MLY	D	225	1	3,4,11	0.86	0	2,4,13	1.40	0
1	MLY	B	261	1	9,10,11	0.51	0	6,11,13	0.06	0
1	MLY	E	225	1	3,4,11	0.86	0	2,4,13	1.36	0
1	MLY	C	310	1	9,10,11	0.51	0	6,11,13	0.07	0
1	SNM	B	204	1	5,6,8	1.41	0	3,7,10	0.30	0
1	MLY	A	211	1	3,4,11	0.85	0	2,4,13	1.32	0
1	MLY	B	219	1	3,4,11	0.85	0	2,4,13	1.33	0
1	MLY	B	218	1	3,4,11	0.86	0	2,4,13	1.36	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	C	252	1	-	1/8/9/11	-
1	MLY	C	219	1	-	0/1/2/11	-
1	MLY	B	252	1	-	1/8/9/11	-
1	MLY	C	225	1	-	0/1/2/11	-
1	MLY	B	225	1	-	1/1/2/11	-
1	MLY	E	310	1	-	5/8/9/11	-
1	SNM	E	204	1	-	1/5/6/10	-
1	MLY	A	218	1	-	0/1/2/11	-
1	MLY	E	261	1	-	4/8/9/11	-
1	SNM	D	204	1	-	1/5/6/10	-
1	MLY	D	211	1	-	1/1/2/11	-
1	MLY	E	252	1	-	4/8/9/11	-
1	MLY	D	261	1	-	3/8/9/11	-
1	MLY	F	310	1	-	6/8/9/11	-
1	MLY	E	218	1	-	0/1/2/11	-
1	MLY	E	219	1	-	0/1/2/11	-
1	MLY	D	252	1	-	1/8/9/11	-
1	MLY	F	211	1	-	1/1/2/11	-
1	MLY	A	261	1	-	4/8/9/11	-
1	SNM	A	204	1	-	0/5/6/10	-
1	MLY	F	225	1	-	0/1/2/11	-
1	MLY	D	219	1	-	1/1/2/11	-
1	MLY	F	218	1	-	0/1/2/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SNM	C	204	1	-	0/5/6/10	-
1	MLY	A	219	1	-	0/1/2/11	-
1	MLY	B	310	1	-	5/8/9/11	-
1	MLY	C	211	1	-	1/1/2/11	-
1	MLY	C	261	1	-	2/8/9/11	-
1	MLY	D	218	1	-	0/1/2/11	-
1	MLY	A	252	1	-	1/8/9/11	-
1	MLY	F	252	1	-	1/8/9/11	-
1	MLY	C	218	1	-	0/1/2/11	-
1	MLY	F	261	1	-	4/8/9/11	-
1	MLY	D	310	1	-	6/8/9/11	-
1	MLY	A	225	1	-	0/1/2/11	-
1	SNM	F	204	1	-	1/5/6/10	-
1	MLY	F	219	1	-	0/1/2/11	-
1	MLY	A	310	1	-	5/8/9/11	-
1	MLY	E	211	1	-	0/1/2/11	-
1	MLY	B	211	1	-	0/1/2/11	-
1	MLY	D	225	1	-	0/1/2/11	-
1	MLY	B	261	1	-	3/8/9/11	-
1	MLY	E	225	1	-	0/1/2/11	-
1	MLY	C	310	1	-	5/8/9/11	-
1	SNM	B	204	1	-	1/5/6/10	-
1	MLY	A	211	1	-	0/1/2/11	-
1	MLY	B	219	1	-	0/1/2/11	-
1	MLY	B	218	1	-	0/1/2/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	310	MLY	N-CA-CB-CG
1	A	310	MLY	C-CA-CB-CG
1	B	310	MLY	N-CA-CB-CG
1	B	310	MLY	C-CA-CB-CG
1	C	310	MLY	N-CA-CB-CG

There are no ring outliers.

9 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	204	SNM	1	0
1	D	204	SNM	1	0
1	E	252	MLY	1	0
1	A	204	SNM	1	0
1	C	204	SNM	1	0
1	C	261	MLY	1	0
1	F	204	SNM	2	0
1	B	261	MLY	1	0
1	B	204	SNM	1	0

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	$\# Z > 2$
2	BMA	D	401	-	12,12,12	0.45	0	17,17,17	0.52	0
2	BMA	E	401	-	12,12,12	0.46	0	17,17,17	0.55	0
3	QQ7	D	403	-	105,105,105	0.11	0	182,182,182	0.21	0
2	BMA	E	402	-	12,12,12	0.46	0	17,17,17	0.50	0
2	BMA	C	401	-	12,12,12	0.45	0	17,17,17	0.53	0
2	BMA	F	402	-	12,12,12	0.45	0	17,17,17	0.49	0
2	BMA	A	401	-	12,12,12	0.45	0	17,17,17	0.53	0
2	BMA	B	402	-	12,12,12	0.45	0	17,17,17	0.51	0
2	BMA	F	401	-	12,12,12	0.46	0	17,17,17	0.53	0
3	QQ7	B	403	-	105,105,105	0.11	0	182,182,182	0.21	0
3	QQ7	C	403	-	105,105,105	0.11	0	182,182,182	0.21	0
3	QQ7	A	403	-	105,105,105	0.11	0	182,182,182	0.21	0
2	BMA	C	402	-	12,12,12	0.46	0	17,17,17	0.50	0
2	BMA	D	402	-	12,12,12	0.46	0	17,17,17	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BMA	B	401	-	12,12,12	0.46	0	17,17,17	0.53	0
3	QQ7	F	403	-	105,105,105	0.11	0	182,182,182	0.22	0
2	BMA	A	402	-	12,12,12	0.45	0	17,17,17	0.50	0
3	QQ7	E	403	-	105,105,105	0.11	0	182,182,182	0.22	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
2	BMA	D	401	-	-	0/2/22/22	0/1/1/1
2	BMA	B	401	-	-	0/2/22/22	0/1/1/1
2	BMA	E	401	-	-	0/2/22/22	0/1/1/1
3	QQ7	D	403	-	14/14/56/56	-	-
2	BMA	E	402	-	-	0/2/22/22	0/1/1/1
2	BMA	C	401	-	-	0/2/22/22	0/1/1/1
2	BMA	A	401	-	-	0/2/22/22	0/1/1/1
3	QQ7	B	403	-	14/14/56/56	-	-
3	QQ7	C	403	-	14/14/56/56	-	-
2	BMA	B	402	-	-	0/2/22/22	0/1/1/1
2	BMA	F	401	-	-	0/2/22/22	0/1/1/1
3	QQ7	A	403	-	14/14/56/56	-	-
2	BMA	C	402	-	-	0/2/22/22	0/1/1/1
2	BMA	D	402	-	-	0/2/22/22	0/1/1/1
2	BMA	A	402	-	-	0/2/22/22	0/1/1/1
3	QQ7	F	403	-	14/14/56/56	-	-
2	BMA	F	402	-	-	0/2/22/22	0/1/1/1
3	QQ7	E	403	-	14/14/56/56	-	-

There are no bond length outliers.

There are no bond angle outliers.

5 of 84 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	403	QQ7	N11
3	A	403	QQ7	N25
3	A	403	QQ7	N09
3	A	403	QQ7	N08
3	A	403	QQ7	N03

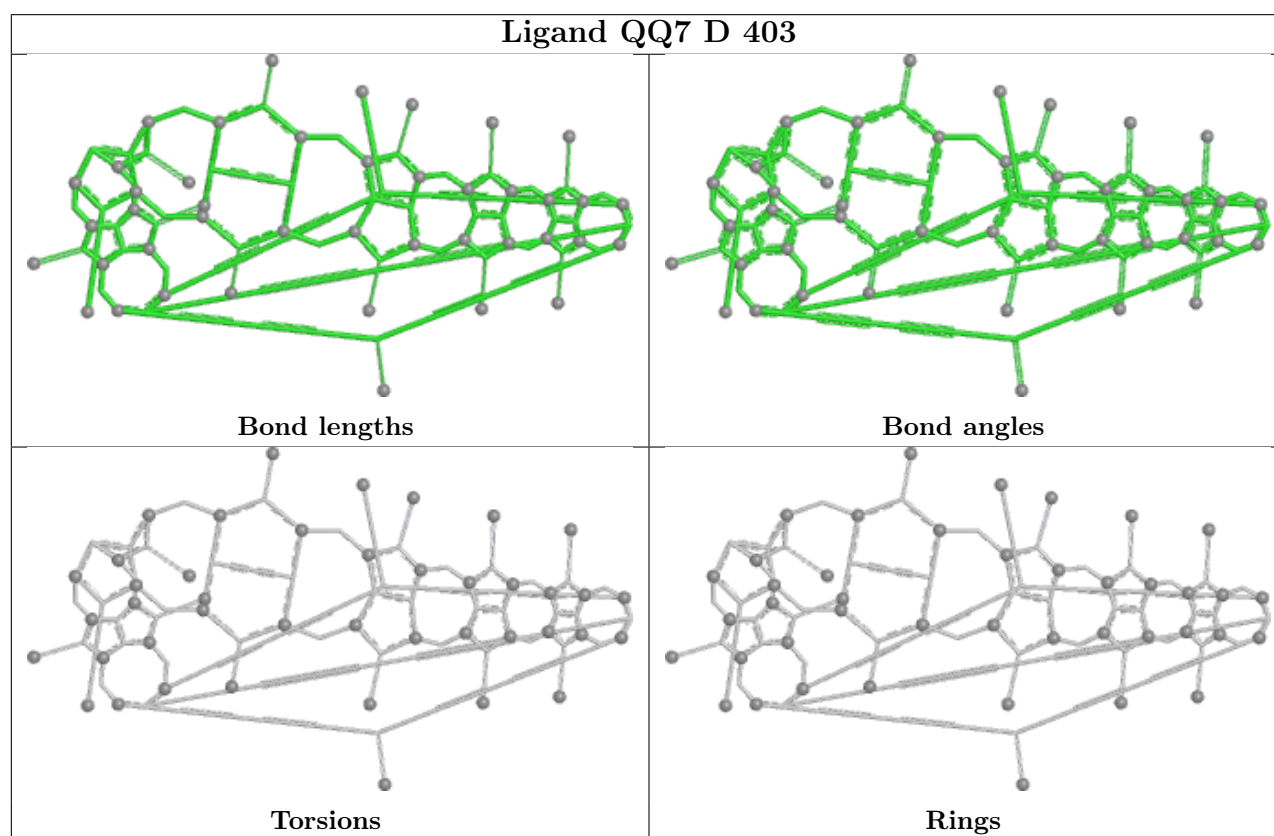
There are no torsion outliers.

There are no ring outliers.

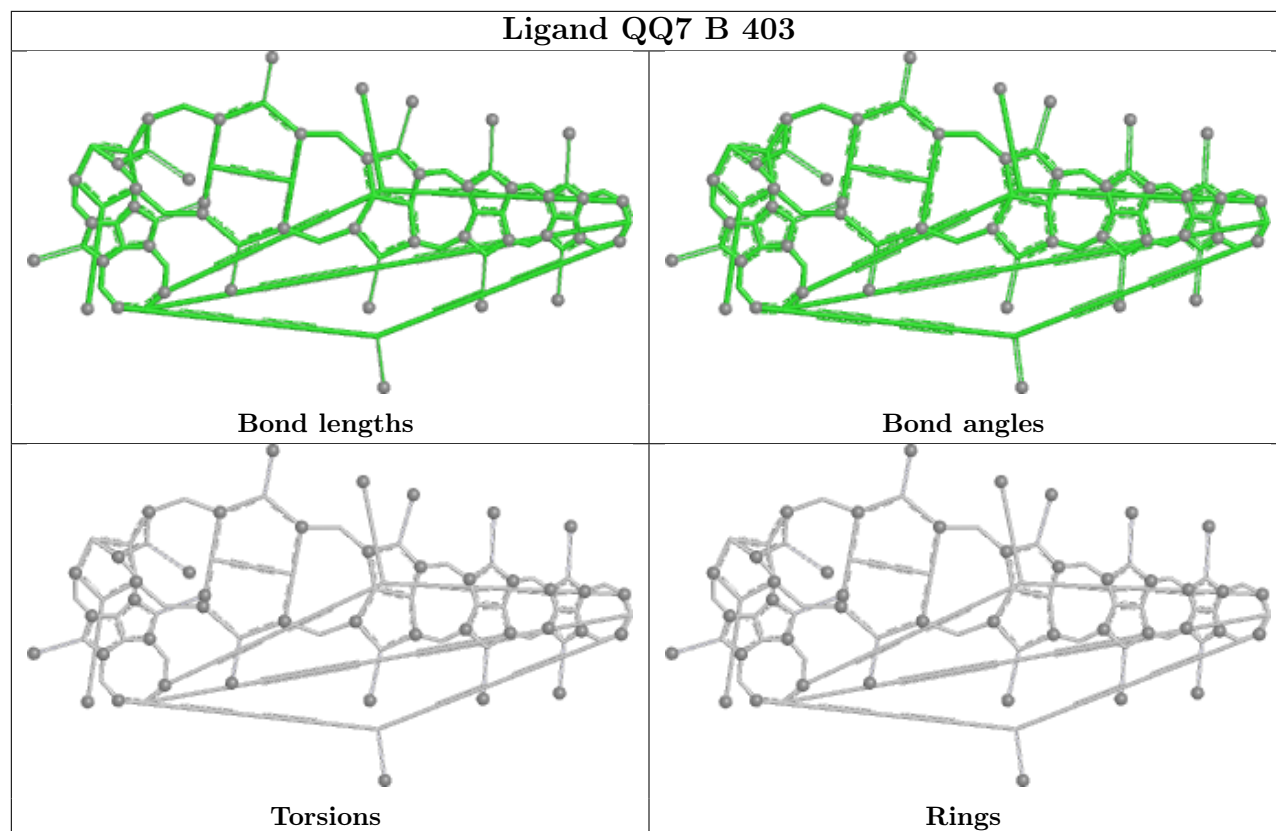
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	403	QQ7	1	0
3	B	403	QQ7	2	0
3	C	403	QQ7	2	0

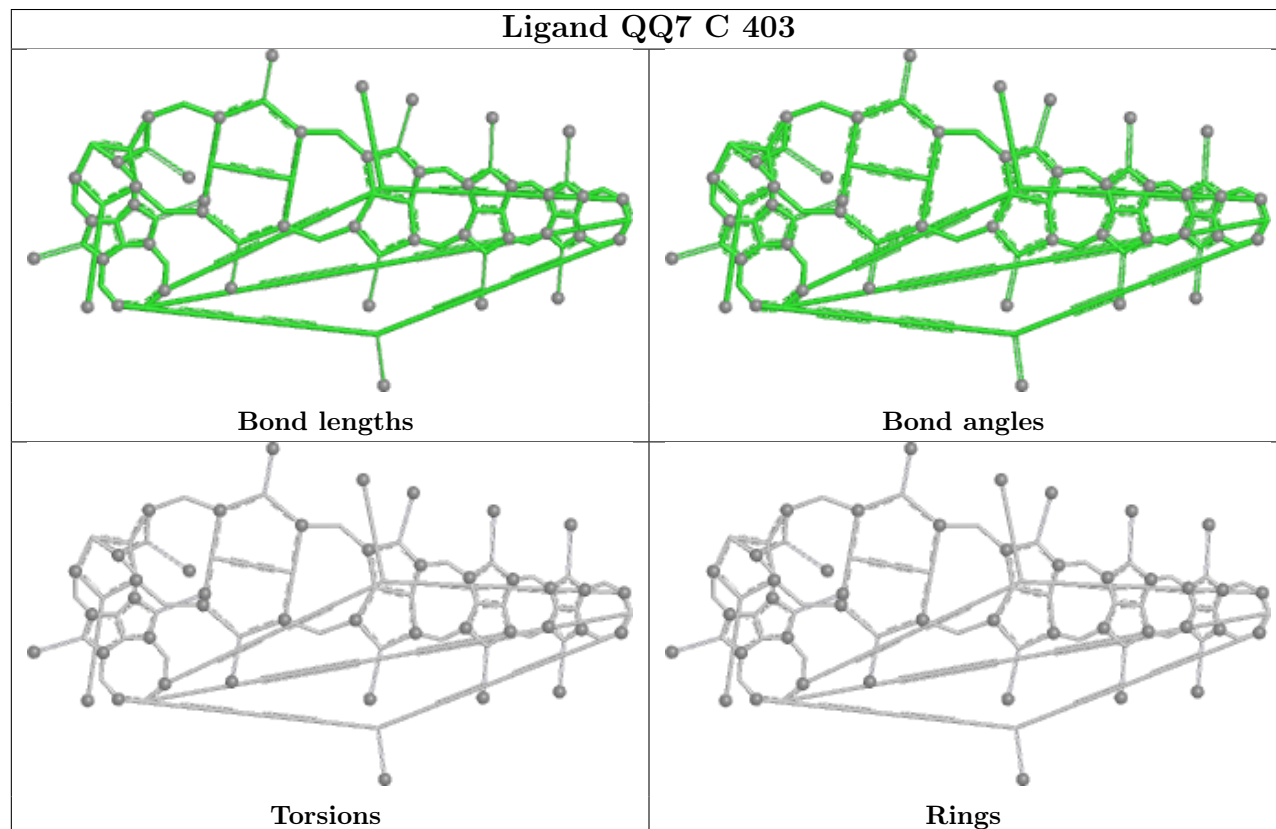
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



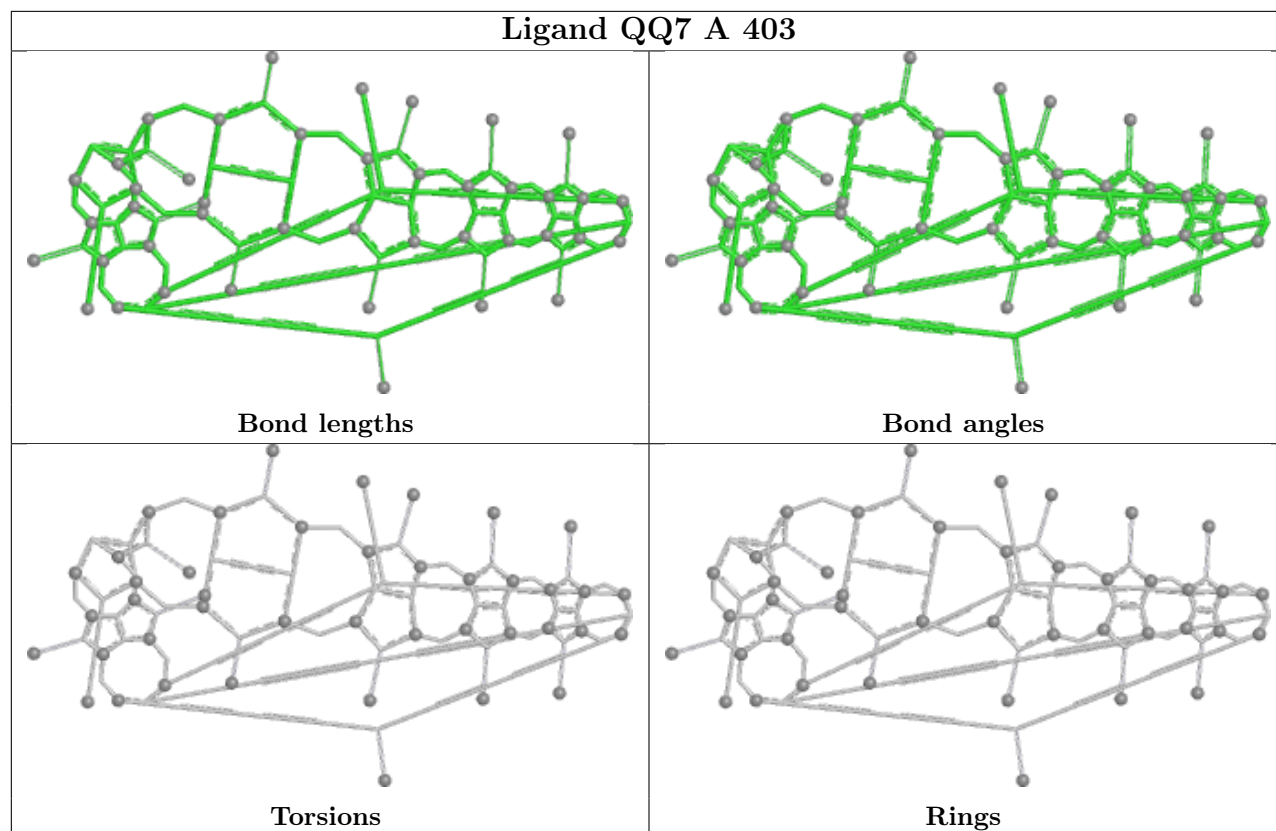
Ligand QQ7 B 403



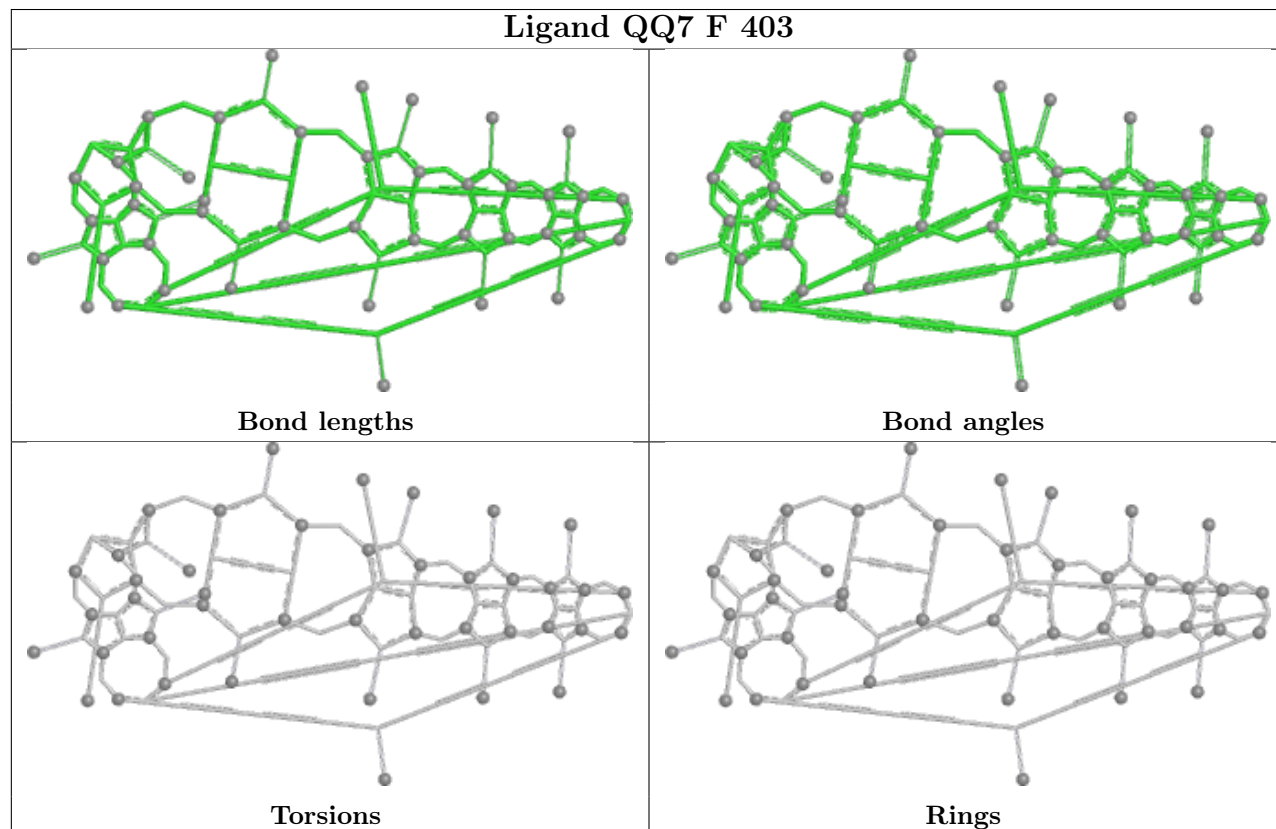
Ligand QQ7 C 403

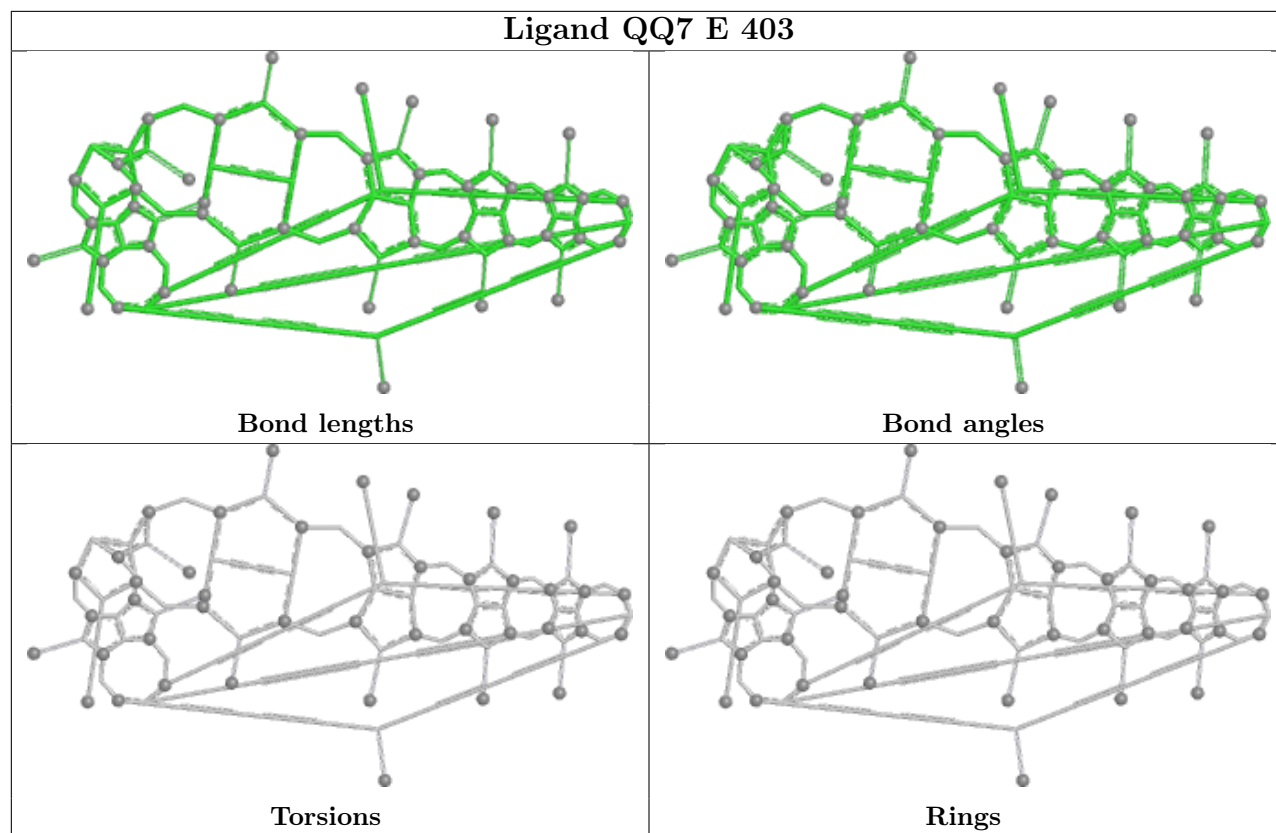


Ligand QQ7 A 403



Ligand QQ7 F 403





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	105/114 (92%)	-1.18	1 (0%) 79 76	35, 65, 344, 556	0
1	B	105/114 (92%)	-1.14	1 (0%) 79 76	39, 65, 331, 423	0
1	C	105/114 (92%)	-1.17	0 100 100	38, 66, 322, 522	0
1	D	105/114 (92%)	-1.06	1 (0%) 79 76	41, 69, 365, 566	0
1	E	105/114 (92%)	-1.12	1 (0%) 79 76	38, 68, 386, 525	0
1	F	105/114 (92%)	-1.14	0 100 100	41, 69, 359, 519	0
All	All	630/684 (92%)	-1.14	4 (0%) 85 83	35, 68, 359, 566	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	205	SER	3.4
1	A	205	SER	3.2
1	E	205	SER	2.5
1	B	205	SER	2.1

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	MLY	D	218	5/12	0.78	0.09	275,278,286,287	0
1	MLY	F	211	5/12	0.90	0.09	197,202,208,213	0
1	MLY	E	218	5/12	0.90	0.09	196,200,203,205	0
1	SNM	C	204	7/9	0.91	0.09	209,212,214,216	0
1	MLY	F	218	5/12	0.91	0.08	213,217,226,226	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	MLY	B	218	5/12	0.93	0.06	229,232,237,240	0
1	MLY	F	219	5/12	0.93	0.08	300,304,313,316	0
1	SNM	A	204	7/9	0.94	0.11	256,259,263,265	0
1	SNM	F	204	7/9	0.94	0.19	276,279,284,284	0
1	MLY	A	211	5/12	0.95	0.04	238,243,245,248	0
1	MLY	B	219	5/12	0.95	0.07	485,488,495,497	0
1	MLY	C	211	5/12	0.95	0.04	199,204,206,210	0
1	MLY	F	225	5/12	0.95	0.06	173,175,180,181	0
1	MLY	A	219	5/12	0.96	0.07	534,537,543,547	0
1	MLY	D	211	5/12	0.96	0.05	175,180,181,185	0
1	MLY	C	219	5/12	0.96	0.07	574,574,583,585	0
1	MLY	E	219	5/12	0.96	0.08	195,199,202,207	0
1	SNM	E	204	7/9	0.96	0.21	364,368,371,374	0
1	MLY	D	225	5/12	0.96	0.07	146,149,154,155	0
1	MLY	E	225	5/12	0.96	0.08	149,151,157,158	0
1	MLY	D	252	11/12	0.96	0.08	109,119,131,135	0
1	MLY	A	218	5/12	0.97	0.05	206,208,215,216	0
1	SNM	B	204	7/9	0.97	0.08	236,239,242,244	0
1	MLY	A	225	5/12	0.97	0.04	145,147,153,154	0
1	MLY	B	225	5/12	0.97	0.06	153,155,161,162	0
1	MLY	F	252	11/12	0.97	0.06	88,100,112,117	0
1	SNM	D	204	7/9	0.97	0.13	222,226,229,231	0
1	MLY	D	219	5/12	0.97	0.07	197,200,209,210	0
1	MLY	C	218	5/12	0.98	0.04	337,340,347,348	0
1	MLY	E	211	5/12	0.98	0.05	185,190,193,198	0
1	MLY	C	225	5/12	0.98	0.06	124,126,130,132	0
1	MLY	B	211	5/12	0.98	0.04	160,165,168,170	0
1	MLY	B	310	11/12	0.98	0.05	74,81,98,100	0
1	MLY	E	252	11/12	0.98	0.05	104,116,128,132	0
1	MLY	C	252	11/12	0.99	0.04	78,90,103,108	0
1	MLY	C	261	11/12	0.99	0.05	59,67,86,90	0
1	MLY	C	310	11/12	0.99	0.04	68,73,92,93	0
1	MLY	A	261	11/12	0.99	0.05	58,66,89,92	0
1	MLY	D	261	11/12	0.99	0.06	67,77,97,98	0
1	MLY	D	310	11/12	0.99	0.05	70,74,90,92	0
1	MLY	A	310	11/12	0.99	0.05	65,71,89,89	0
1	MLY	E	261	11/12	0.99	0.05	66,76,96,98	0
1	MLY	E	310	11/12	0.99	0.06	65,70,88,89	0
1	MLY	B	252	11/12	0.99	0.05	83,94,105,109	0
1	MLY	F	261	11/12	0.99	0.04	71,80,102,102	0
1	MLY	F	310	11/12	0.99	0.07	65,71,88,91	0
1	MLY	B	261	11/12	0.99	0.04	53,63,81,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	MLY	A	252	11/12	0.99	0.06	102,112,126,131	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

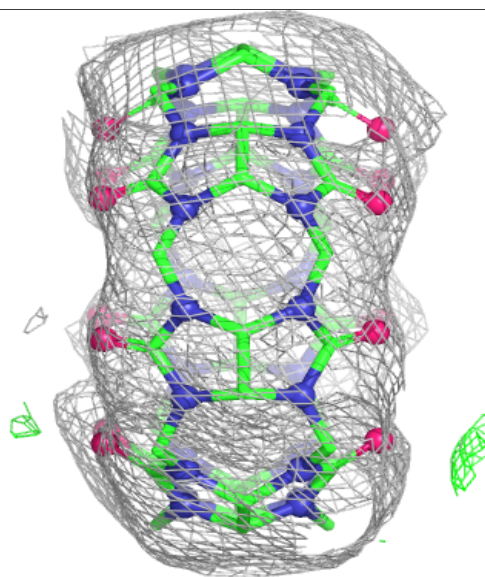
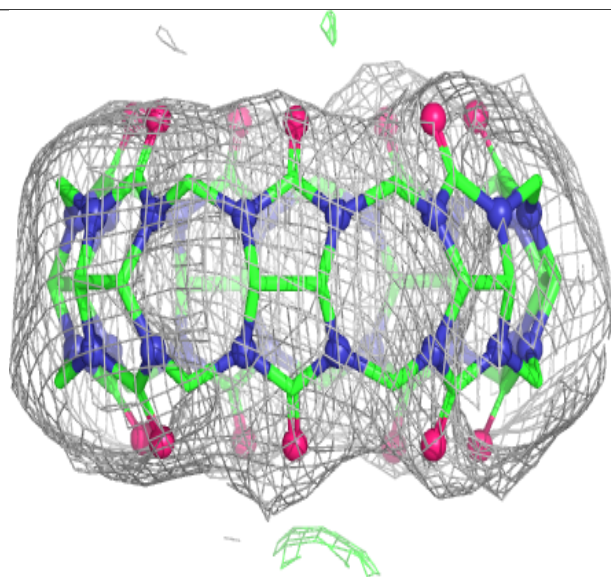
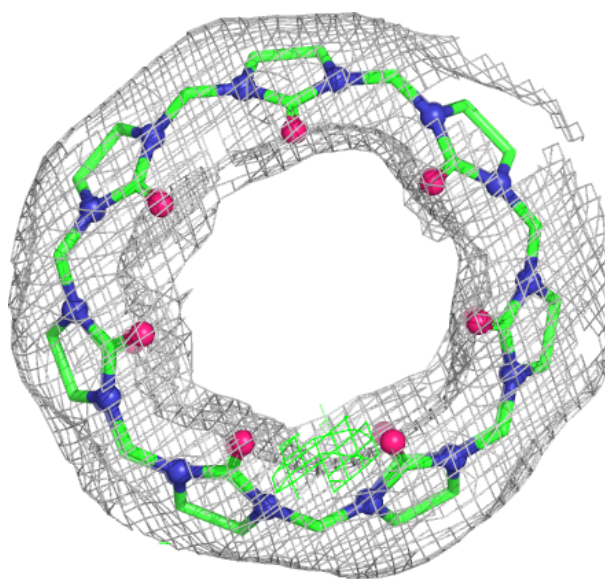
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BMA	A	402	12/12	0.98	0.04	46,58,61,66	0
2	BMA	A	401	12/12	0.99	0.04	59,73,76,77	0
2	BMA	B	401	12/12	0.99	0.05	69,77,82,84	0
2	BMA	B	402	12/12	0.99	0.04	49,56,58,63	0
2	BMA	C	401	12/12	0.99	0.04	58,67,70,71	0
2	BMA	C	402	12/12	0.99	0.04	54,60,63,69	0
2	BMA	D	401	12/12	0.99	0.04	59,69,70,71	0
2	BMA	D	402	12/12	0.99	0.03	47,58,61,68	0
2	BMA	E	401	12/12	0.99	0.05	58,71,74,79	0
2	BMA	E	402	12/12	0.99	0.04	49,60,65,71	0
2	BMA	F	401	12/12	0.99	0.04	61,73,77,82	0
2	BMA	F	402	12/12	0.99	0.04	50,61,64,69	0
3	QQ7	A	403	84/84	0.99	0.03	60,79,90,94	0
3	QQ7	B	403	84/84	0.99	0.04	61,75,85,89	0
3	QQ7	C	403	84/84	0.99	0.03	56,74,87,91	0
3	QQ7	D	403	84/84	0.99	0.03	64,80,87,91	0
3	QQ7	E	403	84/84	0.99	0.03	60,77,87,90	0
3	QQ7	F	403	84/84	0.99	0.03	64,83,91,95	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.

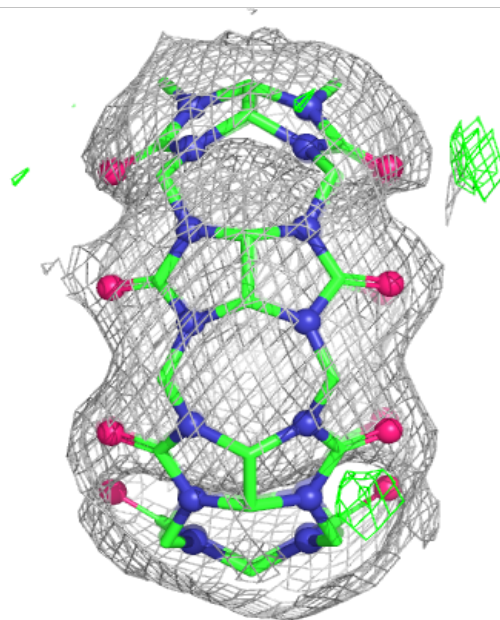
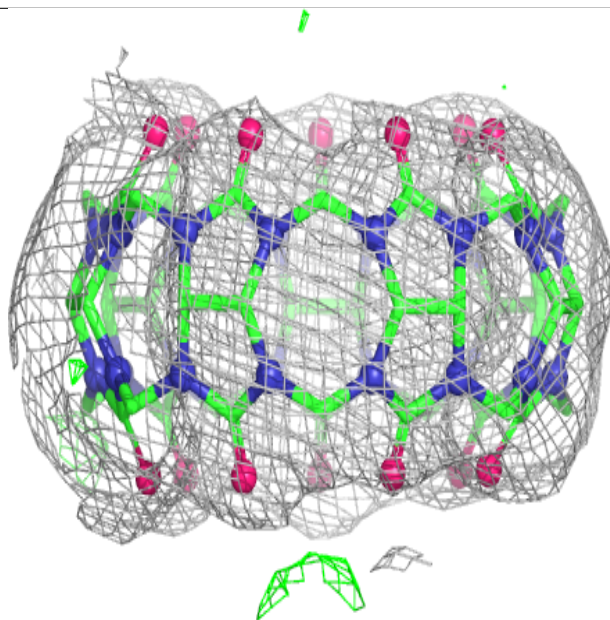
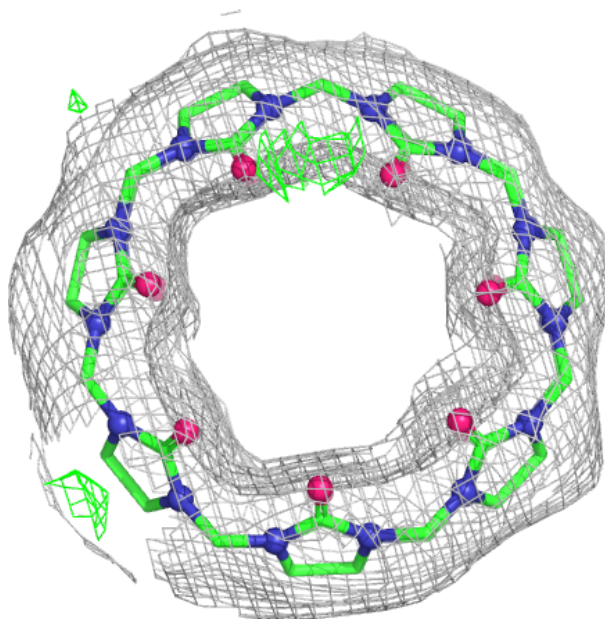
Electron density around QQ7 A 403:

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



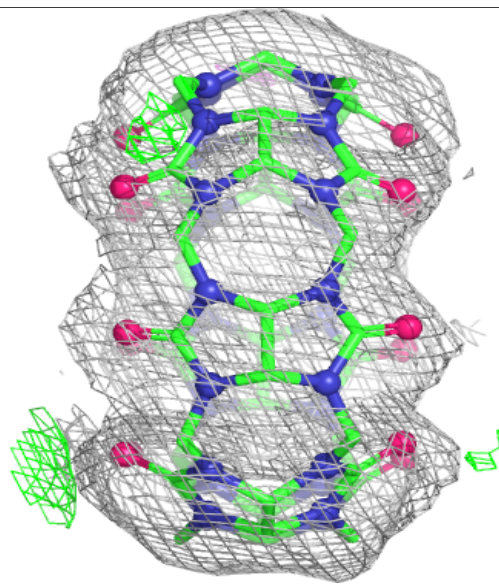
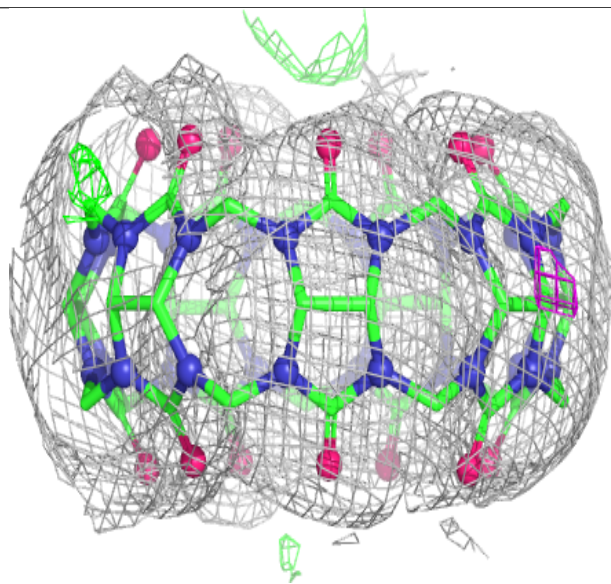
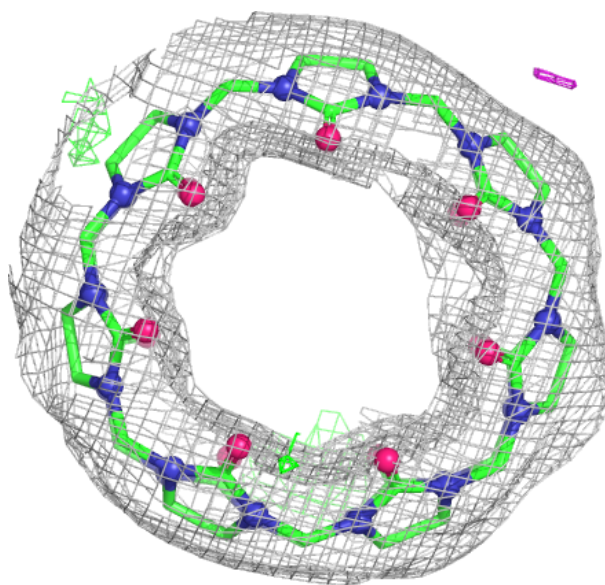
Electron density around QQ7 B 403:

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



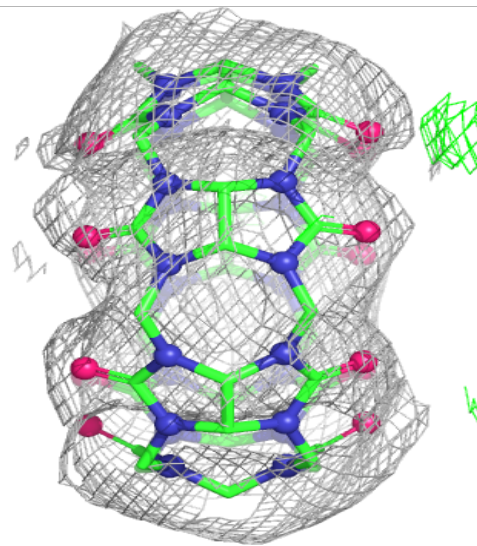
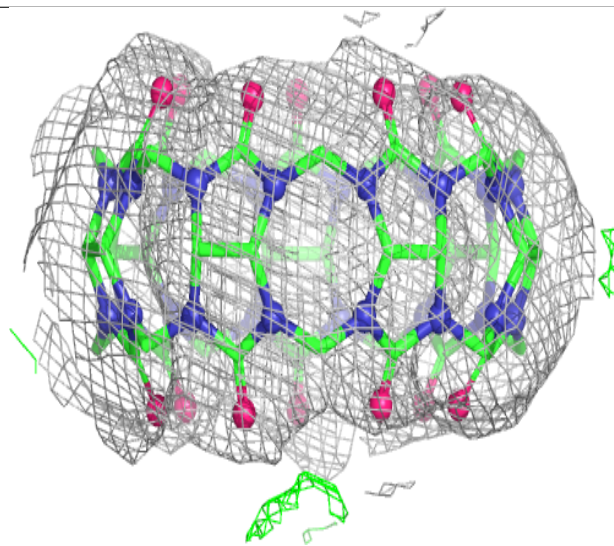
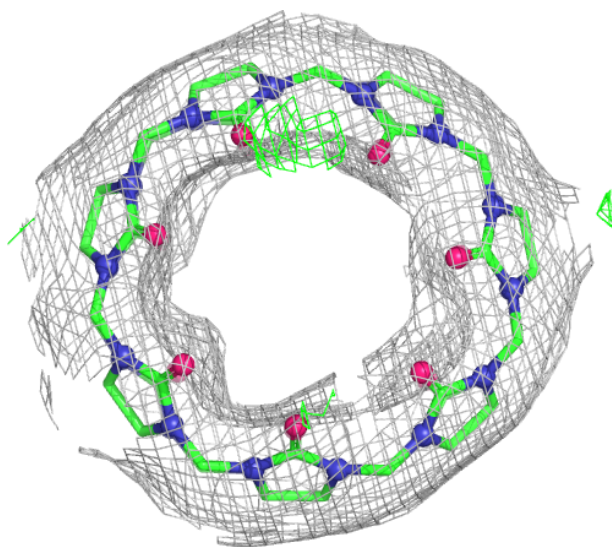
Electron density around QQ7 C 403:

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



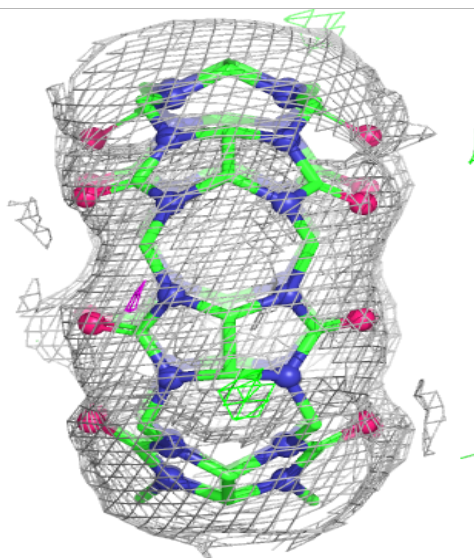
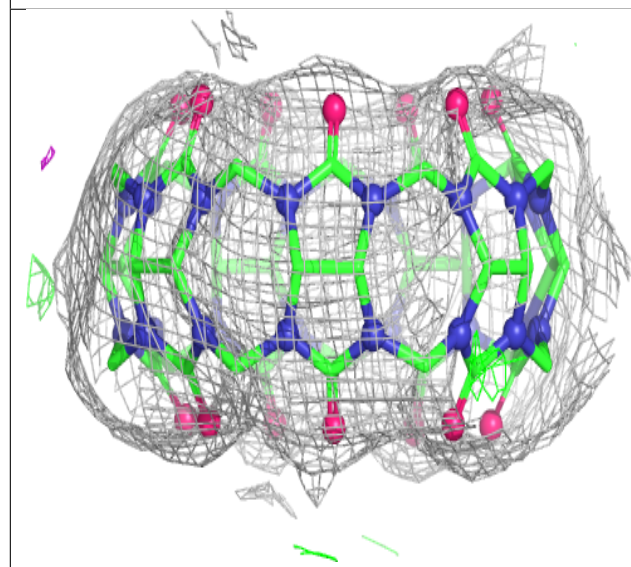
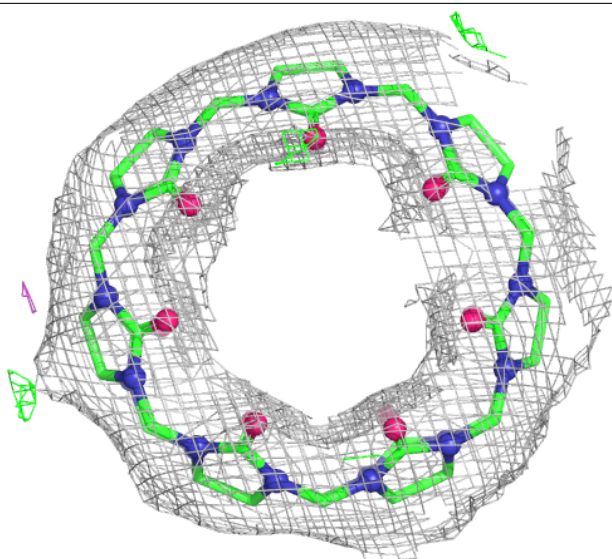
Electron density around QQ7 D 403:

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



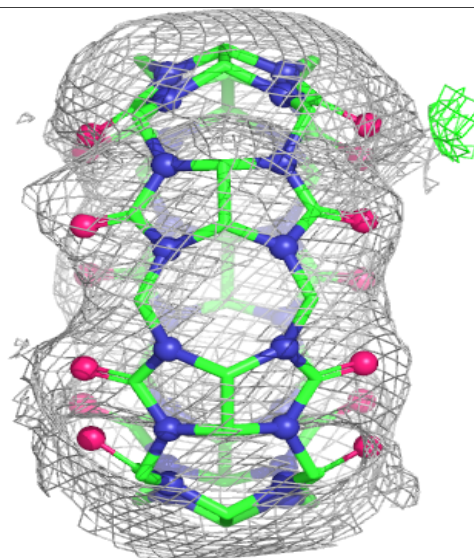
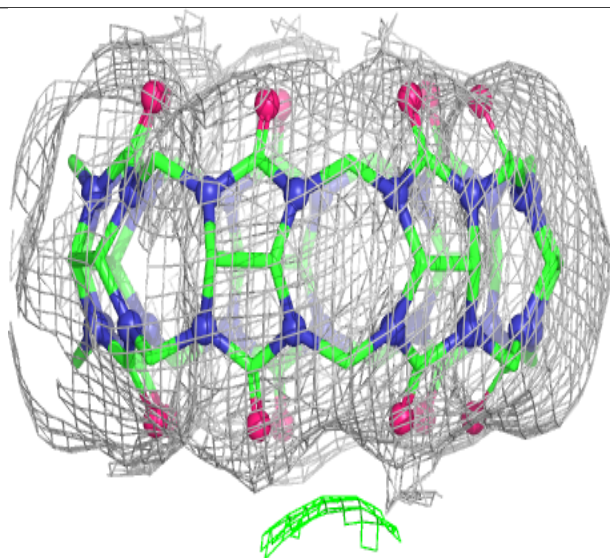
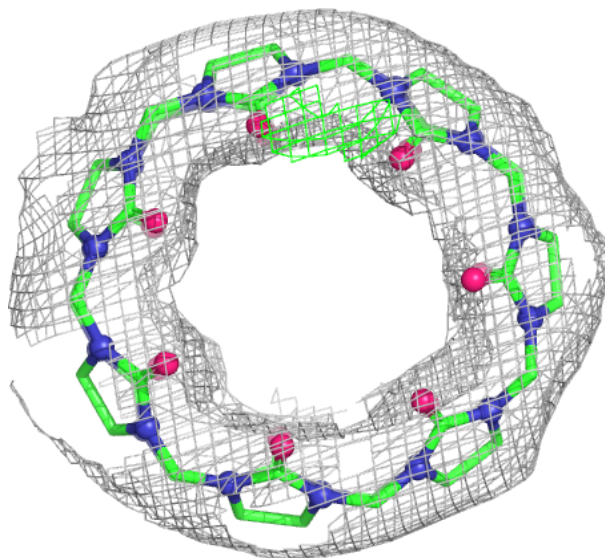
Electron density around QQ7 E 403:

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



Electron density around QQ7 F 403:

$2mF_o-DF_c$ (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.