



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:15 PM UTC

PDB ID : 6U9W / pdb_00006u9w
EMDB ID : EMD-20703
Title : Cryo electron microscopy structure of the ATP-gated rat P2X7 ion channel in the ATP-bound, open state
Authors : Mansoor, S.E.; McCarthy, A.E.
Deposited on : 2019-09-09
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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/EMValidationReportHelp>
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:

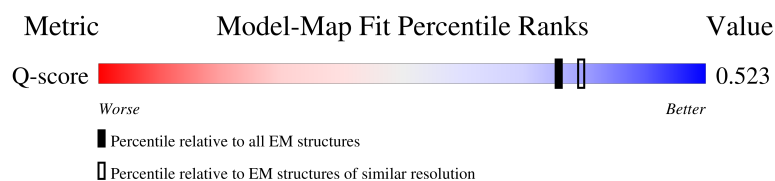
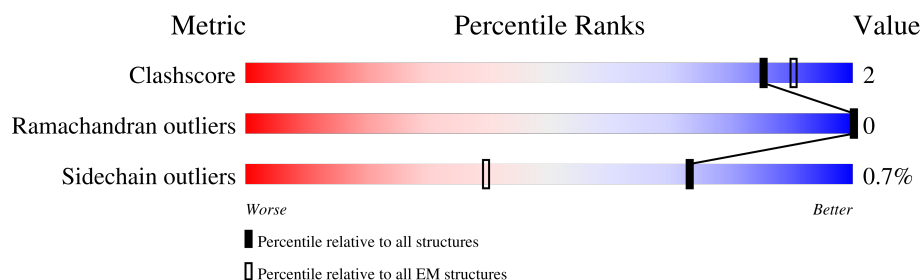
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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:
ELECTRON MICROSCOPY

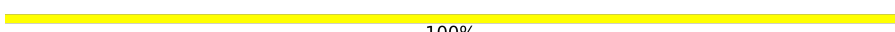
The reported resolution of this entry is 3.30 Å.

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.



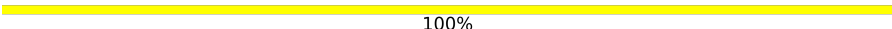
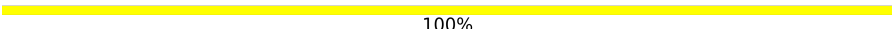
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	609	 88% 8%
1	B	609	 87% 5% 8%
1	C	609	 87% 5% 8%
2	D	2	 100%

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Mol	Chain	Length	Quality of chain
2	E	2	 50% 50%
2	F	2	 100%
2	G	2	 50% 50%
2	H	2	 100%
2	I	2	 50% 50%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 27434 atoms, of which 13400 are hydrogens and 0 are deuteriums.

In the tables below, 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 P2X purinoceptor 7.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	562	Total	C	H	N	O	S	0	0
			8738	2853	4295	761	793	36		
1	B	562	Total	C	H	N	O	S	0	0
			8738	2853	4295	761	793	36		
1	C	562	Total	C	H	N	O	S	0	0
			8738	2853	4295	761	793	36		

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	596	SER	-	expression tag	UNP Q64663
A	597	ASN	-	expression tag	UNP Q64663
A	598	SER	-	expression tag	UNP Q64663
A	599	ALA	-	expression tag	UNP Q64663
A	600	VAL	-	expression tag	UNP Q64663
A	601	ASP	-	expression tag	UNP Q64663
A	602	ALA	-	expression tag	UNP Q64663
A	603	GLY	-	expression tag	UNP Q64663
A	604	LEU	-	expression tag	UNP Q64663
A	605	GLU	-	expression tag	UNP Q64663
A	606	VAL	-	expression tag	UNP Q64663
A	607	LEU	-	expression tag	UNP Q64663
A	608	PHE	-	expression tag	UNP Q64663
A	609	GLN	-	expression tag	UNP Q64663
B	596	SER	-	expression tag	UNP Q64663
B	597	ASN	-	expression tag	UNP Q64663
B	598	SER	-	expression tag	UNP Q64663
B	599	ALA	-	expression tag	UNP Q64663
B	600	VAL	-	expression tag	UNP Q64663
B	601	ASP	-	expression tag	UNP Q64663
B	602	ALA	-	expression tag	UNP Q64663
B	603	GLY	-	expression tag	UNP Q64663
B	604	LEU	-	expression tag	UNP Q64663
B	605	GLU	-	expression tag	UNP Q64663

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Chain	Residue	Modelled	Actual	Comment	Reference
B	606	VAL	-	expression tag	UNP Q64663
B	607	LEU	-	expression tag	UNP Q64663
B	608	PHE	-	expression tag	UNP Q64663
B	609	GLN	-	expression tag	UNP Q64663
C	596	SER	-	expression tag	UNP Q64663
C	597	ASN	-	expression tag	UNP Q64663
C	598	SER	-	expression tag	UNP Q64663
C	599	ALA	-	expression tag	UNP Q64663
C	600	VAL	-	expression tag	UNP Q64663
C	601	ASP	-	expression tag	UNP Q64663
C	602	ALA	-	expression tag	UNP Q64663
C	603	GLY	-	expression tag	UNP Q64663
C	604	LEU	-	expression tag	UNP Q64663
C	605	GLU	-	expression tag	UNP Q64663
C	606	VAL	-	expression tag	UNP Q64663
C	607	LEU	-	expression tag	UNP Q64663
C	608	PHE	-	expression tag	UNP Q64663
C	609	GLN	-	expression tag	UNP Q64663

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

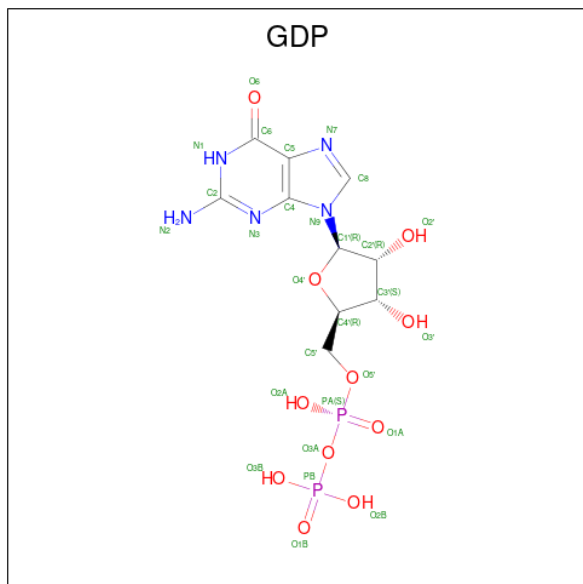


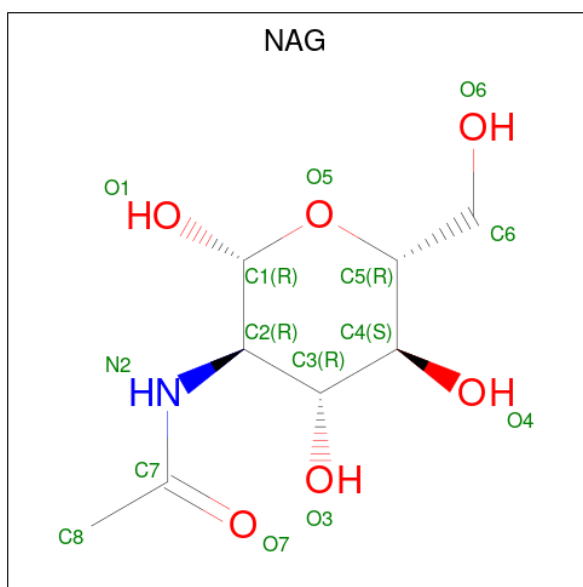
Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	2	Total 53	C 16	H 25	N 2	O 10	0	0
2	E	2	Total 53	C 16	H 25	N 2	O 10	0	0
2	F	2	Total 53	C 16	H 25	N 2	O 10	0	0
2	G	2	Total 53	C 16	H 25	N 2	O 10	0	0
2	H	2	Total 53	C 16	H 25	N 2	O 10	0	0
2	I	2	Total 53	C 16	H 25	N 2	O 10	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	2	Total	Zn	0
			2	2	
3	B	2	Total	Zn	0
			2	2	
3	C	2	Total	Zn	0
			2	2	

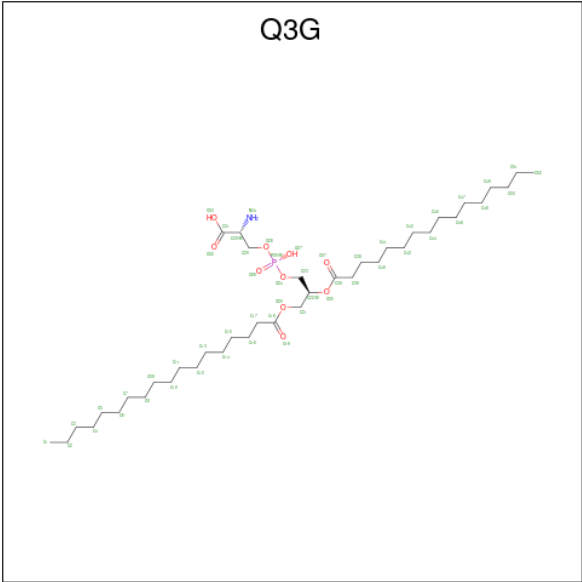
- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).





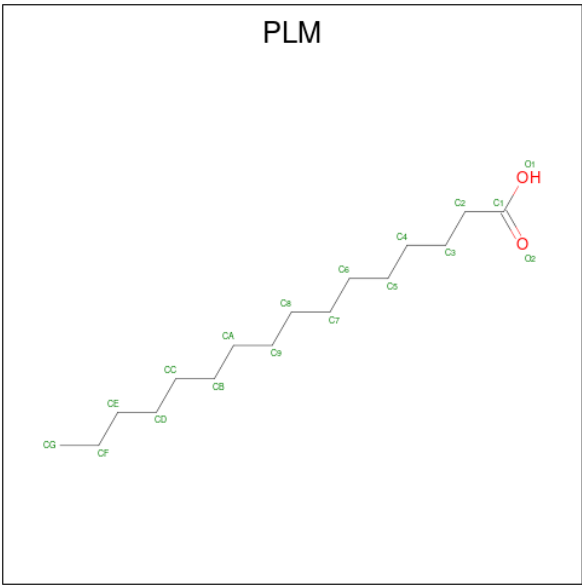
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	A	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	B	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	C	1	Total	C	H	N	O	0
			27	8	13	1	5	
5	C	1	Total	C	H	N	O	0
			27	8	13	1	5	

- Molecule 6 is O-[(R)-[(2S)-2-(hexadecanoyloxy)-3-(octadecanoyloxy)propoxy](hydroxy)phosphoryl]-D-serine (CCD ID: Q3G) (formula: C₄₀H₇₈NO₁₀P).



Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	N	O	P	0
			43	31	1	10	1	
6	B	1	Total	C	N	O	P	0
			43	31	1	10	1	
6	C	1	Total	C	N	O	P	0
			43	31	1	10	1	

- Molecule 7 is PALMITIC ACID (CCD ID: PLM) (formula: C₁₆H₃₂O₂).



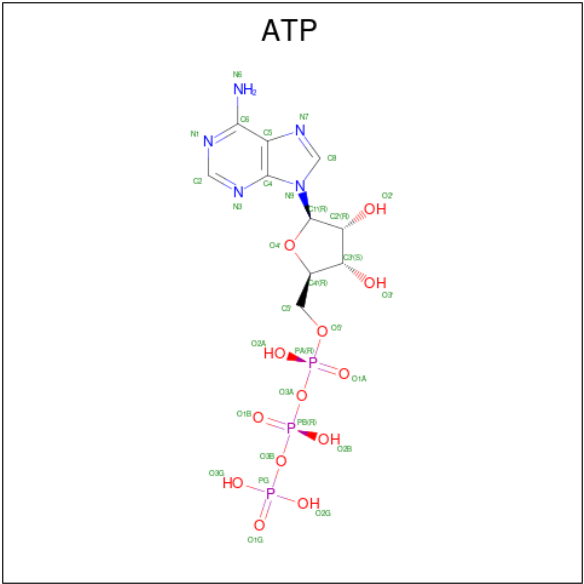
Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	H	O	0
			48	16	31	1	

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Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	H	O	0
			21	8	12	1	
7	A	1	Total	C	H	O	0
			30	11	18	1	
7	A	1	Total	C	H	O	0
			21	8	12	1	
7	B	1	Total	C	H	O	0
			48	16	31	1	
7	B	1	Total	C	H	O	0
			21	8	12	1	
7	B	1	Total	C	H	O	0
			29	11	17	1	
7	B	1	Total	C	H	O	0
			21	8	12	1	
7	C	1	Total	C	H	O	0
			48	16	31	1	
7	C	1	Total	C	H	O	0
			21	8	12	1	
7	C	1	Total	C	H	O	0
			30	11	18	1	
7	C	1	Total	C	H	O	0
			21	8	12	1	

- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

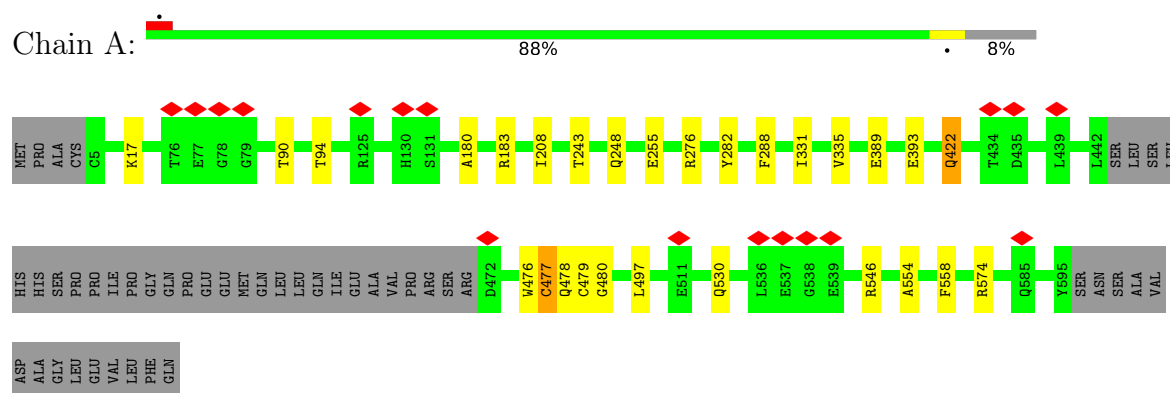


Mol	Chain	Residues	Atoms						AltConf
8	A	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
8	B	1	Total 43	C 10	H 12	N 5	O 13	P 3	0
8	C	1	Total 43	C 10	H 12	N 5	O 13	P 3	0

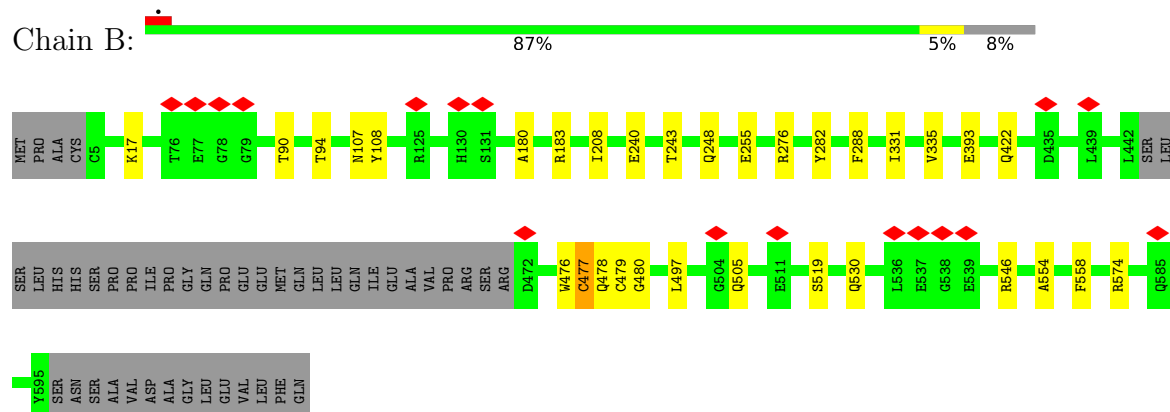
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

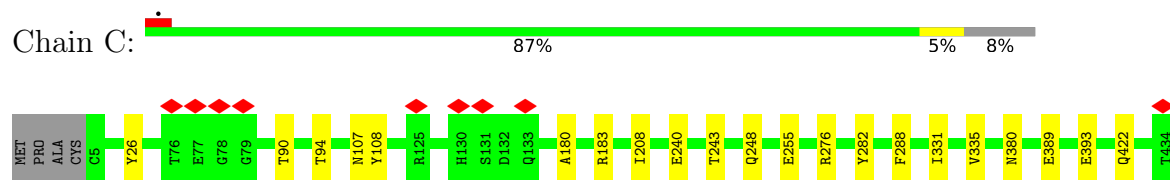
- Molecule 1: P2X purinoceptor 7

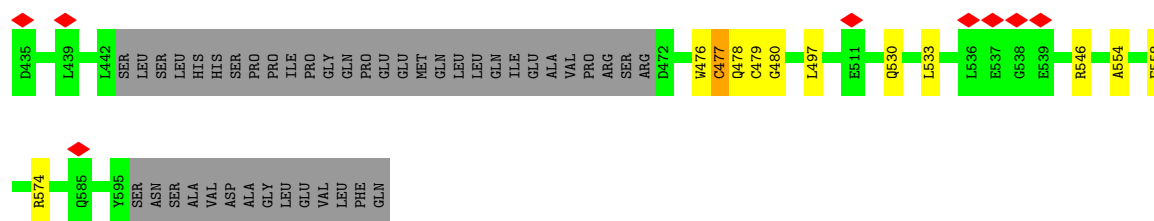


- Molecule 1: P2X purinoceptor 7



- Molecule 1: P2X purinoceptor 7





- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  50% 50%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 50%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  100%

MAG1
MAG2

- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	109570	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.166	Depositor
Minimum map value	-0.099	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0209	Depositor
Map size ($\text{\AA}$)	342.40002, 342.40002, 342.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

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: PLM, ATP, NAG, GDP, ZN, Q3G

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	0.19	0/4561	0.39	0/6185
1	B	0.24	2/4561 (0.0%)	0.40	0/6185
1	C	0.23	1/4561 (0.0%)	0.40	0/6185
All	All	0.22	3/13683 (0.0%)	0.40	0/18555

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	240	GLU	C-N	6.14	1.41	1.33
1	B	519	SER	C-N	5.70	1.41	1.34
1	B	240	GLU	C-N	5.28	1.40	1.33

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	4443	4295	4295	18	0
1	B	4443	4295	4295	19	0
1	C	4443	4295	4295	20	0
2	D	28	25	25	3	0
2	E	28	25	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	28	25	25	3	0
2	G	28	25	25	0	0
2	H	28	25	25	3	0
2	I	28	25	25	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	28	11	11	2	0
4	B	28	11	11	2	0
4	C	28	11	11	2	0
5	A	28	26	26	0	0
5	B	28	26	26	0	0
5	C	28	26	26	0	0
6	A	43	0	0	1	0
6	B	43	0	0	1	0
6	C	43	0	0	1	0
7	A	47	73	73	0	0
7	B	47	72	72	0	0
7	C	47	73	73	0	0
8	A	31	12	12	0	0
8	B	31	12	12	0	0
8	C	31	12	12	0	0
All	All	14034	13400	13400	60	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 2.

All (60) 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:D:1:NAG:O3	2:D:2:NAG:O5	1.98	0.82
2:H:1:NAG:O3	2:H:2:NAG:O5	1.98	0.82
2:F:1:NAG:O3	2:F:2:NAG:O5	1.98	0.81
2:D:1:NAG:O3	2:D:1:NAG:O7	2.09	0.71
2:H:1:NAG:O3	2:H:1:NAG:O7	2.09	0.70
2:F:1:NAG:O3	2:F:1:NAG:O7	2.09	0.69
1:C:574:ARG:NH1	4:C:704:GDP:O6	2.25	0.68
1:A:248:GLN:O	1:A:282:TYR:OH	2.14	0.64
1:A:574:ARG:NH1	4:A:703:GDP:O6	2.31	0.63
1:A:180:ALA:O	1:A:183:ARG:NH1	2.31	0.63
1:B:422:GLN:NE2	1:B:476:TRP:O	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:LYS:NZ	1:C:389:GLU:OE1	2.37	0.58
1:A:478:GLN:OE1	1:A:478:GLN:N	2.36	0.58
1:B:393:GLU:N	1:B:393:GLU:OE1	2.36	0.58
1:B:478:GLN:N	1:B:478:GLN:OE1	2.37	0.58
1:C:478:GLN:N	1:C:478:GLN:OE1	2.37	0.57
1:B:248:GLN:O	1:B:282:TYR:OH	2.18	0.57
1:B:180:ALA:O	1:B:183:ARG:NH1	2.36	0.57
1:A:90:THR:O	1:A:94:THR:OG1	2.23	0.57
1:A:393:GLU:N	1:A:393:GLU:OE1	2.37	0.56
1:B:243:THR:HB	2:F:1:NAG:O6	2.05	0.55
1:C:554:ALA:O	1:C:558:PHE:N	2.39	0.55
1:A:422:GLN:NE2	1:A:476:TRP:O	2.40	0.55
1:A:477:CYS:SG	1:A:480:GLY:N	2.78	0.55
1:C:393:GLU:N	1:C:393:GLU:OE1	2.38	0.55
1:B:574:ARG:NH1	4:B:703:GDP:O6	2.40	0.54
1:C:422:GLN:NE2	1:C:476:TRP:O	2.39	0.54
6:C:711:Q3G:C44	6:C:711:Q3G:C40	2.86	0.54
6:A:710:Q3G:C40	6:A:710:Q3G:C44	2.86	0.53
6:B:710:Q3G:C40	6:B:710:Q3G:C44	2.86	0.53
1:B:90:THR:O	1:B:94:THR:OG1	2.27	0.53
1:C:180:ALA:O	1:C:183:ARG:NH1	2.42	0.52
1:C:546:ARG:NH1	4:C:704:GDP:O3A	2.42	0.52
1:A:554:ALA:O	1:A:558:PHE:N	2.43	0.52
1:C:477:CYS:SG	1:C:480:GLY:N	2.79	0.51
1:B:554:ALA:O	1:B:558:PHE:N	2.43	0.51
1:C:90:THR:O	1:C:94:THR:OG1	2.29	0.51
1:A:255:GLU:OE2	1:A:276:ARG:NH1	2.45	0.50
1:C:530:GLN:N	1:C:530:GLN:OE1	2.44	0.50
1:B:546:ARG:NH1	4:B:703:GDP:O3A	2.44	0.50
1:B:477:CYS:SG	1:B:480:GLY:N	2.81	0.49
1:B:530:GLN:N	1:B:530:GLN:OE1	2.46	0.49
1:A:288:PHE:HD2	1:C:208:ILE:HD13	1.77	0.49
1:A:530:GLN:N	1:A:530:GLN:OE1	2.46	0.48
1:C:26:TYR:OH	1:C:380:ASN:ND2	2.48	0.47
1:C:107:ASN:OD1	1:C:108:TYR:N	2.48	0.47
1:C:248:GLN:O	1:C:282:TYR:OH	2.21	0.47
1:B:331:ILE:O	1:B:335:VAL:HG23	2.15	0.46
1:C:255:GLU:OE2	1:C:276:ARG:NH1	2.50	0.44
1:A:208:ILE:HD13	1:B:288:PHE:HD2	1.82	0.44
1:B:255:GLU:OE2	1:B:276:ARG:NH1	2.51	0.44
1:B:208:ILE:HD13	1:C:288:PHE:HD2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:389:GLU:OE1	1:B:17:LYS:NZ	2.52	0.43
1:A:331:ILE:O	1:A:335:VAL:HG23	2.19	0.42
1:C:331:ILE:O	1:C:335:VAL:HG23	2.19	0.42
1:A:243:THR:HB	2:D:1:NAG:O6	2.19	0.42
1:B:505:GLN:HG2	1:C:533:LEU:HD22	2.02	0.41
1:B:107:ASN:OD1	1:B:108:TYR:N	2.54	0.41
1:A:546:ARG:NH1	4:A:703:GDP:O3A	2.54	0.40
1:C:243:THR:HB	2:H:1:NAG:O6	2.22	0.40

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 PDB entries followed by that with respect to all EM entries.

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	558/609 (92%)	536 (96%)	22 (4%)	0	100	100
1	B	558/609 (92%)	537 (96%)	21 (4%)	0	100	100
1	C	558/609 (92%)	539 (97%)	19 (3%)	0	100	100
All	All	1674/1827 (92%)	1612 (96%)	62 (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 PDB entries followed by that with respect to all EM entries.

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	474/546 (87%)	470 (99%)	4 (1%)	73	79
1	B	474/546 (87%)	471 (99%)	3 (1%)	78	81
1	C	474/546 (87%)	471 (99%)	3 (1%)	78	81
All	All	1422/1638 (87%)	1412 (99%)	10 (1%)	73	80

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	422	GLN
1	A	477	CYS
1	A	479	CYS
1	A	497	LEU
1	B	477	CYS
1	B	479	CYS
1	B	497	LEU
1	C	477	CYS
1	C	479	CYS
1	C	497	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	HIS
1	A	481	ASN
1	B	12	GLN
1	B	481	ASN
1	C	62	HIS
1	C	201	HIS
1	C	481	ASN
1	C	524	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

12 monosaccharides 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	NAG	D	1	1,2	14,14,15	0.29	0	17,19,21	0.56	0
2	NAG	D	2	2	14,14,15	0.29	0	17,19,21	0.55	0
2	NAG	E	1	1,2	14,14,15	0.39	0	17,19,21	0.57	0
2	NAG	E	2	2	14,14,15	0.99	1 (7%)	17,19,21	1.48	2 (11%)
2	NAG	F	1	1,2	14,14,15	0.29	0	17,19,21	0.56	0
2	NAG	F	2	2	14,14,15	0.29	0	17,19,21	0.56	0
2	NAG	G	1	1,2	14,14,15	0.34	0	17,19,21	0.53	0
2	NAG	G	2	2	14,14,15	0.92	1 (7%)	17,19,21	1.50	2 (11%)
2	NAG	H	1	1,2	14,14,15	0.29	0	17,19,21	0.55	0
2	NAG	H	2	2	14,14,15	0.30	0	17,19,21	0.55	0
2	NAG	I	1	1,2	14,14,15	0.39	0	17,19,21	0.57	0
2	NAG	I	2	2	14,14,15	1.02	1 (7%)	17,19,21	1.50	2 (11%)

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	NAG	D	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	3/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1
2	NAG	G	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	3/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	H	2	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	I	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	I	2	2	-	3/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	2	NAG	O5-C1	3.56	1.49	1.43
2	E	2	NAG	O5-C1	3.45	1.49	1.43
2	G	2	NAG	O5-C1	3.30	1.49	1.43

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	2	NAG	C1-O5-C5	5.35	119.36	112.19
2	G	2	NAG	C1-O5-C5	5.31	119.31	112.19
2	E	2	NAG	C1-O5-C5	5.25	119.22	112.19
2	G	2	NAG	C2-N2-C7	2.67	126.48	122.90
2	E	2	NAG	C2-N2-C7	2.65	126.45	122.90
2	I	2	NAG	C2-N2-C7	2.61	126.40	122.90

There are no chirality outliers.

All (27) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	F	2	NAG	O5-C5-C6-O6
2	H	2	NAG	O5-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	F	2	NAG	C4-C5-C6-O6
2	H	2	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6
2	H	1	NAG	C4-C5-C6-O6
2	E	2	NAG	C8-C7-N2-C2
2	E	2	NAG	O7-C7-N2-C2
2	G	2	NAG	C8-C7-N2-C2
2	G	2	NAG	O7-C7-N2-C2
2	I	2	NAG	C8-C7-N2-C2
2	I	2	NAG	O7-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6

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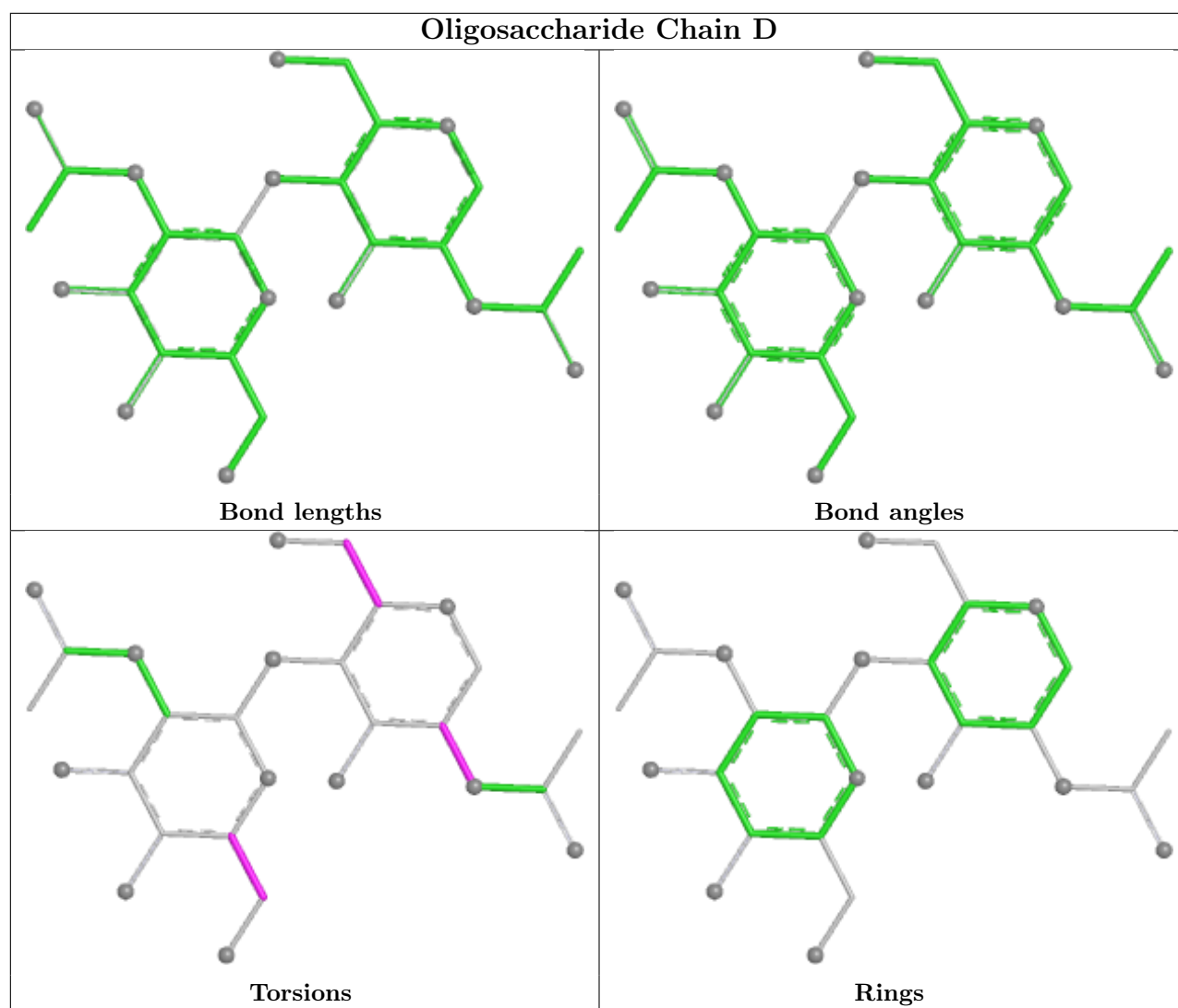
Mol	Chain	Res	Type	Atoms
2	H	1	NAG	O5-C5-C6-O6
2	G	2	NAG	O5-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
2	I	2	NAG	O5-C5-C6-O6
2	D	1	NAG	C1-C2-N2-C7
2	F	1	NAG	C1-C2-N2-C7
2	H	1	NAG	C1-C2-N2-C7
2	D	1	NAG	C3-C2-N2-C7
2	F	1	NAG	C3-C2-N2-C7
2	H	1	NAG	C3-C2-N2-C7

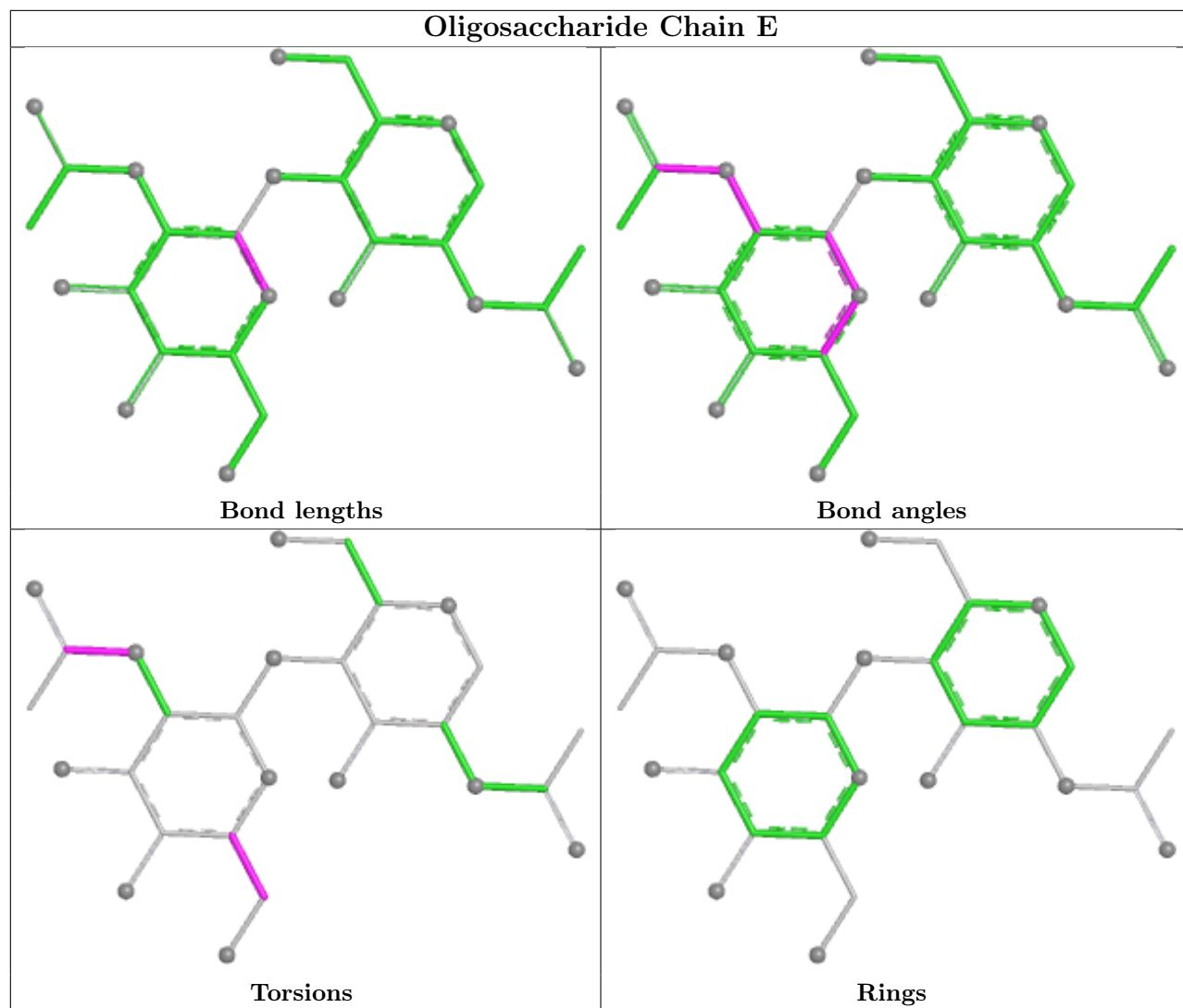
There are no ring outliers.

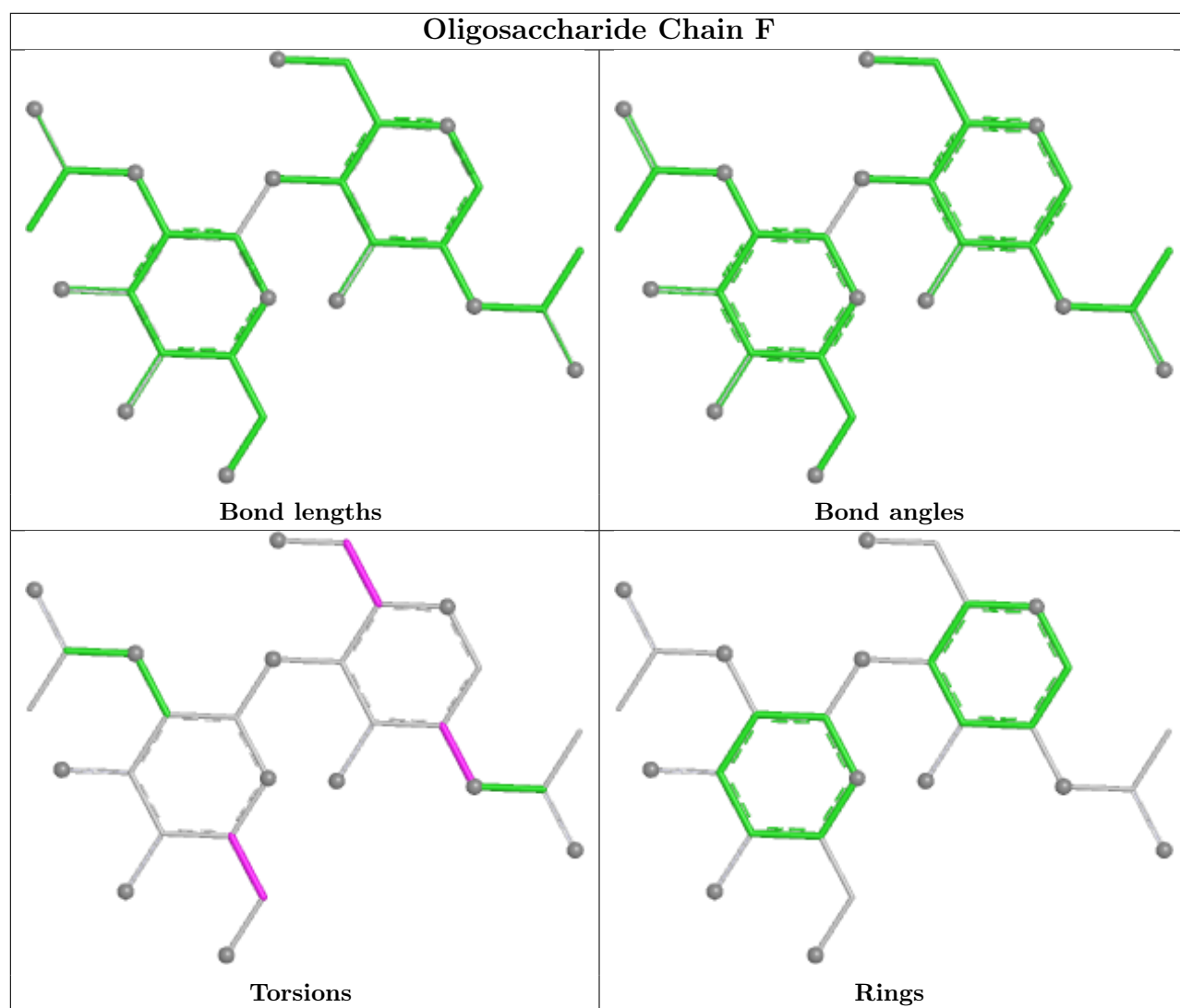
6 monomers are involved in 9 short contacts:

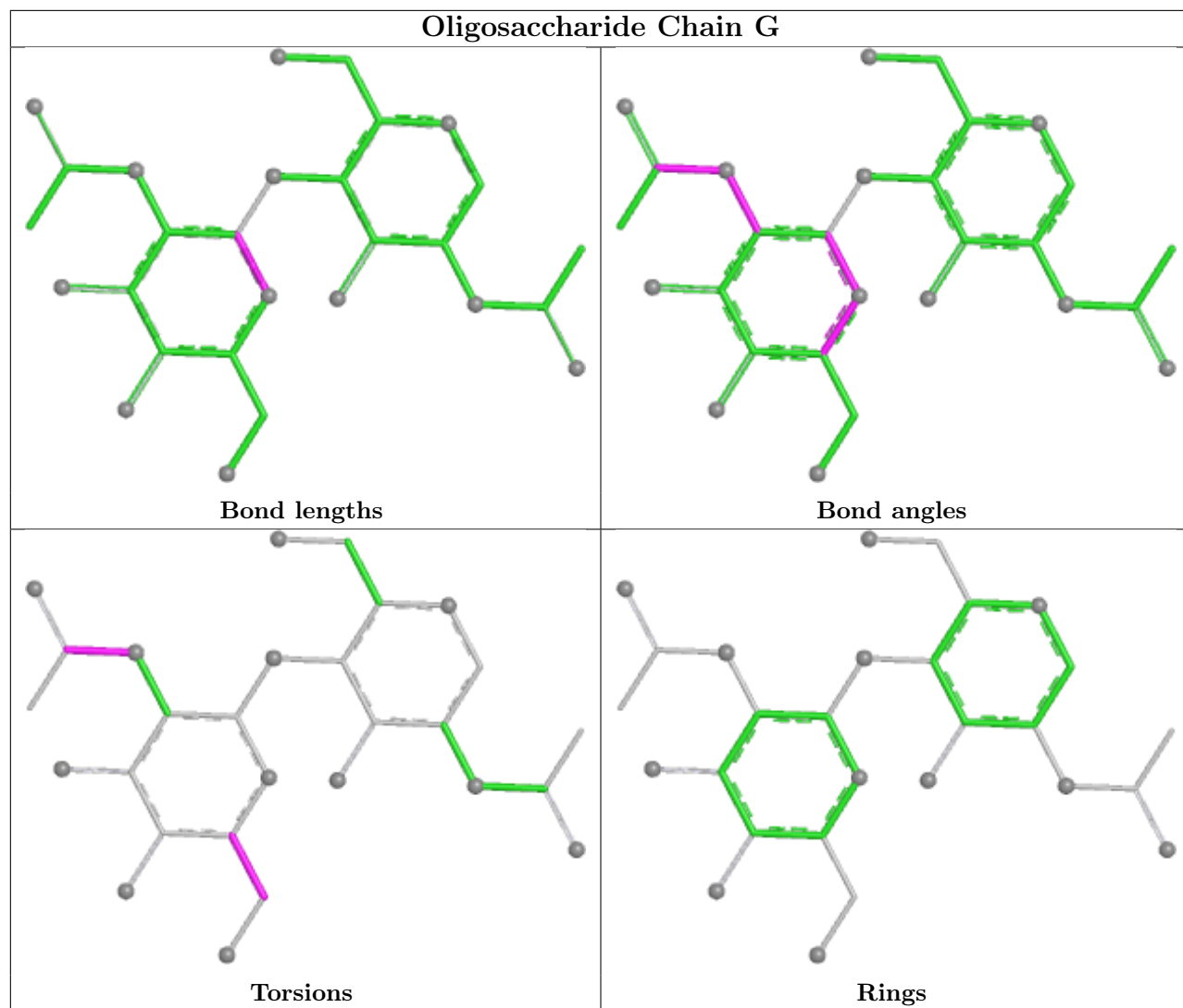
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	NAG	1	0
2	D	1	NAG	3	0
2	H	2	NAG	1	0
2	F	2	NAG	1	0
2	F	1	NAG	3	0
2	H	1	NAG	3	0

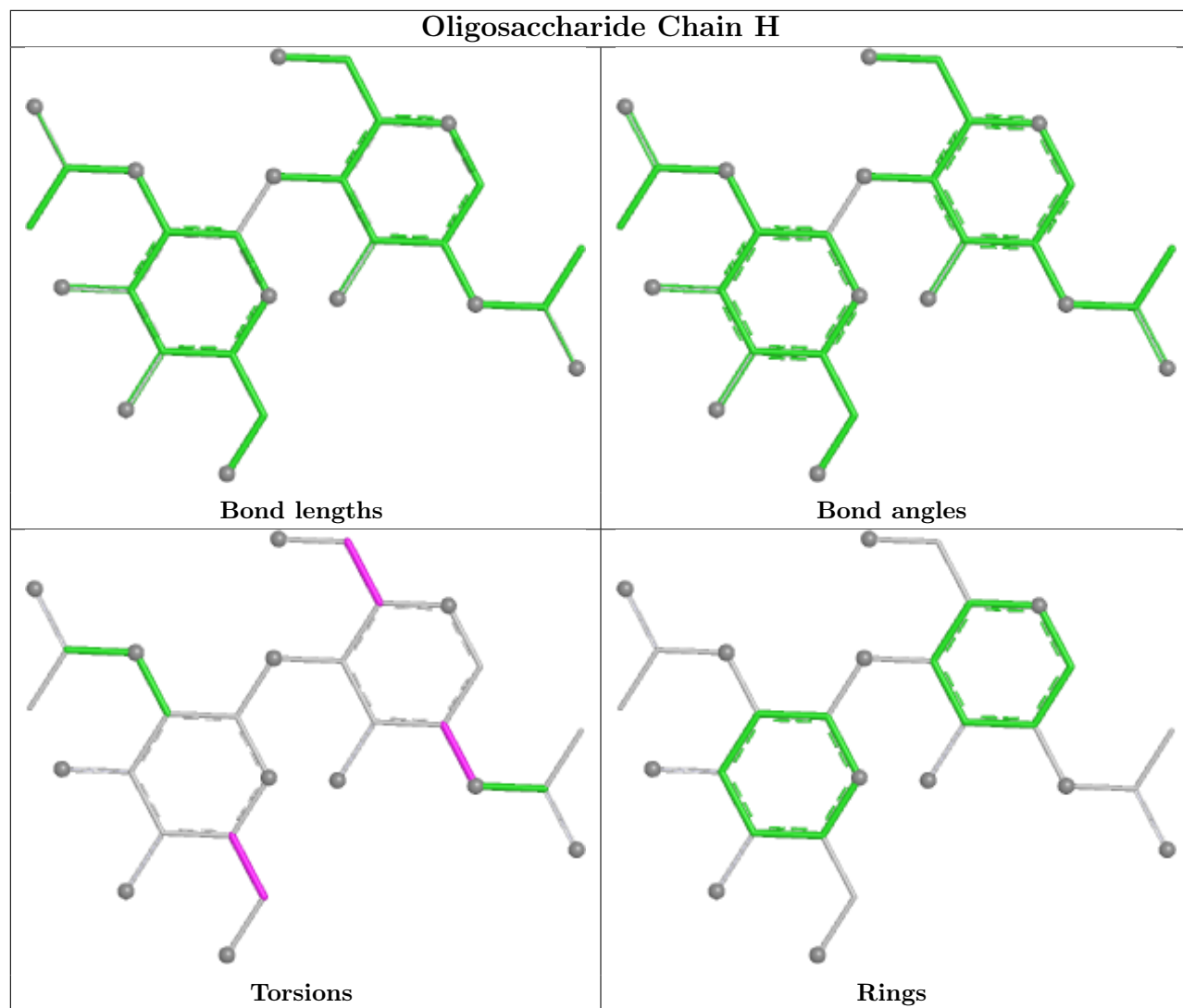
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

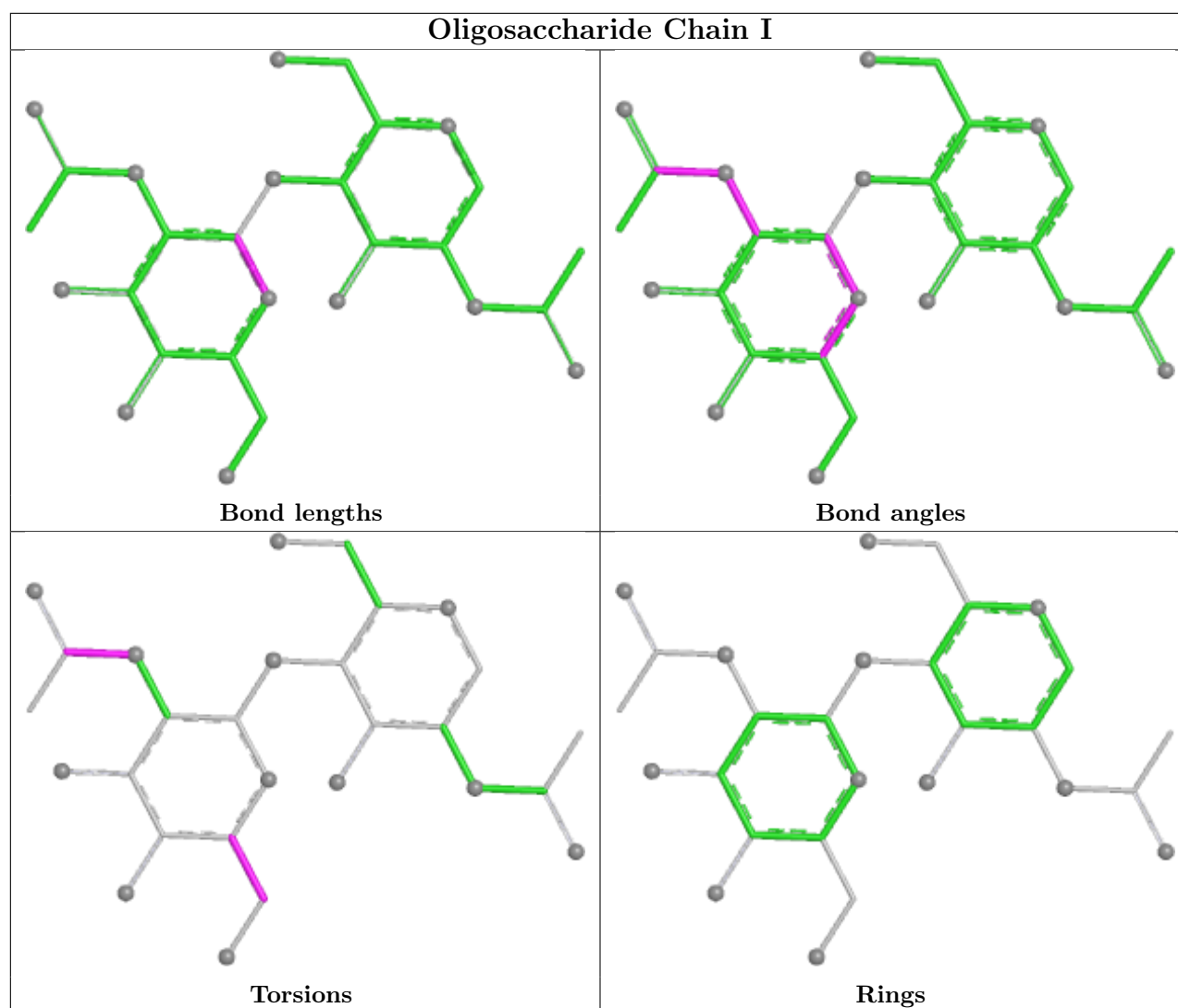












5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 6 are monoatomic - leaving 27 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	$\# Z > 2$
7	PLM	B	714	1	7,8,17	0.26	0	6,7,17	0.45	0
5	NAG	C	705	1	14,14,15	0.20	0	17,19,21	0.81	1 (5%)
7	PLM	A	713	1	10,11,17	0.22	0	9,10,17	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	ATP	B	715	-	32,33,33	3.26	16 (50%)	48,52,52	2.76	13 (27%)
7	PLM	A	712	1	7,8,17	0.26	0	6,7,17	0.44	0
7	PLM	C	714	1	10,11,17	0.21	0	9,10,17	0.51	0
5	NAG	C	706	1	14,14,15	0.45	0	17,19,21	0.33	0
5	NAG	B	705	1	14,14,15	0.47	0	17,19,21	0.34	0
7	PLM	A	711	1	15,16,17	0.17	0	14,15,17	0.54	0
6	Q3G	A	710	-	41,42,51	1.18	5 (12%)	43,49,58	1.01	2 (4%)
7	PLM	A	714	1	7,8,17	0.26	0	6,7,17	0.45	0
7	PLM	B	711	1	15,16,17	0.17	0	14,15,17	0.54	0
7	PLM	C	713	1	7,8,17	0.26	0	6,7,17	0.45	0
6	Q3G	B	710	-	41,42,51	1.18	5 (12%)	43,49,58	1.01	2 (4%)
5	NAG	B	704	1	14,14,15	0.21	0	17,19,21	0.82	1 (5%)
7	PLM	C	712	1	15,16,17	0.17	0	14,15,17	0.55	0
8	ATP	A	715	-	32,33,33	3.28	16 (50%)	48,52,52	2.76	13 (27%)
7	PLM	B	713	1	10,11,17	0.22	0	9,10,17	0.47	0
8	ATP	C	701	-	32,33,33	3.26	16 (50%)	48,52,52	2.77	13 (27%)
4	GDP	C	704	-	29,30,30	3.41	15 (51%)	45,47,47	1.92	10 (22%)
4	GDP	B	703	-	29,30,30	3.42	15 (51%)	45,47,47	1.92	10 (22%)
7	PLM	B	712	1	7,8,17	0.25	0	6,7,17	0.46	0
4	GDP	A	703	-	29,30,30	3.41	15 (51%)	45,47,47	1.92	10 (22%)
5	NAG	A	705	1	14,14,15	0.46	0	17,19,21	0.33	0
6	Q3G	C	711	-	41,42,51	1.18	5 (12%)	43,49,58	1.01	2 (4%)
7	PLM	C	715	1	7,8,17	0.26	0	6,7,17	0.46	0
5	NAG	A	704	1	14,14,15	0.19	0	17,19,21	0.82	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PLM	B	714	1	-	1/6/6/15	-
5	NAG	C	705	1	-	3/6/23/26	0/1/1/1
7	PLM	A	713	1	-	3/9/9/15	-
8	ATP	B	715	-	-	5/22/38/38	0/3/3/3
7	PLM	A	712	1	-	1/6/6/15	-
7	PLM	C	714	1	-	3/9/9/15	-
5	NAG	C	706	1	-	2/6/23/26	0/1/1/1
5	NAG	B	705	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	PLM	A	711	1	-	4/14/14/15	-
6	Q3G	A	710	-	-	18/48/48/57	-
7	PLM	A	714	1	-	1/6/6/15	-
7	PLM	B	711	1	-	5/14/14/15	-
7	PLM	C	713	1	-	1/6/6/15	-
6	Q3G	B	710	-	-	18/48/48/57	-
5	NAG	B	704	1	-	3/6/23/26	0/1/1/1
7	PLM	C	712	1	-	4/14/14/15	-
8	ATP	A	715	-	-	5/22/38/38	0/3/3/3
7	PLM	B	713	1	-	3/9/9/15	-
8	ATP	C	701	-	-	5/22/38/38	0/3/3/3
4	GDP	C	704	-	-	0/16/32/32	0/3/3/3
4	GDP	B	703	-	-	1/16/32/32	0/3/3/3
7	PLM	B	712	1	-	1/6/6/15	-
4	GDP	A	703	-	-	1/16/32/32	0/3/3/3
5	NAG	A	705	1	-	2/6/23/26	0/1/1/1
6	Q3G	C	711	-	-	18/48/48/57	-
7	PLM	C	715	1	-	1/6/6/15	-
5	NAG	A	704	1	-	3/6/23/26	0/1/1/1

All (108) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	701	ATP	C2'-C3'	-10.33	1.25	1.53
8	A	715	ATP	C2'-C3'	-10.33	1.25	1.53
8	B	715	ATP	C2'-C3'	-10.33	1.25	1.53
4	B	703	GDP	C3'-C4'	-8.76	1.30	1.53
4	C	704	GDP	C3'-C4'	-8.75	1.30	1.53
4	A	703	GDP	C3'-C4'	-8.71	1.30	1.53
4	A	703	GDP	O4'-C4'	7.70	1.62	1.45
4	B	703	GDP	O4'-C4'	7.68	1.62	1.45
4	C	704	GDP	O4'-C4'	7.65	1.62	1.45
8	A	715	ATP	PA-O3A	6.55	1.66	1.59
8	C	701	ATP	PA-O3A	6.51	1.66	1.59
4	B	703	GDP	C4-N3	6.48	1.49	1.34
4	C	704	GDP	C4-N3	6.48	1.49	1.34
4	A	703	GDP	C4-N3	6.46	1.49	1.34
8	B	715	ATP	PA-O3A	6.45	1.66	1.59
8	B	715	ATP	PB-O3A	6.38	1.66	1.59
8	A	715	ATP	PB-O3A	6.37	1.66	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	701	ATP	PB-O3A	6.26	1.66	1.59
4	B	703	GDP	C2-N3	5.26	1.45	1.33
4	A	703	GDP	C2-N3	5.26	1.45	1.33
4	A	703	GDP	PA-O3A	5.23	1.65	1.59
4	C	704	GDP	C2-N3	5.22	1.45	1.33
4	C	704	GDP	PA-O3A	5.15	1.65	1.59
4	B	703	GDP	PA-O3A	5.15	1.65	1.59
4	C	704	GDP	O4'-C1'	-4.78	1.31	1.42
4	B	703	GDP	O4'-C1'	-4.77	1.31	1.42
4	A	703	GDP	O4'-C1'	-4.75	1.31	1.42
4	B	703	GDP	C2-N2	4.65	1.45	1.34
4	A	703	GDP	C2-N2	4.63	1.45	1.34
4	C	704	GDP	C2-N2	4.63	1.45	1.34
8	B	715	ATP	O4'-C1'	-4.28	1.32	1.42
8	A	715	ATP	O4'-C1'	-4.27	1.32	1.42
8	C	701	ATP	O4'-C1'	-4.21	1.32	1.42
8	C	701	ATP	C2'-C1'	4.09	1.66	1.53
8	A	715	ATP	C2'-C1'	4.07	1.66	1.53
8	B	715	ATP	C2'-C1'	4.03	1.66	1.53
8	A	715	ATP	PB-O3B	4.02	1.63	1.59
6	C	711	Q3G	C46-C45	-3.99	1.31	1.51
6	B	710	Q3G	C46-C45	-3.99	1.31	1.51
6	A	710	Q3G	C46-C45	-3.97	1.32	1.51
8	C	701	ATP	PB-O3B	3.93	1.63	1.59
8	B	715	ATP	PB-O3B	3.84	1.63	1.59
8	C	701	ATP	C6-N6	3.65	1.43	1.34
8	A	715	ATP	C6-N6	3.62	1.43	1.34
8	B	715	ATP	C6-N6	3.62	1.43	1.34
8	B	715	ATP	C5'-C4'	-3.47	1.41	1.51
8	A	715	ATP	C5'-C4'	-3.46	1.41	1.51
8	C	701	ATP	C5'-C4'	-3.45	1.41	1.51
8	C	701	ATP	O3'-C3'	3.08	1.50	1.43
8	A	715	ATP	O3'-C3'	3.07	1.50	1.43
8	A	715	ATP	PA-O5'	3.04	1.71	1.59
8	B	715	ATP	C3'-C4'	3.04	1.60	1.53
8	C	701	ATP	PA-O5'	3.02	1.71	1.59
8	B	715	ATP	PA-O5'	3.00	1.71	1.59
8	B	715	ATP	O3'-C3'	3.00	1.50	1.43
8	A	715	ATP	C3'-C4'	2.98	1.60	1.53
8	C	701	ATP	C3'-C4'	2.98	1.60	1.53
8	B	715	ATP	C5-C4	-2.90	1.33	1.39
8	A	715	ATP	C5-C4	-2.89	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	703	GDP	O2'-C2'	-2.86	1.35	1.43
8	C	701	ATP	C5-C4	-2.85	1.34	1.39
4	A	703	GDP	O2'-C2'	-2.85	1.35	1.43
4	B	703	GDP	C5-N7	-2.80	1.33	1.39
4	C	704	GDP	C5-N7	-2.80	1.33	1.39
4	C	704	GDP	O2'-C2'	-2.80	1.36	1.43
4	A	703	GDP	C5-N7	-2.80	1.33	1.39
4	A	703	GDP	C2-N1	2.75	1.44	1.37
4	C	704	GDP	O3'-C3'	2.74	1.49	1.43
4	B	703	GDP	C2-N1	2.73	1.44	1.37
4	A	703	GDP	O3'-C3'	2.72	1.49	1.43
4	C	704	GDP	C2-N1	2.72	1.44	1.37
4	B	703	GDP	O3'-C3'	2.71	1.49	1.43
8	A	715	ATP	O4'-C4'	2.70	1.51	1.45
8	C	701	ATP	O4'-C4'	2.69	1.51	1.45
8	A	715	ATP	C5-N7	-2.69	1.34	1.39
8	B	715	ATP	C5-N7	-2.69	1.34	1.39
8	B	715	ATP	C8-N9	-2.68	1.33	1.37
6	B	710	Q3G	O35-C22	-2.67	1.40	1.46
6	C	711	Q3G	O35-C22	-2.66	1.40	1.46
8	B	715	ATP	O4'-C4'	2.66	1.50	1.45
8	A	715	ATP	C8-N9	-2.66	1.33	1.37
8	C	701	ATP	C5-N7	-2.65	1.34	1.39
8	C	701	ATP	C8-N9	-2.65	1.33	1.37
6	A	710	Q3G	O35-C22	-2.64	1.40	1.46
4	C	704	GDP	O6-C6	-2.57	1.18	1.23
4	B	703	GDP	O6-C6	-2.46	1.18	1.23
4	A	703	GDP	O6-C6	-2.45	1.18	1.23
4	C	704	GDP	C5-C6	2.38	1.53	1.44
4	B	703	GDP	C5-C6	2.38	1.53	1.44
6	A	710	Q3G	O20-C18	2.37	1.40	1.33
6	C	711	Q3G	O20-C18	2.37	1.40	1.33
4	A	703	GDP	C5-C6	2.36	1.53	1.44
8	B	715	ATP	O2'-C2'	2.36	1.48	1.43
6	B	710	Q3G	O20-C18	2.35	1.40	1.33
4	B	703	GDP	C6-N1	2.34	1.43	1.38
8	C	701	ATP	O2'-C2'	2.33	1.48	1.43
4	A	703	GDP	C6-N1	2.32	1.43	1.38
8	A	715	ATP	O2'-C2'	2.31	1.48	1.43
4	C	704	GDP	C6-N1	2.28	1.43	1.38
6	A	710	Q3G	O20-C21	-2.27	1.40	1.45
4	C	704	GDP	C4-N9	-2.24	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	710	Q3G	O20-C21	-2.22	1.40	1.45
6	C	711	Q3G	O20-C21	-2.22	1.40	1.45
4	A	703	GDP	C4-N9	-2.21	1.32	1.38
4	B	703	GDP	C4-N9	-2.18	1.32	1.38
6	B	710	Q3G	O35-C36	2.15	1.40	1.34
6	A	710	Q3G	O35-C36	2.15	1.40	1.34
6	C	711	Q3G	O35-C36	2.14	1.40	1.34

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	701	ATP	N6-C6-N1	-9.25	97.77	118.38
8	A	715	ATP	N6-C6-N1	-9.23	97.83	118.38
8	B	715	ATP	N6-C6-N1	-9.17	97.94	118.38
8	A	715	ATP	C5-C6-N6	7.41	141.63	123.29
8	C	701	ATP	C5-C6-N6	7.39	141.59	123.29
8	B	715	ATP	C5-C6-N6	7.34	141.45	123.29
8	C	701	ATP	C5-C4-N3	-5.89	118.61	126.72
8	B	715	ATP	C5-C4-N3	-5.84	118.67	126.72
8	C	701	ATP	N3-C2-N1	-5.80	119.81	128.58
8	A	715	ATP	C5-C4-N3	-5.80	118.74	126.72
8	B	715	ATP	N3-C2-N1	-5.77	119.85	128.58
8	A	715	ATP	N3-C2-N1	-5.74	119.89	128.58
4	B	703	GDP	C1'-N9-C8	-5.58	110.89	126.73
4	C	704	GDP	C1'-N9-C8	-5.53	111.01	126.73
4	A	703	GDP	C1'-N9-C8	-5.51	111.07	126.73
8	C	701	ATP	C4-N9-C1'	-5.37	114.08	126.63
8	A	715	ATP	C4-N9-C1'	-5.30	114.23	126.63
8	B	715	ATP	C4-N9-C1'	-5.28	114.28	126.63
8	B	715	ATP	N3-C4-N9	4.88	135.46	127.17
8	C	701	ATP	N3-C4-N9	4.79	135.32	127.17
8	A	715	ATP	N3-C4-N9	4.77	135.28	127.17
4	C	704	GDP	C5-C4-N3	-4.71	120.90	128.39
4	A	703	GDP	C5-C4-N3	-4.70	120.91	128.39
4	B	703	GDP	C5-C4-N3	-4.66	120.97	128.39
8	B	715	ATP	N9-C8-N7	-4.58	107.44	113.94
8	A	715	ATP	N9-C8-N7	-4.56	107.47	113.94
8	C	701	ATP	N9-C8-N7	-4.49	107.57	113.94
4	B	703	GDP	C1'-N9-C4	4.39	139.45	126.49
4	C	704	GDP	C1'-N9-C4	4.35	139.33	126.49
4	A	703	GDP	C1'-N9-C4	4.32	139.24	126.49
8	C	701	ATP	C1'-N9-C8	4.29	136.62	127.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	703	GDP	C2-N3-C4	4.19	119.52	112.30
8	A	715	ATP	C1'-N9-C8	4.18	136.37	127.09
4	B	703	GDP	C2-N3-C4	4.16	119.47	112.30
4	C	704	GDP	C2-N3-C4	4.13	119.41	112.30
8	B	715	ATP	C1'-N9-C8	4.12	136.23	127.09
6	A	710	Q3G	O35-C36-C38	3.98	120.10	111.48
6	C	711	Q3G	O35-C36-C38	3.97	120.08	111.48
6	B	710	Q3G	O35-C36-C38	3.97	120.07	111.48
8	C	701	ATP	C2-N3-C4	3.78	121.07	111.83
8	B	715	ATP	C2-N3-C4	3.75	120.98	111.83
8	A	715	ATP	C2-N3-C4	3.72	120.91	111.83
8	B	715	ATP	C4-N9-C8	3.56	109.48	105.74
4	B	703	GDP	N9-C8-N7	-3.53	106.86	113.40
4	A	703	GDP	N9-C8-N7	-3.51	106.89	113.40
4	C	704	GDP	N9-C8-N7	-3.50	106.91	113.40
8	A	715	ATP	C4-N9-C8	3.48	109.39	105.74
8	C	701	ATP	C4-N9-C8	3.38	109.28	105.74
8	A	715	ATP	C3'-C2'-C1'	3.13	107.38	101.46
8	C	701	ATP	C3'-C2'-C1'	3.12	107.36	101.46
4	A	703	GDP	N9-C4-N3	3.08	132.11	125.95
4	C	704	GDP	N9-C4-N3	3.06	132.07	125.95
4	B	703	GDP	N9-C4-N3	3.05	132.05	125.95
8	B	715	ATP	C3'-C2'-C1'	2.99	107.13	101.46
4	C	704	GDP	C2-N1-C6	-2.93	119.79	125.11
4	A	703	GDP	C2-N1-C6	-2.92	119.82	125.11
4	B	703	GDP	C2-N1-C6	-2.89	119.87	125.11
8	B	715	ATP	C5-N7-C8	2.89	107.99	103.45
8	A	715	ATP	C5-N7-C8	2.89	107.99	103.45
8	C	701	ATP	C5-N7-C8	2.88	107.98	103.45
6	A	710	Q3G	O20-C18-C17	2.81	120.40	111.83
6	B	710	Q3G	O20-C18-C17	2.80	120.37	111.83
6	C	711	Q3G	O20-C18-C17	2.77	120.30	111.83
5	A	704	NAG	C2-N2-C7	2.76	126.60	122.90
5	B	704	NAG	C2-N2-C7	2.73	126.56	122.90
5	C	705	NAG	C2-N2-C7	2.70	126.52	122.90
4	A	703	GDP	C5-C6-N1	2.56	119.76	113.25
4	B	703	GDP	C5-C6-N1	2.55	119.74	113.25
4	C	704	GDP	C5-C6-N1	2.54	119.73	113.25
4	B	703	GDP	O6-C6-C5	-2.53	119.86	126.53
4	A	703	GDP	O6-C6-C5	-2.51	119.91	126.53
4	C	704	GDP	O6-C6-C5	-2.50	119.92	126.53
4	B	703	GDP	C8-N7-C5	2.25	108.26	104.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	715	ATP	C6-C5-C4	2.23	120.22	117.18
8	B	715	ATP	C6-C5-C4	2.23	120.22	117.18
4	A	703	GDP	C8-N7-C5	2.21	108.20	104.26
8	C	701	ATP	C6-C5-C4	2.21	120.20	117.18
4	C	704	GDP	C8-N7-C5	2.21	108.20	104.26

There are no chirality outliers.

All (114) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	712	PLM	O2-C1-C2-C3
7	A	713	PLM	O2-C1-C2-C3
7	A	713	PLM	C1-C2-C3-C4
7	A	714	PLM	O2-C1-C2-C3
7	B	711	PLM	O2-C1-C2-C3
7	B	712	PLM	O2-C1-C2-C3
7	B	713	PLM	O2-C1-C2-C3
7	B	714	PLM	O2-C1-C2-C3
7	C	713	PLM	O2-C1-C2-C3
7	C	714	PLM	O2-C1-C2-C3
7	C	714	PLM	C1-C2-C3-C4
7	C	715	PLM	O2-C1-C2-C3
8	A	715	ATP	PB-O3B-PG-O3G
8	B	715	ATP	PB-O3B-PG-O3G
8	C	701	ATP	PB-O3B-PG-O3G
6	A	710	Q3G	C38-C36-O35-C22
6	B	710	Q3G	C38-C36-O35-C22
6	C	711	Q3G	C38-C36-O35-C22
6	A	710	Q3G	O37-C36-O35-C22
6	B	710	Q3G	O37-C36-O35-C22
6	C	711	Q3G	O37-C36-O35-C22
5	A	704	NAG	C8-C7-N2-C2
5	A	704	NAG	O7-C7-N2-C2
5	B	704	NAG	C8-C7-N2-C2
5	B	704	NAG	O7-C7-N2-C2
5	C	705	NAG	C8-C7-N2-C2
5	C	705	NAG	O7-C7-N2-C2
6	A	710	Q3G	C17-C18-O20-C21
6	B	710	Q3G	C17-C18-O20-C21
6	C	711	Q3G	C17-C18-O20-C21
5	C	705	NAG	O5-C5-C6-O6
6	A	710	Q3G	N34-C30-C31-O33

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Mol	Chain	Res	Type	Atoms
6	B	710	Q3G	N34-C30-C31-O33
6	C	711	Q3G	N34-C30-C31-O33
5	A	704	NAG	O5-C5-C6-O6
7	A	711	PLM	C3-C4-C5-C6
7	C	712	PLM	C3-C4-C5-C6
6	A	710	Q3G	C12-C13-C14-C15
6	B	710	Q3G	C12-C13-C14-C15
6	C	711	Q3G	C12-C13-C14-C15
6	A	710	Q3G	C15-C16-C17-C18
6	B	710	Q3G	C15-C16-C17-C18
6	C	711	Q3G	C15-C16-C17-C18
7	B	711	PLM	C3-C4-C5-C6
6	A	710	Q3G	O19-C18-O20-C21
6	B	710	Q3G	O19-C18-O20-C21
6	C	711	Q3G	O19-C18-O20-C21
6	A	710	Q3G	C40-C41-C42-C43
6	B	710	Q3G	C40-C41-C42-C43
6	C	711	Q3G	C40-C41-C42-C43
6	A	710	Q3G	C36-C38-C39-C40
6	B	710	Q3G	C36-C38-C39-C40
6	C	711	Q3G	C36-C38-C39-C40
5	A	705	NAG	O5-C5-C6-O6
6	A	710	Q3G	C42-C43-C44-C45
6	B	710	Q3G	C42-C43-C44-C45
6	C	711	Q3G	C42-C43-C44-C45
5	B	704	NAG	O5-C5-C6-O6
6	A	710	Q3G	C38-C39-C40-C41
6	B	710	Q3G	C38-C39-C40-C41
6	C	711	Q3G	C38-C39-C40-C41
5	A	705	NAG	C4-C5-C6-O6
5	B	705	NAG	O5-C5-C6-O6
5	B	705	NAG	C4-C5-C6-O6
6	A	710	Q3G	C11-C12-C13-C14
6	B	710	Q3G	C11-C12-C13-C14
6	C	711	Q3G	C11-C12-C13-C14
6	A	710	Q3G	C45-C46-C47-C48
6	C	711	Q3G	C45-C46-C47-C48
6	B	710	Q3G	C45-C46-C47-C48
4	A	703	GDP	PB-O3A-PA-O1A
7	A	711	PLM	CB-CC-CD-CE
7	B	711	PLM	CB-CC-CD-CE
6	A	710	Q3G	N34-C30-C31-O32

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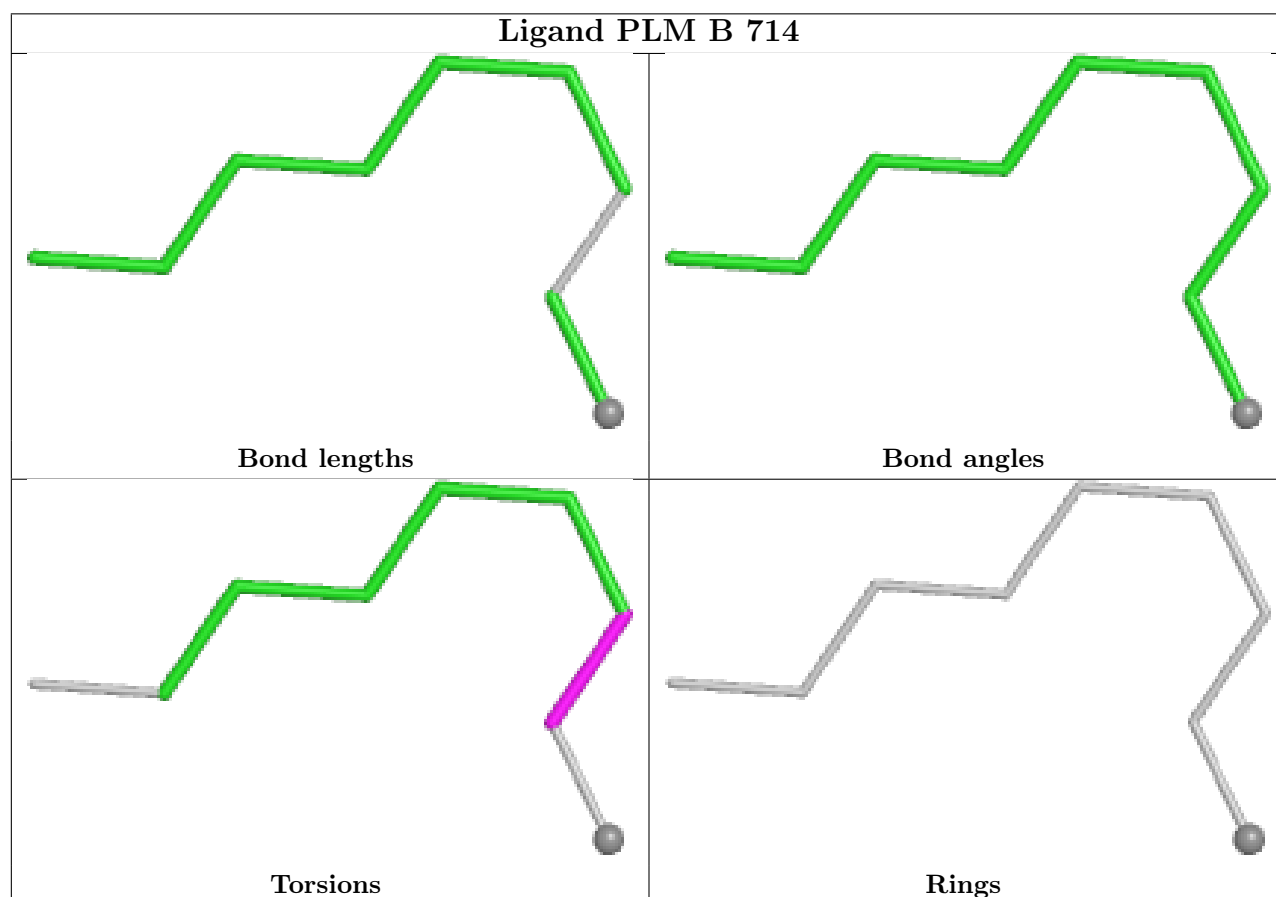
Mol	Chain	Res	Type	Atoms
6	B	710	Q3G	N34-C30-C31-O32
6	C	711	Q3G	N34-C30-C31-O32
7	C	714	PLM	C3-C4-C5-C6
7	C	712	PLM	CB-CC-CD-CE
6	B	710	Q3G	C48-C49-C50-C51
6	A	710	Q3G	C48-C49-C50-C51
6	C	711	Q3G	C48-C49-C50-C51
7	A	711	PLM	C9-CA-CB-CC
7	A	713	PLM	C3-C4-C5-C6
4	B	703	GDP	PB-O3A-PA-O1A
7	A	711	PLM	C1-C2-C3-C4
7	B	711	PLM	C1-C2-C3-C4
7	B	713	PLM	C1-C2-C3-C4
7	C	712	PLM	C1-C2-C3-C4
5	C	706	NAG	C4-C5-C6-O6
7	C	712	PLM	C9-CA-CB-CC
5	C	706	NAG	O5-C5-C6-O6
7	B	711	PLM	C9-CA-CB-CC
7	B	713	PLM	C3-C4-C5-C6
8	B	715	ATP	PB-O3A-PA-O1A
6	A	710	Q3G	O35-C22-C23-O24
6	B	710	Q3G	O35-C22-C23-O24
6	C	711	Q3G	O35-C22-C23-O24
8	A	715	ATP	C3'-C4'-C5'-O5'
8	B	715	ATP	C3'-C4'-C5'-O5'
8	C	701	ATP	C3'-C4'-C5'-O5'
8	A	715	ATP	PB-O3A-PA-O1A
8	C	701	ATP	PB-O3A-PA-O1A
8	C	701	ATP	PB-O3B-PG-O1G
8	A	715	ATP	PB-O3B-PG-O2G
8	B	715	ATP	PB-O3B-PG-O2G
8	A	715	ATP	O4'-C4'-C5'-O5'
6	A	710	Q3G	C21-C22-C23-O24
6	B	710	Q3G	C21-C22-C23-O24
6	C	711	Q3G	C21-C22-C23-O24
8	B	715	ATP	O4'-C4'-C5'-O5'
6	A	710	Q3G	C46-C47-C48-C49
6	B	710	Q3G	C46-C47-C48-C49
6	C	711	Q3G	C46-C47-C48-C49
8	C	701	ATP	O4'-C4'-C5'-O5'

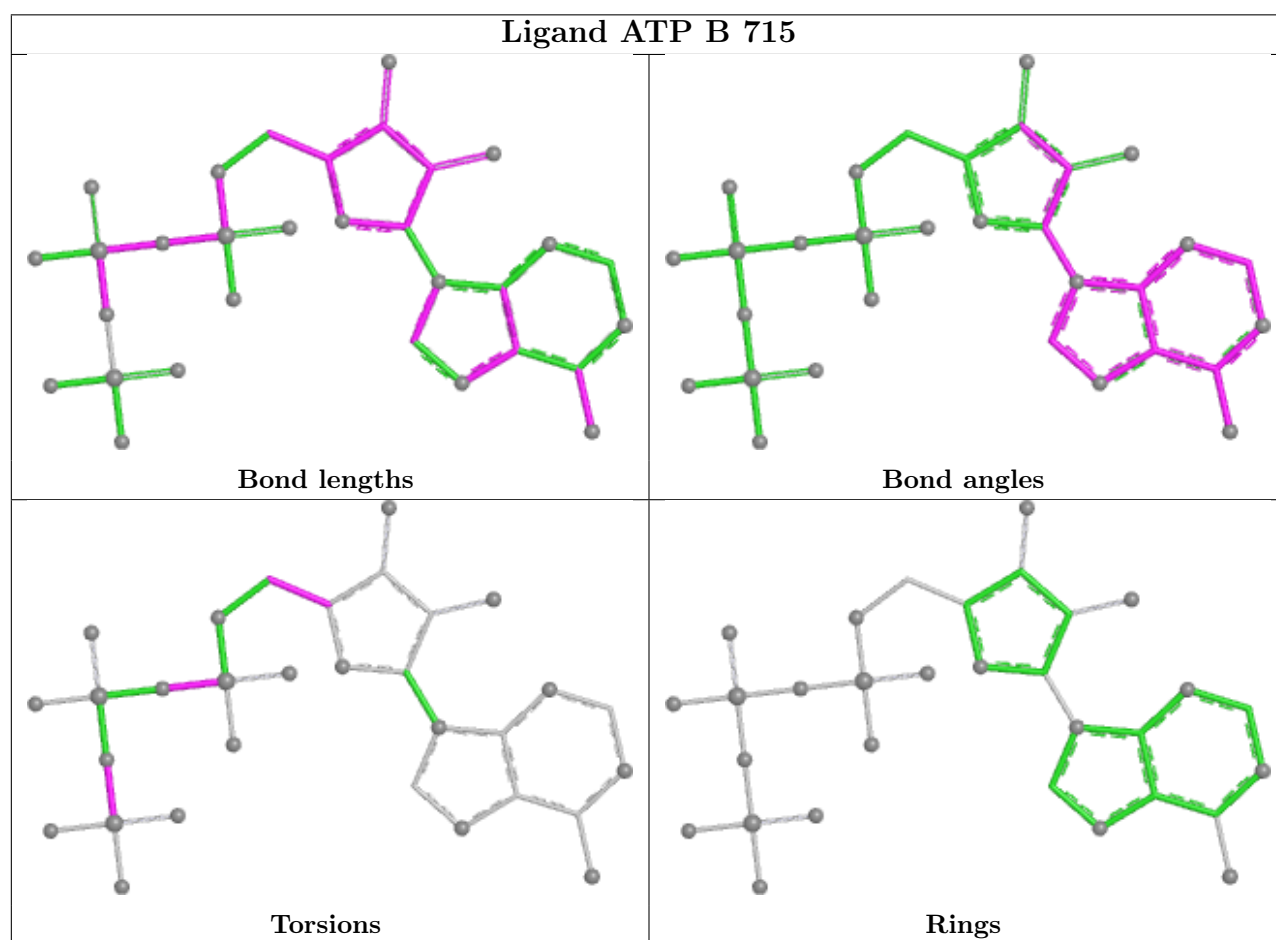
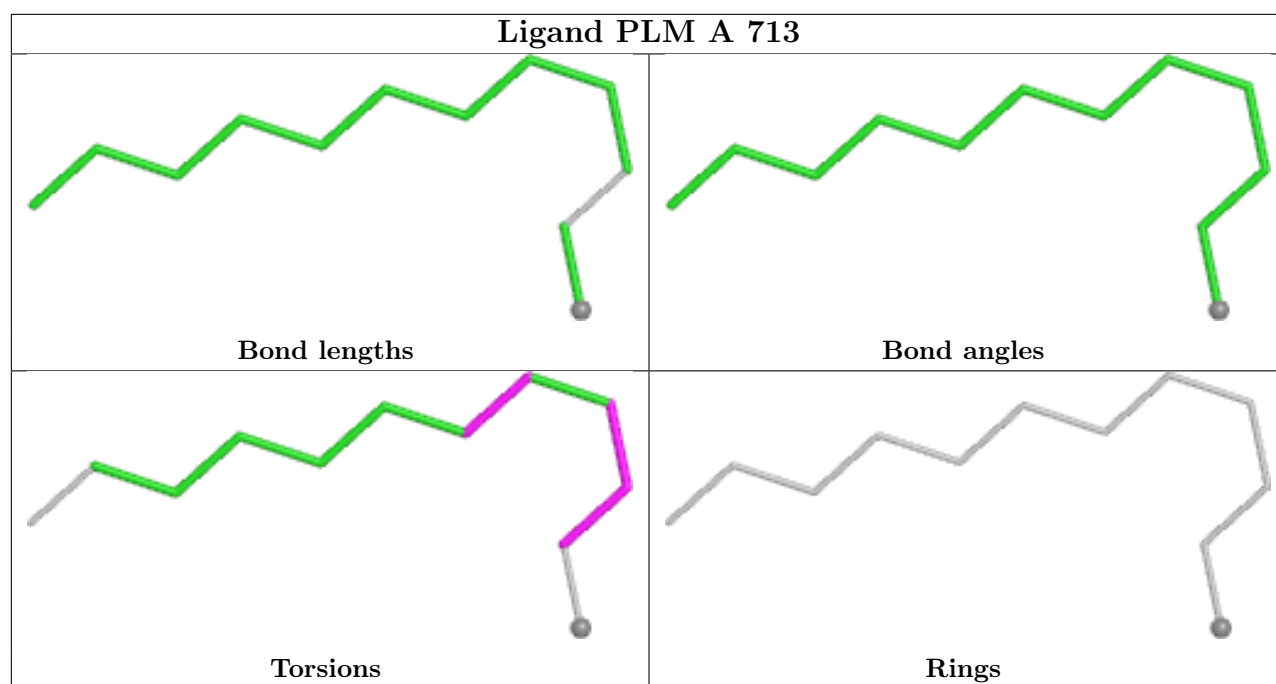
There are no ring outliers.

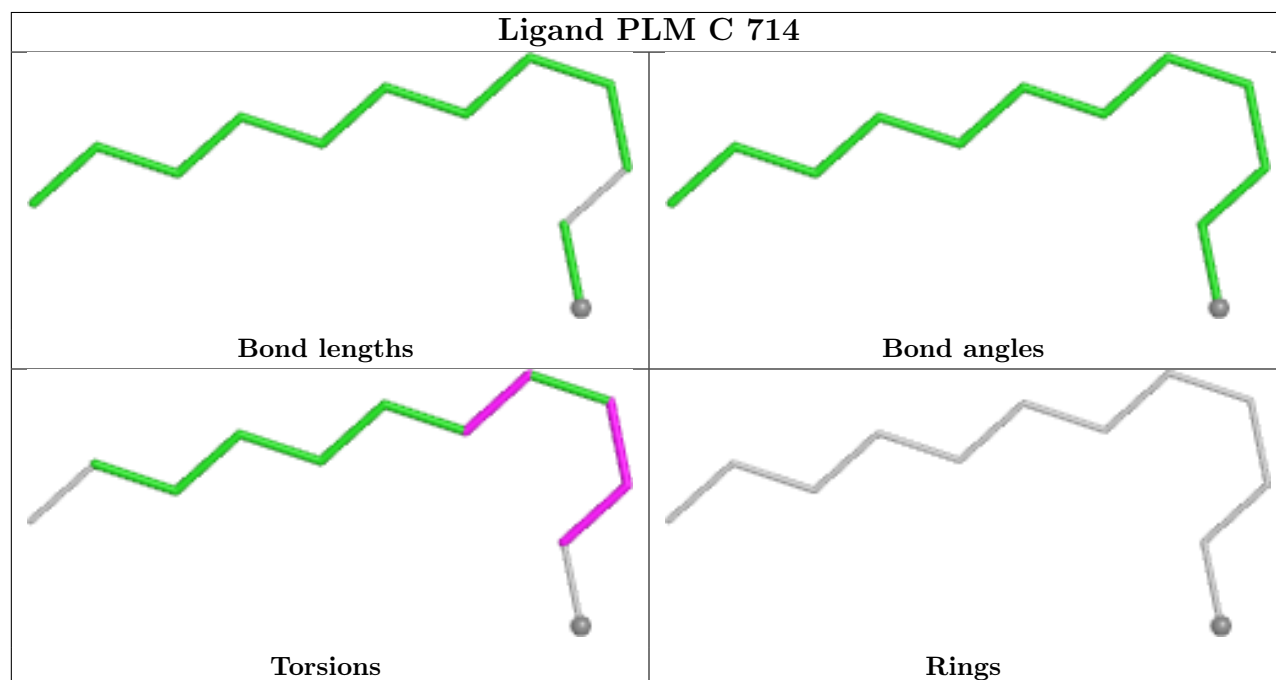
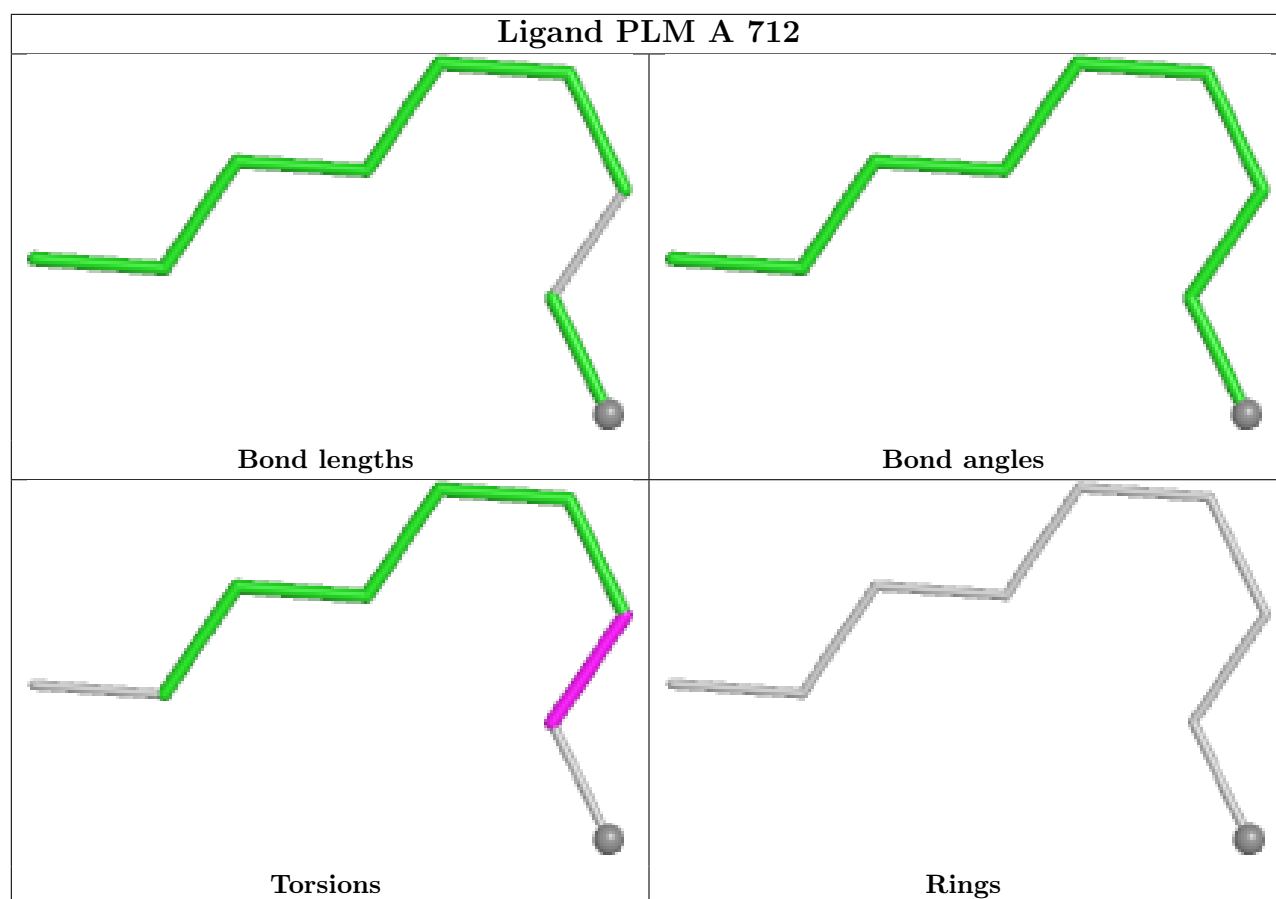
6 monomers are involved in 9 short contacts:

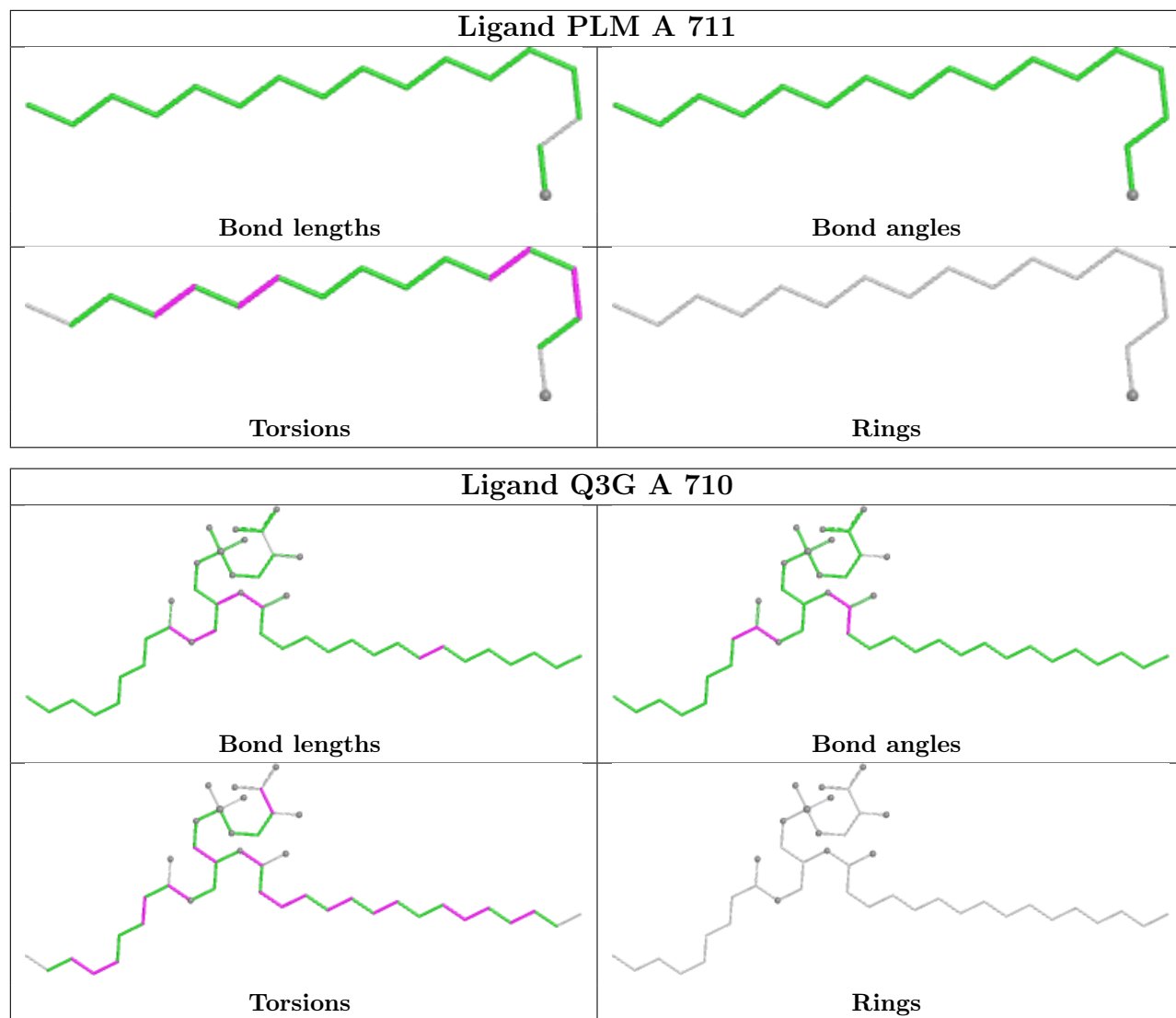
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	710	Q3G	1	0
6	B	710	Q3G	1	0
4	C	704	GDP	2	0
4	B	703	GDP	2	0
4	A	703	GDP	2	0
6	C	711	Q3G	1	0

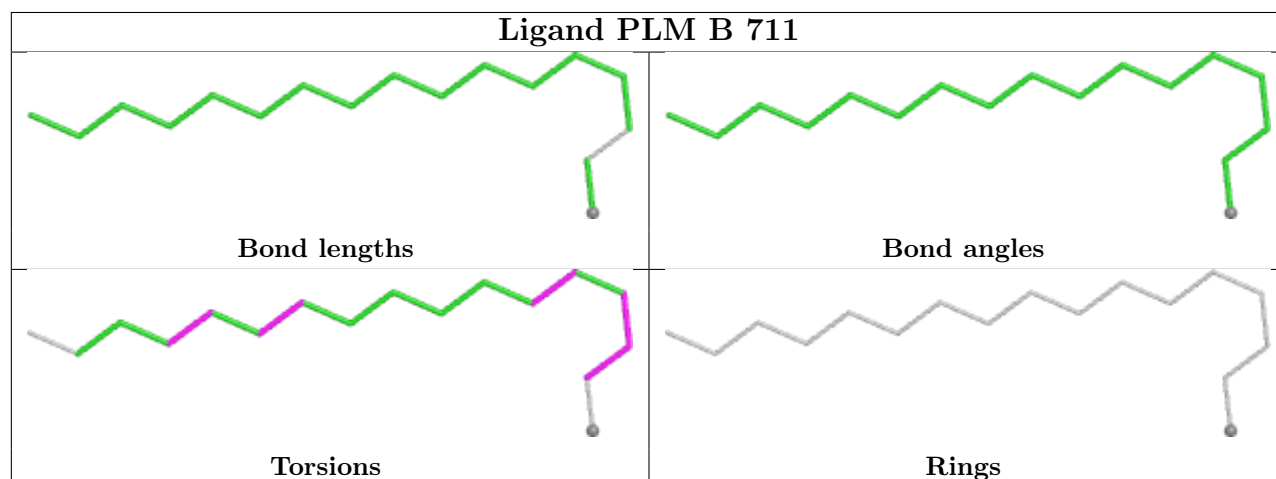
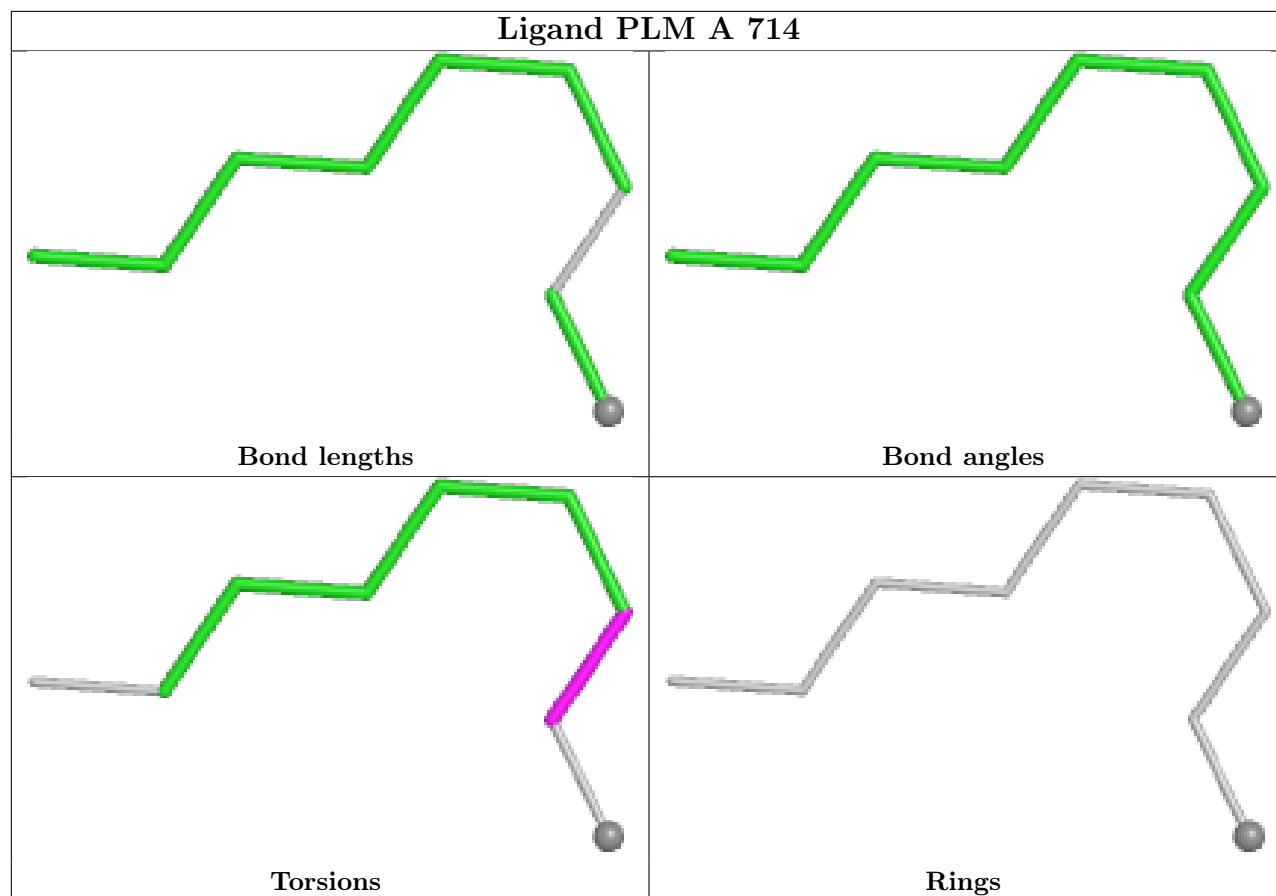
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

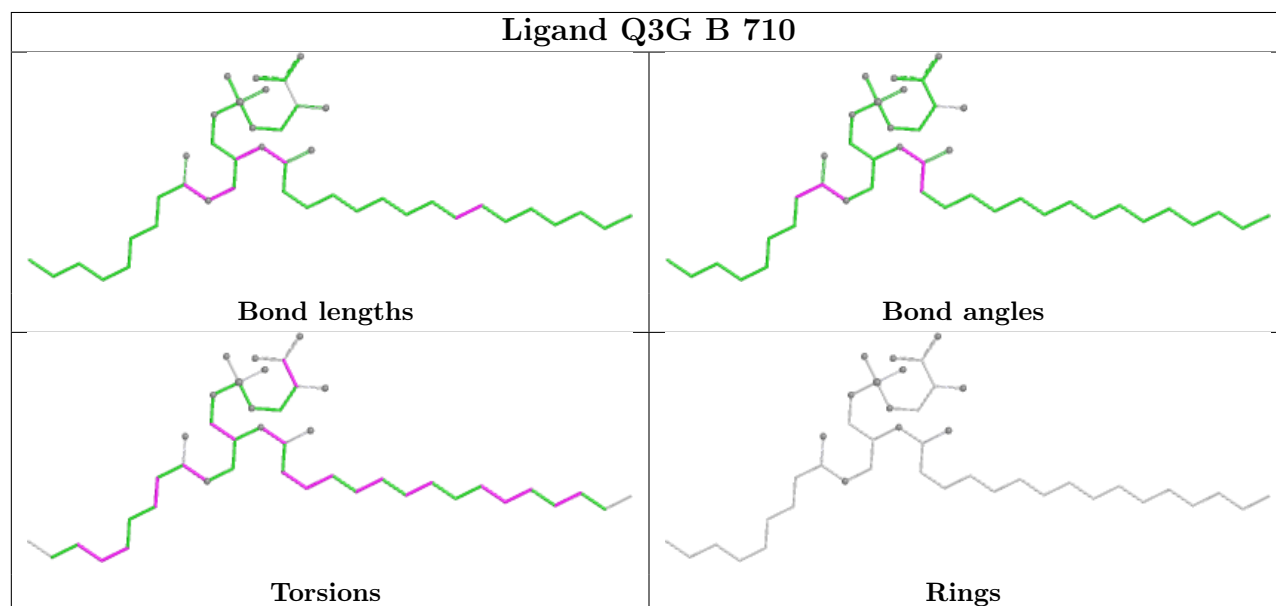
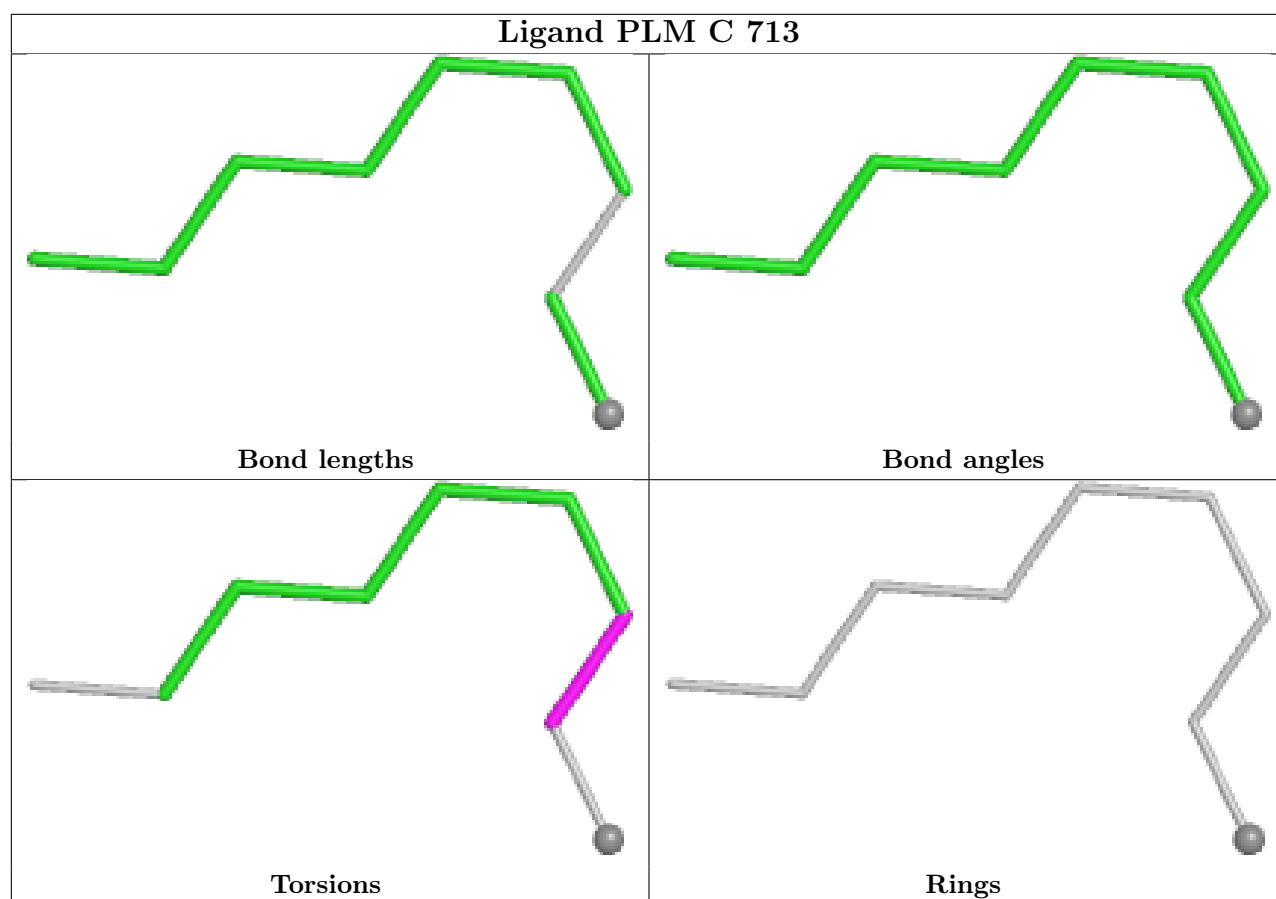


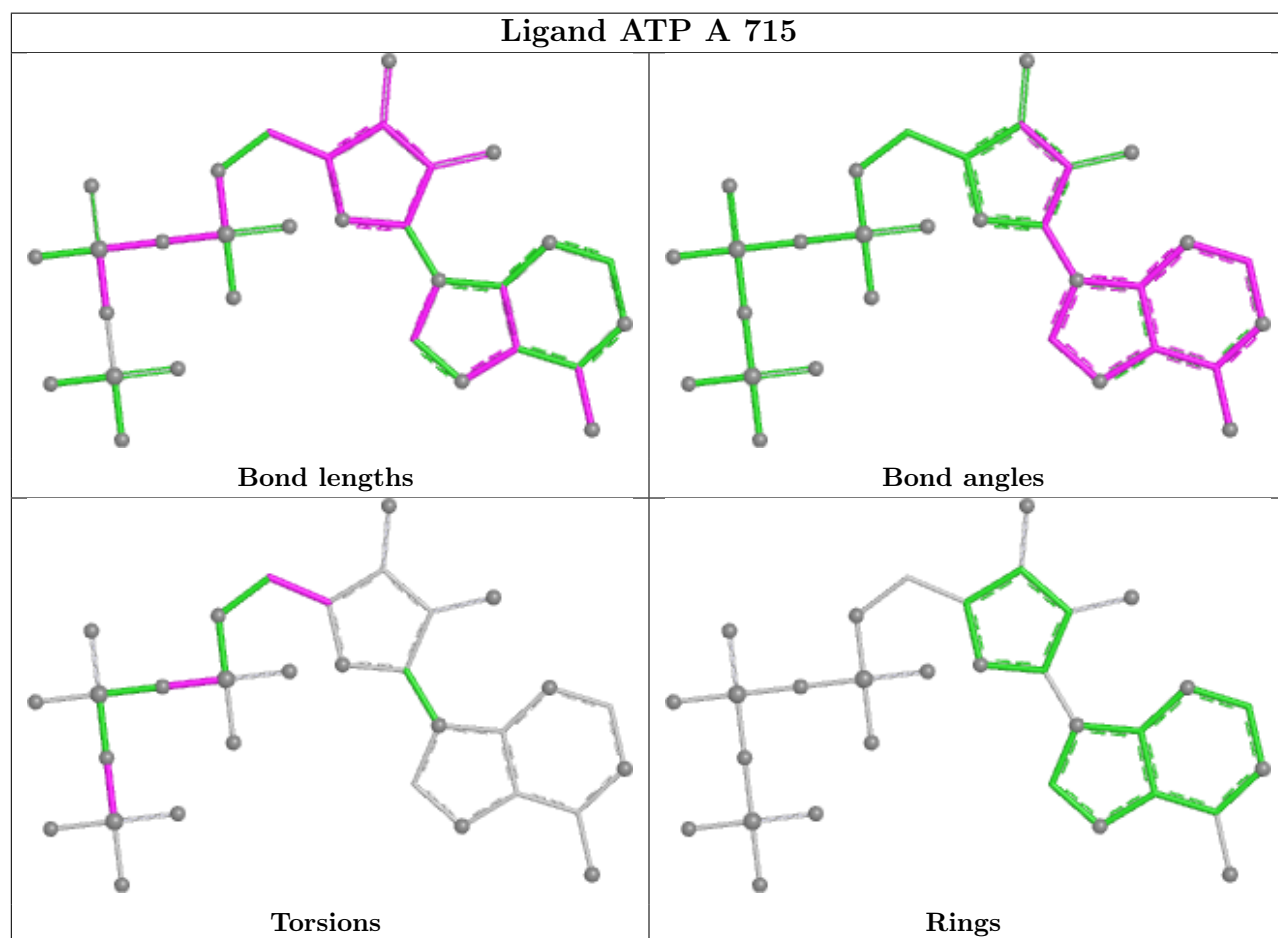
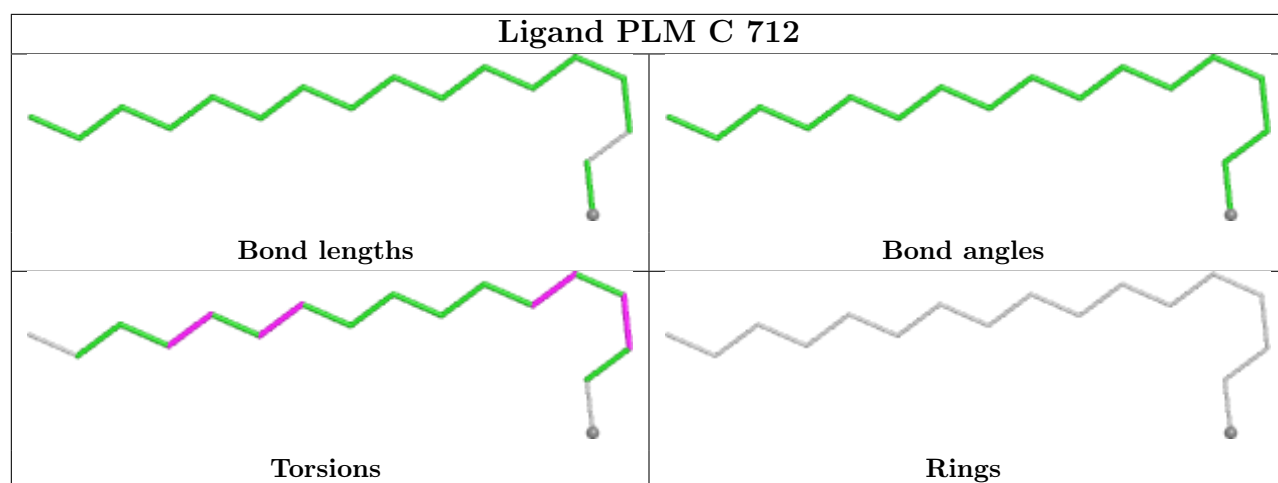


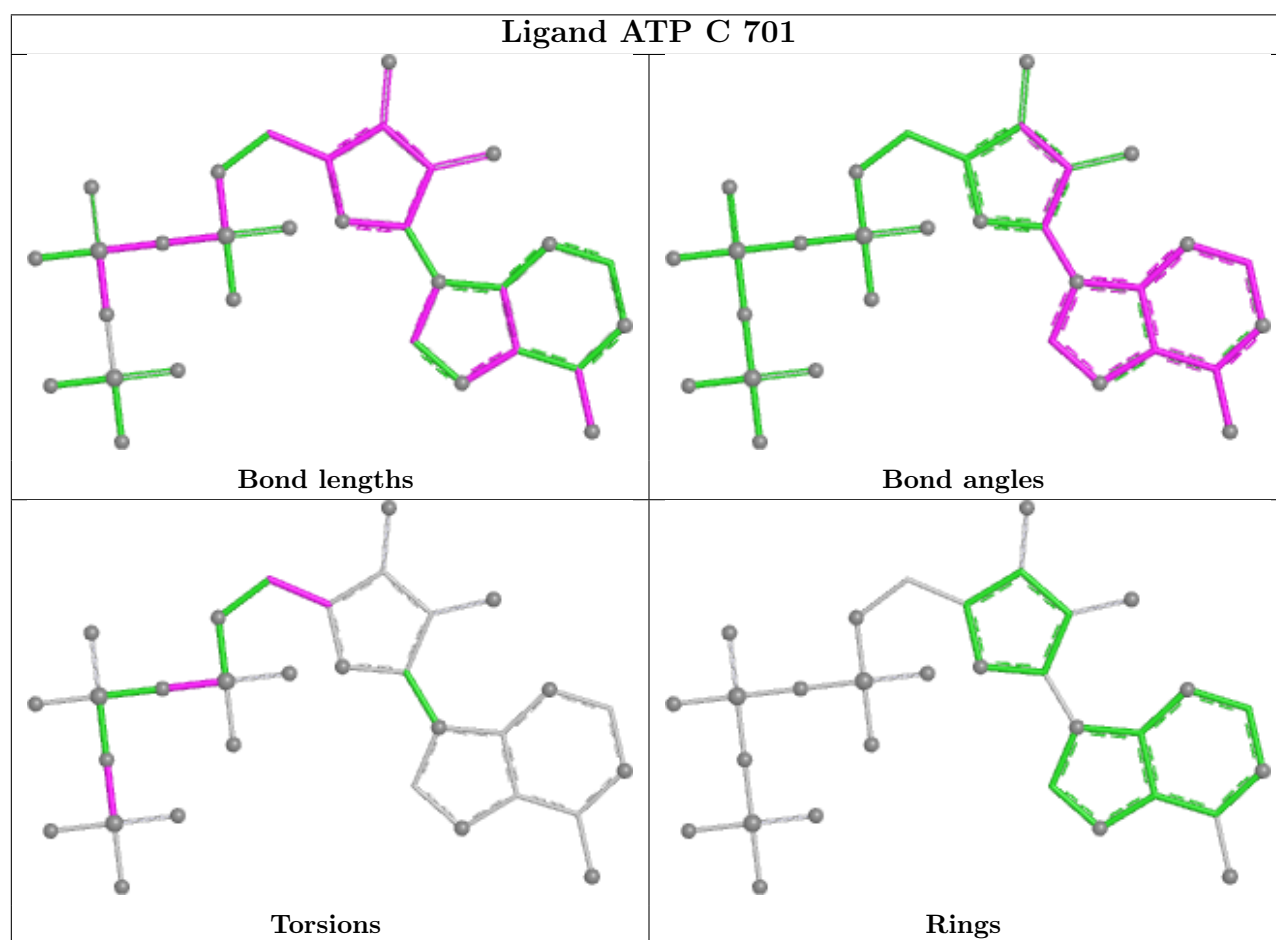
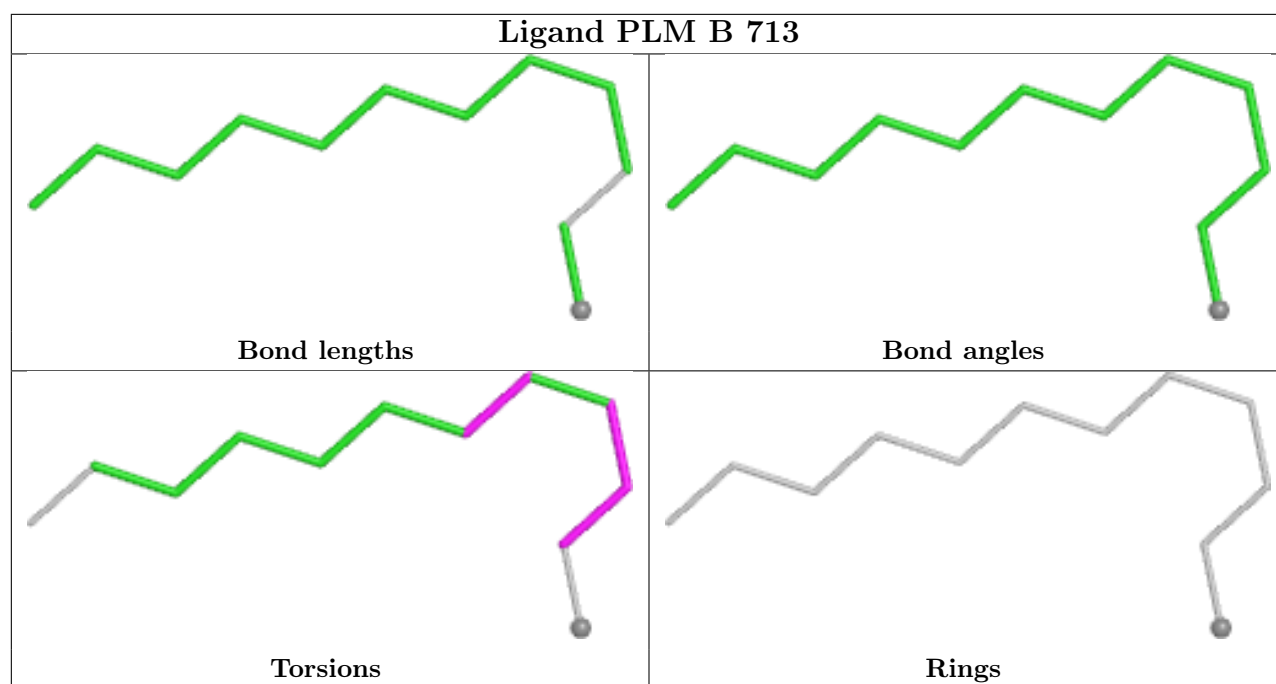


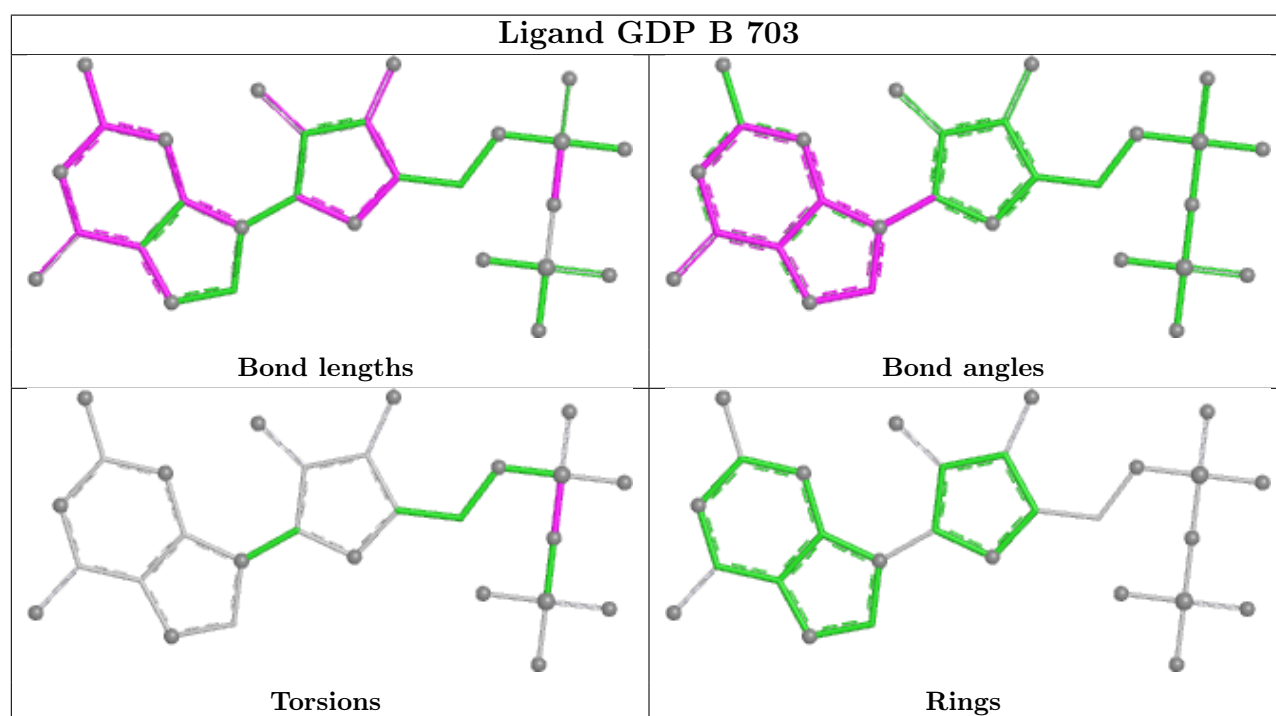
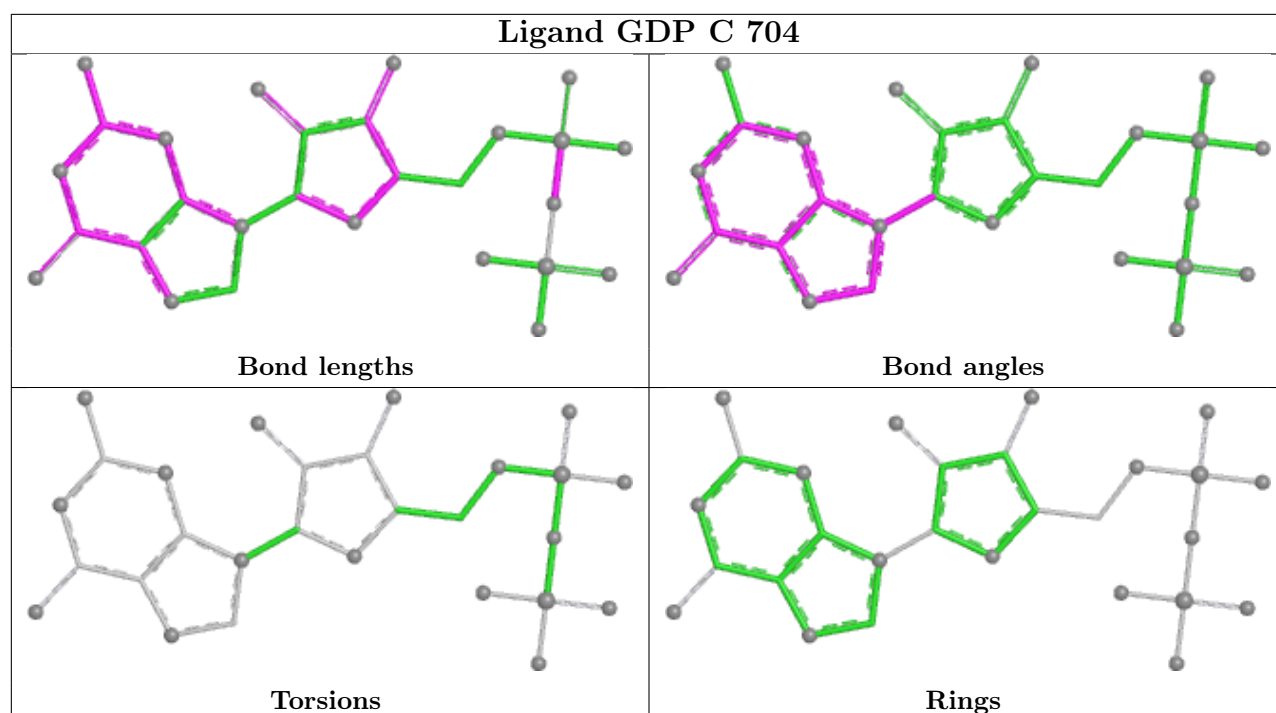


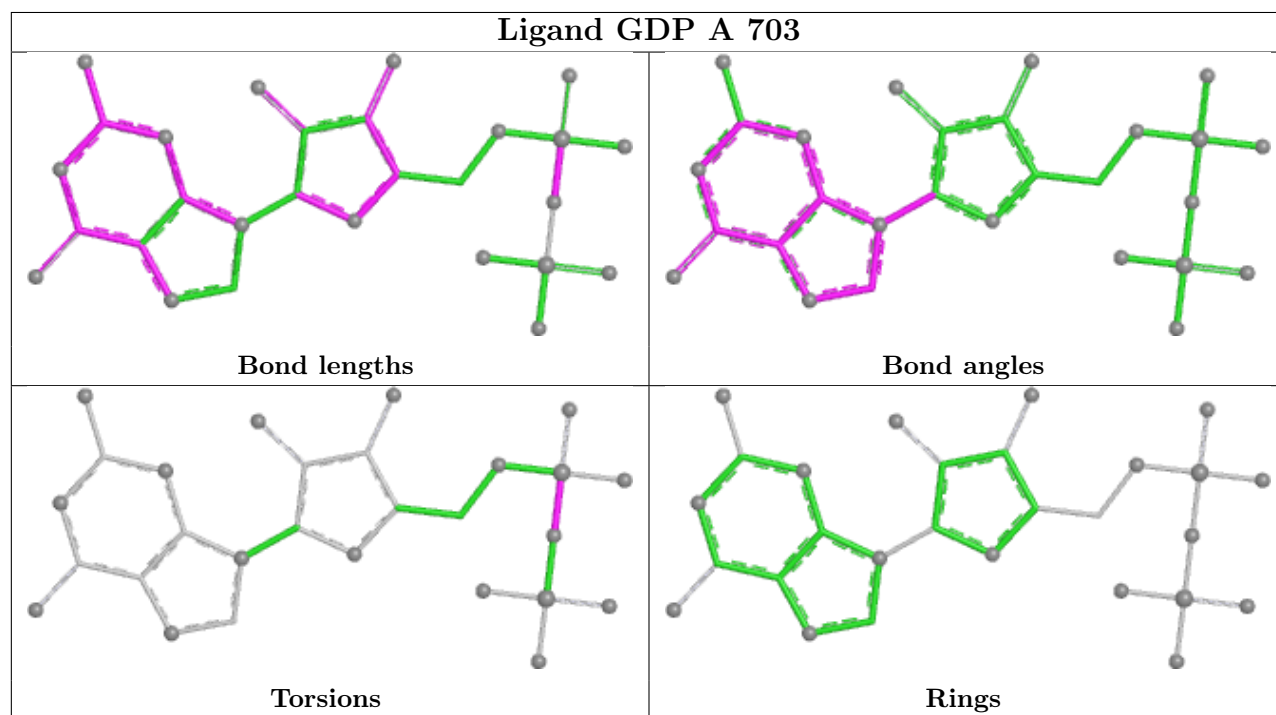
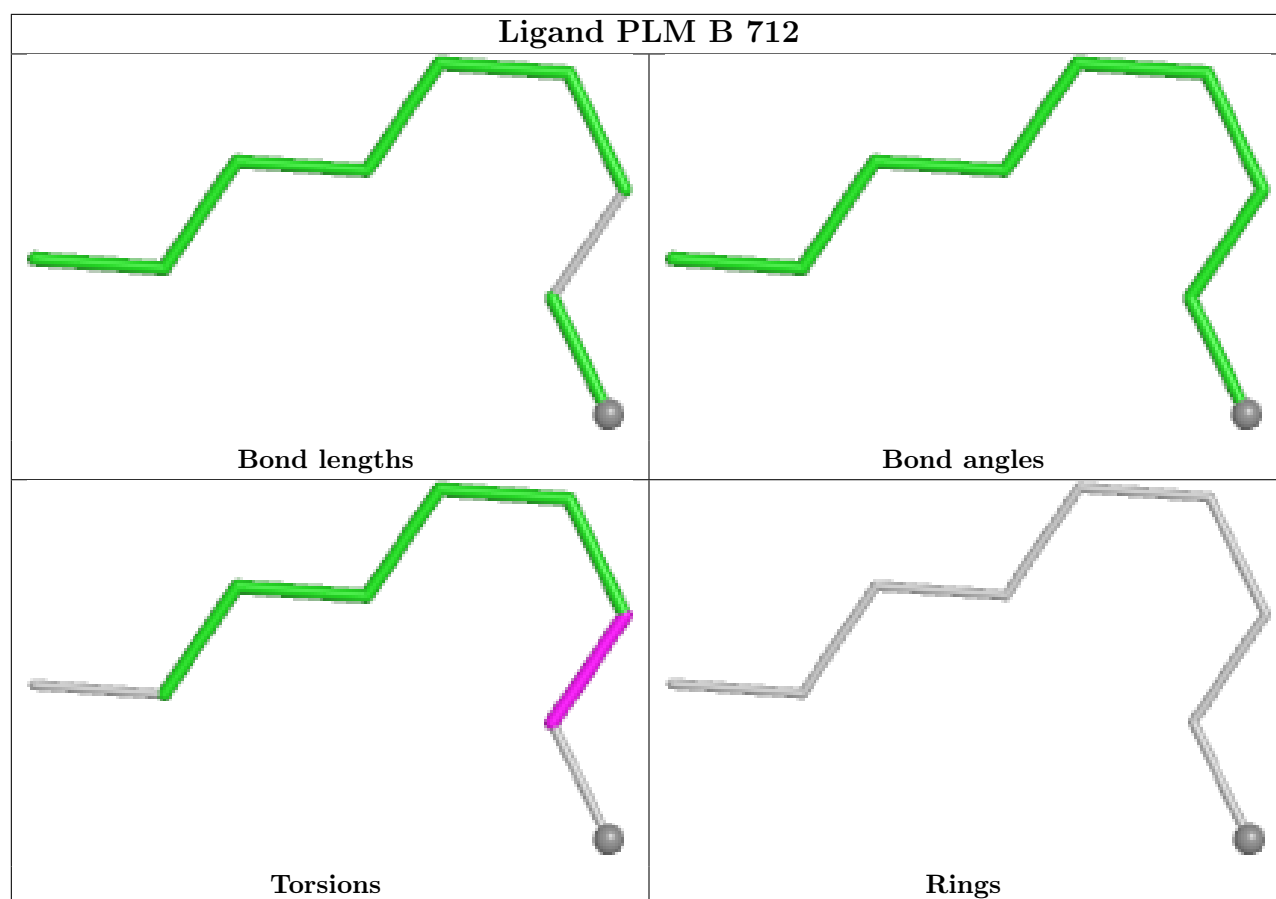


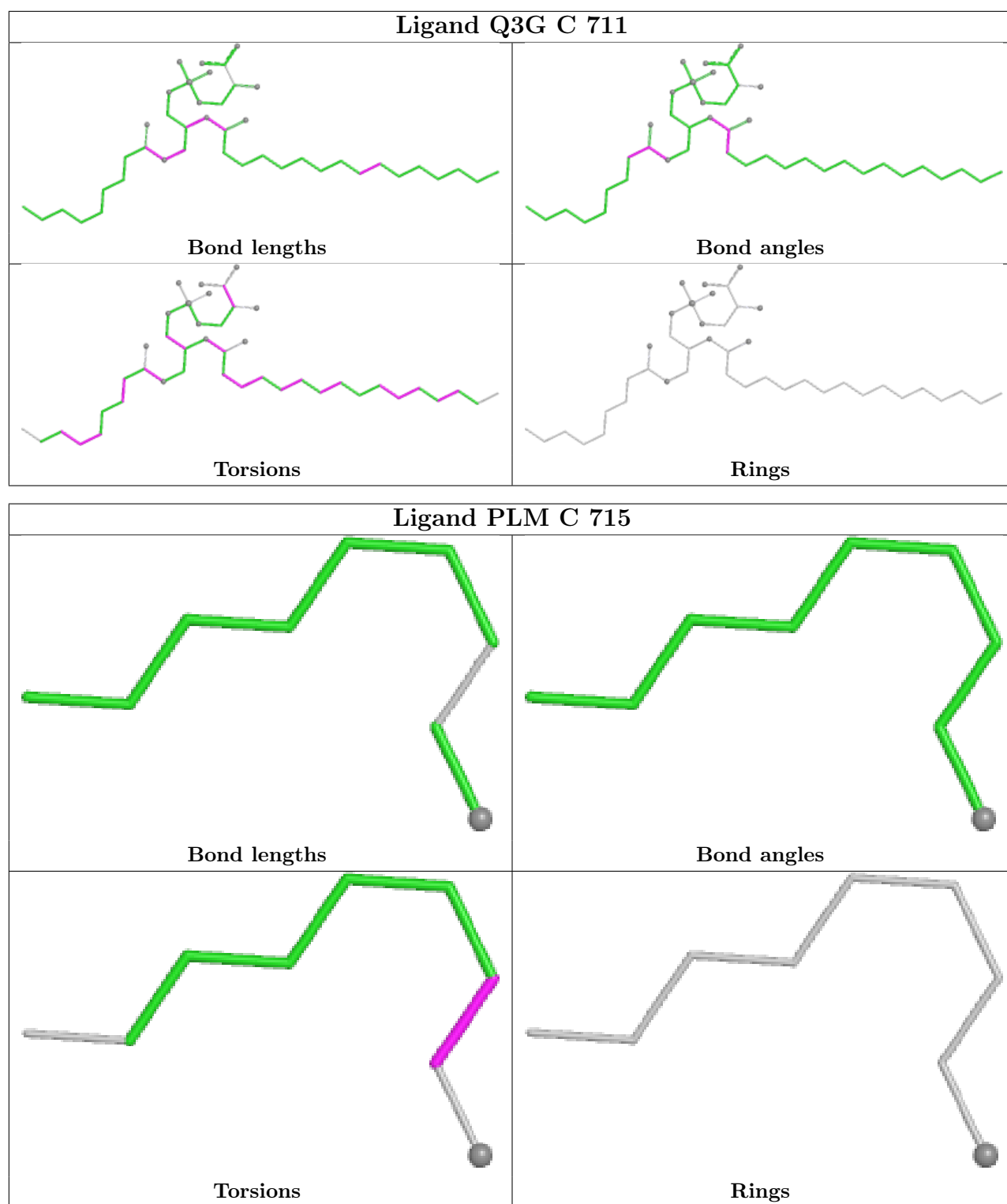












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

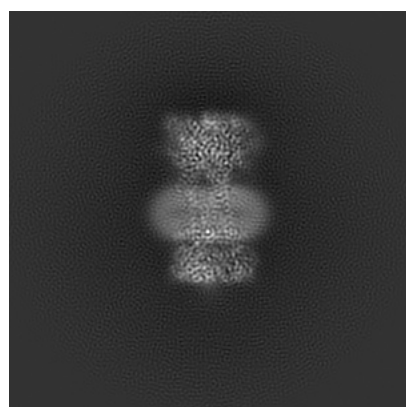
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20703. These allow visual inspection of the internal detail of the map and identification of artifacts.

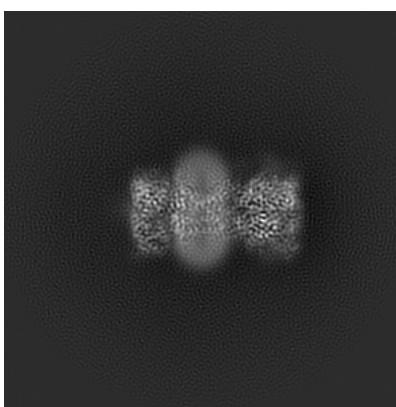
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

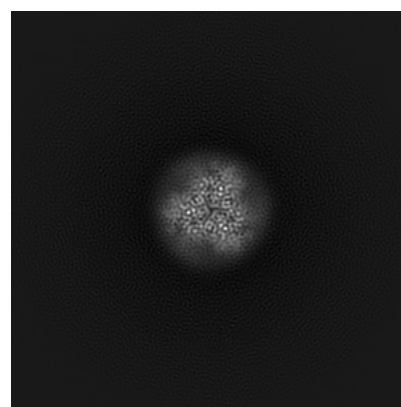
6.1.1 Primary map



X



Y

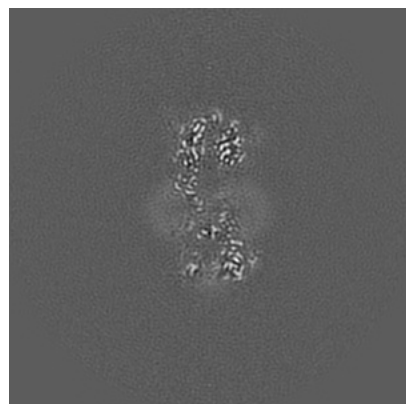


Z

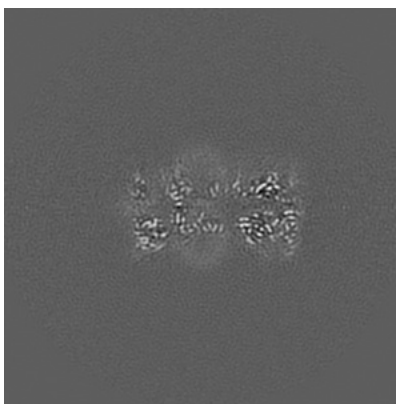
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

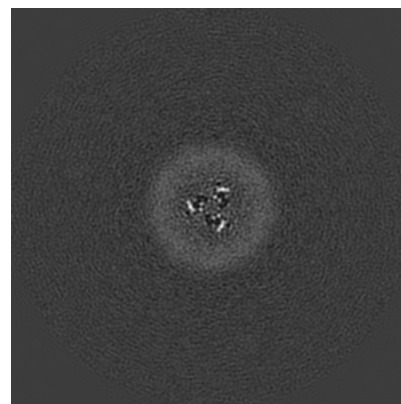
6.2.1 Primary map



X Index: 160



Y Index: 160

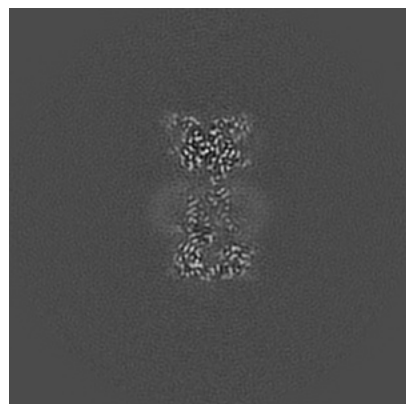


Z Index: 160

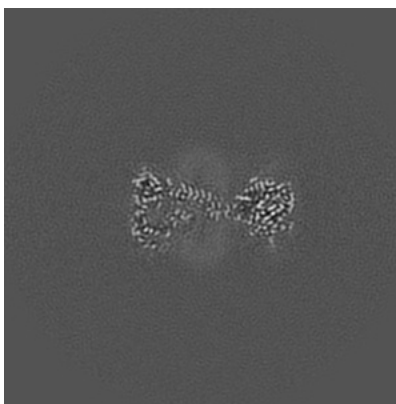
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

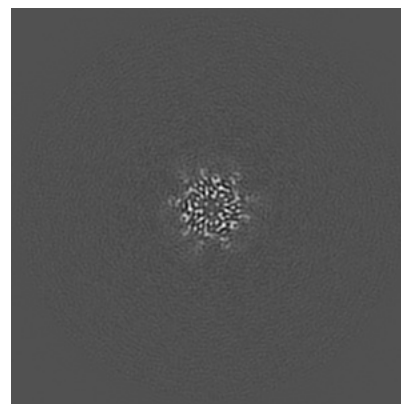
6.3.1 Primary map



X Index: 171



Y Index: 148

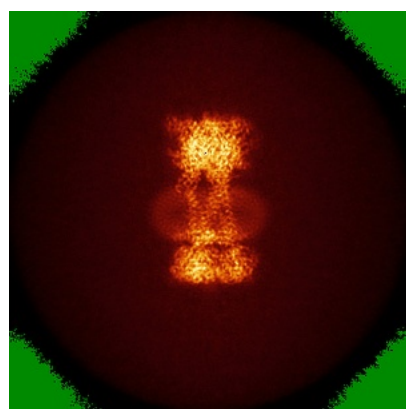


Z Index: 206

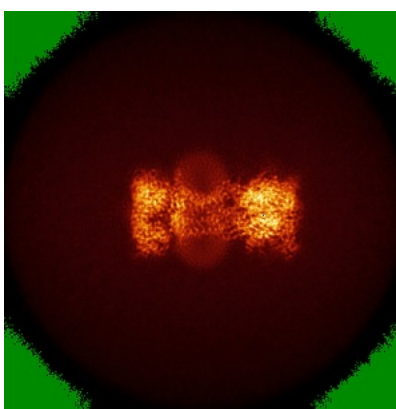
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

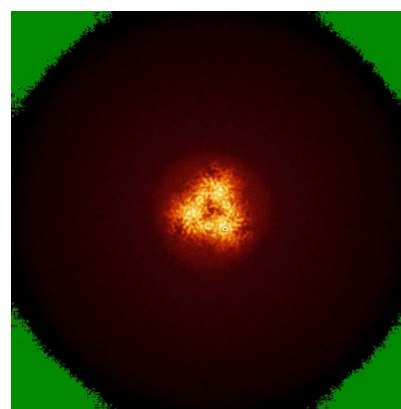
6.4.1 Primary map



X



Y

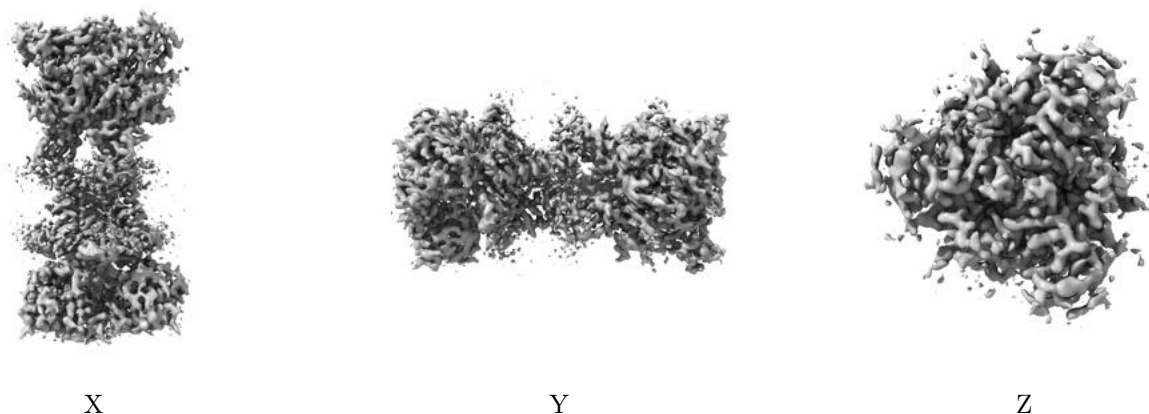


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0209. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

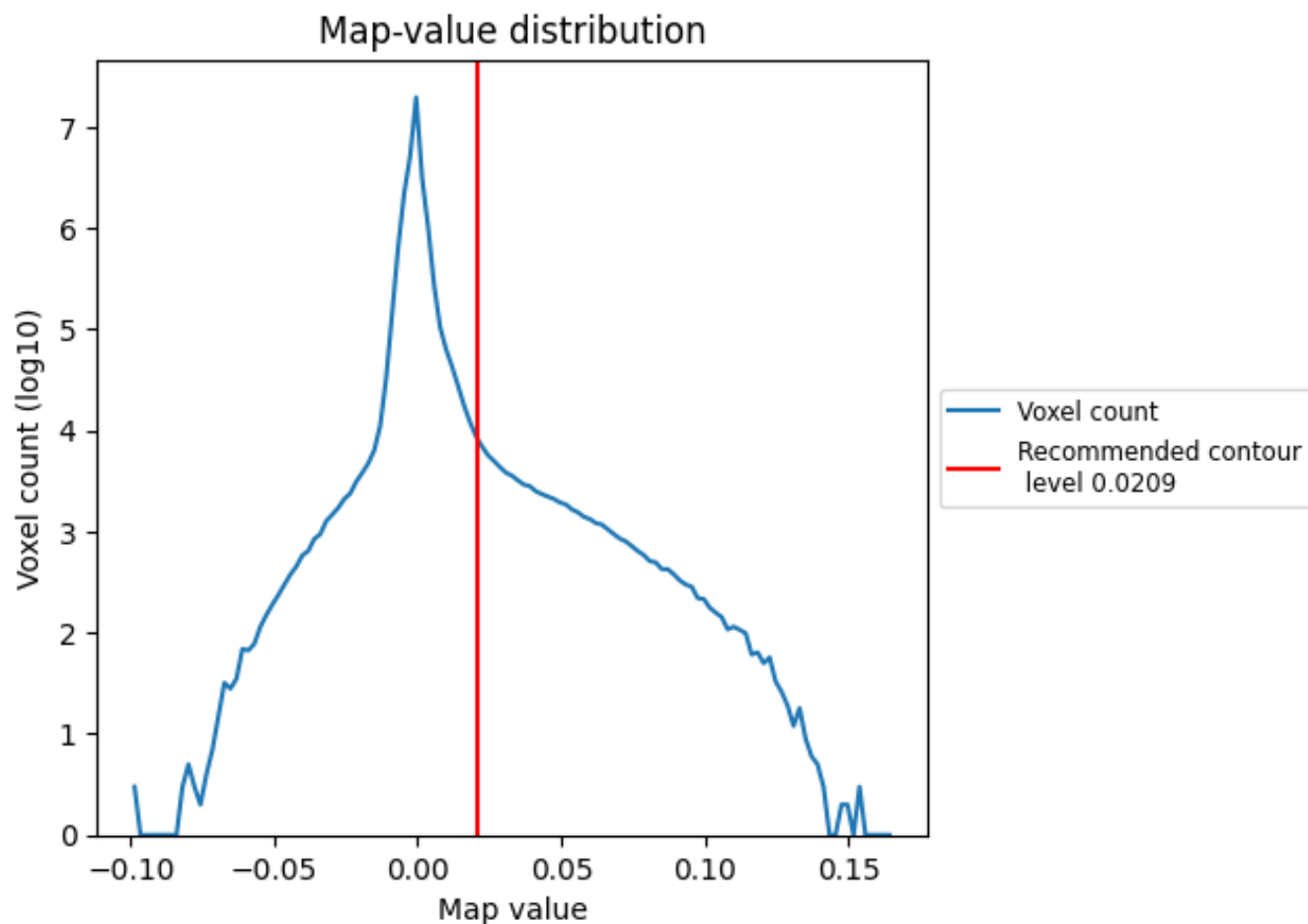
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

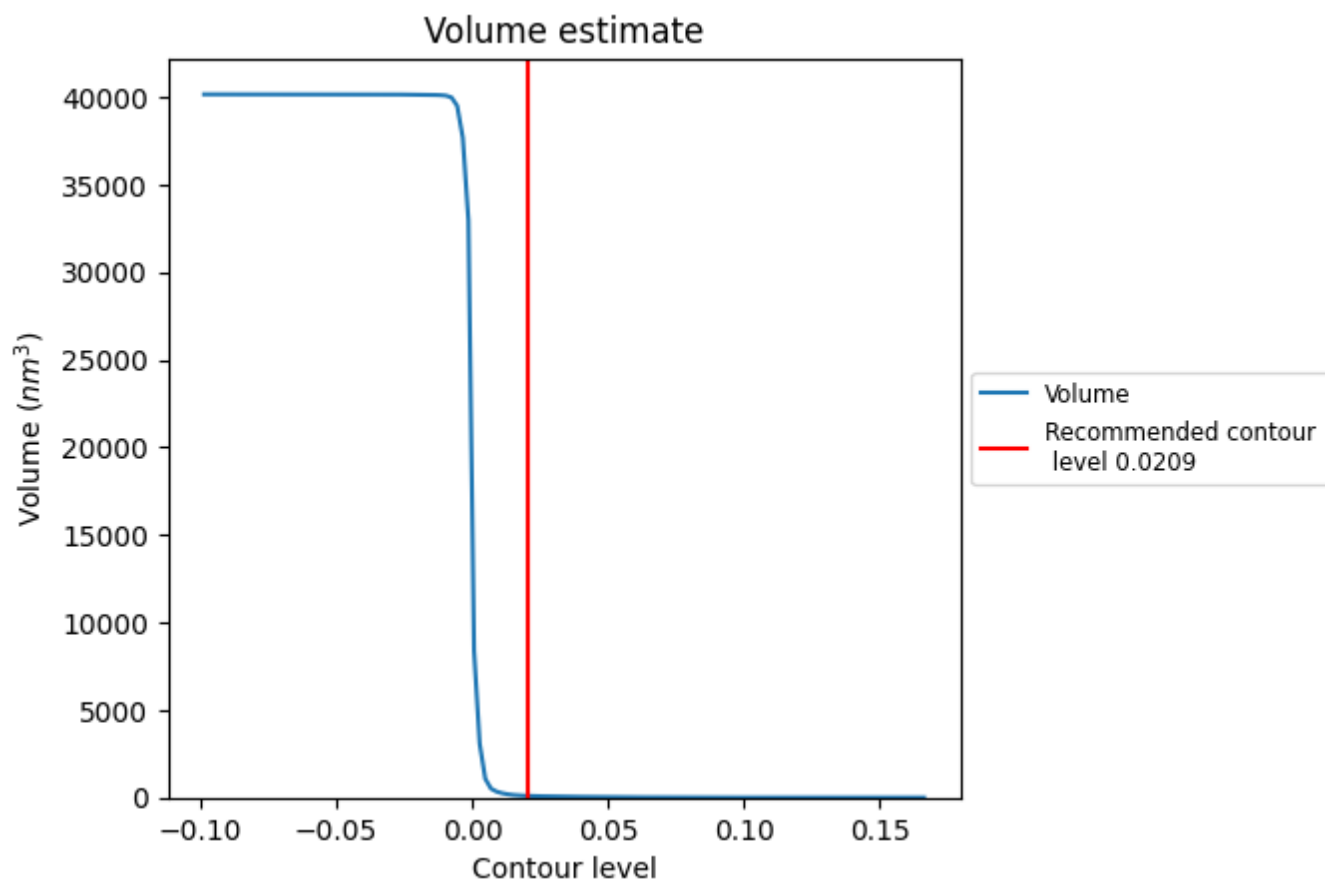
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

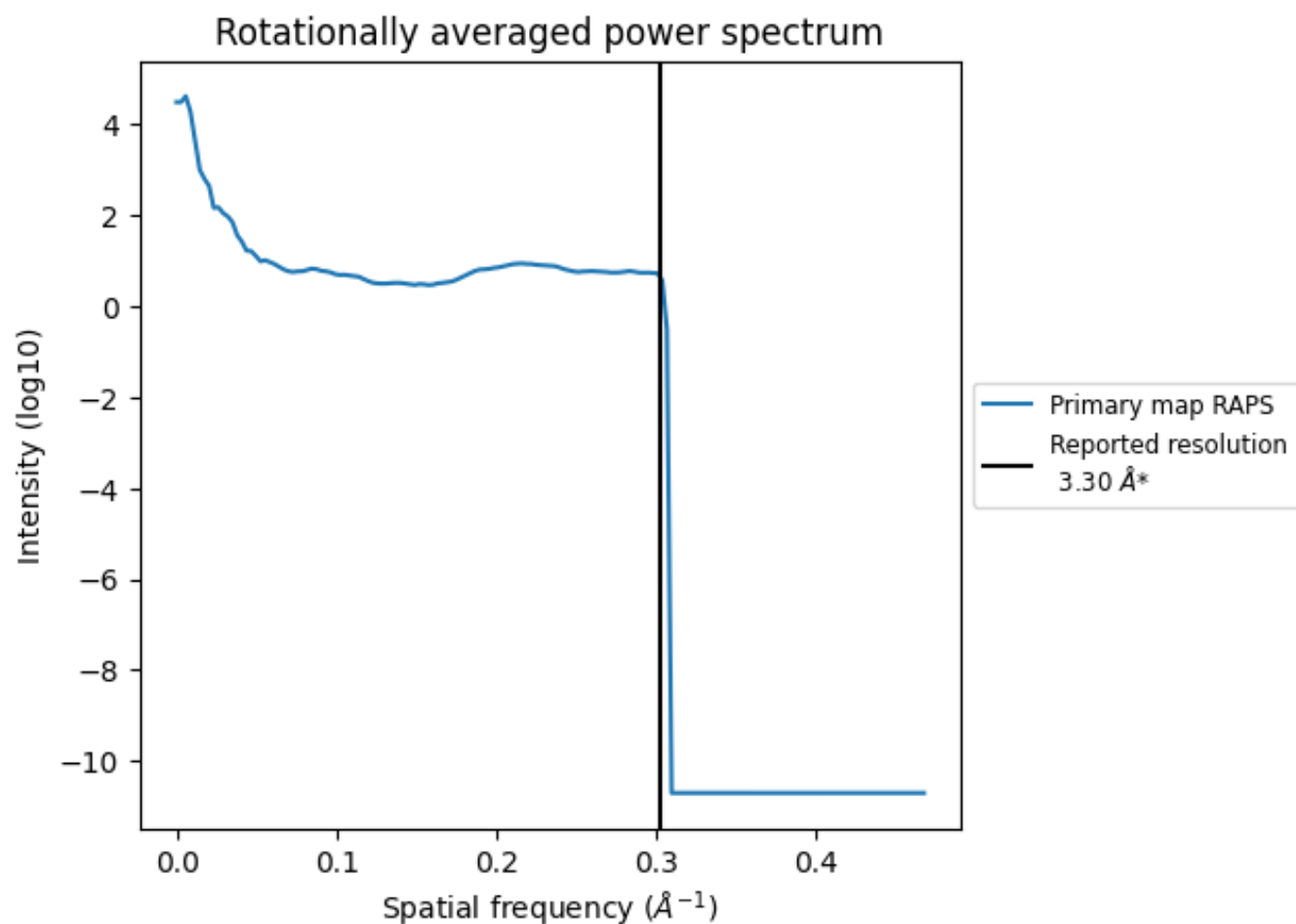
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 94 nm³; this corresponds to an approximate mass of 85 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

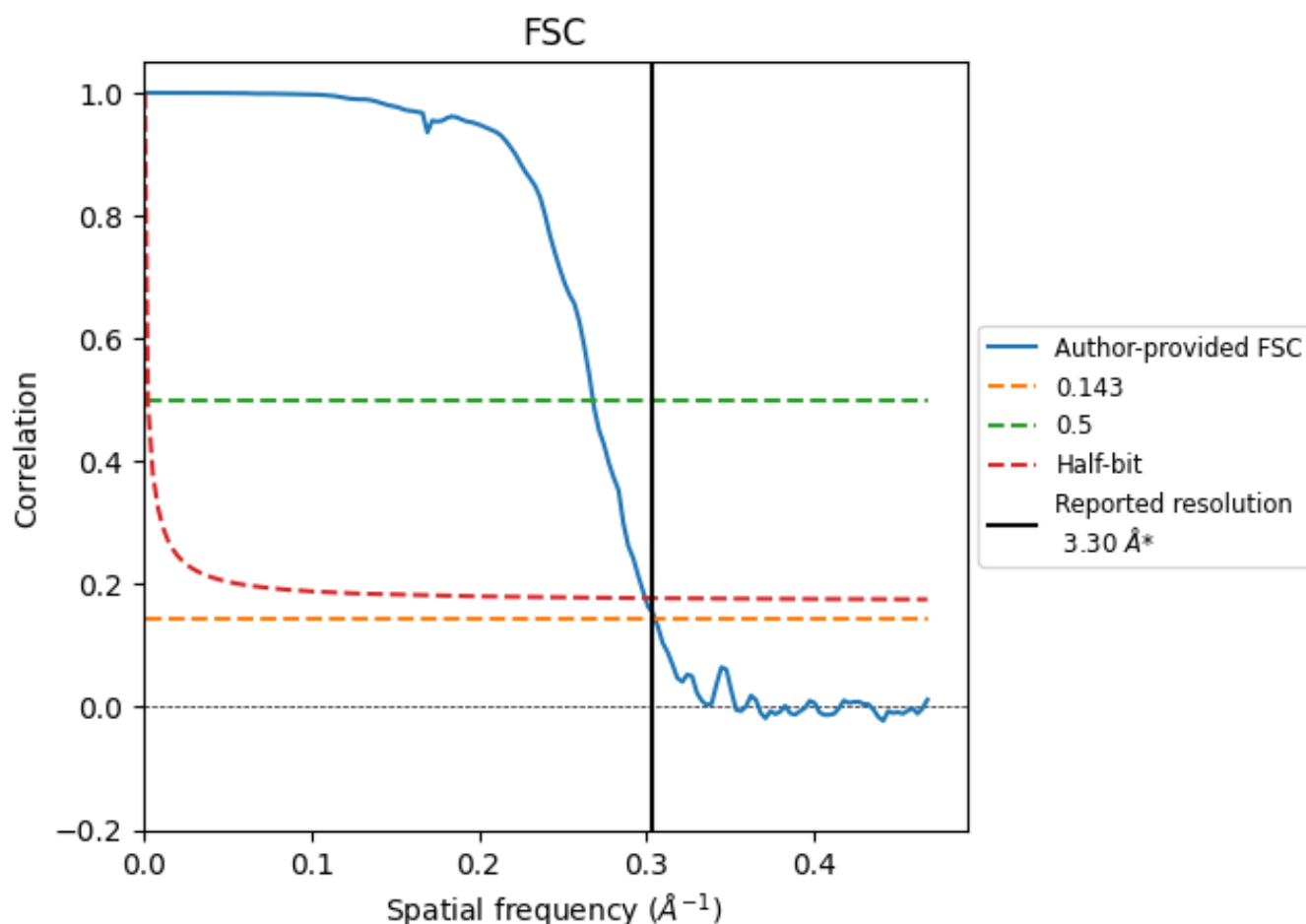


*Reported resolution corresponds to spatial frequency of 0.303 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.28	3.73	3.34
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

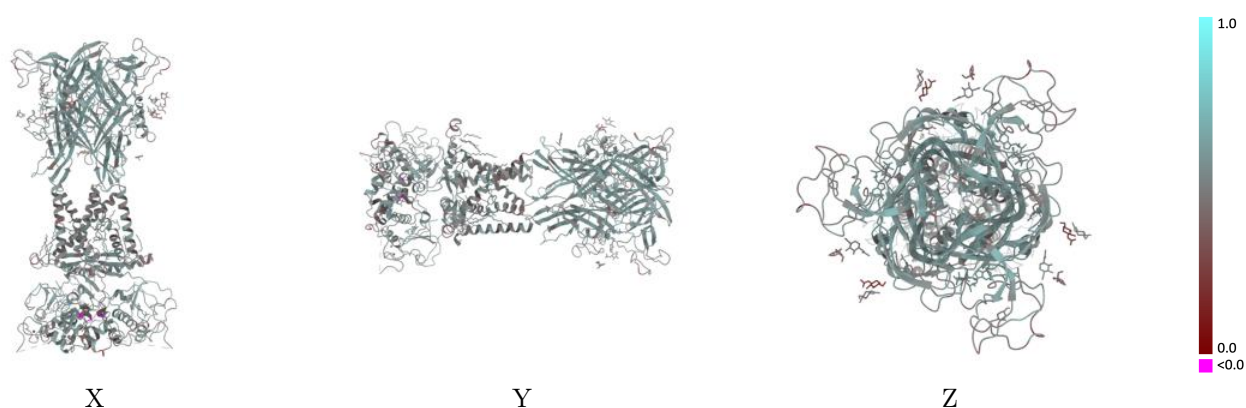
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20703 and PDB model 6U9W. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

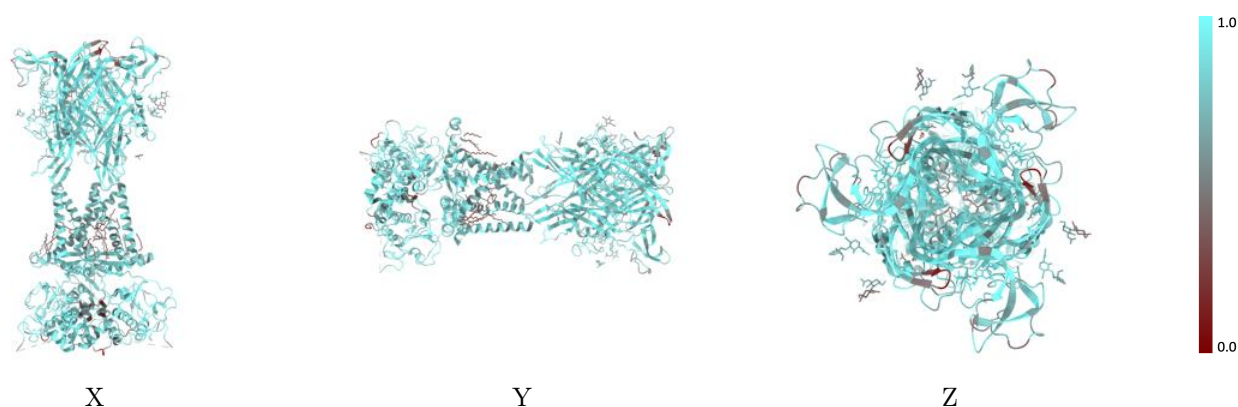
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



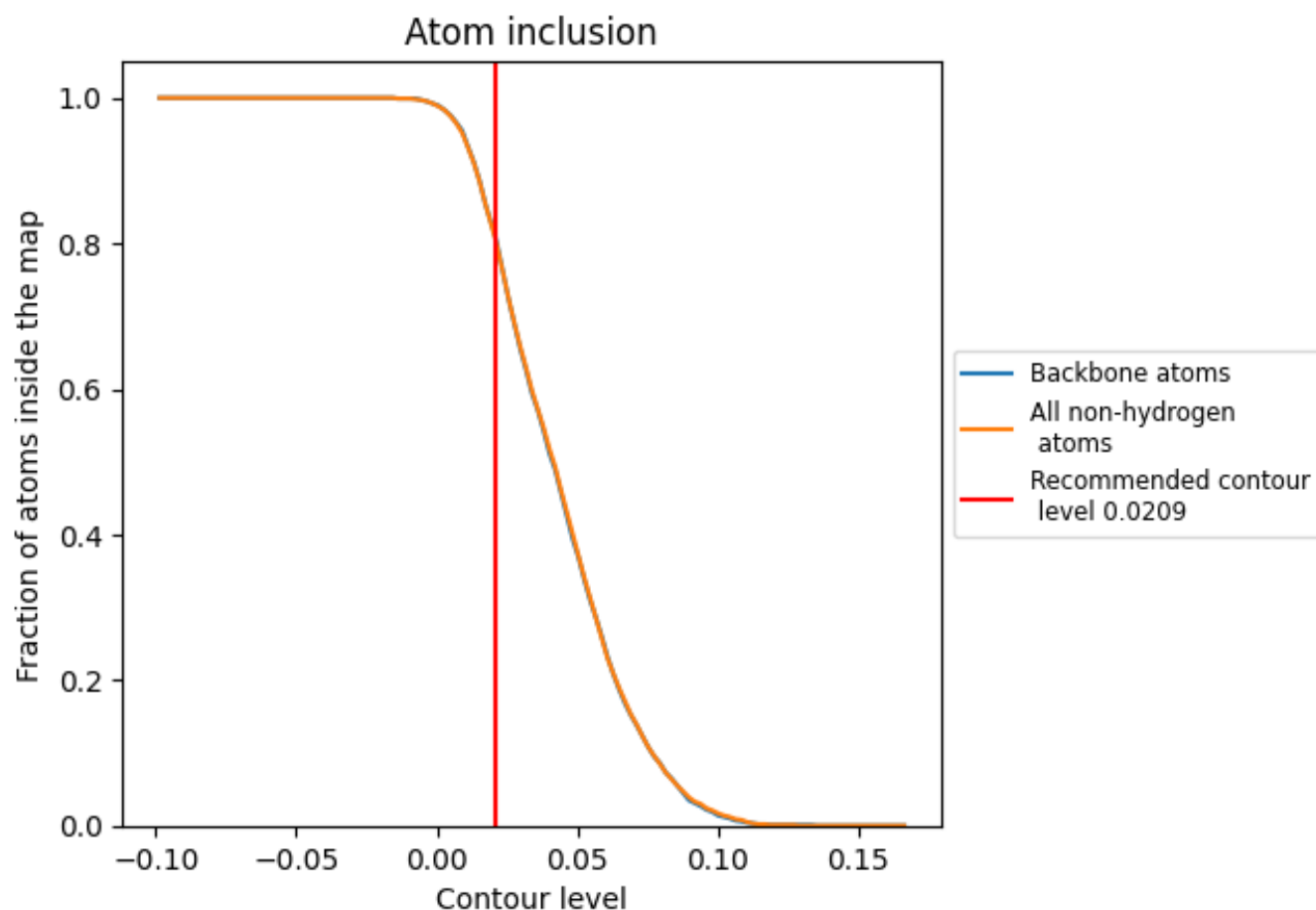
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0209).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0209) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8060	0.5230
A	0.8100	0.5250
B	0.8120	0.5250
C	0.8120	0.5250
D	0.5360	0.3560
E	0.7140	0.4630
F	0.5360	0.3410
G	0.7140	0.4430
H	0.5360	0.3420
I	0.6790	0.4410

1.0

0.0

<0.0