



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:30 AM UTC

PDB ID : 9Z9W / pdb_00009z9w
EMDB ID : EMD-73957
Title : Destabilized open state sheep connexin-50 in DMPC nanodiscs at low pH
Authors : Jarodsky, J.M.; Myers, J.B.; Reichow, S.L.
Deposited on : 2025-11-18
Resolution : 2.20 Å(reported)
Based on initial model : 7jjp

This is a wwPDB EM 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/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:

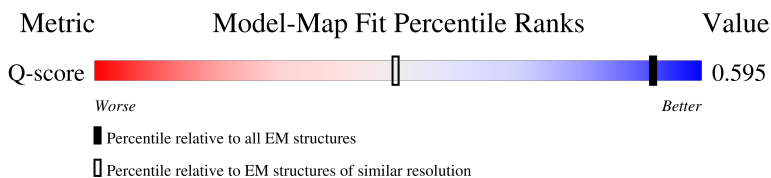
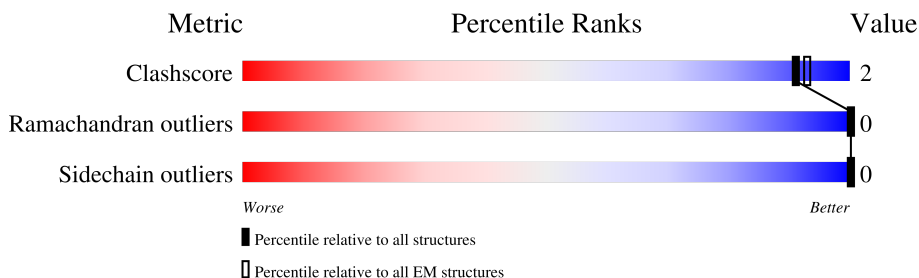
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.20 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	3184 (1.71 - 2.70)

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	440	
1	B	440	
1	C	440	
1	D	440	

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Mol	Chain	Length	Quality of chain
1	E	440	 41% . 58%
1	F	440	 41% . 58%
1	G	440	 41% . 58%
1	H	440	 41% . 58%
1	I	440	 41% . 58%
1	J	440	 41% . 58%
1	K	440	 41% . 58%
1	L	440	 41% . 58%

2 Entry composition

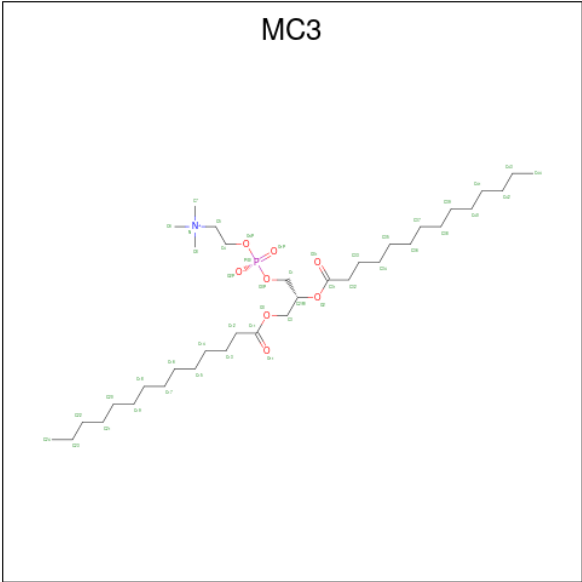
There are 3 unique types of molecules in this entry. The entry contains 45108 atoms, of which 23472 are hydrogens and 0 are deuteriums.

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 Gap junction alpha-8 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	B	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	C	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	D	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	E	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	F	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	G	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	H	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	I	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	J	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	K	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0
1	L	187	Total 3027	C 1004	H 1507	N 247	O 259	S 10	0	0

- Molecule 2 is 1,2-DIMYRISTOYL-RAC-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: MC3) (formula: C₃₆H₇₂NO₈P).



Mol	Chain	Residues	Atoms					AltConf
2	A	1	Total	C	H			0
			33	11	22			
2	A	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	A	1	Total	C	H			0
			30	10	20			
2	A	1	Total	C	H			0
			39	13	26			
2	A	1	Total	C	H			0
			15	5	10			
2	A	1	Total	C	H			0
			33	11	22			
2	A	1	Total	C	H			0
			33	11	22			
2	A	1	Total	C	H			0
			12	4	8			
2	A	1	Total	C	H			0
			33	11	22			
2	A	1	Total	C	H			0
			24	8	16			
2	A	1	Total	C	H			0
			33	11	22			
2	A	1	Total	C	H			0
			21	7	14			
2	A	1	Total	C	H			0
			20	7	13			
2	A	1	Total	C	H			0
			39	13	26			

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Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	H	0
			33	11	22	
2	A	1	Total	C	H	0
			39	13	26	
2	A	1	Total	C	H	0
			36	12	24	
2	A	1	Total	C	H	0
			33	11	22	
2	A	1	Total	C	H	0
			30	10	20	
2	A	1	Total	C	H	0
			24	8	16	
2	A	1	Total	C	H	0
			21	7	14	
2	A	1	Total	C	H	0
			15	5	10	
2	A	1	Total	C	H	0
			15	5	10	
2	A	1	Total	C	H	0
			18	6	12	
2	B	1	Total	C	H	0
			39	13	26	
2	B	1	Total	C	H	0
			33	11	22	
2	B	1	Total	C	H	0
			39	13	26	
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			33	11	22	
2	B	1	Total	C	H	0
			30	10	20	
2	B	1	Total	C	H	0
			24	8	16	
2	B	1	Total	C	H	0
			21	7	14	
2	B	1	Total	C	H	0
			15	5	10	
2	B	1	Total	C	H	0
			15	5	10	
2	B	1	Total	C	H	0
			18	6	12	

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Mol	Chain	Residues	Atoms					AltConf
2	B	1	Total 33	C 11	H 22			0
2	B	1	Total 55	C 17	H 30	O 7	P 1	0
2	B	1	Total 30	C 10	H 20			0
2	B	1	Total 39	C 13	H 26			0
2	B	1	Total 15	C 5	H 10			0
2	B	1	Total 33	C 11	H 22			0
2	B	1	Total 33	C 11	H 22			0
2	B	1	Total 12	C 4	H 8			0
2	B	1	Total 33	C 11	H 22			0
2	B	1	Total 24	C 8	H 16			0
2	B	1	Total 33	C 11	H 22			0
2	B	1	Total 21	C 7	H 14			0
2	B	1	Total 20	C 7	H 13			0
2	C	1	Total 39	C 13	H 26			0
2	C	1	Total 33	C 11	H 22			0
2	C	1	Total 39	C 13	H 26			0
2	C	1	Total 36	C 12	H 24			0
2	C	1	Total 33	C 11	H 22			0
2	C	1	Total 30	C 10	H 20			0
2	C	1	Total 24	C 8	H 16			0
2	C	1	Total 21	C 7	H 14			0

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Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	H			0
			15	5	10			
2	C	1	Total	C	H			0
			15	5	10			
2	C	1	Total	C	H			0
			18	6	12			
2	C	1	Total	C	H			0
			33	11	22			
2	C	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	C	1	Total	C	H			0
			30	10	20			
2	C	1	Total	C	H			0
			39	13	26			
2	C	1	Total	C	H			0
			15	5	10			
2	C	1	Total	C	H			0
			33	11	22			
2	C	1	Total	C	H			0
			33	11	22			
2	C	1	Total	C	H			0
			12	4	8			
2	C	1	Total	C	H			0
			33	11	22			
2	C	1	Total	C	H			0
			24	8	16			
2	C	1	Total	C	H			0
			33	11	22			
2	C	1	Total	C	H			0
			21	7	14			
2	C	1	Total	C	H			0
			20	7	13			
2	D	1	Total	C	H			0
			39	13	26			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			39	13	26			
2	D	1	Total	C	H			0
			36	12	24			
2	D	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	D	1	Total	C	H			0
			30	10	20			
2	D	1	Total	C	H			0
			24	8	16			
2	D	1	Total	C	H			0
			21	7	14			
2	D	1	Total	C	H			0
			15	5	10			
2	D	1	Total	C	H			0
			15	5	10			
2	D	1	Total	C	H			0
			18	6	12			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	D	1	Total	C	H			0
			30	10	20			
2	D	1	Total	C	H			0
			39	13	26			
2	D	1	Total	C	H			0
			15	5	10			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			12	4	8			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			24	8	16			
2	D	1	Total	C	H			0
			33	11	22			
2	D	1	Total	C	H			0
			21	7	14			
2	D	1	Total	C	H			0
			20	7	13			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			36	12	24			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			30	10	20			
2	E	1	Total	C	H			0
			24	8	16			
2	E	1	Total	C	H			0
			21	7	14			
2	E	1	Total	C	H			0
			15	5	10			
2	E	1	Total	C	H			0
			15	5	10			
2	E	1	Total	C	H			0
			18	6	12			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	E	1	Total	C	H			0
			30	10	20			
2	E	1	Total	C	H			0
			39	13	26			
2	E	1	Total	C	H			0
			15	5	10			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			12	4	8			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			24	8	16			
2	E	1	Total	C	H			0
			33	11	22			
2	E	1	Total	C	H			0
			21	7	14			

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Mol	Chain	Residues	Atoms					AltConf
2	E	1	Total	C	H			0
			20	7	13			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			36	12	24			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			30	10	20			
2	F	1	Total	C	H			0
			24	8	16			
2	F	1	Total	C	H			0
			21	7	14			
2	F	1	Total	C	H			0
			15	5	10			
2	F	1	Total	C	H			0
			15	5	10			
2	F	1	Total	C	H			0
			18	6	12			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	F	1	Total	C	H			0
			30	10	20			
2	F	1	Total	C	H			0
			39	13	26			
2	F	1	Total	C	H			0
			15	5	10			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			12	4	8			
2	F	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	F	1	Total	C	H			0
			24	8	16			
2	F	1	Total	C	H			0
			33	11	22			
2	F	1	Total	C	H			0
			21	7	14			
2	F	1	Total	C	H			0
			20	7	13			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	G	1	Total	C	H			0
			30	10	20			
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			15	5	10			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			12	4	8			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			24	8	16			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			21	7	14			
2	G	1	Total	C	H			0
			20	7	13			
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			33	11	22			
2	G	1	Total	C	H			0
			39	13	26			
2	G	1	Total	C	H			0
			36	12	24			

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Mol	Chain	Residues	Atoms			AltConf
2	G	1	Total	C	H	0
			33	11	22	
2	G	1	Total	C	H	0
			30	10	20	
2	G	1	Total	C	H	0
			24	8	16	
2	G	1	Total	C	H	0
			21	7	14	
2	G	1	Total	C	H	0
			15	5	10	
2	G	1	Total	C	H	0
			15	5	10	
2	G	1	Total	C	H	0
			18	6	12	
2	H	1	Total	C	H	0
			39	13	26	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			39	13	26	
2	H	1	Total	C	H	0
			36	12	24	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			30	10	20	
2	H	1	Total	C	H	0
			24	8	16	
2	H	1	Total	C	H	0
			21	7	14	
2	H	1	Total	C	H	0
			15	5	10	
2	H	1	Total	C	H	0
			15	5	10	
2	H	1	Total	C	H	0
			18	6	12	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			55	17	30	
				O	P	
				7	1	
2	H	1	Total	C	H	0
			30	10	20	

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Mol	Chain	Residues	Atoms			AltConf
2	H	1	Total	C	H	0
			39	13	26	
2	H	1	Total	C	H	0
			15	5	10	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			12	4	8	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			24	8	16	
2	H	1	Total	C	H	0
			33	11	22	
2	H	1	Total	C	H	0
			21	7	14	
2	H	1	Total	C	H	0
			20	7	13	
2	I	1	Total	C	H	0
			39	13	26	
2	I	1	Total	C	H	0
			33	11	22	
2	I	1	Total	C	H	0
			39	13	26	
2	I	1	Total	C	H	0
			36	12	24	
2	I	1	Total	C	H	0
			33	11	22	
2	I	1	Total	C	H	0
			30	10	20	
2	I	1	Total	C	H	0
			24	8	16	
2	I	1	Total	C	H	0
			21	7	14	
2	I	1	Total	C	H	0
			15	5	10	
2	I	1	Total	C	H	0
			15	5	10	
2	I	1	Total	C	H	0
			18	6	12	

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Mol	Chain	Residues	Atoms					AltConf
2	I	1	Total 33	C 11	H 22			0
2	I	1	Total 55	C 17	H 30	O 7	P 1	0
2	I	1	Total 30	C 10	H 20			0
2	I	1	Total 39	C 13	H 26			0
2	I	1	Total 15	C 5	H 10			0
2	I	1	Total 33	C 11	H 22			0
2	I	1	Total 33	C 11	H 22			0
2	I	1	Total 12	C 4	H 8			0
2	I	1	Total 33	C 11	H 22			0
2	I	1	Total 24	C 8	H 16			0
2	I	1	Total 33	C 11	H 22			0
2	I	1	Total 21	C 7	H 14			0
2	I	1	Total 20	C 7	H 13			0
2	J	1	Total 39	C 13	H 26			0
2	J	1	Total 33	C 11	H 22			0
2	J	1	Total 39	C 13	H 26			0
2	J	1	Total 36	C 12	H 24			0
2	J	1	Total 33	C 11	H 22			0
2	J	1	Total 30	C 10	H 20			0
2	J	1	Total 24	C 8	H 16			0
2	J	1	Total 21	C 7	H 14			0

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Mol	Chain	Residues	Atoms					AltConf
2	J	1	Total	C	H			0
			15	5	10			
2	J	1	Total	C	H			0
			15	5	10			
2	J	1	Total	C	H			0
			18	6	12			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	J	1	Total	C	H			0
			30	10	20			
2	J	1	Total	C	H			0
			39	13	26			
2	J	1	Total	C	H			0
			15	5	10			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			12	4	8			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			24	8	16			
2	J	1	Total	C	H			0
			33	11	22			
2	J	1	Total	C	H			0
			21	7	14			
2	J	1	Total	C	H			0
			20	7	13			
2	K	1	Total	C	H			0
			39	13	26			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H			0
			39	13	26			
2	K	1	Total	C	H			0
			36	12	24			
2	K	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	K	1	Total	C	H			0
			30	10	20			
2	K	1	Total	C	H			0
			24	8	16			
2	K	1	Total	C	H			0
			21	7	14			
2	K	1	Total	C	H			0
			15	5	10			
2	K	1	Total	C	H			0
			15	5	10			
2	K	1	Total	C	H			0
			18	6	12			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	K	1	Total	C	H			0
			30	10	20			
2	K	1	Total	C	H			0
			39	13	26			
2	K	1	Total	C	H			0
			15	5	10			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H			0
			12	4	8			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H			0
			24	8	16			
2	K	1	Total	C	H			0
			33	11	22			
2	K	1	Total	C	H			0
			21	7	14			
2	K	1	Total	C	H			0
			20	7	13			
2	L	1	Total	C	H			0
			39	13	26			
2	L	1	Total	C	H			0
			33	11	22			

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Mol	Chain	Residues	Atoms					AltConf
2	L	1	Total	C	H			0
			39	13	26			
2	L	1	Total	C	H			0
			36	12	24			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H			0
			30	10	20			
2	L	1	Total	C	H			0
			24	8	16			
2	L	1	Total	C	H			0
			21	7	14			
2	L	1	Total	C	H			0
			15	5	10			
2	L	1	Total	C	H			0
			15	5	10			
2	L	1	Total	C	H			0
			18	6	12			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H	O	P	0
			55	17	30	7	1	
2	L	1	Total	C	H			0
			30	10	20			
2	L	1	Total	C	H			0
			39	13	26			
2	L	1	Total	C	H			0
			15	5	10			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H			0
			12	4	8			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H			0
			24	8	16			
2	L	1	Total	C	H			0
			33	11	22			
2	L	1	Total	C	H			0
			21	7	14			

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Mol	Chain	Residues	Atoms			AltConf
2	L	1	Total	C	H	0
			20	7	13	

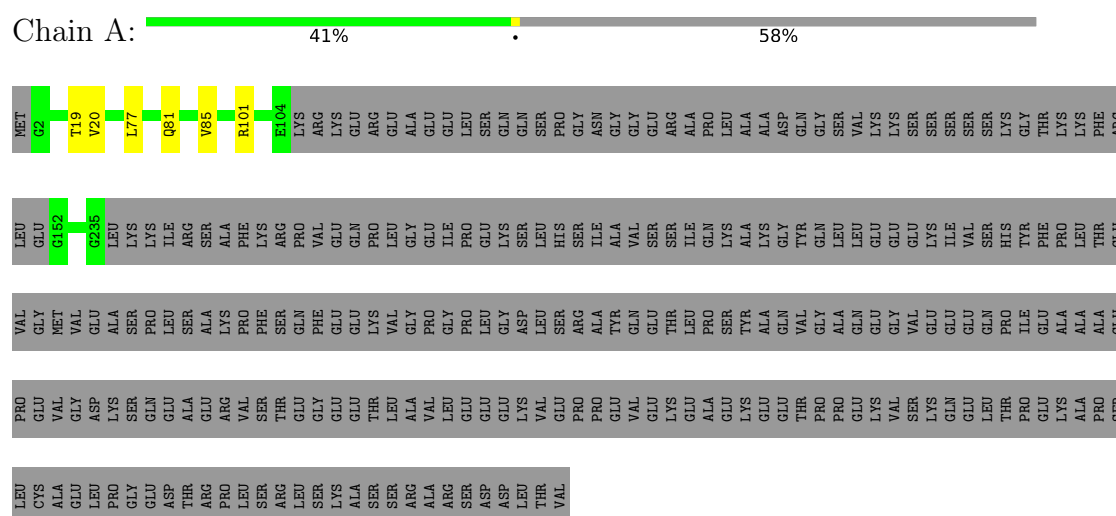
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	48	Total	O	0
			48	48	
3	B	48	Total	O	0
			48	48	
3	C	48	Total	O	0
			48	48	
3	D	48	Total	O	0
			48	48	
3	E	48	Total	O	0
			48	48	
3	F	48	Total	O	0
			48	48	
3	G	49	Total	O	0
			49	49	
3	H	47	Total	O	0
			47	47	
3	I	48	Total	O	0
			48	48	
3	J	48	Total	O	0
			48	48	
3	K	48	Total	O	0
			48	48	
3	L	48	Total	O	0
			48	48	

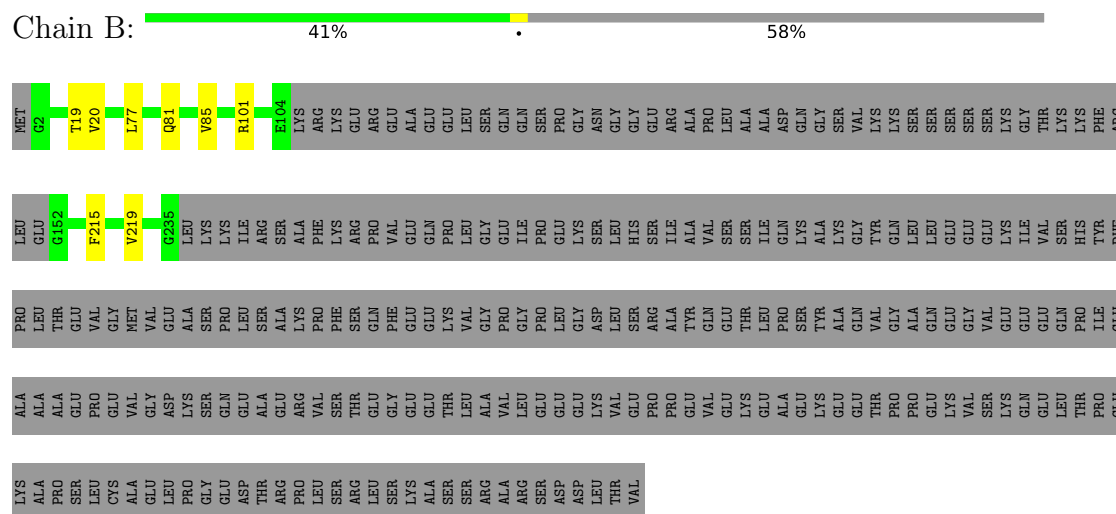
3 Residue-property plots [i](#)

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 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: Gap junction alpha-8 protein



- Molecule 1: Gap junction alpha-8 protein



- Molecule 1: Gap junction alpha-8 protein

[illegible]

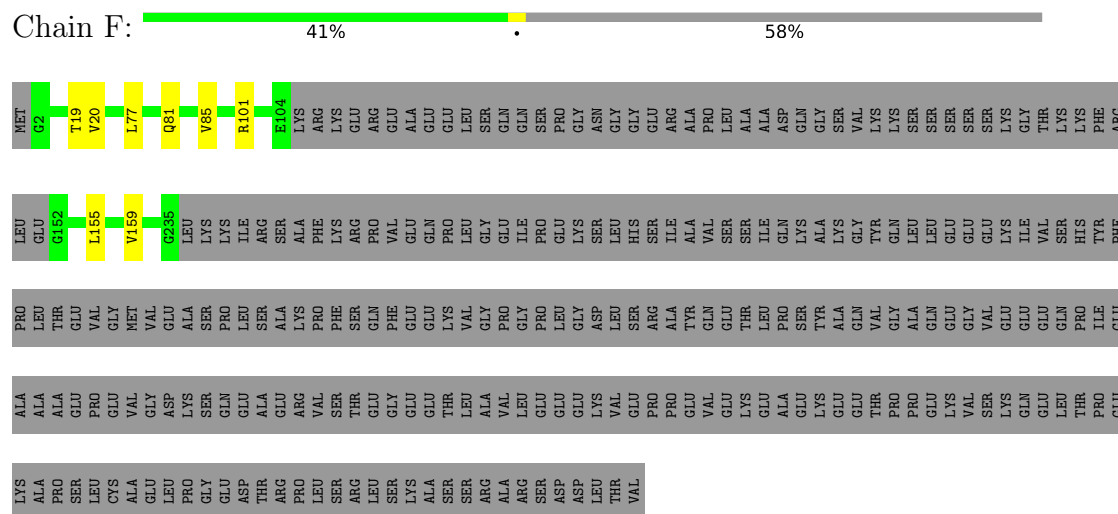
Chain D: 40% . 58%

GLU	GLU	GLU	PHE	LEU	MET
LYS	LYS	PRO	LEU	GLU	G2
ALA	ALA	ALA	THR		T19
PRO	PRO	GLU	GLU	F215	V20
SER	SER	VAL	VAL	H216	
LEU	CYS	GLY	GLY		L77
	ALA	VAL	VAL	V219	Q81
GLU	GLU	GLY	GLU		
LEU	ASP	GLY	GLU	G235	V85
PRO	PRO	LYS	ALA	LEU	
GLY	SER	SER	SER	LYS	R101
GLU	GLN	PRO	PRO	LYS	
ASP	ASP	GLU	LEU	ILE	E104
THR	THR	ALA	SER	ARG	LYS
PRO	ARG	GLU	ALA	SER	ARG
PRO	PRO	ARG	LYS	ALA	LYS
LEU	LEU	VAL	PRO	PHE	LYS
SER	SER	SER	PHE	LYS	GLU
ARG	ARG	THR	SER	ARG	ARG
LEU	LEU	GLU	GLN	PRO	GLU
LYS	SER	GLY	PHE	VAL	ALA
ALA	LYS	GLU	GLU	GLU	GLU
ALA	ALA	GLU	GLU	GLN	LEU
SER	SER	THR	LYS	PRO	SER
ARG	ARG	VAL	GLY	GLY	GLN
LEU	LEU	VAL	PRO	GLU	GLN
ARG	ARG	LEU	GLY	ILE	SER
SER	SER	GLU	PRO	PRO	PRO
ASP	ASP	GLU	LEU	GLY	GLY
LEU	LEU	GLU	GLY	LYS	ASN
THR	THR	VAL	ASP	SER	GLY
VAL	VAL	GLU	SER	LEU	GLY
			GLU	HIS	GLU
			SER	SER	ARG
			ARG	ILE	ALA
			ALA	ALA	PRO
			GLN	VAL	LEU
			THR	SER	ALA
			GLU	SER	ALA
			LEU	ILE	ASP
			PRO	GLN	GLN
			SER	LYS	GLY
			LYS	ALA	SER
			GLU	LYS	VAL
			GLN	GLY	LYS
			VAL	TTR	LYS
			GLY	GLN	SER
			ALA	LEU	SER
			GLN	LEU	SER
			GLY	GLU	SER
			GLY	GLU	SER
			VAL	GLU	LYS
			GLU	GLU	GLY
			THR	GLU	THR
			PRO	GLU	LYS
			THR	GLN	LYS
			THR	ILE	ARG
			PRO	VAL	THR
			ILE	TTR	ARG

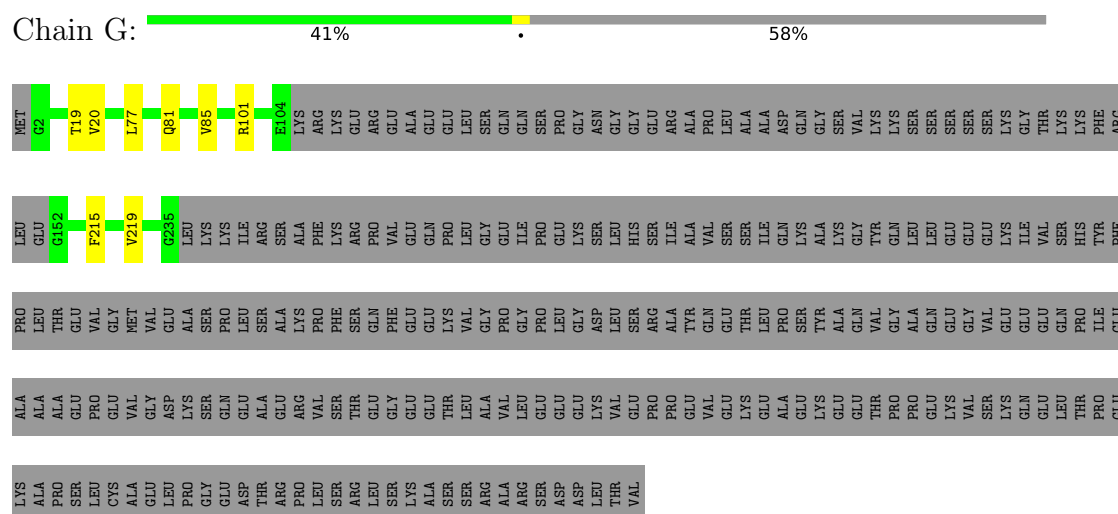
Chain E: 41% . 58%

LEU	PRO	VAL	LEU	GLY	GLY	VAL	LEU	MET
CYS	GLU	GLY	GLU	MET	GLY	G152	GLU	G2
ALA	VAL	VAL	VAL	VAL	VAL	G235	VAL	T19
LEU	ASP	GLU	GLU	GLU	ALA	LEU	LEU	V20
PRO	LYS	ALA	ALA	ALA	LYS	LYS	LYS	L77
GLY	SER	SER	PRO	SER	PRO	PHE	PHE	Q81
GLU	GLN	GLU	LEU	LEU	ILE	LYS	ARG	Q81
ASP	GLU	ALA	SER	SER	ARG	SER	SER	V85
THR	THR	ALA	ALA	ALA	ALA	ALA	ALA	V85
ARG	GLU	ARG	LYS	LYS	LYS	LYS	LYS	R101
PRO	ARG	VAL	PRO	PHE	ARG	ARG	ARG	R101
LEU	SER	SER	SER	SER	LYS	LYS	LYS	E104
ARG	THR	GLY	GLN	GLN	PRO	VAL	VAL	E104
LYS	GLU	GLY	PHE	PHE	VAL	VAL	ARG	LYS
ALA	GLU	GLU	GLU	GLU	GLU	GLU	LYS	LYS
SER	GLU	THR	THR	LYS	PRO	GLN	GLU	GLU
SER	LEU	VAL	VAL	VAL	VAL	VAL	GLY	ALA
ASP	GLU	ALA	ALA	GLY	GLY	ILE	GLU	GLU
ASP	GLU	GLU	GLU	LEU	LEU	PRO	LEU	LEU
LEU	LYS	ASP	ASP	GLY	ASP	GLY	SER	SER
LEU	VAL	VAL	VAL	VAL	LEU	LEU	GLN	GLN
THR	GLU	GLU	GLU	THR	LEU	HIS	SER	PRO
VAL	GLU	SER	SER	ARG	SER	SER	GLY	GLY
	PRO	PRO	ALA	ALA	ILE	ILE	ASN	ASN
	GLU	GLU	GLU	TYR	ALA	ALA	GLY	GLY
	VAL	VAL	GLN	VAL	VAL	VAL	GLY	GLY
	GLU	GLU	SER	SER	SER	SER	ARG	ARG
	LYS	LYS	LEU	LEU	ILE	ILE	ALA	ALA
	GLU	GLU	GLN	GLN	GLN	GLN	PRO	PRO
	ALA	GLU	ALA	ALA	LEU	LEU	LYS	LYS
	GLU	GLY	GLU	GLU	GLU	GLU	LYS	LYS
	VAL	GLY	GLY	GLY	GLU	GLU	LYS	LYS
	SER	VAL	VAL	VAL	VAL	GLU	SER	SER
	LYS	GLN	GLN	GLN	ALA	LYS	GLY	GLY
	GLU	VAL	VAL	VAL	TYR	TYR	GLN	GLN
	THR	GLY	GLY	GLY	THR	THR	VAL	VAL
	PRO	GLU	GLU	GLU	ILE	ILE	SER	SER
	LYS	ALA	ALA	ALA	ALA	ALA	SER	SER
	THR	LEU	LEU	LEU	GLN	GLN	SER	SER
	VAL	THR	THR	THR	PRO	HIS	SER	SER
	PRO	ILE	ILE	ILE	TYR	TYR	LYS	LYS
	LYS	ALA	ALA	ALA	PHE	PHE	THR	THR
	THR	GLU	GLU	GLU	GLU	GLU	PRO	PRO
	ALA	ALA	ALA	ALA	ALA	ALA	LYS	LYS
	PRO	PRO	GLU	GLU	THR	THR	LYS	LYS
	SER	GLU	GLU	GLU	ALA	ALA	PHE	PHE
							ARG	ARG

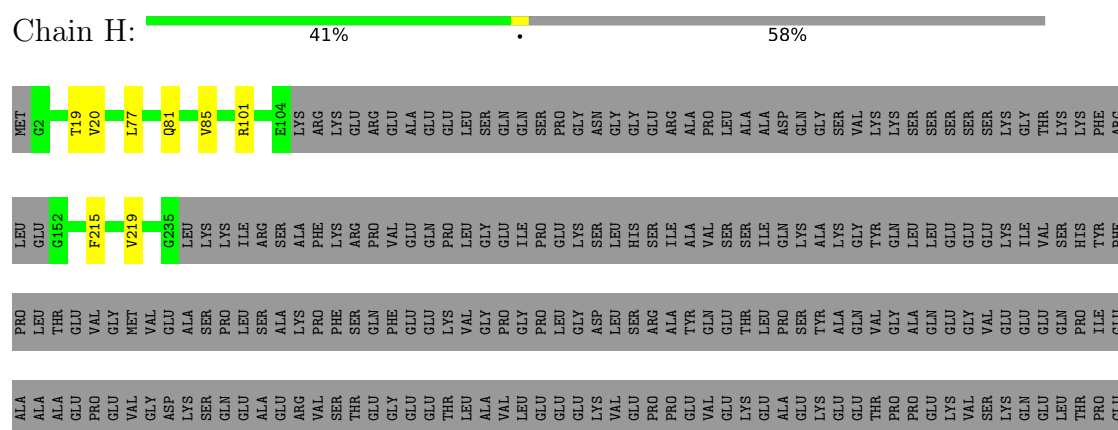
- Molecule 1: Gap junction alpha-8 protein



- Molecule 1: Gap junction alpha-8 protein

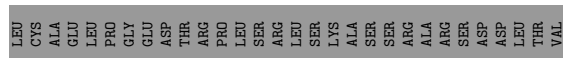


- Molecule 1: Gap junction alpha-8 protein



LEU	CYS	ALA	GLU	LEU	PRO	GLY	GLU	ASP	THR	ARG	PRO	LEU	SER	ARG	LEU	SER	LYS	ALA	SER	SER	ARG	ALA	ARG	SER	ASP	ASP	LEU	THR	VAL
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain L: 41% . 58%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	218088	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.00	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	29000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.375	Depositor
Minimum map value	-2.214	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	307.8144, 307.8144, 307.8144	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8016, 0.8016, 0.8016	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MC3

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	0.08	0/1565	0.22	0/2132
1	B	0.09	0/1565	0.22	0/2132
1	C	0.09	0/1565	0.22	0/2132
1	D	0.09	0/1565	0.22	0/2132
1	E	0.09	0/1565	0.22	0/2132
1	F	0.09	0/1565	0.22	0/2132
1	G	0.09	0/1565	0.22	0/2132
1	H	0.09	0/1565	0.22	0/2132
1	I	0.09	0/1565	0.22	0/2132
1	J	0.09	0/1565	0.22	0/2132
1	K	0.09	0/1565	0.22	0/2132
1	L	0.09	0/1565	0.22	0/2132
All	All	0.09	0/18780	0.22	0/25584

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	1520	1507	1497	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1520	1507	1497	6	0
1	C	1520	1507	1497	6	0
1	D	1520	1507	1497	7	0
1	E	1520	1507	1497	5	0
1	F	1520	1507	1497	6	0
1	G	1520	1507	1497	6	0
1	H	1520	1507	1497	6	0
1	I	1520	1507	1497	6	0
1	J	1520	1507	1497	6	0
1	K	1520	1507	1497	5	0
1	L	1520	1507	1497	5	0
2	A	235	449	372	0	0
2	B	235	449	372	0	0
2	C	235	449	372	0	0
2	D	235	449	372	0	0
2	E	235	449	372	0	0
2	F	235	449	372	0	0
2	G	235	449	372	0	0
2	H	235	449	372	0	0
2	I	235	449	372	0	0
2	J	235	449	372	0	0
2	K	235	449	372	0	0
2	L	235	449	372	0	0
3	A	48	0	0	0	0
3	B	48	0	0	0	0
3	C	48	0	0	0	0
3	D	48	0	0	0	0
3	E	48	0	0	0	0
3	F	48	0	0	0	0
3	G	49	0	0	0	0
3	H	47	0	0	0	0
3	I	48	0	0	0	0
3	J	48	0	0	0	0
3	K	48	0	0	0	0
3	L	48	0	0	0	0
All	All	21636	23472	22428	69	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.

The worst 5 of 69 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:B:81:GLN:O	1:B:85:VAL:HG22	2.06	0.56
1:C:81:GLN:O	1:C:85:VAL:HG22	2.06	0.56
1:H:81:GLN:O	1:H:85:VAL:HG22	2.06	0.56
1:I:81:GLN:O	1:I:85:VAL:HG22	2.06	0.56
1:D:81:GLN:O	1:D:85:VAL:HG22	2.06	0.56

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	B	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	C	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	D	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	E	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	F	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	G	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	H	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	I	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	J	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	K	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
1	L	183/440 (42%)	181 (99%)	2 (1%)	0	100	100
All	All	2196/5280 (42%)	2172 (99%)	24 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	170/385 (44%)	170 (100%)	0	100	100
1	B	170/385 (44%)	170 (100%)	0	100	100
1	C	170/385 (44%)	170 (100%)	0	100	100
1	D	170/385 (44%)	170 (100%)	0	100	100
1	E	170/385 (44%)	170 (100%)	0	100	100
1	F	170/385 (44%)	170 (100%)	0	100	100
1	G	170/385 (44%)	170 (100%)	0	100	100
1	H	170/385 (44%)	170 (100%)	0	100	100
1	I	170/385 (44%)	170 (100%)	0	100	100
1	J	170/385 (44%)	170 (100%)	0	100	100
1	K	170/385 (44%)	170 (100%)	0	100	100
1	L	170/385 (44%)	170 (100%)	0	100	100
All	All	2040/4620 (44%)	2040 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	58	GLN
1	L	58	GLN
1	F	58	GLN
1	G	58	GLN
1	H	57	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

288 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	MC3	C	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	B	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	D	509	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	E	511	-	5,5,45	0.36	0	4,4,53	0.61	0
2	MC3	J	509	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	K	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	F	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	I	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	I	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	J	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	B	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	D	507	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	D	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	L	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	C	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	C	522	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	K	502	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	D	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	F	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	H	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	520	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	K	511	-	5,5,45	0.36	0	4,4,53	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	G	520	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	J	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	D	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	E	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	G	515	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	G	516	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	H	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	I	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	E	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	I	506	-	9,9,45	0.36	0	8,8,53	0.81	0
2	MC3	L	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	B	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	D	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	D	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	D	521	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	I	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	A	519	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	K	509	-	4,4,45	0.36	0	3,3,53	0.57	0
2	MC3	K	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	G	512	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	F	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	F	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	H	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	H	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	C	523	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	D	503	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	C	503	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	I	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	C	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	L	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	K	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	L	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	G	501	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	D	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	C	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	H	511	-	5,5,45	0.36	0	4,4,53	0.62	0
2	MC3	K	521	-	7,7,45	0.36	0	6,6,53	0.76	0
2	MC3	J	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	L	511	-	5,5,45	0.36	0	4,4,53	0.62	0
2	MC3	L	504	-	11,11,45	0.36	0	10,10,53	0.84	0
2	MC3	B	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	C	519	-	3,3,45	0.43	0	2,2,53	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	A	506	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	C	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	D	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	H	504	-	11,11,45	0.35	0	10,10,53	0.83	0
2	MC3	B	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	L	503	-	12,12,45	0.34	0	11,11,53	0.85	0
2	MC3	F	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	F	504	-	11,11,45	0.35	0	10,10,53	0.84	0
2	MC3	E	522	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	J	510	-	4,4,45	0.38	0	3,3,53	0.58	0
2	MC3	K	517	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	J	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	G	505	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	A	515	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	H	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	J	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	K	504	-	11,11,45	0.35	0	10,10,53	0.83	0
2	MC3	K	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	A	513	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	F	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	G	513	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	A	502	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	B	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	A	508	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	A	509	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	E	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	G	503	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	K	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	E	519	-	3,3,45	0.43	0	2,2,53	0.75	0
2	MC3	F	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	A	517	-	11,11,45	0.35	0	10,10,53	0.83	0
2	MC3	I	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	K	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	C	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	A	507	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	I	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	L	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	F	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	L	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	E	508	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	C	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	J	512	-	10,10,45	0.34	0	9,9,53	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	E	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	E	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	G	506	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	I	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	B	508	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	L	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	C	508	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	K	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	C	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	E	504	-	11,11,45	0.36	0	10,10,53	0.84	0
2	MC3	J	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	K	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	H	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	D	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	E	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	F	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	I	504	-	11,11,45	0.35	0	10,10,53	0.83	0
2	MC3	K	505	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	G	508	-	3,3,45	0.43	0	2,2,53	0.75	0
2	MC3	G	517	-	11,11,45	0.35	0	10,10,53	0.84	0
2	MC3	E	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	J	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	K	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	D	504	-	11,11,45	0.35	0	10,10,53	0.84	0
2	MC3	J	502	-	10,10,45	0.35	0	9,9,53	0.84	0
2	MC3	C	504	-	11,11,45	0.35	0	10,10,53	0.83	0
2	MC3	G	509	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	G	514	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	D	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	B	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	H	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	L	508	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	L	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	G	507	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	D	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	G	523	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	B	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	A	503	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	L	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	D	511	-	5,5,45	0.37	0	4,4,53	0.62	0
2	MC3	J	508	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	C	501	-	12,12,45	0.35	0	11,11,53	0.82	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	I	514	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	K	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	E	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	J	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	C	509	-	4,4,45	0.36	0	3,3,53	0.57	0
2	MC3	L	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	I	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	J	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	E	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	E	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	F	508	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	B	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	E	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	J	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	B	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	F	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	511	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	A	510	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	L	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	G	504	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	F	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	F	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	D	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	B	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	H	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	B	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	G	524	-	5,5,45	0.36	0	4,4,53	0.61	0
2	MC3	H	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	I	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	I	511	-	5,5,45	0.37	0	4,4,53	0.62	0
2	MC3	C	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	A	522	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	B	511	-	5,5,45	0.36	0	4,4,53	0.62	0
2	MC3	G	521	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	J	503	-	12,12,45	0.34	0	11,11,53	0.85	0
2	MC3	D	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	K	503	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	C	511	-	5,5,45	0.36	0	4,4,53	0.62	0
2	MC3	C	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	E	503	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	H	508	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	J	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	J	507	-	7,7,45	0.36	0	6,6,53	0.75	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	I	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	L	505	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	I	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	L	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	I	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	H	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	L	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	K	508	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	D	516	-	4,4,45	0.38	0	3,3,53	0.59	0
2	MC3	A	514	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	I	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	H	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	B	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	H	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	I	519	-	3,3,45	0.43	0	2,2,53	0.75	0
2	MC3	J	511	-	5,5,45	0.36	0	4,4,53	0.61	0
2	MC3	E	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	A	504	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	E	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	F	515	-	12,12,45	0.35	0	11,11,53	0.84	0
2	MC3	H	506	-	9,9,45	0.36	0	8,8,53	0.81	0
2	MC3	J	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	K	522	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	A	524	-	5,5,45	0.36	0	4,4,53	0.62	0
2	MC3	B	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	E	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	F	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	B	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	H	512	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	H	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	L	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	B	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	C	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	G	502	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	I	518	-	10,10,45	0.34	0	9,9,53	0.82	0
2	MC3	H	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	A	521	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	E	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	G	510	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	G	511	-	10,10,45	0.35	0	9,9,53	0.82	0
2	MC3	L	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	E	512	-	10,10,45	0.34	0	9,9,53	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	C	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	H	503	-	12,12,45	0.34	0	11,11,53	0.85	0
2	MC3	B	504	-	11,11,45	0.35	0	10,10,53	0.84	0
2	MC3	C	514	-	9,9,45	0.35	0	8,8,53	0.82	0
2	MC3	D	519	-	3,3,45	0.43	0	2,2,53	0.74	0
2	MC3	D	502	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	I	524	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	F	511	-	5,5,45	0.37	0	4,4,53	0.62	0
2	MC3	F	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	H	517	-	10,10,45	0.35	0	9,9,53	0.81	0
2	MC3	K	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	B	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	H	524	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	H	516	-	4,4,45	0.38	0	3,3,53	0.59	0
2	MC3	J	524	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	K	501	-	12,12,45	0.34	0	11,11,53	0.82	0
2	MC3	L	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	B	506	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	J	505	-	10,10,45	0.34	0	9,9,53	0.82	0
2	MC3	F	507	-	7,7,45	0.36	0	6,6,53	0.75	0
2	MC3	L	518	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	K	516	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	E	520	-	10,10,45	0.36	0	9,9,53	0.84	0
2	MC3	A	505	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	L	513	-	24,24,45	0.51	0	26,28,53	0.88	1 (3%)
2	MC3	F	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	I	503	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	D	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	J	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	J	504	-	11,11,45	0.35	0	10,10,53	0.84	0
2	MC3	C	515	-	12,12,45	0.35	0	11,11,53	0.85	0
2	MC3	A	501	-	10,10,45	0.34	0	9,9,53	0.83	0
2	MC3	A	523	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	D	508	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	F	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	B	503	-	12,12,45	0.34	0	11,11,53	0.85	0
2	MC3	D	513	-	24,24,45	0.52	0	26,28,53	0.88	1 (3%)
2	MC3	F	506	-	9,9,45	0.36	0	8,8,53	0.81	0
2	MC3	H	523	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	F	520	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	K	524	-	6,6,45	0.37	0	5,5,53	0.70	0
2	MC3	A	516	-	12,12,45	0.34	0	11,11,53	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	C	505	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	F	503	-	12,12,45	0.34	0	11,11,53	0.85	0
2	MC3	G	522	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	G	518	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	G	519	-	9,9,45	0.35	0	8,8,53	0.81	0
2	MC3	E	510	-	4,4,45	0.37	0	3,3,53	0.58	0
2	MC3	I	508	-	6,6,45	0.36	0	5,5,53	0.70	0
2	MC3	L	502	-	10,10,45	0.35	0	9,9,53	0.83	0
2	MC3	I	509	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	512	-	6,6,45	0.36	0	5,5,53	0.69	0
2	MC3	B	501	-	12,12,45	0.35	0	11,11,53	0.82	0
2	MC3	B	523	-	6,6,45	0.36	0	5,5,53	0.70	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	MC3	C	520	-	-	0/8/8/49	-
2	MC3	B	509	-	-	0/2/2/49	-
2	MC3	D	509	-	-	0/2/2/49	-
2	MC3	E	511	-	-	0/3/3/49	-
2	MC3	J	509	-	-	0/2/2/49	-
2	MC3	K	514	-	-	0/7/7/49	-
2	MC3	F	524	-	-	0/4/4/49	-
2	MC3	I	507	-	-	0/5/5/49	-
2	MC3	I	522	-	-	0/8/8/49	-
2	MC3	J	514	-	-	0/7/7/49	-
2	MC3	B	516	-	-	0/2/2/49	-
2	MC3	D	507	-	-	0/5/5/49	-
2	MC3	D	522	-	-	0/8/8/49	-
2	MC3	L	506	-	-	0/7/7/49	-
2	MC3	C	507	-	-	0/5/5/49	-
2	MC3	C	522	-	-	0/8/8/49	-
2	MC3	K	502	-	-	0/8/8/49	-
2	MC3	D	506	-	-	0/7/7/49	-
2	MC3	F	523	-	-	0/4/4/49	-
2	MC3	H	509	-	-	0/2/2/49	-
2	MC3	A	520	-	-	0/5/5/49	-
2	MC3	K	511	-	-	0/3/3/49	-
2	MC3	G	520	-	-	0/5/5/49	-
2	MC3	J	523	-	-	0/4/4/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	D	518	-	-	0/8/8/49	-
2	MC3	E	515	-	-	0/10/10/49	-
2	MC3	G	515	-	-	0/8/8/49	-
2	MC3	G	516	-	-	0/10/10/49	-
2	MC3	H	515	-	-	0/10/10/49	-
2	MC3	I	521	-	-	0/5/5/49	-
2	MC3	E	513	-	-	8/24/24/49	-
2	MC3	I	506	-	-	0/7/7/49	-
2	MC3	L	510	-	-	0/2/2/49	-
2	MC3	B	521	-	-	0/5/5/49	-
2	MC3	D	517	-	-	0/8/8/49	-
2	MC3	D	512	-	-	0/8/8/49	-
2	MC3	D	521	-	-	0/5/5/49	-
2	MC3	I	513	-	-	8/24/24/49	-
2	MC3	A	519	-	-	0/7/7/49	-
2	MC3	K	509	-	-	0/2/2/49	-
2	MC3	K	510	-	-	0/2/2/49	-
2	MC3	G	512	-	-	0/4/4/49	-
2	MC3	F	505	-	-	0/8/8/49	-
2	MC3	F	519	-	-	0/1/1/49	-
2	MC3	H	501	-	-	0/10/10/49	-
2	MC3	H	514	-	-	0/7/7/49	-
2	MC3	C	523	-	-	0/4/4/49	-
2	MC3	D	503	-	-	0/10/10/49	-
2	MC3	C	503	-	-	0/10/10/49	-
2	MC3	I	516	-	-	0/2/2/49	-
2	MC3	C	512	-	-	0/8/8/49	-
2	MC3	L	515	-	-	0/10/10/49	-
2	MC3	K	506	-	-	0/7/7/49	-
2	MC3	L	512	-	-	0/8/8/49	-
2	MC3	G	501	-	-	0/8/8/49	-
2	MC3	D	524	-	-	0/4/4/49	-
2	MC3	C	516	-	-	0/2/2/49	-
2	MC3	H	511	-	-	0/3/3/49	-
2	MC3	K	521	-	-	0/5/5/49	-
2	MC3	J	513	-	-	8/24/24/49	-
2	MC3	L	511	-	-	0/3/3/49	-
2	MC3	L	504	-	-	0/9/9/49	-
2	MC3	B	514	-	-	0/7/7/49	-
2	MC3	C	519	-	-	0/1/1/49	-
2	MC3	A	506	-	-	0/8/8/49	-
2	MC3	C	524	-	-	0/4/4/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	D	501	-	-	0/10/10/49	-
2	MC3	H	504	-	-	0/9/9/49	-
2	MC3	B	505	-	-	0/8/8/49	-
2	MC3	L	503	-	-	0/10/10/49	-
2	MC3	F	522	-	-	0/8/8/49	-
2	MC3	F	504	-	-	0/9/9/49	-
2	MC3	E	522	-	-	0/8/8/49	-
2	MC3	J	510	-	-	0/2/2/49	-
2	MC3	K	517	-	-	0/8/8/49	-
2	MC3	J	517	-	-	0/8/8/49	-
2	MC3	G	505	-	-	0/2/2/49	-
2	MC3	A	515	-	-	0/8/8/49	-
2	MC3	H	505	-	-	0/8/8/49	-
2	MC3	J	518	-	-	0/8/8/49	-
2	MC3	K	504	-	-	0/9/9/49	-
2	MC3	K	518	-	-	0/8/8/49	-
2	MC3	A	513	-	-	0/4/4/49	-
2	MC3	F	517	-	-	0/8/8/49	-
2	MC3	G	513	-	-	0/4/4/49	-
2	MC3	A	502	-	-	8/24/24/49	-
2	MC3	B	520	-	-	0/8/8/49	-
2	MC3	A	508	-	-	0/1/1/49	-
2	MC3	A	509	-	-	0/8/8/49	-
2	MC3	E	506	-	-	0/7/7/49	-
2	MC3	G	503	-	-	0/7/7/49	-
2	MC3	K	523	-	-	0/4/4/49	-
2	MC3	E	519	-	-	0/1/1/49	-
2	MC3	F	513	-	-	8/24/24/49	-
2	MC3	A	517	-	-	0/9/9/49	-
2	MC3	I	523	-	-	0/4/4/49	-
2	MC3	K	512	-	-	0/8/8/49	-
2	MC3	C	506	-	-	0/7/7/49	-
2	MC3	A	507	-	-	0/8/8/49	-
2	MC3	I	502	-	-	0/8/8/49	-
2	MC3	L	517	-	-	0/8/8/49	-
2	MC3	F	516	-	-	0/2/2/49	-
2	MC3	L	507	-	-	0/5/5/49	-
2	MC3	E	508	-	-	0/4/4/49	-
2	MC3	C	521	-	-	0/5/5/49	-
2	MC3	J	512	-	-	0/8/8/49	-
2	MC3	E	509	-	-	0/2/2/49	-
2	MC3	A	518	-	-	0/8/8/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	E	516	-	-	0/2/2/49	-
2	MC3	G	506	-	-	0/8/8/49	-
2	MC3	I	512	-	-	0/8/8/49	-
2	MC3	B	508	-	-	0/4/4/49	-
2	MC3	L	524	-	-	0/4/4/49	-
2	MC3	C	508	-	-	0/4/4/49	-
2	MC3	K	520	-	-	0/8/8/49	-
2	MC3	C	513	-	-	8/24/24/49	-
2	MC3	E	504	-	-	0/9/9/49	-
2	MC3	J	515	-	-	0/10/10/49	-
2	MC3	K	515	-	-	0/10/10/49	-
2	MC3	H	520	-	-	0/8/8/49	-
2	MC3	D	514	-	-	0/7/7/49	-
2	MC3	E	517	-	-	0/8/8/49	-
2	MC3	F	512	-	-	0/8/8/49	-
2	MC3	I	504	-	-	0/9/9/49	-
2	MC3	K	505	-	-	0/8/8/49	-
2	MC3	G	508	-	-	0/1/1/49	-
2	MC3	G	517	-	-	0/9/9/49	-
2	MC3	E	507	-	-	0/5/5/49	-
2	MC3	J	519	-	-	0/1/1/49	-
2	MC3	K	519	-	-	0/1/1/49	-
2	MC3	D	504	-	-	0/9/9/49	-
2	MC3	J	502	-	-	0/8/8/49	-
2	MC3	C	504	-	-	0/9/9/49	-
2	MC3	G	509	-	-	0/8/8/49	-
2	MC3	G	514	-	-	0/10/10/49	-
2	MC3	D	523	-	-	0/4/4/49	-
2	MC3	B	518	-	-	0/8/8/49	-
2	MC3	H	518	-	-	0/8/8/49	-
2	MC3	L	508	-	-	0/4/4/49	-
2	MC3	L	509	-	-	0/2/2/49	-
2	MC3	G	507	-	-	0/8/8/49	-
2	MC3	D	520	-	-	0/8/8/49	-
2	MC3	G	523	-	-	0/2/2/49	-
2	MC3	B	512	-	-	0/8/8/49	-
2	MC3	A	503	-	-	0/7/7/49	-
2	MC3	L	522	-	-	0/8/8/49	-
2	MC3	D	511	-	-	0/3/3/49	-
2	MC3	J	508	-	-	0/4/4/49	-
2	MC3	C	501	-	-	0/10/10/49	-
2	MC3	I	514	-	-	0/7/7/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	K	507	-	-	0/5/5/49	-
2	MC3	E	505	-	-	0/8/8/49	-
2	MC3	J	522	-	-	0/8/8/49	-
2	MC3	C	509	-	-	0/2/2/49	-
2	MC3	L	523	-	-	0/4/4/49	-
2	MC3	I	517	-	-	0/8/8/49	-
2	MC3	J	506	-	-	0/7/7/49	-
2	MC3	E	524	-	-	0/4/4/49	-
2	MC3	E	521	-	-	0/5/5/49	-
2	MC3	F	508	-	-	0/4/4/49	-
2	MC3	B	515	-	-	0/10/10/49	-
2	MC3	E	502	-	-	0/8/8/49	-
2	MC3	J	521	-	-	0/5/5/49	-
2	MC3	B	513	-	-	8/24/24/49	-
2	MC3	F	509	-	-	0/2/2/49	-
2	MC3	A	511	-	-	0/8/8/49	-
2	MC3	A	510	-	-	0/5/5/49	-
2	MC3	L	514	-	-	0/7/7/49	-
2	MC3	G	504	-	-	0/10/10/49	-
2	MC3	F	514	-	-	0/7/7/49	-
2	MC3	F	518	-	-	0/8/8/49	-
2	MC3	D	505	-	-	0/8/8/49	-
2	MC3	B	519	-	-	0/1/1/49	-
2	MC3	H	502	-	-	0/8/8/49	-
2	MC3	B	502	-	-	0/8/8/49	-
2	MC3	G	524	-	-	0/3/3/49	-
2	MC3	H	519	-	-	0/1/1/49	-
2	MC3	I	510	-	-	0/2/2/49	-
2	MC3	I	511	-	-	0/3/3/49	-
2	MC3	C	502	-	-	0/8/8/49	-
2	MC3	A	522	-	-	0/2/2/49	-
2	MC3	B	511	-	-	0/3/3/49	-
2	MC3	G	521	-	-	0/4/4/49	-
2	MC3	J	503	-	-	0/10/10/49	-
2	MC3	D	510	-	-	0/2/2/49	-
2	MC3	K	503	-	-	0/10/10/49	-
2	MC3	C	511	-	-	0/3/3/49	-
2	MC3	C	510	-	-	0/2/2/49	-
2	MC3	E	503	-	-	0/10/10/49	-
2	MC3	H	508	-	-	0/4/4/49	-
2	MC3	J	516	-	-	0/2/2/49	-
2	MC3	J	507	-	-	0/5/5/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	I	501	-	-	0/10/10/49	-
2	MC3	L	505	-	-	0/8/8/49	-
2	MC3	I	520	-	-	0/8/8/49	-
2	MC3	L	521	-	-	0/5/5/49	-
2	MC3	I	515	-	-	0/10/10/49	-
2	MC3	H	510	-	-	0/2/2/49	-
2	MC3	L	520	-	-	0/8/8/49	-
2	MC3	K	508	-	-	0/4/4/49	-
2	MC3	D	516	-	-	0/2/2/49	-
2	MC3	A	514	-	-	0/10/10/49	-
2	MC3	I	505	-	-	0/8/8/49	-
2	MC3	H	507	-	-	0/5/5/49	-
2	MC3	B	522	-	-	0/8/8/49	-
2	MC3	H	522	-	-	0/8/8/49	-
2	MC3	I	519	-	-	0/1/1/49	-
2	MC3	J	511	-	-	0/3/3/49	-
2	MC3	E	501	-	-	0/10/10/49	-
2	MC3	A	504	-	-	0/10/10/49	-
2	MC3	E	523	-	-	0/4/4/49	-
2	MC3	F	515	-	-	0/10/10/49	-
2	MC3	H	506	-	-	0/7/7/49	-
2	MC3	J	501	-	-	0/10/10/49	-
2	MC3	K	522	-	-	0/8/8/49	-
2	MC3	A	524	-	-	0/3/3/49	-
2	MC3	B	510	-	-	0/2/2/49	-
2	MC3	E	518	-	-	0/8/8/49	-
2	MC3	F	502	-	-	0/8/8/49	-
2	MC3	B	517	-	-	0/8/8/49	-
2	MC3	H	512	-	-	0/8/8/49	-
2	MC3	H	521	-	-	0/5/5/49	-
2	MC3	L	519	-	-	0/1/1/49	-
2	MC3	B	507	-	-	0/5/5/49	-
2	MC3	C	517	-	-	0/8/8/49	-
2	MC3	G	502	-	-	8/24/24/49	-
2	MC3	I	518	-	-	0/8/8/49	-
2	MC3	H	513	-	-	8/24/24/49	-
2	MC3	A	521	-	-	0/4/4/49	-
2	MC3	E	514	-	-	0/7/7/49	-
2	MC3	G	510	-	-	0/5/5/49	-
2	MC3	G	511	-	-	0/8/8/49	-
2	MC3	L	501	-	-	0/10/10/49	-
2	MC3	E	512	-	-	0/8/8/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	C	518	-	-	0/8/8/49	-
2	MC3	H	503	-	-	0/10/10/49	-
2	MC3	B	504	-	-	0/9/9/49	-
2	MC3	C	514	-	-	0/7/7/49	-
2	MC3	D	519	-	-	0/1/1/49	-
2	MC3	D	502	-	-	0/8/8/49	-
2	MC3	I	524	-	-	0/4/4/49	-
2	MC3	F	511	-	-	0/3/3/49	-
2	MC3	F	510	-	-	0/2/2/49	-
2	MC3	H	517	-	-	0/8/8/49	-
2	MC3	K	513	-	-	8/24/24/49	-
2	MC3	B	524	-	-	0/4/4/49	-
2	MC3	H	524	-	-	0/4/4/49	-
2	MC3	H	516	-	-	0/2/2/49	-
2	MC3	J	524	-	-	0/4/4/49	-
2	MC3	K	501	-	-	0/10/10/49	-
2	MC3	L	516	-	-	0/2/2/49	-
2	MC3	B	506	-	-	0/7/7/49	-
2	MC3	J	505	-	-	0/8/8/49	-
2	MC3	F	507	-	-	0/5/5/49	-
2	MC3	L	518	-	-	0/8/8/49	-
2	MC3	K	516	-	-	0/2/2/49	-
2	MC3	E	520	-	-	0/8/8/49	-
2	MC3	A	505	-	-	0/2/2/49	-
2	MC3	L	513	-	-	8/24/24/49	-
2	MC3	F	521	-	-	0/5/5/49	-
2	MC3	I	503	-	-	0/10/10/49	-
2	MC3	D	515	-	-	0/10/10/49	-
2	MC3	J	520	-	-	0/8/8/49	-
2	MC3	J	504	-	-	0/9/9/49	-
2	MC3	C	515	-	-	0/10/10/49	-
2	MC3	A	501	-	-	0/8/8/49	-
2	MC3	A	523	-	-	0/2/2/49	-
2	MC3	D	508	-	-	0/4/4/49	-
2	MC3	F	501	-	-	0/10/10/49	-
2	MC3	B	503	-	-	0/10/10/49	-
2	MC3	D	513	-	-	8/24/24/49	-
2	MC3	F	506	-	-	0/7/7/49	-
2	MC3	H	523	-	-	0/4/4/49	-
2	MC3	F	520	-	-	0/8/8/49	-
2	MC3	K	524	-	-	0/4/4/49	-
2	MC3	A	516	-	-	0/10/10/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	C	505	-	-	0/8/8/49	-
2	MC3	F	503	-	-	0/10/10/49	-
2	MC3	G	522	-	-	0/2/2/49	-
2	MC3	G	518	-	-	0/8/8/49	-
2	MC3	G	519	-	-	0/7/7/49	-
2	MC3	E	510	-	-	0/2/2/49	-
2	MC3	I	508	-	-	0/4/4/49	-
2	MC3	L	502	-	-	0/8/8/49	-
2	MC3	I	509	-	-	0/2/2/49	-
2	MC3	A	512	-	-	0/4/4/49	-
2	MC3	B	501	-	-	0/10/10/49	-
2	MC3	B	523	-	-	0/4/4/49	-

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	513	MC3	O2P-P-O1P	2.25	119.59	110.83
2	J	513	MC3	O2P-P-O1P	2.25	119.59	110.83
2	E	513	MC3	O2P-P-O1P	2.24	119.56	110.83
2	G	502	MC3	O2P-P-O1P	2.24	119.56	110.83
2	B	513	MC3	O2P-P-O1P	2.24	119.55	110.83

There are no chirality outliers.

5 of 96 torsion outliers are listed below:

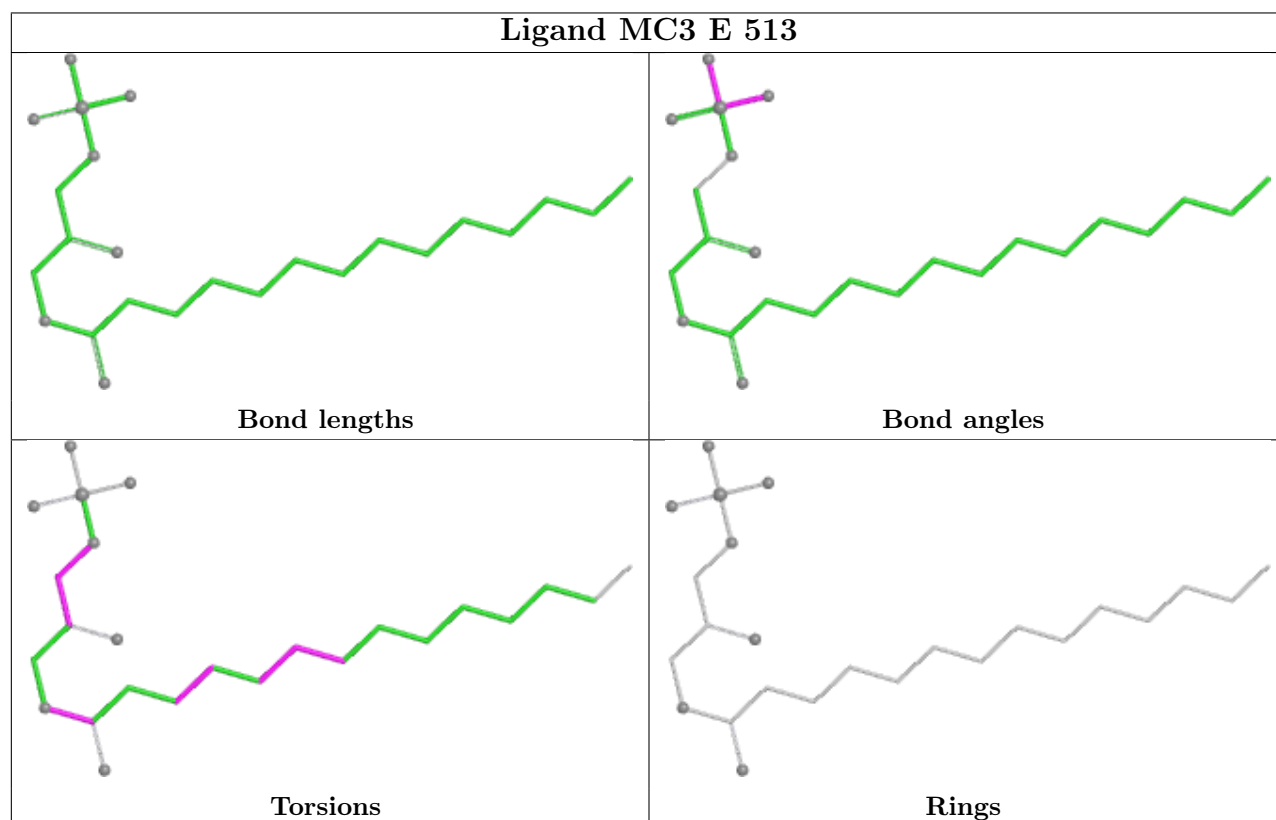
Mol	Chain	Res	Type	Atoms
2	A	502	MC3	O3P-C1-C2-C3
2	B	513	MC3	O3P-C1-C2-C3
2	C	513	MC3	O3P-C1-C2-C3
2	D	513	MC3	O3P-C1-C2-C3
2	E	513	MC3	O3P-C1-C2-C3

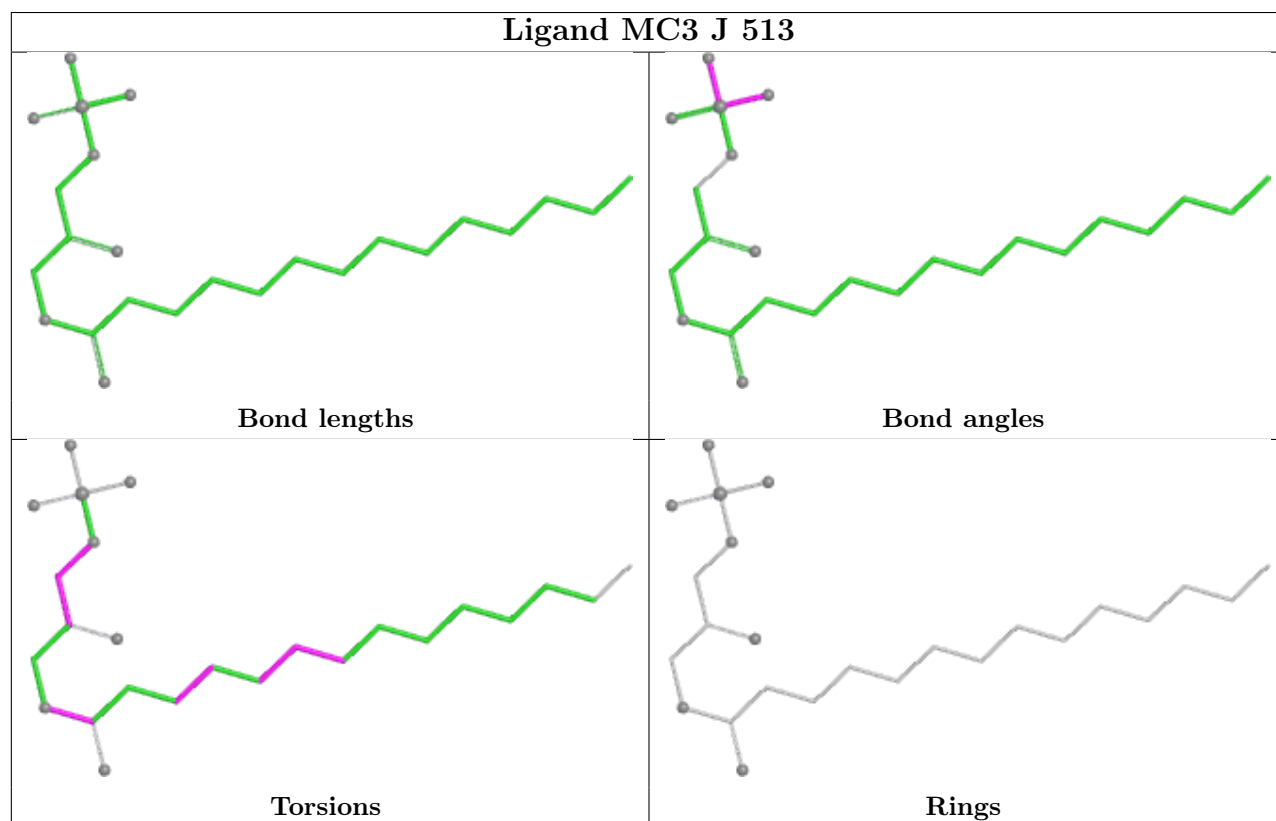
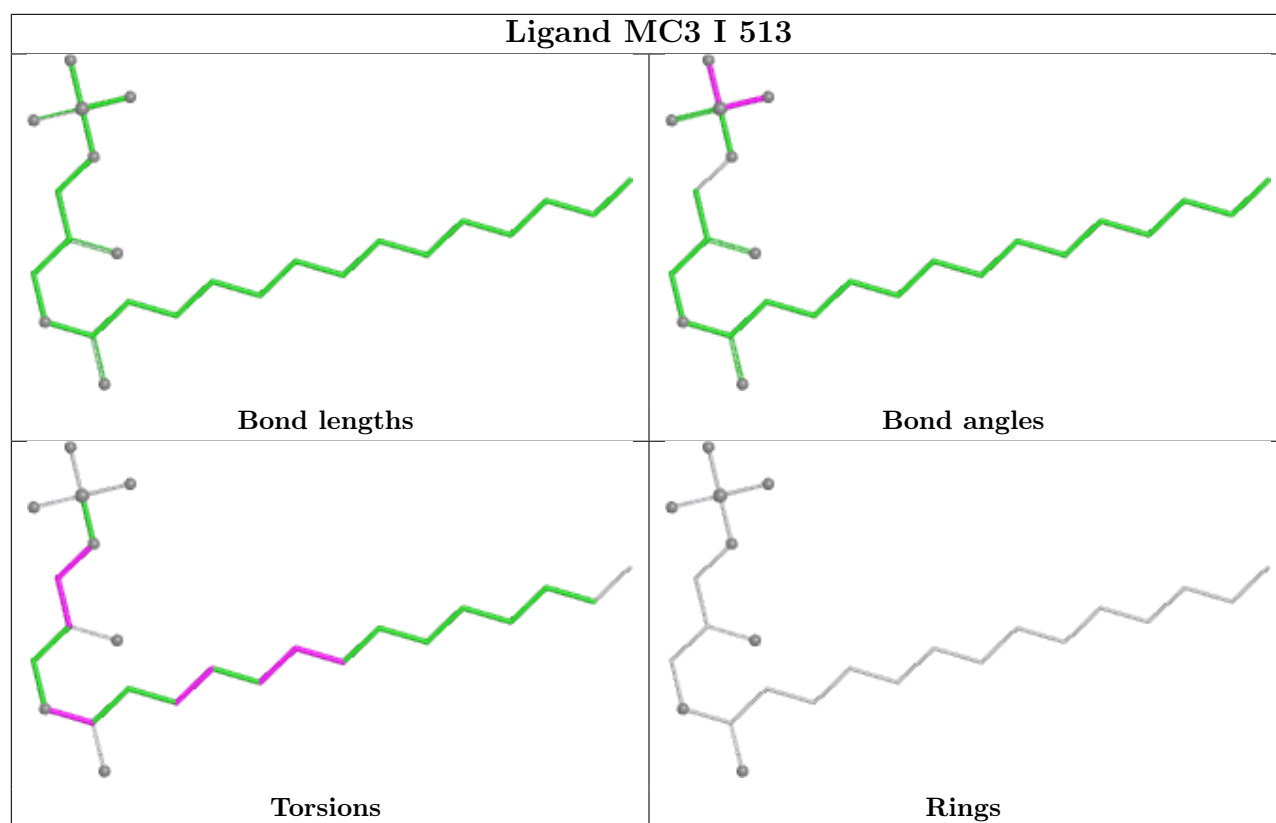
There are no ring outliers.

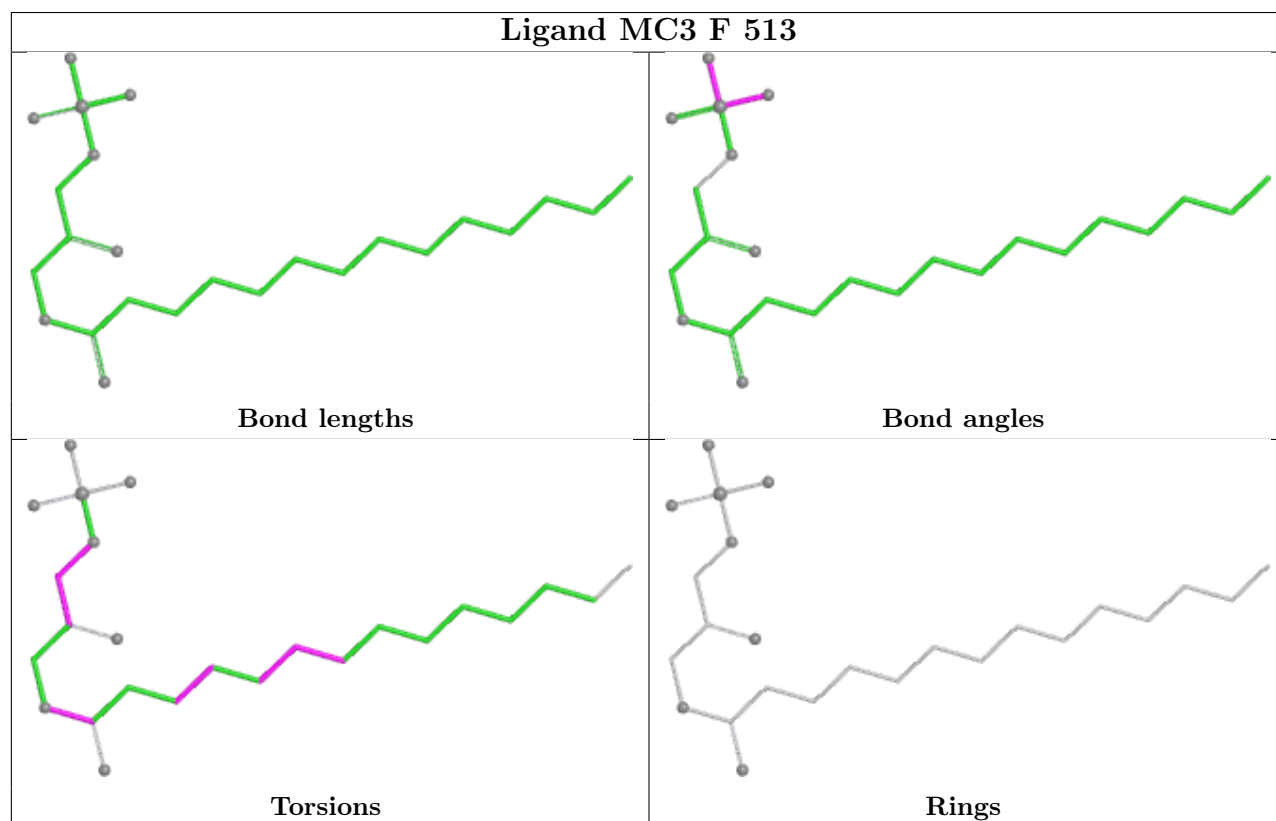
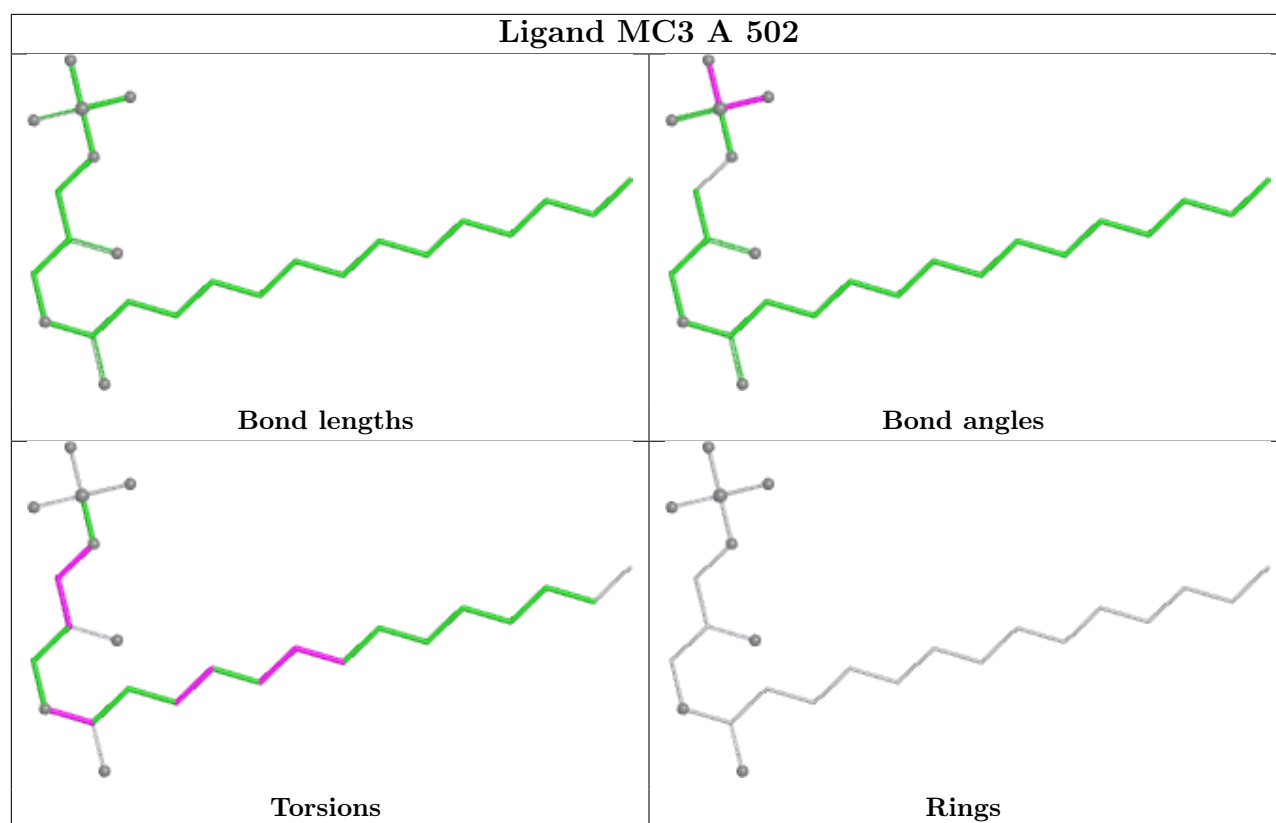
No monomer is involved in short contacts.

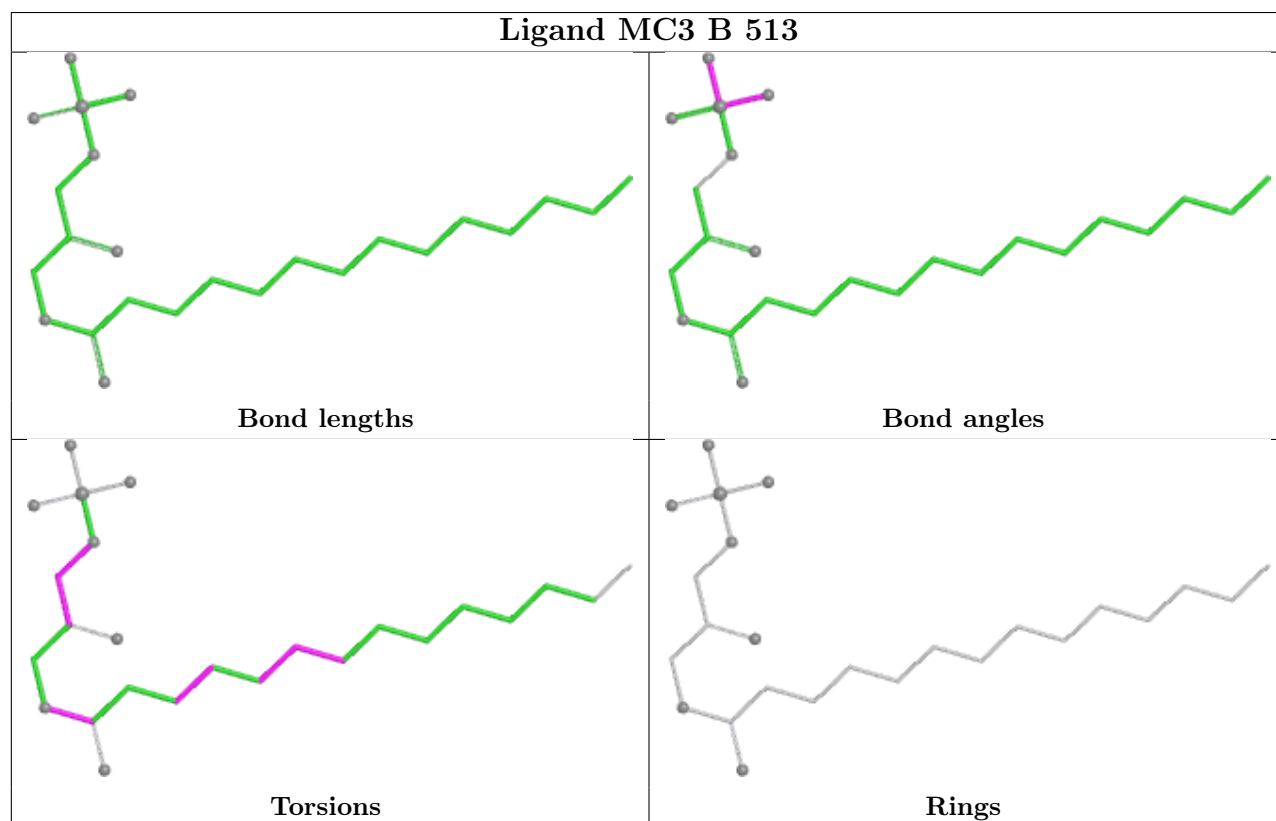
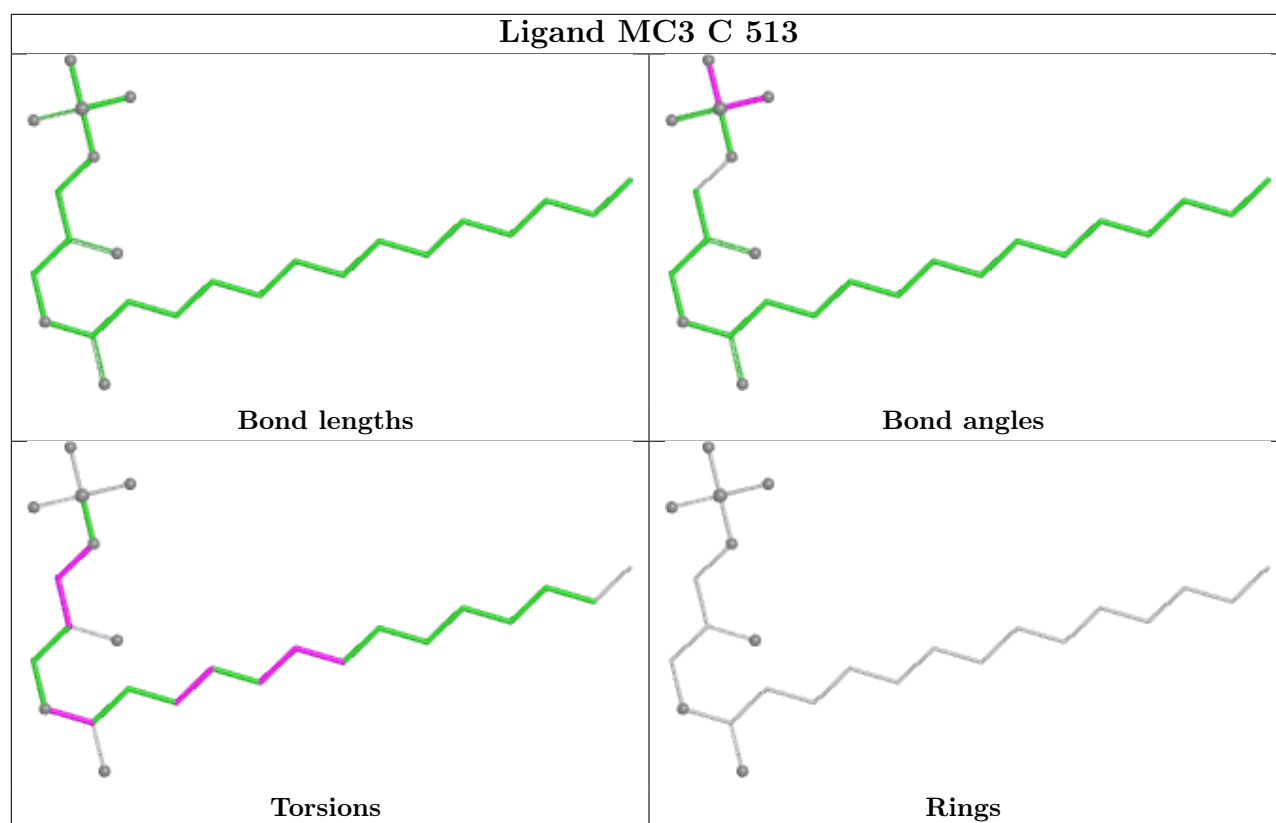
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

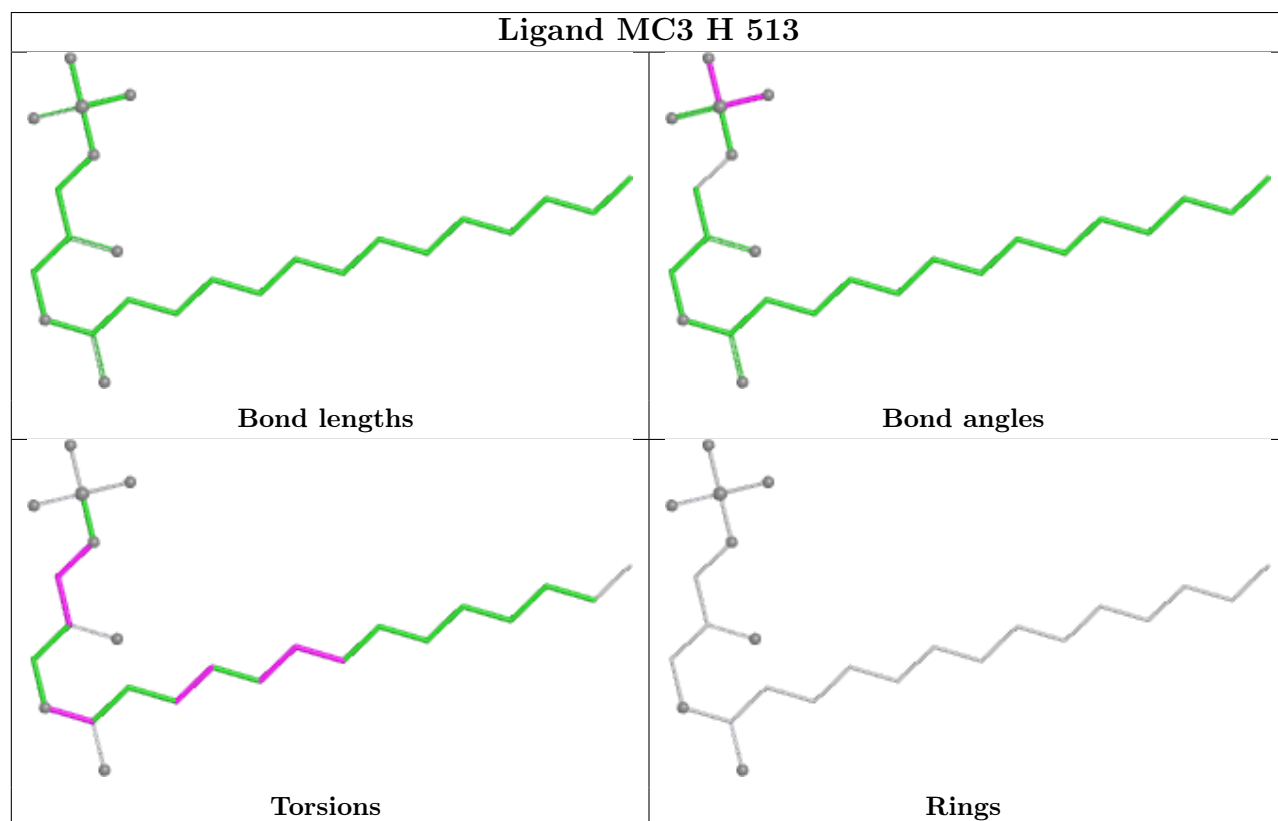
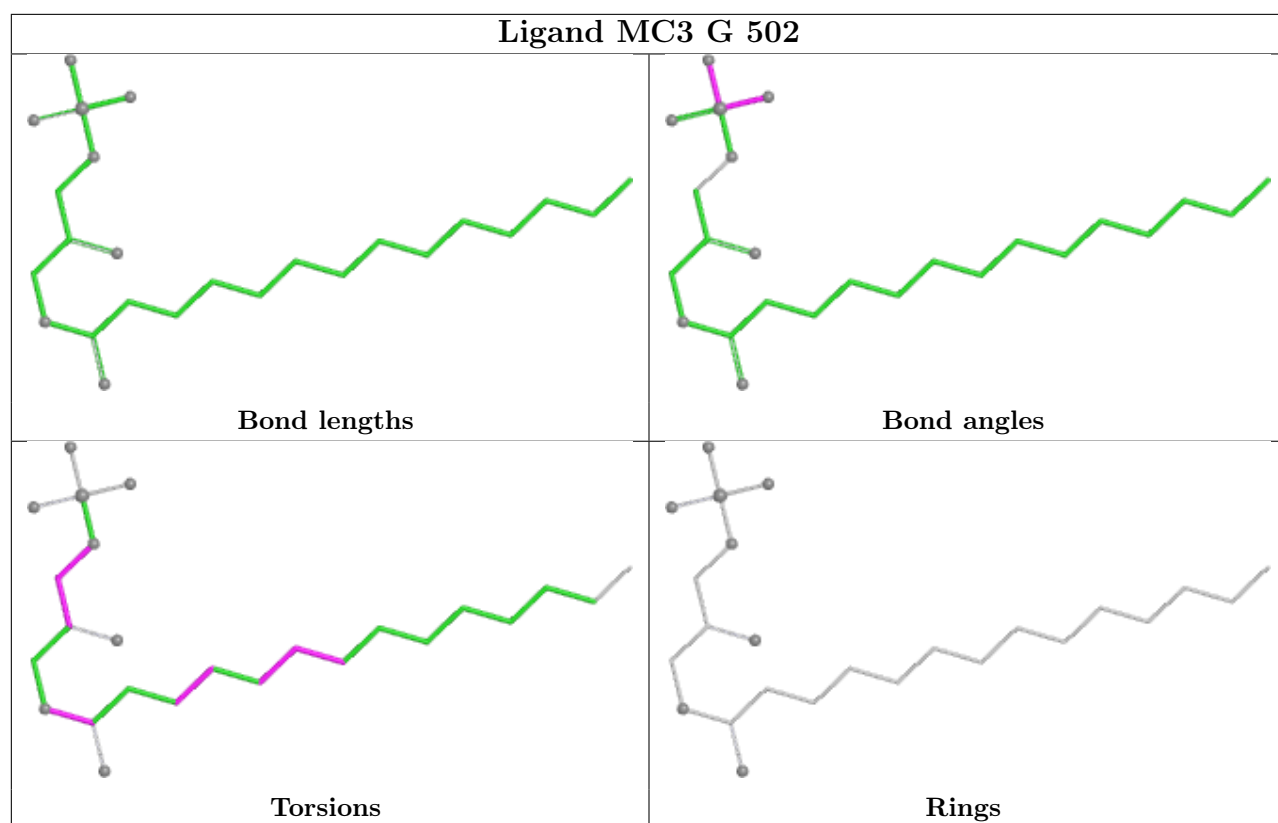
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

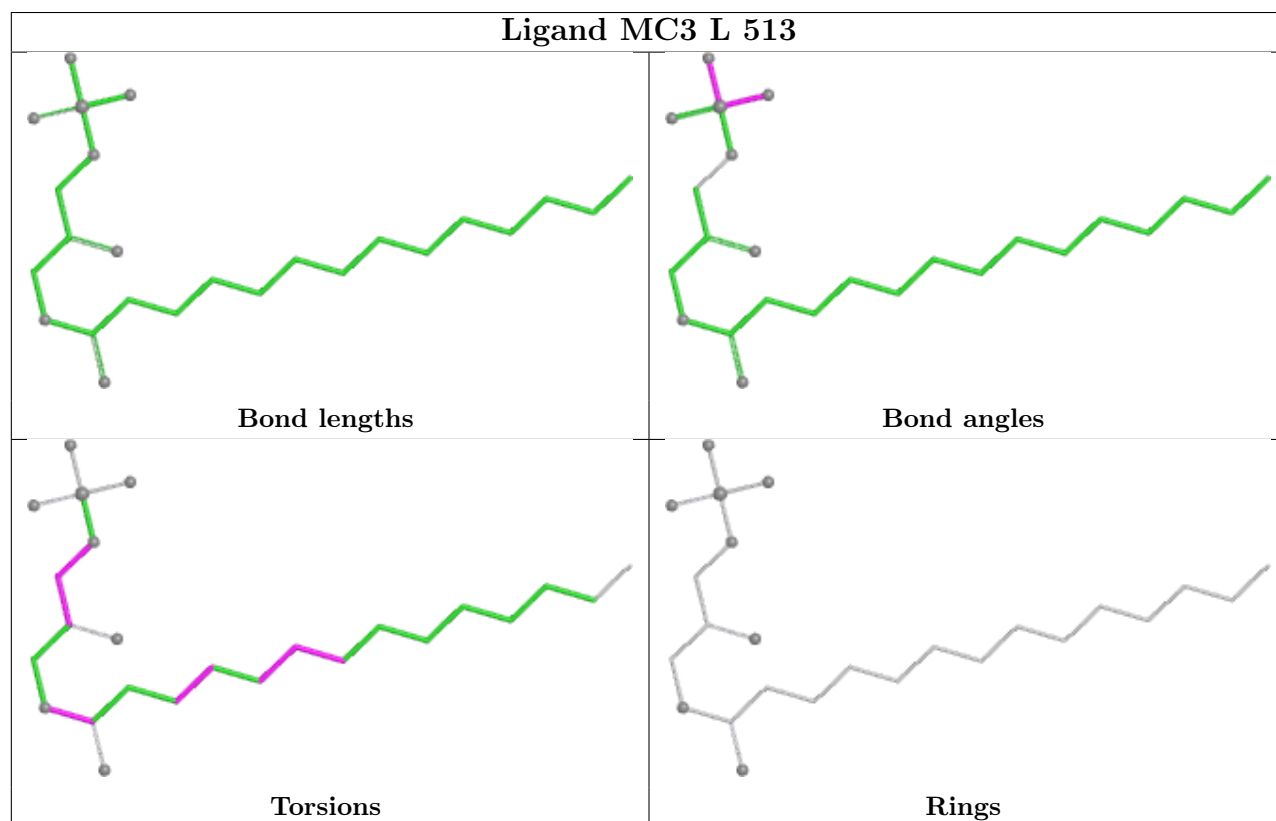
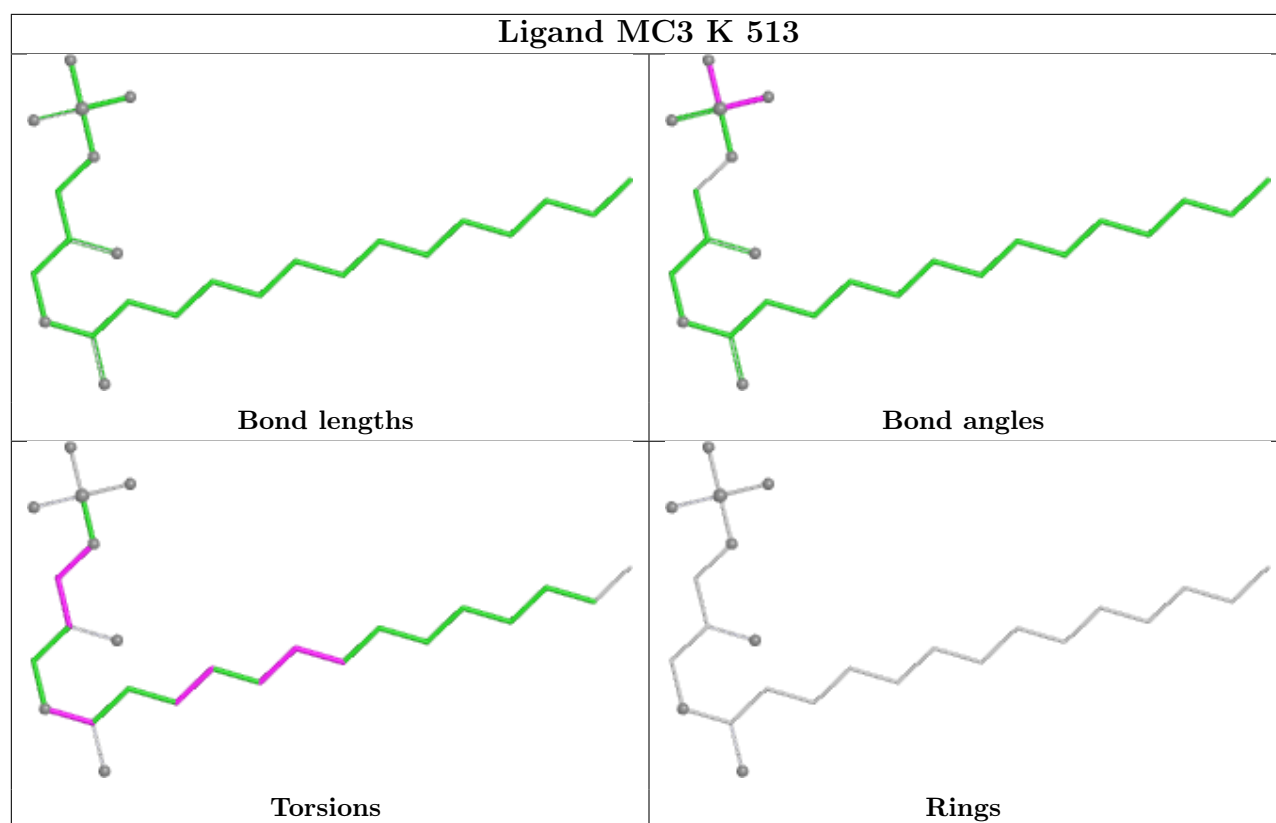


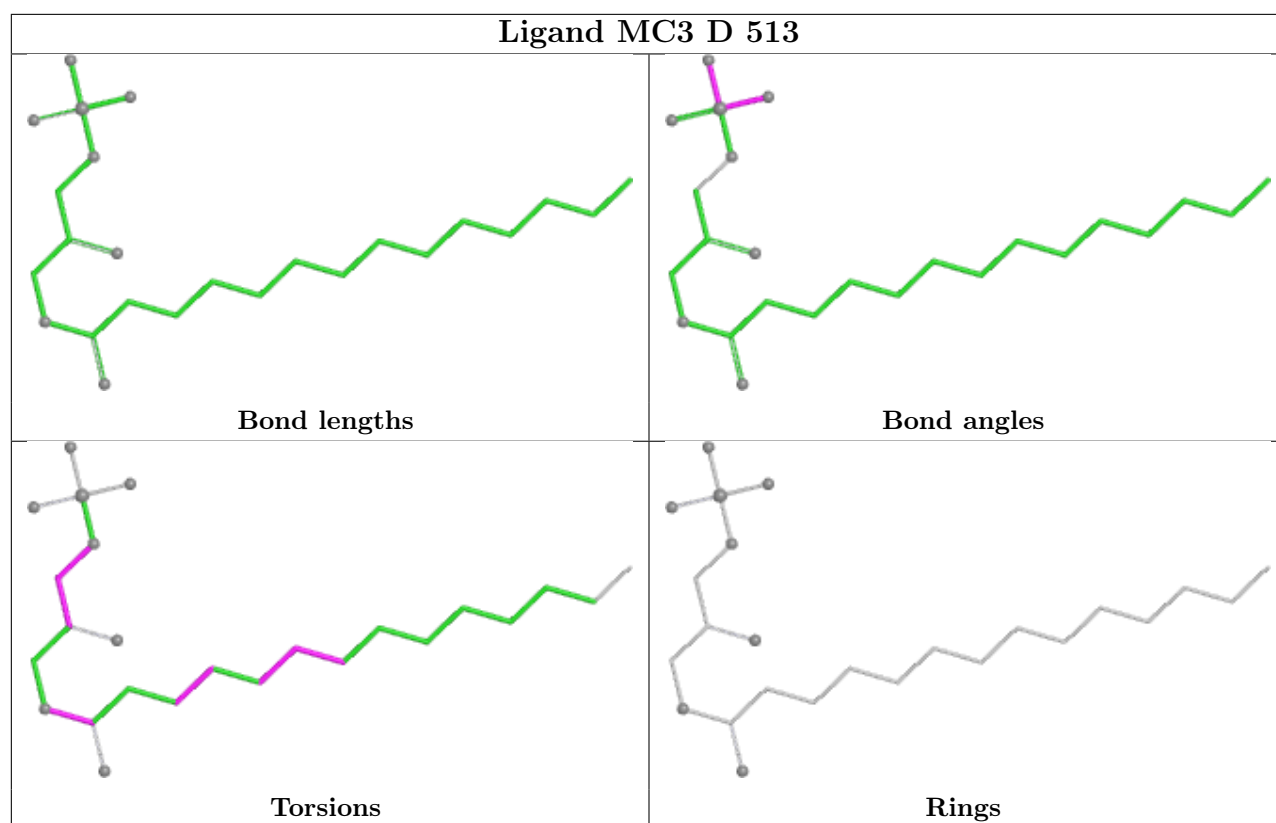












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

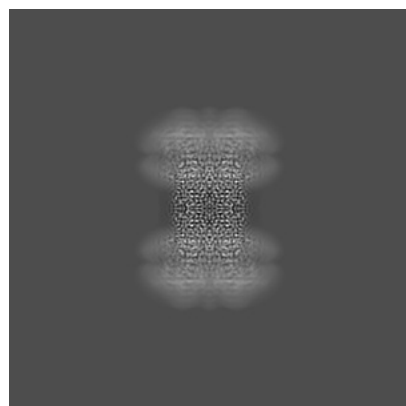
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73957. These allow visual inspection of the internal detail of the map and identification of artifacts.

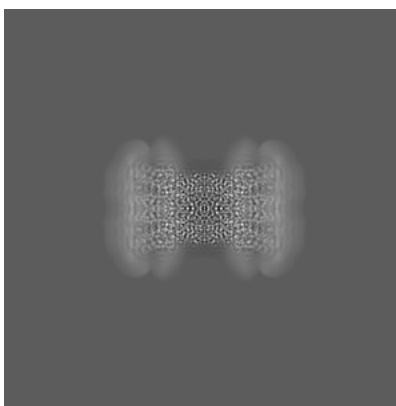
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

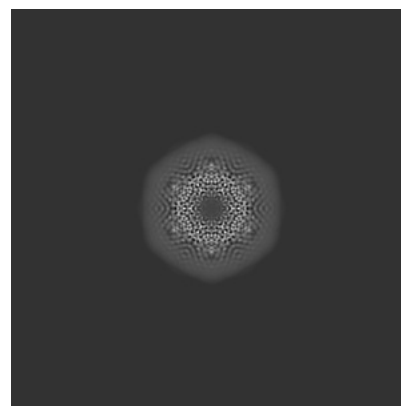
6.1.1 Primary map



X

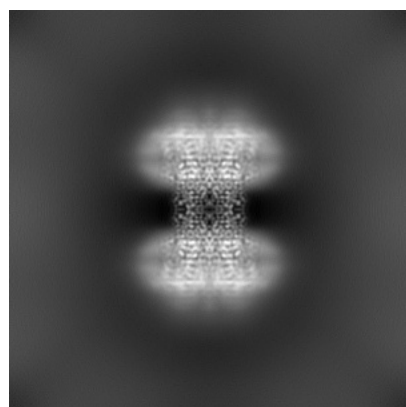


Y

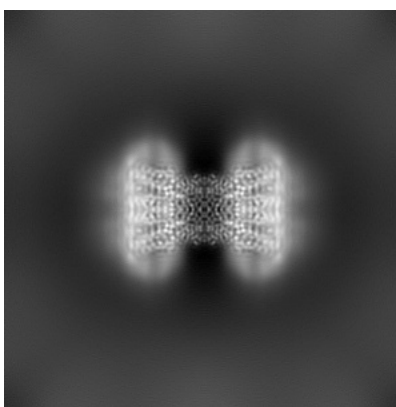


Z

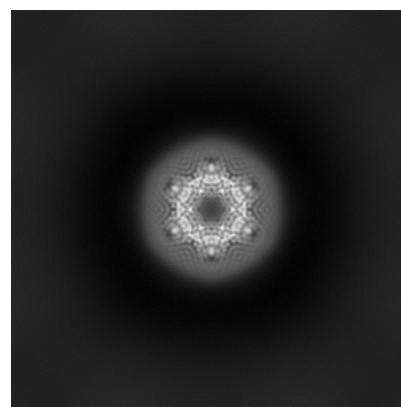
6.1.2 Raw map



X



Y

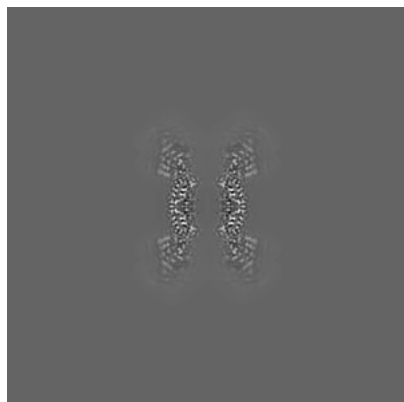


Z

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

6.2 Central slices [i](#)

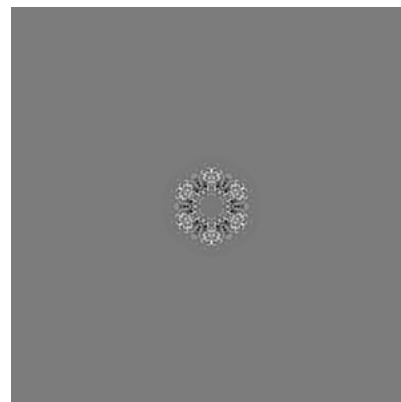
6.2.1 Primary map



X Index: 192

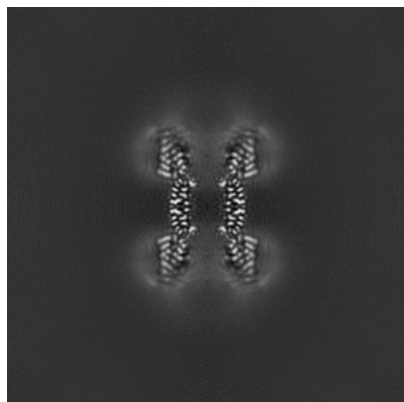


Y Index: 192

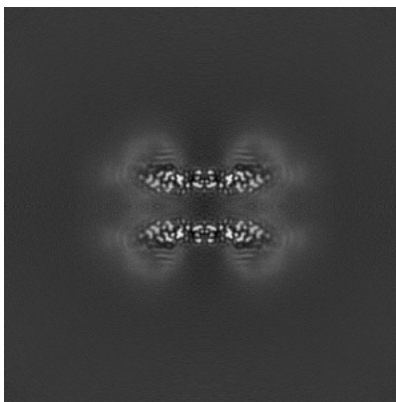


Z Index: 192

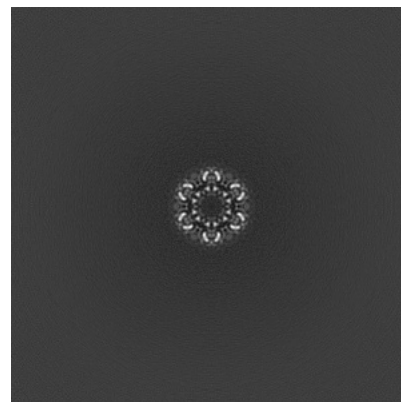
6.2.2 Raw map



X Index: 192



Y Index: 192

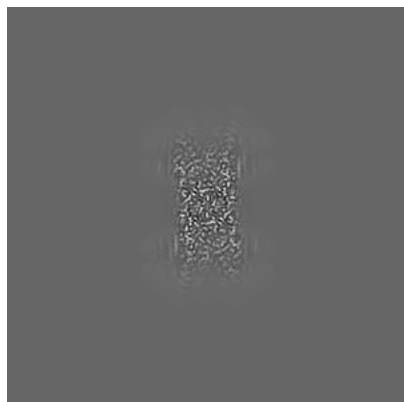


Z Index: 192

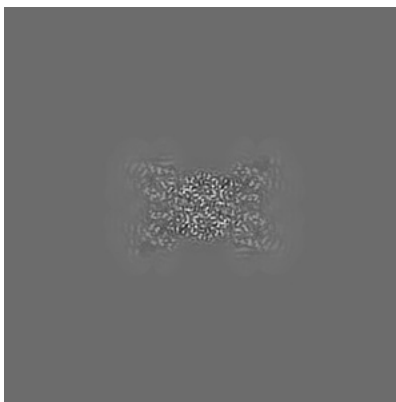
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

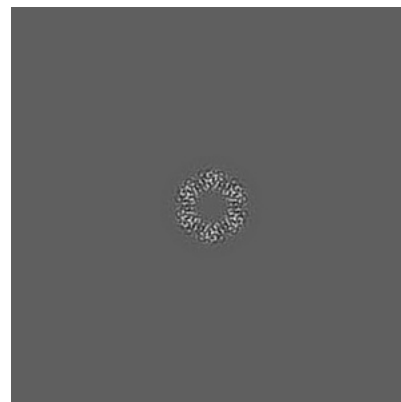
6.3.1 Primary map



X Index: 171

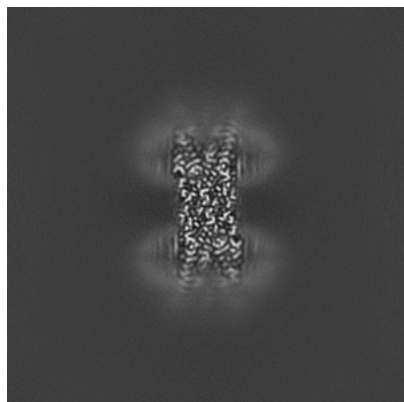


Y Index: 174

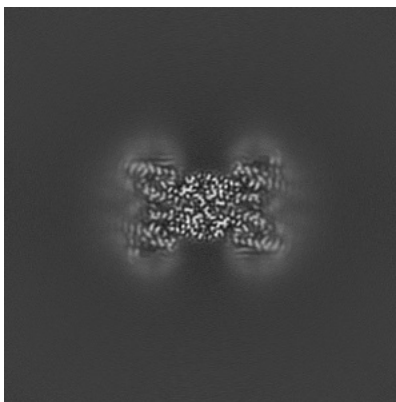


Z Index: 204

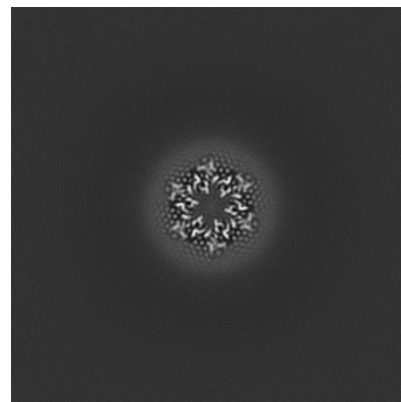
6.3.2 Raw map



X Index: 171



Y Index: 174

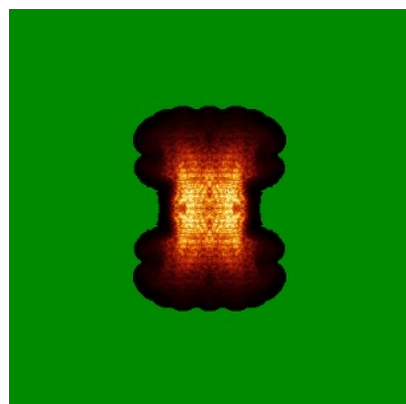


Z Index: 223

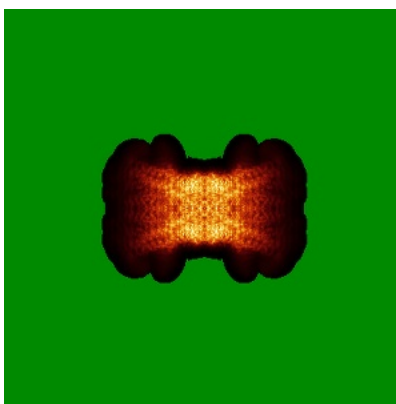
The images above show the largest variance slices of the map in three orthogonal directions.

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

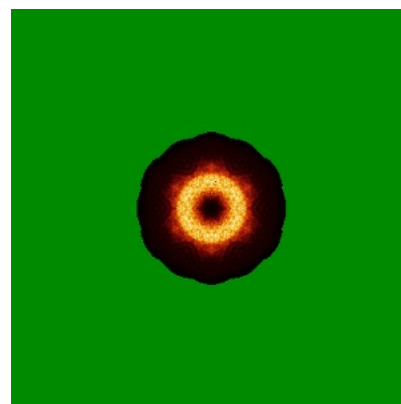
6.4.1 Primary map



X

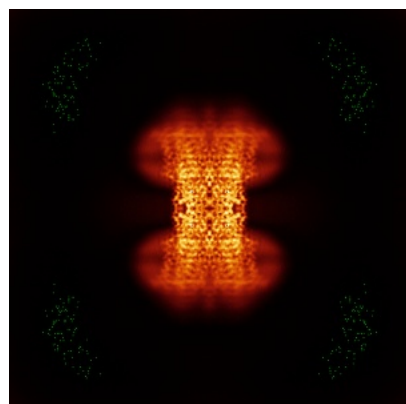


Y

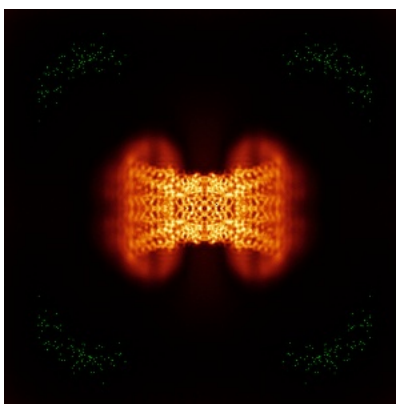


Z

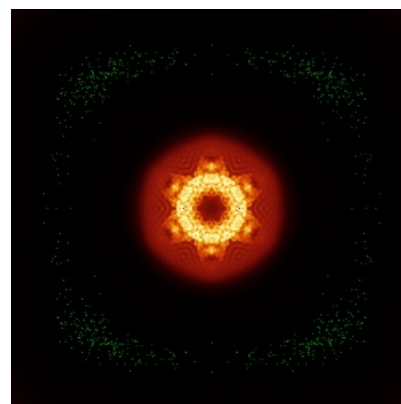
6.4.2 Raw map



X



Y

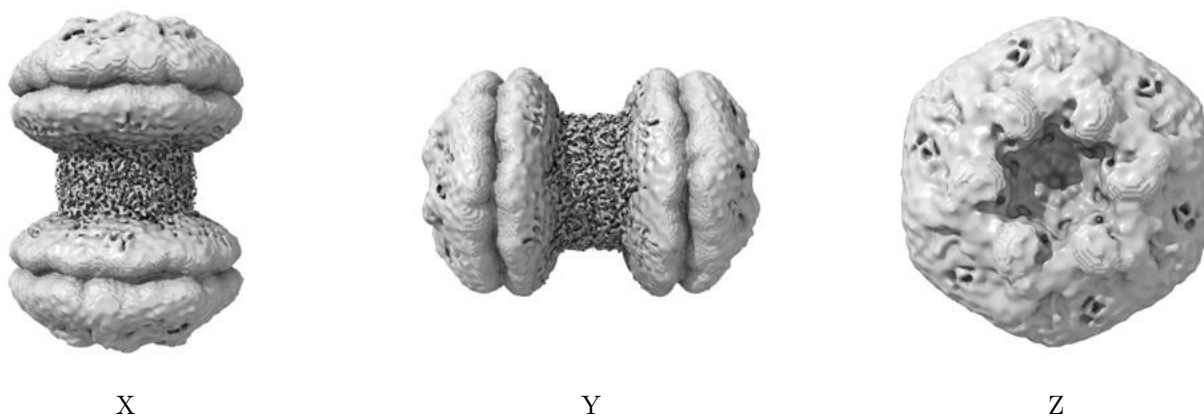


Z

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.

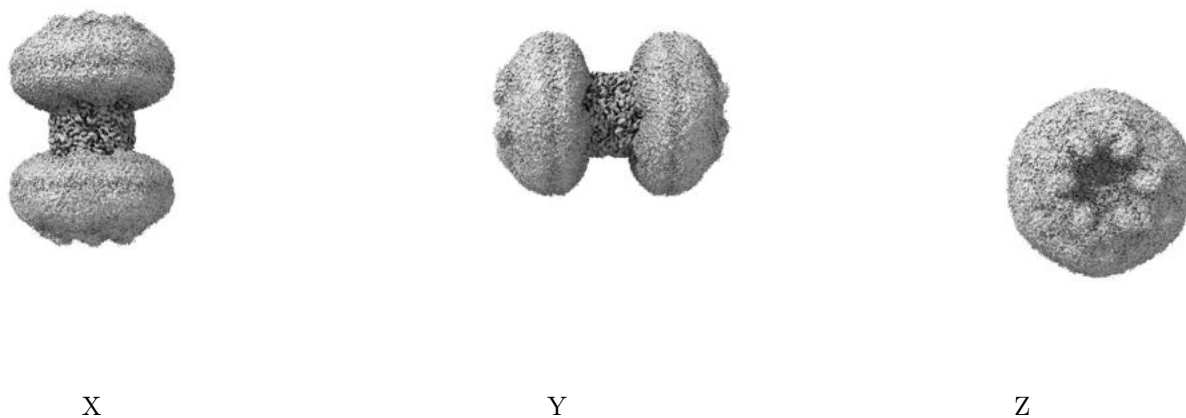
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

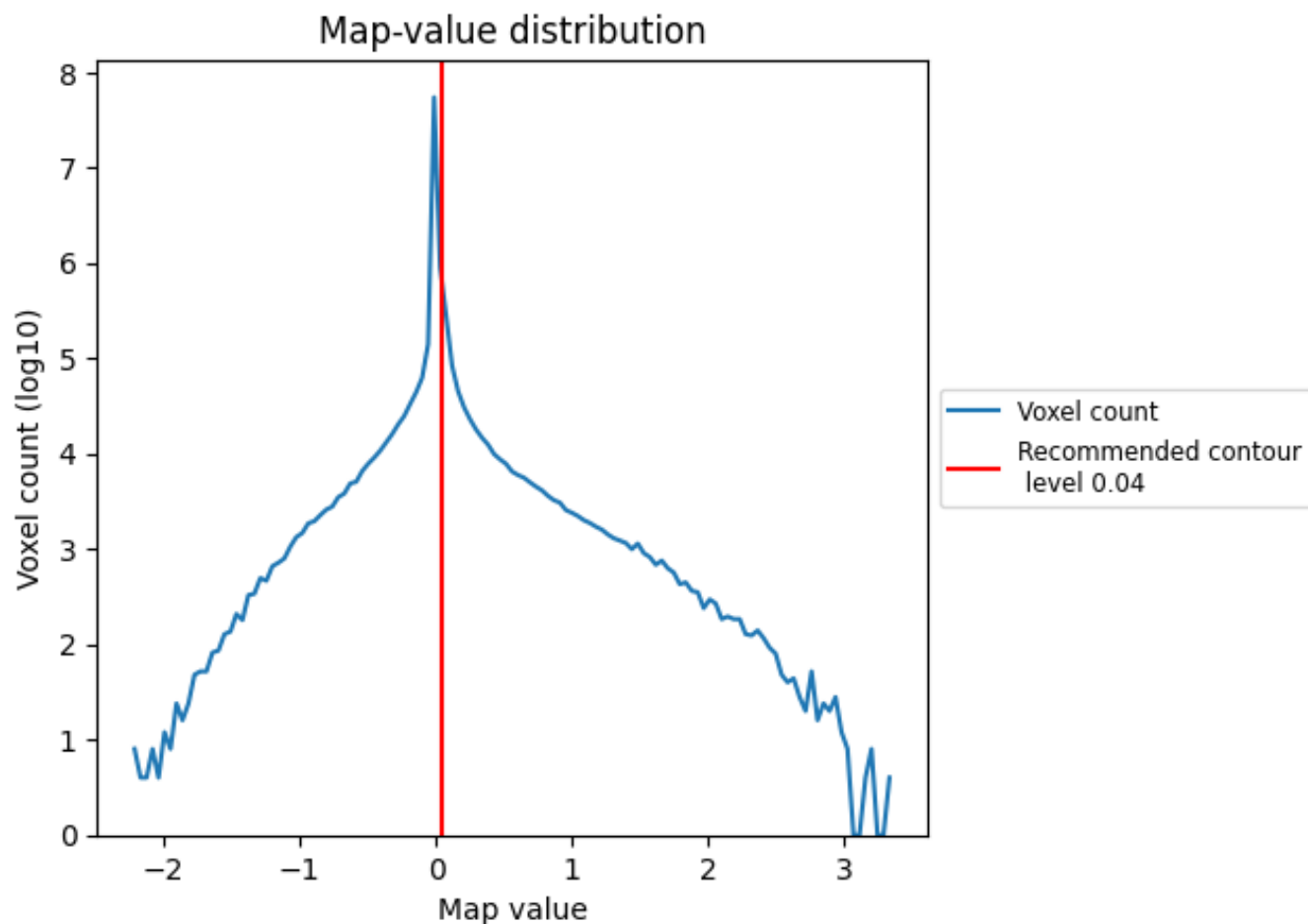
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

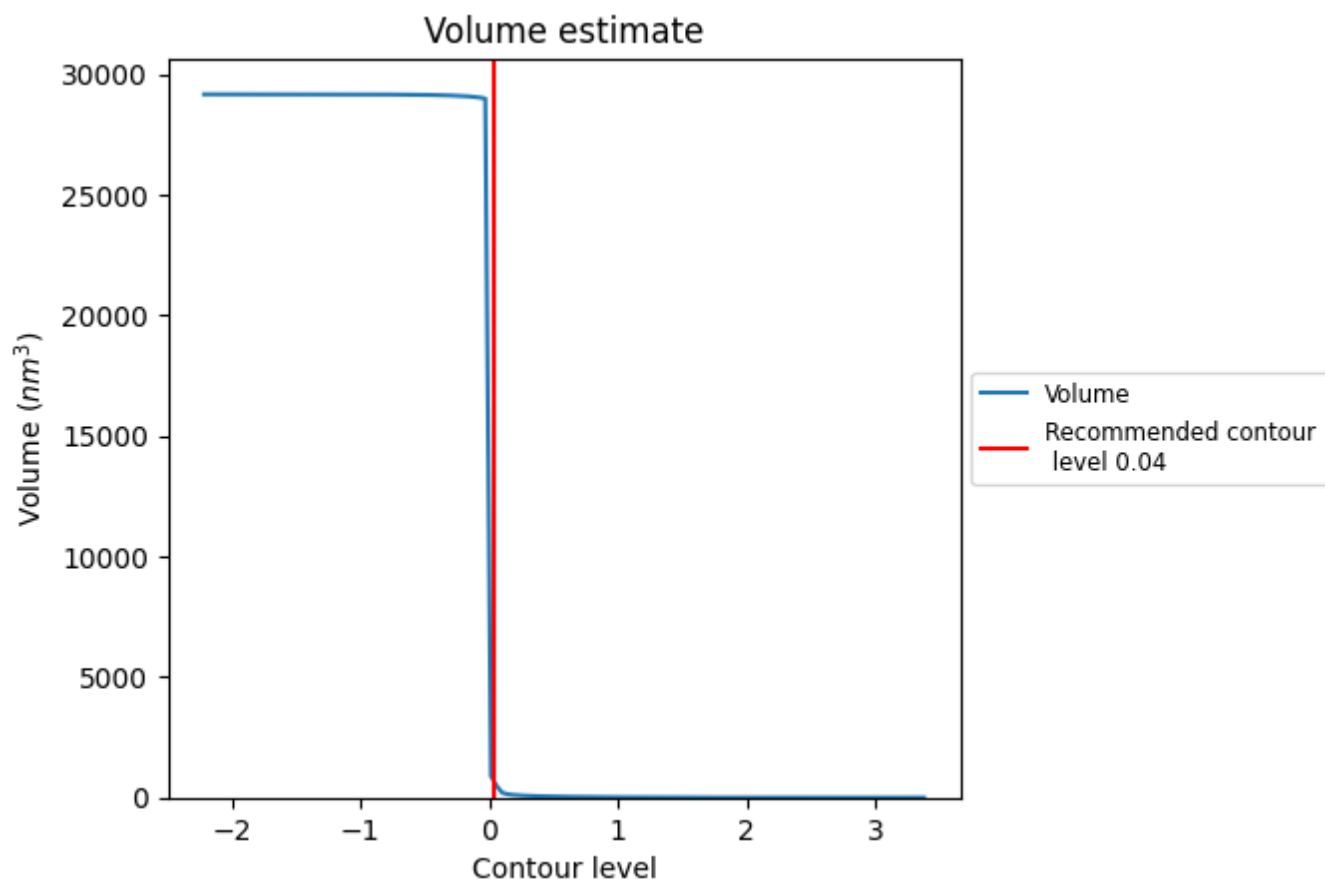
This section contains the results of statistical analysis of the map.

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.

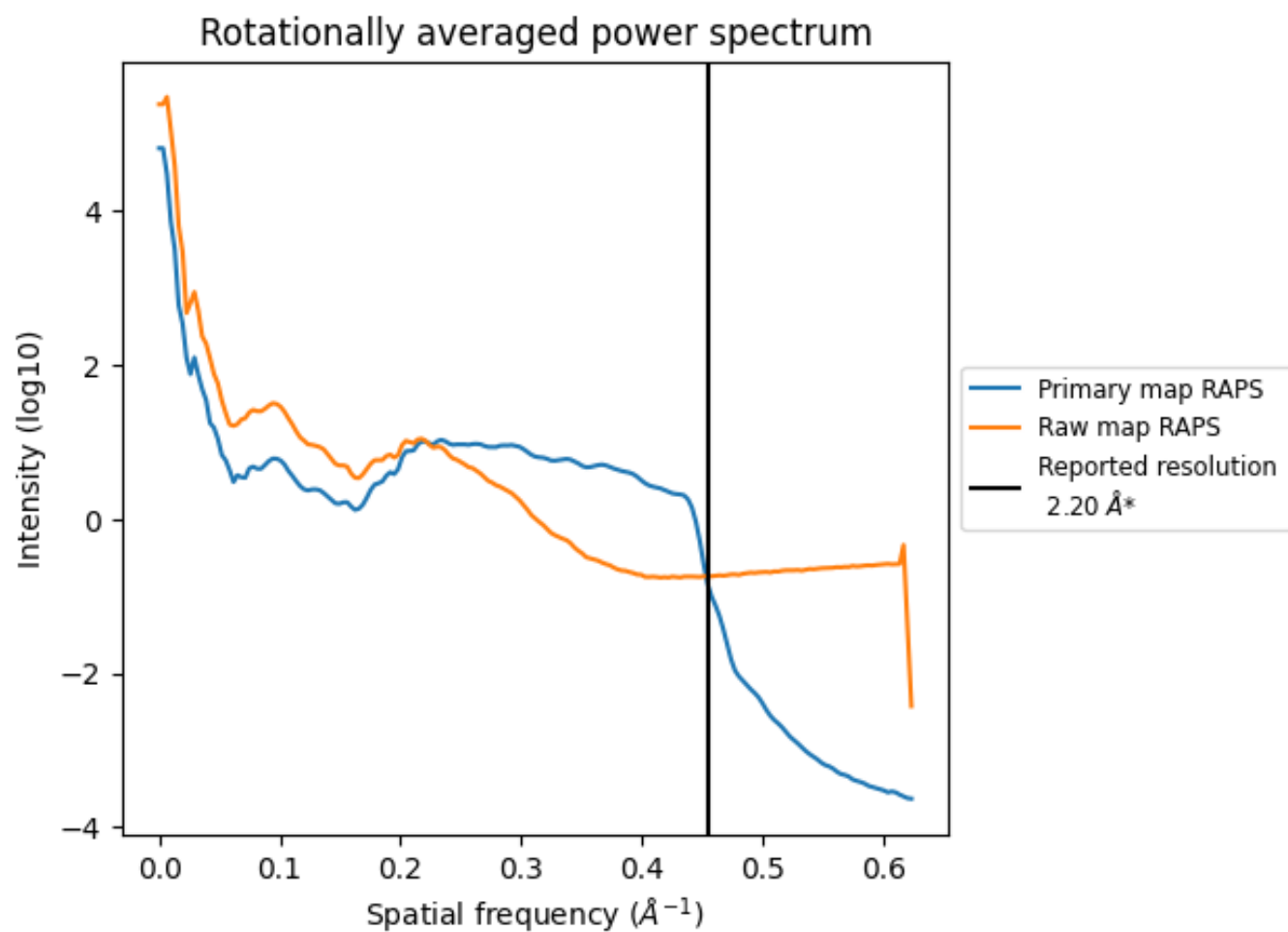
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 640 nm³; this corresponds to an approximate mass of 578 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 ⓘ

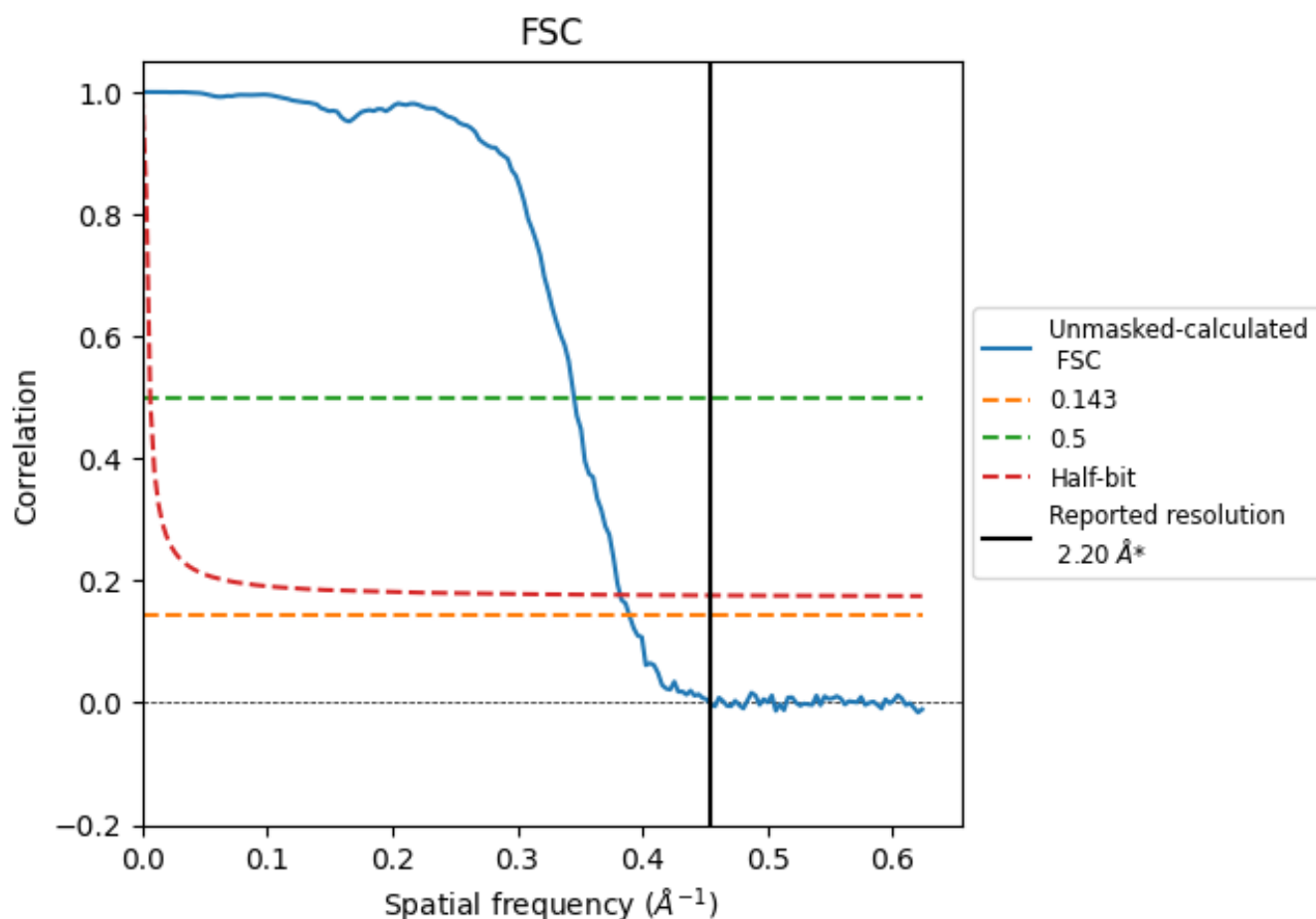


*Reported resolution corresponds to spatial frequency of $0.455 \text{ \AA}^{-1}$

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 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

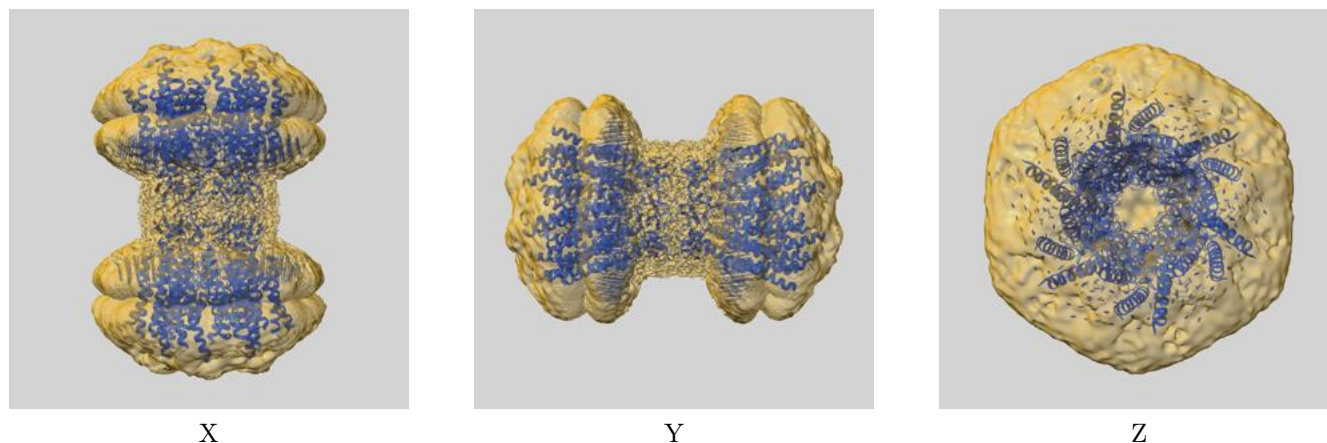
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.57	2.90	2.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.57 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

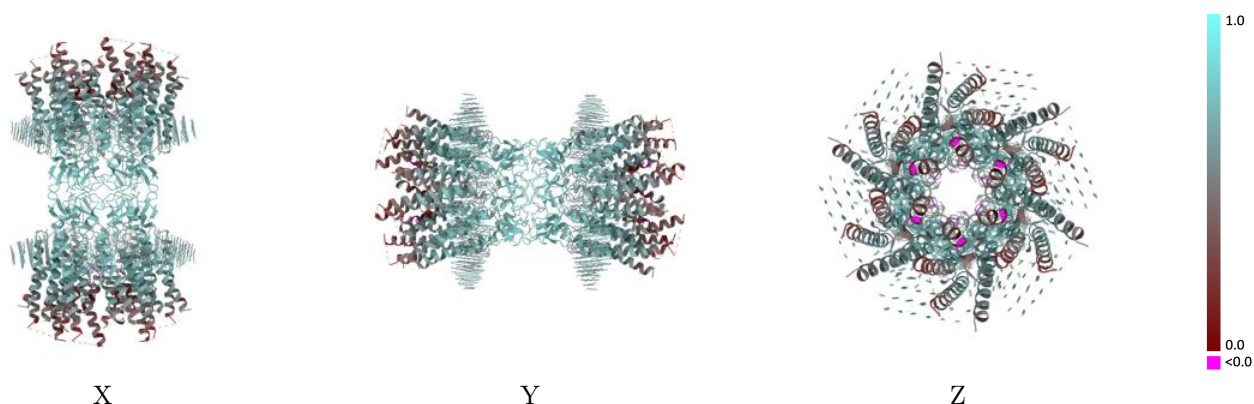
This section contains information regarding the fit between EMDB map EMD-73957 and PDB model 9Z9W. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



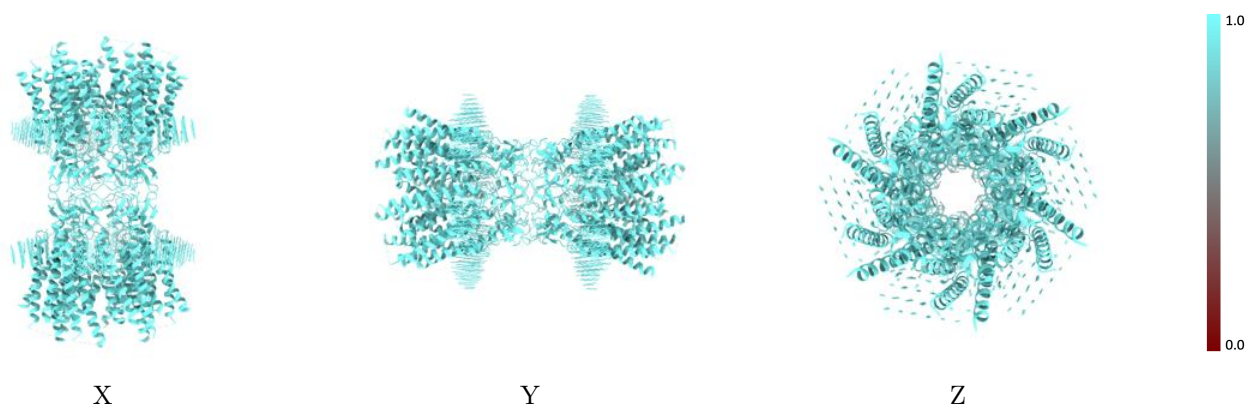
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



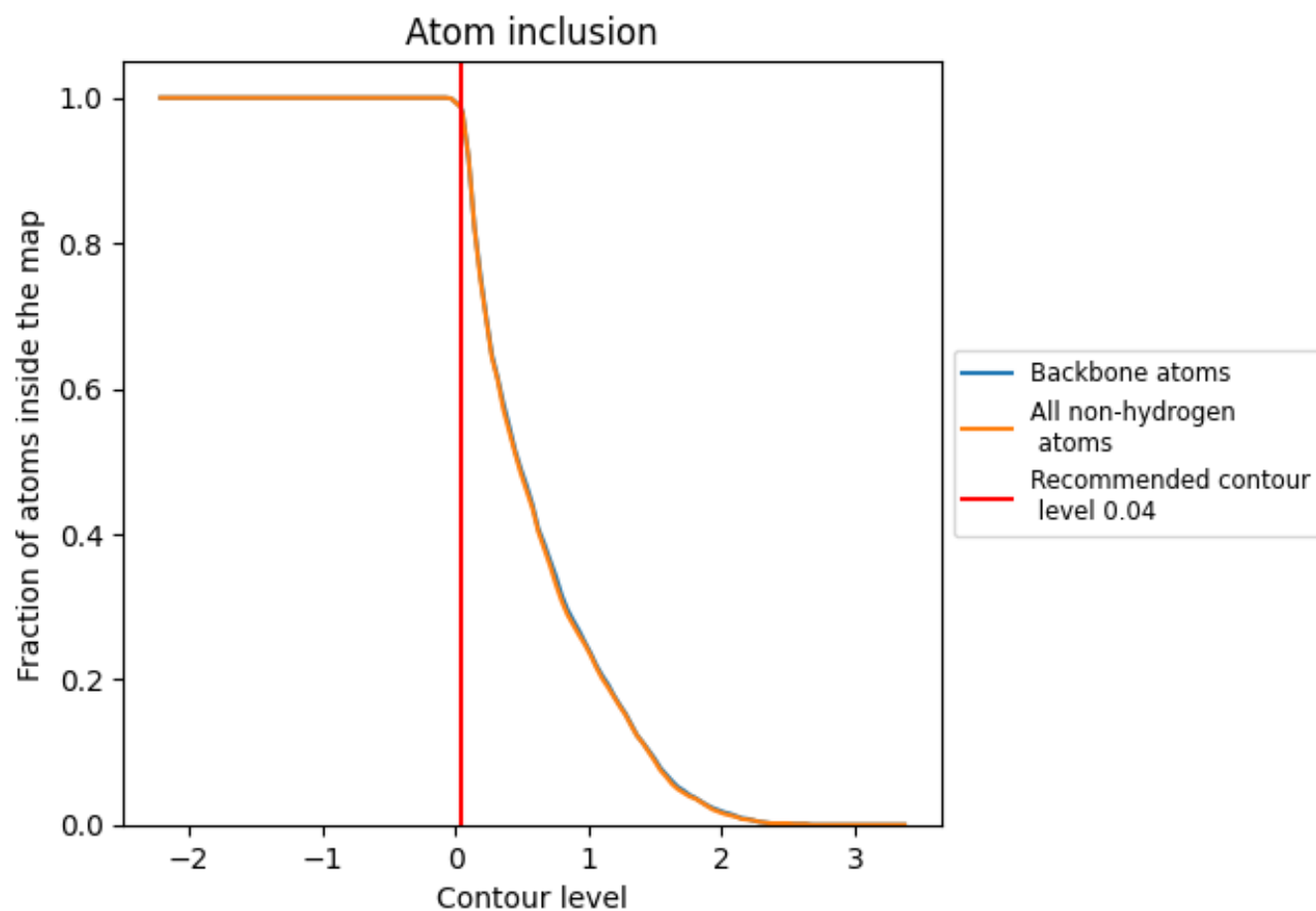
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9870	0.5950
A	0.9890	0.5930
B	0.9870	0.5930
C	0.9880	0.5940
D	0.9900	0.5950
E	0.9870	0.5950
F	0.9890	0.5950
G	0.9880	0.5960
H	0.9870	0.5950
I	0.9880	0.5960
J	0.9900	0.5960
K	0.9870	0.5940
L	0.9890	0.5940

1.0

0.0

<0.0