



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 01:04 AM UTC

PDB ID : 9Z8L / pdb_00009z8l
EMDB ID : EMD-73896
Title : Destabilized open state sheep connexin-50 in DMPC nanodiscs at neutral 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 : 7jkc

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
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

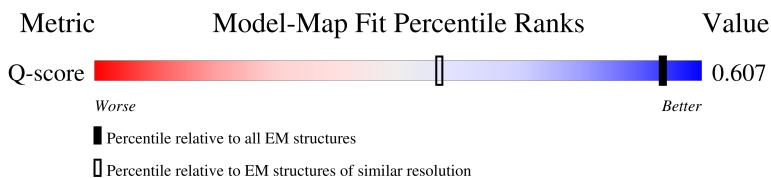
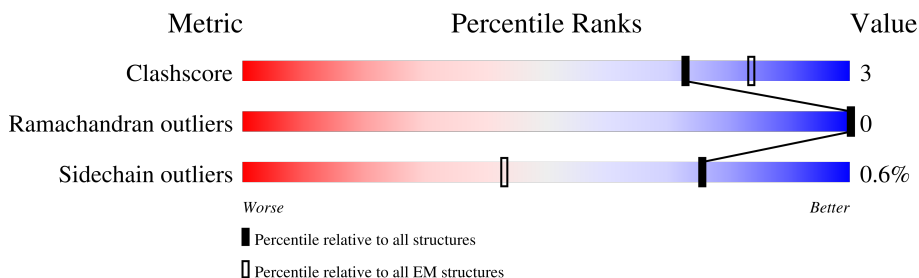
1 Overall quality at a glance

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	 38%5%58%
1	F	440	 38%5%58%
1	G	440	 38%5%58%
1	H	440	 38%5%58%
1	I	440	 38%5%58%
1	J	440	 38%5%58%
1	K	440	 38%5%58%
1	L	440	 38%5%58%

2 Entry composition

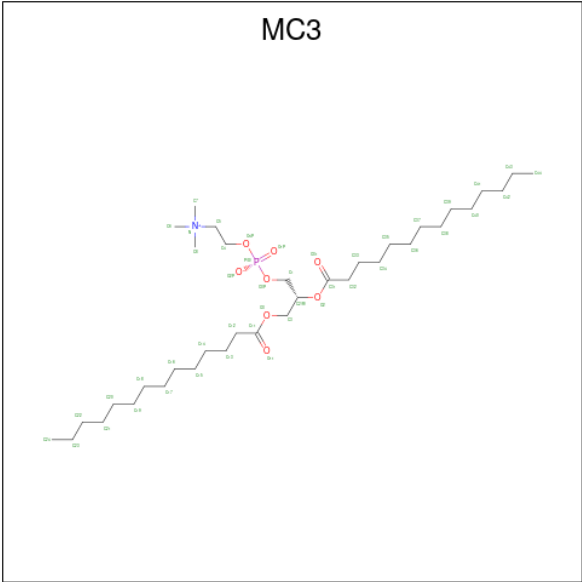
There are 3 unique types of molecules in this entry. The entry contains 45264 atoms, of which 23496 are hydrogens and 0 are deuteriums.

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	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	B	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	C	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	D	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	E	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	F	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	G	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	H	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	I	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	J	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	K	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		
1	L	187	Total	C	H	N	O	S	0	0
			3019	1004	1499	247	259	10		

- 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
			36	12	24	
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
			31	11	20	
2	A	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	A	1	Total	C	H	0
			32	11	21	
2	A	1	Total	C	H	0
			21	7	14	
2	A	1	Total	C	H	0
			24	8	16	
2	A	1	Total	C	H	0
			24	8	16	
2	A	1	Total	C	H	0
			30	10	20	
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
			36	12	24	
2	A	1	Total	C	H	0
			36	12	24	
2	A	1	Total	C	H	0
			30	10	20	
2	A	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	A	1	Total	C	H	0
			15	5	10	
2	A	1	Total	C	H	0
			21	7	14	
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
			36	12	24	
2	B	1	Total	C	H	0
			30	10	20	
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			24	8	16	
2	B	1	Total	C	H	0
			33	11	22	
2	B	1	Total	C	H	0
			27	9	18	
2	B	1	Total	C	H	0
			15	5	10	
2	B	1	Total	C	H	0
			21	7	14	
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			39	13	26	

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Mol	Chain	Residues	Atoms			AltConf
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			31	11	20	
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			15	5	10	
2	B	1	Total	C	H	0
			33	11	22	
2	B	1	Total	C	H	0
			36	12	24	
2	B	1	Total	C	H	0
			32	11	21	
2	B	1	Total	C	H	0
			21	7	14	
2	B	1	Total	C	H	0
			24	8	16	
2	B	1	Total	C	H	0
			24	8	16	
2	B	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
			36	12	24	
2	C	1	Total	C	H	0
			36	12	24	
2	C	1	Total	C	H	0
			30	10	20	
2	C	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	C	1	Total	C	H	0
			15	5	10	
2	C	1	Total	C	H	0
			21	7	14	

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Mol	Chain	Residues	Atoms			AltConf
2	C	1	Total	C	H	0
			36	12	24	
2	C	1	Total	C	H	0
			39	13	26	
2	C	1	Total	C	H	0
			36	12	24	
2	C	1	Total	C	H	0
			31	11	20	
2	C	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	C	1	Total	C	H	0
			32	11	21	
2	C	1	Total	C	H	0
			21	7	14	
2	C	1	Total	C	H	0
			24	8	16	
2	C	1	Total	C	H	0
			24	8	16	
2	C	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
			36	12	24	
2	D	1	Total	C	H	0
			36	12	24	
2	D	1	Total	C	H	0
			30	10	20	
2	D	1	Total	C	H	0
			36	12	24	
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
			27	9	18	

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Mol	Chain	Residues	Atoms			AltConf
2	D	1	Total	C	H	0
			15	5	10	
2	D	1	Total	C	H	0
			21	7	14	
2	D	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	D	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	D	1	Total	C	H	0
			32	11	21	
2	D	1	Total	C	H	0
			21	7	14	
2	D	1	Total	C	H	0
			24	8	16	
2	D	1	Total	C	H	0
			24	8	16	
2	D	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
			36	12	24	
2	E	1	Total	C	H	0
			36	12	24	
2	E	1	Total	C	H	0
			30	10	20	
2	E	1	Total	C	H	0
			36	12	24	
2	E	1	Total	C	H	0
			24	8	16	

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Mol	Chain	Residues	Atoms			AltConf
2	E	1	Total	C	H	0
			33	11	22	
2	E	1	Total	C	H	0
			27	9	18	
2	E	1	Total	C	H	0
			15	5	10	
2	E	1	Total	C	H	0
			21	7	14	
2	E	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	E	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	E	1	Total	C	H	0
			32	11	21	
2	E	1	Total	C	H	0
			21	7	14	
2	E	1	Total	C	H	0
			24	8	16	
2	E	1	Total	C	H	0
			24	8	16	
2	E	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
			36	12	24	
2	F	1	Total	C	H	0
			36	12	24	
2	F	1	Total	C	H	0
			30	10	20	

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Mol	Chain	Residues	Atoms			AltConf
2	F	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	F	1	Total	C	H	0
			15	5	10	
2	F	1	Total	C	H	0
			21	7	14	
2	F	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	F	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	F	1	Total	C	H	0
			32	11	21	
2	F	1	Total	C	H	0
			21	7	14	
2	F	1	Total	C	H	0
			24	8	16	
2	F	1	Total	C	H	0
			24	8	16	
2	F	1	Total	C	H	0
			30	10	20	
2	G	1	Total	C	H	0
			36	12	24	
2	G	1	Total	C	H	0
			39	13	26	

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Mol	Chain	Residues	Atoms			AltConf
2	G	1	Total	C	H	0
			36	12	24	
2	G	1	Total	C	H	0
			31	11	20	
2	G	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	G	1	Total	C	H	0
			32	11	21	
2	G	1	Total	C	H	0
			21	7	14	
2	G	1	Total	C	H	0
			24	8	16	
2	G	1	Total	C	H	0
			24	8	16	
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
			36	12	24	
2	G	1	Total	C	H	0
			36	12	24	
2	G	1	Total	C	H	0
			30	10	20	
2	G	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	G	1	Total	C	H	0
			15	5	10	
2	G	1	Total	C	H	0
			21	7	14	

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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
			36	12	24	
2	H	1	Total	C	H	0
			36	12	24	
2	H	1	Total	C	H	0
			30	10	20	
2	H	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	H	1	Total	C	H	0
			15	5	10	
2	H	1	Total	C	H	0
			21	7	14	
2	H	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	H	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	H	1	Total	C	H	0
			32	11	21	
2	H	1	Total	C	H	0
			21	7	14	
2	H	1	Total	C	H	0
			24	8	16	

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Mol	Chain	Residues	Atoms			AltConf
2	H	1	Total	C	H	0
			24	8	16	
2	H	1	Total	C	H	0
			30	10	20	
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
			36	12	24	
2	I	1	Total	C	H	0
			30	10	20	
2	I	1	Total	C	H	0
			36	12	24	
2	I	1	Total	C	H	0
			24	8	16	
2	I	1	Total	C	H	0
			33	11	22	
2	I	1	Total	C	H	0
			27	9	18	
2	I	1	Total	C	H	0
			15	5	10	
2	I	1	Total	C	H	0
			21	7	14	
2	I	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	I	1	Total	C	H	0
			36	12	24	
2	I	1	Total	C	H	0
			15	5	10	
2	I	1	Total	C	H	0
			33	11	22	
2	I	1	Total	C	H	0
			36	12	24	
2	I	1	Total	C	H	0
			32	11	21	

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Mol	Chain	Residues	Atoms			AltConf
2	I	1	Total	C	H	0
			21	7	14	
2	I	1	Total	C	H	0
			24	8	16	
2	I	1	Total	C	H	0
			24	8	16	
2	I	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
			36	12	24	
2	J	1	Total	C	H	0
			36	12	24	
2	J	1	Total	C	H	0
			30	10	20	
2	J	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	J	1	Total	C	H	0
			15	5	10	
2	J	1	Total	C	H	0
			21	7	14	
2	J	1	Total	C	H	0
			36	12	24	
2	J	1	Total	C	H	0
			39	13	26	
2	J	1	Total	C	H	0
			36	12	24	
2	J	1	Total	C	H	0
			31	11	20	
2	J	1	Total	C	H	0
			36	12	24	
2	J	1	Total	C	H	0
			15	5	10	
2	J	1	Total	C	H	0
			33	11	22	

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Mol	Chain	Residues	Atoms			AltConf
2	J	1	Total	C	H	0
			36	12	24	
2	J	1	Total	C	H	0
			32	11	21	
2	J	1	Total	C	H	0
			21	7	14	
2	J	1	Total	C	H	0
			24	8	16	
2	J	1	Total	C	H	0
			24	8	16	
2	J	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
			36	12	24	
2	K	1	Total	C	H	0
			36	12	24	
2	K	1	Total	C	H	0
			30	10	20	
2	K	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	K	1	Total	C	H	0
			15	5	10	
2	K	1	Total	C	H	0
			21	7	14	
2	K	1	Total	C	H	0
			36	12	24	
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
			31	11	20	
2	K	1	Total	C	H	0
			36	12	24	

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Mol	Chain	Residues	Atoms			AltConf
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
			36	12	24	
2	K	1	Total	C	H	0
			32	11	21	
2	K	1	Total	C	H	0
			21	7	14	
2	K	1	Total	C	H	0
			24	8	16	
2	K	1	Total	C	H	0
			24	8	16	
2	K	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
			36	12	24	
2	L	1	Total	C	H	0
			36	12	24	
2	L	1	Total	C	H	0
			30	10	20	
2	L	1	Total	C	H	0
			36	12	24	
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
			27	9	18	
2	L	1	Total	C	H	0
			15	5	10	
2	L	1	Total	C	H	0
			21	7	14	
2	L	1	Total	C	H	0
			36	12	24	
2	L	1	Total	C	H	0
			39	13	26	
2	L	1	Total	C	H	0
			36	12	24	

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Mol	Chain	Residues	Atoms			AltConf
2	L	1	Total	C	H	0
			31	11	20	
2	L	1	Total	C	H	0
			36	12	24	
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
			36	12	24	
2	L	1	Total	C	H	0
			32	11	21	
2	L	1	Total	C	H	0
			21	7	14	
2	L	1	Total	C	H	0
			24	8	16	
2	L	1	Total	C	H	0
			24	8	16	
2	L	1	Total	C	H	0
			30	10	20	

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		AltConf
3	A	63	Total	O	0
			63	63	
3	B	63	Total	O	0
			63	63	
3	C	63	Total	O	0
			63	63	
3	D	63	Total	O	0
			63	63	
3	E	63	Total	O	0
			63	63	
3	F	63	Total	O	0
			63	63	
3	G	63	Total	O	0
			63	63	
3	H	63	Total	O	0
			63	63	
3	I	63	Total	O	0
			63	63	

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Mol	Chain	Residues	Atoms		AltConf
3	J	63	Total 63	O 63	0
3	K	63	Total 63	O 63	0
3	L	63	Total 63	O 63	0

[illegible]

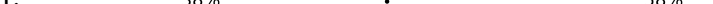
Chain D: 38% . 58%

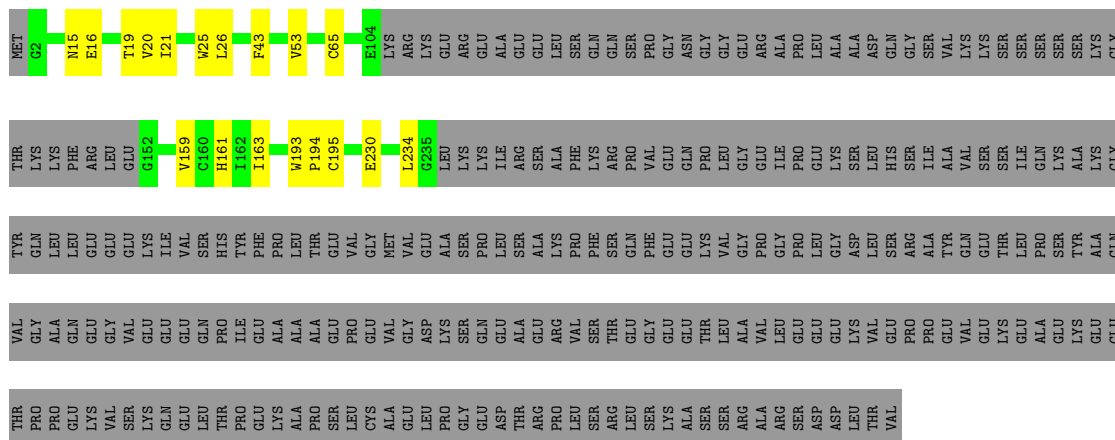
LYS	TYR	ALA	LYS	MET
GLU	ALA	LYS	GLY	G2
GLU	GLN	GLY	THR	
THR	VAL	GLY	LYS	N15
PRO	GLY	GLN	LYS	E16
PRO	ALA	LEU	PHE	
GLU	GLN	LEU	ARG	T19
LYS	GLU	GLU	LEU	V20
VAL	GLY	GLU	GLU	I21
SER	VAL	GLY	G152	
LYS	GLU	LYS	LYS	V25
GLN	GLU	ILE	V159	L26
GLU	GLN	VAL	C160	
LEU	GLN	LEU	H161	R33
THR	PRO	HIS	I162	
PRO	ILE	TYR	I163	F43
GLU	GLU	PHE		
LYS	ALA	PRO	V193	V53
ALA	ALA	LEU	P194	
PRO	ALA	THR	C195	G65
SER	GLU	GLU		
LEU	PRO	VAL	V219	E104
CYS	GLU	GLY		LYS
ALA	VAL	MET	E230	ARG
GLU	GLY	VAL		LYS
LEU	ASP	GLU	C235	GLU
PRO	LYS	ALA	LEU	ARG
GLY	SER	SER	LYS	GLU
GLU	GLN	PRO	LYS	ALA
ASP	GLU	LEU	ILE	GLU
THR	ALA	SER	ARG	GLU
ARG	GLU	ALA	SER	LEU
PRO	ARG	LYS	ALA	SER
LEU	VAL	PRO	PHE	GLN
SER	SER	PHE	LYS	GLN
ARG	THR	SER	ARG	SER
LEU	GLU	SER	PRO	PRO
SER	GLY	PHE	VAL	GLY
LYS	GLU	GLU	GLN	GLY
ALA	THR	GLY	LYS	GLY
SER	LEU	VAL	LEU	GLU
ARG	ALA	GLY	GLY	ARG
ALA	VAL	PRO	GLU	ALA
ARG	LEU	GLY	ILE	PRO
SER	GLU	PRO	PRO	LEU
ASP	GLU	LEU	GLY	ALA
ASP	GLU	ASP	LYS	ALA
LEU	LYS	ASP	SER	ASP
THR	VAL	LEU	LEU	ASP
VAL	VAL	GLU	HIS	GLY
	PRO	ARG	SER	SER
	PRO	ALA	ILE	VAL
	GLU	TYR	ALA	LYS
	VAL	GLN	VAL	LYS
	GLU	THR	VAL	LYS
	LYS	THR	ILE	SER
	GLU	LEU	GLN	SER
	ALA	PRO	LYS	SER
	GLU	SER	GLY	SER

Chain E: 38% . 58%

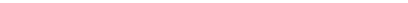
[illegible]

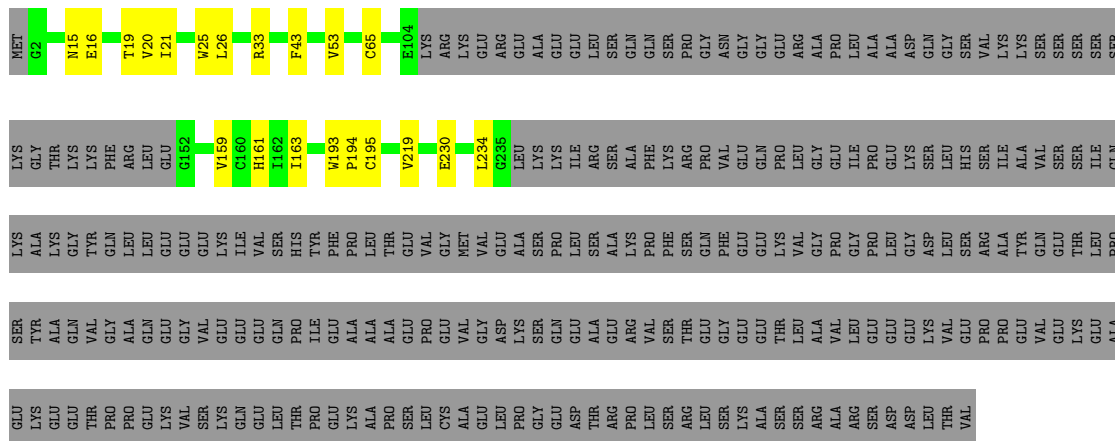
- Molecule 1: Gap junction alpha-8 protein

Chain I:  38% . 58%



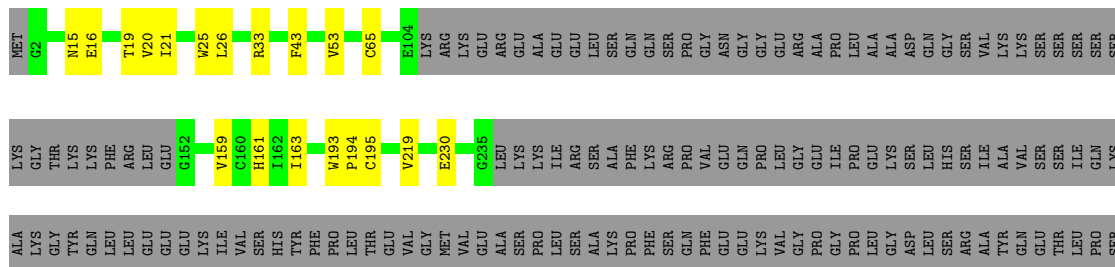
- Molecule 1: Gap junction alpha-8 protein

Chain J:  38% 5% 58%



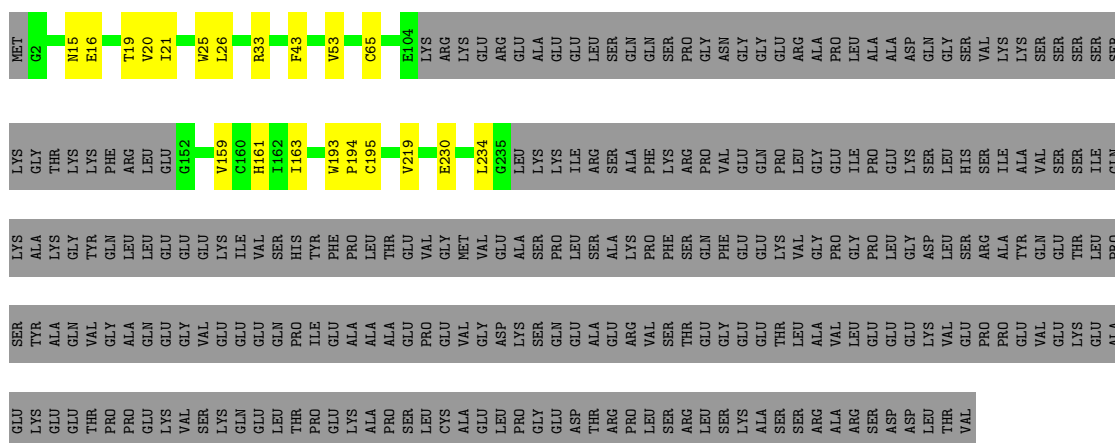
- Molecule 1: Gap junction alpha-8 protein

Chain K: 38% . 58%



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

Chain L: 38% 5% 58%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D6	Depositor
Number of particles used	75136	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)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.860	Depositor
Minimum map value	-1.282	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	315.648, 315.648, 315.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.822, 0.822, 0.822	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: 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	0.35	0/1565	0.32	0/2132
1	B	0.35	0/1565	0.32	0/2132
1	C	0.35	0/1565	0.32	0/2132
1	D	0.35	0/1565	0.32	0/2132
1	E	0.35	0/1565	0.32	0/2132
1	F	0.35	0/1565	0.32	0/2132
1	G	0.35	0/1565	0.32	0/2132
1	H	0.35	0/1565	0.32	0/2132
1	I	0.35	0/1565	0.32	0/2132
1	J	0.35	0/1565	0.32	0/2132
1	K	0.35	0/1565	0.32	0/2132
1	L	0.35	0/1565	0.32	0/2132
All	All	0.35	0/18780	0.32	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 [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	1520	1499	1497	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1520	1499	1497	11	0
1	C	1520	1499	1497	12	0
1	D	1520	1499	1497	11	0
1	E	1520	1499	1497	12	0
1	F	1520	1499	1497	13	0
1	G	1520	1499	1497	13	0
1	H	1520	1499	1497	12	0
1	I	1520	1499	1497	11	0
1	J	1520	1499	1497	12	0
1	K	1520	1499	1497	11	0
1	L	1520	1499	1497	12	0
2	A	231	459	403	0	0
2	B	231	459	403	0	0
2	C	231	459	403	0	0
2	D	231	459	403	0	0
2	E	231	459	403	0	0
2	F	231	459	403	0	0
2	G	231	459	403	0	0
2	H	231	459	403	0	0
2	I	231	459	403	0	0
2	J	231	459	403	0	0
2	K	231	459	403	0	0
2	L	231	459	403	0	0
3	A	63	0	0	1	0
3	B	63	0	0	1	0
3	C	63	0	0	1	0
3	D	63	0	0	1	0
3	E	63	0	0	1	0
3	F	63	0	0	1	0
3	G	63	0	0	1	0
3	H	63	0	0	1	0
3	I	63	0	0	1	0
3	J	63	0	0	1	0
3	K	63	0	0	1	0
3	L	63	0	0	1	0
All	All	21768	23496	22800	143	0

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

All (143) 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:C:25:TRP:CE3	1:C:26:LEU:HD12	2.44	0.53
1:E:25:TRP:CE3	1:E:26:LEU:HD12	2.44	0.53
1:B:25:TRP:CE3	1:B:26:LEU:HD12	2.44	0.53
1:F:25:TRP:CE3	1:F:26:LEU:HD12	2.44	0.53
1:G:25:TRP:CE3	1:G:26:LEU:HD12	2.44	0.53
1:I:25:TRP:CE3	1:I:26:LEU:HD12	2.44	0.53
1:J:25:TRP:CE3	1:J:26:LEU:HD12	2.44	0.53
1:L:25:TRP:CE3	1:L:26:LEU:HD12	2.44	0.53
1:A:25:TRP:CE3	1:A:26:LEU:HD12	2.44	0.53
1:H:25:TRP:CE3	1:H:26:LEU:HD12	2.44	0.53
1:K:25:TRP:CE3	1:K:26:LEU:HD12	2.44	0.53
1:D:25:TRP:CE3	1:D:26:LEU:HD12	2.44	0.53
1:B:25:TRP:HE3	1:B:26:LEU:HD12	1.75	0.52
1:I:25:TRP:HE3	1:I:26:LEU:HD12	1.75	0.52
1:D:25:TRP:HE3	1:D:26:LEU:HD12	1.75	0.52
1:H:25:TRP:HE3	1:H:26:LEU:HD12	1.75	0.51
1:K:25:TRP:HE3	1:K:26:LEU:HD12	1.75	0.51
1:A:25:TRP:HE3	1:A:26:LEU:HD12	1.75	0.51
1:C:25:TRP:HE3	1:C:26:LEU:HD12	1.75	0.51
1:G:25:TRP:HE3	1:G:26:LEU:HD12	1.75	0.51
1:J:25:TRP:HE3	1:J:26:LEU:HD12	1.75	0.51
1:F:25:TRP:HE3	1:F:26:LEU:HD12	1.75	0.51
3:A:627:HOH:O	1:H:53:VAL:CG2	2.59	0.50
1:A:53:VAL:CG2	3:H:627:HOH:O	2.59	0.50
1:F:53:VAL:CG2	3:I:628:HOH:O	2.60	0.50
1:L:25:TRP:HE3	1:L:26:LEU:HD12	1.75	0.50
3:B:628:HOH:O	1:G:53:VAL:CG2	2.60	0.50
1:E:25:TRP:HE3	1:E:26:LEU:HD12	1.75	0.50
3:C:627:HOH:O	1:L:53:VAL:CG2	2.60	0.50
1:E:53:VAL:CG2	3:J:627:HOH:O	2.60	0.50
1:B:53:VAL:CG2	3:G:627:HOH:O	2.59	0.49
3:F:627:HOH:O	1:I:53:VAL:CG2	2.59	0.49
1:D:53:VAL:CG2	3:K:627:HOH:O	2.60	0.49
3:D:627:HOH:O	1:K:53:VAL:CG2	2.60	0.49
1:C:53:VAL:CG2	3:L:627:HOH:O	2.59	0.49
3:E:627:HOH:O	1:J:53:VAL:CG2	2.60	0.49
1:K:159:VAL:O	1:K:163:ILE:HG12	2.17	0.45
1:D:159:VAL:O	1:D:163:ILE:HG12	2.17	0.45
1:A:159:VAL:O	1:A:163:ILE:HG12	2.17	0.45
1:B:159:VAL:O	1:B:163:ILE:HG12	2.17	0.45
1:C:159:VAL:O	1:C:163:ILE:HG12	2.17	0.45
1:H:159:VAL:O	1:H:163:ILE:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:159:VAL:O	1:I:163:ILE:HG12	2.17	0.45
1:J:159:VAL:O	1:J:163:ILE:HG12	2.17	0.45
1:L:159:VAL:O	1:L:163:ILE:HG12	2.17	0.45
1:E:159:VAL:O	1:E:163:ILE:HG12	2.17	0.45
1:F:159:VAL:O	1:F:163:ILE:HG12	2.17	0.45
1:B:15:ASN:OD1	1:B:16:GLU:N	2.50	0.45
1:G:159:VAL:O	1:G:163:ILE:HG12	2.17	0.45
1:I:15:ASN:OD1	1:I:16:GLU:N	2.50	0.45
1:D:15:ASN:OD1	1:D:16:GLU:N	2.50	0.45
1:K:15:ASN:OD1	1:K:16:GLU:N	2.50	0.45
1:A:15:ASN:OD1	1:A:16:GLU:N	2.50	0.44
1:H:15:ASN:OD1	1:H:16:GLU:N	2.50	0.44
1:C:15:ASN:OD1	1:C:16:GLU:N	2.50	0.44
1:J:15:ASN:OD1	1:J:16:GLU:N	2.50	0.44
1:D:65:CYS:SG	1:D:195:CYS:SG	3.16	0.44
1:K:65:CYS:SG	1:K:195:CYS:SG	3.16	0.44
1:F:15:ASN:OD1	1:F:16:GLU:N	2.50	0.44
1:G:15:ASN:OD1	1:G:16:GLU:N	2.50	0.44
1:H:65:CYS:SG	1:H:195:CYS:SG	3.16	0.44
1:J:65:CYS:SG	1:J:195:CYS:SG	3.15	0.44
1:C:65:CYS:SG	1:C:195:CYS:SG	3.16	0.44
1:I:65:CYS:SG	1:I:195:CYS:SG	3.15	0.44
1:A:65:CYS:SG	1:A:195:CYS:SG	3.16	0.44
1:B:65:CYS:SG	1:B:195:CYS:SG	3.16	0.44
1:E:15:ASN:OD1	1:E:16:GLU:N	2.50	0.44
1:L:15:ASN:OD1	1:L:16:GLU:N	2.50	0.44
1:E:19:THR:HG22	1:E:20:VAL:N	2.33	0.44
1:E:65:CYS:SG	1:E:195:CYS:SG	3.16	0.44
1:L:65:CYS:SG	1:L:195:CYS:SG	3.16	0.44
1:L:19:THR:HG22	1:L:20:VAL:N	2.33	0.43
1:F:65:CYS:SG	1:F:195:CYS:SG	3.16	0.43
1:G:19:THR:HG22	1:G:20:VAL:N	2.33	0.43
1:D:19:THR:HG22	1:D:20:VAL:N	2.33	0.43
1:F:19:THR:HG22	1:F:20:VAL:N	2.33	0.43
1:K:19:THR:HG22	1:K:20:VAL:N	2.33	0.43
1:G:65:CYS:SG	1:G:195:CYS:SG	3.15	0.43
1:H:19:THR:HG22	1:H:20:VAL:N	2.33	0.43
1:A:19:THR:HG22	1:A:20:VAL:N	2.33	0.43
1:L:43:PHE:CD1	1:L:43:PHE:N	2.87	0.43
1:E:43:PHE:CD1	1:E:43:PHE:N	2.87	0.42
1:C:19:THR:HG22	1:C:20:VAL:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:19:THR:HG22	1:J:20:VAL:N	2.33	0.42
1:I:19:THR:HG22	1:I:20:VAL:N	2.33	0.42
1:B:19:THR:HG22	1:B:20:VAL:N	2.33	0.42
1:K:43:PHE:CD1	1:K:43:PHE:N	2.87	0.42
1:D:43:PHE:CD1	1:D:43:PHE:N	2.87	0.42
1:F:43:PHE:CD1	1:F:43:PHE:N	2.87	0.42
1:G:43:PHE:CD1	1:G:43:PHE:N	2.87	0.41
1:H:33:ARG:HG2	1:H:219:VAL:HG11	2.02	0.41
1:A:33:ARG:HG2	1:A:219:VAL:HG11	2.02	0.41
1:B:234:LEU:C	1:B:234:LEU:HD23	2.46	0.41
1:C:33:ARG:HG2	1:C:219:VAL:HG11	2.02	0.41
1:F:234:LEU:C	1:F:234:LEU:HD23	2.46	0.41
1:I:43:PHE:CD1	1:I:43:PHE:N	2.87	0.41
1:I:234:LEU:C	1:I:234:LEU:HD23	2.46	0.41
1:C:43:PHE:CD1	1:C:43:PHE:N	2.87	0.41
1:D:193:TRP:CG	1:D:194:PRO:HA	2.56	0.41
1:E:21:ILE:HG21	1:E:230:GLU:OE1	2.21	0.41
1:F:193:TRP:CG	1:F:194:PRO:HA	2.56	0.41
1:G:193:TRP:CG	1:G:194:PRO:HA	2.56	0.41
1:G:234:LEU:C	1:G:234:LEU:HD23	2.46	0.41
1:H:21:ILE:HG21	1:H:230:GLU:OE1	2.21	0.41
1:H:234:LEU:C	1:H:234:LEU:HD23	2.46	0.41
1:K:193:TRP:CG	1:K:194:PRO:HA	2.56	0.41
1:A:21:ILE:HG21	1:A:230:GLU:OE1	2.21	0.41
1:A:234:LEU:C	1:A:234:LEU:HD23	2.46	0.41
1:B:21:ILE:HG21	1:B:230:GLU:OE1	2.21	0.41
1:B:193:TRP:CG	1:B:194:PRO:HA	2.56	0.41
1:C:193:TRP:CG	1:C:194:PRO:HA	2.56	0.41
1:F:33:ARG:HG2	1:F:219:VAL:HG11	2.02	0.41
1:I:21:ILE:HG21	1:I:230:GLU:OE1	2.21	0.41
1:J:33:ARG:HG2	1:J:219:VAL:HG11	2.02	0.41
1:J:43:PHE:CD1	1:J:43:PHE:N	2.87	0.41
1:J:193:TRP:CG	1:J:194:PRO:HA	2.56	0.41
1:L:21:ILE:HG21	1:L:230:GLU:OE1	2.21	0.41
1:B:43:PHE:CD1	1:B:43:PHE:N	2.87	0.41
1:D:21:ILE:HG21	1:D:230:GLU:OE1	2.21	0.41
1:E:193:TRP:CG	1:E:194:PRO:HA	2.56	0.41
1:G:33:ARG:HG2	1:G:219:VAL:HG11	2.02	0.41
1:H:43:PHE:CD1	1:H:43:PHE:N	2.87	0.41
1:L:193:TRP:CG	1:L:194:PRO:HA	2.56	0.41
1:A:43:PHE:CD1	1:A:43:PHE:N	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:234:LEU:HD23	1:J:234:LEU:C	2.46	0.41
1:K:21:ILE:HG21	1:K:230:GLU:OE1	2.21	0.41
1:C:234:LEU:HD23	1:C:234:LEU:C	2.46	0.41
1:D:33:ARG:HG2	1:D:219:VAL:HG11	2.02	0.41
1:E:234:LEU:HD23	1:E:234:LEU:C	2.46	0.41
1:I:193:TRP:CG	1:I:194:PRO:HA	2.56	0.41
1:K:33:ARG:HG2	1:K:219:VAL:HG11	2.02	0.41
1:L:234:LEU:HD23	1:L:234:LEU:C	2.46	0.41
1:G:20:VAL:HG13	1:G:21:ILE:N	2.36	0.41
1:H:193:TRP:CG	1:H:194:PRO:HA	2.56	0.41
1:A:193:TRP:CG	1:A:194:PRO:HA	2.56	0.40
1:F:20:VAL:HG13	1:F:21:ILE:N	2.37	0.40
1:C:21:ILE:HG21	1:C:230:GLU:OE1	2.21	0.40
1:F:21:ILE:HG21	1:F:230:GLU:OE1	2.21	0.40
1:G:21:ILE:HG21	1:G:230:GLU:OE1	2.21	0.40
1:J:21:ILE:HG21	1:J:230:GLU:OE1	2.21	0.40
1:A:20:VAL:HG13	1:A:21:ILE:N	2.37	0.40
1:L:33:ARG:HG2	1:L:219:VAL:HG11	2.02	0.40
1:E:20:VAL:HG13	1:E:21:ILE:N	2.36	0.40

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%)	180 (98%)	3 (2%)	0	100	100
1	B	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	C	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	D	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	E	183/440 (42%)	180 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	G	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	H	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	I	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	J	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	K	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
1	L	183/440 (42%)	180 (98%)	3 (2%)	0	100	100
All	All	2196/5280 (42%)	2160 (98%)	36 (2%)	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%)	169 (99%)	1 (1%)	78	89
1	B	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	C	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	D	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	E	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	F	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	G	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	H	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	I	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	J	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	K	170/385 (44%)	169 (99%)	1 (1%)	78	89
1	L	170/385 (44%)	169 (99%)	1 (1%)	78	89
All	All	2040/4620 (44%)	2028 (99%)	12 (1%)	76	89

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	161	HIS
1	B	161	HIS
1	C	161	HIS
1	D	161	HIS
1	E	161	HIS
1	F	161	HIS
1	G	161	HIS
1	H	161	HIS
1	I	161	HIS
1	J	161	HIS
1	K	161	HIS
1	L	161	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	98	HIS
1	B	58	GLN
1	B	98	HIS
1	C	58	GLN
1	C	98	HIS
1	D	58	GLN
1	D	98	HIS
1	E	58	GLN
1	E	98	HIS
1	F	58	GLN
1	F	98	HIS
1	G	58	GLN
1	G	98	HIS
1	H	58	GLN
1	H	98	HIS
1	I	58	GLN
1	I	98	HIS
1	J	58	GLN
1	J	98	HIS
1	K	58	GLN
1	K	98	HIS
1	L	58	GLN
1	L	98	HIS

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

276 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	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	B	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	L	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	I	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	C	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	K	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	I	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	C	509	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	G	504	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	L	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	B	506	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	B	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	C	504	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	C	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	L	522	-	7,7,45	0.34	0	6,6,53	0.76	0
2	MC3	F	510	-	6,6,45	0.35	0	5,5,53	0.70	0
2	MC3	E	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	F	518	-	11,11,45	0.31	0	10,10,53	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	E	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	J	511	-	11,11,45	0.27	0	10,10,53	0.82	0
2	MC3	C	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	A	513	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	J	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	B	512	-	12,12,45	0.29	0	11,11,53	0.80	0
2	MC3	D	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	J	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	F	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	K	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	F	512	-	12,12,45	0.29	0	11,11,53	0.80	0
2	MC3	F	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	E	504	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	F	517	-	10,10,45	0.32	0	9,9,53	0.81	0
2	MC3	F	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	A	502	-	12,12,45	0.29	0	11,11,53	0.81	0
2	MC3	D	512	-	12,12,45	0.29	0	11,11,53	0.81	0
2	MC3	J	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	J	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	K	522	-	7,7,45	0.33	0	6,6,53	0.75	0
2	MC3	G	513	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	H	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	D	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	J	520	-	6,6,45	0.35	0	5,5,53	0.72	0
2	MC3	D	517	-	10,10,45	0.32	0	9,9,53	0.82	0
2	MC3	J	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	K	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	F	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	K	517	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	L	520	-	6,6,45	0.36	0	5,5,53	0.73	0
2	MC3	E	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	G	516	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	K	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	G	514	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	L	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	D	513	-	11,11,45	0.30	0	10,10,53	0.81	0
2	MC3	I	513	-	11,11,45	0.30	0	10,10,53	0.81	0
2	MC3	L	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	H	517	-	10,10,45	0.32	0	9,9,53	0.82	0
2	MC3	G	503	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	F	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	D	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	I	502	-	11,11,45	0.31	0	10,10,53	0.83	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	L	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	B	523	-	9,9,45	0.34	0	8,8,53	0.82	0
2	MC3	H	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	J	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	G	505	-	11,11,45	0.31	0	10,10,53	0.81	0
2	MC3	L	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	E	506	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	D	510	-	6,6,45	0.35	0	5,5,53	0.70	0
2	MC3	G	515	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	J	514	-	10,10,45	0.31	0	9,9,53	0.83	0
2	MC3	L	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	B	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	K	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	H	509	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	C	503	-	11,11,45	0.32	0	10,10,53	0.84	0
2	MC3	L	517	-	10,10,45	0.32	0	9,9,53	0.81	0
2	MC3	A	510	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	L	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	F	506	-	7,7,45	0.35	0	6,6,53	0.74	0
2	MC3	F	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	C	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	D	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	G	522	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	I	504	-	9,9,45	0.33	0	8,8,53	0.79	0
2	MC3	K	515	-	11,11,45	0.32	0	10,10,53	0.82	0
2	MC3	A	505	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	C	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	D	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	H	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	J	502	-	11,11,45	0.32	0	10,10,53	0.83	0
2	MC3	H	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	B	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	H	512	-	12,12,45	0.29	0	11,11,53	0.81	0
2	MC3	A	516	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	E	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	A	517	-	9,9,45	0.33	0	8,8,53	0.79	0
2	MC3	E	517	-	10,10,45	0.32	0	9,9,53	0.81	0
2	MC3	L	506	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	D	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	E	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	K	512	-	12,12,45	0.29	0	11,11,53	0.80	0
2	MC3	H	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	K	514	-	10,10,45	0.30	0	9,9,53	0.82	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	E	522	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	B	504	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	H	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	I	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	L	514	-	10,10,45	0.31	0	9,9,53	0.83	0
2	MC3	G	517	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	F	507	-	10,10,45	0.34	0	9,9,53	0.82	0
2	MC3	B	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	G	521	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	L	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	J	506	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	J	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	I	512	-	12,12,45	0.30	0	11,11,53	0.81	0
2	MC3	G	523	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	A	521	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	B	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	D	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	F	504	-	9,9,45	0.33	0	8,8,53	0.79	0
2	MC3	A	507	-	10,10,45	0.32	0	9,9,53	0.82	0
2	MC3	C	522	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	C	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	I	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	B	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	K	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	A	511	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	A	523	-	6,6,45	0.35	0	5,5,53	0.70	0
2	MC3	J	512	-	12,12,45	0.29	0	11,11,53	0.80	0
2	MC3	G	506	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	L	509	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	A	515	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	H	519	-	10,10,45	0.32	0	9,9,53	0.83	0
2	MC3	H	514	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	E	513	-	11,11,45	0.29	0	10,10,53	0.81	0
2	MC3	B	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	B	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	G	508	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	G	501	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	G	512	-	7,7,45	0.34	0	6,6,53	0.76	0
2	MC3	C	518	-	11,11,45	0.31	0	10,10,53	0.85	0
2	MC3	B	518	-	11,11,45	0.32	0	10,10,53	0.85	0
2	MC3	D	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	K	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	H	506	-	7,7,45	0.34	0	6,6,53	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	D	511	-	11,11,45	0.27	0	10,10,53	0.82	0
2	MC3	J	519	-	10,10,45	0.32	0	9,9,53	0.82	0
2	MC3	I	522	-	7,7,45	0.34	0	6,6,53	0.76	0
2	MC3	C	515	-	11,11,45	0.32	0	10,10,53	0.82	0
2	MC3	G	509	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	L	504	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	J	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	D	504	-	9,9,45	0.32	0	8,8,53	0.78	0
2	MC3	E	512	-	12,12,45	0.30	0	11,11,53	0.81	0
2	MC3	F	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	L	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	C	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	J	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	A	514	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	G	519	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	H	521	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	I	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	L	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	H	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	H	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	F	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	E	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	D	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	G	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	G	520	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	F	523	-	9,9,45	0.34	0	8,8,53	0.82	0
2	MC3	K	505	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	F	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	I	521	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	K	504	-	9,9,45	0.32	0	8,8,53	0.78	0
2	MC3	I	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	E	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	A	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	J	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	F	522	-	7,7,45	0.33	0	6,6,53	0.75	0
2	MC3	K	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	C	517	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	C	514	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	D	506	-	7,7,45	0.35	0	6,6,53	0.74	0
2	MC3	K	506	-	7,7,45	0.34	0	6,6,53	0.73	0
2	MC3	E	520	-	6,6,45	0.35	0	5,5,53	0.72	0
2	MC3	B	517	-	10,10,45	0.32	0	9,9,53	0.81	0
2	MC3	I	519	-	10,10,45	0.33	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	A	501	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	H	520	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	B	520	-	6,6,45	0.35	0	5,5,53	0.72	0
2	MC3	E	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	C	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	E	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	508	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	H	518	-	11,11,45	0.31	0	10,10,53	0.85	0
2	MC3	I	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	H	504	-	9,9,45	0.32	0	8,8,53	0.79	0
2	MC3	F	511	-	11,11,45	0.27	0	10,10,53	0.82	0
2	MC3	A	519	-	7,7,45	0.34	0	6,6,53	0.73	0
2	MC3	F	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	L	511	-	11,11,45	0.26	0	10,10,53	0.82	0
2	MC3	D	508	-	8,8,45	0.34	0	7,7,53	0.80	0
2	MC3	J	504	-	9,9,45	0.32	0	8,8,53	0.78	0
2	MC3	H	522	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	B	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	D	507	-	10,10,45	0.33	0	9,9,53	0.81	0
2	MC3	K	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	C	512	-	12,12,45	0.29	0	11,11,53	0.81	0
2	MC3	D	522	-	7,7,45	0.34	0	6,6,53	0.76	0
2	MC3	H	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	K	513	-	11,11,45	0.30	0	10,10,53	0.82	0
2	MC3	D	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	D	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	K	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	D	501	-	12,12,45	0.28	0	11,11,53	0.82	0
2	MC3	D	514	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	I	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	K	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	K	501	-	12,12,45	0.27	0	11,11,53	0.81	0
2	MC3	F	503	-	11,11,45	0.32	0	10,10,53	0.84	0
2	MC3	A	522	-	4,4,45	0.37	0	3,3,53	0.59	0
2	MC3	B	521	-	7,7,45	0.35	0	6,6,53	0.75	0
2	MC3	L	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	F	514	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	B	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	C	510	-	6,6,45	0.35	0	5,5,53	0.71	0
2	MC3	E	501	-	12,12,45	0.28	0	11,11,53	0.81	0
2	MC3	G	502	-	12,12,45	0.29	0	11,11,53	0.81	0
2	MC3	J	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	A	504	-	10,10,45	0.31	0	9,9,53	0.82	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MC3	A	506	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	B	522	-	7,7,45	0.33	0	6,6,53	0.75	0
2	MC3	J	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	J	517	-	10,10,45	0.32	0	9,9,53	0.82	0
2	MC3	L	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	K	518	-	11,11,45	0.31	0	10,10,53	0.85	0
2	MC3	C	511	-	11,11,45	0.27	0	10,10,53	0.82	0
2	MC3	B	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	E	518	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	A	503	-	11,11,45	0.30	0	10,10,53	0.81	0
2	MC3	E	514	-	10,10,45	0.31	0	9,9,53	0.82	0
2	MC3	E	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	B	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	A	512	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	E	519	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	I	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	I	509	-	4,4,45	0.36	0	3,3,53	0.59	0
2	MC3	I	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	I	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	C	516	-	4,4,45	0.36	0	3,3,53	0.57	0
2	MC3	E	515	-	11,11,45	0.31	0	10,10,53	0.82	0
2	MC3	K	503	-	11,11,45	0.32	0	10,10,53	0.84	0
2	MC3	G	507	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	G	510	-	6,6,45	0.35	0	5,5,53	0.73	0
2	MC3	A	520	-	10,10,45	0.33	0	9,9,53	0.82	0
2	MC3	H	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	I	506	-	7,7,45	0.34	0	6,6,53	0.74	0
2	MC3	J	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	C	506	-	7,7,45	0.35	0	6,6,53	0.74	0
2	MC3	E	523	-	9,9,45	0.34	0	8,8,53	0.81	0
2	MC3	H	513	-	11,11,45	0.30	0	10,10,53	0.81	0
2	MC3	F	502	-	11,11,45	0.31	0	10,10,53	0.83	0
2	MC3	B	514	-	10,10,45	0.30	0	9,9,53	0.82	0
2	MC3	L	505	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	H	516	-	4,4,45	0.37	0	3,3,53	0.57	0
2	MC3	A	509	-	10,10,45	0.33	0	9,9,53	0.83	0
2	MC3	G	511	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	L	512	-	12,12,45	0.29	0	11,11,53	0.80	0
2	MC3	I	503	-	11,11,45	0.31	0	10,10,53	0.84	0
2	MC3	J	522	-	7,7,45	0.34	0	6,6,53	0.75	0
2	MC3	C	508	-	8,8,45	0.34	0	7,7,53	0.79	0
2	MC3	I	514	-	10,10,45	0.30	0	9,9,53	0.82	0
2	MC3	I	517	-	10,10,45	0.33	0	9,9,53	0.82	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	521	-	-	0/5/5/49	-
2	MC3	B	503	-	-	0/9/9/49	-
2	MC3	L	515	-	-	0/9/9/49	-
2	MC3	I	508	-	-	0/6/6/49	-
2	MC3	C	507	-	-	0/8/8/49	-
2	MC3	K	510	-	-	0/4/4/49	-
2	MC3	I	520	-	-	0/4/4/49	-
2	MC3	C	509	-	-	0/2/2/49	-
2	MC3	G	504	-	-	0/8/8/49	-
2	MC3	L	513	-	-	0/9/9/49	-
2	MC3	B	506	-	-	0/5/5/49	-
2	MC3	B	510	-	-	0/4/4/49	-
2	MC3	C	504	-	-	0/7/7/49	-
2	MC3	C	501	-	-	0/10/10/49	-
2	MC3	L	522	-	-	0/5/5/49	-
2	MC3	F	510	-	-	0/4/4/49	-
2	MC3	E	508	-	-	0/6/6/49	-
2	MC3	F	518	-	-	0/9/9/49	-
2	MC3	E	521	-	-	0/5/5/49	-
2	MC3	J	511	-	-	0/9/9/49	-
2	MC3	C	519	-	-	0/8/8/49	-
2	MC3	A	513	-	-	0/7/7/49	-
2	MC3	J	518	-	-	0/9/9/49	-
2	MC3	B	512	-	-	0/10/10/49	-
2	MC3	D	502	-	-	0/9/9/49	-
2	MC3	J	505	-	-	0/9/9/49	-
2	MC3	F	508	-	-	0/6/6/49	-
2	MC3	K	502	-	-	0/9/9/49	-
2	MC3	F	512	-	-	0/10/10/49	-
2	MC3	F	516	-	-	0/2/2/49	-
2	MC3	E	504	-	-	0/7/7/49	-
2	MC3	F	517	-	-	0/8/8/49	-
2	MC3	F	521	-	-	0/5/5/49	-
2	MC3	A	502	-	-	0/10/10/49	-
2	MC3	D	512	-	-	0/10/10/49	-
2	MC3	J	501	-	-	0/10/10/49	-
2	MC3	J	516	-	-	0/2/2/49	-
2	MC3	K	522	-	-	0/5/5/49	-
2	MC3	G	513	-	-	0/7/7/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	H	510	-	-	0/4/4/49	-
2	MC3	D	516	-	-	0/2/2/49	-
2	MC3	J	520	-	-	0/4/4/49	-
2	MC3	D	517	-	-	0/8/8/49	-
2	MC3	J	521	-	-	0/5/5/49	-
2	MC3	K	516	-	-	0/2/2/49	-
2	MC3	F	515	-	-	0/9/9/49	-
2	MC3	K	517	-	-	0/8/8/49	-
2	MC3	L	520	-	-	0/4/4/49	-
2	MC3	E	503	-	-	0/9/9/49	-
2	MC3	G	516	-	-	0/9/9/49	-
2	MC3	K	508	-	-	0/6/6/49	-
2	MC3	G	514	-	-	0/10/10/49	-
2	MC3	L	523	-	-	0/7/7/49	-
2	MC3	D	513	-	-	0/9/9/49	-
2	MC3	I	513	-	-	0/9/9/49	-
2	MC3	L	502	-	-	0/9/9/49	-
2	MC3	H	517	-	-	0/8/8/49	-
2	MC3	G	503	-	-	0/9/9/49	-
2	MC3	F	505	-	-	0/9/9/49	-
2	MC3	D	503	-	-	0/9/9/49	-
2	MC3	I	502	-	-	0/9/9/49	-
2	MC3	L	521	-	-	0/5/5/49	-
2	MC3	B	523	-	-	0/7/7/49	-
2	MC3	H	508	-	-	0/6/6/49	-
2	MC3	J	507	-	-	0/8/8/49	-
2	MC3	G	505	-	-	0/9/9/49	-
2	MC3	L	510	-	-	0/4/4/49	-
2	MC3	E	506	-	-	0/5/5/49	-
2	MC3	D	510	-	-	0/4/4/49	-
2	MC3	G	515	-	-	0/9/9/49	-
2	MC3	J	514	-	-	0/8/8/49	-
2	MC3	L	501	-	-	0/10/10/49	-
2	MC3	B	515	-	-	0/9/9/49	-
2	MC3	K	511	-	-	0/9/9/49	-
2	MC3	H	509	-	-	0/2/2/49	-
2	MC3	C	503	-	-	0/9/9/49	-
2	MC3	L	517	-	-	0/8/8/49	-
2	MC3	A	510	-	-	0/4/4/49	-
2	MC3	L	508	-	-	0/6/6/49	-
2	MC3	F	506	-	-	0/5/5/49	-
2	MC3	F	509	-	-	0/2/2/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	C	520	-	-	0/4/4/49	-
2	MC3	D	515	-	-	0/9/9/49	-
2	MC3	G	522	-	-	0/2/2/49	-
2	MC3	I	504	-	-	0/7/7/49	-
2	MC3	K	515	-	-	0/9/9/49	-
2	MC3	A	505	-	-	0/9/9/49	-
2	MC3	C	523	-	-	0/7/7/49	-
2	MC3	D	520	-	-	0/4/4/49	-
2	MC3	H	507	-	-	0/8/8/49	-
2	MC3	J	502	-	-	0/9/9/49	-
2	MC3	H	503	-	-	0/9/9/49	-
2	MC3	B	508	-	-	0/6/6/49	-
2	MC3	H	512	-	-	0/10/10/49	-
2	MC3	A	516	-	-	0/9/9/49	-
2	MC3	E	511	-	-	0/9/9/49	-
2	MC3	A	517	-	-	0/7/7/49	-
2	MC3	E	517	-	-	0/8/8/49	-
2	MC3	L	506	-	-	0/5/5/49	-
2	MC3	D	518	-	-	0/9/9/49	-
2	MC3	E	510	-	-	0/4/4/49	-
2	MC3	K	512	-	-	0/10/10/49	-
2	MC3	H	515	-	-	0/9/9/49	-
2	MC3	K	514	-	-	0/8/8/49	-
2	MC3	E	522	-	-	0/5/5/49	-
2	MC3	B	504	-	-	0/7/7/49	-
2	MC3	H	511	-	-	0/9/9/49	-
2	MC3	I	510	-	-	0/4/4/49	-
2	MC3	L	514	-	-	0/8/8/49	-
2	MC3	G	517	-	-	0/7/7/49	-
2	MC3	F	507	-	-	0/8/8/49	-
2	MC3	B	519	-	-	0/8/8/49	-
2	MC3	G	521	-	-	0/6/6/49	-
2	MC3	L	507	-	-	0/8/8/49	-
2	MC3	J	506	-	-	0/5/5/49	-
2	MC3	J	510	-	-	0/4/4/49	-
2	MC3	I	512	-	-	0/10/10/49	-
2	MC3	G	523	-	-	0/4/4/49	-
2	MC3	A	521	-	-	0/6/6/49	-
2	MC3	B	505	-	-	0/9/9/49	-
2	MC3	D	519	-	-	0/8/8/49	-
2	MC3	F	504	-	-	0/7/7/49	-
2	MC3	A	507	-	-	0/8/8/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	C	522	-	-	0/5/5/49	-
2	MC3	C	513	-	-	0/9/9/49	-
2	MC3	I	516	-	-	0/2/2/49	-
2	MC3	B	511	-	-	0/9/9/49	-
2	MC3	K	519	-	-	0/8/8/49	-
2	MC3	A	511	-	-	0/5/5/49	-
2	MC3	A	523	-	-	0/4/4/49	-
2	MC3	J	512	-	-	0/10/10/49	-
2	MC3	G	506	-	-	0/2/2/49	-
2	MC3	L	509	-	-	0/2/2/49	-
2	MC3	A	515	-	-	0/9/9/49	-
2	MC3	H	519	-	-	0/8/8/49	-
2	MC3	H	514	-	-	0/8/8/49	-
2	MC3	E	513	-	-	0/9/9/49	-
2	MC3	B	513	-	-	0/9/9/49	-
2	MC3	B	501	-	-	0/10/10/49	-
2	MC3	G	508	-	-	0/9/9/49	-
2	MC3	G	501	-	-	0/9/9/49	-
2	MC3	G	512	-	-	0/5/5/49	-
2	MC3	C	518	-	-	0/9/9/49	-
2	MC3	B	518	-	-	0/9/9/49	-
2	MC3	D	521	-	-	0/5/5/49	-
2	MC3	K	521	-	-	0/5/5/49	-
2	MC3	H	506	-	-	0/5/5/49	-
2	MC3	D	511	-	-	0/9/9/49	-
2	MC3	J	519	-	-	0/8/8/49	-
2	MC3	I	522	-	-	0/5/5/49	-
2	MC3	C	515	-	-	0/9/9/49	-
2	MC3	G	509	-	-	0/8/8/49	-
2	MC3	L	504	-	-	0/7/7/49	-
2	MC3	J	513	-	-	0/9/9/49	-
2	MC3	D	504	-	-	0/7/7/49	-
2	MC3	E	512	-	-	0/10/10/49	-
2	MC3	F	519	-	-	0/8/8/49	-
2	MC3	L	519	-	-	0/8/8/49	-
2	MC3	C	505	-	-	0/9/9/49	-
2	MC3	J	509	-	-	0/2/2/49	-
2	MC3	A	514	-	-	0/10/10/49	-
2	MC3	G	519	-	-	0/5/5/49	-
2	MC3	H	521	-	-	0/5/5/49	-
2	MC3	I	518	-	-	0/9/9/49	-
2	MC3	L	503	-	-	0/9/9/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	H	501	-	-	0/10/10/49	-
2	MC3	H	523	-	-	0/7/7/49	-
2	MC3	F	520	-	-	0/4/4/49	-
2	MC3	E	509	-	-	0/2/2/49	-
2	MC3	D	505	-	-	0/9/9/49	-
2	MC3	G	518	-	-	0/9/9/49	-
2	MC3	G	520	-	-	0/8/8/49	-
2	MC3	F	523	-	-	0/7/7/49	-
2	MC3	K	505	-	-	0/9/9/49	-
2	MC3	F	501	-	-	0/10/10/49	-
2	MC3	I	521	-	-	0/5/5/49	-
2	MC3	K	504	-	-	0/7/7/49	-
2	MC3	I	511	-	-	0/9/9/49	-
2	MC3	E	505	-	-	0/9/9/49	-
2	MC3	A	518	-	-	0/9/9/49	-
2	MC3	J	515	-	-	0/9/9/49	-
2	MC3	F	522	-	-	0/5/5/49	-
2	MC3	K	520	-	-	0/4/4/49	-
2	MC3	C	517	-	-	0/8/8/49	-
2	MC3	C	514	-	-	0/8/8/49	-
2	MC3	D	506	-	-	0/5/5/49	-
2	MC3	K	506	-	-	0/5/5/49	-
2	MC3	E	520	-	-	0/4/4/49	-
2	MC3	B	517	-	-	0/8/8/49	-
2	MC3	I	519	-	-	0/8/8/49	-
2	MC3	A	501	-	-	0/9/9/49	-
2	MC3	H	520	-	-	0/4/4/49	-
2	MC3	B	520	-	-	0/4/4/49	-
2	MC3	E	507	-	-	0/8/8/49	-
2	MC3	C	502	-	-	0/9/9/49	-
2	MC3	E	516	-	-	0/2/2/49	-
2	MC3	A	508	-	-	0/9/9/49	-
2	MC3	H	518	-	-	0/9/9/49	-
2	MC3	I	505	-	-	0/9/9/49	-
2	MC3	H	504	-	-	0/7/7/49	-
2	MC3	F	511	-	-	0/9/9/49	-
2	MC3	A	519	-	-	0/5/5/49	-
2	MC3	F	513	-	-	0/9/9/49	-
2	MC3	L	511	-	-	0/9/9/49	-
2	MC3	D	508	-	-	0/6/6/49	-
2	MC3	J	504	-	-	0/7/7/49	-
2	MC3	H	522	-	-	0/5/5/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	B	516	-	-	0/2/2/49	-
2	MC3	D	507	-	-	0/8/8/49	-
2	MC3	K	507	-	-	0/8/8/49	-
2	MC3	C	512	-	-	0/10/10/49	-
2	MC3	D	522	-	-	0/5/5/49	-
2	MC3	H	505	-	-	0/9/9/49	-
2	MC3	K	513	-	-	0/9/9/49	-
2	MC3	D	523	-	-	0/7/7/49	-
2	MC3	D	509	-	-	0/2/2/49	-
2	MC3	K	509	-	-	0/2/2/49	-
2	MC3	D	501	-	-	0/10/10/49	-
2	MC3	D	514	-	-	0/8/8/49	-
2	MC3	I	501	-	-	0/10/10/49	-
2	MC3	K	523	-	-	0/7/7/49	-
2	MC3	K	501	-	-	0/10/10/49	-
2	MC3	F	503	-	-	0/9/9/49	-
2	MC3	A	522	-	-	0/2/2/49	-
2	MC3	B	521	-	-	0/5/5/49	-
2	MC3	L	518	-	-	0/9/9/49	-
2	MC3	F	514	-	-	0/8/8/49	-
2	MC3	B	507	-	-	0/8/8/49	-
2	MC3	C	510	-	-	0/4/4/49	-
2	MC3	E	501	-	-	0/10/10/49	-
2	MC3	G	502	-	-	0/10/10/49	-
2	MC3	J	503	-	-	0/9/9/49	-
2	MC3	A	504	-	-	0/8/8/49	-
2	MC3	A	506	-	-	0/2/2/49	-
2	MC3	B	522	-	-	0/5/5/49	-
2	MC3	J	508	-	-	0/6/6/49	-
2	MC3	J	517	-	-	0/8/8/49	-
2	MC3	L	516	-	-	0/2/2/49	-
2	MC3	K	518	-	-	0/9/9/49	-
2	MC3	C	511	-	-	0/9/9/49	-
2	MC3	B	509	-	-	0/2/2/49	-
2	MC3	E	518	-	-	0/9/9/49	-
2	MC3	A	503	-	-	0/9/9/49	-
2	MC3	E	514	-	-	0/8/8/49	-
2	MC3	E	502	-	-	0/9/9/49	-
2	MC3	B	502	-	-	0/9/9/49	-
2	MC3	A	512	-	-	0/5/5/49	-
2	MC3	E	519	-	-	0/8/8/49	-
2	MC3	I	507	-	-	0/8/8/49	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MC3	I	509	-	-	0/2/2/49	-
2	MC3	I	515	-	-	0/9/9/49	-
2	MC3	I	523	-	-	0/7/7/49	-
2	MC3	C	516	-	-	0/2/2/49	-
2	MC3	E	515	-	-	0/9/9/49	-
2	MC3	K	503	-	-	0/9/9/49	-
2	MC3	G	507	-	-	0/8/8/49	-
2	MC3	G	510	-	-	0/4/4/49	-
2	MC3	A	520	-	-	0/8/8/49	-
2	MC3	H	502	-	-	0/9/9/49	-
2	MC3	I	506	-	-	0/5/5/49	-
2	MC3	J	523	-	-	0/7/7/49	-
2	MC3	C	506	-	-	0/5/5/49	-
2	MC3	E	523	-	-	0/7/7/49	-
2	MC3	H	513	-	-	0/9/9/49	-
2	MC3	F	502	-	-	0/9/9/49	-
2	MC3	B	514	-	-	0/8/8/49	-
2	MC3	L	505	-	-	0/9/9/49	-
2	MC3	H	516	-	-	0/2/2/49	-
2	MC3	A	509	-	-	0/8/8/49	-
2	MC3	G	511	-	-	0/5/5/49	-
2	MC3	L	512	-	-	0/10/10/49	-
2	MC3	I	503	-	-	0/9/9/49	-
2	MC3	J	522	-	-	0/5/5/49	-
2	MC3	C	508	-	-	0/6/6/49	-
2	MC3	I	514	-	-	0/8/8/49	-
2	MC3	I	517	-	-	0/8/8/49	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

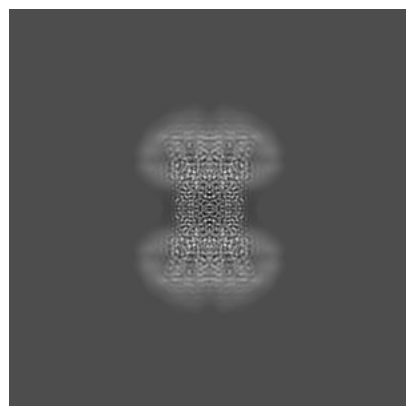
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73896. These allow visual inspection of the internal detail of the map and identification of artifacts.

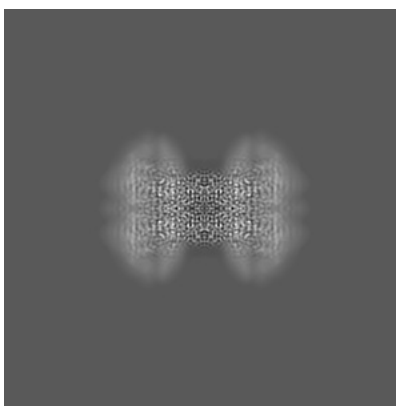
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

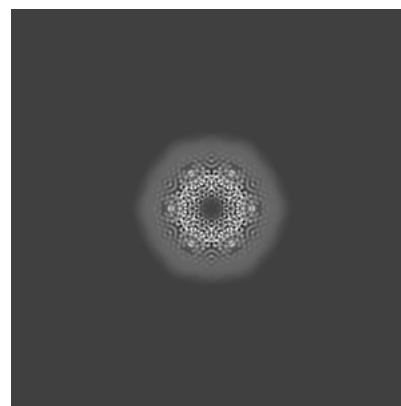
6.1.1 Primary map



X

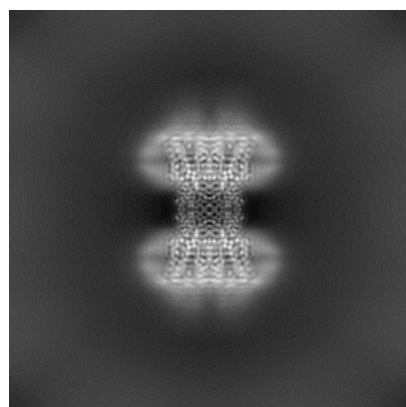


Y

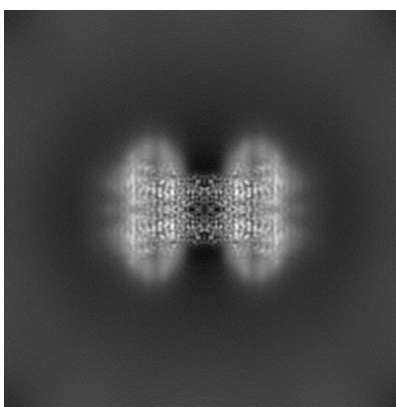


Z

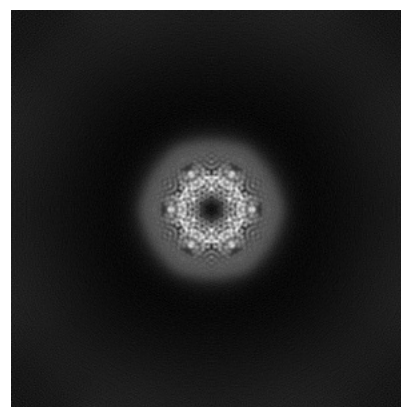
6.1.2 Raw map



X



Y



Z

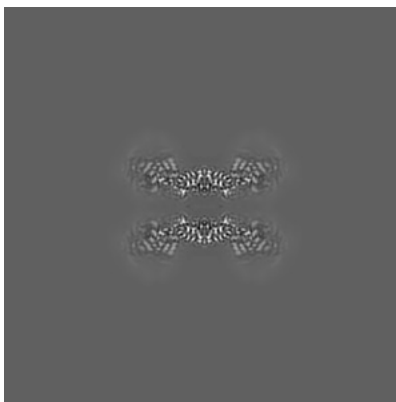
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

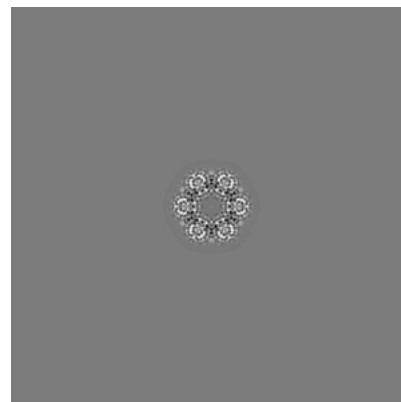
6.2.1 Primary map



X Index: 192

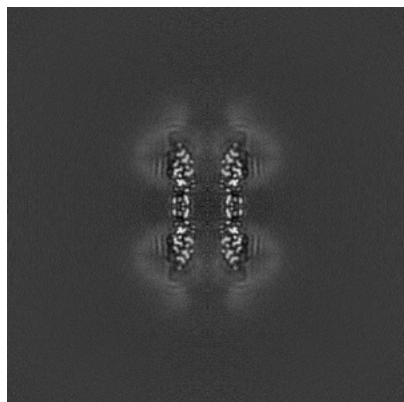


Y Index: 192

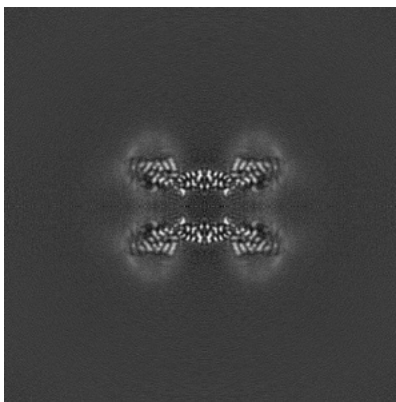


Z Index: 192

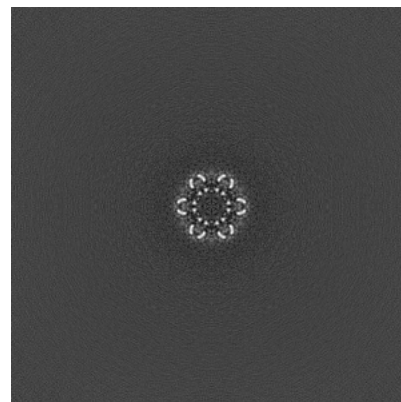
6.2.2 Raw map



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](#)

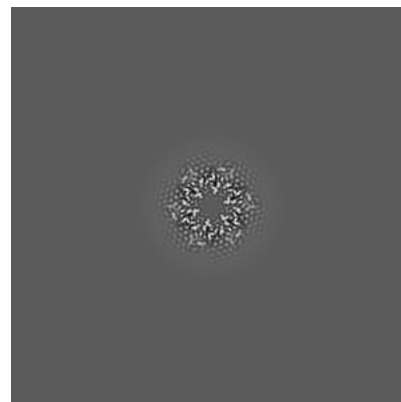
6.3.1 Primary map



X Index: 175

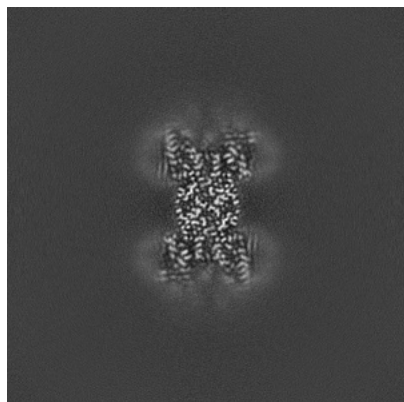


Y Index: 172

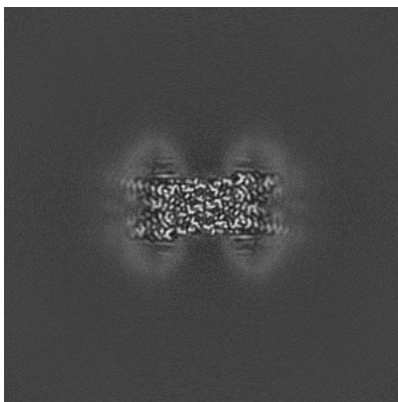


Z Index: 222

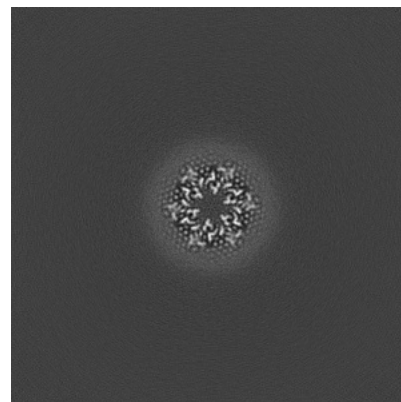
6.3.2 Raw map



X Index: 209



Y Index: 172

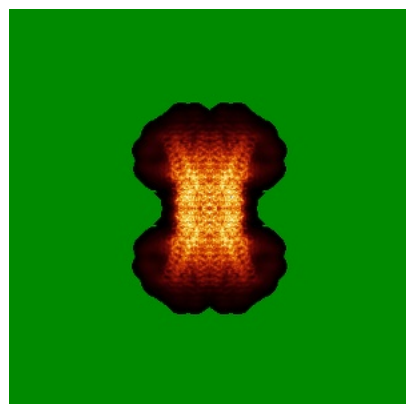


Z Index: 222

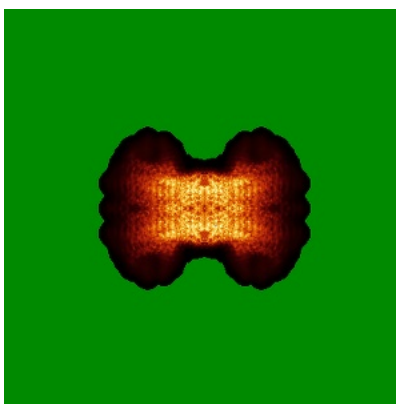
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

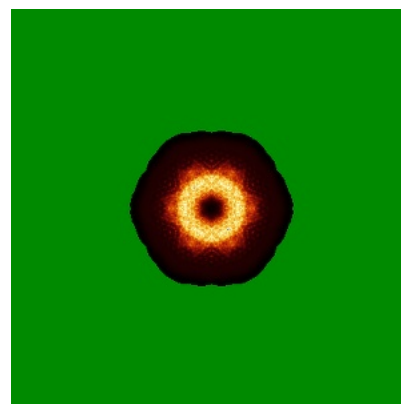
6.4.1 Primary map



X

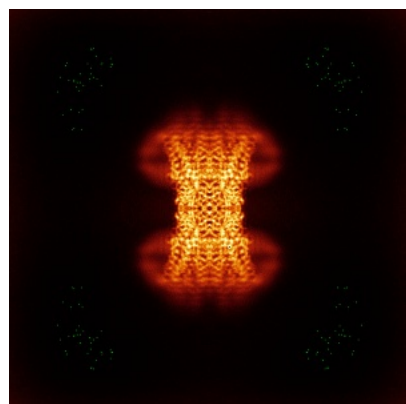


Y

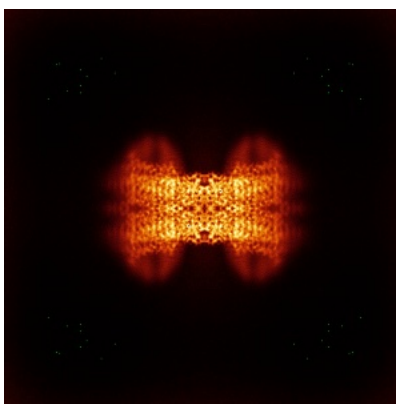


Z

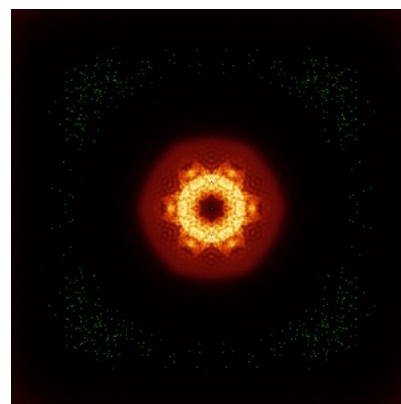
6.4.2 Raw map



X



Y

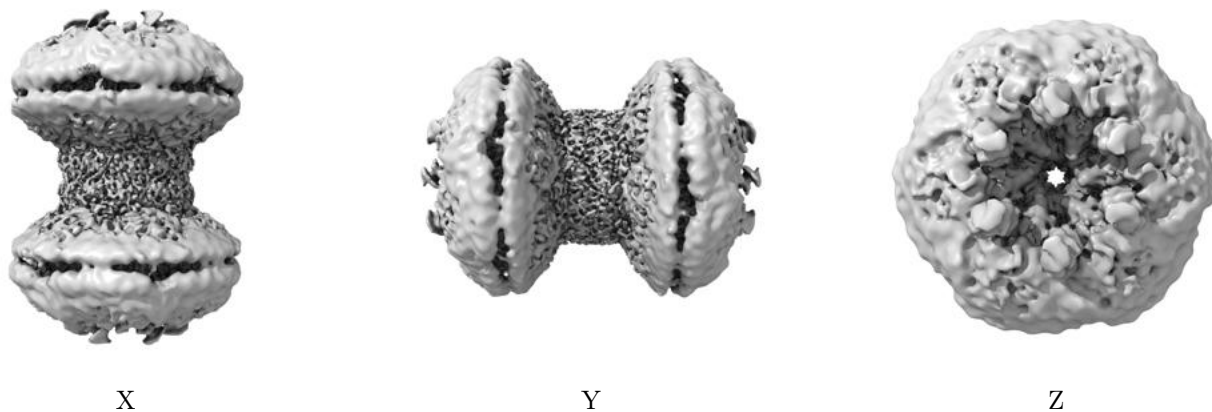


Z

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.

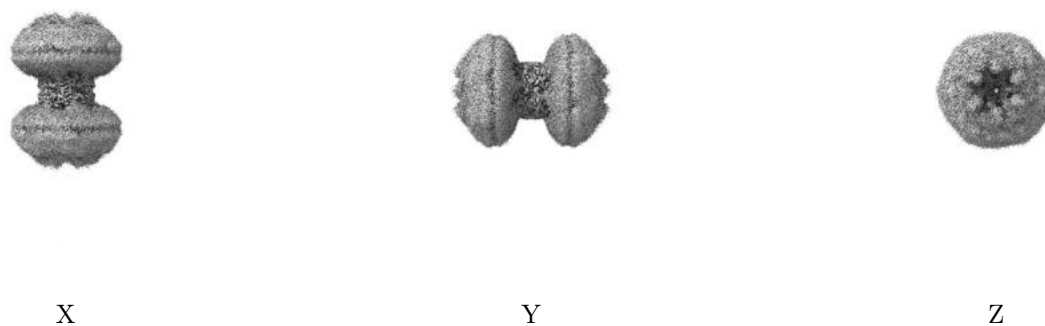
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

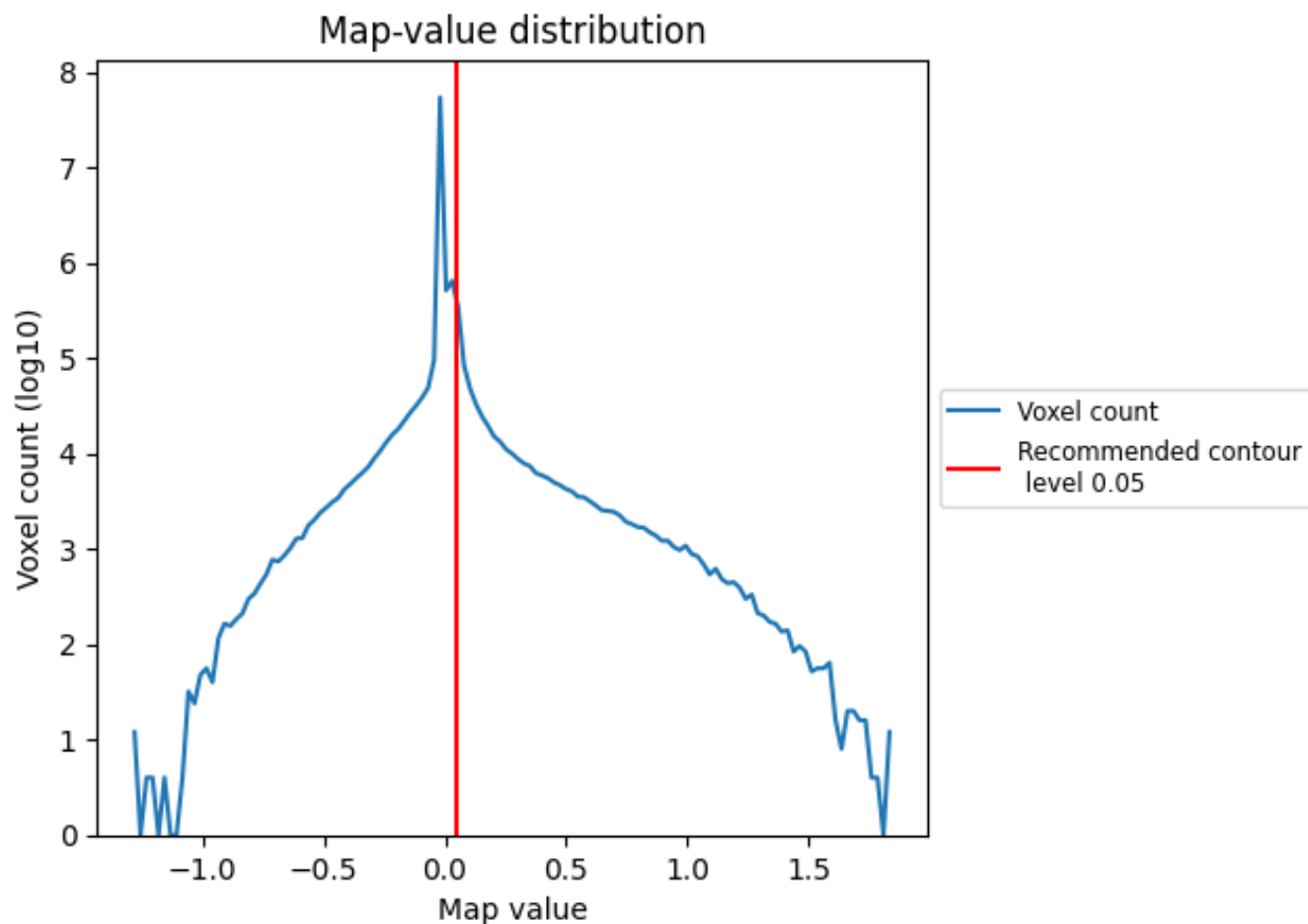
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

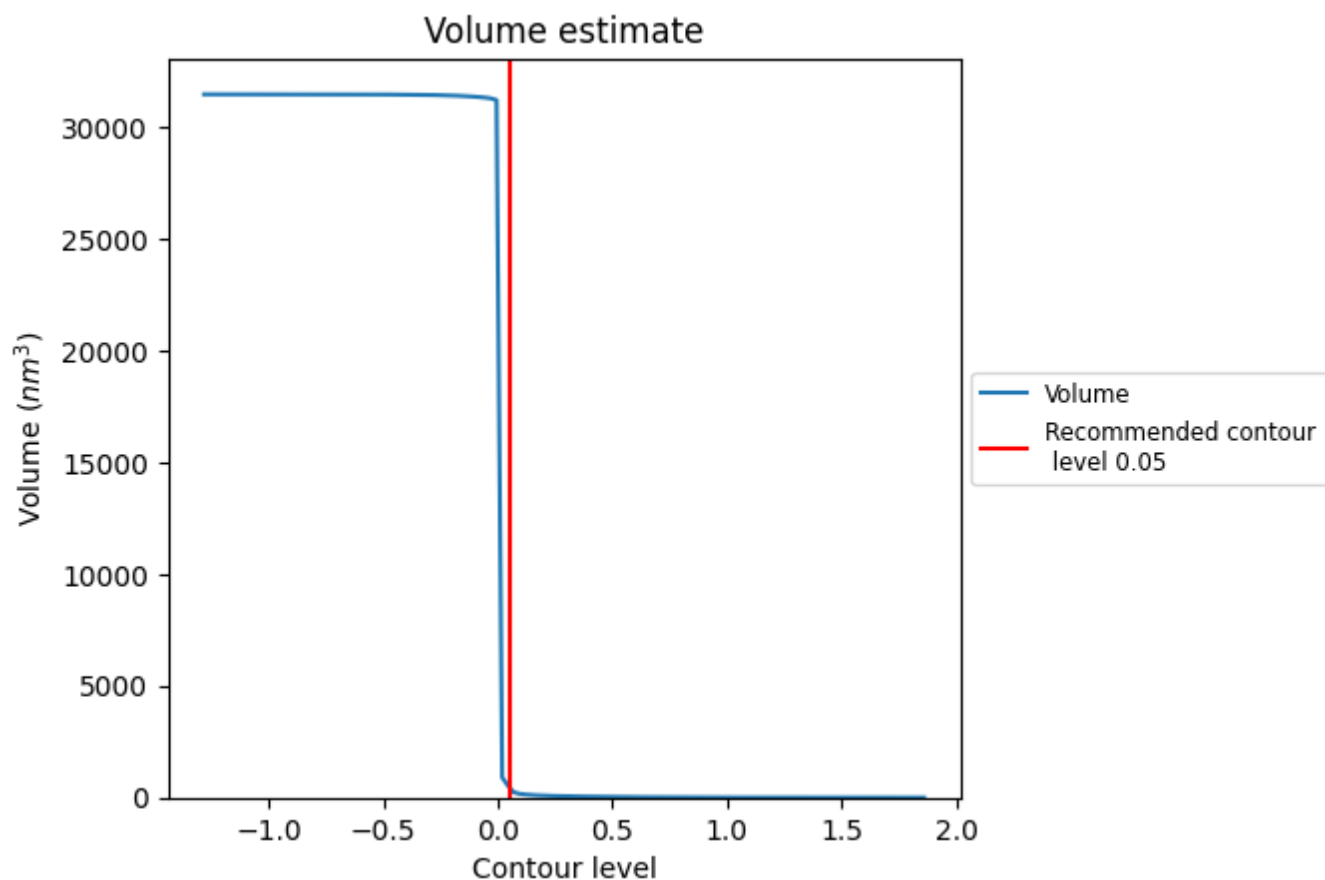
This section contains the results of statistical analysis of the map.

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.

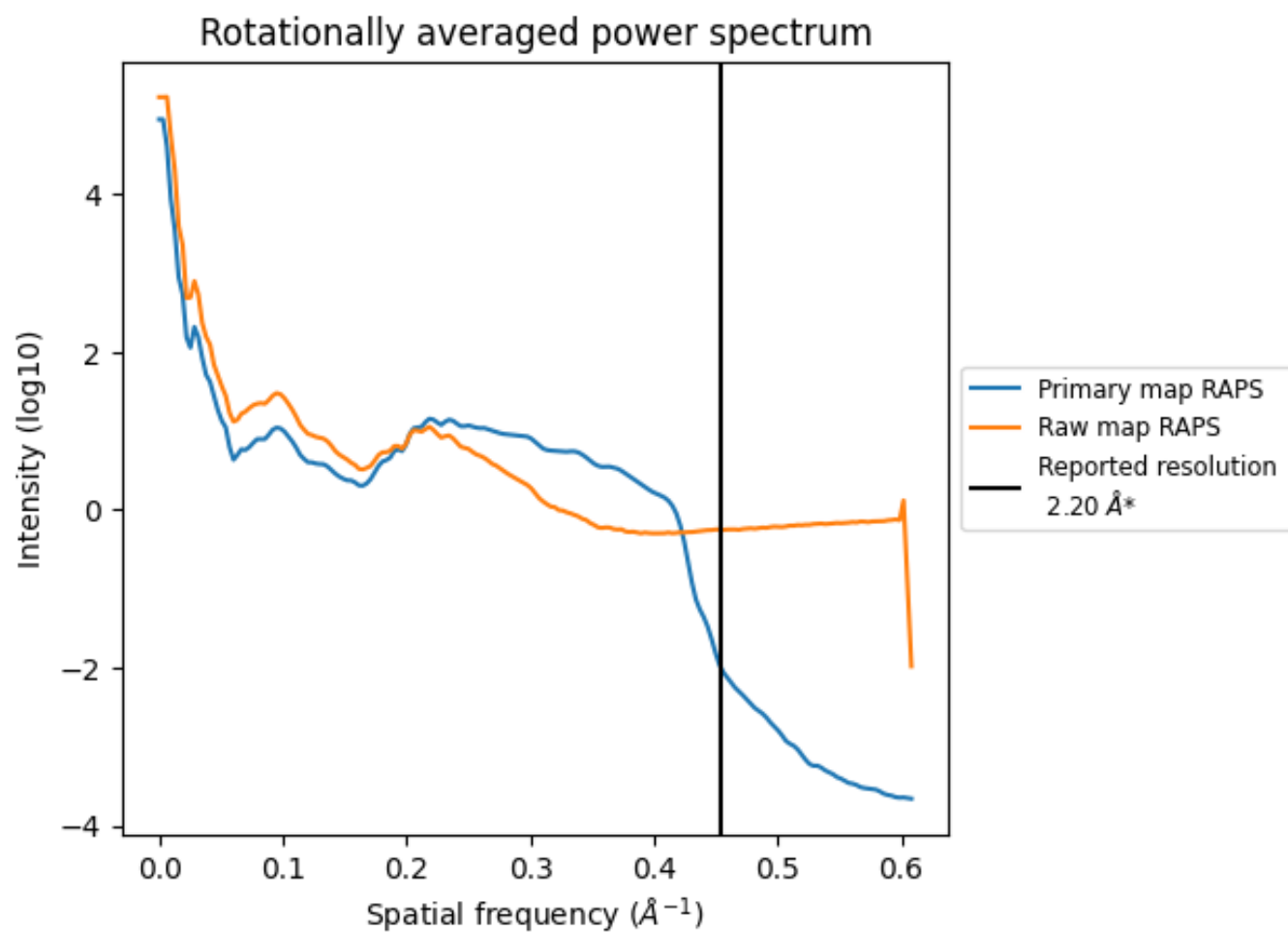
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 462 nm³; this corresponds to an approximate mass of 417 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 ⓘ

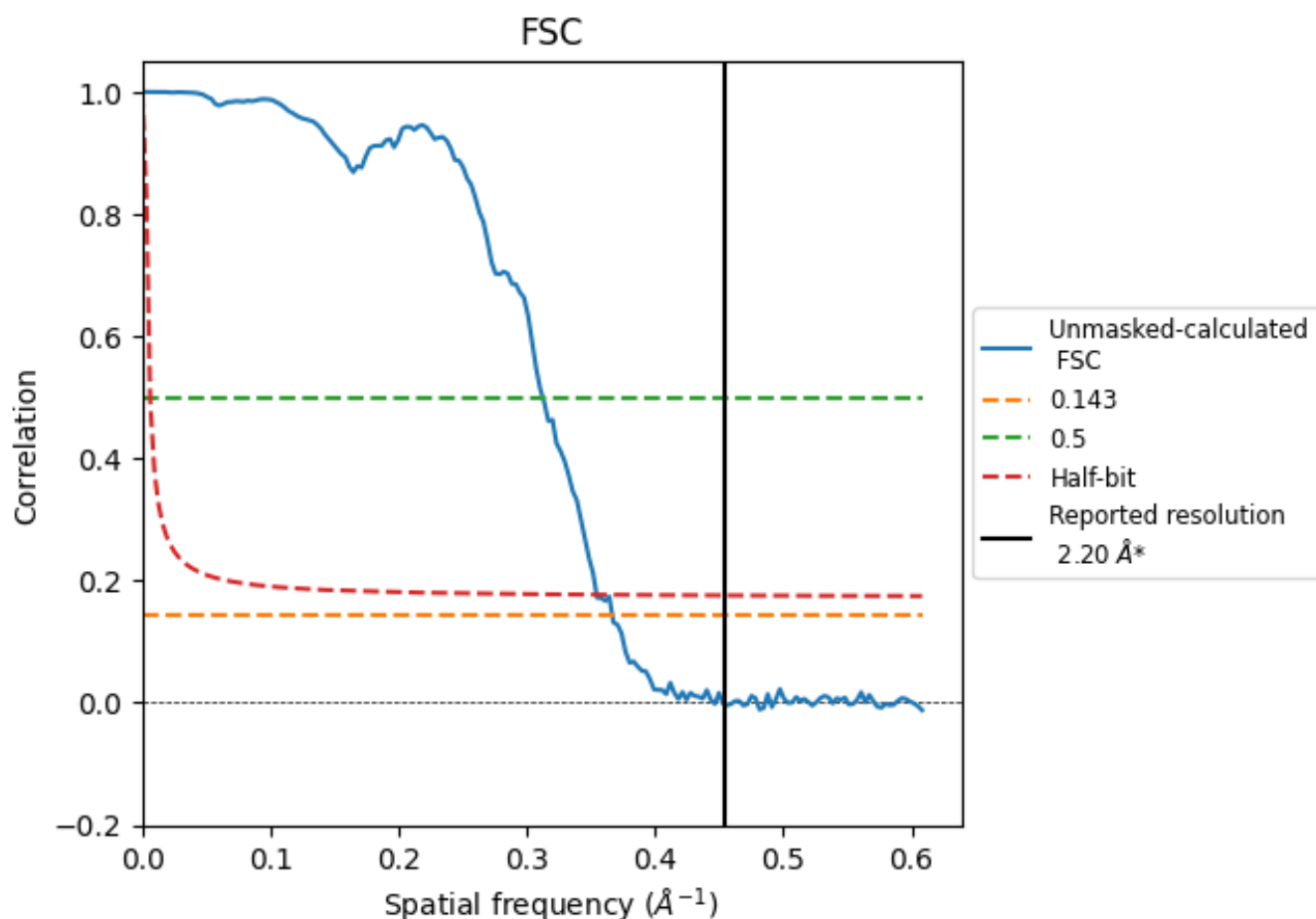


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

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](#)

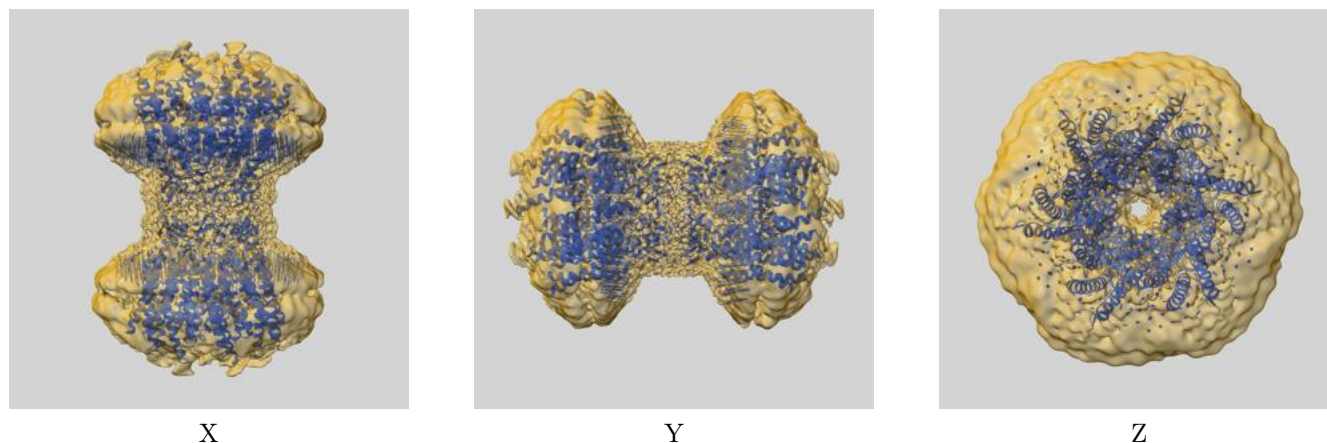
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.73	3.20	2.82

*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 2.73 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

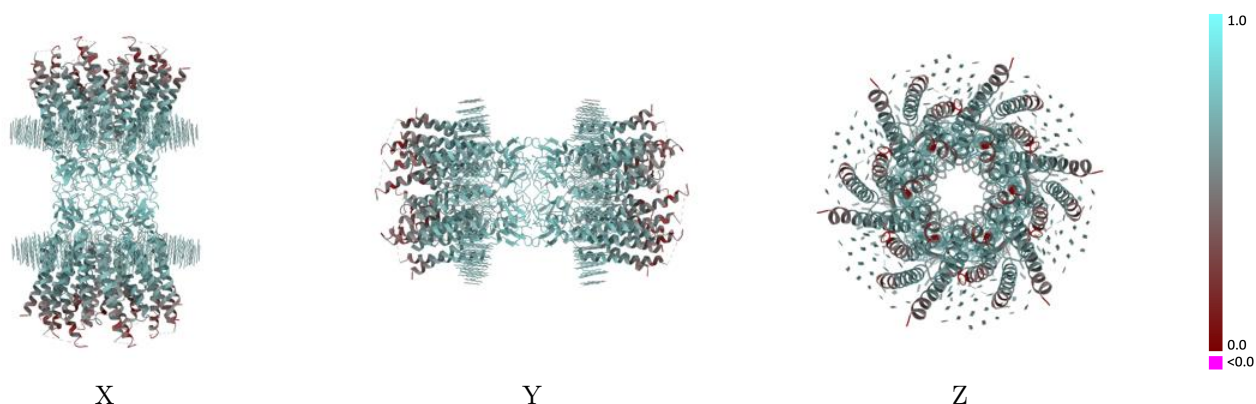
This section contains information regarding the fit between EMDB map EMD-73896 and PDB model 9Z8L. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



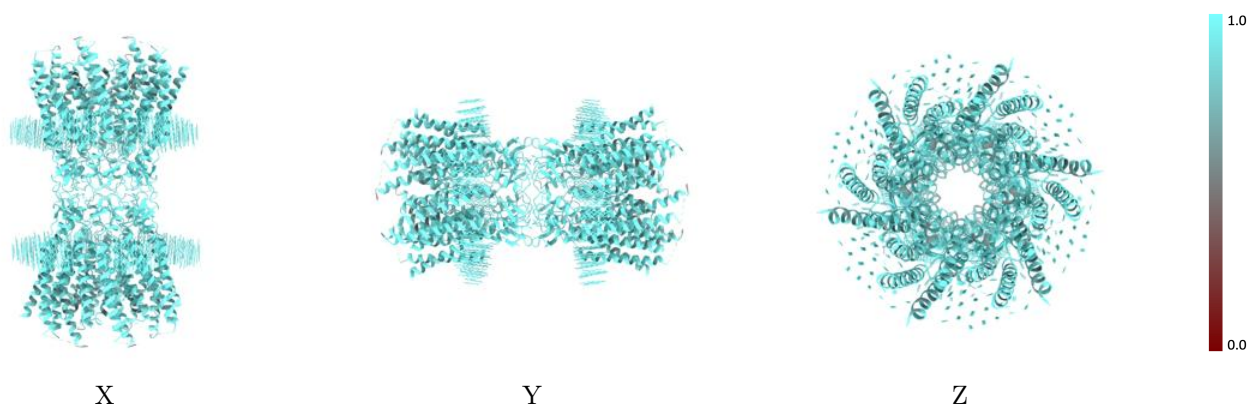
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



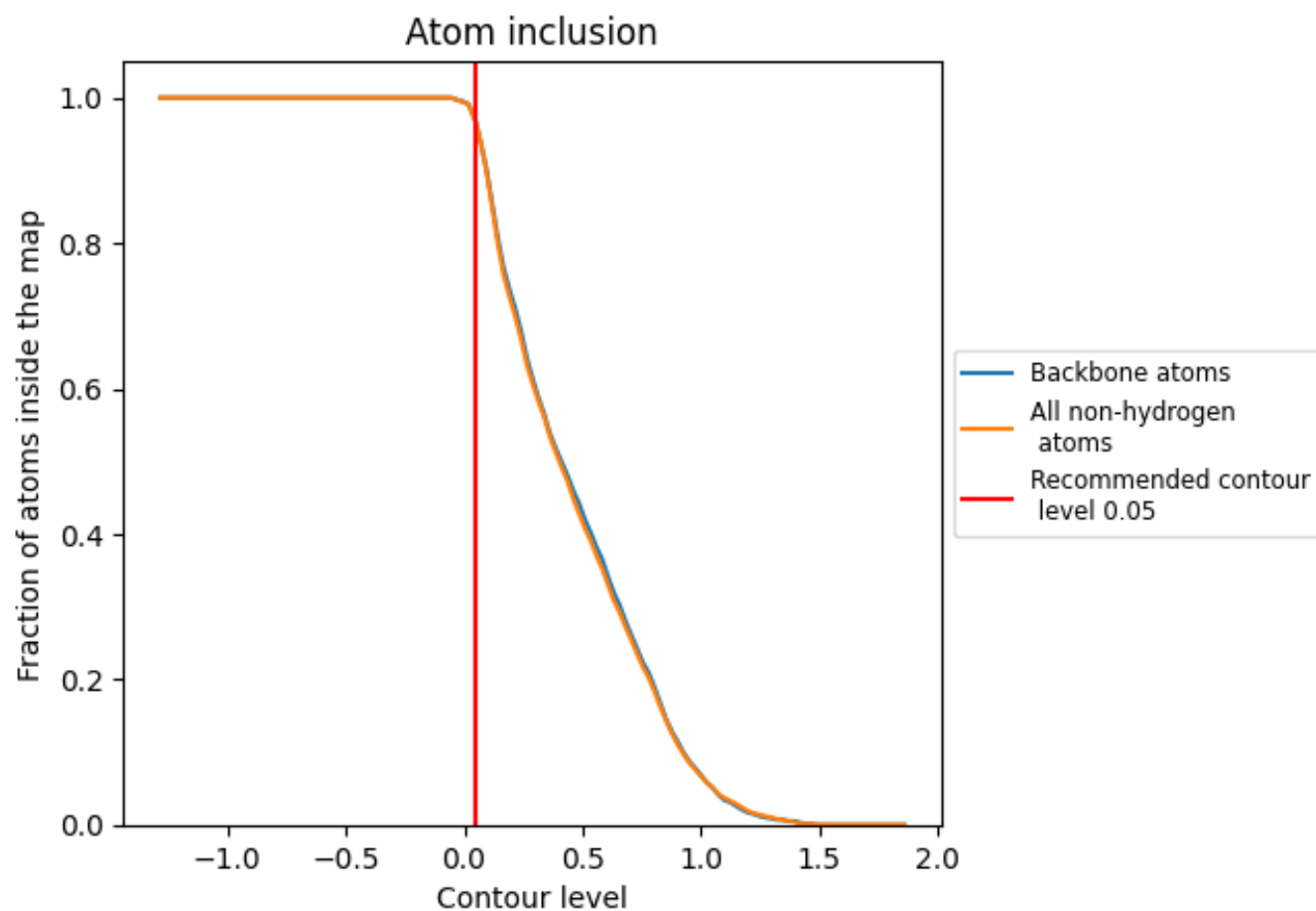
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9660	0.6070
A	0.9670	0.6080
B	0.9660	0.6070
C	0.9680	0.6070
D	0.9660	0.6060
E	0.9660	0.6070
F	0.9680	0.6080
G	0.9670	0.6080
H	0.9630	0.6080
I	0.9660	0.6070
J	0.9680	0.6070
K	0.9650	0.6060
L	0.9660	0.6060

1.0

0.0

<0.0