



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 03:41 PM UTC

PDB ID : 6ULG / pdb_00006ulg
EMDB ID : EMD-20814
Title : Cryo-EM structure of the FLCN-FNIP2-Rag-Ragulator complex
Authors : Shen, K.; Rogala, K.B.; Yu, Z.H.; Sabatini, D.M.
Deposited on : 2019-10-08
Resolution : 3.31 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

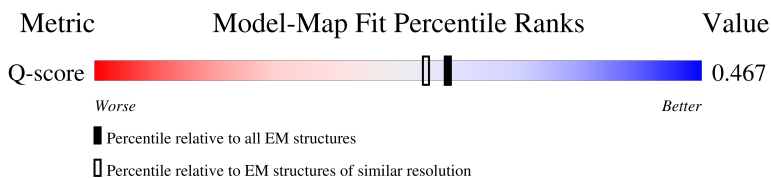
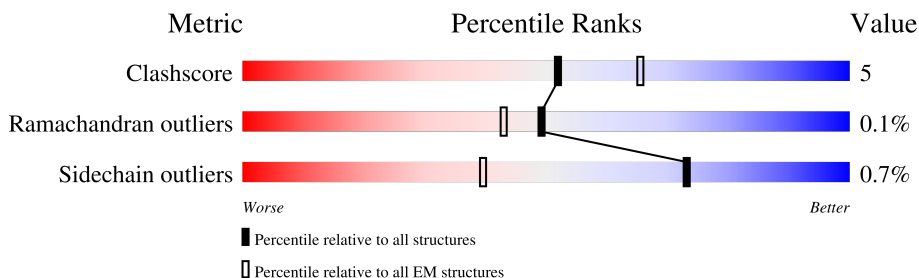
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.31 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	14550 (2.81 - 3.81)

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	L	579	 66% 13% 21%
2	A	124	 84% 14% .
3	B	125	 86% 13% .
4	C	91	 85% 15%

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Mol	Chain	Length	Quality of chain
5	D	99	 78% 8% 14%
6	E	161	 57% 8% 34%
7	F	313	 77% 10% 13%
8	G	399	 65% 12% 22%
9	N	1114	 37% 6% 57%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 16351 atoms, of which 0 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 Folliculin.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	458	Total	C	N	O	S	0	0
			3632	2325	631	651	25		

- Molecule 2 is a protein called Regulator complex protein LAMTOR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	121	Total	C	N	O	S	0	0
			939	604	158	176	1		

- Molecule 3 is a protein called Regulator complex protein LAMTOR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	125	Total	C	N	O	S	1	0
			950	596	163	183	8		

- Molecule 4 is a protein called Regulator complex protein LAMTOR5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	91	Total	C	N	O	S	1	0
			672	409	116	139	8		

- Molecule 5 is a protein called Regulator complex protein LAMTOR4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	85	Total	C	N	O	S	0	0
			647	407	116	123	1		

- Molecule 6 is a protein called Regulator complex protein LAMTOR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	106	Total	C	N	O	S	0	0
			829	524	142	161	2		

- Molecule 7 is a protein called Ras-related GTP-binding protein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	273	Total	C	N	O	S	0	0
			2246	1431	387	412	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	21	ASN	THR	engineered mutation	UNP Q7L523

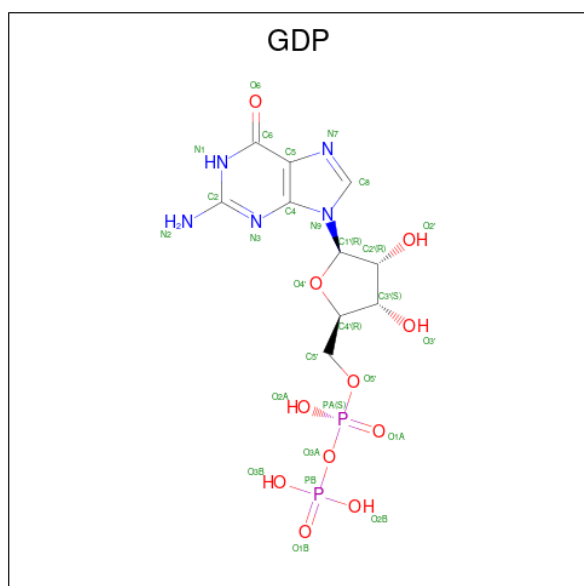
- Molecule 8 is a protein called Ras-related GTP-binding protein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	310	Total	C	N	O	S	0	0
			2506	1614	403	475	14		

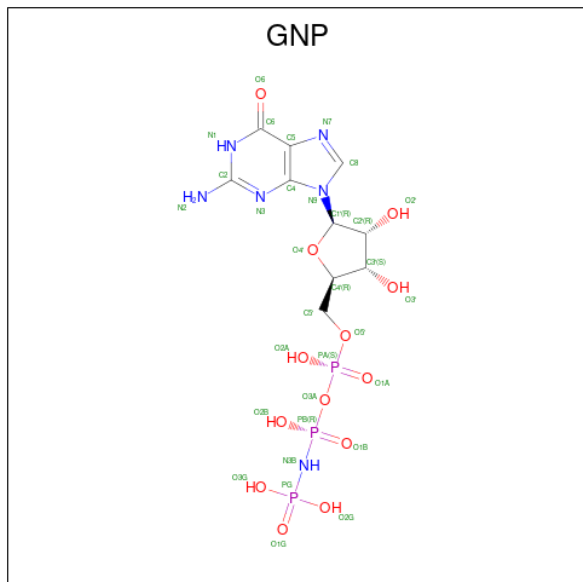
- Molecule 9 is a protein called Folliculin-interacting protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	483	Total	C	N	O	S	0	0
			3869	2481	659	703	26		

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



- Molecule 11 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
11	G	1	Total	C	N	O	P	0
			32	10	6	13	3	

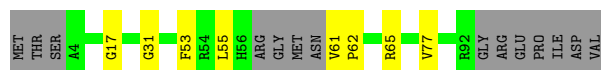
- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
12	G	1	Total	Mg	0
			1	1	



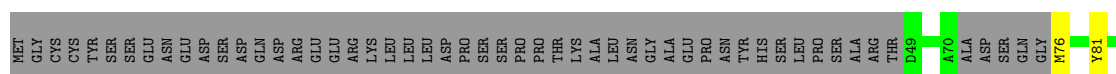
- Molecule 5: Regulator complex protein LAMTOR4

Chain D: 78% 8% 14%



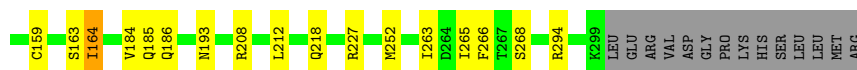
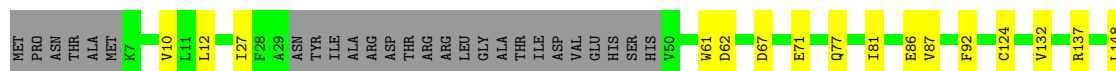
- Molecule 6: Regulator complex protein LAMTOR1

Chain E: 57% 8% 34%



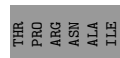
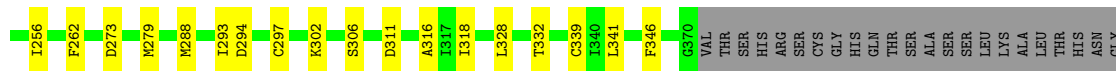
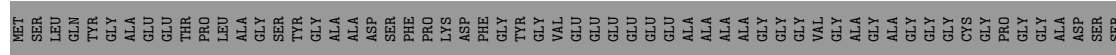
- Molecule 7: Ras-related GTP-binding protein A

Chain F: 77% 10% 13%



- Molecule 8: Ras-related GTP-binding protein C

Chain G: 65% 12% 22%



- Molecule 9: Folliculin-interacting protein 2

Chain N: 37% 6% 57%

LEU	GLY	ASP	SER	ASP	GLU	ALA	CYS	THR	ARG	CYS	VAL	ALA	PRO	GLY	T504	ARG	SER	LEU	ASP	THR	MET
ASP	GLY	LEU	TYR	VAL	GLN	ASN	PRO	PHE	GLN	PRO	PHE	GLN	ASP	GLU	V505	R308	SER	LEU	GLN	GLU	ALA
ASP	ASP	VAL	GLY	ILE	ASN	ARG	GLY	ILE	GLY	CYS	GLY	ILE	PRO	GLY	V506	K309	PHE	ILE	THR	VAL	PRO
GLU	GLU	LYS	VAL	SER	LEU	SER	GLY	SER	SER	PRO	GLY	PHE	PRO	GLY	V507	I316	TYR	ILE	TYR	ILE	LEU
ALA	ALA	ALA	GLY	ALA	SER	GLY	ALA	PHE	ARG	GLY	THR	ASN	PRO	GLY	K509	F317	ASN	ILE	ASN	ILE	LYS
CYS	CYS	GLU	GLY	GLU	GLY	ALA	GLY	ALA	LEU	GLY	THR	PRO	PRO	GLY	Q515	S318	SER	GLN	GLN	SER	LEU
ALA	GLU	GLY	GLY	GLY	GLY	GLY	GLY	SER	PRO	ASP	ASP	PRO	PRO	ASP	L518	L339	ASP	ALA	ALA	PHE	LEU
ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	L521	R346	SER	PRO	CYS	ASN	ASN
ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	T522	V392	GLY	PRO	CYS	LYS	LYS
MET	MET	VAL	VAL	VAL	GLY	GLY	GLY	VAL	VAL	GLY	VAL	VAL	VAL	GLY	S528	R394	SER	GLY	GLN	GLY	GLY
MET	GLY	ASP	PHE	PHE	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	E529	SER	SER	SER	GLY	SER	SER
ASP	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	L530	I428	ASN	ASN	THR	THR	GLY
LEU	LEU	VAL	VAL	VAL	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	Q531	N429	SER	THR	SER	SER	GLY
LEU	HIS	GLY	PRO	PRO	PHE	GLY	ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	S538	K430	SER	ASN	SER	SER	SER
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	N431	GLN	GLN	SER	ALA	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	Q432	ASN	ASN	SER	ALA	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	F433	SER	SER	SER	ALA	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	L438	LEU	GLY	SER	ALA	ALA
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	V441	ARG	CYS	ARG	ILE	ARG
GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	THR	THR	ILE	SER	ALA
VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	GLN	GLN	THR	SER	PRO
GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	VAL	THR	THR	GLY	SER	LYS
GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	ASP	SER	ASN	SER	HIS	GLY
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	LEU	LEU	SER	GLY	GLY
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	GLY	GLY	ALA	SER	PRO
PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	ASN	ALA	HIS	GLY	ALA
ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	GLY	GLY	ALA	THR	ALA
ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	GLY	GLY	GLN	SER	GLY
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	PHE	THR	THR
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ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
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ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	GLY	GLY	THR	ASN	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN	ASN										

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	126984	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	59.2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 BASE (4k x 4k)	Depositor
Maximum map value	0.106	Depositor
Minimum map value	-0.059	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.002	Depositor
Map size (Å)	374.4, 374.4, 374.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, GNP

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	L	0.26	0/3718	0.57	4/5031 (0.1%)
2	A	0.22	0/956	0.49	0/1297
3	B	0.31	0/961	0.63	2/1301 (0.2%)
4	C	0.19	0/678	0.41	0/919
5	D	0.20	0/654	0.52	0/883
6	E	0.26	0/844	0.40	0/1146
7	F	0.25	0/2287	0.56	1/3076 (0.0%)
8	G	0.26	0/2559	0.55	3/3455 (0.1%)
9	N	0.28	0/3943	0.71	5/5325 (0.1%)
All	All	0.26	0/16600	0.59	15/22433 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
8	G	0	2
9	N	0	2
All	All	0	4

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	N	1005	SER	CA-C-N	8.58	130.55	121.97
9	N	1005	SER	C-N-CA	8.58	130.55	121.97
9	N	1047	PRO	N-CA-CB	7.79	111.43	103.25
9	N	430	LYS	CA-C-N	6.35	133.67	121.54
9	N	430	LYS	C-N-CA	6.35	133.67	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	100	LYS	CA-C-N	5.69	132.42	121.54
1	L	100	LYS	C-N-CA	5.69	132.42	121.54
8	G	219	SER	CA-C-N	-5.59	111.91	121.97
8	G	219	SER	C-N-CA	-5.59	111.91	121.97
3	B	116	GLU	CA-C-N	-5.52	113.70	119.83
3	B	116	GLU	C-N-CA	-5.52	113.70	119.83
8	G	108	SER	N-CA-C	5.51	118.94	111.17
7	F	164	ILE	N-CA-C	-5.22	107.74	113.43
1	L	136	GLY	CA-C-N	5.01	131.11	121.54
1	L	136	GLY	C-N-CA	5.01	131.11	121.54

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	G	107	SER	Peptide
8	G	119	GLY	Peptide
9	N	163	PRO	Peptide
9	N	54	ASP	Peptide

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	L	3632	0	3629	45	0
2	A	939	0	963	13	0
3	B	950	0	959	14	0
4	C	672	0	670	11	0
5	D	647	0	657	6	0
6	E	829	0	832	12	0
7	F	2246	0	2243	20	0
8	G	2506	0	2474	30	0
9	N	3869	0	3928	42	0
10	F	28	0	12	0	0
11	G	32	0	12	1	0
12	G	1	0	0	0	0
All	All	16351	0	16379	175	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 5.

All (175) 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)
6:E:99:LEU:HD11	6:E:102:TRP:HB2	1.54	0.90
3:B:112:VAL:O	3:B:116:GLU:HB2	1.90	0.71
8:G:230:SER:O	8:G:234:GLN:HB2	1.94	0.68
9:N:339:LEU:HD22	9:N:961:LEU:HD11	1.79	0.64
9:N:346:ARG:HH22	9:N:987:LEU:HB2	1.63	0.64
9:N:175:ARG:HB3	9:N:179:PHE:HB2	1.81	0.61
4:C:78:LYS:HB3	4:C:83:THR:HG22	1.81	0.61
7:F:252:MET:HG3	8:G:318:ILE:HG12	1.83	0.61
9:N:432:GLN:HB3	9:N:1027:VAL:HG21	1.83	0.60
6:E:112:THR:HG22	6:E:114:GLN:H	1.67	0.60
1:L:131:CYS:SG	1:L:132:GLU:N	2.75	0.60
9:N:956:MET:SD	9:N:956:MET:N	2.75	0.60
8:G:80:VAL:HG21	8:G:220:ILE:HD12	1.82	0.60
1:L:178:ASP:HB2	9:N:480:PRO:HG2	1.84	0.59
7:F:86:GLU:HG3	7:F:87:VAL:HG23	1.84	0.59
2:A:102:LEU:HD22	4:C:47:VAL:HG21	1.84	0.59
9:N:531:GLN:HG2	9:N:562:VAL:HG22	1.85	0.58
4:C:44:VAL:HG11	5:D:53:PHE:HB2	1.85	0.58
1:L:16:PRO:O	1:L:122:ARG:NH1	2.36	0.58
6:E:99:LEU:CD1	6:E:102:TRP:HB2	2.32	0.58
1:L:339:GLN:NE2	1:L:459:SER:O	2.37	0.58
2:A:80:VAL:HG12	2:A:93:ILE:HG12	1.86	0.58
9:N:392:VAL:HG23	9:N:394:ARG:HE	1.69	0.57
9:N:981:THR:HG22	9:N:1012:GLN:HB3	1.86	0.57
5:D:65:ARG:HH22	6:E:121:SER:HB2	1.70	0.57
8:G:151:MET:SD	8:G:198:ARG:NH1	2.79	0.56
1:L:518:LEU:HD22	1:L:550:LEU:HD13	1.89	0.55
3:B:86:VAL:HG22	3:B:112:VAL:HG23	1.88	0.55
8:G:141:ILE:HD11	8:G:232:VAL:HG11	1.89	0.55
7:F:218:GLN:OE1	7:F:227:ARG:NH1	2.39	0.55
9:N:506:VAL:HA	9:N:1002:ASP:HB3	1.88	0.55
1:L:339:GLN:HE22	1:L:460:LEU:HA	1.72	0.55
1:L:233:ARG:NH2	8:G:297:CYS:SG	2.80	0.55
9:N:996:CYS:SG	9:N:1013:ARG:NH1	2.80	0.54
1:L:346:PHE:HB2	1:L:390:VAL:HG21	1.89	0.54
1:L:373:GLN:NE2	1:L:415:CYS:SG	2.80	0.54
4:C:22:LEU:HB3	4:C:85:ALA:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:25:SER:OG	2:A:26:ASP:N	2.40	0.54
9:N:507:VAL:HG22	9:N:1003:LYS:HA	1.89	0.54
1:L:98:HIS:HA	1:L:105:LYS:HA	1.90	0.54
4:C:67:LEU:HB2	4:C:74:ILE:HB	1.90	0.53
1:L:233:ARG:NH1	8:G:294:ASP:OD1	2.41	0.53
1:L:227:THR:OG1	1:L:232:GLN:OE1	2.27	0.53
7:F:208:ARG:NH1	7:F:268:SER:O	2.42	0.53
9:N:393:PRO:HA	9:N:572:VAL:HG22	1.90	0.53
1:L:233:ARG:HH22	8:G:293:ILE:HG22	1.74	0.53
9:N:988:ASP:OD1	9:N:988:ASP:N	2.42	0.53
2:A:20:HIS:HB3	2:A:40:ALA:HB2	1.91	0.53
1:L:137:ARG:O	1:L:155:THR:OG1	2.27	0.52
2:A:99:ASN:ND2	4:C:46:SER:OG	2.42	0.52
8:G:256:ILE:HG23	8:G:341:LEU:HB3	1.91	0.52
3:B:87:ALA:HB2	3:B:116:GLU:HG3	1.91	0.52
2:A:57:THR:HG23	2:A:68:ASN:HB3	1.90	0.52
8:G:77:ILE:HG23	8:G:225:ILE:HD11	1.92	0.52
7:F:266:PHE:HA	7:F:294:ARG:HD3	1.91	0.51
7:F:265:ILE:O	7:F:294:ARG:NH2	2.43	0.51
8:G:302:LYS:NZ	8:G:306:SER:OG	2.43	0.51
8:G:273:ASP:OD1	8:G:273:ASP:N	2.40	0.51
9:N:997:ILE:H	9:N:1012:GLN:HG2	1.75	0.51
9:N:429:ASN:HA	9:N:433:PHE:HB3	1.93	0.51
1:L:176:MET:HG3	1:L:182:LEU:HD13	1.93	0.51
8:G:69:LEU:HD12	8:G:120:GLN:HB3	1.92	0.50
7:F:132:VAL:HG23	7:F:137:ARG:HG2	1.93	0.50
1:L:514:LYS:HD2	1:L:539:LEU:HG	1.94	0.50
6:E:159:GLY:O	7:F:193:ASN:ND2	2.44	0.50
3:B:75:ASP:HB2	3:B:101:PHE:HZ	1.76	0.50
9:N:55:CYS:HB3	9:N:309:LYS:HA	1.93	0.50
1:L:176:MET:HB2	1:L:182:LEU:HD22	1.93	0.50
1:L:543:GLU:OE1	1:L:546:ASN:ND2	2.45	0.49
2:A:11:LYS:HB3	6:E:105:LEU:HD11	1.95	0.49
1:L:345:VAL:HG13	1:L:386:SER:HB2	1.94	0.49
3:B:49:ALA:HB1	3:B:83:ILE:HD11	1.95	0.49
9:N:1038:ILE:HG13	9:N:1055:LEU:HD12	1.93	0.49
8:G:144:ILE:HD11	8:G:157:LEU:HD22	1.93	0.49
8:G:63:ARG:HB2	8:G:137:THR:HG22	1.95	0.49
3:B:41:ASP:N	3:B:41:ASP:OD1	2.46	0.49
7:F:27:ILE:HG23	7:F:212:LEU:HD21	1.94	0.49
2:A:112:PRO:HG2	6:E:102:TRP:HE1	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:401:ARG:O	1:L:416:ASN:N	2.46	0.48
9:N:509:LYS:H	9:N:968:GLU:HB3	1.78	0.48
7:F:62:ASP:OD1	7:F:62:ASP:N	2.43	0.48
2:A:74:TYR:HB2	3:B:71:PHE:HB3	1.94	0.48
7:F:266:PHE:HB2	7:F:294:ARG:HB2	1.95	0.48
2:A:59:GLN:OE1	3:B:51:ASN:ND2	2.47	0.48
8:G:208:LEU:HB3	8:G:211:LEU:HD12	1.96	0.48
8:G:341:LEU:HD11	8:G:346:PHE:HD1	1.79	0.48
1:L:492:ASN:HB3	1:L:495:LEU:HD12	1.96	0.47
8:G:288:MET:HG3	8:G:318:ILE:HD12	1.96	0.47
1:L:135:PRO:HG2	9:N:160:ILE:HG23	1.96	0.47
9:N:506:VAL:H	9:N:966:SER:HB2	1.80	0.47
9:N:979:VAL:O	9:N:983:HIS:ND1	2.48	0.47
1:L:157:PHE:O	1:L:201:GLN:NE2	2.48	0.47
7:F:92:PHE:HZ	7:F:148:LEU:HD11	1.79	0.47
6:E:99:LEU:HD11	6:E:102:TRP:CB	2.36	0.47
2:A:16:VAL:HG13	2:A:102:LEU:HD23	1.96	0.47
3:B:10:VAL:HG13	6:E:148:VAL:HG21	1.96	0.47
8:G:256:ILE:HG21	8:G:339:CYS:HB3	1.97	0.46
9:N:502:THR:HG23	9:N:998:ILE:HB	1.98	0.46
1:L:145:ASP:N	1:L:145:ASP:OD1	2.48	0.46
3:B:19:VAL:HA	3:B:95:ALA:HA	1.98	0.46
5:D:55:LEU:HB2	5:D:62:PRO:HG3	1.98	0.46
7:F:67:ASP:O	7:F:71:GLU:HB3	2.16	0.46
8:G:63:ARG:NE	8:G:136:GLY:O	2.46	0.45
9:N:54:ASP:OD2	9:N:60:ARG:NE	2.47	0.45
1:L:518:LEU:HA	1:L:535:LEU:HD21	1.98	0.45
4:C:21:VAL:HG23	4:C:86:VAL:HG12	1.98	0.45
1:L:211:GLU:HG3	1:L:218:ARG:HH21	1.82	0.45
1:L:440:GLU:HB2	1:L:466:VAL:HG23	1.98	0.45
9:N:985:PRO:HG3	9:N:997:ILE:HG12	1.99	0.45
9:N:501:LEU:HB3	9:N:997:ILE:HD12	1.99	0.45
8:G:219:SER:OG	8:G:222:ASP:OD1	2.35	0.45
9:N:515:GLN:HG2	9:N:573:ARG:HH11	1.81	0.45
8:G:180:VAL:HA	8:G:183:LEU:HD13	1.99	0.45
9:N:46:GLU:HG2	9:N:318:SER:HB3	1.98	0.45
1:L:7:LEU:HD13	1:L:254:LEU:HD21	1.98	0.45
8:G:108:SER:O	8:G:108:SER:OG	2.30	0.44
8:G:130:TYR:HA	8:G:133:ILE:HG12	1.99	0.44
7:F:252:MET:HE2	7:F:263:ILE:HD12	1.99	0.44
8:G:174:GLU:HG2	8:G:232:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:181:ASP:OD1	8:G:181:ASP:N	2.37	0.44
9:N:441:VAL:HG11	9:N:521:LEU:HD21	1.98	0.44
9:N:1034:LEU:HD13	9:N:1058:ARG:HG2	1.98	0.44
7:F:184:VAL:HG23	7:F:186:GLN:HG2	2.00	0.44
8:G:311:ASP:OD1	8:G:311:ASP:N	2.50	0.44
3:B:109:GLN:HA	3:B:112:VAL:HG12	2.00	0.44
1:L:269:LEU:HD22	9:N:530:LEU:HD23	1.99	0.44
1:L:402:ILE:HG22	1:L:417:PHE:HB2	2.00	0.43
3:B:112:VAL:O	3:B:116:GLU:CB	2.64	0.43
1:L:82:CYS:SG	1:L:83:GLU:N	2.90	0.43
4:C:78:LYS:HA	4:C:83:THR:HA	2.00	0.43
1:L:142:PHE:HB2	1:L:186:TRP:HZ3	1.84	0.43
9:N:438:LEU:HA	9:N:441:VAL:HG22	2.00	0.43
4:C:13:MET:HE3	4:C:13:MET:HB3	1.92	0.43
5:D:61:VAL:HA	5:D:62:PRO:HD3	1.96	0.43
1:L:389:GLU:HA	1:L:392:ARG:HD2	2.00	0.42
2:A:16:VAL:HB	2:A:19:LEU:HB2	2.01	0.42
6:E:76:MET:HE2	6:E:81:TYR:HB2	2.01	0.42
4:C:21:VAL:HG12	4:C:34:ARG:HB2	2.02	0.42
7:F:12:LEU:HB3	7:F:62:ASP:HB3	2.01	0.42
1:L:486:ILE:HD12	1:L:486:ILE:HA	1.86	0.42
9:N:167:MET:HG3	9:N:316:ILE:HG13	2.02	0.42
1:L:352:MET:HA	1:L:355:VAL:HG12	2.02	0.42
9:N:980:HIS:HA	9:N:983:HIS:CE1	2.55	0.42
1:L:356:LEU:O	1:L:360:SER:OG	2.35	0.42
1:L:283:LEU:HB3	1:L:558:SER:HB2	2.02	0.42
9:N:66:SER:O	9:N:66:SER:OG	2.35	0.42
9:N:518:LEU:O	9:N:522:THR:OG1	2.35	0.42
3:B:1:MET:HE2	3:B:1:MET:HB3	1.95	0.41
3:B:15:ASN:HA	3:B:19:VAL:HG23	2.01	0.41
7:F:124:CYS:HB2	7:F:159:CYS:HB3	2.02	0.41
1:L:87:SER:OG	1:L:89:ALA:O	2.36	0.41
5:D:65:ARG:NH2	6:E:118:VAL:O	2.51	0.41
7:F:61:TRP:HH2	7:F:81:ILE:HA	1.84	0.41
1:L:534:LYS:HD3	1:L:534:LYS:HA	1.71	0.41
5:D:17:GLY:HA2	5:D:31:GLY:HA3	2.01	0.41
1:L:430:VAL:O	1:L:433:SER:OG	2.33	0.41
1:L:441:VAL:O	1:L:442:HIS:ND1	2.53	0.41
2:A:9:LEU:HD12	2:A:9:LEU:HA	1.91	0.41
9:N:438:LEU:HA	9:N:438:LEU:HD23	1.82	0.41
8:G:279:MET:HE3	8:G:279:MET:HB3	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:96:THR:N	11:G:401:GNP:O1G	2.53	0.41
9:N:530:LEU:HB2	9:N:566:GLU:HG2	2.02	0.41
1:L:130:SER:OG	1:L:131:CYS:N	2.53	0.41
9:N:508:GLY:HA3	9:N:968:GLU:HG2	2.01	0.41
1:L:86:ARG:O	1:L:110:GLN:NE2	2.53	0.41
1:L:134:CYS:HB2	1:L:141:ILE:HD11	2.02	0.41
7:F:77:GLN:HA	7:F:81:ILE:HB	2.03	0.41
7:F:163:SER:OG	7:F:164:ILE:N	2.53	0.41
4:C:45:ILE:HG21	4:C:85:ALA:HB2	2.03	0.40
9:N:995:VAL:HG12	9:N:996:CYS:H	1.86	0.40
6:E:135:ILE:HD13	6:E:135:ILE:HA	1.92	0.40
9:N:487:GLN:NE2	9:N:528:SER:O	2.54	0.40
8:G:316:ALA:HB3	8:G:328:LEU:HB3	2.03	0.40
9:N:504:THR:HB	9:N:964:THR:HG22	2.03	0.40
1:L:2:ASN:HB3	1:L:3:ALA:H	1.61	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	L	450/579 (78%)	410 (91%)	39 (9%)	1 (0%)	43	72
2	A	119/124 (96%)	112 (94%)	7 (6%)	0	100	100
3	B	124/125 (99%)	114 (92%)	10 (8%)	0	100	100
4	C	90/91 (99%)	87 (97%)	3 (3%)	0	100	100
5	D	81/99 (82%)	77 (95%)	4 (5%)	0	100	100
6	E	102/161 (63%)	98 (96%)	4 (4%)	0	100	100
7	F	269/313 (86%)	256 (95%)	12 (4%)	1 (0%)	30	60
8	G	308/399 (77%)	283 (92%)	25 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	N	471/1114 (42%)	403 (86%)	67 (14%)	1 (0%)	43	72
All	All	2014/3005 (67%)	1840 (91%)	171 (8%)	3 (0%)	49	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	N	1047	PRO
1	L	559	LYS
7	F	185	GLN

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	L	403/503 (80%)	403 (100%)	0	100	100
2	A	105/108 (97%)	105 (100%)	0	100	100
3	B	99/98 (101%)	99 (100%)	0	100	100
4	C	78/77 (101%)	78 (100%)	0	100	100
5	D	71/83 (86%)	70 (99%)	1 (1%)	59	72
6	E	93/141 (66%)	90 (97%)	3 (3%)	34	60
7	F	252/287 (88%)	251 (100%)	1 (0%)	84	83
8	G	283/340 (83%)	280 (99%)	3 (1%)	65	74
9	N	433/955 (45%)	428 (99%)	5 (1%)	63	74
All	All	1817/2592 (70%)	1804 (99%)	13 (1%)	73	79

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	D	77	VAL
6	E	97	SER
6	E	98	SER
6	E	148	VAL

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Mol	Chain	Res	Type
7	F	10	VAL
8	G	110	VAL
8	G	262	PHE
8	G	332	THR
9	N	43	ASP
9	N	428	ILE
9	N	507	VAL
9	N	1006	VAL
9	N	1098	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	110	GLN
1	L	111	HIS
1	L	123	GLN
1	L	147	GLN
1	L	255	HIS
1	L	285	GLN
1	L	339	GLN
1	L	373	GLN
1	L	416	ASN
1	L	429	HIS
1	L	494	ASN
1	L	502	GLN
1	L	513	ASN
1	L	533	GLN
2	A	20	HIS
2	A	59	GLN
3	B	51	ASN
4	C	30	ASN
4	C	77	GLN
4	C	79	HIS
6	E	114	GLN
7	F	72	ASN
7	F	107	GLN
7	F	115	GLN
7	F	116	ASN
7	F	179	GLN
7	F	222	GLN
7	F	237	GLN
8	G	357	HIS

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Mol	Chain	Res	Type
9	N	70	GLN
9	N	549	ASN
9	N	980	HIS
9	N	983	HIS

5.3.3 RNA [i](#)

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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	GDP	F	500	-	29,30,30	1.15	3 (10%)	45,47,47	1.80	8 (17%)
11	GNP	G	401	12	34,34,34	1.52	6 (17%)	47,54,54	0.83	1 (2%)

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
10	GDP	F	500	-	-	2/16/32/32	0/3/3/3
11	GNP	G	401	12	-	9/18/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	G	401	GNP	O6-C6	4.99	1.33	1.23
11	G	401	GNP	PB-O3A	4.21	1.64	1.59
10	F	500	GDP	C5-C4	2.87	1.46	1.38
11	G	401	GNP	PG-N3B	2.82	1.70	1.63
11	G	401	GNP	PB-O1B	2.78	1.50	1.46
11	G	401	GNP	PG-O1G	2.66	1.50	1.46
10	F	500	GDP	C6-N1	-2.47	1.34	1.38
11	G	401	GNP	PB-O2B	-2.20	1.51	1.56
10	F	500	GDP	C5-N7	-2.14	1.34	1.39

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	F	500	GDP	C5-C4-N3	-5.92	118.96	128.39
10	F	500	GDP	C2-N3-C4	4.95	120.82	112.30
10	F	500	GDP	N9-C4-N3	4.76	135.48	125.95
10	F	500	GDP	C6-C5-N7	3.01	135.77	130.29
10	F	500	GDP	O6-C6-C5	-2.38	120.24	126.53
10	F	500	GDP	C2'-C1'-N9	-2.34	106.74	113.25
10	F	500	GDP	C4-C5-N7	-2.27	107.07	110.67
10	F	500	GDP	C3'-C2'-C1'	2.25	105.73	101.46
11	G	401	GNP	O1B-PB-N3B	-2.22	108.51	111.77

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	G	401	GNP	PB-N3B-PG-O1G
11	G	401	GNP	PG-N3B-PB-O1B
11	G	401	GNP	PG-N3B-PB-O3A
11	G	401	GNP	PA-O3A-PB-O2B
11	G	401	GNP	C5'-O5'-PA-O3A
11	G	401	GNP	C5'-O5'-PA-O2A
11	G	401	GNP	C3'-C4'-C5'-O5'
11	G	401	GNP	O4'-C4'-C5'-O5'
10	F	500	GDP	C5'-O5'-PA-O3A

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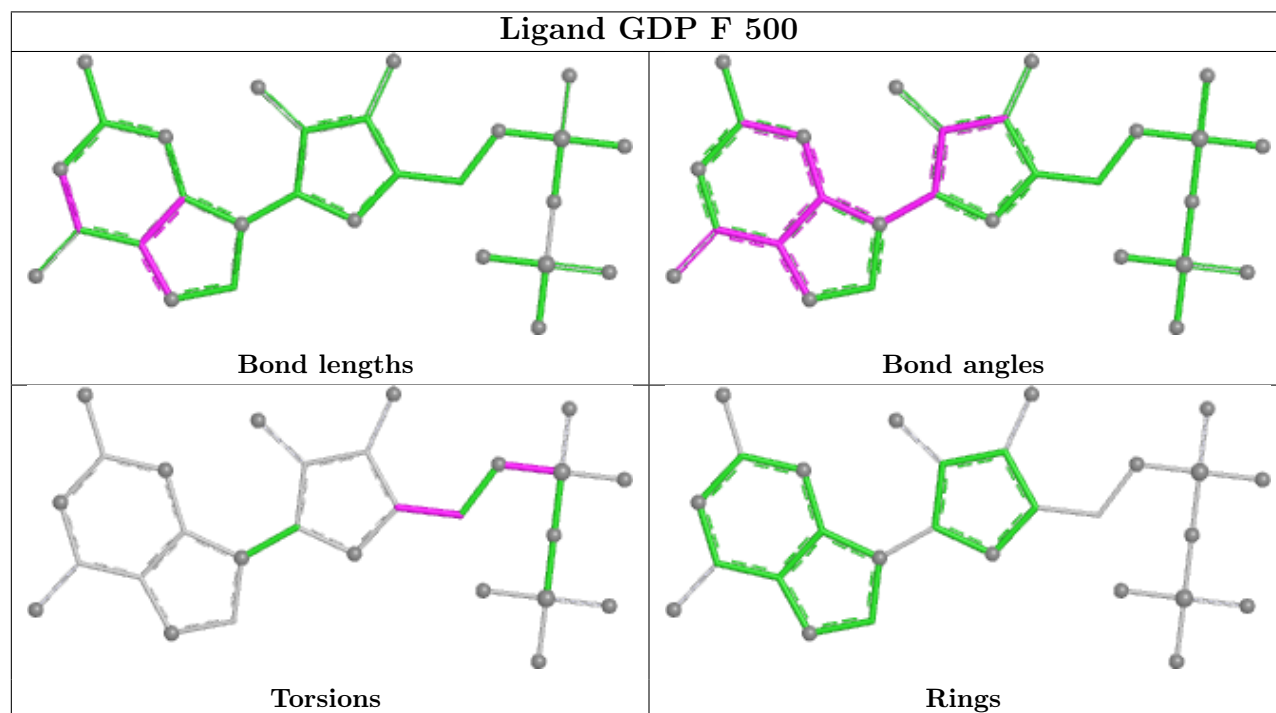
Mol	Chain	Res	Type	Atoms
10	F	500	GDP	C3'-C4'-C5'-O5'
11	G	401	GNP	PA-O3A-PB-O1B

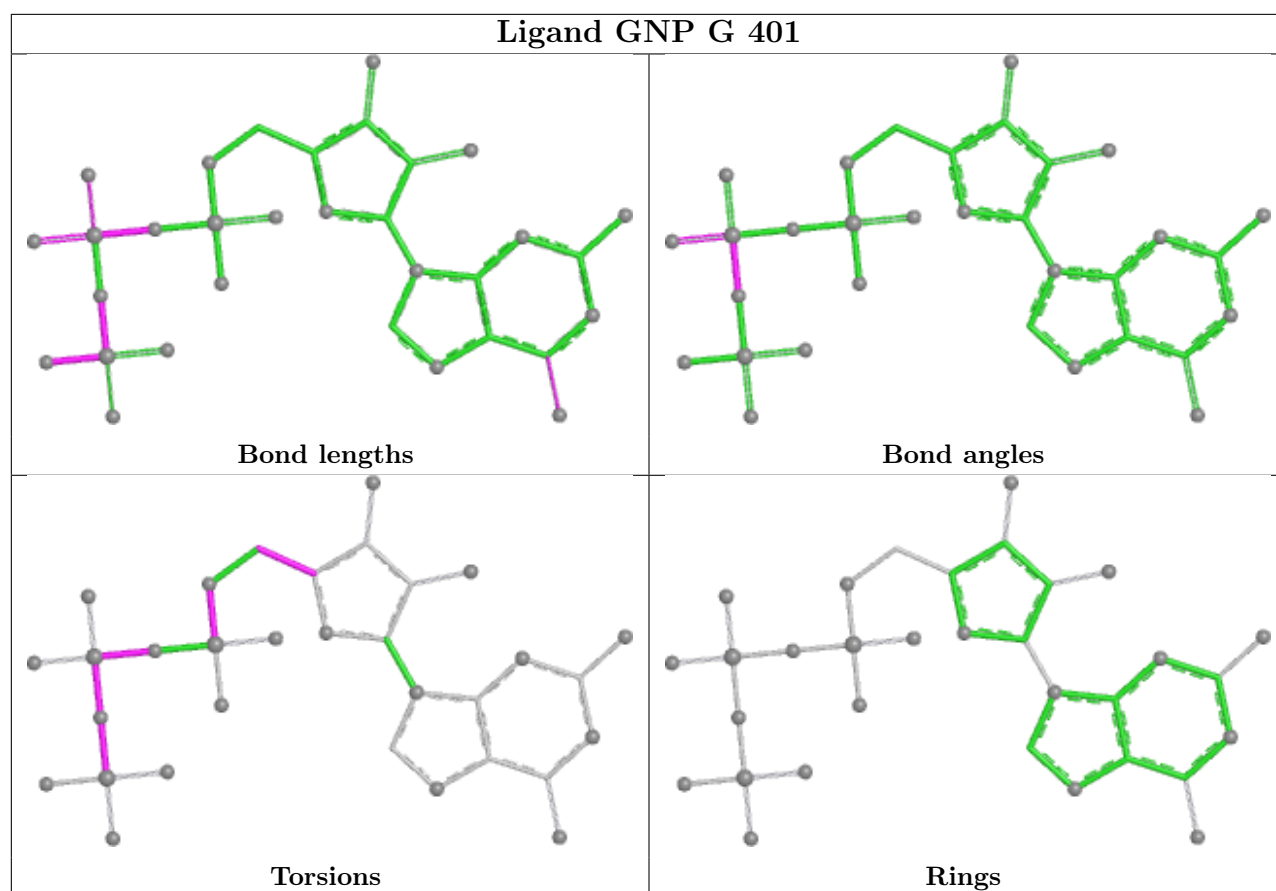
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	G	401	GNP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

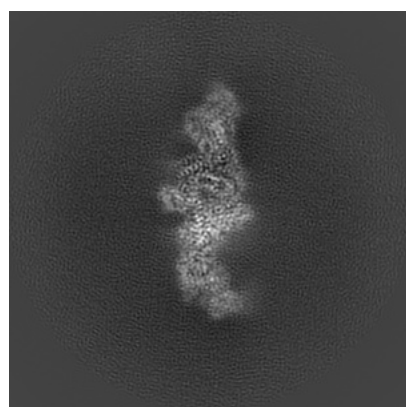
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20814. These allow visual inspection of the internal detail of the map and identification of artifacts.

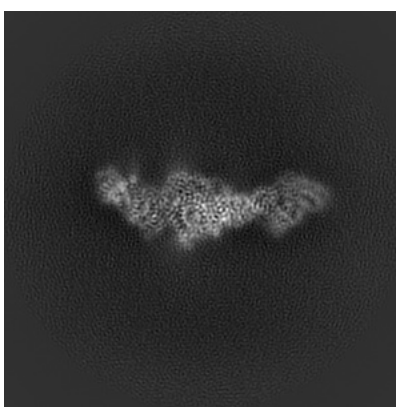
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

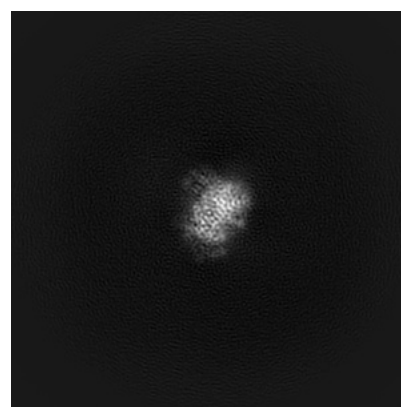
6.1.1 Primary map



X



Y

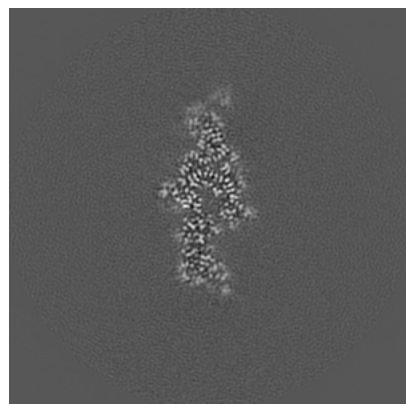


Z

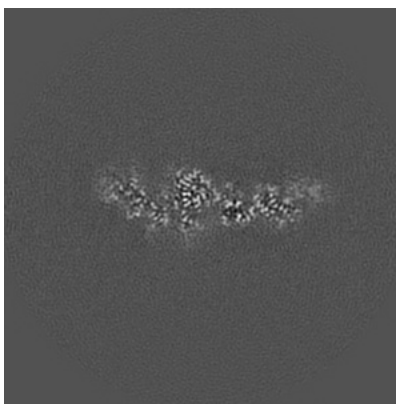
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

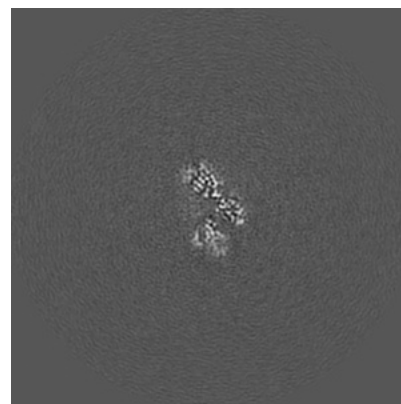
6.2.1 Primary map



X Index: 180



Y Index: 180

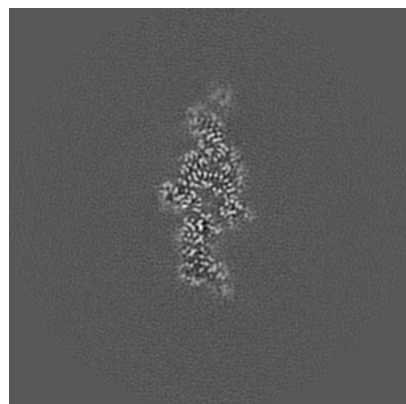


Z Index: 180

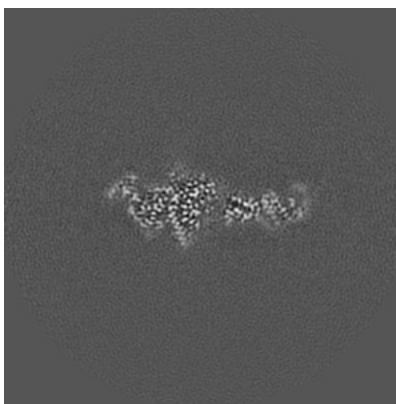
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

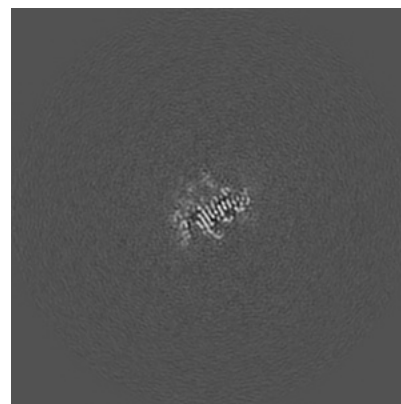
6.3.1 Primary map



X Index: 181



Y Index: 173

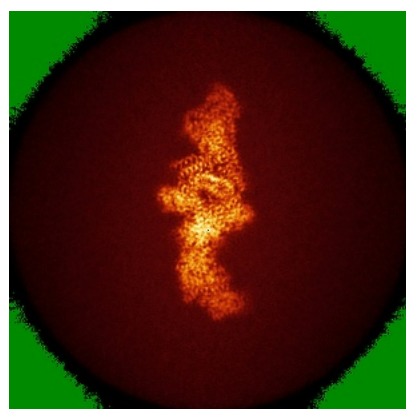


Z Index: 162

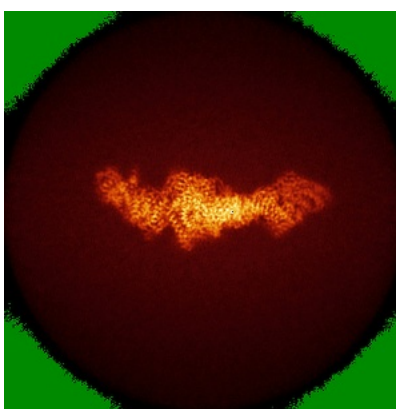
The images above show the largest variance slices of the map in three orthogonal directions.

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

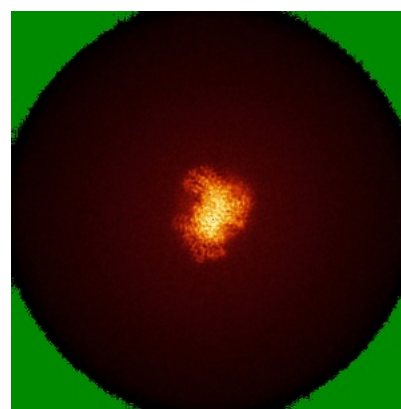
6.4.1 Primary map



X



Y

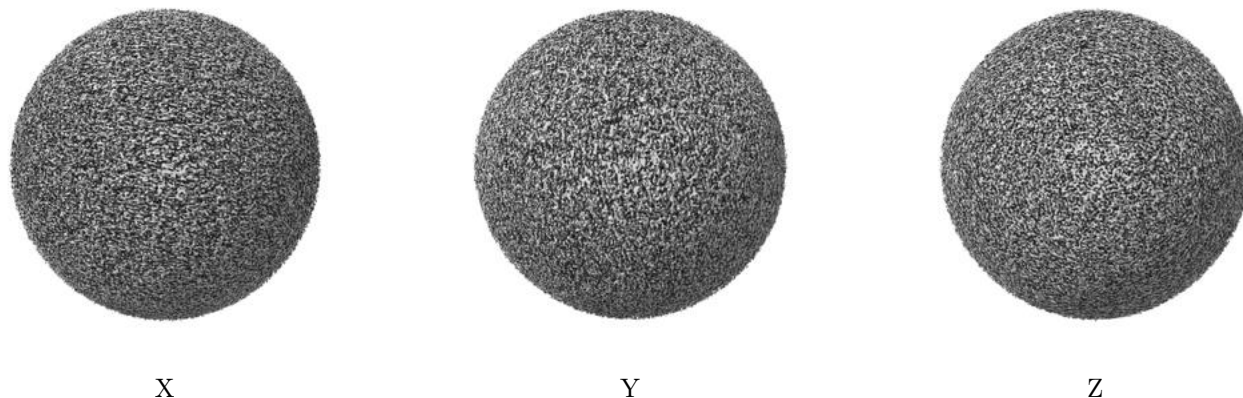


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.002. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

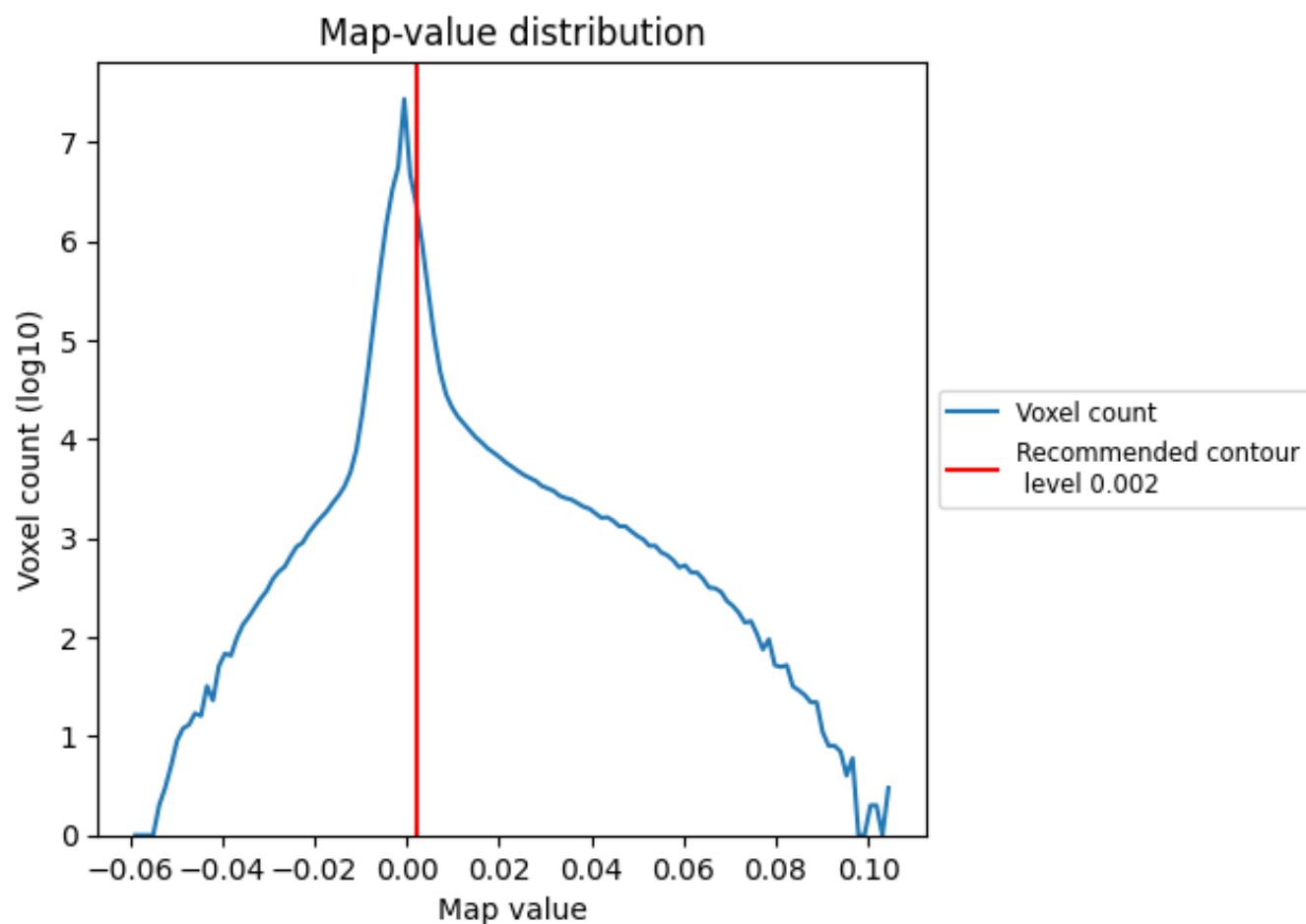
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

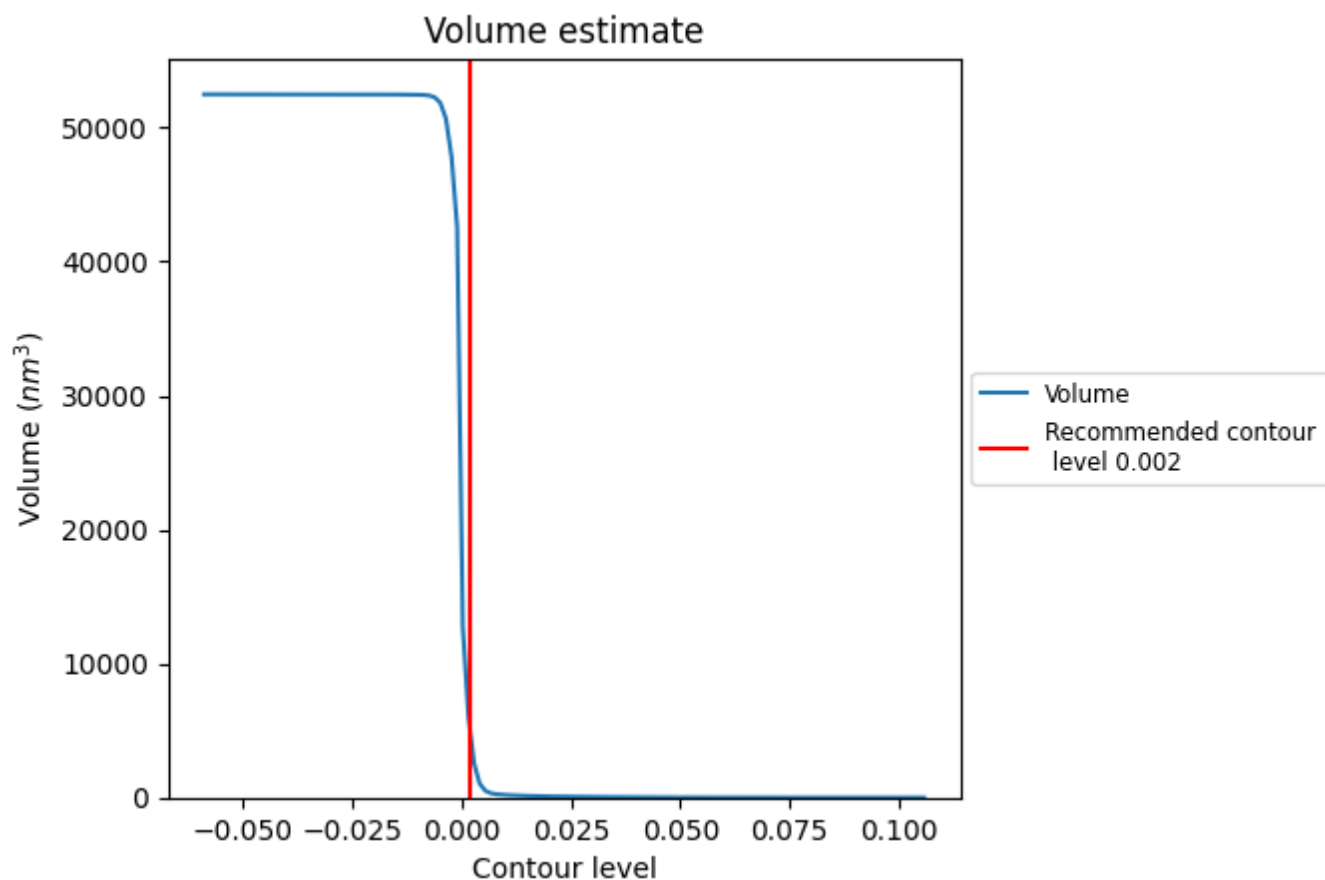
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

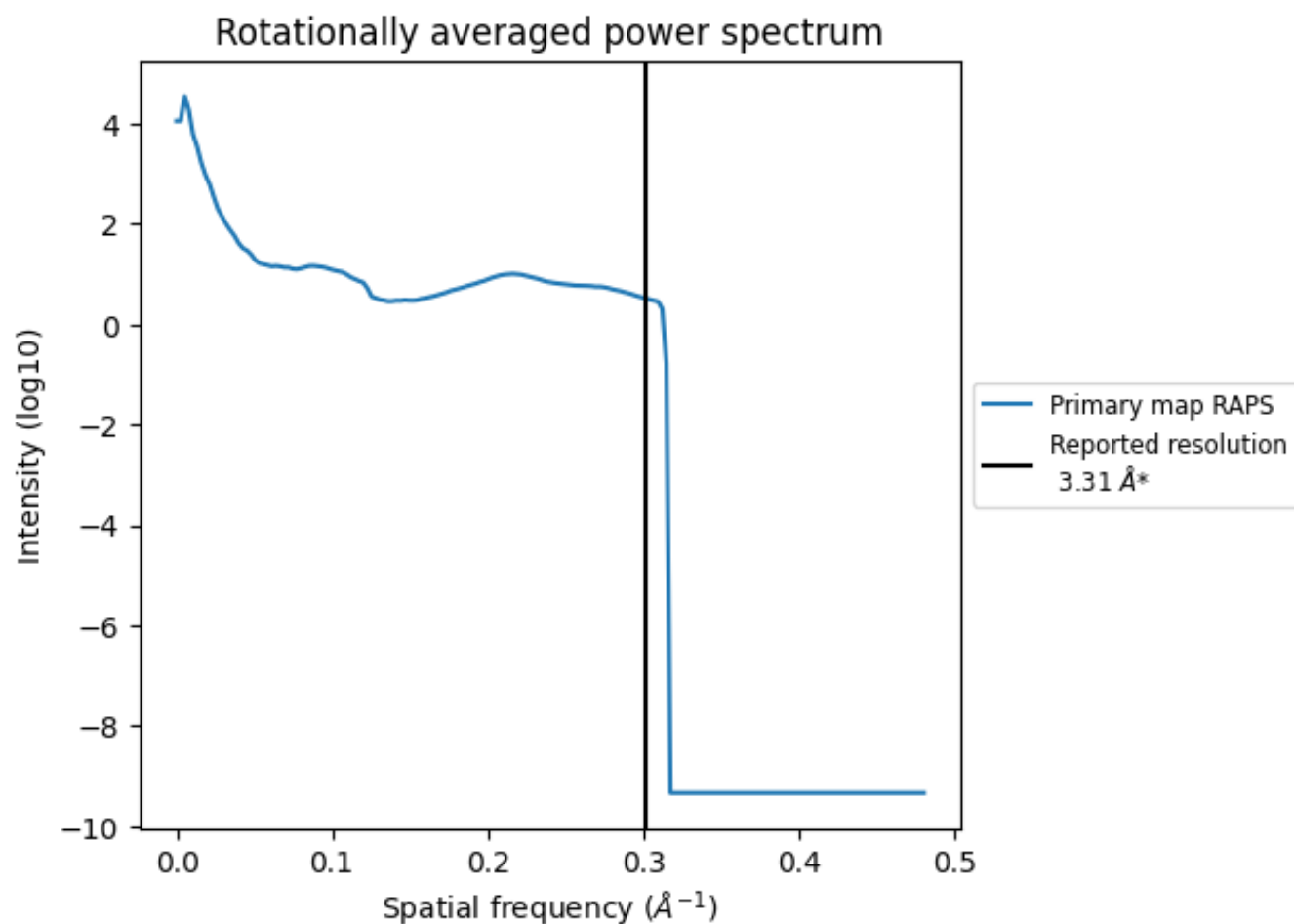
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4938 nm^3 ; this corresponds to an approximate mass of 4460 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 $0.302 \text{ \AA}^{-1}$

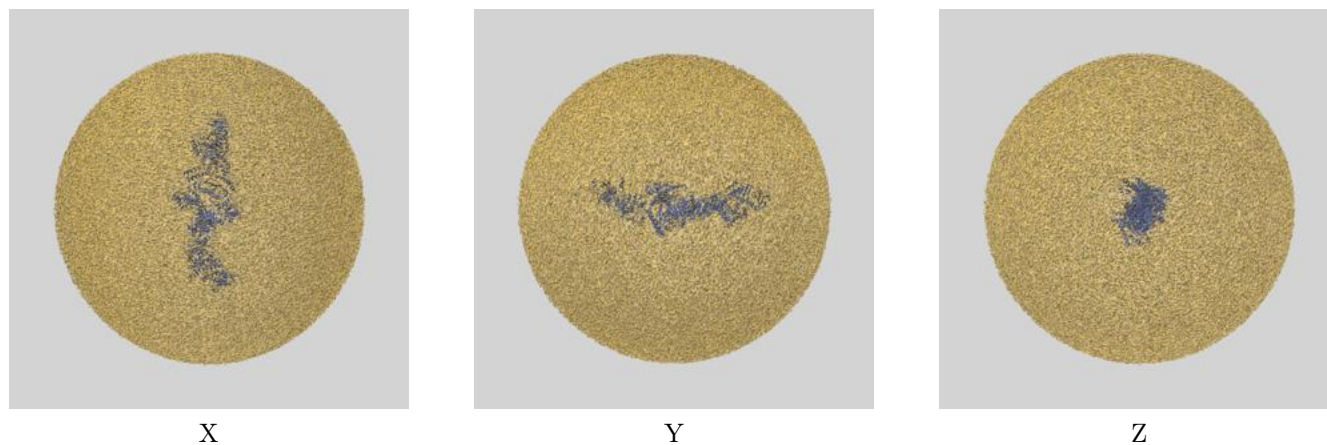
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

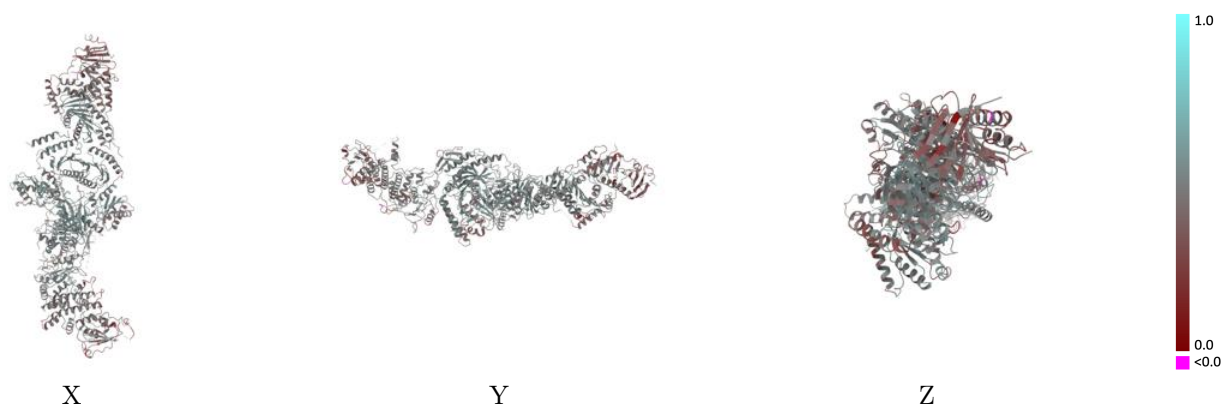
This section contains information regarding the fit between EMDB map EMD-20814 and PDB model 6ULG. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



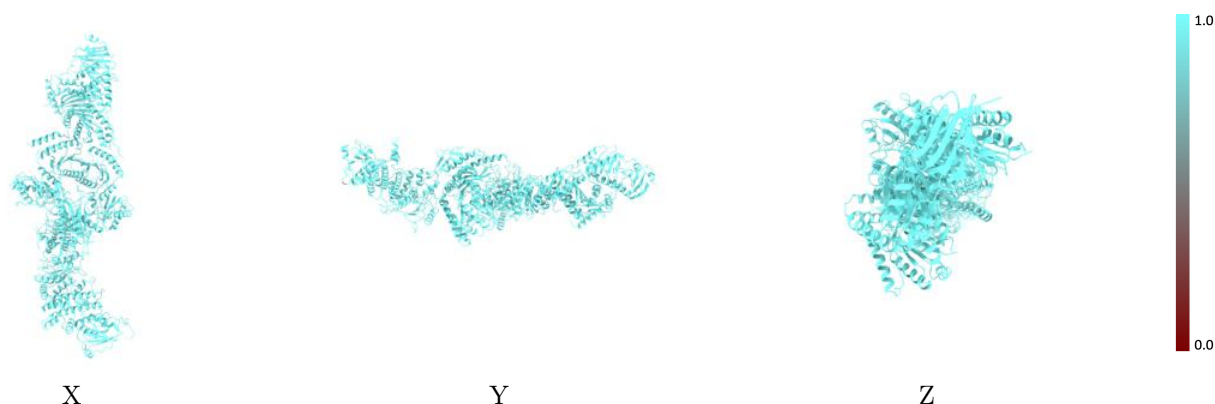
The images above show the 3D surface view of the map at the recommended contour level 0.002 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



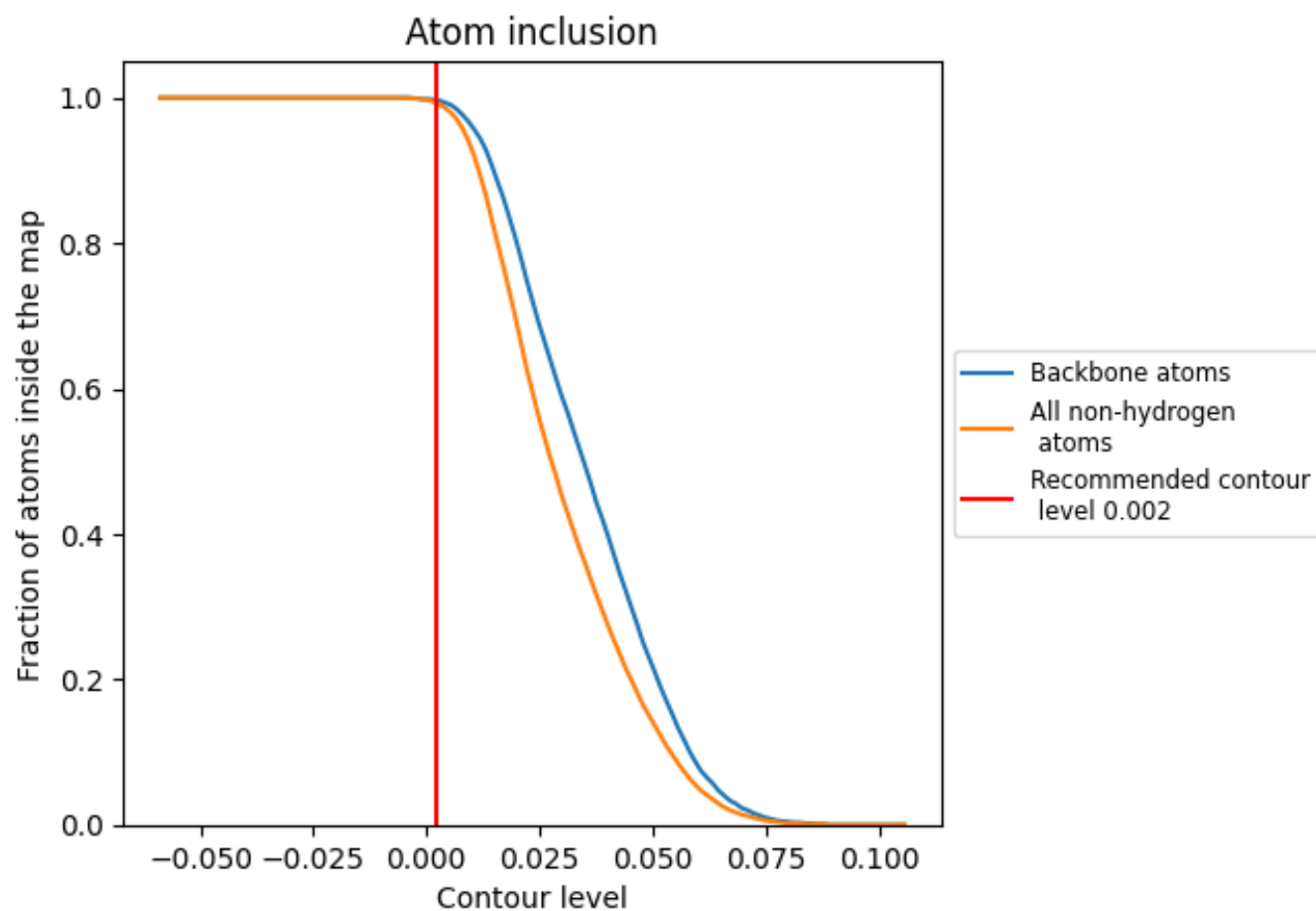
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.002).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% 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 (0.002) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9930	0.4670
A	0.9960	0.4760
B	0.9950	0.4880
C	0.9970	0.4410
D	0.9950	0.3670
E	1.0000	0.4100
F	0.9940	0.4860
G	0.9940	0.5010
L	0.9940	0.4630
N	0.9890	0.4630

1.0

0.0

<0.0