



Full wwPDB EM Validation Report ⓘ

Apr 6, 2026 – 12:52 AM UTC

PDB ID : 9UNL / pdb_00009unl
EMDB ID : EMD-64355
Title : Cryo-EM structure of the human prohibitin complex
Authors : Hong, S.X.; Guan, Z.Y.; Wang, Q.; Yin, P.
Deposited on : 2025-04-23
Resolution : 2.80 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:

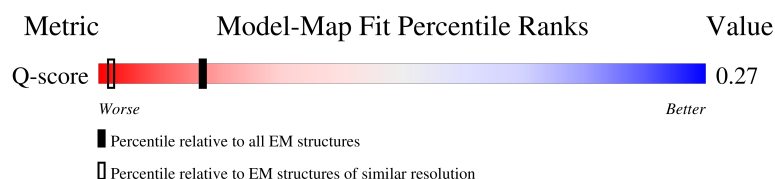
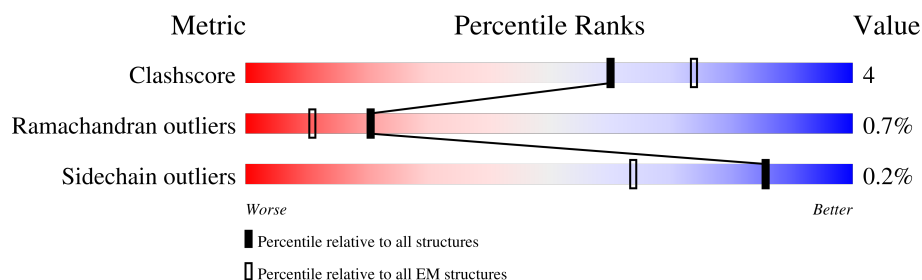
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.80 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	11806 (2.30 - 3.30)

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	296	
1	C	296	
1	E	296	
1	G	296	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	I	296	
1	K	296	
1	M	296	
1	O	296	
1	Q	296	
1	S	296	
1	U	296	
2	B	299	
2	D	299	
2	F	299	
2	H	299	
2	J	299	
2	L	299	
2	N	299	
2	P	299	
2	R	299	
2	T	299	
2	V	299	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 28626 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 Prohibitin 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	250	Total	C	N	O	S	0	0
			1948	1229	345	373	1		
1	C	249	Total	C	N	O	S	0	0
			1940	1223	344	372	1		
1	A	249	Total	C	N	O	S	0	0
			1940	1223	344	372	1		
1	U	85	Total	C	N	O		0	0
			643	398	116	129			
1	S	91	Total	C	N	O		0	0
			691	429	122	140			
1	Q	81	Total	C	N	O		0	0
			613	379	110	124			
1	O	91	Total	C	N	O		0	0
			691	429	122	140			
1	M	75	Total	C	N	O		0	0
			567	353	102	112			
1	K	76	Total	C	N	O		0	0
			575	359	103	113			
1	I	250	Total	C	N	O	S	0	0
			1948	1229	345	373	1		
1	G	250	Total	C	N	O	S	0	0
			1948	1229	345	373	1		

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	273	LEU	-	expression tag	UNP P35232
E	274	GLU	-	expression tag	UNP P35232
E	275	ASP	-	expression tag	UNP P35232
E	276	TYR	-	expression tag	UNP P35232
E	277	LYS	-	expression tag	UNP P35232
E	278	ASP	-	expression tag	UNP P35232
E	279	HIS	-	expression tag	UNP P35232
E	280	ASP	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	281	GLY	-	expression tag	UNP P35232
E	282	ASP	-	expression tag	UNP P35232
E	283	TYR	-	expression tag	UNP P35232
E	284	LYS	-	expression tag	UNP P35232
E	285	ASP	-	expression tag	UNP P35232
E	286	HIS	-	expression tag	UNP P35232
E	287	ASP	-	expression tag	UNP P35232
E	288	ILE	-	expression tag	UNP P35232
E	289	ASP	-	expression tag	UNP P35232
E	290	TYR	-	expression tag	UNP P35232
E	291	LYS	-	expression tag	UNP P35232
E	292	ASP	-	expression tag	UNP P35232
E	293	ASP	-	expression tag	UNP P35232
E	294	ASP	-	expression tag	UNP P35232
E	295	ASP	-	expression tag	UNP P35232
E	296	LYS	-	expression tag	UNP P35232
C	273	LEU	-	expression tag	UNP P35232
C	274	GLU	-	expression tag	UNP P35232
C	275	ASP	-	expression tag	UNP P35232
C	276	TYR	-	expression tag	UNP P35232
C	277	LYS	-	expression tag	UNP P35232
C	278	ASP	-	expression tag	UNP P35232
C	279	HIS	-	expression tag	UNP P35232
C	280	ASP	-	expression tag	UNP P35232
C	281	GLY	-	expression tag	UNP P35232
C	282	ASP	-	expression tag	UNP P35232
C	283	TYR	-	expression tag	UNP P35232
C	284	LYS	-	expression tag	UNP P35232
C	285	ASP	-	expression tag	UNP P35232
C	286	HIS	-	expression tag	UNP P35232
C	287	ASP	-	expression tag	UNP P35232
C	288	ILE	-	expression tag	UNP P35232
C	289	ASP	-	expression tag	UNP P35232
C	290	TYR	-	expression tag	UNP P35232
C	291	LYS	-	expression tag	UNP P35232
C	292	ASP	-	expression tag	UNP P35232
C	293	ASP	-	expression tag	UNP P35232
C	294	ASP	-	expression tag	UNP P35232
C	295	ASP	-	expression tag	UNP P35232
C	296	LYS	-	expression tag	UNP P35232
A	273	LEU	-	expression tag	UNP P35232
A	274	GLU	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	ASP	-	expression tag	UNP P35232
A	276	TYR	-	expression tag	UNP P35232
A	277	LYS	-	expression tag	UNP P35232
A	278	ASP	-	expression tag	UNP P35232
A	279	HIS	-	expression tag	UNP P35232
A	280	ASP	-	expression tag	UNP P35232
A	281	GLY	-	expression tag	UNP P35232
A	282	ASP	-	expression tag	UNP P35232
A	283	TYR	-	expression tag	UNP P35232
A	284	LYS	-	expression tag	UNP P35232
A	285	ASP	-	expression tag	UNP P35232
A	286	HIS	-	expression tag	UNP P35232
A	287	ASP	-	expression tag	UNP P35232
A	288	ILE	-	expression tag	UNP P35232
A	289	ASP	-	expression tag	UNP P35232
A	290	TYR	-	expression tag	UNP P35232
A	291	LYS	-	expression tag	UNP P35232
A	292	ASP	-	expression tag	UNP P35232
A	293	ASP	-	expression tag	UNP P35232
A	294	ASP	-	expression tag	UNP P35232
A	295	ASP	-	expression tag	UNP P35232
A	296	LYS	-	expression tag	UNP P35232
U	273	LEU	-	expression tag	UNP P35232
U	274	GLU	-	expression tag	UNP P35232
U	275	ASP	-	expression tag	UNP P35232
U	276	TYR	-	expression tag	UNP P35232
U	277	LYS	-	expression tag	UNP P35232
U	278	ASP	-	expression tag	UNP P35232
U	279	HIS	-	expression tag	UNP P35232
U	280	ASP	-	expression tag	UNP P35232
U	281	GLY	-	expression tag	UNP P35232
U	282	ASP	-	expression tag	UNP P35232
U	283	TYR	-	expression tag	UNP P35232
U	284	LYS	-	expression tag	UNP P35232
U	285	ASP	-	expression tag	UNP P35232
U	286	HIS	-	expression tag	UNP P35232
U	287	ASP	-	expression tag	UNP P35232
U	288	ILE	-	expression tag	UNP P35232
U	289	ASP	-	expression tag	UNP P35232
U	290	TYR	-	expression tag	UNP P35232
U	291	LYS	-	expression tag	UNP P35232
U	292	ASP	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
U	293	ASP	-	expression tag	UNP P35232
U	294	ASP	-	expression tag	UNP P35232
U	295	ASP	-	expression tag	UNP P35232
U	296	LYS	-	expression tag	UNP P35232
S	273	LEU	-	expression tag	UNP P35232
S	274	GLU	-	expression tag	UNP P35232
S	275	ASP	-	expression tag	UNP P35232
S	276	TYR	-	expression tag	UNP P35232
S	277	LYS	-	expression tag	UNP P35232
S	278	ASP	-	expression tag	UNP P35232
S	279	HIS	-	expression tag	UNP P35232
S	280	ASP	-	expression tag	UNP P35232
S	281	GLY	-	expression tag	UNP P35232
S	282	ASP	-	expression tag	UNP P35232
S	283	TYR	-	expression tag	UNP P35232
S	284	LYS	-	expression tag	UNP P35232
S	285	ASP	-	expression tag	UNP P35232
S	286	HIS	-	expression tag	UNP P35232
S	287	ASP	-	expression tag	UNP P35232
S	288	ILE	-	expression tag	UNP P35232
S	289	ASP	-	expression tag	UNP P35232
S	290	TYR	-	expression tag	UNP P35232
S	291	LYS	-	expression tag	UNP P35232
S	292	ASP	-	expression tag	UNP P35232
S	293	ASP	-	expression tag	UNP P35232
S	294	ASP	-	expression tag	UNP P35232
S	295	ASP	-	expression tag	UNP P35232
S	296	LYS	-	expression tag	UNP P35232
Q	273	LEU	-	expression tag	UNP P35232
Q	274	GLU	-	expression tag	UNP P35232
Q	275	ASP	-	expression tag	UNP P35232
Q	276	TYR	-	expression tag	UNP P35232
Q	277	LYS	-	expression tag	UNP P35232
Q	278	ASP	-	expression tag	UNP P35232
Q	279	HIS	-	expression tag	UNP P35232
Q	280	ASP	-	expression tag	UNP P35232
Q	281	GLY	-	expression tag	UNP P35232
Q	282	ASP	-	expression tag	UNP P35232
Q	283	TYR	-	expression tag	UNP P35232
Q	284	LYS	-	expression tag	UNP P35232
Q	285	ASP	-	expression tag	UNP P35232
Q	286	HIS	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
Q	287	ASP	-	expression tag	UNP P35232
Q	288	ILE	-	expression tag	UNP P35232
Q	289	ASP	-	expression tag	UNP P35232
Q	290	TYR	-	expression tag	UNP P35232
Q	291	LYS	-	expression tag	UNP P35232
Q	292	ASP	-	expression tag	UNP P35232
Q	293	ASP	-	expression tag	UNP P35232
Q	294	ASP	-	expression tag	UNP P35232
Q	295	ASP	-	expression tag	UNP P35232
Q	296	LYS	-	expression tag	UNP P35232
O	273	LEU	-	expression tag	UNP P35232
O	274	GLU	-	expression tag	UNP P35232
O	275	ASP	-	expression tag	UNP P35232
O	276	TYR	-	expression tag	UNP P35232
O	277	LYS	-	expression tag	UNP P35232
O	278	ASP	-	expression tag	UNP P35232
O	279	HIS	-	expression tag	UNP P35232
O	280	ASP	-	expression tag	UNP P35232
O	281	GLY	-	expression tag	UNP P35232
O	282	ASP	-	expression tag	UNP P35232
O	283	TYR	-	expression tag	UNP P35232
O	284	LYS	-	expression tag	UNP P35232
O	285	ASP	-	expression tag	UNP P35232
O	286	HIS	-	expression tag	UNP P35232
O	287	ASP	-	expression tag	UNP P35232
O	288	ILE	-	expression tag	UNP P35232
O	289	ASP	-	expression tag	UNP P35232
O	290	TYR	-	expression tag	UNP P35232
O	291	LYS	-	expression tag	UNP P35232
O	292	ASP	-	expression tag	UNP P35232
O	293	ASP	-	expression tag	UNP P35232
O	294	ASP	-	expression tag	UNP P35232
O	295	ASP	-	expression tag	UNP P35232
O	296	LYS	-	expression tag	UNP P35232
M	273	LEU	-	expression tag	UNP P35232
M	274	GLU	-	expression tag	UNP P35232
M	275	ASP	-	expression tag	UNP P35232
M	276	TYR	-	expression tag	UNP P35232
M	277	LYS	-	expression tag	UNP P35232
M	278	ASP	-	expression tag	UNP P35232
M	279	HIS	-	expression tag	UNP P35232
M	280	ASP	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
M	281	GLY	-	expression tag	UNP P35232
M	282	ASP	-	expression tag	UNP P35232
M	283	TYR	-	expression tag	UNP P35232
M	284	LYS	-	expression tag	UNP P35232
M	285	ASP	-	expression tag	UNP P35232
M	286	HIS	-	expression tag	UNP P35232
M	287	ASP	-	expression tag	UNP P35232
M	288	ILE	-	expression tag	UNP P35232
M	289	ASP	-	expression tag	UNP P35232
M	290	TYR	-	expression tag	UNP P35232
M	291	LYS	-	expression tag	UNP P35232
M	292	ASP	-	expression tag	UNP P35232
M	293	ASP	-	expression tag	UNP P35232
M	294	ASP	-	expression tag	UNP P35232
M	295	ASP	-	expression tag	UNP P35232
M	296	LYS	-	expression tag	UNP P35232
K	273	LEU	-	expression tag	UNP P35232
K	274	GLU	-	expression tag	UNP P35232
K	275	ASP	-	expression tag	UNP P35232
K	276	TYR	-	expression tag	UNP P35232
K	277	LYS	-	expression tag	UNP P35232
K	278	ASP	-	expression tag	UNP P35232
K	279	HIS	-	expression tag	UNP P35232
K	280	ASP	-	expression tag	UNP P35232
K	281	GLY	-	expression tag	UNP P35232
K	282	ASP	-	expression tag	UNP P35232
K	283	TYR	-	expression tag	UNP P35232
K	284	LYS	-	expression tag	UNP P35232
K	285	ASP	-	expression tag	UNP P35232
K	286	HIS	-	expression tag	UNP P35232
K	287	ASP	-	expression tag	UNP P35232
K	288	ILE	-	expression tag	UNP P35232
K	289	ASP	-	expression tag	UNP P35232
K	290	TYR	-	expression tag	UNP P35232
K	291	LYS	-	expression tag	UNP P35232
K	292	ASP	-	expression tag	UNP P35232
K	293	ASP	-	expression tag	UNP P35232
K	294	ASP	-	expression tag	UNP P35232
K	295	ASP	-	expression tag	UNP P35232
K	296	LYS	-	expression tag	UNP P35232
I	273	LEU	-	expression tag	UNP P35232
I	274	GLU	-	expression tag	UNP P35232

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	275	ASP	-	expression tag	UNP P35232
I	276	TYR	-	expression tag	UNP P35232
I	277	LYS	-	expression tag	UNP P35232
I	278	ASP	-	expression tag	UNP P35232
I	279	HIS	-	expression tag	UNP P35232
I	280	ASP	-	expression tag	UNP P35232
I	281	GLY	-	expression tag	UNP P35232
I	282	ASP	-	expression tag	UNP P35232
I	283	TYR	-	expression tag	UNP P35232
I	284	LYS	-	expression tag	UNP P35232
I	285	ASP	-	expression tag	UNP P35232
I	286	HIS	-	expression tag	UNP P35232
I	287	ASP	-	expression tag	UNP P35232
I	288	ILE	-	expression tag	UNP P35232
I	289	ASP	-	expression tag	UNP P35232
I	290	TYR	-	expression tag	UNP P35232
I	291	LYS	-	expression tag	UNP P35232
I	292	ASP	-	expression tag	UNP P35232
I	293	ASP	-	expression tag	UNP P35232
I	294	ASP	-	expression tag	UNP P35232
I	295	ASP	-	expression tag	UNP P35232
I	296	LYS	-	expression tag	UNP P35232
G	273	LEU	-	expression tag	UNP P35232
G	274	GLU	-	expression tag	UNP P35232
G	275	ASP	-	expression tag	UNP P35232
G	276	TYR	-	expression tag	UNP P35232
G	277	LYS	-	expression tag	UNP P35232
G	278	ASP	-	expression tag	UNP P35232
G	279	HIS	-	expression tag	UNP P35232
G	280	ASP	-	expression tag	UNP P35232
G	281	GLY	-	expression tag	UNP P35232
G	282	ASP	-	expression tag	UNP P35232
G	283	TYR	-	expression tag	UNP P35232
G	284	LYS	-	expression tag	UNP P35232
G	285	ASP	-	expression tag	UNP P35232
G	286	HIS	-	expression tag	UNP P35232
G	287	ASP	-	expression tag	UNP P35232
G	288	ILE	-	expression tag	UNP P35232
G	289	ASP	-	expression tag	UNP P35232
G	290	TYR	-	expression tag	UNP P35232
G	291	LYS	-	expression tag	UNP P35232
G	292	ASP	-	expression tag	UNP P35232

Continued on next page...

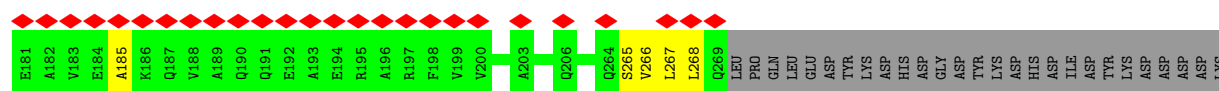
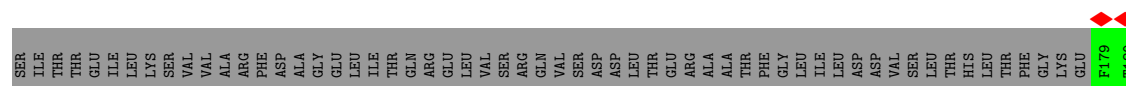
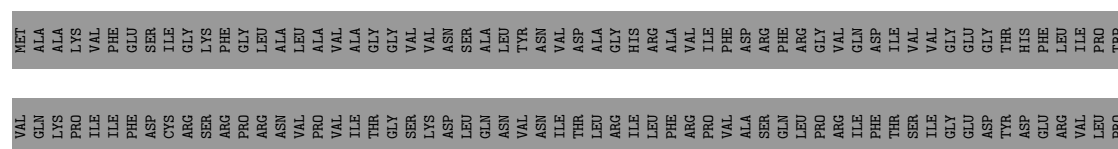
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	293	ASP	-	expression tag	UNP P35232
G	294	ASP	-	expression tag	UNP P35232
G	295	ASP	-	expression tag	UNP P35232
G	296	LYS	-	expression tag	UNP P35232

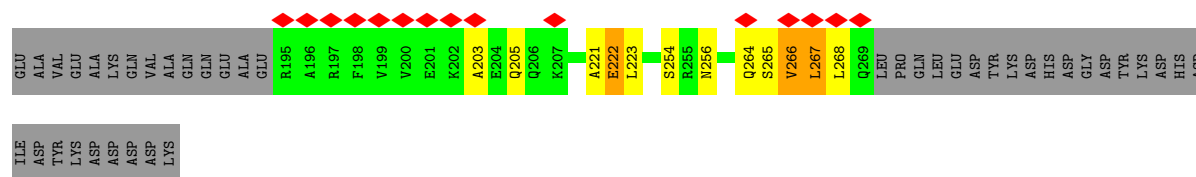
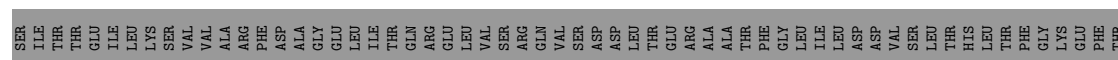
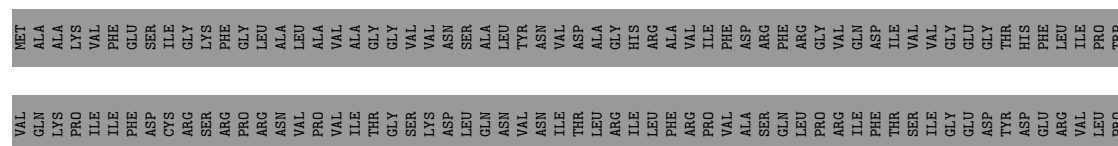
- Molecule 2 is a protein called Prohibitin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	262	Total	C	N	O	S	0	0
			2075	1307	376	389	3		
2	D	263	Total	C	N	O	S	0	0
			2084	1313	378	390	3		
2	B	262	Total	C	N	O	S	0	0
			2075	1307	376	389	3		
2	V	105	Total	C	N	O	S	0	0
			823	508	152	162	1		
2	T	105	Total	C	N	O	S	0	0
			823	508	152	162	1		
2	R	97	Total	C	N	O	S	0	0
			758	468	141	148	1		
2	P	105	Total	C	N	O	S	0	0
			823	508	152	162	1		
2	N	97	Total	C	N	O	S	0	0
			758	468	141	148	1		
2	L	96	Total	C	N	O	S	0	0
			753	465	140	147	1		
2	J	262	Total	C	N	O	S	0	0
			2075	1307	376	389	3		
2	H	262	Total	C	N	O	S	0	0
			2075	1307	376	389	3		

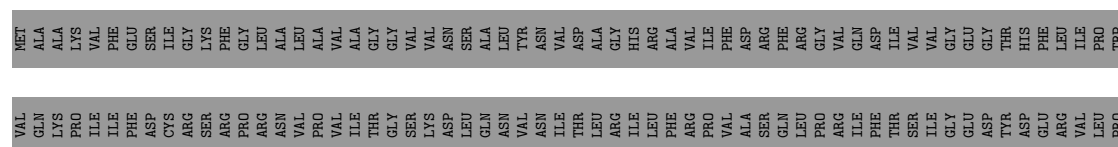
- Molecule 1: Prohibitin 1

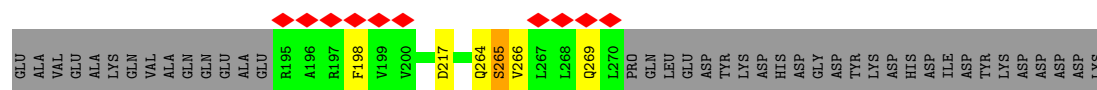


- Molecule 1: Prohibitin 1

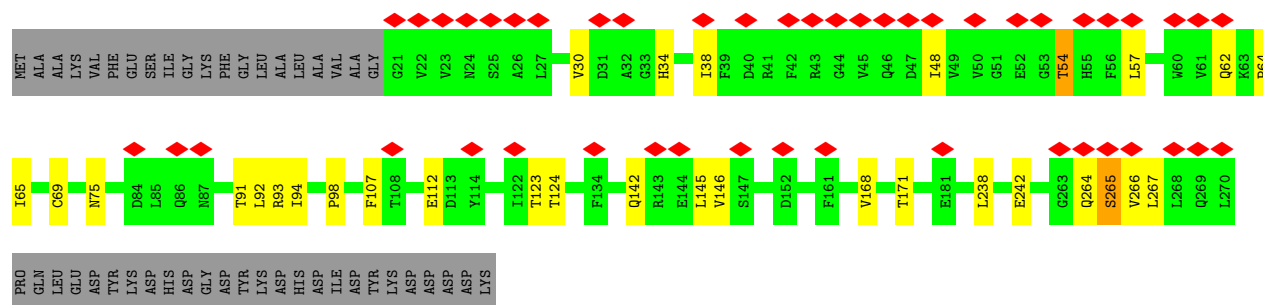


- Molecule 1: Prohibitin 1

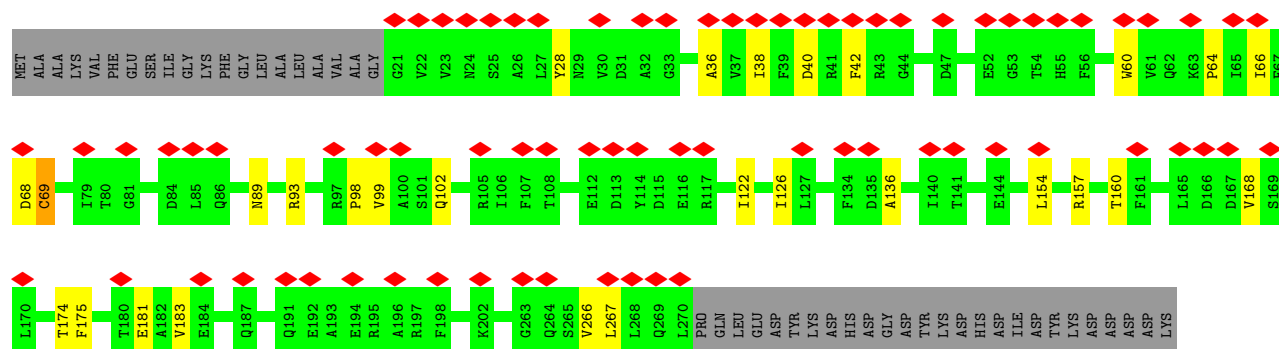
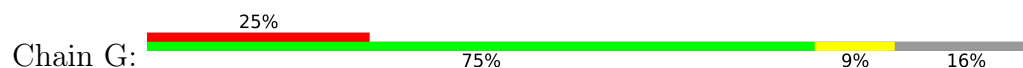




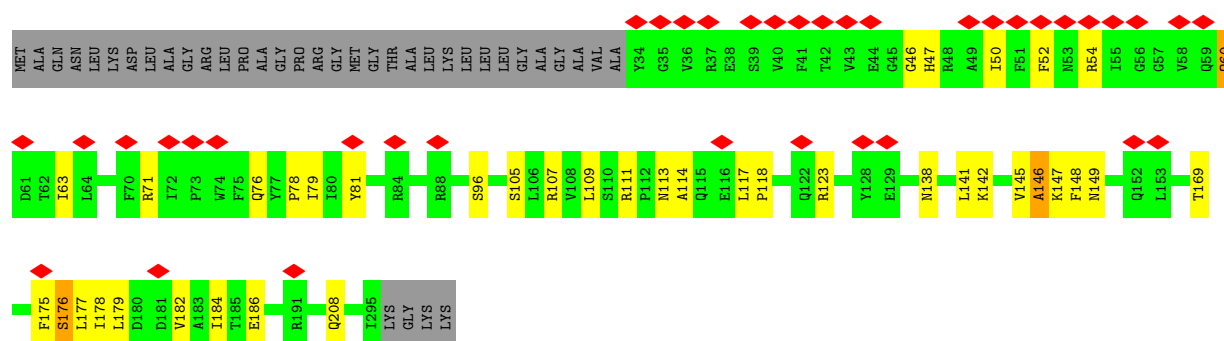
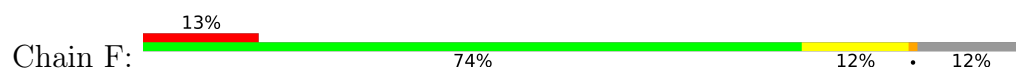
- Molecule 1: Prohibitin 1



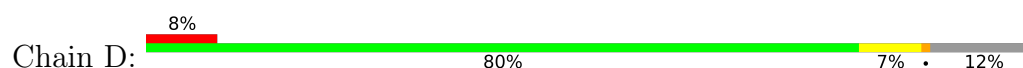
- Molecule 1: Prohibitin 1



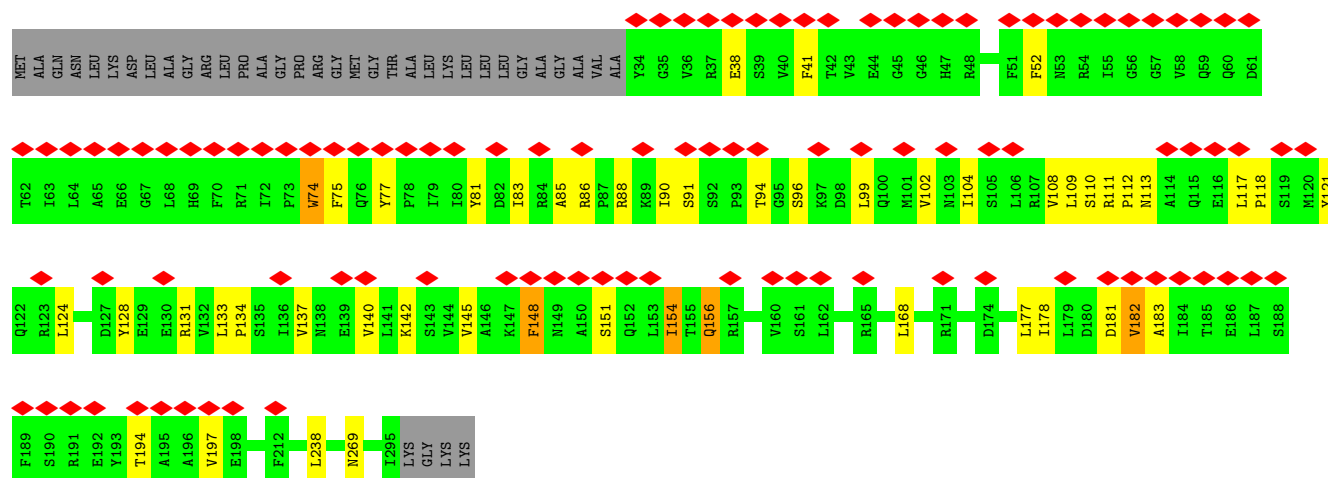
- Molecule 2: Prohibitin-2



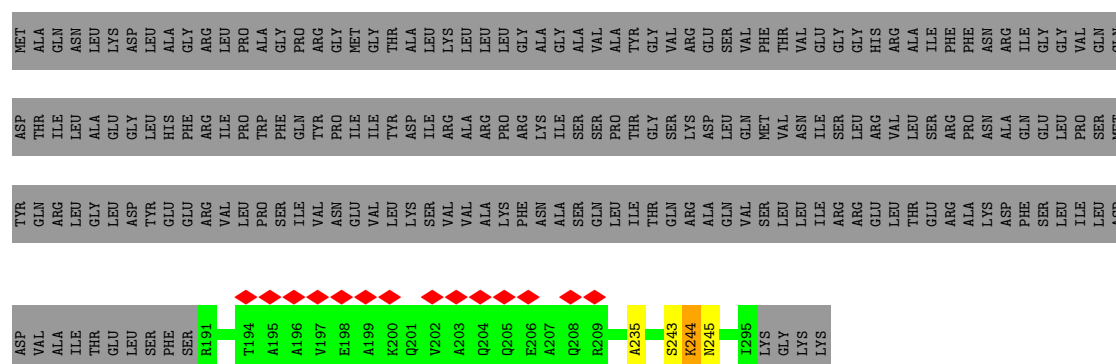
- Molecule 2: Prohibitin-2



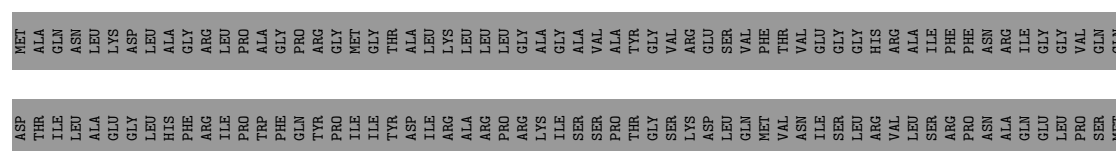
- Molecule 2: Prohibitin-2

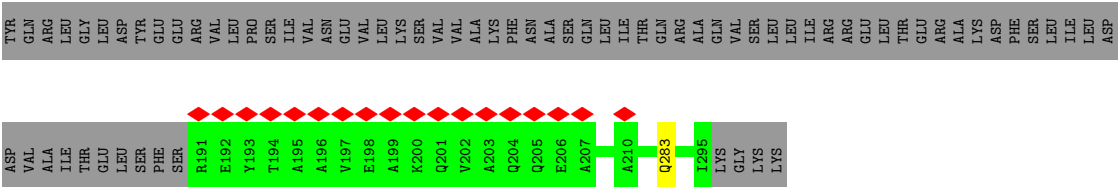


- Molecule 2: Prohibitin-2

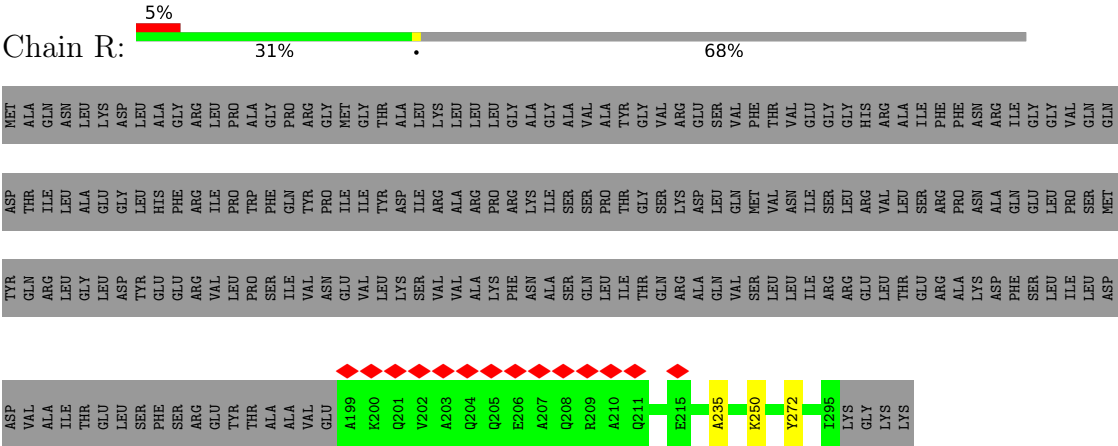


- Molecule 2: Prohibitin-2

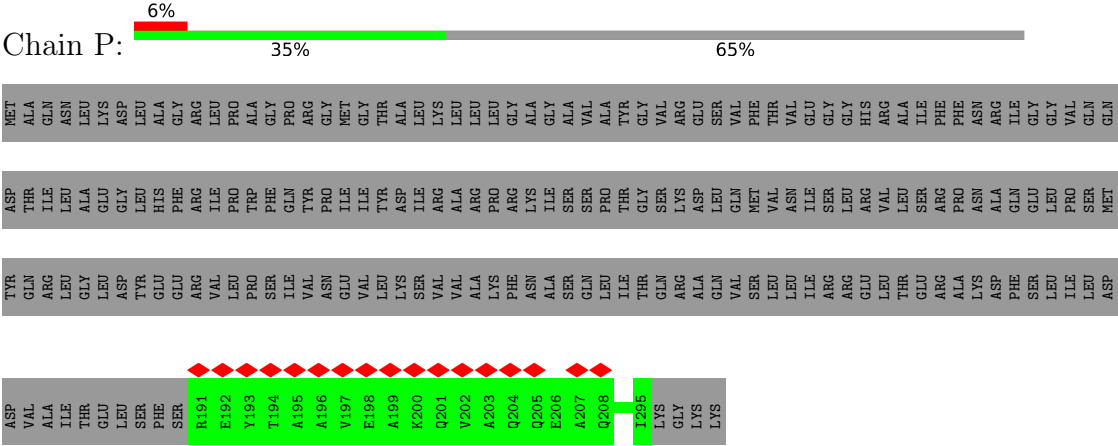




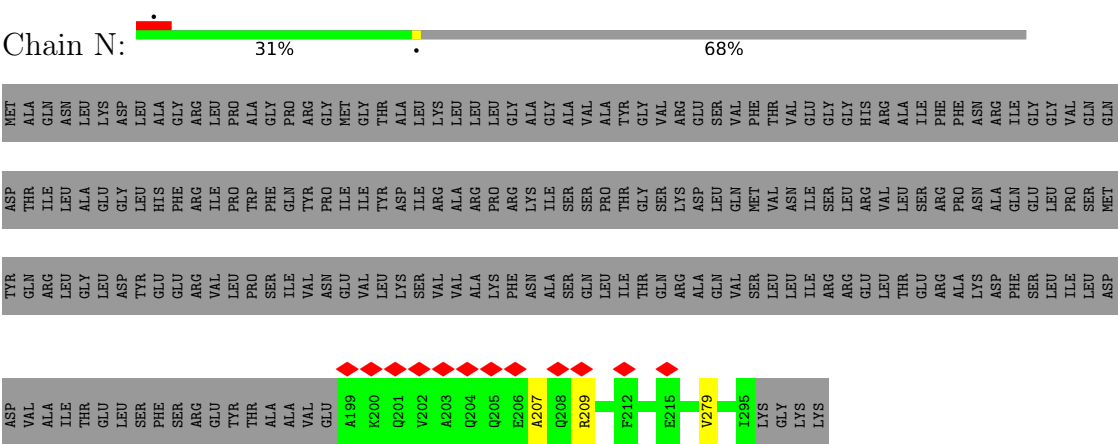
• Molecule 2: Prohibitin-2



• Molecule 2: Prohibitin-2



• Molecule 2: Prohibitin-2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	268512	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	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.694	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	419.84, 419.84, 419.84	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	Depositor

5 Model quality

5.1 Standard geometry

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	0.25	0/1967	0.61	4/2665 (0.2%)
1	C	0.27	0/1967	0.62	0/2665
1	E	0.26	0/1975	0.57	0/2676
1	G	0.25	0/1975	0.60	2/2676 (0.1%)
1	I	0.27	0/1975	0.58	0/2676
1	K	0.27	0/578	0.56	1/777 (0.1%)
1	M	0.27	0/570	0.62	0/766
1	O	0.24	0/695	0.46	0/935
1	Q	0.23	0/616	0.41	0/828
1	S	0.27	0/695	0.48	0/935
1	U	0.25	0/646	0.47	0/868
2	B	0.28	0/2103	0.68	4/2837 (0.1%)
2	D	0.29	0/2112	0.64	6/2848 (0.2%)
2	F	0.29	0/2103	0.62	5/2837 (0.2%)
2	H	0.25	0/2103	0.54	0/2837
2	J	0.30	0/2103	0.70	4/2837 (0.1%)
2	L	0.26	0/757	0.51	0/1013
2	N	0.24	0/762	0.42	0/1020
2	P	0.25	0/828	0.44	0/1110
2	R	0.26	0/762	0.48	0/1020
2	T	0.25	0/828	0.40	0/1110
2	V	0.25	0/828	0.45	0/1110
All	All	0.27	0/28948	0.58	26/39046 (0.1%)

There are no bond length outliers.

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	VAL	CA-C-N	8.01	136.12	121.70
1	A	78	VAL	C-N-CA	8.01	136.12	121.70
2	B	74	TRP	CA-C-N	7.77	135.69	121.70
2	B	74	TRP	C-N-CA	7.77	135.69	121.70
2	F	146	ALA	CA-C-N	6.89	134.09	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	146	ALA	C-N-CA	6.89	134.09	121.70
2	D	89	LYS	CA-C-N	6.84	134.01	121.70
2	D	89	LYS	C-N-CA	6.84	134.01	121.70
2	F	60	GLN	CA-C-N	6.64	135.22	121.94
2	F	60	GLN	C-N-CA	6.64	135.22	121.94
2	J	182	VAL	CA-C-N	6.27	132.99	121.70
2	J	182	VAL	C-N-CA	6.27	132.99	121.70
1	G	69	CYS	CA-C-N	5.83	132.19	121.70
1	G	69	CYS	C-N-CA	5.83	132.19	121.70
2	J	68	LEU	CA-C-N	5.76	132.55	121.54
2	J	68	LEU	C-N-CA	5.76	132.55	121.54
2	D	150	ALA	CA-C-N	5.50	131.60	121.70
2	D	150	ALA	C-N-CA	5.50	131.60	121.70
1	K	265	SER	N-CA-C	5.49	117.53	108.48
2	D	90	ILE	CA-C-N	5.48	131.57	121.70
2	D	90	ILE	C-N-CA	5.48	131.57	121.70
2	B	154	ILE	CA-C-N	5.22	131.51	121.54
2	B	154	ILE	C-N-CA	5.22	131.51	121.54
1	A	170	LEU	CA-C-N	5.10	130.88	121.70
1	A	170	LEU	C-N-CA	5.10	130.88	121.70
2	F	146	ALA	N-CA-C	5.02	117.61	109.83

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1940	0	1972	35	0
1	C	1940	0	1972	23	0
1	E	1948	0	1983	17	0
1	G	1948	0	1983	20	0
1	I	1948	0	1983	20	0
1	K	575	0	598	6	0
1	M	567	0	587	12	0
1	O	691	0	702	8	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	613	0	625	7	0
1	S	691	0	702	6	0
1	U	643	0	660	6	0
2	B	2075	0	2121	35	0
2	D	2084	0	2134	18	0
2	F	2075	0	2121	29	0
2	H	2075	0	2121	18	0
2	J	2075	0	2121	33	0
2	L	753	0	779	2	0
2	N	758	0	784	3	0
2	P	823	0	844	0	0
2	R	758	0	784	3	0
2	T	823	0	844	1	0
2	V	823	0	844	2	0
All	All	28626	0	29264	258	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 4.

All (258) 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:U:266:VAL:HB	1:S:267:LEU:HB2	1.52	0.92
2:B:96:SER:HB3	2:B:151:SER:H	1.39	0.86
2:H:105:SER:O	2:H:185:THR:HA	1.91	0.71
1:A:78:VAL:HB	1:A:79:ILE:HA	1.73	0.70
2:B:74:TRP:N	2:B:75:PHE:HB2	2.08	0.67
2:B:74:TRP:H	2:B:75:PHE:HB2	1.61	0.66
2:B:81:TYR:OH	2:B:118:PRO:O	2.15	0.64
2:B:90:ILE:HG13	2:B:137:VAL:HG11	1.79	0.63
2:J:182:VAL:HA	2:J:183:ALA:HB3	1.81	0.63
2:J:50:ILE:HG22	2:J:79:ILE:HB	1.82	0.62
1:A:39:PHE:HB3	1:A:63:LYS:HB3	1.82	0.62
1:A:32:ALA:H	2:B:77:TYR:HB3	1.63	0.62
1:A:39:PHE:HB2	1:A:65:ILE:HD11	1.82	0.62
1:C:38:ILE:HA	1:C:64:PRO:HB3	1.82	0.61
1:A:89:ASN:HB3	1:A:174:THR:HB	1.84	0.59
1:I:142:GLN:HB2	1:I:146:VAL:HG23	1.83	0.58
2:J:113:ASN:HB3	2:J:116:GLU:HB2	1.85	0.58
1:C:28:TYR:O	1:C:55:HIS:HB3	2.04	0.58
2:D:105:SER:H	2:D:186:GLU:HB2	1.69	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:54:THR:O	2:D:54:ARG:HB2	2.04	0.57
2:F:113:ASN:O	2:F:117:LEU:HG	2.05	0.57
1:A:90:ILE:HA	1:A:172:HIS:O	2.03	0.57
1:A:78:VAL:HB	1:A:79:ILE:CA	2.34	0.57
1:A:113:ASP:HB3	1:A:116:GLU:HG3	1.87	0.57
2:B:134:PRO:HA	2:B:137:VAL:HG12	1.87	0.56
1:O:267:LEU:H	1:M:266:VAL:HG12	1.70	0.56
1:I:91:THR:OG1	1:I:171:THR:OG1	2.24	0.56
2:J:38:GLU:HB2	2:J:73:PRO:HB3	1.89	0.55
2:F:50:ILE:O	2:F:78:PRO:HA	2.06	0.55
2:F:146:ALA:H	2:F:147:LYS:HB2	1.72	0.55
2:F:147:LYS:O	2:F:149:ASN:N	2.36	0.55
2:F:96:SER:HB2	2:F:148:PHE:HA	1.89	0.55
1:A:78:VAL:CB	1:A:79:ILE:HA	2.37	0.54
1:M:268:LEU:HB2	1:K:269:GLN:HA	1.89	0.54
1:C:28:TYR:HB2	1:C:57:LEU:HD23	1.88	0.54
2:D:90:ILE:HG13	2:D:134:PRO:HA	1.89	0.54
1:G:68:ASP:N	1:G:68:ASP:OD1	2.38	0.54
1:C:266:VAL:HG21	1:A:267:LEU:O	2.07	0.54
1:G:69:CYS:HB3	1:G:98:PRO:HD2	1.90	0.54
1:A:165:LEU:HD21	1:A:168:VAL:HG23	1.89	0.54
1:K:217:ASP:HB3	2:J:238:LEU:HD21	1.90	0.54
1:O:268:LEU:HD23	1:M:267:LEU:HG	1.89	0.53
2:F:179:LEU:HD23	2:F:179:LEU:H	1.73	0.53
2:B:128:TYR:HA	2:B:131:ARG:HB3	1.91	0.53
1:A:166:ASP:O	1:A:167:ASP:HB2	2.07	0.53
1:C:253:ARG:HD3	1:C:257:ILE:HB	1.91	0.53
2:B:83:ILE:HG23	2:B:112:PRO:HD2	1.91	0.53
1:C:253:ARG:HD2	2:D:269:ASN:HB3	1.91	0.52
1:M:203:ALA:HB1	2:L:226:VAL:HG11	1.90	0.52
1:M:265:SER:OG	1:K:266:VAL:N	2.35	0.52
2:J:140:VAL:O	2:J:144:VAL:HG23	2.09	0.52
1:A:32:ALA:HB1	2:B:52:PHE:O	2.09	0.52
2:J:167:GLU:O	2:J:168:LEU:HB3	2.10	0.52
2:B:124:LEU:HB3	2:B:128:TYR:HB3	1.92	0.52
1:M:254:SER:OG	1:M:256:ASN:OD1	2.27	0.52
1:O:266:VAL:HG13	1:M:267:LEU:HB2	1.93	0.51
1:E:107:PHE:CG	1:E:107:PHE:O	2.62	0.51
2:F:50:ILE:HB	2:F:79:ILE:HB	1.92	0.51
1:C:80:THR:O	1:C:87:ASN:HA	2.11	0.51
1:C:261:PRO:HG2	1:C:264:GLN:HG3	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:69:CYS:HA	1:I:98:PRO:HD2	1.92	0.51
1:C:25:SER:O	1:C:59:PRO:HA	2.10	0.51
1:A:183:VAL:O	1:A:186:LYS:HG2	2.11	0.51
2:F:141:LEU:O	2:F:145:VAL:HG22	2.10	0.51
2:J:104:ILE:HD11	2:J:145:VAL:HG23	1.92	0.51
2:F:52:PHE:O	2:F:76:GLN:HA	2.10	0.51
1:E:175:PHE:O	1:E:177:LYS:N	2.44	0.50
1:A:140:ILE:HG23	1:A:141:THR:HG23	1.92	0.50
2:J:107:ARG:HB3	2:J:184:ILE:HG13	1.93	0.50
1:G:99:VAL:HB	1:G:102:GLN:HB3	1.93	0.50
1:E:265:SER:HB2	1:G:266:VAL:H	1.76	0.50
2:J:184:ILE:HG22	2:J:185:THR:HB	1.94	0.49
2:J:170:GLU:O	2:J:173:LYS:HG2	2.11	0.49
2:B:85:ALA:HA	2:B:110:SER:O	2.12	0.49
1:A:85:LEU:HD21	1:A:136:ALA:HB2	1.95	0.49
1:I:57:LEU:HD13	1:I:64:PRO:HB3	1.95	0.49
2:J:108:VAL:HA	2:J:182:VAL:O	2.13	0.49
1:C:123:THR:HA	1:C:154:LEU:HD21	1.95	0.49
1:A:110:ILE:HD12	1:A:114:TYR:HA	1.94	0.49
1:G:93:ARG:O	1:G:168:VAL:HA	2.13	0.49
1:E:31:ASP:OD1	2:F:54:ARG:NH1	2.46	0.48
2:F:138:ASN:O	2:F:142:LYS:HG2	2.13	0.48
2:B:109:LEU:HB2	2:B:181:ASP:HB2	1.94	0.48
2:J:113:ASN:HB2	2:J:117:LEU:HD23	1.93	0.48
1:C:65:ILE:HD13	1:C:112:GLU:HB2	1.96	0.48
1:C:92:LEU:HD12	1:C:123:THR:HB	1.96	0.48
1:A:268:LEU:HB3	1:U:269:GLN:HB3	1.95	0.48
1:A:147:SER:HA	1:A:170:LEU:HD13	1.95	0.48
1:U:261:PRO:HG2	1:U:264:GLN:HG3	1.96	0.48
2:N:279:VAL:HG12	2:N:279:VAL:O	2.13	0.48
2:J:136:ILE:HG22	2:J:168:LEU:HD12	1.94	0.48
1:E:267:LEU:HA	1:G:266:VAL:HG23	1.95	0.48
1:C:266:VAL:HG21	1:A:267:LEU:H	1.79	0.48
1:A:112:GLU:OE1	1:A:112:GLU:N	2.45	0.48
2:B:182:VAL:HG12	2:B:183:ALA:N	2.29	0.48
2:H:41:PHE:HB2	2:H:71:ARG:HD2	1.96	0.48
1:A:38:ILE:HG13	1:A:50:VAL:HG11	1.96	0.47
1:G:181:GLU:OE2	2:F:208:GLN:NE2	2.46	0.47
1:Q:264:GLN:O	1:O:265:SER:HB3	2.15	0.47
1:M:221:ALA:O	1:M:222:GLU:HB2	2.14	0.47
1:E:107:PHE:O	1:E:107:PHE:CD2	2.67	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:264:GLN:O	1:I:264:GLN:NE2	2.47	0.47
2:B:94:THR:O	2:B:102:VAL:HB	2.14	0.47
2:B:108:VAL:HG22	2:B:183:ALA:HB2	1.95	0.47
1:C:143:ARG:HG3	2:D:147:LYS:HG3	1.95	0.47
2:H:267:SER:OG	2:H:269:ASN:ND2	2.47	0.47
1:E:92:LEU:HD21	1:E:94:ILE:HD11	1.97	0.47
1:M:265:SER:HB3	1:K:265:SER:H	1.79	0.47
1:A:127:LEU:HA	1:A:130:VAL:HG22	1.97	0.47
2:J:42:THR:O	2:J:67:GLY:N	2.47	0.47
2:J:117:LEU:HA	2:J:120:MET:HB2	1.97	0.47
2:H:94:THR:O	2:H:101:MET:HA	2.15	0.47
2:H:94:THR:HB	2:H:145:VAL:HG21	1.97	0.47
2:H:126:LEU:O	2:H:126:LEU:HG	2.14	0.47
2:D:150:ALA:H	2:D:151:SER:CB	2.28	0.47
1:C:88:VAL:HG22	1:C:175:PHE:CD1	2.50	0.47
1:I:142:GLN:HB3	1:I:145:LEU:HB2	1.97	0.47
2:F:52:PHE:HA	2:F:60:GLN:HB3	1.97	0.47
2:F:109:LEU:HB3	2:F:182:VAL:HB	1.97	0.47
2:F:111:ARG:HB2	2:F:178:ILE:HB	1.97	0.46
2:D:90:ILE:N	2:D:91:SER:HB2	2.29	0.46
2:J:52:PHE:O	2:J:76:GLN:HA	2.15	0.46
2:J:167:GLU:O	2:J:169:THR:N	2.49	0.46
1:E:70:ARG:HB2	2:F:123:ARG:O	2.16	0.46
1:M:222:GLU:O	1:M:223:LEU:C	2.57	0.46
1:G:183:VAL:HB	2:H:99:LEU:HB2	1.97	0.46
2:F:105:SER:HB3	2:F:186:GLU:HB2	1.98	0.46
2:D:157:ARG:HA	2:D:160:VAL:HG12	1.97	0.46
1:A:170:LEU:HA	1:A:171:THR:HB	1.97	0.46
2:F:52:PHE:HA	2:F:60:GLN:CB	2.46	0.46
2:V:243:SER:O	2:V:244:LYS:HB3	2.16	0.46
2:H:89:LYS:HA	2:H:107:ARG:HA	1.97	0.46
1:I:265:SER:OG	1:I:266:VAL:N	2.47	0.46
1:C:82:SER:HB2	1:C:83:LYS:HA	1.98	0.46
1:Q:267:LEU:HD11	2:R:272:TYR:CE2	2.51	0.46
1:I:75:ASN:HA	1:I:93:ARG:HA	1.98	0.46
1:I:267:LEU:O	1:G:267:LEU:HA	2.16	0.46
2:J:160:VAL:O	2:J:164:ILE:HG23	2.16	0.45
2:D:48:ARG:NE	2:D:48:ARG:HA	2.31	0.45
2:D:149:ASN:O	2:D:160:VAL:HB	2.16	0.45
1:I:266:VAL:HG13	1:G:266:VAL:HG13	1.99	0.45
1:C:52:GLU:OE1	2:D:57:GLY:HA3	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:HIS:O	1:C:174:THR:N	2.49	0.45
1:M:205:GLN:NE2	2:N:207:ALA:O	2.42	0.45
1:G:28:TYR:CD1	1:G:28:TYR:C	2.94	0.45
1:S:184:GLU:O	1:S:188:VAL:HG23	2.16	0.45
2:F:176:SER:OG	2:F:177:LEU:N	2.50	0.45
2:B:113:ASN:HA	2:B:178:ILE:HG13	1.99	0.45
2:D:151:SER:N	2:D:154:ILE:O	2.49	0.45
2:B:91:SER:HA	2:B:104:ILE:O	2.17	0.45
2:H:111:ARG:O	2:H:178:ILE:N	2.50	0.45
1:S:265:SER:HB3	1:Q:265:SER:HB3	1.98	0.45
1:A:265:SER:HB2	1:U:265:SER:HB2	1.99	0.44
1:E:36:ALA:HA	1:E:65:ILE:O	2.17	0.44
1:A:191:GLN:HE22	2:B:197:VAL:HG23	1.83	0.44
2:H:114:ALA:O	2:H:117:LEU:HG	2.18	0.44
1:I:123:THR:OG1	1:I:124:THR:N	2.50	0.44
1:G:38:ILE:HG12	1:G:64:PRO:HG3	1.99	0.44
1:O:267:LEU:H	1:M:266:VAL:CG1	2.30	0.44
1:I:92:LEU:HD11	1:I:168:VAL:HG13	1.99	0.44
2:H:49:ALA:HA	2:H:79:ILE:O	2.16	0.44
2:F:50:ILE:HG23	2:F:63:ILE:HG12	1.99	0.44
1:G:154:LEU:HD13	1:G:168:VAL:HG11	1.99	0.44
1:A:85:LEU:HD22	1:A:88:VAL:HG21	2.00	0.44
1:O:185:ALA:HB1	2:N:209:ARG:HD3	2.00	0.44
1:G:40:ASP:OD1	1:G:42:PHE:HB3	2.17	0.44
1:U:221:ALA:O	1:U:222:GLU:HB3	2.17	0.44
2:T:283:GLN:CD	2:T:283:GLN:H	2.25	0.44
2:J:185:THR:OG1	2:J:186:GLU:N	2.46	0.43
2:H:154:ILE:HG13	2:H:154:ILE:O	2.16	0.43
1:E:254:SER:OG	1:E:256:ASN:OD1	2.32	0.43
2:B:81:TYR:OH	2:B:121:TYR:N	2.51	0.43
2:F:46:GLY:N	2:F:47:HIS:HA	2.33	0.43
2:D:104:ILE:HG12	2:D:186:GLU:O	2.18	0.43
2:B:86:ARG:O	2:B:109:LEU:HA	2.18	0.43
1:U:235:LEU:HD22	2:V:235:ALA:HB2	2.01	0.43
1:Q:265:SER:OG	1:Q:266:VAL:N	2.51	0.43
2:B:154:ILE:HG22	2:B:156:GLN:HB2	1.99	0.43
2:B:96:SER:HB2	2:B:148:PHE:HA	2.00	0.43
1:I:112:GLU:H	1:I:112:GLU:CD	2.21	0.43
1:I:238:LEU:O	1:I:242:GLU:HG2	2.19	0.43
2:H:172:ALA:HB1	2:H:177:LEU:O	2.19	0.43
1:S:236:ILE:HD13	2:R:250:LYS:HD2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:157:ARG:O	1:G:160:THR:OG1	2.26	0.43
2:F:47:HIS:N	2:F:81:TYR:O	2.52	0.43
2:J:68:LEU:O	2:J:69:HIS:HB2	2.18	0.43
2:J:116:GLU:N	2:J:116:GLU:OE1	2.52	0.42
2:H:53:ASN:HA	2:H:76:GLN:HA	2.00	0.42
2:F:169:THR:HG22	2:F:179:LEU:HB2	2.01	0.42
2:F:81:TYR:CE2	2:F:114:ALA:HB2	2.54	0.42
2:B:96:SER:HB3	2:B:151:SER:N	2.19	0.42
2:B:104:ILE:HD11	2:B:145:VAL:HG11	2.00	0.42
2:J:47:HIS:CE1	2:J:80:ILE:HG23	2.54	0.42
1:C:261:PRO:HD3	2:D:272:TYR:HB2	2.01	0.42
1:I:38:ILE:HG23	1:I:62:GLN:HA	2.00	0.42
2:J:48:ARG:HB2	2:J:82:ASP:HB2	2.00	0.42
2:D:150:ALA:HA	2:D:160:VAL:HB	2.01	0.42
2:H:106:LEU:HA	2:H:184:ILE:O	2.20	0.42
1:S:265:SER:HB3	1:Q:265:SER:CB	2.50	0.42
2:F:96:SER:HA	2:F:145:VAL:O	2.20	0.42
1:G:60:TRP:CD1	1:G:60:TRP:C	2.97	0.42
2:J:162:LEU:O	2:J:165:ARG:HG2	2.20	0.42
1:A:183:VAL:HG11	2:B:99:LEU:HB2	2.01	0.42
1:S:261:PRO:HG2	1:S:264:GLN:HB3	2.01	0.42
2:D:150:ALA:HB3	2:D:151:SER:HA	2.00	0.42
1:I:38:ILE:HD12	1:I:48:ILE:HG13	2.02	0.42
2:B:112:PRO:HA	2:B:177:LEU:HA	2.01	0.42
1:A:146:VAL:O	1:A:150:VAL:HG23	2.20	0.42
1:G:36:ALA:HA	1:G:66:ILE:HA	2.02	0.42
1:G:175:PHE:CD1	1:G:175:PHE:N	2.88	0.42
2:F:175:PHE:O	2:F:176:SER:C	2.62	0.42
1:A:28:TYR:OH	1:A:38:ILE:HG12	2.20	0.41
1:A:257:ILE:O	2:B:269:ASN:HB2	2.20	0.41
1:C:88:VAL:HG22	1:C:175:PHE:CG	2.55	0.41
1:K:198:PHE:HB2	2:L:203:ALA:HB1	2.02	0.41
1:G:89:ASN:HB2	1:G:174:THR:HB	2.01	0.41
2:F:117:LEU:N	2:F:118:PRO:HD2	2.35	0.41
2:D:103:ASN:HB2	2:D:188:SER:HB3	2.00	0.41
2:B:88:ARG:CZ	2:B:133:LEU:HB3	2.51	0.41
2:B:194:THR:HA	2:B:197:VAL:HB	2.01	0.41
1:G:122:ILE:HG12	1:G:126:ILE:HD12	2.02	0.41
2:J:50:ILE:HD13	2:J:52:PHE:HB2	2.02	0.41
1:I:65:ILE:HG21	1:I:107:PHE:CD1	2.55	0.41
1:I:94:ILE:HD12	1:I:123:THR:HG22	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:91:THR:HB	1:E:172:HIS:HB2	2.02	0.41
1:C:93:ARG:HB3	1:C:169:SER:HB3	2.03	0.41
2:F:71:ARG:NH2	2:F:76:GLN:O	2.48	0.41
2:J:81:TYR:CE2	2:J:118:PRO:HD3	2.56	0.41
2:F:107:ARG:HB2	2:F:184:ILE:HB	2.02	0.41
2:J:94:THR:HG23	2:J:145:VAL:HB	2.03	0.41
1:E:40:ASP:O	1:E:44:GLY:N	2.45	0.41
1:E:92:LEU:HB3	1:E:127:LEU:HD11	2.01	0.41
1:C:268:LEU:O	1:C:269:GLN:HB2	2.21	0.41
1:A:170:LEU:HB3	1:A:171:THR:HG22	2.03	0.41
1:Q:235:LEU:HD22	2:R:235:ALA:HB2	2.03	0.41
1:I:30:VAL:CG2	1:I:34:HIS:HB2	2.51	0.41
2:B:38:GLU:HA	2:B:41:PHE:HB2	2.03	0.41
2:B:109:LEU:CB	2:B:181:ASP:HB2	2.51	0.41
2:J:91:SER:OG	2:J:103:ASN:OD1	2.30	0.41
2:J:93:PRO:HA	2:J:102:VAL:O	2.20	0.41
2:J:111:ARG:HG2	2:J:178:ILE:HG23	2.02	0.41
1:A:78:VAL:HG21	1:A:89:ASN:HA	2.02	0.41
1:A:130:VAL:HB	1:A:150:VAL:HG22	2.02	0.41
2:H:279:VAL:HG12	2:H:279:VAL:O	2.20	0.41
1:Q:266:VAL:HB	1:O:266:VAL:HB	2.03	0.40
1:I:54:THR:OG1	2:J:77:TYR:OH	2.38	0.40
2:D:106:LEU:HA	2:D:184:ILE:O	2.21	0.40
1:E:92:LEU:CB	1:E:127:LEU:HD11	2.51	0.40
2:B:111:ARG:HB2	2:B:178:ILE:HB	2.03	0.40
2:J:69:HIS:HA	2:J:70:PHE:HA	1.94	0.40
2:H:140:VAL:HG11	2:H:168:LEU:HG	2.03	0.40
2:H:289:ARG:NH1	2:H:293:SER:OG	2.54	0.40
1:E:106:ILE:O	1:E:108:THR:N	2.54	0.40
2:B:140:VAL:HG11	2:B:168:LEU:HG	2.03	0.40
1:O:265:SER:OG	1:O:266:VAL:N	2.55	0.40
1:E:61:VAL:O	1:E:62:GLN:HB2	2.21	0.40
1:E:157:ARG:HA	1:E:157:ARG:NE	2.36	0.40
1:A:235:LEU:HA	2:B:238:LEU:HD23	2.03	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	247/296 (83%)	220 (89%)	24 (10%)	3 (1%)	10	34
1	C	247/296 (83%)	216 (87%)	29 (12%)	2 (1%)	16	44
1	E	248/296 (84%)	232 (94%)	16 (6%)	0	100	100
1	G	248/296 (84%)	216 (87%)	31 (12%)	1 (0%)	30	60
1	I	248/296 (84%)	229 (92%)	17 (7%)	2 (1%)	16	44
1	K	74/296 (25%)	70 (95%)	4 (5%)	0	100	100
1	M	73/296 (25%)	65 (89%)	4 (6%)	4 (6%)	1	4
1	O	89/296 (30%)	86 (97%)	3 (3%)	0	100	100
1	Q	79/296 (27%)	75 (95%)	3 (4%)	1 (1%)	9	31
1	S	89/296 (30%)	84 (94%)	5 (6%)	0	100	100
1	U	83/296 (28%)	76 (92%)	7 (8%)	0	100	100
2	B	260/299 (87%)	225 (86%)	32 (12%)	3 (1%)	10	34
2	D	261/299 (87%)	237 (91%)	24 (9%)	0	100	100
2	F	260/299 (87%)	229 (88%)	30 (12%)	1 (0%)	30	60
2	H	260/299 (87%)	233 (90%)	26 (10%)	1 (0%)	30	60
2	J	260/299 (87%)	231 (89%)	24 (9%)	5 (2%)	6	22
2	L	94/299 (31%)	90 (96%)	4 (4%)	0	100	100
2	N	95/299 (32%)	93 (98%)	2 (2%)	0	100	100
2	P	103/299 (34%)	99 (96%)	4 (4%)	0	100	100
2	R	95/299 (32%)	93 (98%)	2 (2%)	0	100	100
2	T	103/299 (34%)	101 (98%)	2 (2%)	0	100	100
2	V	103/299 (34%)	98 (95%)	3 (3%)	2 (2%)	6	22
All	All	3619/6545 (55%)	3298 (91%)	296 (8%)	25 (1%)	20	47

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	103	LEU
1	M	264	GLN
1	I	54	THR
1	I	265	SER
1	G	136	ALA
2	B	182	VAL
2	V	244	LYS
2	V	245	ASN
2	J	69	HIS
1	C	102	GLN
1	A	78	VAL
1	A	144	GLU
1	A	167	ASP
1	Q	262	ALA
2	F	176	SER
2	B	156	GLN
2	J	43	VAL
1	M	267	LEU
2	H	279	VAL
2	B	148	PHE
2	J	97	LYS
1	M	222	GLU
2	J	148	PHE
1	M	266	VAL
2	J	279	VAL

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	209/247 (85%)	208 (100%)	1 (0%)	81	93
1	C	209/247 (85%)	209 (100%)	0	100	100
1	E	210/247 (85%)	210 (100%)	0	100	100
1	G	210/247 (85%)	210 (100%)	0	100	100
1	I	210/247 (85%)	210 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	58/247 (24%)	58 (100%)	0	100	100
1	M	57/247 (23%)	57 (100%)	0	100	100
1	O	69/247 (28%)	69 (100%)	0	100	100
1	Q	61/247 (25%)	61 (100%)	0	100	100
1	S	69/247 (28%)	69 (100%)	0	100	100
1	U	64/247 (26%)	64 (100%)	0	100	100
2	B	221/248 (89%)	219 (99%)	2 (1%)	70	89
2	D	222/248 (90%)	222 (100%)	0	100	100
2	F	221/248 (89%)	221 (100%)	0	100	100
2	H	221/248 (89%)	220 (100%)	1 (0%)	81	93
2	J	221/248 (89%)	220 (100%)	1 (0%)	81	93
2	L	79/248 (32%)	79 (100%)	0	100	100
2	N	79/248 (32%)	79 (100%)	0	100	100
2	P	85/248 (34%)	85 (100%)	0	100	100
2	R	79/248 (32%)	79 (100%)	0	100	100
2	T	85/248 (34%)	85 (100%)	0	100	100
2	V	85/248 (34%)	85 (100%)	0	100	100
All	All	3024/5445 (56%)	3019 (100%)	5 (0%)	85	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LEU
2	B	117	LEU
2	B	142	LYS
2	J	177	LEU
2	H	71	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	264	GLN
1	C	142	GLN
1	A	75	ASN
1	A	191	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	O	187	GLN
1	K	205	GLN
1	K	226	ASN
1	G	75	ASN
1	G	86	GLN
2	F	69	HIS
2	D	219	GLN
2	V	219	GLN
2	N	205	GLN
2	N	269	ASN
2	J	100	GLN
2	H	60	GLN
2	H	122	GLN
2	H	138	ASN
2	H	269	ASN

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](#)

There are no ligands in this entry.

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.

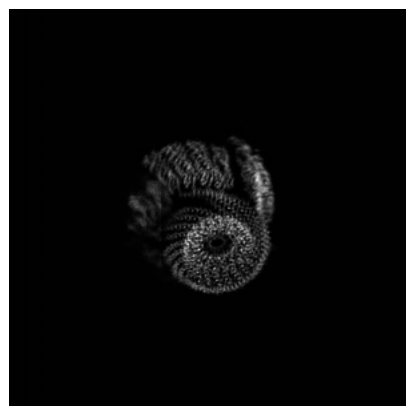
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64355. These allow visual inspection of the internal detail of the map and identification of artifacts.

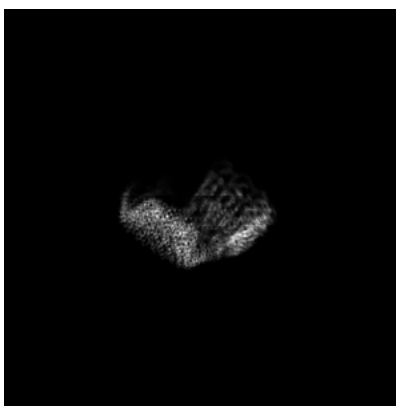
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

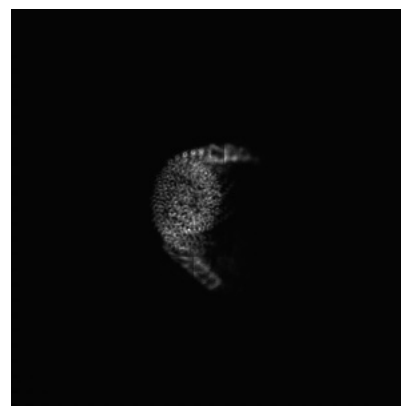
6.1.1 Primary map



X

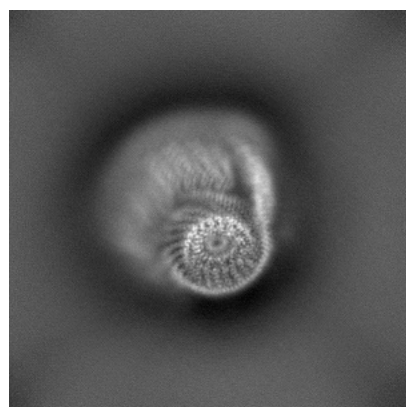


Y

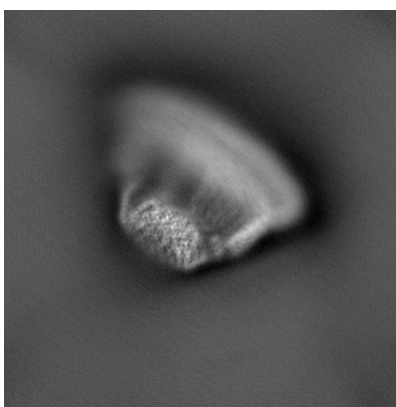


Z

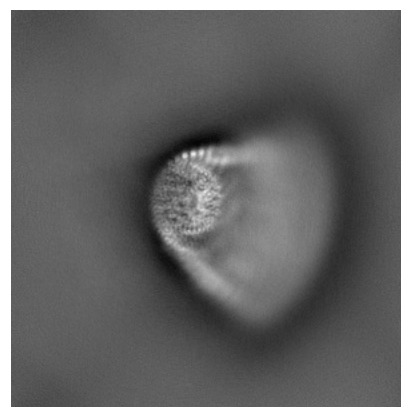
6.1.2 Raw map



X



Y

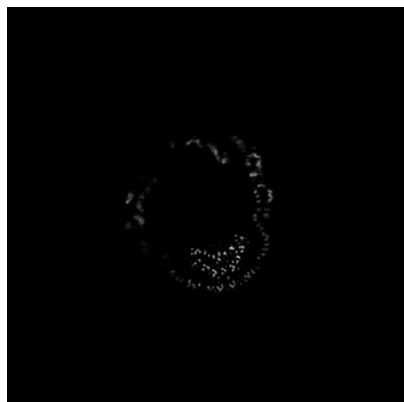


Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 256

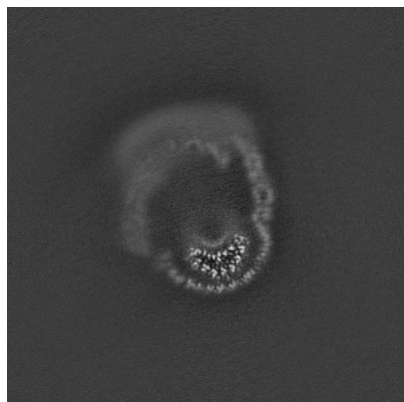


Y Index: 256

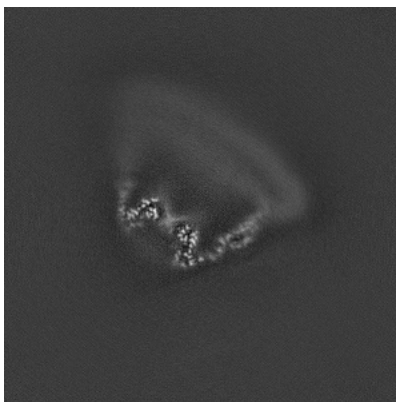


Z Index: 256

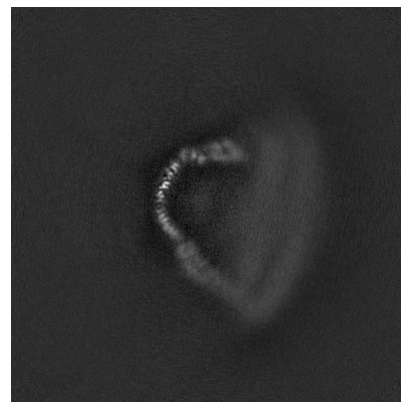
6.2.2 Raw map



X Index: 256



Y Index: 256

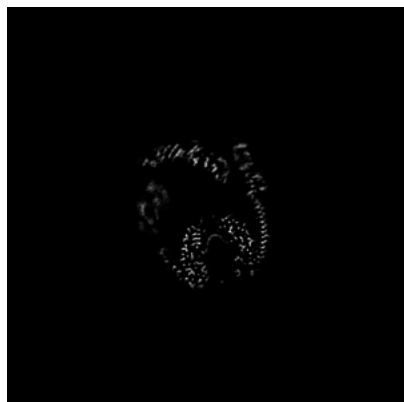


Z Index: 256

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

6.3 Largest variance slices [i](#)

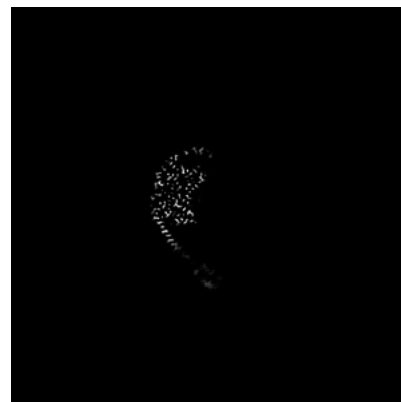
6.3.1 Primary map



X Index: 234

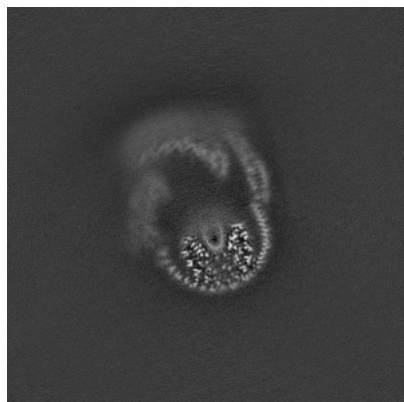


Y Index: 229

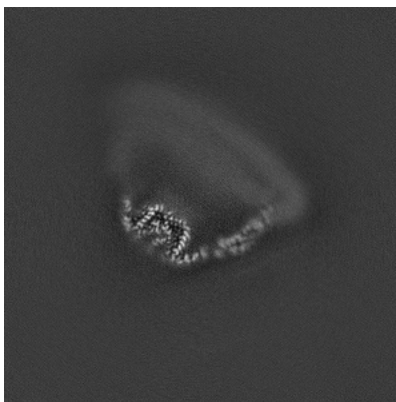


Z Index: 232

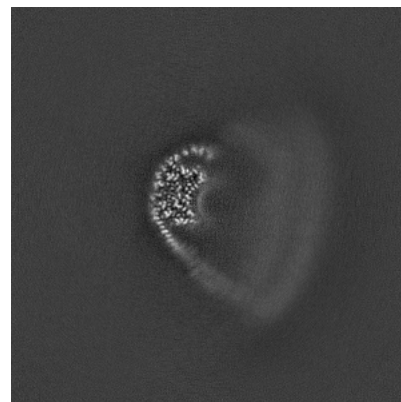
6.3.2 Raw map



X Index: 243



Y Index: 236

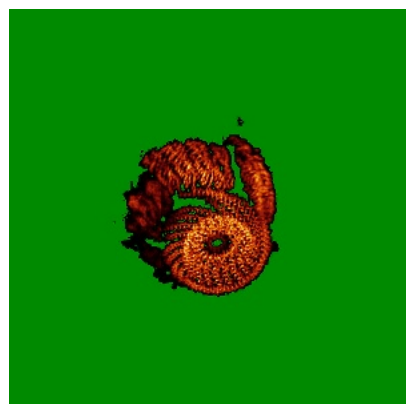


Z Index: 232

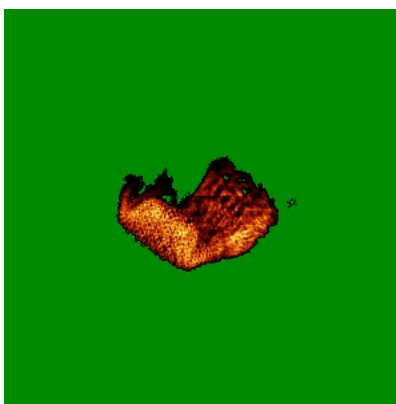
The images above show the largest variance slices of the map in three orthogonal directions.

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

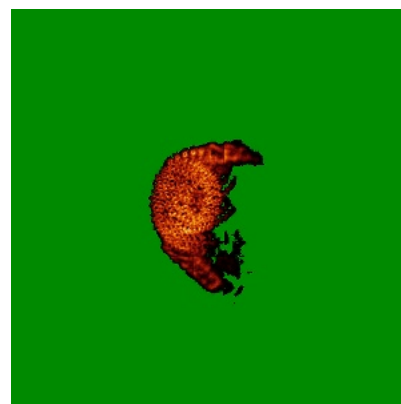
6.4.1 Primary map



X

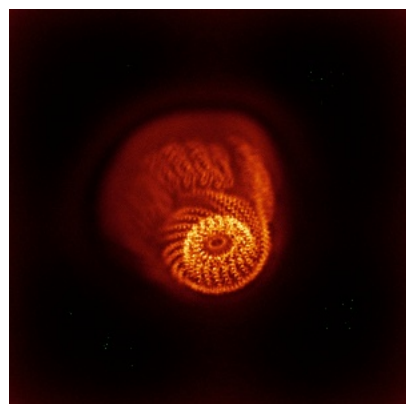


Y

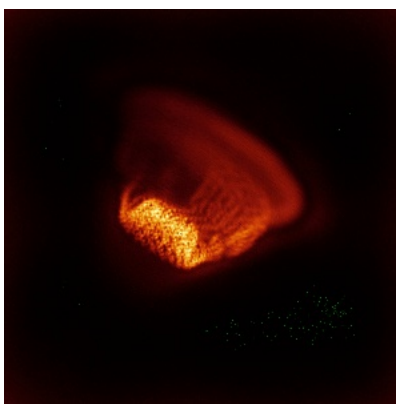


Z

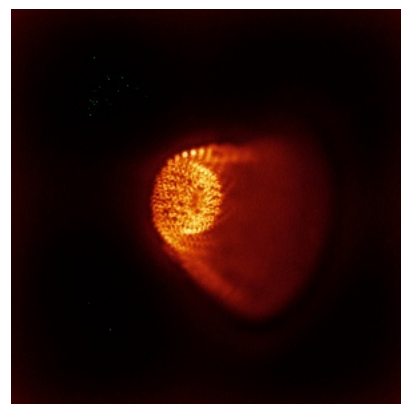
6.4.2 Raw map



X



Y

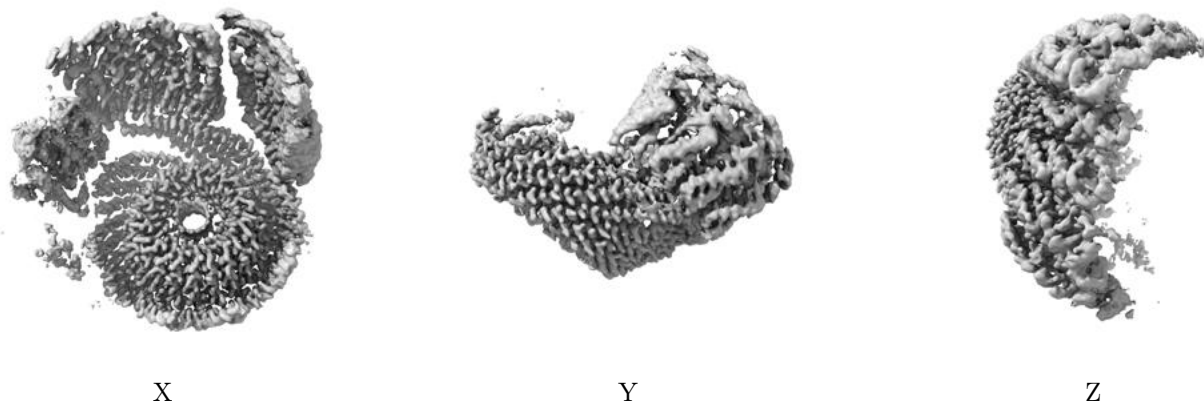


Z

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

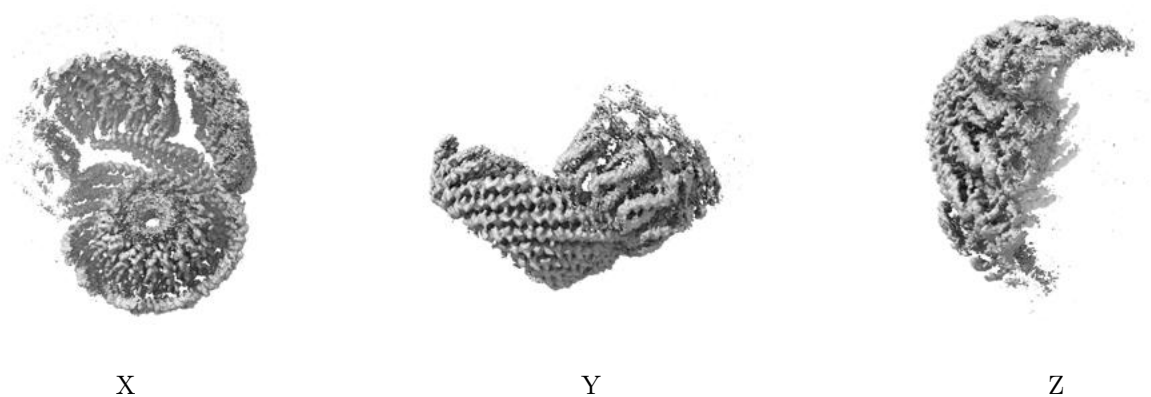
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. 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.

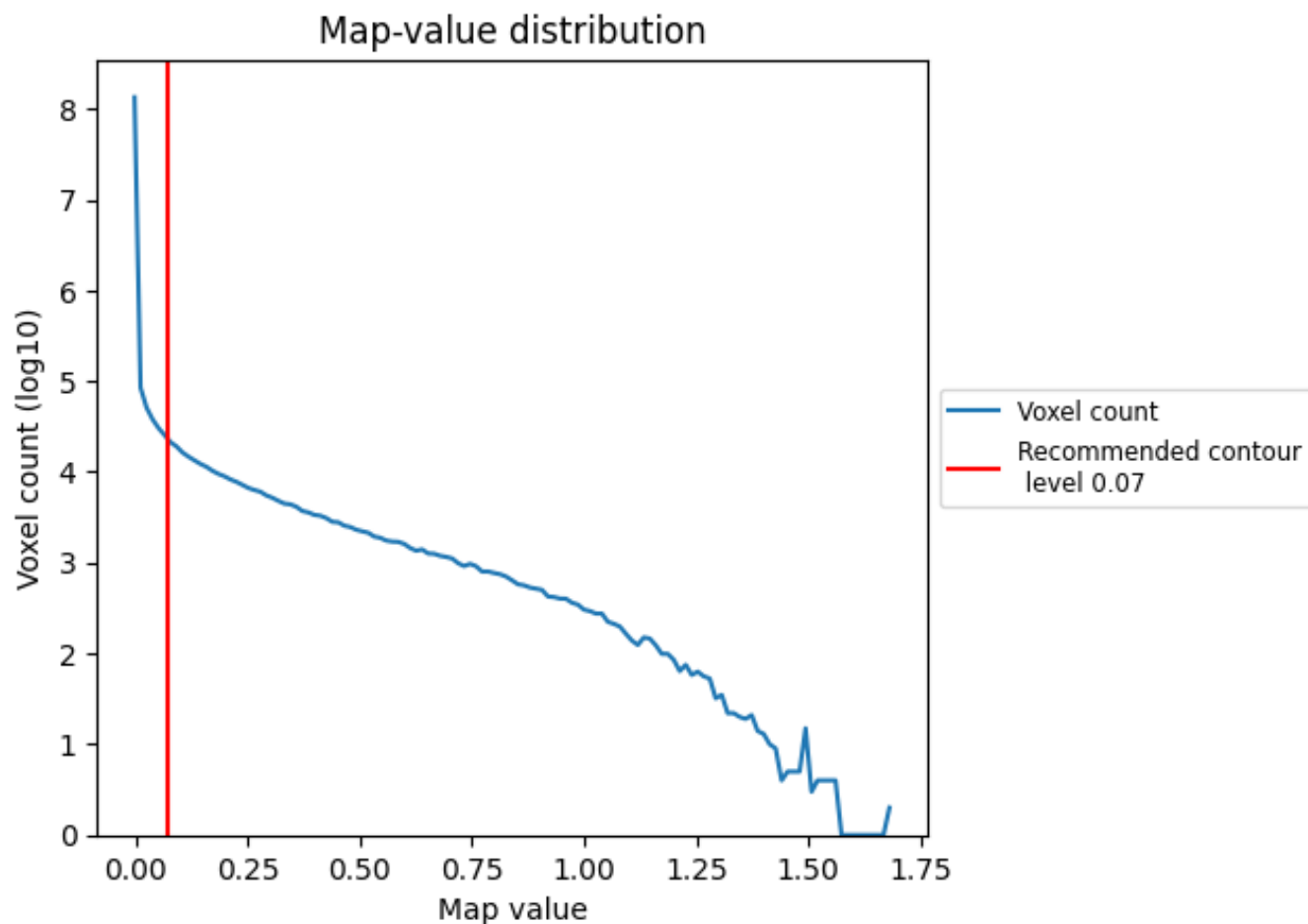
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

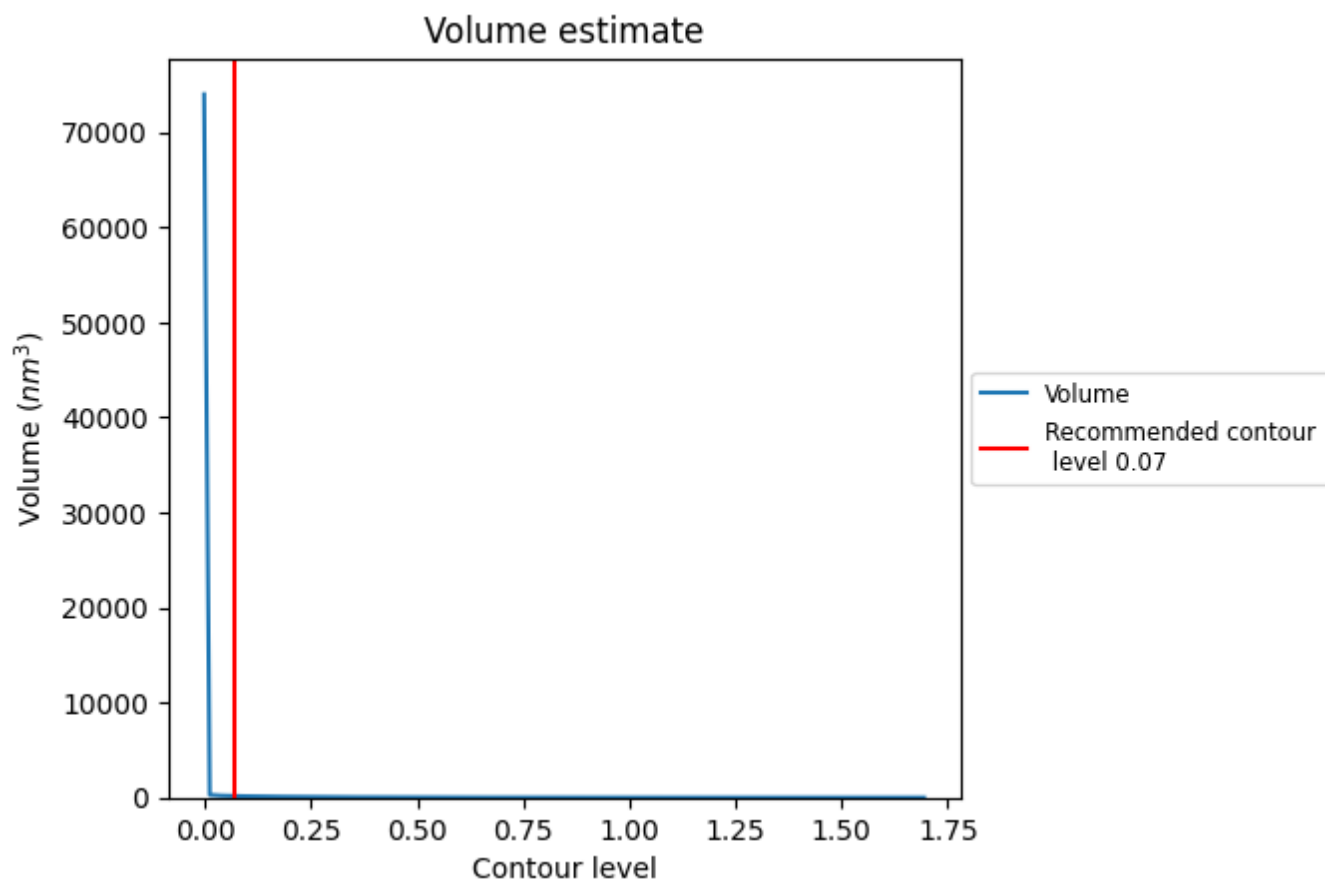
This section contains the results of statistical analysis of the map.

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.

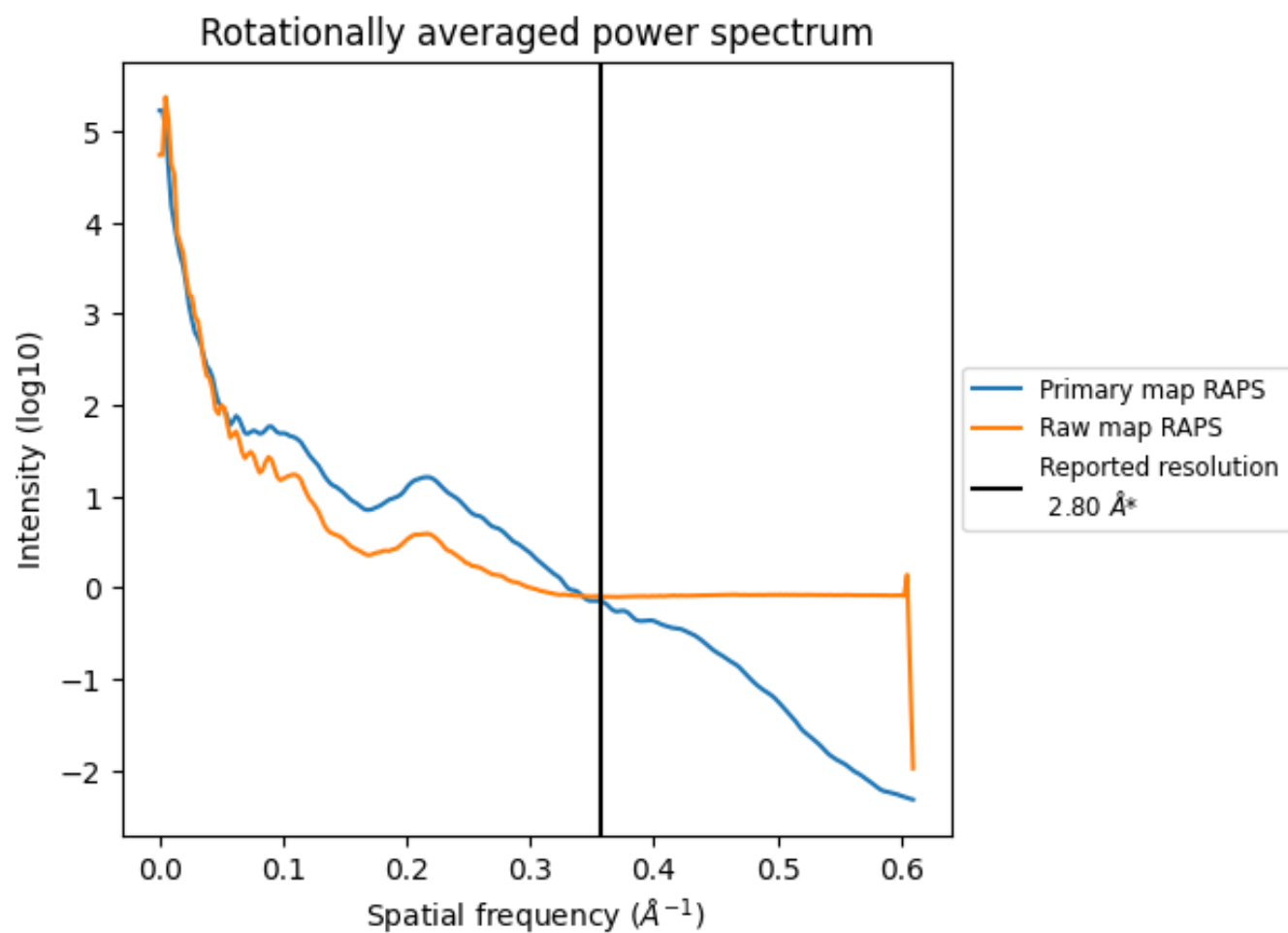
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 162 nm^3 ; this corresponds to an approximate mass of 147 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 ⓘ

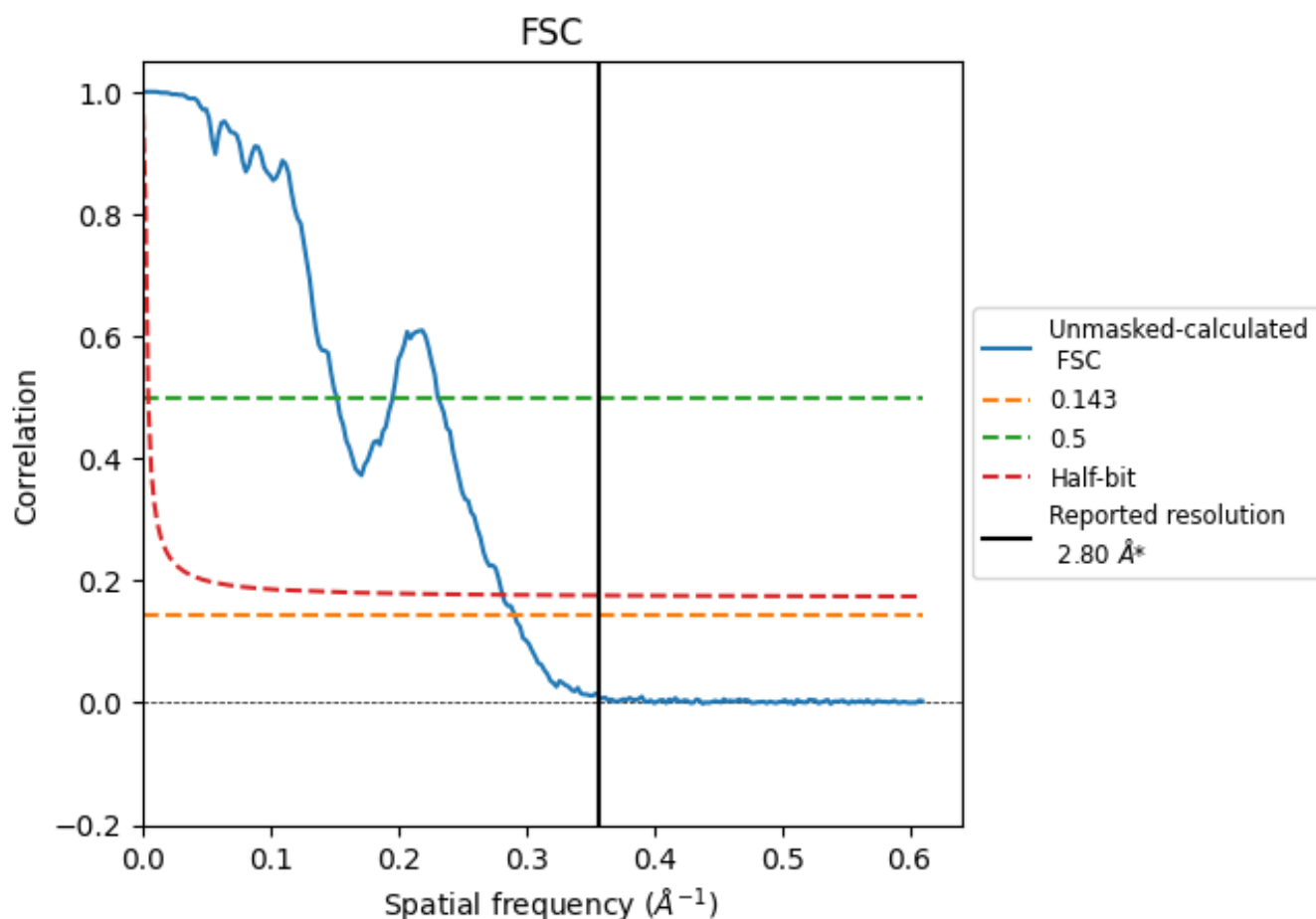


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 Å⁻¹

8.2 Resolution estimates [i](#)

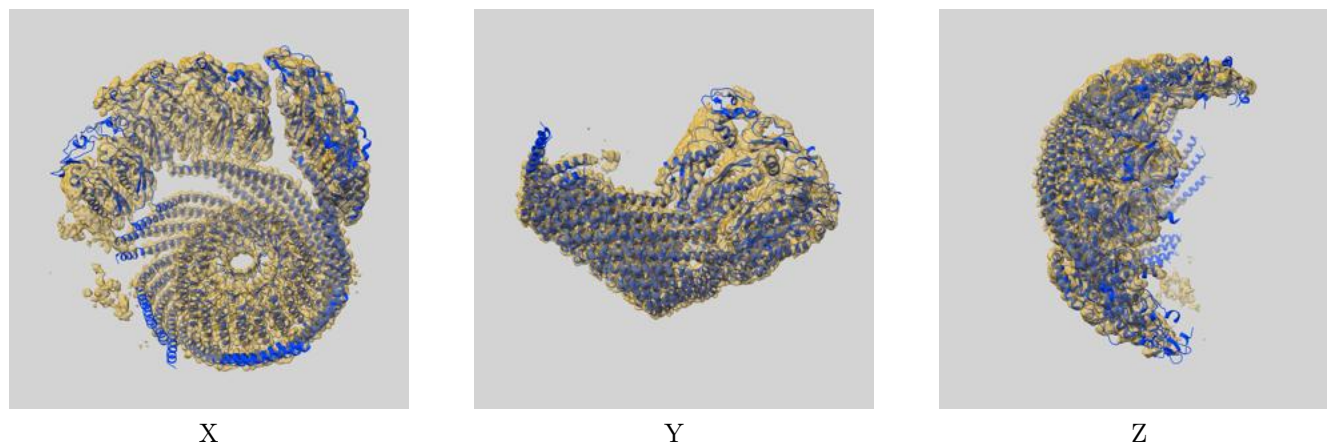
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.43	6.57	3.55

*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 3.43 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

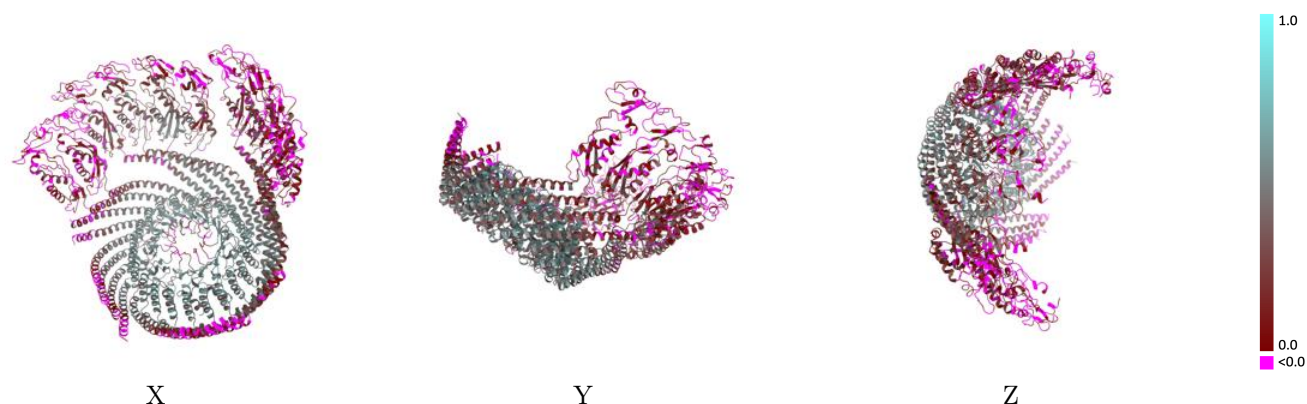
This section contains information regarding the fit between EMDB map EMD-64355 and PDB model 9UNL. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



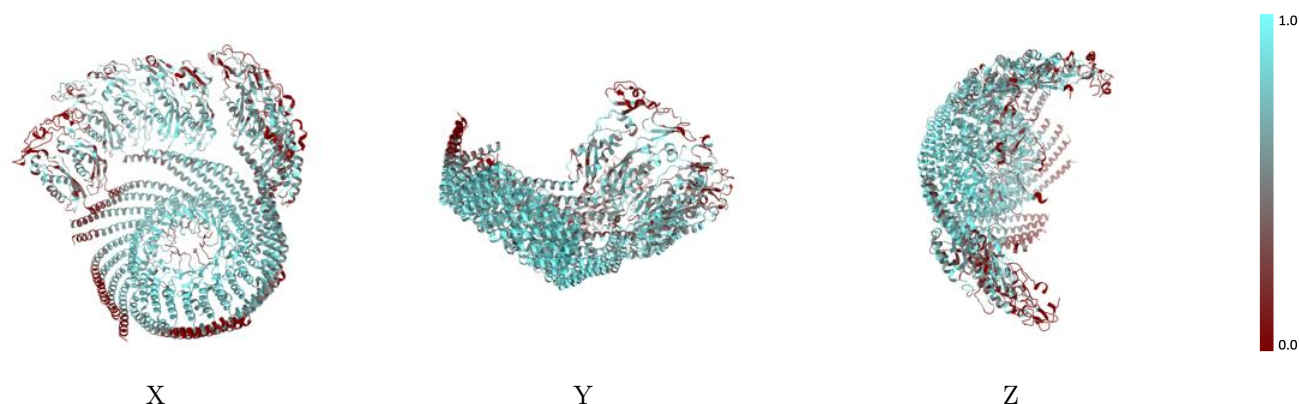
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



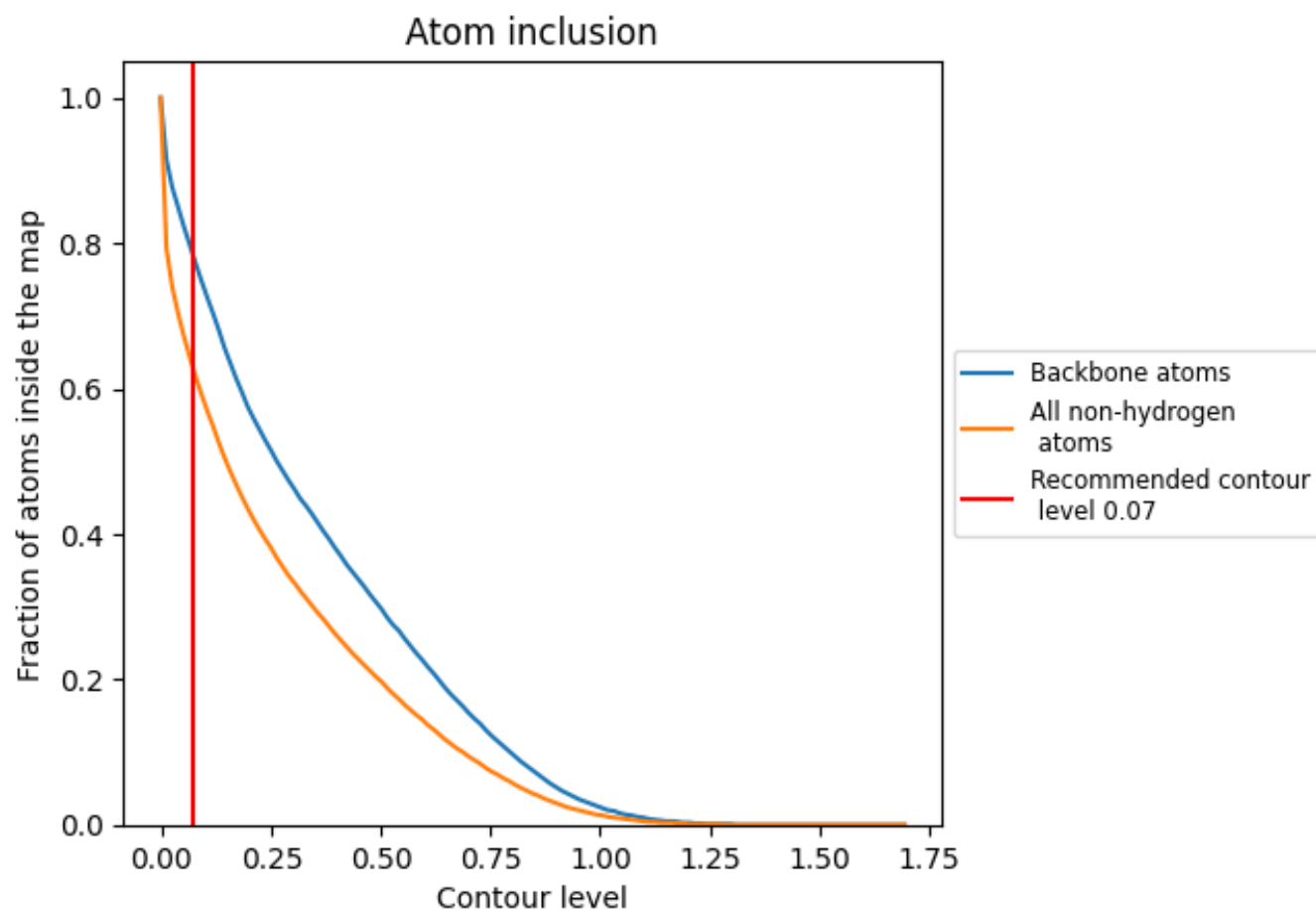
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 63% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6310	 0.2700
A	 0.4630	 0.1490
B	 0.5010	 0.1730
C	 0.6090	 0.1890
D	 0.7320	 0.3030
E	 0.7370	 0.3330
F	 0.6860	 0.2810
G	 0.5510	 0.1770
H	 0.6610	 0.2430
I	 0.6270	 0.2100
J	 0.5770	 0.1980
K	 0.6770	 0.3990
L	 0.7380	 0.4020
M	 0.6740	 0.3630
N	 0.6940	 0.3930
O	 0.5600	 0.3060
P	 0.6610	 0.3730
Q	 0.6190	 0.3380
R	 0.7140	 0.4090
S	 0.5740	 0.3150
T	 0.6840	 0.3830
U	 0.6670	 0.3650
V	 0.7420	 0.4140

