



Full wwPDB EM Validation Report ⓘ

Jul 19, 2025 – 03:14 PM EDT

PDB ID : 9N81 / pdb_00009n81
EMDB ID : EMD-49108
Title : A gap-filling complex with Pol mu engaged in the NHEJ Pathway
Authors : Li, J.; Liu, L.; Gellert, M.; Yang, W.
Deposited on : 2025-02-07
Resolution : 2.80 Å(reported)
Based on initial model : 9CQ3

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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

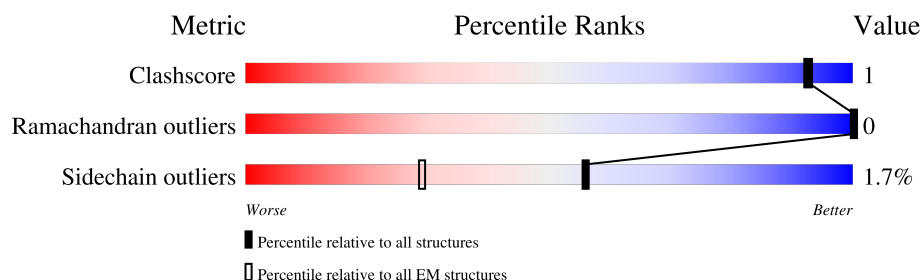
1 Overall quality at a glance

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.








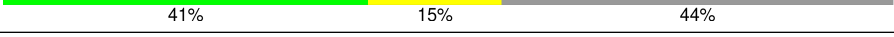

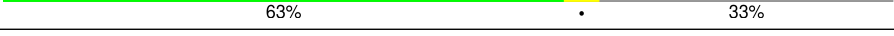
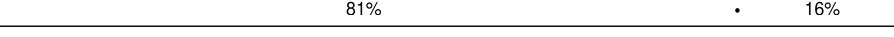

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	612	
1	a	612	
2	B	732	
2	b	732	
3	C	302	
3	c	302	
4	D	336	
4	E	336	

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Mol	Chain	Length	Quality of chain
4	d	336	
4	e	336	
5	F	914	
5	f	914	
6	G	218	
6	H	218	
7	I	68	
8	J	68	
9	K	51	
10	L	50	
11	M	512	
11	m	512	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 41888 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 X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	516	Total	C	N	O	S	0	0
			4169	2665	704	781	19		
1	a	507	Total	C	N	O	S	0	0
			4094	2617	693	766	18		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P12956
A	-1	PRO	-	expression tag	UNP P12956
A	0	VAL	-	expression tag	UNP P12956
a	-2	GLY	-	expression tag	UNP P12956
a	-1	PRO	-	expression tag	UNP P12956
a	0	VAL	-	expression tag	UNP P12956

- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	512	Total	C	N	O	S	1	0
			4115	2631	691	770	23		
2	b	511	Total	C	N	O	S	0	0
			4100	2623	686	768	23		

- Molecule 3 is a protein called Non-homologous end-joining factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	238	Total	C	N	O	S	0	0
			1887	1207	317	348	15		
3	c	235	Total	C	N	O	S	0	0
			1869	1195	314	345	15		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q9H9Q4
C	-1	PRO	-	expression tag	UNP Q9H9Q4
C	0	VAL	-	expression tag	UNP Q9H9Q4
c	-2	GLY	-	expression tag	UNP Q9H9Q4
c	-1	PRO	-	expression tag	UNP Q9H9Q4
c	0	VAL	-	expression tag	UNP Q9H9Q4

- Molecule 4 is a protein called DNA repair protein XRCC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	202	Total	C	N	O	S	0	0
			1633	1034	279	313	7		
4	E	201	Total	C	N	O	S	0	0
			1628	1031	278	312	7		
4	d	200	Total	C	N	O	S	0	0
			1623	1028	277	311	7		
4	e	200	Total	C	N	O	S	0	0
			1623	1028	277	311	7		

- Molecule 5 is a protein called DNA ligase 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	679	Total	C	N	O	S	0	0
			5503	3504	945	1021	33		
5	f	255	Total	C	N	O	S	0	0
			2069	1315	349	392	13		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	GLY	-	expression tag	UNP P49917
F	-1	PRO	-	expression tag	UNP P49917
F	0	VAL	-	expression tag	UNP P49917
f	-2	GLY	-	expression tag	UNP P49917
f	-1	PRO	-	expression tag	UNP P49917
f	0	VAL	-	expression tag	UNP P49917

- Molecule 6 is a protein called Protein PAXX.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	23	Total	C	N	O	S	0	0
			165	105	27	32	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	23	Total	C	N	O	S	0	0
			165	105	27	32	1		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-13	MET	-	expression tag	UNP Q9BUH6
G	-12	GLY	-	expression tag	UNP Q9BUH6
G	-11	SER	-	expression tag	UNP Q9BUH6
G	-10	SER	-	expression tag	UNP Q9BUH6
G	-9	HIS	-	expression tag	UNP Q9BUH6
G	-8	HIS	-	expression tag	UNP Q9BUH6
G	-7	HIS	-	expression tag	UNP Q9BUH6
G	-6	HIS	-	expression tag	UNP Q9BUH6
G	-5	HIS	-	expression tag	UNP Q9BUH6
G	-4	HIS	-	expression tag	UNP Q9BUH6
G	-3	SER	-	expression tag	UNP Q9BUH6
G	-2	GLN	-	expression tag	UNP Q9BUH6
G	-1	ASP	-	expression tag	UNP Q9BUH6
G	0	PRO	-	expression tag	UNP Q9BUH6
H	-13	MET	-	expression tag	UNP Q9BUH6
H	-12	GLY	-	expression tag	UNP Q9BUH6
H	-11	SER	-	expression tag	UNP Q9BUH6
H	-10	SER	-	expression tag	UNP Q9BUH6
H	-9	HIS	-	expression tag	UNP Q9BUH6
H	-8	HIS	-	expression tag	UNP Q9BUH6
H	-7	HIS	-	expression tag	UNP Q9BUH6
H	-6	HIS	-	expression tag	UNP Q9BUH6
H	-5	HIS	-	expression tag	UNP Q9BUH6
H	-4	HIS	-	expression tag	UNP Q9BUH6
H	-3	SER	-	expression tag	UNP Q9BUH6
H	-2	GLN	-	expression tag	UNP Q9BUH6
H	-1	ASP	-	expression tag	UNP Q9BUH6
H	0	PRO	-	expression tag	UNP Q9BUH6

- Molecule 7 is a DNA chain called DNA (38-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	38	Total	C	N	O	P	0	0
			771	370	131	232	38		

- Molecule 8 is a DNA chain called DNA (42-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	42	Total	C	N	O	P	0	0
			857	410	154	251	42		

- Molecule 9 is a DNA chain called DNA (34-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	34	Total	C	N	O	P	0	0
			702	335	136	198	33		

- Molecule 10 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	37	Total	C	N	O	P	0	0
			763	364	137	225	37		

- Molecule 11 is a protein called DNA-directed DNA/RNA polymerase mu.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	428	Total	C	N	O	S	0	0
			3389	2139	622	614	14		
11	m	96	Total	C	N	O	S	0	0
			732	457	135	134	6		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-17	HIS	-	expression tag	UNP Q9NP87
M	-16	HIS	-	expression tag	UNP Q9NP87
M	-15	HIS	-	expression tag	UNP Q9NP87
M	-14	HIS	-	expression tag	UNP Q9NP87
M	-13	HIS	-	expression tag	UNP Q9NP87
M	-12	HIS	-	expression tag	UNP Q9NP87
M	-11	SER	-	expression tag	UNP Q9NP87
M	-10	SER	-	expression tag	UNP Q9NP87
M	-9	GLY	-	expression tag	UNP Q9NP87
M	-8	LEU	-	expression tag	UNP Q9NP87
M	-7	GLU	-	expression tag	UNP Q9NP87
M	-6	VAL	-	expression tag	UNP Q9NP87
M	-5	LEU	-	expression tag	UNP Q9NP87
M	-4	PHE	-	expression tag	UNP Q9NP87
M	-3	GLN	-	expression tag	UNP Q9NP87
M	-2	GLY	-	expression tag	UNP Q9NP87
M	-1	PRO	-	expression tag	UNP Q9NP87

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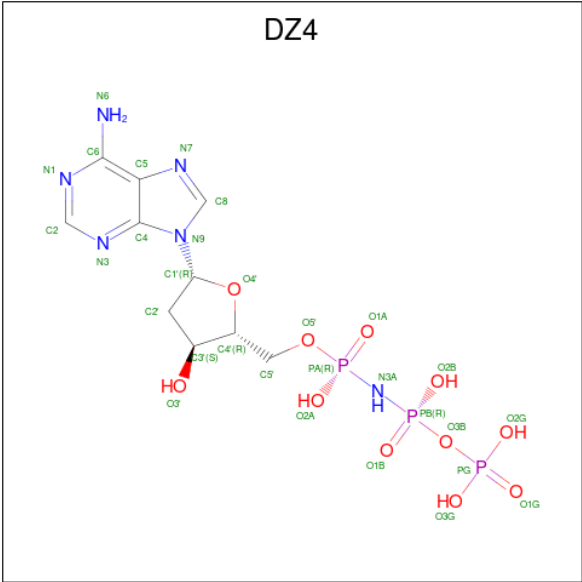
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Chain	Residue	Modelled	Actual	Comment	Reference
M	0	HIS	-	expression tag	UNP Q9NP87
m	-17	HIS	-	expression tag	UNP Q9NP87
m	-16	HIS	-	expression tag	UNP Q9NP87
m	-15	HIS	-	expression tag	UNP Q9NP87
m	-14	HIS	-	expression tag	UNP Q9NP87
m	-13	HIS	-	expression tag	UNP Q9NP87
m	-12	HIS	-	expression tag	UNP Q9NP87
m	-11	SER	-	expression tag	UNP Q9NP87
m	-10	SER	-	expression tag	UNP Q9NP87
m	-9	GLY	-	expression tag	UNP Q9NP87
m	-8	LEU	-	expression tag	UNP Q9NP87
m	-7	GLU	-	expression tag	UNP Q9NP87
m	-6	VAL	-	expression tag	UNP Q9NP87
m	-5	LEU	-	expression tag	UNP Q9NP87
m	-4	PHE	-	expression tag	UNP Q9NP87
m	-3	GLN	-	expression tag	UNP Q9NP87
m	-2	GLY	-	expression tag	UNP Q9NP87
m	-1	PRO	-	expression tag	UNP Q9NP87
m	0	HIS	-	expression tag	UNP Q9NP87

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

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

- Molecule 13 is 2'-deoxy-5'-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]amino}phosphoryl]adenosine (CCD ID: DZ4) (formula: C₁₀H₁₇N₆O₁₁P₃).

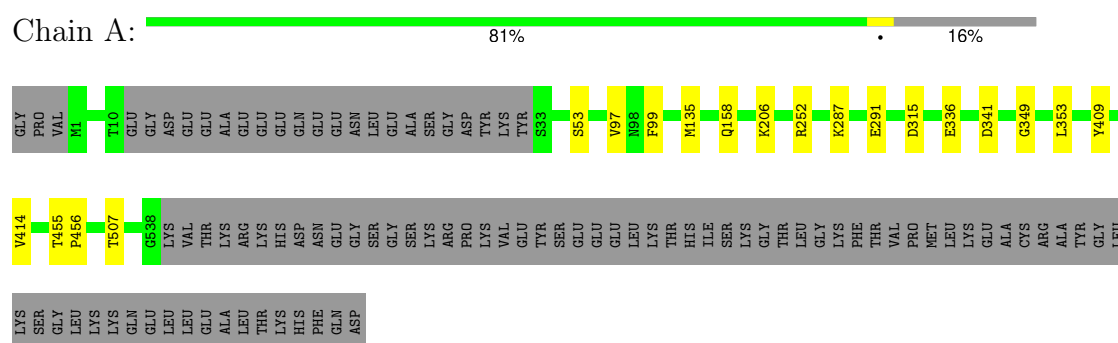


Mol	Chain	Residues	Atoms					AltConf
13	M	1	Total	C	N	O	P	0
			30	10	6	11	3	

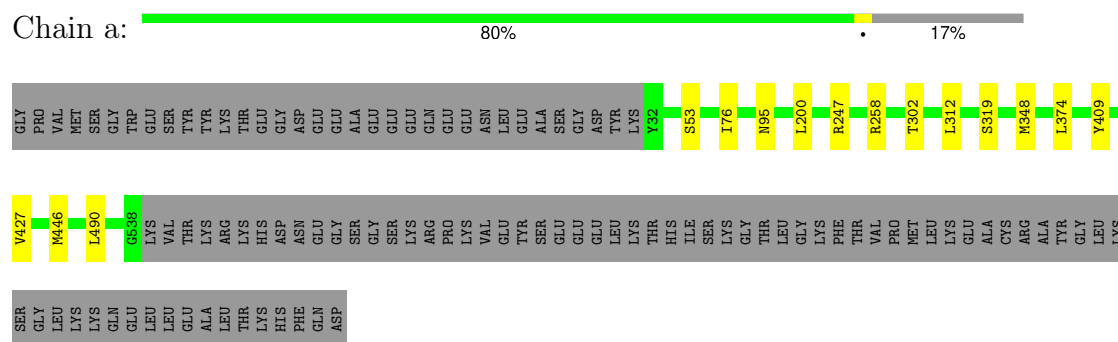
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

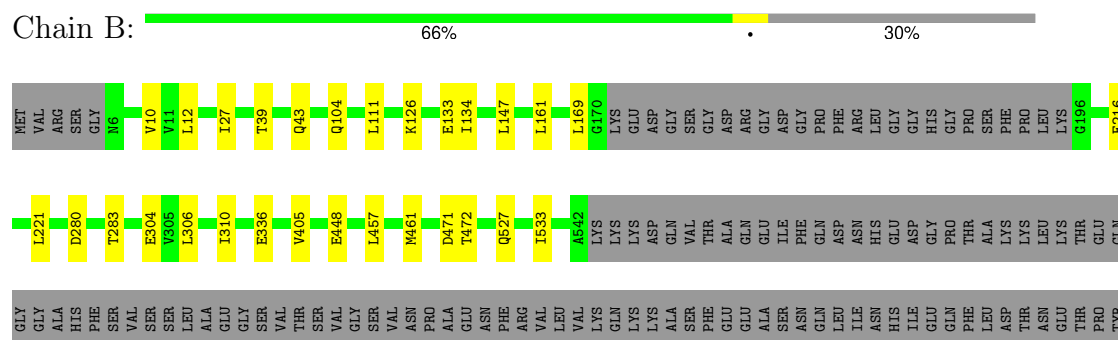
- Molecule 1: X-ray repair cross-complementing protein 6

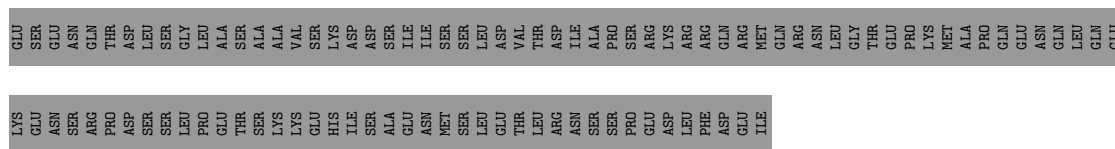


- Molecule 1: X-ray repair cross-complementing protein 6

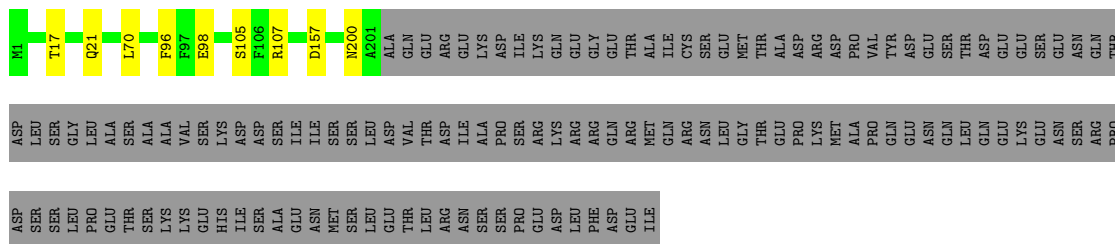


- Molecule 2: X-ray repair cross-complementing protein 5

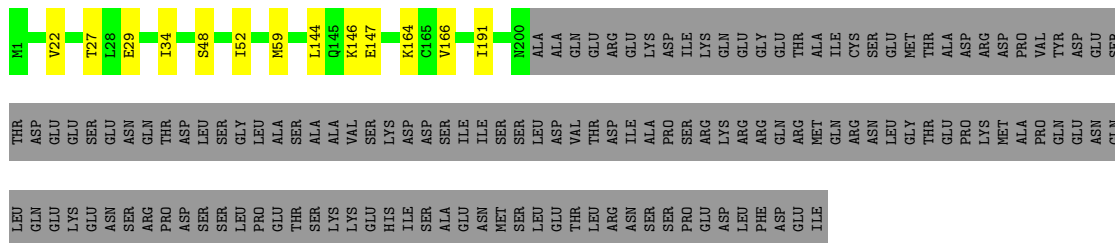




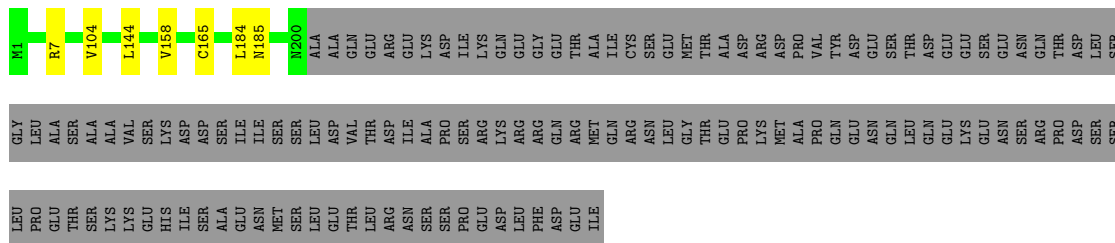
- Molecule 4: DNA repair protein XRCC4



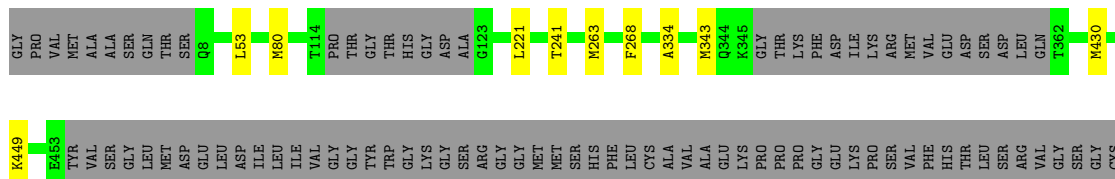
- Molecule 4: DNA repair protein XRCC4



- Molecule 4: DNA repair protein XRCC4



- Molecule 5: DNA ligase 4



ALA	PRO	LYS	MET	LYS	VAL	ILE	GLY	ILE	ILE	GLU	HIS	LEU	LYS	ALA	ASN	PRO	ASN	THR	ASN	VAL	ASN	K654	V690	V700	S794	D798	R837	I840	E844 L845	A850	K857	L910	TTF
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- Molecule 5: DNA ligase 4

Chain f: 26% 72%

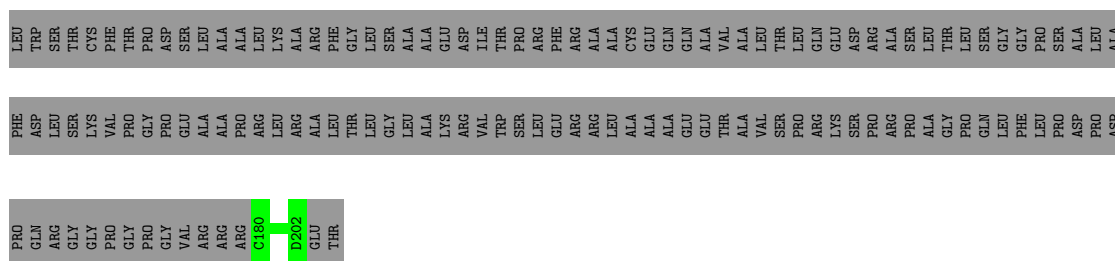
[illegible]

V662	S672	Q673	L678	A683	L726	C747	T750	E757	D758	S764	Y765	L771	N772	Y777	T840	F847	H848	H869	V872	L910	T916
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- Molecule 6: Protein PAXX

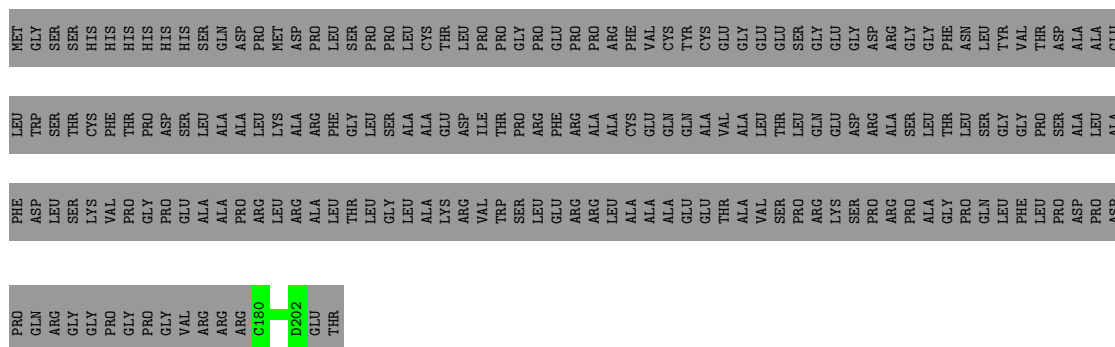
Chain G:  11% 89%

NET	GLY	SER	SER	HIS	HIS	HIS	HIS	HIS	SER	GLN	ASP	PRO	NET	ASP	PRO	LEU	SER	THR	LEU	PRO	PRO	GLY	PRO	GLU	PRO	PRO	ARG	PHE	VAL	CYS	TYR	CYS	GLU	GLY	GLY	GLU	GLU	SER	GLY	GLY	GLY	GLY	ASP	ASP	ARG	GLY	PHE	ASN	LEU	TYR	VAL	THR	ASP	ALA	ALA	THR
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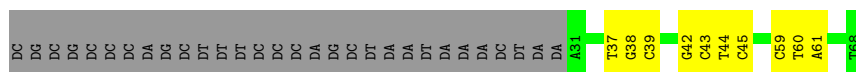
- Molecule 6: Protein PAXX

Chain H: 11% 89%



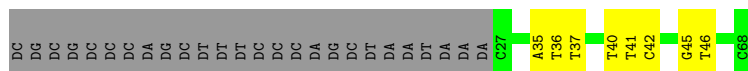
- Molecule 7: DNA (38-MER)

Chain I: 41% 15% 44%



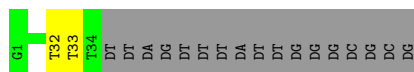
- Molecule 8: DNA (42-MER)

Chain J:  50% 12% 38%



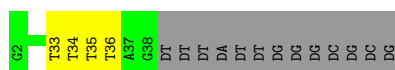
- Molecule 9: DNA (34-MER)

Chain K:  63% 3% 33%



- Molecule 10: DNA (37-MER)

Chain L:  66% 8% 26%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	671447	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47.42	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.586	Depositor
Minimum map value	-0.200	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	426.496, 426.496, 426.496	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.833, 0.833, 0.833	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: DZ4, MG

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	0.09	0/4252	0.22	0/5728
1	a	0.08	0/4175	0.21	0/5626
2	B	0.09	0/4196	0.24	0/5661
2	b	0.08	0/4181	0.21	0/5642
3	C	0.08	0/1926	0.23	0/2610
3	c	0.09	0/1907	0.23	0/2584
4	D	0.11	0/1662	0.24	0/2235
4	E	0.12	0/1657	0.24	0/2228
4	d	0.11	0/1652	0.22	0/2221
4	e	0.10	0/1652	0.22	0/2221
5	F	0.08	0/5617	0.21	0/7568
5	f	0.09	0/2118	0.23	0/2862
6	G	0.07	0/169	0.18	0/226
6	H	0.06	0/169	0.17	0/226
7	I	0.17	0/861	0.42	0/1325
8	J	0.17	0/960	0.44	0/1478
9	K	0.19	0/790	0.44	0/1219
10	L	0.19	0/855	0.45	0/1317
11	M	0.10	0/3468	0.21	0/4695
11	m	0.09	0/749	0.24	0/1017
All	All	0.10	0/43016	0.25	0/58689

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4169	0	4230	11	0
1	a	4094	0	4161	3	0
2	B	4115	0	4156	19	0
2	b	4100	0	4141	9	0
3	C	1887	0	1901	5	0
3	c	1869	0	1882	7	0
4	D	1633	0	1625	4	0
4	E	1628	0	1620	2	0
4	d	1623	0	1615	6	0
4	e	1623	0	1615	6	0
5	F	5503	0	5504	13	0
5	f	2069	0	2011	9	0
6	G	165	0	160	0	0
6	H	165	0	160	0	0
7	I	771	0	432	6	0
8	J	857	0	475	5	0
9	K	702	0	384	1	0
10	L	763	0	420	4	0
11	M	3389	0	3359	9	0
11	m	732	0	726	1	0
12	M	1	0	0	0	0
13	M	30	0	13	0	0
All	All	41888	0	40590	108	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 1.

All (108) 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)
4:d:144:LEU:HB3	4:e:144:LEU:HD22	1.70	0.73
5:f:773:GLN:O	5:f:777:VAL:HG23	1.89	0.72
5:F:263:MET:HE2	5:F:268:PHE:CD1	2.32	0.64
8:J:36:DT:H2'	8:J:37:DT:H71	1.80	0.64
3:c:18:LEU:O	3:c:18:LEU:HD12	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:457:LEU:HD22	2:B:533:ILE:HD12	1.81	0.62
4:D:66:TYR:O	4:D:70:LEU:HD23	2.03	0.58
1:A:353:LEU:HD21	1:A:414:VAL:HG13	1.85	0.58
2:b:55:ALA:HB2	2:b:83:LEU:HD22	1.87	0.57
2:B:39:THR:O	2:B:43:GLN:HG3	2.05	0.57
5:f:678:LEU:HD22	5:f:726:LEU:HD23	1.91	0.52
5:F:334:ALA:HB1	5:F:343:MET:HE2	1.92	0.52
5:f:759:ASP:C	5:f:759:ASP:OD1	2.52	0.52
4:d:166:VAL:HG23	5:f:847:PHE:HA	1.92	0.51
4:e:158:VAL:HG22	5:f:840:ILE:HD13	1.93	0.51
3:C:100:VAL:HG13	3:C:101:ALA:H	1.76	0.50
4:e:144:LEU:O	4:e:144:LEU:HD23	2.12	0.50
10:L:35:DT:H2'	10:L:36:DT:H72	1.94	0.49
4:D:178:LYS:O	4:D:181:ILE:HG13	2.13	0.49
11:M:189:LEU:HD13	11:M:193:VAL:HG23	1.94	0.49
1:a:446:MET:HE1	2:b:264:TYR:HB2	1.95	0.49
4:d:164:LYS:HD2	4:d:164:LYS:C	2.38	0.48
2:B:133:GLU:C	2:B:134:ILE:HD13	2.38	0.48
5:F:887:LYS:N	5:F:887:LYS:HD3	2.28	0.48
2:b:15:ASP:OD1	2:b:15:ASP:C	2.57	0.47
2:b:457:LEU:HD22	2:b:533:ILE:CD1	2.44	0.47
2:B:471:ASP:O	2:B:472:THR:HG23	2.15	0.47
5:F:844:GLU:OE1	5:F:844:GLU:HA	2.14	0.47
8:J:35:DA:H2'	8:J:36:DT:H71	1.97	0.47
11:M:199:LEU:HD11	11:M:213:VAL:HG11	1.96	0.47
2:B:448:GLU:H	2:B:448:GLU:CD	2.23	0.47
1:A:315:ASP:OD1	1:A:315:ASP:C	2.58	0.46
3:C:138:PRO:O	3:C:142:MET:HG3	2.16	0.46
5:F:80:MET:HA	5:F:80:MET:HE2	1.98	0.46
2:B:104:GLN:HA	2:B:104:GLN:OE1	2.16	0.46
2:B:134:ILE:HD13	2:B:134:ILE:N	2.31	0.46
11:M:36:GLU:N	11:M:37:PRO:CD	2.78	0.46
3:c:9:LEU:O	3:c:222:THR:HG21	2.16	0.46
11:m:35:VAL:HG23	11:m:35:VAL:O	2.16	0.46
4:d:22:VAL:HG12	4:d:34:ILE:HG22	1.97	0.45
11:M:343:GLU:CG	11:M:343:GLU:O	2.64	0.45
8:J:45:DG:H2'	8:J:46:DT:H71	1.97	0.45
1:a:76:ILE:HG21	1:a:247:ARG:HA	1.98	0.45
2:B:336:GLU:N	2:B:336:GLU:OE2	2.50	0.45
10:L:34:DT:H2'	10:L:35:DT:H72	1.99	0.45
3:c:67:ALA:CB	4:e:104:VAL:HG12	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:40:DT:C6	8:J:41:DT:H72	2.52	0.45
1:A:158:GLN:N	1:A:158:GLN:OE1	2.50	0.45
7:I:42:DG:C4	7:I:43:DC:C5	3.05	0.45
4:d:27:THR:HG22	4:d:29:GLU:H	1.83	0.44
5:F:700:VAL:HG23	5:F:700:VAL:O	2.16	0.44
2:b:381:ILE:HG22	2:b:412:ILE:HD11	1.99	0.44
8:J:41:DT:C2	8:J:42:DC:C5	3.06	0.44
2:B:280:ASP:OD2	2:B:283:THR:HG22	2.18	0.43
3:C:40:ASP:OD1	3:C:40:ASP:C	2.61	0.43
3:c:67:ALA:HB1	4:e:104:VAL:HG12	2.00	0.43
3:C:100:VAL:HG13	3:C:101:ALA:N	2.32	0.43
7:I:44:DT:C2	7:I:45:DC:C5	3.06	0.43
7:I:60:DT:C2	7:I:61:DA:N7	2.87	0.43
10:L:33:DT:H2'	10:L:34:DT:H72	2.00	0.43
4:D:1:MET:HE2	4:D:1:MET:HA	2.00	0.43
1:A:287:LYS:HD2	2:B:310:ILE:HG21	2.01	0.43
2:B:10:VAL:HG12	2:B:12:LEU:HD12	2.01	0.43
2:B:221:LEU:C	2:B:221:LEU:HD13	2.44	0.43
5:F:430:MET:HE2	5:F:449:LYS:HA	2.01	0.43
5:f:757:GLU:OE1	5:f:757:GLU:HA	2.19	0.43
3:c:79:LEU:O	3:c:79:LEU:HD23	2.19	0.42
2:b:264:TYR:O	2:b:362:LEU:HD23	2.19	0.42
1:A:341:ASP:N	1:A:341:ASP:OD1	2.51	0.42
11:M:351:MET:HE2	11:M:351:MET:CA	2.48	0.42
10:L:34:DT:C2'	10:L:35:DT:H72	2.50	0.42
1:A:507:THR:HG23	2:B:405:VAL:CG2	2.50	0.42
11:M:226:GLU:HA	11:M:226:GLU:OE1	2.19	0.42
5:F:53:LEU:HD23	5:F:53:LEU:O	2.19	0.42
1:A:336:GLU:CD	1:A:336:GLU:C	2.88	0.42
2:B:527:GLN:HA	2:B:527:GLN:OE1	2.20	0.42
4:D:157:ASP:OD1	4:D:157:ASP:C	2.62	0.42
7:I:37:DT:C2	7:I:38:DG:C8	3.07	0.42
5:F:80:MET:HE2	5:F:80:MET:CA	2.50	0.42
1:A:291:GLU:HG3	5:F:690:VAL:HG12	2.01	0.42
2:B:216:GLU:CD	2:B:216:GLU:C	2.88	0.42
11:M:343:GLU:O	11:M:343:GLU:HG2	2.19	0.42
2:b:87:ASP:OD1	2:b:87:ASP:N	2.53	0.41
2:b:138:LEU:HD11	2:b:165:LEU:HD21	2.02	0.41
5:f:771:LEU:HD12	5:f:771:LEU:O	2.20	0.41
1:A:455:THR:HG22	1:A:456:PRO:HD2	2.01	0.41
4:E:96:PHE:C	4:E:96:PHE:CD1	2.98	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:e:158:VAL:HG13	5:f:840:ILE:HD11	2.01	0.41
3:C:152:GLU:OE2	3:c:197:LYS:HE3	2.21	0.41
7:I:38:DG:C4	7:I:39:DC:C5	3.09	0.41
9:K:32:DT:H2'	9:K:33:DT:H72	2.03	0.41
11:M:173:GLU:HA	11:M:173:GLU:OE1	2.20	0.41
2:B:147:LEU:HD22	2:B:147:LEU:N	2.36	0.41
2:B:304:GLU:OE2	2:B:304:GLU:C	2.63	0.41
7:I:59:DC:C2'	7:I:60:DT:H71	2.50	0.41
1:a:258:ARG:HE	1:a:374:LEU:HD11	1.85	0.41
5:f:869:HIS:O	5:f:872:VAL:HG22	2.19	0.41
11:M:26:ARG:HH11	11:M:26:ARG:HG3	1.85	0.41
1:A:97:VAL:HG11	1:A:99:PHE:CE1	2.56	0.41
5:F:794:SER:O	5:F:798:ASP:OD2	2.38	0.41
5:F:837:ARG:O	5:F:840:ILE:HG22	2.21	0.41
3:c:149:GLN:O	3:c:153:LEU:HD23	2.21	0.41
4:d:48:SER:O	4:d:52:ILE:HG22	2.21	0.41
5:F:845:LEU:O	5:F:850:ALA:HB3	2.21	0.40
4:E:98:GLU:HB3	4:E:107:ARG:HA	2.03	0.40
2:B:27:ILE:O	2:B:27:ILE:HG22	2.21	0.40
2:b:11:VAL:HG21	2:b:118:ILE:HG13	2.02	0.40
1:A:349:GLY:HA2	2:B:461:MET:HE2	2.04	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	512/612 (84%)	500 (98%)	12 (2%)	0	100	100
1	a	505/612 (82%)	496 (98%)	9 (2%)	0	100	100
2	B	509/732 (70%)	500 (98%)	9 (2%)	0	100	100
2	b	507/732 (69%)	503 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	234/302 (78%)	224 (96%)	10 (4%)	0	100	100
3	c	231/302 (76%)	223 (96%)	8 (4%)	0	100	100
4	D	200/336 (60%)	193 (96%)	7 (4%)	0	100	100
4	E	199/336 (59%)	195 (98%)	4 (2%)	0	100	100
4	d	198/336 (59%)	196 (99%)	2 (1%)	0	100	100
4	e	198/336 (59%)	192 (97%)	6 (3%)	0	100	100
5	F	671/914 (73%)	657 (98%)	14 (2%)	0	100	100
5	f	253/914 (28%)	244 (96%)	9 (4%)	0	100	100
6	G	21/218 (10%)	21 (100%)	0	0	100	100
6	H	21/218 (10%)	21 (100%)	0	0	100	100
11	M	420/512 (82%)	404 (96%)	16 (4%)	0	100	100
11	m	94/512 (18%)	93 (99%)	1 (1%)	0	100	100
All	All	4773/7924 (60%)	4662 (98%)	111 (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	468/550 (85%)	463 (99%)	5 (1%)	70	90
1	a	460/550 (84%)	450 (98%)	10 (2%)	47	79
2	B	464/649 (72%)	459 (99%)	5 (1%)	70	90
2	b	463/649 (71%)	459 (99%)	4 (1%)	75	92
3	C	210/264 (80%)	202 (96%)	8 (4%)	28	62
3	c	208/264 (79%)	205 (99%)	3 (1%)	62	87
4	D	180/303 (59%)	172 (96%)	8 (4%)	24	56
4	E	180/303 (59%)	174 (97%)	6 (3%)	33	67
4	d	180/303 (59%)	176 (98%)	4 (2%)	47	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	e	180/303 (59%)	176 (98%)	4 (2%)	47	79
5	F	611/810 (75%)	609 (100%)	2 (0%)	91	97
5	f	231/810 (28%)	223 (96%)	8 (4%)	31	65
6	G	18/173 (10%)	18 (100%)	0	100	100
6	H	18/173 (10%)	18 (100%)	0	100	100
11	M	360/428 (84%)	357 (99%)	3 (1%)	79	93
11	m	77/428 (18%)	74 (96%)	3 (4%)	27	61
All	All	4308/6960 (62%)	4235 (98%)	73 (2%)	56	84

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	SER
1	A	135	MET
1	A	206	LYS
1	A	252	ARG
1	A	409	TYR
2	B	111	LEU
2	B	126	LYS
2	B	161	LEU
2	B	169	LEU
2	B	306	LEU
3	C	16	LEU
3	C	41	LEU
3	C	49	VAL
3	C	78	ASN
3	C	107	ARG
3	C	110	SER
3	C	167	TYR
3	C	182	GLU
4	D	34	ILE
4	D	37	THR
4	D	40	HIS
4	D	66	TYR
4	D	84	TYR
4	D	87	ASN
4	D	166	VAL
4	D	184	LEU
4	E	17	THR
4	E	21	GLN

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Mol	Chain	Res	Type
4	E	70	LEU
4	E	105	SER
4	E	157	ASP
4	E	200	ASN
5	F	221	LEU
5	F	241	THR
11	M	25	THR
11	M	68	HIS
11	M	476	GLU
1	a	53	SER
1	a	95	ASN
1	a	200	LEU
1	a	302	THR
1	a	312	LEU
1	a	319	SER
1	a	348	MET
1	a	409	TYR
1	a	427	VAL
1	a	490	LEU
2	b	83	LEU
2	b	87	ASP
2	b	246	HIS
2	b	339	CYS
3	c	18	LEU
3	c	26	LYS
3	c	49	VAL
4	d	59	MET
4	d	146	LYS
4	d	147	GLU
4	d	191	ILE
4	e	7	ARG
4	e	165	CYS
4	e	184	LEU
4	e	185	ASN
5	f	662	VAL
5	f	672	SER
5	f	673	GLN
5	f	747	CYS
5	f	750	THR
5	f	764	SER
5	f	765	TYR
5	f	848	HIS

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Mol	Chain	Res	Type
11	m	34	LEU
11	m	95	THR
11	m	107	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	GLN
1	A	128	GLN
1	A	264	ASN
1	A	320	GLN
2	B	45	GLN
2	B	103	GLN
2	B	404	GLN
2	B	500	HIS
2	B	509	GLN
2	B	511	HIS
2	B	517	ASN
4	D	112	ASN
4	D	141	ASN
4	E	21	GLN
5	F	200	GLN
5	F	215	HIS
5	F	227	GLN
5	F	716	ASN
5	F	869	HIS
11	M	329	HIS
1	a	65	GLN
1	a	98	ASN
1	a	320	GLN
2	b	330	GLN
3	c	42	GLN
3	c	43	GLN
3	c	133	GLN
4	d	145	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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
13	DZ4	M	502	12	28,32,32	1.18	2 (7%)	33,50,50	1.21	2 (6%)

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
13	DZ4	M	502	12	-	3/15/34/34	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	502	DZ4	C8-N7	-2.49	1.30	1.34
13	M	502	DZ4	C4-N3	-2.15	1.32	1.35

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	502	DZ4	N3-C2-N1	-4.56	122.48	128.67
13	M	502	DZ4	C2'-C1'-N9	-2.12	109.70	114.61

There are no chirality outliers.

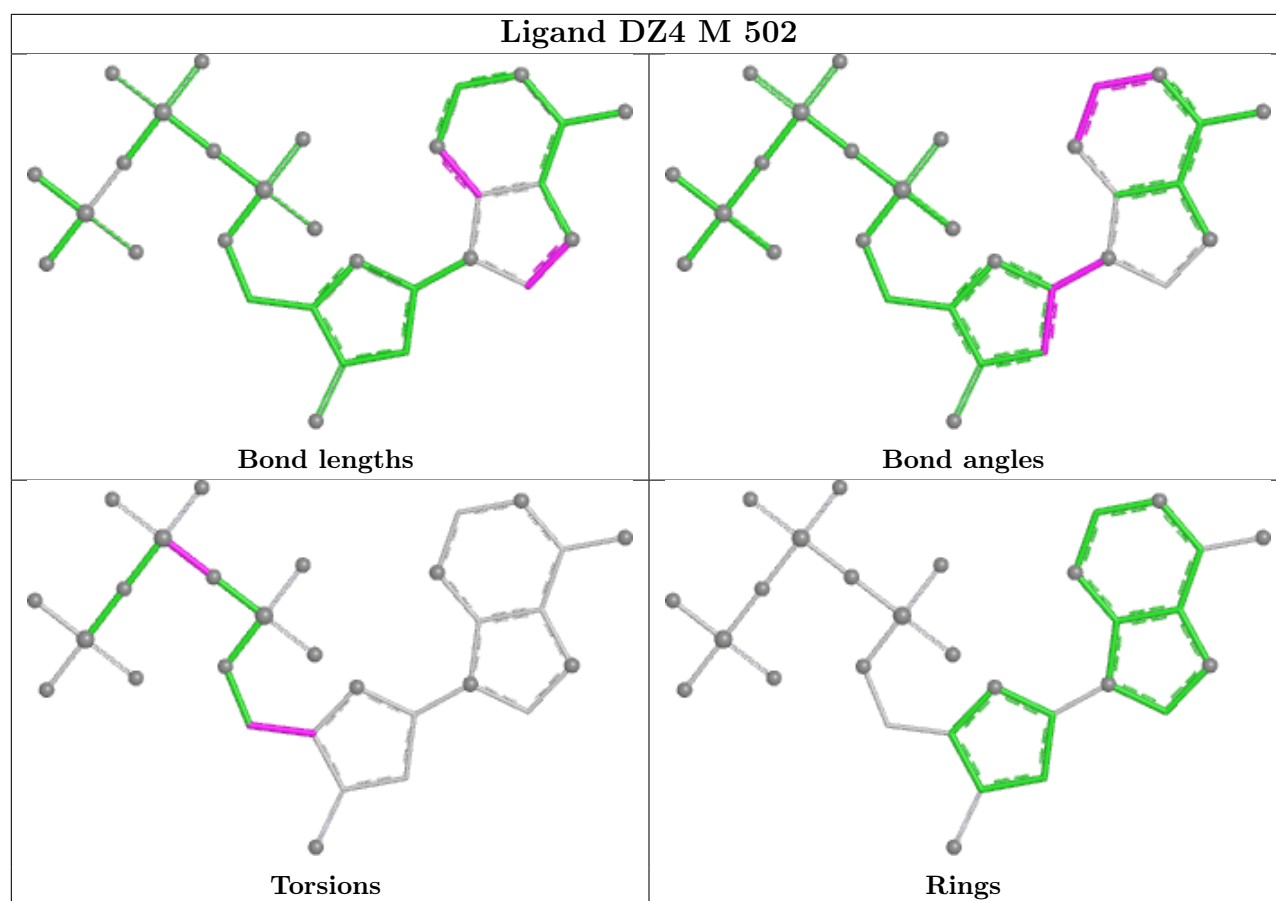
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	M	502	DZ4	O4'-C4'-C5'-O5'
13	M	502	DZ4	C3'-C4'-C5'-O5'
13	M	502	DZ4	PA-N3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

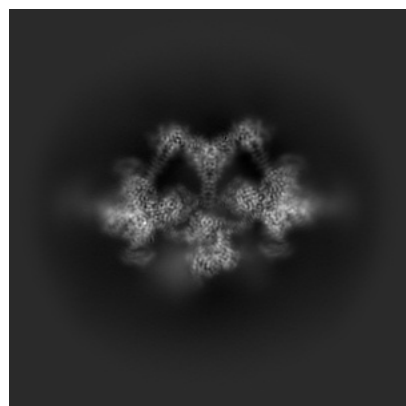
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49108. These allow visual inspection of the internal detail of the map and identification of artifacts.

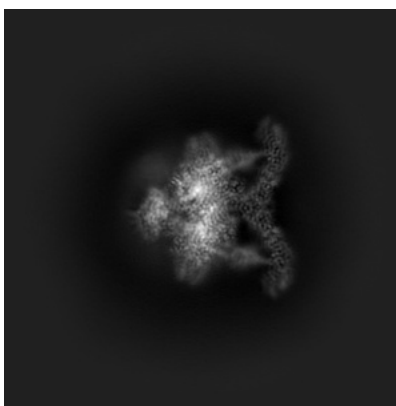
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

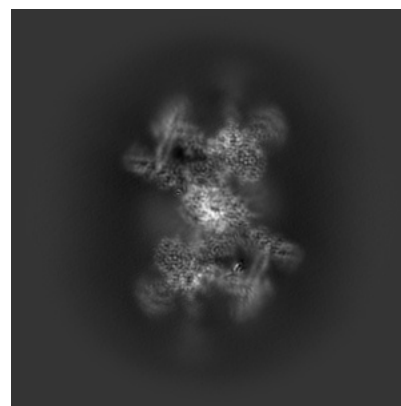
6.1.1 Primary map



X

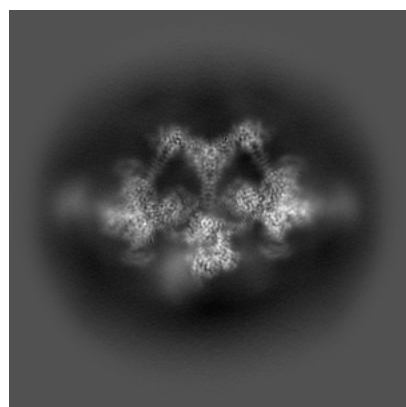


Y

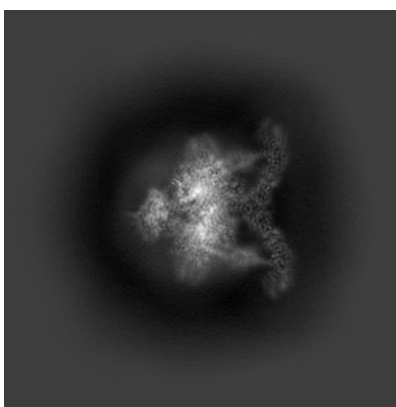


Z

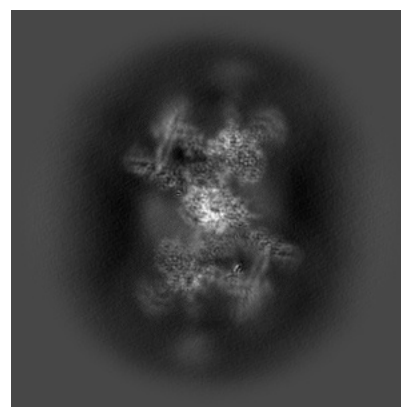
6.1.2 Raw map



X



Y



Z

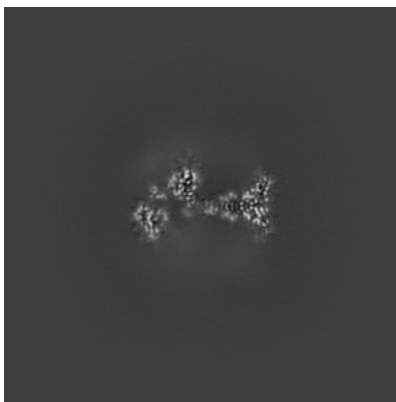
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

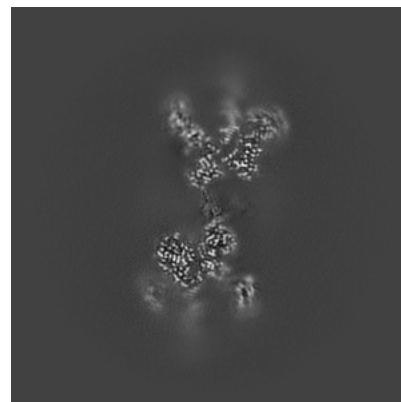
6.2.1 Primary map



X Index: 256

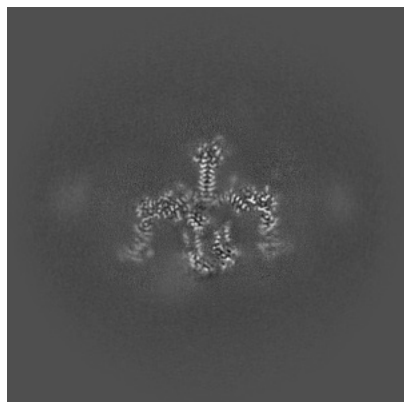


Y Index: 256

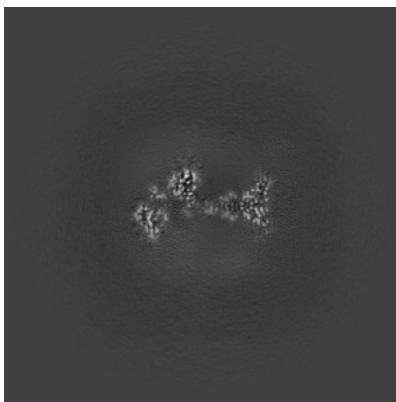


Z Index: 256

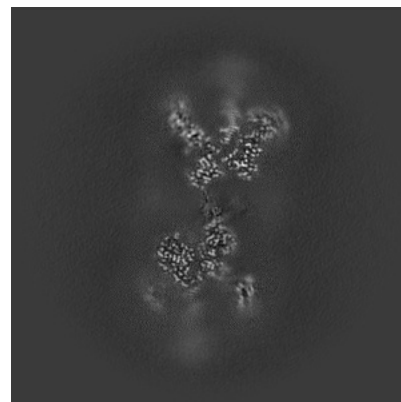
6.2.2 Raw map



X Index: 256



Y Index: 256

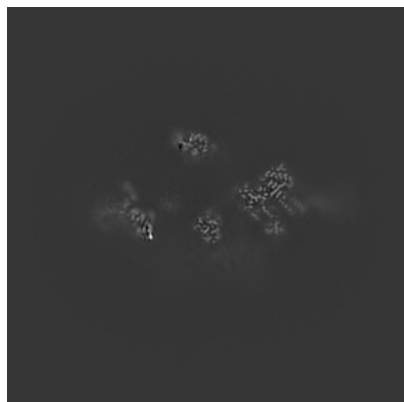


Z Index: 256

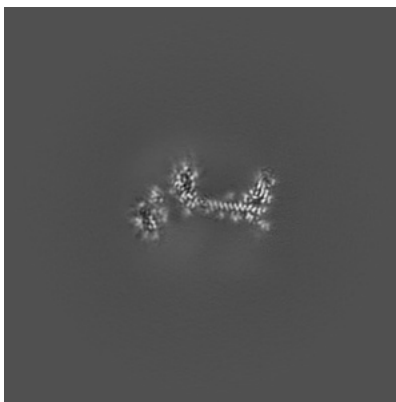
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

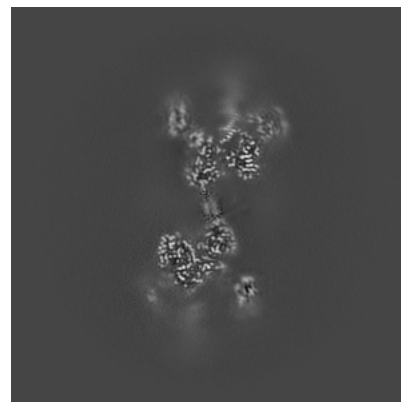
6.3.1 Primary map



X Index: 289

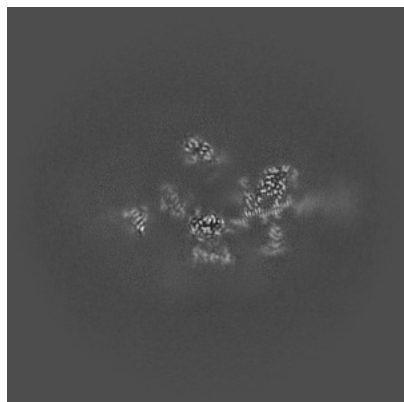


Y Index: 251

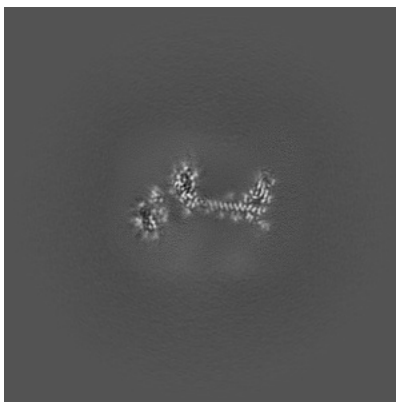


Z Index: 259

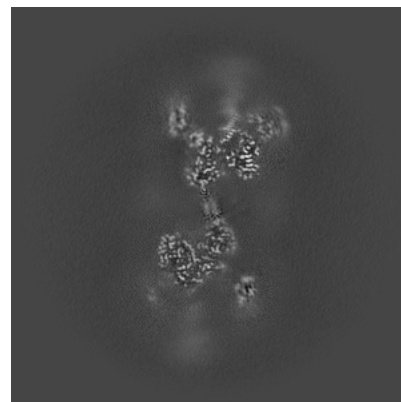
6.3.2 Raw map



X Index: 278



Y Index: 251

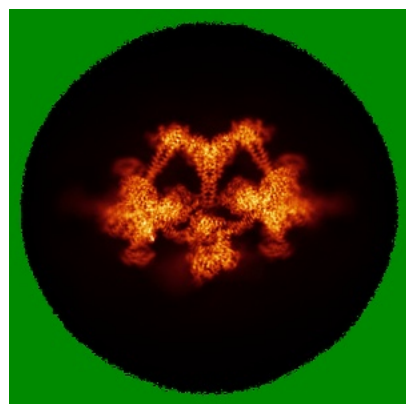


Z Index: 259

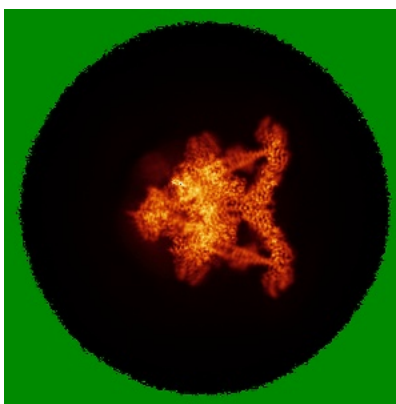
The images above show the largest variance slices of the map in three orthogonal directions.

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

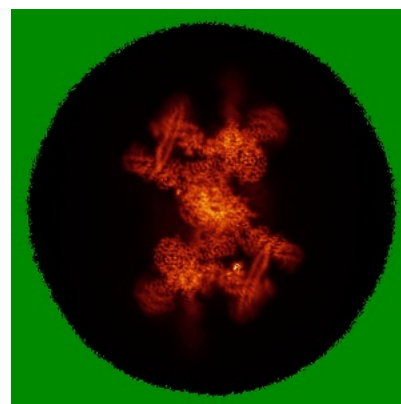
6.4.1 Primary map



X

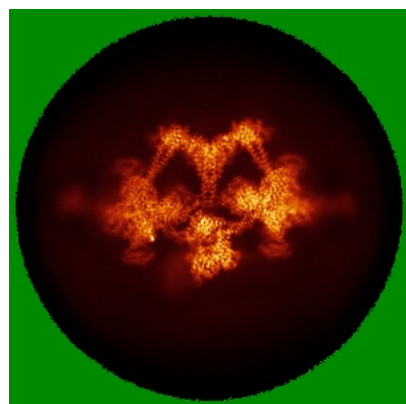


Y

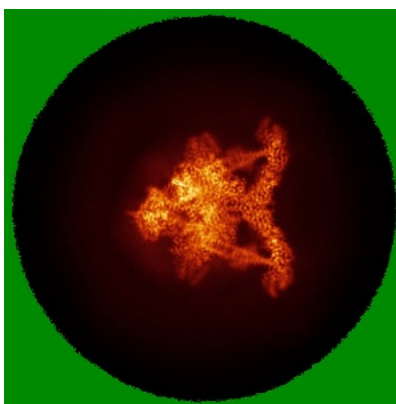


Z

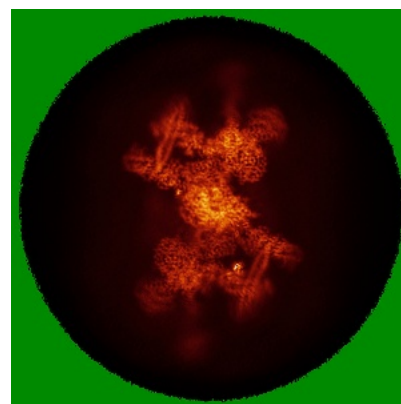
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06. 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



X



Y



Z

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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

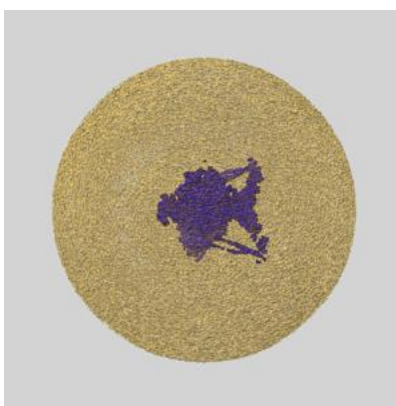
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

6.6.1 emd_49108_msk_1.map [i](#)



X



Y

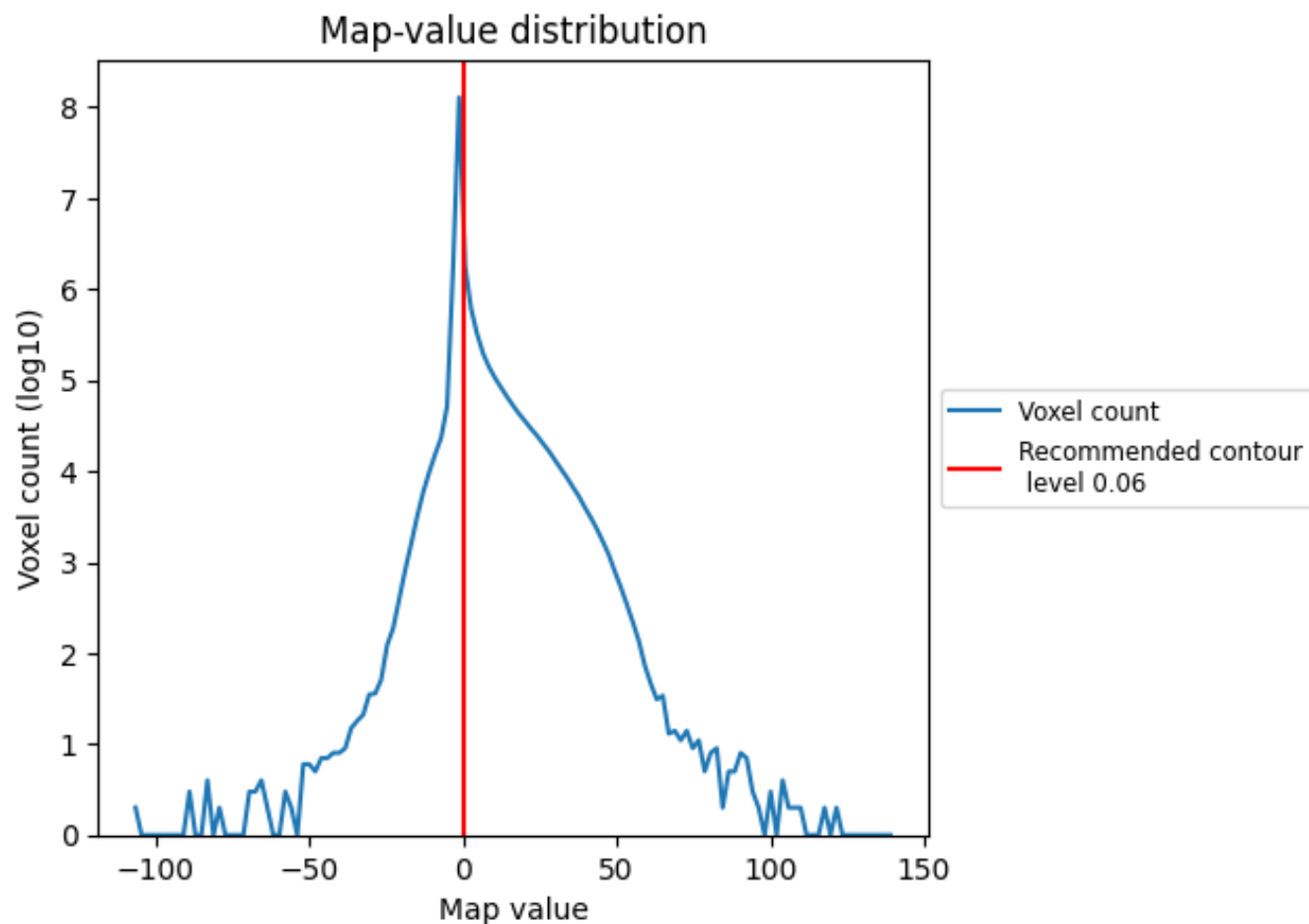


Z

7 Map analysis [i](#)

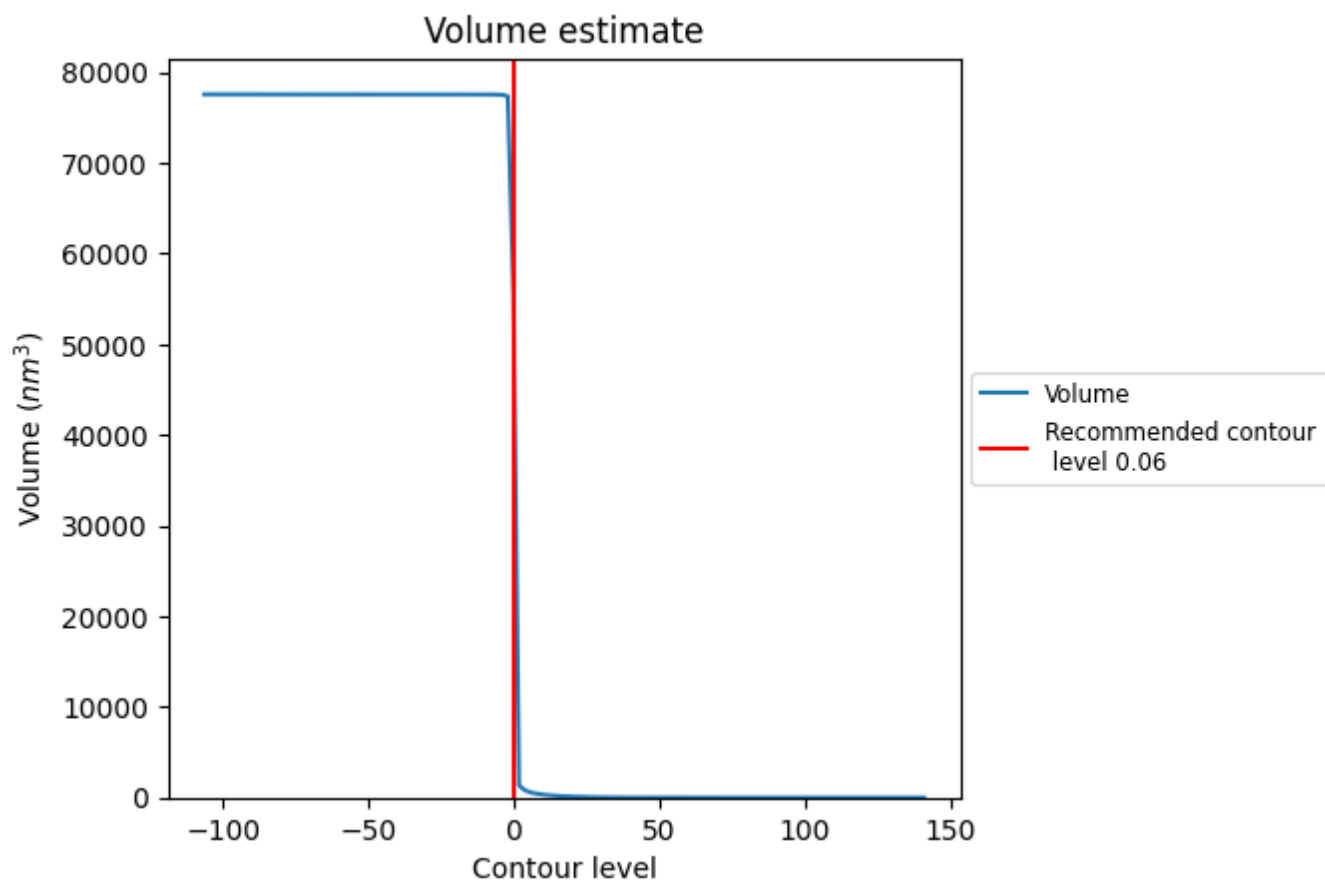
This section contains the results of statistical analysis of the map.

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.

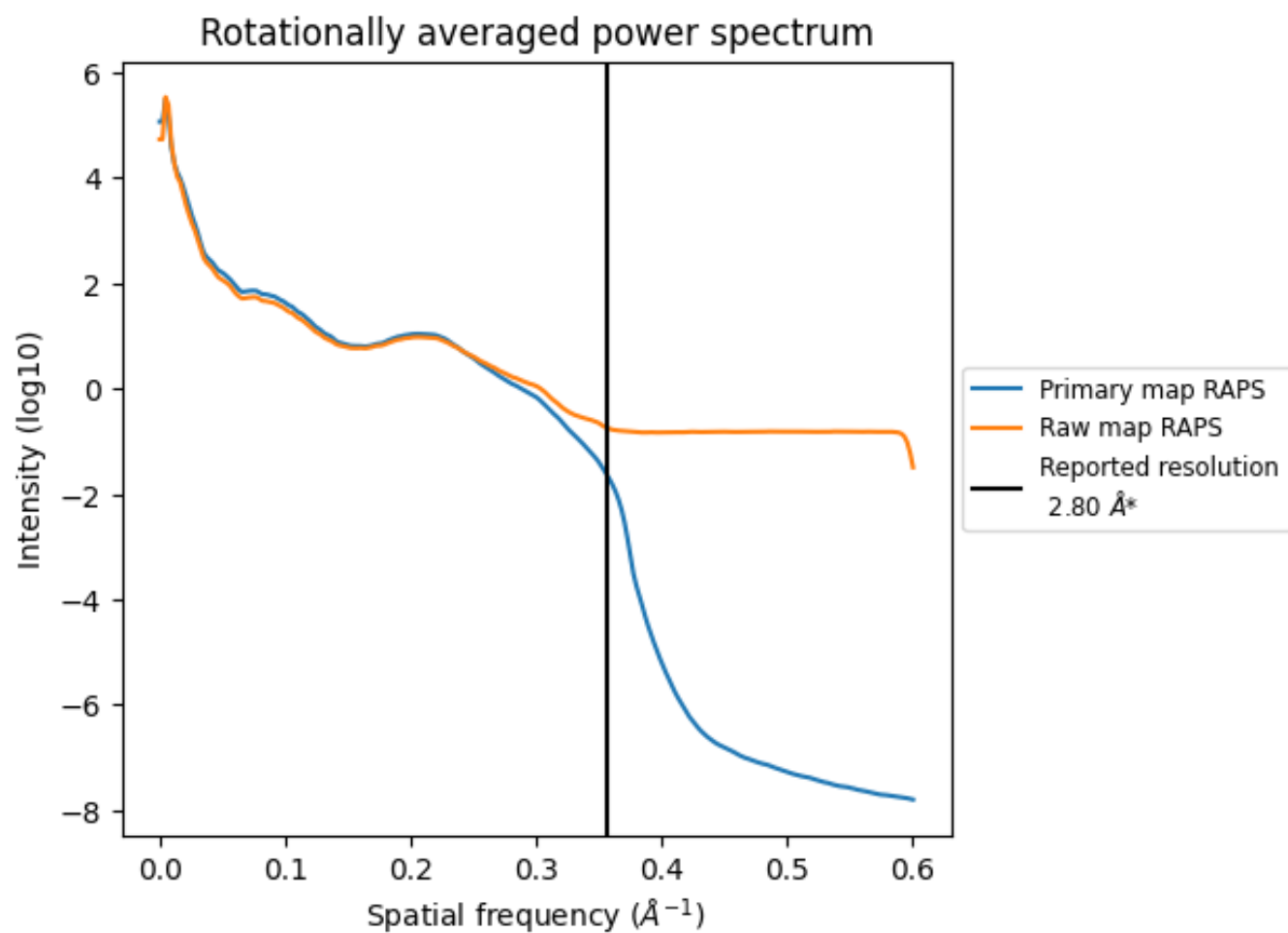
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 50910 nm³; this corresponds to an approximate mass of 45988 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 ⓘ

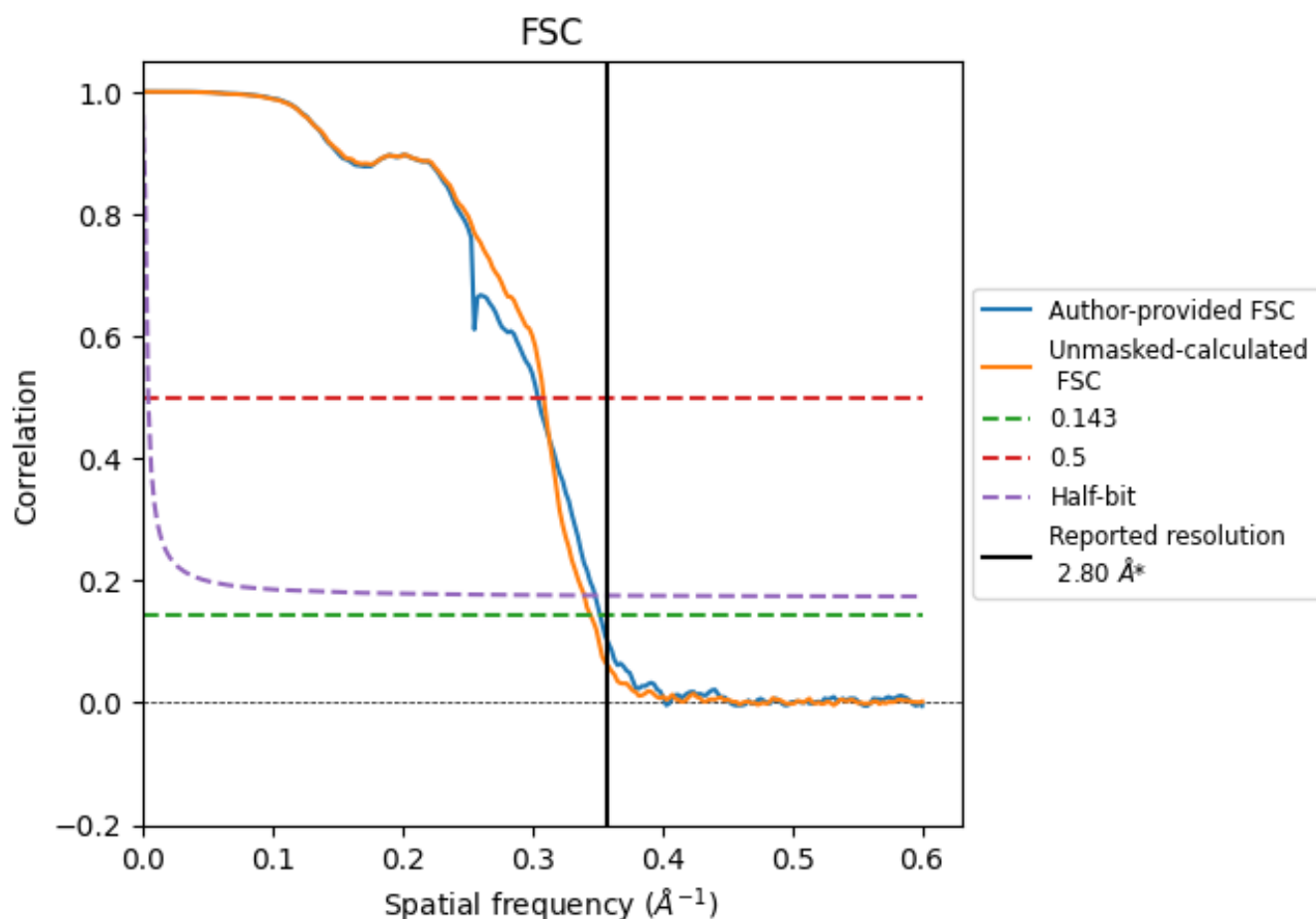


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

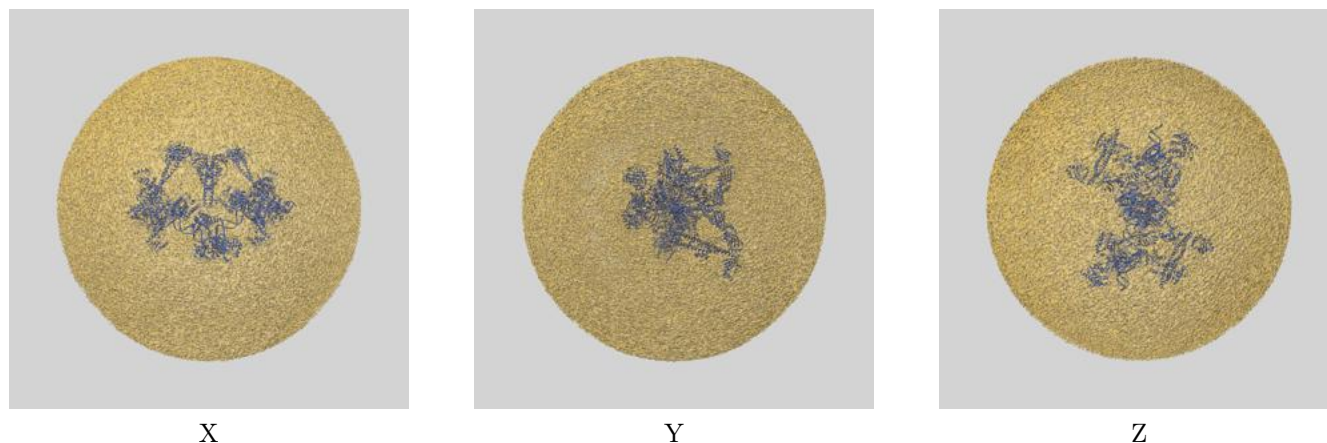
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.28	2.87
Unmasked-calculated*	2.90	3.24	2.94

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

9 Map-model fit [i](#)

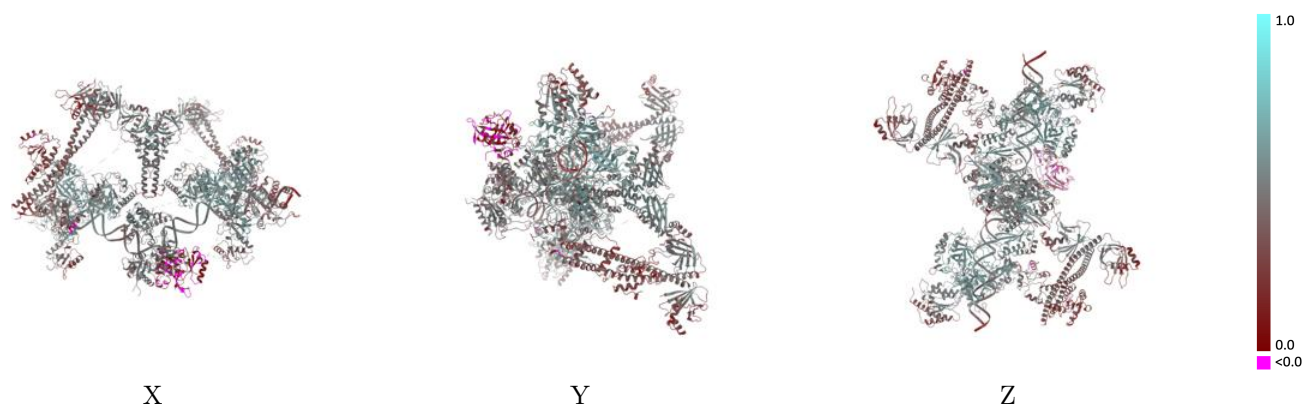
This section contains information regarding the fit between EMDB map EMD-49108 and PDB model 9N81. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



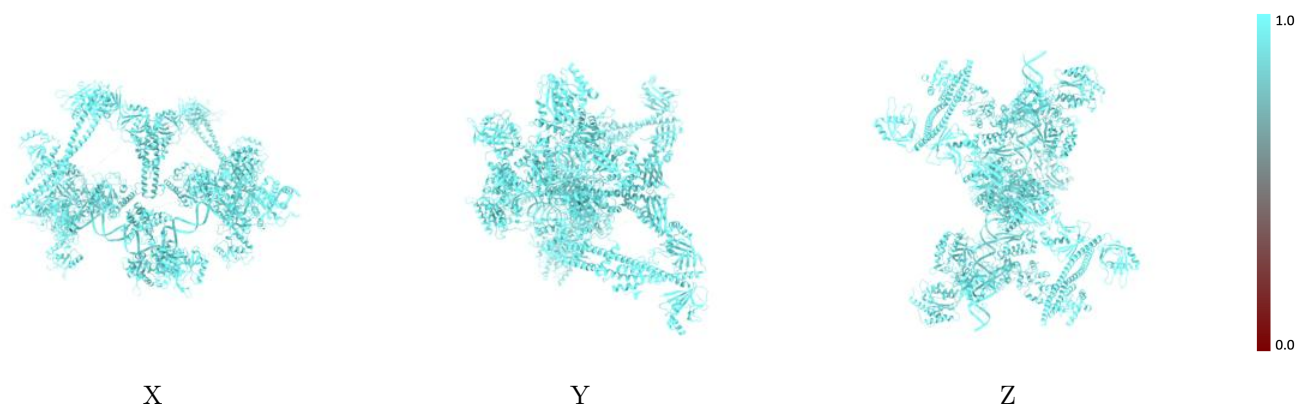
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



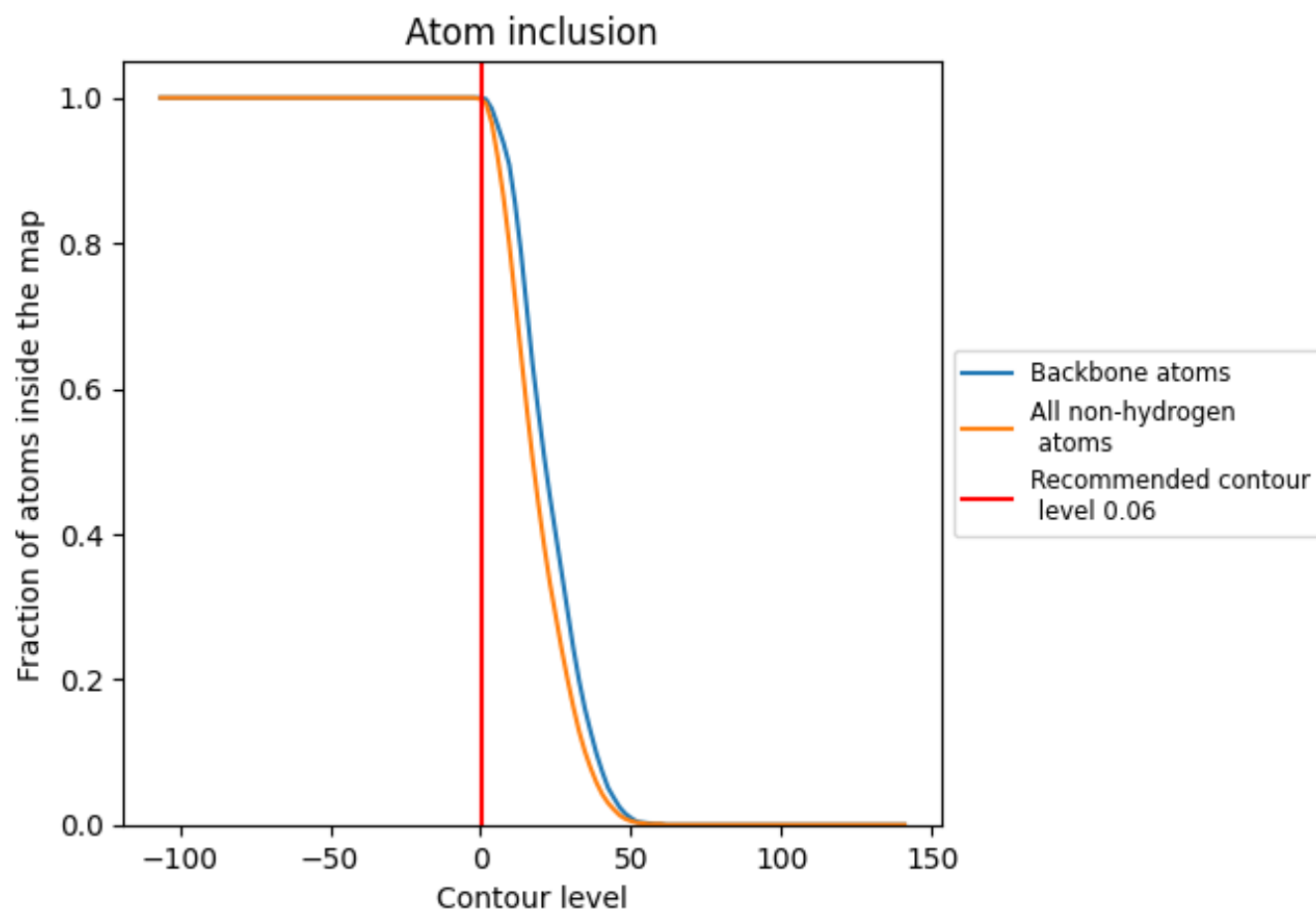
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).











































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9980	 0.4410
A	 0.9980	 0.5350
B	 1.0000	 0.4960
C	 0.9970	 0.4780
D	 0.9980	 0.3510
E	 0.9940	 0.4050
F	 0.9990	 0.3040
G	 1.0000	 0.5440
H	 0.9940	 0.5160
I	 1.0000	 0.4240
J	 1.0000	 0.4510
K	 1.0000	 0.4590
L	 1.0000	 0.4690
M	 0.9990	 0.4470
a	 0.9990	 0.5400
b	 1.0000	 0.5020
c	 0.9980	 0.4690
d	 0.9980	 0.3650
e	 0.9980	 0.4190
f	 0.9960	 0.2980
m	 0.9940	 0.3680

