



wwPDB EM Validation Summary Report ⓘ

Jul 25, 2026 – 01:14 PM EDT

PDB ID : 9Z0H / pdb_00009z0h
EMDB ID : EMD-73706
Title : Trypanosoma brucei mitochondrial RNA-editing catalytic complex 2, U-insertion (RECC2)
Authors : Liu, Y.T.; Jih, J.; Zhou, Z.H.; Aphasizhev, R.
Deposited on : 2025-11-01
Resolution : 2.79 Å(reported)

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

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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.dev133
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) : 2.50

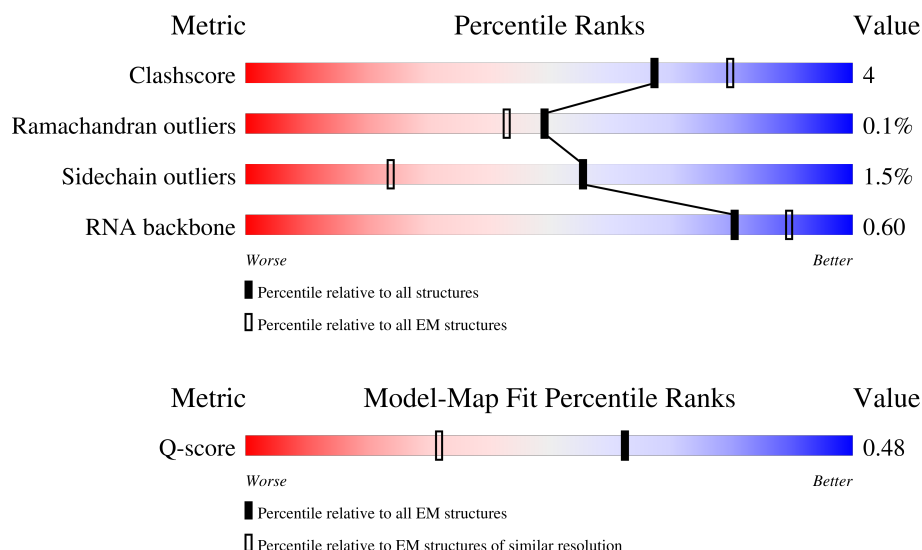
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

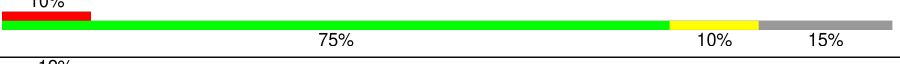
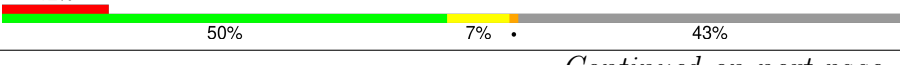
The reported resolution of this entry is 2.79 Å.

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	-
RNA backbone	8273	3508	-
Q-score	-	25397	10811 (2.29 - 3.29)

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	384	
2	B	411	
3	C	538	

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Mol	Chain	Length	Quality of chain
4	D	414	
5	E	164	
5	H	164	
5	J	164	
6	F	393	
7	G	587	
7	K	587	
8	I	218	
9	L	169	
10	O	762	
11	R	77	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 23367 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 RNA editing complex protein MP44.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	374	Total	C	N	O	S	0	0
			2991	1887	546	539	19		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	HIS	ARG	conflict	UNP Q86MV8
A	43	VAL	LEU	conflict	UNP Q86MV8
A	315	ILE	PHE	conflict	UNP Q86MV8
A	383	TYR	-	expression tag	UNP Q86MV8
A	384	ARG	-	expression tag	UNP Q86MV8

- Molecule 2 is a protein called KREPB7.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	348	Total	C	N	O	S	0	0
			2859	1838	491	506	24		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	5	THR	ALA	conflict	UNP A0A3L6L1W9

- Molecule 3 is a protein called RNA editing complex protein MP61.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	309	Total	C	N	O	S	0	0
			2532	1615	452	451	14		

- Molecule 4 is a protein called RNA editing complex protein MP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	365	Total	C	N	O	S	0	0
			2890	1808	530	536	16		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	207	PHE	LEU	conflict	UNP Q86MV9
D	228	ASP	GLY	conflict	UNP Q86MV9
D	324	ALA	VAL	conflict	UNP Q86MV9

- Molecule 5 is a protein called MP18 RNA editing complex protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	114	Total	C	N	O	S	0	0
			895	567	155	170	3		
5	H	118	Total	C	N	O	S	0	0
			931	588	165	175	3		
5	J	119	Total	C	N	O	S	0	0
			936	589	166	176	5		

- Molecule 6 is a protein called RNA-editing complex protein MP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	129	Total	C	N	O	S	0	0
			1040	663	179	192	6		

- Molecule 7 is a protein called KREPA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	178	Total	C	N	O	S	0	0
			1342	841	233	261	7		
7	K	184	Total	C	N	O	S	0	0
			1393	872	244	270	7		

- Molecule 8 is a protein called RNA editing complex protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	195	Total	C	N	O	S	0	0
			1487	914	274	287	12		

- Molecule 9 is a protein called KREPA5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	139	Total	C	N	O	S	0	0
			1115	704	201	203	7		

- Molecule 10 is a protein called RNA-editing complex protein MP81.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	142	Total	C	N	O	S	0	0
			1105	682	192	225	6		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	9	ASP	GLY	conflict	UNP Q95W15
O	12	CYS	SER	conflict	UNP Q95W15
O	35	SER	ALA	conflict	UNP Q95W15
O	76	GLY	GLU	conflict	UNP Q95W15
O	244	GLY	GLU	conflict	UNP Q95W15
O	293	SER	PRO	conflict	UNP Q95W15
O	594	SER	ASN	conflict	UNP Q95W15

- Molecule 11 is a RNA chain called tRNA-valine (anticodon AAC).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	77	Total	C	N	O	P	0	0
			1645	732	290	546	77		

- Molecule 12 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
12	B	1	Total	Zn	0
			1	1	
12	C	1	Total	Zn	0
			1	1	
12	D	1	Total	Zn	0
			1	1	
12	K	1	Total	Zn	0
			1	1	
12	O	1	Total	Zn	0
			1	1	

- Molecule 13 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
13	C	2	Total	Mg	0
			2	2	

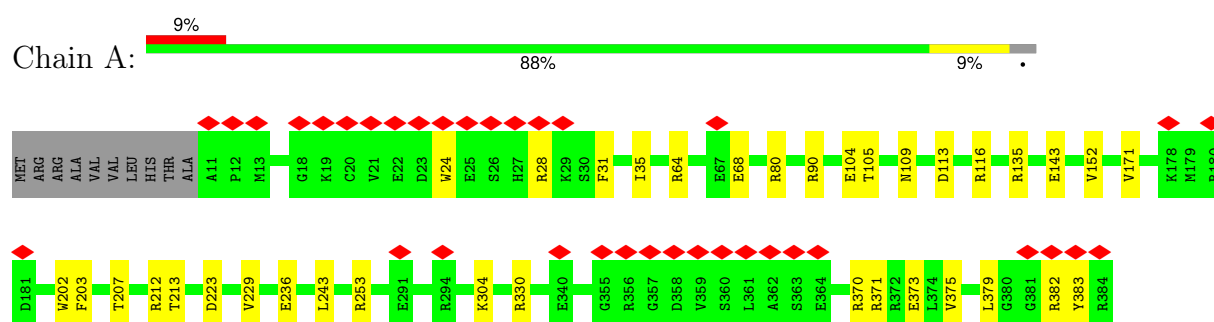
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		AltConf
14	A	56	Total	O	0
			56	56	
14	B	5	Total	O	0
			5	5	
14	C	3	Total	O	0
			3	3	
14	D	15	Total	O	0
			15	15	
14	E	16	Total	O	0
			16	16	
14	F	21	Total	O	0
			21	21	
14	G	9	Total	O	0
			9	9	
14	H	9	Total	O	0
			9	9	
14	I	1	Total	O	0
			1	1	
14	K	1	Total	O	0
			1	1	
14	R	63	Total	O	0
			63	63	

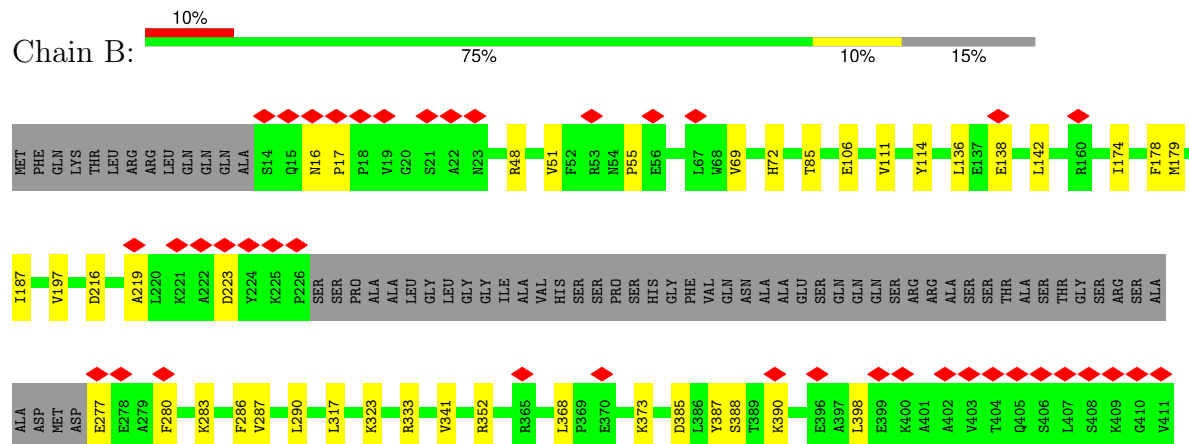
3 Residue-property plots

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.

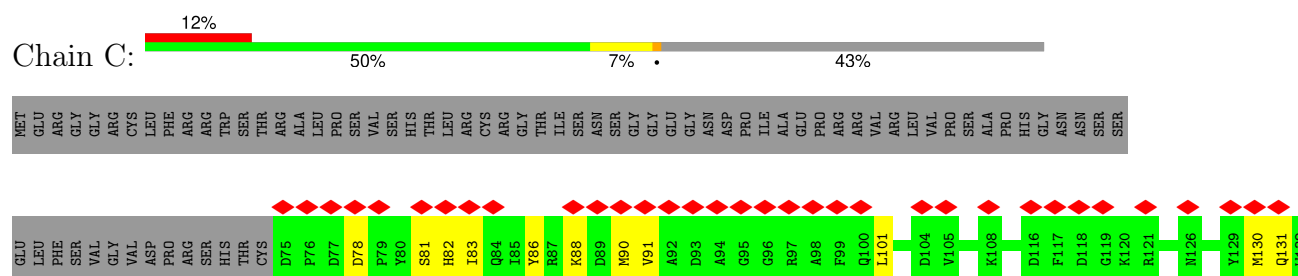
• Molecule 1: RNA editing complex protein MP44



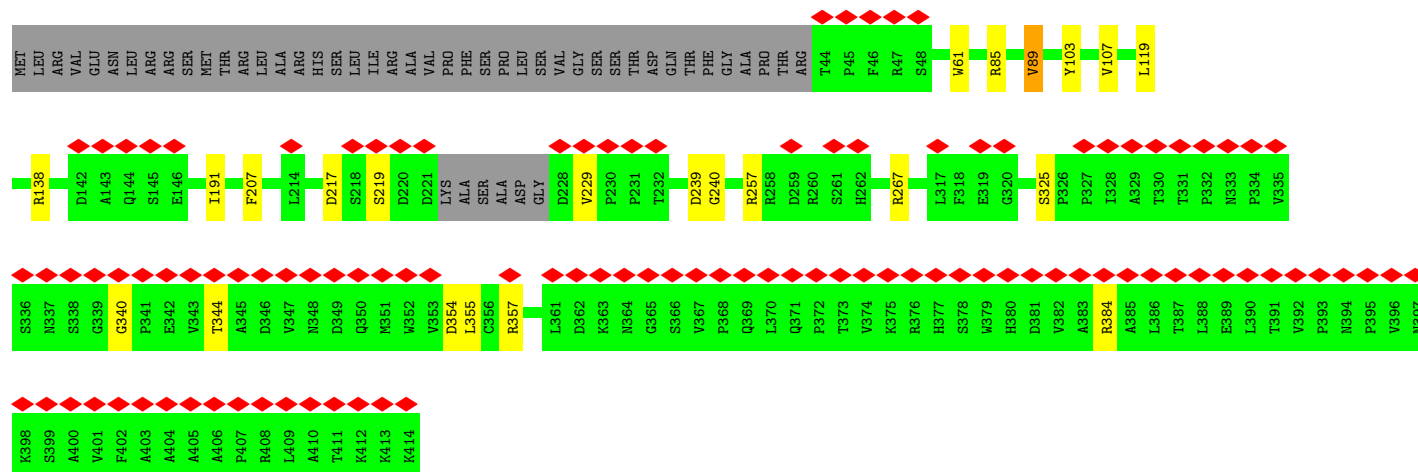
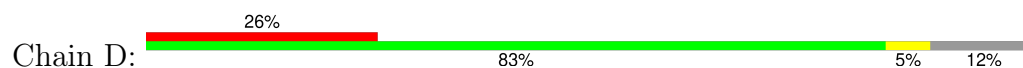
• Molecule 2: KREPB7



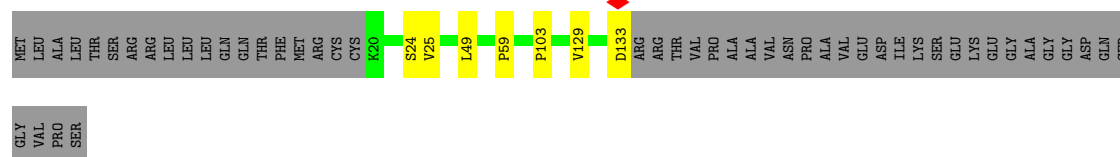
• Molecule 3: RNA editing complex protein MP61



- Molecule 4: RNA editing complex protein MP46



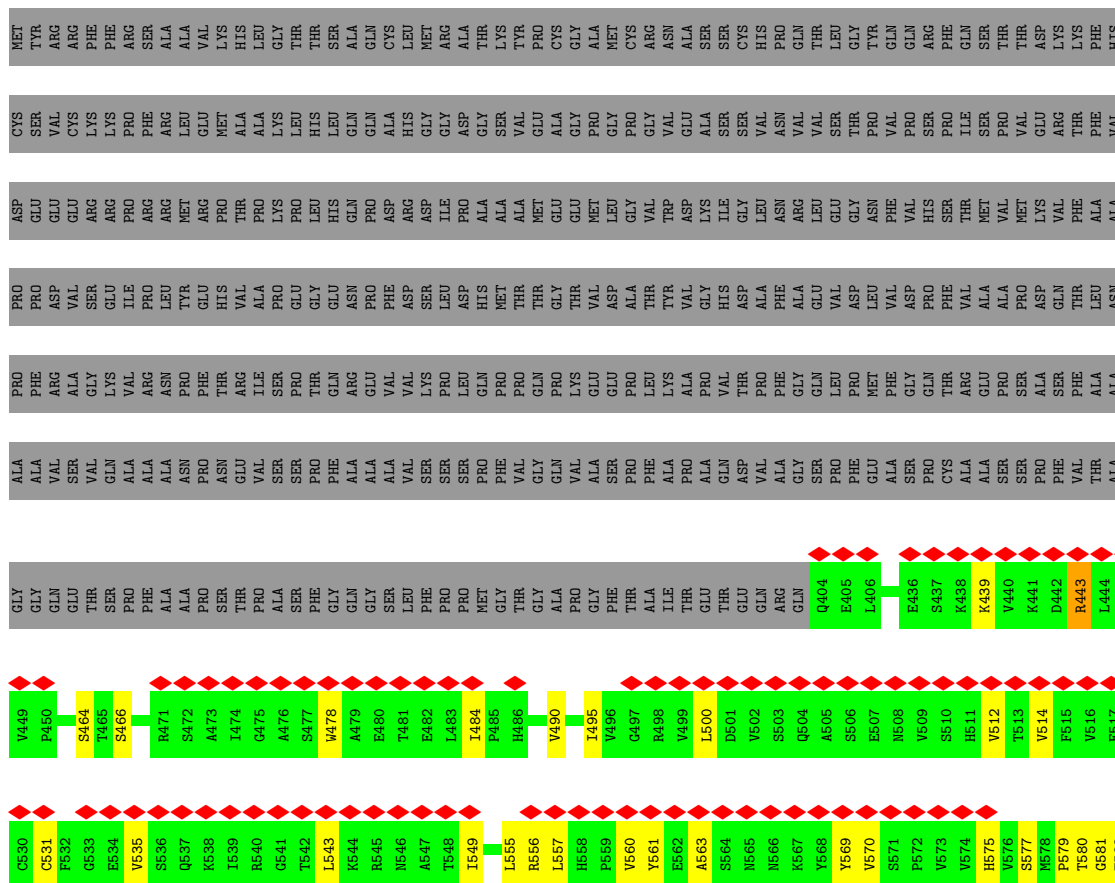
- Molecule 5: MP18 RNA editing complex protein, putative



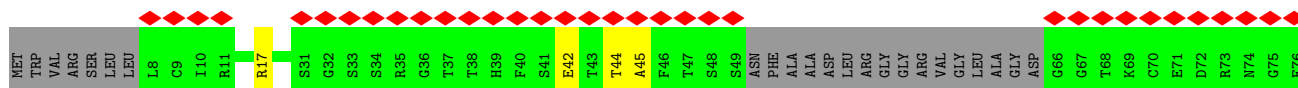
- Molecule 5: MP18 RNA editing complex protein, putative

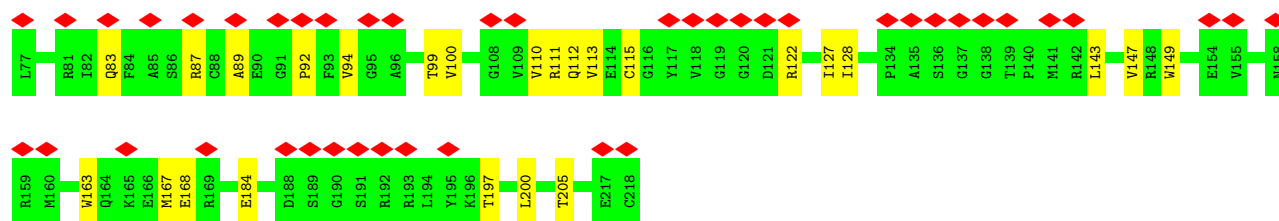


- Molecule 7: KREPA2

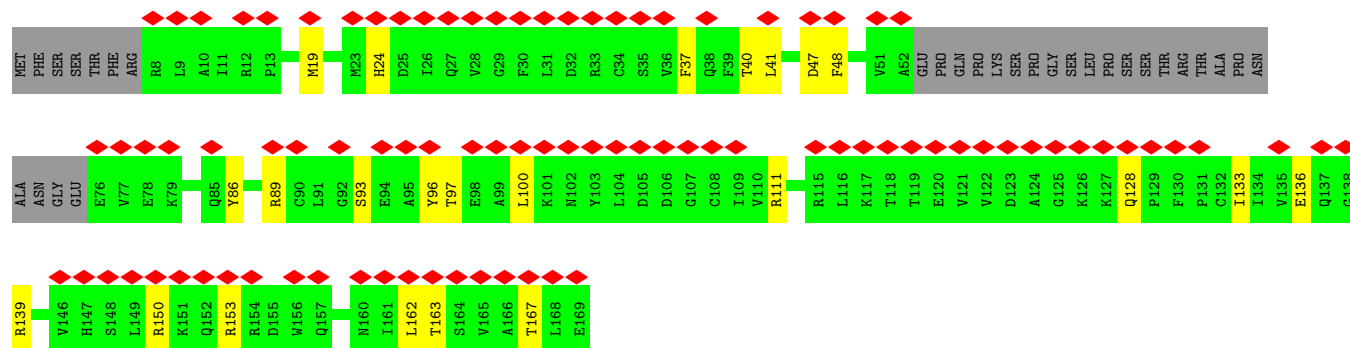


- Molecule 8: RNA editing complex protein

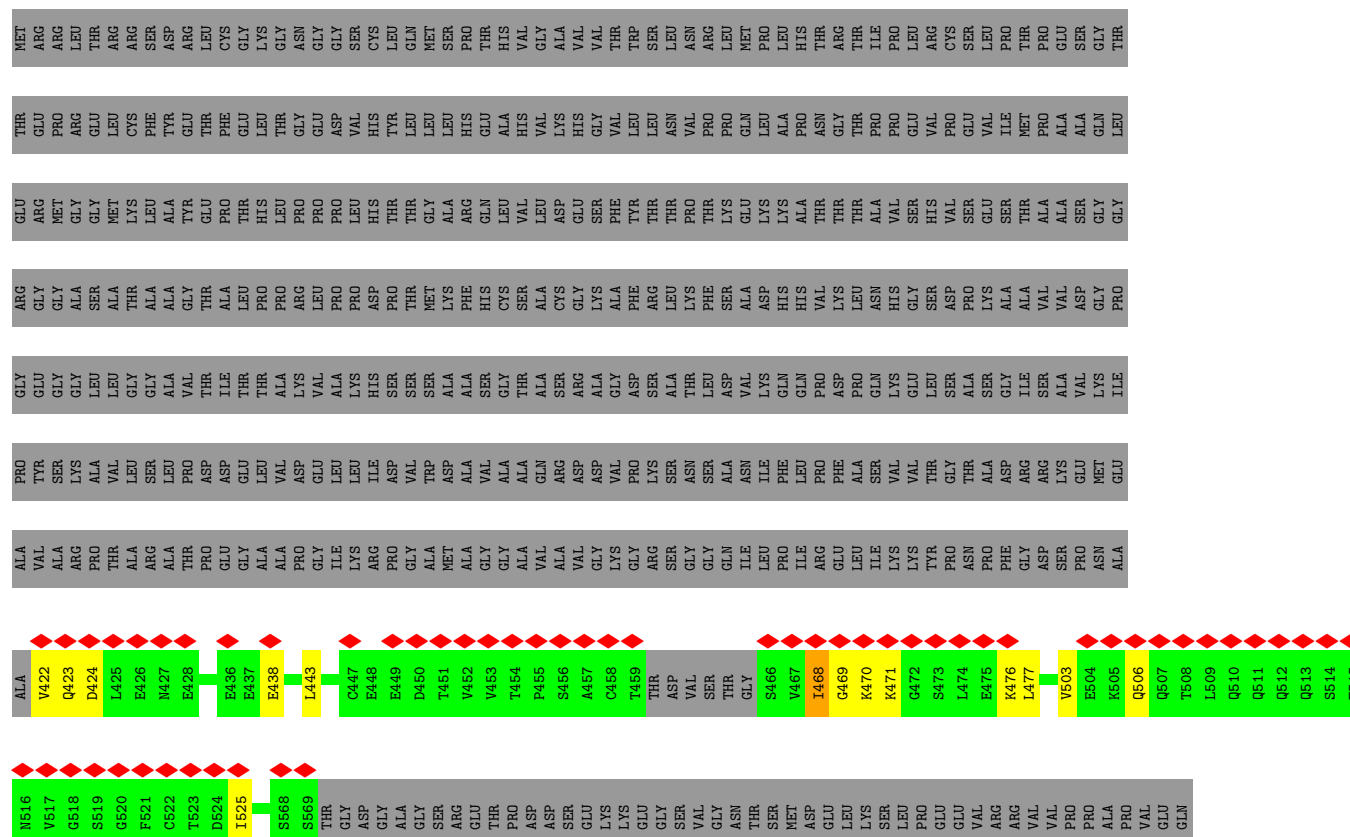




• Molecule 9: KREPA5



• Molecule 10: RNA-editing complex protein MP81

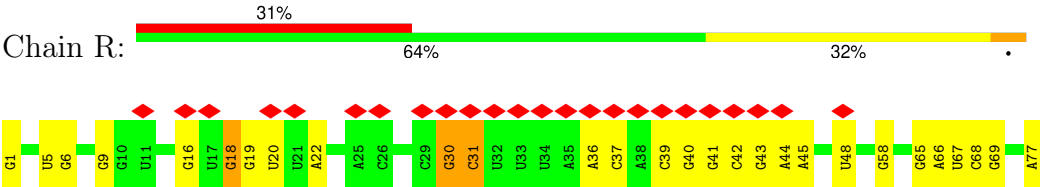


ASP
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PRO
ASP

ASP
ASP
VAL
SER
LYS
ARG
LEU
HIS
ALA
TYR
PRO
PHE
TLE
GLN
VAL
U20
VAL
PRO
PRO
LEU
GLY
TYR
VAL
LYS
VAL
VAL
GLY

● Molecule 11: tRNA-valine (anticodon AAC)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	496750	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS, TFS KRIOS	Depositor
Voltage (kV)	300, 300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45, 45	Depositor
Minimum defocus (nm)	1000, 600	Depositor
Maximum defocus (nm)	3000, 2800	Depositor
Magnification	81000, 130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k), FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	76.638	Depositor
Minimum map value	-50.207	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.016	Depositor
Recommended contour level	8.12	Depositor
Map size ($\text{\AA}$)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	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: ZN, 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	0.14	0/3054	0.34	0/4132
2	B	0.14	0/2940	0.31	0/3986
3	C	0.14	0/2599	0.31	0/3513
4	D	0.14	0/2951	0.31	0/3998
5	E	0.13	0/916	0.33	0/1248
5	H	0.12	0/952	0.35	0/1296
5	J	0.08	0/957	0.26	0/1302
6	F	0.12	0/1071	0.30	0/1455
7	G	0.11	0/1369	0.36	0/1856
7	K	0.11	0/1421	0.32	0/1927
8	I	0.11	0/1509	0.30	0/2034
9	L	0.09	0/1131	0.25	0/1526
10	O	0.10	0/1119	0.25	0/1510
11	R	0.58	5/1837 (0.3%)	0.39	2/2861 (0.1%)
All	All	0.20	5/23826 (0.0%)	0.32	2/32644 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	H	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	R	1	G	C3'-O3'	-15.34	1.19	1.42
11	R	1	G	OP3-P	8.61	1.65	1.48
11	R	1	G	C6-O6	8.05	1.40	1.24
11	R	1	G	C2-N2	5.77	1.46	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	R	1	G	N7-C5	5.36	1.50	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	R	1	G	OP1-P-OP2	-6.11	101.27	119.60
11	R	1	G	C3'-C2'-C1'	5.03	106.33	101.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	H	131	HIS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2991	0	3052	24	0
2	B	2859	0	2801	24	0
3	C	2532	0	2464	27	0
4	D	2890	0	2871	15	0
5	E	895	0	877	4	0
5	H	931	0	919	7	0
5	J	936	0	920	10	0
6	F	1040	0	988	5	0
7	G	1342	0	1337	11	0
7	K	1393	0	1392	22	0
8	I	1487	0	1475	19	0
9	L	1115	0	1143	15	0
10	O	1105	0	1096	8	0
11	R	1645	0	829	17	0
12	B	1	0	0	0	0
12	C	1	0	0	0	0
12	D	1	0	0	0	0
12	K	1	0	0	0	0
12	O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	C	2	0	0	0	0
14	A	56	0	0	0	0
14	B	5	0	0	0	0
14	C	3	0	0	0	0
14	D	15	0	0	0	0
14	E	16	0	0	0	0
14	F	21	0	0	1	0
14	G	9	0	0	0	0
14	H	9	0	0	0	0
14	I	1	0	0	0	0
14	K	1	0	0	0	0
14	R	63	0	0	0	0
All	All	23367	0	22164	172	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.

The worst 5 of 172 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:A:382:ARG:HH11	1:A:383:TYR:HB2	1.48	0.77
8:I:110:VAL:HG22	8:I:128:ILE:HG12	1.66	0.75
3:C:164:LYS:O	3:C:168:HIS:ND1	2.24	0.71
2:B:323:LYS:NZ	3:C:319:GLY:O	2.25	0.70
2:B:48:ARG:NH2	2:B:85:THR:OG1	2.26	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	372/384 (97%)	364 (98%)	8 (2%)	0	100	100
2	B	344/411 (84%)	339 (98%)	5 (2%)	0	100	100
3	C	307/538 (57%)	300 (98%)	7 (2%)	0	100	100
4	D	361/414 (87%)	351 (97%)	10 (3%)	0	100	100
5	E	112/164 (68%)	110 (98%)	2 (2%)	0	100	100
5	H	116/164 (71%)	112 (97%)	3 (3%)	1 (1%)	14	41
5	J	117/164 (71%)	111 (95%)	6 (5%)	0	100	100
6	F	127/393 (32%)	121 (95%)	6 (5%)	0	100	100
7	G	174/587 (30%)	153 (88%)	20 (12%)	1 (1%)	21	51
7	K	182/587 (31%)	174 (96%)	8 (4%)	0	100	100
8	I	191/218 (88%)	188 (98%)	3 (2%)	0	100	100
9	L	135/169 (80%)	131 (97%)	4 (3%)	0	100	100
10	O	138/762 (18%)	132 (96%)	6 (4%)	0	100	100
All	All	2676/4955 (54%)	2586 (97%)	88 (3%)	2 (0%)	49	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	H	135	ARG
7	G	491	SER

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	331/339 (98%)	329 (99%)	2 (1%)	78	92
2	B	309/357 (87%)	303 (98%)	6 (2%)	50	81
3	C	270/461 (59%)	265 (98%)	5 (2%)	50	81
4	D	321/362 (89%)	318 (99%)	3 (1%)	70	89
5	E	104/145 (72%)	101 (97%)	3 (3%)	37	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	H	108/145 (74%)	106 (98%)	2 (2%)	50	81
5	J	109/145 (75%)	108 (99%)	1 (1%)	70	89
6	F	114/327 (35%)	112 (98%)	2 (2%)	51	82
7	G	152/486 (31%)	148 (97%)	4 (3%)	40	75
7	K	158/486 (32%)	154 (98%)	4 (2%)	42	76
8	I	162/178 (91%)	159 (98%)	3 (2%)	50	81
9	L	125/151 (83%)	125 (100%)	0	100	100
10	O	126/623 (20%)	124 (98%)	2 (2%)	55	83
All	All	2389/4205 (57%)	2352 (98%)	37 (2%)	55	84

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	I	83	GLN
10	O	423	GLN
8	I	100	VAL
7	K	464	SER
3	C	325	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
8	I	164	GLN
10	O	423	GLN
5	J	96	ASN
10	O	431	ASN
4	D	109	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	R	76/77 (98%)	8 (10%)	1 (1%)

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	R	9	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	R	16	G
11	R	18	G
11	R	19	G
11	R	30	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	R	30	G

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 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

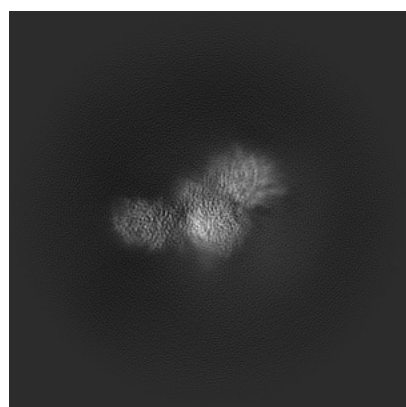
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-73706. These allow visual inspection of the internal detail of the map and identification of artifacts.

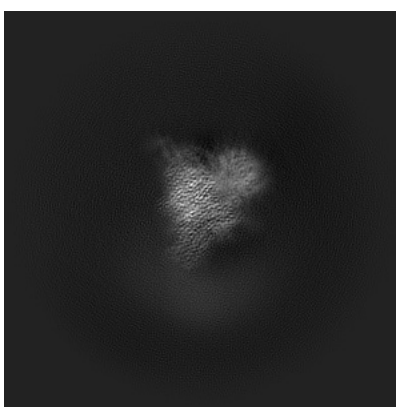
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

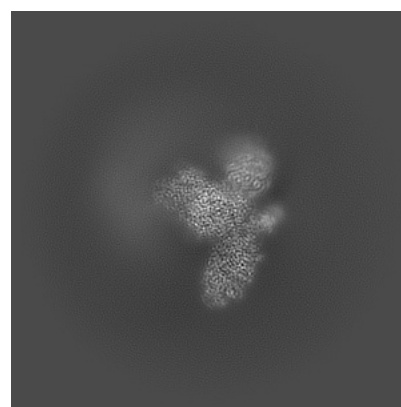
6.1.1 Primary map



X



Y

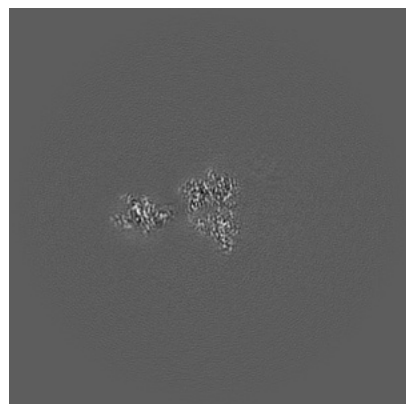


Z

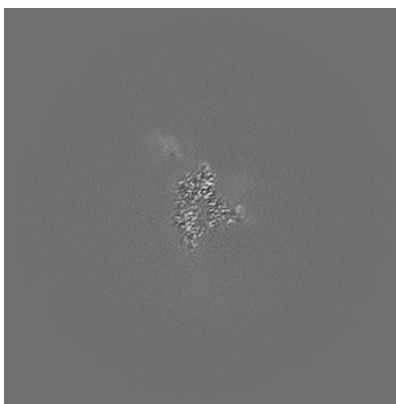
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

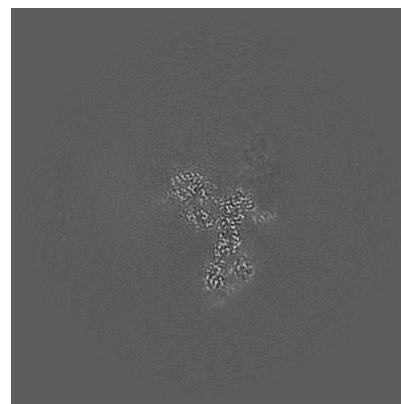
6.2.1 Primary map



X Index: 192



Y Index: 192

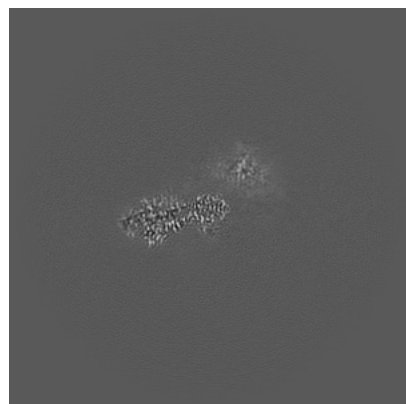


Z Index: 192

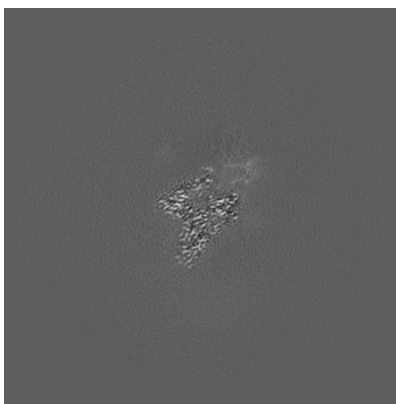
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

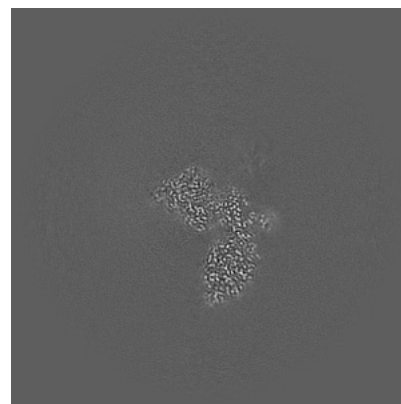
6.3.1 Primary map



X Index: 218



Y Index: 206

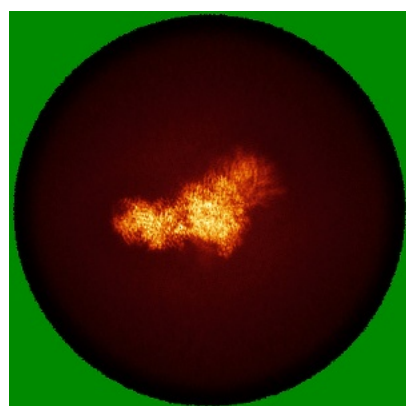


Z Index: 181

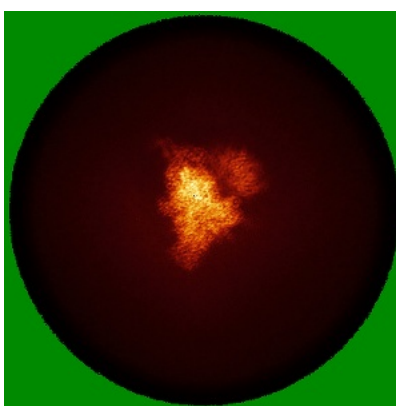
The images above show the largest variance slices of the map in three orthogonal directions.

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

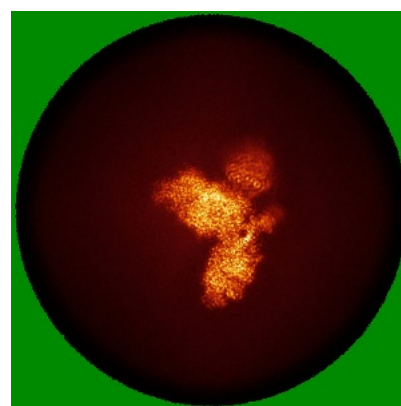
6.4.1 Primary map



X



Y

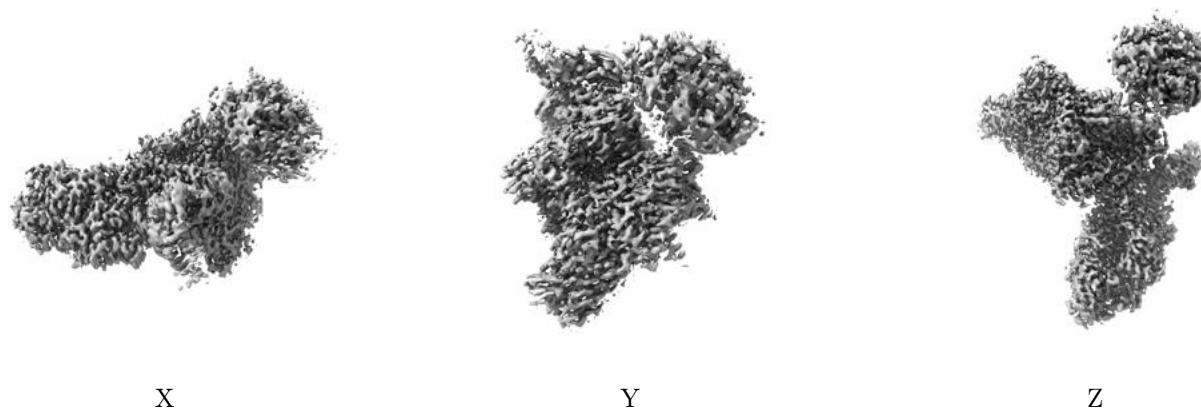


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 8.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

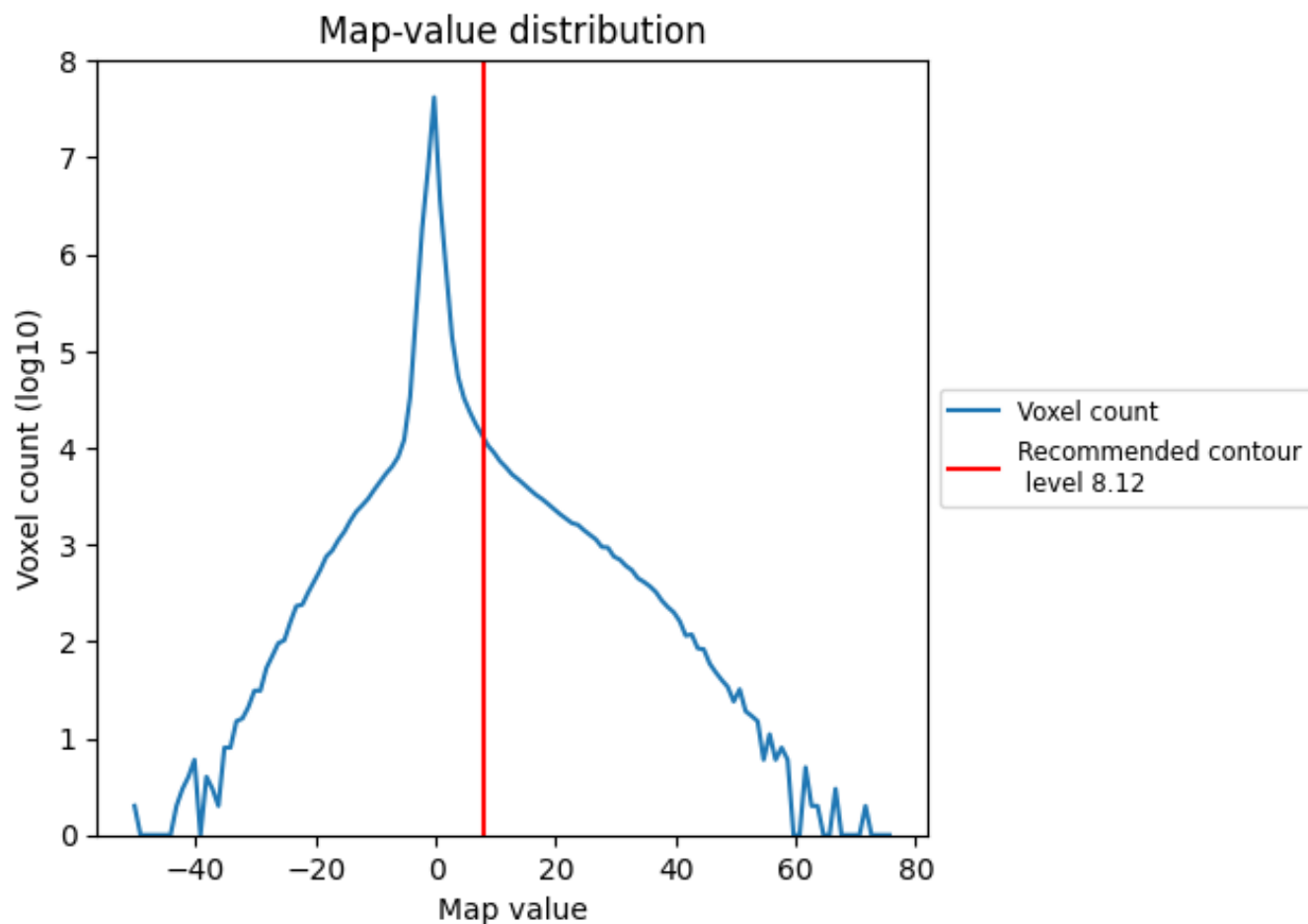
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

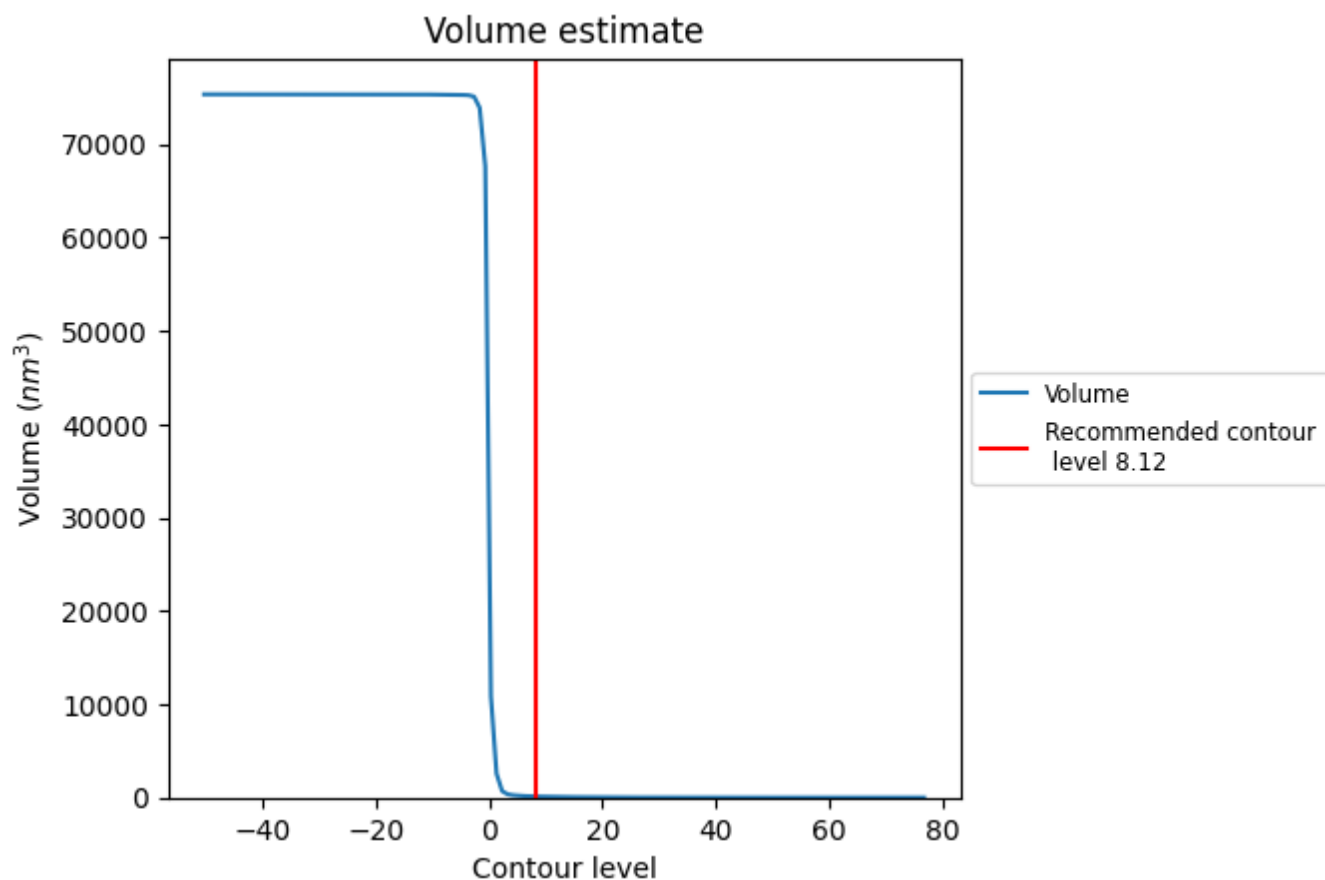
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

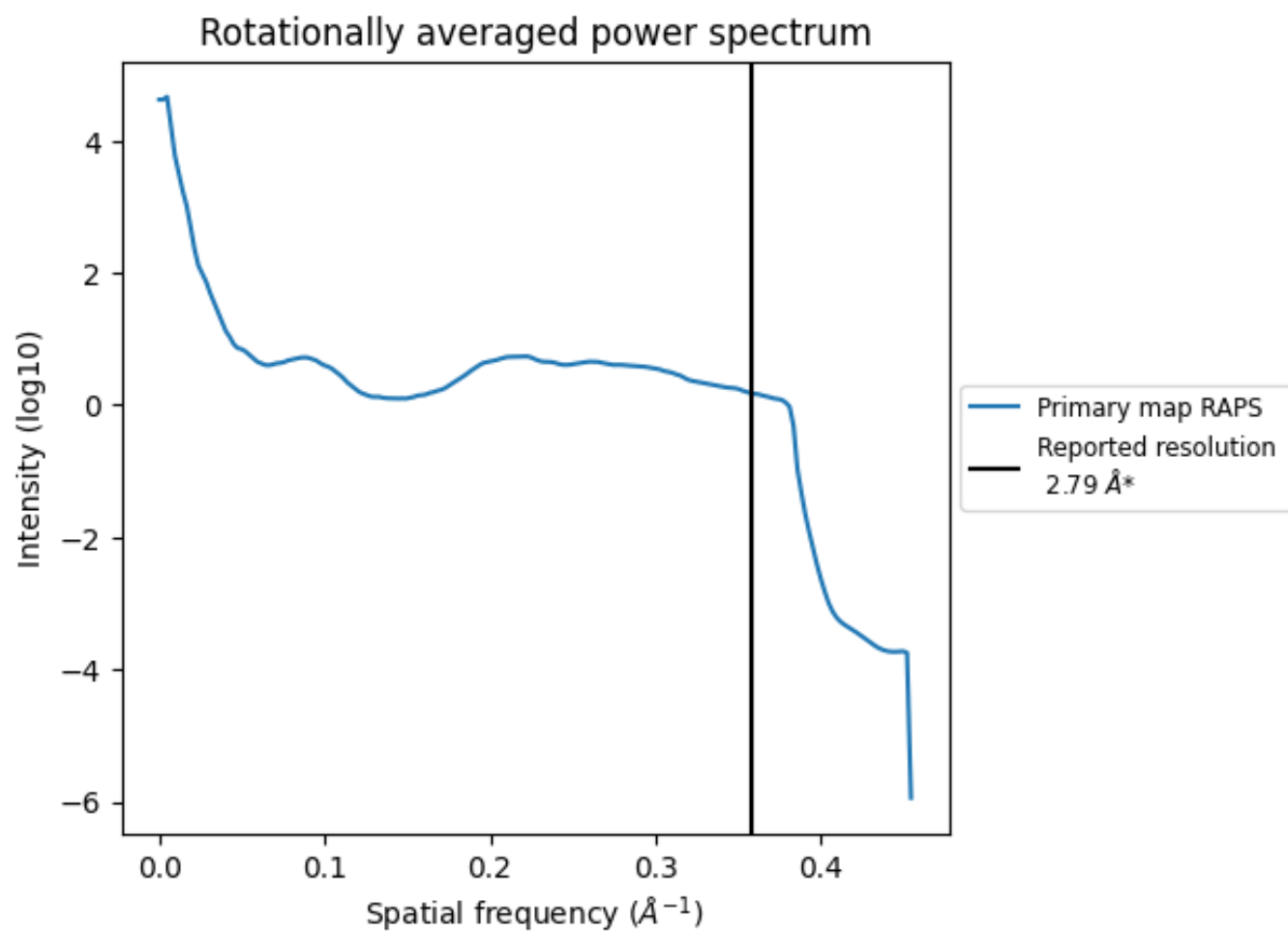
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 118 nm^3 ; this corresponds to an approximate mass of 107 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 0.358 Å⁻¹

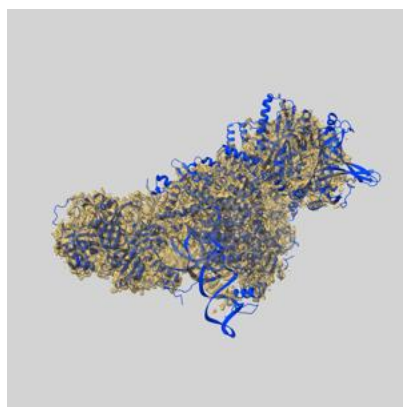
8 Fourier-Shell correlation

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

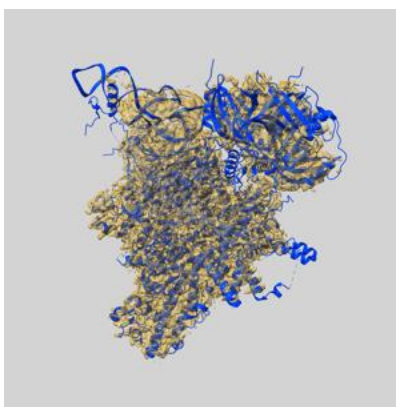
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-73706 and PDB model 9Z0H. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

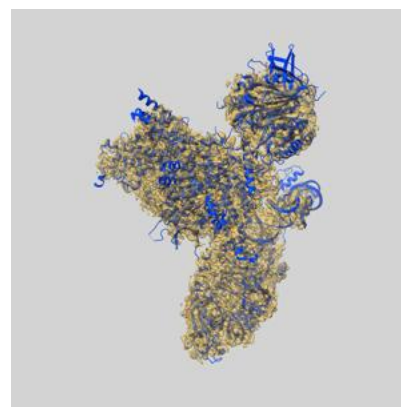
9.1 Map-model overlay [i](#)



X



Y



Z

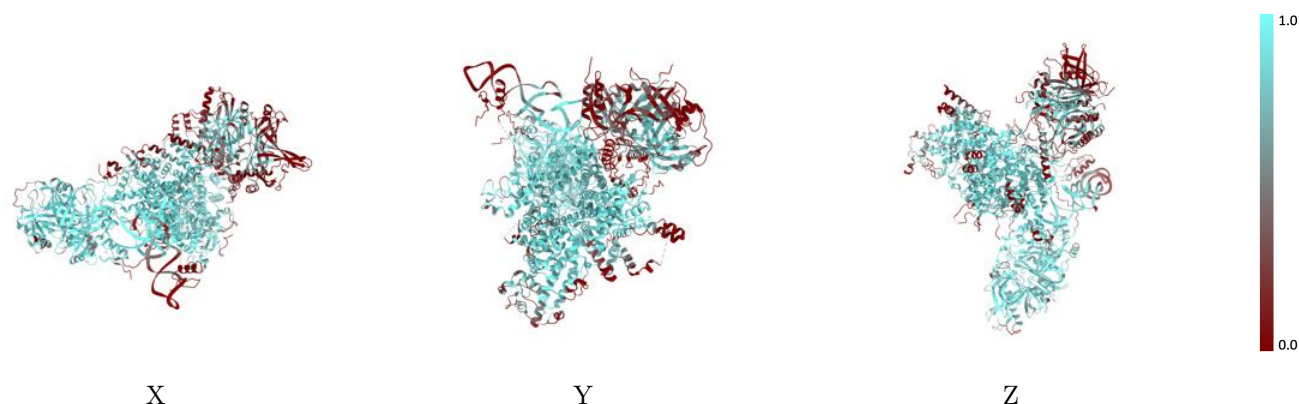
The images above show the 3D surface view of the map at the recommended contour level 8.12 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



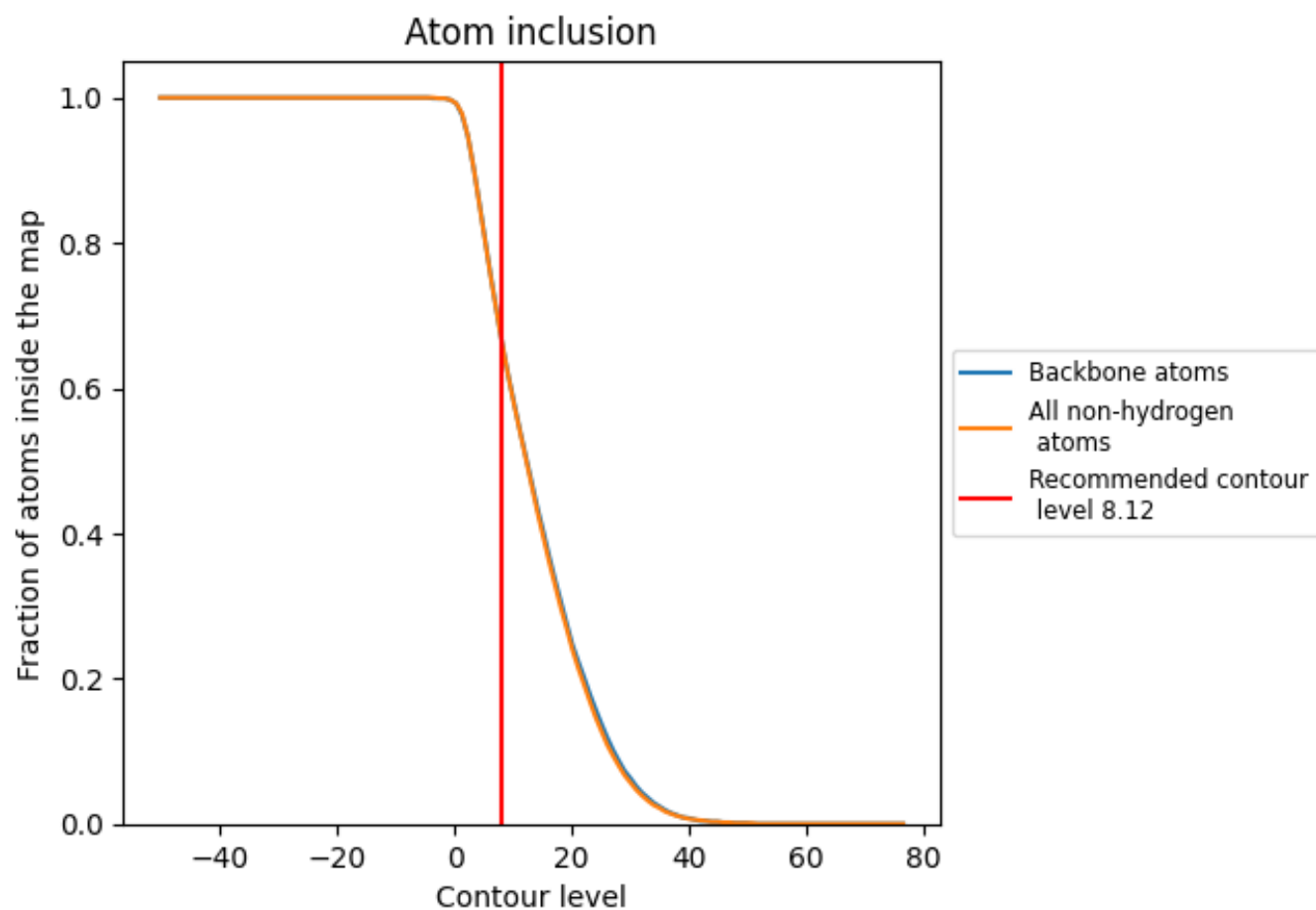
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (8.12).

9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 66% 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 (8.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6630	 0.4800
A	 0.8230	 0.5640
B	 0.8110	 0.5640
C	 0.7220	 0.5360
D	 0.6520	 0.4760
E	 0.9110	 0.5990
F	 0.8290	 0.5720
G	 0.5840	 0.4300
H	 0.8370	 0.5590
I	 0.4940	 0.3490
J	 0.5550	 0.3740
K	 0.3510	 0.3450
L	 0.2880	 0.2560
O	 0.5290	 0.4520
R	 0.6390	 0.4400

