



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 11:54 PM UTC

PDB ID : 3J0Q / pdb_00003j0q
EMDB ID : EMD-5329
Title : Core of mammalian 80S pre-ribosome in complex with tRNAs fitted to a 10.6Å cryo-em map: rotated PRE state 2
Authors : Budkevich, T.; Giesebrecht, J.; Altman, R.; Munro, J.; Mielke, T.; Nierhaus, K.; Blanchard, S.; Spahn, C.M.
Deposited on : 2011-10-11
Resolution : 10.60 Å(reported)
Based on initial models : 3O58, 2XZM

This is a wwPDB EM Validation Summary 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

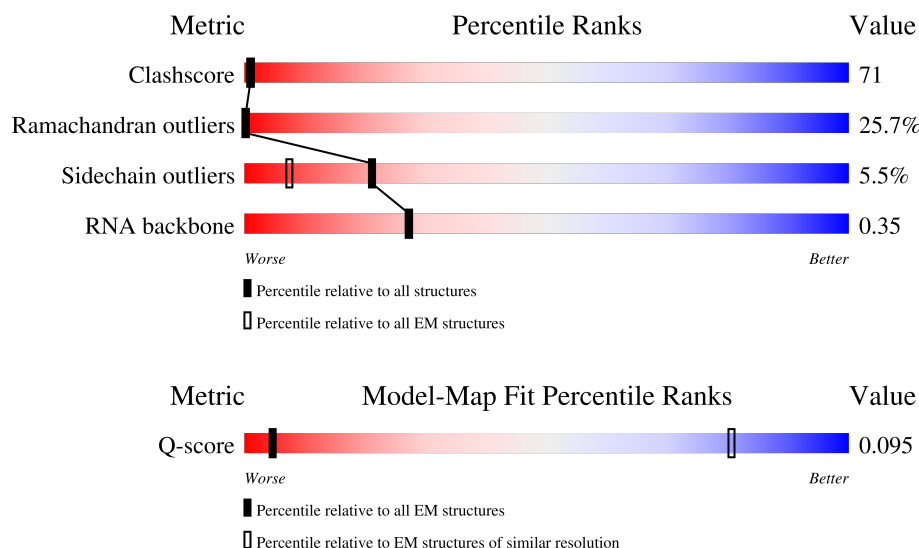
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.60 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.



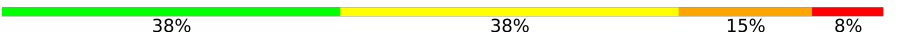
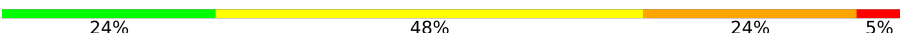
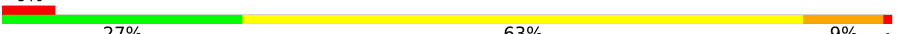
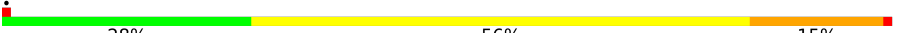
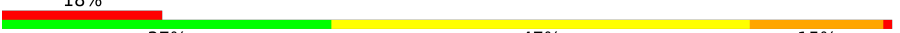
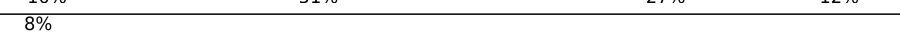
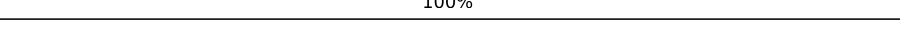
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	97 (10.10 - 11.10)

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	48	
2	c	17	
3	d	7	

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Mol	Chain	Length	Quality of chain
4	g	31	
5	G	13	
6	f	21	
7	h	111	
8	S	125	
9	L	141	
10	X	68	
11	2	112	
12	3	12	
13	9	19	
14	7	50	
15	B	213	
16	J	219	
17	k	165	
18	W	77	
18	Y	77	
19	y	3	
20	w	2	

2 Entry composition

There are 20 unique types of molecules in this entry. The entry contains 18327 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 RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	48	Total	C	N	O	P	0	0
			1029	459	190	332	48		

- Molecule 2 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	17	Total	C	N	O	P	0	0
			362	162	66	117	17		

- Molecule 3 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	7	Total	C	N	O	P	0	0
			155	69	33	46	7		

- Molecule 4 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	g	31	Total	C	N	O	P	0	0
			660	295	118	216	31		

- Molecule 5 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	13	Total	C	N	O	P	0	0
			276	123	49	91	13		

- Molecule 6 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	21	Total	C	N	O	P	0	0
			452	200	79	152	21		

- Molecule 7 is a RNA chain called 40S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	111	Total	C	N	O	P	0	0
			2368	1060	431	766	111		

- Molecule 8 is a protein called Ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	S	125	Total	C	N	O	S	0	0
			985	632	173	176	4		

- Molecule 9 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	141	Total	C	N	O	S	0	0
			1097	691	221	180	5		

- Molecule 10 is a protein called Ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	X	68	Total	C	N	O	S	0	0
			554	350	113	90	1		

- Molecule 11 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	2	112	Total	C	N	O	P	0	0
			2392	1070	435	775	112		

- Molecule 12 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	3	12	Total	C	N	O	P	0	0
			259	116	50	81	12		

- Molecule 13 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	9	19	Total	C	N	O	P	0	0
			408	183	78	128	19		

- Molecule 14 is a RNA chain called 60S ribosomal RNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	7	50	Total	C	N	O	P	0	0
			1054	471	173	360	50		

- Molecule 15 is a protein called Ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	B	213	Total	C	N	O		0	0
			1055	629	213	213			

- Molecule 16 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	208	Total	C	N	O		0	0
			1027	611	208	208			

- Molecule 17 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	165	Total	C	N	O		0	0
			810	480	165	165			

- Molecule 18 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
18	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 19 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	y	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

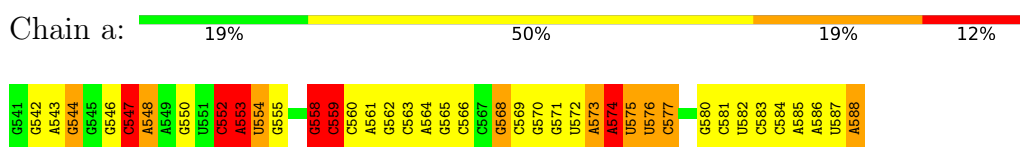
- Molecule 20 is a RNA chain called mRNA fragment.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	w	2	Total	C	N	O	P	0	0
			44	20	10	12	2		

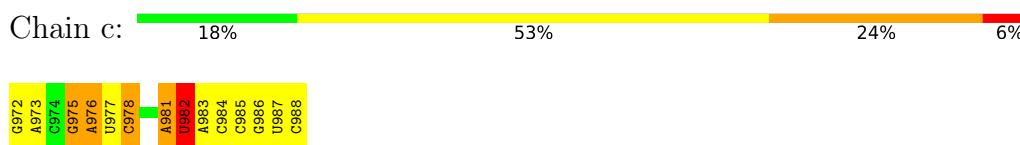
3 Residue-property plots

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.

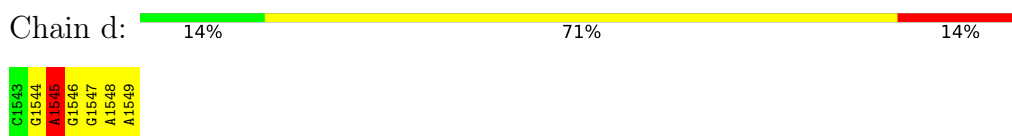
- Molecule 1: 40S ribosomal RNA fragment



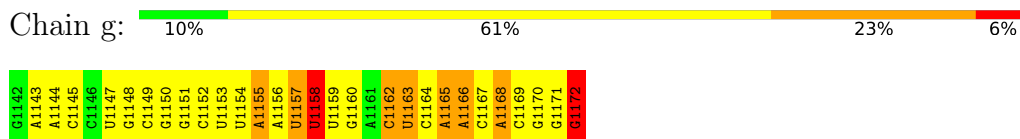
- Molecule 2: 40S ribosomal RNA fragment



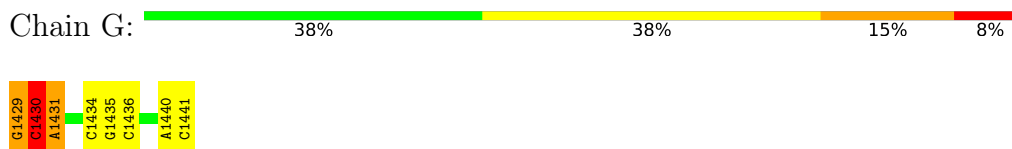
- Molecule 3: 40S ribosomal RNA fragment



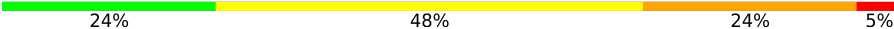
- Molecule 4: 40S ribosomal RNA fragment

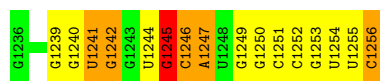


- Molecule 5: 40S ribosomal RNA fragment

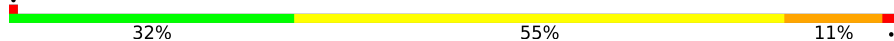


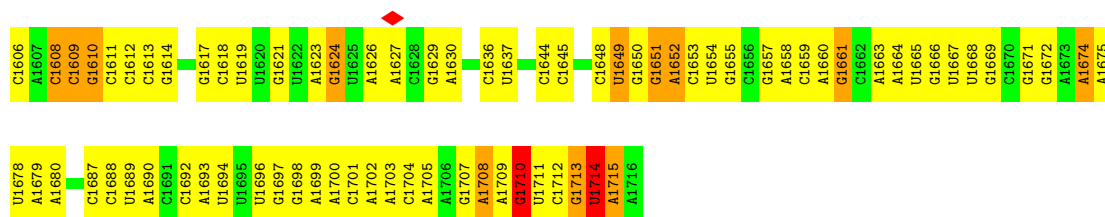
- Molecule 6: 40S ribosomal RNA fragment

Chain f: 

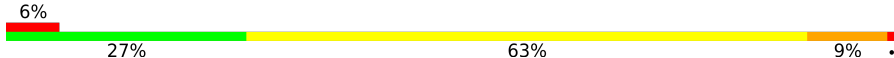


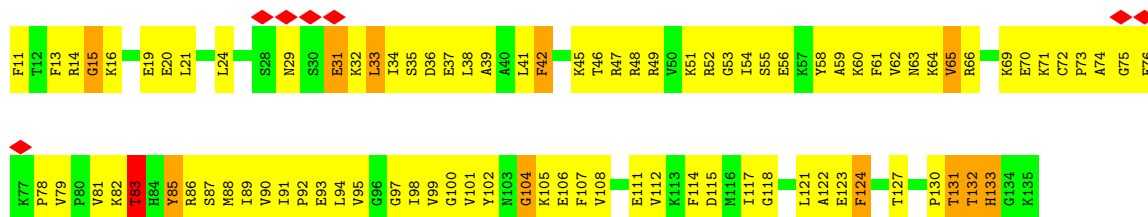
- Molecule 7: 40S ribosomal RNA fragment

Chain h: 



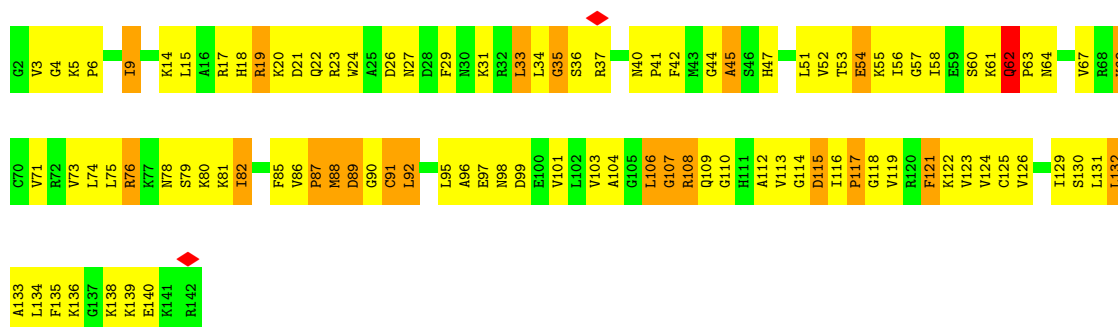
- Molecule 8: Ribosomal protein S15

Chain S: 



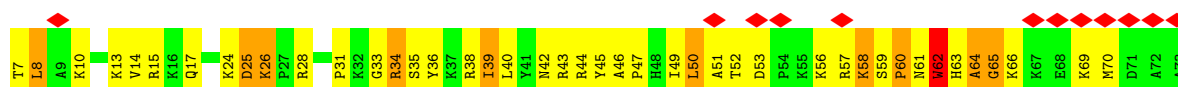
- Molecule 9: Ribosomal protein S23

Chain L: 



- Molecule 10: Ribosomal protein S30

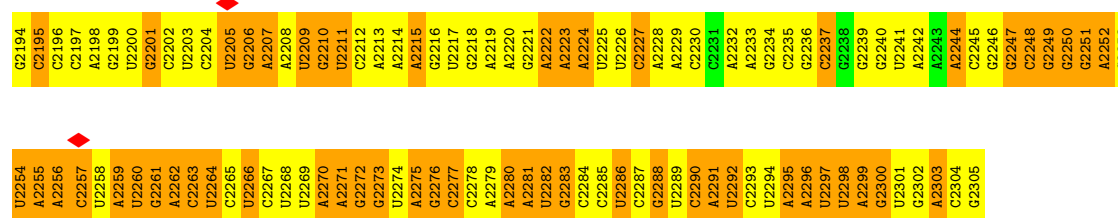
Chain X: 



A74

- Molecule 11: 60S ribosomal RNA fragment

Chain 2:  48% 49%



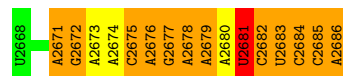
- Molecule 12: 60S ribosomal RNA fragment

Chain 3:  25% 33% 42%



- Molecule 13: 60S ribosomal RNA fragment

Chain 9:  16% 16% 63% 5%



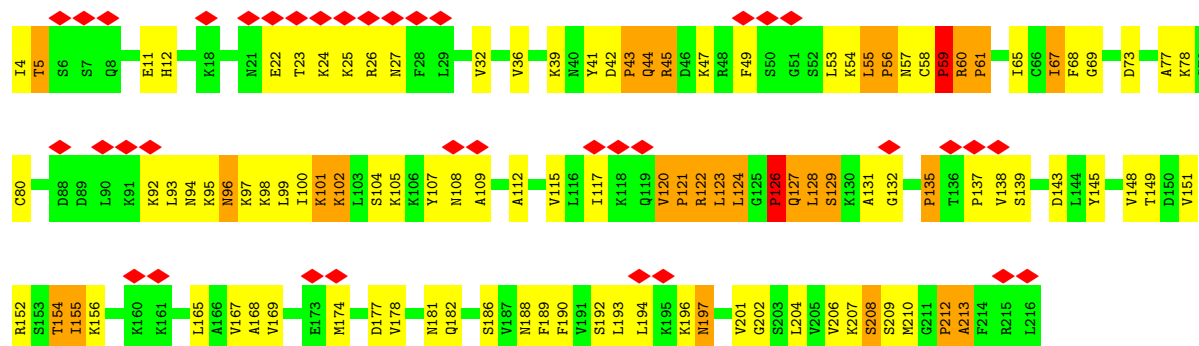
- Molecule 14: 60S ribosomal RNA fragment

Chain 7:  44% 54%



- Molecule 15: Ribosomal protein L10a

Chain B:  17% 49% 37% 13%



- Molecule 19: mRNA fragment

Chain y:  100%

U19
U20
C21

- Molecule 20: mRNA fragment

Chain w:  100%

A14
A15

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23347	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF CORRECTION OF EACH DEFOCUS GROUP VOLUME PRIOR TO BACK PROJECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	17103.236	Depositor
Minimum map value	-2542.373	Depositor
Average map value	275.672	Depositor
Map value standard deviation	1215.576	Depositor
Recommended contour level	1000	Depositor
Map size ($\text{\AA}$)	453.6, 453.6, 453.6	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.52, 2.52, 2.52	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	0.52	0/1151	0.97	7/1793 (0.4%)
2	c	0.46	0/404	0.94	4/627 (0.6%)
3	d	0.40	0/174	0.93	1/270 (0.4%)
4	g	0.47	0/737	0.94	5/1146 (0.4%)
5	G	0.42	0/307	0.92	2/476 (0.4%)
6	f	0.45	0/504	0.90	3/785 (0.4%)
7	h	0.38	0/2650	0.70	3/4127 (0.1%)
8	S	0.44	0/1003	1.05	7/1342 (0.5%)
9	L	0.55	0/1114	1.05	3/1485 (0.2%)
10	X	0.43	0/566	1.19	5/753 (0.7%)
11	2	0.58	0/2677	0.64	0/4170
12	3	0.11	0/290	0.24	0/450
13	9	0.62	0/457	0.80	2/710 (0.3%)
14	7	0.59	0/1174	0.74	3/1825 (0.2%)
15	B	0.51	0/1054	1.05	12/1468 (0.8%)
16	J	1.00	0/1025	1.37	21/1424 (1.5%)
17	k	0.85	0/809	1.34	17/1122 (1.5%)
18	W	1.60	5/1832 (0.3%)	1.46	18/2855 (0.6%)
18	Y	1.60	6/1832 (0.3%)	1.46	16/2855 (0.6%)
19	y	0.44	0/65	0.54	0/98
20	w	0.42	0/49	0.62	0/74
All	All	0.85	11/19874 (0.1%)	1.04	129/29855 (0.4%)

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
1	a	0	3
3	d	0	1
4	g	0	2
7	h	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	k	0	1
18	W	0	5
18	Y	0	5
All	All	0	19

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	Y	30	G	C2'-C1'	-6.36	1.43	1.53
18	W	30	G	C2'-C1'	-6.33	1.43	1.53
18	Y	45	G	C1'-N9	-5.89	1.39	1.48
18	W	45	G	C1'-N9	-5.86	1.39	1.48
18	Y	14	A	C1'-N9	-5.65	1.39	1.48

The worst 5 of 129 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	k	139	THR	N-CA-C	-9.78	101.00	113.72
8	S	131	THR	N-CA-C	9.43	124.61	109.24
7	h	1714	U	N1-C1'-C2'	8.95	125.42	112.00
17	k	166	LYS	N-CA-C	-8.87	102.01	112.92
10	X	58	LYS	N-CA-C	8.85	121.75	110.33

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	547	C	Sidechain
1	a	559	C	Sidechain
1	a	574	A	Sidechain
3	d	1545	A	Sidechain
4	g	1157	U	Sidechain

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	1029	0	521	100	0
2	c	362	0	185	18	0
3	d	155	0	77	46	0
4	g	660	0	335	51	0
5	G	276	0	142	13	0
6	f	452	0	226	25	0
7	h	2368	0	1196	128	0
8	S	985	0	1026	116	0
9	L	1097	0	1169	118	0
10	X	554	0	604	68	0
11	2	2392	0	1208	408	0
12	3	259	0	125	91	0
13	9	408	0	199	258	0
14	7	1054	0	529	187	0
15	B	1055	0	449	127	0
16	J	1027	0	468	117	0
17	k	810	0	353	255	0
18	W	1640	0	825	180	0
18	Y	1640	0	825	198	0
19	y	60	0	31	33	0
20	w	44	0	23	16	0
All	All	18327	0	10516	2044	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 71.

The worst 5 of 2044 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)
13:9:2674:A:H61	17:k:23:VAL:CA	1.05	1.66
13:9:2680:A:C2	17:k:57:PHE:CB	1.83	1.60
13:9:2683:U:H1'	17:k:20:ASN:CB	1.13	1.53
13:9:2677:G:C6	17:k:56:THR:CB	1.93	1.51
7:h:1709:A:H5'	19:y:19:U:C4'	1.20	1.50

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	
8	S	123/125 (98%)	90 (73%)	25 (20%)	8 (6%)	1	12
9	L	139/141 (99%)	106 (76%)	18 (13%)	15 (11%)	0	6
10	X	66/68 (97%)	48 (73%)	12 (18%)	6 (9%)	0	8
15	B	211/213 (99%)	76 (36%)	67 (32%)	68 (32%)	0	0
16	J	204/219 (93%)	80 (39%)	52 (26%)	72 (35%)	0	0
17	k	163/165 (99%)	57 (35%)	42 (26%)	64 (39%)	0	0
All	All	906/931 (97%)	457 (50%)	216 (24%)	233 (26%)	0	1

5 of 233 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	S	15	GLY
9	L	45	ALA
9	L	62	GLN
9	L	87	PRO
9	L	88	MET

5.3.2 Protein sidechains [i](#)

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	
8	S	105/105 (100%)	101 (96%)	4 (4%)	29	50
9	L	113/113 (100%)	104 (92%)	9 (8%)	11	31
10	X	57/57 (100%)	55 (96%)	2 (4%)	32	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	275/275 (100%)	260 (94%)	15 (6%)	21	41

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	L	69	LYS
10	X	34	ARG
9	L	82	ILE
10	X	62	TRP
9	L	106	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
10	X	42	ASN
10	X	17	GLN
9	L	78	ASN
9	L	62	GLN
9	L	98	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	47/48 (97%)	16 (34%)	0
11	2	111/112 (99%)	55 (49%)	9 (8%)
12	3	11/12 (91%)	6 (54%)	1 (9%)
13	9	18/19 (94%)	13 (72%)	1 (5%)
14	7	49/50 (98%)	29 (59%)	5 (10%)
18	W	76/77 (98%)	17 (22%)	0
18	Y	76/77 (98%)	17 (22%)	0
19	y	2/3 (66%)	0	0
2	c	16/17 (94%)	4 (25%)	0
20	w	1/2 (50%)	0	0
3	d	6/7 (85%)	2 (33%)	0
4	g	30/31 (96%)	8 (26%)	0
5	G	12/13 (92%)	2 (16%)	1 (8%)
6	f	20/21 (95%)	5 (25%)	0
7	h	110/111 (99%)	12 (10%)	0
All	All	585/600 (97%)	186 (31%)	17 (2%)

5 of 186 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	544	G
1	a	547	C
1	a	548	A
1	a	552	C
1	a	553	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
14	7	2851	A
14	7	2872	A
11	2	2281	A
11	2	2290	C
11	2	2297	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

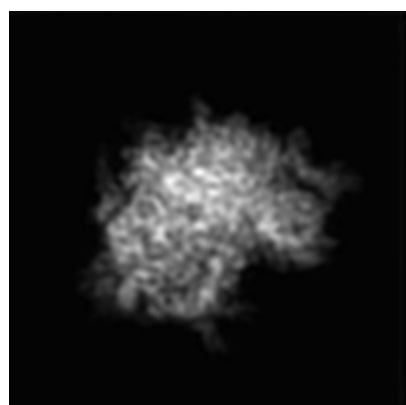
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5329. These allow visual inspection of the internal detail of the map and identification of artifacts.

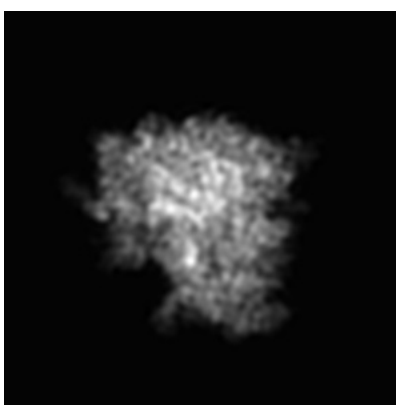
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

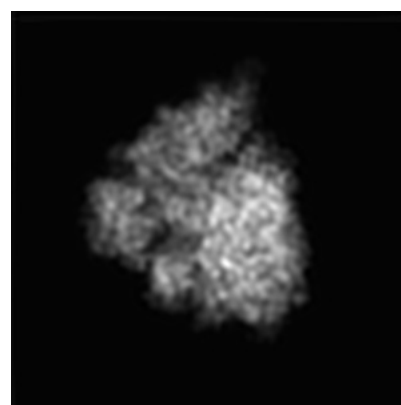
6.1.1 Primary map



X



Y

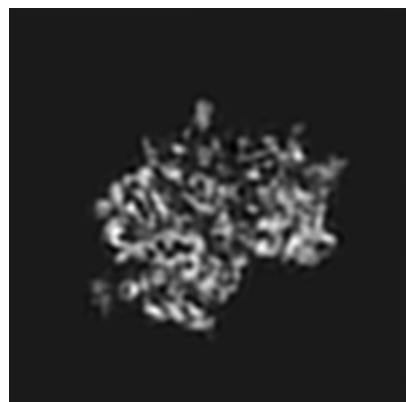


Z

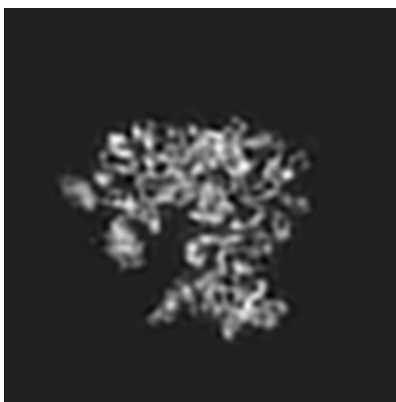
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

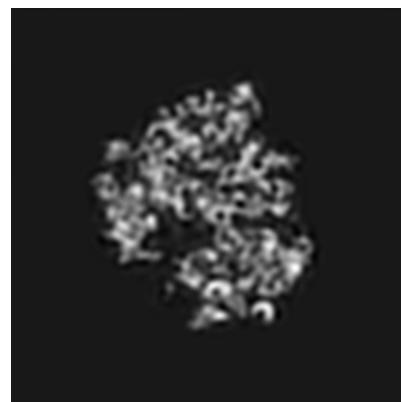
6.2.1 Primary map



X Index: 90



Y Index: 90

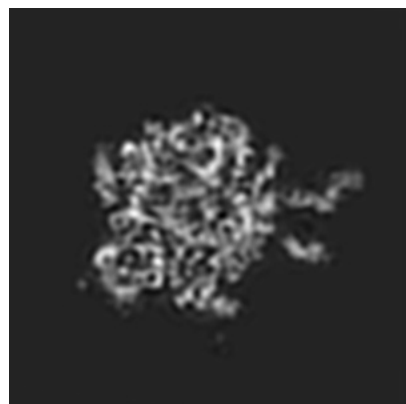


Z Index: 90

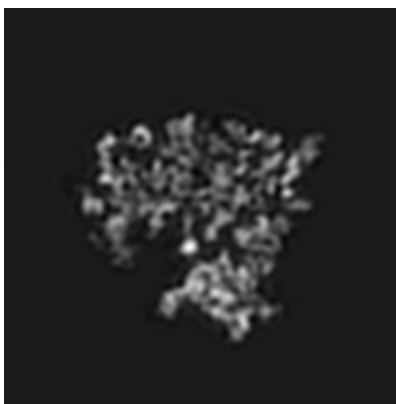
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

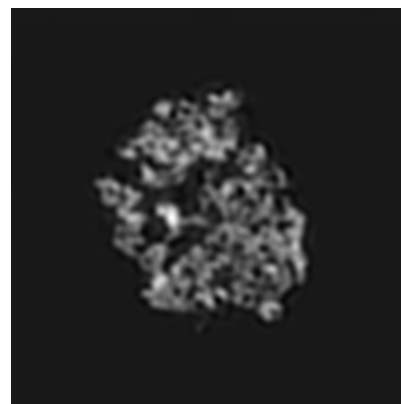
6.3.1 Primary map



X Index: 107



Y Index: 85

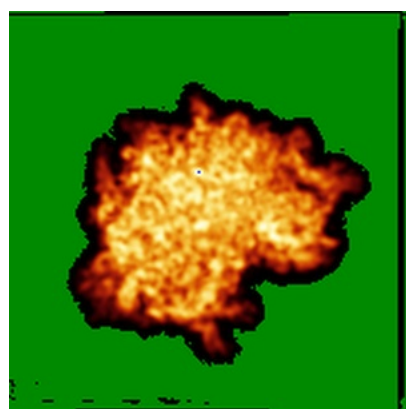


Z Index: 83

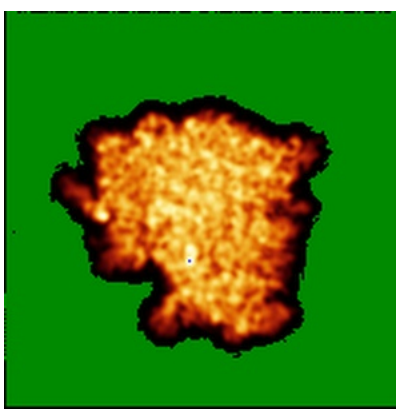
The images above show the largest variance slices of the map in three orthogonal directions.

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

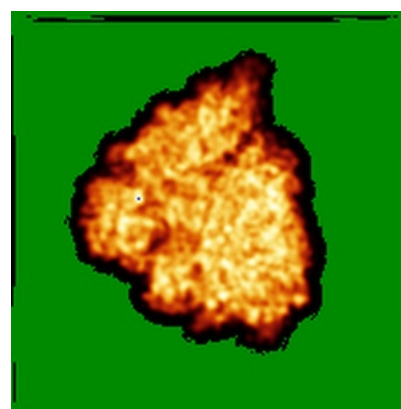
6.4.1 Primary map



X



Y

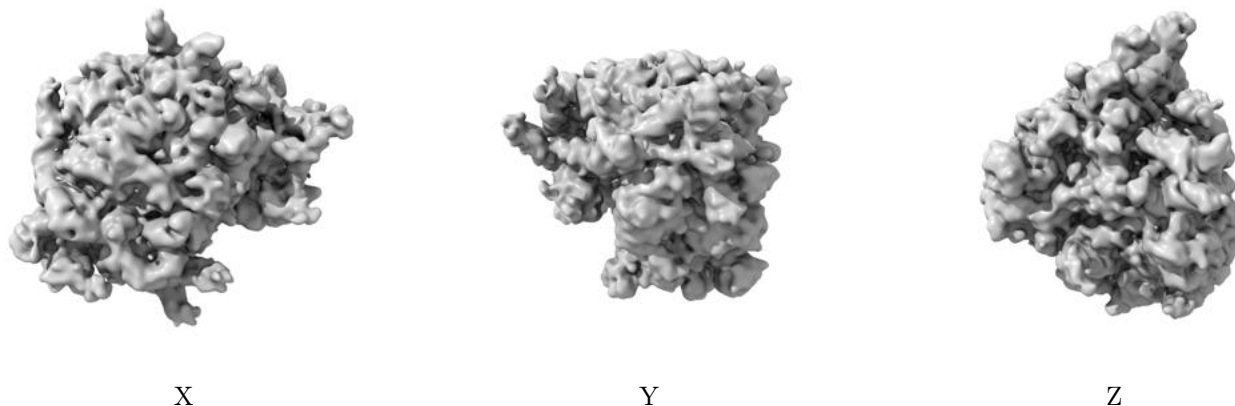


Z

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 1000.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

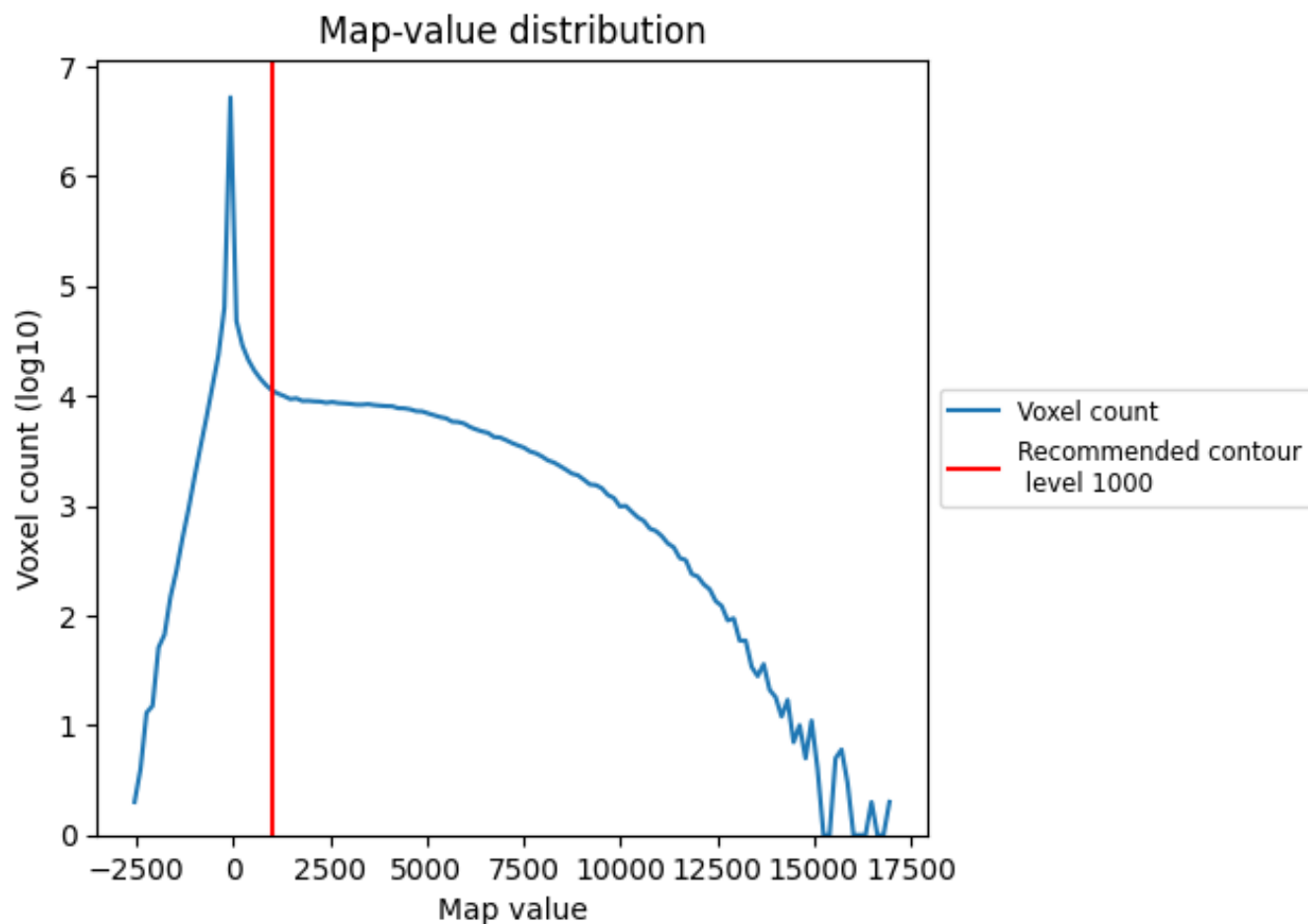
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

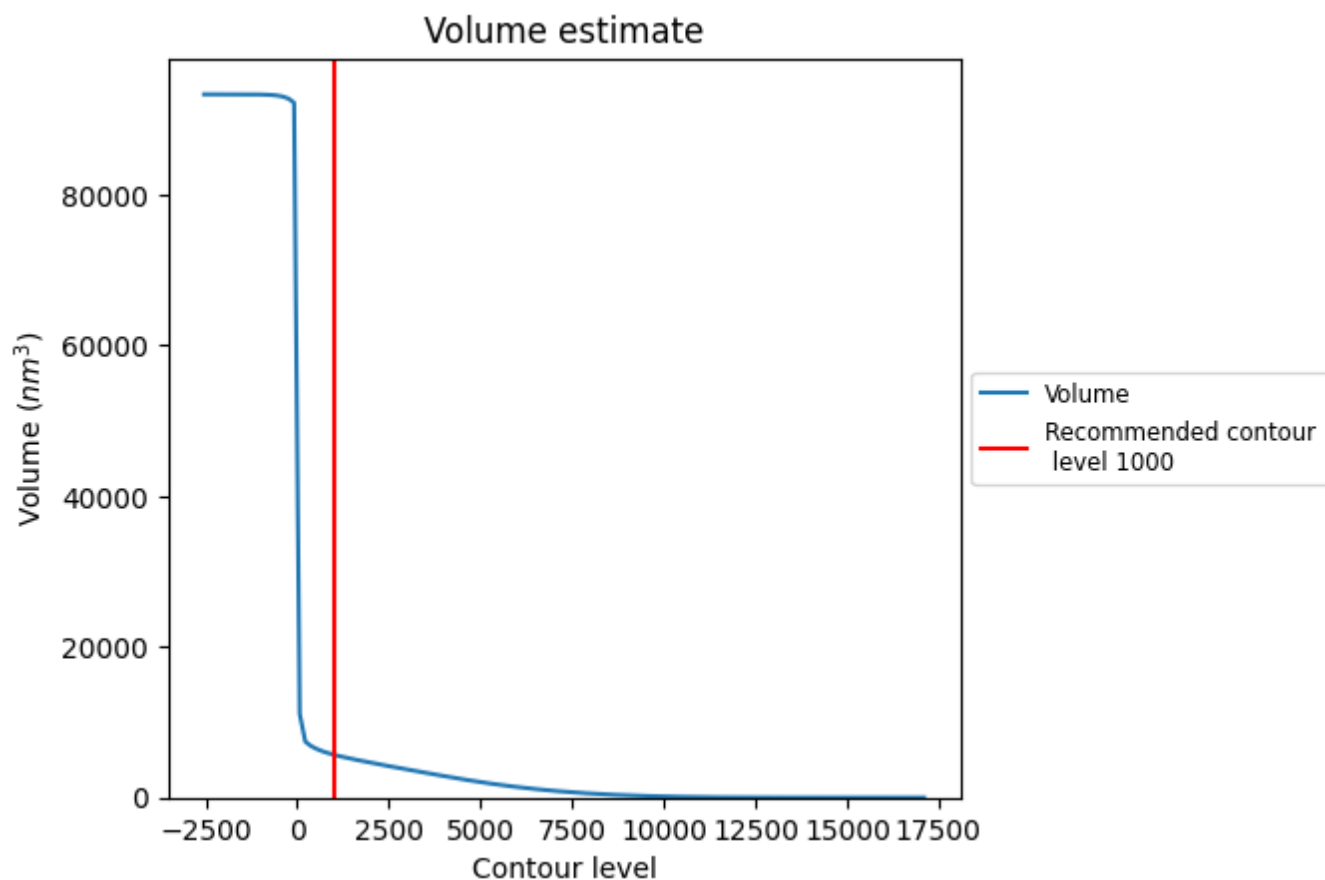
This section contains the results of statistical analysis of the map.

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.

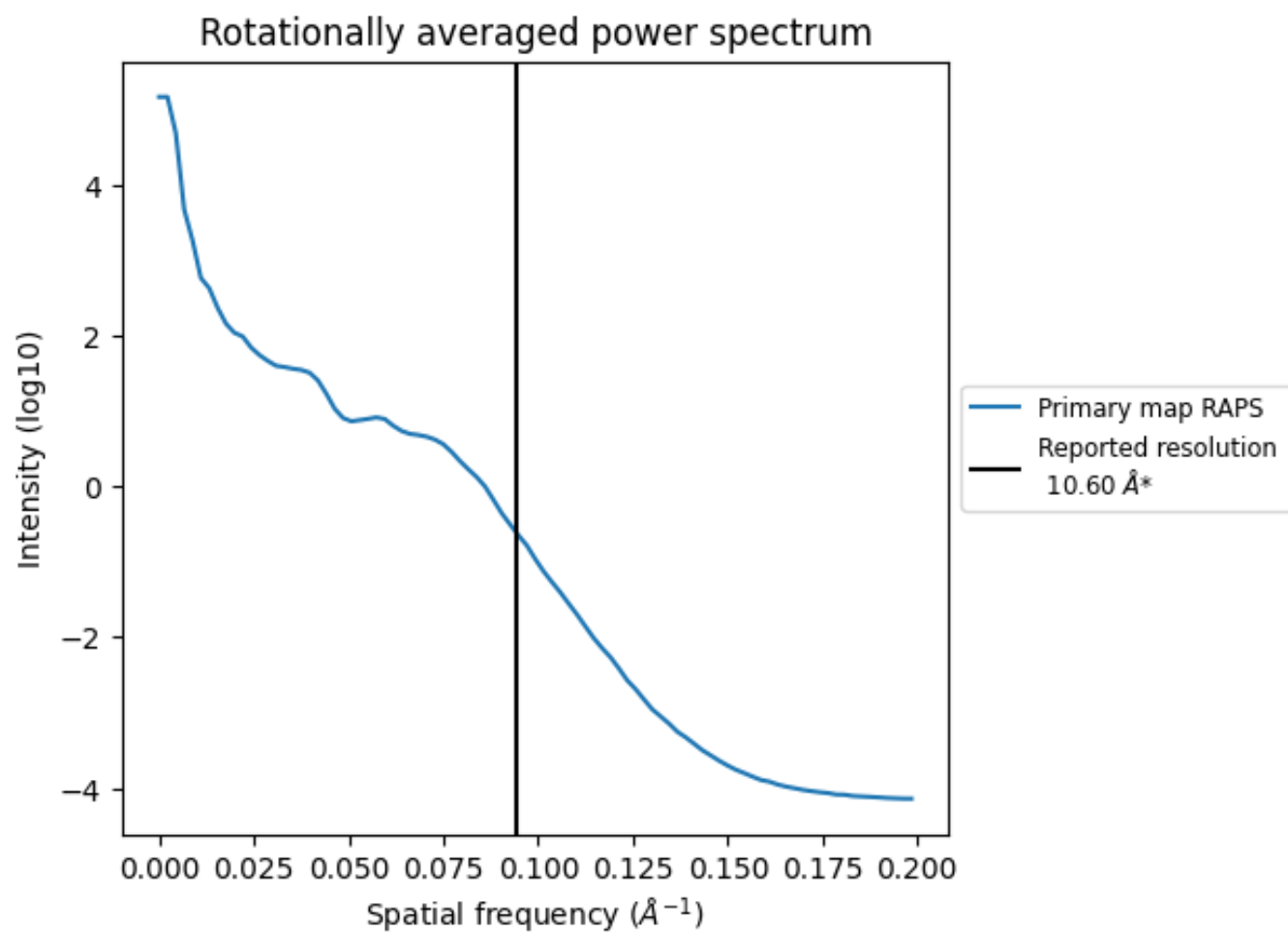
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5682 nm^3 ; this corresponds to an approximate mass of 5133 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 0.094 Å⁻¹

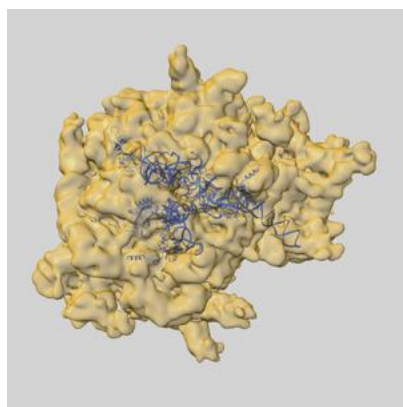
8 Fourier-Shell correlation ⓘ

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

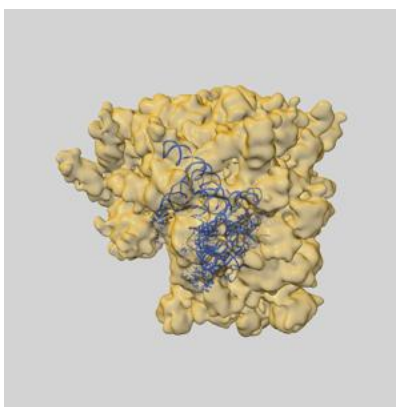
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5329 and PDB model 3J0Q. Per-residue inclusion information can be found in section [3](#) on page [7](#).

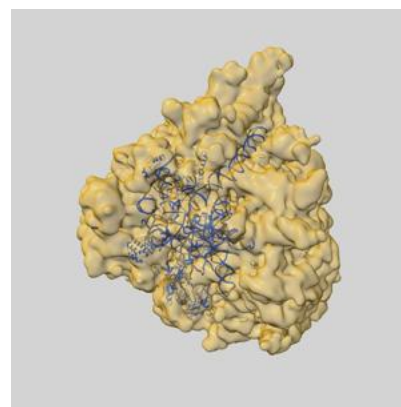
9.1 Map-model overlay [i](#)



X



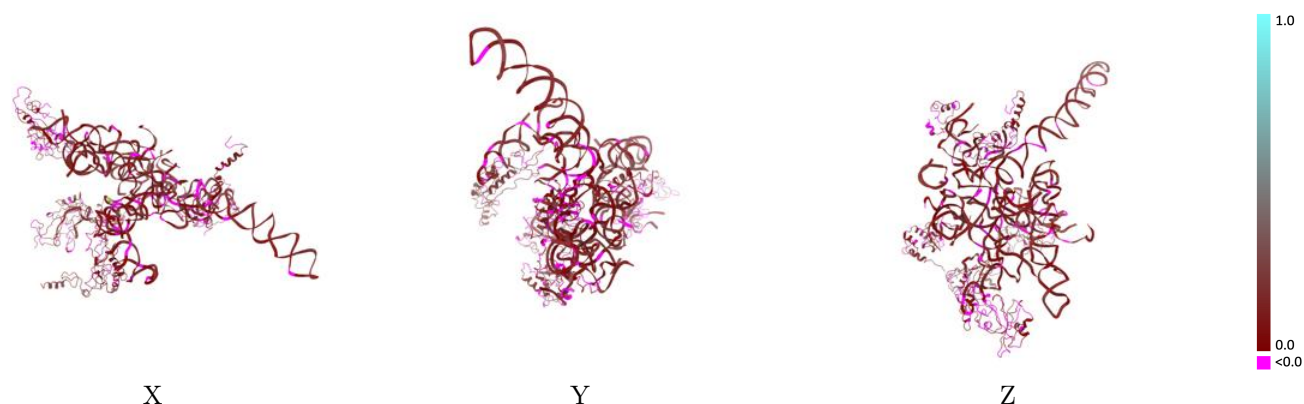
Y



Z

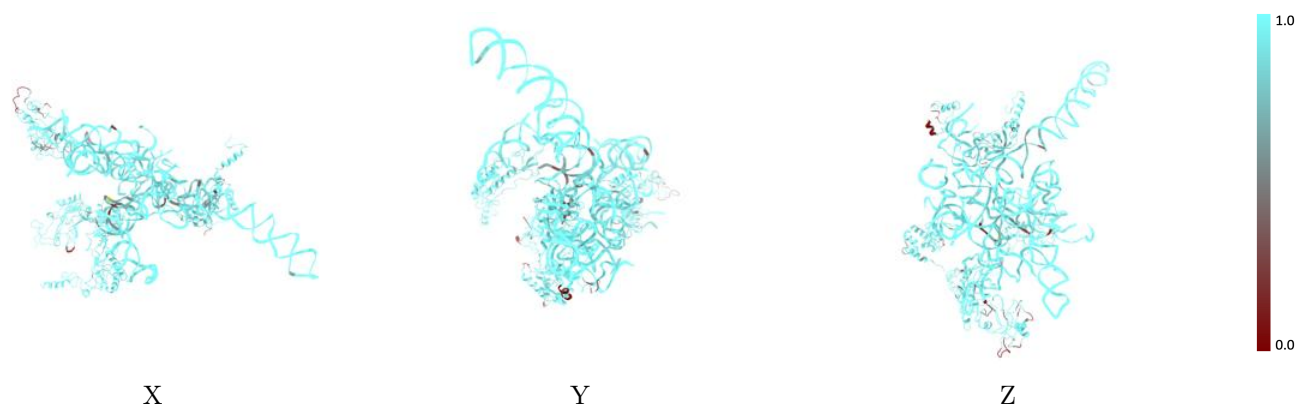
The images above show the 3D surface view of the map at the recommended contour level 1000.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



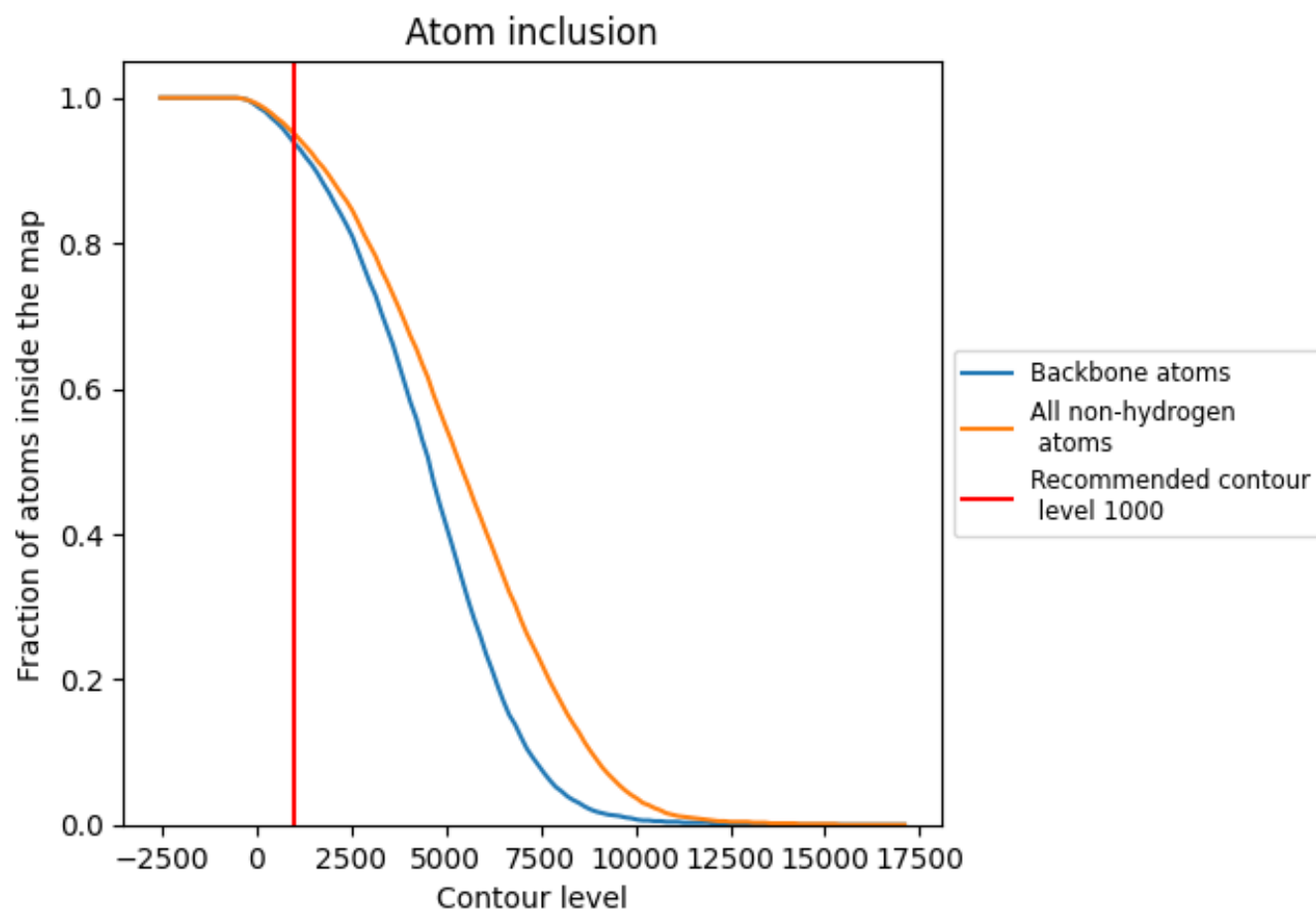
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1000).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 95% 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 (1000) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.0950
2	 0.9790	 0.1170
3	 1.0000	 0.0550
7	 0.9930	 0.1040
9	 0.9980	 0.1260
B	 0.8130	 0.0120
G	 1.0000	 0.1230
J	 0.9930	 0.1220
L	 0.9340	 0.0550
S	 0.9290	 0.0730
W	 0.9780	 0.1260
X	 0.7930	 0.0320
Y	 0.8680	 0.0770
a	 1.0000	 0.1180
c	 0.9920	 0.0990
d	 1.0000	 0.1270
f	 1.0000	 0.1510
g	 0.9970	 0.0850
h	 0.9520	 0.1060
k	 0.9720	 0.1040
w	 0.8410	 -0.0740
y	 0.9830	 0.0890

