



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 12:43 AM UTC

PDB ID : 7ABH / pdb_00007abh
EMDB ID : EMD-11696
Title : Human pre-Bact-2 spliceosome (SF3b/U2 snRNP portion)
Authors : Townsend, C.; Kastner, B.; Leelaram, M.N.; Bertram, K.; Stark, H.;
Luehrmann, R.
Deposited on : 2020-09-07
Resolution : 4.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

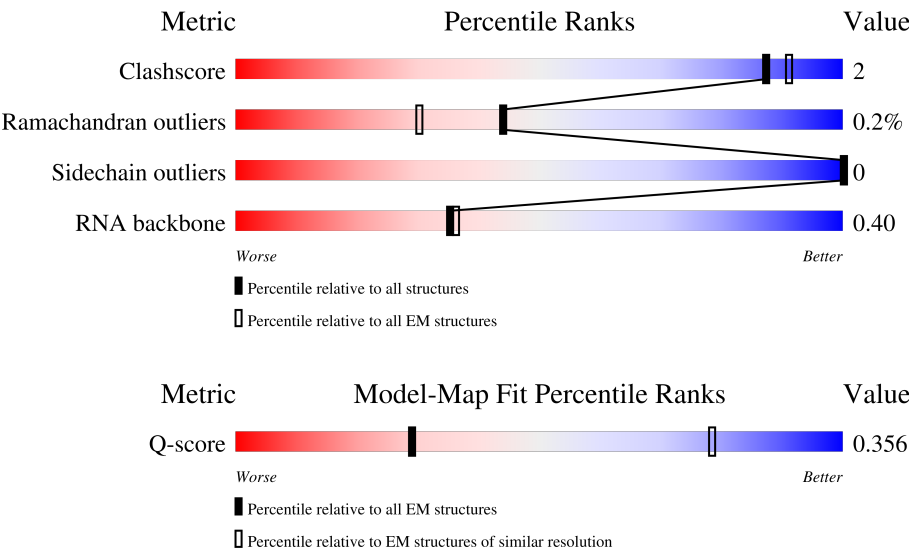
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	L	802	6% 94%
2	y	110	32% 87% 9%
3	Z	230	7% 6% 88%

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Mol	Chain	Length	Quality of chain
4	F	464	
5	4	501	
6	u	1304	
7	T	895	
8	E	1217	
9	w	424	
10	x	86	
11	z	125	
12	0	396	
13	1	322	
14	Y	904	
15	2	188	
16	7	393	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 17922 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 Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	L	48	Total	C	N	O	0	0
			237	141	48	48		

- Molecule 2 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	y	100	Total	C	N	O	0	0
			498	298	100	100		

- Molecule 3 is a RNA chain called MINX M3 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	28	Total	C	N	O	P	0	0
			579	260	87	204	28		

- Molecule 4 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	75	Total	C	N	O	0	0
			374	224	75	75		

- Molecule 5 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	108	Total	C	N	O	0	0
			541	325	108	108		

- Molecule 6 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	u	932	Total	C	N	O	0	0
			4704	2840	932	932		

- Molecule 7 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	T	183	Total	C	N	O	0	0
			942	576	183	183		

- Molecule 8 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	E	1177	Total	C	N	O	0	0
			5926	3572	1177	1177		

- Molecule 9 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	w	78	Total	C	N	O	0	0
			391	235	78	78		

- Molecule 10 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	x	79	Total	C	N	O	0	0
			397	239	79	79		

- Molecule 11 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	z	108	Total	C	N	O	0	0
			544	328	108	108		

- Molecule 12 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	0	150	Total	C	N	O	0	0
			761	461	150	150		

- Molecule 13 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	1	122	Total	C	N	O	0	0
			607	363	122	122		

- Molecule 14 is a protein called Serine/arginine repetitive matrix protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	Y	95	Total	C	N	O	0	0
			478	288	95	95		

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	2	37	Total	C	N	O	P	0	0
			778	349	126	266	37		

- Molecule 16 is a protein called DNA/RNA-binding protein KIN17.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	7	33	Total	C	N	O	0	0
			165	99	33	33		

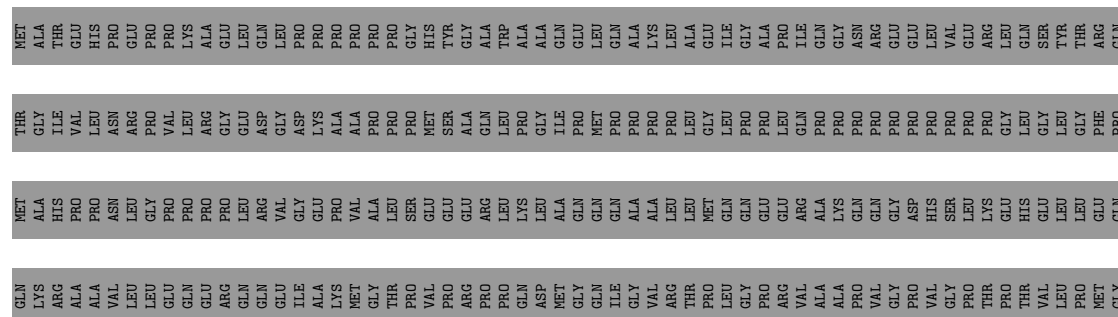
3 Residue-property plots

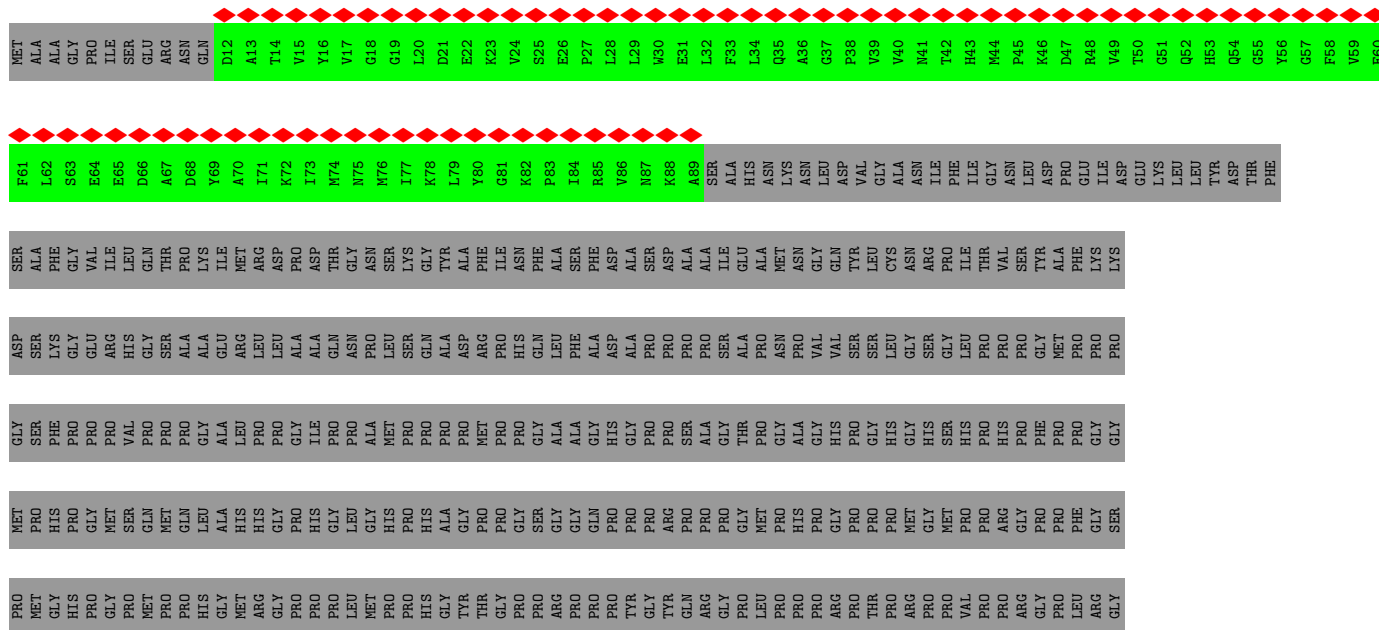
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

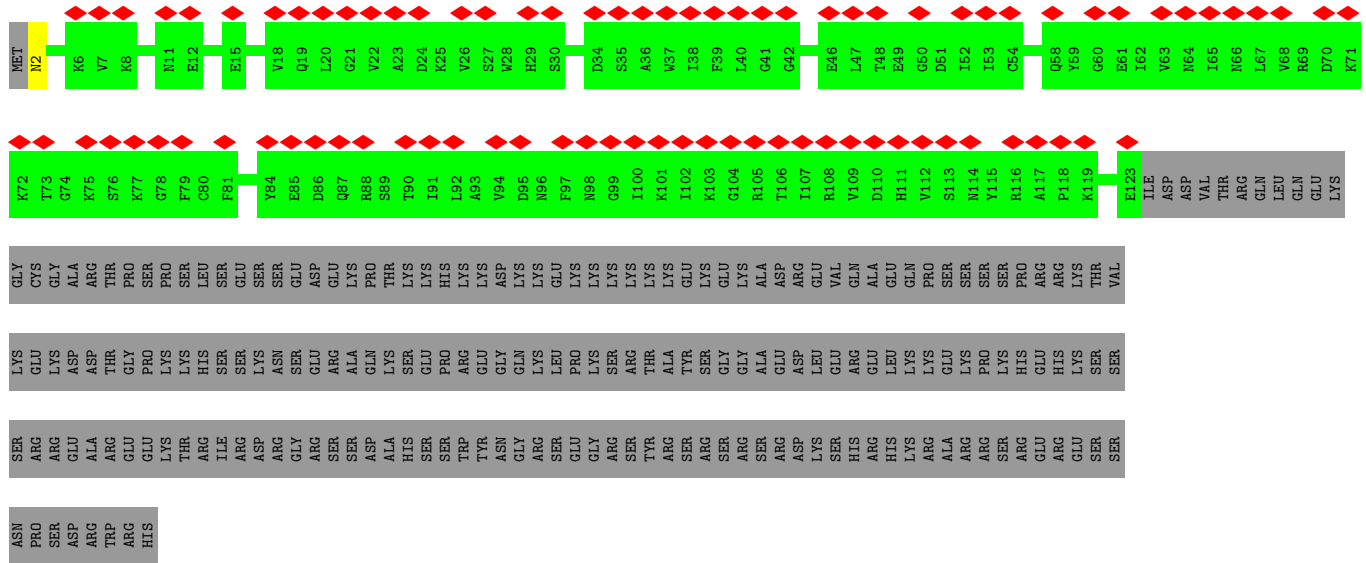
- Molecule 1: Cell division cycle 5-like protein



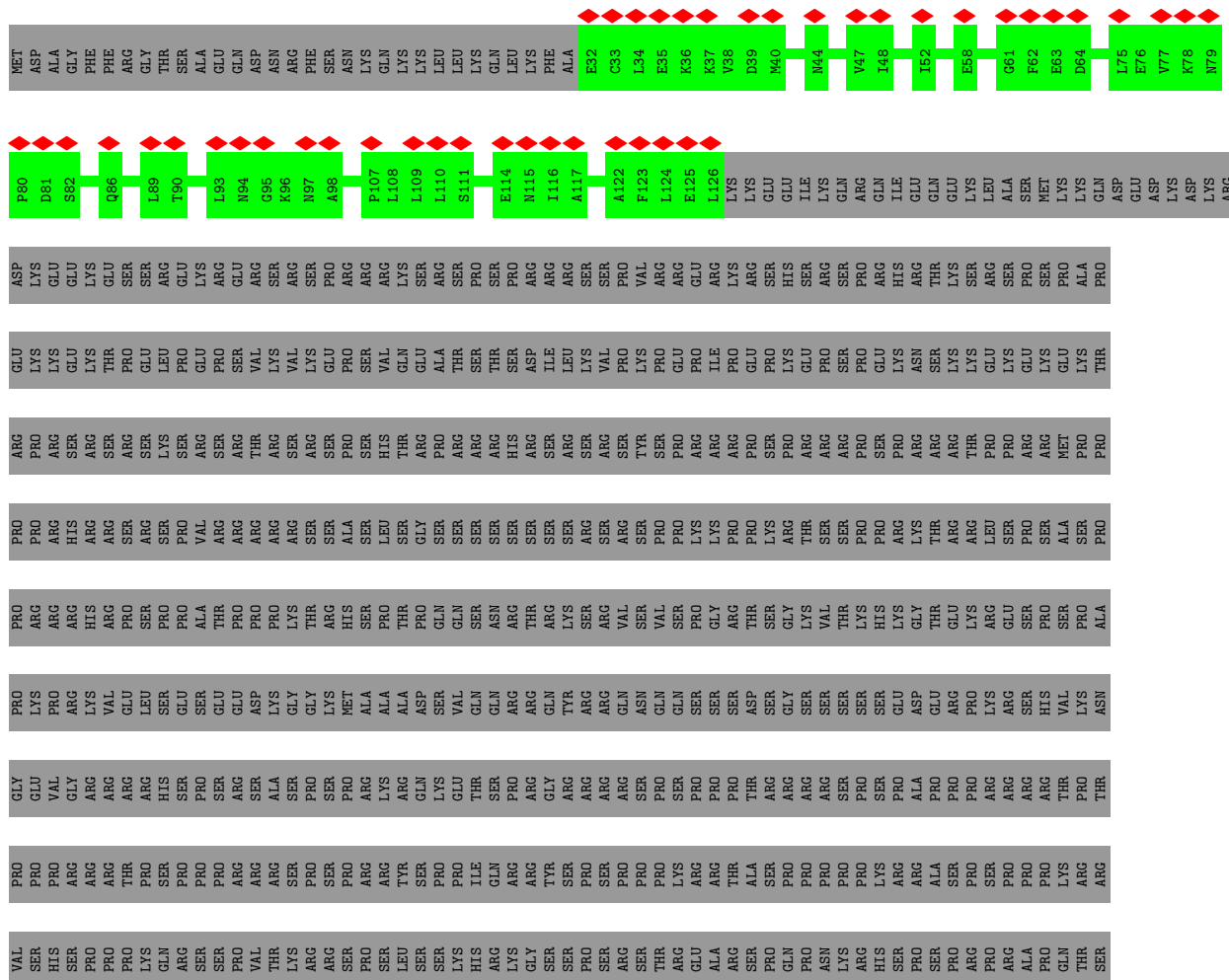








- Molecule 14: Serine/arginine repetitive matrix protein 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39336	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.108	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.047	Depositor
Map size (Å)	445.44, 445.44, 445.44	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.11	0/236	0.25	0/327
2	y	0.13	0/501	0.31	0/697
3	Z	0.11	0/642	0.29	0/994
4	F	0.10	0/374	0.28	0/521
5	4	0.20	0/544	0.37	0/759
6	u	0.18	0/4748	0.35	0/6646
7	T	0.13	0/957	0.31	0/1341
8	E	0.31	0/5980	0.42	0/8363
9	w	0.12	0/394	0.29	0/549
10	x	0.17	0/399	0.32	0/557
11	z	0.12	0/548	0.30	0/766
12	0	0.14	0/770	0.35	0/1079
13	1	0.11	0/609	0.29	0/848
14	Y	0.10	0/481	0.27	0/672
15	2	0.15	0/867	0.35	0/1346
16	7	0.08	0/164	0.20	0/228
All	All	0.22	0/18214	0.36	0/25693

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 [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	L	237	0	113	0	0
2	y	498	0	241	2	0
3	Z	579	0	296	8	0
4	F	374	0	178	2	0
5	4	541	0	266	0	0
6	u	4704	0	2383	7	0
7	T	942	0	490	1	0
8	E	5926	0	2964	28	0
9	w	391	0	197	0	0
10	x	397	0	191	0	0
11	z	544	0	264	1	0
12	0	761	0	376	1	0
13	1	607	0	279	1	0
14	Y	478	0	226	0	0
15	2	778	0	391	5	0
16	7	165	0	68	1	0
All	All	17922	0	8923	50	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 2.

All (50) 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)
8:E:405:SER:CB	8:E:406:PRO:HD3	1.75	1.16
8:E:405:SER:CB	8:E:406:PRO:CD	2.42	0.97
8:E:12:THR:CB	8:E:403:SER:CB	2.44	0.94
8:E:1107:THR:O	8:E:1115:GLU:CB	2.29	0.79
8:E:1106:LYS:CB	8:E:1116:SER:O	2.32	0.77
8:E:12:THR:CB	8:E:403:SER:CA	2.72	0.68
8:E:923:GLY:O	8:E:945:VAL:N	2.20	0.68
8:E:445:SER:N	8:E:766:ALA:O	2.28	0.66
3:Z:156:U:H3	15:2:33:G:H1	0.73	0.65
3:Z:156:U:O4	15:2:33:G:O6	2.16	0.64
3:Z:167:U:OP1	13:1:2:ASN:N	2.32	0.63
15:2:44:U:O2'	15:2:45:C:O5'	2.16	0.63
8:E:12:THR:CB	8:E:403:SER:HA	2.27	0.62
4:F:56:CYS:O	4:F:60:LEU:N	2.31	0.62
8:E:406:PRO:O	8:E:427:CYS:HA	2.00	0.61
8:E:636:GLN:O	8:E:670:GLN:N	2.34	0.61
8:E:1106:LYS:CA	8:E:1116:SER:O	2.48	0.61
2:y:58:CYS:N	2:y:63:GLY:O	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:1107:THR:O	8:E:1115:GLU:CA	2.49	0.60
11:z:53:THR:O	11:z:57:ARG:N	2.35	0.60
12:0:261:LEU:N	12:0:273:MET:O	2.35	0.58
3:Z:146:G:N2	3:Z:147:U:O4	2.37	0.58
8:E:1106:LYS:HA	8:E:1118:VAL:H	1.68	0.58
3:Z:156:U:O2	15:2:33:G:N2	2.25	0.56
8:E:943:THR:CB	8:E:976:LYS:CB	2.86	0.54
8:E:93:GLN:O	8:E:97:ASN:N	2.41	0.53
8:E:1107:THR:O	8:E:1115:GLU:HA	2.09	0.52
3:Z:153:U:P	6:u:1105:GLU:CB	2.99	0.51
6:u:813:PRO:O	6:u:817:HIS:N	2.41	0.51
8:E:1181:GLN:O	8:E:1185:MET:N	2.45	0.50
8:E:511:LEU:N	8:E:515:ALA:O	2.45	0.49
8:E:355:ASN:HA	8:E:402:ASP:O	2.13	0.49
8:E:1106:LYS:C	8:E:1116:SER:O	2.56	0.48
4:F:19:SER:O	4:F:23:ASN:N	2.46	0.47
6:u:1237:LEU:O	6:u:1241:ILE:N	2.47	0.47
8:E:784:THR:O	8:E:802:THR:N	2.46	0.46
3:Z:153:U:OP1	6:u:1105:GLU:CB	2.65	0.45
6:u:1110:VAL:O	6:u:1113:THR:N	2.50	0.44
8:E:85:GLY:O	8:E:107:PHE:N	2.48	0.44
16:7:151:ARG:O	16:7:155:LEU:N	2.44	0.44
3:Z:163:C:O2'	3:Z:164:C:O5'	2.36	0.44
6:u:1000:ILE:O	6:u:1004:ILE:N	2.48	0.44
2:y:41:THR:O	2:y:71:TYR:N	2.46	0.43
8:E:466:ILE:N	8:E:513:ASP:O	2.53	0.42
8:E:1107:THR:N	8:E:1116:SER:O	2.53	0.42
6:u:1259:ARG:N	15:2:56:A:OP1	2.48	0.41
8:E:1106:LYS:CA	8:E:1118:VAL:H	2.34	0.41
7:T:573:ASP:O	7:T:577:LYS:N	2.53	0.41
8:E:316:GLU:O	8:E:323:THR:N	2.52	0.40
8:E:638:GLU:N	8:E:668:GLY:O	2.49	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	L	46/802 (6%)	46 (100%)	0	0	100	100
2	y	98/110 (89%)	94 (96%)	4 (4%)	0	100	100
4	F	73/464 (16%)	71 (97%)	2 (3%)	0	100	100
5	4	106/501 (21%)	96 (91%)	10 (9%)	0	100	100
6	u	922/1304 (71%)	881 (96%)	41 (4%)	0	100	100
7	T	175/895 (20%)	163 (93%)	12 (7%)	0	100	100
8	E	1165/1217 (96%)	1079 (93%)	78 (7%)	8 (1%)	18	55
9	w	76/424 (18%)	74 (97%)	2 (3%)	0	100	100
10	x	77/86 (90%)	68 (88%)	9 (12%)	0	100	100
11	z	106/125 (85%)	94 (89%)	12 (11%)	0	100	100
12	0	148/396 (37%)	133 (90%)	15 (10%)	0	100	100
13	1	120/322 (37%)	111 (92%)	9 (8%)	0	100	100
14	Y	93/904 (10%)	92 (99%)	1 (1%)	0	100	100
16	7	31/393 (8%)	31 (100%)	0	0	100	100
All	All	3236/7943 (41%)	3033 (94%)	195 (6%)	8 (0%)	44	77

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	405	SER
8	E	773	VAL
8	E	920	VAL
8	E	769	LYS
8	E	921	ALA
8	E	406	PRO
8	E	1109	LEU
8	E	402	ASP

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	
2	y	4/95 (4%)	4 (100%)	0	100	100
4	F	1/382 (0%)	1 (100%)	0	100	100
5	4	4/446 (1%)	4 (100%)	0	100	100
6	u	49/1104 (4%)	49 (100%)	0	100	100
7	T	19/776 (2%)	19 (100%)	0	100	100
8	E	60/1051 (6%)	60 (100%)	0	100	100
9	w	4/336 (1%)	4 (100%)	0	100	100
10	x	3/77 (4%)	3 (100%)	0	100	100
11	z	5/109 (5%)	5 (100%)	0	100	100
12	0	10/349 (3%)	10 (100%)	0	100	100
13	1	3/291 (1%)	3 (100%)	0	100	100
14	Y	4/831 (0%)	4 (100%)	0	100	100
All	All	166/5847 (3%)	166 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
15	2	36/188 (19%)	9 (25%)	2 (5%)
3	Z	27/230 (11%)	12 (44%)	1 (3%)
All	All	63/418 (15%)	21 (33%)	3 (4%)

All (21) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	Z	147	U
3	Z	149	A
3	Z	151	A
3	Z	153	U
3	Z	155	A
3	Z	159	U

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Mol	Chain	Res	Type
3	Z	160	G
3	Z	161	U
3	Z	162	C
3	Z	163	C
3	Z	164	C
3	Z	167	U
15	2	30	A
15	2	31	G
15	2	40	C
15	2	44	U
15	2	45	C
15	2	46	U
15	2	47	U
15	2	48	A
15	2	49	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	Z	163	C
15	2	44	U
15	2	46	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

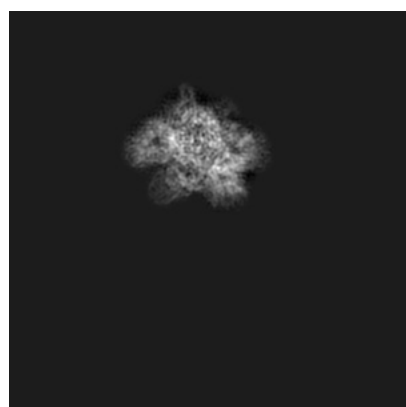
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11696. These allow visual inspection of the internal detail of the map and identification of artifacts.

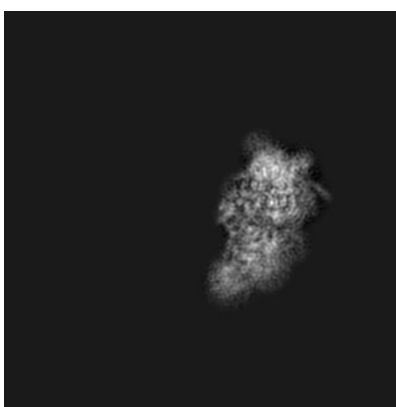
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

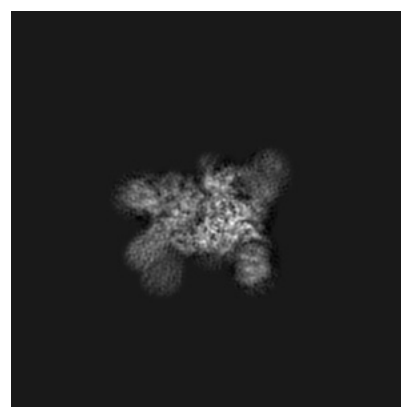
6.1.1 Primary map



X



Y

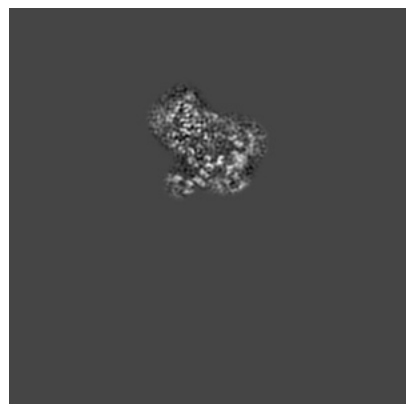


Z

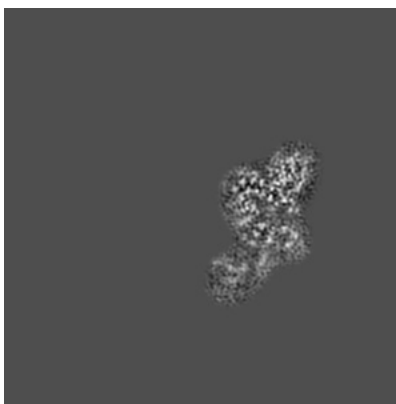
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 192



Y Index: 192

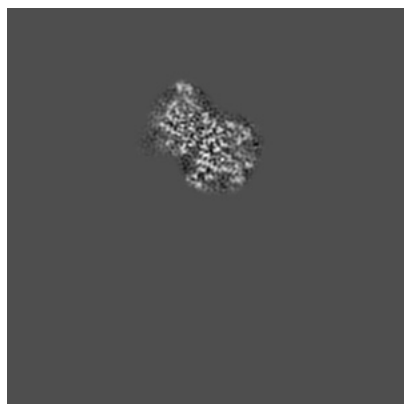


Z Index: 192

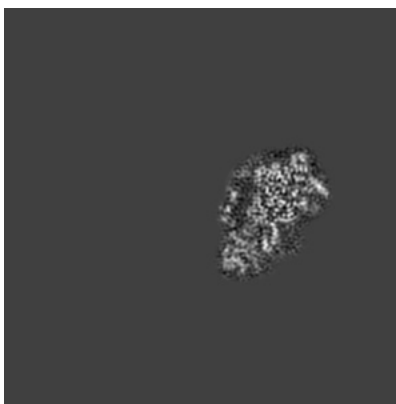
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

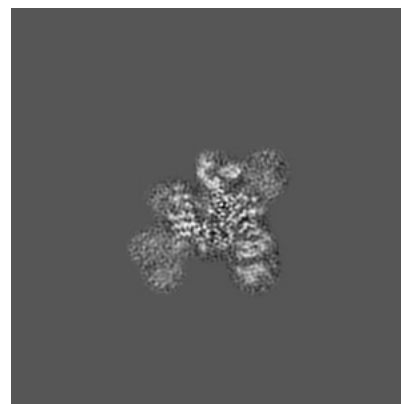
6.3.1 Primary map



X Index: 208



Y Index: 175

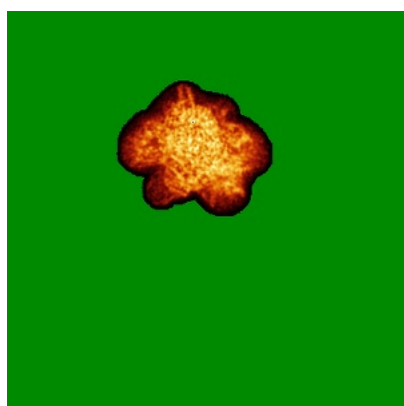


Z Index: 259

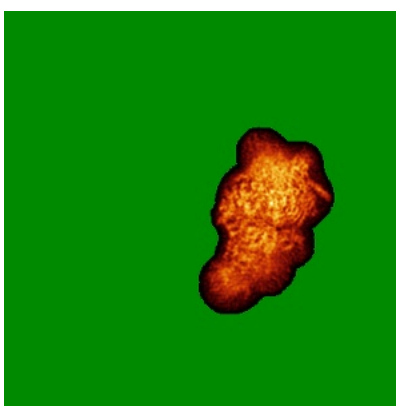
The images above show the largest variance slices of the map in three orthogonal directions.

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

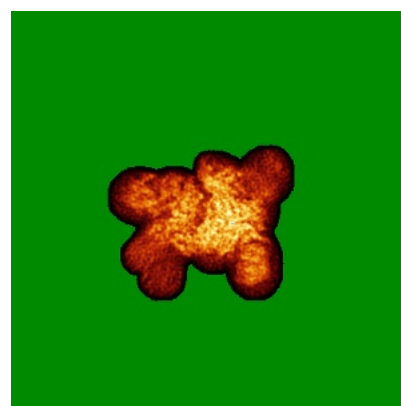
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.047. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

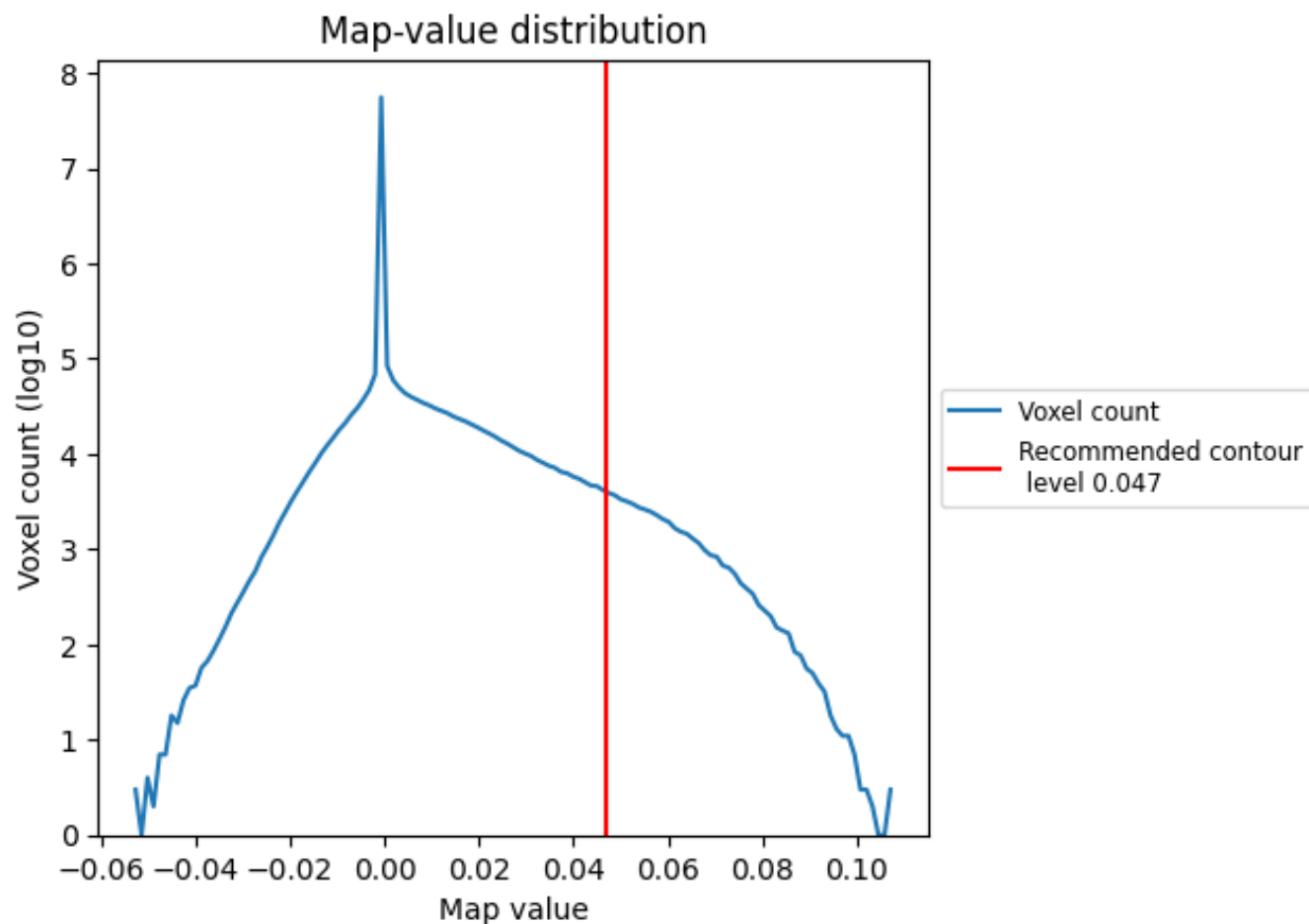
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

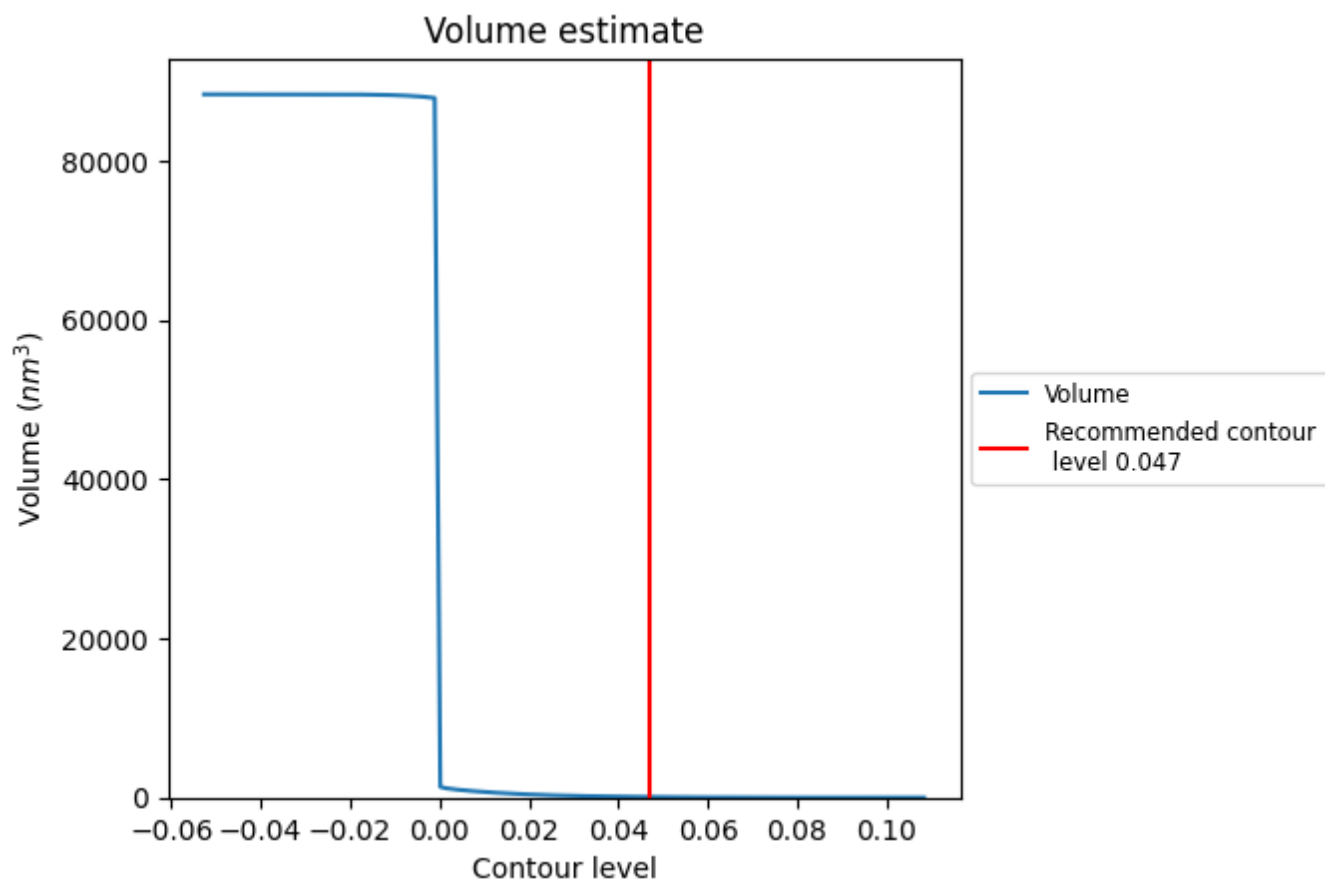
This section contains the results of statistical analysis of the map.

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.

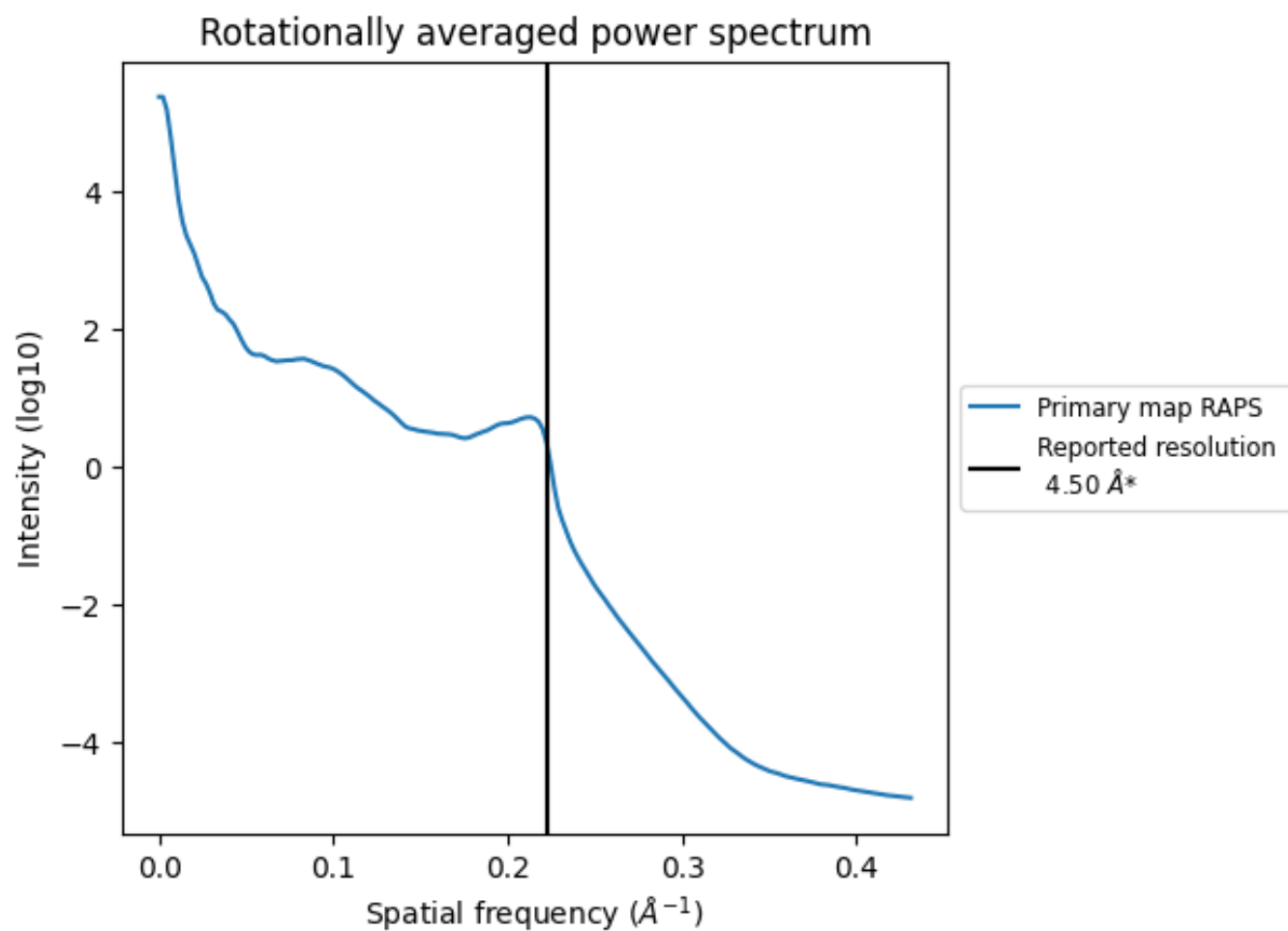
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 74 nm^3 ; this corresponds to an approximate mass of 67 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 0.222 Å⁻¹

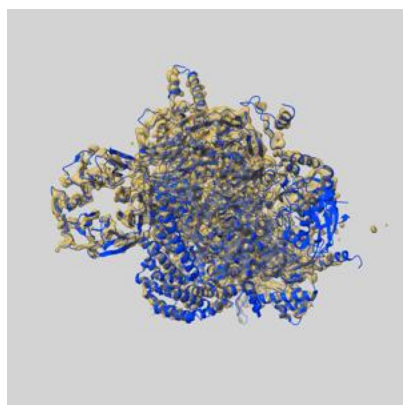
8 Fourier-Shell correlation

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

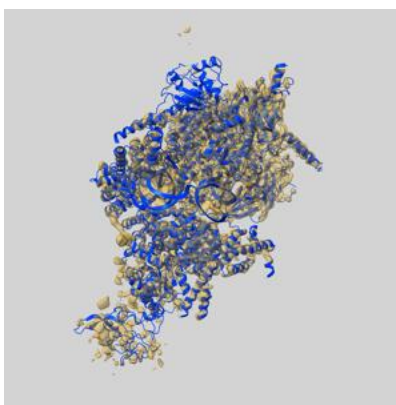
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11696 and PDB model 7ABH. Per-residue inclusion information can be found in section [3](#) on page [7](#).

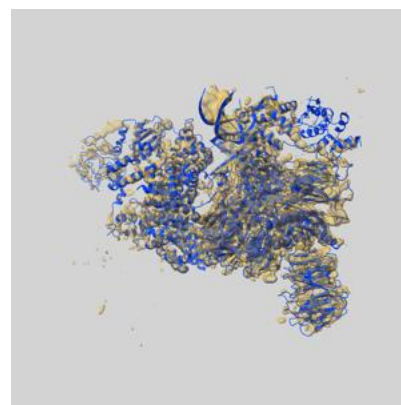
9.1 Map-model overlay [i](#)



X



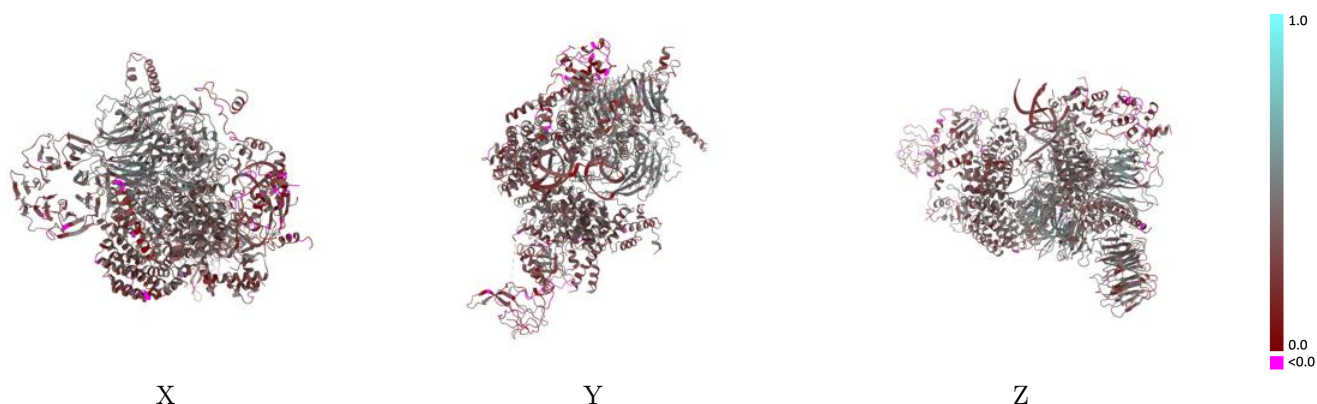
Y



Z

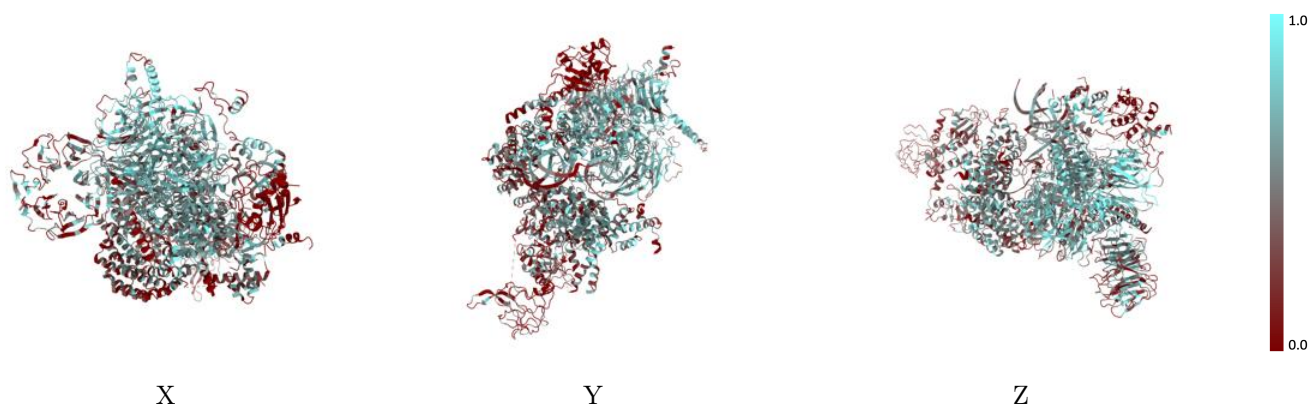
The images above show the 3D surface view of the map at the recommended contour level 0.047 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



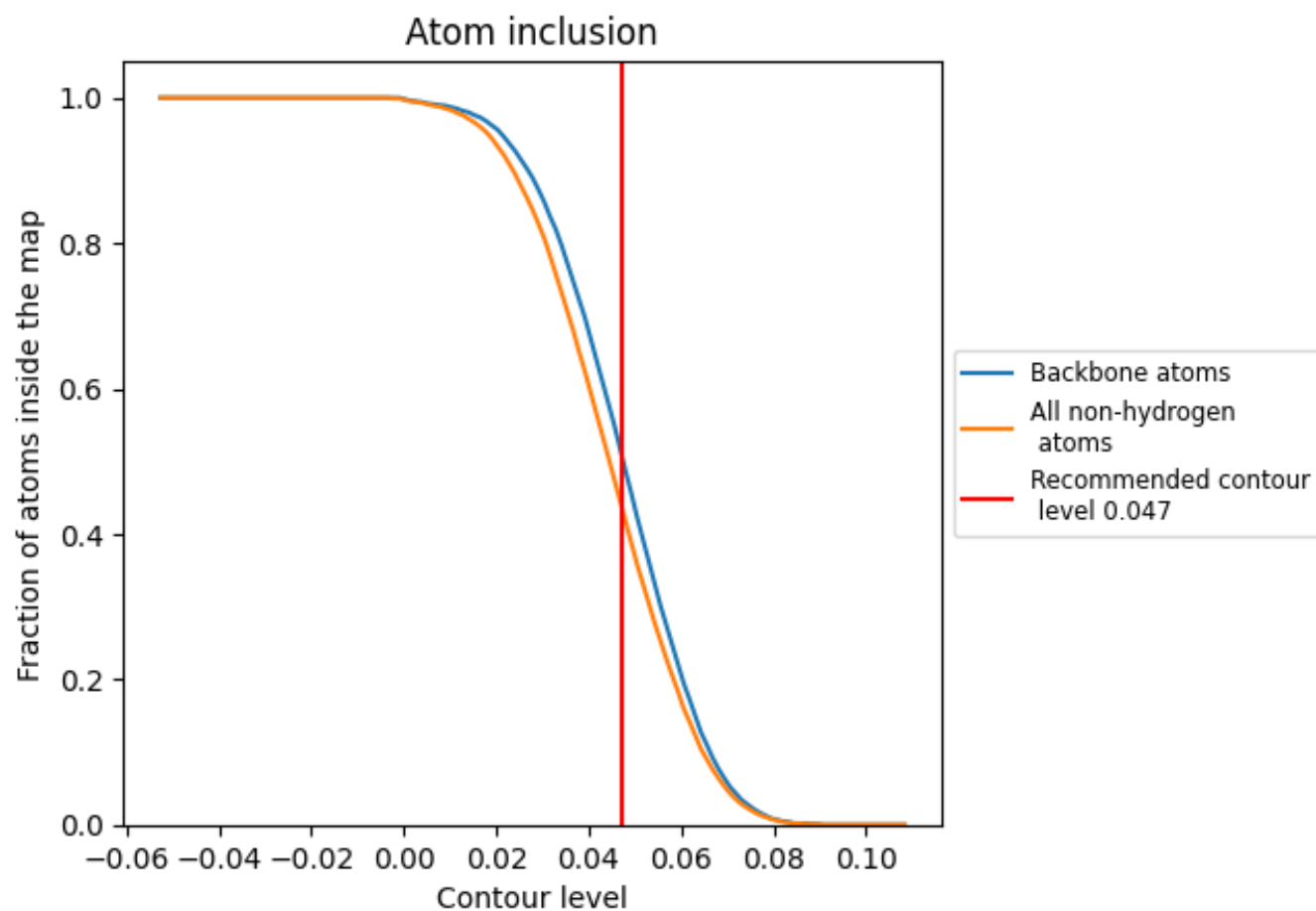
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.047).

9.4 Atom inclusion [i](#)



At the recommended contour level, 51% of all backbone atoms, 44% 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 (0.047) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4400	 0.3560
0	 0.1310	 0.2330
1	 0.3360	 0.3570
2	 0.4220	 0.2720
4	 0.4440	 0.3010
7	 0.1700	 0.1720
E	 0.5480	 0.4230
F	 0.4040	 0.2960
L	 0.3500	 0.3230
T	 0.3250	 0.3250
Y	 0.4390	 0.3400
Z	 0.2990	 0.3010
u	 0.4600	 0.3480
w	 0.0030	 0.1820
x	 0.5790	 0.4020
y	 0.5380	 0.4210
z	 0.2650	 0.3080

