



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:03 AM UTC

PDB ID : 6QKL / pdb_00006qkl
EMDB ID : EMD-3145
Title : Mechanism of eIF6 release from the nascent 60S ribosomal subunit
Authors : Kargas, V.; Warren, A.J.
Deposited on : 2019-01-29
Resolution : 3.30 Å(reported)

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:

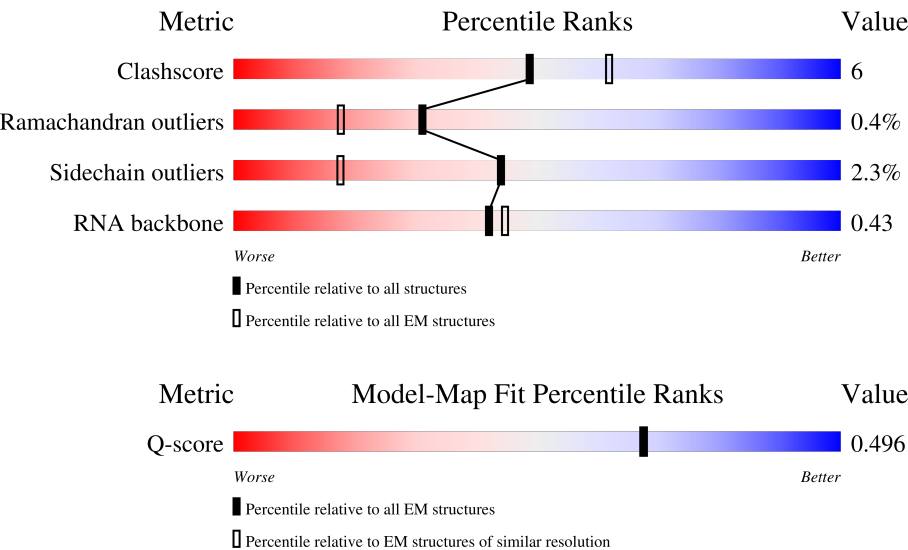
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	N	3741	
2	A	398	
3	B	188	

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Mol	Chain	Length	Quality of chain
4	E	136	
5	F	217	
6	G	69	
7	H	52	
8	I	224	
9	J	250	
10	C	205	
11	D	166	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 39284 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 26S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	1158	Total	C	N	O	P	0	0
			24677	11044	4417	8061	1155		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	388	Total	C	N	O	S	0	0
			3098	1971	583	533	11		

- Molecule 3 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	185	Total	C	N	O	S	0	0
			1467	932	260	269	6		

- Molecule 4 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	128	Total	C	N	O	S	0	0
			963	608	178	170	7		

- Molecule 5 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	216	Total	C	N	O	S	0	0
			1713	1074	331	296	12		

- Molecule 6 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	53	Total	C	N	O	S	0	0
			453	297	79	74	3		

- Molecule 7 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	51	Total	C	N	O	S	0	0
			417	263	86	62	6		

- Molecule 8 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	224	Total	C	N	O	S	0	0
			1679	1046	289	334	10		

- Molecule 9 is a protein called Ribosome maturation protein SBDS.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	250	Total	C	N	O	S	0	0
			2005	1267	349	378	11		

- Molecule 10 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C	205	Total	C	N	O	S	0	0
			1567	996	271	292	8		

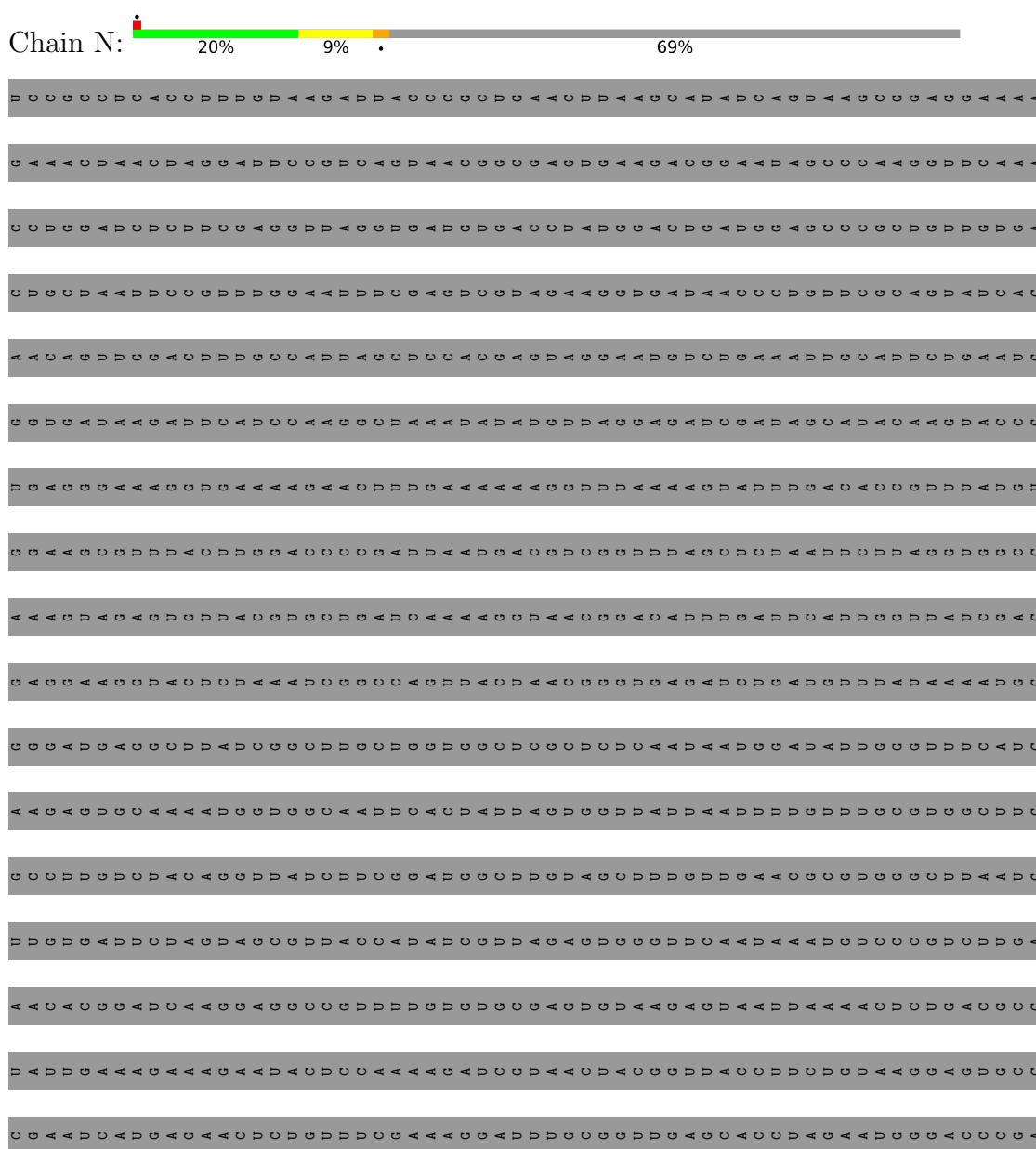
- Molecule 11 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	D	166	Total	C	N	O	S	0	0
			1245	790	220	228	7		

3 Residue-property plots [i](#)

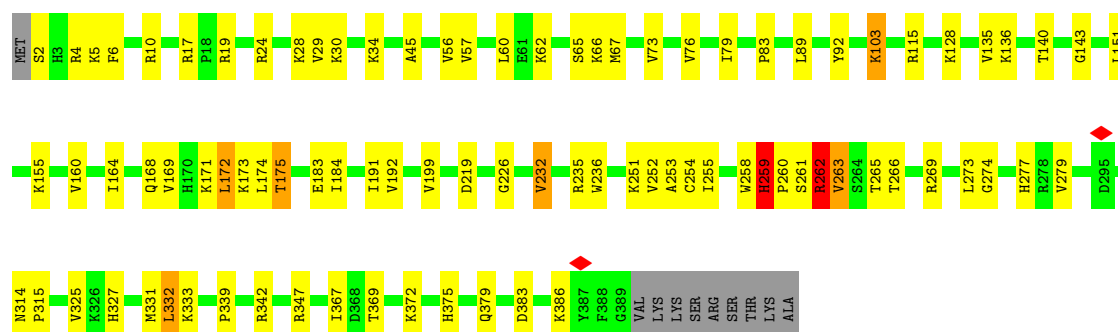
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 26S RIBOSOMAL RNA

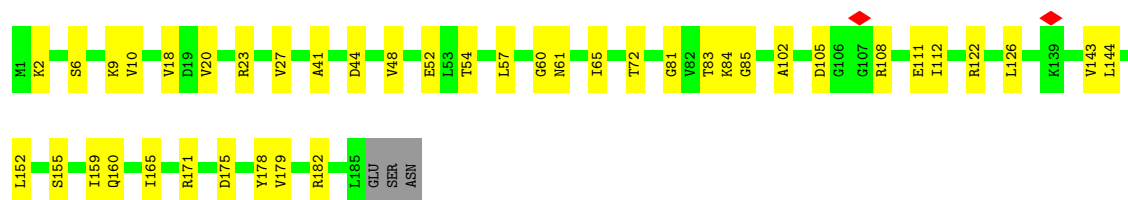
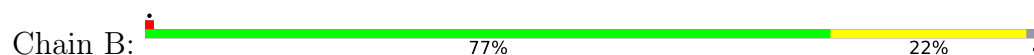




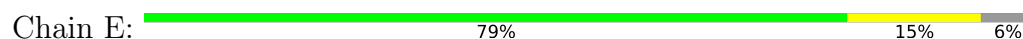




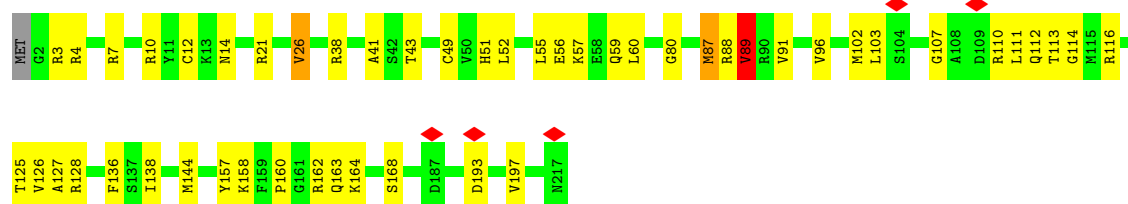
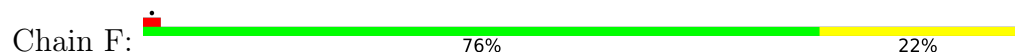
• Molecule 3: 60S ribosomal protein L9



• Molecule 4: 60S ribosomal protein L23



• Molecule 5: 60S ribosomal protein L10



• Molecule 6: 60S ribosomal protein L24

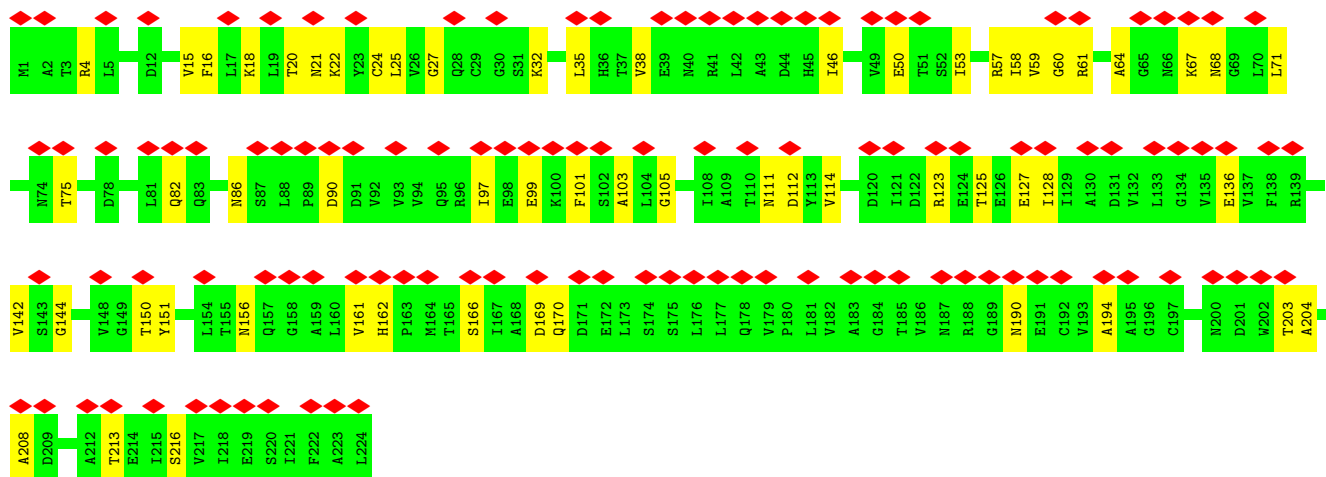
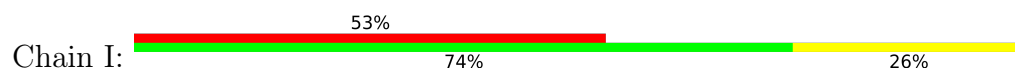


• Molecule 7: Ubiquitin-60S ribosomal protein L40

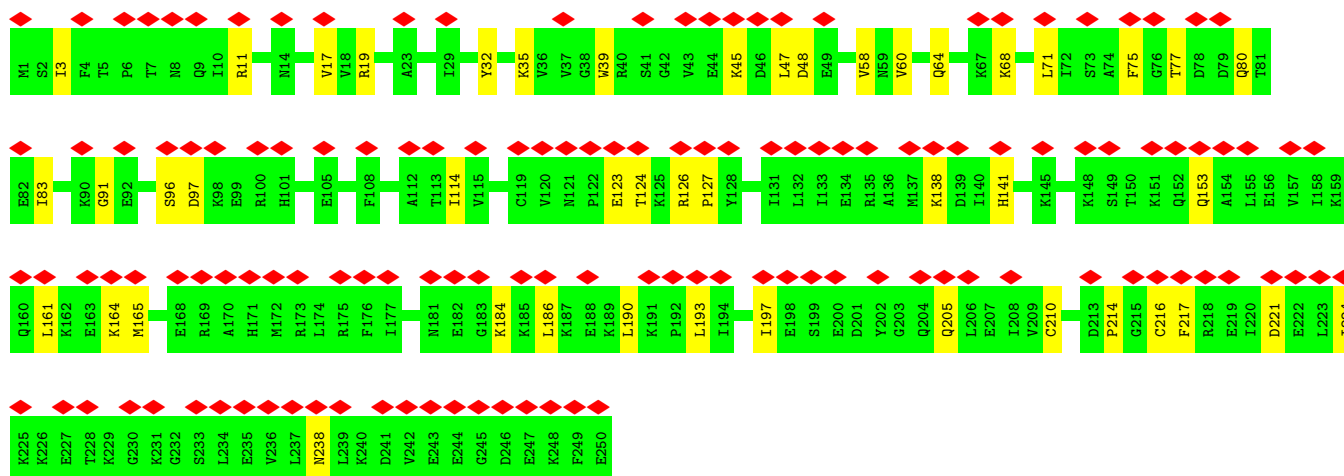
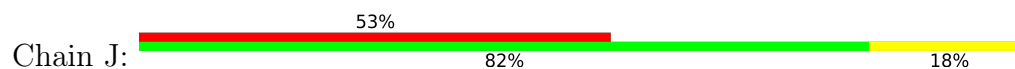




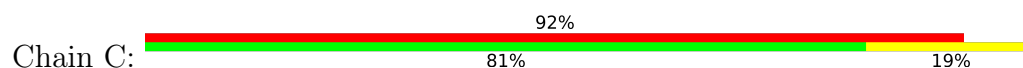
• Molecule 8: Eukaryotic translation initiation factor 6

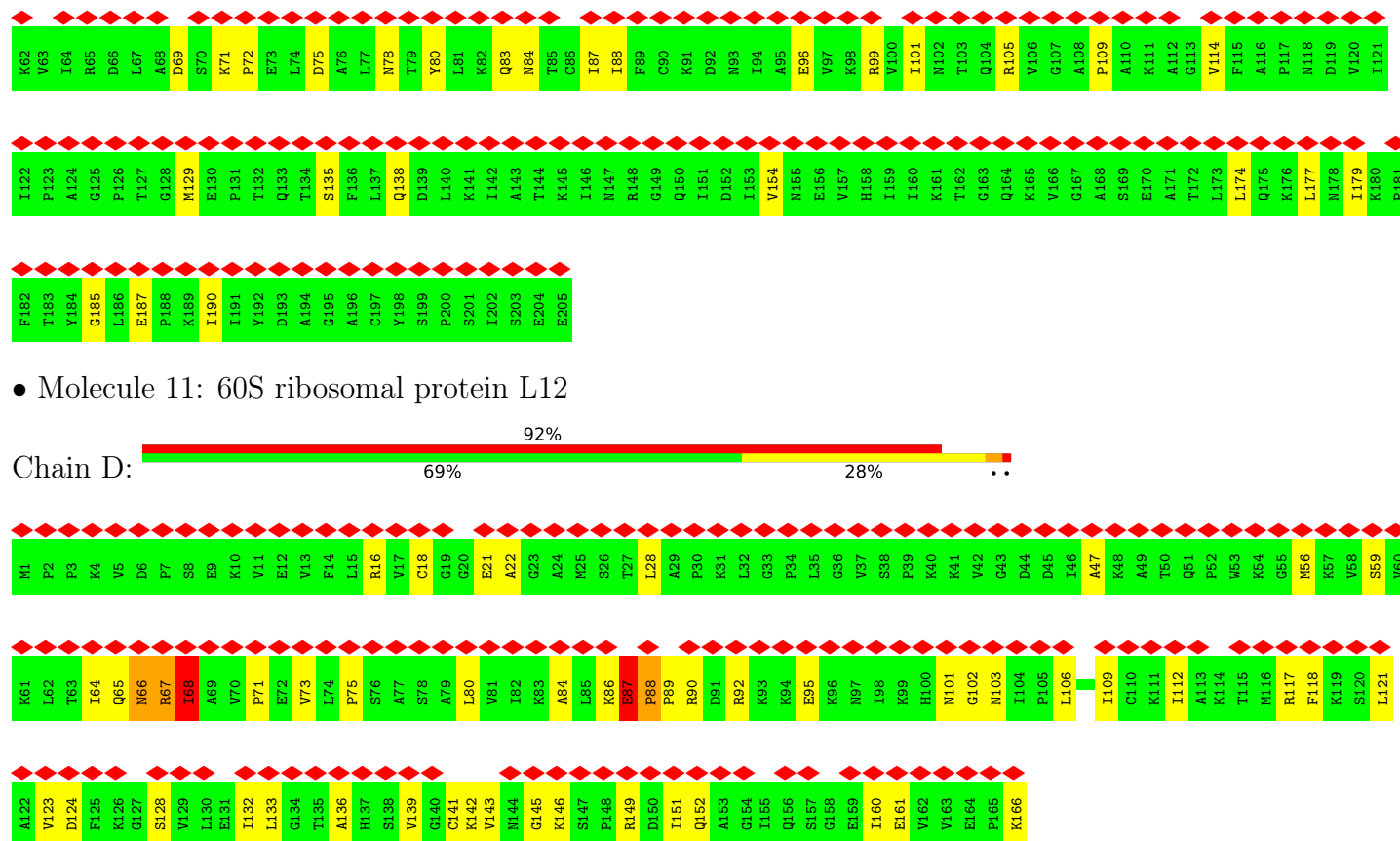


• Molecule 9: Ribosome maturation protein SBDS



• Molecule 10: 60S acidic ribosomal protein P0





- Molecule 11: 60S ribosomal protein L12

92%

Chain D:

69%

28%

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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43063	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	2200	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.554	Depositor
Minimum map value	-1.083	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.14	Depositor
Map size ($\text{\AA}$)	399.0, 399.0, 399.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.33, 1.33, 1.33	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	N	0.52	3/27610 (0.0%)	0.53	9/43014 (0.0%)
2	A	0.52	0/3163	0.73	5/4239 (0.1%)
3	B	0.39	0/1486	0.63	0/1999
4	E	0.44	0/978	0.63	0/1316
5	F	0.41	0/1744	0.70	5/2335 (0.2%)
6	G	0.35	0/466	0.58	0/624
7	H	0.44	0/423	0.64	0/560
8	I	0.30	0/1699	0.70	0/2316
9	J	0.27	0/2028	0.65	3/2715 (0.1%)
10	C	0.23	0/1588	0.58	0/2137
11	D	0.32	0/1265	0.83	5/1702 (0.3%)
All	All	0.47	3/42450 (0.0%)	0.58	27/62957 (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
2	A	1	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	2660	G	O3'-P	-7.33	1.50	1.61
1	N	2659	G	O3'-P	-5.84	1.52	1.61
1	N	3272	G	O3'-P	-5.66	1.52	1.61

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	2660	G	C1'-C2'-O2'	-11.49	91.16	108.40
11	D	151	ILE	N-CA-C	-8.08	103.37	111.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	262	ARG	CG-CD-NE	-7.75	94.94	112.00
11	D	88	PRO	N-CA-C	7.47	119.82	110.70
1	N	3273	A	C1'-C2'-O2'	-6.96	97.95	108.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	259	HIS	CA

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	N	24677	0	12445	144	0
2	A	3098	0	3224	64	0
3	B	1467	0	1538	22	0
4	E	963	0	1016	16	0
5	F	1713	0	1766	38	0
6	G	453	0	454	6	0
7	H	417	0	466	9	0
8	I	1679	0	1676	33	0
9	J	2005	0	2097	29	0
10	C	1567	0	1653	21	0
11	D	1245	0	1338	39	0
All	All	39284	0	27673	371	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 6.

The worst 5 of 371 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)
11:D:86:LYS:O	11:D:87:GLU:O	1.72	1.06
1:N:1457:G:H21	1:N:1521:A:N6	1.66	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:110:ARG:HE	9:J:11:ARG:NE	1.69	0.90
5:F:110:ARG:HG2	5:F:111:LEU:HG	1.55	0.87
1:N:1457:G:H21	1:N:1521:A:H62	1.19	0.87

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	
2	A	386/398 (97%)	353 (92%)	31 (8%)	2 (0%)	24	55
3	B	183/188 (97%)	168 (92%)	15 (8%)	0	100	100
4	E	126/136 (93%)	116 (92%)	10 (8%)	0	100	100
5	F	214/217 (99%)	195 (91%)	18 (8%)	1 (0%)	24	55
6	G	51/69 (74%)	48 (94%)	3 (6%)	0	100	100
7	H	49/52 (94%)	42 (86%)	7 (14%)	0	100	100
8	I	222/224 (99%)	194 (87%)	27 (12%)	1 (0%)	24	55
9	J	248/250 (99%)	219 (88%)	28 (11%)	1 (0%)	30	60
10	C	203/205 (99%)	176 (87%)	27 (13%)	0	100	100
11	D	164/166 (99%)	139 (85%)	23 (14%)	2 (1%)	10	37
All	All	1846/1905 (97%)	1650 (89%)	189 (10%)	7 (0%)	31	60

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	123	ARG
5	F	89	VAL
9	J	47	LEU
11	D	68	ILE

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Mol	Chain	Res	Type
11	D	87	GLU

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	A	328/337 (97%)	316 (96%)	12 (4%)	30	58
3	B	165/168 (98%)	163 (99%)	2 (1%)	63	75
4	E	103/108 (95%)	103 (100%)	0	100	100
5	F	179/180 (99%)	176 (98%)	3 (2%)	53	71
6	G	50/65 (77%)	49 (98%)	1 (2%)	48	68
7	H	47/48 (98%)	43 (92%)	4 (8%)	10	33
8	I	187/190 (98%)	184 (98%)	3 (2%)	55	72
9	J	226/228 (99%)	224 (99%)	2 (1%)	70	78
10	C	171/172 (99%)	166 (97%)	5 (3%)	37	62
11	D	139/139 (100%)	135 (97%)	4 (3%)	37	62
All	All	1595/1635 (98%)	1559 (98%)	36 (2%)	44	66

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	C	21	THR
11	D	139	VAL
10	C	114	VAL
11	D	66	ASN
3	B	20	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
9	J	86	GLN
10	C	155	ASN

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Mol	Chain	Res	Type
9	J	181	ASN
10	C	83	GLN
11	D	152	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	N	1153/3741 (30%)	266 (23%)	10 (0%)

5 of 266 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	N	1225	G
1	N	1231	U
1	N	1233	G
1	N	1236	G
1	N	1240	U

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	N	2515	G
1	N	2995	G
1	N	3457	U
1	N	1519	C
1	N	1525	G

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

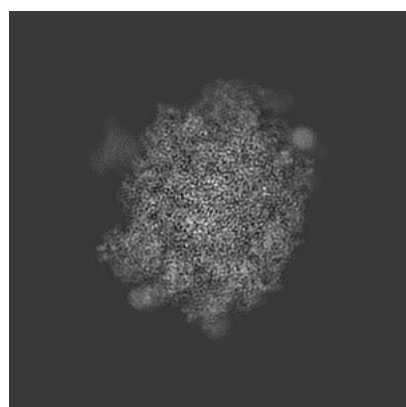
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3145. These allow visual inspection of the internal detail of the map and identification of artifacts.

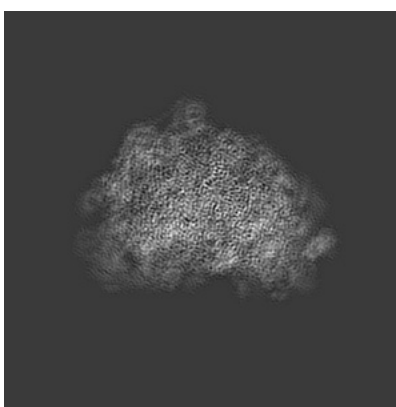
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

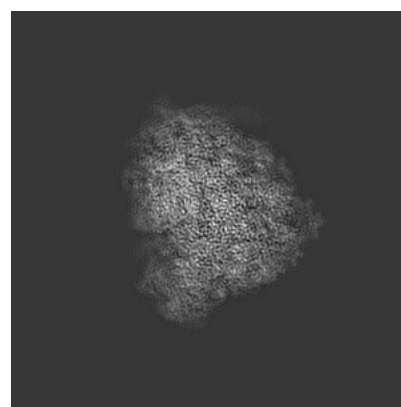
6.1.1 Primary map



X



Y

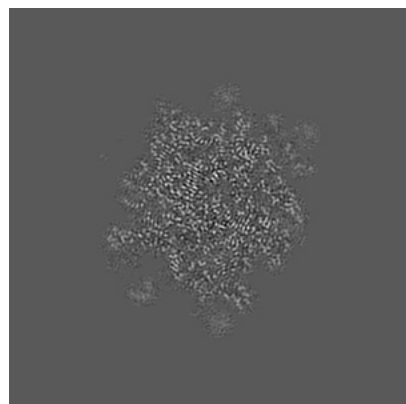


Z

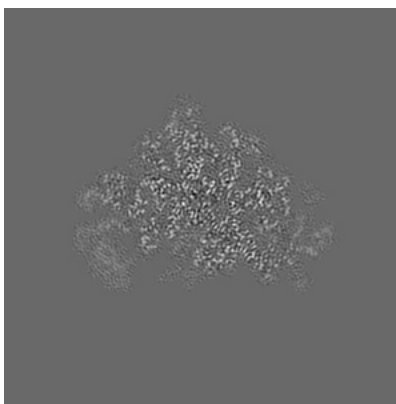
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150

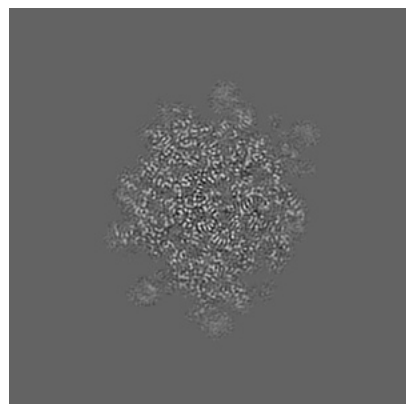


Z Index: 150

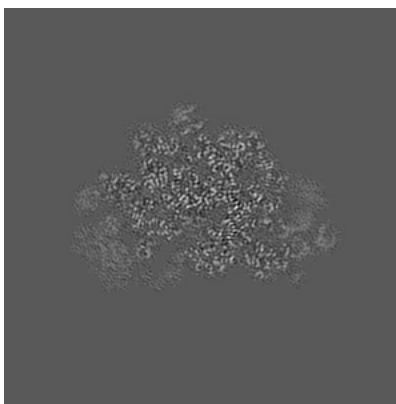
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

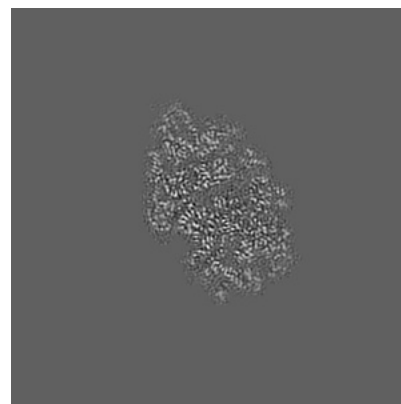
6.3.1 Primary map



X Index: 153



Y Index: 155

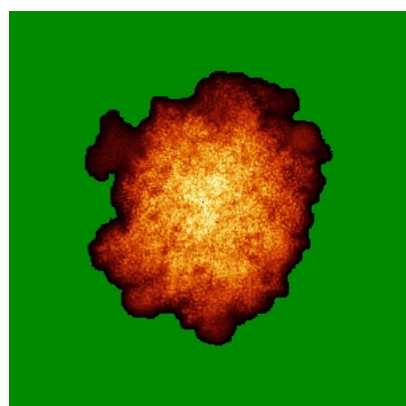


Z Index: 161

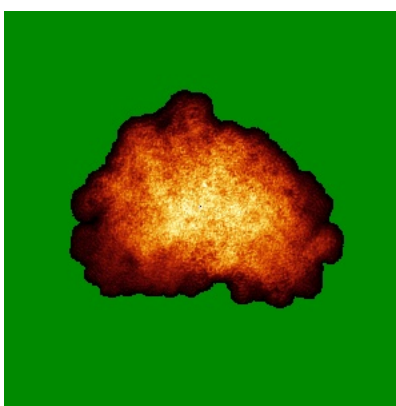
The images above show the largest variance slices of the map in three orthogonal directions.

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

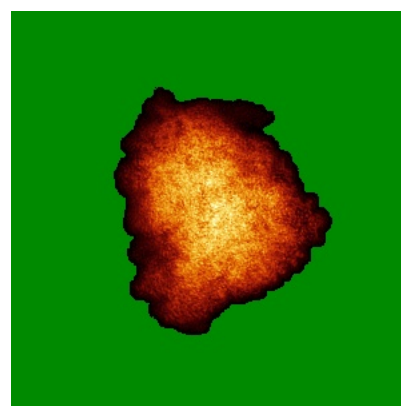
6.4.1 Primary map



X



Y

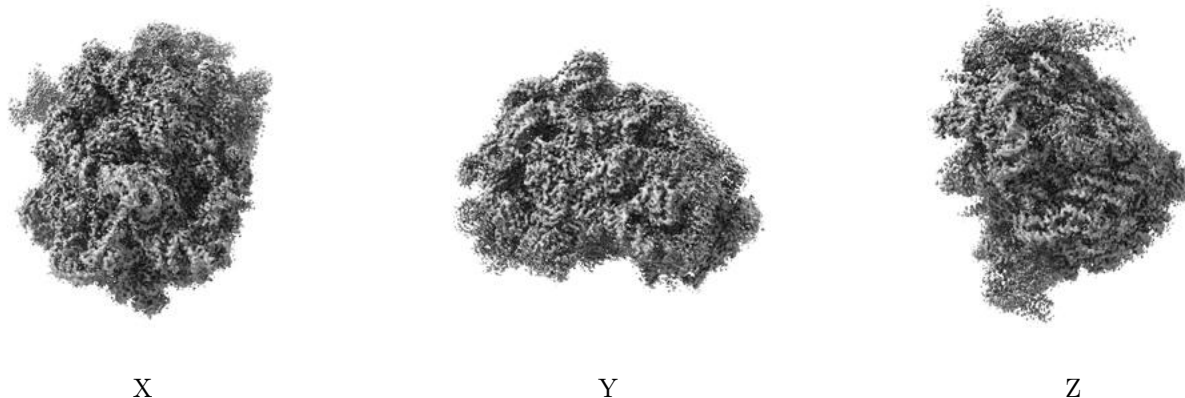


Z

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

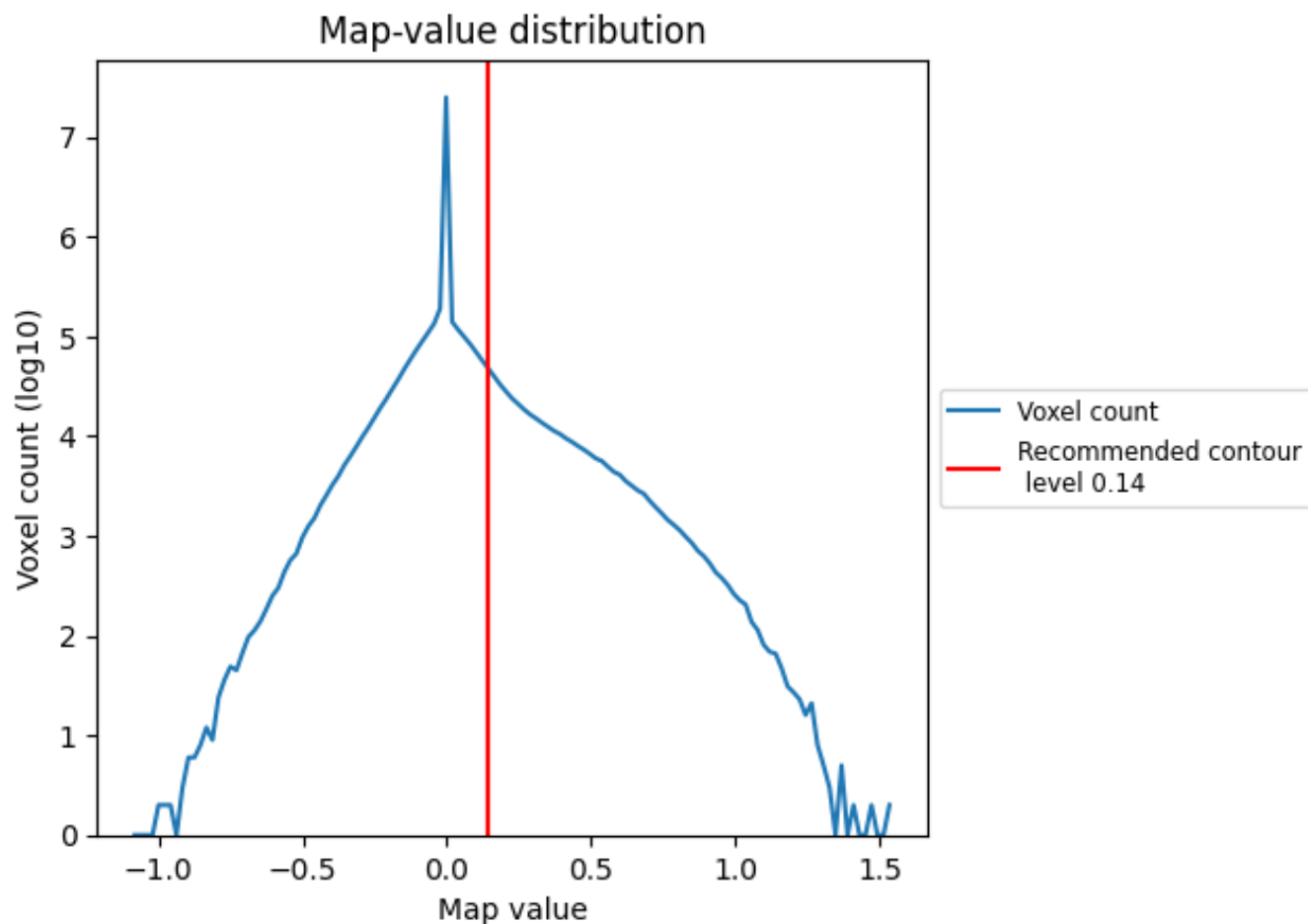
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

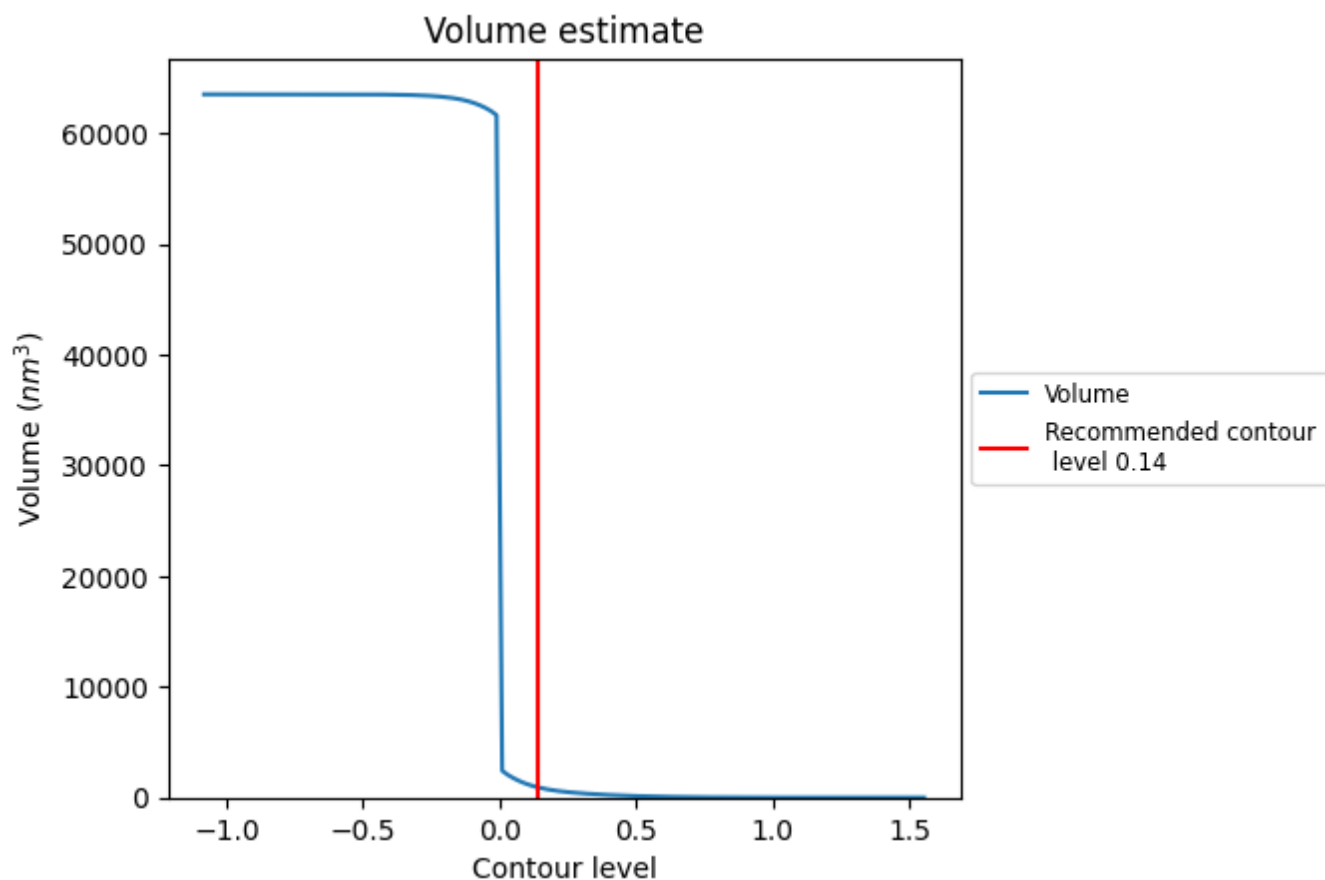
This section contains the results of statistical analysis of the map.

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.

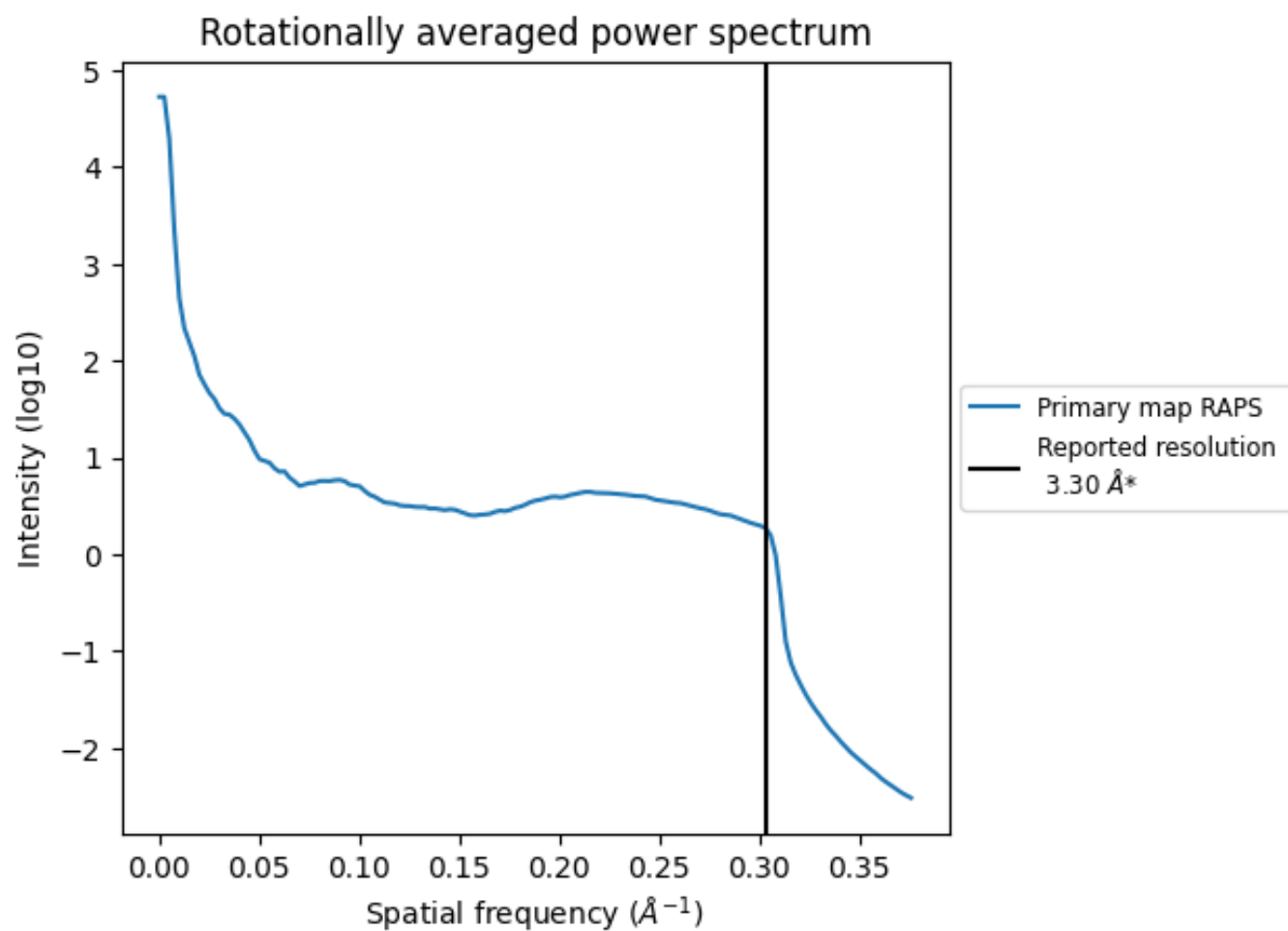
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 926 nm³; this corresponds to an approximate mass of 837 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 0.303 Å⁻¹

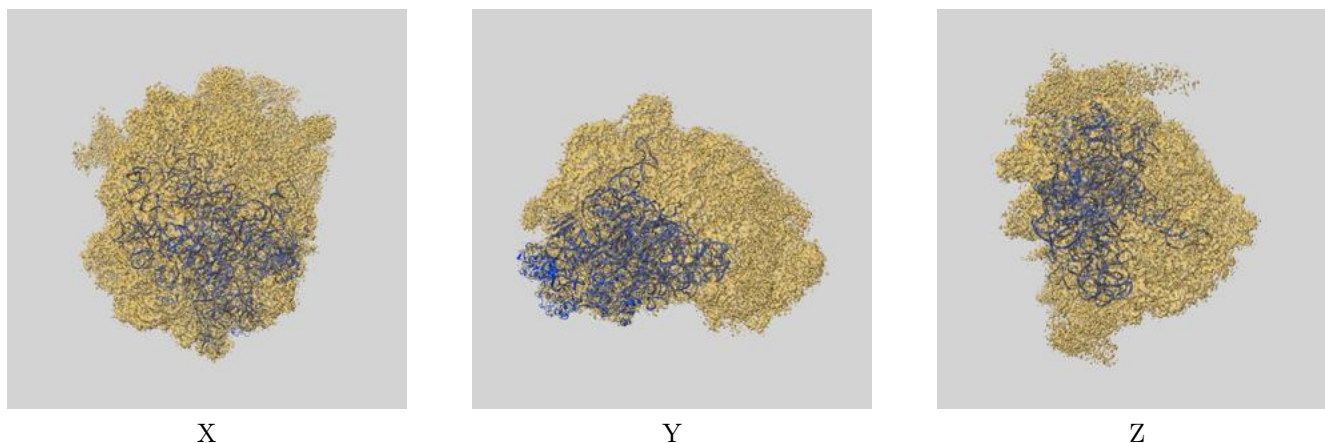
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

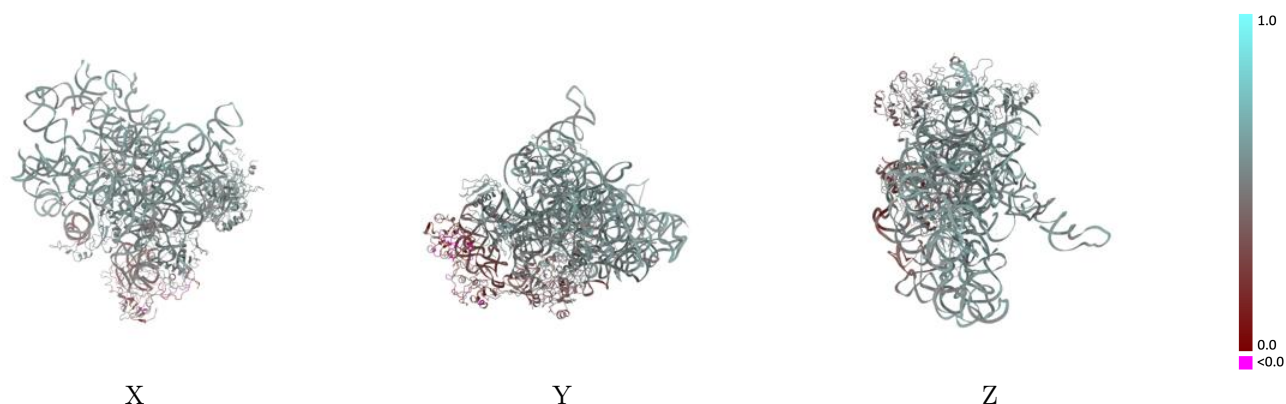
This section contains information regarding the fit between EMDB map EMD-3145 and PDB model 6QKL. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



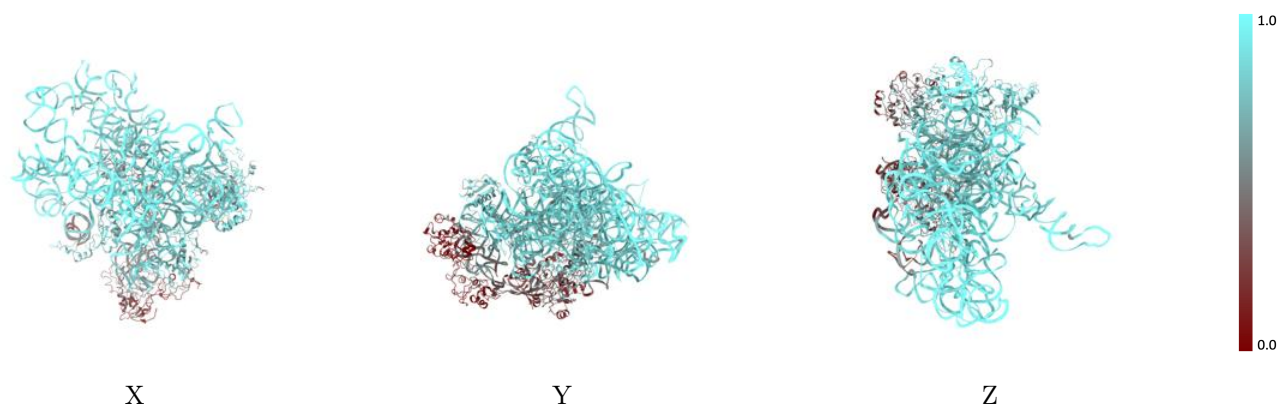
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



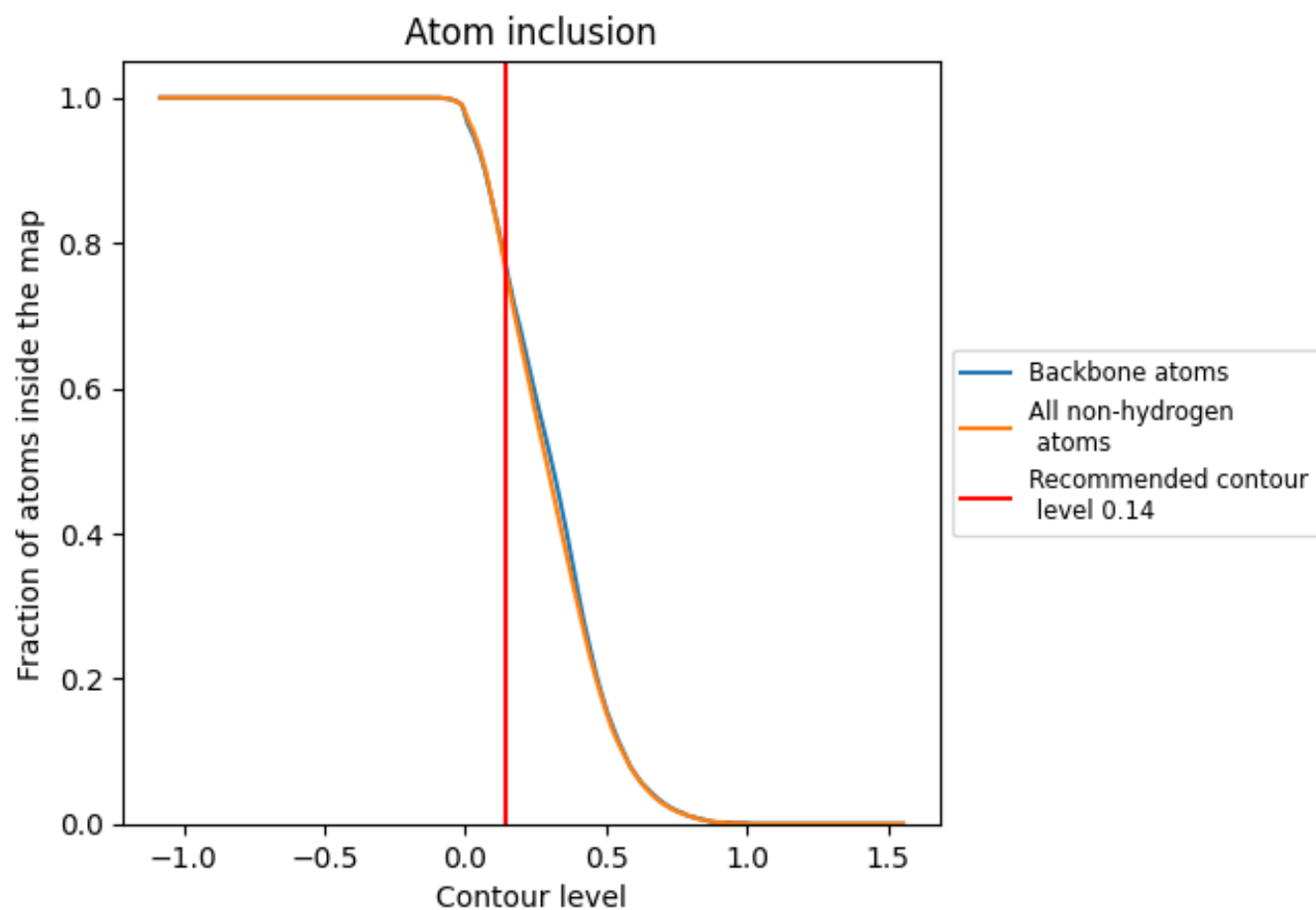
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 77% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7690	0.4960
A	0.8360	0.5460
B	0.8010	0.5270
C	0.1230	0.2530
D	0.1530	0.2800
E	0.8400	0.5560
F	0.7890	0.5290
G	0.7970	0.5280
H	0.8540	0.5450
I	0.3870	0.4180
J	0.3840	0.3850
N	0.8810	0.5230

1.0

0.0

<0.0