



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:58 PM UTC

PDB ID : 6H25 / pdb_00006h25
EMDB ID : EMD-0128
Title : Human nuclear RNA exosome EXO-10-MPP6 complex
Authors : Gerlach, P.; Schuller, J.M.; Falk, S.; Basquin, J.; Conti, E.
Deposited on : 2018-07-13
Resolution : 3.80 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:

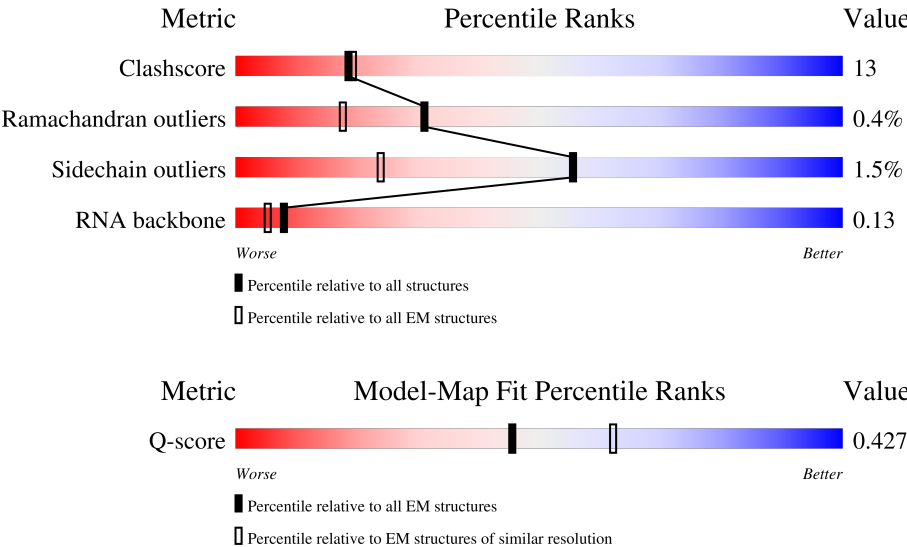
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	10198 (3.30 - 4.30)

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	443	
2	B	249	
3	C	278	

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Mol	Chain	Length	Quality of chain
4	D	237	75%14%11%
5	E	295	79%17%..
6	F	276	82%6%12%
7	G	293	5%63%8%.28%
8	H	297	78%13%.7%
9	I	199	22%..75%
10	J	962	7%72%16%.10%
11	K	166	16%5%..78%
12	R	44	..9%86%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 22138 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 Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	287	Total	C	N	O	S	0	0
			2221	1400	394	410	17		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q06265
A	-2	PRO	-	expression tag	UNP Q06265
A	-1	ASP	-	expression tag	UNP Q06265
A	0	SER	-	expression tag	UNP Q06265

- Molecule 2 is a protein called Exosome complex component RRP41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	239	Total	C	N	O	S	0	0
			1771	1096	332	334	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q9NPD3
B	-2	PRO	-	expression tag	UNP Q9NPD3
B	-1	ASP	-	expression tag	UNP Q9NPD3
B	0	SER	-	expression tag	UNP Q9NPD3

- Molecule 3 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	264	Total	C	N	O	S	0	0
			1923	1209	315	385	14		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	ARG	-	expression tag	UNP Q96B26
C	0	SER	-	expression tag	UNP Q96B26

- Molecule 4 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	210	Total	C	N	O	S	0	0
			1570	982	280	297	11		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	ARG	-	expression tag	UNP Q9NQT4
D	0	SER	-	expression tag	UNP Q9NQT4

- Molecule 5 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	287	Total	C	N	O	S	0	0
			2144	1345	364	420	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP Q15024
E	-2	PRO	-	expression tag	UNP Q15024
E	-1	ASP	-	expression tag	UNP Q15024
E	0	SER	-	expression tag	UNP Q15024

- Molecule 6 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	244	Total	C	N	O	S	0	0
			1752	1097	326	322	7		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP Q5RKV6
F	-2	PRO	-	expression tag	UNP Q5RKV6
F	-1	ASP	-	expression tag	UNP Q5RKV6
F	0	SER	-	expression tag	UNP Q5RKV6

- Molecule 7 is a protein called Exosome complex component RRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	210	Total	C	N	O	S	0	0
			1527	979	272	267	9		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-17	GLY	-	expression tag	UNP Q9NQT5
G	-16	SER	-	expression tag	UNP Q9NQT5
G	-15	GLY	-	expression tag	UNP Q9NQT5
G	-14	SER	-	expression tag	UNP Q9NQT5
G	-13	GLY	-	expression tag	UNP Q9NQT5
G	-12	SER	-	expression tag	UNP Q9NQT5
G	-11	GLY	-	expression tag	UNP Q9NQT5
G	-10	SER	-	expression tag	UNP Q9NQT5
G	-9	GLY	-	expression tag	UNP Q9NQT5
G	-8	SER	-	expression tag	UNP Q9NQT5
G	-7	GLY	-	expression tag	UNP Q9NQT5
G	-6	SER	-	expression tag	UNP Q9NQT5
G	-5	GLY	-	expression tag	UNP Q9NQT5
G	-4	SER	-	expression tag	UNP Q9NQT5
G	-3	GLY	-	expression tag	UNP Q9NQT5
G	-2	SER	-	expression tag	UNP Q9NQT5
G	-1	GLY	-	expression tag	UNP Q9NQT5
G	0	SER	-	expression tag	UNP Q9NQT5

- Molecule 8 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	275	Total	C	N	O	S	0	0
			2066	1306	364	384	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-3	GLY	-	expression tag	UNP Q13868
H	-2	PRO	-	expression tag	UNP Q13868
H	-1	ASP	-	expression tag	UNP Q13868
H	0	SER	-	expression tag	UNP Q13868

- Molecule 9 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	50	Total	C	N	O	S	0	0
			373	233	66	70	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	GLY	-	expression tag	UNP Q9Y3B2
I	-2	PRO	-	expression tag	UNP Q9Y3B2
I	-1	ASP	-	expression tag	UNP Q9Y3B2
I	0	SER	-	expression tag	UNP Q9Y3B2

- Molecule 10 is a protein called Exosome complex exonuclease RRP44.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	868	Total	C	N	O	S	0	0
			6488	4100	1176	1184	28		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLY	-	expression tag	UNP Q9Y2L1
J	-2	PRO	-	expression tag	UNP Q9Y2L1
J	-1	ASP	-	expression tag	UNP Q9Y2L1
J	0	SER	-	expression tag	UNP Q9Y2L1
J	146	ASN	ASP	engineered mutation	UNP Q9Y2L1
J	487	ASN	ASP	engineered mutation	UNP Q9Y2L1

- Molecule 11 is a protein called M-phase phosphoprotein 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	37	Total	C	N	O	0	0
			183	109	37	37		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-5	GLY	-	expression tag	UNP Q99547
K	-4	PRO	-	expression tag	UNP Q99547
K	-3	ASP	-	expression tag	UNP Q99547
K	-2	SER	-	expression tag	UNP Q99547
K	-1	ALA	-	expression tag	UNP Q99547
K	0	SER	-	expression tag	UNP Q99547

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Chain	Residue	Modelled	Actual	Comment	Reference
K	8	LYS	ARG	conflict	UNP Q99547

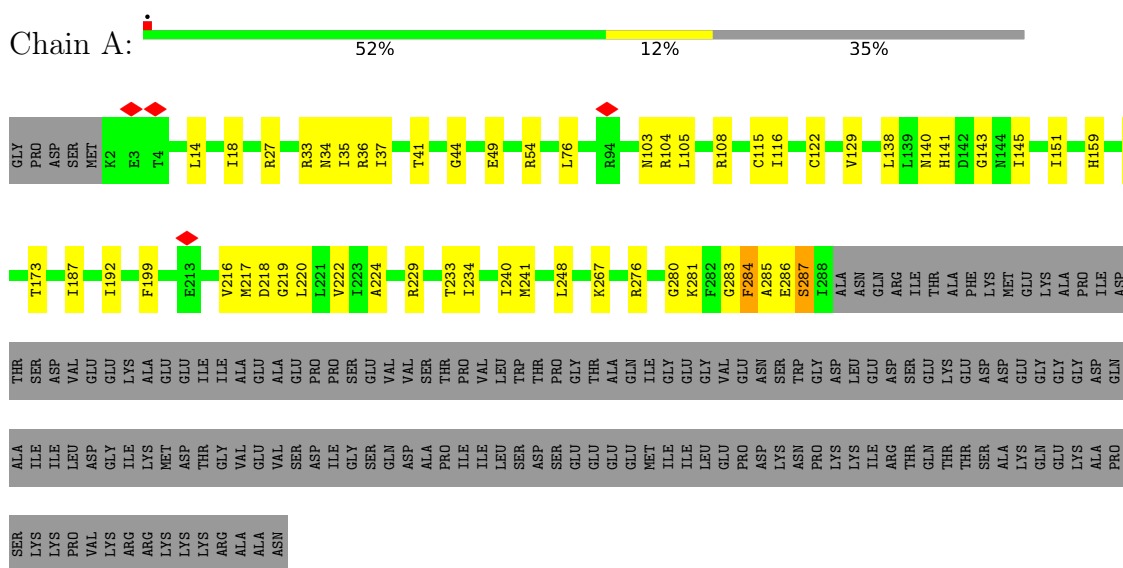
- Molecule 12 is a RNA chain called U44 ssRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	R	6	Total	C	N	O	P	0	0
			120	54	12	48	6		

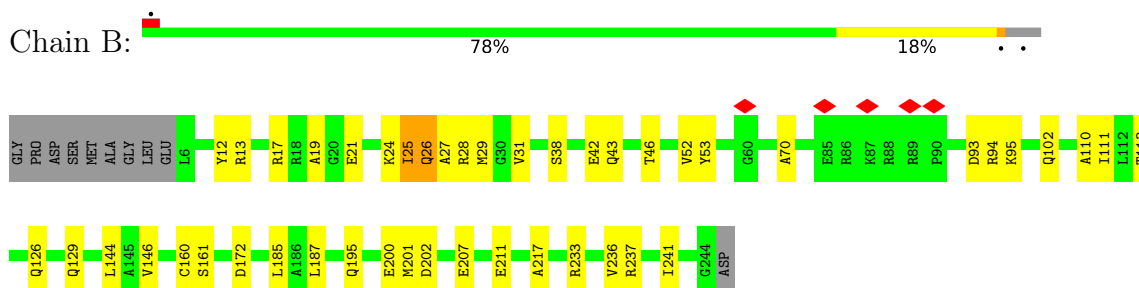
3 Residue-property plots

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.

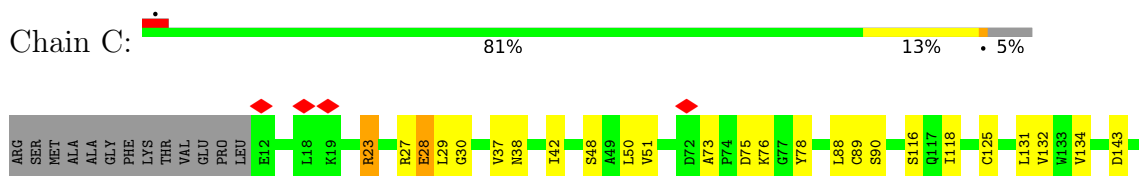
• Molecule 1: Exosome complex component RRP45



• Molecule 2: Exosome complex component RRP41



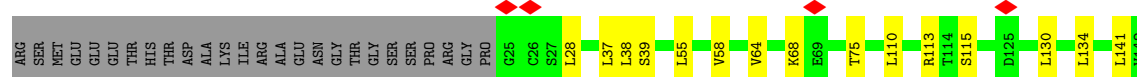
• Molecule 3: Exosome complex component RRP43





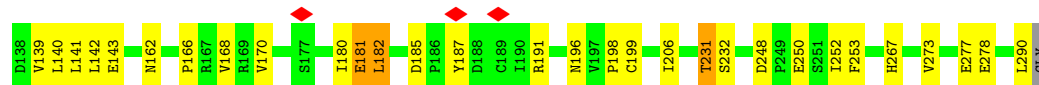
• Molecule 4: Exosome complex component RRP46

Chain D: 75% 14% 11%



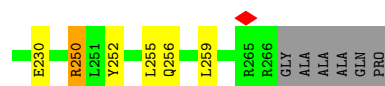
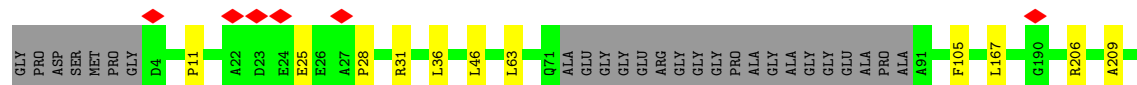
• Molecule 5: Exosome complex component RRP42

Chain E: 79% 17% 4%



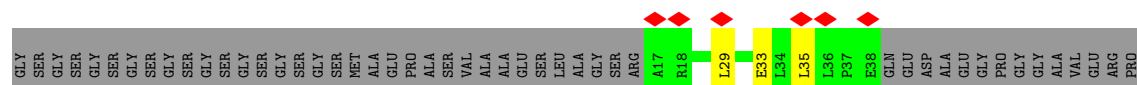
• Molecule 6: Exosome complex component MTR3

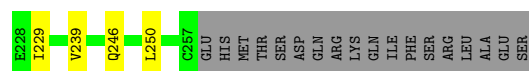
Chain F: 82% 6% 12%



• Molecule 7: Exosome complex component RRP40

Chain G: 5% 63% 8% 28%





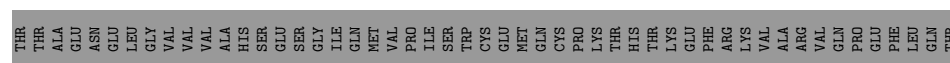
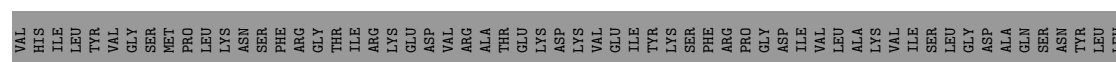
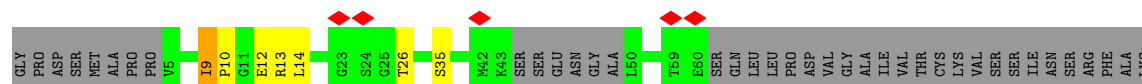
• Molecule 8: Exosome complex component RRP4

Chain H: 78% 13% 7%



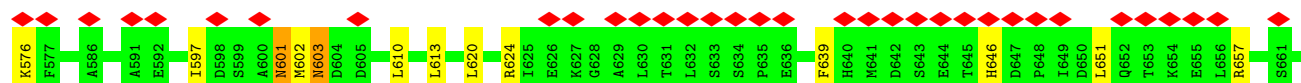
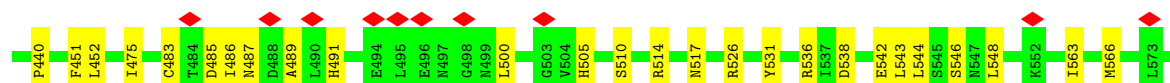
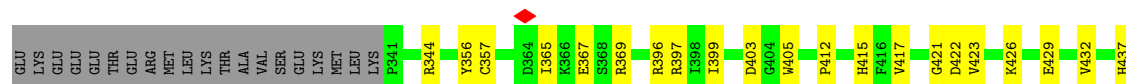
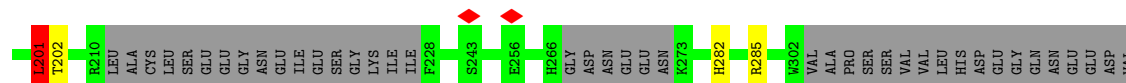
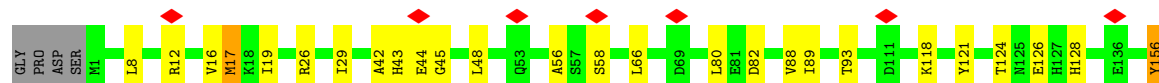
• Molecule 9: Exosome complex component CSL4

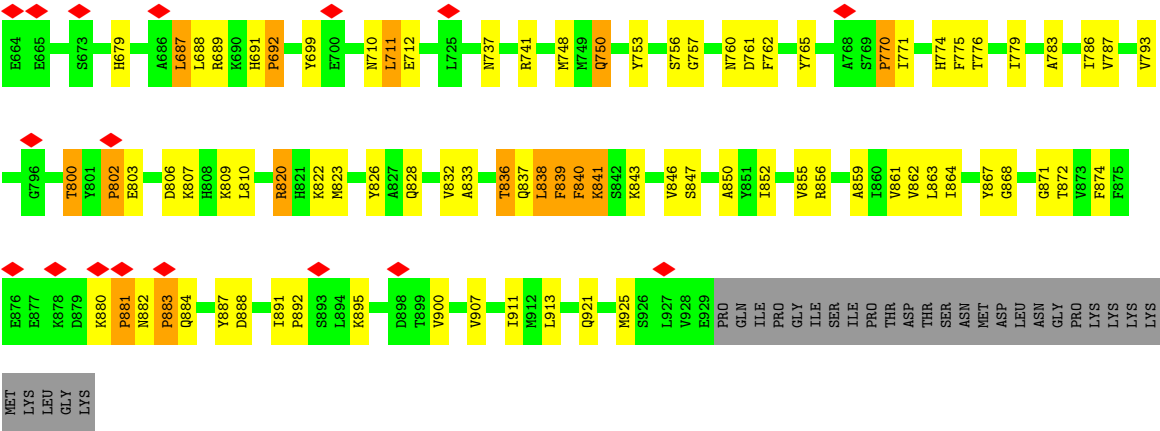
Chain I: 22% 75%



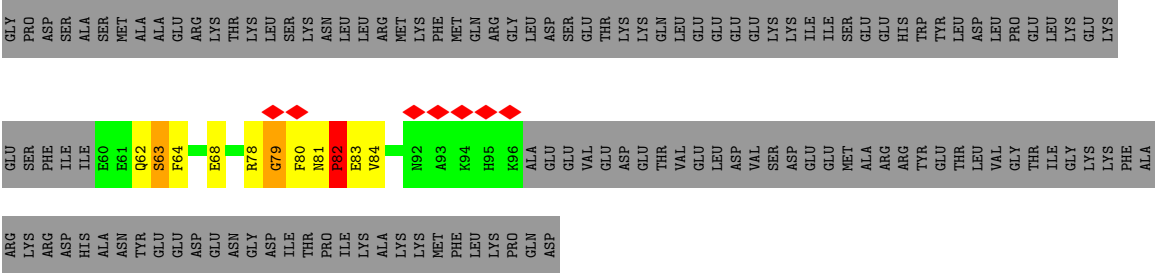
• Molecule 10: Exosome complex exonuclease RRP44

Chain J: 7% 72% 16% 10%





• Molecule 11: M-phase phosphoprotein 6



• Molecule 12: U44 ssRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110958	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 ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.366	Depositor
Minimum map value	-0.241	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	337.5, 337.5, 337.5	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	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	0.33	0/2254	0.64	2/3043 (0.1%)
2	B	0.43	0/1795	0.73	2/2431 (0.1%)
3	C	0.33	0/1953	0.65	0/2662
4	D	0.31	0/1590	0.60	0/2151
5	E	0.34	0/2175	0.74	1/2950 (0.0%)
6	F	0.30	0/1781	0.58	1/2425 (0.0%)
7	G	0.22	0/1549	0.60	2/2100 (0.1%)
8	H	0.27	0/2094	0.64	1/2832 (0.0%)
9	I	0.24	0/378	0.77	3/509 (0.6%)
10	J	0.31	0/6621	0.72	12/9018 (0.1%)
11	K	0.86	0/182	1.10	1/252 (0.4%)
12	R	0.45	0/131	0.78	0/200
All	All	0.33	0/22503	0.68	25/30573 (0.1%)

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
3	C	0	1

There are no bond length outliers.

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	181	GLU	N-CA-C	14.71	126.81	111.07
10	J	802	PRO	CA-N-CD	-9.79	98.29	112.00
10	J	883	PRO	CA-N-CD	-9.78	98.31	112.00
10	J	881	PRO	CA-N-CD	-9.67	98.46	112.00
10	J	770	PRO	CA-N-CD	-9.56	98.62	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	23	ARG	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	2221	0	2240	81	0
2	B	1771	0	1751	72	0
3	C	1923	0	1877	33	0
4	D	1570	0	1603	41	0
5	E	2144	0	2110	61	0
6	F	1752	0	1752	18	0
7	G	1527	0	1530	23	0
8	H	2066	0	2069	56	0
9	I	373	0	368	8	0
10	J	6488	0	6153	256	0
11	K	183	0	76	11	0
12	R	120	0	61	12	0
All	All	22138	0	21590	570	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 13.

The worst 5 of 570 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)
2:B:241:ILE:CD1	8:H:20:ARG:HB3	1.34	1.52
2:B:126:GLN:NE2	5:E:140:LEU:HD21	1.18	1.47
10:J:639:PHE:CE1	10:J:651:LEU:HD21	1.57	1.40
11:K:78:ARG:O	11:K:80:PHE:N	1.58	1.36
1:A:267:LYS:CD	1:A:286:GLU:OE2	1.81	1.29

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	285/443 (64%)	275 (96%)	9 (3%)	1 (0%)	30	62
2	B	237/249 (95%)	223 (94%)	14 (6%)	0	100	100
3	C	262/278 (94%)	249 (95%)	12 (5%)	1 (0%)	30	62
4	D	208/237 (88%)	202 (97%)	6 (3%)	0	100	100
5	E	285/295 (97%)	253 (89%)	31 (11%)	1 (0%)	30	62
6	F	240/276 (87%)	232 (97%)	8 (3%)	0	100	100
7	G	204/293 (70%)	196 (96%)	8 (4%)	0	100	100
8	H	267/297 (90%)	254 (95%)	13 (5%)	0	100	100
9	I	46/199 (23%)	44 (96%)	2 (4%)	0	100	100
10	J	860/962 (89%)	800 (93%)	57 (7%)	3 (0%)	36	67
11	K	35/166 (21%)	23 (66%)	6 (17%)	6 (17%)	0	2
All	All	2929/3695 (79%)	2751 (94%)	166 (6%)	12 (0%)	31	62

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	PHE
10	J	761	ASP
11	K	63	SER
11	K	79	GLY
11	K	81	ASN

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	242/384 (63%)	241 (100%)	1 (0%)	84	83
2	B	174/189 (92%)	171 (98%)	3 (2%)	53	67
3	C	208/237 (88%)	208 (100%)	0	100	100
4	D	170/195 (87%)	170 (100%)	0	100	100
5	E	236/255 (92%)	230 (98%)	6 (2%)	42	61
6	F	164/191 (86%)	163 (99%)	1 (1%)	78	79
7	G	150/230 (65%)	149 (99%)	1 (1%)	76	77
8	H	218/257 (85%)	214 (98%)	4 (2%)	51	67
9	I	41/173 (24%)	40 (98%)	1 (2%)	43	62
10	J	645/856 (75%)	628 (97%)	17 (3%)	40	60
All	All	2248/2967 (76%)	2214 (98%)	34 (2%)	55	69

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	J	820	ARG
10	J	836	THR
10	J	840	PHE
8	H	20	ARG
7	G	225	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
10	J	288	HIS
10	J	737	ASN
10	J	517	ASN
10	J	640	HIS
10	J	825	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	R	6/44 (13%)	3 (50%)	1 (16%)

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	R	40	U
12	R	41	U
12	R	44	U

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	R	39	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 [i](#)

There are no chain breaks in this entry.

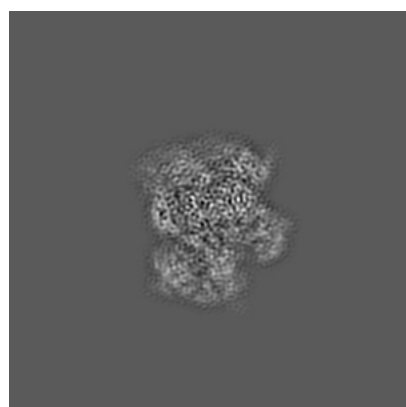
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0128. These allow visual inspection of the internal detail of the map and identification of artifacts.

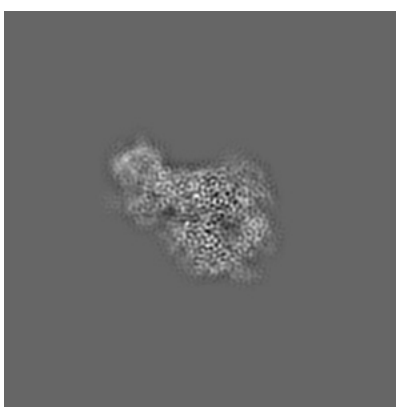
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

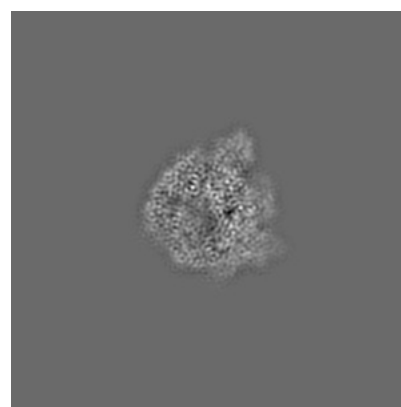
6.1.1 Primary map



X



Y

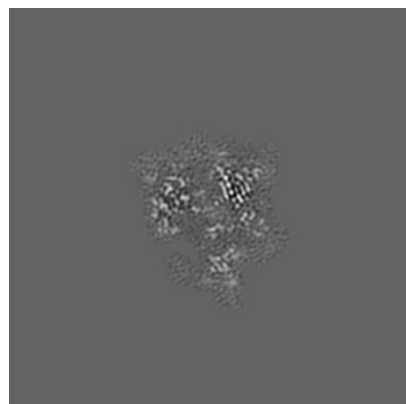


Z

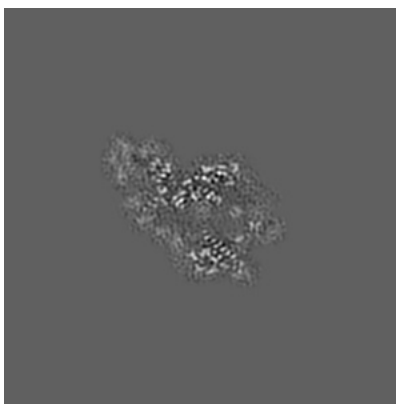
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

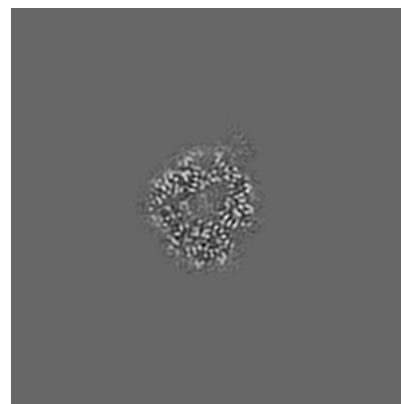
6.2.1 Primary map



X Index: 125



Y Index: 125

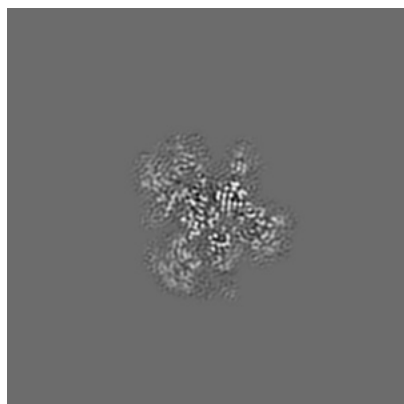


Z Index: 125

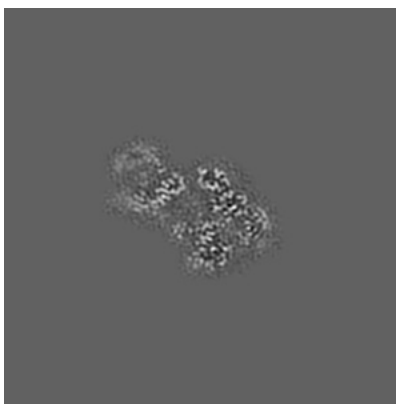
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

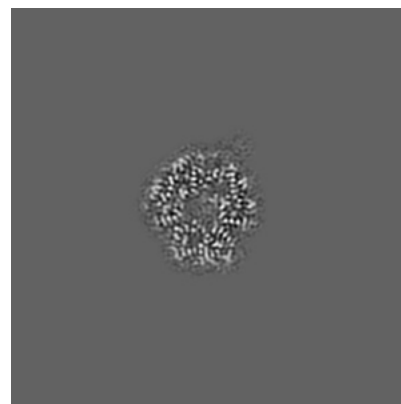
6.3.1 Primary map



X Index: 138



Y Index: 135

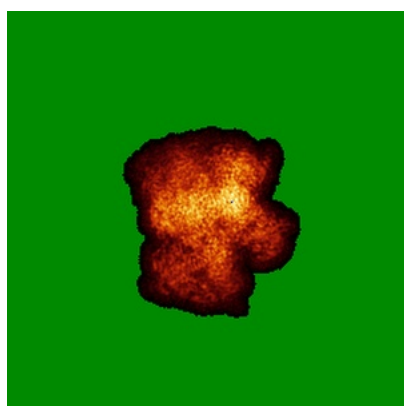


Z Index: 127

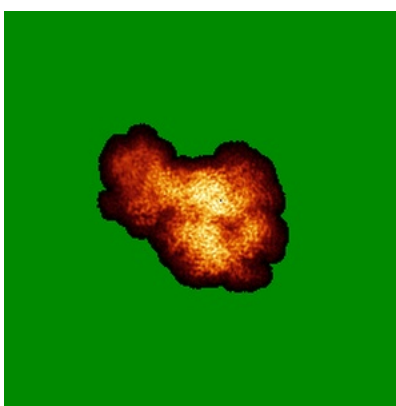
The images above show the largest variance slices of the map in three orthogonal directions.

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

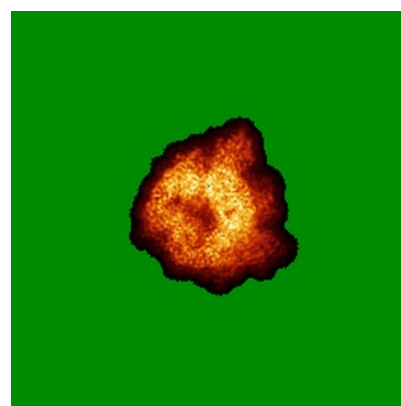
6.4.1 Primary map



X



Y

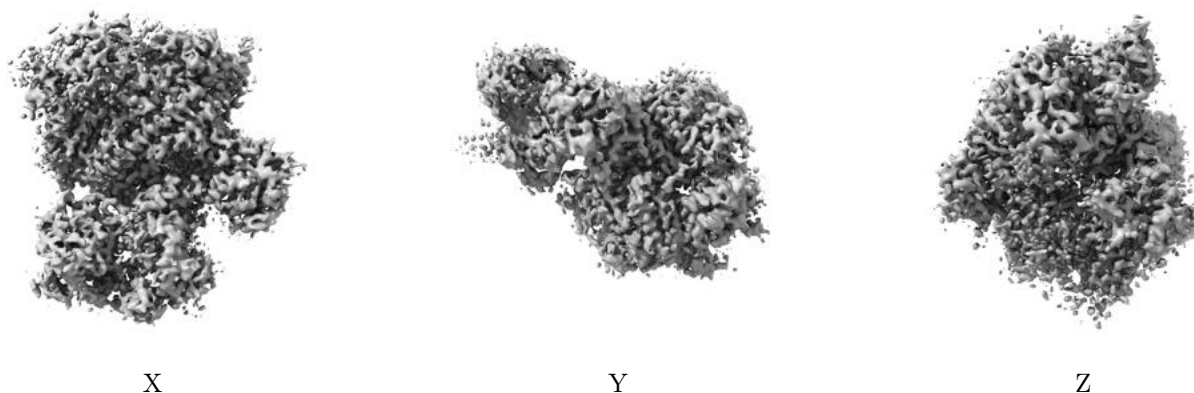


Z

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

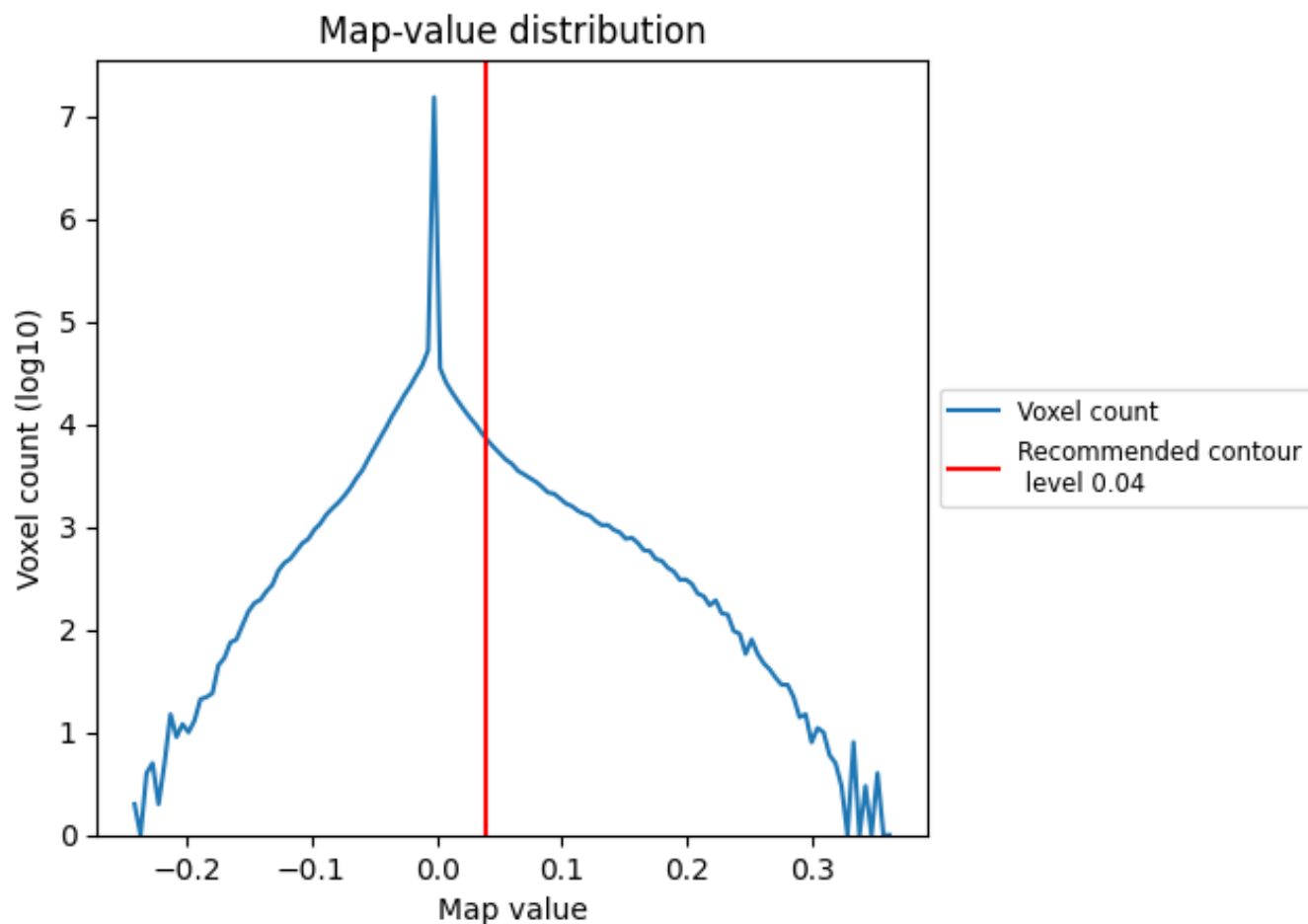
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

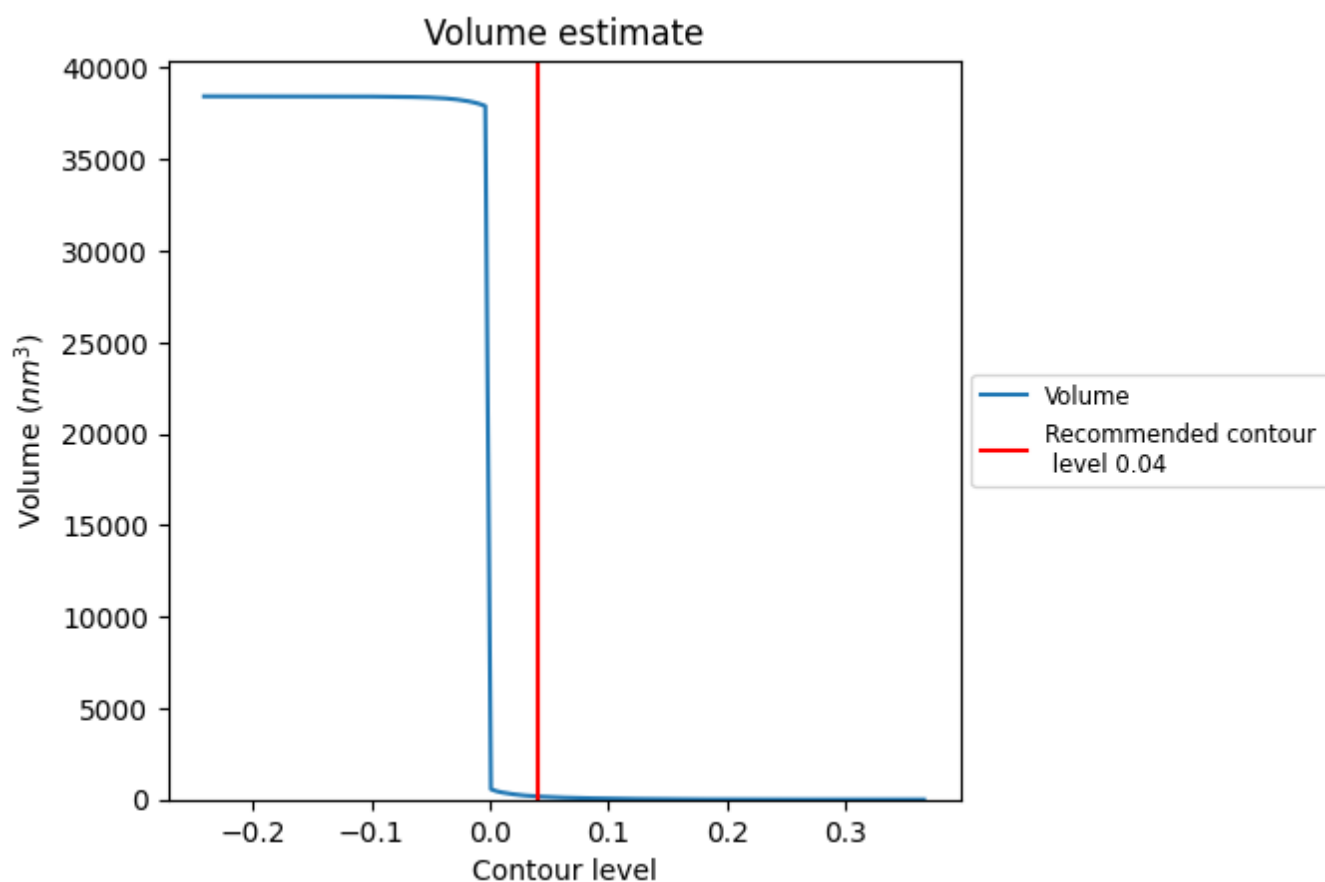
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

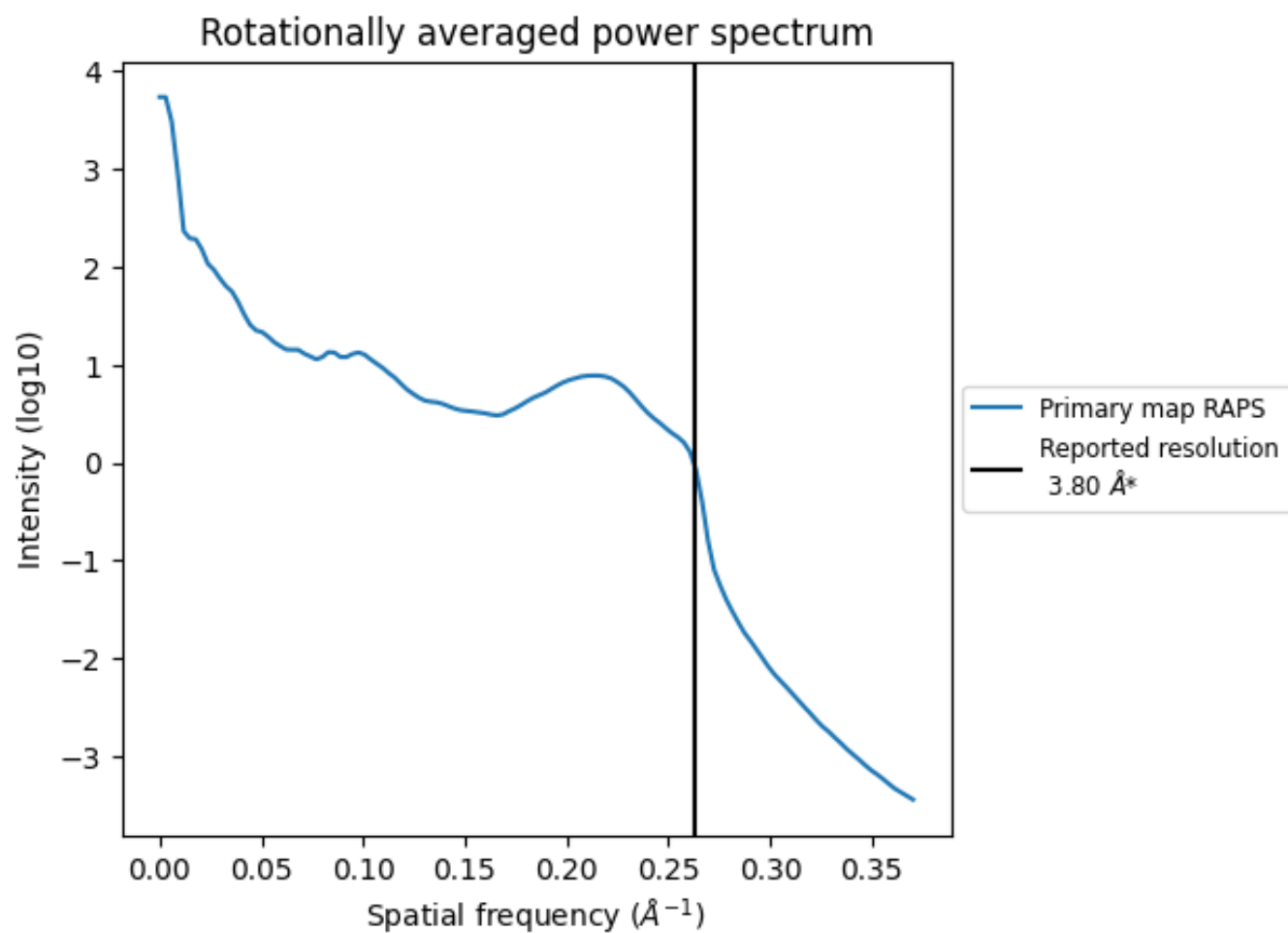
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 171 nm³; this corresponds to an approximate mass of 154 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

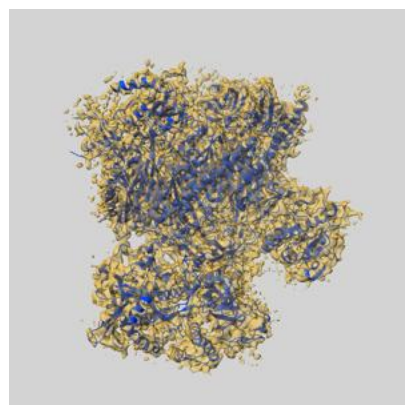
8 Fourier-Shell correlation ⓘ

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

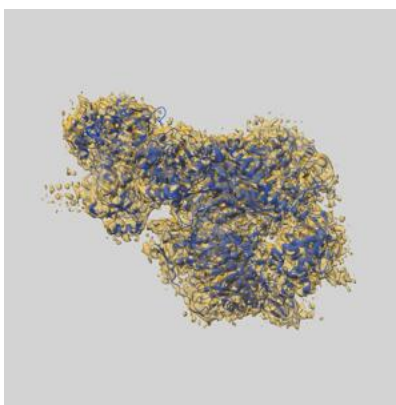
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0128 and PDB model 6H25. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

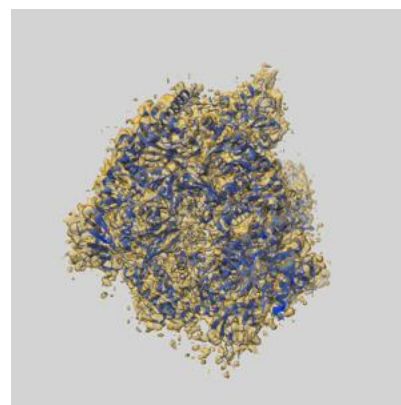
9.1 Map-model overlay [i](#)



X



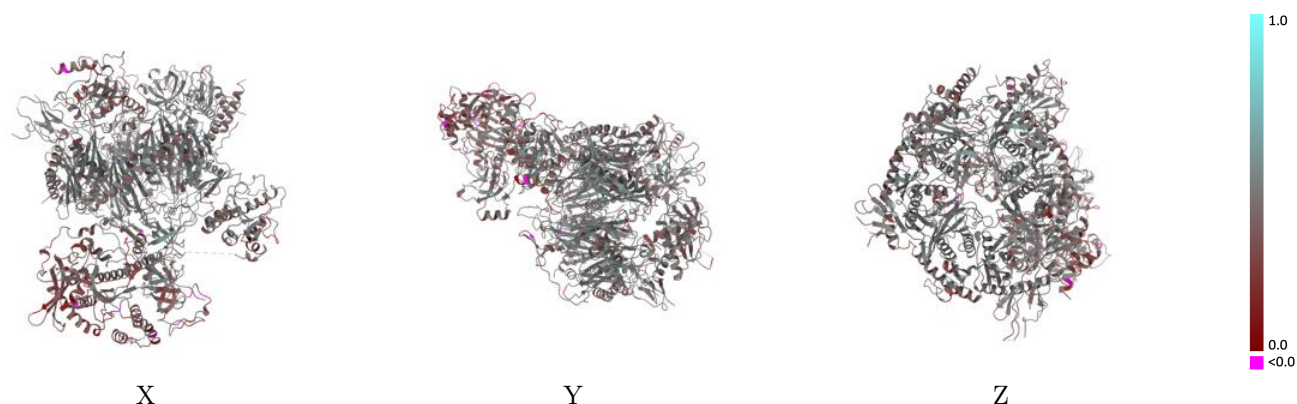
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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](#)



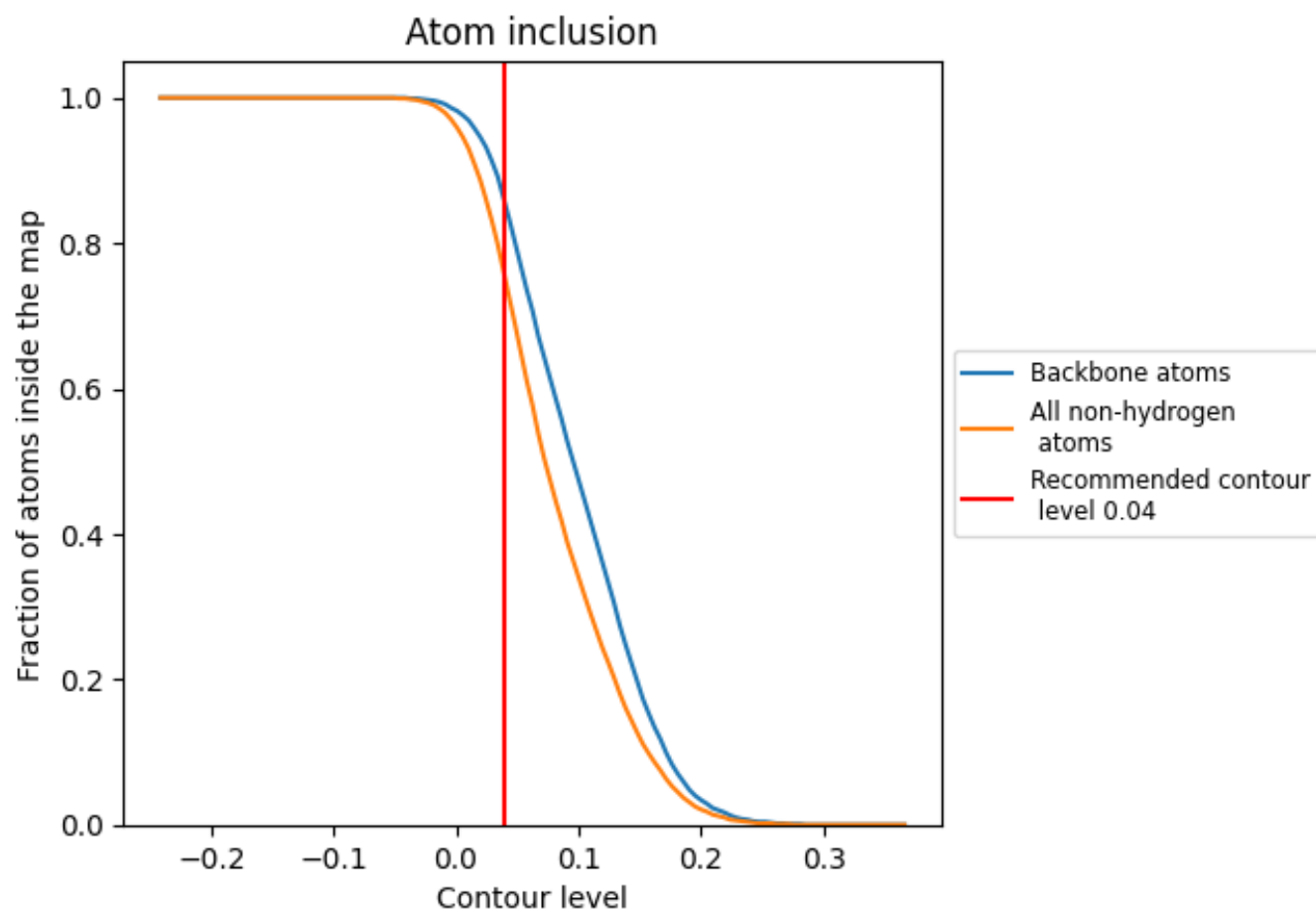
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 75% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7530	0.4270
A	0.7690	0.4540
B	0.7860	0.4630
C	0.7670	0.4330
D	0.7540	0.4540
E	0.7850	0.4540
F	0.7670	0.4550
G	0.6810	0.4220
H	0.7640	0.4320
I	0.7220	0.4170
J	0.7360	0.3830
K	0.7000	0.3840
R	0.8250	0.4740

1.0

0.0

<0.0