



wwPDB EM Validation Summary Report ⓘ

May 12, 2025 – 06:58 PM EDT

PDB ID : 6O9Z / pdb_00006o9z
EMDB ID : EMD-0664
Title : Electron cryo-microscopy of the eukaryotic translation initiation factor 2B bound to eukaryotic translation initiation factor 2 from Homo sapiens
Authors : Nguyen, H.C.; Kenner, L.R.; Frost, A.S.
Deposited on : 2019-03-15
Resolution : 3.03 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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

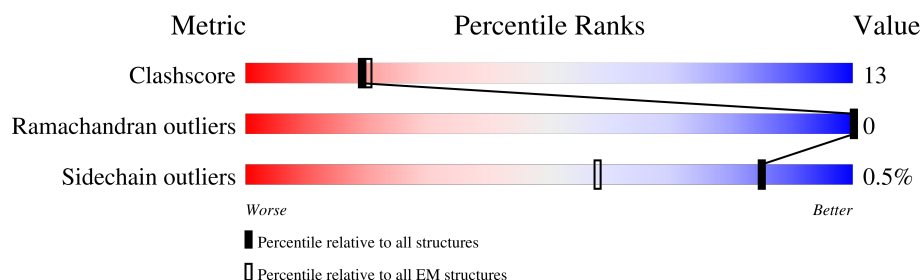
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.03 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	721	
1	B	721	
2	C	368	
2	D	368	
3	E	523	
3	F	523	
4	G	305	
4	H	305	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	I	452	<div><div></div><div>14%</div><div>41%</div><div>12%</div><div>47%</div></div>
5	J	452	<div><div></div><div>15%</div><div>42%</div><div>11%</div><div>47%</div></div>
6	L	323	<div><div></div><div>12%</div><div>53%</div><div></div><div>46%</div></div>
6	M	323	<div><div></div><div>12%</div><div>52%</div><div></div><div>46%</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25788 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 Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	426	Total	C	N	O	S	0	0
			3172	2043	524	590	15		
1	B	426	Total	C	N	O	S	0	0
			3172	2043	524	590	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	587	VAL	ILE	conflict	UNP Q13144
B	587	VAL	ILE	conflict	UNP Q13144

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	317	Total	C	N	O	S	0	0
			2415	1558	394	448	15		
2	D	318	Total	C	N	O	S	0	0
			2425	1564	397	449	15		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	MET	-	initiating methionine	UNP P49770
C	-15	HIS	-	expression tag	UNP P49770
C	-14	HIS	-	expression tag	UNP P49770
C	-13	HIS	-	expression tag	UNP P49770
C	-12	HIS	-	expression tag	UNP P49770
C	-11	HIS	-	expression tag	UNP P49770
C	-10	HIS	-	expression tag	UNP P49770
C	-9	GLY	-	expression tag	UNP P49770
C	-8	GLY	-	expression tag	UNP P49770
C	-7	GLY	-	expression tag	UNP P49770
C	-6	SER	-	expression tag	UNP P49770

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLU	-	expression tag	UNP P49770
C	-4	ASN	-	expression tag	UNP P49770
C	-3	LEU	-	expression tag	UNP P49770
C	-2	TYR	-	expression tag	UNP P49770
C	-1	PHE	-	expression tag	UNP P49770
C	0	GLN	-	expression tag	UNP P49770
C	1	SER	-	expression tag	UNP P49770
D	-16	MET	-	initiating methionine	UNP P49770
D	-15	HIS	-	expression tag	UNP P49770
D	-14	HIS	-	expression tag	UNP P49770
D	-13	HIS	-	expression tag	UNP P49770
D	-12	HIS	-	expression tag	UNP P49770
D	-11	HIS	-	expression tag	UNP P49770
D	-10	HIS	-	expression tag	UNP P49770
D	-9	GLY	-	expression tag	UNP P49770
D	-8	GLY	-	expression tag	UNP P49770
D	-7	GLY	-	expression tag	UNP P49770
D	-6	SER	-	expression tag	UNP P49770
D	-5	GLU	-	expression tag	UNP P49770
D	-4	ASN	-	expression tag	UNP P49770
D	-3	LEU	-	expression tag	UNP P49770
D	-2	TYR	-	expression tag	UNP P49770
D	-1	PHE	-	expression tag	UNP P49770
D	0	GLN	-	expression tag	UNP P49770
D	1	SER	-	expression tag	UNP P49770

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	353	Total	C	N	O	S	0	0
			2683	1733	443	493	14		
3	F	353	Total	C	N	O	S	0	0
			2683	1733	443	493	14		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	290	Total	C	N	O	S	0	0
			2080	1352	347	372	9		
4	H	290	Total	C	N	O	S	0	0
			2080	1352	347	372	9		

- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit gamma.

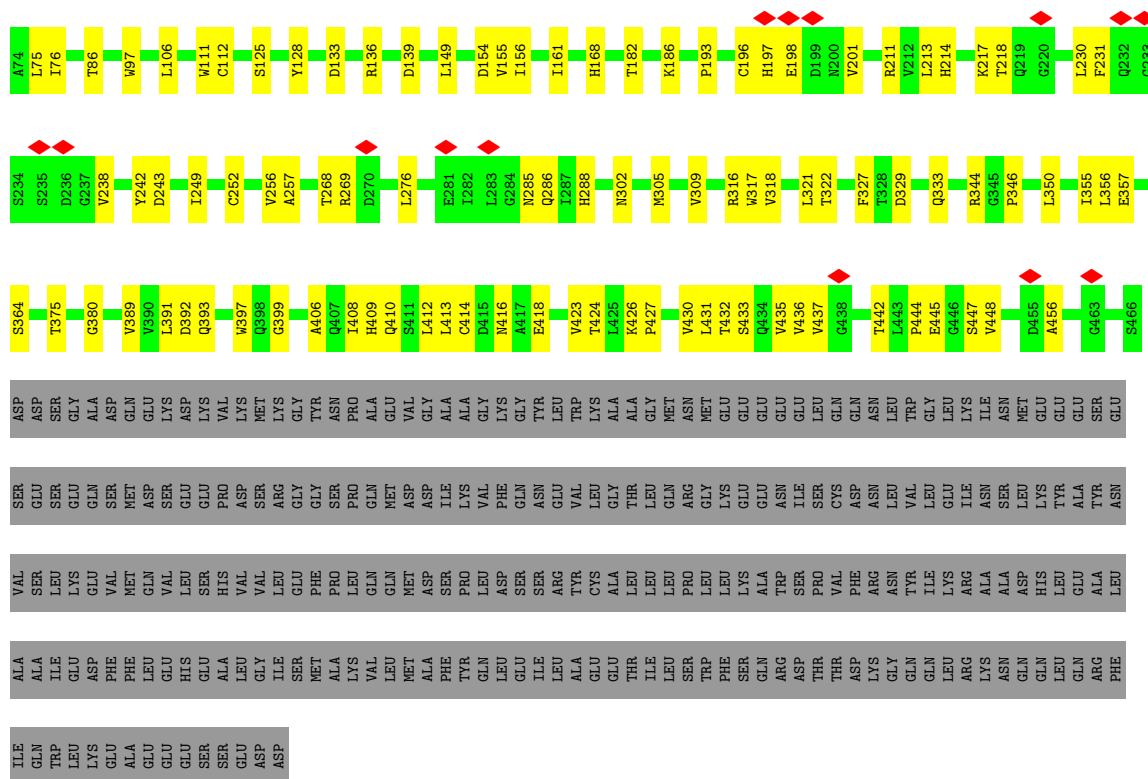
Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	240	Total	C	N	O	S	0	0
			1609	1050	266	285	8		
5	J	240	Total	C	N	O	S	0	0
			1609	1050	266	285	8		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

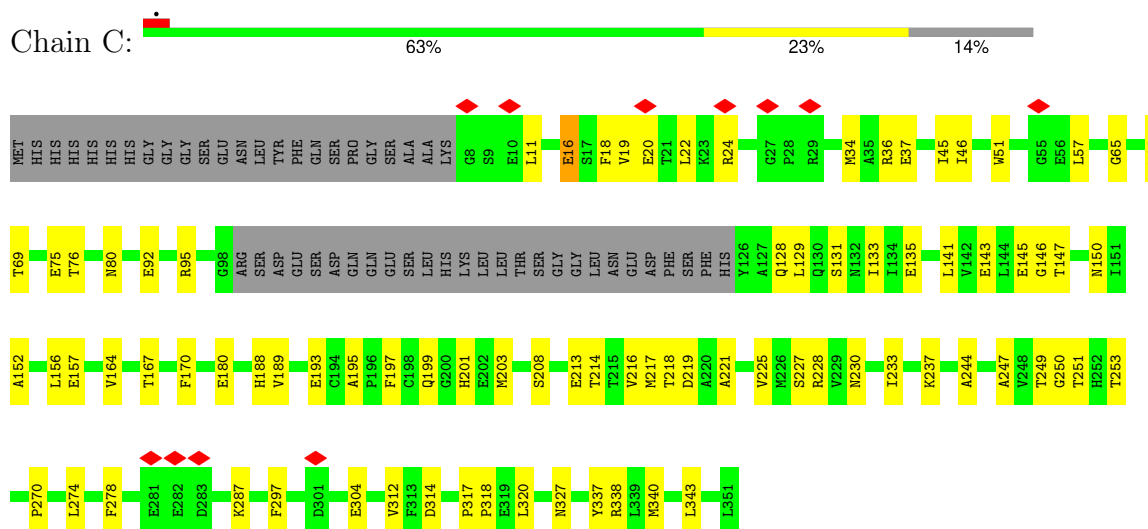
Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	176	Total	C	N	O	P S	0	0
			930	553	192	183	1 1		
6	M	176	Total	C	N	O	P S	0	0
			930	553	192	183	1 1		

There are 18 discrepancies between the modelled and reference sequences:

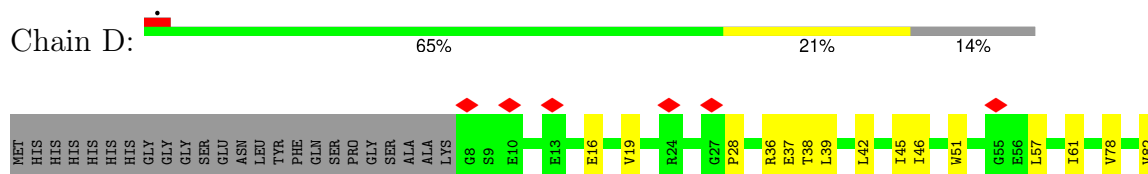
Chain	Residue	Modelled	Actual	Comment	Reference
L	-8	MET	-	initiating methionine	UNP P05198
L	-7	ASP	-	expression tag	UNP P05198
L	-6	TYR	-	expression tag	UNP P05198
L	-5	LYS	-	expression tag	UNP P05198
L	-4	ASP	-	expression tag	UNP P05198
L	-3	ASP	-	expression tag	UNP P05198
L	-2	ASP	-	expression tag	UNP P05198
L	-1	ASP	-	expression tag	UNP P05198
L	0	LYS	-	expression tag	UNP P05198
M	-8	MET	-	initiating methionine	UNP P05198
M	-7	ASP	-	expression tag	UNP P05198
M	-6	TYR	-	expression tag	UNP P05198
M	-5	LYS	-	expression tag	UNP P05198
M	-4	ASP	-	expression tag	UNP P05198
M	-3	ASP	-	expression tag	UNP P05198
M	-2	ASP	-	expression tag	UNP P05198
M	-1	ASP	-	expression tag	UNP P05198
M	0	LYS	-	expression tag	UNP P05198



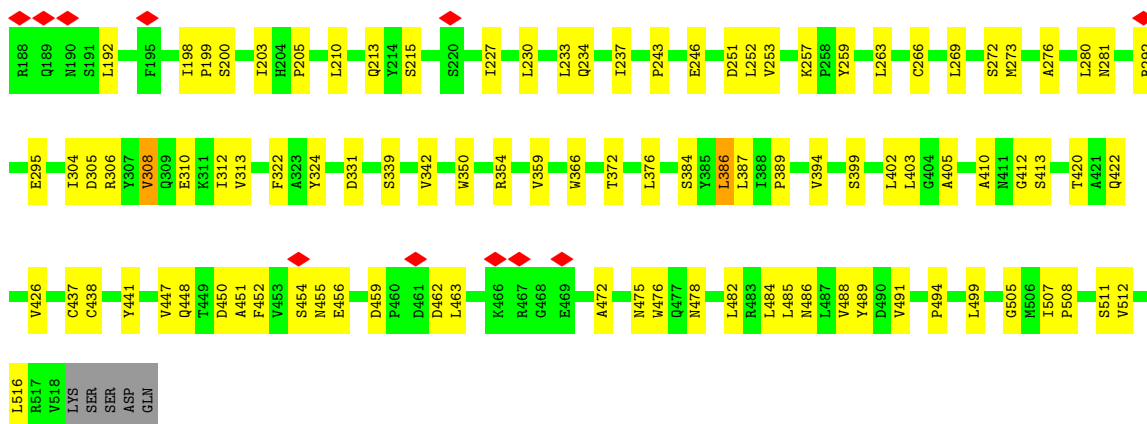
• Molecule 2: Translation initiation factor eIF-2B subunit beta



• Molecule 2: Translation initiation factor eIF-2B subunit beta

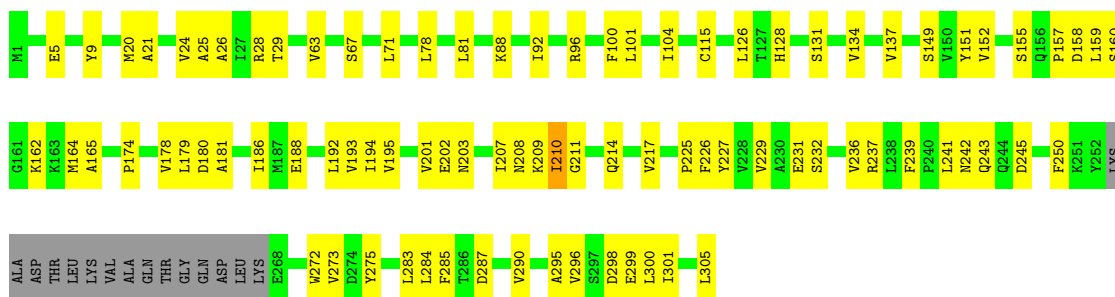






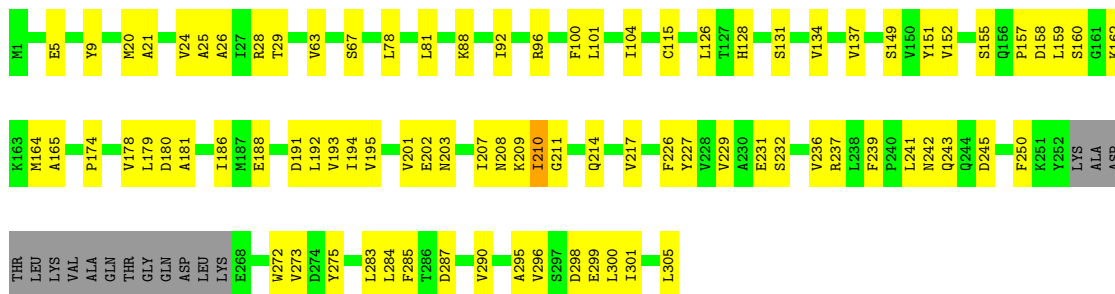
- Molecule 4: Translation initiation factor eIF-2B subunit alpha

Chain G: 67% 28% 5%



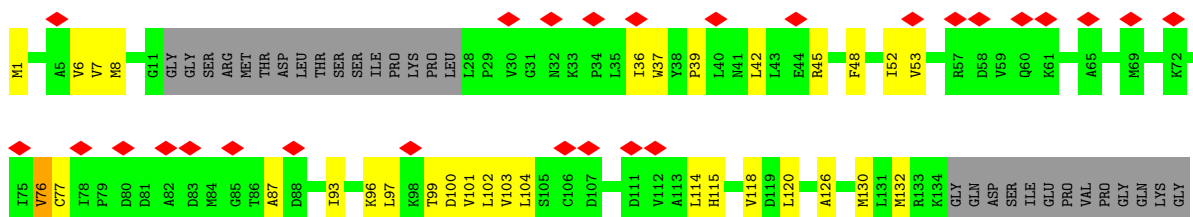
- Molecule 4: Translation initiation factor eIF-2B subunit alpha

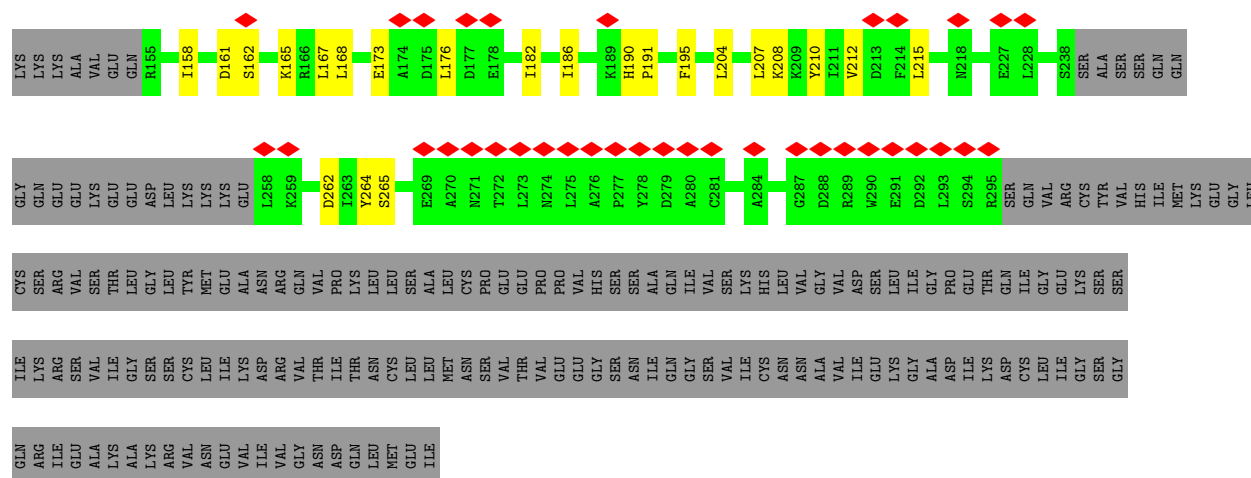
Chain H: 67% 28% 5%



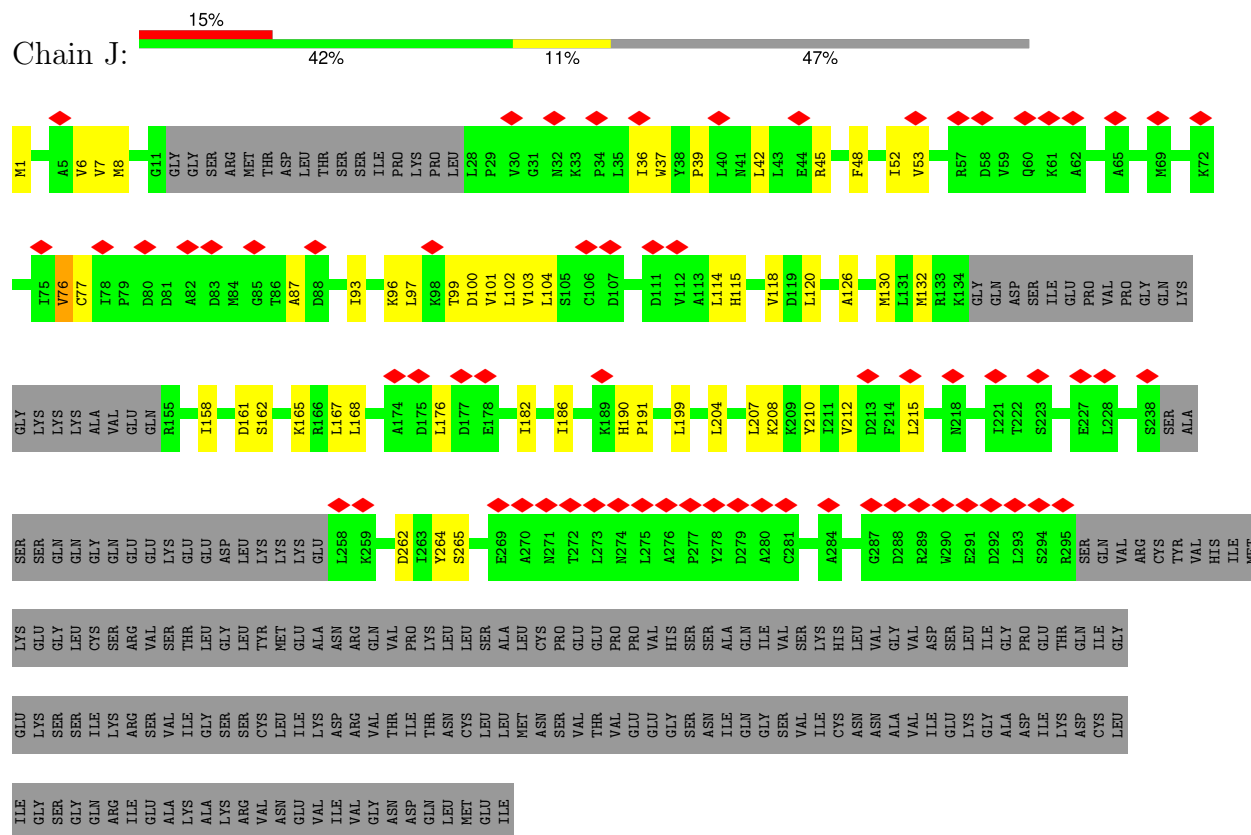
- Molecule 5: Translation initiation factor eIF-2B subunit gamma

Chain I: 14% 41% 12% 47%

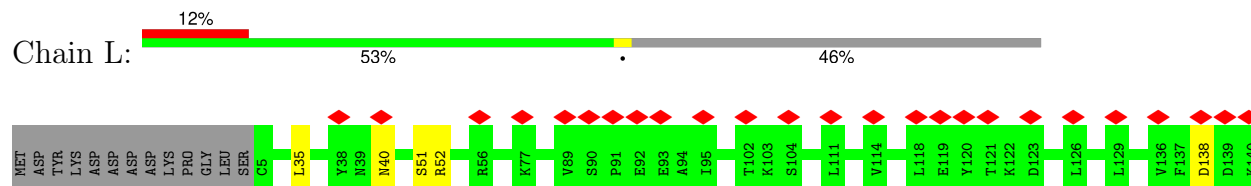


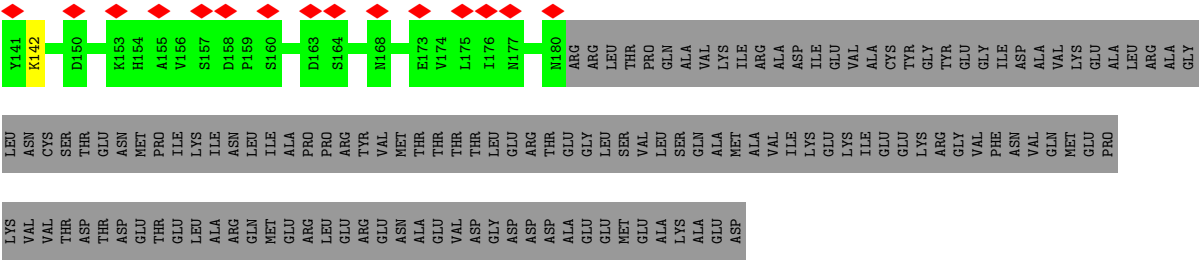


• Molecule 5: Translation initiation factor eIF-2B subunit gamma

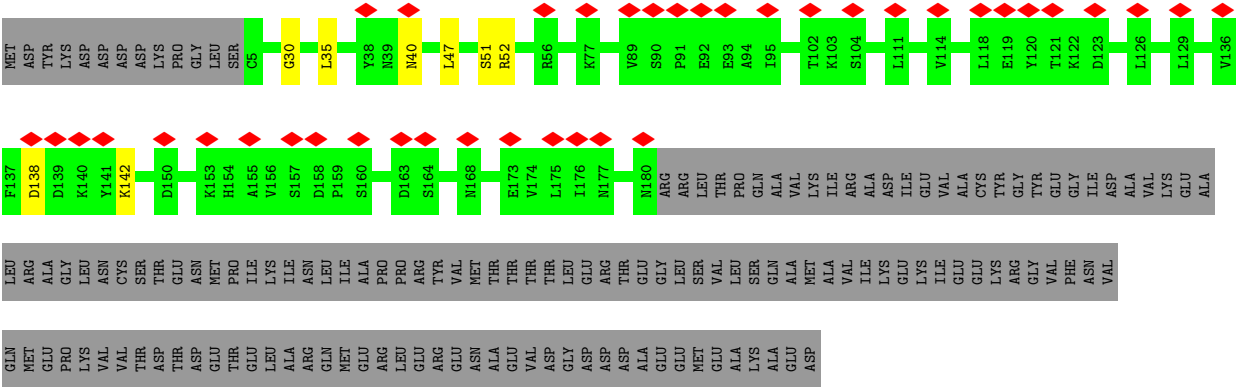


• Molecule 6: Eukaryotic translation initiation factor 2 subunit 1





● Molecule 6: Eukaryotic translation initiation factor 2 subunit 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34014	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 ($e^-/\text{\AA}^2$)	80	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	14.365	Depositor
Minimum map value	-8.686	Depositor
Average map value	-0.011	Depositor
Map value standard deviation	0.787	Depositor
Recommended contour level	1.9	Depositor
Map size (Å)	289.344, 289.344, 289.344	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82199997, 0.82199997, 0.82199997	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.35	0/3236	0.53	0/4403
1	B	0.35	0/3236	0.54	0/4403
2	C	0.39	0/2460	0.54	0/3318
2	D	0.39	0/2471	0.53	0/3333
3	E	0.38	0/2732	0.60	0/3699
3	F	0.38	0/2732	0.59	0/3699
4	G	0.42	0/2114	0.66	0/2867
4	H	0.42	0/2114	0.66	0/2867
5	I	0.25	0/1630	0.56	0/2219
5	J	0.25	0/1630	0.56	0/2219
6	L	0.19	0/918	0.44	0/1268
6	M	0.19	0/918	0.44	0/1268
All	All	0.36	0/26191	0.57	0/35563

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	A	3172	0	3018	70	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3172	0	3018	72	0
2	C	2415	0	2390	66	0
2	D	2425	0	2397	62	0
3	E	2683	0	2685	84	0
3	F	2683	0	2685	83	0
4	G	2080	0	2010	73	0
4	H	2080	0	2010	73	0
5	I	1609	0	1377	42	0
5	J	1609	0	1377	41	0
6	L	930	0	484	4	0
6	M	930	0	484	5	0
All	All	25788	0	23935	622	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 622 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)
4:H:210:ILE:H	4:H:210:ILE:HD12	1.42	0.84
4:G:210:ILE:HD12	4:G:210:ILE:H	1.42	0.83
3:E:199:PRO:HG3	5:I:48:PHE:H	1.44	0.82
3:F:199:PRO:HG3	5:J:48:PHE:H	1.47	0.80
2:C:253:THR:HG21	3:F:422:GLN:HE21	1.48	0.79

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	424/721 (59%)	402 (95%)	22 (5%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	424/721 (59%)	402 (95%)	22 (5%)	0	100	100
2	C	313/368 (85%)	305 (97%)	8 (3%)	0	100	100
2	D	314/368 (85%)	301 (96%)	13 (4%)	0	100	100
3	E	351/523 (67%)	342 (97%)	9 (3%)	0	100	100
3	F	351/523 (67%)	342 (97%)	9 (3%)	0	100	100
4	G	286/305 (94%)	269 (94%)	17 (6%)	0	100	100
4	H	286/305 (94%)	270 (94%)	16 (6%)	0	100	100
5	I	232/452 (51%)	223 (96%)	9 (4%)	0	100	100
5	J	232/452 (51%)	223 (96%)	9 (4%)	0	100	100
6	L	173/323 (54%)	165 (95%)	8 (5%)	0	100	100
6	M	173/323 (54%)	165 (95%)	8 (5%)	0	100	100
All	All	3559/5384 (66%)	3409 (96%)	150 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	347/626 (55%)	346 (100%)	1 (0%)	91	95
1	B	347/626 (55%)	346 (100%)	1 (0%)	91	95
2	C	265/312 (85%)	264 (100%)	1 (0%)	89	94
2	D	266/312 (85%)	266 (100%)	0	100	100
3	E	307/444 (69%)	305 (99%)	2 (1%)	81	90
3	F	307/444 (69%)	305 (99%)	2 (1%)	81	90
4	G	199/260 (76%)	198 (100%)	1 (0%)	86	93
4	H	199/260 (76%)	198 (100%)	1 (0%)	86	93
5	I	127/398 (32%)	125 (98%)	2 (2%)	58	79
5	J	127/398 (32%)	125 (98%)	2 (2%)	58	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	L	12/287 (4%)	12 (100%)	0	100	100
6	M	12/287 (4%)	12 (100%)	0	100	100
All	All	2515/4654 (54%)	2502 (100%)	13 (0%)	85	93

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	G	210	ILE
4	H	210	ILE
5	J	162	SER
5	I	162	SER
5	J	76	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	242	ASN
4	H	156	GLN
2	D	277	GLN
3	F	422	GLN
2	D	261	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SEP	M	51	6	8,9,10	1.55	1 (12%)	7,12,14	1.40	1 (14%)
6	SEP	L	51	6	8,9,10	1.55	1 (12%)	7,12,14	1.37	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SEP	M	51	6	-	1/6/8/10	-
6	SEP	L	51	6	-	1/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	51	SEP	P-O1P	3.38	1.61	1.50
6	M	51	SEP	P-O1P	3.35	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	51	SEP	OG-CB-CA	3.17	111.23	108.14
6	L	51	SEP	OG-CB-CA	3.11	111.17	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	51	SEP	N-CA-CB-OG
6	M	51	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

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.

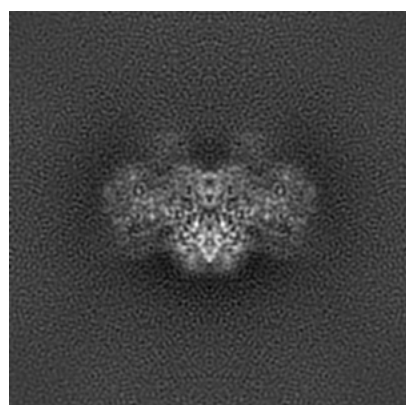
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0664. These allow visual inspection of the internal detail of the map and identification of artifacts.

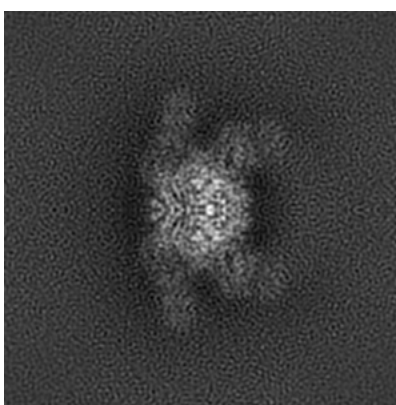
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

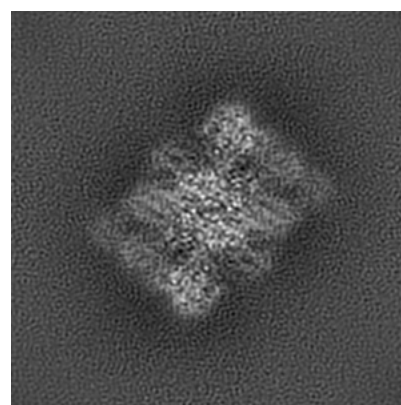
6.1.1 Primary map



X



Y

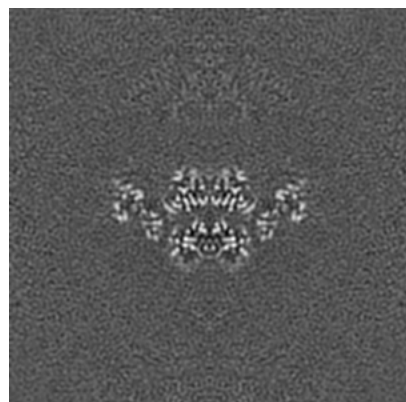


Z

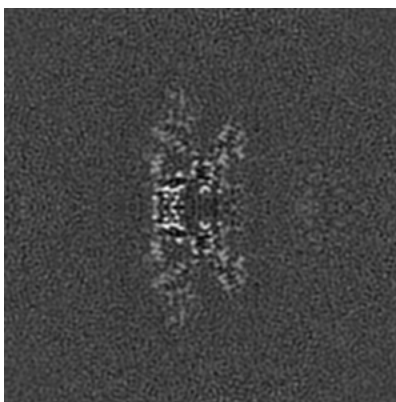
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

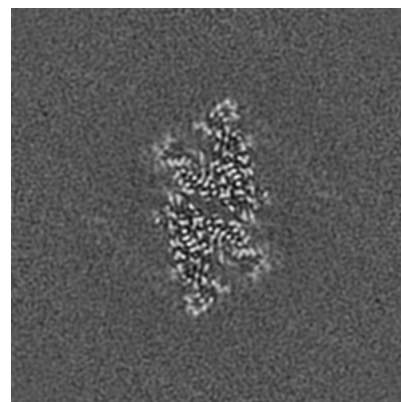
6.2.1 Primary map



X Index: 176



Y Index: 176

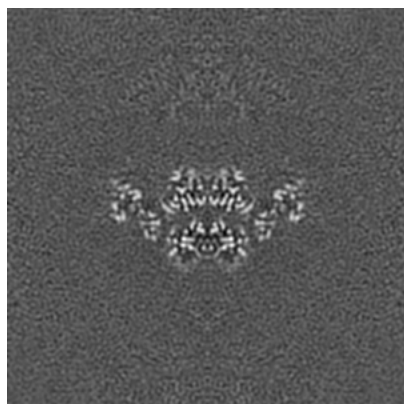


Z Index: 176

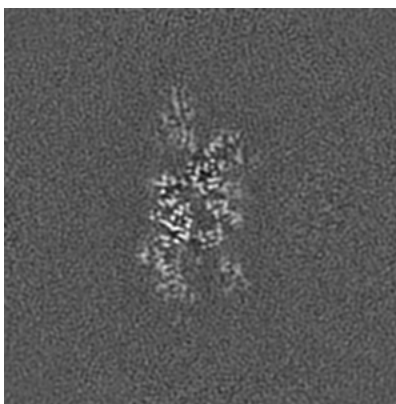
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

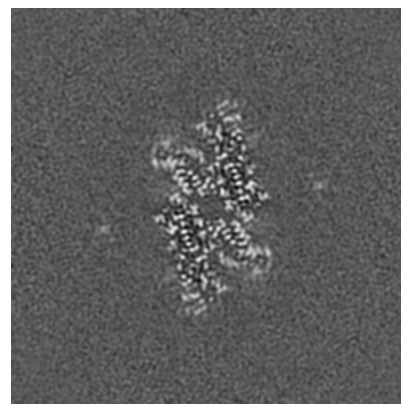
6.3.1 Primary map



X Index: 176



Y Index: 181

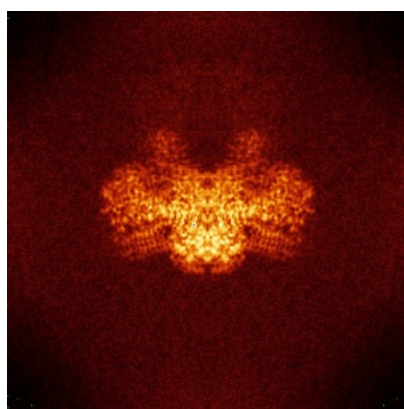


Z Index: 174

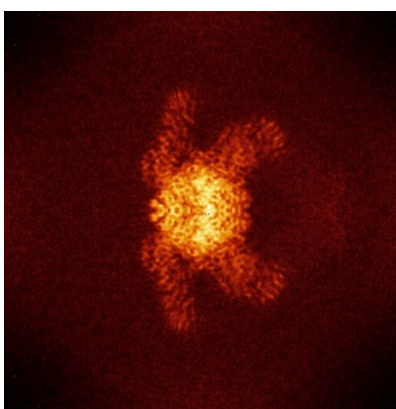
The images above show the largest variance slices of the map in three orthogonal directions.

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

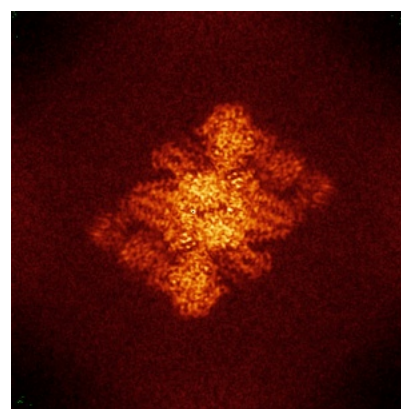
6.4.1 Primary map



X



Y

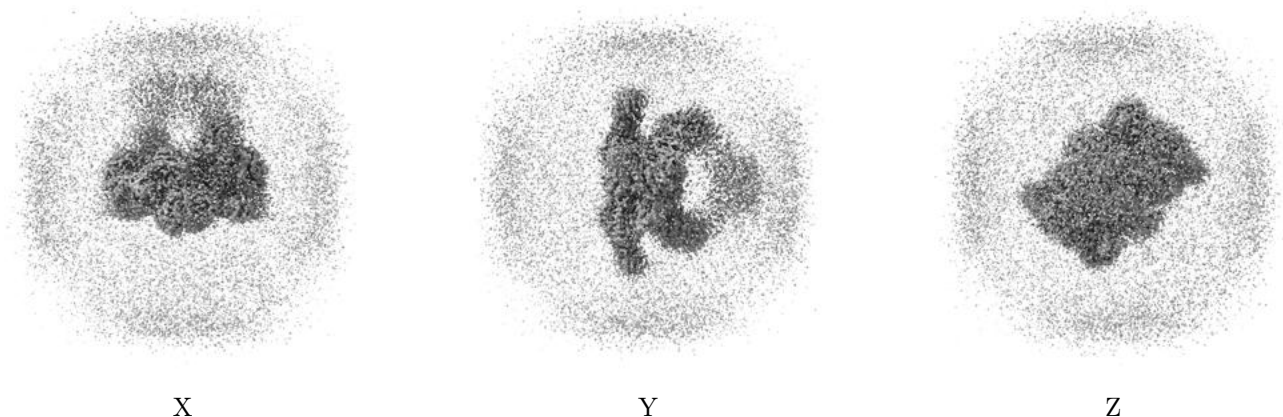


Z

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

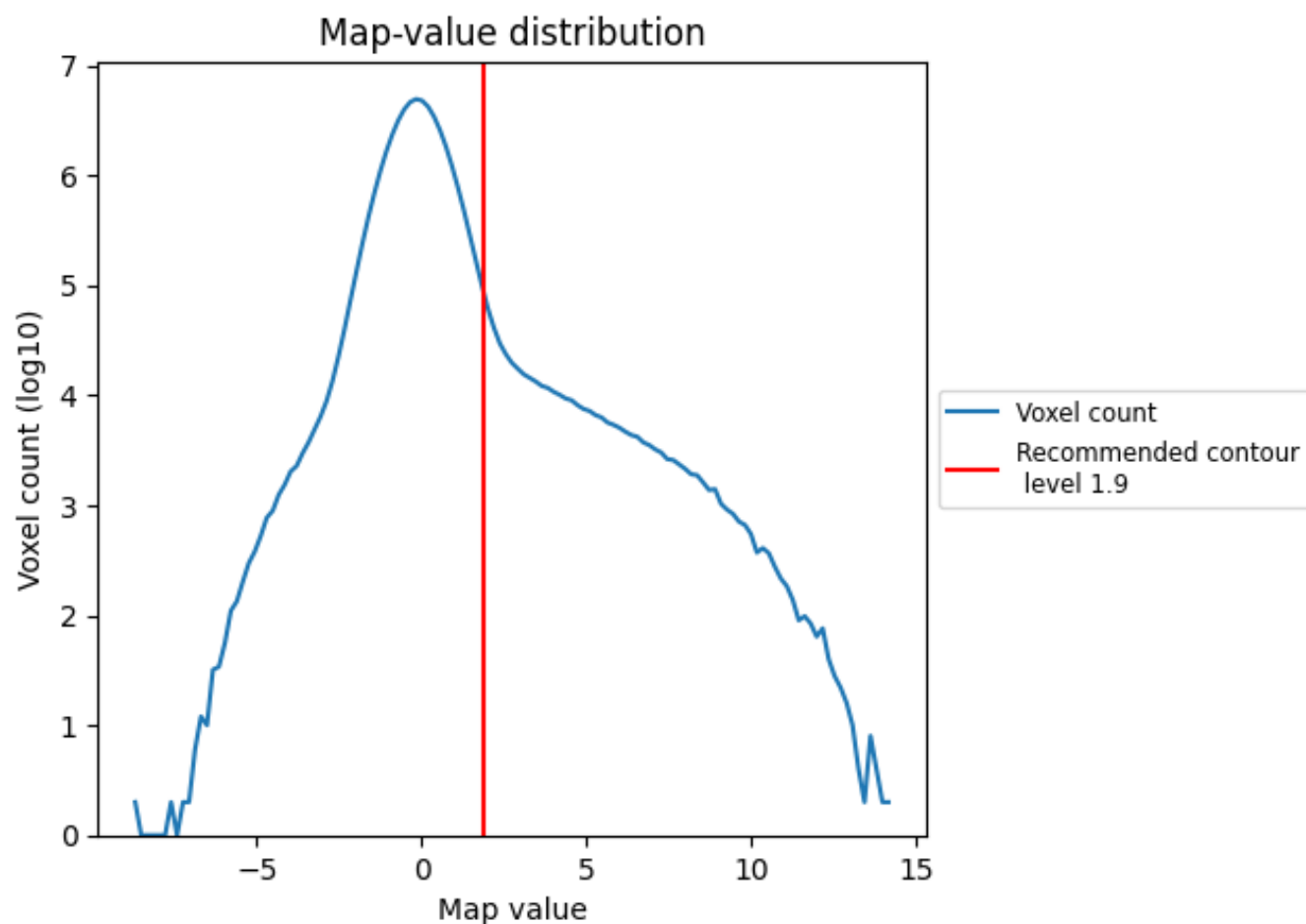
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

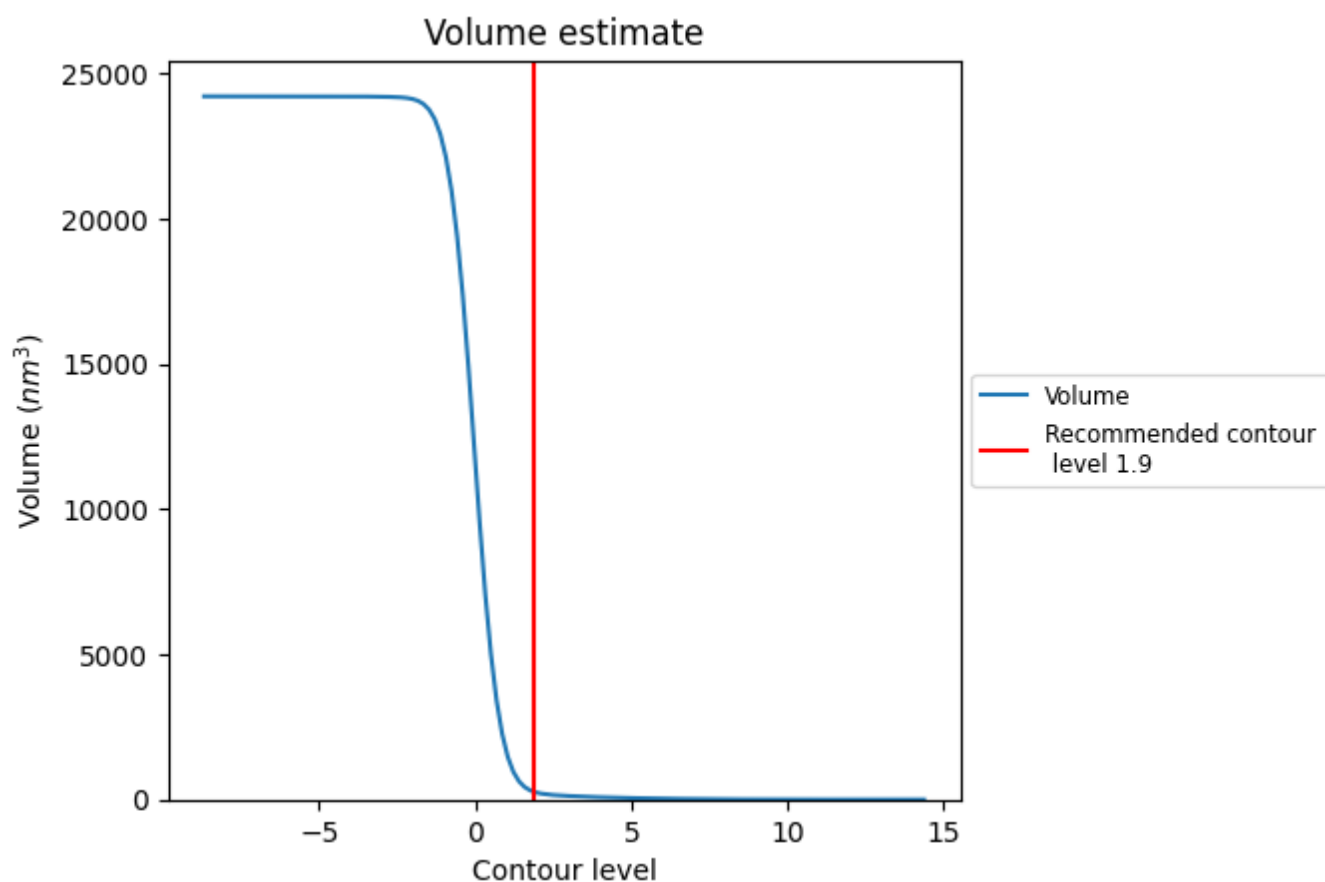
This section contains the results of statistical analysis of the map.

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.

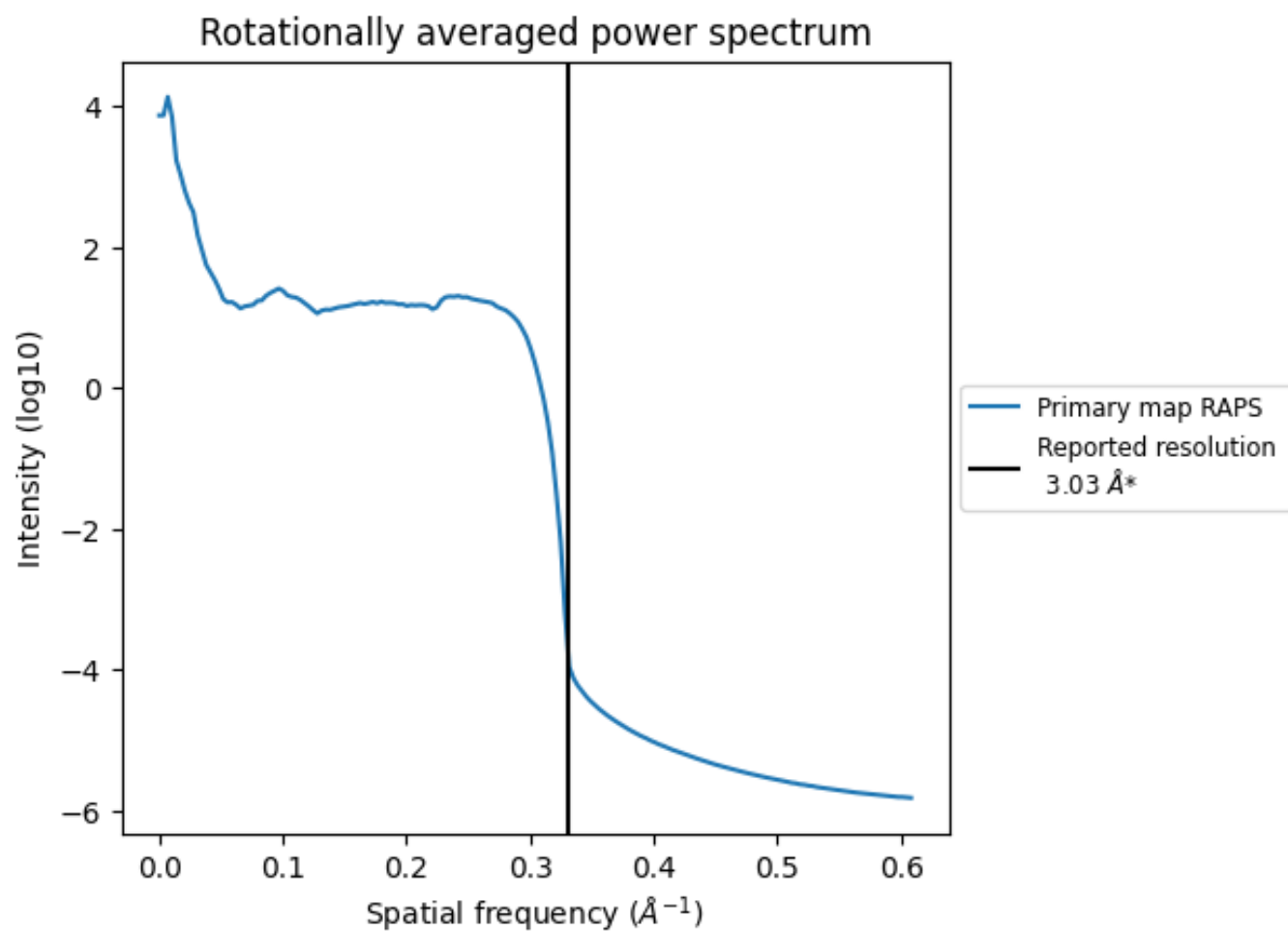
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 261 nm³; this corresponds to an approximate mass of 236 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 0.330 Å⁻¹

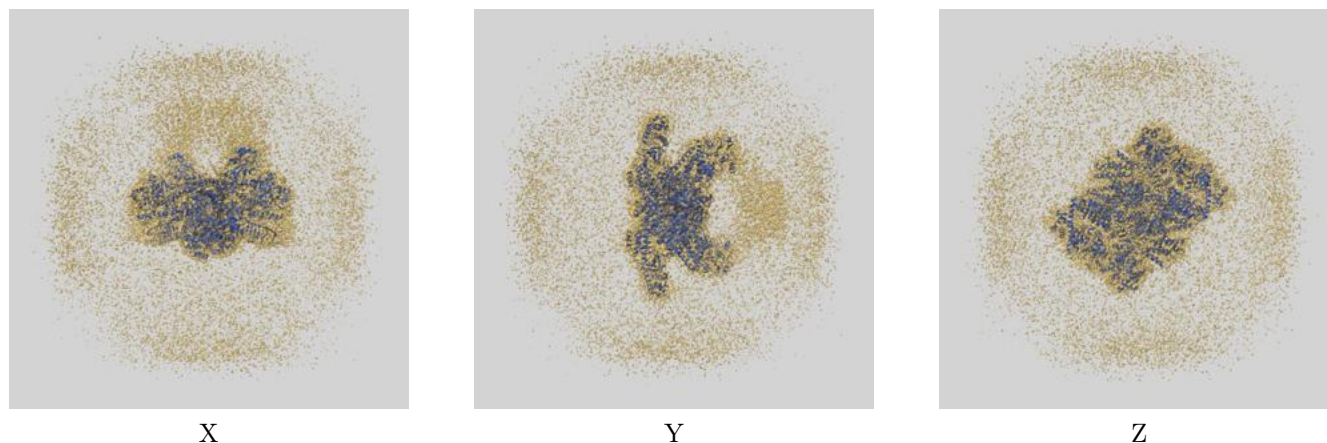
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

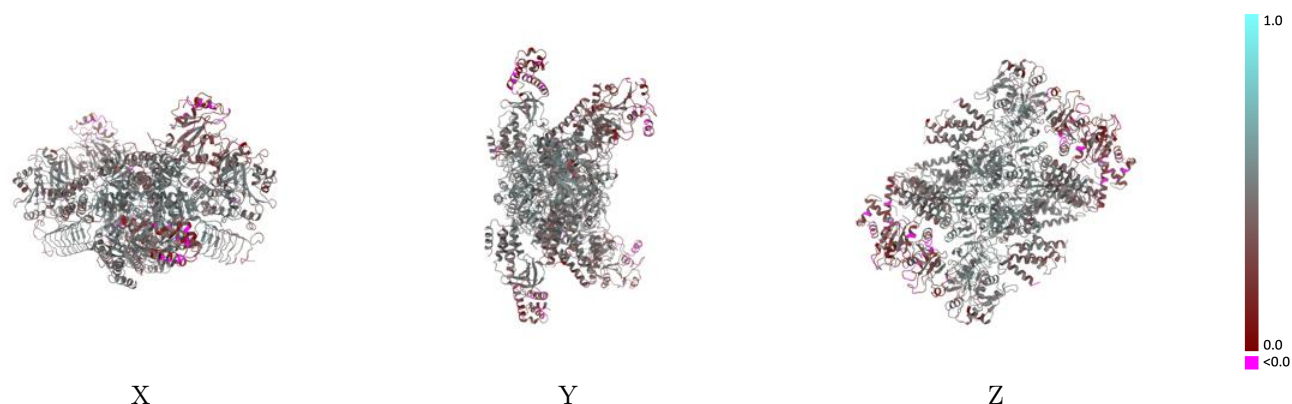
This section contains information regarding the fit between EMDB map EMD-0664 and PDB model 6O9Z. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



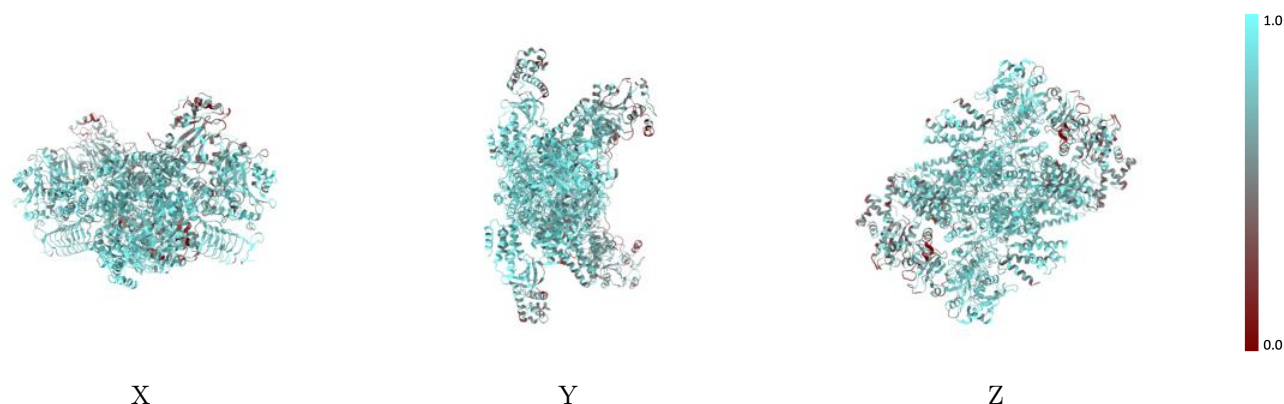
The images above show the 3D surface view of the map at the recommended contour level 1.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



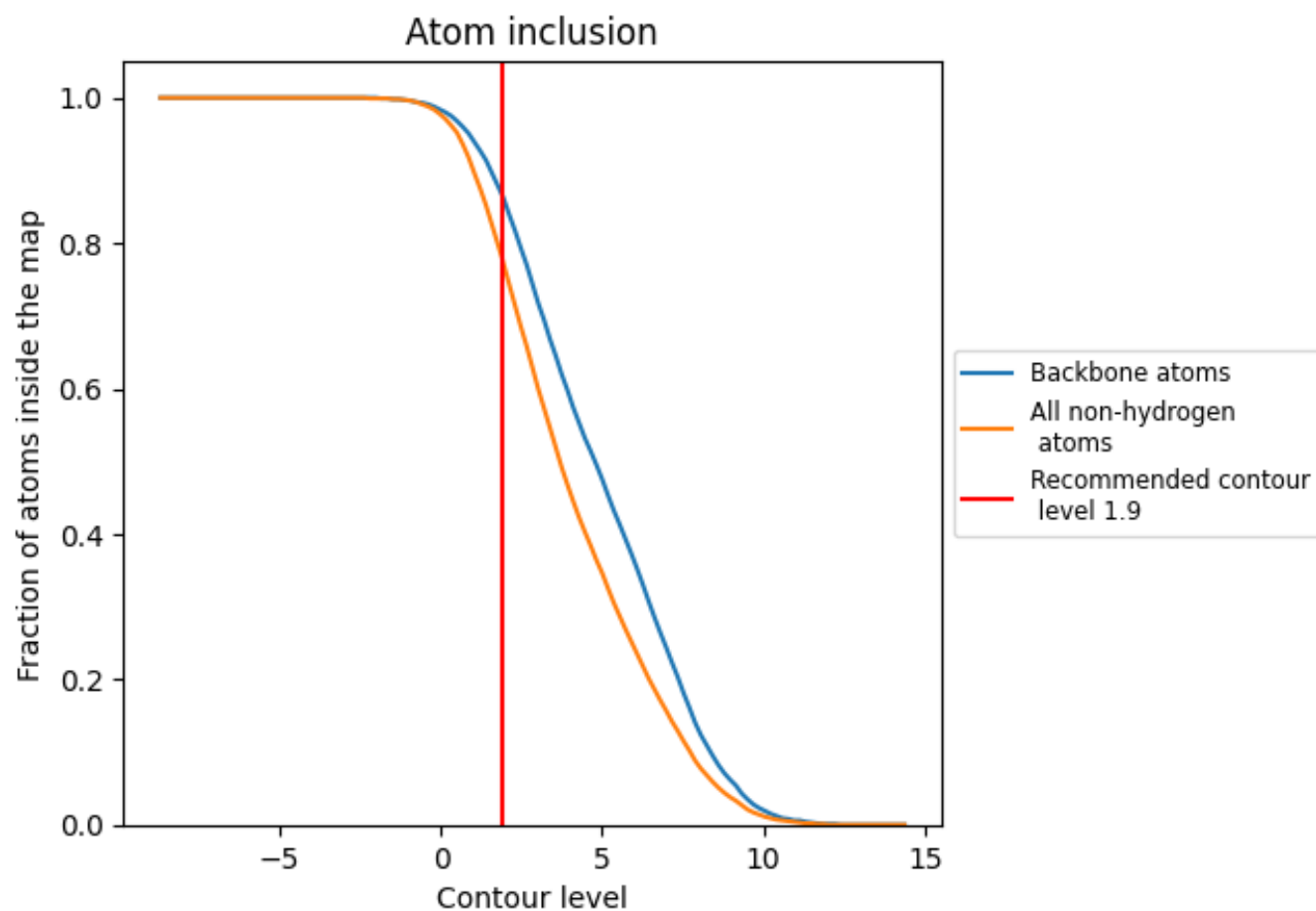
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (1.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7790</div>	<div><div></div>0.4410</div>
A	<div><div></div>0.8180</div>	<div><div></div>0.4580</div>
B	<div><div></div>0.8150</div>	<div><div></div>0.4580</div>
C	<div><div></div>0.8030</div>	<div><div></div>0.4650</div>
D	<div><div></div>0.8010</div>	<div><div></div>0.4660</div>
E	<div><div></div>0.7770</div>	<div><div></div>0.4720</div>
F	<div><div></div>0.7770</div>	<div><div></div>0.4720</div>
G	<div><div></div>0.8900</div>	<div><div></div>0.4930</div>
H	<div><div></div>0.8890</div>	<div><div></div>0.4910</div>
I	<div><div></div>0.5890</div>	<div><div></div>0.3140</div>
J	<div><div></div>0.5870</div>	<div><div></div>0.3110</div>
L	<div><div></div>0.6770</div>	<div><div></div>0.3330</div>
M	<div><div></div>0.6770</div>	<div><div></div>0.3330</div>

1.0

0.0

<0.0