



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:11 PM UTC

PDB ID : 7VLK / pdb_00007vlk
EMDB ID : EMD-32023
Title : eIF2B-SFSV NSs C2-imposed
Authors : Kashiwagi, K.; Ito, T.
Deposited on : 2021-10-04
Resolution : 2.27 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:

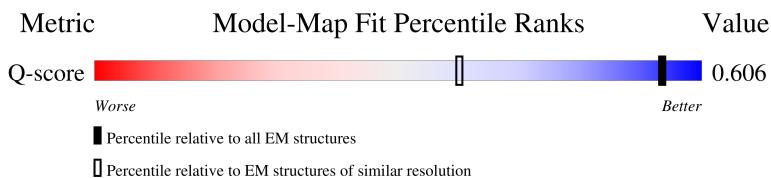
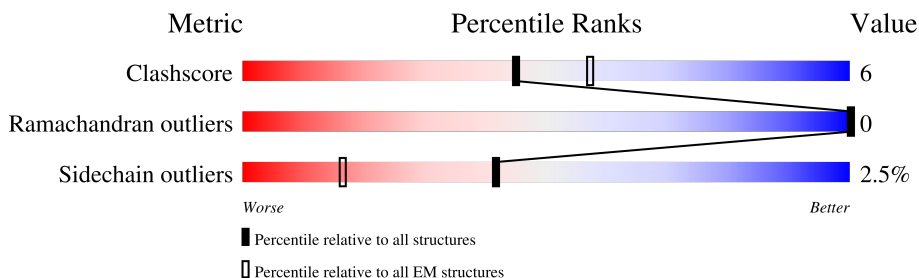
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.27 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.



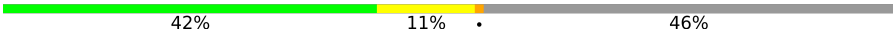
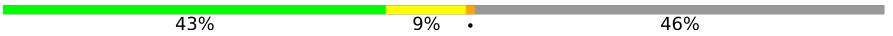
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3593 (1.77 - 2.77)

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	307	 76% 20% .
1	B	307	 78% 18% .
2	C	351	 79% 16% 5%
2	D	351	 78% 17% 5%

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Mol	Chain	Length	Quality of chain
3	E	452	
3	F	452	
4	G	523	
4	H	523	
5	I	721	
5	J	721	
6	K	261	
6	L	261	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28774 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 alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	294	Total	C	N	O	S	0	0
			2279	1464	378	425	12		
1	B	294	Total	C	N	O	S	0	0
			2279	1464	378	425	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q14232
A	0	PRO	-	expression tag	UNP Q14232
B	-1	GLY	-	expression tag	UNP Q14232
B	0	PRO	-	expression tag	UNP Q14232

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	333	Total	C	N	O	S	0	0
			2613	1652	460	486	15		
2	D	333	Total	C	N	O	S	0	0
			2613	1652	460	486	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	242	Total	C	N	O	S	0	0
			1802	1162	303	328	9		
3	F	242	Total	C	N	O	S	0	0
			1802	1162	303	328	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	356	Total	C	N	O	S	0	0
			2771	1752	494	511	14		
4	H	356	Total	C	N	O	S	0	0
			2771	1752	494	511	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	427	Total	C	N	O	S	0	0
			3333	2103	590	625	15		
5	J	427	Total	C	N	O	S	0	0
			3333	2103	590	625	15		

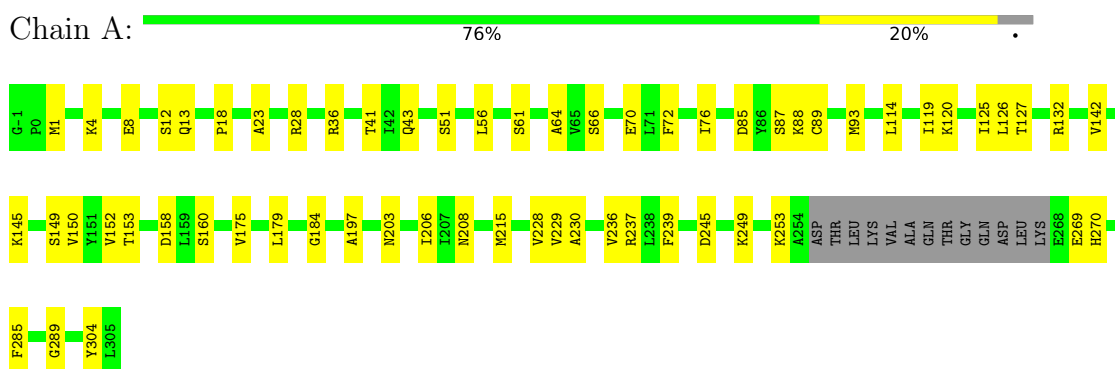
- Molecule 6 is a protein called Non-structural protein NS-S.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	197	Total	C	N	O	S	0	0
			1589	1011	274	290	14		
6	L	197	Total	C	N	O	S	0	0
			1589	1011	274	290	14		

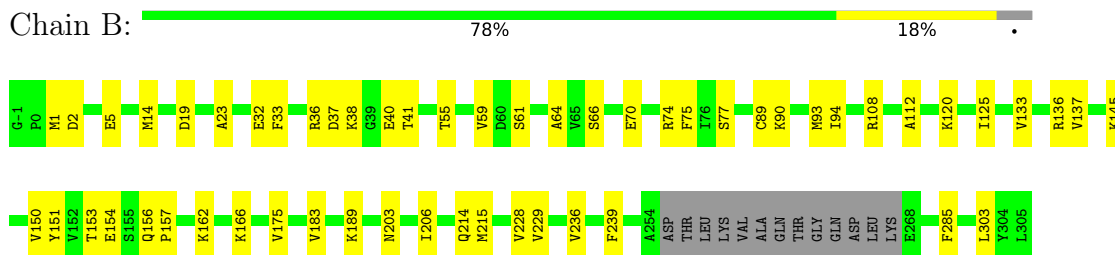
3 Residue-property plots

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.

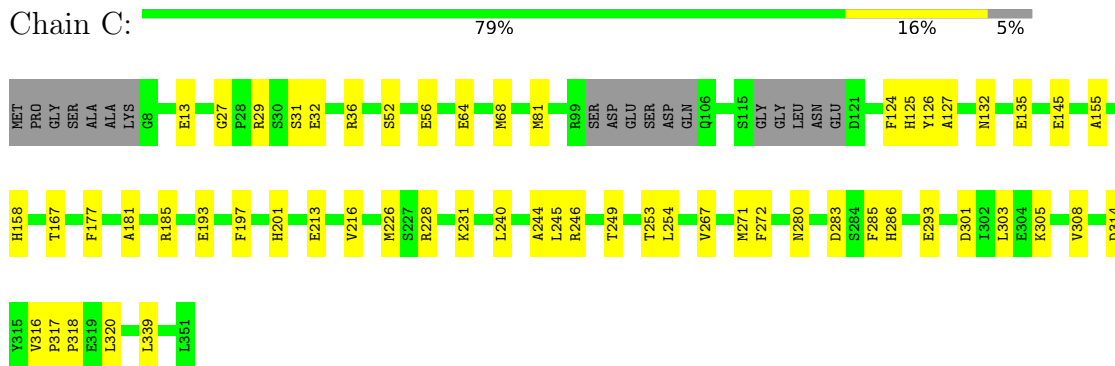
- Molecule 1: Translation initiation factor eIF-2B subunit alpha



- Molecule 1: Translation initiation factor eIF-2B subunit alpha



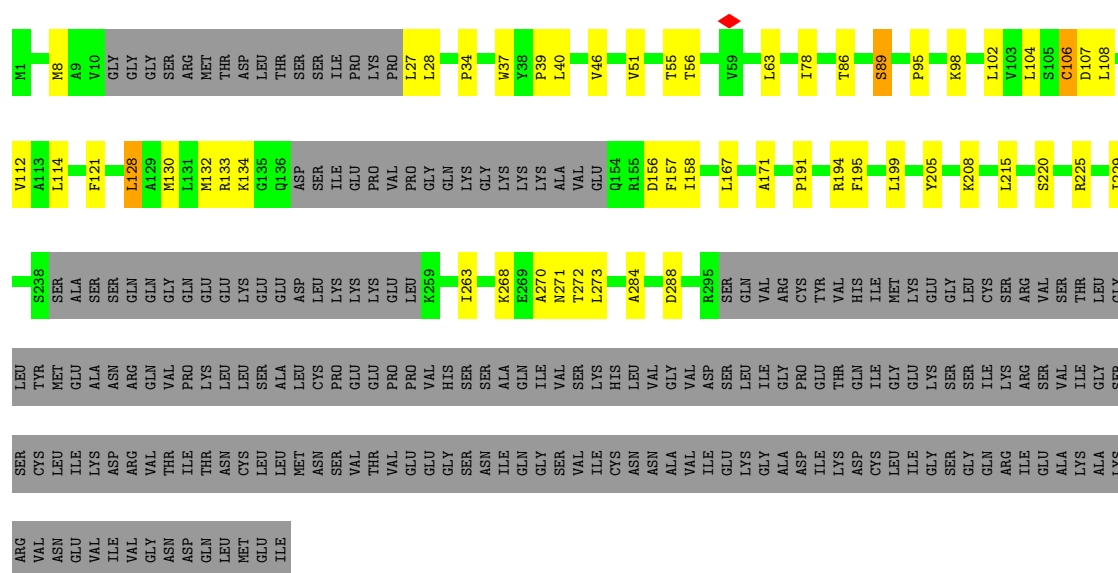
- Molecule 2: Translation initiation factor eIF-2B subunit beta



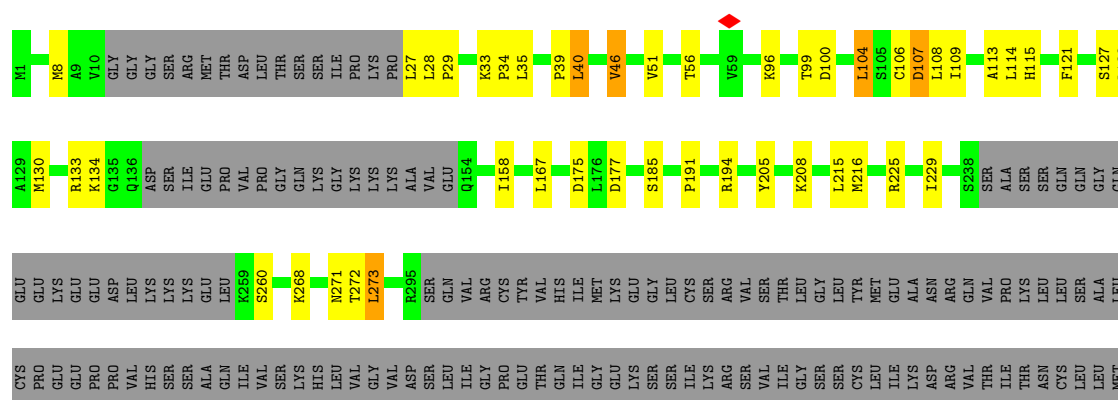
- Molecule 2: Translation initiation factor eIF-2B subunit beta

V308	T147	MT
V312	A155	PR0
F313	H158	SER
D314	T167	ALA
V316	F177	ALA
P317	A181	LYS
P318	E193	G8
F319	F197	R14
L320	C198	G27
I321	Q199	P28
M340	G200	E32
L351	H201	R36
	E213	Q44
	V216	E64
	D219	M68
	I222	I89
	F223	Y93
	R228	L96
	K231	H97
A241	A241	G98
A244	A244	R99
L245	L245	SER
T249	T249	ASP
V267	V267	ASP
P270	P270	GLU
N280	N280	SER
D283	D283	ASP
H286	H286	GLN
K287	K287	Q106
P291	P291	L113
E293	E293	T114
V294	V294	S115
L295	L295	GLY
D301	D301	LEU
V305	V305	ASN
		GLU
		D121
		Q128
		S131
		N132
		I133
		T134
		E135
		E145
		G148

Chain E: 42% 11% 46%

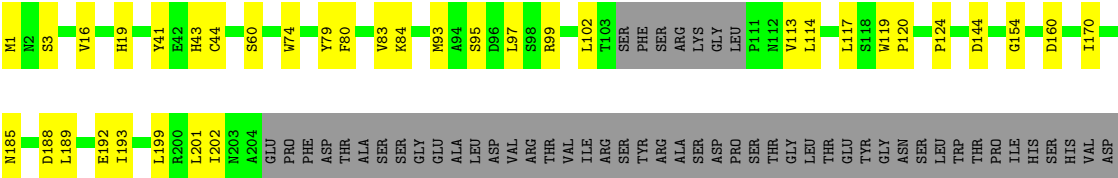


Chain F: 43% 9% . 46%



HIS
VAL
ASP
GLU
ASN
ASP
GLU
SER
SER
SER
ASP
SER
ASP
ASP
PHE

● Molecule 6: Non-structural protein NS-S



GLU
ASN
ASP
GLU
SER
SER
SER
ASP
SER
ASP
PHE

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	888479	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	43.821	Depositor
Minimum map value	-22.302	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	331.6, 331.6, 331.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.829, 0.829, 0.829	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	A	0.09	0/2316	0.25	0/3127
1	B	0.11	0/2316	0.29	0/3127
2	C	0.09	0/2662	0.24	0/3597
2	D	0.08	0/2662	0.22	0/3597
3	E	0.11	0/1828	0.33	0/2480
3	F	0.10	0/1828	0.30	0/2480
4	G	0.09	0/2823	0.24	0/3836
4	H	0.09	0/2823	0.25	0/3836
5	I	0.09	0/3402	0.27	0/4631
5	J	0.09	0/3402	0.27	0/4631
6	K	0.09	0/1627	0.29	0/2196
6	L	0.08	0/1627	0.25	0/2196
All	All	0.09	0/29316	0.27	0/39734

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	2279	0	2353	34	0
1	B	2279	0	2353	36	0
2	C	2613	0	2623	32	0
2	D	2613	0	2623	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1802	0	1753	35	0
3	F	1802	0	1753	31	0
4	G	2771	0	2834	34	0
4	H	2771	0	2834	37	0
5	I	3333	0	3302	37	0
5	J	3333	0	3302	34	0
6	K	1589	0	1554	22	0
6	L	1589	0	1554	21	0
All	All	28774	0	28838	362	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 362 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)
3:F:104:LEU:HD11	3:F:108:LEU:HD22	1.69	0.73
1:A:245:ASP:OD2	4:G:326:LYS:NZ	2.22	0.73
3:F:33:LYS:HG3	3:F:34:PRO:HD2	1.70	0.73
3:E:8:MET:SD	3:E:89:SER:OG	2.47	0.72
5:J:181:MET:HB3	5:J:287:ILE:HG12	1.71	0.72

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	268/307 (87%)	262 (98%)	6 (2%)	0	100	100
1	B	290/307 (94%)	283 (98%)	7 (2%)	0	100	100
2	C	327/351 (93%)	319 (98%)	8 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	327/351 (93%)	321 (98%)	6 (2%)	0	100	100
3	E	234/452 (52%)	230 (98%)	4 (2%)	0	100	100
3	F	234/452 (52%)	229 (98%)	5 (2%)	0	100	100
4	G	354/523 (68%)	353 (100%)	1 (0%)	0	100	100
4	H	354/523 (68%)	353 (100%)	1 (0%)	0	100	100
5	I	425/721 (59%)	408 (96%)	17 (4%)	0	100	100
5	J	425/721 (59%)	413 (97%)	12 (3%)	0	100	100
6	K	193/261 (74%)	188 (97%)	5 (3%)	0	100	100
6	L	193/261 (74%)	191 (99%)	2 (1%)	0	100	100
All	All	3624/5230 (69%)	3550 (98%)	74 (2%)	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	250/261 (96%)	244 (98%)	6 (2%)	43	59
1	B	250/261 (96%)	247 (99%)	3 (1%)	63	77
2	C	285/298 (96%)	279 (98%)	6 (2%)	47	63
2	D	285/298 (96%)	281 (99%)	4 (1%)	59	74
3	E	178/398 (45%)	171 (96%)	7 (4%)	28	41
3	F	178/398 (45%)	165 (93%)	13 (7%)	13	16
4	G	312/444 (70%)	308 (99%)	4 (1%)	61	76
4	H	312/444 (70%)	307 (98%)	5 (2%)	55	71
5	I	374/626 (60%)	361 (96%)	13 (4%)	32	45
5	J	374/626 (60%)	363 (97%)	11 (3%)	37	52
6	K	176/233 (76%)	172 (98%)	4 (2%)	44	60
6	L	176/233 (76%)	173 (98%)	3 (2%)	53	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3150/4520 (70%)	3071 (98%)	79 (2%)	42 58

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	331	THR
5	J	433	SER
5	I	429	SER
5	J	208	THR
6	K	195	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
5	J	384	HIS
5	J	388	ASN
2	D	349	HIS
2	D	277	GLN
5	J	407	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

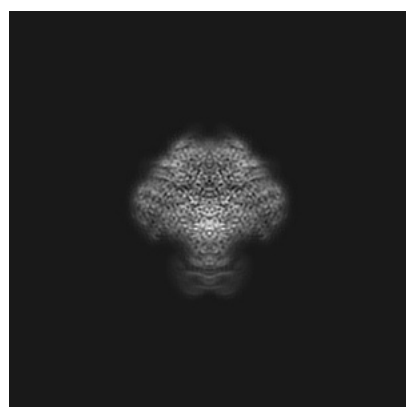
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32023. These allow visual inspection of the internal detail of the map and identification of artifacts.

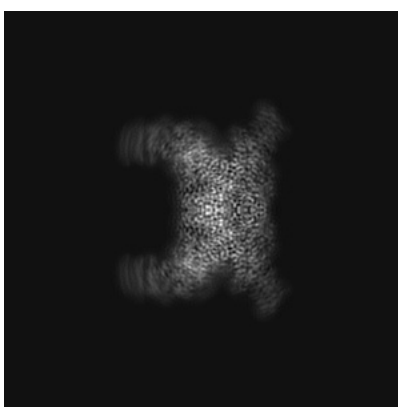
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

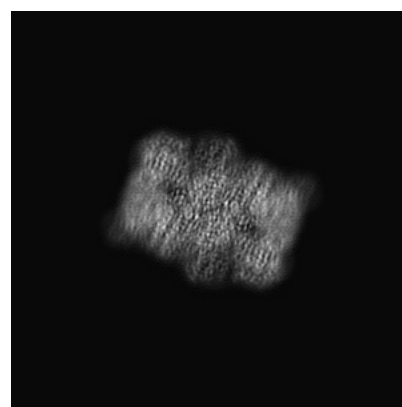
6.1.1 Primary map



X



Y

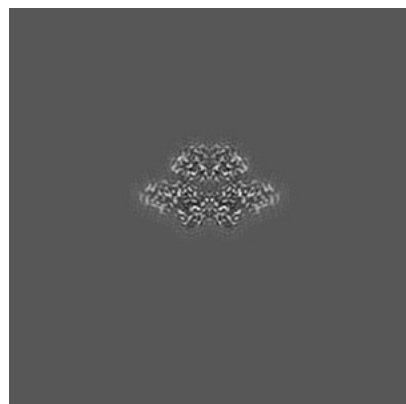


Z

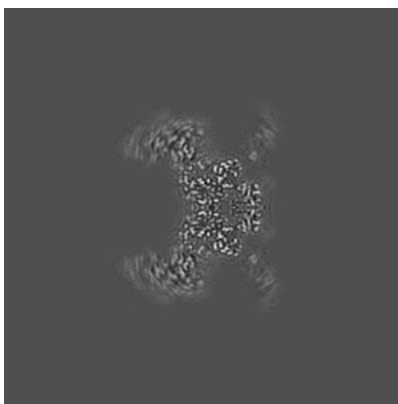
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

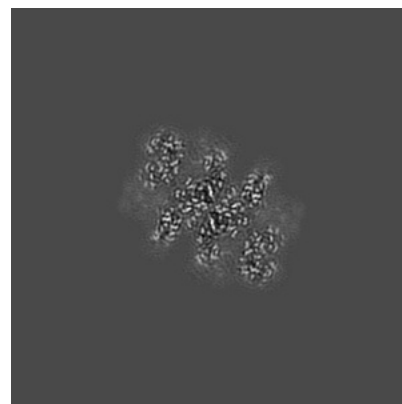
6.2.1 Primary map



X Index: 200



Y Index: 200

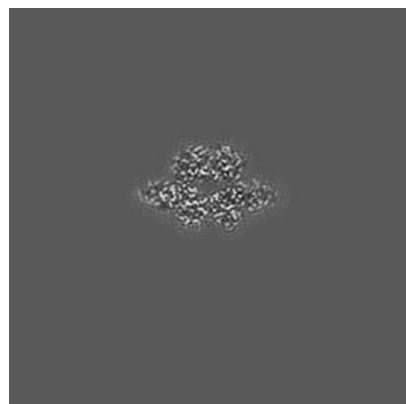


Z Index: 200

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

6.3 Largest variance slices [i](#)

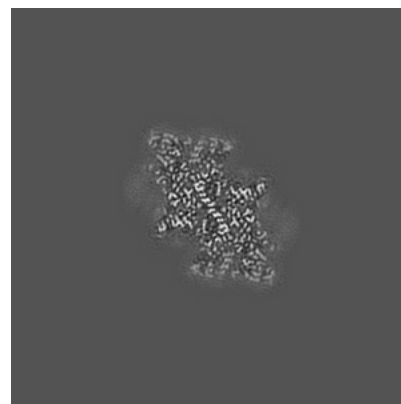
6.3.1 Primary map



X Index: 198



Y Index: 187

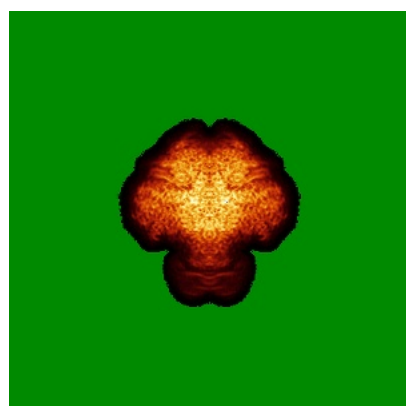


Z Index: 208

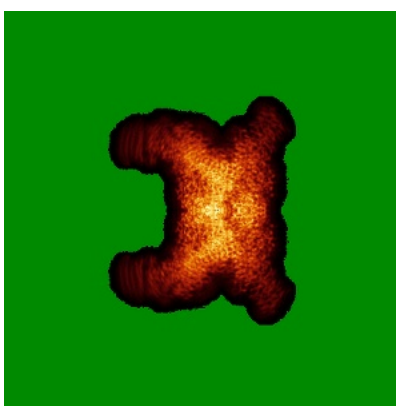
The images above show the largest variance slices of the map in three orthogonal directions.

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

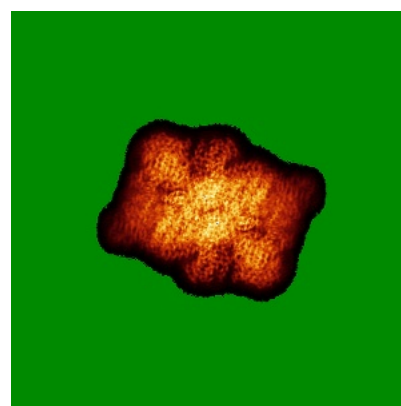
6.4.1 Primary map



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](#)

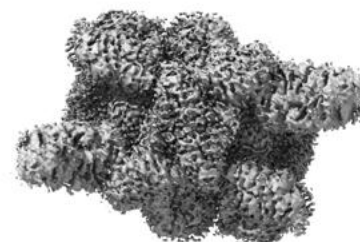
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

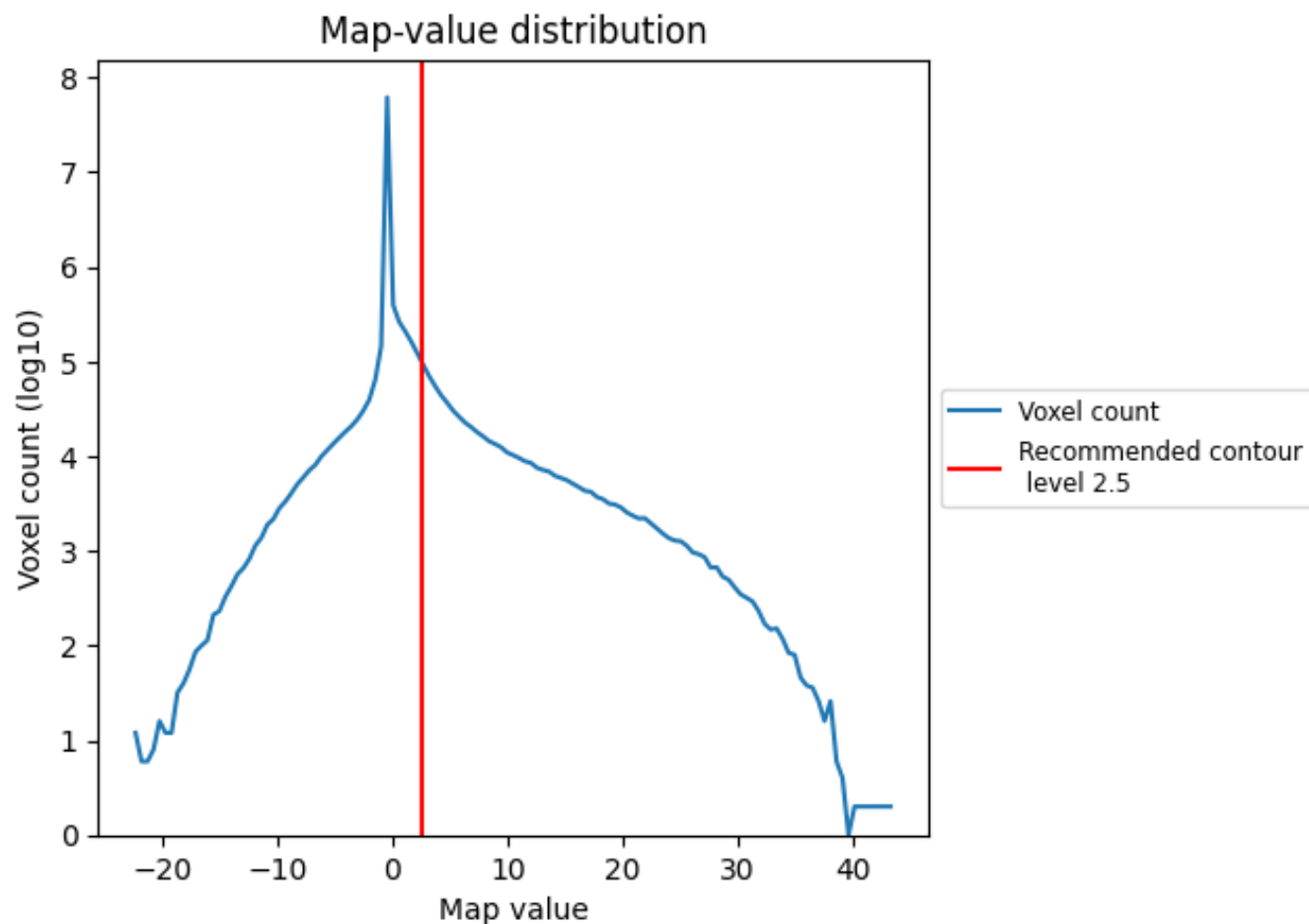
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

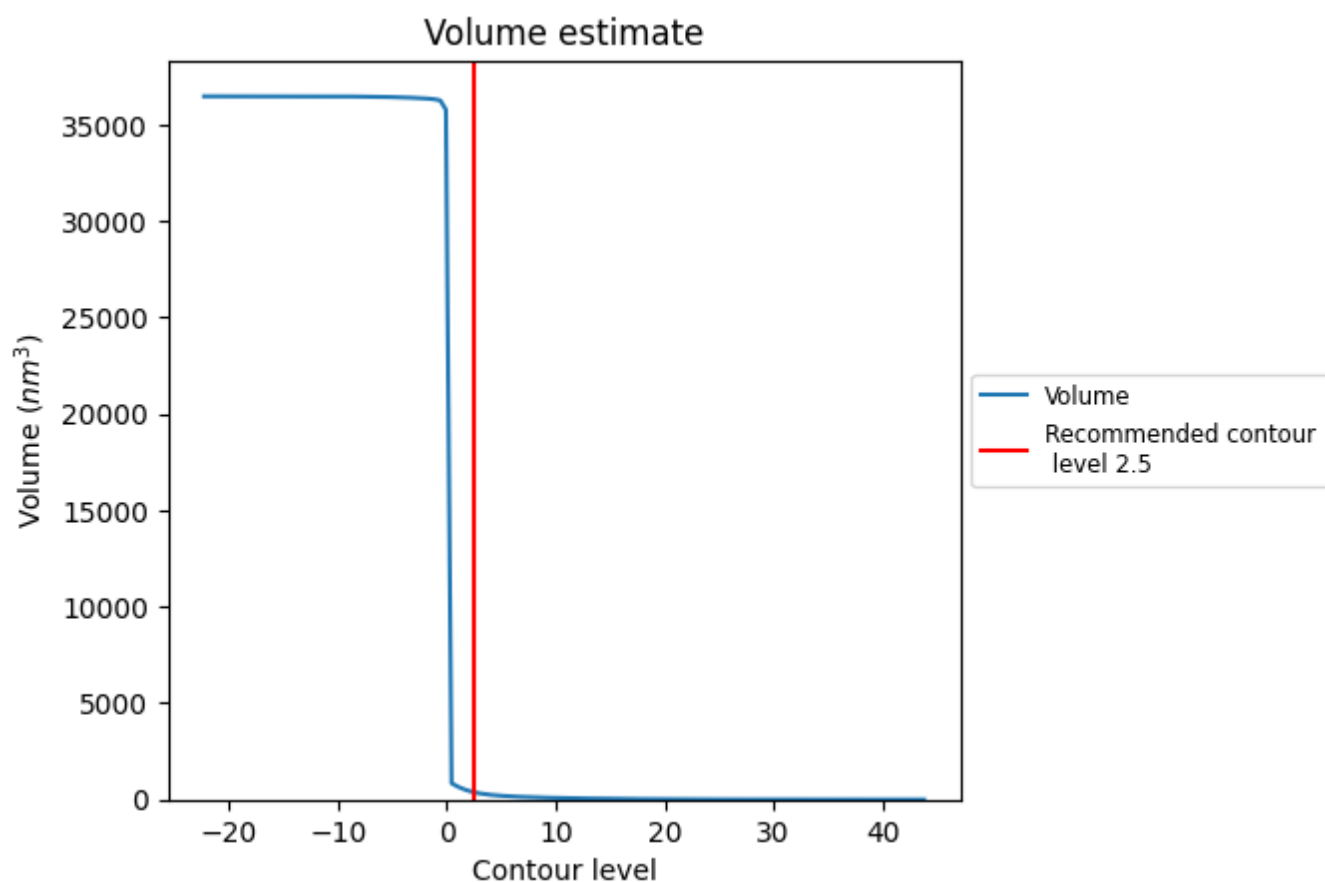
This section contains the results of statistical analysis of the map.

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.

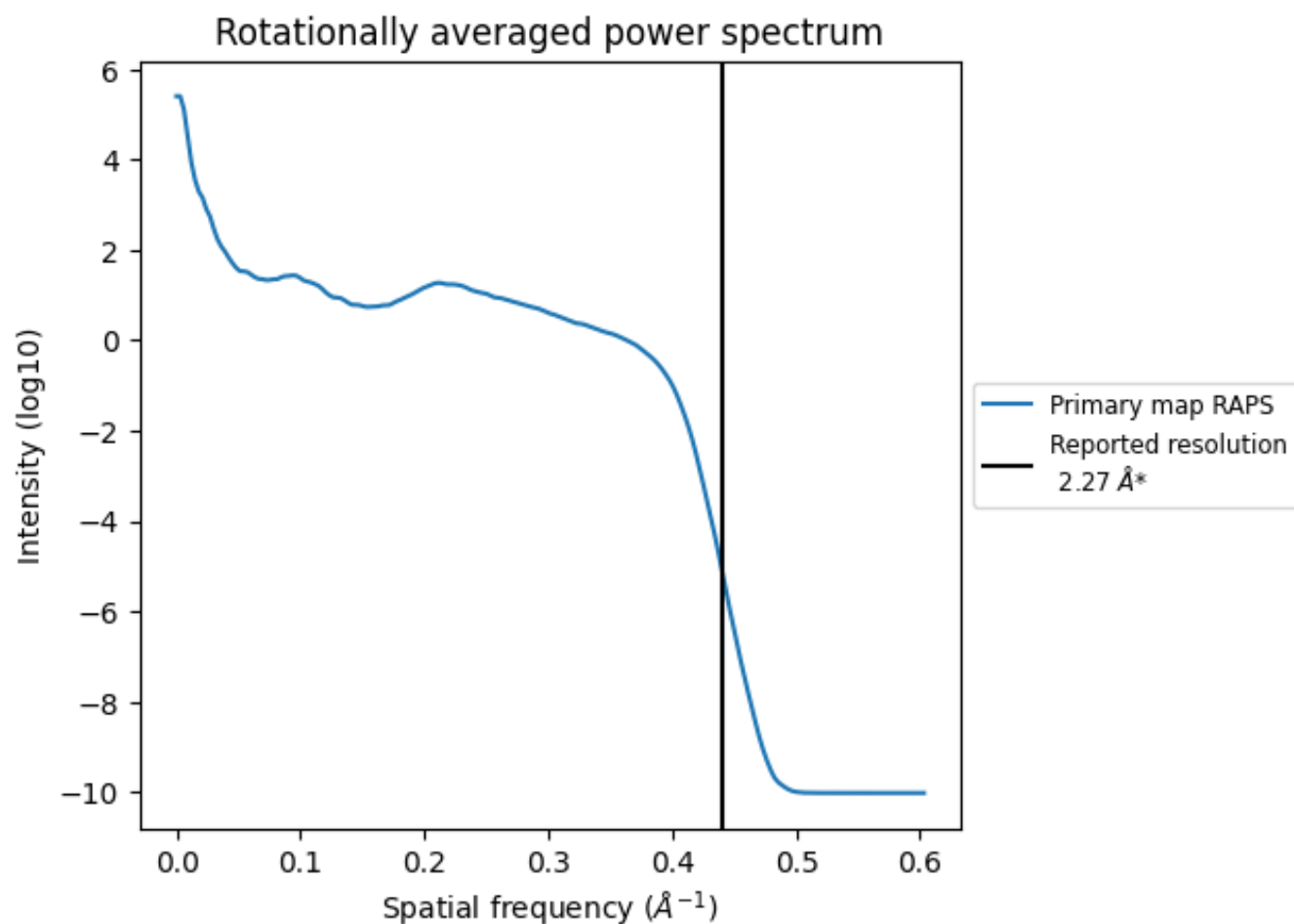
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 378 nm^3 ; this corresponds to an approximate mass of 342 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 0.441 Å⁻¹

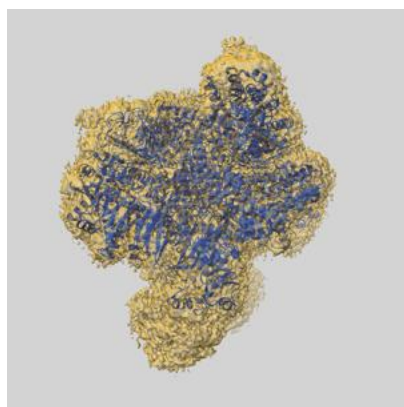
8 Fourier-Shell correlation

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

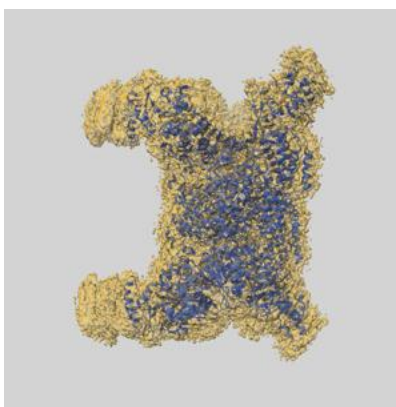
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32023 and PDB model 7VLK. Per-residue inclusion information can be found in section 3 on page 6.

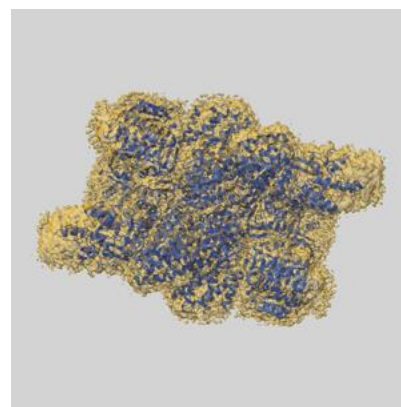
9.1 Map-model overlay [i](#)



X



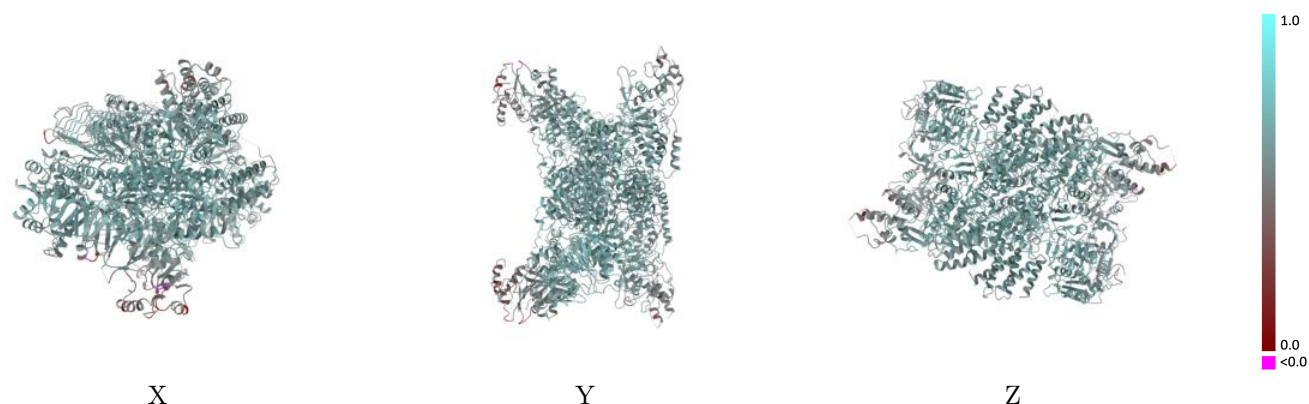
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5 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](#)

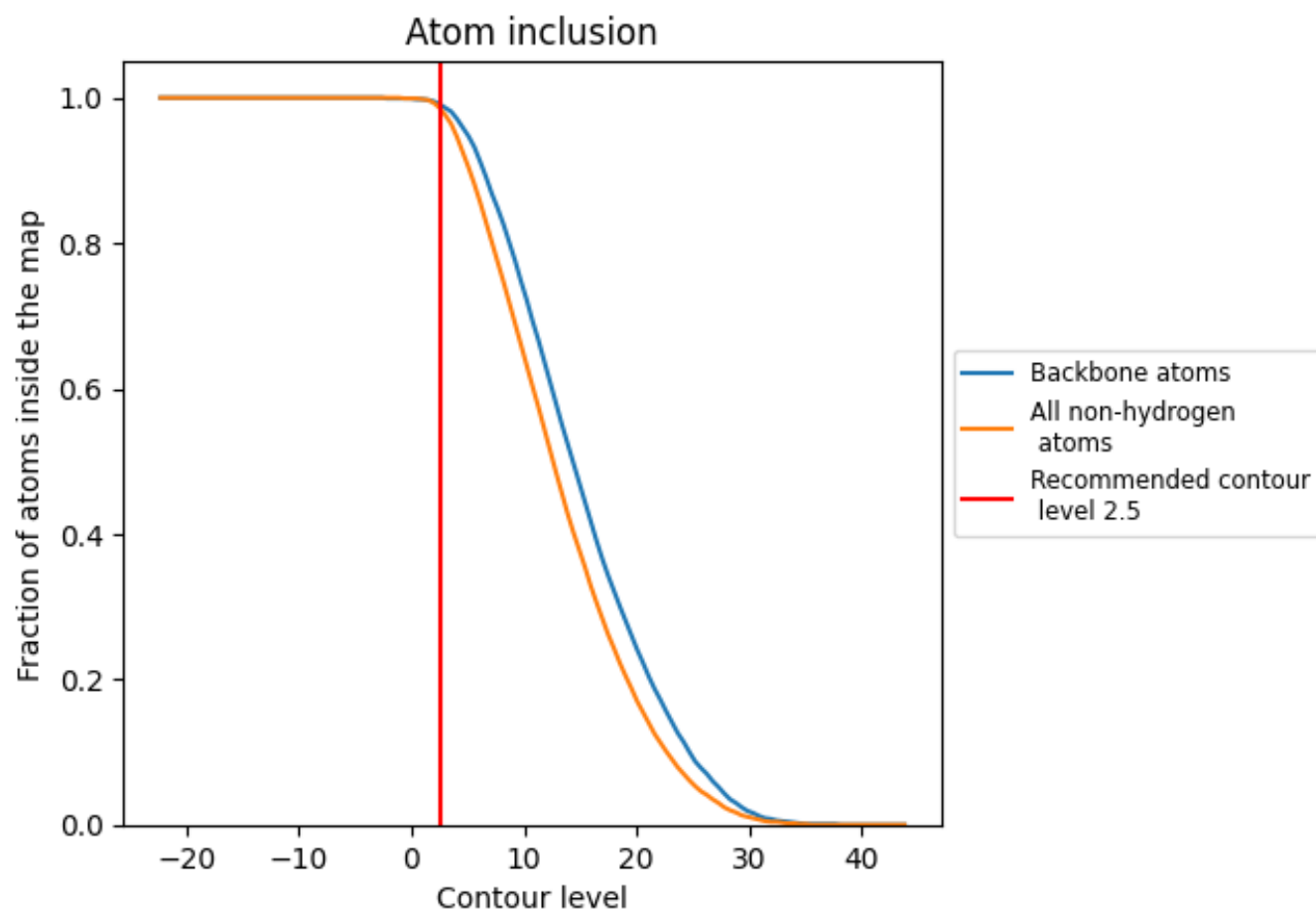


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9860	0.6060
A	0.9890	0.6170
B	0.9900	0.6170
C	0.9900	0.6300
D	0.9890	0.6340
E	0.9720	0.5250
F	0.9720	0.5240
G	0.9960	0.6530
H	0.9960	0.6540
I	0.9870	0.6070
J	0.9880	0.6040
K	0.9730	0.5610
L	0.9730	0.5610

1.0

0.0

<0.0