Full wwPDB EM Validation Report (i)

Jul 3, 2024 – 01:10 am BST

PDB ID	:	7NKQ
EMDB ID	:	EMD-12446
Title	:	Mycobacterium smegmatis ATP synthase b-delta state 3
Authors	:	Montgomery, M.G.; Petri, J.; Spikes, T.E.; Walker, J.E.
Deposited on	:	2021-02-18
Resolution	:	2.98 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

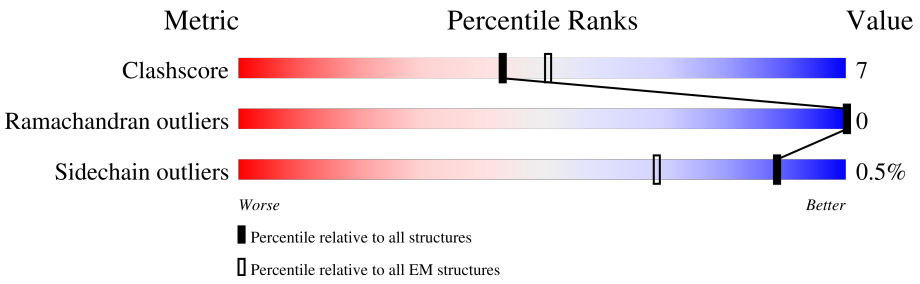
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.98 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 <=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	548	5% 17% • 81%
1	B	548	6% 11% • 88%
1	C	548	• 7% • 92%
2	D	475	• 9% • 89%
2	E	475	• 9% • 90%
2	F	475	• 8% 92%
3	d	445	24% 74% 26%
4	b	180	13% 21% 79%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10621 atoms, of which 5312 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 ATP synthase subunit alpha.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	A	104	1500	476	735	123	165	1	0	0
1	B	64	917	289	445	78	104	1	0	0
1	C	45	643	206	308	53	75	1	0	0

- Molecule 2 is a protein called ATP synthase subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
2	D	50	752	231	379	72	69	1	0	0
2	E	48	721	222	366	66	66	1	0	0
2	F	36	559	172	286	53	48		0	0

- Molecule 3 is a protein called ATP synthase subunit b-delta.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
3	d	330	5002	1525	2531	452	492	2	0	0

- Molecule 4 is a protein called ATP synthase subunit b.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	H	N	O		
4	b	37	527	157	262	49	59	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	171	HIS	-	expression tag	UNP A0R204

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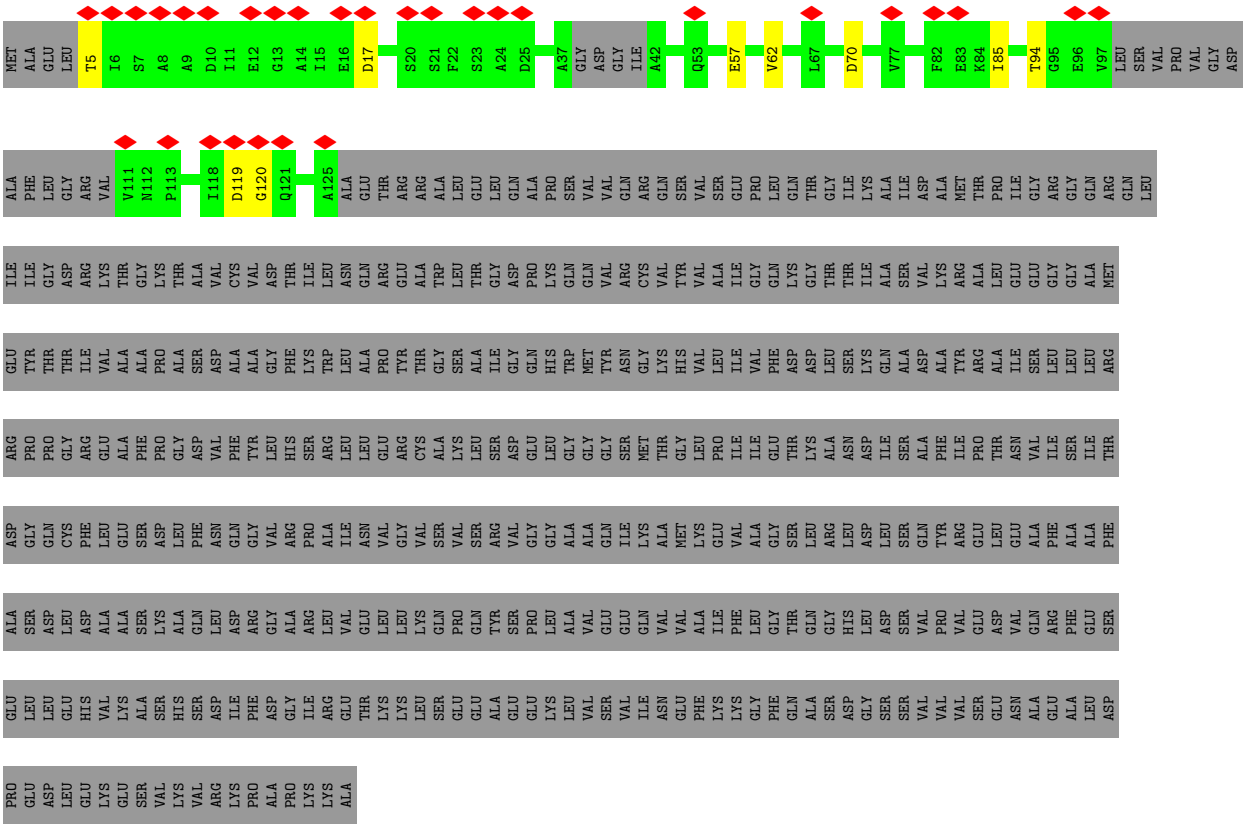
Chain	Residue	Modelled	Actual	Comment	Reference
b	172	HIS	-	expression tag	UNP A0R204
b	173	HIS	-	expression tag	UNP A0R204
b	174	HIS	-	expression tag	UNP A0R204
b	175	HIS	-	expression tag	UNP A0R204
b	176	HIS	-	expression tag	UNP A0R204
b	177	HIS	-	expression tag	UNP A0R204
b	178	HIS	-	expression tag	UNP A0R204
b	179	HIS	-	expression tag	UNP A0R204
b	180	HIS	-	expression tag	UNP A0R204

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.

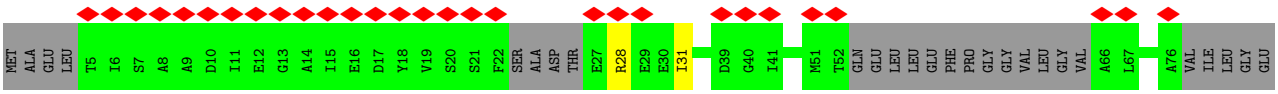
- Molecule 1: ATP synthase subunit alpha

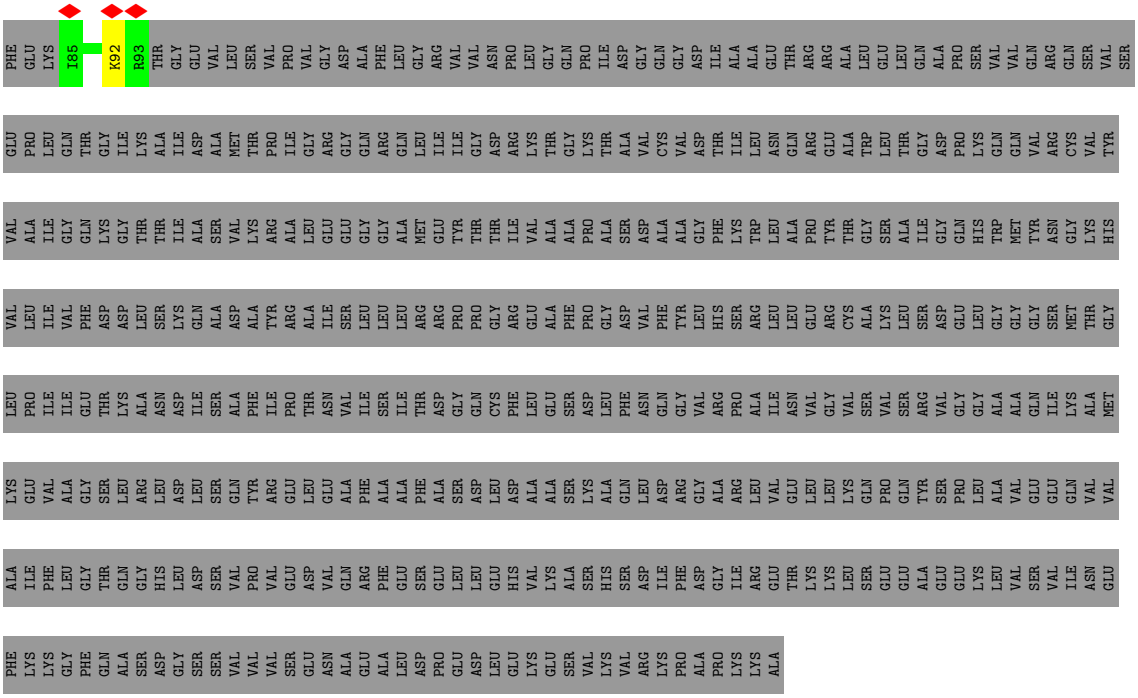
Chain A:



- Molecule 1: ATP synthase subunit alpha

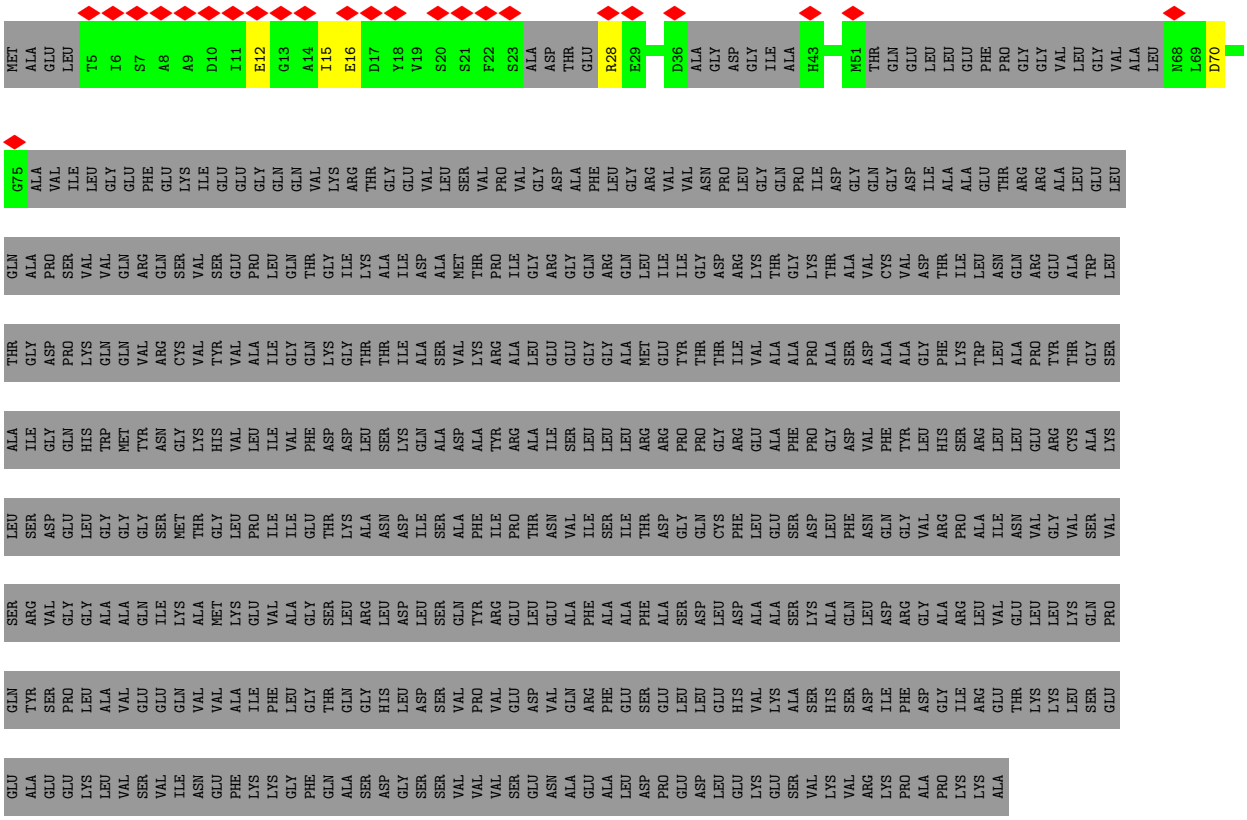
Chain B:





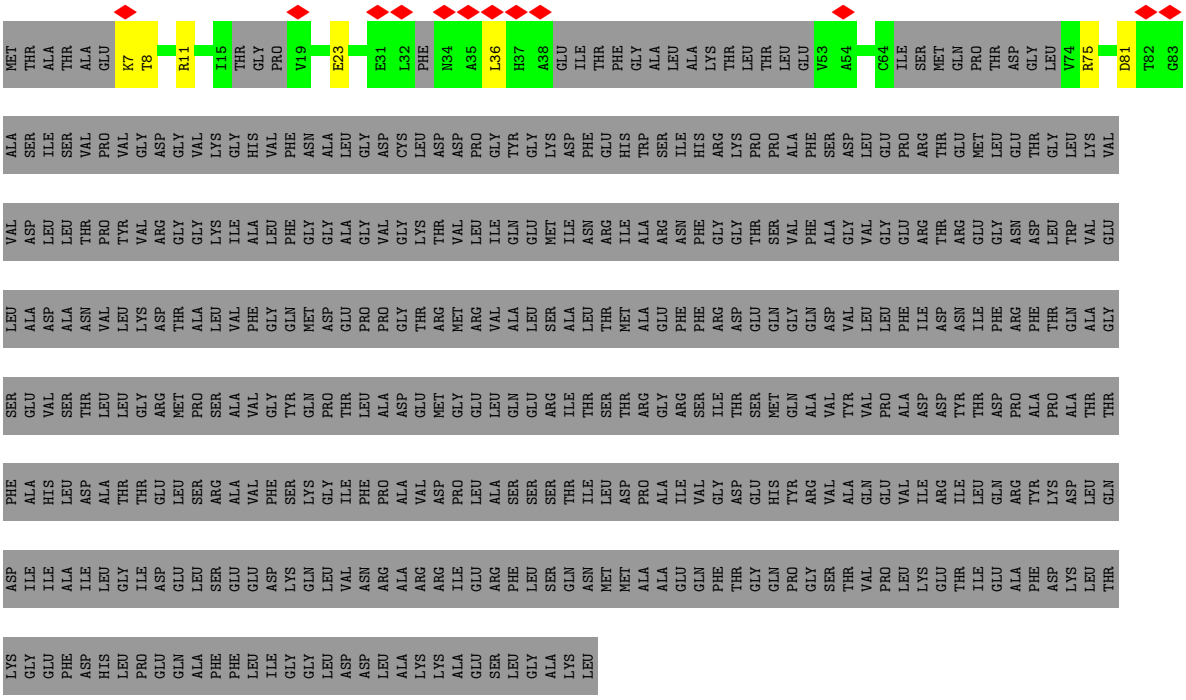
• Molecule 1: ATP synthase subunit alpha

Chain C: 7% 92%



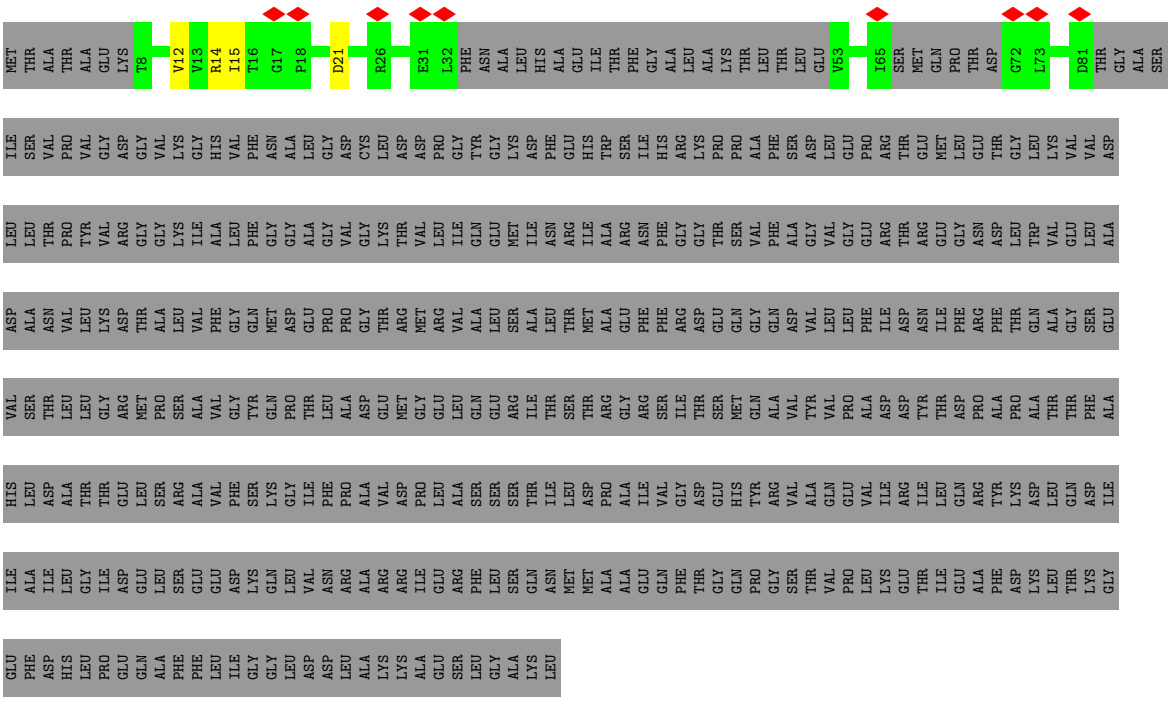
• Molecule 2: ATP synthase subunit beta

Chain D: 9% 89%



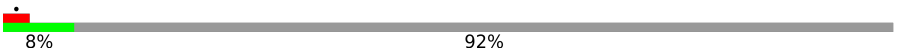
- Molecule 2: ATP synthase subunit beta

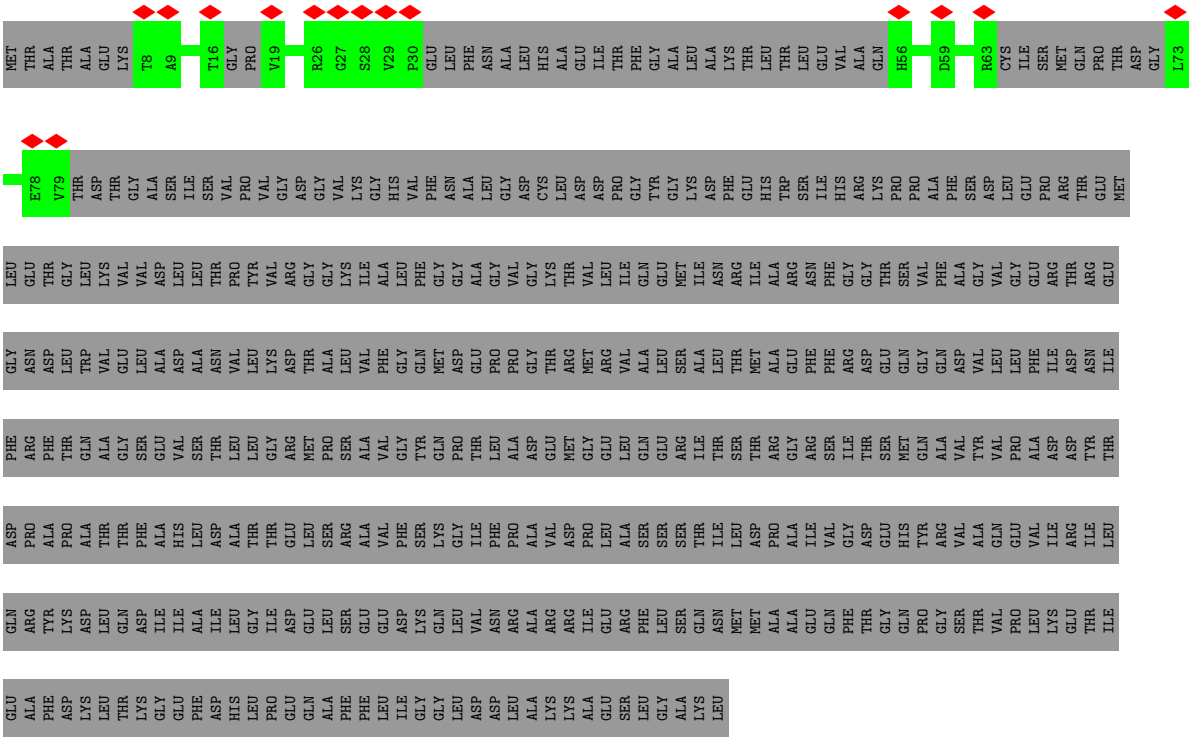
Chain E: 9% 90%



- Molecule 2: ATP synthase subunit beta

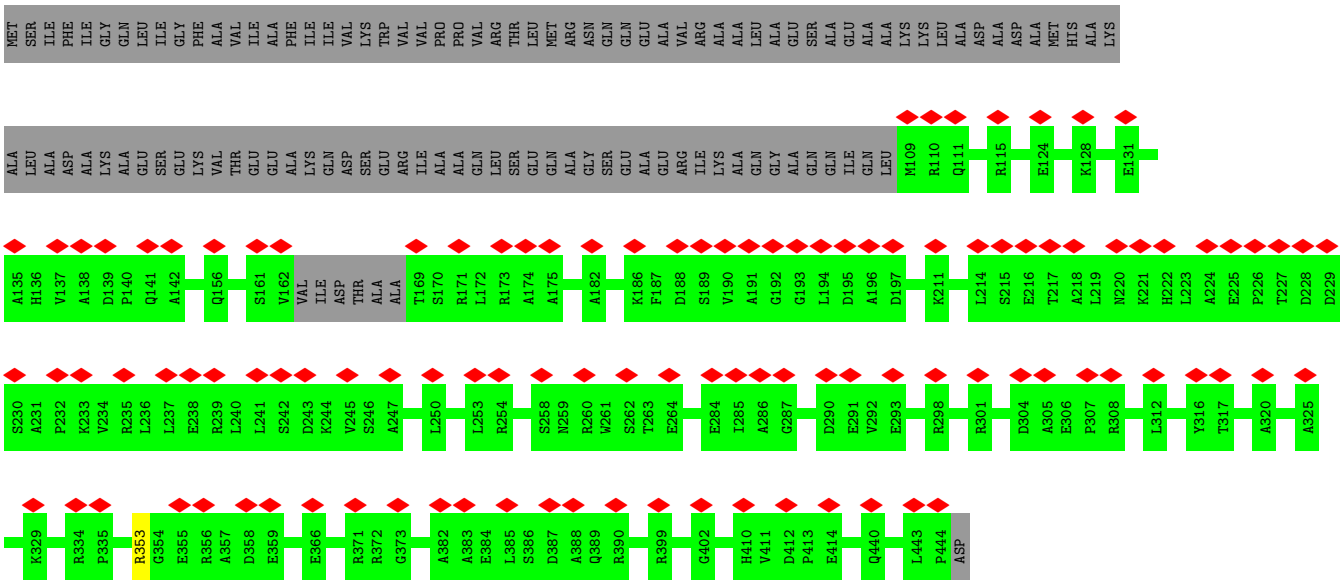
Chain F:





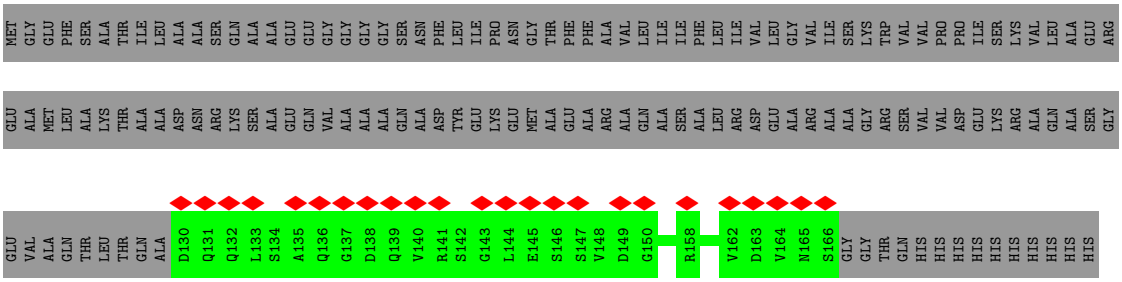
- Molecule 3: ATP synthase subunit b-delta

Chain d:



- Molecule 4: ATP synthase subunit b

Chain b:


MET GLY GLU PHE SER ALA THR ILE LEU ALA ALA SER GLN ALA ALA GLU GLU GLY GLY GLY GLY SER ASN PHE LEU ILE PRO ASN GLY THR PHE PHE ALA VAL LEU ILE ILE PHE LEU ILE VAL LEU GLY VAL ILE SER LYS TRP VAL VAL PRO PRO ILE SER LYS VAL LEU ALA GLU ARG
GLU ALA MET LEU ALA LYS THR ALA ALA ASP ASN ARG LYS SER ALA GLU GLN VAL ALA ALA ALA GLN ALA ASP TYR GLU LYS GLU MET ALA GLU ALA ARG ALA GLN ALA SER ALA LEU ARG ASP GLU ALA ARG ALA ALA GLY ARG SER VAL VAL ASP GLU LYS ARG ALA GLN ALA SER GLY
GLU VAL ALA GLN THR LEU THR GLN ALA D130 Q131 Q132 L133 S134 A135 Q136 G137 D138 Q139 V140 R141 S142 G143 L144 E145 S146 S147 V148 D149 G150 R158 V162 D163 V164 N165 S166 GLY GLY THR GLN HIS HIS HIS HIS HIS HIS HIS HIS HIS HIS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85548	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 ($e^-/Å^2$)	59.86	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.071	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0176	Depositor
Map size (Å)	415.0, 415.0, 415.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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	0.31	0/772	0.46	0/1045
1	B	0.29	0/473	0.46	0/635
1	C	0.30	0/336	0.46	0/451
2	D	0.33	0/373	0.55	0/500
2	E	0.38	0/357	0.59	0/483
2	F	0.30	0/273	0.58	0/366
3	d	0.26	0/2492	0.52	0/3381
4	b	0.23	0/264	0.50	0/354
All	All	0.29	0/5340	0.51	0/7215

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	765	735	735	6	0
1	B	472	445	445	2	0
1	C	335	308	308	4	0
2	D	373	379	379	5	0
2	E	355	366	366	2	0
2	F	273	286	286	0	0
3	d	2471	2531	2531	0	0
4	b	265	262	262	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5309	5312	5312	18	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 7.

All (18) 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:D:36:LEU:HD23	2:D:81:ASP:HA	1.86	0.58
1:B:31:ILE:HD12	1:B:92:LYS:NZ	2.21	0.54
1:C:12:GLU:O	1:C:16:GLU:OE1	2.24	0.54
2:E:14:ARG:NH1	2:E:21:ASP:OD2	2.41	0.53
1:A:119:ASP:OD1	1:A:120:GLY:N	2.42	0.53
2:D:11:ARG:NH1	2:D:23:GLU:OE1	2.42	0.52
1:C:70:ASP:O	2:D:75:ARG:NH1	2.43	0.51
1:C:15:ILE:HG23	1:C:16:GLU:OE1	2.12	0.50
1:A:70:ASP:N	1:A:70:ASP:OD1	2.45	0.49
2:E:12:VAL:HG11	2:E:15:ILE:HD11	1.96	0.47
1:A:17:ASP:N	1:A:17:ASP:OD1	2.46	0.47
1:A:5:THR:O	1:A:5:THR:HG23	2.15	0.47
1:C:12:GLU:HA	1:C:15:ILE:HG22	1.96	0.46
1:A:57:GLU:OE2	1:A:94:THR:HG22	2.15	0.46
2:D:81:ASP:OD2	2:D:81:ASP:O	2.35	0.45
1:A:62:VAL:HG11	1:A:85:ILE:HD11	1.99	0.44
2:D:7:LYS:O	2:D:8:THR:OG1	2.29	0.41
1:B:31:ILE:HD12	1:B:92:LYS:HZ1	1.84	0.41

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	98/548 (18%)	97 (99%)	1 (1%)	0	100	100
1	B	56/548 (10%)	54 (96%)	2 (4%)	0	100	100
1	C	37/548 (7%)	36 (97%)	1 (3%)	0	100	100
2	D	40/475 (8%)	40 (100%)	0	0	100	100
2	E	42/475 (9%)	41 (98%)	1 (2%)	0	100	100
2	F	28/475 (6%)	27 (96%)	1 (4%)	0	100	100
3	d	326/445 (73%)	314 (96%)	12 (4%)	0	100	100
4	b	35/180 (19%)	35 (100%)	0	0	100	100
All	All	662/3694 (18%)	644 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	82/441 (19%)	82 (100%)	0	100	100
1	B	50/441 (11%)	49 (98%)	1 (2%)	55	81
1	C	38/441 (9%)	37 (97%)	1 (3%)	46	76
2	D	41/388 (11%)	41 (100%)	0	100	100
2	E	40/388 (10%)	40 (100%)	0	100	100
2	F	31/388 (8%)	31 (100%)	0	100	100
3	d	262/347 (76%)	261 (100%)	1 (0%)	91	97
4	b	30/134 (22%)	30 (100%)	0	100	100
All	All	574/2968 (19%)	571 (100%)	3 (0%)	89	95

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	28	ARG
1	C	28	ARG

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Mol	Chain	Res	Type
3	d	353	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	d	112	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 monosaccharides 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.

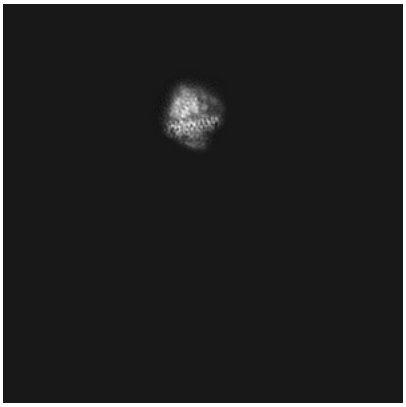
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-12446. These allow visual inspection of the internal detail of the map and identification of artifacts.

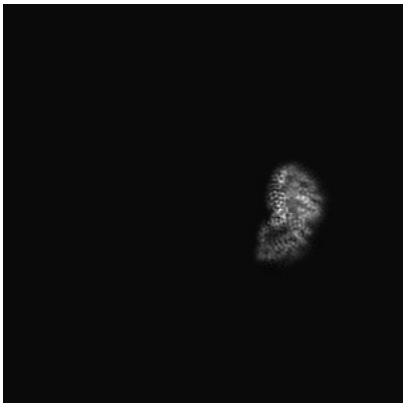
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

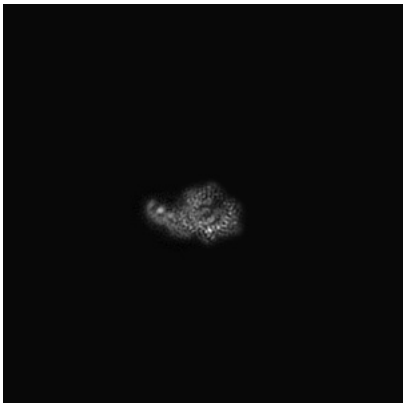
6.1.1 Primary map



X



Y



Z

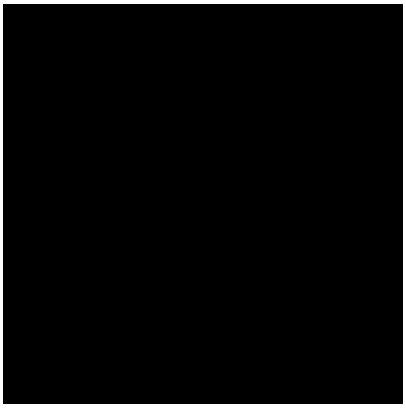
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

6.2.1 Primary map

X Index: 250

Y Index: 250



Z Index: 250

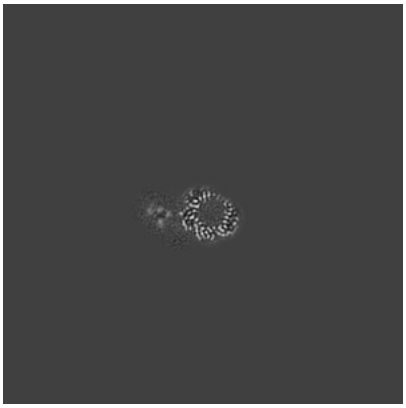
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 257

Y Index: 221

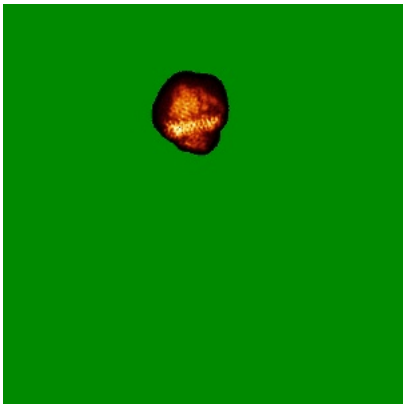


Z Index: 346

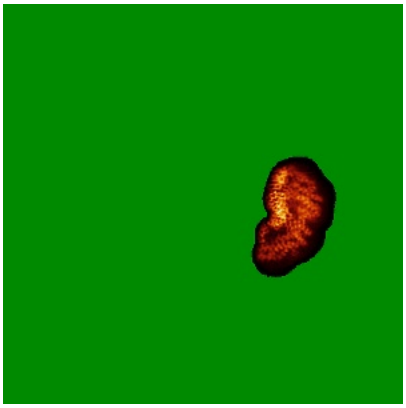
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

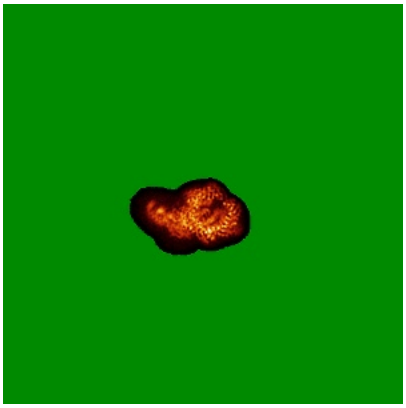
6.4.1 Primary map



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 0.0176. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

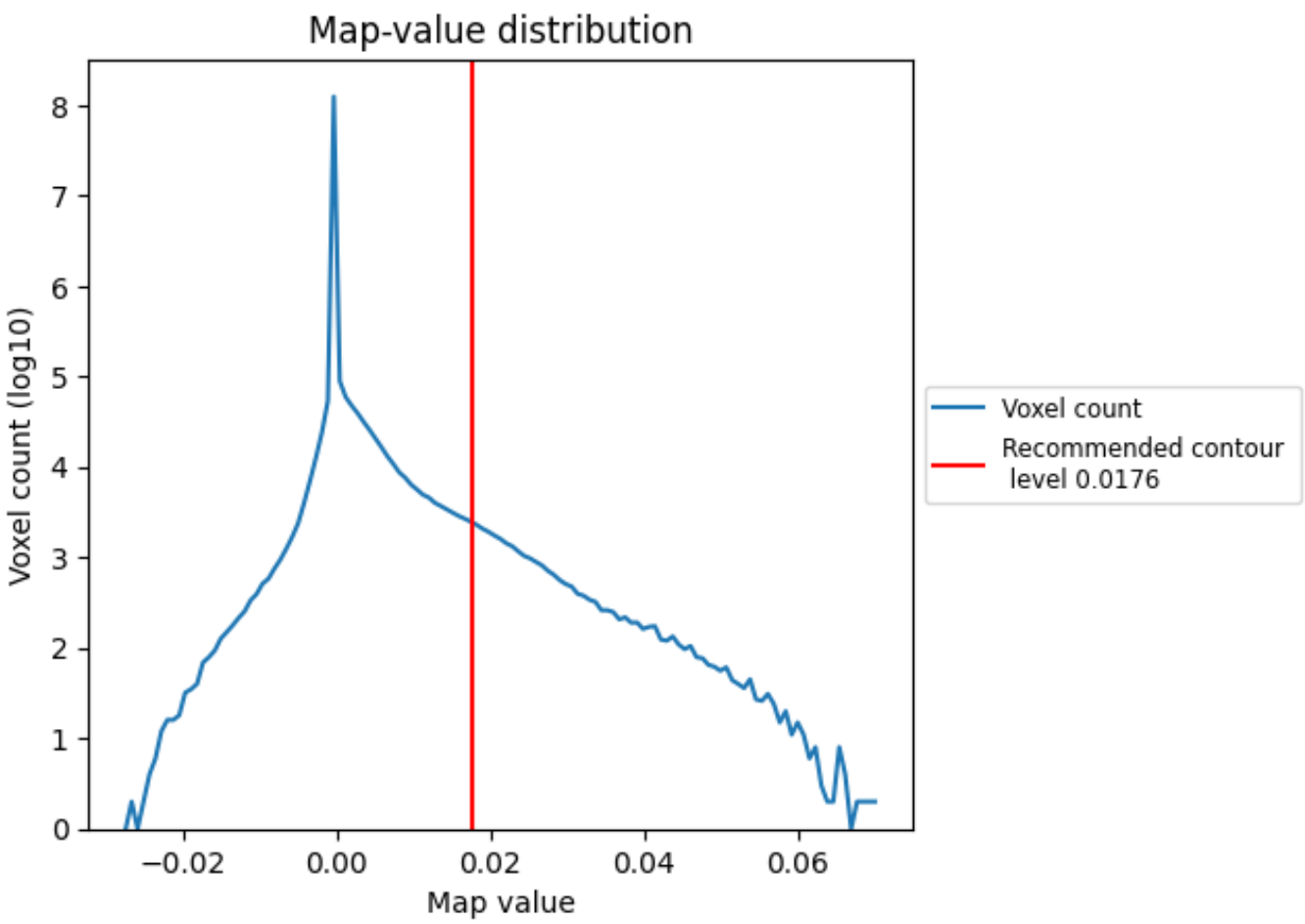
6.6 Mask visualisation (i)

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

7 Map analysis (i)

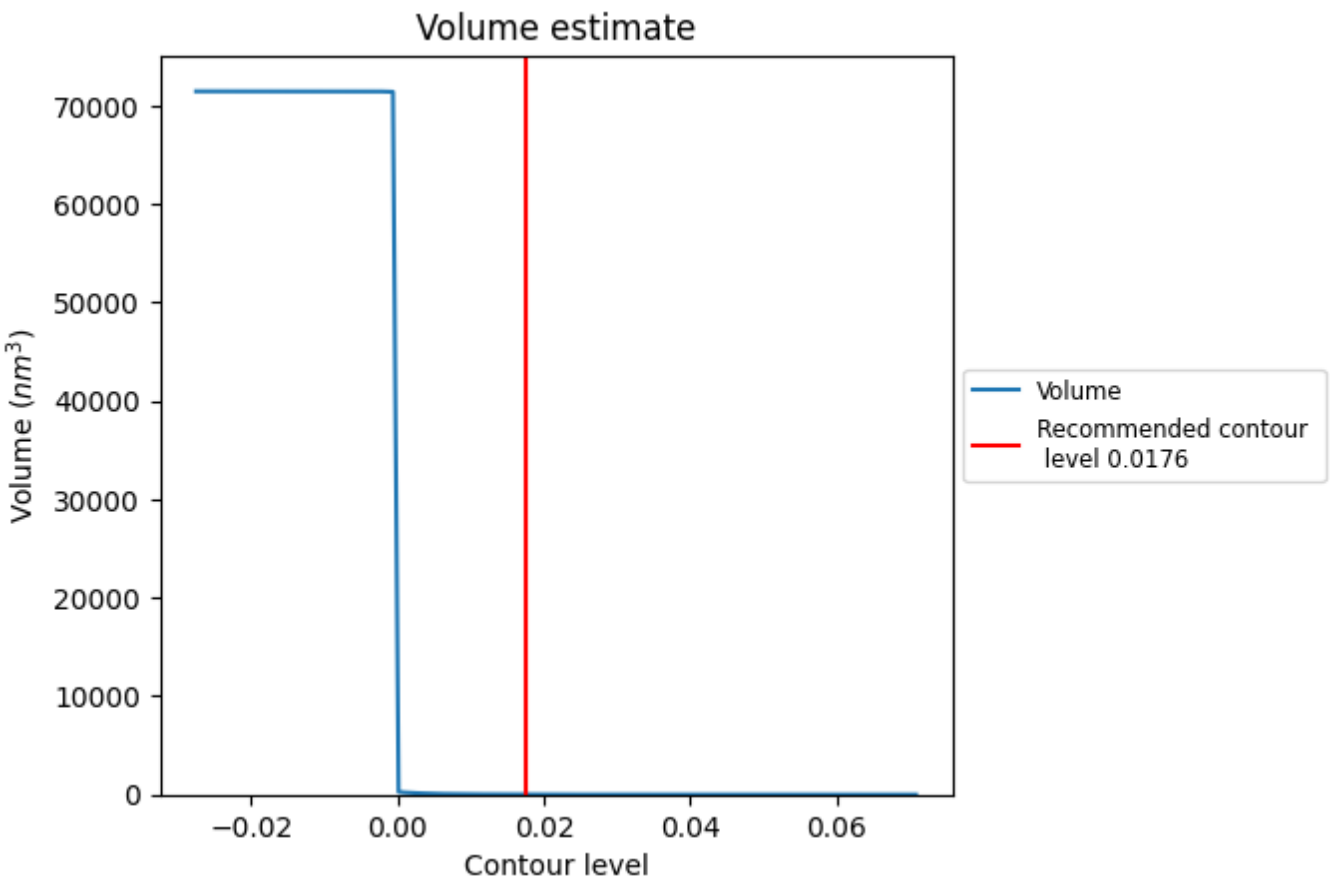
This section contains the results of statistical analysis of the map.

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.

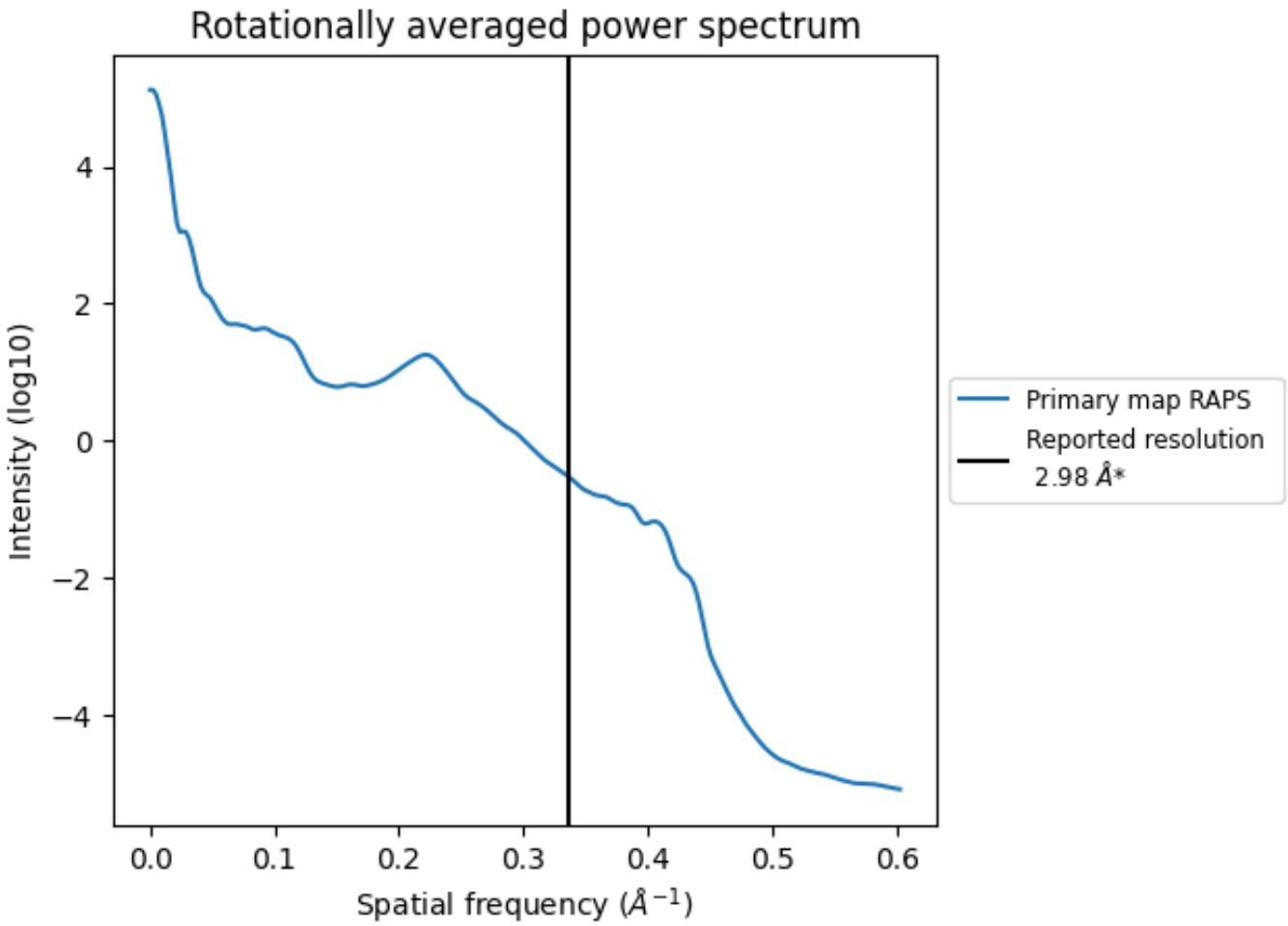
7.2 Volume estimate (i)



The volume at the recommended contour level is 16 nm^3; this corresponds to an approximate mass of 14 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)

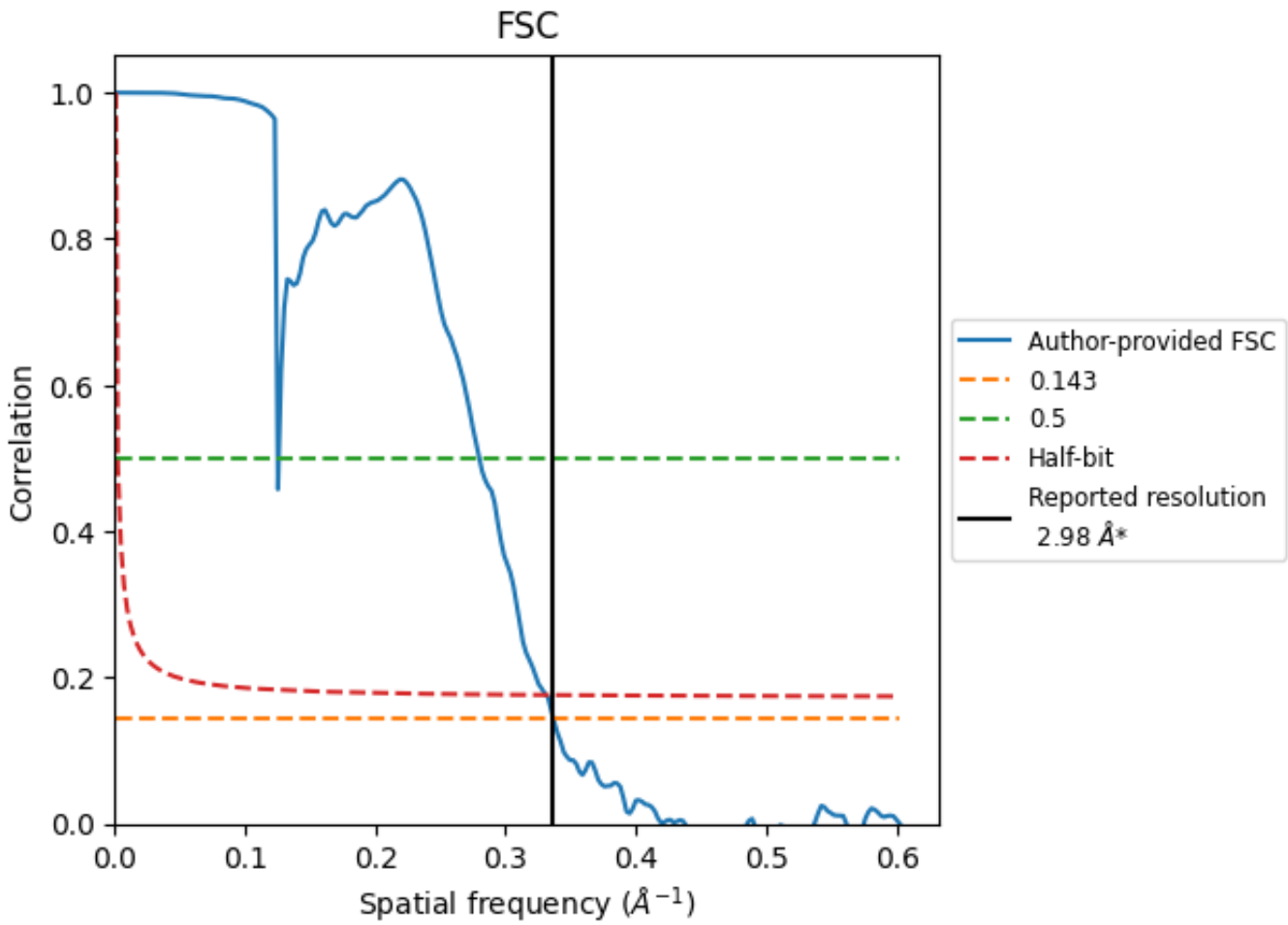


*Reported resolution corresponds to spatial frequency of 0.336 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.336 Å^{-1}

8.2 Resolution estimates (i)

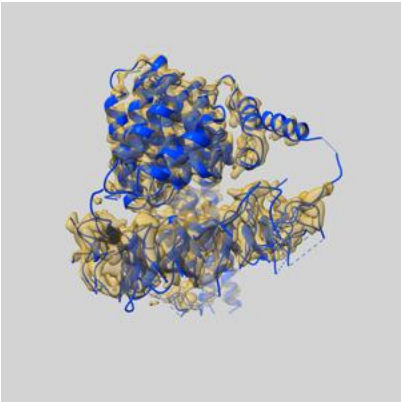
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.98	-	-
Author-provided FSC curve	2.97	7.99	3.02
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

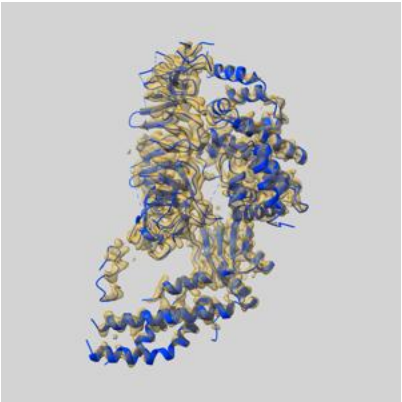
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-12446 and PDB model 7NKQ. Per-residue inclusion information can be found in section 3 on page 5.

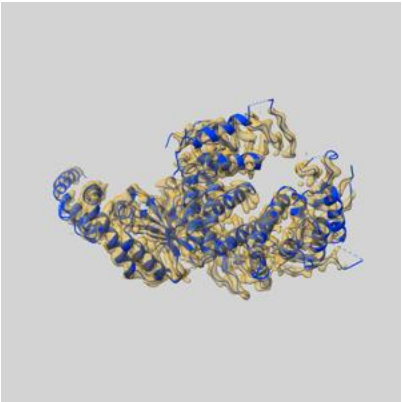
9.1 Map-model overlay (i)



X



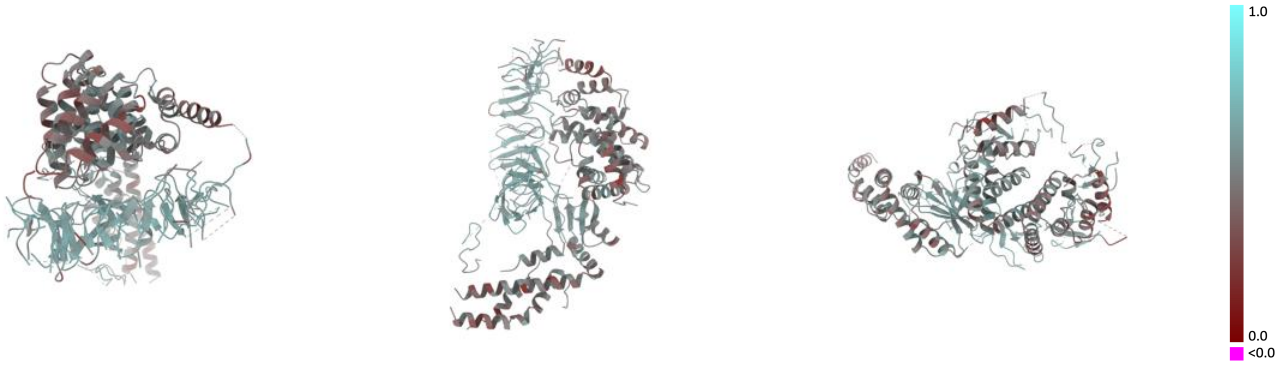
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0176 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.

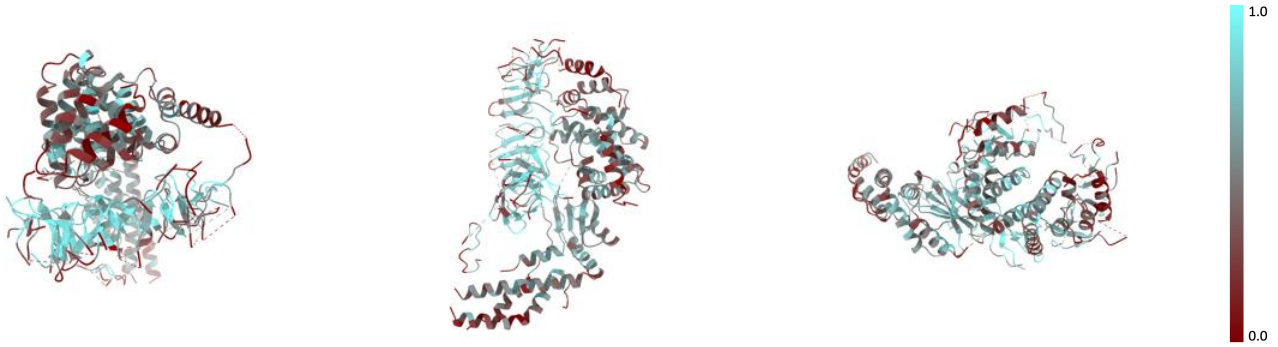
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

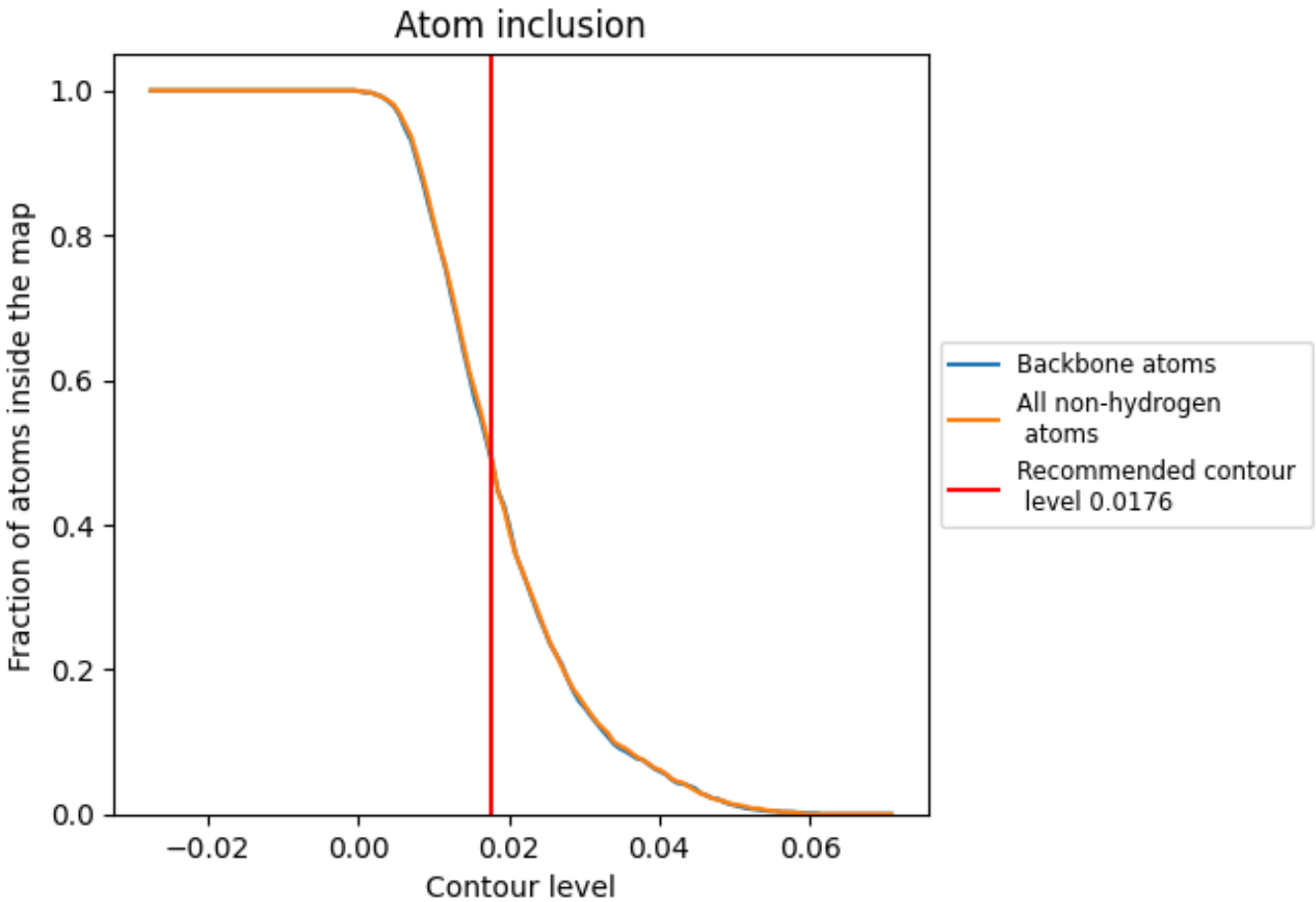
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0176).

9.4 Atom inclusion (i)



At the recommended contour level, 49% of all backbone atoms, 50% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0176) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4990	0.5070
A	0.5750	0.5540
B	0.3940	0.4750
C	0.3670	0.4790
D	0.5980	0.5800
E	0.7160	0.5940
F	0.4790	0.5540
b	0.3220	0.4460
d	0.5040	0.4800