



wwPDB EM Validation Summary Report ⓘ

Mar 3, 2024 – 04:36 PM EST

PDB ID : 5VOY
EMDB ID : EMD-8725
Title : Yeast V-ATPase in complex with Legionella pneumophila effector SidK (rotational state 2)
Authors : Zhao, J.
Deposited on : 2017-05-03
Resolution : 7.90 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:

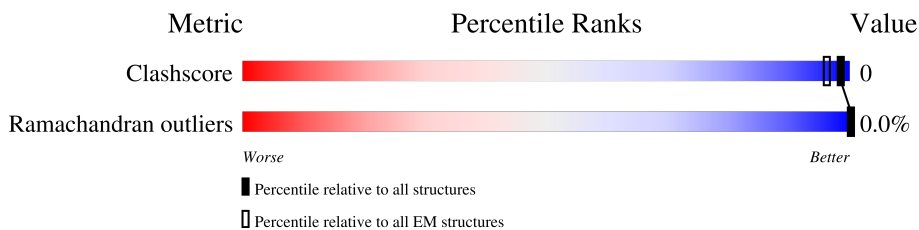
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 7.90 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

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	617	5% 96% .
1	C	617	. 96% .
1	E	617	5% 96% .
2	B	517	6% 88% 12%
2	D	517	5% 88% 12%
2	F	517	7% 88% 12%
3	G	233	9% 94% 6%
3	I	233	. 93% 7%
3	K	233	. 93% 7%

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Mol	Chain	Length	Quality of chain
4	H	114	14% 92% 8%
4	J	114	10% 92% 8%
4	L	114	7% 92% 8%
5	M	256	• 82% 18%
6	N	118	13% 97% •
7	O	392	23% 100%
8	P	478	17% 97% •
9	Q	345	19% 100%
10	R	213	17% 100%
11	S	164	9% 89% • 10%
12	T	160	9% 94% 6%
12	U	160	11% 94% 6%
12	V	160	11% 93% 7%
12	W	160	9% 94% 6%
12	X	160	11% 94% 6%
12	Y	160	9% 94% 6%
12	Z	160	9% 92% 8%
12	a	160	11% 92% 8%
13	b	840	6% 75% 25%
14	c	73	10% 78% 22%
15	d	54	19% 100%
16	e	573	10% 44% 56%
16	f	573	9% 44% 56%
16	g	573	9% 44% 56%

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 34724 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 V-type proton ATPase catalytic subunit A,V-type proton ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
1	A	593	2371	1186	593	592	0	0
1	C	593	2371	1186	593	592	0	0
1	E	593	2371	1186	593	592	0	0

- Molecule 2 is a protein called V-type proton ATPase subunit B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	457	1827	914	457	456	0	0
2	D	457	1827	914	457	456	0	0
2	F	457	1827	914	457	456	0	0

- Molecule 3 is a protein called V-type proton ATPase subunit E.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	G	218	871	436	218	217	0	0
3	I	217	867	434	217	216	0	0
3	K	217	867	434	217	216	0	0

- Molecule 4 is a protein called V-type proton ATPase subunit G.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	H	105	419	210	105	104	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	J	105	Total	C	N	O	0	0
			419	210	105	104		
4	L	105	Total	C	N	O	0	0
			419	210	105	104		

- Molecule 5 is a protein called V-type proton ATPase subunit D.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	M	210	Total	C	N	O	0	0
			839	420	210	209		

- Molecule 6 is a protein called V-type proton ATPase subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	N	115	Total	C	N	O	0	0
			459	230	115	114		

- Molecule 7 is a protein called V-type proton ATPase subunit C.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	392	Total	C	N	O	0	0
			1567	784	392	391		

- Molecule 8 is a protein called V-type proton ATPase subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	462	Total	C	N	O	0	0
			1847	924	462	461		

- Molecule 9 is a protein called V-type proton ATPase subunit d.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Q	345	Total	C	N	O	0	0
			1379	690	345	344		

- Molecule 10 is a protein called V-type proton ATPase subunit c’.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	213	Total	C	N	O	0	0
			851	426	213	212		

- Molecule 11 is a protein called V-type proton ATPase subunit c'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	S	147	587	294	147	146	0	0

- Molecule 12 is a protein called V-type proton ATPase subunit c.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	T	150	599	300	150	149	0	0
12	U	150	599	300	150	149	0	0
12	V	149	595	298	149	148	0	0
12	W	150	599	300	150	149	0	0
12	X	150	599	300	150	149	0	0
12	Y	150	599	300	150	149	0	0
12	Z	148	591	296	148	147	0	0
12	a	148	591	296	148	147	0	0

- Molecule 13 is a protein called V-type proton ATPase subunit a, vacuolar isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	b	634	2529	1268	634	627	0	0

- Molecule 14 is a protein called V-type proton ATPase subunit e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	c	57	227	114	57	56	0	0

- Molecule 15 is a protein called V-type proton ATPase subunit f.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	d	54	214	108	54	52	0	0

- Molecule 16 is a protein called effector protein SidK.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	e	250	999	500	250	249	0	0
16	f	250	999	500	250	249	0	0
16	g	250	999	500	250	249	0	0

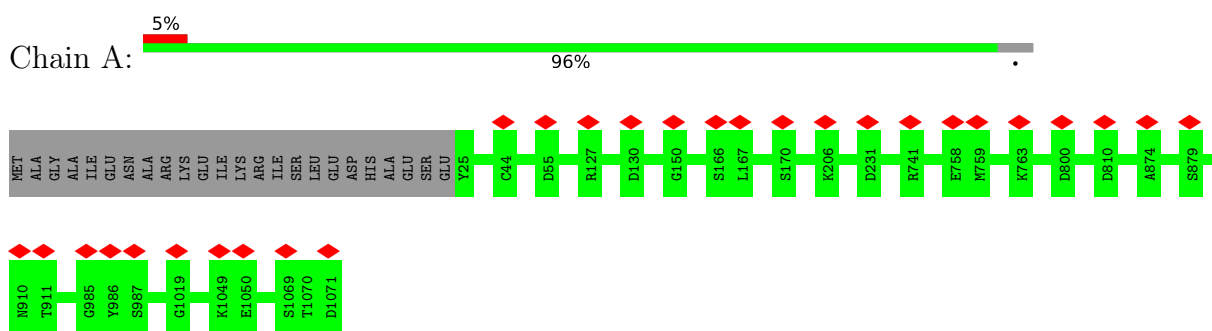
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	89	LEU	GLN	conflict	UNP G8UUS6
f	89	LEU	GLN	conflict	UNP G8UUS6
g	89	LEU	GLN	conflict	UNP G8UUS6

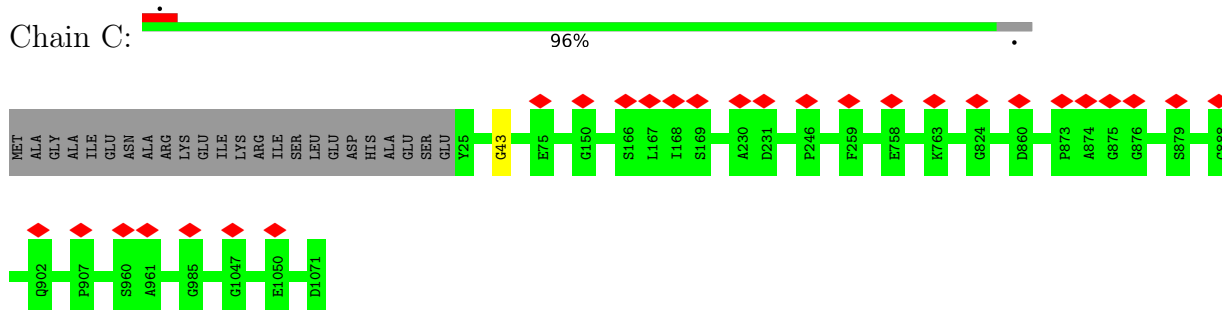
3 Residue-property plots [i](#)

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.

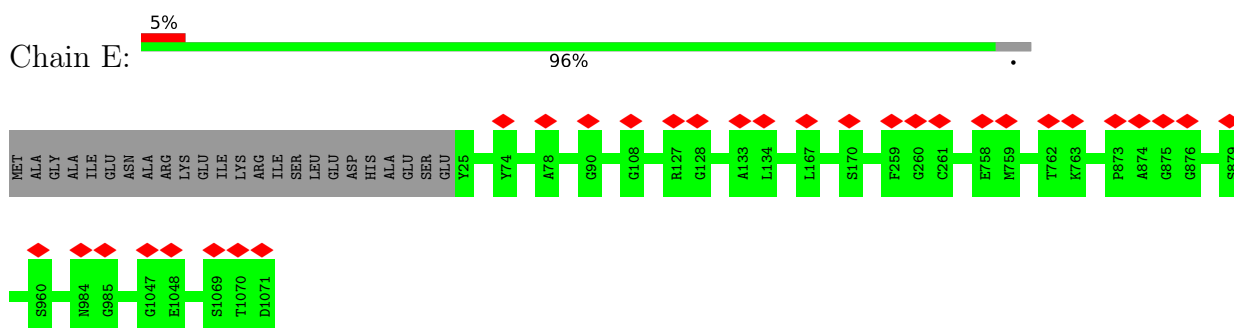
- Molecule 1: V-type proton ATPase catalytic subunit A,V-type proton ATPase catalytic subunit A




- Molecule 1: V-type proton ATPase catalytic subunit A,V-type proton ATPase catalytic subunit A

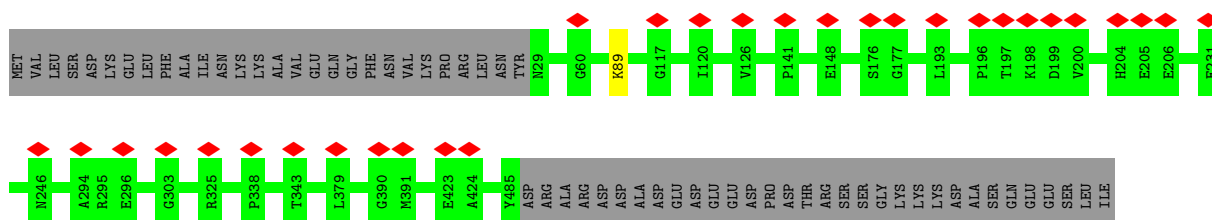


- Molecule 1: V-type proton ATPase catalytic subunit A,V-type proton ATPase catalytic subunit A




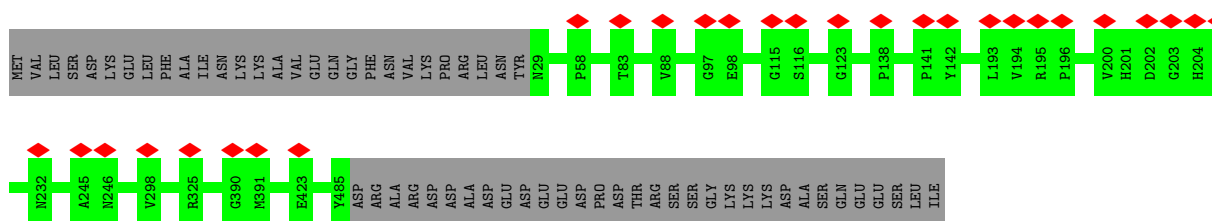
- Molecule 2: V-type proton ATPase subunit B

Chain B: 




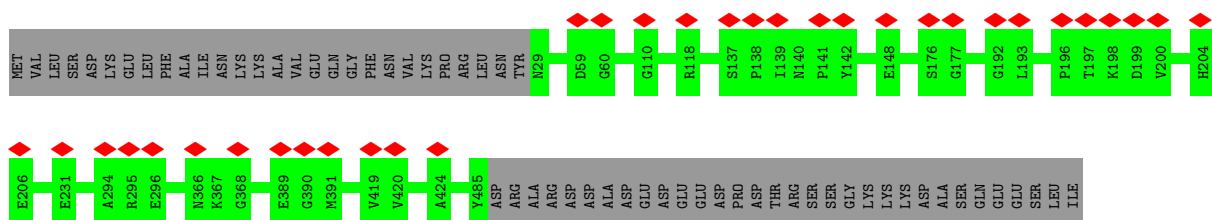
- Molecule 2: V-type proton ATPase subunit B

Chain D: 

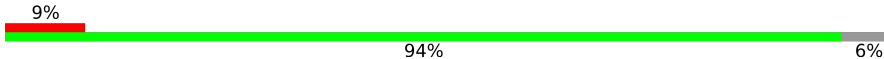


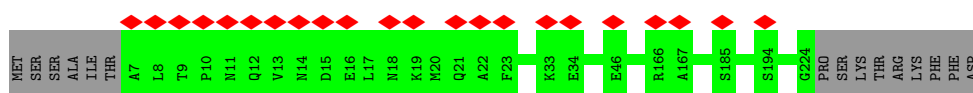
- Molecule 2: V-type proton ATPase subunit B

Chain F: 

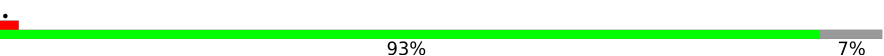


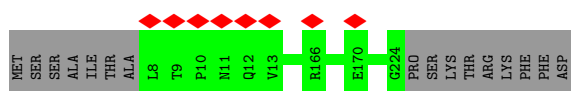
- Molecule 3: V-type proton ATPase subunit E

Chain G: 



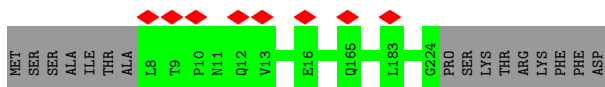
- Molecule 3: V-type proton ATPase subunit E

Chain I: 

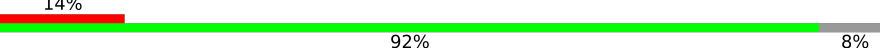


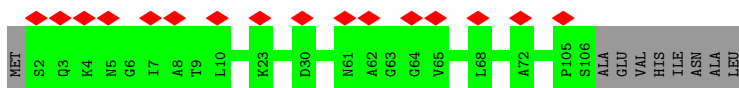
- Molecule 3: V-type proton ATPase subunit E

Chain K:  93% 7%

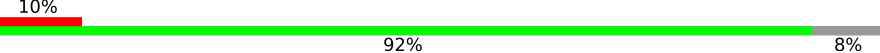


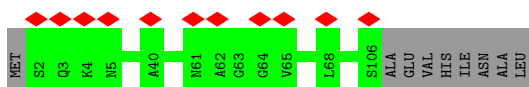
- Molecule 4: V-type proton ATPase subunit G

Chain H:  14% 92% 8%

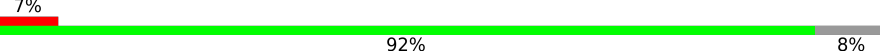


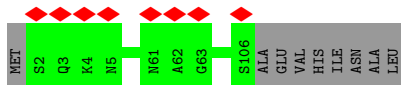
- Molecule 4: V-type proton ATPase subunit G

Chain J:  10% 92% 8%




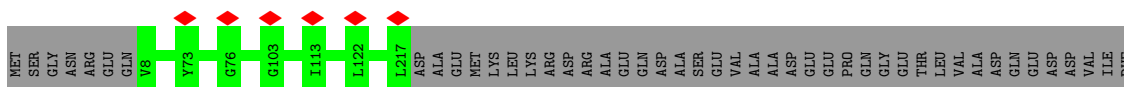
- Molecule 4: V-type proton ATPase subunit G

Chain L:  7% 92% 8%



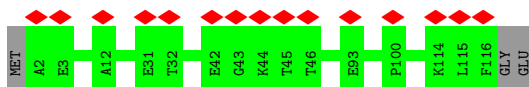
- Molecule 5: V-type proton ATPase subunit D

Chain M:  82% 18%



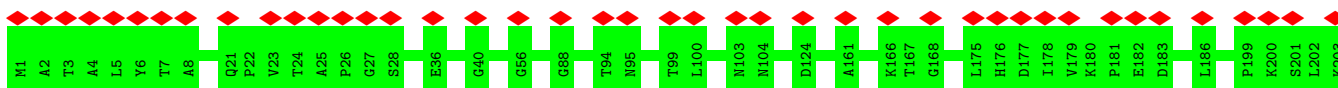
- Molecule 6: V-type proton ATPase subunit F

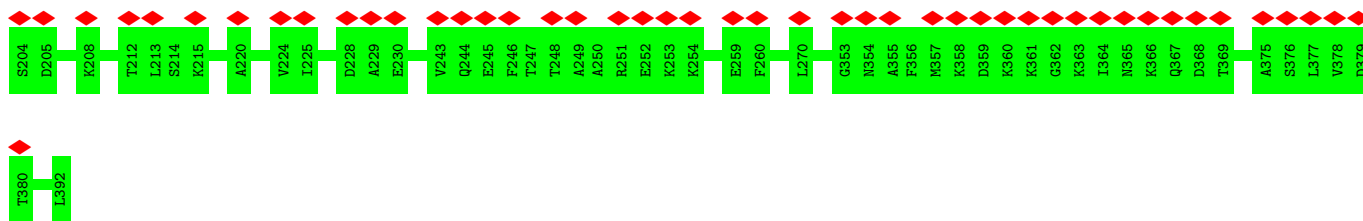
Chain N:  13% 97%



- Molecule 7: V-type proton ATPase subunit C

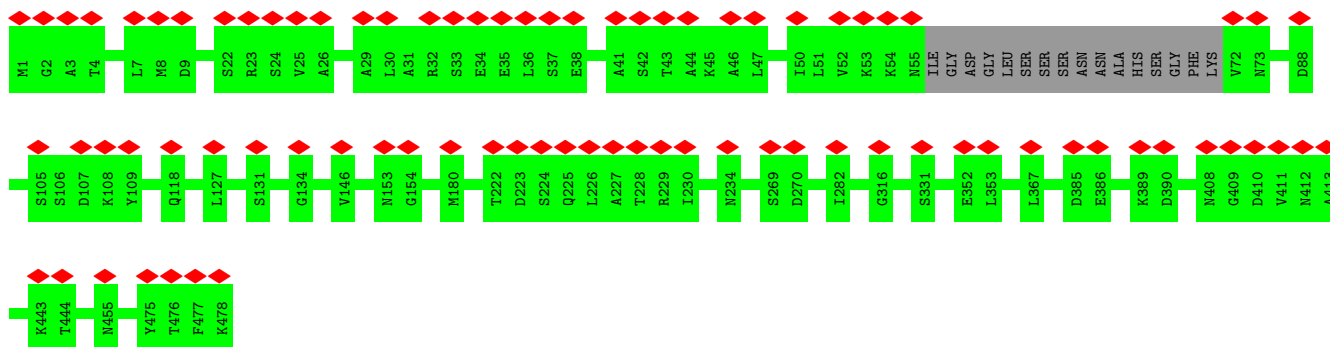
Chain O:  23% 100%





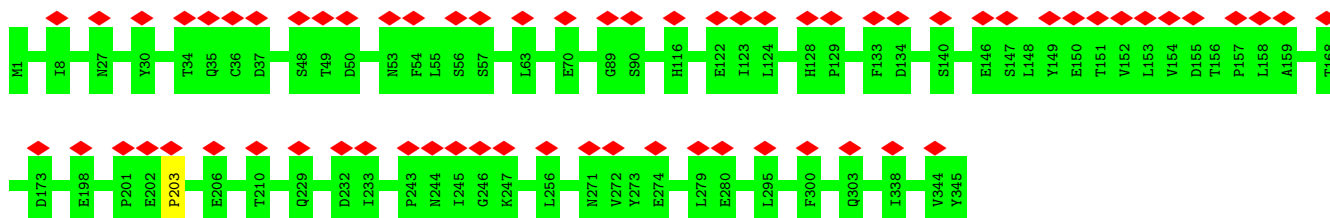
- Molecule 8: V-type proton ATPase subunit H

Chain P: 17% 97%



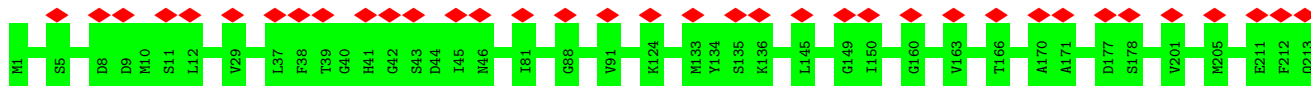
- Molecule 9: V-type proton ATPase subunit d

Chain Q: 19% 100%



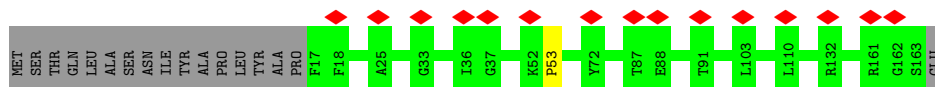
- Molecule 10: V-type proton ATPase subunit c''

Chain R: 17% 100%

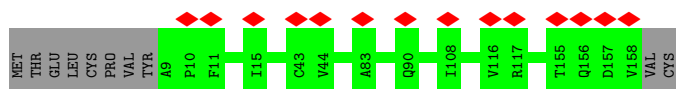
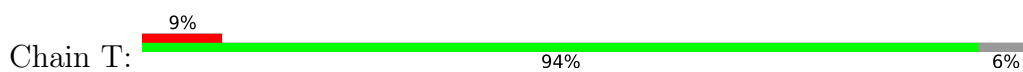


- Molecule 11: V-type proton ATPase subunit c'

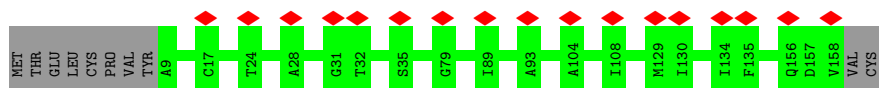
Chain S: 9% 89% 10%



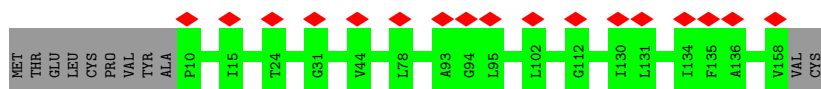
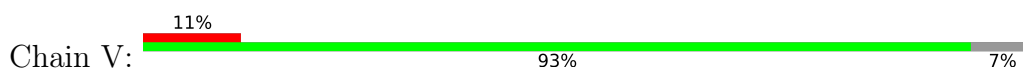
- Molecule 12: V-type proton ATPase subunit c



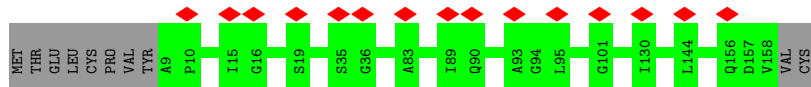
- Molecule 12: V-type proton ATPase subunit c



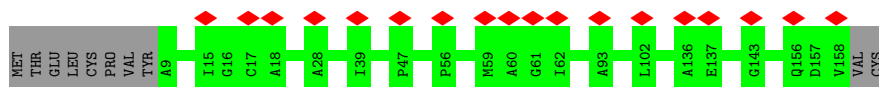
- Molecule 12: V-type proton ATPase subunit c



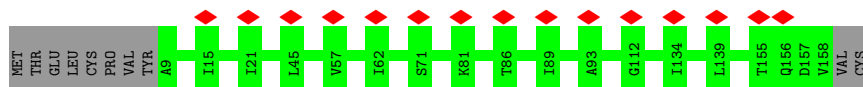
- Molecule 12: V-type proton ATPase subunit c



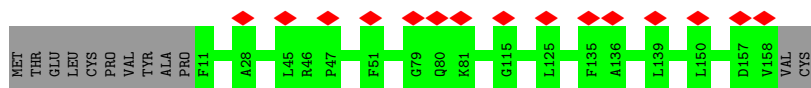
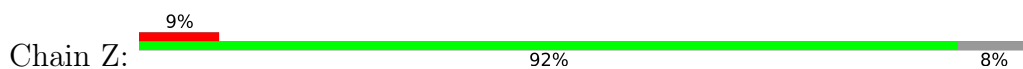
- Molecule 12: V-type proton ATPase subunit c



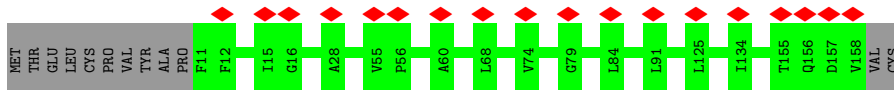
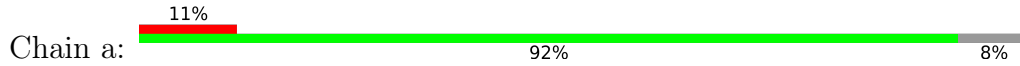
- Molecule 12: V-type proton ATPase subunit c



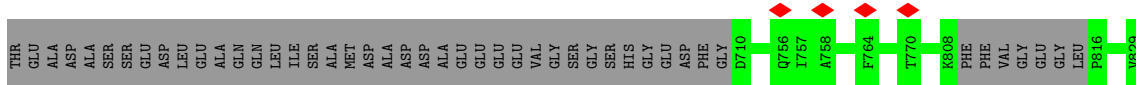
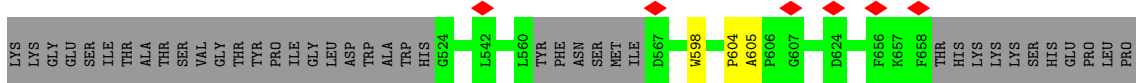
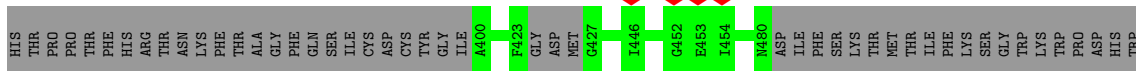
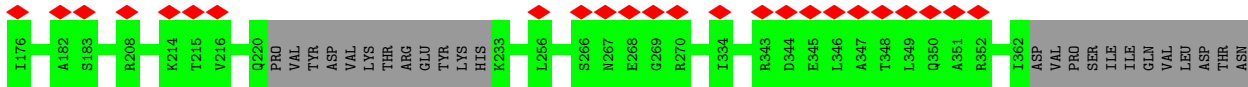
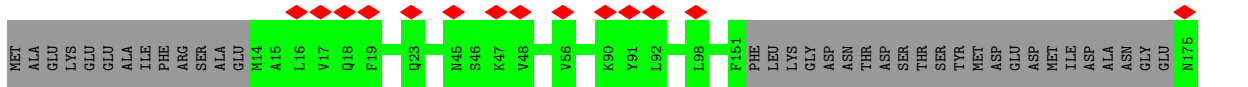
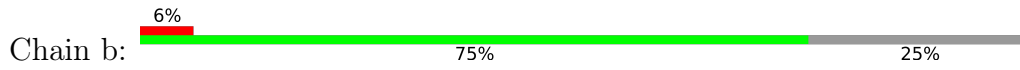
- Molecule 12: V-type proton ATPase subunit c



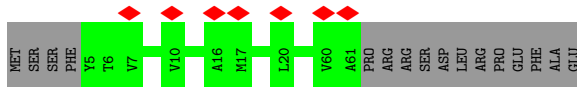
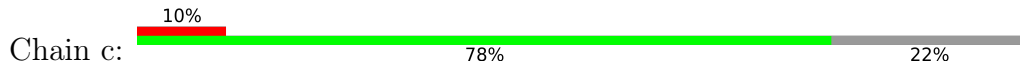
- Molecule 12: V-type proton ATPase subunit c



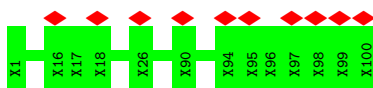
- Molecule 13: V-type proton ATPase subunit a, vacuolar isoform



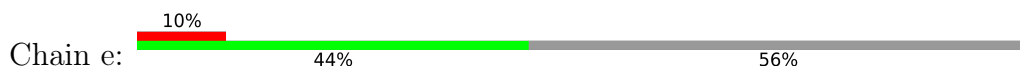
- Molecule 14: V-type proton ATPase subunit e



- Molecule 15: V-type proton ATPase subunit f



- Molecule 16: effector protein SidK



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11125	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.2	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	0.131	Depositor
Minimum map value	-0.040	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	371.2, 371.2, 371.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	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	0.23	0/2370	0.44	0/2961
1	C	0.23	0/2370	0.44	0/2961
1	E	0.23	0/2370	0.45	0/2961
2	B	0.23	0/1826	0.44	0/2281
2	D	0.23	0/1826	0.45	0/2281
2	F	0.24	0/1826	0.44	0/2281
3	G	0.23	0/870	0.41	0/1086
3	I	0.24	0/866	0.39	0/1081
3	K	0.23	0/866	0.40	0/1081
4	H	0.23	0/418	0.37	0/521
4	J	0.22	0/418	0.35	0/521
4	L	0.22	0/418	0.35	0/521
5	M	0.23	0/838	0.38	0/1046
6	N	0.23	0/458	0.43	0/571
7	O	0.23	0/1566	0.42	0/1956
8	P	0.22	0/1845	0.38	0/2303
9	Q	0.22	0/1378	0.38	0/1721
10	R	0.22	0/850	0.45	0/1061
11	S	0.23	0/586	0.43	0/731
12	T	0.23	0/598	0.39	0/746
12	U	0.23	0/598	0.40	0/746
12	V	0.23	0/594	0.39	0/741
12	W	0.23	0/598	0.41	0/746
12	X	0.23	0/598	0.40	0/746
12	Y	0.23	0/598	0.39	0/746
12	Z	0.23	0/590	0.41	0/736
12	a	0.23	0/590	0.42	0/736
13	b	0.22	0/2520	0.46	2/3136 (0.1%)
14	c	0.21	0/226	0.42	0/281
16	e	0.22	0/998	0.38	0/1246
16	f	0.22	0/998	0.38	0/1246
16	g	0.22	0/998	0.38	0/1246
All	All	0.23	0/34469	0.42	2/43024 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
13	b	598	TRP	N-CA-C	5.53	125.94	111.00
13	b	605	ALA	C-N-CA	5.09	143.38	122.00

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	2371	0	662	0	0
1	C	2371	0	662	1	0
1	E	2371	0	662	0	0
2	B	1827	0	501	1	0
2	D	1827	0	501	0	0
2	F	1827	0	501	0	0
3	G	871	0	226	0	0
3	I	867	0	225	0	0
3	K	867	0	225	0	0
4	H	419	0	115	0	0
4	J	419	0	115	0	0
4	L	419	0	115	0	0
5	M	839	0	228	0	0
6	N	459	0	117	0	0
7	O	1567	0	404	0	0
8	P	1847	0	480	0	0
9	Q	1379	0	370	0	0
10	R	851	0	261	0	0
11	S	587	0	186	0	0
12	T	599	0	189	0	0
12	U	599	0	189	0	0
12	V	595	0	189	0	0
12	W	599	0	189	0	0
12	X	599	0	189	0	0
12	Y	599	0	189	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	Z	591	0	188	0	0
12	a	591	0	188	0	0
13	b	2529	0	681	0	0
14	c	227	0	56	0	0
15	d	214	0	5	0	0
16	e	999	0	256	0	0
16	f	999	0	256	0	0
16	g	999	0	256	0	0
All	All	34724	0	9576	1	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 0.

All (1) 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:89:LYS:H	1:C:43:GLY:H	1.63	0.47

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	591/617 (96%)	571 (97%)	20 (3%)	0	100	100
1	C	591/617 (96%)	567 (96%)	24 (4%)	0	100	100
1	E	591/617 (96%)	566 (96%)	25 (4%)	0	100	100
2	B	455/517 (88%)	441 (97%)	14 (3%)	0	100	100
2	D	455/517 (88%)	444 (98%)	11 (2%)	0	100	100
2	F	455/517 (88%)	442 (97%)	13 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	G	216/233 (93%)	212 (98%)	4 (2%)	0	100	100
3	I	215/233 (92%)	211 (98%)	4 (2%)	0	100	100
3	K	215/233 (92%)	211 (98%)	4 (2%)	0	100	100
4	H	103/114 (90%)	102 (99%)	1 (1%)	0	100	100
4	J	103/114 (90%)	103 (100%)	0	0	100	100
4	L	103/114 (90%)	103 (100%)	0	0	100	100
5	M	208/256 (81%)	205 (99%)	3 (1%)	0	100	100
6	N	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
7	O	390/392 (100%)	378 (97%)	12 (3%)	0	100	100
8	P	458/478 (96%)	440 (96%)	18 (4%)	0	100	100
9	Q	343/345 (99%)	325 (95%)	17 (5%)	1 (0%)	41	77
10	R	211/213 (99%)	189 (90%)	22 (10%)	0	100	100
11	S	145/164 (88%)	142 (98%)	2 (1%)	1 (1%)	22	63
12	T	148/160 (92%)	144 (97%)	4 (3%)	0	100	100
12	U	148/160 (92%)	143 (97%)	5 (3%)	0	100	100
12	V	147/160 (92%)	145 (99%)	2 (1%)	0	100	100
12	W	148/160 (92%)	145 (98%)	3 (2%)	0	100	100
12	X	148/160 (92%)	146 (99%)	2 (1%)	0	100	100
12	Y	148/160 (92%)	145 (98%)	3 (2%)	0	100	100
12	Z	146/160 (91%)	144 (99%)	2 (1%)	0	100	100
12	a	146/160 (91%)	143 (98%)	3 (2%)	0	100	100
13	b	616/840 (73%)	584 (95%)	31 (5%)	1 (0%)	47	81
14	c	55/73 (75%)	44 (80%)	11 (20%)	0	100	100
16	e	248/573 (43%)	244 (98%)	4 (2%)	0	100	100
16	f	248/573 (43%)	244 (98%)	4 (2%)	0	100	100
16	g	248/573 (43%)	242 (98%)	6 (2%)	0	100	100
All	All	8555/10321 (83%)	8274 (97%)	278 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	b	604	PRO
9	Q	203	PRO

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Mol	Chain	Res	Type
11	S	53	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	d	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	31:UNK	C	78:UNK	N	11.30

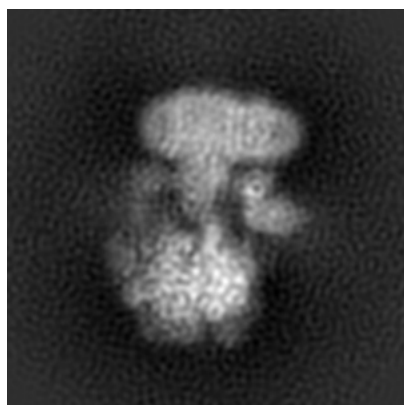
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8725. These allow visual inspection of the internal detail of the map and identification of artifacts.

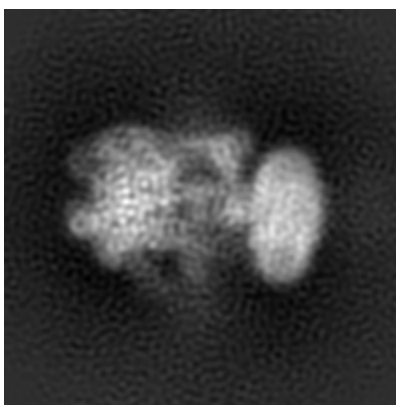
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

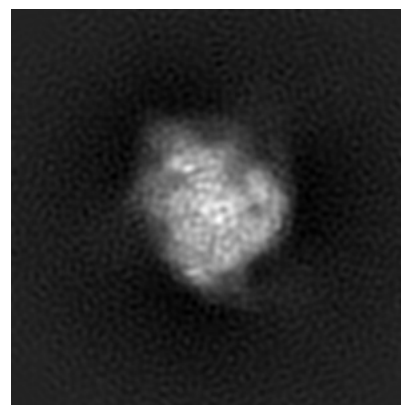
6.1.1 Primary map



X



Y

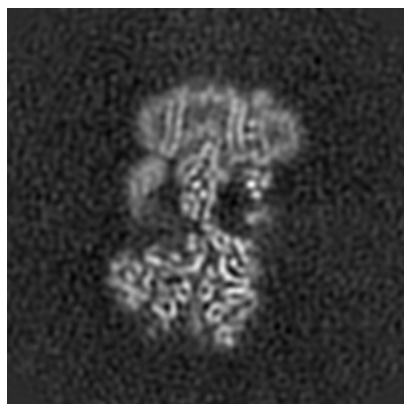


Z

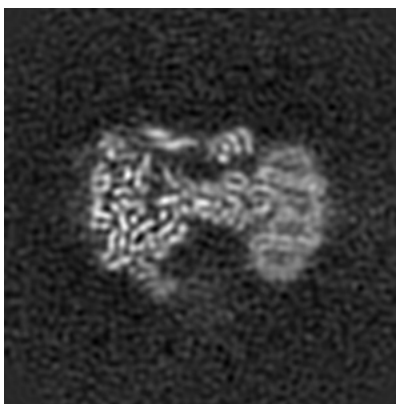
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

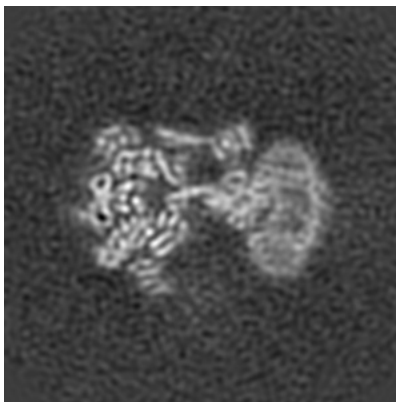
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

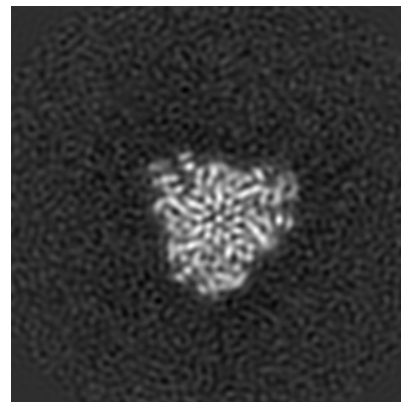
6.3.1 Primary map



X Index: 132



Y Index: 131

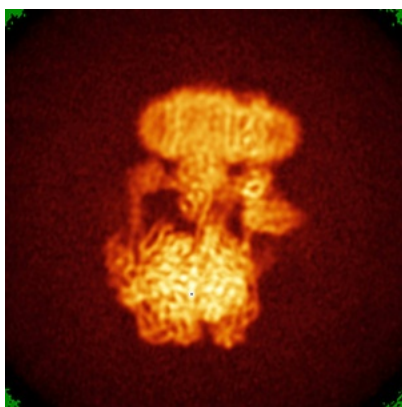


Z Index: 76

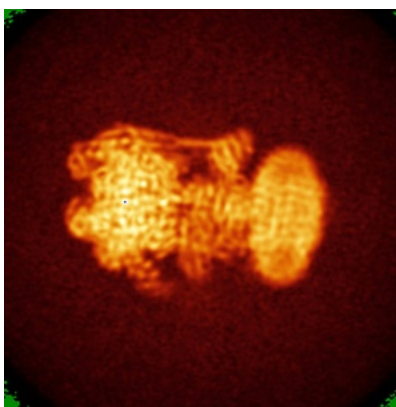
The images above show the largest variance slices of the map in three orthogonal directions.

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

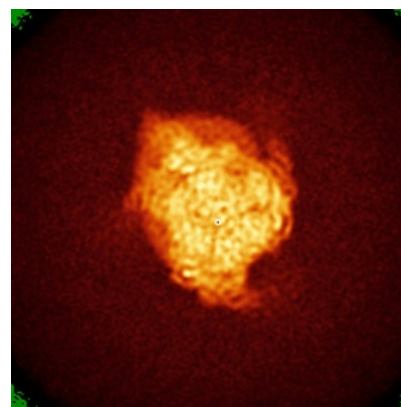
6.4.1 Primary map



X



Y

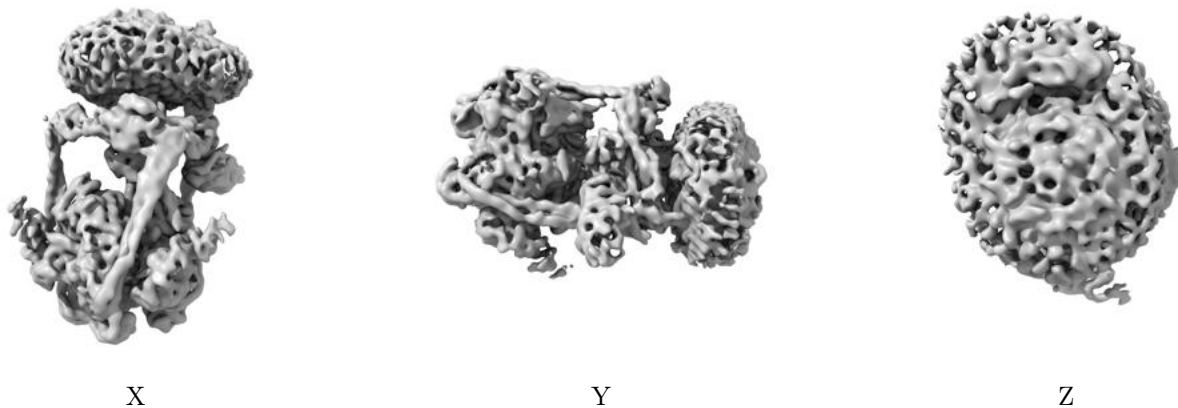


Z

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.

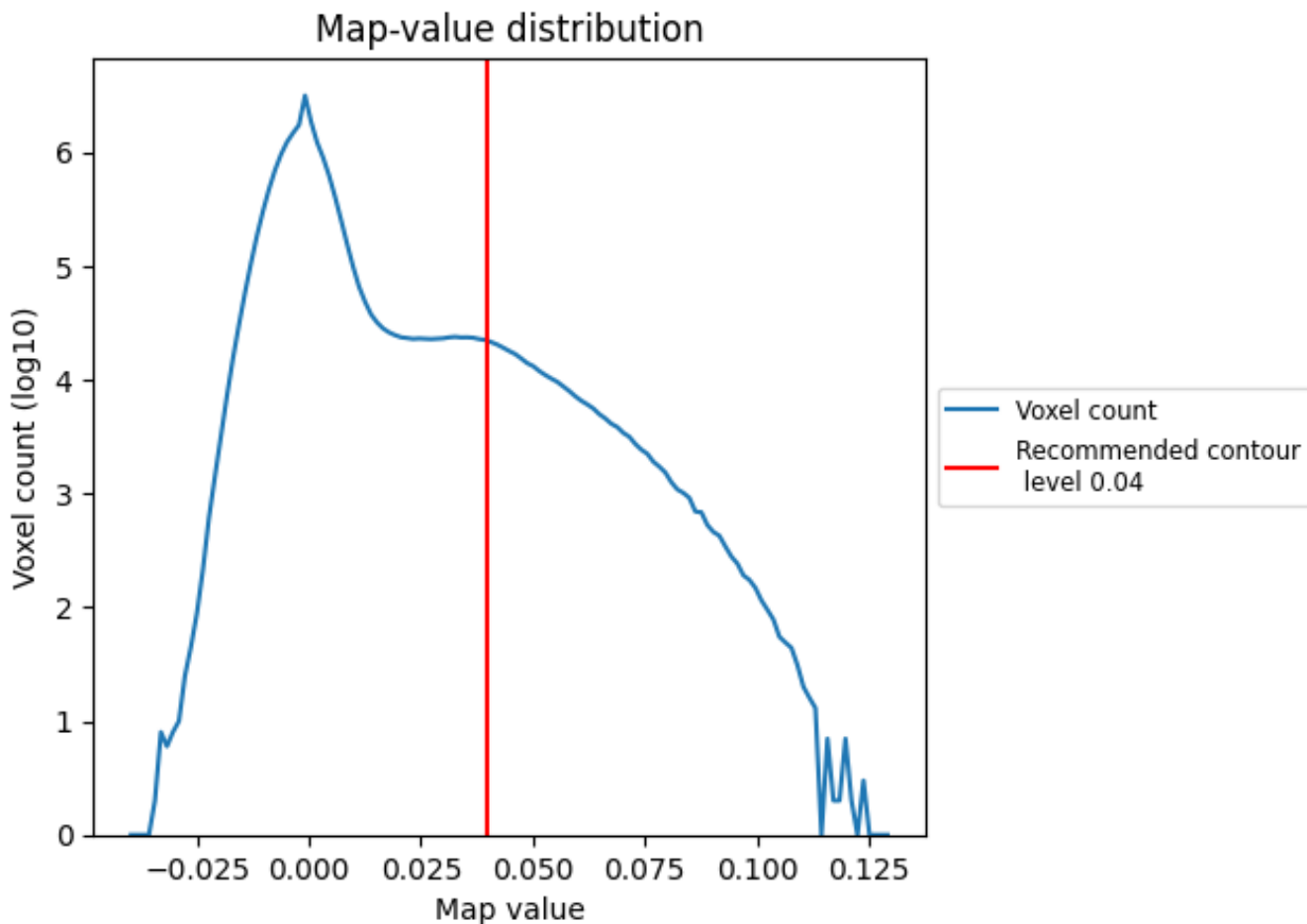
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

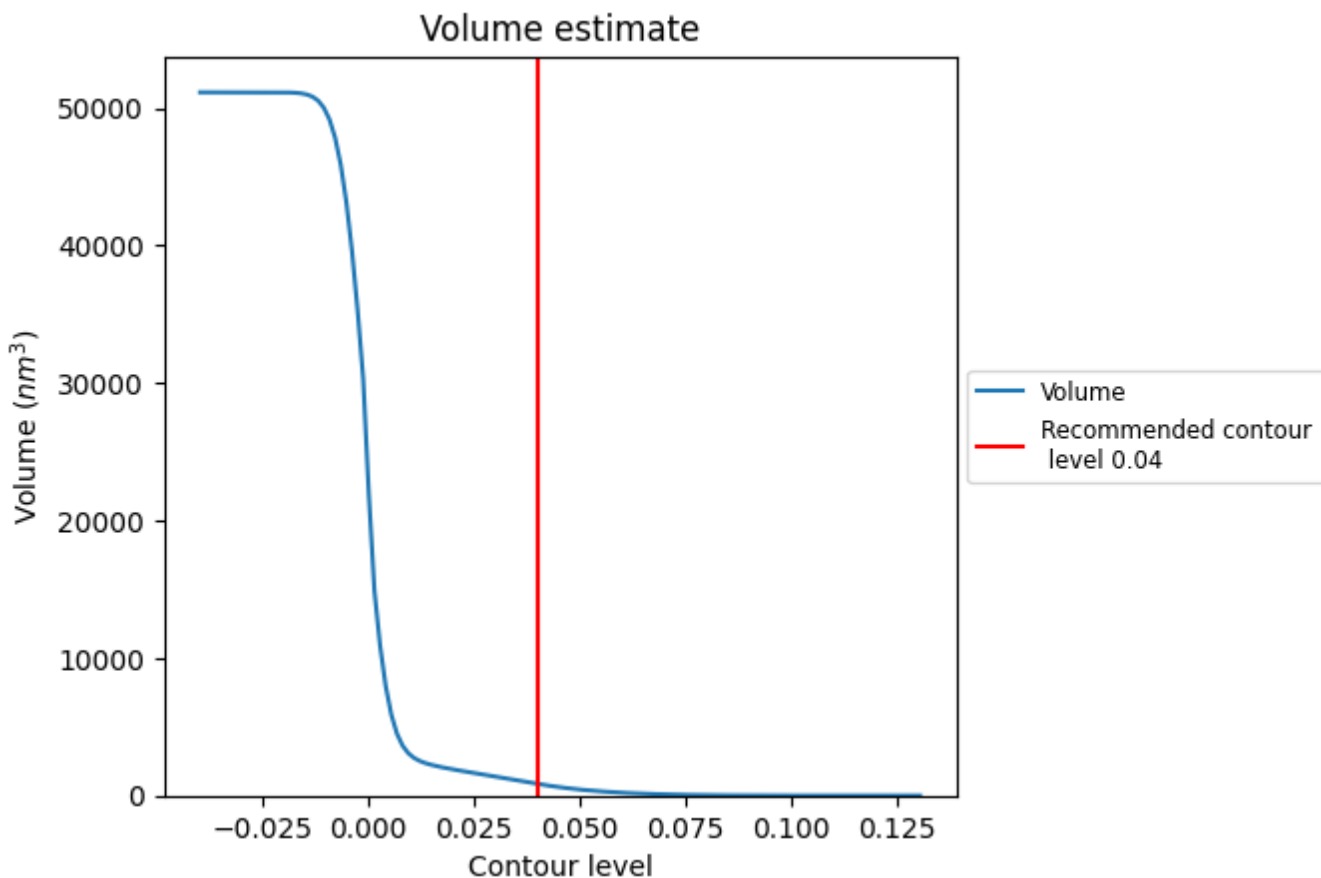
This section contains the results of statistical analysis of the map.

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.

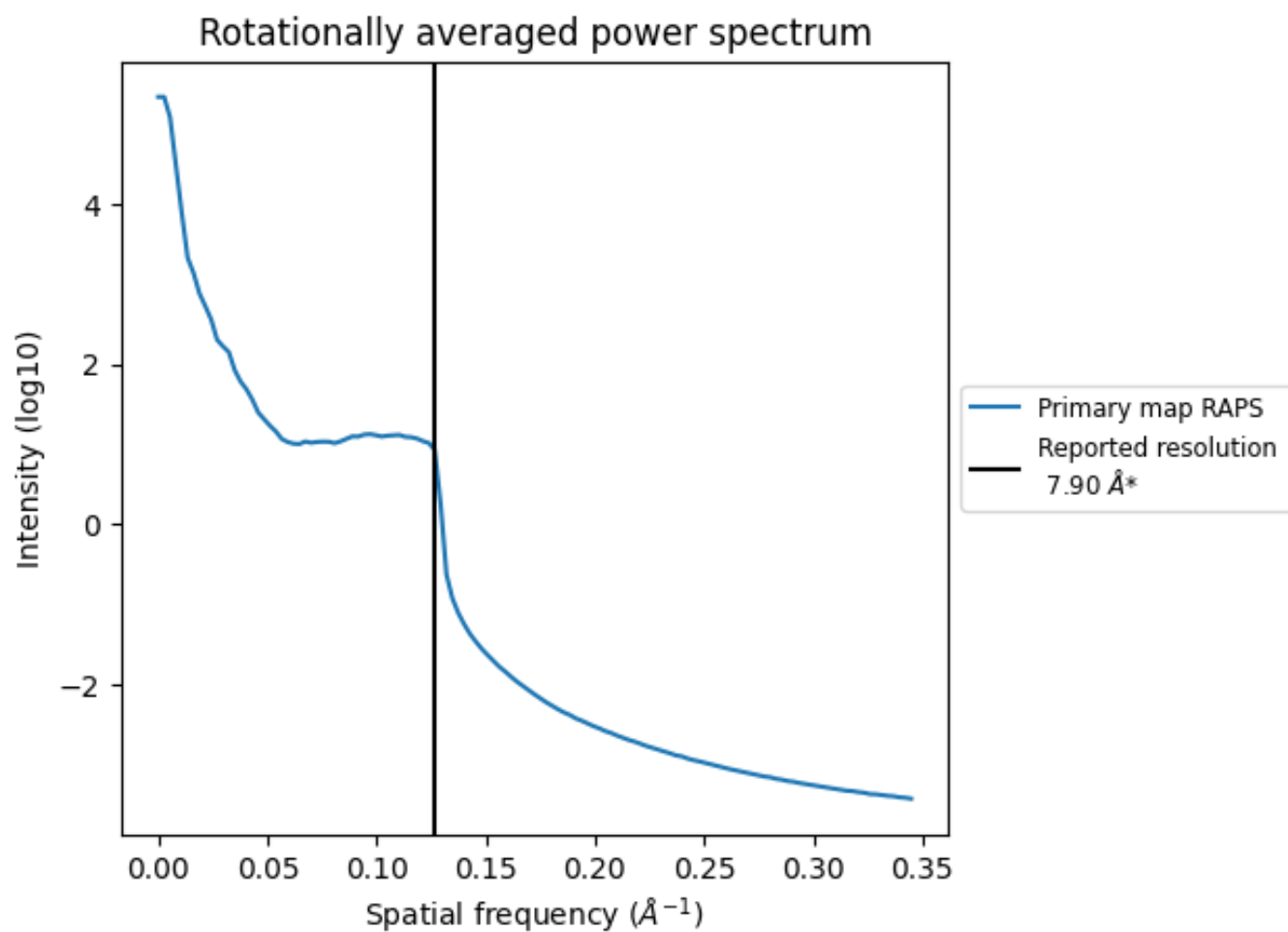
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 855 nm³; this corresponds to an approximate mass of 772 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 0.127 Å⁻¹

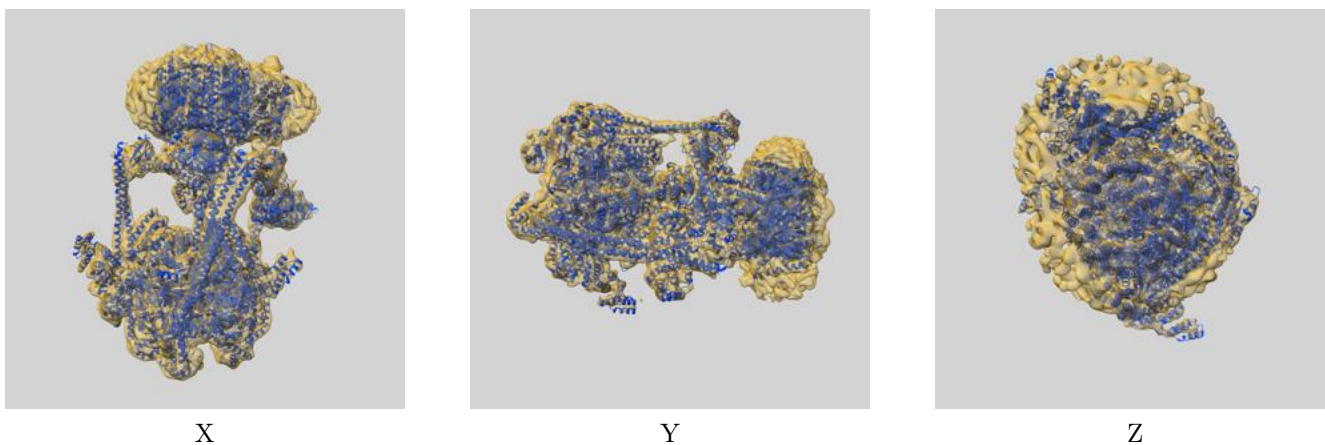
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

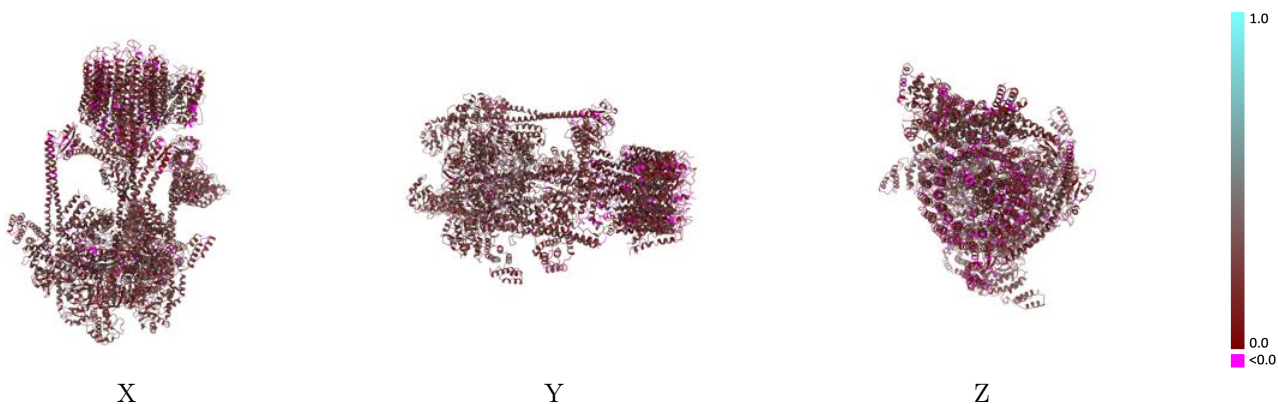
This section contains information regarding the fit between EMDB map EMD-8725 and PDB model 5VOY. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



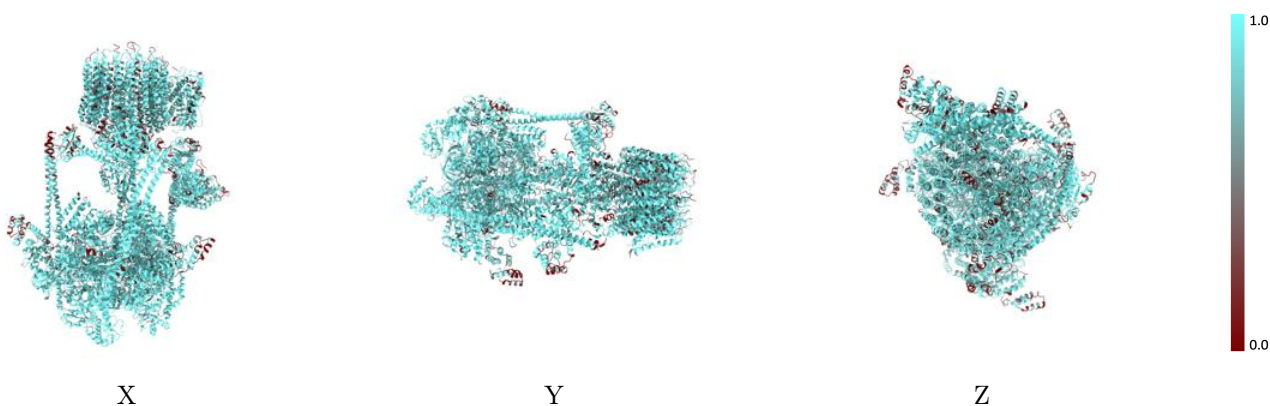
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



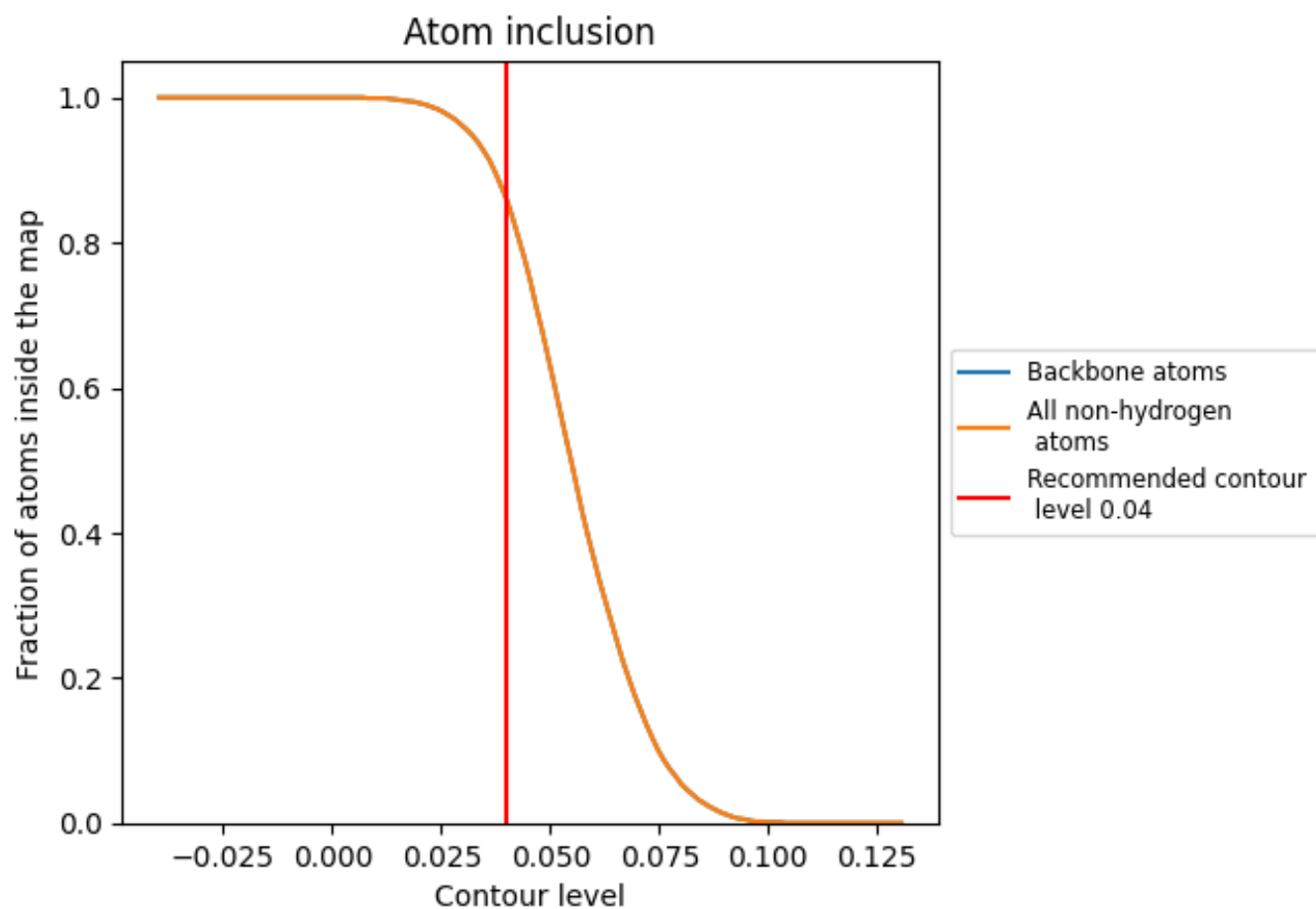
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 86% 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	 0.8590	 0.2110
A	 0.9320	 0.2320
B	 0.9050	 0.2230
C	 0.9210	 0.2310
D	 0.9070	 0.2290
E	 0.9170	 0.2240
F	 0.8990	 0.2200
G	 0.8750	 0.2340
H	 0.8070	 0.2080
I	 0.9520	 0.2630
J	 0.8710	 0.2220
K	 0.9450	 0.2680
L	 0.9090	 0.2410
M	 0.9430	 0.2360
N	 0.8300	 0.2080
O	 0.7270	 0.1760
P	 0.7900	 0.2210
Q	 0.7500	 0.1670
R	 0.7730	 0.1480
S	 0.8600	 0.1700
T	 0.8580	 0.1770
U	 0.8450	 0.1850
V	 0.8570	 0.1800
W	 0.8450	 0.1600
X	 0.8250	 0.1210
Y	 0.8680	 0.1540
Z	 0.8660	 0.1650
a	 0.8240	 0.1430
b	 0.8900	 0.2100
c	 0.8500	 0.1650
d	 0.7380	 0.1250
e	 0.7180	 0.2390
f	 0.7610	 0.2480
g	 0.7240	 0.2430

