



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:54 AM EST

PDB ID : 3J9T  
EMDB ID : EMD-6284  
Title : Yeast V-ATPase state 1  
Authors : Zhao, J.; Benlekbir, S.; Rubinstein, J.L.  
Deposited on : 2015-02-23  
Resolution : 6.90 Å(reported)  
Based on initial models : 1HO8, 4DL0, 4RND, 1U7L

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

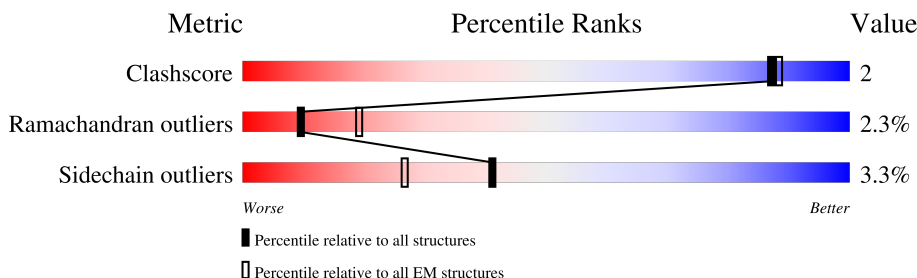
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.90 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
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  $\geq 3$ , 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	M	256	
2	N	118	
3	A	616	
3	C	616	
3	E	616	
4	B	517	
4	D	517	
4	F	517	

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Mol	Chain	Length	Quality of chain
5	Q	345	
6	H	114	
6	J	114	
6	L	114	
7	G	233	
7	I	233	
7	K	233	
8	P	478	
9	b	840	
10	O	392	
11	R	160	
11	S	160	
11	T	160	
11	U	160	
11	V	160	
11	W	160	
11	X	160	
11	Y	160	
11	Z	160	
11	a	160	

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 57659 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 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	210	Total	C	N	O	S	0	0
			1691	1061	305	321	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
2	N	115	Total	C	N	O	0	0
			928	589	157	182		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	593	Total	C	N	O	S	0	0
			4578	2904	760	894	20		
3	C	593	Total	C	N	O	S	0	0
			4578	2904	760	894	20		
3	E	593	Total	C	N	O	S	0	0
			4578	2904	760	894	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	457	Total	C	N	O	S	0	0
			3585	2266	612	695	12		
4	D	457	Total	C	N	O	S	0	0
			3585	2266	612	695	12		
4	F	457	Total	C	N	O	S	0	0
			3585	2266	612	695	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Q	345	Total	C	N	O	S	0	0
			2802	1779	454	555	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	105	Total	C	N	O		0	0
			824	517	144	163			
6	H	105	Total	C	N	O		0	0
			824	517	144	163			
6	J	105	Total	C	N	O		0	0
			824	517	144	163			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	217	Total	C	N	O	S	0	0
			1731	1083	296	347	5		
7	G	217	Total	C	N	O	S	0	0
			1731	1083	296	347	5		
7	I	217	Total	C	N	O	S	0	0
			1731	1083	296	347	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	461	Total	C	N	O	S	0	0
			3712	2373	623	704	12		

- Molecule 9 is a protein called V-type proton ATPase subunit a, vacuolar isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	312	Total	C	N	O	S	0	0
			2540	1614	434	489	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	392	Total	C	N	O	S	0	0
			3122	2005	516	596	5		

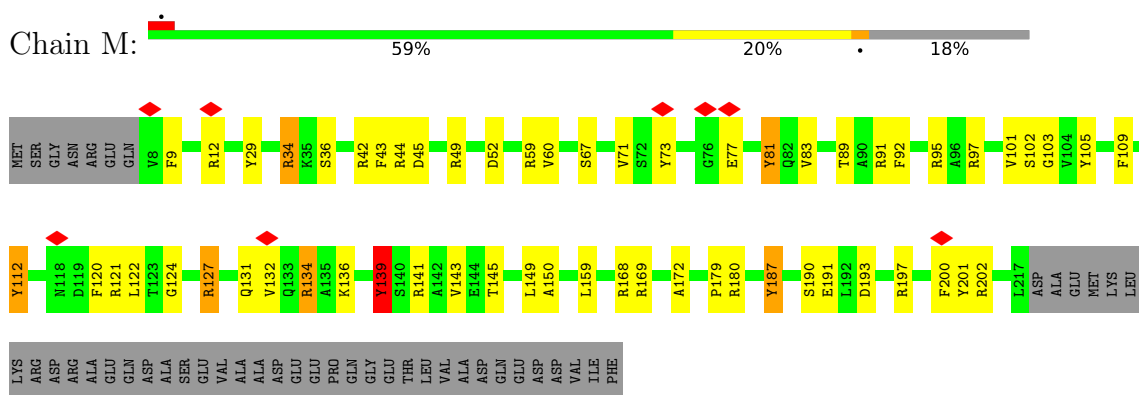
- Molecule 11 is a protein called V-type proton ATPase subunit c.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	R	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	U	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	V	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	T	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	W	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	S	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	X	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	Z	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	a	150	Total 1071	C 704	N 173	O 187	S 7	0	0

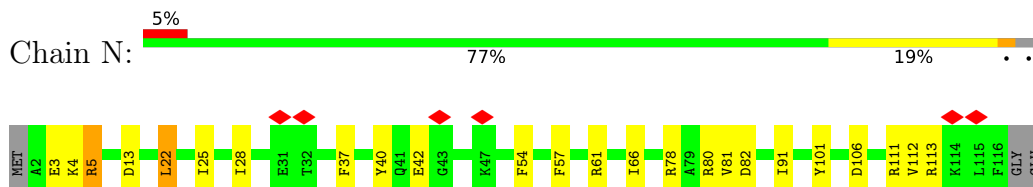
### 3 Residue-property plots

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.

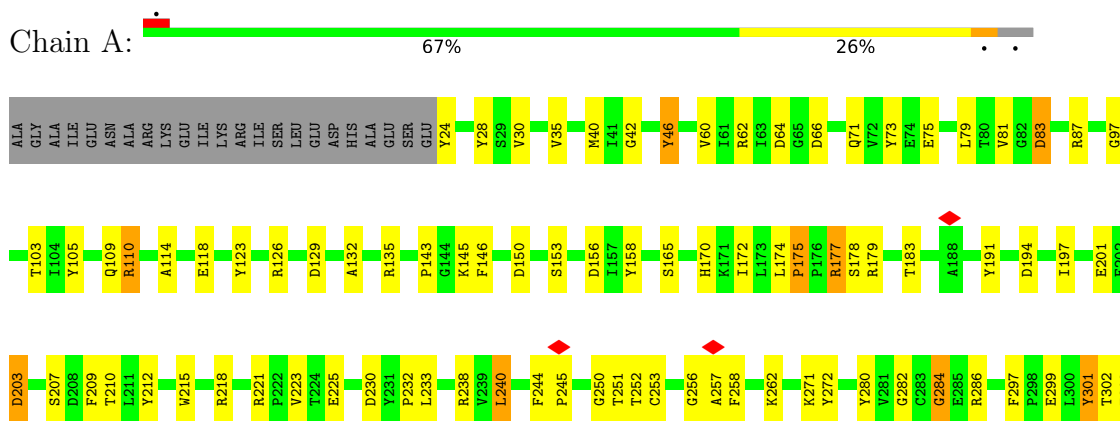
- Molecule 1: V-type proton ATPase subunit D

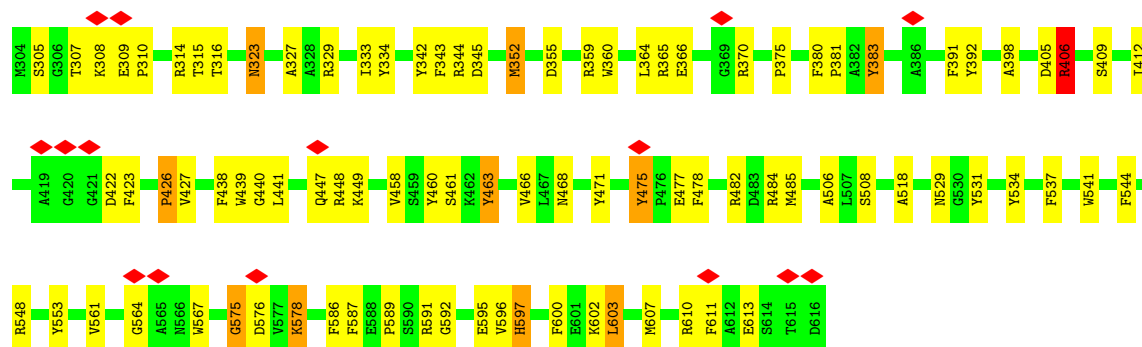


- Molecule 2: V-type proton ATPase subunit F



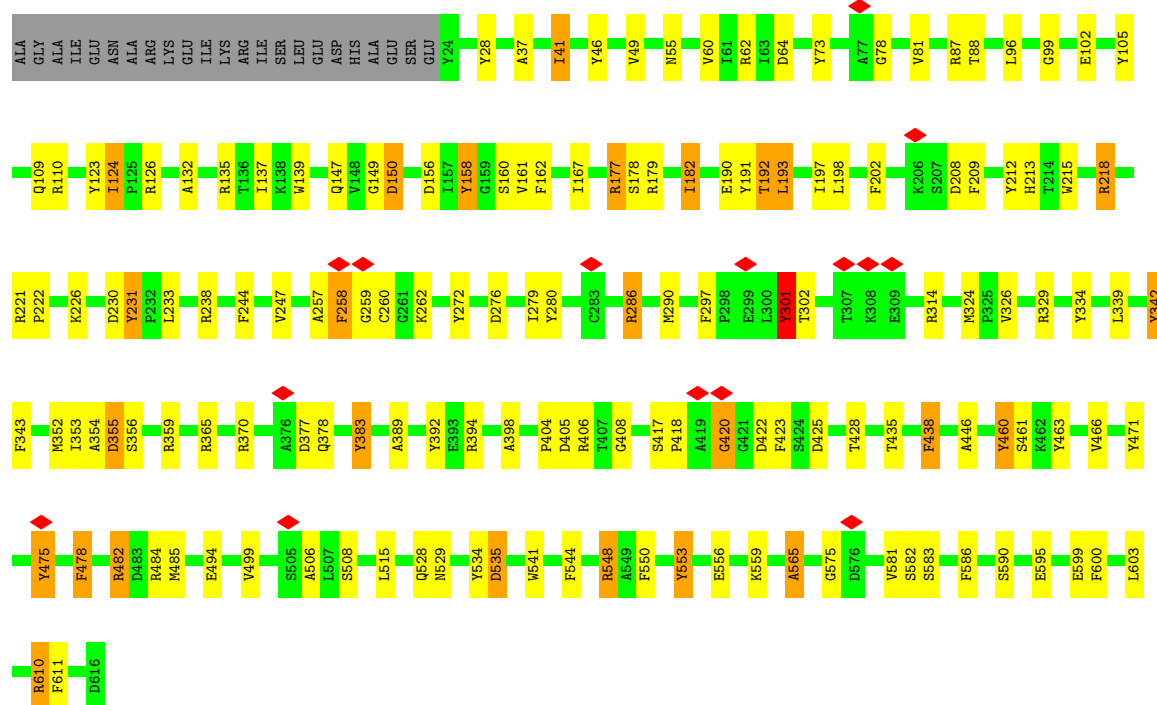
- Molecule 3: V-type proton ATPase catalytic subunit A





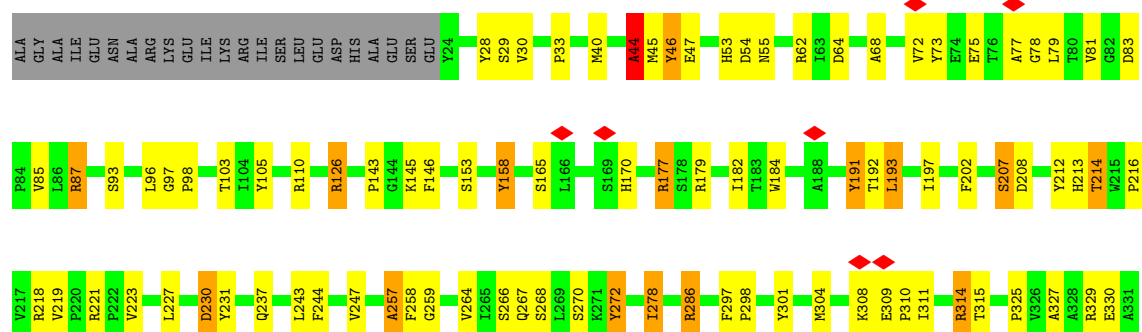
• Molecule 3: V-type proton ATPase catalytic subunit A

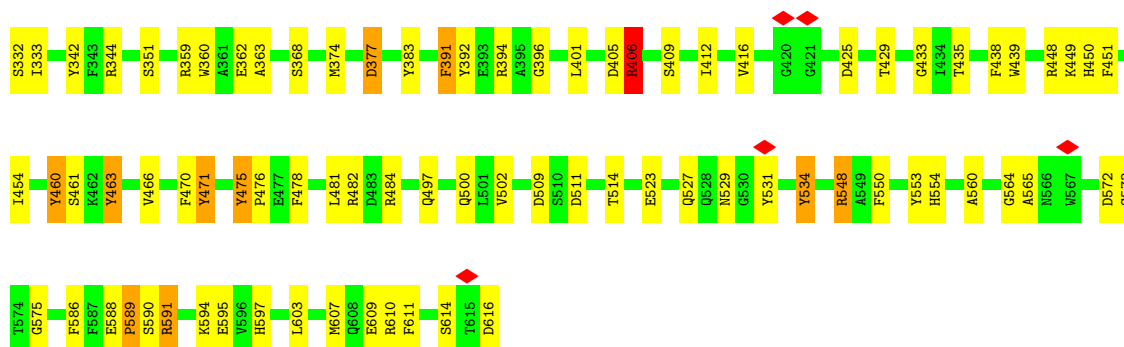
Chain C: 72% 20%



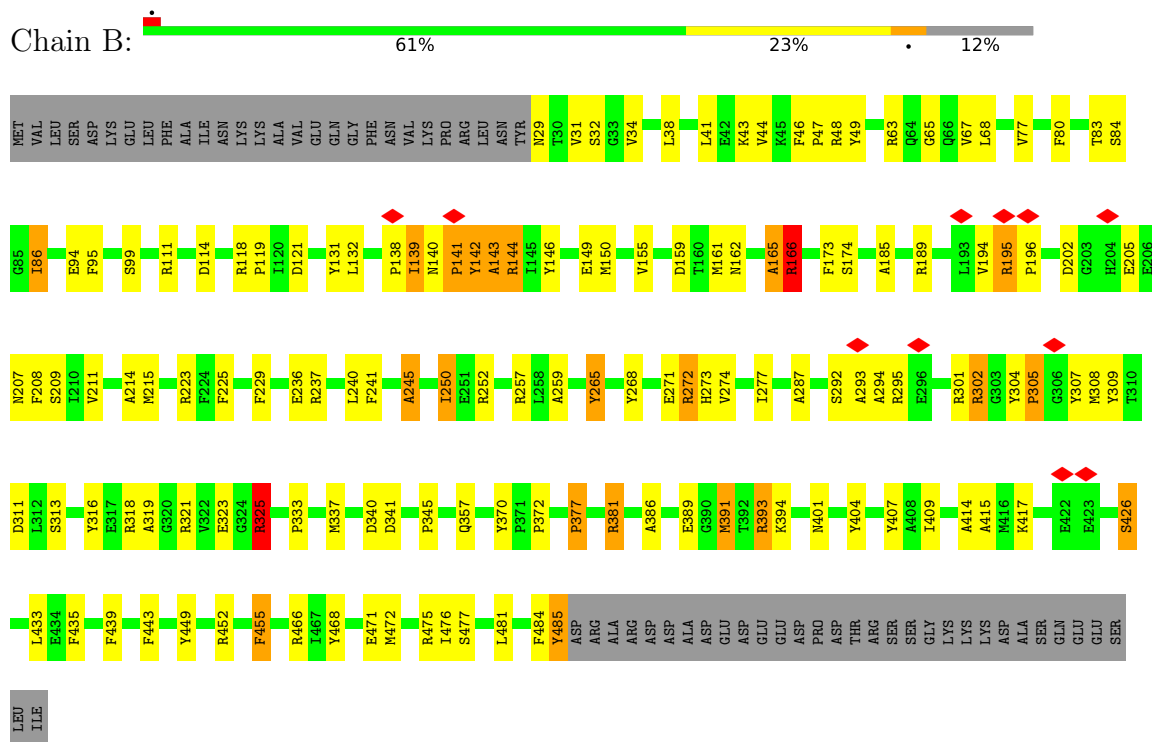
• Molecule 3: V-type proton ATPase catalytic subunit A

Chain E: 68% 24%



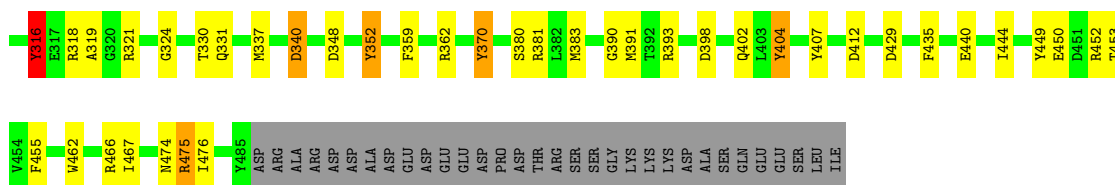


• Molecule 4: V-type proton ATPase subunit B

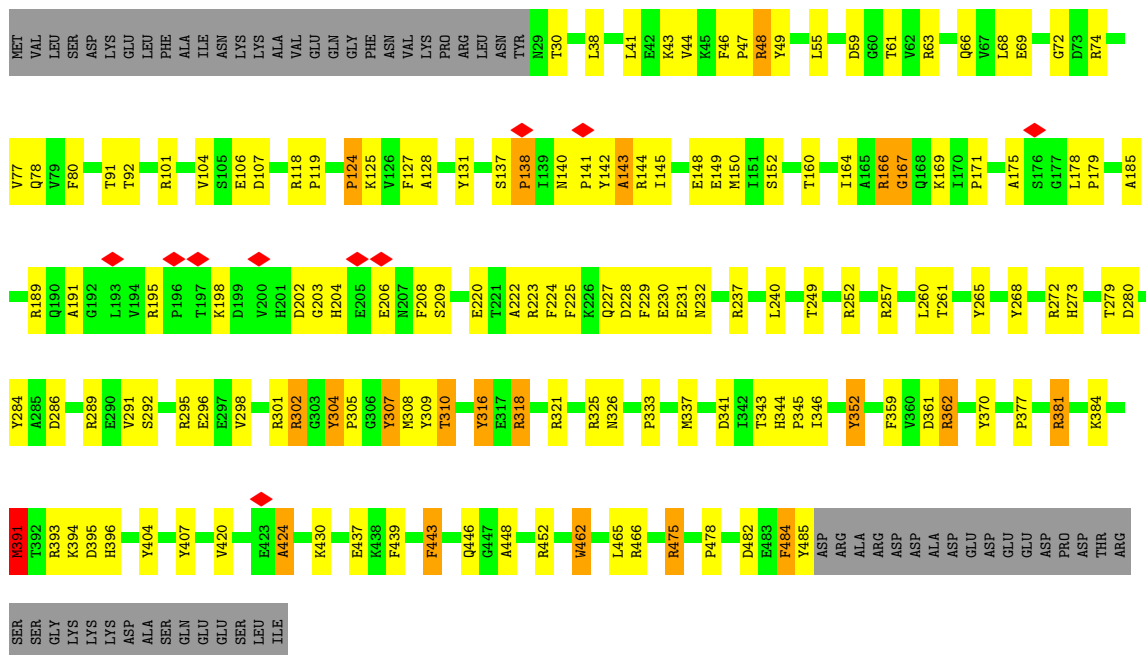


• Molecule 4: V-type proton ATPase subunit B

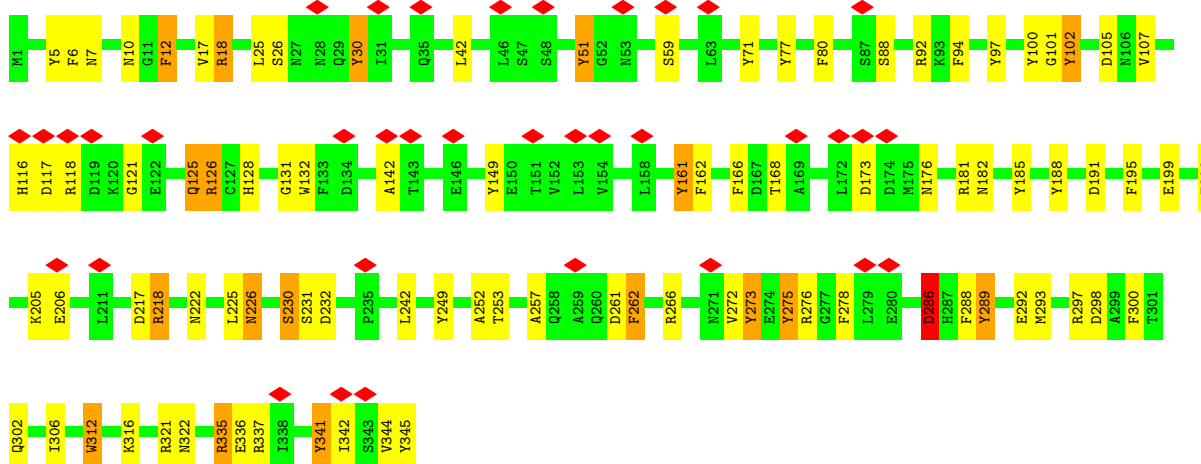
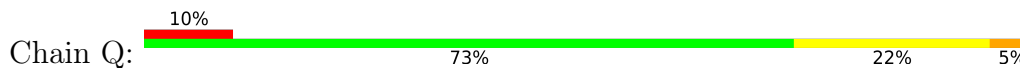





• Molecule 4: V-type proton ATPase subunit B



• Molecule 5: V-type proton ATPase subunit d



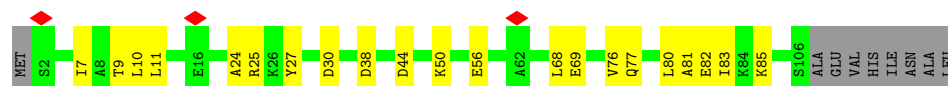
• Molecule 6: V-type proton ATPase subunit G

Chain L:  76% 14% 8%



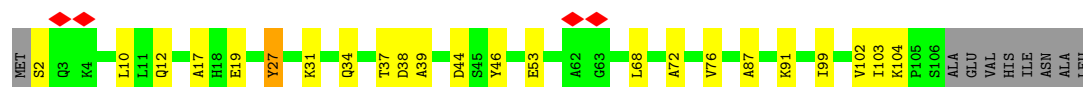
- Molecule 6: V-type proton ATPase subunit G

Chain H:  74% 18% 8%



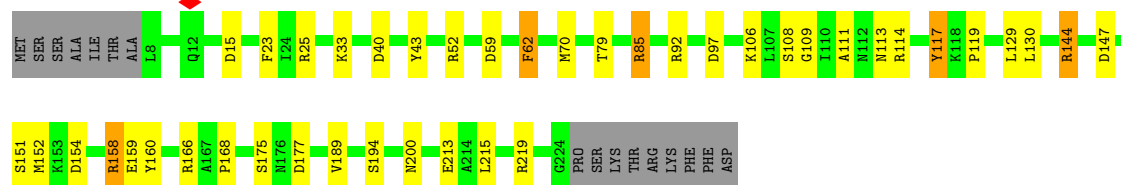
- Molecule 6: V-type proton ATPase subunit G

Chain J:  72% 19% 8%



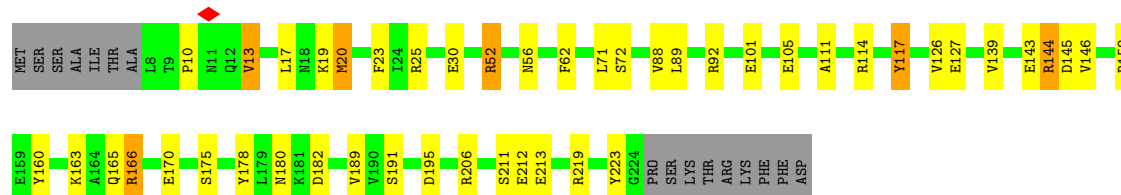
- Molecule 7: V-type proton ATPase subunit E

Chain K:  75% 16% 7%



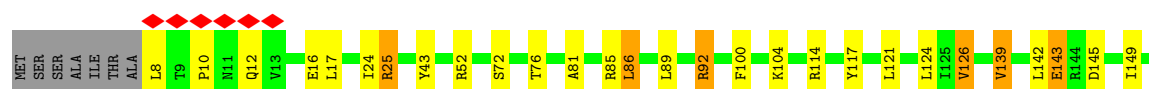
- Molecule 7: V-type proton ATPase subunit E

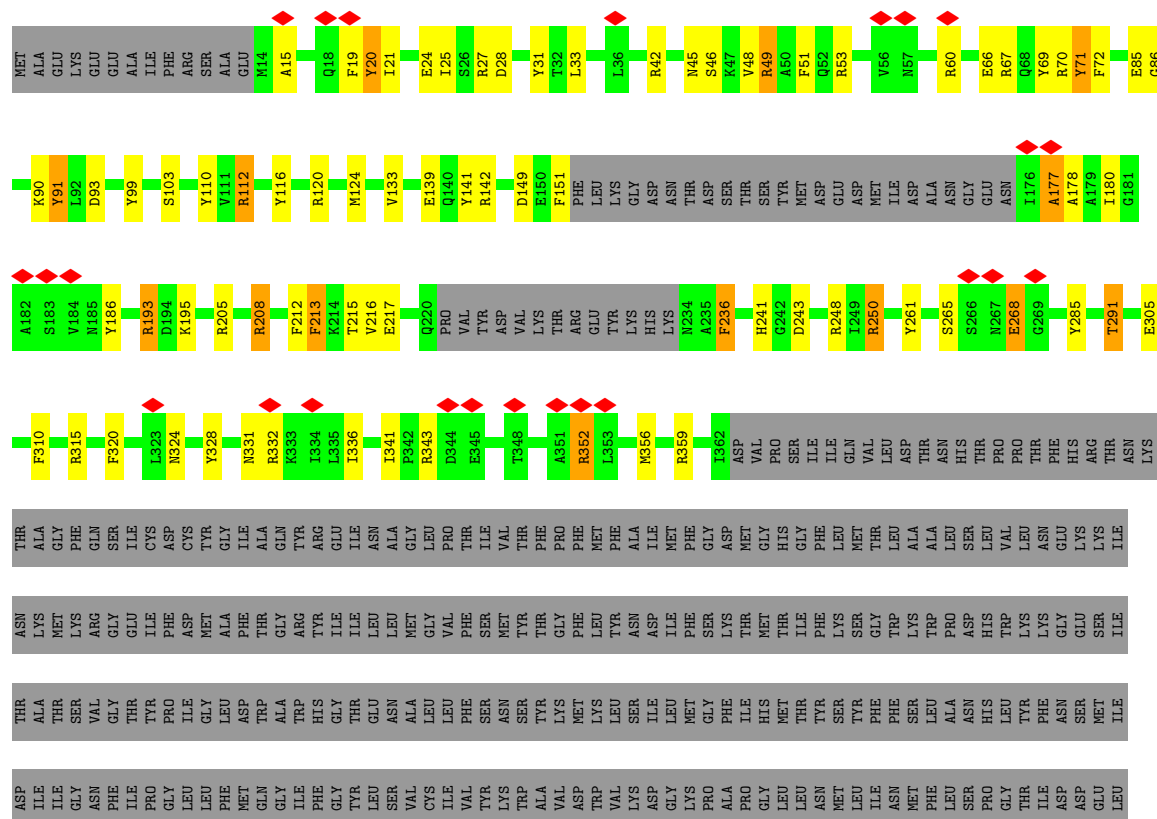
Chain G:  73% 18% 7%

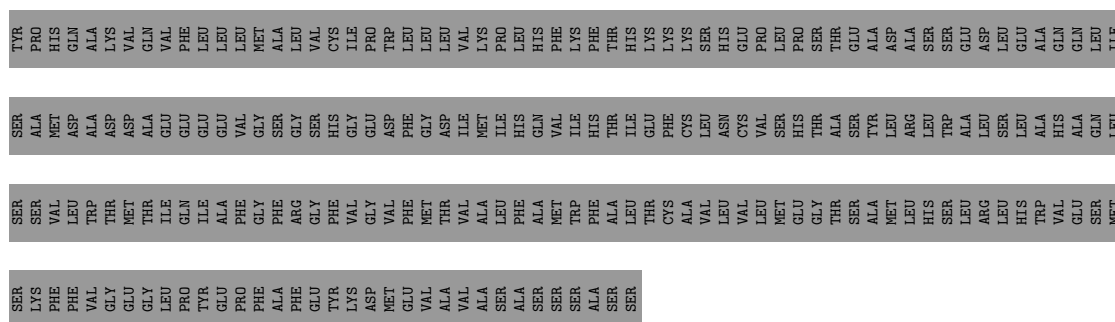


- Molecule 7: V-type proton ATPase subunit E

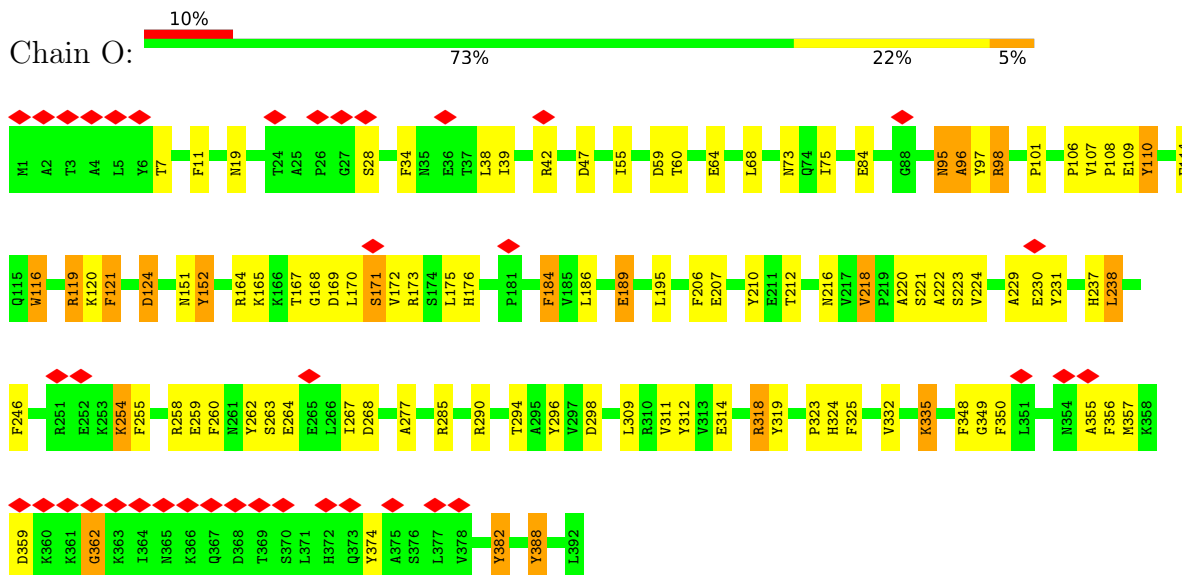
Chain I:  76% 14% 7%



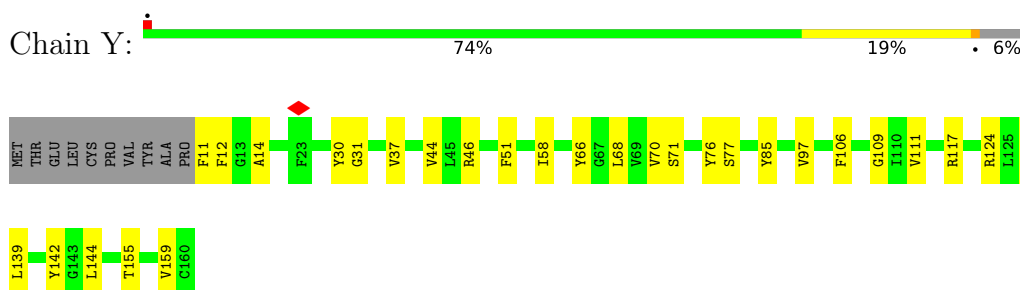




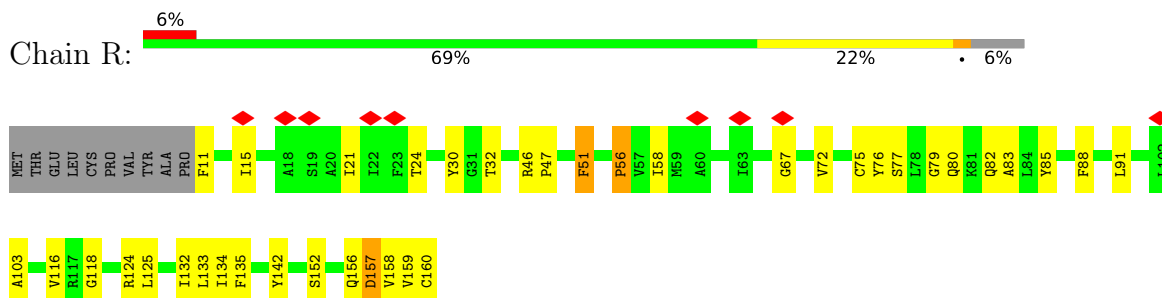
- Molecule 10: V-type proton ATPase subunit C



- Molecule 11: V-type proton ATPase subunit c

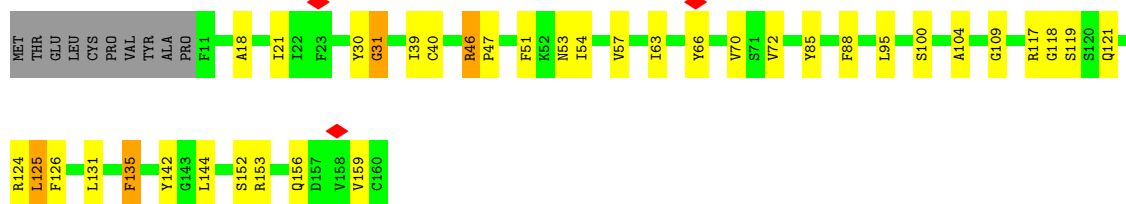


- Molecule 11: V-type proton ATPase subunit c



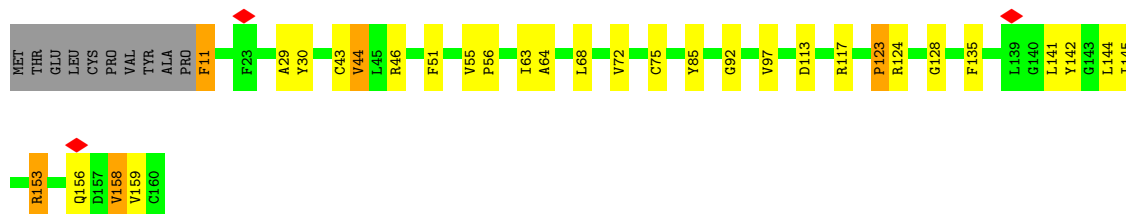
- Molecule 11: V-type proton ATPase subunit c

Chain U:  71% 21% 6%




- Molecule 11: V-type proton ATPase subunit c

Chain V:  74% 16% 6%



- Molecule 11: V-type proton ATPase subunit c

Chain T:  78% 14% 6%



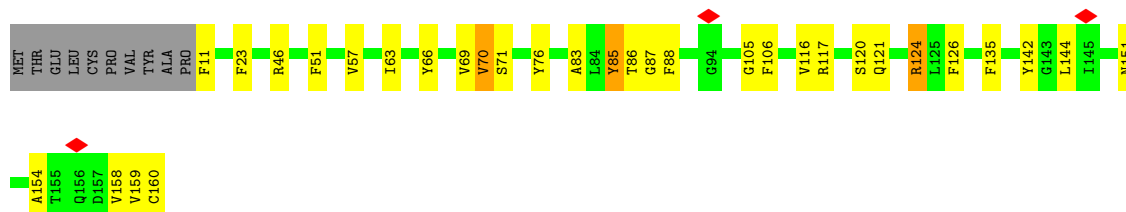
- Molecule 11: V-type proton ATPase subunit c

Chain W:  72% 18% 6%

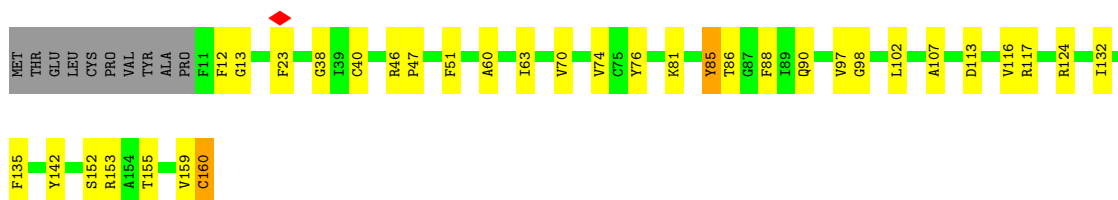


- Molecule 11: V-type proton ATPase subunit c


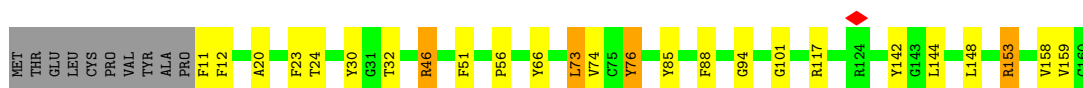
Chain S:  74% 18% 6%




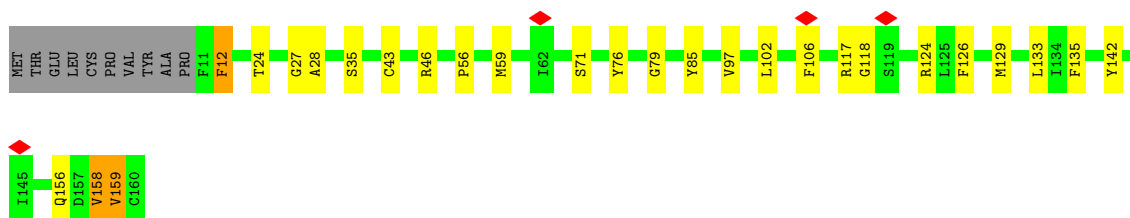
## • Molecule 11: V-type proton ATPase subunit c

Chain X:  72% 20% • 6%

## • Molecule 11: V-type proton ATPase subunit c

Chain Z:  78% 13% • 6%

## • Molecule 11: V-type proton ATPase subunit c

Chain a:  77% 15% • 6%

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	50503	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	7000	Depositor
Magnification	34483	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum map value	0.156	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.03	Depositor
Map size ( $\text{\AA}$ )	371.2, 371.2, 371.2	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.45, 1.45, 1.45	Depositor

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	M	1.76	20/1710 (1.2%)	1.95	49/2295 (2.1%)
2	N	1.68	7/944 (0.7%)	1.85	21/1277 (1.6%)
3	A	1.75	44/4677 (0.9%)	2.02	134/6339 (2.1%)
3	C	1.71	34/4677 (0.7%)	1.91	109/6339 (1.7%)
3	E	1.78	53/4677 (1.1%)	1.96	122/6339 (1.9%)
4	B	1.72	27/3654 (0.7%)	1.99	99/4953 (2.0%)
4	D	1.72	40/3654 (1.1%)	2.00	78/4953 (1.6%)
4	F	1.74	34/3654 (0.9%)	2.02	109/4953 (2.2%)
5	Q	1.75	23/2861 (0.8%)	1.99	73/3880 (1.9%)
6	H	1.58	2/828 (0.2%)	1.76	14/1098 (1.3%)
6	J	1.62	3/828 (0.4%)	1.85	20/1098 (1.8%)
6	L	1.65	6/828 (0.7%)	1.69	10/1098 (0.9%)
7	G	1.72	21/1743 (1.2%)	1.82	30/2338 (1.3%)
7	I	1.70	18/1743 (1.0%)	1.82	30/2338 (1.3%)
7	K	1.71	17/1743 (1.0%)	1.77	31/2338 (1.3%)
8	P	1.65	21/3766 (0.6%)	1.85	63/5087 (1.2%)
9	b	1.73	18/2578 (0.7%)	2.03	81/3479 (2.3%)
10	O	1.69	25/3185 (0.8%)	1.95	81/4314 (1.9%)
11	R	1.65	8/1086 (0.7%)	1.96	26/1472 (1.8%)
11	S	1.67	10/1086 (0.9%)	1.89	21/1472 (1.4%)
11	T	1.65	9/1086 (0.8%)	1.89	27/1472 (1.8%)
11	U	1.65	7/1086 (0.6%)	1.91	19/1472 (1.3%)
11	V	1.68	6/1086 (0.6%)	1.94	22/1472 (1.5%)
11	W	1.69	7/1086 (0.6%)	2.07	36/1472 (2.4%)
11	X	1.72	15/1086 (1.4%)	1.87	20/1472 (1.4%)
11	Y	1.64	6/1086 (0.6%)	1.93	26/1472 (1.8%)
11	Z	1.65	7/1086 (0.6%)	1.85	18/1472 (1.2%)
11	a	1.68	10/1086 (0.9%)	1.87	24/1472 (1.6%)
All	All	1.71	498/58610 (0.8%)	1.93	1393/79236 (1.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	M	0	7
2	N	0	2
3	A	0	11
3	C	0	14
3	E	0	12
4	B	0	13
4	D	0	13
4	F	0	11
5	Q	0	14
6	L	0	2
7	G	0	4
7	I	0	3
7	K	0	5
8	P	0	9
9	b	0	14
10	O	0	12
11	S	0	1
11	T	0	4
11	U	0	2
11	V	0	2
11	W	0	4
11	X	0	1
11	Z	0	2
11	a	0	2
All	All	0	164

The worst 5 of 498 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	X	160	CYS	CB-SG	11.36	2.01	1.82
8	P	392	TYR	CG-CD2	9.03	1.50	1.39
3	E	268	SER	CA-CB	8.92	1.66	1.52
9	b	248	ARG	NE-CZ	8.29	1.43	1.33
3	C	110	ARG	CD-NE	8.22	1.60	1.46

The worst 5 of 1393 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	406	ARG	NE-CZ-NH1	17.62	129.11	120.30
1	M	91	ARG	NE-CZ-NH1	17.37	128.98	120.30
4	B	485	TYR	CB-CG-CD1	17.28	131.37	121.00
4	D	111	ARG	NE-CZ-NH1	16.88	128.74	120.30
3	E	329	ARG	NE-CZ-NH1	16.34	128.47	120.30

There are no chirality outliers.

5 of 164 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	112	TYR	Sidechain
1	M	134	ARG	Sidechain
1	M	139	TYR	Sidechain
1	M	34	ARG	Sidechain
1	M	81	TYR	Sidechain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	1691	0	1740	8	0
2	N	928	0	926	4	0
3	A	4578	0	4519	13	0
3	C	4578	0	4519	11	0
3	E	4578	0	4519	15	0
4	B	3585	0	3567	16	0
4	D	3585	0	3567	12	0
4	F	3585	0	3567	16	0
5	Q	2802	0	2689	9	0
6	H	824	0	877	5	0
6	J	824	0	877	5	0
6	L	824	0	877	3	0
7	G	1731	0	1797	6	0
7	I	1731	0	1797	7	0
7	K	1731	0	1797	1	0
8	P	3712	0	3829	11	0
9	b	2540	0	2537	0	0
10	O	3122	0	3155	8	0
11	R	1071	0	1141	2	0
11	S	1071	0	1141	3	0
11	T	1071	0	1141	3	0
11	U	1071	0	1141	11	0
11	V	1071	0	1141	24	0
11	W	1071	0	1141	5	0
11	X	1071	0	1141	4	0
11	Y	1071	0	1141	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	Z	1071	0	1141	8	0
11	a	1071	0	1141	0	0
All	All	57659	0	58566	191	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 2.

The worst 5 of 191 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)
11:X:160:CYS:SG	11:X:160:CYS:CB	2.01	1.47
11:V:141:LEU:HA	11:V:144:LEU:CD2	1.71	1.21
11:V:141:LEU:O	11:V:144:LEU:HG	1.48	1.13
11:V:141:LEU:HA	11:V:144:LEU:HD21	1.23	1.08
11:Z:66:TYR:HB3	11:Z:144:LEU:HD22	1.33	1.05

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	M	208/256 (81%)	206 (99%)	2 (1%)	0	100	100
2	N	113/118 (96%)	102 (90%)	10 (9%)	1 (1%)	17	57
3	A	591/616 (96%)	541 (92%)	31 (5%)	19 (3%)	4	26
3	C	591/616 (96%)	538 (91%)	37 (6%)	16 (3%)	5	31
3	E	591/616 (96%)	542 (92%)	32 (5%)	17 (3%)	4	29
4	B	455/517 (88%)	413 (91%)	27 (6%)	15 (3%)	4	26
4	D	455/517 (88%)	416 (91%)	25 (6%)	14 (3%)	4	27
4	F	455/517 (88%)	411 (90%)	30 (7%)	14 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	Q	343/345 (99%)	318 (93%)	18 (5%)	7 (2%)	7	38
6	H	103/114 (90%)	99 (96%)	3 (3%)	1 (1%)	15	54
6	J	103/114 (90%)	100 (97%)	3 (3%)	0	100	100
6	L	103/114 (90%)	98 (95%)	4 (4%)	1 (1%)	15	54
7	G	215/233 (92%)	207 (96%)	7 (3%)	1 (0%)	29	69
7	I	215/233 (92%)	208 (97%)	6 (3%)	1 (0%)	29	69
7	K	215/233 (92%)	205 (95%)	9 (4%)	1 (0%)	29	69
8	P	457/478 (96%)	431 (94%)	18 (4%)	8 (2%)	8	40
9	b	306/840 (36%)	274 (90%)	25 (8%)	7 (2%)	6	34
10	O	390/392 (100%)	350 (90%)	21 (5%)	19 (5%)	2	20
11	R	148/160 (92%)	138 (93%)	6 (4%)	4 (3%)	5	31
11	S	148/160 (92%)	140 (95%)	6 (4%)	2 (1%)	11	46
11	T	148/160 (92%)	143 (97%)	5 (3%)	0	100	100
11	U	148/160 (92%)	140 (95%)	5 (3%)	3 (2%)	7	38
11	V	148/160 (92%)	139 (94%)	5 (3%)	4 (3%)	5	31
11	W	148/160 (92%)	137 (93%)	8 (5%)	3 (2%)	7	38
11	X	148/160 (92%)	138 (93%)	8 (5%)	2 (1%)	11	46
11	Y	148/160 (92%)	139 (94%)	8 (5%)	1 (1%)	22	63
11	Z	148/160 (92%)	136 (92%)	9 (6%)	3 (2%)	7	38
11	a	148/160 (92%)	138 (93%)	7 (5%)	3 (2%)	7	38
All	All	7389/8469 (87%)	6847 (93%)	375 (5%)	167 (2%)	9	34

5 of 167 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	257	ALA
3	A	475	TYR
4	B	292	SER
3	C	475	TYR
3	C	529	ASN

### 5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	183/221 (83%)	181 (99%)	2 (1%)	73	84
2	N	102/104 (98%)	101 (99%)	1 (1%)	76	86
3	A	497/515 (96%)	479 (96%)	18 (4%)	35	59
3	C	497/515 (96%)	472 (95%)	25 (5%)	24	49
3	E	497/515 (96%)	473 (95%)	24 (5%)	25	51
4	B	391/444 (88%)	370 (95%)	21 (5%)	22	47
4	D	391/444 (88%)	384 (98%)	7 (2%)	59	77
4	F	391/444 (88%)	374 (96%)	17 (4%)	29	53
5	Q	309/309 (100%)	296 (96%)	13 (4%)	30	54
6	H	87/94 (93%)	84 (97%)	3 (3%)	37	60
6	J	87/94 (93%)	87 (100%)	0	100	100
6	L	87/94 (93%)	84 (97%)	3 (3%)	37	60
7	G	194/208 (93%)	190 (98%)	4 (2%)	53	72
7	I	194/208 (93%)	189 (97%)	5 (3%)	46	66
7	K	194/208 (93%)	189 (97%)	5 (3%)	46	66
8	P	426/439 (97%)	417 (98%)	9 (2%)	53	72
9	b	275/728 (38%)	265 (96%)	10 (4%)	35	59
10	O	348/348 (100%)	339 (97%)	9 (3%)	46	66
11	R	110/119 (92%)	104 (94%)	6 (6%)	21	47
11	S	110/119 (92%)	106 (96%)	4 (4%)	35	59
11	T	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	U	110/119 (92%)	106 (96%)	4 (4%)	35	59
11	V	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	W	110/119 (92%)	109 (99%)	1 (1%)	78	87
11	X	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	Y	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	Z	110/119 (92%)	108 (98%)	2 (2%)	59	77
11	a	110/119 (92%)	108 (98%)	2 (2%)	59	77
All	All	6250/7122 (88%)	6043 (97%)	207 (3%)	41	61

5 of 207 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	Q	59	SER
8	P	368	LEU
11	S	124	ARG
5	Q	161	TYR
6	L	104	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
5	Q	302	GLN
8	P	412	ASN
11	R	90	GLN
6	L	12	GLN
8	P	206	HIS

### 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 ⓘ

There are no chain breaks in this entry.

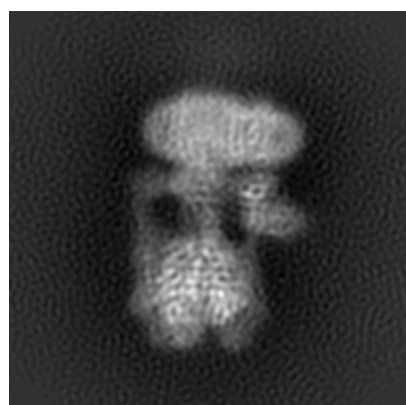
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6284. These allow visual inspection of the internal detail of the map and identification of artifacts.

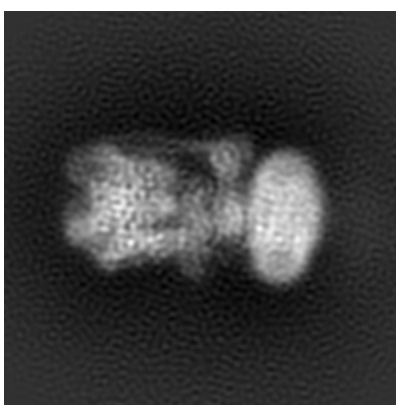
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

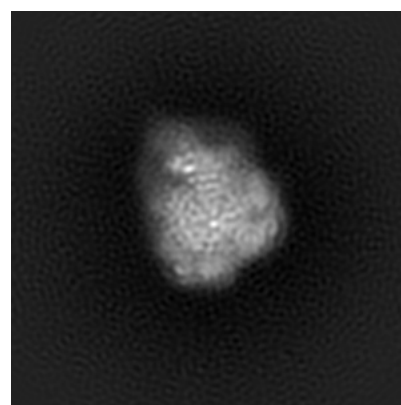
#### 6.1.1 Primary map



X



Y

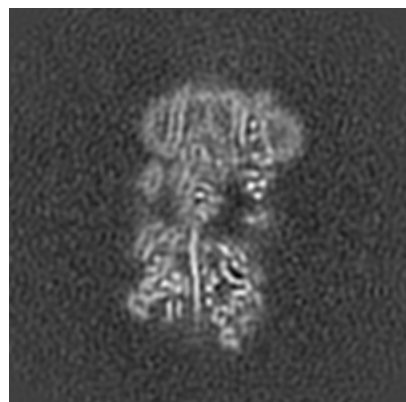


Z

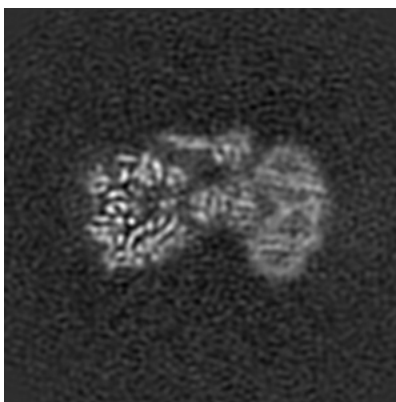
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

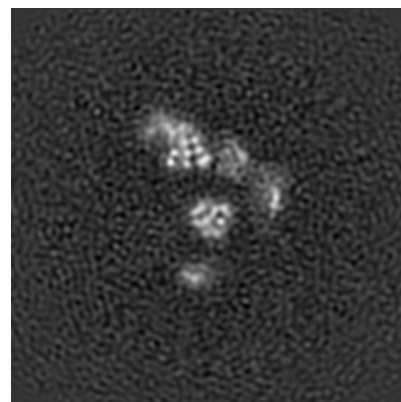
#### 6.2.1 Primary map



X Index: 128



Y Index: 128

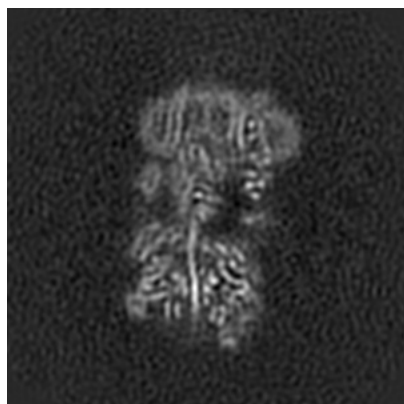


Z Index: 128

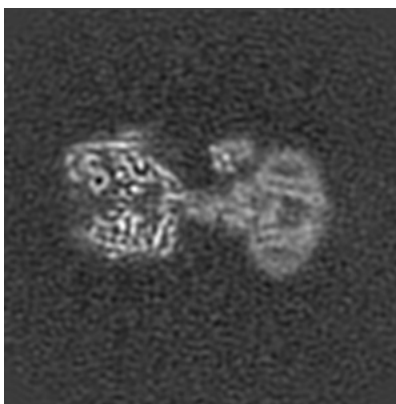
The images above show central slices of the map in three orthogonal directions.

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

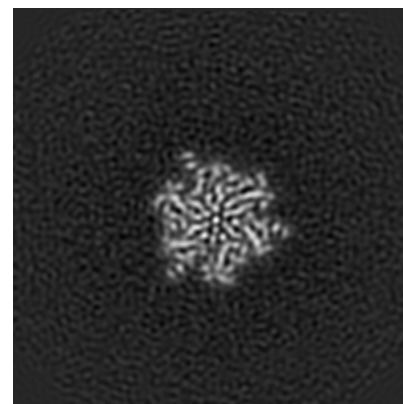
### 6.3.1 Primary map



X Index: 129



Y Index: 115



Z Index: 75

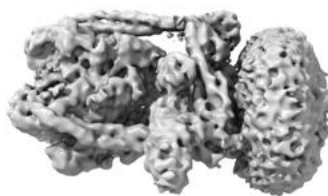
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

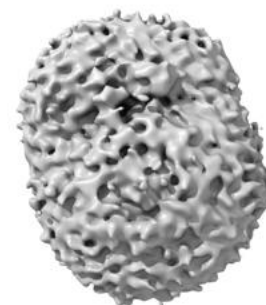
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

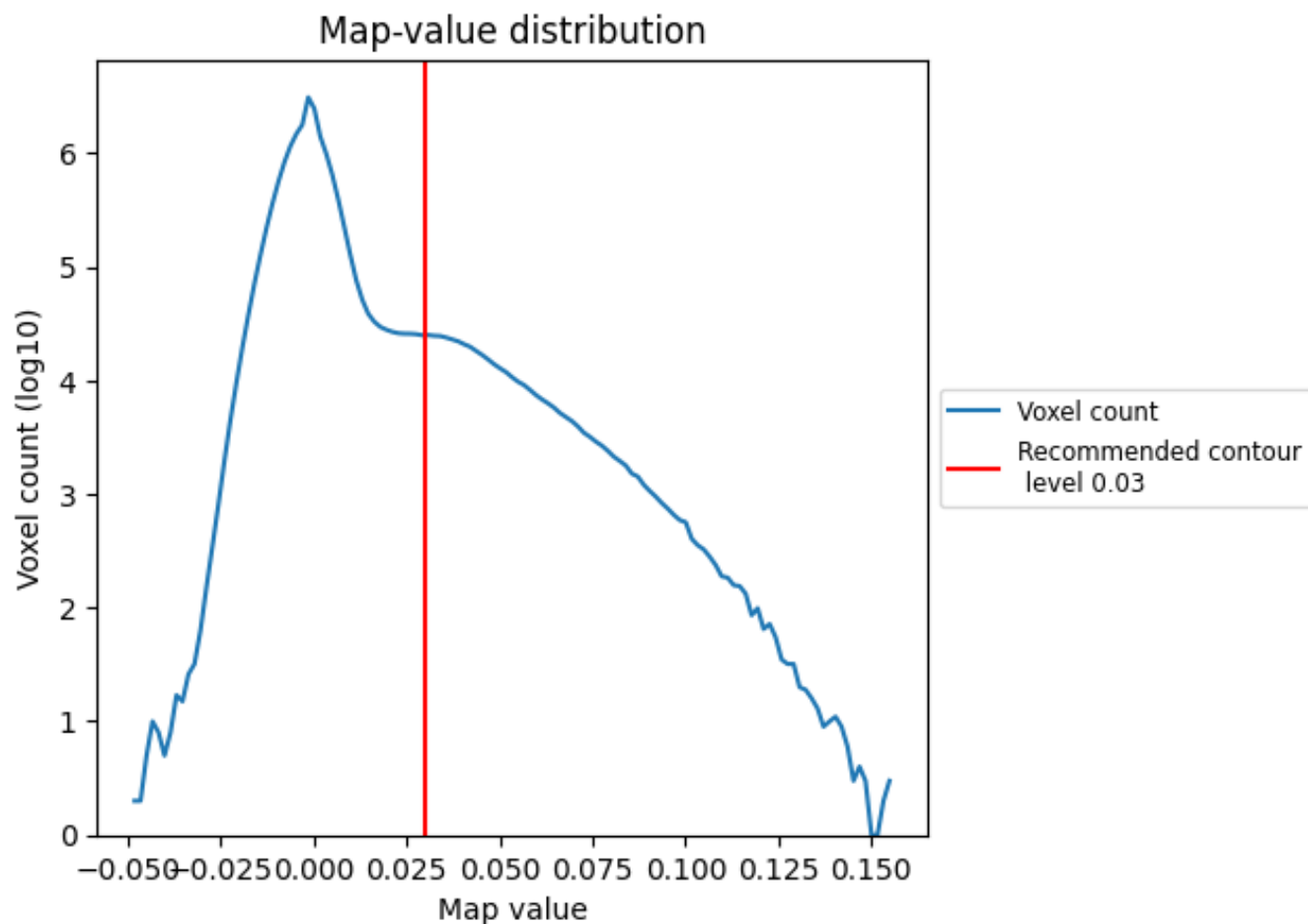
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

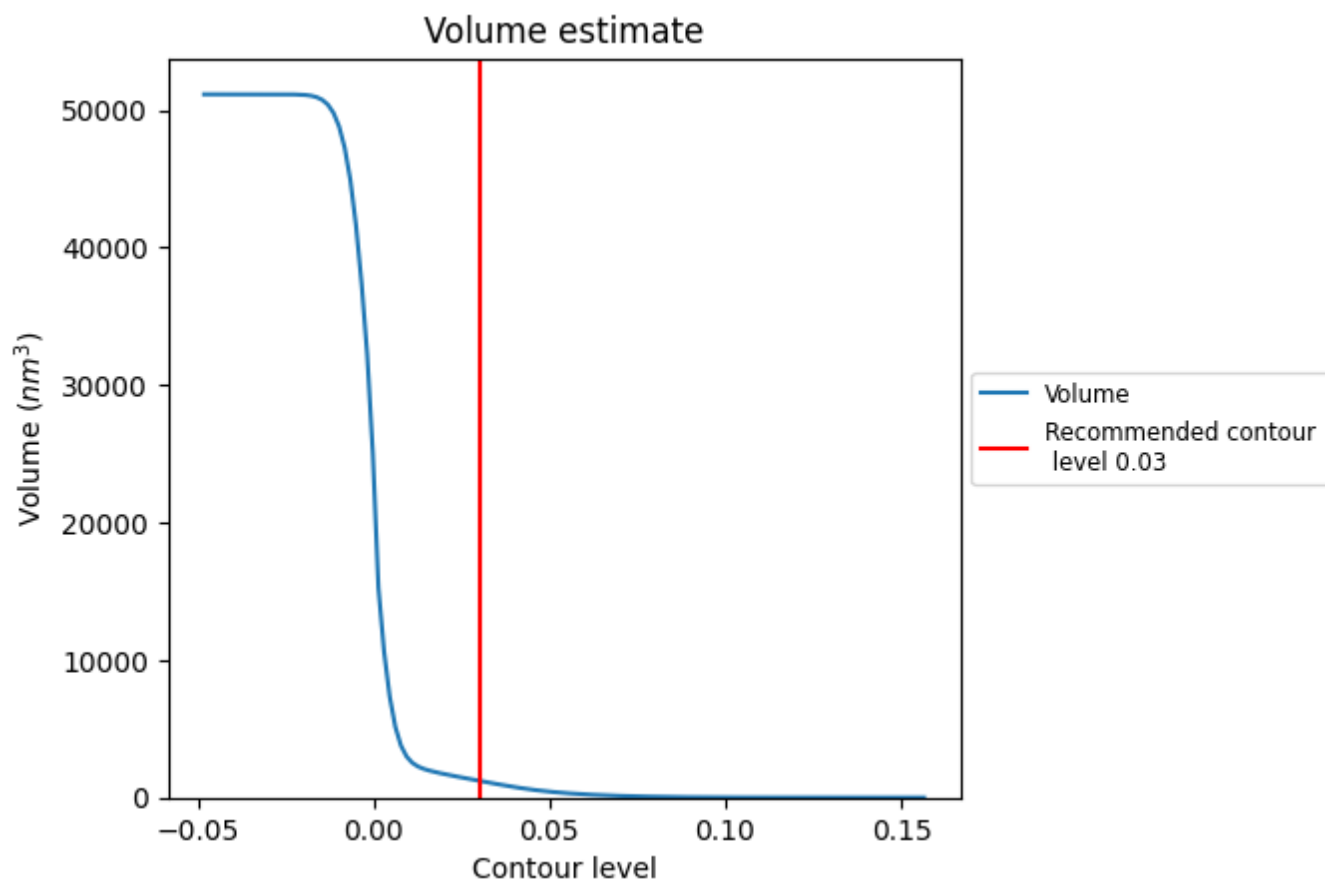
This section contains the results of statistical analysis of the map.

### 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.

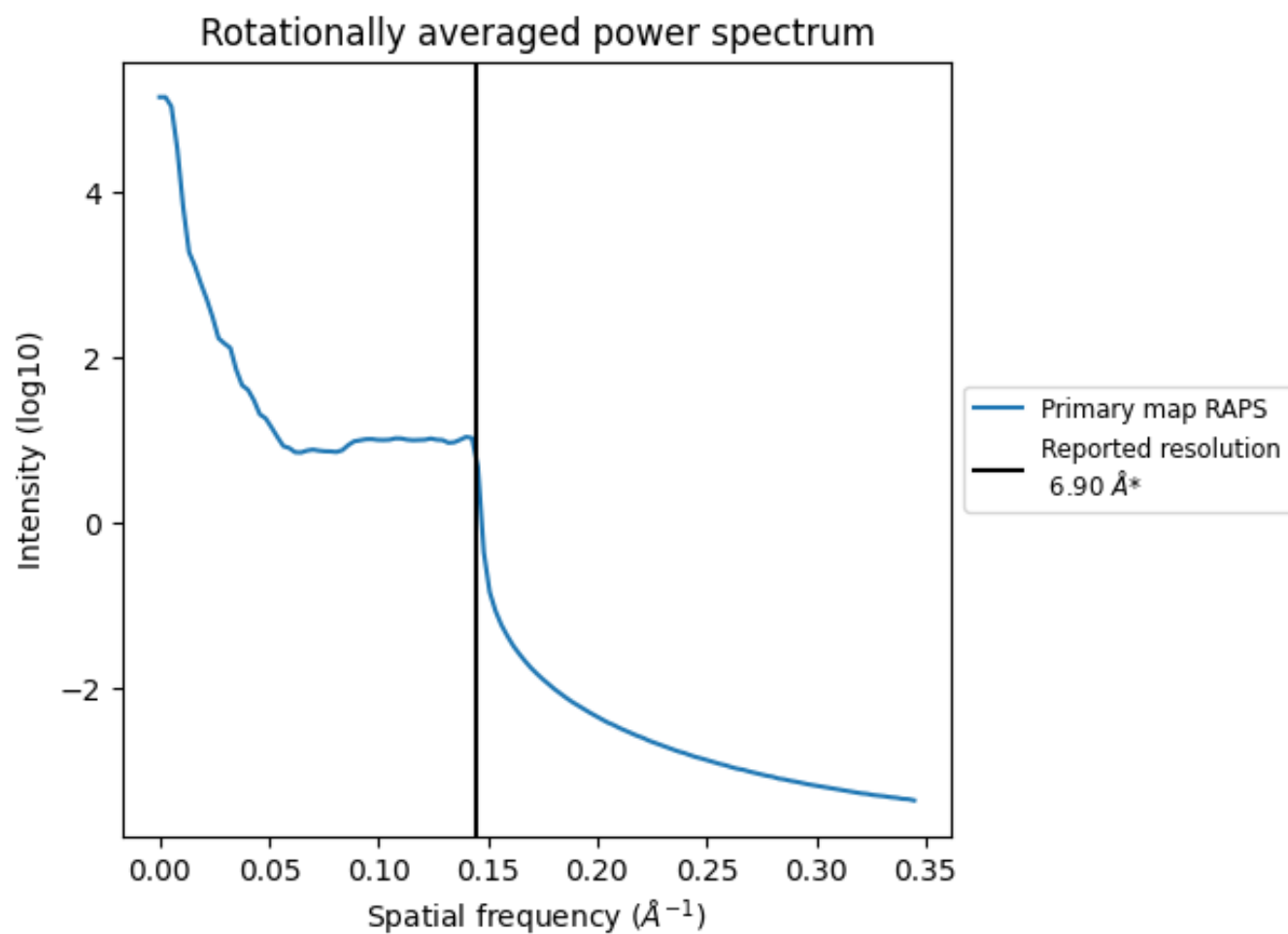
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1220 nm<sup>3</sup>; this corresponds to an approximate mass of 1102 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 ⓘ

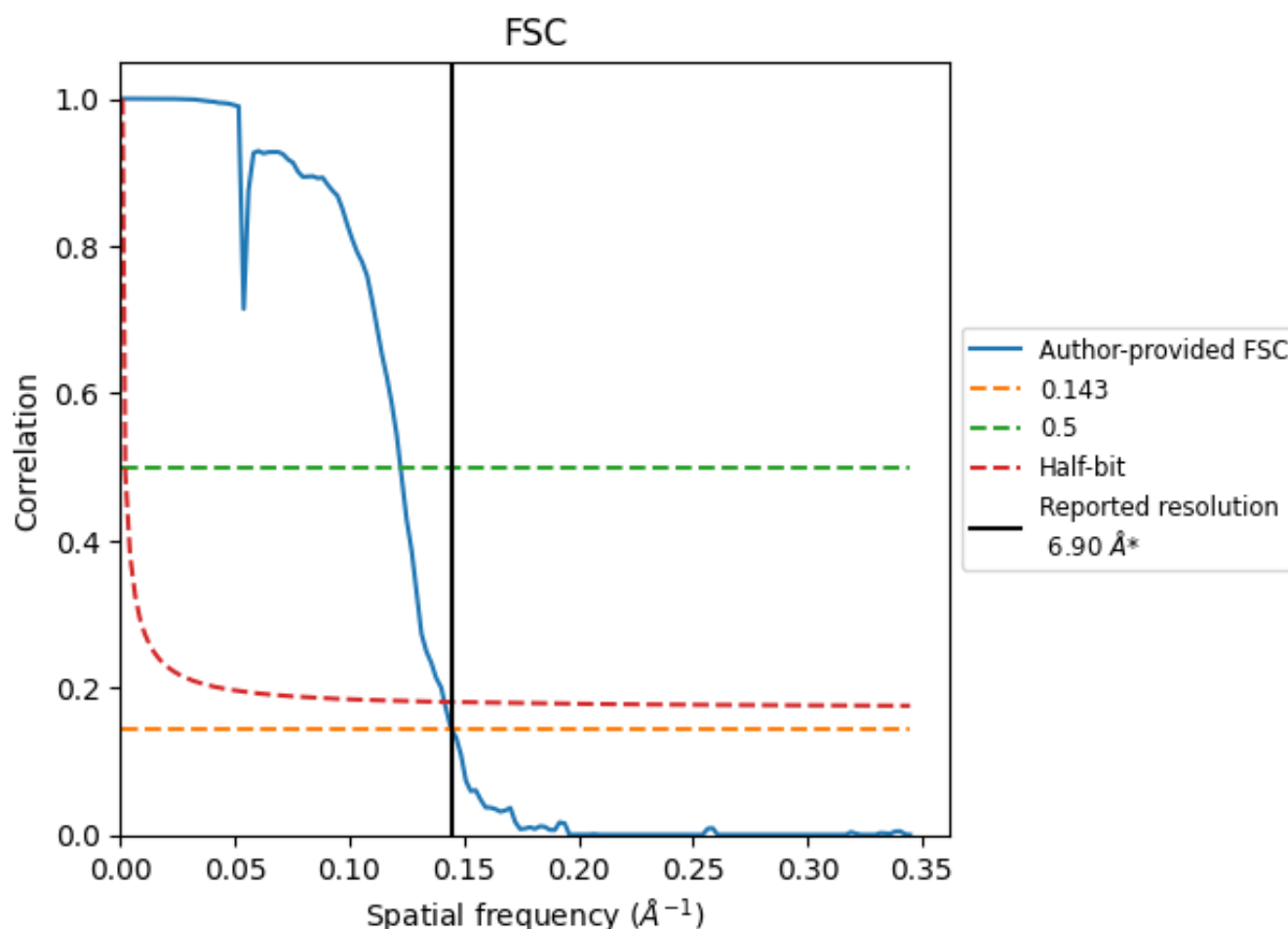


\*Reported resolution corresponds to spatial frequency of 0.145 Å<sup>-1</sup>

## 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 0.145  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

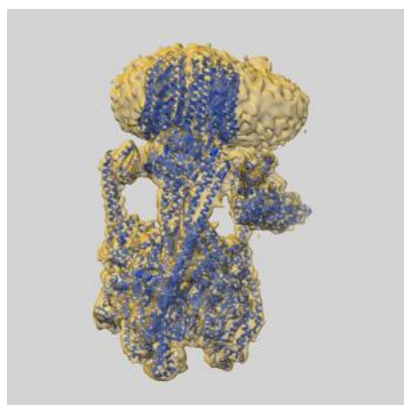
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.90	-	-
Author-provided FSC curve	6.92	8.17	7.07
Unmasked-calculated*	-	-	-

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

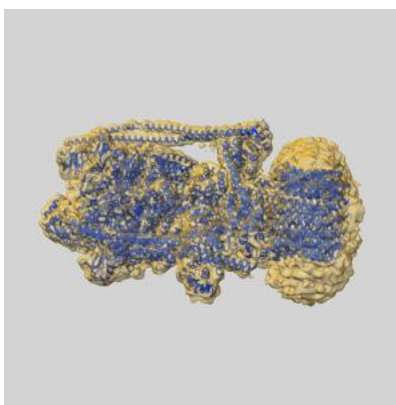
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6284 and PDB model 3J9T. Per-residue inclusion information can be found in section [3](#) on page [7](#).

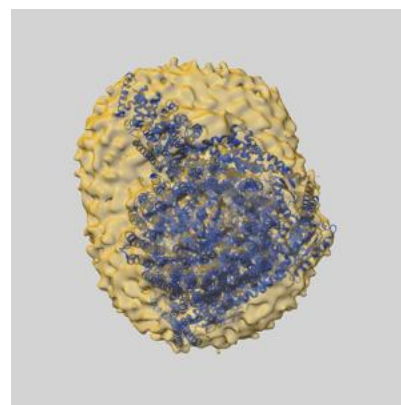
### 9.1 Map-model overlay [i](#)



X



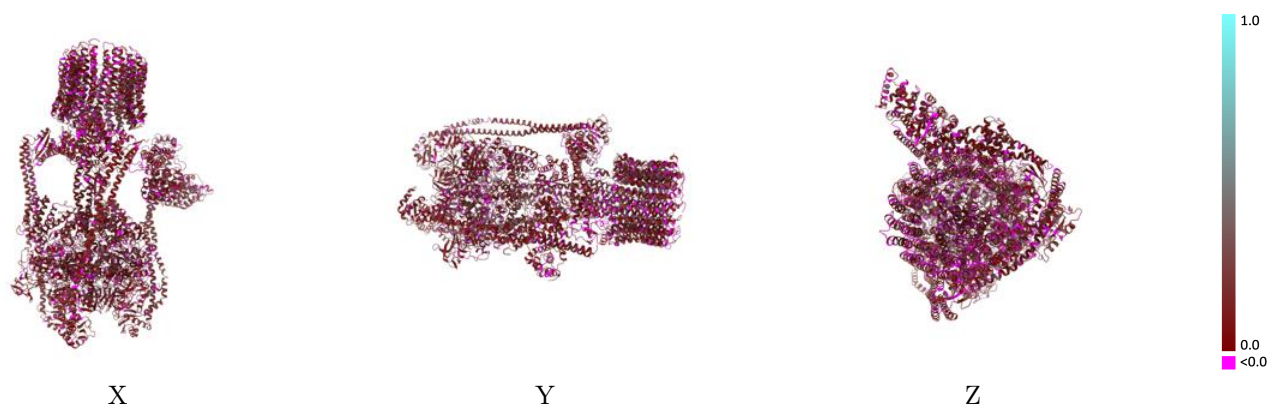
Y



Z

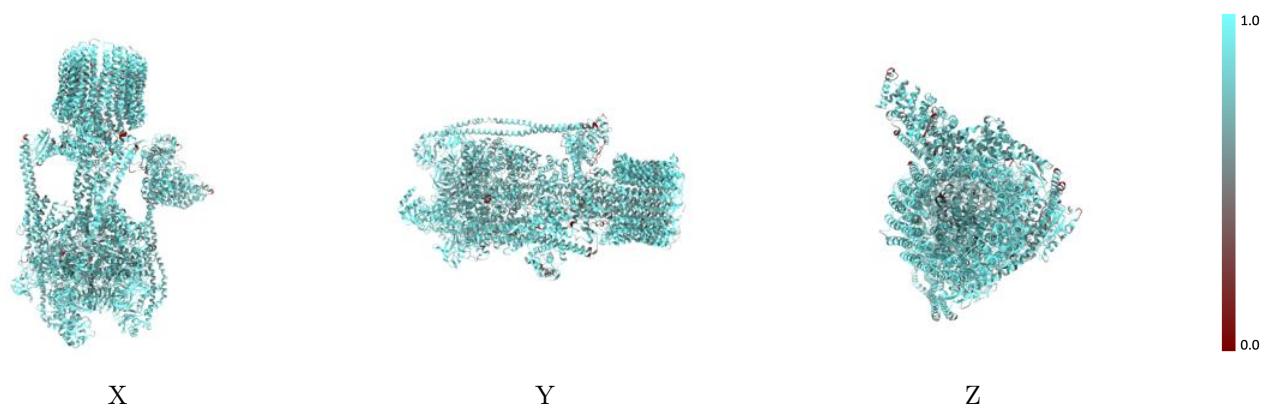
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



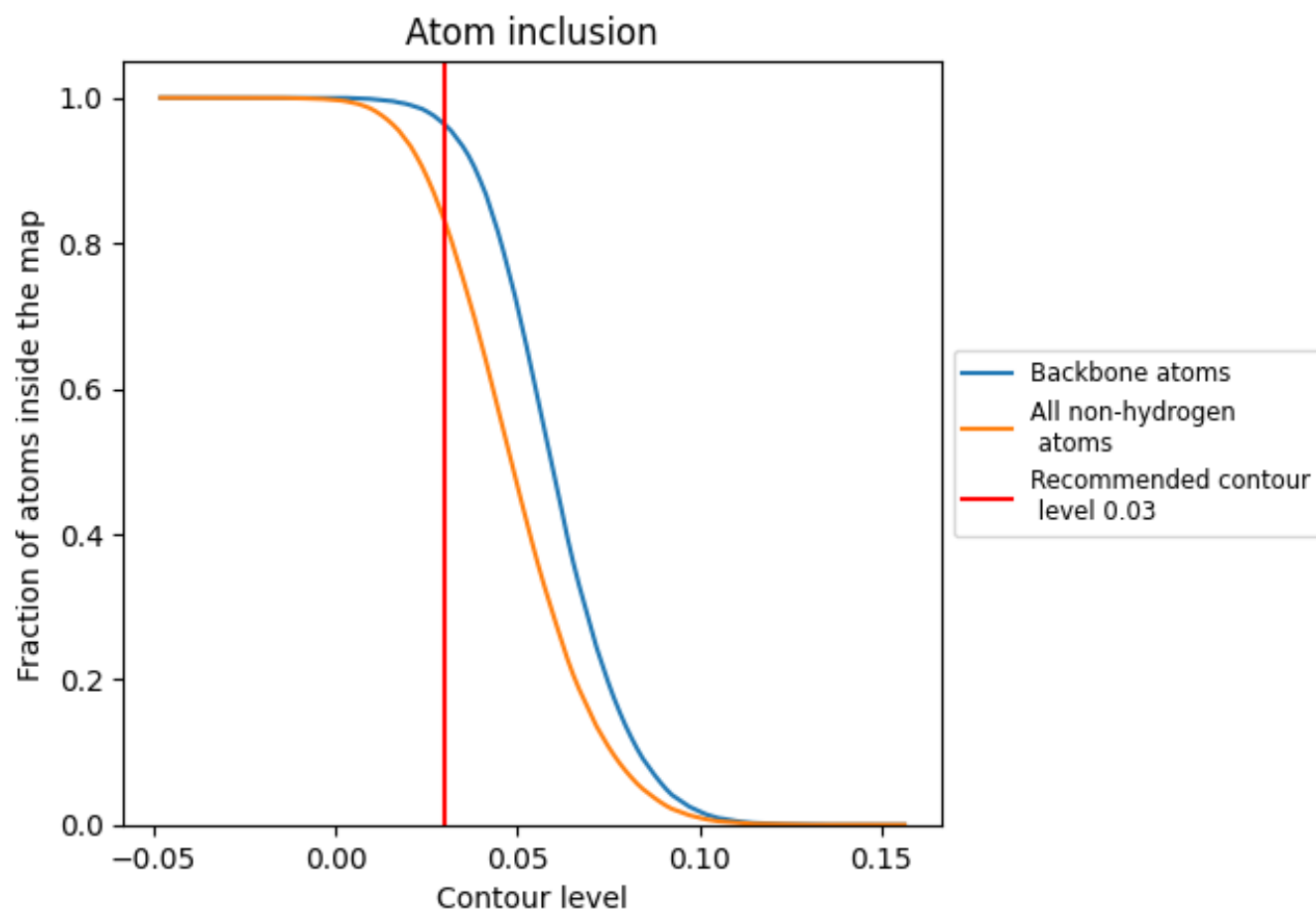
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).



























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 83% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8301	 0.1280
A	 0.8394	 0.1420
B	 0.8193	 0.1320
C	 0.8403	 0.1390
D	 0.8181	 0.1290
E	 0.8501	 0.1400
F	 0.8224	 0.1320
G	 0.8370	 0.1440
H	 0.8032	 0.1400
I	 0.8247	 0.1460
J	 0.7800	 0.1530
K	 0.8335	 0.1500
L	 0.7934	 0.1500
M	 0.8045	 0.1160
N	 0.8085	 0.1430
O	 0.7923	 0.1220
P	 0.8082	 0.1290
Q	 0.7790	 0.0950
R	 0.8800	 0.0950
S	 0.9017	 0.0960
T	 0.9036	 0.1140
U	 0.8790	 0.1250
V	 0.8280	 0.1130
W	 0.8289	 0.1210
X	 0.8819	 0.1210
Y	 0.9112	 0.1130
Z	 0.9017	 0.0940
a	 0.8724	 0.0990
b	 0.7876	 0.1030

