



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 02:47 AM EST

PDB ID : 3J9V  
EMDB ID : EMD-6286  
Title : Yeast V-ATPase state 3  
Authors : Zhao, J.; Benlekbir, S.; Rubinstein, J.L.  
Deposited on : 2015-02-23  
Resolution : 8.30 Å(reported)  
Based on initial models : 4RND, 1HO8, 4DL0, 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

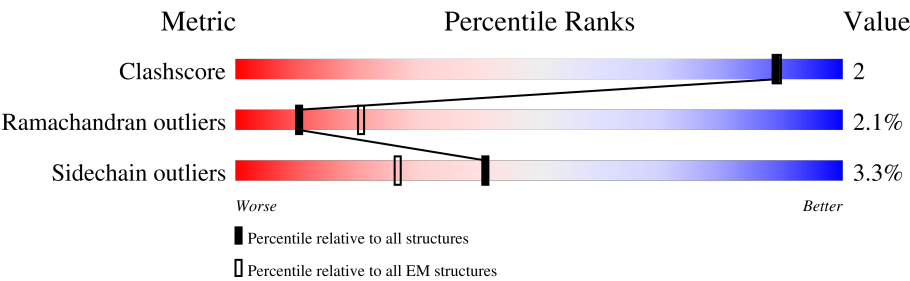


# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 8.30 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



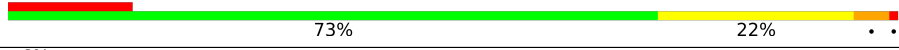



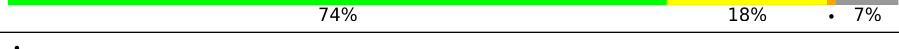
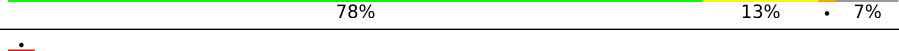
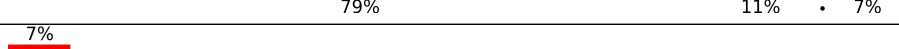
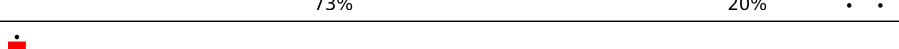
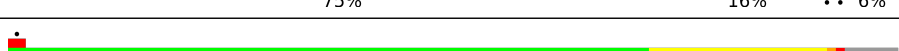



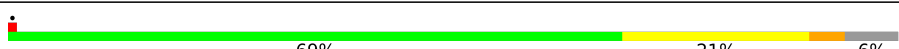





The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey 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	b	840	<div><div>10%</div><div>27%9%63%</div></div>
2	O	392	<div><div>79%17%</div></div>
3	M	256	<div><div>9%61%18%18%</div></div>
4	N	118	<div><div>80%16%</div></div>
5	A	616	<div><div>72%21%</div></div>
5	C	616	<div><div>70%22%</div></div>
5	E	616	<div><div>5%68%22%5%</div></div>
6	B	517	<div><div>65%19%5%12%</div></div>

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Mol	Chain	Length	Quality of chain
6	D	517	
6	F	517	
7	Q	345	
8	H	114	
8	J	114	
8	L	114	
9	G	233	
9	I	233	
9	K	233	
10	P	478	
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 a, vacuolar isoform.

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

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

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

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

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

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

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

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

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

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



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

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

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

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

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

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

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

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

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

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



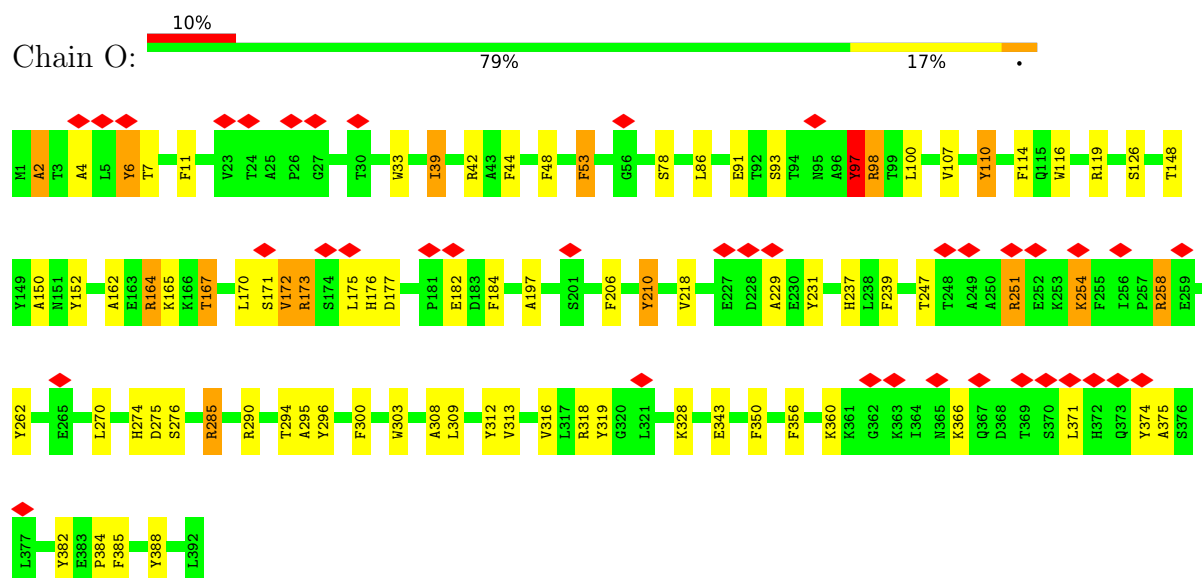
Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	U	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	X	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	Y	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	W	150	Total 1071	C 704	N 173	O 187	S 7	0	0
11	Z	150	Total 1071	C 704	N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



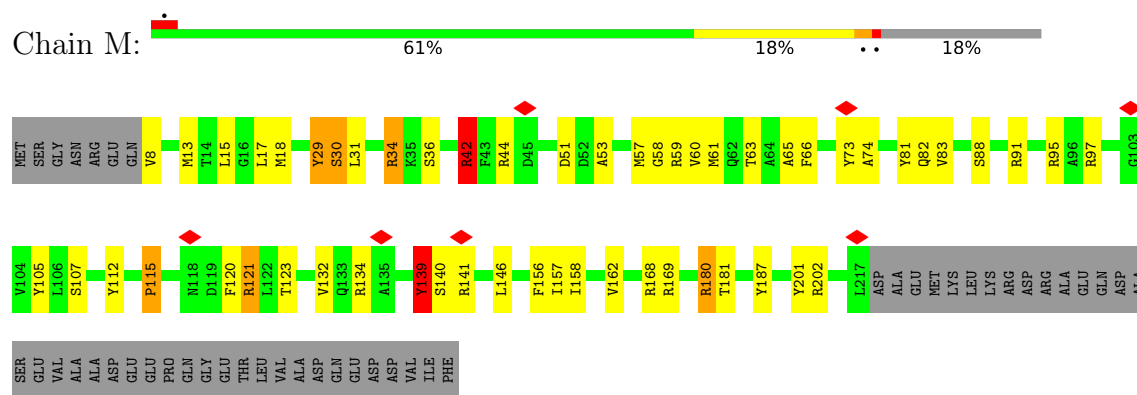




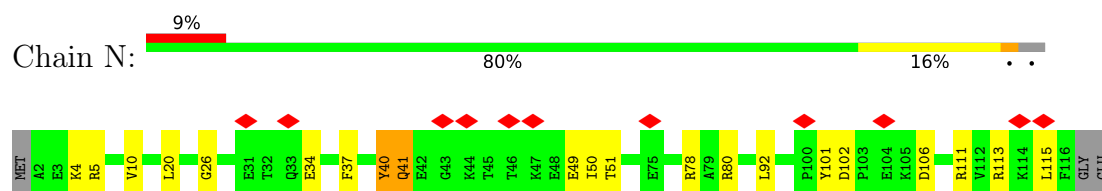
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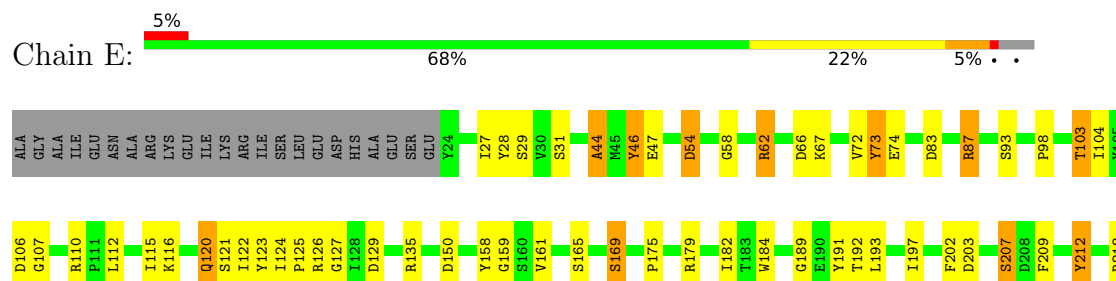
- Molecule 3: V-type proton ATPase subunit D



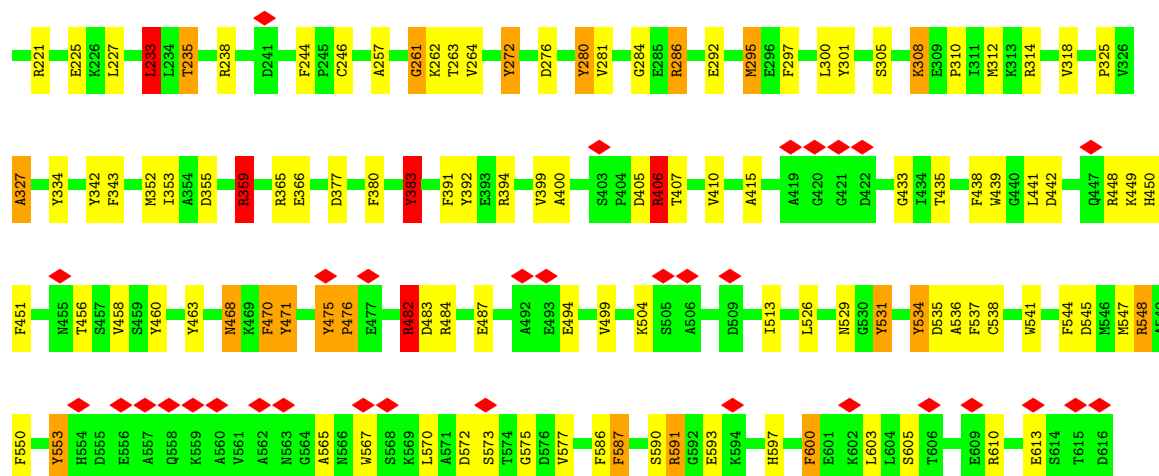
- Molecule 4: V-type proton ATPase subunit F



- Molecule 5: V-type proton ATPase catalytic subunit A

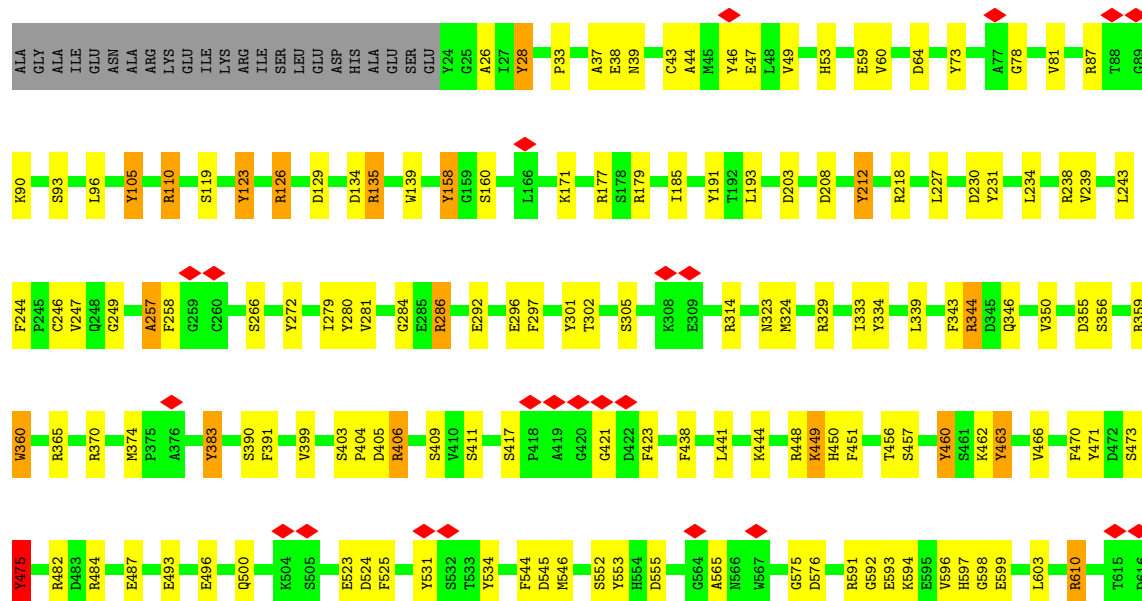






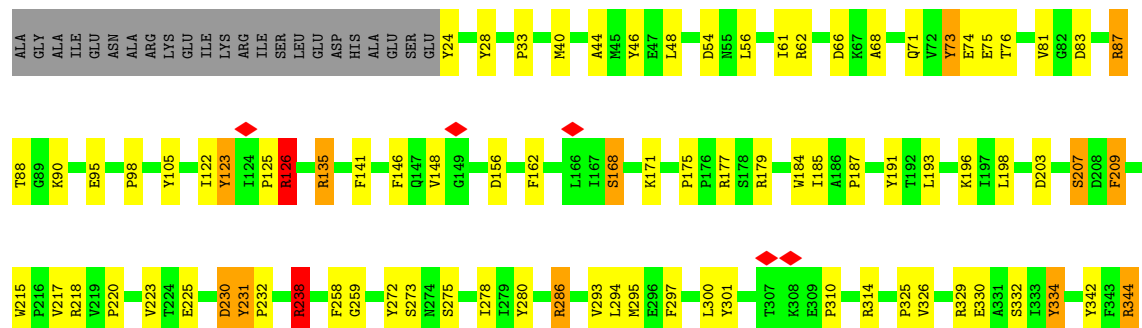
• Molecule 5: V-type proton ATPase catalytic subunit A

Chain A: 72% 21%

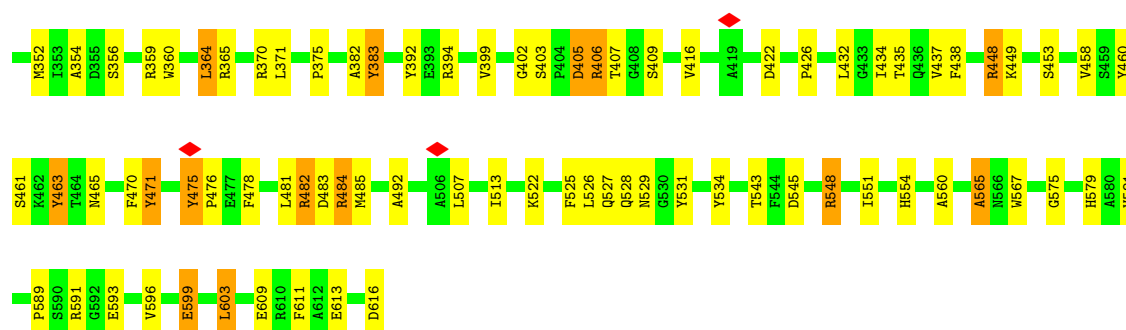


• Molecule 5: V-type proton ATPase catalytic subunit A

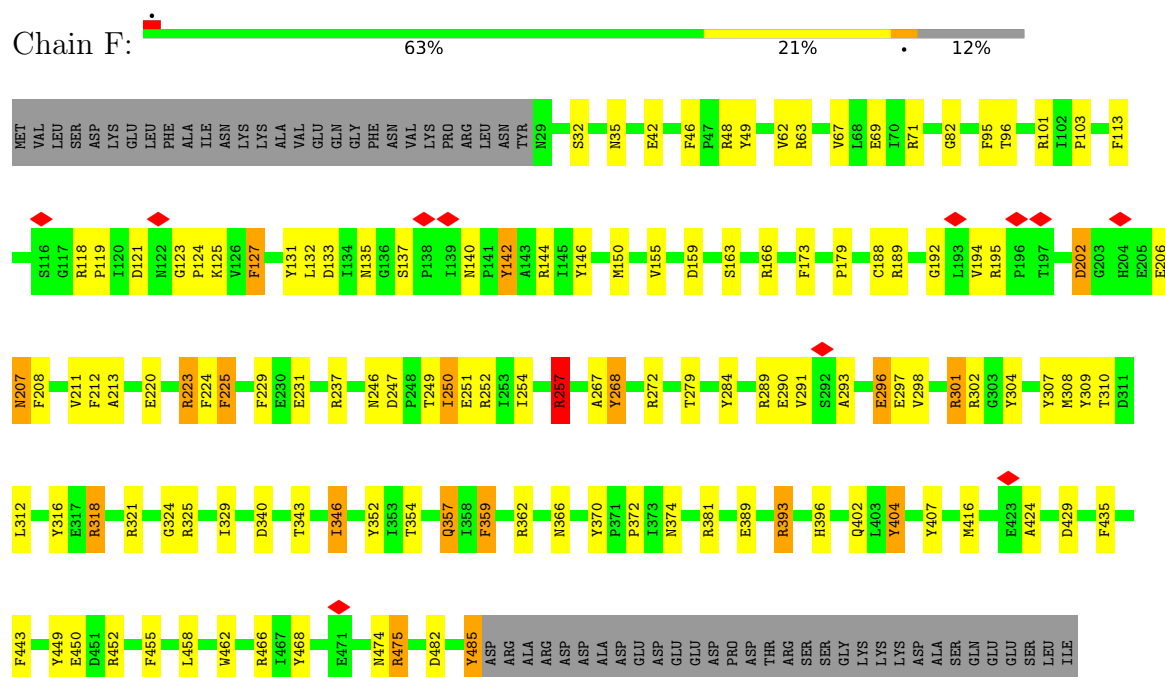
Chain C: 70% 22%



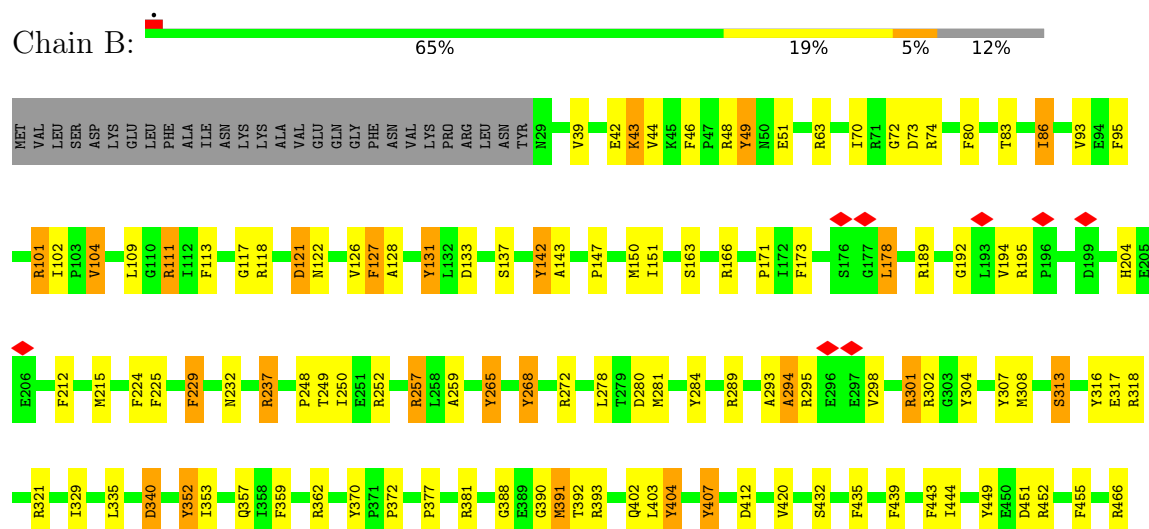




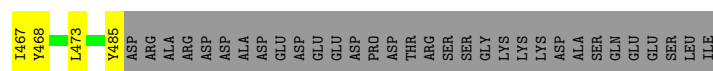
• Molecule 6: V-type proton ATPase subunit B



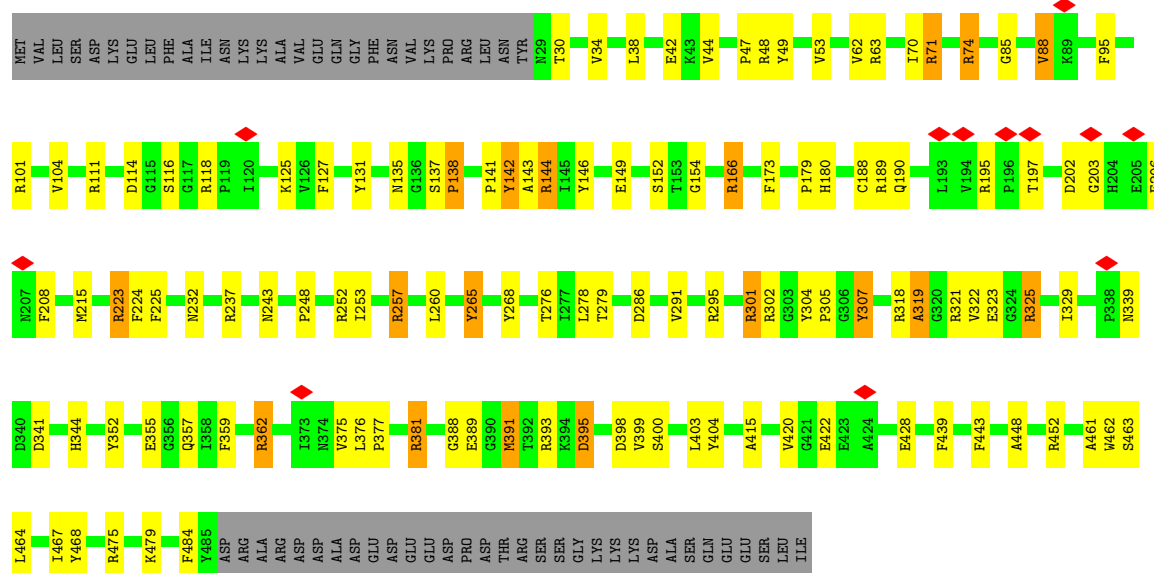
• Molecule 6: V-type proton ATPase subunit B



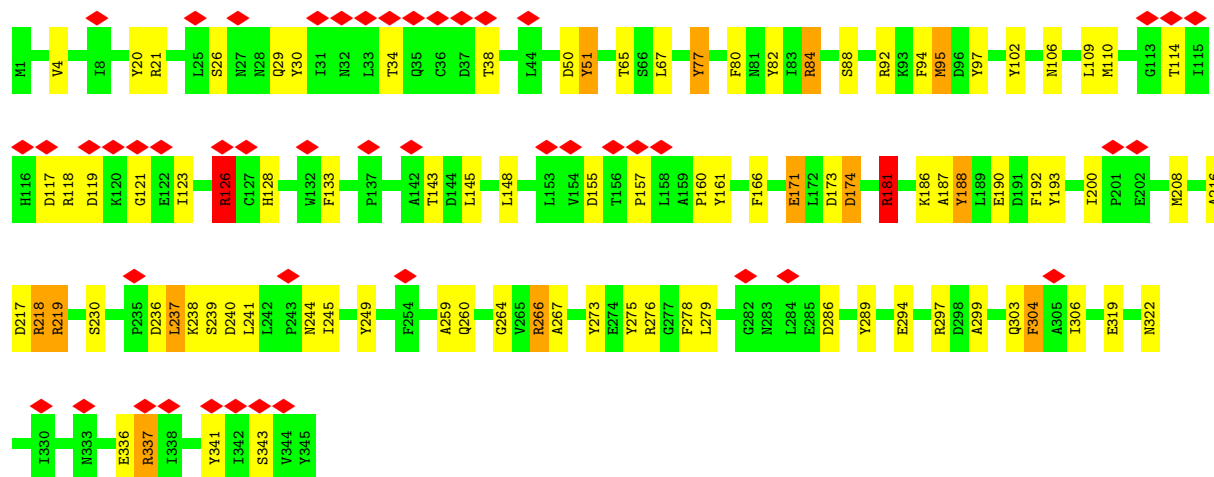
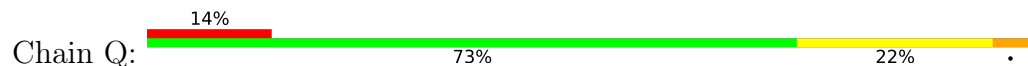




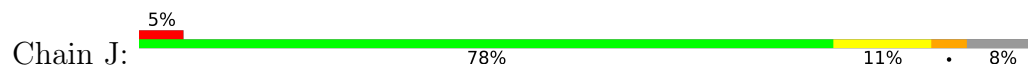
• Molecule 6: V-type proton ATPase subunit B



• Molecule 7: V-type proton ATPase subunit d




• Molecule 8: V-type proton ATPase subunit G






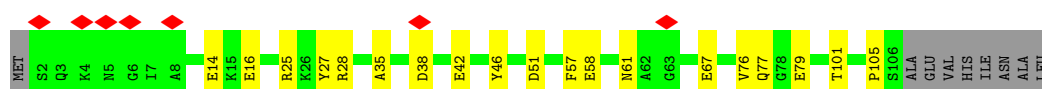
- Molecule 8: V-type proton ATPase subunit G

Chain L:  77% 13% 8%




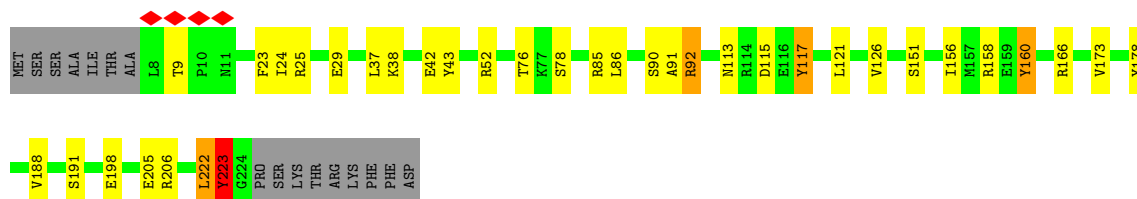
- Molecule 8: V-type proton ATPase subunit G

Chain H:  75% 17% 8%




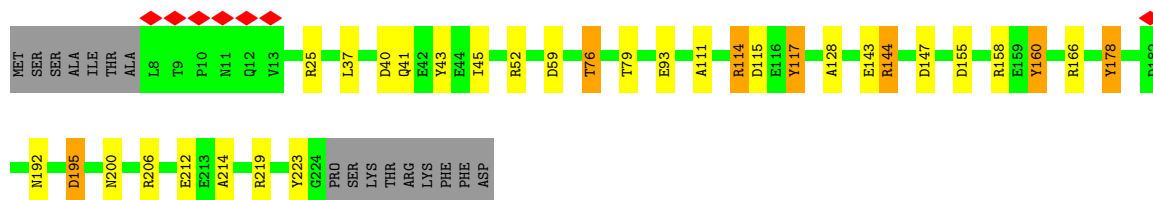
- Molecule 9: V-type proton ATPase subunit E

Chain I:  78% 13% 7%




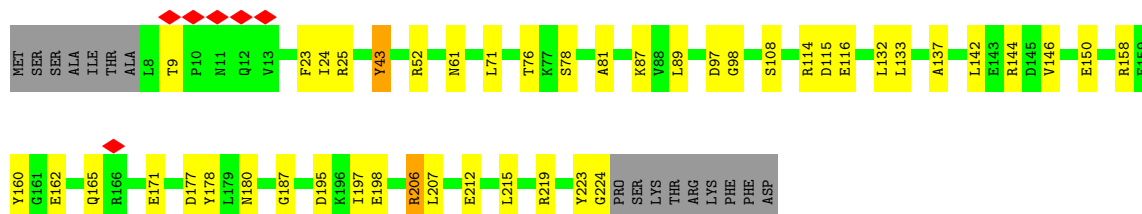
- Molecule 9: V-type proton ATPase subunit E

Chain K:  79% 11% 7%



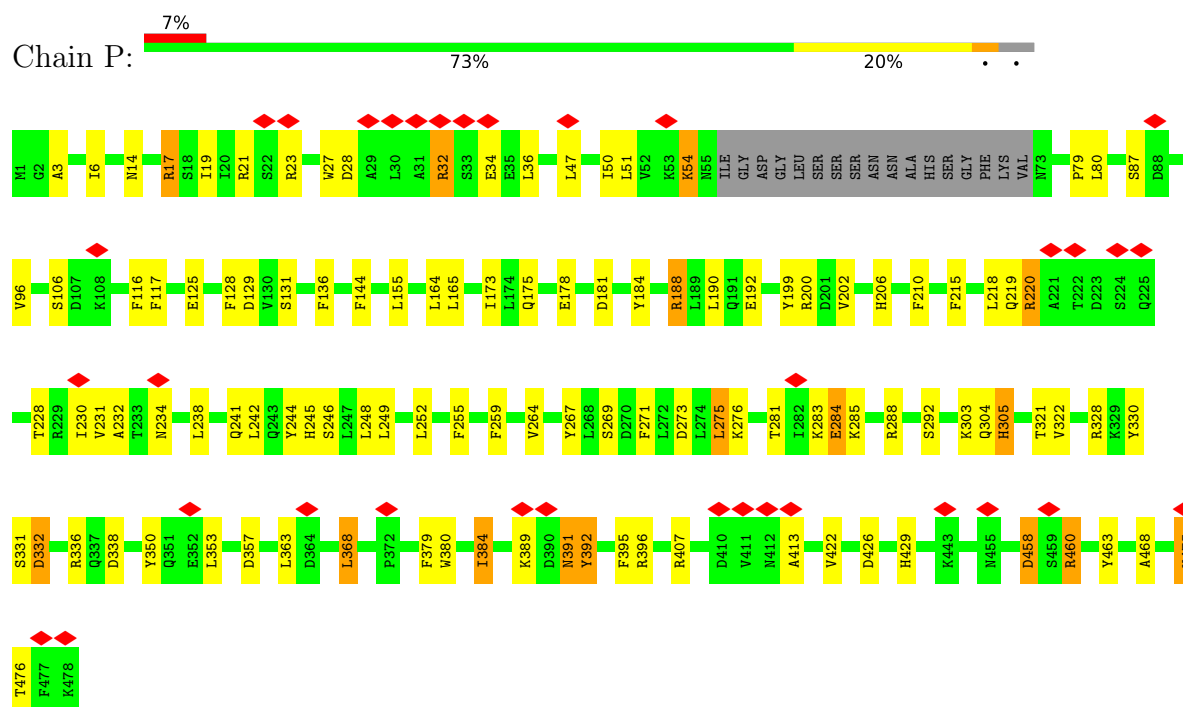
- Molecule 9: V-type proton ATPase subunit E

Chain G:  74% 18% 7%

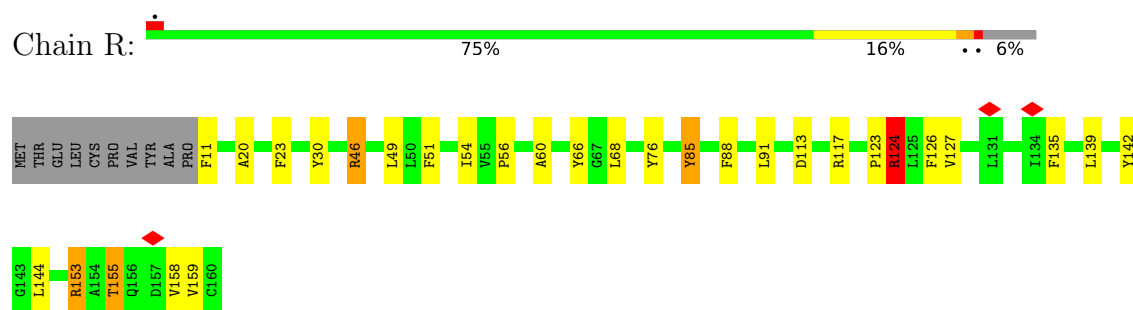


- Molecule 10: V-type proton ATPase subunit H

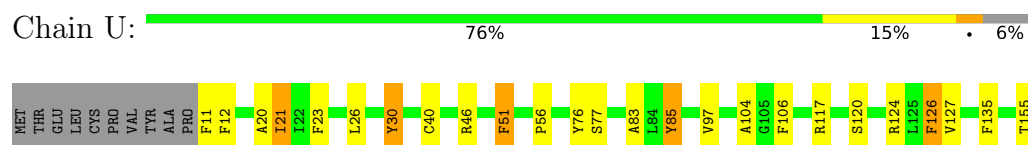




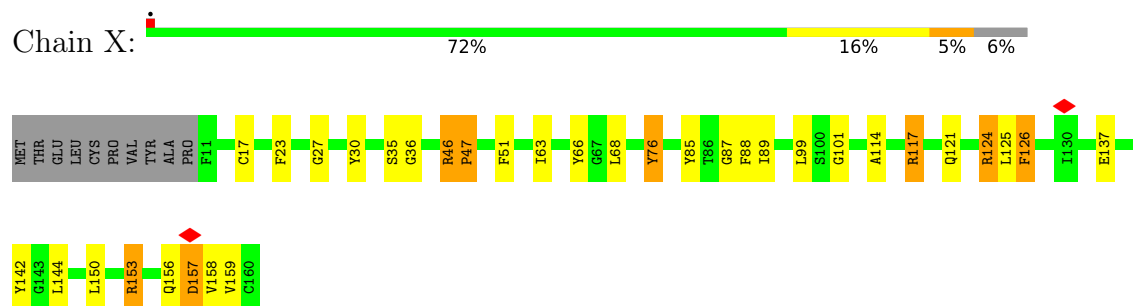
- Molecule 11: V-type proton ATPase subunit c



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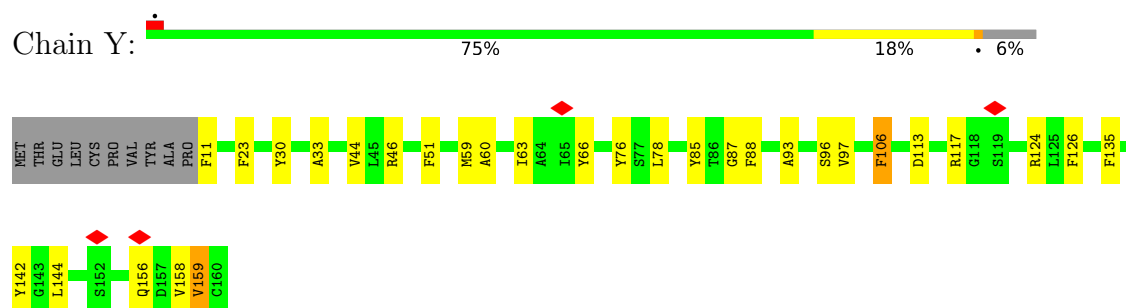


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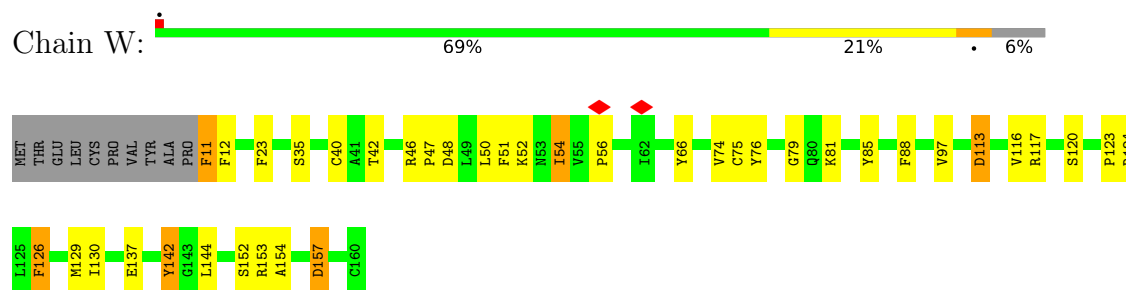




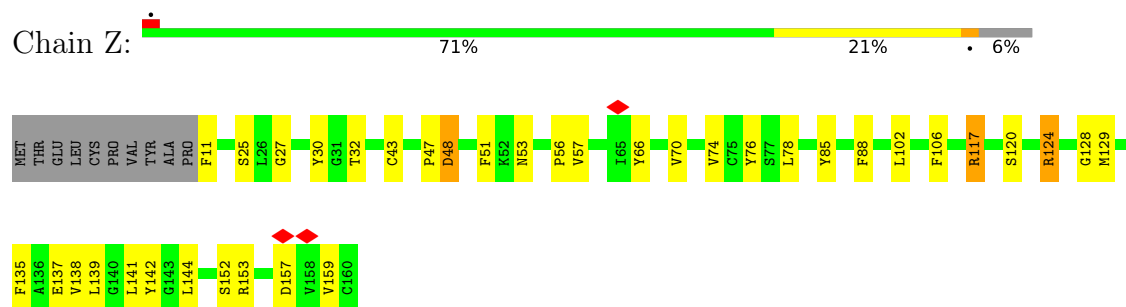
- Molecule 11: V-type proton ATPase subunit c



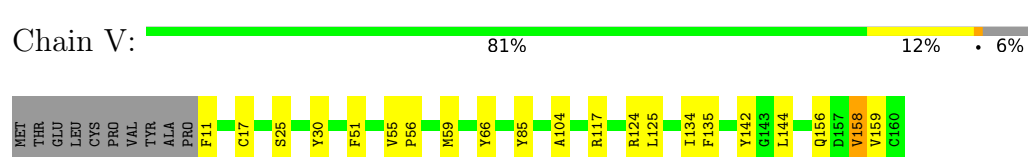
- Molecule 11: V-type proton ATPase subunit c



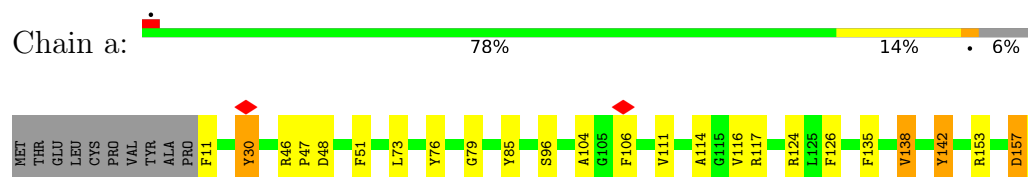
- Molecule 11: V-type proton ATPase subunit c



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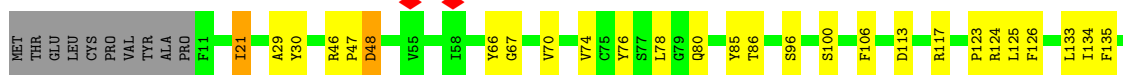
- Molecule 11: V-type proton ATPase subunit c



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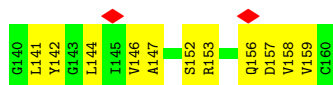
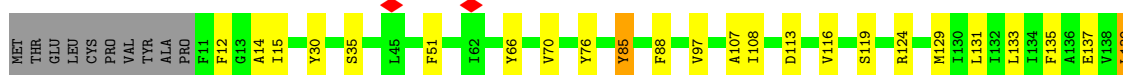


Chain S:  72% 20% 6%



- Molecule 11: V-type proton ATPase subunit c

Chain T:  72% 21% 6%





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17595	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	0.120	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	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	b	1.76	22/2578 (0.9%)	2.07	83/3479 (2.4%)
2	O	1.68	27/3185 (0.8%)	1.90	63/4314 (1.5%)
3	M	1.76	16/1710 (0.9%)	1.87	43/2295 (1.9%)
4	N	1.68	8/944 (0.8%)	1.83	14/1277 (1.1%)
5	A	1.72	46/4677 (1.0%)	1.95	105/6339 (1.7%)
5	C	1.71	35/4677 (0.7%)	1.96	108/6339 (1.7%)
5	E	1.75	61/4677 (1.3%)	1.97	125/6339 (2.0%)
6	B	1.72	38/3654 (1.0%)	1.99	90/4953 (1.8%)
6	D	1.72	31/3654 (0.8%)	1.98	88/4953 (1.8%)
6	F	1.74	34/3654 (0.9%)	1.91	90/4953 (1.8%)
7	Q	1.74	28/2861 (1.0%)	1.96	78/3880 (2.0%)
8	H	1.70	8/828 (1.0%)	1.76	10/1098 (0.9%)
8	J	1.63	5/828 (0.6%)	1.72	9/1098 (0.8%)
8	L	1.59	3/828 (0.4%)	1.76	13/1098 (1.2%)
9	G	1.68	12/1743 (0.7%)	1.86	33/2338 (1.4%)
9	I	1.70	10/1743 (0.6%)	1.84	30/2338 (1.3%)
9	K	1.67	9/1743 (0.5%)	1.84	29/2338 (1.2%)
10	P	1.68	25/3766 (0.7%)	1.87	74/5087 (1.5%)
11	R	1.63	3/1086 (0.3%)	2.03	30/1472 (2.0%)
11	S	1.77	7/1086 (0.6%)	1.79	19/1472 (1.3%)
11	T	1.60	4/1086 (0.4%)	1.97	25/1472 (1.7%)
11	U	1.65	6/1086 (0.6%)	2.05	23/1472 (1.6%)
11	V	1.67	4/1086 (0.4%)	1.84	17/1472 (1.2%)
11	W	1.67	9/1086 (0.8%)	1.95	30/1472 (2.0%)
11	X	1.72	7/1086 (0.6%)	1.86	22/1472 (1.5%)
11	Y	1.63	3/1086 (0.3%)	1.90	27/1472 (1.8%)
11	Z	1.68	7/1086 (0.6%)	1.87	18/1472 (1.2%)
11	a	1.68	7/1086 (0.6%)	1.97	24/1472 (1.6%)
All	All	1.70	475/58610 (0.8%)	1.93	1320/79236 (1.7%)

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	b	0	11
2	O	0	10
3	M	0	4
5	A	0	14
5	C	0	17
5	E	0	19
6	B	0	20
6	D	0	8
6	F	0	11
7	Q	0	6
8	J	0	2
8	L	0	1
9	G	0	4
9	I	0	3
9	K	0	4
10	P	0	9
11	R	0	3
11	S	0	1
11	T	0	1
11	U	0	3
11	W	0	1
11	X	0	7
11	Y	0	3
11	Z	0	2
11	a	0	3
All	All	0	167

The worst 5 of 475 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	393	ARG	CZ-NH2	9.92	1.46	1.33
10	P	246	SER	CA-CB	9.62	1.67	1.52
6	B	257	ARG	NE-CZ	8.88	1.44	1.33
5	E	334	TYR	CE1-CZ	8.71	1.49	1.38
6	F	101	ARG	CZ-NH1	8.52	1.44	1.33

The worst 5 of 1320 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	62	ARG	NE-CZ-NH1	19.24	129.92	120.30
11	U	12	PHE	CB-CG-CD1	18.18	133.52	120.80
1	b	285	TYR	CB-CG-CD1	16.96	131.18	121.00
6	D	325	ARG	NE-CZ-NH2	-16.76	111.92	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	285	TYR	CB-CG-CD2	-16.54	111.07	121.00

There are no chirality outliers.

5 of 167 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	b	61	ARG	Sidechain
1	b	69	TYR	Sidechain
1	b	73	TYR	Sidechain
1	b	86	GLY	Peptide
1	b	91	TYR	Sidechain

## 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	b	2540	0	2537	0	0
2	O	3122	0	3155	6	0
3	M	1691	0	1740	7	0
4	N	928	0	926	1	0
5	A	4578	0	4519	15	0
5	C	4578	0	4519	23	0
5	E	4578	0	4519	20	0
6	B	3585	0	3567	11	0
6	D	3585	0	3567	14	0
6	F	3585	0	3567	14	0
7	Q	2802	0	2689	11	0
8	H	824	0	877	1	0
8	J	824	0	877	0	0
8	L	824	0	877	0	0
9	G	1731	0	1797	2	0
9	I	1731	0	1797	6	0
9	K	1731	0	1797	2	0
10	P	3712	0	3829	13	0
11	R	1071	0	1141	5	0
11	S	1071	0	1141	4	0
11	T	1071	0	1141	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	U	1071	0	1141	0	0
11	V	1071	0	1141	2	0
11	W	1071	0	1141	8	0
11	X	1071	0	1141	7	0
11	Y	1071	0	1141	2	0
11	Z	1071	0	1141	7	0
11	a	1071	0	1141	0	0
All	All	57659	0	58566	169	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 169 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:S:66:TYR:HB3	11:S:144:LEU:HD22	1.32	1.07
11:T:66:TYR:HB3	11:T:144:LEU:HD22	1.36	1.06
11:X:66:TYR:HB3	11:X:144:LEU:HD22	1.38	1.02
11:R:66:TYR:HB3	11:R:144:LEU:HD22	1.45	0.97
11:X:66:TYR:CB	11:X:144:LEU:HD22	2.05	0.86

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	b	306/840 (36%)	283 (92%)	16 (5%)	7 (2%)	6	34
2	O	390/392 (100%)	359 (92%)	19 (5%)	12 (3%)	4	27
3	M	208/256 (81%)	201 (97%)	6 (3%)	1 (0%)	29	69
4	N	113/118 (96%)	103 (91%)	8 (7%)	2 (2%)	8	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	591/616 (96%)	543 (92%)	34 (6%)	14 (2%)	6	33
5	C	591/616 (96%)	540 (91%)	35 (6%)	16 (3%)	5	31
5	E	591/616 (96%)	536 (91%)	43 (7%)	12 (2%)	7	38
6	B	455/517 (88%)	415 (91%)	32 (7%)	8 (2%)	8	40
6	D	455/517 (88%)	406 (89%)	34 (8%)	15 (3%)	4	26
6	F	455/517 (88%)	405 (89%)	39 (9%)	11 (2%)	6	33
7	Q	343/345 (99%)	312 (91%)	24 (7%)	7 (2%)	7	38
8	H	103/114 (90%)	101 (98%)	0	2 (2%)	8	38
8	J	103/114 (90%)	99 (96%)	2 (2%)	2 (2%)	8	38
8	L	103/114 (90%)	99 (96%)	2 (2%)	2 (2%)	8	38
9	G	215/233 (92%)	205 (95%)	8 (4%)	2 (1%)	17	57
9	I	215/233 (92%)	209 (97%)	6 (3%)	0	100	100
9	K	215/233 (92%)	207 (96%)	5 (2%)	3 (1%)	11	46
10	P	457/478 (96%)	429 (94%)	19 (4%)	9 (2%)	7	38
11	R	148/160 (92%)	138 (93%)	6 (4%)	4 (3%)	5	31
11	S	148/160 (92%)	139 (94%)	7 (5%)	2 (1%)	11	46
11	T	148/160 (92%)	137 (93%)	7 (5%)	4 (3%)	5	31
11	U	148/160 (92%)	135 (91%)	10 (7%)	3 (2%)	7	38
11	V	148/160 (92%)	139 (94%)	7 (5%)	2 (1%)	11	46
11	W	148/160 (92%)	143 (97%)	4 (3%)	1 (1%)	22	63
11	X	148/160 (92%)	138 (93%)	6 (4%)	4 (3%)	5	31
11	Y	148/160 (92%)	140 (95%)	5 (3%)	3 (2%)	7	38
11	Z	148/160 (92%)	138 (93%)	6 (4%)	4 (3%)	5	31
11	a	148/160 (92%)	136 (92%)	8 (5%)	4 (3%)	5	31
All	All	7389/8469 (87%)	6835 (92%)	398 (5%)	156 (2%)	10	36

5 of 156 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	167	THR
2	O	172	VAL
5	E	475	TYR
6	F	125	LYS
6	F	207	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	b	275/728 (38%)	261 (95%)	14 (5%)	24	48
2	O	348/348 (100%)	345 (99%)	3 (1%)	78	87
3	M	183/221 (83%)	177 (97%)	6 (3%)	38	61
4	N	102/104 (98%)	100 (98%)	2 (2%)	55	74
5	A	497/515 (96%)	480 (97%)	17 (3%)	37	60
5	C	497/515 (96%)	477 (96%)	20 (4%)	31	55
5	E	497/515 (96%)	473 (95%)	24 (5%)	25	51
6	B	391/444 (88%)	374 (96%)	17 (4%)	29	53
6	D	391/444 (88%)	377 (96%)	14 (4%)	35	59
6	F	391/444 (88%)	373 (95%)	18 (5%)	27	52
7	Q	309/309 (100%)	302 (98%)	7 (2%)	50	70
8	H	87/94 (93%)	86 (99%)	1 (1%)	73	84
8	J	87/94 (93%)	83 (95%)	4 (5%)	27	52
8	L	87/94 (93%)	85 (98%)	2 (2%)	50	70
9	G	194/208 (93%)	191 (98%)	3 (2%)	65	80
9	I	194/208 (93%)	193 (100%)	1 (0%)	88	93
9	K	194/208 (93%)	192 (99%)	2 (1%)	76	86
10	P	426/439 (97%)	413 (97%)	13 (3%)	40	62
11	R	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	S	110/119 (92%)	102 (93%)	8 (7%)	14	39
11	T	110/119 (92%)	106 (96%)	4 (4%)	35	59
11	U	110/119 (92%)	104 (94%)	6 (6%)	21	47
11	V	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	W	110/119 (92%)	104 (94%)	6 (6%)	21	47
11	X	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	Y	110/119 (92%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	Z	110/119 (92%)	107 (97%)	3 (3%)	44	65
11	a	110/119 (92%)	109 (99%)	1 (1%)	78	87
All	All	6250/7122 (88%)	6045 (97%)	205 (3%)	41	61

5 of 205 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	C	478	PHE
8	J	52	LYS
11	S	148	LEU
5	C	593	GLU
6	D	362	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
5	C	71	GLN
11	Y	151	ASN
6	D	190	GLN
11	U	90	GLN
11	a	151	ASN

### 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.



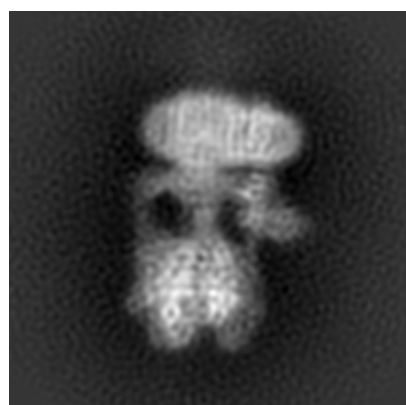
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6286. These allow visual inspection of the internal detail of the map and identification of artifacts.

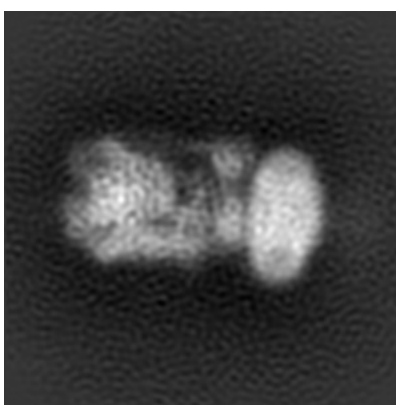
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

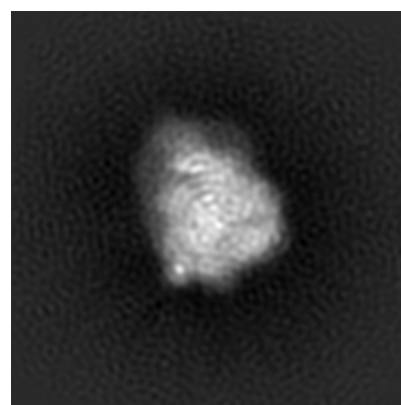
#### 6.1.1 Primary map



X



Y

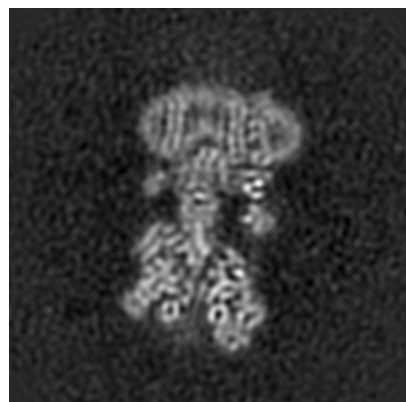


Z

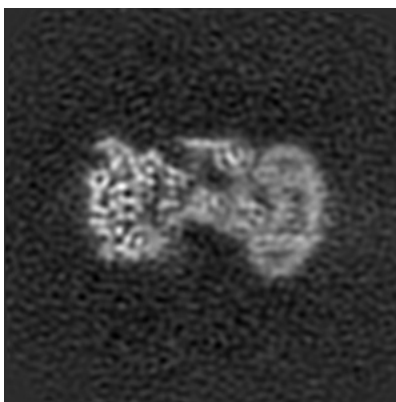
The images above show the map projected in three orthogonal directions.

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

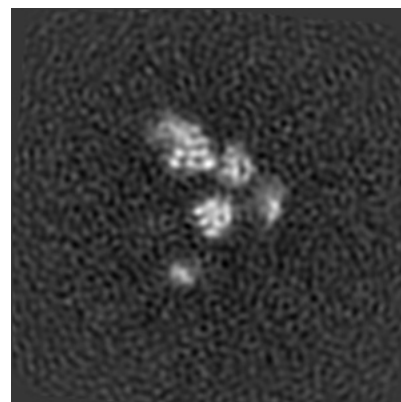
#### 6.2.1 Primary map



X Index: 128



Y Index: 128



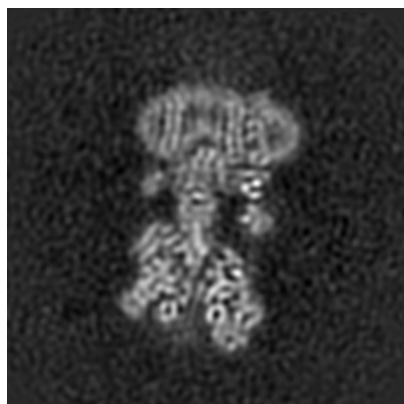
Z Index: 128



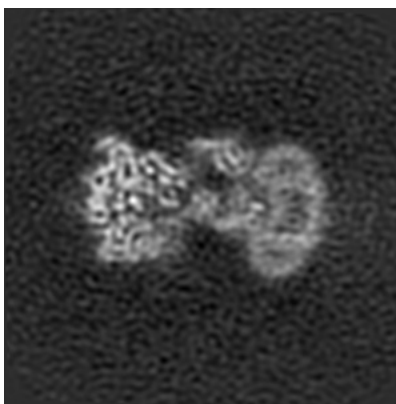
The images above show central slices of the map in three orthogonal directions.

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

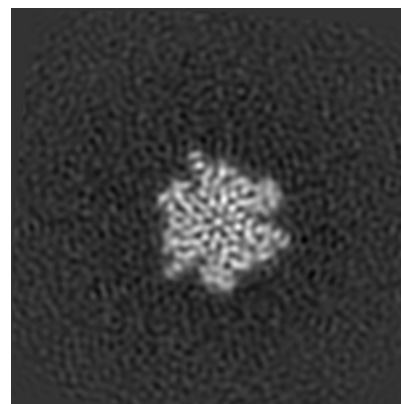
### 6.3.1 Primary map



X Index: 128



Y Index: 130



Z Index: 74

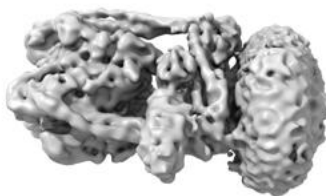
The images above show the largest variance slices of the map in three orthogonal directions.

## 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

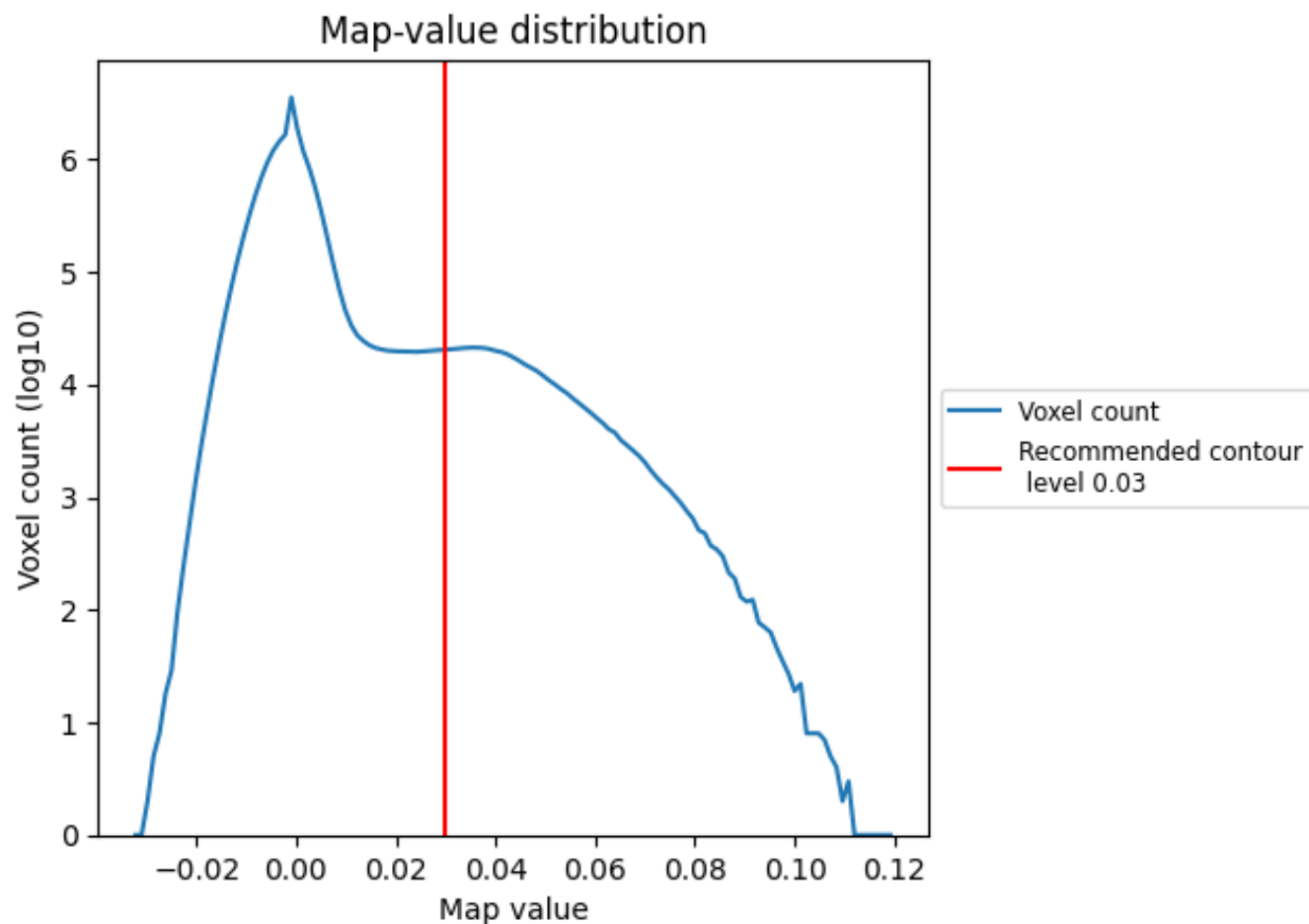
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

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

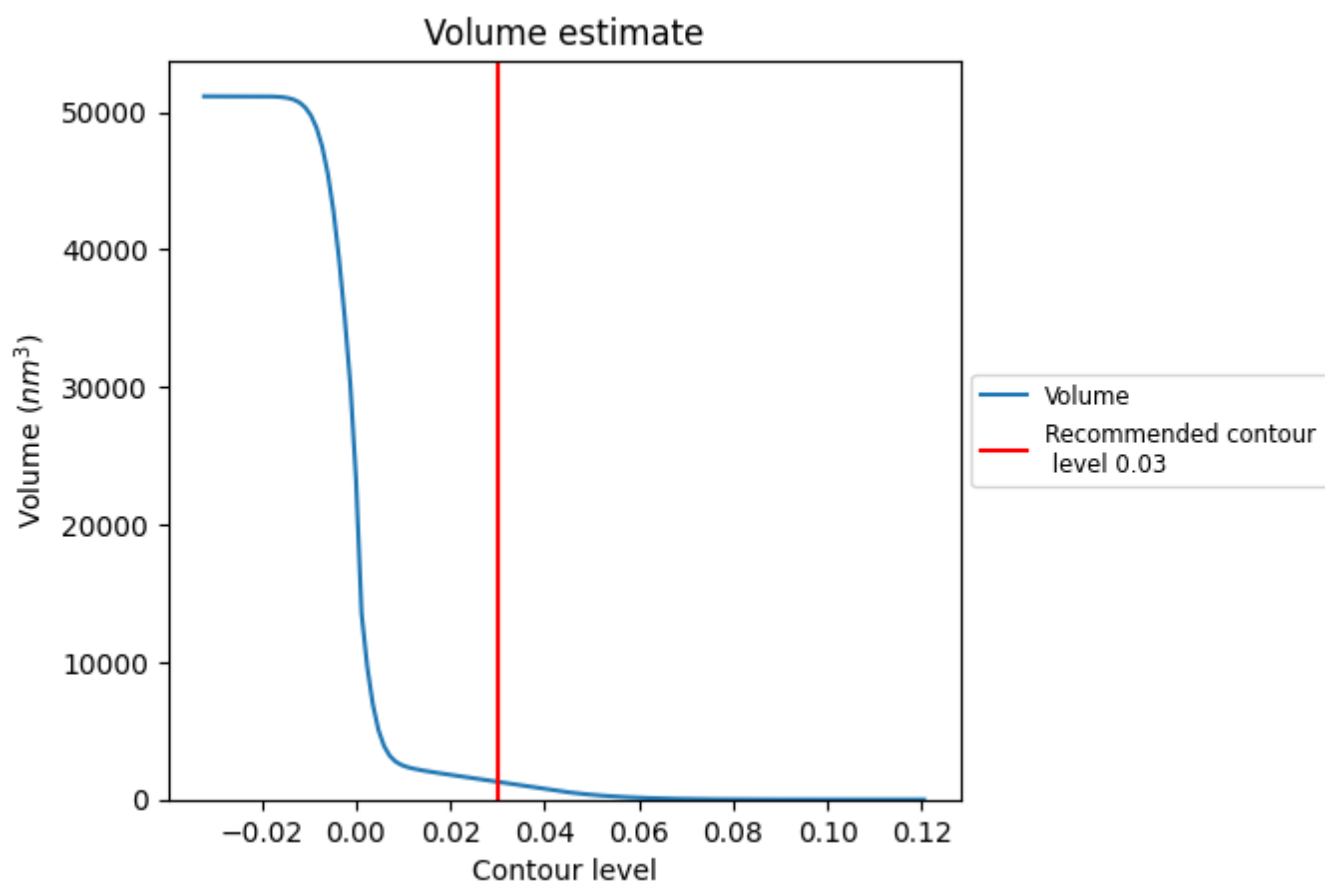
### 7.1 Map-value distribution [i](#)



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](#)

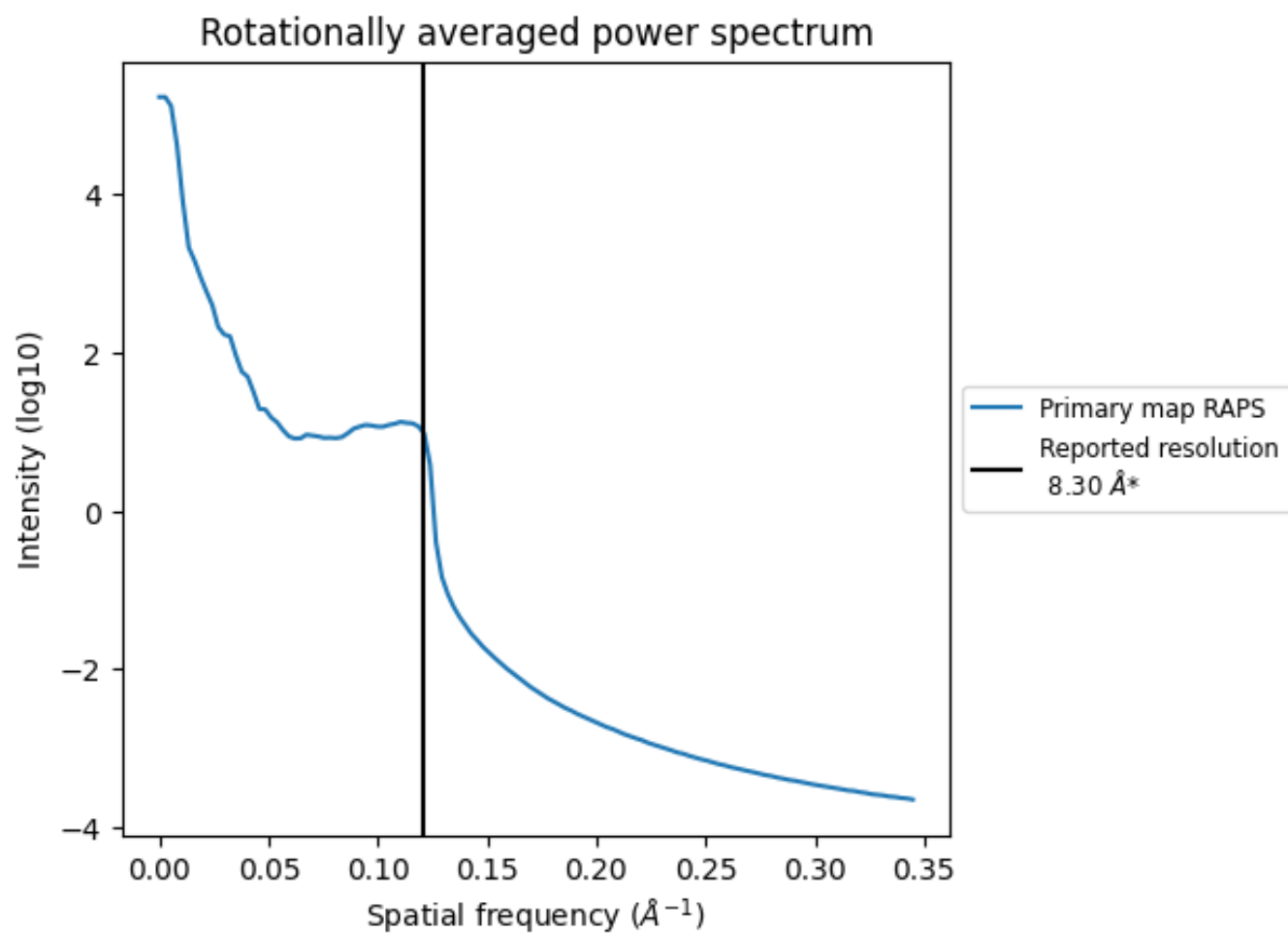


The volume at the recommended contour level is 1299 nm<sup>3</sup>; this corresponds to an approximate mass of 1174 kDa.

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 ⓘ



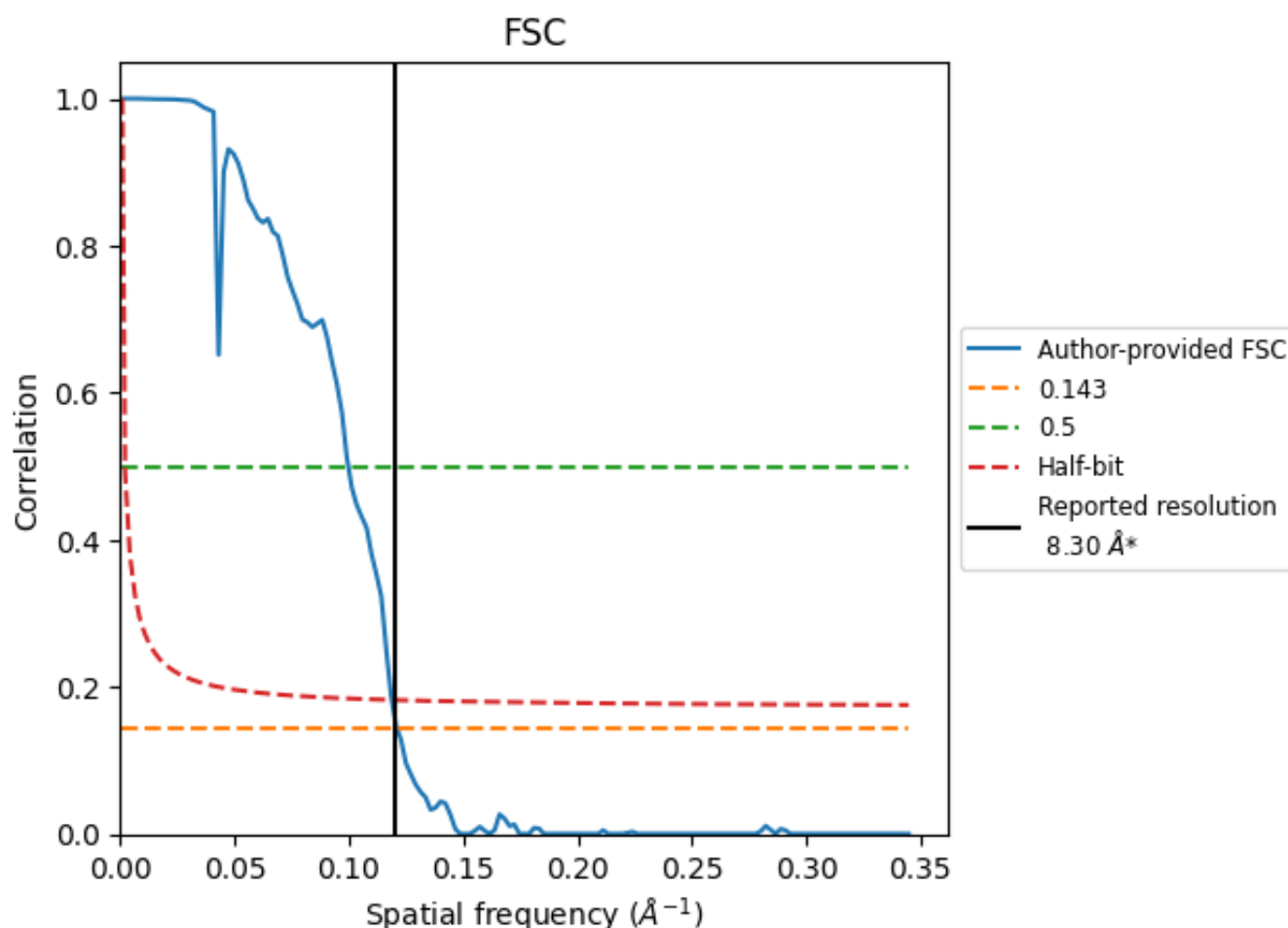
\*Reported resolution corresponds to spatial frequency of 0.120 Å<sup>-1</sup>



## 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 0.120 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.30	-	-
Author-provided FSC curve	8.26	10.02	8.42
Unmasked-calculated*	-	-	-

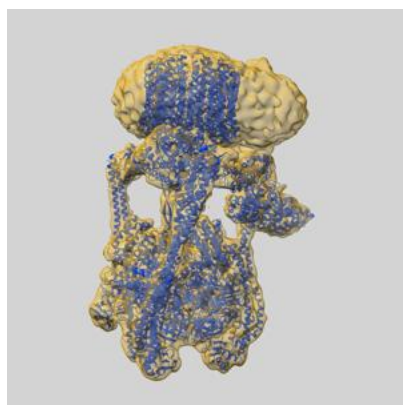
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



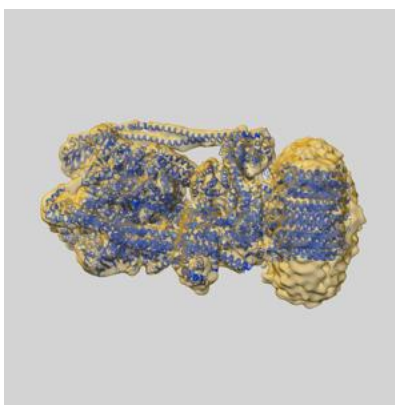
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-6286 and PDB model 3J9V. Per-residue inclusion information can be found in section [3](#) on page [7](#).

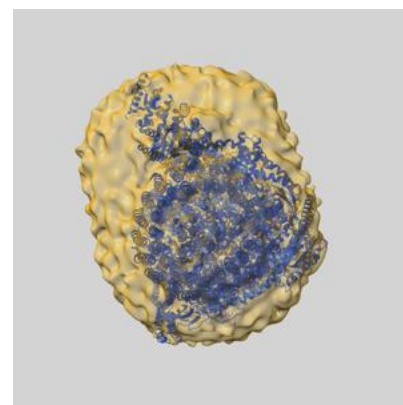
### 9.1 Map-model overlay [i](#)



X



Y

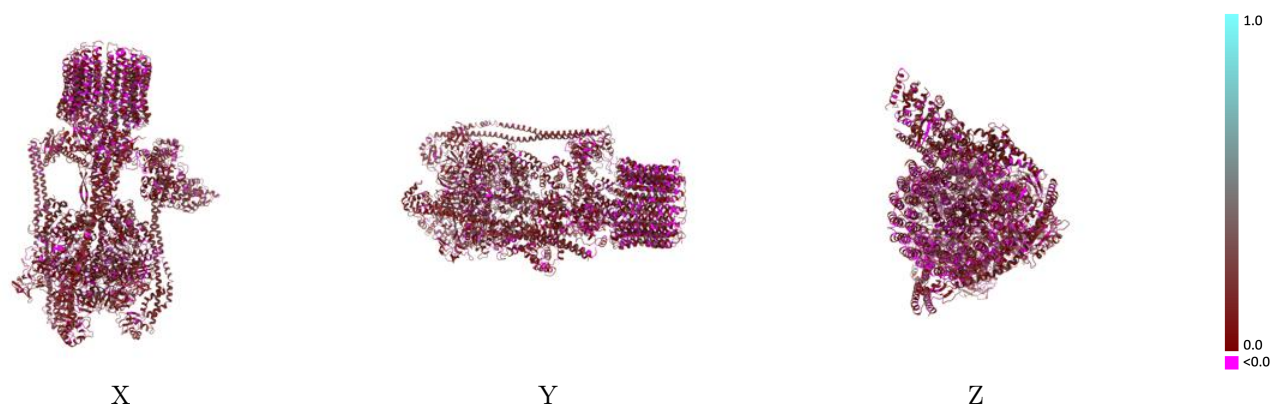


Z

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.

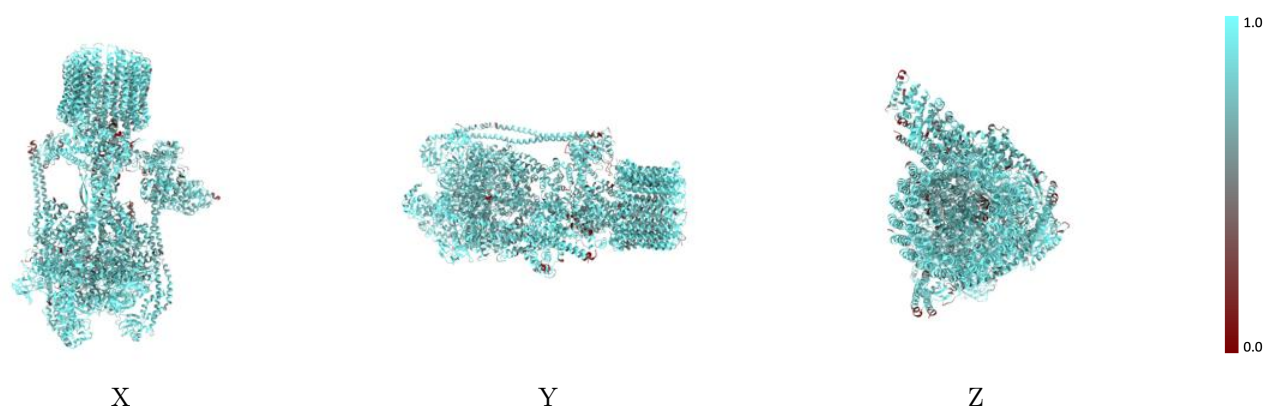


## 9.2 Q-score mapped to coordinate model [i](#)



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.

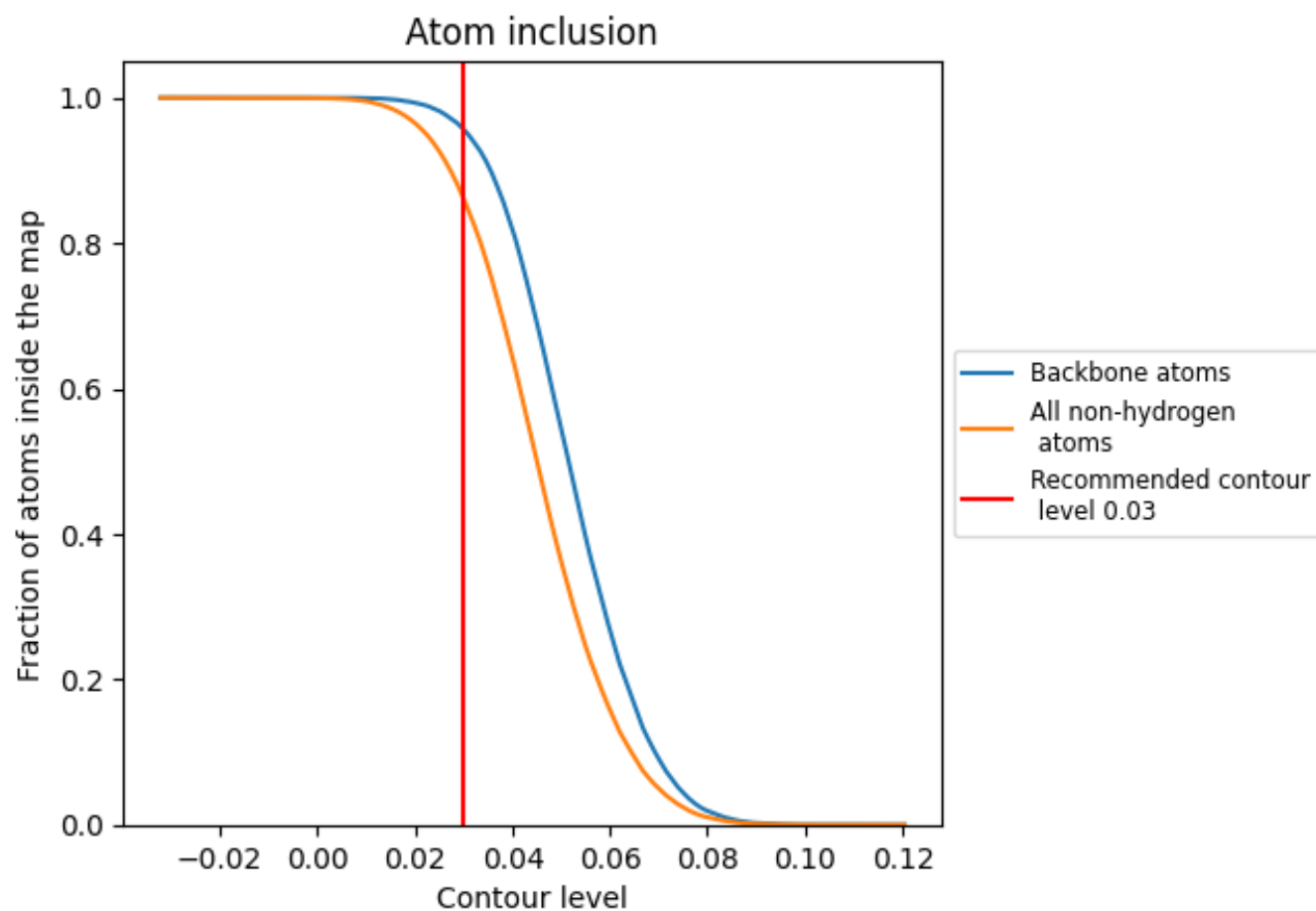
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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, 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8608	 0.1150
A	 0.8810	 0.1250
B	 0.8729	 0.1170
C	 0.8799	 0.1280
D	 0.8540	 0.1180
E	 0.8481	 0.1260
F	 0.8780	 0.1140
G	 0.8529	 0.1400
H	 0.7897	 0.1460
I	 0.8681	 0.1490
J	 0.8007	 0.1560
K	 0.8669	 0.1430
L	 0.8142	 0.1600
M	 0.8458	 0.1150
N	 0.8107	 0.1060
O	 0.8046	 0.1150
P	 0.8295	 0.1260
Q	 0.7696	 0.0740
R	 0.9234	 0.0670
S	 0.9310	 0.0500
T	 0.9093	 0.1000
U	 0.9376	 0.0970
V	 0.9518	 0.0850
W	 0.9386	 0.0670
X	 0.9282	 0.0780
Y	 0.8885	 0.1050
Z	 0.8724	 0.0920
a	 0.8989	 0.0920
b	 0.8381	 0.1140

