



## wwPDB EM Validation Summary Report ⓘ

Nov 21, 2022 – 10:38 PM EST

PDB ID : 7U8O  
EMDB ID : EMD-26385  
Title : Structure of porcine V-ATPase with mEAK7 and SidK, Rotary state 2  
Authors : Tan, Y.Z.; Keon, K.A.  
Deposited on : 2022-03-09  
Resolution : 3.50 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](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

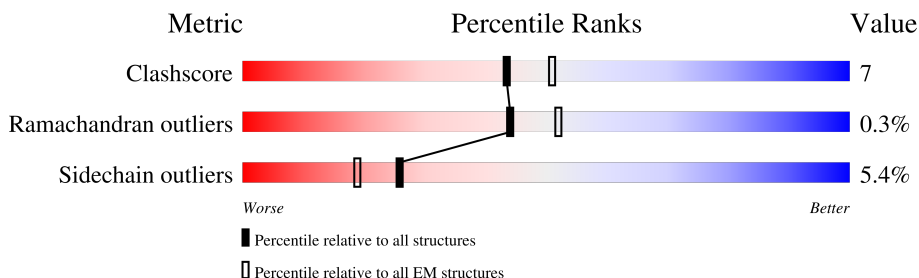
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.50 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.
















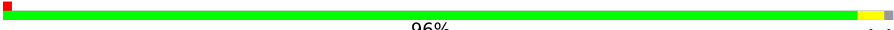

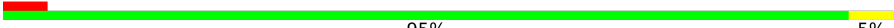
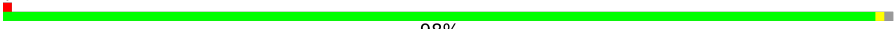



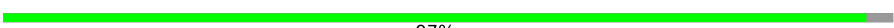

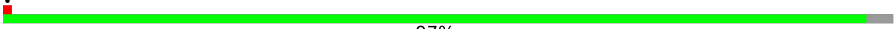


Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	A	617	
1	B	617	
1	C	617	
2	D	515	
2	E	515	
2	F	515	
3	G	382	
4	H	247	

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Mol	Chain	Length	Quality of chain
5	I	226	 79% 17%
5	J	226	 82% 13%
5	K	226	 79% 16%
6	L	119	 6% 67% 22% 8%
7	M	118	 85% 8% 7%
7	N	118	 86% 6% 7%
7	O	118	 84% 8% 8%
8	Q	337	 60% 7% 34%
8	R	337	 53% 8% 39%
8	S	337	 55% 11% 33%
9	T	483	 13% 88% 12%
10	U	456	 74% 10% 16%
11	a	838	 86% 11%
12	b	205	 96%
13	c	469	 39% 56%
14	d	351	 5% 95% 5%
15	e	81	 98%
16	f	98	 86% 14%
17	g	155	 94%
17	h	155	 93%
17	i	155	 97%
17	j	155	 94%
17	k	155	 97%
17	l	155	 93%
17	m	155	 88% 9%

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Mol	Chain	Length	Quality of chain
17	n	155	<div><div></div><div>93%</div><div></div></div>
17	o	155	<div><div></div><div>93%</div><div></div></div>
18	p	351	<div><div></div><div>15%</div><div></div><div>85%</div></div>

## 2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 68632 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	600	Total	C	N	O	S	0	0
			4661	2957	790	889	25		
1	B	588	Total	C	N	O	S	0	0
			4579	2903	777	875	24		
1	C	587	Total	C	N	O	S	0	0
			4577	2904	776	873	24		

- Molecule 2 is a protein called Vacuolar proton pump subunit B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	458	Total	C	N	O	S	0	0
			3590	2278	615	676	21		
2	E	456	Total	C	N	O	S	0	0
			3572	2266	611	674	21		
2	F	456	Total	C	N	O	S	0	0
			3572	2266	611	674	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	360	Total	C	N	O	S	0	0
			1791	1070	360	360	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	213	Total	C	N	O	S	0	0
			1717	1089	309	314	5		

- Molecule 5 is a protein called V-type proton ATPase subunit E 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	217	Total	C	N	O	S	0	0
			1614	1013	295	300	6		
5	J	218	Total	C	N	O	S	0	0
			1608	1008	296	298	6		
5	K	217	Total	C	N	O	S	0	0
			1707	1073	308	319	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	109	Total	C	N	O	S	0	0
			865	548	153	162	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	110	Total	C	N	O	S	0	0
			682	419	130	131	2		
7	N	110	Total	C	N	O	S	0	0
			661	404	128	128	1		
7	O	108	Total	C	N	O	S	0	0
			679	418	130	130	1		

- Molecule 8 is a protein called Bacterial effector protein SidK.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	224	Total	C	N	O	S	0	0
			1824	1162	306	346	10		
8	R	206	Total	C	N	O	S	0	0
			1685	1073	285	319	8		
8	S	226	Total	C	N	O	S	0	0
			1832	1167	308	346	11		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
9	T	427	Total	C	N	O	0	0
			2124	1268	428	428		

- Molecule 10 is a protein called TLDc protein mEAK-7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	U	383	Total	C	N	O	S	0	0
			2400	1481	449	459	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	750	Total	C	N	O	S	0	0
			5635	3662	947	991	35		

- Molecule 12 is a protein called V-type proton ATPase 21 kDa proteolipid subunit isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	b	203	Total	C	N	O	S	0	0
			1498	993	237	258	10		

- Molecule 13 is a protein called ATPase H<sup>+</sup> transporting accessory protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	c	205	Total	C	N	O	S	0	0
			1661	1084	269	301	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	d	350	Total	C	N	O	S	0	0
			2835	1829	462	530	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	80	Total	C	N	O	S	0	0
			652	451	98	98	5		

- Molecule 16 is a protein called Ribonuclease kappa.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	84	Total	C	N	O	S	0	0
			653	433	100	114	6		

- Molecule 17 is a protein called V-type proton ATPase proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	g	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	h	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	i	150	Total	C	N	O	S	0	0
			1052	695	164	186	7		
17	j	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	k	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	l	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	m	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	n	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		
17	o	150	Total	C	N	O	S	0	0
			1058	698	167	186	7		

- Molecule 18 is a protein called ATPase H(+)-transporting lysosomal accessory protein 2.

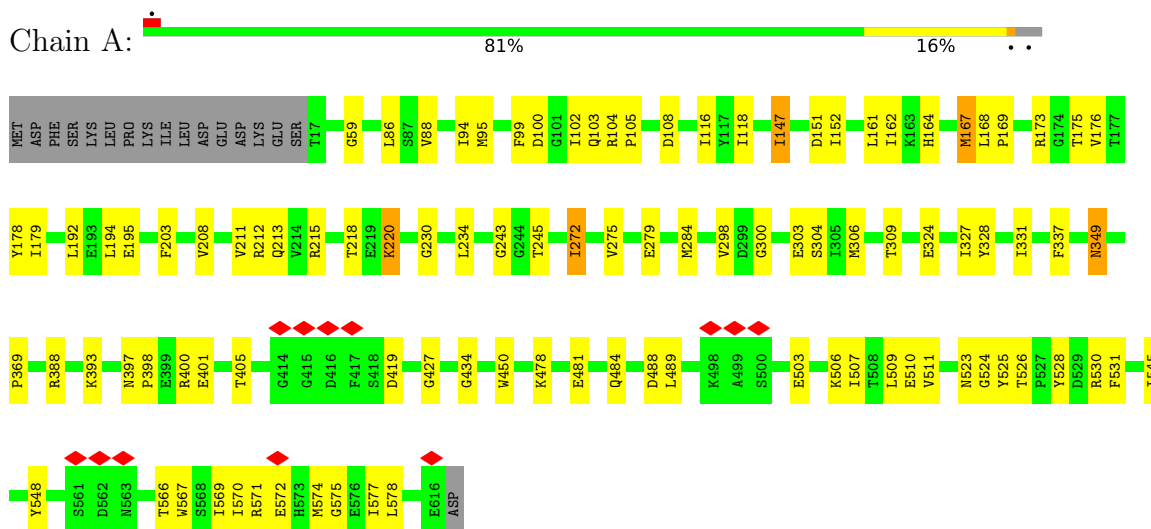
Mol	Chain	Residues	Atoms					AltConf	Trace
18	p	53	Total	C	N	O	S	0	0
			442	297	65	76	4		



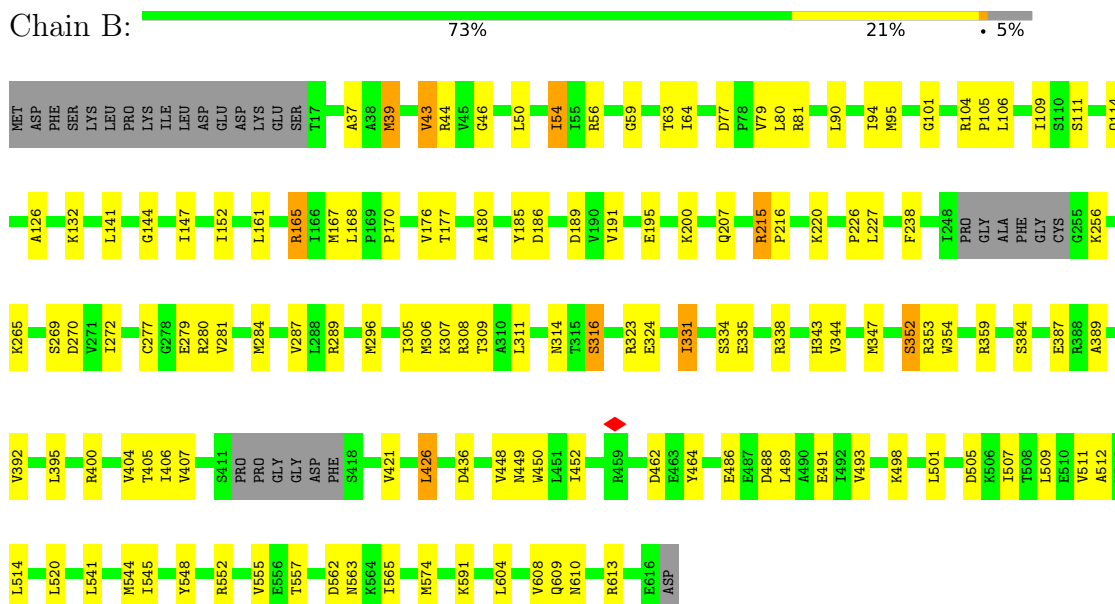
### 3 Residue-property plots

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.

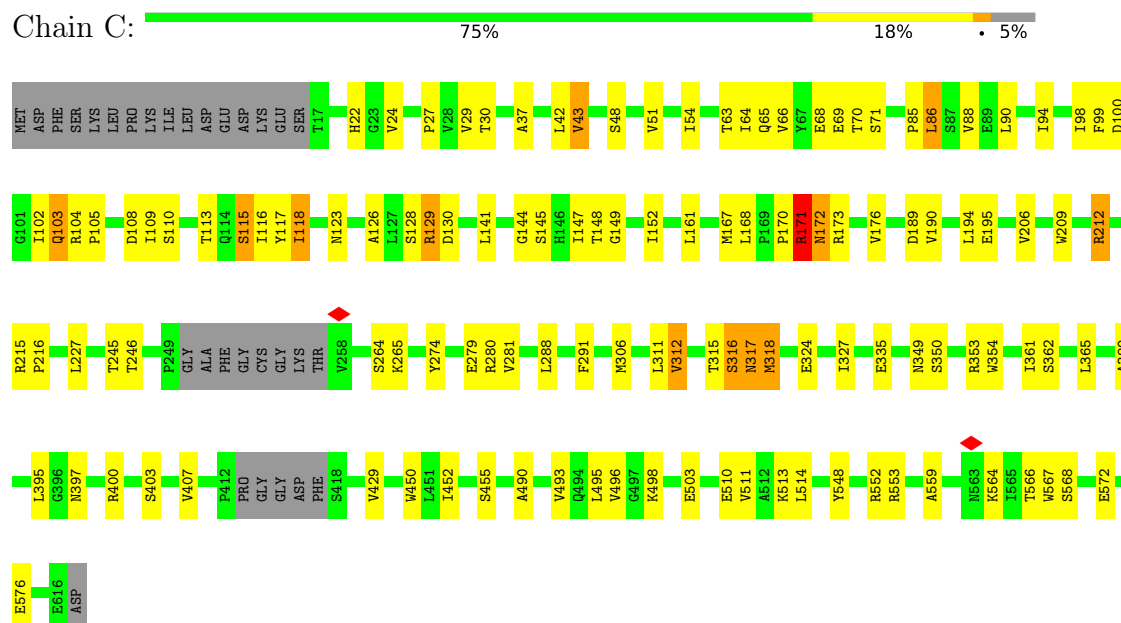
- Molecule 1: V-type proton ATPase catalytic subunit A



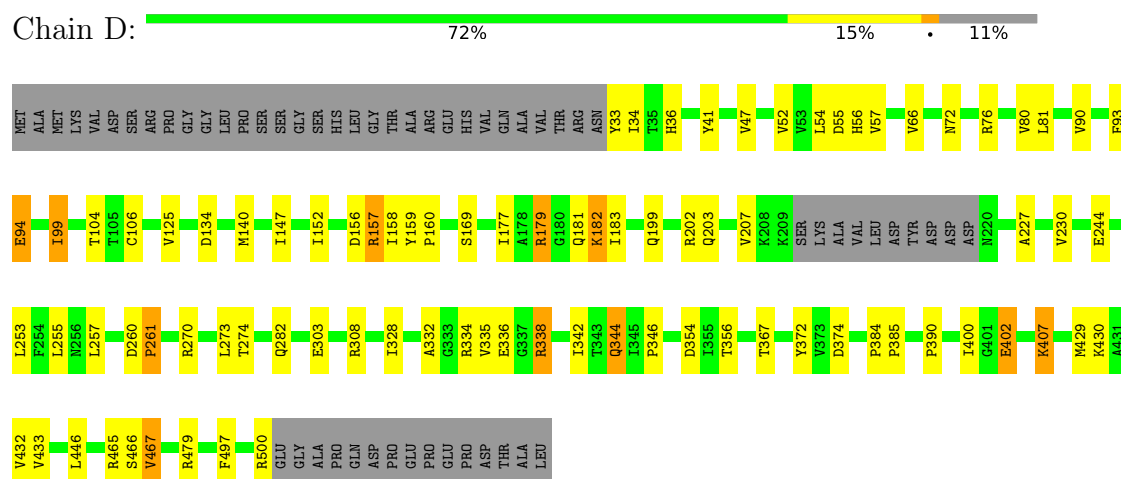
- Molecule 1: V-type proton ATPase catalytic subunit A



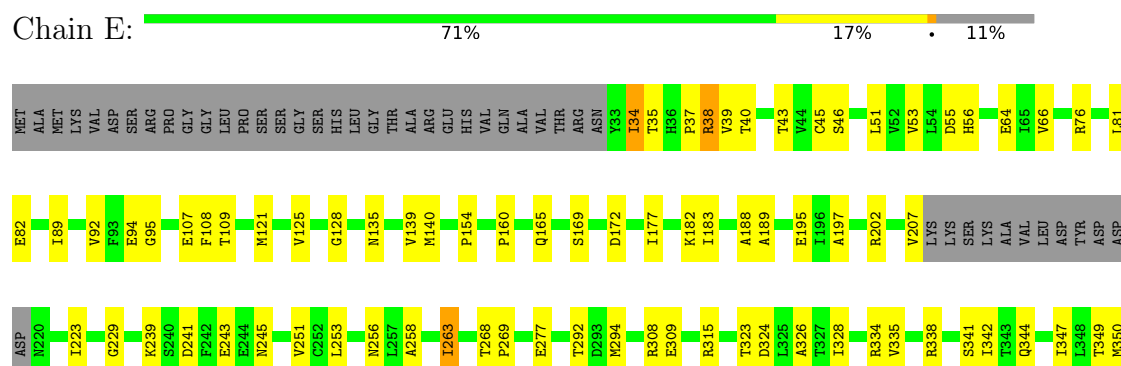
- Molecule 1: V-type proton ATPase catalytic subunit A



- Molecule 2: Vacuolar proton pump subunit B



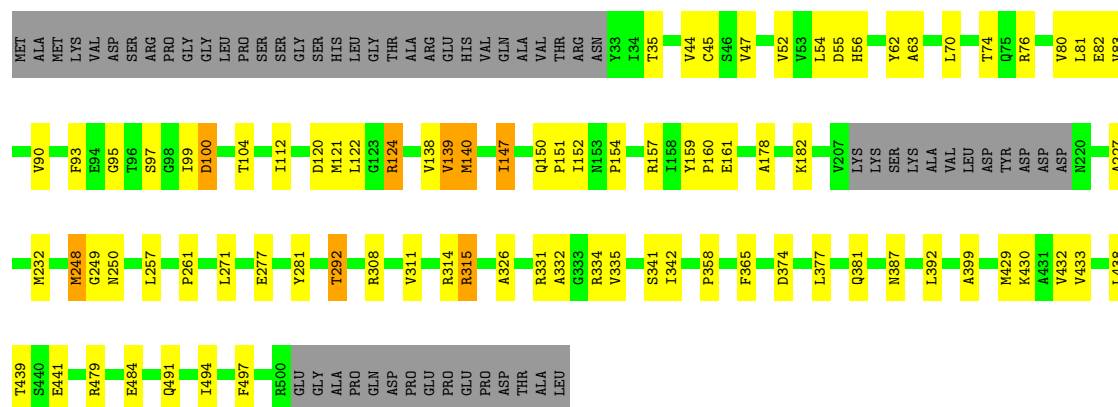
- Molecule 2: Vacuolar proton pump subunit B





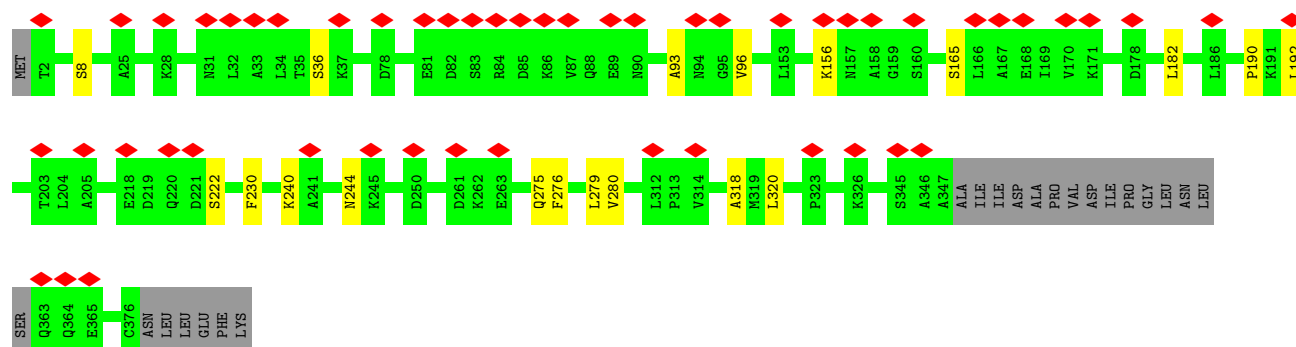
• Molecule 2: Vacuolar proton pump subunit B

Chain F: 72% 15% 11%



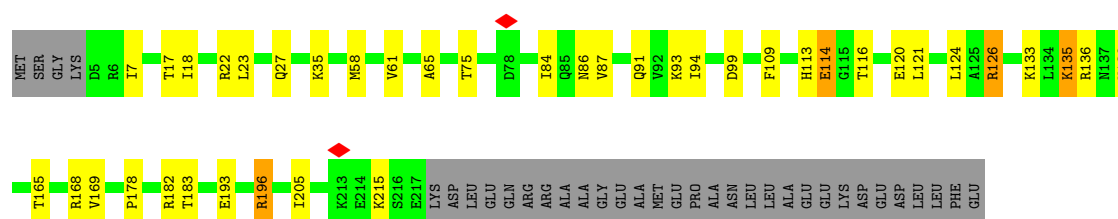
• Molecule 3: V-type proton ATPase subunit C

Chain G: 14% 89% 5% 6%



• Molecule 4: V-type proton ATPase subunit D

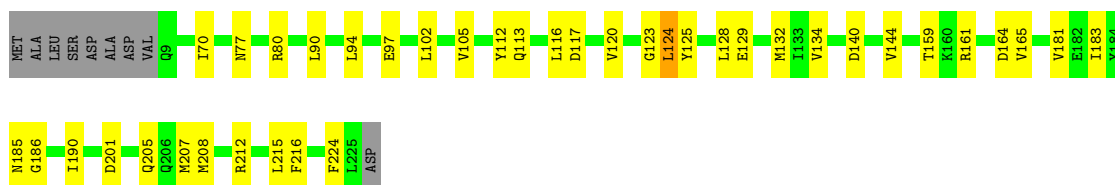
Chain H: 70% 15% 14%




• Molecule 5: V-type proton ATPase subunit E 1

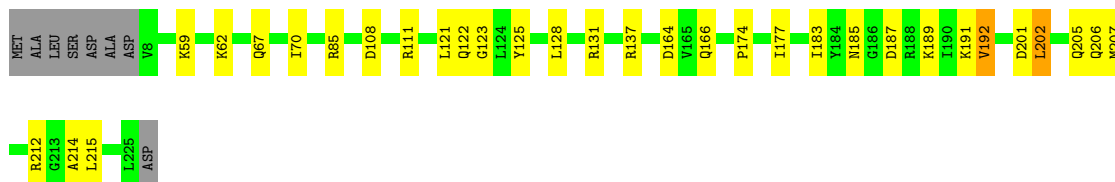
Chain I: 79% 17% 4%






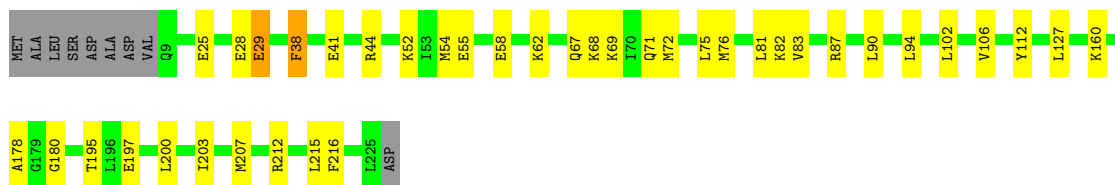
- Molecule 5: V-type proton ATPase subunit E 1

Chain J:  82% 13% . .



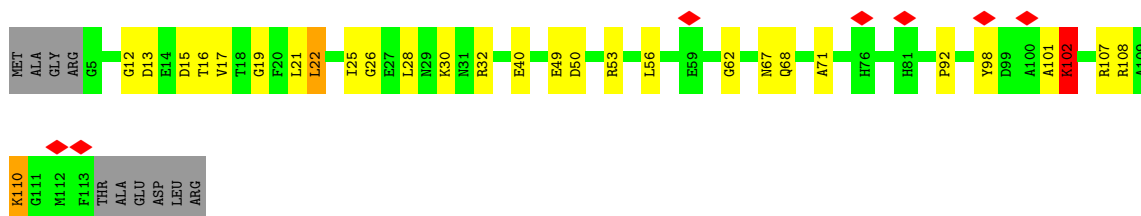
- Molecule 5: V-type proton ATPase subunit E 1

Chain K:  79% 16% . .




- Molecule 6: V-type proton ATPase subunit F

Chain L:  67% 22% 6% 8%




- Molecule 7: V-type proton ATPase subunit G

Chain M:  85% 8% 7%

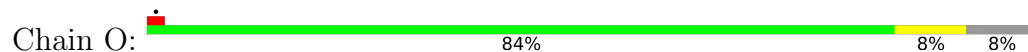


- Molecule 7: V-type proton ATPase subunit G

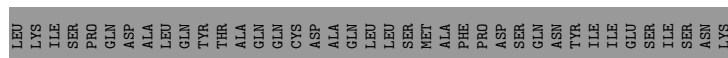
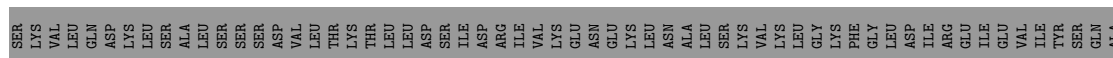
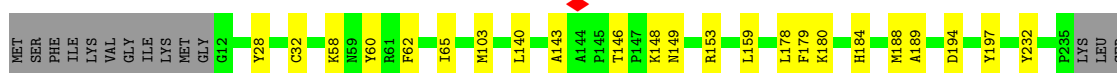
Chain N:  86% 6% 7%



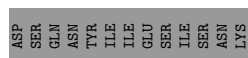
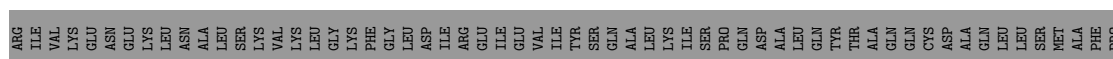
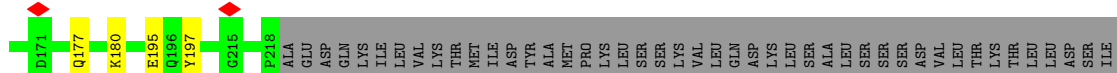
- Molecule 7: V-type proton ATPase subunit G



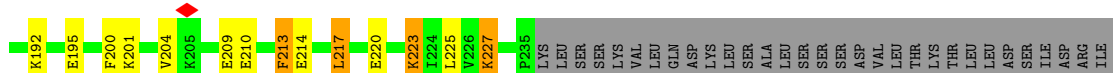
- Molecule 8: Bacterial effector protein SidK

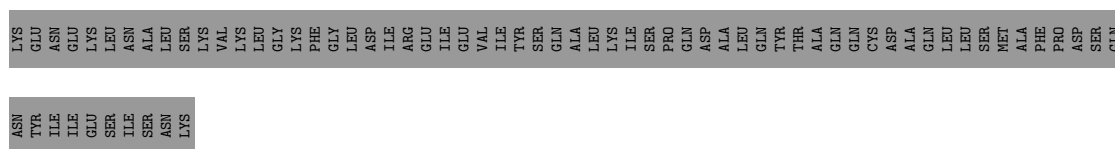


- Molecule 8: Bacterial effector protein SidK

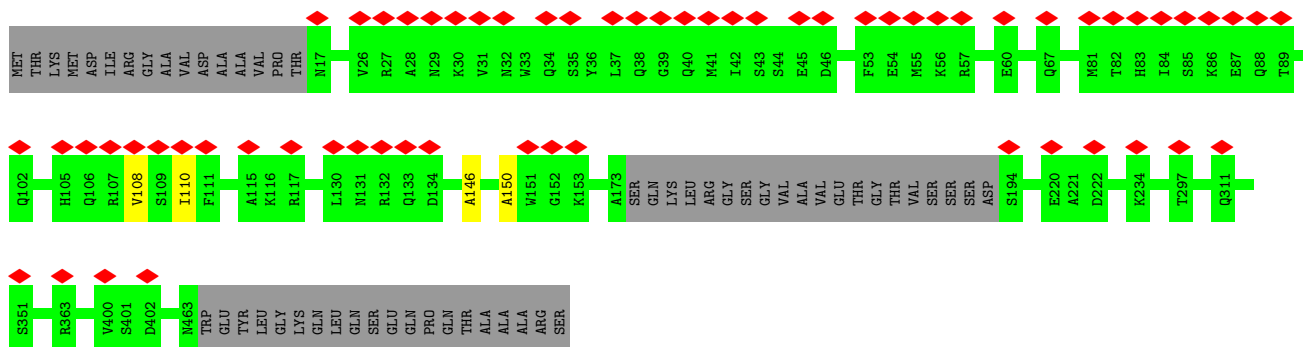
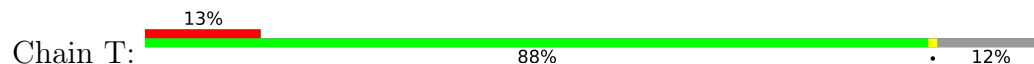


- Molecule 8: Bacterial effector protein SidK

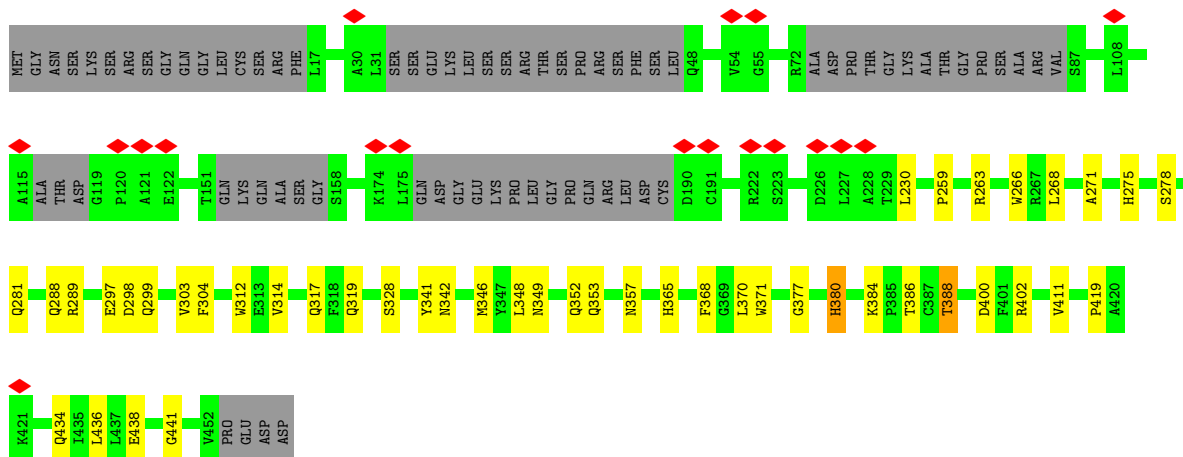




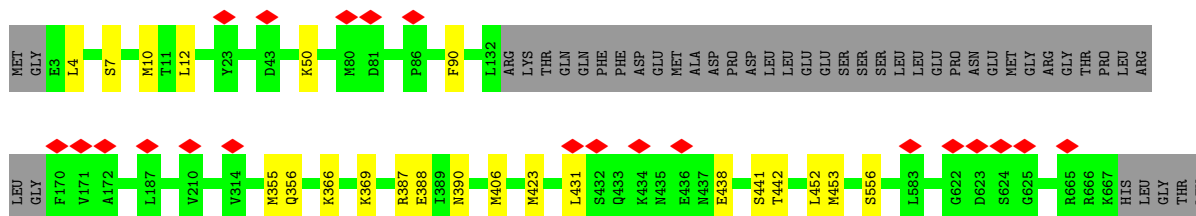
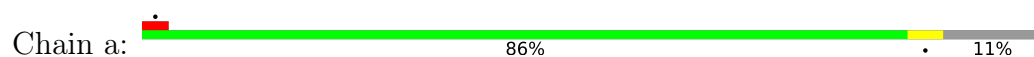
• Molecule 9: V-type proton ATPase subunit H

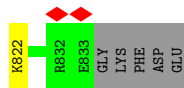


• Molecule 10: TLDC protein mEAK-7



• Molecule 11: V-type proton ATPase subunit a

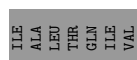
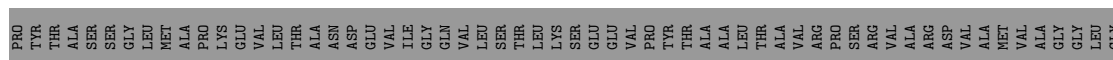
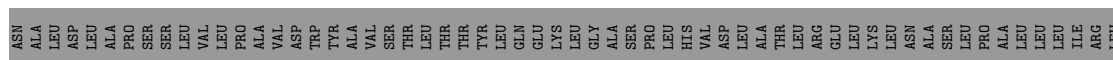
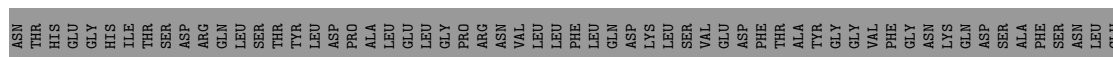
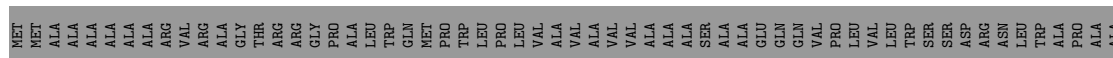




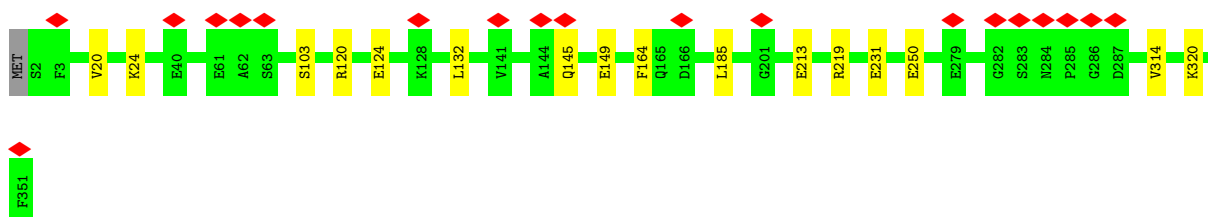
- Chain b:  96%



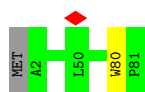
- Chain c:  39% 56%



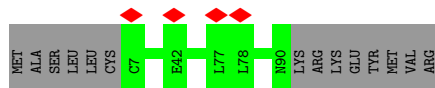
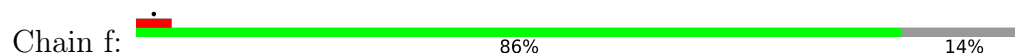
- Chain d: 



- Chain e:  98%



- Molecule 16: Ribonuclease kappa



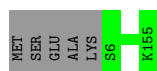
- Molecule 17: V-type proton ATPase proteolipid subunit



- Molecule 17: V-type proton ATPase proteolipid subunit



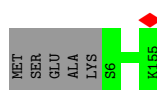
- Molecule 17: V-type proton ATPase proteolipid subunit



- Molecule 17: V-type proton ATPase proteolipid subunit



- Molecule 17: V-type proton ATPase proteolipid subunit



- Molecule 17: V-type proton ATPase proteolipid subunit







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31814	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	36	Depositor
Minimum defocus (nm)	787.921	Depositor
Maximum defocus (nm)	2554.877	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.692	Depositor
Minimum map value	-0.560	Depositor
Average map value	0.026	Depositor
Map value standard deviation	0.135	Depositor
Recommended contour level	0.8	Depositor
Map size ( $\text{\AA}$ )	476.1, 476.1, 476.1	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.3225, 1.3225, 1.3225	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	A	0.51	0/4757	0.79	0/6446
1	B	0.54	0/4668	0.78	0/6322
1	C	0.54	0/4668	0.78	0/6324
2	D	0.55	0/3662	0.83	0/4961
2	E	0.48	0/3644	0.73	0/4939
2	F	0.56	0/3644	0.82	0/4939
3	G	0.23	0/1789	0.39	0/2495
4	H	0.47	0/1735	0.76	0/2321
5	I	0.32	0/1628	0.55	0/2197
5	J	0.35	0/1621	0.60	0/2188
5	K	0.41	0/1722	0.67	0/2313
6	L	0.52	0/879	0.90	0/1186
7	M	0.32	0/687	0.50	0/943
7	N	0.34	0/666	0.51	0/917
7	O	0.47	0/685	0.65	0/942
8	Q	0.45	0/1858	0.67	0/2505
8	R	0.54	0/1717	0.79	0/2315
8	S	0.50	0/1866	0.72	0/2515
9	T	0.23	0/2122	0.36	0/2959
10	U	0.34	0/2437	0.53	0/3335
11	a	0.45	0/5767	0.69	0/7838
12	b	0.44	0/1532	0.73	0/2083
13	c	0.58	0/1716	0.87	0/2338
14	d	0.53	0/2901	0.77	0/3930
15	e	0.56	0/679	0.85	0/934
16	f	0.58	0/669	0.82	0/907
17	g	0.48	0/1073	0.76	0/1453
17	h	0.46	0/1073	0.73	0/1453
17	i	0.37	0/1067	0.60	0/1446
17	j	0.39	0/1073	0.66	0/1453
17	k	0.44	0/1073	0.75	0/1453
17	l	0.48	0/1073	0.77	0/1453
17	m	0.48	0/1073	0.74	0/1453
17	n	0.53	0/1073	0.82	0/1453

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
17	o	0.52	0/1073	0.79	0/1453
18	p	0.46	0/456	0.70	0/625
All	All	0.48	0/69826	0.73	0/94787

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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	4661	0	4653	64	0
1	B	4579	0	4575	78	0
1	C	4577	0	4577	70	0
2	D	3590	0	3581	47	0
2	E	3572	0	3555	49	0
2	F	3572	0	3555	60	0
3	G	1791	0	797	10	0
4	H	1717	0	1822	21	0
5	I	1614	0	1567	33	0
5	J	1608	0	1558	22	0
5	K	1707	0	1739	23	0
6	L	865	0	872	12	0
7	M	682	0	499	9	0
7	N	661	0	447	6	0
7	O	679	0	494	5	0
8	Q	1824	0	1835	19	0
8	R	1685	0	1691	12	0
8	S	1832	0	1843	23	0
9	T	2124	0	947	2	0
10	U	2400	0	1768	32	0
11	a	5635	0	5264	0	0
12	b	1498	0	1548	0	0
13	c	1661	0	1566	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	d	2835	0	2770	0	0
15	e	652	0	668	0	0
16	f	653	0	652	0	0
17	g	1058	0	1136	0	0
17	h	1058	0	1136	0	0
17	i	1052	0	1125	0	0
17	j	1058	0	1136	0	0
17	k	1058	0	1136	0	0
17	l	1058	0	1136	0	0
17	m	1058	0	1136	0	0
17	n	1058	0	1136	0	0
17	o	1058	0	1136	0	0
18	p	442	0	438	0	0
All	All	68632	0	65494	528	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 528 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)
1:B:95:MET:HE1	1:B:308:ARG:C	1.91	0.90
1:A:95:MET:CE	1:A:337:PHE:CE2	2.54	0.90
1:A:95:MET:HE1	1:A:337:PHE:CE2	2.09	0.86
1:C:117:TYR:HE1	2:F:152:ILE:CD1	1.92	0.83
1:B:95:MET:CE	1:B:308:ARG:C	2.49	0.80

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	598/617 (97%)	559 (94%)	37 (6%)	2 (0%)	41	75
1	B	582/617 (94%)	546 (94%)	35 (6%)	1 (0%)	47	81
1	C	581/617 (94%)	539 (93%)	38 (6%)	4 (1%)	22	61
2	D	454/515 (88%)	424 (93%)	28 (6%)	2 (0%)	34	72
2	E	452/515 (88%)	432 (96%)	19 (4%)	1 (0%)	47	81
2	F	452/515 (88%)	418 (92%)	32 (7%)	2 (0%)	34	72
3	G	356/382 (93%)	350 (98%)	6 (2%)	0	100	100
4	H	211/247 (85%)	203 (96%)	8 (4%)	0	100	100
5	I	215/226 (95%)	204 (95%)	11 (5%)	0	100	100
5	J	216/226 (96%)	212 (98%)	4 (2%)	0	100	100
5	K	215/226 (95%)	213 (99%)	1 (0%)	1 (0%)	29	68
6	L	107/119 (90%)	98 (92%)	6 (6%)	3 (3%)	5	32
7	M	108/118 (92%)	107 (99%)	1 (1%)	0	100	100
7	N	108/118 (92%)	105 (97%)	1 (1%)	2 (2%)	8	40
7	O	106/118 (90%)	106 (100%)	0	0	100	100
8	Q	222/337 (66%)	215 (97%)	7 (3%)	0	100	100
8	R	204/337 (60%)	194 (95%)	8 (4%)	2 (1%)	15	54
8	S	224/337 (66%)	209 (93%)	15 (7%)	0	100	100
9	T	423/483 (88%)	410 (97%)	13 (3%)	0	100	100
10	U	371/456 (81%)	348 (94%)	23 (6%)	0	100	100
11	a	744/838 (89%)	708 (95%)	33 (4%)	3 (0%)	34	72
12	b	201/205 (98%)	192 (96%)	8 (4%)	1 (0%)	29	68
13	c	203/469 (43%)	178 (88%)	22 (11%)	3 (2%)	10	45
14	d	348/351 (99%)	319 (92%)	28 (8%)	1 (0%)	41	75
15	e	78/81 (96%)	76 (97%)	1 (1%)	1 (1%)	12	48
16	f	82/98 (84%)	81 (99%)	1 (1%)	0	100	100
17	g	148/155 (96%)	143 (97%)	4 (3%)	1 (1%)	22	61
17	h	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
17	i	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
17	j	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
17	k	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
17	l	148/155 (96%)	147 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	m	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
17	n	148/155 (96%)	144 (97%)	4 (3%)	0	100	100
17	o	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
18	p	51/351 (14%)	49 (96%)	2 (4%)	0	100	100
All	All	9244/10914 (85%)	8802 (95%)	412 (4%)	30 (0%)	44	75

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	N	111	HIS
7	N	112	GLU
11	a	90	PHE
2	F	331	ARG
12	b	31	LEU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	508/525 (97%)	485 (96%)	23 (4%)	27	61
1	B	500/525 (95%)	465 (93%)	35 (7%)	15	46
1	C	501/525 (95%)	457 (91%)	44 (9%)	10	38
2	D	392/438 (90%)	368 (94%)	24 (6%)	18	51
2	E	390/438 (89%)	372 (95%)	18 (5%)	27	61
2	F	390/438 (89%)	374 (96%)	16 (4%)	30	63
3	G	1/344 (0%)	1 (100%)	0	100	100
4	H	184/211 (87%)	168 (91%)	16 (9%)	10	38
5	I	150/197 (76%)	147 (98%)	3 (2%)	55	79
5	J	148/197 (75%)	143 (97%)	5 (3%)	37	68
5	K	175/197 (89%)	170 (97%)	5 (3%)	42	71
6	L	93/100 (93%)	83 (89%)	10 (11%)	6	30

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	M	36/101 (36%)	34 (94%)	2 (6%)	21	54
7	N	29/101 (29%)	28 (97%)	1 (3%)	37	68
7	O	36/101 (36%)	32 (89%)	4 (11%)	6	28
8	Q	203/305 (67%)	201 (99%)	2 (1%)	76	88
8	R	188/305 (62%)	176 (94%)	12 (6%)	17	50
8	S	203/305 (67%)	188 (93%)	15 (7%)	13	44
9	T	1/429 (0%)	1 (100%)	0	100	100
10	U	147/382 (38%)	141 (96%)	6 (4%)	30	63
11	a	540/743 (73%)	513 (95%)	27 (5%)	24	58
12	b	156/158 (99%)	151 (97%)	5 (3%)	39	69
13	c	179/387 (46%)	162 (90%)	17 (10%)	8	34
14	d	305/306 (100%)	290 (95%)	15 (5%)	25	59
15	e	71/72 (99%)	71 (100%)	0	100	100
16	f	70/83 (84%)	70 (100%)	0	100	100
17	g	105/109 (96%)	101 (96%)	4 (4%)	33	65
17	h	105/109 (96%)	99 (94%)	6 (6%)	20	53
17	i	104/109 (95%)	104 (100%)	0	100	100
17	j	105/109 (96%)	101 (96%)	4 (4%)	33	65
17	k	105/109 (96%)	105 (100%)	0	100	100
17	l	105/109 (96%)	99 (94%)	6 (6%)	20	53
17	m	105/109 (96%)	91 (87%)	14 (13%)	4	21
17	n	105/109 (96%)	99 (94%)	6 (6%)	20	53
17	o	105/109 (96%)	99 (94%)	6 (6%)	20	53
18	p	48/311 (15%)	46 (96%)	2 (4%)	30	63
All	All	6588/9205 (72%)	6235 (95%)	353 (5%)	26	55

5 of 353 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	S	220	GLU
13	c	343	ARG
10	U	384	LYS
11	a	739	TYR
14	d	219	ARG



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
13	c	359	GLN
17	g	123	GLN
17	n	123	GLN
17	i	123	GLN
1	C	317	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.

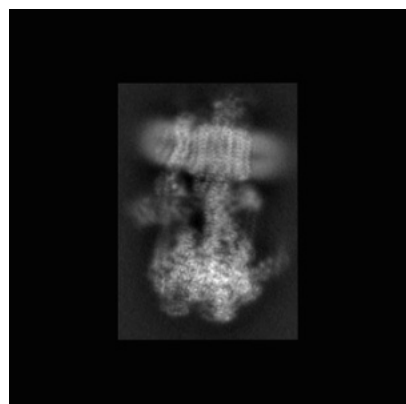
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26385. These allow visual inspection of the internal detail of the map and identification of artifacts.

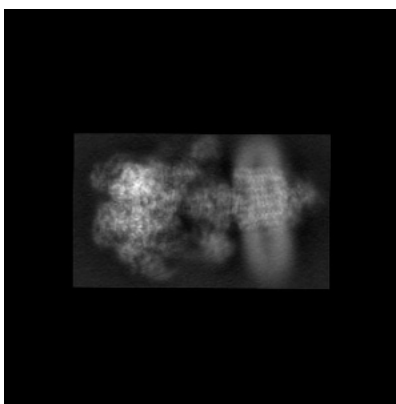
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

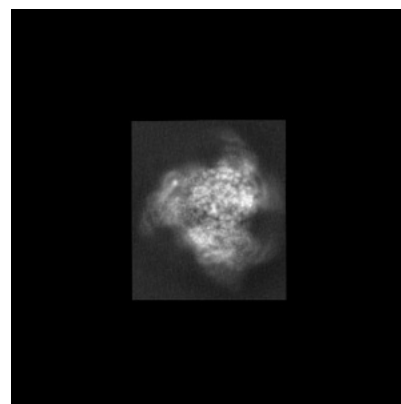
#### 6.1.1 Primary map



X

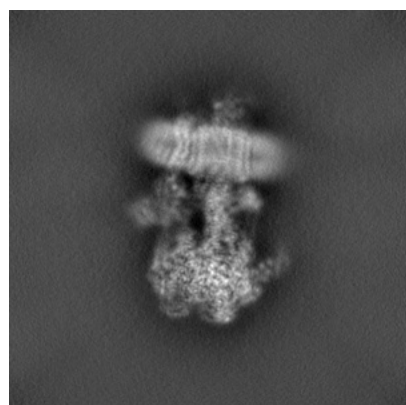


Y

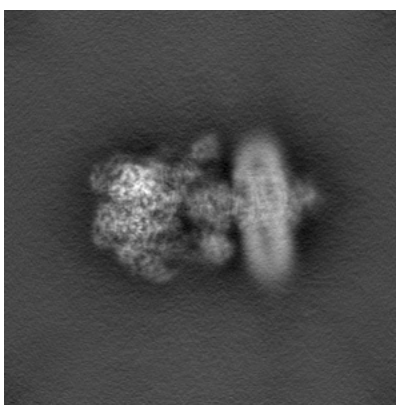


Z

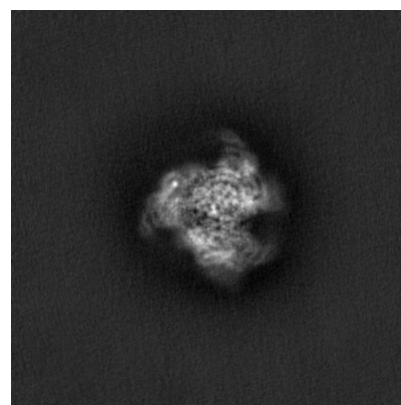
#### 6.1.2 Raw map



X



Y

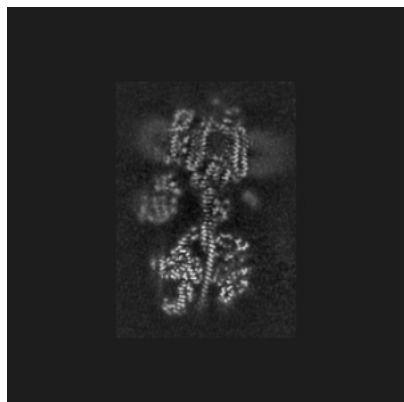


Z

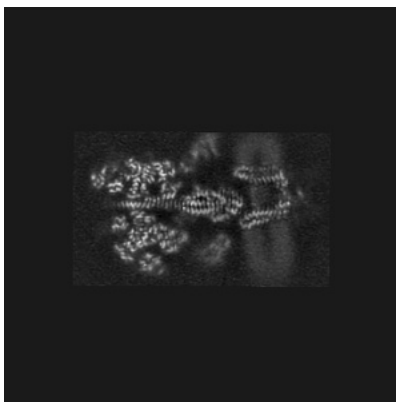
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

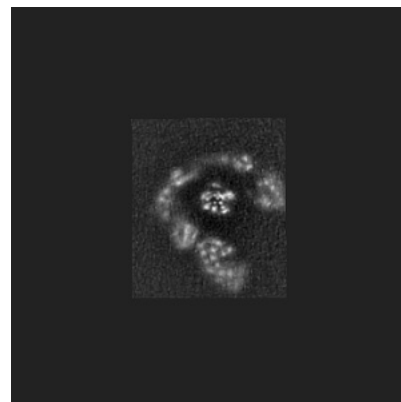
### 6.2.1 Primary map



X Index: 180

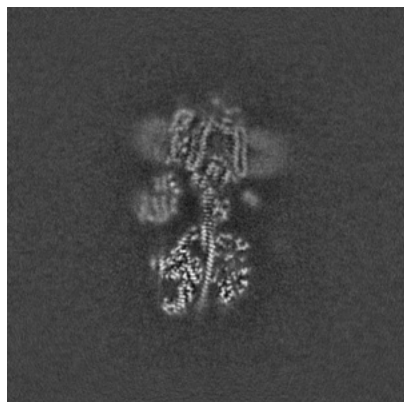


Y Index: 180

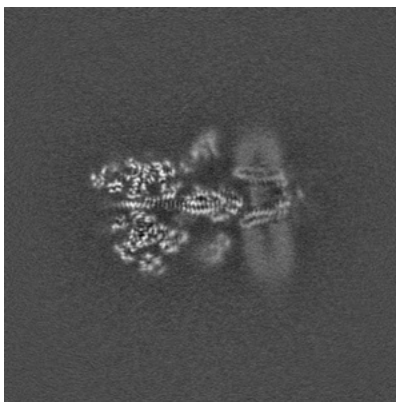


Z Index: 180

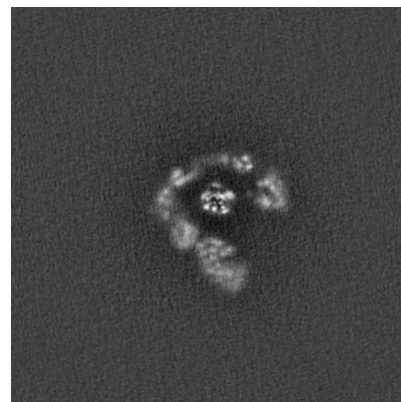
### 6.2.2 Raw map



X Index: 180



Y Index: 180

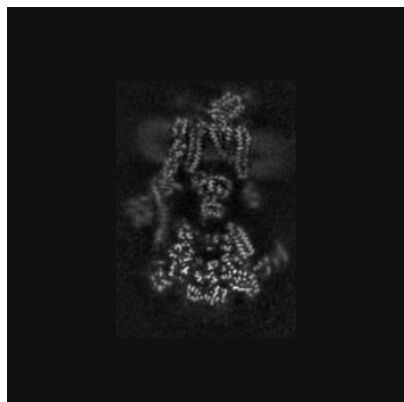


Z Index: 180

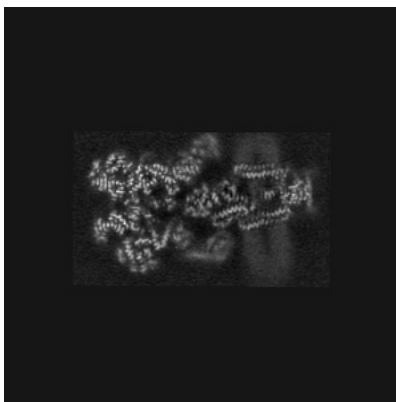
The images above show central slices of the map in three orthogonal directions.

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

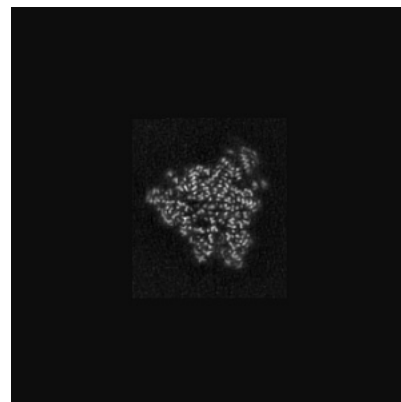
### 6.3.1 Primary map



X Index: 193

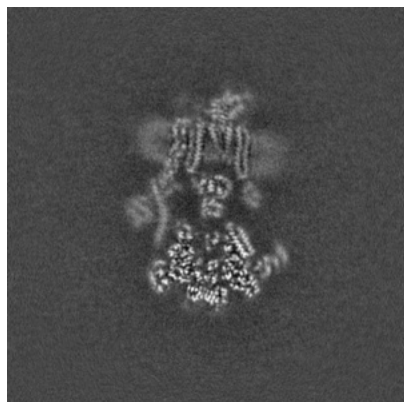


Y Index: 188

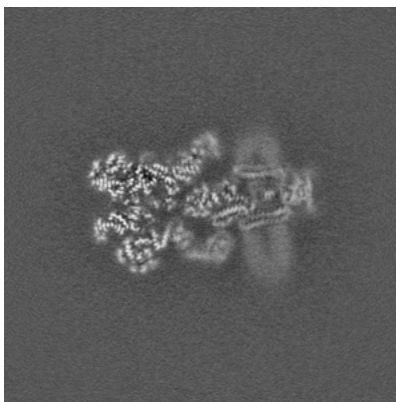


Z Index: 116

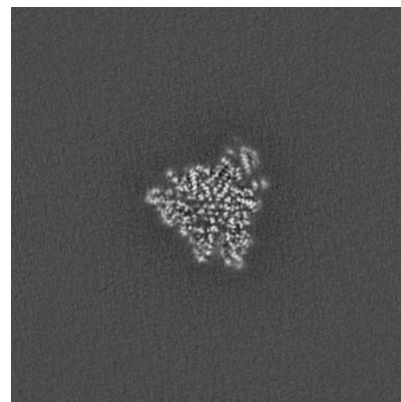
### 6.3.2 Raw map



X Index: 194



Y Index: 188

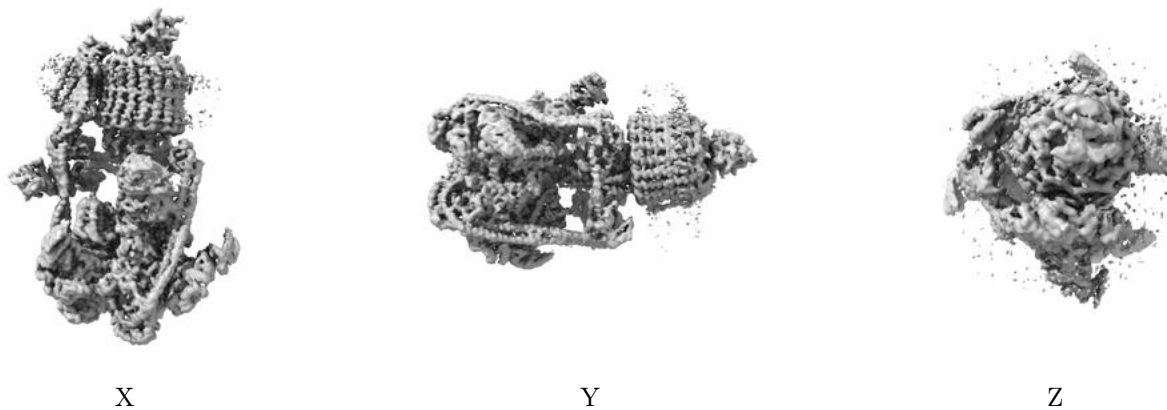


Z Index: 116

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

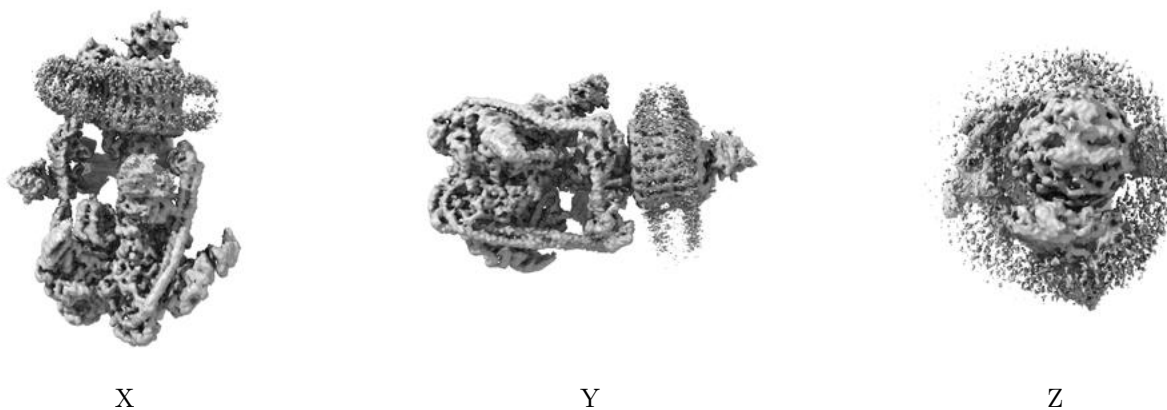
## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

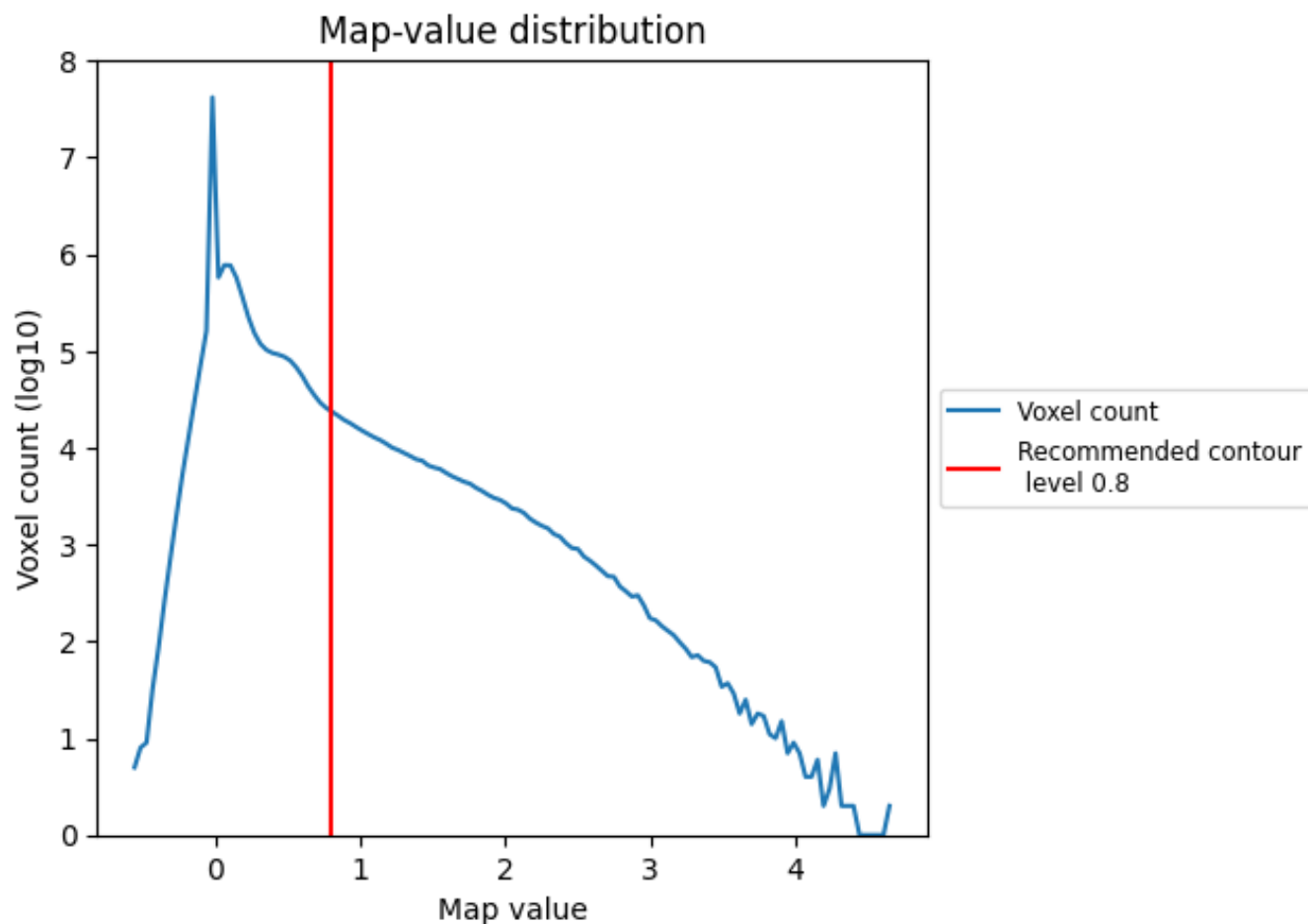
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

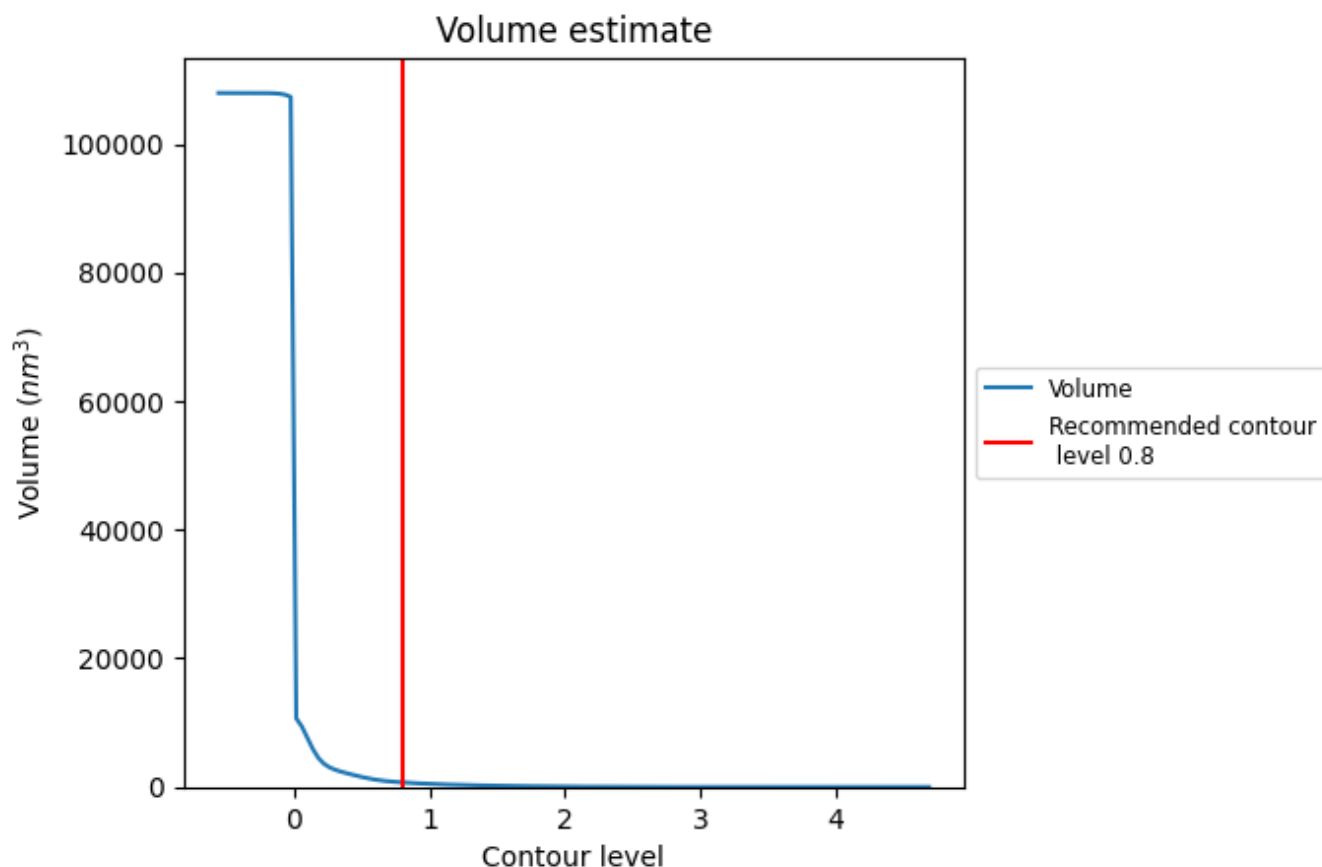
This section contains the results of statistical analysis of the map.

### 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.

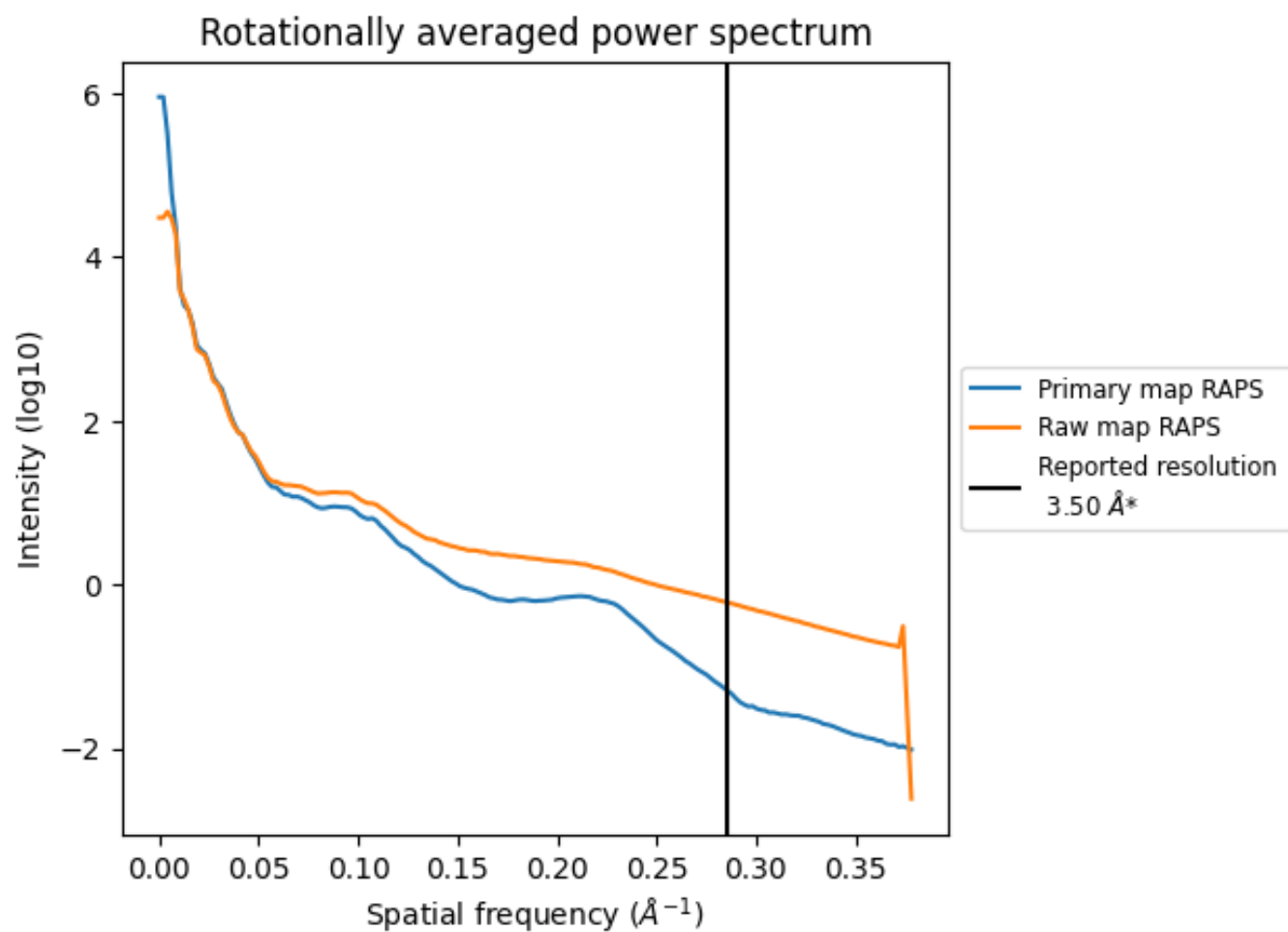
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 707  $\text{nm}^3$ ; this corresponds to an approximate mass of 639 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 ⓘ



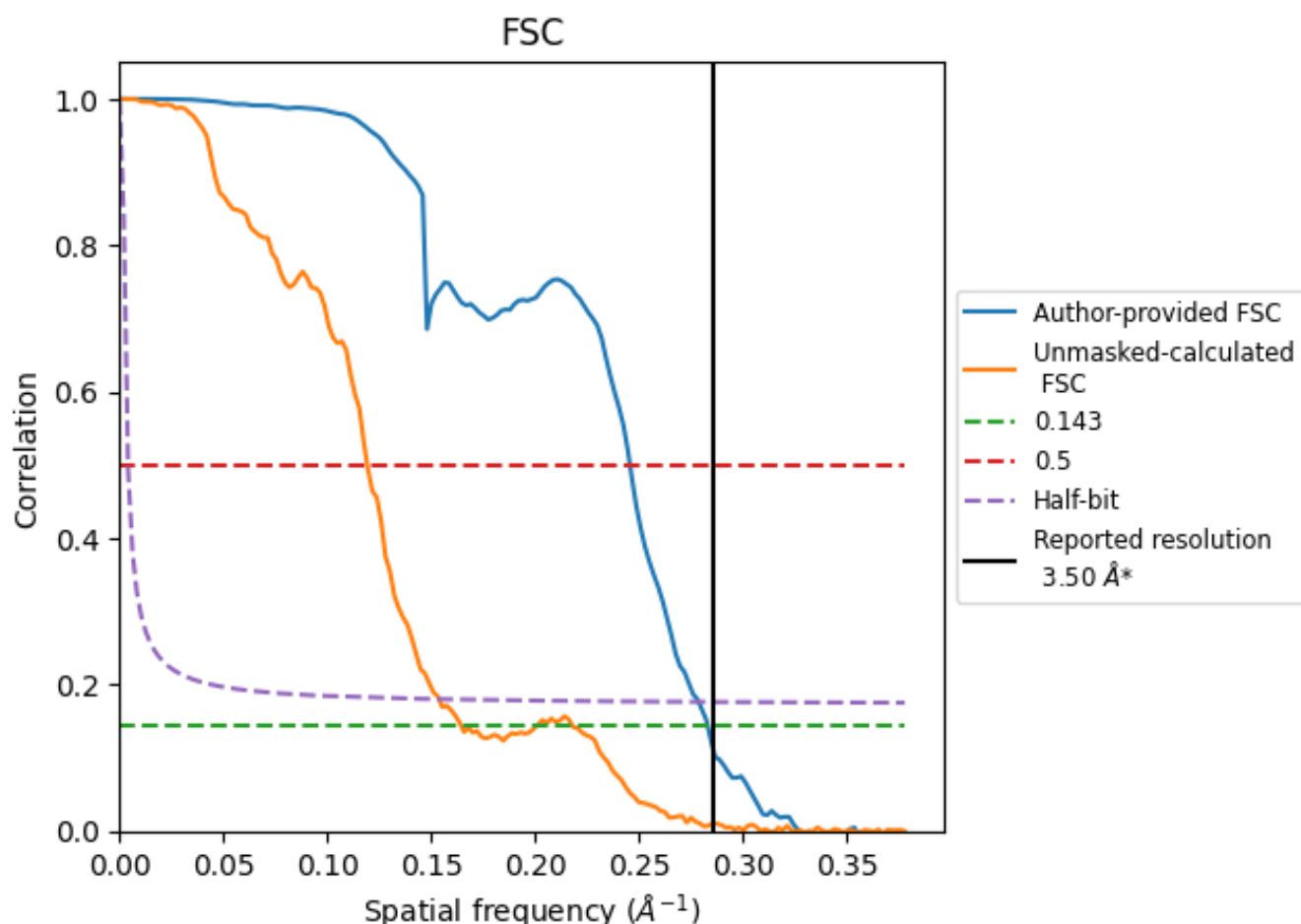
\*Reported resolution corresponds to spatial frequency of 0.286 Å<sup>-1</sup>



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

## 8.2 Resolution estimates [i](#)

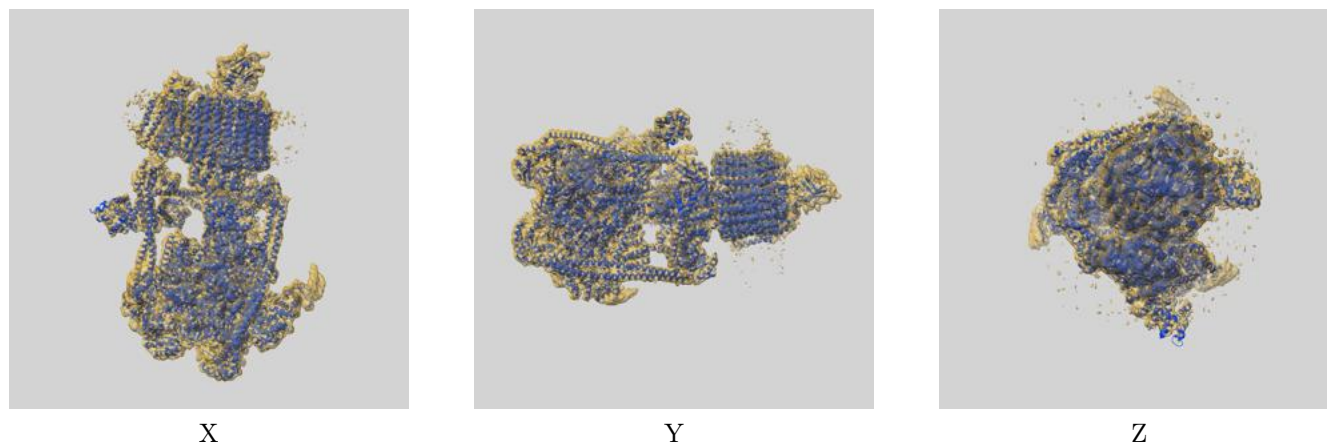
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.53	4.07	3.59
Unmasked-calculated*	6.08	8.38	6.50

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.08 differs from the reported value 3.5 by more than 10 %

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

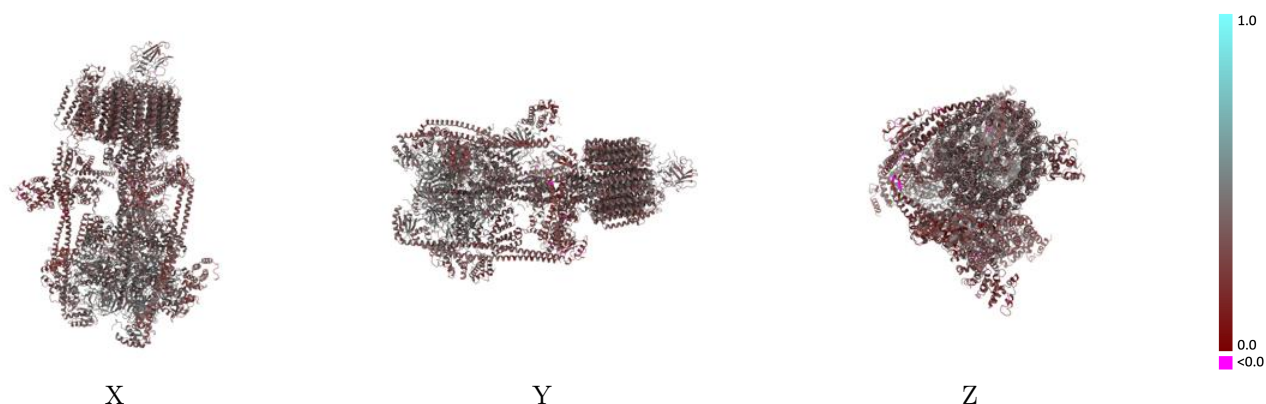
This section contains information regarding the fit between EMDB map EMD-26385 and PDB model 7U8O. Per-residue inclusion information can be found in section [3](#) on page [9](#).

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



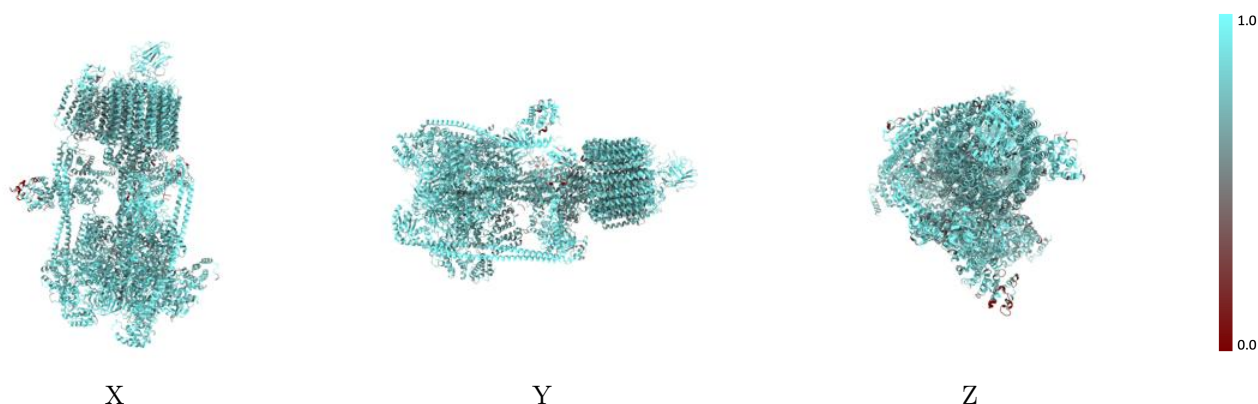
The images above show the 3D surface view of the map at the recommended contour level 0.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



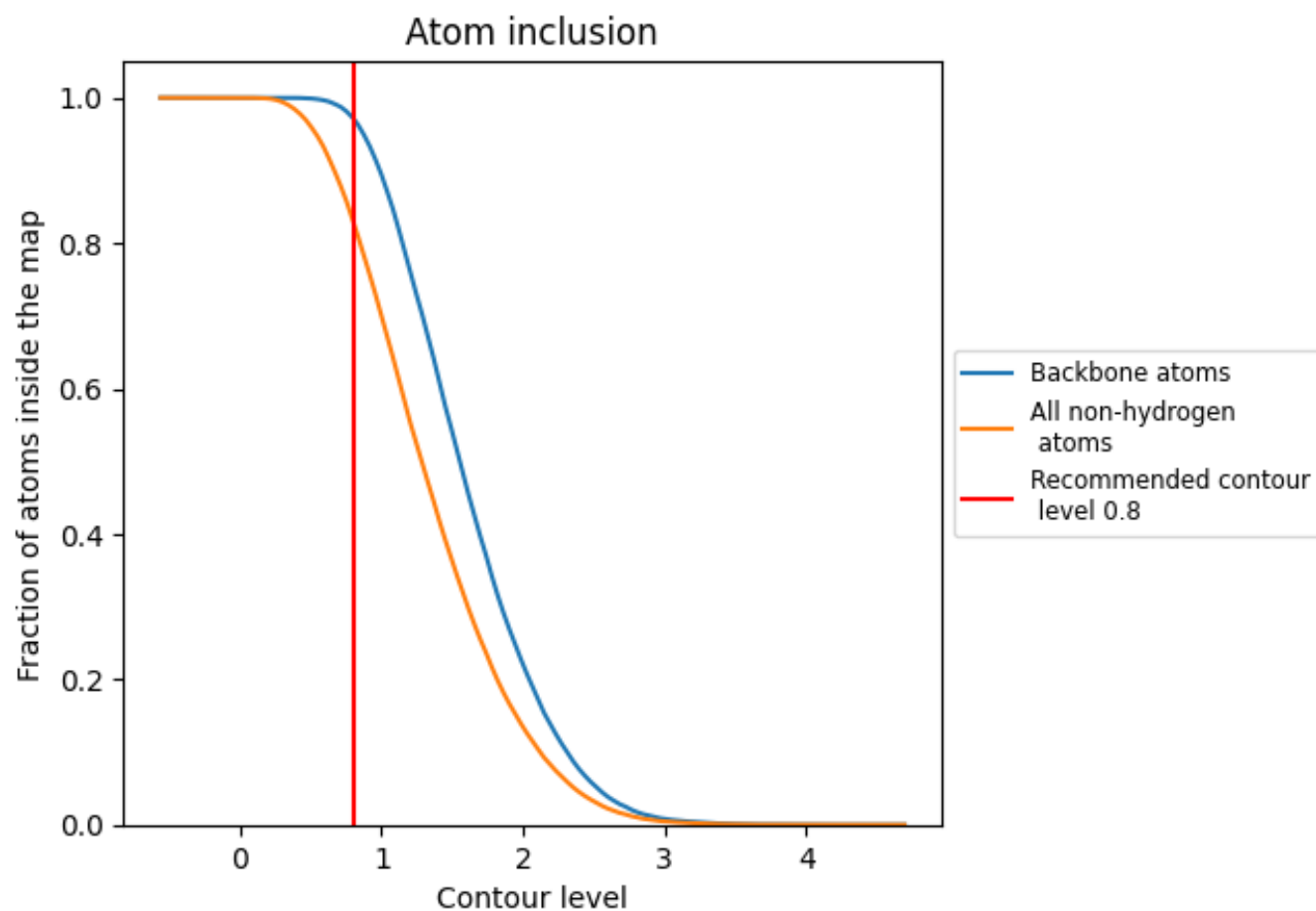
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.8).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8301	 0.3710
A	 0.8482	 0.3930
B	 0.8869	 0.4170
C	 0.8723	 0.4050
D	 0.9065	 0.4360
E	 0.8977	 0.4330
F	 0.9052	 0.4300
G	 0.7739	 0.2760
H	 0.7813	 0.3750
I	 0.8767	 0.3670
J	 0.8902	 0.3740
K	 0.8365	 0.3580
L	 0.7220	 0.3550
M	 0.8810	 0.3390
N	 0.9555	 0.3540
O	 0.9069	 0.3520
Q	 0.8058	 0.3220
R	 0.8113	 0.3220
S	 0.7983	 0.3220
T	 0.7740	 0.2660
U	 0.8917	 0.3760
a	 0.7558	 0.3190
b	 0.7946	 0.3800
c	 0.8548	 0.3750
d	 0.7315	 0.3650
e	 0.7769	 0.3550
f	 0.7384	 0.3090
g	 0.7975	 0.3780
h	 0.8128	 0.3810
i	 0.8188	 0.3640
j	 0.8357	 0.3700
k	 0.7861	 0.3680
l	 0.7526	 0.3530
m	 0.7479	 0.3470
n	 0.7440	 0.3490



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Chain	Atom inclusion	Q-score
o	 0.7431	 0.3560
p	 0.7912	 0.3770