



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:15 AM UTC

PDB ID : 7UZF / pdb_00007uzf
EMDB ID : EMD-26909
Title : Rat Kidney V-ATPase with SidK, State 1
Authors : Rubinstein, J.L.; Abbas, Y.M.
Deposited on : 2022-05-09
Resolution : 3.80 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

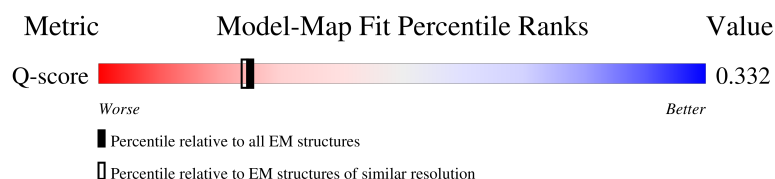
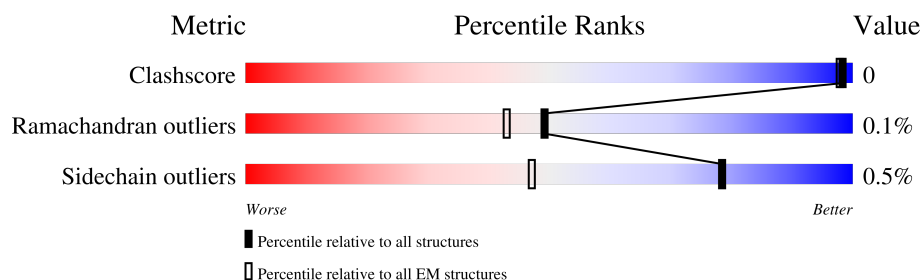
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

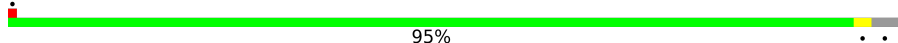
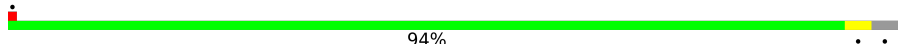
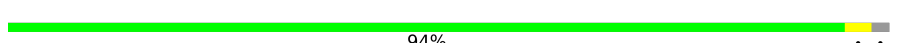
The reported resolution of this entry is 3.80 Å.

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.



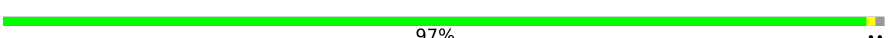
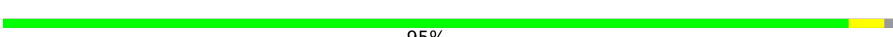
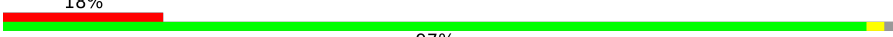
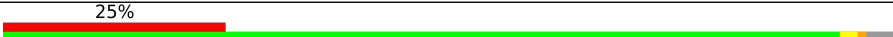
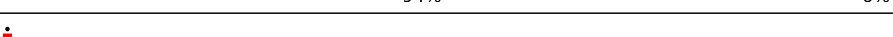
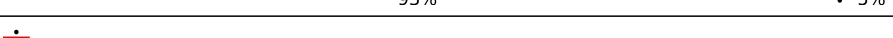
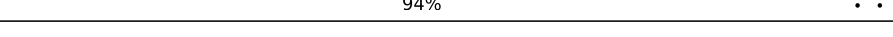
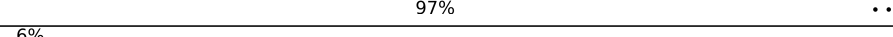
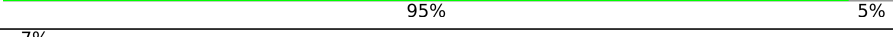
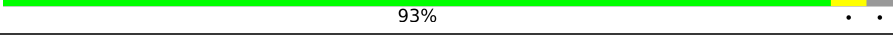
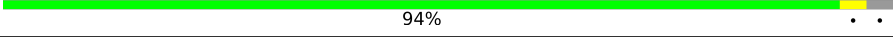
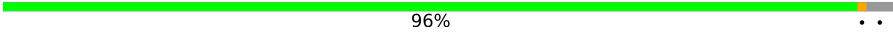
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	617	 95%
1	B	617	 94%
1	C	617	 94%
2	D	511	 89% 10%

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Mol	Chain	Length	Quality of chain
2	E	511	
2	F	511	
3	G	382	
4	H	247	
5	I	226	
5	J	226	
5	K	226	
6	L	119	
7	M	118	
7	N	118	
7	O	118	
8	P	483	
9	Q	280	
9	R	280	
9	S	280	
10	a	838	
11	b	205	
12	c	463	
13	d	351	
14	e	81	
15	f	98	
16	g	155	
16	h	155	
16	i	155	
16	j	155	

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Mol	Chain	Length	Quality of chain
16	k	155	96%
16	l	155	95%
16	m	155	96%
16	n	155	94%
16	o	155	94%
17	p	350	14% 85%

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 71930 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 ATPase H⁺-transporting V1 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	597	Total	C	N	O	S	0	0
			4632	2936	783	887	26		
1	B	600	Total	C	N	O	S	0	0
			4651	2949	786	889	27		
1	C	602	Total	C	N	O	S	0	0
			4666	2957	788	894	27		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	460	Total	C	N	O	S	0	0
			3604	2287	614	683	20		
2	E	460	Total	C	N	O	S	0	0
			3603	2286	615	682	20		
2	F	457	Total	C	N	O	S	0	0
			3576	2269	610	677	20		

- Molecule 3 is a protein called V-type proton ATPase subunit C 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	358	Total	C	N	O	S	0	0
			2919	1873	492	545	9		

- Molecule 4 is a protein called ATPase H⁺-transporting V1 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	218	Total	C	N	O	S	0	0
			1760	1116	316	323	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	223	Total	C	N	O	S	0	0
			1808	1137	319	342	10		
5	J	223	Total	C	N	O	S	0	0
			1808	1137	319	342	10		
5	K	223	Total	C	N	O	S	0	0
			1808	1137	319	342	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	110	Total	C	N	O	S	0	0
			875	553	157	163	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	112	Total	C	N	O	S	0	0
			920	563	173	181	3		
7	N	114	Total	C	N	O	S	0	0
			935	571	176	185	3		
7	O	114	Total	C	N	O	S	0	0
			935	571	176	185	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	431	Total	C	N	O	S	0	0
			3537	2243	610	658	26		

- Molecule 9 is a protein called Effector SidK.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	263	Total	C	N	O	S	0	0
			2126	1350	357	409	10		
9	R	264	Total	C	N	O	S	0	0
			2130	1352	358	410	10		
9	S	267	Total	C	N	O	S	0	0
			2155	1369	362	413	11		

- Molecule 10 is a protein called V-type proton ATPase 116 kDa subunit a isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	a	757	Total	C	N	O	S	0	0
			6164	4025	1032	1066	41		

- Molecule 11 is a protein called ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA_a.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	b	203	Total	C	N	O	S	0	0
			1503	996	237	259	11		

- Molecule 12 is a protein called V-type proton ATPase subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	204	Total	C	N	O	S	0	0
			1652	1087	259	297	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	d	348	Total	C	N	O	S	0	0
			2817	1817	458	528	14		

- Molecule 14 is a protein called V-type proton ATPase subunit e 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	e	77	Total	C	N	O	S	0	0
			623	431	97	92	3		

- Molecule 15 is a protein called Ribonuclease K.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	f	84	Total	C	N	O	S	0	0
			652	431	101	114	6		

- Molecule 16 is a protein called V-type proton ATPase 16 kDa proteolipid subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	g	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	h	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		

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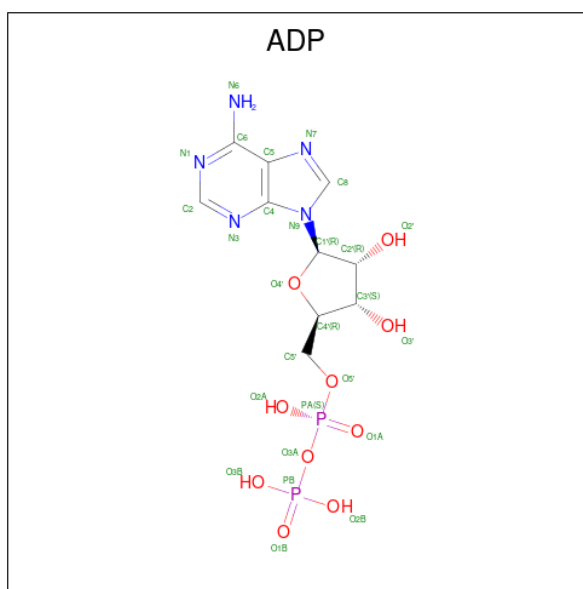
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Mol	Chain	Residues	Atoms					AltConf	Trace
16	i	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	j	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	k	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	l	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	m	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	n	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		
16	o	150	Total	C	N	O	S	0	0
			1069	699	171	191	8		

- Molecule 17 is a protein called Renin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	p	51	Total	C	N	O	S	0	0
			423	284	62	75	2		

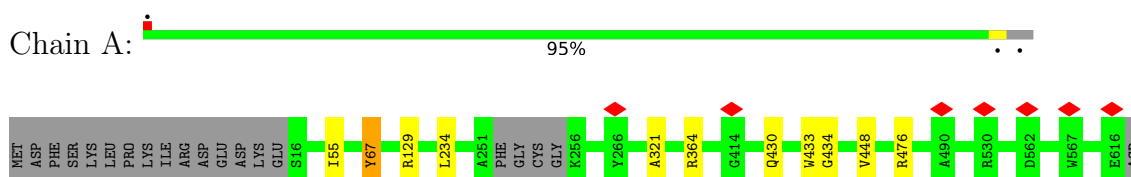
- Molecule 18 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



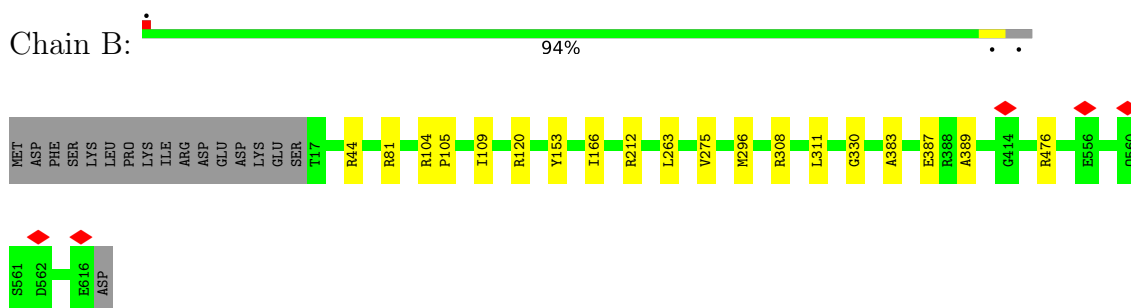
3 Residue-property plots

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.

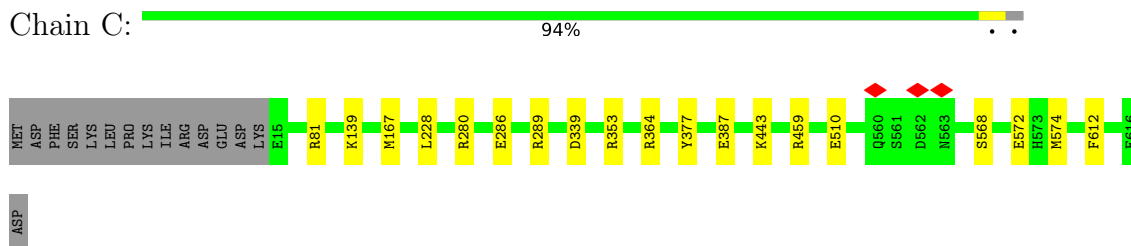
- Molecule 1: ATPase H⁺-transporting V1 subunit A



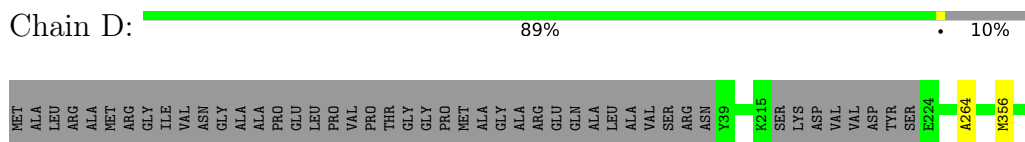
- Molecule 1: ATPase H⁺-transporting V1 subunit A

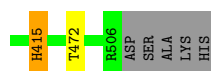


- Molecule 1: ATPase H⁺-transporting V1 subunit A



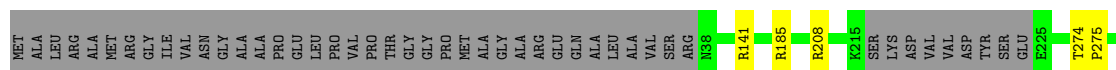
- Molecule 2: V-type proton ATPase subunit B, brain isoform





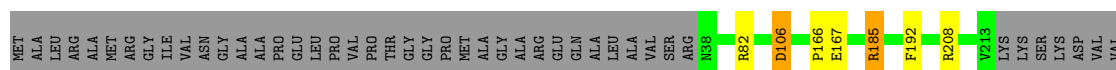
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain E: 88% 10%



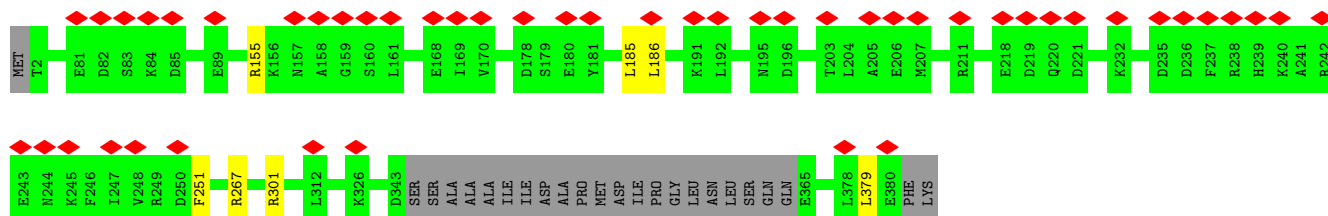
- Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain F: 84% 5% 11%



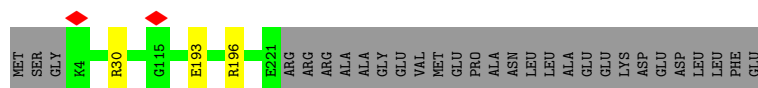
- Molecule 3: V-type proton ATPase subunit C 1

Chain G: 13% 92% 6%



- Molecule 4: ATPase H⁺-transporting V1 subunit D

Chain H: 87% 12%



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

Chain I: 97% 2%

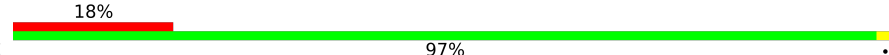


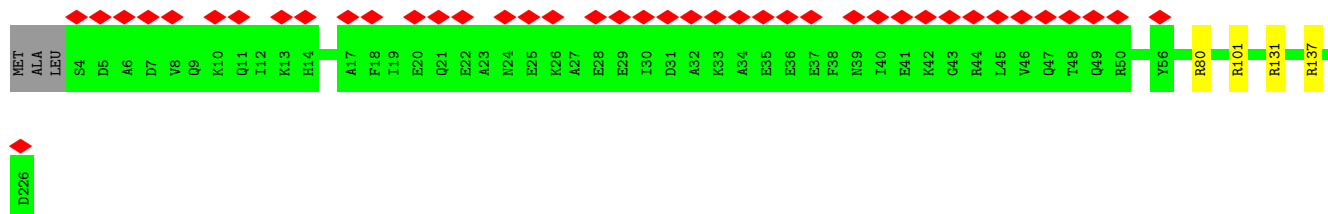
- Molecule 5: V-type proton ATPase subunit E 1

Chain J:  95%

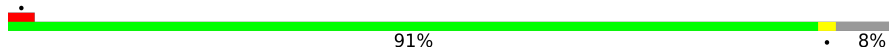


- Molecule 5: V-type proton ATPase subunit E 1

Chain K:  18% 97%

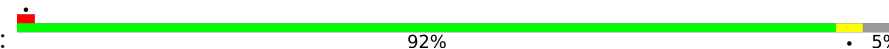


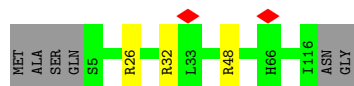
- Molecule 6: V-type proton ATPase subunit F

Chain L:  91% 8%

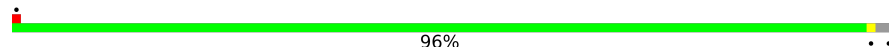


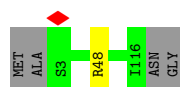
- Molecule 7: V-type proton ATPase subunit G

Chain M:  92% 5%

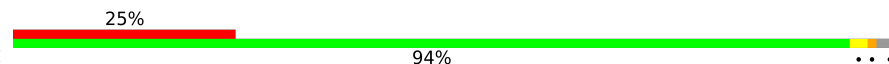


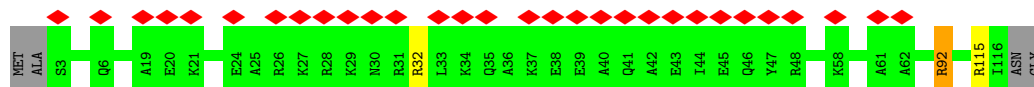
- Molecule 7: V-type proton ATPase subunit G

Chain N:  96%



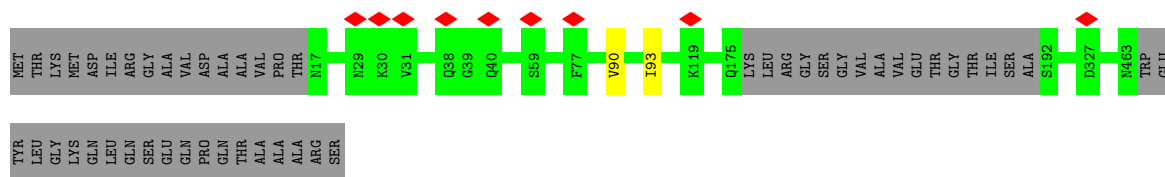
- Molecule 7: V-type proton ATPase subunit G

Chain O:  25% 94%



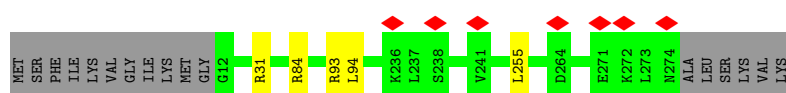
- Molecule 8: V-type proton ATPase subunit H

Chain P:  89% 11%

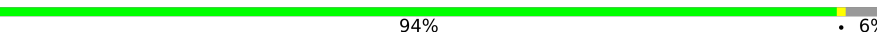


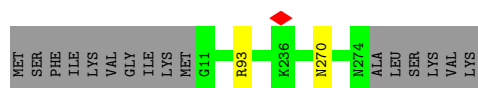
- Molecule 9: Effector SidK

Chain Q:  92% 6%



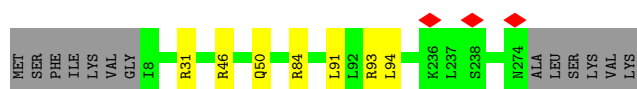
- Molecule 9: Effector SidK

Chain R:  94% 6%



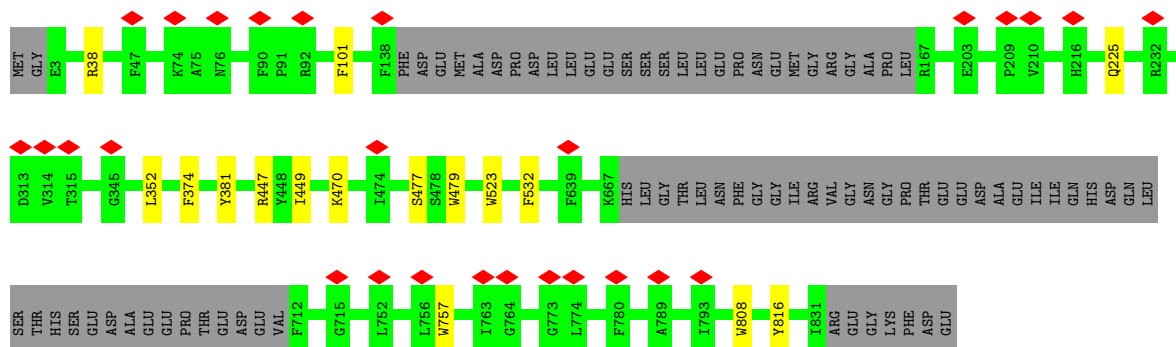
- Molecule 9: Effector SidK

Chain S:  93% 5%

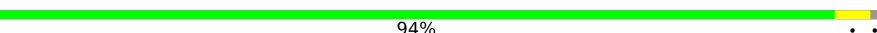


- Molecule 10: V-type proton ATPase 116 kDa subunit a isoform 1

Chain a:  88% 10%

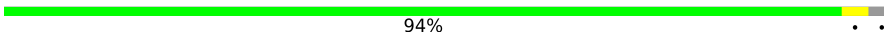


- Molecule 11: ATPase, H⁺ transporting, V0 subunit B (Predicted), isoform CRA_a

Chain b:  94% 6%

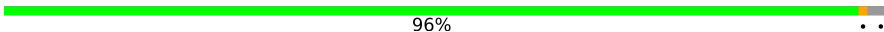


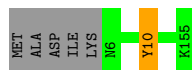
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:  94% ..

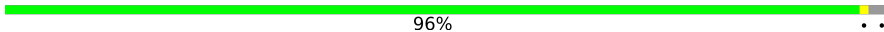


- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:  96% ..

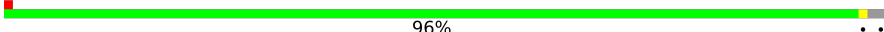


- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:  96% ..

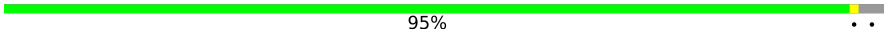


- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:  96% ..

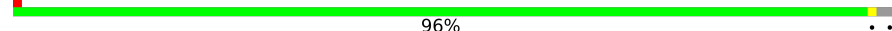


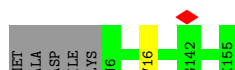
- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain l:  95% ..

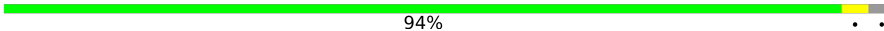


- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain m:  96% ..



- Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain n:  94% ..



● Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain o:

94%

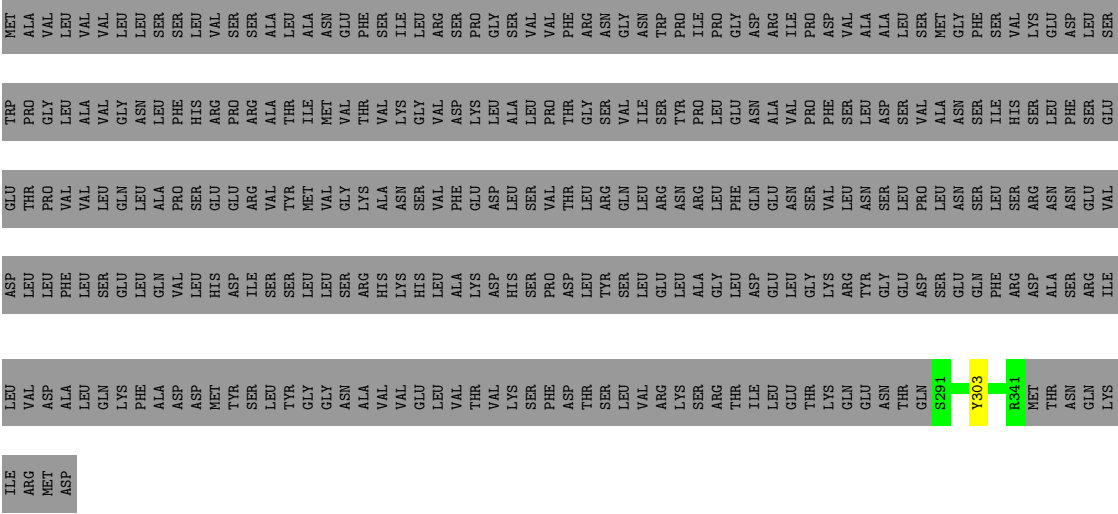


● Molecule 17: Renin receptor

Chain p:

14%

85%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45083	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	44.825	Depositor
Minimum defocus (nm)	100	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	70.456	Depositor
Minimum map value	-45.496	Depositor
Average map value	0.008	Depositor
Map value standard deviation	1.338	Depositor
Recommended contour level	4	Depositor
Map size (Å)	449.65, 449.65, 449.65	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3225, 1.3225, 1.3225	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.73	0/4725	1.19	3/6396 (0.0%)
1	B	0.73	0/4746	1.21	8/6425 (0.1%)
1	C	0.72	0/4761	1.19	3/6445 (0.0%)
2	D	0.74	0/3675	1.21	2/4979 (0.0%)
2	E	0.74	0/3674	1.22	7/4978 (0.1%)
2	F	0.73	0/3647	1.22	11/4944 (0.2%)
3	G	0.75	0/2973	1.26	3/4016 (0.1%)
4	H	0.71	0/1778	1.16	1/2377 (0.0%)
5	I	0.68	0/1825	1.22	1/2442 (0.0%)
5	J	0.69	0/1825	1.17	3/2442 (0.1%)
5	K	0.69	0/1825	1.21	3/2442 (0.1%)
6	L	0.77	0/889	1.31	2/1199 (0.2%)
7	M	0.74	0/928	1.28	3/1236 (0.2%)
7	N	0.71	0/943	1.27	1/1256 (0.1%)
7	O	0.74	0/943	1.30	3/1256 (0.2%)
8	P	0.74	0/3604	1.25	0/4854
9	Q	0.70	0/2160	1.24	3/2910 (0.1%)
9	R	0.68	0/2164	1.23	1/2915 (0.0%)
9	S	0.72	0/2189	1.25	6/2947 (0.2%)
10	a	0.75	0/6322	1.24	4/8551 (0.0%)
11	b	0.72	0/1537	1.18	2/2088 (0.1%)
12	c	0.73	0/1707	1.22	4/2324 (0.2%)
13	d	0.72	0/2882	1.20	5/3903 (0.1%)
14	e	0.78	0/648	1.24	0/891
15	f	0.73	0/668	1.20	0/907
16	g	0.74	0/1084	1.17	3/1466 (0.2%)
16	h	0.74	0/1084	1.16	1/1466 (0.1%)
16	i	0.73	0/1084	1.17	0/1466
16	j	0.74	0/1084	1.17	0/1466
16	k	0.71	0/1084	1.09	0/1466
16	l	0.73	0/1084	1.14	1/1466 (0.1%)
16	m	0.75	0/1084	1.18	0/1466

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	n	0.75	0/1084	1.17	1/1466 (0.1%)
16	o	0.75	0/1084	1.19	2/1466 (0.1%)
17	p	0.77	0/436	1.20	0/598
All	All	0.73	0/73230	1.21	87/98915 (0.1%)

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	A	0	2
1	C	0	3
2	D	0	1
2	E	0	1
2	F	0	3
5	J	0	2
5	K	0	1
7	O	0	1
10	a	0	1
11	b	0	2
13	d	0	2
16	g	0	1
16	h	0	1
16	i	0	1
16	j	0	1
16	o	0	2
17	p	0	1
All	All	0	26

There are no bond length outliers.

The worst 5 of 87 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	Q	93	ARG	NE-CZ-NH2	6.78	125.30	119.20
1	C	81	ARG	NE-CZ-NH2	6.66	125.20	119.20
1	B	308	ARG	NE-CZ-NH2	6.41	124.97	119.20
13	d	7	LEU	CB-CA-C	6.39	122.67	110.27
2	E	185	ARG	NE-CZ-NH2	6.21	124.79	119.20

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	364	ARG	Sidechain
1	A	67	TYR	Sidechain
1	C	280	ARG	Sidechain
1	C	364	ARG	Sidechain
1	C	377	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	A	4632	0	4628	3	0
1	B	4651	0	4644	6	0
1	C	4666	0	4655	4	0
2	D	3604	0	3608	2	0
2	E	3603	0	3608	1	0
2	F	3576	0	3576	6	0
3	G	2919	0	2961	3	0
4	H	1760	0	1869	1	0
5	I	1808	0	1880	1	0
5	J	1808	0	1880	1	0
5	K	1808	0	1880	0	0
6	L	875	0	883	0	0
7	M	920	0	918	0	0
7	N	935	0	931	0	0
7	O	935	0	931	0	0
8	P	3537	0	3510	1	0
9	Q	2126	0	2165	1	0
9	R	2130	0	2168	0	0
9	S	2155	0	2201	2	0
10	a	6164	0	6197	5	0
11	b	1503	0	1551	2	0
12	c	1652	0	1584	7	0
13	d	2817	0	2756	0	0
14	e	623	0	641	0	0
15	f	652	0	647	0	0
16	g	1069	0	1136	2	0
16	h	1069	0	1136	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	i	1069	0	1136	0	0
16	j	1069	0	1136	0	0
16	k	1069	0	1136	0	0
16	l	1069	0	1136	0	0
16	m	1069	0	1136	1	0
16	n	1069	0	1136	3	0
16	o	1069	0	1136	1	0
17	p	423	0	416	0	0
18	C	27	0	12	0	0
All	All	71930	0	72924	45	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

The worst 5 of 45 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:A:234:LEU:HD21	1:A:448:VAL:HG21	1.82	0.61
1:C:387:GLU:HG3	2:D:264:ALA:HB3	1.88	0.54
1:B:104:ARG:HB3	1:B:109:ILE:HD11	1.92	0.52
1:B:387:GLU:HG3	2:F:264:ALA:HB3	1.91	0.52
3:G:379:LEU:H	3:G:379:LEU:HD23	1.75	0.51

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	593/617 (96%)	564 (95%)	28 (5%)	1 (0%)	43 73
1	B	598/617 (97%)	575 (96%)	22 (4%)	1 (0%)	43 73

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	600/617 (97%)	578 (96%)	21 (4%)	1 (0%)	43	73
2	D	456/511 (89%)	436 (96%)	20 (4%)	0	100	100
2	E	456/511 (89%)	430 (94%)	26 (6%)	0	100	100
2	F	453/511 (89%)	433 (96%)	20 (4%)	0	100	100
3	G	354/382 (93%)	348 (98%)	6 (2%)	0	100	100
4	H	216/247 (87%)	212 (98%)	4 (2%)	0	100	100
5	I	221/226 (98%)	218 (99%)	3 (1%)	0	100	100
5	J	221/226 (98%)	217 (98%)	4 (2%)	0	100	100
5	K	221/226 (98%)	216 (98%)	5 (2%)	0	100	100
6	L	108/119 (91%)	104 (96%)	4 (4%)	0	100	100
7	M	110/118 (93%)	109 (99%)	1 (1%)	0	100	100
7	N	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
7	O	112/118 (95%)	111 (99%)	1 (1%)	0	100	100
8	P	427/483 (88%)	422 (99%)	5 (1%)	0	100	100
9	Q	261/280 (93%)	256 (98%)	5 (2%)	0	100	100
9	R	262/280 (94%)	258 (98%)	4 (2%)	0	100	100
9	S	265/280 (95%)	257 (97%)	8 (3%)	0	100	100
10	a	751/838 (90%)	728 (97%)	23 (3%)	0	100	100
11	b	201/205 (98%)	198 (98%)	3 (2%)	0	100	100
12	c	202/463 (44%)	189 (94%)	13 (6%)	0	100	100
13	d	346/351 (99%)	338 (98%)	7 (2%)	1 (0%)	36	67
14	e	75/81 (93%)	73 (97%)	2 (3%)	0	100	100
15	f	82/98 (84%)	81 (99%)	1 (1%)	0	100	100
16	g	148/155 (96%)	148 (100%)	0	0	100	100
16	h	148/155 (96%)	146 (99%)	2 (1%)	0	100	100
16	i	148/155 (96%)	145 (98%)	2 (1%)	1 (1%)	18	51
16	j	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
16	k	148/155 (96%)	147 (99%)	1 (1%)	0	100	100
16	l	148/155 (96%)	147 (99%)	1 (1%)	0	100	100
16	m	148/155 (96%)	145 (98%)	3 (2%)	0	100	100
16	n	148/155 (96%)	145 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	o	148/155 (96%)	148 (100%)	0	0	100	100
17	p	49/350 (14%)	44 (90%)	5 (10%)	0	100	100
All	All	9084/10268 (88%)	8822 (97%)	257 (3%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	i	10	TYR
1	B	389	ALA
1	C	139	LYS
13	d	339	ARG
1	A	434	GLY

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	506/524 (97%)	505 (100%)	1 (0%)	87	87
1	B	507/524 (97%)	504 (99%)	3 (1%)	78	79
1	C	509/524 (97%)	502 (99%)	7 (1%)	59	70
2	D	394/431 (91%)	392 (100%)	2 (0%)	81	81
2	E	394/431 (91%)	394 (100%)	0	100	100
2	F	391/431 (91%)	382 (98%)	9 (2%)	44	63
3	G	325/344 (94%)	325 (100%)	0	100	100
4	H	189/212 (89%)	189 (100%)	0	100	100
5	I	196/198 (99%)	196 (100%)	0	100	100
5	J	196/198 (99%)	195 (100%)	1 (0%)	81	81
5	K	196/198 (99%)	196 (100%)	0	100	100
6	L	94/100 (94%)	94 (100%)	0	100	100
7	M	97/101 (96%)	97 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	N	99/101 (98%)	99 (100%)	0	100	100
7	O	99/101 (98%)	99 (100%)	0	100	100
8	P	389/428 (91%)	389 (100%)	0	100	100
9	Q	241/255 (94%)	240 (100%)	1 (0%)	84	83
9	R	241/255 (94%)	240 (100%)	1 (0%)	84	83
9	S	244/255 (96%)	244 (100%)	0	100	100
10	a	674/743 (91%)	673 (100%)	1 (0%)	88	89
11	b	156/158 (99%)	152 (97%)	4 (3%)	40	60
12	c	182/395 (46%)	181 (100%)	1 (0%)	81	81
13	d	303/306 (99%)	300 (99%)	3 (1%)	68	74
14	e	65/68 (96%)	65 (100%)	0	100	100
15	f	70/83 (84%)	70 (100%)	0	100	100
16	g	109/113 (96%)	108 (99%)	1 (1%)	70	74
16	h	109/113 (96%)	108 (99%)	1 (1%)	70	74
16	i	109/113 (96%)	109 (100%)	0	100	100
16	j	109/113 (96%)	109 (100%)	0	100	100
16	k	109/113 (96%)	108 (99%)	1 (1%)	70	74
16	l	109/113 (96%)	108 (99%)	1 (1%)	70	74
16	m	109/113 (96%)	109 (100%)	0	100	100
16	n	109/113 (96%)	109 (100%)	0	100	100
16	o	109/113 (96%)	109 (100%)	0	100	100
17	p	46/313 (15%)	46 (100%)	0	100	100
All	All	7784/8694 (90%)	7746 (100%)	38 (0%)	78	81

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	b	70	TYR
16	h	12	SER
11	b	153	VAL
13	d	24	LYS
16	l	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
9	S	132	GLN
13	d	84	HIS
10	a	41	ASN
10	a	548	HIS
16	i	78	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
18	ADP	C	801	-	28,29,29	1.07	1 (3%)	43,45,45	1.22	6 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
18	ADP	C	801	-	-	5/16/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	C	801	ADP	C5-C4	-2.34	1.34	1.39

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	C	801	ADP	C4-C5-N7	2.97	113.98	110.58
18	C	801	ADP	O2A-PA-O3A	2.85	114.98	107.27
18	C	801	ADP	C5-C4-N3	-2.54	123.22	126.72
18	C	801	ADP	C2-N1-C6	-2.26	115.01	118.73
18	C	801	ADP	C5-C6-N1	2.12	122.89	117.51

There are no chirality outliers.

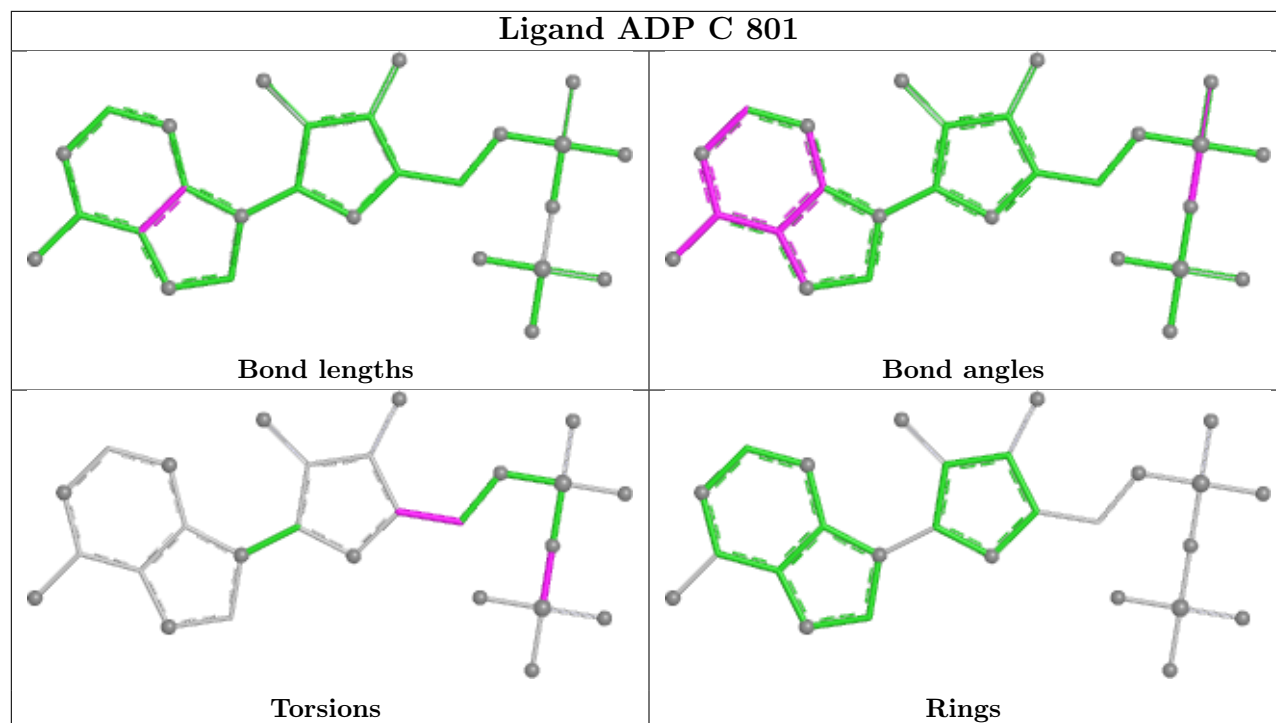
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
18	C	801	ADP	O4'-C4'-C5'-O5'
18	C	801	ADP	PA-O3A-PB-O1B
18	C	801	ADP	C3'-C4'-C5'-O5'
18	C	801	ADP	PA-O3A-PB-O2B
18	C	801	ADP	PA-O3A-PB-O3B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

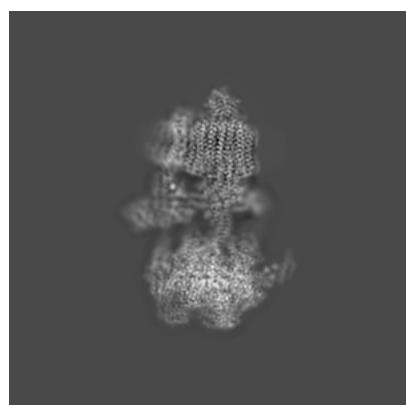
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26909. These allow visual inspection of the internal detail of the map and identification of artifacts.

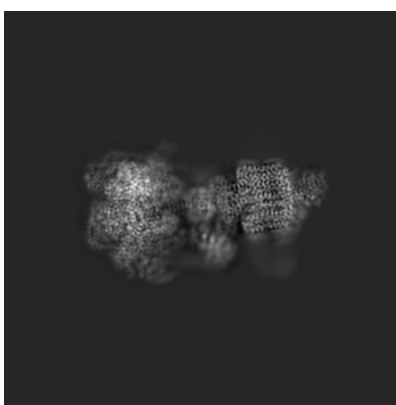
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

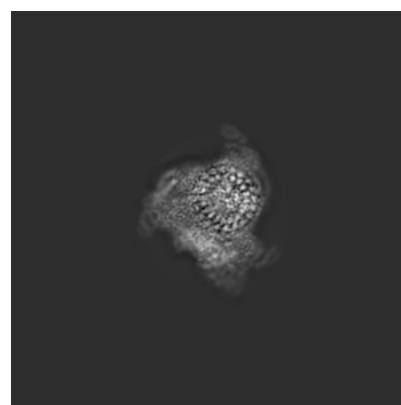
6.1.1 Primary map



X



Y



Z

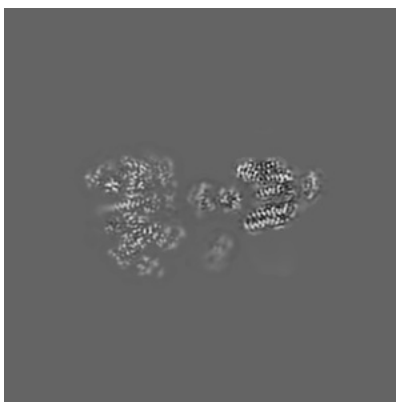
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 170



Y Index: 170

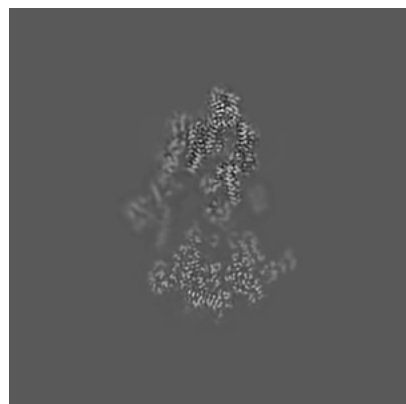


Z Index: 170

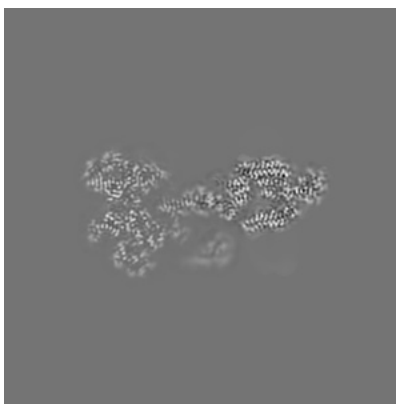
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

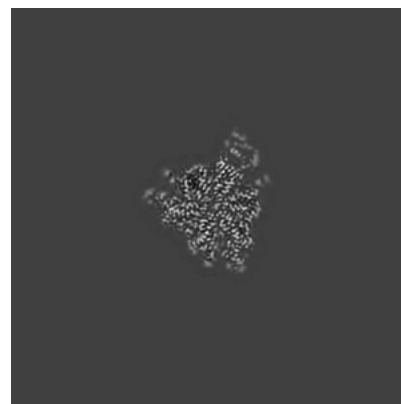
6.3.1 Primary map



X Index: 184



Y Index: 179

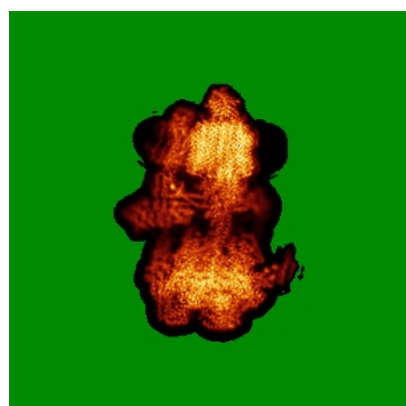


Z Index: 110

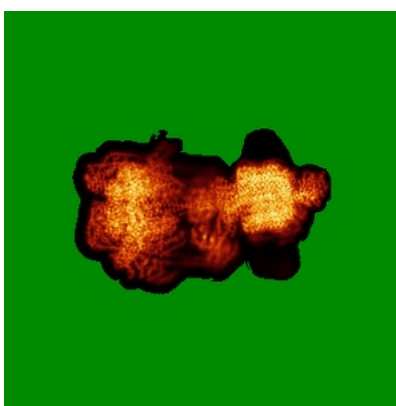
The images above show the largest variance slices of the map in three orthogonal directions.

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

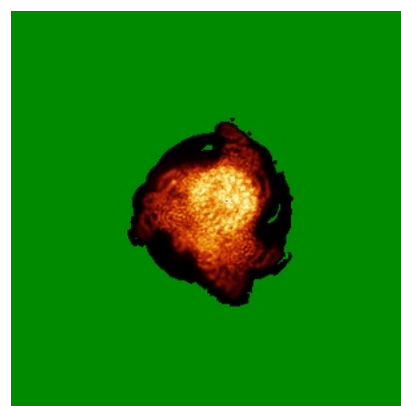
6.4.1 Primary map



X



Y

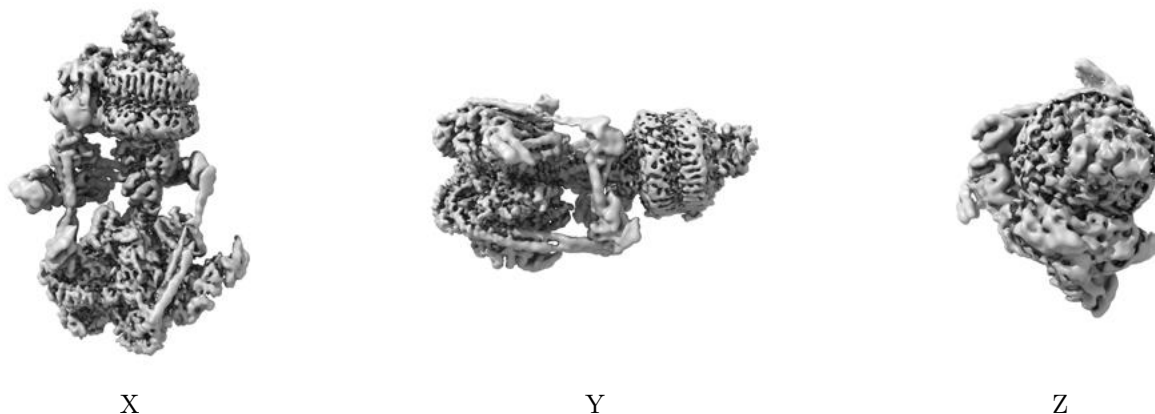


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

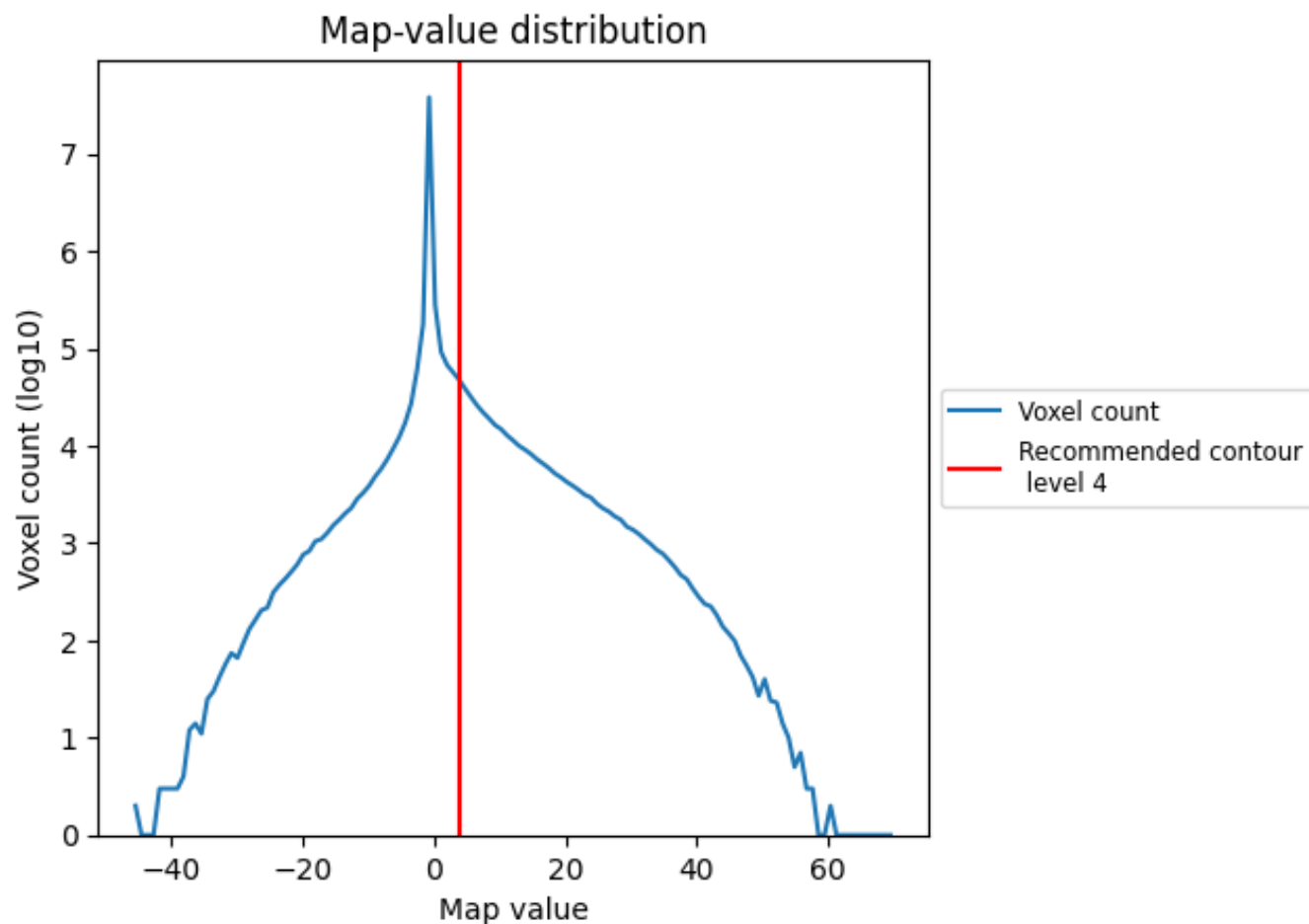
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

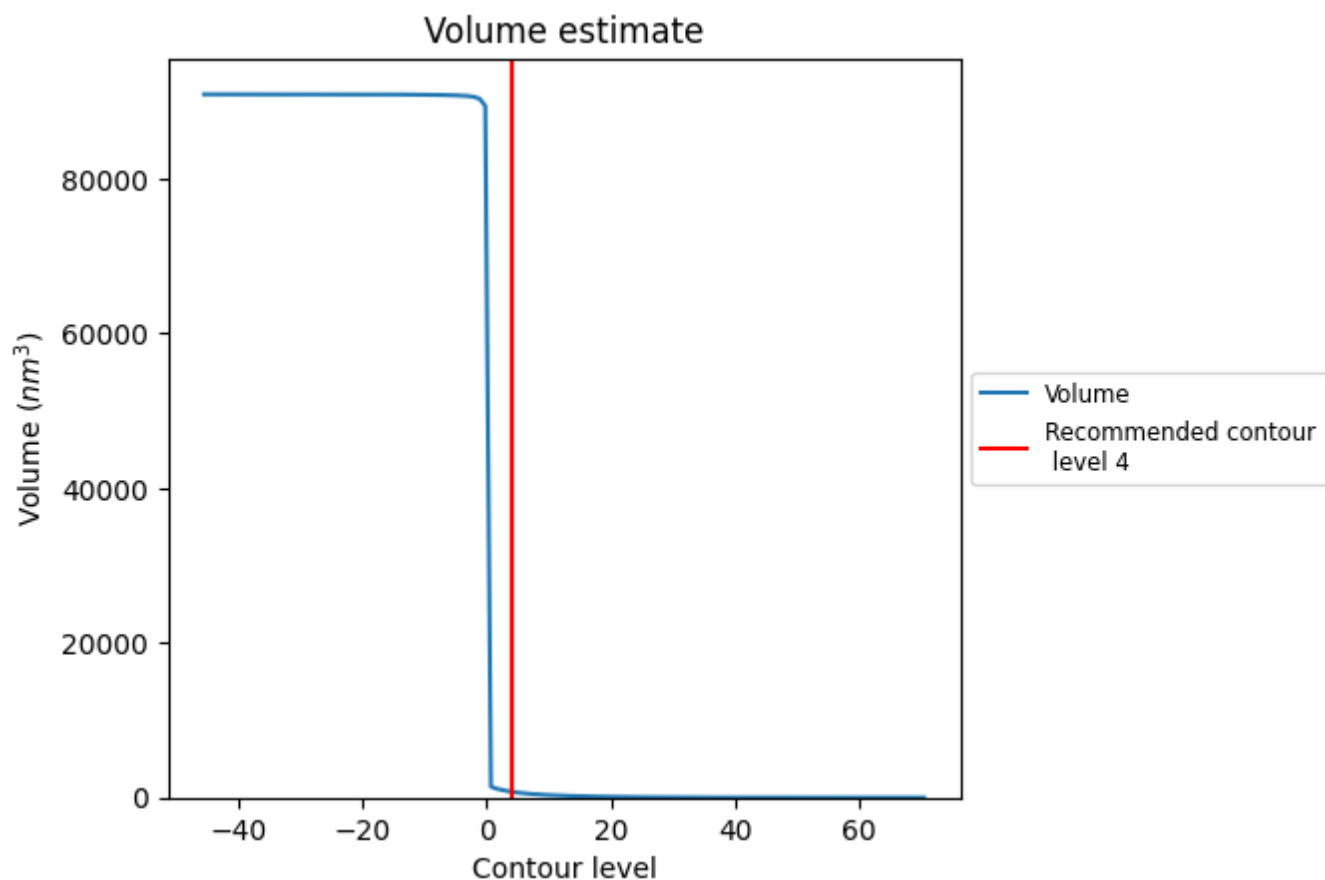
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

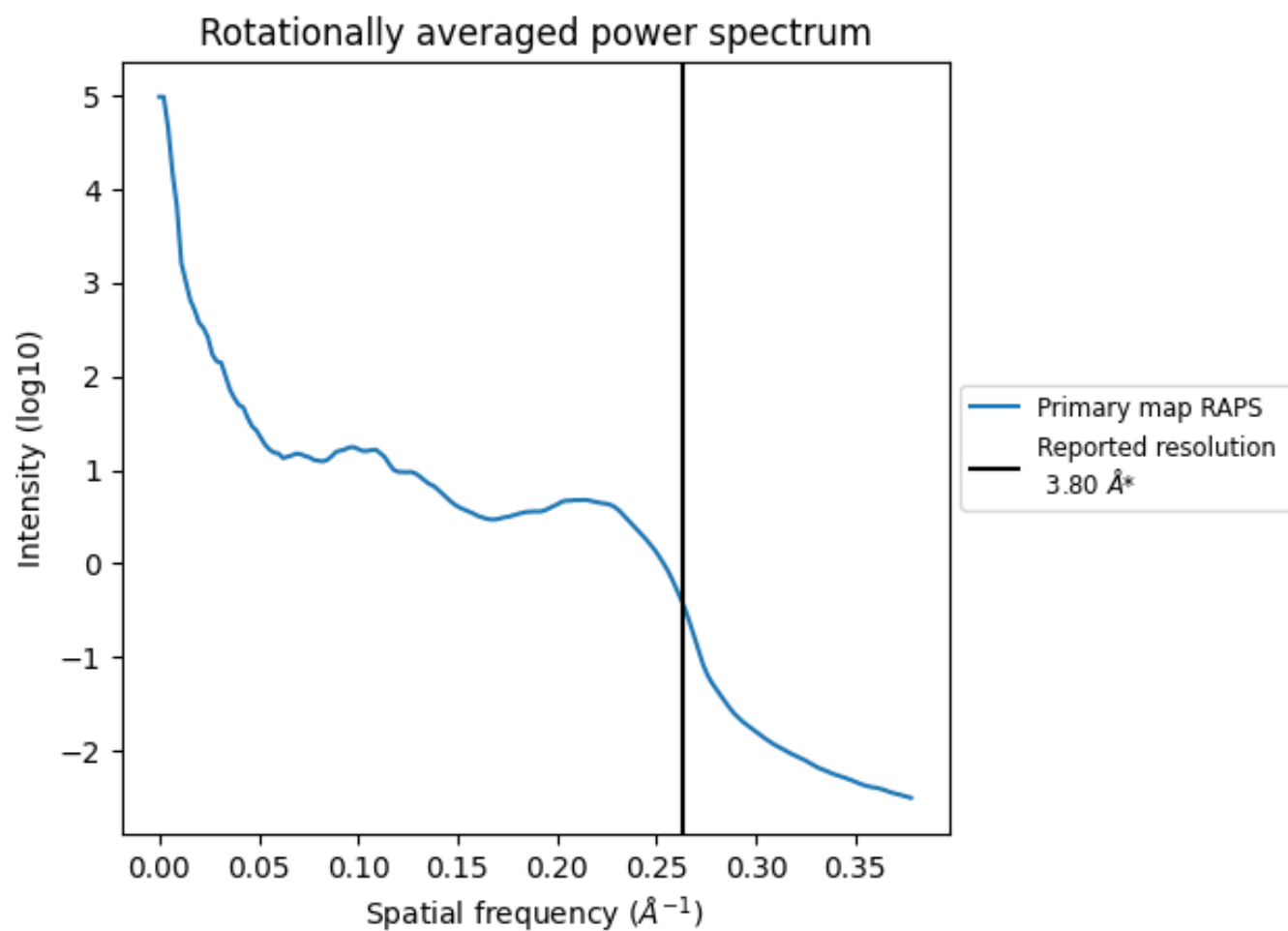
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 758 nm³; this corresponds to an approximate mass of 685 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 0.263 Å⁻¹

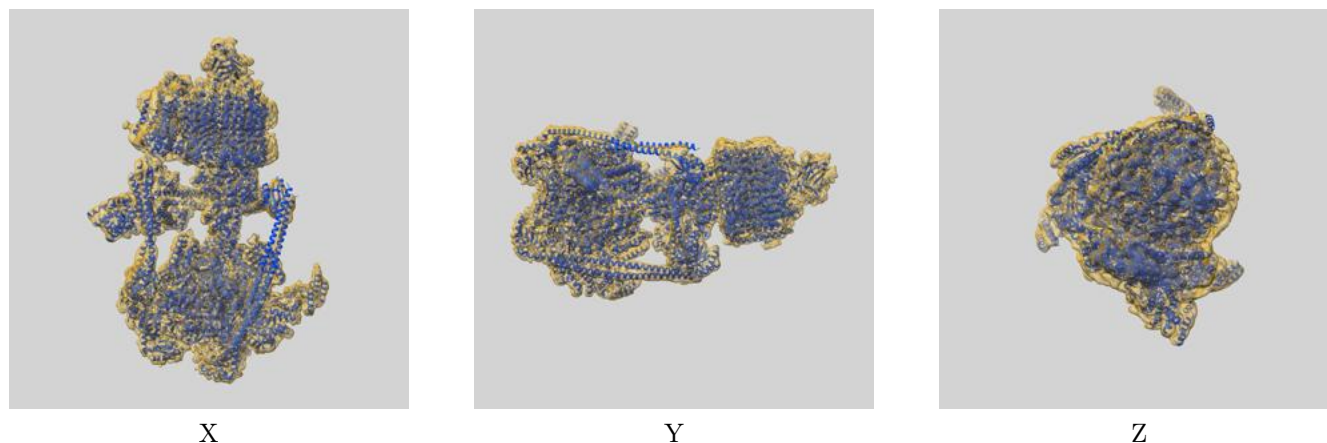
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

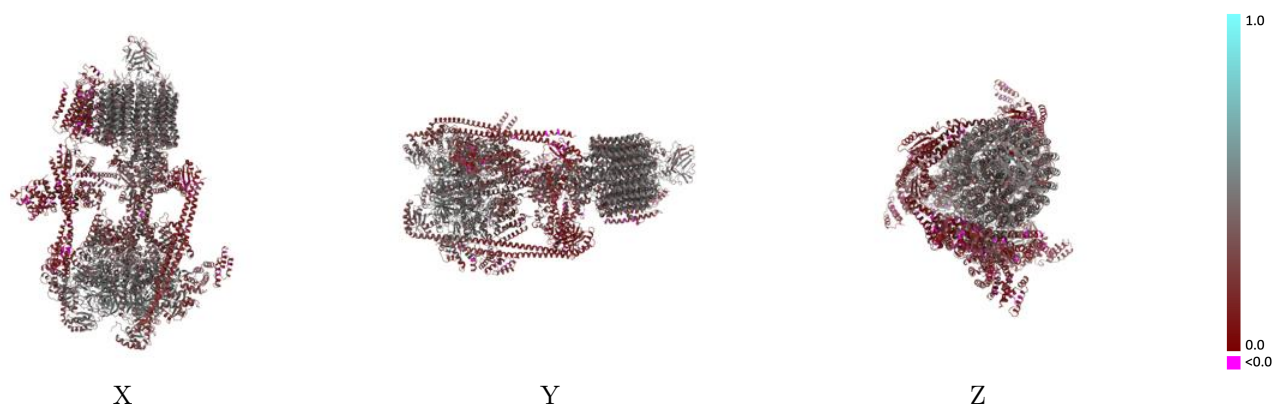
This section contains information regarding the fit between EMDB map EMD-26909 and PDB model 7UZF. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



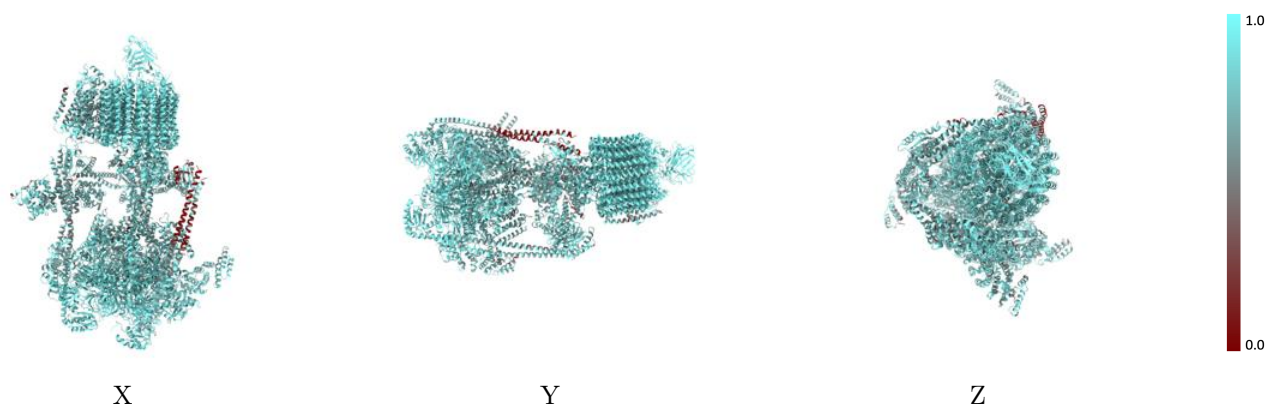
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



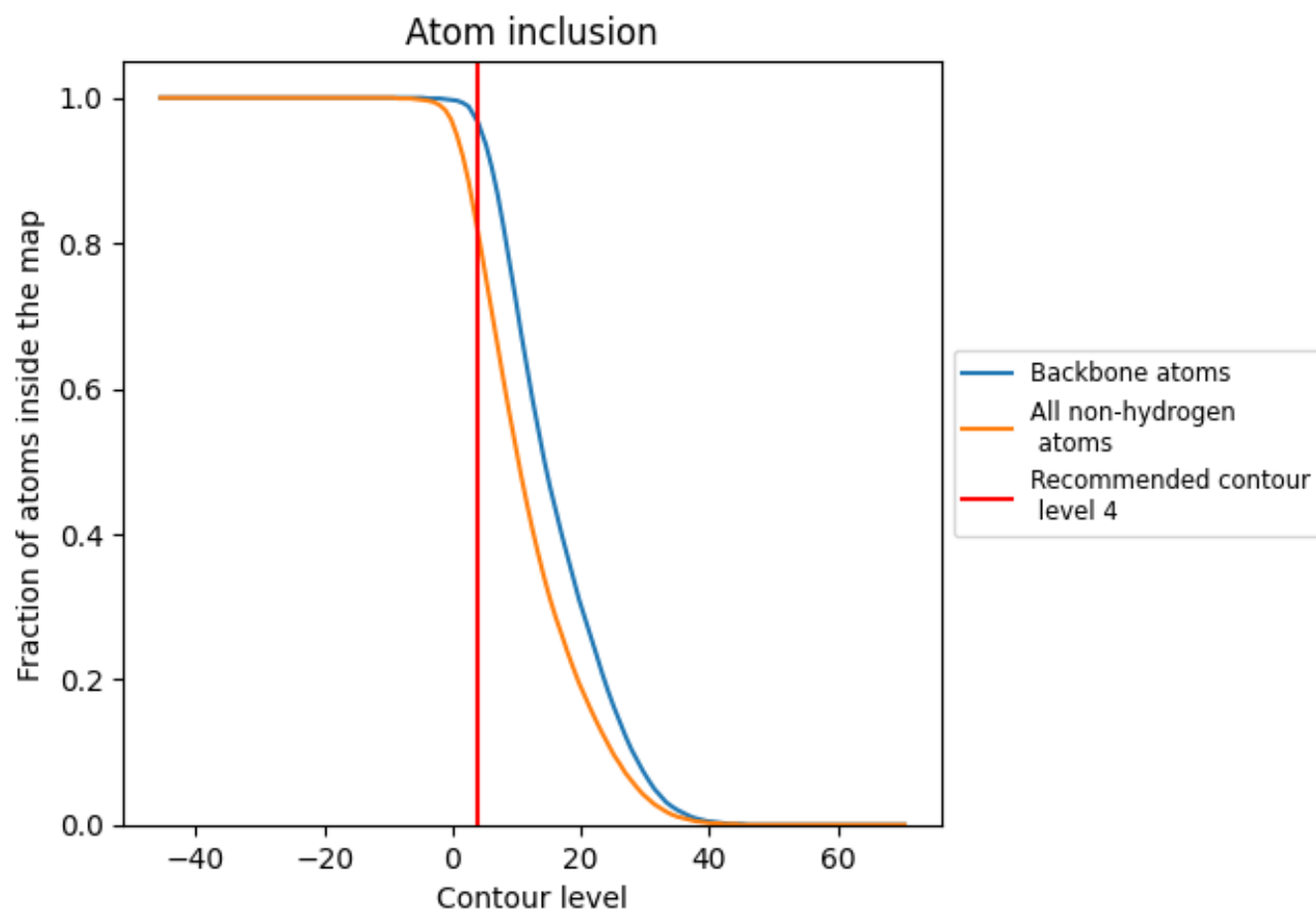
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 82% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8150	 0.3320
A	 0.8450	 0.3890
B	 0.8420	 0.3830
C	 0.8620	 0.4050
D	 0.8690	 0.4160
E	 0.8880	 0.4360
F	 0.8560	 0.4060
G	 0.6710	 0.1440
H	 0.7980	 0.3450
I	 0.7970	 0.2990
J	 0.8010	 0.2910
K	 0.6660	 0.2770
L	 0.7570	 0.2920
M	 0.7310	 0.2310
N	 0.7710	 0.2470
O	 0.5830	 0.2160
P	 0.7820	 0.1670
Q	 0.7490	 0.2400
R	 0.7920	 0.2690
S	 0.7550	 0.2510
a	 0.7610	 0.1960
b	 0.8880	 0.4350
c	 0.9010	 0.4180
d	 0.8470	 0.3890
e	 0.7550	 0.1860
f	 0.7320	 0.1450
g	 0.8830	 0.4290
h	 0.8850	 0.4310
i	 0.8730	 0.4240
j	 0.8700	 0.4150
k	 0.8660	 0.4160
l	 0.8730	 0.4260
m	 0.8810	 0.4300
n	 0.8780	 0.4420
o	 0.8810	 0.4370
p	 0.8670	 0.3960

