Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 05:30 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 Full wwPDB EM Validation 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:

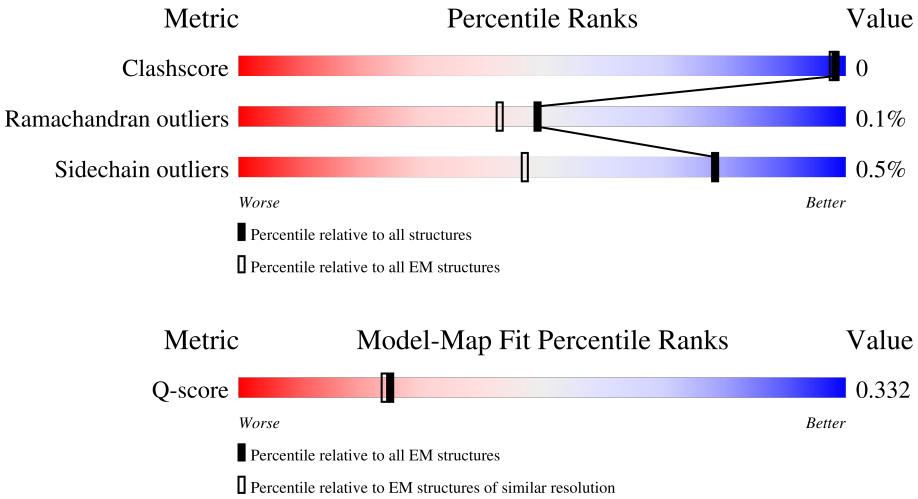
EMDB validation analysis	:	0.0.1.dev132
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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.



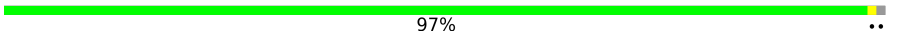
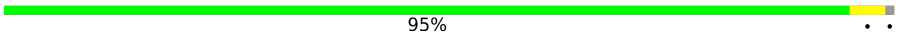
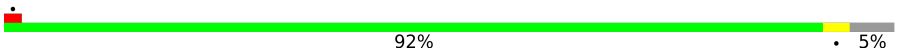
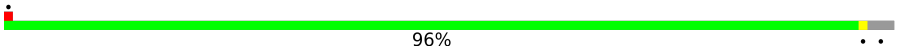
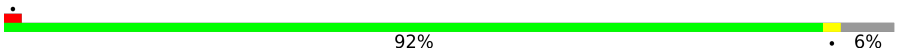
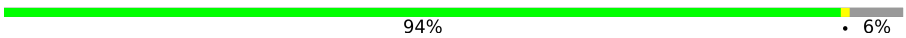
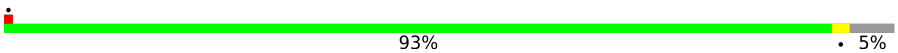
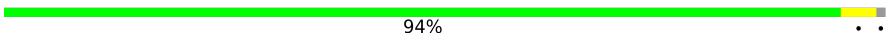
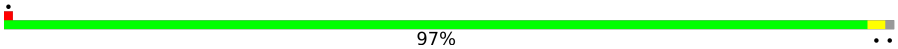
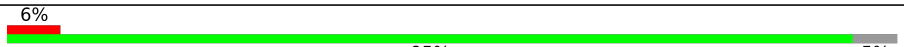
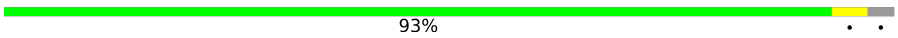
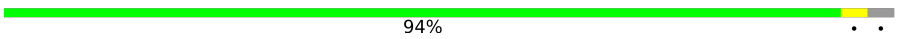
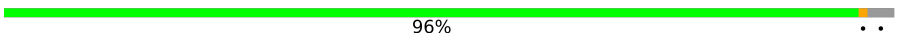
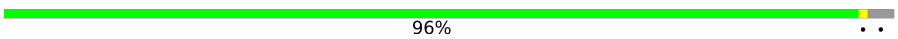
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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 <=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%

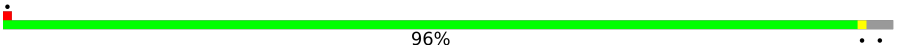
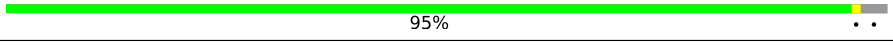
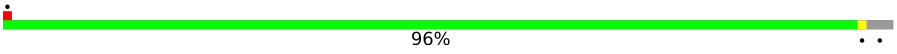
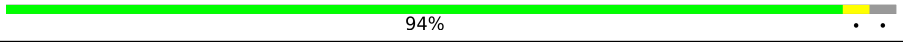
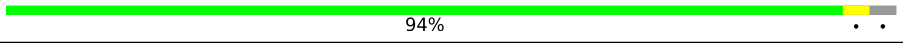
Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
16	k	155	
16	l	155	
16	m	155	
16	n	155	
16	o	155	
17	p	350	

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		

Continued on next page...

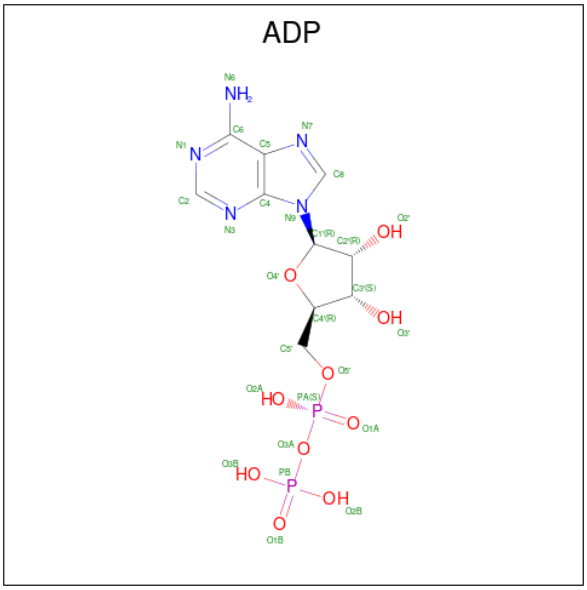
Continued from previous page...

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).



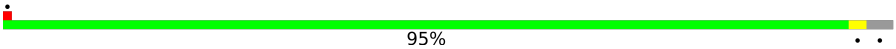
Mol	Chain	Residues	Atoms					AltConf
18	C	1	Total	C	N	O	P	0
			27	10	5	10	2	

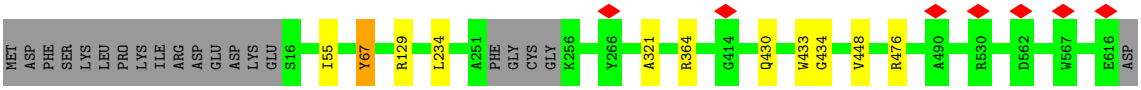
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

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

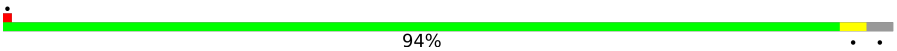
Chain A:

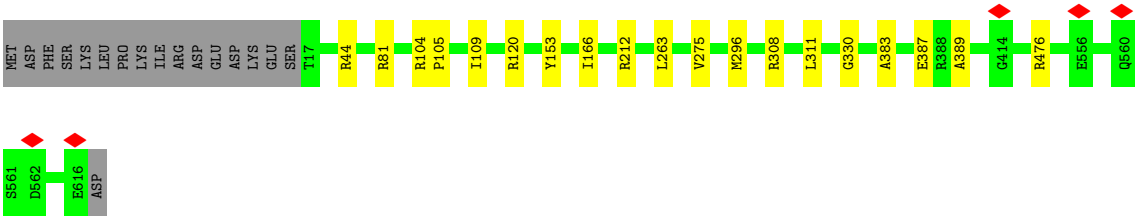




• Molecule 1: ATPase H+-transporting V1 subunit A

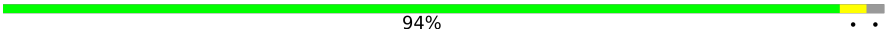
Chain B:





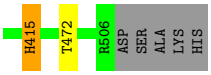
• Molecule 1: ATPase H+-transporting V1 subunit A

Chain C:



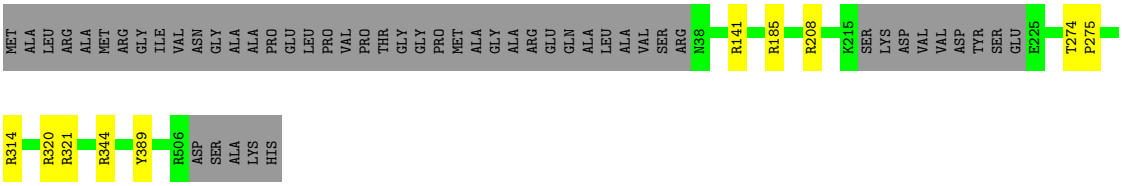
• Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain D:



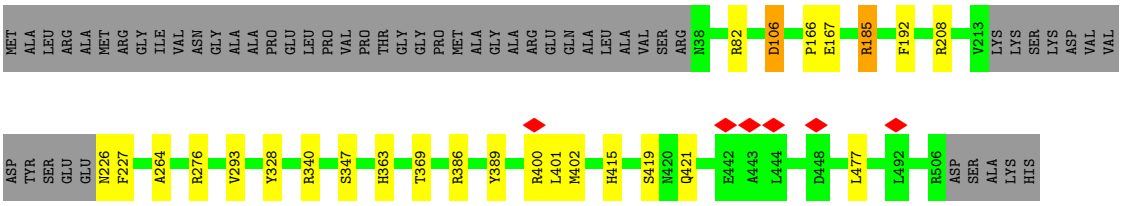
• Molecule 2: V-type proton ATPase subunit B, brain isoform

Chain E:



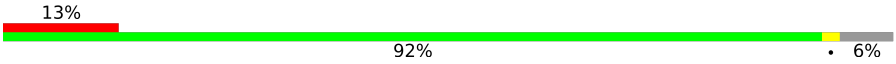
• Molecule 2: V-type proton ATPase subunit B, brain isoform

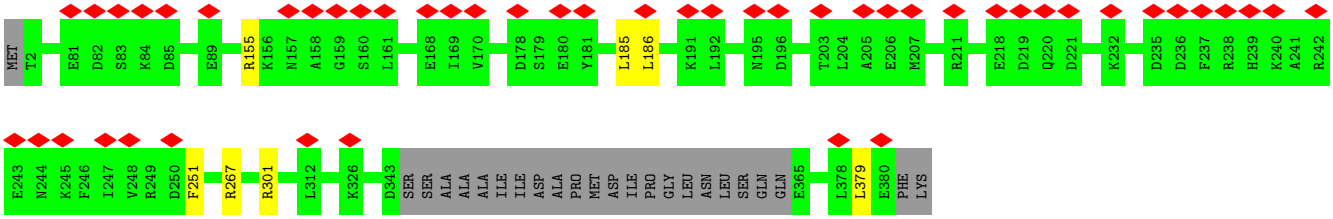
Chain F:



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

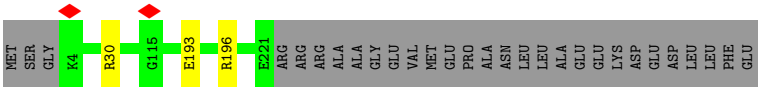
Chain G:





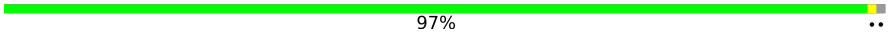
• Molecule 4: ATPase H+-transporting V1 subunit D

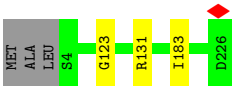
Chain H:



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

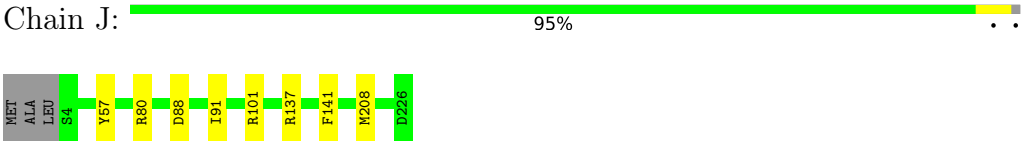
Chain I:





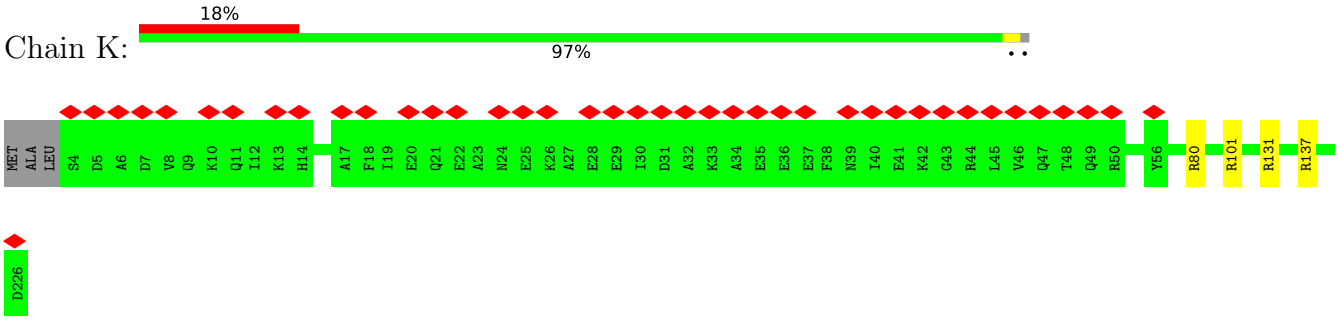
• Molecule 5: V-type proton ATPase subunit E 1

Chain J:



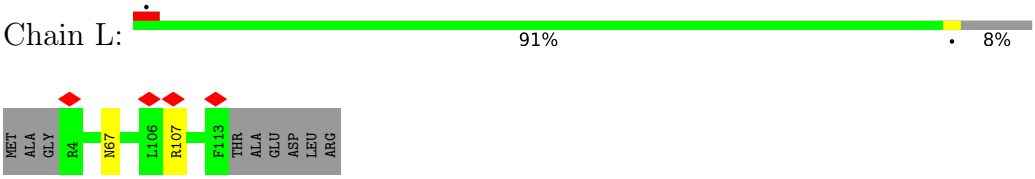
• Molecule 5: V-type proton ATPase subunit E 1

Chain K:



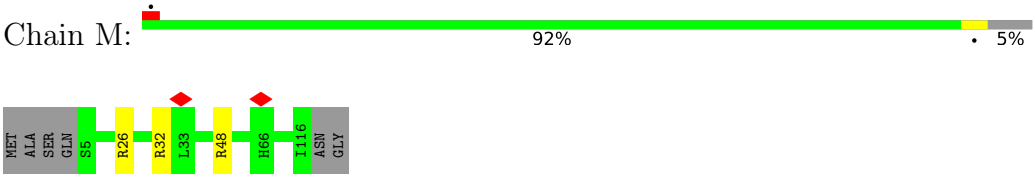
• Molecule 6: V-type proton ATPase subunit F

Chain L:



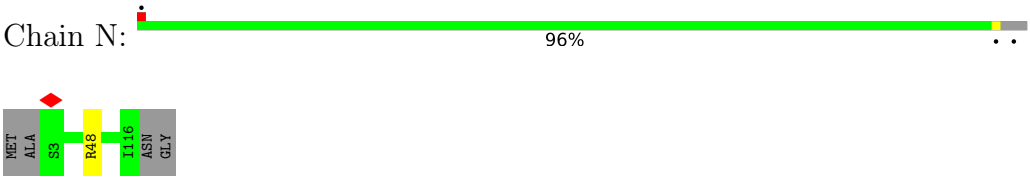
• Molecule 7: V-type proton ATPase subunit G

Chain M:



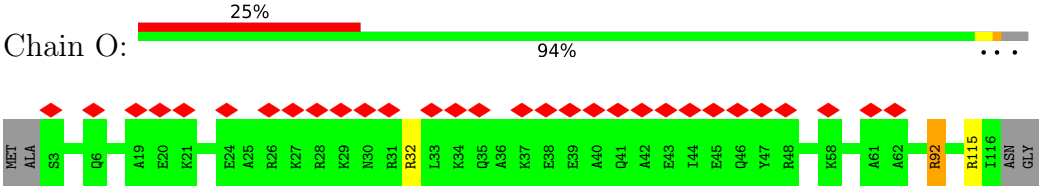
• Molecule 7: V-type proton ATPase subunit G

Chain N:



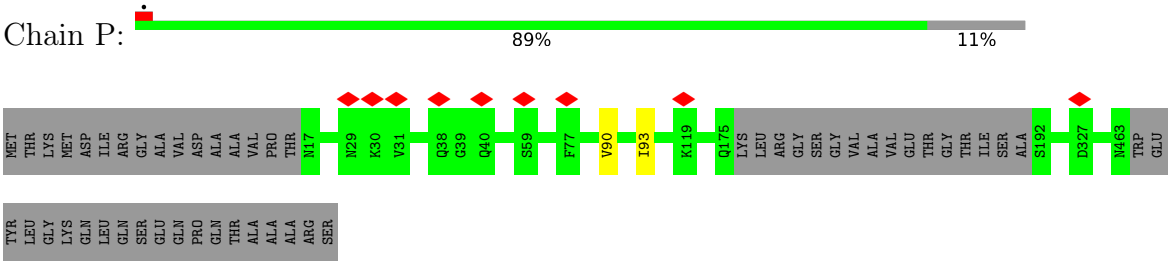
• Molecule 7: V-type proton ATPase subunit G

Chain O:



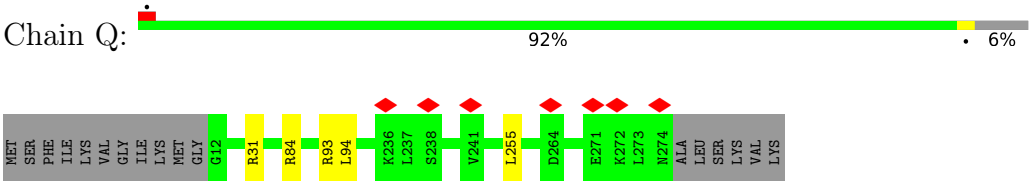
• Molecule 8: V-type proton ATPase subunit H

Chain P:



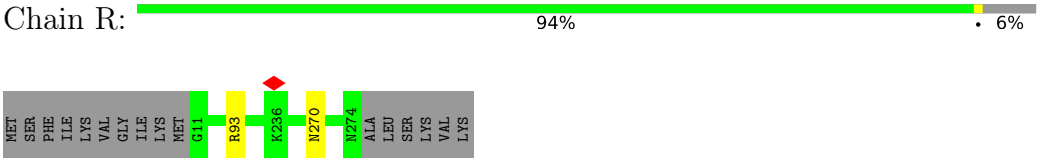
• Molecule 9: Effector SidK

Chain Q:



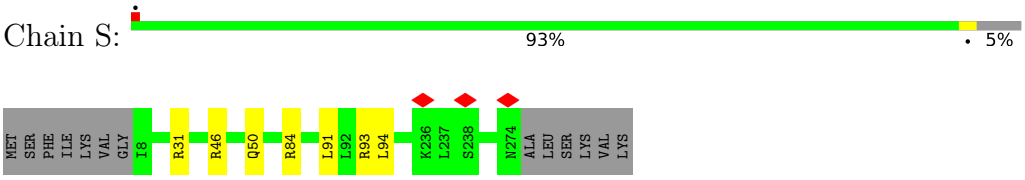
• Molecule 9: Effector SidK

Chain R:



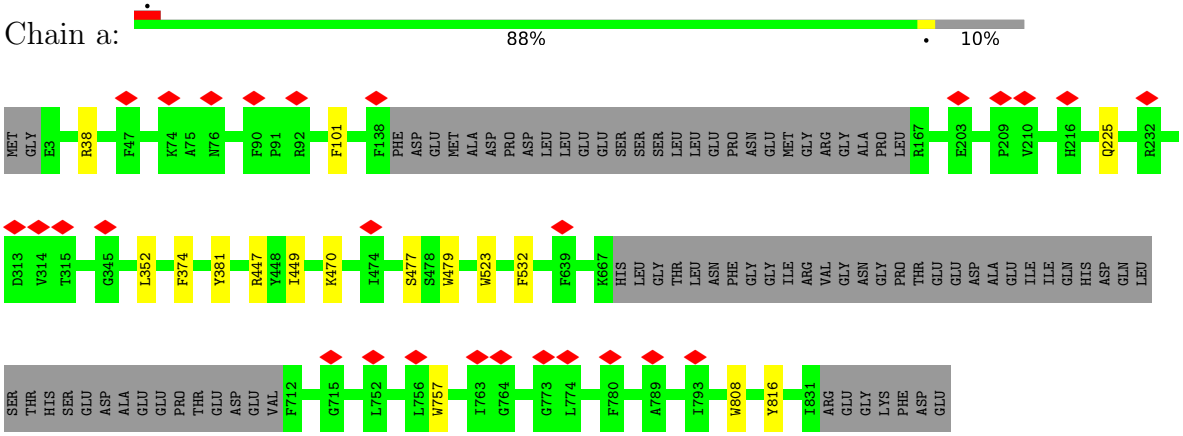
• Molecule 9: Effector SidK

Chain S:



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

Chain a:

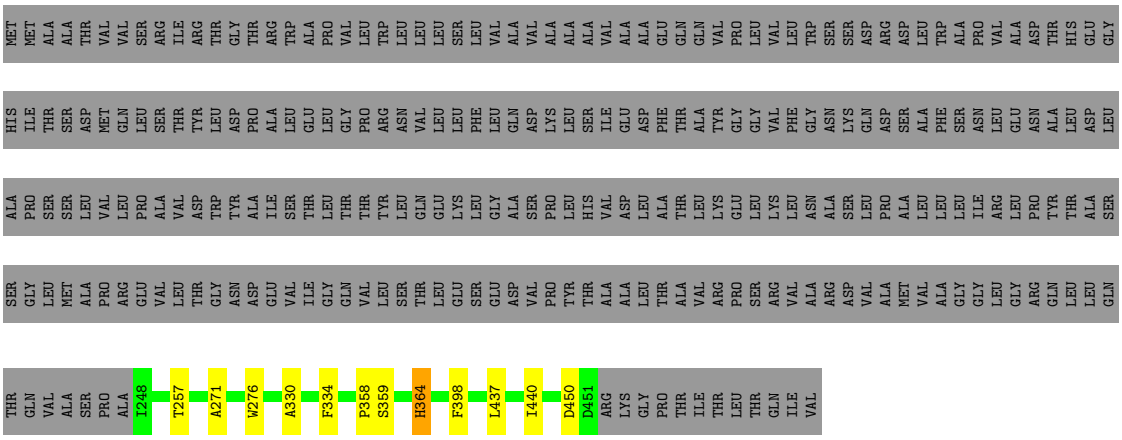


• Molecule 11: ATPase, H+ transporting, V0 subunit B (Predicted), isoform CRA_a

Chain b:

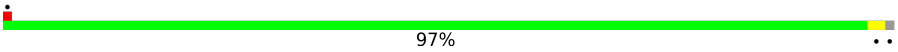
• Molecule 12: V-type proton ATPase subunit S1

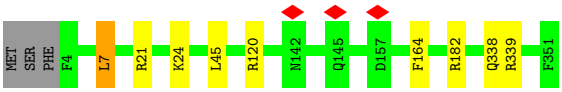
Chain c:



• Molecule 13: V-type proton ATPase subunit

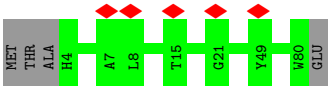
Chain d:





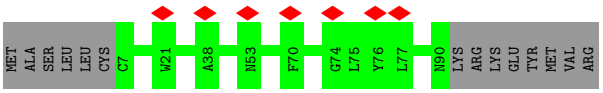
• Molecule 14: V-type proton ATPase subunit e 2

Chain e:



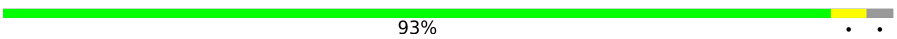
• Molecule 15: Ribonuclease K

Chain f:



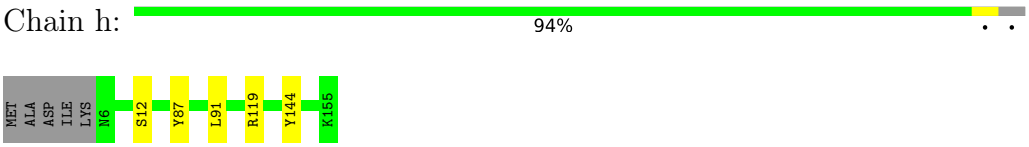
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain g:



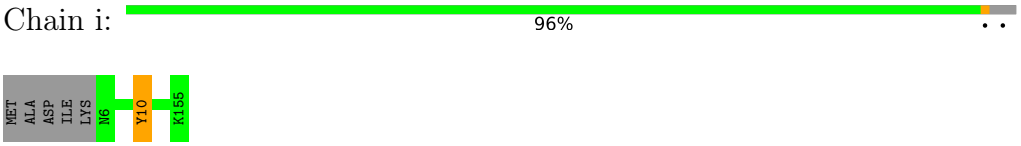
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain h:



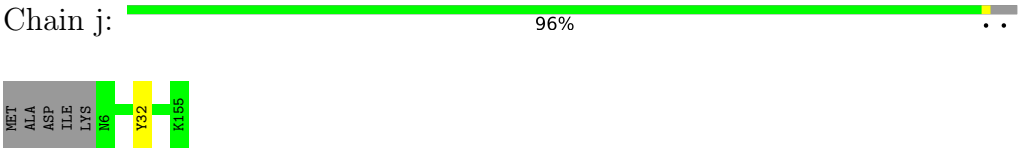
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain i:



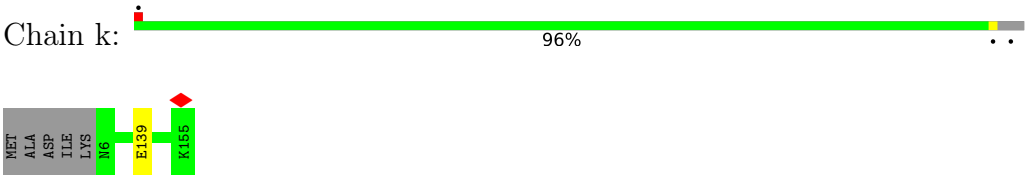
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain j:



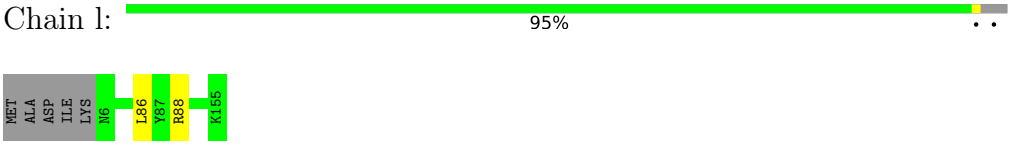
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain k:



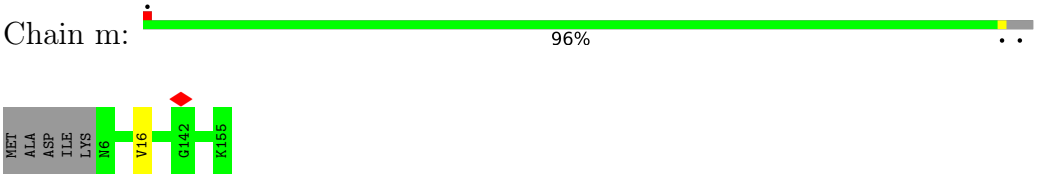
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain l:



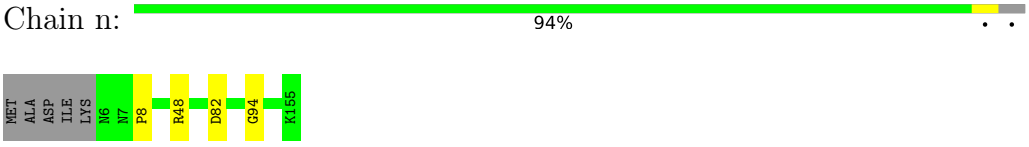
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

Chain m:



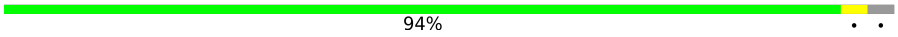
• Molecule 16: V-type proton ATPase 16 kDa proteolipid subunit

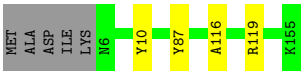
Chain n:



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

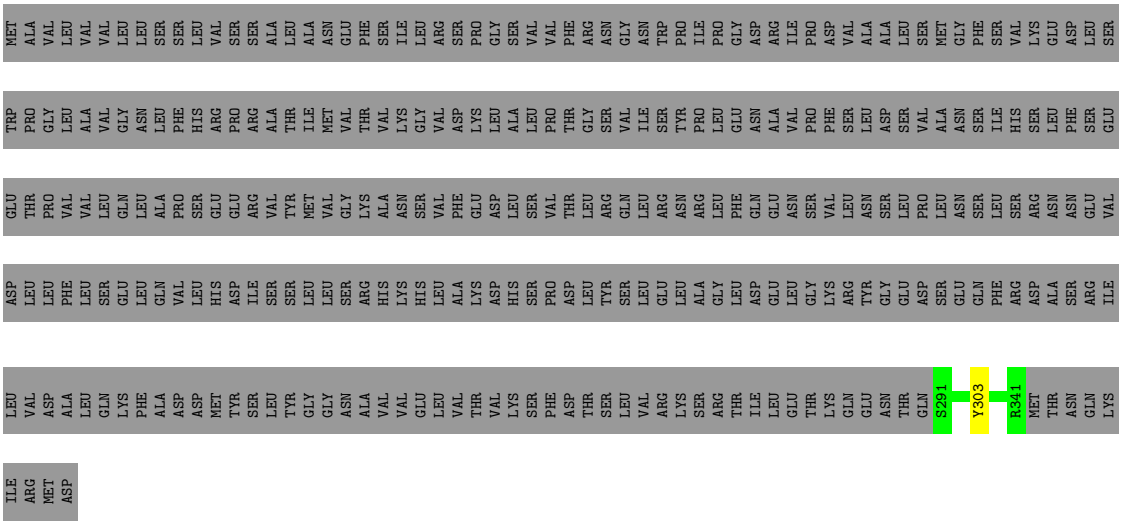
Chain o:





• Molecule 17: Renin receptor

Chain p:



4 Experimental information (i)

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 ($e^-/Å^2$)	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.

All (87) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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
10	a	225	GLN	OE1-CD-NE2	-6.19	116.41	122.60
2	E	321	ARG	NE-CZ-NH2	6.11	124.69	119.20
13	d	7	LEU	N-CA-CB	-6.04	99.79	110.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	308	ARG	CD-NE-CZ	5.99	132.79	124.40
5	K	80	ARG	NE-CZ-NH2	5.96	124.57	119.20
10	a	101	PHE	CA-CB-CG	5.86	119.66	113.80
1	A	129	ARG	NE-CZ-NH2	5.81	124.43	119.20
9	R	93	ARG	NE-CZ-NH2	5.79	124.41	119.20
9	S	93	ARG	NE-CZ-NH2	5.78	124.40	119.20
6	L	107	ARG	NE-CZ-NH2	5.77	124.39	119.20
9	S	46	ARG	NE-CZ-NH2	5.76	124.38	119.20
2	E	141	ARG	NE-CZ-NH2	5.68	124.31	119.20
2	F	106	ASP	CA-CB-CG	5.60	118.20	112.60
11	b	51	ASN	CA-CB-CG	-5.60	107.00	112.60
1	B	120	ARG	NE-CZ-NH2	5.59	124.23	119.20
5	I	131	ARG	NE-CZ-NH2	5.59	124.23	119.20
13	d	338	GLN	OE1-CD-NE2	-5.57	117.03	122.60
13	d	182	ARG	NE-CZ-NH2	5.56	124.21	119.20
2	E	344	ARG	NE-CZ-NH2	5.52	124.17	119.20
1	B	105	PRO	N-CA-CB	5.52	106.93	103.23
10	a	447	ARG	NE-CZ-NH2	5.51	124.16	119.20
5	K	131	ARG	NE-CZ-NH2	5.51	124.16	119.20
7	M	48	ARG	NE-CZ-NH2	5.49	124.14	119.20
7	M	26	ARG	NE-CZ-NH2	5.48	124.13	119.20
5	J	141	PHE	CA-CB-CG	5.47	119.27	113.80
2	F	192	PHE	CA-CB-CG	5.47	119.27	113.80
7	O	32	ARG	NE-CZ-NH2	5.46	124.11	119.20
2	F	400	ARG	NE-CZ-NH2	5.44	124.09	119.20
7	N	48	ARG	NE-CZ-NH2	5.43	124.08	119.20
1	B	476	ARG	NE-CZ-NH2	5.40	124.06	119.20
7	O	115	ARG	NE-CZ-NH2	5.40	124.06	119.20
5	J	80	ARG	NE-CZ-NH2	5.40	124.06	119.20
16	o	116	ALA	CA-C-N	5.39	125.82	119.94
16	o	116	ALA	C-N-CA	5.39	125.82	119.94
1	A	476	ARG	NE-CZ-NH2	5.38	124.04	119.20
12	c	450	ASP	N-CA-C	5.38	117.62	110.53
9	S	31	ARG	NE-CZ-NH2	5.34	124.01	119.20
2	F	363	HIS	CB-CG-CD2	-5.34	124.26	131.20
16	g	48	ARG	NE-CZ-NH2	5.34	124.00	119.20
2	D	363	HIS	CB-CG-CD2	-5.33	124.27	131.20
2	F	208	ARG	NE-CZ-NH2	5.33	124.00	119.20
3	G	301	ARG	NE-CZ-NH2	5.33	123.99	119.20
3	G	155	ARG	NE-CZ-NH2	5.30	123.97	119.20
9	Q	31	ARG	NE-CZ-NH2	5.29	123.96	119.20
1	B	44	ARG	NE-CZ-NH2	5.27	123.94	119.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	314	ARG	NE-CZ-NH2	5.26	123.94	119.20
2	F	386	ARG	NE-CZ-NH2	5.26	123.94	119.20
3	G	267	ARG	NE-CZ-NH2	5.26	123.93	119.20
12	c	364	HIS	CB-CG-CD2	-5.26	124.37	131.20
12	c	257	THR	CA-C-N	5.24	129.66	122.06
12	c	257	THR	C-N-CA	5.24	129.66	122.06
2	D	415	HIS	CA-CB-CG	5.21	119.01	113.80
7	M	32	ARG	NE-CZ-NH2	5.20	123.88	119.20
9	S	84	ARG	NE-CZ-NH2	5.15	123.83	119.20
16	n	48	ARG	NE-CZ-NH2	5.14	123.83	119.20
13	d	120	ARG	NE-CZ-NH2	5.12	123.80	119.20
2	E	320	ARG	NE-CZ-NH2	5.11	123.80	119.20
16	l	88	ARG	NE-CZ-NH2	5.10	123.79	119.20
1	B	81	ARG	NE-CZ-NH2	5.09	123.78	119.20
5	J	101	ARG	NE-CZ-NH2	5.09	123.78	119.20
2	F	369	THR	CA-C-N	5.09	125.59	119.94
2	F	369	THR	C-N-CA	5.09	125.59	119.94
9	Q	84	ARG	NE-CZ-NH2	5.09	123.78	119.20
11	b	34	ARG	NE-CZ-NH2	5.09	123.78	119.20
1	A	55	ILE	CB-CA-C	5.09	115.74	110.70
6	L	67	ASN	OD1-CG-ND2	-5.08	117.52	122.60
10	a	38	ARG	NE-CZ-NH2	5.07	123.76	119.20
2	E	208	ARG	NE-CZ-NH2	5.06	123.76	119.20
1	C	81	ARG	NH1-CZ-NH2	-5.05	112.73	119.30
2	F	276	ARG	NE-CZ-NH2	5.05	123.74	119.20
16	g	116	ALA	CA-C-N	5.04	125.58	119.98
16	g	116	ALA	C-N-CA	5.04	125.58	119.98
7	O	92	ARG	NE-CZ-NH2	5.04	123.73	119.20
2	F	421	GLN	OE1-CD-NE2	-5.03	117.57	122.60
16	h	119	ARG	NE-CZ-NH2	5.03	123.73	119.20
1	C	459	ARG	NE-CZ-NH2	5.02	123.71	119.20
1	B	212	ARG	NE-CZ-NH2	5.01	123.71	119.20
5	K	101	ARG	NE-CZ-NH2	5.01	123.71	119.20
4	H	30	ARG	NE-CZ-NH2	5.00	123.70	119.20
9	S	50	GLN	CA-C-N	5.00	126.98	120.28
9	S	50	GLN	C-N-CA	5.00	126.98	120.28
2	F	340	ARG	NE-CZ-NH2	5.00	123.70	119.20

There are no chirality outliers.

All (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
2	D	389	TYR	Sidechain
2	E	389	TYR	Sidechain
2	F	185	ARG	Sidechain
2	F	389	TYR	Sidechain
2	F	82	ARG	Sidechain
5	J	137	ARG	Sidechain
5	J	57	TYR	Sidechain
5	K	137	ARG	Sidechain
7	O	92	ARG	Sidechain
10	a	816	TYR	Sidechain
11	b	26	TYR	Sidechain
11	b	8	TYR	Sidechain
13	d	164	PHE	Sidechain
13	d	21	ARG	Sidechain
16	g	32	TYR	Sidechain
16	h	144	TYR	Sidechain
16	i	10	TYR	Sidechain
16	j	32	TYR	Sidechain
16	o	10	TYR	Sidechain
16	o	119	ARG	Sidechain
17	p	303	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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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.

All (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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:186:LEU:HD13	3:G:251:PHE:H	1.76	0.51
1:B:275:VAL:HG11	1:B:330:GLY:HA3	1.94	0.49
16:g:44:MET:HG2	16:g:122:ALA:HB2	1.95	0.49
11:b:33:PHE:CG	12:c:358:PRO:HG3	2.48	0.48
1:A:67:TYR:CE1	1:A:321:ALA:HB1	2.49	0.48
16:h:87:TYR:CZ	16:h:91:LEU:HD11	2.49	0.47
12:c:334:PHE:CE1	12:c:359:SER:CB	2.97	0.47
3:G:185:LEU:C	3:G:186:LEU:HD12	2.39	0.46
2:D:406:ILE:HD12	2:D:415:HIS:CE1	2.50	0.46
9:Q:94:LEU:C	9:Q:94:LEU:HD23	2.40	0.46
10:a:470:LYS:HE3	10:a:757:TRP:CE2	2.51	0.45
10:a:374:PHE:CE2	10:a:449:ILE:HG22	2.51	0.45
12:c:364:HIS:CD2	12:c:364:HIS:C	2.94	0.45
8:P:90:VAL:HA	8:P:93:ILE:HG22	1.99	0.44
1:C:574:MET:HE1	1:C:612:PHE:CE2	2.53	0.44
1:C:167:MET:HE1	1:C:339:ASP:C	2.43	0.43
12:c:334:PHE:CE1	12:c:359:SER:HB2	2.53	0.43
16:m:16:VAL:HG13	16:n:94:GLY:HA3	2.00	0.43
12:c:437:LEU:HA	12:c:440:ILE:HG22	1.99	0.43
2:F:166:PRO:HG2	2:F:401:LEU:HD13	2.01	0.43
2:E:274:THR:HB	2:E:275:PRO:HD3	2.00	0.43
4:H:193:GLU:CD	4:H:196:ARG:HH22	2.27	0.42
5:I:123:GLY:HA3	5:I:183:ILE:HD13	2.02	0.42
5:J:88:ASP:HA	5:J:91:ILE:HG22	2.00	0.42
1:B:387:GLU:CG	2:F:264:ALA:HB3	2.50	0.42
12:c:271:ALA:HB2	12:c:276:TRP:CD2	2.55	0.41
16:g:44:MET:SD	16:g:44:MET:C	3.04	0.41
1:B:383:ALA:HB1	2:F:264:ALA:HB1	2.02	0.41
1:B:153:TYR:CZ	1:B:166:ILE:HG22	2.56	0.41
10:a:381:TYR:HB3	10:a:808:TRP:CD2	2.55	0.41
1:C:353:ARG:HD2	2:F:328:TYR:CZ	2.56	0.41
9:S:91:LEU:HD13	9:S:91:LEU:C	2.46	0.41
2:F:415:HIS:CD2	2:F:477:LEU:HD21	2.56	0.41
12:c:330:ALA:HB2	16:n:8:PRO:HA	2.02	0.40
11:b:58:ILE:CD1	11:b:105:ILE:HA	2.51	0.40
9:S:94:LEU:HD23	9:S:94:LEU:C	2.47	0.40
10:a:523:TRP:CE2	10:a:532:PHE:CE2	3.10	0.40
10:a:477:SER:HB2	10:a:479:TRP:CD1	2.56	0.40
1:A:234:LEU:HD22	1:A:433:TRP:CD1	2.57	0.40
16:n:82:ASP:HA	16:o:87:TYR:CD1	2.56	0.40

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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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 (i)

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

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
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
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

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	430	GLN
1	B	263	LEU
1	B	296	MET
1	B	311	LEU
1	C	228	LEU
1	C	286	GLU
1	C	289	ARG
1	C	443	LYS
1	C	510	GLU
1	C	568	SER
1	C	572	GLU
2	D	356	MET
2	D	472	THR
2	F	106	ASP
2	F	167	GLU
2	F	185	ARG
2	F	226	ASN
2	F	227	PHE
2	F	293	VAL
2	F	347	SER
2	F	402	MET
2	F	419	SER
5	J	208	MET
9	Q	255	LEU
9	R	270	ASN
10	a	352	LEU
11	b	34	ARG
11	b	67	TRP
11	b	70	TYR
11	b	153	VAL
12	c	398	PHE
13	d	7	LEU
13	d	24	LYS
13	d	45	LEU
16	g	139	GLU
16	h	12	SER
16	k	139	GLU
16	l	86	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (78) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	HIS
1	A	184	ASN
1	A	231	GLN
1	A	543	ASN
1	B	140	ASN
1	B	157	ASN
1	B	231	GLN
1	B	543	ASN
1	C	22	HIS
1	C	146	HIS
1	C	231	GLN
1	C	444	HIS
1	C	484	GLN
1	C	521	GLN
2	D	73	HIS
2	D	200	ASN
2	D	205	GLN
2	D	209	GLN
2	D	251	ASN
2	D	415	HIS
2	D	461	ASN
2	E	181	ASN
2	E	292	HIS
2	F	97	GLN
2	F	181	ASN
2	F	200	ASN
2	F	384	HIS
3	G	74	GLN
3	G	200	GLN
3	G	214	ASN
3	G	317	GLN
3	G	322	GLN
4	H	111	HIS
5	I	9	GLN
5	I	63	GLN
5	I	67	GLN
5	J	9	GLN
5	J	24	ASN
5	K	9	GLN
5	K	66	GLN
7	M	10	GLN
7	M	50	GLN
7	N	6	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
7	O	6	GLN
7	O	10	GLN
8	P	17	ASN
8	P	384	ASN
8	P	435	GLN
8	P	439	ASN
9	Q	40	ASN
9	Q	132	GLN
9	Q	149	ASN
9	Q	177	GLN
9	Q	196	GLN
9	Q	243	GLN
9	R	40	ASN
9	R	176	ASN
9	S	132	GLN
10	a	14	GLN
10	a	41	ASN
10	a	115	GLN
10	a	269	GLN
10	a	273	ASN
10	a	489	ASN
10	a	524	ASN
10	a	548	HIS
11	b	197	GLN
12	c	364	HIS
12	c	391	HIS
12	c	392	ASN
13	d	13	ASN
13	d	84	HIS
13	d	152	ASN
13	d	340	HIS
15	f	64	GLN
16	i	78	ASN
16	o	123	GLN
17	p	327	ASN

5.3.3 RNA

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

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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
18	C	801	ADP	N6-C6-N1	-2.05	113.82	118.38

There are no chirality outliers.

All (5) torsion outliers are listed below:

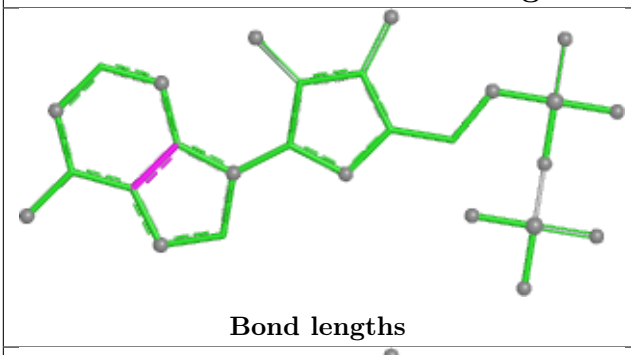
Mol	Chain	Res	Type	Atoms
18	C	801	ADP	O4'-C4'-C5'-O5'
18	C	801	ADP	PA-O3A-PB-O1B
18	C	801	ADP	C3'-C4'-C5'-O5'
18	C	801	ADP	PA-O3A-PB-O2B
18	C	801	ADP	PA-O3A-PB-O3B

There are no ring outliers.

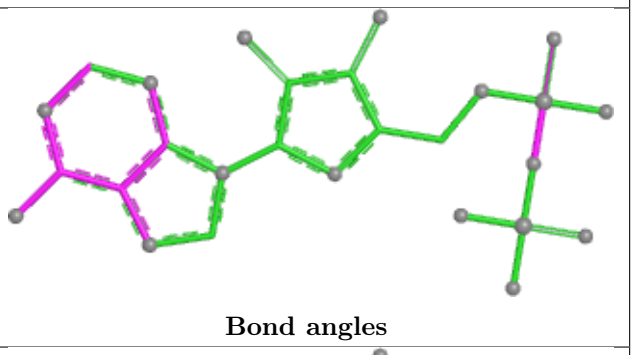
No monomer is involved in short contacts.

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 then 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.

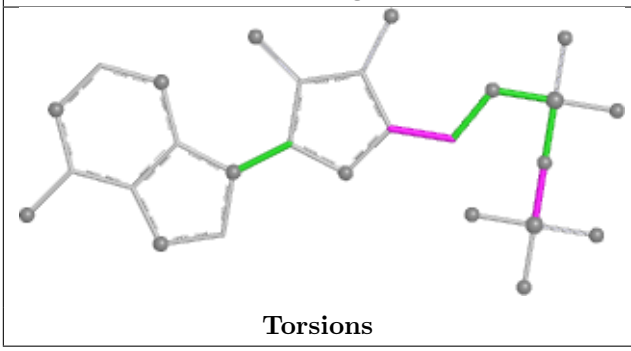
Ligand ADP C 801



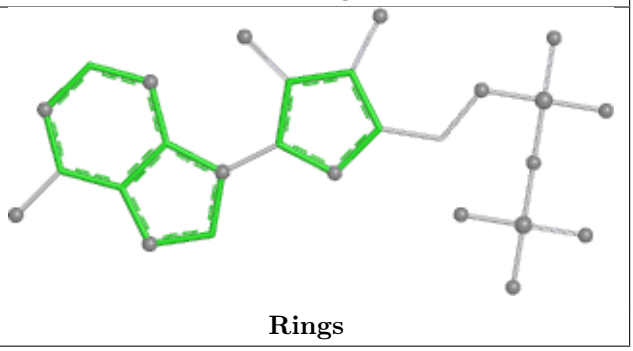
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

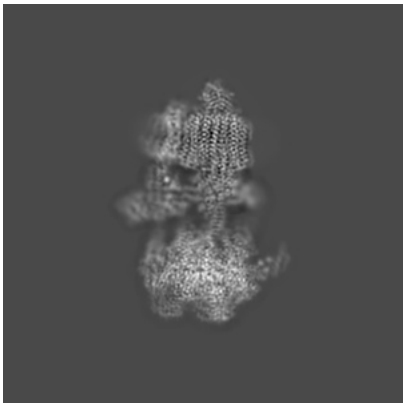
6 Map visualisation

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.

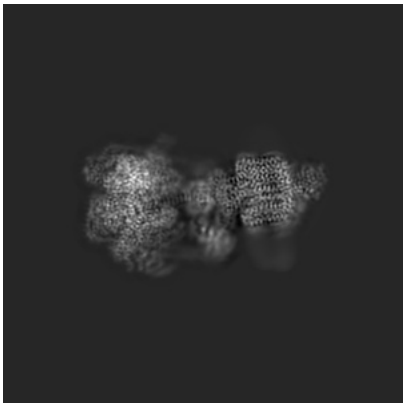
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

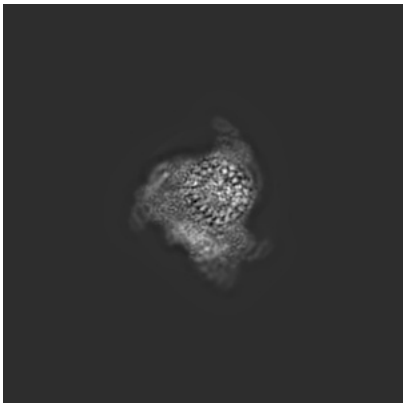
6.1.1 Primary map



X



Y



Z

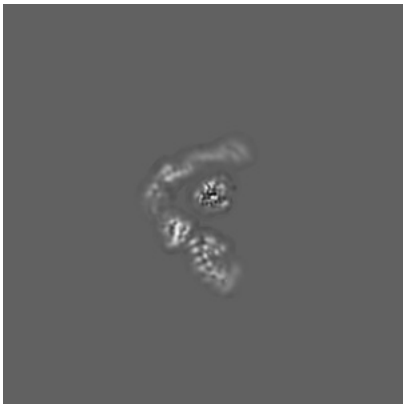
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map

X Index: 170

Y Index: 170

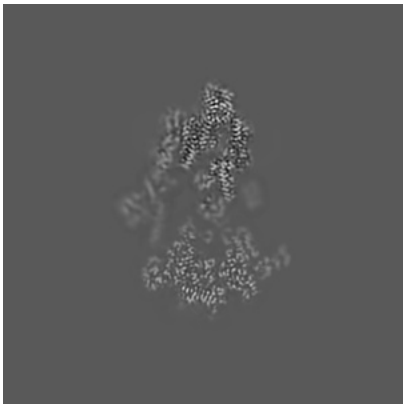


Z Index: 170

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

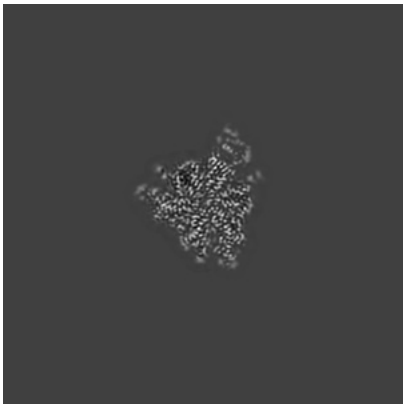
6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 184

Y Index: 179

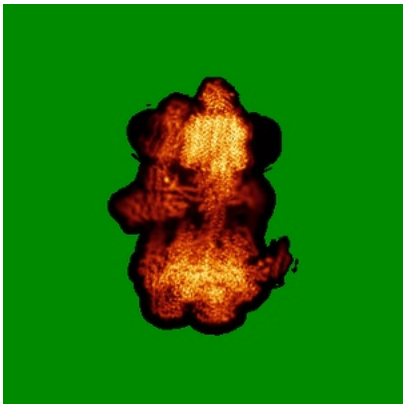


Z Index: 110

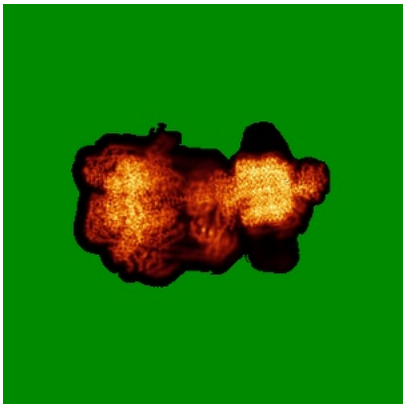
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

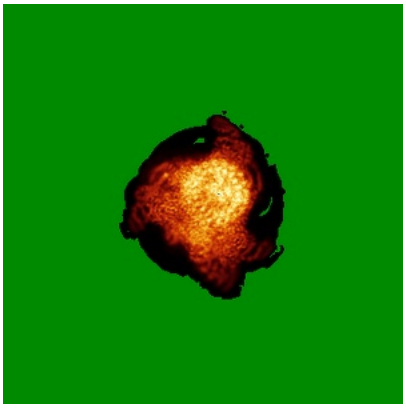
6.4.1 Primary map



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

X Y Z

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.

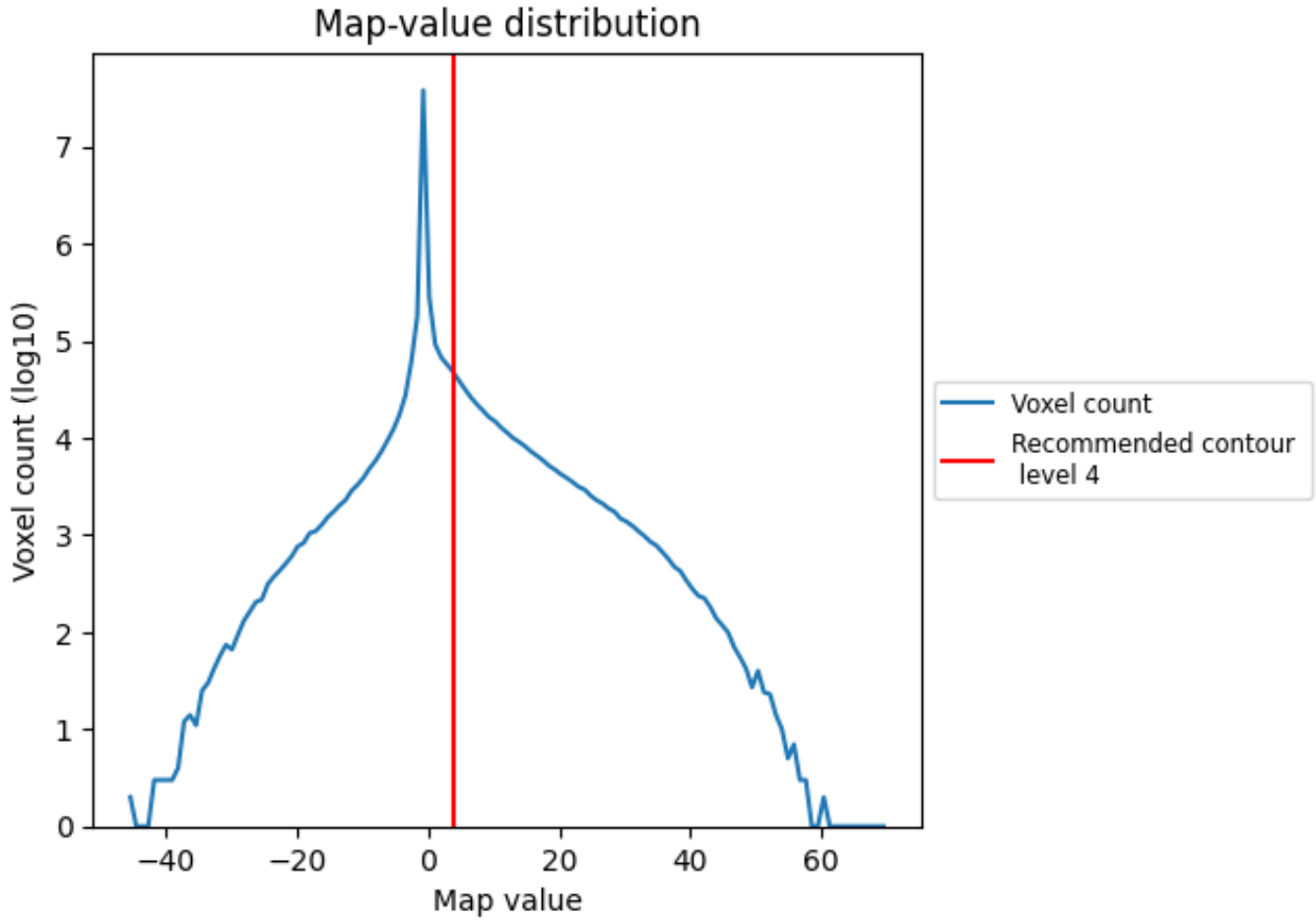
6.6 Mask visualisation (i)

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

7 Map analysis

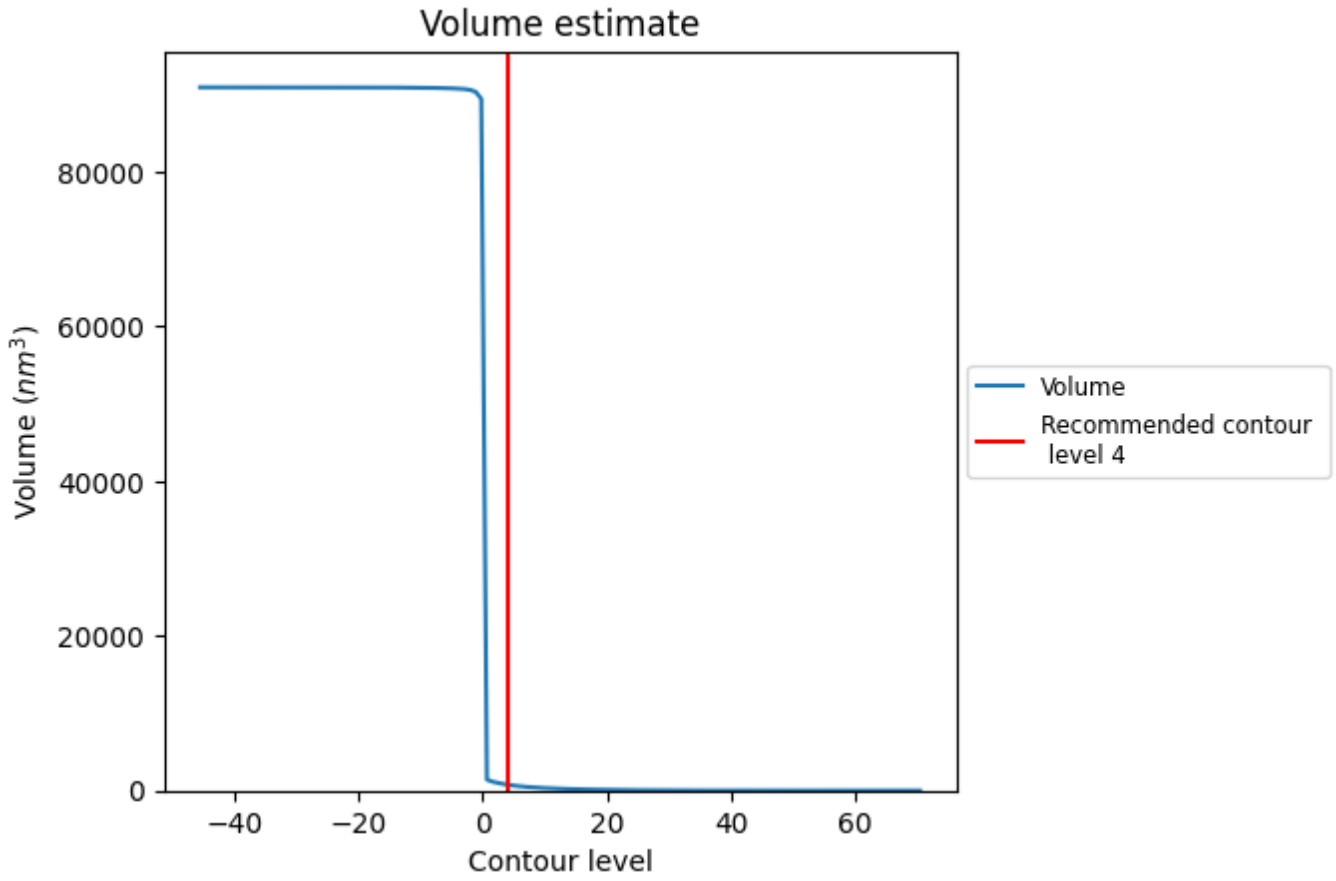
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

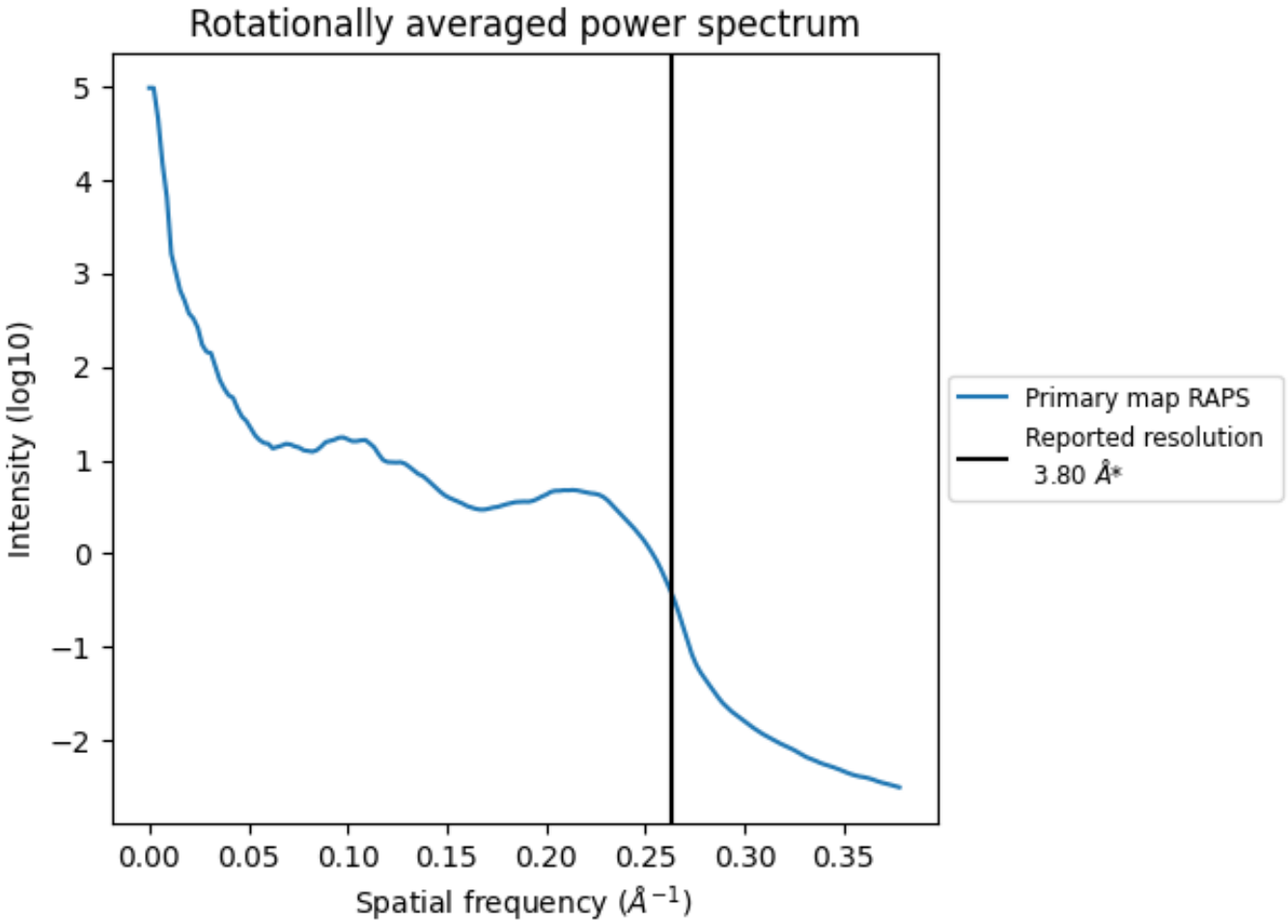
7.2 Volume estimate



The volume at the recommended contour level is 758 nm^3; 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 (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

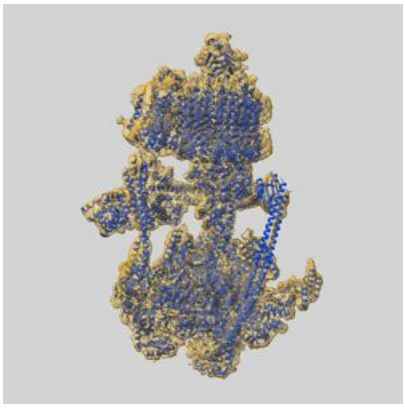
8 Fourier-Shell correlation

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

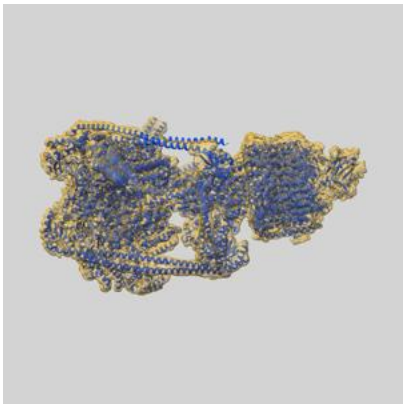
9 Map-model fit

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.

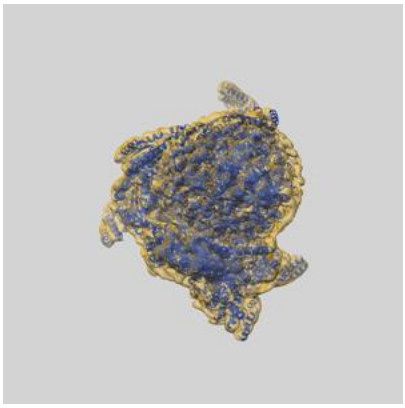
9.1 Map-model overlay



X



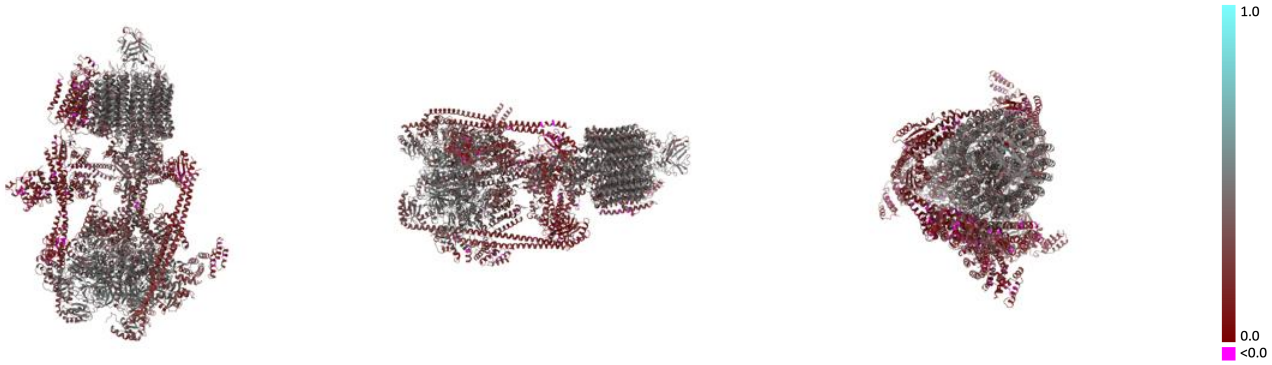
Y



Z

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.

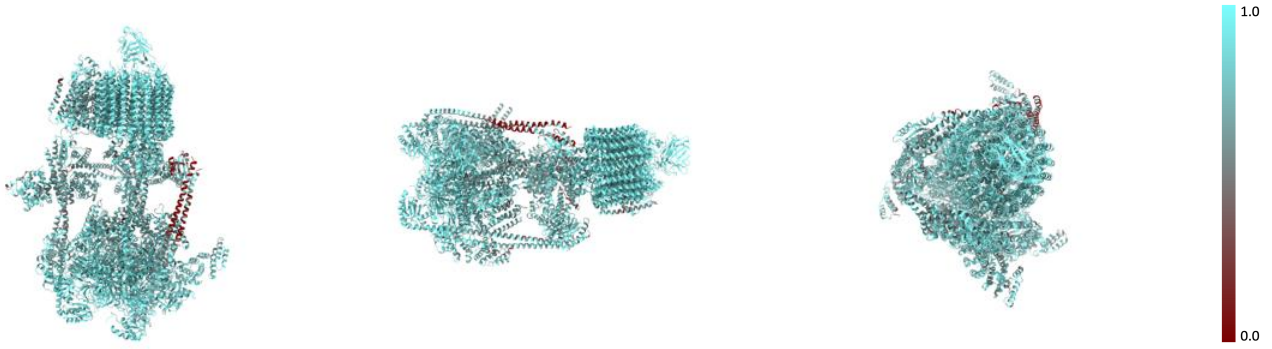
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

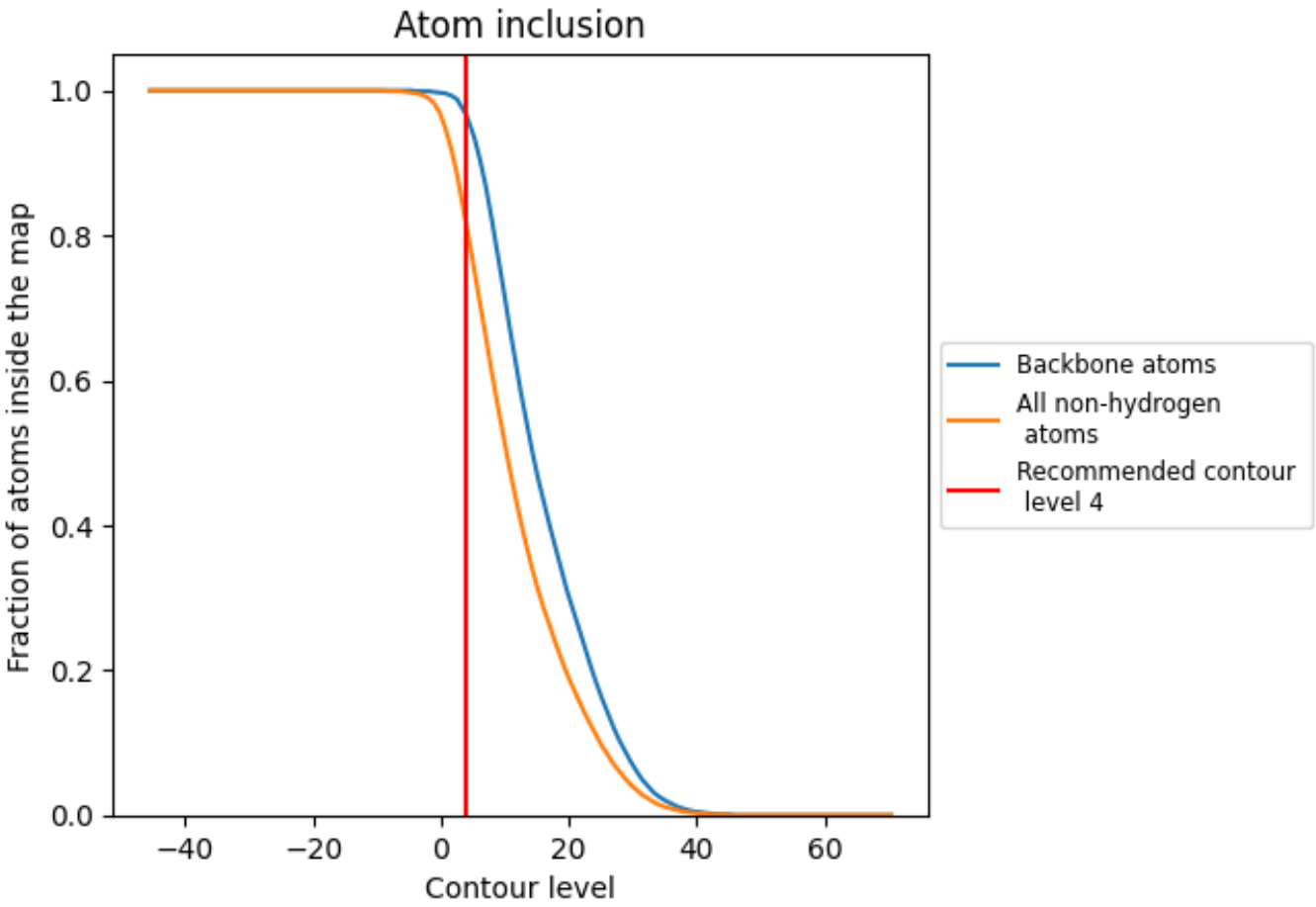
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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