



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 10:26 pm BST

PDB ID : 6R86
EMDB ID : EMD-4752
Title : Yeast Vms1-60S ribosomal subunit complex (post-state)
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;
Neupert, W.; Beckmann, R.
Deposited on : 2019-03-31
Resolution : 3.40 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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

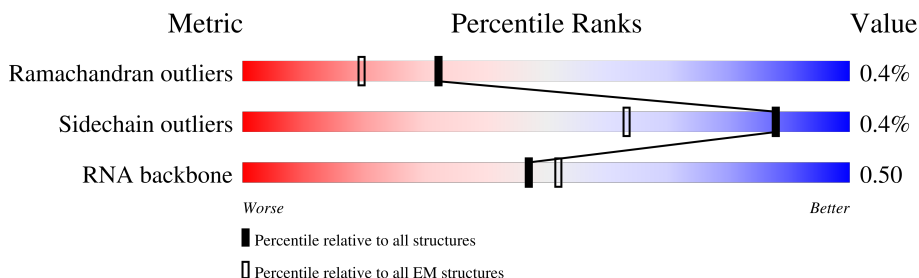
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.



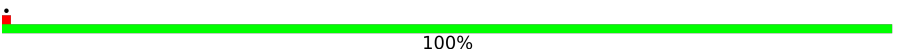
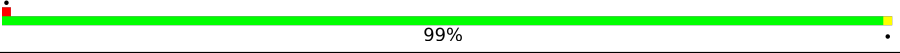
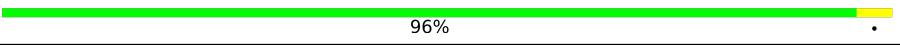
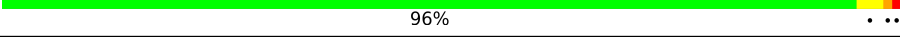
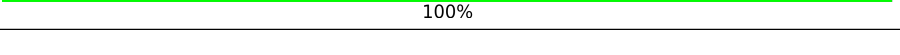
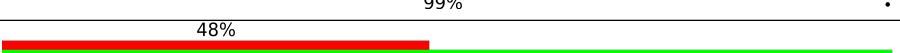
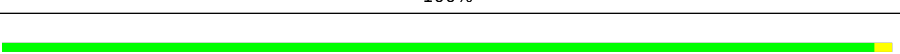
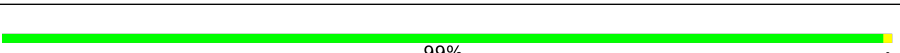
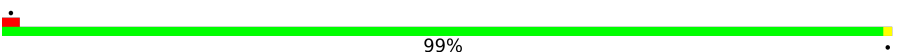
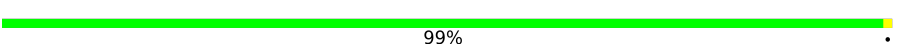
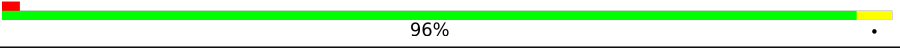
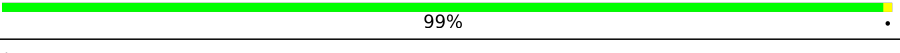
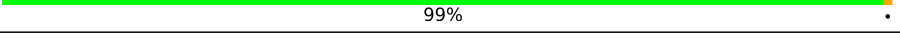
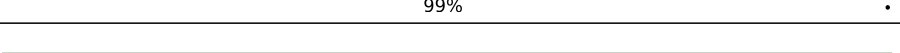
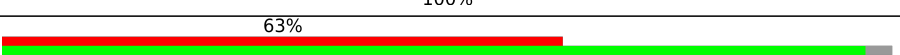
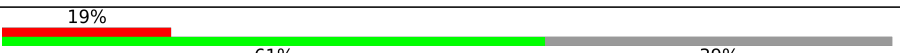


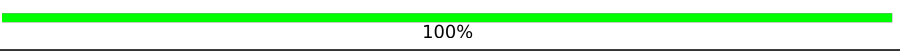

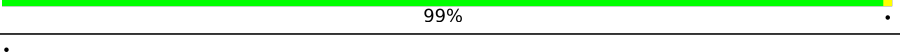
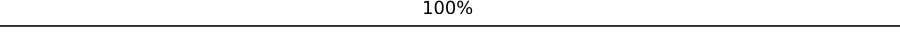
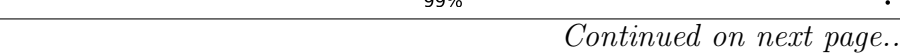


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	R	475	<div> <div>23%</div> <div>74%</div> <div>25%</div> </div>
2	X	224	<div>100%</div>
3	i	112	<div>100%</div>
4	J	222	<div>98%</div>
5	j	119	<div>97%</div>
6	K	233	<div>98%</div>
7	k	99	<div>99%</div>
8	7	191	<div>98%</div>

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Mol	Chain	Length	Quality of chain
9	l	87	 100%
10	M	169	 99%
11	m	77	 96%
12	N	193	 96%
13	n	50	 100%
14	O	136	 99%
15	o	52	 48% 100%
16	p	203	 98%
17	Q	197	 99%
18	5	183	 99%
19	S	185	 99%
20	s	220	 96%
21	T	152	 99%
22	U	172	 99%
23	V	159	 99%
24	W	100	 100%
25	P	155	 63% 97%
26	r	197	 19% 61% 39%
27	x	136	 100%
28	3	121	 74% 23%
29	Y	62	 100%
30	4	158	 72% 27%
31	Z	121	 99%
32	a	126	 100%
33	b	135	 99%

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Mol	Chain	Length	Quality of chain
34	C	105	
35	c	148	
36	D	91	
37	d	58	
38	E	252	
39	e	97	
40	F	386	
41	f	109	
42	G	361	
43	g	127	
44	H	296	
45	h	106	
46	I	175	
47	L	204	
48	1	3260	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 132446 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 Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	R	356	Total	C	N	O	S	Se	0	0
			2784	1776	495	500	12	1		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	224	Total	C	N	O	S	0	0
			1633	1019	279	328	7		

- Molecule 3 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	i	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 5 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	j	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 6 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 7 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	k	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 8 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 9 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 10 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 11 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	m	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 12 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	N	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 13 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	5	183	Total	C	N	O		0	0
			1420	882	281	257			

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	s	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	152	Total	C	N	O	0	0
			1228	763	260	205		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L12-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	P	150	Total	C	N	O	0	0
			737	437	150	150		

- Molecule 26 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	r	121	Total	C	N	O	S	0	0
			967	621	170	173	3		

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	x	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 28 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 29 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Y	62	Total	C	N	O	S	0	0
			513	330	101	81	1		

- Molecule 30 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 31 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 32 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	a	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 33 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	b	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 34 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	C	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 35 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 36 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	D	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 37 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	d	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 38 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 39 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	F	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	f	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	G	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 43 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	g	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 44 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	H	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 45 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	h	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 46 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	I	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 47 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	L	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 48 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	1	3260	Total	C	N	O	P	0	0
			69730	31146	12569	22755	3260		

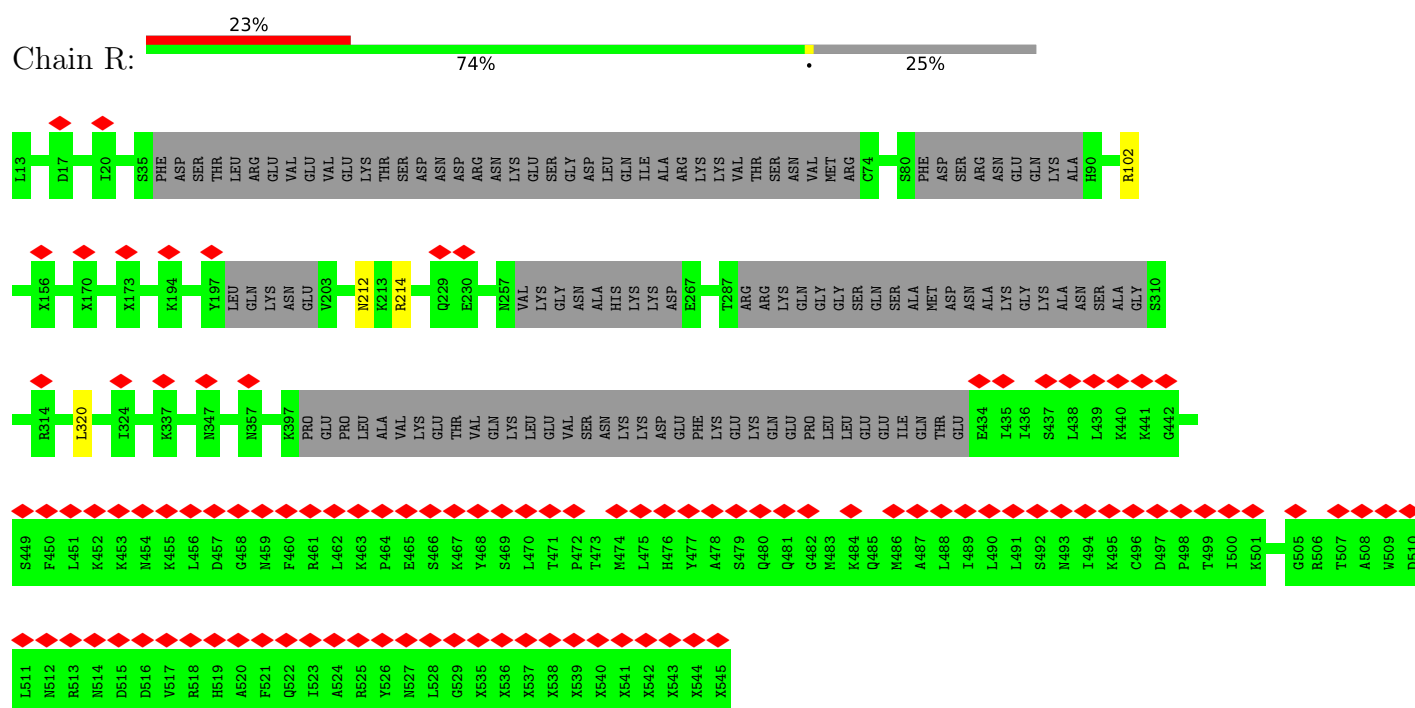
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	R	1	Total 1	Zn 1	0

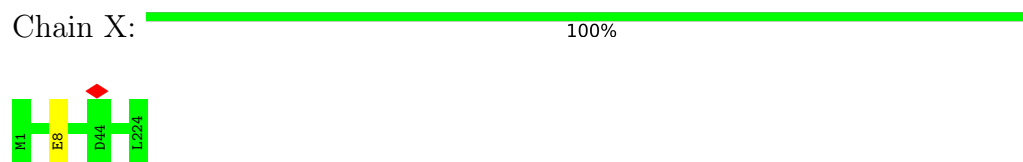
3 Residue-property plots

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

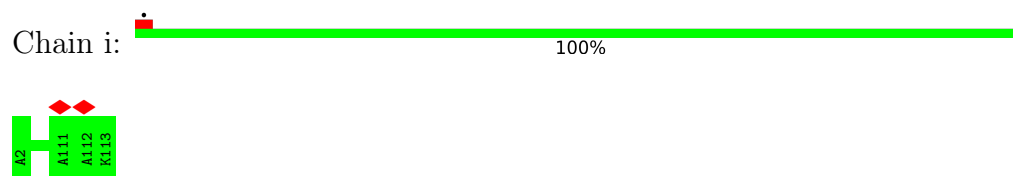
- Molecule 1: Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1,Protein VMS1



- Molecule 2: Eukaryotic translation initiation factor 6



- Molecule 3: 60S ribosomal protein L34-A



- Molecule 4: 60S ribosomal protein L7-A

Chain J:  98% .



- Molecule 5: 60S ribosomal protein L35-A

Chain j:  97% ..



- Molecule 6: 60S ribosomal protein L8-A

Chain K:  98% .



- Molecule 7: 60S ribosomal protein L36-A

Chain k:  99% .



- Molecule 8: 60S ribosomal protein L9-A

Chain 7:  98% .



- Molecule 9: 60S ribosomal protein L37-A

Chain l:  100% .



- Molecule 10: 60S ribosomal protein L11-B

Chain M:  99% .



- Molecule 11: 60S ribosomal protein L38

Chain m: 96%



- Molecule 12: 60S ribosomal protein L13-A

Chain N: 96%



- Molecule 13: 60S ribosomal protein L39

Chain n: 100%

There are no outlier residues recorded for this chain.

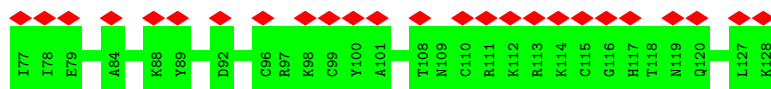
- Molecule 14: 60S ribosomal protein L14-A

Chain O: 99%



- Molecule 15: Ubiquitin-60S ribosomal protein L40

Chain o: 48%
100%



- Molecule 16: 60S ribosomal protein L15-A

Chain p: 98%

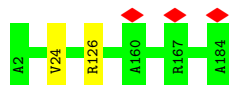


- Molecule 17: 60S ribosomal protein L16-A

Chain Q: 99%



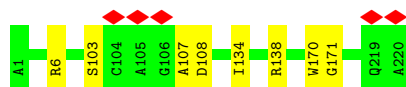
- Molecule 18: 60S ribosomal protein L17-A



- Molecule 19: 60S ribosomal protein L18-A



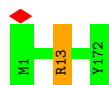
- Molecule 20: 60S ribosomal protein L10



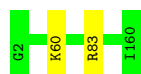
- Molecule 21: 60S ribosomal protein L19-A



- Molecule 22: 60S ribosomal protein L20-A



- Molecule 23: 60S ribosomal protein L21-A

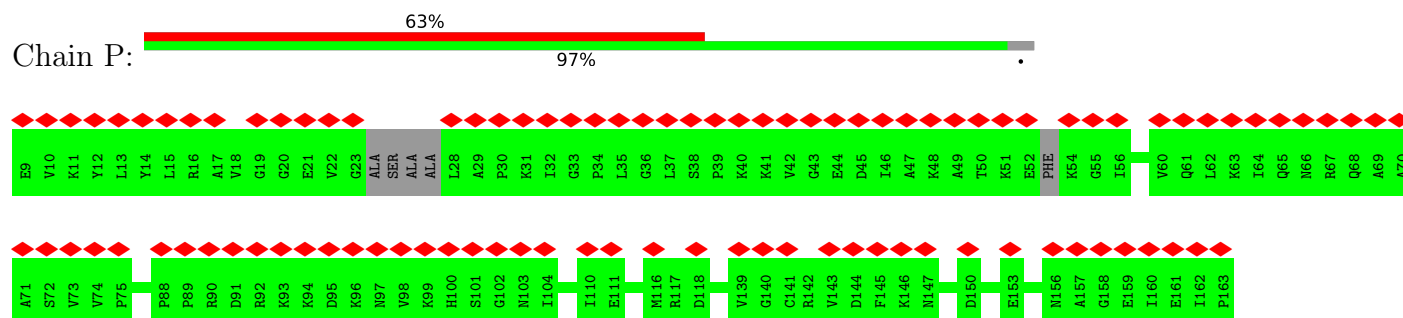


- Molecule 24: 60S ribosomal protein L22-A

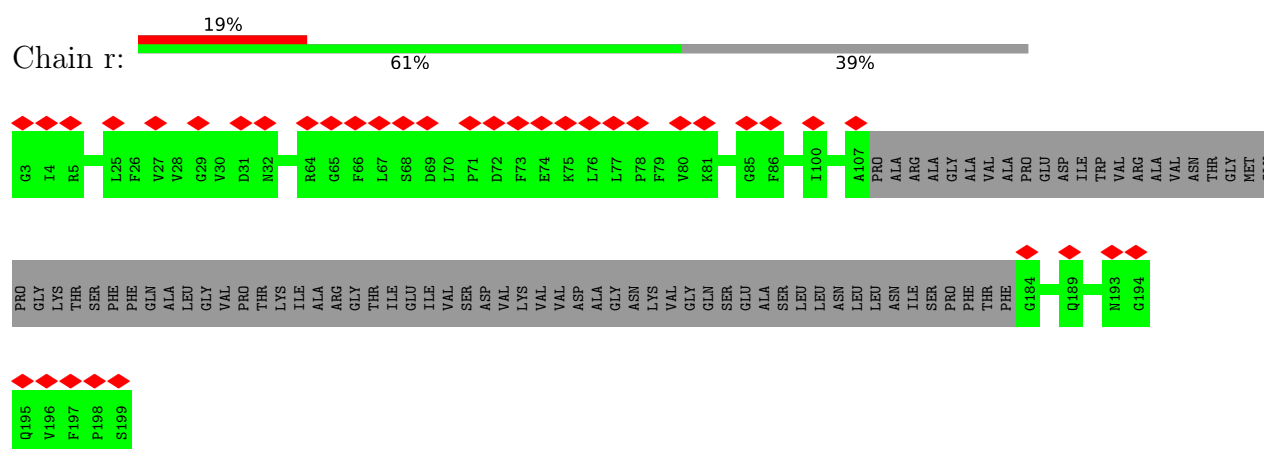


There are no outlier residues recorded for this chain.

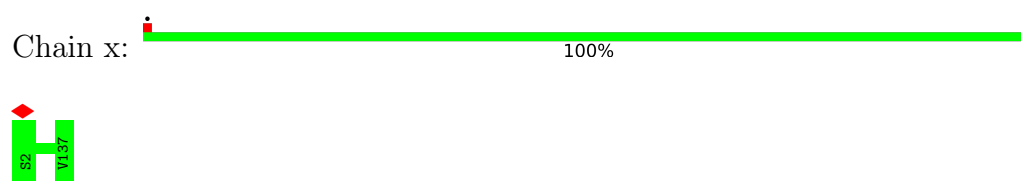
- Molecule 25: 60S ribosomal protein L12-A



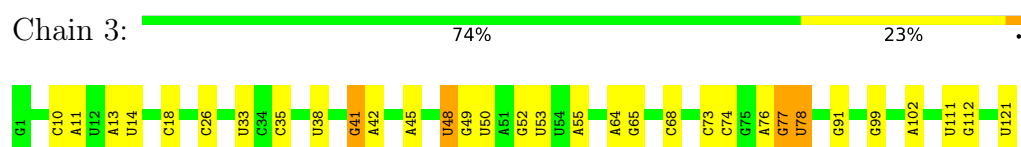
- Molecule 26: 60S acidic ribosomal protein P0



- Molecule 27: 60S ribosomal protein L23-A



- Molecule 28: 5S ribosomal RNA



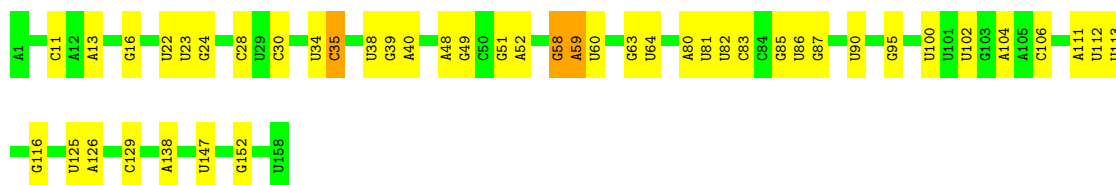
- Molecule 29: 60S ribosomal protein L24-A



There are no outlier residues recorded for this chain.

- Molecule 30: 5.8S ribosomal RNA





- Molecule 31: 60S ribosomal protein L25

Chain Z: 99%



- Molecule 32: 60S ribosomal protein L26-A

Chain a: 100%



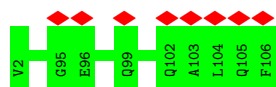
- Molecule 33: 60S ribosomal protein L27-A

Chain b: 99%



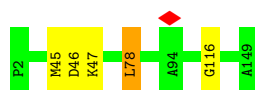
- Molecule 34: 60S ribosomal protein L42-A

Chain C: 8% 100%



- Molecule 35: 60S ribosomal protein L28

Chain c: 97%



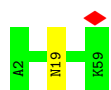
- Molecule 36: 60S ribosomal protein L43-A

Chain D: 98%



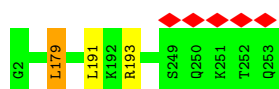
- Molecule 37: 60S ribosomal protein L29

Chain d:  98%



- Molecule 38: 60S ribosomal protein L2-A

Chain E:  99%



- Molecule 39: 60S ribosomal protein L30

Chain e:  100%



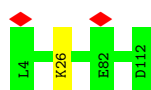
- Molecule 40: 60S ribosomal protein L3

Chain F:  99%



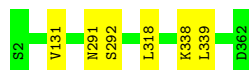
- Molecule 41: 60S ribosomal protein L31-A

Chain f:  99%



- Molecule 42: 60S ribosomal protein L4-A

Chain G:  98%

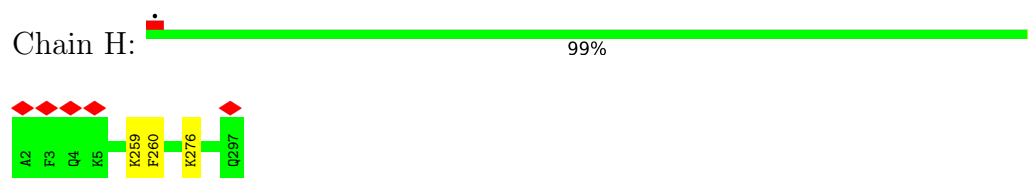


- Molecule 43: 60S ribosomal protein L32

Chain g:  100%

There are no outlier residues recorded for this chain.

- Molecule 44: 60S ribosomal protein L5

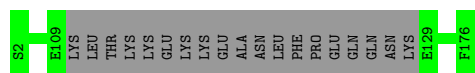
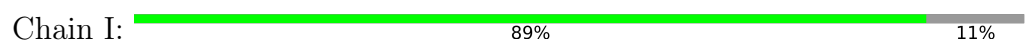


- Molecule 45: 60S ribosomal protein L33-A



There are no outlier residues recorded for this chain.

- Molecule 46: 60S ribosomal protein L6-A



- Molecule 47: 60S ribosomal protein L1-A



- Molecule 48: 25S ribosomal RNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	115812	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.812	Depositor
Minimum map value	-0.588	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.025	Depositor
Map size (\AA)	429.264, 429.264, 429.264	wwPDB
Map dimensions	396, 396, 396	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	R	0.27	0/2631	0.51	1/3532 (0.0%)
2	X	0.30	0/1653	0.54	0/2255
3	i	0.43	0/890	0.59	0/1189
4	J	0.44	0/1821	0.61	0/2451
5	j	0.34	0/978	0.62	0/1301
6	K	0.38	0/1836	0.63	0/2481
7	k	0.36	0/778	0.62	0/1034
8	7	0.34	0/1539	0.55	0/2073
9	l	0.47	0/696	0.64	0/923
10	M	0.30	0/1374	0.59	0/1842
11	m	0.34	0/618	0.62	1/826 (0.1%)
12	N	0.42	0/1568	0.68	4/2106 (0.2%)
13	n	0.42	0/443	0.65	0/588
14	O	0.37	0/1068	0.58	0/1438
15	o	0.28	0/423	0.57	0/562
16	p	0.52	0/1757	0.67	1/2354 (0.0%)
17	Q	0.42	0/1585	0.57	1/2128 (0.0%)
18	5	0.39	0/1443	0.62	0/1944
19	S	0.38	0/1465	0.65	1/1965 (0.1%)
20	s	0.36	0/1807	0.66	1/2425 (0.0%)
21	T	0.37	0/1245	0.61	0/1661
22	U	0.43	0/1481	0.60	0/1990
23	V	0.42	0/1300	0.58	0/1743
24	W	0.35	0/812	0.55	0/1099
25	P	0.25	0/734	0.53	0/1015
26	r	0.27	0/982	0.57	0/1320
27	x	0.42	0/1018	0.62	0/1369
28	3	0.57	0/2883	1.11	18/4491 (0.4%)
29	Y	0.38	0/525	0.55	0/696
30	4	0.69	0/3746	1.09	13/5832 (0.2%)
31	Z	0.42	0/979	0.61	1/1321 (0.1%)
32	a	0.35	0/1004	0.58	0/1341

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.35	0/1118	0.54	0/1497
34	C	0.35	0/860	0.61	0/1136
35	c	0.45	0/1204	0.66	0/1612
36	D	0.46	0/701	0.65	0/934
37	d	0.34	0/473	0.51	0/629
38	E	0.48	0/1948	0.66	2/2617 (0.1%)
39	e	0.33	0/751	0.53	0/1008
40	F	0.47	1/3146 (0.0%)	0.63	0/4228
41	f	0.44	0/890	0.59	0/1196
42	G	0.41	0/2800	0.62	0/3790
43	g	0.38	0/1041	0.57	0/1394
44	H	0.36	0/2425	0.56	0/3271
45	h	0.46	0/868	0.58	0/1168
46	I	0.33	0/1260	0.54	0/1694
47	L	0.28	0/1634	0.58	0/2195
48	1	0.70	2/78052 (0.0%)	1.16	494/121690 (0.4%)
All	All	0.59	3/142253 (0.0%)	0.99	538/209354 (0.3%)

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
2	X	0	1
4	J	0	2
5	j	0	2
6	K	0	3
7	k	0	1
8	7	0	1
10	M	0	1
11	m	0	2
12	N	0	3
14	O	0	1
20	s	0	4
33	b	0	1
35	c	0	3
36	D	0	1
37	d	0	1
38	E	0	1
40	F	0	1
42	G	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
44	H	0	1
All	All	0	34

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	F	237	LYS	C-N	-7.03	1.17	1.34
48	1	3047	U	N3-C4	-5.82	1.33	1.38
48	1	3186	A	N9-C4	-5.00	1.34	1.37

The worst 5 of 538 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	1	2080	C	N1-C2-O2	13.81	127.19	118.90
48	1	3278	C	C2-N1-C1'	13.74	133.91	118.80
48	1	3278	C	N1-C2-O2	13.45	126.97	118.90
48	1	2080	C	N3-C2-O2	-12.68	113.02	121.90
48	1	2080	C	C2-N1-C1'	10.80	130.68	118.80

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	J	157	ASN	Peptide
4	J	232	ARG	Peptide
2	X	8	GLU	Peptide
5	j	90	ARG	Peptide
5	j	91	ALA	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	R	300/475 (63%)	284 (95%)	16 (5%)	0	100	100
2	X	222/224 (99%)	211 (95%)	11 (5%)	0	100	100
3	i	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
4	J	220/222 (99%)	202 (92%)	16 (7%)	2 (1%)	14	41
5	j	117/119 (98%)	109 (93%)	5 (4%)	3 (3%)	4	22
6	K	231/233 (99%)	215 (93%)	14 (6%)	2 (1%)	14	41
7	k	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
8	7	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
9	l	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
10	M	167/169 (99%)	145 (87%)	22 (13%)	0	100	100
11	m	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
12	N	191/193 (99%)	173 (91%)	14 (7%)	4 (2%)	5	24
13	n	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
14	O	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
15	o	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
16	p	201/203 (99%)	182 (90%)	16 (8%)	3 (2%)	8	30
17	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
18	5	181/183 (99%)	163 (90%)	18 (10%)	0	100	100
19	S	183/185 (99%)	171 (93%)	12 (7%)	0	100	100
20	s	218/220 (99%)	194 (89%)	22 (10%)	2 (1%)	14	41
21	T	150/152 (99%)	141 (94%)	8 (5%)	1 (1%)	19	47
22	U	170/172 (99%)	158 (93%)	11 (6%)	1 (1%)	22	50
23	V	157/159 (99%)	145 (92%)	12 (8%)	0	100	100
24	W	98/100 (98%)	89 (91%)	9 (9%)	0	100	100
25	P	144/155 (93%)	124 (86%)	20 (14%)	0	100	100
26	r	117/197 (59%)	108 (92%)	9 (8%)	0	100	100
27	x	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
29	Y	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
31	Z	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
32	a	124/126 (98%)	118 (95%)	6 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	b	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	44
34	C	103/105 (98%)	89 (86%)	14 (14%)	0	100	100
35	c	146/148 (99%)	128 (88%)	16 (11%)	2 (1%)	9	31
36	D	89/91 (98%)	82 (92%)	7 (8%)	0	100	100
37	d	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
38	E	250/252 (99%)	229 (92%)	21 (8%)	0	100	100
39	e	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
40	F	384/386 (100%)	354 (92%)	29 (8%)	1 (0%)	37	66
41	f	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
42	G	359/361 (99%)	325 (90%)	32 (9%)	2 (1%)	22	50
43	g	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
44	H	294/296 (99%)	274 (93%)	18 (6%)	2 (1%)	19	47
45	h	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
46	I	152/175 (87%)	147 (97%)	5 (3%)	0	100	100
47	L	202/204 (99%)	165 (82%)	37 (18%)	0	100	100
All	All	7086/7457 (95%)	6532 (92%)	528 (8%)	26 (0%)	32	60

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	s	108	ASP
35	c	47	LYS
35	c	78	LEU
42	G	339	LEU
4	J	158	LYS

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	R	288/392 (74%)	285 (99%)	3 (1%)	73	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	X	177/192 (92%)	177 (100%)	0	100	100
3	i	95/95 (100%)	95 (100%)	0	100	100
4	J	186/186 (100%)	186 (100%)	0	100	100
5	j	104/104 (100%)	104 (100%)	0	100	100
6	K	187/191 (98%)	187 (100%)	0	100	100
7	k	81/81 (100%)	81 (100%)	0	100	100
8	7	171/171 (100%)	169 (99%)	2 (1%)	67	80
9	l	70/70 (100%)	70 (100%)	0	100	100
10	M	147/147 (100%)	147 (100%)	0	100	100
11	m	68/68 (100%)	68 (100%)	0	100	100
12	N	154/154 (100%)	153 (99%)	1 (1%)	84	90
13	n	45/45 (100%)	45 (100%)	0	100	100
14	O	107/107 (100%)	107 (100%)	0	100	100
15	o	47/47 (100%)	47 (100%)	0	100	100
16	p	175/175 (100%)	173 (99%)	2 (1%)	70	81
17	Q	160/160 (100%)	160 (100%)	0	100	100
18	5	140/145 (97%)	138 (99%)	2 (1%)	62	77
19	S	150/150 (100%)	150 (100%)	0	100	100
20	s	184/186 (99%)	183 (100%)	1 (0%)	86	91
21	T	126/126 (100%)	126 (100%)	0	100	100
22	U	156/156 (100%)	155 (99%)	1 (1%)	84	90
23	V	136/136 (100%)	134 (98%)	2 (2%)	60	76
24	W	87/87 (100%)	87 (100%)	0	100	100
26	r	105/166 (63%)	105 (100%)	0	100	100
27	x	104/104 (100%)	104 (100%)	0	100	100
29	Y	54/54 (100%)	54 (100%)	0	100	100
31	Z	104/105 (99%)	104 (100%)	0	100	100
32	a	109/109 (100%)	109 (100%)	0	100	100
33	b	115/115 (100%)	115 (100%)	0	100	100
34	C	90/90 (100%)	90 (100%)	0	100	100
35	c	118/118 (100%)	117 (99%)	1 (1%)	79	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	D	71/71 (100%)	70 (99%)	1 (1%)	62	77
37	d	46/46 (100%)	46 (100%)	0	100	100
38	E	193/194 (100%)	192 (100%)	1 (0%)	86	91
39	e	81/81 (100%)	81 (100%)	0	100	100
40	F	319/322 (99%)	318 (100%)	1 (0%)	91	95
41	f	92/96 (96%)	91 (99%)	1 (1%)	70	81
42	G	288/288 (100%)	288 (100%)	0	100	100
43	g	109/109 (100%)	109 (100%)	0	100	100
44	H	244/244 (100%)	244 (100%)	0	100	100
45	h	90/90 (100%)	90 (100%)	0	100	100
46	I	134/152 (88%)	134 (100%)	0	100	100
47	L	185/185 (100%)	181 (98%)	4 (2%)	47	68
All	All	5892/6110 (96%)	5869 (100%)	23 (0%)	88	93

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	c	78	LEU
40	F	104	THR
38	E	193	ARG
41	f	26	LYS
16	p	183	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
33	b	57	HIS
45	h	42	GLN
37	d	12	GLN
47	L	57	ASN
42	G	110	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	3	120/121 (99%)	28 (23%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	4	157/158 (99%)	36 (22%)	5 (3%)
48	1	3257/3260 (99%)	906 (27%)	158 (4%)
All	All	3534/3539 (99%)	970 (27%)	164 (4%)

5 of 970 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
28	3	10	C
28	3	11	A
28	3	13	A
28	3	14	U
28	3	33	U

5 of 164 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	1	2282	U
48	1	2911	A
48	1	2385	G
48	1	2617	U
48	1	3156	U

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	R	4
48	1	3
40	F	1

The worst 5 of 8 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	173:UNK	C	188:SER	N	30.28
1	R	105:ARG	C	113:UNK	N	19.44
1	1	1980:C	O3'	2042:G	P	19.07
1	R	529:GLY	C	535:UNK	N	17.02
1	R	123:UNK	C	156:UNK	N	12.97

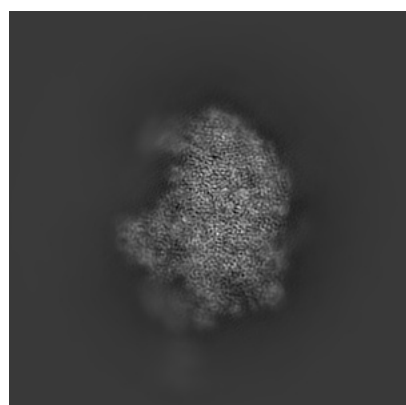
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4752. These allow visual inspection of the internal detail of the map and identification of artifacts.

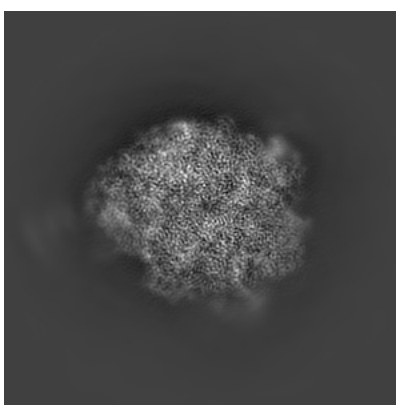
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

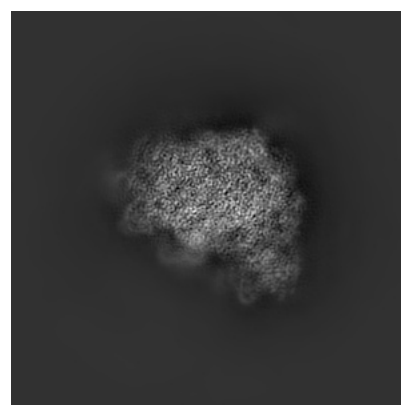
6.1.1 Primary map



X



Y

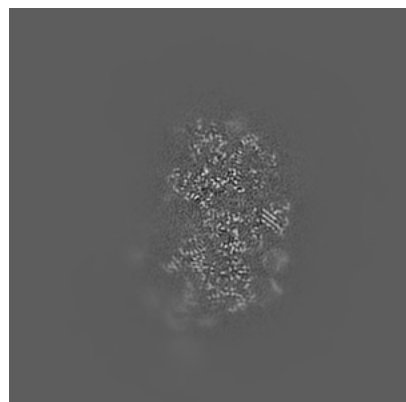


Z

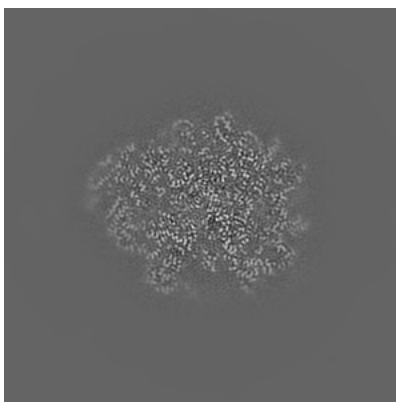
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

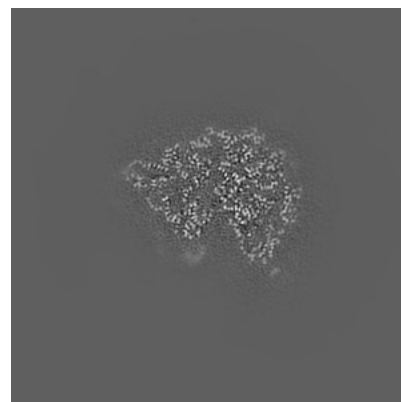
6.2.1 Primary map



X Index: 198



Y Index: 198

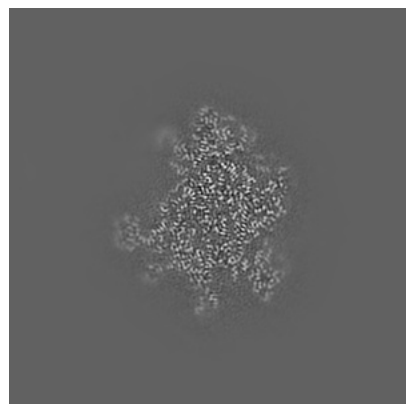


Z Index: 198

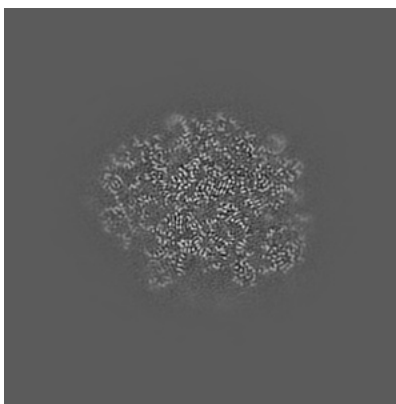
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

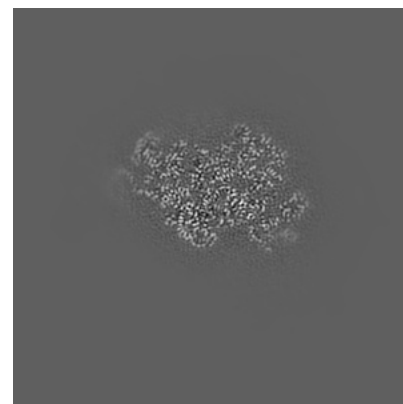
6.3.1 Primary map



X Index: 235



Y Index: 206

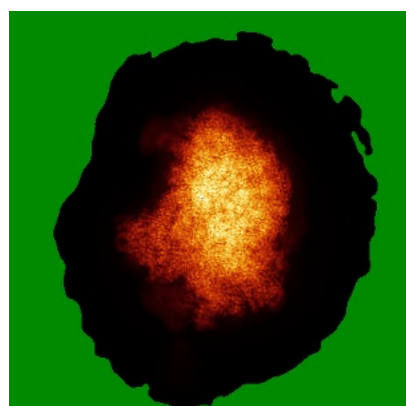


Z Index: 217

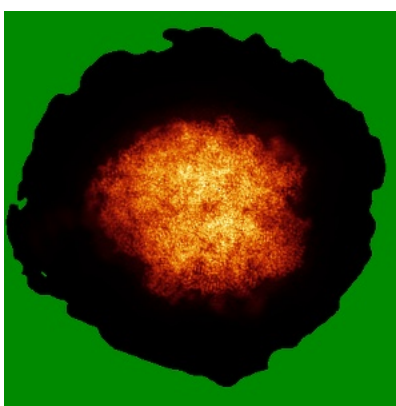
The images above show the largest variance slices of the map in three orthogonal directions.

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

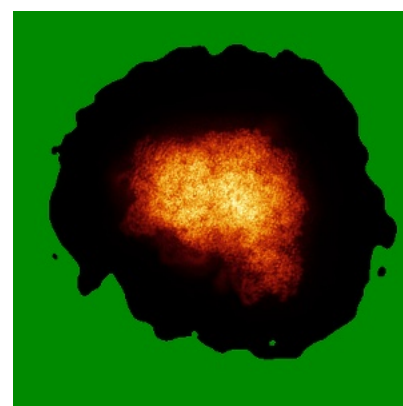
6.4.1 Primary map



X



Y

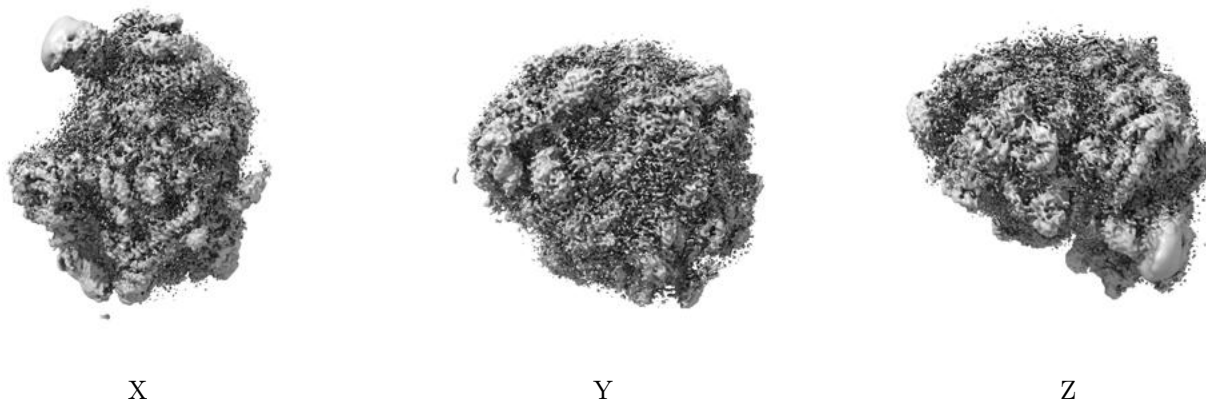


Z

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 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

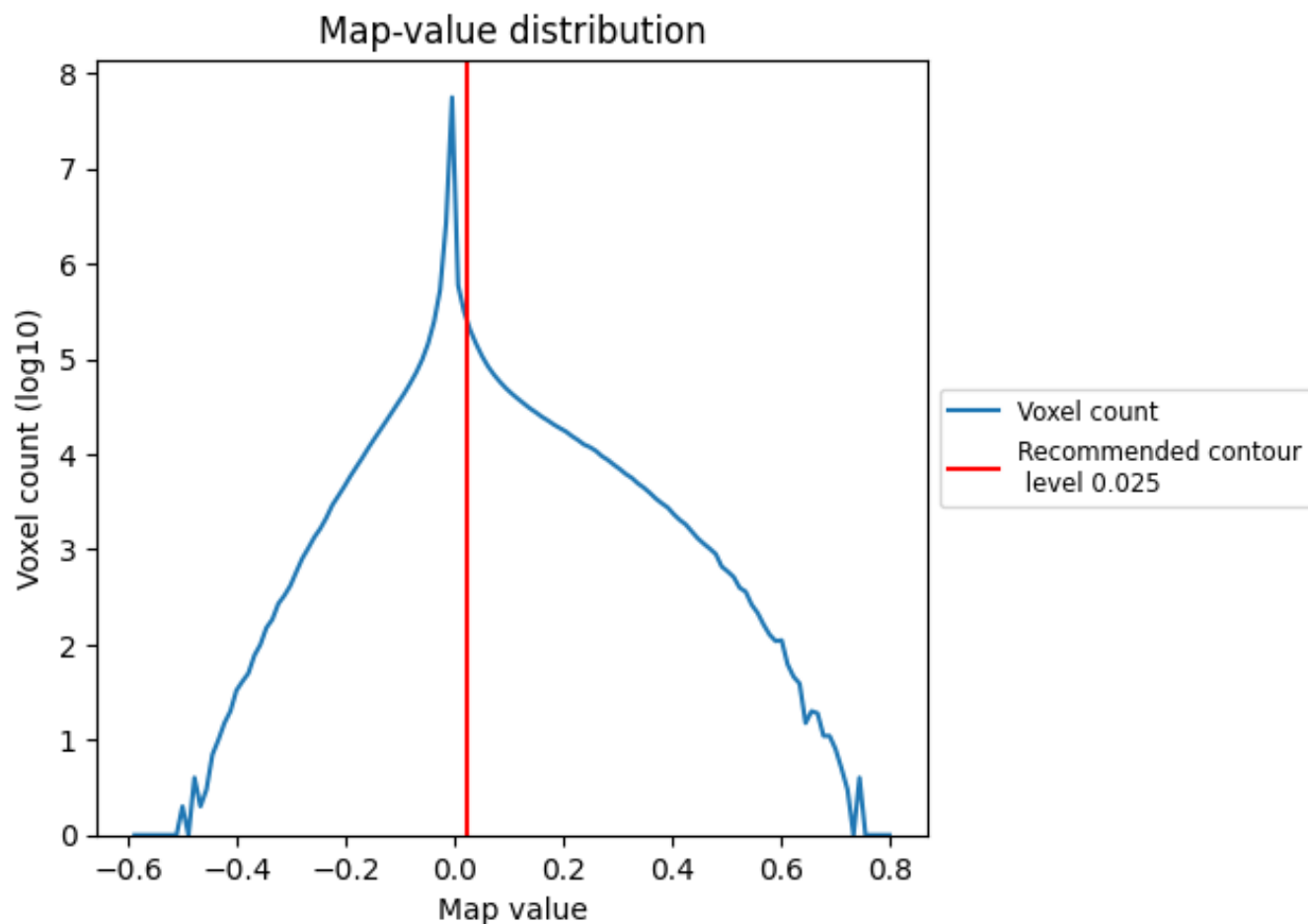
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

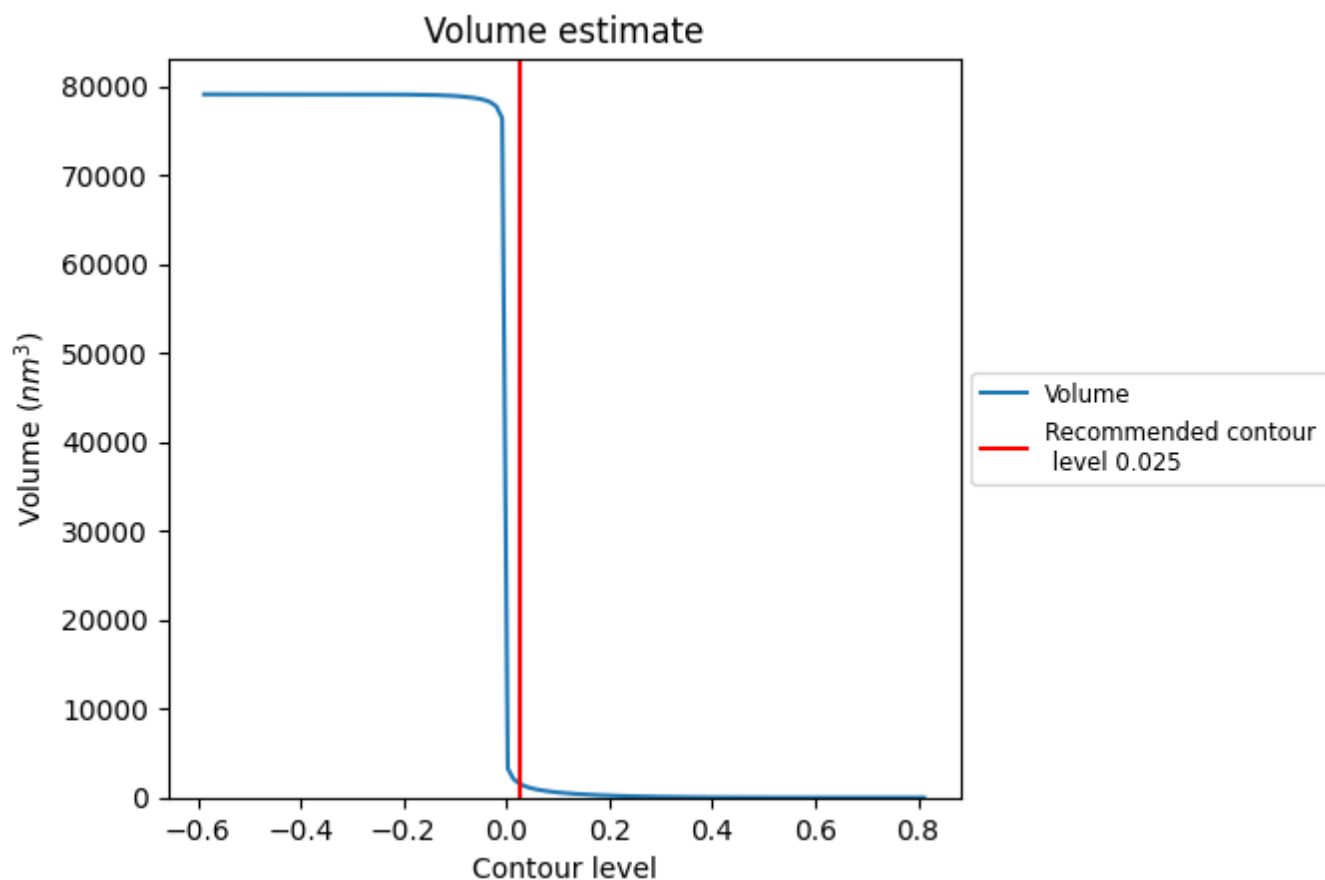
This section contains the results of statistical analysis of the map.

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.

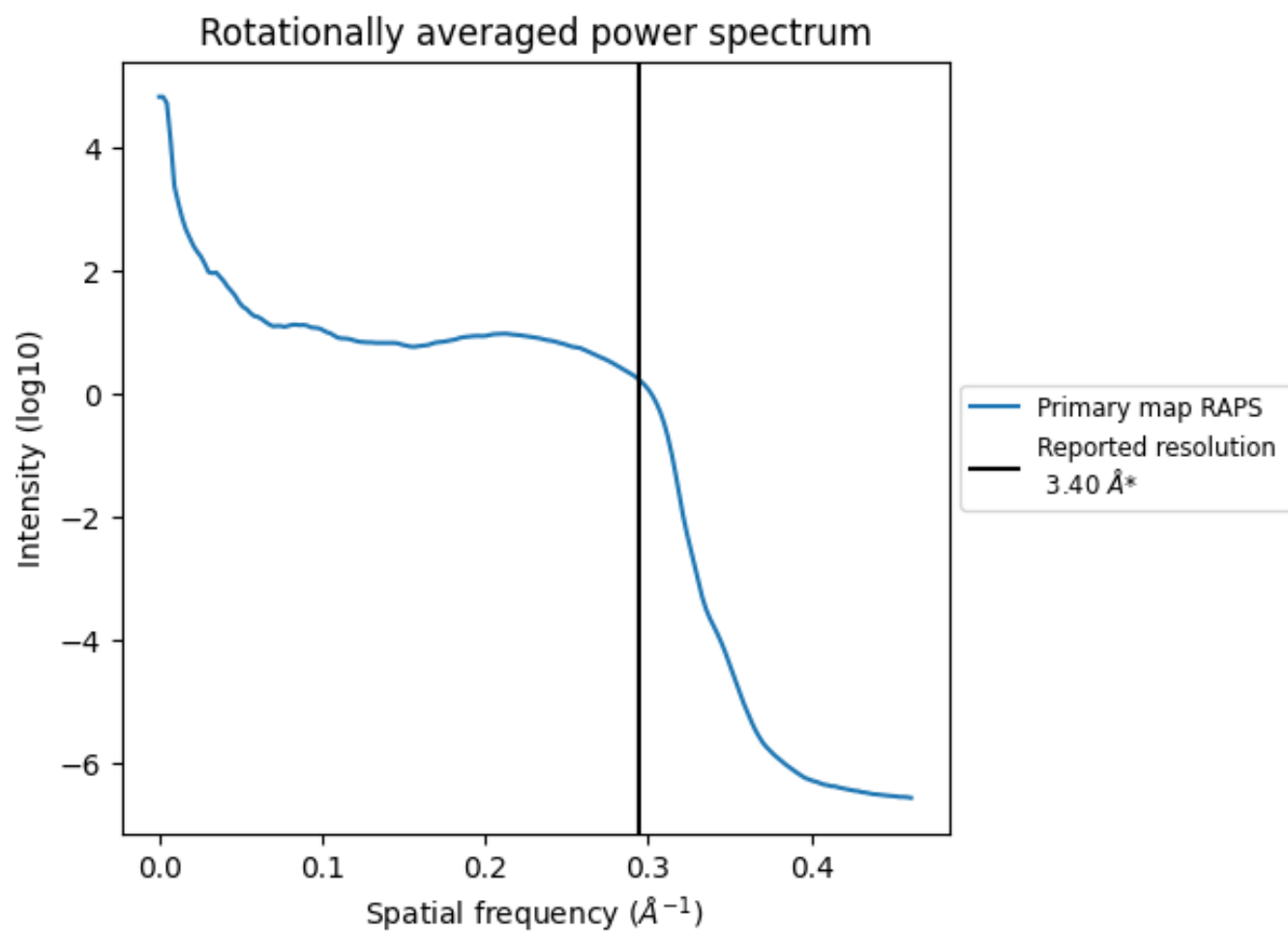
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1583 nm³; this corresponds to an approximate mass of 1430 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 0.294 Å⁻¹

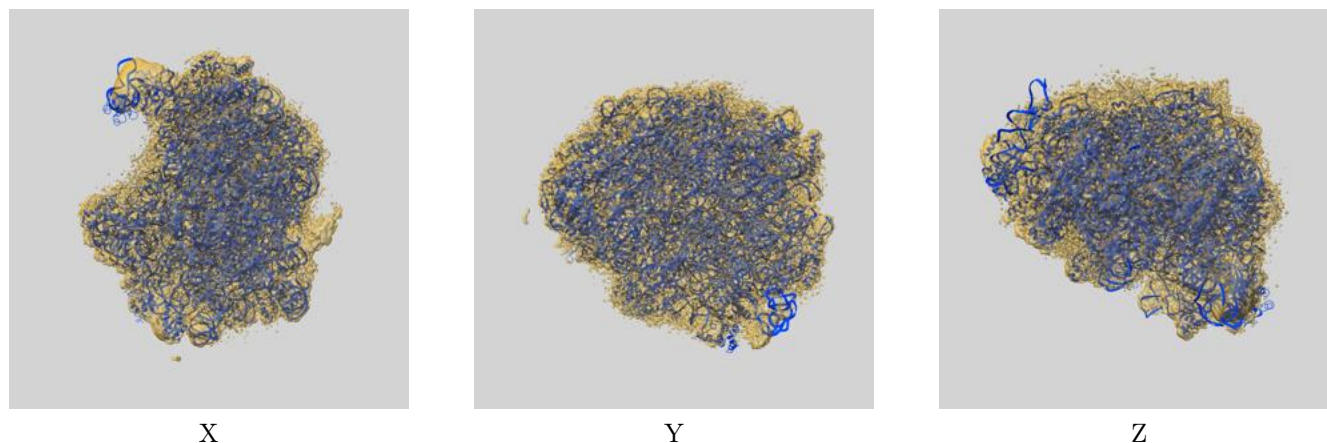
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

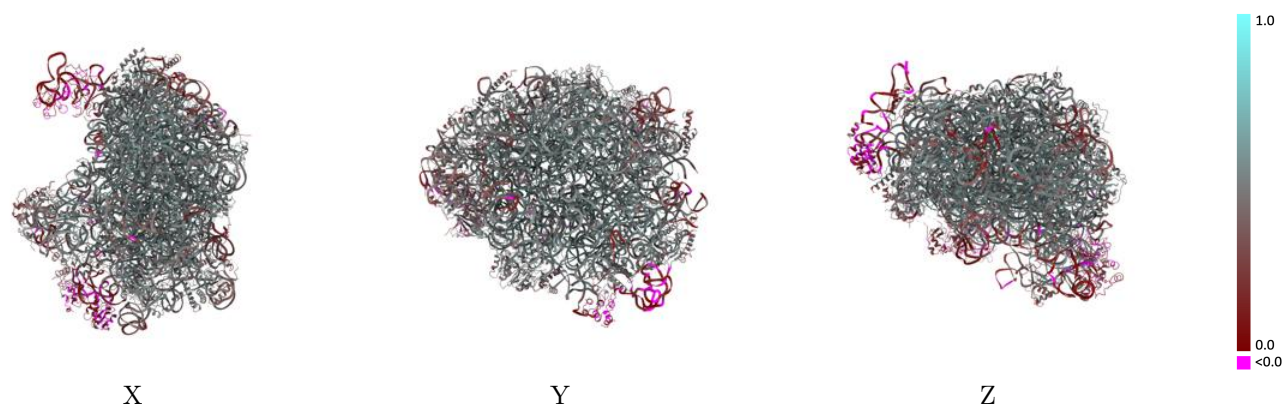
This section contains information regarding the fit between EMDB map EMD-4752 and PDB model 6R86. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



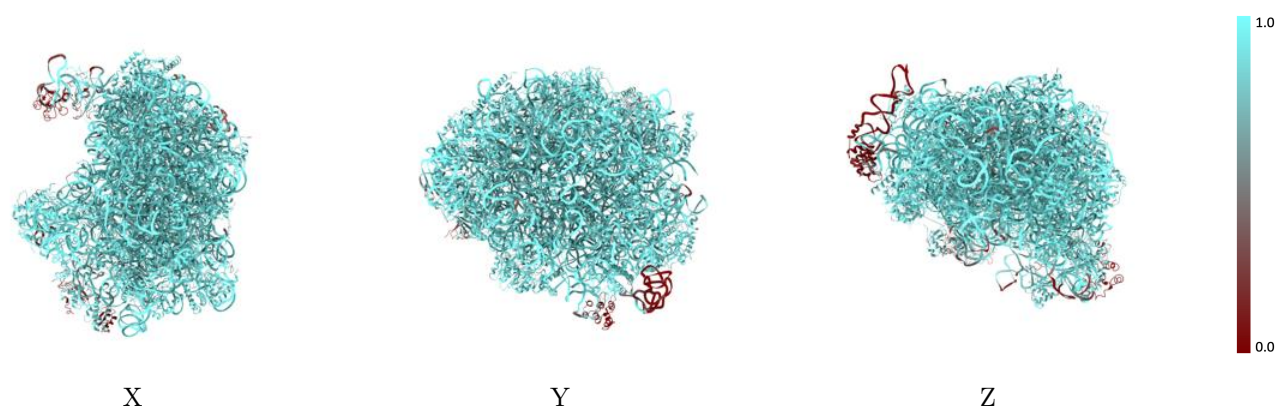
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



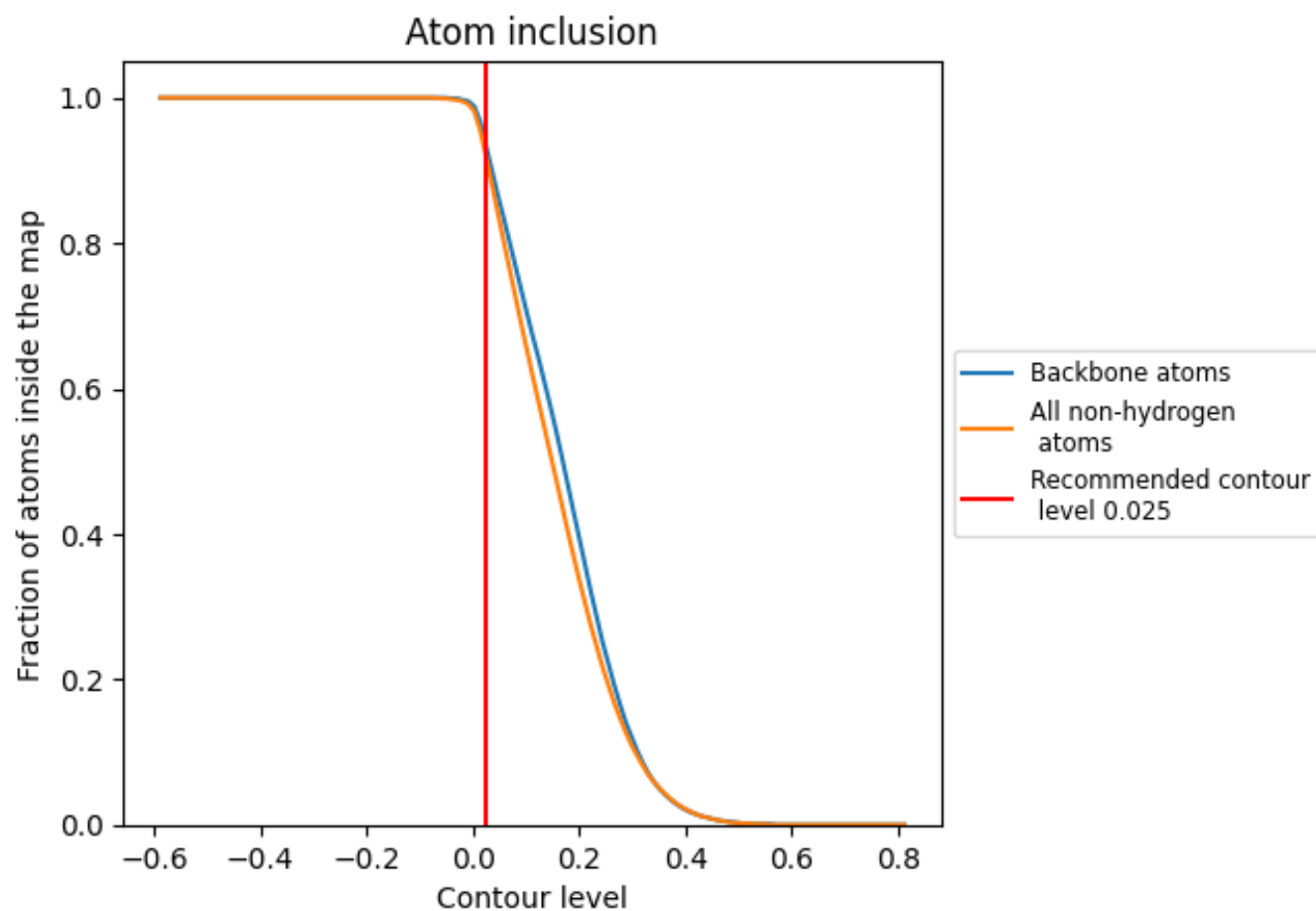
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.025).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





























The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.4620
1	 0.9430	 0.4680
3	 0.9850	 0.4910
4	 0.9750	 0.5130
5	 0.9210	 0.4980
7	 0.9150	 0.4580
C	 0.8560	 0.4840
D	 0.9220	 0.5110
E	 0.9330	 0.5330
F	 0.9440	 0.5170
G	 0.9400	 0.5110
H	 0.9070	 0.4360
I	 0.9110	 0.4590
J	 0.9400	 0.5070
K	 0.9180	 0.4680
L	 0.3870	 0.0560
M	 0.8700	 0.3790
N	 0.9360	 0.5050
O	 0.9230	 0.4740
P	 0.3660	 0.0790
Q	 0.9510	 0.5190
R	 0.6070	 0.1760
S	 0.9340	 0.5090
T	 0.9300	 0.5060
U	 0.9180	 0.4900
V	 0.9430	 0.5100
W	 0.9050	 0.4440
X	 0.9220	 0.4450
Y	 0.9400	 0.5090
Z	 0.9440	 0.5110
a	 0.9250	 0.5030
b	 0.9240	 0.4710
c	 0.9560	 0.5330
d	 0.9180	 0.4880
e	 0.9040	 0.4580



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Chain	Atom inclusion	Q-score
f	 0.9070	 0.4930
g	 0.9440	 0.5280
h	 0.9460	 0.5350
i	 0.9170	 0.5070
j	 0.9240	 0.4930
k	 0.9230	 0.4740
l	 0.9590	 0.5480
m	 0.9100	 0.4610
n	 0.9590	 0.5320
o	 0.4270	 0.1660
p	 0.9570	 0.5540
r	 0.6380	 0.0610
s	 0.8920	 0.4590
x	 0.9410	 0.5320