



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 09:39 PM UTC

PDB ID : 6R84 / pdb_00006r84
EMDB ID : EMD-4751
Title : Yeast Vms1 (Q295L)-60S ribosomal subunit complex (pre-state with Arb1)
Authors : Su, T.; Izawa, T.; Cheng, J.; Yamashita, Y.; Berninghausen, O.; Inada, T.;
Neupert, W.; Beckmann, R.
Deposited on : 2019-03-31
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

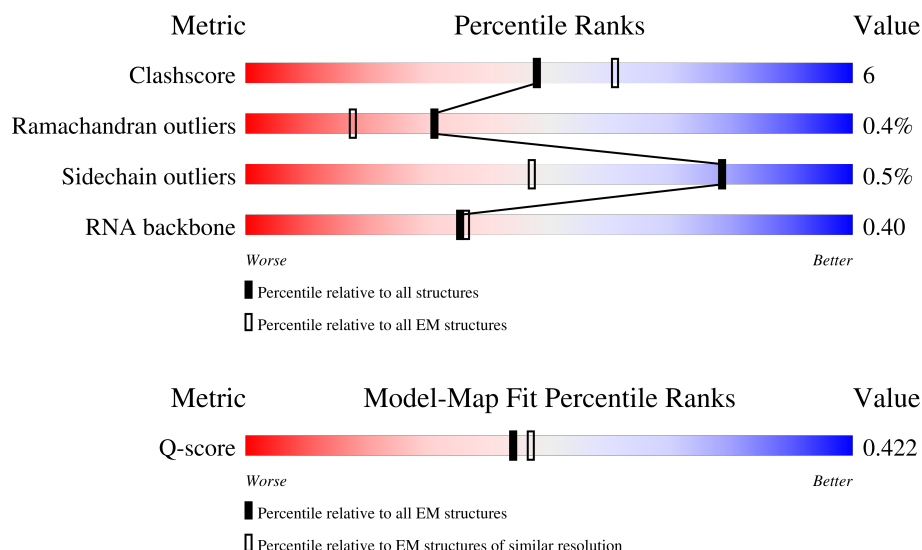
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.60 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.



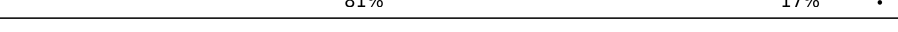
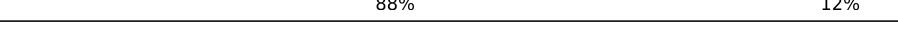
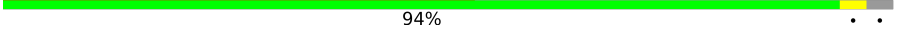
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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

Mol	Chain	Length	Quality of chain
1	A	519	
2	R	433	
3	X	224	

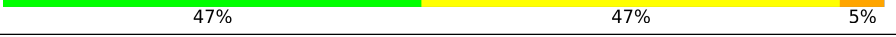
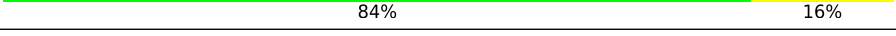
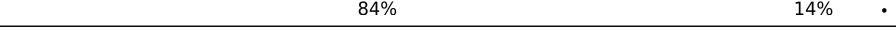
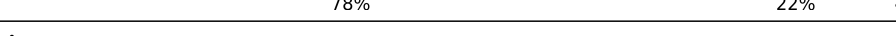
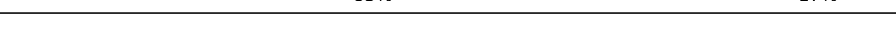
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Mol	Chain	Length	Quality of chain
4	i	112	 82% 17%
5	J	222	 83% 17%
6	j	119	 86% 12%
7	K	233	 88% 10%
8	k	99	 92% 8%
9	7	191	 84% 16%
10	l	87	 79% 21%
11	M	169	 81% 18%
12	m	77	 94% 6%
13	N	193	 78% 20%
14	n	50	 82% 18%
15	O	136	 86% 14%
16	o	52	 85% 15%
17	p	203	 72% 27%
18	Q	197	 87% 13%
19	5	183	 81% 17%
20	S	185	 88% 12%
21	s	220	 74% 22%
22	T	152	 85% 15%
23	U	172	 82% 17%
24	V	159	 86% 14%
25	W	100	 89% 10%
26	P	155	 53% 94%
27	r	197	 14% 49% 12% 39%
28	x	136	 76% 24%

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Mol	Chain	Length	Quality of chain
29	3	121	 56% 36% 7%
30	Y	62	 87% 13%
31	4	158	 52% 37% 11%
32	Z	121	 88% 12%
33	a	126	 84% 16%
34	B	76	 47% 47% 5%
35	b	135	 85% 13%
36	C	105	 88% 12%
37	c	148	 84% 16%
38	D	91	 81% 19%
39	d	58	 84% 14%
40	E	252	 80% 20%
41	e	97	 84% 16%
42	F	386	 78% 22%
43	f	109	 85% 15%
44	G	361	 84% 15%
45	g	127	 86% 14%
46	H	296	 83% 16%
47	h	106	 83% 17%
48	I	175	 77% 13% 11%
49	L	204	 41% 81% 19%
50	1	3316	 54% 37% 9%

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 138804 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 ABC transporter ATP-binding protein ARB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	446	Total	C	N	O	S	0	0
			3522	2232	610	668	12		

- Molecule 2 is a protein called Protein VMS1,Vms1,Protein VMS1,Vms1.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	R	360	Total	C	N	O	S	Se	0	0
			2804	1788	499	504	12	1		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	?	-	PHE	deletion	UNP Q04311
R	?	-	ASP	deletion	UNP Q04311
R	?	-	SER	deletion	UNP Q04311
R	?	-	THR	deletion	UNP Q04311
R	?	-	LEU	deletion	UNP Q04311
R	?	-	ARG	deletion	UNP Q04311
R	?	-	GLU	deletion	UNP Q04311
R	?	-	VAL	deletion	UNP Q04311
R	?	-	GLU	deletion	UNP Q04311
R	?	-	VAL	deletion	UNP Q04311
R	?	-	GLU	deletion	UNP Q04311
R	?	-	LYS	deletion	UNP Q04311
R	?	-	THR	deletion	UNP Q04311
R	?	-	SER	deletion	UNP Q04311
R	?	-	ASP	deletion	UNP Q04311
R	?	-	ASN	deletion	UNP Q04311
R	?	-	ASP	deletion	UNP Q04311
R	?	-	ARG	deletion	UNP Q04311
R	?	-	ASN	deletion	UNP Q04311
R	?	-	LYS	deletion	UNP Q04311
R	?	-	GLU	deletion	UNP Q04311

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Chain	Residue	Modelled	Actual	Comment	Reference
R	?	-	SER	deletion	UNP Q04311
R	?	-	GLY	deletion	UNP Q04311
R	?	-	ASP	deletion	UNP Q04311
R	?	-	LEU	deletion	UNP Q04311
R	?	-	GLN	deletion	UNP Q04311
R	?	-	ILE	deletion	UNP Q04311
R	?	-	ALA	deletion	UNP Q04311
R	?	-	ARG	deletion	UNP Q04311
R	?	-	LYS	deletion	UNP Q04311
R	?	-	LYS	deletion	UNP Q04311
R	?	-	VAL	deletion	UNP Q04311
R	?	-	THR	deletion	UNP Q04311
R	?	-	SER	deletion	UNP Q04311
R	?	-	ASN	deletion	UNP Q04311
R	?	-	VAL	deletion	UNP Q04311
R	?	-	MET	deletion	UNP Q04311
R	?	-	ARG	deletion	UNP Q04311
R	?	-	PHE	deletion	UNP Q04311
R	?	-	ASP	deletion	UNP Q04311
R	?	-	SER	deletion	UNP Q04311
R	?	-	ARG	deletion	UNP Q04311
R	?	-	ASN	deletion	UNP Q04311
R	?	-	GLU	deletion	UNP Q04311
R	?	-	GLN	deletion	UNP Q04311
R	?	-	LYS	deletion	UNP Q04311
R	?	-	ALA	deletion	UNP Q04311
R	187	SER	-	linker	UNP Q04311

- Molecule 3 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 4 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 7 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 9 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	7	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 10 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 12 is a protein called 60S ribosomal protein L38.

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

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L39.

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

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 16 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	5	183	Total	C	N	O	0	0
			1420	882	281	257		

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L10.

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

- Molecule 22 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 24 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 26 is a protein called 60S ribosomal protein L12-A.

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

- Molecule 27 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 28 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 29 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 30 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 31 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 32 is a protein called 60S ribosomal protein L25.

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

- Molecule 33 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 34 is a RNA chain called tRNA-Ala.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

- Molecule 35 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L28.

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

- Molecule 38 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L29.

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

- Molecule 40 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L30.

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

- Molecule 42 is a protein called 60S ribosomal protein L3.

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

- Molecule 43 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L32.

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

- Molecule 46 is a protein called 60S ribosomal protein L5.

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

- Molecule 47 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L1-A.

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

- Molecule 50 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	1	3316	Total	C	N	O	P	0	0
			70924	31675	12770	23163	3316		

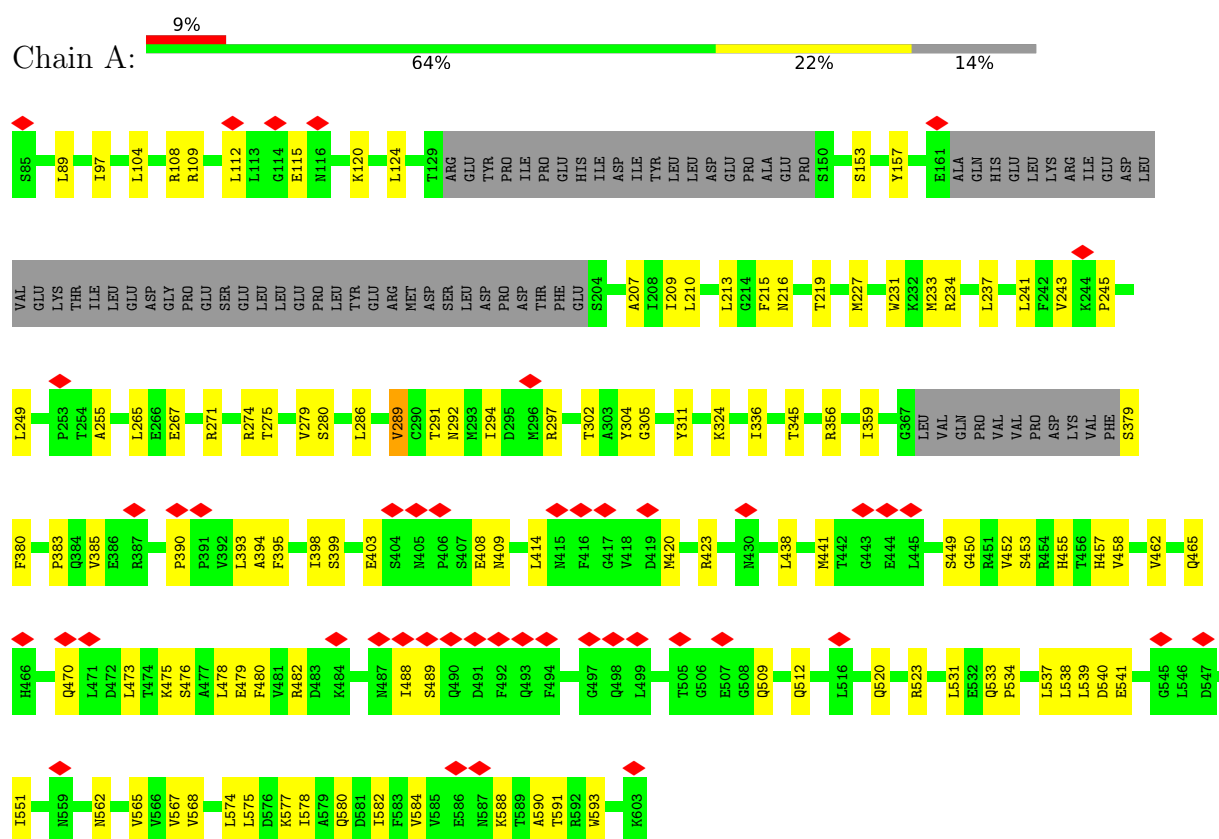
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

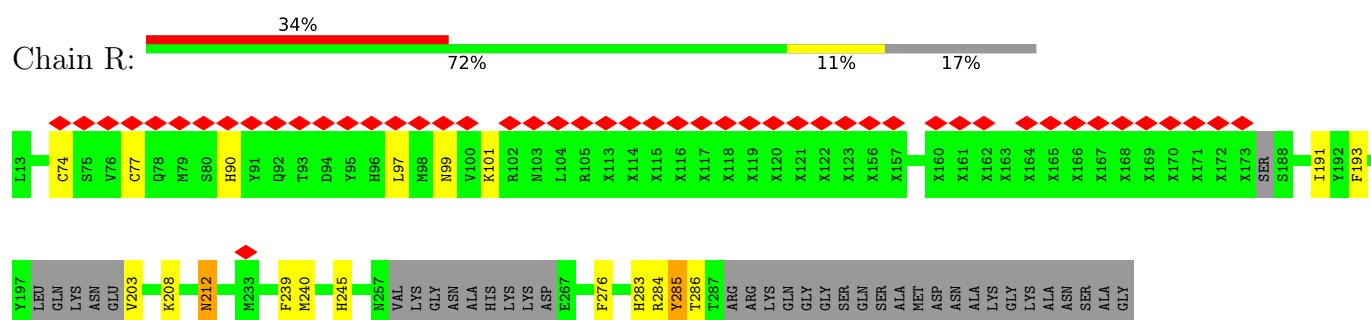
3 Residue-property plots

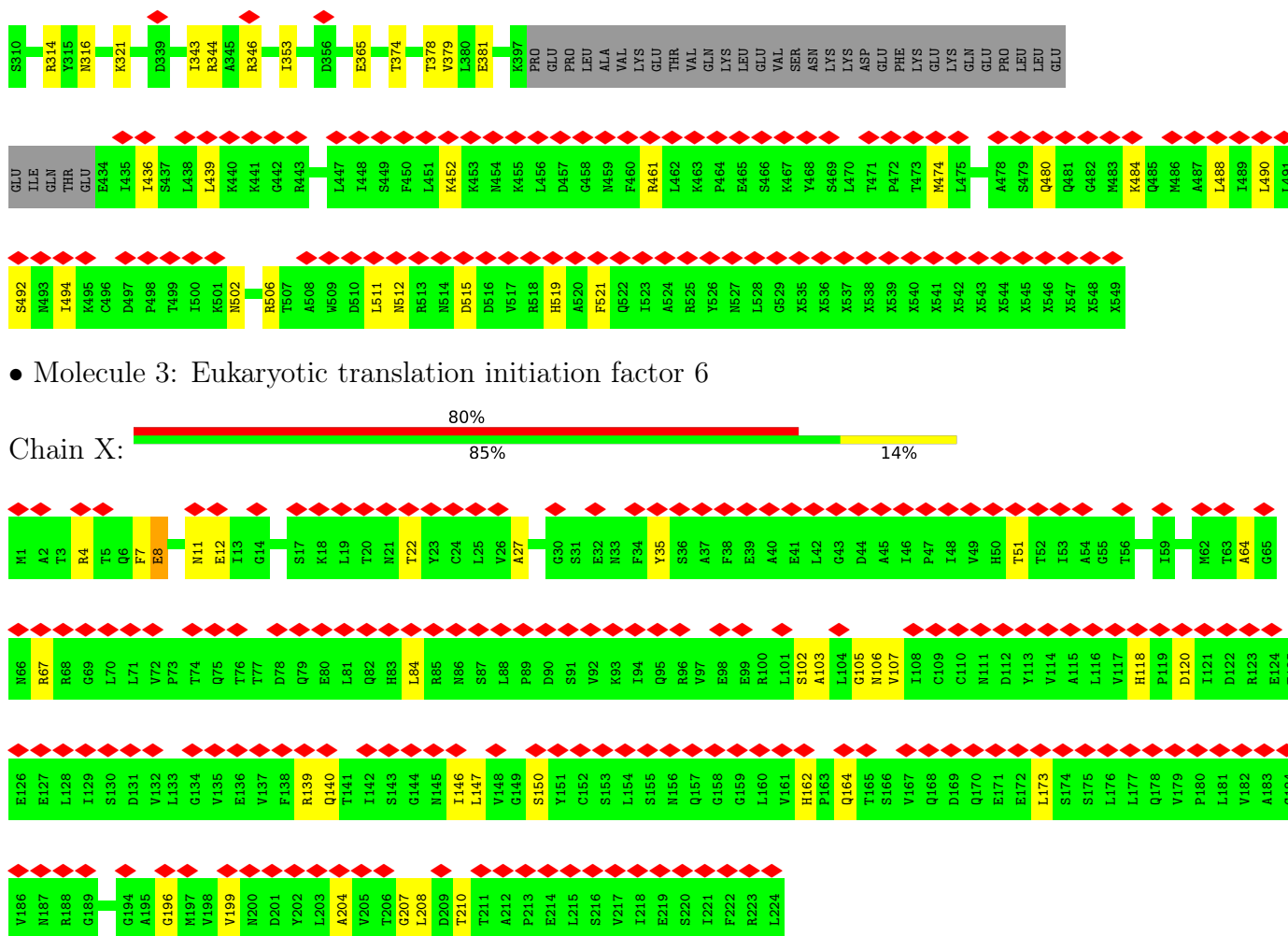
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: ABC transporter ATP-binding protein ARB1

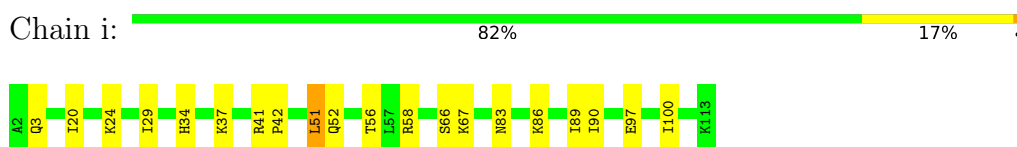


- Molecule 2: Protein VMS1,Vms1,Protein VMS1,Vms1

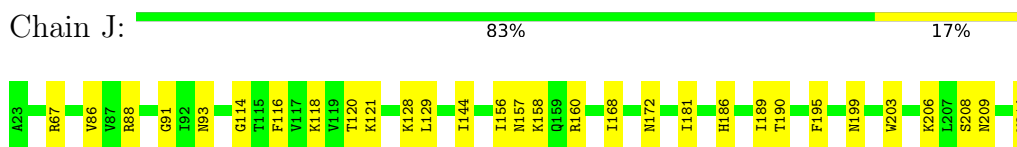




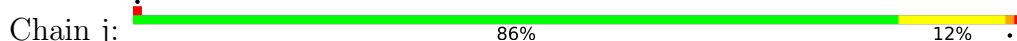
• Molecule 4: 60S ribosomal protein L34-A



• Molecule 5: 60S ribosomal protein L7-A

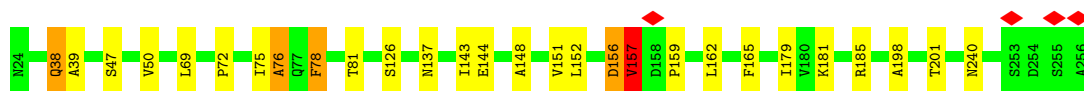
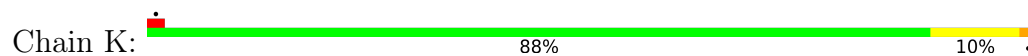


• Molecule 6: 60S ribosomal protein L35-A





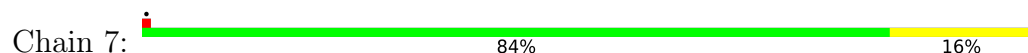
- Molecule 7: 60S ribosomal protein L8-A



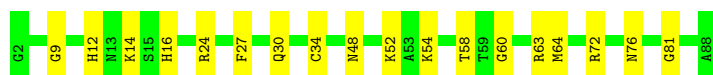
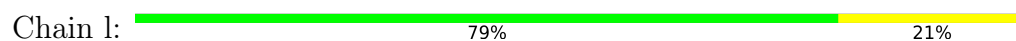
- Molecule 8: 60S ribosomal protein L36-A



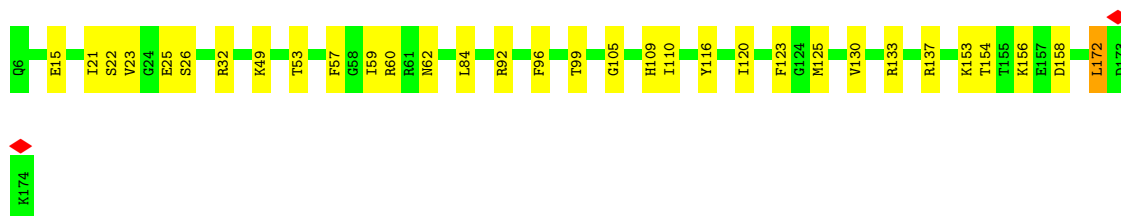
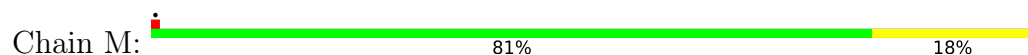
- Molecule 9: 60S ribosomal protein L9-A



- Molecule 10: 60S ribosomal protein L37-A



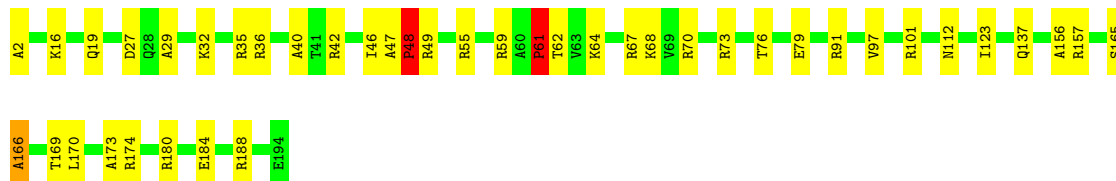
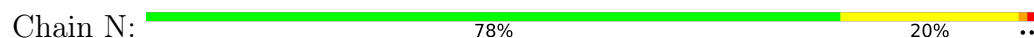
- Molecule 11: 60S ribosomal protein L11-B



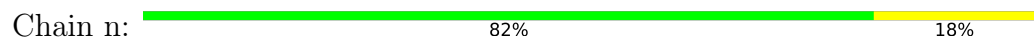
- Molecule 12: 60S ribosomal protein L38



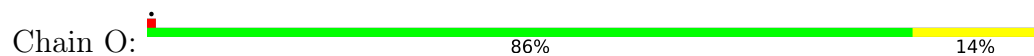
- Molecule 13: 60S ribosomal protein L13-A



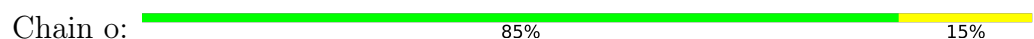
- Molecule 14: 60S ribosomal protein L39



- Molecule 15: 60S ribosomal protein L14-A



- Molecule 16: Ubiquitin-60S ribosomal protein L40



- Molecule 17: 60S ribosomal protein L15-A



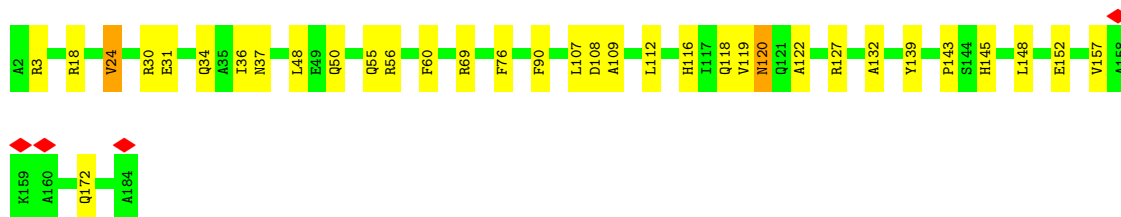
- Molecule 18: 60S ribosomal protein L16-A

Chain Q:  87% 13%



- Molecule 19: 60S ribosomal protein L17-A

Chain 5:  81% 17%



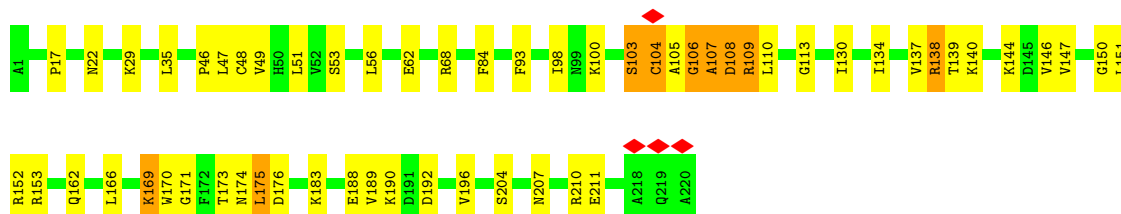
- Molecule 20: 60S ribosomal protein L18-A

Chain S:  88% 12%



- Molecule 21: 60S ribosomal protein L10

Chain s:  74% 22%



- Molecule 22: 60S ribosomal protein L19-A

Chain T:  85% 15%



- Molecule 23: 60S ribosomal protein L20-A

Chain U:  82% 17%



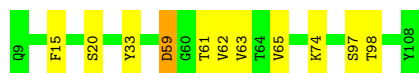
- Molecule 24: 60S ribosomal protein L21-A

Chain V:  86% 14%

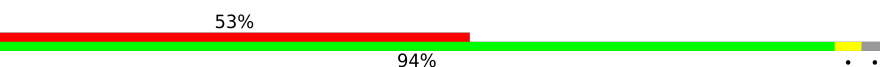


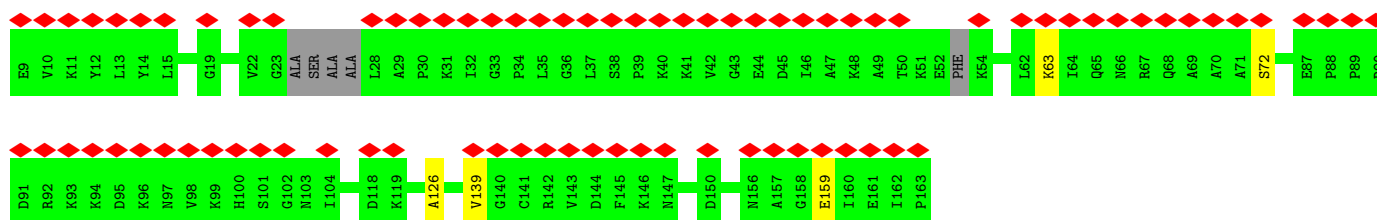
- Molecule 25: 60S ribosomal protein L22-A

Chain W:  89% 10%

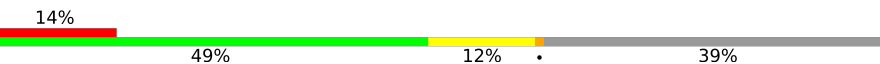


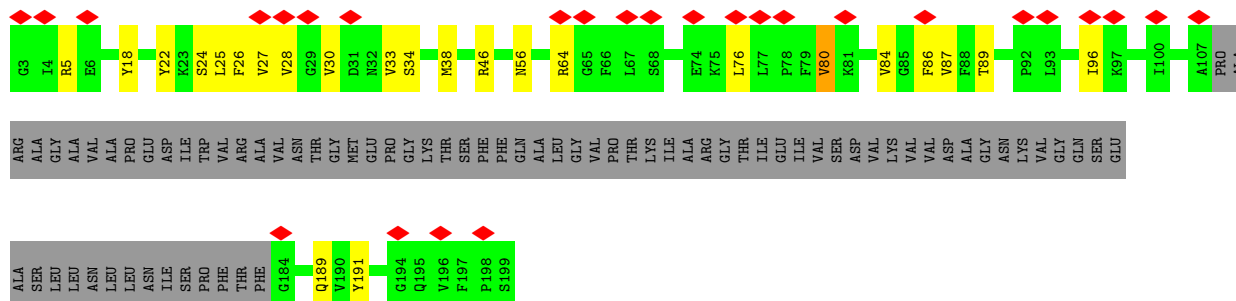
- Molecule 26: 60S ribosomal protein L12-A

Chain P:  53% 94%



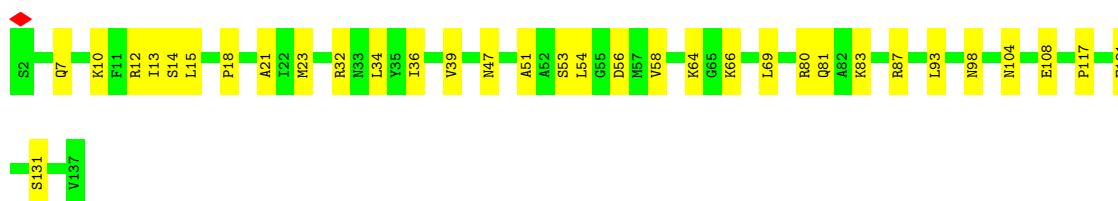
- Molecule 27: 60S acidic ribosomal protein P0

Chain r:  14% 49% 12% 39%



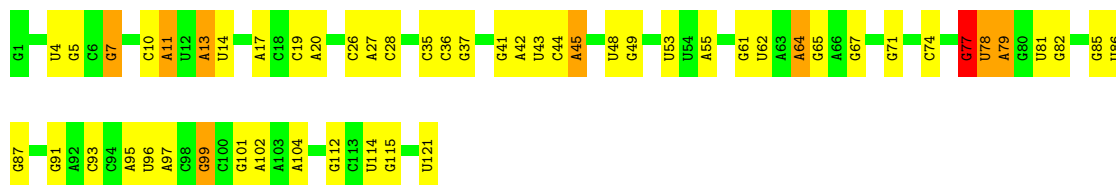
- Molecule 28: 60S ribosomal protein L23-A

Chain x:  76% 24%



- Molecule 29: 5S rRNA

Chain 3:  56% 36% 7%



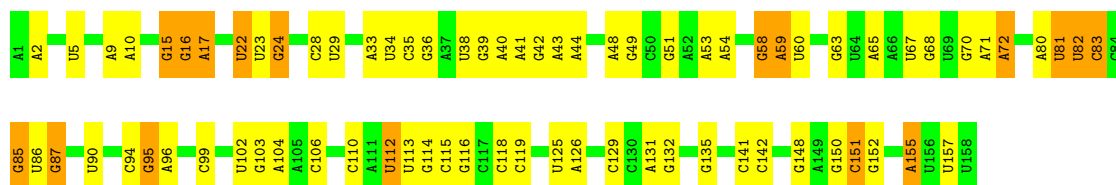
- Molecule 30: 60S ribosomal protein L24-A

Chain Y:  87% 13%



- Molecule 31: 5.8S rRNA

Chain 4:  52% 37% 11%



- Molecule 32: 60S ribosomal protein L25

Chain Z:  88% 12%



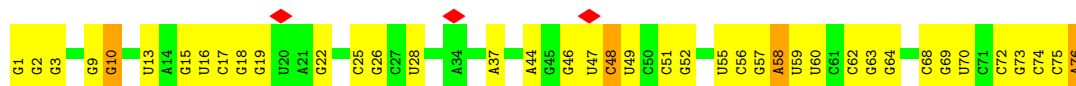
- Molecule 33: 60S ribosomal protein L26-A

Chain a:  84% 16%



- Molecule 34: tRNA-Ala

Chain B:  47% 47% 5%



- Molecule 35: 60S ribosomal protein L27-A

Chain b:  85% 13%



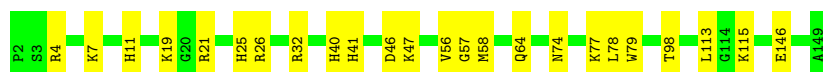
- Molecule 36: 60S ribosomal protein L42-A

Chain C:  88% 12%



- Molecule 37: 60S ribosomal protein L28

Chain c:  84% 16%



- Molecule 38: 60S ribosomal protein L43-A

Chain D:  81% 19%



- Molecule 39: 60S ribosomal protein L29

Chain d:  84% 14%



- Molecule 40: 60S ribosomal protein L2-A

Chain E:  80% 20%

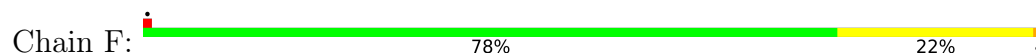


- Molecule 41: 60S ribosomal protein L30

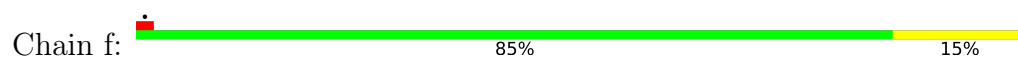
Chain e:  84% 16%



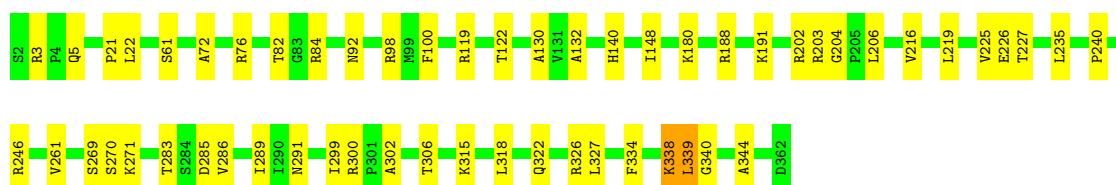
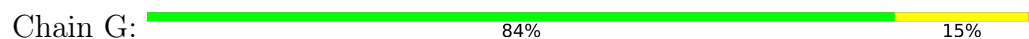
- Molecule 42: 60S ribosomal protein L3



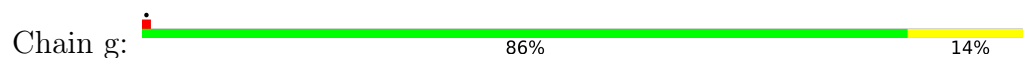
- Molecule 43: 60S ribosomal protein L31-A



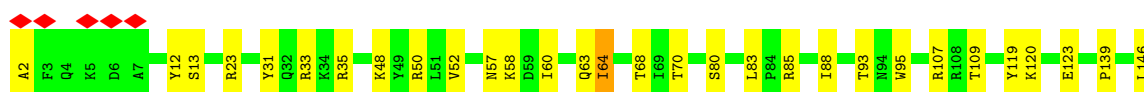
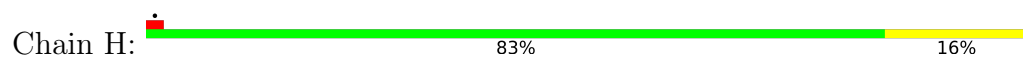
- Molecule 44: 60S ribosomal protein L4-A



- Molecule 45: 60S ribosomal protein L32



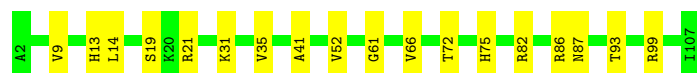
- Molecule 46: 60S ribosomal protein L5





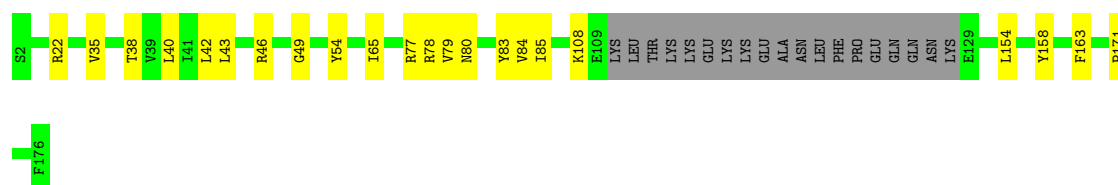
- Molecule 47: 60S ribosomal protein L33-A

Chain h: 83% 17%



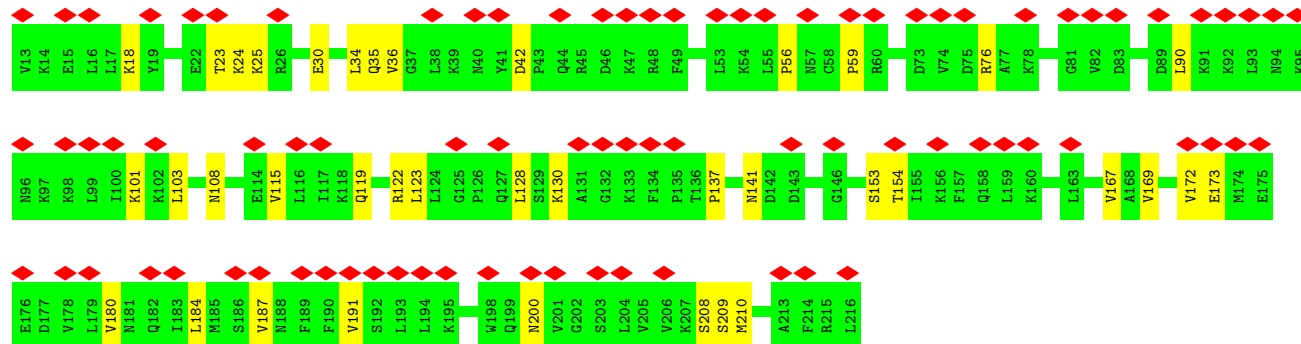
- Molecule 48: 60S ribosomal protein L6-A

Chain I: 77% 13% 11%



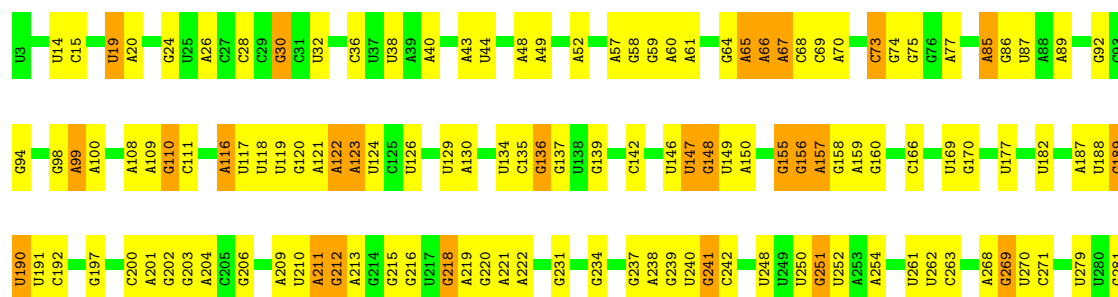
- Molecule 49: 60S ribosomal protein L1-A

Chain L: 41% 81% 19%



- Molecule 50: 25S rRNA

Chain 1: 54% 37% 9%



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A1503	G1408	U1329	G1248	A1169	G1072	G994	A896	C804	U707	A619	A529	A374	A285
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G1507	G1412	U1331	A1251	G1178	C1076	G999	A906	A807	A709	A622	G531	G376	G287
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A1575	U1496	U1398	G1322	A1243	A1159	G1063	U985	U889				A522	A522
G1576		A1399	G1323	A1244		A1064							

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A1884	U1885	A1886	A1887	U1888	G1889	U1892	A1893	G1896	A1897	G1898	U1899	A1900	U1901	G1902	G1906	C1907	A1908	U1909	A1913	U1914	U1916	U1920	C1926	U1927	G1928	U1929	A1930	U1931	A1932	G1935	U1938	U1939	G1940	A1945	A1946	G1947	U1948	G1953	U1954	U1955	A1956	U1957	U1958	G1959	A1960	U1961	A1962							
A1787	C1788	C1792	U1793	U1794	U1795	U1796	U1797	G1808	A1813	A1814	U1815	U1816	U1817	U1818	U1819	U1820	U1821	C1822	G1830	U1831	A1835	U1839	U1840	A1841	U1842	U1843	C1846	U1847	G1848	U1849	A1850	G1851	U1852	U1853	U1854	U1855	G1863	A1864	U1865	C1866	A1867	U1868	C1869	U1870	U1876	U1877	U1878	A1879	U1880	A1881				
A1683	U1688	C1695	U1696	C1709	U1710	G1713	A1714	U1715	U1716	U1717	U1718	G1719	U1722	A1723	U1724	C1725	G1730	U1740	U1741	U1742	U1746	U1749	A1750	U1751	G1752	G1756	A1760	C1761	U1762	U1763	U1765	G1766	G1769	U1770	C1771	U1772	C1773	G1775	U1778	C1779	G1780	U1785	G1786											
C1578	C1579	C1580	C1581	C1582	A1583	A1588	A1589	G1590	G1591	U1592	A1593	A1594	U1595	C1596	A1602	A1603	G1604	U1605	U1606	A1613	C1614	C1615	U1616	U1620	A1621	U1622	G1623	U1626	U1627	C1628	U1629	U1630	C1631	G1634	U1635	A1638	C1644	U1645	G1646	A1656	C1657	C1660	G1661	C1662	C1663	G1664	G1678							

U3357	A3273	A3187	C3093	U2996	C2889
U3358	A3274	U3190	A3094	G2997	A2890
G3361	G3276	G3191	G3098	U2998	U2891
A3362	U3277	C3194	G3109	U2999	A2892
U3363	C3278	U3195	C3110	A3000	G2895
U3368	A3279	U3196	U3111	C3001	A2896
G3369	G3286	U3197	G3112	C3002	
A3370	U3287	U3198	A3113	A3005	C2899
G3375	G3288	G3205	A3114	G3009	A2900
A3376	G3289	C3206	C3115	U3010	G2901
A3376	G3290	U3207	G3116	A3011	U2904
G3377	G3291	U3207	C3117	A3012	
C3378	A3292	G3208	C3118		A2911
U3382	U3293	A3209	U3119	G3015	G2912
G3383	A3294	A3210	C3120	A3016	A2919
U3386	A3295	U3121	U3121	A3017	U2920
	A3296	U3214	A3122	C3018	U2921
		A3215			G2922
A3305	A3305	G3216	A3129	A3021	U2924
U3306	U3306	C3217	A3130	G3022	
A3307	A3307	A3218	U3131	A3023	A2941
C3308	C3308	G3219		U3024	C2942
G3309	G3309	G3220	A3139	A3024	C2943
A3310	A3310	C3221	G3140	G3025	U2944
		U3222	A3141	G3026	A2946
U3313	U3313	A3227	A3142	A3040	G2947
A3316	A3316	C3228	C3143	U3041	C2948
U3317	U3317		C3144	U3042	U2949
G3318	G3318	U3231	G3147	G3043	G2950
U3319	U3319	G3232		G3044	G2951
A3322	A3322	A3234	A3150	U3047	
A3323	A3323	C3234	U3151	A3048	U2954
C3324	C3324	U3237	U3152	A3049	U2955
			U3153	U3050	
A3330	A3330	A3243	C3154	U3051	G2964
U3331	U3331	A3244	U3155	U3056	U2966
U3332	U3332	A3245	U3156	U3057	A2971
G3333	G3333	G3246	U3157	G3058	G2972
U3334	U3334	G3247	G3158	U3059	G2973
A3335	A3335		C3162	U3066	
		G3253	A3163	U3067	A2976
G3340	G3340	G3254		G3068	G2977
U3341	U3341	U3255	A3170	G3069	U2978
		G3256	U3171	C3066	U2979
A3344	A3344	C3257	G3172	U3068	
G3345	G3345	U3258	G3173		C2983
U3346	U3346	U3259	A3174	U3078	
A3347	A3347	G3260	U3175	U3079	A2976
G3348	G3348		G3176	G3080	G2977
		G3263			U2978
U3351	U3351	A3268	U3179	A3086	U2979
U3352	U3352	U3269	A3180	A3087	
G3353	G3353	U3270	C3181	G3088	
U3354	U3354	G3271	U3185		C2983
U3355	U3355	C3272	A3186		U2992
G3356	G3356				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31832	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	0.560	Depositor
Minimum map value	-0.382	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.025	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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	A	0.22	0/3583	0.58	0/4831
2	R	0.25	0/2631	0.56	0/3532
3	X	0.20	0/1653	0.55	0/2255
4	i	0.53	0/890	0.85	3/1189 (0.3%)
5	J	0.44	0/1821	0.70	0/2451
6	j	0.35	0/978	0.86	8/1301 (0.6%)
7	K	0.37	0/1836	0.75	8/2481 (0.3%)
8	k	0.38	0/778	0.74	0/1034
9	7	0.42	0/1539	0.68	1/2073 (0.0%)
10	l	0.56	0/696	0.90	0/923
11	M	0.29	0/1374	0.76	2/1842 (0.1%)
12	m	0.35	0/618	0.64	0/826
13	N	0.43	0/1568	0.84	4/2106 (0.2%)
14	n	0.60	0/443	0.84	0/588
15	O	0.39	0/1068	0.70	0/1438
16	o	0.42	0/423	0.78	1/562 (0.2%)
17	p	0.56	0/1757	0.89	4/2354 (0.2%)
18	Q	0.51	0/1585	0.77	0/2128
19	5	0.49	0/1443	0.83	2/1944 (0.1%)
20	S	0.38	0/1465	0.74	0/1965
21	s	0.41	0/1807	0.82	5/2425 (0.2%)
22	T	0.45	0/1245	0.79	0/1661
23	U	0.49	0/1481	0.80	1/1990 (0.1%)
24	V	0.41	0/1300	0.73	0/1743
25	W	0.34	0/812	0.71	1/1099 (0.1%)
26	P	0.24	0/734	0.84	1/1015 (0.1%)
27	r	0.21	0/982	0.64	1/1320 (0.1%)
28	x	0.44	0/1018	0.71	0/1369
29	3	0.36	0/2883	0.49	1/4491 (0.0%)
30	Y	0.41	0/525	0.70	0/696
31	4	0.47	0/3746	0.53	0/5832
32	Z	0.46	0/979	0.71	0/1321

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.39	0/1004	0.73	0/1341
34	B	0.22	0/1810	0.39	0/2821
35	b	0.39	0/1118	0.73	1/1497 (0.1%)
36	C	0.39	0/860	0.78	0/1136
37	c	0.44	0/1204	0.78	0/1612
38	D	0.48	0/701	0.76	0/934
39	d	0.40	0/473	0.68	0/629
40	E	0.56	0/1948	0.81	4/2617 (0.2%)
41	e	0.34	0/751	0.68	0/1008
42	F	0.57	1/3146 (0.0%)	0.79	0/4228
43	f	0.50	0/890	0.74	0/1196
44	G	0.44	0/2800	0.80	0/3790
45	g	0.45	0/1041	0.73	0/1394
46	H	0.31	0/2425	0.64	0/3271
47	h	0.51	0/868	0.71	0/1168
48	I	0.33	0/1260	0.65	0/1694
49	L	0.24	0/1634	0.74	1/2195 (0.0%)
50	l	0.46	0/79382	0.57	17/123763 (0.0%)
All	All	0.44	1/148976 (0.0%)	0.63	66/219079 (0.0%)

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	1
3	X	0	1
5	J	0	2
6	j	0	2
7	K	0	3
9	7	0	1
11	M	0	1
12	m	0	1
13	N	0	3
21	s	0	2
23	U	0	1
35	b	0	1
37	c	0	1
39	d	0	1
42	F	0	1
44	G	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	H	0	1
All	All	0	27

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	F	237	LYS	C-N	-13.03	1.13	1.33

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	N	48	PRO	CA-C-N	9.06	139.97	121.48
13	N	48	PRO	C-N-CA	9.06	139.97	121.48
49	L	191	VAL	N-CA-C	-6.59	106.31	112.83
13	N	61	PRO	CA-C-N	6.52	133.99	121.54
13	N	61	PRO	C-N-CA	6.52	133.99	121.54

There are no chirality outliers.

5 of 27 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	289	VAL	Peptide
5	J	157	ASN	Peptide
5	J	232	ARG	Peptide
3	X	8	GLU	Peptide
6	j	90	ARG	Peptide

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	3522	0	3534	74	0
2	R	2804	0	2687	46	0
3	X	1633	0	1596	21	0
4	i	880	0	945	11	0
5	J	1784	0	1862	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	j	969	0	1078	10	0
7	K	1804	0	1877	19	0
8	k	771	0	849	7	0
9	7	1518	0	1587	21	0
10	l	681	0	687	17	0
11	M	1353	0	1383	19	0
12	m	612	0	682	3	0
13	N	1543	0	1608	29	0
14	n	436	0	475	5	0
15	O	1053	0	1149	15	0
16	o	417	0	459	7	0
17	p	1720	0	1779	45	0
18	Q	1555	0	1659	16	0
19	5	1420	0	1437	21	0
20	S	1441	0	1543	20	0
21	s	1770	0	1808	57	0
22	T	1228	0	1314	17	0
23	U	1445	0	1487	19	0
24	V	1276	0	1323	18	0
25	W	796	0	812	6	0
26	P	737	0	341	2	0
27	r	967	0	991	17	0
28	x	1003	0	1048	24	0
29	3	2579	0	1304	32	0
30	Y	513	0	540	6	0
31	4	3353	0	1695	40	0
32	Z	964	0	1025	12	0
33	a	993	0	1081	16	0
34	B	1622	0	820	44	0
35	b	1092	0	1155	16	0
36	C	847	0	918	8	0
37	c	1173	0	1215	17	0
38	D	694	0	738	13	0
39	d	462	0	491	7	0
40	E	1914	0	1981	38	0
41	e	743	0	797	12	0
42	F	3075	0	3141	59	0
43	f	876	0	912	12	0
44	G	2748	0	2859	39	0
45	g	1020	0	1090	13	0
46	H	2375	0	2325	31	0
47	h	850	0	880	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	I	1239	0	1326	14	0
49	L	1609	0	1701	24	0
50	1	70924	0	35641	632	0
51	R	1	0	0	0	0
All	All	138804	0	101635	1339	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 6.

The worst 5 of 1339 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:345:THR:HG21	21:s:109:ARG:NH1	1.62	1.14
2:R:286:THR:HG22	2:R:316:ASN:HB3	1.35	1.06
2:R:286:THR:HG22	2:R:316:ASN:CB	1.86	1.05
1:A:345:THR:CG2	21:s:109:ARG:NH1	2.22	1.03
2:R:284:ARG:NH1	34:B:1:G:C8	2.31	0.99

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	438/519 (84%)	411 (94%)	27 (6%)	0	100	100
2	R	300/433 (69%)	286 (95%)	14 (5%)	0	100	100
3	X	222/224 (99%)	206 (93%)	16 (7%)	0	100	100
4	i	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
5	J	220/222 (99%)	205 (93%)	13 (6%)	2 (1%)	14	46
6	j	117/119 (98%)	110 (94%)	4 (3%)	3 (3%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	K	231/233 (99%)	211 (91%)	19 (8%)	1 (0%)	30	61
8	k	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
9	7	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
10	l	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
11	M	167/169 (99%)	148 (89%)	19 (11%)	0	100	100
12	m	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
13	N	191/193 (99%)	171 (90%)	16 (8%)	4 (2%)	5	31
14	n	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
15	O	134/136 (98%)	119 (89%)	15 (11%)	0	100	100
16	o	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
17	p	201/203 (99%)	179 (89%)	19 (10%)	3 (2%)	8	37
18	Q	195/197 (99%)	187 (96%)	8 (4%)	0	100	100
19	5	181/183 (99%)	164 (91%)	17 (9%)	0	100	100
20	S	183/185 (99%)	169 (92%)	14 (8%)	0	100	100
21	s	218/220 (99%)	187 (86%)	26 (12%)	5 (2%)	5	30
22	T	150/152 (99%)	142 (95%)	7 (5%)	1 (1%)	18	51
23	U	170/172 (99%)	156 (92%)	13 (8%)	1 (1%)	21	54
24	V	157/159 (99%)	144 (92%)	13 (8%)	0	100	100
25	W	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
26	P	144/155 (93%)	122 (85%)	22 (15%)	0	100	100
27	r	117/197 (59%)	110 (94%)	7 (6%)	0	100	100
28	x	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
30	Y	60/62 (97%)	56 (93%)	4 (7%)	0	100	100
32	Z	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
33	a	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
35	b	133/135 (98%)	117 (88%)	15 (11%)	1 (1%)	16	49
36	C	103/105 (98%)	92 (89%)	11 (11%)	0	100	100
37	c	146/148 (99%)	129 (88%)	14 (10%)	3 (2%)	5	31
38	D	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
39	d	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	34
40	E	250/252 (99%)	223 (89%)	27 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	e	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
42	F	384/386 (100%)	349 (91%)	34 (9%)	1 (0%)	36	65
43	f	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
44	G	359/361 (99%)	324 (90%)	34 (10%)	1 (0%)	36	65
45	g	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
46	H	294/296 (99%)	271 (92%)	23 (8%)	0	100	100
47	h	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
48	I	152/175 (87%)	143 (94%)	9 (6%)	0	100	100
49	L	202/204 (99%)	165 (82%)	37 (18%)	0	100	100
All	All	7524/7934 (95%)	6877 (91%)	620 (8%)	27 (0%)	31	61

5 of 27 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	s	104	CYS
21	s	106	GLY
37	c	47	LYS
44	G	339	LEU
5	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	A	386/456 (85%)	385 (100%)	1 (0%)	86	83
2	R	288/349 (82%)	286 (99%)	2 (1%)	76	78
3	X	177/192 (92%)	177 (100%)	0	100	100
4	i	95/95 (100%)	94 (99%)	1 (1%)	65	74
5	J	186/186 (100%)	186 (100%)	0	100	100
6	j	104/104 (100%)	104 (100%)	0	100	100
7	K	187/191 (98%)	186 (100%)	1 (0%)	81	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	k	81/81 (100%)	81 (100%)	0	100	100
9	7	171/171 (100%)	169 (99%)	2 (1%)	63	73
10	l	70/70 (100%)	70 (100%)	0	100	100
11	M	147/147 (100%)	146 (99%)	1 (1%)	76	78
12	m	68/68 (100%)	68 (100%)	0	100	100
13	N	154/154 (100%)	154 (100%)	0	100	100
14	n	45/45 (100%)	45 (100%)	0	100	100
15	O	107/107 (100%)	107 (100%)	0	100	100
16	o	47/47 (100%)	47 (100%)	0	100	100
17	p	175/175 (100%)	172 (98%)	3 (2%)	53	69
18	Q	160/160 (100%)	158 (99%)	2 (1%)	61	72
19	5	140/145 (97%)	138 (99%)	2 (1%)	59	71
20	S	150/150 (100%)	150 (100%)	0	100	100
21	s	184/186 (99%)	182 (99%)	2 (1%)	65	74
22	T	126/126 (100%)	125 (99%)	1 (1%)	73	77
23	U	156/156 (100%)	155 (99%)	1 (1%)	78	79
24	V	136/136 (100%)	136 (100%)	0	100	100
25	W	87/87 (100%)	87 (100%)	0	100	100
27	r	105/166 (63%)	105 (100%)	0	100	100
28	x	104/104 (100%)	103 (99%)	1 (1%)	68	75
30	Y	54/54 (100%)	54 (100%)	0	100	100
32	Z	104/105 (99%)	104 (100%)	0	100	100
33	a	109/109 (100%)	108 (99%)	1 (1%)	70	76
35	b	115/115 (100%)	115 (100%)	0	100	100
36	C	90/90 (100%)	90 (100%)	0	100	100
37	c	118/118 (100%)	117 (99%)	1 (1%)	73	77
38	D	71/71 (100%)	71 (100%)	0	100	100
39	d	46/46 (100%)	46 (100%)	0	100	100
40	E	193/194 (100%)	189 (98%)	4 (2%)	47	65
41	e	81/81 (100%)	81 (100%)	0	100	100
42	F	319/322 (99%)	315 (99%)	4 (1%)	61	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	f	92/96 (96%)	92 (100%)	0	100	100
44	G	288/288 (100%)	288 (100%)	0	100	100
45	g	109/109 (100%)	109 (100%)	0	100	100
46	H	244/244 (100%)	243 (100%)	1 (0%)	84	81
47	h	90/90 (100%)	90 (100%)	0	100	100
48	I	134/152 (88%)	134 (100%)	0	100	100
49	L	185/185 (100%)	184 (100%)	1 (0%)	81	80
All	All	6278/6523 (96%)	6246 (100%)	32 (0%)	78	80

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	F	104	THR
42	F	324	VAL
18	Q	84	LEU
18	Q	34	VAL
46	H	64	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
23	U	122	HIS
35	b	29	HIS
46	H	63	GLN
24	V	5	HIS
27	r	32	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	3	120/121 (99%)	29 (24%)	1 (0%)
31	4	157/158 (99%)	47 (29%)	4 (2%)
34	B	75/76 (98%)	16 (21%)	0
50	1	3312/3316 (99%)	967 (29%)	155 (4%)
All	All	3664/3671 (99%)	1059 (28%)	160 (4%)

5 of 1059 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	3	7	G
29	3	11	A
29	3	13	A
29	3	14	U
29	3	26	C

5 of 160 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	1	2385	G
50	1	3022	G
50	1	2447	A
50	1	2727	A
50	1	3179	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	R	5
50	1	4
42	F	1

The worst 5 of 10 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	35:SER	C	74:CYS	N	41.41
1	1	2087:C	O3'	2093:A	P	28.40
1	R	529:GLY	C	535:UNK	N	19.42
1	R	105:ARG	C	113:UNK	N	18.44
1	R	123:UNK	C	156:UNK	N	13.45

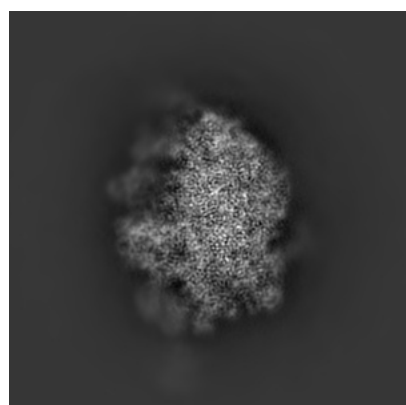
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4751. These allow visual inspection of the internal detail of the map and identification of artifacts.

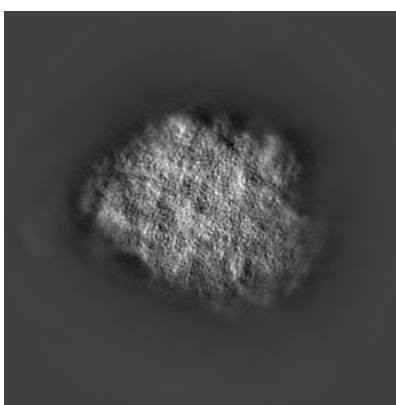
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

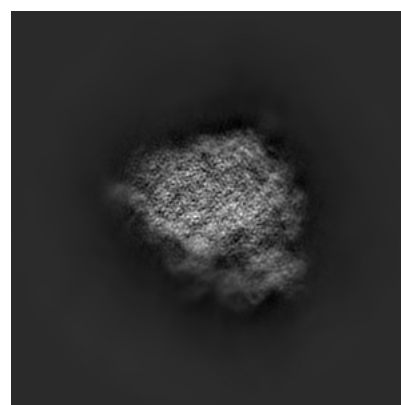
6.1.1 Primary map



X



Y

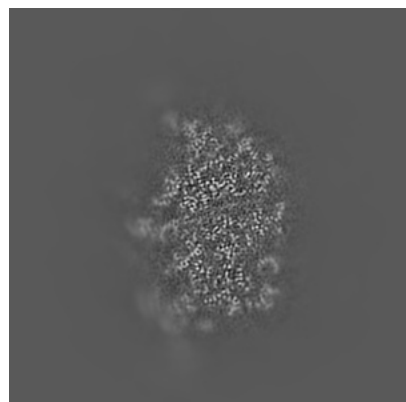


Z

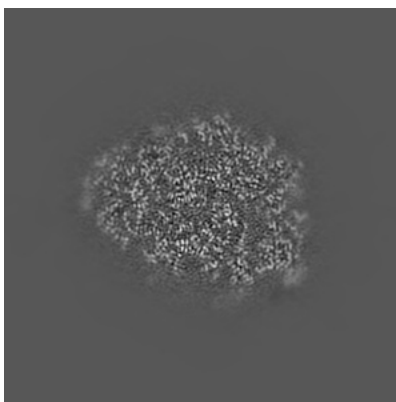
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

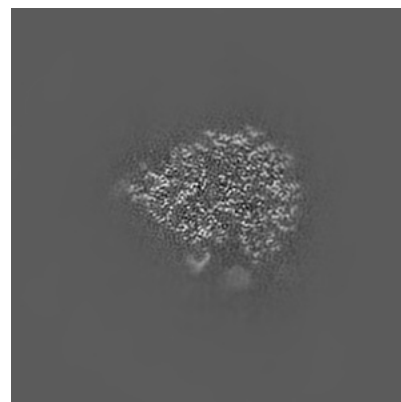
6.2.1 Primary map



X Index: 198



Y Index: 198

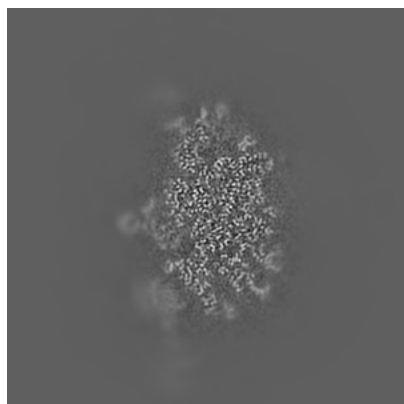


Z Index: 198

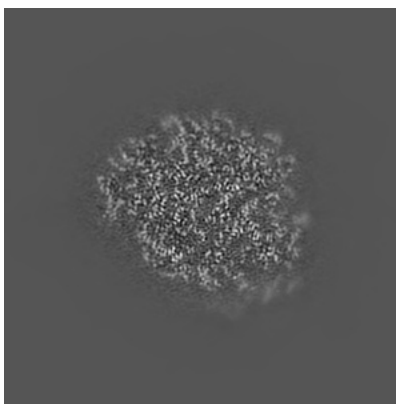
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

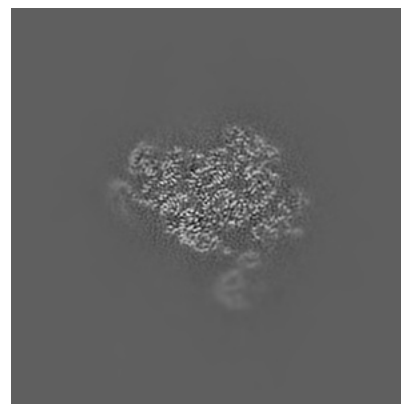
6.3.1 Primary map



X Index: 183



Y Index: 209

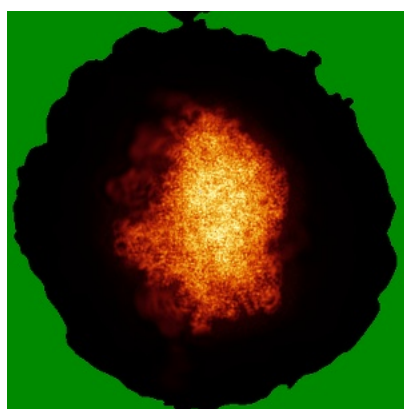


Z Index: 214

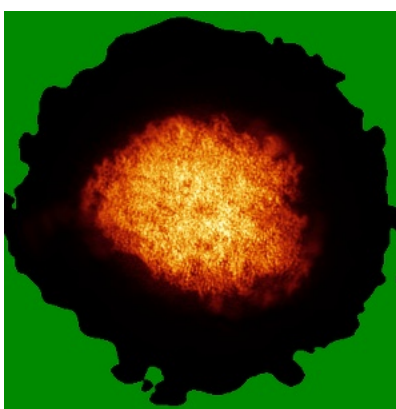
The images above show the largest variance slices of the map in three orthogonal directions.

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

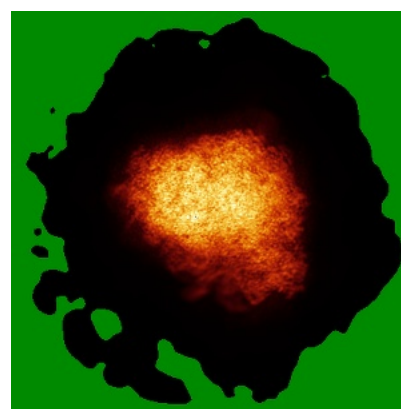
6.4.1 Primary map



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.

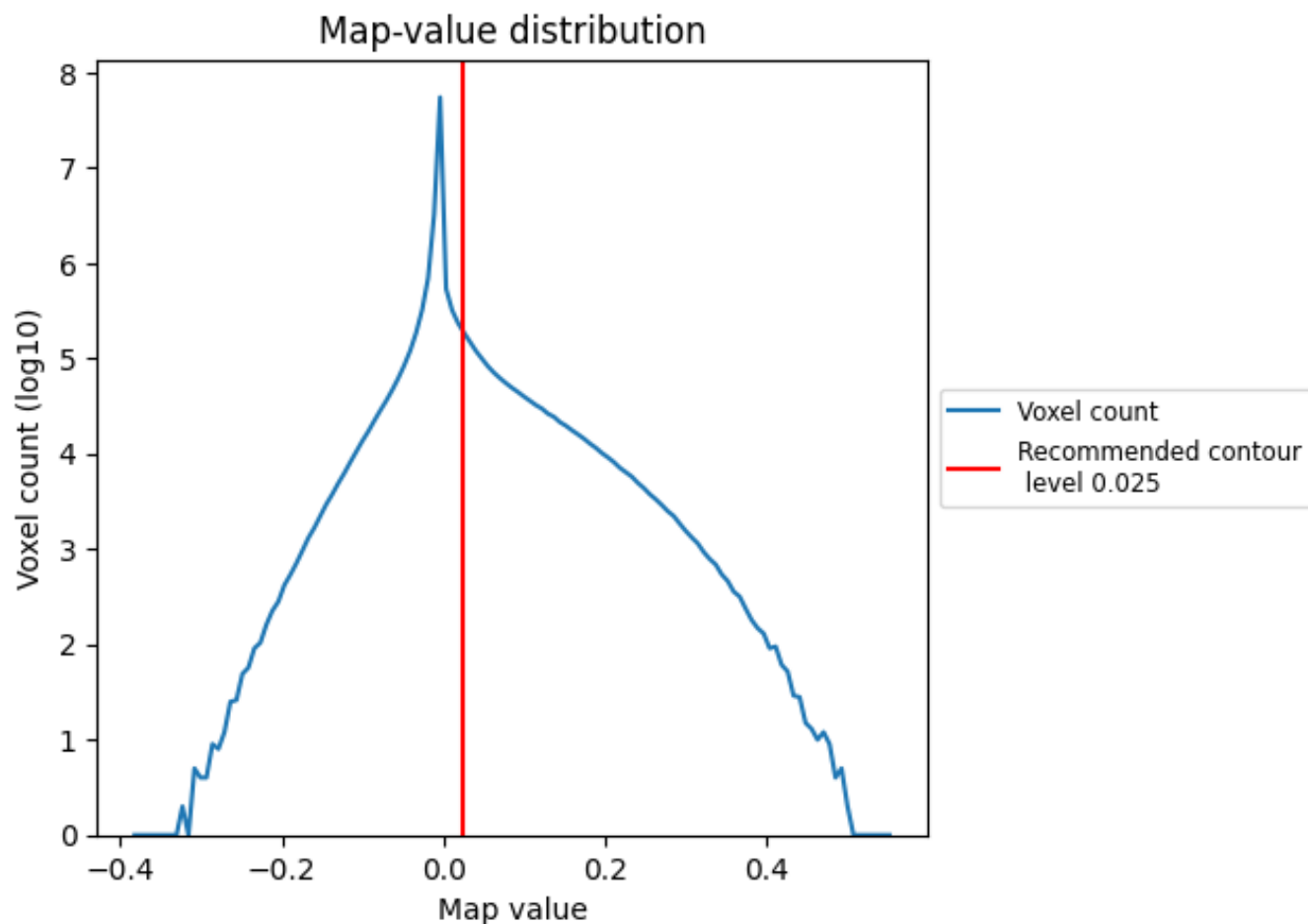
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

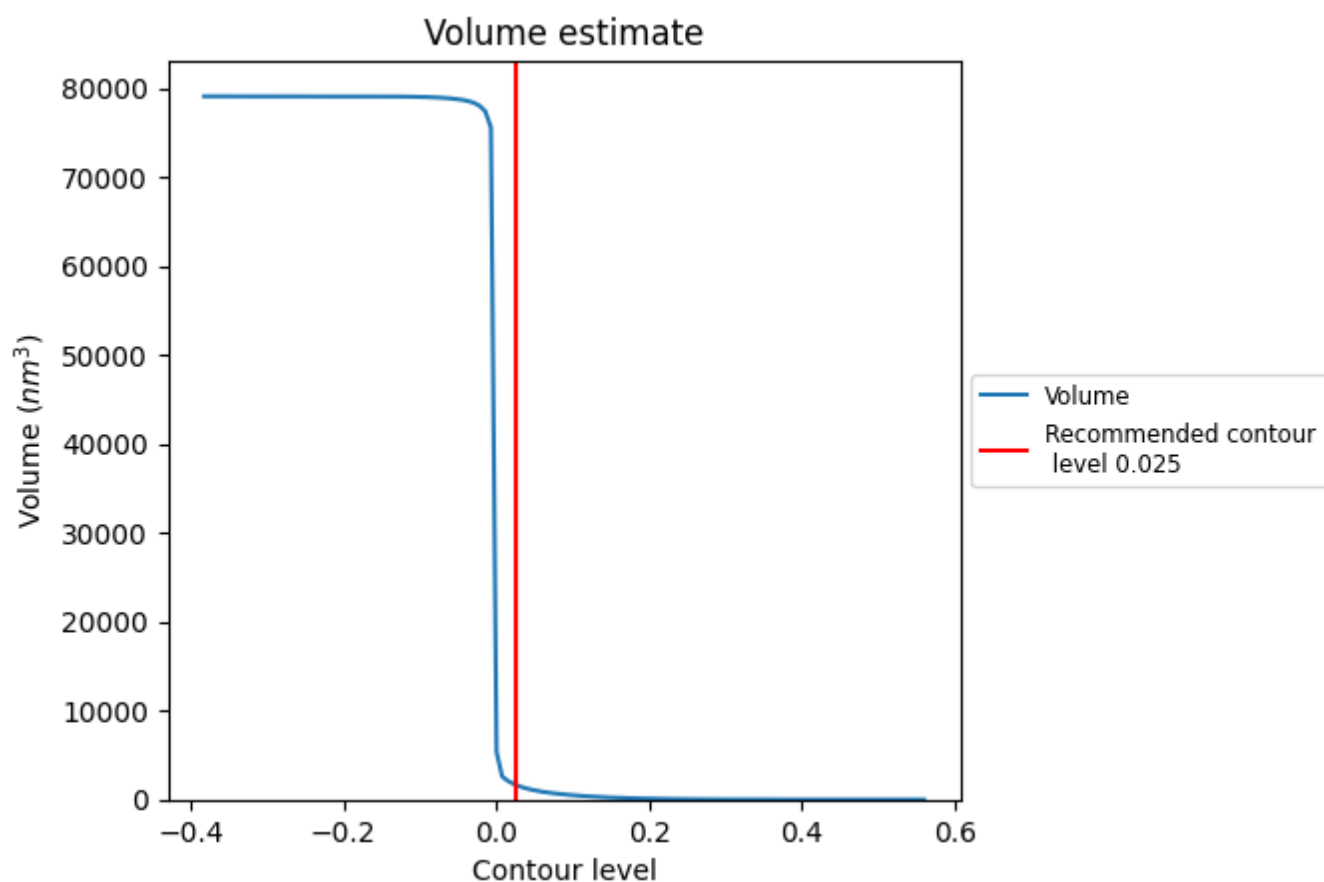
This section contains the results of statistical analysis of the map.

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.

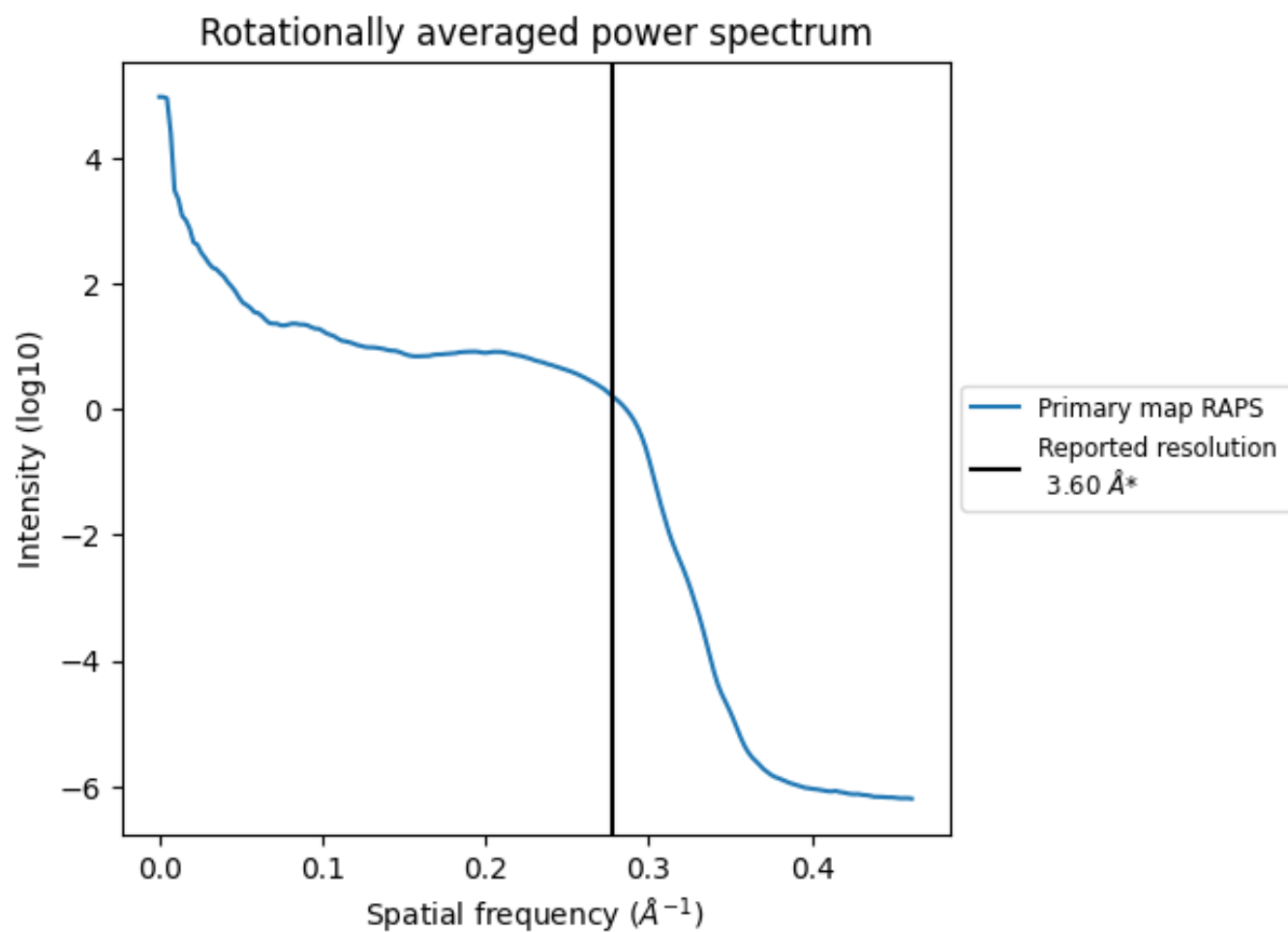
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1693 nm³; this corresponds to an approximate mass of 1530 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 0.278 Å⁻¹

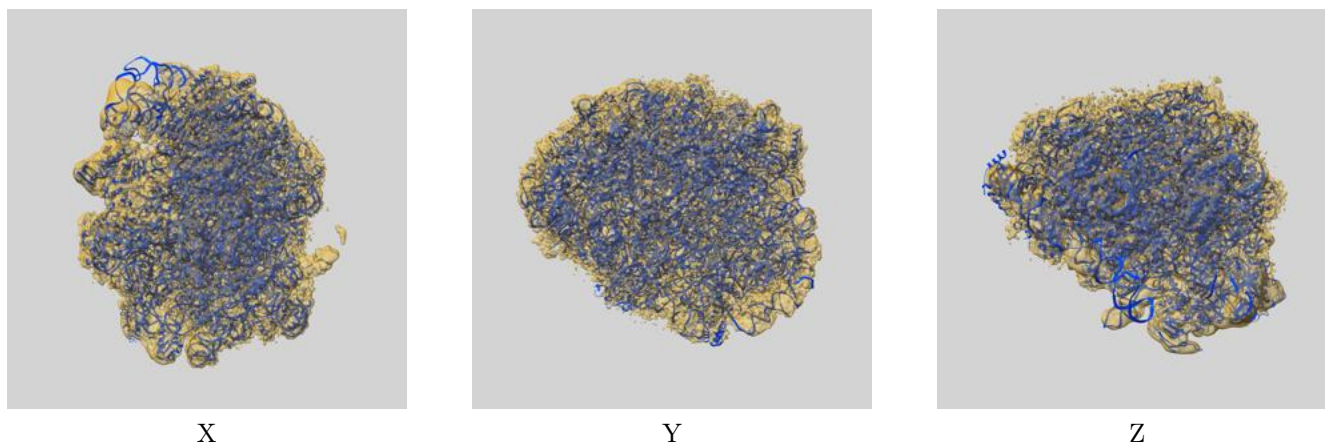
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

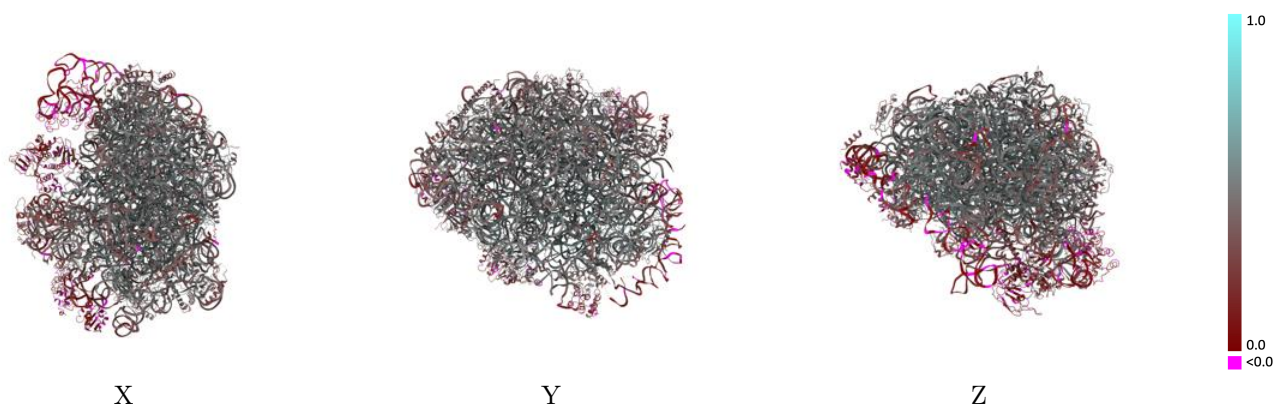
This section contains information regarding the fit between EMDB map EMD-4751 and PDB model 6R84. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



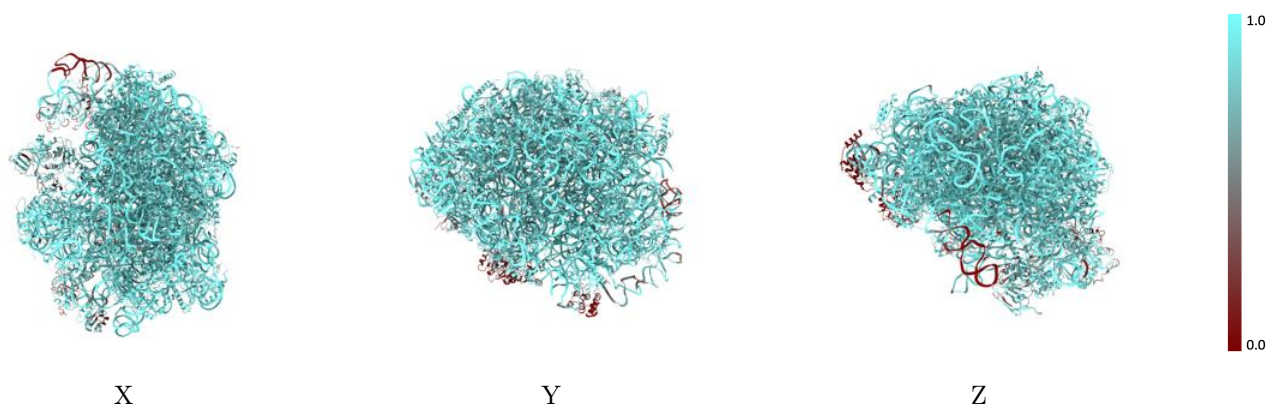
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



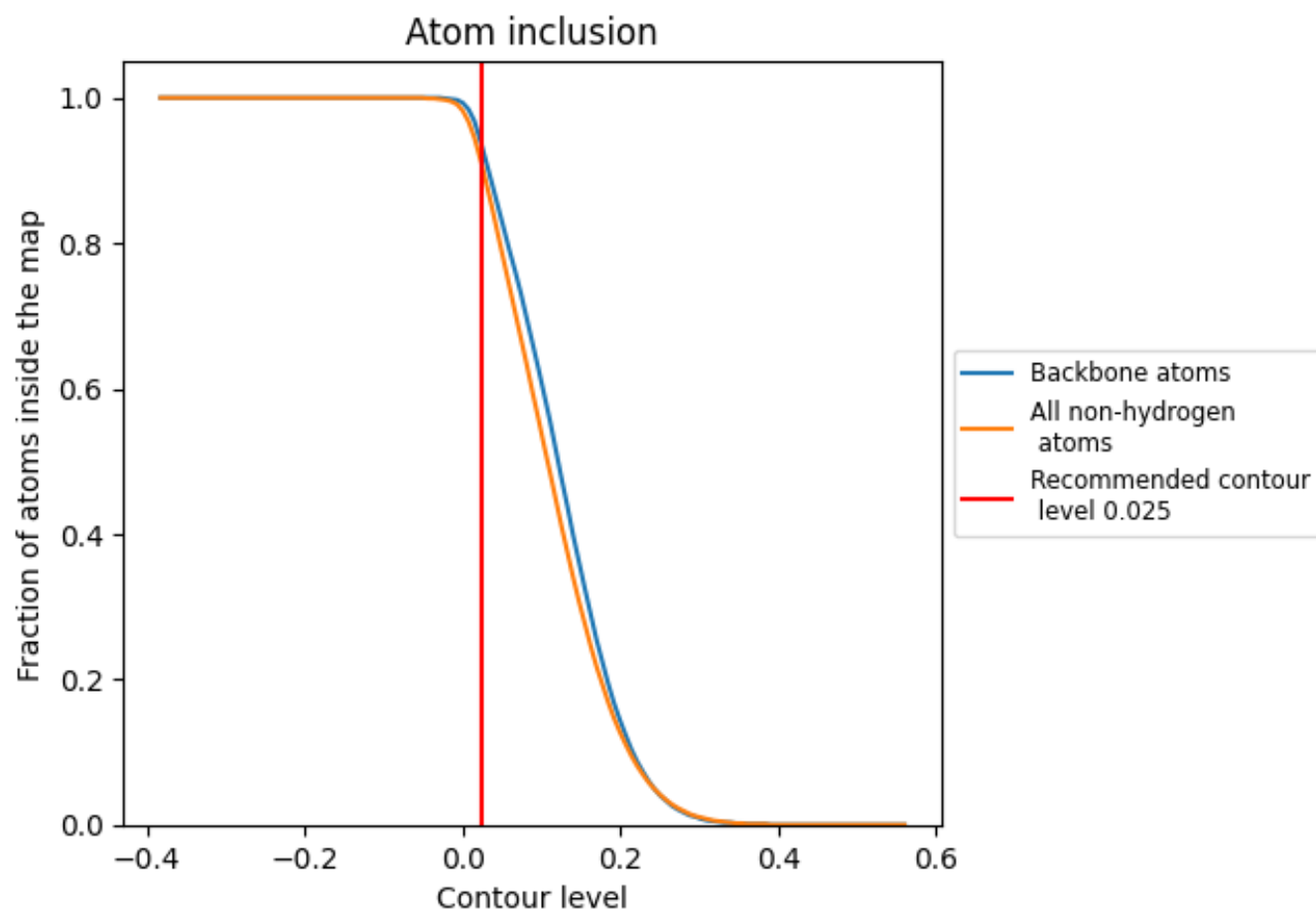
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 91% 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	 0.9070	 0.4220
1	 0.9510	 0.4380
3	 0.9850	 0.4350
4	 0.9810	 0.4760
5	 0.9190	 0.4750
7	 0.9030	 0.4520
A	 0.7480	 0.1760
B	 0.9240	 0.2640
C	 0.8840	 0.4570
D	 0.9310	 0.4890
E	 0.9220	 0.5030
F	 0.9320	 0.4880
G	 0.9150	 0.4590
H	 0.8750	 0.3560
I	 0.8810	 0.4160
J	 0.9060	 0.4460
K	 0.8950	 0.4130
L	 0.5220	 0.0610
M	 0.8660	 0.3550
N	 0.9140	 0.4410
O	 0.9270	 0.4450
P	 0.4630	 0.1180
Q	 0.9390	 0.4920
R	 0.5590	 0.2560
S	 0.9210	 0.4640
T	 0.9250	 0.4730
U	 0.9140	 0.4760
V	 0.9010	 0.4590
W	 0.9080	 0.4110
X	 0.2340	 0.2510
Y	 0.9340	 0.4640
Z	 0.9200	 0.4840
a	 0.9180	 0.4570
b	 0.9010	 0.4480
c	 0.9300	 0.4670



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Chain	Atom inclusion	Q-score
d	 0.8940	 0.4180
e	 0.9040	 0.4300
f	 0.9120	 0.4770
g	 0.9110	 0.4850
h	 0.9270	 0.4970
i	 0.9200	 0.4920
j	 0.9140	 0.4500
k	 0.8750	 0.4260
l	 0.9560	 0.5230
m	 0.8480	 0.4190
n	 0.9420	 0.5110
o	 0.9330	 0.4730
p	 0.9340	 0.5050
r	 0.7010	 0.0920
s	 0.8790	 0.4360
x	 0.9180	 0.4790