



wwPDB EM Validation Summary Report ⓘ

Nov 9, 2024 – 11:25 pm GMT

PDB ID : 6R84
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.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

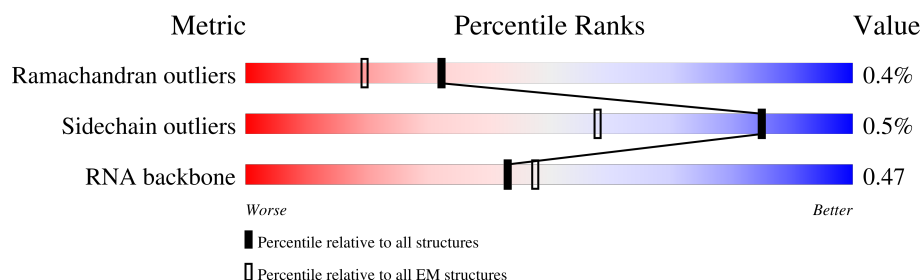
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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.



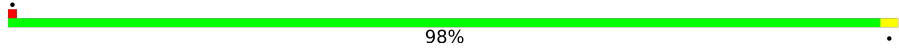
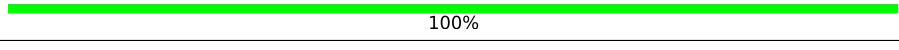
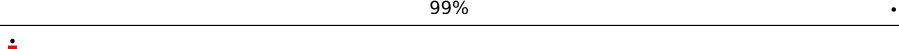
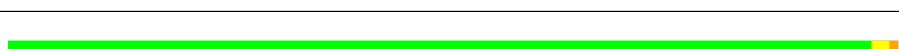

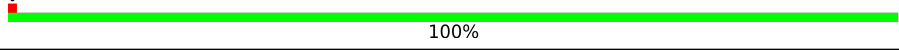
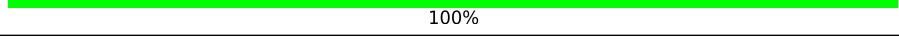
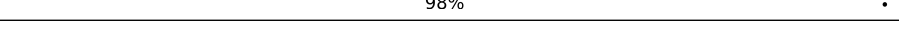

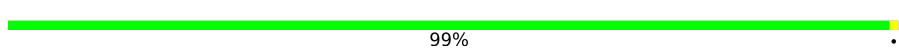
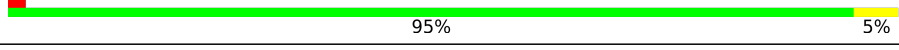
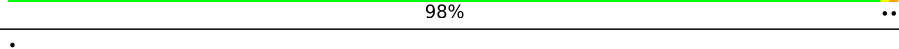
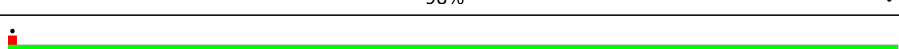
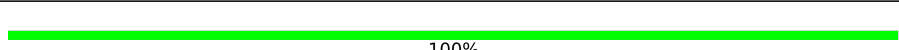
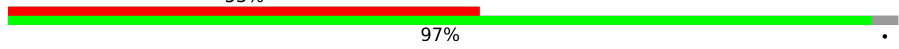

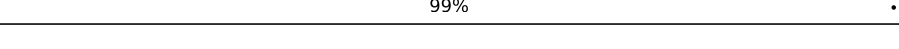


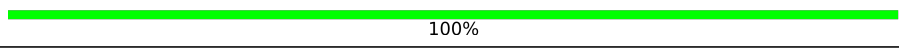
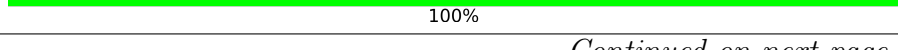



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A	519	
2	R	433	
3	X	224	
4	i	112	
5	J	222	
6	j	119	
7	K	233	
8	k	99	


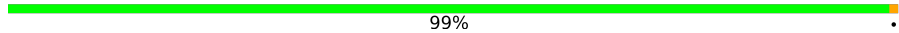
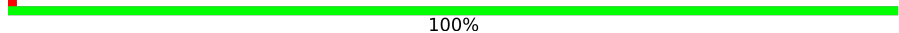
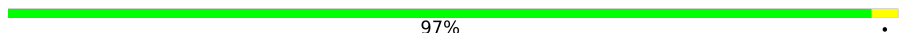
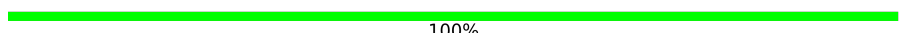
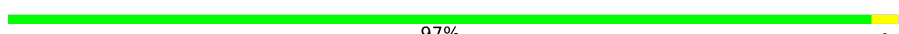
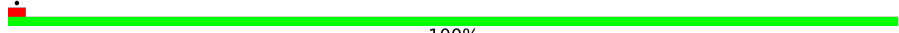







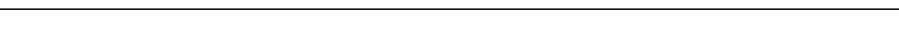
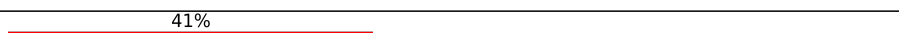
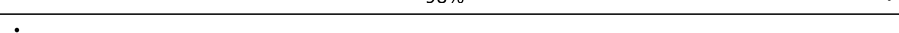
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Mol	Chain	Length	Quality of chain
9	7	191	
10	l	87	
11	M	169	
12	m	77	
13	N	193	
14	n	50	
15	O	136	
16	o	52	
17	p	203	
18	Q	197	
19	5	183	
20	S	185	
21	s	220	
22	T	152	
23	U	172	
24	V	159	
25	W	100	
26	P	155	
27	r	197	
28	x	136	
29	3	121	
30	Y	62	
31	4	158	
32	Z	121	
33	a	126	

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Mol	Chain	Length	Quality of chain
34	B	76	 79%18%
35	b	135	 99%
36	C	105	 100%
37	c	148	 97%
38	D	91	 100%
39	d	58	 97%
40	E	252	 100%
41	e	97	 100%
42	F	386	 99%
43	f	109	 100%
44	G	361	 99%
45	g	127	 100%
46	H	296	 99%
47	h	106	 100%
48	I	175	 88%11%
49	L	204	 41%98%
50	1	3316	 64%31%5%

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
			1441	908	290	241	2	0

- 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
			1770	1121	335	307	7	0

- 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
			1228	763	260	205		0

- 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
			1445	930	267	244	4	0

- 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
			1276	805	246	221	4	0

- 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
			796	516	131	149		0

- 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		

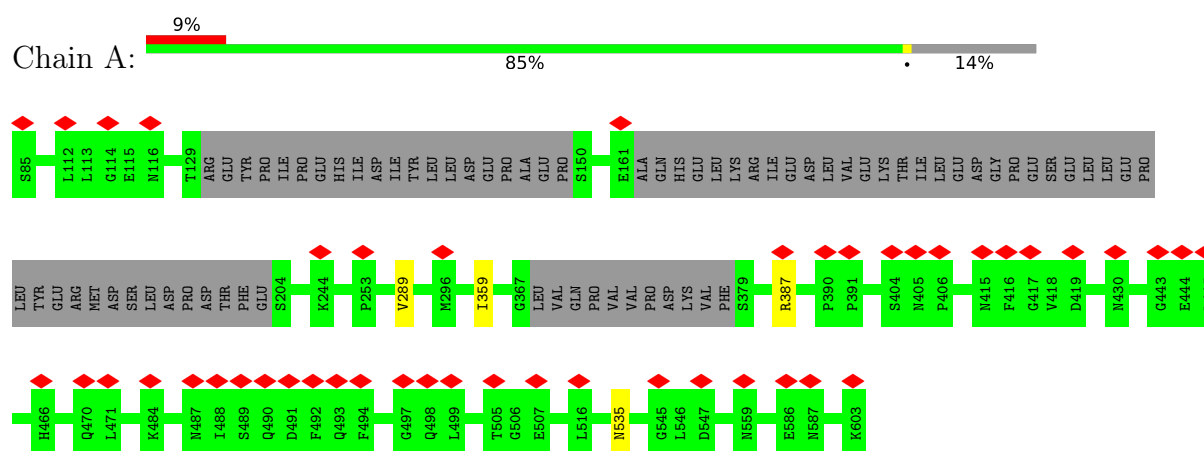
- Molecule 51 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

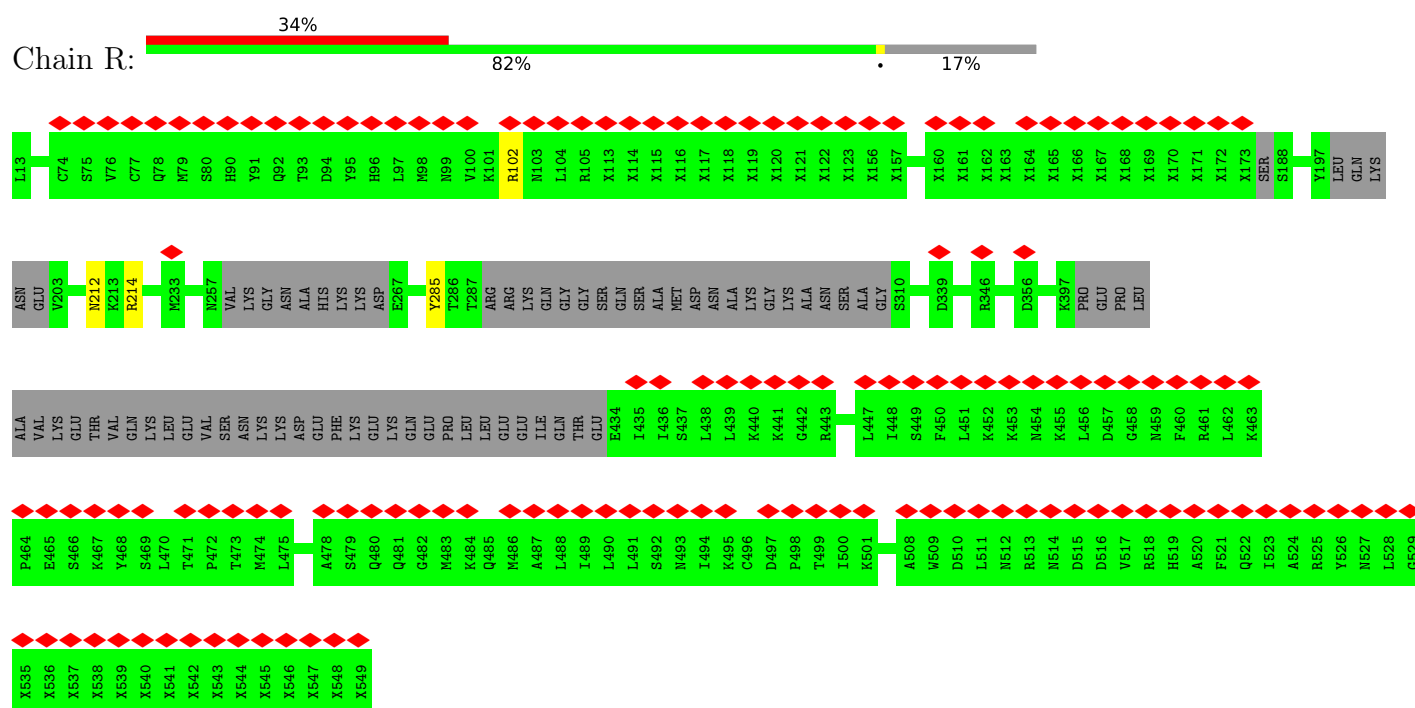
3 Residue-property plots

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.

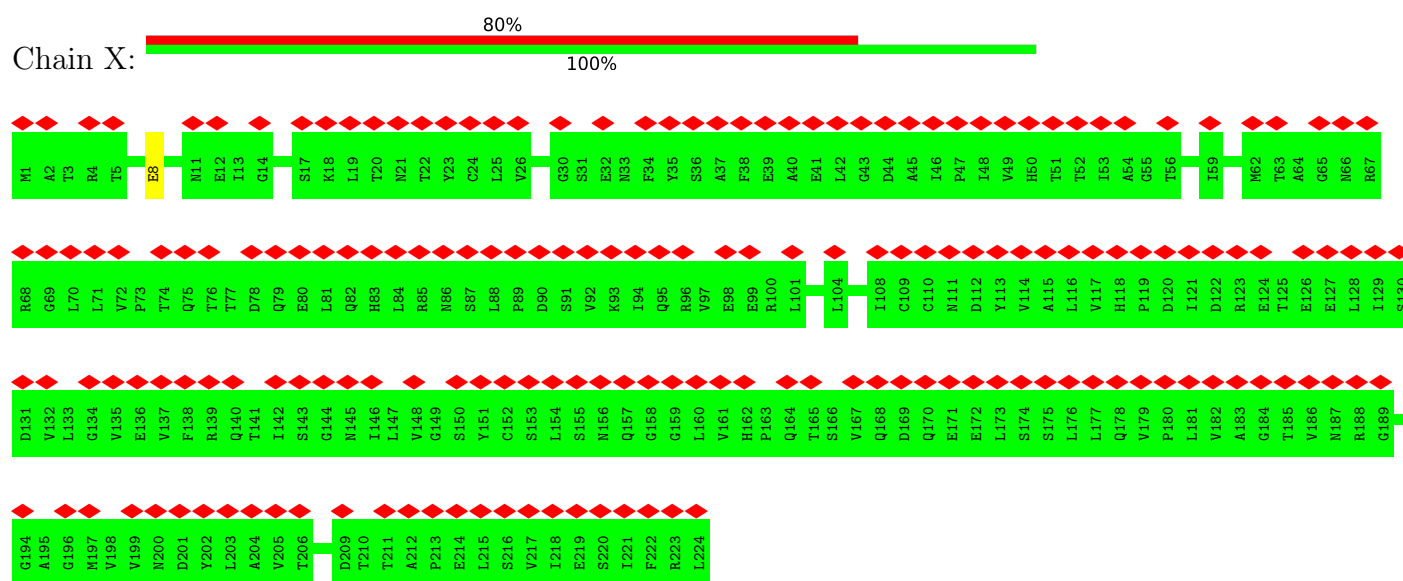
- Molecule 1: ABC transporter ATP-binding protein ARB1



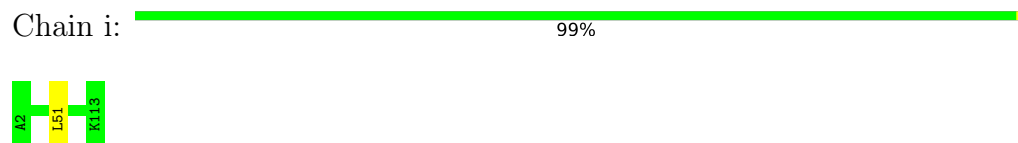
- Molecule 2: Protein VMS1,Vms1,Protein VMS1,Vms1



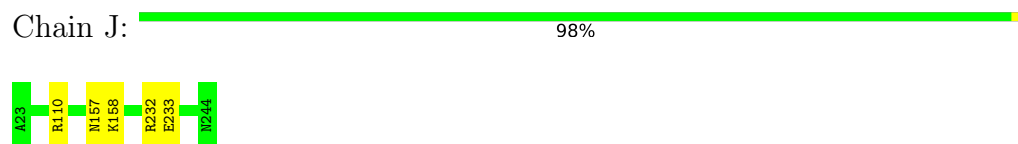
- Molecule 3: Eukaryotic translation initiation factor 6



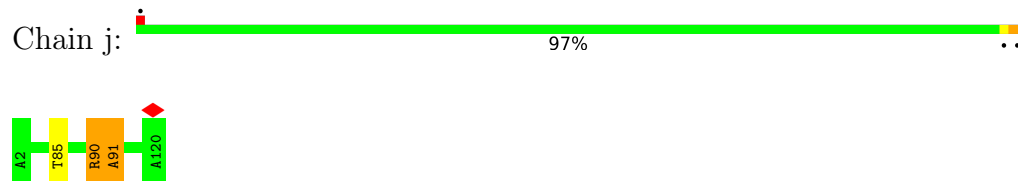
- Molecule 4: 60S ribosomal protein L34-A



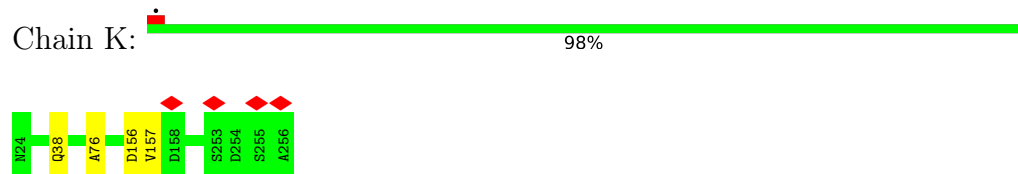
- Molecule 5: 60S ribosomal protein L7-A



- Molecule 6: 60S ribosomal protein L35-A

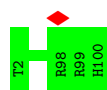


- Molecule 7: 60S ribosomal protein L8-A



- Molecule 8: 60S ribosomal protein L36-A





- Molecule 9: 60S ribosomal protein L9-A

Chain 7: 98%



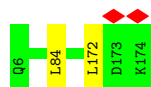
- Molecule 10: 60S ribosomal protein L37-A

Chain l: 100%

There are no outlier residues recorded for this chain.

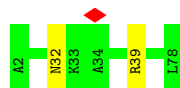
- Molecule 11: 60S ribosomal protein L11-B

Chain M: 99%



- Molecule 12: 60S ribosomal protein L38

Chain m: 97%



- Molecule 13: 60S ribosomal protein L13-A

Chain N: 97%



- Molecule 14: 60S ribosomal protein L39

Chain n: 100%

There are no outlier residues recorded for this chain.

- Molecule 15: 60S ribosomal protein L14-A

Chain O: 100%



- Molecule 16: Ubiquitin-60S ribosomal protein L40

Chain o: 100%

There are no outlier residues recorded for this chain.

- Molecule 17: 60S ribosomal protein L15-A

Chain p: 98%



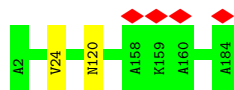
- Molecule 18: 60S ribosomal protein L16-A

Chain Q: 100%

There are no outlier residues recorded for this chain.

- Molecule 19: 60S ribosomal protein L17-A

Chain 5: 99%



- Molecule 20: 60S ribosomal protein L18-A

Chain S: 99%



- Molecule 21: 60S ribosomal protein L10

Chain s: 95% 5%

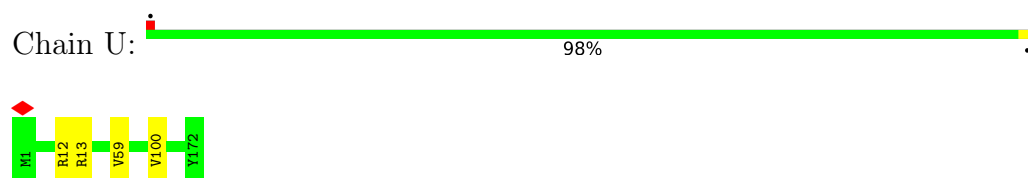


- Molecule 22: 60S ribosomal protein L19-A

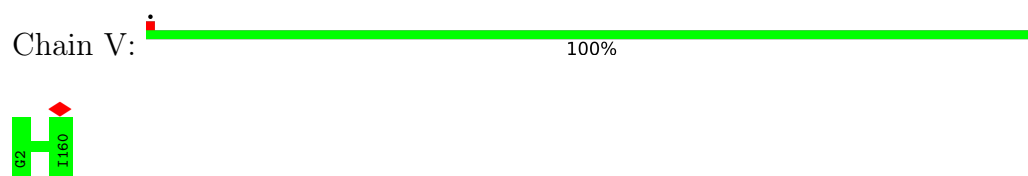
Chain T: 98% ..



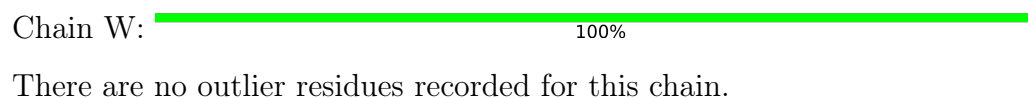
- Molecule 23: 60S ribosomal protein L20-A



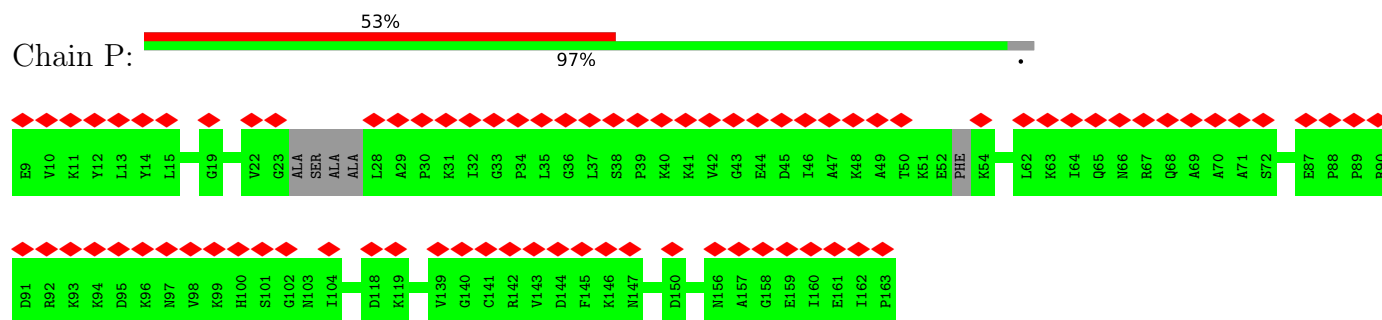
- Molecule 24: 60S ribosomal protein L21-A



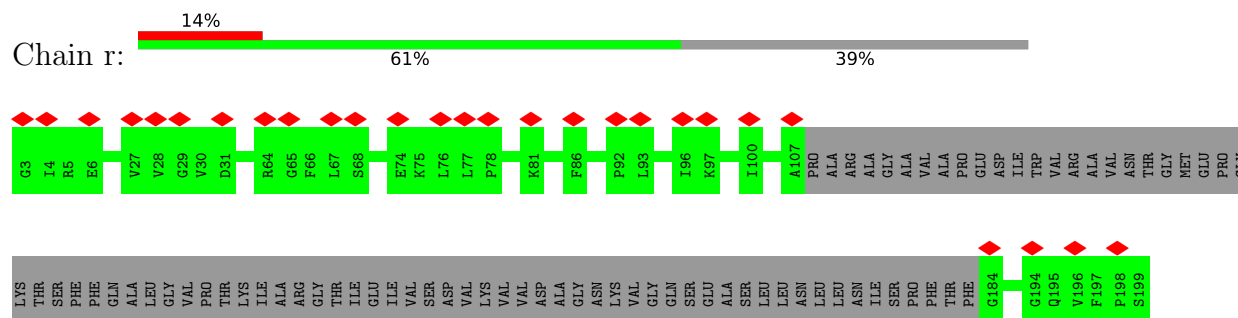
- Molecule 25: 60S ribosomal protein L22-A



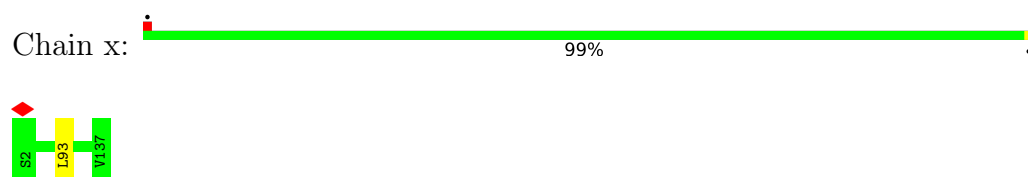
- Molecule 26: 60S ribosomal protein L12-A



- Molecule 27: 60S acidic ribosomal protein P0

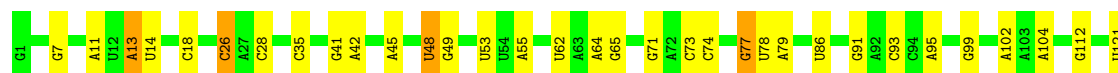


- Molecule 28: 60S ribosomal protein L23-A



- Molecule 29: 5S rRNA

Chain 3:  73% 24%



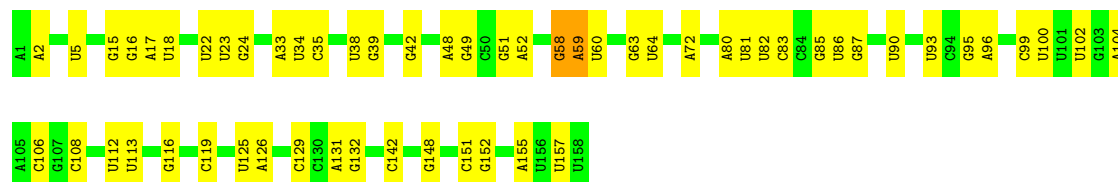
- Molecule 30: 60S ribosomal protein L24-A

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: 5.8S rRNA

Chain 4:  64% 35%



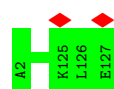
- Molecule 32: 60S ribosomal protein L25

Chain Z:  100%


There are no outlier residues recorded for this chain.

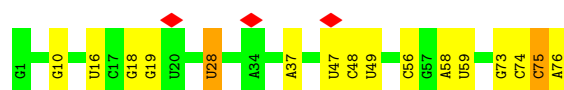
- Molecule 33: 60S ribosomal protein L26-A

Chain a:  100%



- Molecule 34: tRNA-Ala

Chain B:  79% 18%



- Molecule 35: 60S ribosomal protein L27-A

Chain b:  99%



- Molecule 36: 60S ribosomal protein L42-A

Chain C:  100%



- Molecule 37: 60S ribosomal protein L28

Chain c:  97%



- Molecule 38: 60S ribosomal protein L43-A

Chain D:  100%

There are no outlier residues recorded for this chain.

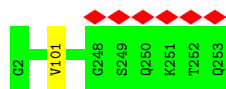
- Molecule 39: 60S ribosomal protein L29

Chain d:  97%



- Molecule 40: 60S ribosomal protein L2-A

Chain E:  100%



- Molecule 41: 60S ribosomal protein L30

Chain e:  100%

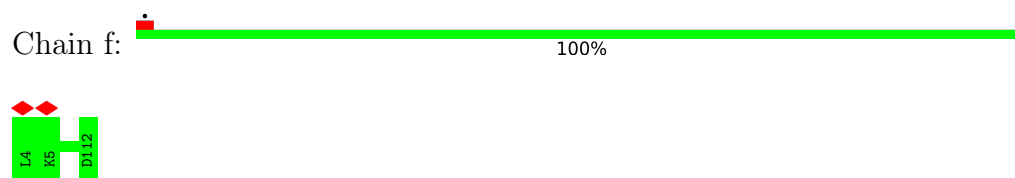


- Molecule 42: 60S ribosomal protein L3

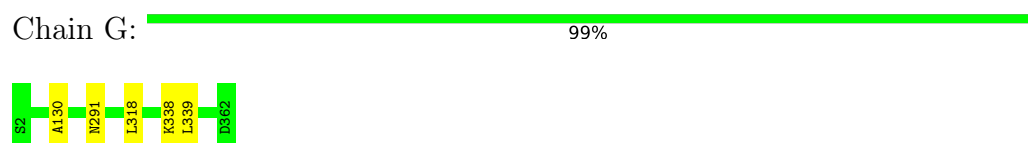
Chain F:  99%



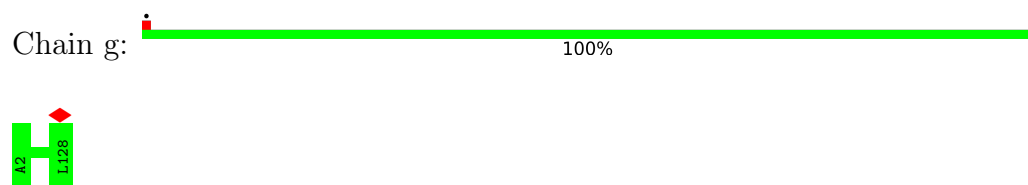
- Molecule 43: 60S ribosomal protein L31-A



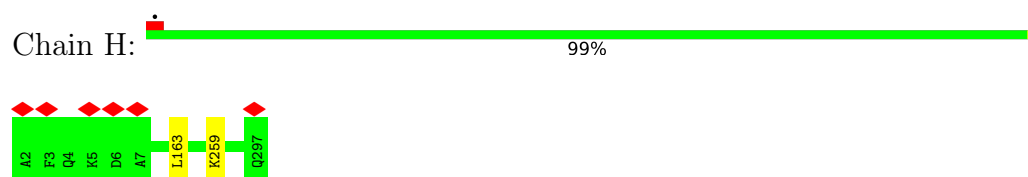
- Molecule 44: 60S ribosomal protein L4-A



- Molecule 45: 60S ribosomal protein L32



- Molecule 46: 60S ribosomal protein L5

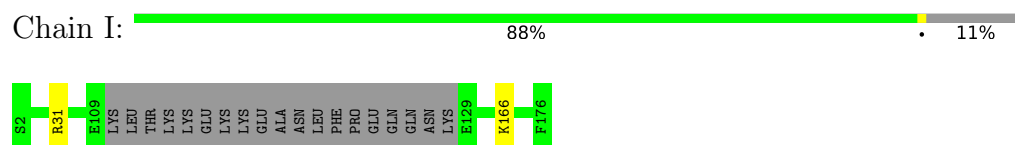


- Molecule 47: 60S ribosomal protein L33-A

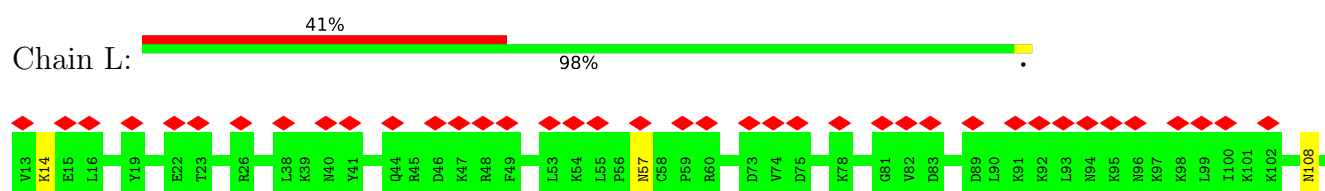


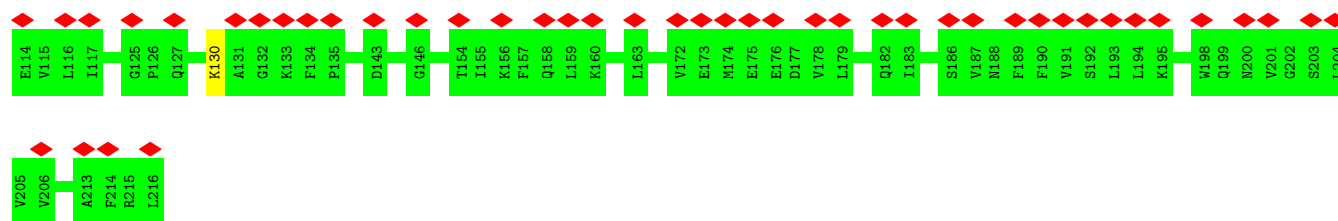
There are no outlier residues recorded for this chain.

- Molecule 48: 60S ribosomal protein L6-A



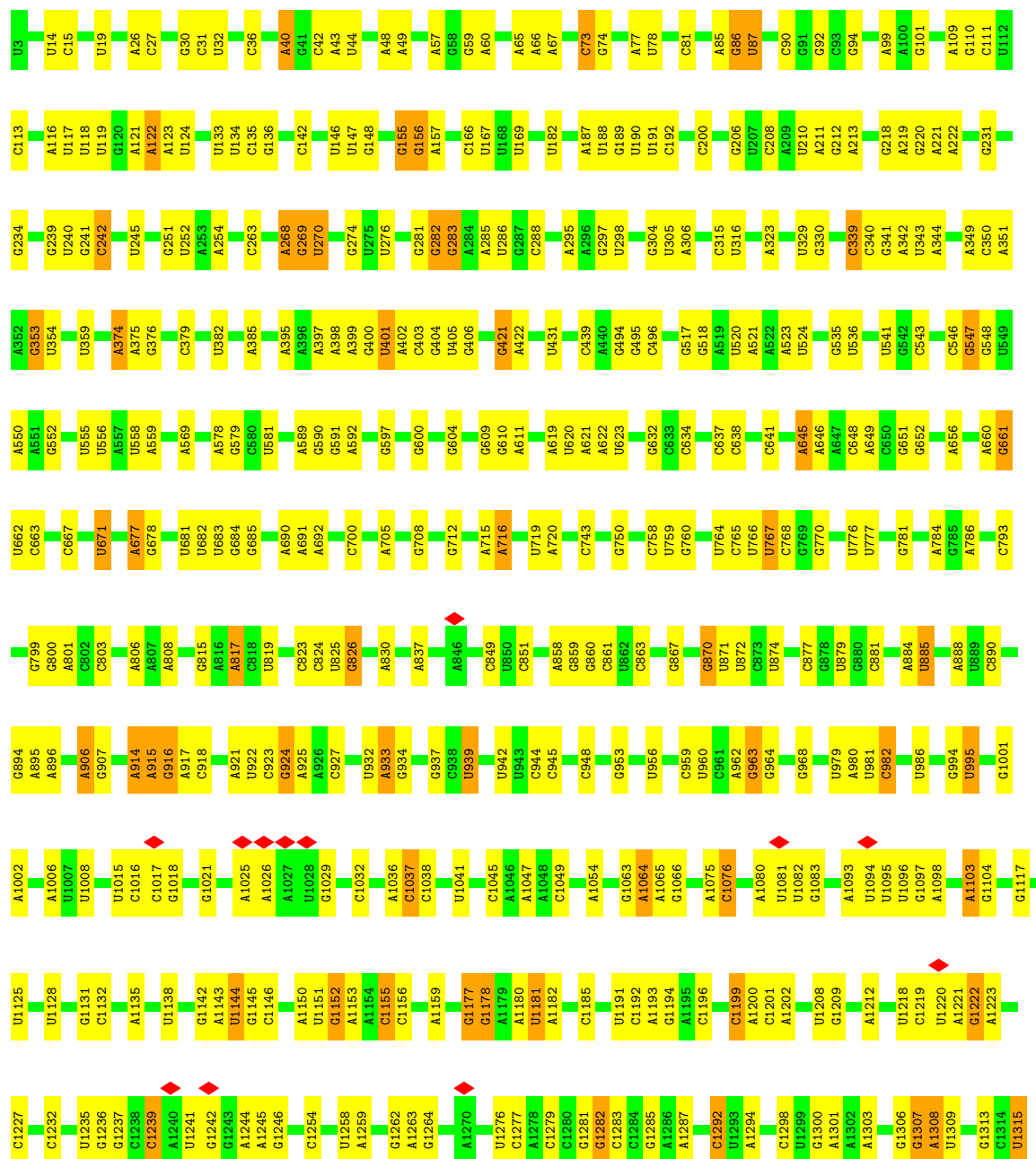
- Molecule 49: 60S ribosomal protein L1-A





• Molecule 50: 25S rRNA

Chain 1: 64% 31% 5%



U2722	G2614	A2500	G2393	A2279	C2163	A2047	C1977	C1870	C1762	A1613	A1535	C1437	C1316
G2726	G2615	U2504	G2394	A2280	G2169	G2048	A1978	U1871	U1763	A1620	G1536	G1443	A1317
U2727	U2617	U2505	A2281	A2282	U2170	A2049	G1979	C1872	U1764	G1623	G1542	G1446	C1320
G2728	G2618	U2506	G2282	G2283	U2176	G2052	C1980	U1876	G1769	U1629	U1549	G1447	U1322
U2729	G2619	C2507	C2284	C2285	G2177	C2053	G1981	G1878	U1630	U1449	C1550	U1448	C1323
G2730	C2622	U2508	G2403	C2286	A2178	C2054	U1986	U1880	C1770	A1451	U1551	U1449	U1324
C2737	C2626	U2510	C2405	G2288	C2179	U2056	U1990	A1881	U1772	A1638	G1552	U1451	U1325
C2742	A2626	A2511	C2406	U2288	U2184	G2057	U1991	A1886	G1774	U1554	U1553	U1329	U1329
U2752	A2628	U2513	U2411	A2299	G2187	G2058	U1992	A1901	G1775	U1555	U1554	A1455	A1330
G2753	U2629	U2514	G2412	A2300	A2188	U2059	G1993	U1888	C1771	U1645	U1555	A1456	U1331
G2754	A2635	A2515	C2415	C2306	G2194	U2081	G1994	U1889	G1780	A1646	C1556	C1459	A1332
C2755	A2636	G2522	G2418	G2307	G2199	U2082	A1995	G1893	C1788	A1657	A1557	C1459	C1333
G2761	A2637	A2523	A2419	A2308	G2205	U2085	C1996	A1892	U1785	A1657	A1558	C1469	C1339
A2762	C2638	C2531	A2419	A2309	G2206	A2086	U1997	A1893	G1796	C1657	G1561	U1477	C1345
U2763	A2642	U2532	A2424	A2313	A2207	A2087	G1998	A1900	G1794	G1685	C1563	A1481	U1348
C2764	G2643	G2533	G2434	G2315	G2218	C2093	U2000	G1902	U1795	C1685	U1564	A1482	G1349
C2772	C2644	U2434	U2434	U2336	G2228	C2094	G2007	G1906	A1797	C1670	G1565	C1478	A1350
C2773	U2652	G2435	G2435	U2339	G2228	C2101	U2001	U1906	A1696	C1670	A1566	A1481	U1351
U2777	U2655	G2440	G2440	C2322	G2210	U2102	G2002	A1909	A1813	A1683	U1568	A1482	A1352
G2778	A2656	A2441	A2441	U2340	G2218	A2107	G2003	A1913	U1814	U1688	U1569	G1483	U1353
U2783	A2657	C2444	C2444	A2341	G2218	G2111	G2005	U1926	U1815	U1570	U1570	U1484	G1354
G2796	C2666	U2542	U2542	U2336	G2228	U2112	G2006	G1927	U1817	U1571	U1571	G1485	A1355
C2797	A2674	C2546	A2447	C2339	G2237	C2114	G2008	A1930	U1818	U1696	G1573	G1487	G1357
C2798	G2675	U2547	G2448	U2340	A2243	G2121	G2009	U1931	U1820	A1714	A1574	G1488	G1365
A2799	A2676	G2548	U2453	A2341	A2244	G2122	U2010	U1932	C1822	A1715	G1575	G1492	G1366
G2800	G2677	G2549	G2454	U2342	A2244	G2122	U2011	A1933	U1716	U1495	U1368	G1493	U1367
A2801	A2678	U2550	A2459	C2343	C2248	C2128	U2012	G1935	U1717	C1496	G1380	U1494	U1368
A2802	U2681	C2552	A2462	C2354	G2249	A2131	C2013	U1938	G1719	C1499	A1386	C1502	G1387
A2803	U2688	U2553	A2468	C2359	G2250	C2132	U2014	G1939	A1841	C1503	A1390	C1391	C1392
A2804	A2689	A2554	G2469	C2362	G2253	U2137	C2015	U1948	U1842	C1507	G1396	C1508	C1397
A2808	G2690	A2561	C2470	A2363	U2254	U2141	U2016	G1951	C1843	C1507	U1397	U1511	U1398
C2810	A2694	U2569	U2471	G2364	A2256	U2137	G2017	G1952	C1846	G1507	C1396	U1512	C1397
G2814	A2703	U2570	U2472	G2365	C2257	A2138	C2018	G1953	A1847	C1508	A1588	A1515	G1417
G2815	G2815	U2571	C2366	C2366	U2258	A2139	U2019	G1954	G1848	A1589	A1589	U1523	A1418
G2816	G2816	C2572	C2366	C2366	U2258	A2140	A2020	U1955	C1849	A1741	G1590	G1525	A1419
A2817	A2817	G2573	C2476	A2372	G2261	U2141	G2021	U1958	G1851	U1742	A1593	G1525	A1419
U2827	C2707	G2585	G2477	A2373	A2262	A2142	G2022	A1959	C1854	A1749	A1594	G1528	C1432
G2828	C2711	A2583	C2478	G2374	C2263	A2143	C2023	A1960	U1855	A1750	U1595	A1529	A1433
U2829	U2712	C2584	G2376	G2375	C2267	A2145	G2024	G1961	C1856	G1751	C1597	G1529	A1434
G2830	U2713	A2595	G2377	G2376	U2268	C2146	G2025	A1962	C1857	A1752	A1603	U1530	A1435
C2836	A2715	G2606	C2378	C2378	U2269	U2153	A2026	G1963	C1857	C1756	A1604	C1531	U1436
U2842	U2716	G2607	G2385	A2271	A2271	A2158	U2032	G1964	C1866	C1756	A1605	G1528	C1432
U2845	G2720	U2612	A2386	G2272	G2272	U2159	G2033	A1971	A1867	A1760	C1608	A1529	A1433
	A2721	U2613	U2388	G2273	U2274	G2160	C2034	A1972	C1868	C1761		C1531	A1435
							G2035	G1973	C1869				
							C2038						
							C2039						
							U2040						
							U2041						
							U2044						
							G2045						
							U2046						



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 (\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 [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/3583	0.51	0/4831
2	R	0.30	0/2631	0.50	0/3532
3	X	0.27	0/1653	0.50	0/2255
4	i	0.58	0/890	0.64	0/1189
5	J	0.48	0/1821	0.59	0/2451
6	j	0.39	0/978	0.63	0/1301
7	K	0.42	0/1836	0.62	0/2481
8	k	0.40	0/778	0.61	0/1034
9	7	0.46	0/1539	0.59	0/2073
10	l	0.58	0/696	0.72	0/923
11	M	0.33	0/1374	0.60	0/1842
12	m	0.38	0/618	0.61	0/826
13	N	0.44	0/1568	0.66	1/2106 (0.0%)
14	n	0.58	0/443	0.73	0/588
15	O	0.44	0/1068	0.60	0/1438
16	o	0.45	0/423	0.61	0/562
17	p	0.61	0/1757	0.72	1/2354 (0.0%)
18	Q	0.55	0/1585	0.62	0/2128
19	5	0.52	0/1443	0.68	0/1944
20	S	0.41	0/1465	0.63	1/1965 (0.1%)
21	s	0.45	0/1807	0.71	2/2425 (0.1%)
22	T	0.47	0/1245	0.66	1/1661 (0.1%)
23	U	0.55	1/1481 (0.1%)	0.65	0/1990
24	V	0.47	0/1300	0.61	0/1743
25	W	0.43	0/812	0.56	0/1099
26	P	0.25	0/734	0.53	0/1015
27	r	0.27	0/982	0.57	0/1320
28	x	0.48	0/1018	0.62	0/1369
29	3	0.75	0/2883	1.17	14/4491 (0.3%)
30	Y	0.46	0/525	0.58	0/696
31	4	0.97	0/3746	1.16	15/5832 (0.3%)
32	Z	0.50	0/979	0.60	0/1321

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	a	0.40	0/1004	0.60	0/1341
34	B	0.43	0/1810	1.06	2/2821 (0.1%)
35	b	0.44	0/1118	0.59	0/1497
36	C	0.43	0/860	0.63	0/1136
37	c	0.46	0/1204	0.68	0/1612
38	D	0.54	0/701	0.66	0/934
39	d	0.37	0/473	0.54	0/629
40	E	0.58	0/1948	0.70	0/2617
41	e	0.42	0/751	0.58	0/1008
42	F	0.58	1/3146 (0.0%)	0.69	1/4228 (0.0%)
43	f	0.54	0/890	0.62	0/1196
44	G	0.47	0/2800	0.66	0/3790
45	g	0.48	0/1041	0.60	0/1394
46	H	0.36	0/2425	0.57	1/3271 (0.0%)
47	h	0.57	0/868	0.60	0/1168
48	I	0.38	0/1260	0.55	0/1694
49	L	0.28	0/1634	0.59	0/2195
50	1	0.95	4/79382 (0.0%)	1.26	679/123763 (0.5%)
All	All	0.78	6/148976 (0.0%)	1.05	718/219079 (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
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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	F	237	LYS	C-N	-8.92	1.13	1.34
50	1	2828	G	N7-C5	-5.89	1.35	1.39
50	1	2951	G	N7-C5	-5.38	1.36	1.39
50	1	2911	A	N9-C4	-5.16	1.34	1.37
50	1	3047	U	N3-C4	-5.11	1.33	1.38

The worst 5 of 718 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	1	2080	C	N1-C2-O2	14.11	127.37	118.90
50	1	2080	C	N3-C2-O2	-13.39	112.52	121.90
50	1	3278	C	N1-C2-O2	13.38	126.93	118.90
50	1	1432	C	C2-N1-C1'	13.14	133.25	118.80
50	1	3278	C	C2-N1-C1'	12.02	132.03	118.80

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

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

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	48
6	j	117/119 (98%)	110 (94%)	4 (3%)	3 (3%)	4	28
7	K	231/233 (99%)	211 (91%)	19 (8%)	1 (0%)	30	63
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	33
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	39
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	31
22	T	150/152 (99%)	142 (95%)	7 (5%)	1 (1%)	19	53
23	U	170/172 (99%)	156 (92%)	13 (8%)	1 (1%)	22	55
24	V	157/159 (99%)	144 (92%)	13 (8%)	0	100	100
25	W	98/100 (98%)	91 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	51
36	C	103/105 (98%)	92 (89%)	11 (11%)	0	100	100
37	c	146/148 (99%)	129 (88%)	14 (10%)	3 (2%)	5	33
38	D	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
39	d	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	7	35
40	E	250/252 (99%)	223 (89%)	27 (11%)	0	100	100
41	e	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
42	F	384/386 (100%)	349 (91%)	34 (9%)	1 (0%)	37	67
43	f	107/109 (98%)	97 (91%)	10 (9%)	0	100	100
44	G	359/361 (99%)	324 (90%)	34 (10%)	1 (0%)	37	67
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%)	32	63

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%)	383 (99%)	3 (1%)	79	88
2	R	288/349 (82%)	284 (99%)	4 (1%)	62	79
3	X	177/192 (92%)	177 (100%)	0	100	100
4	i	95/95 (100%)	94 (99%)	1 (1%)	70	83
5	J	186/186 (100%)	185 (100%)	1 (0%)	86	93
6	j	104/104 (100%)	104 (100%)	0	100	100
7	K	187/191 (98%)	187 (100%)	0	100	100
8	k	81/81 (100%)	81 (100%)	0	100	100
9	7	171/171 (100%)	169 (99%)	2 (1%)	67	82
10	l	70/70 (100%)	70 (100%)	0	100	100
11	M	147/147 (100%)	146 (99%)	1 (1%)	81	90
12	m	68/68 (100%)	67 (98%)	1 (2%)	60	78
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%)	174 (99%)	1 (1%)	84	92
18	Q	160/160 (100%)	160 (100%)	0	100	100
19	5	140/145 (97%)	138 (99%)	2 (1%)	62	79
20	S	150/150 (100%)	150 (100%)	0	100	100
21	s	184/186 (99%)	182 (99%)	2 (1%)	70	83
22	T	126/126 (100%)	124 (98%)	2 (2%)	58	76
23	U	156/156 (100%)	155 (99%)	1 (1%)	84	92
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	x	104/104 (100%)	103 (99%)	1 (1%)	73	85
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%)	109 (100%)	0	100	100
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%)	79	88
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%)	192 (100%)	1 (0%)	86	93
41	e	81/81 (100%)	81 (100%)	0	100	100
42	F	319/322 (99%)	318 (100%)	1 (0%)	91	96
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%)	244 (100%)	0	100	100
47	h	90/90 (100%)	90 (100%)	0	100	100
48	I	134/152 (88%)	132 (98%)	2 (2%)	60	78
49	L	185/185 (100%)	181 (98%)	4 (2%)	47	69
All	All	6278/6523 (96%)	6247 (100%)	31 (0%)	85	93

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	5	24	VAL
49	L	14	LYS
21	s	138	ARG
49	L	108	ASN
42	F	104	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
20	S	73	GLN

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Mol	Chain	Res	Type
35	b	57	HIS
47	h	42	GLN
21	s	208	ASN
23	U	142	GLN

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%)	966 (29%)	155 (4%)
All	All	3664/3671 (99%)	1058 (28%)	160 (4%)

5 of 1058 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 ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

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
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

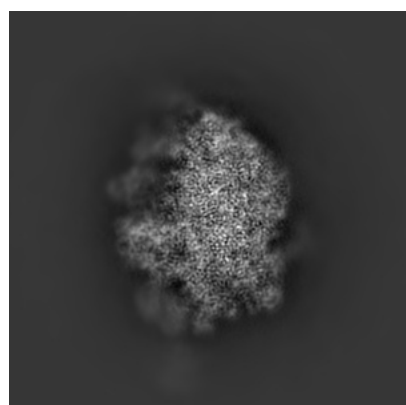
6 Map visualisation [i](#)

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.

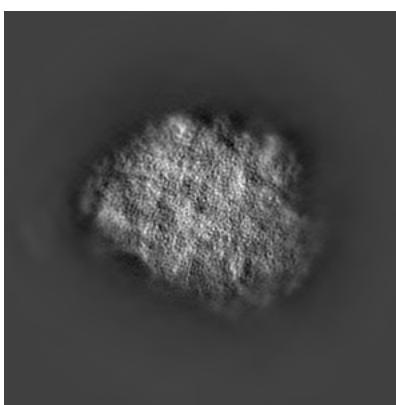
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

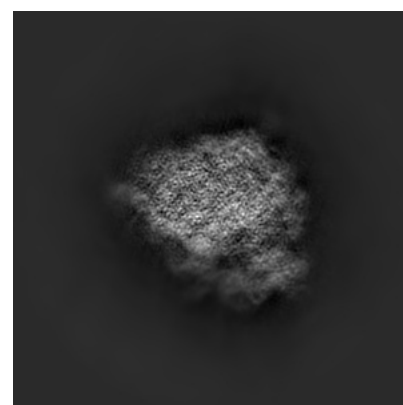
6.1.1 Primary map



X



Y

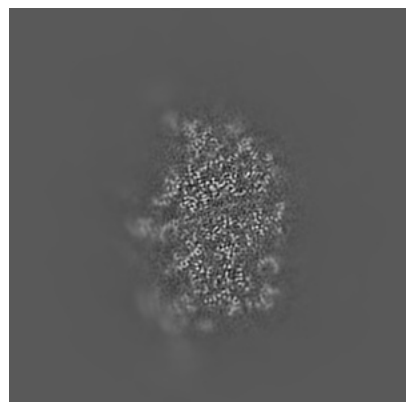


Z

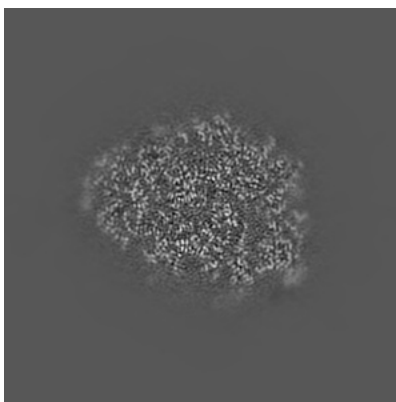
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

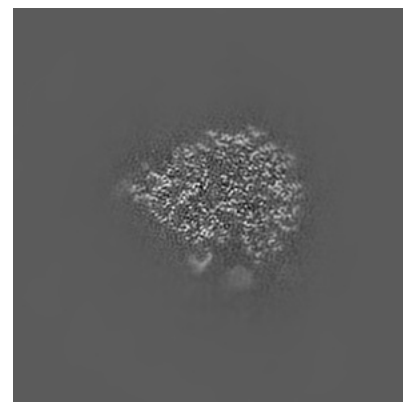
6.2.1 Primary map



X Index: 198



Y Index: 198

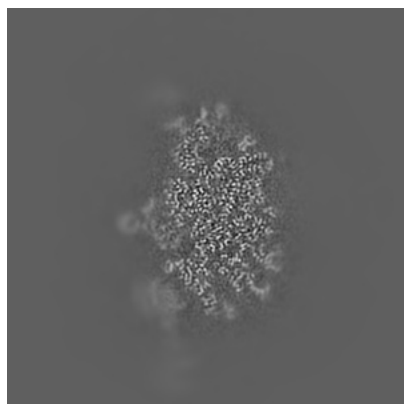


Z Index: 198

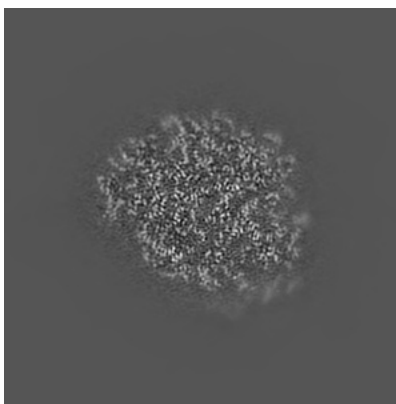
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

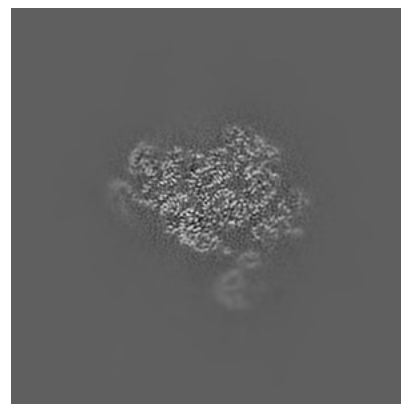
6.3.1 Primary map



X Index: 183



Y Index: 209

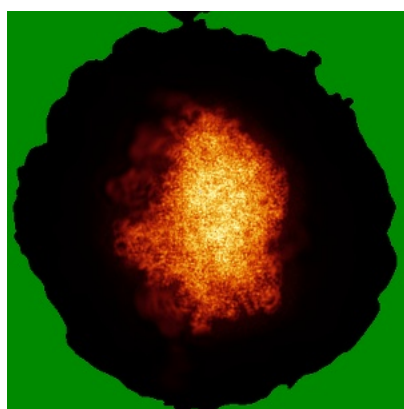


Z Index: 214

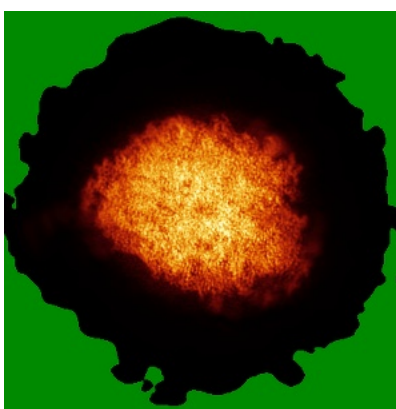
The images above show the largest variance slices of the map in three orthogonal directions.

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

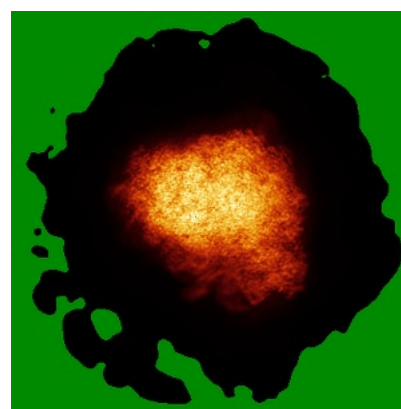
6.4.1 Primary map



X



Y

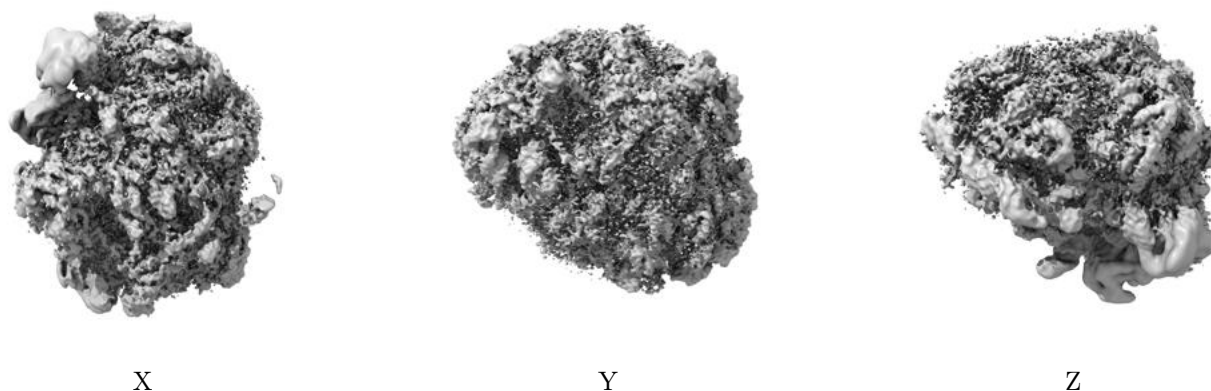


Z

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.

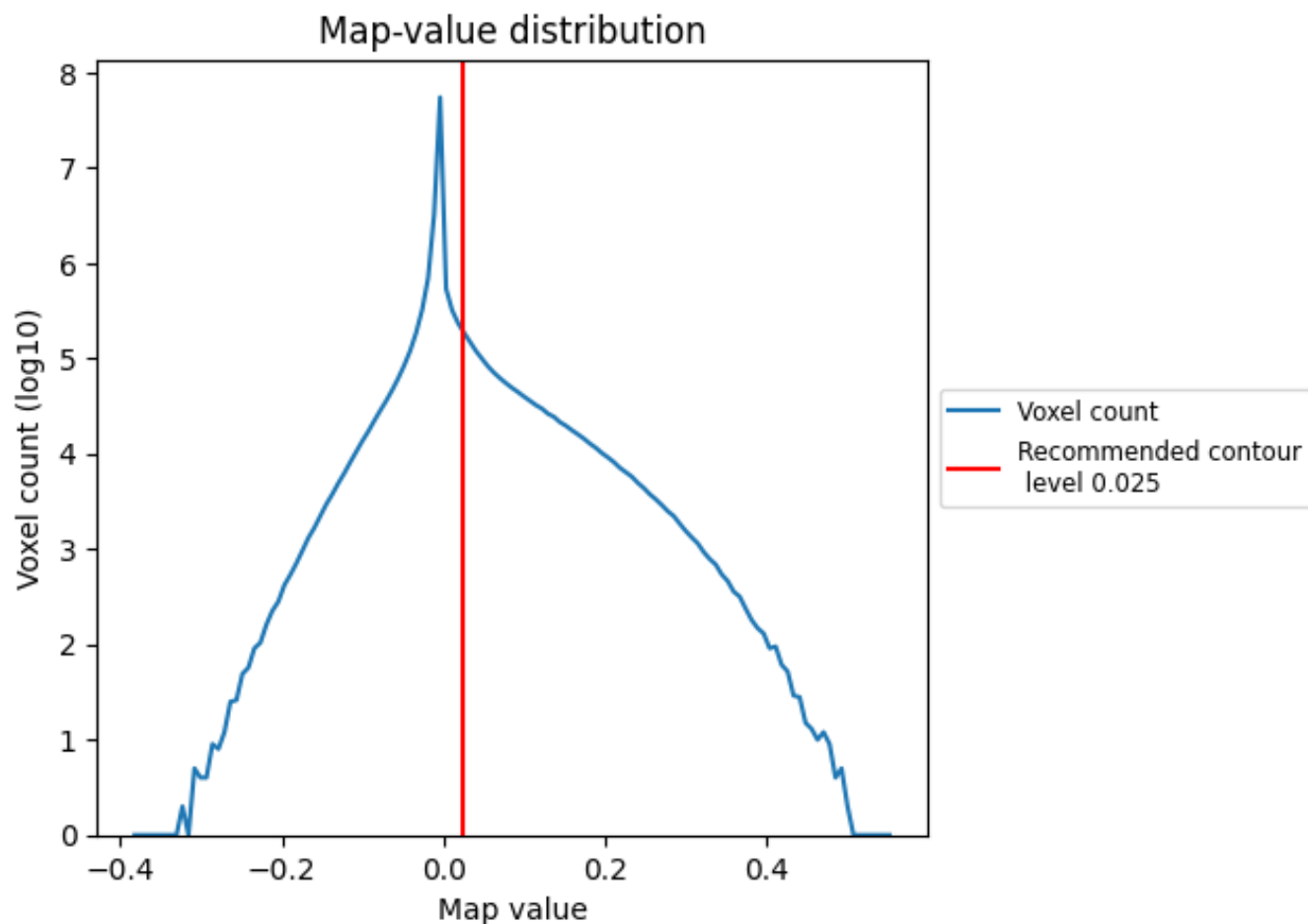
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

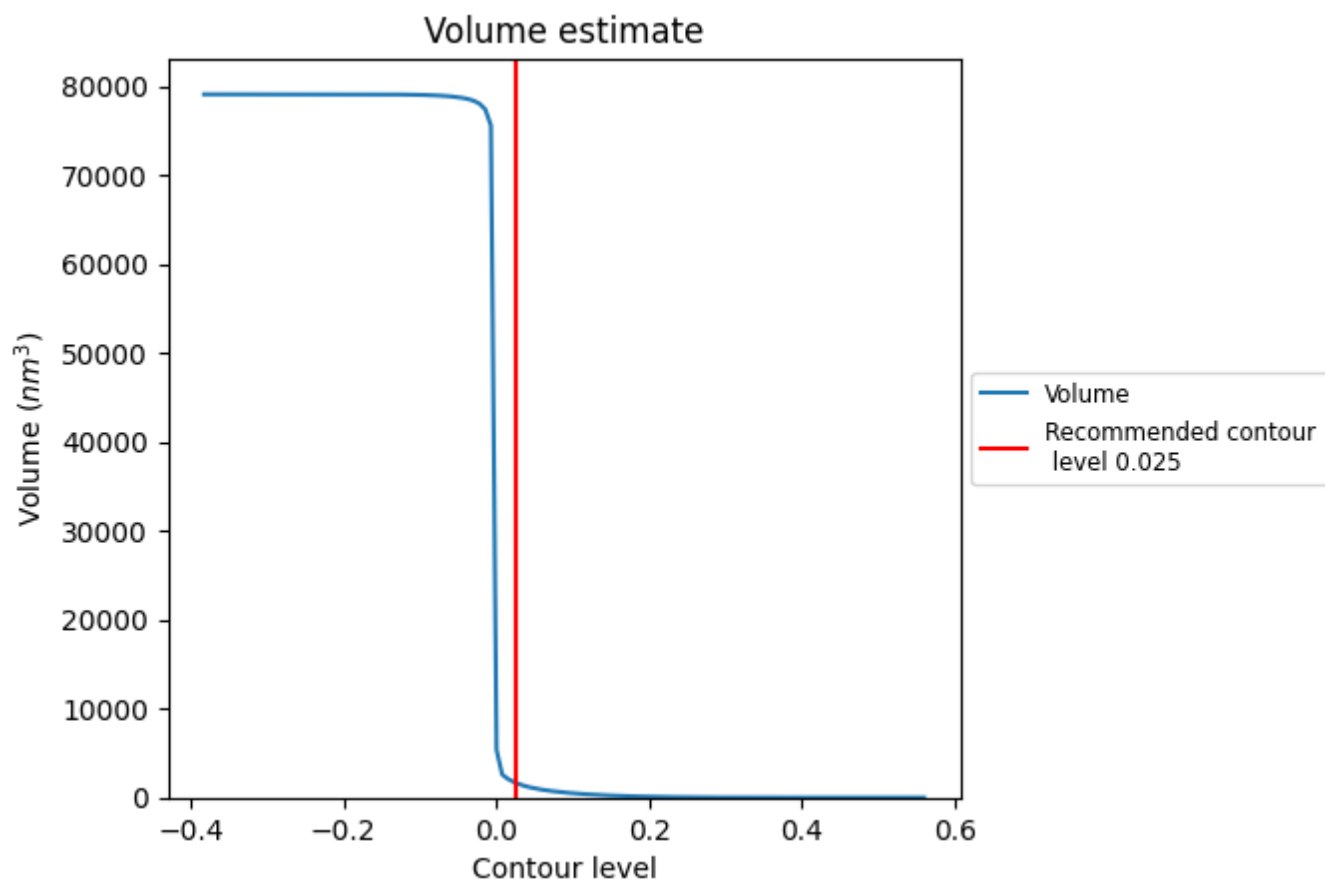
This section contains the results of statistical analysis of the map.

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.

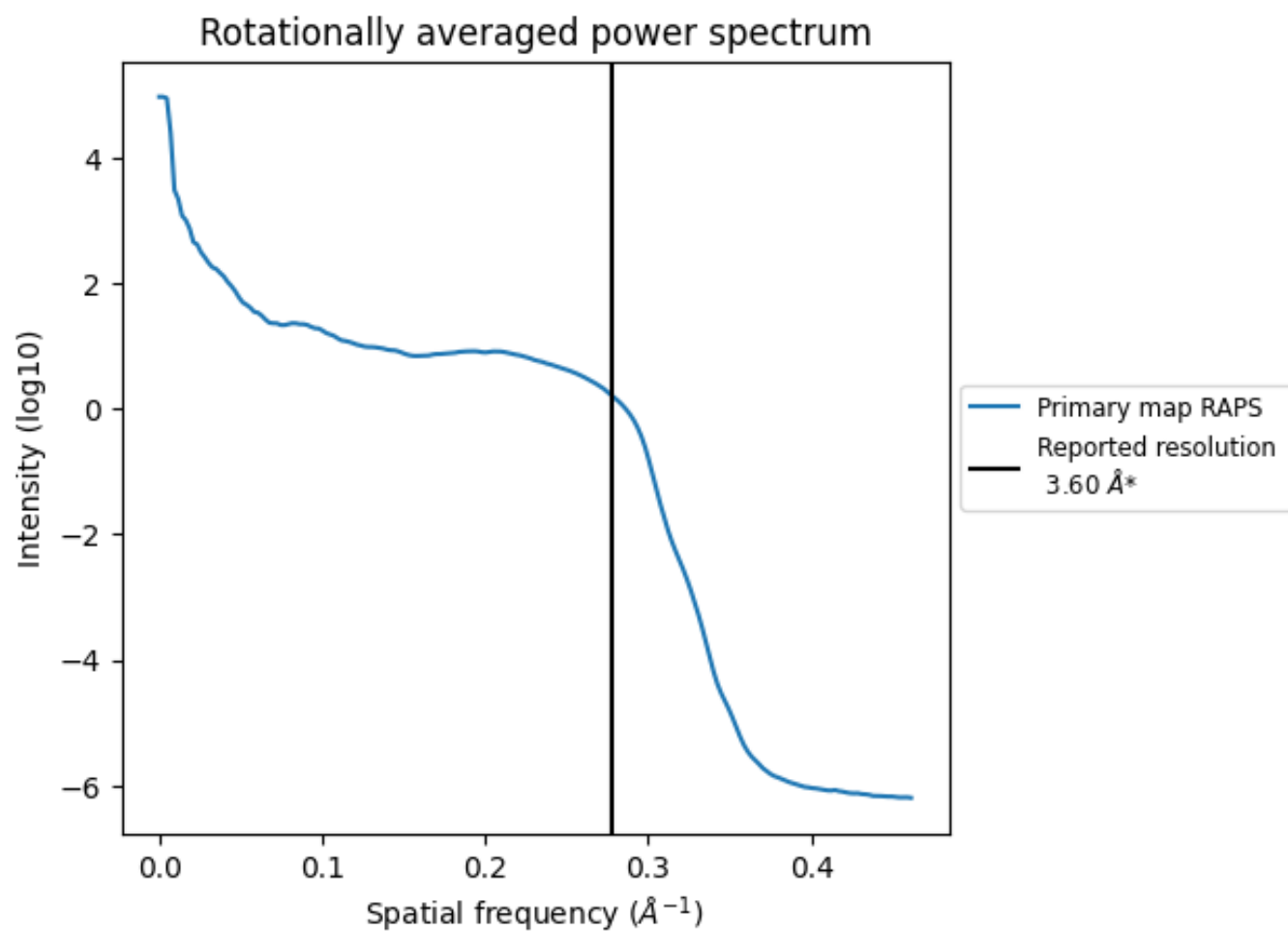
7.2 Volume estimate [i](#)



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

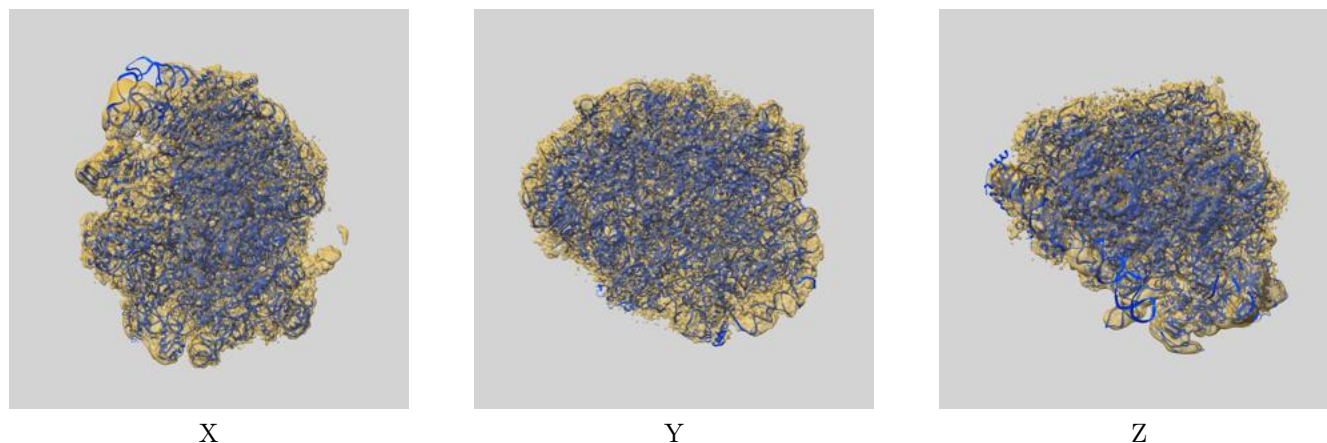
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

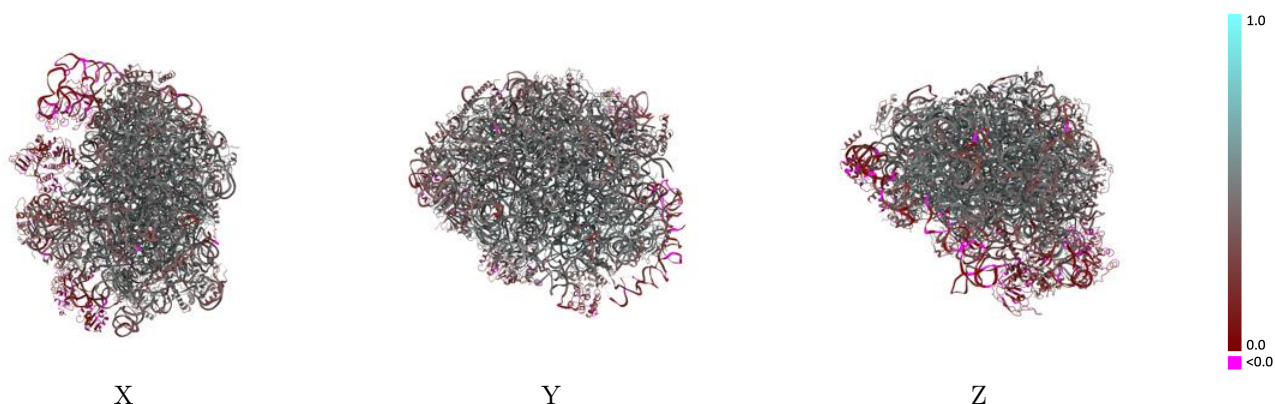
This section contains information regarding the fit between EMDB map EMD-4751 and PDB model 6R84. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



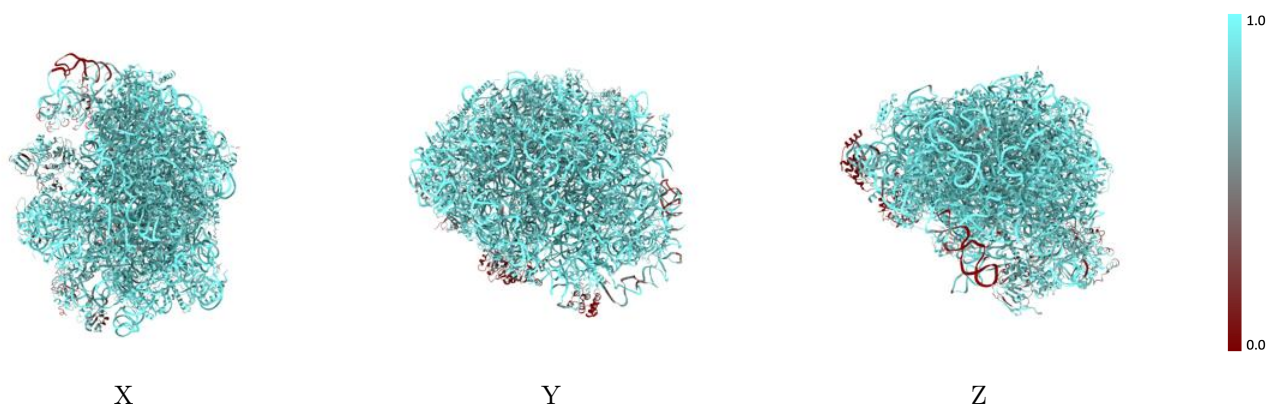
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



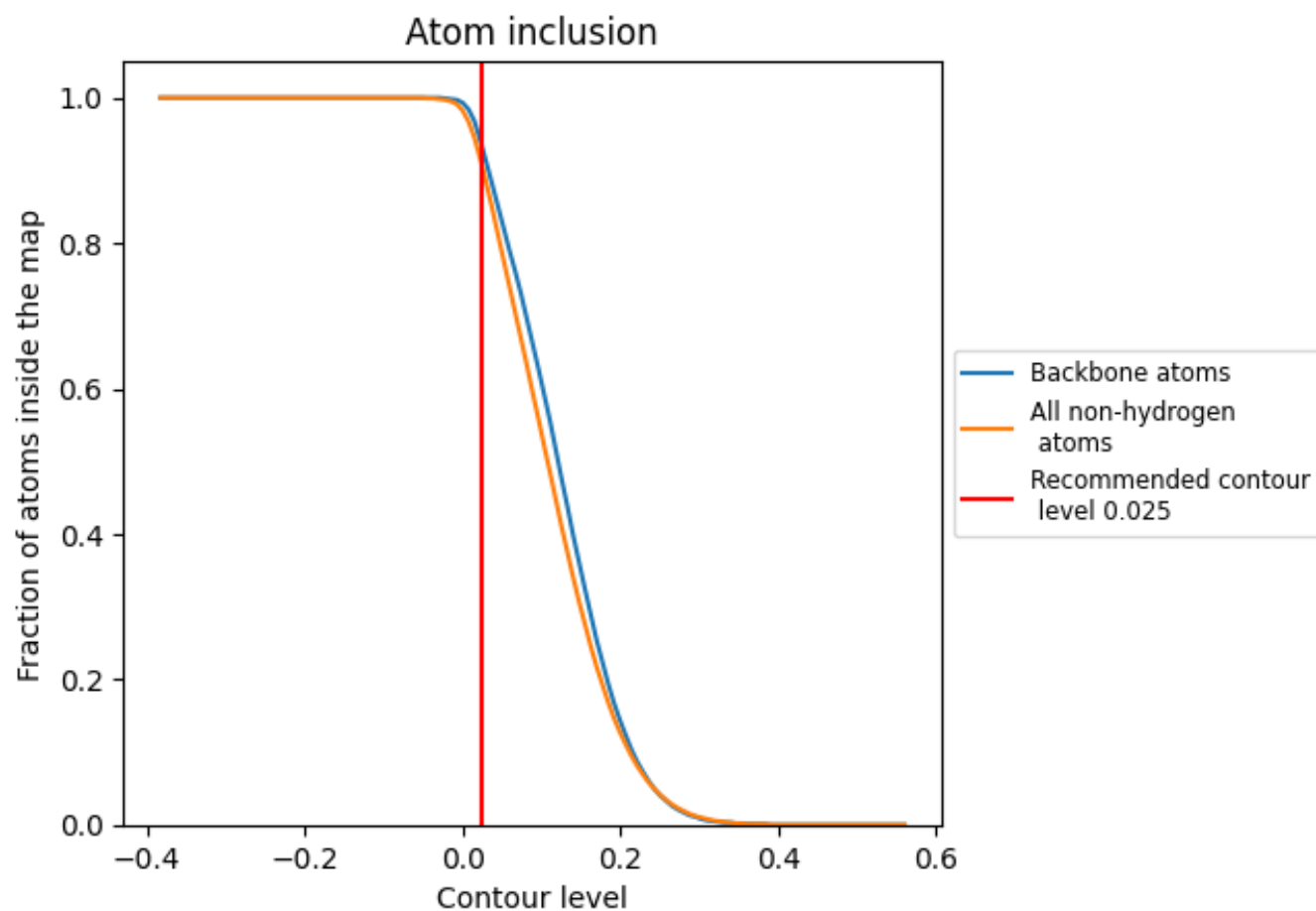
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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