



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 09:31 PM UTC

PDB ID : 7PWO / pdb_00007pwo
EMDB ID : EMD-13683
Title : Cryo-EM structure of Giardia lamblia ribosome at 2.75 Å resolution
Authors : Hiregange, D.G.; Rivalta, A.; Bose, T.; Breiner-Goldstein, E.; Samiya, S.; Cimicata, G.; Kulakova, L.; Zimmerman, E.; Bashan, A.; Herzberg, O.; Yonath, A.
Deposited on : 2021-10-07
Resolution : 2.75 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

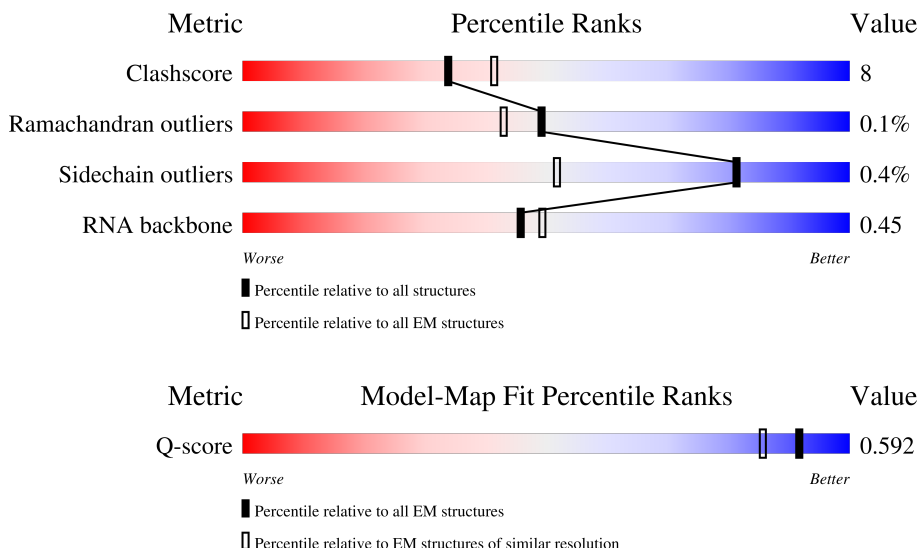
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.75 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	10570 (2.25 - 3.25)

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	T1	139	
2	N1	154	
3	J1	189	

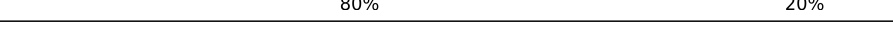
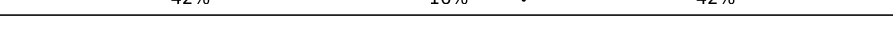
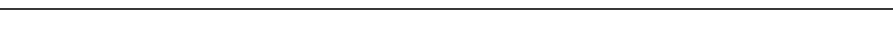
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Mol	Chain	Length	Quality of chain
4	D1	217	
5	X1	143	
6	S1	154	
7	Q1	158	
8	C1	242	
9	B1	248	
10	b1	124	
11	a1	109	
12	V1	89	
13	R1	137	
14	K1	134	
15	I1	174	
16	e1	69	
17	H1	190	
18	n1	41	
19	c1	64	
20	O1	145	
21	W1	130	
22	E1	268	
23	L1	199	
24	U1	126	
25	1	2707	
26	3	120	
27	42	139	
28	A2	251	

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Mol	Chain	Length	Quality of chain
29	B2	379	 81% 19%
30	C2	316	 79% 20% .
31	D2	297	 68% 21% 10%
32	F2	235	 77% 14% 9%
33	G2	225	 59% 22% 19%
34	H2	185	 78% 21% ..
35	I2	210	 80% 15% 5%
36	J2	173	 73% 21% . 5%
37	L2	234	 66% 15% 19%
38	M2	131	 79% 18% .
39	N2	204	 86% 14%
40	O2	197	 79% 20% .
41	P2	164	 73% 21% 6%
42	Q2	179	 80% 20% .
43	R2	196	 64% 24% .. 10%
44	S2	173	 82% 18%
45	T2	159	 81% 14% . .
46	U2	171	 42% 16% . 42%
47	V2	142	 86% 12% .
48	X2	141	 68% 14% 18%
49	Y2	135	 87% 11% .
50	Z2	135	 75% 21% .
51	a2	149	 82% 17% ..
52	b2	62	 81% 10% 10%
53	c2	109	 79% 13% 8%

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Mol	Chain	Length	Quality of chain
54	d2	106	
55	e2	136	
56	f2	123	
57	g2	120	
58	h2	124	
59	i2	90	
60	j2	89	
61	k2	77	
62	l2	51	
63	m2	127	
64	o2	106	
65	p2	94	
66	w2	14	
67	W2	102	
68	E	3	
69	d1	137	
70	F1	190	
71	Y1	132	
72	G1	248	
73	2	1452	
74	A1	245	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
75	K	1	2894	-	-	X	-

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 163704 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 Ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T1	108	Total	C	N	O	S	0	0
			795	503	148	142	2		

- Molecule 2 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N1	152	Total	C	N	O	S	0	0
			1192	759	227	201	5		

- Molecule 3 is a protein called Ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J1	166	Total	C	N	O	S	0	0
			1322	827	257	232	6		

- Molecule 4 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D1	182	Total	C	N	O	S	0	0
			1402	890	254	244	14		

- Molecule 5 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X1	142	Total	C	N	O	S	0	0
			1104	697	219	184	4		

- Molecule 6 is a protein called Ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	S1	133	Total	C	N	O	S	0	0
			1055	651	210	188	6		

- Molecule 7 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Q1	125	Total	C	N	O	S	0	0
			960	603	190	164	3		

- Molecule 8 is a protein called Ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C1	212	Total	C	N	O	S	0	0
			1641	1043	298	296	4		

- Molecule 9 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B1	218	Total	C	N	O	S	0	0
			1758	1113	323	309	13		

- Molecule 10 is a protein called Ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	b1	79	Total	C	N	O	S	0	0
			614	389	105	114	6		

- Molecule 11 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a1	97	Total	C	N	O	S	0	0
			785	484	162	131	8		

- Molecule 12 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	V1	82	Total	C	N	O	S	0	0
			605	377	112	110	6		

- Molecule 13 is a protein called Ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R1	99	Total	C	N	O	S	0	0
			767	476	141	147	3		

- Molecule 14 is a protein called Ribosomal protein S10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K1	83	Total	C	N	O	S	0	0
			689	446	116	123	4		

- Molecule 15 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I1	163	Total	C	N	O	S	0	0
			1282	804	246	229	3		

- Molecule 16 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	e1	37	Total	C	N	O	S	0	0
			291	185	59	46	1		

- Molecule 17 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H1	162	Total	C	N	O	S	0	0
			1195	773	210	207	5		

- Molecule 18 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n1	24	Total	C	N	O	S	0	0
			217	134	55	25	3		

- Molecule 19 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	c1	55	Total	C	N	O	S	0	0
			439	269	89	80	1		

- Molecule 20 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O1	126	Total	C	N	O	S	0	0
			935	572	189	170	4		

- Molecule 21 is a protein called Ribosomal protein S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W1	129	Total	C	N	O	S	0	0
			1031	659	192	177	3		

- Molecule 22 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E1	258	Total	C	N	O	S	0	0
			2062	1320	378	352	12		

- Molecule 23 is a protein called SSU ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	L1	181	Total	C	N	O	S	0	0
			1487	936	296	248	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L1	12	SER	GLY	conflict	UNP V6TVJ7

- Molecule 24 is a protein called Ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U1	74	Total	C	N	O	S	0	0
			609	394	111	102	2		

- Molecule 25 is a RNA chain called rRNA 28S.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	1	2448	Total	C	N	O	P	0	0
			52571	23373	9743	17007	2448		

- Molecule 26 is a RNA chain called rRNA 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3	117	Total	C	N	O	P	0	0
			2501	1116	458	810	117		

- Molecule 27 is a RNA chain called rRNA 5.8S.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	42	138	Total	C	N	O	P	0	0
			2958	1315	553	952	138		

- Molecule 28 is a protein called Ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A2	250	Total	C	N	O	S	0	0
			1873	1157	383	320	13		

- Molecule 29 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B2	378	Total	C	N	O	S	0	0
			2987	1886	566	514	21		

- Molecule 30 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	C2	314	Total	C	N	O	S	0	0
			2446	1539	474	424	9		

- Molecule 31 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	D2	266	Total	C	N	O	S	0	0
			2115	1341	391	375	8		

- Molecule 32 is a protein called Ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	F2	214	Total	C	N	O	S	0	0
			1730	1100	315	310	5		

- Molecule 33 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	G2	182	Total	C	N	O	S	0	0
			1446	921	264	255	6		

- Molecule 34 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	H2	184	Total	C	N	O	S	0	0
			1442	912	263	257	10		

- Molecule 35 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	I2	200	Total	C	N	O	S	0	0
			1621	1019	321	273	8		

- Molecule 36 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	J2	164	Total	C	N	O	S	0	0
			1305	821	246	233	5		

- Molecule 37 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L2	189	Total	C	N	O	S	0	0
			1512	942	309	255	6		

- Molecule 38 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M2	128	Total	C	N	O	S	0	0
			990	626	178	181	5		

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N2	204	Total	C	N	O	S	0	0
			1712	1083	358	265	6		

- Molecule 40 is a protein called Ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O2	195	Total	C	N	O	S	0	0
			1587	997	310	267	13		

- Molecule 41 is a protein called Ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P2	154	Total	C	N	O	S	0	0
			1235	781	239	211	4		

- Molecule 42 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q2	178	Total	C	N	O	S	0	0
			1402	871	279	243	9		

- Molecule 43 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R2	177	Total	C	N	O	S	0	0
			1463	902	313	243	5		

- Molecule 44 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S2	173	Total	C	N	O	S	0	0
			1418	895	274	240	9		

- Molecule 45 is a protein called Ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T2	153	Total	C	N	O	S	0	0
			1226	766	252	201	7		

- Molecule 46 is a protein called Ribosomal protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U2	100	Total	C	N	O	S	0	0
			820	524	141	153	2		

- Molecule 47 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V2	139	Total	C	N	O	S	0	0
			1063	668	207	183	5		

- Molecule 48 is a protein called Ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	X2	116	Total	C	N	O	S	0	0
			936	601	169	163	3		

- Molecule 49 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Y2	133	Total	C	N	O	S	0	0
			1076	665	219	184	8		

- Molecule 50 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Z2	129	Total	C	N	O	S	0	0
			980	623	179	173	5		

- Molecule 51 is a protein called Ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a2	148	Total	C	N	O	S	0	0
			1201	759	240	199	3		

- Molecule 52 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	b2	56	Total	C	N	O	S	0	0
			463	280	104	77	2		

- Molecule 53 is a protein called Ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	c2	100	Total	C	N	O	S	0	0
			750	470	132	144	4		

- Molecule 54 is a protein called Ribosomal protein L31B.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	d2	94	Total	C	N	O		0	0
			752	482	149	121			

- Molecule 55 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	e2	126	Total	C	N	O	S	0	0
			1039	661	207	165	6		

- Molecule 56 is a protein called Ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	f2	123	Total	C	N	O	S	0	0
			974	619	180	171	4		

- Molecule 57 is a protein called Ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	g2	99	Total	C	N	O	S	0	0
			798	493	167	134	4		

- Molecule 58 is a protein called Ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	h2	120	Total	C	N	O	S	0	0
			960	610	185	160	5		

- Molecule 59 is a protein called Ribosomal protein L36-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	i2	85	Total	C	N	O	S	0	0
			691	438	138	111	4		

- Molecule 60 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	j2	87	Total	C	N	O	S	0	0
			692	423	146	116	7		

- Molecule 61 is a protein called Ribosomal L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	k2	66	Total	C	N	O	S	0	0
			504	320	86	94	4		

- Molecule 62 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	l2	50	Total	C	N	O	0	0
			434	278	91	65		

- Molecule 63 is a protein called Ubiquitin/Ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	m2	51	Total	C	N	O	S	0	0
			421	257	88	69	7		

- Molecule 64 is a protein called Ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	o2	94	Total	C	N	O	S	0	0
			762	474	157	126	5		

- Molecule 65 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	p2	91	Total	C	N	O	S	0	0
			708	436	144	122	6		

- Molecule 66 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	w2	14	Total	C	N	O	P	0	0
			299	133	56	96	14		

- Molecule 67 is a protein called Ribosomal protein L24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	W2	65	Total	C	N	O	S	0	0
			540	343	110	85	2		

- Molecule 68 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	E	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 69 is a protein called Ribosomal protein S29A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	d1	48	Total	C	N	O	S	0	0
			392	250	72	65	5		

- Molecule 70 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	F1	161	Total	C	N	O	S	0	0
			1246	771	240	227	8		

- Molecule 71 is a protein called Ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Y1	91	Total	C	N	O	S	0	0
			713	454	126	127	6		

- Molecule 72 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	G1	189	Total	C	N	O	S	0	0
			1453	914	280	249	10		

- Molecule 73 is a RNA chain called rRNA 18S.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	2	1355	Total	C	N	O	P	0	0
			29096	12946	5388	9407	1355		

- Molecule 74 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	A1	194	Total	C	N	O	S	0	0
			1546	998	269	271	8		

- Molecule 75 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
75	N1	3	Total	K	0
			3	3	
75	X1	1	Total	K	0
			1	1	
75	S1	2	Total	K	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
75	b1	2	Total 2	K 2	0
75	a1	1	Total 1	K 1	0
75	I1	2	Total 2	K 2	0
75	O1	5	Total 5	K 5	0
75	W1	1	Total 1	K 1	0
75	E1	4	Total 4	K 4	0
75	L1	4	Total 4	K 4	0
75	U1	1	Total 1	K 1	0
75	1	181	Total 181	K 181	0
75	3	1	Total 1	K 1	0
75	42	2	Total 2	K 2	0
75	A2	4	Total 4	K 4	0
75	B2	3	Total 3	K 3	0
75	C2	4	Total 4	K 4	0
75	I2	1	Total 1	K 1	0
75	L2	1	Total 1	K 1	0
75	N2	2	Total 2	K 2	0
75	V2	1	Total 1	K 1	0
75	a2	2	Total 2	K 2	0
75	e2	1	Total 1	K 1	0
75	j2	1	Total 1	K 1	0

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Mol	Chain	Residues	Atoms		AltConf
75	o2	1	Total 1	K 1	0
75	G1	1	Total 1	K 1	0
75	2	222	Total 222	K 222	0
75	A1	1	Total 1	K 1	0

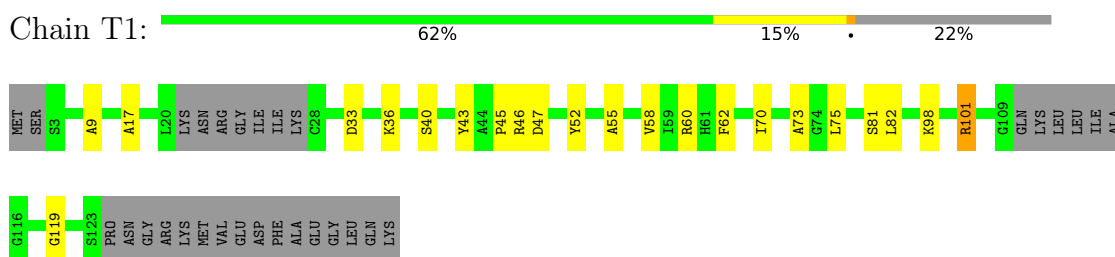
- Molecule 76 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
76	N1	1	Total 1	Mg 1	0
76	E1	1	Total 1	Mg 1	0
76	L1	1	Total 1	Mg 1	0
76	1	71	Total 71	Mg 71	0
76	42	1	Total 1	Mg 1	0
76	C2	1	Total 1	Mg 1	0
76	F2	1	Total 1	Mg 1	0
76	P2	1	Total 1	Mg 1	0
76	V2	1	Total 1	Mg 1	0
76	b2	1	Total 1	Mg 1	0
76	o2	1	Total 1	Mg 1	0
76	G1	1	Total 1	Mg 1	0
76	2	19	Total 19	Mg 19	0

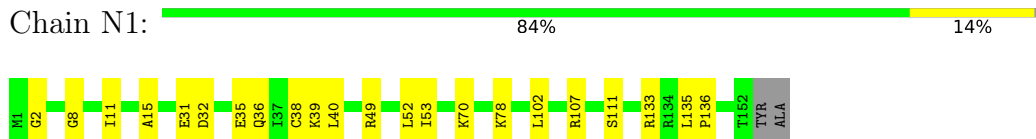
3 Residue-property plots [i](#)

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

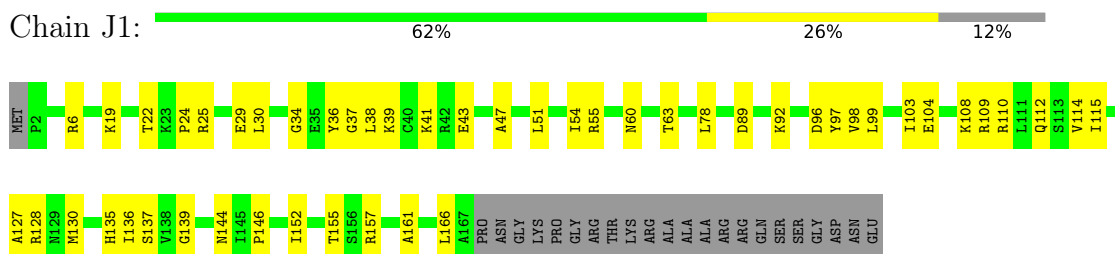
• Molecule 1: Ribosomal protein S19e



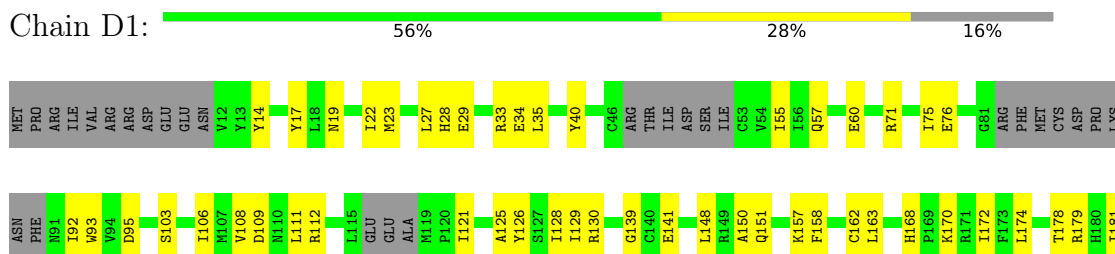
• Molecule 2: Ribosomal protein S13



• Molecule 3: Ribosomal protein S9

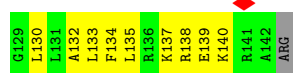
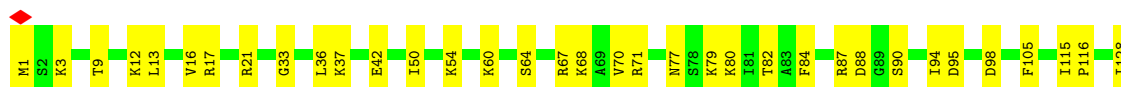


• Molecule 4: Ribosomal protein S3





• Molecule 5: Ribosomal protein S23



• Molecule 6: Ribosomal protein S18

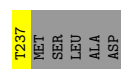


• Molecule 7: Ribosomal protein S16



• Molecule 8: Ribosomal protein S2





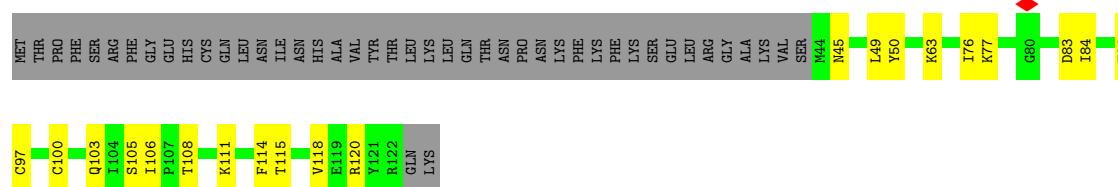
- Molecule 9: 40S ribosomal protein S3a

Chain B1: 63% 25% 12%



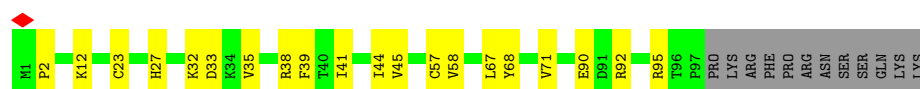
- Molecule 10: Ribosomal protein S27

Chain b1: 48% 16% 36%



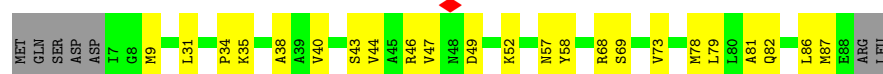
- Molecule 11: 40S ribosomal protein S26

Chain a1: 71% 18% 11%



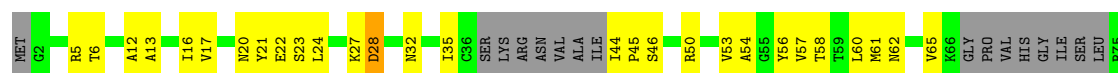
- Molecule 12: 40S ribosomal protein S21

Chain V1: 66% 26% 8%



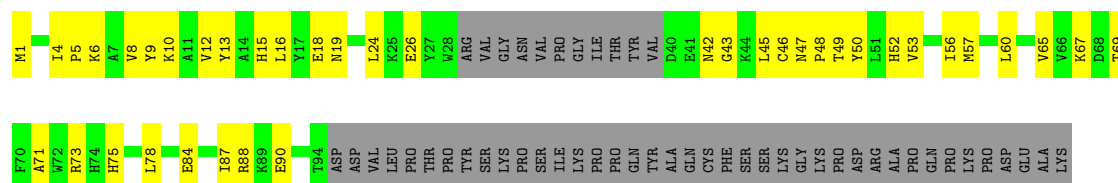
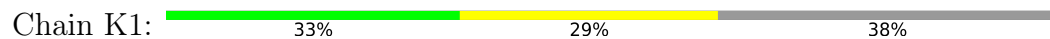
- Molecule 13: Ribosomal protein S17

Chain R1: 42% 30% 28%





- Molecule 14: Ribosomal protein S10B



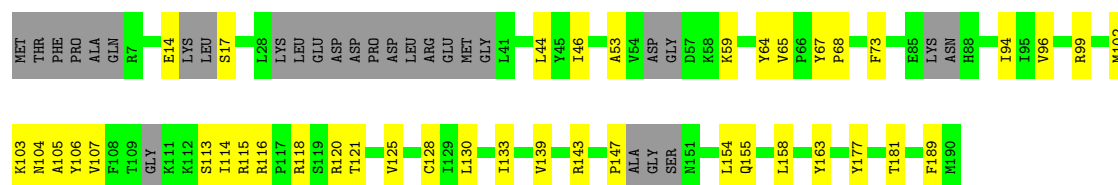
- Molecule 15: 40S ribosomal protein S8



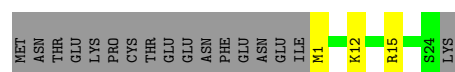
- Molecule 16: 40S ribosomal protein S30



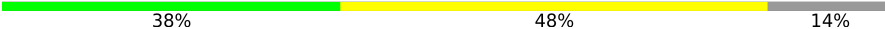
- Molecule 17: 40S ribosomal protein S7

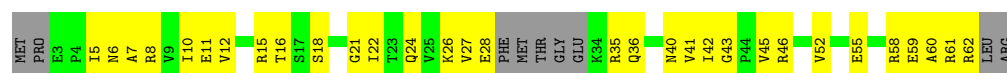


- Molecule 18: Ribosomal protein eL41



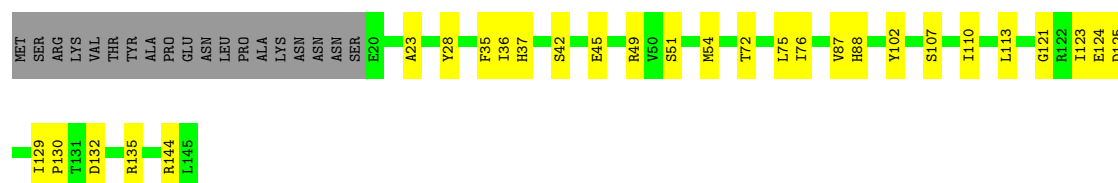
- Molecule 19: Ribosomal protein S28

Chain c1: 



- Molecule 20: Ribosomal protein S14

Chain O1: 



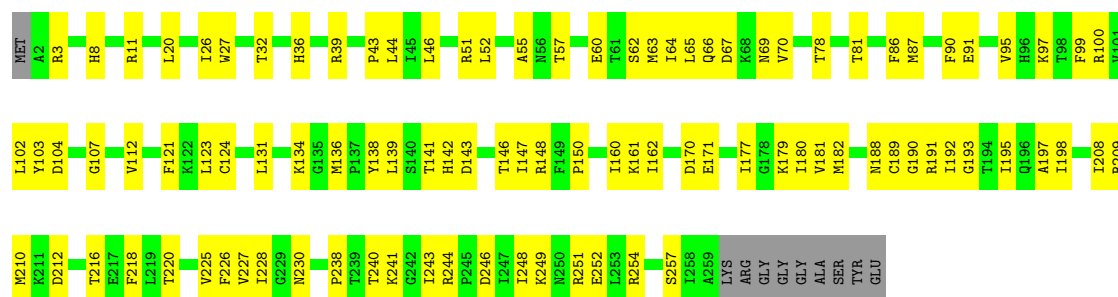
- Molecule 21: Ribosomal protein S15A

Chain W1: 



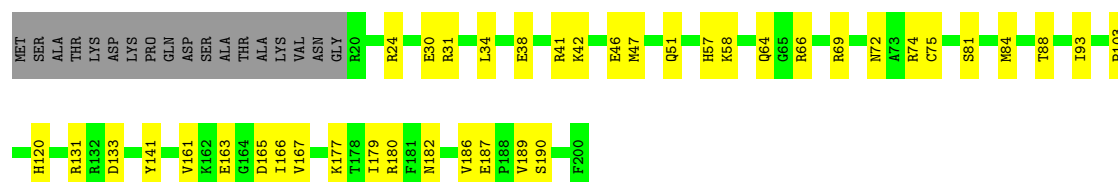
- Molecule 22: 40S ribosomal protein S4

Chain E1: 

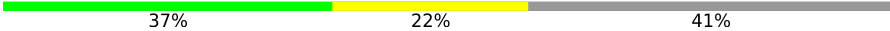


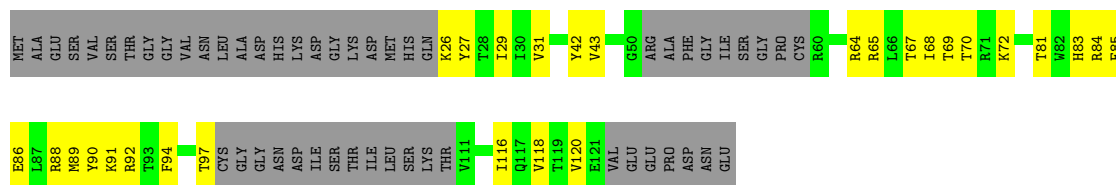
- Molecule 23: SSU ribosomal protein S17P

Chain L1: 



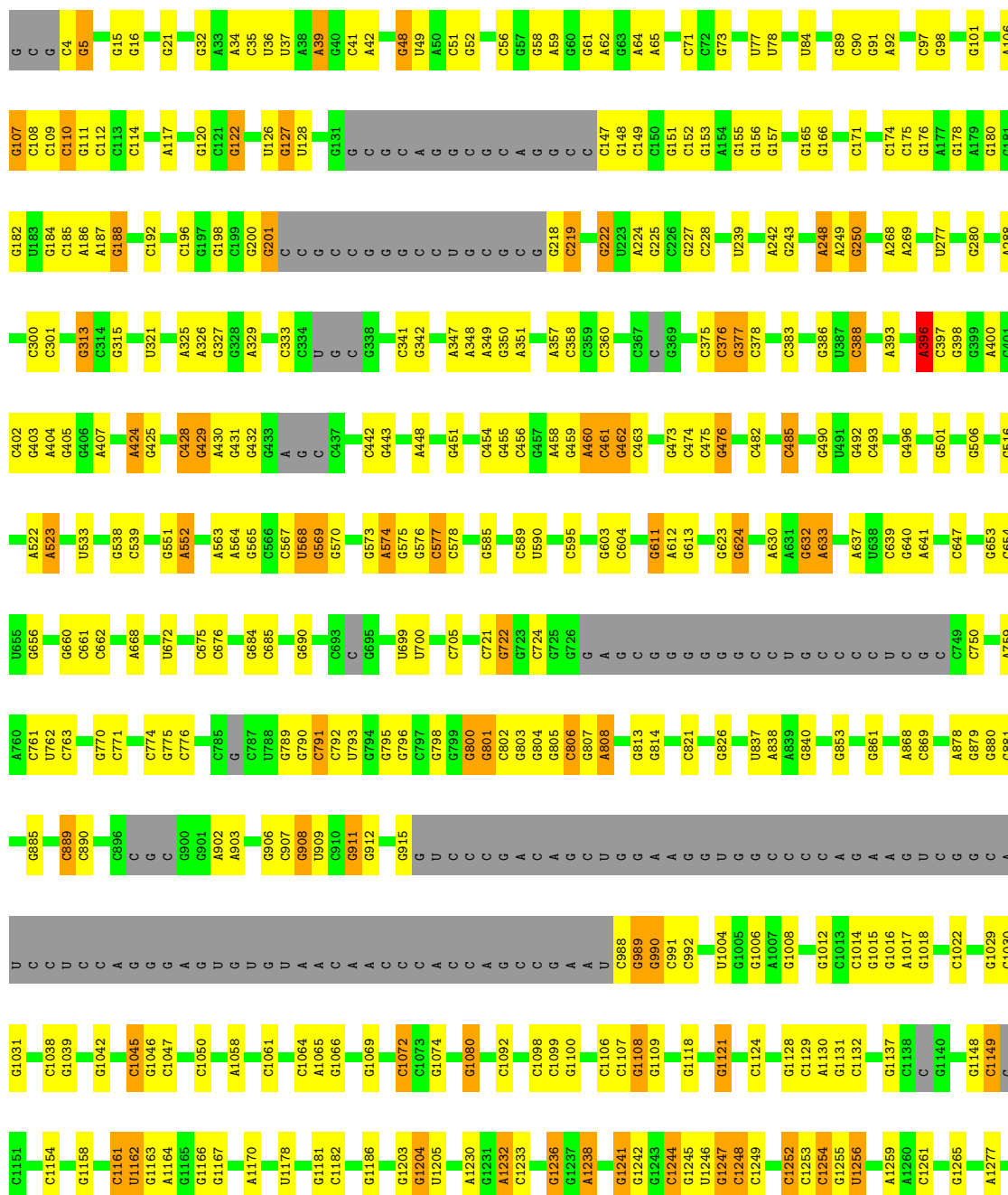
- Molecule 24: Ribosomal protein S20

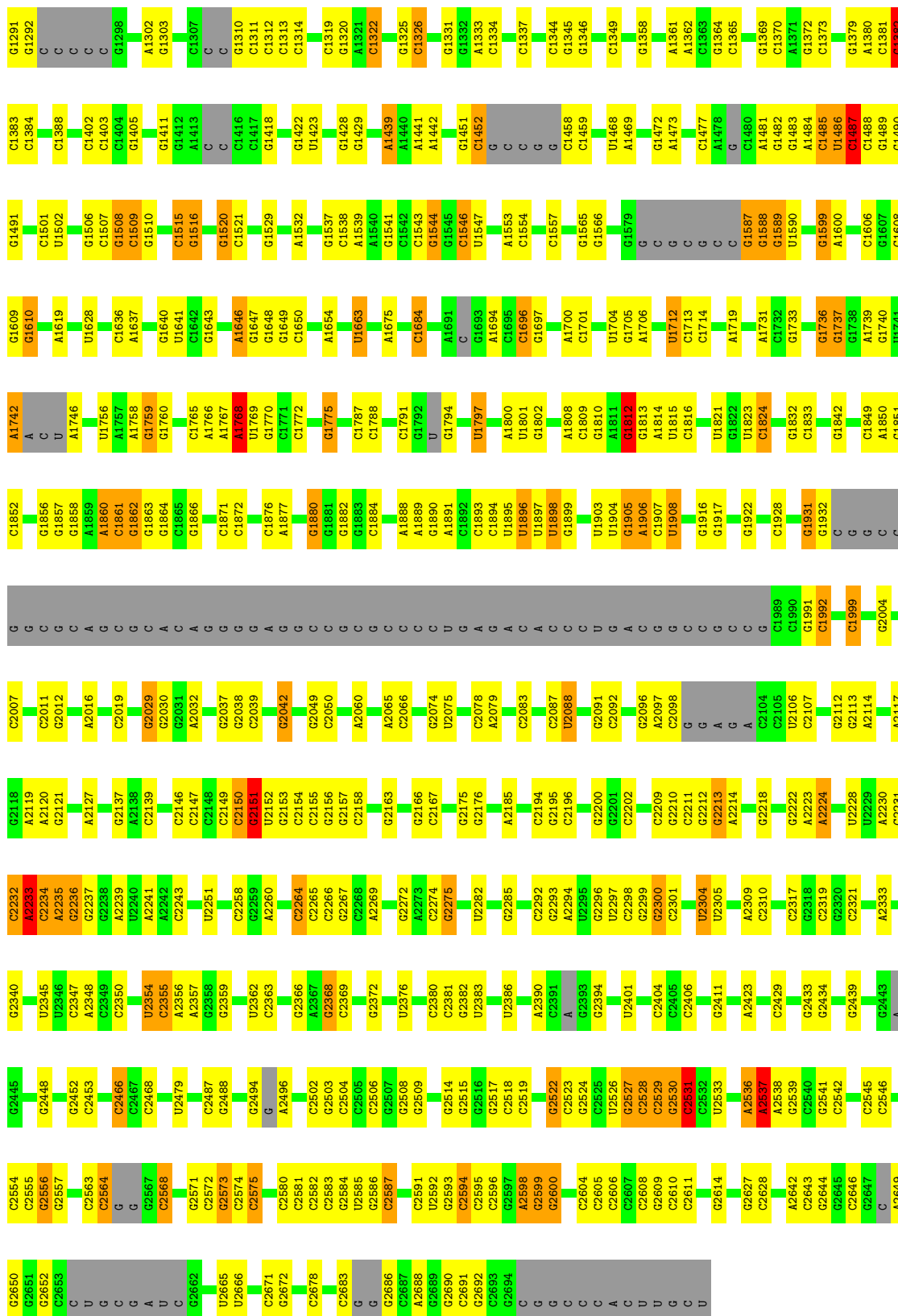
Chain U1: 



• Molecule 25: rRNA 28S

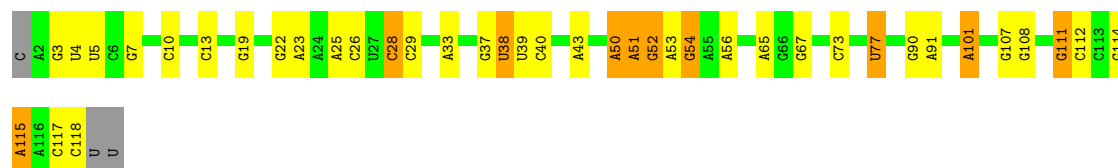
Chain 1: 





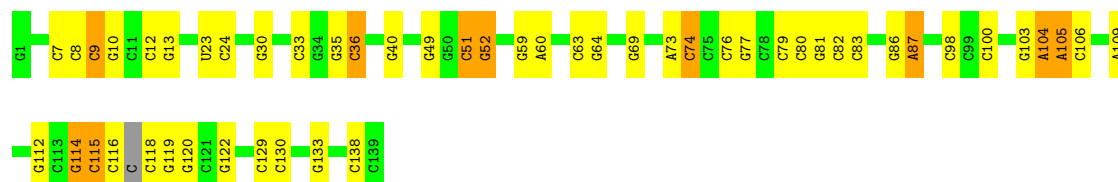
- Molecule 26: rRNA 5S





- Molecule 27: rRNA 5.8S

Chain 42: 63% 29% 7% .



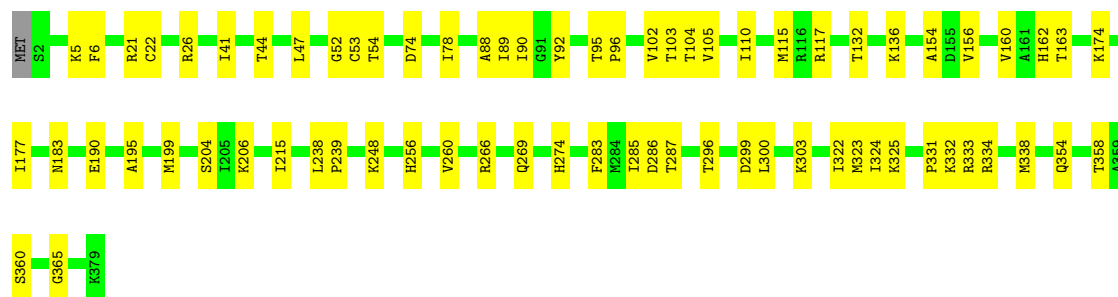
- Molecule 28: Ribosomal protein L2

Chain A2: 91% 8%



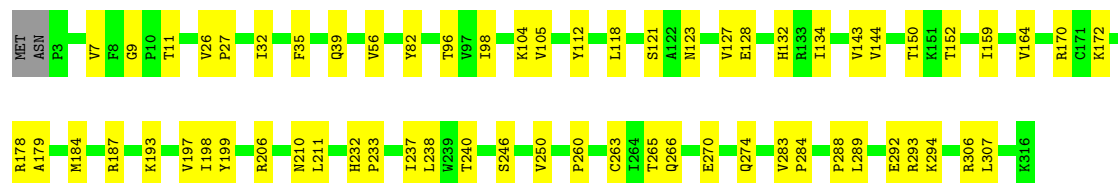
- Molecule 29: Ribosomal protein L3

Chain B2: 81% 19%



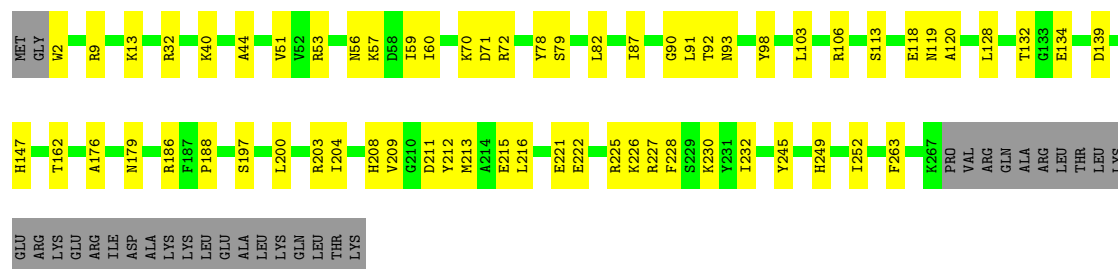
- Molecule 30: Ribosomal protein L4

Chain C2: 79% 20% .



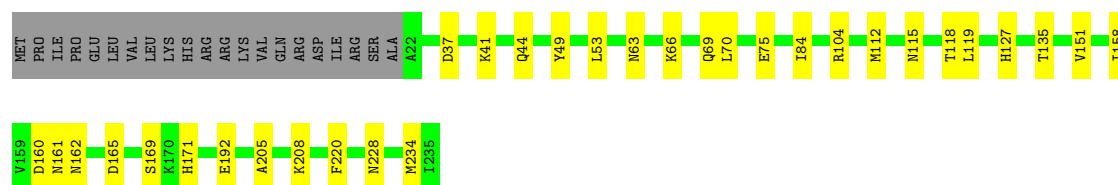
- Molecule 31: Ribosomal protein L5

Chain D2: 68% 21% 10%



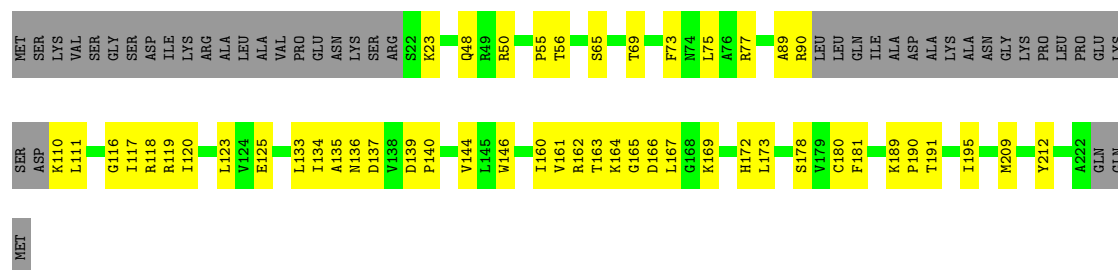
• Molecule 32: Ribosomal protein L7

Chain F2: 77% 14% 9%



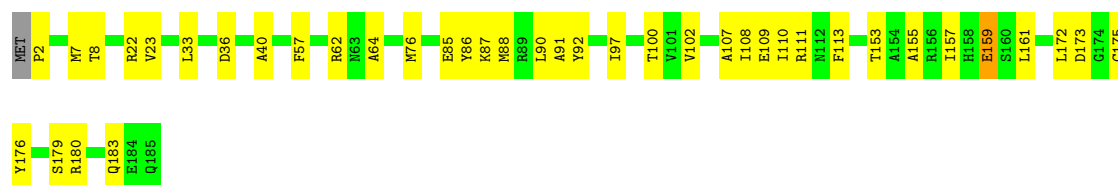
• Molecule 33: 60S ribosomal protein L7a

Chain G2: 59% 22% 19%



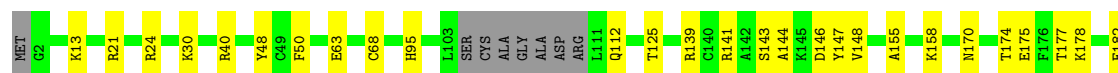
• Molecule 34: Ribosomal protein L6

Chain H2: 78% 21% ..



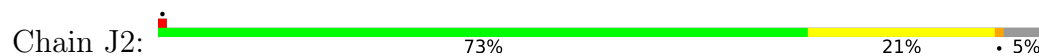
• Molecule 35: Ribosomal protein L10

Chain I2: 80% 15% 5%

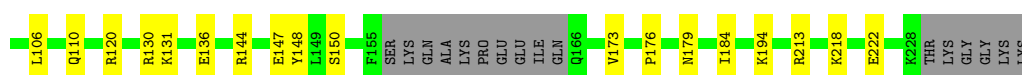




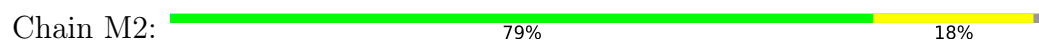
- Molecule 36: Ribosomal protein L11



- Molecule 37: 60S ribosomal protein L13



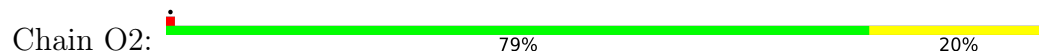
- Molecule 38: Ribosomal protein L14



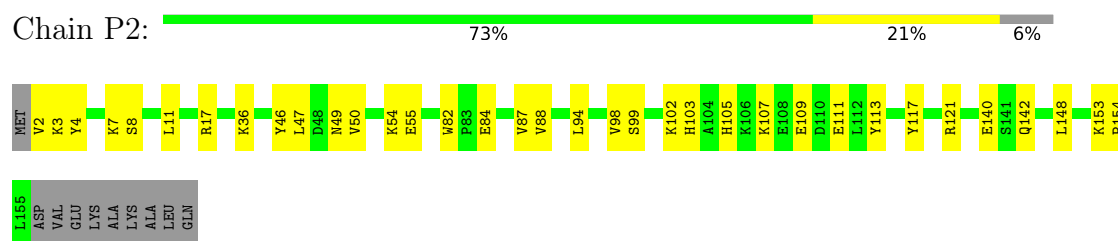
- Molecule 39: Ribosomal protein L15



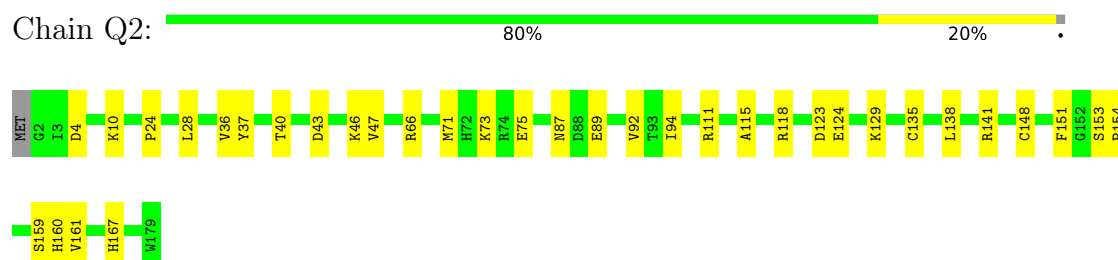
- Molecule 40: Ribosomal protein L13a



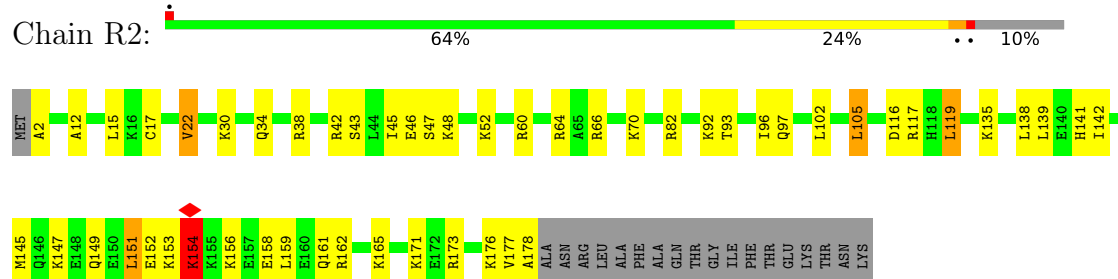
- Molecule 41: Ribosomal protein L17



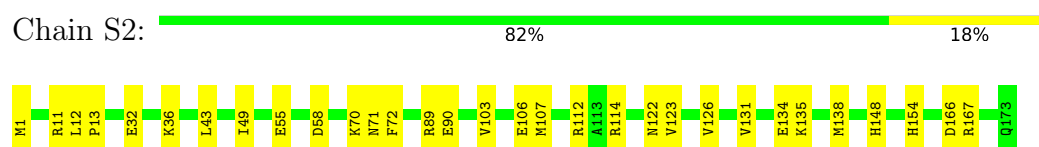
- Molecule 42: Ribosomal protein L18



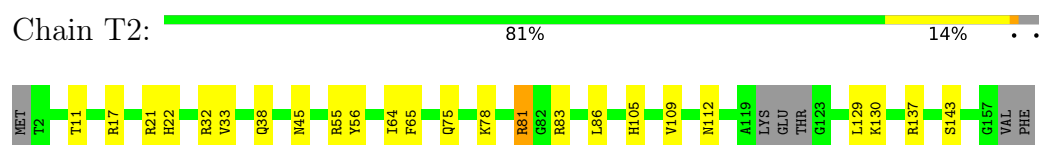
- Molecule 43: Ribosomal protein L19



- Molecule 44: 60S ribosomal protein L18a

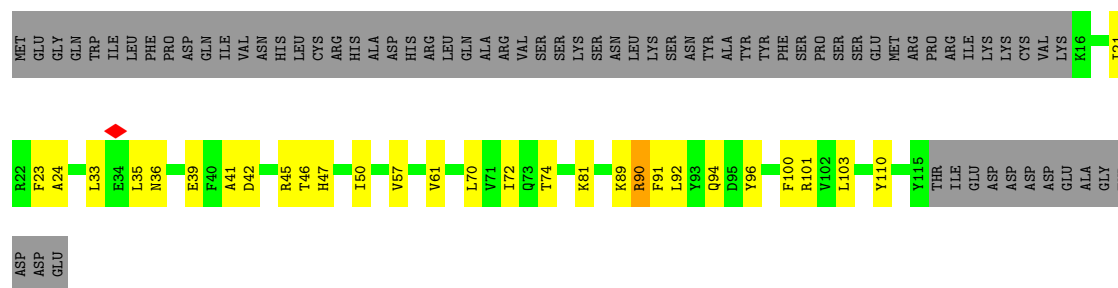


- Molecule 45: Ribosomal protein L21



- Molecule 46: Ribosomal protein eL22





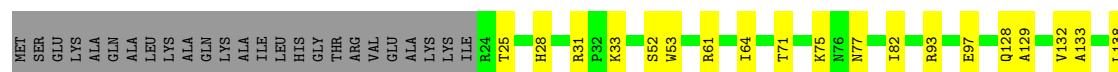
- Molecule 47: Ribosomal protein L23

Chain V2: 86% 12% .



- Molecule 48: Ribosomal protein L23A

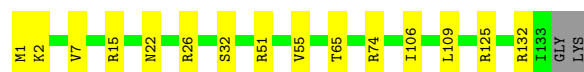
Chain X2: 68% 14% 18%



A139

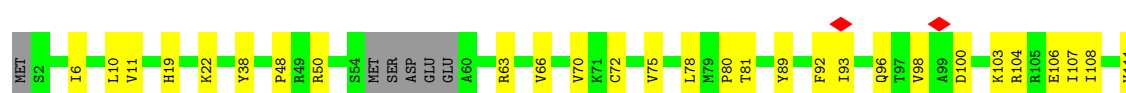
- Molecule 49: Ribosomal protein L26

Chain Y2: 87% 11% .



- Molecule 50: 60S ribosomal protein L27

Chain Z2: 75% 21% .



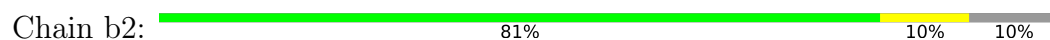
A135

- Molecule 51: Ribosomal protein L27a

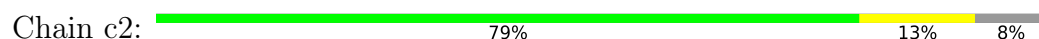
Chain a2: 82% 17% ..



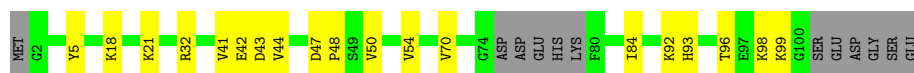
- Molecule 52: 60S ribosomal protein L29



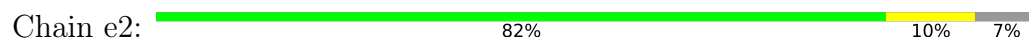
- Molecule 53: Ribosomal protein L30



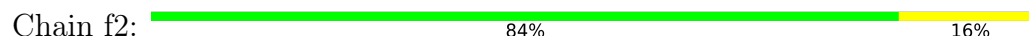
- Molecule 54: Ribosomal protein L31B



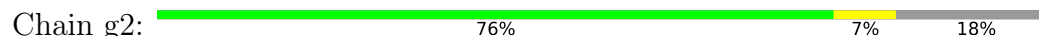
- Molecule 55: Ribosomal protein L32



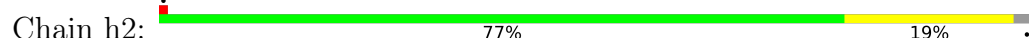
- Molecule 56: Ribosomal protein L35a

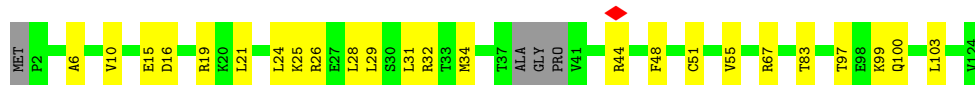


- Molecule 57: Ribosomal protein L34



- Molecule 58: Ribosomal protein L35





- Molecule 59: Ribosomal protein L36-1

Chain i2: 87% 8% 6%



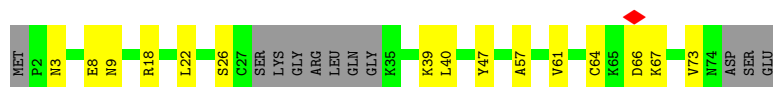
- Molecule 60: Ribosomal protein L37

Chain j2: 84% 13% .



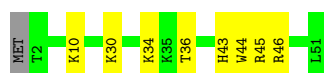
- Molecule 61: Ribosomal L38e

Chain k2: 66% 19% 14%



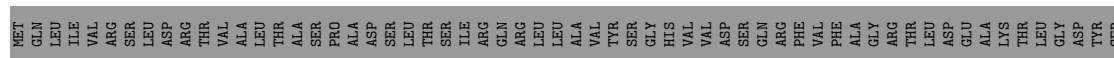
- Molecule 62: Ribosomal protein L39

Chain l2: 82% 16% .



- Molecule 63: Ubiquitin/Ribosomal protein L40e

Chain m2: 33% 7% 60%



- Molecule 64: Ribosomal protein L44

Chain o2: 75% 13% 11%



- Molecule 65: Ribosomal protein L37a

MET
A2
V8
T11
R20
L26
E30
Q33
T38
C39
P40
F41
C42
D45
T82
R85
L88
E91
D92
ALA
GLN

- | |
|-----|
| A1 |
| G2 |
| |
| G5 |
| C68 |
| C69 |
| G70 |
| C71 |
| C72 |
| A73 |
| C74 |
| C75 |
| A76 |

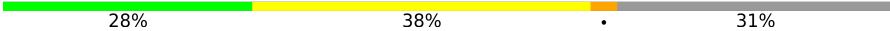
- | MET |
|-----|
| V2 |
| M22 |
| Z23 |
| R24 |
| K27 |
| V28 |
| W45 |
| K49 |
| L54 |
| R58 |
| E63 |
| V64 |
| I65 |
| LYS |
| ALA |
| ARG |
| GLU |
| VAL |
| THR |
| ARG |
| LYS |
| ALA |
| VAL |
| SER |
| LYS |
| ARG |
| ASN |
| PHE |
| LEU |
| SER |
| ILE |
| ASP |
| ASP |
| SER |
| LYS |
| LEU |
| GLU |
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| LEU |
| LYS |
| SER |
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| TYR |
| SER |
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| VAL |

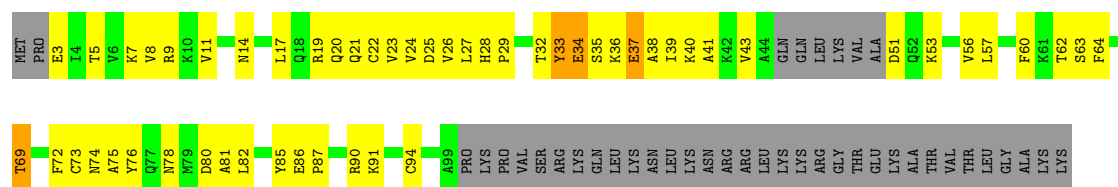
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|-----|-----|-----|
| C74 | C75 | A76 |
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- [illegible]

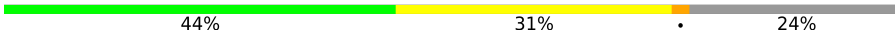
- | | |
|------|----|
| K145 | K146 | A147 | A148 | F149 | R150 | K151 | V152 | R153 | P154 | F155 | A156 | E157 | C158 | L159 | A160 | E161 | M164 | N165 | A166 | A167 | D171 | K172 | S173 | Y174 | R179 | M180 | S181 | R184 | I185 | A186 | N189 | R190 | K191 | K192 | K193 | K194 | K195 | K196 | K197 | K198 | K199 | K200 | K201 | K202 | K203 | K204 | K205 | K206 | K207 | K208 | K209 | K210 | K211 | K212 | K213 | K214 | K215 | K216 | K217 | K218 | K219 | K220 | K221 | K222 | K223 | K224 | K225 | K226 | K227 | K228 | K229 | K230 | K231 | K232 | K233 | K234 | K235 | K236 | K237 | K238 | K239 | K240 | K241 | K242 | K243 | K244 | K245 | K246 | K247 | K248 | K249 | A250 | K251 | C252 | P253 | V254 | V255 | E256 | R257 | L258 | T259 | N260 | S261 | L262 | M263 | M264 | H265 | G266 | R267 | R268 | R269 | R270 | R271 | R272 | R273 | R274 | R275 | R276 | R277 | R278 | R279 | R280 | R281 | R282 | R283 | R284 | R285 | R286 | R287 | R288 | R289 | R290 | R291 | R292 | R293 | R294 | R295 | R296 | R297 | R298 | R299 | R300 | R301 | R302 | R303 | R304 | R305 | R306 | R307 | R308 | R309 | R310 | R311 | R312 | R313 | R314 | R315 | R316 | R317 | R318 | R319 | R320 | R321 | R322 | R323 | R324 | R325 | R326 | R327 | R328 | R329 | R330 | R331 | R332 | R333 | R334 | R335 | R336 | R337 | R338 | R339 | R340 | R341 | R342 | R343 | R344 | R345 | R346 | R347 | R348 | R349 | R350 | R351 | R352 | R353 | R354 | R355 | R356 | R357 | R358 | R359 | R360 | R361 | R362 | R363 | R364 | R365 | R366 | R367 | R368 | R369 | R370 | R371 | R372 | R373 | R374 | R375 | R376 | R377 | R378 | R379 | R380 | R381 | R382 | R383 | R384 | R385 | R386 | R387 | R388 | R389 | R390 | R391 | R392 | R393 | R394 | R395 | R396 | R397 | R398 | R399 | R400 | R401 | R402 | R403 | R404 | R405 | R406 | R407 | R408 | R409 | R410 | R411 | R412 | R413 | R414 | R415 | R416 | R417 | R418 | R419 | R420 | R421 | R422 | R423 | R424 | R425 | R426 | R427 | R428 | R429 | R430 | R431 | R432 | R433 | R434 | R435 | R436 | R437 | R438 | R439 | R440 | R441 | R442 | R443 | R444 | R445 | R446 | R447 | R448 | R449 | R450 | R451 | R452 | R453 | R454 | R455 | R456 | R457 | R458 | R459 | R460 | R461 | R462 | R463 | R464 | R465 | R466 | R467 | R468 | R469 | R470 | R471 | R472 | R473 | R474 | R475 | R476 | R477 | R478 | R479 | R480 | R481 | R482 | R483 | R484 | R485 | R486 | R487 | R488 | R489 | R490 | R491 | R492 | R493 | R494 | R495 | R496 | R497 | R498 | R499 | R500 | R501 | R502 | R503 | R504 | R505 | R506 | R507 | R508 | R509 | R510 | R511 | R512 | R513 | R514 | R515 | R516 | R517 | R518 | R519 | R520 | R521 | R522 | R523 | R524 | R525 | R526 | R527 | R528 | R529 | R530 | R531 | R532 | R533 | R534 | R535 | R536 | R537 | R538 | R539 | R540 | R541 | R542 | R543 | R544 | R545 | R546 | R547 | R548 | R549 | R550 | R551 | R552 | R553 | R554 | R555 | R556 | R557 | R558 | R559 | R560 | R561 | R562 | R563 | R564 | R565 | R566 | R567 | R568 | R569 | R570 | R571 | R572 | R573 | R574 | R575 | R576 | R577 | R578 | R579 | R580 | R581 | R582 | R583 | R584 | R585 | R586 | R587 | R588 | R589 | R590 | R591 | R592 | R593 | R594 | R595 | R596 | R597 | R598 | R599 | R600 | R601 | R602 | R603 | R604 | R605 | R606 | R607 | R608 | R609 | R610 | R611 | R612 | R613 | R614 | R615 | R616 | R617 | R618 | R619 | R620 | R621 | R622 | R623 | R624 | R625 | R626 | R627 | R628 | R629 | R630 | R631 | R632 | R633 | R634 | R635 | R636 | R637 | R638 | R639 | R640 | R641 | R642 | R643 | R644 | R645 | R646 | R647 | R648 | R649 | R650 | R651 | R652 | R653 | R654 | R655 | R656 | R657 | R658 | R659 | R660 | R661 | R662 | R663 | R664 | R665 | R666 | R667 | R668 | R6 |
|------|----|

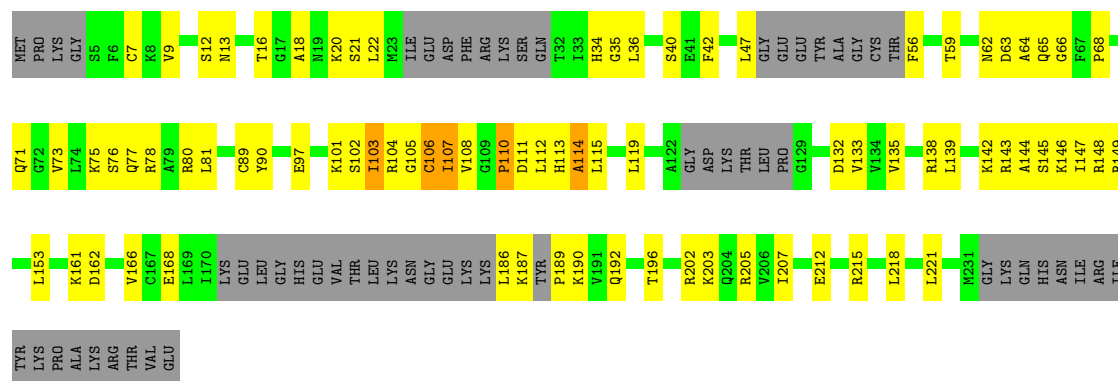
- 

Chain Y1:  28% 38% 31%



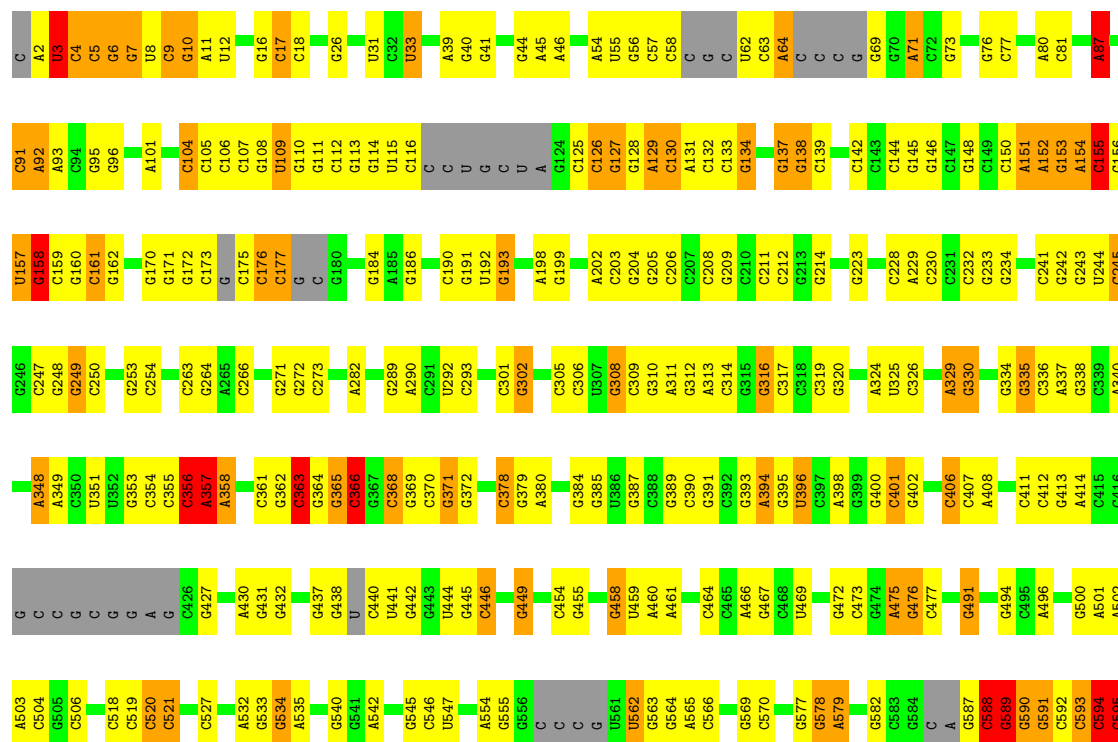
• Molecule 72: 40S ribosomal protein S6

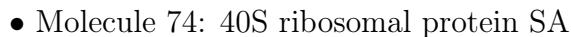
Chain G1:  44% 31% 24%



• Molecule 73: rRNA 18S

Chain 2:  46% 34% 11% 7%





Response	Percentage
Doing a good job	65%
Not doing a good job	14%
Don't know	21%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	91058	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.087	Depositor
Minimum map value	-0.030	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0055	Depositor
Map size ($\text{\AA}$)	374.0, 374.0, 374.0	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4OC, 7MG, MG, 5MC, OMC, 4AC, OMU, MA6, M7A, A2M, OMG, C4J, K

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	T1	0.28	0/812	0.56	0/1098
2	N1	0.29	0/1215	0.57	0/1634
3	J1	0.30	0/1340	0.64	0/1796
4	D1	0.28	0/1422	0.59	0/1909
5	X1	0.28	0/1119	0.59	0/1498
6	S1	0.28	0/1070	0.67	0/1435
7	Q1	0.33	0/968	0.68	0/1295
8	C1	0.34	0/1674	0.62	0/2259
9	B1	0.30	0/1793	0.57	0/2419
10	b1	0.29	0/628	1.12	2/852 (0.2%)
11	a1	0.28	0/797	0.53	0/1072
12	V1	0.52	0/613	0.77	0/823
13	R1	0.38	0/773	0.71	1/1037 (0.1%)
14	K1	0.28	0/707	0.67	0/957
15	I1	0.27	0/1302	0.57	0/1746
16	e1	0.25	0/294	0.50	0/392
17	H1	0.31	0/1211	0.56	0/1640
18	n1	0.36	0/219	0.74	0/280
19	c1	0.63	0/439	0.85	0/585
20	O1	0.31	0/947	0.60	0/1273
21	W1	0.40	0/1048	0.64	0/1412
22	E1	0.30	0/2108	0.61	1/2845 (0.0%)
23	L1	0.29	0/1520	0.61	0/2037
24	U1	0.32	0/619	0.66	0/833
25	1	0.41	1/58145 (0.0%)	0.56	97/90686 (0.1%)
26	3	0.33	0/2797	0.49	4/4359 (0.1%)
27	42	0.35	0/3277	0.45	0/5109
28	A2	0.40	0/1906	0.61	0/2561
29	B2	0.38	0/3058	0.63	0/4129
30	C2	0.37	0/2498	0.63	0/3388
31	D2	0.28	0/2157	0.54	0/2899
32	F2	0.32	0/1760	0.57	0/2374

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	G2	0.31	0/1472	0.65	0/1989
34	H2	0.34	0/1469	0.63	1/1985 (0.1%)
35	I2	0.29	0/1657	0.57	0/2219
36	J2	0.29	0/1325	0.58	0/1776
37	L2	0.33	0/1533	0.58	0/2052
38	M2	0.28	0/1002	0.59	0/1349
39	N2	0.35	0/1755	0.58	0/2353
40	O2	0.35	0/1618	0.58	0/2169
41	P2	0.35	0/1261	0.65	0/1688
42	Q2	0.29	0/1425	0.54	0/1907
43	R2	0.92	0/1478	1.21	1/1954 (0.1%)
44	S2	0.31	0/1452	0.59	0/1955
45	T2	0.31	0/1251	0.61	1/1682 (0.1%)
46	U2	0.42	0/836	0.67	0/1124
47	V2	0.32	0/1083	0.60	0/1458
48	X2	0.31	0/956	0.58	0/1293
49	Y2	0.31	0/1091	0.62	0/1454
50	Z2	0.29	0/997	0.53	0/1352
51	a2	0.42	0/1231	0.67	0/1647
52	b2	0.30	0/471	0.55	0/624
53	c2	0.28	0/758	0.61	0/1025
54	d2	0.32	0/764	0.68	0/1026
55	e2	0.36	0/1063	0.60	0/1418
56	f2	0.29	0/994	0.57	0/1338
57	g2	0.28	0/813	0.52	0/1092
58	h2	0.30	0/971	0.59	0/1295
59	i2	0.31	0/700	0.58	0/927
60	j2	0.33	0/708	0.54	0/941
61	k2	0.26	0/507	0.54	0/679
62	l2	0.32	0/445	0.62	0/594
63	m2	0.27	0/426	0.54	0/568
64	o2	0.33	0/773	0.58	0/1023
65	p2	0.34	0/717	0.70	0/956
66	w2	0.56	0/332	1.01	6/511 (1.2%)
67	W2	0.31	0/551	0.58	0/738
68	E	0.26	0/68	0.52	0/103
69	d1	0.53	0/400	0.82	0/532
70	F1	0.97	0/1264	1.19	2/1697 (0.1%)
71	Y1	0.50	0/724	0.80	1/971 (0.1%)
72	G1	0.51	0/1466	0.83	0/1956
73	2	0.36	0/32117	0.61	111/50066 (0.2%)
74	A1	0.24	0/1580	0.47	0/2149
All	All	0.38	1/173740 (0.0%)	0.60	228/254267 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	1	49	OMU	O3'-P	5.20	1.61	1.56

The worst 5 of 228 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	b1	96	PHE	CA-C-N	18.33	147.09	121.61
10	b1	96	PHE	C-N-CA	18.33	147.09	121.61
73	2	155	C	P-O3'-C3'	-8.91	106.83	120.20
73	2	595	G	P-O3'-C3'	-8.83	106.96	120.20
73	2	138	G	P-O3'-C3'	-8.64	107.24	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	T1	795	0	763	24	0
2	N1	1192	0	1256	19	0
3	J1	1322	0	1378	40	0
4	D1	1402	0	1424	47	0
5	X1	1104	0	1194	35	0
6	S1	1055	0	1076	66	0
7	Q1	960	0	1037	52	0
8	C1	1641	0	1687	50	0
9	B1	1758	0	1797	45	0
10	b1	614	0	604	14	0
11	a1	785	0	817	17	0
12	V1	605	0	606	22	0
13	R1	767	0	759	54	0
14	K1	689	0	671	36	0
15	I1	1282	0	1336	28	0
16	e1	291	0	306	7	0
17	H1	1195	0	1171	28	0
18	n1	217	0	259	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	c1	439	0	473	26	0
20	O1	935	0	934	22	0
21	W1	1031	0	1082	36	0
22	E1	2062	0	2145	70	0
23	L1	1487	0	1510	24	0
24	U1	609	0	648	34	0
25	1	52571	0	26733	359	0
26	3	2501	0	1269	27	0
27	42	2958	0	1517	21	0
28	A2	1873	0	1932	17	0
29	B2	2987	0	3022	45	0
30	C2	2446	0	2535	47	0
31	D2	2115	0	2135	50	0
32	F2	1730	0	1766	23	0
33	G2	1446	0	1508	35	0
34	H2	1442	0	1480	26	0
35	I2	1621	0	1634	23	0
36	J2	1305	0	1318	32	0
37	L2	1512	0	1607	26	0
38	M2	990	0	1022	21	0
39	N2	1712	0	1790	24	0
40	O2	1587	0	1634	35	0
41	P2	1235	0	1265	26	0
42	Q2	1402	0	1478	23	0
43	R2	1463	0	1567	44	0
44	S2	1418	0	1410	25	0
45	T2	1226	0	1256	25	0
46	U2	820	0	806	23	0
47	V2	1063	0	1109	12	0
48	X2	936	0	984	16	0
49	Y2	1076	0	1139	15	0
50	Z2	980	0	974	20	0
51	a2	1201	0	1233	21	0
52	b2	463	0	489	4	0
53	c2	750	0	775	12	0
54	d2	752	0	804	13	0
55	e2	1039	0	1095	9	0
56	f2	974	0	995	13	0
57	g2	798	0	832	4	0
58	h2	960	0	1046	15	0
59	i2	691	0	748	5	0
60	j2	692	0	680	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	k2	504	0	535	8	0
62	l2	434	0	468	6	0
63	m2	421	0	441	7	0
64	o2	762	0	805	11	0
65	p2	708	0	745	11	0
66	w2	299	0	156	7	0
67	W2	540	0	575	8	0
68	E	62	0	34	0	0
69	d1	392	0	387	18	0
70	F1	1246	0	1268	97	0
71	Y1	713	0	729	55	0
72	G1	1453	0	1532	69	0
73	2	29096	0	14772	421	0
74	A1	1546	0	1576	39	0
75	1	181	0	0	2	0
75	2	222	0	0	0	0
75	3	1	0	0	0	0
75	42	2	0	0	0	0
75	A1	1	0	0	0	0
75	A2	4	0	0	0	0
75	B2	3	0	0	0	0
75	C2	4	0	0	0	0
75	E1	4	0	0	0	0
75	G1	1	0	0	0	0
75	I1	2	0	0	0	0
75	I2	1	0	0	0	0
75	L1	4	0	0	0	0
75	L2	1	0	0	0	0
75	N1	3	0	0	0	0
75	N2	2	0	0	0	0
75	O1	5	0	0	0	0
75	S1	2	0	0	0	0
75	U1	1	0	0	0	0
75	V2	1	0	0	0	0
75	W1	1	0	0	0	0
75	X1	1	0	0	0	0
75	a1	1	0	0	0	0
75	a2	2	0	0	0	0
75	b1	2	0	0	0	0
75	e2	1	0	0	0	0
75	j2	1	0	0	0	0
75	o2	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
76	1	71	0	0	0	0
76	2	19	0	0	0	0
76	42	1	0	0	0	0
76	C2	1	0	0	0	0
76	E1	1	0	0	0	0
76	F2	1	0	0	0	0
76	G1	1	0	0	0	0
76	L1	1	0	0	0	0
76	N1	1	0	0	0	0
76	P2	1	0	0	0	0
76	V2	1	0	0	0	0
76	b2	1	0	0	0	0
76	o2	1	0	0	0	0
All	All	163704	0	122543	2339	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 8.

The worst 5 of 2339 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)
13:R1:91:LYS:O	74:A1:203:LYS:NZ	1.72	1.21
13:R1:88:ALA:HB2	74:A1:206:LEU:HD21	1.22	1.13
72:G1:104:ARG:HG2	72:G1:105:GLY:H	1.27	0.98
13:R1:107:GLN:NE2	74:A1:45:ASP:OD2	1.96	0.97
13:R1:88:ALA:CB	74:A1:206:LEU:HD21	1.96	0.95

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	T1	102/139 (73%)	97 (95%)	5 (5%)	0	100	100
2	N1	150/154 (97%)	142 (95%)	8 (5%)	0	100	100
3	J1	164/189 (87%)	153 (93%)	11 (7%)	0	100	100
4	D1	174/217 (80%)	163 (94%)	11 (6%)	0	100	100
5	X1	140/143 (98%)	130 (93%)	10 (7%)	0	100	100
6	S1	131/154 (85%)	113 (86%)	18 (14%)	0	100	100
7	Q1	119/158 (75%)	108 (91%)	11 (9%)	0	100	100
8	C1	210/242 (87%)	195 (93%)	15 (7%)	0	100	100
9	B1	216/248 (87%)	207 (96%)	9 (4%)	0	100	100
10	b1	77/124 (62%)	71 (92%)	6 (8%)	0	100	100
11	a1	95/109 (87%)	90 (95%)	5 (5%)	0	100	100
12	V1	80/89 (90%)	72 (90%)	8 (10%)	0	100	100
13	R1	93/137 (68%)	87 (94%)	6 (6%)	0	100	100
14	K1	79/134 (59%)	70 (89%)	9 (11%)	0	100	100
15	I1	159/174 (91%)	147 (92%)	12 (8%)	0	100	100
16	e1	31/69 (45%)	29 (94%)	2 (6%)	0	100	100
17	H1	148/190 (78%)	133 (90%)	15 (10%)	0	100	100
18	n1	22/41 (54%)	22 (100%)	0	0	100	100
19	c1	51/64 (80%)	47 (92%)	4 (8%)	0	100	100
20	O1	124/145 (86%)	121 (98%)	3 (2%)	0	100	100
21	W1	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
22	E1	256/268 (96%)	234 (91%)	22 (9%)	0	100	100
23	L1	179/199 (90%)	169 (94%)	10 (6%)	0	100	100
24	U1	68/126 (54%)	63 (93%)	5 (7%)	0	100	100
28	A2	248/251 (99%)	237 (96%)	11 (4%)	0	100	100
29	B2	376/379 (99%)	357 (95%)	19 (5%)	0	100	100
30	C2	312/316 (99%)	295 (95%)	17 (5%)	0	100	100
31	D2	264/297 (89%)	247 (94%)	17 (6%)	0	100	100
32	F2	212/235 (90%)	209 (99%)	3 (1%)	0	100	100
33	G2	178/225 (79%)	173 (97%)	5 (3%)	0	100	100
34	H2	182/185 (98%)	172 (94%)	10 (6%)	0	100	100
35	I2	196/210 (93%)	187 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	J2	158/173 (91%)	144 (91%)	14 (9%)	0	100	100
37	L2	185/234 (79%)	183 (99%)	2 (1%)	0	100	100
38	M2	126/131 (96%)	115 (91%)	11 (9%)	0	100	100
39	N2	202/204 (99%)	192 (95%)	10 (5%)	0	100	100
40	O2	193/197 (98%)	186 (96%)	7 (4%)	0	100	100
41	P2	152/164 (93%)	143 (94%)	9 (6%)	0	100	100
42	Q2	176/179 (98%)	169 (96%)	7 (4%)	0	100	100
43	R2	175/196 (89%)	166 (95%)	9 (5%)	0	100	100
44	S2	171/173 (99%)	165 (96%)	6 (4%)	0	100	100
45	T2	149/159 (94%)	145 (97%)	4 (3%)	0	100	100
46	U2	98/171 (57%)	90 (92%)	8 (8%)	0	100	100
47	V2	137/142 (96%)	133 (97%)	4 (3%)	0	100	100
48	X2	114/141 (81%)	109 (96%)	5 (4%)	0	100	100
49	Y2	131/135 (97%)	126 (96%)	5 (4%)	0	100	100
50	Z2	125/135 (93%)	115 (92%)	10 (8%)	0	100	100
51	a2	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
52	b2	54/62 (87%)	54 (100%)	0	0	100	100
53	c2	98/109 (90%)	97 (99%)	1 (1%)	0	100	100
54	d2	90/106 (85%)	81 (90%)	9 (10%)	0	100	100
55	e2	124/136 (91%)	119 (96%)	5 (4%)	0	100	100
56	f2	121/123 (98%)	114 (94%)	7 (6%)	0	100	100
57	g2	97/120 (81%)	94 (97%)	3 (3%)	0	100	100
58	h2	116/124 (94%)	114 (98%)	2 (2%)	0	100	100
59	i2	81/90 (90%)	76 (94%)	5 (6%)	0	100	100
60	j2	85/89 (96%)	83 (98%)	2 (2%)	0	100	100
61	k2	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
62	l2	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
63	m2	49/127 (39%)	46 (94%)	3 (6%)	0	100	100
64	o2	92/106 (87%)	90 (98%)	2 (2%)	0	100	100
65	p2	89/94 (95%)	85 (96%)	4 (4%)	0	100	100
67	W2	63/102 (62%)	59 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	d1	46/137 (34%)	40 (87%)	6 (13%)	0	100	100
70	F1	157/190 (83%)	127 (81%)	27 (17%)	3 (2%)	6	12
71	Y1	87/132 (66%)	76 (87%)	10 (12%)	1 (1%)	11	22
72	G1	177/248 (71%)	134 (76%)	37 (21%)	6 (3%)	3	5
74	A1	192/245 (78%)	185 (96%)	7 (4%)	0	100	100
All	All	9329/10892 (86%)	8754 (94%)	565 (6%)	10 (0%)	49	71

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
72	G1	103	ILE
72	G1	114	ALA
72	G1	106	CYS
70	F1	34	PHE
72	G1	65	GLN

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	T1	78/115 (68%)	77 (99%)	1 (1%)	61	76
2	N1	123/130 (95%)	123 (100%)	0	100	100
3	J1	141/164 (86%)	141 (100%)	0	100	100
4	D1	142/182 (78%)	142 (100%)	0	100	100
5	X1	113/114 (99%)	113 (100%)	0	100	100
6	S1	112/131 (86%)	112 (100%)	0	100	100
7	Q1	101/130 (78%)	101 (100%)	0	100	100
8	C1	176/201 (88%)	176 (100%)	0	100	100
9	B1	196/220 (89%)	196 (100%)	0	100	100
10	b1	70/112 (62%)	70 (100%)	0	100	100
11	a1	90/103 (87%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	V1	62/72 (86%)	62 (100%)	0	100	100
13	R1	81/123 (66%)	80 (99%)	1 (1%)	63	78
14	K1	73/119 (61%)	73 (100%)	0	100	100
15	I1	138/148 (93%)	138 (100%)	0	100	100
16	e1	30/58 (52%)	30 (100%)	0	100	100
17	H1	116/170 (68%)	116 (100%)	0	100	100
18	n1	21/38 (55%)	21 (100%)	0	100	100
19	c1	49/57 (86%)	48 (98%)	1 (2%)	48	69
20	O1	91/113 (80%)	91 (100%)	0	100	100
21	W1	114/115 (99%)	114 (100%)	0	100	100
22	E1	225/232 (97%)	225 (100%)	0	100	100
23	L1	155/173 (90%)	155 (100%)	0	100	100
24	U1	68/110 (62%)	68 (100%)	0	100	100
28	A2	189/192 (98%)	189 (100%)	0	100	100
29	B2	312/313 (100%)	312 (100%)	0	100	100
30	C2	261/263 (99%)	260 (100%)	1 (0%)	84	91
31	D2	210/242 (87%)	210 (100%)	0	100	100
32	F2	184/204 (90%)	184 (100%)	0	100	100
33	G2	159/198 (80%)	159 (100%)	0	100	100
34	H2	160/164 (98%)	160 (100%)	0	100	100
35	I2	166/177 (94%)	166 (100%)	0	100	100
36	J2	137/149 (92%)	136 (99%)	1 (1%)	76	86
37	L2	159/197 (81%)	159 (100%)	0	100	100
38	M2	103/111 (93%)	102 (99%)	1 (1%)	68	81
39	N2	174/175 (99%)	174 (100%)	0	100	100
40	O2	164/165 (99%)	164 (100%)	0	100	100
41	P2	130/139 (94%)	130 (100%)	0	100	100
42	Q2	154/155 (99%)	154 (100%)	0	100	100
43	R2	149/167 (89%)	144 (97%)	5 (3%)	32	57
44	S2	147/154 (96%)	147 (100%)	0	100	100
45	T2	126/133 (95%)	126 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	U2	87/153 (57%)	86 (99%)	1 (1%)	65	79
47	V2	112/114 (98%)	112 (100%)	0	100	100
48	X2	104/123 (85%)	104 (100%)	0	100	100
49	Y2	114/115 (99%)	114 (100%)	0	100	100
50	Z2	101/119 (85%)	101 (100%)	0	100	100
51	a2	126/127 (99%)	125 (99%)	1 (1%)	73	84
52	b2	51/57 (90%)	51 (100%)	0	100	100
53	c2	84/92 (91%)	84 (100%)	0	100	100
54	d2	78/92 (85%)	78 (100%)	0	100	100
55	e2	112/120 (93%)	112 (100%)	0	100	100
56	f2	102/103 (99%)	102 (100%)	0	100	100
57	g2	87/100 (87%)	87 (100%)	0	100	100
58	h2	102/107 (95%)	102 (100%)	0	100	100
59	i2	72/78 (92%)	72 (100%)	0	100	100
60	j2	70/74 (95%)	70 (100%)	0	100	100
61	k2	56/68 (82%)	56 (100%)	0	100	100
62	l2	46/48 (96%)	46 (100%)	0	100	100
63	m2	46/110 (42%)	45 (98%)	1 (2%)	45	67
64	o2	81/93 (87%)	81 (100%)	0	100	100
65	p2	71/73 (97%)	71 (100%)	0	100	100
67	W2	58/92 (63%)	58 (100%)	0	100	100
69	d1	41/116 (35%)	39 (95%)	2 (5%)	22	43
70	F1	132/157 (84%)	119 (90%)	13 (10%)	7	15
71	Y1	77/113 (68%)	75 (97%)	2 (3%)	40	63
72	G1	153/213 (72%)	151 (99%)	2 (1%)	61	76
74	A1	168/217 (77%)	168 (100%)	0	100	100
All	All	7980/9302 (86%)	7947 (100%)	33 (0%)	81	91

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	F1	174	TYR
71	Y1	37	GLU

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Mol	Chain	Res	Type
72	G1	107	ILE
51	a2	10	LYS
46	U2	90	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
37	L2	121	GLN
45	T2	105	HIS
71	Y1	14	ASN
37	L2	171	GLN
42	Q2	177	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
25	1	2420/2707 (89%)	411 (16%)	24 (0%)
26	3	116/120 (96%)	16 (13%)	2 (1%)
27	42	136/139 (97%)	35 (25%)	2 (1%)
66	w2	12/14 (85%)	4 (33%)	0
68	E	2/3 (66%)	1 (50%)	0
73	2	1335/1452 (91%)	310 (23%)	17 (1%)
All	All	4021/4435 (90%)	777 (19%)	45 (1%)

5 of 777 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
25	1	5	G
25	1	21	G
25	1	39	A
25	1	42	A
25	1	48	G

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
73	2	8	U
73	2	600	G
73	2	204	G
73	2	589	G

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Mol	Chain	Res	Type
73	2	835	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

40 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	OMG	1	313	25	23,26,27	2.28	8 (34%)	32,38,41	1.83	10 (31%)
73	M7A	2	1390	73	19,25,26	0.39	0	25,37,40	0.61	0
73	MA6	2	1434	73	23,26,27	1.49	4 (17%)	33,38,41	3.19	12 (36%)
73	4OC	2	1325	73	20,23,24	3.06	8 (40%)	25,32,35	0.97	1 (4%)
25	OMG	1	2237	75,25	23,26,27	1.25	3 (13%)	32,38,41	2.12	7 (21%)
25	OMG	1	1204	25	23,26,27	2.24	8 (34%)	32,38,41	2.10	14 (43%)
73	OMG	2	1035	73,75	23,26,27	2.33	8 (34%)	32,38,41	1.96	8 (25%)
25	OMG	1	1121	25	23,26,27	1.23	3 (13%)	32,38,41	2.17	7 (21%)
73	OMG	2	371	73	23,26,27	1.25	3 (13%)	32,38,41	2.13	7 (21%)
25	5MC	1	1765	25	19,22,23	3.48	8 (42%)	26,32,35	1.10	3 (11%)
25	OMC	1	1824	25	19,22,23	0.78	0	25,31,34	1.24	1 (4%)
25	OMC	1	1684	75,25	19,22,23	2.77	7 (36%)	25,31,34	0.98	1 (4%)
27	OMG	42	133	27,25	23,26,27	2.28	9 (39%)	32,38,41	1.73	7 (21%)
25	OMG	1	2042	25,68	23,26,27	2.31	7 (30%)	32,38,41	1.86	7 (21%)
25	OMG	1	2074	25	23,26,27	2.24	8 (34%)	32,38,41	1.79	8 (25%)
25	OMU	1	1908	25	19,22,23	4.30	15 (78%)	25,31,34	2.00	8 (32%)
73	7MG	2	1261	73	23,26,27	3.52	10 (43%)	27,39,42	2.23	9 (33%)
73	A2M	2	348	73,76	22,25,26	3.18	9 (40%)	30,36,39	2.98	11 (36%)
25	A2M	1	393	25	22,25,26	3.18	10 (45%)	30,36,39	2.90	11 (36%)
73	A2M	2	87	73,75	22,25,26	3.30	10 (45%)	30,36,39	2.94	13 (43%)
25	OMU	1	1897	75,25	19,22,23	2.94	7 (36%)	25,31,34	1.88	4 (16%)
73	4AC	2	1426	73,75	21,24,25	4.43	16 (76%)	28,34,37	1.42	3 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
73	OMG	2	1011	73	23,26,27	1.22	3 (13%)	32,38,41	2.10	8 (25%)
25	A2M	1	1768	25	22,25,26	3.24	10 (45%)	30,36,39	3.18	16 (53%)
73	OMU	2	1314	73	19,22,23	2.95	8 (42%)	25,31,34	1.86	5 (20%)
25	OMG	1	1520	25	23,26,27	1.23	3 (13%)	32,38,41	2.17	7 (21%)
25	A2M	1	523	25	22,25,26	3.14	10 (45%)	30,36,39	2.95	11 (36%)
73	OMG	2	868	73	23,26,27	2.31	8 (34%)	32,38,41	1.61	7 (21%)
73	C4J	2	933	73	25,29,30	3.29	9 (36%)	28,42,45	1.39	4 (14%)
25	OMU	1	1896	75,25	19,22,23	2.94	8 (42%)	25,31,34	1.86	5 (20%)
25	OMG	1	1882	75,25	23,26,27	1.21	3 (13%)	32,38,41	2.31	9 (28%)
25	OMG	1	1775	25	23,26,27	2.27	7 (30%)	32,38,41	1.99	10 (31%)
25	OMU	1	49	75,25	19,22,23	2.98	7 (36%)	25,31,34	1.81	6 (24%)
25	OMG	1	386	25	23,26,27	1.20	3 (13%)	32,38,41	2.23	8 (25%)
25	A2M	1	396	75,25	22,25,26	1.50	5 (22%)	30,36,39	2.04	8 (26%)
25	OMG	1	624	75,25	23,26,27	2.27	8 (34%)	32,38,41	2.10	10 (31%)
73	MA6	2	1435	73	23,26,27	1.46	5 (21%)	33,38,41	3.40	13 (39%)
25	OMC	1	2380	25	19,22,23	2.83	8 (42%)	25,31,34	0.89	1 (4%)
25	5MC	1	2292	75,25	19,22,23	3.58	8 (42%)	26,32,35	1.29	3 (11%)
73	OMC	2	104	73	19,22,23	0.83	0	25,31,34	1.03	1 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	OMG	1	313	25	-	2/9/27/28	0/3/3/3
73	M7A	2	1390	73	-	1/7/37/38	0/3/3/3
73	MA6	2	1434	73	-	0/11/29/30	0/3/3/3
73	4OC	2	1325	73	-	0/9/29/30	0/2/2/2
25	OMG	1	2237	75,25	-	0/9/27/28	0/3/3/3
25	OMG	1	1204	25	-	0/9/27/28	0/3/3/3
73	OMG	2	1035	73,75	-	1/9/27/28	0/3/3/3
25	OMG	1	1121	25	-	2/9/27/28	0/3/3/3
73	OMG	2	371	73	-	2/9/27/28	0/3/3/3
25	5MC	1	1765	25	-	0/7/25/26	0/2/2/2
25	OMC	1	1824	25	-	1/9/27/28	0/2/2/2
25	OMC	1	1684	75,25	-	4/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	OMG	42	133	27,25	-	0/9/27/28	0/3/3/3
25	OMG	1	2042	25,68	-	0/9/27/28	0/3/3/3
25	OMG	1	2074	25	-	1/9/27/28	0/3/3/3
25	OMU	1	1908	25	-	2/9/27/28	0/2/2/2
73	7MG	2	1261	73	-	0/7/37/38	0/3/3/3
73	A2M	2	348	73,76	-	0/9/27/28	0/3/3/3
25	A2M	1	393	25	-	0/9/27/28	0/3/3/3
73	A2M	2	87	73,75	-	3/9/27/28	0/3/3/3
25	OMU	1	1897	75,25	-	0/9/27/28	0/2/2/2
73	4AC	2	1426	73,75	-	2/11/29/30	0/2/2/2
73	OMG	2	1011	73	-	1/9/27/28	0/3/3/3
25	A2M	1	1768	25	-	3/9/27/28	0/3/3/3
73	OMU	2	1314	73	-	0/9/27/28	0/2/2/2
25	OMG	1	1520	25	-	1/9/27/28	0/3/3/3
25	A2M	1	523	25	-	1/9/27/28	0/3/3/3
73	OMG	2	868	73	-	5/9/27/28	0/3/3/3
73	C4J	2	933	73	-	6/16/34/35	0/2/2/2
25	OMU	1	1896	75,25	-	0/9/27/28	0/2/2/2
25	OMG	1	1882	75,25	-	0/9/27/28	0/3/3/3
25	OMG	1	1775	25	-	2/9/27/28	0/3/3/3
25	OMU	1	49	75,25	-	1/9/27/28	0/2/2/2
25	OMG	1	386	25	-	0/9/27/28	0/3/3/3
25	A2M	1	396	75,25	-	1/9/27/28	0/3/3/3
25	OMG	1	624	75,25	-	1/9/27/28	0/3/3/3
73	MA6	2	1435	73	-	3/11/29/30	0/3/3/3
25	OMC	1	2380	25	-	0/9/27/28	0/2/2/2
25	5MC	1	2292	75,25	-	4/7/25/26	0/2/2/2
73	OMC	2	104	73	-	1/9/27/28	0/2/2/2

The worst 5 of 274 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	2	933	C4J	C6-C5	11.86	1.52	1.35
25	1	1908	OMU	C3'-C2'	-10.61	1.29	1.53
25	1	2292	5MC	C6-C5	9.04	1.49	1.34
73	2	1426	4AC	O4'-C1'	8.93	1.62	1.42
25	1	523	A2M	C3'-C4'	-8.82	1.30	1.53

The worst 5 of 284 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
73	2	1435	MA6	N1-C6-N6	-12.51	101.61	116.86
73	2	1434	MA6	N1-C6-N6	-11.74	102.55	116.86
73	2	1435	MA6	C5-C6-N6	8.85	139.34	125.33
73	2	1434	MA6	C5-C6-N6	7.92	137.87	125.33
25	1	1768	A2M	N6-C6-N1	-6.70	103.47	118.38

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	1	49	OMU	C1'-C2'-O2'-CM2
25	1	313	OMG	O4'-C4'-C5'-O5'
25	1	396	A2M	C1'-C2'-O2'-CM'
25	1	523	A2M	C1'-C2'-O2'-CM'
25	1	624	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

17 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
73	2	1434	MA6	2	0
73	2	371	OMG	7	0
25	1	1824	OMC	1	0
25	1	1684	OMC	1	0
25	1	2042	OMG	1	0
73	2	1261	7MG	3	0
73	2	348	A2M	3	0
73	2	87	A2M	1	0
73	2	1011	OMG	1	0
25	1	1768	A2M	1	0
73	2	1314	OMU	3	0
25	1	1520	OMG	2	0
25	1	523	A2M	1	0
25	1	1896	OMU	1	0
25	1	396	A2M	2	0
25	1	624	OMG	1	0
73	2	104	OMC	1	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 556 ligands modelled in this entry, 556 are 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
66	w2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w2	5:G	O3'	68:C	P	17.08

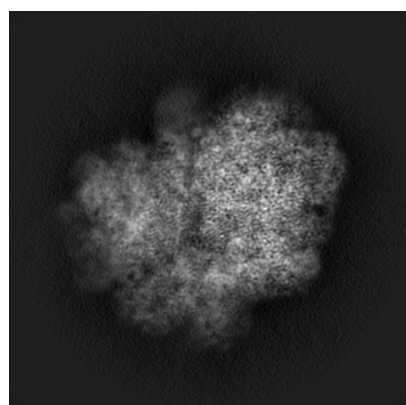
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13683. These allow visual inspection of the internal detail of the map and identification of artifacts.

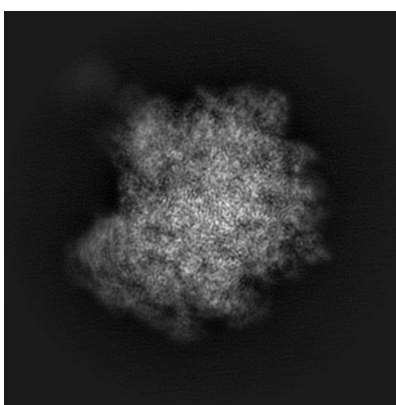
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

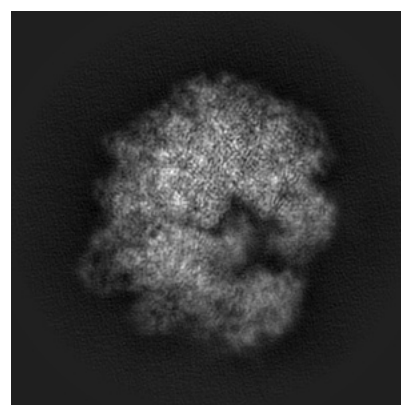
6.1.1 Primary map



X



Y

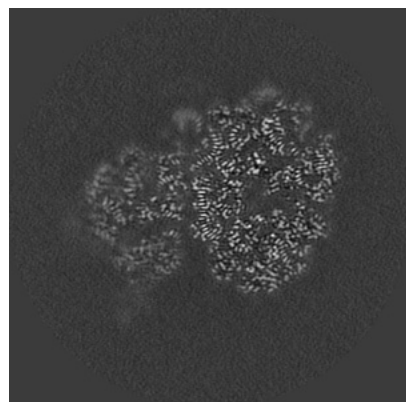


Z

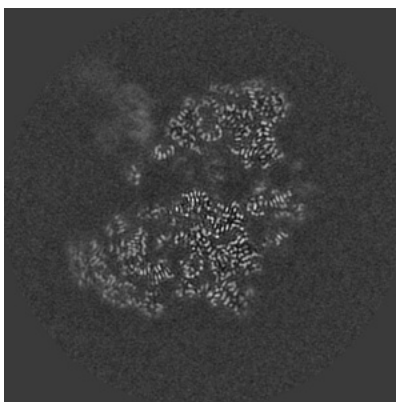
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

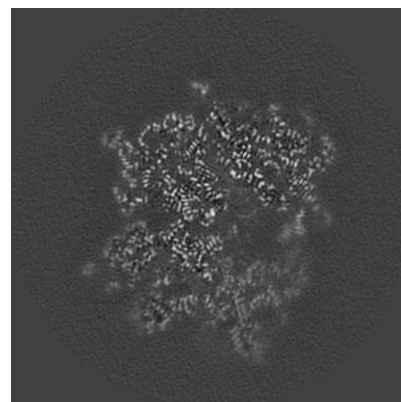
6.2.1 Primary map



X Index: 220



Y Index: 220

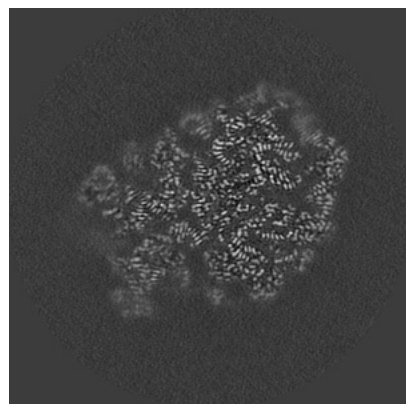


Z Index: 220

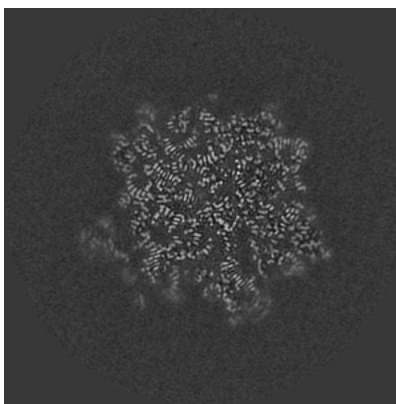
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

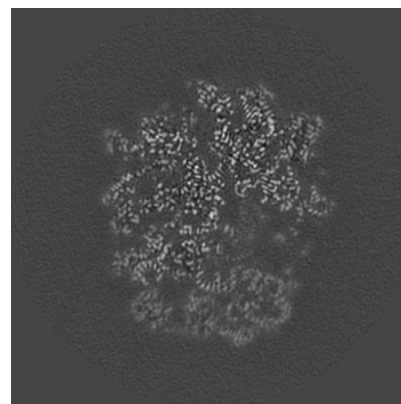
6.3.1 Primary map



X Index: 211



Y Index: 254

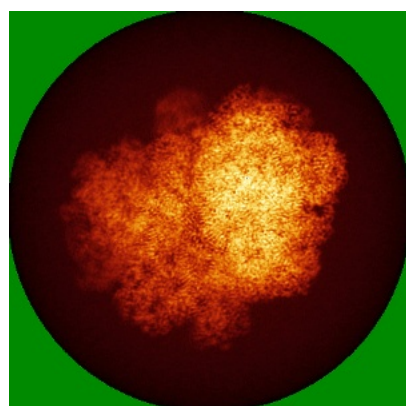


Z Index: 237

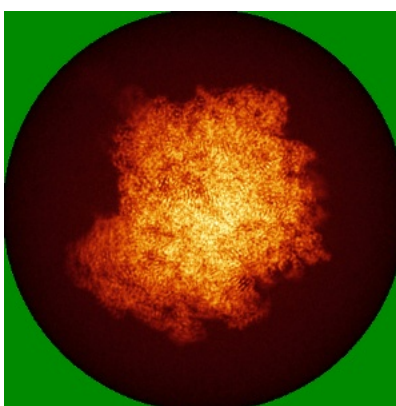
The images above show the largest variance slices of the map in three orthogonal directions.

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

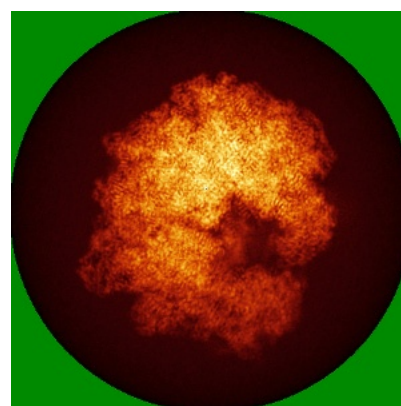
6.4.1 Primary map



X



Y



Z

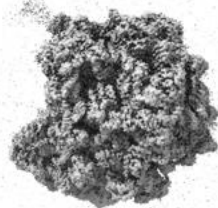
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0055. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

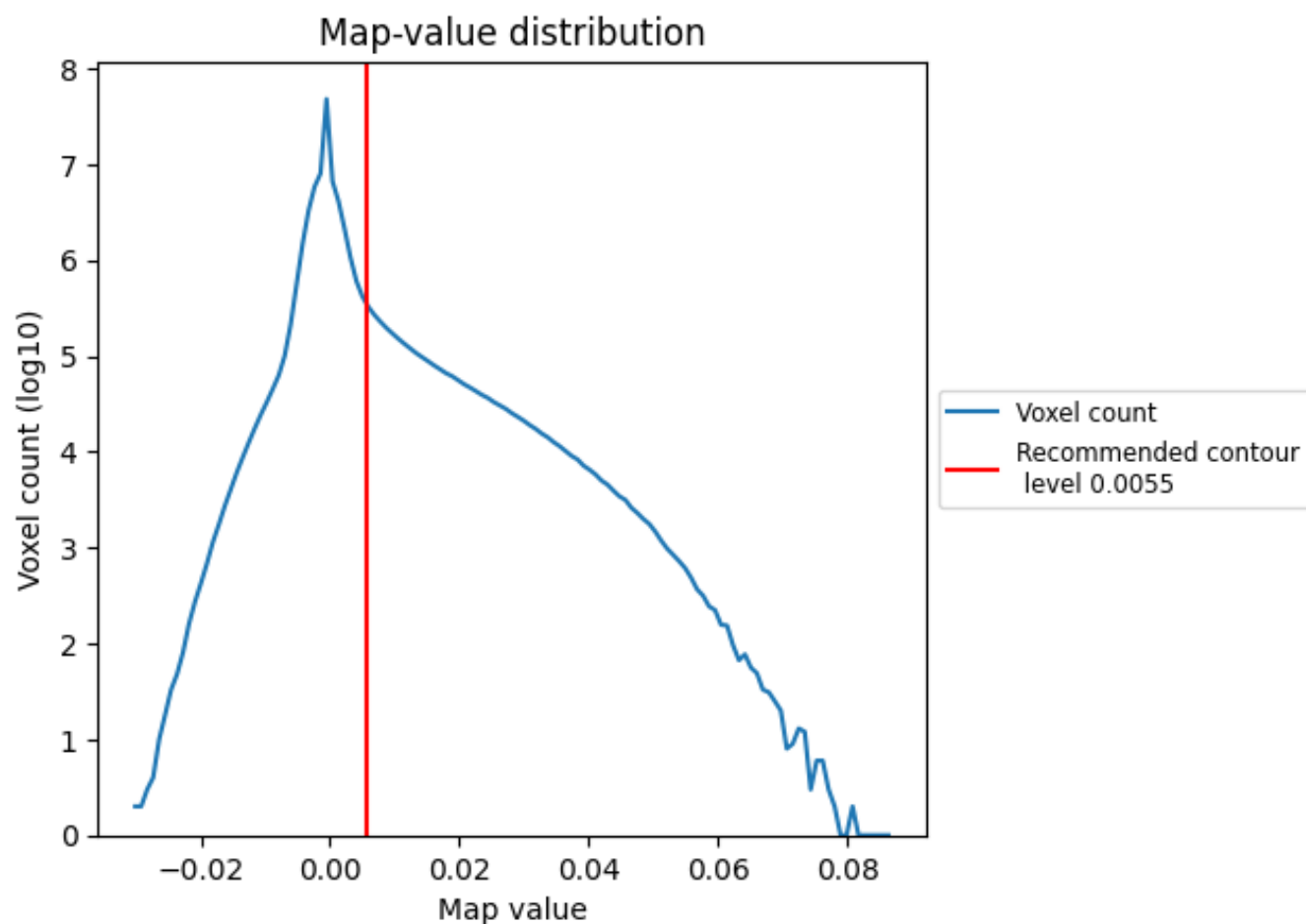
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

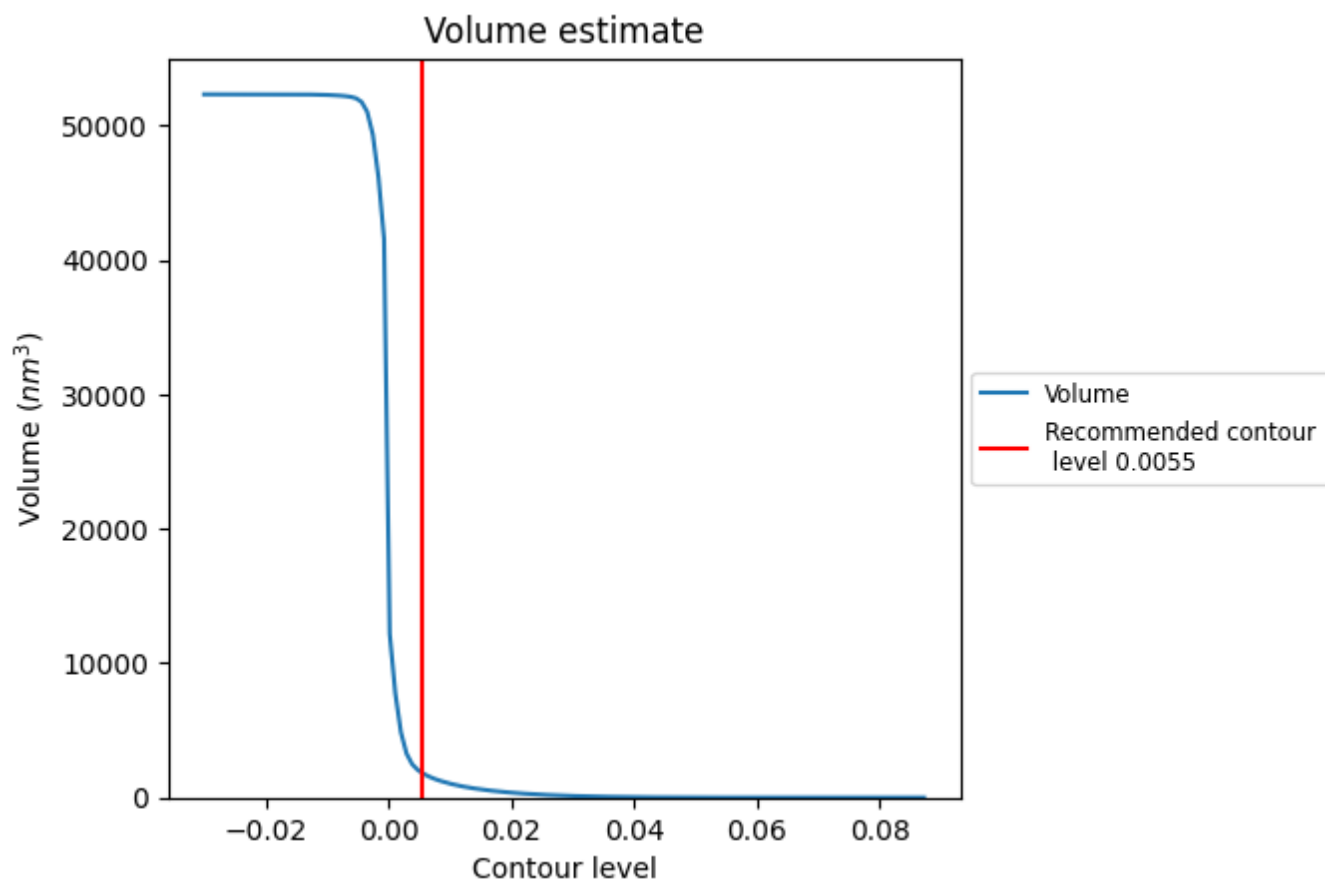
This section contains the results of statistical analysis of the map.

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.

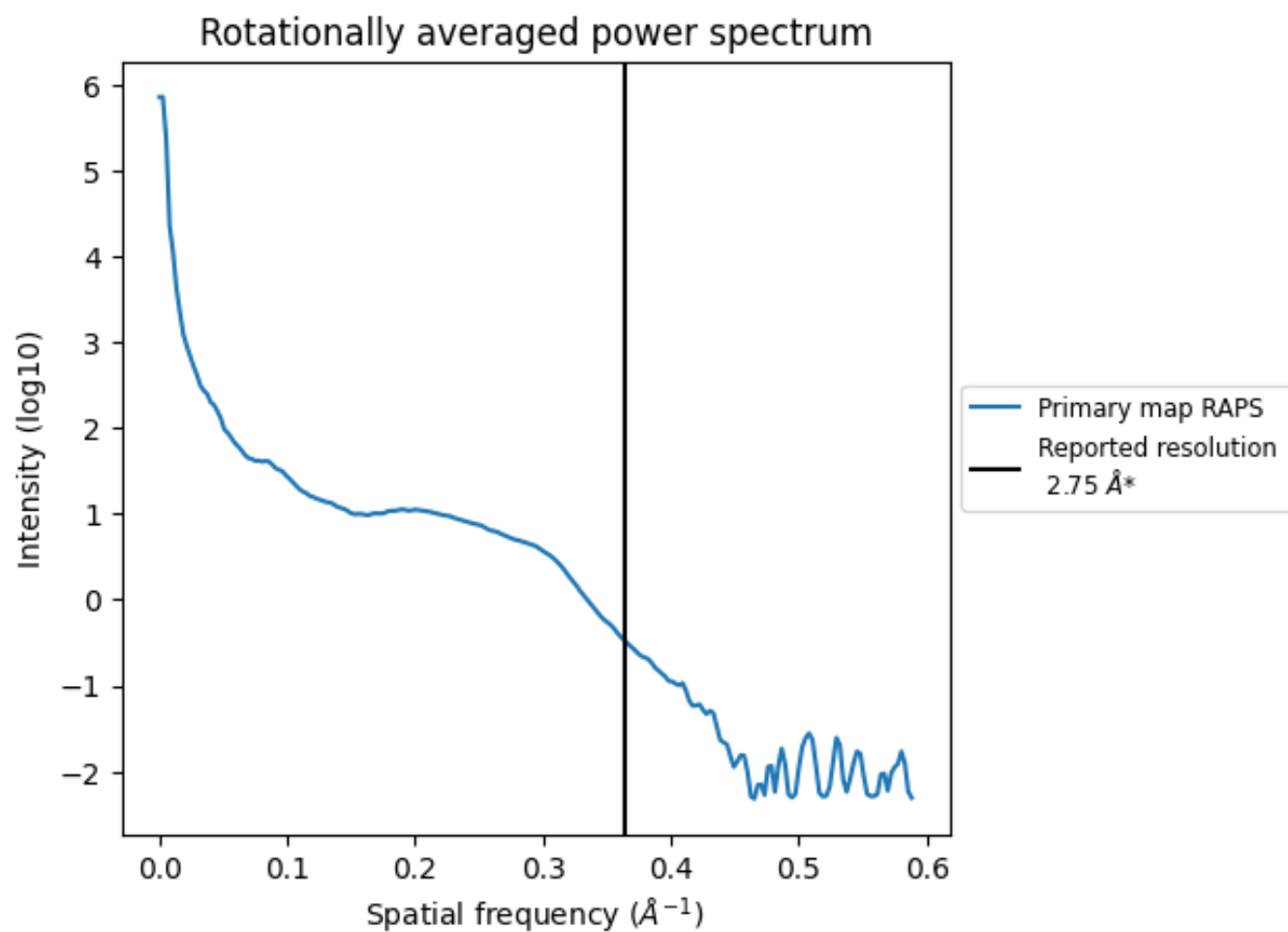
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1818 nm³; this corresponds to an approximate mass of 1643 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 0.364 Å⁻¹

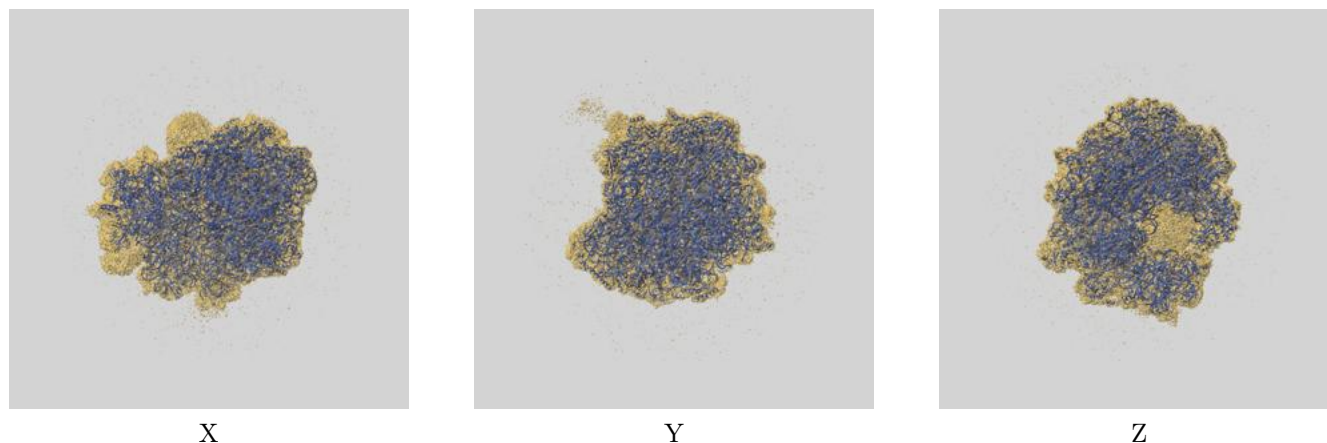
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

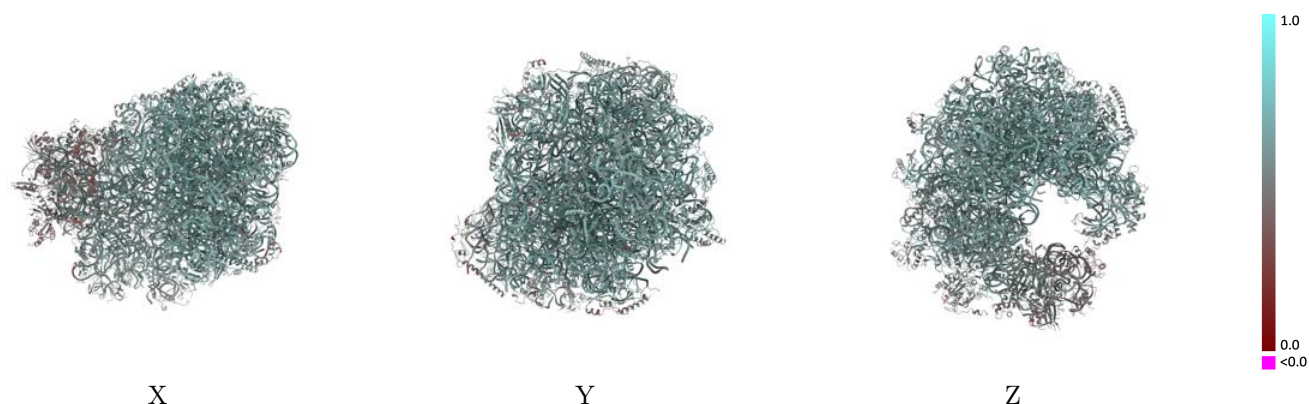
This section contains information regarding the fit between EMDB map EMD-13683 and PDB model 7PWO. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



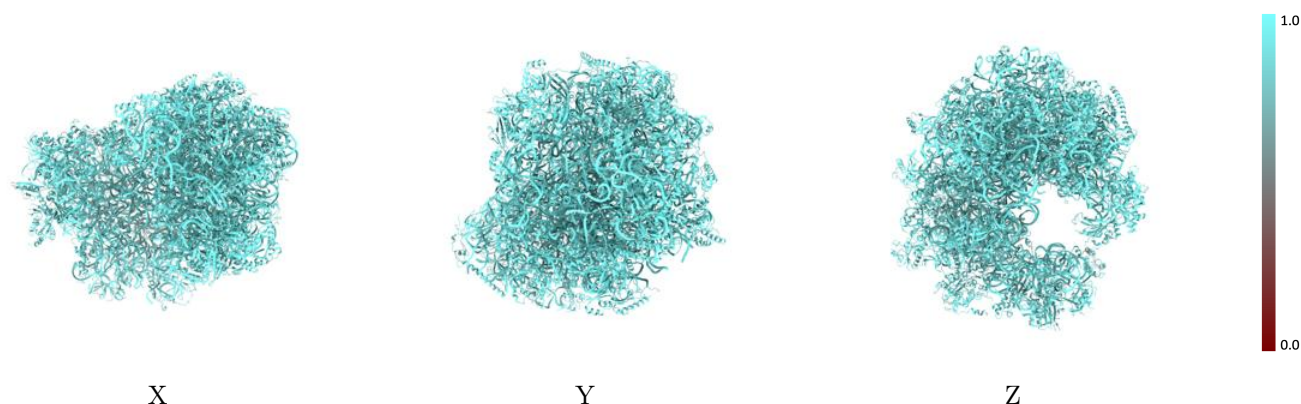
The images above show the 3D surface view of the map at the recommended contour level 0.0055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



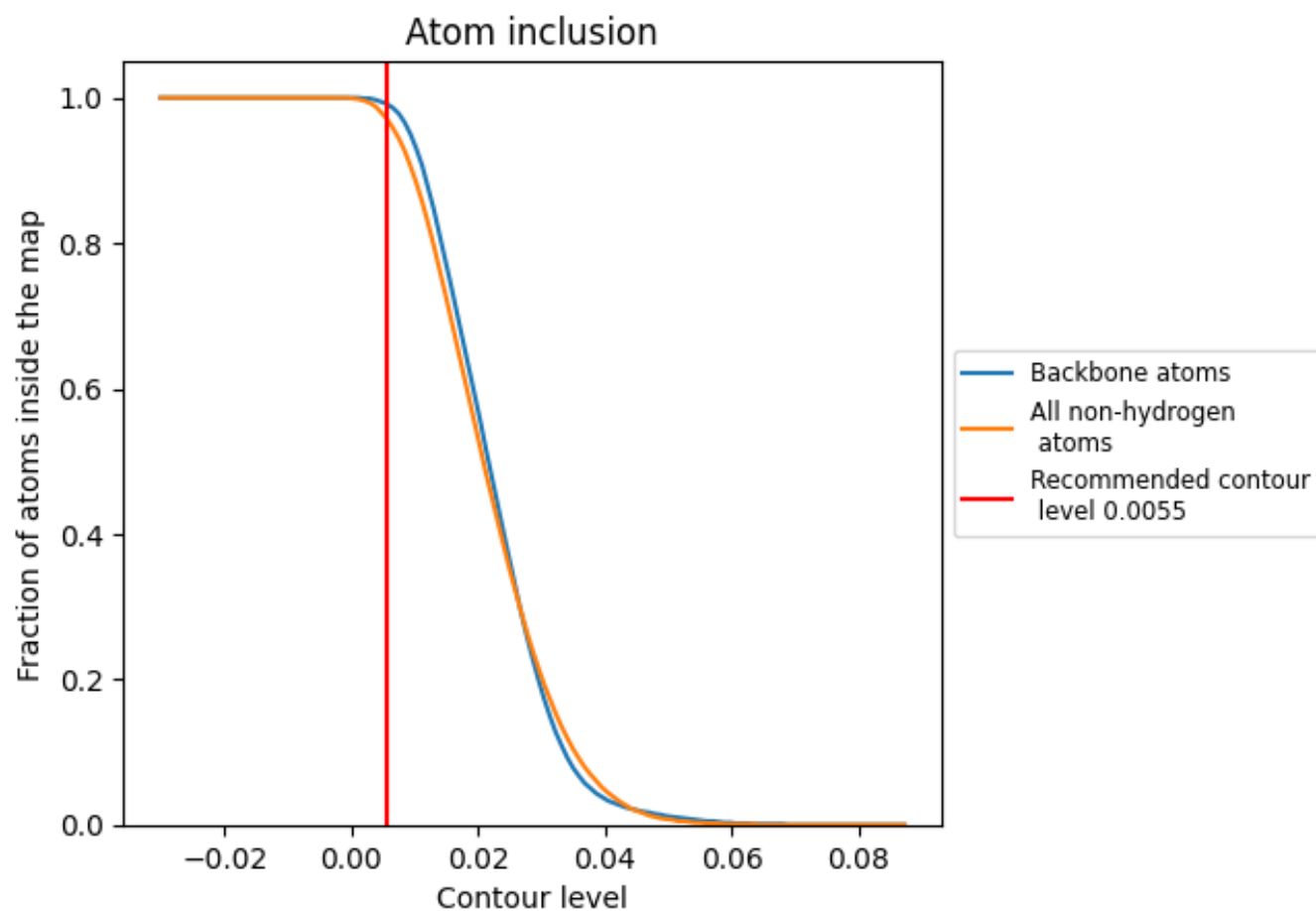
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0055).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 97% 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 (0.0055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9720	 0.5920
1	 0.9970	 0.6340
2	 0.9870	 0.5740
3	 0.9960	 0.6040
42	 0.9980	 0.6210
A1	 0.9310	 0.5090
A2	 0.9820	 0.6460
B1	 0.9560	 0.5680
B2	 0.9770	 0.6130
C1	 0.9490	 0.5640
C2	 0.9640	 0.5950
D1	 0.8850	 0.4780
D2	 0.9540	 0.5680
E	 0.9030	 0.5790
E1	 0.9430	 0.5520
F1	 0.8810	 0.4750
F2	 0.9550	 0.5930
G1	 0.9090	 0.4790
G2	 0.9550	 0.5700
H1	 0.9590	 0.5280
H2	 0.9600	 0.5790
I1	 0.9560	 0.5920
I2	 0.9510	 0.5960
J1	 0.9280	 0.5360
J2	 0.9350	 0.5310
K1	 0.8530	 0.3860
L1	 0.9420	 0.5840
L2	 0.9690	 0.6020
M2	 0.9590	 0.5640
N1	 0.9440	 0.5820
N2	 0.9870	 0.6420
O1	 0.9650	 0.5950
O2	 0.9520	 0.5890
P2	 0.9650	 0.6040
Q1	 0.8710	 0.4730



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Chain	Atom inclusion	Q-score
Q2	 0.9670	 0.6010
R1	 0.8450	 0.4340
R2	 0.9370	 0.5780
S1	 0.8360	 0.3980
S2	 0.9680	 0.6000
T1	 0.9200	 0.4740
T2	 0.9770	 0.6200
U1	 0.8810	 0.4840
U2	 0.9290	 0.5230
V1	 0.9260	 0.5240
V2	 0.9660	 0.6180
W1	 0.9530	 0.5830
W2	 0.9830	 0.6170
X1	 0.9400	 0.5680
X2	 0.9660	 0.6060
Y1	 0.9070	 0.4860
Y2	 0.9660	 0.5870
Z2	 0.9450	 0.5350
a1	 0.9590	 0.5970
a2	 0.9850	 0.6280
b1	 0.9370	 0.5380
b2	 0.9780	 0.6180
c1	 0.8810	 0.4950
c2	 0.9490	 0.5770
d1	 0.9080	 0.4680
d2	 0.9680	 0.6060
e1	 0.9390	 0.5350
e2	 0.9740	 0.6100
f2	 0.9520	 0.5860
g2	 0.9660	 0.6160
h2	 0.9380	 0.5630
i2	 0.9390	 0.5710
j2	 0.9860	 0.6420
k2	 0.9110	 0.5130
l2	 0.9740	 0.6230
m2	 0.9780	 0.6030
n1	 0.9700	 0.6280
o2	 0.9660	 0.6340
p2	 0.9740	 0.6250
w2	 0.9730	 0.5790