



## wwPDB EM Validation Summary Report ⓘ

Mar 26, 2026 – 04:06 PM UTC

PDB ID : 7OLC / pdb\_00007olc  
EMDB ID : EMD-12976  
Title : Thermophilic eukaryotic 80S ribosome at idle POST state  
Authors : Kisonaite, M.; Wild, K.; Sinning, I.  
Deposited on : 2021-05-19  
Resolution : 2.90 Å (reported)  
Based on initial model : 4V88

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

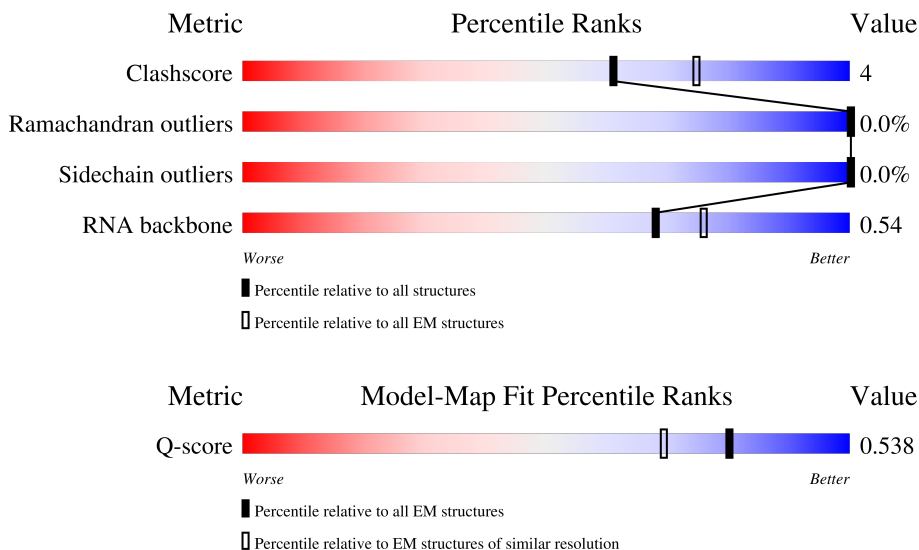
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 2.90 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.








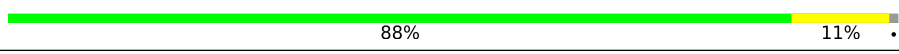
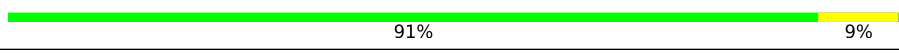
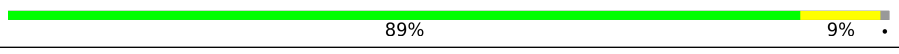

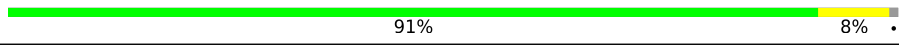




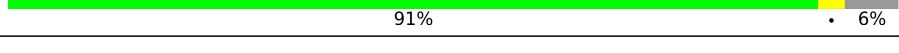

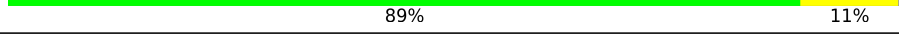

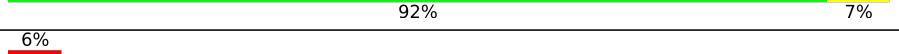

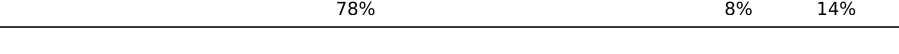
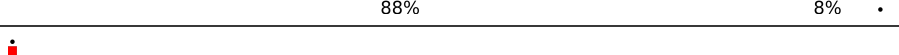
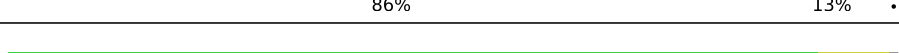
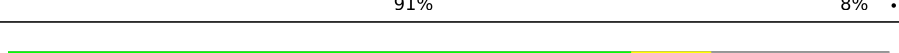

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 ( 2.40 - 3.40 )

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  $\geq 3$ , 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	1	3337	
2	2	1796	
3	3	120	











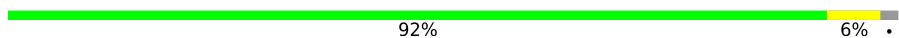













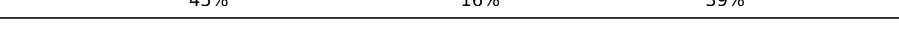
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Mol	Chain	Length	Quality of chain
4	4	156	 79% 17%
5	A	316	 13% 72% 27%
6	B	302	 8% 89%
7	C	614	 10% 10% 87%
8	LA	254	 86% 13%
9	LB	392	 88% 11%
10	LC	365	 91% 9%
11	LD	304	 89% 9%
12	LE	200	 88% 9%
13	LF	249	 91% 8%
14	LG	262	 81% 8% 10%
15	LH	192	 83% 16%
16	LI	219	 89% 10%
17	LJ	173	 78% 18%
18	LK	165	 68% 91% 6%
19	LL	213	 85% 13%
20	LM	142	 89% 11%
21	LN	203	 82% 18%
22	LO	204	 92% 7%
23	LP	187	 6% 88% 11%
24	LQ	213	 78% 8% 14%
25	LR	192	 88% 8%
26	LS	174	 86% 13%
27	LT	160	 91% 8%
28	LU	127	 70% 9% 20%

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Mol	Chain	Length	Quality of chain
29	LV	139	 89% 8%
30	LW	161	 14% 73% 10% 17%
31	LX	156	 64% 13% 22%
32	LY	138	 83% 14%
33	LZ	135	 87% 13%
34	La	149	 86% 13%
35	Lb	65	 86% 9% 5%
36	Lc	108	 80% 10% 10%
37	Ld	120	 81% 12% 7%
38	Le	131	 88% 7% 5%
39	Lf	109	 92% 6%
40	Lg	119	 86% 8% 6%
41	Lh	126	 84% 13%
42	Li	110	 80% 13% 7%
43	Lj	95	 80% 11% 9%
44	Lk	81	 79% 15% 6%
45	Ll	51	 90% 8%
46	Lm	128	 36% 5% 59%
47	Ln	25	 84% 12%
47	Lr	25	 8% 80% 16%
48	Lo	106	 90% 8%
49	Lp	92	 86% 13%
50	Lq	147	 90% 6%
51	Ls	312	 39% 45% 16% 39%
52	SA	285	 64% 9% 27%


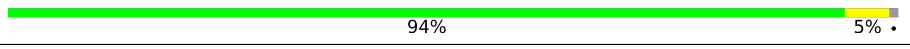


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Mol	Chain	Length	Quality of chain
53	SB	255	76% 15% 9%
54	SC	263	70% 12% 18%
55	SD	254	72% 13% 16%
56	SE	264	84% 14%
57	SF	212	6% 76% 18% 6%
58	SG	239	77% 20%
59	SH	203	78% 18%
60	SI	202	84% 15%
61	SJ	190	78% 16% 6%
62	SK	159	36% 19% 44%
63	SL	161	81% 12% 7%
64	SM	144	65% 65% 17% 18%
65	SN	151	89% 11%
66	SO	150	70% 19% 10%
67	SP	153	8% 57% 18% 25%
68	SQ	143	74% 22%
69	SR	143	71% 18% 10%
70	SS	156	52% 36% 12%
71	ST	153	70% 23% 7%
72	SU	116	8% 78% 11% 11%
73	SV	98	78% 10% 12%
74	SW	130	87% 12%
75	SX	145	83% 14%
76	SY	136	6% 79% 18%
77	SZ	99	42% 27% 30%

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Mol	Chain	Length	Quality of chain
78	Sa	119	 70% 18% 13%
79	Sb	82	 94% 5%
80	Sc	68	 79% 10% 10%
81	Sd	56	 66% 27% 7%
82	Se	62	 58% 6% 35%
83	Sf	154	 24% 39% 8% 53%

## 2 Entry composition [i](#)

There are 86 unique types of molecules in this entry. The entry contains 207344 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 RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	3191	68242	30465	12334	22252	3191	0	0

- Molecule 2 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1765	37645	16822	6706	12352	1765	0	0

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	119	2535	1132	453	831	119	0	0

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	156	3319	1484	589	1090	156	0	0

- Molecule 5 is a protein called Putative guanine nucleotide-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	A	312	2438	1534	424	468	12	0	0

- Molecule 6 is a protein called HABP4\_PA1-RBP1 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	B	32	244	145	49	50	0	0

- Molecule 7 is a protein called Ribosome-associated molecular chaperone SSB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	C	78	619	388	106	123	2	0	0

- Molecule 8 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LA	252	1925	1203	385	334	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	LB	387	3088	1964	576	535	13	0	0

- Molecule 10 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	LC	363	2758	1741	527	481	9	0	0

- Molecule 11 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	LD	300	2440	1545	431	461	3	0	0

- Molecule 12 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LE	194	1518	974	274	267	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	LF	247	2017	1294	376	344	3	0	0

- Molecule 14 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	LG	235	1900	1218	351	326	5	0	0

- Molecule 15 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	LH	191	1505	955	269	275	6	0	0

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

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Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 16 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	LI	217	1760	1109	343	299	9	0	0

- Molecule 17 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	LJ	167	1367	854	268	239	6	0	0

- Molecule 18 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	LK	155	762	452	155	155	0	0

- Molecule 19 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	LL	209	1666	1037	340	287	2	0	0

- Molecule 20 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	LM	141	1125	714	216	194	1	0	0

- Molecule 21 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	LN	202	1703	1062	360	277	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	LO	203	1613	1036	305	267	5	0	0

- Molecule 23 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	LP	186	1472	912	295	262	3	0	0

- Molecule 24 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	LQ	183	1481	935	306	238	2	0	0

- Molecule 25 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	LR	184	1506	928	324	249	5	0	0

- Molecule 26 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	LS	173	1425	917	266	238	4	0	0

- Molecule 27 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	LT	158	1266	803	246	215	2	0	0

- Molecule 28 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LU	101	819	532	142	144	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LV	135	994	633	185	169	7	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LW	133	1075	667	221	185	2	0	0

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	?	-	LYS	deletion	UNP G0S1P9
LW	?	-	VAL	deletion	UNP G0S1P9
LW	?	-	ARG	deletion	UNP G0S1P9
LW	?	-	PHE	deletion	UNP G0S1P9
LW	?	-	PRO	deletion	UNP G0S1P9
LW	?	-	ILE	deletion	UNP G0S1P9
LW	?	-	SER	deletion	UNP G0S1P9
LW	?	-	HIS	deletion	UNP G0S1P9
LW	?	-	GLU	deletion	UNP G0S1P9
LW	?	-	GLY	deletion	UNP G0S1P9
LW	?	-	ASP	deletion	UNP G0S1P9
LW	?	-	ASN	deletion	UNP G0S1P9
LW	?	-	GLY	deletion	UNP G0S1P9
LW	?	-	ASP	deletion	UNP G0S1P9
LW	?	-	ILE	deletion	UNP G0S1P9
LW	?	-	SER	deletion	UNP G0S1P9
LW	?	-	HIS	deletion	UNP G0S1P9
LW	?	-	PRO	deletion	UNP G0S1P9
LW	?	-	GLU	deletion	UNP G0S1P9
LW	?	-	GLU	deletion	UNP G0S1P9
LW	?	-	ILE	deletion	UNP G0S1P9
LW	?	-	ARG	deletion	UNP G0S1P9
LW	?	-	THR	deletion	UNP G0S1P9
LW	?	-	GLY	deletion	UNP G0S1P9
LW	?	-	ARG	deletion	UNP G0S1P9

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Chain	Residue	Modelled	Actual	Comment	Reference
LW	?	-	ARG	deletion	UNP G0S1P9
LW	?	-	LYS	deletion	UNP G0S1P9
LW	?	-	ILE	deletion	UNP G0S1P9
LW	?	-	ALA	deletion	UNP G0S1P9
LW	?	-	PRO	deletion	UNP G0S1P9
LW	?	-	ALA	deletion	UNP G0S1P9
LW	?	-	THR	deletion	UNP G0S1P9
LW	?	-	ARG	deletion	UNP G0S1P9
LW	?	-	GLN	deletion	UNP G0S1P9
LW	?	-	LEU	deletion	UNP G0S1P9
LW	?	-	ARG	deletion	UNP G0S1P9
LW	?	-	ALA	deletion	UNP G0S1P9
LW	?	-	GLU	deletion	UNP G0S1P9
LW	?	-	VAL	deletion	UNP G0S1P9
LW	?	-	GLN	deletion	UNP G0S1P9
LW	?	-	LYS	deletion	UNP G0S1P9
LW	?	-	THR	deletion	UNP G0S1P9
LW	?	-	SER	deletion	UNP G0S1P9
LW	?	-	MET	deletion	UNP G0S1P9

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	LX	121	965	620	175	170	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	LY	134	1065	664	215	184	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	LZ	135	1111	713	207	187	4	0	0

- Molecule 34 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	La	148	1180	745	239	194	2	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
La	1	MET	TYR	conflict	UNP G0SGT6
La	3	THR	-	insertion	UNP G0SGT6
La	4	ARG	VAL	conflict	UNP G0SGT6
La	6	SER	GLN	conflict	UNP G0SGT6
La	7	LYS	ASP	conflict	UNP G0SGT6
La	8	THR	LYS	conflict	UNP G0SGT6
La	9	ARG	LYS	conflict	UNP G0SGT6
La	10	LYS	ALA	conflict	UNP G0SGT6
La	11	HIS	PRO	conflict	UNP G0SGT6
La	13	GLY	PRO	conflict	UNP G0SGT6
La	14	HIS	ARG	conflict	UNP G0SGT6
La	16	SER	-	insertion	UNP G0SGT6
La	17	ALA	-	insertion	UNP G0SGT6
La	18	GLY	-	insertion	UNP G0SGT6
La	19	LYS	ARG	conflict	UNP G0SGT6
La	20	GLY	ARG	conflict	UNP G0SGT6

- Molecule 35 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	Lb	62	508	310	112	86		0	0

- Molecule 36 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	Lc	97	722	458	125	134	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	Ld	112	911	575	178	157	1	0	0

- Molecule 38 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Le	124	Total	C	N	O	S	0	0
			1001	629	205	161	6		

- Molecule 39 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lf	107	Total	C	N	O	S	0	0
			853	540	170	142	1		

- Molecule 40 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lg	112	Total	C	N	O	S	0	0
			891	554	181	152	4		

- Molecule 41 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Lh	122	Total	C	N	O	0	0
			1003	637	198	168		

- Molecule 42 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Li	102	Total	C	N	O	S	0	0
			836	515	184	136	1		

- Molecule 43 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lj	86	Total	C	N	O	S	0	0
			684	418	152	109	5		

- Molecule 44 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	?	-	LYS	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89
Lk	?	-	ILE	deletion	UNP G0SG89
Lk	?	-	ALA	deletion	UNP G0SG89
Lk	?	-	PHE	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	PRO	deletion	UNP G0SG89
Lk	?	-	LEU	deletion	UNP G0SG89
Lk	?	-	THR	deletion	UNP G0SG89
Lk	?	-	ALA	deletion	UNP G0SG89

- Molecule 45 is a protein called eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	Ll	50	435	275	97	63	0	0

- Molecule 46 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Lm	52	418	261	86	65	6	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	1	MET	SER	conflict	UNP G0S8G4
Lm	2	GLN	ARG	conflict	UNP G0S8G4

- Molecule 47 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	Ln	24	224	136	61	26	1	0	0
47	Lr	24	224	136	61	26	1	0	0

- Molecule 48 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lo	104	Total	C	N	O	S	0	0
			822	520	161	136	5		

- Molecule 49 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lp	91	Total	C	N	O	S	0	0
			697	430	138	123	6		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Lq	141	Total	C	N	O	0	0
			1083	678	215	190		

- Molecule 51 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ls	189	Total	C	N	O	S	0	0
			1449	927	250	265	7		

- Molecule 52 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SA	208	Total	C	N	O	S	0	0
			1641	1051	289	295	6		

- Molecule 53 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SB	232	Total	C	N	O	S	0	0
			1871	1190	351	325	5		

- Molecule 54 is a protein called 40S ribosomal protein S2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	216	Total	C	N	O	S	0	0
			1672	1074	294	301	3		

- Molecule 55 is a protein called 40S ribosomal protein S3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SD	214	Total	C	N	O	S	0	0
			1688	1068	307	305	8		

- Molecule 56 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SE	261	Total	C	N	O	S	0	0
			2072	1314	389	362	7		

- Molecule 57 is a protein called 40S ribosomal protein s5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SF	199	Total	C	N	O	S	0	0
			1557	971	294	285	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SG	232	Total	C	N	O	S	0	0
			1875	1171	376	323	5		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	SH	195	Total	C	N	O	0	0
			1562	983	300	279		

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SI	201	Total	C	N	O	S	0	0
			1621	1009	330	281	1		

- Molecule 61 is a protein called 40S ribosomal protein s9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SJ	179	Total	C	N	O	S	0	0
			1466	933	290	241	2		

- Molecule 62 is a protein called 40S ribosomal protein s10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SK	89	742	487	124	129	2	0	0

- Molecule 63 is a protein called 40S ribosomal protein S11-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	SL	150	1222	780	236	201	5	0	0

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	SM	118	923	577	167	171	8	0	0

- Molecule 65 is a protein called 40S ribosomal protein S13-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	SN	150	1182	756	220	205	1	0	0

- Molecule 66 is a protein called 40S ribosomal protein S14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	SO	135	1002	614	199	184	5	0	0

- Molecule 67 is a protein called 40S ribosomal protein s15-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	SP	115	917	583	172	159	3	0	0

- Molecule 68 is a protein called 40S ribosomal protein S16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	SQ	138	1081	693	202	184	2	0	0

- Molecule 69 is a protein called 40S ribosomal protein S17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	SR	128	1045	657	190	195	3	0	0

- Molecule 70 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	SS	137	1118	699	222	196	1	0	0

- Molecule 71 is a protein called 40S ribosomal protein S19-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	ST	142	1117	694	221	201	1	0	0

- Molecule 72 is a protein called 40S ribosomal protein S20-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	SU	103	819	517	150	148	4	0	0

- Molecule 73 is a protein called 40S ribosomal protein S21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	SV	86	664	408	124	128	4	0	0

- Molecule 74 is a protein called 40S ribosomal protein S22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SW	129	1037	659	195	178	5	0	0

- Molecule 75 is a protein called 40S ribosomal protein s23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	SX	142	1099	694	215	188	2	0	0

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SY	132	Total	C	N	O	S	0	0
			1061	668	209	182	2		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	69	Total	C	N	O	S	0	0
			546	345	101	98	2		

- Molecule 78 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sa	104	Total	C	N	O	S	0	0
			839	518	177	137	7		

- Molecule 79 is a protein called Ribosomal protein s27-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sb	81	Total	C	N	O	S	0	0
			611	386	111	107	7		

- Molecule 80 is a protein called 40S ribosomal protein S28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sc	61	Total	C	N	O	S	0	0
			484	298	97	88	1		

- Molecule 81 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sd	52	Total	C	N	O	S	0	0
			419	261	84	70	4		

- Molecule 82 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	Se	40	Total	C	N	O	0	0
			322	202	67	53		

- Molecule 83 is a protein called 40S ribosomal protein S27a-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sf	73	Total	C	N	O	S	0	0
			604	382	115	101	6		

- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
84	1	415	Total	Mg	0
			415	415	
84	2	121	Total	Mg	0
			121	121	
84	3	8	Total	Mg	0
			8	8	
84	4	11	Total	Mg	0
			11	11	
84	LA	1	Total	Mg	0
			1	1	
84	LB	1	Total	Mg	0
			1	1	
84	LI	1	Total	Mg	0
			1	1	
84	LN	3	Total	Mg	0
			3	3	
84	LP	1	Total	Mg	0
			1	1	
84	LT	2	Total	Mg	0
			2	2	
84	LV	1	Total	Mg	0
			1	1	
84	Lb	1	Total	Mg	0
			1	1	
84	Lo	1	Total	Mg	0
			1	1	
84	SN	1	Total	Mg	0
			1	1	
84	SO	1	Total	Mg	0
			1	1	
84	SQ	1	Total	Mg	0
			1	1	
84	SX	1	Total	Mg	0
			1	1	

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	Lg	1	Total 1	Zn 1	0
85	Lj	1	Total 1	Zn 1	0
85	Lm	1	Total 1	Zn 1	0
85	Lo	1	Total 1	Zn 1	0
85	Lp	1	Total 1	Zn 1	0
85	Sa	1	Total 1	Zn 1	0
85	Sb	1	Total 1	Zn 1	0
85	Sd	1	Total 1	Zn 1	0

- Molecule 86 is water.

Mol	Chain	Residues	Atoms		AltConf
86	1	748	Total 748	O 748	0
86	2	136	Total 136	O 136	0
86	4	20	Total 20	O 20	0
86	LB	3	Total 3	O 3	0
86	LC	3	Total 3	O 3	0
86	LD	1	Total 1	O 1	0
86	LN	6	Total 6	O 6	0
86	LO	5	Total 5	O 5	0
86	LP	2	Total 2	O 2	0
86	LQ	1	Total 1	O 1	0
86	LT	4	Total 4	O 4	0
86	LW	4	Total 4	O 4	0

*Continued on next page...*

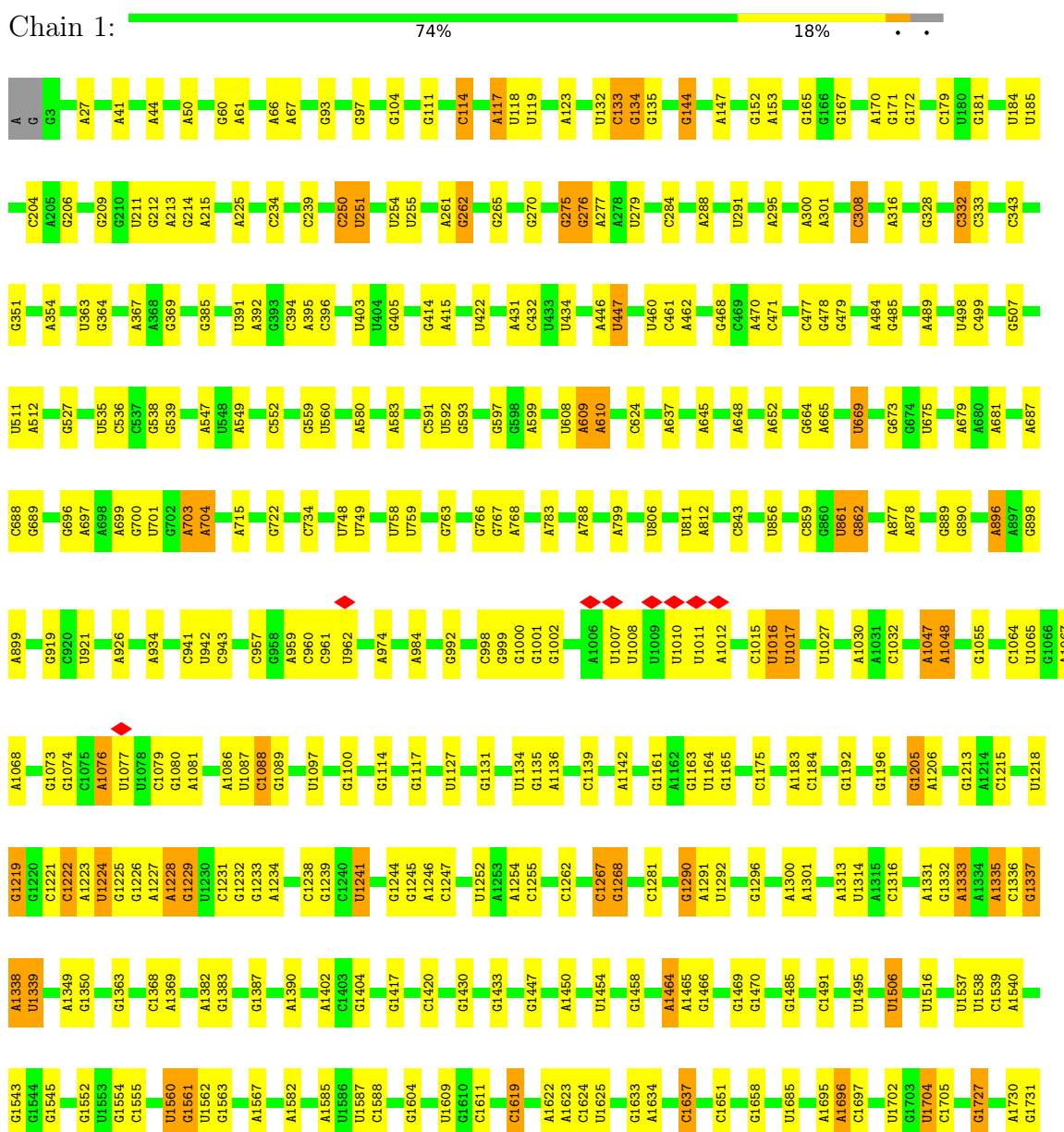
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
86	Lb	1	Total 1	O 1	0
86	Ld	1	Total 1	O 1	0
86	Le	4	Total 4	O 4	0
86	Lj	1	Total 1	O 1	0
86	SL	2	Total 2	O 2	0
86	SN	2	Total 2	O 2	0
86	Sa	1	Total 1	O 1	0

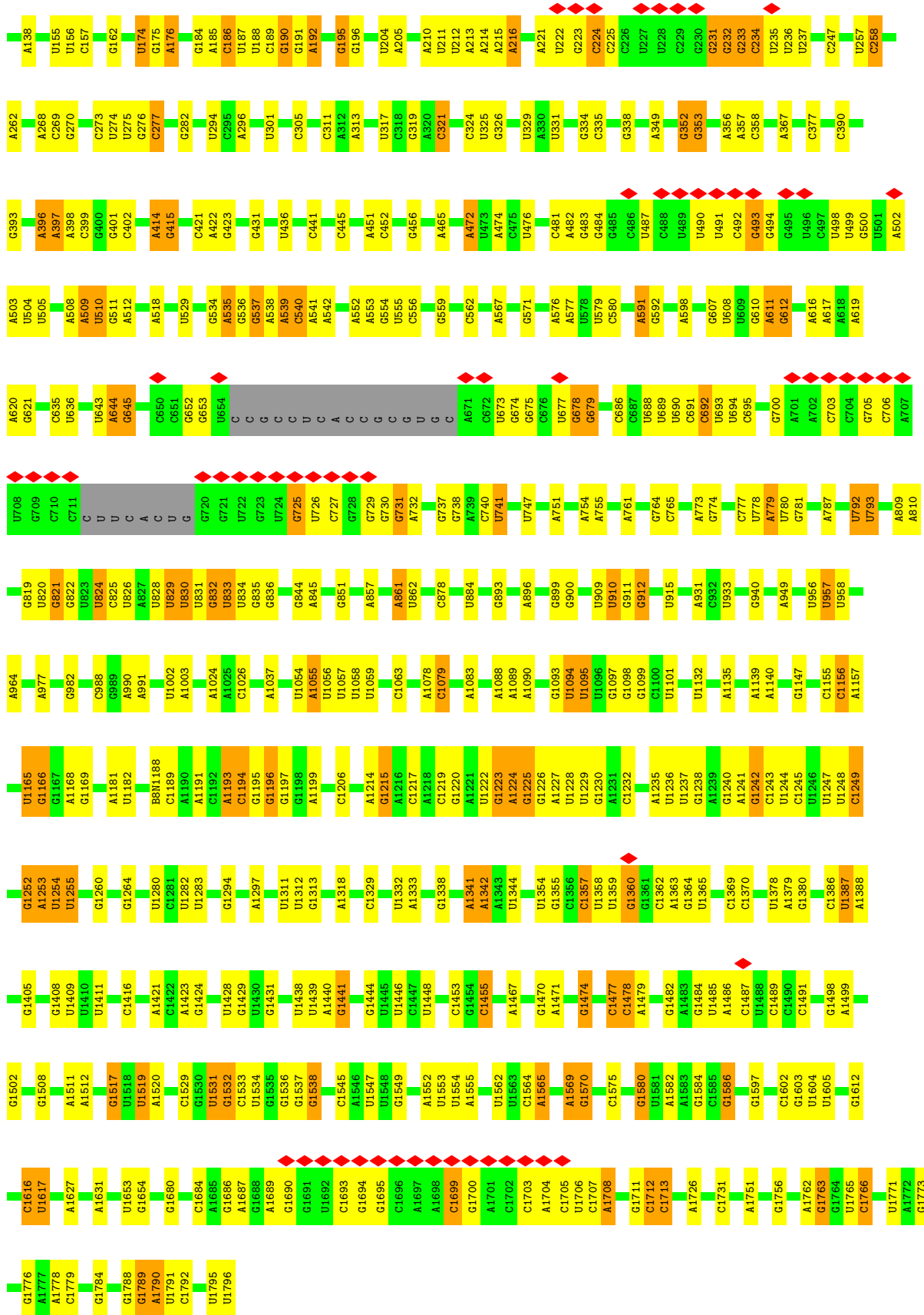
### 3 Residue-property plots

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

- Molecule 1: 26S rRNA

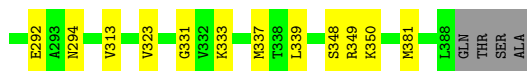












- Molecule 10: 60S ribosomal protein L4-like protein

Chain LC: 91% 9%



- Molecule 11: 60S ribosomal protein l5-like protein

Chain LD: 89% 9%



GLU

- Molecule 12: 60S ribosomal protein L6

Chain LE: 88% 9%



- Molecule 13: 60S ribosomal protein l7-like protein

Chain LF: 91% 8%



- Molecule 14: 60S ribosomal protein L8

Chain LG: 81% 8% 10%

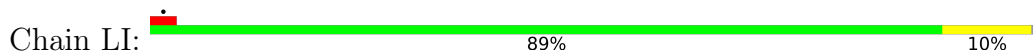


- Molecule 15: 60S ribosomal protein l9-like protein

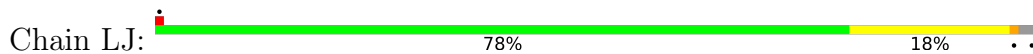
Chain LH: 83% 16%



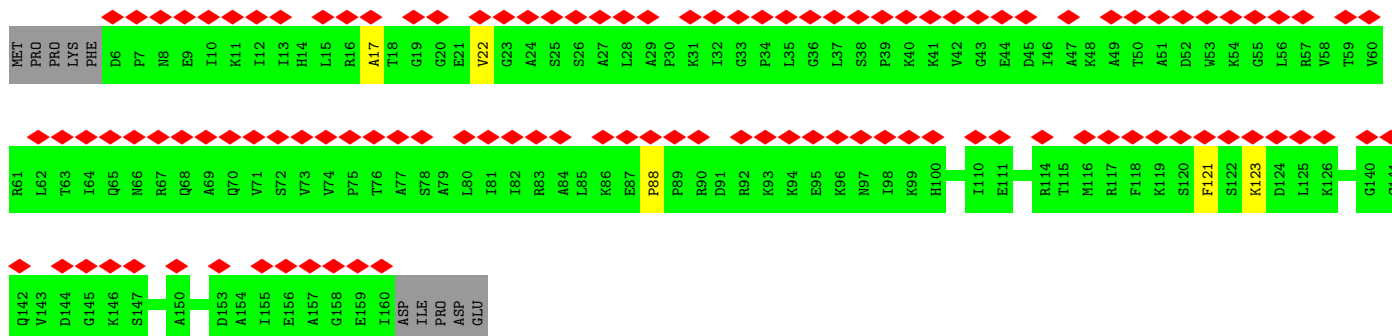
- Molecule 16: 60S ribosomal protein L10-like protein



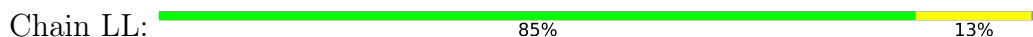
- Molecule 17: Putative ribosomal protein



- Molecule 18: 60S ribosomal protein L12-like protein



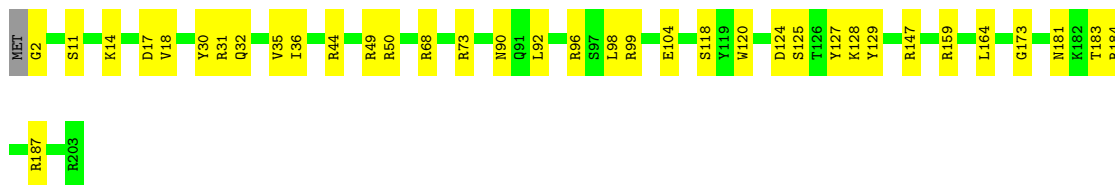
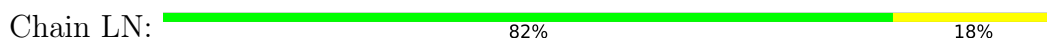
- Molecule 19: 60S ribosomal protein L13



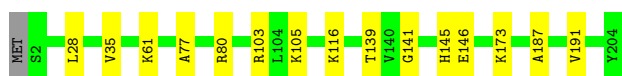
- Molecule 20: 60S ribosomal protein L14-like protein



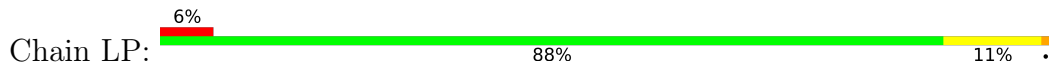
• Molecule 21: Ribosomal protein L15



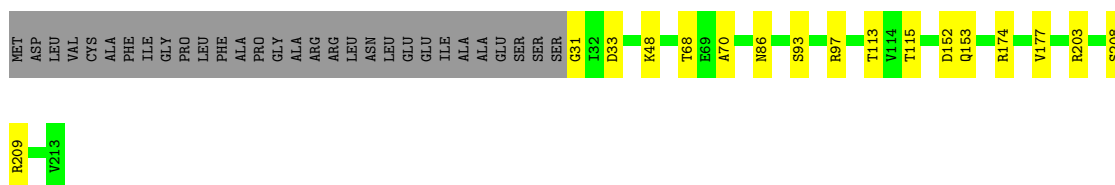
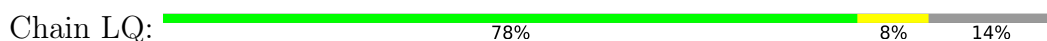
• Molecule 22: 60S ribosomal protein L16-like protein



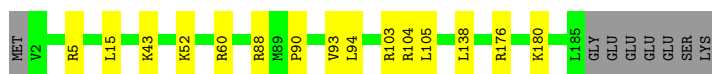
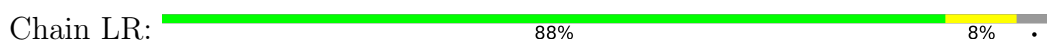
• Molecule 23: 60S ribosomal protein l17-like protein



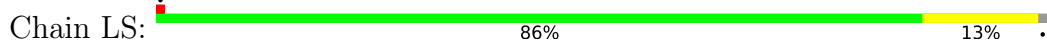
• Molecule 24: Ribosomal protein L18-like protein



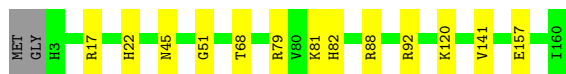
• Molecule 25: Ribosomal protein L19



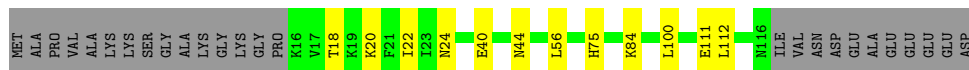
• Molecule 26: 60S ribosomal protein L20



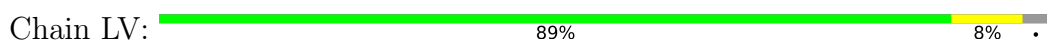
• Molecule 27: 60S ribosomal protein l21-like protein



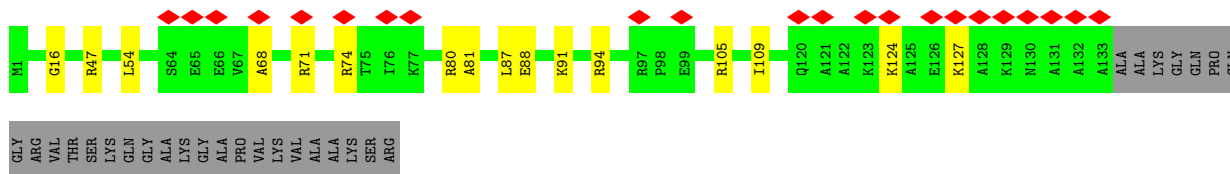
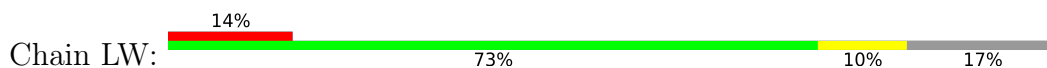
• Molecule 28: 60S ribosomal protein L22-like protein



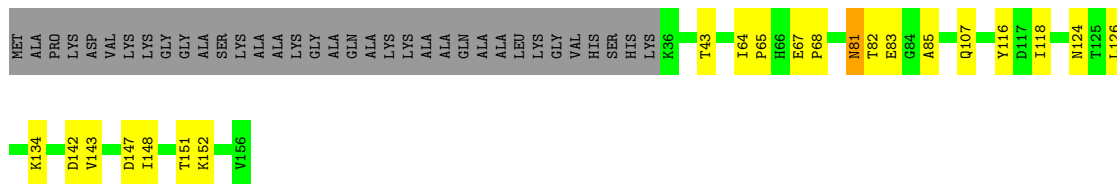
• Molecule 29: 60S ribosomal protein l23-like protein



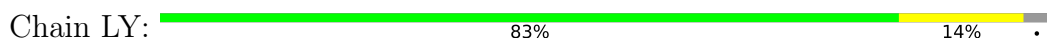
• Molecule 30: 60S ribosomal protein L24-like protein




• Molecule 31: 60S ribosomal protein L25-like protein



• Molecule 32: 60S ribosomal protein L26-like protein




• Molecule 33: 60S ribosomal protein L27

Chain LZ:  87% 13%




- Molecule 34: 60S ribosomal protein L28-like protein

Chain La:  86% 13%




- Molecule 35: 60S ribosomal protein L29

Chain Lb:  86% 9% 5%




- Molecule 36: 60S ribosomal protein l30-like protein

Chain Lc:  80% 10% 10%




- Molecule 37: Putative 60S ribosomal protein

Chain Ld:  81% 12% 7%



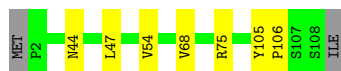
- Molecule 38: 60S ribosomal protein L32-like protein

Chain Le:  88% 7% 5%



- Molecule 39: 60S ribosomal protein l33-like protein

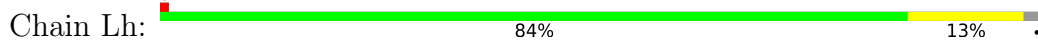
Chain Lf:  92% 6%



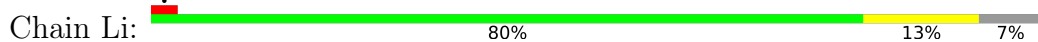
- Molecule 40: Ribosomal protein l34-like protein



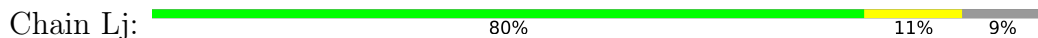
- Molecule 41: Dolichyl-diphosphooligosaccharide--protein glycotransferase



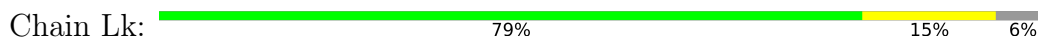
- Molecule 42: 60S ribosomal protein L36



- Molecule 43: Ribosomal protein L37



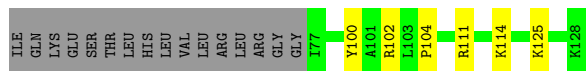
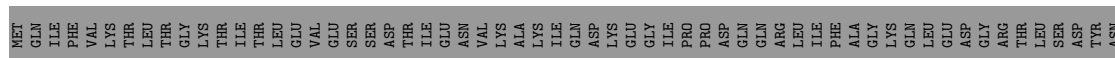
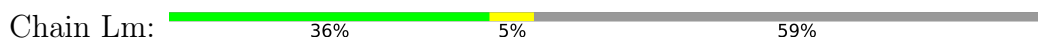
- Molecule 44: 60S ribosomal protein L38-like protein



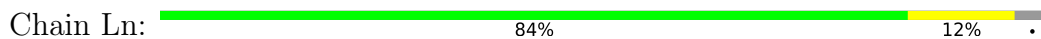
- Molecule 45: eL39



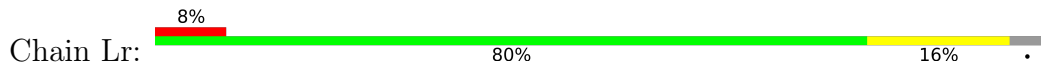
- Molecule 46: Ubiquitin



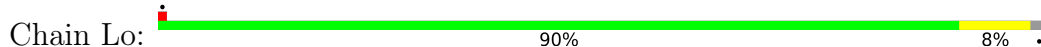
- Molecule 47: 60S ribosomal protein L41-A



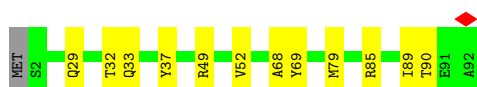
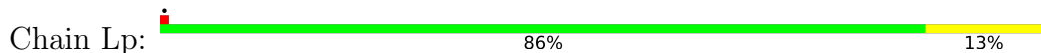
- Molecule 47: 60S ribosomal protein L41-A



- Molecule 48: 60S ribosomal protein L44-like protein



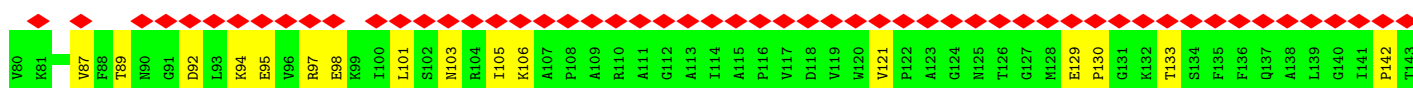
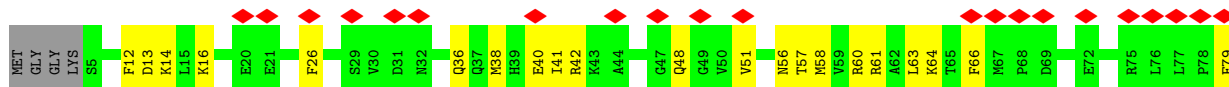
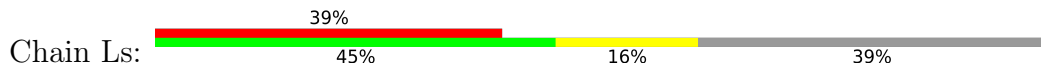
- Molecule 49: 60S ribosomal protein L43-like protein

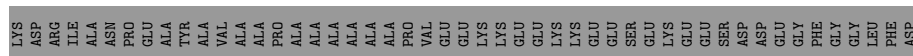
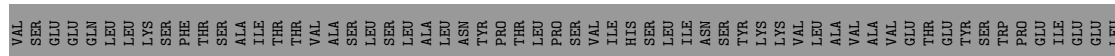


- Molecule 50: Putative 60S ribosomal protein

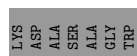


- Molecule 51: 60S acidic ribosomal protein P0

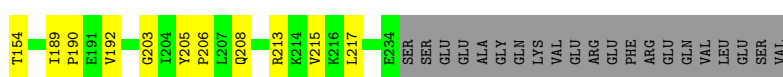
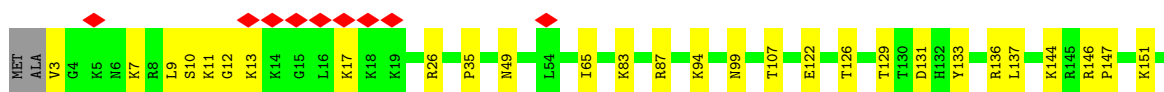
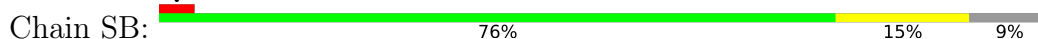




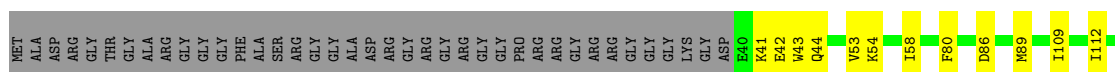
• Molecule 52: 40S ribosomal protein S0



• Molecule 53: 40S ribosomal protein S1



• Molecule 54: 40S ribosomal protein S2-like protein



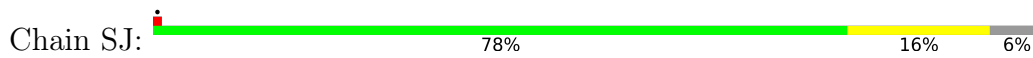
• Molecule 55: 40S ribosomal protein S3-like protein







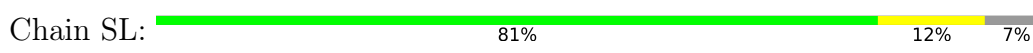
• Molecule 61: 40S ribosomal protein s9-like protein



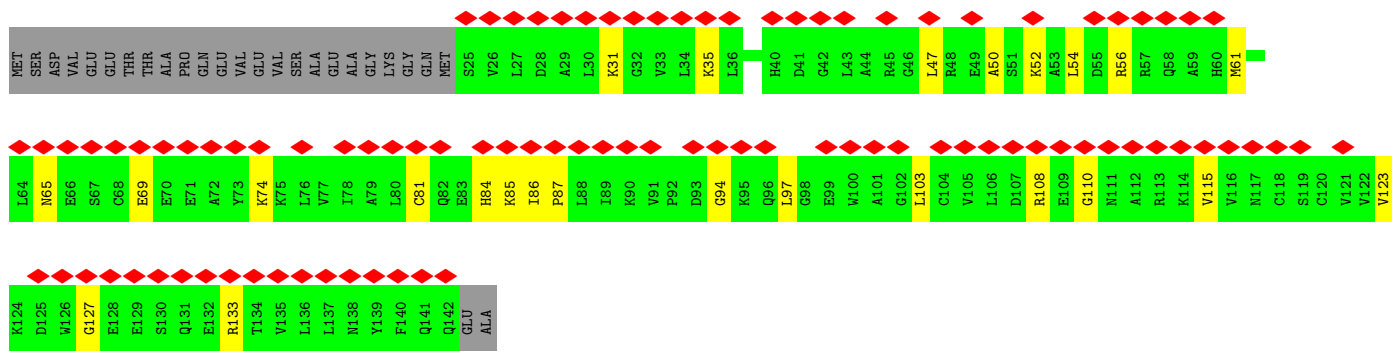
• Molecule 62: 40S ribosomal protein s10-like protein




• Molecule 63: 40S ribosomal protein S11-like protein



• Molecule 64: 40S ribosomal protein S12



• Molecule 65: 40S ribosomal protein S13-like protein

Chain SN:  89% 11%



- Molecule 66: 40S ribosomal protein S14-like protein

Chain SO:  70% 19% 10%




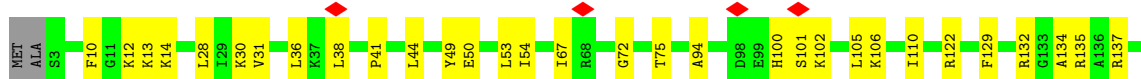
- Molecule 67: 40S ribosomal protein s15-like protein

Chain SP:  8% 57% 18% 25%



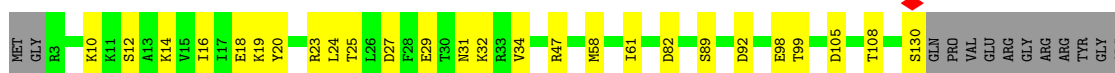
- Molecule 68: 40S ribosomal protein S16-like protein

Chain SQ:  74% 22%



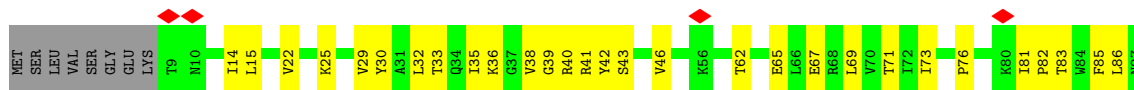
- Molecule 69: 40S ribosomal protein S17-like protein

Chain SR:  71% 18% 10%

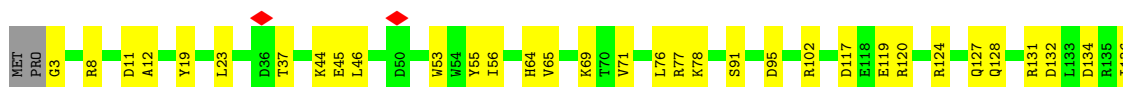


- Molecule 70: Putative ribosomal protein

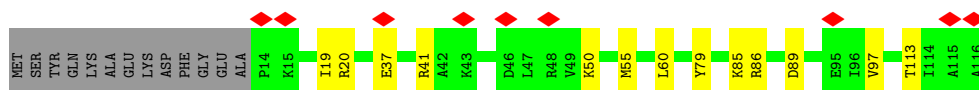
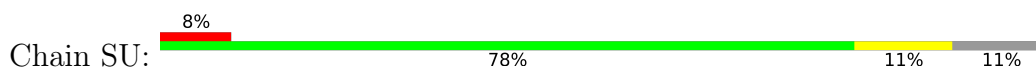
Chain SS:  52% 36% 12%



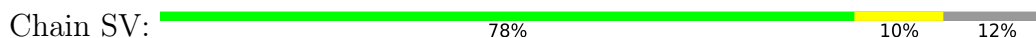
- Molecule 71: 40S ribosomal protein S19-like protein



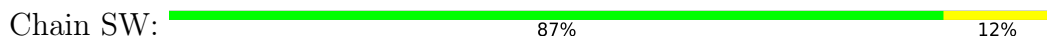
- Molecule 72: 40S ribosomal protein S20-like protein



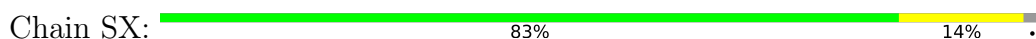
- Molecule 73: 40S ribosomal protein S21-like protein



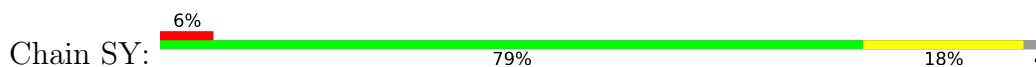
- Molecule 74: 40S ribosomal protein S22-like protein



- Molecule 75: 40S ribosomal protein s23-like protein

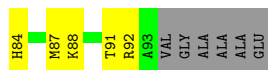


- Molecule 76: 40S ribosomal protein S24





• Molecule 77: 40S ribosomal protein S25



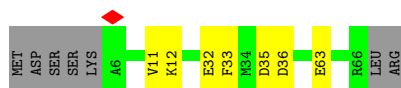
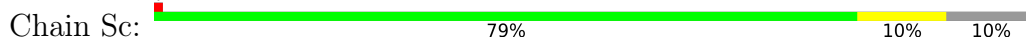
• Molecule 78: 40S ribosomal protein S26



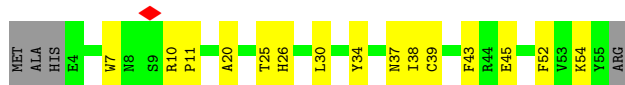
• Molecule 79: Ribosomal protein s27-like protein



• Molecule 80: 40S ribosomal protein S28-like protein



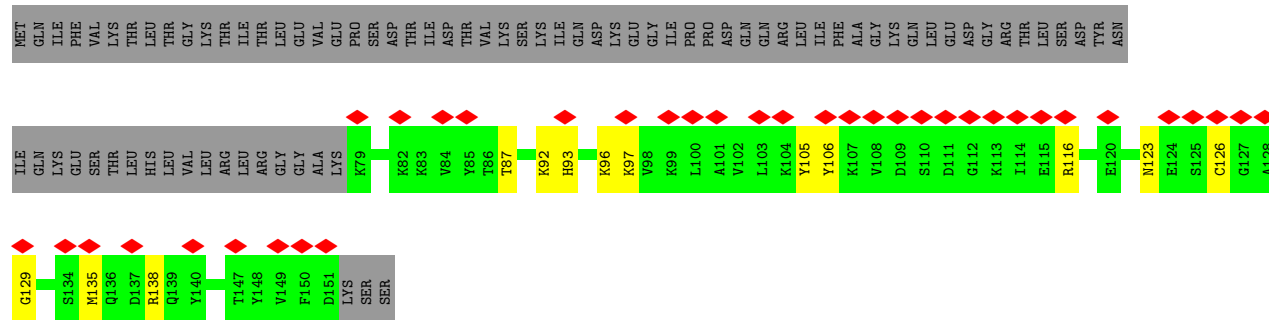
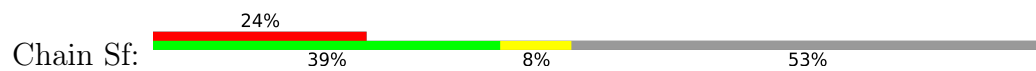
• Molecule 81: uS14



• Molecule 82: 40S ribosomal protein S30



• Molecule 83: 40S ribosomal protein S27a-like protein



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	279818	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 ( $e^-/\text{\AA}^2$ )	32.51	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	18.276	Depositor
Minimum map value	-8.430	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.534	Depositor
Recommended contour level	1.3	Depositor
Map size (Å)	534.60004, 534.60004, 534.60004	wwPDB
Map dimensions	486, 486, 486	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: MG, OMG, B8N, SAC, 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	1	0.17	0/76339	0.21	0/119028
2	2	0.13	0/42072	0.20	0/65562
3	3	0.15	0/2833	0.18	0/4413
4	4	0.15	0/3710	0.17	0/5778
5	A	0.09	0/2495	0.28	0/3390
6	B	0.15	0/243	0.36	0/316
7	C	0.09	0/622	0.25	0/827
8	LA	0.18	0/1964	0.32	0/2641
9	LB	0.17	0/3156	0.33	0/4238
10	LC	0.15	0/2815	0.28	0/3795
11	LD	0.14	0/2487	0.28	0/3341
12	LE	0.12	0/1547	0.29	0/2081
13	LF	0.15	0/2055	0.28	0/2758
14	LG	0.13	0/1929	0.25	0/2579
15	LH	0.15	0/1525	0.31	0/2050
16	LI	0.15	0/1797	0.28	0/2413
17	LJ	0.12	0/1389	0.31	0/1856
18	LK	0.08	0/761	0.30	0/1056
19	LL	0.14	0/1695	0.30	0/2276
20	LM	0.14	0/1144	0.28	0/1539
21	LN	0.17	0/1740	0.29	0/2332
22	LO	0.15	0/1638	0.27	0/2197
23	LP	0.15	0/1495	0.31	0/2014
24	LQ	0.15	0/1507	0.29	0/2017
25	LR	0.14	0/1525	0.22	0/2028
26	LS	0.16	0/1460	0.29	0/1965
27	LT	0.15	0/1292	0.25	0/1738
28	LU	0.10	0/832	0.27	0/1112
29	LV	0.16	0/1012	0.32	0/1361
30	LW	0.13	0/1088	0.26	0/1443
31	LX	0.15	0/981	0.35	0/1324
32	LY	0.14	0/1079	0.26	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	LZ	0.13	0/1134	0.26	0/1519
34	La	0.17	0/1212	0.30	0/1627
35	Lb	0.13	0/518	0.33	0/684
36	Lc	0.14	0/731	0.25	0/983
37	Ld	0.18	0/925	0.33	0/1238
38	Le	0.15	0/1019	0.26	0/1358
39	Lf	0.17	0/874	0.28	0/1176
40	Lg	0.16	0/904	0.33	0/1210
41	Lh	0.14	0/1014	0.25	0/1349
42	Li	0.13	0/844	0.25	0/1115
43	Lj	0.16	0/697	0.30	0/922
44	Lk	0.16	0/640	0.28	0/850
45	Ll	0.16	0/445	0.32	0/593
46	Lm	0.14	0/424	0.25	0/561
47	Ln	0.17	0/225	0.26	0/289
47	Lr	0.10	0/225	0.23	0/289
48	Lo	0.15	0/835	0.27	0/1105
49	Lp	0.16	0/705	0.31	0/940
50	Lq	0.13	0/1101	0.27	0/1482
51	Ls	0.10	0/1477	0.30	0/1995
52	SA	0.13	0/1683	0.30	0/2299
53	SB	0.14	0/1900	0.32	0/2551
54	SC	0.12	0/1703	0.26	0/2303
55	SD	0.10	0/1712	0.27	0/2299
56	SE	0.11	0/2112	0.29	0/2842
57	SF	0.10	0/1578	0.29	0/2130
58	SG	0.10	0/1906	0.26	0/2547
59	SH	0.11	0/1587	0.30	0/2140
60	SI	0.13	0/1654	0.28	0/2213
61	SJ	0.12	0/1489	0.27	0/1993
62	SK	0.12	0/764	0.32	0/1038
63	SL	0.13	0/1249	0.26	0/1678
64	SM	0.10	0/934	0.33	0/1255
65	SN	0.16	0/1205	0.28	0/1627
66	SO	0.16	0/1014	0.39	2/1361 (0.1%)
67	SP	0.09	0/932	0.28	0/1248
68	SQ	0.10	0/1098	0.31	0/1472
69	SR	0.11	0/1060	0.30	0/1424
70	SS	0.10	0/1133	0.30	0/1520
71	ST	0.12	0/1137	0.31	0/1533
72	SU	0.10	0/828	0.30	0/1112
73	SV	0.13	0/671	0.28	0/900
74	SW	0.13	0/1055	0.31	0/1416

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
75	SX	0.14	0/1116	0.29	0/1489
76	SY	0.10	0/1075	0.23	0/1431
77	SZ	0.08	0/550	0.25	0/736
78	Sa	0.16	0/852	0.28	0/1136
79	Sb	0.12	0/623	0.34	0/843
80	Sc	0.12	0/487	0.34	0/653
81	Sd	0.08	0/427	0.24	0/570
82	Se	0.10	0/325	0.28	0/427
83	Sf	0.08	0/614	0.28	0/813
All	All	0.15	0/220649	0.24	2/323195 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
9	LB	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
66	SO	63	ALA	CA-C-N	5.46	131.96	121.54
66	SO	63	ALA	C-N-CA	5.46	131.96	121.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	LB	257	HIS	Peptide

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	68242	0	34375	266	0
2	2	37645	0	18955	279	0
3	3	2535	0	1284	12	0
4	4	3319	0	1678	16	0
5	A	2438	0	2385	63	0
6	B	244	0	233	6	0
7	C	619	0	654	11	0
8	LA	1925	0	1999	22	0
9	LB	3088	0	3206	33	0
10	LC	2758	0	2883	21	0
11	LD	2440	0	2431	22	0
12	LE	1518	0	1619	13	0
13	LF	2017	0	2130	15	0
14	LG	1900	0	2066	15	0
15	LH	1505	0	1581	20	0
16	LI	1760	0	1798	13	0
17	LJ	1367	0	1405	22	0
18	LK	762	0	362	3	0
19	LL	1666	0	1756	21	0
20	LM	1125	0	1198	10	0
21	LN	1703	0	1767	29	0
22	LO	1613	0	1706	9	0
23	LP	1472	0	1518	15	0
24	LQ	1481	0	1596	15	0
25	LR	1506	0	1603	12	0
26	LS	1425	0	1484	17	0
27	LT	1266	0	1328	11	0
28	LU	819	0	864	8	0
29	LV	994	0	1054	7	0
30	LW	1075	0	1146	12	0
31	LX	965	0	1050	15	0
32	LY	1065	0	1156	17	0
33	LZ	1111	0	1181	14	0
34	La	1180	0	1203	16	0
35	Lb	508	0	526	6	0
36	Lc	722	0	766	7	0
37	Ld	911	0	965	12	0
38	Le	1001	0	1070	6	0
39	Lf	853	0	880	4	0
40	Lg	891	0	958	8	0
41	Lh	1003	0	1116	12	0
42	Li	836	0	915	12	0
43	Lj	684	0	712	6	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Lk	632	0	693	7	0
45	Ll	435	0	473	3	0
46	Lm	418	0	459	6	0
47	Ln	224	0	271	3	0
47	Lr	224	0	271	2	0
48	Lo	822	0	891	7	0
49	Lp	697	0	737	9	0
50	Lq	1083	0	1140	8	0
51	Ls	1449	0	1488	36	0
52	SA	1641	0	1650	17	0
53	SB	1871	0	1989	28	0
54	SC	1672	0	1777	23	0
55	SD	1688	0	1750	27	0
56	SE	2072	0	2155	23	0
57	SF	1557	0	1608	29	0
58	SG	1875	0	1983	31	0
59	SH	1562	0	1641	23	0
60	SI	1621	0	1645	23	0
61	SJ	1466	0	1582	22	0
62	SK	742	0	738	26	0
63	SL	1222	0	1289	16	0
64	SM	923	0	946	16	0
65	SN	1182	0	1264	11	0
66	SO	1002	0	1034	22	0
67	SP	917	0	978	22	0
68	SQ	1081	0	1151	24	0
69	SR	1045	0	1083	15	0
70	SS	1118	0	1172	39	0
71	ST	1117	0	1133	30	0
72	SU	819	0	895	10	0
73	SV	664	0	662	8	0
74	SW	1037	0	1076	10	0
75	SX	1099	0	1169	16	0
76	SY	1061	0	1150	17	0
77	SZ	546	0	591	18	0
78	Sa	839	0	891	15	0
79	Sb	611	0	633	3	0
80	Sc	484	0	513	4	0
81	Sd	419	0	418	11	0
82	Se	322	0	365	3	0
83	Sf	604	0	640	13	0
84	1	415	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	2	121	0	0	0	0
84	3	8	0	0	0	0
84	4	11	0	0	0	0
84	LA	1	0	0	0	0
84	LB	1	0	0	0	0
84	LI	1	0	0	0	0
84	LN	3	0	0	0	0
84	LP	1	0	0	0	0
84	LT	2	0	0	0	0
84	LV	1	0	0	0	0
84	Lb	1	0	0	0	0
84	Lo	1	0	0	0	0
84	SN	1	0	0	0	0
84	SO	1	0	0	0	0
84	SQ	1	0	0	0	0
84	SX	1	0	0	0	0
85	Lg	1	0	0	0	0
85	Lj	1	0	0	0	0
85	Lm	1	0	0	0	0
85	Lo	1	0	0	0	0
85	Lp	1	0	0	0	0
85	Sa	1	0	0	0	0
85	Sb	1	0	0	0	0
85	Sd	1	0	0	0	0
86	1	748	0	0	30	0
86	2	136	0	0	3	0
86	4	20	0	0	3	0
86	LB	3	0	0	0	0
86	LC	3	0	0	0	0
86	LD	1	0	0	0	0
86	LN	6	0	0	0	0
86	LO	5	0	0	0	0
86	LP	2	0	0	0	0
86	LQ	1	0	0	0	0
86	LT	4	0	0	0	0
86	LW	4	0	0	0	0
86	Lb	1	0	0	0	0
86	Ld	1	0	0	0	0
86	Le	4	0	0	0	0
86	Lj	1	0	0	0	0
86	SL	2	0	0	1	0
86	SN	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	Sa	1	0	0	0	0
All	All	207344	0	154556	1509	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 4.

The worst 5 of 1509 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)
2:2:191:G:HO2'	2:2:192:A:H8	1.05	1.02
60:SI:87:ASN:HB3	60:SI:90:LEU:HD23	1.60	0.83
2:2:1474:G:OP1	71:ST:44:LYS:NZ	2.13	0.81
2:2:691:C:H4'	2:2:692:C:H5'	1.63	0.80
68:SQ:28:LEU:HD21	68:SQ:30:LYS:HE2	1.63	0.80

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	A	310/316 (98%)	293 (94%)	17 (6%)	0	100	100
6	B	28/302 (9%)	19 (68%)	9 (32%)	0	100	100
7	C	76/614 (12%)	76 (100%)	0	0	100	100
8	LA	250/254 (98%)	239 (96%)	11 (4%)	0	100	100
9	LB	385/392 (98%)	366 (95%)	18 (5%)	1 (0%)	36	65
10	LC	361/365 (99%)	343 (95%)	18 (5%)	0	100	100
11	LD	298/304 (98%)	291 (98%)	7 (2%)	0	100	100
12	LE	192/200 (96%)	174 (91%)	18 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
14	LG	233/262 (89%)	229 (98%)	4 (2%)	0	100	100
15	LH	189/192 (98%)	183 (97%)	6 (3%)	0	100	100
16	LI	215/219 (98%)	201 (94%)	14 (6%)	0	100	100
17	LJ	165/173 (95%)	160 (97%)	5 (3%)	0	100	100
18	LK	153/165 (93%)	133 (87%)	18 (12%)	2 (1%)	9	32
19	LL	207/213 (97%)	201 (97%)	6 (3%)	0	100	100
20	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
21	LN	200/203 (98%)	192 (96%)	8 (4%)	0	100	100
22	LO	201/204 (98%)	193 (96%)	8 (4%)	0	100	100
23	LP	184/187 (98%)	173 (94%)	10 (5%)	1 (0%)	24	54
24	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
25	LR	182/192 (95%)	178 (98%)	4 (2%)	0	100	100
26	LS	171/174 (98%)	167 (98%)	4 (2%)	0	100	100
27	LT	156/160 (98%)	151 (97%)	5 (3%)	0	100	100
28	LU	99/127 (78%)	94 (95%)	5 (5%)	0	100	100
29	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
30	LW	131/161 (81%)	126 (96%)	5 (4%)	0	100	100
31	LX	119/156 (76%)	113 (95%)	6 (5%)	0	100	100
32	LY	132/138 (96%)	129 (98%)	3 (2%)	0	100	100
33	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
34	La	146/149 (98%)	136 (93%)	10 (7%)	0	100	100
35	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
36	Lc	95/108 (88%)	94 (99%)	1 (1%)	0	100	100
37	Ld	110/120 (92%)	108 (98%)	2 (2%)	0	100	100
38	Le	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
39	Lf	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
40	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
41	Lh	120/126 (95%)	117 (98%)	3 (2%)	0	100	100
42	Li	100/110 (91%)	94 (94%)	6 (6%)	0	100	100
43	Lj	84/95 (88%)	79 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Lk	74/81 (91%)	72 (97%)	2 (3%)	0	100	100
45	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
46	Lm	50/128 (39%)	50 (100%)	0	0	100	100
47	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lr	22/25 (88%)	22 (100%)	0	0	100	100
48	Lo	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
49	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	Lq	139/147 (95%)	134 (96%)	5 (4%)	0	100	100
51	Ls	187/312 (60%)	183 (98%)	4 (2%)	0	100	100
52	SA	206/285 (72%)	193 (94%)	13 (6%)	0	100	100
53	SB	230/255 (90%)	216 (94%)	14 (6%)	0	100	100
54	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100
55	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
56	SE	259/264 (98%)	246 (95%)	13 (5%)	0	100	100
57	SF	197/212 (93%)	181 (92%)	16 (8%)	0	100	100
58	SG	230/239 (96%)	220 (96%)	10 (4%)	0	100	100
59	SH	193/203 (95%)	185 (96%)	8 (4%)	0	100	100
60	SI	199/202 (98%)	192 (96%)	7 (4%)	0	100	100
61	SJ	177/190 (93%)	169 (96%)	8 (4%)	0	100	100
62	SK	87/159 (55%)	87 (100%)	0	0	100	100
63	SL	148/161 (92%)	146 (99%)	2 (1%)	0	100	100
64	SM	116/144 (81%)	105 (90%)	11 (10%)	0	100	100
65	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
66	SO	133/150 (89%)	127 (96%)	6 (4%)	0	100	100
67	SP	113/153 (74%)	109 (96%)	4 (4%)	0	100	100
68	SQ	136/143 (95%)	129 (95%)	7 (5%)	0	100	100
69	SR	126/143 (88%)	123 (98%)	3 (2%)	0	100	100
70	SS	135/156 (86%)	123 (91%)	12 (9%)	0	100	100
71	ST	140/153 (92%)	134 (96%)	6 (4%)	0	100	100
72	SU	101/116 (87%)	94 (93%)	7 (7%)	0	100	100
73	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
75	SX	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
76	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
77	SZ	67/99 (68%)	66 (98%)	1 (2%)	0	100	100
78	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
79	Sb	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
80	Sc	59/68 (87%)	54 (92%)	5 (8%)	0	100	100
81	Sd	50/56 (89%)	48 (96%)	2 (4%)	0	100	100
82	Se	38/62 (61%)	37 (97%)	1 (3%)	0	100	100
83	Sf	71/154 (46%)	62 (87%)	9 (13%)	0	100	100
All	All	11698/13795 (85%)	11185 (96%)	509 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	LK	88	PRO
18	LK	22	VAL
23	LP	163	VAL
9	LB	257	HIS

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A	271/274 (99%)	271 (100%)	0	100	100
6	B	21/224 (9%)	21 (100%)	0	100	100
7	C	68/511 (13%)	68 (100%)	0	100	100
8	LA	196/198 (99%)	196 (100%)	0	100	100
9	LB	327/331 (99%)	327 (100%)	0	100	100
10	LC	284/285 (100%)	284 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LD	250/253 (99%)	250 (100%)	0	100	100
12	LE	162/166 (98%)	162 (100%)	0	100	100
13	LF	213/215 (99%)	213 (100%)	0	100	100
14	LG	203/222 (91%)	203 (100%)	0	100	100
15	LH	168/169 (99%)	168 (100%)	0	100	100
16	LI	182/183 (100%)	182 (100%)	0	100	100
17	LJ	145/150 (97%)	144 (99%)	1 (1%)	76	92
19	LL	172/176 (98%)	172 (100%)	0	100	100
20	LM	116/117 (99%)	116 (100%)	0	100	100
21	LN	179/180 (99%)	179 (100%)	0	100	100
22	LO	161/162 (99%)	161 (100%)	0	100	100
23	LP	151/152 (99%)	151 (100%)	0	100	100
24	LQ	155/178 (87%)	155 (100%)	0	100	100
25	LR	153/160 (96%)	153 (100%)	0	100	100
26	LS	153/154 (99%)	153 (100%)	0	100	100
27	LT	134/135 (99%)	134 (100%)	0	100	100
28	LU	89/108 (82%)	89 (100%)	0	100	100
29	LV	99/102 (97%)	99 (100%)	0	100	100
30	LW	107/125 (86%)	107 (100%)	0	100	100
31	LX	108/129 (84%)	107 (99%)	1 (1%)	70	90
32	LY	117/119 (98%)	117 (100%)	0	100	100
33	LZ	121/121 (100%)	121 (100%)	0	100	100
34	La	121/122 (99%)	121 (100%)	0	100	100
35	Lb	53/55 (96%)	53 (100%)	0	100	100
36	Lc	78/88 (89%)	78 (100%)	0	100	100
37	Ld	97/105 (92%)	96 (99%)	1 (1%)	68	89
38	Le	107/114 (94%)	107 (100%)	0	100	100
39	Lf	88/90 (98%)	88 (100%)	0	100	100
40	Lg	97/102 (95%)	97 (100%)	0	100	100
41	Lh	109/112 (97%)	109 (100%)	0	100	100
42	Li	86/93 (92%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	Lj	70/78 (90%)	70 (100%)	0	100	100
44	Lk	73/77 (95%)	73 (100%)	0	100	100
45	Ll	45/46 (98%)	45 (100%)	0	100	100
46	Lm	47/115 (41%)	47 (100%)	0	100	100
47	Ln	22/23 (96%)	22 (100%)	0	100	100
47	Lr	22/23 (96%)	22 (100%)	0	100	100
48	Lo	88/90 (98%)	88 (100%)	0	100	100
49	Lp	73/74 (99%)	73 (100%)	0	100	100
50	Lq	109/112 (97%)	109 (100%)	0	100	100
51	Ls	155/255 (61%)	155 (100%)	0	100	100
52	SA	178/225 (79%)	178 (100%)	0	100	100
53	SB	203/223 (91%)	203 (100%)	0	100	100
54	SC	181/206 (88%)	181 (100%)	0	100	100
55	SD	182/206 (88%)	181 (100%)	1 (0%)	81	93
56	SE	219/221 (99%)	219 (100%)	0	100	100
57	SF	167/178 (94%)	167 (100%)	0	100	100
58	SG	198/204 (97%)	198 (100%)	0	100	100
59	SH	169/177 (96%)	169 (100%)	0	100	100
60	SI	163/164 (99%)	163 (100%)	0	100	100
61	SJ	154/162 (95%)	154 (100%)	0	100	100
62	SK	77/126 (61%)	77 (100%)	0	100	100
63	SL	133/143 (93%)	133 (100%)	0	100	100
64	SM	101/121 (84%)	101 (100%)	0	100	100
65	SN	129/130 (99%)	129 (100%)	0	100	100
66	SO	102/117 (87%)	102 (100%)	0	100	100
67	SP	99/132 (75%)	99 (100%)	0	100	100
68	SQ	111/115 (96%)	111 (100%)	0	100	100
69	SR	119/131 (91%)	119 (100%)	0	100	100
70	SS	120/135 (89%)	120 (100%)	0	100	100
71	ST	114/124 (92%)	114 (100%)	0	100	100
72	SU	93/103 (90%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	SV	69/80 (86%)	69 (100%)	0	100	100
74	SW	112/113 (99%)	112 (100%)	0	100	100
75	SX	113/116 (97%)	113 (100%)	0	100	100
76	SY	112/115 (97%)	112 (100%)	0	100	100
77	SZ	60/80 (75%)	60 (100%)	0	100	100
78	Sa	91/103 (88%)	91 (100%)	0	100	100
79	Sb	70/71 (99%)	70 (100%)	0	100	100
80	Sc	54/61 (88%)	54 (100%)	0	100	100
81	Sd	43/46 (94%)	43 (100%)	0	100	100
82	Se	34/51 (67%)	34 (100%)	0	100	100
83	Sf	66/139 (48%)	66 (100%)	0	100	100
All	All	9881/11391 (87%)	9877 (100%)	4 (0%)	100	100

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	LJ	40	GLN
31	LX	81	ASN
37	Ld	105	ASN
55	SD	177	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 87 such sidechains are listed below:

Mol	Chain	Res	Type
55	SD	59	GLN
62	SK	48	GLN
55	SD	224	GLN
57	SF	145	GLN
68	SQ	5	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	476 (14%)	39 (1%)
2	2	1761/1796 (98%)	311 (17%)	34 (1%)
3	3	118/120 (98%)	9 (7%)	1 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	4	155/156 (99%)	20 (12%)	0
All	All	5222/5409 (96%)	816 (15%)	74 (1%)

5 of 816 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A
1	1	41	A
1	1	44	A
1	1	50	A
1	1	60	G

5 of 74 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	832	G
2	2	1616	C
2	2	1165	U
2	2	1341	A
1	1	2503	C

## 5.4 Non-standard residues in protein, DNA, RNA chains

3 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
2	B8N	2	1188	2	25,29,30	2.58	5 (20%)	28,42,45	1.32	4 (14%)
1	OMG	1	2578	1	23,26,27	0.50	0	32,38,41	0.44	0
22	SAC	LO	2	22	7,8,9	1.03	0	7,9,11	1.05	0

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
2	B8N	2	1188	2	-	1/16/34/35	0/2/2/2
1	OMG	1	2578	1	-	2/9/27/28	0/3/3/3
22	SAC	LO	2	22	-	2/7/8/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1188	B8N	O4-C4	9.58	1.42	1.23
2	2	1188	B8N	C2-N3	-3.87	1.32	1.38
2	2	1188	B8N	C4-N3	-3.80	1.33	1.40
2	2	1188	B8N	C4-C5	-3.51	1.39	1.47
2	2	1188	B8N	C6-C5	3.14	1.39	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1188	B8N	N3-C2-N1	3.42	120.90	116.72
2	2	1188	B8N	C4-N3-C2	-3.26	121.61	125.62
2	2	1188	B8N	O4'-C1'-C2'	2.09	108.04	105.15
2	2	1188	B8N	C1'-C5-C4	2.02	120.68	117.61

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	LO	2	SAC	N-CA-CB-OG
22	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
2	2	1188	B8N	C31-C32-C33-C34
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 579 ligands modelled in this entry, 579 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](#)

There are no chain breaks in this entry.

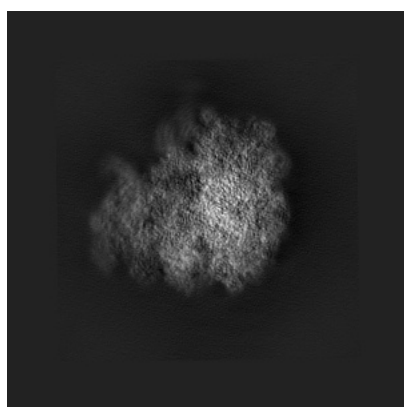
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12976. These allow visual inspection of the internal detail of the map and identification of artifacts.

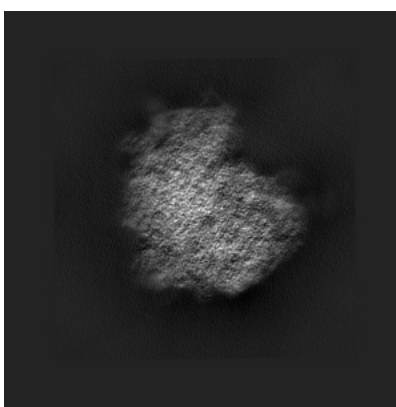
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

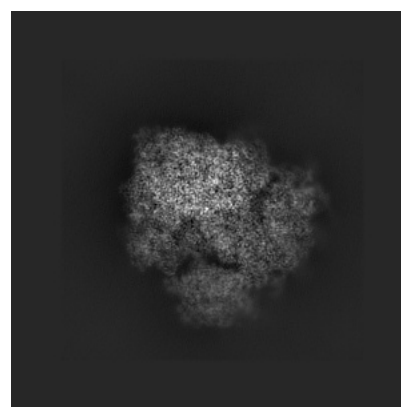
#### 6.1.1 Primary map



X



Y

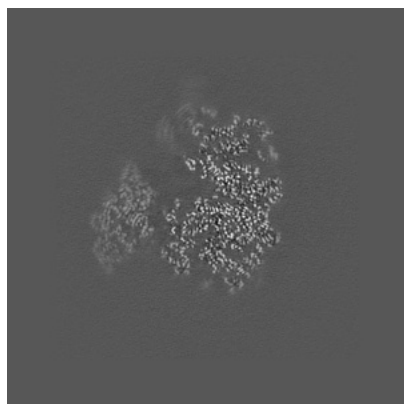


Z

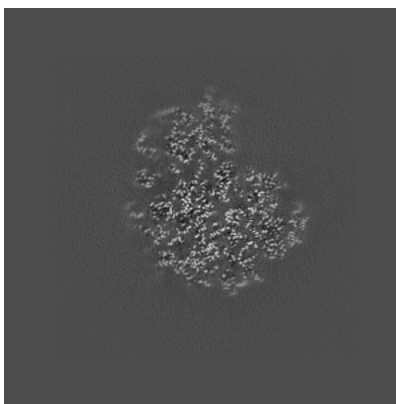
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

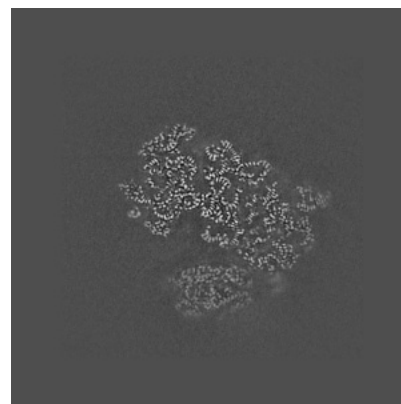
#### 6.2.1 Primary map



X Index: 243



Y Index: 243

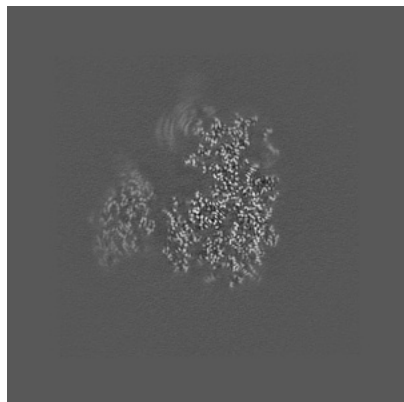


Z Index: 243

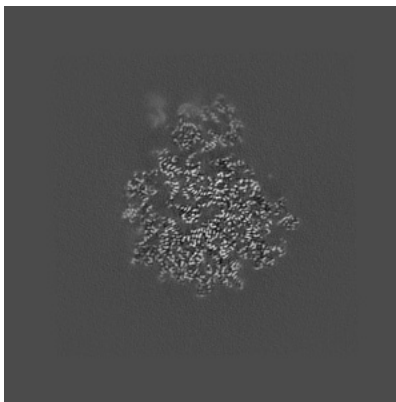
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

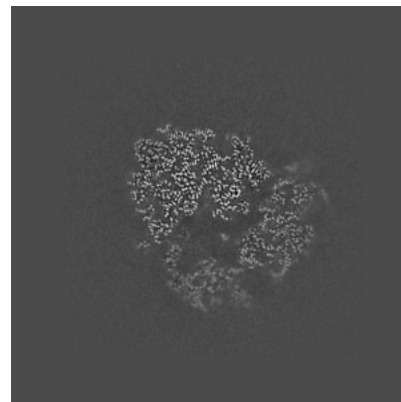
### 6.3.1 Primary map



X Index: 247



Y Index: 267

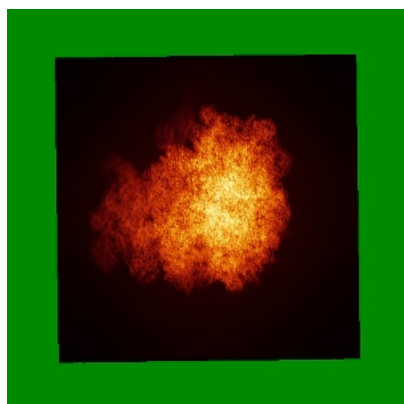


Z Index: 258

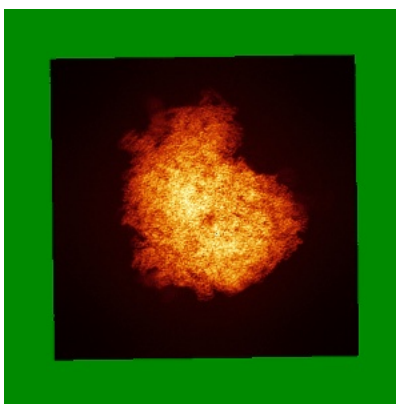
The images above show the largest variance slices of the map in three orthogonal directions.

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

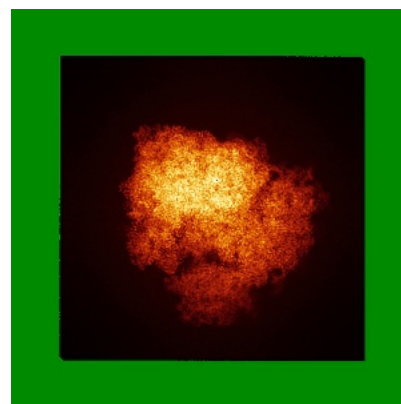
### 6.4.1 Primary map



X



Y

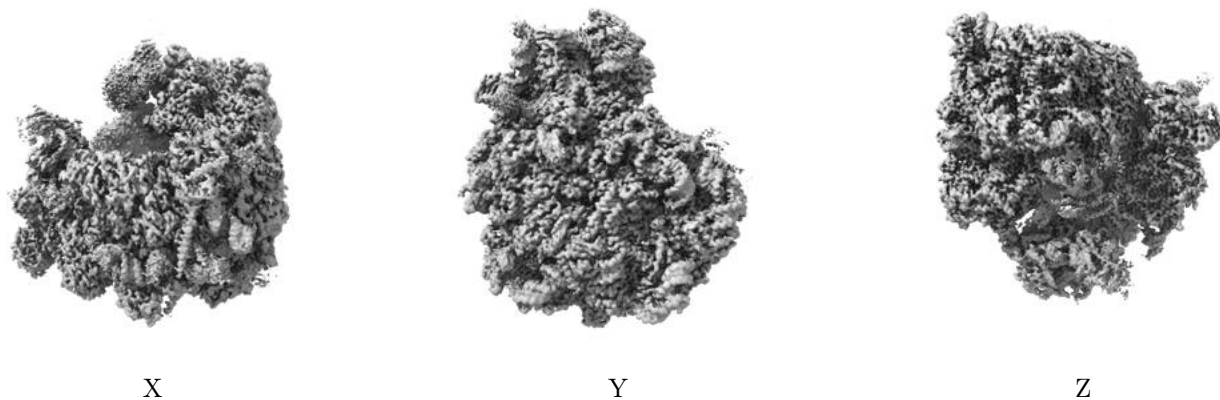


Z

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

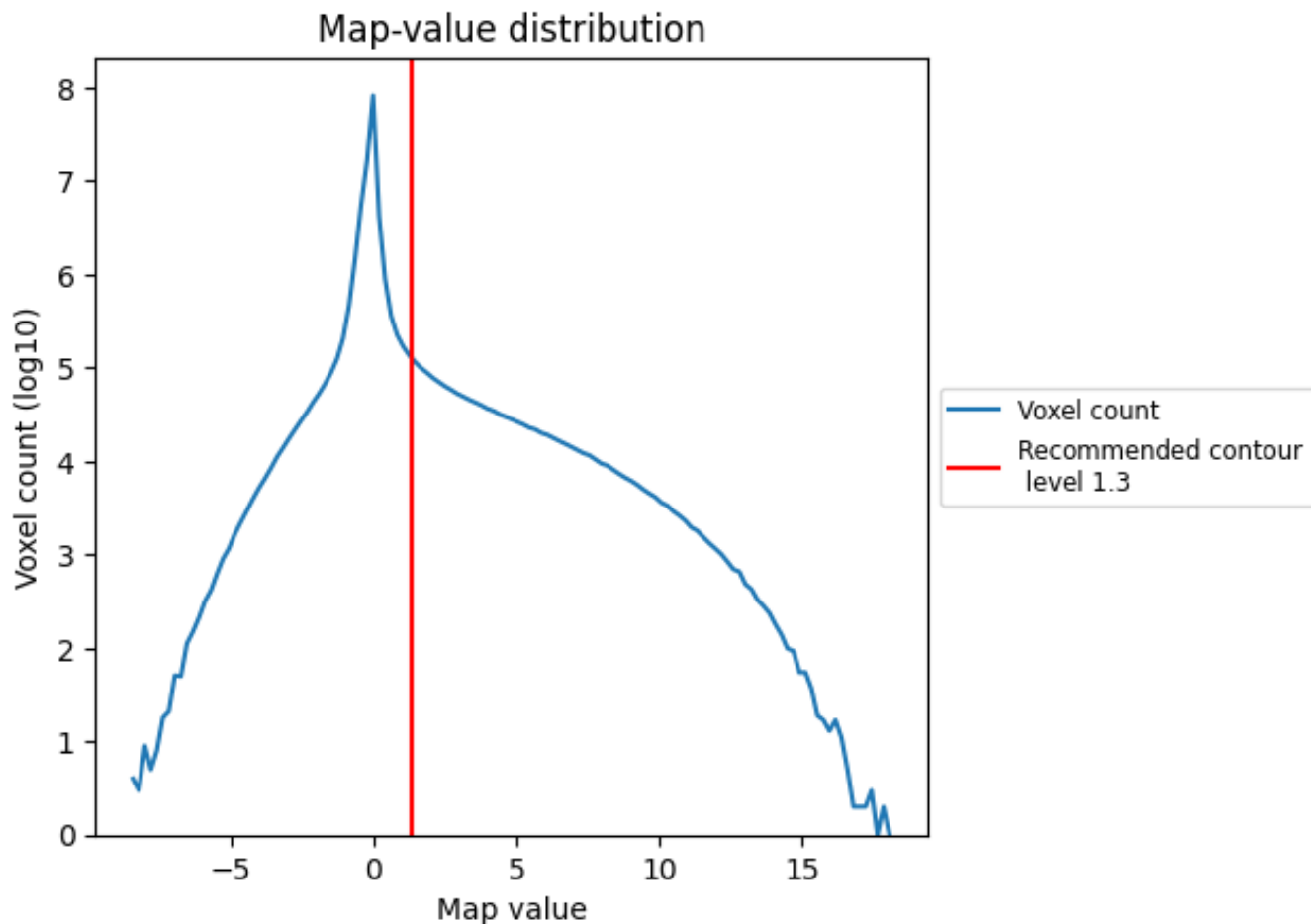
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

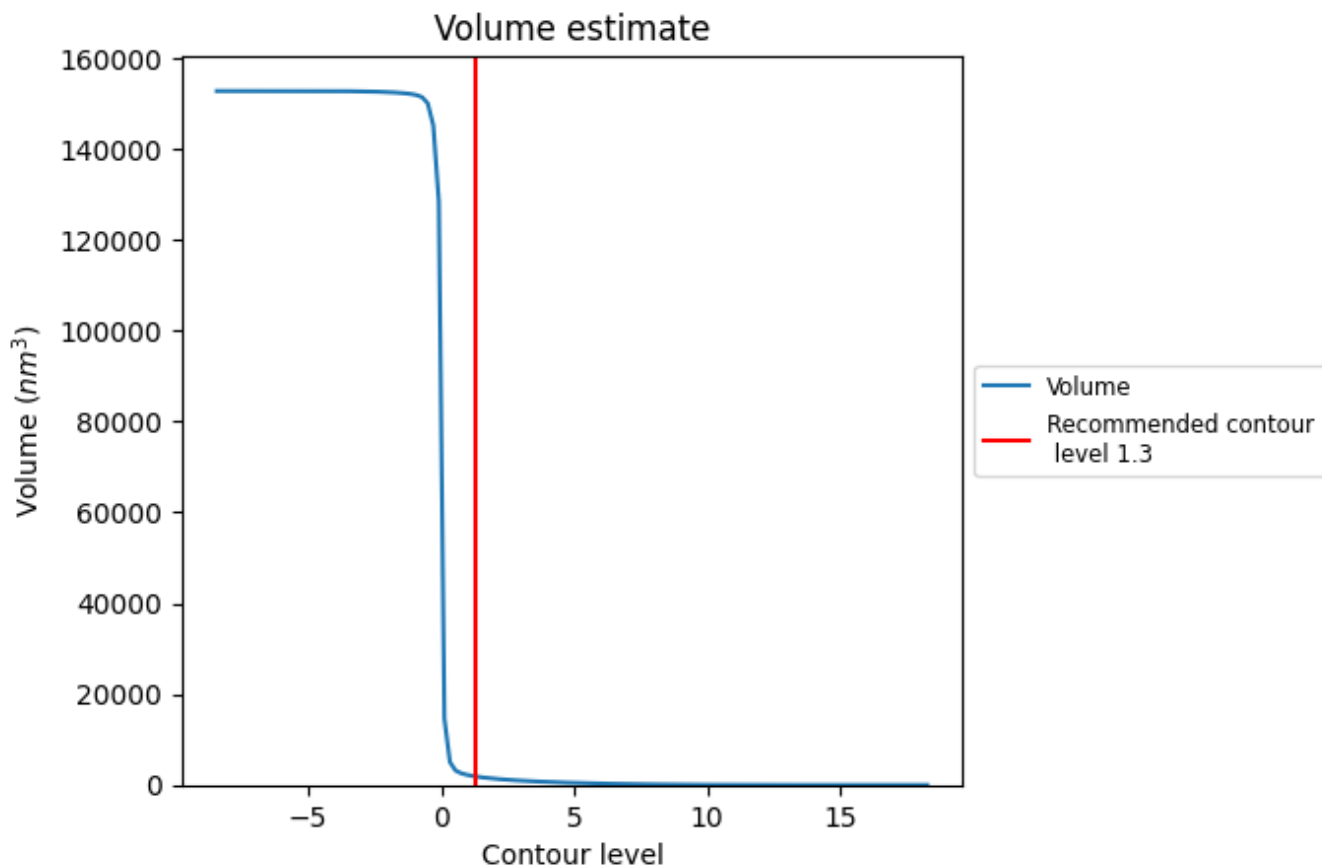
This section contains the results of statistical analysis of the map.

### 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.

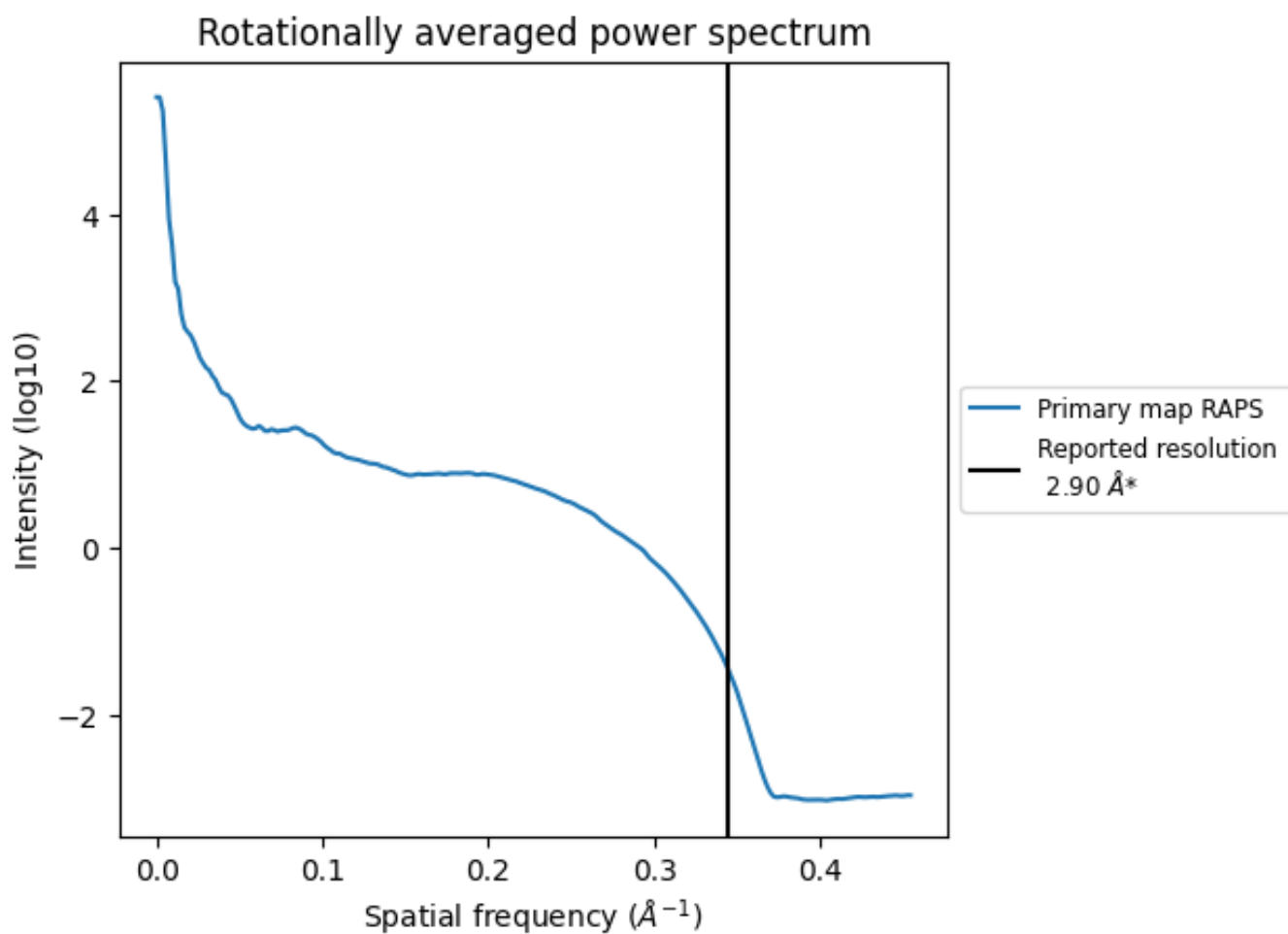
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1875 nm<sup>3</sup>; this corresponds to an approximate mass of 1694 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

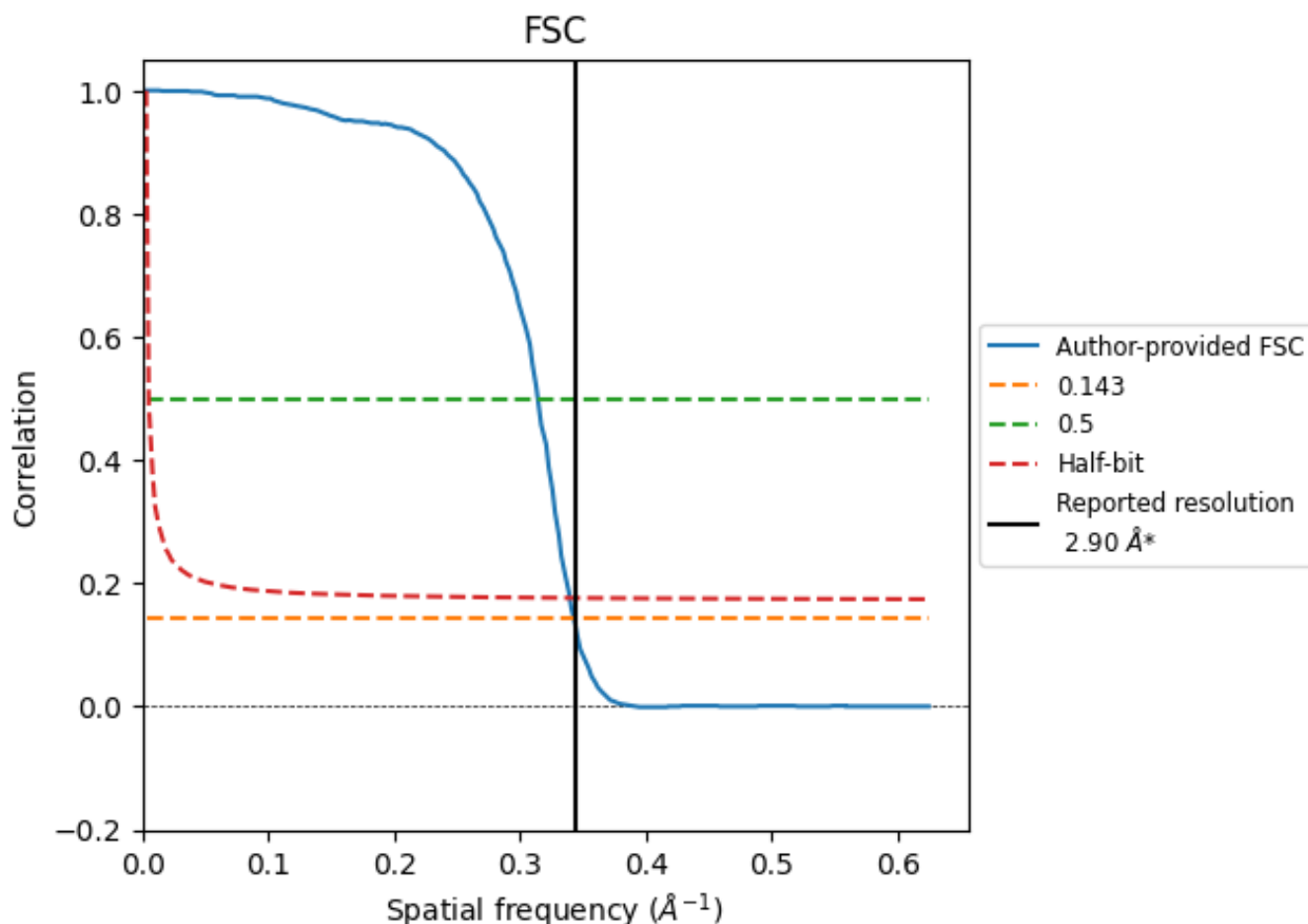


\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [\(i\)](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [\(i\)](#)



\*Reported resolution corresponds to spatial frequency of 0.345 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

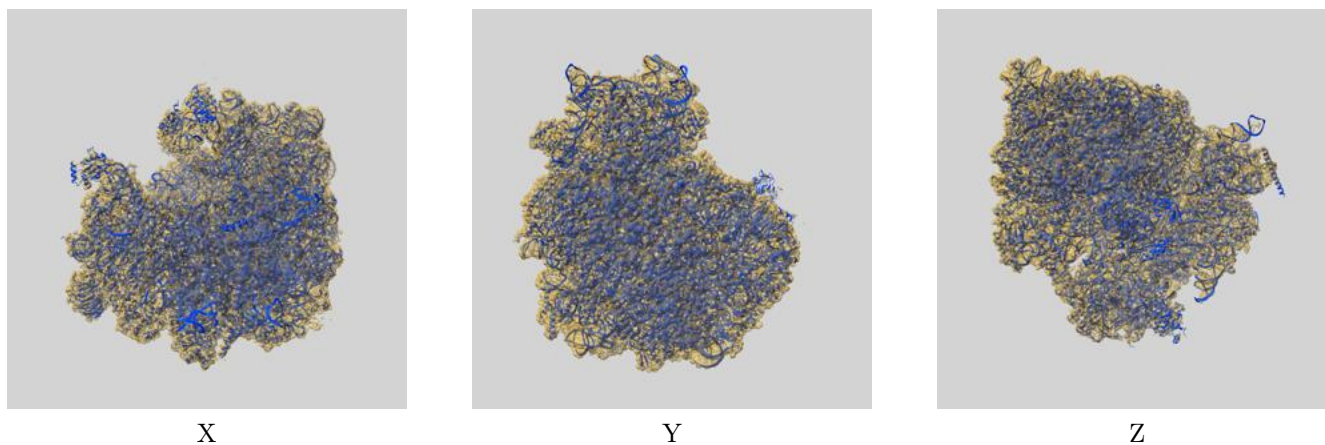
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.92	3.18	2.94
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

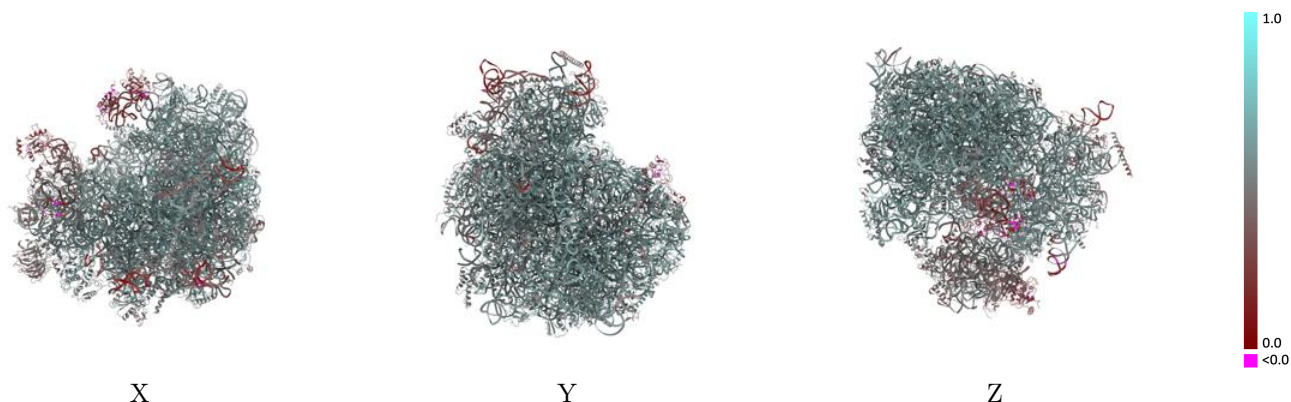
This section contains information regarding the fit between EMDB map EMD-12976 and PDB model 7OLC. Per-residue inclusion information can be found in section 3 on page 25.

### 9.1 Map-model overlay [i](#)



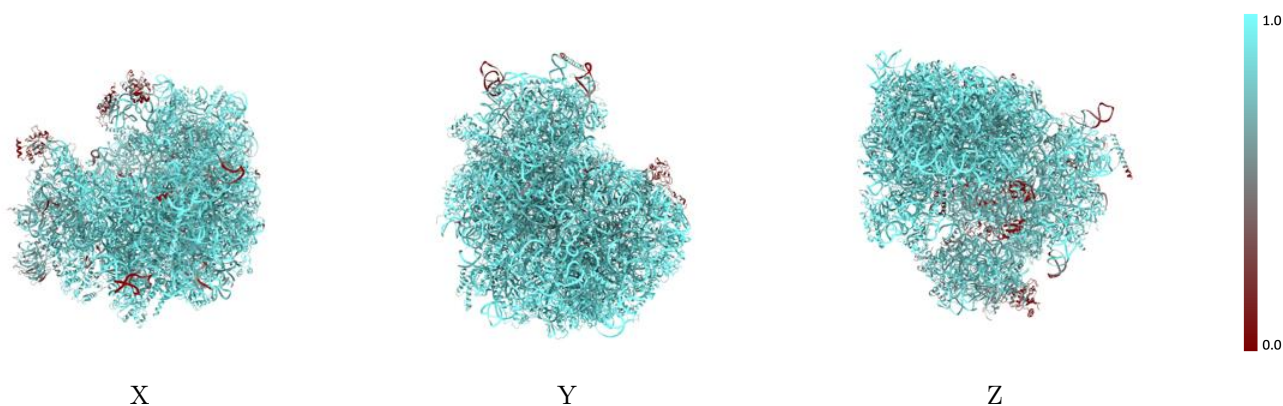
The images above show the 3D surface view of the map at the recommended contour level 1.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



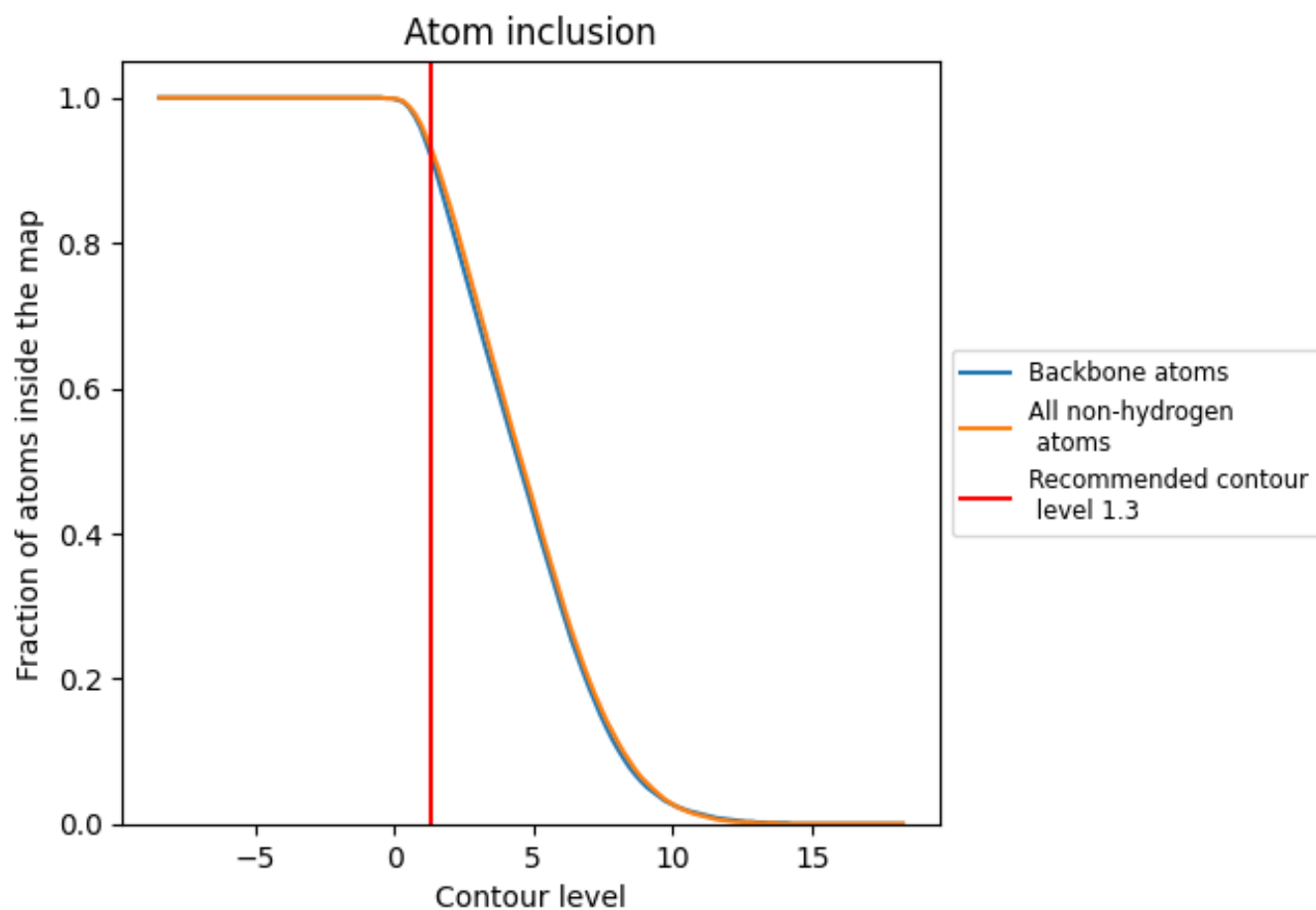
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.3).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 93% 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 (1.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9330	 0.5380
1	 0.9860	 0.5640
2	 0.9410	 0.5140
3	 0.9990	 0.5860
4	 0.9910	 0.5580
A	 0.6780	 0.4190
B	 0.7500	 0.4500
C	 0.2640	 0.4510
LA	 0.9710	 0.5830
LB	 0.9790	 0.5870
LC	 0.9680	 0.5750
LD	 0.9350	 0.5470
LE	 0.9280	 0.5400
LF	 0.9610	 0.5790
LG	 0.9440	 0.5460
LH	 0.9570	 0.5650
LI	 0.9530	 0.5750
LJ	 0.9030	 0.5140
LK	 0.3070	 0.2010
LL	 0.9560	 0.5590
LM	 0.9540	 0.5730
LN	 0.9830	 0.5860
LO	 0.9740	 0.5830
LP	 0.9130	 0.5560
LQ	 0.9740	 0.5870
LR	 0.9560	 0.5620
LS	 0.9780	 0.5850
LT	 0.9740	 0.5730
LU	 0.9180	 0.5080
LV	 0.9740	 0.5820
LW	 0.7460	 0.4870
LX	 0.9370	 0.5450
LY	 0.9560	 0.5620
LZ	 0.9560	 0.5570
La	 0.9770	 0.5810



















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Chain	Atom inclusion	Q-score
Lb	 0.9350	 0.5320
Lc	 0.9630	 0.5620
Ld	 0.9200	 0.5550
Le	 0.9750	 0.5880
Lf	 0.9730	 0.5950
Lg	 0.9660	 0.5640
Lh	 0.9250	 0.5330
Li	 0.9110	 0.5270
Lj	 0.9850	 0.5870
Lk	 0.8960	 0.5050
Ll	 0.9610	 0.5500
Lm	 0.9780	 0.5780
Ln	 0.9700	 0.5840
Lo	 0.9540	 0.5770
Lp	 0.9600	 0.5640
Lq	 0.9590	 0.5720
Lr	 0.8280	 0.5060
Ls	 0.3000	 0.2350
SA	 0.9430	 0.5430
SB	 0.9050	 0.5320
SC	 0.9430	 0.5600
SD	 0.7710	 0.4710
SE	 0.9380	 0.5540
SF	 0.8020	 0.4640
SG	 0.9130	 0.5210
SH	 0.9010	 0.5030
SI	 0.9060	 0.5450
SJ	 0.9450	 0.5490
SK	 0.7880	 0.3950
SL	 0.9460	 0.5720
SM	 0.1950	 0.2690
SN	 0.9450	 0.5560
SO	 0.9420	 0.5420
SP	 0.7610	 0.3860
SQ	 0.7880	 0.4660
SR	 0.8680	 0.5010
SS	 0.8110	 0.4280
ST	 0.7920	 0.4260
SU	 0.7150	 0.4540
SV	 0.9470	 0.5470
SW	 0.9480	 0.5640
SX	 0.9470	 0.5690

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Chain	Atom inclusion	Q-score
SY	 0.8730	 0.5330
SZ	 0.7920	 0.4180
Sa	 0.9270	 0.5450
Sb	 0.9470	 0.5290
Sc	 0.9010	 0.5120
Sd	 0.9180	 0.5090
Se	 0.9290	 0.5320
Sf	 0.4260	 0.2630