



wwPDB EM Validation Summary Report ⓘ

May 19, 2024 – 11:12 am BST

PDB ID : 6T4Q
EMDB ID : EMD-10377
Title : Structure of yeast 80S ribosome stalled on the CGA-CCG inhibitory codon combination.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-14
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

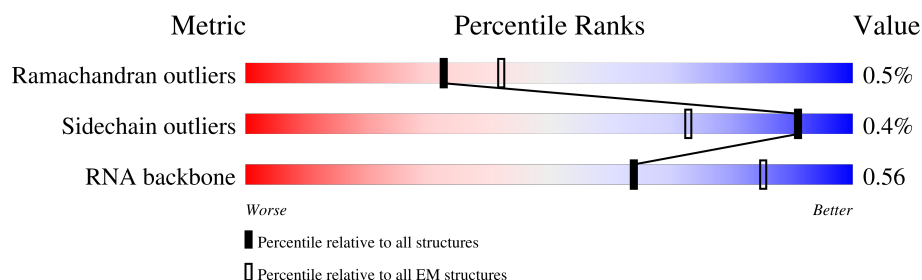
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

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 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



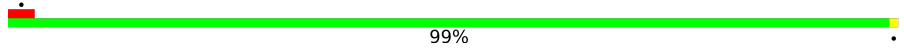
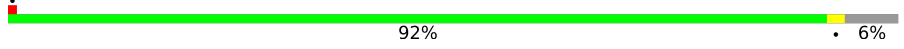
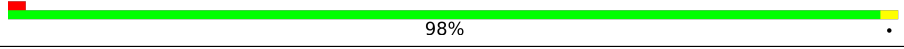
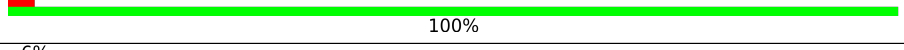
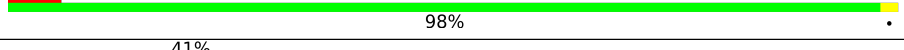
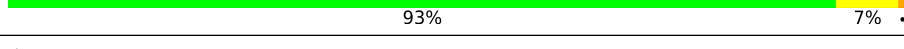
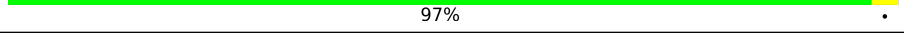
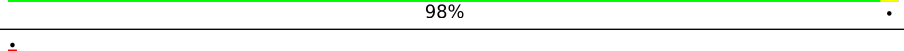
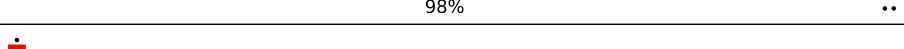
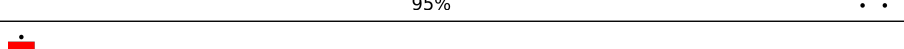
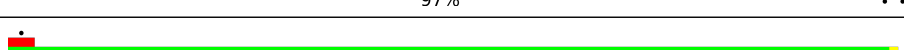
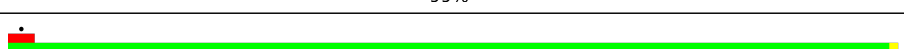
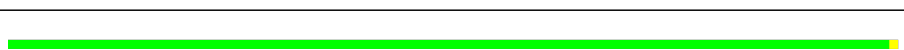
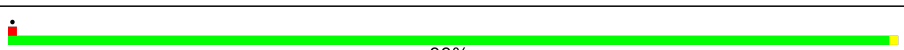
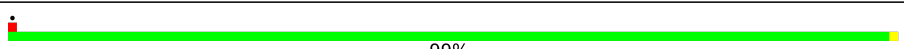
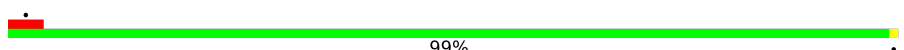
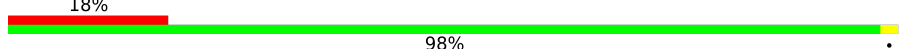
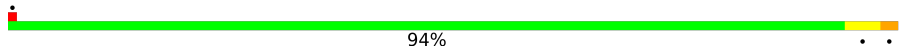
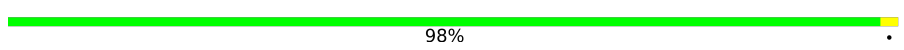
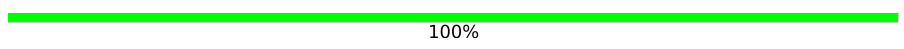
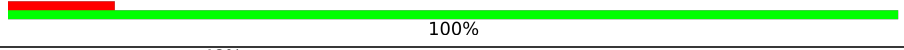
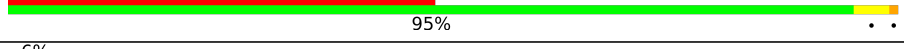
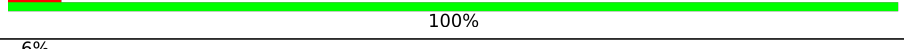
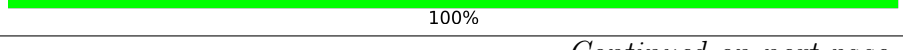

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	C2	1798	
2	SB	232	
3	SP	117	
4	SC	216	
5	SD	222	
6	SE	258	
7	SF	206	
8	SG	228	



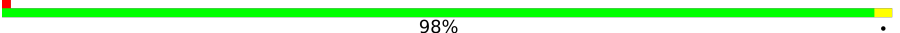
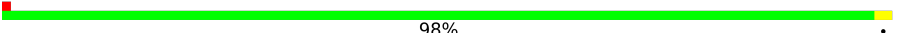
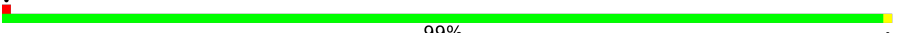
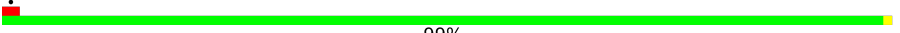









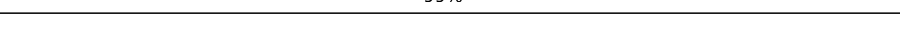
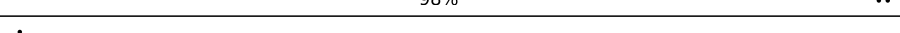
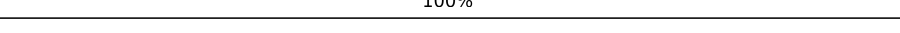
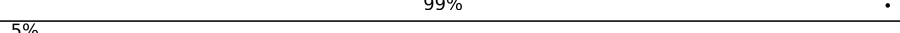
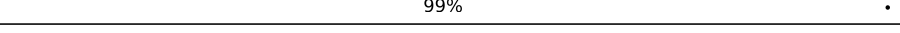
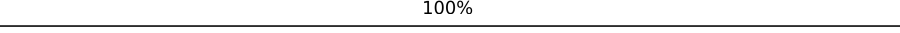
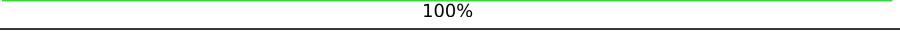
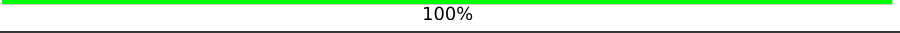
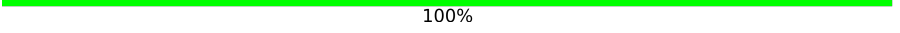
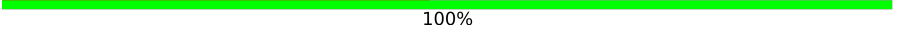
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Mol	Chain	Length	Quality of chain
9	SH	184	 99%
10	SI	198	 92% 6%
11	SJ	184	 98%
12	SK	92	 100%
13	SL	144	 98%
14	SM	121	 93% 41% 7%
15	SN	150	 97%
16	SO	127	 98%
17	SQ	141	 98%
18	SR	125	 95%
19	SS	145	 97%
20	ST	143	 99%
21	SU	100	 99%
22	SV	87	 99%
23	SW	129	 99%
24	SX	144	 99%
25	SY	134	 99%
26	SZ	82	 98%
27	Sa	97	 94%
28	Sb	81	 98%
29	Sd	53	 100%
30	Se	60	 100%
31	Sf	73	 95%
32	Sg	312	 100%
33	Sc	63	 100%

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Mol	Chain	Length	Quality of chain
34	C4	121	 90% 10%
35	C3	158	 80% 20%
36	LA	251	 98% .
37	LB	386	 98% .
38	LC	361	 99% .
39	LD	294	 99% .
40	LE	175	 95% 5%
41	LF	222	 100%
42	LG	233	 99% .
43	LH	191	 100%
44	LI	218	 99% .
45	LJ	169	 99% .
46	LL	193	 98% .
47	LM	136	 100%
48	LN	203	 99% .
49	LO	197	 98% ..
50	LP	183	 100%
51	LQ	185	 99% .
52	LR	188	 5% 99% .
53	LS	171	 100%
54	LT	159	 100%
55	LU	100	 100%
56	LV	136	 100%
57	LW	126	 48% 100%
58	LX	121	 98% .

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Mol	Chain	Length	Quality of chain
59	LY	125	100%
60	LZ	135	99%
61	La	148	98%
62	Lb	58	5% 93% 5%
63	Lc	96	100%
64	Ld	109	6% 99%
65	Le	127	99%
66	Lf	106	100%
67	Lg	112	100%
68	Lh	119	97%
69	Li	99	99%
70	Lj	85	99%
71	Lk	77	100%
72	Ll	50	100%
73	Lm	52	100%
74	Ln	25	100%
75	Lo	103	99%
76	Lp	91	100%
77	C1	3184	82% 18%
78	5	30	67% 53% 47%
79	6	76	5% 82% 18%
80	7	75	77% 23%
81	8	6	17% 100%
82	SA	206	99%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 203581 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 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 3 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 5 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	SD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 6 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 7 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 8 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 9 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	SH	184	Total	C	N	O	S	0	0
			1473	946	263	264			

- Molecule 10 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SI	187	Total	C	N	O	S	0	0
			1476	916	295	263	2		

- Molecule 11 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SJ	184	Total	C	N	O	S	0	0
			1479	935	285	258	1		

- Molecule 12 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	SK	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 13 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 14 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SM	121	Total	C	N	O	S	0	0
			875	551	153	169	2		

- Molecule 15 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 16 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	SQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 19 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ST	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 21 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	SY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	SZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Sb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 29 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 30 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 31 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sf	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Sf	97	ALA	LYS	conflict	UNP P05759

- Molecule 32 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sg	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 33 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Sc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 34 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 35 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 36 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 37 is a protein called 60S ribosomal protein L3.

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

- Molecule 38 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 40 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	132	ALA	THR	conflict	UNP P05739
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 41 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 44 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 45 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 46 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LP	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 51 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LR	188	Total	C	N	O	S	0	0
			1515	932	323	260			

- Molecule 53 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 54 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 56 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	LW	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 58 is a protein called 60S ribosomal protein L25.

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

- Molecule 59 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LY	125	Total	C	N	O	S	0	0
			984	620	191	173			

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

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

- Molecule 61 is a protein called 60S ribosomal protein L28.

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

- Molecule 62 is a protein called 60S ribosomal protein L29.

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

- Molecule 63 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 64 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 65 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 66 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 70 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 71 is a protein called 60S ribosomal protein L38.

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

- Molecule 72 is a protein called 60S ribosomal protein L39.

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

- Molecule 73 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 74 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 75 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 76 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 77 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	C1	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	5	30	Total	C	N	O	P	1	0
			666	298	127	210	31		

- Molecule 79 is a RNA chain called ICG tRNA Arg (P/P).

Mol	Chain	Residues	Atoms					AltConf	Trace
79	6	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 80 is a RNA chain called tRNA (E/E).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	7	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	11	C	U	conflict	GB 176418

- Molecule 81 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	8	6	Total	C	N	O	S	0	0
			53	33	10	9	1		

- Molecule 82 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	SA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 83 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	C2	84	Total	Mg	0
			84	84	
83	SF	1	Total	Mg	0
			1	1	
83	C4	1	Total	Mg	0
			1	1	
83	C3	1	Total	Mg	0
			1	1	
83	LA	2	Total	Mg	0
			2	2	
83	LB	2	Total	Mg	0
			2	2	
83	LF	1	Total	Mg	0
			1	1	
83	LN	2	Total	Mg	0
			2	2	
83	LP	1	Total	Mg	0
			1	1	
83	LR	2	Total	Mg	0
			2	2	
83	LV	1	Total	Mg	0
			1	1	
83	La	1	Total	Mg	0
			1	1	
83	Le	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
83	Lg	1	Total 1	Mg 1	0
83	Lj	1	Total 1	Mg 1	0
83	C1	187	Total 187	Mg 187	0
83	6	1	Total 1	Mg 1	0

- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

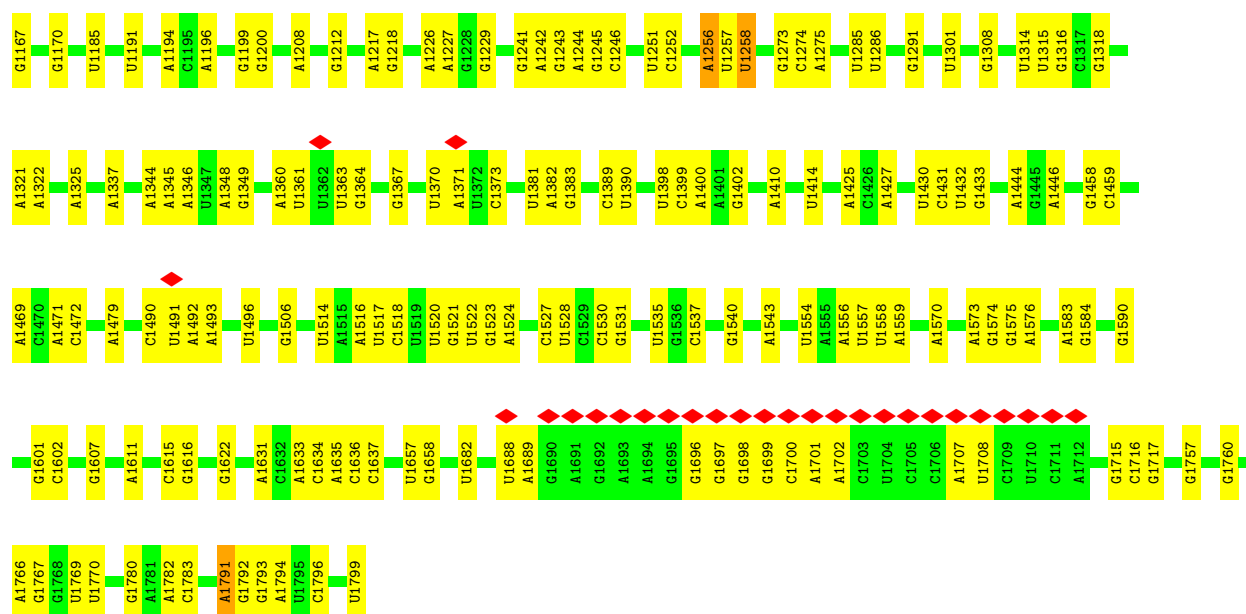
Mol	Chain	Residues	Atoms		AltConf
84	Sd	1	Total 1	Zn 1	0
84	Sf	1	Total 1	Zn 1	0
84	Lg	1	Total 1	Zn 1	0
84	Lj	1	Total 1	Zn 1	0
84	Lm	1	Total 1	Zn 1	0
84	Lo	1	Total 1	Zn 1	0
84	Lp	1	Total 1	Zn 1	0

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.

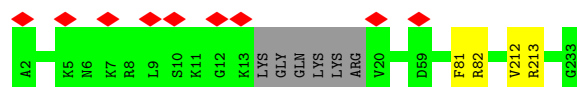
• Molecule 1: 18S rRNA





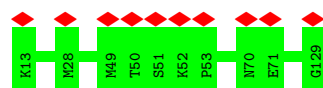
• Molecule 2: 40S ribosomal protein S1-A

Chain SB: 96%



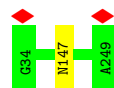
• Molecule 3: 40S ribosomal protein S15

Chain SP: 9% 100%



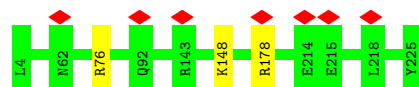
• Molecule 4: 40S ribosomal protein S2

Chain SC: 100%



• Molecule 5: 40S ribosomal protein S3

Chain SD: 99%



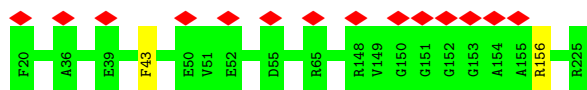
• Molecule 6: 40S ribosomal protein S4-A

Chain SE:  99%



- Molecule 7: Rps5p

Chain SF:  99%



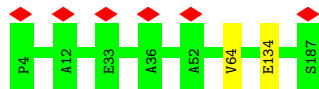
- Molecule 8: 40S ribosomal protein S6-A

Chain SG:  98%



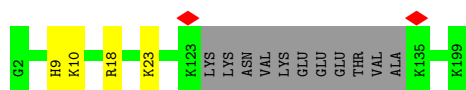
- Molecule 9: 40S ribosomal protein S7-A

Chain SH:  99%



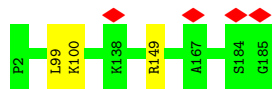
- Molecule 10: 40S ribosomal protein S8-A

Chain SI:  92% 6%



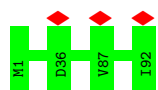
- Molecule 11: 40S ribosomal protein S9-A

Chain SJ:  98%

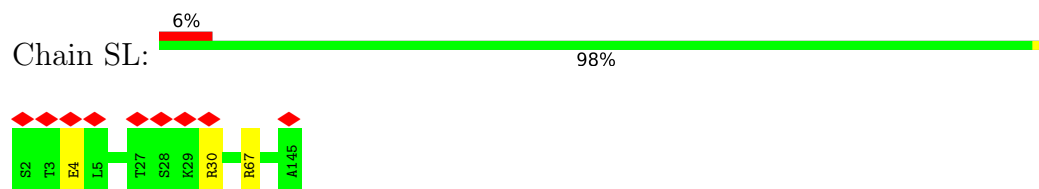


- Molecule 12: 40S ribosomal protein S10-A

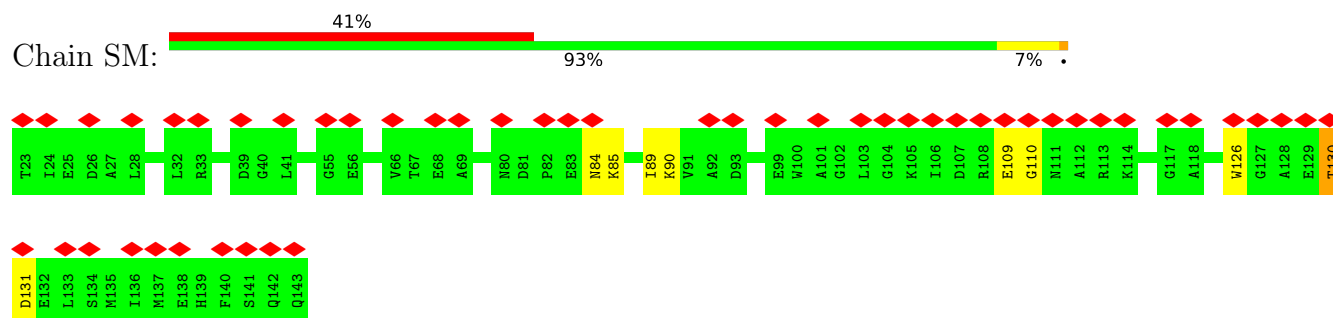
Chain SK:  100%



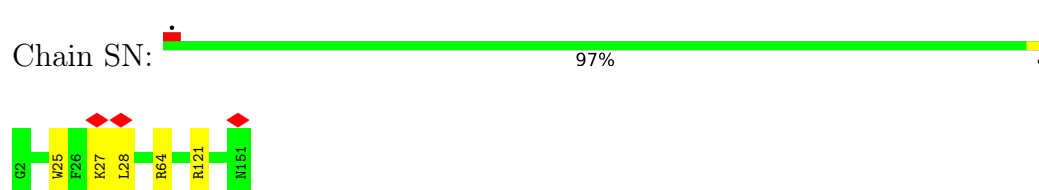
- Molecule 13: 40S ribosomal protein S11-A



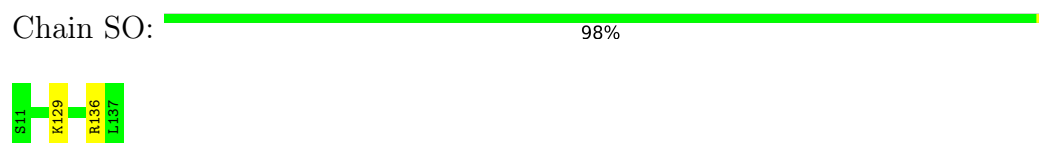
- Molecule 14: 40S ribosomal protein S12



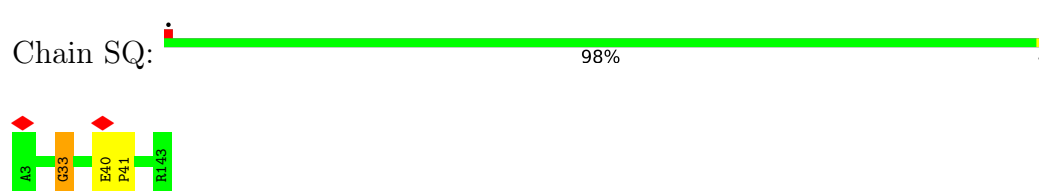
- Molecule 15: 40S ribosomal protein S13



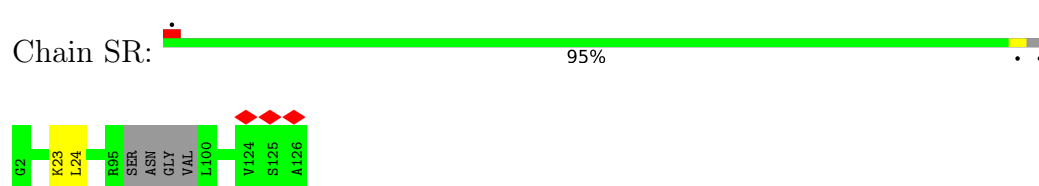
- Molecule 16: 40S ribosomal protein S14-B



- Molecule 17: 40S ribosomal protein S16-A

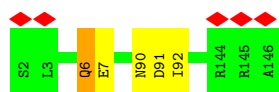


- Molecule 18: 40S ribosomal protein S17-A



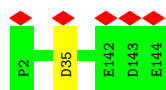
- Molecule 19: 40S ribosomal protein S18-A

Chain SS:  97% . .



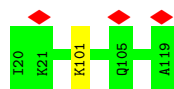
- Molecule 20: 40S ribosomal protein S19-A

Chain ST:  99% .



- Molecule 21: 40S ribosomal protein S20

Chain SU:  99% .



- Molecule 22: 40S ribosomal protein S21-A

Chain SV:  99% .



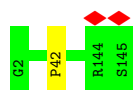
- Molecule 23: 40S ribosomal protein S22-A

Chain SW:  99% .



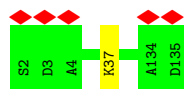
- Molecule 24: 40S ribosomal protein S23-A

Chain SX:  99% .

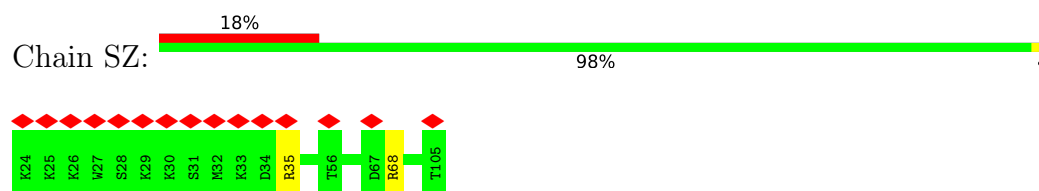


- Molecule 25: 40S ribosomal protein S24-A

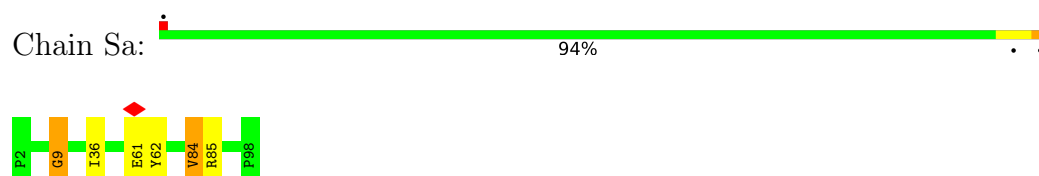
Chain SY:  99% .



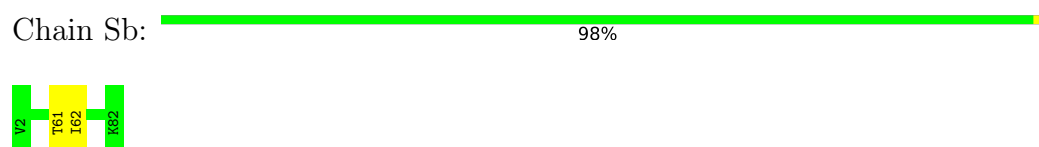
- Molecule 26: 40S ribosomal protein S25-A



- Molecule 27: 40S ribosomal protein S26-B



- Molecule 28: 40S ribosomal protein S27-A

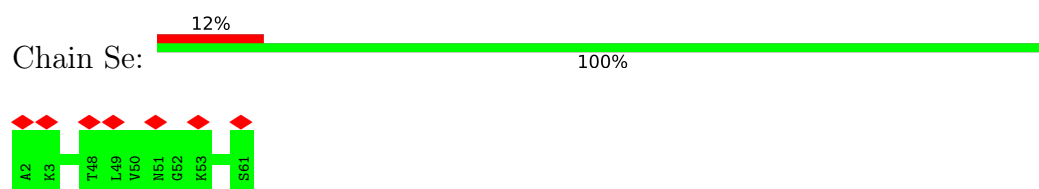


- Molecule 29: 40S ribosomal protein S29-A

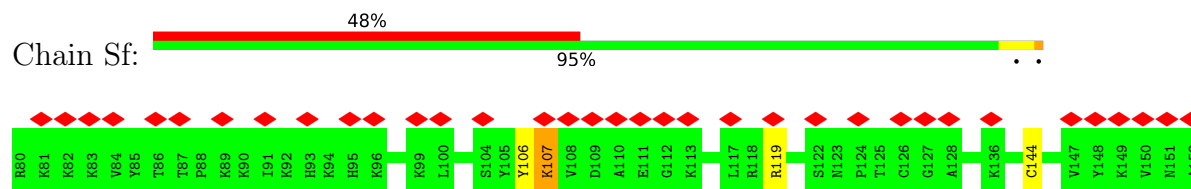


There are no outlier residues recorded for this chain.

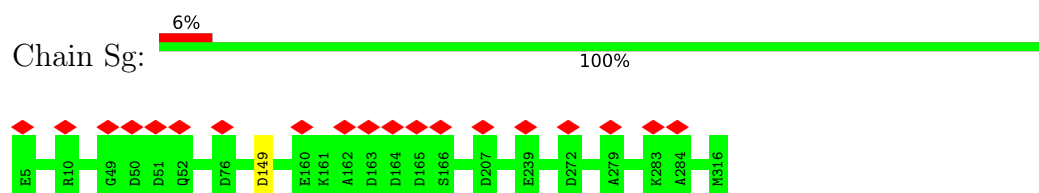
- Molecule 30: 40S ribosomal protein S30-A



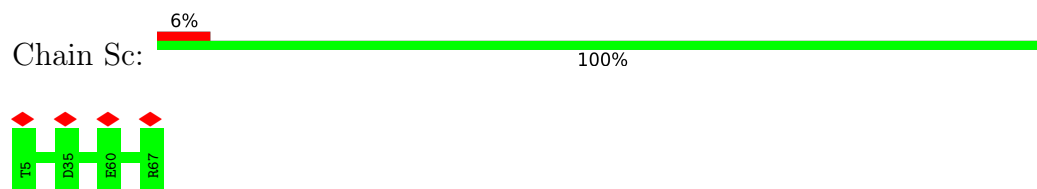
- Molecule 31: Ubiquitin-40S ribosomal protein S31



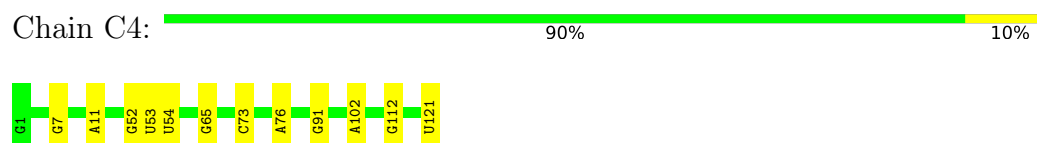
- Molecule 32: Guanine nucleotide-binding protein subunit beta-like protein



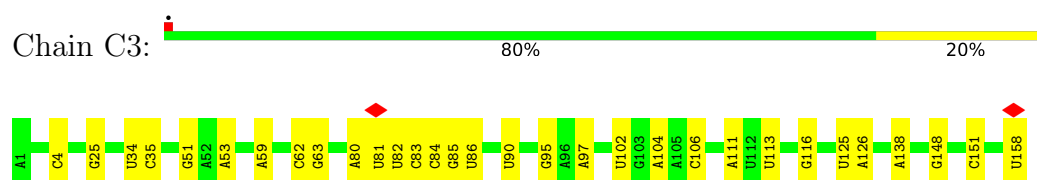
- Molecule 33: 40S ribosomal protein S28-A



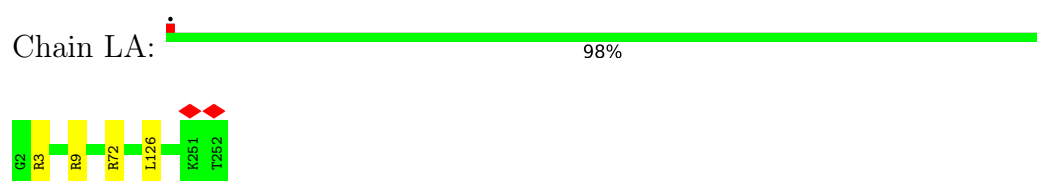
- Molecule 34: 5S rRNA



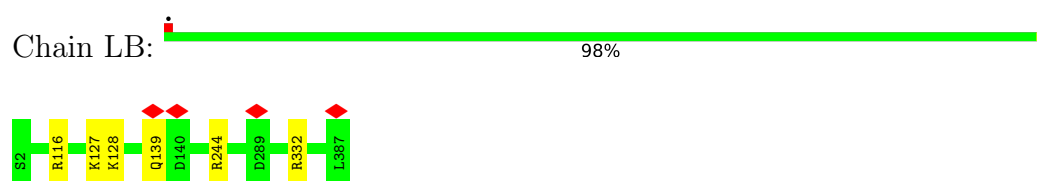
- Molecule 35: 5.8S rRNA



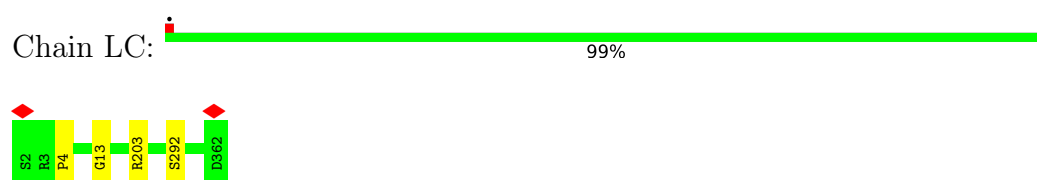
- Molecule 36: 60S ribosomal protein L2-A



- Molecule 37: 60S ribosomal protein L3

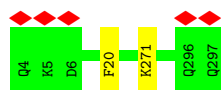


- Molecule 38: 60S ribosomal protein L4-A

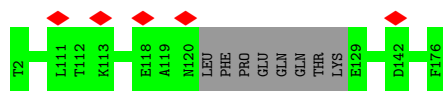


- Molecule 39: 60S ribosomal protein L5

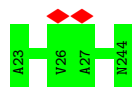




- Molecule 40: 60S ribosomal protein L6-B



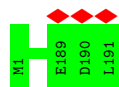
- Molecule 41: 60S ribosomal protein L7-A



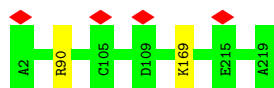
- Molecule 42: 60S ribosomal protein L8-A



- Molecule 43: 60S ribosomal protein L9-A



- Molecule 44: 60S ribosomal protein L10

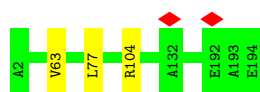


- Molecule 45: 60S ribosomal protein L11-B



- Molecule 46: 60S ribosomal protein L13-A

Chain LL:  98%



- Molecule 47: 60S ribosomal protein L14-A

Chain LM:  100%



- Molecule 48: 60S ribosomal protein L15-A

Chain LN:  99%



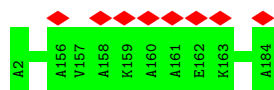
- Molecule 49: 60S ribosomal protein L16-A

Chain LO:  98%



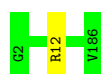
- Molecule 50: 60S ribosomal protein L17-A

Chain LP:  100%



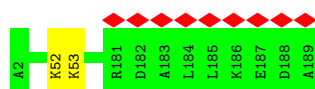
- Molecule 51: 60S ribosomal protein L18-A

Chain LQ:  99%



- Molecule 52: 60S ribosomal protein L19-A

Chain LR:  5% 99%



- Molecule 53: 60S ribosomal protein L20-A

Chain LS:  100%

There are no outlier residues recorded for this chain.

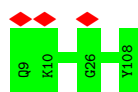
- Molecule 54: 60S ribosomal protein L21-A

Chain LT:  100%

There are no outlier residues recorded for this chain.

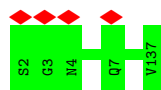
- Molecule 55: 60S ribosomal protein L22-A

Chain LU:  100%



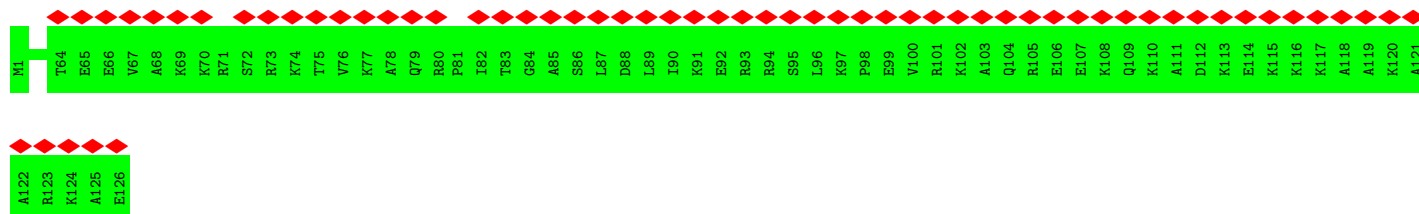
- Molecule 56: 60S ribosomal protein L23-A

Chain LV:  100%



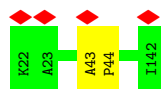
- Molecule 57: 60S ribosomal protein L24-A

Chain LW:  48% 100%



- Molecule 58: 60S ribosomal protein L25

Chain LX:  98%



- Molecule 59: 60S ribosomal protein L26-A

Chain LY:  100%

There are no outlier residues recorded for this chain.

- Molecule 60: 60S ribosomal protein L27-A

Chain LZ:  99% .



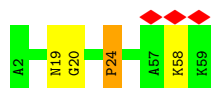
- Molecule 61: 60S ribosomal protein L28

Chain La:  98% ..



- Molecule 62: 60S ribosomal protein L29

Chain Lb:  5% 93% 5% .



- Molecule 63: 60S ribosomal protein L30

Chain Lc:  100%

There are no outlier residues recorded for this chain.

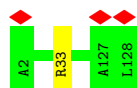
- Molecule 64: 60S ribosomal protein L31-A

Chain Ld:  6% 99% .



- Molecule 65: 60S ribosomal protein L32

Chain Le:  99% .



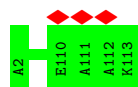
- Molecule 66: 60S ribosomal protein L33-A

Chain Lf:  100%

There are no outlier residues recorded for this chain.

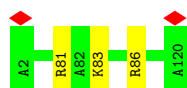
- Molecule 67: 60S ribosomal protein L34-A

Chain Lg:  100%



- Molecule 68: 60S ribosomal protein L35-A

Chain Lh:  97%



- Molecule 69: 60S ribosomal protein L36-A

Chain Li:  99%



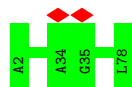
- Molecule 70: 60S ribosomal protein L37-A

Chain Lj:  99%



- Molecule 71: 60S ribosomal protein L38

Chain Lk:  100%



- Molecule 72: 60S ribosomal protein L39

Chain Ll:  100%

There are no outlier residues recorded for this chain.

- Molecule 73: Ubiquitin-60S ribosomal protein L40

Chain Lm:  100%

There are no outlier residues recorded for this chain.

- Molecule 74: 60S ribosomal protein L41-A

Chain Ln:  100%

There are no outlier residues recorded for this chain.

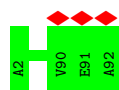
• Molecule 75: 60S ribosomal protein L42-A

Chain Lo:  99%


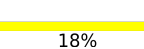


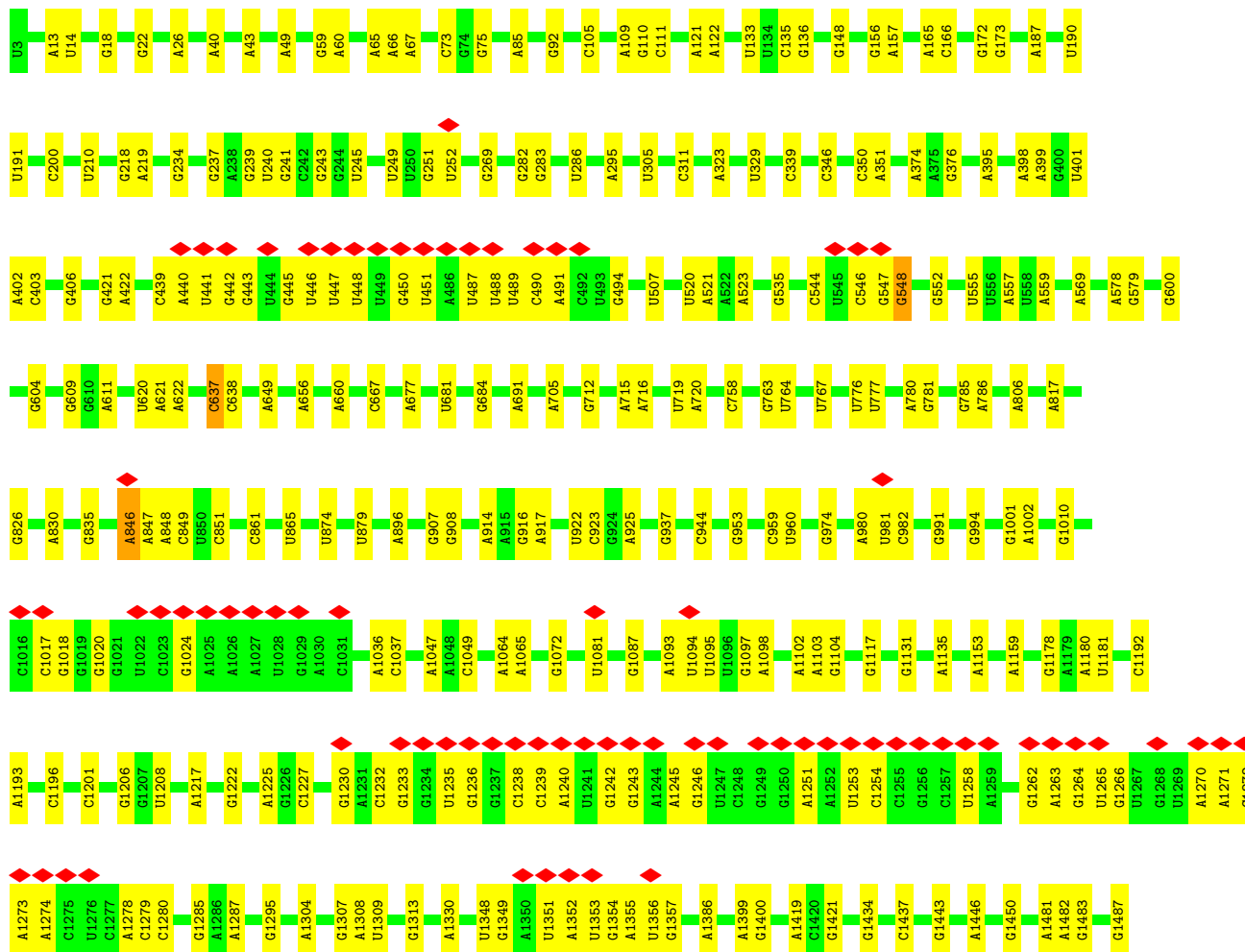
• Molecule 76: 60S ribosomal protein L43-A

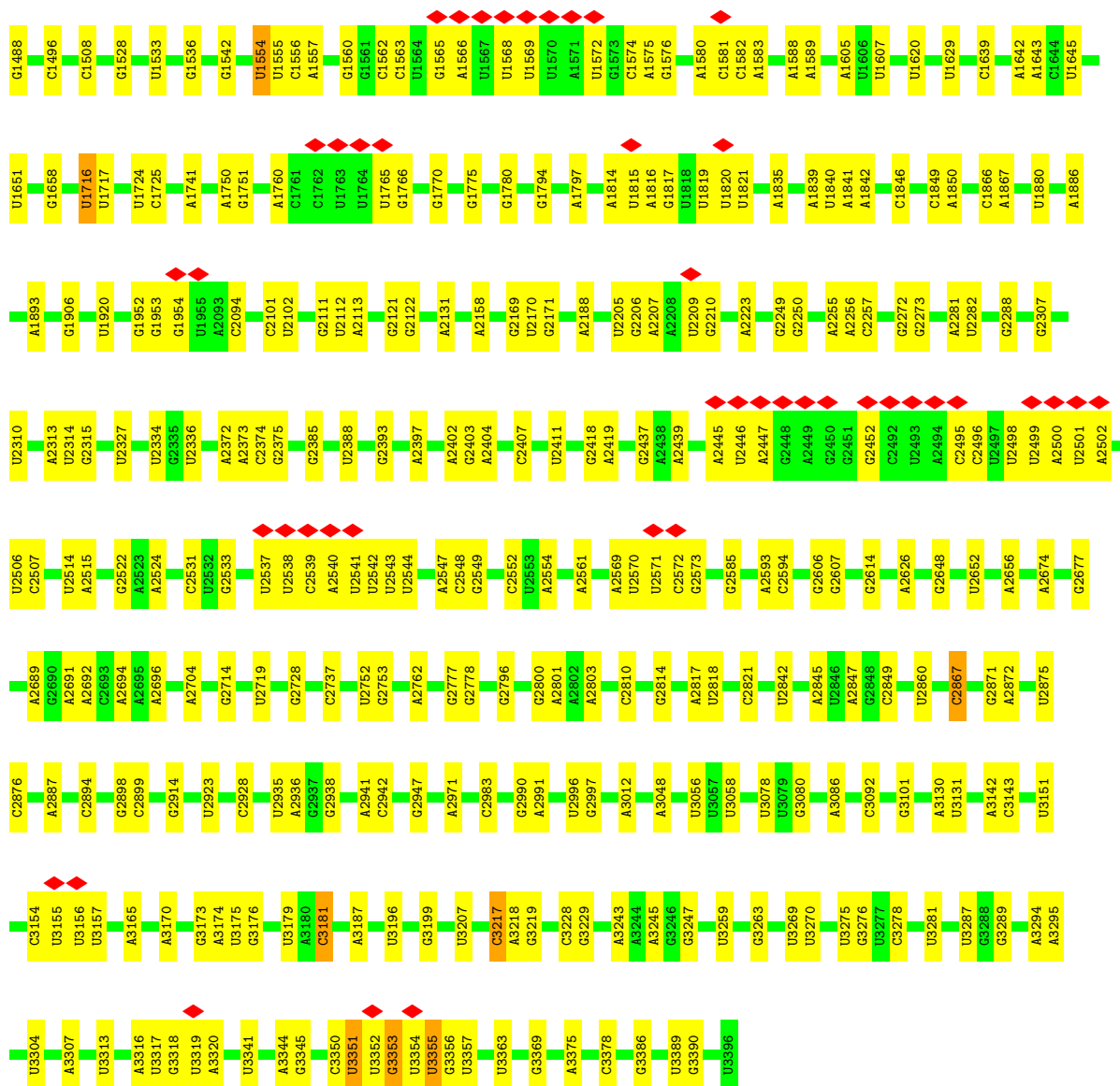
Chain Lp:  100%



• Molecule 77: 25S rRNA

Chain C1:  82%  18%

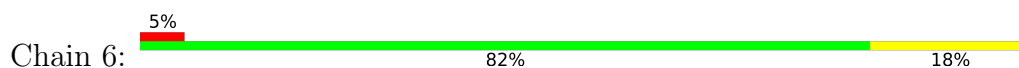




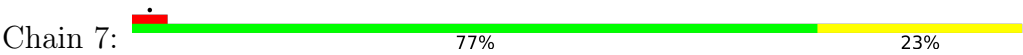
- Molecule 78: mRNA



- Molecule 79: ICG tRNA Arg (P/P)



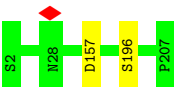
- Molecule 80: tRNA (E/E)



- Molecule 81: nascent chain



- Molecule 82: 40S ribosomal protein S0-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	550205	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 ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.531	Depositor
Minimum map value	-0.739	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.035	Depositor
Recommended contour level	0.0612	Depositor
Map size (Å)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	C2	0.99	8/42053 (0.0%)	0.94	46/65522 (0.1%)
2	SB	0.35	0/1823	0.62	0/2447
3	SP	0.30	0/936	0.55	0/1259
4	SC	0.39	0/1656	0.57	0/2251
5	SD	0.32	0/1754	0.53	0/2361
6	SE	0.39	0/2097	0.58	0/2823
7	SF	0.30	0/1625	0.56	0/2197
8	SG	0.32	0/1839	0.62	0/2460
9	SH	0.33	0/1498	0.58	0/2019
10	SI	0.40	0/1501	0.62	0/2006
11	SJ	0.35	0/1504	0.60	0/2016
12	SK	0.32	0/769	0.50	0/1039
13	SL	0.47	0/1185	0.59	0/1598
14	SM	0.32	0/883	0.71	0/1199
15	SN	0.40	0/1215	0.67	1/1638 (0.1%)
16	SO	0.38	0/937	0.67	0/1261
17	SQ	0.34	0/1125	0.55	0/1510
18	SR	0.30	0/957	0.53	0/1283
19	SS	0.29	0/1211	0.59	0/1628
20	ST	0.32	0/1130	0.54	1/1517 (0.1%)
21	SU	0.31	0/807	0.55	0/1091
22	SV	0.38	0/682	0.59	0/921
23	SW	0.43	0/1038	0.61	1/1395 (0.1%)
24	SX	0.40	0/1139	0.62	0/1518
25	SY	0.33	0/1087	0.54	0/1449
26	SZ	0.29	0/661	0.59	0/888
27	Sa	0.40	0/782	0.73	0/1047
28	Sb	0.37	0/620	0.59	0/838
29	Sd	0.35	0/452	0.53	0/600
30	Se	0.32	0/480	0.56	0/639
31	Sf	0.29	0/567	0.66	0/764
32	Sg	0.28	0/2436	0.53	0/3318

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sc	0.32	0/493	0.64	0/663
34	C4	0.57	0/2883	0.85	0/4491
35	C3	0.78	0/3746	0.92	1/5832 (0.0%)
36	LA	0.49	0/1933	0.71	3/2598 (0.1%)
37	LB	0.45	0/3146	0.61	2/4228 (0.0%)
38	LC	0.46	0/2800	0.59	0/3790
39	LD	0.36	0/2400	0.55	0/3239
40	LE	0.38	0/1327	0.54	0/1790
41	LF	0.45	0/1821	0.53	0/2451
42	LG	0.41	0/1836	0.53	0/2481
43	LH	0.38	0/1529	0.53	0/2060
44	LI	0.40	0/1801	0.55	0/2416
45	LJ	0.32	0/1371	0.58	0/1838
46	LL	0.45	0/1568	0.65	0/2106
47	LM	0.37	0/1068	0.57	0/1438
48	LN	0.52	0/1757	0.69	0/2354
49	LO	0.46	0/1585	0.58	0/2128
50	LP	0.45	0/1439	0.63	0/1938
51	LQ	0.43	0/1465	0.61	0/1965
52	LR	0.42	0/1532	0.63	0/2043
53	LS	0.43	0/1473	0.55	0/1980
54	LT	0.43	0/1300	0.56	0/1743
55	LU	0.38	0/812	0.54	0/1099
56	LV	0.43	0/1018	0.59	0/1369
57	LW	0.38	0/850	0.52	0/1152
58	LX	0.44	0/979	0.58	0/1321
59	LY	0.41	0/995	0.63	0/1329
60	LZ	0.43	0/1118	0.54	0/1497
61	La	0.48	0/1204	0.62	0/1612
62	Lb	0.37	0/473	0.57	0/629
63	Lc	0.42	0/745	0.54	0/1001
64	Ld	0.44	0/890	0.60	0/1196
65	Le	0.44	0/1038	0.61	2/1390 (0.1%)
66	Lf	0.49	0/868	0.60	0/1168
67	Lg	0.46	0/890	0.63	0/1189
68	Lh	0.39	0/978	0.60	1/1301 (0.1%)
69	Li	0.35	0/772	0.56	0/1026
70	Lj	0.53	0/685	0.76	1/908 (0.1%)
71	Lk	0.36	0/618	0.53	0/826
72	Ll	0.43	0/443	0.64	0/588
73	Lm	0.40	0/423	0.54	0/562
74	Ln	0.43	0/230	0.66	0/296
75	Lo	0.43	0/836	0.61	0/1104

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lp	0.46	0/701	0.66	0/934
77	C1	1.08	7/76214 (0.0%)	0.95	44/118821 (0.0%)
78	5	0.29	0/746	0.77	0/1161
79	6	0.42	0/1810	0.87	0/2817
80	7	0.32	0/1773	0.82	0/2759
81	8	0.33	0/54	0.77	0/71
82	SA	0.34	0/1644	0.53	0/2249
All	All	0.83	15/218529 (0.0%)	0.83	103/321449 (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
2	SB	0	1
6	SE	0	1
8	SG	0	1
9	SH	0	1
13	SL	0	1
14	SM	0	3
15	SN	0	1
17	SQ	0	2
19	SS	0	2
27	Sa	0	4
28	Sb	0	1
31	Sf	0	2
37	LB	0	2
38	LC	0	1
42	LG	0	2
45	LJ	0	1
49	LO	0	1
58	LX	0	1
61	La	0	1
62	Lb	0	3
64	Ld	0	1
68	Lh	0	1
All	All	0	34

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C2	629	U	C5-C6	152.50	2.71	1.34
77	C1	846	A	C5-C6	135.50	2.63	1.41
77	C1	846	A	N3-C4	88.94	1.88	1.34
77	C1	846	A	C6-N1	83.90	1.94	1.35
77	C1	846	A	C5-C4	82.38	1.96	1.38

The worst 5 of 103 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	629	U	C2-N3-C4	44.00	153.40	127.00
77	C1	846	A	C2-N3-C4	40.91	131.06	110.60
77	C1	846	A	C4-C5-N7	-38.76	91.32	110.70
1	C2	629	U	C4-C5-C6	-36.39	97.87	119.70
77	C1	846	A	C6-C5-N7	31.79	154.55	132.30

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	SB	81	PHE	Peptide
6	SE	42	LEU	Peptide
8	SG	68	LEU	Peptide
9	SH	64	VAL	Peptide
13	SL	4	GLU	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SB	222/232 (96%)	192 (86%)	27 (12%)	3 (1%)	11	22
3	SP	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
4	SC	214/216 (99%)	197 (92%)	16 (8%)	1 (0%)	29	52
5	SD	220/222 (99%)	211 (96%)	9 (4%)	0	100	100
6	SE	256/258 (99%)	235 (92%)	20 (8%)	1 (0%)	34	57
7	SF	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
8	SG	226/228 (99%)	209 (92%)	14 (6%)	3 (1%)	12	24
9	SH	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	29	52
10	SI	183/198 (92%)	166 (91%)	14 (8%)	3 (2%)	9	19
11	SJ	182/184 (99%)	162 (89%)	18 (10%)	2 (1%)	14	30
12	SK	90/92 (98%)	75 (83%)	15 (17%)	0	100	100
13	SL	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
14	SM	119/121 (98%)	80 (67%)	32 (27%)	7 (6%)	1	1
15	SN	148/150 (99%)	136 (92%)	10 (7%)	2 (1%)	11	22
16	SO	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
17	SQ	139/141 (99%)	126 (91%)	11 (8%)	2 (1%)	11	22
18	SR	117/125 (94%)	109 (93%)	6 (5%)	2 (2%)	9	18
19	SS	143/145 (99%)	126 (88%)	13 (9%)	4 (3%)	5	7
20	ST	141/143 (99%)	127 (90%)	14 (10%)	0	100	100
21	SU	98/100 (98%)	90 (92%)	8 (8%)	0	100	100
22	SV	85/87 (98%)	72 (85%)	12 (14%)	1 (1%)	13	27
23	SW	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
24	SX	142/144 (99%)	121 (85%)	20 (14%)	1 (1%)	22	43
25	SY	132/134 (98%)	123 (93%)	8 (6%)	1 (1%)	19	39
26	SZ	80/82 (98%)	66 (82%)	13 (16%)	1 (1%)	12	24
27	Sa	95/97 (98%)	77 (81%)	14 (15%)	4 (4%)	3	3
28	Sb	79/81 (98%)	70 (89%)	8 (10%)	1 (1%)	12	24
29	Sd	51/53 (96%)	51 (100%)	0	0	100	100
30	Se	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
31	Sf	71/73 (97%)	45 (63%)	25 (35%)	1 (1%)	11	22
32	Sg	310/312 (99%)	279 (90%)	31 (10%)	0	100	100
33	Sc	61/63 (97%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LA	249/251 (99%)	234 (94%)	14 (6%)	1 (0%)	34	57
37	LB	384/386 (100%)	357 (93%)	26 (7%)	1 (0%)	41	64
38	LC	359/361 (99%)	326 (91%)	31 (9%)	2 (1%)	25	47
39	LD	292/294 (99%)	273 (94%)	18 (6%)	1 (0%)	41	64
40	LE	163/175 (93%)	156 (96%)	7 (4%)	0	100	100
41	LF	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
42	LG	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
43	LH	189/191 (99%)	175 (93%)	14 (7%)	0	100	100
44	LI	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
45	LJ	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
46	LL	191/193 (99%)	171 (90%)	18 (9%)	2 (1%)	15	32
47	LM	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
48	LN	201/203 (99%)	188 (94%)	12 (6%)	1 (0%)	29	52
49	LO	195/197 (99%)	188 (96%)	5 (3%)	2 (1%)	15	32
50	LP	181/183 (99%)	168 (93%)	13 (7%)	0	100	100
51	LQ	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
52	LR	186/188 (99%)	180 (97%)	4 (2%)	2 (1%)	14	30
53	LS	169/171 (99%)	162 (96%)	7 (4%)	0	100	100
54	LT	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
55	LU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
56	LV	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
57	LW	124/126 (98%)	113 (91%)	11 (9%)	0	100	100
58	LX	119/121 (98%)	114 (96%)	4 (3%)	1 (1%)	19	39
59	LY	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
60	LZ	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
61	La	146/148 (99%)	127 (87%)	17 (12%)	2 (1%)	11	22
62	Lb	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	8	16
63	Lc	94/96 (98%)	94 (100%)	0	0	100	100
64	Ld	107/109 (98%)	96 (90%)	11 (10%)	0	100	100
65	Le	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
66	Lf	104/106 (98%)	102 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	Lg	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
68	Lh	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
69	Li	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
70	Lj	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
71	Lk	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
72	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
73	Lm	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
74	Ln	23/25 (92%)	23 (100%)	0	0	100	100
75	Lo	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
76	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
81	8	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
82	SA	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	15	32
All	All	10988/11175 (98%)	10103 (92%)	826 (8%)	59 (0%)	32	52

5 of 59 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	SE	43	PRO
8	SG	68	LEU
10	SI	10	LYS
27	Sa	84	VAL
49	LO	111[A]	PRO

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	
2	SB	200/205 (98%)	200 (100%)	0	100	100
3	SP	95/98 (97%)	95 (100%)	0	100	100
4	SC	175/175 (100%)	175 (100%)	0	100	100
5	SD	182/182 (100%)	179 (98%)	3 (2%)	62	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	SE	220/220 (100%)	219 (100%)	1 (0%)	88	96
7	SF	172/173 (99%)	170 (99%)	2 (1%)	71	87
8	SG	189/195 (97%)	188 (100%)	1 (0%)	88	96
9	SH	163/165 (99%)	163 (100%)	0	100	100
10	SI	148/159 (93%)	147 (99%)	1 (1%)	84	94
11	SJ	156/157 (99%)	155 (99%)	1 (1%)	86	95
12	SK	77/85 (91%)	77 (100%)	0	100	100
13	SL	129/129 (100%)	127 (98%)	2 (2%)	62	82
14	SM	88/98 (90%)	88 (100%)	0	100	100
15	SN	127/127 (100%)	126 (99%)	1 (1%)	81	92
16	SO	91/96 (95%)	89 (98%)	2 (2%)	52	76
17	SQ	117/117 (100%)	117 (100%)	0	100	100
18	SR	101/113 (89%)	101 (100%)	0	100	100
19	SS	128/128 (100%)	128 (100%)	0	100	100
20	ST	115/115 (100%)	115 (100%)	0	100	100
21	SU	93/93 (100%)	92 (99%)	1 (1%)	73	88
22	SV	71/74 (96%)	71 (100%)	0	100	100
23	SW	110/110 (100%)	110 (100%)	0	100	100
24	SX	119/119 (100%)	119 (100%)	0	100	100
25	SY	112/112 (100%)	112 (100%)	0	100	100
26	SZ	67/73 (92%)	66 (98%)	1 (2%)	65	83
27	Sa	83/83 (100%)	83 (100%)	0	100	100
28	Sb	70/70 (100%)	70 (100%)	0	100	100
29	Sd	47/47 (100%)	47 (100%)	0	100	100
30	Se	50/51 (98%)	50 (100%)	0	100	100
31	Sf	56/63 (89%)	54 (96%)	2 (4%)	35	61
32	Sg	250/257 (97%)	249 (100%)	1 (0%)	91	97
33	Sc	55/56 (98%)	55 (100%)	0	100	100
36	LA	190/193 (98%)	189 (100%)	1 (0%)	88	96
37	LB	319/322 (99%)	318 (100%)	1 (0%)	92	98
38	LC	288/288 (100%)	287 (100%)	1 (0%)	92	98

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	LD	241/243 (99%)	240 (100%)	1 (0%)	91	97
40	LE	138/153 (90%)	138 (100%)	0	100	100
41	LF	186/186 (100%)	186 (100%)	0	100	100
42	LG	187/191 (98%)	186 (100%)	1 (0%)	88	96
43	LH	168/171 (98%)	168 (100%)	0	100	100
44	LI	185/185 (100%)	183 (99%)	2 (1%)	73	88
45	LJ	146/147 (99%)	146 (100%)	0	100	100
46	LL	154/154 (100%)	153 (99%)	1 (1%)	86	95
47	LM	107/107 (100%)	107 (100%)	0	100	100
48	LN	175/175 (100%)	174 (99%)	1 (1%)	86	95
49	LO	160/160 (100%)	159 (99%)	1 (1%)	86	95
50	LP	138/145 (95%)	138 (100%)	0	100	100
51	LQ	150/150 (100%)	149 (99%)	1 (1%)	84	94
52	LR	152/153 (99%)	152 (100%)	0	100	100
53	LS	155/155 (100%)	155 (100%)	0	100	100
54	LT	136/136 (100%)	136 (100%)	0	100	100
55	LU	87/87 (100%)	87 (100%)	0	100	100
56	LV	104/104 (100%)	104 (100%)	0	100	100
57	LW	56/107 (52%)	56 (100%)	0	100	100
58	LX	104/105 (99%)	104 (100%)	0	100	100
59	LY	108/108 (100%)	108 (100%)	0	100	100
60	LZ	115/115 (100%)	114 (99%)	1 (1%)	78	91
61	La	118/118 (100%)	117 (99%)	1 (1%)	81	92
62	Lb	46/46 (100%)	45 (98%)	1 (2%)	52	76
63	Lc	81/81 (100%)	81 (100%)	0	100	100
64	Ld	92/96 (96%)	92 (100%)	0	100	100
65	Le	108/109 (99%)	108 (100%)	0	100	100
66	Lf	90/90 (100%)	90 (100%)	0	100	100
67	Lg	95/95 (100%)	95 (100%)	0	100	100
68	Lh	104/104 (100%)	103 (99%)	1 (1%)	76	90
69	Li	80/81 (99%)	79 (99%)	1 (1%)	69	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	Lj	69/69 (100%)	69 (100%)	0	100	100
71	Lk	68/68 (100%)	68 (100%)	0	100	100
72	Ll	45/45 (100%)	45 (100%)	0	100	100
73	Lm	47/47 (100%)	47 (100%)	0	100	100
74	Ln	22/23 (96%)	22 (100%)	0	100	100
75	Lo	87/88 (99%)	86 (99%)	1 (1%)	73	88
76	Lp	71/71 (100%)	71 (100%)	0	100	100
81	8	5/6 (83%)	5 (100%)	0	100	100
82	SA	170/173 (98%)	170 (100%)	0	100	100
All	All	9203/9395 (98%)	9167 (100%)	36 (0%)	91	97

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	LO	176[A]	LYS
75	Lo	80	ARG
51	LQ	12	ARG
62	Lb	58	LYS
16	SO	129	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
33	Sc	43	ASN
66	Lf	75	HIS
39	LD	274	GLN
67	Lg	108	GLN
55	LU	9	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1768/1798 (98%)	462 (26%)	50 (2%)
34	C4	120/121 (99%)	11 (9%)	1 (0%)
35	C3	157/158 (99%)	30 (19%)	1 (0%)
77	C1	3180/3184 (99%)	564 (17%)	38 (1%)
78	5	28/30 (93%)	12 (42%)	2 (7%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
79	6	75/76 (98%)	14 (18%)	0
80	7	74/75 (98%)	17 (22%)	0
All	All	5402/5442 (99%)	1110 (20%)	92 (1%)

5 of 1110 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C2	2	A
1	C2	4	C
1	C2	17	C
1	C2	25	C
1	C2	26	A

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
77	C1	637	C
77	C1	1716	U
77	C1	763	G
77	C1	1307	G
77	C1	2112	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 298 ligands modelled in this entry, 298 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
77	C1	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C1	1955:U	O3'	2093:A	P	25.82
1	C1	2452:G	O3'	2492:C	P	17.25
1	C1	451:U	O3'	486:A	P	9.70

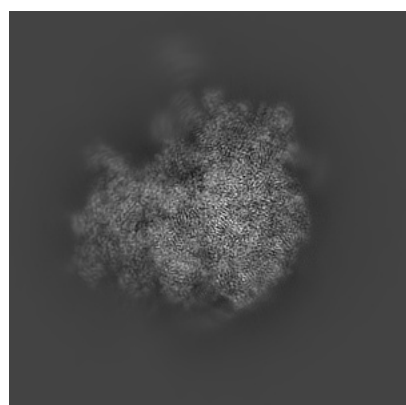
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10377. These allow visual inspection of the internal detail of the map and identification of artifacts.

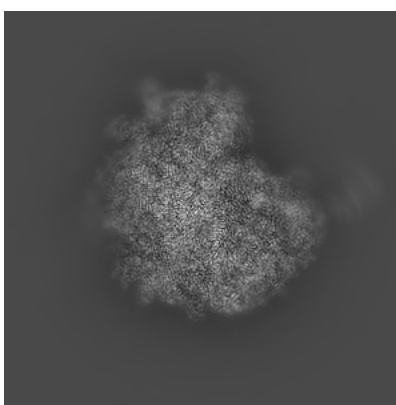
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

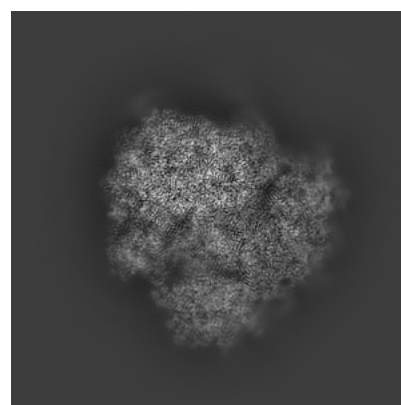
6.1.1 Primary map



X



Y

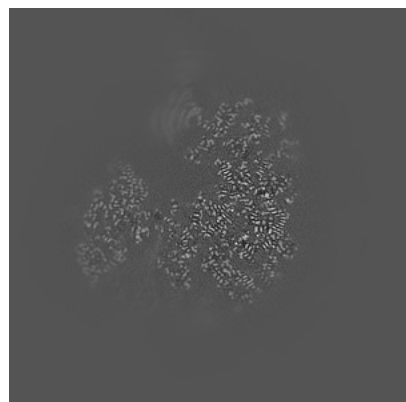


Z

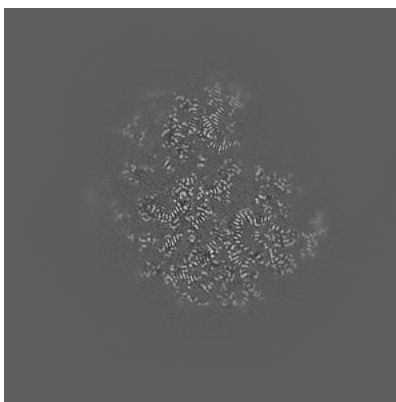
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

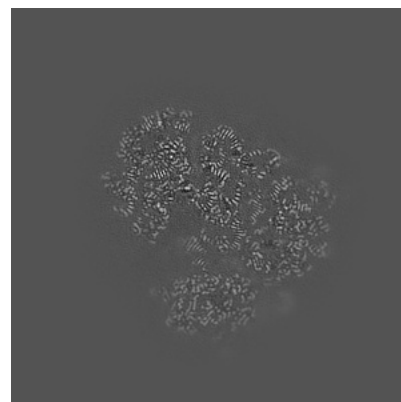
6.2.1 Primary map



X Index: 200



Y Index: 200

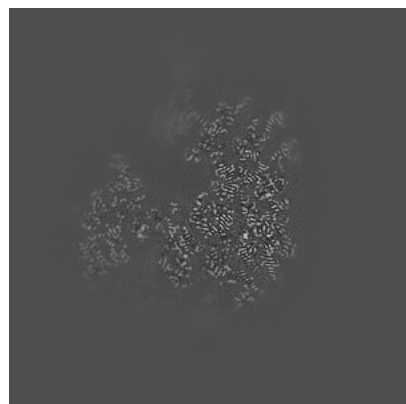


Z Index: 200

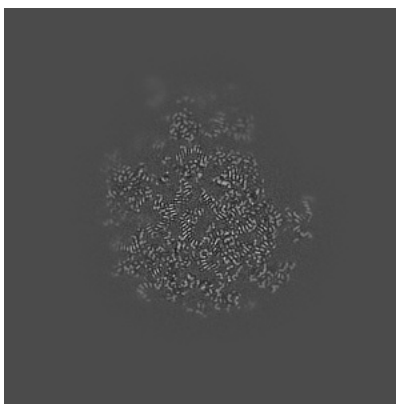
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

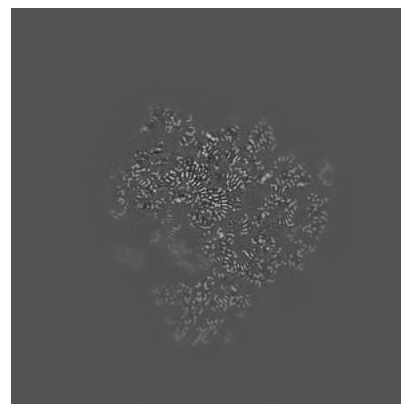
6.3.1 Primary map



X Index: 203



Y Index: 232

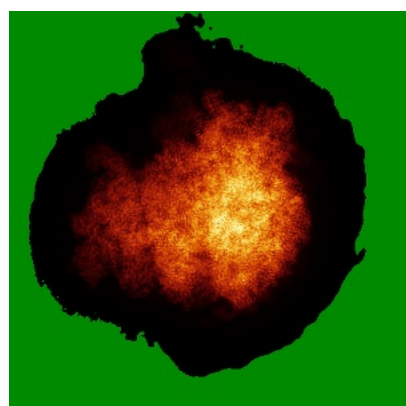


Z Index: 181

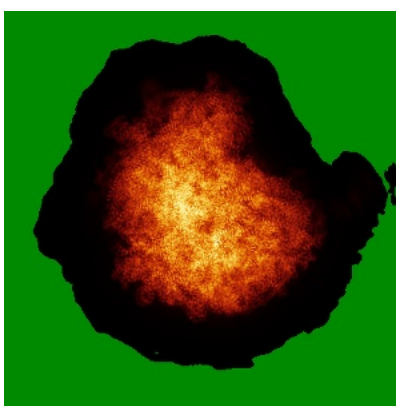
The images above show the largest variance slices of the map in three orthogonal directions.

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

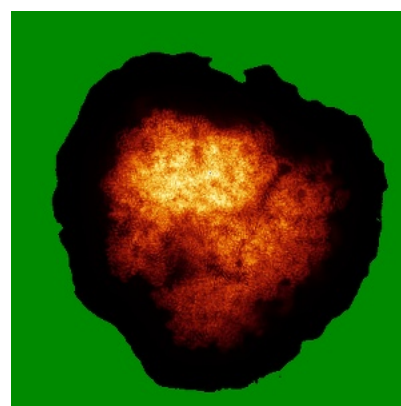
6.4.1 Primary map



X



Y

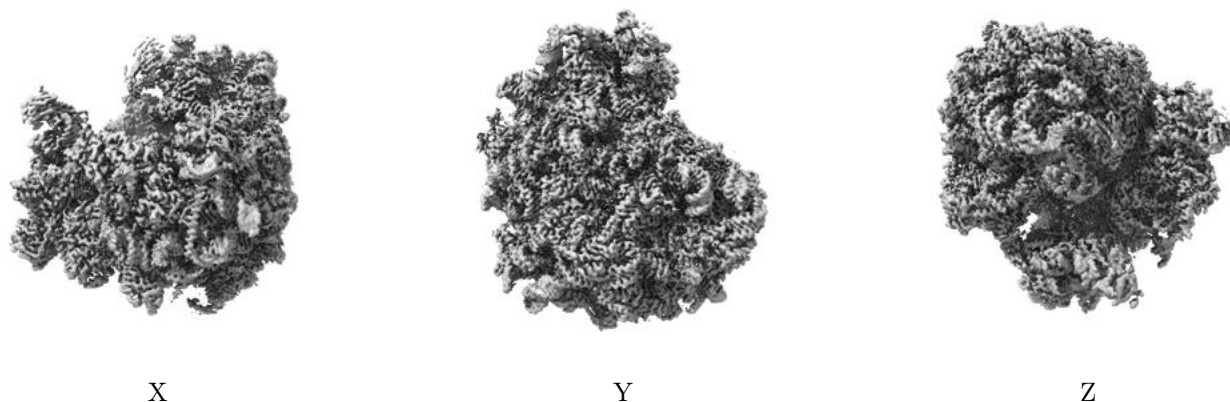


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0612. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

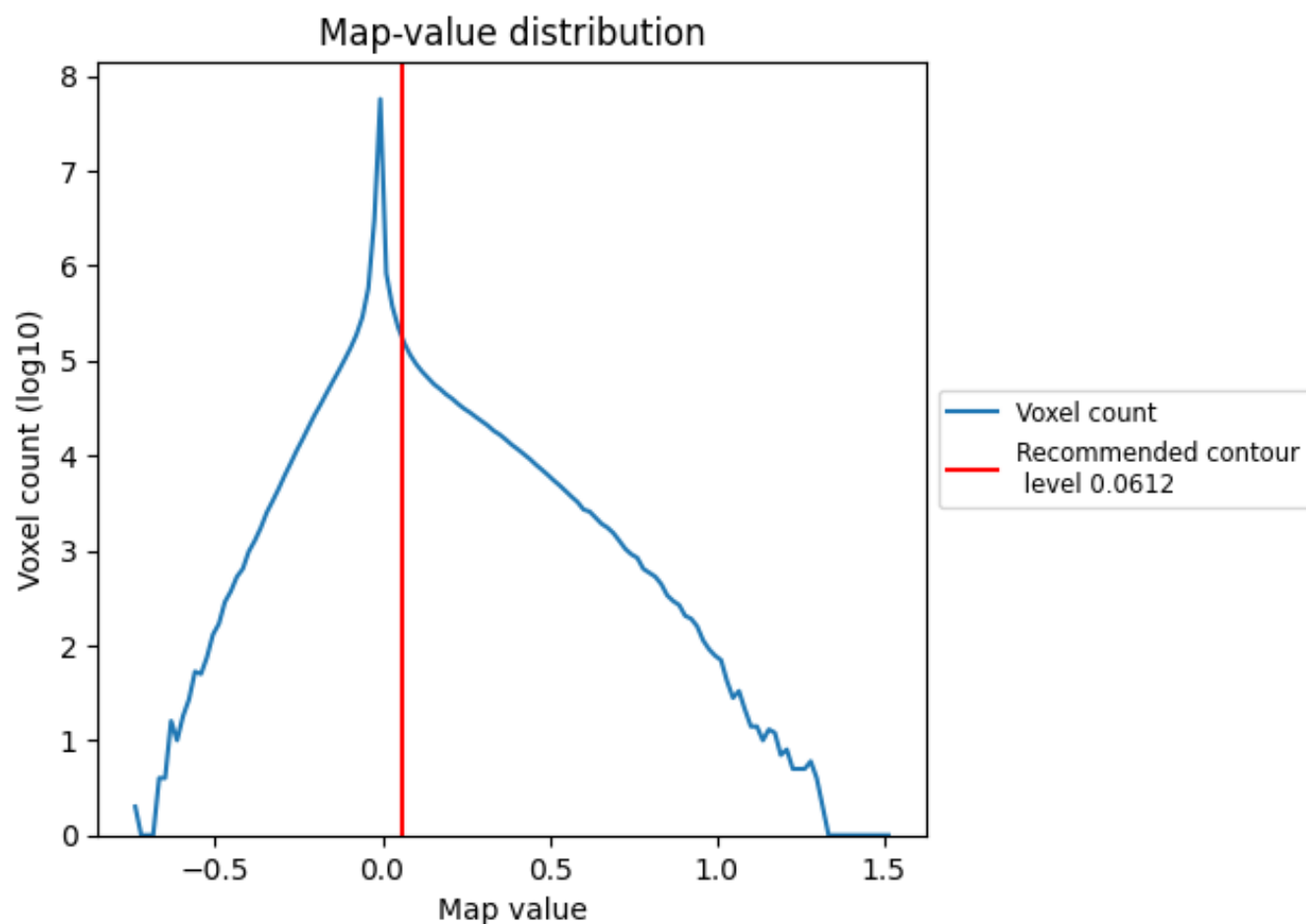
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

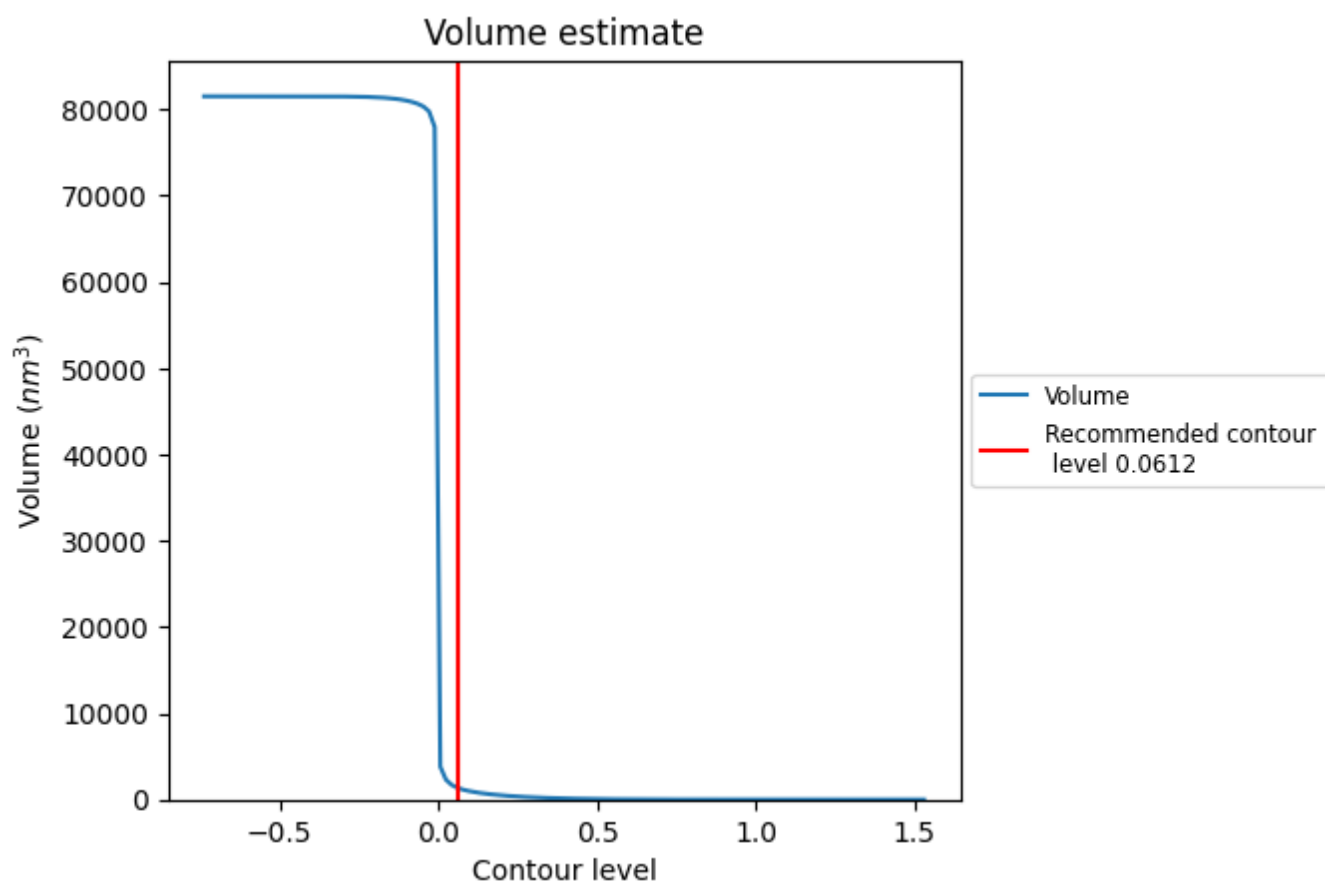
This section contains the results of statistical analysis of the map.

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.

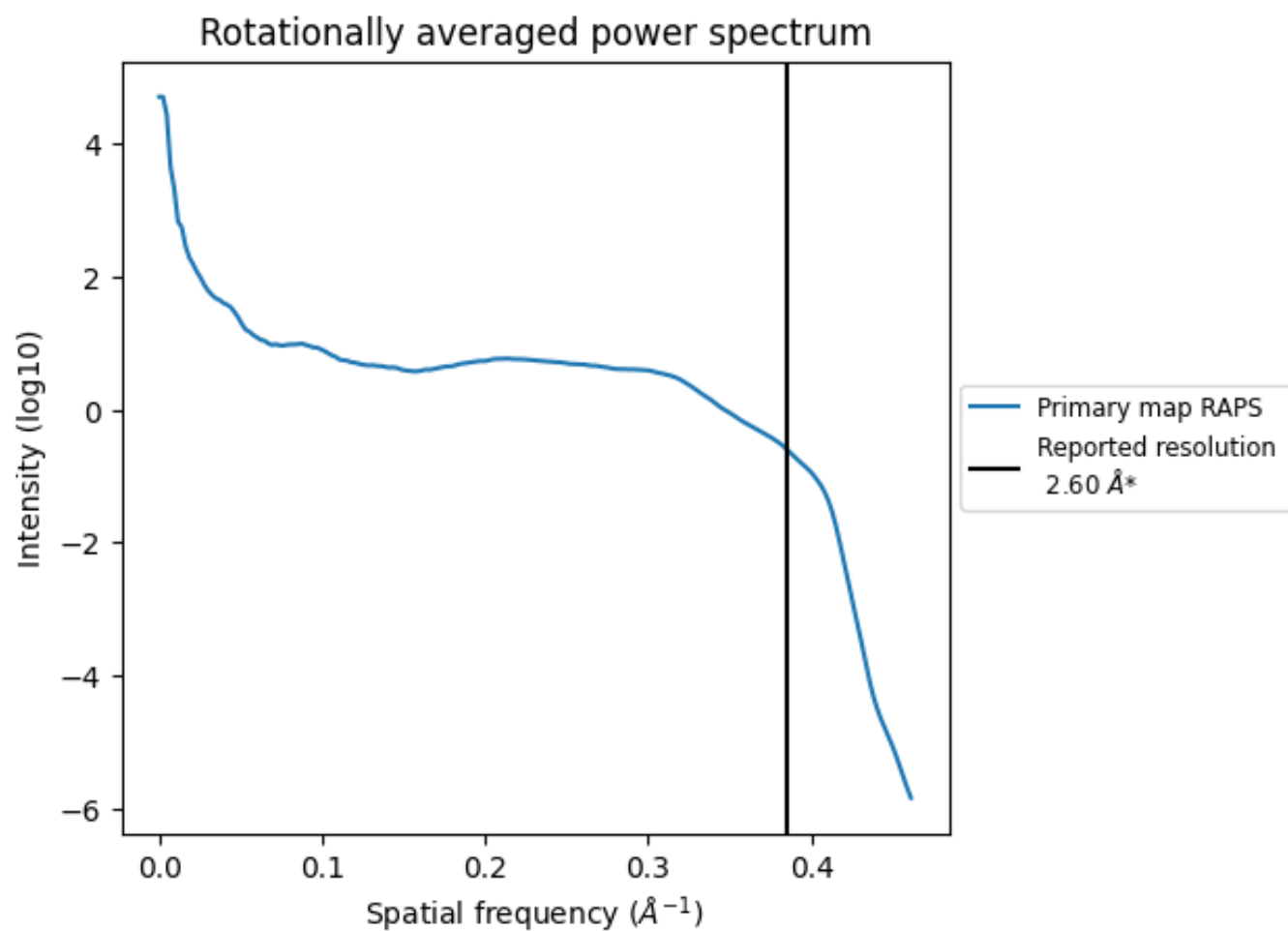
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1353 nm^3 ; this corresponds to an approximate mass of 1222 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 ⓘ

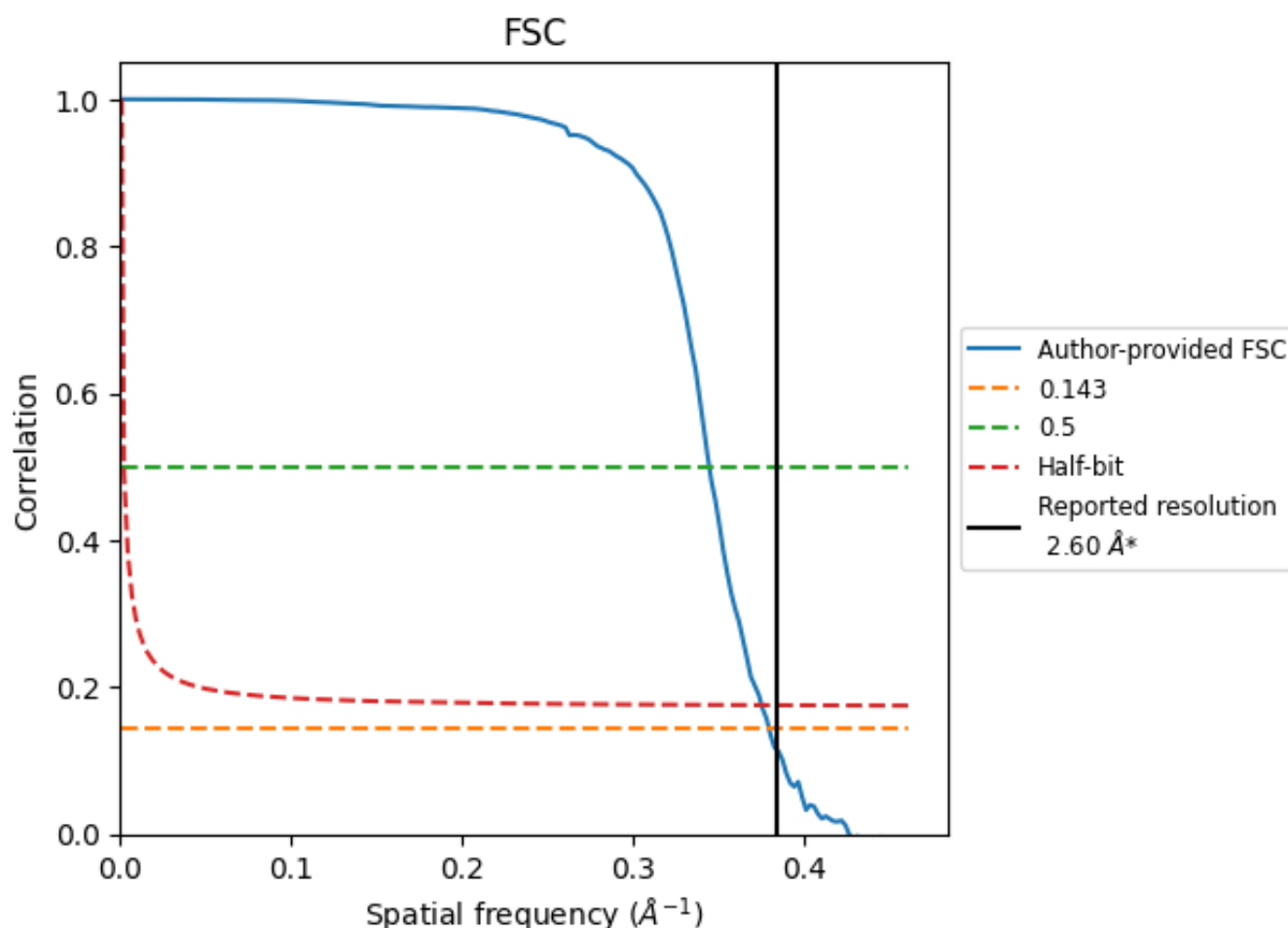


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

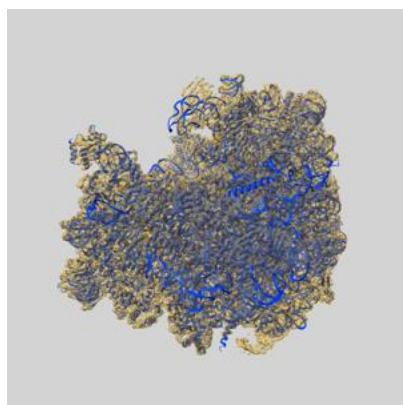
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.63	2.90	2.66
Unmasked-calculated*	-	-	-

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

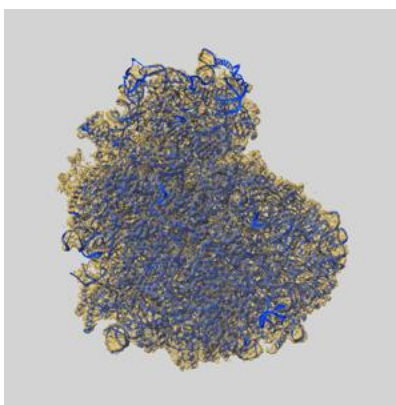
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10377 and PDB model 6T4Q. Per-residue inclusion information can be found in section [3](#) on page [20](#).

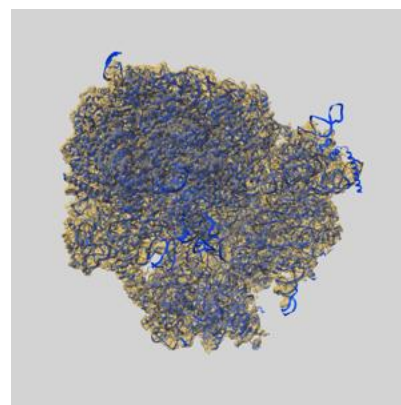
9.1 Map-model overlay [i](#)



X



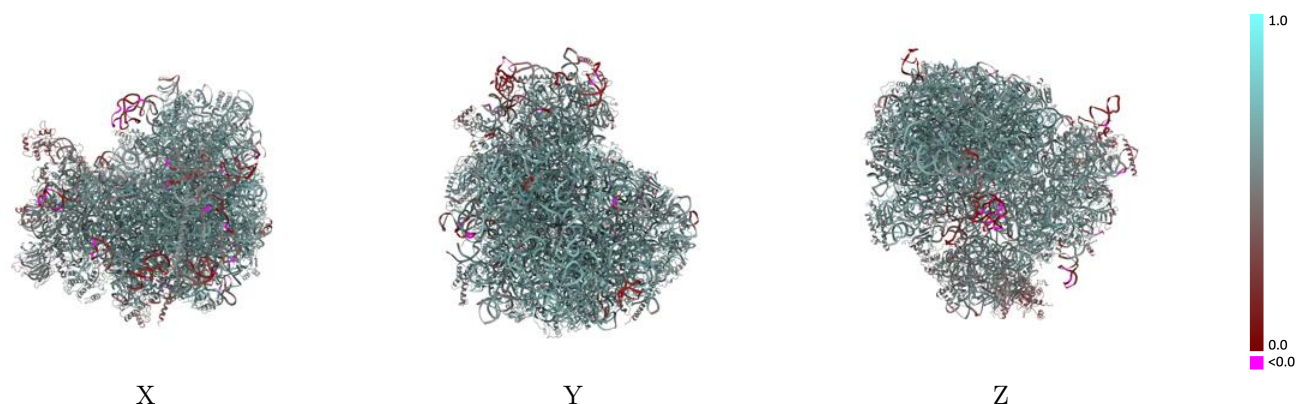
Y



Z

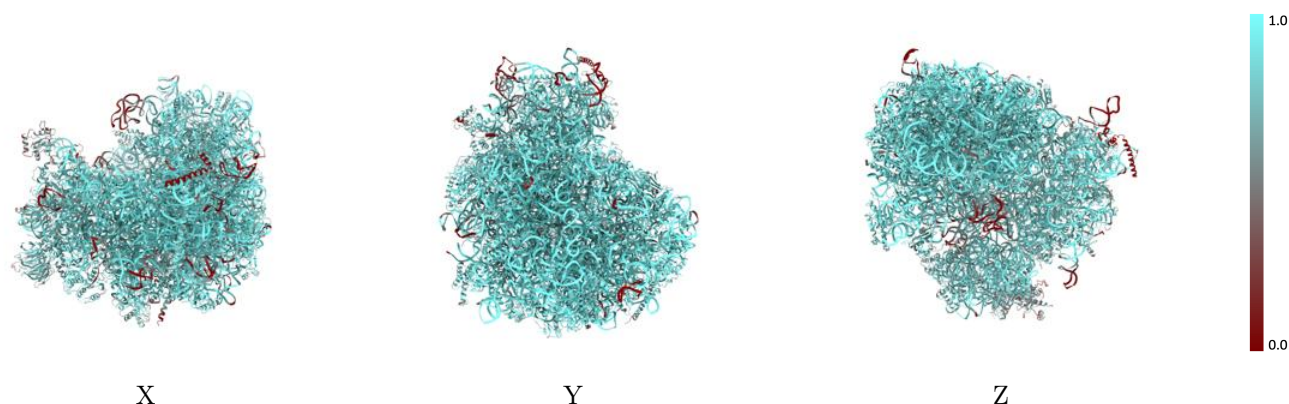
The images above show the 3D surface view of the map at the recommended contour level 0.0612 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



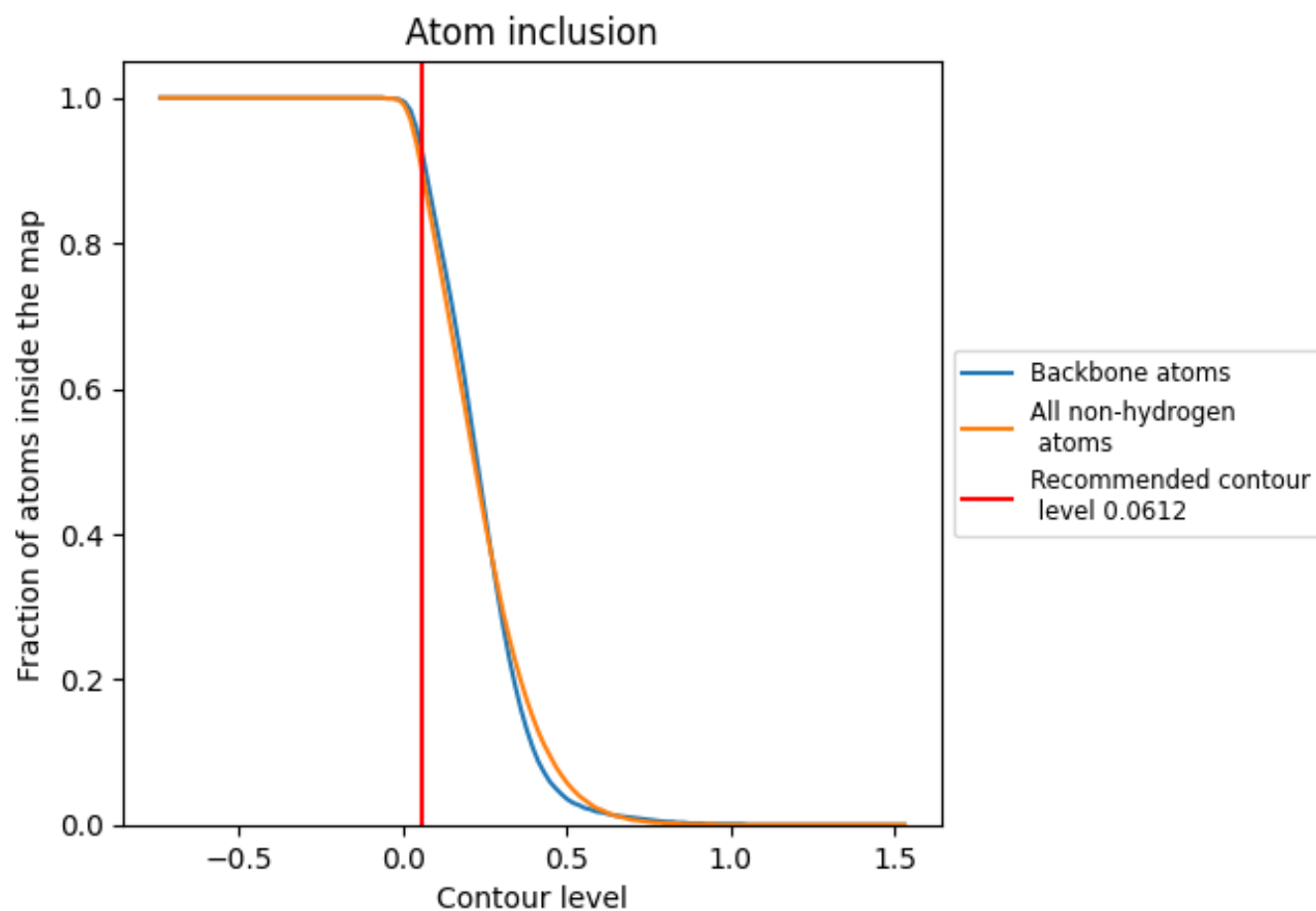
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0612).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.0612) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.5810
5	 0.3570	 0.3060
6	 0.8510	 0.5020
7	 0.7840	 0.4560
8	 0.6800	 0.4490
C1	 0.9450	 0.6100
C2	 0.9050	 0.5580
C3	 0.9720	 0.6360
C4	 0.9860	 0.6100
LA	 0.9500	 0.6530
LB	 0.9310	 0.6220
LC	 0.9150	 0.6150
LD	 0.8400	 0.5450
LE	 0.8640	 0.5640
LF	 0.9030	 0.6030
LG	 0.8590	 0.5660
LH	 0.8820	 0.5850
LI	 0.8610	 0.5850
LJ	 0.8060	 0.5300
LL	 0.8890	 0.5950
LM	 0.8810	 0.5820
LN	 0.9680	 0.6520
LO	 0.9230	 0.6160
LP	 0.9020	 0.6240
LQ	 0.9200	 0.6200
LR	 0.8500	 0.5850
LS	 0.9100	 0.6110
LT	 0.9060	 0.6070
LU	 0.8350	 0.5370
LV	 0.9080	 0.6270
LW	 0.5920	 0.5090
LX	 0.9040	 0.6010
LY	 0.9040	 0.6050
LZ	 0.8740	 0.5870
La	 0.9270	 0.6320















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Chain	Atom inclusion	Q-score
Lb	 0.8300	 0.5600
Lc	 0.8980	 0.6050
Ld	 0.8850	 0.6020
Le	 0.9260	 0.6370
Lf	 0.9460	 0.6440
Lg	 0.9030	 0.6240
Lh	 0.8840	 0.5950
Li	 0.8540	 0.5680
Lj	 0.9710	 0.6660
Lk	 0.8200	 0.5570
Ll	 0.9470	 0.6550
Lm	 0.8840	 0.5910
Ln	 0.9380	 0.6330
Lo	 0.8930	 0.6130
Lp	 0.9060	 0.6310
SA	 0.8720	 0.5610
SB	 0.8190	 0.5610
SC	 0.8890	 0.5940
SD	 0.7670	 0.5140
SE	 0.8770	 0.5820
SF	 0.7460	 0.5070
SG	 0.7870	 0.5170
SH	 0.7810	 0.5070
SI	 0.8890	 0.5910
SJ	 0.8290	 0.5460
SK	 0.7570	 0.4790
SL	 0.8790	 0.6100
SM	 0.4430	 0.3060
SN	 0.8710	 0.5750
SO	 0.8760	 0.5760
SP	 0.7060	 0.4700
SQ	 0.8200	 0.5410
SR	 0.7800	 0.5120
SS	 0.7500	 0.4880
ST	 0.7820	 0.5060
SU	 0.7560	 0.5060
SV	 0.8710	 0.5710
SW	 0.9110	 0.6200
SX	 0.8870	 0.5910
SY	 0.8100	 0.5200
SZ	 0.6490	 0.4540
Sa	 0.8750	 0.5780

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Chain	Atom inclusion	Q-score
Sb	 0.8550	 0.5700
Sc	 0.7590	 0.5310
Sd	 0.9010	 0.5780
Se	 0.7390	 0.5250
Sf	 0.4490	 0.2770
Sg	 0.7160	 0.4840