



wwPDB EM Validation Summary Report ⓘ

Dec 11, 2022 – 07:50 pm GMT

PDB ID : 6T7I
EMDB ID : EMD-10396
Title : Structure of yeast 80S ribosome stalled on the CGA-CGA inhibitory codon combination.
Authors : Tesina, P.; Buschauer, R.; Cheng, J.; Berninghausen, O.; Becker, R.; Beckmann, R.
Deposited on : 2019-10-22
Resolution : 3.20 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:

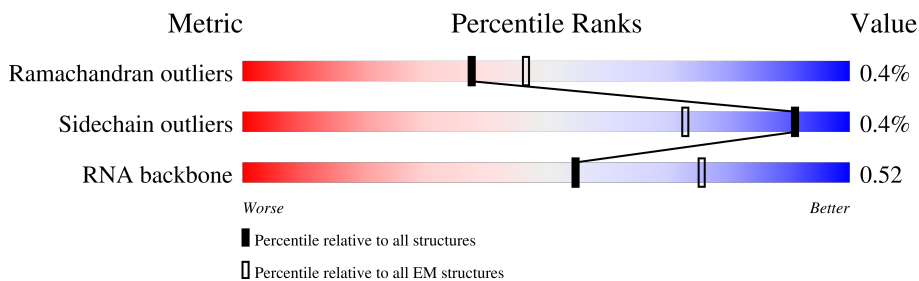
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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.



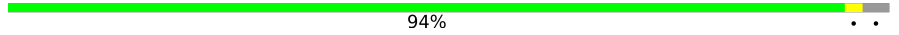
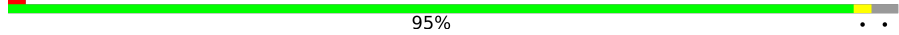
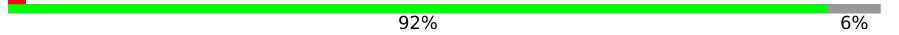
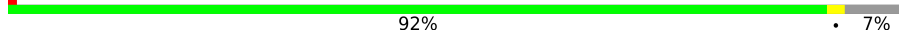



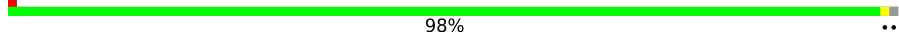

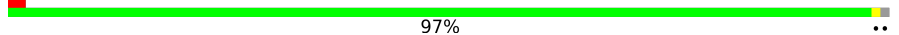

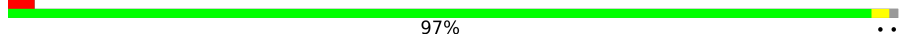



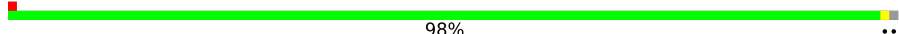
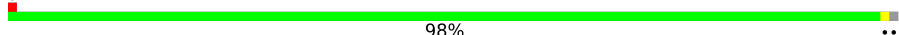
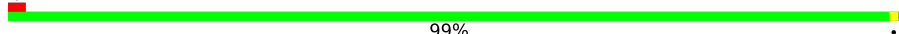


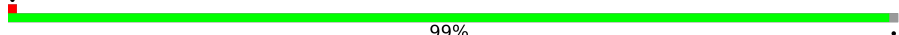
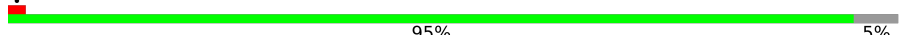
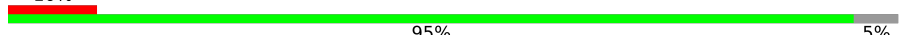

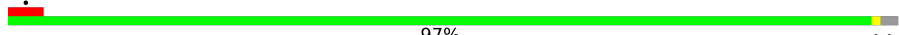
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1800	
2	SA	252	
3	SB	255	
4	SP	142	
5	SC	254	
6	SD	240	
7	SE	261	
8	SF	225	

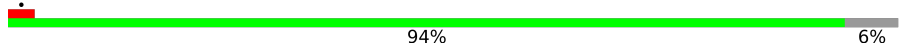

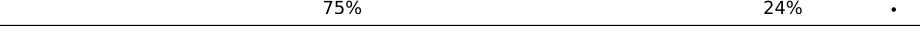
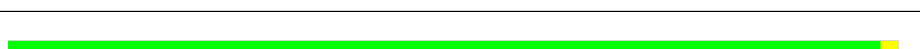

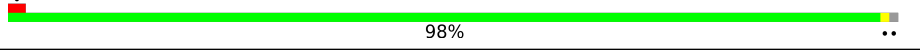
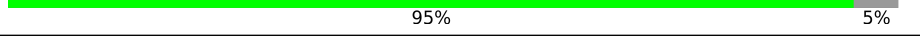
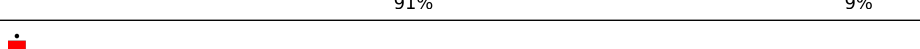

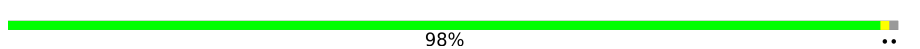
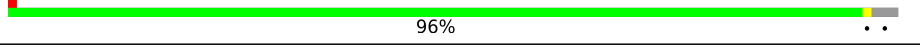
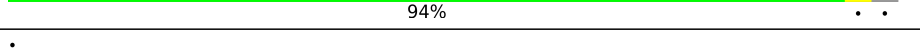
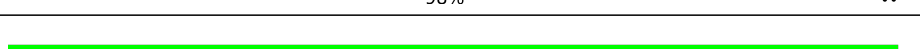
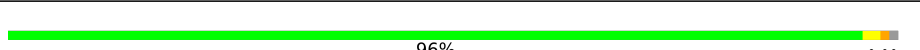
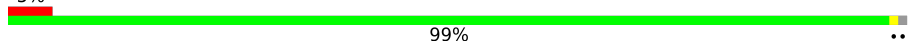
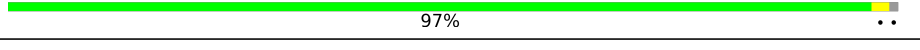
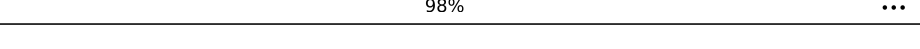


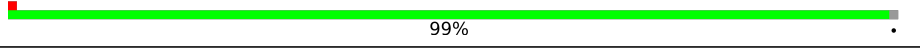




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Mol	Chain	Length	Quality of chain
9	SG	236	 94%
10	SH	190	 95%
11	SI	200	 92% 6%
12	SJ	197	 92% 7%
13	SK	105	 88% 12%
14	SL	156	 91% 8%
15	SM	143	 11% 80% 15%
16	SN	151	 98%
17	SO	137	 92% 7%
18	SQ	143	 97%
19	SR	136	 88% 11%
20	SS	146	 97%
21	ST	144	 99%
22	SU	121	 83% 17%
23	SV	87	 99%
24	SW	130	 98%
25	SX	145	 98%
26	SY	135	 99%
27	SZ	108	 14% 76% 24%
28	Sa	119	 78% 18%
29	Sb	82	 99%
30	Sd	56	 95% 5%
31	Se	63	 10% 95% 5%
32	Sf	152	 6% 47% 52%
33	Sg	319	 97%


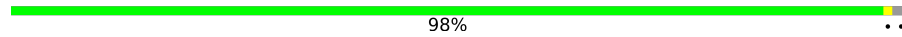
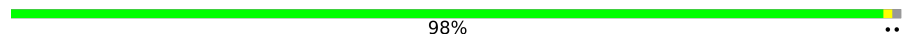
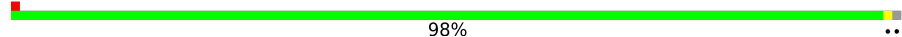
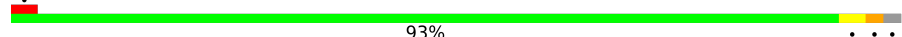
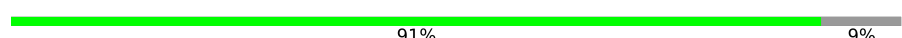
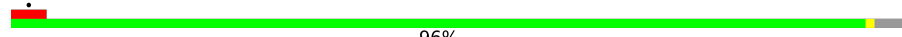
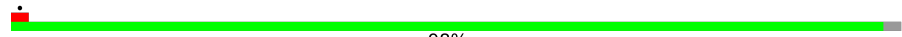



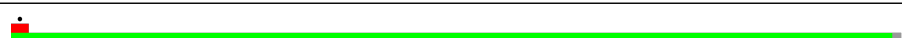

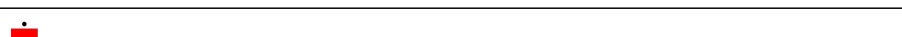
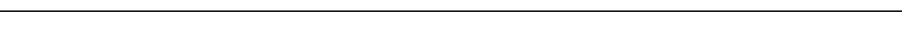
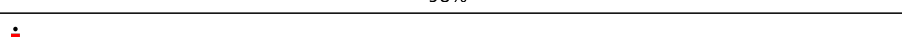
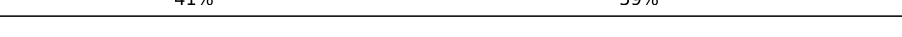
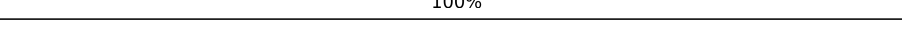
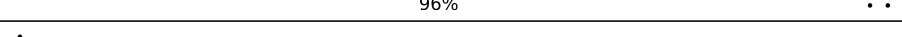
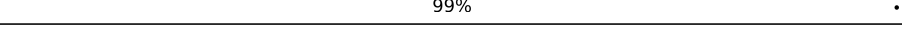
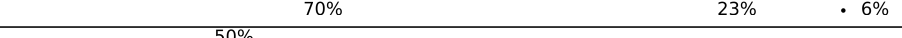
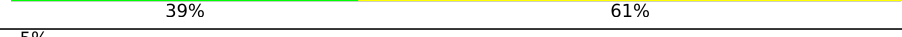

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Mol	Chain	Length	Quality of chain
34	Sc	67	 94% 6%
35	C4	121	 88% 12%
36	C3	158	 75% 24%
37	LA	254	 98% ..
38	LB	387	 98% .
39	LC	362	 99% .
40	LD	297	 98% ..
41	LE	176	 95% 5%
42	LF	244	 91% 9%
43	LG	256	 89% . 9%
44	LH	191	 99% .
45	LI	221	 98% ..
46	LJ	174	 96% ..
47	LL	199	 94% . .
48	LM	138	 98% ..
49	LN	204	 100%
50	LO	199	 96% ...
51	LP	184	 99% ..
52	LQ	186	 97% ..
53	LR	189	 98% ...
54	LS	172	 99% .
55	LT	160	 99% .
56	LU	121	 83% 17%
57	LV	137	 99% .
58	LW	155	39% 81% 19%

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Mol	Chain	Length	Quality of chain
59	LX	142	
60	LY	127	
61	LZ	136	
62	La	149	
63	Lb	59	
64	Lc	105	
65	Ld	113	
66	Le	130	
67	Lf	107	
68	Lg	121	
69	Lh	120	
70	Li	100	
71	Lj	88	
72	Lk	78	
73	Ll	51	
74	Lm	128	
75	Ln	25	
76	Lo	106	
77	Lp	92	
78	C1	3396	
79	5	18	
80	6	76	
81	7	75	

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 202973 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 ribosomal RNA.

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

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S15.

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

- Molecule 5 is a protein called 40S ribosomal protein S2.

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

- Molecule 6 is a protein called 40S ribosomal protein S3.

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

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 8 is a protein called Rps5p.

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

- Molecule 9 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S12.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 22 is a protein called 40S ribosomal protein S20.

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

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S26-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 34 is a protein called 40S ribosomal protein S28-B.

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

- Molecule 35 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 36 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 37 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 38 is a protein called 60S ribosomal protein L3.

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

- Molecule 39 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L5.

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

- Molecule 41 is a protein called 60S ribosomal protein L6-B.

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

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 42 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L10.

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

- Molecule 46 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L24-B.

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

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	5	ILE	VAL	conflict	UNP P24000
LW	104	GLN	ASN	conflict	UNP P24000
LW	109	GLN	LEU	conflict	UNP P24000
LW	112	ASP	ASN	conflict	UNP P24000
LW	117	LYS	ARG	conflict	UNP P24000
LW	119	ALA	GLU	conflict	UNP P24000

- Molecule 59 is a protein called 60S ribosomal protein L25.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L28.

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

- Molecule 63 is a protein called 60S ribosomal protein L29.

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

- Molecule 64 is a protein called 60S ribosomal protein L30.

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

- Molecule 65 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 66 is a protein called 60S ribosomal protein L32.

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

- Molecule 67 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L38.

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

- Molecule 73 is a protein called 60S ribosomal protein L39.

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

- Molecule 74 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 75 is a protein called 60S ribosomal protein L41-B.

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

- Molecule 76 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 78 is a RNA chain called 25S ribosomal RNA.

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

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	5	18	Total	C	N	O	P	1	0
			409	183	78	129	19		

- Molecule 80 is a RNA chain called ICG tRNA Arg.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	6	76	Total	C	N	O	P	0	0
			1621	723	290	532	76		

- Molecule 81 is a RNA chain called tRNA (E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
81	7	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

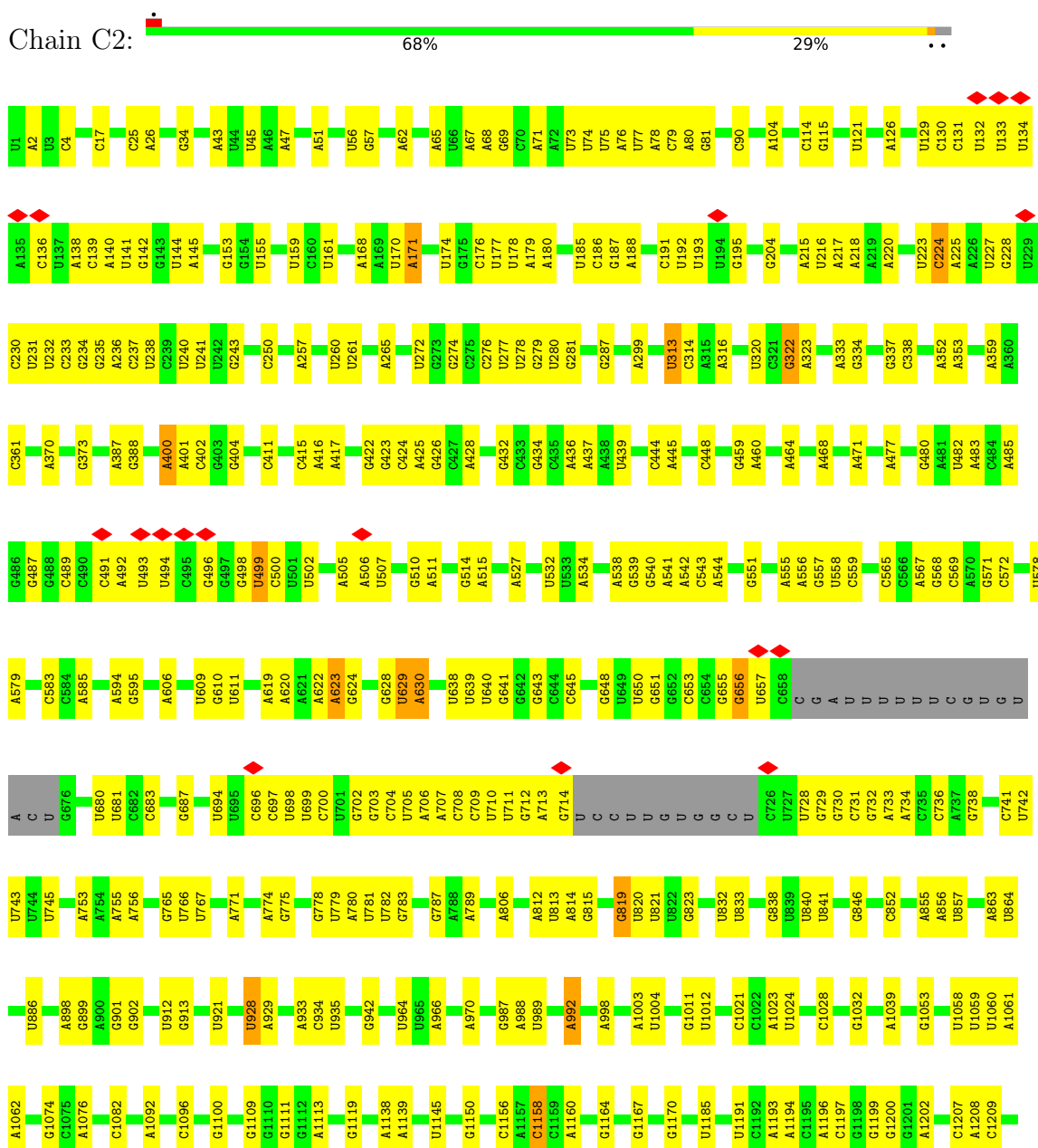
There is a discrepancy between the modelled and reference sequences:

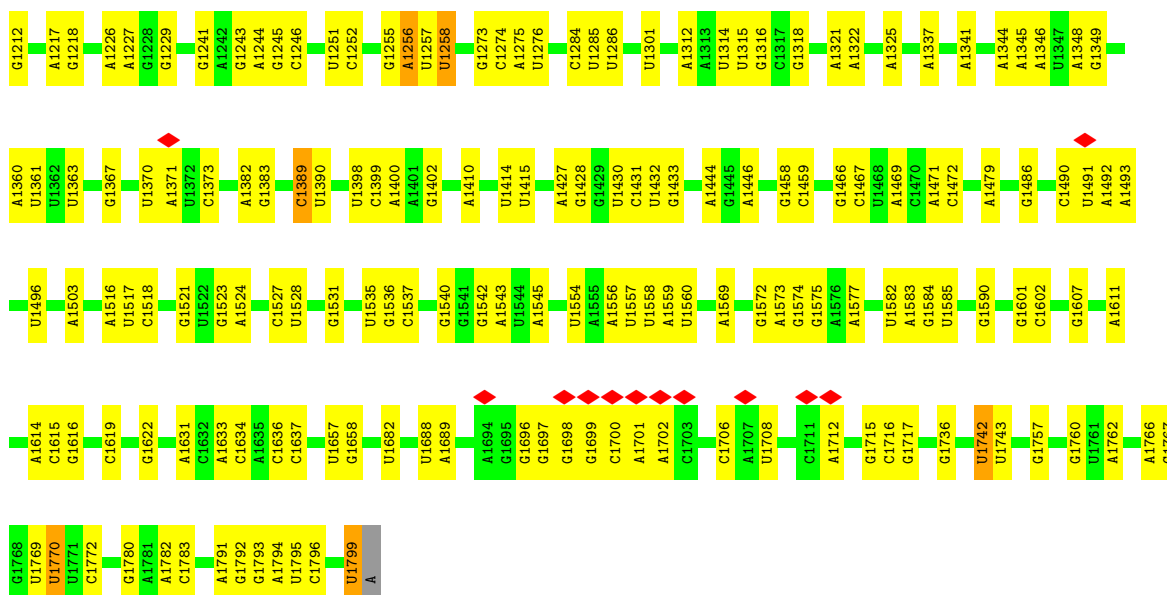
Chain	Residue	Modelled	Actual	Comment	Reference
7	11	C	U	conflict	GB 176418

3 Residue-property plots [i](#)

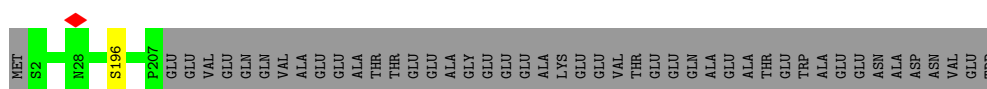
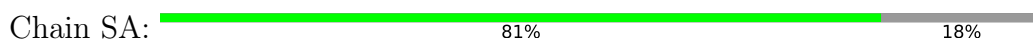
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





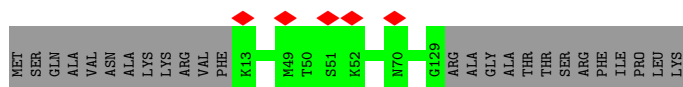
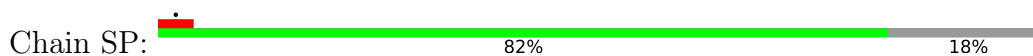
- Molecule 2: 40S ribosomal protein S0-A



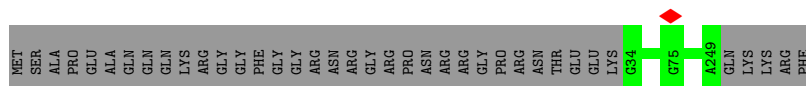
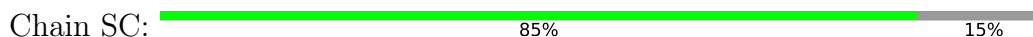
- Molecule 3: 40S ribosomal protein S1-A



- Molecule 4: 40S ribosomal protein S15

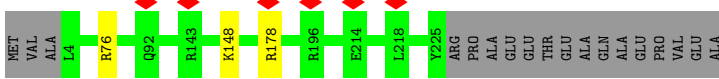


- Molecule 5: 40S ribosomal protein S2



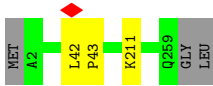
- Molecule 6: 40S ribosomal protein S3

Chain SD:  91% 8%



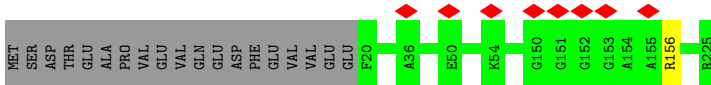
- Molecule 7: 40S ribosomal protein S4-A

Chain SE:  98%



- Molecule 8: Rps5p

Chain SF:  91% 8%



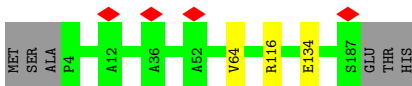
- Molecule 9: 40S ribosomal protein S6-A

Chain SG:  94%




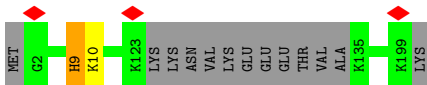
- Molecule 10: 40S ribosomal protein S7-A

Chain SH:  95%



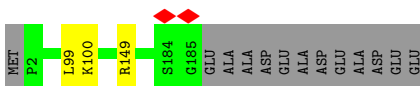
- Molecule 11: 40S ribosomal protein S8-A

Chain SI:  92% 6%

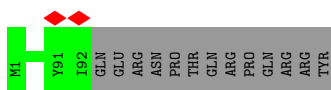
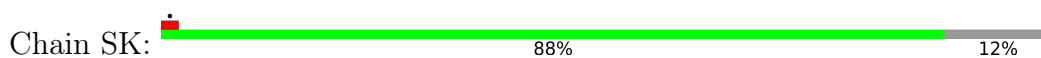


- Molecule 12: 40S ribosomal protein S9-A

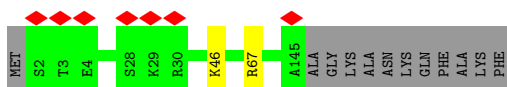
Chain SJ:  92% 7%



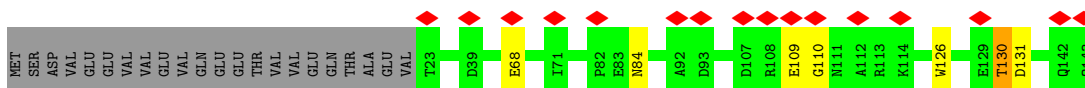
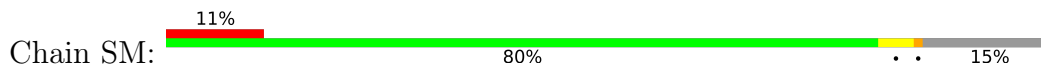
- Molecule 13: 40S ribosomal protein S10-A



- Molecule 14: 40S ribosomal protein S11-A



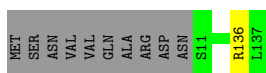
- Molecule 15: 40S ribosomal protein S12



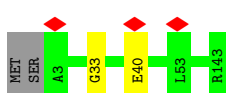
- Molecule 16: 40S ribosomal protein S13



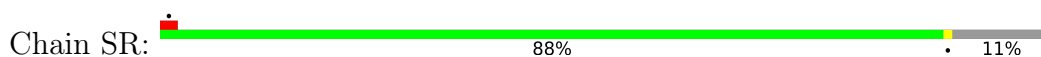
- Molecule 17: 40S ribosomal protein S14-A

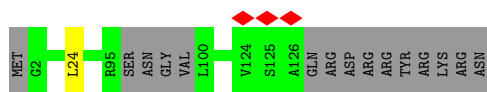


- Molecule 18: 40S ribosomal protein S16-A

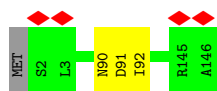


- Molecule 19: 40S ribosomal protein S17-B

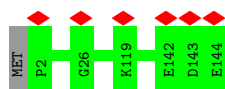




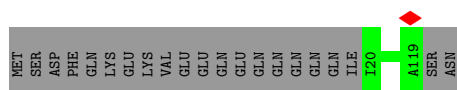
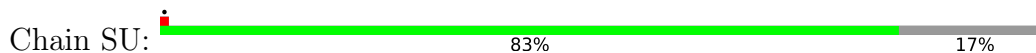
- Molecule 20: 40S ribosomal protein S18-A



- Molecule 21: 40S ribosomal protein S19-A



- Molecule 22: 40S ribosomal protein S20



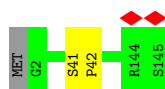
- Molecule 23: 40S ribosomal protein S21-A



- Molecule 24: 40S ribosomal protein S22-A



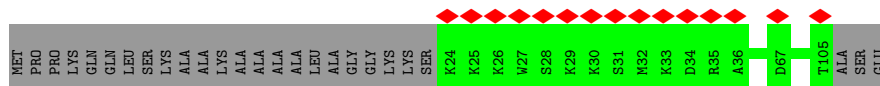
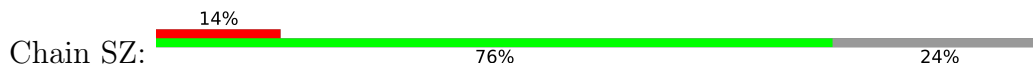
- Molecule 25: 40S ribosomal protein S23-A



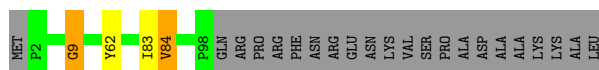
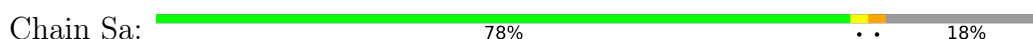
- Molecule 26: 40S ribosomal protein S24-A



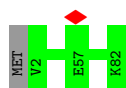
- Molecule 27: 40S ribosomal protein S25-A



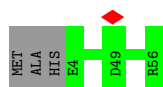
- Molecule 28: 40S ribosomal protein S26-A



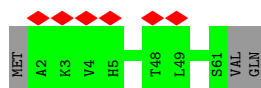
- Molecule 29: 40S ribosomal protein S27-A



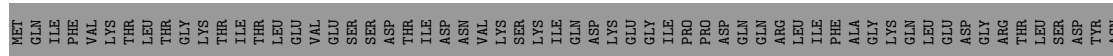
- Molecule 30: 40S ribosomal protein S29-A

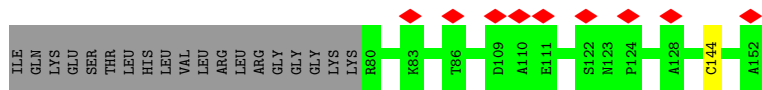


- Molecule 31: 40S ribosomal protein S30-A

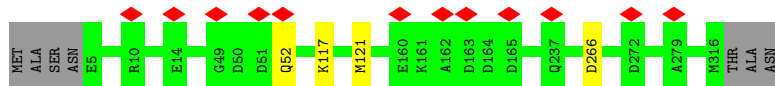


- Molecule 32: Ubiquitin-40S ribosomal protein S31

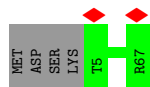




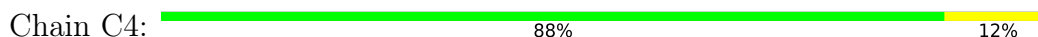
• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein



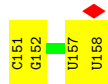
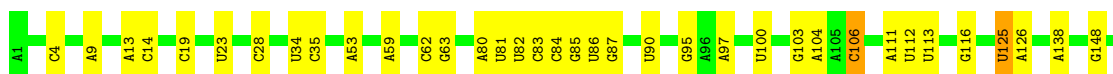
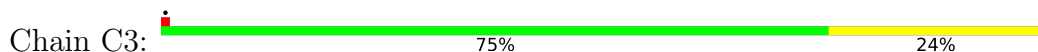
• Molecule 34: 40S ribosomal protein S28-B



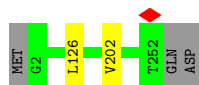
• Molecule 35: 5S ribosomal RNA



• Molecule 36: 5.8S ribosomal RNA



• Molecule 37: 60S ribosomal protein L2-A

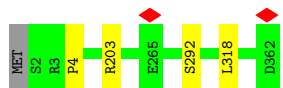


• Molecule 38: 60S ribosomal protein L3

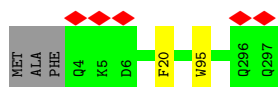




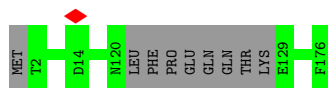
- Molecule 39: 60S ribosomal protein L4-A



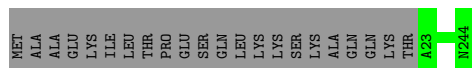
- Molecule 40: 60S ribosomal protein L5



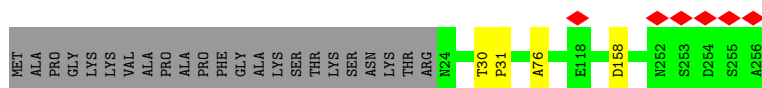
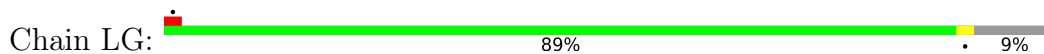
- Molecule 41: 60S ribosomal protein L6-B



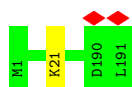
- Molecule 42: 60S ribosomal protein L7-A



- Molecule 43: 60S ribosomal protein L8-A

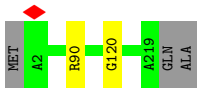


- Molecule 44: 60S ribosomal protein L9-A



- Molecule 45: 60S ribosomal protein L10

Chain LI:  98%



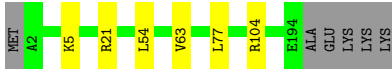
- Molecule 46: 60S ribosomal protein L11-A

Chain LJ:  96%



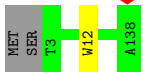
- Molecule 47: 60S ribosomal protein L13-A

Chain LL:  94%



- Molecule 48: 60S ribosomal protein L14-A

Chain LM:  98%



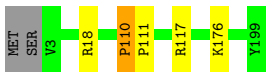
- Molecule 49: 60S ribosomal protein L15-A

Chain LN:  100%



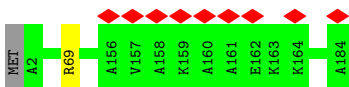
- Molecule 50: 60S ribosomal protein L16-A

Chain LO:  96%



- Molecule 51: 60S ribosomal protein L17-A

Chain LP:  99%



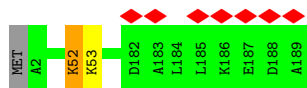
- Molecule 52: 60S ribosomal protein L18-A

Chain LQ:  97%



- Molecule 53: 60S ribosomal protein L19-A

Chain LR:  98%



- Molecule 54: 60S ribosomal protein L20-A

Chain LS:  99%




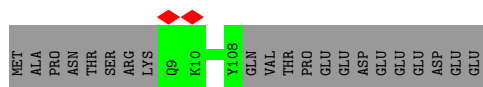
- Molecule 55: 60S ribosomal protein L21-A

Chain LT:  99%



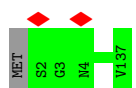
- Molecule 56: 60S ribosomal protein L22-A

Chain LU:  83% 17%




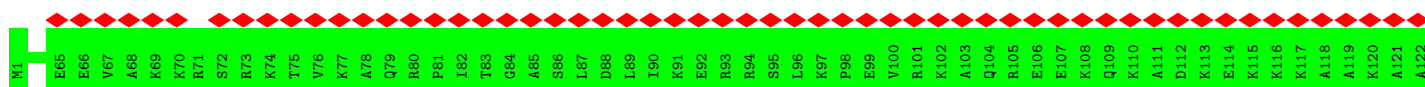
- Molecule 57: 60S ribosomal protein L23-A

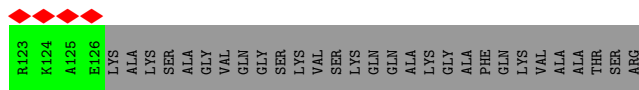
Chain LV:  99%



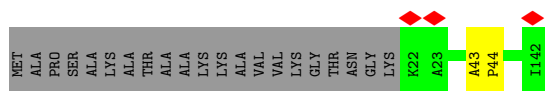
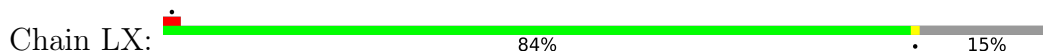
- Molecule 58: 60S ribosomal protein L24-B

Chain LW:  39% 81% 19%

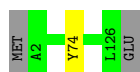




- Molecule 59: 60S ribosomal protein L25



- Molecule 60: 60S ribosomal protein L26-A



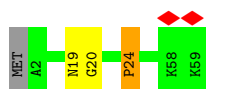
- Molecule 61: 60S ribosomal protein L27-A



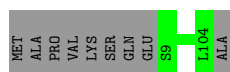
- Molecule 62: 60S ribosomal protein L28



- Molecule 63: 60S ribosomal protein L29

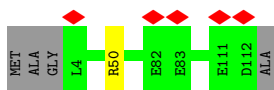


- Molecule 64: 60S ribosomal protein L30



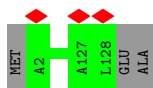
- Molecule 65: 60S ribosomal protein L31-A

Chain Ld:  96%



- Molecule 66: 60S ribosomal protein L32

Chain Le:  98%



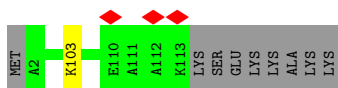
- Molecule 67: 60S ribosomal protein L33-A

Chain Lf:  99%



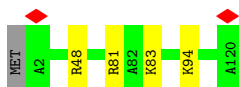
- Molecule 68: 60S ribosomal protein L34-A

Chain Lg:  92% 7%



- Molecule 69: 60S ribosomal protein L35-A

Chain Lh:  96%



- Molecule 70: 60S ribosomal protein L36-A

Chain Li:  99%



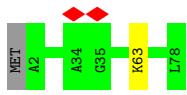
- Molecule 71: 60S ribosomal protein L37-A

Chain Lj:  97%



- Molecule 72: 60S ribosomal protein L38

Chain Lk:  97%



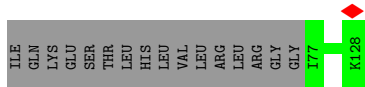
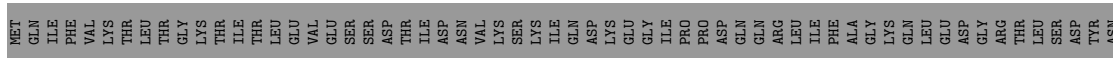
- Molecule 73: 60S ribosomal protein L39

Chain Ll:  98%



- Molecule 74: Ubiquitin-60S ribosomal protein L40

Chain Lm:  41% 59%



- Molecule 75: 60S ribosomal protein L41-B

Chain Ln:  100%

There are no outlier residues recorded for this chain.

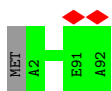
- Molecule 76: 60S ribosomal protein L42-A

Chain Lo:  96%



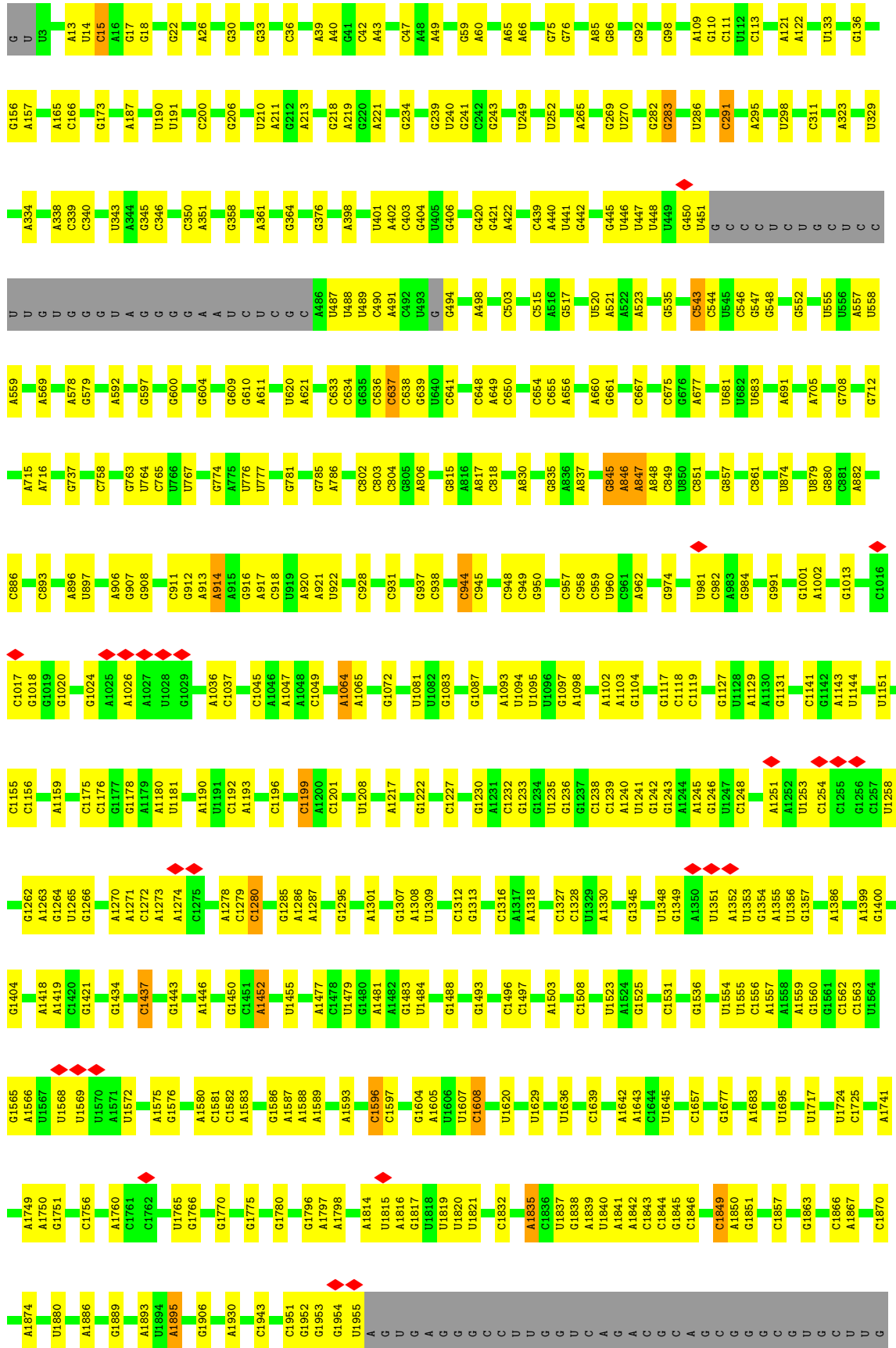
- Molecule 77: 60S ribosomal protein L43-A

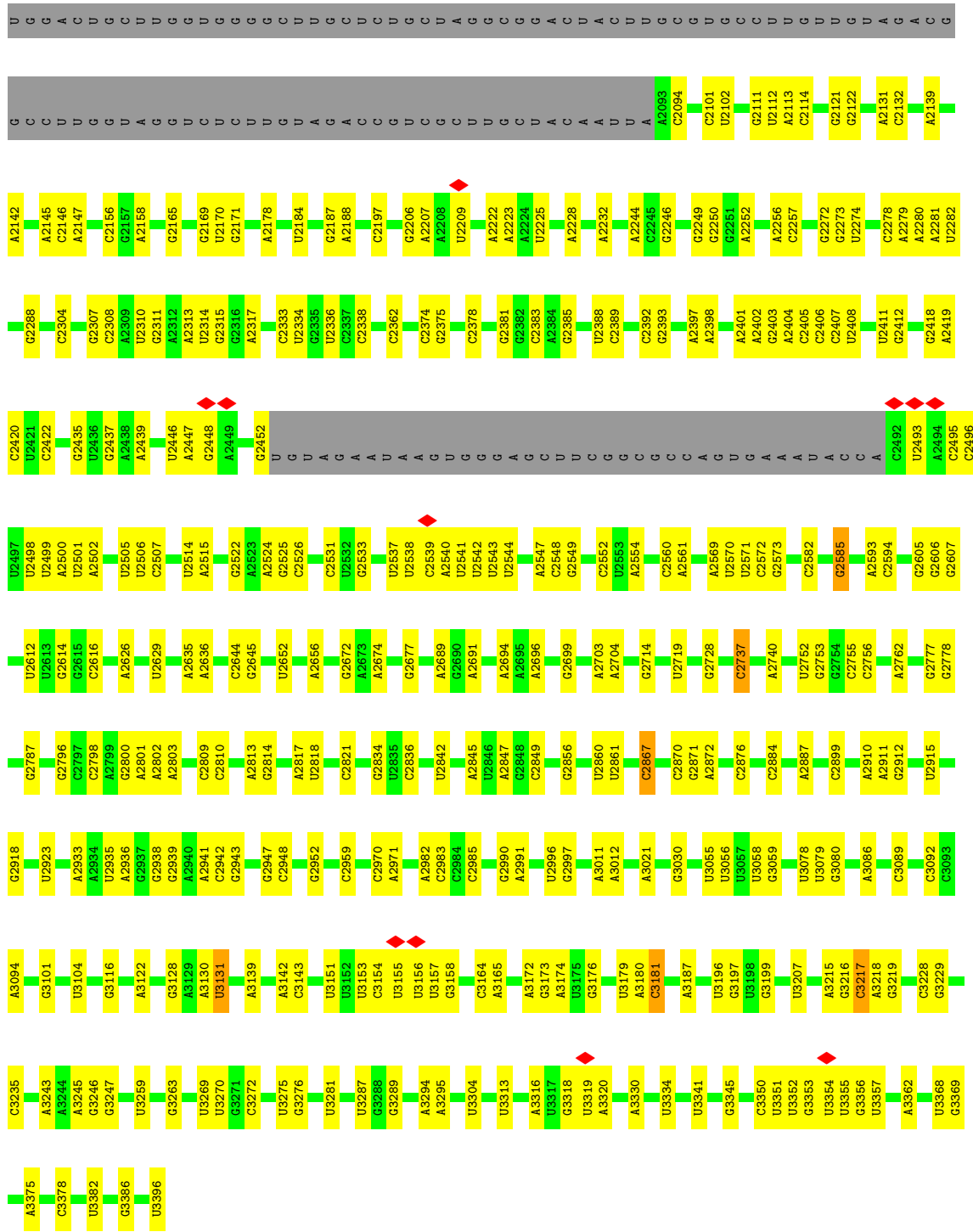
Chain Lp:  99%



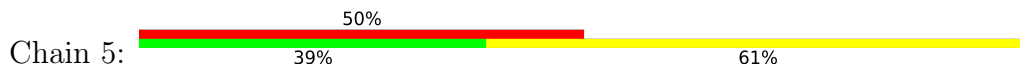
- Molecule 78: 25S ribosomal RNA

Chain C1:  70% 23% 6%

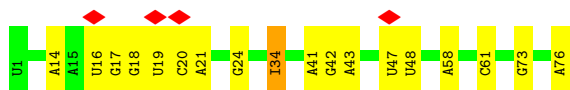
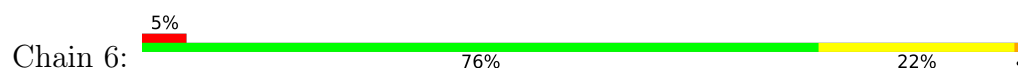




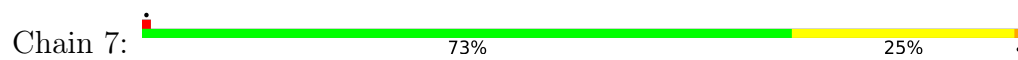
• Molecule 79: mRNA



• Molecule 80: ICG tRNA Arg



- Molecule 81: tRNA (E-site)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	334959	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	0.318	Depositor
Minimum map value	-0.153	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.022	Depositor
Map size (Å)	381.15, 381.15, 381.15	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.847, 0.847, 0.847	Depositor

5 Model quality

5.1 Standard geometry

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	1.19	10/42053 (0.0%)	1.05	55/65522 (0.1%)
2	SA	0.40	0/1644	0.51	0/2249
3	SB	0.50	0/1823	0.59	0/2447
4	SP	0.35	0/936	0.52	0/1259
5	SC	0.51	0/1656	0.57	0/2251
6	SD	0.38	0/1754	0.53	0/2361
7	SE	0.47	0/2097	0.56	0/2823
8	SF	0.38	0/1625	0.55	0/2197
9	SG	0.39	0/1839	0.60	0/2460
10	SH	0.39	0/1498	0.53	0/2019
11	SI	0.55	0/1501	0.63	0/2006
12	SJ	0.42	0/1504	0.58	0/2016
13	SK	0.35	0/769	0.49	0/1039
14	SL	0.67	0/1185	0.58	0/1598
15	SM	0.29	0/883	0.60	0/1199
16	SN	0.58	0/1215	0.59	0/1638
17	SO	0.60	0/937	0.64	0/1261
18	SQ	0.40	0/1125	0.56	0/1510
19	SR	0.35	0/957	0.53	0/1283
20	SS	0.36	0/1211	0.56	0/1628
21	ST	0.38	0/1130	0.53	0/1517
22	SU	0.37	0/807	0.55	0/1091
23	SV	0.44	0/682	0.59	0/921
24	SW	0.58	0/1038	0.61	1/1395 (0.1%)
25	SX	0.61	0/1139	0.62	0/1518
26	SY	0.39	0/1087	0.53	0/1449
27	SZ	0.34	0/661	0.56	0/888
28	Sa	0.59	0/782	0.69	0/1047
29	Sb	0.46	0/620	0.57	0/838
30	Sd	0.44	0/452	0.54	0/600
31	Se	0.39	0/480	0.53	0/639
32	Sf	0.31	0/567	0.58	0/764
33	Sg	0.31	0/2436	0.52	0/3318
34	Sc	0.42	0/493	0.67	0/663

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	C4	1.19	0/2883	1.09	2/4491 (0.0%)
36	C3	1.33	1/3746 (0.0%)	1.18	15/5832 (0.3%)
37	LA	0.90	1/1933 (0.1%)	0.70	0/2598
38	LB	0.86	0/3146	0.64	0/4228
39	LC	0.81	0/2800	0.62	0/3790
40	LD	0.63	0/2400	0.57	0/3239
41	LE	0.59	0/1327	0.55	0/1790
42	LF	0.87	0/1821	0.58	0/2451
43	LG	0.66	0/1836	0.58	0/2481
44	LH	0.69	0/1529	0.57	0/2060
45	LI	0.75	1/1801 (0.1%)	0.60	0/2416
46	LJ	0.55	0/1371	0.60	0/1838
47	LL	0.78	2/1568 (0.1%)	0.65	0/2106
48	LM	0.67	0/1068	0.62	0/1438
49	LN	1.01	0/1757	0.71	0/2354
50	LO	0.87	0/1585	0.62	1/2128 (0.0%)
51	LP	0.84	0/1439	0.67	2/1938 (0.1%)
52	LQ	0.77	0/1465	0.68	0/1965
53	LR	0.71	0/1532	0.64	0/2043
54	LS	0.84	0/1473	0.60	0/1980
55	LT	0.84	0/1300	0.61	0/1743
56	LU	0.58	0/812	0.54	0/1099
57	LV	0.82	0/1018	0.64	0/1369
58	LW	0.62	0/850	0.53	0/1152
59	LX	0.75	0/979	0.61	0/1321
60	LY	0.66	0/995	0.62	0/1329
61	LZ	0.67	0/1118	0.56	0/1497
62	La	0.87	0/1204	0.64	0/1612
63	Lb	0.62	0/473	0.65	0/629
64	Lc	0.71	0/745	0.57	0/1001
65	Ld	0.78	0/890	0.63	0/1196
66	Le	0.81	0/1038	0.60	0/1390
67	Lf	0.95	0/868	0.65	0/1168
68	Lg	0.83	0/890	0.66	0/1189
69	Lh	0.63	0/978	0.61	0/1301
70	Li	0.61	0/772	0.57	0/1026
71	Lj	0.97	0/685	0.71	0/908
72	Lk	0.57	0/618	0.54	0/826
73	Ll	0.81	0/443	0.61	0/588
74	Lm	0.71	0/423	0.58	0/562
75	Ln	0.70	0/230	0.71	0/296
76	Lo	0.77	0/836	0.62	0/1104
77	Lp	0.87	0/701	0.69	0/934

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	C1	1.59	104/76214 (0.1%)	1.20	157/118821 (0.1%)
79	5	0.59	0/458	0.89	0/712
80	6	0.81	2/1810 (0.1%)	0.95	0/2817
81	7	0.61	0/1773	0.94	1/2759 (0.0%)
All	All	1.18	121/218187 (0.1%)	0.98	234/320929 (0.1%)

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
3	SB	0	2
7	SE	0	1
10	SH	0	2
11	SI	0	1
15	SM	0	3
18	SQ	0	2
20	SS	0	1
25	SX	0	1
28	Sa	0	2
32	Sf	0	1
38	LB	0	3
39	LC	0	1
43	LG	0	2
44	LH	0	1
48	LM	0	1
50	LO	0	1
52	LQ	0	1
53	LR	0	1
59	LX	0	1
61	LZ	0	1
63	Lb	0	3
69	Lh	0	1
All	All	0	33

The worst 5 of 121 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C2	629	U	C5-C6	151.67	2.70	1.34
78	C1	846	A	C5-C6	134.98	2.62	1.41
78	C1	846	A	N3-C4	91.08	1.89	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	C1	846	A	C5-C4	83.20	1.97	1.38
78	C1	846	A	C6-N1	82.04	1.93	1.35

The worst 5 of 234 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C2	629	U	C2-N3-C4	43.21	152.93	127.00
78	C1	846	A	C2-N3-C4	40.73	130.96	110.60
78	C1	846	A	C4-C5-N7	-39.06	91.17	110.70
1	C2	629	U	C4-C5-C6	-34.99	98.71	119.70
78	C1	846	A	C6-C5-N7	31.94	154.66	132.30

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	SB	151	LYS	Peptide
3	SB	81	PHE	Peptide
7	SE	42	LEU	Peptide
10	SH	134	GLU	Peptide
10	SH	64	VAL	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	SA	204/252 (81%)	182 (89%)	21 (10%)	1 (0%)	29	67
3	SB	222/255 (87%)	188 (85%)	32 (14%)	2 (1%)	17	56

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	SP	115/142 (81%)	101 (88%)	14 (12%)	0	100	100
5	SC	214/254 (84%)	190 (89%)	24 (11%)	0	100	100
6	SD	220/240 (92%)	211 (96%)	9 (4%)	0	100	100
7	SE	256/261 (98%)	229 (90%)	26 (10%)	1 (0%)	34	69
8	SF	204/225 (91%)	187 (92%)	17 (8%)	0	100	100
9	SG	226/236 (96%)	204 (90%)	19 (8%)	3 (1%)	12	47
10	SH	182/190 (96%)	160 (88%)	22 (12%)	0	100	100
11	SI	183/200 (92%)	163 (89%)	18 (10%)	2 (1%)	14	51
12	SJ	182/197 (92%)	164 (90%)	16 (9%)	2 (1%)	14	51
13	SK	90/105 (86%)	79 (88%)	11 (12%)	0	100	100
14	SL	142/156 (91%)	120 (84%)	22 (16%)	0	100	100
15	SM	119/143 (83%)	83 (70%)	32 (27%)	4 (3%)	3	24
16	SN	148/151 (98%)	132 (89%)	15 (10%)	1 (1%)	22	61
17	SO	125/137 (91%)	106 (85%)	19 (15%)	0	100	100
18	SQ	139/143 (97%)	121 (87%)	18 (13%)	0	100	100
19	SR	117/136 (86%)	106 (91%)	10 (8%)	1 (1%)	17	56
20	SS	143/146 (98%)	127 (89%)	14 (10%)	2 (1%)	11	46
21	ST	141/144 (98%)	126 (89%)	15 (11%)	0	100	100
22	SU	98/121 (81%)	90 (92%)	8 (8%)	0	100	100
23	SV	85/87 (98%)	73 (86%)	11 (13%)	1 (1%)	13	49
24	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
25	SX	142/145 (98%)	118 (83%)	23 (16%)	1 (1%)	22	61
26	SY	132/135 (98%)	119 (90%)	12 (9%)	1 (1%)	19	58
27	SZ	80/108 (74%)	67 (84%)	13 (16%)	0	100	100
28	Sa	95/119 (80%)	71 (75%)	20 (21%)	4 (4%)	3	20
29	Sb	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
30	Sd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
31	Se	58/63 (92%)	51 (88%)	7 (12%)	0	100	100
32	Sf	71/152 (47%)	45 (63%)	26 (37%)	0	100	100
33	Sg	310/319 (97%)	280 (90%)	29 (9%)	1 (0%)	41	74
34	Sc	61/67 (91%)	54 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	LA	249/254 (98%)	220 (88%)	28 (11%)	1 (0%)	34	69
38	LB	384/387 (99%)	337 (88%)	45 (12%)	2 (0%)	29	67
39	LC	359/362 (99%)	331 (92%)	26 (7%)	2 (1%)	25	64
40	LD	292/297 (98%)	270 (92%)	21 (7%)	1 (0%)	41	74
41	LE	163/176 (93%)	145 (89%)	18 (11%)	0	100	100
42	LF	220/244 (90%)	200 (91%)	20 (9%)	0	100	100
43	LG	231/256 (90%)	208 (90%)	22 (10%)	1 (0%)	34	69
44	LH	189/191 (99%)	174 (92%)	15 (8%)	0	100	100
45	LI	216/221 (98%)	200 (93%)	16 (7%)	0	100	100
46	LJ	167/174 (96%)	145 (87%)	20 (12%)	2 (1%)	13	49
47	LL	191/199 (96%)	162 (85%)	26 (14%)	3 (2%)	9	43
48	LM	134/138 (97%)	125 (93%)	9 (7%)	0	100	100
49	LN	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
50	LO	195/199 (98%)	182 (93%)	11 (6%)	2 (1%)	15	54
51	LP	181/184 (98%)	163 (90%)	18 (10%)	0	100	100
52	LQ	183/186 (98%)	165 (90%)	18 (10%)	0	100	100
53	LR	186/189 (98%)	178 (96%)	6 (3%)	2 (1%)	14	51
54	LS	169/172 (98%)	158 (94%)	11 (6%)	0	100	100
55	LT	157/160 (98%)	145 (92%)	12 (8%)	0	100	100
56	LU	98/121 (81%)	89 (91%)	9 (9%)	0	100	100
57	LV	134/137 (98%)	126 (94%)	8 (6%)	0	100	100
58	LW	124/155 (80%)	116 (94%)	8 (6%)	0	100	100
59	LX	119/142 (84%)	107 (90%)	11 (9%)	1 (1%)	19	58
60	LY	123/127 (97%)	115 (94%)	8 (6%)	0	100	100
61	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
62	La	146/149 (98%)	125 (86%)	19 (13%)	2 (1%)	11	46
63	Lb	56/59 (95%)	45 (80%)	10 (18%)	1 (2%)	8	41
64	Lc	94/105 (90%)	93 (99%)	1 (1%)	0	100	100
65	Ld	107/113 (95%)	91 (85%)	16 (15%)	0	100	100
66	Le	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
67	Lf	104/107 (97%)	97 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Lg	110/121 (91%)	101 (92%)	9 (8%)	0	100	100
69	Lh	117/120 (98%)	109 (93%)	8 (7%)	0	100	100
70	Li	97/100 (97%)	91 (94%)	6 (6%)	0	100	100
71	Lj	83/88 (94%)	76 (92%)	7 (8%)	0	100	100
72	Lk	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
73	Ll	48/51 (94%)	42 (88%)	6 (12%)	0	100	100
74	Lm	50/128 (39%)	45 (90%)	5 (10%)	0	100	100
75	Ln	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
76	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
77	Lp	89/92 (97%)	80 (90%)	9 (10%)	0	100	100
All	All	10984/11880 (92%)	9852 (90%)	1085 (10%)	47 (0%)	38	69

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	SG	68	LEU
11	SI	10	LYS
28	Sa	84	VAL
37	LA	126	LEU
62	La	78	LEU

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	
2	SA	170/210 (81%)	170 (100%)	0	100	100
3	SB	200/224 (89%)	200 (100%)	0	100	100
4	SP	95/118 (80%)	95 (100%)	0	100	100
5	SC	175/205 (85%)	175 (100%)	0	100	100
6	SD	182/195 (93%)	179 (98%)	3 (2%)	62	84
7	SE	220/222 (99%)	219 (100%)	1 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	SF	172/191 (90%)	171 (99%)	1 (1%)	86	94
9	SG	189/201 (94%)	187 (99%)	2 (1%)	73	88
10	SH	163/170 (96%)	162 (99%)	1 (1%)	86	94
11	SI	148/161 (92%)	148 (100%)	0	100	100
12	SJ	156/166 (94%)	155 (99%)	1 (1%)	86	94
13	SK	77/98 (79%)	77 (100%)	0	100	100
14	SL	129/137 (94%)	127 (98%)	2 (2%)	62	84
15	SM	88/119 (74%)	87 (99%)	1 (1%)	73	88
16	SN	127/128 (99%)	126 (99%)	1 (1%)	81	93
17	SO	91/105 (87%)	90 (99%)	1 (1%)	73	88
18	SQ	117/119 (98%)	117 (100%)	0	100	100
19	SR	101/124 (82%)	101 (100%)	0	100	100
20	SS	128/129 (99%)	128 (100%)	0	100	100
21	ST	115/116 (99%)	115 (100%)	0	100	100
22	SU	93/114 (82%)	93 (100%)	0	100	100
23	SV	71/74 (96%)	71 (100%)	0	100	100
24	SW	110/111 (99%)	110 (100%)	0	100	100
25	SX	119/120 (99%)	119 (100%)	0	100	100
26	SY	112/113 (99%)	112 (100%)	0	100	100
27	SZ	67/89 (75%)	67 (100%)	0	100	100
28	Sa	83/101 (82%)	83 (100%)	0	100	100
29	Sb	70/71 (99%)	70 (100%)	0	100	100
30	Sd	47/49 (96%)	47 (100%)	0	100	100
31	Se	50/54 (93%)	50 (100%)	0	100	100
32	Sf	56/135 (42%)	56 (100%)	0	100	100
33	Sg	250/262 (95%)	247 (99%)	3 (1%)	71	88
34	Sc	55/60 (92%)	55 (100%)	0	100	100
37	LA	190/196 (97%)	190 (100%)	0	100	100
38	LB	319/323 (99%)	317 (99%)	2 (1%)	86	94
39	LC	288/289 (100%)	287 (100%)	1 (0%)	92	96
40	LD	241/245 (98%)	240 (100%)	1 (0%)	91	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	LE	138/155 (89%)	138 (100%)	0	100	100
42	LF	186/205 (91%)	186 (100%)	0	100	100
43	LG	187/208 (90%)	186 (100%)	1 (0%)	88	95
44	LH	168/171 (98%)	168 (100%)	0	100	100
45	LI	185/187 (99%)	184 (100%)	1 (0%)	88	95
46	LJ	146/150 (97%)	146 (100%)	0	100	100
47	LL	154/159 (97%)	153 (99%)	1 (1%)	86	94
48	LM	107/109 (98%)	107 (100%)	0	100	100
49	LN	175/176 (99%)	175 (100%)	0	100	100
50	LO	160/162 (99%)	158 (99%)	2 (1%)	69	87
51	LP	138/146 (94%)	138 (100%)	0	100	100
52	LQ	150/151 (99%)	147 (98%)	3 (2%)	55	80
53	LR	152/154 (99%)	152 (100%)	0	100	100
54	LS	155/156 (99%)	155 (100%)	0	100	100
55	LT	136/137 (99%)	136 (100%)	0	100	100
56	LU	87/107 (81%)	87 (100%)	0	100	100
57	LV	104/105 (99%)	104 (100%)	0	100	100
58	LW	56/127 (44%)	56 (100%)	0	100	100
59	LX	104/118 (88%)	104 (100%)	0	100	100
60	LY	108/110 (98%)	107 (99%)	1 (1%)	78	91
61	LZ	115/116 (99%)	114 (99%)	1 (1%)	78	91
62	La	118/119 (99%)	118 (100%)	0	100	100
63	Lb	46/47 (98%)	46 (100%)	0	100	100
64	Lc	81/88 (92%)	81 (100%)	0	100	100
65	Ld	92/97 (95%)	91 (99%)	1 (1%)	73	88
66	Le	108/111 (97%)	108 (100%)	0	100	100
67	Lf	90/91 (99%)	90 (100%)	0	100	100
68	Lg	95/103 (92%)	94 (99%)	1 (1%)	73	88
69	Lh	104/105 (99%)	101 (97%)	3 (3%)	42	74
70	Li	80/82 (98%)	80 (100%)	0	100	100
71	Lj	69/71 (97%)	69 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	Lk	68/69 (99%)	67 (98%)	1 (2%)	65	85
73	Ll	45/46 (98%)	45 (100%)	0	100	100
74	Lm	47/116 (40%)	47 (100%)	0	100	100
75	Ln	22/23 (96%)	22 (100%)	0	100	100
76	Lo	87/91 (96%)	86 (99%)	1 (1%)	73	88
77	Lp	71/72 (99%)	71 (100%)	0	100	100
All	All	9198/9984 (92%)	9160 (100%)	38 (0%)	91	95

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	LQ	55	SER
69	Lh	94	LYS
60	LY	74	TYR
68	Lg	103	LYS
76	Lo	80	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
39	LC	320	ASN
72	Lk	57	ASN
45	LI	51	HIS
71	Lj	76	ASN
66	Le	6	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C2	1768/1800 (98%)	508 (28%)	55 (3%)
35	C4	120/121 (99%)	13 (10%)	1 (0%)
36	C3	157/158 (99%)	33 (21%)	2 (1%)
78	C1	3180/3396 (93%)	662 (20%)	41 (1%)
79	5	16/18 (88%)	9 (56%)	2 (12%)
80	6	75/76 (98%)	18 (24%)	0
81	7	74/75 (98%)	20 (27%)	0
All	All	5390/5644 (95%)	1263 (23%)	101 (1%)

5 of 1263 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 101 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	C3	125	U
78	C1	1273	A
79	5	34	U
78	C1	65	A
78	C1	763	G

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](#)

There are no ligands in this entry.

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
45	LI	1
47	LL	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	LI	120:GLY	C	121:LYS	N	1.19
1	LL	54:LEU	C	55:ARG	N	1.19

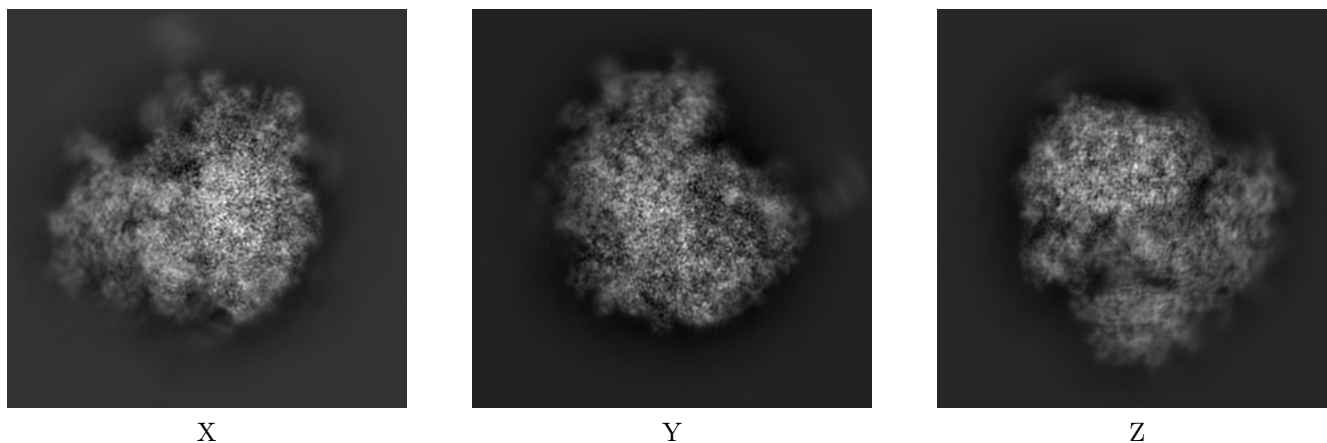
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10396. 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](#)

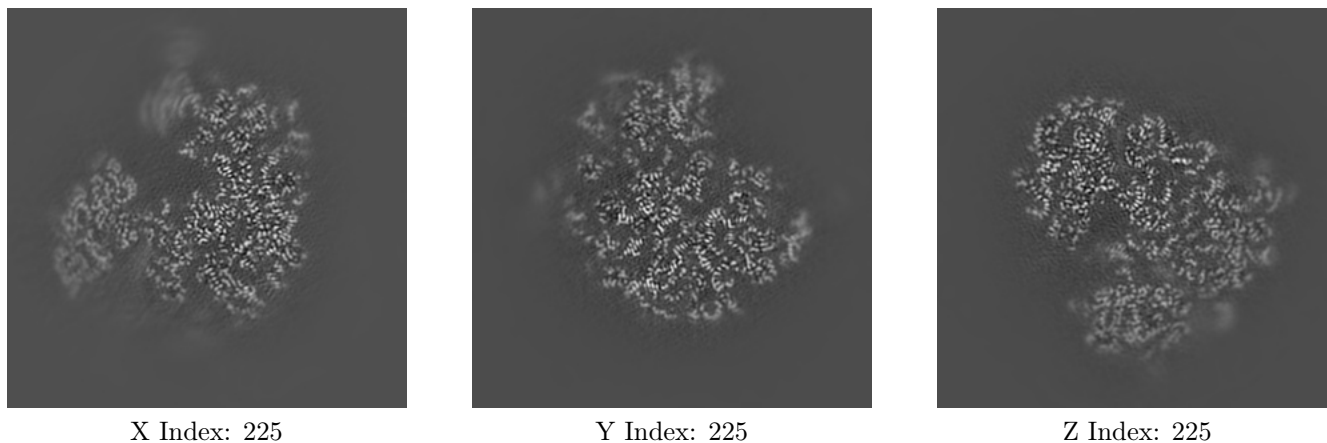
6.1.1 Primary map



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

6.2 Central slices [i](#)

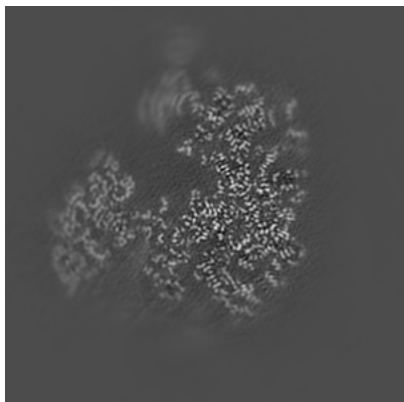
6.2.1 Primary map



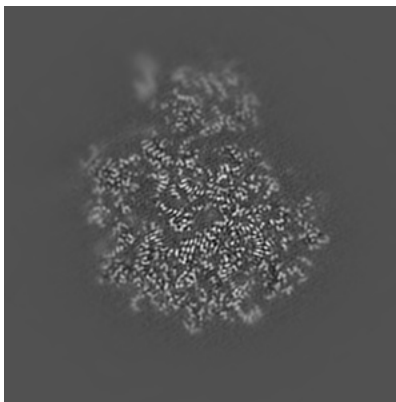
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

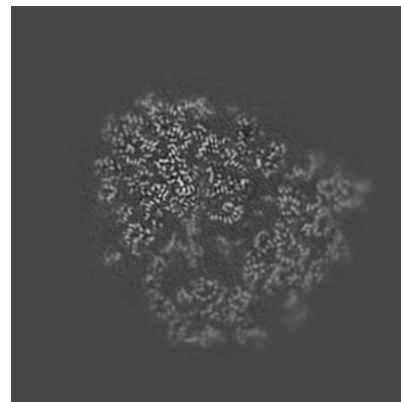
6.3.1 Primary map



X Index: 224



Y Index: 257



Z Index: 237

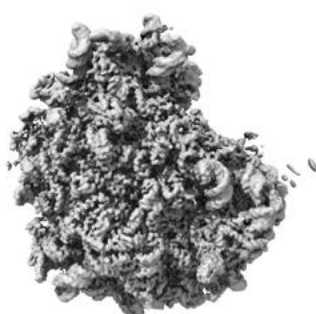
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

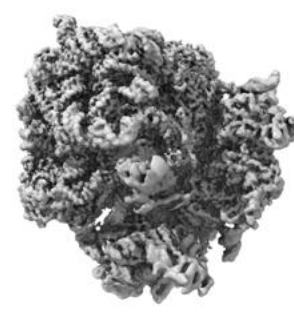
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.022. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

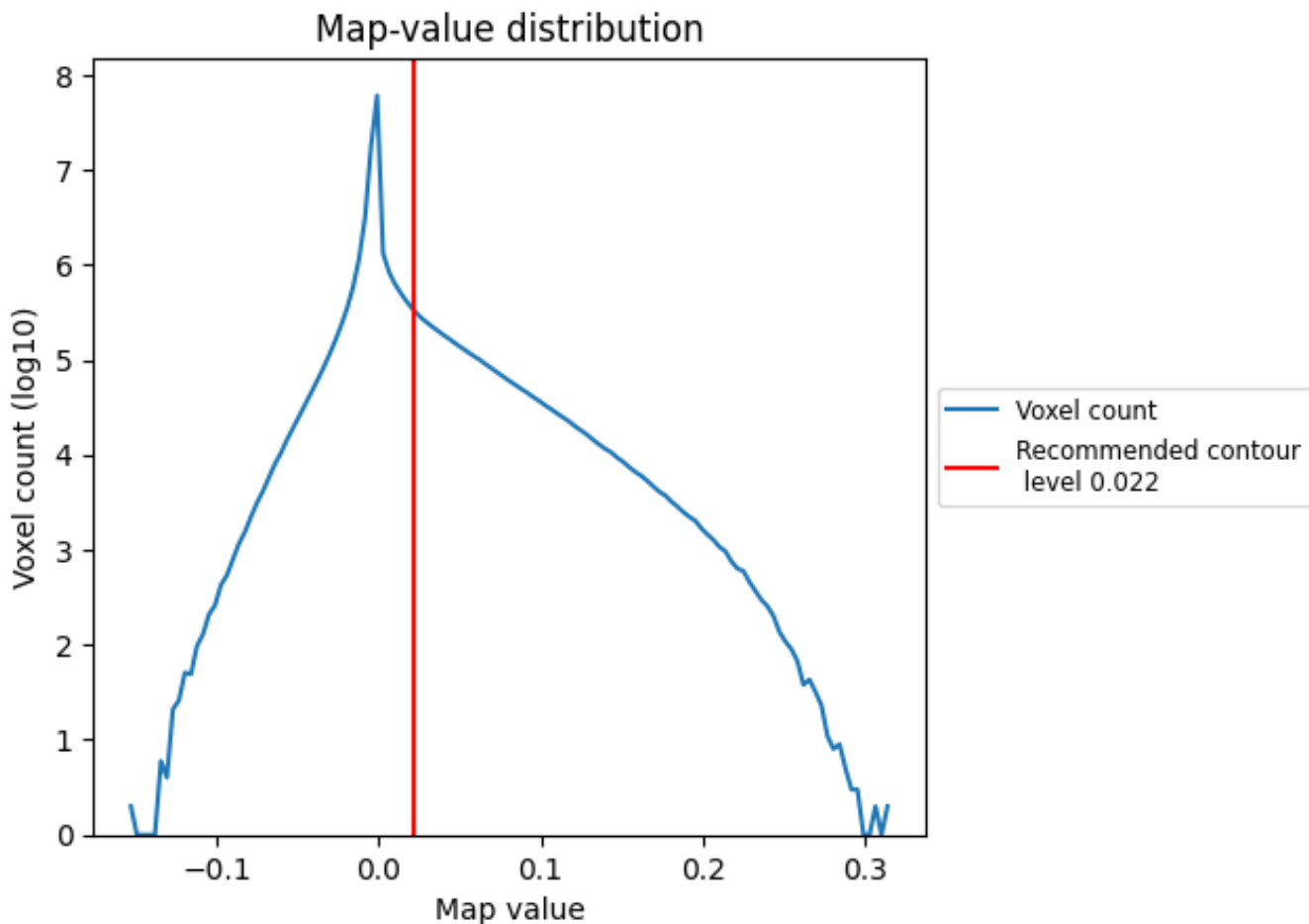
6.5 Mask visualisation

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

7 Map analysis [i](#)

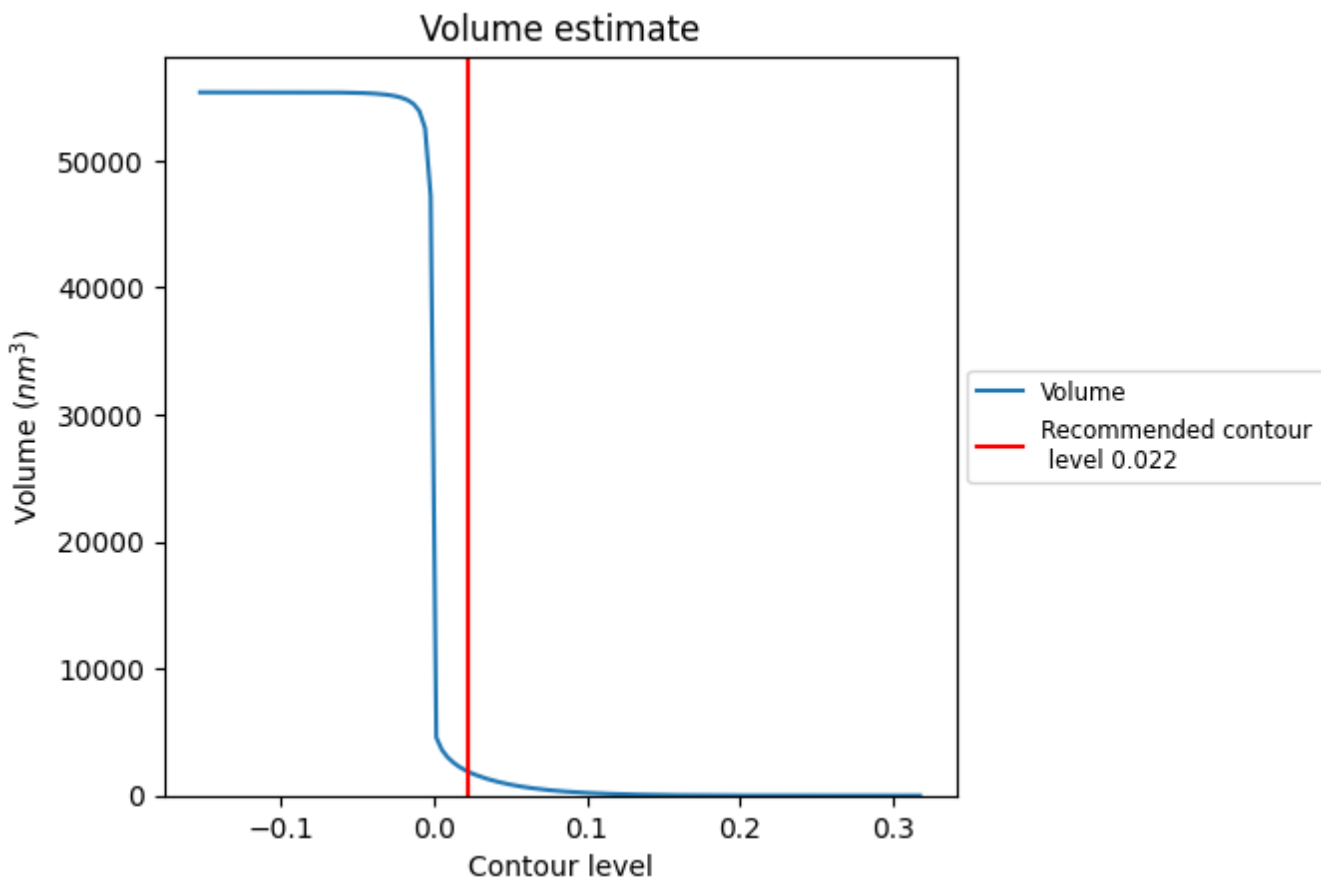
This section contains the results of statistical analysis of the map.

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.

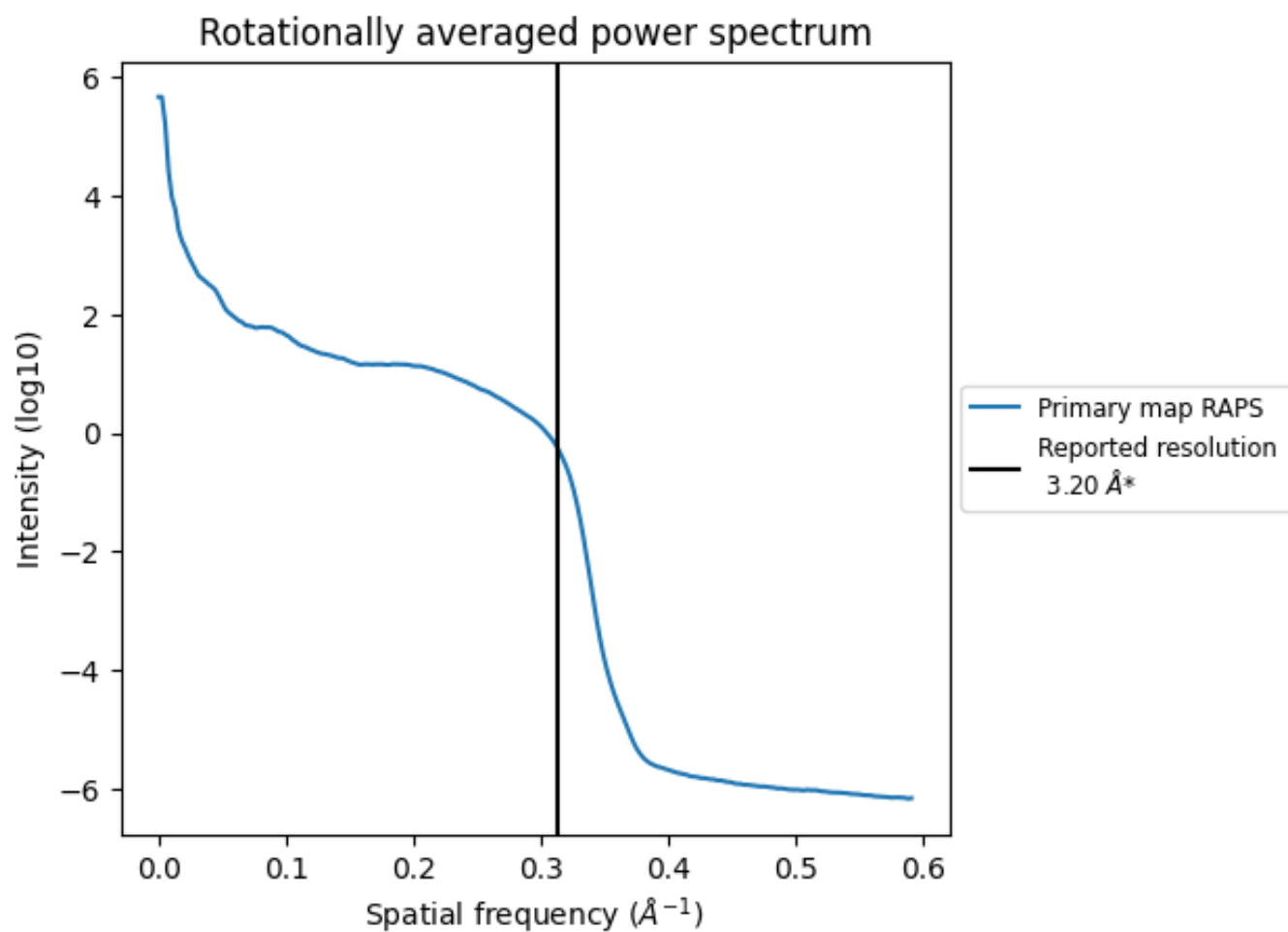
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1906 nm³; this corresponds to an approximate mass of 1722 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 0.312\AA^{-1}

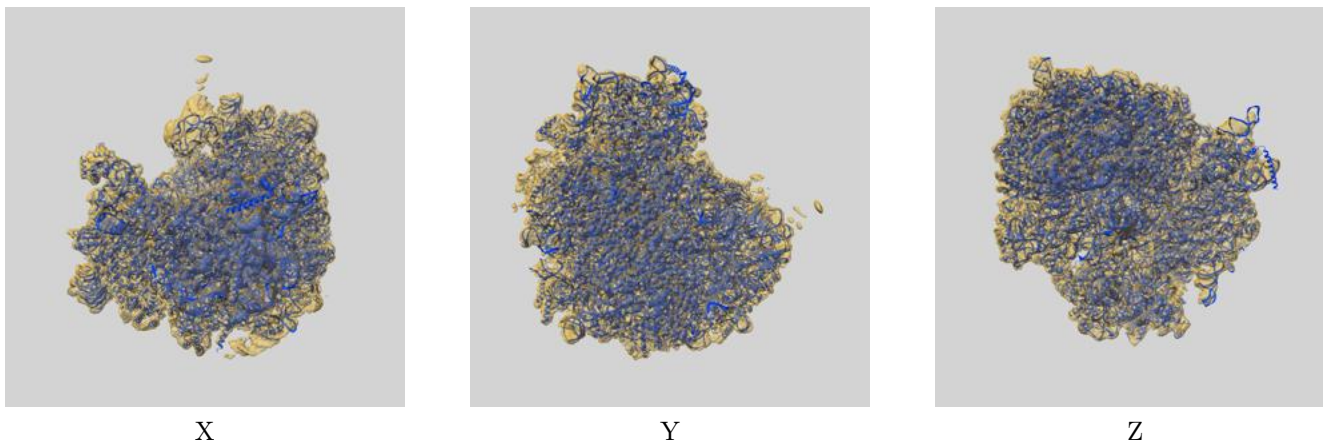
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

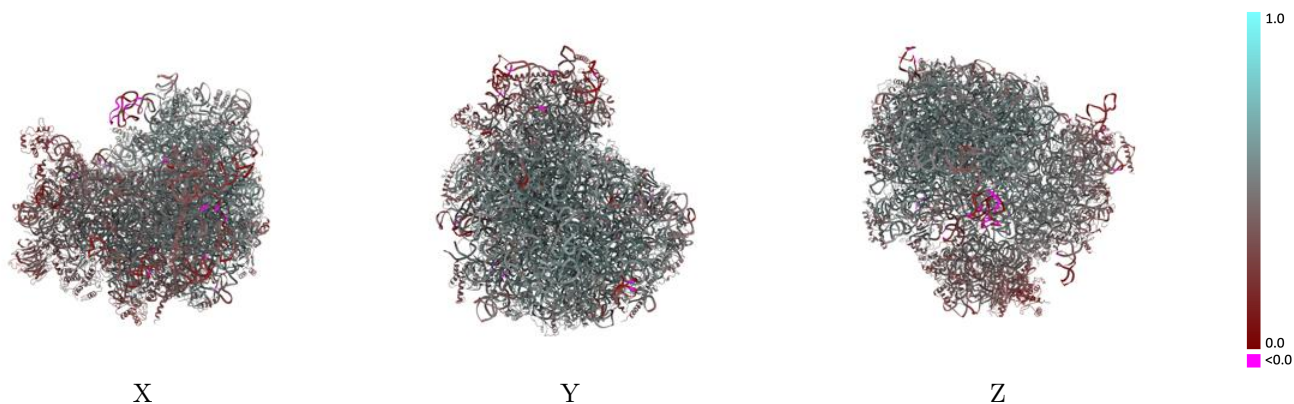
This section contains information regarding the fit between EMDB map EMD-10396 and PDB model 6T7I. Per-residue inclusion information can be found in section 3 on page 19.

9.1 Map-model overlay [i](#)



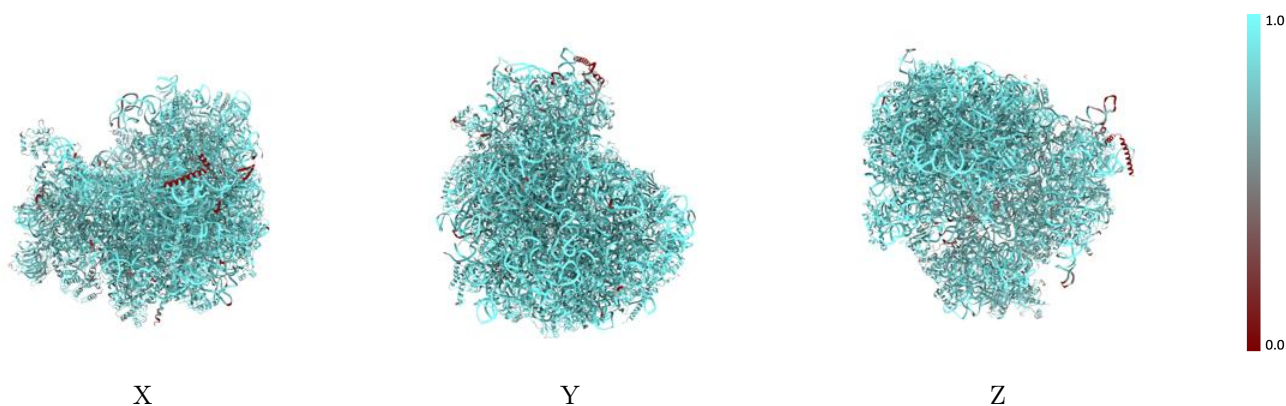
The images above show the 3D surface view of the map at the recommended contour level 0.022 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



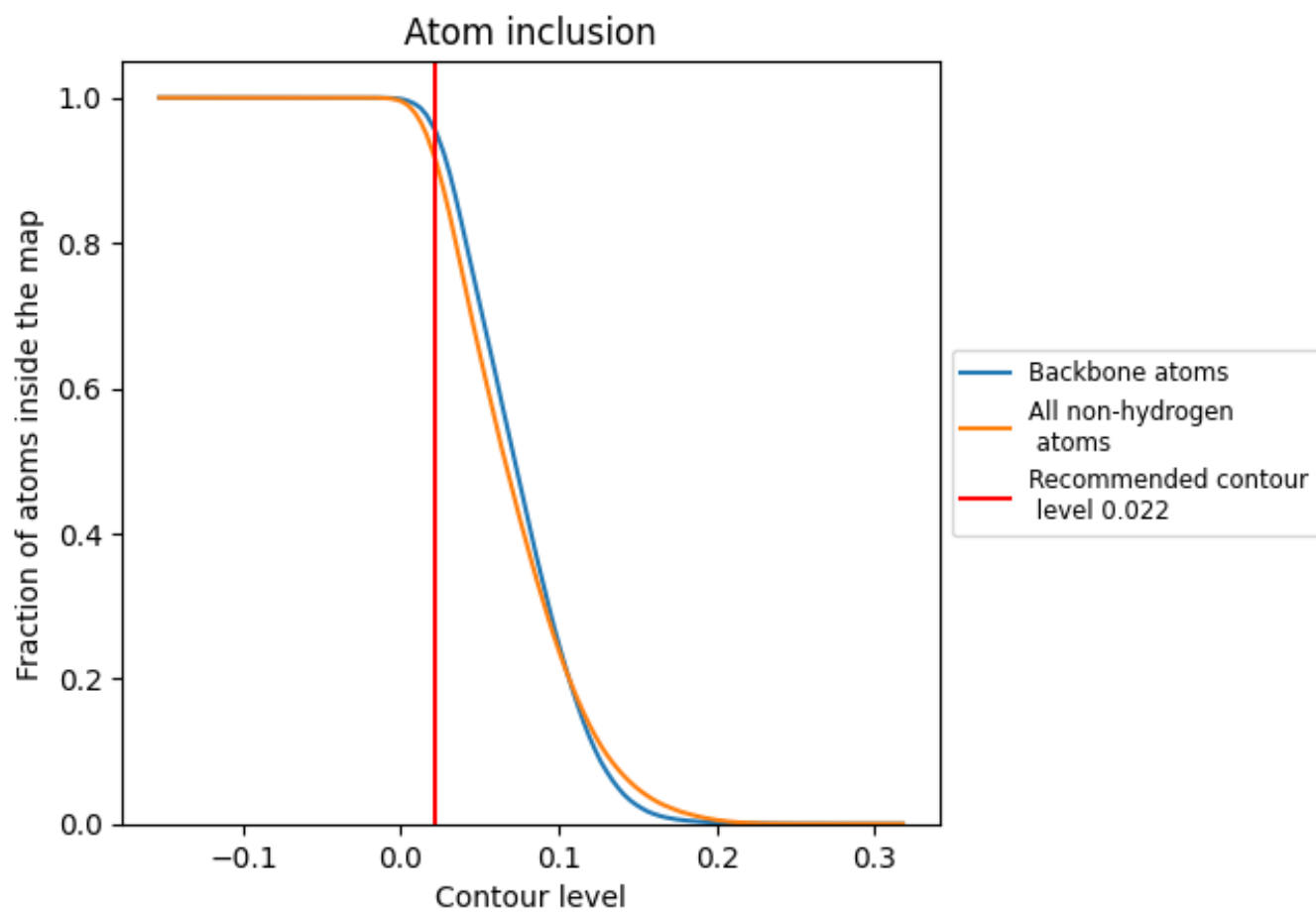
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.022).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.022) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9137	 0.4770
5	 0.4935	 0.3330
6	 0.9229	 0.4380
7	 0.9207	 0.3810
C1	 0.9687	 0.5180
C2	 0.9530	 0.4370
C3	 0.9779	 0.5320
C4	 0.9922	 0.5230
LA	 0.8934	 0.5530
LB	 0.9127	 0.5270
LC	 0.9017	 0.5110
LD	 0.8833	 0.4580
LE	 0.8812	 0.4710
LF	 0.9036	 0.5090
LG	 0.8640	 0.4610
LH	 0.8797	 0.4960
LI	 0.8724	 0.5100
LJ	 0.8491	 0.4570
LL	 0.8944	 0.4970
LM	 0.9055	 0.4910
LN	 0.9108	 0.5550
LO	 0.8963	 0.5210
LP	 0.8839	 0.5170
LQ	 0.9047	 0.5250
LR	 0.8392	 0.4770
LS	 0.8881	 0.5270
LT	 0.8968	 0.5270
LU	 0.8593	 0.4450
LV	 0.8693	 0.5360
LW	 0.5488	 0.4120
LX	 0.8705	 0.4980
LY	 0.8871	 0.5050
LZ	 0.8768	 0.4660
La	 0.9037	 0.5350
Lb	 0.8451	 0.4970













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Chain	Atom inclusion	Q-score
Lc	 0.8772	 0.4840
Ld	 0.8471	 0.5120
Le	 0.8981	 0.5390
Lf	 0.9160	 0.5550
Lg	 0.8801	 0.5190
Lh	 0.8664	 0.4840
Li	 0.8568	 0.4710
Lj	 0.9146	 0.5690
Lk	 0.8214	 0.4450
Ll	 0.9012	 0.5450
Lm	 0.8983	 0.5340
Ln	 0.8317	 0.5400
Lo	 0.8882	 0.5340
Lp	 0.8445	 0.5320
SA	 0.8338	 0.4070
SB	 0.8228	 0.4540
SC	 0.8299	 0.4480
SD	 0.7654	 0.3790
SE	 0.8297	 0.4370
SF	 0.7741	 0.3850
SG	 0.8210	 0.3840
SH	 0.7971	 0.3670
SI	 0.8637	 0.4700
SJ	 0.8244	 0.4070
SK	 0.7832	 0.3240
SL	 0.8475	 0.4950
SM	 0.6867	 0.2040
SN	 0.8589	 0.4640
SO	 0.8761	 0.4770
SP	 0.7843	 0.3560
SQ	 0.8007	 0.3940
SR	 0.7993	 0.3700
SS	 0.8016	 0.3730
ST	 0.7928	 0.3630
SU	 0.7980	 0.3610
SV	 0.8392	 0.4260
SW	 0.8427	 0.4700
SX	 0.8373	 0.4980
SY	 0.8232	 0.3760
SZ	 0.6851	 0.3340
Sa	 0.8647	 0.4850
Sb	 0.8486	 0.4430

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Chain	Atom inclusion	Q-score
Sc	 0.7696	 0.4350
Sd	 0.8818	 0.4380
Se	 0.7675	 0.4320
Sf	 0.7366	 0.2250
Sg	 0.7787	 0.3210