



wwPDB EM Validation Summary Report ⓘ

Feb 14, 2024 – 02:40 pm GMT

PDB ID : 8000
EMDB ID : EMD-17004
Title : Chaetomium thermophilum Methionine Aminopeptidase 2 autoproteolysis product at the 80S ribosome
Authors : Klein, M.A.; Wild, K.; Kisonaite, M.; Sinning, I.
Deposited on : 2023-04-04
Resolution : 3.10 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:

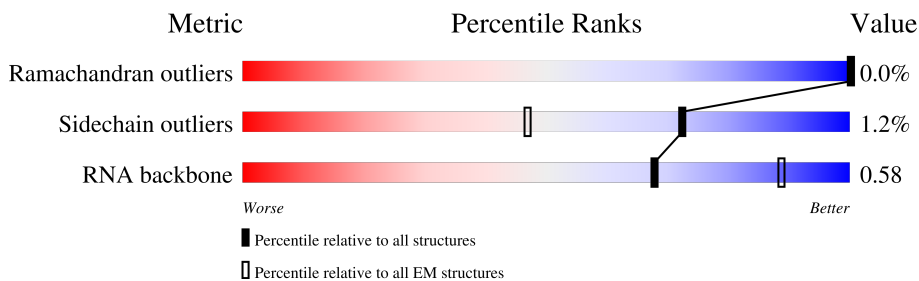
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 3.10 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	1	3337	80% 15% .
2	2	1796	80% 18% .
3	3	120	91% 8% .
4	4	156	87% 13%
5	A	316	7% 98% ..
6	B	302	10% . 89%
7	C	614	12% 87%
8	LA	254	99% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	LB	388	99%
10	LC	365	99%
11	LD	304	98%
12	LE	200	96%
13	LF	249	99%
14	LG	262	89% 10%
15	LH	192	99%
16	LI	219	99%
17	LJ	173	94%
18	LK	165	63% 93% 6%
19	LL	213	98%
20	LM	142	99%
21	LN	203	100%
22	LO	204	98%
23	LP	186	6% 98%
24	LQ	213	85% 14%
25	LR	192	95%
26	LS	174	99%
27	LT	160	98%
28	LU	127	77% 20%
29	LV	139	97%
30	LW	161	13% 80% 17%
31	LX	156	76% 22%
32	LY	138	95%
33	LZ	135	99%

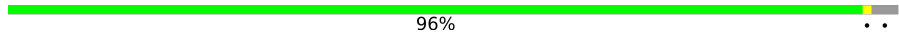
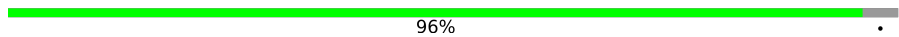
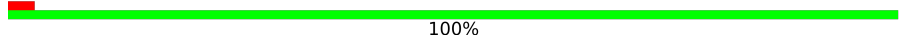
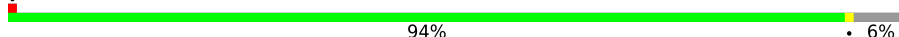

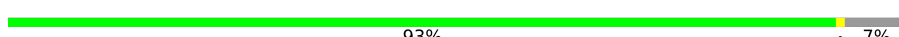




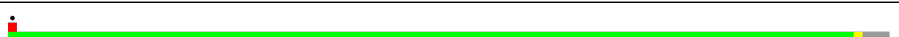


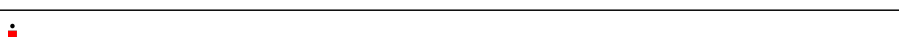
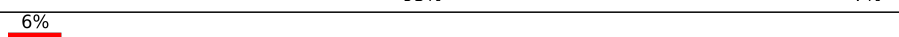
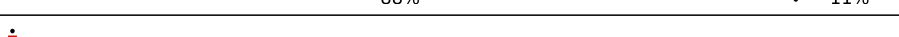

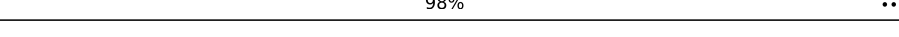
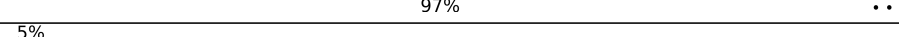
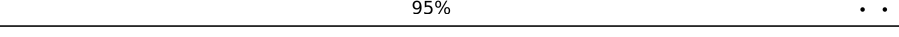


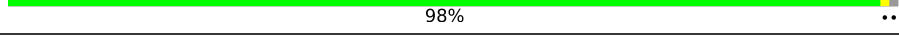

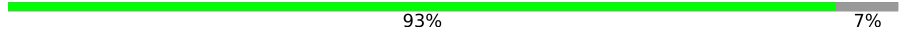
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	La	149	98%
35	Lb	65	94% 5%
36	Lc	108	89% 10%
37	Ld	120	93% 7%
38	Le	131	94% 5%
39	Lf	109	98%
40	Lg	119	94% 6%
41	Lh	126	97%
42	Li	110	91% 7%
43	Lj	95	91% 9%
44	Lk	80	90% 5% 5%
45	Ll	51	98%
46	Lm	128	40% 59%
47	Ln	25	96%
47	Lr	25	16% 92%
48	Lo	106	98%
49	Lp	92	99%
50	Lq	147	96%
51	Ls	312	37% 58% 39%
52	SA	285	73% 27%
53	SB	255	91% 9%
54	SC	263	81% 18%
55	SD	254	82% 16%
56	SE	264	98%
57	SF	212	93% 6%


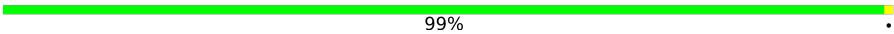
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
58	SG	239	 96%
59	SH	203	 96%
60	SI	202	 100%
61	SJ	190	 94% 6%
62	SK	159	 55% 44%
63	SL	161	 93% 7%
64	SM	144	 47% 80% 18%
65	SN	151	 99%
66	SO	150	 88% 10%
67	SP	153	 7% 73% 25%
68	SQ	143	 95%
69	SR	143	 84% 6% 10%
70	SS	156	 87% 12%
71	ST	153	 93% 7%
72	SU	116	 6% 88% 11%
73	SV	98	 86% 12%
74	SW	130	 98%
75	SX	145	 97%
76	SY	136	 5% 95%
77	SZ	99	 67% 30%
78	Sa	119	 84% 13%
79	Sb	82	 98%
80	Sc	68	 87% 10%
81	Sd	56	 93% 7%
82	Se	61	 72% 28%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
83	Sf	154	
84	D	371	

2 Entry composition

There are 85 unique types of molecules in this entry. The entry contains 208770 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 28S rRNA.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	2578	OMG	N	conflict	GB 7OLC_1

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

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1	U	N	conflict	GB 7OLC_2
2	1188	B8N	N	conflict	GB 7OLC_2

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	1	A	N	conflict	GB 7OLC_3

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

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

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

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

- Molecule 6 is a protein called Hyaluronan/mRNA-binding protein domain-containing protein.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 17 is a protein called Putative ribosomal protein.

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

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

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

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

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

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

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

- Molecule 21 is a protein called Ribosomal protein L15.

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

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

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

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

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

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

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

- Molecule 25 is a protein called Ribosomal protein L19.

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

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

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

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

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

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

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

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

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

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

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	5	GLU	ASP	conflict	UNP G2Q623
LW	7	THR	SER	conflict	UNP G2Q623
LW	102	ASN	SER	conflict	UNP G2Q623
LW	117	ALA	GLN	conflict	UNP G2Q623
LW	139	PRO	ALA	conflict	UNP G2Q623
LW	140	GLN	ALA	conflict	UNP G2Q623

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
LW	154	VAL	ILE	conflict	UNP G2Q623
LW	157	ALA	GLN	conflict	UNP G2Q623

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

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

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

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

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

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

- Molecule 34 is a protein called Ribosomal protein L18e/L15P domain-containing protein.

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

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
La	70	ARG	ALA	conflict	UNP G2QB77
La	72	SER	THR	conflict	UNP G2QB77
La	84	SER	ALA	conflict	UNP G2QB77
La	85	ASP	GLU	conflict	UNP G2QB77
La	86	VAL	THR	conflict	UNP G2QB77
La	94	GLN	ALA	conflict	UNP G2QB77
La	96	LYS	THR	conflict	UNP G2QB77
La	120	GLU	GLN	conflict	UNP G2QB77
La	123	VAL	PHE	conflict	UNP G2QB77
La	139	LYS	THR	conflict	UNP G2QB77

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 43 is a protein called Ribosomal protein L37.

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lk	5	VAL	ILE	conflict	UNP G2Q8J4
Lk	6	SER	GLY	conflict	UNP G2Q8J4
Lk	53	ASP	GLU	conflict	UNP G2Q8J4
Lk	78	LYS	SER	conflict	UNP G2Q8J4

- Molecule 45 is a protein called 60S ribosomal protein L39.

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

- Molecule 46 is a protein called Ubiquitin-like domain-containing protein.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Lm	24	GLU	ASP	conflict	UNP A0A2A9PNA8
Lm	28	ALA	SER	conflict	UNP A0A2A9PNA8

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 70 is a protein called Putative ribosomal protein.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 81 is a protein called 40S ribosomal protein S29.

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
82	Se	44	353	222	74	57	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Se	4	ALA	-	insertion	UNP Q2H4C5

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

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

- Molecule 84 is a protein called Methionine aminopeptidase 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	D	371	2911	1832	513	559	7	0	0

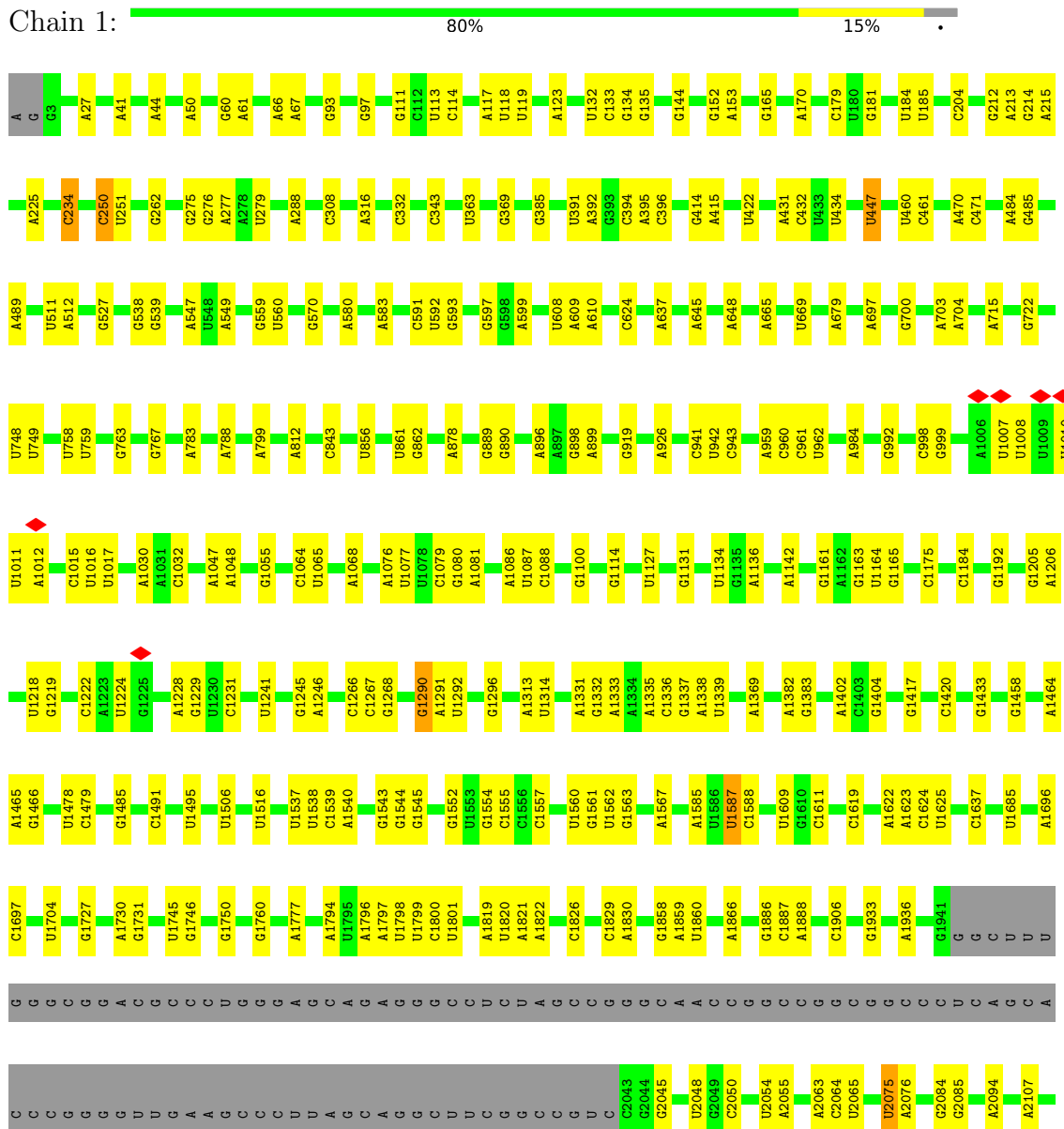
- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

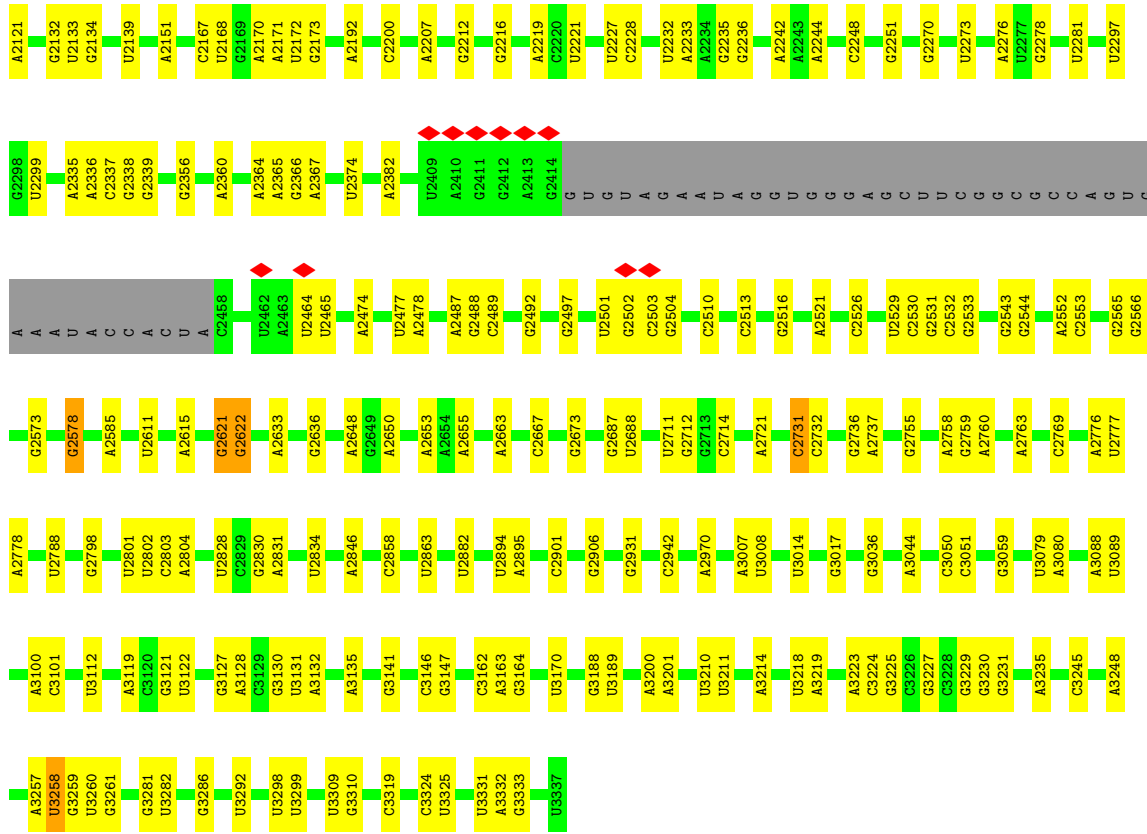
Mol	Chain	Residues	Atoms		AltConf
85	Lg	1	Total	Zn	0
			1	1	
85	Lj	1	Total	Zn	0
			1	1	
85	Lm	1	Total	Zn	0
			1	1	
85	Lo	1	Total	Zn	0
			1	1	
85	Lp	1	Total	Zn	0
			1	1	
85	Sa	1	Total	Zn	0
			1	1	
85	Sb	1	Total	Zn	0
			1	1	
85	Sd	1	Total	Zn	0
			1	1	

3 Residue-property plots [\(i\)](#)

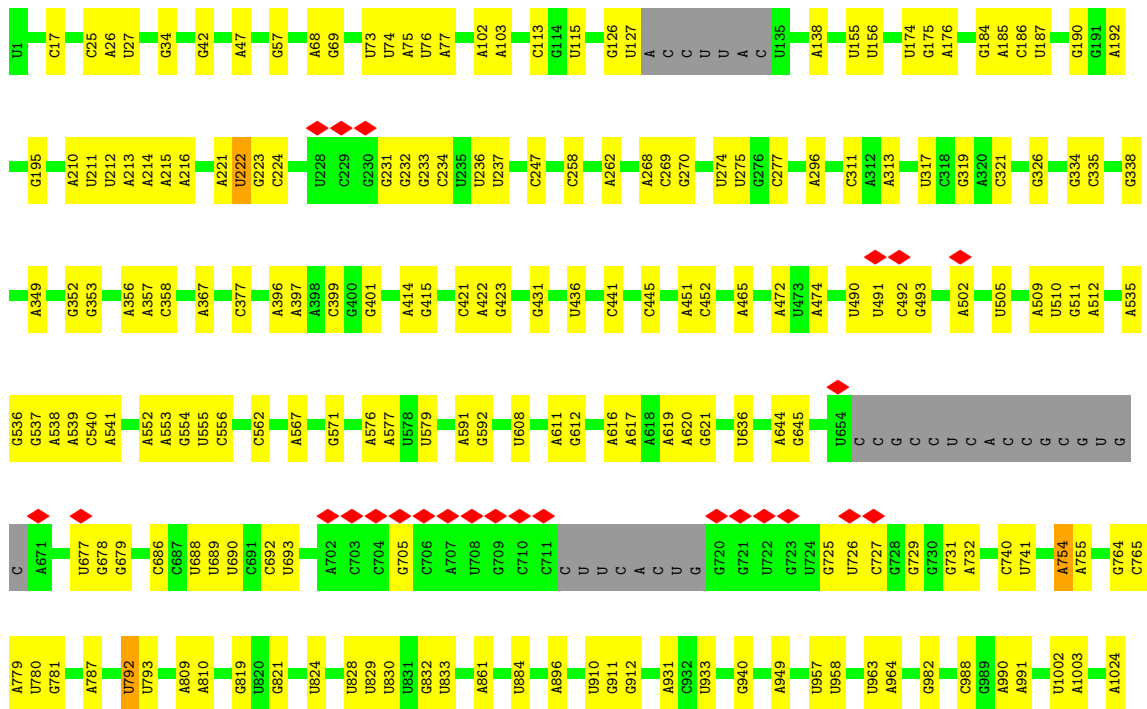
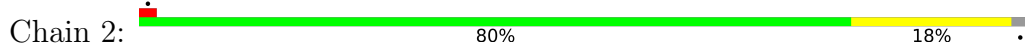
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

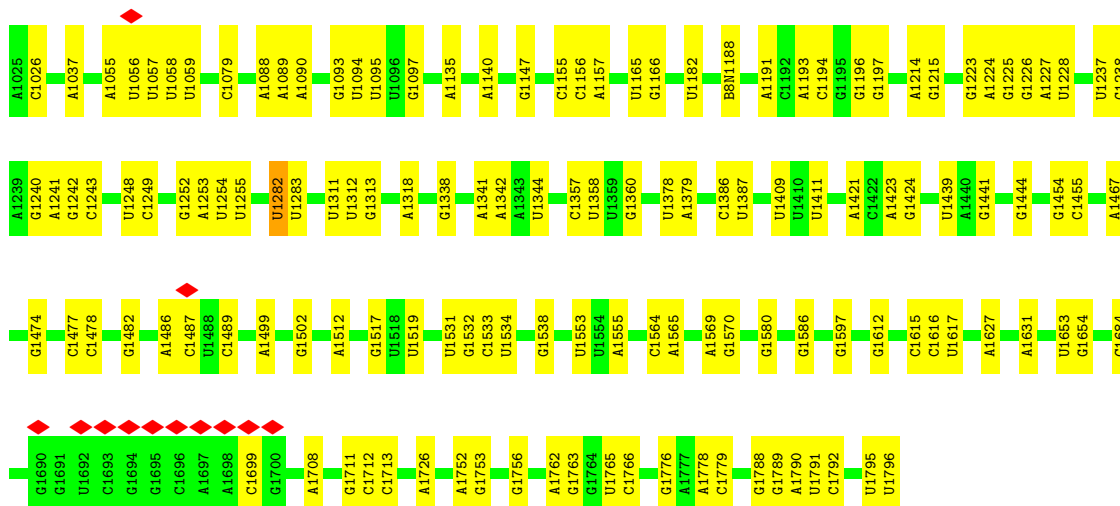
- Molecule 1: 28S rRNA



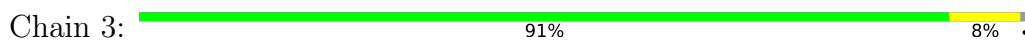


• Molecule 2: 18S rRNA

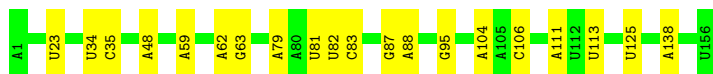
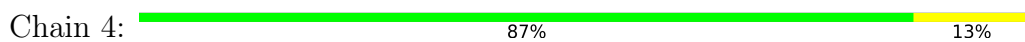




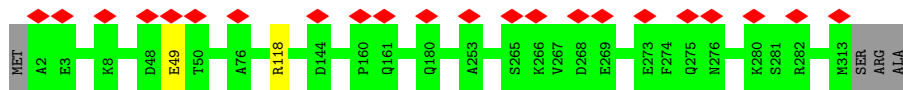
• Molecule 3: 5S rRNA



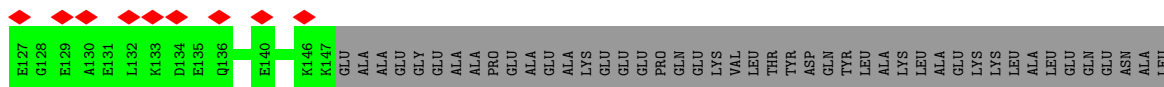
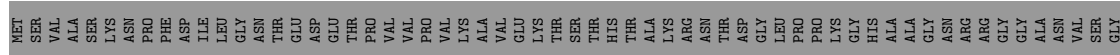
• Molecule 4: 5.8S rRNA



• Molecule 5: Putative guanine nucleotide-binding protein



• Molecule 6: Hyaluronan/mRNA-binding protein domain-containing protein





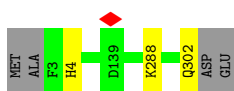
- Molecule 10: 60S ribosomal protein L4-like protein

Chain LC: 99%



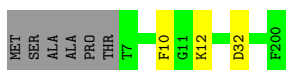
- Molecule 11: 60S ribosomal protein I5-like protein

Chain LD: 98%



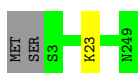
- Molecule 12: 60S ribosomal protein L6

Chain LE: 96%



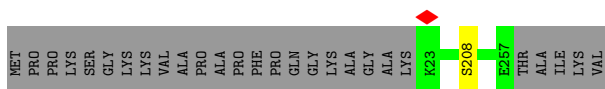
- Molecule 13: 60S ribosomal protein I7-like protein

Chain LF: 99%



- Molecule 14: 60S ribosomal protein L8

Chain LG: 89% 10%



- Molecule 15: 60S ribosomal protein I9-like protein

Chain LH: 99%



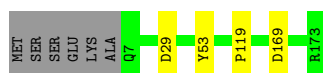
- Molecule 16: 60S ribosomal protein L10-like protein

Chain LI: 99%



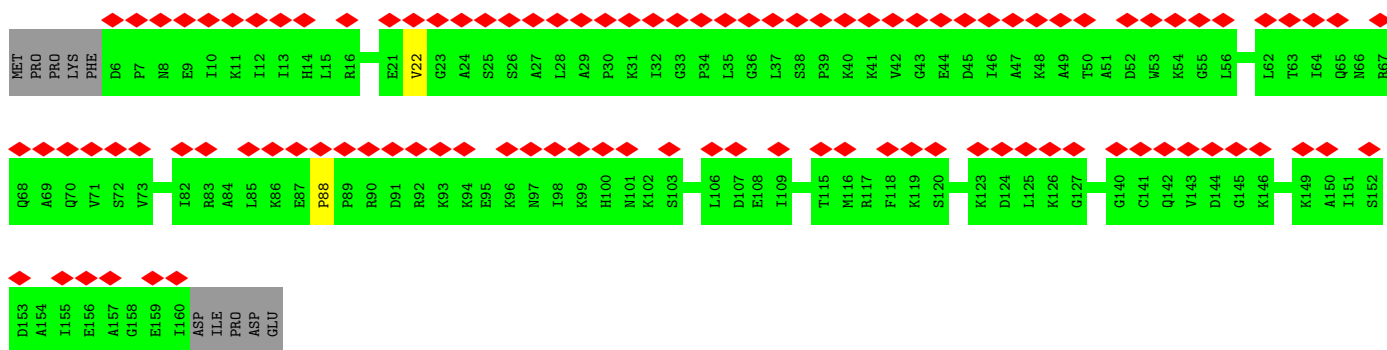
- Molecule 17: Putative ribosomal protein

Chain LJ: 94%



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

Chain LK: 93% 6%



- Molecule 19: 60S ribosomal protein L13

Chain LL: 98%



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

Chain LM: 99%



- Molecule 21: Ribosomal protein L15

Chain LN: 100%

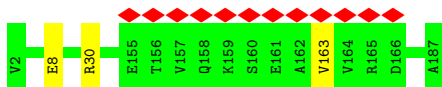


- Molecule 22: 60S ribosomal protein L16-like protein

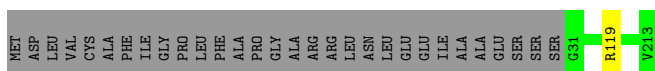
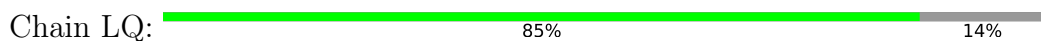
Chain LO: 98%



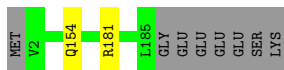
- Molecule 23: 60S ribosomal protein l17-like protein



- Molecule 24: Ribosomal protein L18-like protein



- Molecule 25: Ribosomal protein L19



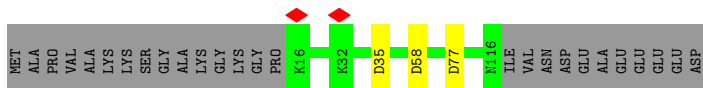
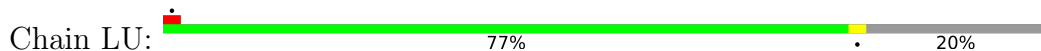
- Molecule 26: 60S ribosomal protein L20



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

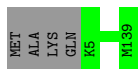


- Molecule 28: 60S ribosomal protein L22-like protein

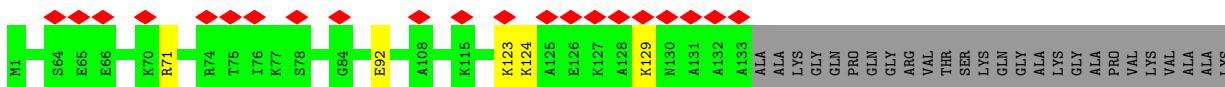
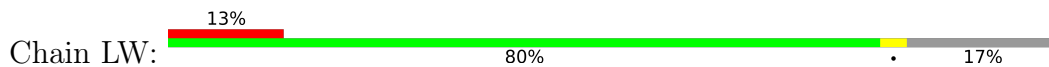


- Molecule 29: 60S ribosomal protein l23-like protein

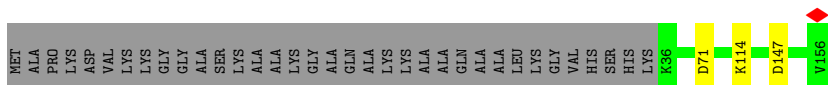
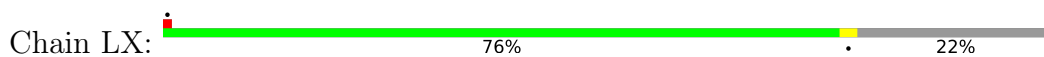




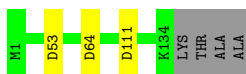
- Molecule 30: 60S ribosomal protein L24



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



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



- Molecule 33: 60S ribosomal protein L27




- Molecule 34: Ribosomal protein L18e/L15P domain-containing protein

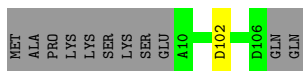


- Molecule 35: 60S ribosomal protein L29



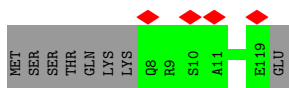
- Molecule 36: 60S ribosomal protein l30-like protein

Chain Lc:  89% 10%



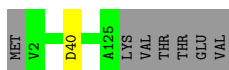
- Molecule 37: Putative 60S ribosomal protein

Chain Ld:  93% 7%



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

Chain Le:  94% 5%



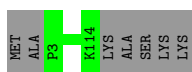
- Molecule 39: 60S ribosomal protein l33-like protein

Chain Lf:  98%



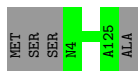
- Molecule 40: Ribosomal protein l34-like protein

Chain Lg:  94% 6%



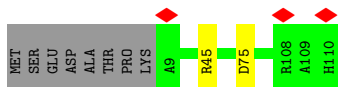
- Molecule 41: dolichyl-diphosphooligosaccharide--protein glycotransferase

Chain Lh:  97%



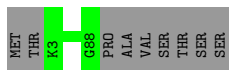
- Molecule 42: 60S ribosomal protein L36

Chain Li:  91% 7%



- Molecule 43: Ribosomal protein L37

Chain Lj:  91% 9%



- Molecule 44: 60S ribosomal protein L38

Chain Lk:  90% 5% 5%



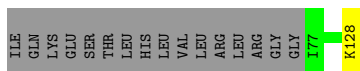
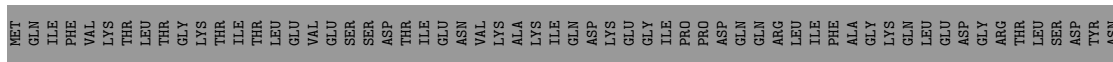
- Molecule 45: 60S ribosomal protein L39

Chain Ll:  98%



- Molecule 46: Ubiquitin-like domain-containing protein

Chain Lm:  40% 59%



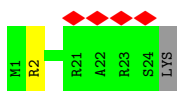
- Molecule 47: 60S ribosomal protein L41-A

Chain Ln:  96%



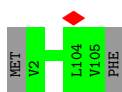
- Molecule 47: 60S ribosomal protein L41-A

Chain Lr:  16% 92%

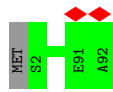


- Molecule 48: 60S ribosomal protein L44-like protein

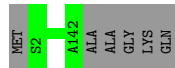
Chain Lo:  98%



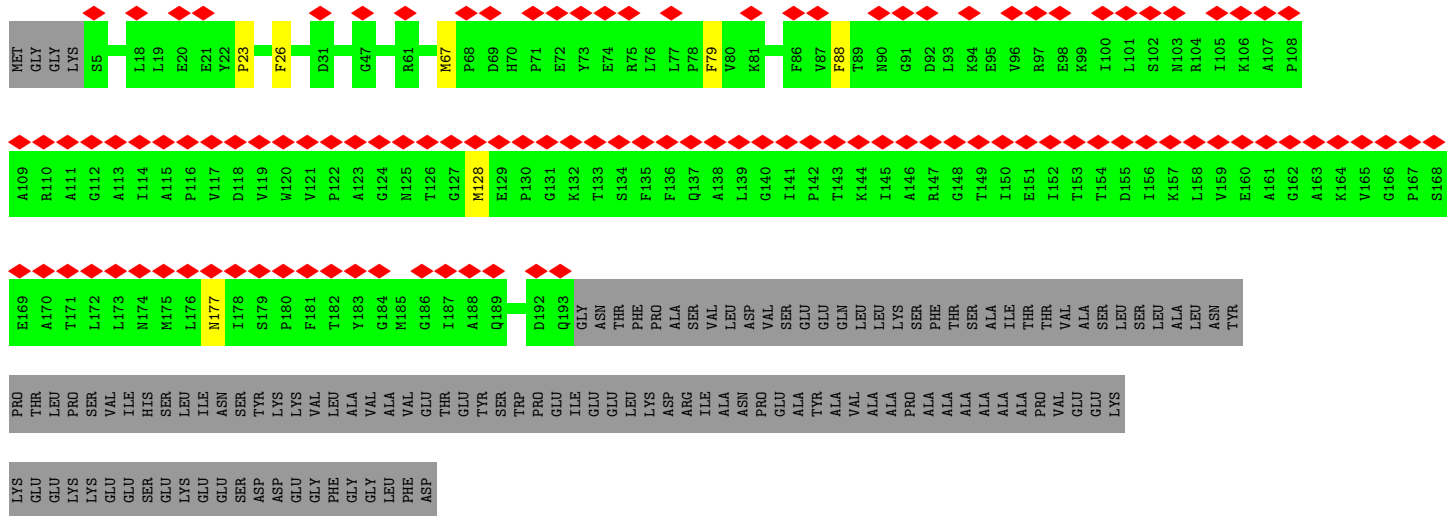
- Molecule 49: 60S ribosomal protein L43-like protein



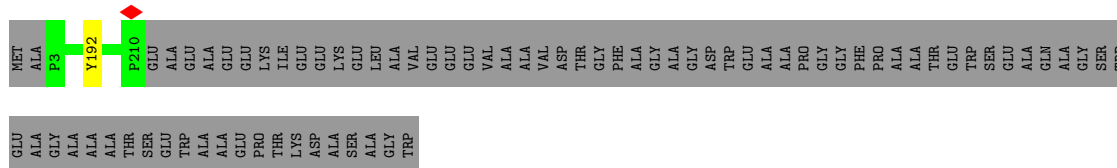
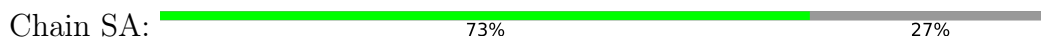
- Molecule 50: Putative 60S ribosomal protein



- Molecule 51: 60S acidic ribosomal protein P0

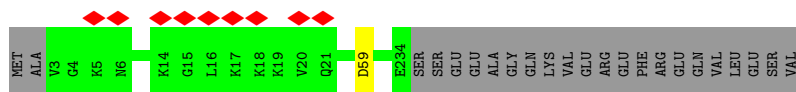


- Molecule 52: 40S ribosomal protein S0

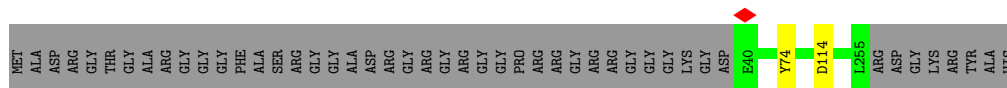
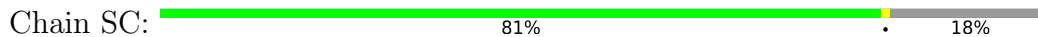


- Molecule 53: 40S ribosomal protein S1

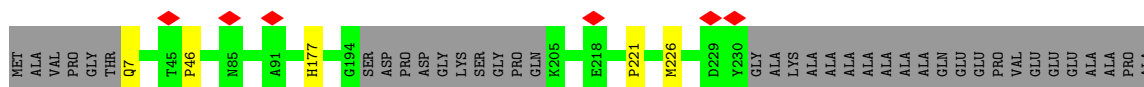
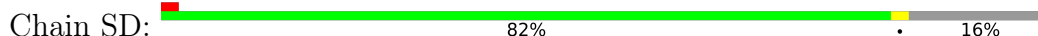




• Molecule 54: 40S ribosomal protein S2-like protein

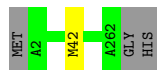


• Molecule 55: 40S ribosomal protein S3-like protein

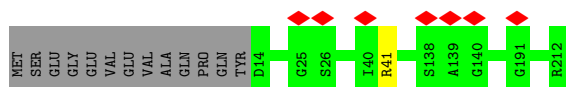


GLU
GLN

• Molecule 56: 40S ribosomal protein S4



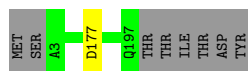
• Molecule 57: 40S ribosomal protein s5-like protein



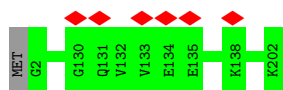
• Molecule 58: 40S ribosomal protein S6



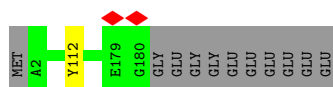
• Molecule 59: 40S ribosomal protein S7



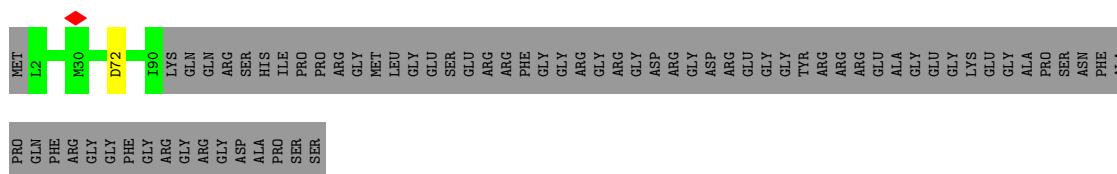
- Molecule 60: 40S ribosomal protein S8



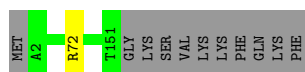
- Molecule 61: 40S ribosomal protein s9-like protein



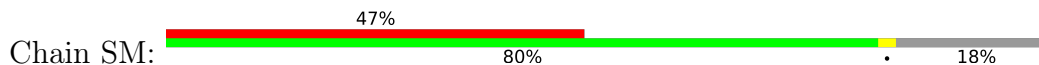
- Molecule 62: 40S ribosomal protein s10-like protein



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



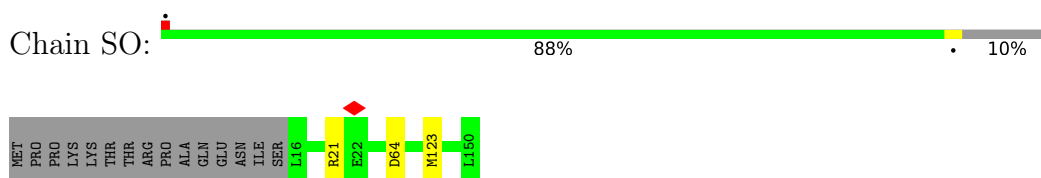
- Molecule 64: 40S ribosomal protein S12



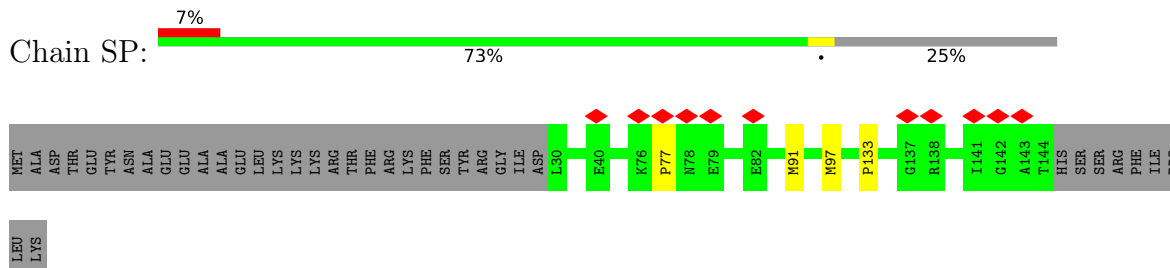
- Molecule 65: 40S ribosomal protein S13-like protein



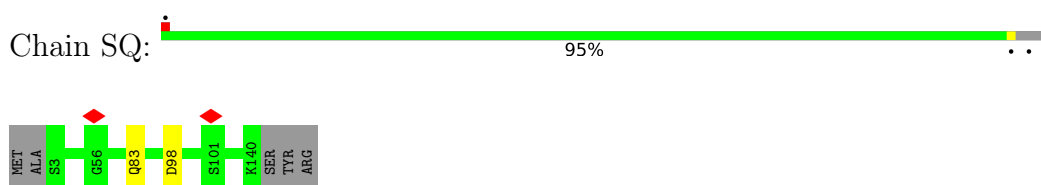
- Molecule 66: 40S ribosomal protein S14-like protein



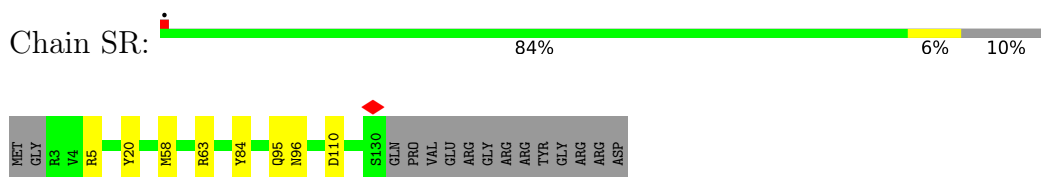
- Molecule 67: 40S ribosomal protein s15-like protein



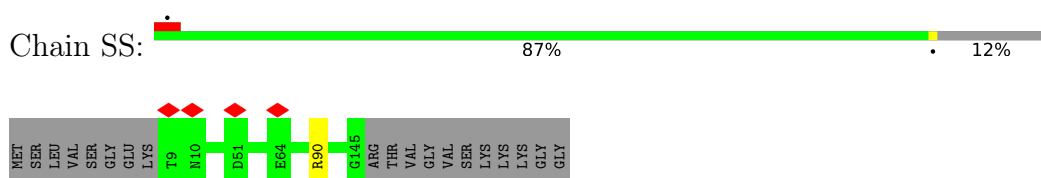
- Molecule 68: 40S ribosomal protein S16-like protein



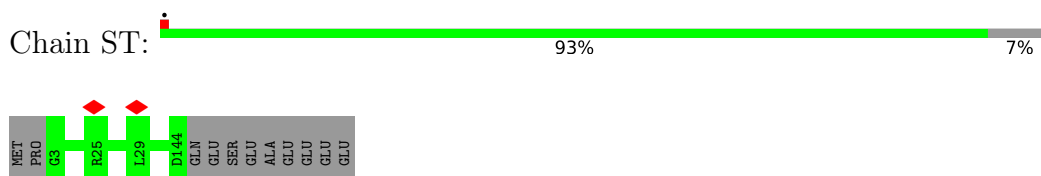
- Molecule 69: 40S ribosomal protein S17-like protein



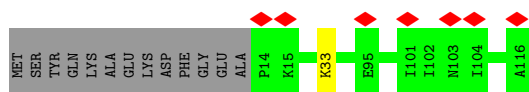
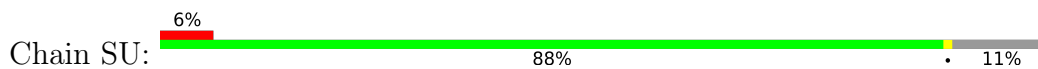
- Molecule 70: Putative ribosomal protein



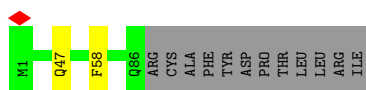
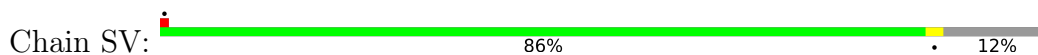
- Molecule 71: 40S ribosomal protein S19-like protein



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



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



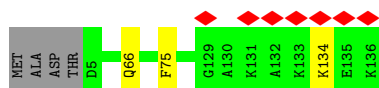
• Molecule 74: 40S ribosomal protein S22-like protein



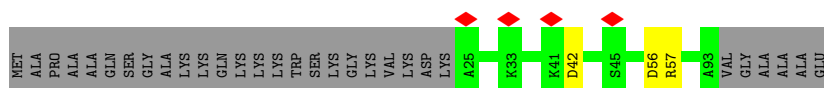
• Molecule 75: 40S ribosomal protein s23-like protein



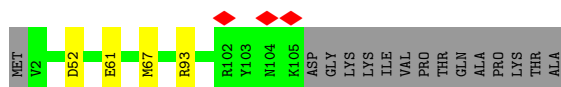
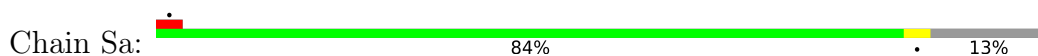
• Molecule 76: 40S ribosomal protein S24



• Molecule 77: 40S ribosomal protein S25



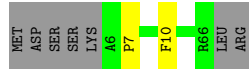
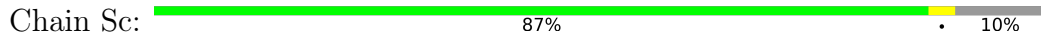
• Molecule 78: 40S ribosomal protein S26



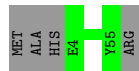
- Molecule 79: Ribosomal protein s27-like protein



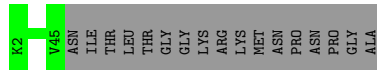
- Molecule 80: 40S ribosomal protein S28-like protein



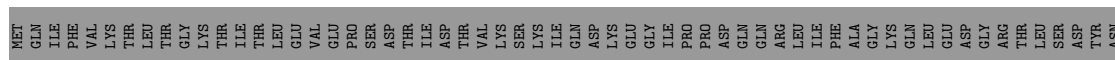
- Molecule 81: 40S ribosomal protein S29



- Molecule 82: 40S ribosomal protein S30



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



- Molecule 84: Methionine aminopeptidase 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	119160	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 ($e^-/\text{\AA}^2$)	54.8	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2100	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	1.870	Depositor
Minimum map value	-0.608	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.22	Depositor
Map size (\AA)	666.0, 666.0, 666.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.11, 1.11, 1.11	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: B8N, SAC, OMG, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	1	0.30	0/76339	0.80	22/119028 (0.0%)
2	2	0.26	0/42072	0.80	9/65562 (0.0%)
3	3	0.27	0/2833	0.80	0/4413
4	4	0.29	0/3710	0.78	0/5778
5	A	0.25	0/2495	0.54	0/3390
6	B	0.27	0/243	0.60	0/316
7	C	0.34	0/622	0.69	1/827 (0.1%)
8	LA	0.27	0/1964	0.56	0/2641
9	LB	0.25	0/3156	0.53	0/4238
10	LC	0.25	0/2815	0.51	0/3795
11	LD	0.26	0/2487	0.51	0/3341
12	LE	0.26	0/1547	0.51	0/2081
13	LF	0.26	0/2055	0.51	0/2758
14	LG	0.25	0/1929	0.50	0/2579
15	LH	0.25	0/1525	0.52	0/2050
16	LI	0.25	0/1797	0.55	0/2413
17	LJ	0.50	1/1389 (0.1%)	0.61	0/1856
18	LK	0.24	0/761	0.51	0/1056
19	LL	0.25	0/1695	0.56	0/2276
20	LM	0.25	0/1144	0.53	0/1539
21	LN	0.25	0/1740	0.58	0/2332
22	LO	0.26	0/1638	0.51	0/2197
23	LP	0.25	0/1495	0.55	0/2014
24	LQ	0.26	0/1507	0.58	0/2017
25	LR	0.24	0/1525	0.54	0/2028
26	LS	0.26	0/1460	0.52	0/1965
27	LT	0.26	0/1292	0.57	0/1738
28	LU	0.26	0/832	0.51	0/1112
29	LV	0.26	0/1012	0.54	0/1361
30	LW	0.25	0/1088	0.58	0/1443
31	LX	0.24	0/981	0.52	0/1324
32	LY	0.26	0/1079	0.59	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.25	0/1134	0.54	0/1519
34	La	0.25	0/1212	0.57	0/1627
35	Lb	0.26	0/518	0.55	0/684
36	Lc	0.27	0/731	0.49	0/983
37	Ld	0.26	0/925	0.54	0/1238
38	Le	0.24	0/1019	0.53	0/1358
39	Lf	0.26	0/874	0.56	0/1176
40	Lg	0.25	0/904	0.58	0/1210
41	Lh	0.24	0/1014	0.51	0/1349
42	Li	0.25	0/844	0.64	1/1115 (0.1%)
43	Lj	0.26	0/697	0.60	0/922
44	Lk	0.28	0/640	0.59	1/850 (0.1%)
45	Ll	0.23	0/445	0.58	0/593
46	Lm	0.25	0/424	0.54	0/561
47	Ln	0.23	0/225	0.69	0/289
47	Lr	0.21	0/225	0.68	0/289
48	Lo	0.27	0/835	0.61	0/1105
49	Lp	0.25	0/705	0.57	0/940
50	Lq	0.25	0/1101	0.52	0/1482
51	Ls	0.31	1/1477 (0.1%)	0.53	0/1995
52	SA	0.25	0/1683	0.50	0/2299
53	SB	0.24	0/1900	0.53	0/2551
54	SC	0.25	0/1703	0.50	0/2303
55	SD	2.45	2/1712 (0.1%)	1.08	3/2299 (0.1%)
56	SE	0.25	0/2112	0.55	0/2842
57	SF	0.24	0/1578	0.55	0/2130
58	SG	0.24	0/1906	0.55	0/2547
59	SH	0.25	0/1587	0.57	0/2140
60	SI	0.26	0/1654	0.56	0/2213
61	SJ	0.25	0/1489	0.55	0/1993
62	SK	0.25	0/764	0.53	0/1038
63	SL	0.26	0/1249	0.55	0/1678
64	SM	0.25	0/934	0.55	0/1255
65	SN	0.25	0/1205	0.50	0/1627
66	SO	0.26	0/1014	0.63	0/1361
67	SP	0.64	1/932 (0.1%)	0.74	2/1248 (0.2%)
68	SQ	0.25	0/1098	0.57	0/1472
69	SR	0.28	0/1060	0.57	0/1424
70	SS	0.25	0/1133	0.59	0/1520
71	ST	0.24	0/1137	0.59	0/1533
72	SU	0.23	0/828	0.55	0/1112
73	SV	0.27	0/671	0.59	0/900
74	SW	0.26	0/1055	0.58	0/1416

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	SX	0.27	0/1116	0.54	0/1489
76	SY	0.27	0/1075	0.58	0/1431
77	SZ	0.26	0/550	0.72	0/736
78	Sa	0.26	0/852	0.59	0/1136
79	Sb	0.26	0/623	0.58	0/843
80	Sc	5.21	1/487 (0.2%)	1.97	2/653 (0.3%)
81	Sd	0.25	0/427	0.59	0/570
82	Se	0.24	0/357	0.60	0/470
83	Sf	2.02	1/614 (0.2%)	0.99	2/813 (0.2%)
84	D	0.26	0/2972	0.51	0/4023
All	All	0.44	7/223653 (0.0%)	0.72	43/327261 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	LB	0	1
84	D	0	1
All	All	0	2

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
80	Sc	7	PRO	N-CD	114.94	3.08	1.47
55	SD	221	PRO	N-CD	99.56	2.87	1.47
83	Sf	122	PRO	N-CD	49.71	2.17	1.47
67	SP	77	PRO	N-CD	17.78	1.72	1.47
55	SD	46	PRO	N-CD	16.56	1.71	1.47

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	Sc	7	PRO	N-CD-CG	-36.22	48.87	103.20
55	SD	221	PRO	CA-N-CD	-29.54	70.14	111.50
55	SD	221	PRO	N-CD-CG	-29.47	58.99	103.20
80	Sc	7	PRO	CA-N-CD	-29.09	70.78	111.50
83	Sf	122	PRO	N-CD-CG	-20.97	71.74	103.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
84	D	384	ARG	Sidechain
9	LB	257	HIS	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	
5	A	310/316 (98%)	294 (95%)	16 (5%)	0	100	100
6	B	28/302 (9%)	19 (68%)	9 (32%)	0	100	100
7	C	76/614 (12%)	76 (100%)	0	0	100	100
8	LA	250/254 (98%)	236 (94%)	14 (6%)	0	100	100
9	LB	385/388 (99%)	367 (95%)	17 (4%)	1 (0%)	41	73
10	LC	361/365 (99%)	345 (96%)	16 (4%)	0	100	100
11	LD	298/304 (98%)	291 (98%)	7 (2%)	0	100	100
12	LE	192/200 (96%)	176 (92%)	16 (8%)	0	100	100
13	LF	245/249 (98%)	237 (97%)	8 (3%)	0	100	100
14	LG	233/262 (89%)	228 (98%)	5 (2%)	0	100	100
15	LH	189/192 (98%)	183 (97%)	6 (3%)	0	100	100
16	LI	215/219 (98%)	202 (94%)	13 (6%)	0	100	100
17	LJ	165/173 (95%)	159 (96%)	6 (4%)	0	100	100
18	LK	153/165 (93%)	134 (88%)	17 (11%)	2 (1%)	12	42
19	LL	207/213 (97%)	201 (97%)	6 (3%)	0	100	100
20	LM	139/142 (98%)	136 (98%)	3 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	LN	200/203 (98%)	191 (96%)	9 (4%)	0	100	100
22	LO	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
23	LP	184/186 (99%)	175 (95%)	8 (4%)	1 (0%)	29	64
24	LQ	181/213 (85%)	174 (96%)	7 (4%)	0	100	100
25	LR	182/192 (95%)	178 (98%)	4 (2%)	0	100	100
26	LS	171/174 (98%)	166 (97%)	5 (3%)	0	100	100
27	LT	156/160 (98%)	150 (96%)	6 (4%)	0	100	100
28	LU	99/127 (78%)	95 (96%)	4 (4%)	0	100	100
29	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
30	LW	131/161 (81%)	126 (96%)	5 (4%)	0	100	100
31	LX	119/156 (76%)	112 (94%)	7 (6%)	0	100	100
32	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
33	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
34	La	146/149 (98%)	137 (94%)	9 (6%)	0	100	100
35	Lb	60/65 (92%)	58 (97%)	2 (3%)	0	100	100
36	Lc	95/108 (88%)	95 (100%)	0	0	100	100
37	Ld	110/120 (92%)	107 (97%)	3 (3%)	0	100	100
38	Le	122/131 (93%)	119 (98%)	3 (2%)	0	100	100
39	Lf	105/109 (96%)	99 (94%)	6 (6%)	0	100	100
40	Lg	110/119 (92%)	104 (94%)	6 (6%)	0	100	100
41	Lh	120/126 (95%)	118 (98%)	2 (2%)	0	100	100
42	Li	100/110 (91%)	94 (94%)	6 (6%)	0	100	100
43	Lj	84/95 (88%)	80 (95%)	4 (5%)	0	100	100
44	Lk	74/80 (92%)	72 (97%)	2 (3%)	0	100	100
45	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
46	Lm	50/128 (39%)	50 (100%)	0	0	100	100
47	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lr	22/25 (88%)	22 (100%)	0	0	100	100
48	Lo	102/106 (96%)	98 (96%)	4 (4%)	0	100	100
49	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
50	Lq	139/147 (95%)	133 (96%)	6 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	Ls	187/312 (60%)	184 (98%)	3 (2%)	0	100	100
52	SA	206/285 (72%)	193 (94%)	13 (6%)	0	100	100
53	SB	230/255 (90%)	216 (94%)	14 (6%)	0	100	100
54	SC	214/263 (81%)	206 (96%)	8 (4%)	0	100	100
55	SD	210/254 (83%)	199 (95%)	11 (5%)	0	100	100
56	SE	259/264 (98%)	248 (96%)	11 (4%)	0	100	100
57	SF	197/212 (93%)	182 (92%)	15 (8%)	0	100	100
58	SG	230/239 (96%)	221 (96%)	9 (4%)	0	100	100
59	SH	193/203 (95%)	185 (96%)	8 (4%)	0	100	100
60	SI	199/202 (98%)	192 (96%)	7 (4%)	0	100	100
61	SJ	177/190 (93%)	171 (97%)	6 (3%)	0	100	100
62	SK	87/159 (55%)	87 (100%)	0	0	100	100
63	SL	148/161 (92%)	146 (99%)	2 (1%)	0	100	100
64	SM	116/144 (81%)	104 (90%)	12 (10%)	0	100	100
65	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
66	SO	133/150 (89%)	127 (96%)	6 (4%)	0	100	100
67	SP	113/153 (74%)	108 (96%)	5 (4%)	0	100	100
68	SQ	136/143 (95%)	130 (96%)	6 (4%)	0	100	100
69	SR	126/143 (88%)	123 (98%)	3 (2%)	0	100	100
70	SS	135/156 (86%)	123 (91%)	12 (9%)	0	100	100
71	ST	140/153 (92%)	135 (96%)	5 (4%)	0	100	100
72	SU	101/116 (87%)	94 (93%)	7 (7%)	0	100	100
73	SV	84/98 (86%)	82 (98%)	2 (2%)	0	100	100
74	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
75	SX	140/145 (97%)	131 (94%)	9 (6%)	0	100	100
76	SY	130/136 (96%)	128 (98%)	2 (2%)	0	100	100
77	SZ	67/99 (68%)	66 (98%)	1 (2%)	0	100	100
78	Sa	102/119 (86%)	99 (97%)	3 (3%)	0	100	100
79	Sb	79/82 (96%)	75 (95%)	4 (5%)	0	100	100
80	Sc	59/68 (87%)	54 (92%)	5 (8%)	0	100	100
81	Sd	50/56 (89%)	48 (96%)	2 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
82	Se	42/61 (69%)	39 (93%)	3 (7%)	0	100	100
83	Sf	71/154 (46%)	62 (87%)	9 (13%)	0	100	100
84	D	369/371 (100%)	365 (99%)	4 (1%)	0	100	100
All	All	12071/14159 (85%)	11564 (96%)	503 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	A	271/274 (99%)	269 (99%)	2 (1%)	84	93
6	B	21/224 (9%)	19 (90%)	2 (10%)	8	31
7	C	68/511 (13%)	67 (98%)	1 (2%)	65	85
8	LA	196/198 (99%)	195 (100%)	1 (0%)	88	94
9	LB	327/328 (100%)	325 (99%)	2 (1%)	86	94
10	LC	284/285 (100%)	284 (100%)	0	100	100
11	LD	250/253 (99%)	247 (99%)	3 (1%)	71	88
12	LE	162/166 (98%)	159 (98%)	3 (2%)	57	81
13	LF	213/215 (99%)	212 (100%)	1 (0%)	88	94
14	LG	203/222 (91%)	202 (100%)	1 (0%)	88	94
15	LH	168/169 (99%)	167 (99%)	1 (1%)	86	94
16	LI	182/183 (100%)	181 (100%)	1 (0%)	88	94
17	LJ	145/150 (97%)	142 (98%)	3 (2%)	53	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	LL	172/176 (98%)	171 (99%)	1 (1%)	86	94
20	LM	116/117 (99%)	115 (99%)	1 (1%)	78	91
21	LN	179/180 (99%)	179 (100%)	0	100	100
22	LO	161/162 (99%)	158 (98%)	3 (2%)	57	81
23	LP	151/151 (100%)	149 (99%)	2 (1%)	69	87
24	LQ	155/178 (87%)	154 (99%)	1 (1%)	86	94
25	LR	153/160 (96%)	151 (99%)	2 (1%)	69	87
26	LS	153/154 (99%)	153 (100%)	0	100	100
27	LT	134/135 (99%)	133 (99%)	1 (1%)	84	93
28	LU	89/108 (82%)	86 (97%)	3 (3%)	37	69
29	LV	99/102 (97%)	99 (100%)	0	100	100
30	LW	107/125 (86%)	102 (95%)	5 (5%)	26	59
31	LX	108/129 (84%)	105 (97%)	3 (3%)	43	73
32	LY	117/119 (98%)	114 (97%)	3 (3%)	46	74
33	LZ	121/121 (100%)	119 (98%)	2 (2%)	60	83
34	La	121/122 (99%)	119 (98%)	2 (2%)	60	83
35	Lb	53/55 (96%)	52 (98%)	1 (2%)	57	81
36	Lc	78/88 (89%)	77 (99%)	1 (1%)	69	87
37	Ld	97/105 (92%)	97 (100%)	0	100	100
38	Le	107/114 (94%)	106 (99%)	1 (1%)	78	91
39	Lf	88/90 (98%)	88 (100%)	0	100	100
40	Lg	97/102 (95%)	97 (100%)	0	100	100
41	Lh	109/112 (97%)	109 (100%)	0	100	100
42	Li	86/93 (92%)	85 (99%)	1 (1%)	71	88
43	Lj	70/78 (90%)	70 (100%)	0	100	100
44	Lk	73/77 (95%)	70 (96%)	3 (4%)	30	64
45	Ll	45/46 (98%)	45 (100%)	0	100	100
46	Lm	47/115 (41%)	46 (98%)	1 (2%)	53	79
47	Ln	22/23 (96%)	22 (100%)	0	100	100
47	Lr	22/23 (96%)	21 (96%)	1 (4%)	27	60
48	Lo	88/90 (98%)	88 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Lp	73/74 (99%)	73 (100%)	0	100	100
50	Lq	109/112 (97%)	109 (100%)	0	100	100
51	Ls	155/255 (61%)	149 (96%)	6 (4%)	32	65
52	SA	178/225 (79%)	177 (99%)	1 (1%)	86	94
53	SB	203/223 (91%)	202 (100%)	1 (0%)	88	94
54	SC	181/206 (88%)	179 (99%)	2 (1%)	73	89
55	SD	182/206 (88%)	179 (98%)	3 (2%)	62	84
56	SE	219/221 (99%)	218 (100%)	1 (0%)	88	94
57	SF	167/178 (94%)	166 (99%)	1 (1%)	86	94
58	SG	198/204 (97%)	196 (99%)	2 (1%)	76	90
59	SH	169/177 (96%)	168 (99%)	1 (1%)	86	94
60	SI	163/164 (99%)	163 (100%)	0	100	100
61	SJ	154/162 (95%)	153 (99%)	1 (1%)	86	94
62	SK	77/126 (61%)	76 (99%)	1 (1%)	69	87
63	SL	133/143 (93%)	132 (99%)	1 (1%)	81	92
64	SM	101/121 (84%)	98 (97%)	3 (3%)	41	71
65	SN	129/130 (99%)	129 (100%)	0	100	100
66	SO	102/117 (87%)	99 (97%)	3 (3%)	42	72
67	SP	99/132 (75%)	97 (98%)	2 (2%)	55	80
68	SQ	111/115 (96%)	109 (98%)	2 (2%)	59	82
69	SR	119/131 (91%)	111 (93%)	8 (7%)	16	46
70	SS	120/135 (89%)	119 (99%)	1 (1%)	81	92
71	ST	114/124 (92%)	114 (100%)	0	100	100
72	SU	93/103 (90%)	92 (99%)	1 (1%)	73	89
73	SV	69/80 (86%)	67 (97%)	2 (3%)	42	72
74	SW	112/113 (99%)	111 (99%)	1 (1%)	78	91
75	SX	113/116 (97%)	111 (98%)	2 (2%)	59	82
76	SY	112/115 (97%)	109 (97%)	3 (3%)	44	74
77	SZ	60/80 (75%)	57 (95%)	3 (5%)	24	57
78	Sa	91/103 (88%)	87 (96%)	4 (4%)	28	61
79	Sb	70/71 (99%)	69 (99%)	1 (1%)	67	86

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
80	Sc	54/61 (88%)	53 (98%)	1 (2%)	57	81
81	Sd	43/46 (94%)	43 (100%)	0	100	100
82	Se	37/50 (74%)	37 (100%)	0	100	100
83	Sf	66/139 (48%)	64 (97%)	2 (3%)	41	71
84	D	315/315 (100%)	314 (100%)	1 (0%)	92	96
All	All	10199/11701 (87%)	10079 (99%)	120 (1%)	72	88

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	Lm	128	LYS
77	SZ	57	ARG
55	SD	226	MET
77	SZ	56	ASP
83	Sf	119	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
59	SH	17	GLN
62	SK	31	HIS
61	SJ	137	GLN
67	SP	73	GLN
37	Ld	105	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3188/3337 (95%)	477 (14%)	39 (1%)
2	2	1760/1796 (97%)	316 (17%)	34 (1%)
3	3	118/120 (98%)	9 (7%)	1 (0%)
4	4	155/156 (99%)	20 (12%)	0
All	All	5221/5409 (96%)	822 (15%)	74 (1%)

5 of 822 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	27	A

Continued on next page...

Continued from previous page...

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

5 of 74 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	832	G
2	2	1616	C
2	2	1165	U
2	2	1341	A
1	1	2532	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
22	SAC	LO	2	22	7,8,9	1.03	0	8,9,11	0.91	0
1	OMG	1	2578	1	18,26,27	1.14	2 (11%)	19,38,41	0.82	1 (5%)
2	B8N	2	1188	2	24,29,30	2.47	4 (16%)	29,42,45	1.23	3 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	SAC	LO	2	22	-	3/7/8/10	-
1	OMG	1	2578	1	-	2/5/27/28	0/3/3/3
2	B8N	2	1188	2	-	1/16/34/35	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1188	B8N	O4-C4	9.23	1.42	1.23
2	2	1188	B8N	C2-N3	-3.69	1.32	1.38
2	2	1188	B8N	C4-N3	-3.50	1.33	1.40
2	2	1188	B8N	C6-C5	3.32	1.39	1.34
1	1	2578	OMG	C8-N7	-2.84	1.30	1.35

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1188	B8N	N3-C2-N1	2.99	120.98	116.76
2	2	1188	B8N	C4-N3-C2	-2.98	121.69	125.46
1	1	2578	OMG	O6-C6-C5	2.32	128.90	124.37
2	2	1188	B8N	O4'-C1'-C2'	2.25	108.31	105.14

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	LO	2	SAC	O-C-CA-CB
22	LO	2	SAC	N-CA-CB-OG
22	LO	2	SAC	C-CA-CB-OG
1	1	2578	OMG	O4'-C4'-C5'-O5'
1	1	2578	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

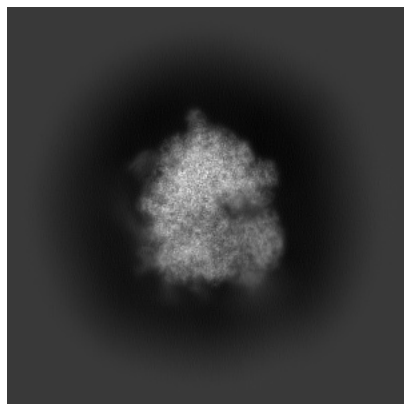
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17004. These allow visual inspection of the internal detail of the map and identification of artifacts.

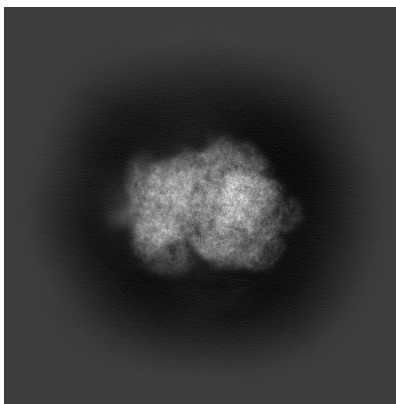
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

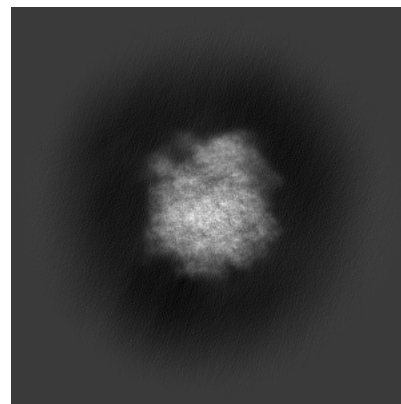
6.1.1 Primary map



X

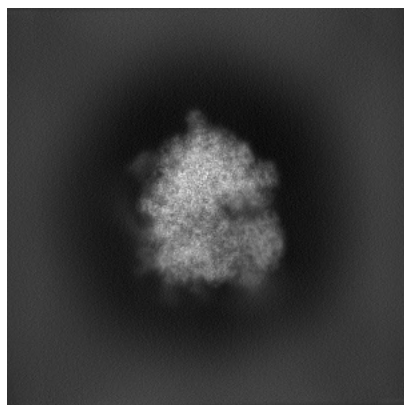


Y

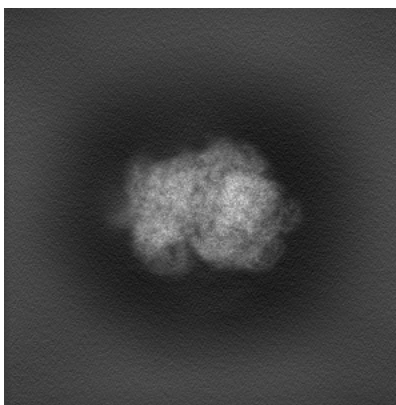


Z

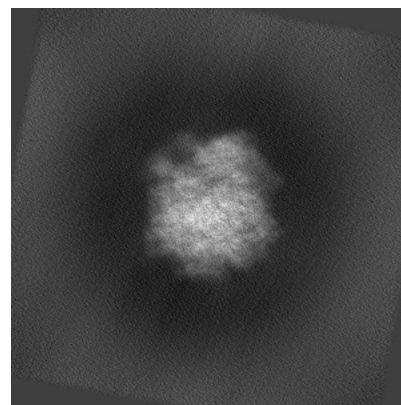
6.1.2 Raw map



X



Y

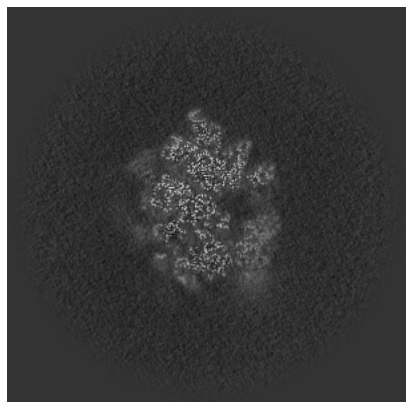


Z

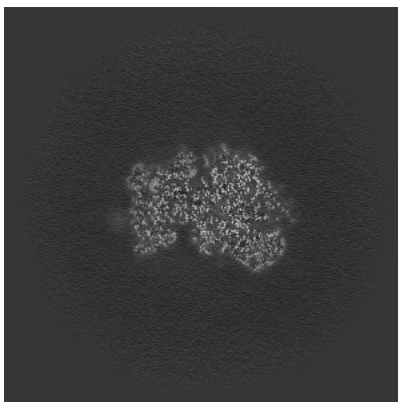
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

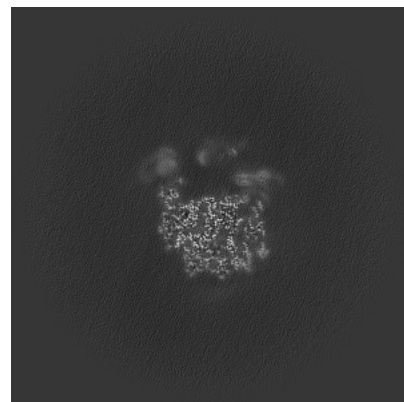
6.2.1 Primary map



X Index: 300

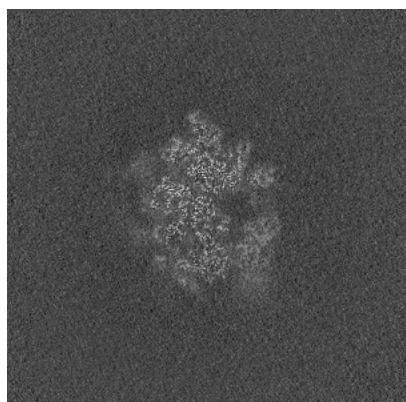


Y Index: 300

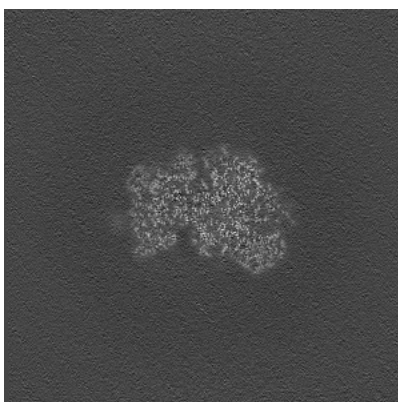


Z Index: 300

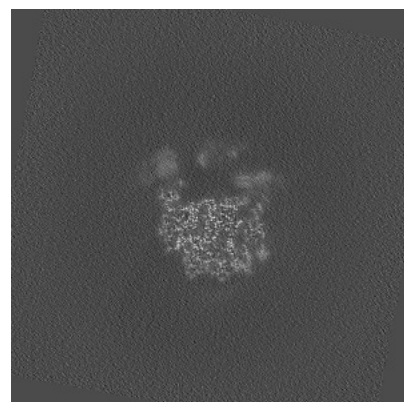
6.2.2 Raw map



X Index: 300



Y Index: 300

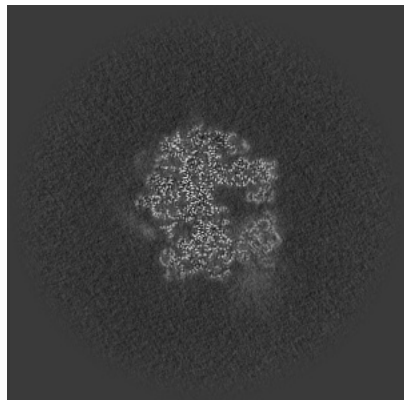


Z Index: 300

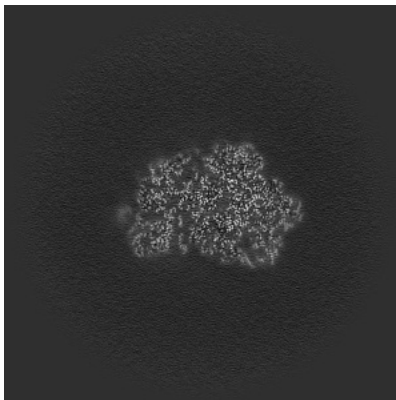
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

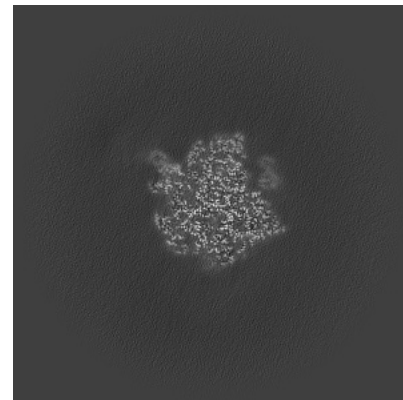
6.3.1 Primary map



X Index: 317

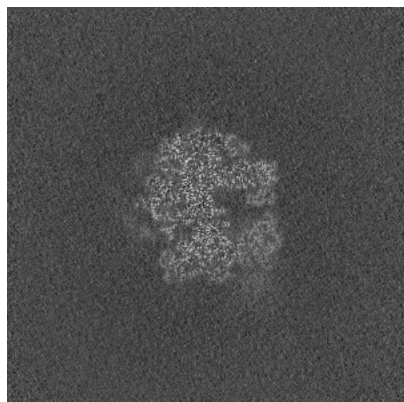


Y Index: 286

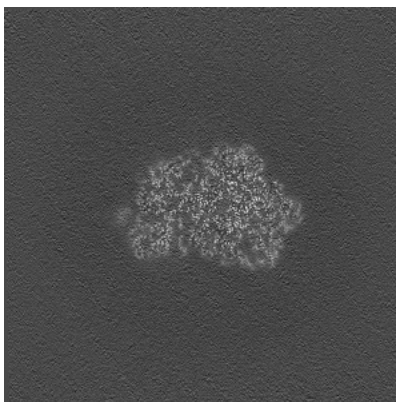


Z Index: 337

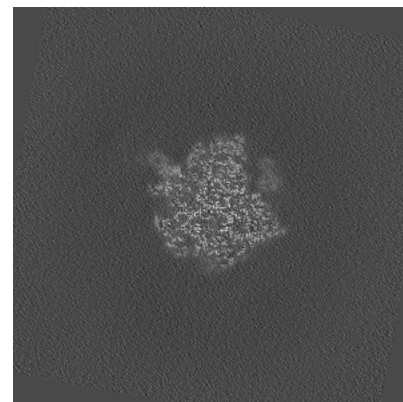
6.3.2 Raw map



X Index: 317



Y Index: 286

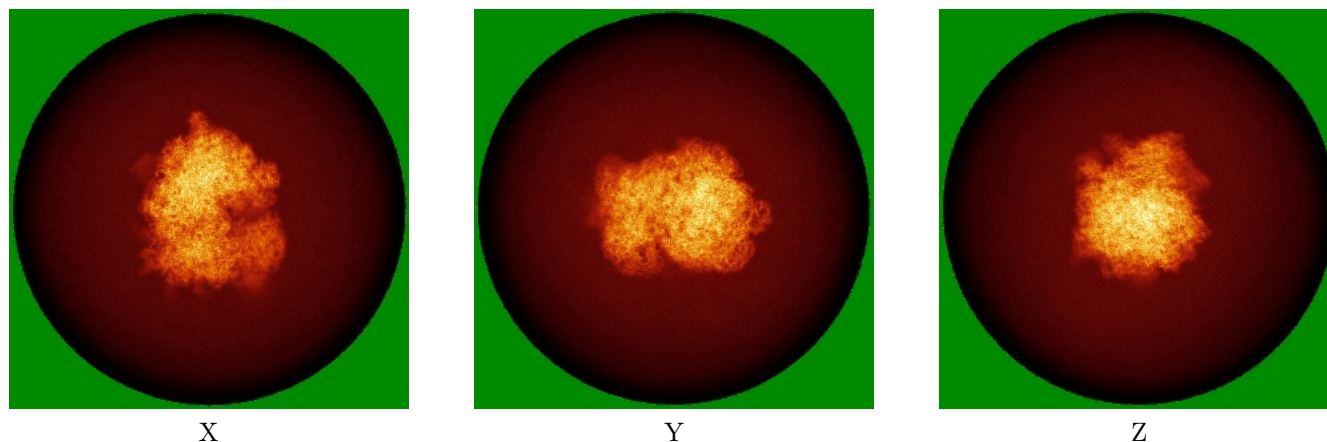


Z Index: 337

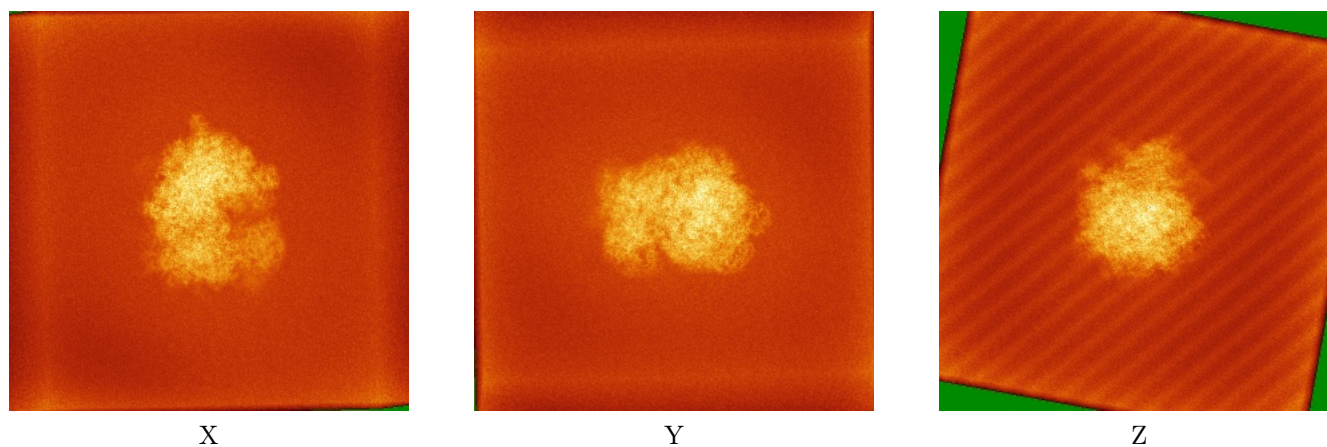
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



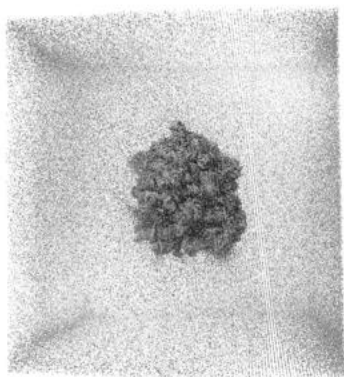
Y



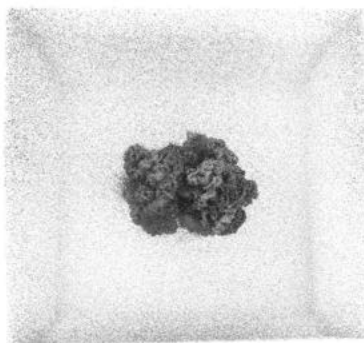
Z

The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

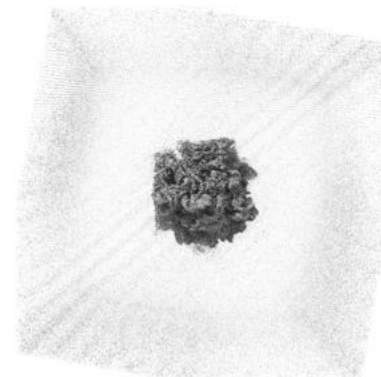
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

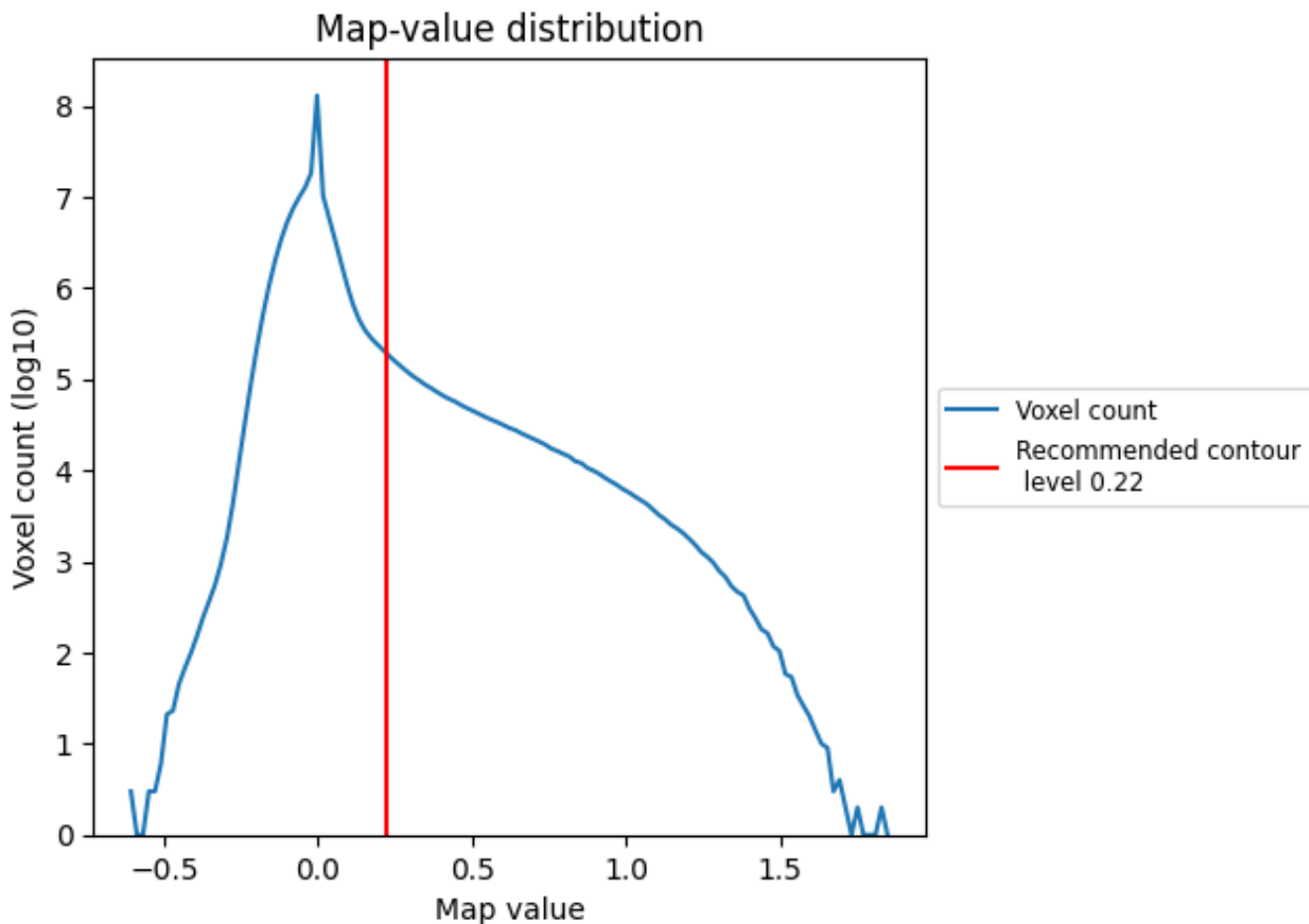
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

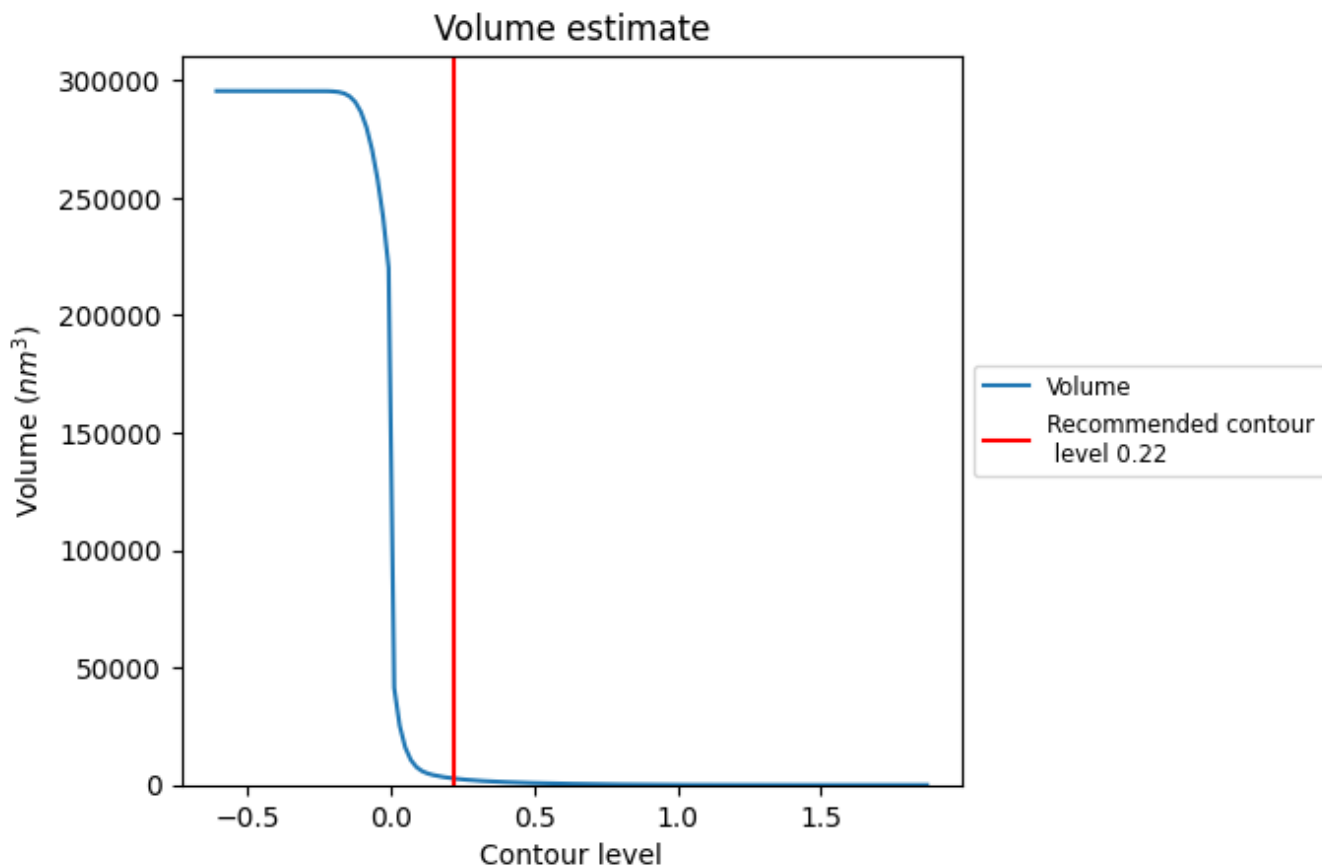
This section contains the results of statistical analysis of the map.

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.

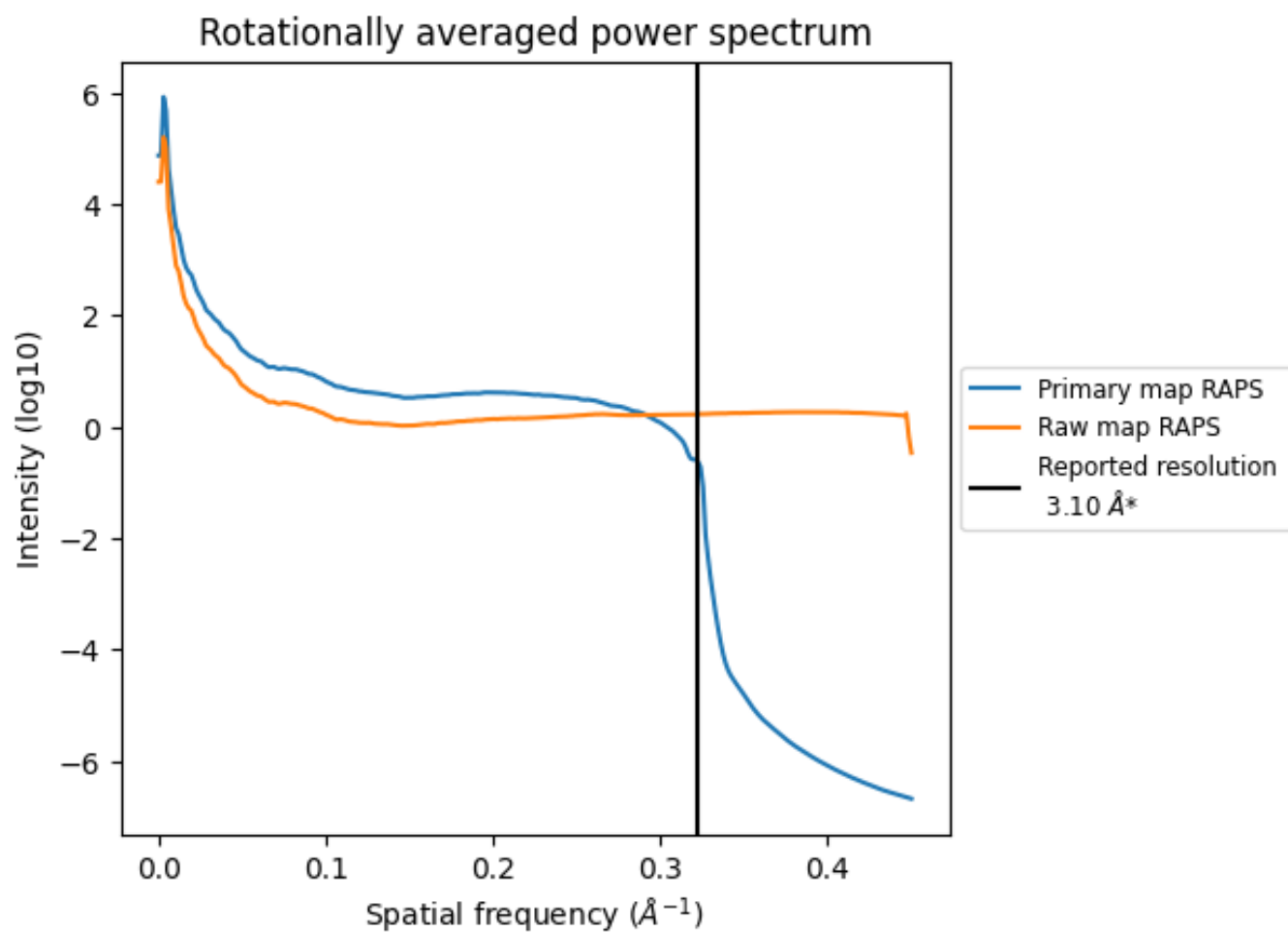
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2763 nm^3 ; this corresponds to an approximate mass of 2496 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](#)

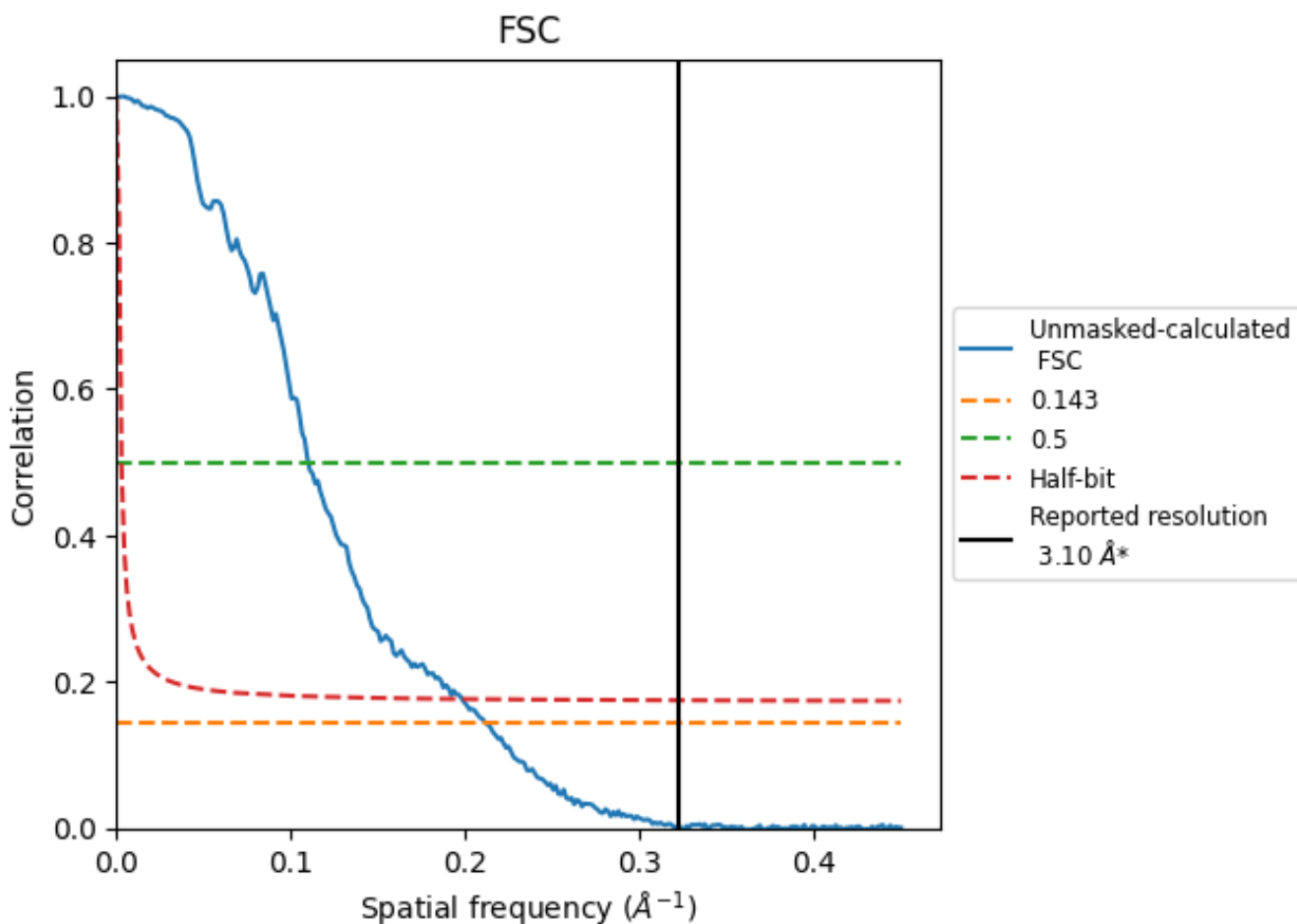


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

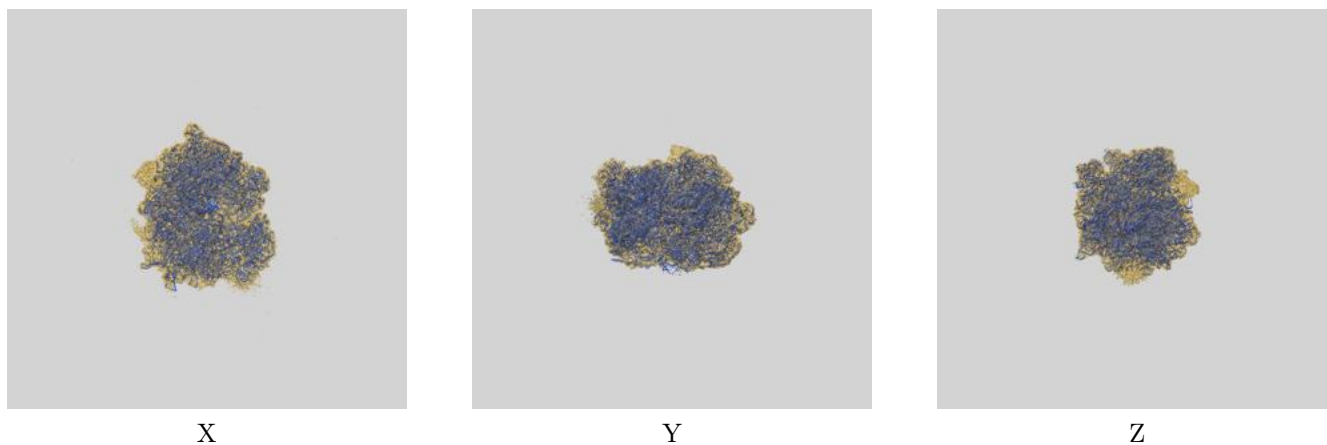
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.72	9.08	5.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.72 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

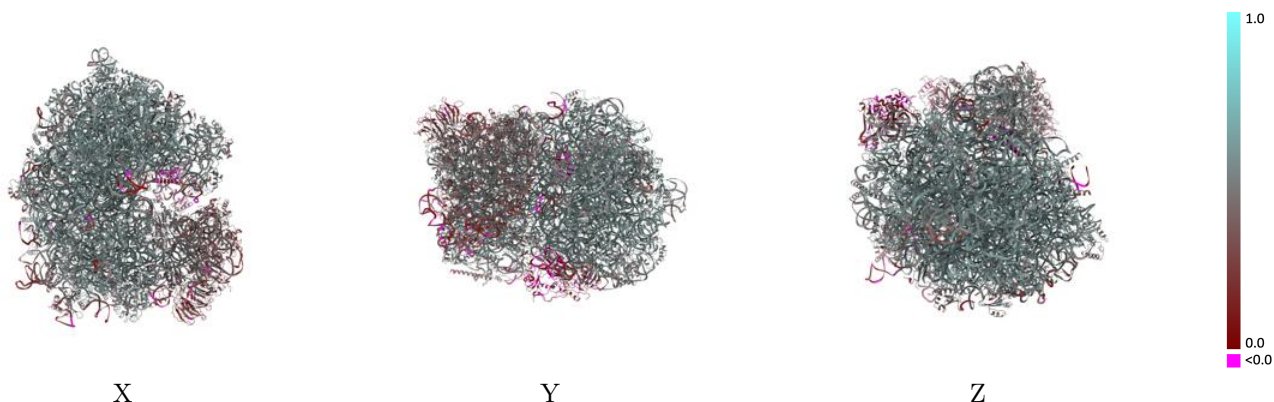
This section contains information regarding the fit between EMDB map EMD-17004 and PDB model 8000. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)



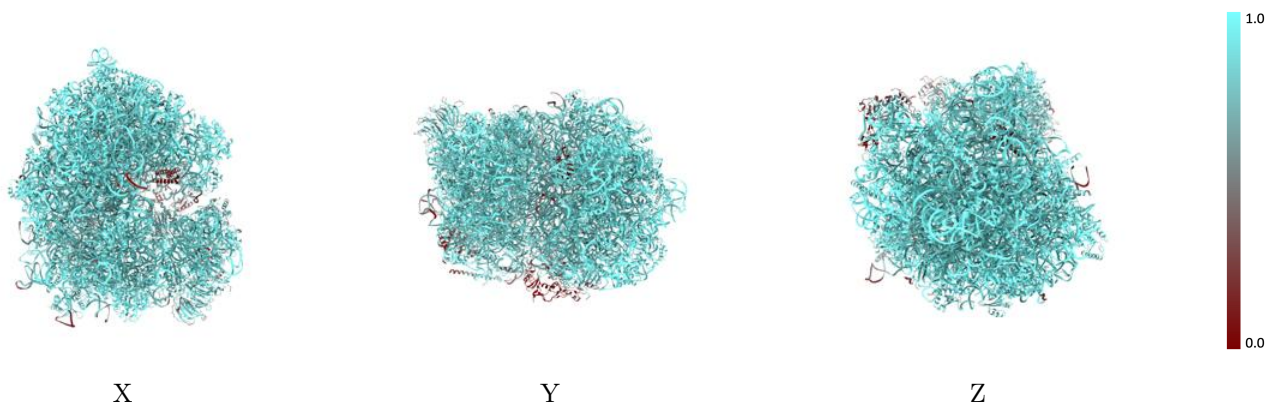
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



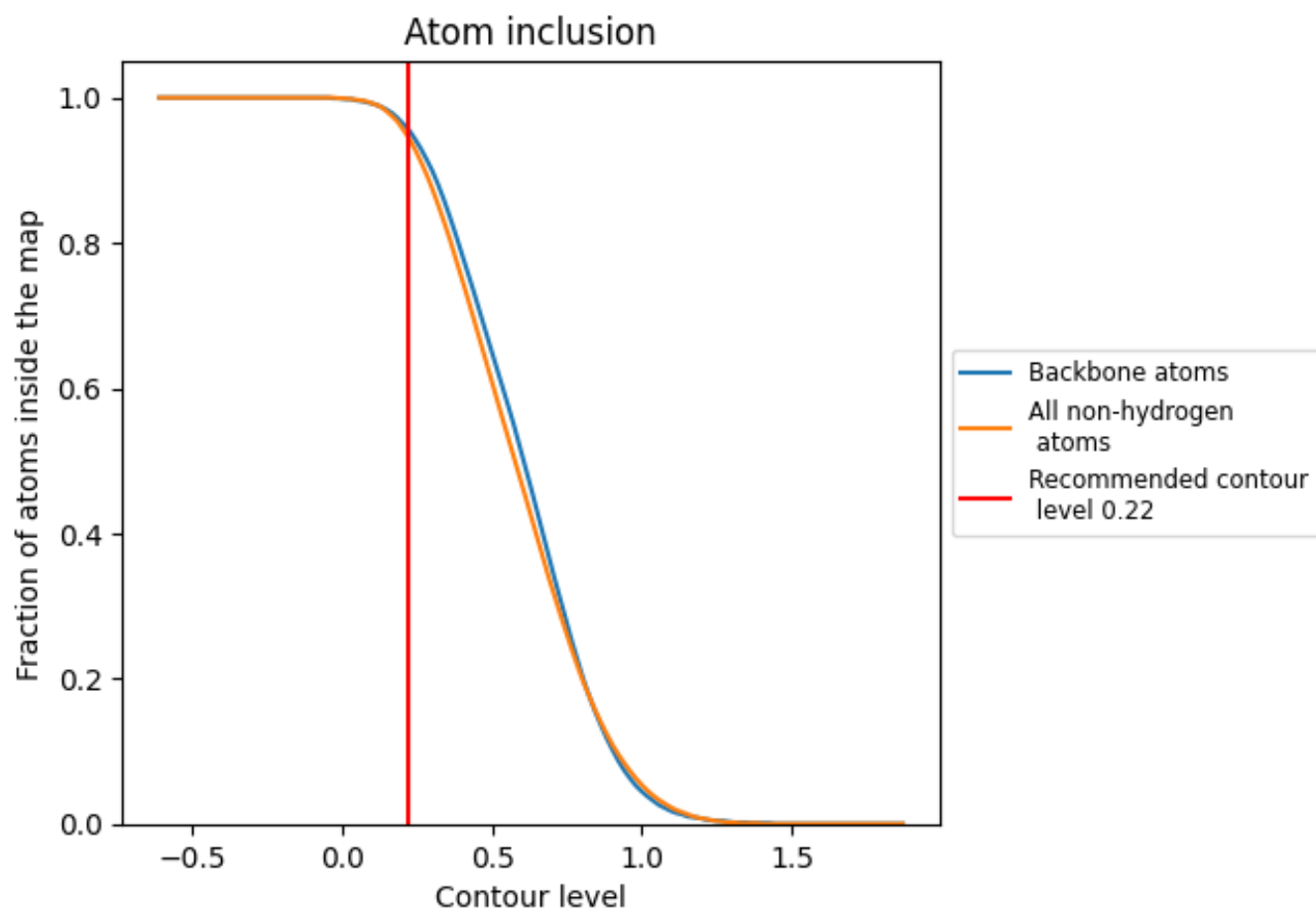
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.4940
1	 0.9860	 0.5310
2	 0.9600	 0.4630
3	 0.9990	 0.5300
4	 0.9900	 0.5360
A	 0.7890	 0.2830
B	 0.5680	 0.2140
C	 0.0880	 0.0170
D	 0.8550	 0.4440
LA	 0.9800	 0.5690
LB	 0.9770	 0.5490
LC	 0.9790	 0.5530
LD	 0.9440	 0.4910
LE	 0.9620	 0.4950
LF	 0.9760	 0.5440
LG	 0.9490	 0.5090
LH	 0.9440	 0.5080
LI	 0.9450	 0.5300
LJ	 0.9210	 0.4610
LK	 0.3400	 0.1100
LL	 0.9710	 0.5420
LM	 0.9730	 0.5170
LN	 0.9970	 0.5710
LO	 0.9870	 0.5440
LP	 0.9240	 0.5150
LQ	 0.9940	 0.5680
LR	 0.9640	 0.5410
LS	 0.9870	 0.5480
LT	 0.9770	 0.5440
LU	 0.9140	 0.4490
LV	 0.9830	 0.5620
LW	 0.7770	 0.4090
LX	 0.9590	 0.5210
LY	 0.9810	 0.5360
LZ	 0.9800	 0.5310





















Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
La	 0.9880	 0.5700
Lb	 0.9640	 0.5040
Lc	 0.9760	 0.5310
Ld	 0.9310	 0.5200
Le	 0.9930	 0.5660
Lf	 0.9980	 0.5630
Lg	 0.9810	 0.5510
Lh	 0.9580	 0.5150
Li	 0.9520	 0.5050
Lj	 0.9950	 0.5790
Lk	 0.9120	 0.4860
Ll	 0.9980	 0.5520
Lm	 0.9730	 0.5390
Ln	 0.9900	 0.5740
Lo	 0.9620	 0.5300
Lp	 0.9540	 0.5470
Lq	 0.9860	 0.5460
Lr	 0.8280	 0.4600
Ls	 0.3360	 0.1420
SA	 0.9600	 0.4990
SB	 0.9110	 0.4900
SC	 0.9570	 0.5220
SD	 0.8430	 0.3590
SE	 0.9650	 0.5170
SF	 0.8470	 0.3920
SG	 0.9360	 0.4620
SH	 0.9230	 0.4690
SI	 0.9350	 0.5110
SJ	 0.9620	 0.5120
SK	 0.9290	 0.3020
SL	 0.9760	 0.5450
SM	 0.3590	 0.1780
SN	 0.9640	 0.5380
SO	 0.9570	 0.5130
SP	 0.7780	 0.2790
SQ	 0.9050	 0.3790
SR	 0.8740	 0.3980
SS	 0.8570	 0.3640
ST	 0.8990	 0.3730
SU	 0.8630	 0.3800
SV	 0.9520	 0.5190
SW	 0.9810	 0.5450

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SX	 0.9630	 0.5360
SY	 0.9040	 0.4810
SZ	 0.8290	 0.3560
Sa	 0.9440	 0.5150
Sb	 0.9640	 0.5100
Sc	 0.8900	 0.4380
Sd	 0.9730	 0.4040
Se	 0.9210	 0.4950
Sf	 0.5140	 0.1400