



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:45 AM UTC

PDB ID : 9I78 / pdb_00009i78
EMDB ID : EMD-52656
Title : Cryo-EM structure of Chaetomium thermophilum ribosome-bound SND3 translocon
Authors : Yang, T.J.; McDowell, M.A.
Deposited on : 2025-01-31
Resolution : 2.20 Å (reported)
Based on initial models : 7OLC, .

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

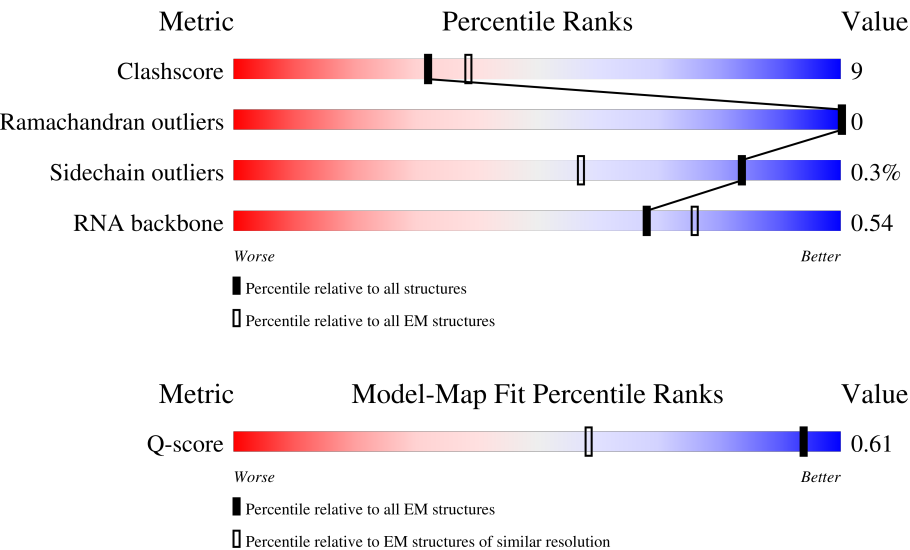
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.20 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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	476	
2	2	124	
3	3	70	



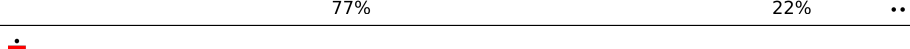
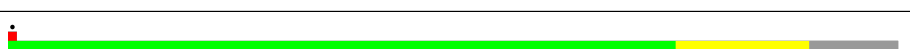



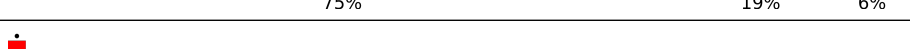
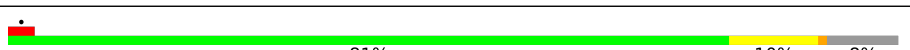


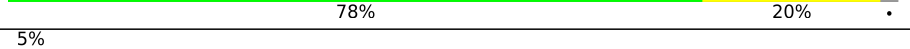

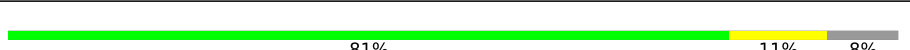


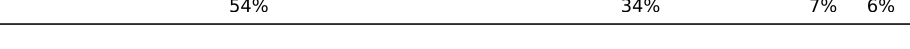





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Mol	Chain	Length	Quality of chain
4	4	455	
5	6	224	
6	7	278	
7	LA	254	
8	LB	392	
9	LC	365	
10	LD	304	
11	LE	200	
12	LF	249	
13	LG	262	
14	LH	192	
15	LI	219	
16	LJ	173	
17	LL	213	
18	LM	142	
19	LN	203	
20	LO	204	
21	LP	187	
22	LQ	213	
23	LR	192	
24	LS	174	
25	LT	160	
26	LU	127	
27	LV	139	
28	LX	156	

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Mol	Chain	Length	Quality of chain
29	LY	138	
30	LZ	135	
31	La	149	
32	Lb	65	
33	Lc	108	
34	Ld	120	
35	Le	131	
36	Lf	109	
37	Lg	119	
38	Lh	126	
39	Li	110	
40	Lj	95	
41	Lk	81	
42	Ll	51	
43	Lm	128	
44	Ln	25	
45	Lo	106	
46	Lp	92	
47	Lq	147	
48	L1	3337	
49	L2	156	
50	L3	120	

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 133840 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Translocon Sec61/SecY plug domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	462	Total	C	N	O	S	0	0
			3579	2338	577	640	24		

- Molecule 2 is a protein called SEC61 beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	98	Total	C	N	O	S	0	0
			717	451	137	128	1		

- Molecule 3 is a protein called SEC61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	65	Total	C	N	O	S	0	0
			524	343	91	89	1		

- Molecule 4 is a protein called CCDC47.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	371	Total	C	N	O	S	0	0
			2990	1907	523	554	6		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	53	ASP	-	insertion	UNP G0S5M5
4	54	TYR	-	insertion	UNP G0S5M5
4	55	LYS	-	insertion	UNP G0S5M5
4	56	ASP	-	insertion	UNP G0S5M5
4	57	ASP	-	insertion	UNP G0S5M5
4	58	ASP	-	insertion	UNP G0S5M5
4	59	ASP	-	insertion	UNP G0S5M5
4	60	LYS	-	insertion	UNP G0S5M5

- Molecule 5 is a protein called Putative inorganic phosphate transporter protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	188	Total	C	N	O	S	0	0
			1443	934	239	259	11		

There are 33 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	192	GLY	-	expression tag	UNP G0RYQ7
6	193	SER	-	expression tag	UNP G0RYQ7
6	194	GLY	-	expression tag	UNP G0RYQ7
6	195	SER	-	expression tag	UNP G0RYQ7
6	196	ALA	-	expression tag	UNP G0RYQ7
6	197	TRP	-	expression tag	UNP G0RYQ7
6	198	SER	-	expression tag	UNP G0RYQ7
6	199	HIS	-	expression tag	UNP G0RYQ7
6	200	PRO	-	expression tag	UNP G0RYQ7
6	201	GLN	-	expression tag	UNP G0RYQ7
6	202	PHE	-	expression tag	UNP G0RYQ7
6	203	GLU	-	expression tag	UNP G0RYQ7
6	204	LYS	-	expression tag	UNP G0RYQ7
6	205	GLY	-	expression tag	UNP G0RYQ7
6	206	GLY	-	expression tag	UNP G0RYQ7
6	207	GLY	-	expression tag	UNP G0RYQ7
6	208	SER	-	expression tag	UNP G0RYQ7
6	209	GLY	-	expression tag	UNP G0RYQ7
6	210	GLY	-	expression tag	UNP G0RYQ7
6	211	GLY	-	expression tag	UNP G0RYQ7
6	212	SER	-	expression tag	UNP G0RYQ7
6	213	GLY	-	expression tag	UNP G0RYQ7
6	214	GLY	-	expression tag	UNP G0RYQ7
6	215	SER	-	expression tag	UNP G0RYQ7
6	216	ALA	-	expression tag	UNP G0RYQ7
6	217	TRP	-	expression tag	UNP G0RYQ7
6	218	SER	-	expression tag	UNP G0RYQ7
6	219	HIS	-	expression tag	UNP G0RYQ7
6	220	PRO	-	expression tag	UNP G0RYQ7
6	221	GLN	-	expression tag	UNP G0RYQ7
6	222	PHE	-	expression tag	UNP G0RYQ7
6	223	GLU	-	expression tag	UNP G0RYQ7
6	224	LYS	-	expression tag	UNP G0RYQ7

- Molecule 6 is a protein called Translocon-associated protein subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	7	30	Total	C	N	O	0	0
			267	190	35	42		

- Molecule 7 is a protein called 60S ribosomal protein L2-like protein.

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

- Molecule 8 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 9 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 10 is a protein called 60S ribosomal protein l5-like protein.

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

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	180	Total	C	N	O	S	0	0
			1416	909	255	249	3		

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

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

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	234	Total	C	N	O	S	0	0
			1891	1212	349	325	5		

- Molecule 14 is a protein called 60S ribosomal protein l9-like protein.

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

There are 37 discrepancies between the modelled and reference sequences:

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

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

- Molecule 15 is a protein called 60S ribosomal protein L10-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	208	Total	C	N	O	S	0	0
			1699	1073	331	287	8		

- Molecule 16 is a protein called Putative ribosomal protein.

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

- Molecule 17 is a protein called 60S ribosomal protein L13.

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

- Molecule 18 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 19 is a protein called Ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	204	Total	C	N	O	S	0	0
			1613	1036	305	267	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LO	2	ACE	-	acetylation	UNP G0SH61

- Molecule 21 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	170	Total	C	N	O	S	0	0
			1349	835	272	239	3		

- Molecule 22 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 23 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	179	Total	C	N	O	S	0	0
			1466	903	315	243	5		

- Molecule 24 is a protein called 60S ribosomal protein L20.

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

- Molecule 25 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 26 is a protein called 60S ribosomal protein L22-like protein.

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

- Molecule 27 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	132	Total	C	N	O	S	0	0
			970	619	178	166	7		

- Molecule 28 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 29 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 30 is a protein called 60S ribosomal protein L27.

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

- Molecule 31 is a protein called 60S ribosomal protein L28-like protein.

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

- Molecule 32 is a protein called 60S ribosomal protein L29.

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

- Molecule 33 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 34 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	109	Total	C	N	O	S	0	0
			885	561	171	152	1		

- Molecule 35 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	123	Total	C	N	O	S	0	0
			994	624	204	160	6		

- Molecule 36 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 37 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 38 is a protein called Dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	101	Total	C	N	O	S	0	0
			826	509	181	135	1		

- Molecule 40 is a protein called Ribosomal protein L37.

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

- Molecule 41 is a protein called 60S ribosomal protein L38-like protein.

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

- Molecule 42 is a protein called Ribosomal protein eL39.

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

- Molecule 43 is a protein called Putative ribosomal protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L44-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	98	Total	C	N	O	S	0	0
			784	495	154	130	5		

- Molecule 46 is a protein called 60S ribosomal protein L43-like protein.

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

- Molecule 47 is a protein called Putative 60S ribosomal protein.

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

- Molecule 48 is a RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L1	3146	Total	C	N	O	P	0	0
			67284	30038	12169	21931	3146		

- Molecule 49 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L2	149	Total	C	N	O	P	0	0
			3173	1419	567	1038	149		

- Molecule 50 is a RNA chain called 5S rRNA.

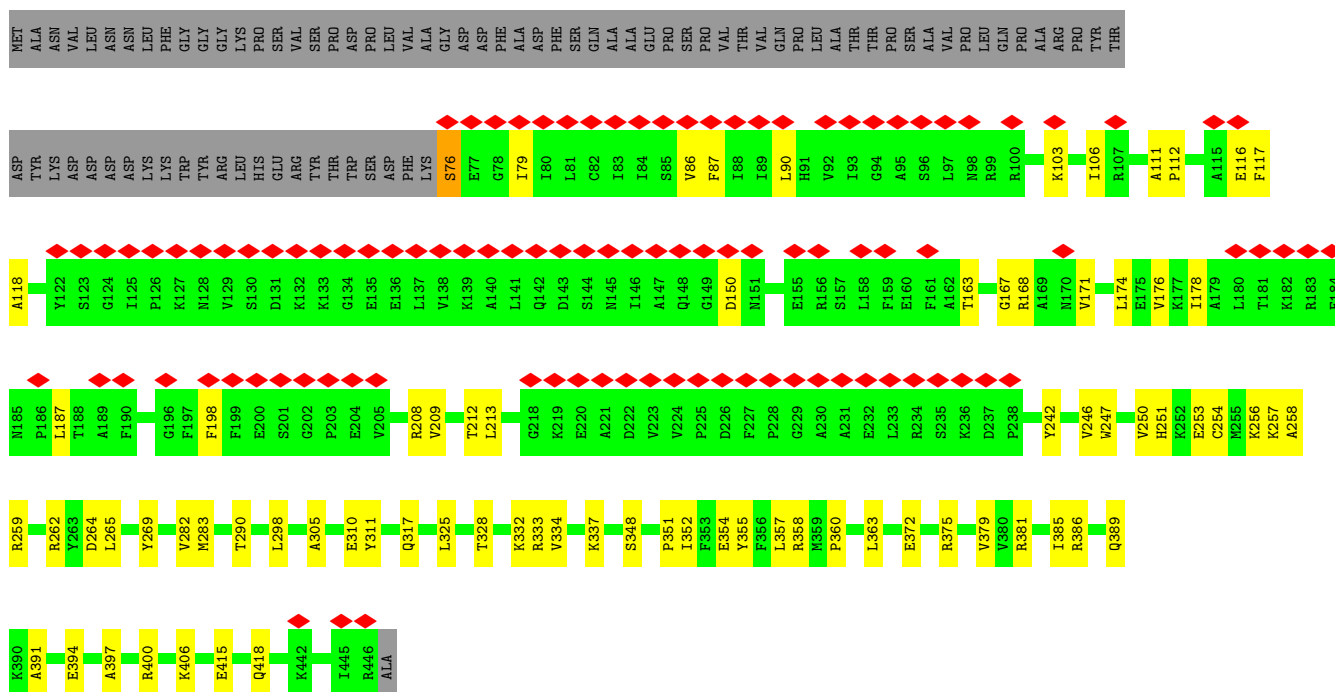
Mol	Chain	Residues	Atoms					AltConf	Trace
50	L3	119	Total	C	N	O	P	0	0
			2535	1132	453	831	119		

There is a discrepancy between the modelled and reference sequences:

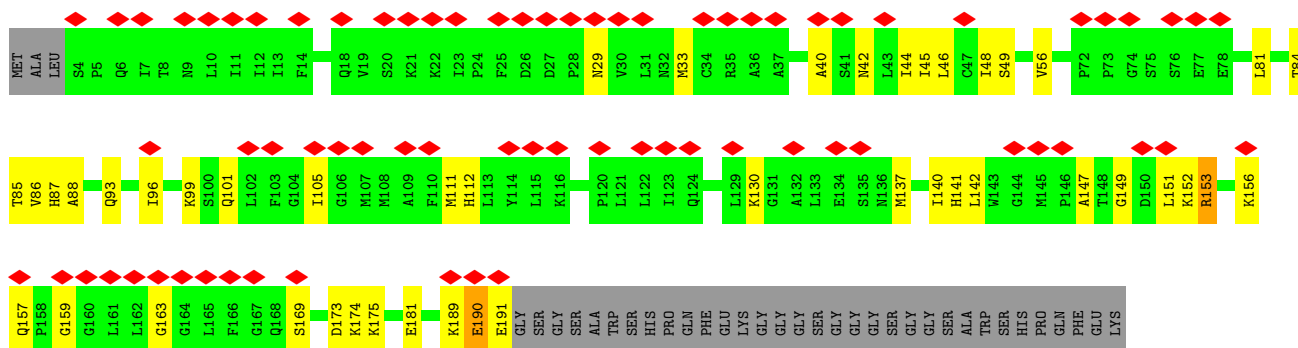
Chain	Residue	Modelled	Actual	Comment	Reference
L3	1	A	N	conflict	GB 7OLC_3

- Molecule 51 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

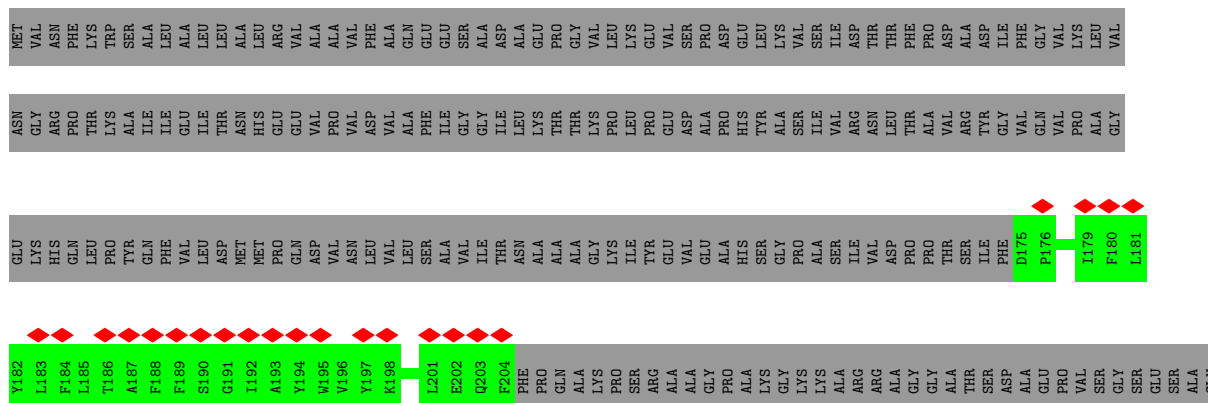
Mol	Chain	Residues	Atoms		AltConf
51	LC	2	Total	Mg	0
			2	2	
51	LN	1	Total	Mg	0
			1	1	
51	LQ	1	Total	Mg	0
			1	1	
51	Lb	2	Total	Mg	0
			2	2	
51	L1	359	Total	Mg	0
			359	359	
51	L2	14	Total	Mg	0
			14	14	



- Molecule 5: Putative inorganic phosphate transporter protein




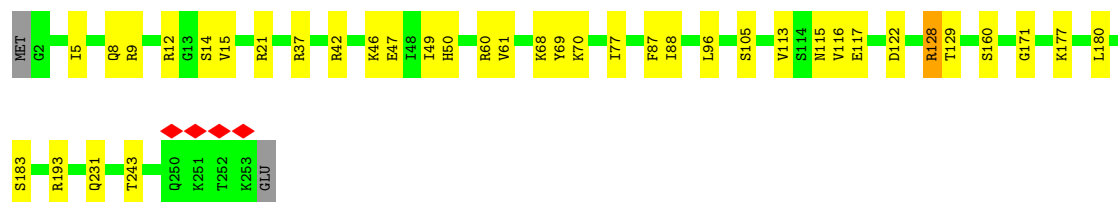
- Molecule 6: Translocon-associated protein subunit alpha




GLY
ASN
THR
SER
GLY
ALA
GLY
GLY
LYS
GLU
TYR
ASP
GLU
SER
TRP
ILE
PRO
ALA
HIS
HIS
ILE
ASN
ARG
PRO
VAL
ALA
ARG
LYS
VAL
LYS
GLY
GLY
SER
LYS
SER
LYS

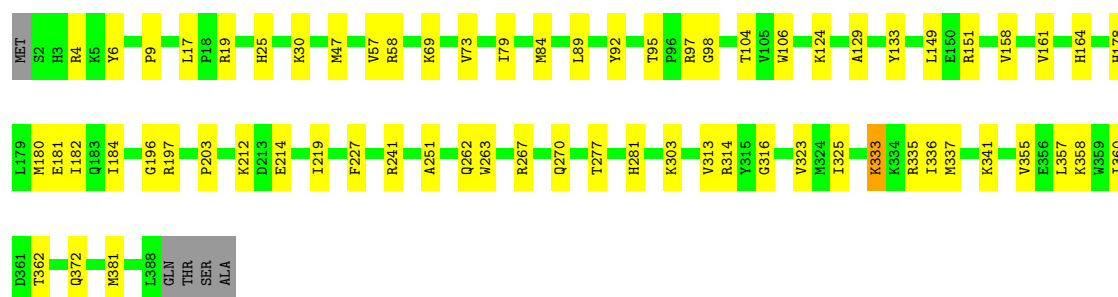
- Molecule 7: 60S ribosomal protein L2-like protein

Chain LA:  84% 15%



- Molecule 8: 60S ribosomal protein L3-like protein

Chain LB:  82% 17%




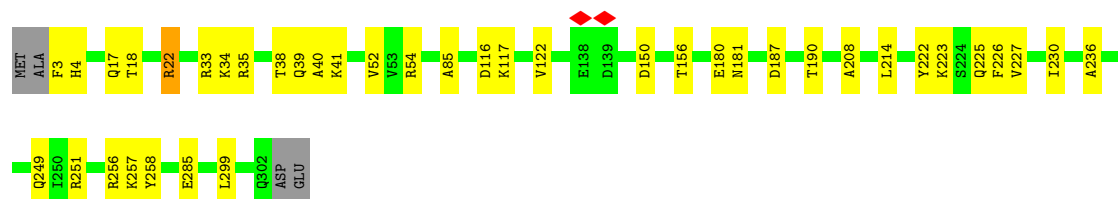
- Molecule 9: 60S ribosomal protein L4-like protein

Chain LC:  89% 10%




- Molecule 10: 60S ribosomal protein l5-like protein

Chain LD:  85% 13%




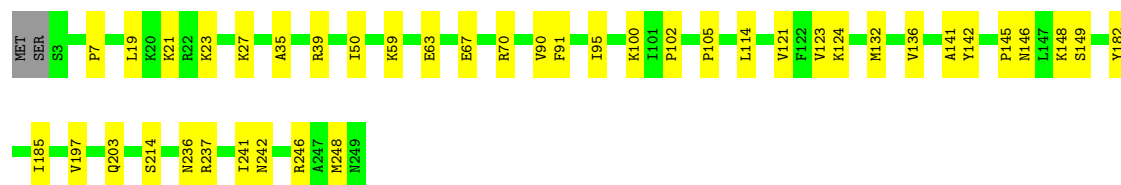
- Molecule 11: 60S ribosomal protein L6

Chain LE:  76% 13% 10%



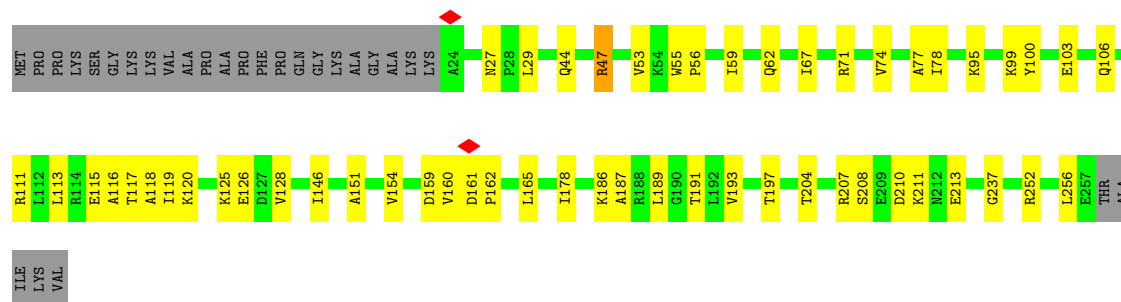
- Molecule 12: 60S ribosomal protein l7-like protein

Chain LF:  83% 16%




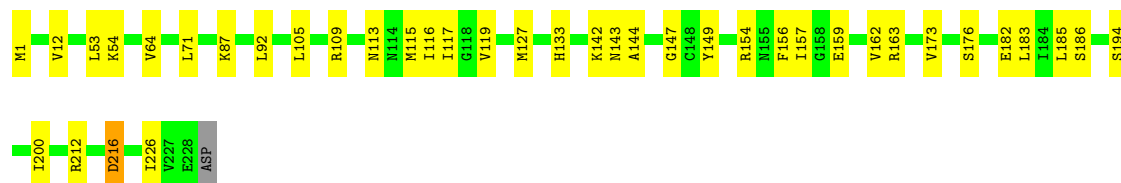
- Molecule 13: 60S ribosomal protein L8

Chain LG:  69% 20% 11%




- Molecule 14: 60S ribosomal protein l9-like protein

Chain LH:  79% 20%



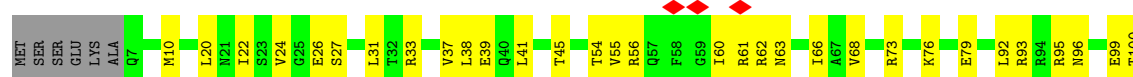
- Molecule 15: 60S ribosomal protein L10-like protein

Chain LI:  77% 18% 5%

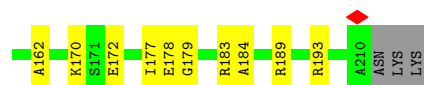
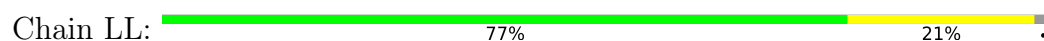




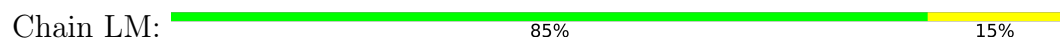
- Molecule 16: Putative ribosomal protein



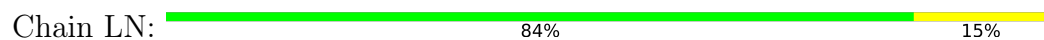
- Molecule 17: 60S ribosomal protein L13



- Molecule 18: 60S ribosomal protein L14-like protein



- Molecule 19: Ribosomal protein L15

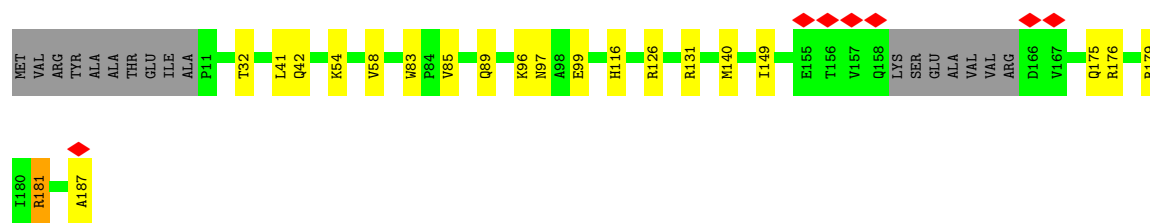


- Molecule 20: 60S ribosomal protein L16-like protein



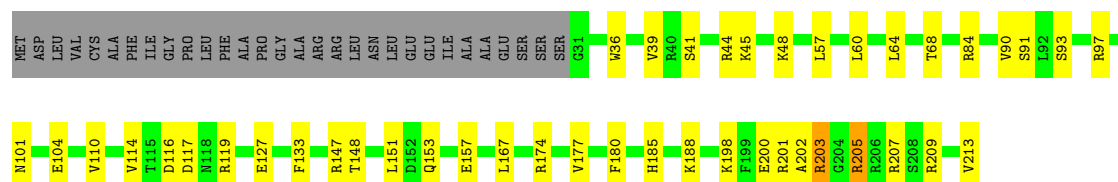
- Molecule 21: 60S ribosomal protein l17-like protein





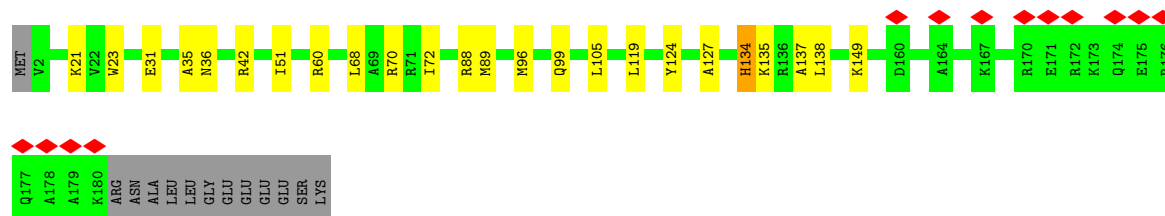
- Molecule 22: Ribosomal protein L18-like protein

Chain LQ: 65% 20% 14%



- Molecule 23: Ribosomal protein L19

Chain LR: 7% 81% 12% 7%



- Molecule 24: 60S ribosomal protein L20

Chain LS: 89% 11%



- Molecule 25: 60S ribosomal protein l21-like protein

Chain LT: 85% 13%



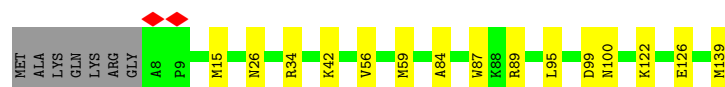
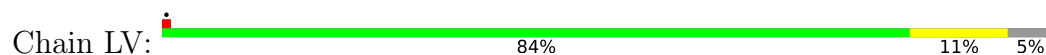
- Molecule 26: 60S ribosomal protein L22-like protein

Chain LU: 46% 33% 20%

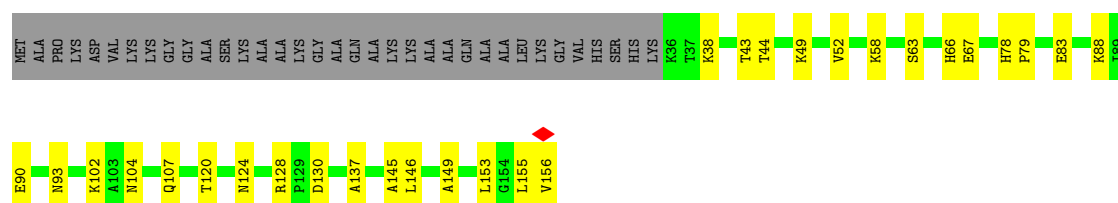




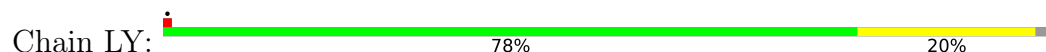
- Molecule 27: 60S ribosomal protein l23-like protein



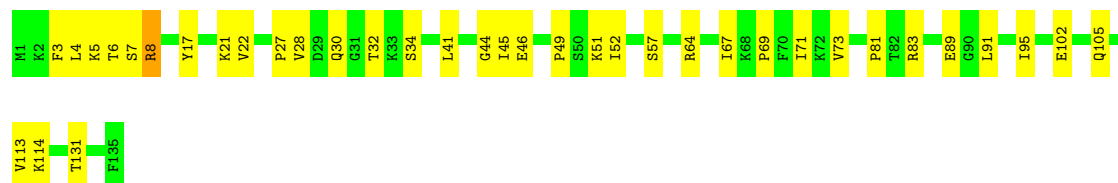
- Molecule 28: 60S ribosomal protein L25-like protein



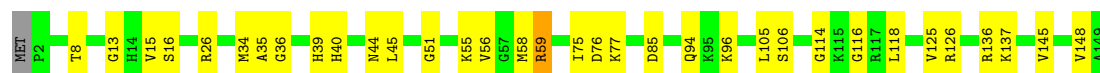
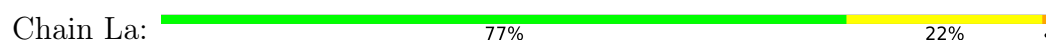
- Molecule 29: 60S ribosomal protein L26-like protein



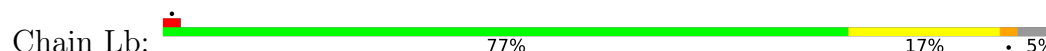
- Molecule 30: 60S ribosomal protein L27

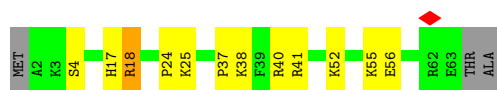


- Molecule 31: 60S ribosomal protein L28-like protein

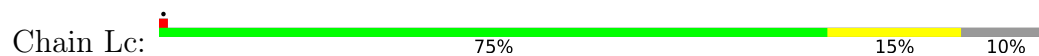


- Molecule 32: 60S ribosomal protein L29

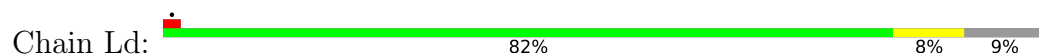




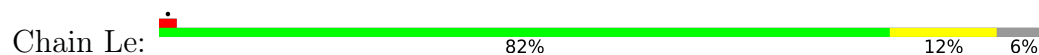
- Molecule 33: 60S ribosomal protein l30-like protein



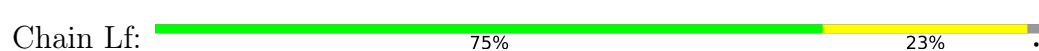
- Molecule 34: Putative 60S ribosomal protein



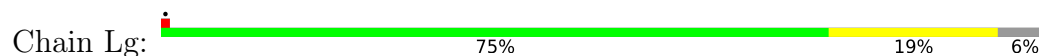
- Molecule 35: 60S ribosomal protein L32-like protein



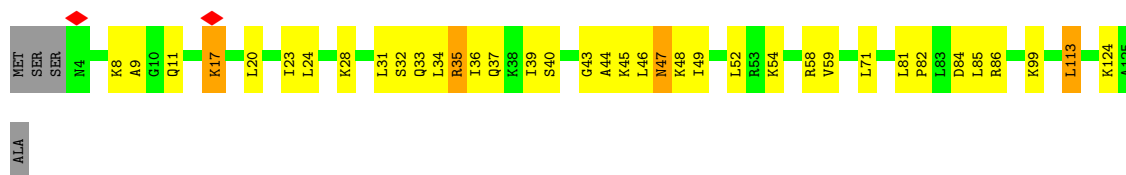
- Molecule 36: 60S ribosomal protein l33-like protein



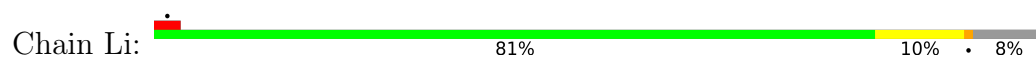
- Molecule 37: Ribosomal protein l34-like protein



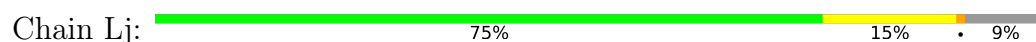
- Molecule 38: Dolichyl-diphosphooligosaccharide--protein glycotransferase



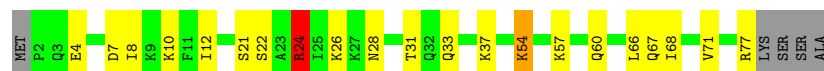
- Molecule 39: 60S ribosomal protein L36



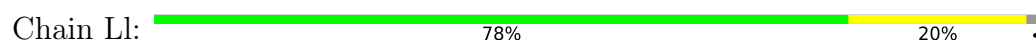
- Molecule 40: Ribosomal protein L37



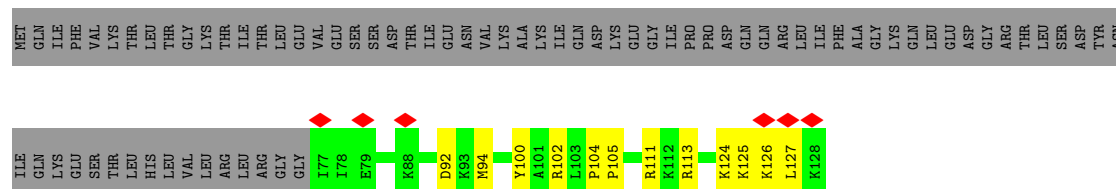
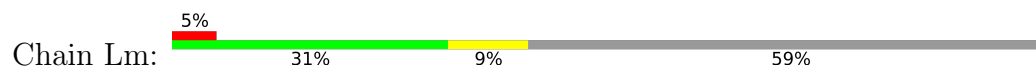
- Molecule 41: 60S ribosomal protein L38-like protein



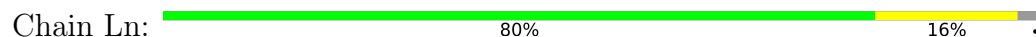
- Molecule 42: Ribosomal protein eL39



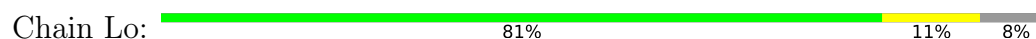
- Molecule 43: Putative ribosomal protein



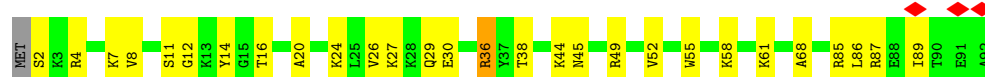
- Molecule 44: 60S ribosomal protein L41-A



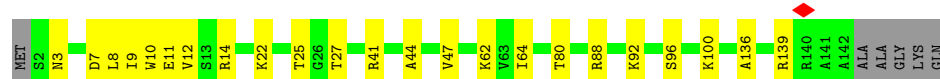
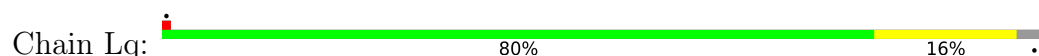
- Molecule 45: 60S ribosomal protein L44-like protein



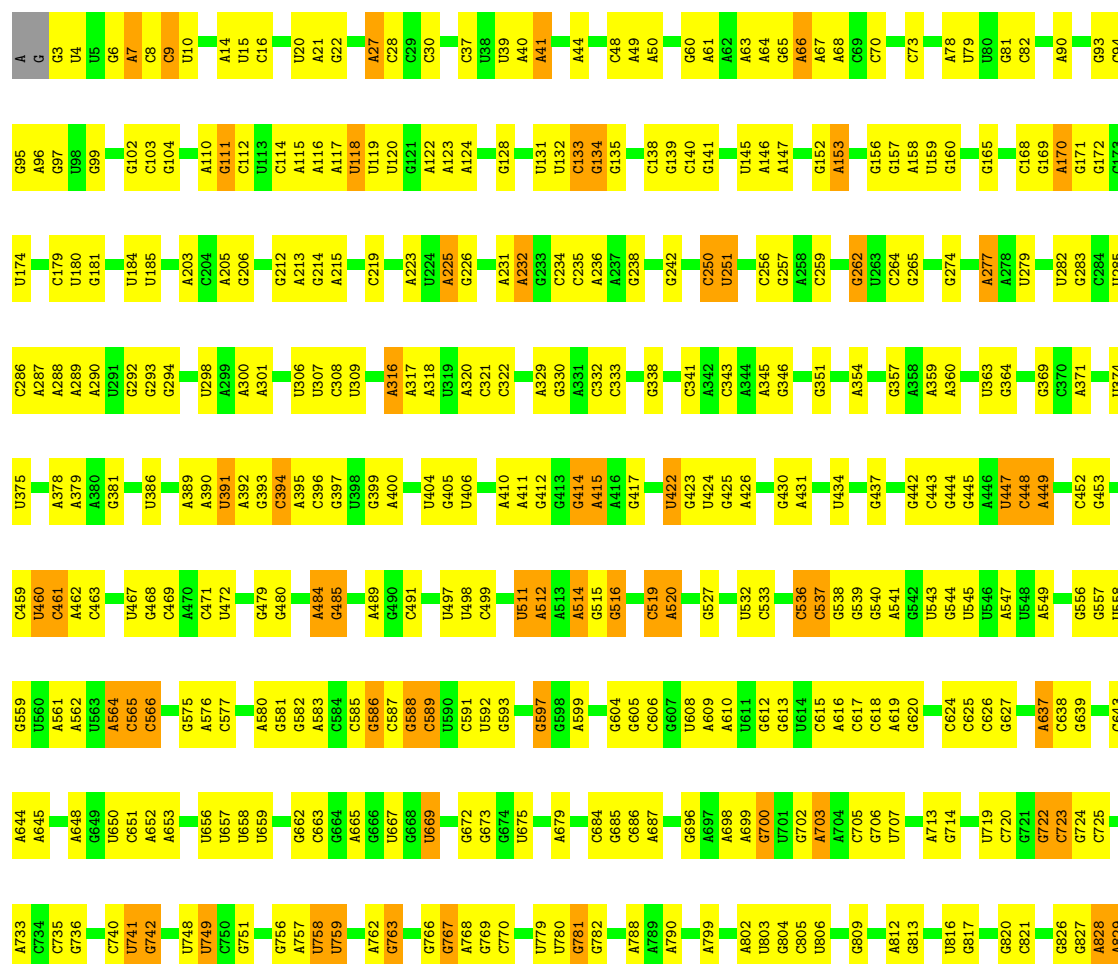
- Molecule 46: 60S ribosomal protein L43-like protein



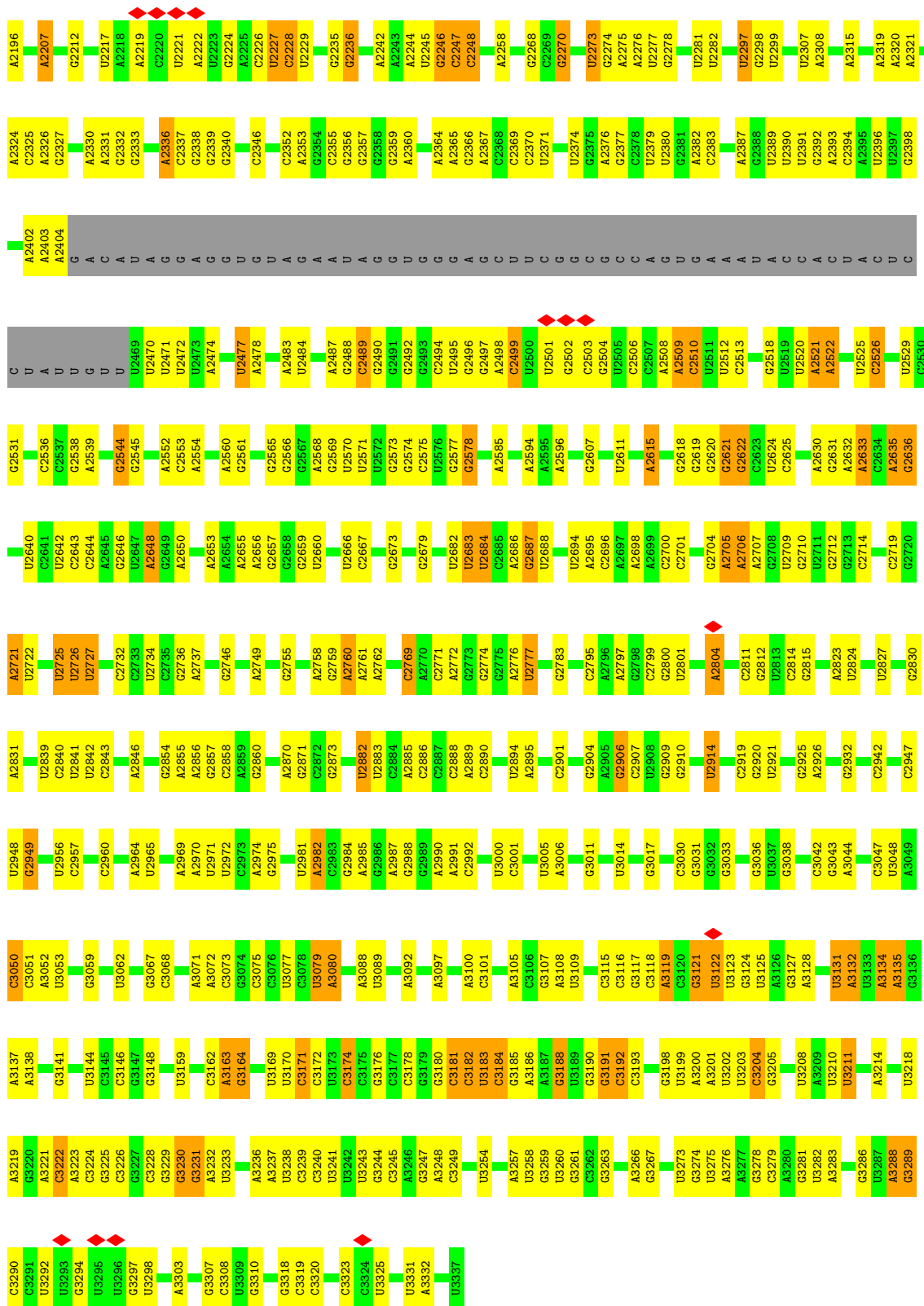
- Molecule 47: Putative 60S ribosomal protein



- Molecule 48: 26S rRNA



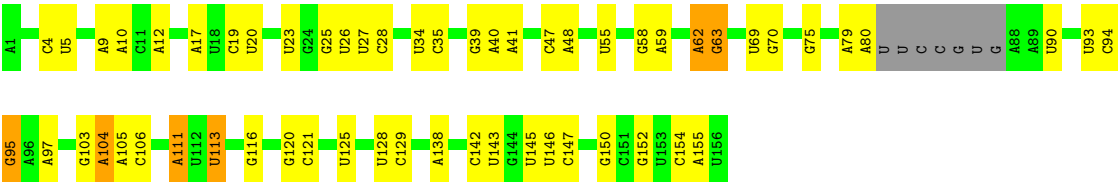
U2100	A1866	A	U	U1562	U1480	U1330	G1226	A1023	U937	A830
A2101	A1875	G	U	G1563	A1460	G1331	A1227	A1024	U938	C831
A2102	A1875	C	A	A1567	A1464	G1332	A1228	A1029	C941	U832
U2103	A1875	A	A	A1568	A1465	A1333	G1229	A1030	U942	C833
U2104	A1879	C	A	A1569	G1466	A1334	G1233	A1031	C945	U834
A2105	A1886	G	G	C1576	G1469	A1335	G1239	C1032	G945	G835
A2106	C1887	G	G	C1577	G1476	G1336	G1239	A1047	U837	G836
A2107	A1888	C	C	G1578	U1477	G1337	G1240	A1048	G950	G838
U2111	A1890	U	U	U1581	U1477	A1338	U1241	C1052	C951	G839
A2112	A1891	C	U	U1584	C1480	U1339	U1242	G1053	A840	A840
A2115	U1892	G	U	A1585	A1481	G1345	A1243	U1054	G955	G841
U2116	A1893	C	U	A1586	U1482	A1346	G1244	G1055	U956	G842
U2121	G1894	C	G	C1595	G1485	G1347	G1245	A1062	C960	C843
G2122	A1895	C	C	U1596	G1486	U1361	C1247	A1063	C961	U853
G2123	U1896	C	C	G1597	A1487	G1362	G1251	A1064	U962	U854
G2124	U1905	C	G	U1600	C1491	U1370	U1252	C1066	C964	C855
U2127	C1906	G	G	G1615	G1508	A1376	A1253	A1076	U967	U856
G2132	G1907	C	C	A1618	G1511	A1382	C1258	A1077	U968	U861
U2133	G1914	A	C	U1619	U1506	G1374	C1259	U1078	U969	G869
U2137	G1920	C	C	C1611	A1507	G1375	A1256	U1079	U970	A870
U2143	C1921	C	G	G1615	G1508	A1376	A1257	A974	A974	A878
C2144	U1922	C	G	A1618	G1511	A1382	C1258	G975	G975	G882
G2148	G1933	C	U	U1623	C1515	G1387	U1261	G1080	U977	A883
U2149	C	C	G	U1624	U1516	A1390	C1263	A1081	G981	U887
G2151	C	C	A	U1625	U1517	A1390	C1263	U1077	G982	G888
U2166	C	C	G	G1626	U1518	U1398	C1267	G983	G983	G889
U2167	C	C	U	A1627	U1518	U1399	U1268	A1086	A984	G890
U2168	C	C	U	U1628	A1522	U1400	A1269	A1089	U990	C893
G2169	C	C	U	C1629	C1534	A1401	A1270	A1090	A991	A896
A2170	C	C	G	U1637	G1535	A1402	U1271	C1091	G992	A897
A2171	C	C	G	G1638	U1536	A1416	U1273	A995	C996	G898
U2172	C	C	A	U1639	U1536	G1417	A1274	C997	U997	A899
G2173	C	C	U	C1640	U1539	A1418	C1275	C998	A903	A903
A2176	C	C	U	G1641	A1540	U1419	C1280	C1004	C905	U904
A2177	C	C	G	C1643	G1543	C1420	C1280	G1005	G906	C906
A2182	C	C	G	C1652	G1544	G1426	G1290	A	G919	G919
A2183	C	C	G	C1657	G1546	G1427	A1291	U	C920	C920
G2184	C	C	G	U1657	C1547	U1428	U1292	U1009	U925	U925
A2185	C	C	G	G1758	A1548	A1429	C1299	U1010	A926	A926
A2186	C	C	A	U1660	C1549	U1442	C1299	U1011	C927	C927
A2187	C	C	A	U1661	U1550	C1443	A1301	A1012	C928	C928
U2188	C	C	U	U1662	C1551	A1444	A1301	U1016	G929	G929
U2189	C	C	A	U1666	C1552	A1445	A1309	U1017	C930	C930
A2192	C	C	A	U1667	U1553	G1449	C1310	U1017	A934	A934
G2193	C	C	U	U1668	G1554	U1454	A1314	U1020	G935	G935
C2194	C	C	G	C1670	C1555	U1454	A1314	C1021	U936	U936
A2195	C	C	G	U1671	U1560	G1455	C1322	G1140		
	C	C	G		G1561		C1323			
							U1324			



• Molecule 49: 5.8S rRNA

Chain L2:





• Molecule 50: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	119533	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	40.187	Depositor
Minimum map value	-12.158	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Map size (Å)	535.68, 535.68, 535.68	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04625, 1.04625, 1.04625	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, ACE, MG

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	0.23	1/3659 (0.0%)	0.44	0/4965
2	2	0.13	0/730	0.33	0/990
3	3	0.26	0/533	0.55	0/718
4	4	0.15	0/3047	0.35	0/4104
5	6	0.38	1/1470 (0.1%)	0.54	0/1982
6	7	0.11	0/279	0.40	0/381
7	LA	0.17	0/1964	0.34	0/2641
8	LB	0.17	0/3156	0.34	0/4238
9	LC	0.17	0/2815	0.36	2/3795 (0.1%)
10	LD	0.18	0/2487	0.34	0/3341
11	LE	0.19	0/1442	0.41	1/1938 (0.1%)
12	LF	0.21	0/2055	0.35	0/2758
13	LG	0.24	0/1920	0.43	0/2568
14	LH	0.20	0/1525	0.39	0/2050
15	LI	0.20	0/1735	0.39	0/2328
16	LJ	0.21	0/1389	0.42	0/1856
17	LL	0.24	0/1695	0.43	0/2276
18	LM	0.13	0/1144	0.26	0/1539
19	LN	0.22	0/1740	0.34	0/2332
20	LO	0.21	0/1645	0.32	0/2207
21	LP	0.17	0/1370	0.34	0/1842
22	LQ	0.26	0/1507	0.45	1/2017 (0.0%)
23	LR	0.20	0/1485	0.35	0/1974
24	LS	0.17	0/1460	0.35	0/1965
25	LT	0.27	0/1292	0.45	1/1738 (0.1%)
26	LU	0.32	1/832 (0.1%)	0.55	2/1112 (0.2%)
27	LV	0.14	0/988	0.32	0/1331
28	LX	0.15	0/981	0.31	0/1324
29	LY	0.41	1/1079 (0.1%)	0.62	1/1443 (0.1%)
30	LZ	0.31	0/1134	0.48	0/1519
31	La	0.33	0/1212	0.47	0/1627
32	Lb	0.51	2/518 (0.4%)	0.54	0/684

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.14	0/731	0.28	0/983
34	Ld	0.26	0/899	0.36	0/1204
35	Le	0.14	0/1012	0.29	0/1348
36	Lf	0.20	0/874	0.34	0/1176
37	Lg	0.24	0/904	0.39	0/1210
38	Lh	0.53	0/1014	0.70	1/1349 (0.1%)
39	Li	0.26	0/833	0.41	0/1100
40	Lj	0.29	0/697	0.38	0/922
41	Lk	0.24	0/640	0.41	0/850
42	Ll	0.15	0/445	0.29	0/593
43	Lm	0.23	0/424	0.34	0/561
44	Ln	0.11	0/225	0.28	0/289
45	Lo	0.14	0/797	0.29	0/1054
46	Lp	0.22	0/705	0.40	0/940
47	Lq	0.15	0/1101	0.35	0/1482
48	L1	0.18	0/75268	0.31	0/117356
49	L2	0.17	0/3547	0.27	0/5522
50	L3	0.15	0/2833	0.24	0/4413
All	All	0.20	6/143237 (0.0%)	0.34	9/209935 (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
5	6	0	1
7	LA	0	1
9	LC	0	1
10	LD	0	2
11	LE	0	1
13	LG	0	1
14	LH	0	1
16	LJ	0	1
17	LL	0	1
19	LN	0	1
21	LP	0	1
22	LQ	0	3
25	LT	0	3
26	LU	0	1
29	LY	0	1
30	LZ	0	1

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	La	0	2
32	Lb	0	1
37	Lg	0	1
38	Lh	0	1
39	Li	0	1
41	Lk	0	1
43	Lm	0	1
46	Lp	0	1
All	All	0	30

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	6	174	LYS	C-N	8.09	1.44	1.33
32	Lb	24	PRO	C-N	-7.01	1.24	1.33
32	Lb	17	HIS	C-N	-5.65	1.26	1.33
29	LY	73	TYR	C-N	-5.57	1.26	1.33
26	LU	81	ARG	C-N	5.50	1.41	1.33

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	LC	201	ARG	N-CA-CB	-6.93	100.30	110.49
26	LU	81	ARG	CA-C-N	-6.33	111.70	120.38
26	LU	81	ARG	C-N-CA	-6.33	111.70	120.38
38	Lh	47	ASN	N-CA-C	-6.24	105.79	113.41
9	LC	121	PHE	CA-CB-CG	6.07	119.87	113.80

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	6	153	ARG	Sidechain
7	LA	128	ARG	Sidechain
9	LC	201	ARG	Sidechain
10	LD	22	ARG	Sidechain
10	LD	35	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	3579	0	3685	108	0
2	2	717	0	757	9	0
3	3	524	0	549	17	0
4	4	2990	0	3052	78	0
5	6	1443	0	1520	55	0
6	7	267	0	255	0	0
7	LA	1925	0	1999	35	0
8	LB	3088	0	3206	46	0
9	LC	2758	0	2883	31	0
10	LD	2440	0	2431	37	0
11	LE	1416	0	1509	26	0
12	LF	2017	0	2130	50	0
13	LG	1891	0	2053	49	0
14	LH	1505	0	1581	40	0
15	LI	1699	0	1735	40	0
16	LJ	1367	0	1405	75	0
17	LL	1666	0	1756	59	0
18	LM	1125	0	1198	14	0
19	LN	1703	0	1767	28	0
20	LO	1613	0	1706	22	0
21	LP	1349	0	1388	24	0
22	LQ	1481	0	1596	37	0
23	LR	1466	0	1557	39	0
24	LS	1425	0	1484	24	0
25	LT	1266	0	1328	28	0
26	LU	819	0	864	32	0
27	LV	970	0	1026	13	0
28	LX	965	0	1050	34	0
29	LY	1065	0	1156	34	0
30	LZ	1111	0	1181	30	0
31	La	1180	0	1203	37	0
32	Lb	508	0	526	12	0
33	Lc	722	0	766	14	0
34	Ld	885	0	939	15	0
35	Le	994	0	1061	13	0
36	Lf	853	0	880	21	0
37	Lg	891	0	962	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lh	1003	0	1116	50	0
39	Li	826	0	908	16	0
40	Lj	684	0	716	20	0
41	Lk	632	0	693	16	0
42	Ll	435	0	473	9	0
43	Lm	418	0	463	9	0
44	Ln	224	0	271	2	0
45	Lo	784	0	849	9	0
46	Lp	697	0	741	29	0
47	Lq	1083	0	1140	26	0
48	L1	67284	0	33893	861	0
49	L2	3173	0	1605	37	0
50	L3	2535	0	1284	28	0
51	L1	359	0	0	0	0
51	L2	14	0	0	0	0
51	LC	2	0	0	0	0
51	LN	1	0	0	0	0
51	LQ	1	0	0	0	0
51	Lb	2	0	0	0	0
All	All	133840	0	100296	1982	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 1982 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:52:TYR:CE2	1:1:149:ILE:HD11	1.27	1.65
1:1:52:TYR:HE2	1:1:149:ILE:CD1	1.09	1.63
16:LJ:27:SER:HA	16:LJ:31:LEU:CD1	1.34	1.58
3:3:25:ARG:CZ	28:LX:156:VAL:HG21	1.44	1.46
1:1:132:VAL:HG13	1:1:309:MET:CE	1.52	1.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	460/476 (97%)	444 (96%)	16 (4%)	0	100	100
2	2	96/124 (77%)	95 (99%)	1 (1%)	0	100	100
3	3	63/70 (90%)	63 (100%)	0	0	100	100
4	4	369/455 (81%)	366 (99%)	3 (1%)	0	100	100
5	6	186/224 (83%)	180 (97%)	6 (3%)	0	100	100
6	7	28/278 (10%)	27 (96%)	1 (4%)	0	100	100
7	LA	250/254 (98%)	246 (98%)	4 (2%)	0	100	100
8	LB	385/392 (98%)	377 (98%)	8 (2%)	0	100	100
9	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
10	LD	298/304 (98%)	293 (98%)	5 (2%)	0	100	100
11	LE	178/200 (89%)	172 (97%)	6 (3%)	0	100	100
12	LF	245/249 (98%)	239 (98%)	6 (2%)	0	100	100
13	LG	232/262 (88%)	223 (96%)	9 (4%)	0	100	100
14	LH	189/192 (98%)	185 (98%)	4 (2%)	0	100	100
15	LI	204/219 (93%)	201 (98%)	3 (2%)	0	100	100
16	LJ	165/173 (95%)	161 (98%)	4 (2%)	0	100	100
17	LL	207/213 (97%)	199 (96%)	8 (4%)	0	100	100
18	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
19	LN	200/203 (98%)	193 (96%)	7 (4%)	0	100	100
20	LO	202/204 (99%)	199 (98%)	3 (2%)	0	100	100
21	LP	166/187 (89%)	164 (99%)	2 (1%)	0	100	100
22	LQ	181/213 (85%)	171 (94%)	10 (6%)	0	100	100
23	LR	177/192 (92%)	174 (98%)	3 (2%)	0	100	100
24	LS	171/174 (98%)	168 (98%)	3 (2%)	0	100	100
25	LT	156/160 (98%)	155 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	LU	99/127 (78%)	97 (98%)	2 (2%)	0	100	100
27	LV	130/139 (94%)	129 (99%)	1 (1%)	0	100	100
28	LX	119/156 (76%)	115 (97%)	4 (3%)	0	100	100
29	LY	132/138 (96%)	128 (97%)	4 (3%)	0	100	100
30	LZ	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
31	La	146/149 (98%)	135 (92%)	11 (8%)	0	100	100
32	Lb	60/65 (92%)	59 (98%)	1 (2%)	0	100	100
33	Lc	95/108 (88%)	93 (98%)	2 (2%)	0	100	100
34	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
35	Le	121/131 (92%)	117 (97%)	4 (3%)	0	100	100
36	Lf	105/109 (96%)	102 (97%)	3 (3%)	0	100	100
37	Lg	110/119 (92%)	105 (96%)	5 (4%)	0	100	100
38	Lh	120/126 (95%)	110 (92%)	10 (8%)	0	100	100
39	Li	99/110 (90%)	96 (97%)	3 (3%)	0	100	100
40	Lj	84/95 (88%)	80 (95%)	4 (5%)	0	100	100
41	Lk	74/81 (91%)	72 (97%)	2 (3%)	0	100	100
42	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
43	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
44	Ln	22/25 (88%)	22 (100%)	0	0	100	100
45	Lo	96/106 (91%)	95 (99%)	1 (1%)	0	100	100
46	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
47	Lq	139/147 (95%)	133 (96%)	6 (4%)	0	100	100
All	All	7486/8382 (89%)	7286 (97%)	200 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	391/400 (98%)	389 (100%)	2 (0%)	81	90
2	2	76/93 (82%)	76 (100%)	0	100	100
3	3	57/58 (98%)	57 (100%)	0	100	100
4	4	319/390 (82%)	318 (100%)	1 (0%)	86	93
5	6	158/181 (87%)	156 (99%)	2 (1%)	61	76
6	7	27/222 (12%)	27 (100%)	0	100	100
7	LA	196/198 (99%)	196 (100%)	0	100	100
8	LB	327/331 (99%)	326 (100%)	1 (0%)	86	93
9	LC	284/285 (100%)	284 (100%)	0	100	100
10	LD	250/253 (99%)	249 (100%)	1 (0%)	84	92
11	LE	151/166 (91%)	150 (99%)	1 (1%)	76	87
12	LF	213/215 (99%)	213 (100%)	0	100	100
13	LG	202/222 (91%)	202 (100%)	0	100	100
14	LH	168/169 (99%)	167 (99%)	1 (1%)	78	89
15	LI	176/183 (96%)	176 (100%)	0	100	100
16	LJ	145/150 (97%)	145 (100%)	0	100	100
17	LL	172/176 (98%)	172 (100%)	0	100	100
18	LM	116/117 (99%)	116 (100%)	0	100	100
19	LN	179/180 (99%)	179 (100%)	0	100	100
20	LO	162/162 (100%)	162 (100%)	0	100	100
21	LP	139/152 (91%)	139 (100%)	0	100	100
22	LQ	155/178 (87%)	154 (99%)	1 (1%)	78	89
23	LR	149/160 (93%)	148 (99%)	1 (1%)	76	87
24	LS	153/154 (99%)	153 (100%)	0	100	100
25	LT	134/135 (99%)	134 (100%)	0	100	100
26	LU	89/108 (82%)	89 (100%)	0	100	100
27	LV	97/102 (95%)	97 (100%)	0	100	100
28	LX	108/129 (84%)	107 (99%)	1 (1%)	70	84
29	LY	117/119 (98%)	117 (100%)	0	100	100
30	LZ	121/121 (100%)	121 (100%)	0	100	100
31	La	121/122 (99%)	120 (99%)	1 (1%)	73	85
32	Lb	53/55 (96%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lc	78/88 (89%)	78 (100%)	0	100	100
34	Ld	94/105 (90%)	94 (100%)	0	100	100
35	Le	106/114 (93%)	105 (99%)	1 (1%)	70	84
36	Lf	88/90 (98%)	88 (100%)	0	100	100
37	Lg	97/102 (95%)	97 (100%)	0	100	100
38	Lh	109/112 (97%)	107 (98%)	2 (2%)	51	68
39	Li	85/93 (91%)	84 (99%)	1 (1%)	63	78
40	Lj	70/78 (90%)	69 (99%)	1 (1%)	59	75
41	Lk	73/77 (95%)	71 (97%)	2 (3%)	39	53
42	Ll	45/46 (98%)	45 (100%)	0	100	100
43	Lm	47/115 (41%)	47 (100%)	0	100	100
44	Ln	22/23 (96%)	22 (100%)	0	100	100
45	Lo	85/90 (94%)	85 (100%)	0	100	100
46	Lp	73/74 (99%)	73 (100%)	0	100	100
47	Lq	109/112 (97%)	109 (100%)	0	100	100
All	All	6386/7005 (91%)	6366 (100%)	20 (0%)	84	93

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	Lh	17	LYS
40	Lj	84	LYS
41	Lk	54	LYS
41	Lk	24	ARG
10	LD	180	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
35	Le	66	HIS
39	Li	24	HIS
46	Lp	29	GLN
13	LG	62	GLN
12	LF	242	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
48	L1	3142/3337 (94%)	532 (16%)	54 (1%)
49	L2	147/156 (94%)	17 (11%)	0
50	L3	118/120 (98%)	8 (6%)	1 (0%)
All	All	3407/3613 (94%)	557 (16%)	55 (1%)

5 of 557 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
48	L1	7	A
48	L1	9	C
48	L1	15	U
48	L1	16	C
48	L1	27	A

5 of 55 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	L1	1793	A
48	L1	2227	U
50	L3	72	G
48	L1	3230	G
48	L1	1796	A

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
48	OMG	L1	2578	48	23,26,27	0.49	0	32,38,41	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
48	OMG	L1	2578	48	-	3/9/27/28	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
48	L1	2578	OMG	O4'-C4'-C5'-O5'
48	L1	2578	OMG	C3'-C4'-C5'-O5'
48	L1	2578	OMG	C1'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
48	L1	2578	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 379 ligands modelled in this entry, 379 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

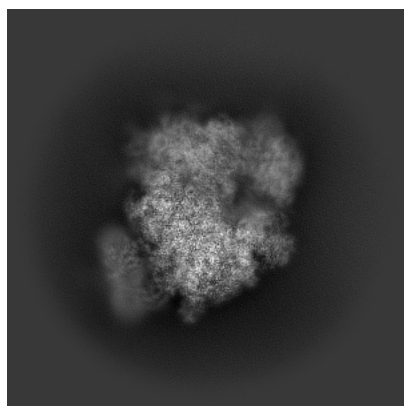
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52656. These allow visual inspection of the internal detail of the map and identification of artifacts.

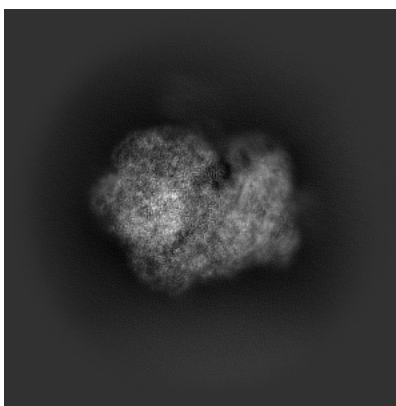
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

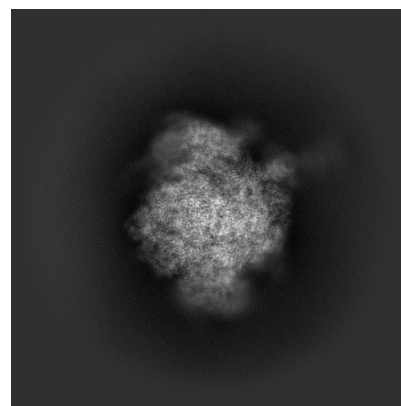
6.1.1 Primary map



X

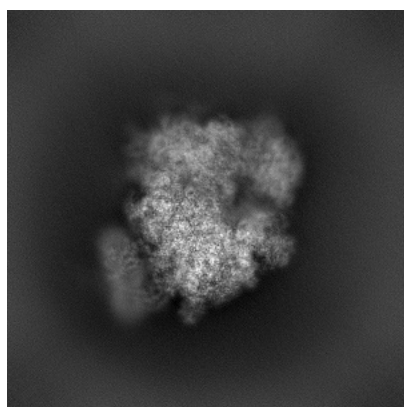


Y

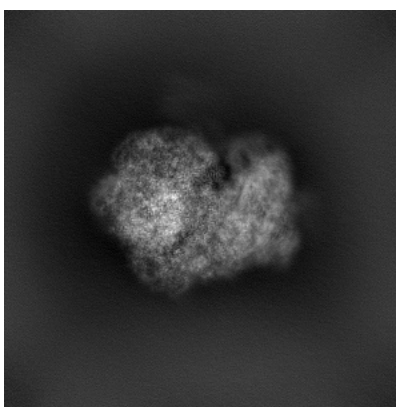


Z

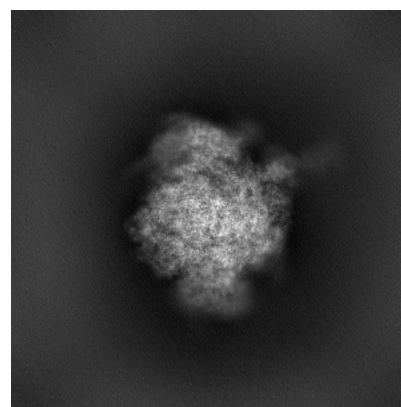
6.1.2 Raw map



X



Y

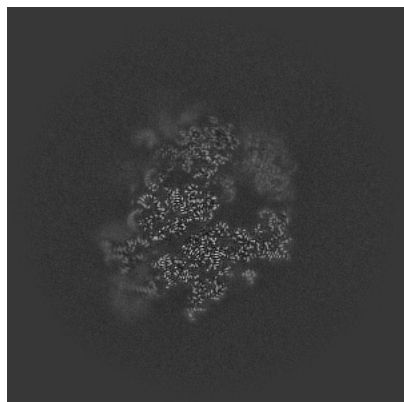


Z

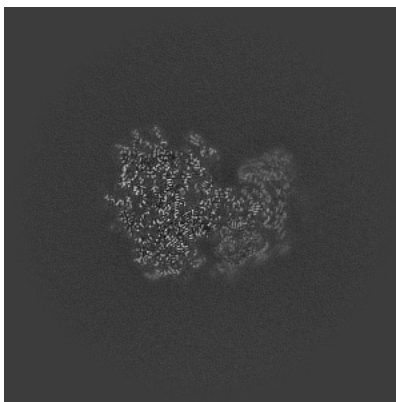
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

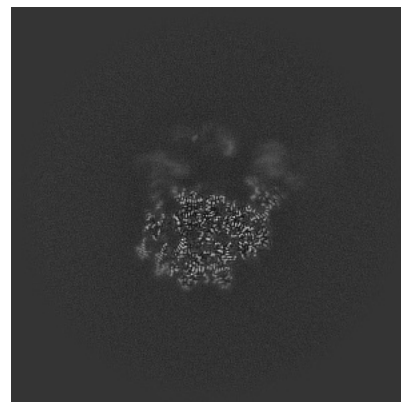
6.2.1 Primary map



X Index: 256

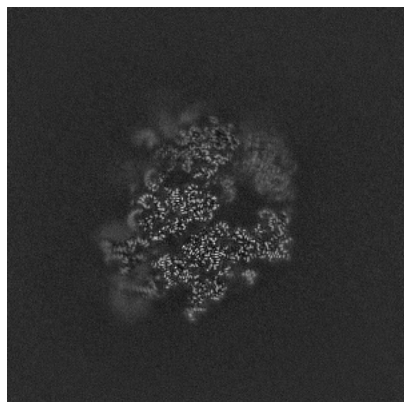


Y Index: 256

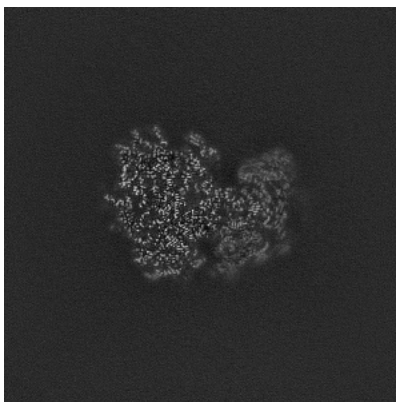


Z Index: 256

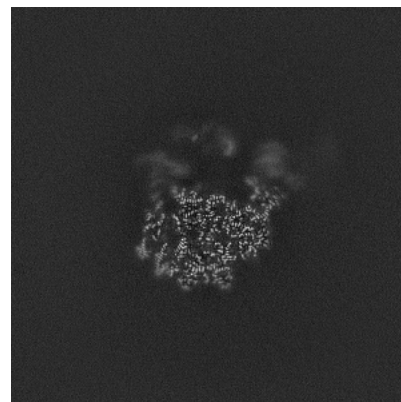
6.2.2 Raw map



X Index: 256



Y Index: 256

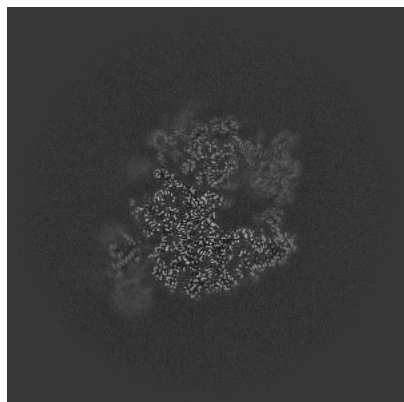


Z Index: 256

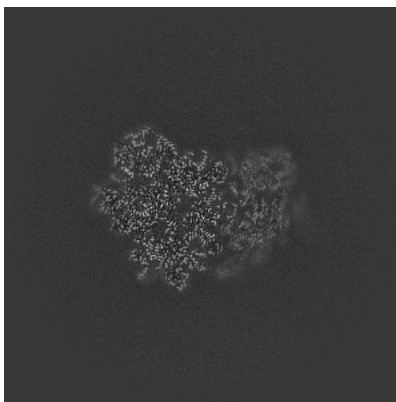
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

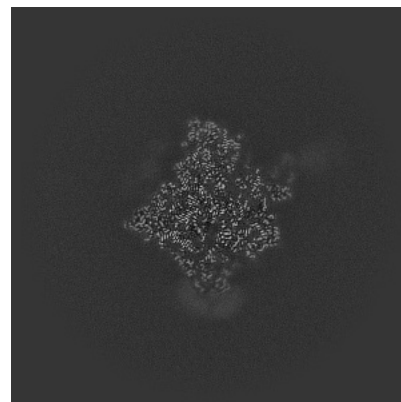
6.3.1 Primary map



X Index: 239

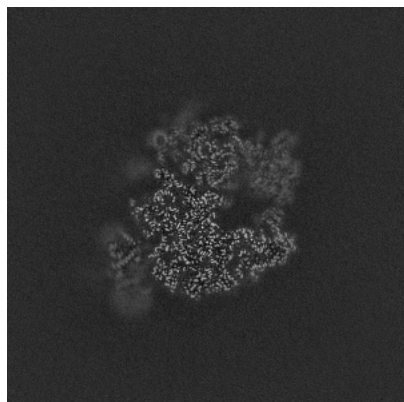


Y Index: 242

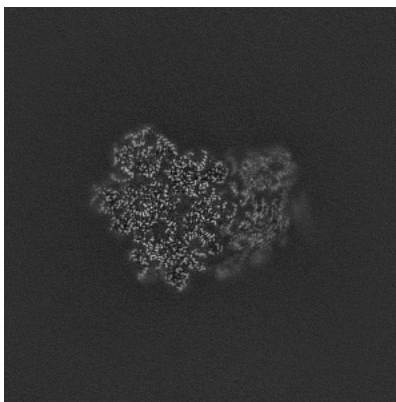


Z Index: 214

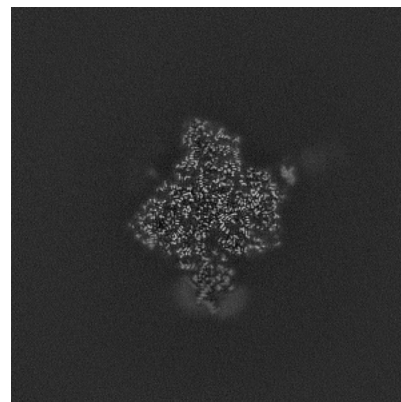
6.3.2 Raw map



X Index: 239



Y Index: 242

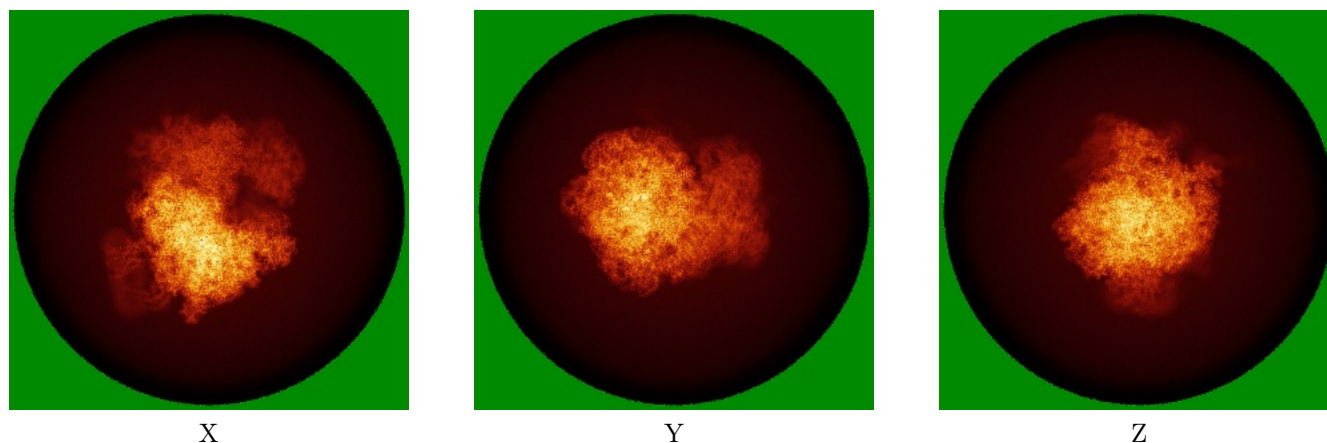


Z Index: 207

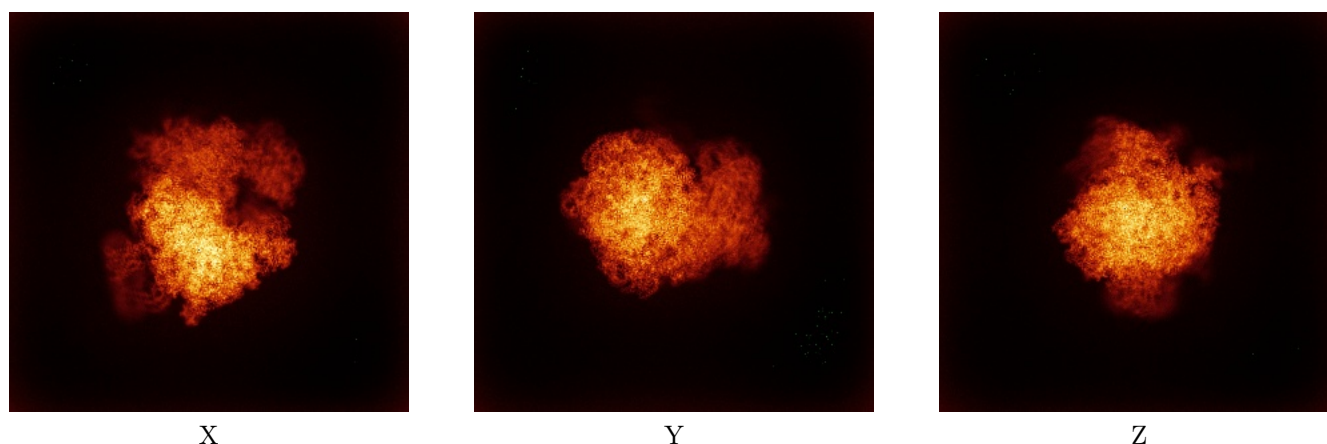
The images above show the largest variance slices of the map in three orthogonal directions.

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](#)

This section was not generated.

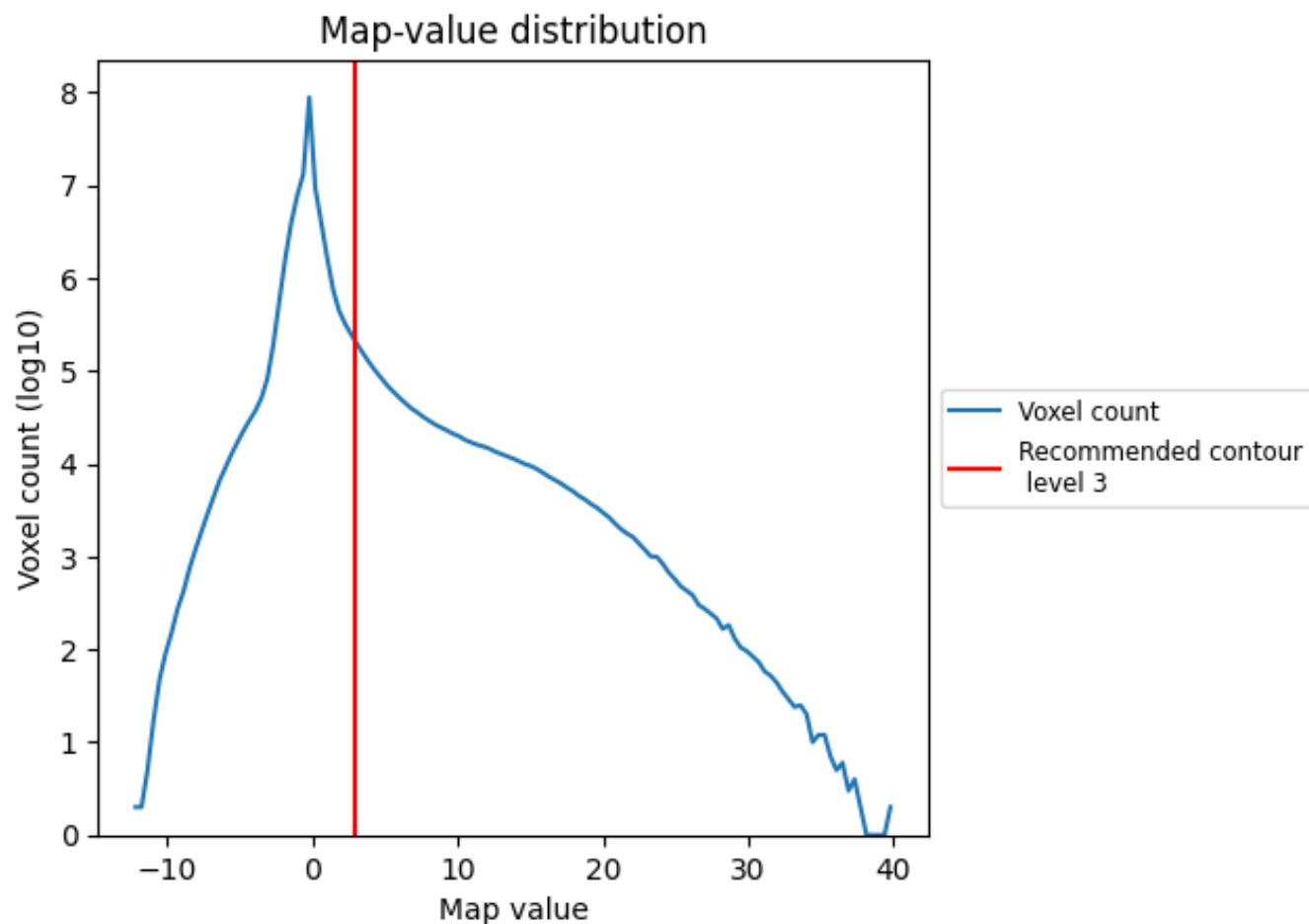
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

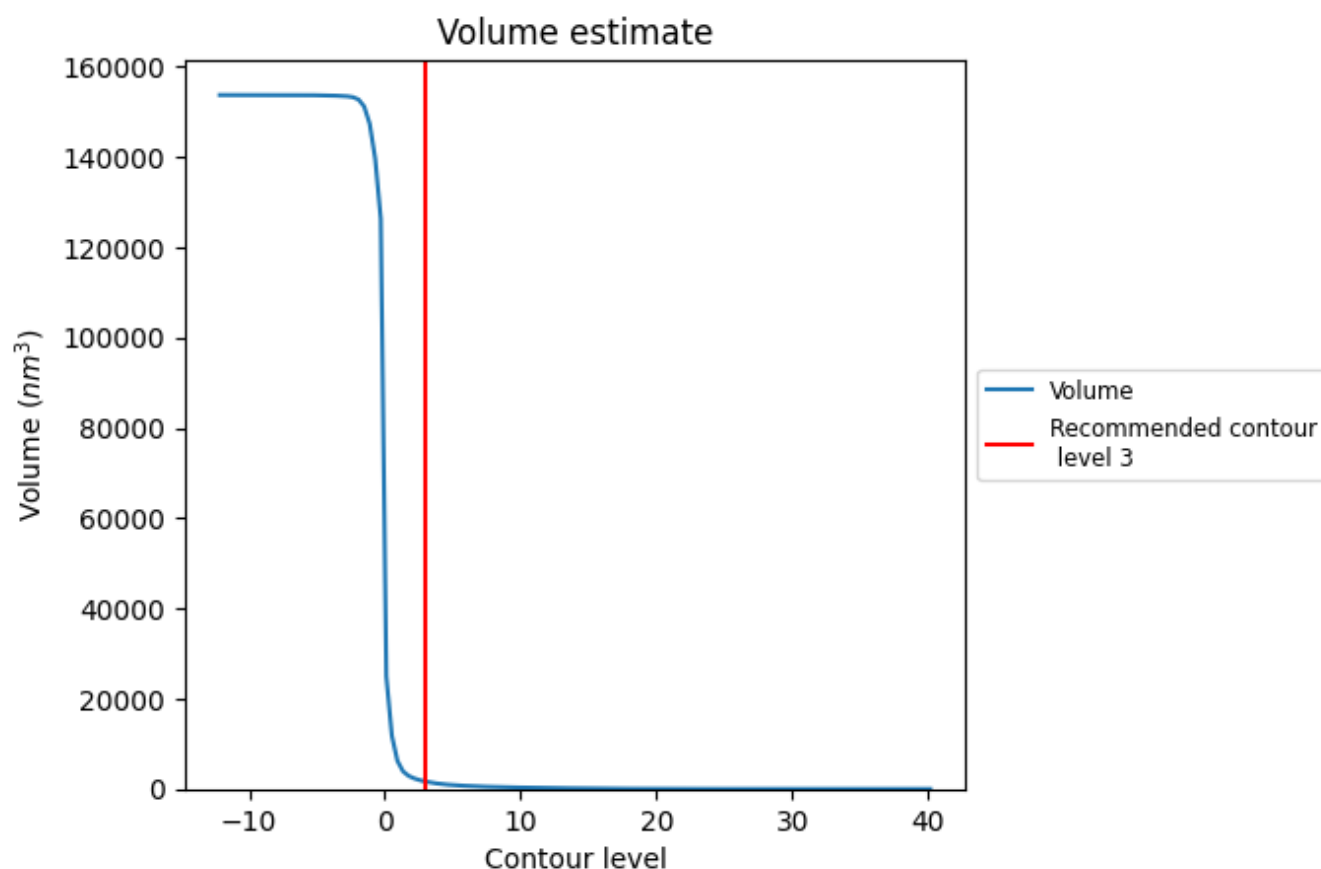
This section contains the results of statistical analysis of the map.

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.

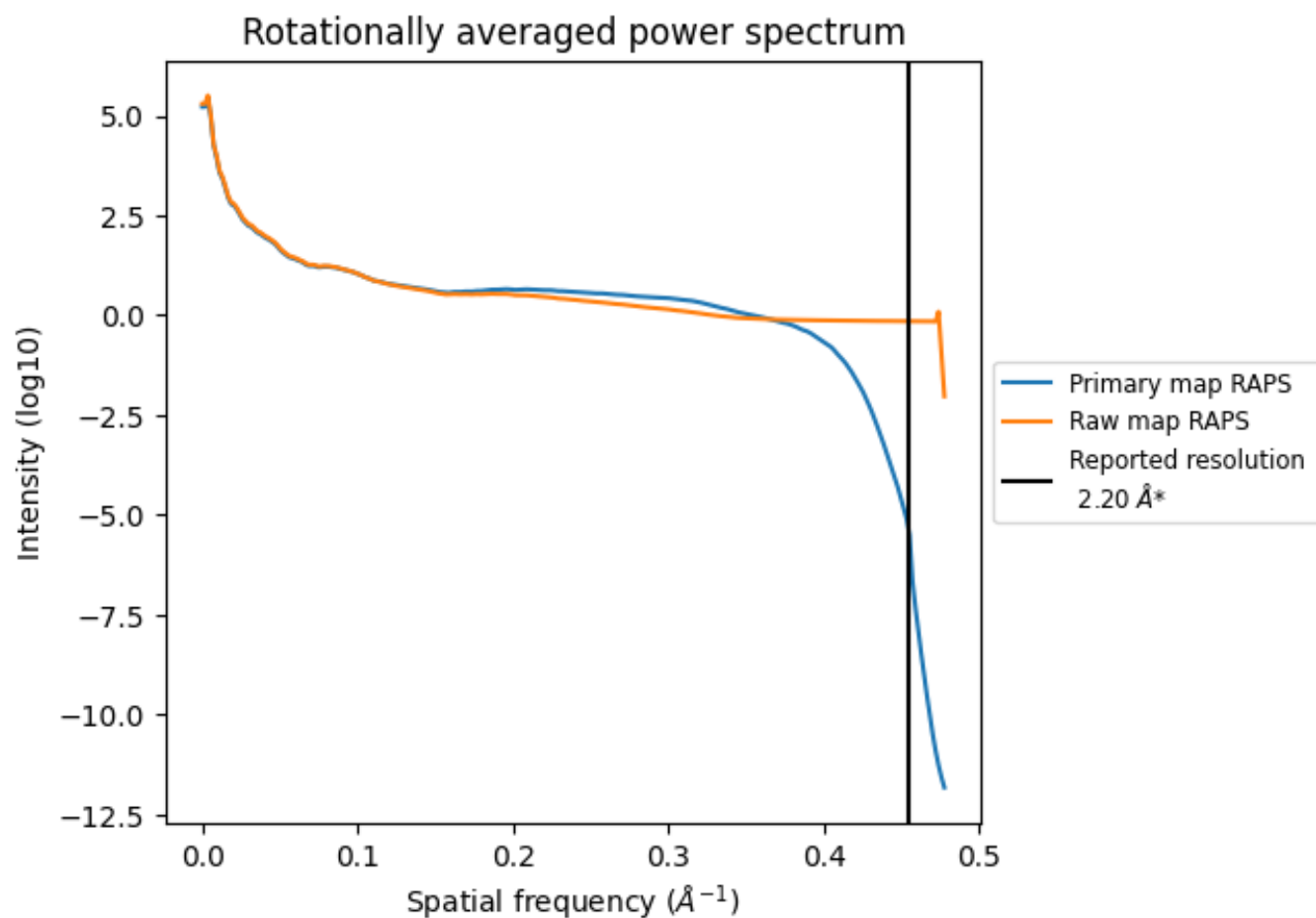
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1640 nm^3 ; this corresponds to an approximate mass of 1481 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

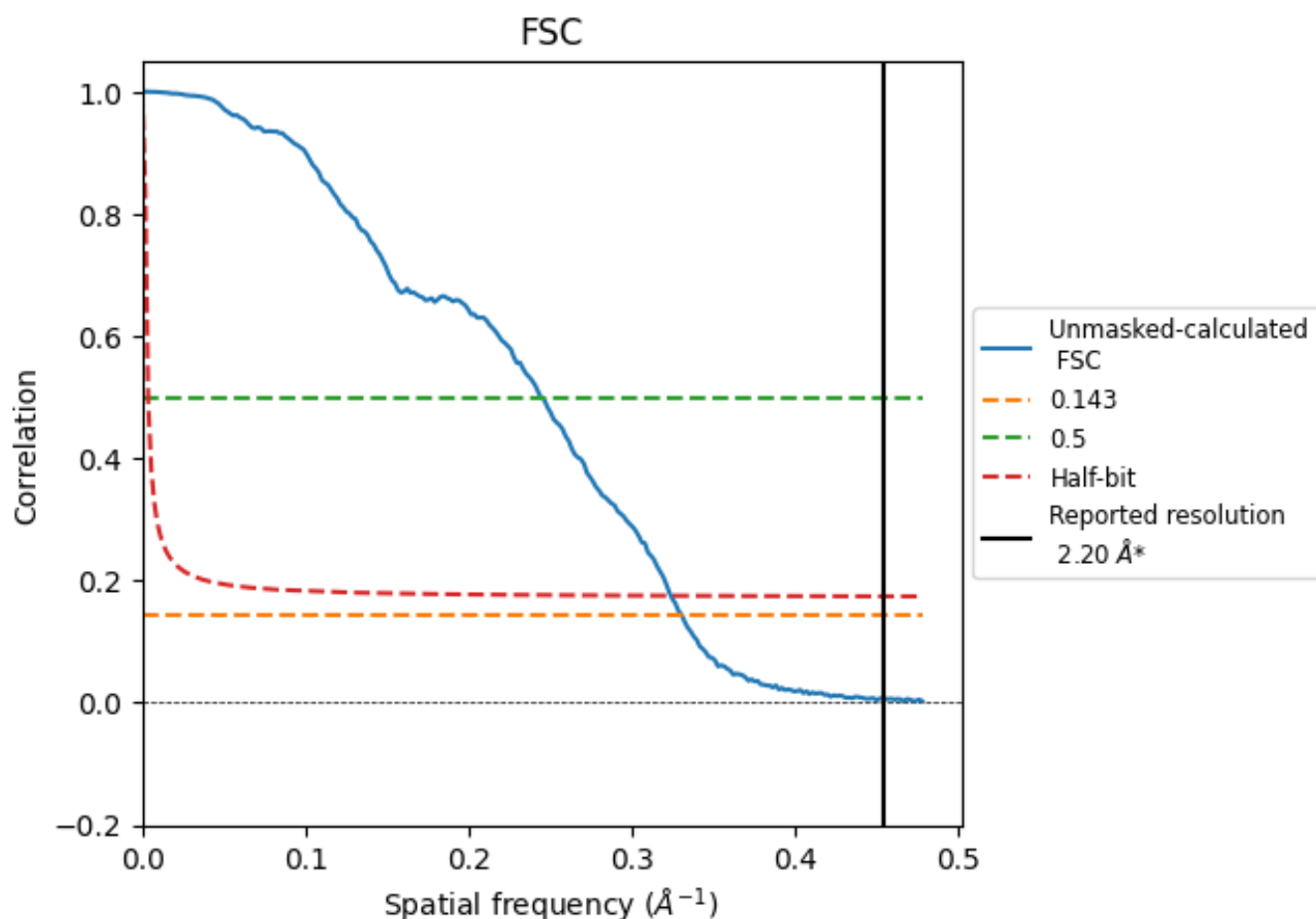


*Reported resolution corresponds to spatial frequency of 0.455 \AA^{-1}

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 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

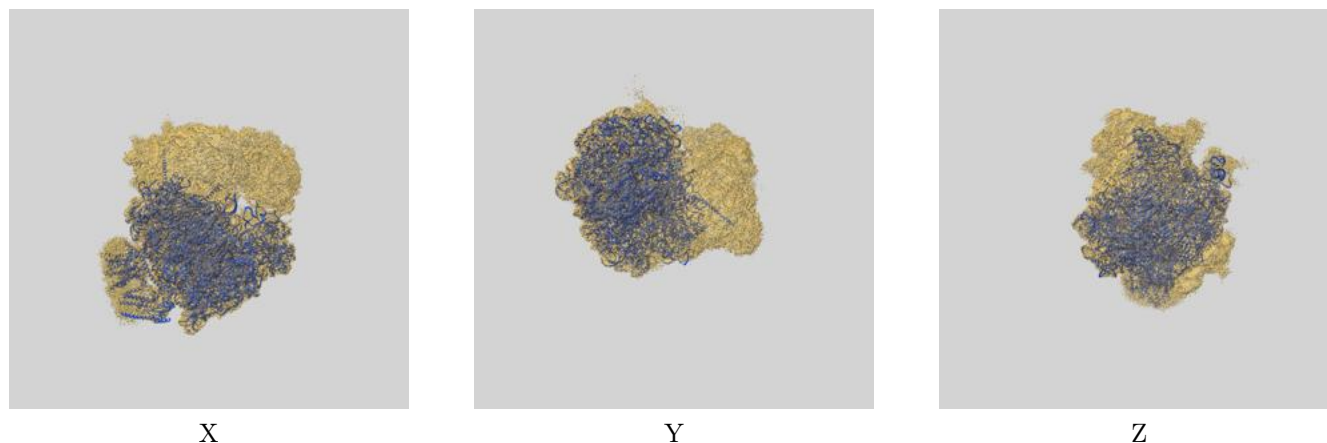
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.02	4.09	3.09

*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 3.02 differs from the reported value 2.2 by more than 10 %

9 Map-model fit [i](#)

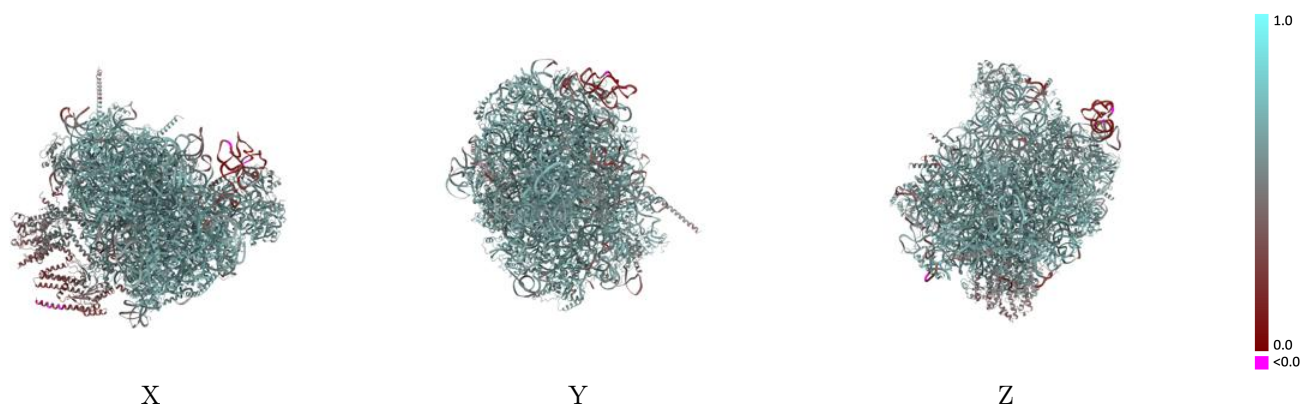
This section contains information regarding the fit between EMDB map EMD-52656 and PDB model 9I78. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



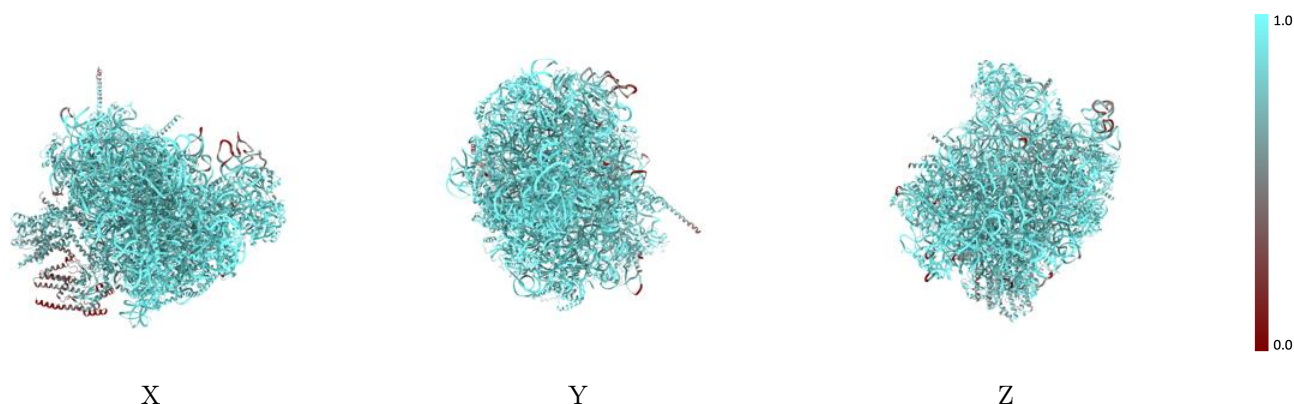
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



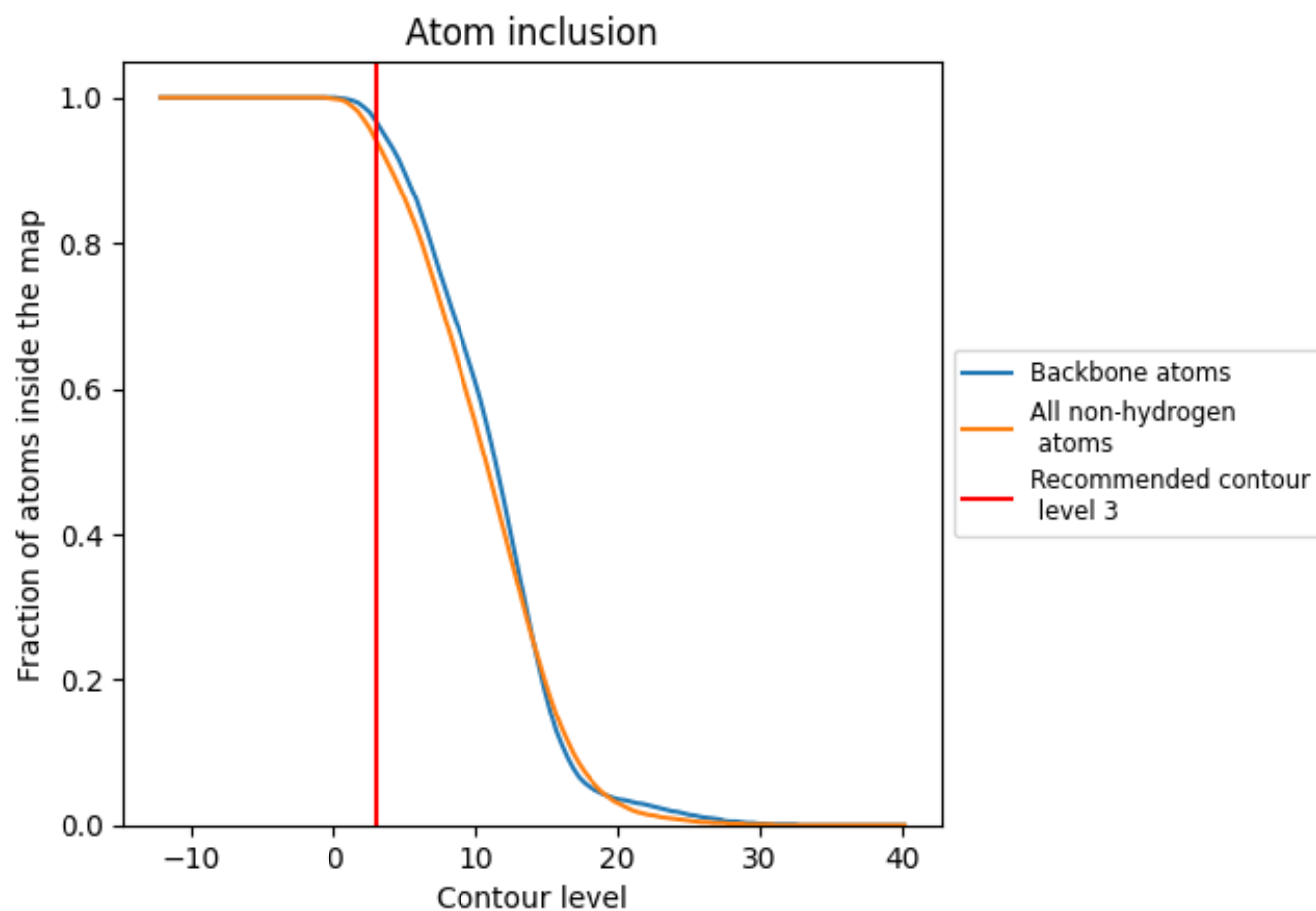
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.6100
1	 0.7860	 0.4600
2	 0.7410	 0.4670
3	 0.6970	 0.4120
4	 0.5890	 0.3930
6	 0.5020	 0.3130
7	 0.3170	 0.2490
L1	 0.9710	 0.6170
L2	 0.9900	 0.6380
L3	 0.9990	 0.6330
LA	 0.9570	 0.6630
LB	 0.9780	 0.6610
LC	 0.9740	 0.6620
LD	 0.9420	 0.6120
LE	 0.9400	 0.6140
LF	 0.9700	 0.6540
LG	 0.9310	 0.6120
LH	 0.9370	 0.6070
LI	 0.9600	 0.6340
LJ	 0.8780	 0.5330
LL	 0.9560	 0.6390
LM	 0.9700	 0.6430
LN	 0.9930	 0.6790
LO	 0.9780	 0.6620
LP	 0.9330	 0.6440
LQ	 0.9850	 0.6670
LR	 0.8920	 0.6100
LS	 0.9780	 0.6550
LT	 0.9610	 0.6440
LU	 0.8880	 0.5510
LV	 0.9620	 0.6610
LX	 0.9410	 0.6390
LY	 0.9470	 0.6420
LZ	 0.9580	 0.6230
La	 0.9760	 0.6600



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Chain	Atom inclusion	Q-score
Lb	 0.9410	 0.5950
Lc	 0.9450	 0.6180
Ld	 0.9280	 0.6340
Le	 0.9770	 0.6720
Lf	 0.9900	 0.6720
Lg	 0.9410	 0.6310
Lh	 0.8960	 0.5840
Li	 0.9110	 0.5920
Lj	 0.9830	 0.6690
Lk	 0.8750	 0.5730
Ll	 0.9590	 0.6510
Lm	 0.7010	 0.5500
Ln	 0.7980	 0.5700
Lo	 0.9620	 0.6570
Lp	 0.9120	 0.6200
Lq	 0.9640	 0.6470