



wwPDB EM Validation Summary Report ⓘ

Sep 6, 2026 – 06:14 PM EDT

PDB ID : 11HE / pdb_000011he
EMDB ID : EMD-75687
Title : Rabbit 60S ribosomal subunit with eEF2 domain IV closed
Authors : Seraj, Z.; Zottig, X.; Huang, C.H.; Loveland, A.B.; Diggs, S.; Sholi, E.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2026-02-24
Resolution : 2.86 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:

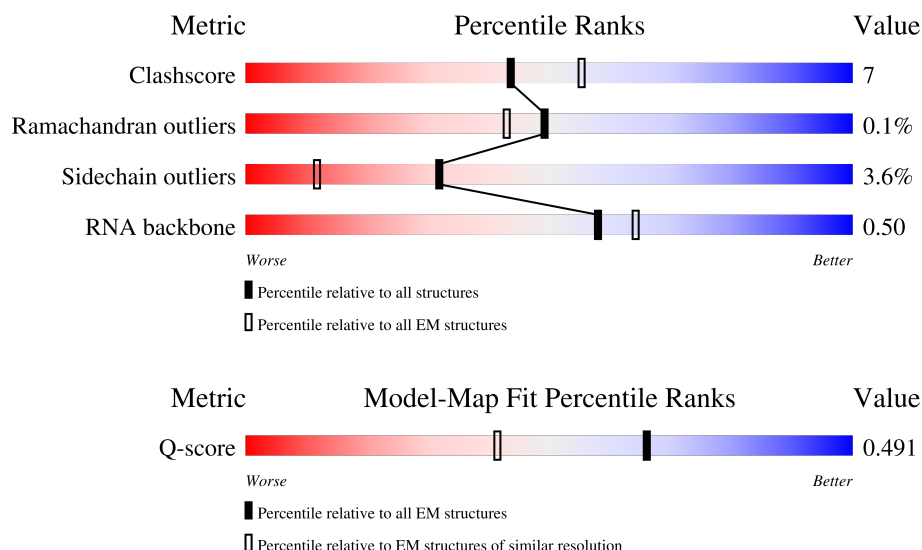
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 2.86 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.



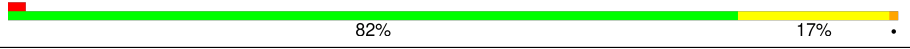
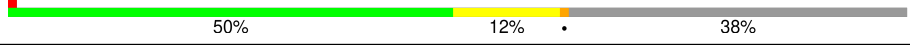
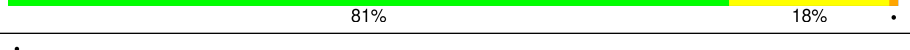
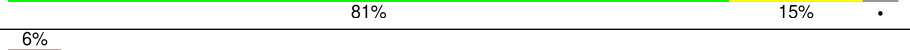
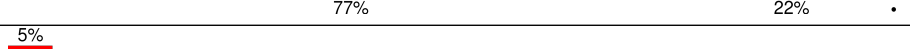
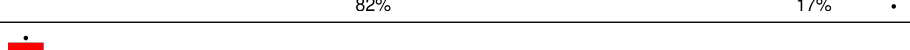
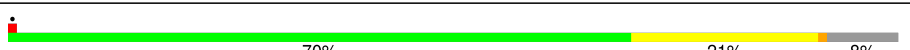
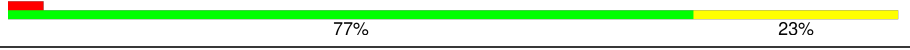
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	58	156	
2	5	120	
3	L8	345	

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Mol	Chain	Length	Quality of chain
4	L3	394	
5	L4	362	
6	L5	293	
7	L6	347	
8	L7	225	
9	aa	240	
10	L9	190	
11	10	213	
12	11	170	
13	13	210	
14	14	138	
15	15	203	
16	bb	199	
17	17	153	
18	19	180	
19	20	192	
20	21	159	
21	22	99	
22	23	131	
23	24	63	
24	cc	118	
25	26	134	
26	27	135	
27	dd	147	
28	29	245	

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Mol	Chain	Length	Quality of chain
29	30	98	
30	31	107	
31	32	128	
32	ee	109	
33	34	114	
34	35	122	
35	36	102	
36	37	86	
37	38	69	
38	39	50	
39	40	52	
40	42	104	
41	ff	91	
42	gg	124	
43	s	196	
44	t	153	
45	EB	375	
46	u	206	
47	Q	188	
48	ES	5070	
49	28	4807	
50	v	857	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 147611 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 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	58	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L8	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L3	394	Total	C	N	O	S	0	0
			3173	2020	597	543	13		

- Molecule 5 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L4	362	Total	C	N	O	S	0	0
			2884	1812	577	481	14		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	293	Total	C	N	O	S	0	0
			2392	1512	438	428	14		

- Molecule 7 is a protein called large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L6	216	Total	C	N	O	S	0	0
			1728	1115	329	281	3		

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 9 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	aa	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L9	190	Total	C	N	O	S	0	0
			1517	954	284	273	6		

- Molecule 11 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	10	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	11	170	Total	C	N	O	S	0	0
			1363	861	254	242	6		

- Molecule 13 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	13	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	14	138	Total	C	N	O	S	0	0
			1138	727	221	183	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	15	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 16 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	bb	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	17	153	Total	C	N	O	S	0	0
			1243	777	241	216	9		

- Molecule 18 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	19	159	Total	C	N	O	S	0	0
			1325	825	283	208	9		

- Molecule 19 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	20	176	Total	C	N	O	S	0	0
			1461	930	285	235	11		

- Molecule 20 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	21	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 21 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	22	99	Total	C	N	O	S	0	0
			810	519	141	148	2		

- Molecule 22 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	23	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 23 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	24	63	Total	C	N	O	S	0	0
			529	337	103	86	3		

- Molecule 24 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	cc	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	26	134	Total	C	N	O	S	0	0
			1116	700	226	187	3		

- Molecule 26 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	27	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 27 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	dd	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 28 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	29	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 29 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	30	98	Total	C	N	O	S	0	0
			762	481	134	141	6		

- Molecule 30 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	31	107	Total	C	N	O	S	0	0
			889	560	171	156	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	32	128	Total	C	N	O	S	0	0
			1054	667	216	166	5		

- Molecule 32 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ee	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 33 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	34	114	Total	C	N	O	S	0	0
			907	566	187	148	6		

- Molecule 34 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	35	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 35 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	36	102	Total	C	N	O	S	0	0
			831	520	176	130	5		

- Molecule 36 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	37	86	Total	C	N	O	S	0	0
			706	434	155	112	5		

- Molecule 37 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	38	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 38 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	39	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 39 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	40	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	42	104	Total	C	N	O	S	0	0
			852	533	174	139	6		

- Molecule 41 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ff	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	gg	124	Total	C	N	O	S	0	0
			991	615	202	168	6		

- Molecule 43 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1508	959	263	277	9		

- Molecule 44 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1161	722	218	218	3		

- Molecule 45 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EB	375	Total	C	N	O	S	0	0
			2932	1844	509	562	17		

- Molecule 46 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	u	206	Total	C	N	O	S	0	0
			1655	1058	297	292	8		

- Molecule 47 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 48 is a RNA chain called ES27L.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ES	67	Total	C	N	O	P	0	0
			1444	639	266	472	67		

- Molecule 49 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	28	3486	Total	C	N	O	P	0	0
			74767	33297	13700	24284	3486		

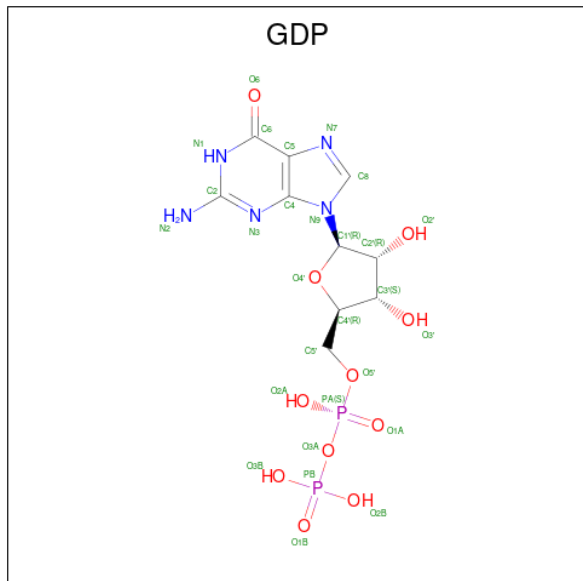
- Molecule 50 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	822	Total	C	N	O	S	0	0
			6409	4073	1097	1195	44		

- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn).

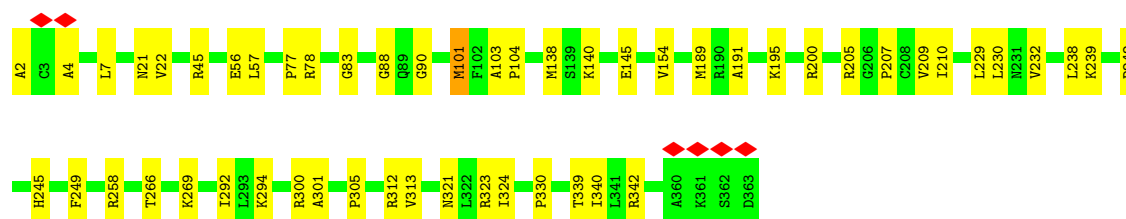
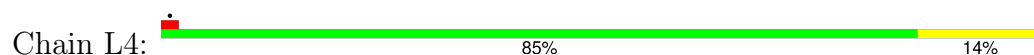
Mol	Chain	Residues	Atoms		AltConf
51	34	1	Total	Zn	0
			1	1	
51	37	1	Total	Zn	0
			1	1	
51	ff	1	Total	Zn	0
			1	1	

- Molecule 52 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

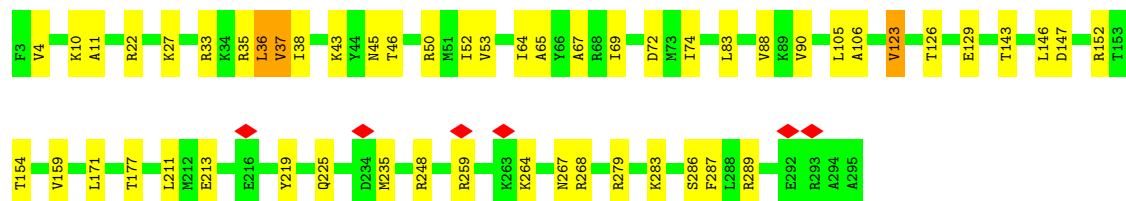
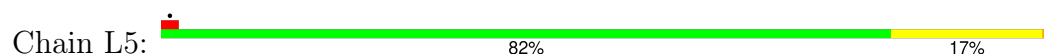




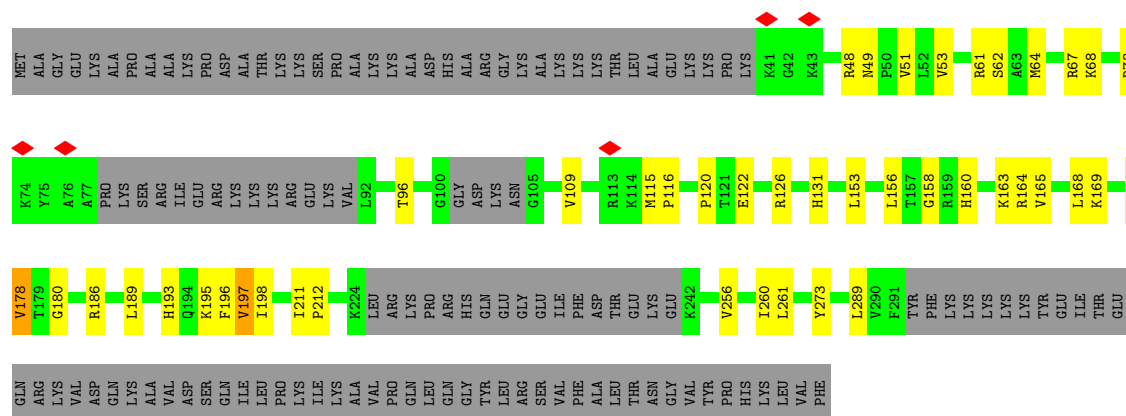
- Molecule 5: 60S ribosomal protein L4



- Molecule 6: 60S ribosomal protein L5

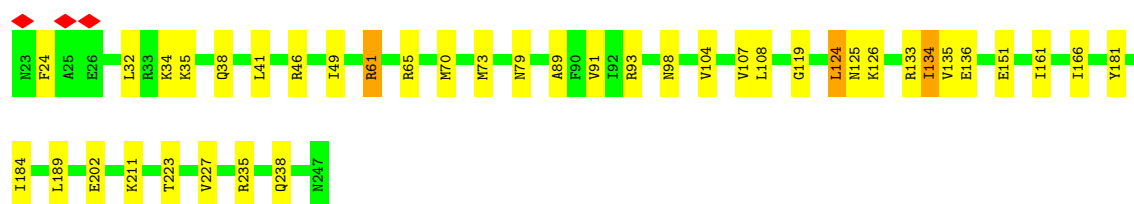


- Molecule 7: large ribosomal subunit protein eL6



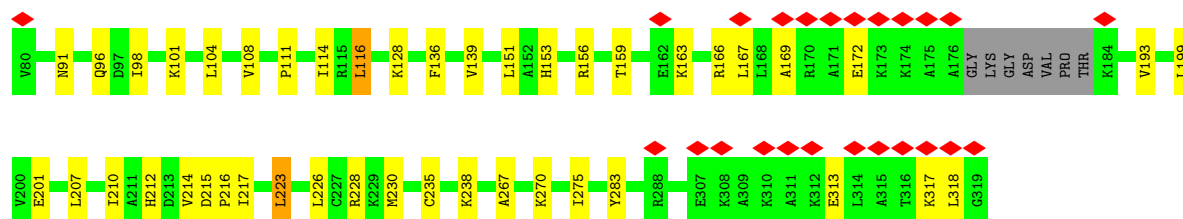
- Molecule 8: 60S ribosomal protein L7

Chain L7:  82% 16%



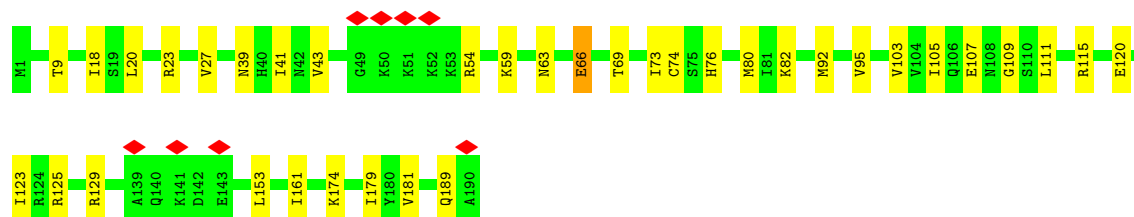
- Molecule 9: Large ribosomal subunit protein eL8

Chain aa:  10% 79% 18%



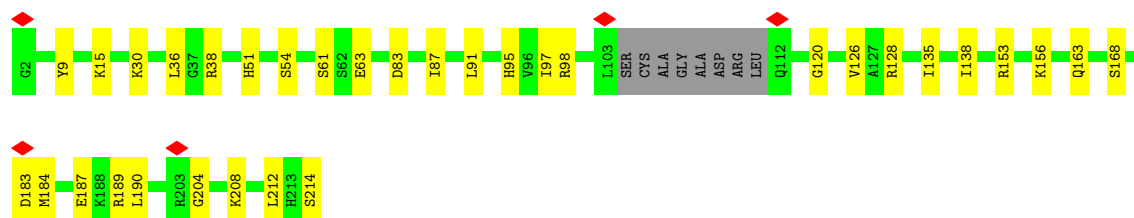
- Molecule 10: 60S ribosomal protein L9

Chain L9:  81% 18%



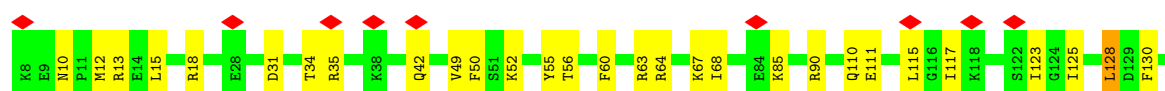
- Molecule 11: Ribosomal protein L10

Chain 10:  81% 15%



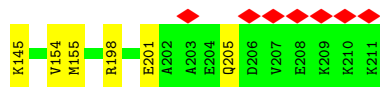
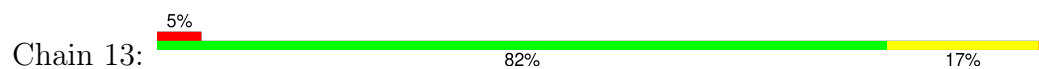
- Molecule 12: 60S ribosomal protein L11

Chain 11:  6% 77% 22%

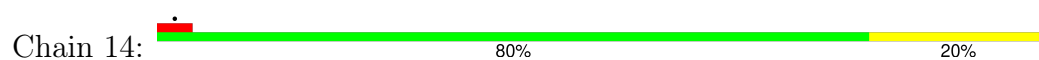




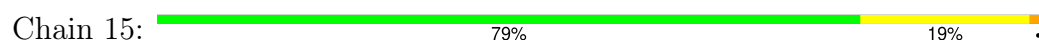
- Molecule 13: Large ribosomal subunit protein eL13



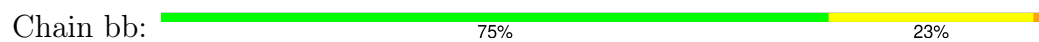
- Molecule 14: 60S ribosomal protein L14



- Molecule 15: 60S ribosomal protein L15



- Molecule 16: Large ribosomal subunit protein uL13



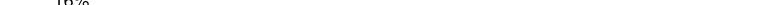
- Molecule 17: 60S ribosomal protein L17

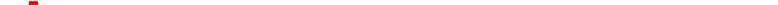


- Chain 19:
-
- 7% 73% 16% 12%
- A156 D157 Q158 A159 E160 ALA ARG ARG ARG SER THR LYS GLU ALA ARG LYS ARG ARG ARG LYS GLU ARG LEU GLN ALA LYS LYS
- S2 R3 L4 L10 K19 T29 I41 L44 L49 R60 R66 R70 R71 R74 G77 I78 G79 R80 R81 R96 I101 L105 L106 H118 M119 Y120 M134 K135 R136 I137 L138 M139 E140 H141 L145 K149 A150 R151 K152 K153 L154 L155

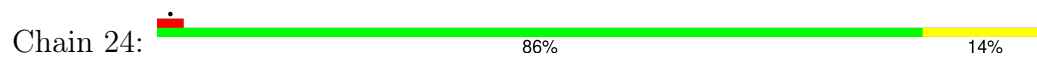
- Chain 20:
-
- Sequence logo for Chain 20. The y-axis represents information content in bits. The x-axis lists amino acids. A color scale at the top indicates conservation levels: green (70%), yellow (21%), and grey (8%).
- | Position | Amino Acid | Information Content (bits) |
|----------|------------|----------------------------|
| 1 | E130 | 0.15 |
| 2 | E131 | 0.10 |
| 3 | R139 | 0.10 |
| 4 | L159 | 0.25 |
| 5 | R160 | 0.15 |
| 6 | K164 | 0.10 |
| 7 | P165 | 0.10 |
| 8 | R166 | 0.10 |
| 9 | R171 | 0.10 |
| 10 | P172 | 0.10 |
| 11 | F176 | 0.15 |
| 12 | ARG | 0.05 |
| 13 | GLN | 0.05 |
| 14 | HIS | 0.05 |
| 15 | LYS | 0.05 |
| 16 | PRO | 0.05 |
| 17 | ARG | 0.05 |
| 18 | PHE | 0.05 |
| 19 | THR | 0.05 |
| 20 | THR | 0.05 |
| 21 | LYS | 0.05 |
| 22 | ARG | 0.05 |
| 23 | PRO | 0.05 |
| 24 | ASN | 0.05 |
| 25 | THR | 0.05 |
| 26 | PHE | 0.05 |
| 27 | PHE | 0.05 |
| 28 | M1 | 0.10 |
| 29 | T6 | 0.10 |
| 30 | V13 | 0.10 |
| 31 | G14 | 0.15 |
| 32 | R15 | 0.10 |
| 33 | C16 | 0.10 |
| 34 | L17 | 0.10 |
| 35 | P18 | 0.10 |
| 36 | T19 | 0.10 |
| 37 | P20 | 0.10 |
| 38 | R23 | 0.20 |
| 39 | L27 | 0.10 |
| 40 | M30 | 0.10 |
| 41 | A34 | 0.10 |
| 42 | P35 | 0.10 |
| 43 | V39 | 0.10 |
| 44 | R43 | 0.10 |
| 45 | F44 | 0.10 |
| 46 | V48 | 0.10 |
| 47 | M54 | 0.10 |
| 48 | V62 | 0.10 |
| 49 | Y63 | 0.10 |
| 50 | V67 | 0.10 |
| 51 | L73 | 0.10 |
| 52 | K76 | 0.10 |
| 53 | N77 | 0.15 |
| 54 | F78 | 0.10 |
| 55 | G79 | 0.10 |
| 56 | I80 | 0.10 |
| 57 | R83 | 0.10 |
| 58 | L100 | 0.10 |
| 59 | T101 | 0.10 |
| 60 | T102 | 0.10 |
| 61 | T107 | 0.10 |
| 62 | R111 | 0.10 |
| 63 | R116 | 0.10 |
| 64 | I126 | 0.20 |
| 65 | M127 | 0.20 |
| 66 | K128 | 0.15 |
| 67 | V129 | 0.10 |

- Chain 21:
- 
- 5% 80% 20%
- 
- T2 R8 M14 F19 R20 L27 K31 K32 I33 Y34 K35 V40 V48 M52 P53 H54 K55 G62 Q69 V76 A86 K87 E94 H95 I96 K97 R102 L106 E111 K117 E118 A119 K120 E121 K122 V126 Q127 P132 A133 T142
- M144 G145 P155 F158 M159 A160

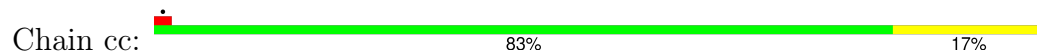
- Chain 22: 

- Chain 23: 
- 

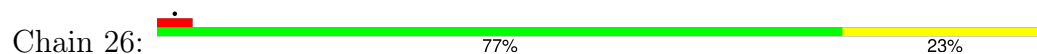
- WORLDWIDE
PDB
PROTEIN DATA BANK



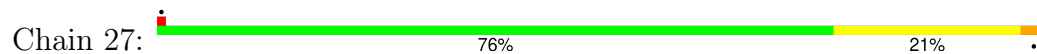
- Molecule 24: Large ribosomal subunit protein uL23



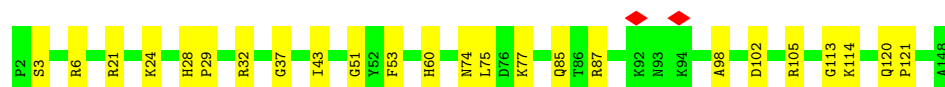
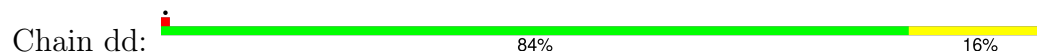
- Molecule 25: 60S ribosomal protein L26



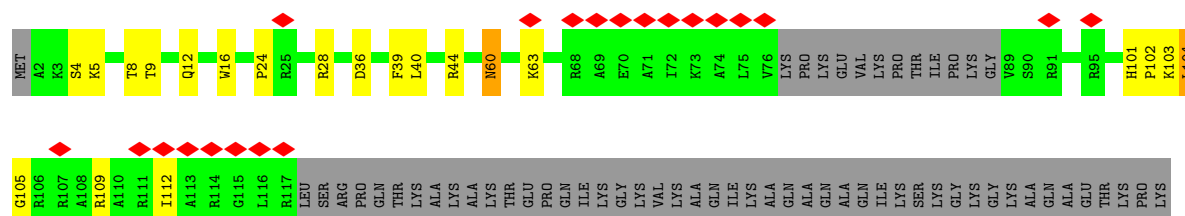
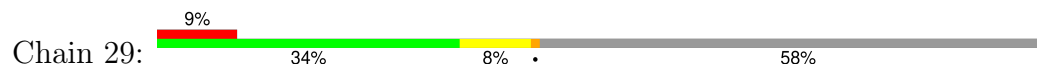
- Molecule 26: 60S ribosomal protein L27



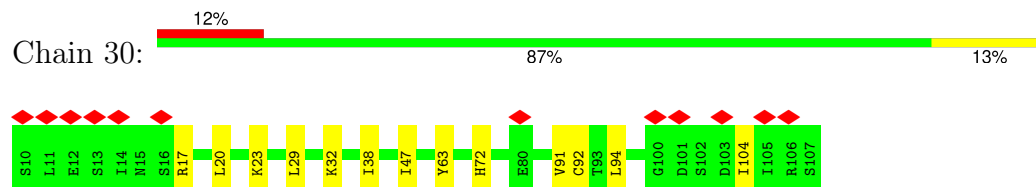
- Molecule 27: 60S ribosomal protein L27a



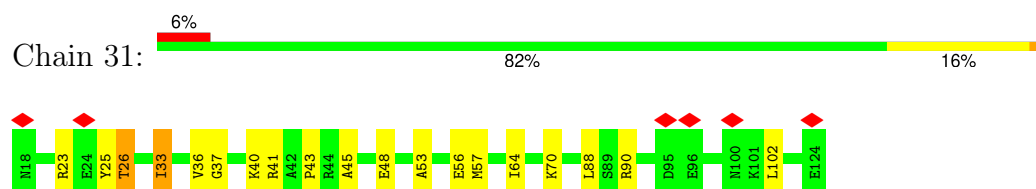
- Molecule 28: Large ribosomal subunit protein eL29



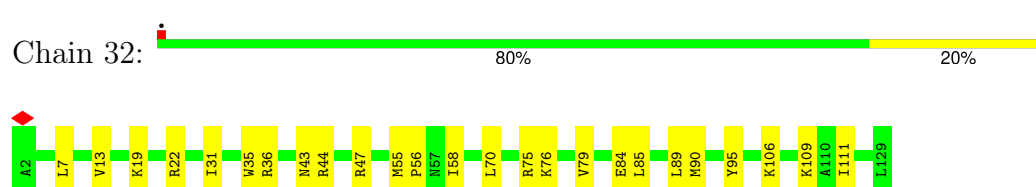
- Molecule 29: 60S ribosomal protein L30



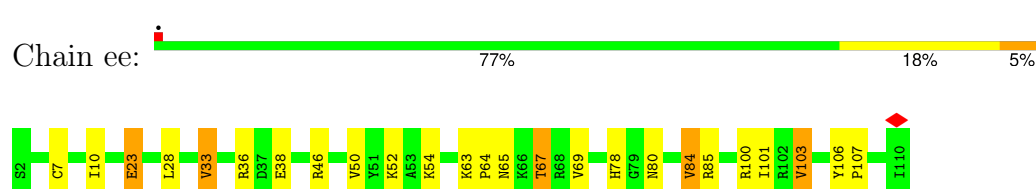
- Molecule 30: 60S ribosomal protein L31



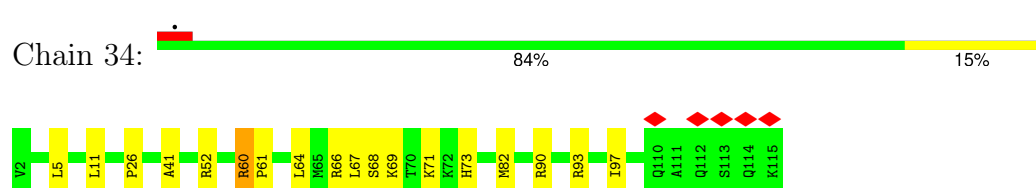
- Molecule 31: Large ribosomal subunit protein eL32



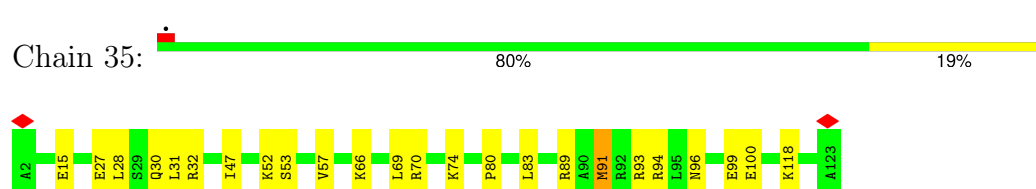
- Molecule 32: Large ribosomal subunit protein eL33



- Molecule 33: 60S ribosomal protein L34

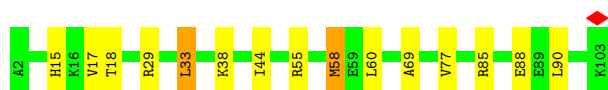


- Molecule 34: 60S ribosomal protein L35



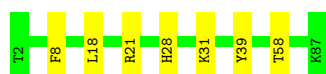
- Molecule 35: 60S ribosomal protein L36

Chain 36:  85% 13%



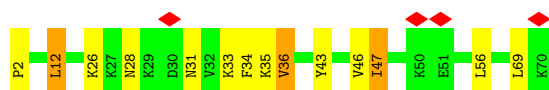
- Molecule 36: 60S ribosomal protein L37

Chain 37:  92% 8%



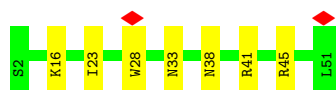
- Molecule 37: Large ribosomal subunit protein eL38

Chain 38:  6% 80% 16%



- Molecule 38: 60S ribosomal protein L39

Chain 39:  86% 14%



- Molecule 39: Large ribosomal subunit protein eL40

Chain 40:  6% 81% 17%



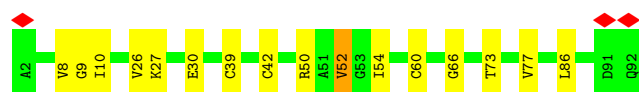
- Molecule 40: eL42

Chain 42:  82% 17%

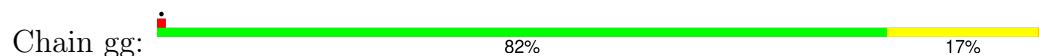


- Molecule 41: 60S ribosomal protein L37a

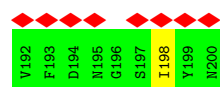
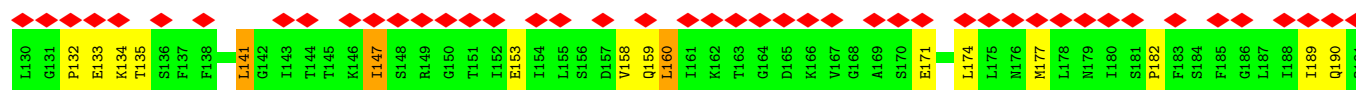
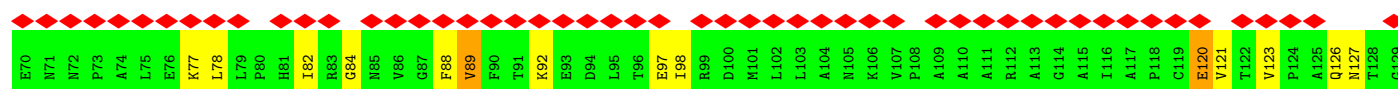
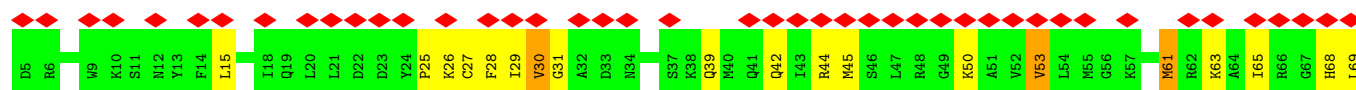
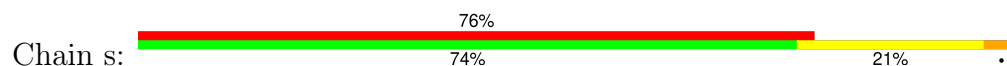
Chain ff:  82% 16%



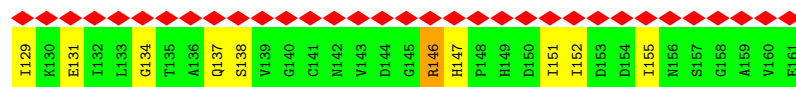
- Molecule 42: 60S ribosomal protein L28



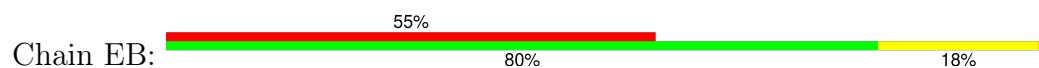
- Molecule 43: 60S acidic ribosomal protein P0

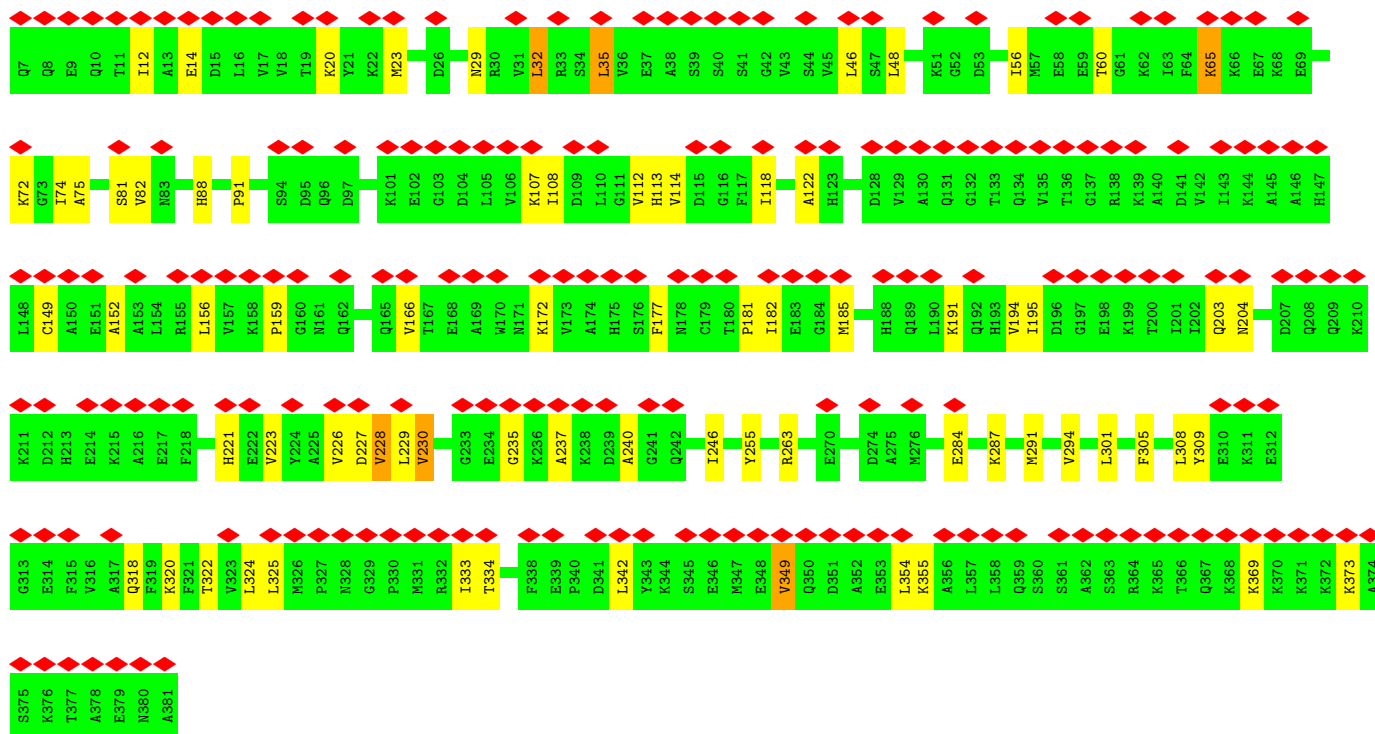


- Molecule 44: uL11



- Molecule 45: Proliferation-associated protein 2G4

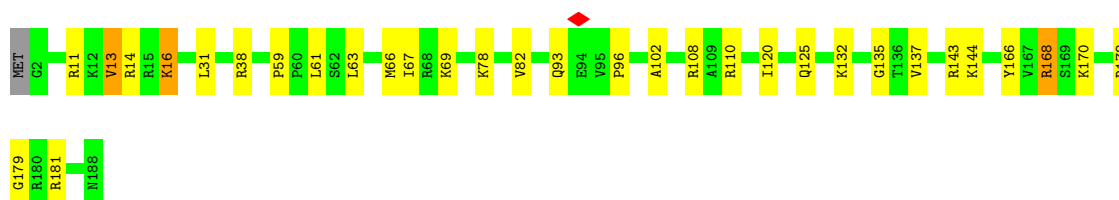
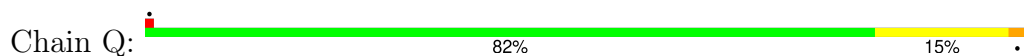




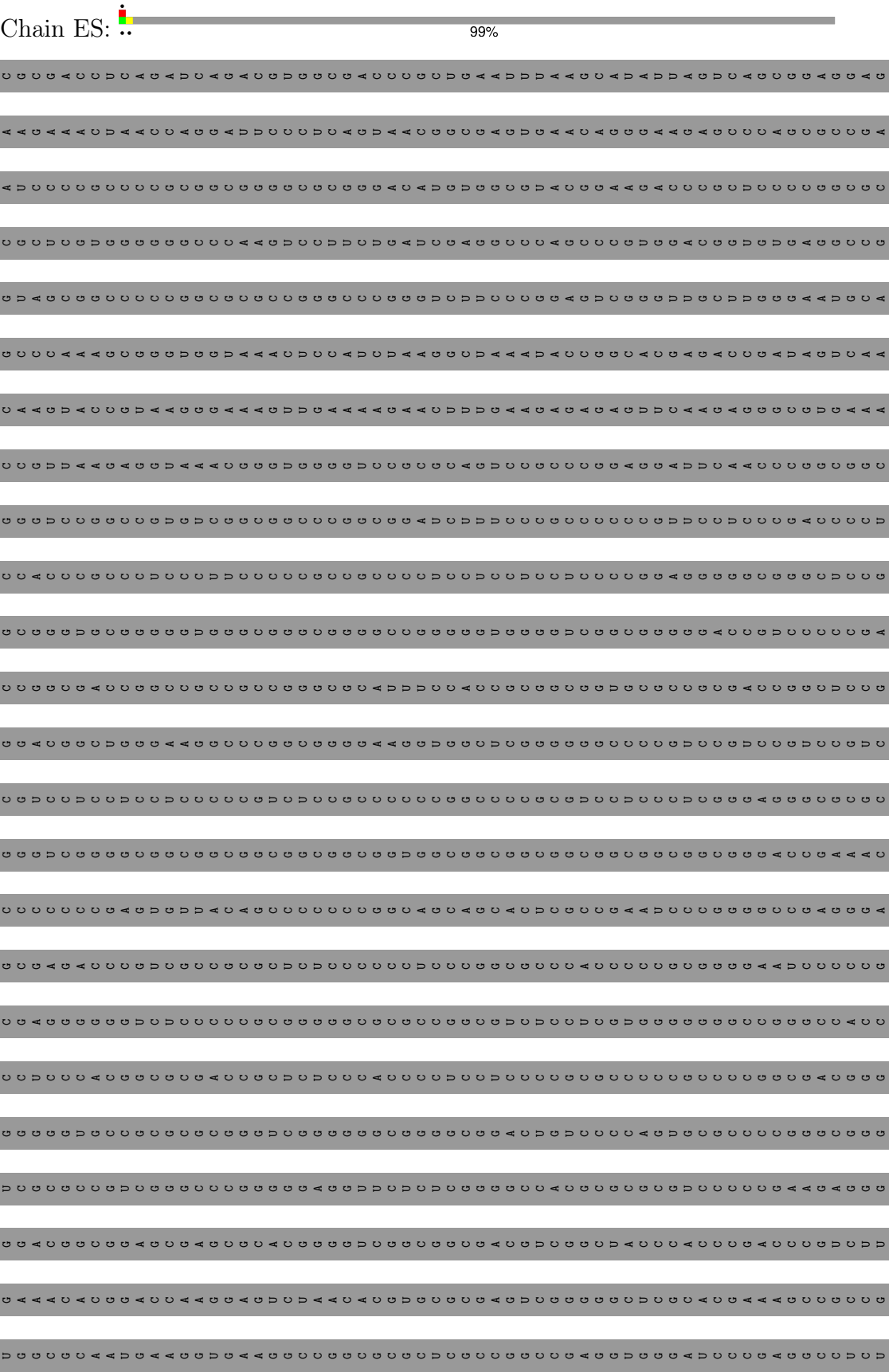
• Molecule 46: 60S ribosomal protein L10a



• Molecule 47: Large ribosomal subunit protein eL18

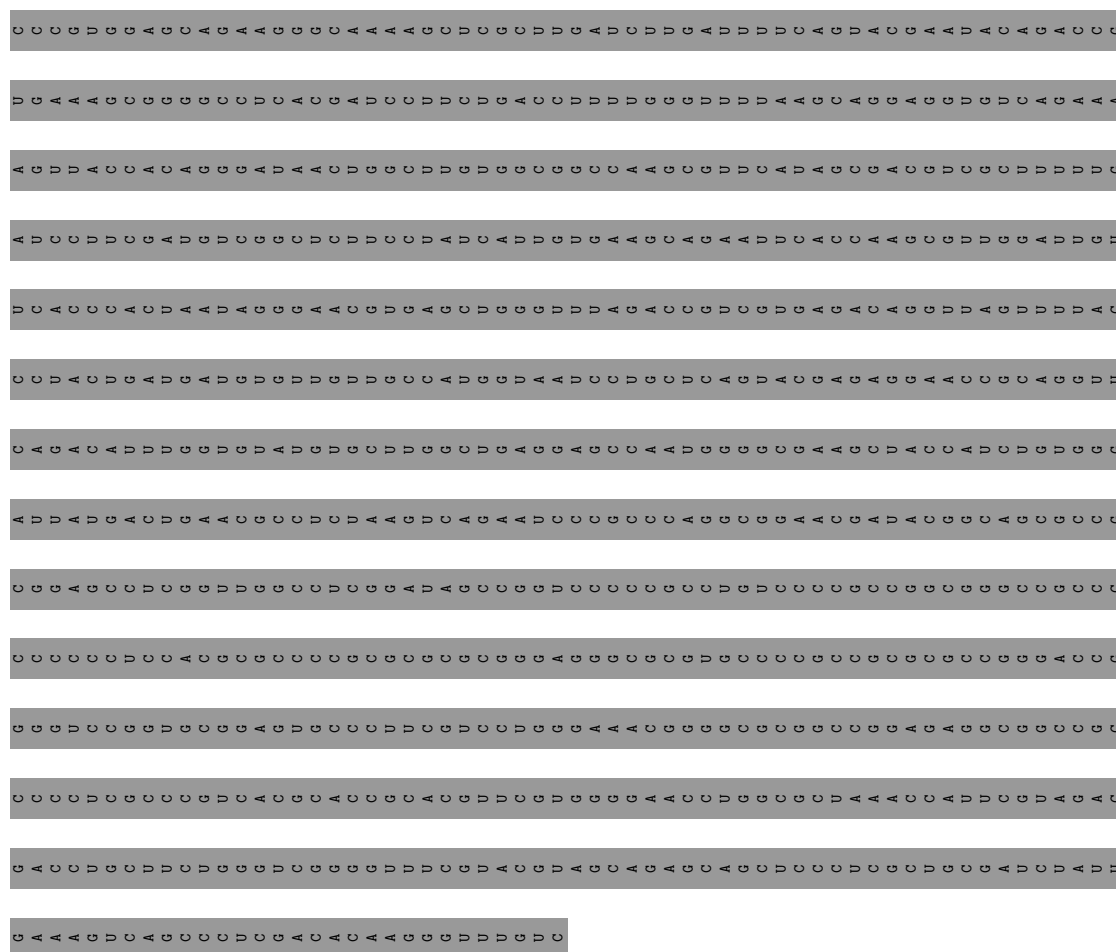


● Molecule 48: ES27L



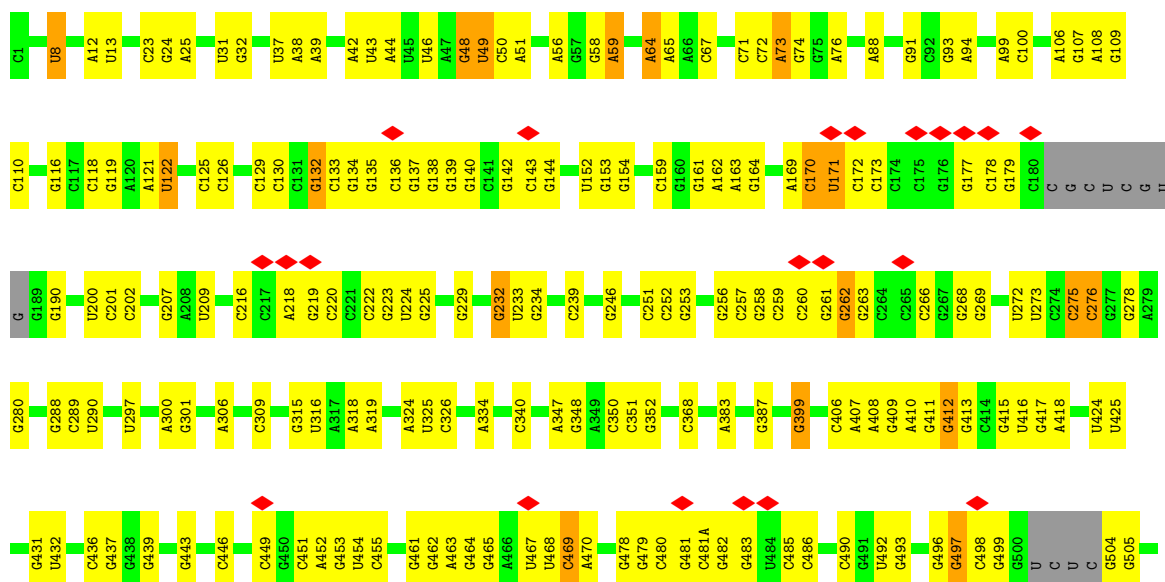


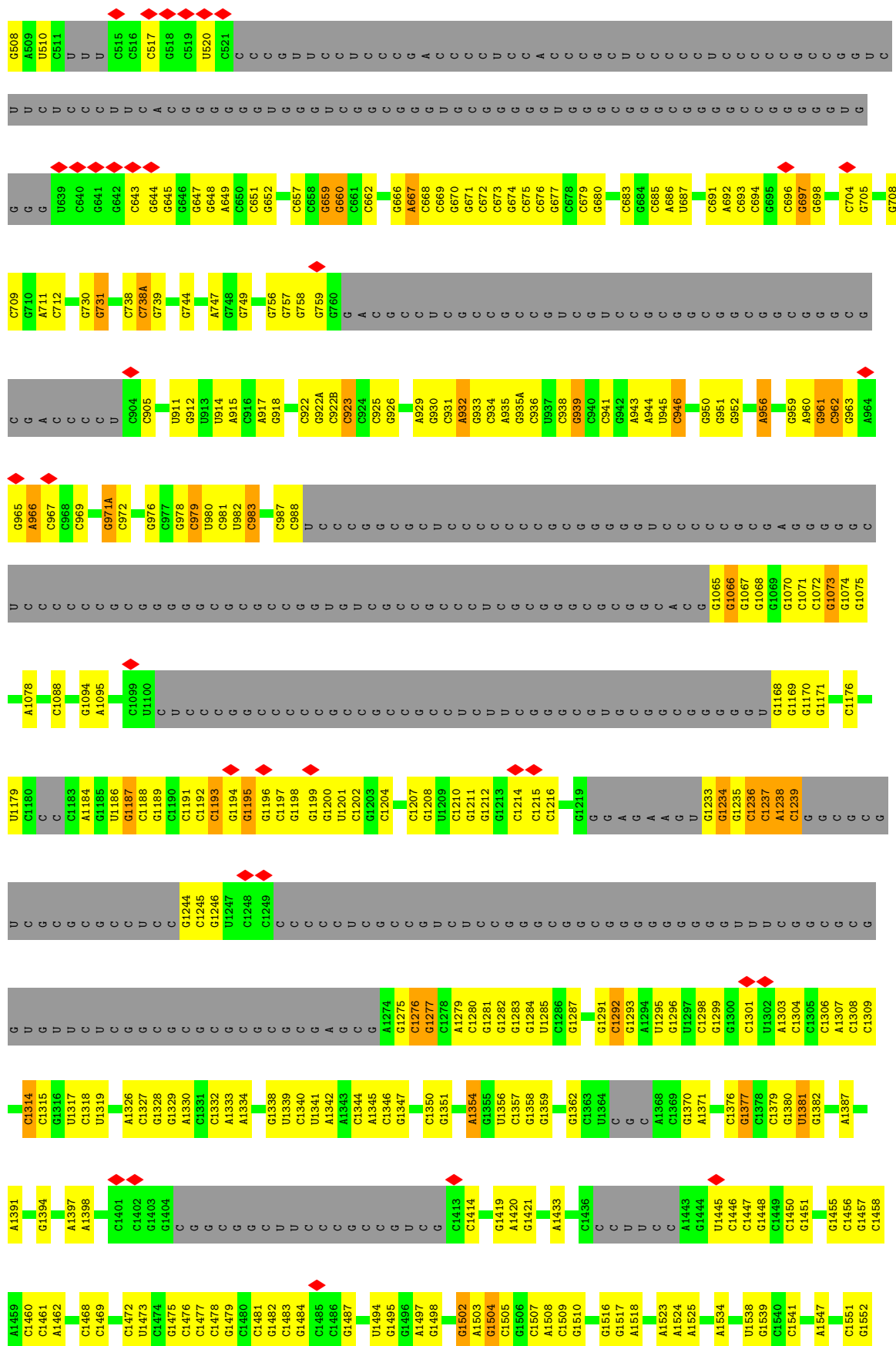




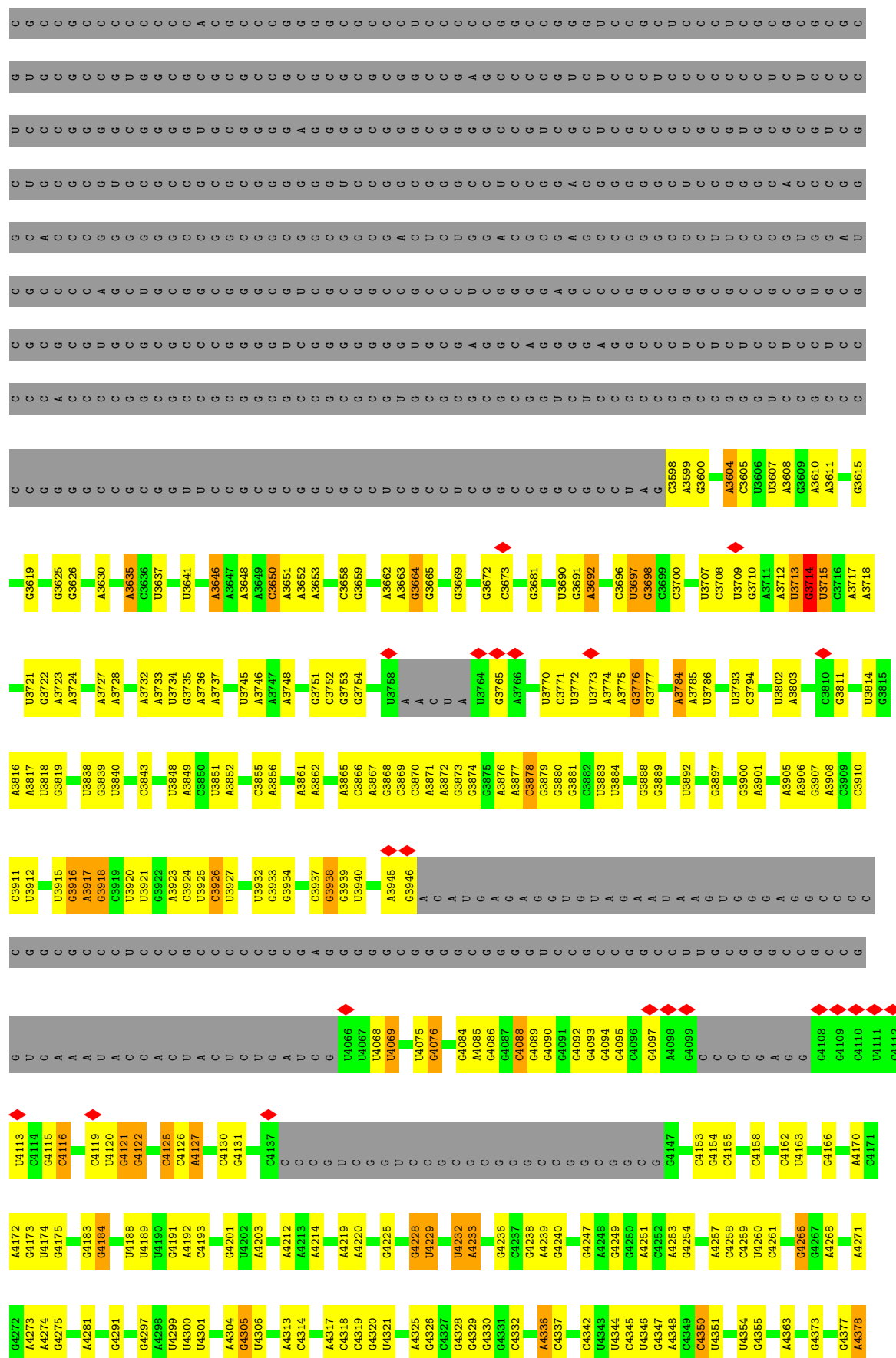
• Molecule 49: 28S rRNA

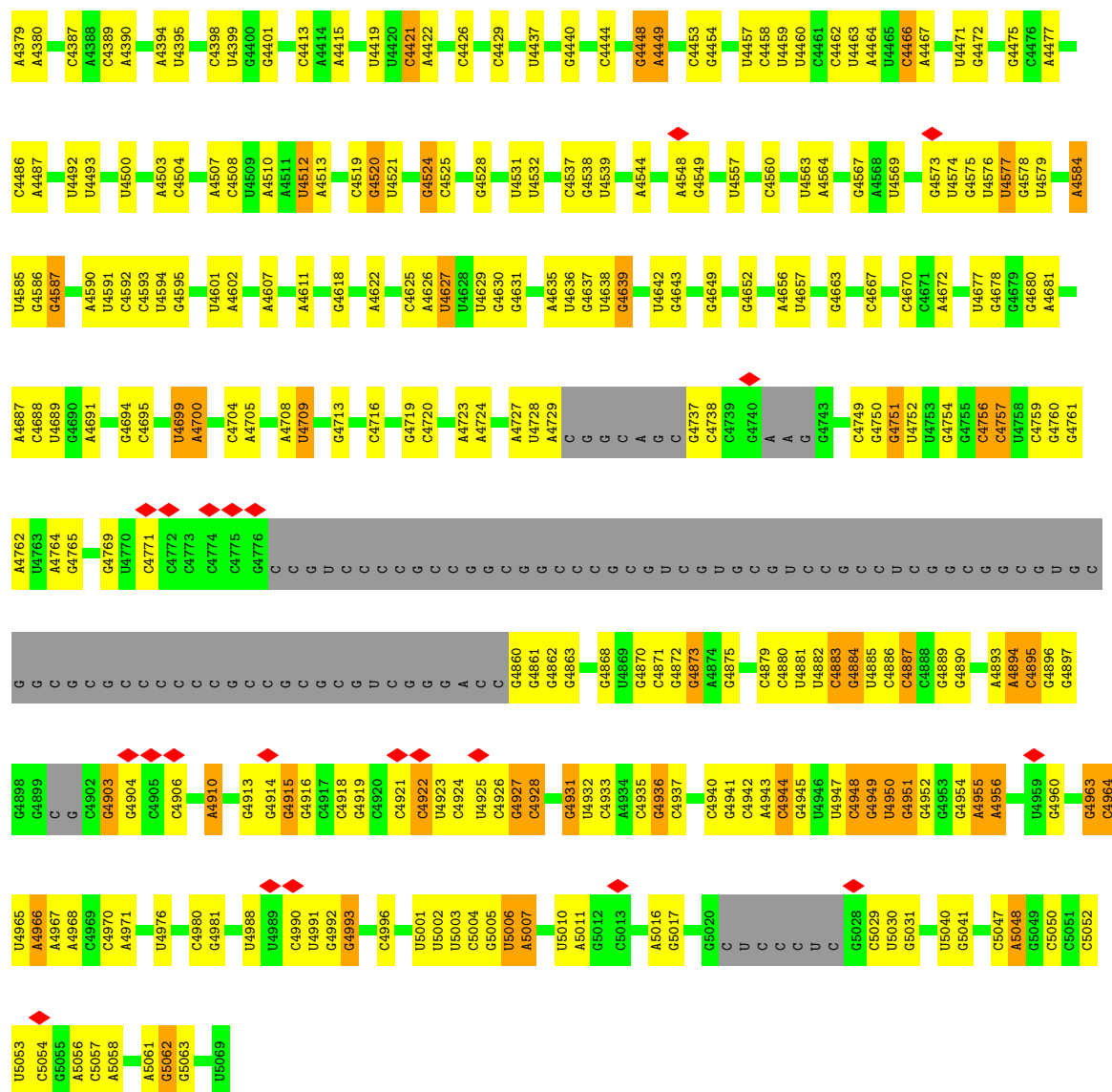
Chain 28: 41% 27% 27%



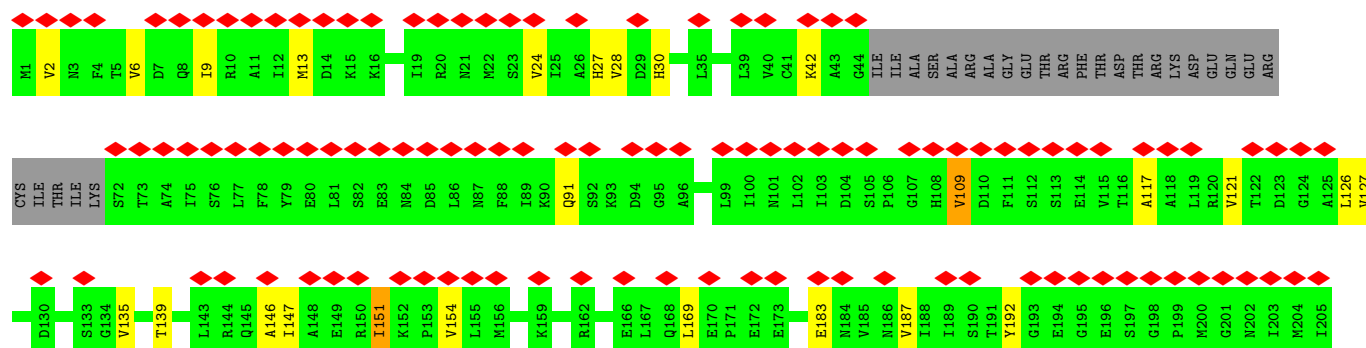
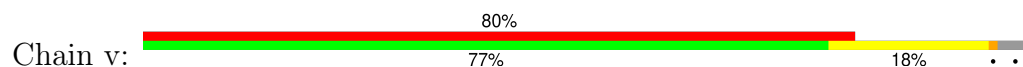


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G	C2786	U2707	C2615	G2506	A2417	G2294	G2052	U1974	G1883	A1776	A1669	A1558
C	A2787	U2708	G	A2507	G	G	G	G1975	G1884	U1781	G1677	G1559
C	U2788	C2709	A2623	A2513	G2421	G2297	G2055	G1976	G1885	A1787	U1677	A1560
G	A2789	C2710	G	G	C2422	U	A2056	G1977	C1893	A1788	A1682	G1561
U	U2790	G2711	C2627	U2519	U2425	C	G2058	G1978	A1897	C1789	U1683	G1562
C	G	C2712	G	G2521	U2428	C	C	U1979	U1910	U1790	U1684	A1563
U	G2713	G2714	G	G2522	G	C	C	U1980	G1911	A1794	G1685	A1564
G	G2715	U2716	G2634	G2528	G2433	C	C	G1981	G1914	G1797	C1686	A1565
G	C2717	U2718	U2635	U2529	G2434	C	C	A1984	C1917	G1802	C1690	C1566
G	A2796	G2719	U2636	U2530	U2439	G	G	G1985	A1803	G1803	G1574	G1577
G	C2797	C2720	U2637	U2537	G2440	C	C	U1986	U1917	U1578	G1577	U1578
G	A2798	G2721	U2638	U2538	C2441	G	G	G1987	A1804	A1804	C	G
G	G	U2722	U2639	U2539	G	G	G	U1988	A1805	A1805	A	G
G	U2723	U2723	A2642	C2539	C2441	G	G	G1989	G1806	G1806	A	G
G	U2724	U2724	G2643	C2540	G2448	C	C	U1990	G1807	G1807	A	G
C	A2725	A2725	G2644	C2541	A2449	C	C	G1991	C1808	C1808	C	G
C	G2726	G2726	U2645	C2542	G2450	C	C	U1992	C1809	C1809	C	G
G	C2727	U2727	A2646	C2543	G	C	C	U1993	C1810	C1810	C	G
A	U2728	U2728	U2647	G2544	G	C	C	U1994	C1811	C1811	C	G
A	G2823	G2732	G2648	U2545	G	C	C	U1995	C1812	C1812	C	G
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G	U2827	G2736	G2655	C2549	G2468	C	C	U1999	G1818	G1818	C	G
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G	A2836	C2739	U2661	U2553	G	C	C	U2001	U1820	U1820	C	G
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G	A2870	U2763	G	G	G	C	C	U2018	U1859	U1859	C	G
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A	G	A2765	G	G	G	C	C	U2020	U1861	U1861	C	G
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C	G	G	G	G	G	C	C	U2045	U1987	U1987	C	G
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C	G	G	G	G	G	C	C	U2067	U2009	U2009	C	G
C	G	G	G	G	G	C	C	U2068	U2010	U2010	C	G
C	G	G	G	G	G	C	C	U2069	U2011	U2011	C	G
C	G	G	G	G	G	C	C	U2070	U2012	U2012	C	G
C	G	G	G	G	G	C	C	U2071	U2013	U2013	C	G
C	G	G	G	G	G	C	C	U2072	U2014	U2014	C	G
C	G	G	G	G	G	C	C	U2073	U2015	U2015	C	G
C	G	G	G	G	G	C	C	U2074	U2016	U2016	C	G
C	G	G	G	G	G	C	C	U2075	U2017	U2017	C	G
C	G	G	G	G	G	C	C	U2076	U2018	U2018	C	G
C	G	G	G	G	G	C	C	U2077	U2019	U2019	C	G
C	G	G	G	G	G	C	C	U2078	U2020	U2020	C	G
C	G	G	G	G	G	C	C	U2079	U2021	U2021	C	G
C	G	G	G	G	G	C	C	U2080	U2022	U2022	C	G
C	G	G	G	G	G	C	C	U2081	U2023	U2023	C	G
C	G	G	G	G	G	C	C	U2082	U2024	U2024	C	G
C	G	G	G	G	G	C	C	U2083	U2025	U2025	C	G
C	G	G	G	G	G	C	C	U2084	U2026	U2026	C	G
C	G	G	G	G	G	C	C	U2085	U2027	U2027	C	G
C	G	G	G	G	G	C	C	U2086	U2028	U2028	C	G
C	G	G	G	G	G	C	C	U2087	U2029	U2029	C	G
C	G	G	G	G	G	C	C	U2088	U2030	U2030	C	G
C	G	G	G	G	G	C	C	U2089	U2031	U2031	C	G
C	G	G	G	G	G	C	C	U2090	U2032	U2032	C	G
C	G	G	G	G	G	C	C	U2091	U2033	U2033	C	G
C	G	G	G	G	G	C	C	U2092	U2034	U2034	C	G
C	G	G	G	G	G	C	C	U2093	U2035	U2035	C	G
C	G	G	G	G	G	C	C	U2094	U2036	U2036	C	G
C	G	G	G	G	G	C	C	U2095	U2037	U2037	C	G
C	G	G	G	G	G	C	C	U2096	U2038	U2038	C	G
C	G	G	G	G	G	C	C	U2097	U2039	U2039	C	G
C	G	G	G	G	G	C	C	U2098	U2040	U2040	C	G
C	G	G	G	G	G	C	C	U2099	U2041	U2041	C	G
C	G	G	G	G	G	C	C	U2100	U2042	U2042	C	G
C	G	G	G	G	G	C	C	U2101	U2043	U2043	C	G
C	G	G	G	G	G	C	C	U2102	U2044	U2044	C	G
C	G	G	G	G	G	C	C	U2103	U2045	U2045	C	G
C	G	G	G	G	G	C	C	U2104	U2046	U2046	C	G
C	G	G	G	G	G	C	C	U2105	U2047	U2047	C	G
C	G	G	G	G	G	C	C	U2106	U2048	U2048	C	G
C	G	G	G	G	G	C	C	U2107	U2049	U2049	C	G
C	G	G	G	G	G	C	C	U2108	U2050	U2050	C	G
C	G	G	G	G	G	C	C	U2109	U2051	U2051	C	G
C	G	G	G	G	G	C	C	U2110	U2052	U2052	C</	





• Molecule 50: Elongation factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	22323	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 ($e^-/\text{\AA}^2$)	39	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	31.991	Depositor
Minimum map value	-14.192	Depositor
Average map value	0.003	Depositor
Map value standard deviation	1.049	Depositor
Recommended contour level	3.8	Depositor
Map size ($\text{\AA}$)	664.0, 664.0, 664.0	wwPDB
Map dimensions	800, 800, 800	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	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: ZN, GDP

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	58	0.19	0/3581	0.29	0/5577
2	5	0.17	0/2858	0.25	0/4455
3	L8	0.20	0/1936	0.36	0/2596
4	L3	0.20	0/3241	0.33	0/4339
5	L4	0.19	0/2938	0.31	0/3946
6	L5	0.17	0/2438	0.33	0/3264
7	L6	0.17	0/1761	0.31	0/2362
8	L7	0.20	0/1911	0.31	0/2549
9	aa	0.19	0/1910	0.34	0/2569
10	L9	0.19	0/1536	0.36	0/2063
11	10	0.19	0/1702	0.31	0/2272
12	11	0.20	0/1386	0.37	0/1852
13	13	0.18	0/1733	0.34	0/2316
14	14	0.17	0/1159	0.32	0/1547
15	15	0.22	0/1746	0.37	0/2338
16	bb	0.21	0/1662	0.35	0/2222
17	17	0.19	0/1269	0.35	0/1700
18	19	0.16	0/1341	0.29	0/1776
19	20	0.19	0/1500	0.33	0/2012
20	21	0.19	0/1326	0.30	0/1770
21	22	0.15	0/824	0.34	0/1104
22	23	0.19	0/993	0.32	0/1332
23	24	0.18	0/542	0.30	0/720
24	cc	0.18	0/984	0.30	0/1323
25	26	0.18	0/1133	0.34	0/1504
26	27	0.16	0/1130	0.29	0/1507
27	dd	0.20	0/1191	0.31	0/1590
28	29	0.16	0/861	0.28	0/1138
29	30	0.15	0/772	0.29	0/1034
30	31	0.19	0/904	0.33	0/1216
31	32	0.20	0/1072	0.34	0/1429
32	ee	0.22	0/895	0.37	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	34	0.18	0/917	0.33	0/1220
34	35	0.16	0/1021	0.32	0/1348
35	36	0.17	0/842	0.30	0/1112
36	37	0.20	0/721	0.31	0/952
37	38	0.18	0/575	0.35	0/761
38	39	0.21	0/459	0.34	0/608
39	40	0.17	0/435	0.33	0/575
40	42	0.18	0/865	0.31	0/1140
41	ff	0.18	0/718	0.35	0/953
42	gg	0.19	0/1007	0.33	0/1349
43	s	0.15	0/1531	0.36	0/2064
44	t	0.15	0/1175	0.40	0/1582
45	EB	0.14	0/2979	0.30	0/4000
46	u	0.15	0/1681	0.38	0/2255
47	Q	0.21	0/1539	0.36	0/2054
48	ES	0.17	0/1609	0.38	0/2502
49	28	0.20	1/83633 (0.0%)	0.32	5/130425 (0.0%)
50	v	0.21	0/6536	0.41	0/8828
All	All	0.19	1/158478 (0.0%)	0.32	5/232348 (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
50	v	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	28	3715	U	O3'-P	-12.54	1.42	1.61

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	28	3715	U	P-O3'-C3'	14.39	141.79	120.20
49	28	3714	G	O3'-P-O5'	-14.35	82.48	104.00
49	28	3715	U	OP2-P-O3'	-9.77	78.69	108.00
49	28	3715	U	O3'-P-O5'	8.50	116.75	104.00
49	28	3714	G	P-O3'-C3'	-5.79	111.51	120.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	v	500	SER	Peptide

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	58	3208	0	1629	39	0
2	5	2558	0	1296	21	0
3	L8	1898	0	1993	38	0
4	L3	3173	0	3310	53	0
5	L4	2884	0	3053	35	0
6	L5	2392	0	2424	36	0
7	L6	1728	0	1887	31	0
8	L7	1875	0	1995	26	0
9	aa	1879	0	2027	25	0
10	L9	1517	0	1597	22	0
11	10	1664	0	1712	19	0
12	11	1363	0	1399	23	0
13	13	1702	0	1820	23	0
14	14	1138	0	1211	16	0
15	15	1701	0	1749	33	0
16	bb	1630	0	1778	33	0
17	17	1243	0	1274	10	0
18	19	1325	0	1457	20	0
19	20	1461	0	1508	32	0
20	21	1298	0	1366	26	0
21	22	810	0	833	9	0
22	23	979	0	1039	10	0
23	24	529	0	541	5	0
24	cc	967	0	1040	12	0
25	26	1116	0	1205	17	0
26	27	1107	0	1182	15	0
27	dd	1162	0	1209	24	0
28	29	848	0	920	14	0
29	30	762	0	794	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	31	889	0	930	15	0
31	32	1054	0	1147	16	0
32	ee	876	0	912	19	0
33	34	907	0	998	11	0
34	35	1013	0	1147	19	0
35	36	831	0	916	7	0
36	37	706	0	737	3	0
37	38	569	0	637	10	0
38	39	447	0	480	6	0
39	40	429	0	469	6	0
40	42	852	0	924	13	0
41	ff	708	0	756	10	0
42	gg	991	0	1044	13	0
43	s	1508	0	1564	27	0
44	t	1161	0	1218	32	0
45	EB	2932	0	2967	40	0
46	u	1655	0	1760	37	0
47	Q	1515	0	1634	25	0
48	ES	1444	0	735	35	0
49	28	74767	0	37771	800	0
50	v	6409	0	6476	83	0
51	34	1	0	0	0	0
51	37	1	0	0	0	0
51	ff	1	0	0	0	0
52	v	28	0	12	0	0
All	All	147611	0	110482	1677	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 7.

The worst 5 of 1677 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)
41:ff:42:CYS:HB3	41:ff:60:CYS:SG	1.85	1.17
49:28:2007:G:H21	49:28:2012:A:N6	1.47	1.13
49:28:2007:G:N2	49:28:2012:A:H62	1.48	1.10
49:28:4421:C:H42	49:28:4475:G:N2	1.59	0.99
49:28:4421:C:N4	49:28:4475:G:H22	1.64	0.95

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	
3	L8	246/345 (71%)	236 (96%)	10 (4%)	0	100	100
4	L3	392/394 (100%)	383 (98%)	9 (2%)	0	100	100
5	L4	360/362 (99%)	350 (97%)	10 (3%)	0	100	100
6	L5	291/293 (99%)	275 (94%)	14 (5%)	2 (1%)	18	35
7	L6	208/347 (60%)	200 (96%)	8 (4%)	0	100	100
8	L7	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
9	aa	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
10	L9	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
11	10	201/213 (94%)	196 (98%)	5 (2%)	0	100	100
12	11	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
13	13	208/210 (99%)	199 (96%)	8 (4%)	1 (0%)	24	42
14	14	136/138 (99%)	134 (98%)	2 (2%)	0	100	100
15	15	201/203 (99%)	192 (96%)	8 (4%)	1 (0%)	24	42
16	bb	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
17	17	151/153 (99%)	149 (99%)	2 (1%)	0	100	100
18	19	157/180 (87%)	155 (99%)	2 (1%)	0	100	100
19	20	174/192 (91%)	169 (97%)	5 (3%)	0	100	100
20	21	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
21	22	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
22	23	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
23	24	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
24	cc	116/118 (98%)	113 (97%)	3 (3%)	0	100	100
25	26	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
26	27	133/135 (98%)	127 (96%)	6 (4%)	0	100	100
27	dd	145/147 (99%)	135 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	29	100/245 (41%)	96 (96%)	4 (4%)	0	100	100
29	30	96/98 (98%)	96 (100%)	0	0	100	100
30	31	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
31	32	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
32	ee	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
33	34	112/114 (98%)	112 (100%)	0	0	100	100
34	35	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
35	36	100/102 (98%)	96 (96%)	4 (4%)	0	100	100
36	37	84/86 (98%)	84 (100%)	0	0	100	100
37	38	67/69 (97%)	67 (100%)	0	0	100	100
38	39	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
39	40	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
40	42	102/104 (98%)	97 (95%)	5 (5%)	0	100	100
41	ff	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
42	gg	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
43	s	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
44	t	151/153 (99%)	135 (89%)	16 (11%)	0	100	100
45	EB	373/375 (100%)	364 (98%)	9 (2%)	0	100	100
46	u	204/206 (99%)	189 (93%)	15 (7%)	0	100	100
47	Q	185/188 (98%)	180 (97%)	5 (3%)	0	100	100
50	v	816/857 (95%)	800 (98%)	14 (2%)	2 (0%)	43	62
All	All	8051/8616 (93%)	7800 (97%)	245 (3%)	6 (0%)	49	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	15	77	LYS
50	v	738	PRO
50	v	739	ARG
13	13	64	VAL
6	L5	36	LEU

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	
3	L8	190/263 (72%)	182 (96%)	8 (4%)	26	51
4	L3	342/342 (100%)	330 (96%)	12 (4%)	32	57
5	L4	302/302 (100%)	296 (98%)	6 (2%)	48	71
6	L5	247/247 (100%)	241 (98%)	6 (2%)	43	67
7	L6	190/302 (63%)	184 (97%)	6 (3%)	34	59
8	L7	196/196 (100%)	188 (96%)	8 (4%)	27	52
9	aa	200/205 (98%)	192 (96%)	8 (4%)	28	53
10	L9	169/169 (100%)	163 (96%)	6 (4%)	31	56
11	10	175/180 (97%)	173 (99%)	2 (1%)	65	81
12	11	143/143 (100%)	139 (97%)	4 (3%)	38	62
13	13	175/175 (100%)	168 (96%)	7 (4%)	28	53
14	14	117/117 (100%)	114 (97%)	3 (3%)	40	65
15	15	171/171 (100%)	164 (96%)	7 (4%)	27	52
16	bb	171/171 (100%)	162 (95%)	9 (5%)	20	42
17	17	134/134 (100%)	131 (98%)	3 (2%)	45	69
18	19	141/159 (89%)	139 (99%)	2 (1%)	59	78
19	20	157/173 (91%)	153 (98%)	4 (2%)	42	66
20	21	139/139 (100%)	136 (98%)	3 (2%)	45	69
21	22	89/89 (100%)	87 (98%)	2 (2%)	45	69
22	23	101/101 (100%)	97 (96%)	4 (4%)	28	53
23	24	55/55 (100%)	54 (98%)	1 (2%)	51	73
24	cc	106/106 (100%)	104 (98%)	2 (2%)	50	72
25	26	124/124 (100%)	118 (95%)	6 (5%)	23	46
26	27	117/117 (100%)	110 (94%)	7 (6%)	17	36
27	dd	119/119 (100%)	118 (99%)	1 (1%)	73	86
28	29	84/184 (46%)	81 (96%)	3 (4%)	31	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	30	84/84 (100%)	83 (99%)	1 (1%)	63	80
30	31	98/98 (100%)	96 (98%)	2 (2%)	48	71
31	32	114/114 (100%)	112 (98%)	2 (2%)	51	73
32	ee	88/88 (100%)	83 (94%)	5 (6%)	18	39
33	34	98/98 (100%)	95 (97%)	3 (3%)	35	60
34	35	109/109 (100%)	107 (98%)	2 (2%)	51	73
35	36	86/86 (100%)	81 (94%)	5 (6%)	18	38
36	37	73/73 (100%)	71 (97%)	2 (3%)	39	63
37	38	64/64 (100%)	61 (95%)	3 (5%)	23	47
38	39	47/47 (100%)	47 (100%)	0	100	100
39	40	48/48 (100%)	47 (98%)	1 (2%)	47	70
40	42	92/92 (100%)	91 (99%)	1 (1%)	65	81
41	ff	74/74 (100%)	72 (97%)	2 (3%)	39	63
42	gg	107/108 (99%)	102 (95%)	5 (5%)	23	47
43	s	164/164 (100%)	147 (90%)	17 (10%)	7	14
44	t	126/126 (100%)	117 (93%)	9 (7%)	13	28
45	EB	321/321 (100%)	304 (95%)	17 (5%)	20	42
46	u	186/186 (100%)	177 (95%)	9 (5%)	23	46
47	Q	164/165 (99%)	159 (97%)	5 (3%)	36	61
50	v	701/730 (96%)	667 (95%)	34 (5%)	22	45
All	All	6998/7358 (95%)	6743 (96%)	255 (4%)	32	56

5 of 255 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	26	79	VAL
50	v	2	VAL
34	35	91	MET
47	Q	168	ARG
50	v	402	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 124 such sidechains are listed below:

Mol	Chain	Res	Type
19	20	156	HIS
46	u	184	HIS
25	26	127	GLN
46	u	158	GLN
50	v	291	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	58	149/156 (95%)	31 (20%)	1 (0%)
2	5	119/120 (99%)	12 (10%)	0
48	ES	63/5070 (1%)	14 (22%)	1 (1%)
49	28	3460/4807 (71%)	720 (20%)	45 (1%)
All	All	3791/10153 (37%)	777 (20%)	47 (1%)

5 of 777 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	58	2	G
1	58	16	G
1	58	23	C
1	58	34	U
1	58	35	C

5 of 47 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	28	2266	C
49	28	3697	U
49	28	2502	A
49	28	2661	U
49	28	3888	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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
52	GDP	v	900	-	29,30,30	3.59	13 (44%)	45,47,47	2.17	13 (28%)

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
52	GDP	v	900	-	-	4/16/32/32	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	v	900	GDP	O6-C6	9.62	1.41	1.23
52	v	900	GDP	C2'-C3'	-8.47	1.30	1.53
52	v	900	GDP	O4'-C4'	-7.09	1.29	1.45
52	v	900	GDP	O4'-C1'	6.08	1.56	1.42
52	v	900	GDP	C2-N2	4.88	1.45	1.34

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	v	900	GDP	C5-C4-N3	-6.93	117.36	128.39
52	v	900	GDP	C2-N3-C4	5.86	122.39	112.30
52	v	900	GDP	N9-C4-N3	4.90	135.74	125.95
52	v	900	GDP	C2'-C3'-C4'	4.31	110.93	102.61
52	v	900	GDP	C8-N7-C5	3.28	110.10	104.26

There are no chirality outliers.

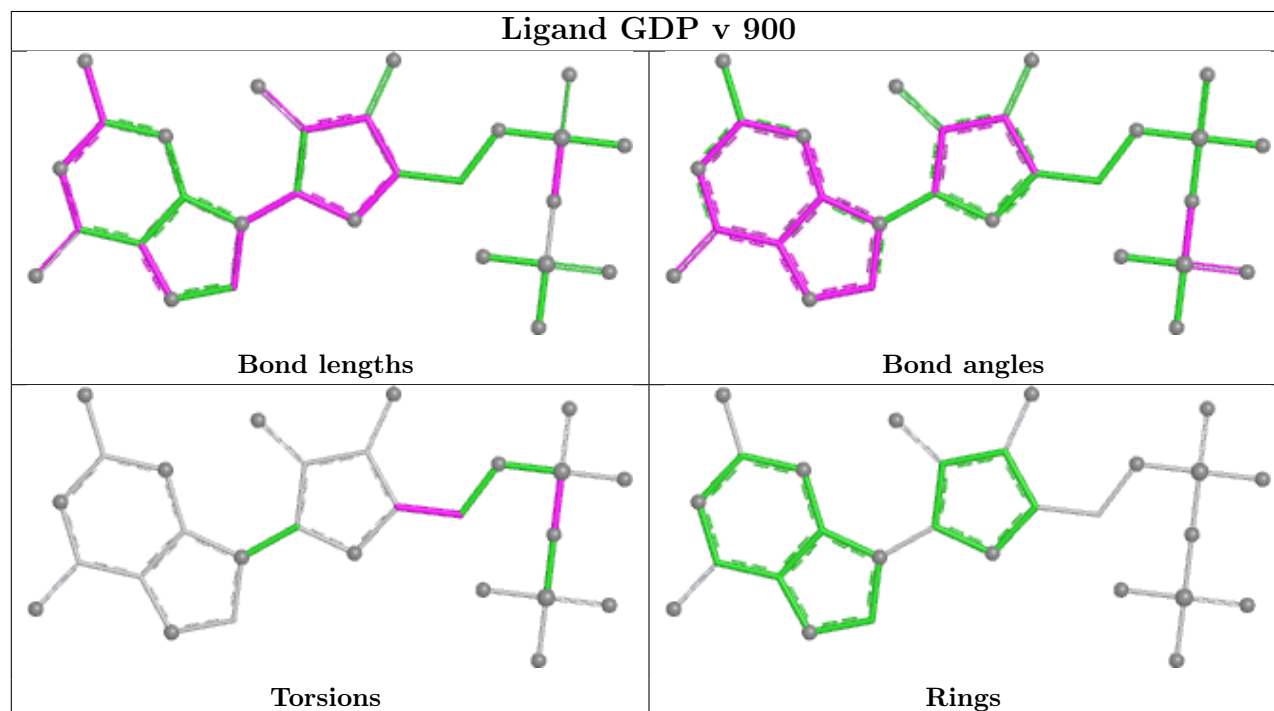
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
52	v	900	GDP	C3'-C4'-C5'-O5'
52	v	900	GDP	O4'-C4'-C5'-O5'
52	v	900	GDP	PB-O3A-PA-O2A
52	v	900	GDP	PB-O3A-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
49	28	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	28	3944:G	O3'	3945:A	P	4.51
1	28	2025:A	O3'	2026:A	P	3.18

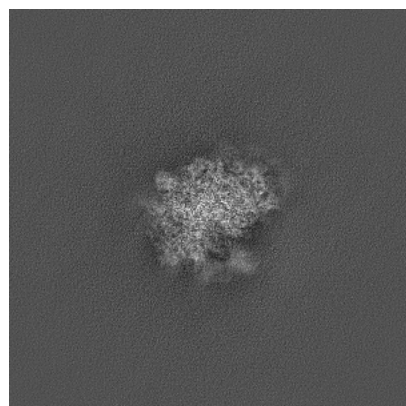
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75687. These allow visual inspection of the internal detail of the map and identification of artifacts.

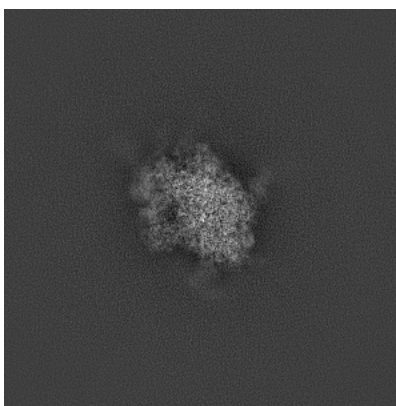
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

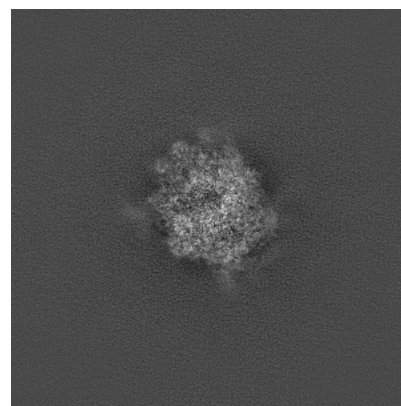
6.1.1 Primary map



X

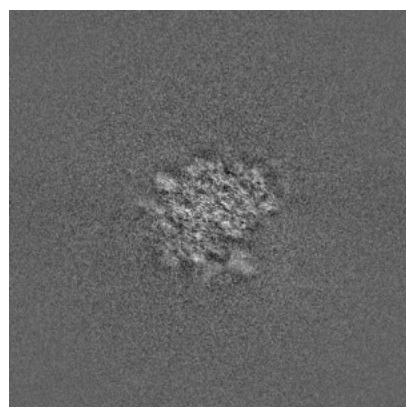


Y

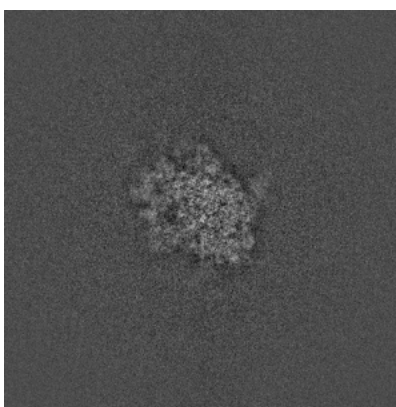


Z

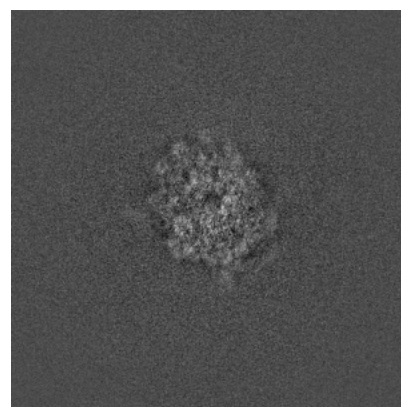
6.1.2 Raw map



X



Y

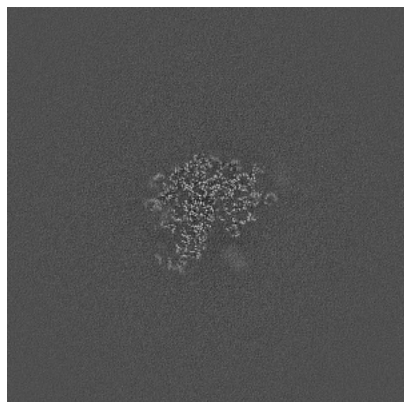


Z

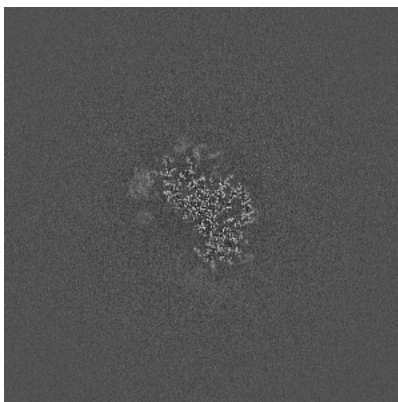
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

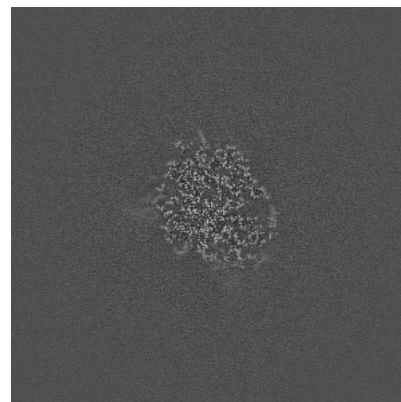
6.2.1 Primary map



X Index: 400

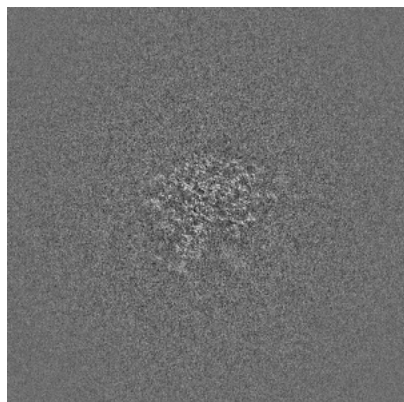


Y Index: 400

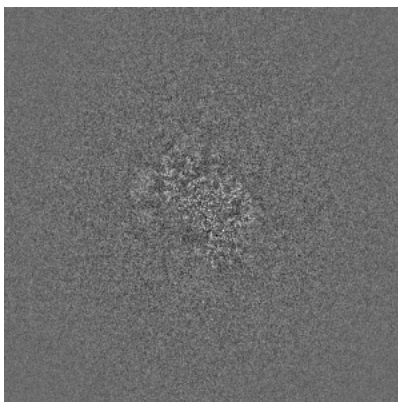


Z Index: 400

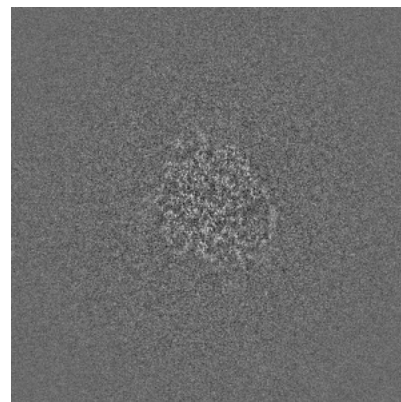
6.2.2 Raw map



X Index: 400



Y Index: 400

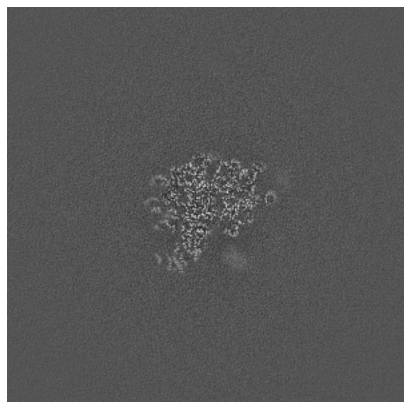


Z Index: 400

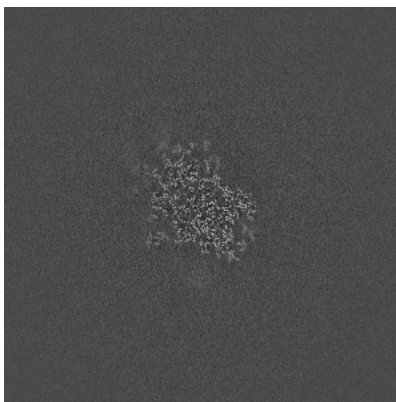
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

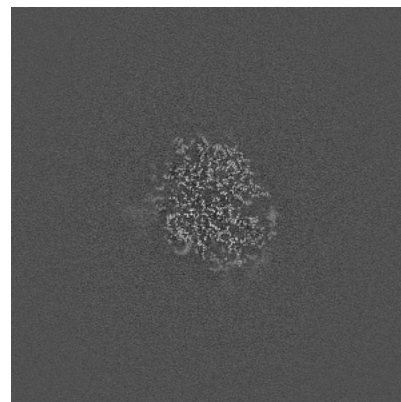
6.3.1 Primary map



X Index: 397

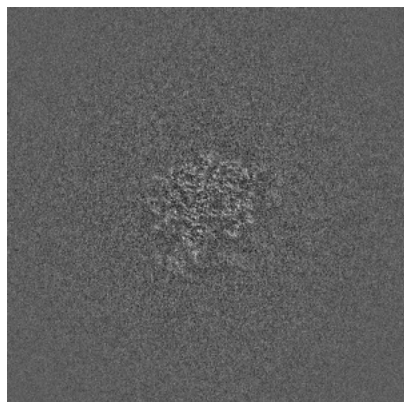


Y Index: 380

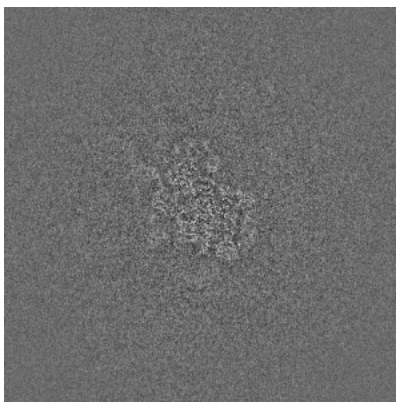


Z Index: 403

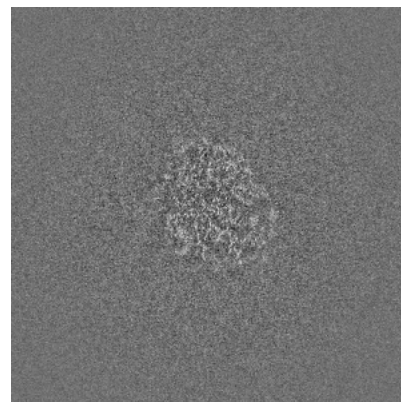
6.3.2 Raw map



X Index: 396



Y Index: 384

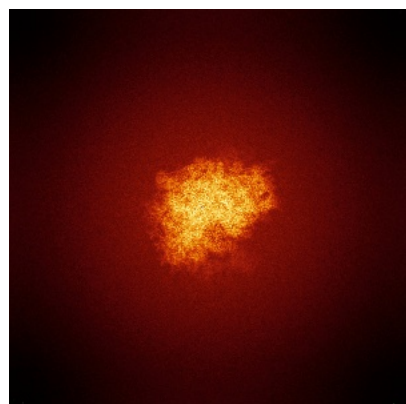


Z Index: 403

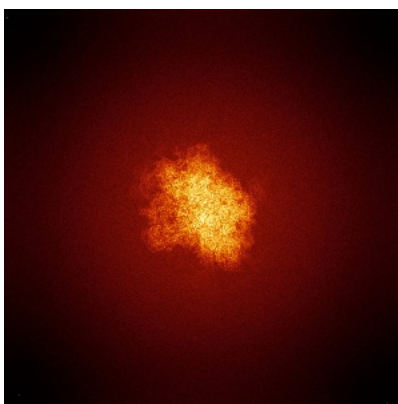
The images above show the largest variance slices of the map in three orthogonal directions.

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

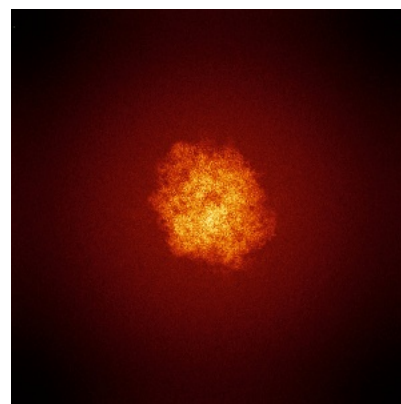
6.4.1 Primary map



X

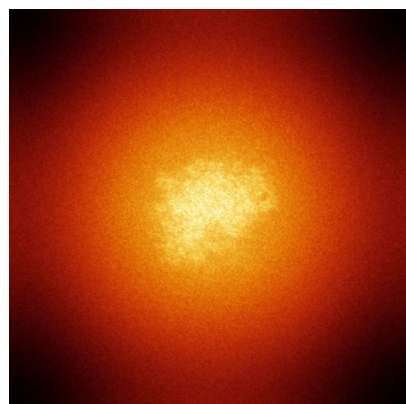


Y

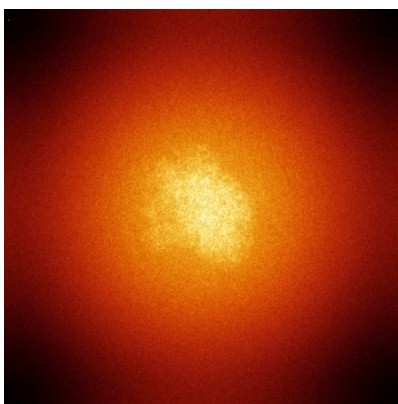


Z

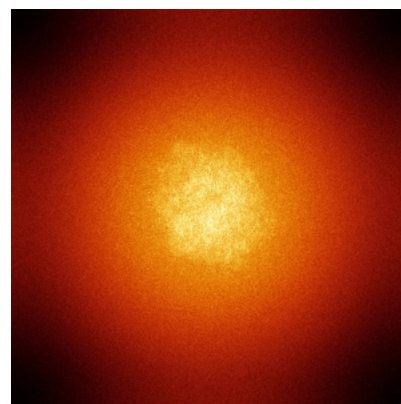
6.4.2 Raw map



X



Y

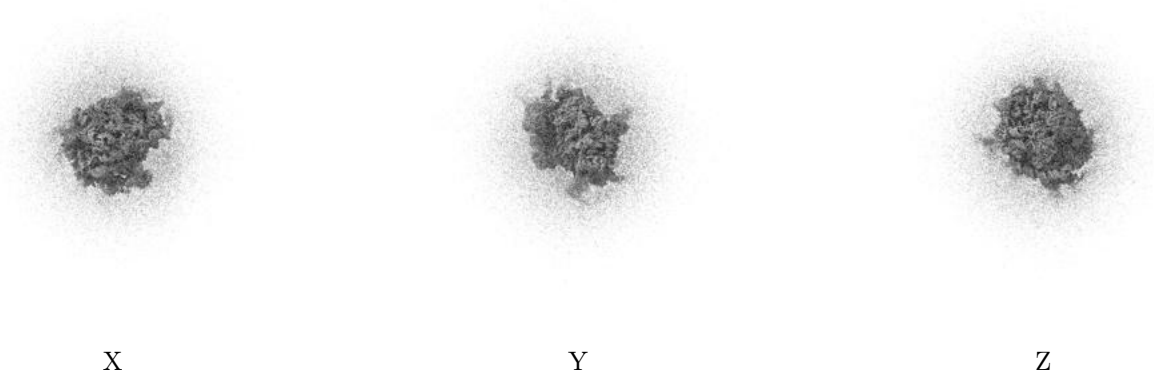


Z

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

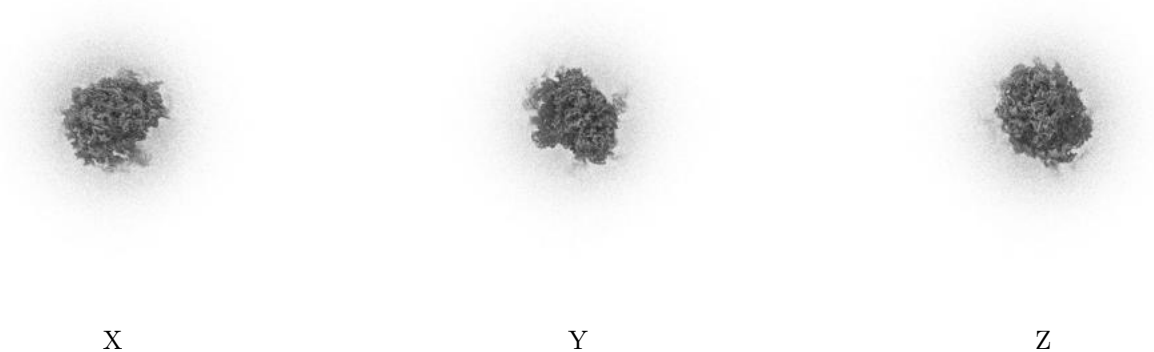
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.8. 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



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.

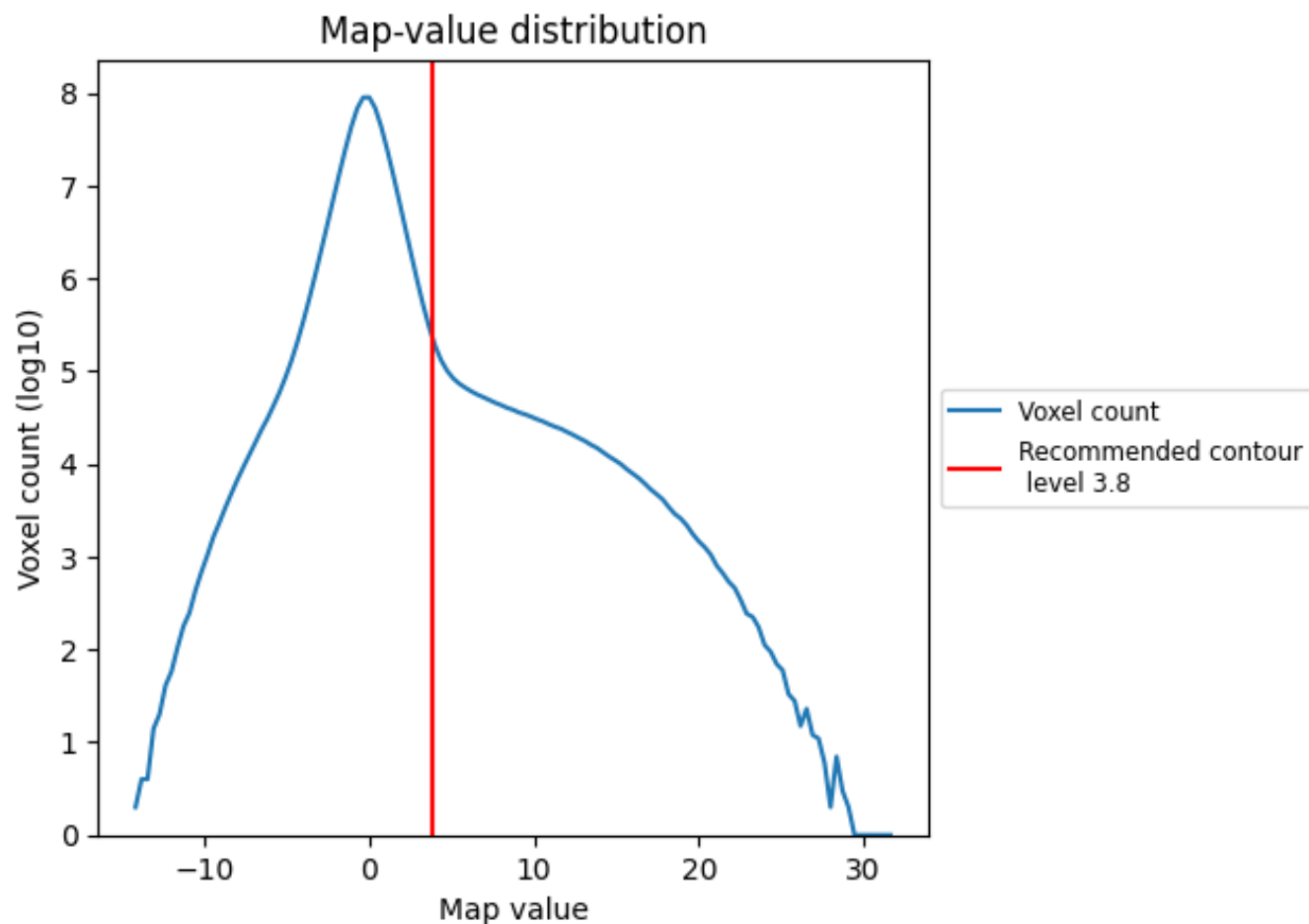
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

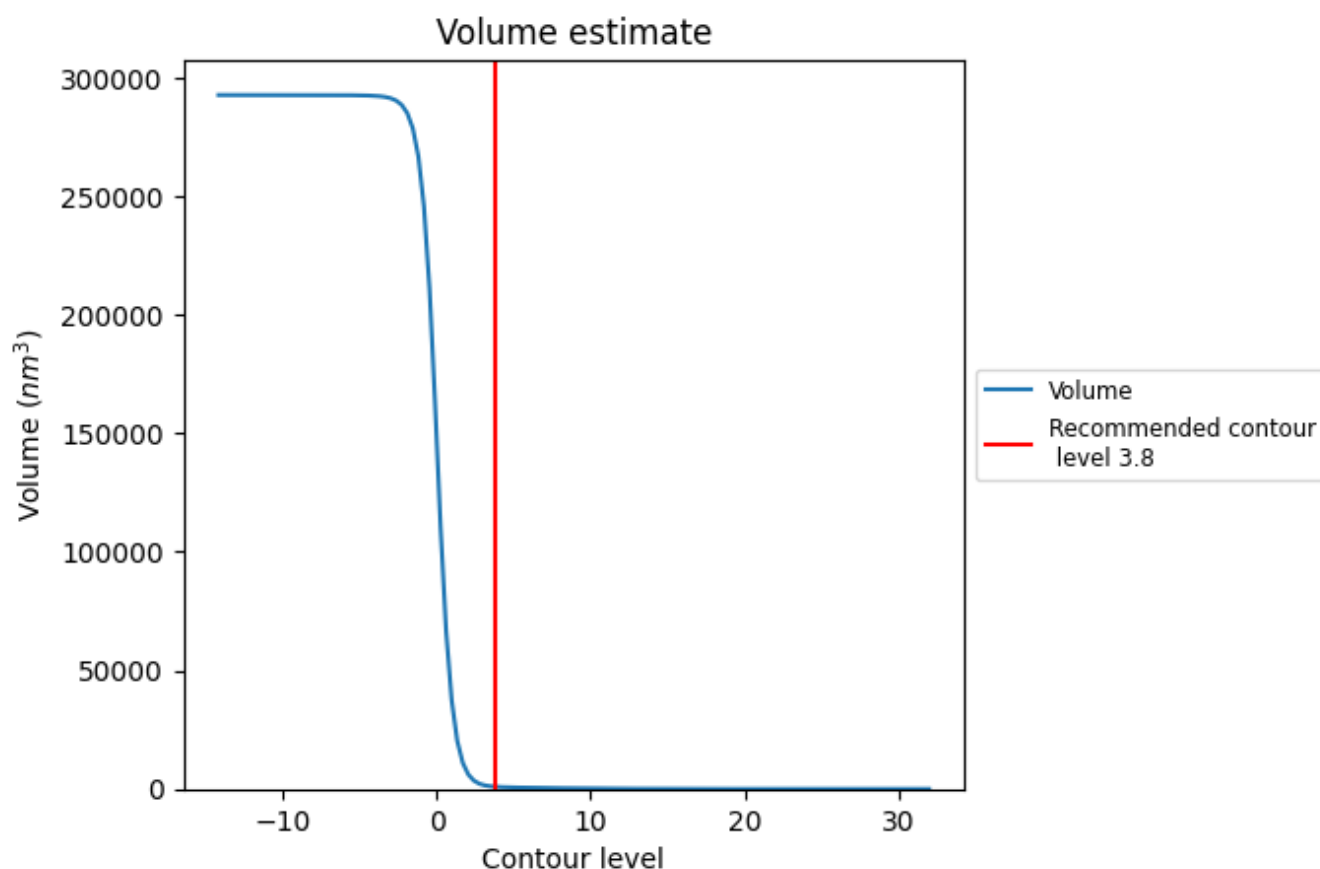
This section contains the results of statistical analysis of the map.

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.

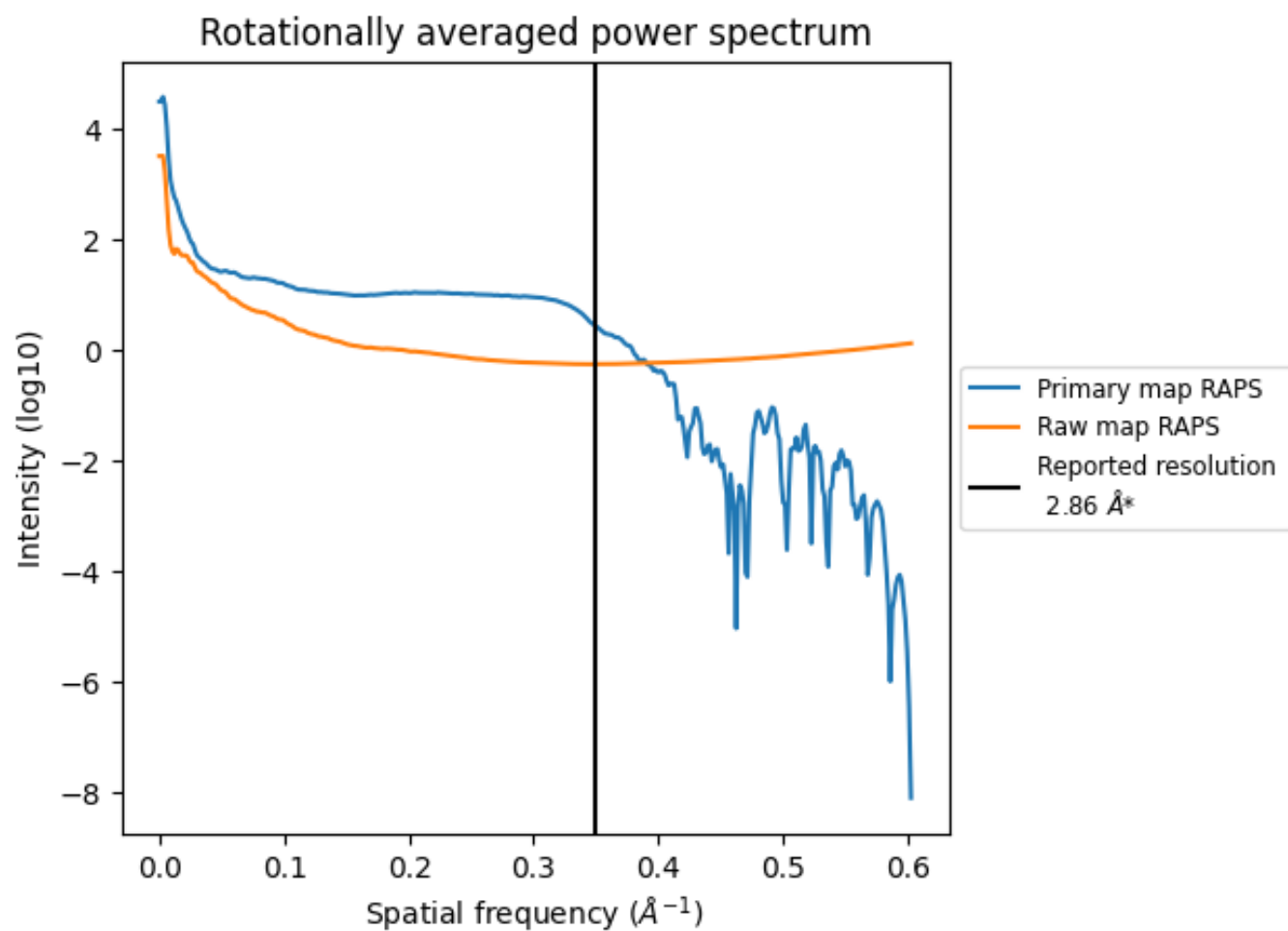
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 940 nm³; this corresponds to an approximate mass of 849 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 ⓘ

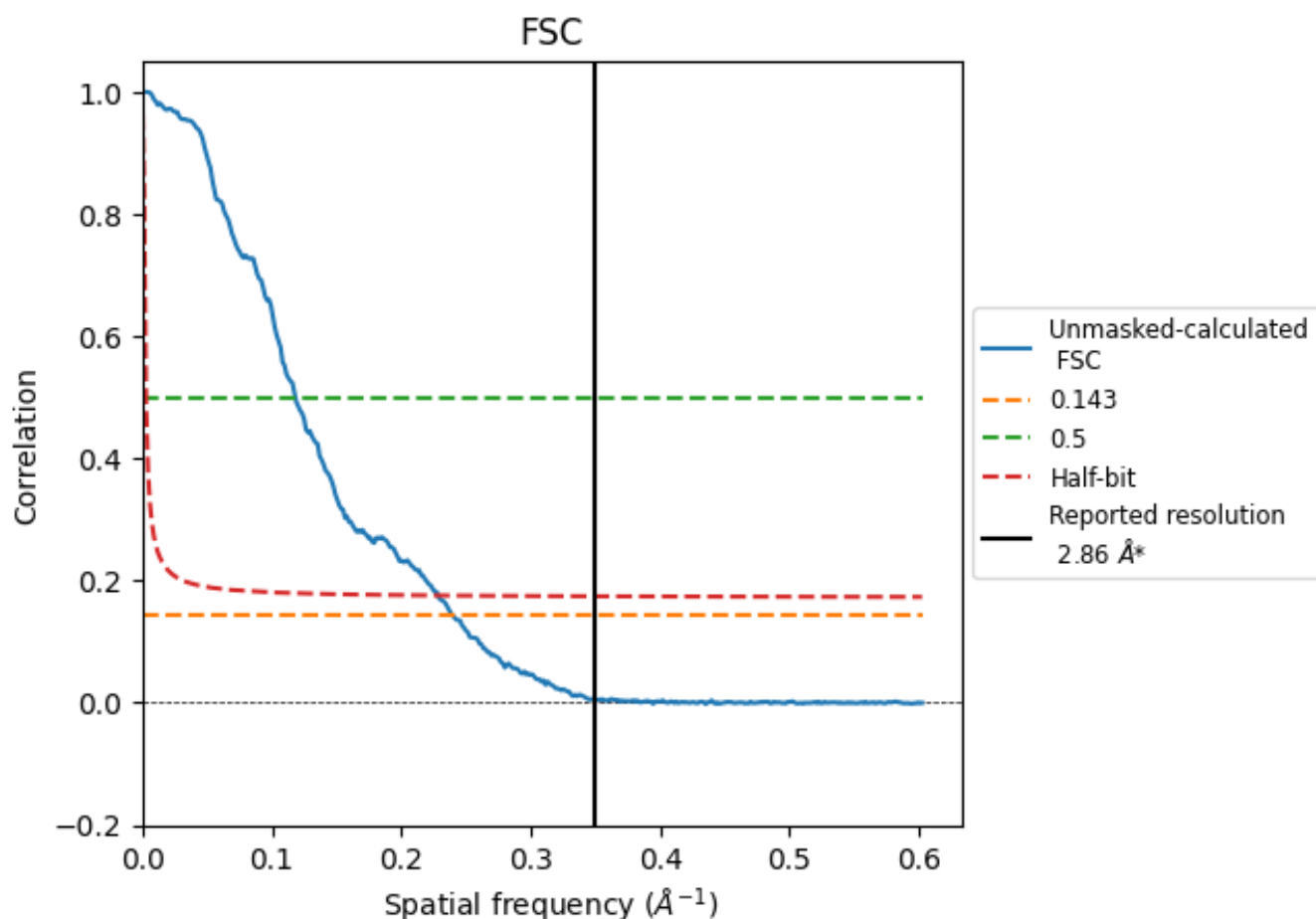


*Reported resolution corresponds to spatial frequency of 0.350 Å⁻¹

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 0.350 Å⁻¹

8.2 Resolution estimates [i](#)

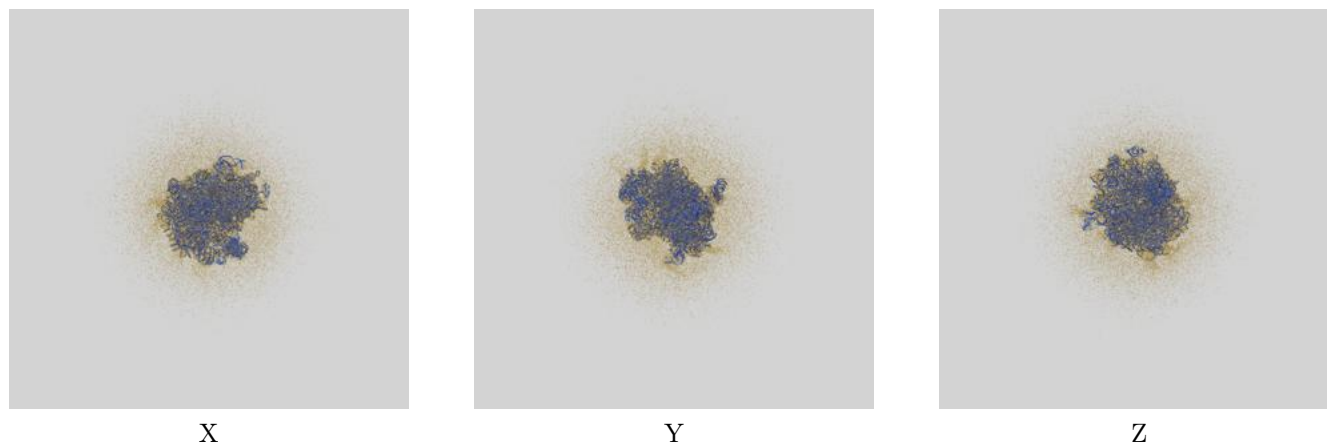
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.86	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.18	8.45	4.38

*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 4.18 differs from the reported value 2.86 by more than 10 %

9 Map-model fit [i](#)

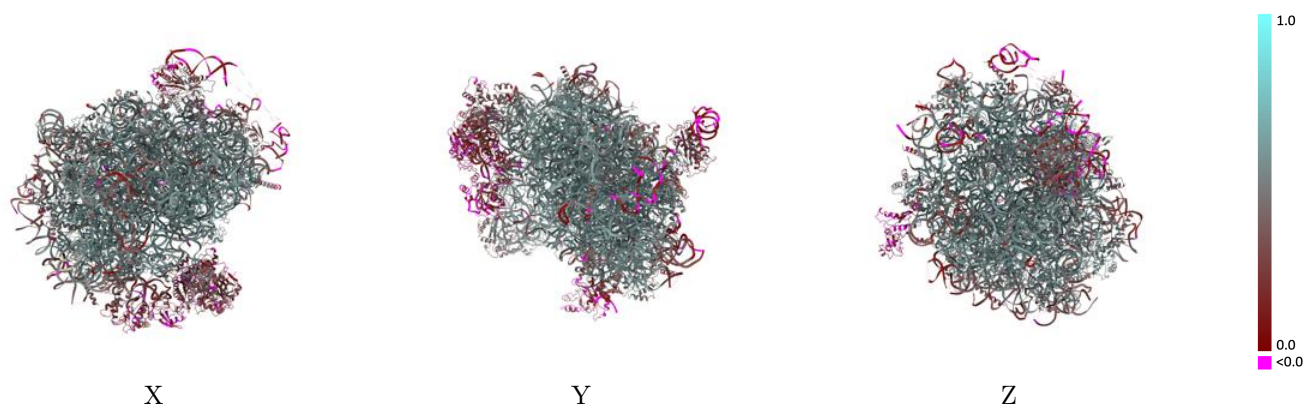
This section contains information regarding the fit between EMDB map EMD-75687 and PDB model 11HE. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



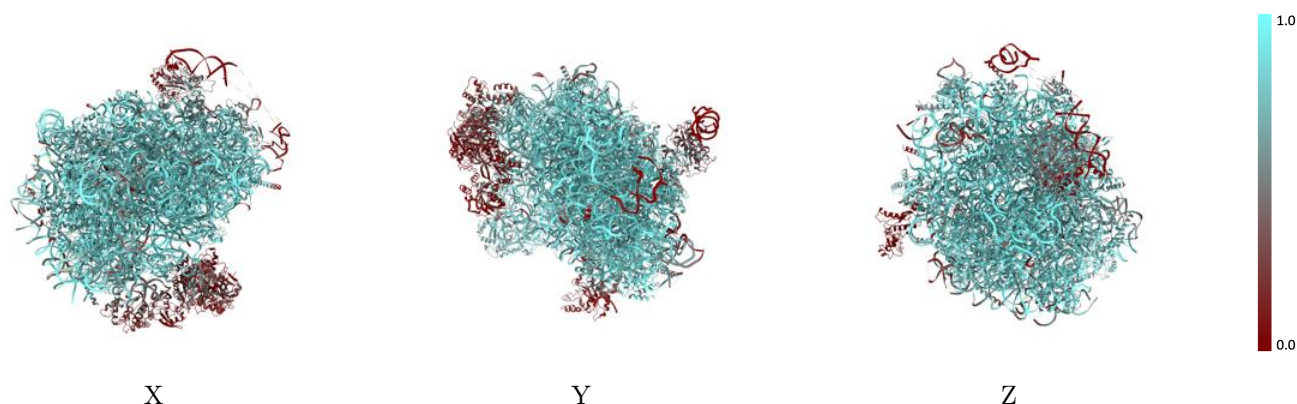
The images above show the 3D surface view of the map at the recommended contour level 3.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



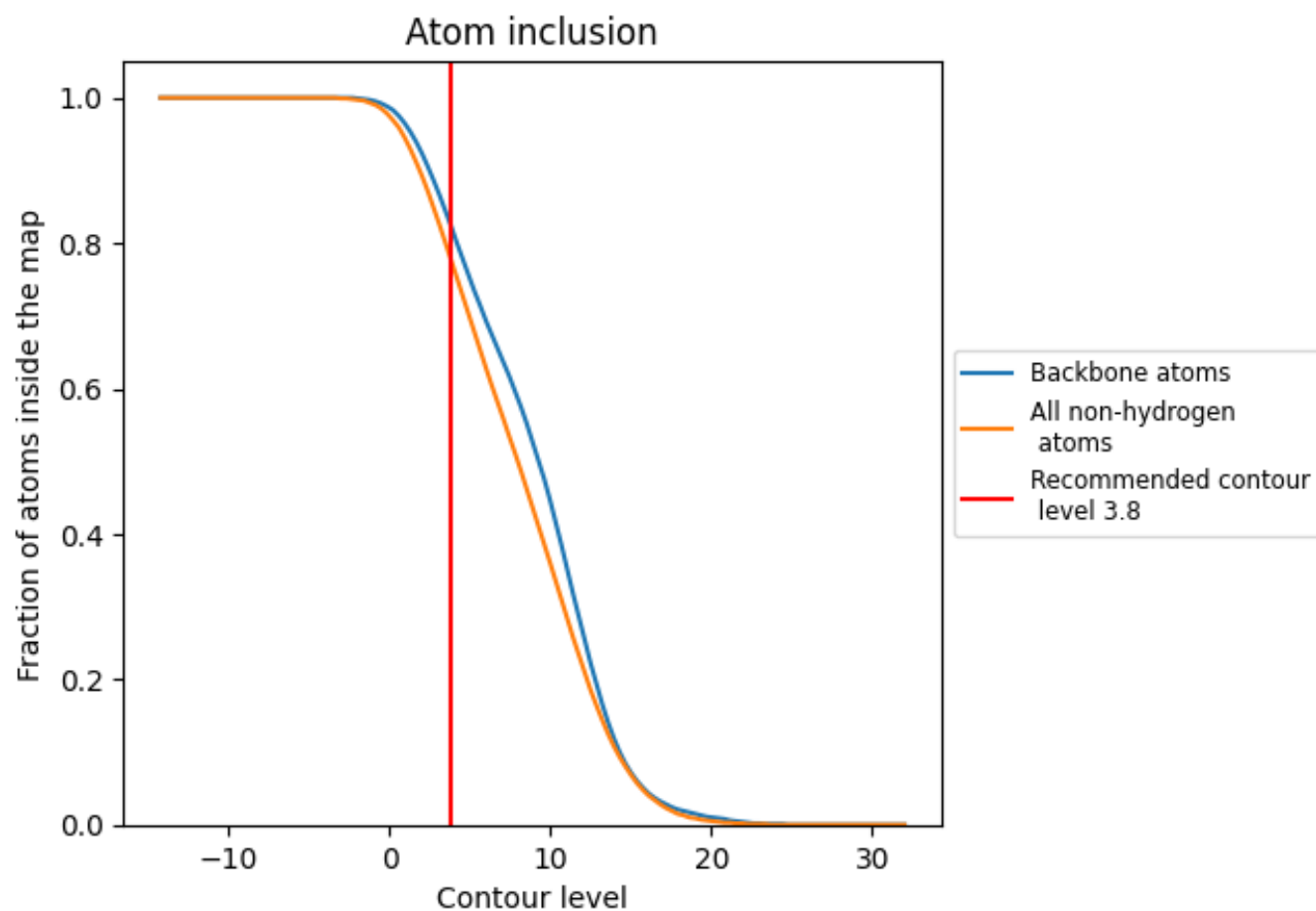
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 78% 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 (3.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7800	 0.4910
10	 0.8120	 0.5290
11	 0.6750	 0.4140
13	 0.8000	 0.5200
14	 0.8330	 0.5300
15	 0.8860	 0.5860
17	 0.8530	 0.5620
19	 0.7660	 0.5020
20	 0.8570	 0.5590
21	 0.8020	 0.5310
22	 0.6170	 0.3860
23	 0.8190	 0.5540
24	 0.8080	 0.5360
26	 0.8250	 0.5310
27	 0.7880	 0.5120
28	 0.8670	 0.5200
29	 0.6660	 0.4380
30	 0.7030	 0.4640
31	 0.7870	 0.5160
32	 0.8570	 0.5760
34	 0.8040	 0.5470
35	 0.7810	 0.5200
36	 0.7950	 0.5090
37	 0.8740	 0.5750
38	 0.6710	 0.4450
39	 0.8240	 0.5500
40	 0.7810	 0.5100
42	 0.8090	 0.5250
5	 0.9250	 0.5650
58	 0.8840	 0.5410
EB	 0.3820	 0.2900
ES	 0.0310	 0.0430
L3	 0.8390	 0.5540
L4	 0.8440	 0.5550
L5	 0.7840	 0.5010



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Chain	Atom inclusion	Q-score
L6	 0.7990	 0.5120
L7	 0.8560	 0.5660
L8	 0.8540	 0.5700
L9	 0.7600	 0.5110
Q	 0.8690	 0.5710
aa	 0.7340	 0.4710
bb	 0.8540	 0.5640
cc	 0.8080	 0.5330
dd	 0.8720	 0.5770
ee	 0.8790	 0.5800
ff	 0.8100	 0.5390
gg	 0.8600	 0.5640
s	 0.2790	 0.2310
t	 0.0760	 0.0790
u	 0.0310	 0.0530
v	 0.2000	 0.2160