



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:19 AM UTC

PDB ID : 7QEP / pdb_00007qep
EMDB ID : EMD-13936
Title : Cryo-EM structure of the ribosome from Encephalitozoon cuniculi
Authors : Nicholson, D.; Ranson, N.A.; Melnikov, S.V.
Deposited on : 2021-12-03
Resolution : 2.70 Å (reported)
Based on initial models : 4V88, 6RM3

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:

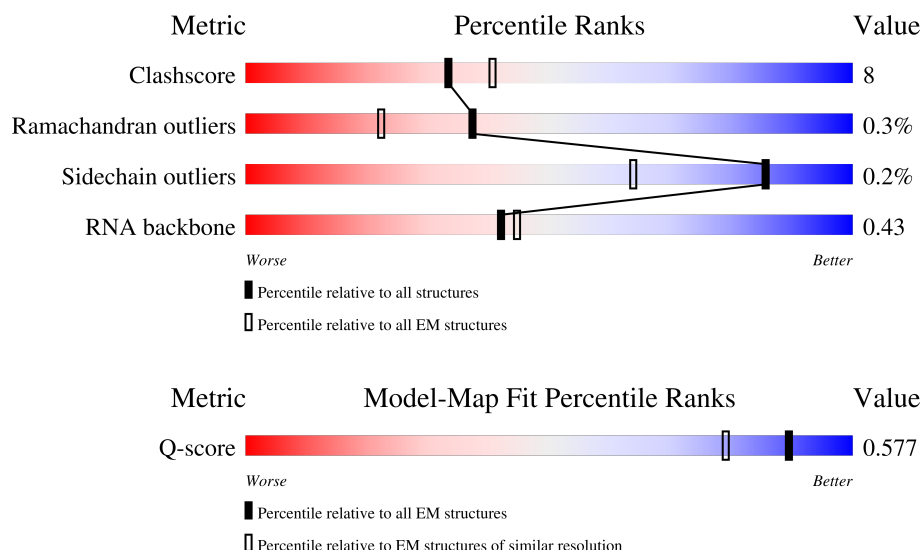
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 2.70 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	10327 (2.20 - 3.20)

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	RA	334	97% 54% 43% .
2	1	2486	69% 20% 7% .
3	2	119	74% 22% .

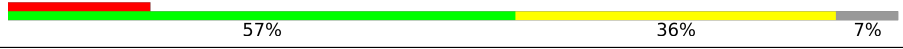
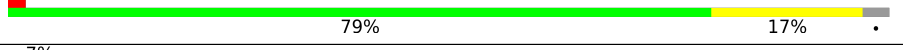
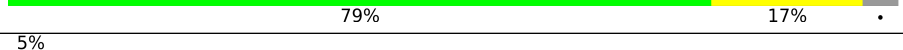
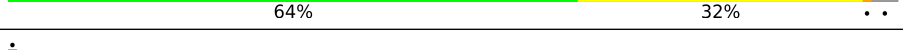
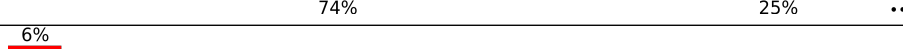
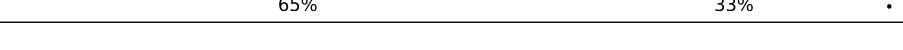
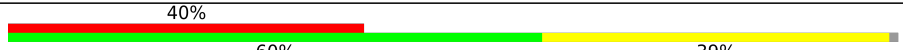
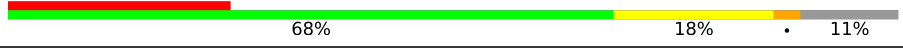
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Mol	Chain	Length	Quality of chain
4	3	1300	
5	C0	96	
6	C1	156	
7	C2	134	
8	C3	148	
9	C4	134	
10	C5	148	
11	C6	145	
12	C7	120	
13	C8	153	
14	C9	137	
15	D0	120	
16	D1	70	
17	D2	128	
18	D3	140	
19	D4	131	
20	D5	109	
21	D6	105	
22	D7	85	
23	D8	65	
24	D9	66	
25	E1	152	
26	L1	219	
27	L2	239	
28	L3	383	

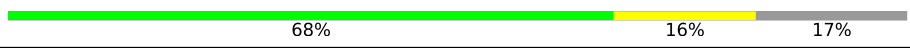
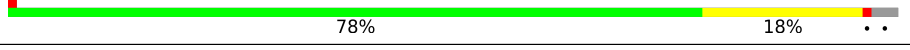
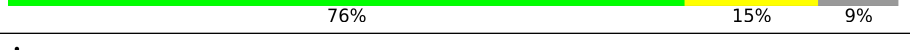
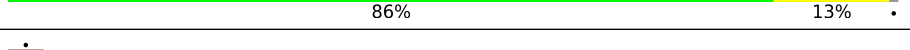
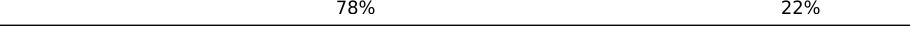
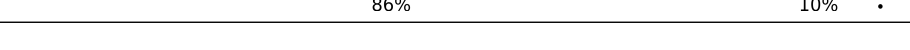
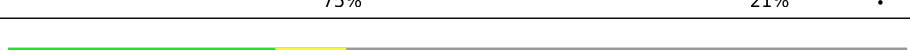
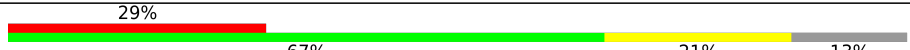
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Mol	Chain	Length	Quality of chain
29	L4	335	
30	L5	287	
31	L6	171	
32	L7	239	
33	L8	206	
34	L9	183	
35	M0	219	
36	M1	173	
37	M3	163	
38	M4	106	
39	M5	204	
40	M6	198	
41	M7	183	
42	M8	200	
43	M9	171	
44	MD	171	
45	MS	73	
46	N0	188	
47	N1	160	
48	N2	112	
49	N3	146	
50	N4	100	
51	N5	105	
52	N6	143	
53	N7	126	

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Mol	Chain	Length	Quality of chain
54	N8	147	
55	N9	57	
56	O0	108	
57	O1	111	
58	O2	139	
59	O3	113	
60	O4	110	
61	O5	122	
62	O6	94	
63	O7	90	
64	O9	52	
65	P0	131	
66	P2	104	
67	P3	89	
68	S0	252	
69	S1	239	
70	S2	242	
71	S3	216	
72	S4	268	
73	S5	189	
74	S6	217	
75	S7	170	
76	S8	173	
77	S9	184	

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 166143 atoms, of which 31 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 Guanine nucleotide binding protein beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	RA	328	Total	C	N	O	S	0	0
			2537	1594	427	502	14		

- Molecule 2 is a RNA chain called 5.8S-23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2319	Total	C	N	O	P	0	0
			49833	22195	9045	16274	2319		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 13560063

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	119	Total	C	N	O	P	0	0
			2550	1138	469	824	119		

- Molecule 4 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	1295	Total	C	N	O	P	0	0
			27838	12399	5052	9092	1295		

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C0	81	Total	C	N	O	S	0	0
			686	449	122	112	3		

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C1	141	Total	C	N	O	S	0	0
			1126	718	206	194	8		

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C2	118	Total	C	N	O	S	0	0
			879	548	154	166	11		

- Molecule 8 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C3	146	Total	C	N	O	S	0	0
			1166	736	221	205	4		

- Molecule 9 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C4	126	Total	C	N	O	S	0	0
			942	583	192	163	4		

- Molecule 10 is a protein called RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	C5	116	Total	C	N	O	S	0	0
			903	576	167	154	6		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C6	141	Total	C	N	O	S	0	0
			1132	727	202	197	6		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C7	117	Total	C	N	O	S	0	0
			962	611	166	180	5		

- Molecule 13 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C8	141	Total	C	N	O	S	0	0
			1121	692	220	203	6		

- Molecule 14 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	C9	135	Total	C	N	O	S	0	0
			1089	690	187	206	6		

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	D0	93	Total	C	N	O	S	0	0
			779	498	137	140	4		

- Molecule 16 is a protein called ECU11_0225 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	D1	68	Total	C	N	O	S	0	0
			518	323	89	103	3		

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN S15A (S22 in yeast).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	D2	127	Total	C	N	O	S	0	0
			1012	639	190	176	7		

- Molecule 18 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	D3	137	Total	C	N	O	S	0	0
			1052	669	196	185	2		

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	D4	127	Total	C	N	O	S	0	0
			1056	668	199	186	3		

- Molecule 20 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	D5	87	Total	C	N	O	S	0	0
			691	424	141	123	3		

- Molecule 21 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	D6	101	Total	C	N	O	S	0	0
			801	494	161	139	7		

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	D7	82	Total	C	N	O	S	0	0
			633	391	117	117	8		

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	D8	57	Total	C	N	O	S	0	0
			446	278	84	81	3		

- Molecule 24 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	D9	65	Total	C	N	O	S	0	0
			524	334	96	88	6		

- Molecule 25 is a protein called Similarity to monoubiquitin/carboxy-extension protein fusion.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	E1	58	Total	C	N	O	0	0
			276	168	58	50		

- Molecule 26 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	L1	206	Total	C	N	O	0	0
			1016	604	206	206		

- Molecule 27 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L2	232	Total	C	N	O	S	0	0
			1759	1098	328	324	9		

- Molecule 28 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	L3	363	Total	C	N	O	S	0	0
			2827	1781	539	491	16		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L4	329	Total	C	N	O	S	0	0
			2596	1621	488	474	13		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	L5	283	Total	C	N	O	S	0	0
			2273	1421	425	420	7		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	L6	159	Total	C	N	O	S	0	0
			1279	811	220	241	7		

- Molecule 32 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	L7	231	Total	C	N	O	S	0	0
			1903	1203	352	337	11		

- Molecule 33 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	L8	197	Total	C	N	O	S	0	0
			1573	1015	269	282	7		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L9	182	Total	C	N	O	S	1	0
			1443	909	265	260	9		

- Molecule 35 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M0	211	Total	C	N	O	S	0	0
			1706	1079	329	291	7		

- Molecule 36 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M1	167	Total	C	N	O	S	0	0
			1336	845	247	237	7		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	M3	161	Total	C	N	O	S	0	0
			1308	825	253	225	5		

- Molecule 38 is a protein called ECU06_1215 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M4	104	Total	C	N	O	S	0	0
			848	537	150	160	1		

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M5	203	Total	C	N	O	S	0	0
			1657	1031	335	279	12		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L13A (L16).

Mol	Chain	Residues	Atoms					AltConf	Trace
40	M6	196	Total	C	N	O	S	0	0
			1577	1001	291	276	9		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	M7	174	Total	C	N	O	S	0	0
			1363	861	263	234	5		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	M8	186	Total	C	N	O	S	0	0
			1470	929	266	266	9		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M9	170	Total	C	N	O	S	0	0
			1398	864	285	238	11		

- Molecule 44 is a protein called Uncharacterized protein ECU01_0250.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	MD	170	Total	C	N	O	S	0	0
			1349	848	230	260	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
MD	59	GLY	SER	variant	UNP Q8SWQ4

- Molecule 45 is a protein called ECU06_1135 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	MS	68	Total	C	N	O	S	0	0
			592	372	121	97	2		

- Molecule 46 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	N0	178	Total	C	N	O	S	0	0
			1438	929	249	254	6		

- Molecule 47 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	N1	159	Total	C	N	O	S	0	0
			1288	812	249	220	7		

- Molecule 48 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	N2	93	Total	C	N	O	S	0	0
			735	477	130	125	3		

- Molecule 49 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	N3	135	Total	C	N	O	S	0	0
			1058	666	206	179	7		

- Molecule 50 is a protein called Similarity to 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N4	89	Total	C	N	O	S	0	0
			709	443	136	126	4		

- Molecule 51 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	N5	93	Total	C	N	O	S	0	0
			720	460	123	134	3		

- Molecule 52 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N6	142	Total	C	N	O	S	0	0
			1171	730	230	208	3		

- Molecule 53 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	N7	118	Total	C	N	O	S	0	0
			938	617	162	154	5		

- Molecule 54 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	N8	146	Total	C	N	O	S	0	0
			1196	763	232	198	3		

- Molecule 55 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	N9	55	Total	C	N	O	S	0	0
			437	272	90	74	1		

- Molecule 56 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	O0	90	Total	C	N	O	S	0	0
			692	442	122	124	4		

- Molecule 57 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	O1	108	Total	C	N	O	S	0	0
			879	559	164	153	3		

- Molecule 58 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	O2	128	Total	C	N	O	S	0	0
			1062	674	215	169	4		

- Molecule 59 is a protein called 60S RIBOSOMAL PROTEIN L35A (L33).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	O3	109	Total	C	N	O	S	0	0
			861	543	166	149	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O4	100	Total	C	N	O	S	0	0
			807	493	177	131	6		

- Molecule 61 is a protein called 60S ribosomal protein L35-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O5	121	Total	C	N	O	S	0	0
			981	609	201	170	1		

- Molecule 62 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	O6	94	Total	C	N	O	S	0	0
			735	461	147	125	2		

- Molecule 63 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	O7	86	Total	C	N	O	S	0	0
			691	416	152	115	8		

- Molecule 64 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	O9	50	Total	C	N	O	S	0	0
			434	271	97	63	3		

- Molecule 65 is a protein called UBIQUITIN/ L40 RIBOSOMAL PROTEIN FUSION.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	P0	49	Total	C	N	O	S	0	0
			381	230	75	68	8		

- Molecule 66 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	P2	97	Total	C	N	O	S	0	0
			788	492	167	125	4		

- Molecule 67 is a protein called 60S RIBOSOMAL PROTEIN L37A (L43).

Mol	Chain	Residues	Atoms					AltConf	Trace
67	P3	86	Total	C	N	O	S	0	0
			664	419	128	111	6		

- Molecule 68 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	S0	203	Total	C	N	O	S	0	0
			1584	1017	272	289	6		

- Molecule 69 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	S1	209	Total	C	N	O	S	0	0
			1670	1058	299	300	13		

- Molecule 70 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	S2	217	Total	C	N	O	S	0	0
			1636	1037	293	300	6		

- Molecule 71 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	S3	210	Total	C	N	O	S	0	0
			1658	1057	295	298	8		

- Molecule 72 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	S4	259	Total	C	N	O	S	0	0
			2045	1301	361	374	9		

- Molecule 73 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	S5	188	Total	C	N	O	S	0	0
			1461	905	282	269	5		

- Molecule 74 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S6	204	Total	C	N	O	S	0	0
			1680	1049	321	301	9		

- Molecule 75 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	S7	149	Total	C	N	O	S	0	0
			1173	745	212	208	8		

- Molecule 76 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S8	164	Total	C	N	O	S	0	0
			1300	812	255	230	3		

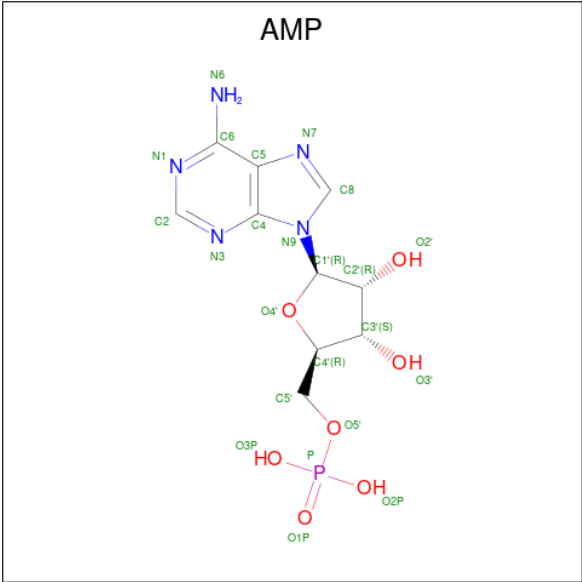
- Molecule 77 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	S9	171	Total	C	N	O	S	0	0
			1374	873	255	241	5		

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

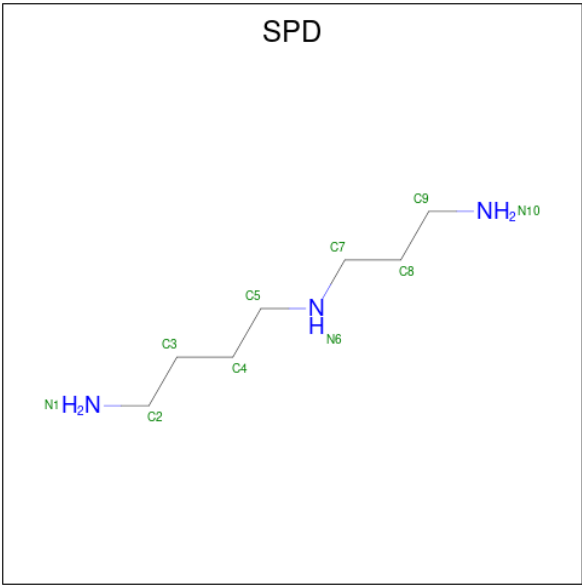
Mol	Chain	Residues	Atoms		AltConf
78	D6	1	Total	Zn	0
			1	1	
78	D7	1	Total	Zn	0
			1	1	
78	D9	1	Total	Zn	0
			1	1	
78	E1	1	Total	Zn	0
			1	1	
78	O7	1	Total	Zn	0
			1	1	
78	P0	1	Total	Zn	0
			1	1	
78	P2	1	Total	Zn	0
			1	1	
78	P3	1	Total	Zn	0
			1	1	

- Molecule 79 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
79	L9	1	Total	C	H	N	O	P	0
			35	10	12	5	7	1	

- Molecule 80 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).

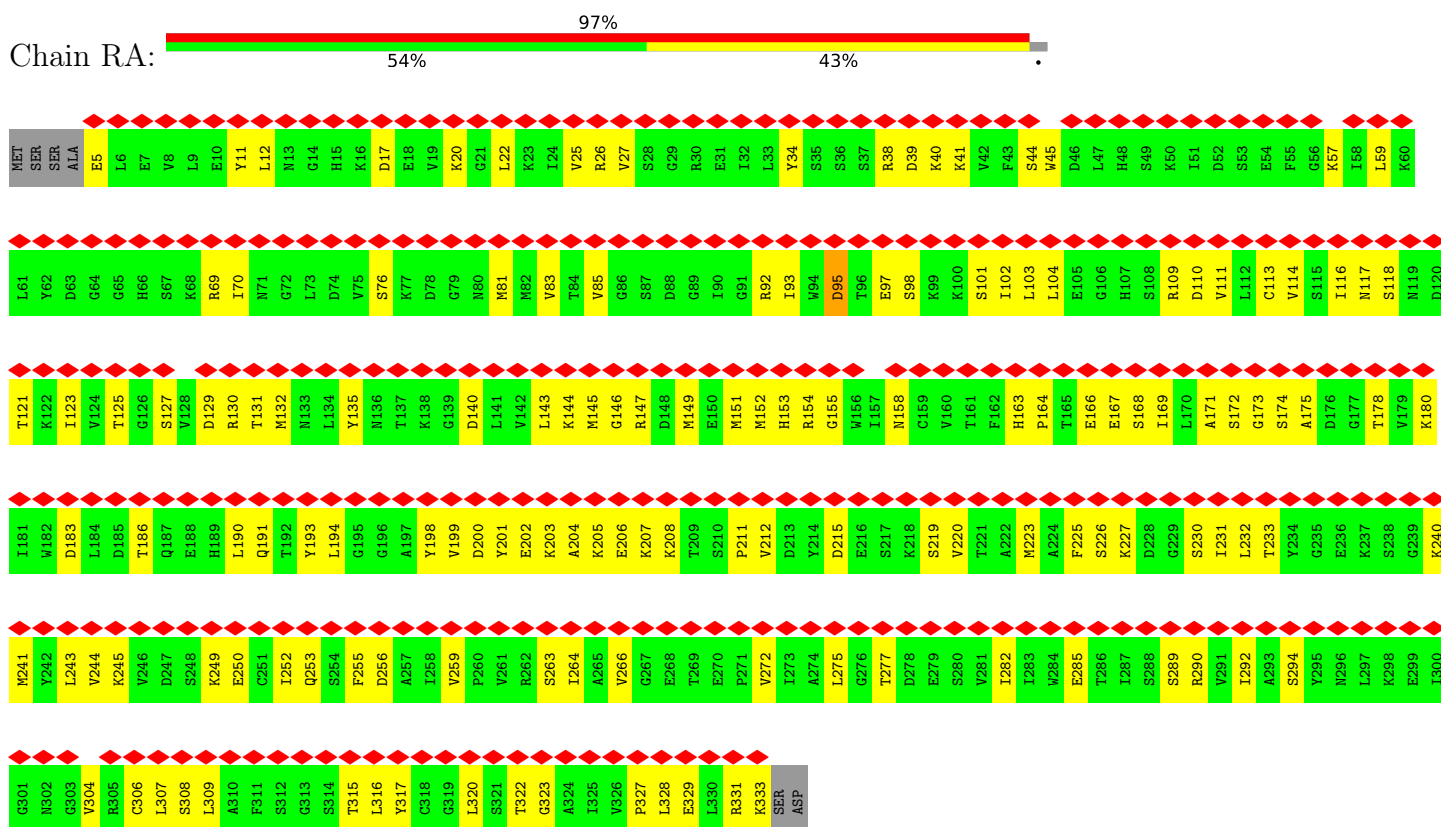


Mol	Chain	Residues	Atoms				AltConf
80	N8	1	Total	C	H	N	0
			29	7	19	3	

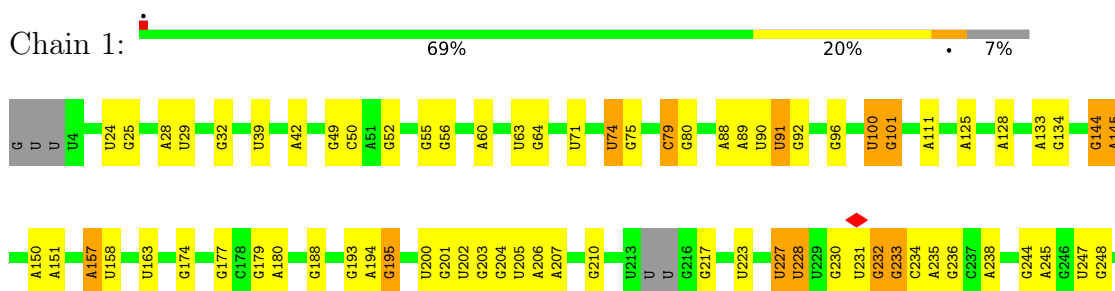
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

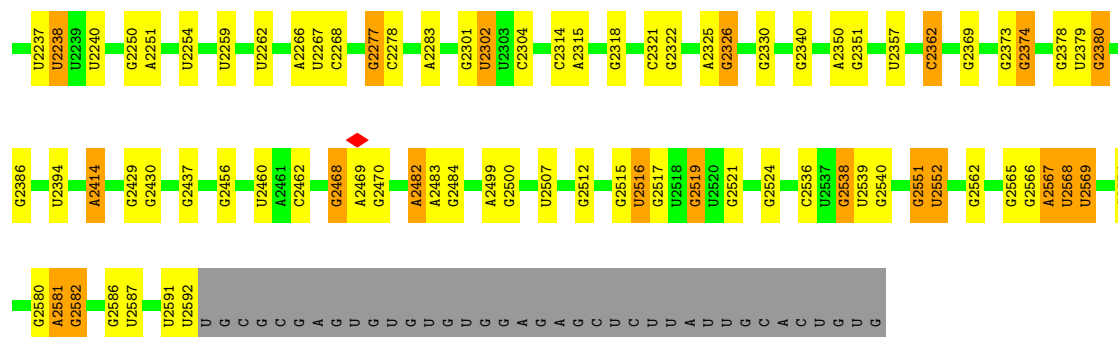
- Molecule 1: Guanine nucleotide binding protein beta subunit



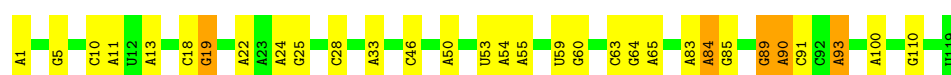
- Molecule 2: 5.8S-23S ribosomal RNA



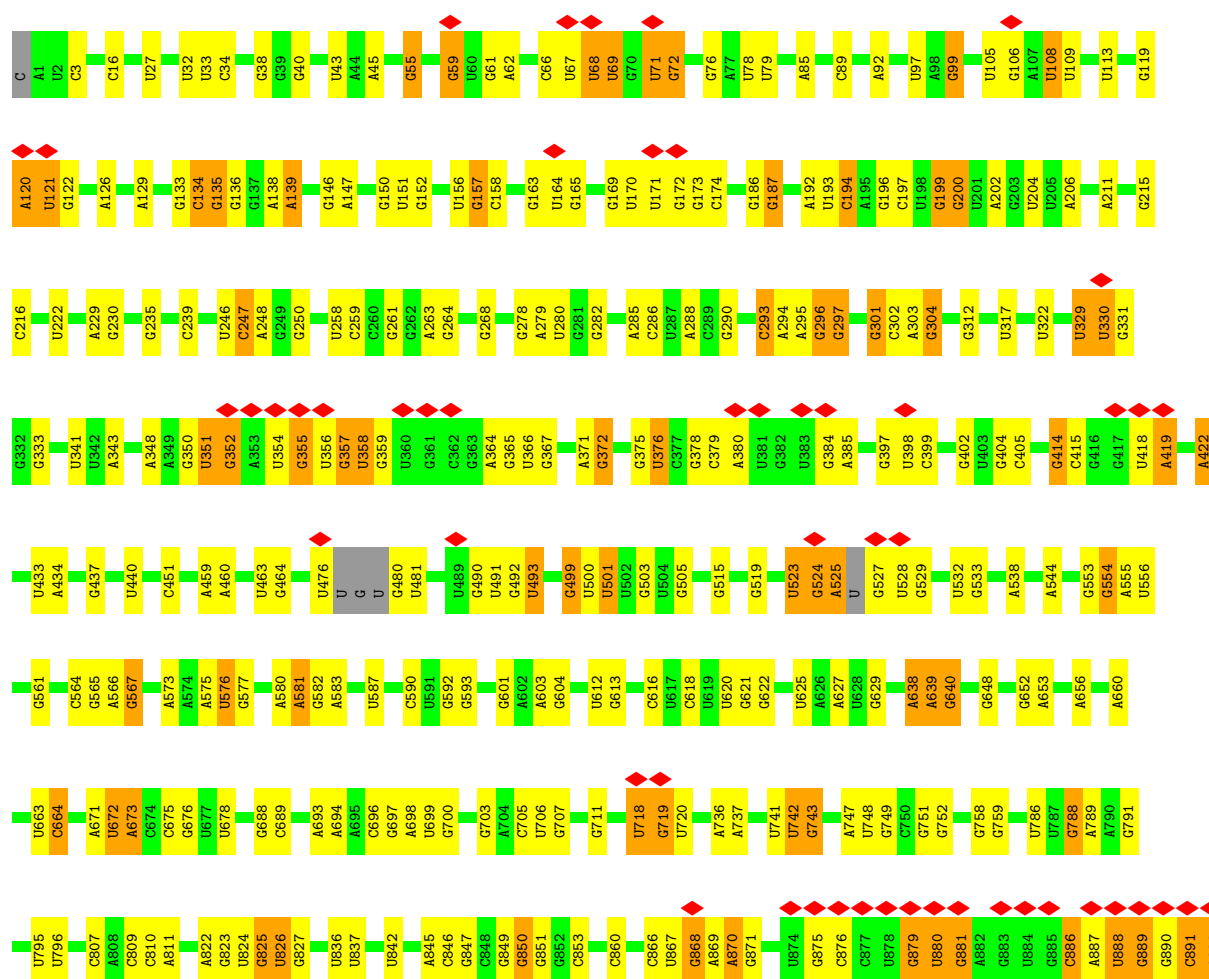


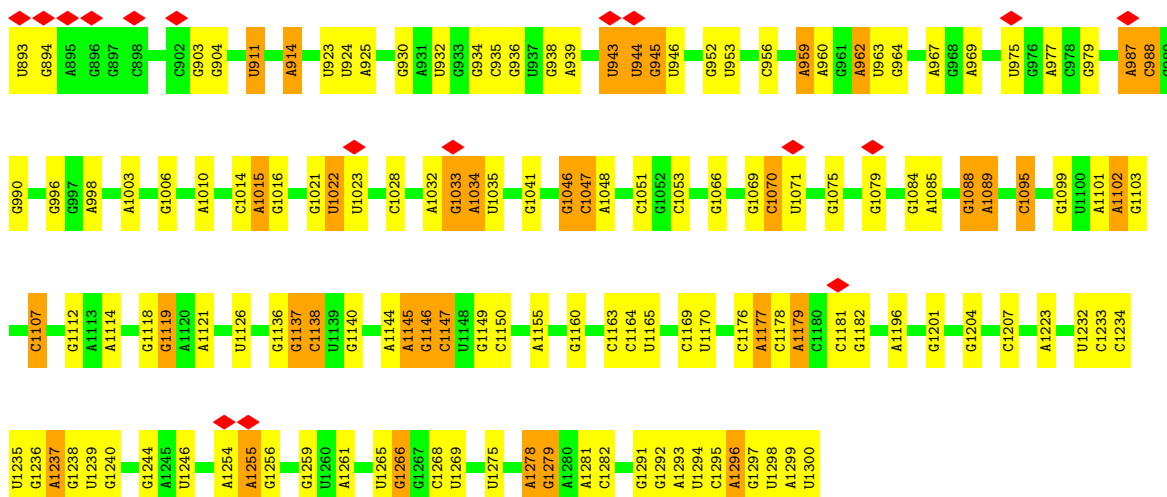


• Molecule 3: 5S ribosomal RNA

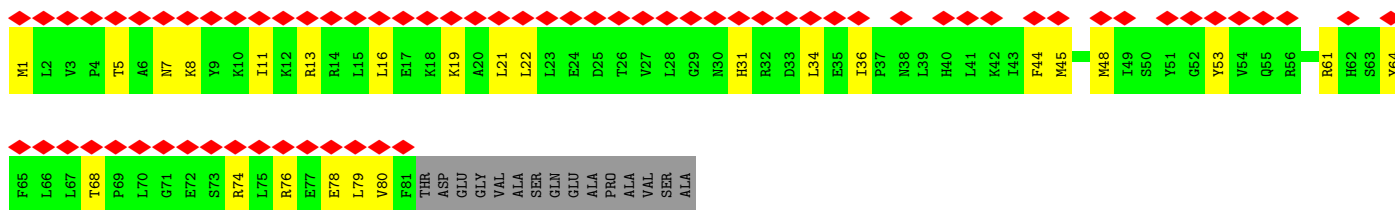
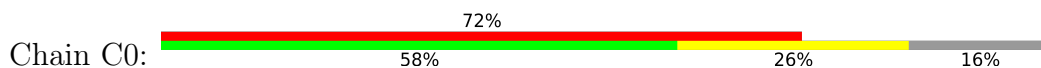


• Molecule 4: 18S ribosomal RNA

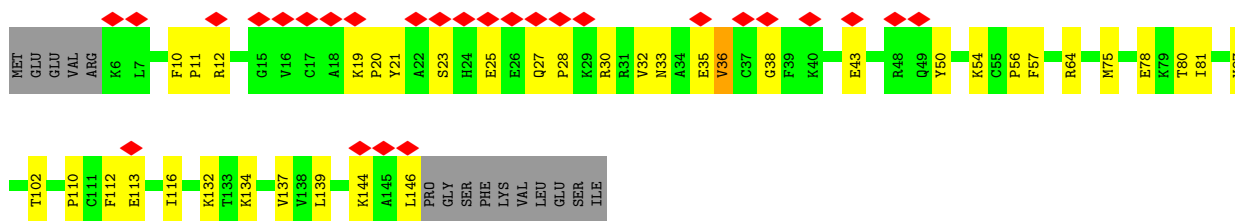




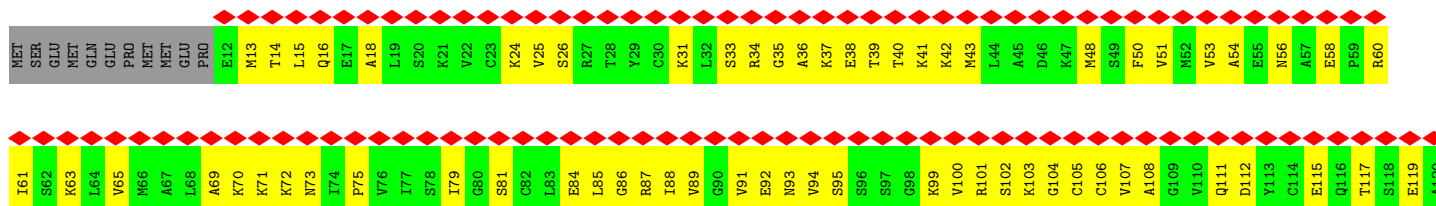
• Molecule 5: 40S RIBOSOMAL PROTEIN S10



• Molecule 6: 40S RIBOSOMAL PROTEIN S11

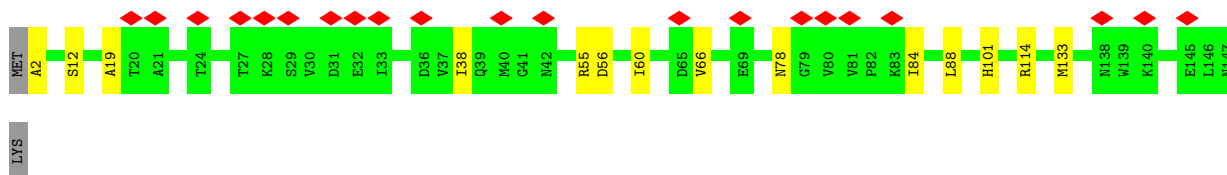
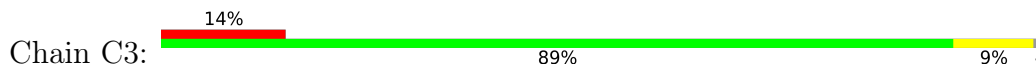


• Molecule 7: 40S RIBOSOMAL PROTEIN S12

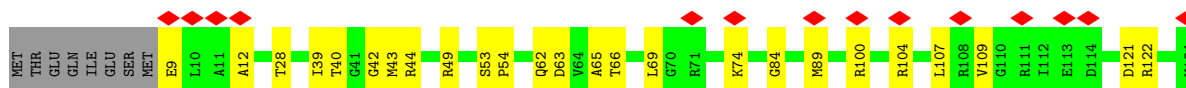
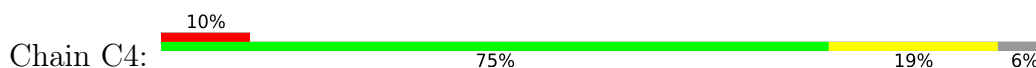




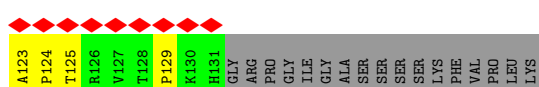
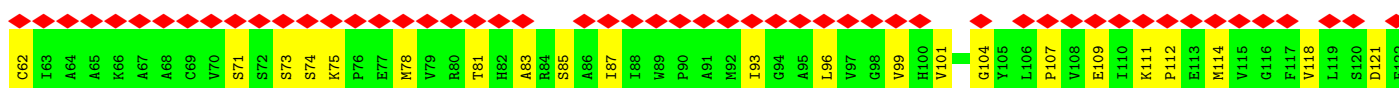
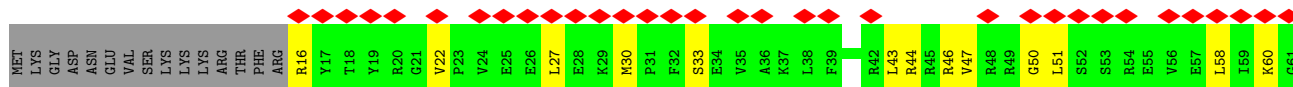
• Molecule 8: 40S ribosomal protein S13



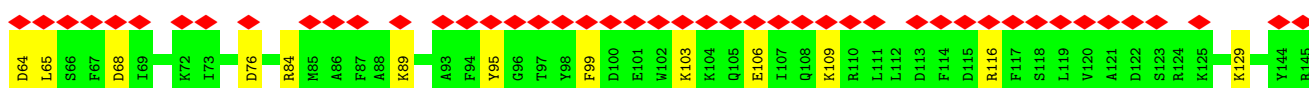
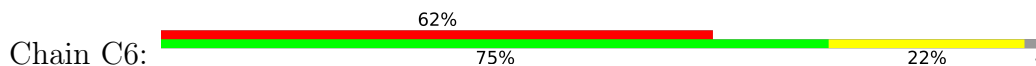
• Molecule 9: 40S ribosomal protein S14



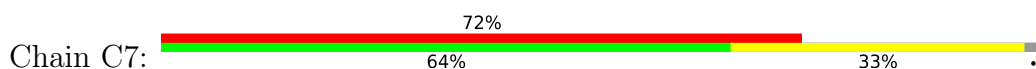
• Molecule 10: RIBOSOMAL PROTEIN S15

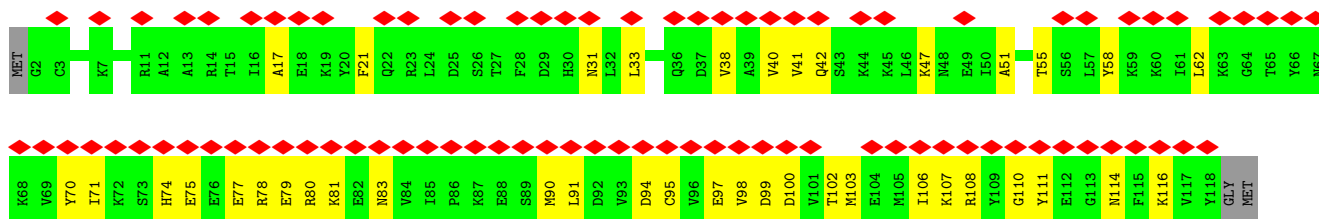


• Molecule 11: 40S RIBOSOMAL PROTEIN S16

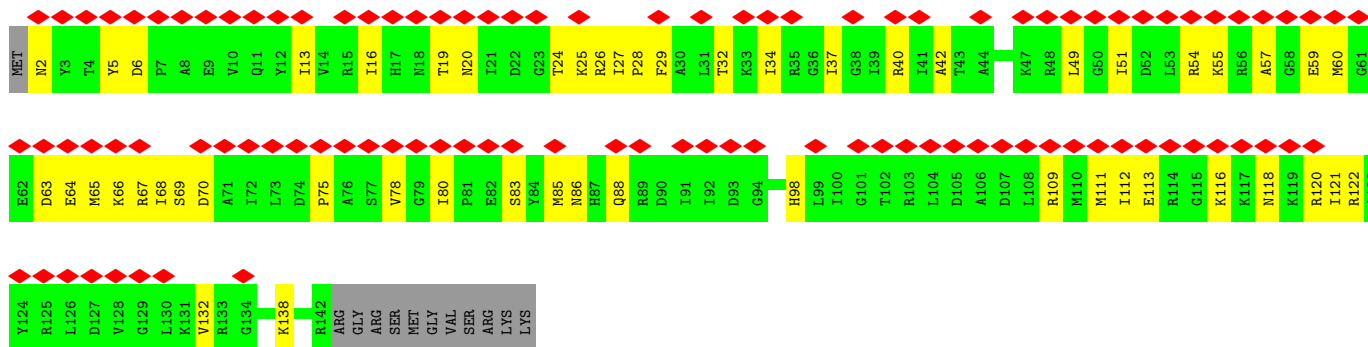


• Molecule 12: 40S ribosomal protein S17





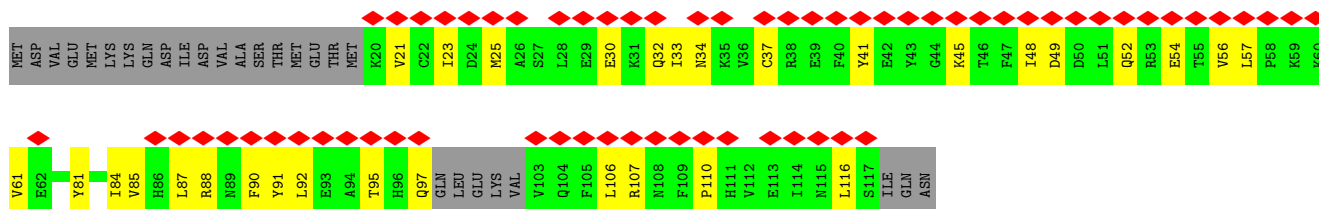
• Molecule 13: 40S ribosomal protein S18



• Molecule 14: 40S ribosomal protein S19

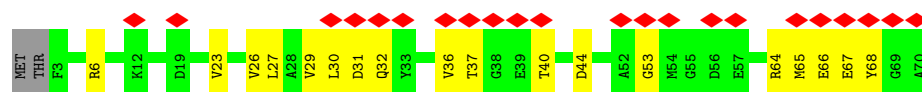


• Molecule 15: 40S RIBOSOMAL PROTEIN S20

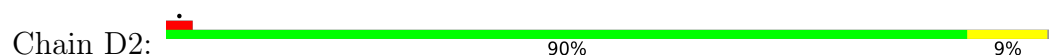


• Molecule 16: ECU11_0225 protein

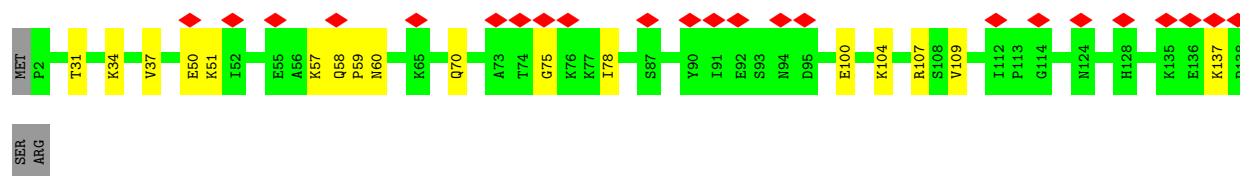
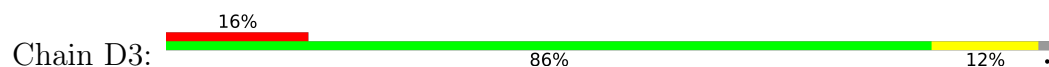




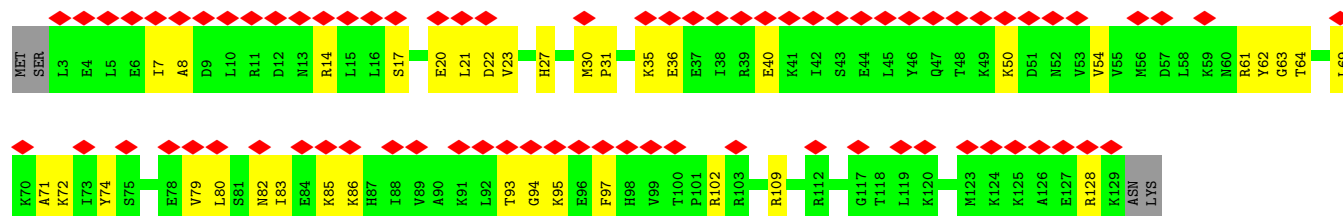
- Molecule 17: 40S RIBOSOMAL PROTEIN S15A (S22 in yeast)



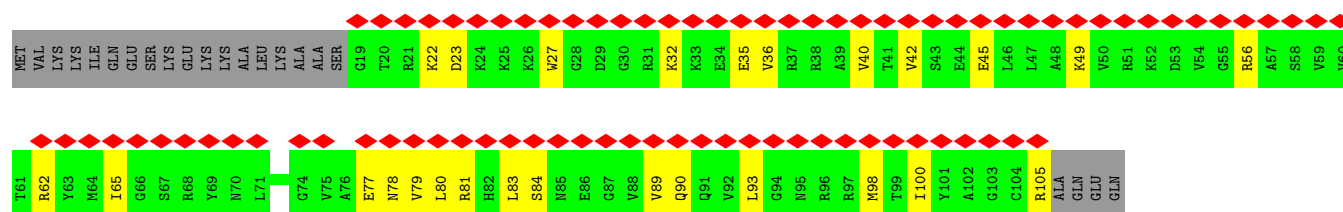
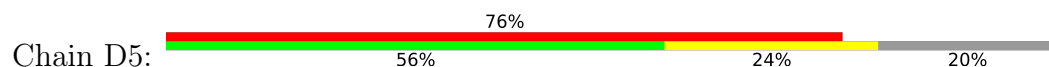
- Molecule 18: 40S ribosomal protein S23



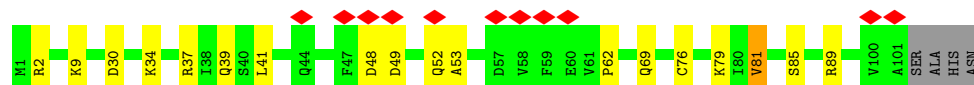
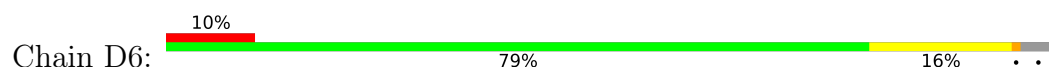
- Molecule 19: 40S RIBOSOMAL PROTEIN S24



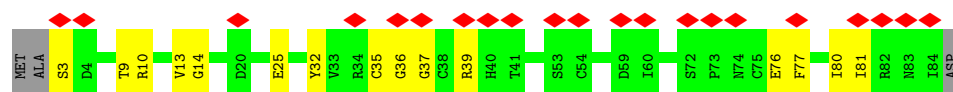
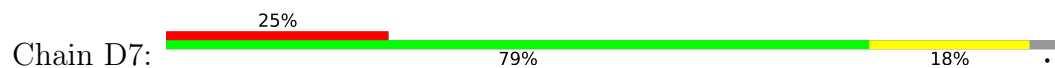
- Molecule 20: 40S ribosomal protein S25



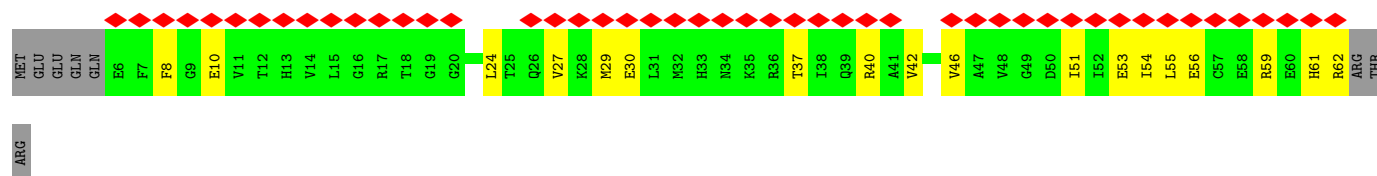
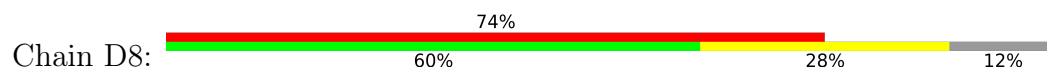
- Molecule 21: 40S ribosomal protein S26



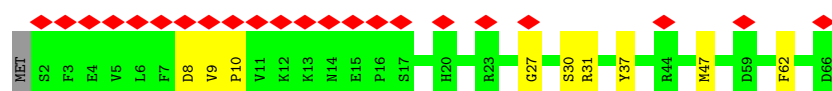
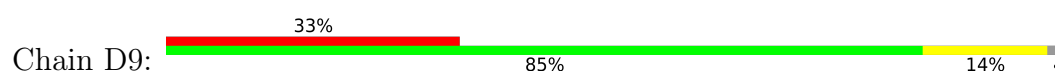
- Molecule 22: 40S RIBOSOMAL PROTEIN S27



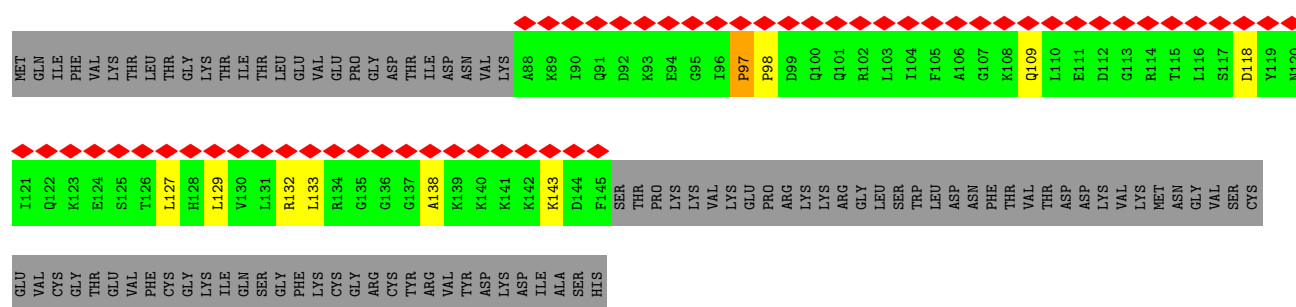
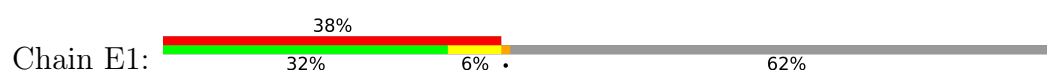
- Molecule 23: 40S RIBOSOMAL PROTEIN S28



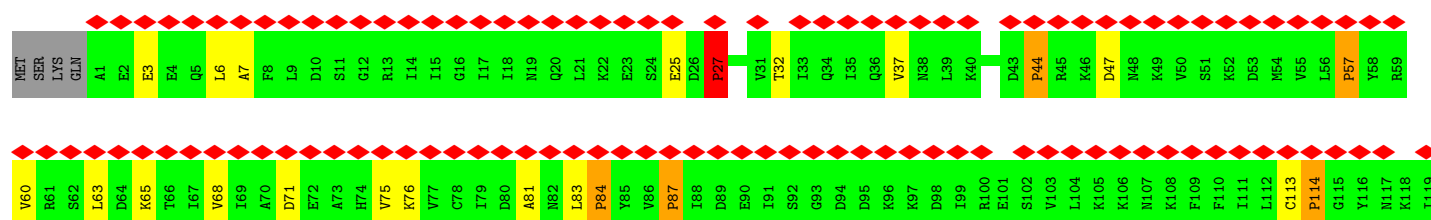
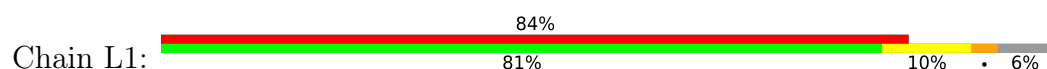
- Molecule 24: 40S ribosomal protein S29

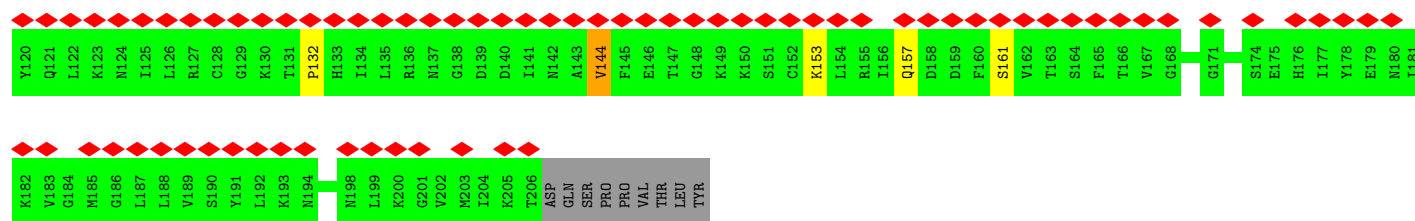


- Molecule 25: Similarity to monoubiquitin/carboxy-extension protein fusion

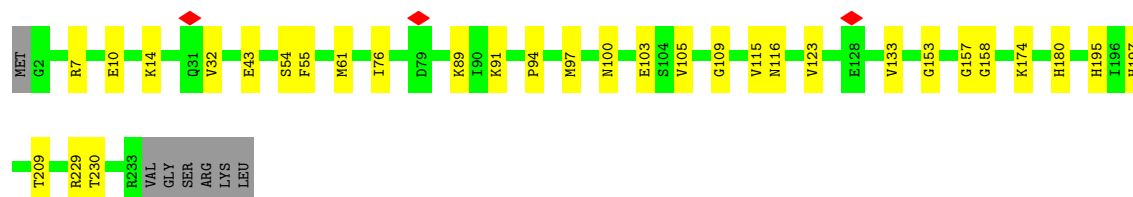
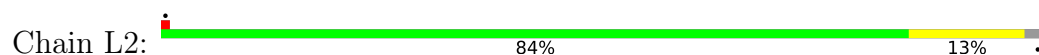


- Molecule 26: 60S ribosomal protein L1

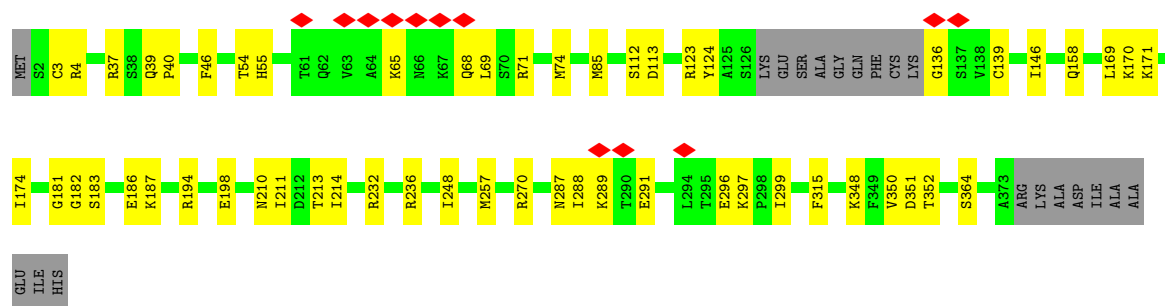
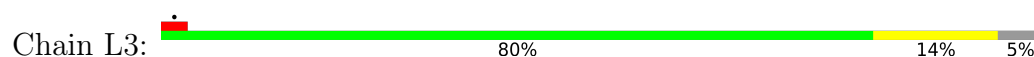




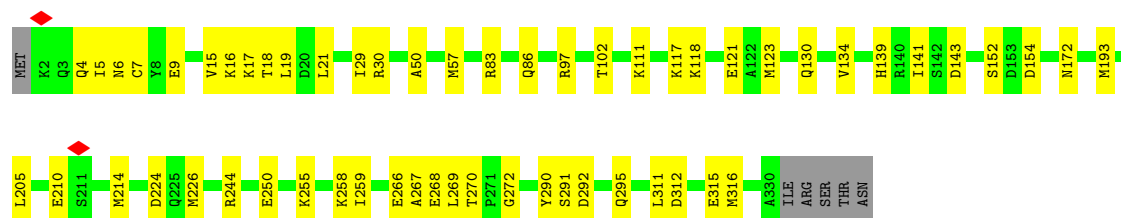
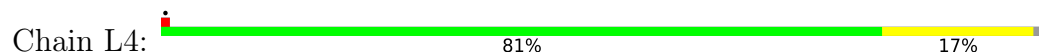
- Molecule 27: 60S ribosomal protein L8



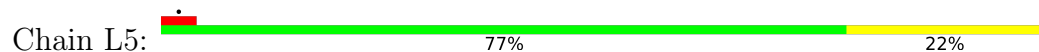
- Molecule 28: 60S ribosomal protein L3



- Molecule 29: 60S RIBOSOMAL PROTEIN L4

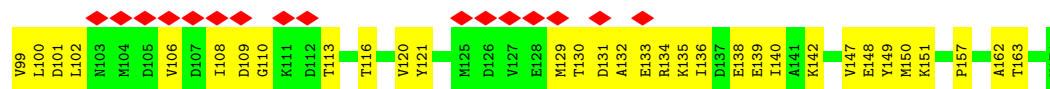
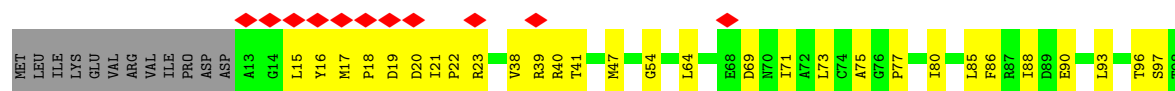


- Molecule 30: 60S RIBOSOMAL PROTEIN L5

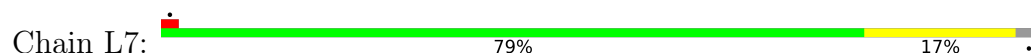




• Molecule 31: 60S RIBOSOMAL PROTEIN L6



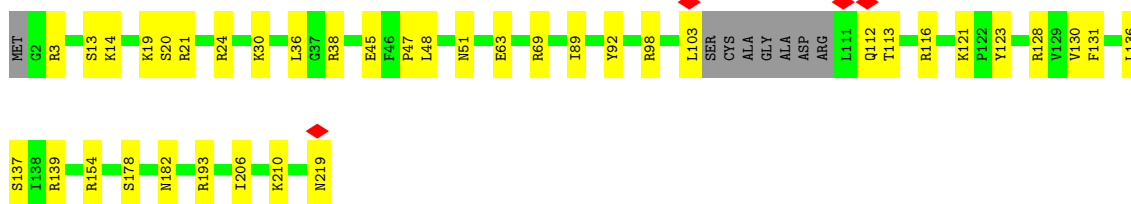
• Molecule 32: 60S ribosomal protein L7



• Molecule 33: 60S ribosomal protein L7a

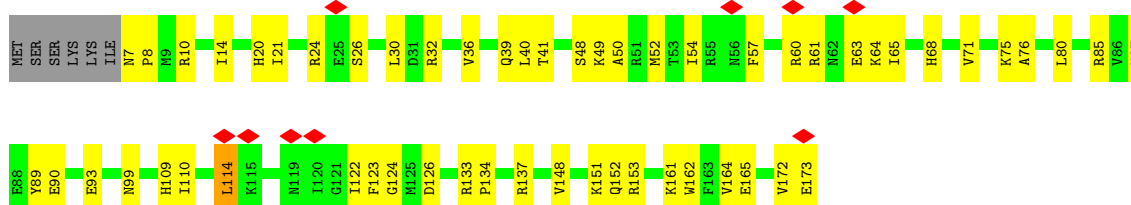


Chain M0:  79% 17%



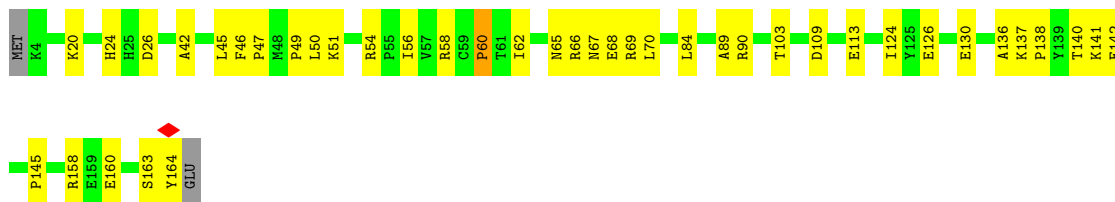
- Molecule 36: 60S ribosomal protein L11

Chain M1:  5% 64% 32%



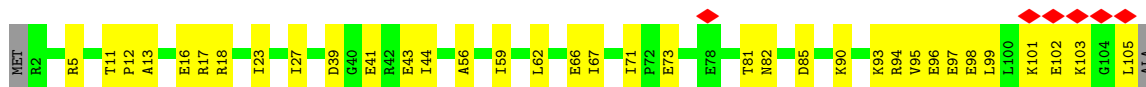
- Molecule 37: 60S RIBOSOMAL PROTEIN L13

Chain M3:  74% 25%



- Molecule 38: ECU06_1215 protein

Chain M4:  6% 65% 33%



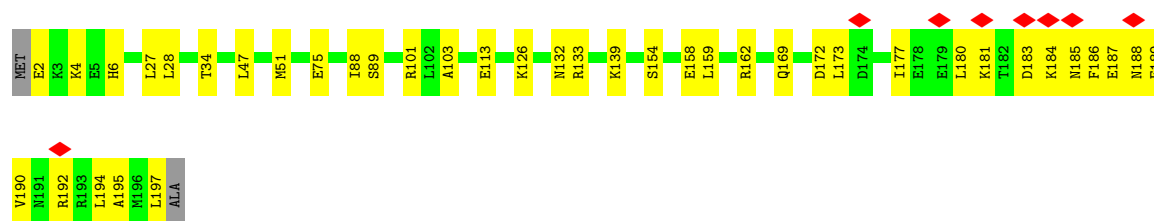
- Molecule 39: Ribosomal protein L15

Chain M5:  87% 12%

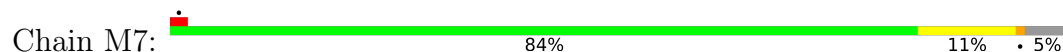


- Molecule 40: 60S RIBOSOMAL PROTEIN L13A (L16)

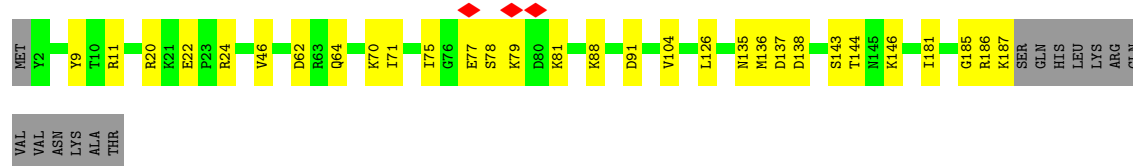
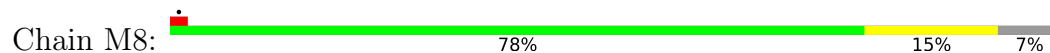
Chain M6:  79% 20%



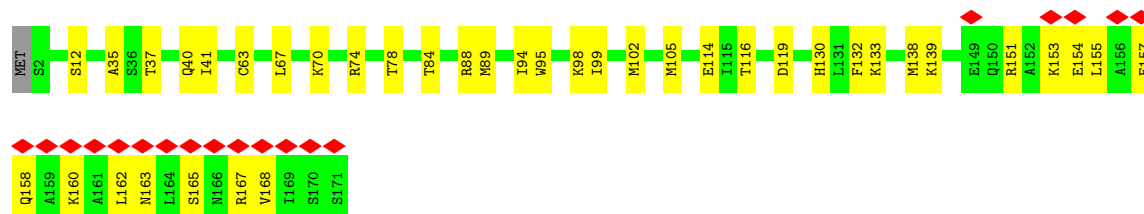
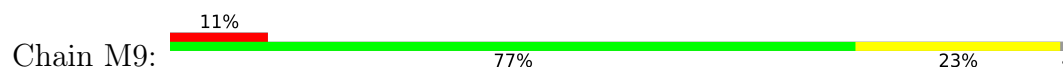
• Molecule 41: 60S RIBOSOMAL PROTEIN L17



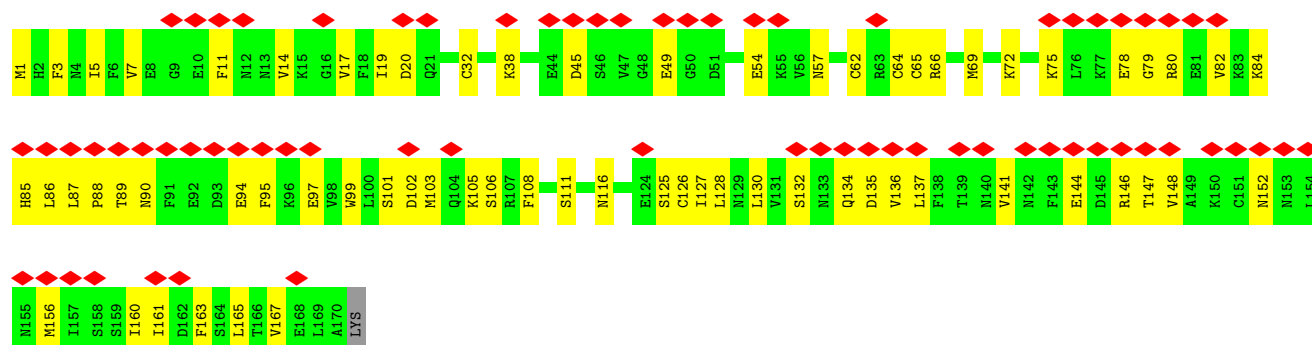
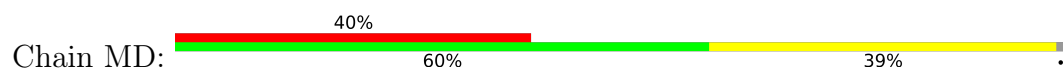
• Molecule 42: 60S RIBOSOMAL PROTEIN L18



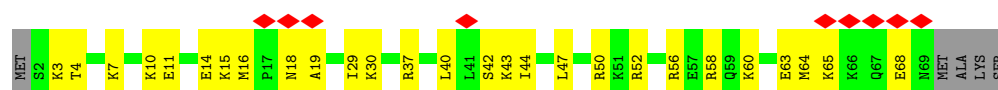
• Molecule 43: 60S RIBOSOMAL PROTEIN L19



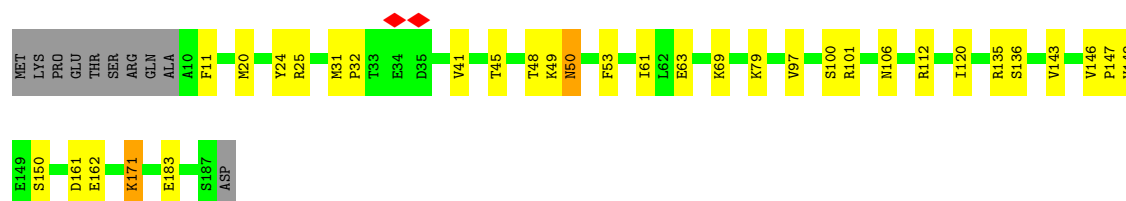
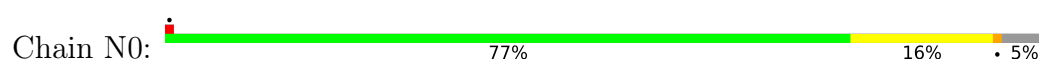
• Molecule 44: Uncharacterized protein ECU01_0250



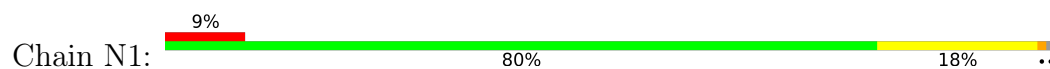
- Molecule 45: ECU06_1135 protein



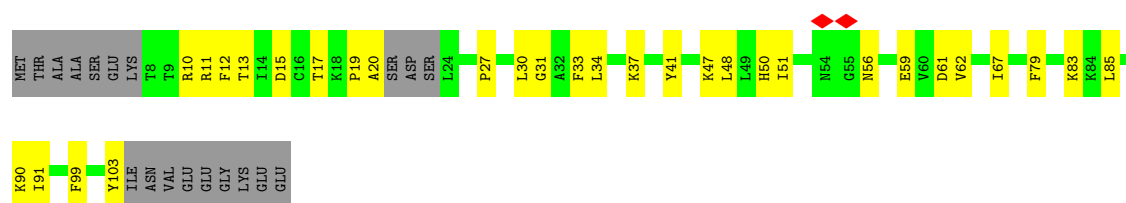
- Molecule 46: 60S ribosomal protein L20



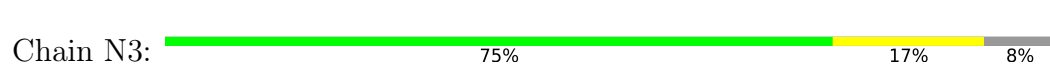
- Molecule 47: 60S ribosomal protein L21



- Molecule 48: 60S ribosomal protein L22



- Molecule 49: 60S ribosomal protein L23



- Molecule 50: Similarity to 60S RIBOSOMAL PROTEIN L24



- Molecule 51: 60S RIBOSOMAL PROTEIN L23A

Chain N5:  81% 8% 11%



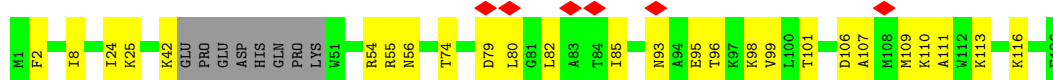
- Molecule 52: 60S RIBOSOMAL PROTEIN L26

Chain N6:  82% 17% ..



- Molecule 53: 60S RIBOSOMAL PROTEIN L27

Chain N7:  5% 73% 21% 6%



- Molecule 54: 60S ribosomal protein L27a

Chain N8:  80% 20% .



- Molecule 55: 60S ribosomal protein L29

Chain N9:  81% 16% .



- Molecule 56: 60S RIBOSOMAL PROTEIN L30

Chain O0:  68% 16% 17%



- Molecule 57: 60S ribosomal protein L31

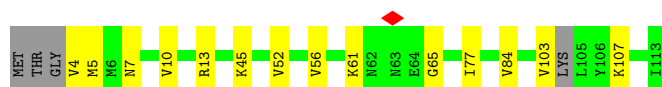
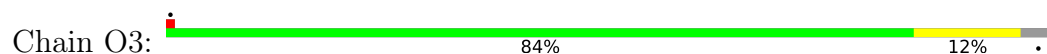
Chain O1:  78% 18% ..



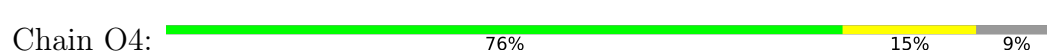
- Molecule 58: 60S ribosomal protein L32



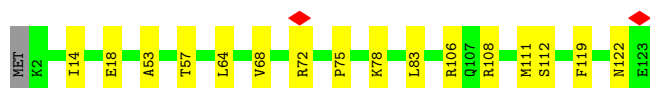
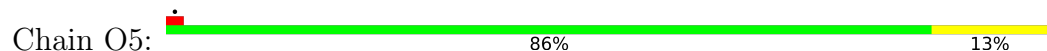
- Molecule 59: 60S RIBOSOMAL PROTEIN L35A (L33)



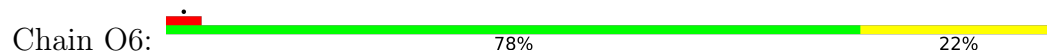
- Molecule 60: 60S ribosomal protein L34



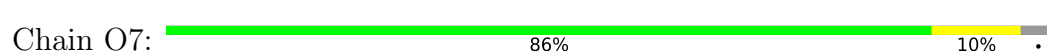
- Molecule 61: 60S ribosomal protein L35-1



- Molecule 62: 60S ribosomal protein L36



- Molecule 63: 60S ribosomal protein L37



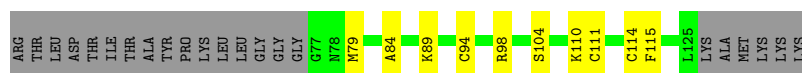
- Molecule 64: 60S ribosomal protein L39

Chain O9:  75% 21% .



- Molecule 65: UBIQUITIN/ L40 RIBOSOMAL PROTEIN FUSION

Chain P0:  30% 8% 63%



- Molecule 66: 60S ribosomal protein L44

Chain P2:  74% 19% 7%



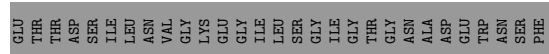
- Molecule 67: 60S RIBOSOMAL PROTEIN L37A (L43)

Chain P3:  84% 12% .



- Molecule 68: 40S ribosomal protein S0

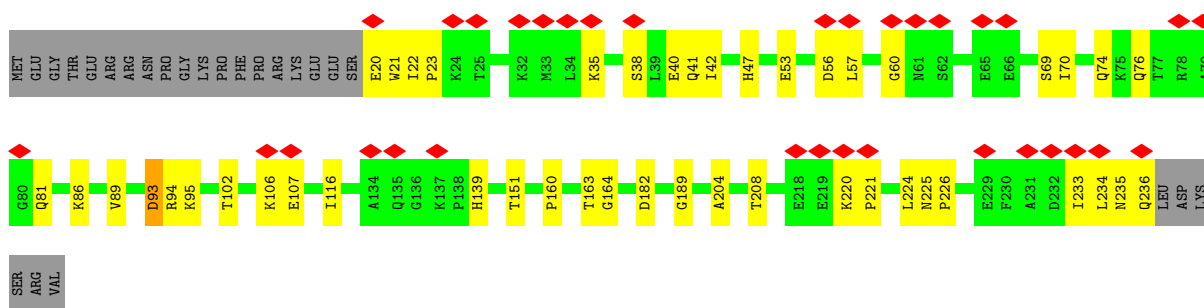
Chain S0:  36% 54% 27% 19%



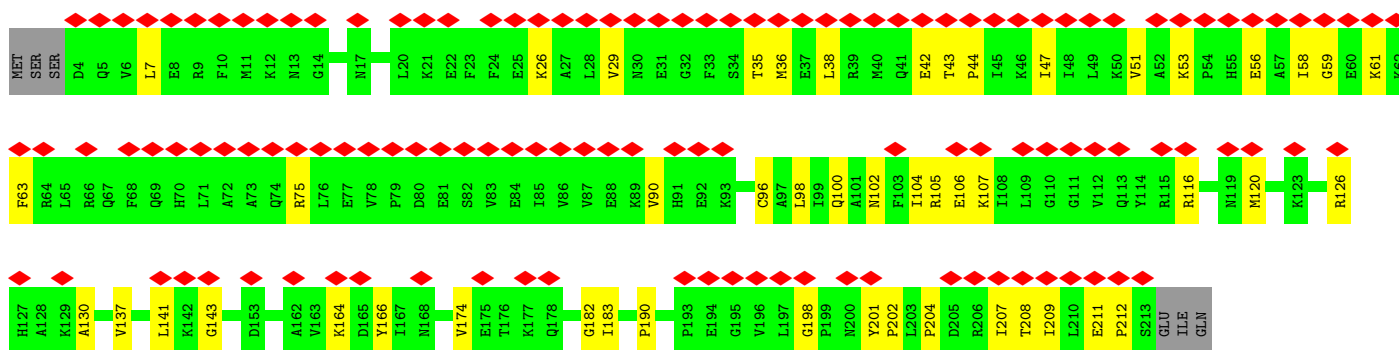
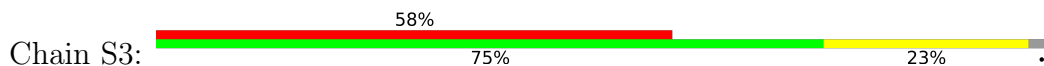
- Molecule 69: 40S ribosomal protein S1

Chain S1:  29% 67% 21% 13%

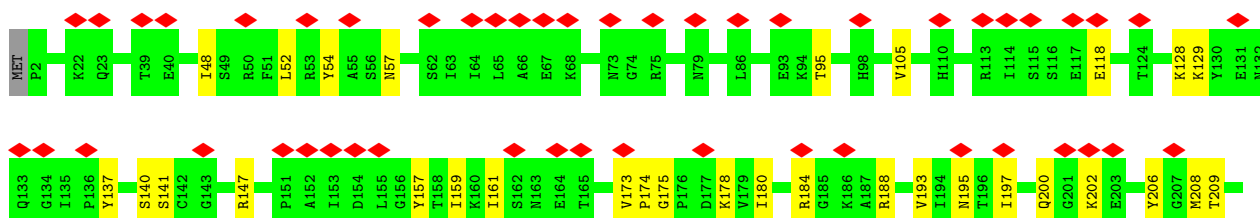
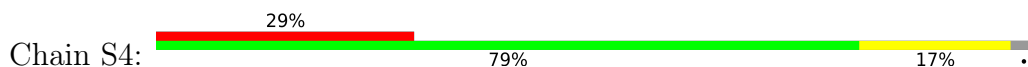
● Molecule 70: 40S RIBOSOMAL PROTEIN S2

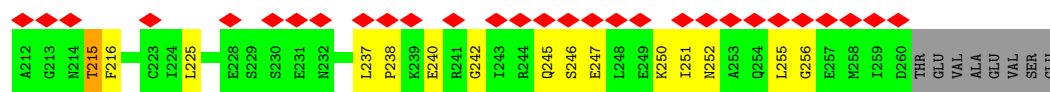


- Molecule 71: 40S ribosomal protein S3

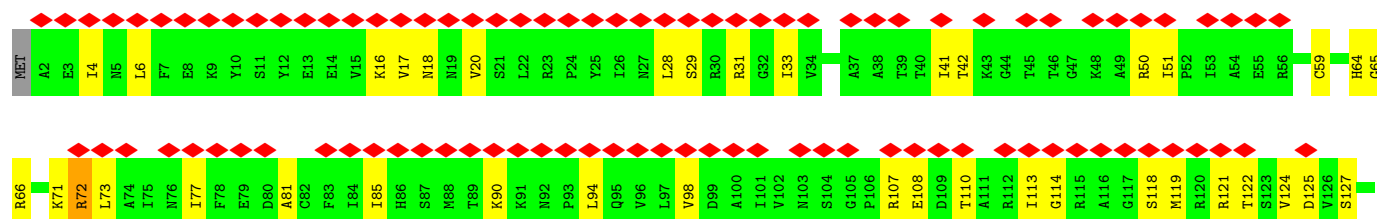
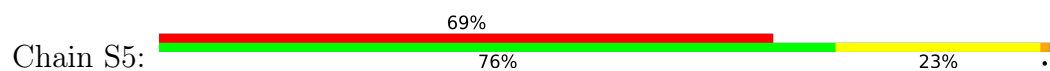


- Molecule 72: 40S ribosomal protein S4

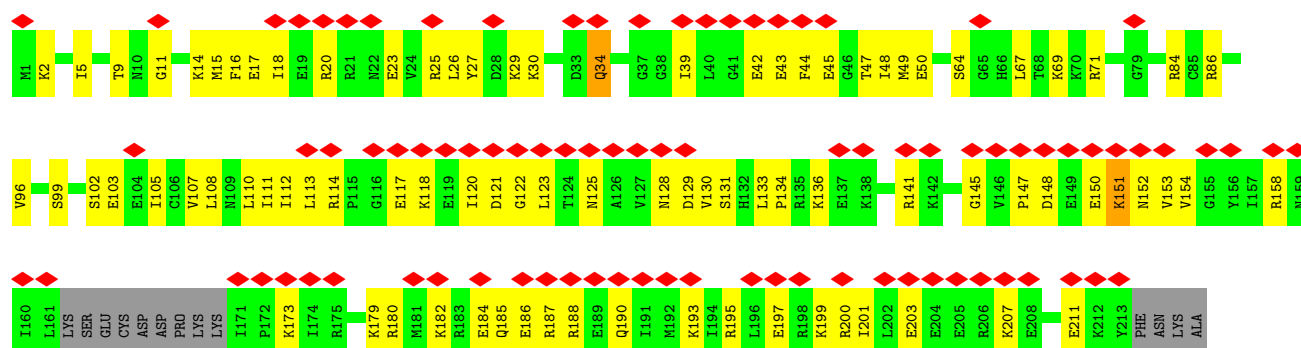
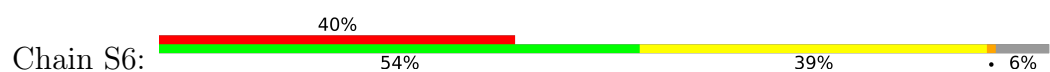




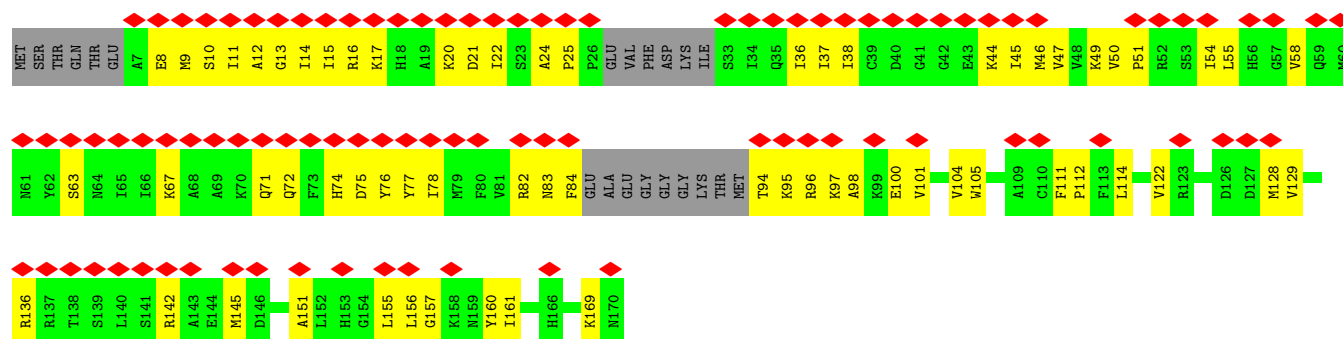
• Molecule 73: 40S ribosomal protein S5



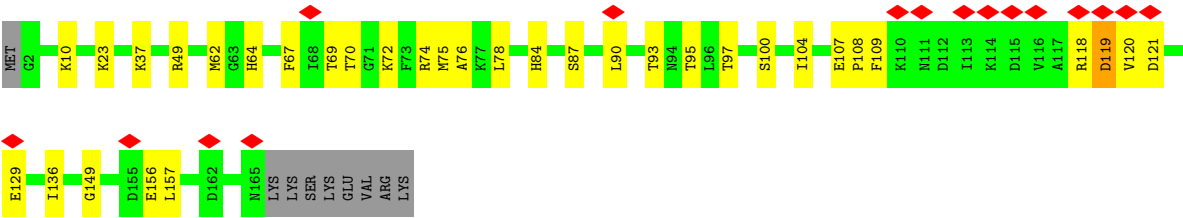
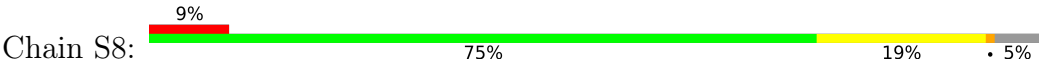
• Molecule 74: 40S ribosomal protein S6



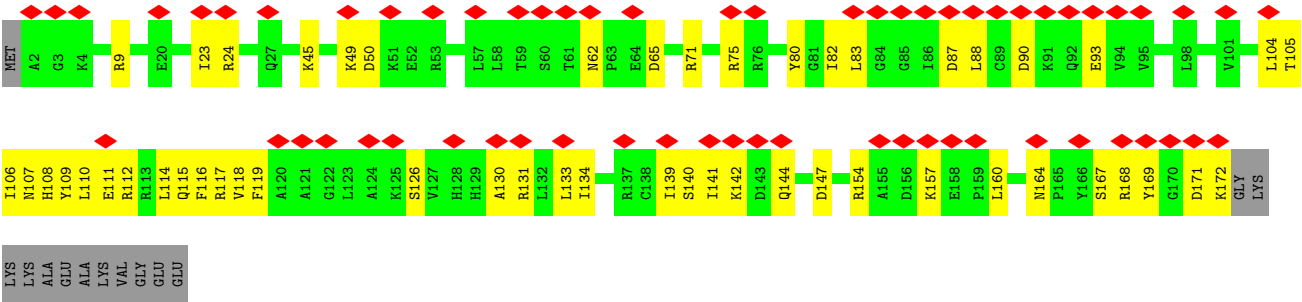
• Molecule 75: 40S ribosomal protein S7



• Molecule 76: 40S ribosomal protein S8



• Molecule 77: 40S ribosomal protein S9



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108005	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2600	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.928	Depositor
Minimum map value	-0.411	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	440.832, 440.832, 440.832	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.861, 0.861, 0.861	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, ZN, AMP

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	RA	0.32	0/2576	0.52	0/3470
2	1	0.51	1/55780 (0.0%)	0.52	0/87016
3	2	0.41	0/2854	0.35	0/4449
4	3	0.51	0/31169	0.46	0/48638
5	C0	0.35	0/701	0.53	0/943
6	C1	0.39	0/1150	0.53	0/1543
7	C2	0.24	0/884	0.48	0/1180
8	C3	0.42	0/1190	0.52	0/1601
9	C4	0.42	0/952	0.63	1/1276 (0.1%)
10	C5	0.34	0/923	0.49	0/1246
11	C6	0.43	0/1150	0.59	0/1538
12	C7	0.34	0/975	0.49	0/1306
13	C8	0.39	0/1133	0.60	0/1516
14	C9	0.37	0/1109	0.52	0/1490
15	D0	0.33	0/794	0.58	0/1066
16	D1	0.33	0/522	0.40	0/701
17	D2	0.44	0/1029	0.52	0/1375
18	D3	0.40	0/1068	0.53	0/1430
19	D4	0.29	0/1070	0.47	0/1426
20	D5	0.33	0/696	0.58	0/928
21	D6	0.42	0/813	0.59	0/1082
22	D7	0.37	0/645	0.48	0/865
23	D8	0.35	0/451	0.59	0/603
24	D9	0.42	0/538	0.64	0/718
25	E1	0.22	0/275	0.70	2/375 (0.5%)
26	L1	0.24	0/1015	0.78	7/1411 (0.5%)
27	L2	0.38	0/1788	0.60	0/2408
28	L3	0.37	0/2876	0.61	0/3854
29	L4	0.37	0/2634	0.59	0/3533
30	L5	0.28	0/2315	0.43	0/3097
31	L6	0.23	0/1299	0.50	0/1753
32	L7	0.33	0/1936	0.51	0/2580

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	L8	0.27	0/1600	0.45	0/2156
34	L9	0.35	0/1462	0.56	0/1961
35	M0	0.34	0/1738	0.57	0/2319
36	M1	0.25	0/1357	0.52	0/1813
37	M3	0.39	0/1333	0.55	0/1785
38	M4	0.26	0/857	0.46	0/1150
39	M5	0.42	0/1684	0.61	0/2244
40	M6	0.33	0/1602	0.46	0/2142
41	M7	0.39	0/1389	0.57	0/1865
42	M8	0.33	0/1494	0.47	0/2003
43	M9	0.33	0/1413	0.47	0/1866
44	MD	0.19	0/1368	0.49	0/1842
45	MS	0.32	0/597	0.57	0/782
46	N0	0.36	0/1470	0.55	0/1980
47	N1	0.37	0/1313	0.62	0/1759
48	N2	0.20	0/748	0.46	0/1001
49	N3	0.35	0/1074	0.60	1/1438 (0.1%)
50	N4	0.31	0/719	0.53	0/959
51	N5	0.33	0/730	0.52	0/983
52	N6	0.31	0/1187	0.53	0/1576
53	N7	0.24	0/954	0.47	0/1279
54	N8	0.45	0/1230	0.72	2/1648 (0.1%)
55	N9	0.39	0/447	0.56	0/597
56	O0	0.27	0/701	0.42	0/939
57	O1	0.32	0/889	0.49	0/1194
58	O2	0.38	0/1084	0.55	0/1448
59	O3	0.35	0/876	0.56	0/1180
60	O4	0.37	0/817	0.53	0/1085
61	O5	0.33	0/988	0.47	0/1314
62	O6	0.28	0/742	0.49	0/988
63	O7	0.42	0/702	0.62	0/927
64	O9	0.37	0/441	0.57	0/580
65	P0	0.34	0/383	0.51	0/503
66	P2	0.34	0/800	0.58	0/1056
67	P3	0.32	0/673	0.45	0/893
68	S0	0.30	0/1615	0.45	0/2189
69	S1	0.37	0/1701	0.49	0/2275
70	S2	0.38	0/1660	0.51	0/2238
71	S3	0.34	0/1684	0.50	0/2263
72	S4	0.35	0/2087	0.49	0/2810
73	S5	0.37	0/1478	0.56	0/1989
74	S6	0.34	0/1700	0.55	0/2259
75	S7	0.29	0/1191	0.47	0/1602

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	S8	0.42	0/1323	0.59	1/1769 (0.1%)
77	S9	0.31	0/1397	0.50	0/1874
All	All	0.44	1/177008 (0.0%)	0.51	14/256940 (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
1	RA	0	1
6	C1	0	1
7	C2	0	1
14	C9	0	1
32	L7	0	1
34	L9	0	2
37	M3	0	1
43	M9	0	1
50	N4	0	2
62	O6	0	1
70	S2	0	1
72	S4	0	1
74	S6	0	1
All	All	0	15

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	519	A	C1'-N9	-5.49	1.39	1.48

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	N3	53	GLY	N-CA-C	8.44	120.65	112.04
26	L1	27	PRO	N-CA-CB	8.08	111.74	103.25
26	L1	57	PRO	N-CA-CB	7.59	111.22	103.25
26	L1	114	PRO	N-CA-CB	7.51	111.14	103.25
26	L1	44	PRO	N-CA-CB	7.46	111.08	103.25

There are no chirality outliers.

5 of 15 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C1	36	VAL	Peptide
7	C2	104	GLY	Peptide
14	C9	113	GLU	Peptide
32	L7	227	HIS	Peptide
1	RA	95	ASP	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	RA	2537	0	2550	150	0
2	1	49833	0	24957	256	0
3	2	2550	0	1288	11	0
4	3	27838	0	13926	194	0
5	C0	686	0	730	22	0
6	C1	1126	0	1172	35	0
7	C2	879	0	937	80	0
8	C3	1166	0	1210	12	0
9	C4	942	0	1005	18	0
10	C5	903	0	945	36	0
11	C6	1132	0	1193	26	0
12	C7	962	0	987	40	0
13	C8	1121	0	1170	45	0
14	C9	1089	0	1103	41	0
15	D0	779	0	787	35	0
16	D1	518	0	526	16	0
17	D2	1012	0	1033	9	0
18	D3	1052	0	1126	12	0
19	D4	1056	0	1135	32	0
20	D5	691	0	727	22	0
21	D6	801	0	820	13	0
22	D7	633	0	621	15	0
23	D8	446	0	457	23	0
24	D9	524	0	518	8	0
25	E1	276	0	128	6	0
26	L1	1016	0	439	10	0
27	L2	1759	0	1817	22	0
28	L3	2827	0	2945	50	0
29	L4	2596	0	2669	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	L5	2273	0	2281	43	0
31	L6	1279	0	1302	67	0
32	L7	1903	0	1962	32	0
33	L8	1573	0	1682	58	0
34	L9	1443	0	1504	39	0
35	M0	1706	0	1750	30	0
36	M1	1336	0	1378	47	0
37	M3	1308	0	1374	34	0
38	M4	848	0	881	34	0
39	M5	1657	0	1719	20	0
40	M6	1577	0	1659	46	0
41	M7	1363	0	1399	16	0
42	M8	1470	0	1551	27	0
43	M9	1398	0	1483	30	0
44	MD	1349	0	1346	65	0
45	MS	592	0	661	24	0
46	N0	1438	0	1490	26	0
47	N1	1288	0	1331	33	0
48	N2	735	0	757	21	0
49	N3	1058	0	1138	21	0
50	N4	709	0	738	30	0
51	N5	720	0	757	6	0
52	N6	1171	0	1219	20	0
53	N7	938	0	1008	28	0
54	N8	1196	0	1207	28	0
55	N9	437	0	442	9	0
56	O0	692	0	736	11	0
57	O1	879	0	946	19	0
58	O2	1062	0	1135	20	0
59	O3	861	0	879	12	0
60	O4	807	0	868	13	0
61	O5	981	0	1075	15	0
62	O6	735	0	796	16	0
63	O7	691	0	715	9	0
64	O9	434	0	478	8	0
65	P0	381	0	394	11	0
66	P2	788	0	860	13	0
67	P3	664	0	708	11	0
68	S0	1584	0	1630	59	0
69	S1	1670	0	1705	34	0
70	S2	1636	0	1731	31	0
71	S3	1658	0	1728	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	S4	2045	0	2092	37	0
73	S5	1461	0	1523	40	0
74	S6	1680	0	1757	87	0
75	S7	1173	0	1206	70	0
76	S8	1300	0	1344	26	0
77	S9	1374	0	1435	45	0
78	D6	1	0	0	0	0
78	D7	1	0	0	0	0
78	D9	1	0	0	0	0
78	E1	1	0	0	0	0
78	O7	1	0	0	0	0
78	P0	1	0	0	0	0
78	P2	1	0	0	0	0
78	P3	1	0	0	0	0
79	L9	23	12	12	0	0
80	N8	10	19	19	0	0
All	All	166112	31	128712	2413	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 8.

The worst 5 of 2413 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)
4:3:573:A:H5''	9:C4:49:ARG:HD3	1.39	1.03
75:S7:49:LYS:HB3	75:S7:83:ASN:HB3	1.44	0.99
50:N4:73:GLN:HE22	74:S6:114:ARG:HB2	1.31	0.95
2:1:2538:G:H2'	2:1:2539:U:H5''	1.48	0.95
73:S5:6:LEU:HD23	73:S5:94:LEU:HD22	1.49	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	RA	326/334 (98%)	264 (81%)	62 (19%)	0	100	100
5	C0	79/96 (82%)	72 (91%)	7 (9%)	0	100	100
6	C1	139/156 (89%)	123 (88%)	16 (12%)	0	100	100
7	C2	116/134 (87%)	102 (88%)	14 (12%)	0	100	100
8	C3	144/148 (97%)	136 (94%)	8 (6%)	0	100	100
9	C4	124/134 (92%)	113 (91%)	11 (9%)	0	100	100
10	C5	114/148 (77%)	107 (94%)	7 (6%)	0	100	100
11	C6	139/145 (96%)	124 (89%)	15 (11%)	0	100	100
12	C7	115/120 (96%)	104 (90%)	11 (10%)	0	100	100
13	C8	139/153 (91%)	126 (91%)	13 (9%)	0	100	100
14	C9	133/137 (97%)	123 (92%)	10 (8%)	0	100	100
15	D0	89/120 (74%)	81 (91%)	8 (9%)	0	100	100
16	D1	66/70 (94%)	65 (98%)	1 (2%)	0	100	100
17	D2	125/128 (98%)	122 (98%)	3 (2%)	0	100	100
18	D3	135/140 (96%)	129 (96%)	6 (4%)	0	100	100
19	D4	125/131 (95%)	113 (90%)	12 (10%)	0	100	100
20	D5	85/109 (78%)	72 (85%)	13 (15%)	0	100	100
21	D6	99/105 (94%)	94 (95%)	5 (5%)	0	100	100
22	D7	80/85 (94%)	68 (85%)	12 (15%)	0	100	100
23	D8	55/65 (85%)	47 (86%)	8 (14%)	0	100	100
24	D9	63/66 (96%)	57 (90%)	6 (10%)	0	100	100
25	E1	56/152 (37%)	47 (84%)	8 (14%)	1 (2%)	6	18
26	L1	204/219 (93%)	151 (74%)	41 (20%)	12 (6%)	1	2
27	L2	230/239 (96%)	204 (89%)	26 (11%)	0	100	100
28	L3	359/383 (94%)	315 (88%)	43 (12%)	1 (0%)	36	60
29	L4	327/335 (98%)	293 (90%)	33 (10%)	1 (0%)	36	60
30	L5	281/287 (98%)	262 (93%)	19 (7%)	0	100	100
31	L6	157/171 (92%)	128 (82%)	28 (18%)	1 (1%)	21	44
32	L7	229/239 (96%)	213 (93%)	16 (7%)	0	100	100
33	L8	195/206 (95%)	163 (84%)	32 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	L9	181/183 (99%)	154 (85%)	27 (15%)	0	100	100
35	M0	207/219 (94%)	190 (92%)	16 (8%)	1 (0%)	24	48
36	M1	165/173 (95%)	143 (87%)	21 (13%)	1 (1%)	21	44
37	M3	159/163 (98%)	144 (91%)	14 (9%)	1 (1%)	21	44
38	M4	102/106 (96%)	93 (91%)	9 (9%)	0	100	100
39	M5	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
40	M6	194/198 (98%)	187 (96%)	7 (4%)	0	100	100
41	M7	172/183 (94%)	157 (91%)	15 (9%)	0	100	100
42	M8	184/200 (92%)	172 (94%)	12 (6%)	0	100	100
43	M9	168/171 (98%)	157 (94%)	11 (6%)	0	100	100
44	MD	168/171 (98%)	138 (82%)	30 (18%)	0	100	100
45	MS	66/73 (90%)	63 (96%)	3 (4%)	0	100	100
46	N0	176/188 (94%)	157 (89%)	16 (9%)	3 (2%)	7	19
47	N1	157/160 (98%)	136 (87%)	19 (12%)	2 (1%)	9	25
48	N2	89/112 (80%)	76 (85%)	13 (15%)	0	100	100
49	N3	133/146 (91%)	127 (96%)	6 (4%)	0	100	100
50	N4	87/100 (87%)	74 (85%)	12 (14%)	1 (1%)	11	29
51	N5	91/105 (87%)	83 (91%)	8 (9%)	0	100	100
52	N6	140/143 (98%)	131 (94%)	7 (5%)	2 (1%)	9	23
53	N7	114/126 (90%)	100 (88%)	14 (12%)	0	100	100
54	N8	144/147 (98%)	123 (85%)	20 (14%)	1 (1%)	18	41
55	N9	53/57 (93%)	47 (89%)	6 (11%)	0	100	100
56	O0	88/108 (82%)	83 (94%)	5 (6%)	0	100	100
57	O1	106/111 (96%)	94 (89%)	10 (9%)	2 (2%)	6	17
58	O2	126/139 (91%)	123 (98%)	3 (2%)	0	100	100
59	O3	105/113 (93%)	97 (92%)	8 (8%)	0	100	100
60	O4	98/110 (89%)	94 (96%)	4 (4%)	0	100	100
61	O5	119/122 (98%)	118 (99%)	1 (1%)	0	100	100
62	O6	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
63	O7	84/90 (93%)	81 (96%)	3 (4%)	0	100	100
64	O9	48/52 (92%)	43 (90%)	5 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
65	P0	47/131 (36%)	42 (89%)	5 (11%)	0	100	100
66	P2	95/104 (91%)	81 (85%)	13 (14%)	1 (1%)	11	29
67	P3	84/89 (94%)	80 (95%)	4 (5%)	0	100	100
68	S0	201/252 (80%)	178 (89%)	23 (11%)	0	100	100
69	S1	205/239 (86%)	184 (90%)	21 (10%)	0	100	100
70	S2	215/242 (89%)	199 (93%)	16 (7%)	0	100	100
71	S3	208/216 (96%)	190 (91%)	18 (9%)	0	100	100
72	S4	257/268 (96%)	228 (89%)	29 (11%)	0	100	100
73	S5	186/189 (98%)	171 (92%)	14 (8%)	1 (0%)	24	48
74	S6	200/217 (92%)	182 (91%)	17 (8%)	1 (0%)	24	48
75	S7	143/170 (84%)	132 (92%)	10 (7%)	1 (1%)	18	41
76	S8	162/173 (94%)	148 (91%)	13 (8%)	1 (1%)	21	44
77	S9	169/184 (92%)	147 (87%)	22 (13%)	0	100	100
All	All	10717/11696 (92%)	9640 (90%)	1042 (10%)	35 (0%)	37	60

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
26	L1	27	PRO
26	L1	37	VAL
26	L1	44	PRO
26	L1	57	PRO
26	L1	83	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	
1	RA	286/291 (98%)	286 (100%)	0	100	100
5	C0	76/86 (88%)	76 (100%)	0	100	100
6	C1	124/138 (90%)	124 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	C2	99/114 (87%)	99 (100%)	0	100	100
8	C3	127/129 (98%)	127 (100%)	0	100	100
9	C4	93/101 (92%)	93 (100%)	0	100	100
10	C5	98/125 (78%)	98 (100%)	0	100	100
11	C6	121/125 (97%)	120 (99%)	1 (1%)	73	88
12	C7	107/109 (98%)	107 (100%)	0	100	100
13	C8	119/129 (92%)	119 (100%)	0	100	100
14	C9	119/121 (98%)	119 (100%)	0	100	100
15	D0	88/114 (77%)	88 (100%)	0	100	100
16	D1	55/57 (96%)	55 (100%)	0	100	100
17	D2	107/108 (99%)	107 (100%)	0	100	100
18	D3	111/114 (97%)	111 (100%)	0	100	100
19	D4	117/121 (97%)	117 (100%)	0	100	100
20	D5	73/91 (80%)	73 (100%)	0	100	100
21	D6	86/89 (97%)	85 (99%)	1 (1%)	63	84
22	D7	71/73 (97%)	71 (100%)	0	100	100
23	D8	48/56 (86%)	48 (100%)	0	100	100
24	D9	57/58 (98%)	57 (100%)	0	100	100
27	L2	192/198 (97%)	192 (100%)	0	100	100
28	L3	298/313 (95%)	297 (100%)	1 (0%)	86	94
29	L4	274/280 (98%)	274 (100%)	0	100	100
30	L5	235/238 (99%)	235 (100%)	0	100	100
31	L6	139/151 (92%)	139 (100%)	0	100	100
32	L7	210/216 (97%)	209 (100%)	1 (0%)	81	92
33	L8	181/190 (95%)	181 (100%)	0	100	100
34	L9	157/157 (100%)	155 (99%)	2 (1%)	61	83
35	M0	179/184 (97%)	179 (100%)	0	100	100
36	M1	143/149 (96%)	143 (100%)	0	100	100
37	M3	139/141 (99%)	138 (99%)	1 (1%)	76	90
38	M4	93/94 (99%)	93 (100%)	0	100	100
39	M5	173/174 (99%)	173 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	M6	167/168 (99%)	167 (100%)	0	100	100
41	M7	142/160 (89%)	140 (99%)	2 (1%)	59	82
42	M8	165/178 (93%)	165 (100%)	0	100	100
43	M9	147/148 (99%)	146 (99%)	1 (1%)	76	90
44	MD	158/159 (99%)	158 (100%)	0	100	100
45	MS	65/69 (94%)	65 (100%)	0	100	100
46	N0	160/169 (95%)	159 (99%)	1 (1%)	78	91
47	N1	137/140 (98%)	136 (99%)	1 (1%)	76	90
48	N2	76/94 (81%)	76 (100%)	0	100	100
49	N3	113/122 (93%)	113 (100%)	0	100	100
50	N4	78/86 (91%)	78 (100%)	0	100	100
51	N5	78/91 (86%)	78 (100%)	0	100	100
52	N6	126/127 (99%)	126 (100%)	0	100	100
53	N7	98/110 (89%)	98 (100%)	0	100	100
54	N8	124/125 (99%)	124 (100%)	0	100	100
55	N9	44/47 (94%)	44 (100%)	0	100	100
56	O0	77/90 (86%)	77 (100%)	0	100	100
57	O1	101/106 (95%)	100 (99%)	1 (1%)	68	86
58	O2	114/125 (91%)	114 (100%)	0	100	100
59	O3	93/99 (94%)	92 (99%)	1 (1%)	65	85
60	O4	87/91 (96%)	87 (100%)	0	100	100
61	O5	102/103 (99%)	102 (100%)	0	100	100
62	O6	74/79 (94%)	74 (100%)	0	100	100
63	O7	73/76 (96%)	73 (100%)	0	100	100
64	O9	44/46 (96%)	44 (100%)	0	100	100
65	P0	41/107 (38%)	41 (100%)	0	100	100
66	P2	84/89 (94%)	84 (100%)	0	100	100
67	P3	67/69 (97%)	67 (100%)	0	100	100
68	S0	176/219 (80%)	176 (100%)	0	100	100
69	S1	184/206 (89%)	184 (100%)	0	100	100
70	S2	177/200 (88%)	177 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	S3	178/184 (97%)	178 (100%)	0	100	100
72	S4	228/236 (97%)	228 (100%)	0	100	100
73	S5	159/160 (99%)	158 (99%)	1 (1%)	78	91
74	S6	182/194 (94%)	182 (100%)	0	100	100
75	S7	127/144 (88%)	127 (100%)	0	100	100
76	S8	140/149 (94%)	140 (100%)	0	100	100
77	S9	147/156 (94%)	147 (100%)	0	100	100
All	All	9128/9755 (94%)	9113 (100%)	15 (0%)	85	95

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	M7	119	ILE
59	O3	84	VAL
41	M7	138	VAL
73	S5	72	ARG
47	N1	153	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
62	O6	63	ASN
74	S6	22	ASN
66	P2	3	ASN
70	S2	81	GLN
77	S9	129	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	1	2305/2486 (92%)	405 (17%)	25 (1%)
3	2	118/119 (99%)	20 (16%)	0
4	3	1292/1300 (99%)	335 (25%)	13 (1%)
All	All	3715/3905 (95%)	760 (20%)	38 (1%)

5 of 760 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	1	24	U
2	1	25	G
2	1	32	G
2	1	39	U
2	1	49	G

5 of 38 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	3	133	G
4	3	891	C
4	3	199	G
4	3	523	U
4	3	1137	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	$\# Z > 2$
80	SPD	N8	201	-	9,9,9	0.42	0	8,8,8	1.18	1 (12%)
79	AMP	L9	201	-	25,25,25	0.33	0	37,38,38	0.42	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
80	SPD	N8	201	-	-	3/7/7/7	-
79	AMP	L9	201	-	-	3/10/26/26	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
80	N8	201	SPD	C4-C5-N6	-2.62	105.03	112.07

There are no chirality outliers.

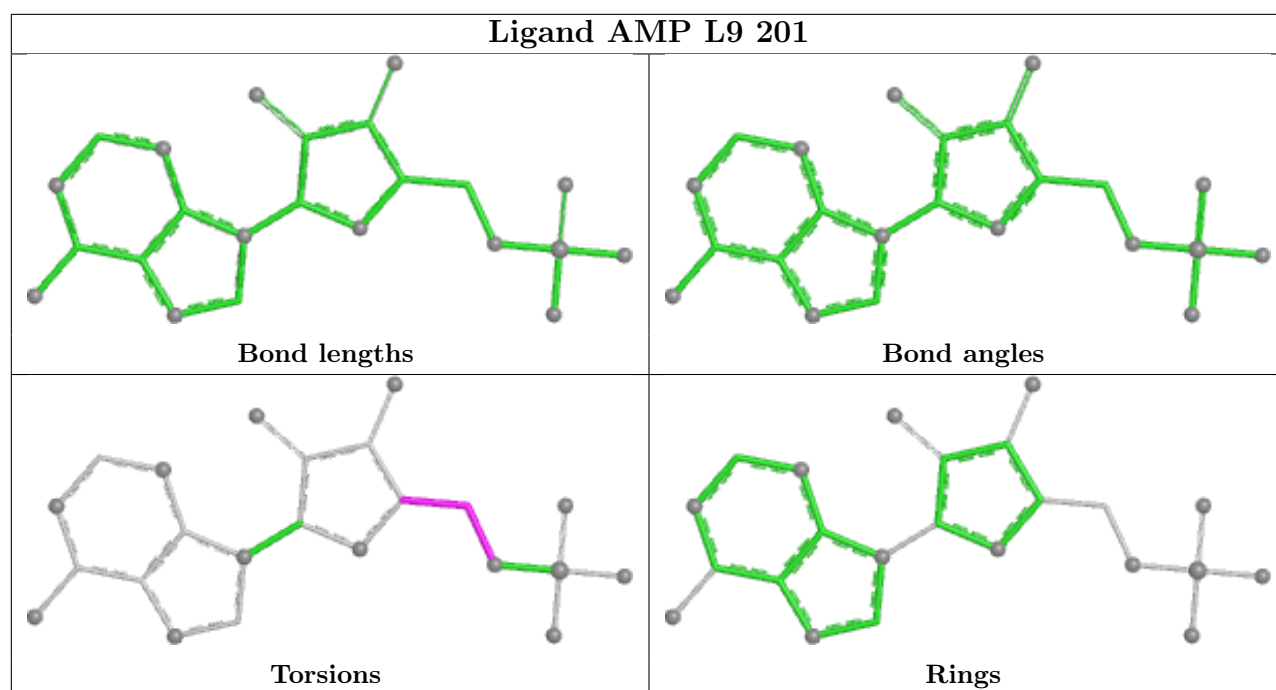
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	L9	201	AMP	O4'-C4'-C5'-O5'
79	L9	201	AMP	C3'-C4'-C5'-O5'
80	N8	201	SPD	N6-C7-C8-C9
80	N8	201	SPD	C4-C5-N6-C7
80	N8	201	SPD	C2-C3-C4-C5

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

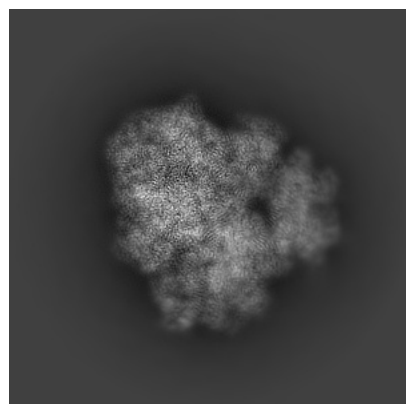
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13936. These allow visual inspection of the internal detail of the map and identification of artifacts.

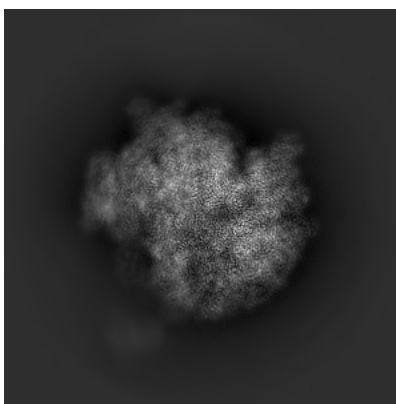
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

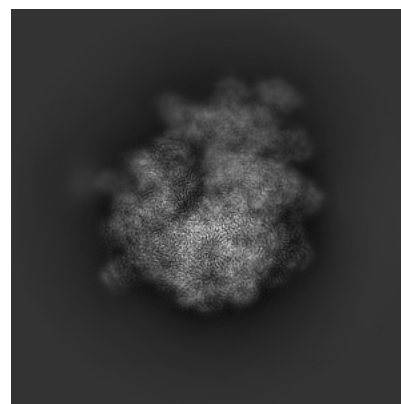
6.1.1 Primary map



X

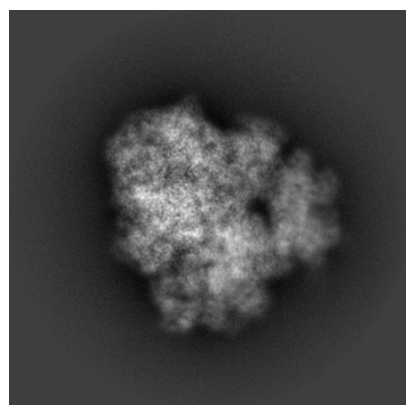


Y

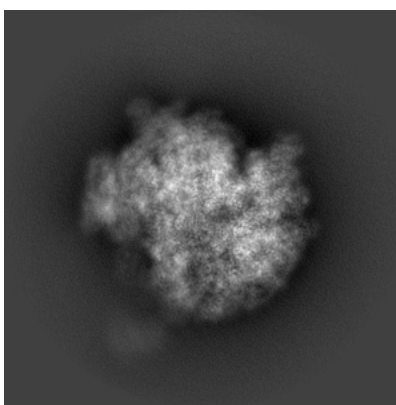


Z

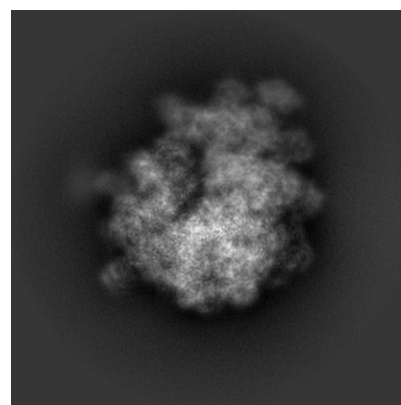
6.1.2 Raw map



X



Y

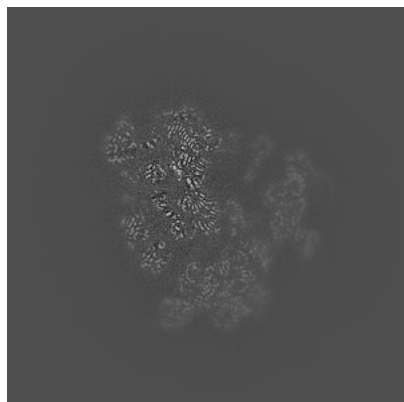


Z

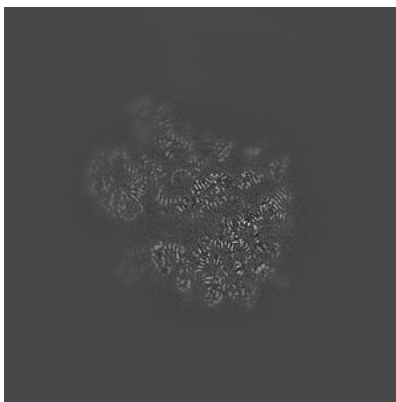
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

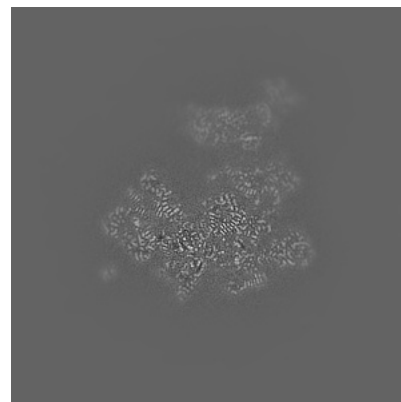
6.2.1 Primary map



X Index: 256

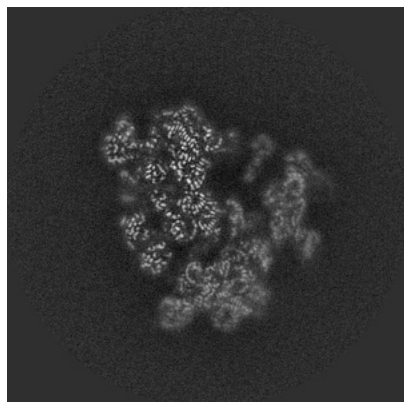


Y Index: 256

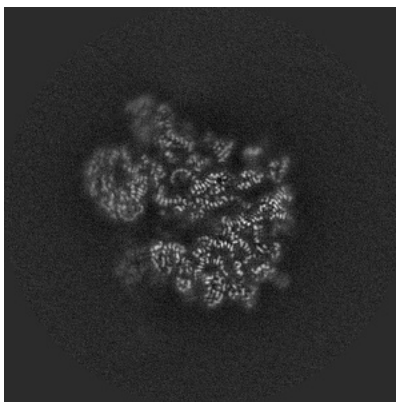


Z Index: 256

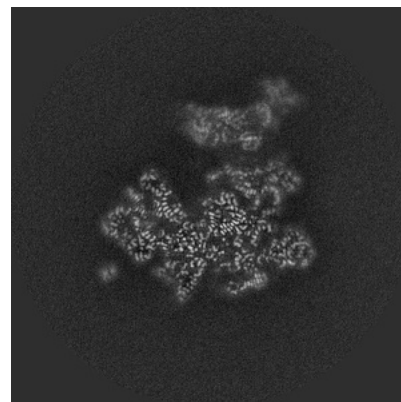
6.2.2 Raw map



X Index: 256



Y Index: 256

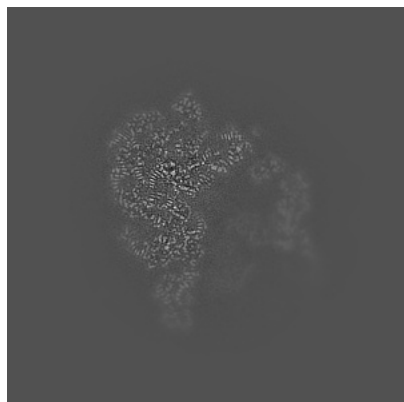


Z Index: 256

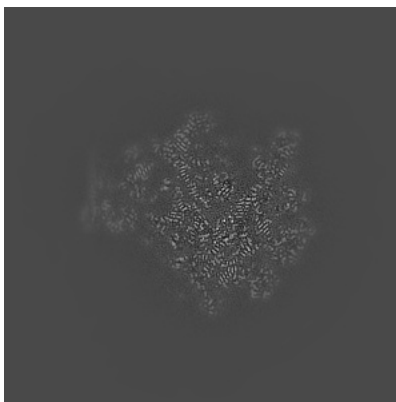
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

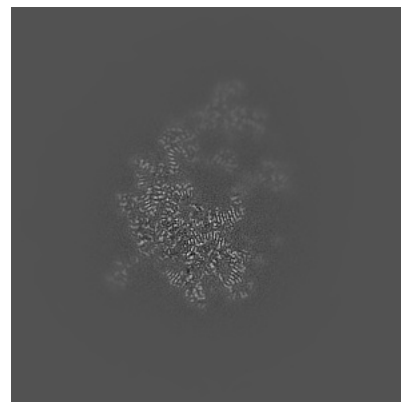
6.3.1 Primary map



X Index: 231

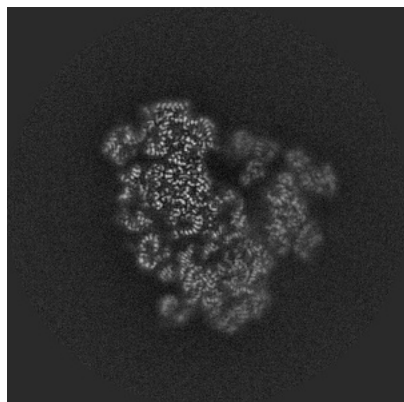


Y Index: 219

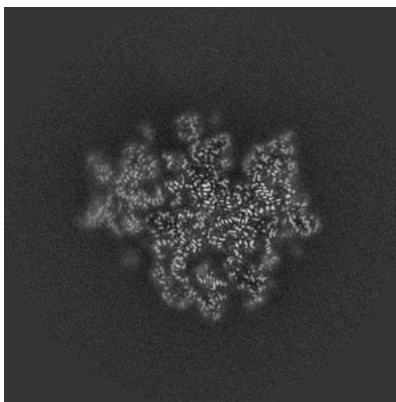


Z Index: 301

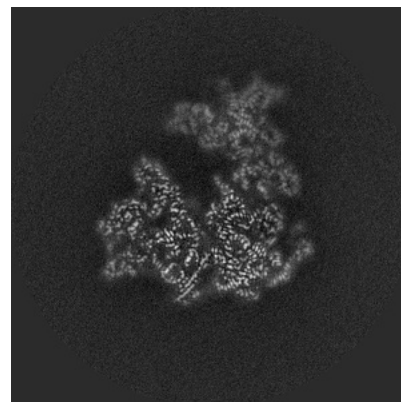
6.3.2 Raw map



X Index: 267



Y Index: 233

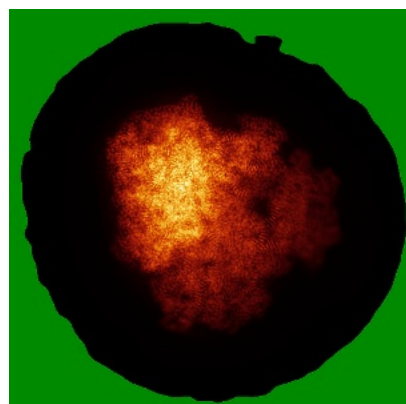


Z Index: 272

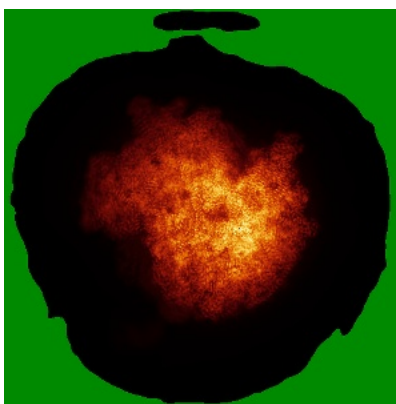
The images above show the largest variance slices of the map in three orthogonal directions.

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

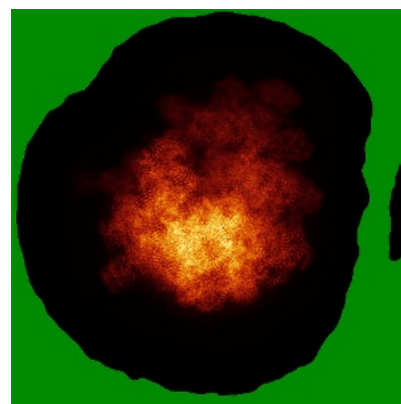
6.4.1 Primary map



X

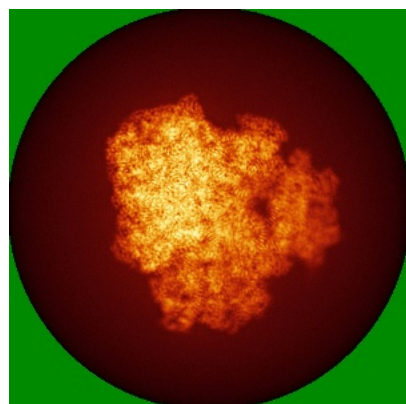


Y

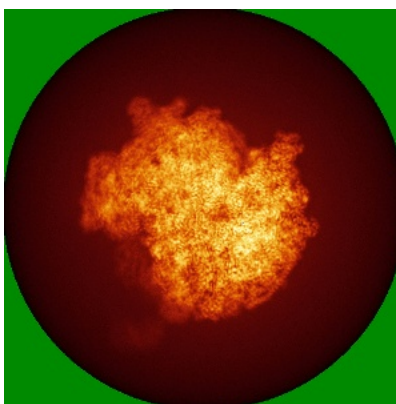


Z

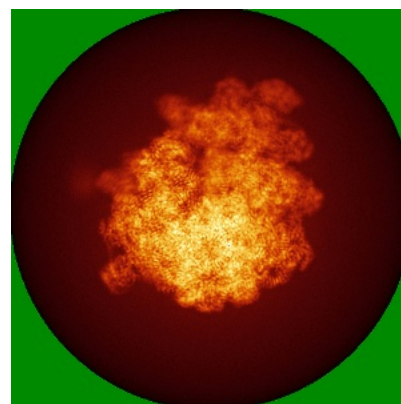
6.4.2 Raw map



X



Y

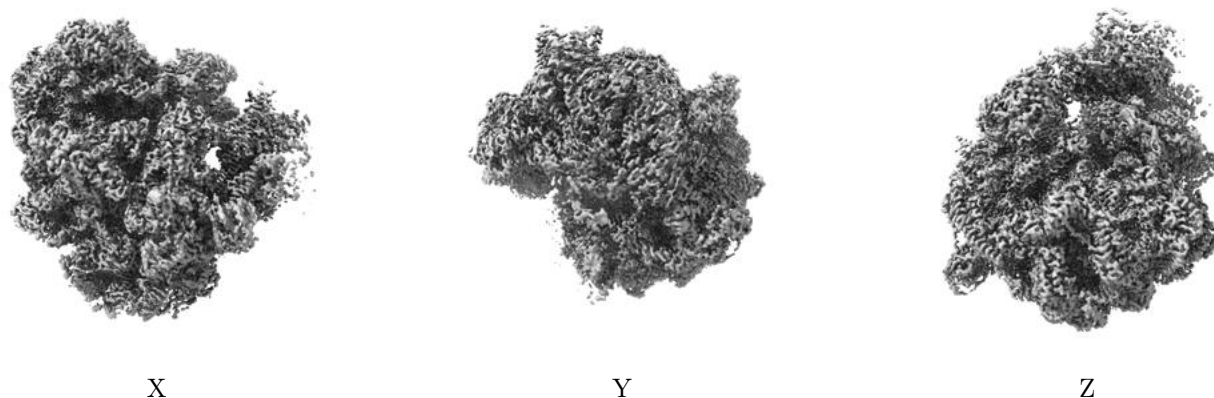


Z

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.

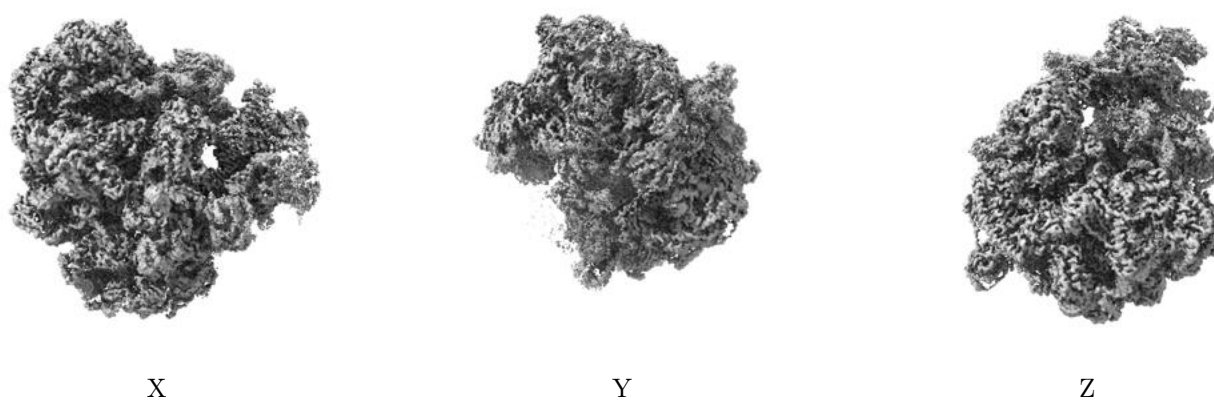
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. 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.

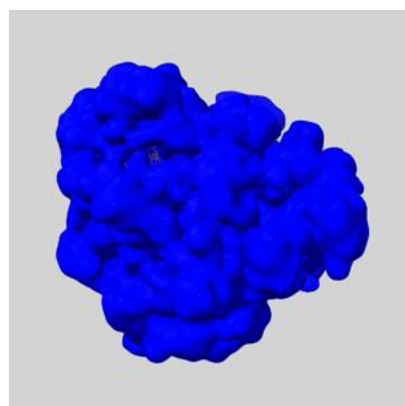
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

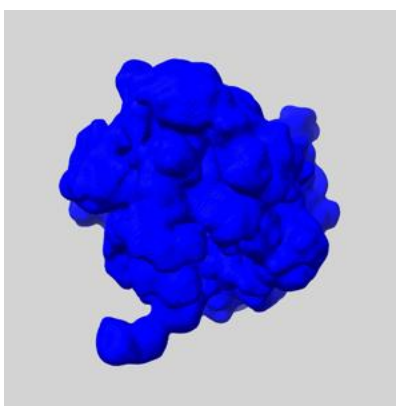
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

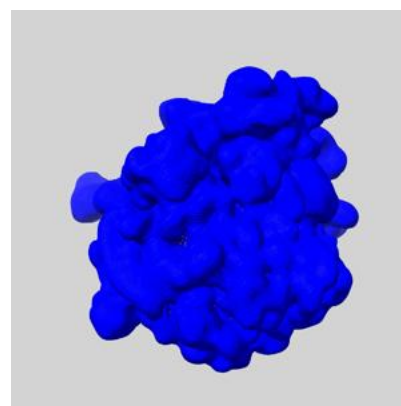
6.6.1 emd_13936_msk_1.map [i](#)



X



Y

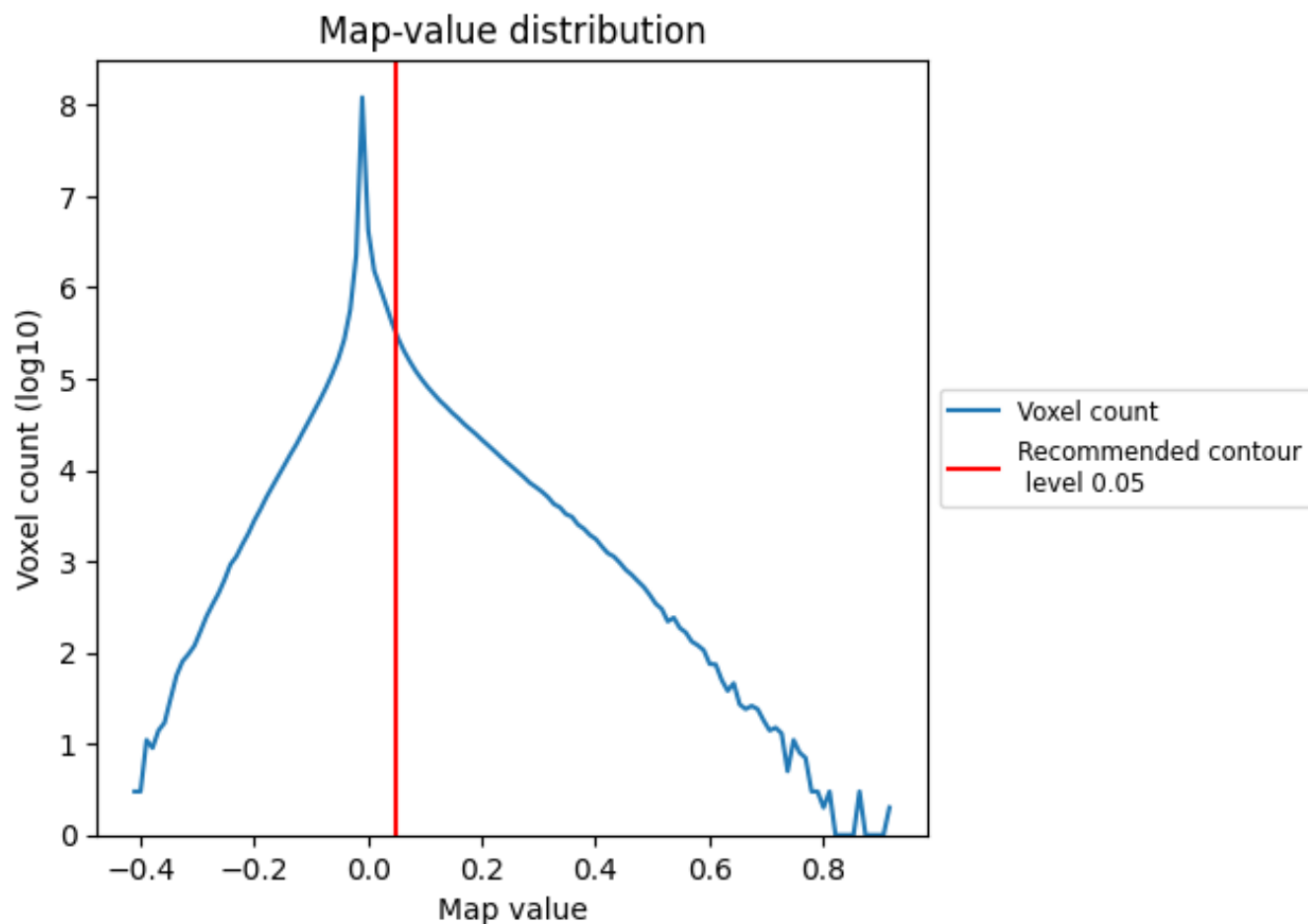


Z

7 Map analysis [i](#)

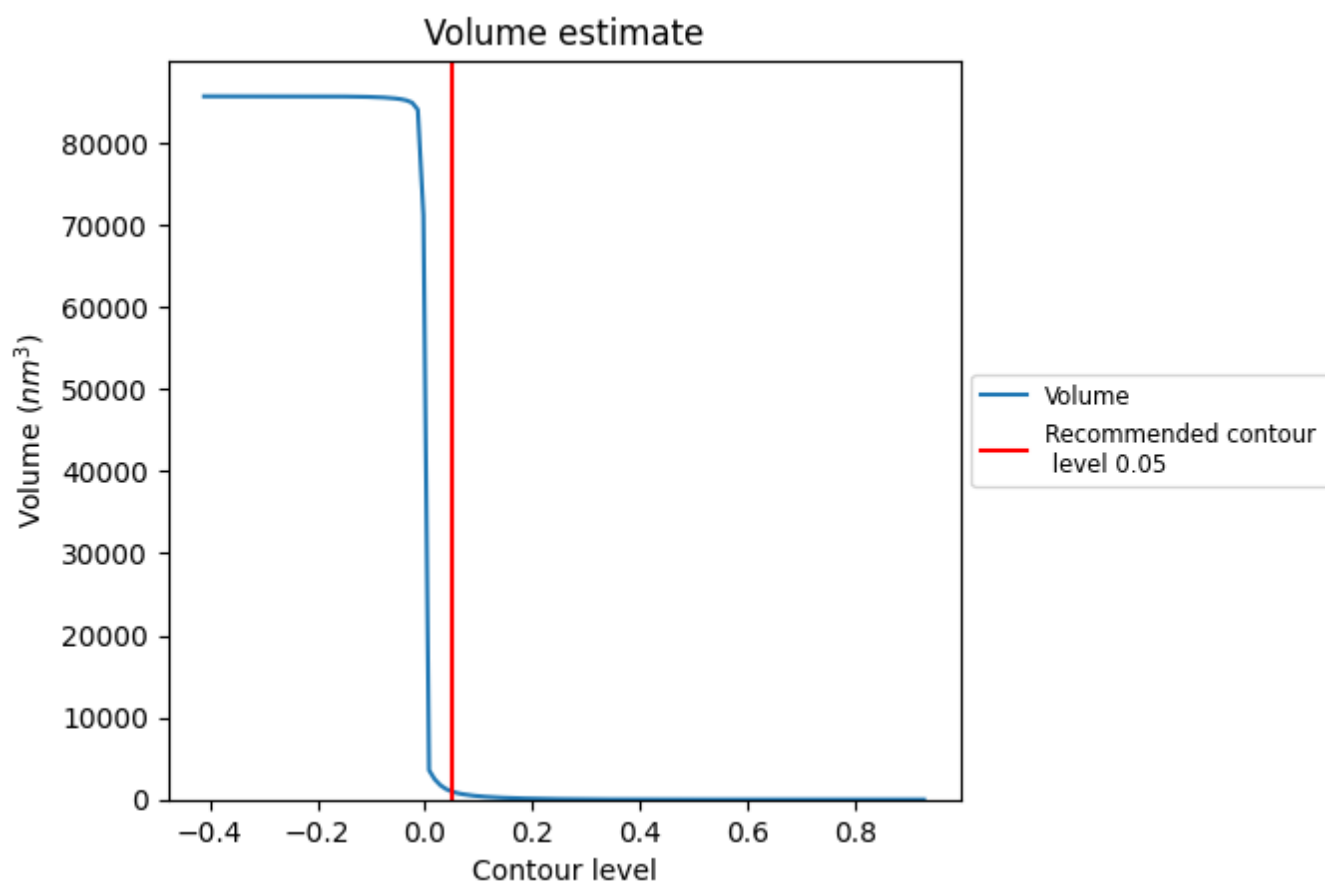
This section contains the results of statistical analysis of the map.

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.

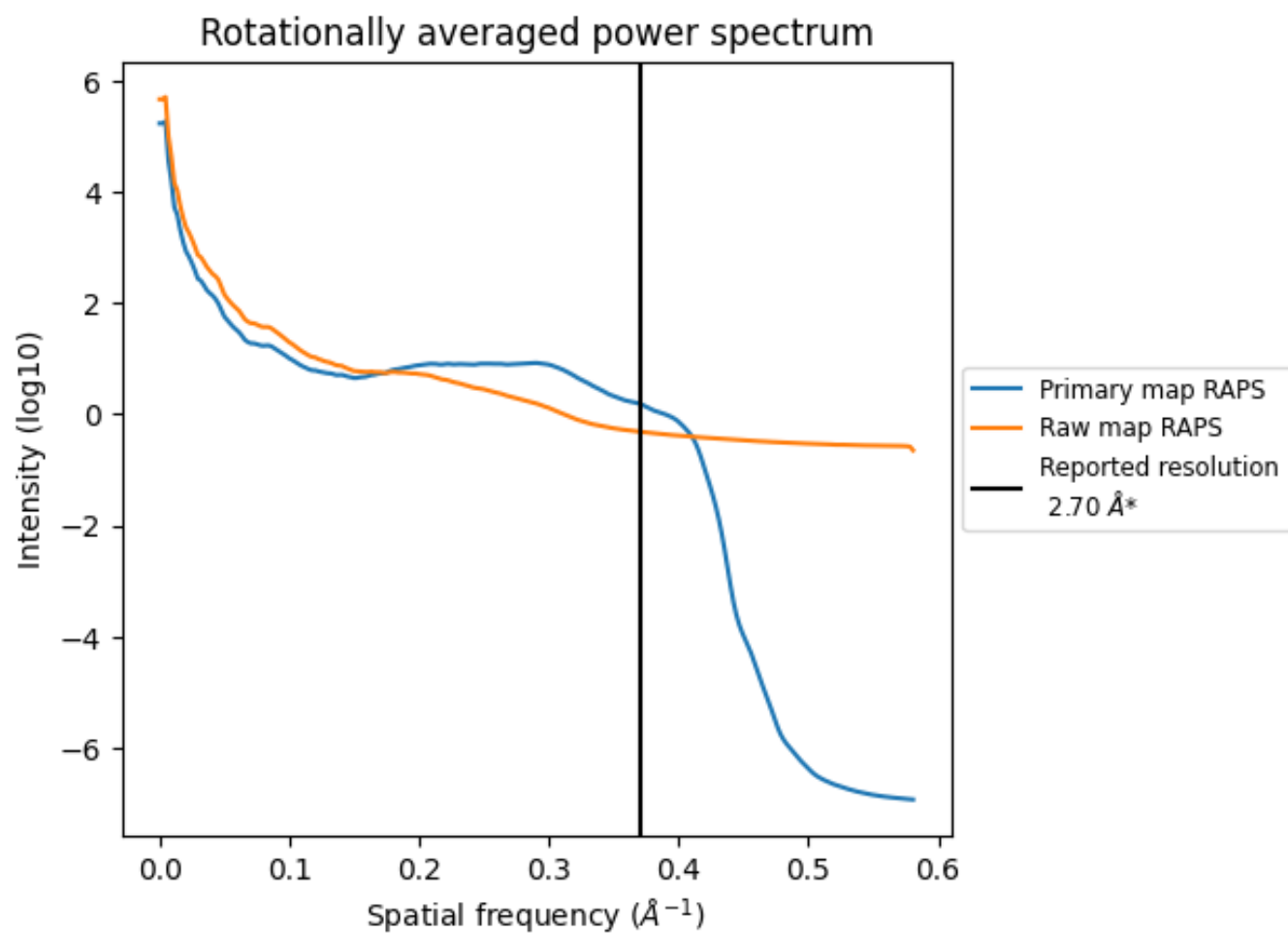
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 982 nm³; this corresponds to an approximate mass of 887 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 ⓘ

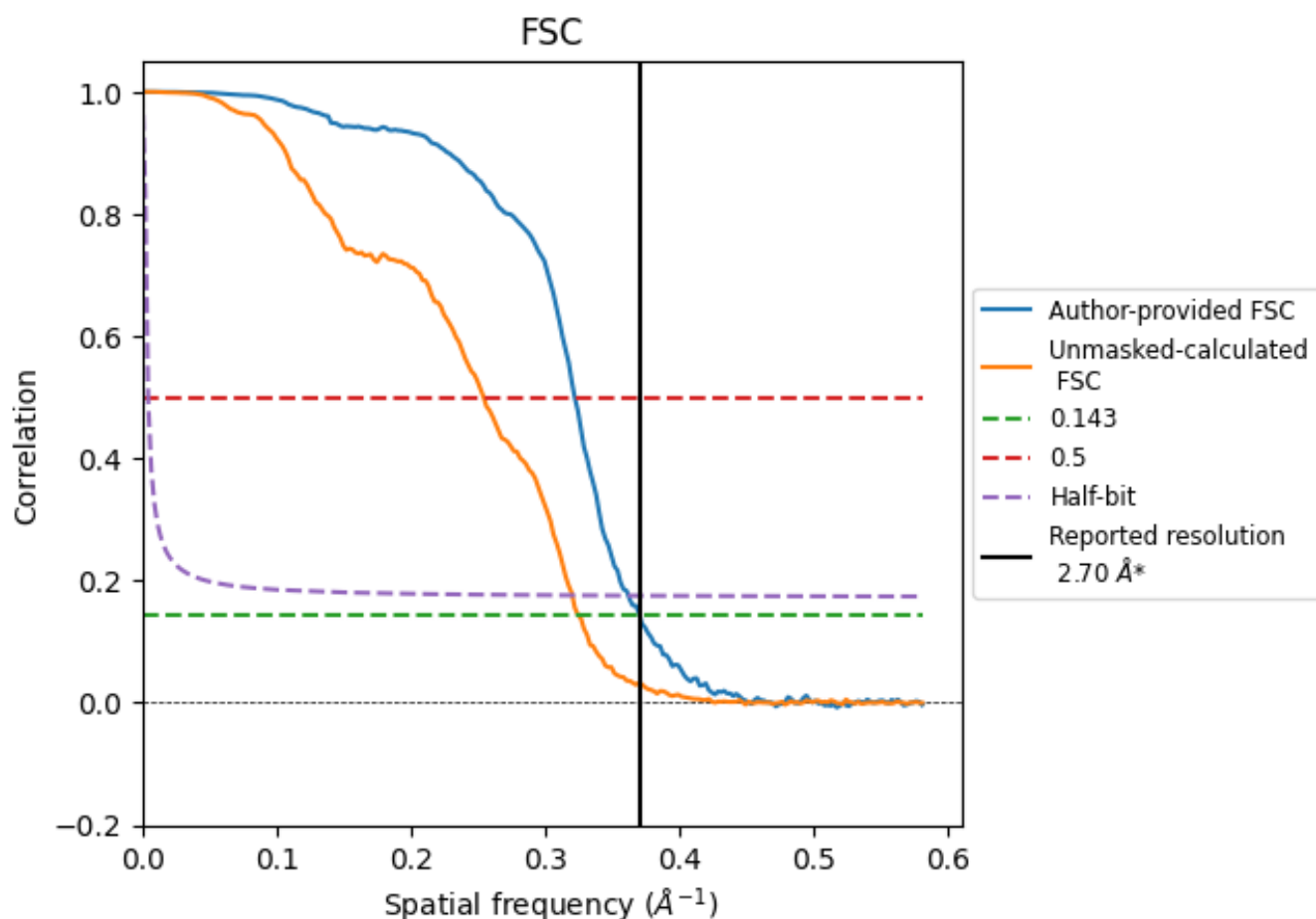


*Reported resolution corresponds to spatial frequency of 0.370 $\text{\AA}^{-1}$

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 0.370 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

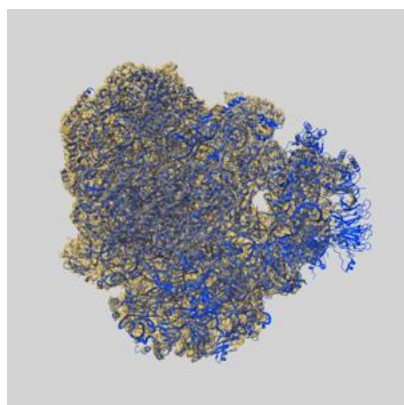
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.70	-	-
Author-provided FSC curve	2.70	3.11	2.76
Unmasked-calculated*	3.08	3.93	3.12

*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 3.08 differs from the reported value 2.7 by more than 10 %

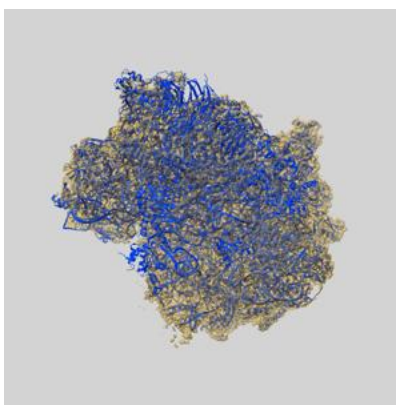
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13936 and PDB model 7QEP. Per-residue inclusion information can be found in section 3 on page 19.

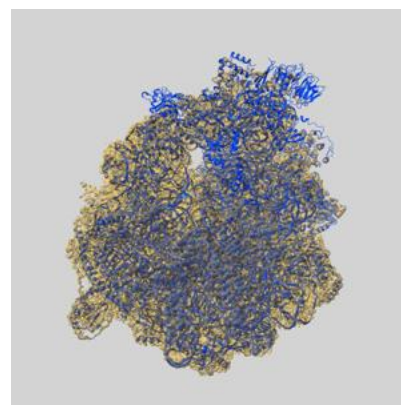
9.1 Map-model overlay [i](#)



X



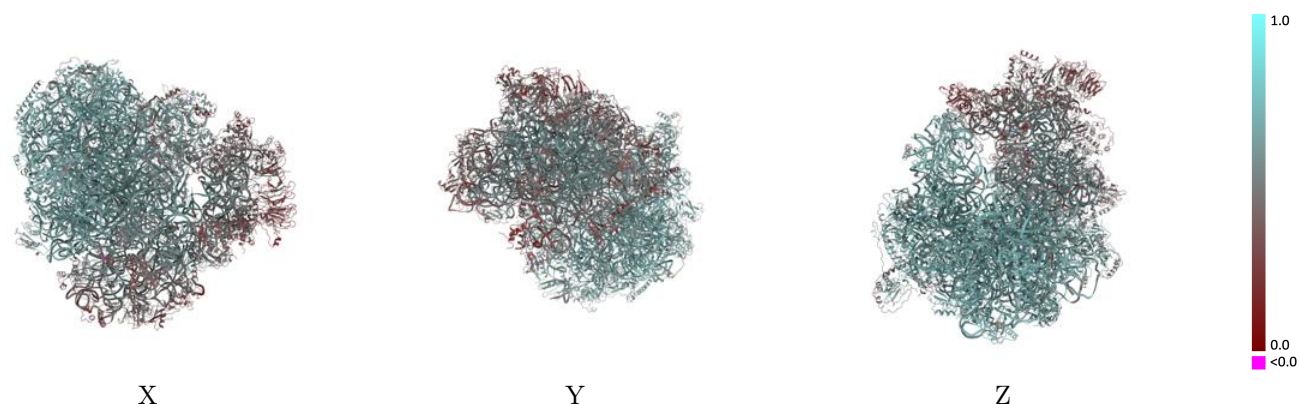
Y



Z

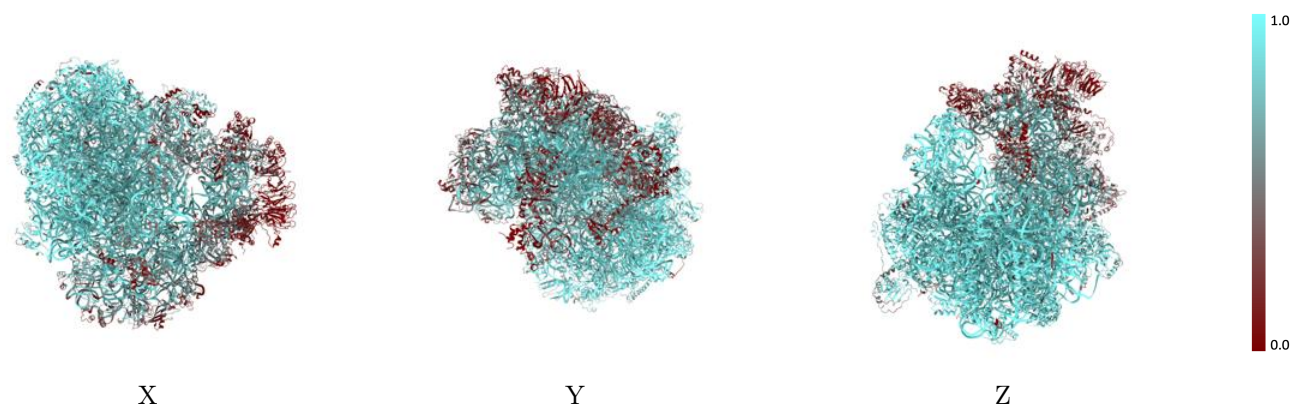
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



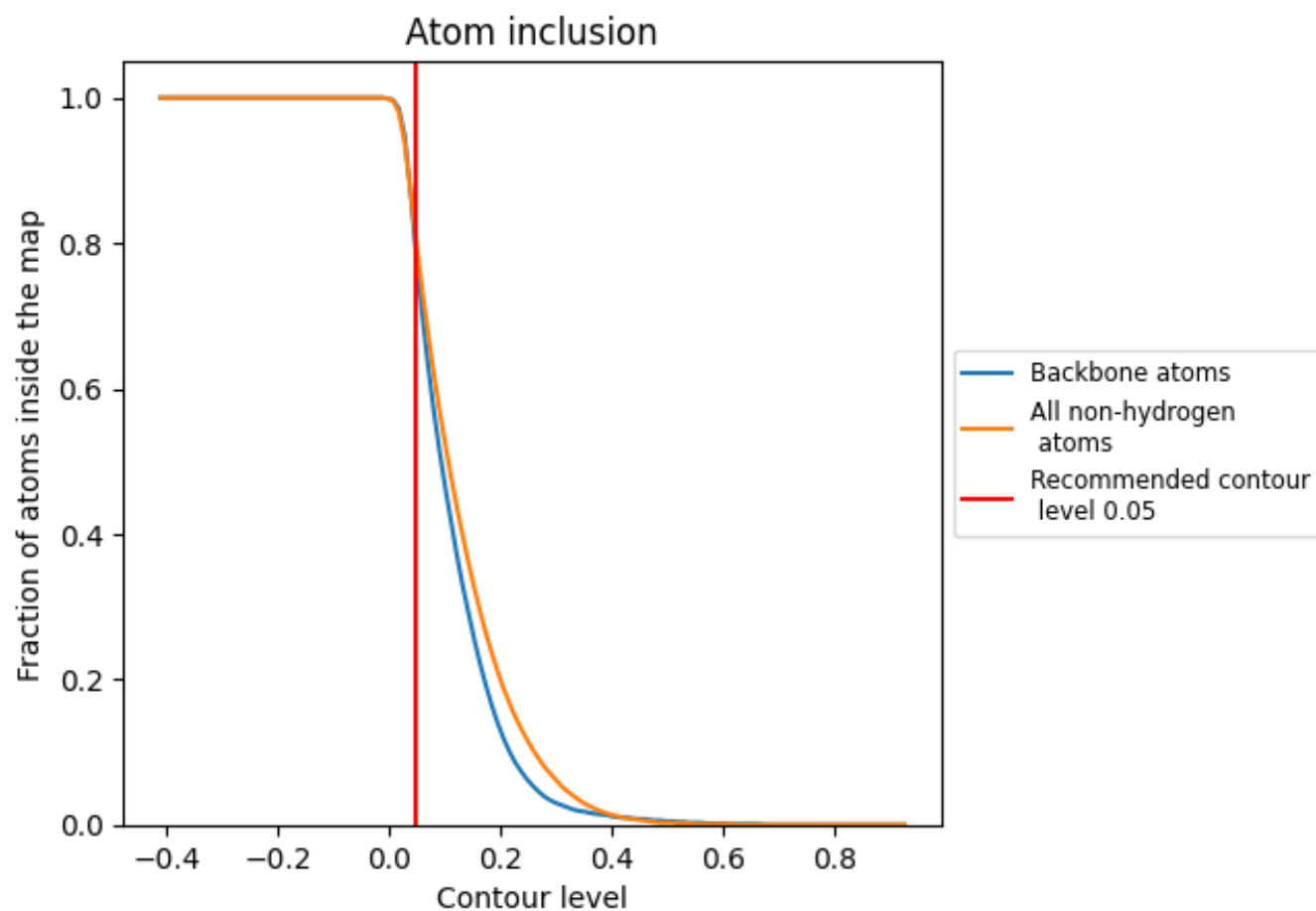
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7980	 0.5770
1	 0.9790	 0.6690
2	 0.9930	 0.6530
3	 0.8510	 0.5350
C0	 0.2100	 0.3530
C1	 0.6450	 0.4840
C2	 0.0050	 0.2160
C3	 0.6940	 0.5110
C4	 0.6680	 0.5340
C5	 0.1980	 0.3310
C6	 0.3300	 0.4370
C7	 0.2410	 0.3760
C8	 0.2830	 0.3840
C9	 0.2990	 0.4130
D0	 0.2340	 0.3920
D1	 0.4810	 0.4570
D2	 0.7580	 0.5260
D3	 0.6350	 0.5220
D4	 0.3570	 0.3660
D5	 0.0920	 0.3430
D6	 0.7680	 0.5650
D7	 0.5750	 0.4580
D8	 0.1330	 0.3740
D9	 0.4900	 0.4530
E1	 0.0000	 0.2250
L1	 0.1490	 0.4190
L2	 0.9160	 0.6480
L3	 0.9150	 0.6450
L4	 0.9040	 0.6390
L5	 0.8670	 0.5940
L6	 0.7150	 0.5330
L7	 0.9010	 0.6340
L8	 0.7990	 0.5610
L9	 0.8800	 0.5990
M0	 0.9160	 0.6420



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Chain	Atom inclusion	Q-score
M1	 0.7730	 0.5600
M3	 0.9190	 0.6320
M4	 0.8100	 0.5770
M5	 0.9700	 0.6760
M6	 0.8550	 0.6160
M7	 0.9310	 0.6590
M8	 0.9360	 0.6440
M9	 0.8180	 0.6010
MD	 0.4480	 0.5150
MS	 0.7500	 0.5740
N0	 0.9270	 0.6340
N1	 0.8560	 0.6250
N2	 0.7780	 0.5420
N3	 0.9190	 0.6550
N4	 0.6820	 0.5790
N5	 0.8920	 0.6310
N6	 0.8880	 0.6280
N7	 0.8240	 0.5560
N8	 0.9360	 0.6520
N9	 0.9300	 0.6510
O0	 0.8470	 0.5930
O1	 0.8960	 0.6250
O2	 0.9240	 0.6470
O3	 0.9430	 0.6480
O4	 0.9530	 0.6510
O5	 0.9050	 0.6310
O6	 0.8120	 0.5880
O7	 0.9800	 0.7020
O9	 0.9490	 0.6580
P0	 0.8840	 0.6140
P2	 0.8950	 0.6340
P3	 0.8970	 0.6430
RA	 0.0330	 0.2920
S0	 0.4150	 0.4290
S1	 0.5330	 0.4770
S2	 0.6520	 0.5210
S3	 0.3520	 0.4310
S4	 0.5480	 0.4340
S5	 0.2850	 0.4270
S6	 0.4820	 0.3970
S7	 0.3240	 0.3880
S8	 0.7080	 0.4810

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Chain	Atom inclusion	Q-score
S9	 0.4770	 0.4100