



wwPDB EM Validation Summary Report ⓘ

Sep 29, 2026 – 06:56 PM JST

PDB ID : 9X4D / pdb_00009x4d
EMDB ID : EMD-66542
Title : Structure of the old Killifish Ribosome
Authors : Kim, J.; Song, J.J.; Kim, Y.
Deposited on : 2025-10-10
Resolution : 2.93 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
MolProbity : 4-5-2 with Phenix2.2
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) : 2.51

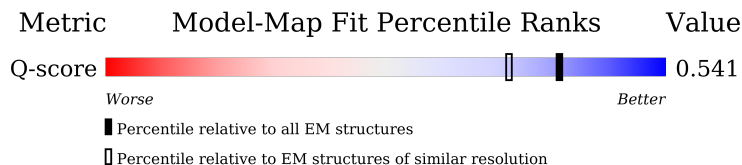
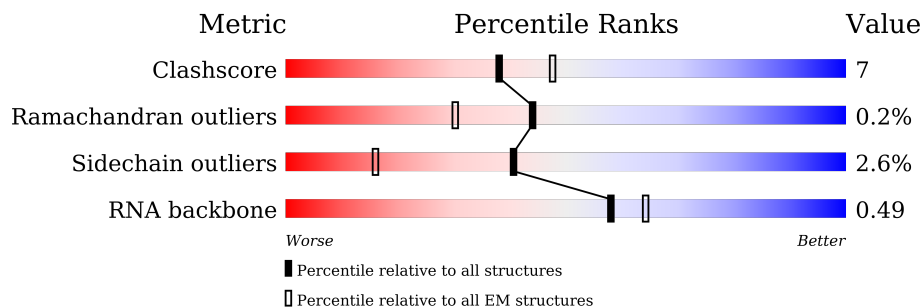
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.93 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.



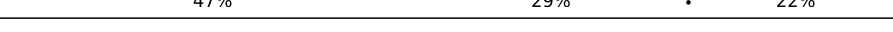
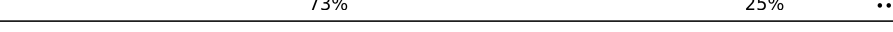
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13037 (2.43 - 3.43)

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	11	51	73% 25% .
2	21	128	7% 27% 10% 63%
3	Z1	136	80% 18% ..

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Mol	Chain	Length	Quality of chain
4	a1	257	
5	b1	64	
6	d2	69	
7	e1	117	
8	f1	110	
9	g1	92	
10	g2	313	
11	h1	297	
12	i1	120	
13	j1	161	
14	k1	192	
15	l1	259	
16	m1	266	
17	m2	132	
18	n1	148	
19	q2	119	
20	r2	130	
21	u2	203	
22	x2	133	
23	y2	143	
24	z2	166	
25	32	84	
26	41	137	
27	42	266	
28	K1	70	

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Mol	Chain	Length	Quality of chain
29	51	25	
30	61	215	
31	71	178	
32	72	151	
33	81	205	
34	82	142	
35	91	116	
36	B1	403	
37	B2	151	
38	C1	375	
39	D1	124	
40	E1	135	
41	F1	245	
42	H1	123	
43	H2	83	
44	I1	105	
45	J1	97	
46	J2	279	
47	K2	208	
48	L1	211	
49	L2	194	
50	M1	137	
51	A2	145	
52	P2	152	
53	i2	134	

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Mol	Chain	Length	Quality of chain
54	w2	247	
55	A1	4024	
56	C2	1838	
57	M2	146	
58	N1	204	
59	N2	73	
60	O1	106	
61	O2	263	
62	P1	184	
63	Q1	188	
64	R1	196	
65	S1	176	
66	S2	146	
67	T1	160	
68	T2	123	
69	U1	129	
70	U2	194	
71	V1	140	
72	W1	157	
73	W2	249	
74	X1	155	
75	Y1	145	
76	Y2	161	
77	k2	317	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 190927 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	11	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 2 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	21	47	Total	C	N	O	S	0	0
			387	238	84	59	6		

- Molecule 3 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z1	135	Total	C	N	O	S	0	0
			1107	715	208	180	4		

- Molecule 4 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a1	246	Total	C	N	O	S	0	0
			1890	1186	387	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b1	50	Total	C	N	O	S	0	0
			428	265	94	68	1		

- Molecule 6 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d2	56	Total	C	N	O	S	0	0
			443	270	91	80	2		

- Molecule 7 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e1	108	Total	C	N	O	S	0	0
			861	540	177	138	6		

- Molecule 8 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f1	109	Total	C	N	O	S	0	0
			872	554	170	144	4		

- Molecule 9 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	g1	88	Total	C	N	O	S	0	0
			686	434	133	113	6		

- Molecule 10 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	g2	209	Total	C	N	O	S	0	0
			1660	1057	292	302	9		

- Molecule 11 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	h1	286	Total	C	N	O	S	0	0
			2311	1465	420	415	11		

- Molecule 12 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i1	119	Total	C	N	O	P	0	0
			2541	1135	460	828	118		

- Molecule 13 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j1	147	Total	C	N	O	P	0	0
			3135	1398	561	1029	147		

- Molecule 14 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k1	189	Total	C	N	O	S	0	0
			1503	947	278	272	6		

- Molecule 15 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l1	210	Total	C	N	O	S	0	0
			1677	1074	324	275	4		

- Molecule 16 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	m1	213	Total	C	N	O	S	0	0
			1730	1108	328	290	4		

- Molecule 17 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	m2	122	Total	C	N	O	S	0	0
			1001	635	195	166	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n1	147	Total	C	N	O	S	0	0
			1159	736	231	187	5		

- Molecule 19 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	q2	93	Total	C	N	O	S	0	0
			744	465	143	132	4		

- Molecule 20 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	r2	129	Total	C	N	O	S	0	0
			1036	660	193	177	6		

- Molecule 21 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u2	177	Total	C	N	O	S	0	0
			1401	881	257	256	7		

- Molecule 22 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	x2	47	Total	C	N	O		0	0
			380	233	85	62			

- Molecule 23 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y2	139	Total	C	N	O	S	0	0
			1083	684	215	181	3		

- Molecule 24 is a protein called Ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z2	37	Total	C	N	O	S	0	0
			317	212	54	47	4		

- Molecule 25 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	32	68	Total	C	N	O	S	0	0
			549	343	106	97	3		

- Molecule 26 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	41	123	Total	C	N	O	S	0	0
			979	610	200	166	3		

- Molecule 27 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	42	210	Total	C	N	O	S	0	0
			1708	1083	307	304	14		

- Molecule 28 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	K1	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

- Molecule 29 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	51	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 30 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	61	104	Total	C	N	O	S	0	0
			836	529	164	136	7		

- Molecule 31 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	71	149	Total	C	N	O	S	0	0
			1212	763	235	209	5		

- Molecule 32 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	72	131	Total	C	N	O	S	0	0
			981	600	193	182	6		

- Molecule 33 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	81	204	Total	C	N	O	S	0	0
			1660	1074	320	263	3		

- Molecule 34 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	82	95	Total	C	N	O	S	0	0
			756	468	155	127	6		

- Molecule 35 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	91	96	Total	C	N	O	S	0	0
			746	471	133	135	7		

- Molecule 36 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B1	394	Total	C	N	O	S	0	0
			3173	2018	597	545	13		

- Molecule 37 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	B2	150	Total	C	N	O	S	0	0
			1205	771	229	204	1		

- Molecule 38 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	C1	349	Total	C	N	O	S	0	0
			2788	1762	547	464	15		

- Molecule 39 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	D1	102	Total	C	N	O	S	0	0
			837	529	165	139	4		

- Molecule 40 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	E1	127	Total	C	N	O	S	0	0
			1042	663	208	165	6		

- Molecule 41 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	F1	226	Total	C	N	O	S	0	0
			1865	1200	360	296	9		

- Molecule 42 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	H1	121	Total	C	N	O	S	0	0
			1003	632	203	167	1		

- Molecule 43 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	H2	83	Total	C	N	O	S	0	0
			645	400	118	123	4		

- Molecule 44 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	I1	100	Total	C	N	O	S	0	0
			811	509	170	127	5		

- Molecule 45 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	J1	86	Total	C	N	O	S	0	0
			706	433	156	113	4		

- Molecule 46 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	J2	216	Total	C	N	O	S	0	0
			1671	1081	286	295	9		

- Molecule 47 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	K2	203	Total	C	N	O	S	0	0
			1652	1040	321	287	4		

- Molecule 48 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L1	202	Total	C	N	O	S	0	0
			1632	1015	341	271	5		

- Molecule 49 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	L2	177	Total	C	N	O	S	0	0
			1473	939	293	239	2		

- Molecule 50 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	M1	133	Total	C	N	O	S	0	0
			1088	694	205	182	7		

- Molecule 51 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	A2	100	Total	C	N	O	S	0	0
			832	526	157	142	7		

- Molecule 52 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	P2	139	Total	C	N	O	S	0	0
			1155	725	234	195	1		

- Molecule 53 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	i2	119	Total	C	N	O	S	0	0
			969	608	180	178	3		

- Molecule 54 is a protein called DNA-(apurinic or apyrimidinic site) lyase.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	w2	206	Total	C	N	O	S	0	0
			1602	1023	290	282	7		

- Molecule 55 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A1	3205	Total	C	N	O	P	0	0
			68707	30615	12552	22335	3205		

- Molecule 56 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	C2	1485	Total	C	N	O	P	0	0
			31719	14168	5722	10344	1485		

- Molecule 57 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	M2	141	Total	C	N	O	S	0	0
			1088	685	208	192	3		

- Molecule 58 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	N1	203	Total	C	N	O	S	0	0
			1697	1066	357	268	6		

- Molecule 59 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	N2	39	Total	C	N	O	S	0	0
			317	196	66	50	5		

- Molecule 60 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	O1	93	Total	C	N	O	S	0	0
			770	484	156	124	6		

- Molecule 61 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	O2	257	Total	C	N	O	S	0	0
			2040	1304	379	348	9		

- Molecule 62 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	P1	152	Total	C	N	O	S	0	0
			1232	770	243	210	9		

- Molecule 63 is a protein called Ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Q1	187	Total	C	N	O	S	0	0
			1510	946	315	244	5		

- Molecule 64 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	R1	171	Total	C	N	O	S	0	0
			1423	880	310	223	10		

- Molecule 65 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	S1	176	Total	C	N	O	S	0	0
			1458	932	286	231	9		

- Molecule 66 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	S2	138	Total	C	N	O	S	0	0
			1090	694	203	190	3		

- Molecule 67 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	T1	157	Total	C	N	O	S	0	0
			1290	818	252	216	4		

- Molecule 68 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	T2	70	Total	C	N	O	S	0	0
			568	367	102	98	1		

- Molecule 69 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	U1	91	Total	C	N	O	S	0	0
			757	488	132	135	2		

- Molecule 70 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	U2	177	Total	C	N	O	S	0	0
			1429	914	260	254	1		

- Molecule 71 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	V1	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

- Molecule 72 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	W1	61	Total	C	N	O	S	0	0
			512	329	100	81	2		

- Molecule 73 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	W2	221	Total	C	N	O	S	0	0
			1791	1120	355	309	7		

- Molecule 74 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	X1	118	Total	C	N	O	S	0	0
			968	619	182	166	1		

- Molecule 75 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Y1	128	Total	C	N	O	S	0	0
			1067	670	219	175	3		

- Molecule 76 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Y2	138	Total	C	N	O	S	0	0
			1121	711	214	191	5		

- Molecule 77 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	k2	270	Total	C	N	O	S	0	0
			2138	1361	371	395	11		

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

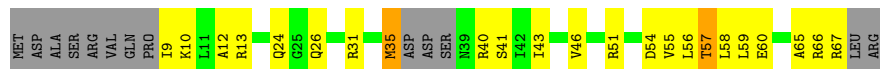
Mol	Chain	Residues	Atoms		AltConf
78	21	1	Total	Zn	0
			1	1	
78	e1	1	Total	Zn	0
			1	1	
78	g1	1	Total	Zn	0
			1	1	
78	82	1	Total	Zn	0
			1	1	
78	J1	1	Total	Zn	0
			1	1	
78	N2	1	Total	Zn	0
			1	1	
78	O1	1	Total	Zn	0
			1	1	

- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

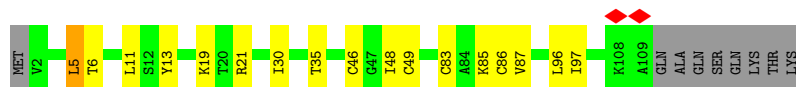
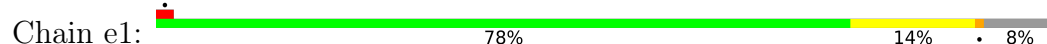
Mol	Chain	Residues	Atoms		AltConf
79	i1	1	Total	Mg	0
			1	1	
79	J1	1	Total	Mg	0
			1	1	
79	A1	62	Total	Mg	0
			62	62	
79	C2	21	Total	Mg	0
			21	21	



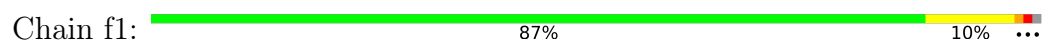
- Molecule 6: Small ribosomal subunit protein eS28



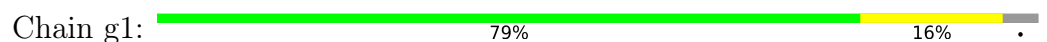
- Molecule 7: Large ribosomal subunit protein eL34



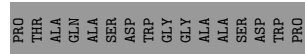
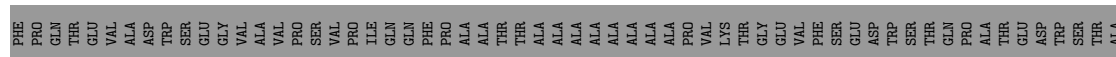
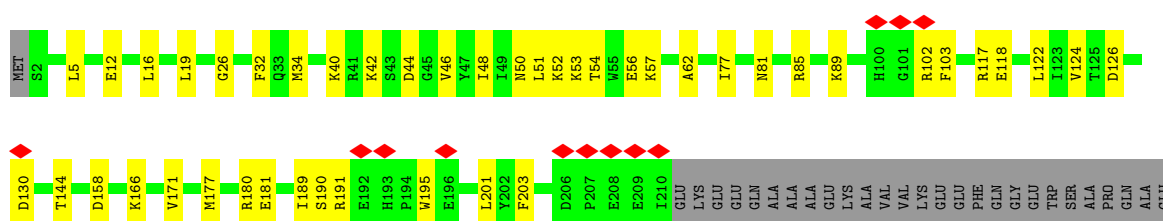
- Molecule 8: Large ribosomal subunit protein eL33



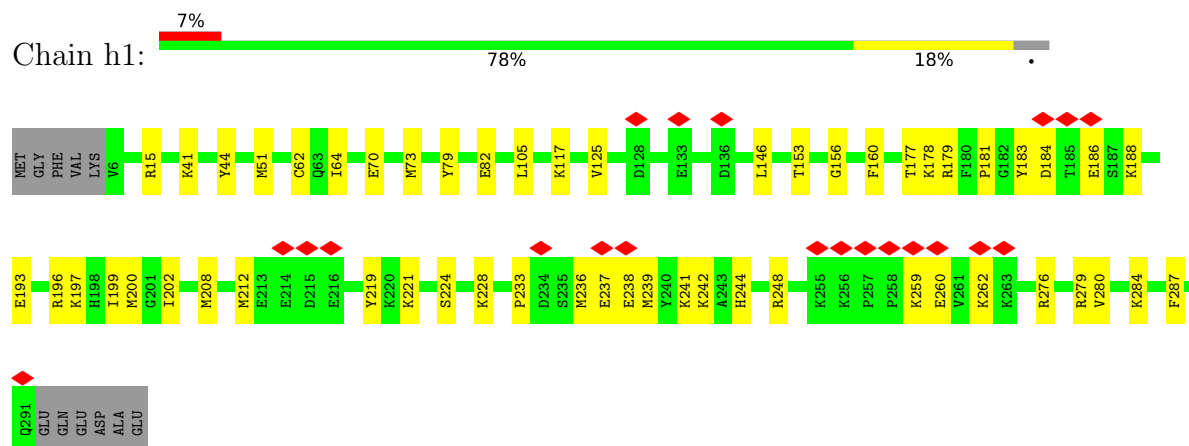
- Molecule 9: Large ribosomal subunit protein eL43



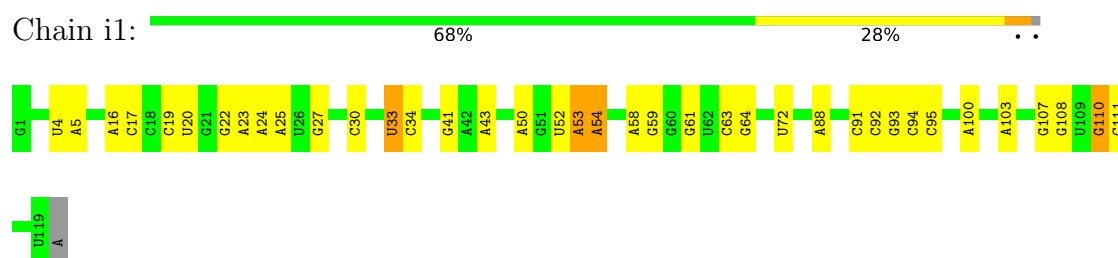
- Molecule 10: Small ribosomal subunit protein uS2



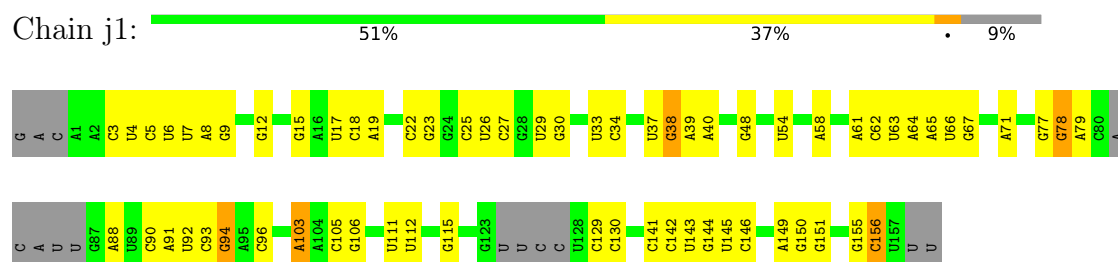
- Molecule 11: Large ribosomal subunit protein uL18



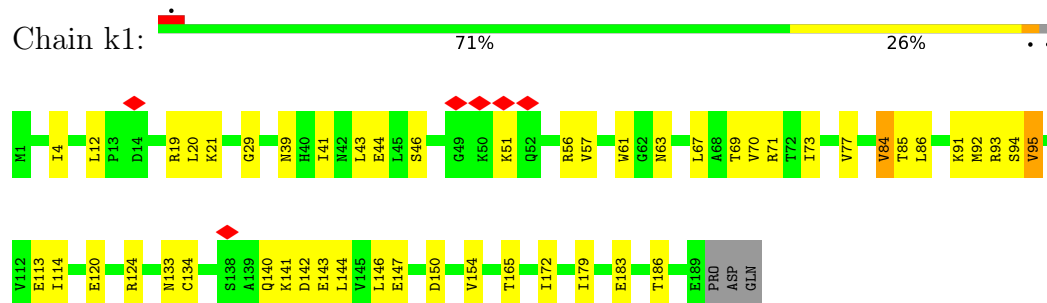
- Molecule 12: 5S rRNA



- Molecule 13: 5.8S rRNA

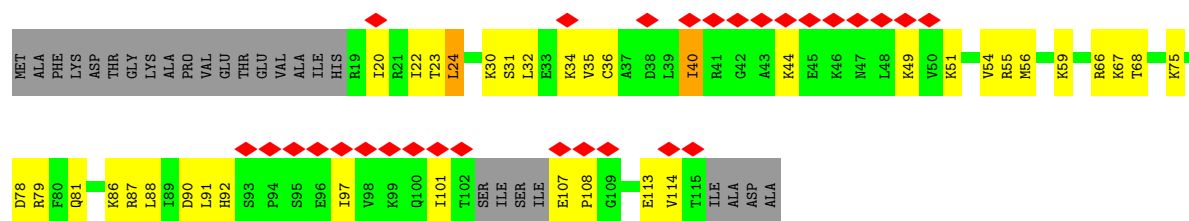


- Molecule 14: Large ribosomal subunit protein uL6



- Molecule 15: Large ribosomal subunit protein eL6





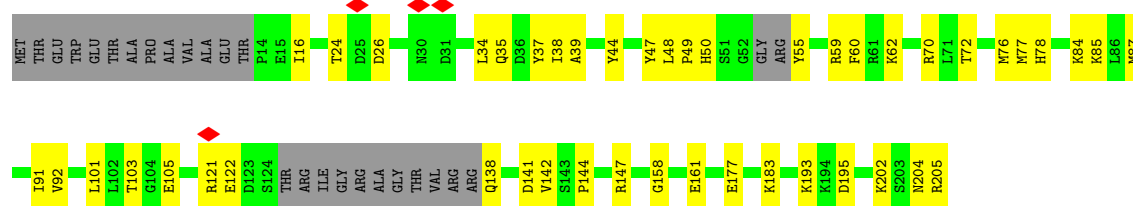
- Molecule 20: Small ribosomal subunit protein uS8

Chain r2: 73% 25% ..



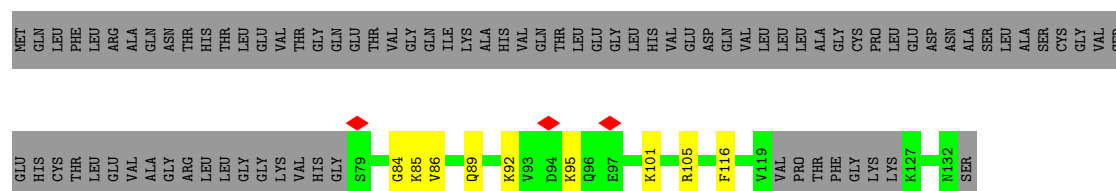
- Molecule 21: Small ribosomal subunit protein uS7

Chain u2: 65% 23% 13%



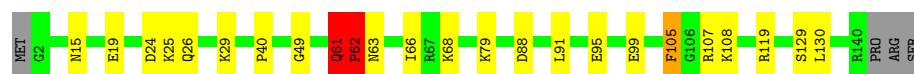
- Molecule 22: FAU ubiquitin like and ribosomal protein S30 fusion a

Chain x2: 29% 7% 65%



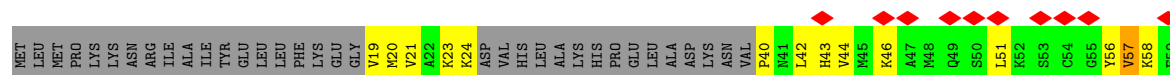
- Molecule 23: Small ribosomal subunit protein uS12

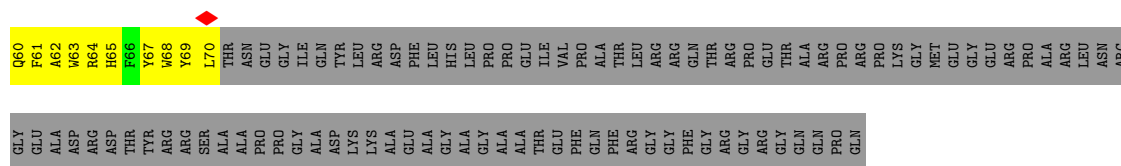
Chain y2: 80% 15% ..



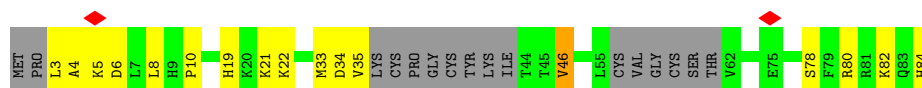
- Molecule 24: Ribosomal protein S10

Chain z2: 7% 8% 14% 78%

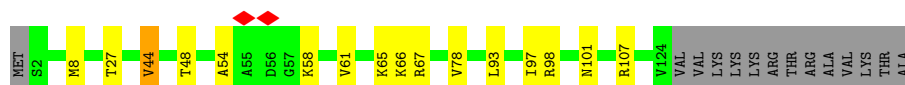
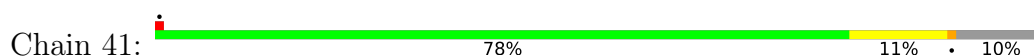




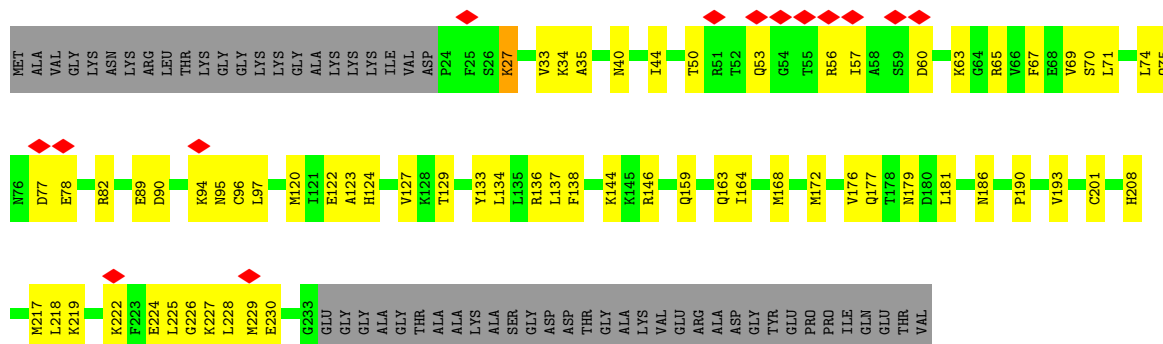
- Molecule 25: 40S ribosomal protein S27



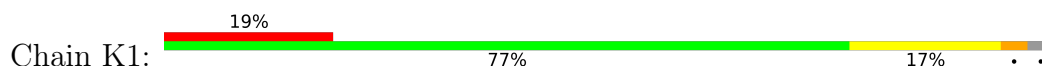
- Molecule 26: Large ribosomal subunit protein eL28



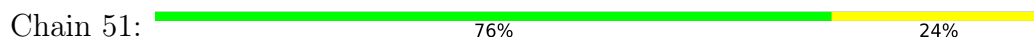
- Molecule 27: Small ribosomal subunit protein eS1



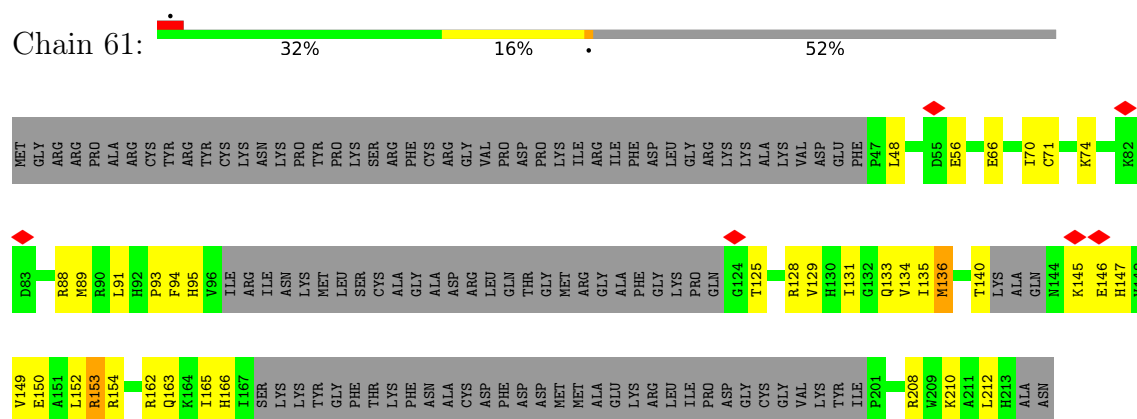
- Molecule 28: Large ribosomal subunit protein eL38



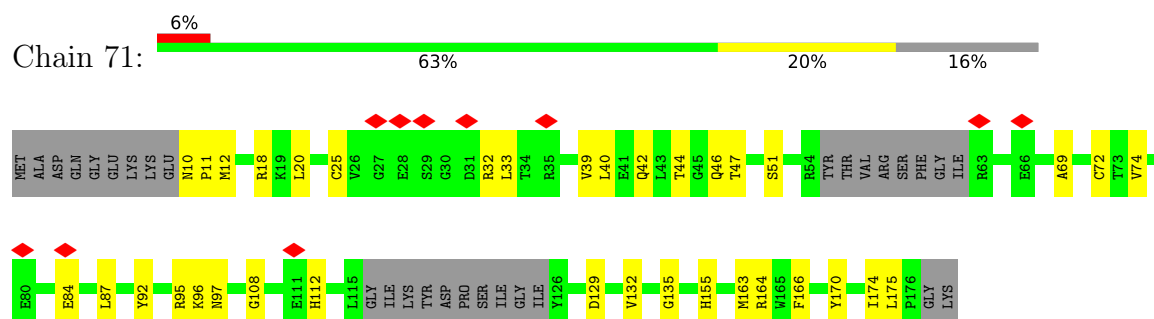
- Molecule 29: Small ribosomal subunit protein eS32



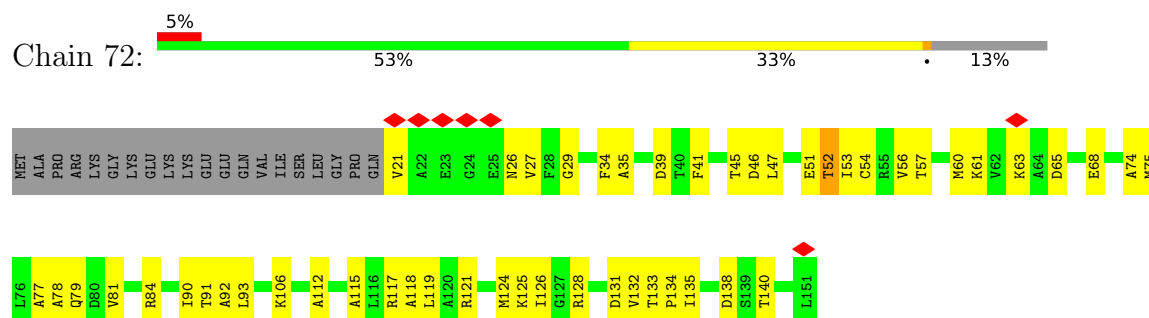
- Molecule 30: Ribosomal protein L10



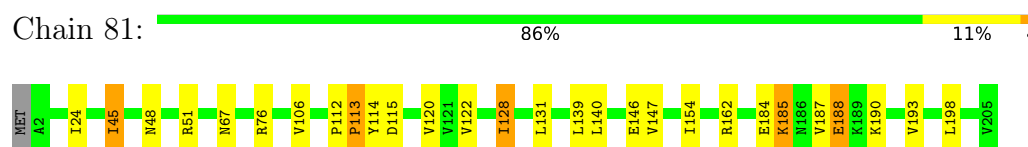
- Molecule 31: Large ribosomal subunit protein uL5



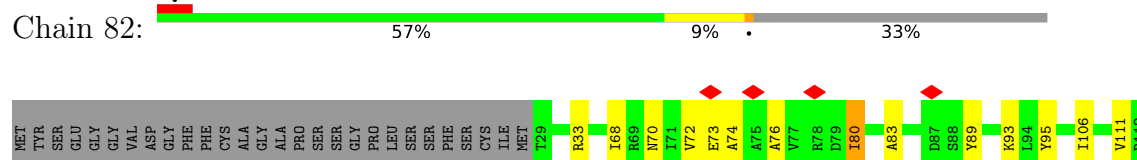
- Molecule 32: Small ribosomal subunit protein uS11

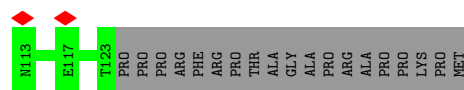


- Molecule 33: Large ribosomal subunit protein uL13

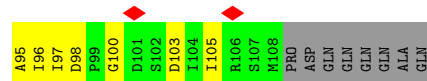
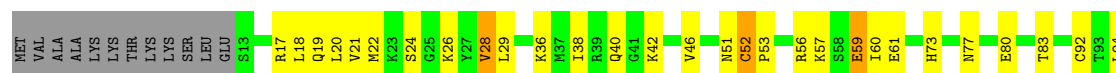


- Molecule 34: 40S ribosomal protein S26

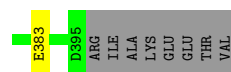
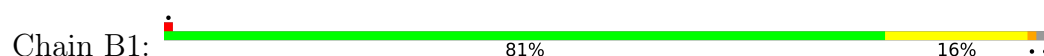




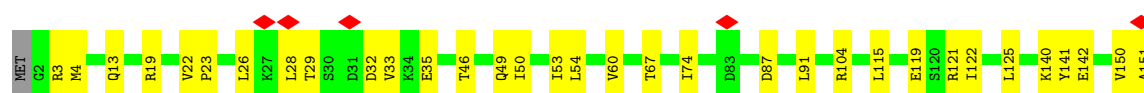
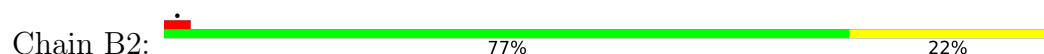
- Molecule 35: Large ribosomal subunit protein eL30



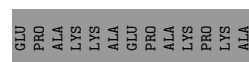
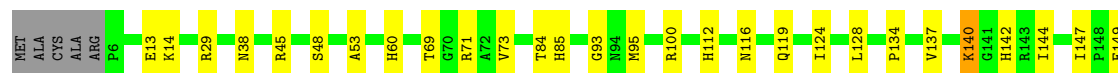
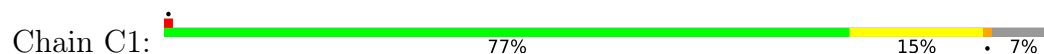
- Molecule 36: Large ribosomal subunit protein uL3



- Molecule 37: Small ribosomal subunit protein uS15



- Molecule 38: Ribosomal protein L4



- Molecule 39: Large ribosomal subunit protein eL31

Chain D1:  70% 10% 18%



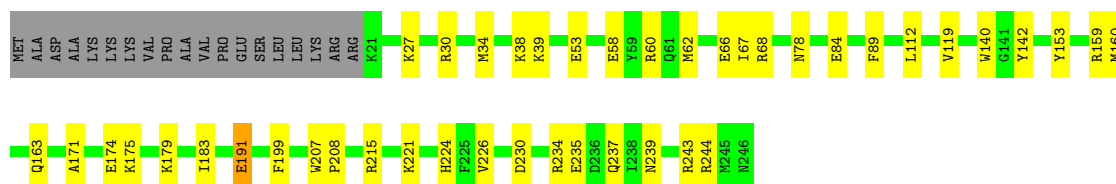
- Molecule 40: 60S ribosomal protein L32

Chain E1:  81% 11% 6%



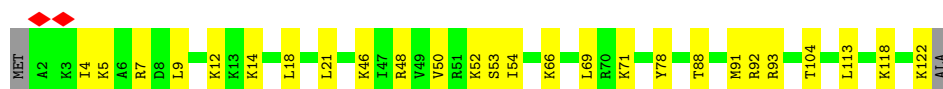
- Molecule 41: Large ribosomal subunit protein uL30

Chain F1:  75% 17% 8%



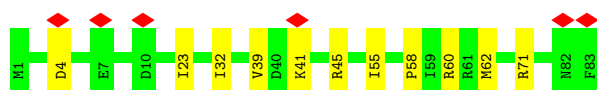
- Molecule 42: Large ribosomal subunit protein uL29

Chain H1:  77% 21% 2%



- Molecule 43: 40S ribosomal protein S21

Chain H2:  7% 87% 13%



- Molecule 44: 60S ribosomal protein L36

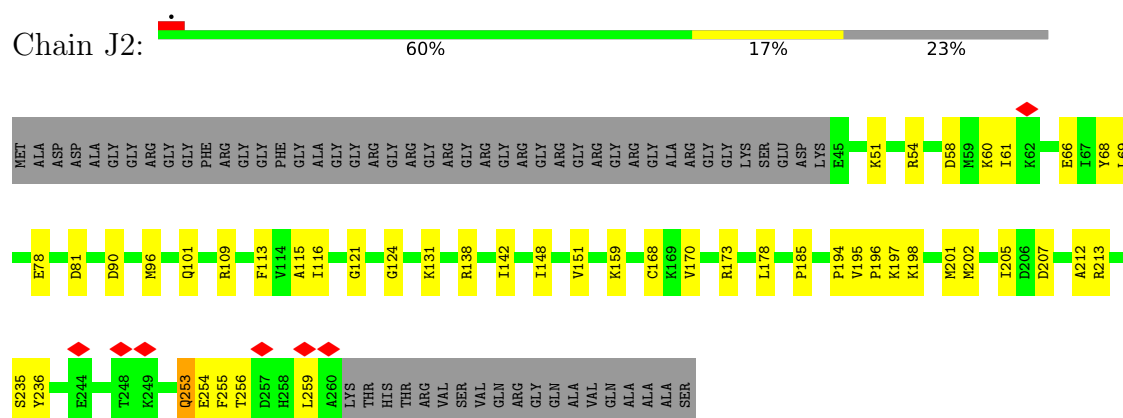
Chain I1:  85% 10% 5%



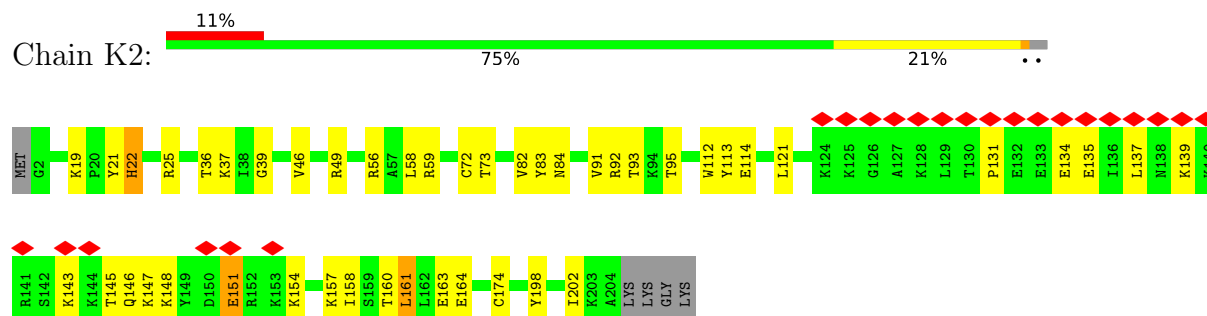
- Molecule 45: Ribosomal protein L37

Chain J1:  82% 6% 11%

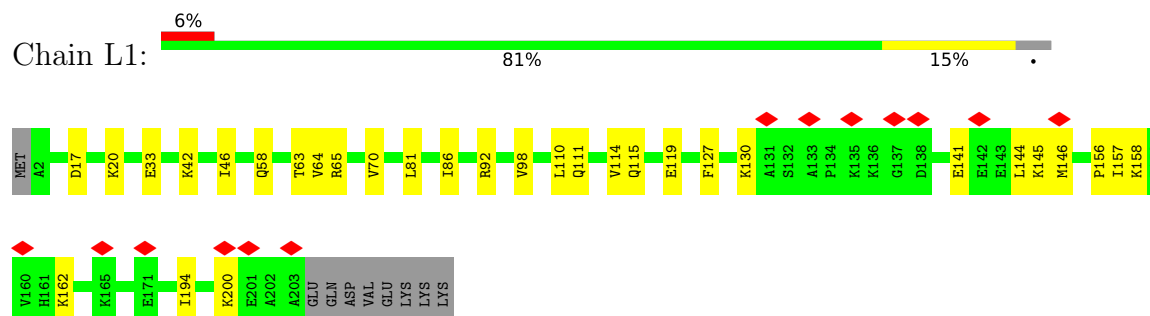
- Molecule 46: Small ribosomal subunit protein uS5



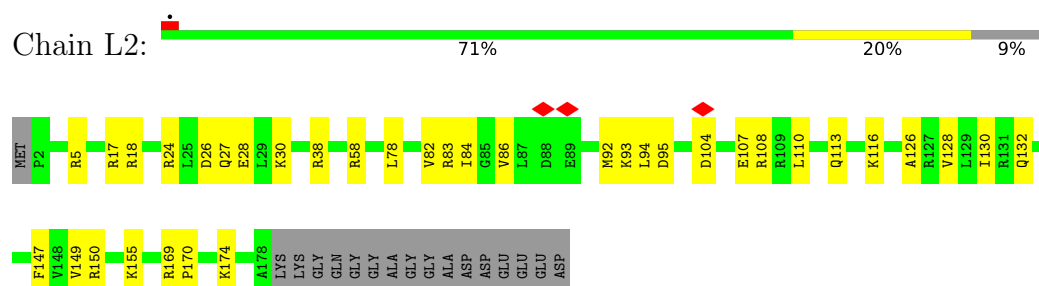
- Molecule 47: 40S ribosomal protein S8



- Molecule 48: 60S ribosomal protein L13



- Molecule 49: Small ribosomal subunit protein uS4

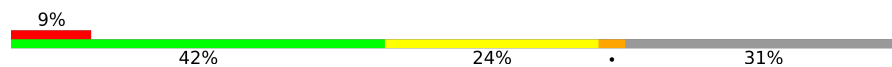


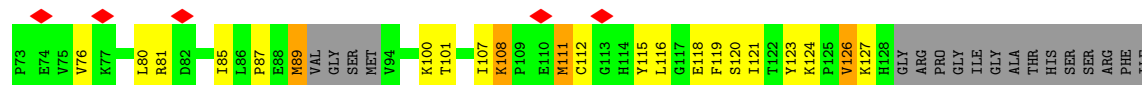
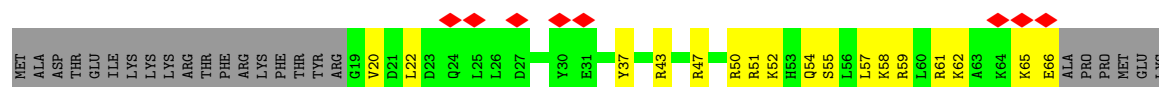
- Molecule 50: Large ribosomal subunit protein eL14

Chain M1: 



- Molecule 51: 40S ribosomal protein S15

Chain A2: 



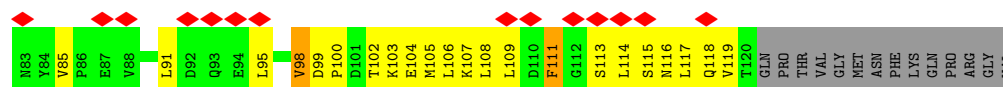
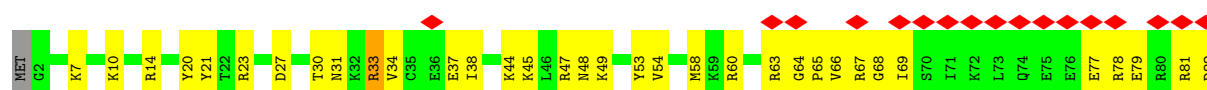
- Molecule 52: Small ribosomal subunit protein uS13

Chain P2: 



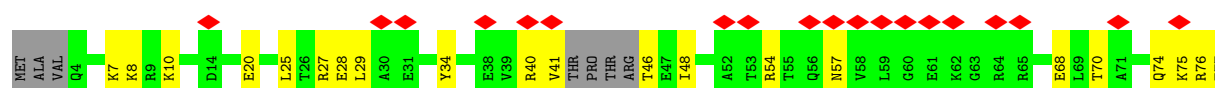
- Molecule 53: Small ribosomal subunit protein eS17

Chain i2: 

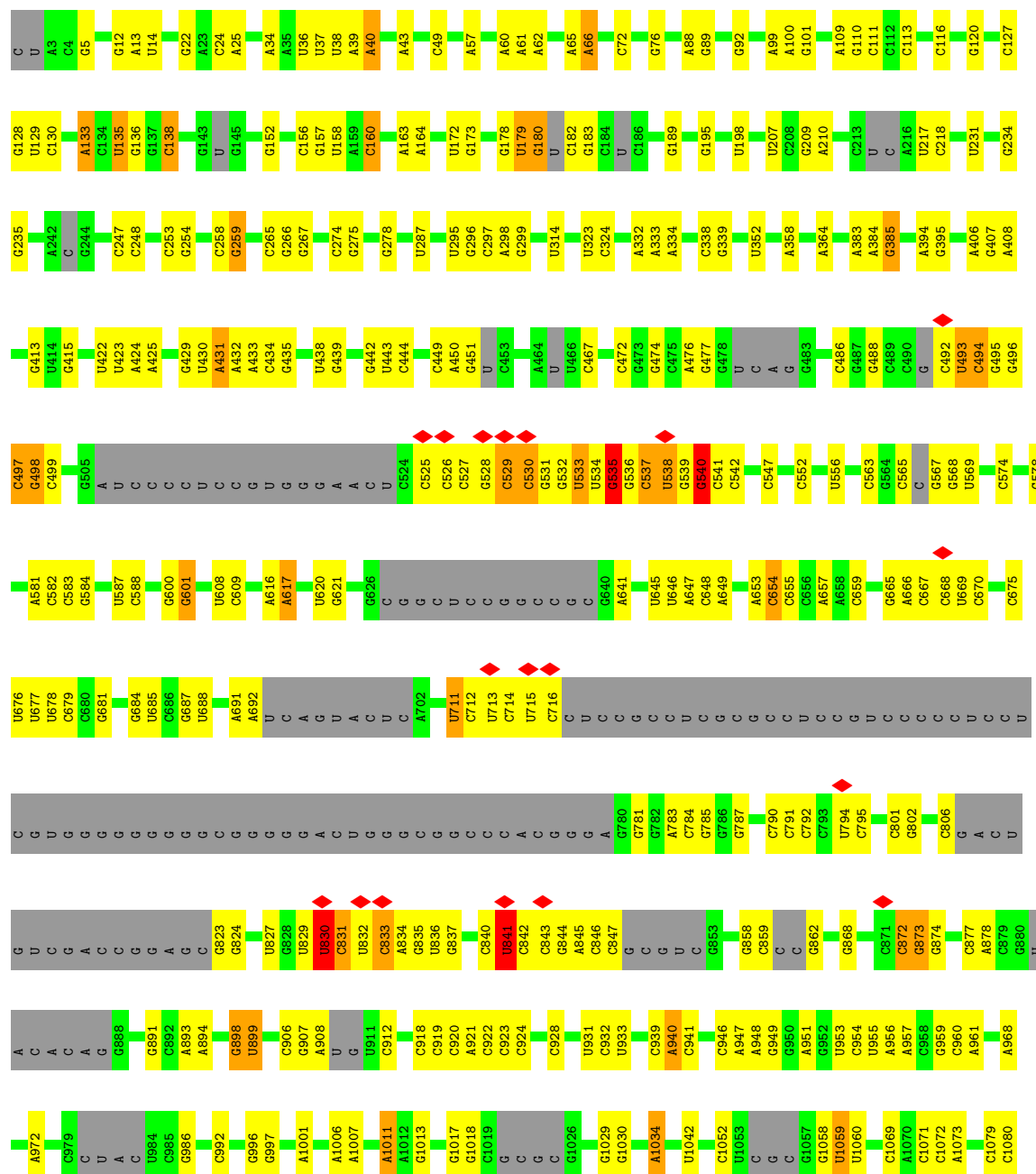


- Molecule 54: DNA-(apurinic or apyrimidinic site) lyase

Chain w2: 

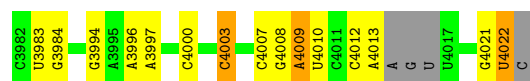


- Molecule 55: 28S rRNA



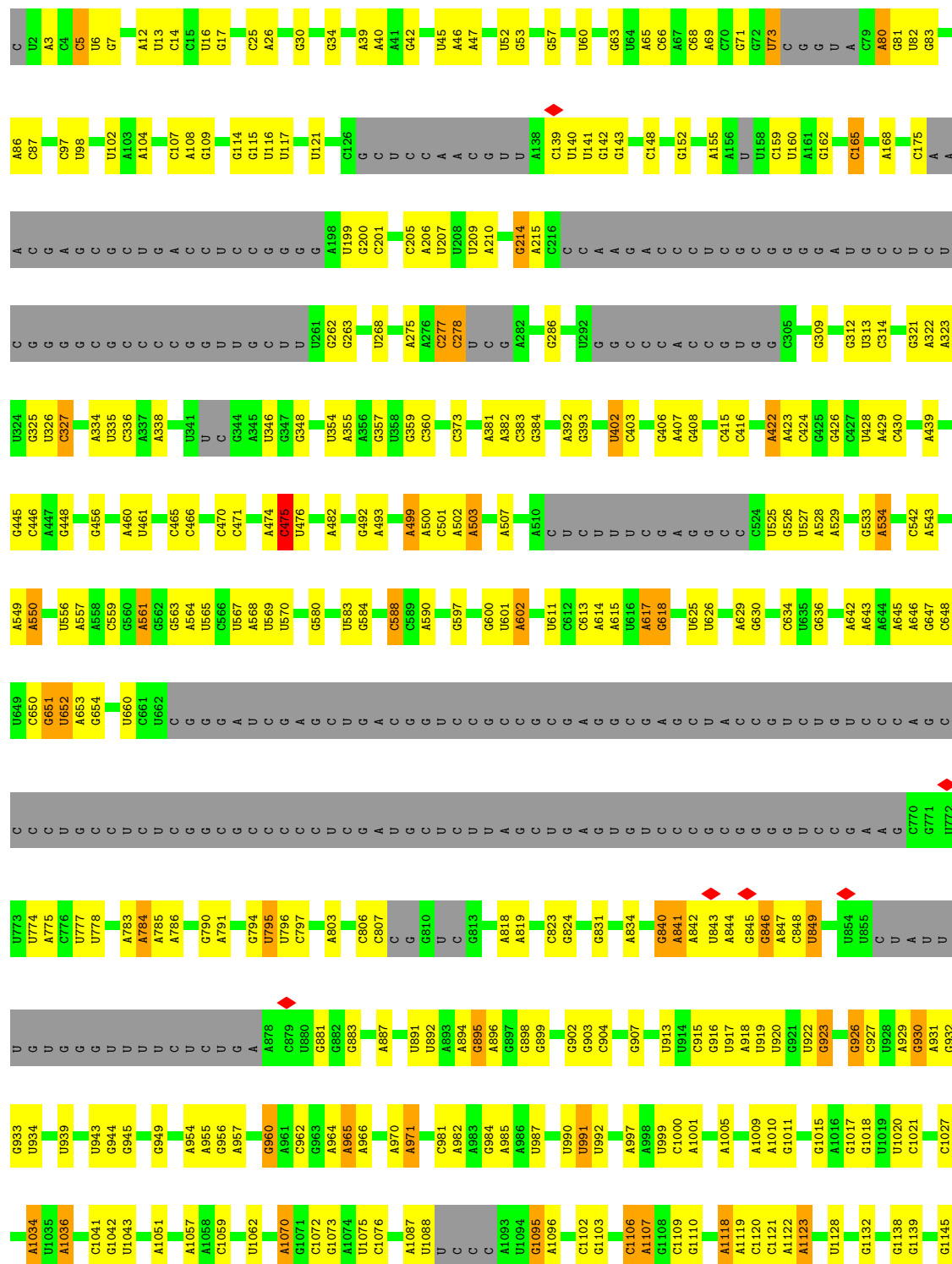
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G1215	G1216	C1222	A1224	C1225	G1228	G1235	C1239	A1242	A1243	G1244	A1245	G1252	C1256	A1257	G1265	C1272	C1273	U1274	A1280	G1281	G1283	G1287	U1288	C1289	G1291	C1294	A1295	G1296	G1301	G1302	C1303	G1309	U1310	C1311	C1313	C1314	C1315	A1316	G1317	G1330	A1373	U1374	U1375	C1376	U1377	C1378	A1379	A1380	A1381	U1385	A1386	A1387																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
U1320	U1321	U1322	C1324	G1327	C1333	G1335	A1336	U1337	G1338	U1340	U1341	A1342	G1343	A1344	G1439	G1440	C1441	C1442	G1448	C1449	C1450	C1451	A1452	C1453	A1461	A1462	G1463	C1464	C1469	U1470	G1471	U1476	G1477	A1482	A1486	C1487	C1488	G1489	A1490	A1491	A1502	G1503	U1512	G1513	C1514	G1515																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
G1516	C1525	A1526	G1527	A1528	C1530	C1531	C1532	A1533	G1535	A1536	A1537	G1540	U1541	G1542	G1546	A1552	U1553	G1554	G1555	G1556	G1557	G1558	G1559	G1560	G1561	G1562	G1563	G1564	G1565	G1566	G1567	G1568	G1569	G1570	G1571	G1572	G1573	G1574	G1575	G1576	G1577	G1578	G1579	G1580	G1581	G1582	G1583	G1584	G1585	G1586	G1587	G1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	G1596	G1597	G1598	G1599	G1600	G1601	G1602	G1603	G1604	G1605	G1606	G1607	G1608	G1609	G1610	G1611	G1612	G1613	G1614	G1615	G1616	G1617	G1618	G1619	G1620	G1621	G1622	G1623	G1624	G1625	G1626	G1627	G1628	G1629	G1630	G1631	G1632	G1633	G1634	G1635	G1636	G1637	G1638	G1639	G1640	G1641	G1642	G1643	G1644	G1645	G1646	G1647	G1648	G1649	G1650	G1651	G1652	G1653	G1654	G1655	G1656	G1657	G1658	G1659	G1660	G1661	G1662	G1663	G1664	G1665	G1666	G1667	G1668	G1669	G1670	G1671	G1672	G1673	G1674	G1675	G1676	G1677	G1678	G1679	G1680	G1681	G1682	G1683	G1684	G1685	G1686	G1687	G1688	G1689	G1690	G1691	G1692	G1693	G1694	G1695	G1696	G1697	G1698	G1699	G1700	G1701	G1702	G1703	G1704	G1705	G1706	G1707	G1708	G1709	G1710	G1711	G1712	G1713	G1714	G1715	G1716	G1717	G1718	G1719	G1720	G1721	G1722	G1723	G1724	G1725	G1726	G1727	G1728	G1729	G1730	G1731	G1732	G1733	G1734	G1735	G1736	G1737	G1738	G1739	G1740	G1741	G1742	G1743	G1744	G1745	G1746	G1747	G1748	G1749	G1750	G1751	G1752	G1753	G1754	G1755	G1756	G1757	G1758	G1759	G1760	G1761	G1762	G1763	G1764	G1765	G1766	G1767	G1768	G1769	G1770	G1771	G1772	G1773	G1774	G1775	G1776	G1777	G1778	G1779	G1780	G1781	G1782	G1783	G1784	G1785	G1786	G1787	G1788	G1789	G1790	G1791	G1792	G1793	G1794	G1795	G1796	G1797	G1798	G1799	G1800	G1801	G1802	G1803	G1804	G1805	G1806	G1807	G1808	G1809	G1810	G1811	G1812	G1813	G1814	G1815	G1816	G1817	G1818	G1819	G1820	G1821	G1822	G1823	G1824	G1825	G1826	G1827	G1828	G1829	G1830	G1831	G1832	G1833	G1834	G1835	G1836	G1837	G1838	G1839	G1840	G1841	G1842	G1843	G1844	G1845	G1846	G1847	G1848	G1849	G1850	G1851	G1852	G1853	G1854	G1855	G1856	G1857	G1858	G1859	G1860	G1861	G1862	G1863	G1864	G1865	G1866	G1867	G1868	G1869	G1870	G1871	G1872	G1873	G1874	G1875	G1876	G1877	G1878	G1879	G1880	G1881	G1882	G1883	G1884	G1885	G1886	G1887	G1888	G1889	G1890	G1891	G1892	G1893	G1894	G1895	G1896	G1897	G1898	G1899	G1900	G1901	G1902	G1903	G1904	G1905	G1906	G1907	G1908	G1909	G1910	G1911	G1912	G1913	G1914	G1915	G1916	G1917	G1918	G1919	G1920	G1921	G1922	G1923	G1924	G1925	G1926	G1927	G1928	G1929	G1930	G1931	G1932	G1933	G1934	G1935	G1936	G1937	G1938	G1939	G1940	G1941	G1942	G1943	G1944	G1945	G1946	G1947	G1948	G1949	G1950	G1951	G1952	G1953	G1954	G1955	G1956	G1957	G1958	G1959	G1960	G1961	G1962	G1963	G1964	G1965	G1966	G1967	G1968	G1969	G1970	G1971	G1972	G1973	G1974	G1975	G1976	G1977	G1978	G1979	G1980	G1981	G1982	G1983	G1984	G1985	G1986	G1987	G1988	G1989	G1990	G1991	G1992	G1993	G1994	G1995	G1996	G1997	G1998	G1999	G2000	G2001	G2002	G2003	G2004	G2005	G2006	G2007	G2008	G2009	G2010	G2011	G2012	G2013	G2014	G2015	G2016	G2017	G2018	G2019	G2020	G2021	G2022	G2023	G2024	G2025	G2026	G2027	G2028	G2029	G2030	G2031	G2032	G2033	G2034	G2035	G2036	G2037	G2038	G2039	G2040	G2041	G2042	G2043	G2044	G2045	G2046	G2047	G2048	G2049	G2050	G2051	G2052	G2053	G2054	G2055	G2056	G2057	G2058	G2059	G2060	G2061	G2062	G2063	G2064	G2065	G2066	G2067	G2068	G2069	G2070	G2071	G2072	G2073	G2074	G2075	G2076	G2077	G2078	G2079	G2080	G2081	G2082	G2083	G2084	G2085	G2086	G2087	G2088	G2089	G2090	G2091	G2092	G2093	G2094	G2095	G2096	G2097	G2098	G2099	G2100	G2101	G2102	G2103	G2104	G2105	G2106	G2107	G2108	G2109	G2110	G2111	G2112	G2113	G2114	G2115	G2116	G2117	G2118	G2119	G2120	G2121	G2122	G2123	G2124	G2125	G2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	G2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	G2142	G2143	G2144	G2145	G2146	G2147	G2148	G2149	G2150	G2151	G2152	G2153	G2154	G2155	G2156	G2157	G2158	G2159	G2160	G2161	G2162	G2163	G2164	G2165	G2166	G2167	G2168	G2169	G2170	G2171	G2172	G2173	G2174	G2175	G2176	G2177	G2178	G2179	G2180	G2181	G2182	G2183	G2184	G2185	G2186	G2187	G2188	G2189	G2190	G2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200	G2201	G2202	G2203	G2204	G2205	G2206	G2207	G2208	G2209	G2210	G2211	G2212	G2213	G2214	G2215	G2216	G2217	G2218	G2219	G2220	G2221	G2222	G2223	G2224	G2225	G2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2238	G2239	G2240	G2241	G2242	G2243	G2244	G2245	G2246	G2247	G2248	G2249	G2250	G2251	G2252	G2253	G2254	G2255	G2256	G2257	G2258	G2259	G2260	G2261	G2262	G2263	G2264	G2265	G2266	G2267	G2268	G2269	G2270	G2271	G2272	G2273	G2274	G2275	G2276	G2277	G2278	G2279	G2280	G2281	G2282	G2283	G2284	G2285	G2286	G2287	G2288	G2289	G2290	G2291	G2292	G2293	G2294	G2295	G2296	G2297	G2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	G2309	G2310	G2311	G2312	G2313	G2314	G2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	G2328	G2329	G2330	G2331	G2332	G2333	G2334	G2335	G2336	G2337	G2338	G2339	G2340	G2341	G2342	G2343	G2344	G2345	G2346	G2347	G2348	G2349	G2350	G2351	G2352	G2353	G2354	G2355	G2356	G2357	G2358	G2359	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	G2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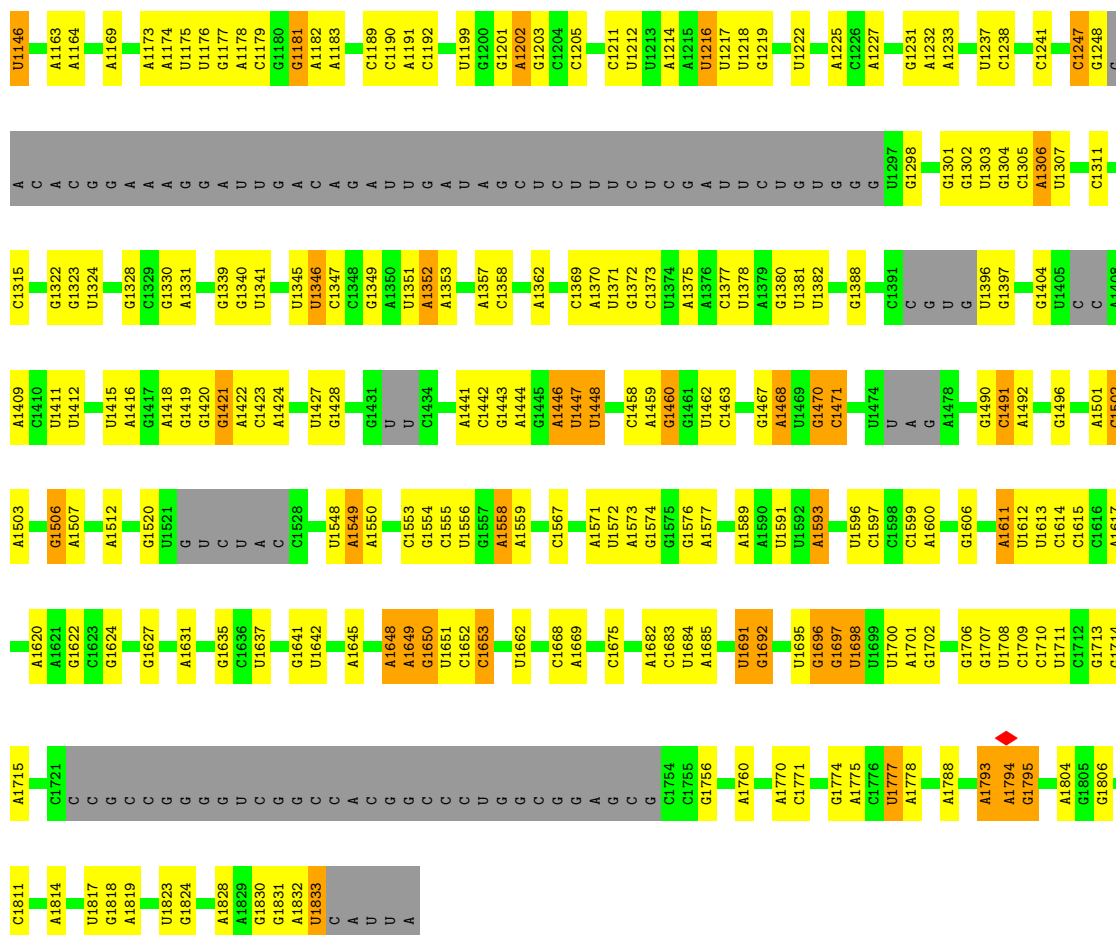




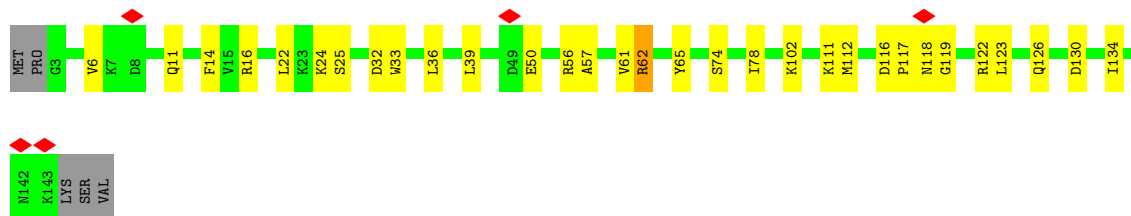
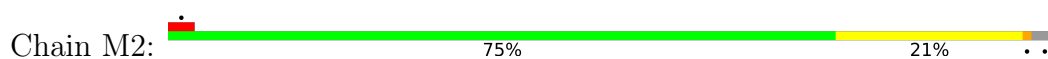
• Molecule 56: 18S rRNA

Chain C2: 50% 26% 19%

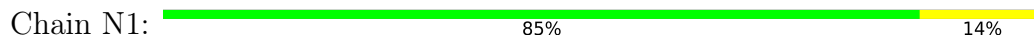




• Molecule 57: Small ribosomal subunit protein eS19

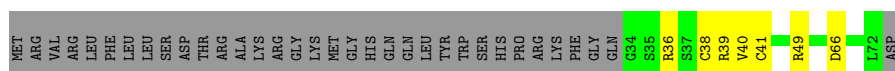


• Molecule 58: Ribosomal protein L15



• Molecule 59: Small ribosomal subunit protein uS14

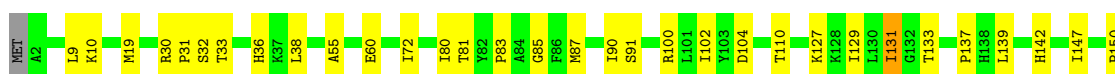
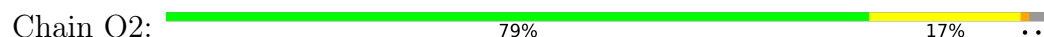




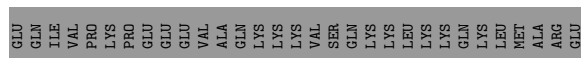
- Molecule 60: 60S ribosomal protein L36a



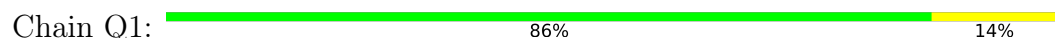
- Molecule 61: 40S ribosomal protein S4



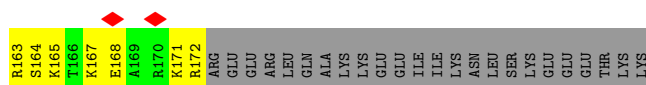
- Molecule 62: Large ribosomal subunit protein uL22



- Molecule 63: Ribosomal protein L18



- Molecule 64: Ribosomal protein L19



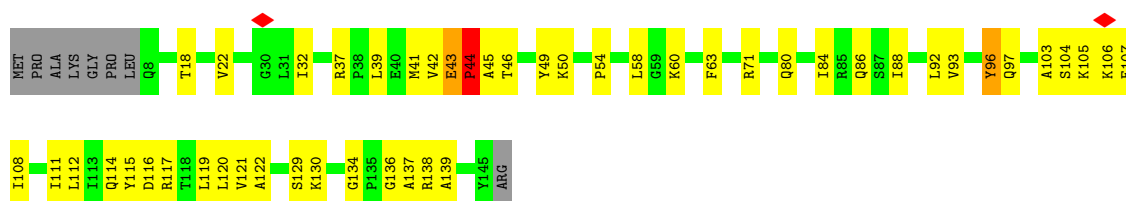
- Molecule 65: 60S ribosomal protein L18a

Chain S1:  85% 13% ..



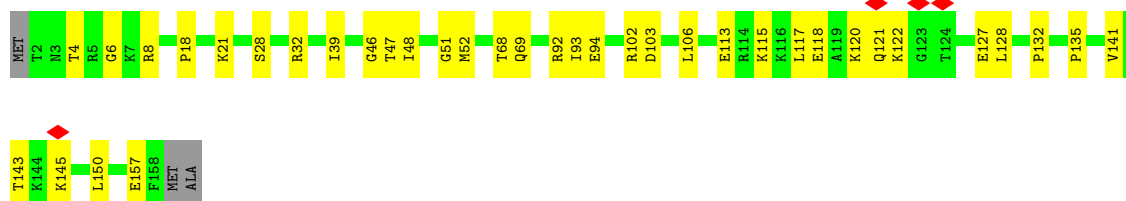
- Molecule 66: Small ribosomal subunit protein uS9

Chain S2:  61% 32% .. 5%



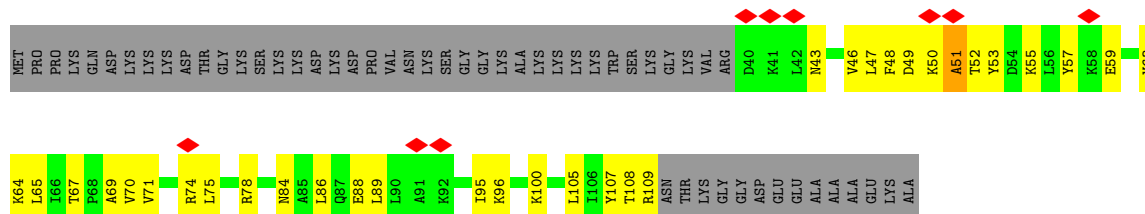
- Molecule 67: Large ribosomal subunit protein eL21

Chain T1:  75% 23% .



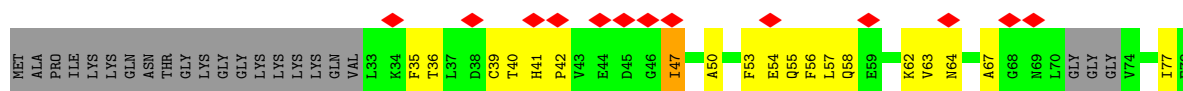
- Molecule 68: 40S ribosomal protein S25

Chain T2:  7% 30% 26% 43%



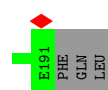
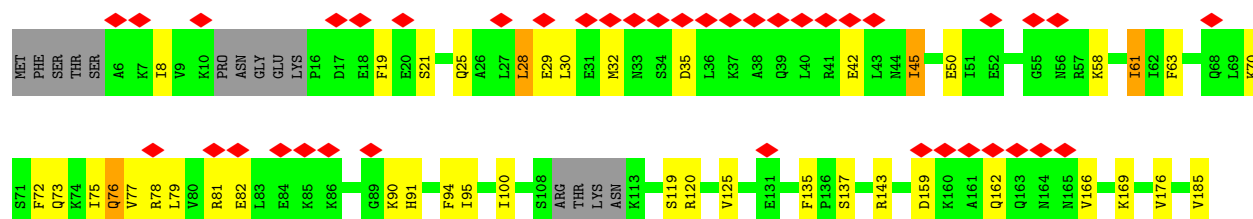
- Molecule 69: Large ribosomal subunit protein eL22

Chain U1:  12% 43% 26% 29%

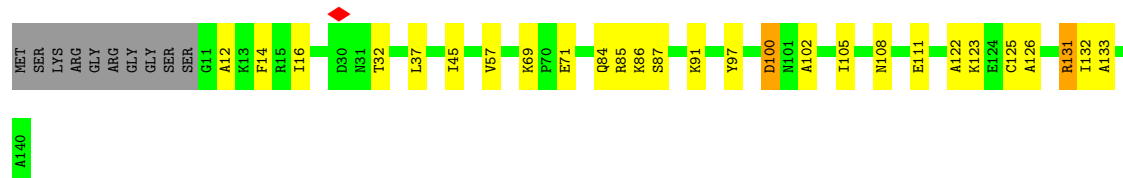
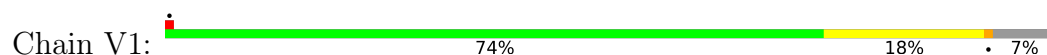




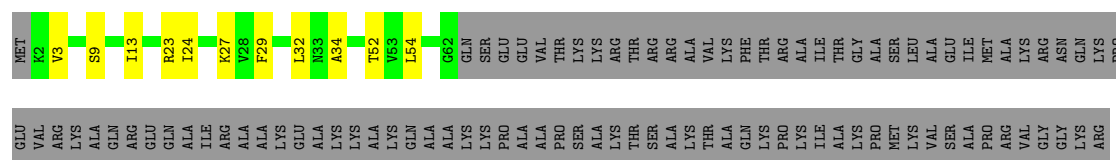
- Molecule 70: 40S ribosomal protein S7



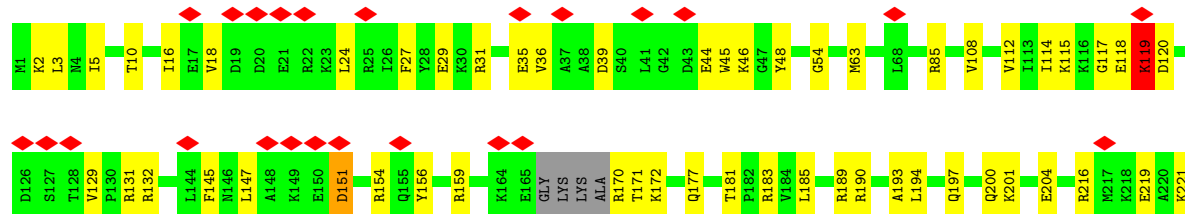
- Molecule 71: Large ribosomal subunit protein uL14

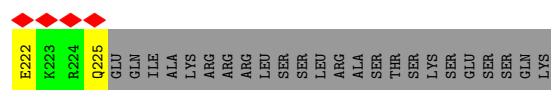


- Molecule 72: Large ribosomal subunit protein eL24

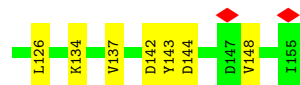
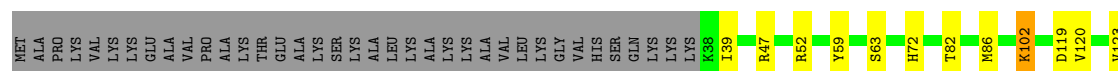


- Molecule 73: 40S ribosomal protein S6

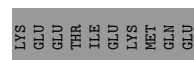




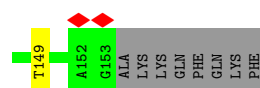
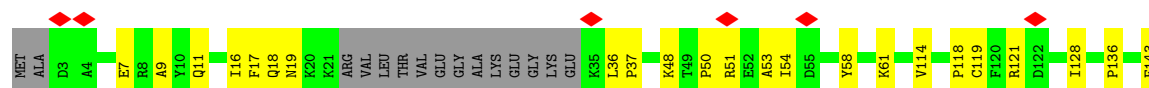
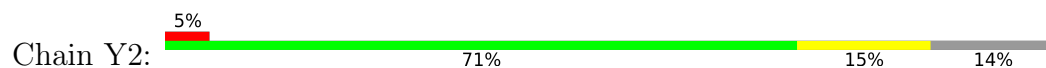
- Molecule 74: Large ribosomal subunit protein uL23



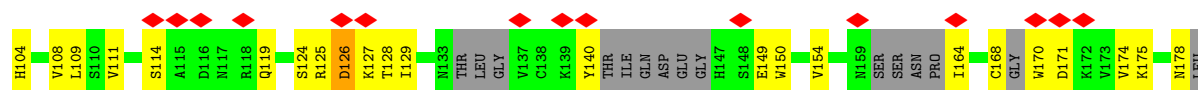
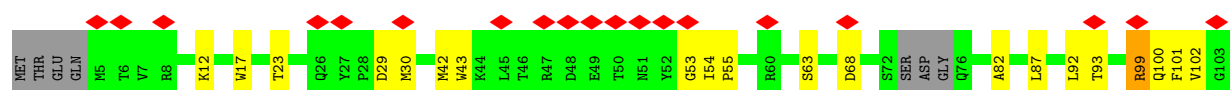
- Molecule 75: Ribosomal protein L26

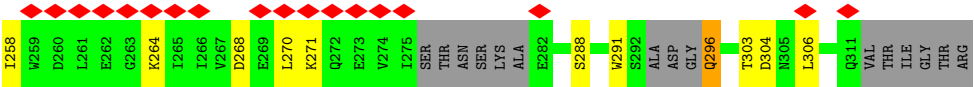


- Molecule 76: Small ribosomal subunit protein uS17



- Molecule 77: Small ribosomal subunit protein RACK1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	115566	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60.23	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.577	Depositor
Minimum map value	-0.032	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	529.92, 529.92, 529.92	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82799995, 0.82799995, 0.82799995	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	11	0.19	0/454	0.39	0/599
2	21	0.15	0/393	0.35	0/519
3	Z1	0.18	0/1130	0.41	0/1507
4	a1	0.18	0/1929	0.40	0/2584
5	b1	0.26	0/438	0.48	0/579
6	d2	0.24	0/443	0.62	0/589
7	e1	0.29	0/871	0.46	0/1161
8	f1	0.23	0/892	0.48	0/1193
9	g1	0.16	0/696	0.38	0/924
10	g2	0.19	0/1699	0.48	0/2308
11	h1	0.17	0/2357	0.40	0/3158
12	i1	0.35	0/2842	0.76	0/4430
13	j1	0.32	0/3501	0.78	0/5451
14	k1	0.19	0/1521	0.43	0/2043
15	l1	0.18	0/1706	0.41	0/2282
16	m1	0.19	0/1764	0.44	0/2374
17	m2	0.20	0/1017	0.44	0/1351
18	n1	0.16	0/1191	0.33	0/1593
19	q2	0.20	0/752	0.54	0/1007
20	r2	0.16	0/1053	0.37	0/1409
21	u2	0.18	0/1421	0.49	0/1908
22	x2	0.17	0/382	0.45	0/501
23	y2	0.26	0/1100	0.52	1/1468 (0.1%)
24	z2	0.24	0/327	0.75	0/436
25	32	0.19	0/558	0.51	0/744
26	41	0.21	0/994	0.37	0/1332
27	42	0.19	0/1735	0.50	1/2321 (0.0%)
28	K1	0.21	0/565	0.57	0/750
29	51	0.20	0/240	0.49	0/305
30	61	0.21	0/853	0.58	0/1139
31	71	0.21	0/1229	0.50	0/1636
32	72	0.22	0/993	0.52	0/1332

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	81	0.23	0/1692	0.46	1/2268 (0.0%)
34	82	0.16	0/766	0.42	0/1024
35	91	0.32	0/756	0.61	1/1013 (0.1%)
36	B1	0.17	0/3243	0.38	0/4345
37	B2	0.16	0/1228	0.40	0/1649
38	C1	0.17	0/2845	0.38	0/3822
39	D1	0.17	0/850	0.39	0/1141
40	E1	0.16	0/1060	0.34	0/1413
41	F1	0.19	0/1901	0.39	0/2539
42	H1	0.17	0/1010	0.40	0/1334
43	H2	0.30	0/653	0.60	0/875
44	I1	0.18	0/823	0.46	0/1092
45	J1	0.16	0/720	0.38	0/953
46	J2	0.17	0/1707	0.42	0/2308
47	K2	0.20	0/1681	0.45	0/2243
48	L1	0.17	0/1661	0.40	0/2218
49	L2	0.17	0/1498	0.40	0/2003
50	M1	0.21	0/1108	0.44	0/1479
51	A2	0.23	0/844	0.60	1/1123 (0.1%)
52	P2	0.22	0/1173	0.63	0/1571
53	i2	0.23	0/980	0.64	0/1314
54	w2	0.21	0/1626	0.55	0/2184
55	A1	0.34	0/76831	0.80	14/119730 (0.0%)
56	C2	0.30	0/35470	0.76	4/55243 (0.0%)
57	M2	0.19	0/1105	0.44	0/1483
58	N1	0.17	0/1740	0.33	0/2327
59	N2	0.14	0/321	0.30	0/423
60	O1	0.17	0/783	0.41	0/1035
61	O2	0.15	0/2081	0.38	0/2800
62	P1	0.27	0/1258	0.46	0/1687
63	Q1	0.18	0/1536	0.36	0/2051
64	R1	0.20	0/1439	0.48	1/1902 (0.1%)
65	S1	0.22	0/1498	0.51	1/2011 (0.0%)
66	S2	0.25	0/1107	0.58	2/1484 (0.1%)
67	T1	0.17	0/1319	0.41	0/1765
68	T2	0.27	0/575	0.58	0/772
69	U1	0.25	0/769	0.61	0/1027
70	U2	0.19	0/1448	0.46	0/1937
71	V1	0.16	0/987	0.38	0/1324
72	W1	0.15	0/525	0.32	0/699
73	W2	0.21	0/1812	0.47	0/2412
74	X1	0.18	0/986	0.41	0/1326
75	Y1	0.18	0/1083	0.41	0/1442

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	Y2	0.22	0/1141	0.40	0/1528
77	k2	0.20	0/2184	0.52	1/2960 (0.0%)
All	All	0.28	0/204869	0.68	28/300212 (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
23	y2	0	1
62	P1	0	1
77	k2	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	k2	126	ASP	N-CA-C	-8.97	102.44	112.57
23	y2	62	PRO	O-C-N	-8.48	111.19	122.64
56	C2	73	U	C3'-C2'-C1'	-6.71	96.13	101.50
55	A1	830	U	P-O3'-C3'	6.59	127.61	119.70
56	C2	1247	C	N3-C2-O2	-6.54	117.32	121.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
62	P1	69	ARG	Sidechain
77	k2	99	ARG	Sidechain
23	y2	62	PRO	Mainchain

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	l1	444	0	483	10	0
2	21	387	0	416	8	0
3	Z1	1107	0	1184	19	0
4	a1	1890	0	1985	35	0
5	b1	428	0	443	4	0
6	d2	443	0	473	21	0
7	e1	861	0	951	10	0
8	f1	872	0	911	9	0
9	g1	686	0	743	14	0
10	g2	1660	0	1655	43	0
11	h1	2311	0	2342	43	0
12	i1	2541	0	1286	19	0
13	j1	3135	0	1590	51	0
14	k1	1503	0	1586	42	0
15	l1	1677	0	1827	25	0
16	m1	1730	0	1845	39	0
17	m2	1001	0	1081	22	0
18	n1	1159	0	1197	10	0
19	q2	744	0	806	33	0
20	r2	1036	0	1082	24	0
21	u2	1401	0	1442	34	0
22	x2	380	0	418	9	0
23	y2	1083	0	1150	21	0
24	z2	317	0	320	26	0
25	32	549	0	562	13	0
26	41	979	0	1040	7	0
27	42	1708	0	1781	46	0
28	K1	559	0	624	10	0
29	51	239	0	289	5	0
30	61	836	0	858	36	0
31	71	1212	0	1254	23	0
32	72	981	0	1005	41	0
33	81	1660	0	1812	18	0
34	82	756	0	799	16	0
35	91	746	0	778	25	0
36	B1	3173	0	3294	50	0
37	B2	1205	0	1292	26	0
38	C1	2788	0	2954	38	0
39	D1	837	0	897	9	0
40	E1	1042	0	1138	10	0
41	F1	1865	0	2002	30	0
42	H1	1003	0	1131	22	0
43	H2	645	0	648	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	I1	811	0	887	8	0
45	J1	706	0	735	5	0
46	J2	1671	0	1751	35	0
47	K2	1652	0	1737	31	0
48	L1	1632	0	1733	22	0
49	L2	1473	0	1585	34	0
50	M1	1088	0	1144	13	0
51	A2	832	0	868	40	0
52	P2	1155	0	1209	50	0
53	i2	969	0	1020	53	0
54	w2	1602	0	1688	66	0
55	A1	68707	0	34705	550	0
56	C2	31719	0	16018	314	0
57	M2	1088	0	1135	22	0
58	N1	1697	0	1743	20	0
59	N2	317	0	323	6	0
60	O1	770	0	832	8	0
61	O2	2040	0	2152	30	0
62	P1	1232	0	1260	19	0
63	Q1	1510	0	1622	19	0
64	R1	1423	0	1566	31	0
65	S1	1458	0	1516	20	0
66	S2	1090	0	1151	42	0
67	T1	1290	0	1356	27	0
68	T2	568	0	619	29	0
69	U1	757	0	782	28	0
70	U2	1429	0	1527	31	0
71	V1	973	0	1034	19	0
72	W1	512	0	525	8	0
73	W2	1791	0	1936	39	0
74	X1	968	0	1039	14	0
75	Y1	1067	0	1162	19	0
76	Y2	1121	0	1178	16	0
77	k2	2138	0	2097	57	0
78	21	1	0	0	0	0
78	82	1	0	0	0	0
78	J1	1	0	0	0	0
78	N2	1	0	0	0	0
78	O1	1	0	0	0	0
78	e1	1	0	0	0	0
78	g1	1	0	0	0	0
79	A1	62	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	C2	21	0	0	0	0
79	J1	1	0	0	0	0
79	i1	1	0	0	0	0
All	All	190927	0	143009	2466	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 2466 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)
33:81:48:ASN:HB3	33:81:51:ARG:HG2	1.40	1.02
30:61:145:LYS:HE2	30:61:145:LYS:H	1.25	1.00
52:P2:113:ARG:HA	52:P2:116:LYS:HE3	1.43	0.99
8:f1:106:TYR:HB3	8:f1:107:PRO:HD2	1.47	0.95
54:w2:54:ARG:HH12	54:w2:57:ASN:HB3	1.30	0.94

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	11	48/51 (94%)	48 (100%)	0	0	100	100
2	21	45/128 (35%)	42 (93%)	3 (7%)	0	100	100
3	Z1	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
4	a1	244/257 (95%)	234 (96%)	10 (4%)	0	100	100
5	b1	48/64 (75%)	42 (88%)	5 (10%)	1 (2%)	5	15
6	d2	52/69 (75%)	51 (98%)	1 (2%)	0	100	100
7	e1	106/117 (91%)	100 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	f1	107/110 (97%)	100 (94%)	5 (5%)	2 (2%)	6	17
9	g1	86/92 (94%)	86 (100%)	0	0	100	100
10	g2	207/313 (66%)	197 (95%)	10 (5%)	0	100	100
11	h1	284/297 (96%)	271 (95%)	13 (5%)	0	100	100
14	k1	187/192 (97%)	180 (96%)	7 (4%)	0	100	100
15	l1	202/259 (78%)	194 (96%)	8 (4%)	0	100	100
16	m1	209/266 (79%)	206 (99%)	3 (1%)	0	100	100
17	m2	120/132 (91%)	116 (97%)	3 (2%)	1 (1%)	16	36
18	n1	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
19	q2	89/119 (75%)	83 (93%)	6 (7%)	0	100	100
20	r2	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
21	u2	171/203 (84%)	164 (96%)	7 (4%)	0	100	100
22	x2	43/133 (32%)	42 (98%)	1 (2%)	0	100	100
23	y2	137/143 (96%)	130 (95%)	5 (4%)	2 (2%)	8	23
24	z2	33/166 (20%)	28 (85%)	4 (12%)	1 (3%)	3	9
25	32	62/84 (74%)	57 (92%)	5 (8%)	0	100	100
26	41	121/137 (88%)	115 (95%)	5 (4%)	1 (1%)	16	36
27	42	208/266 (78%)	198 (95%)	10 (5%)	0	100	100
28	K1	66/70 (94%)	63 (96%)	3 (4%)	0	100	100
29	51	23/25 (92%)	23 (100%)	0	0	100	100
30	61	96/215 (45%)	93 (97%)	3 (3%)	0	100	100
31	71	143/178 (80%)	138 (96%)	5 (4%)	0	100	100
32	72	129/151 (85%)	124 (96%)	4 (3%)	1 (1%)	16	36
33	81	202/205 (98%)	193 (96%)	8 (4%)	1 (0%)	24	49
34	82	93/142 (66%)	89 (96%)	4 (4%)	0	100	100
35	91	94/116 (81%)	90 (96%)	4 (4%)	0	100	100
36	B1	392/403 (97%)	382 (97%)	10 (3%)	0	100	100
37	B2	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
38	C1	347/375 (92%)	340 (98%)	7 (2%)	0	100	100
39	D1	98/124 (79%)	96 (98%)	2 (2%)	0	100	100
40	E1	125/135 (93%)	124 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	F1	224/245 (91%)	217 (97%)	7 (3%)	0	100	100
42	H1	119/123 (97%)	116 (98%)	3 (2%)	0	100	100
43	H2	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
44	I1	98/105 (93%)	96 (98%)	2 (2%)	0	100	100
45	J1	84/97 (87%)	84 (100%)	0	0	100	100
46	J2	214/279 (77%)	208 (97%)	6 (3%)	0	100	100
47	K2	201/208 (97%)	190 (94%)	11 (6%)	0	100	100
48	L1	200/211 (95%)	190 (95%)	10 (5%)	0	100	100
49	L2	175/194 (90%)	169 (97%)	6 (3%)	0	100	100
50	M1	131/137 (96%)	127 (97%)	4 (3%)	0	100	100
51	A2	94/145 (65%)	85 (90%)	9 (10%)	0	100	100
52	P2	137/152 (90%)	127 (93%)	10 (7%)	0	100	100
53	i2	117/134 (87%)	109 (93%)	8 (7%)	0	100	100
54	w2	202/247 (82%)	193 (96%)	9 (4%)	0	100	100
57	M2	139/146 (95%)	132 (95%)	7 (5%)	0	100	100
58	N1	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
59	N2	37/73 (51%)	37 (100%)	0	0	100	100
60	O1	91/106 (86%)	85 (93%)	6 (7%)	0	100	100
61	O2	255/263 (97%)	246 (96%)	9 (4%)	0	100	100
62	P1	150/184 (82%)	146 (97%)	4 (3%)	0	100	100
63	Q1	185/188 (98%)	177 (96%)	6 (3%)	2 (1%)	11	29
64	R1	169/196 (86%)	165 (98%)	3 (2%)	1 (1%)	21	45
65	S1	174/176 (99%)	161 (92%)	10 (6%)	3 (2%)	7	20
66	S2	136/146 (93%)	124 (91%)	8 (6%)	4 (3%)	3	9
67	T1	155/160 (97%)	151 (97%)	4 (3%)	0	100	100
68	T2	68/123 (55%)	65 (96%)	1 (2%)	2 (3%)	3	9
69	U1	85/129 (66%)	78 (92%)	7 (8%)	0	100	100
70	U2	171/194 (88%)	158 (92%)	13 (8%)	0	100	100
71	V1	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
72	W1	59/157 (38%)	59 (100%)	0	0	100	100
73	W2	217/249 (87%)	203 (94%)	13 (6%)	1 (0%)	24	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
74	X1	116/155 (75%)	112 (97%)	4 (3%)	0	100	100
75	Y1	126/145 (87%)	120 (95%)	6 (5%)	0	100	100
76	Y2	134/161 (83%)	130 (97%)	4 (3%)	0	100	100
77	k2	248/317 (78%)	231 (93%)	15 (6%)	2 (1%)	16	36
All	All	10291/12274 (84%)	9862 (96%)	404 (4%)	25 (0%)	44	65

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	f1	107	PRO
65	S1	161	ARG
65	S1	165	PRO
66	S2	44	PRO
66	S2	45	ALA

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	11	47/48 (98%)	47 (100%)	0	100	100
2	21	43/116 (37%)	41 (95%)	2 (5%)	23	48
3	Z1	116/117 (99%)	114 (98%)	2 (2%)	53	73
4	a1	189/199 (95%)	186 (98%)	3 (2%)	55	74
5	b1	46/54 (85%)	44 (96%)	2 (4%)	26	51
6	d2	49/61 (80%)	46 (94%)	3 (6%)	17	38
7	e1	93/101 (92%)	90 (97%)	3 (3%)	34	59
8	f1	90/91 (99%)	88 (98%)	2 (2%)	45	69
9	g1	72/75 (96%)	72 (100%)	0	100	100
10	g2	178/253 (70%)	175 (98%)	3 (2%)	53	73
11	h1	243/252 (96%)	241 (99%)	2 (1%)	73	84
14	k1	168/171 (98%)	162 (96%)	6 (4%)	31	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	l1	183/226 (81%)	177 (97%)	6 (3%)	33	58
16	m1	186/224 (83%)	182 (98%)	4 (2%)	45	69
17	m2	108/114 (95%)	103 (95%)	5 (5%)	24	49
18	n1	118/119 (99%)	116 (98%)	2 (2%)	53	73
19	q2	86/106 (81%)	80 (93%)	6 (7%)	14	32
20	r2	112/113 (99%)	107 (96%)	5 (4%)	24	49
21	u2	151/170 (89%)	147 (97%)	4 (3%)	40	65
22	x2	39/109 (36%)	39 (100%)	0	100	100
23	y2	111/115 (96%)	108 (97%)	3 (3%)	39	64
24	z2	33/134 (25%)	31 (94%)	2 (6%)	17	38
25	32	62/76 (82%)	61 (98%)	1 (2%)	55	74
26	41	108/120 (90%)	103 (95%)	5 (5%)	24	49
27	42	191/229 (83%)	189 (99%)	2 (1%)	68	81
28	K1	63/65 (97%)	61 (97%)	2 (3%)	34	59
29	51	24/24 (100%)	24 (100%)	0	100	100
30	61	89/181 (49%)	85 (96%)	4 (4%)	24	49
31	71	126/149 (85%)	120 (95%)	6 (5%)	23	47
32	72	102/119 (86%)	99 (97%)	3 (3%)	37	62
33	81	174/175 (99%)	165 (95%)	9 (5%)	21	44
34	82	83/119 (70%)	81 (98%)	2 (2%)	43	67
35	91	81/98 (83%)	75 (93%)	6 (7%)	13	30
36	B1	343/351 (98%)	337 (98%)	6 (2%)	53	73
37	B2	129/130 (99%)	129 (100%)	0	100	100
38	C1	296/314 (94%)	287 (97%)	9 (3%)	36	61
39	D1	92/110 (84%)	89 (97%)	3 (3%)	33	58
40	E1	114/121 (94%)	109 (96%)	5 (4%)	25	50
41	F1	194/210 (92%)	191 (98%)	3 (2%)	57	75
42	H1	109/110 (99%)	109 (100%)	0	100	100
43	H2	69/69 (100%)	69 (100%)	0	100	100
44	I1	84/88 (96%)	83 (99%)	1 (1%)	63	78
45	J1	73/80 (91%)	73 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	J2	181/216 (84%)	177 (98%)	4 (2%)	45	69
47	K2	174/178 (98%)	168 (97%)	6 (3%)	32	58
48	L1	168/177 (95%)	164 (98%)	4 (2%)	43	67
49	L2	158/168 (94%)	156 (99%)	2 (1%)	61	77
50	M1	115/118 (98%)	114 (99%)	1 (1%)	70	82
51	A2	92/130 (71%)	88 (96%)	4 (4%)	26	51
52	P2	121/132 (92%)	119 (98%)	2 (2%)	53	73
53	i2	108/121 (89%)	104 (96%)	4 (4%)	30	55
54	w2	170/205 (83%)	167 (98%)	3 (2%)	51	72
57	M2	112/117 (96%)	108 (96%)	4 (4%)	31	56
58	N1	171/172 (99%)	168 (98%)	3 (2%)	51	72
59	N2	34/64 (53%)	33 (97%)	1 (3%)	37	62
60	O1	84/95 (88%)	78 (93%)	6 (7%)	13	31
61	O2	221/226 (98%)	214 (97%)	7 (3%)	34	59
62	P1	132/162 (82%)	129 (98%)	3 (2%)	44	68
63	Q1	159/160 (99%)	157 (99%)	2 (1%)	61	77
64	R1	149/173 (86%)	146 (98%)	3 (2%)	48	70
65	S1	155/155 (100%)	151 (97%)	4 (3%)	40	65
66	S2	113/119 (95%)	109 (96%)	4 (4%)	32	56
67	T1	140/142 (99%)	137 (98%)	3 (2%)	47	70
68	T2	62/104 (60%)	61 (98%)	1 (2%)	55	74
69	U1	84/115 (73%)	83 (99%)	1 (1%)	63	78
70	U2	161/177 (91%)	153 (95%)	8 (5%)	22	46
71	V1	100/107 (94%)	92 (92%)	8 (8%)	11	27
72	W1	53/126 (42%)	52 (98%)	1 (2%)	50	71
73	W2	194/218 (89%)	186 (96%)	8 (4%)	27	52
74	X1	106/135 (78%)	103 (97%)	3 (3%)	38	63
75	Y1	119/134 (89%)	116 (98%)	3 (2%)	42	66
76	Y2	124/142 (87%)	124 (100%)	0	100	100
77	k2	238/274 (87%)	234 (98%)	4 (2%)	53	73
All	All	9065/10468 (87%)	8826 (97%)	239 (3%)	41	65

5 of 239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	C1	85	HIS
73	W2	112	VAL
48	L1	64	VAL
71	V1	132	ILE
77	k2	102	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
53	i2	48	ASN
63	Q1	125	GLN
54	w2	179	GLN
61	O2	224	ASN
65	S1	173	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	i1	118/120 (98%)	13 (11%)	0
13	j1	144/161 (89%)	20 (13%)	0
55	A1	3151/4024 (78%)	526 (16%)	19 (0%)
56	C2	1463/1838 (79%)	256 (17%)	4 (0%)
All	All	4876/6143 (79%)	815 (16%)	23 (0%)

5 of 815 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	i1	25	A
12	i1	30	C
12	i1	33	U
12	i1	50	A
12	i1	53	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	A1	2085	G
55	A1	3918	U
55	A1	3742	U

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Mol	Chain	Res	Type
55	A1	4021	G
55	A1	714	C

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 92 ligands modelled in this entry, 92 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

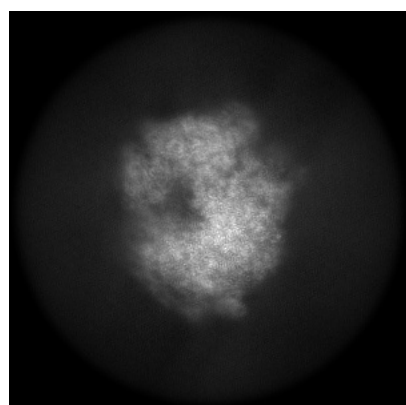
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-66542. These allow visual inspection of the internal detail of the map and identification of artifacts.

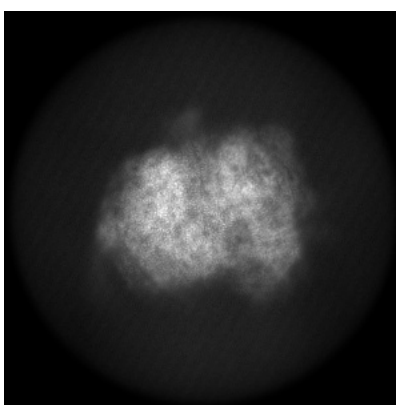
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

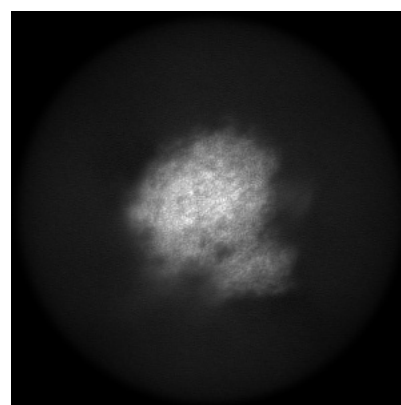
6.1.1 Primary map



X



Y

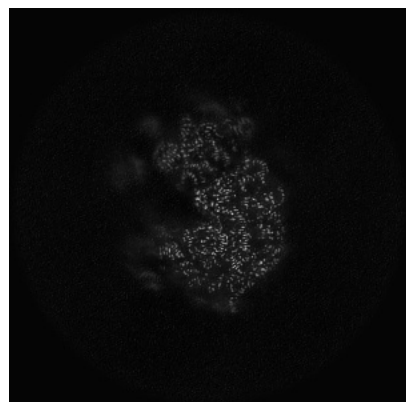


Z

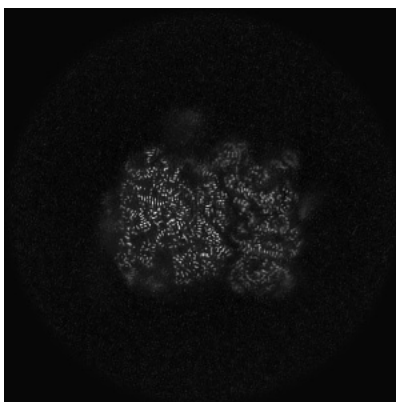
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

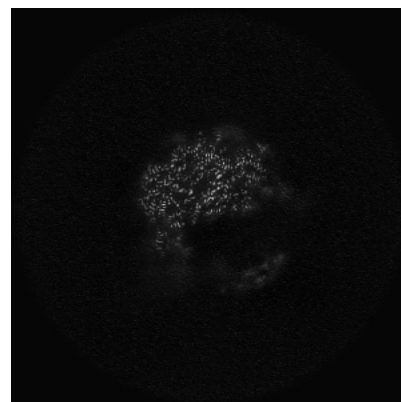
6.2.1 Primary map



X Index: 320



Y Index: 320

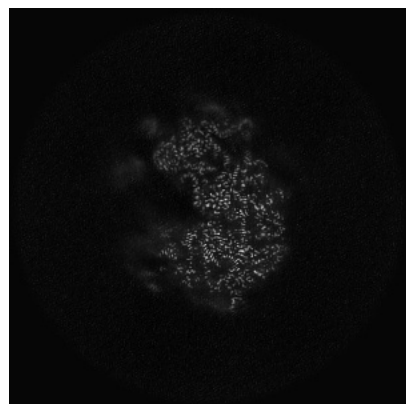


Z Index: 320

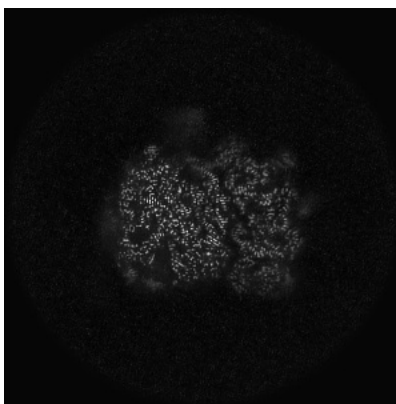
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

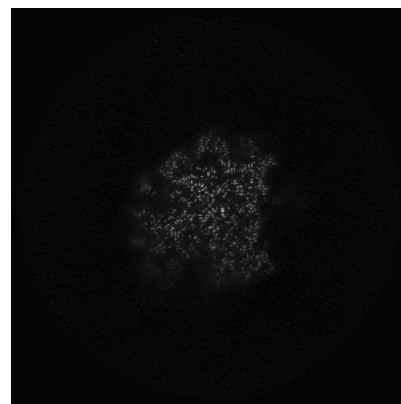
6.3.1 Primary map



X Index: 317



Y Index: 323

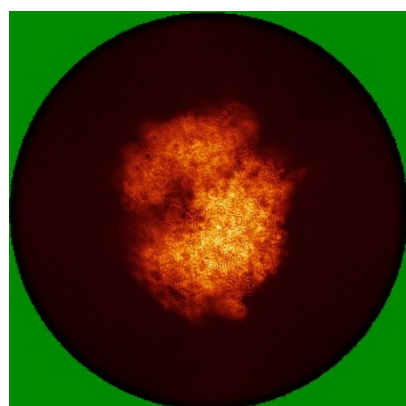


Z Index: 260

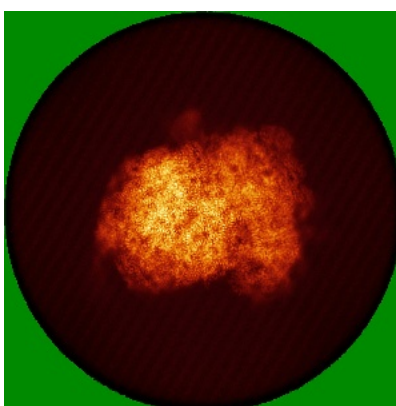
The images above show the largest variance slices of the map in three orthogonal directions.

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

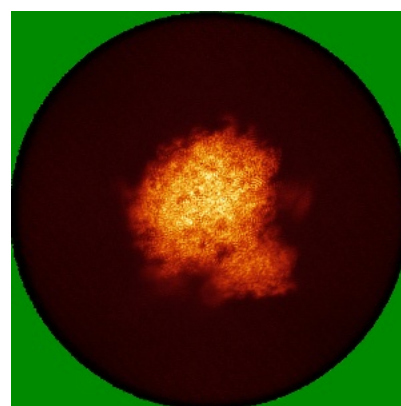
6.4.1 Primary map



X



Y

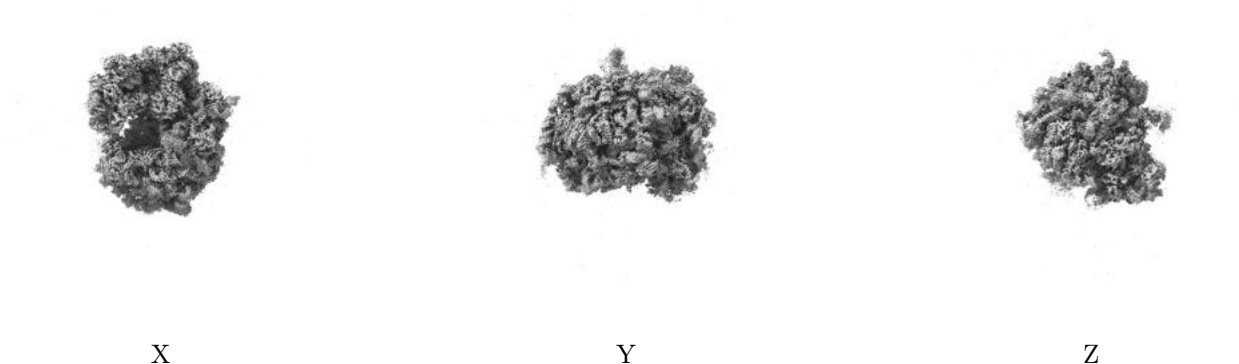


Z

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.

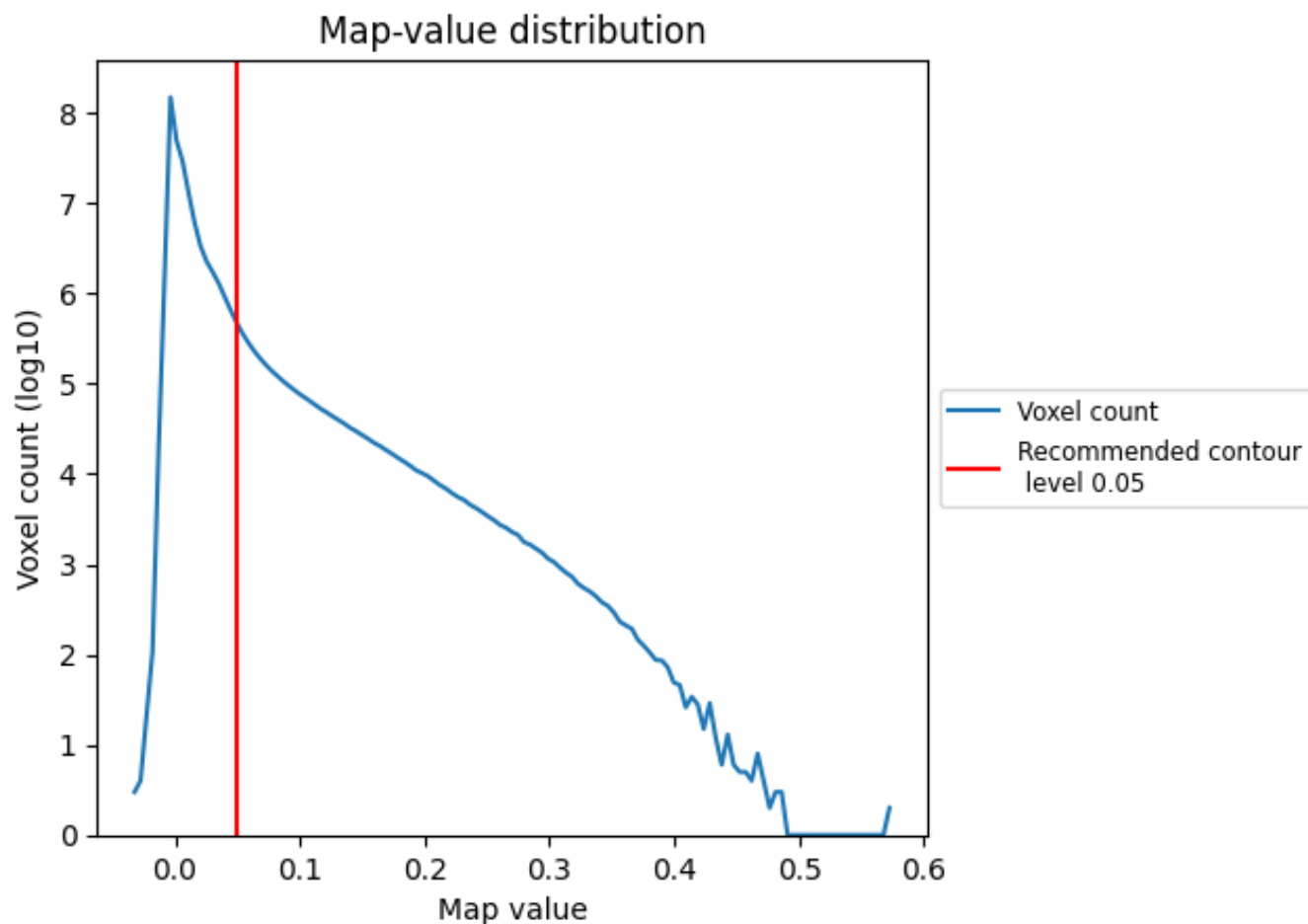
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

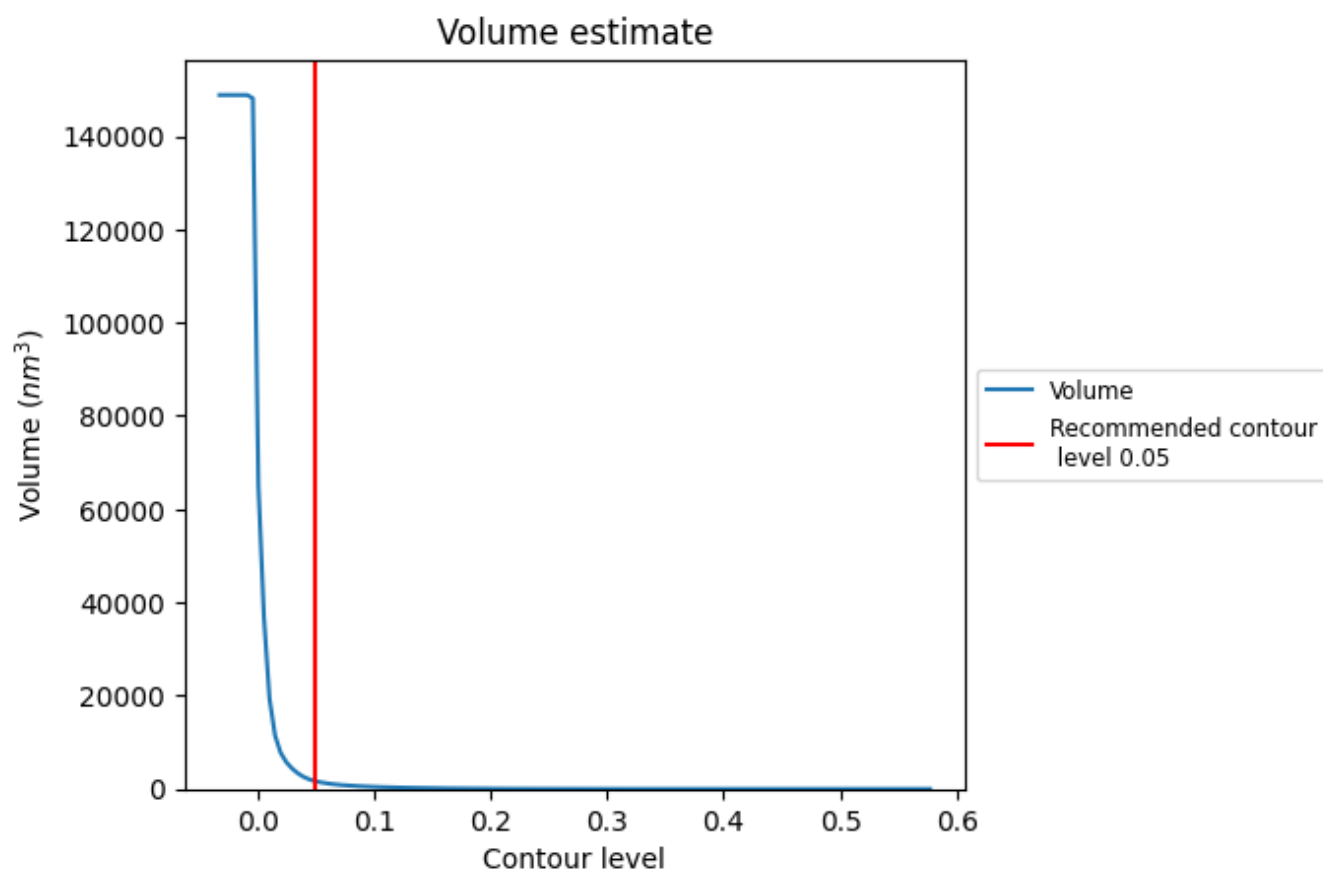
This section contains the results of statistical analysis of the map.

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.

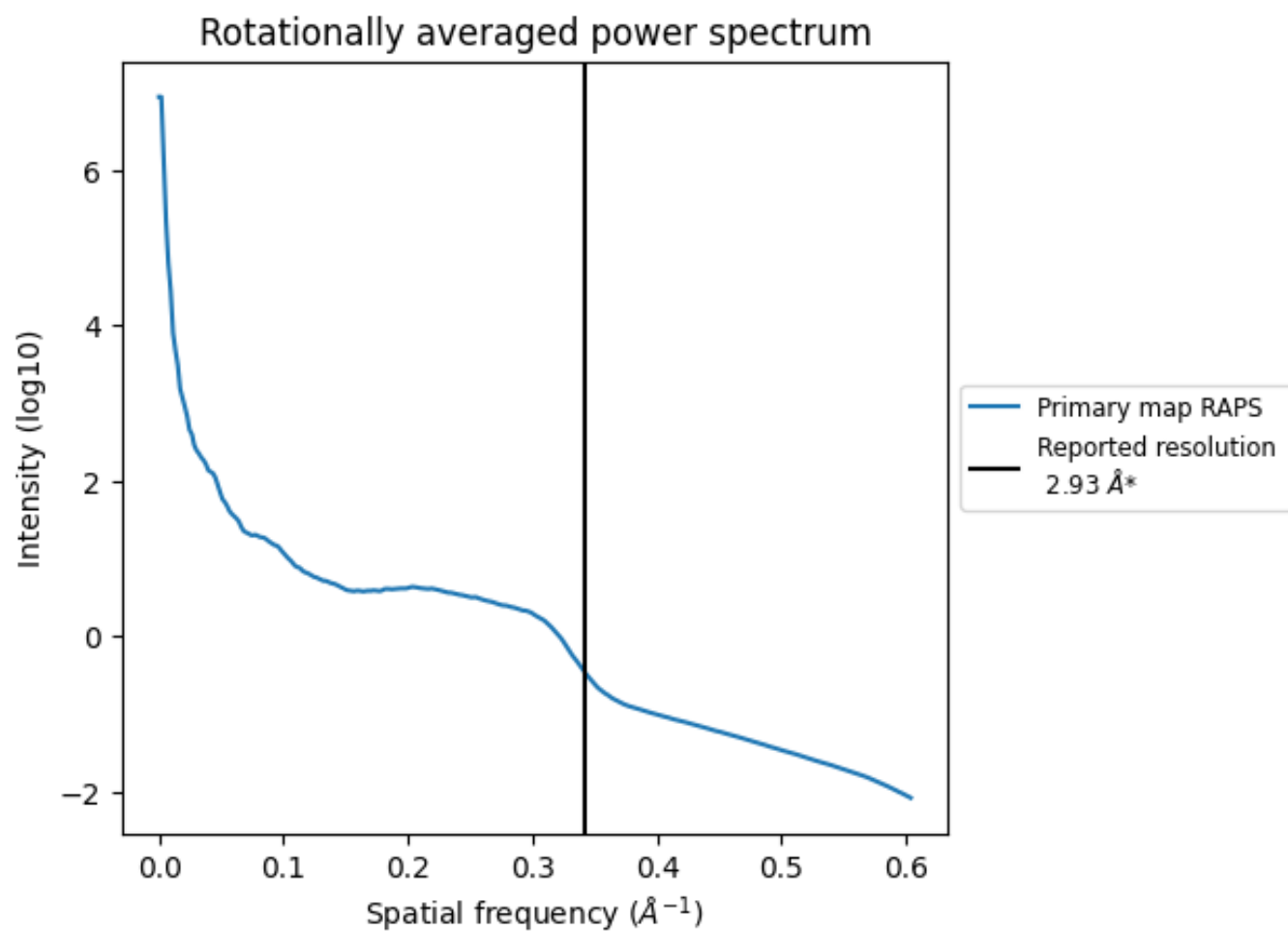
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1665 nm^3 ; this corresponds to an approximate mass of 1504 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 0.341 Å⁻¹

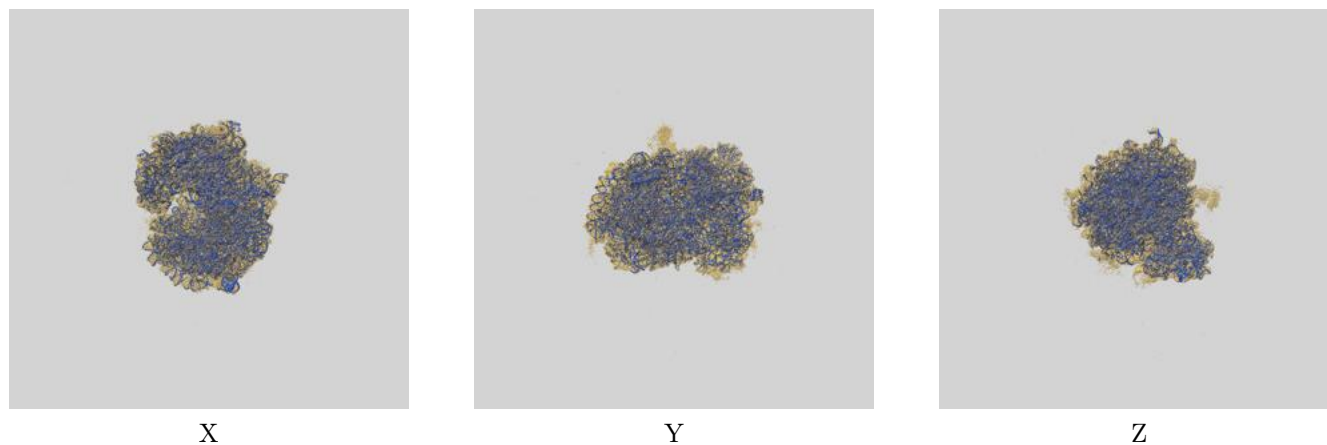
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

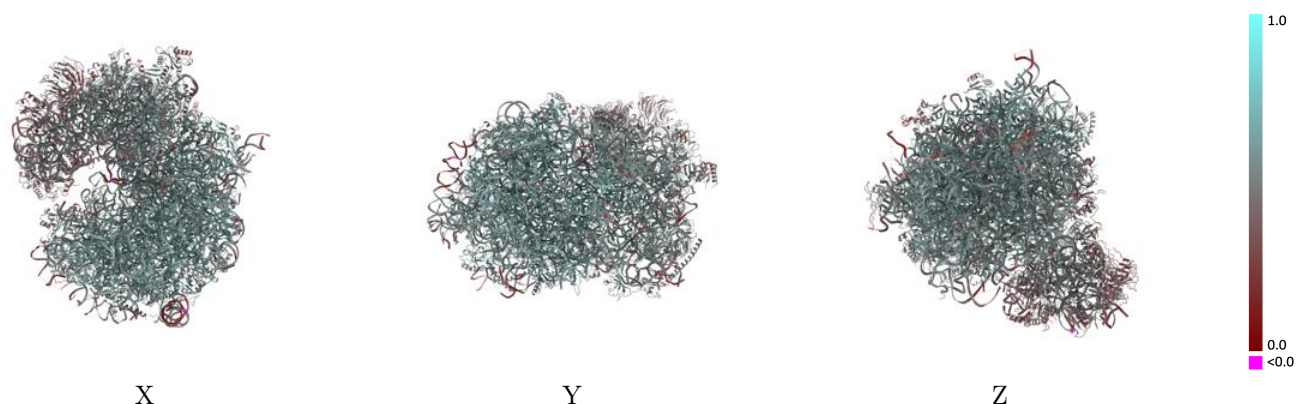
This section contains information regarding the fit between EMDB map EMD-66542 and PDB model 9X4D. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



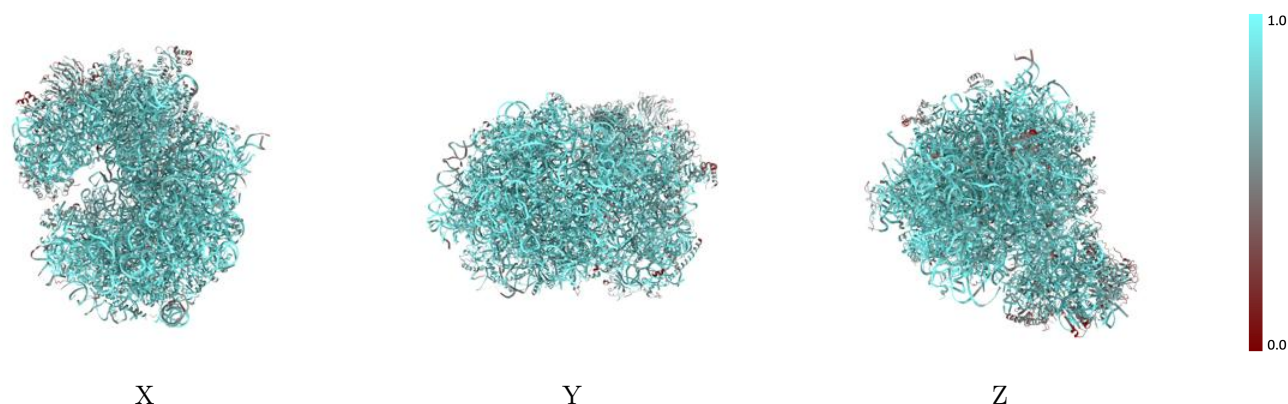
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



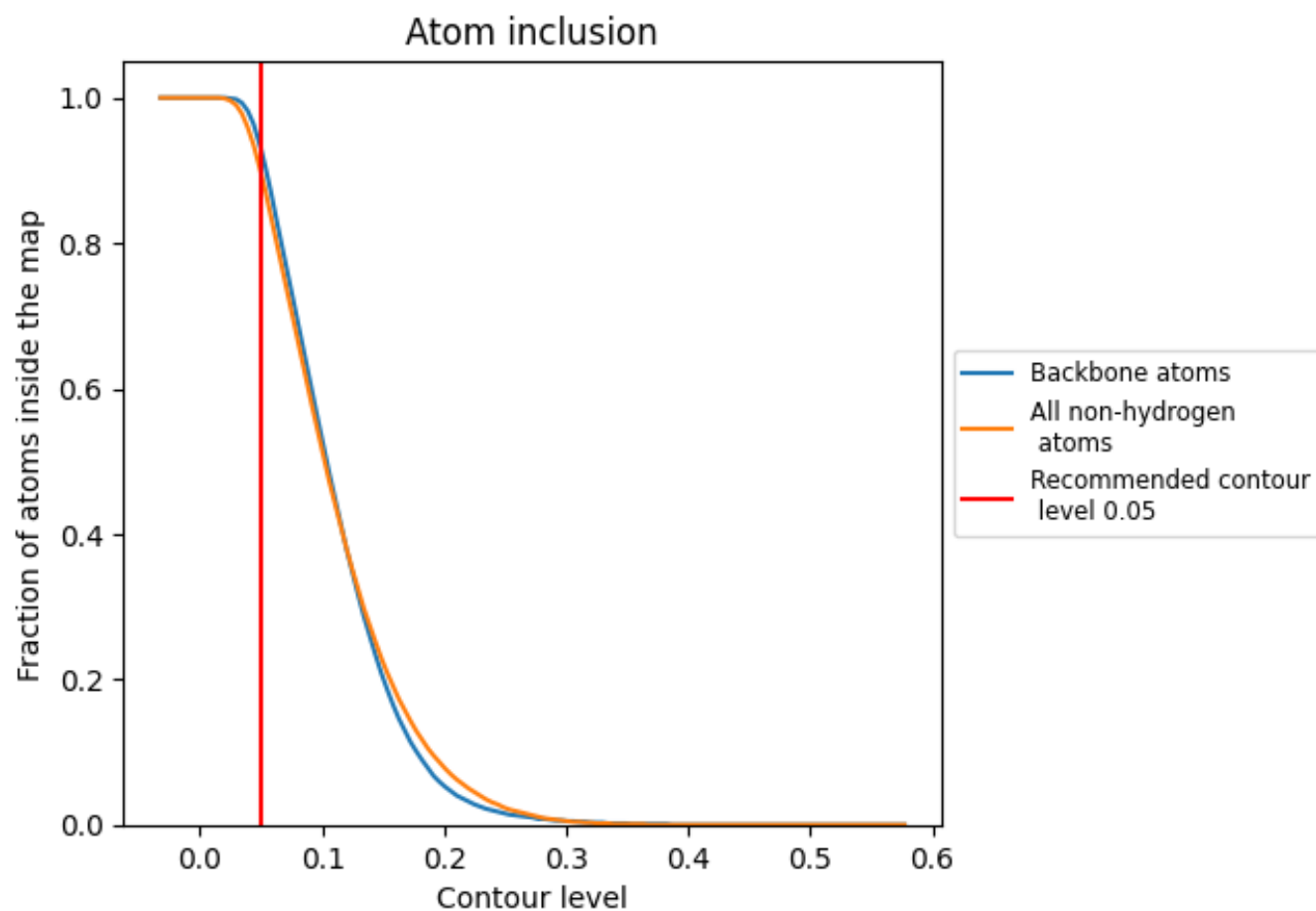
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 93% of all backbone atoms, 90% 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	 0.8960	 0.5410
11	 0.9220	 0.5800
21	 0.7110	 0.5230
32	 0.7780	 0.4990
41	 0.9010	 0.5850
42	 0.7480	 0.4810
51	 0.8670	 0.5560
61	 0.7360	 0.4520
71	 0.7420	 0.4820
72	 0.8010	 0.4800
81	 0.9290	 0.5850
82	 0.7930	 0.5010
91	 0.8750	 0.5330
A1	 0.9500	 0.5680
A2	 0.6750	 0.3970
B1	 0.9010	 0.5880
B2	 0.8110	 0.5170
C1	 0.9100	 0.5910
C2	 0.9530	 0.5120
D1	 0.8940	 0.5700
E1	 0.9240	 0.5910
F1	 0.9140	 0.5820
H1	 0.8710	 0.5650
H2	 0.7100	 0.4990
I1	 0.8540	 0.5490
J1	 0.9660	 0.6100
J2	 0.8160	 0.5170
K1	 0.6950	 0.4890
K2	 0.7500	 0.4980
L1	 0.8480	 0.5620
L2	 0.8500	 0.5130
M1	 0.9020	 0.5700
M2	 0.7610	 0.4570
N1	 0.9670	 0.6140
N2	 0.9080	 0.5200



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Chain	Atom inclusion	Q-score
O1	 0.8750	 0.5760
O2	 0.8660	 0.5320
P1	 0.9380	 0.5930
P2	 0.6610	 0.3890
Q1	 0.9260	 0.6020
R1	 0.8660	 0.5490
S1	 0.9150	 0.5790
S2	 0.7690	 0.4400
T1	 0.8860	 0.5710
T2	 0.6790	 0.3790
U1	 0.6510	 0.4430
U2	 0.6270	 0.4500
V1	 0.8720	 0.5790
W1	 0.9130	 0.6000
W2	 0.6880	 0.4570
X1	 0.8610	 0.5580
Y1	 0.9090	 0.5820
Y2	 0.8340	 0.5460
Z1	 0.8270	 0.5450
a1	 0.9410	 0.6060
b1	 0.8990	 0.5640
d2	 0.7810	 0.4270
e1	 0.9210	 0.5800
f1	 0.9570	 0.6040
g1	 0.8950	 0.5810
g2	 0.7460	 0.4900
h1	 0.8240	 0.5310
i1	 0.9850	 0.5880
i2	 0.5880	 0.4020
j1	 0.9760	 0.5890
k1	 0.8110	 0.5320
k2	 0.5250	 0.3700
l1	 0.8590	 0.5580
m1	 0.8370	 0.5440
m2	 0.8190	 0.4960
n1	 0.9320	 0.6070
q2	 0.5780	 0.4130
r2	 0.8930	 0.5390
u2	 0.7940	 0.4270
w2	 0.6280	 0.3940
x2	 0.7560	 0.4890
y2	 0.8470	 0.5410

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Chain	Atom inclusion	Q-score
z2	 0.5900	 0.3550