



wwPDB EM Validation Summary Report ⓘ

Mar 24, 2026 – 01:05 AM UTC

PDB ID : 6D9J / pdb_00006d9j
EMDB ID : EMD-7836
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-sitetRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-30
Resolution : 3.20 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:

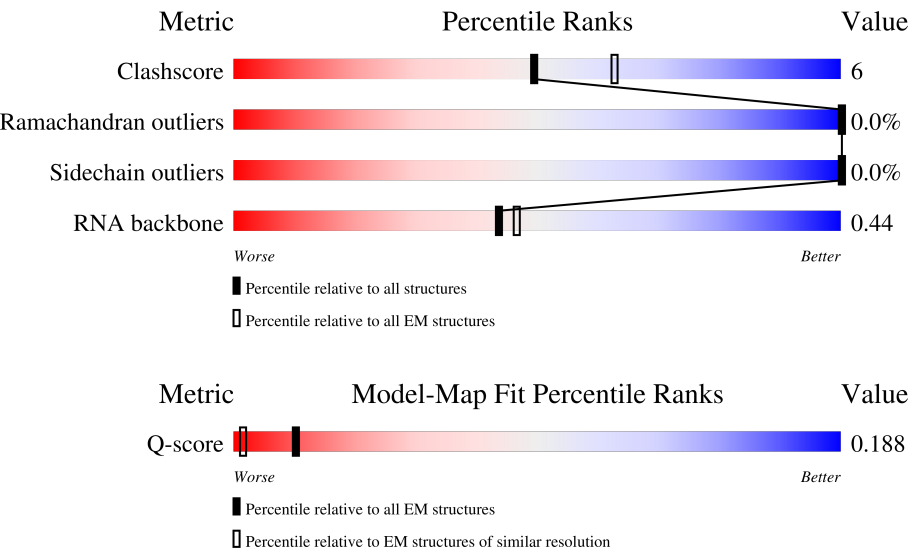
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



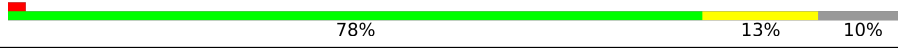
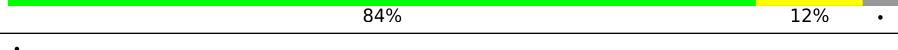
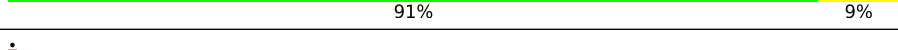
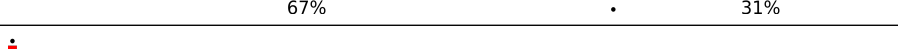
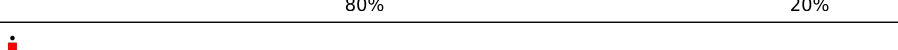
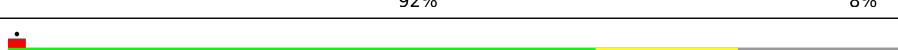
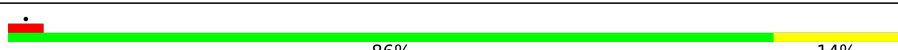
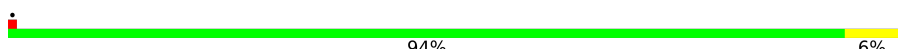
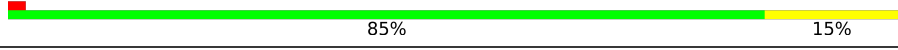
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	392	

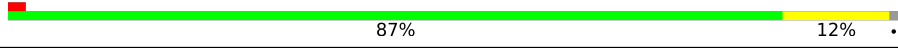
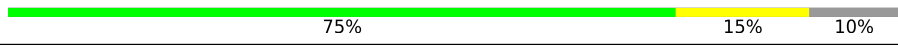
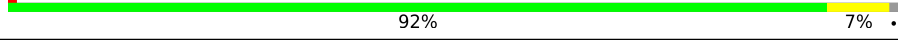
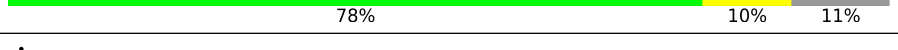
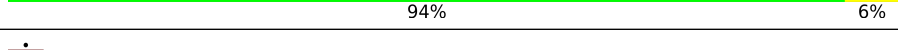
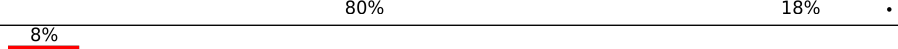
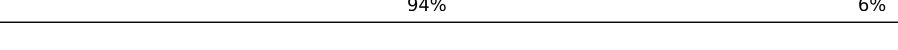
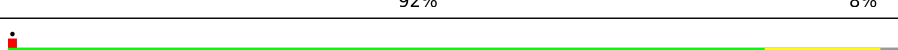
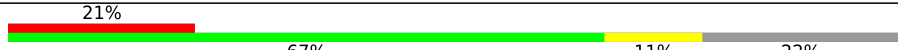
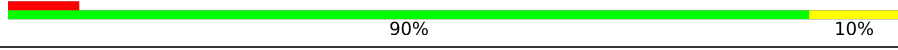
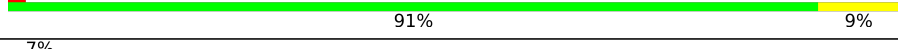
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	242	
8	H	192	
9	I	214	
10	J	178	
11	L	211	
12	M	198	
13	N	204	
14	O	198	
15	P	187	
16	Q	187	
17	R	181	
18	S	176	
19	T	160	
20	U	99	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	

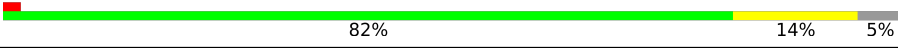
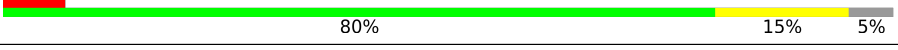
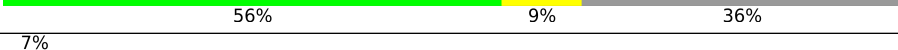
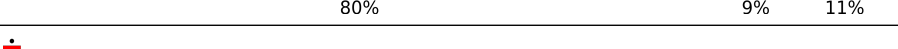
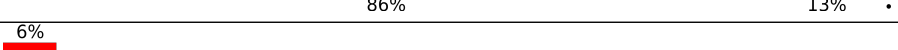
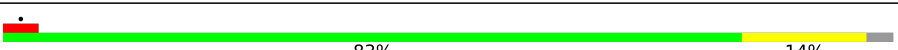
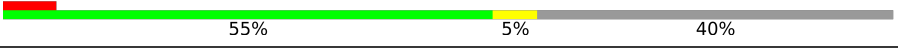
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	
34	i	105	
35	j	97	
36	k	69	
37	l	51	
38	m	52	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	303	
44	t	195	
45	5	3594	
46	7	119	
47	8	151	
48	K	217	
49	2	1697	
50	BB	217	
51	CC	264	
52	DD	221	
53	EE	281	

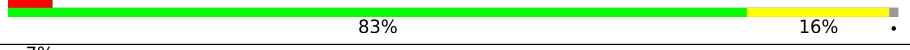
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	FF	262	
55	GG	204	
56	HH	249	
57	II	194	
58	JJ	206	
59	KK	194	
60	LL	149	
61	MM	158	
62	NN	132	
63	OO	151	
64	PP	151	
65	QQ	145	
66	RR	172	
67	SS	135	
68	TT	152	
69	UU	145	
70	VV	119	
71	WW	83	
72	XX	130	
73	YY	143	
74	ZZ	134	
75	aa	125	
76	bb	101	
77	cc	84	
78	dd	69	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	ee	56	
80	ff	133	
81	gg	156	
82	hh	317	
83	3	87	
84	9	856	
85	4	190	

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 227188 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 Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1777	1110	361	300	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 3 is a protein called Ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	LYS	-	expression tag	UNP P19949

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called eL8.

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

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

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

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	137	Total	C	N	O	S	0	0
			1130	722	220	181	7		

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	PRO	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12
M	?	-	LYS	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	ALA	deletion	UNP G1SZ12
M	?	-	GLY	deletion	UNP G1SZ12
M	?	-	GLN	deletion	UNP G1SZ12

- Molecule 13 is a protein called Ribosomal protein L15.

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

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	198	Total	C	N	O	S	0	0
			1623	1046	318	254	5		

- Molecule 15 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 21 is a protein called Ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	106	Total	C	N	O	S	0	0
			860	538	174	144	4		

- Molecule 23 is a protein called eL23.

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

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called 60S ribosomal protein L27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 30 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called eL35.

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

- Molecule 34 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 36 is a protein called eL38.

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

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	262	LEU	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	266	THR	ALA	conflict	UNP A0A1U7UFL5
s	267	LEU	PHE	conflict	UNP A0A1U7UFL5
s	269	ILE	ALA	conflict	UNP A0A1U7UFL5
s	270	ILE	ASP	conflict	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PHE	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PRO	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	272	VAL	ALA	conflict	UNP A0A1U7UFL5
s	273	ARG	ALA	conflict	UNP A0A1U7UFL5
s	274	ASP	ALA	conflict	UNP A0A1U7UFL5
s	275	SER	ALA	conflict	UNP A0A1U7UFL5
s	276	THR	PRO	conflict	UNP A0A1U7UFL5
s	278	ASP	ALA	conflict	UNP A0A1U7UFL5
s	282	ALA	LEU	conflict	UNP A0A1U7UFL5
s	284	GLN	ALA	conflict	UNP A0A1U7UFL5
s	286	SER	ALA	conflict	UNP A0A1U7UFL5
s	290	PRO	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	294	ASN	ASP	conflict	UNP A0A1U7UFL5

- Molecule 44 is a protein called Ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 45 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	5	3594	Total	C	N	O	P	0	0
			77073	34324	14116	25039	3594		

- Molecule 46 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 47 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 48 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	K	212	Total	C	N	O	S	0	0
			1705	1091	306	300	8		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	2	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 50 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 51 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CC	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 52 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	DD	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 53 is a protein called Ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	EE	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 54 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	FF	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 55 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	GG	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	HH	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	II	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	JJ	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JJ	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 59 is a protein called Ribosomal protein S9 (Predicted).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	KK	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 60 is a protein called S10_ plectin domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	LL	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 61 is a protein called Ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	MM	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 62 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	NN	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 63 is a protein called Ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	OO	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 64 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	PP	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	QQ	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 66 is a protein called Ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	RR	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	TT	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 69 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	UU	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 70 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	VV	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 71 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	WW	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 72 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	XX	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	YY	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	ZZ	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 75 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	aa	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	bb	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	cc	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called Ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	dd	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 79 is a protein called eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	ee	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	ff	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 81 is a protein called Ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	gg	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 82 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	hh	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 83 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	3	87	Total	C	N	O	P	0	0
			1860	829	333	612	86		

- Molecule 84 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	9	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 85 is a RNA chain called CrPV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	4	190	Total	C	N	O	P	0	0
			4020	1802	689	1339	190		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	6217	C	-	expression tag	GB 8895506
4	6218	U	-	expression tag	GB 8895506
4	6219	U	-	expression tag	GB 8895506

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
86	p	1	Total	Zn	0
			1	1	
86	2	1	Total	Zn	0
			1	1	
86	bb	1	Total	Zn	0
			1	1	
86	gg	1	Total	Zn	0
			1	1	

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

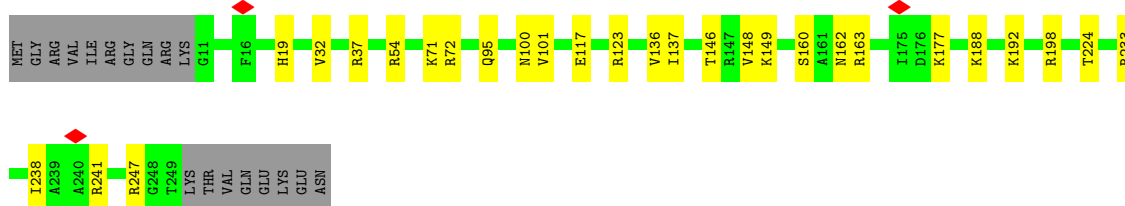
Mol	Chain	Residues	Atoms		AltConf
87	5	2	Total	Mg	0
			2	2	

3 Residue-property plots [i](#)

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

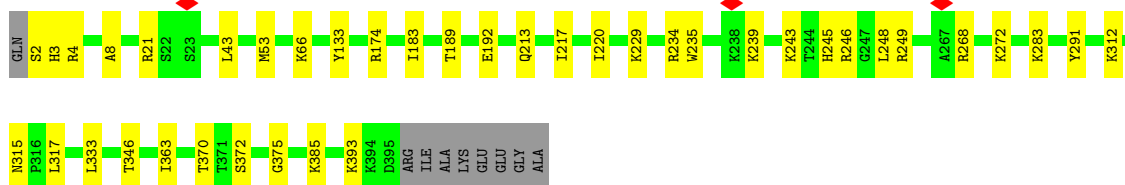
• Molecule 1: Ribosomal protein L8

Chain A: 



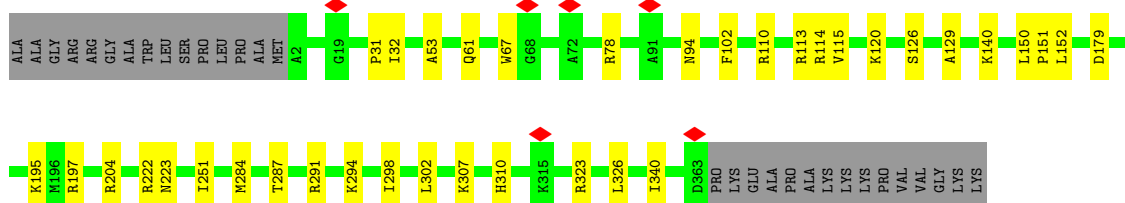
• Molecule 2: uL3

Chain B: 



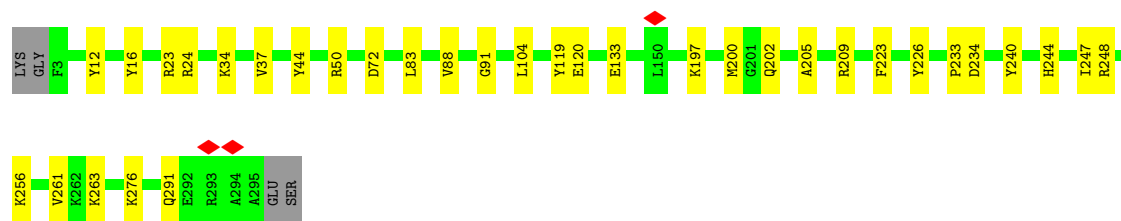
• Molecule 3: Ribosomal protein L4

Chain C: 

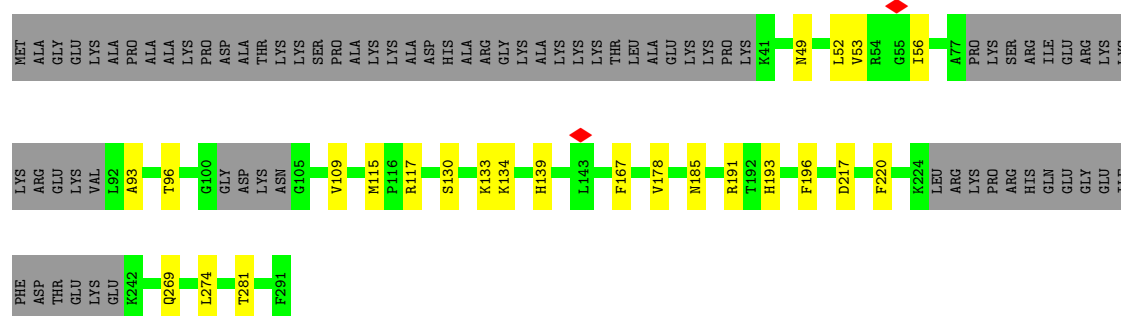


• Molecule 4: Large ribosomal subunit protein uL18

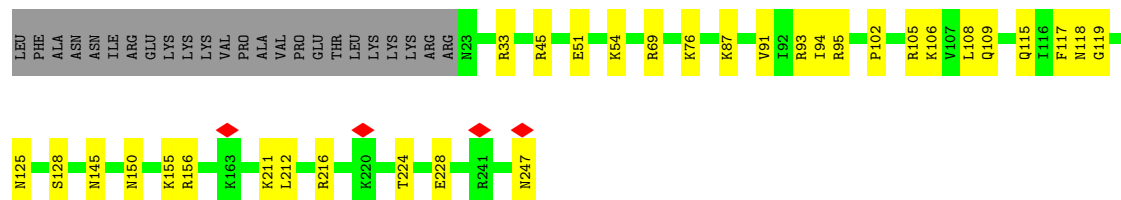
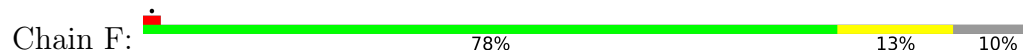
Chain D: 



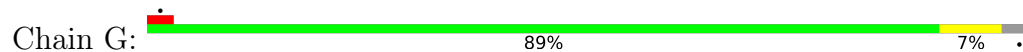
• Molecule 5: 60S ribosomal protein L6



• Molecule 6: uL30



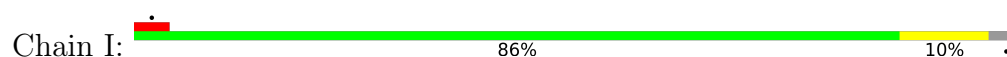
• Molecule 7: eL8



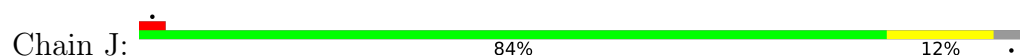
• Molecule 8: 60S ribosomal protein L9



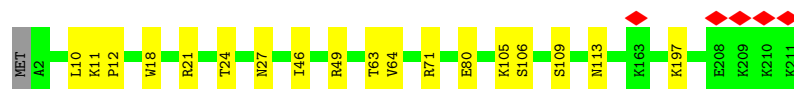
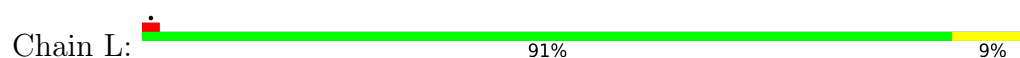
• Molecule 9: 60S ribosomal protein L10



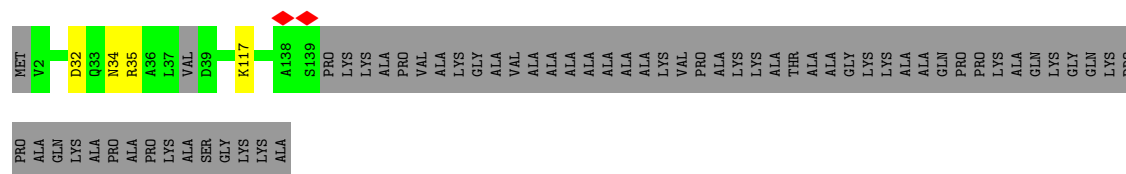
- Molecule 10: Ribosomal protein L11



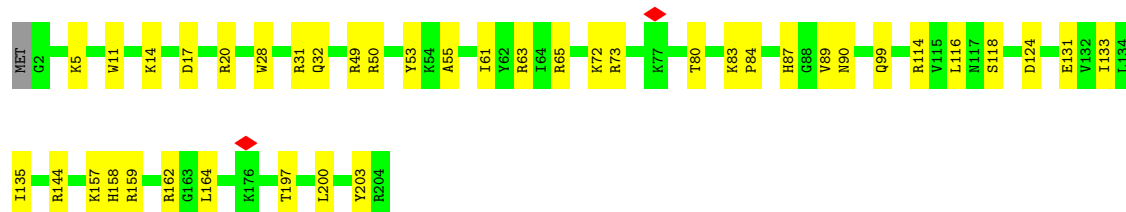
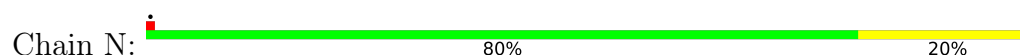
- Molecule 11: 60S ribosomal protein L13



- Molecule 12: Large ribosomal subunit protein eL14



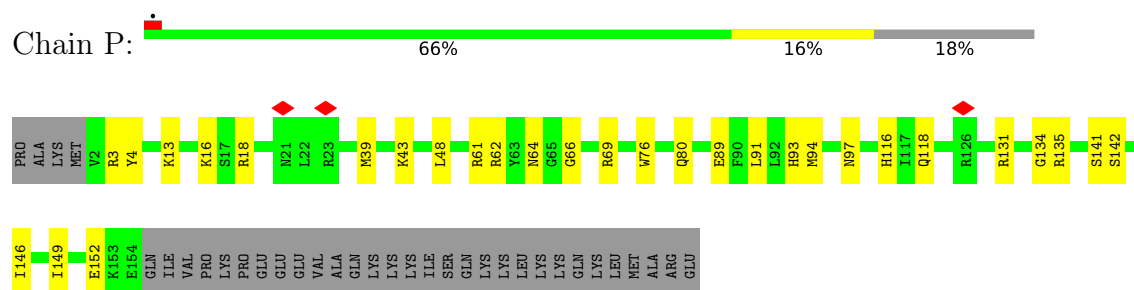
- Molecule 13: Ribosomal protein L15



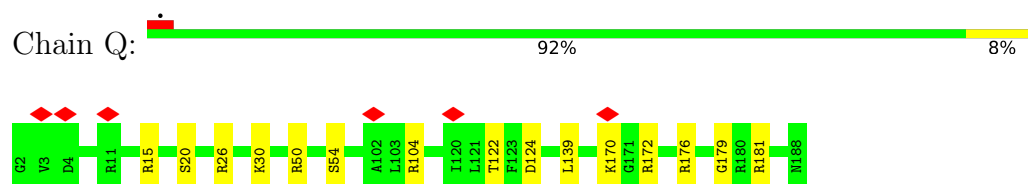
- Molecule 14: uL13



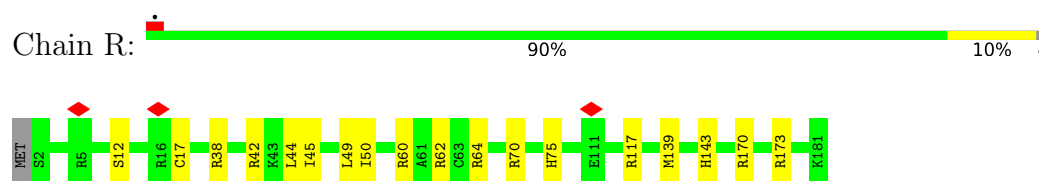
- Molecule 15: Large ribosomal subunit protein uL22



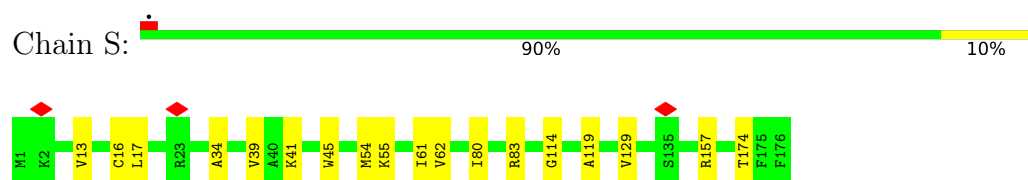
- Molecule 16: eL18



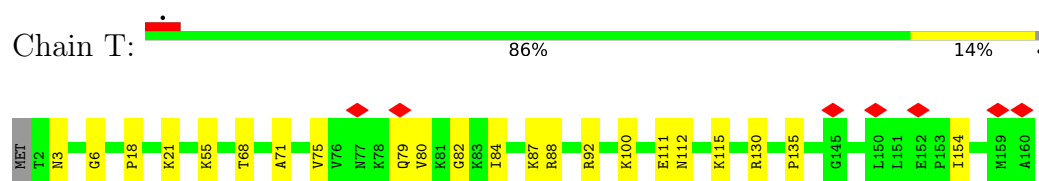
- Molecule 17: eL19



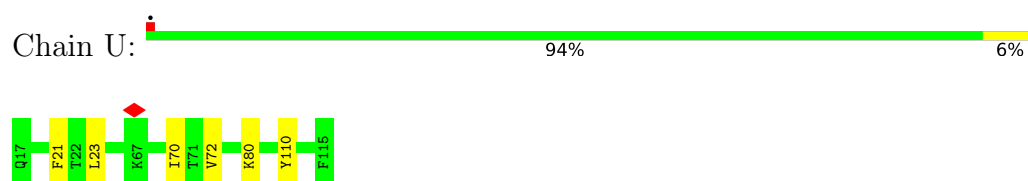
- Molecule 18: eL20



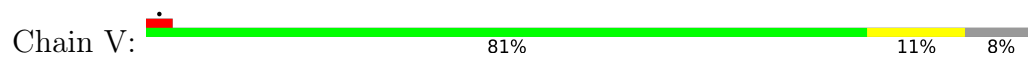
- Molecule 19: eL21



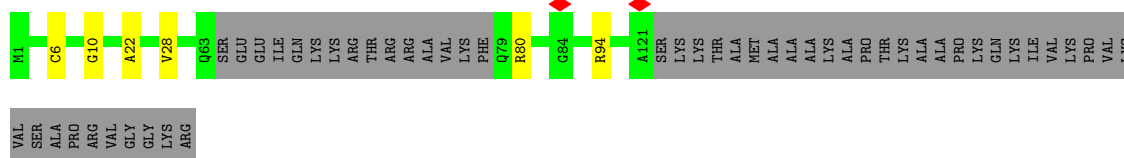
- Molecule 20: eL22



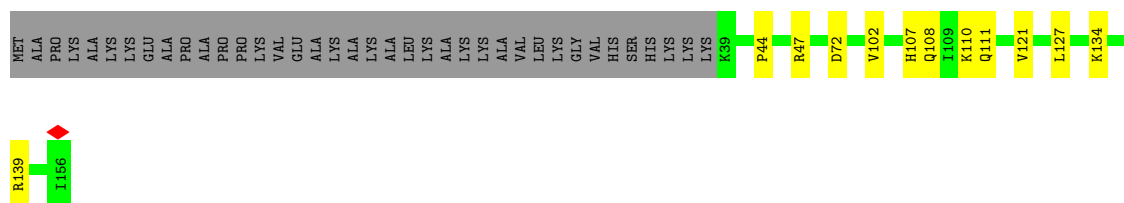
- Molecule 21: Ribosomal protein L23



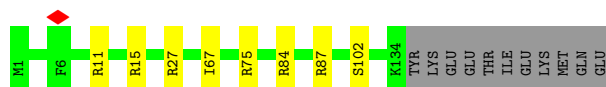
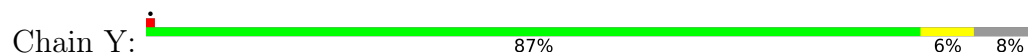
• Molecule 22: eL24



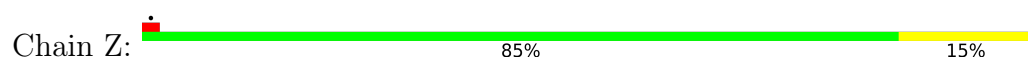
• Molecule 23: eL23



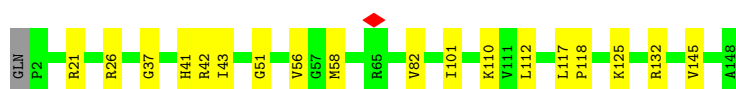
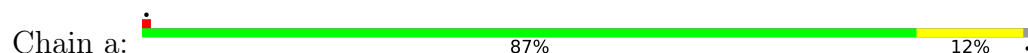
• Molecule 24: uL24



• Molecule 25: 60S ribosomal protein L27

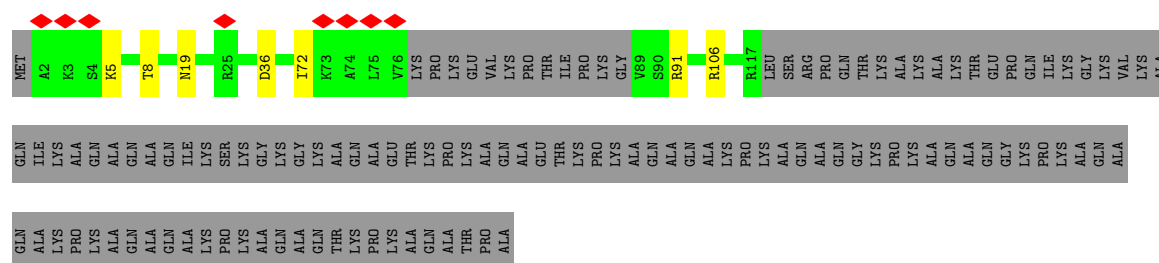


• Molecule 26: uL15



• Molecule 27: eL29

Chain b:  43% 54%



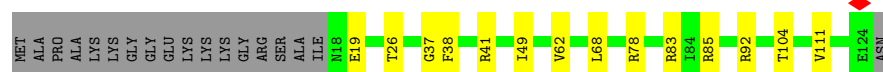
• Molecule 28: eL30

Chain c:  72% 13% 15%



• Molecule 29: eL31

Chain d:  74% 11% 14%



• Molecule 30: Ribosomal protein L32

Chain e:  85% 10% 5%



• Molecule 31: eL33

Chain f:  87% 12%



• Molecule 32: Large ribosomal subunit protein eL34

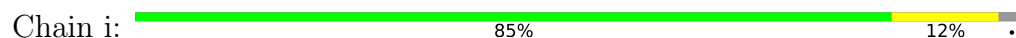
Chain g:  75% 15% 10%



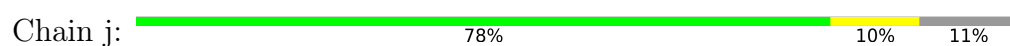
• Molecule 33: eL35



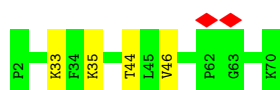
- Molecule 34: 60S ribosomal protein L36



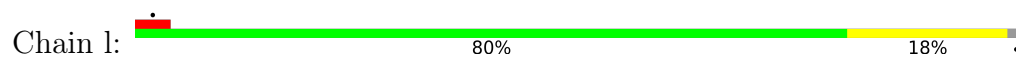
- Molecule 35: Ribosomal protein L37



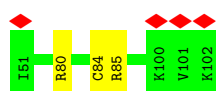
- Molecule 36: eL38



- Molecule 37: eL39



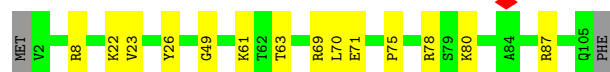
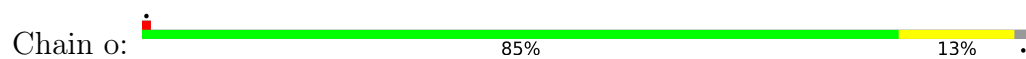
- Molecule 38: eL40



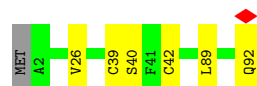
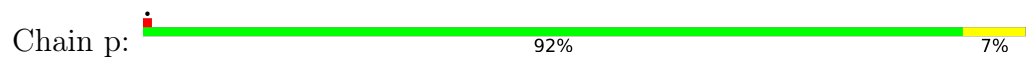
- Molecule 39: eL41



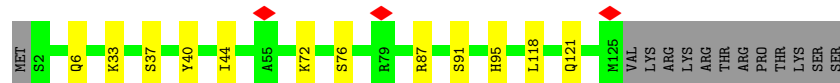
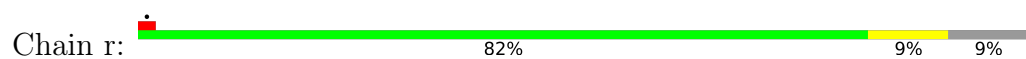
- Molecule 40: Large ribosomal subunit protein eL42



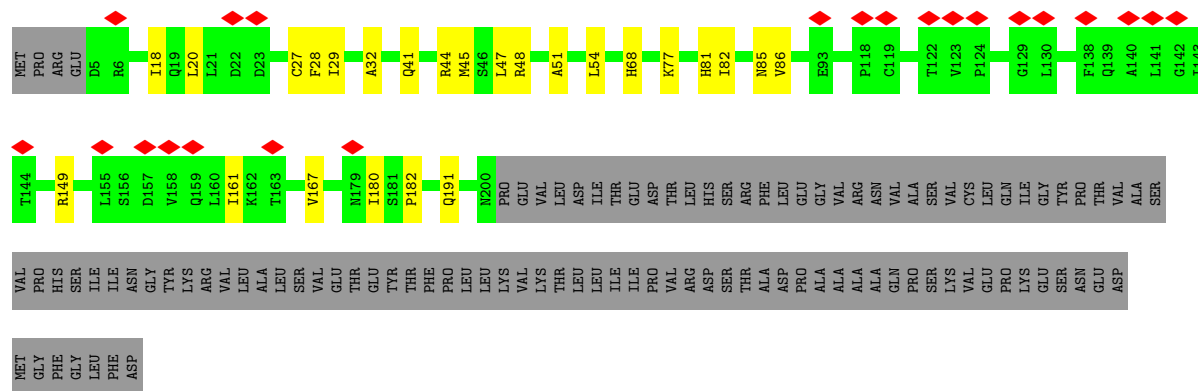
• Molecule 41: eL43



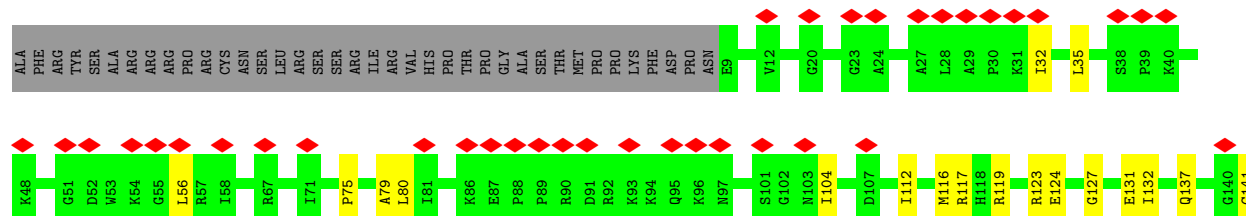
• Molecule 42: eL28



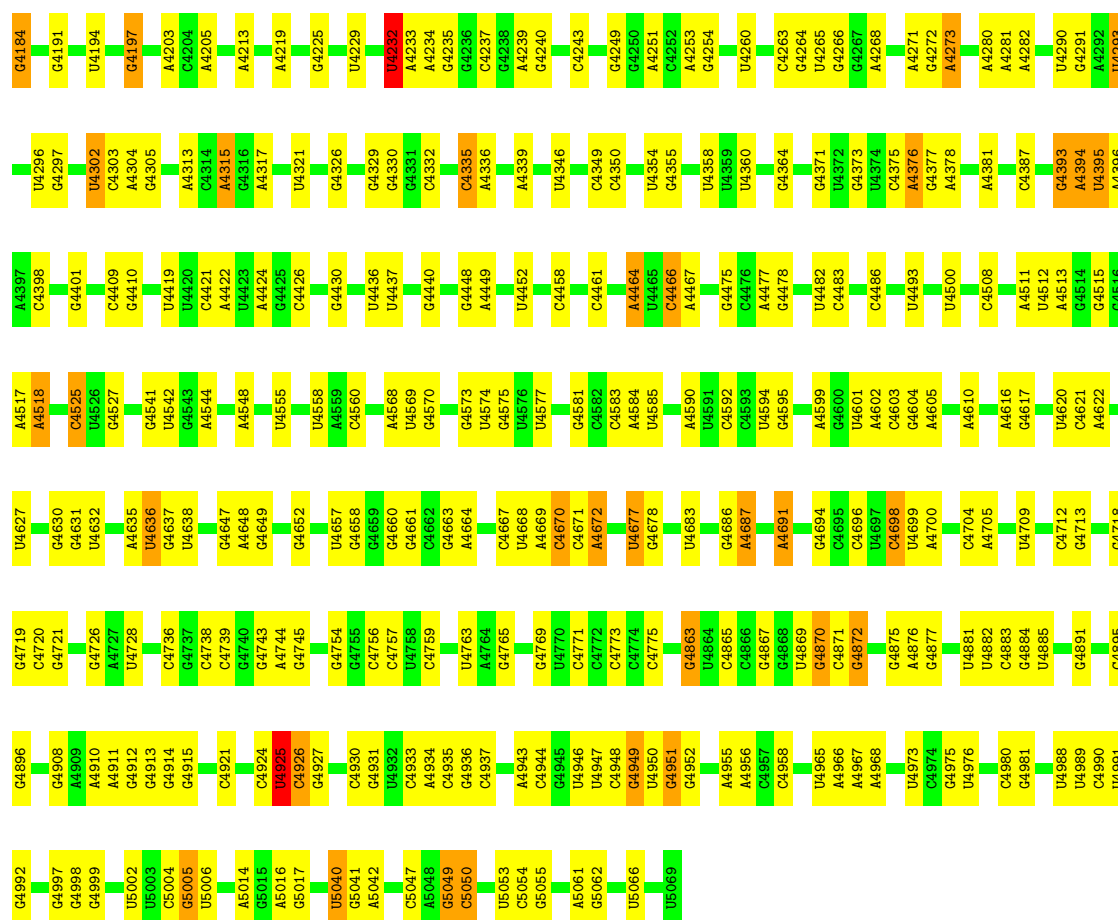
• Molecule 43: 60S acidic ribosomal protein P0

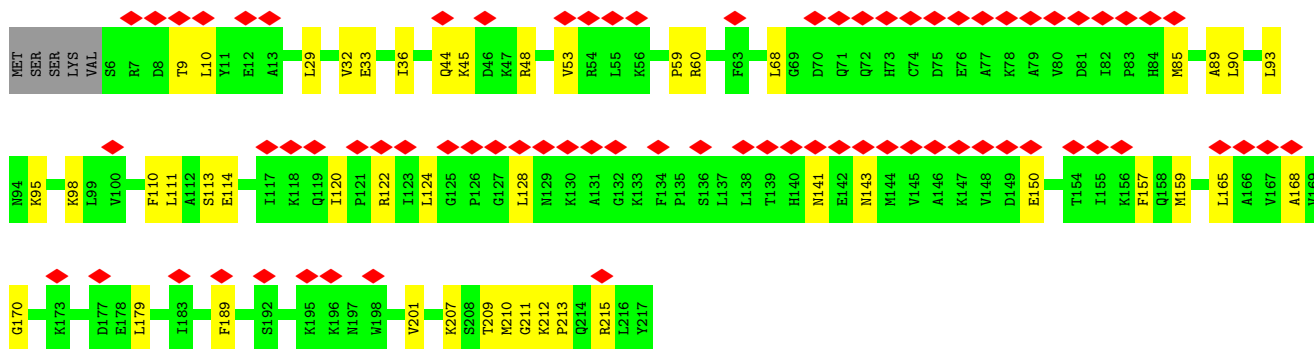


• Molecule 44: Ribosomal protein L12



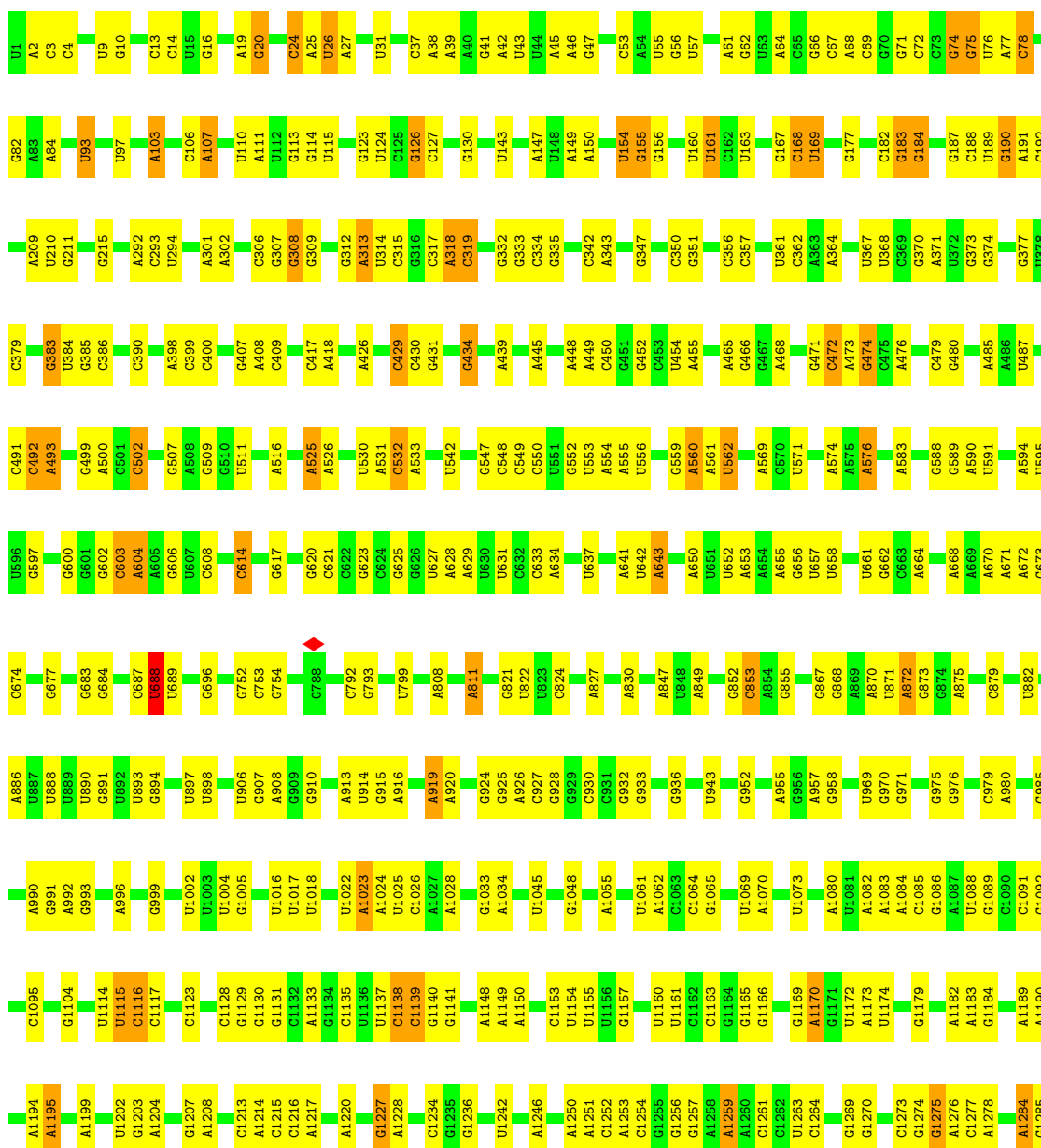
U4066	U4067	U4068	U4069	C4072	A4073	C4074	U4075	A4076	A4077	G4082	U4083	A4084	A4085	A4086	G4087	A4088	G4089	G4097	A4098	C4116	C4119	U4120	G4121	A4122	C4123	C4124	C4125	A4126	G4131	C4134	G4135	C4148	A4157	C4158	C4162	U4163	C4164	G4168	G4169	A4170	C4171	A4178	C4179	G4180	G4183																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
U3915	G3916	A3917	G3918	C3924	U3925	C3926	U3927	A3928	G3938	G3939	A3942	A3943	A3944	C3945	G3946	U3950	G3951	U3957	G3958	U3964	A3965	A3966	G3967	U3968	C4126	G3970	A3971	A3972	G3973	C3975	G4036	G4039	C4040	C4041	G4045	A4047	A4048	U4049	A4050	C4051	A4052	A4053	C4054	U4055	U4063	C4064	G4065																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
A3817	U3818	G3819	G3820	G3823	A3824	A3825	C3826	A3827	A3828	G3829	A3830	G3839	U3840	C3843	U3844	A3845	A3846	U3851	A3852	A3855	C3856	G3857	A3858	C3859	A3860	A3861	A3862	A3863	A3864	A3865	A3866	A3867	A3868	A3869	A3870	A3871	A3872	A3873	A3874	A3875	A3876	A3877	A3878	A3879	A3880	A3881	A3882	A3883	A3884	A3885	A3886	A3887	A3888	A3889	A3890	A3891	A3892	A3893	A3894	A3895	A3896	A3897	A3898	A3899	A3900	A3901	A3902	A3903	A3904	A3905	A3906	A3907	A3908	A3909	A3910	A3911	A3912	A3913	A3914	A3915	A3916	A3917	A3918	A3919	A3920	A3921	A3922	A3923	A3924	A3925	A3926	A3927	A3928	A3929	A3930	A3931	A3932	A3933	A3934	A3935	A3936	A3937	A3938	A3939	A3940	A3941	A3942	A3943	A3944	A3945	A3946	A3947	A3948	A3949	A3950	A3951	A3952	A3953	A3954	A3955	A3956	A3957	A3958	A3959	A3960	A3961	A3962	A3963	A3964	A3965	A3966	A3967	A3968	A3969	A3970	A3971	A3972	A3973	A3974	A3975	A3976	A3977	A3978	A3979	A3980	A3981	A3982	A3983	A3984	A3985	A3986	A3987	A3988	A3989	A3990	A3991	A3992	A3993	A3994	A3995	A3996	A3997	A3998	A3999	A4000	A4001	A4002	A4003	A4004	A4005	A4006	A4007	A4008	A4009	A4010	A4011	A4012	A4013	A4014	A4015	A4016	A4017	A4018	A4019	A4020	A4021	A4022	A4023	A4024	A4025	A4026	A4027	A4028	A4029	A4030	A4031	A4032	A4033	A4034	A4035	A4036	A4037	A4038	A4039	A4040	A4041	A4042	A4043	A4044	A4045	A4046	A4047	A4048	A4049	A4050	A4051	A4052	A4053	A4054	A4055	A4056	A4057	A4058	A4059	A4060	A4061	A4062	A4063	A4064	A4065	A4066	A4067	A4068	A4069	A4070	A4071	A4072	A4073	A4074	A4075	A4076	A4077	A4078	A4079	A4080	A4081	A4082	A4083	A4084	A4085	A4086	A4087	A4088	A4089	A4090	A4091	A4092	A4093	A4094	A4095	A4096	A4097	A4098	A4099	A4100	A4101	A4102	A4103	A4104	A4105	A4106	A4107	A4108	A4109	A4110	A4111	A4112	A4113	A4114	A4115	A4116	A4117	A4118	A4119	A4120	A4121	A4122	A4123	A4124	A4125	A4126	A4127	A4128	A4129	A4130	A4131	A4132	A4133	A4134	A4135	A4136	A4137	A4138	A4139	A4140	A4141	A4142	A4143	A4144	A4145	A4146	A4147	A4148	A4149	A4150	A4151	A4152	A4153	A4154	A4155	A4156	A4157	A4158	A4159	A4160	A4161	A4162	A4163	A4164	A4165	A4166	A4167	A4168	A4169	A4170	A4171	A4172	A4173	A4174	A4175	A4176	A4177	A4178	A4179	A4180	A4181	A4182	A4183	A4184	A4185	A4186	A4187	A4188	A4189	A4190	A4191	A4192	A4193	A4194	A4195	A4196	A4197	A4198	A4199	A4200	A4201	A4202	A4203	A4204	A4205	A4206	A4207	A4208	A4209	A4210	A4211	A4212	A4213	A4214	A4215	A4216	A4217	A4218	A4219	A4220	A4221	A4222	A4223	A4224	A4225	A4226	A4227	A4228	A4229	A4230	A4231	A4232	A4233	A4234	A4235	A4236	A4237	A4238	A4239	A4240	A4241	A4242	A4243	A4244	A4245	A4246	A4247	A4248	A4249	A4250	A4251	A4252	A4253	A4254	A4255	A4256	A4257	A4258	A4259	A4260	A4261	A4262	A4263	A4264	A4265	A4266	A4267	A4268	A4269	A4270	A4271	A4272	A4273	A4274	A4275	A4276	A4277	A4278	A4279	A4280	A4281	A4282	A4283	A4284	A4285	A4286	A4287	A4288	A4289	A4290	A4291	A4292	A4293	A4294	A4295	A4296	A4297	A4298	A4299	A4300	A4301	A4302	A4303	A4304	A4305	A4306	A4307	A4308	A4309	A4310	A4311	A4312	A4313	A4314	A4315	A4316	A4317	A4318	A4319	A4320	A4321	A4322	A4323	A4324	A4325	A4326	A4327	A4328	A4329	A4330	A4331	A4332	A4333	A4334	A4335	A4336	A4337	A4338	A4339	A4340	A4341	A4342	A4343	A4344	A4345	A4346	A4347	A4348	A4349	A4350	A4351	A4352	A4353	A4354	A4355	A4356	A4357	A4358	A4359	A4360	A4361	A4362	A4363	A4364	A4365	A4366	A4367	A4368	A4369	A4370	A4371	A4372	A4373	A4374	A4375	A4376	A4377	A4378	A4379	A4380	A4381	A4382	A4383	A4384	A4385	A4386	A4387	A4388	A4389	A4390	A4391	A4392	A4393	A4394	A4395	A4396	A4397	A4398	A4399	A4400	A4401	A4402	A4403	A4404	A4405	A4406	A4407	A4408	A4409	A4410	A4411	A4412	A4413	A4414	A4415	A4416	A4417	A4418	A4419	A4420	A4421	A4422	A4423	A4424	A4425	A4426	A4427	A4428	A4429	A4430	A4431	A4432	A4433	A4434	A4435	A4436	A4437	A4438	A4439	A4440	A4441	A4442	A4443	A4444	A4445	A4446	A4447	A4448	A4449	A4450	A4451	A4452	A4453	A4454	A4455	A4456	A4457	A4458	A4459	A4460	A4461	A4462	A4463	A4464	A4465	A4466	A4467	A4468	A4469	A4470	A4471	A4472	A4473	A4474	A4475	A4476	A4477	A4478	A4479	A4480	A4481	A4482	A4483	A4484	A4485	A4486	A4487	A4488	A4489	A4490	A4491	A4492	A4493	A4494	A4495	A4496	A4497	A4498	A4499	A4500	A4501	A4502	A4503	A4504	A4505	A4506	A4507	A4508	A4509	A4510	A4511	A4512	A4513	A4514	A4515	A4516	A4517	A4518	A4519	A4520	A4521	A4522	A4523	A4524	A4525	A4526	A4527	A4528	A4529	A4530	A4531	A4532	A4533	A4534	A4535	A4536	A4537	A4538	A4539	A4540	A4541	A4542	A4543	A4544	A4545	A4546	A4547	A4548	A4549	A4550	A4551	A4552	A4553	A4554	A4555	A4556	A4557	A4558	A4559	A4560	A4561	A4562	A4563	A4564	A4565	A4566	A4567	A4568	A4569	A4570	A4571	A4572	A4573	A4574	A4575	A4576	A4577	A4578	A4579	A4580	A4581	A4582	A4583	A4584	A4585	A4586	A4587	A4588	A4589	A4590	A4591	A4592	A4593	A4594	A4595	A4596	A4597	A4598	A4599	A4600	A4601	A4602	A4603	A4604	A4605	A4606	A4607	A4608	A4609	A4610	A4611	A4612	A4613	A4614	A4615	A4616	A4617	A4618	A4619	A4620	A4621	A4622	A4623	A4624	A4625	A4626	A4627	A4628	A4629	A4630	A4631	A4632	A4633	A4634	A4635	A4636	A4637	A4638	A4639	A4640	A4641	A4642	A4643	A4644	A4645	A4646	A4647	A4648	A4649	A4650	A4651	A4652	A4653	A4654	A4655	A4656	A4657	A4658	A4659	A4660	A4661	A4662	A4663	A4664	A4665	A4666	A4667	A4668	A4669	A4670	A4671	A4672	A4673	A4674	A4675	A4676	A4677	A4678	A4679	A4680	A4681	A4682	A4683	A4684	A4685	A4686	A4687	A4688	A4689	A4690	A4691	A4692	A4693	A4694	A4695	A4696	A4697	A4698	A4699	A4700	A4701	A4702	A4703	A4704	A4705	A4706	A4707	A4708	A4709	A4710	A4711	A4712	A4713	A4714	A4715	A4716	A4717	A4718	A4719	A4720	A4721	A4722	A4723	A4724	A4725	A4726	A4727	A4728	A4729	A4730	A4731	A4732	A4733	A4734	A4735	A4736	A4737	A4738	A4739	A4740	A4741	A4742	A4743	A4744	A4745	A4746	A4747	A4748	A4749	A4750	A4751	A4752	A4753	A4754	A4755	A4756	A4757	A4758	A4759	A4760	A4761	A4762	A4763	A4764	A4765	A4766	A4767	A4768	A4769	A4770	A4771	A4772	A4773	A4774	A4775	A4776	A4777	A4778	A4779	A4780	A4781	A4782	A4783	A4784	A4785	A4786	A4787	A4788	A4789	A4790	A4791	A4792	A4793	A4794	A4795	A4796	A4797	A4798	A4799	A4800	A4801	A4802	A4803	A4804	A4805	A4806	A4807	A4808	A4809	A4810	A4811	A4812	A4813	A4814	A4815	A4816	A4817	A4818	A4819	A4820	A4821	A4822	A4823	A4824	A4825	A4826	A4827	A4828	A4829	A4830	A4831	A4832	A4833	A4834	A4835	A4836	A4837	A4838	A4839	A4840	A4841	A4842	A4843	A4844	A4845	A4846	A4847	A4848	A4849	A4850	A4851	A4852	A4853	A4854	A4855	A4856	A4857	A4858	A4859	A4860	A4861	A4862	A4863	A4864	A4865	A4866	A4867	A4868	A4869	A4870	A4871	A4872	A4873	A4874	A4875	A4876	A4877	A4878	A4879	A4880	A4881	A4882	A4883	A4884	A4885	A4886	A4887	A4888	A4889	A4890	A4891	A4892	A4893	A4894	A4895	A4896	A4897	A4898	A4899	A4900	A4901	A4902	A4903	A4904	A4905	A4906	A4907	A4908	A4909	A4910	A4911	A4912	A4913	A4914	A4915	A4916	A4917	A4918	A4919	A4920	A4921	A4922	A4923	A4924	A4925	A4926	A4927	A4928	A4929	A4930	A4931	A4932	A4933	A4934	A4935	A4936	A4937	A4938	A4939	A4940	A4941	A4942	A4943	A4944	A4945	A4946	A4947	A4948	A4949	A4950	A4951	A4952	A4953	A4954	A4955	A4956	A4957	A4958	A4959	A4960	A4961	A4962	A4963	A4964	A4965	A4966	A4967	A4968	A4969	A4970	A4971	A4972	A4973	A4974	A4975	A4976	A4977	A4978	A4979	A4980	A4981	A4982	A4983	A4984	A4985	A4986	A4987	A4988	A4989	A4990	A4991	A4992	A4993	A4994	A4995	A4996	A4997	A4998	A4999	A5000	A5001	A5002	A5003	A5004	A5005	A5006	A5007	A5008	A5009	A5010	A5011	A5012	A5013	A5014	A5015	A5016	A5017	A5018	A5019	A5020	A5021	A5022	A5023	A5024	A5025	A5026	A5027	A5028	A5029	A5030	A5031	A5032	A5033	A5034	A5035	A5036	A5037	A5038	A5039	A5040	A5041	A5042	A5043	A5044	A5045	A5046	A5047	A5048	A5049	A5050	A5051	A5052	A5053	A5054	A5055	A5056	A5057	A5058	A5059	A5060	A5061	A5062	A5063	A5064	A5065	A5066	A5067	A5068	A5069	A5070	A5071	A5072	A5073	A5074	A5075	A5076	A5077	A5078	A5079	A5080	A5081	A5082	A5083	A5084	A5085	A5086	A5087	A5088	A5089	A5090	A5091	A5092	A5093	A5094	A5095	A5096	A5097	A5

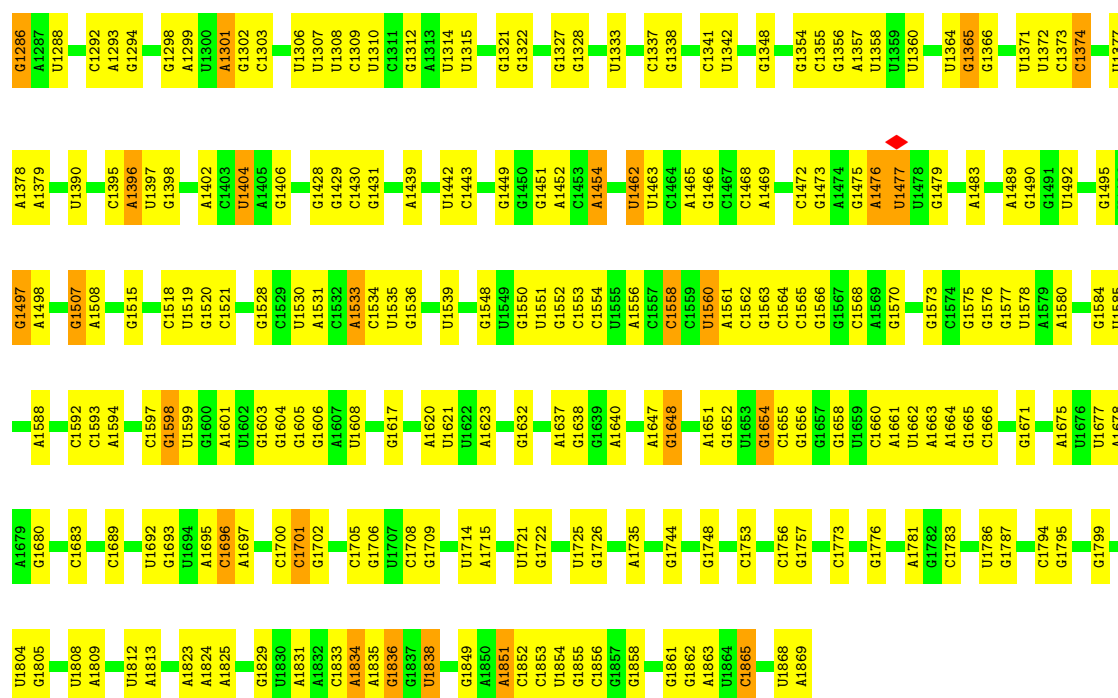




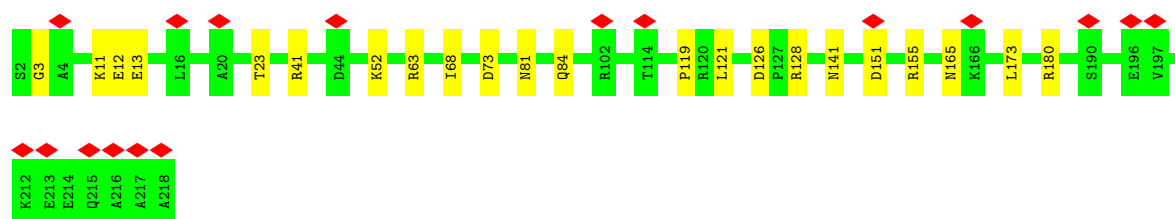
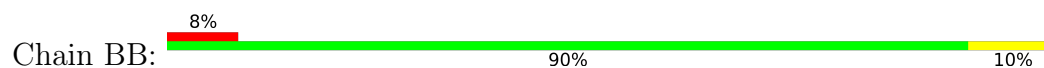
• Molecule 49: 18S rRNA

Chain 2: 61% 35% 5%

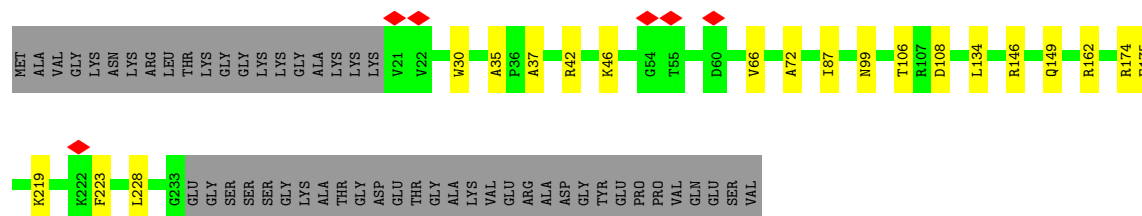
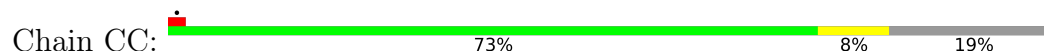




- Molecule 50: uS2



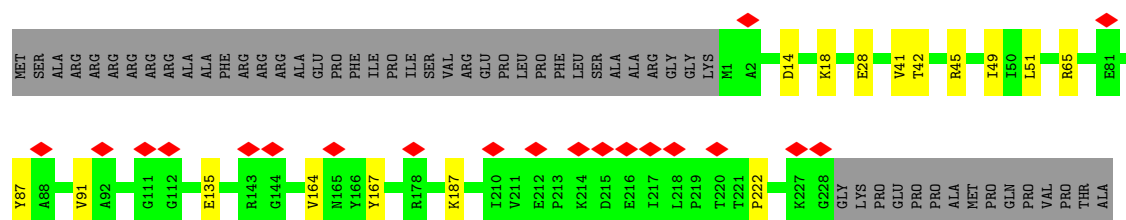
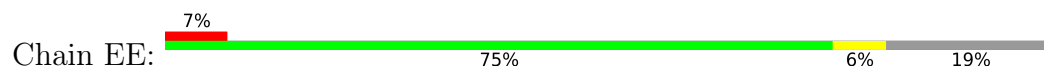
- Molecule 51: 40S ribosomal protein S3a



- Molecule 52: uS5



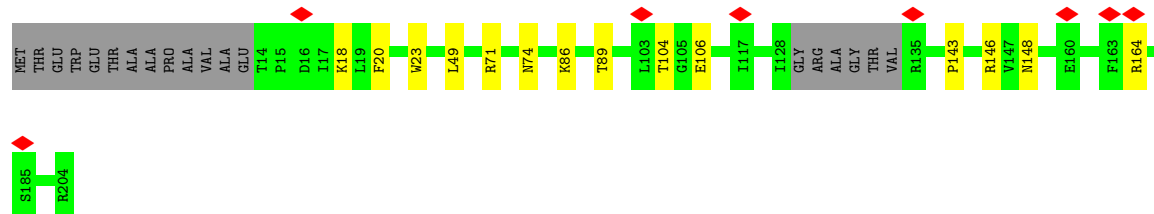
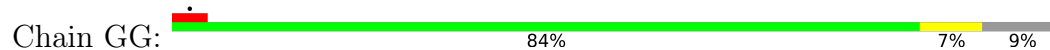
- Molecule 53: Ribosomal protein S3



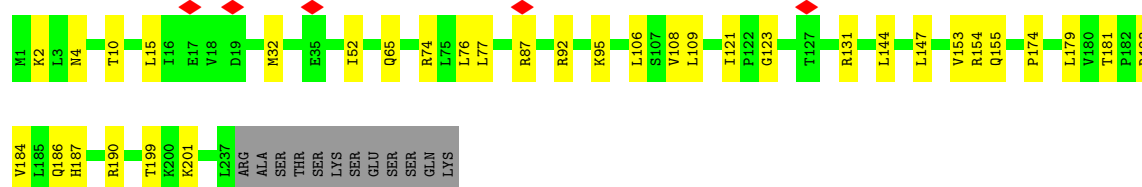
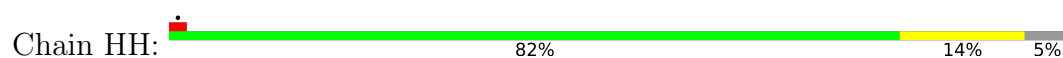
- Molecule 54: eS4



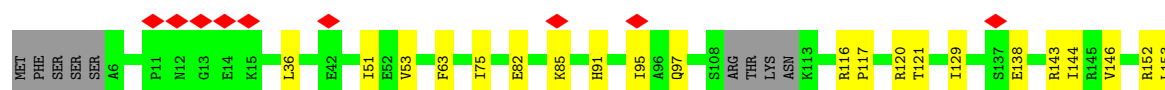
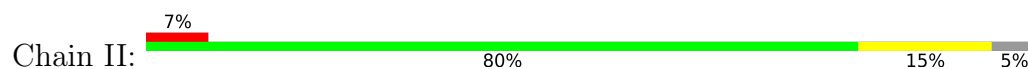
- Molecule 55: Ribosomal protein S5



- Molecule 56: 40S ribosomal protein S6



- Molecule 57: 40S ribosomal protein S7





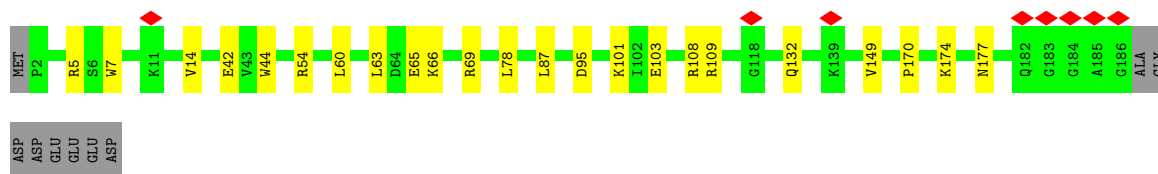
- Molecule 58: 40S ribosomal protein S8

Chain JJ: 88% 12%



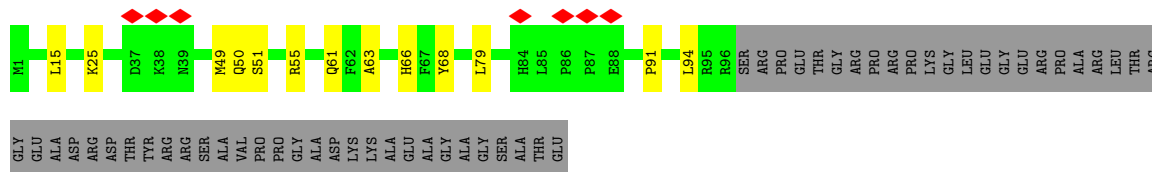
- Molecule 59: Ribosomal protein S9 (Predicted)

Chain KK: 84% 12% 5%



- Molecule 60: S10_pectin domain-containing protein

Chain LL: 5% 56% 9% 36%



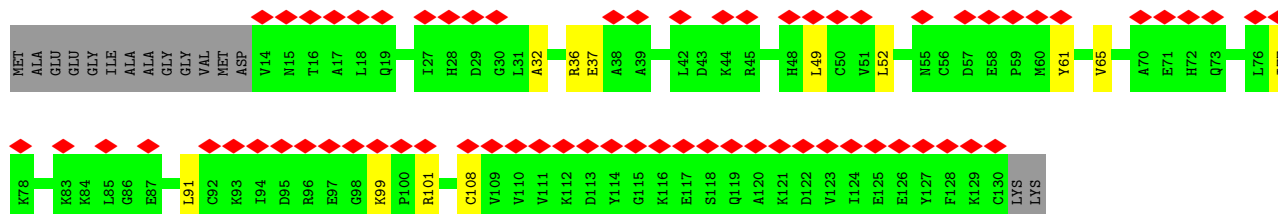
- Molecule 61: Ribosomal protein S11

Chain MM: 7% 83% 8% 9%



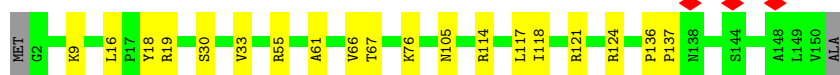
- Molecule 62: 40S ribosomal protein S12

Chain NN: 52% 80% 9% 11%



- Molecule 63: Ribosomal protein S13

Chain OO:  86% 13%



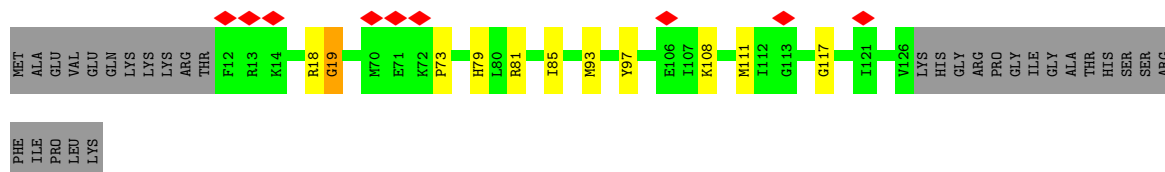
- Molecule 64: Small ribosomal subunit protein uS11

Chain PP:  6% 79% 11% 10%



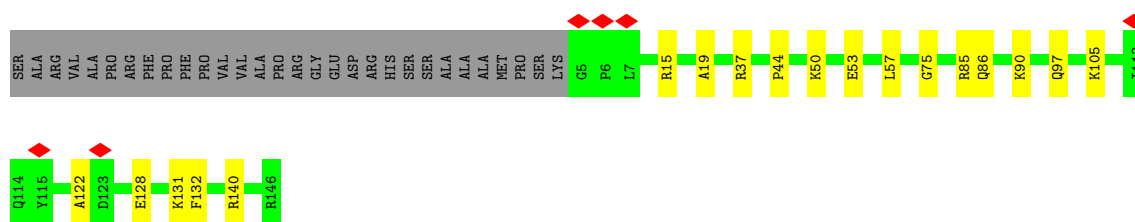
- Molecule 65: uS19

Chain QQ:  6% 72% 7% 21%



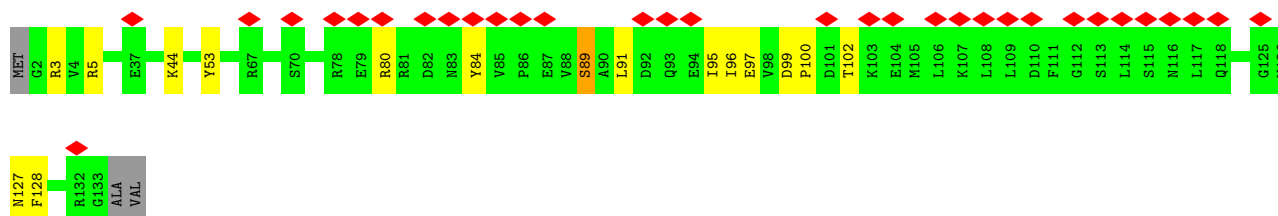
- Molecule 66: Ribosomal protein S16

Chain RR:  72% 10% 17%



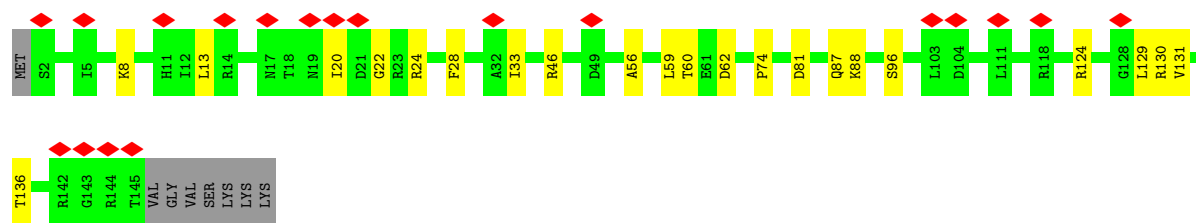
- Molecule 67: eS17

Chain SS:  24% 86% 11% 2%



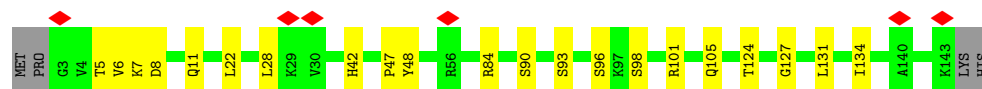
- Molecule 68: uS13

Chain TT:  12% 80% 14% 5%



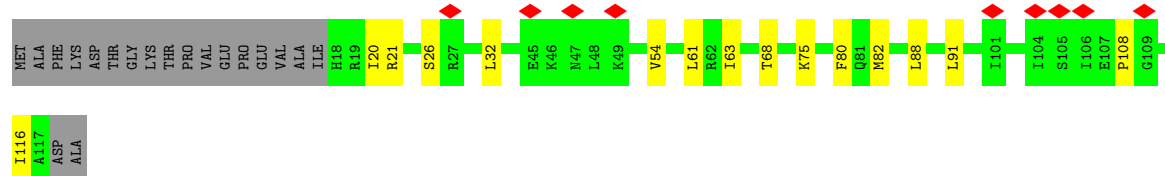
- Molecule 69: eS19

Chain UU: 83% 14% .



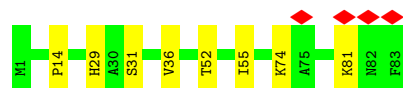
- Molecule 70: uS10

Chain VV: 8% 71% 13% 16%



- Molecule 71: eS21

Chain WW: 5% 90% 10%



- Molecule 72: Ribosomal protein S15a

Chain XX: 82% 18% .



- Molecule 73: Ribosomal protein S23

Chain YY: 85% 14% .

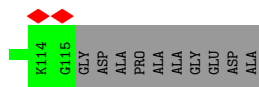
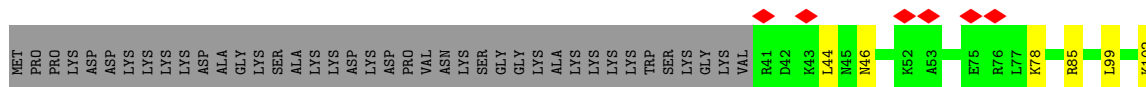


- Molecule 74: 40S ribosomal protein S24

Chain ZZ: 81% 11% 7%



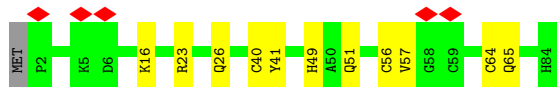
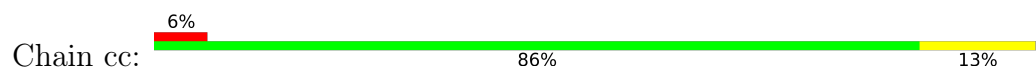
• Molecule 75: eS25



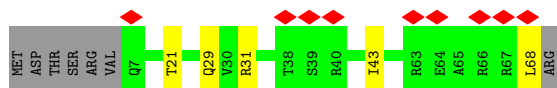
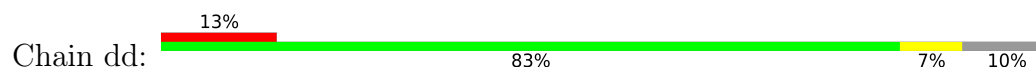
• Molecule 76: eS26



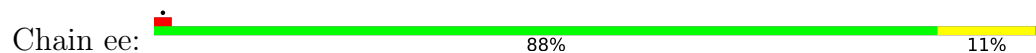
• Molecule 77: 40S ribosomal protein S27



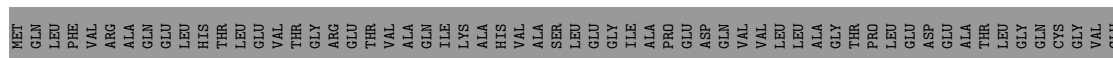
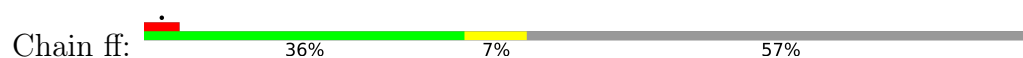
• Molecule 78: Ribosomal protein S28

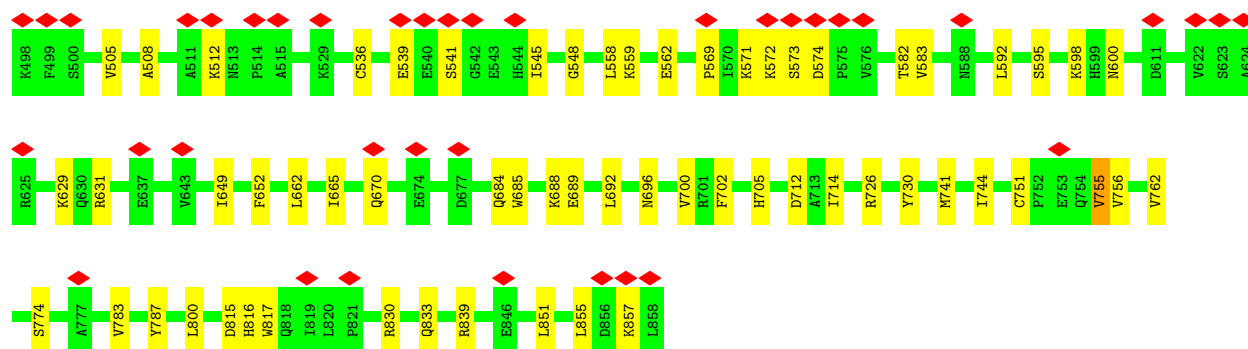


• Molecule 79: eS29

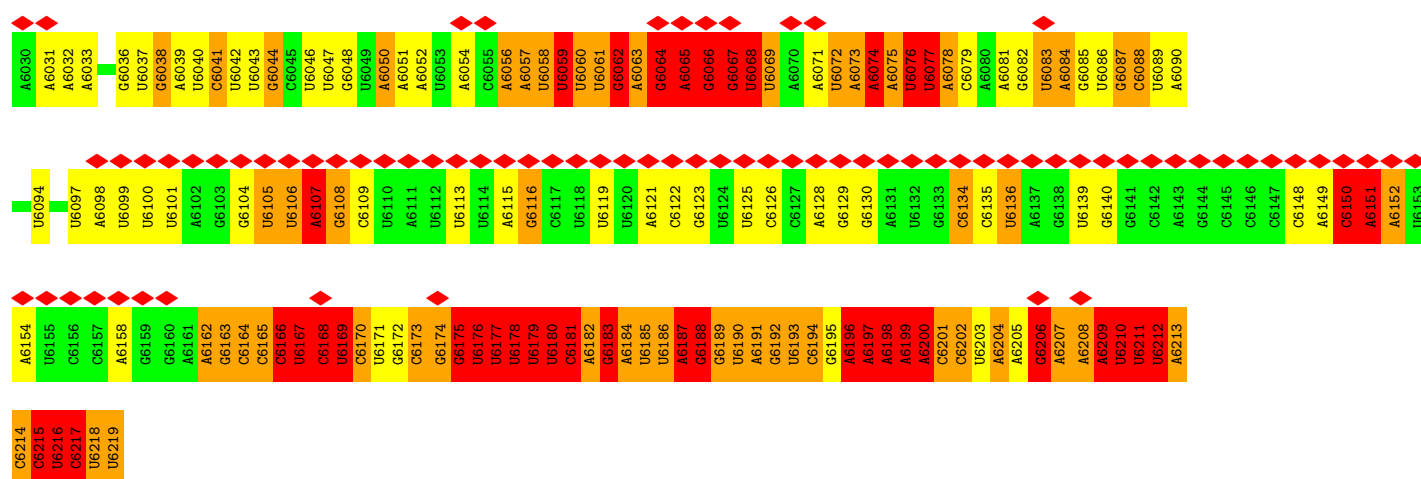
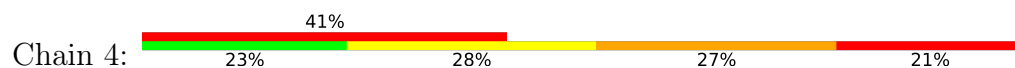


• Molecule 80: 40S ribosomal protein S30





• Molecule 85: CrPV IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.19	0/1812	0.49	0/2439
2	B	0.18	0/3240	0.48	2/4339 (0.0%)
3	C	0.18	0/2936	0.45	0/3943
4	D	0.17	0/2437	0.43	0/3264
5	E	0.18	0/1762	0.46	0/2362
6	F	0.18	0/1911	0.46	0/2549
7	G	0.19	0/1910	0.47	0/2569
8	H	0.18	0/1535	0.49	0/2063
9	I	0.18	0/1702	0.43	0/2272
10	J	0.18	0/1385	0.48	0/1852
11	L	0.24	0/1733	0.49	0/2316
12	M	0.16	0/1150	0.41	0/1534
13	N	0.17	0/1746	0.45	0/2338
14	O	0.17	0/1653	0.43	0/2206
15	P	0.17	0/1268	0.47	0/1700
16	Q	0.18	0/1539	0.46	0/2054
17	R	0.18	0/1524	0.45	0/2013
18	S	0.17	0/1501	0.45	0/2012
19	T	0.18	0/1326	0.42	0/1770
20	U	0.18	0/823	0.47	0/1104
21	V	0.16	0/983	0.42	0/1319
22	W	0.16	0/873	0.45	0/1158
23	X	0.18	0/984	0.43	0/1323
24	Y	0.18	0/1132	0.43	0/1504
25	Z	0.18	0/1130	0.47	0/1507
26	a	0.16	0/1191	0.42	0/1590
27	b	0.16	0/861	0.40	0/1138
28	c	0.17	0/771	0.41	0/1034
29	d	0.21	0/903	0.54	0/1216
30	e	0.17	0/1071	0.47	0/1429
31	f	0.17	0/895	0.48	0/1198
32	g	0.18	0/916	0.45	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.18	0/1021	0.42	0/1348
34	i	0.17	0/841	0.44	0/1112
35	j	0.23	0/720	0.50	0/952
36	k	0.17	0/575	0.41	0/761
37	l	0.19	0/459	0.48	0/608
38	m	0.18	0/435	0.45	0/575
39	n	0.16	0/240	0.41	0/305
40	o	0.14	0/864	0.37	0/1140
41	p	0.17	0/718	0.44	0/953
42	r	0.18	0/1010	0.47	0/1354
43	s	0.19	0/1530	0.45	0/2064
44	t	0.21	0/1174	0.55	0/1582
45	5	0.14	0/86202	0.31	5/134412 (0.0%)
46	7	0.13	0/2836	0.28	0/4421
47	8	0.14	0/3581	0.30	0/5577
48	K	0.23	0/1730	0.60	0/2315
49	2	0.14	0/40500	0.32	2/63092 (0.0%)
50	BB	0.21	0/1747	0.54	0/2374
51	CC	0.18	0/1756	0.46	0/2350
52	DD	0.18	0/1753	0.45	0/2369
53	EE	0.20	0/1796	0.49	0/2417
54	FF	0.17	0/2118	0.47	0/2849
55	GG	0.20	0/1492	0.49	0/2005
56	HH	0.18	0/1946	0.45	0/2590
57	II	0.19	0/1510	0.47	0/2022
58	JJ	0.18	0/1715	0.48	0/2287
59	KK	0.18	0/1550	0.49	0/2069
60	LL	0.17	0/834	0.43	0/1125
61	MM	0.18	0/1195	0.48	0/1597
62	NN	0.21	0/918	0.53	0/1233
63	OO	0.17	0/1226	0.42	0/1649
64	PP	0.17	0/1029	0.46	0/1380
65	QQ	0.18	0/974	0.54	0/1301
66	RR	0.19	0/1146	0.48	0/1534
67	SS	0.22	0/1082	0.56	1/1452 (0.1%)
68	TT	0.20	0/1208	0.53	0/1618
69	UU	0.19	0/1115	0.46	0/1493
70	VV	0.19	0/805	0.44	0/1081
71	WW	0.18	0/643	0.47	0/860
72	XX	0.17	0/1051	0.43	0/1406
73	YY	0.18	0/1116	0.47	0/1490
74	ZZ	0.19	0/1028	0.47	0/1366
75	aa	0.20	0/604	0.48	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	bb	0.17	0/828	0.44	0/1109
77	cc	0.18	0/665	0.46	0/891
78	dd	0.14	0/490	0.38	0/656
79	ee	0.16	0/470	0.45	0/623
80	ff	0.17	0/462	0.47	0/607
81	gg	0.16	0/567	0.42	0/753
82	hh	0.16	0/2492	0.46	0/3391
83	3	0.13	0/2077	0.26	0/3238
84	9	0.20	0/6804	0.54	1/9189 (0.0%)
85	4	0.68	14/4490 (0.3%)	1.55	126/6984 (1.8%)
All	All	0.18	14/243741 (0.0%)	0.44	137/357074 (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
3	C	0	1
50	BB	0	1
65	QQ	0	1
67	SS	0	1
73	YY	0	1
84	9	0	1
85	4	1	14
All	All	1	20

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	4	6218	U	C1'-N1	7.11	1.59	1.48
85	4	6219	U	C1'-N1	7.05	1.59	1.48
85	4	6065	A	O3'-P	6.87	1.71	1.61
85	4	6078	A	O3'-P	-6.68	1.51	1.61
85	4	6217	C	O3'-P	6.52	1.71	1.61

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6068	U	O3'-P-O5'	-25.54	65.70	104.00
85	4	6218	U	O3'-P-O5'	-23.73	68.41	104.00
85	4	6176	U	C1'-C2'-O2'	-21.00	76.91	108.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6215	C	C4'-C3'-O3'	19.37	142.05	113.00
85	4	6187	A	C1'-C2'-O2'	-17.98	84.84	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6210	U	C1'

5 of 20 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	BB	12	GLU	Peptide
3	C	151	PRO	Peptide
65	QQ	19	GLY	Peptide
67	SS	89	SER	Peptide
73	YY	61	GLN	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	A	1777	0	1819	22	0
2	B	3172	0	3310	31	0
3	C	2883	0	3052	28	0
4	D	2391	0	2424	21	0
5	E	1729	0	1887	17	0
6	F	1875	0	1995	20	0
7	G	1879	0	2025	11	0
8	H	1516	0	1597	14	0
9	I	1664	0	1712	14	0
10	J	1362	0	1399	11	0
11	L	1702	0	1820	15	0
12	M	1130	0	1201	3	0
13	N	1701	0	1749	27	0
14	O	1623	0	1771	11	0
15	P	1242	0	1274	22	0
16	Q	1515	0	1634	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	R	1508	0	1664	13	0
18	S	1462	0	1508	11	0
19	T	1298	0	1366	15	0
20	U	809	0	833	3	0
21	V	969	0	1031	11	0
22	W	860	0	903	7	0
23	X	967	0	1040	9	0
24	Y	1115	0	1205	7	0
25	Z	1107	0	1182	13	0
26	a	1162	0	1209	14	0
27	b	848	0	920	5	0
28	c	761	0	794	9	0
29	d	888	0	930	8	0
30	e	1053	0	1147	10	0
31	f	876	0	912	10	0
32	g	906	0	1002	12	0
33	h	1013	0	1147	7	0
34	i	830	0	916	10	0
35	j	705	0	741	9	0
36	k	569	0	637	2	0
37	l	447	0	480	7	0
38	m	429	0	469	2	0
39	n	239	0	289	2	0
40	o	851	0	924	10	0
41	p	708	0	756	4	0
42	r	994	0	1051	8	0
43	s	1507	0	1564	14	0
44	t	1160	0	1218	12	0
45	5	77073	0	38949	466	0
46	7	2538	0	1286	8	0
47	8	3208	0	1629	24	0
48	K	1705	0	1804	143	0
49	2	36229	0	18309	260	0
50	BB	1710	0	1708	16	0
51	CC	1729	0	1803	12	0
52	DD	1716	0	1806	13	0
53	EE	1768	0	1866	9	0
54	FF	2076	0	2177	14	0
55	GG	1471	0	1522	11	0
56	HH	1923	0	2089	24	0
57	II	1488	0	1582	18	0
58	JJ	1686	0	1772	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	KK	1525	0	1640	16	0
60	LL	810	0	836	8	0
61	MM	1175	0	1249	10	0
62	NN	908	0	939	7	0
63	OO	1202	0	1289	15	0
64	PP	1016	0	1039	15	0
65	QQ	956	0	1002	6	0
66	RR	1128	0	1195	12	0
67	SS	1068	0	1121	13	0
68	TT	1190	0	1249	13	0
69	UU	1097	0	1130	16	0
70	VV	795	0	862	11	0
71	WW	636	0	637	7	0
72	XX	1034	0	1080	15	0
73	YY	1098	0	1167	13	0
74	ZZ	1011	0	1083	10	0
75	aa	598	0	656	4	0
76	bb	814	0	865	8	0
77	cc	651	0	672	7	0
78	dd	488	0	514	3	0
79	ee	459	0	451	5	0
80	ff	457	0	502	6	0
81	gg	555	0	565	5	0
82	hh	2436	0	2392	28	0
83	3	1860	0	935	36	0
84	9	6673	0	6750	78	0
85	4	4020	0	2013	738	0
86	2	1	0	0	0	0
86	bb	1	0	0	0	0
86	gg	1	0	0	0	0
86	p	1	0	0	0	0
87	5	2	0	0	0	0
All	All	227188	0	170642	2123	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 6.

The worst 5 of 2123 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)
85:4:6199:A:N6	85:4:6200:A:C5	1.78	1.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6180:U:N3	85:4:6196:A:H2	1.08	1.49
48:K:124:LEU:CA	85:4:6088:C:H42	1.25	1.48
85:4:6178:U:C2	85:4:6179:U:C6	2.00	1.48
85:4:6177:U:H2'	85:4:6178:U:C3'	1.39	1.47

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/257 (92%)	223 (94%)	14 (6%)	0	100	100
2	B	392/403 (97%)	381 (97%)	11 (3%)	0	100	100
3	C	358/392 (91%)	341 (95%)	17 (5%)	0	100	100
4	D	291/297 (98%)	281 (97%)	10 (3%)	0	100	100
5	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
6	F	223/249 (90%)	214 (96%)	9 (4%)	0	100	100
7	G	229/242 (95%)	218 (95%)	11 (5%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
9	I	201/214 (94%)	192 (96%)	9 (4%)	0	100	100
10	J	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
11	L	208/211 (99%)	198 (95%)	10 (5%)	0	100	100
12	M	133/198 (67%)	128 (96%)	5 (4%)	0	100	100
13	N	201/204 (98%)	189 (94%)	12 (6%)	0	100	100
14	O	194/198 (98%)	186 (96%)	8 (4%)	0	100	100
15	P	151/187 (81%)	147 (97%)	4 (3%)	0	100	100
16	Q	185/187 (99%)	179 (97%)	6 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	R	178/181 (98%)	174 (98%)	4 (2%)	0	100	100
18	S	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
19	T	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
20	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
21	V	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
22	W	102/157 (65%)	99 (97%)	3 (3%)	0	100	100
23	X	116/156 (74%)	109 (94%)	7 (6%)	0	100	100
24	Y	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
25	Z	133/136 (98%)	123 (92%)	10 (8%)	0	100	100
26	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	b	100/226 (44%)	99 (99%)	1 (1%)	0	100	100
28	c	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
29	d	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
30	e	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
31	f	107/110 (97%)	98 (92%)	9 (8%)	0	100	100
32	g	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
33	h	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
34	i	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
35	j	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
36	k	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
37	l	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
38	m	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
41	p	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
42	r	122/137 (89%)	119 (98%)	3 (2%)	0	100	100
43	s	194/303 (64%)	186 (96%)	8 (4%)	0	100	100
44	t	151/195 (77%)	135 (89%)	16 (11%)	0	100	100
48	K	204/217 (94%)	182 (89%)	21 (10%)	1 (0%)	24	59
50	BB	215/217 (99%)	202 (94%)	13 (6%)	0	100	100
51	CC	211/264 (80%)	197 (93%)	14 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	DD	219/221 (99%)	216 (99%)	3 (1%)	0	100	100
53	EE	226/281 (80%)	217 (96%)	9 (4%)	0	100	100
54	FF	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
55	GG	181/204 (89%)	173 (96%)	8 (4%)	0	100	100
56	HH	235/249 (94%)	227 (97%)	8 (3%)	0	100	100
57	II	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
58	JJ	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
59	KK	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
60	LL	94/149 (63%)	90 (96%)	4 (4%)	0	100	100
61	MM	139/158 (88%)	132 (95%)	7 (5%)	0	100	100
62	NN	115/132 (87%)	107 (93%)	8 (7%)	0	100	100
63	OO	147/151 (97%)	145 (99%)	2 (1%)	0	100	100
64	PP	134/151 (89%)	126 (94%)	8 (6%)	0	100	100
65	QQ	113/145 (78%)	102 (90%)	10 (9%)	1 (1%)	14	47
66	RR	140/172 (81%)	133 (95%)	7 (5%)	0	100	100
67	SS	130/135 (96%)	119 (92%)	11 (8%)	0	100	100
68	TT	142/152 (93%)	133 (94%)	9 (6%)	0	100	100
69	UU	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
70	VV	98/119 (82%)	96 (98%)	2 (2%)	0	100	100
71	WW	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
72	XX	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
73	YY	139/143 (97%)	131 (94%)	7 (5%)	1 (1%)	18	52
74	ZZ	122/134 (91%)	120 (98%)	2 (2%)	0	100	100
75	aa	73/125 (58%)	72 (99%)	1 (1%)	0	100	100
76	bb	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
77	cc	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
78	dd	60/69 (87%)	60 (100%)	0	0	100	100
79	ee	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
80	ff	55/133 (41%)	49 (89%)	6 (11%)	0	100	100
81	gg	66/156 (42%)	63 (96%)	3 (4%)	0	100	100
82	hh	310/317 (98%)	292 (94%)	18 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
84	9	854/856 (100%)	801 (94%)	53 (6%)	0	100	100
All	All	12554/14095 (89%)	11964 (95%)	587 (5%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
48	K	59	PRO
73	YY	62	PRO
65	QQ	19	GLY

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	A	172/199 (86%)	172 (100%)	0	100	100
2	B	342/348 (98%)	342 (100%)	0	100	100
3	C	302/323 (94%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100
5	E	190/251 (76%)	190 (100%)	0	100	100
6	F	196/218 (90%)	196 (100%)	0	100	100
7	G	200/208 (96%)	200 (100%)	0	100	100
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	175/181 (97%)	175 (100%)	0	100	100
10	J	143/149 (96%)	143 (100%)	0	100	100
11	L	175/176 (99%)	175 (100%)	0	100	100
12	M	116/151 (77%)	116 (100%)	0	100	100
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	170/170 (100%)	170 (100%)	0	100	100
15	P	134/165 (81%)	134 (100%)	0	100	100
16	Q	164/164 (100%)	164 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	R	159/160 (99%)	159 (100%)	0	100	100
18	S	157/157 (100%)	157 (100%)	0	100	100
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	89/89 (100%)	89 (100%)	0	100	100
21	V	100/107 (94%)	100 (100%)	0	100	100
22	W	86/126 (68%)	86 (100%)	0	100	100
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	124 (100%)	0	100	100
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	119 (100%)	0	100	100
27	b	84/172 (49%)	83 (99%)	1 (1%)	63	79
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	98 (100%)	0	100	100
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/106 (92%)	98 (100%)	0	100	100
33	h	109/110 (99%)	109 (100%)	0	100	100
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100
36	k	64/64 (100%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/48 (100%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	108 (100%)	0	100	100
43	s	164/258 (64%)	164 (100%)	0	100	100
44	t	126/163 (77%)	126 (100%)	0	100	100
48	K	190/196 (97%)	190 (100%)	0	100	100
50	BB	180/181 (99%)	180 (100%)	0	100	100
51	CC	194/231 (84%)	194 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	DD	187/187 (100%)	187 (100%)	0	100	100
53	EE	190/232 (82%)	190 (100%)	0	100	100
54	FF	224/224 (100%)	224 (100%)	0	100	100
55	GG	158/170 (93%)	158 (100%)	0	100	100
56	HH	207/218 (95%)	207 (100%)	0	100	100
57	II	165/174 (95%)	165 (100%)	0	100	100
58	JJ	178/178 (100%)	178 (100%)	0	100	100
59	KK	161/168 (96%)	161 (100%)	0	100	100
60	LL	87/125 (70%)	87 (100%)	0	100	100
61	MM	130/142 (92%)	129 (99%)	1 (1%)	73	82
62	NN	99/108 (92%)	99 (100%)	0	100	100
63	OO	130/131 (99%)	130 (100%)	0	100	100
64	PP	106/119 (89%)	106 (100%)	0	100	100
65	QQ	105/130 (81%)	105 (100%)	0	100	100
66	RR	117/140 (84%)	117 (100%)	0	100	100
67	SS	119/121 (98%)	119 (100%)	0	100	100
68	TT	125/132 (95%)	125 (100%)	0	100	100
69	UU	111/116 (96%)	111 (100%)	0	100	100
70	VV	92/107 (86%)	92 (100%)	0	100	100
71	WW	67/67 (100%)	67 (100%)	0	100	100
72	XX	112/113 (99%)	112 (100%)	0	100	100
73	YY	113/114 (99%)	113 (100%)	0	100	100
74	ZZ	107/115 (93%)	107 (100%)	0	100	100
75	aa	66/103 (64%)	66 (100%)	0	100	100
76	bb	88/88 (100%)	88 (100%)	0	100	100
77	cc	75/76 (99%)	75 (100%)	0	100	100
78	dd	55/62 (89%)	55 (100%)	0	100	100
79	ee	48/49 (98%)	48 (100%)	0	100	100
80	ff	47/106 (44%)	47 (100%)	0	100	100
81	gg	61/140 (44%)	61 (100%)	0	100	100
82	hh	272/275 (99%)	272 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
84	9	728/728 (100%)	727 (100%)	1 (0%)	88	91
All	All	10937/12018 (91%)	10934 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	b	72	ILE
61	MM	42	LEU
84	9	158	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
51	CC	147	ASN
63	OO	101	HIS
54	FF	142	HIS
57	II	193	GLN
68	TT	72	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3562/3594 (99%)	902 (25%)	29 (0%)
46	7	118/119 (99%)	16 (13%)	0
47	8	149/151 (98%)	37 (24%)	1 (0%)
49	2	1679/1697 (98%)	409 (24%)	14 (0%)
83	3	86/87 (98%)	25 (29%)	0
85	4	188/190 (98%)	124 (65%)	48 (25%)
All	All	5782/5838 (99%)	1513 (26%)	92 (1%)

5 of 1513 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	5	A
45	5	7	C
45	5	11	G
45	5	12	A
45	5	14	C

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
85	4	6151	A
85	4	6180	U
85	4	6164	C
85	4	6172	G
85	4	6184	A

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 6 ligands modelled in this entry, 6 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	5	36
49	2	20

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
48	K	3
47	8	1
82	hh	1
14	O	1
3	C	1

The worst 5 of 63 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	41.98
1	5	1252:C	O3'	1271:G	P	33.40
1	5	1696:C	O3'	1720:C	P	19.99
1	5	1219:G	O3'	1233:G	P	18.35
1	5	523:C	O3'	638:G	P	18.12

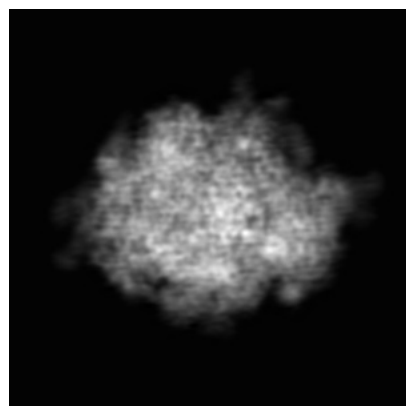
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7836. These allow visual inspection of the internal detail of the map and identification of artifacts.

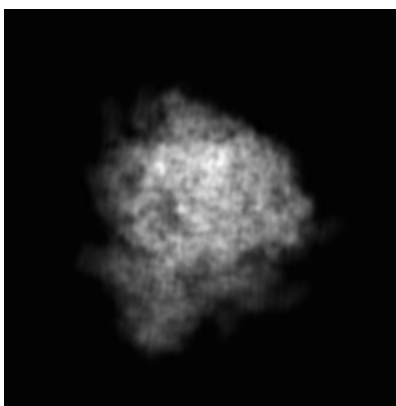
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

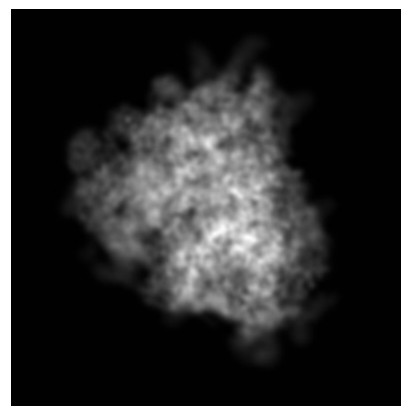
6.1.1 Primary map



X

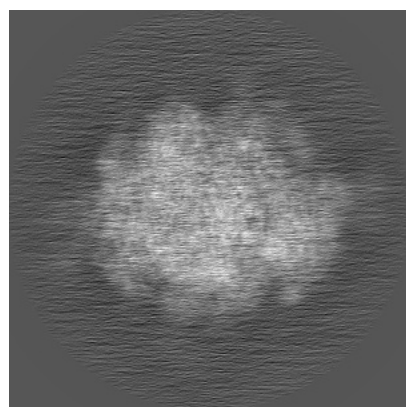


Y

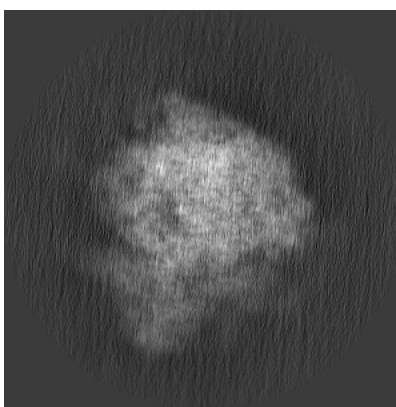


Z

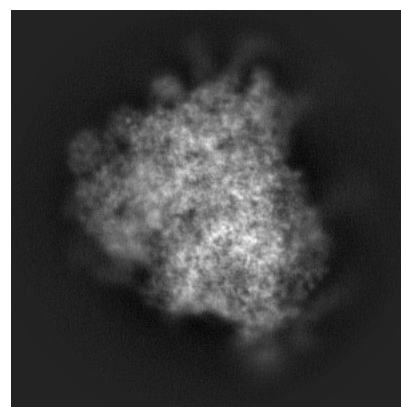
6.1.2 Raw map



X



Y

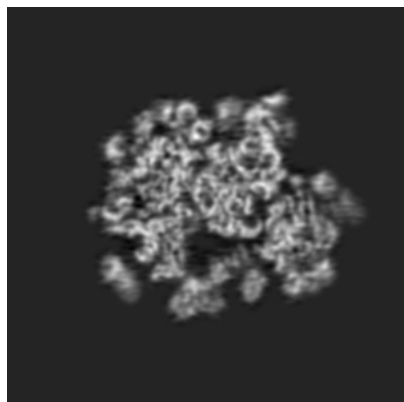


Z

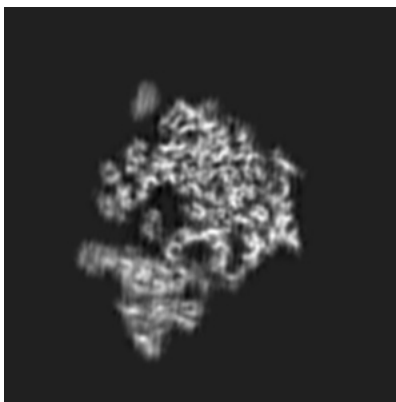
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

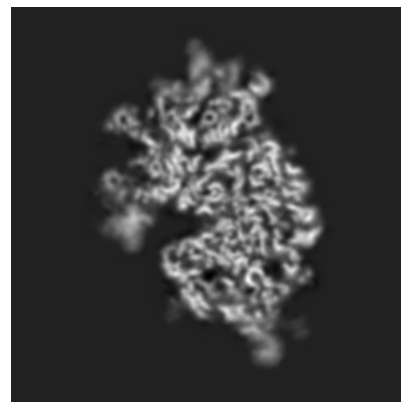
6.2.1 Primary map



X Index: 200

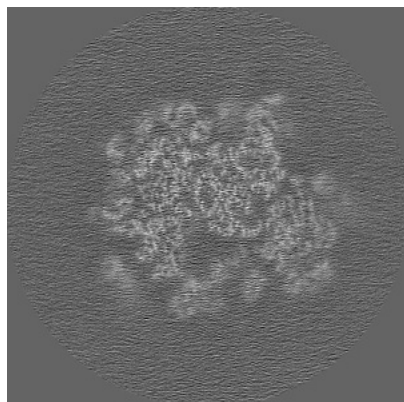


Y Index: 200

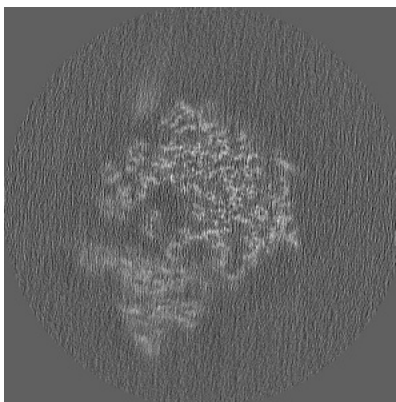


Z Index: 200

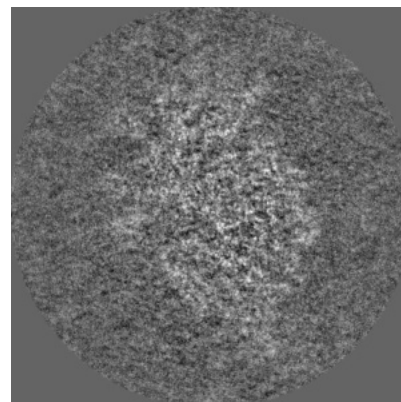
6.2.2 Raw map



X Index: 200



Y Index: 200

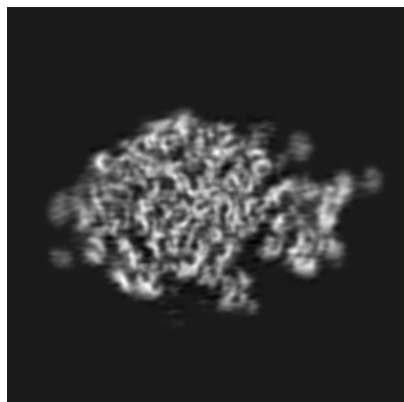


Z Index: 200

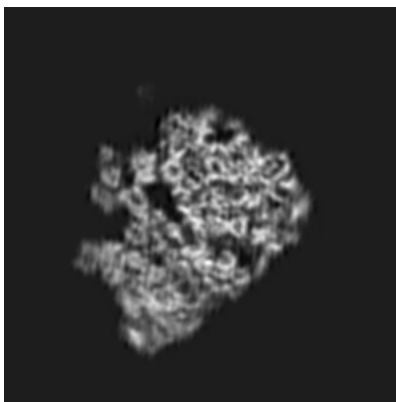
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

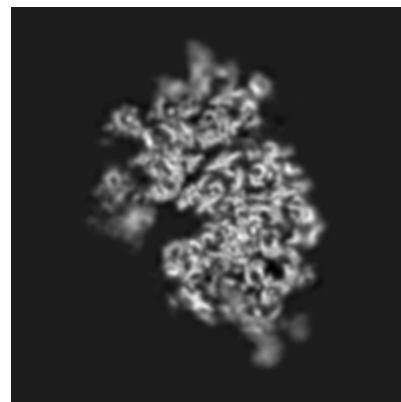
6.3.1 Primary map



X Index: 248

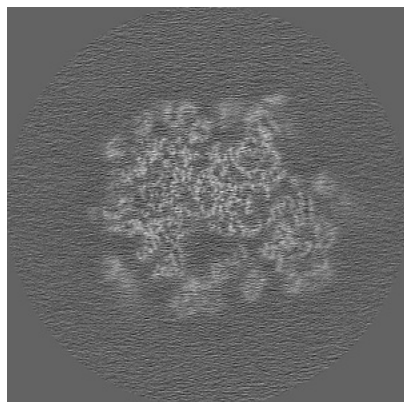


Y Index: 213

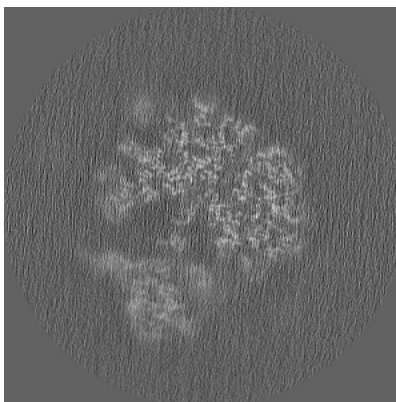


Z Index: 197

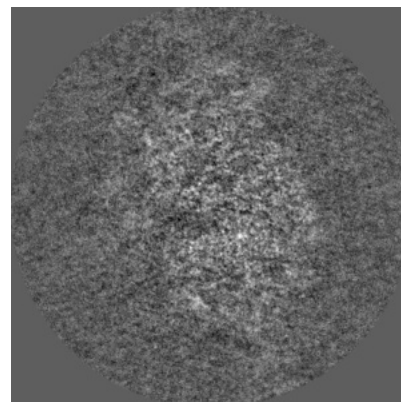
6.3.2 Raw map



X Index: 201



Y Index: 189

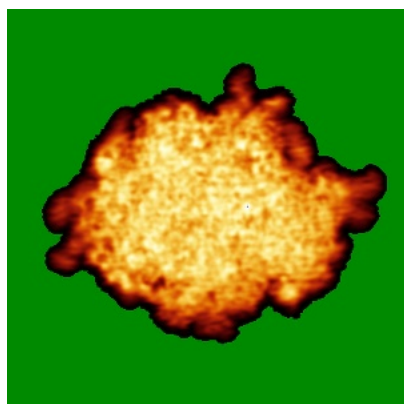


Z Index: 198

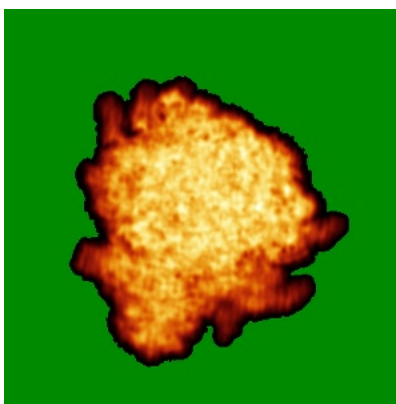
The images above show the largest variance slices of the map in three orthogonal directions.

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

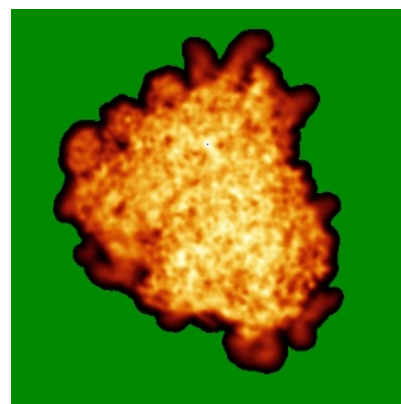
6.4.1 Primary map



X

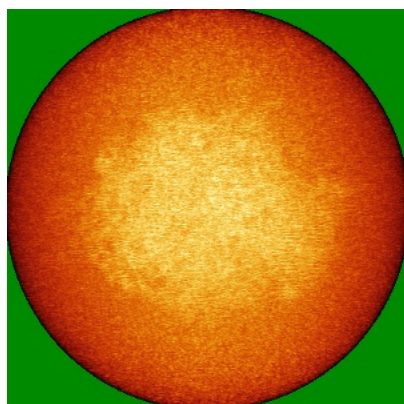


Y

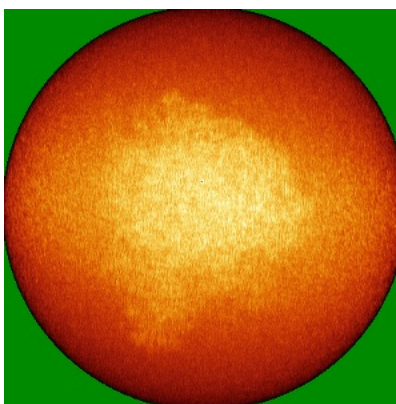


Z

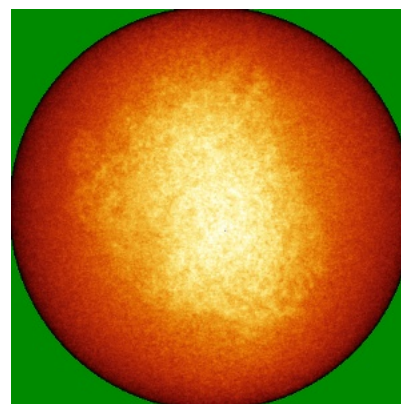
6.4.2 Raw map



X



Y

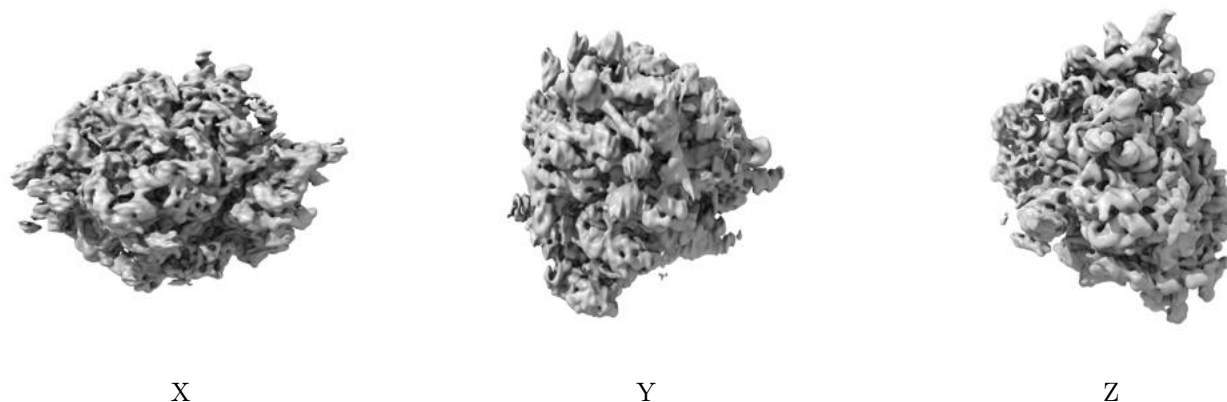


Z

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.

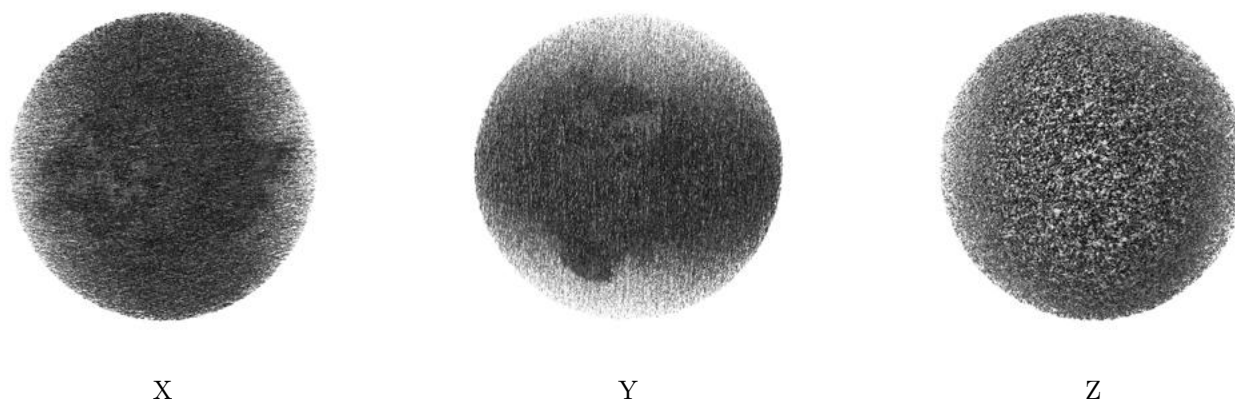
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. 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.

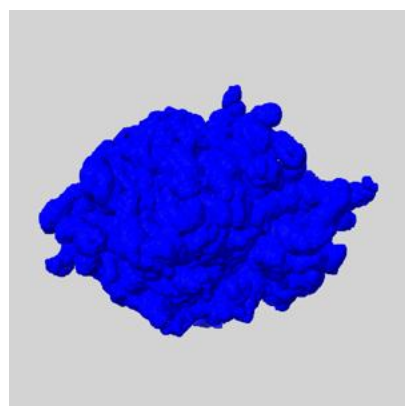
6.6 Mask visualisation [i](#)

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

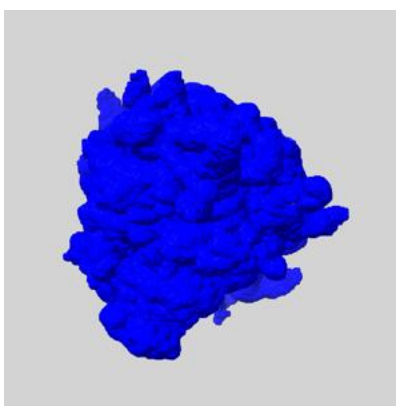
A mask typically either:

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

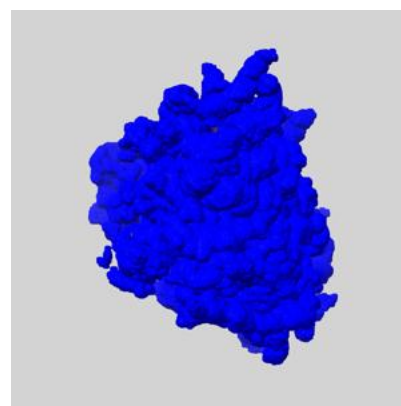
6.6.1 emd_7836_msk_1.map [i](#)



X



Y

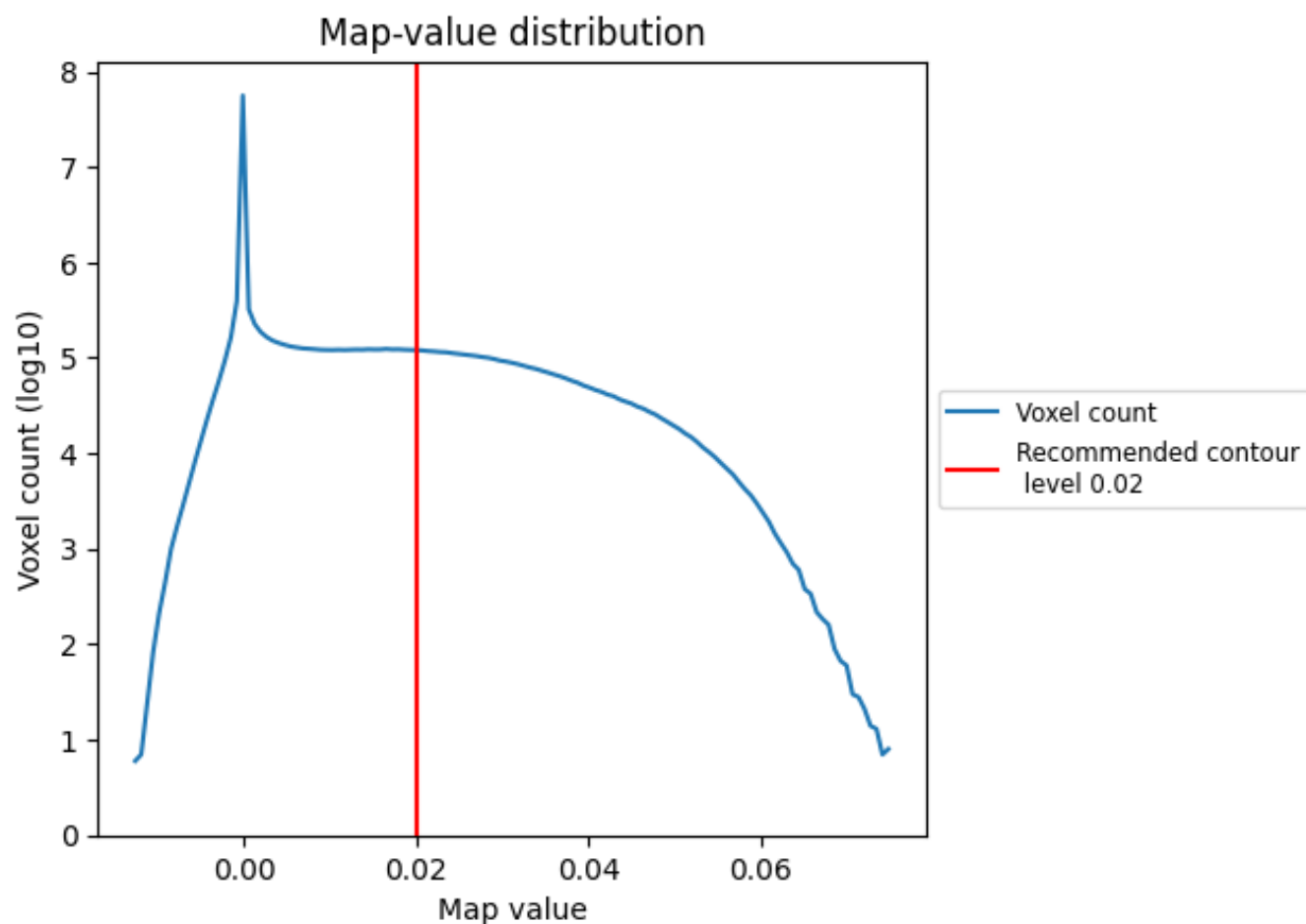


Z

7 Map analysis [i](#)

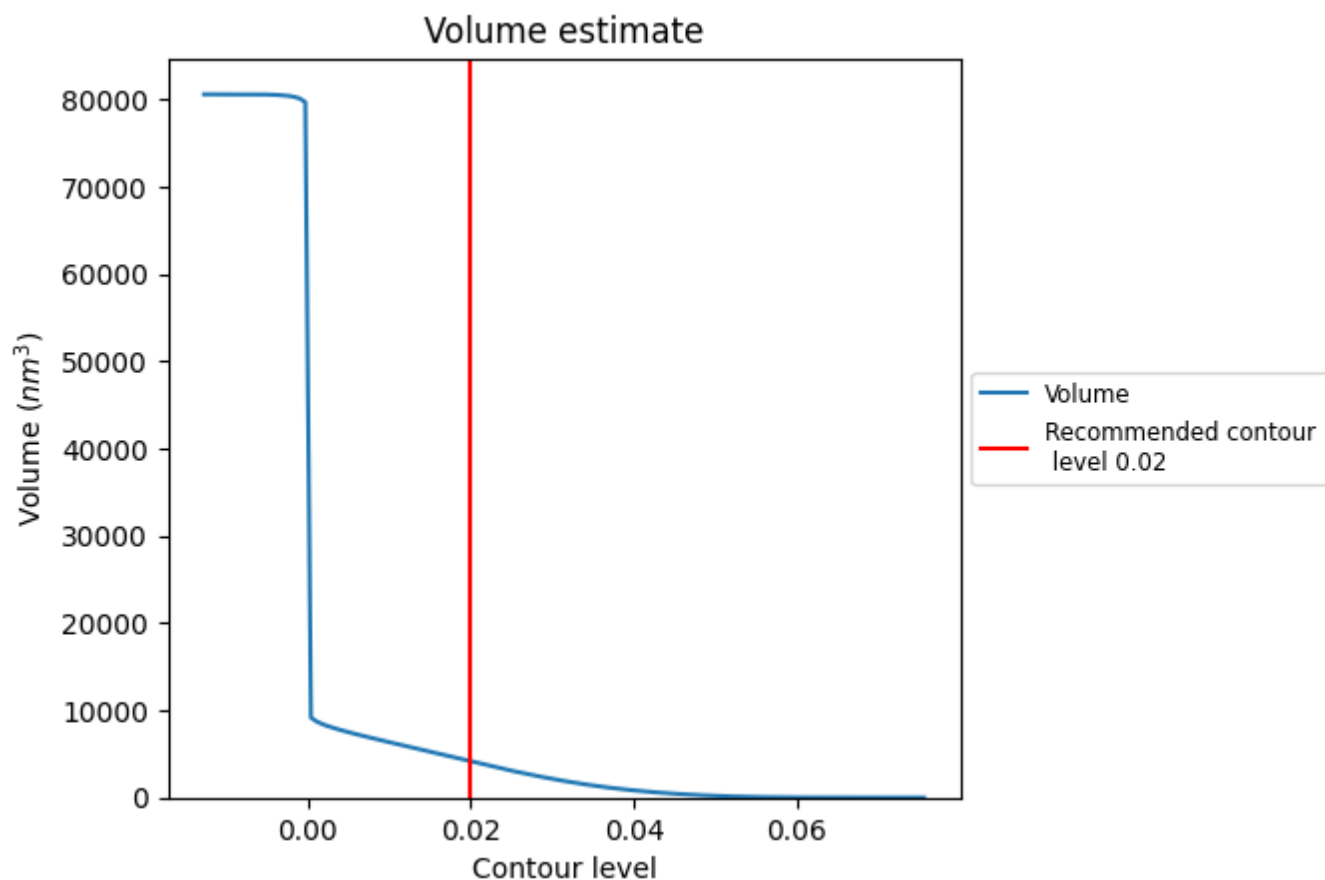
This section contains the results of statistical analysis of the map.

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.

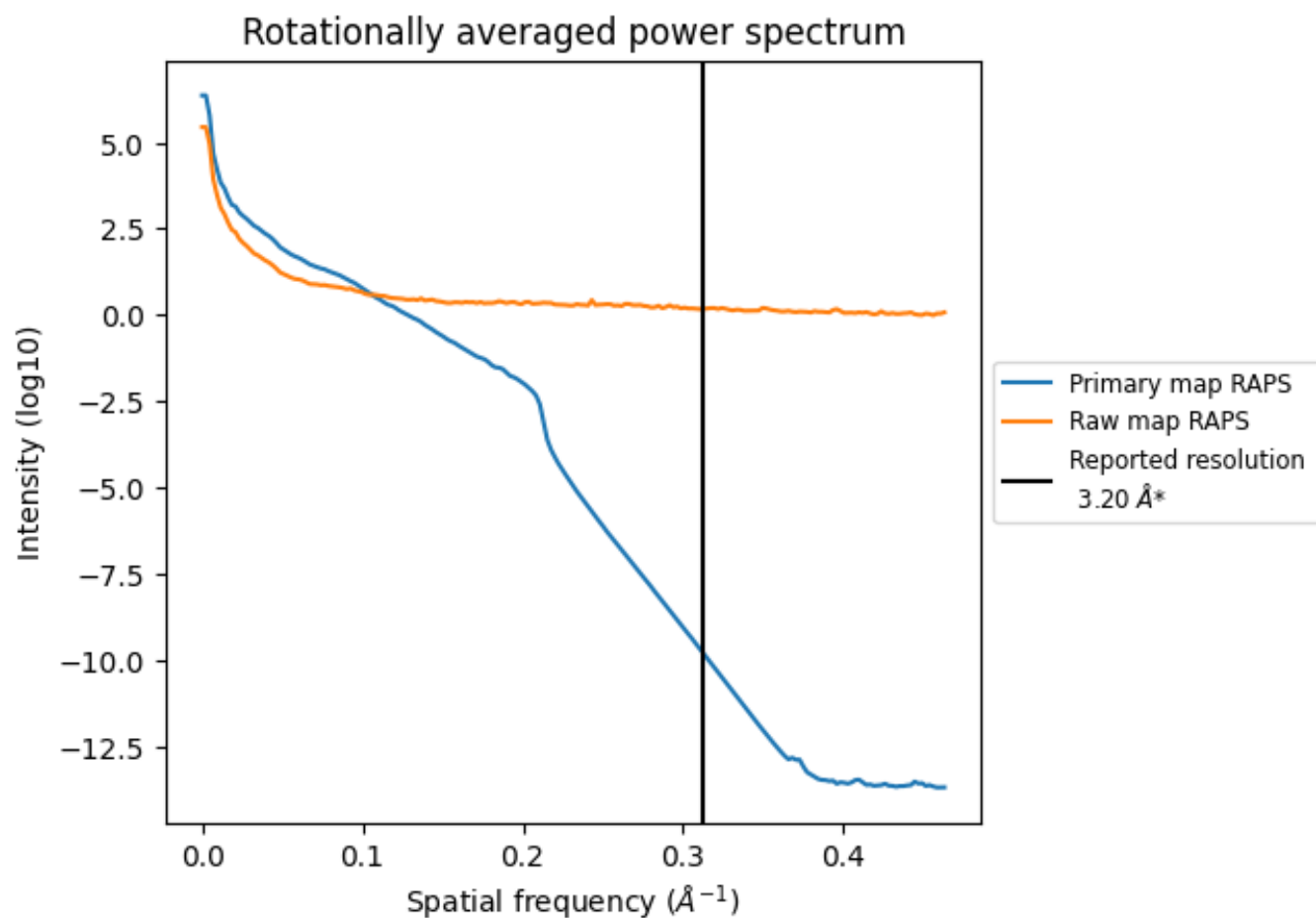
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4136 nm³; this corresponds to an approximate mass of 3736 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 ⓘ

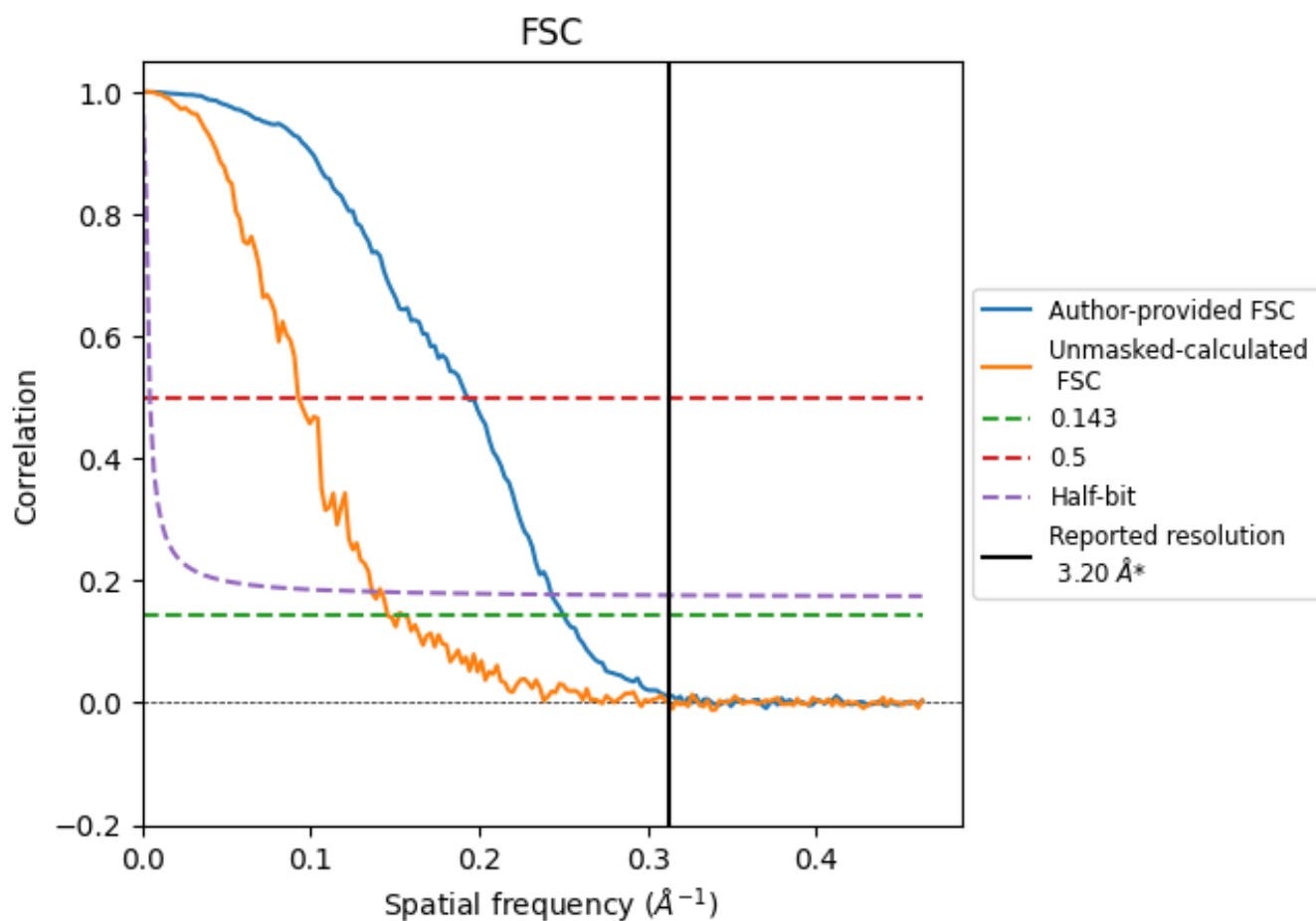


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	6.86	10.79	7.33

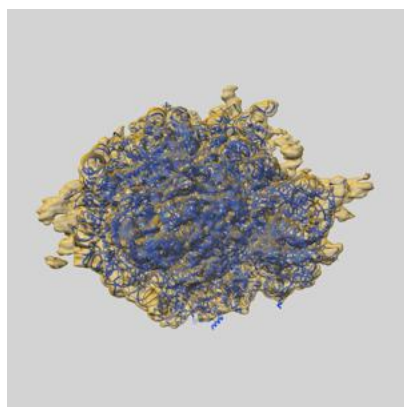
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.00 differs from the reported value 3.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.86 differs from the reported value 3.2 by more than 10 %

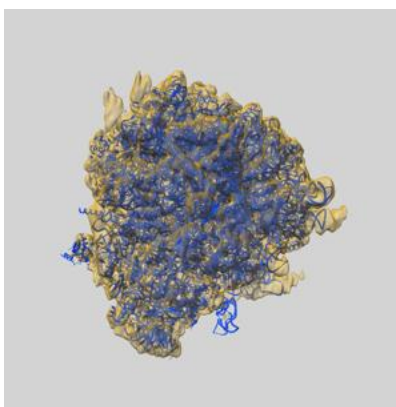
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7836 and PDB model 6D9J. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

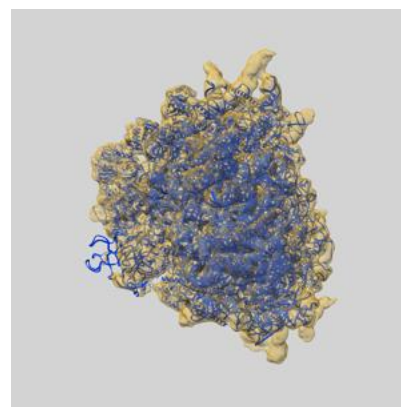
9.1 Map-model overlay [i](#)



X



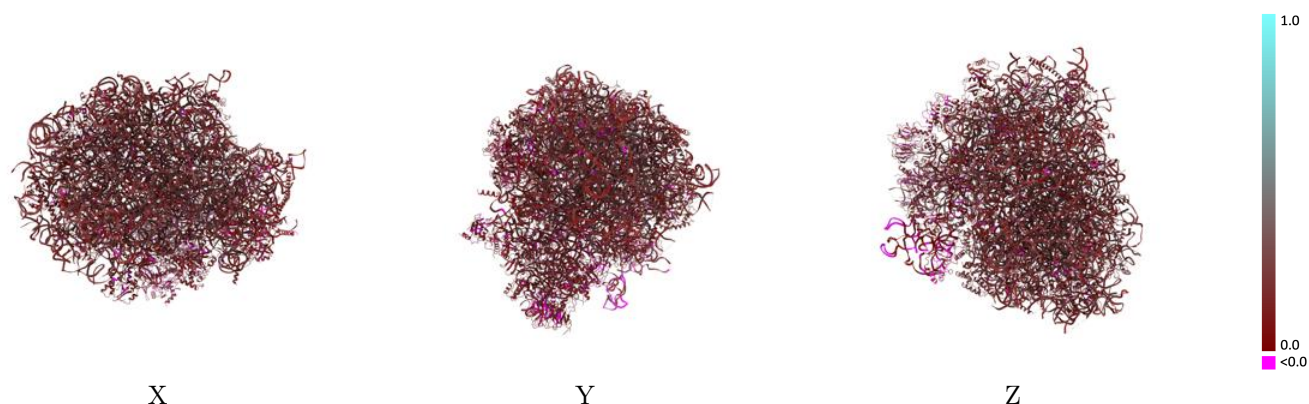
Y



Z

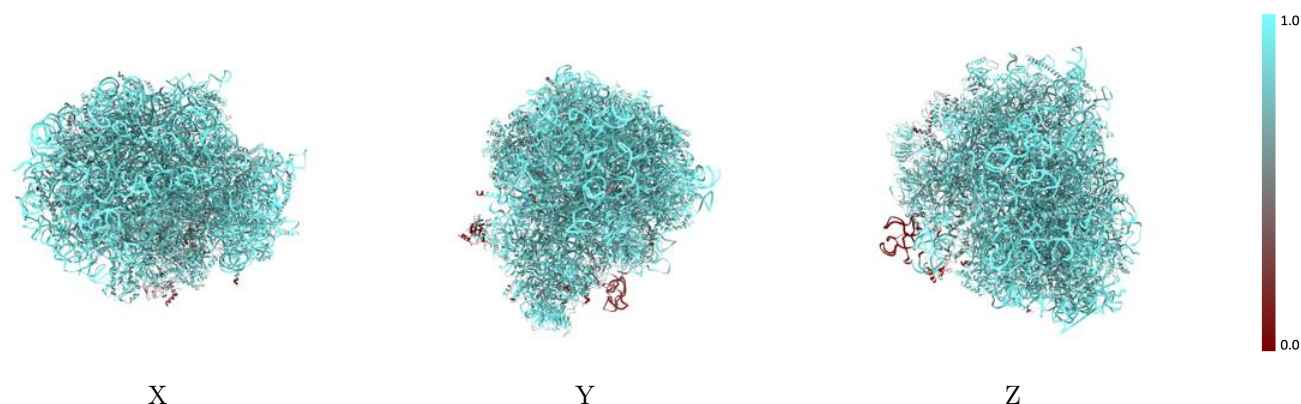
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



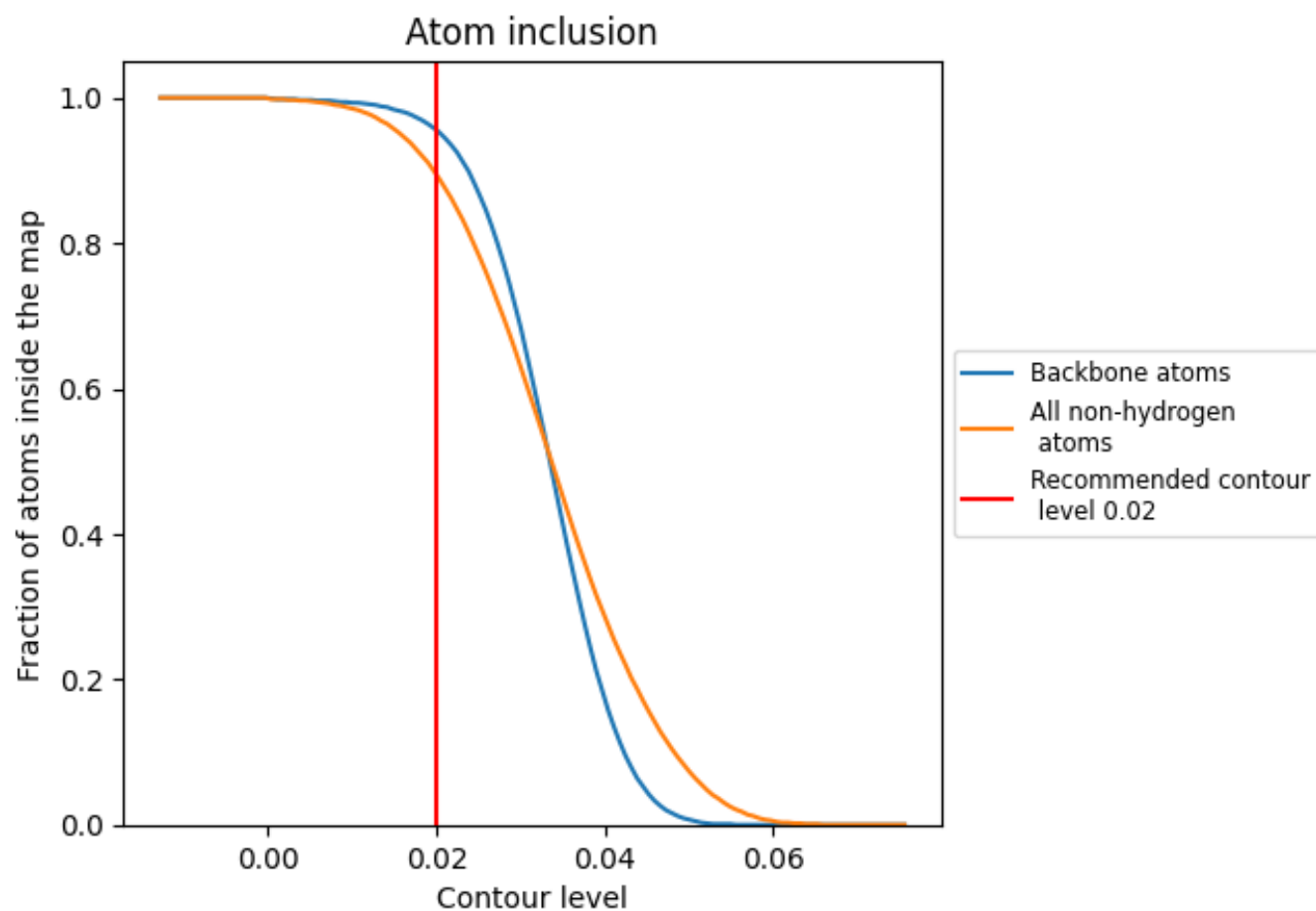
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8950	 0.1880
2	 0.9770	 0.2060
3	 0.7770	 0.1720
4	 0.5300	 0.0620
5	 0.9830	 0.2280
7	 0.9960	 0.2340
8	 0.9800	 0.2140
9	 0.7330	 0.1480
A	 0.8350	 0.1770
B	 0.8230	 0.1750
BB	 0.7880	 0.1530
C	 0.8350	 0.1610
CC	 0.8570	 0.1640
D	 0.8940	 0.1680
DD	 0.8000	 0.1630
E	 0.8520	 0.1690
EE	 0.7810	 0.1540
F	 0.7990	 0.1610
FF	 0.8580	 0.1500
G	 0.8270	 0.1690
GG	 0.8030	 0.1470
H	 0.8070	 0.1740
HH	 0.8570	 0.1460
I	 0.8200	 0.1700
II	 0.7960	 0.1670
J	 0.8450	 0.1570
JJ	 0.8490	 0.1540
K	 0.5690	 0.0670
KK	 0.8150	 0.1510
L	 0.8350	 0.1780
LL	 0.8610	 0.1400
M	 0.9020	 0.1660
MM	 0.8120	 0.1870
N	 0.8410	 0.1420
NN	 0.3300	 0.0790



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
O	 0.8030	 0.1710
OO	 0.8120	 0.1750
P	 0.8720	 0.1570
PP	 0.8460	 0.1530
Q	 0.8000	 0.1630
QQ	 0.8200	 0.1090
R	 0.8240	 0.1720
RR	 0.8210	 0.1110
S	 0.8490	 0.1750
SS	 0.5970	 0.0840
T	 0.8040	 0.1790
TT	 0.7460	 0.1390
U	 0.8410	 0.1780
UU	 0.8590	 0.1220
V	 0.7690	 0.1790
VV	 0.7840	 0.1220
W	 0.8390	 0.1680
WW	 0.7910	 0.1510
X	 0.8170	 0.1620
XX	 0.8150	 0.1770
Y	 0.8820	 0.1560
YY	 0.7550	 0.1600
Z	 0.8910	 0.1650
ZZ	 0.8790	 0.1410
a	 0.8810	 0.1550
aa	 0.7500	 0.1480
b	 0.8070	 0.1590
bb	 0.8250	 0.1560
c	 0.8670	 0.1750
cc	 0.8140	 0.1780
d	 0.8480	 0.1750
dd	 0.7400	 0.1430
e	 0.8280	 0.1830
ee	 0.9050	 0.1340
f	 0.8300	 0.1700
ff	 0.7840	 0.1470
g	 0.8480	 0.1460
gg	 0.5010	 0.0810
h	 0.8320	 0.1750
hh	 0.8710	 0.1260
i	 0.8130	 0.1780
j	 0.8720	 0.1320

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
k	 0.8260	 0.1720
l	 0.8340	 0.1610
m	 0.8070	 0.1570
n	 0.7660	 0.1230
o	 0.8750	 0.1730
p	 0.8200	 0.1710
r	 0.8450	 0.1740
s	 0.7700	 0.1380
t	 0.6520	 0.0890