



## wwPDB EM Validation Summary Report ⓘ

Jun 9, 2026 – 03:32 PM EDT

PDB ID : 9Q1S / pdb\_00009q1s  
EMDB ID : EMD-72137  
Title : NediV IRES (P site) in complex with Rabbit 80S ribosome  
Authors : De, S.; Altomare, C.G.; Abaeva, I.S.; Dadhwal, P.; Garg, P.; Acosta-Reyes, F.; Brown, Z.P.; Pestova, T.V.; Hellen, C.U.T.; Frank, J.  
Deposited on : 2025-08-14  
Resolution : 3.00 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](mailto: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>.

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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

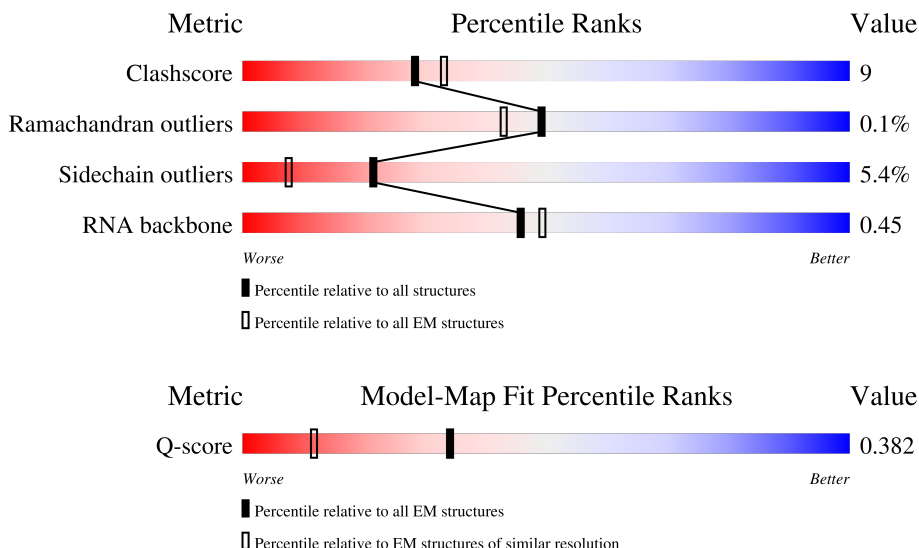
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




The reported resolution of this entry is 3.00 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.















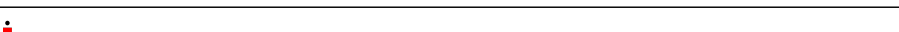

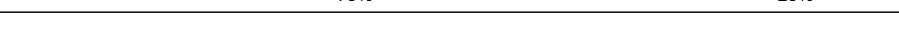

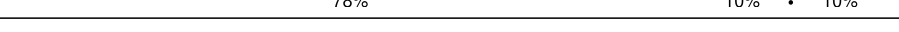








Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 ( 2.50 - 3.50 )

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  $\geq 3$ , 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	9	1670	
2	A	248	
3	B	394	







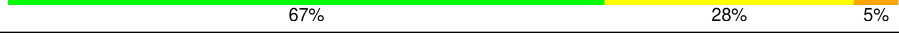
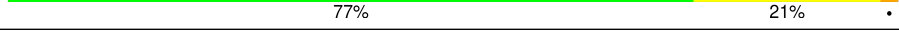
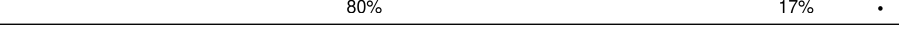
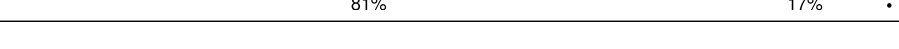
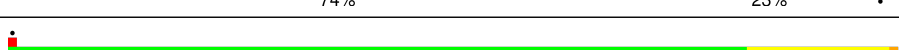

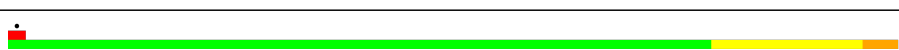

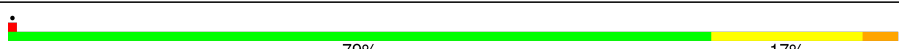





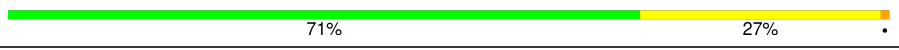
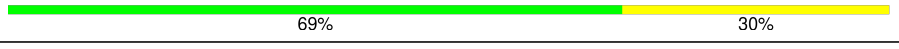



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Mol	Chain	Length	Quality of chain
4	C	362	
5	E	251	
6	G	240	
7	H	190	
8	I	213	
9	J	170	
10	L	210	
11	N	203	
12	O	199	
13	R	180	
14	V	139	
15	W	94	
16	X	118	
17	Y	134	
18	a	147	
19	b	116	
20	e	128	
21	5	3543	
22	7	119	
23	8	156	
24	D	293	
25	F	225	
26	M	138	
27	P	153	
28	Q	187	

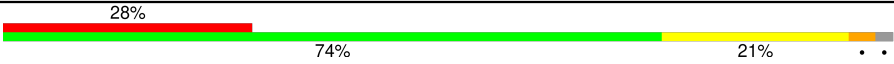







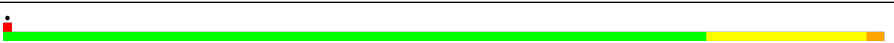

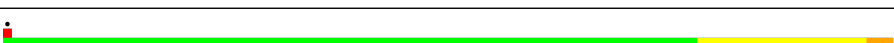


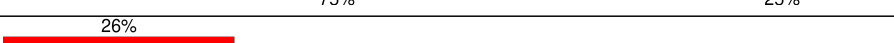
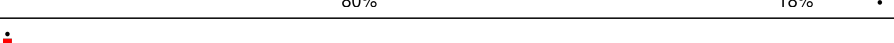
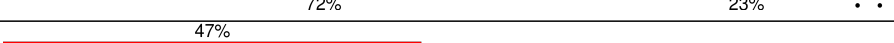
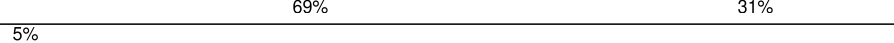
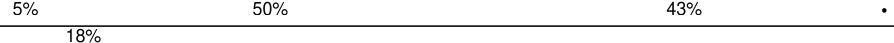
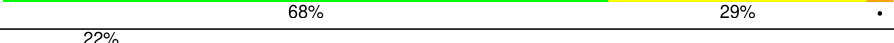






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Mol	Chain	Length	Quality of chain
29	S	176	
30	T	159	
31	U	99	
32	Z	135	
33	c	98	
34	d	107	
35	f	109	
36	g	114	
37	h	122	
38	i	102	
39	j	86	
40	k	69	
41	l	50	
42	m	52	
43	n	25	
44	o	104	
45	p	91	
46	r	124	
47	l	167	
48	K	130	
49	AA	217	
50	BB	213	
51	CC	221	
52	EE	262	
53	GG	224	

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Mol	Chain	Length	Quality of chain
54	HH	189	
55	II	206	
56	JJ	176	
57	LL	151	
58	NN	149	
59	OO	136	
60	VV	83	
61	WW	129	
62	XX	141	
63	YY	124	
64	aa	101	
65	bb	83	
66	ee	57	
67	DD	211	
68	FF	191	
69	KK	78	
70	PP	129	
71	QQ	136	
72	RR	132	
73	SS	144	
74	TT	141	
75	UU	48	
76	ZZ	75	
77	cc	62	
78	dd	55	

## 2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 208701 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	9	1670	Total	C	N	O	P	0	0
			35659	15917	6408	11665	1669		

- Molecule 2 is a protein called 60S ribosomal protein L8.

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

- Molecule 3 is a protein called 60S ribosomal protein L3.

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

- Molecule 4 is a protein called 60S ribosomal protein L4.

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

- Molecule 5 is a protein called Large ribosomal subunit protein eL6.

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 Large ribosomal subunit protein eL8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 7 is a protein called 60S ribosomal protein L9.

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

- Molecule 8 is a protein called Ribosomal protein L10.

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

- Molecule 9 is a protein called 60S ribosomal protein L11.

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

- Molecule 10 is a protein called Large ribosomal subunit protein eL13.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 11 is a protein called 60S ribosomal protein L15.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 13 is a protein called 60S ribosomal protein L19.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	HIS	conflict	UNP G1TYL6
R	151	ARG	HIS	conflict	UNP G1TYL6

- Molecule 14 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	139	Total	C	N	O	S	0	0
			1034	648	199	182	5		

- Molecule 15 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	79	Total	C	N	O	S	0	0
			645	408	127	106	4		

- Molecule 16 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 17 is a protein called 60S ribosomal protein L26.

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

- Molecule 18 is a protein called 60S ribosomal protein L27a.



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

- Molecule 19 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 20 is a protein called Large ribosomal subunit protein eL32.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	3	ALA	SER	conflict	UNP G1TUN8
e	13	VAL	ILE	conflict	UNP G1TUN8
e	16	ARG	TRP	conflict	UNP G1TUN8
e	81	ASN	SER	conflict	UNP G1TUN8
e	98	GLU	LYS	conflict	UNP G1TUN8
e	108	ARG	CYS	conflict	UNP G1TUN8
e	115	ALA	VAL	conflict	UNP G1TUN8

- Molecule 21 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	5	3543	Total	C	N	O	P	0	0
			75972	33833	13910	24686	3543		

- Molecule 22 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 23 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 24 is a protein called 60S ribosomal protein L5.

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

- Molecule 25 is a protein called 60S ribosomal protein L7.

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

- Molecule 26 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 27 is a protein called 60S ribosomal protein L17.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL18.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	4	ASP	ASN	conflict	UNP G1TFE0
Q	14	ARG	TRP	conflict	UNP G1TFE0
Q	53	MET	LEU	conflict	UNP G1TFE0
Q	58	ARG	TRP	conflict	UNP G1TFE0
Q	75	ARG	GLN	conflict	UNP G1TFE0
Q	80	ALA	PRO	conflict	UNP G1TFE0
Q	86	VAL	ILE	conflict	UNP G1TFE0
Q	104	ARG	HIS	conflict	UNP G1TFE0
Q	110	ARG	CYS	conflict	UNP G1TFE0
Q	137	VAL	GLY	conflict	UNP G1TFE0
Q	157	GLY	ARG	conflict	UNP G1TFE0

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 29 is a protein called eL20.

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

- Molecule 30 is a protein called 60S ribosomal protein L21.

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

- Molecule 31 is a protein called eL22.

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

- Molecule 32 is a protein called 60S ribosomal protein L27.

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

- Molecule 33 is a protein called 60S ribosomal protein L30.

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

- Molecule 34 is a protein called 60S ribosomal protein L31.

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

- Molecule 35 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 36 is a protein called 60S ribosomal protein L34.

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

- Molecule 37 is a protein called 60S ribosomal protein L35.

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

- Molecule 38 is a protein called 60S ribosomal protein L36.

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

- Molecule 39 is a protein called 60S ribosomal protein L37.

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

- Molecule 40 is a protein called Large ribosomal subunit protein eL38.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 41 is a protein called 60S ribosomal protein L39.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 43 is a protein called eL41.

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

- Molecule 44 is a protein called eL42.

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

- Molecule 45 is a protein called 60S ribosomal protein L37a.

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

- Molecule 46 is a protein called 60S ribosomal protein L28.

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

- Molecule 47 is a RNA chain called NediV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	167	Total	C	N	O	P	0	0
			3538	1583	612	1176	167		

- Molecule 48 is a protein called eL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	K	130	Total	C	N	O	S	0	0
			1064	680	193	186	5		

- Molecule 49 is a protein called 40S\_SA\_C domain-containing protein.

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

- Molecule 50 is a protein called 40S ribosomal protein S3a.

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

- Molecule 51 is a protein called 40S ribosomal protein S2.

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

- Molecule 52 is a protein called 40S ribosomal protein S4.

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

- Molecule 53 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	GG	224	Total	C	N	O	S	0	0
			1813	1134	362	310	7		

- Molecule 54 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	II	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
II	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 56 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	JJ	176	Total	C	N	O	S	0	0
			1472	938	294	238	2		

- Molecule 57 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 58 is a protein called 40S ribosomal protein S13.

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

- Molecule 59 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 60 is a protein called eS21.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VV	3	ASN	SER	conflict	UNP G1TM82

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
VV	4	ASP	ASN	conflict	UNP G1TM82
VV	33	GLN	PRO	conflict	UNP G1TM82
VV	50	PHE	SER	conflict	UNP G1TM82
VV	75	ALA	SER	conflict	UNP G1TM82
VV	76	ASP	HIS	conflict	UNP G1TM82
VV	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 61 is a protein called 40S ribosomal protein S15a.

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

- Molecule 62 is a protein called 40S ribosomal protein S23.

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

- Molecule 63 is a protein called 40S ribosomal protein S24.

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

- Molecule 64 is a protein called eS26.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	28	ARG	CYS	conflict	UNP G1TFE8
aa	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 65 is a protein called 40S ribosomal protein S27.



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

- Molecule 66 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	DD	211	Total	C	N	O	S	0	0
			1637	1044	298	287	8		

- Molecule 68 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 69 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	KK	78	Total	C	N	O	S	0	0
			658	431	114	107	6		

- Molecule 70 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	PP	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 71 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	QQ	136	Total	C	N	O	S	0	0
			1087	691	206	187	3		

- Molecule 72 is a protein called 40S ribosomal protein S17.

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

- Molecule 73 is a protein called 40S ribosomal protein S18.

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

- Molecule 74 is a protein called Small ribosomal subunit protein eS19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TT	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 75 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	UU	48	Total	C	N	O	S	0	0
			394	244	80	66	4		

- Molecule 76 is a protein called 40S ribosomal protein S25.

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

- Molecule 77 is a protein called 40S ribosomal protein S28.

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

- Molecule 78 is a protein called 40S ribosomal protein S29.

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

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

Mol	Chain	Residues	Atoms		AltConf
79	A	1	Total	Mg	0
			1	1	
79	V	1	Total	Mg	0
			1	1	
79	a	1	Total	Mg	0
			1	1	
79	5	192	Total	Mg	0
			192	192	
79	7	6	Total	Mg	0
			6	6	
79	8	3	Total	Mg	0
			3	3	
79	l	1	Total	Mg	0
			1	1	
79	aa	1	Total	Mg	0
			1	1	

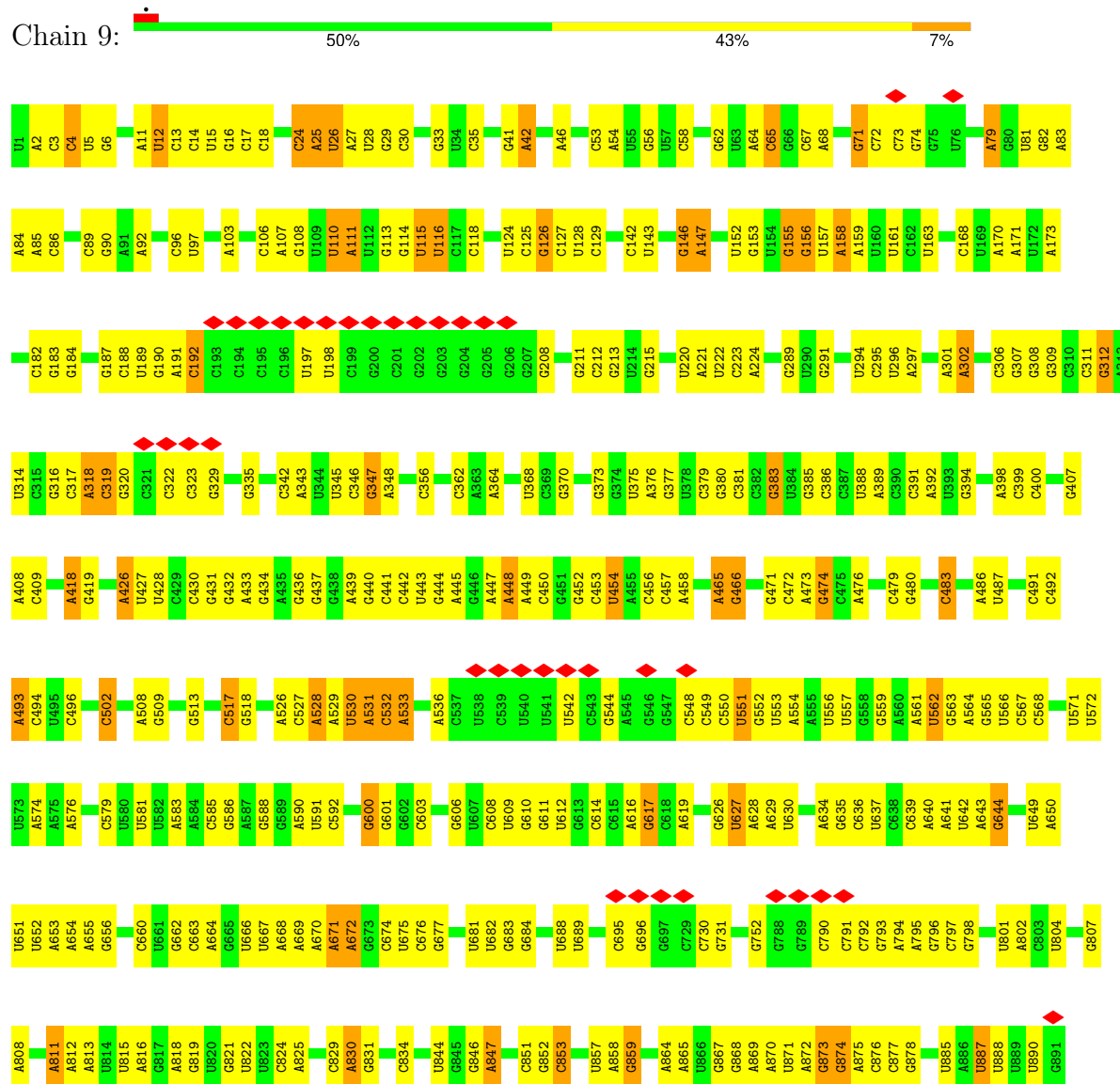
- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

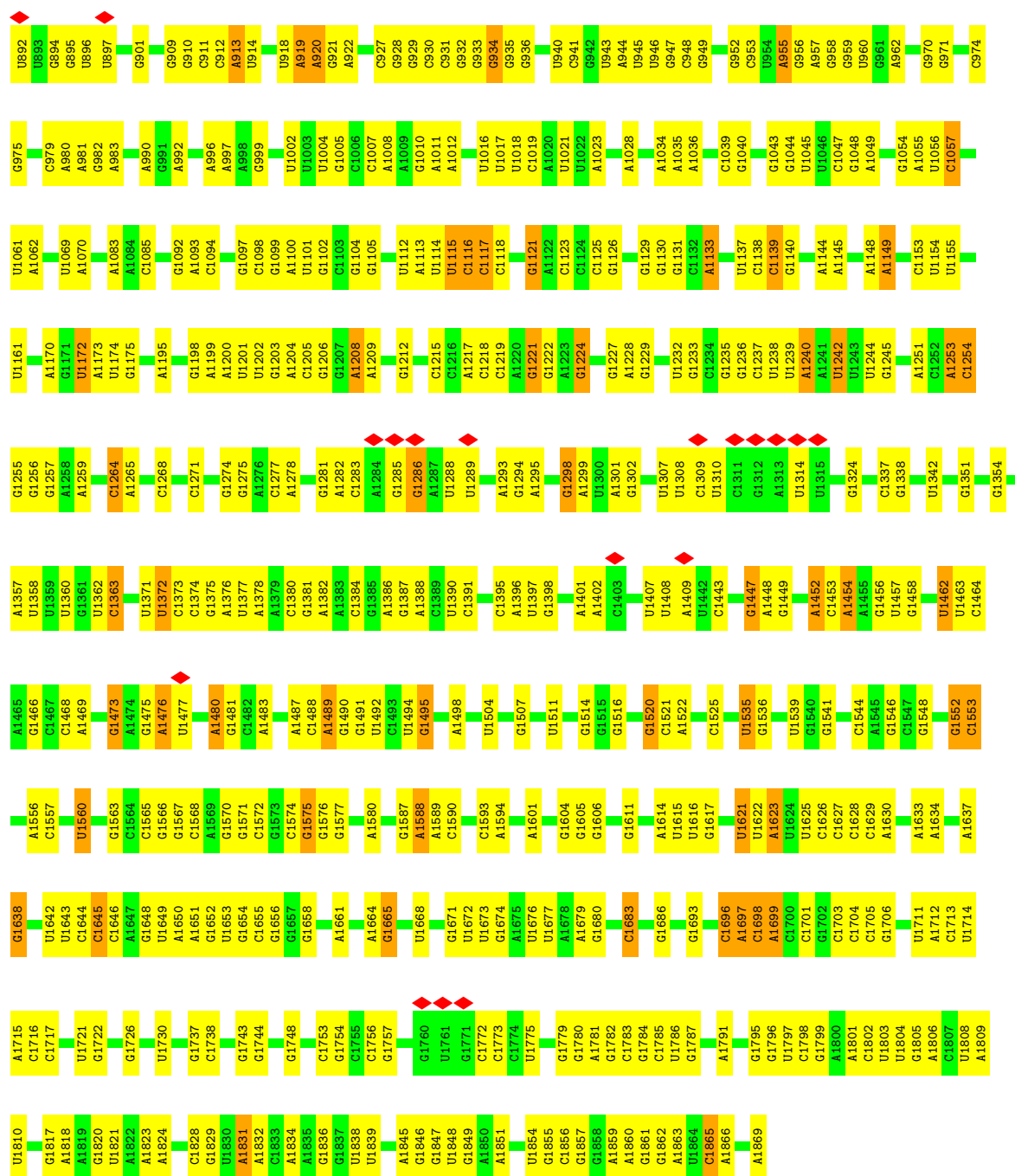
Mol	Chain	Residues	Atoms		AltConf
80	g	1	Total	Zn	0
			1	1	
80	j	1	Total	Zn	0
			1	1	
80	m	1	Total	Zn	0
			1	1	
80	o	1	Total	Zn	0
			1	1	
80	p	1	Total	Zn	0
			1	1	
80	aa	1	Total	Zn	0
			1	1	
80	dd	1	Total	Zn	0
			1	1	

### 3 Residue-property plots

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

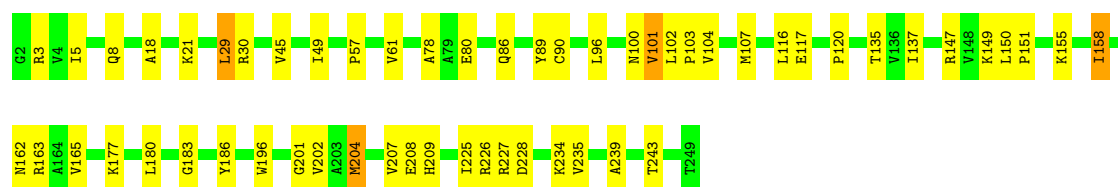
#### • Molecule 1: 18S rRNA






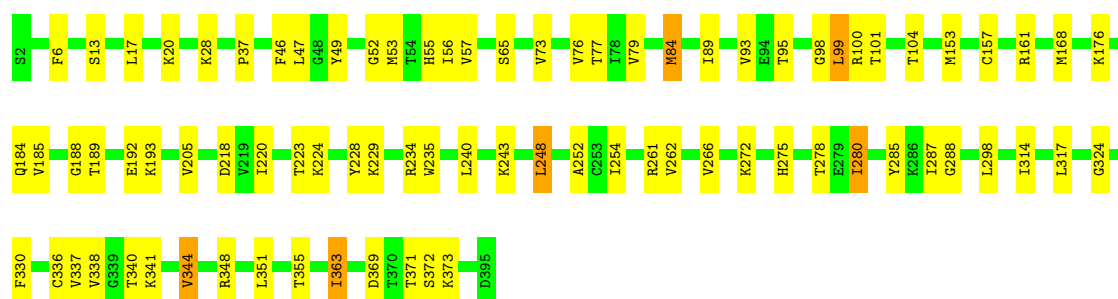
• Molecule 2: 60S ribosomal protein L8

Chain A: 77% 21%




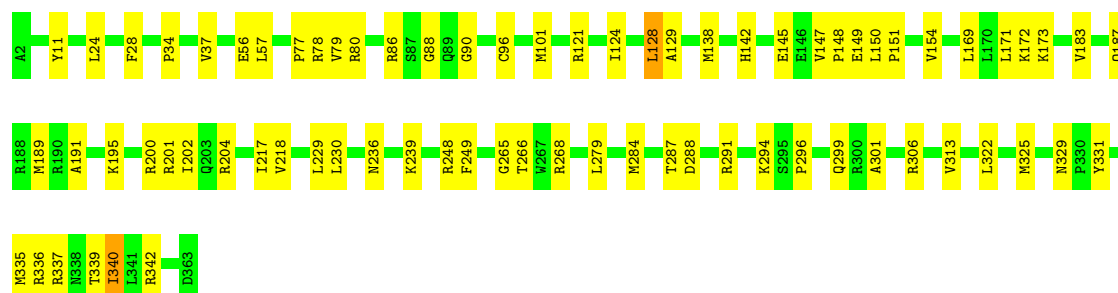
• Molecule 3: 60S ribosomal protein L3

Chain B:  79% 19%



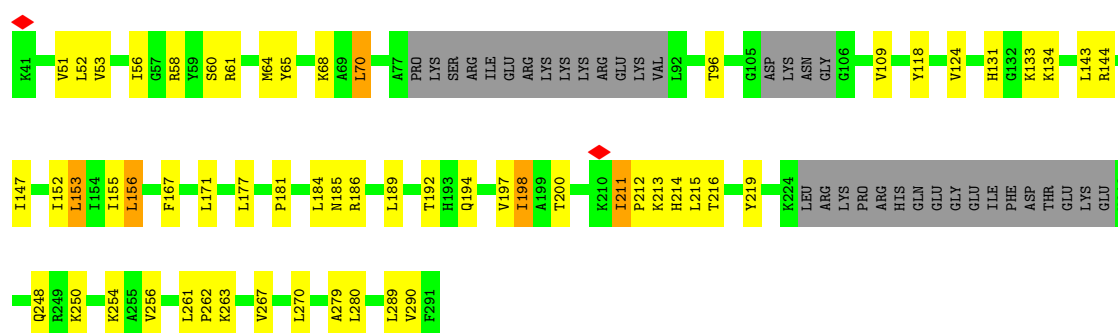
• Molecule 4: 60S ribosomal protein L4

Chain C:  80% 20%



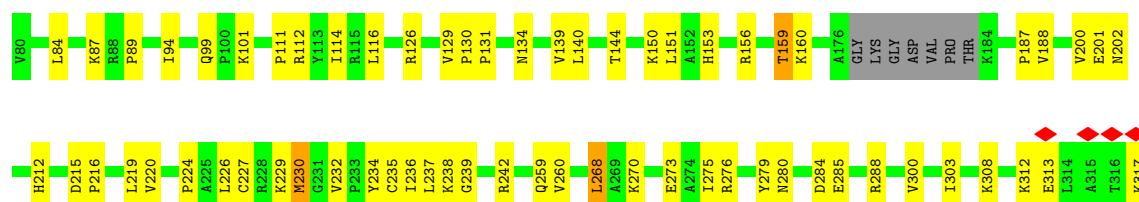
• Molecule 5: Large ribosomal subunit protein eL6

Chain E:  63% 21% 14%



• Molecule 6: Large ribosomal subunit protein eL8

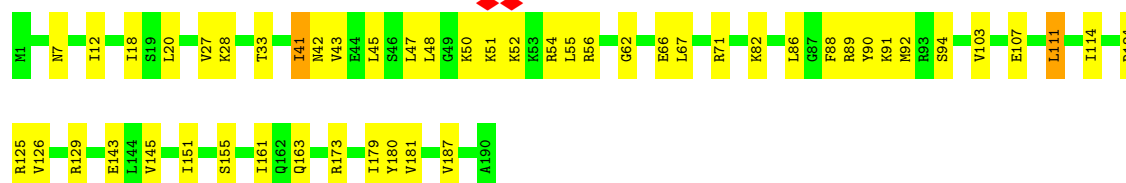
Chain G:  70% 26%





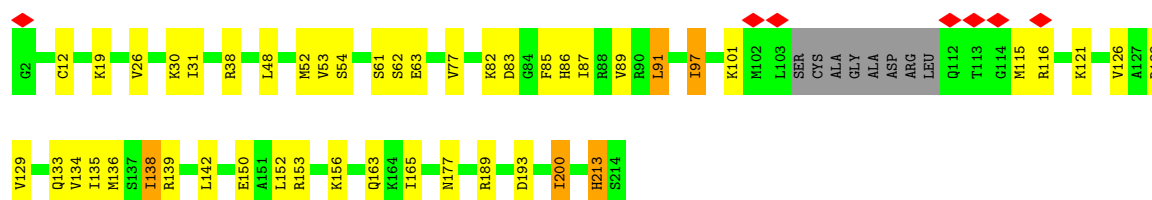
- Molecule 7: 60S ribosomal protein L9

Chain H: 74% 25%



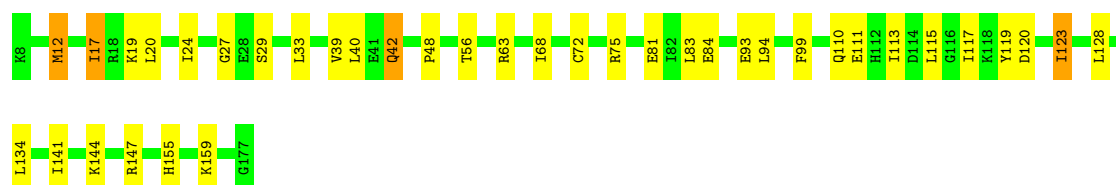
- Molecule 8: Ribosomal protein L10

Chain I: 74% 20%



- Molecule 9: 60S ribosomal protein L11

Chain J: 78% 20%



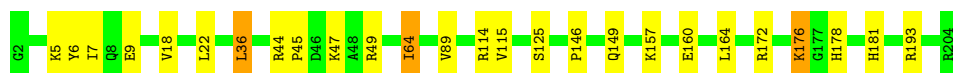
- Molecule 10: Large ribosomal subunit protein eL13

Chain L: 83% 16%

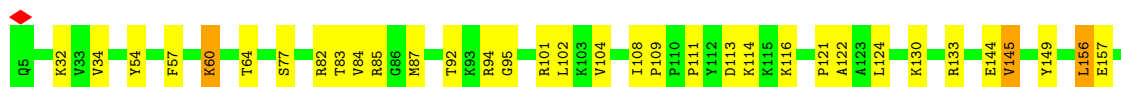
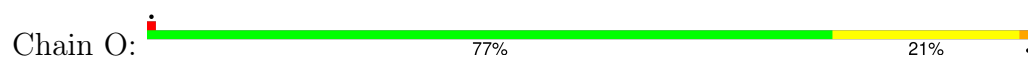


- Molecule 11: 60S ribosomal protein L15

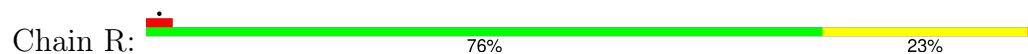
Chain N: 87% 11%



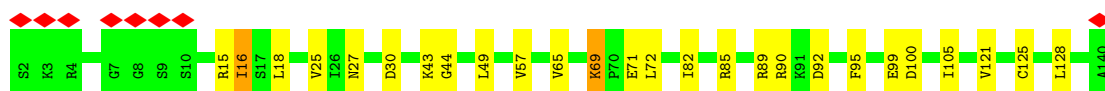
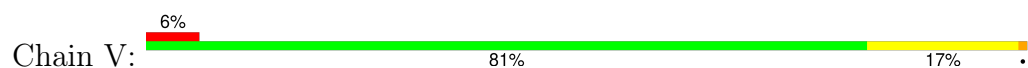
- Molecule 12: Large ribosomal subunit protein uL13



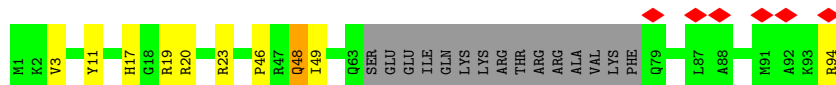
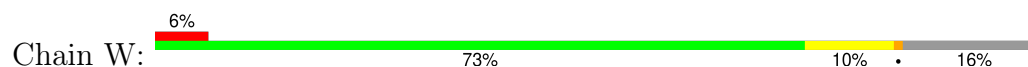
- Molecule 13: 60S ribosomal protein L19



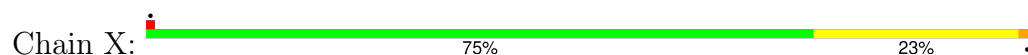
- Molecule 14: Large ribosomal subunit protein uL14



- Molecule 15: Large ribosomal subunit protein eL24

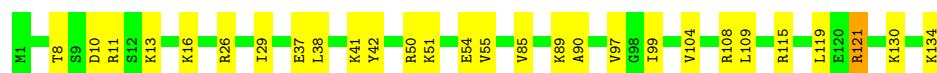


- Molecule 16: Large ribosomal subunit protein uL23



- Molecule 17: 60S ribosomal protein L26





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|----|----|----|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|
| P2 | S3 | R4 | L5 |  | R12 | T22 | G23 | K24 | H25 | R26 | R32 | G36 | H40 | I43 | H49 | P50 | G51 | K55 | V56 | G57 | M58 | R59 | H60 | K64 | P71 | L75 | K94 | A98 | D102 | R105 | Y108 | G113 | L117 | V122 | E134 | I137 | V140 | G143 |
|----|----|----|----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|

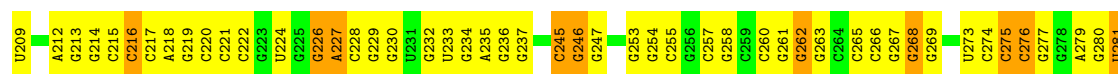
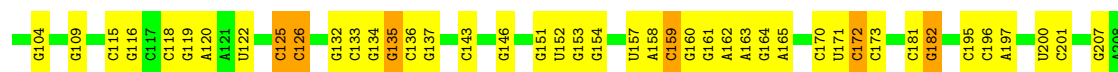


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|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|
| A2 | V8 | K9 | P10 | K11 | I12 | I21 | Q24 | K30 | I31 | I42 | D43 | K43 | R44 | V45 | R46 | Q52 | I58 | T66 | K67 | H68 | M69 | L70 | R75 | K76 | F77 | L78 | V79 | H80 | N81 | L85 | L89 | M90 | C91 | Y95 | I99 | S104 | R108 | I111 | L118 | A119 | I120 |
|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|

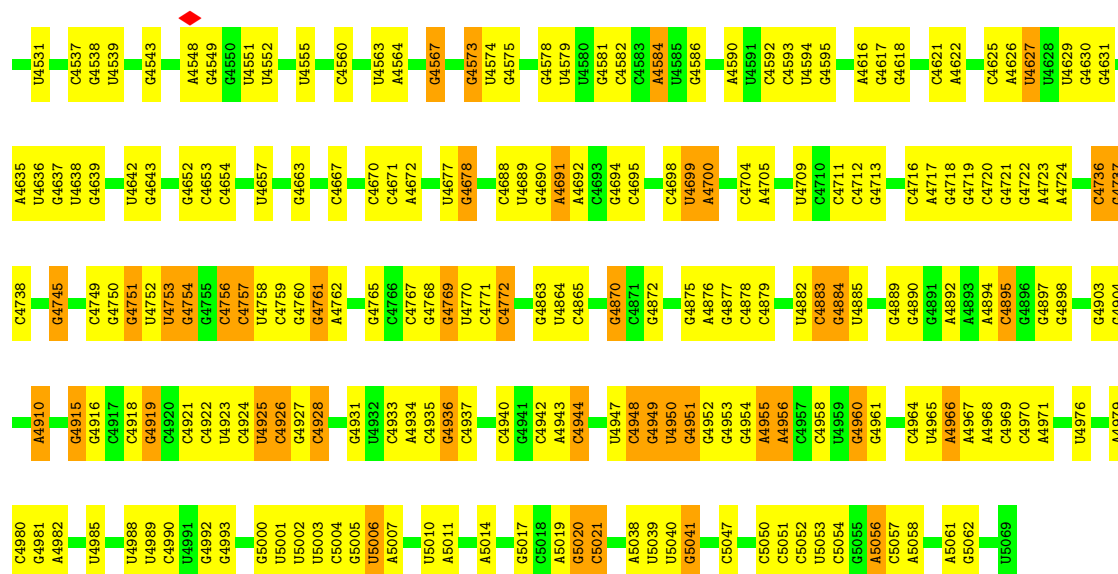


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|----|--|----|----|----|----|----|--|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|-----|--|-----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|-----|-----|--|-----|-----|-----|-----|--|-----|------|
| C1 |  | G4 | A5 | C6 | C7 | U8 |  | A12 | U13 |  | C18 | G19 |  | A26 |  | G29 |  | G32 | A33 |  | U37 |  | A38 | G39 | G40 | C41 | A42 | U43 | A44 | U45 | U46 | A47 | G48 | U49 | C50 |  | G55 | A56 | G57 | G58 | A59 | A60 | A61 | A62 | G63 | A64 | A65 |  | A69 |  | A73 | G74 |  | G91 | C92 | G93 | A94 |  | A99 | G100 |
|----|--|----|----|----|----|----|--|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|-----|--|-----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|-----|-----|--|-----|-----|-----|-----|--|-----|------|



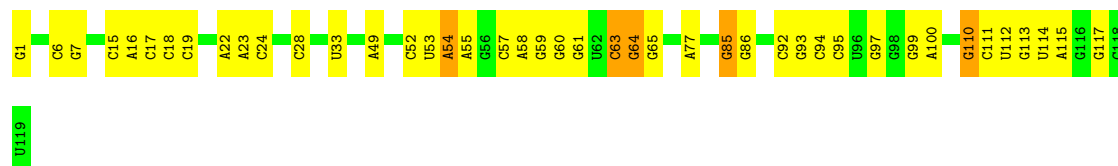
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A2029	G1969	U1882		G1686	G1581	C1485	A1398	C1314	G1189	A966	G670	A747	A408
G2034	C1884	C1883	A1786	U1687	G1586	G1486	G1399	G1314		C967	G671	G749	A409
A2046	G1885	C1884	A1788	G1688	G1587	G1487	G1400	U1317	G1193	C968	C672	U750	A410
U2047	A1886	A1887	C1789	G1689	G1588	G1488	C1401	C1318	G1194	G673	G674	G751	G411
A2048	U1889	U1890	A1794	C1690	U1591	A1491	C1402	C1325	G1195	C972	C675	G752	G412
G2049	G1890	G1891		G1691	G1592	A1492	G1403	C1326	G1196		C676		G413
G2050	C1892	G1893	G1799	G1694	A1593	A1497	G1404	A1326		C975	C677	G758	C414
G2055	A1897	A1898			C1594	C1498	G1405		G1199	G976	C678	G759	C415
G2056	G1899	G1899	A1802	G1724	U1596	C1499	G1406	A1330	U1201	G977	C679	U760	U416
	G1900	G1900	G1803		C1597	C1501	G1406C	C1332	U1202	G978	G680	U761	C491
C2062	G1901	C1731	A1804	U1730	C1598	G1502	C1411	A1333	C1202	U913	G681	U762	A418
G2063	G1902	C1731	A1805	U1731	C1599	G1503	G1411A	A1334	C1202	U914	G682		A419
G2064	G1903	C1732	G1806	G1733	A1600	A1504	C1411B	G1335	C1210	A917	C683	C494	C422
	A1904	C1733	C1807	G1733	A1601	C1505	C1411C	G1336	C1211	G918	C684	C495	C423
G2068	G1905	G1905			U1506	G1506	G1412	A1337	C1212	G919	C685	C496	G424
	U1906	G1906	G1811	A1738	C1507	C1507	G1412	U1338	C1215	G920	A686	C497	U425
A2069	C1907	G1912	C1812	G1739	A1508	A1508	A1420	U1339	C1216	C922		C498	U426
	G1908	C1913		C1740	C1509	C1509	G1421	C1340	C1216	A692	A692	C499	A427
C2073	G1909	C1914	U1817	G1741	G1612	C1510	U1341	U1341	G1234	C922A	C922A	G500	G428
C2074	A1910	C1915	G1818	A1742	A1613	U1511	A1427	A1342	G1235	C923	C923	G504	A429
G2075	A1911	C1916	G1819	A1743	G1617	G1512	U1428	A1343	G1236	C924	C924	G505	G430
G2076	U1912	A1917	U1820	U1744		U1513	C1429	C1344	G1237	C925	C925		G431
	C1913	U1918	G1821	G1745	A1621	U1514	A1433	A1345	C1238	G926	G926		U432
U2080	C1914	G1919	G1822	A1746	U1622	A1515		A1346	A1239	G927	G927	U510	
C2081	C1915	G1920	G1823		G1623	G1516	U1438	G1347	C1239	C928	C928	U511	U440
	C1916	C1921	G1824	A1749	A1623	G1517	U1440	G1351	G1246	A929	A929	C515	C441
U2084	U1917	G1922	A1825	G1750	G1624	A1518	U1441	C1352	U1247	G930	G930	C516	G442
G2085	A1918	G1923	G1826	A1751	G1625	A1518	C1441	C1352	U1247	C931	C931	C517	G443
	A1919	G1924	C1827	G1752		A1523		C1353	G1273	A932	A932	C518	
G2089	G2000	C1931	G1828	G1753	C1628	A1534	C1446	A1354	G1274	C933	C933	C519	C446
U2090	G2001	A1932	G1829	U1754	A1534		C1446	A1354	G1275	C934	C934		
G2092	A2002	G1933	G1830	U1755	A1631	C1541	C1449	G1358	G1276	U1083	G708	G638	C449
G2093	G2003	A1934	G1835	U1757	G1632	A1547	C1450	G1359	G1277	U1084	C709	U639	G450
A2094	U2004	A1939	G1836	G1758	A1633		C1450	G1360	G1278	C1085	G710	C640	C451
	G2005	G1940	A1837	G1759	A1634	A1547		G1361	A1279		A711	G641	A452
G2096	G2006	A1941		G1760	C1635	G1550	G1455	G1362	C1280	G1089	C712	G642	G453
A2097	G2007	A1942	G1840	G1761	U1636	C1551	G1456	C1363	G1281	G1090	C713	G643	U454
G2098	U2008	A1943	G1841	C1762	A1637	G1552	G1457	U1364	G1282	C1091	G714	G644	
A2099	A2009	A1944	G1842	C1763	A1638	G1553	G1458	G1364	G1283	C1092	G715		C455
G2099	A2010	A1944	G1842	G1763	U1639	A1553	A1459	G1370	G1284	C1093	C716	G648	C460
G2100	C2011	G1945		G1764	C1640	A1594	C1460	A1371	G1284	G1094	U717	A649	G461
A2101	A2012	G1946	G1853	A1765	G1641		C1461	A1372	G1291	C938	C718	G462	G462
G2102	A2013	G1948	G1854	A1766	A1642	C1557	A1462	A1373	C1292	C939	C719	C651	A463
A2103	C2014	A1949	G1855	A1767	A1643	A1558	A1462	G1374	G1293	C940		C652	G464
	U2015	G1951		C1768	C1644	A1558	G1465		G1294	C946	C727	C653	G465
A2105	C2016		G1869	G1769	C1645	A1563		G1377	A1295	G951	U728	C654	A466
G2106	A2017	U1957	C1870	A1770	A1646		U1473		G1296	G952	G729	C655	U467
A2107	C2018	A1958	A1871	U1771		C1566	C1474	G1380	C1301	G952	G730		U468
G2108	C2019	U1959	G1872	C1772	G1654		G1475	U1381	C1302	A956	G731	C658	C469
A2109	U2020	A1960	A1873	U1773	U1572	C1573	C1476	G1382	U1302	G957	A732	C662	A471
G2259	G2021	G1961	A1874	C1774	C1661	G1573	C1477	G1383	G1303	G958	G733	G663	
C2260	C2022	A1962	G1875	A1775	C1662	G1574	C1478	G1384	A1304	G959	G734	G664	C474
G2261	G2023	C1963	U1876	A1776	C1663	A1575	G1479	G1385	C1305	A960		C665	G475
G2262	A2025	A1964	G1877	C1777	G1576	G1577	C1480	C1386	C1306	G961	C738	C666	G476
A2263	A2026	C1966	G1878	C1778	A1669	U1578	C1481	A1387	A1307	C962	C738A	G667	C477
			C1879	U1779			G1482		C1308	G963	G739		





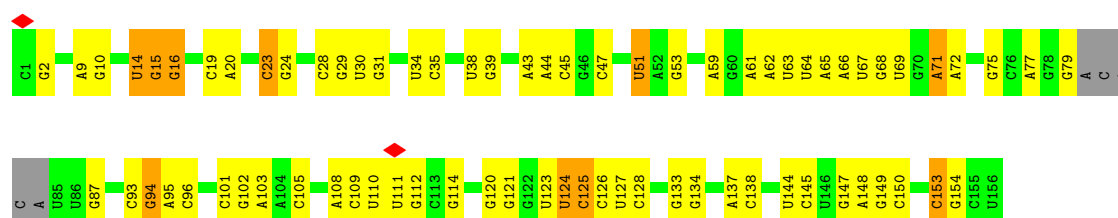
• Molecule 22: 5S rRNA

Chain 7: 64% 32% .



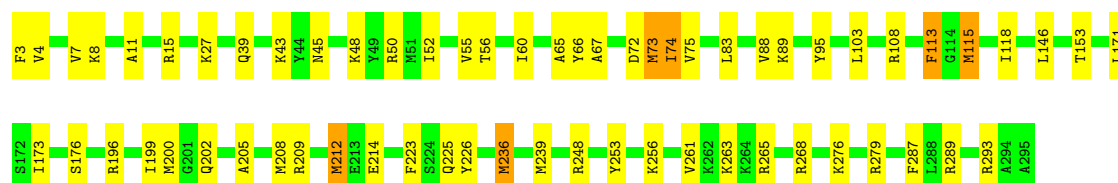
• Molecule 23: 5.8S rRNA

Chain 8: 49% 41% 6% .



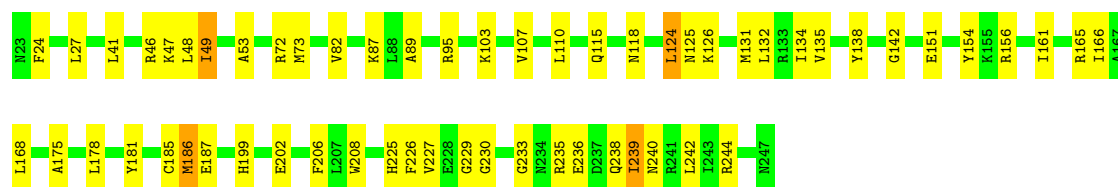
• Molecule 24: 60S ribosomal protein L5

Chain D: 78% 19% .



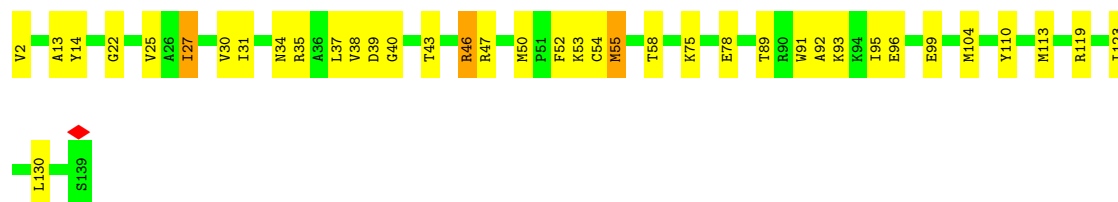
• Molecule 25: 60S ribosomal protein L7

Chain F:  74% 24% .



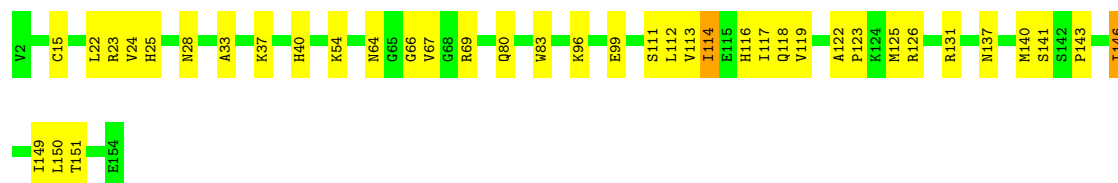
- Molecule 26: 60S ribosomal protein L14

Chain M:  72% 25% .




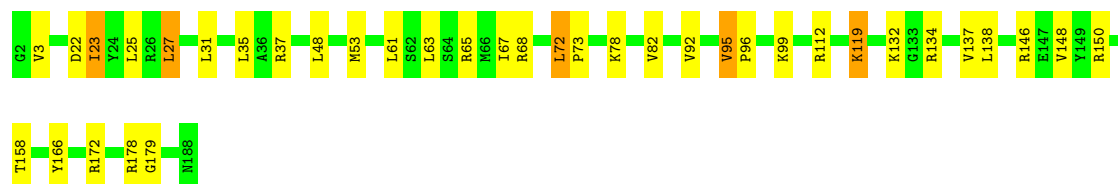
- Molecule 27: 60S ribosomal protein L17

Chain P:  75% 24% .



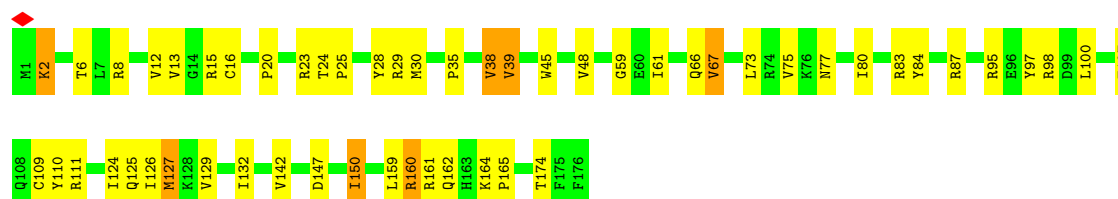
- Molecule 28: Large ribosomal subunit protein eL18

Chain Q:  80% 17% .

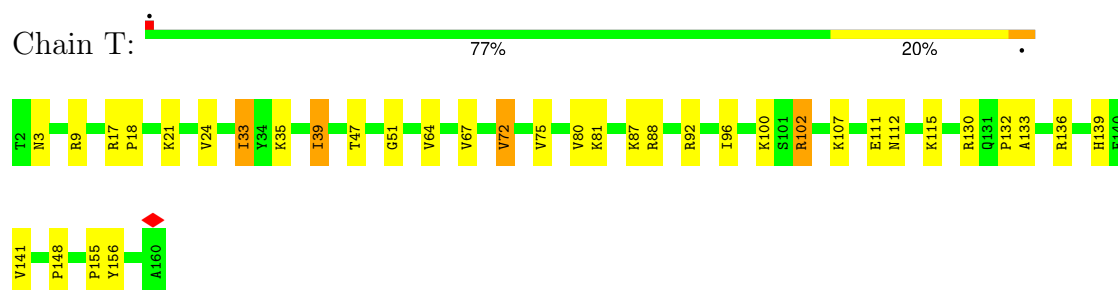


- Molecule 29: eL20

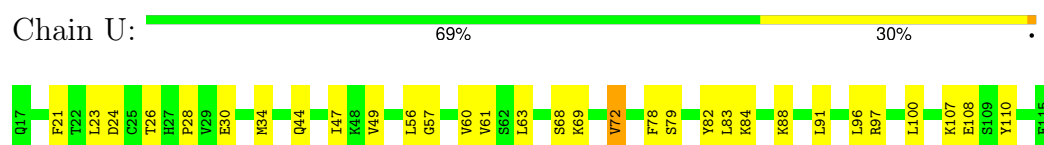
Chain S:  69% 27% .



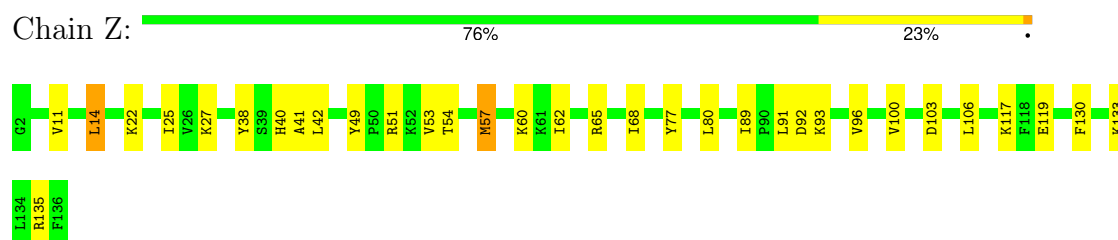
- Molecule 30: 60S ribosomal protein L21



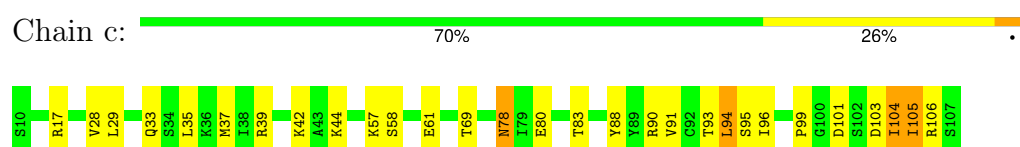
- Molecule 31: eL22



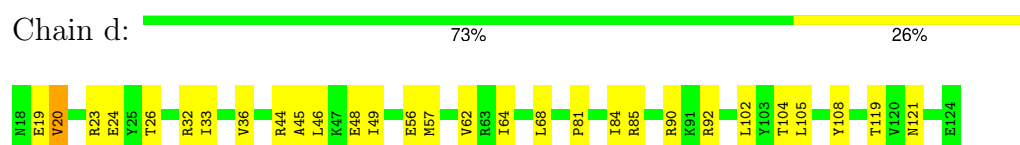
- Molecule 32: 60S ribosomal protein L27



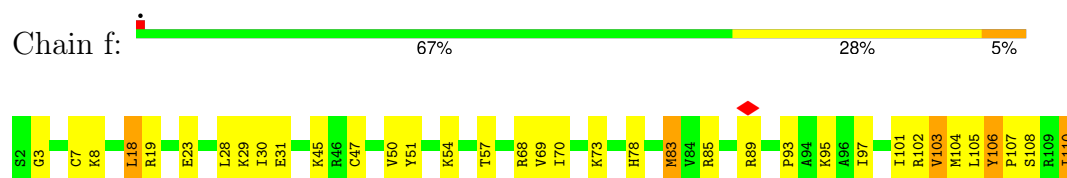
- Molecule 33: 60S ribosomal protein L30




- Molecule 34: 60S ribosomal protein L31



- Molecule 35: Large ribosomal subunit protein eL33




- Molecule 36: 60S ribosomal protein L34

Chain g:  77% 21%




- Molecule 37: 60S ribosomal protein L35

Chain h:  80% 17%



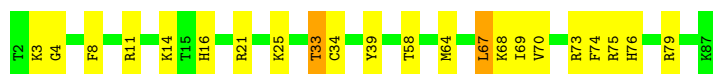
- Molecule 38: 60S ribosomal protein L36

Chain i:  81% 17%




- Molecule 39: 60S ribosomal protein L37

Chain j:  74% 23%




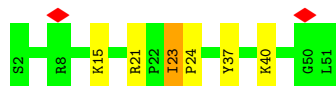
- Molecule 40: Large ribosomal subunit protein eL38

Chain k:  83% 16%




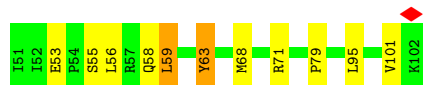
- Molecule 41: 60S ribosomal protein L39

Chain l:  88% 10%




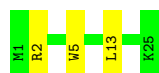
- Molecule 42: Large ribosomal subunit protein eL40

Chain m:  79% 17%




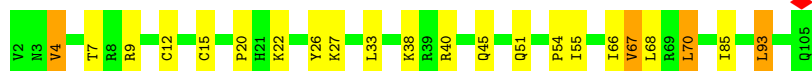
- Molecule 43: eL41

Chain n:  88% 12%




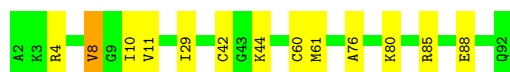
- Molecule 44: eL42

Chain o:  79% 17%



- Molecule 45: 60S ribosomal protein L37a

Chain p:  86% 13%



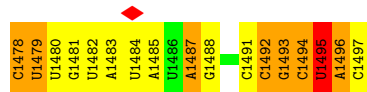
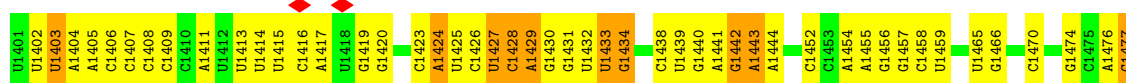
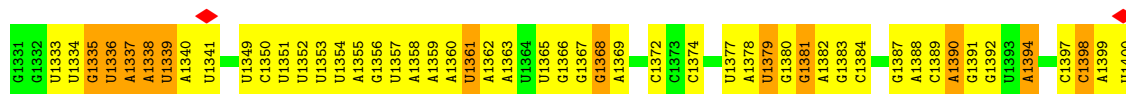
- Molecule 46: 60S ribosomal protein L28

Chain r:  75% 24%



- Molecule 47: NediV IRES

Chain 1:  31% 51% 17%



- Molecule 48: eL1

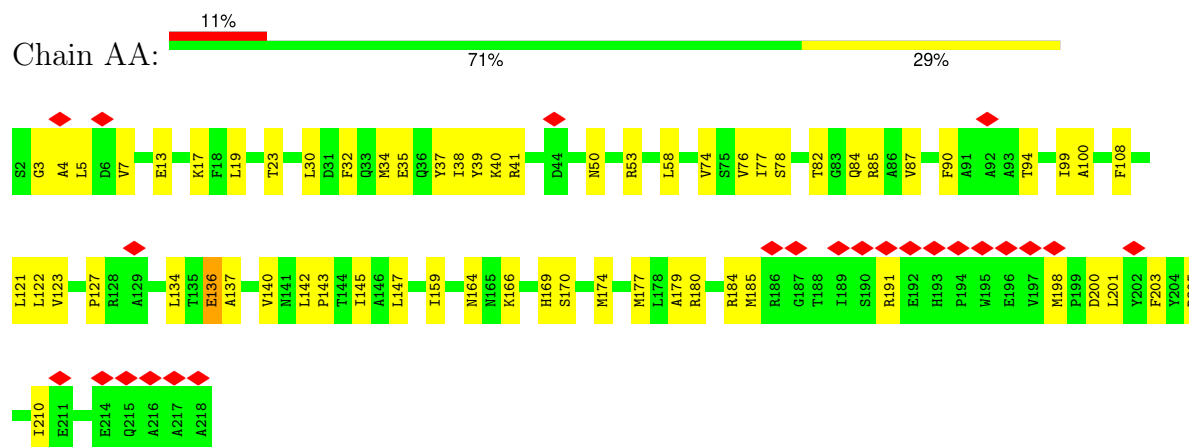
Chain K:  73% 25%



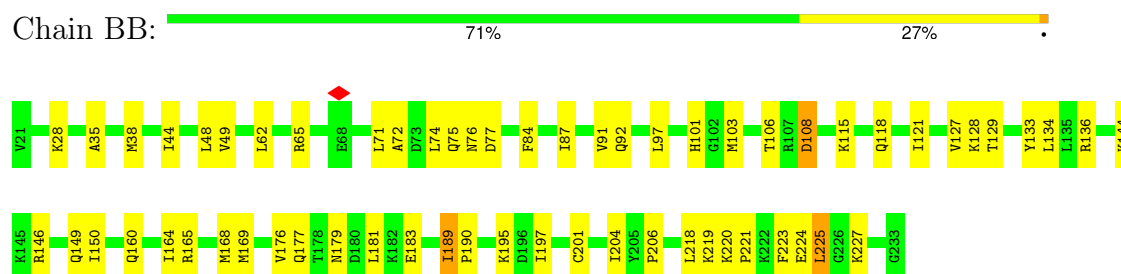




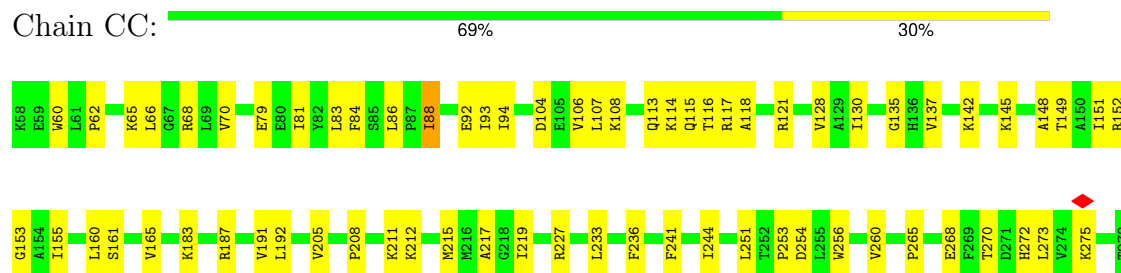
- Molecule 49: 40S\_SA\_C domain-containing protein



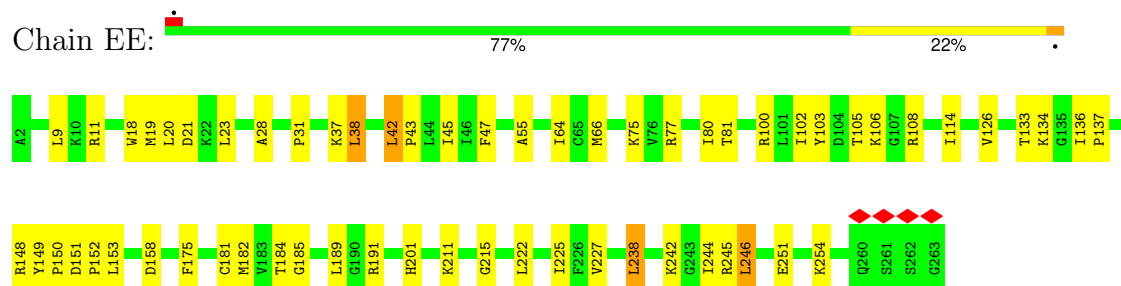
- Molecule 50: 40S ribosomal protein S3a



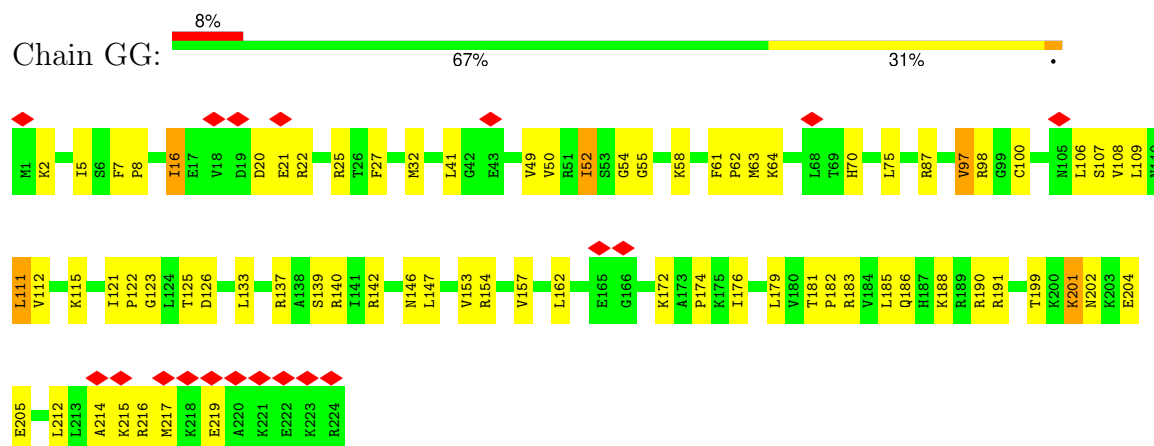
- Molecule 51: 40S ribosomal protein S2



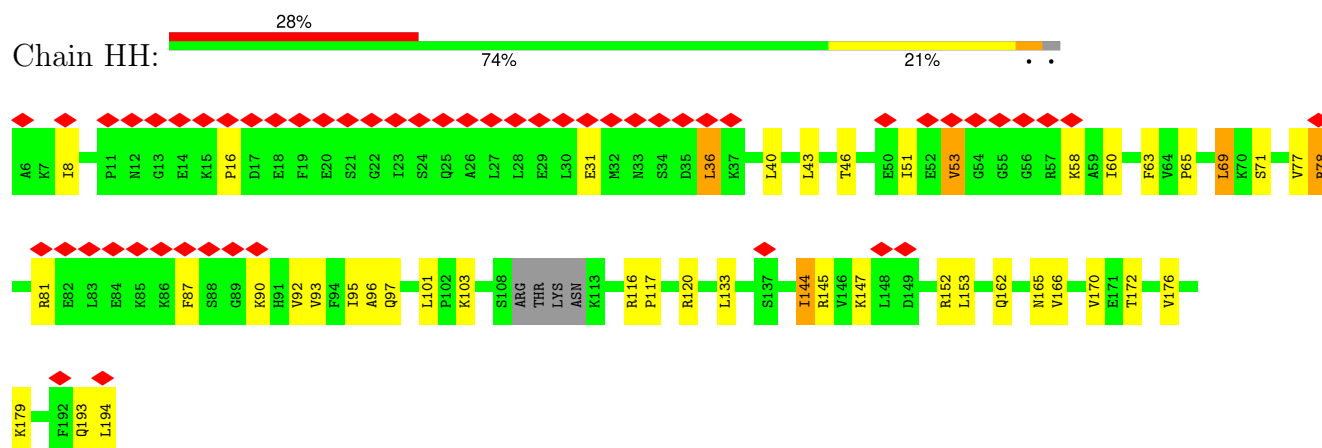
- Molecule 52: 40S ribosomal protein S4



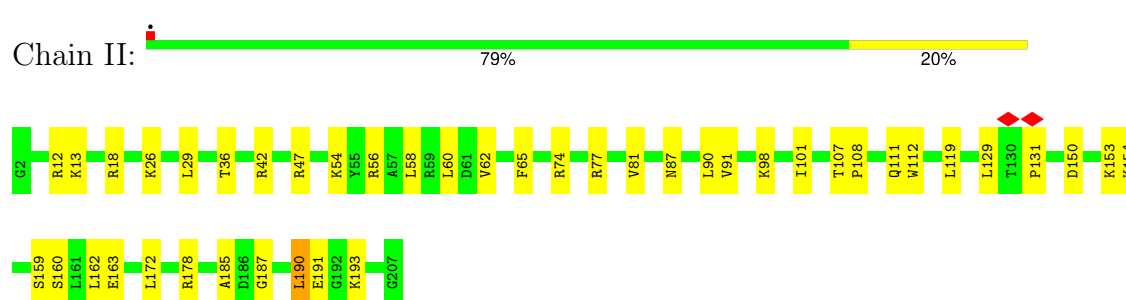
- Molecule 53: Small ribosomal subunit protein eS6



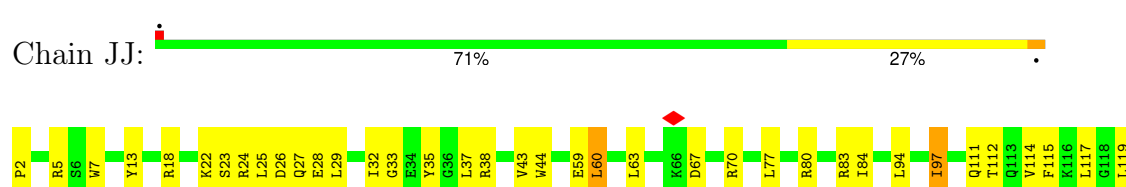
- Molecule 54: Small ribosomal subunit protein eS7

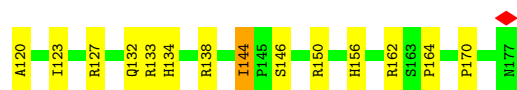


- Molecule 55: 40S ribosomal protein S8



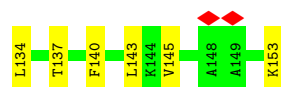
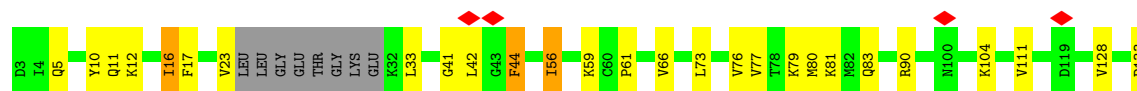
- Molecule 56: Small ribosomal subunit protein uS4





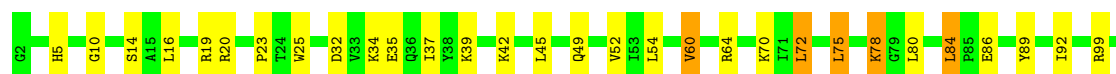
- Molecule 57: Small ribosomal subunit protein uS17

Chain LL: 73% 20% 5%



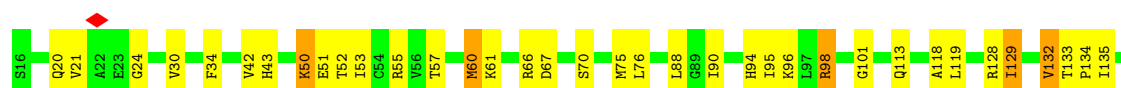
- Molecule 58: 40S ribosomal protein S13

Chain NN: 72% 25%



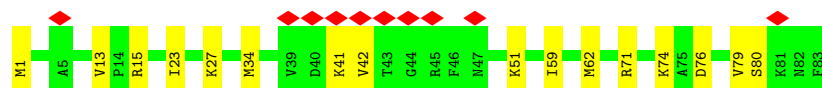
- Molecule 59: Small ribosomal subunit protein uS11

Chain OO: 73% 24%



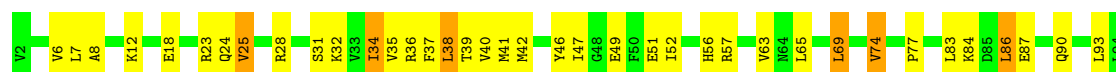
- Molecule 60: eS21

Chain VV: 12% 81% 19%



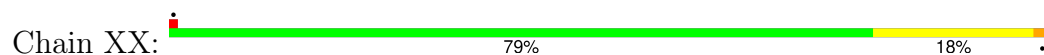
- Molecule 61: 40S ribosomal protein S15a

Chain WW: 64% 31% 5%

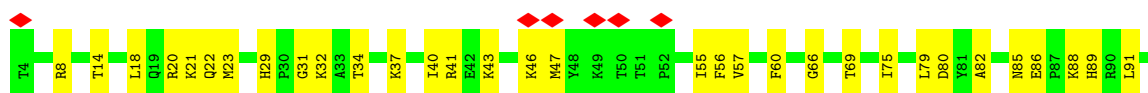




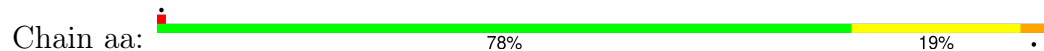
- Molecule 62: 40S ribosomal protein S23



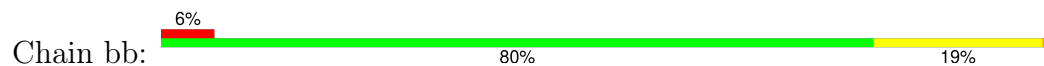
- Molecule 63: 40S ribosomal protein S24



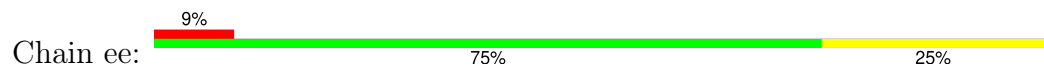
- Molecule 64: eS26



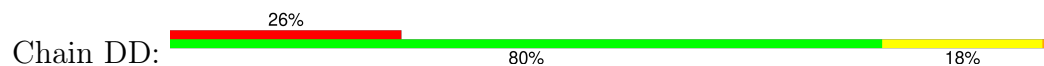
- Molecule 65: 40S ribosomal protein S27

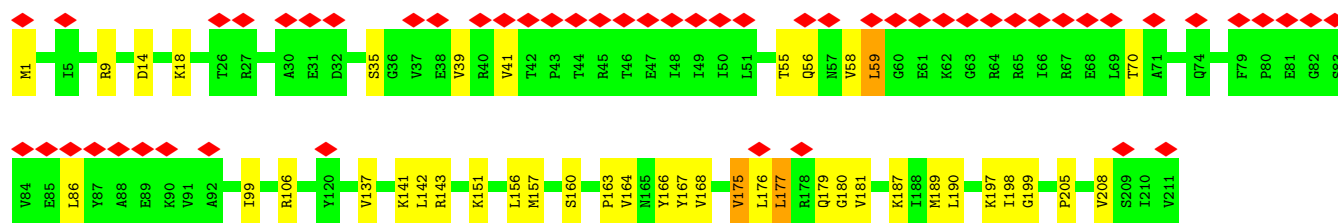


- Molecule 66: Small ribosomal subunit protein eS30



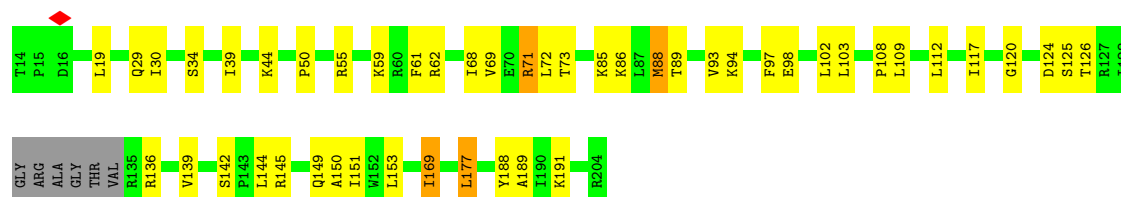
- Molecule 67: Small ribosomal subunit protein uS3





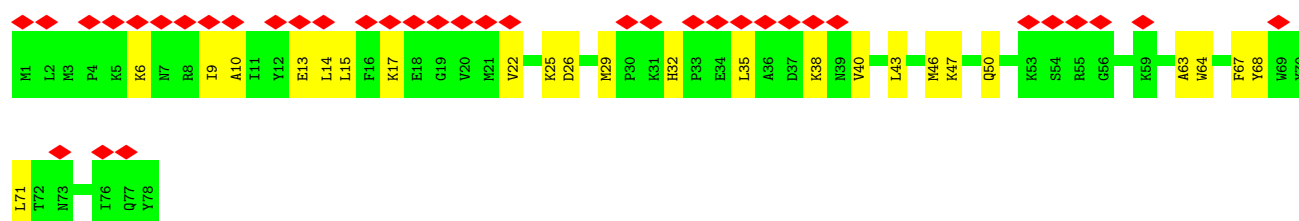
- Molecule 68: Small ribosomal subunit protein uS7

Chain FF: 72% 23%



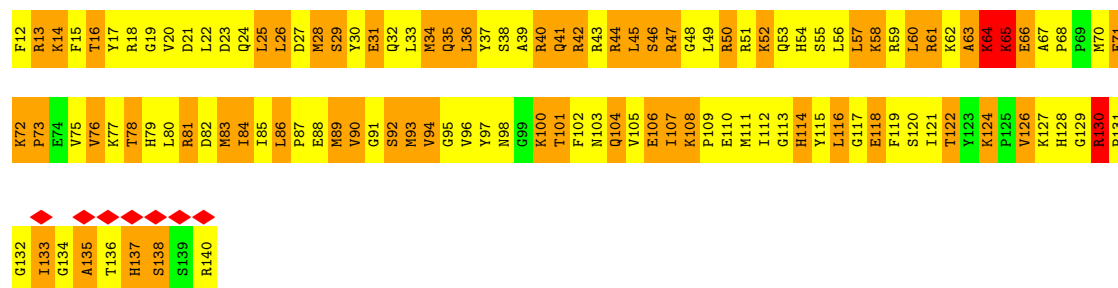
- Molecule 69: Small ribosomal subunit protein eS10

Chain KK: 47% 69% 31%



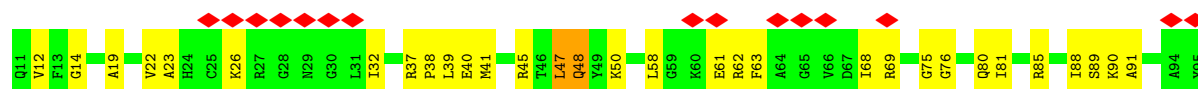
- Molecule 70: Small ribosomal subunit protein uS19

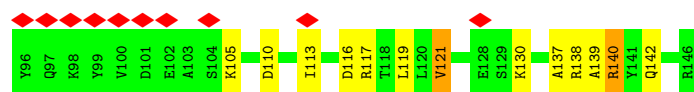
Chain PP: 5% 50% 43%



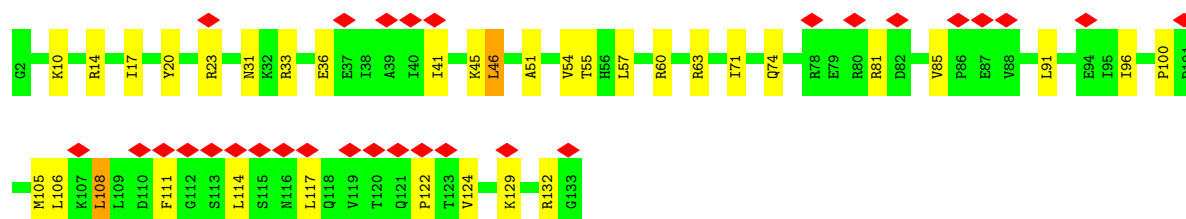
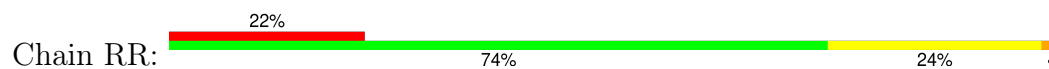
- Molecule 71: Small ribosomal subunit protein uS9

Chain QQ: 18% 68% 29%

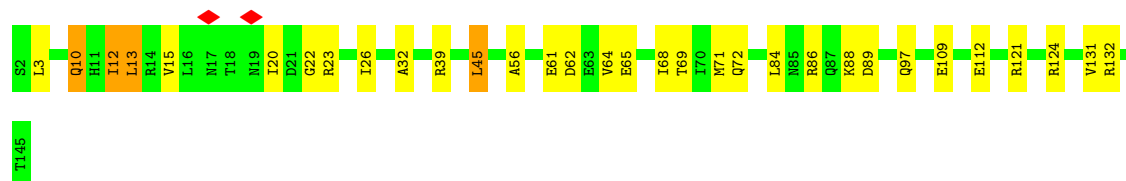
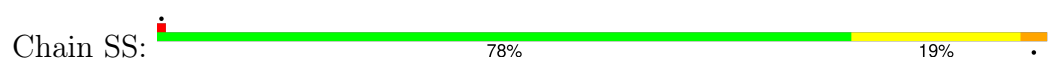




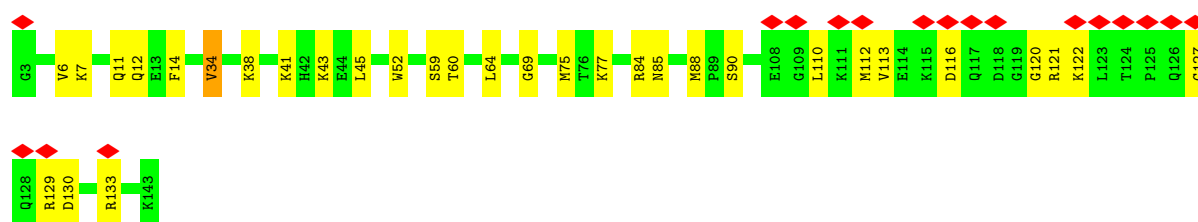
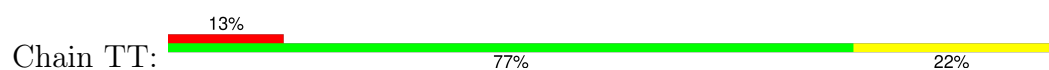
- Molecule 72: 40S ribosomal protein S17



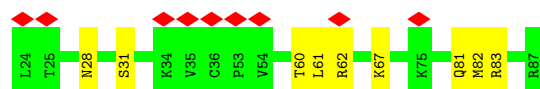
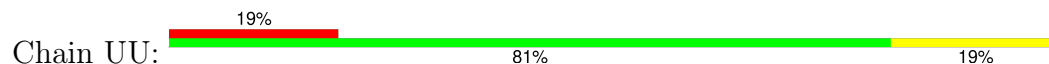
- Molecule 73: 40S ribosomal protein S18



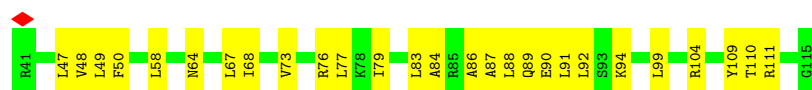
- Molecule 74: Small ribosomal subunit protein eS19



- Molecule 75: uS10



- Molecule 76: 40S ribosomal protein S25



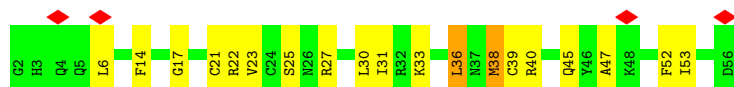
- Molecule 77: 40S ribosomal protein S28

Chain cc:  69% 26% 5%



- Molecule 78: 40S ribosomal protein S29

Chain dd:  7% 65% 31% .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	264326	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	64	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.612	Depositor
Minimum map value	-0.681	Depositor
Average map value	0.063	Depositor
Map value standard deviation	0.161	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	320.0, 320.0, 320.0	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.25, 1.25, 1.25	Depositor



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	9	0.11	1/39866 (0.0%)	0.24	2/62107 (0.0%)
2	A	0.10	0/1936	0.26	0/2596
3	B	0.10	0/3240	0.25	0/4339
4	C	0.09	0/2937	0.25	1/3946 (0.0%)
5	E	0.08	0/1762	0.25	0/2362
6	G	0.09	0/1910	0.26	0/2569
7	H	0.10	0/1535	0.27	0/2063
8	I	0.09	0/1702	0.24	0/2272
9	J	0.08	0/1385	0.25	0/1852
10	L	0.09	0/1733	0.24	0/2316
11	N	0.10	0/1746	0.25	0/2338
12	O	0.10	0/1662	0.26	0/2222
13	R	0.09	0/1524	0.24	0/2013
14	V	0.09	0/1048	0.25	0/1402
15	W	0.09	0/657	0.24	0/873
16	X	0.09	0/984	0.27	0/1323
17	Y	0.09	0/1132	0.23	0/1504
18	a	0.09	0/1191	0.26	0/1590
19	b	0.08	0/861	0.20	0/1138
20	e	0.10	0/1071	0.25	0/1429
21	5	0.11	0/84978	0.26	0/132528
22	7	0.08	0/2836	0.18	0/4421
23	8	0.10	0/3581	0.23	0/5577
24	D	0.08	0/2437	0.24	0/3264
25	F	0.10	0/1911	0.26	0/2549
26	M	0.10	0/1158	0.27	0/1547
27	P	0.10	0/1268	0.32	0/1700
28	Q	0.09	0/1539	0.24	0/2054
29	S	0.11	0/1501	0.27	0/2012
30	T	0.08	0/1326	0.22	0/1770
31	U	0.09	0/823	0.26	0/1104
32	Z	0.09	0/1130	0.24	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	c	0.10	0/771	0.26	0/1034
34	d	0.10	0/903	0.26	0/1216
35	f	0.10	0/895	0.29	0/1198
36	g	0.09	0/916	0.24	0/1220
37	h	0.10	0/1021	0.28	0/1348
38	i	0.09	0/841	0.24	0/1112
39	j	0.09	0/720	0.27	0/952
40	k	0.08	0/575	0.26	0/761
41	l	0.11	0/459	0.28	0/608
42	m	0.08	0/435	0.24	0/575
43	n	0.09	0/240	0.20	0/305
44	o	0.08	0/864	0.22	0/1140
45	p	0.10	0/718	0.25	0/953
46	r	0.09	0/1010	0.29	0/1354
47	1	0.35	0/3951	0.56	2/6150 (0.0%)
48	K	0.10	0/1080	0.30	0/1447
49	AA	0.08	0/1747	0.24	0/2374
50	BB	0.11	0/1756	0.29	0/2350
51	CC	0.09	0/1753	0.26	0/2369
52	EE	0.08	0/2118	0.25	0/2849
53	GG	0.09	0/1836	0.26	0/2445
54	HH	0.08	0/1510	0.22	0/2022
55	II	0.08	0/1715	0.25	0/2287
56	JJ	0.09	0/1497	0.25	0/2001
57	LL	0.09	0/1195	0.25	0/1597
58	NN	0.09	0/1226	0.25	0/1649
59	OO	0.08	0/1029	0.25	0/1380
60	VV	0.08	0/643	0.27	0/860
61	WW	0.11	0/1051	0.34	0/1406
62	XX	0.09	0/1116	0.28	0/1490
63	YY	0.09	0/1028	0.24	0/1366
64	aa	0.11	0/828	0.31	0/1109
65	bb	0.07	0/665	0.25	0/891
66	ee	0.09	0/462	0.23	0/607
67	DD	0.09	0/1662	0.28	0/2234
68	FF	0.08	0/1492	0.26	0/2005
69	KK	0.10	0/677	0.27	0/909
70	PP	0.50	0/1079	0.83	4/1441 (0.3%)
71	QQ	0.10	0/1104	0.27	0/1476
72	RR	0.09	0/1082	0.26	0/1452
73	SS	0.08	0/1208	0.26	0/1618
74	TT	0.08	0/1115	0.23	0/1493
75	UU	0.07	0/399	0.24	0/530

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	ZZ	0.08	0/604	0.25	0/810
77	cc	0.08	0/490	0.27	0/656
78	dd	0.13	0/470	0.32	0/623
All	All	0.12	1/224326 (0.0%)	0.27	9/329959 (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
35	f	0	1
78	dd	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	9	1699	A	O3'-P	-5.33	1.53	1.61

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	1	1495	U	C1'-C2'-O2'	-11.54	94.49	111.80
1	9	1699	A	C3'-C2'-O2'	-8.98	97.23	110.70
47	1	1495	U	O4'-C4'-C3'	-6.55	99.55	106.10
70	PP	134	GLY	N-CA-C	-6.16	107.75	115.08
4	C	340	ILE	N-CA-C	-6.10	106.80	111.62

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
78	dd	38	MET	Peptide
35	f	106	TYR	Peptide

## 5.2 Too-close contacts [i](#)

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	9	35659	0	18015	548	0
2	A	1898	0	1993	35	0
3	B	3172	0	3310	49	0
4	C	2883	0	3053	45	0
5	E	1729	0	1887	32	0
6	G	1879	0	2027	41	0
7	H	1516	0	1597	32	0
8	I	1664	0	1712	28	0
9	J	1362	0	1399	22	0
10	L	1702	0	1820	28	0
11	N	1701	0	1749	20	0
12	O	1630	0	1778	34	0
13	R	1508	0	1664	30	0
14	V	1034	0	1097	16	0
15	W	645	0	668	6	0
16	X	967	0	1040	18	0
17	Y	1115	0	1205	21	0
18	a	1162	0	1209	25	0
19	b	848	0	920	8	0
20	e	1053	0	1147	20	0
21	5	75972	0	38385	1227	0
22	7	2538	0	1286	28	0
23	8	3208	0	1629	38	0
24	D	2391	0	2424	42	0
25	F	1875	0	1995	38	0
26	M	1137	0	1211	23	0
27	P	1242	0	1274	27	0
28	Q	1515	0	1634	24	0
29	S	1462	0	1508	35	0
30	T	1298	0	1366	26	0
31	U	809	0	833	16	0
32	Z	1107	0	1182	21	0
33	c	761	0	794	20	0
34	d	888	0	930	17	0
35	f	876	0	912	23	0
36	g	906	0	998	18	0
37	h	1013	0	1147	16	0
38	i	830	0	916	12	0
39	j	705	0	737	14	0
40	k	569	0	637	6	0
41	l	447	0	480	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	429	0	465	7	0
43	n	239	0	289	2	0
44	o	851	0	920	12	0
45	p	708	0	756	10	0
46	r	994	0	1051	19	0
47	1	3538	0	1789	65	0
48	K	1064	0	1126	19	0
49	AA	1710	0	1708	46	0
50	BB	1729	0	1803	42	0
51	CC	1716	0	1806	42	0
52	EE	2076	0	2177	41	0
53	GG	1813	0	1967	49	0
54	HH	1488	0	1582	29	0
55	II	1686	0	1772	27	0
56	JJ	1472	0	1584	40	0
57	LL	1175	0	1249	20	0
58	NN	1202	0	1289	26	0
59	OO	1016	0	1039	29	0
60	VV	636	0	637	11	0
61	WW	1034	0	1080	31	0
62	XX	1098	0	1167	21	0
63	YY	1011	0	1083	32	0
64	aa	814	0	863	19	0
65	bb	651	0	672	11	0
66	ee	457	0	502	15	0
67	DD	1637	0	1734	24	0
68	FF	1471	0	1522	32	0
69	KK	658	0	674	15	0
70	PP	1058	0	1104	203	0
71	QQ	1087	0	1152	31	0
72	RR	1068	0	1121	25	0
73	SS	1190	0	1249	24	0
74	TT	1097	0	1132	21	0
75	UU	394	0	425	5	0
76	ZZ	598	0	656	18	0
77	cc	488	0	514	16	0
78	dd	459	0	448	16	0
79	5	192	0	0	0	0
79	7	6	0	0	0	0
79	8	3	0	0	0	0
79	A	1	0	0	0	0
79	V	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
79	a	1	0	0	0	0
79	aa	1	0	0	0	0
79	l	1	0	0	0	0
80	aa	1	0	0	0	0
80	dd	1	0	0	0	0
80	g	1	0	0	0	0
80	j	1	0	0	0	0
80	m	1	0	0	0	0
80	o	1	0	0	0	0
80	p	1	0	0	0	0
All	All	208701	0	153675	3419	0

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

The worst 5 of 3419 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)
70:PP:72:LYS:HE3	70:PP:92:SER:CA	1.21	1.61
70:PP:72:LYS:CE	70:PP:92:SER:CA	1.77	1.55
70:PP:72:LYS:CE	70:PP:92:SER:HA	1.37	1.51
70:PP:72:LYS:CE	70:PP:92:SER:C	1.97	1.36
70:PP:72:LYS:NZ	70:PP:92:SER:O	1.69	1.25

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	
2	A	246/248 (99%)	236 (96%)	10 (4%)	0	100	100
3	B	392/394 (100%)	380 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	C	360/362 (99%)	349 (97%)	11 (3%)	0	100	100
5	E	208/251 (83%)	203 (98%)	5 (2%)	0	100	100
6	G	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
7	H	188/190 (99%)	186 (99%)	2 (1%)	0	100	100
8	I	201/213 (94%)	194 (96%)	7 (4%)	0	100	100
9	J	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
10	L	208/210 (99%)	202 (97%)	6 (3%)	0	100	100
11	N	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
12	O	197/199 (99%)	194 (98%)	3 (2%)	0	100	100
13	R	178/180 (99%)	175 (98%)	3 (2%)	0	100	100
14	V	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
15	W	75/94 (80%)	73 (97%)	2 (3%)	0	100	100
16	X	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
17	Y	132/134 (98%)	132 (100%)	0	0	100	100
18	a	145/147 (99%)	143 (99%)	2 (1%)	0	100	100
19	b	100/116 (86%)	97 (97%)	3 (3%)	0	100	100
20	e	126/128 (98%)	124 (98%)	2 (2%)	0	100	100
24	D	291/293 (99%)	283 (97%)	8 (3%)	0	100	100
25	F	223/225 (99%)	213 (96%)	10 (4%)	0	100	100
26	M	136/138 (99%)	129 (95%)	7 (5%)	0	100	100
27	P	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
28	Q	185/187 (99%)	181 (98%)	4 (2%)	0	100	100
29	S	174/176 (99%)	165 (95%)	9 (5%)	0	100	100
30	T	157/159 (99%)	151 (96%)	6 (4%)	0	100	100
31	U	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
32	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
33	c	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
34	d	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
35	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
36	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
37	h	120/122 (98%)	118 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	i	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
39	j	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
40	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
41	l	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
42	m	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
43	n	23/25 (92%)	23 (100%)	0	0	100	100
44	o	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
45	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
46	r	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
48	K	126/130 (97%)	115 (91%)	11 (9%)	0	100	100
49	AA	215/217 (99%)	209 (97%)	6 (3%)	0	100	100
50	BB	211/213 (99%)	199 (94%)	12 (6%)	0	100	100
51	CC	219/221 (99%)	214 (98%)	5 (2%)	0	100	100
52	EE	260/262 (99%)	247 (95%)	13 (5%)	0	100	100
53	GG	222/224 (99%)	215 (97%)	7 (3%)	0	100	100
54	HH	181/189 (96%)	176 (97%)	5 (3%)	0	100	100
55	II	204/206 (99%)	198 (97%)	6 (3%)	0	100	100
56	JJ	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
57	LL	139/151 (92%)	133 (96%)	6 (4%)	0	100	100
58	NN	147/149 (99%)	144 (98%)	3 (2%)	0	100	100
59	OO	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
60	VV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
61	WW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
62	XX	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
63	YY	122/124 (98%)	121 (99%)	1 (1%)	0	100	100
64	aa	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
65	bb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
66	ee	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
67	DD	209/211 (99%)	202 (97%)	7 (3%)	0	100	100
68	FF	181/191 (95%)	172 (95%)	9 (5%)	0	100	100
69	KK	76/78 (97%)	74 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	PP	127/129 (98%)	79 (62%)	40 (32%)	8 (6%)	1	6
71	QQ	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
72	RR	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
73	SS	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
74	TT	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
75	UU	44/48 (92%)	44 (100%)	0	0	100	100
76	ZZ	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
77	cc	60/62 (97%)	60 (100%)	0	0	100	100
78	dd	53/55 (96%)	46 (87%)	7 (13%)	0	100	100
All	All	10683/10948 (98%)	10317 (97%)	358 (3%)	8 (0%)	49	80

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
70	PP	135	ALA
70	PP	65	LYS
70	PP	61	ARG
70	PP	63	ALA
70	PP	73	PRO

### 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	
2	A	190/190 (100%)	183 (96%)	7 (4%)	30	64
3	B	342/342 (100%)	323 (94%)	19 (6%)	19	52
4	C	302/302 (100%)	294 (97%)	8 (3%)	40	72
5	E	190/223 (85%)	176 (93%)	14 (7%)	13	42
6	G	200/205 (98%)	191 (96%)	9 (4%)	24	59
7	H	169/169 (100%)	163 (96%)	6 (4%)	31	65
8	I	175/180 (97%)	165 (94%)	10 (6%)	18	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	J	143/143 (100%)	134 (94%)	9 (6%)	16	48
10	L	175/175 (100%)	168 (96%)	7 (4%)	28	62
11	N	171/171 (100%)	165 (96%)	6 (4%)	32	65
12	O	171/171 (100%)	165 (96%)	6 (4%)	32	65
13	R	159/159 (100%)	155 (98%)	4 (2%)	42	72
14	V	106/106 (100%)	99 (93%)	7 (7%)	15	46
15	W	66/80 (82%)	62 (94%)	4 (6%)	17	49
16	X	106/106 (100%)	100 (94%)	6 (6%)	18	52
17	Y	124/124 (100%)	122 (98%)	2 (2%)	55	79
18	a	119/119 (100%)	116 (98%)	3 (2%)	42	72
19	b	84/95 (88%)	78 (93%)	6 (7%)	13	43
20	e	114/114 (100%)	107 (94%)	7 (6%)	17	49
24	D	247/247 (100%)	233 (94%)	14 (6%)	18	52
25	F	196/196 (100%)	186 (95%)	10 (5%)	21	55
26	M	117/117 (100%)	109 (93%)	8 (7%)	14	45
27	P	134/134 (100%)	129 (96%)	5 (4%)	30	64
28	Q	164/164 (100%)	151 (92%)	13 (8%)	11	39
29	S	157/157 (100%)	138 (88%)	19 (12%)	5	21
30	T	139/139 (100%)	130 (94%)	9 (6%)	15	47
31	U	89/89 (100%)	86 (97%)	3 (3%)	32	66
32	Z	117/117 (100%)	113 (97%)	4 (3%)	32	66
33	c	84/84 (100%)	75 (89%)	9 (11%)	6	26
34	d	98/98 (100%)	94 (96%)	4 (4%)	27	61
35	f	88/88 (100%)	81 (92%)	7 (8%)	11	38
36	g	98/98 (100%)	91 (93%)	7 (7%)	13	43
37	h	109/109 (100%)	104 (95%)	5 (5%)	24	58
38	i	86/86 (100%)	81 (94%)	5 (6%)	18	51
39	j	73/73 (100%)	69 (94%)	4 (6%)	19	53
40	k	64/64 (100%)	61 (95%)	3 (5%)	23	58
41	l	47/47 (100%)	45 (96%)	2 (4%)	26	60
42	m	48/48 (100%)	45 (94%)	3 (6%)	16	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	n	24/24 (100%)	23 (96%)	1 (4%)	26	61
44	o	92/92 (100%)	85 (92%)	7 (8%)	12	41
45	p	74/74 (100%)	73 (99%)	1 (1%)	59	80
46	r	108/108 (100%)	104 (96%)	4 (4%)	30	64
48	K	119/120 (99%)	112 (94%)	7 (6%)	18	50
49	AA	180/181 (99%)	173 (96%)	7 (4%)	28	62
50	BB	194/194 (100%)	187 (96%)	7 (4%)	31	65
51	CC	187/187 (100%)	180 (96%)	7 (4%)	30	64
52	EE	224/224 (100%)	216 (96%)	8 (4%)	31	65
53	GG	195/195 (100%)	185 (95%)	10 (5%)	21	55
54	HH	165/169 (98%)	160 (97%)	5 (3%)	36	69
55	II	178/178 (100%)	176 (99%)	2 (1%)	65	83
56	JJ	158/158 (100%)	153 (97%)	5 (3%)	34	67
57	LL	130/136 (96%)	121 (93%)	9 (7%)	14	45
58	NN	130/130 (100%)	122 (94%)	8 (6%)	16	49
59	OO	106/106 (100%)	98 (92%)	8 (8%)	12	41
60	VV	67/67 (100%)	64 (96%)	3 (4%)	24	59
61	WW	112/112 (100%)	100 (89%)	12 (11%)	6	26
62	XX	113/113 (100%)	108 (96%)	5 (4%)	25	60
63	YY	107/107 (100%)	100 (94%)	7 (6%)	15	47
64	aa	88/88 (100%)	82 (93%)	6 (7%)	14	45
65	bb	75/75 (100%)	73 (97%)	2 (3%)	39	71
66	ee	47/47 (100%)	47 (100%)	0	100	100
67	DD	174/174 (100%)	167 (96%)	7 (4%)	28	62
68	FF	158/161 (98%)	152 (96%)	6 (4%)	29	63
69	KK	70/70 (100%)	69 (99%)	1 (1%)	59	80
70	PP	115/115 (100%)	57 (50%)	58 (50%)	0	0
71	QQ	112/112 (100%)	108 (96%)	4 (4%)	31	65
72	RR	119/119 (100%)	115 (97%)	4 (3%)	32	66
73	SS	125/125 (100%)	120 (96%)	5 (4%)	28	62
74	TT	111/111 (100%)	107 (96%)	4 (4%)	31	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
75	UU	46/46 (100%)	46 (100%)	0	100	100
76	ZZ	66/66 (100%)	66 (100%)	0	100	100
77	cc	55/55 (100%)	52 (94%)	3 (6%)	19	53
78	dd	48/48 (100%)	45 (94%)	3 (6%)	16	48
All	All	9333/9416 (99%)	8833 (95%)	500 (5%)	21	53

5 of 500 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	c	101	ASP
70	PP	64	LYS
46	r	103	HIS
70	PP	50	ARG
70	PP	130	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 142 such sidechains are listed below:

Mol	Chain	Res	Type
64	aa	7	ASN
66	ee	110	GLN
70	PP	24	GLN
24	D	202	GLN
24	D	122	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	9	1653/1670 (98%)	327 (19%)	16 (0%)
21	5	3519/3543 (99%)	756 (21%)	53 (1%)
22	7	118/119 (99%)	11 (9%)	0
23	8	149/156 (95%)	35 (23%)	1 (0%)
47	1	166/167 (99%)	94 (56%)	9 (5%)
All	All	5605/5655 (99%)	1223 (21%)	79 (1%)

5 of 1223 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	9	2	A

*Continued on next page...*

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Mol	Chain	Res	Type
1	9	3	C
1	9	4	C
1	9	12	U
1	9	25	A

5 of 79 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	5	3603	G
47	1	1338	A
21	5	3888	G
21	5	4884	G
47	1	1481	G

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 213 ligands modelled in this entry, 213 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
21	5	25
1	9	19
48	K	1
75	UU	1
5	E	1

The worst 5 of 47 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	42.14
1	5	1252:C	O3'	1271:G	P	34.29
1	9	752:G	O3'	788:G	P	21.44
1	9	1409:A	O3'	1442:U	P	19.85
1	5	1219:G	O3'	1233:G	P	19.34

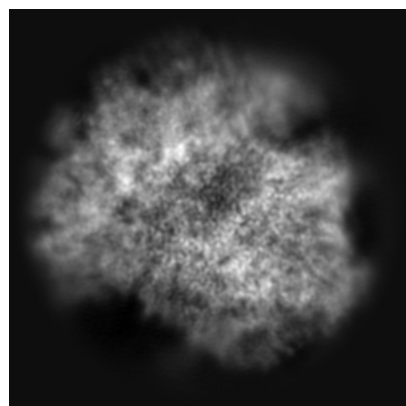
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72137. These allow visual inspection of the internal detail of the map and identification of artifacts.

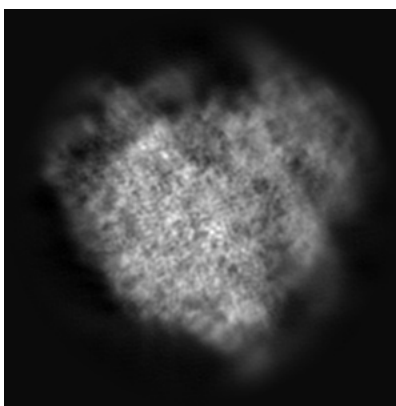
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

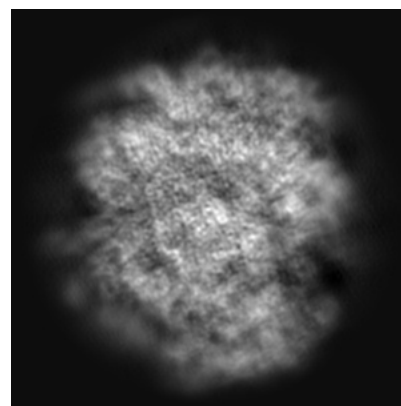
#### 6.1.1 Primary map



X

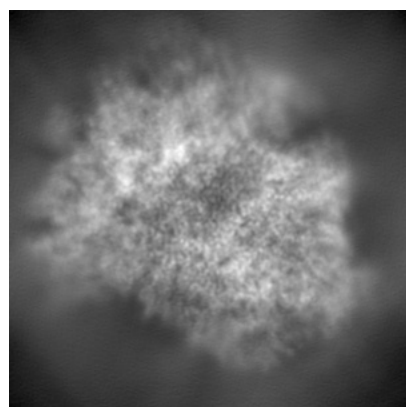


Y

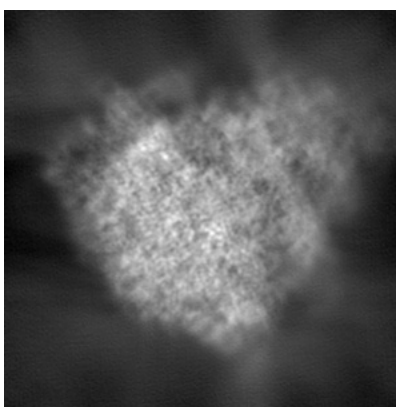


Z

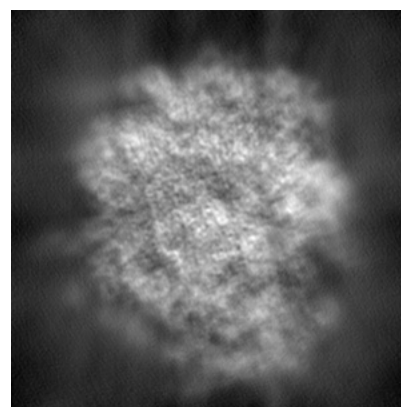
#### 6.1.2 Raw map



X



Y

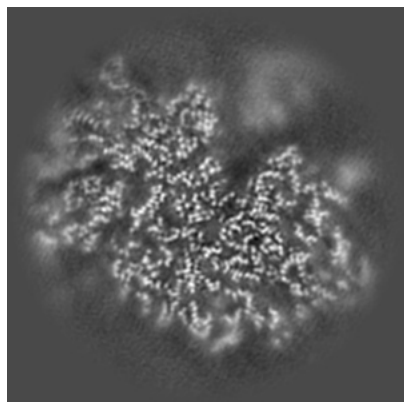


Z

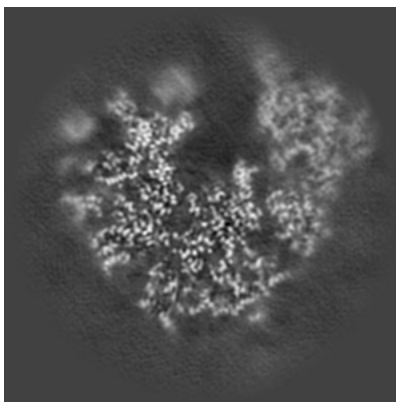
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

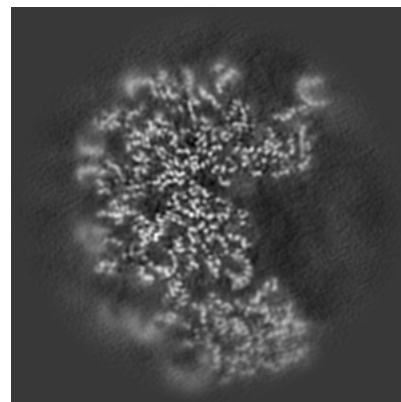
### 6.2.1 Primary map



X Index: 128

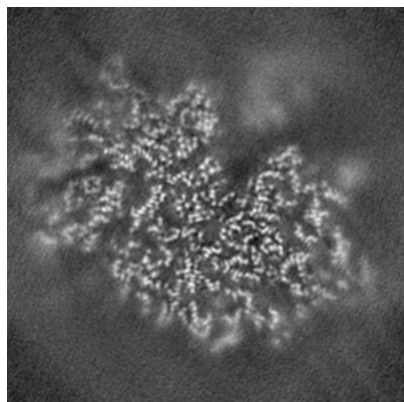


Y Index: 128

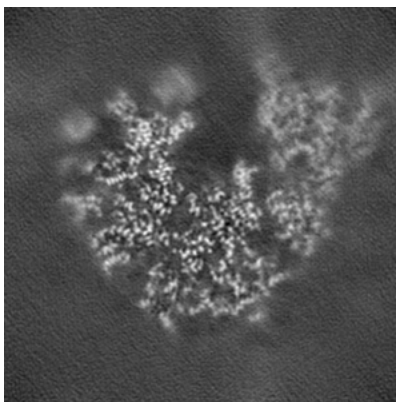


Z Index: 128

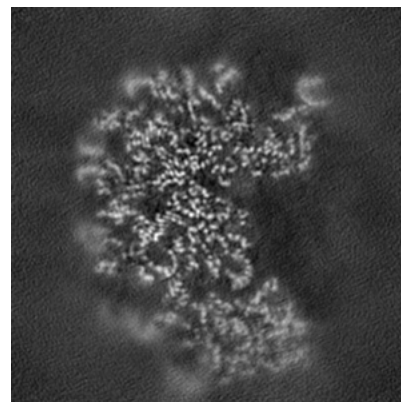
### 6.2.2 Raw map



X Index: 128



Y Index: 128



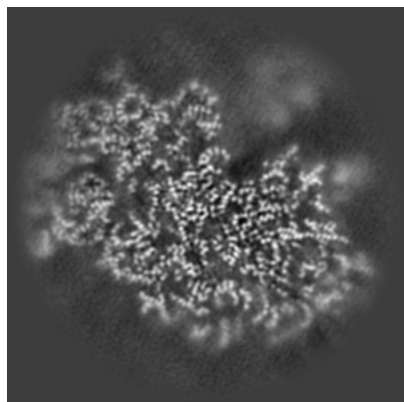
Z Index: 128

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

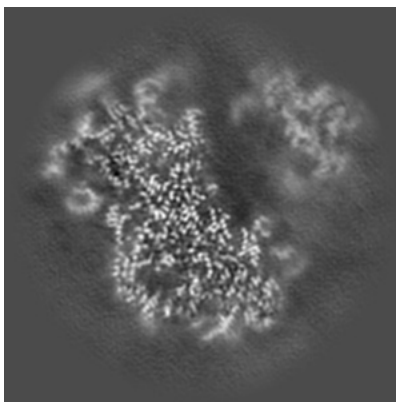


## 6.3 Largest variance slices [i](#)

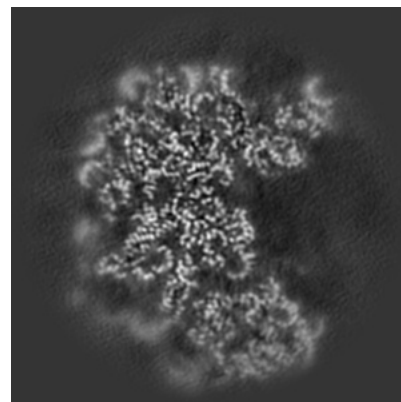
### 6.3.1 Primary map



X Index: 123

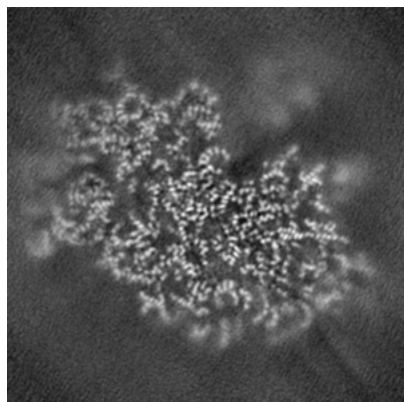


Y Index: 146

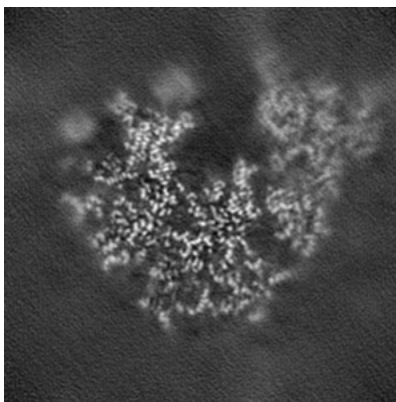


Z Index: 132

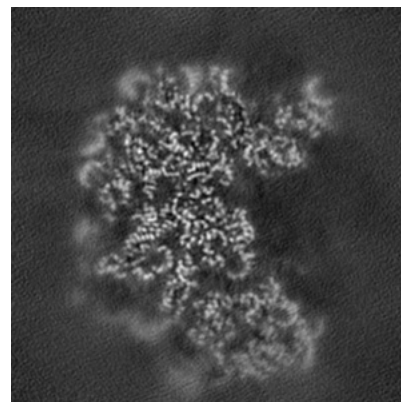
### 6.3.2 Raw map



X Index: 123



Y Index: 127

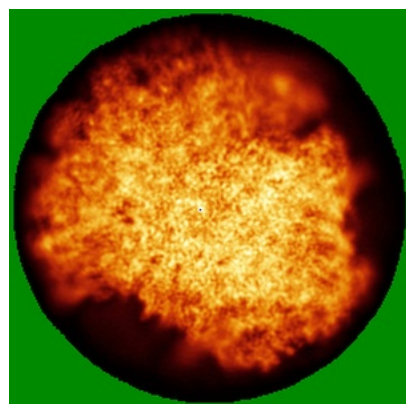


Z Index: 132

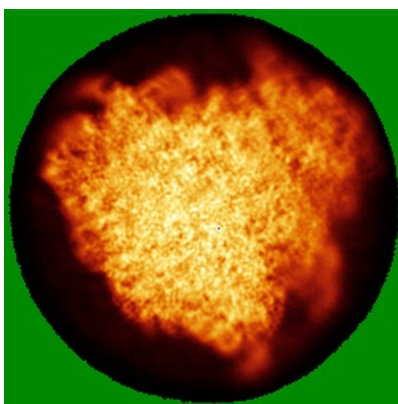
The images above show the largest variance slices of the map in three orthogonal directions.

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

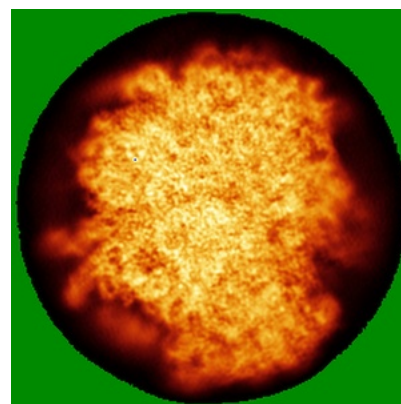
### 6.4.1 Primary map



X

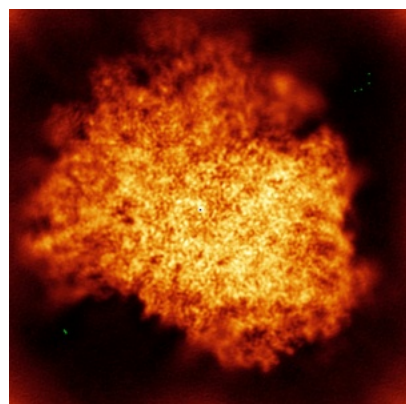


Y

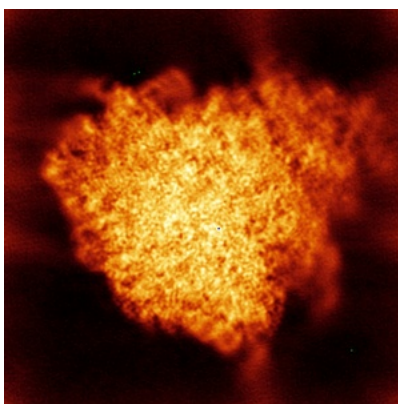


Z

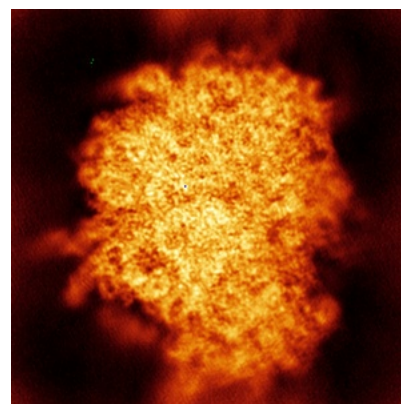
### 6.4.2 Raw map



X



Y

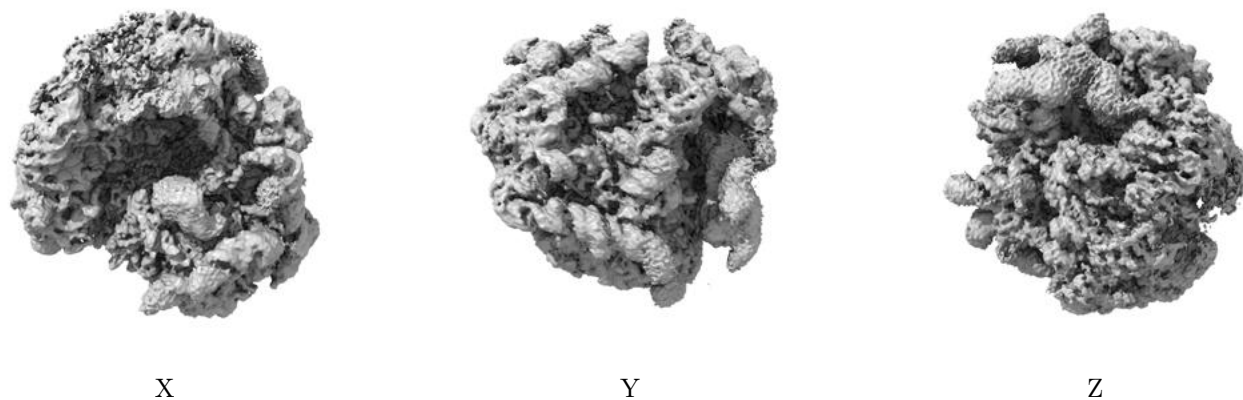


Z

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.

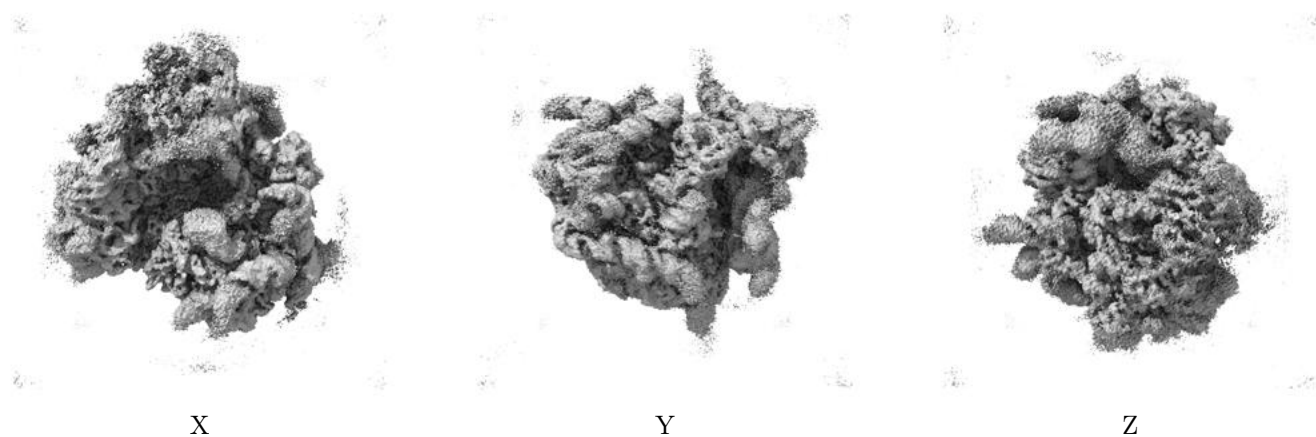
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

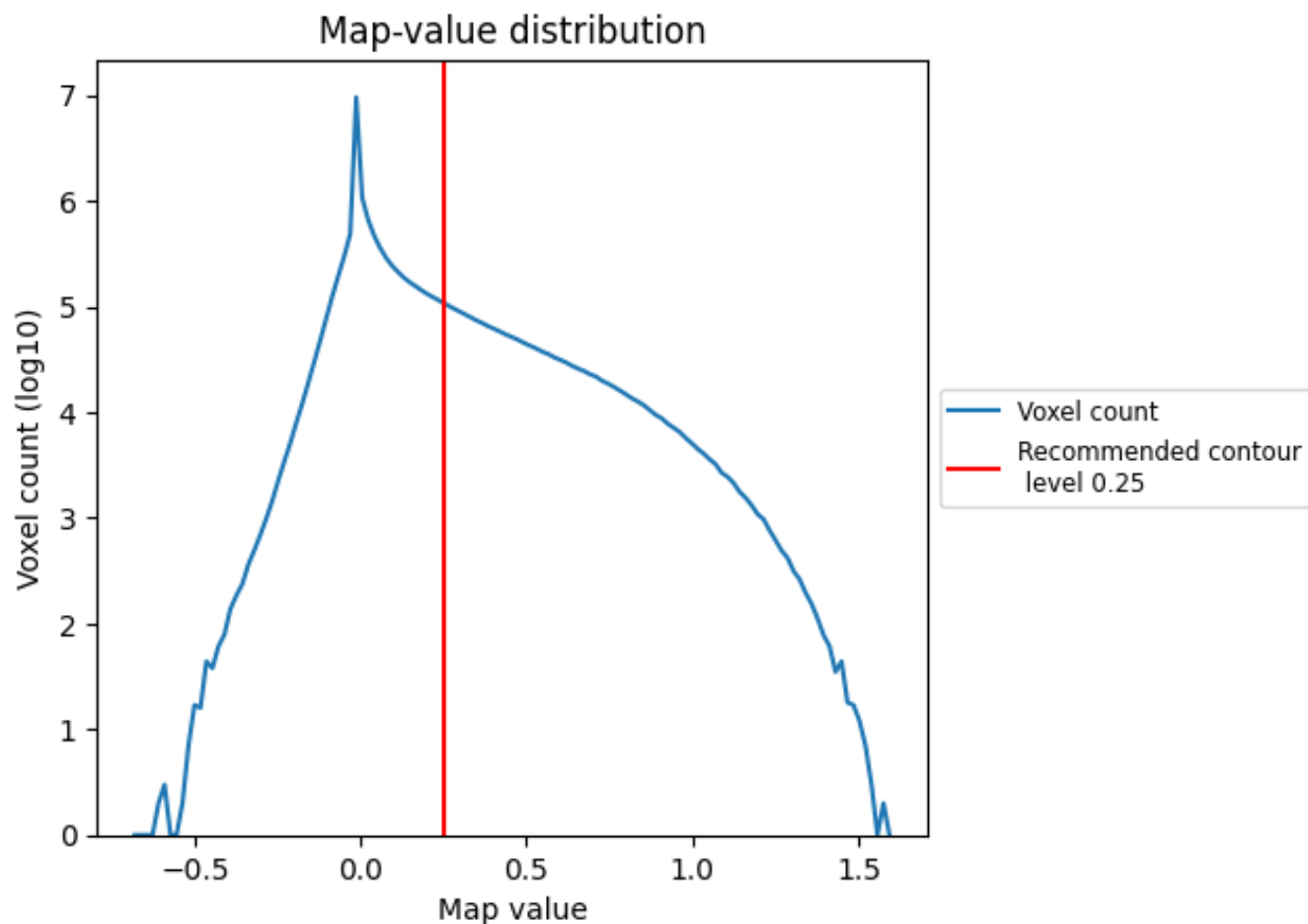
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

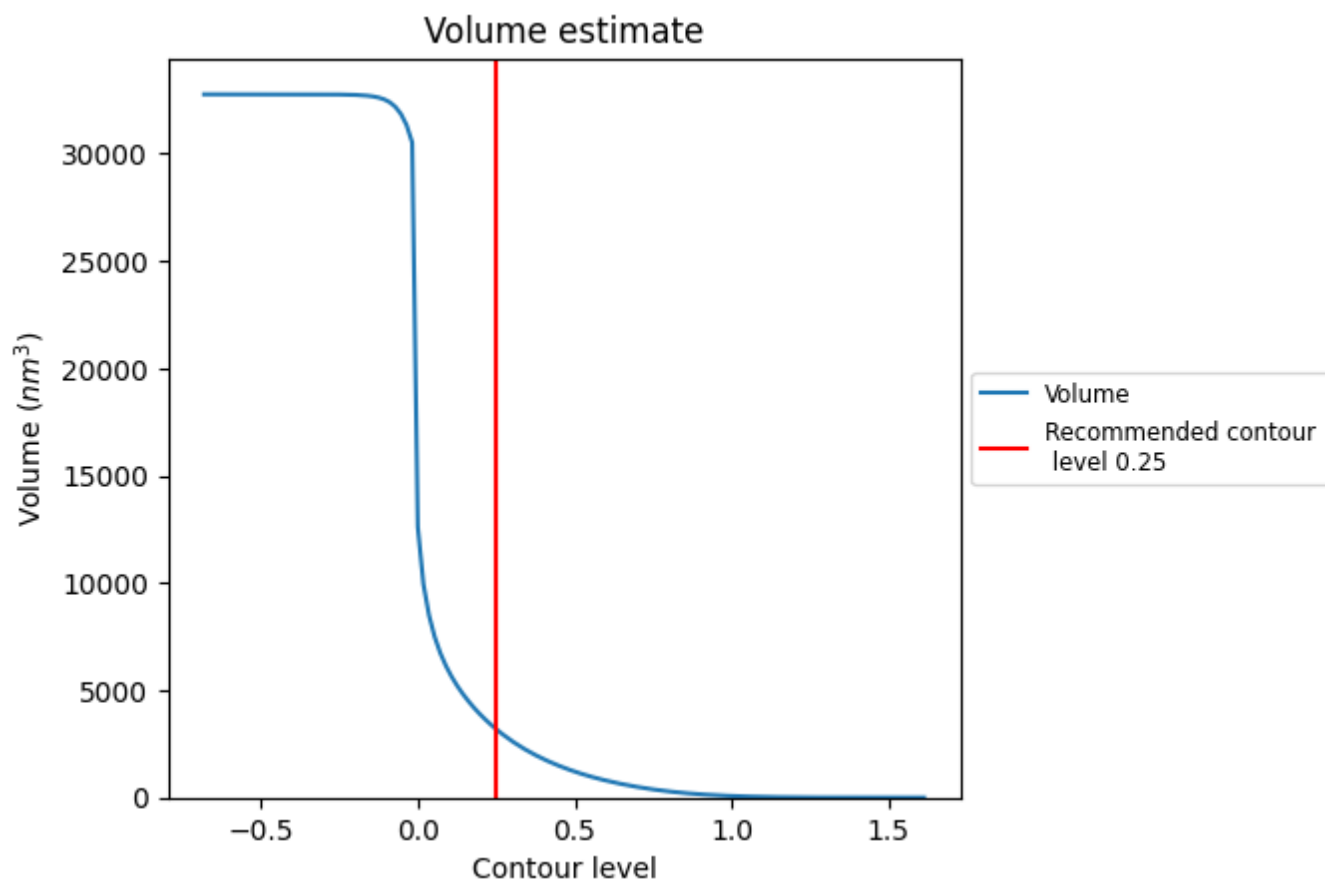
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

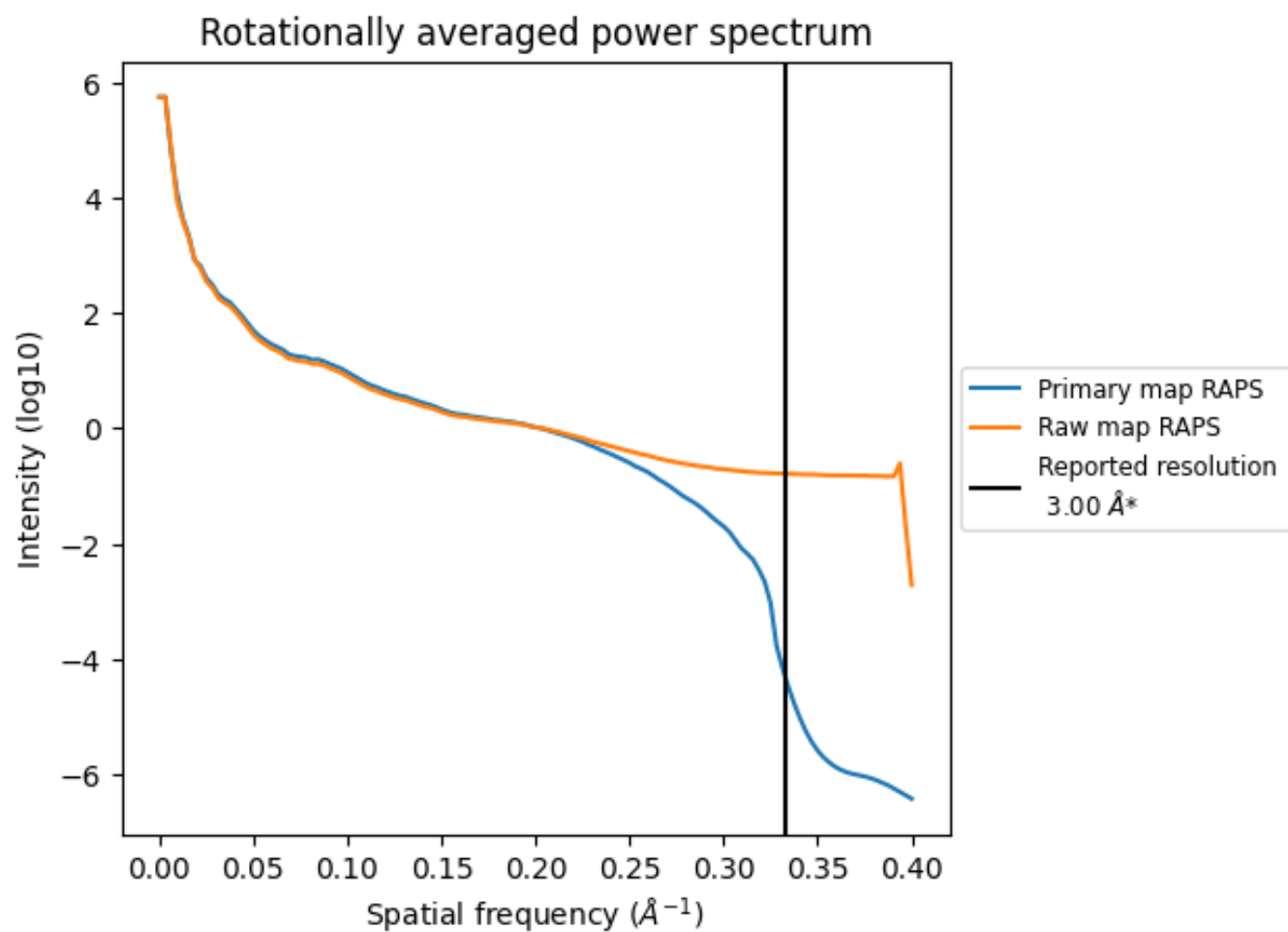
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3185  $\text{nm}^3$ ; this corresponds to an approximate mass of 2877 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 ⓘ

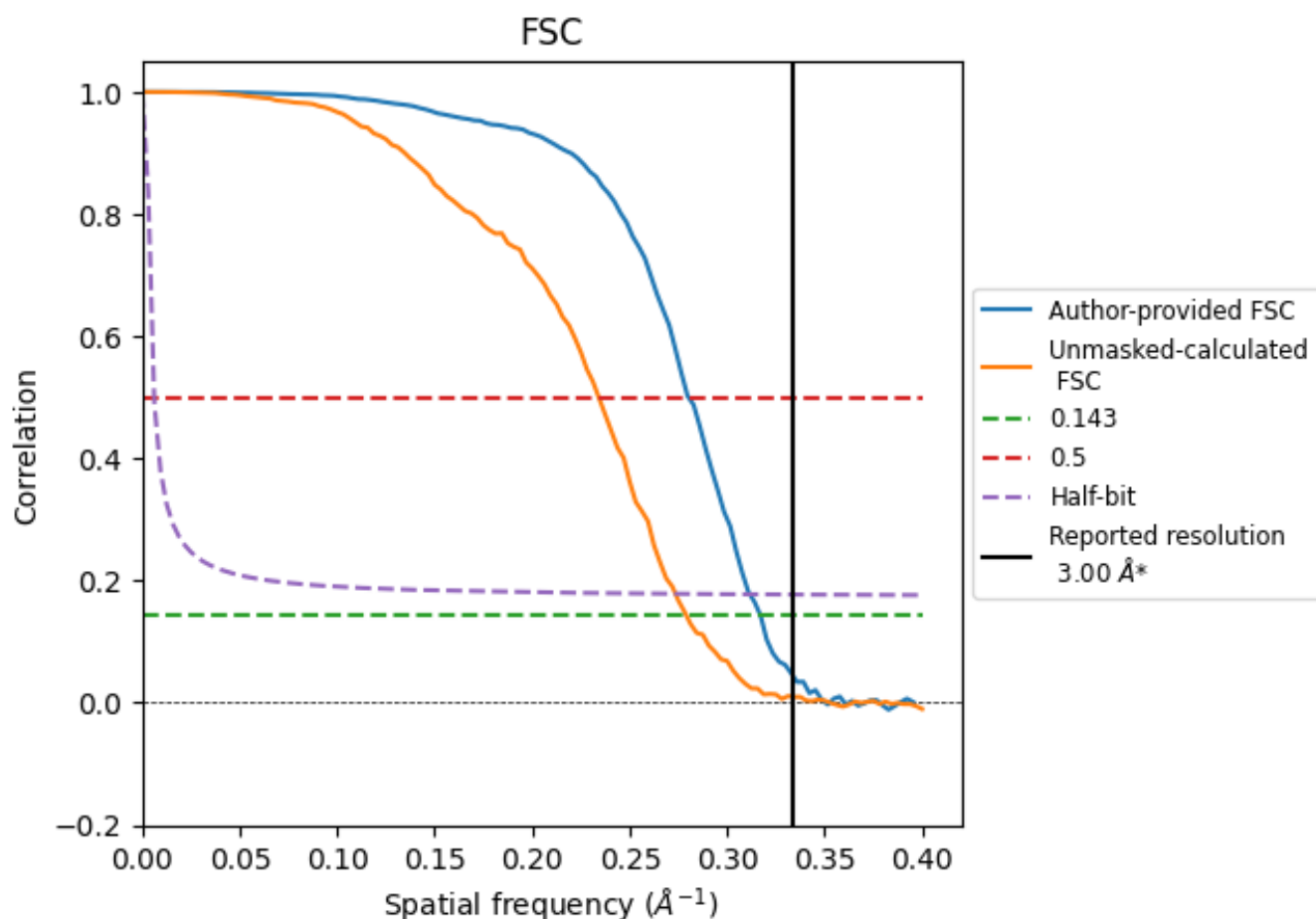


\*Reported resolution corresponds to spatial frequency of 0.333  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.333 \text{ \AA}^{-1}$



## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.15	3.57	3.21
Unmasked-calculated*	3.58	4.27	3.66

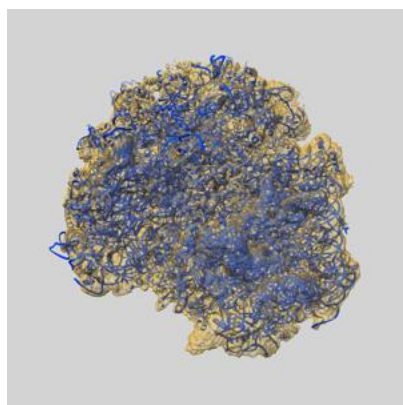
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.58 differs from the reported value 3.0 by more than 10 %



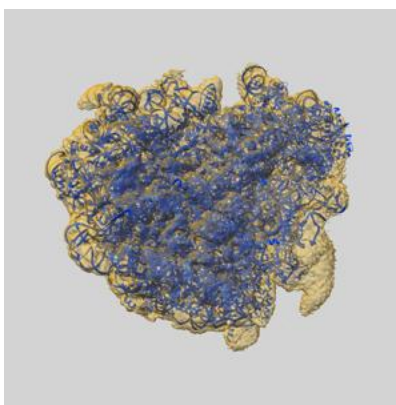
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72137 and PDB model 9Q1S. Per-residue inclusion information can be found in section [3](#) on page [20](#).

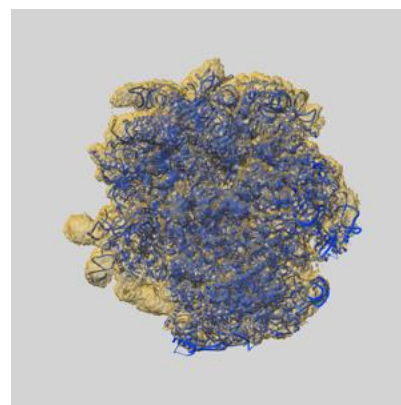
### 9.1 Map-model overlay [i](#)



X



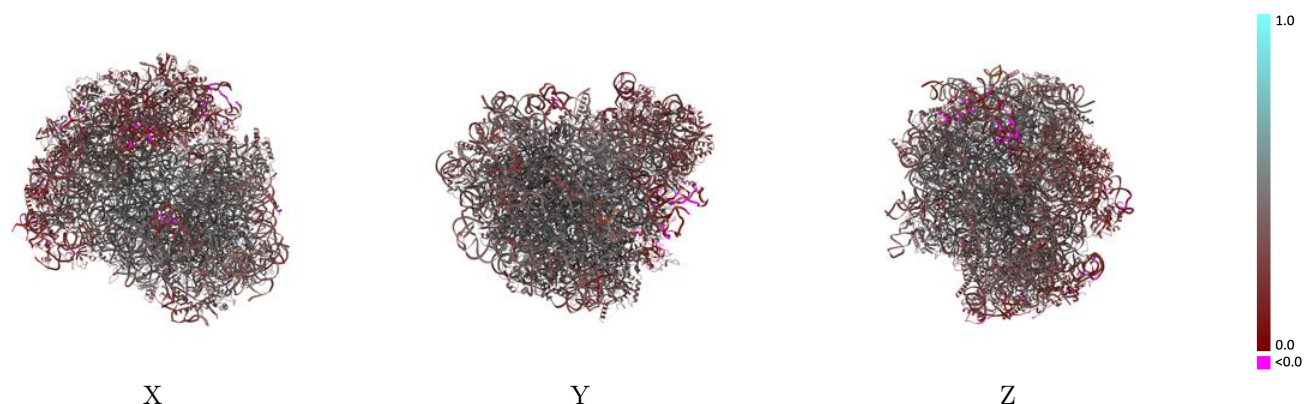
Y



Z

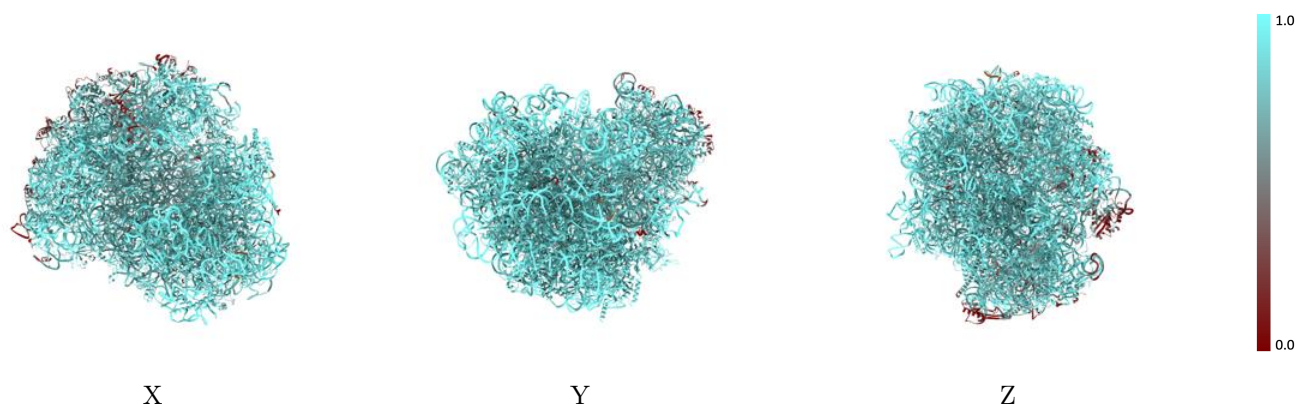
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



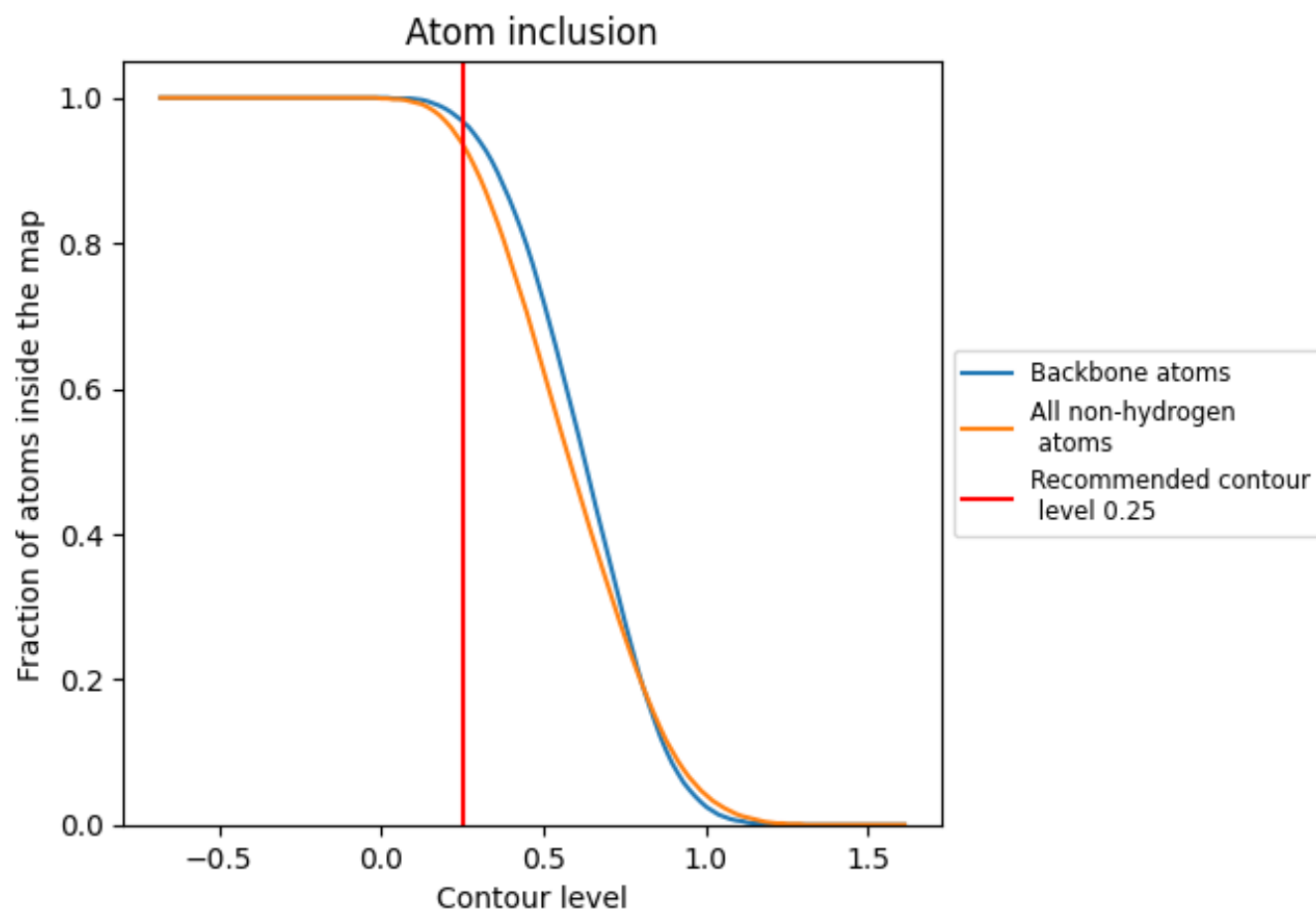
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9370	 0.3820
1	 0.9190	 0.1470
5	 0.9870	 0.4170
7	 0.9960	 0.4230
8	 0.9840	 0.4180
9	 0.9390	 0.3440
A	 0.9230	 0.4710
AA	 0.7620	 0.3390
B	 0.8940	 0.4450
BB	 0.9230	 0.3600
C	 0.9320	 0.4400
CC	 0.9240	 0.3540
D	 0.9710	 0.3820
DD	 0.6020	 0.2740
E	 0.9080	 0.3970
EE	 0.9260	 0.3580
F	 0.9080	 0.4260
FF	 0.9340	 0.3050
G	 0.9240	 0.3630
GG	 0.8140	 0.2160
H	 0.9250	 0.4070
HH	 0.6400	 0.3220
I	 0.9060	 0.4240
II	 0.9190	 0.3670
J	 0.9000	 0.3390
JJ	 0.9060	 0.2460
K	 0.9040	 0.1580
KK	 0.4810	 0.2070
L	 0.9200	 0.4120
LL	 0.8640	 0.4000
M	 0.9550	 0.3890
N	 0.9440	 0.4520
NN	 0.9200	 0.3920
O	 0.8780	 0.4220
OO	 0.9440	 0.3640







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Chain	Atom inclusion	Q-score
P	 0.9420	 0.4550
PP	 0.9290	 0.2510
Q	 0.9230	 0.4480
QQ	 0.6900	 0.2830
R	 0.9170	 0.3970
RR	 0.6350	 0.3010
S	 0.9330	 0.4230
SS	 0.8980	 0.2700
T	 0.9100	 0.4300
TT	 0.7940	 0.2600
U	 0.9940	 0.3710
UU	 0.7070	 0.2840
V	 0.8150	 0.4320
VV	 0.7380	 0.3370
W	 0.8070	 0.3390
WW	 0.8940	 0.3910
X	 0.9170	 0.4170
XX	 0.8640	 0.3730
Y	 0.9580	 0.4100
YY	 0.8830	 0.1770
Z	 0.9800	 0.3990
ZZ	 0.9020	 0.2570
a	 0.9590	 0.4590
aa	 0.9280	 0.3790
b	 0.8750	 0.3660
bb	 0.9010	 0.3500
c	 0.9570	 0.3960
cc	 0.9550	 0.3530
d	 0.9250	 0.4250
dd	 0.8240	 0.2090
e	 0.9040	 0.4640
ee	 0.8550	 0.2660
f	 0.9060	 0.4610
g	 0.9220	 0.4290
h	 0.9300	 0.3900
i	 0.9460	 0.4130
j	 0.9260	 0.4650
k	 0.9530	 0.3910
l	 0.8650	 0.4170
m	 0.9740	 0.4270
n	 0.8900	 0.4140
o	 0.8990	 0.4480

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Chain	Atom inclusion	Q-score
p	 0.9140	 0.4390
r	 0.9110	 0.4230