



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 06:12 PM EDT

PDB ID : 9Q2M / pdb_00009q2m
EMDB ID : EMD-72168
Title : Rabbit ribosomal 80S elongation complex with eEF2, partial P site Ala-tRNA, E site Ala-tRNA on NediV ORF
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 : 2025-08-15
Resolution : 3.30 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
Mogul : 2022.3.0, CSD as543be (2022)
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

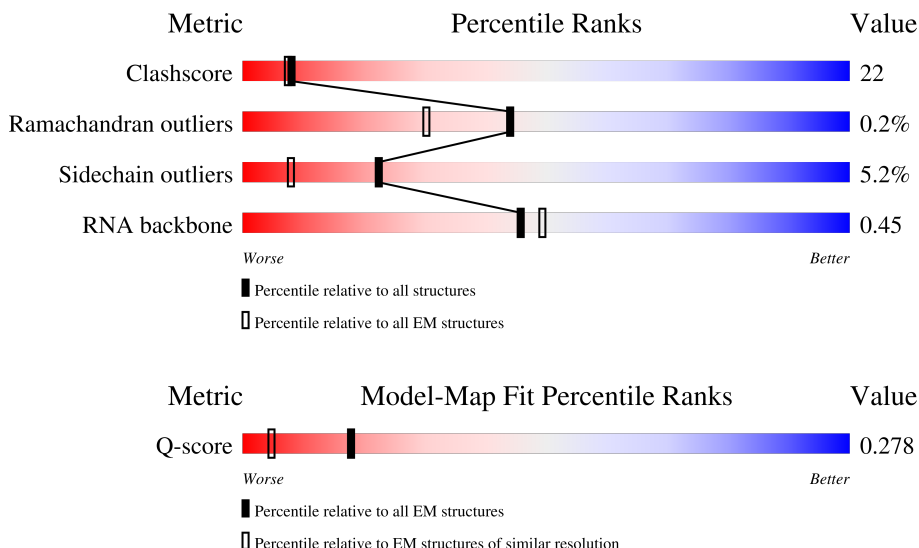
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.




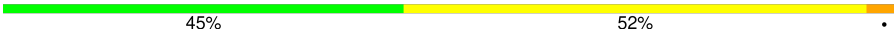


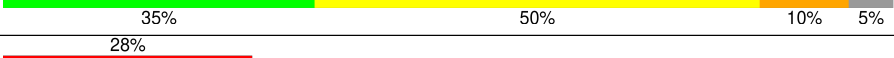
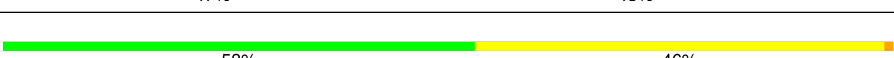
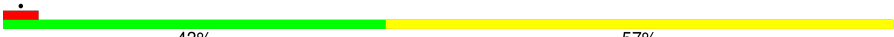
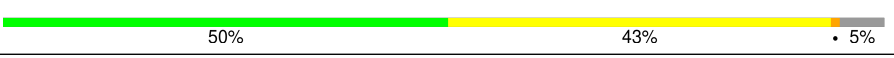

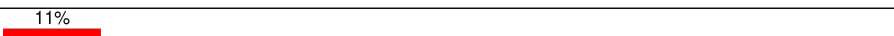
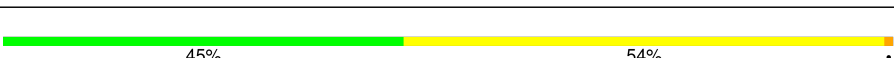
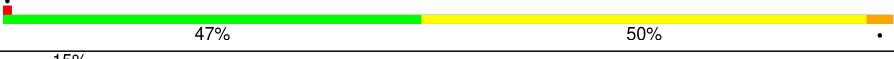




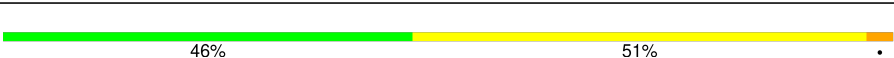
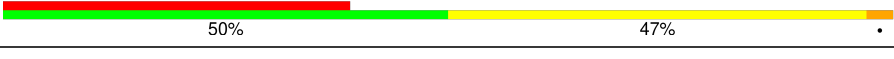





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	R	180	
2	W	106	
3	9	1670	



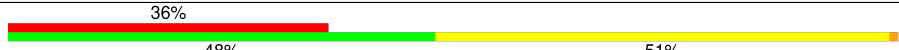
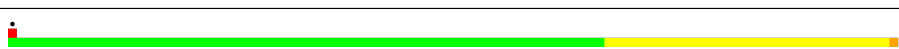

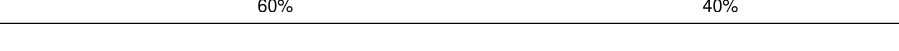
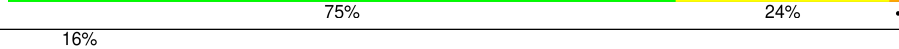

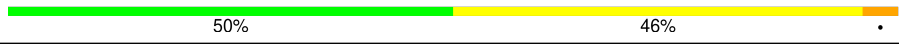




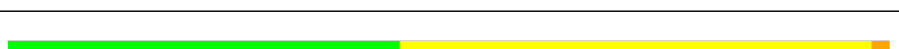

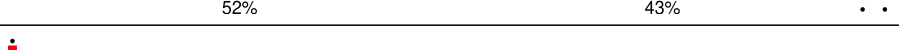


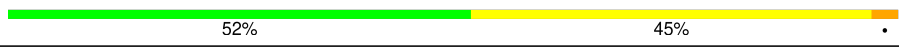



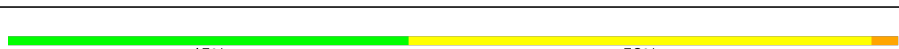

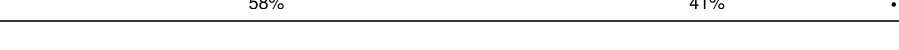
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Mol	Chain	Length	Quality of chain
4	AA	217	
5	BB	213	
6	CC	221	
7	EE	262	
8	GG	237	
9	HH	189	
10	II	206	
11	JJ	185	
12	LL	151	
13	NN	149	
14	OO	136	
15	VV	83	
16	WW	129	
17	XX	141	
18	YY	124	
19	aa	101	
20	bb	83	
21	ee	57	
22	DD	228	
23	FF	191	
24	KK	96	
25	MM	117	
26	PP	115	
27	QQ	141	
28	RR	132	




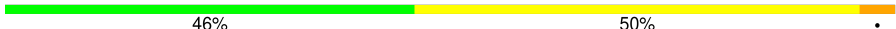


















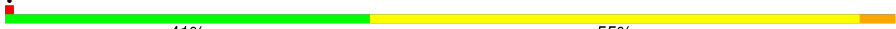


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Mol	Chain	Length	Quality of chain
29	SS	144	
30	TT	141	
31	UU	100	
32	ZZ	75	
33	cc	62	
34	dd	55	
35	ff	68	
36	A	248	
37	B	394	
38	C	362	
39	D	293	
40	E	216	
41	F	225	
42	G	240	
43	H	190	
44	I	213	
45	J	170	
46	L	210	
47	M	138	
48	N	203	
49	O	199	
50	P	153	
51	Q	187	
52	S	176	
53	T	159	



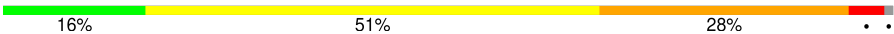
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Mol	Chain	Length	Quality of chain
54	U	99	
55	V	139	
56	X	118	
57	Y	134	
58	Z	135	
59	a	147	
60	b	104	
61	c	98	
62	d	107	
63	e	128	
64	f	109	
65	g	114	
66	h	122	
67	i	102	
68	j	86	
69	k	69	
70	l	50	
71	m	52	
72	n	25	
73	o	104	
74	p	91	
75	r	124	
76	s	196	
77	t	153	
78	5	3543	

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Mol	Chain	Length	Quality of chain
79	7	119	
80	8	156	
81	EF	855	
82	1	11	
83	PT	11	
84	ET	76	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 223342 atoms, of which 6717 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 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	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 2 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 3 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	9	1670	Total	C	N	O	P	0	0
			35655	15916	6405	11665	1669		

- Molecule 4 is a protein called 40S_SA_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	209	Total	C	N	O	S	0	0
			1650	1051	290	301	8		

- Molecule 5 is a protein called 40S ribosomal protein S3a.

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

- Molecule 6 is a protein called 40S ribosomal protein S2.

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

- Molecule 7 is a protein called 40S ribosomal protein S4.

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

- Molecule 8 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GG	226	Total	C	N	O	S	0	0
			1831	1144	365	315	7		

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

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

- Molecule 10 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	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 11 is a protein called 40S ribosomal protein S9.

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

- Molecule 12 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 13 is a protein called 40S ribosomal protein S13.

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

- Molecule 14 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 15 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	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
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 16 is a protein called 40S ribosomal protein S15a.

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

- Molecule 17 is a protein called 40S ribosomal protein S23.

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

- Molecule 18 is a protein called 40S ribosomal protein S24.

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

- Molecule 19 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	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 20 is a protein called 40S ribosomal protein S27.

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

- Molecule 21 is a protein called Small ribosomal subunit protein eS30.

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

- Molecule 22 is a protein called 40S ribosomal protein S3.

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

- Molecule 23 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 24 is a protein called 40S ribosomal protein S10.

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

- Molecule 25 is a protein called 40S ribosomal protein S12.

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

- Molecule 26 is a protein called Small ribosomal subunit protein uS19.

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

- Molecule 27 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	QQ	141	Total	C	N	O	S	0	0
			1116	711	209	193	3		

- Molecule 28 is a protein called 40S ribosomal protein S17.

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

- Molecule 29 is a protein called 40S ribosomal protein S18.

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

- Molecule 30 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	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 31 is a protein called 40S ribosomal protein S20.

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

- Molecule 32 is a protein called 40S ribosomal protein S25.

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

- Molecule 33 is a protein called 40S ribosomal protein S28.

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

- Molecule 34 is a protein called 40S ribosomal protein S29.

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

- Molecule 35 is a protein called 40S ribosomal protein S27a.

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

- Molecule 36 is a protein called 60S ribosomal protein L8.

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

- Molecule 37 is a protein called 60S ribosomal protein L3.

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

- Molecule 38 is a protein called 60S ribosomal protein L4.

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

- Molecule 39 is a protein called 60S ribosomal protein L5.

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

- Molecule 40 is a protein called 60S ribosomal protein L6.

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

- Molecule 41 is a protein called 60S ribosomal protein L7.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	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 43 is a protein called 60S ribosomal protein L9.

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

- Molecule 44 is a protein called Ribosomal protein L10.

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

- Molecule 45 is a protein called 60S ribosomal protein L11.

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

- Molecule 46 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	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 47 is a protein called 60S ribosomal protein L14.

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

- Molecule 48 is a protein called 60S ribosomal protein L15.

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

- Molecule 49 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 50 is a protein called 60S ribosomal protein L17.

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

- Molecule 51 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	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
Q	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 52 is a protein called eL20.

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

- Molecule 53 is a protein called 60S ribosomal protein L21.

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

- Molecule 54 is a protein called Large ribosomal subunit protein eL22.

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

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1

- Molecule 55 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 56 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 57 is a protein called 60S ribosomal protein L26.

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

- Molecule 58 is a protein called 60S ribosomal protein L27.

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

- Molecule 59 is a protein called 60S ribosomal protein L27a.

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

- Molecule 60 is a protein called eL29.

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

- Molecule 61 is a protein called 60S ribosomal protein L30.

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

- Molecule 62 is a protein called 60S ribosomal protein L31.

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

- Molecule 63 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	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

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Chain	Residue	Modelled	Actual	Comment	Reference
e	98	GLU	LYS	conflict	UNP G1TUN8
e	108	ARG	CYS	conflict	UNP G1TUN8
e	115	ALA	VAL	conflict	UNP G1TUN8

- Molecule 64 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 65 is a protein called 60S ribosomal protein L34.

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

- Molecule 66 is a protein called 60S ribosomal protein L35.

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

- Molecule 67 is a protein called 60S ribosomal protein L36.

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

- Molecule 68 is a protein called 60S ribosomal protein L37.

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

- Molecule 69 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	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 70 is a protein called 60S ribosomal protein L39.

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

- Molecule 71 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 72 is a protein called eL41.

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

- Molecule 73 is a protein called eL42.

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

- Molecule 74 is a protein called 60S ribosomal protein L37a.

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

- Molecule 75 is a protein called 60S ribosomal protein L28.

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

- Molecule 76 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 77 is a protein called uL11.

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

- Molecule 78 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	5	3512	Total	C	N	O	P	0	0
			75293	33533	13777	24471	3512		

- Molecule 79 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	7	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

- Molecule 80 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 81 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	EF	835	Total	C	H	N	O	S	0	0
			13123	4144	6607	1117	1211	44		

- Molecule 82 is a RNA chain called NediV ORF.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	1	11	Total	C	H	N	O	P	0	0
			339	103	110	39	76	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
83	PT	11	Total	C	N	O	P	0	0
			233	104	40	78	11		

- Molecule 84 is a RNA chain called E site Ala-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	ET	75	Total	C	N	O	P	0	0
			1595	712	285	524	74		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	aa	1	Total	Mg	0
			1	1	
85	A	1	Total	Mg	0
			1	1	
85	P	1	Total	Mg	0
			1	1	
85	V	1	Total	Mg	0
			1	1	
85	g	1	Total	Mg	0
			1	1	
85	5	190	Total	Mg	0
			190	190	
85	7	6	Total	Mg	0
			6	6	
85	8	4	Total	Mg	0
			4	4	
85	EF	1	Total	Mg	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
86	aa	1	Total	Zn	0
			1	1	
86	dd	1	Total	Zn	0
			1	1	
86	ff	1	Total	Zn	0
			1	1	
86	g	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	j	1	Total 1	Zn 1	0
86	m	1	Total 1	Zn 1	0
86	o	1	Total 1	Zn 1	0
86	p	1	Total 1	Zn 1	0

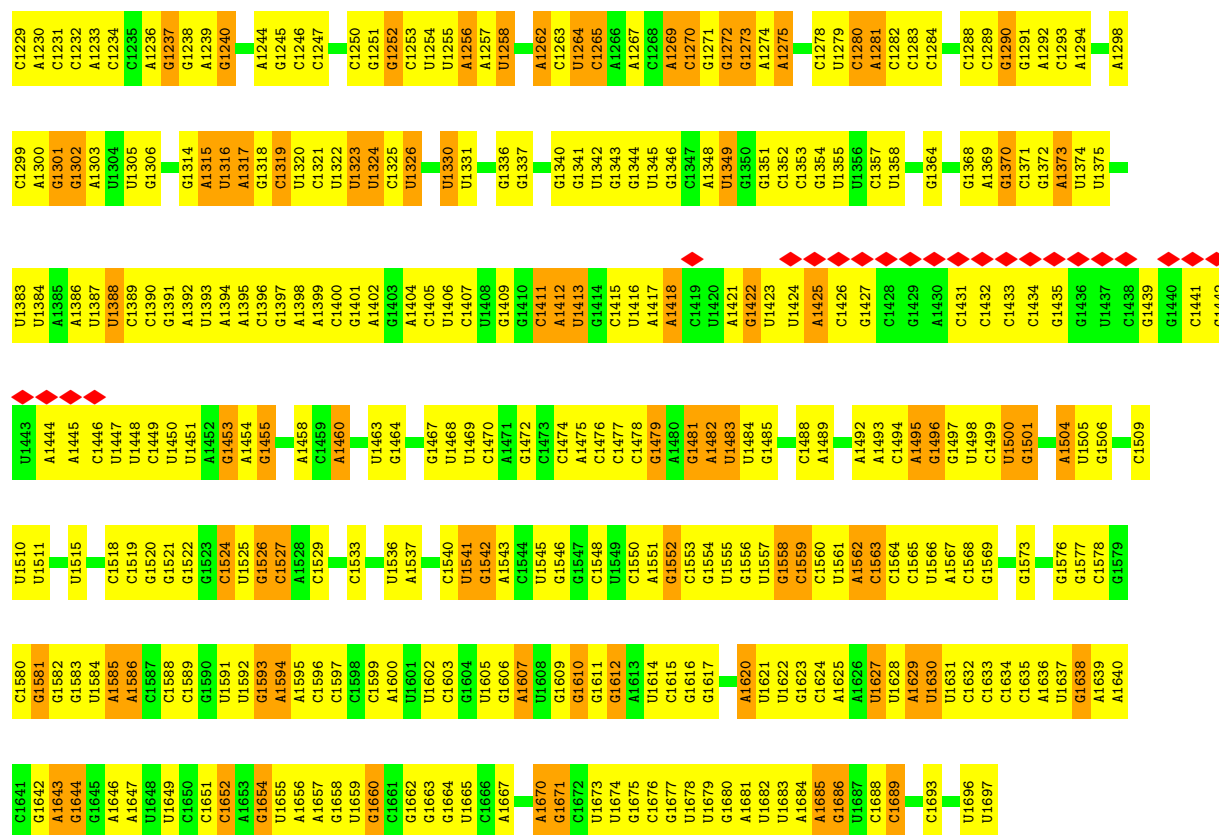
3 Residue-property plots [i](#)

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.

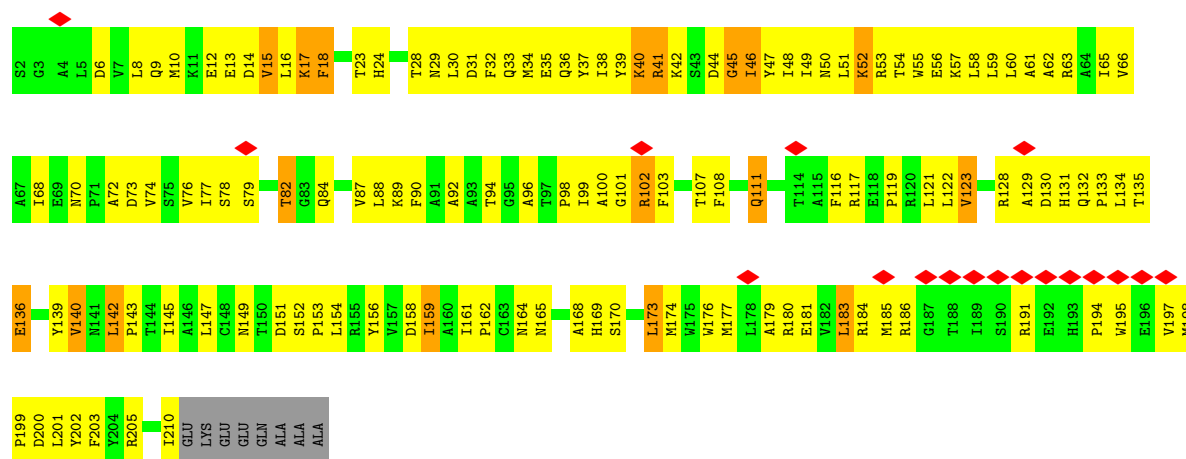
• Molecule 1: 60S ribosomal protein L19





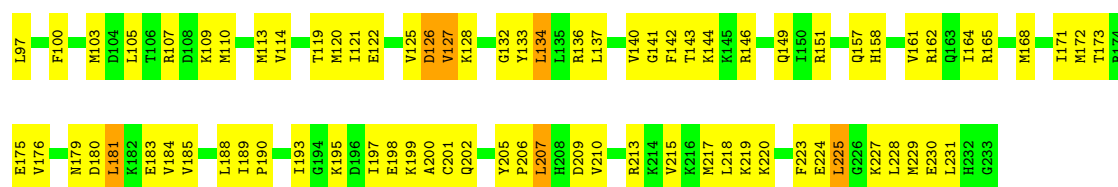


• Molecule 4: 40S_SA_C domain-containing protein

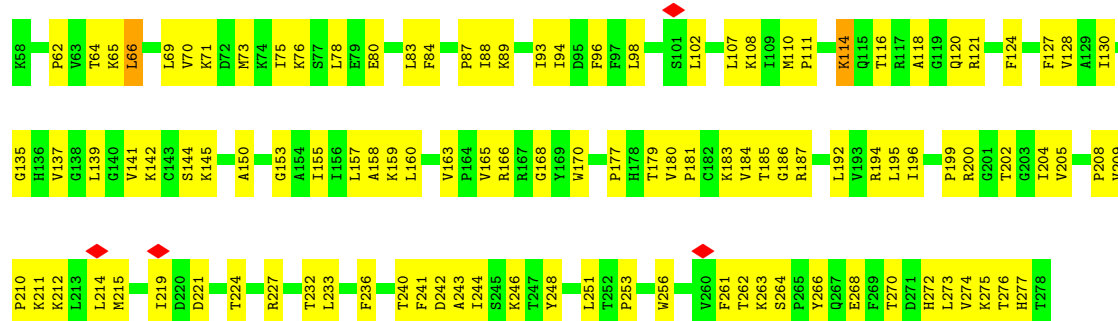


• Molecule 5: 40S ribosomal protein S3a

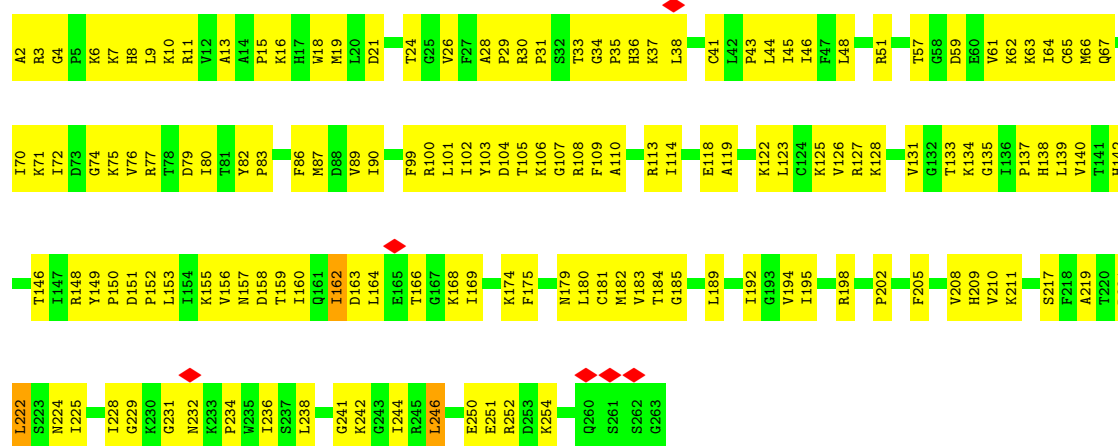




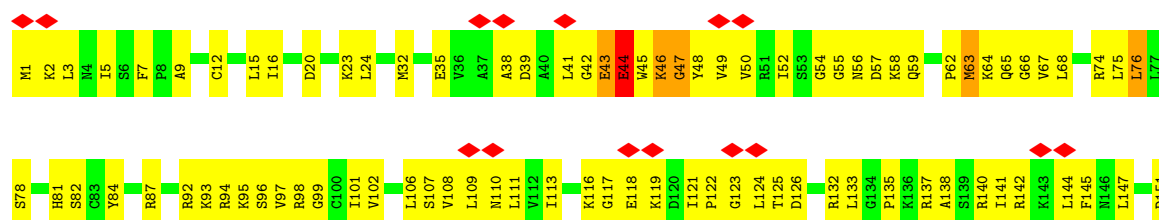
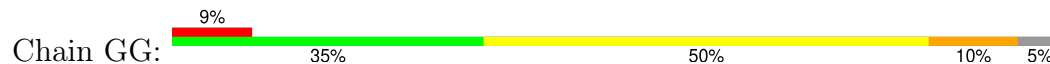
• Molecule 6: 40S ribosomal protein S2

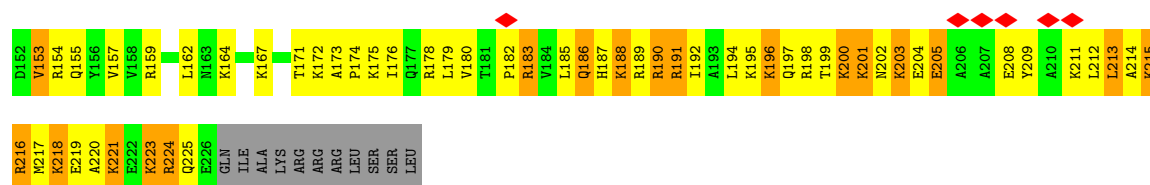


• Molecule 7: 40S ribosomal protein S4

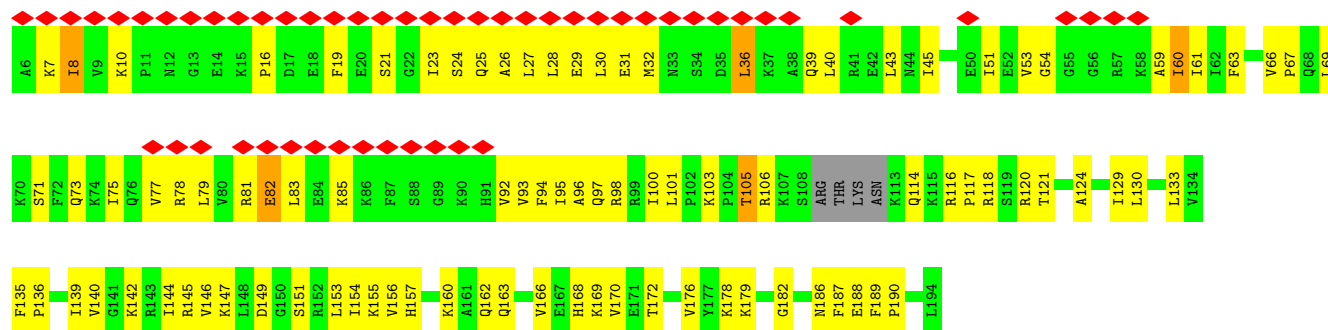


• Molecule 8: 40S ribosomal protein S6





• Molecule 9: Small ribosomal subunit protein eS7




• Molecule 10: 40S ribosomal protein S8

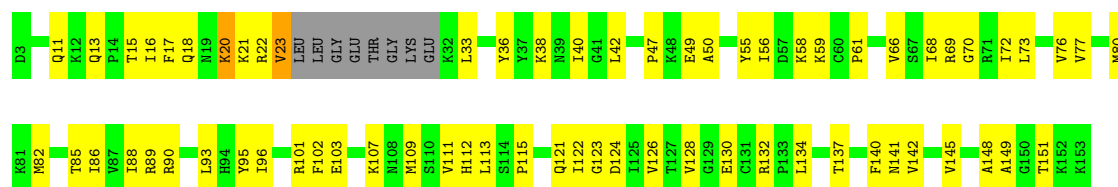


• Molecule 11: 40S ribosomal protein S9



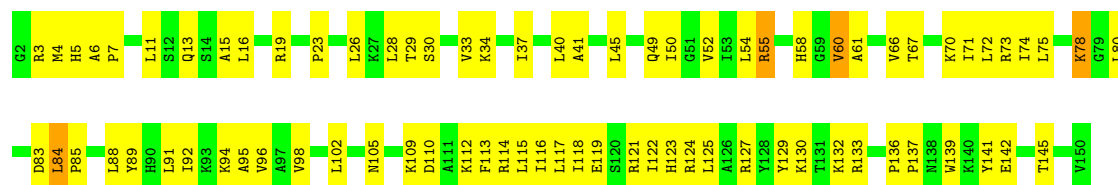
• Molecule 12: Small ribosomal subunit protein uS17

Chain LL: 



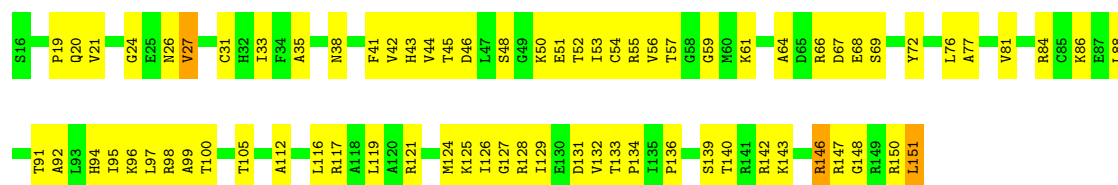
- Molecule 13: 40S ribosomal protein S13

Chain NN: 



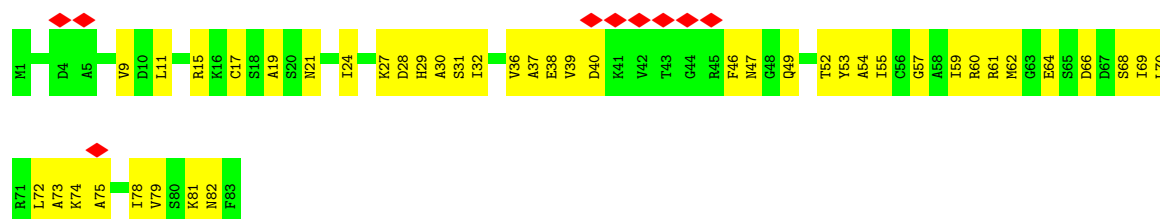
- Molecule 14: Small ribosomal subunit protein uS11

Chain OO: 



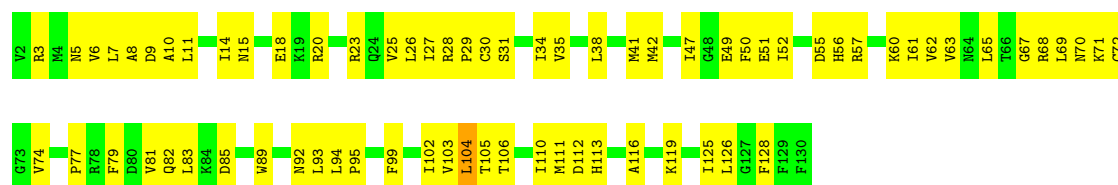
- Molecule 15: eS21

Chain VV: 

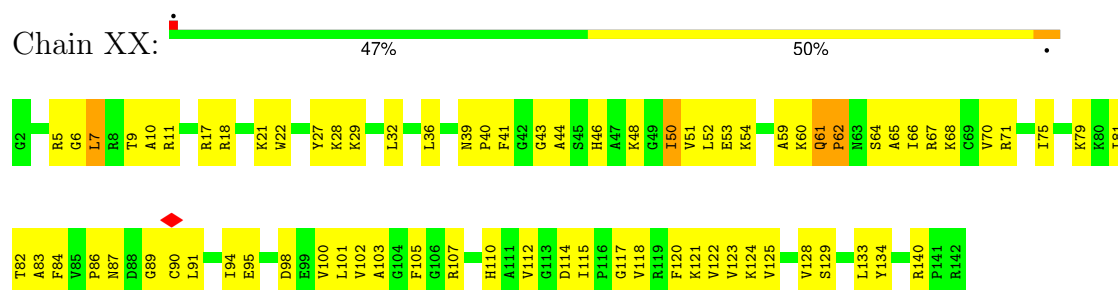


- Molecule 16: 40S ribosomal protein S15a

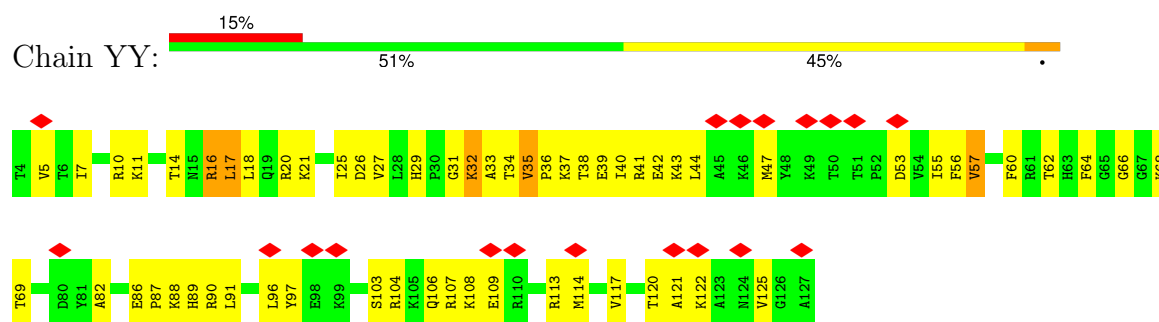
Chain WW: 



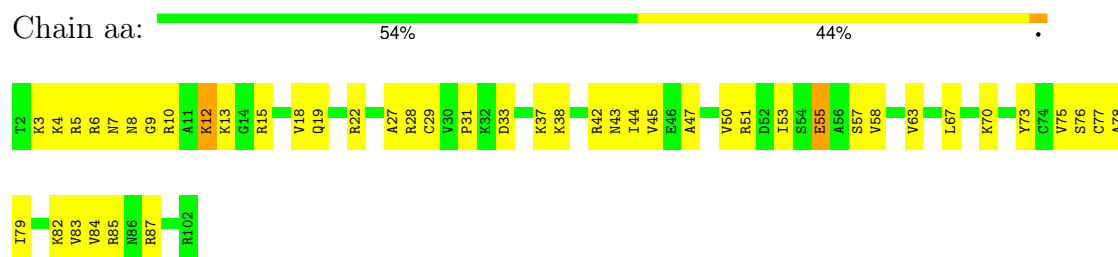
- Molecule 17: 40S ribosomal protein S23



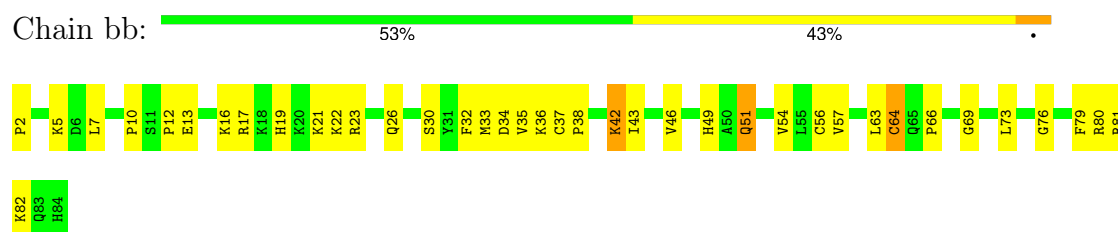
- Molecule 18: 40S ribosomal protein S24



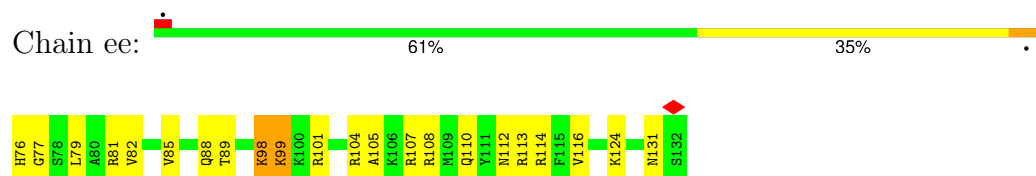
- Molecule 19: eS26



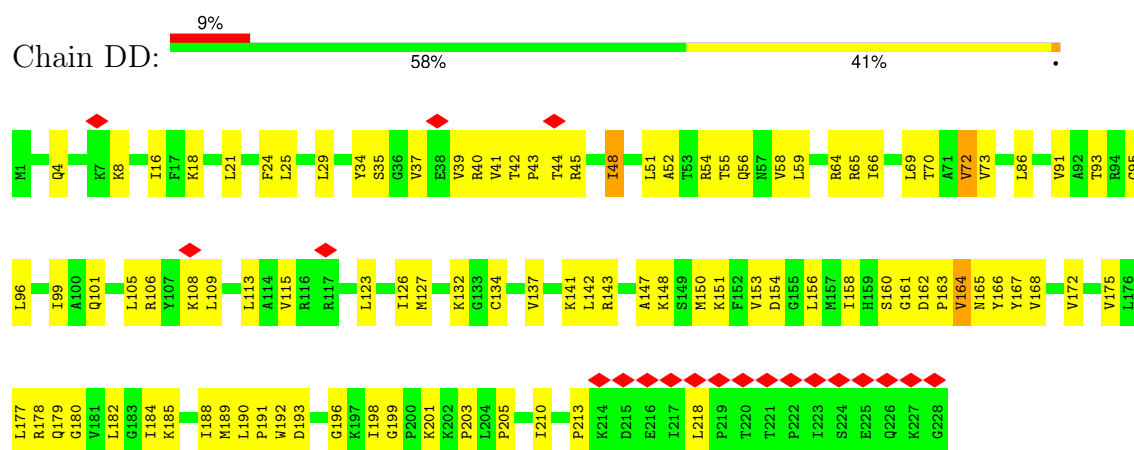
- Molecule 20: 40S ribosomal protein S27



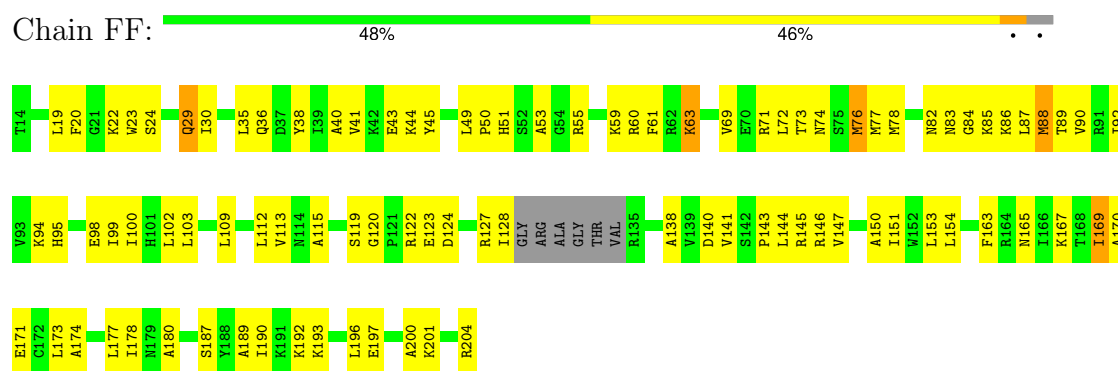
- Molecule 21: Small ribosomal subunit protein eS30



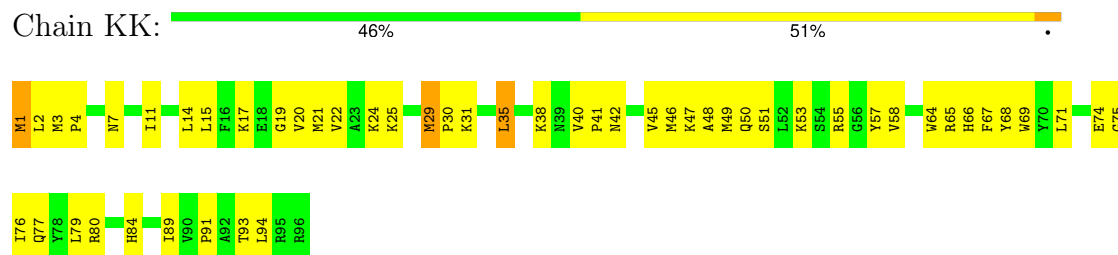
- Molecule 22: 40S ribosomal protein S3



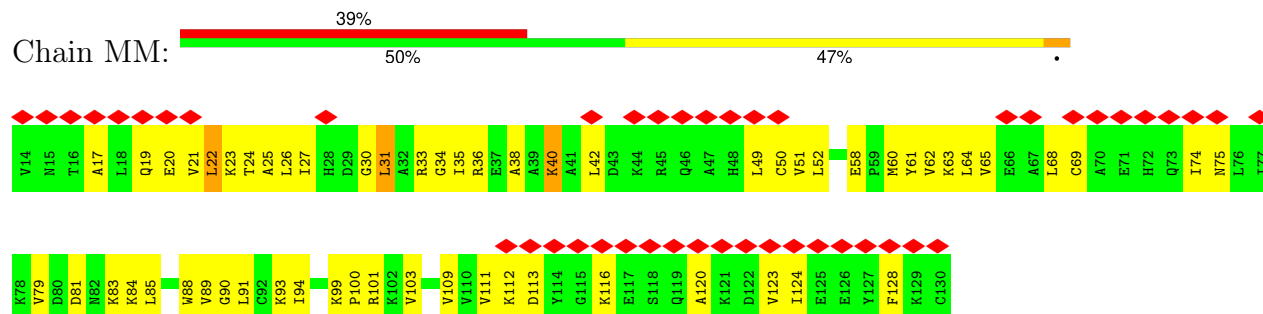
• Molecule 23: Small ribosomal subunit protein uS7



• Molecule 24: 40S ribosomal protein S10

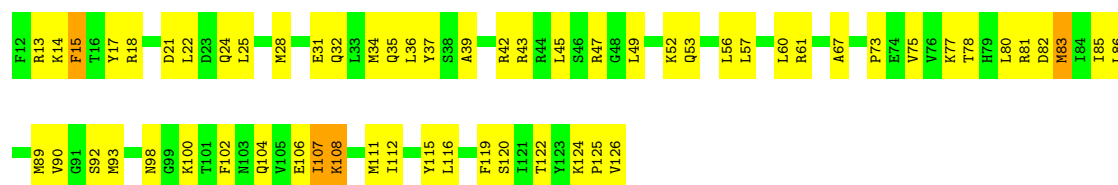


• Molecule 25: 40S ribosomal protein S12



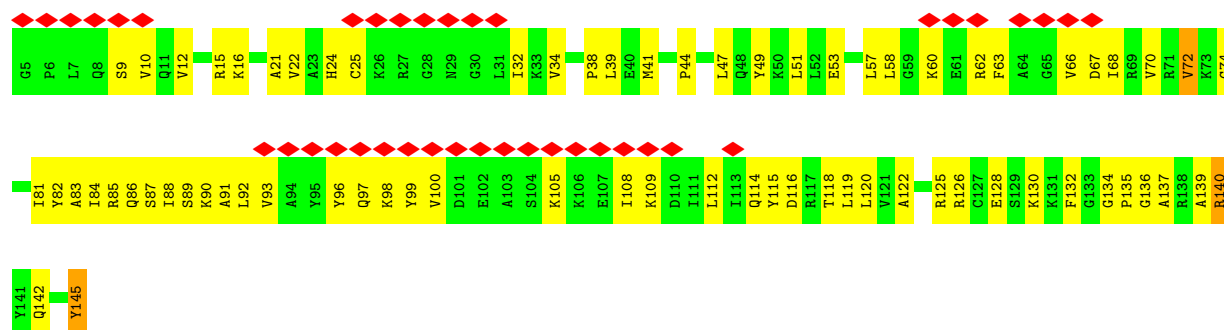
• Molecule 26: Small ribosomal subunit protein uS19

Chain PP: 




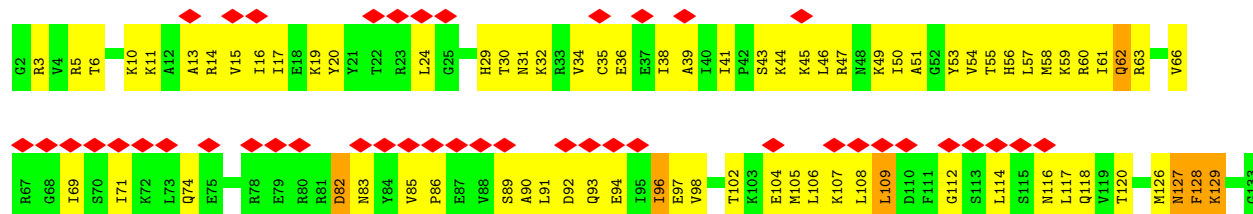
- Molecule 27: Small ribosomal subunit protein uS9

Chain QQ: 



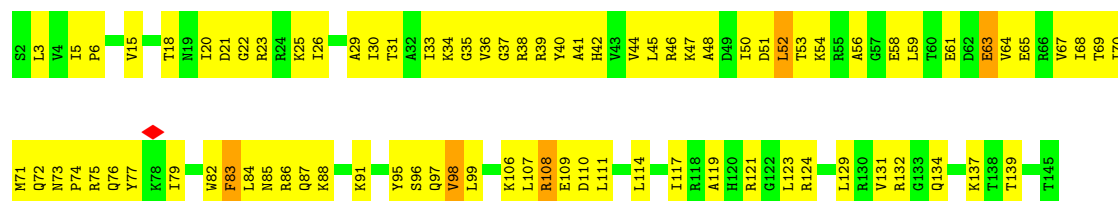
- Molecule 28: 40S ribosomal protein S17

Chain RR: 



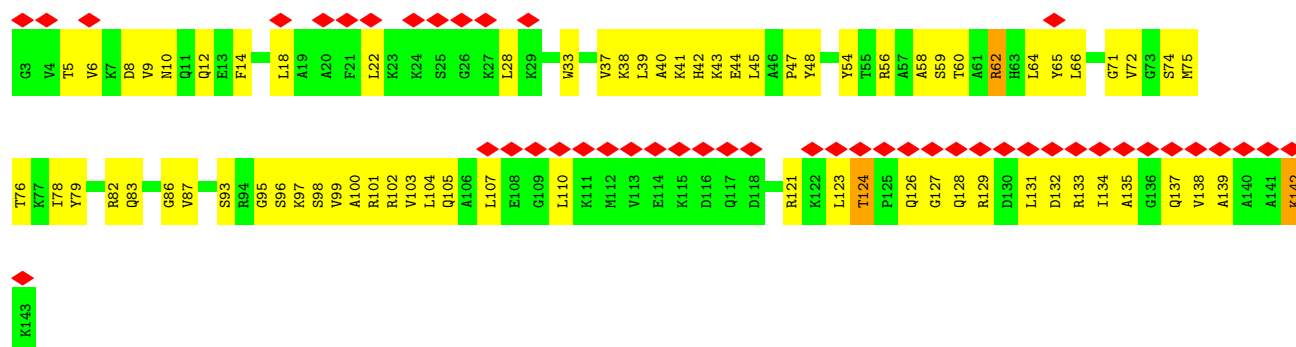
- Molecule 29: 40S ribosomal protein S18

Chain SS: 

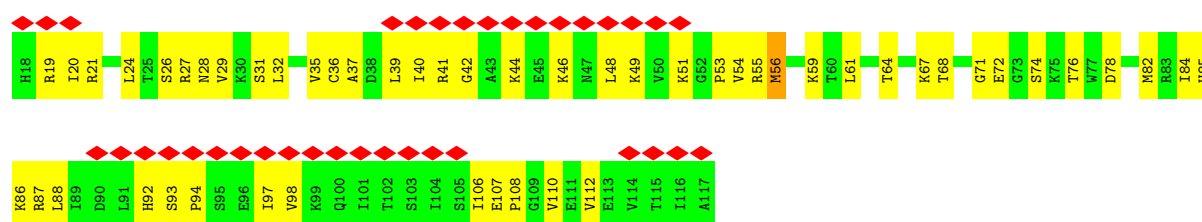


- Molecule 30: Small ribosomal subunit protein eS19

Chain TT: 



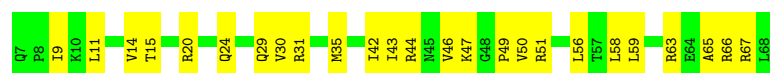
- Molecule 31: 40S ribosomal protein S20



- Molecule 32: 40S ribosomal protein S25



- Molecule 33: 40S ribosomal protein S28



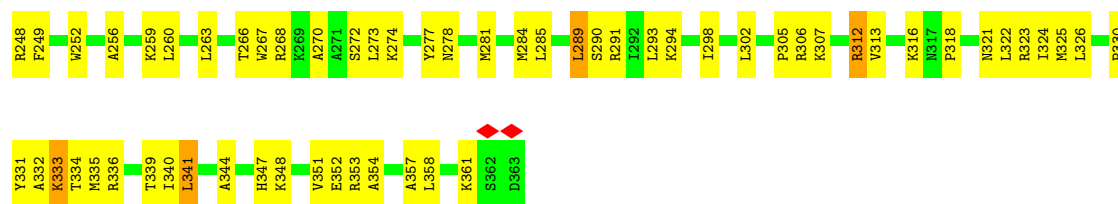
- Molecule 34: 40S ribosomal protein S29



- Molecule 35: 40S ribosomal protein S27a

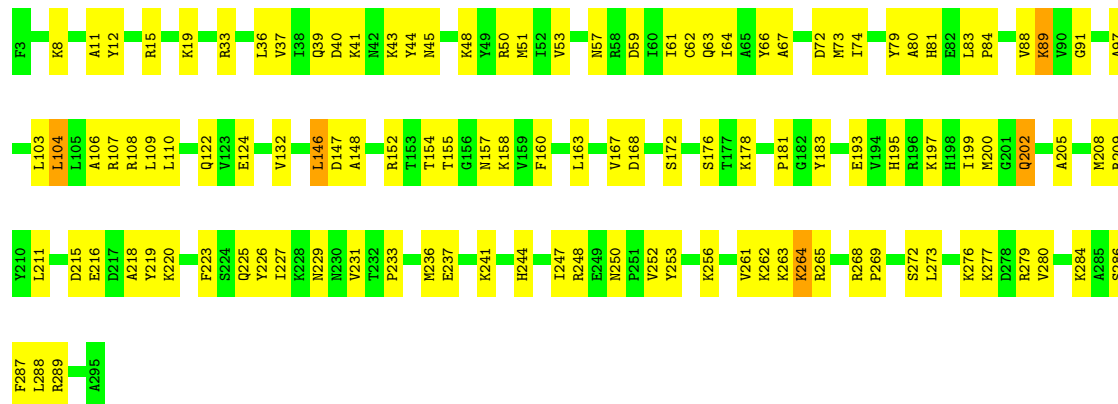






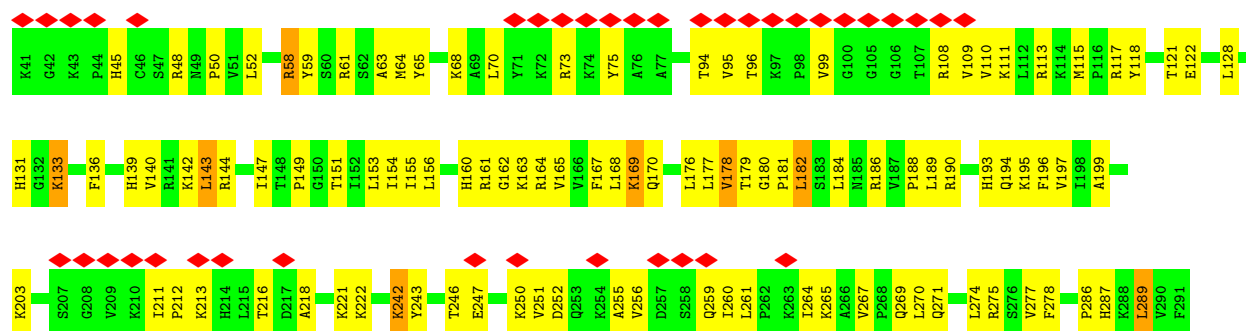
• Molecule 39: 60S ribosomal protein L5

Chain D: 61% 38% .



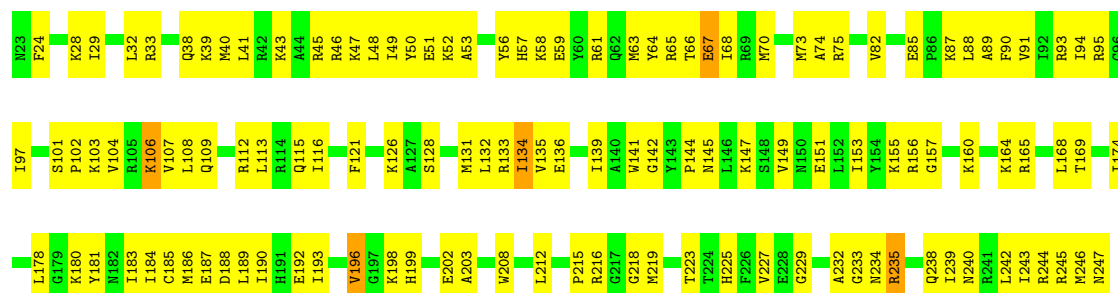
• Molecule 40: 60S ribosomal protein L6

Chain E: 18% 51% 45% .

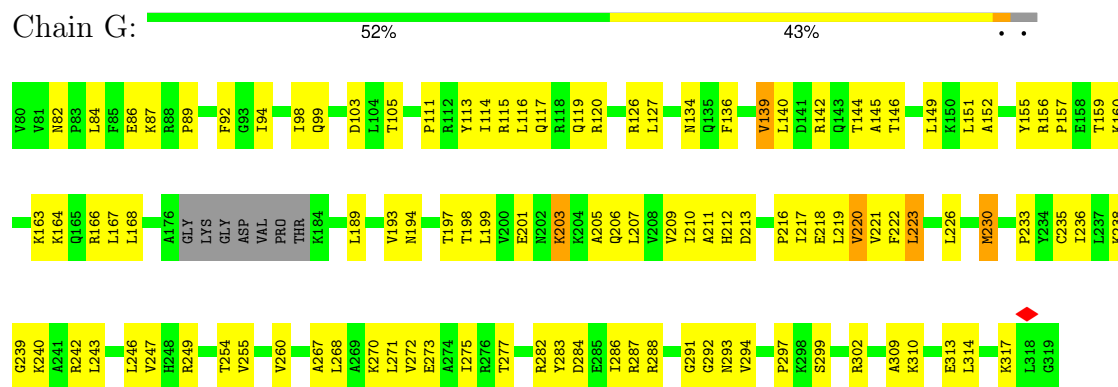


• Molecule 41: 60S ribosomal protein L7

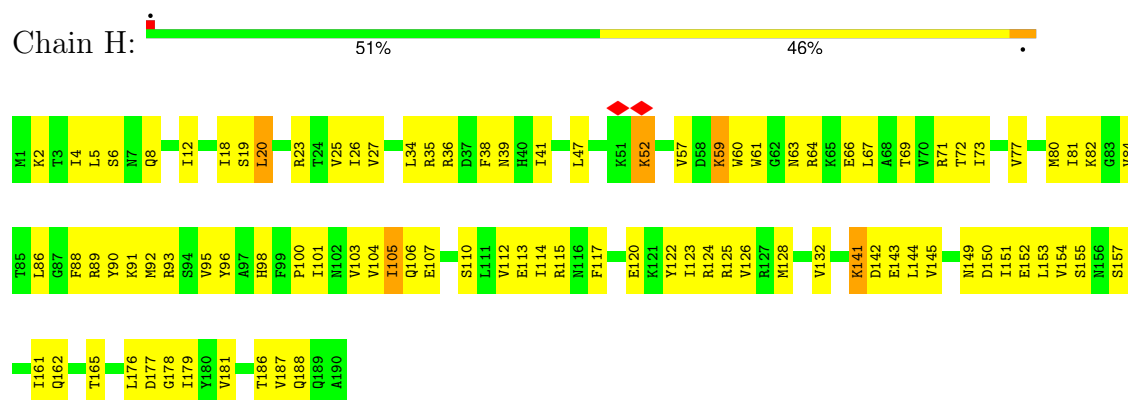
Chain F: 44% 53% .



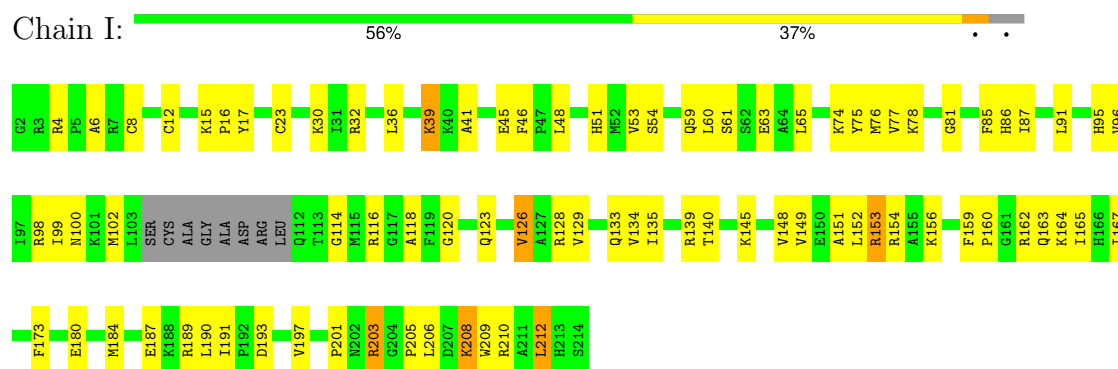
- Molecule 42: Large ribosomal subunit protein eL8



- Molecule 43: 60S ribosomal protein L9



- Molecule 44: Ribosomal protein L10



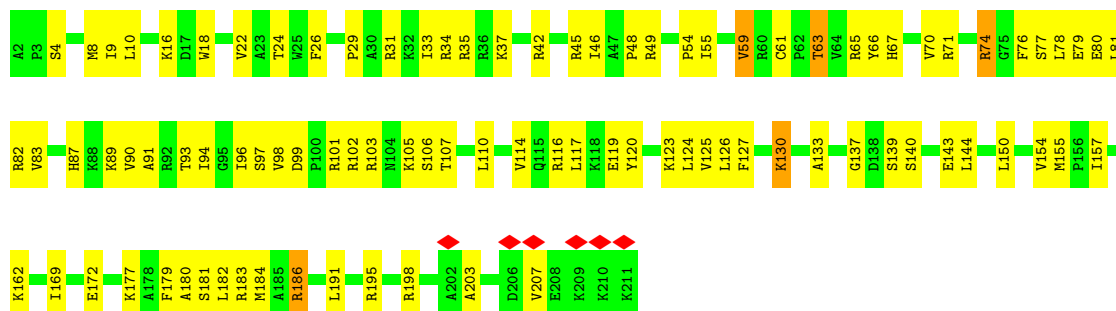
- Molecule 45: 60S ribosomal protein L11





- Molecule 46: Large ribosomal subunit protein eL13

Chain L: 56% 42%



- Molecule 47: 60S ribosomal protein L14

Chain M: 50% 46%



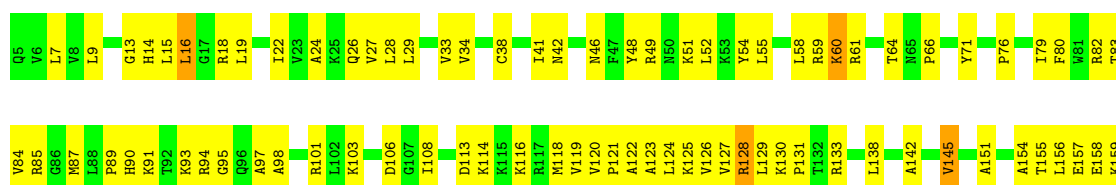
- Molecule 48: 60S ribosomal protein L15

Chain N: 54% 45%



- Molecule 49: Large ribosomal subunit protein uL13

Chain O: 45% 52%





• Molecule 50: 60S ribosomal protein L17

Chain P: 58% 41%



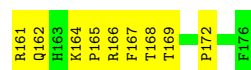
• Molecule 51: Large ribosomal subunit protein eL18

Chain Q: 56% 42%



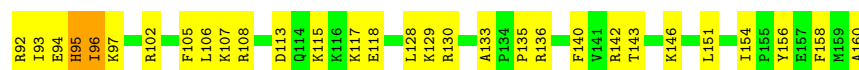
• Molecule 52: eL20

Chain S: 52% 47%

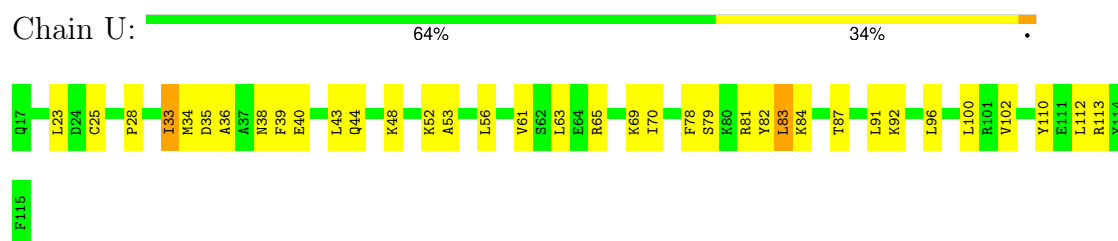


• Molecule 53: 60S ribosomal protein L21

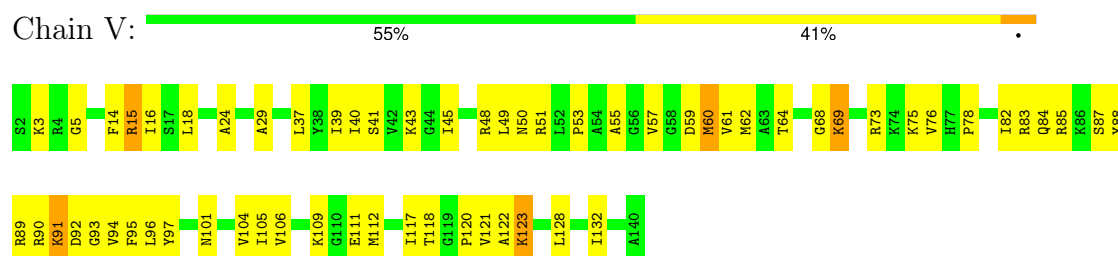
Chain T: 57% 40%



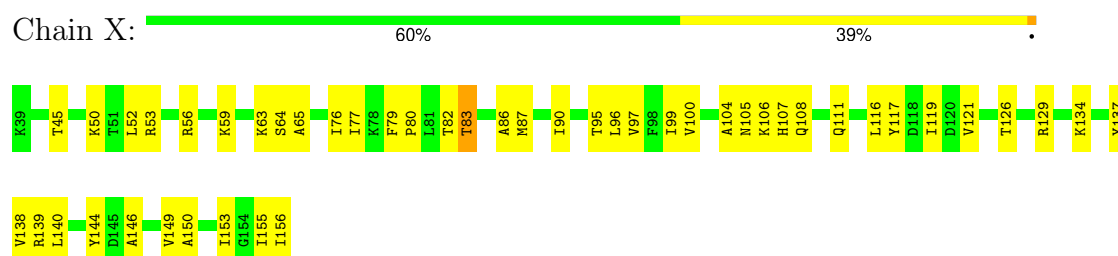
- Molecule 54: Large ribosomal subunit protein eL22



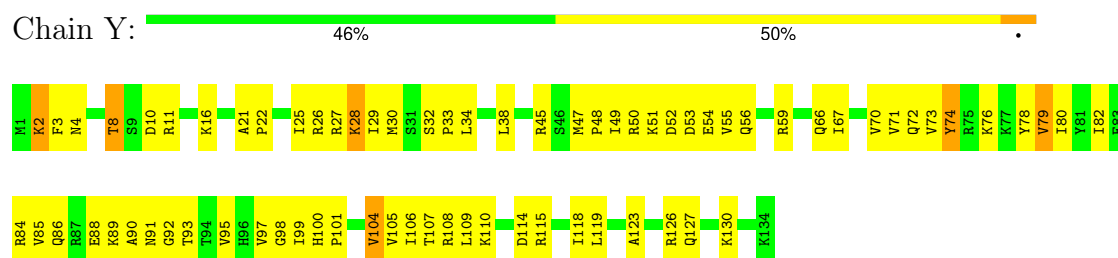
- Molecule 55: Large ribosomal subunit protein uL14



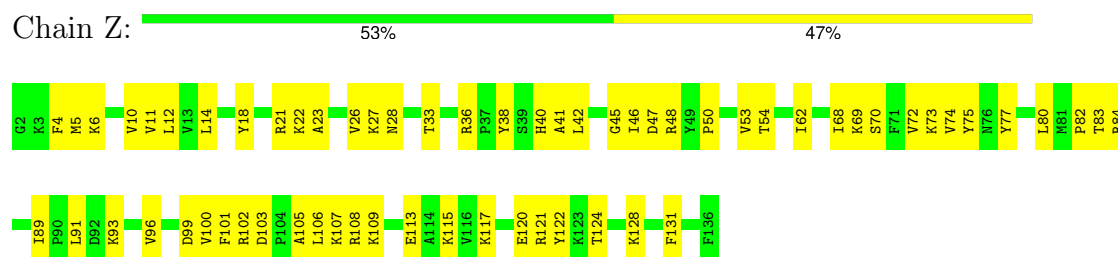
- Molecule 56: Large ribosomal subunit protein uL23



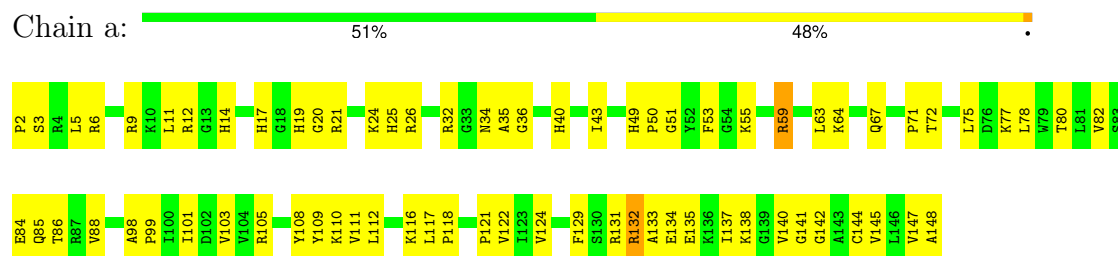
- Molecule 57: 60S ribosomal protein L26



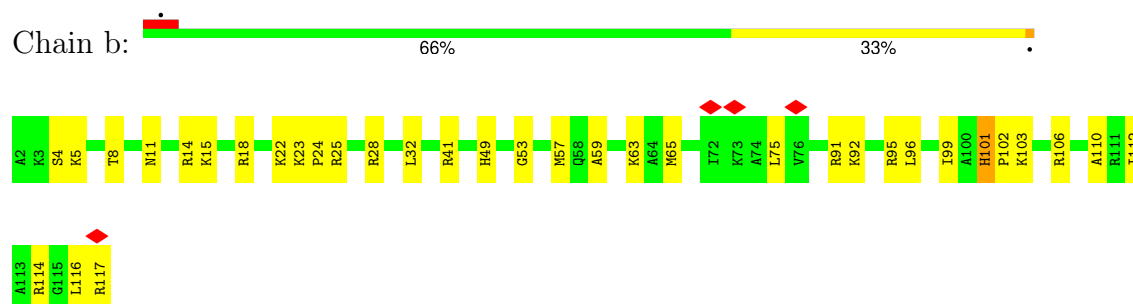
- Molecule 58: 60S ribosomal protein L27



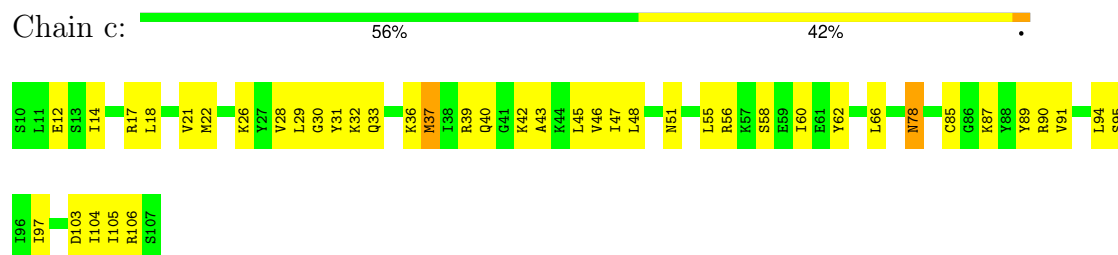
- Molecule 59: 60S ribosomal protein L27a



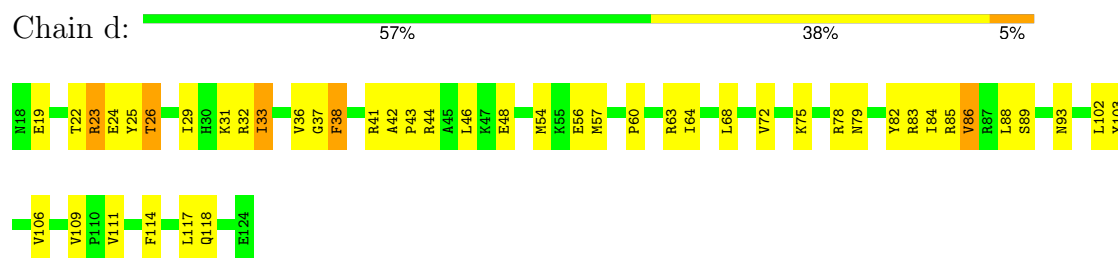
- Molecule 60: eL29



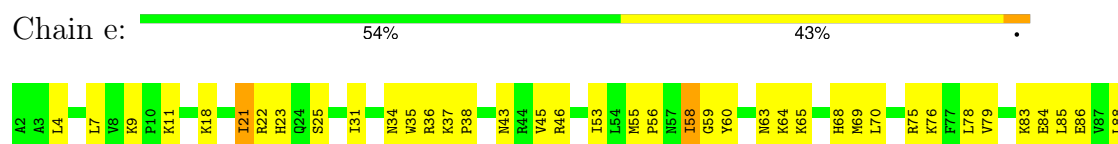
- Molecule 61: 60S ribosomal protein L30

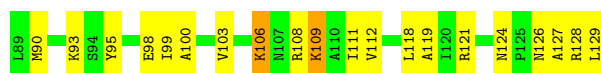


- Molecule 62: 60S ribosomal protein L31



- Molecule 63: Large ribosomal subunit protein eL32





- Molecule 64: Large ribosomal subunit protein eL33

Chain f: 61% 38%



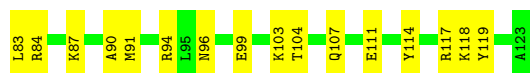
- Molecule 65: 60S ribosomal protein L34

Chain g: 57% 39%



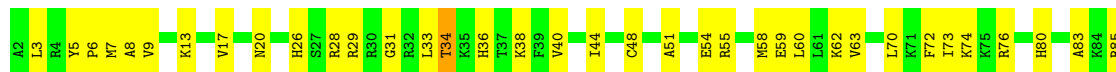
- Molecule 66: 60S ribosomal protein L35

Chain h: 54% 46%



- Molecule 67: 60S ribosomal protein L36

Chain i: 61% 37%



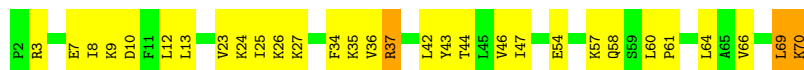
- Molecule 68: 60S ribosomal protein L37

Chain j: 53% 45%



- Molecule 69: Large ribosomal subunit protein eL38

Chain k: 57% 39% .



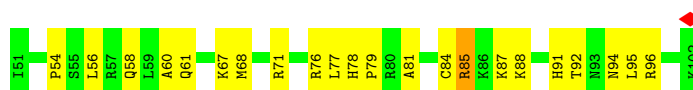
- Molecule 70: 60S ribosomal protein L39

Chain l: 52% 46% .



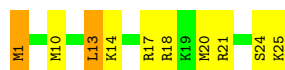
- Molecule 71: Large ribosomal subunit protein eL40

Chain m: 58% 40% .



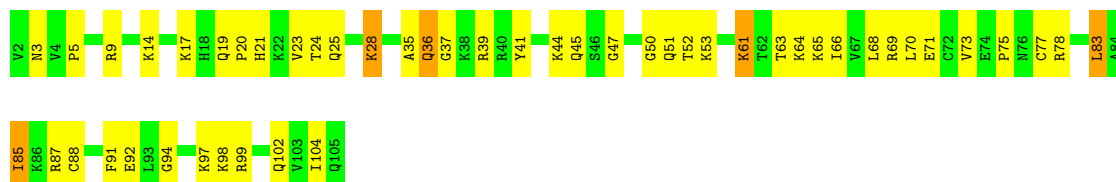
- Molecule 72: eL41

Chain n: 60% 32% 8%



- Molecule 73: eL42

Chain o: 53% 42% 5%

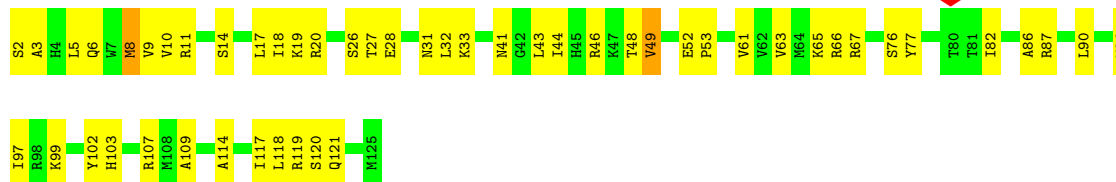


- Molecule 74: 60S ribosomal protein L37a

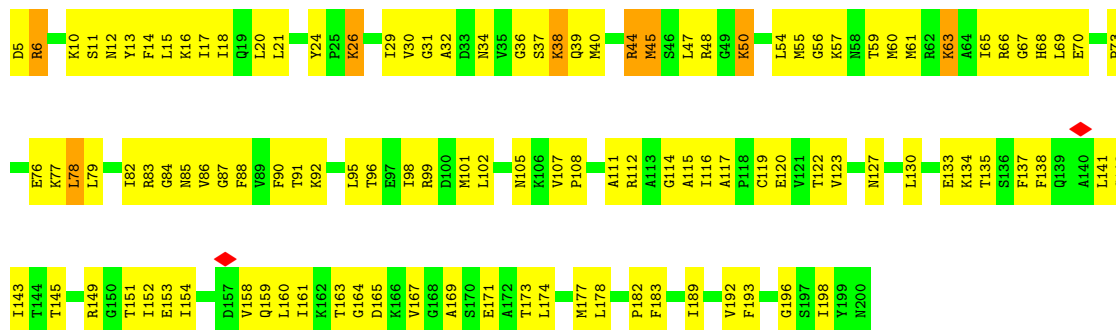
Chain p: 53% 45% .



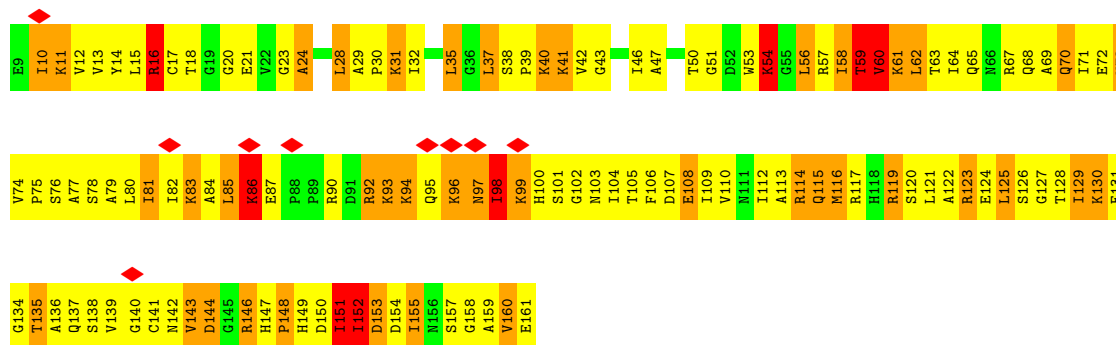
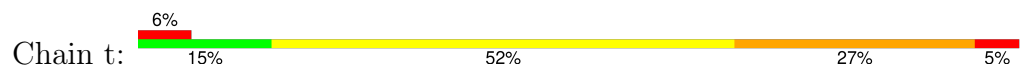
• Molecule 75: 60S ribosomal protein L28



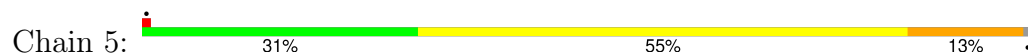
• Molecule 76: 60S acidic ribosomal protein P0



• Molecule 77: uL11



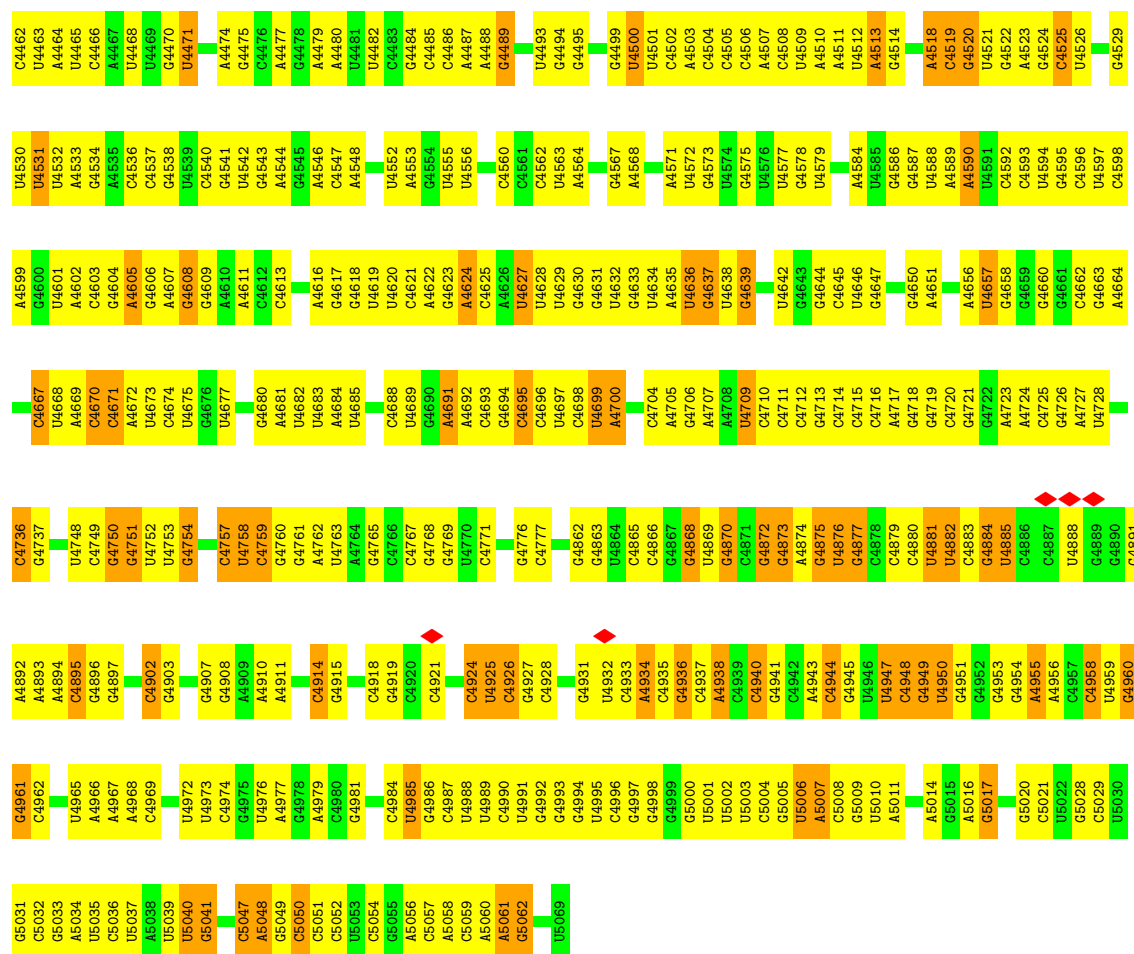
• Molecule 78: 28S rRNA



G1351	G1282	U1186	C979	C922	C712	C640	C449	A385	A306	G232	U150	U68	C1
G1352	G1283	G1187	U980	G522A	C713	G647	G450	A386	A307	U233	G151	A69	C6
G1353	G1284	C981	C922B	C922B	G714	G648	C451	A387	C308	G234	C155	A70	C7
G1354	U1285	G1188	C923	C923	G715	G649	A452	A388	G309	C238	G156	A73	C8
G1355	U1286	G1189	C924	C924	G716	A649	G453	A389	G310	C239	U157	A74	C9
G1356	C1287	C1190	C	C925	G717	C650	U454	C390	G311	G240	A158	A75	A10
G1357	G1288	C1191	C	C926	C718	C651	C455	C391	G312	G241	C159	A76	G11
G1358	G1289	G1192	C	G927	C719	G652	C456	A392	U391	G242	G160	U77	G12
G1359	G1291	G1193	C	C928	G720	U653	C457	A393	G314	A243	A161	U78	U13
G1360	G1292	G1194	C	A929	G721	C654	C458	U392	G315	G244	G162	U79	C14
G1361	G1293	G1195	C	G930	G722	C655	C459	G394	U316	G245	A163	U80	U15
G1362	G1294	G1196	U	G931	G723	C656	C460	A395	A317	G246	G164	C81	A16
G1363	G1295	G1197	C	A932	G724	C657	C461	A396	A318	G247	U82	U82	C18
G1364	G1296	G1198	G	G933	G725	C658	G464	G397	A319	G248	C83	C83	C19
G1365	G1297	G1199	G	C934	G726	C659	G465	G398	C320	C249	U84	U84	U20
G1366	G1298	C1202	C	A935	G727	C660	A466	G399	C321	C250	G85	G85	U21
G1367	G1299	G1203	C	G935A	G728	G664	U467	U404	C322	G251	C172	U86	G22
G1368	G1300	G1204	G	C936	G729	C665	U468	U405	C323	G252	C173	U87	G23
G1369	G1301	C1205	G	C937	G730	C666	C469	C406	A324	G253	G177	A88	G24
G1370	G1302	G1206	G	G938	G731	C667	C470	A408	U325	G254	C178	G91	A25
G1371	G1303	C1207	C	C939	G732	C668	A471	A411	C326	G255	G179	C92	C26
G1372	G1304	G1208	C	C940	G733	C669	C472	G412	U327	G256	C180	G93	C27
G1373	G1305	G1209	G	C941	G734	C670	C473	G413	U333	G257	C181	A89	C28
G1374	G1306	U1209	G	G942	G735	C671	C474	G414	A334	G258	G192	A99	G29
G1375	G1307	G1210	C	A943	G736	C672	C475	G415	A335	G259	G193	C100	C30
G1376	G1308	G1211	C	A944	G737	C673	C476	G416	A336	G260	G194	C101	U31
G1377	G1309	G1212	C	U945	G738	C674	G477	G417	A337	G261	G195	C110	G32
G1378	G1310	G1213	C	C946	G739	C675	C478	A418	A338	G262	G196	G104	A33
G1379	G1311	G1214	C	C947	G740	C676	G479	A419	A339	G263	A197	G105	A34
G1380	G1312	G1215	C	C948	G741	C677	G480	A420	A340	G264	G205	G106	U35
G1381	G1313	G1216	C	C949	G742	C678	C481	A421	A341	G265	U206	G107	U36
G1382	G1314	G1217	C	G950	G743	C679	C482	A422	A342	G266	G207	A108	U37
G1383	G1315	G1218	C	G951	G744	C680	C483	A423	A343	G267	G208	G109	A38
G1384	G1316	G1219	C	C952	G745	C681	C484	U424	A344	G268	G209	C110	A39
G1385	G1317	G1220	C	G953	G746	C682	C485	U425	A345	G269	G214	G114	G40
G1386	G1318	G1221	C	C954	G747	C683	C486	U426	A346	G270	C215	C115	A41
G1387	G1319	G1222	C	C955	G748	C684	C487	A427	A347	G271	C216	C116	A42
G1388	G1320	G1223	C	G956	G749	C685	C488	A428	A348	G272	C217	C117	U43
G1389	G1321	G1224	C	A956	G750	C686	C489	A429	A349	G273	G218	G118	U46
G1390	G1322	G1225	C	G957	G751	C687	C490	G430	A350	U274	C219	G119	A47
G1391	G1323	G1226	C	G958	G752	C688	C491	G431	A351	G275	C220	A120	G48
G1392	G1324	G1227	C	G959	G753	C689	C492	U432	A352	G276	C221	G124	U49
G1393	G1325	G1228	C	A960	G754	C690	C493	U433	A353	G277	C222	C124	G52
G1394	G1326	G1229	C	C961	G755	C691	C494	A434	A354	U278	C223	C125	C53
G1395	G1327	G1230	C	C962	G756	C692	C495	A435	A355	G279	G224	G126	C54
G1396	G1328	G1231	C	G963	G757	C693	C496	C436	A356	U280	G225	G127	G54
G1397	G1329	G1232	C	A964	G758	C694	C497	C437	A357	G281	G226	C128	G55
G1398	G1330	G1233	C	G965	G759	C695	C498	U438	A358	G282	C227	C129	A56
G1399	G1331	G1234	C	C966	G760	C696	C499	A439	A359	G283	C228	G134	G57
G1400	G1332	G1235	C	C967	G761	C697	C500	A440	A360	U284	G229	G135	A58
G1401	G1333	G1236	C	C968	G762	C698	C501	A441	A361	G285	G230	C146	A64
G1402	G1334	G1237	C	G969	G763	C699	C502	A442	A362	G286	G231	A147	A65
G1403	G1335	G1238	C	C970	G764	C700	C503	A443	A363	U287	G232	C148	A66
G1404	G1336	G1239	C	C971	G765	C701	C504	A444	A364	G288	G233	G137	C67
G1405	G1337	G1240	C	C972	G766	C702	C505	A445	A365	C289	G234	G146	A64
G1406	G1338	G1241	C	C973	G767	C703	C506	A446	A366	G290	G235	A147	A65
G1407	G1339	G1242	C	C974	G768	C704	C507	A447	A367	U291	G236	C148	A66
G1408	G1340	G1243	C	C975	G769	C705	C508	A448	A368	G292	G237	G149	A67
G1409	G1341	G1244	C	C976	G770	C706	C509	A449	A369	U293	G238	A149	A68
G1410	G1342	G1245	C	C977	G771	C707	C510	A450	A370	G294	G239	C149	A69
G1411	G1343	G1246	C	C978	G772	C708	C511	A451	A371	U295	G240	G137	A60
G1412	G1344	G1247	C	C979	G773	C709	C512	A452	A372	G296	G241	G146	A64
G1413	G1345	G1248	C	C980	G774	C710	C513	A453	A373	G297	G242	A146	A65
G1414	G1346	G1249	C	C981	G775	C711	C514	A454	A374	G298	G243	C147	A66
G1415	G1347	G1250	C	C982	G776	C712	C515	A455	A375	G299	G244	A147	A67
G1416	G1348	G1251	C	C983	G777	C713	C516	A456	A376	G300	G245	G146	A68
G1417	G1349	G1252	C	C984	G778	C714	C517	A457	A377	G301	G246	A147	A69
G1418	G1350	G1253	C	C985	G779	C715	C518	A458	A378	G302	G247	C148	A70
G1419	G1351	G1254	C	C986	G780	C716	C519	A459	A379	G303	G248	A149	A71
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G1421	G1353	G1256	C	C988	G782	C718	C521	A461	A381	G305	G250	A149	A73
G1422	G1354	G1257	C	C989	G783	C719	C522	A462	A382	G306	G251	G149	A74
G1423	G1355	G1258	C	C990	G784	C720	C523	A463	A383	G307	G252	A149	A75
G1424	G1356	G1259	C	C991	G785	C721	C524	A464	A384	G308	G253	G149	A76
G1425	G1357	G1260	C	C992	G786	C722	C525	A465	A385	G309	G254	A149	A77
G1426	G1358	G1261	C	C993	G787	C723	C526	A466	A386	G310	G255	G149	A78
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G1431	G1363	G1266	C	C998	G792	C728	C531	A471	A391	G315	G260	A149	A83
G1432	G1364	G1267	C	C999	G793	C729	C532	A472	A392	G316	G261	G149	A84
G1433	G1365	G1268	C	C1000	G794	C730	C533	A473	A393	G317	G262	A149	A85
G1434	G1366	G1269	C	C1001	G795	C731	C534	A474	A394	G318	G263	G149	A86
G1435	G1367	G1270	C	C1002	G796	C732	C535	A475	A395	G319	G264	A149	A87
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G1437	G1369	G1272	C	C1004	G798	C734	C537	A477	A397	G321	G266	A149	A89
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G1439	G1371	G1274	C	C1006	G800	C736	C539	A479	A399	G323	G268	A149	A91
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G1443	G1375	G1278	C	C1010	G804	C740	C543	A483	A403	G327	G272	A149	A95
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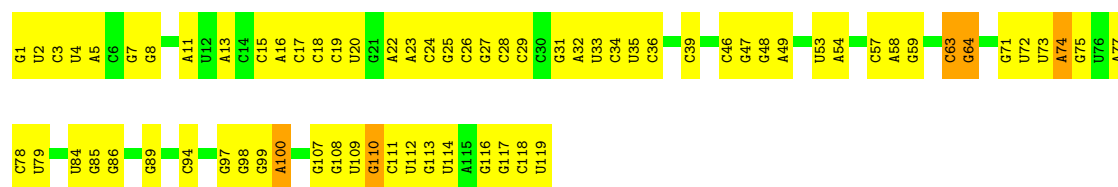
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G2286	G2289	C2289	C2290	G2291	G2292	U2293	G2294	G2295	G2296	G2297	G2298	G2299	A2300	G2301	U2305	G2306	A2307	A2308	G2309	C2310	G2311	U2312	A2313	G2314	G2315	G2316	G2319	G2320	G2321	G2322	C2323	G2324	C2325	G2326	G2327	G2328	U2329	G2330	G2331	A2332	G2333	G2334	A2341	G2342	G2343	U2344	G2345	G2348	A2349	U2350	G2351	U2352	G2355	G2356																																																		
G2357	G2358	U2359	U2362	A2363	G2364	G2365	A2370	G2373	A2374	A2375	G2376	G2377	G2378	A2381	A2382	C2383	A2386	G2387	A2388	G2391	C2392	G2395	A2396	G2402	G2406	G2407	C2410	A2411	U2412	U2413	G2414	U2415	G2416	A2417	A2418	G2419	A2420	G2421	C2422	A2423	G2424	U2425	U2426	G2433	G2434	G2435																																																										
G2439	U2440	C2441	U2444	G2445	G2446	U2447	A2448	A2449	A2453	G2457	C2458	G2459	G2460	G2461	G2465	G2466	U2467	G2468	C2469	C2470	G2471	A2472	A2473	G2474	G2475	G2476	A2477	G2478	G2479	G2480	G2481	A2484	U2485	G2486	G2487	G2488	G2489	U2490	C2491	G2492	U2494	G2502	G2503	G2504	G2505	G2506	A2507	U2508	C2509	A2513	G2517	G2518	U2519	G2520	G2521	G2528	A2529	U2530	G2533	C2534	G2535	A2536	A2537	U2538	G2539	G2540	G2541	G2542	A2543	G2544	U2545	G2546	G2547	G2548	G2549	G2552	A2553	U2554	G2555	G2556	G2557	G2562	C2563	G2564	U2570	G2571	G2572	A2573	G2574	U2575	G2576	U2580	A2581	A2582	G2583	G2584	G2585	G2586	A2587	C2588	G2589	A2590	A2591	U2592
G1426	A1427	C1431	G1432	C1436	C1437	U1438	U1440	U1441	C1442	U1443	G1444	C1445	U1446	G1447	G1448	C1449	G1455	C1456	G1457	C1458	A1459	C1460	C1461	A1462	C1463	C1464	G1465	C1468	C1469	G1470	U1473	C1474	G1475	C1476	C1477	G1478	G1479	C1480	C1481	G1482	A1483	G1484	C1485	G1488	G1492	G1493	U1494	G1495	G1496	A1497	G1498	C1499																																																				
A1500	C1501	G1502	A1503	G1504	C1505	G1506	C1507	A1508	C1509	G1510	U1511	C1512	U1513	U1514	A1515	G1516	G1517	A1518	A1523	G1526	A1527	U1528	A1533	A1534	C1535	U1536	A1537	U1538	G1539	G1543	G1544	G1545	C1546	A1547	C1551	G1552	A1553	A1554	C1557	A1558	G1559	A1563	A1564	C1565	G1566	U1569	G1570	G1571	U1572	G1573	A1574																																																					
A1575	G1576	U1577	C1578	G1579	C1580	G1581	G1586	U1587	U1588	C1589	C1590	U1591	G1592	C1593	C1594	G1595	U1596	G1597	C1598	A1599	A1600	C1603	G1604	G1605	G1608	U1609	C1610	C1611	G1612	C1613	C1614	G1615	U1616	G1617	U1620	A1621	U1622	A1623	G1624	G1625	G1626	C1627	C1628	U1629	A1630	U1631	G1633	A1634	U1635	U1636	U1637	A1638	U1639																																																			
C1640	G1641	A1642	A1643	C1644	G1645	A1646	G1654	G1658	U1659	U1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	A1668	A1669	G1670	G1676	G1680	G1681	A1682	U1683	A1684	C1685	C1686	U1687	G1688	G1689	G1690	G1691	C1692	U1693	C1694	U1695	C1696	C1720	G1721	C1722	A1723	G1724	U1725	U1726	U1727	U1728	A1729	G1732	U1733	G1734	U1735	A1738																																																			
G1739	C1740	G1741	A1742	U1743	U1744	G1745	A1746	U1747	U1748	A1749	G1750	A1751	G1752	G1753	U1754	C1755	U1756	U1757	G1761	G1764	A1765	A1766	G1769	U1770	U1771	C1772	U1773	U1773	A1776	C1777	C1778	U1779	A1780	U1781	U1782	G1783	U1784	C1785	U1786	A1787	G1788	C1789	U1790	U1791	U1792	A1793	A1794	A1795	U1796	U1800	A1801	A1802	G1803	A1804	A1805																																																	
G1806	C1807	G1811	C1812	U1813	U1814	G1815	C1816	U1817	G1818	G1819	C1820	G1821	U1822	G1823	G1824	A1825	G1826	G1827	C1828	G1829	G1830	U1834	G1835	A1837	U1838	U1839	G1840	C1841	G1842	A1843	C1844	U1845	G1846	C1847	U1848	U1849	A1850	G1851	U1852	G1853	G1854	G1855	C1856	C1857	A1858	C1859	U1860	U1861	U1862	U1863	U1866	A1867	A1868	G1869	C1870																																																	
A1871	G1872	A1873	A1874	C1875	U1876	G1877	C1878	U1879	C1880	C1881	U1882	C1884	A1887	C1888	G1889	C1890	C1901	G1902	G1903	G1904	U1905	U1906	A1907	G1910	G1911	G1912	C1913	G1914	C1915	G1916	A1984	U1918	G1919	C1920	C1921	G1922	A1923	C1924	G1925	C1926	U1927	C1928	A1929	U1930	C1931	A1932	G1933	A1934	A1939	G1940	A1941	A1942	A1943	G1948																																																		
G1952	U1953	U1954	U1955	U1956	U1957	U1958	U1959	A1960	G1961	A1962	C1963	A1964	G1965	C1966	A1967	G1968	G1969	A1970	G1971	G1972	G1973	U1974	U1975	G1976	C1977	C1978	A1979	U1980	U1981	G1982	A1983	U1984	G1985	U1986	G1987	G1988	C1989	A1990	A1991	U1992	C1993	C1994	G1995	C1996	U1997	A1998	A1999	G2000	A2001	A2002	G2003	U2004	G2007	U2008	C2011	A2012																																																
U2015	C2016	A2017	C2018	C2019	U2020	G2021	C2022	C2023	G2024	A2025	A2026	U2027	C2028	A2029	A2030	C2031	U2032	C2037	U2038	G2039	A2040	A2041	A2042	G2045	G2046	A2047	U2048	G2049	G2050	C2051	G2052	C2053	U2054	G2055	G2056	G2060	U2061	C2062	G2063	G2064	C2065	C2066	C2067	C2068	A2069	C2070	C2074	G2075	G2076	C2077	C2078	G2079	U2080	C2081																																																		
G2082	C2083	G2084	G2085	G2086	C2087	A2088	G2089	U2090	C2091	G2092	A2093	G2094	A2095	G2096	U2097	G2098	C2099	G2100	A2101	G2102	A2103	A2104	A2105	G2106	U2107	G2108	A2109	G	U	U	U	U	C2258	G2259	C2260	G2261	G2262	A2263	C2264	G2265	C2266	U2267	A2268	G2269	G2270	G2271	C2272	G2273	C2274	G2275	A2276	C2277	G2278	A2279	G2280	U2281	A2282	G2283	G2284	A2285																																												
G2286	G2289	C2289	C2290	G2291	G2292	U2293	G2294	G2295	G2296	G2297	G2298	G2299	A2300	G2301	U2305	G2306	A2307	A2308	G2309	C2310	G2311	U2312	A2313	G2314	G2315	G2316	G2319	G2320	G2321	G2322	C2323	G2324	C2325	G2326	G2327	G2328	U2329	G2330	G2331	A2332	G2333	G2334	A2341	G2342	G2343	U2344	G2345	G2348	A2349	U2350	G2351	U2352	G2355	G2356																																																		
G2357	G2358	U2359	U2362	A2363	G2364	G2365	A2370	G2373	A2374	A2375	G2376	G2377	G2378	A2381	A2382	C2383	A2386	G2387	A2388	G2391	C2392	G2395	A2396	G2402	G2406	G2407	C2410	A2411	U2412	U2413	G2414	U2415	G2416	A2417	A2418	G2419	A2420	G2421	C2422	A2423	G2424	U2425	U2426	G2433	G2434	G2435																																																										
G2439	U2440	C2441	U2444	G2445	G2446	U2447	A2448	A2449	A2453	G2457	C2458	G2459	G2460	G2461	G2465	G2466	U2467	G2468	C2469	C2470	G2471	A2472	A2473	G2474	G2475	G2476	A2477	G2478	G2479	G2480	G2481	A2484	U2485	G2486	G2487	G2488	G2489	U2490	C2491	G2492	U2494	G2502	G2503	G2504	G2505	G2506	A2507	U2508	C2509	A2513	G2517	G2518	U2519	G2520	G2521	G2528	A2529	U2530	G2533	C2534	G2535	A2536	A2537	U2538	G2539	G2540	G2541	G2542	A2543	G2544	U2545	G2546	G2547	G2548	G2549	G2552	A2553	U2554	G2555	G2556	G2557	G2562	C2563	G2564	U2570	G2571	G2572	A2573	G2574	U2575	G2576	U2580	A2581	A2582	G2583	G2584	G2585	G2586	A2587	C2588	G2589	A2590	A2591	U2592





• Molecule 79: 5S rRNA

Chain 7: 41% 55%

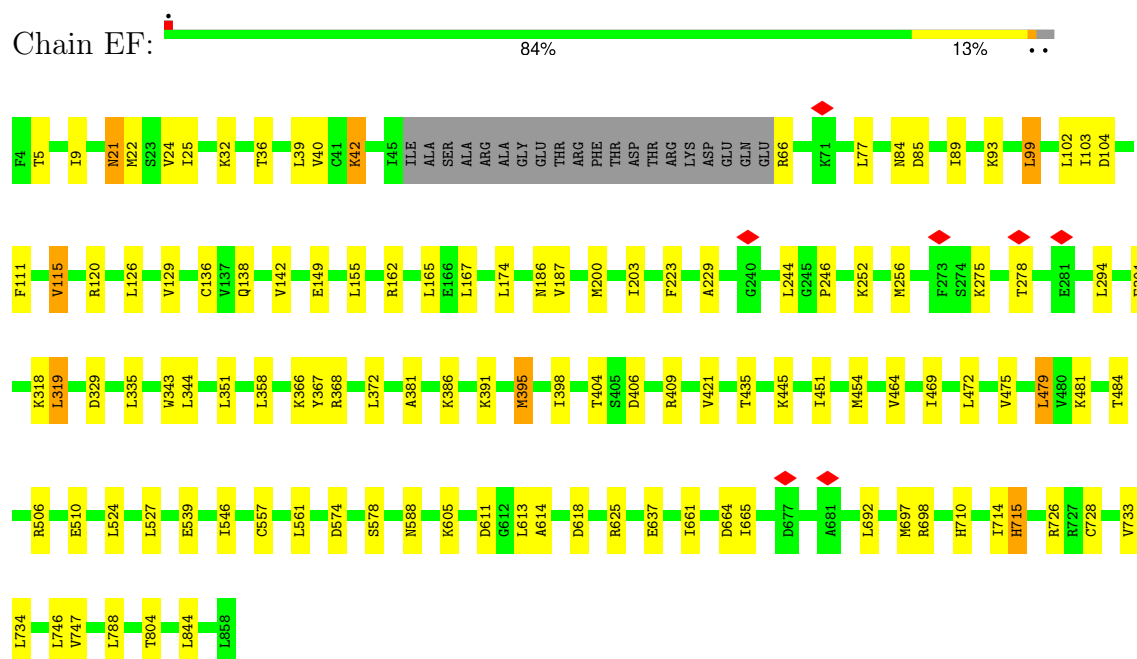


• Molecule 80: 5.8S rRNA

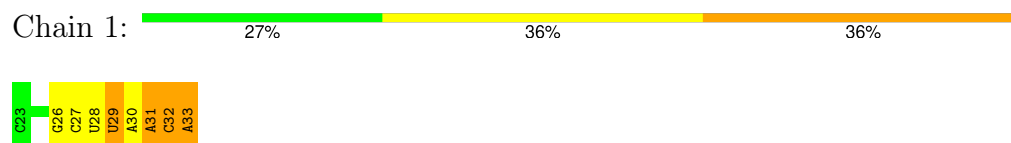
Chain 8: 25% 60% 12%



- Molecule 81: Elongation factor 2



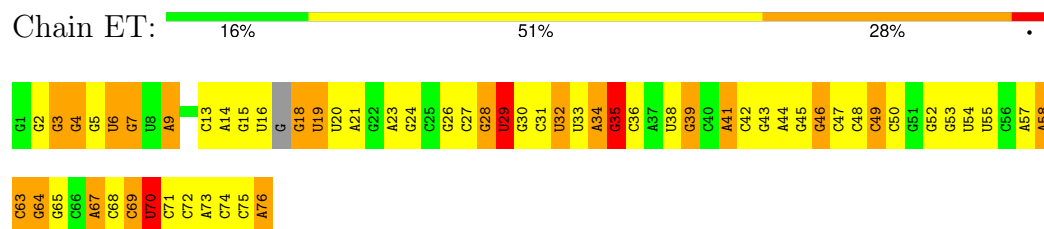
- Molecule 82: NediV ORF



- Molecule 83: P site Ala-tRNA



- Molecule 84: E site Ala-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34773	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	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)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.648	Depositor
Minimum map value	-0.225	Depositor
Average map value	0.029	Depositor
Map value standard deviation	0.060	Depositor
Recommended contour level	0.05	Depositor
Map size (\AA)	298.8, 298.8, 298.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	R	0.14	0/1524	0.30	0/2013
2	W	0.16	0/541	0.37	0/720
3	9	0.12	0/39860	0.27	0/62094
4	AA	0.15	0/1687	0.37	1/2294 (0.0%)
5	BB	0.11	0/1756	0.29	0/2350
6	CC	0.11	0/1753	0.28	0/2369
7	EE	0.11	0/2118	0.27	0/2849
8	GG	0.25	0/1854	0.50	2/2469 (0.1%)
9	HH	0.13	0/1510	0.24	0/2022
10	II	0.11	0/1715	0.27	0/2287
11	JJ	0.09	0/1550	0.25	0/2069
12	LL	0.11	0/1195	0.28	0/1597
13	NN	0.11	0/1226	0.24	0/1649
14	OO	0.10	0/1029	0.26	0/1380
15	VV	0.09	0/643	0.23	0/860
16	WW	0.12	0/1051	0.29	0/1406
17	XX	0.14	0/1116	0.31	0/1490
18	YY	0.10	0/1028	0.25	0/1366
19	aa	0.12	0/828	0.29	0/1109
20	bb	0.10	0/665	0.26	0/891
21	ee	0.09	0/462	0.26	0/607
22	DD	0.11	0/1796	0.30	0/2417
23	FF	0.10	0/1492	0.27	0/2005
24	KK	0.11	0/834	0.28	0/1125
25	MM	0.13	0/918	0.32	0/1233
26	PP	0.11	0/974	0.29	0/1301
27	QQ	0.09	0/1134	0.24	0/1520
28	RR	0.13	0/1082	0.35	0/1452
29	SS	0.10	0/1208	0.28	0/1618
30	TT	0.09	0/1115	0.25	0/1493
31	UU	0.10	0/805	0.28	0/1081
32	ZZ	0.10	0/604	0.26	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	cc	0.09	0/490	0.25	0/656
34	dd	0.09	0/470	0.25	0/623
35	ff	0.10	0/567	0.26	0/753
36	A	0.16	0/1936	0.32	0/2596
37	B	0.14	0/3240	0.32	0/4339
38	C	0.13	0/2937	0.30	0/3946
39	D	0.12	0/2437	0.27	0/3264
40	E	0.10	0/1762	0.25	0/2362
41	F	0.13	0/1911	0.31	0/2549
42	G	0.12	0/1910	0.27	0/2569
43	H	0.13	0/1535	0.29	0/2063
44	I	0.13	0/1702	0.25	0/2272
45	J	0.12	0/1385	0.29	0/1852
46	L	0.13	0/1733	0.28	0/2316
47	M	0.12	0/1158	0.27	0/1547
48	N	0.15	0/1746	0.30	0/2338
49	O	0.15	0/1662	0.30	0/2222
50	P	0.14	0/1268	0.32	0/1700
51	Q	0.15	0/1539	0.31	0/2054
52	S	0.13	0/1501	0.29	0/2012
53	T	0.14	0/1326	0.27	0/1770
54	U	0.11	0/823	0.28	0/1104
55	V	0.13	0/1048	0.29	0/1402
56	X	0.12	0/984	0.27	0/1323
57	Y	0.12	0/1132	0.26	0/1504
58	Z	0.13	0/1130	0.30	0/1507
59	a	0.15	0/1191	0.30	0/1590
60	b	0.12	0/861	0.28	0/1138
61	c	0.11	0/771	0.25	0/1034
62	d	0.14	0/903	0.28	0/1216
63	e	0.15	0/1071	0.32	0/1429
64	f	0.15	0/895	0.34	0/1198
65	g	0.13	0/916	0.29	0/1220
66	h	0.12	0/1021	0.26	0/1348
67	i	0.12	0/841	0.28	0/1112
68	j	0.16	0/720	0.32	0/952
69	k	0.12	0/575	0.28	0/761
70	l	0.14	0/459	0.27	0/608
71	m	0.11	0/435	0.28	0/575
72	n	0.12	0/240	0.21	0/305
73	o	0.13	0/864	0.28	0/1140
74	p	0.13	0/718	0.29	0/953
75	r	0.12	0/1010	0.28	0/1354

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	s	0.14	0/1530	0.32	0/2064
77	t	0.51	0/1174	0.92	10/1582 (0.6%)
78	5	0.16	10/84212 (0.0%)	0.29	0/131319
79	7	0.12	0/2836	0.23	0/4421
80	8	0.14	0/3581	0.27	0/5577
81	EF	0.32	1/6623 (0.0%)	0.60	1/8943 (0.0%)
82	1	0.62	2/254 (0.8%)	0.32	0/392
83	PT	0.42	0/259	0.76	0/401
84	ET	0.76	16/1780 (0.9%)	0.50	0/2771
All	All	0.17	29/232145 (0.0%)	0.31	14/339992 (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
17	XX	0	1
28	RR	0	2
37	B	0	1
64	f	0	1
81	EF	0	1
All	All	0	6

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	ET	39	G	C1'-N9	-7.44	1.36	1.48
84	ET	2	G	C1'-N9	-7.38	1.36	1.48
84	ET	4	G	C1'-N9	-7.26	1.37	1.48
84	ET	64	G	C1'-N9	-7.23	1.37	1.48
84	ET	3	G	C1'-N9	-7.18	1.37	1.48

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	GG	44	GLU	N-CA-C	-8.52	102.15	112.54
8	GG	47	GLY	N-CA-C	-7.63	104.50	115.64
77	t	83	LYS	N-CA-C	-7.10	103.58	111.82
77	t	144	ASP	N-CA-C	-6.22	103.09	111.54
77	t	151	ILE	N-CA-C	-6.16	104.28	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
37	B	258	HIS	Peptide
28	RR	127	ASN	Peptide
28	RR	129	LYS	Peptide
17	XX	61	GLN	Peptide
64	f	106	TYR	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	R	1508	0	1664	88	0
2	W	528	0	541	53	0
3	9	35655	0	18015	1209	0
4	AA	1650	0	1654	196	0
5	BB	1729	0	1803	128	0
6	CC	1716	0	1806	102	0
7	EE	2076	0	2177	159	0
8	GG	1831	0	1978	223	0
9	HH	1488	0	1582	85	0
10	II	1686	0	1772	96	0
11	JJ	1525	0	1640	115	0
12	LL	1175	0	1249	66	0
13	NN	1202	0	1289	93	0
14	OO	1016	0	1039	82	0
15	VV	636	0	637	46	0
16	WW	1034	0	1080	84	0
17	XX	1098	0	1167	82	0
18	YY	1011	0	1083	64	0
19	aa	814	0	863	56	0
20	bb	651	0	672	35	0
21	ee	457	0	502	32	0
22	DD	1768	0	1866	105	0
23	FF	1471	0	1522	109	0
24	KK	810	0	836	50	0
25	MM	908	0	939	58	0
26	PP	956	0	1002	66	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	QQ	1116	0	1182	75	0
28	RR	1068	0	1121	123	0
29	SS	1190	0	1249	94	0
30	TT	1097	0	1132	81	0
31	UU	795	0	862	52	0
32	ZZ	598	0	656	29	0
33	cc	488	0	514	30	0
34	dd	459	0	448	19	0
35	ff	555	0	563	21	0
36	A	1898	0	1993	137	0
37	B	3172	0	3310	190	0
38	C	2883	0	3053	163	0
39	D	2391	0	2424	110	0
40	E	1729	0	1887	112	0
41	F	1875	0	1995	120	0
42	G	1879	0	2027	99	0
43	H	1516	0	1597	94	0
44	I	1664	0	1712	95	0
45	J	1362	0	1399	73	0
46	L	1702	0	1820	95	0
47	M	1137	0	1211	72	0
48	N	1701	0	1749	95	0
49	O	1630	0	1778	109	0
50	P	1242	0	1274	58	0
51	Q	1515	0	1634	91	0
52	S	1462	0	1508	92	0
53	T	1298	0	1366	76	0
54	U	809	0	833	33	0
55	V	1034	0	1097	64	0
56	X	967	0	1040	40	0
57	Y	1115	0	1205	77	0
58	Z	1107	0	1182	55	0
59	a	1162	0	1209	85	0
60	b	848	0	920	32	0
61	c	761	0	794	44	0
62	d	888	0	930	40	0
63	e	1053	0	1147	51	0
64	f	876	0	912	34	0
65	g	906	0	998	52	0
66	h	1013	0	1147	52	0
67	i	830	0	916	48	0
68	j	705	0	737	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
69	k	569	0	637	35	0
70	l	447	0	480	28	0
71	m	429	0	465	23	0
72	n	239	0	289	19	0
73	o	851	0	920	44	0
74	p	708	0	756	50	0
75	r	994	0	1051	49	0
76	s	1507	0	1564	142	0
77	t	1160	0	1215	272	0
78	5	75293	0	38042	2167	0
79	7	2538	0	1286	72	0
80	8	3208	0	1629	115	0
81	EF	6516	6607	6604	38	0
82	1	229	110	120	12	0
83	PT	233	0	119	80	0
84	ET	1595	0	810	79	0
85	5	190	0	0	0	0
85	7	6	0	0	0	0
85	8	4	0	0	0	0
85	A	1	0	0	0	0
85	EF	1	0	0	0	0
85	P	1	0	0	0	0
85	V	1	0	0	0	0
85	aa	1	0	0	0	0
85	g	1	0	0	0	0
86	aa	1	0	0	0	0
86	dd	1	0	0	0	0
86	ff	1	0	0	0	0
86	g	1	0	0	0	0
86	j	1	0	0	0	0
86	m	1	0	0	0	0
86	o	1	0	0	0	0
86	p	1	0	0	0	0
All	All	216625	6717	162896	8355	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 22.

The worst 5 of 8355 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)
8:GG:221:LYS:CA	8:GG:224:ARG:HH12	1.11	1.57
8:GG:221:LYS:HA	8:GG:224:ARG:CZ	1.47	1.40
77:t:92:ARG:NH1	77:t:93:LYS:HD3	1.47	1.28
77:t:154:ASP:HA	77:t:158:GLY:CA	1.67	1.25
8:GG:221:LYS:HA	8:GG:224:ARG:NH1	0.93	1.23

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	R	178/180 (99%)	174 (98%)	4 (2%)	0	100	100
2	W	61/106 (58%)	58 (95%)	3 (5%)	0	100	100
4	AA	207/217 (95%)	198 (96%)	9 (4%)	0	100	100
5	BB	211/213 (99%)	200 (95%)	11 (5%)	0	100	100
6	CC	219/221 (99%)	216 (99%)	3 (1%)	0	100	100
7	EE	260/262 (99%)	251 (96%)	9 (4%)	0	100	100
8	GG	224/237 (94%)	220 (98%)	4 (2%)	0	100	100
9	HH	181/189 (96%)	177 (98%)	4 (2%)	0	100	100
10	II	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
11	JJ	183/185 (99%)	181 (99%)	2 (1%)	0	100	100
12	LL	139/151 (92%)	134 (96%)	5 (4%)	0	100	100
13	NN	147/149 (99%)	145 (99%)	2 (1%)	0	100	100
14	OO	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
15	VV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
16	WW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
17	XX	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	18	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	YY	122/124 (98%)	122 (100%)	0	0	100	100
19	aa	99/101 (98%)	98 (99%)	1 (1%)	0	100	100
20	bb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
21	ee	55/57 (96%)	54 (98%)	1 (2%)	0	100	100
22	DD	226/228 (99%)	222 (98%)	3 (1%)	1 (0%)	30	60
23	FF	181/191 (95%)	176 (97%)	5 (3%)	0	100	100
24	KK	94/96 (98%)	92 (98%)	2 (2%)	0	100	100
25	MM	115/117 (98%)	107 (93%)	8 (7%)	0	100	100
26	PP	113/115 (98%)	108 (96%)	5 (4%)	0	100	100
27	QQ	139/141 (99%)	135 (97%)	4 (3%)	0	100	100
28	RR	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
29	SS	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
30	TT	139/141 (99%)	138 (99%)	1 (1%)	0	100	100
31	UU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
32	ZZ	73/75 (97%)	73 (100%)	0	0	100	100
33	cc	60/62 (97%)	56 (93%)	4 (7%)	0	100	100
34	dd	53/55 (96%)	53 (100%)	0	0	100	100
35	ff	66/68 (97%)	63 (96%)	3 (4%)	0	100	100
36	A	246/248 (99%)	230 (94%)	16 (6%)	0	100	100
37	B	392/394 (100%)	380 (97%)	12 (3%)	0	100	100
38	C	360/362 (99%)	350 (97%)	10 (3%)	0	100	100
39	D	291/293 (99%)	280 (96%)	11 (4%)	0	100	100
40	E	208/216 (96%)	206 (99%)	2 (1%)	0	100	100
41	F	223/225 (99%)	214 (96%)	8 (4%)	1 (0%)	30	60
42	G	229/240 (95%)	224 (98%)	5 (2%)	0	100	100
43	H	188/190 (99%)	185 (98%)	3 (2%)	0	100	100
44	I	201/213 (94%)	193 (96%)	8 (4%)	0	100	100
45	J	168/170 (99%)	164 (98%)	4 (2%)	0	100	100
46	L	208/210 (99%)	202 (97%)	6 (3%)	0	100	100
47	M	136/138 (99%)	126 (93%)	10 (7%)	0	100	100
48	N	201/203 (99%)	197 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	O	197/199 (99%)	192 (98%)	5 (2%)	0	100	100
50	P	151/153 (99%)	145 (96%)	6 (4%)	0	100	100
51	Q	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
52	S	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
53	T	157/159 (99%)	149 (95%)	8 (5%)	0	100	100
54	U	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
55	V	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
56	X	116/118 (98%)	111 (96%)	5 (4%)	0	100	100
57	Y	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
58	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
59	a	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
60	b	100/104 (96%)	98 (98%)	2 (2%)	0	100	100
61	c	96/98 (98%)	94 (98%)	2 (2%)	0	100	100
62	d	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
63	e	126/128 (98%)	120 (95%)	6 (5%)	0	100	100
64	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
65	g	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
66	h	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
67	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
68	j	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
69	k	67/69 (97%)	67 (100%)	0	0	100	100
70	l	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
71	m	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
72	n	23/25 (92%)	23 (100%)	0	0	100	100
73	o	102/104 (98%)	100 (98%)	2 (2%)	0	100	100
74	p	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
75	r	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
76	s	194/196 (99%)	183 (94%)	11 (6%)	0	100	100
77	t	151/153 (99%)	114 (76%)	24 (16%)	13 (9%)	0	4
81	EF	830/855 (97%)	762 (92%)	65 (8%)	3 (0%)	30	60
All	All	11982/12272 (98%)	11529 (96%)	434 (4%)	19 (0%)	44	71

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	XX	62	PRO
77	t	60	VAL
77	t	98	ILE
77	t	143	VAL
77	t	24	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	159/159 (100%)	146 (92%)	13 (8%)	10	35
2	W	55/86 (64%)	53 (96%)	2 (4%)	31	58
4	AA	175/181 (97%)	157 (90%)	18 (10%)	7	25
5	BB	194/194 (100%)	185 (95%)	9 (5%)	24	53
6	CC	187/187 (100%)	181 (97%)	6 (3%)	34	60
7	EE	224/224 (100%)	217 (97%)	7 (3%)	35	60
8	GG	197/207 (95%)	173 (88%)	24 (12%)	5	19
9	HH	165/169 (98%)	159 (96%)	6 (4%)	31	58
10	II	178/178 (100%)	173 (97%)	5 (3%)	38	62
11	JJ	161/161 (100%)	160 (99%)	1 (1%)	78	81
12	LL	130/136 (96%)	124 (95%)	6 (5%)	24	53
13	NN	130/130 (100%)	125 (96%)	5 (4%)	29	57
14	OO	106/106 (100%)	103 (97%)	3 (3%)	38	62
15	VV	67/67 (100%)	66 (98%)	1 (2%)	57	72
16	WW	112/112 (100%)	110 (98%)	2 (2%)	51	70
17	XX	113/113 (100%)	109 (96%)	4 (4%)	32	58
18	YY	107/107 (100%)	99 (92%)	8 (8%)	12	38
19	aa	88/88 (100%)	83 (94%)	5 (6%)	18	47
20	bb	75/75 (100%)	71 (95%)	4 (5%)	20	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	ee	47/47 (100%)	44 (94%)	3 (6%)	16	44
22	DD	190/190 (100%)	183 (96%)	7 (4%)	30	58
23	FF	158/161 (98%)	152 (96%)	6 (4%)	29	57
24	KK	87/87 (100%)	82 (94%)	5 (6%)	18	47
25	MM	99/99 (100%)	94 (95%)	5 (5%)	21	50
26	PP	105/105 (100%)	100 (95%)	5 (5%)	23	52
27	QQ	116/116 (100%)	111 (96%)	5 (4%)	26	54
28	RR	119/119 (100%)	113 (95%)	6 (5%)	22	50
29	SS	125/125 (100%)	120 (96%)	5 (4%)	28	56
30	TT	111/111 (100%)	106 (96%)	5 (4%)	24	53
31	UU	92/92 (100%)	90 (98%)	2 (2%)	45	66
32	ZZ	66/66 (100%)	64 (97%)	2 (3%)	36	61
33	cc	55/55 (100%)	55 (100%)	0	100	100
34	dd	48/48 (100%)	47 (98%)	1 (2%)	47	67
35	ff	61/61 (100%)	58 (95%)	3 (5%)	22	51
36	A	190/190 (100%)	179 (94%)	11 (6%)	18	47
37	B	342/342 (100%)	327 (96%)	15 (4%)	25	54
38	C	302/302 (100%)	285 (94%)	17 (6%)	19	47
39	D	247/247 (100%)	240 (97%)	7 (3%)	38	62
40	E	190/190 (100%)	179 (94%)	11 (6%)	18	47
41	F	196/196 (100%)	185 (94%)	11 (6%)	19	47
42	G	200/205 (98%)	192 (96%)	8 (4%)	28	56
43	H	169/169 (100%)	161 (95%)	8 (5%)	23	52
44	I	175/180 (97%)	167 (95%)	8 (5%)	24	53
45	J	143/143 (100%)	135 (94%)	8 (6%)	19	47
46	L	175/175 (100%)	169 (97%)	6 (3%)	32	59
47	M	117/117 (100%)	110 (94%)	7 (6%)	17	46
48	N	171/171 (100%)	165 (96%)	6 (4%)	32	58
49	O	171/171 (100%)	163 (95%)	8 (5%)	23	52
50	P	134/134 (100%)	132 (98%)	2 (2%)	57	72
51	Q	164/164 (100%)	156 (95%)	8 (5%)	22	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	S	157/157 (100%)	151 (96%)	6 (4%)	29	57
53	T	139/139 (100%)	131 (94%)	8 (6%)	18	47
54	U	89/89 (100%)	85 (96%)	4 (4%)	24	53
55	V	106/106 (100%)	99 (93%)	7 (7%)	15	43
56	X	106/106 (100%)	101 (95%)	5 (5%)	23	52
57	Y	124/124 (100%)	116 (94%)	8 (6%)	15	43
58	Z	117/117 (100%)	115 (98%)	2 (2%)	53	71
59	a	119/119 (100%)	116 (98%)	3 (2%)	42	64
60	b	84/84 (100%)	81 (96%)	3 (4%)	31	58
61	c	84/84 (100%)	81 (96%)	3 (4%)	31	58
62	d	98/98 (100%)	92 (94%)	6 (6%)	17	45
63	e	114/114 (100%)	105 (92%)	9 (8%)	11	36
64	f	88/88 (100%)	83 (94%)	5 (6%)	18	47
65	g	98/98 (100%)	92 (94%)	6 (6%)	17	45
66	h	109/109 (100%)	107 (98%)	2 (2%)	51	70
67	i	86/86 (100%)	84 (98%)	2 (2%)	44	66
68	j	73/73 (100%)	71 (97%)	2 (3%)	39	63
69	k	64/64 (100%)	60 (94%)	4 (6%)	16	44
70	l	47/47 (100%)	46 (98%)	1 (2%)	47	67
71	m	48/48 (100%)	47 (98%)	1 (2%)	47	67
72	n	24/24 (100%)	22 (92%)	2 (8%)	10	34
73	o	92/92 (100%)	86 (94%)	6 (6%)	15	43
74	p	74/74 (100%)	72 (97%)	2 (3%)	39	63
75	r	108/108 (100%)	105 (97%)	3 (3%)	38	62
76	s	164/164 (100%)	155 (94%)	9 (6%)	19	48
77	t	126/126 (100%)	82 (65%)	44 (35%)	0	1
81	EF	710/726 (98%)	650 (92%)	60 (8%)	10	33
All	All	10436/10522 (99%)	9893 (95%)	543 (5%)	22	49

5 of 543 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
77	t	94	LYS

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Mol	Chain	Res	Type
77	t	133	LEU
77	t	93	LYS
81	EF	481	LYS
36	A	207	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 169 such sidechains are listed below:

Mol	Chain	Res	Type
49	O	14	HIS
63	e	43	ASN
50	P	80	GLN
56	X	105	ASN
68	j	16	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	9	1653/1670 (98%)	354 (21%)	19 (1%)
78	5	3488/3543 (98%)	747 (21%)	59 (1%)
79	7	118/119 (99%)	9 (7%)	0
80	8	149/156 (95%)	30 (20%)	1 (0%)
82	1	10/11 (90%)	4 (40%)	0
83	PT	10/11 (90%)	9 (90%)	0
84	ET	73/76 (96%)	21 (28%)	1 (1%)
All	All	5501/5586 (98%)	1174 (21%)	80 (1%)

5 of 1174 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	9	2	A
3	9	3	C
3	9	4	C
3	9	14	C
3	9	25	A

5 of 80 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
78	5	2266	C
78	5	4699	U

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Mol	Chain	Res	Type
78	5	2474	G
78	5	3904	G
78	5	4936	G

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	DDE	EF	715	81	18,20,21	1.03	1 (5%)	17,28,30	1.08	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	DDE	EF	715	81	-	5/20/21/23	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	EF	715	DDE	CD2-CG	2.68	1.41	1.36

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	EF	715	DDE	CAU-CBW-CBI	-3.36	104.65	111.22

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
81	EF	715	DDE	CA-CB-CG-ND1
81	EF	715	DDE	OAG-CBI-CBW-CAU
81	EF	715	DDE	CA-CB-CG-CD2
81	EF	715	DDE	NAD-CBI-CBW-CAU
81	EF	715	DDE	CAT-CAU-CBW-CBI

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
81	EF	715	DDE	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 214 ligands modelled in this entry, 214 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
78	5	26
3	9	20

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Mol	Chain	Number of breaks
40	E	3
60	b	1

The worst 5 of 50 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	9	1219:A	O3'	1220:A	P	46.96
1	b	76:VAL	C	89:VAL	N	37.07
1	E	77:ALA	C	92:LEU	N	30.34
1	5	1219:G	O3'	1233:G	P	22.45
1	9	1119:G	O3'	1121:G	P	19.74

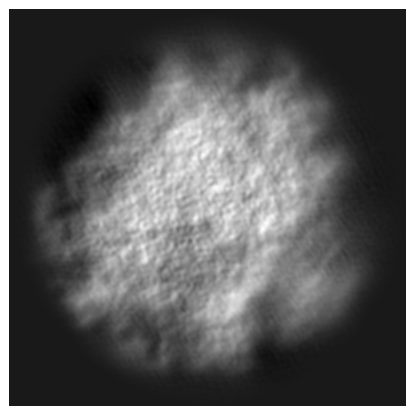
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72168. These allow visual inspection of the internal detail of the map and identification of artifacts.

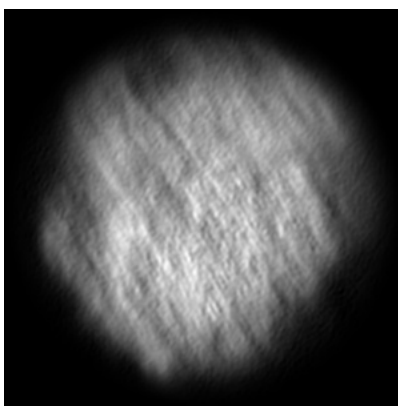
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

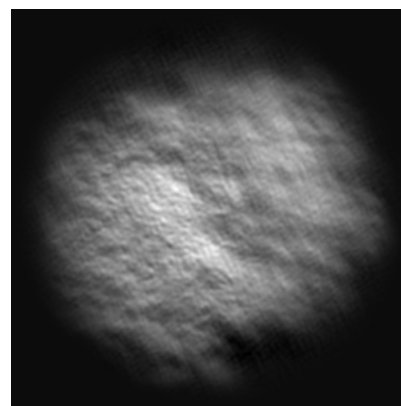
6.1.1 Primary map



X

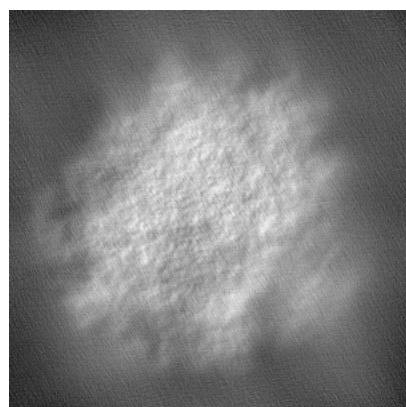


Y

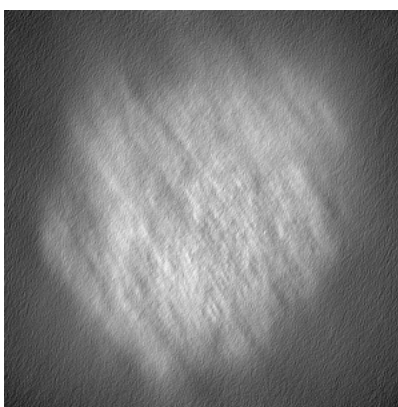


Z

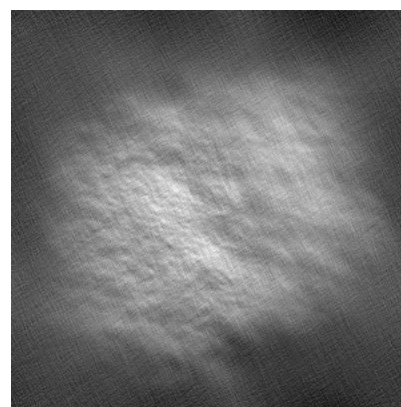
6.1.2 Raw map



X



Y

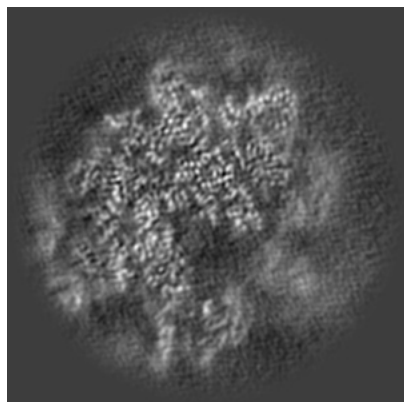


Z

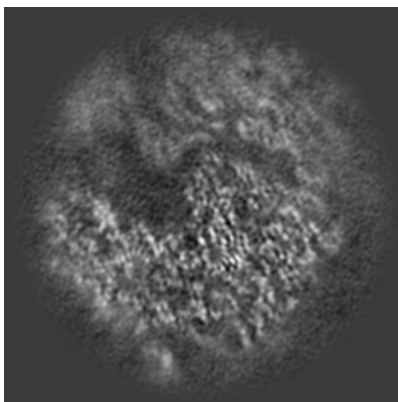
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

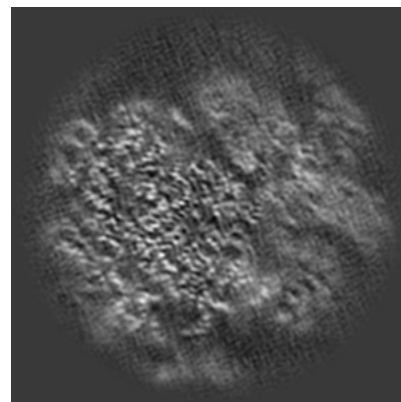
6.2.1 Primary map



X Index: 180

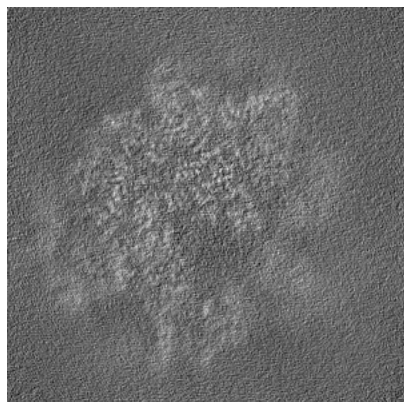


Y Index: 180

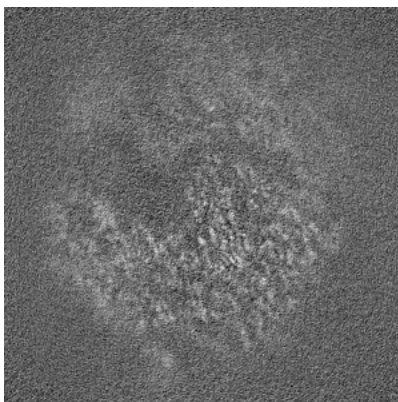


Z Index: 180

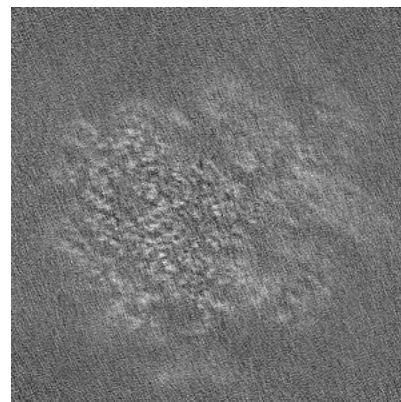
6.2.2 Raw map



X Index: 180



Y Index: 180

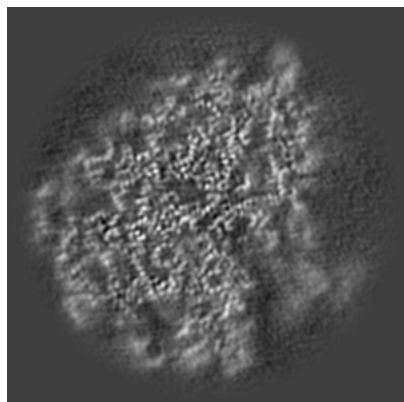


Z Index: 180

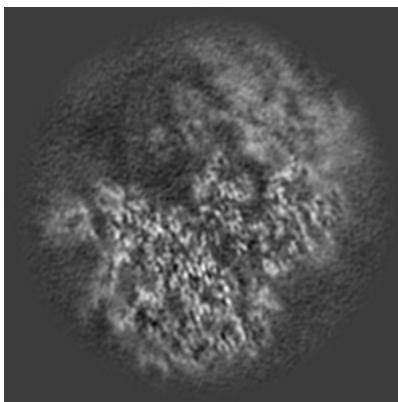
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

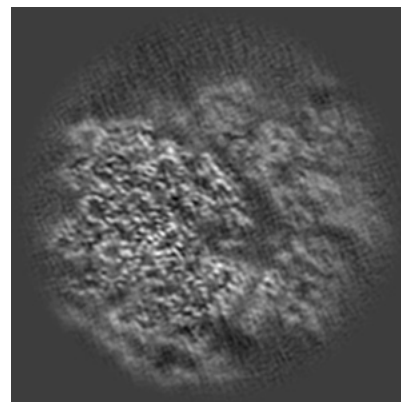
6.3.1 Primary map



X Index: 148

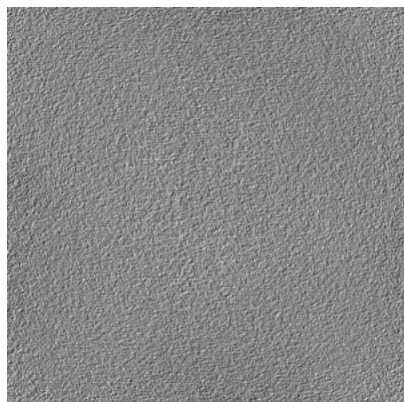


Y Index: 149

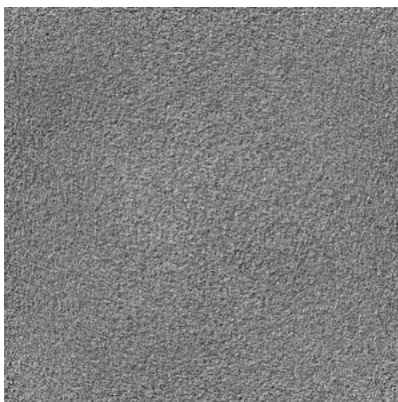


Z Index: 171

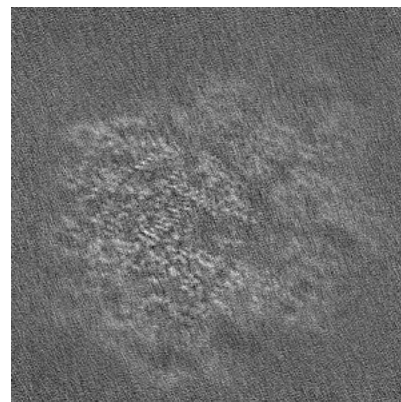
6.3.2 Raw map



X Index: 0



Y Index: 0

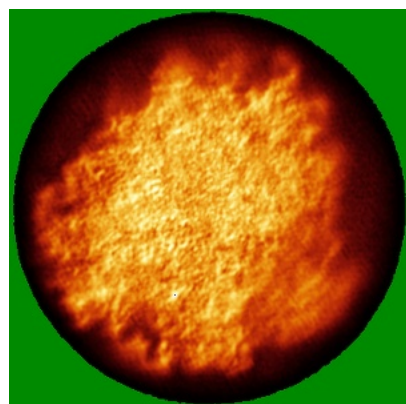


Z Index: 174

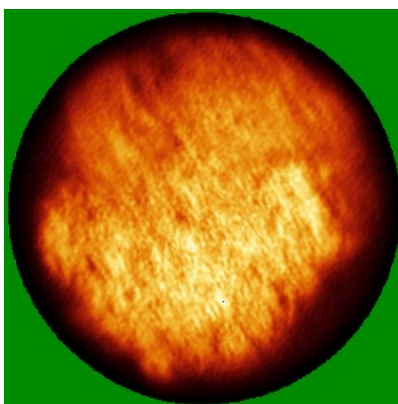
The images above show the largest variance slices of the map in three orthogonal directions.

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

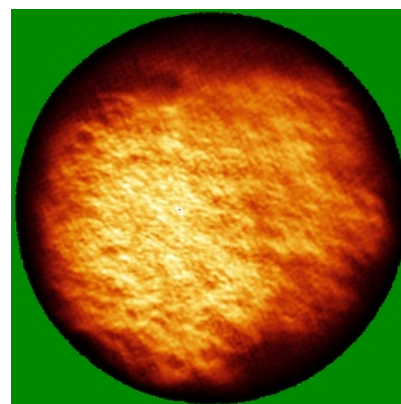
6.4.1 Primary map



X

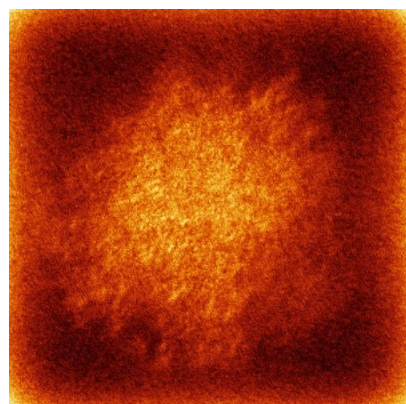


Y

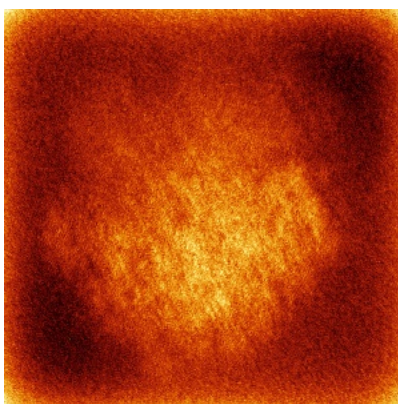


Z

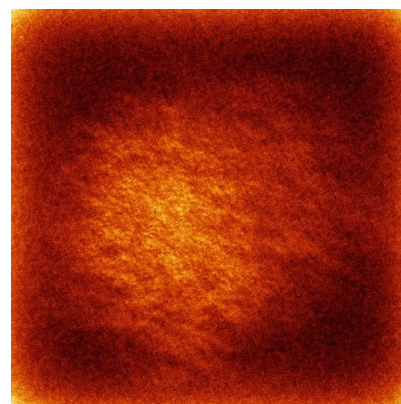
6.4.2 Raw map



X



Y

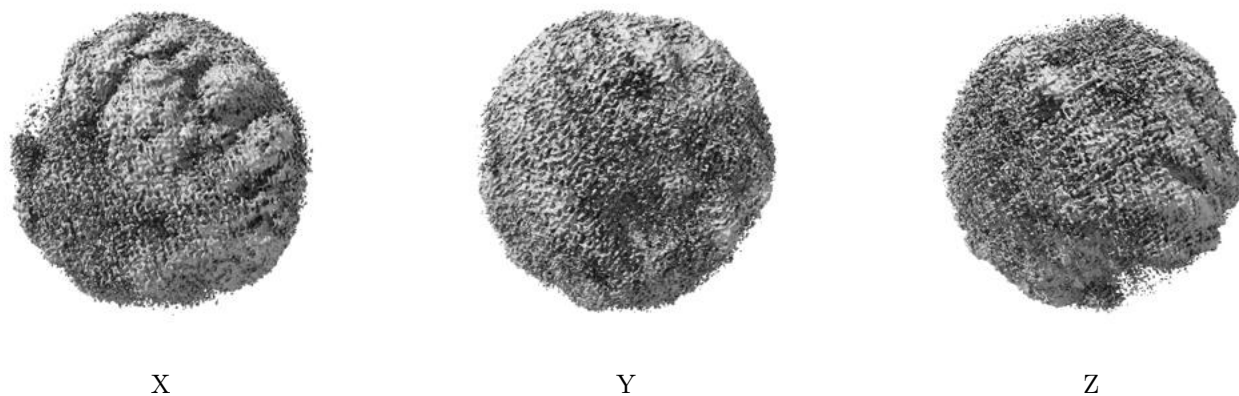


Z

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

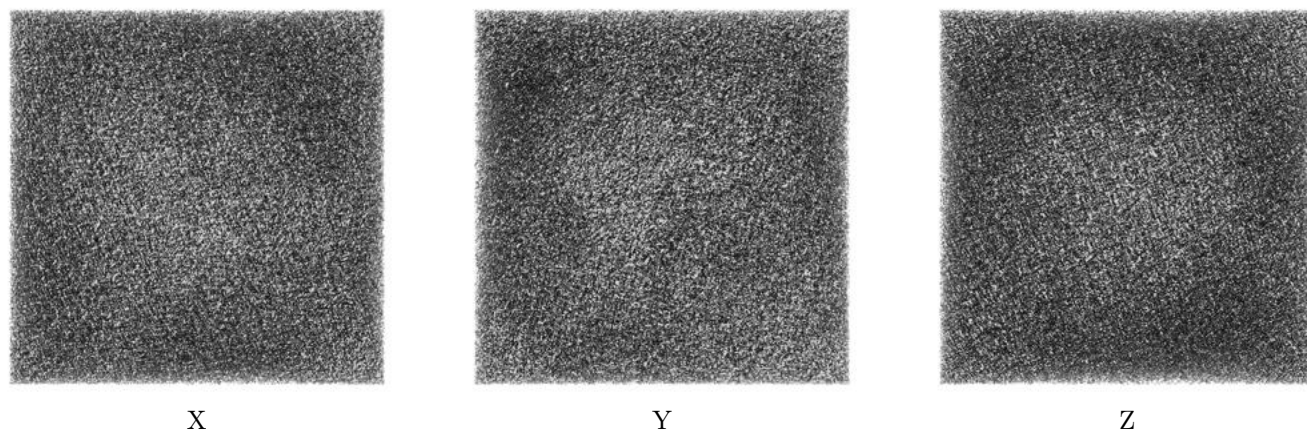
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

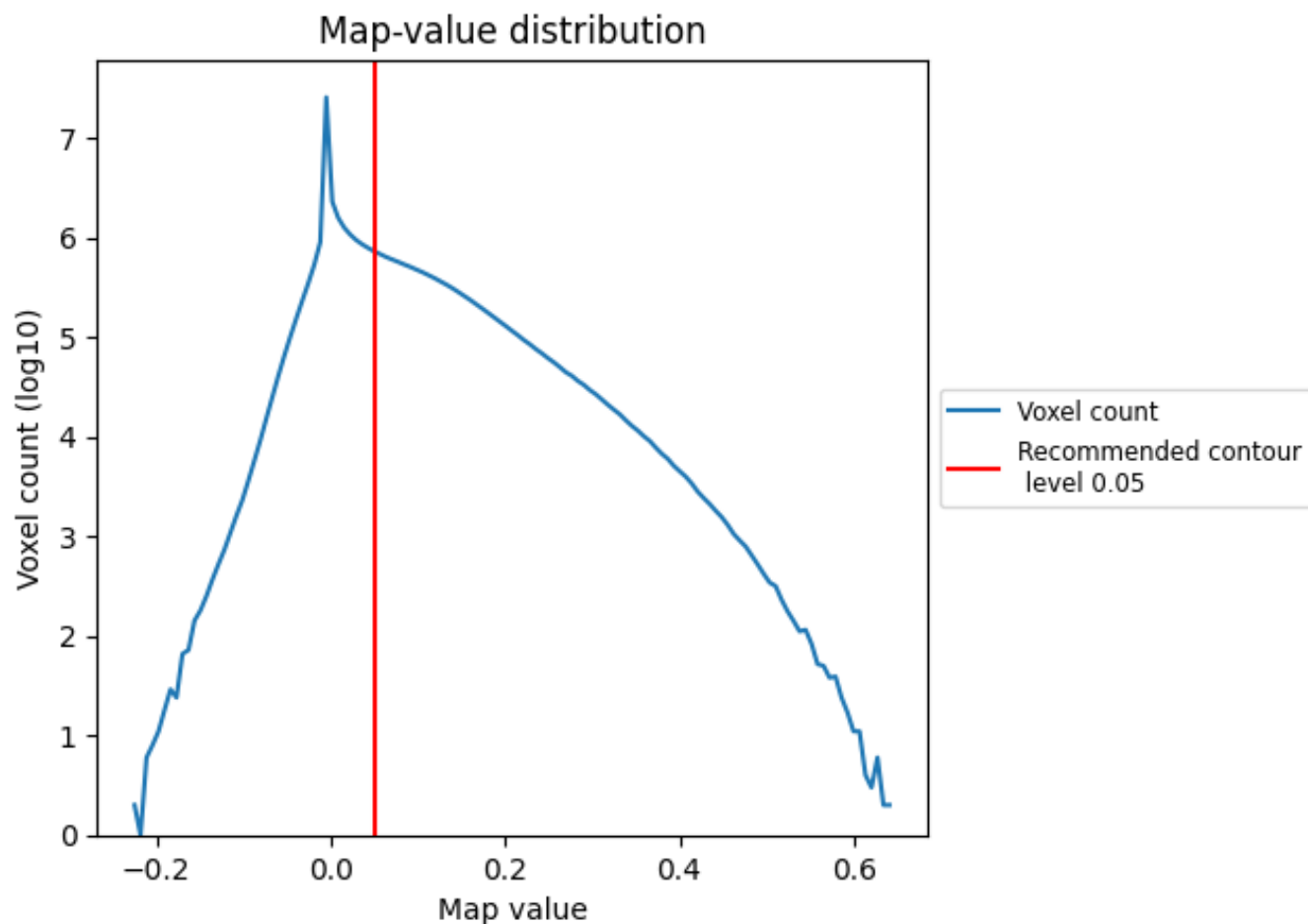
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

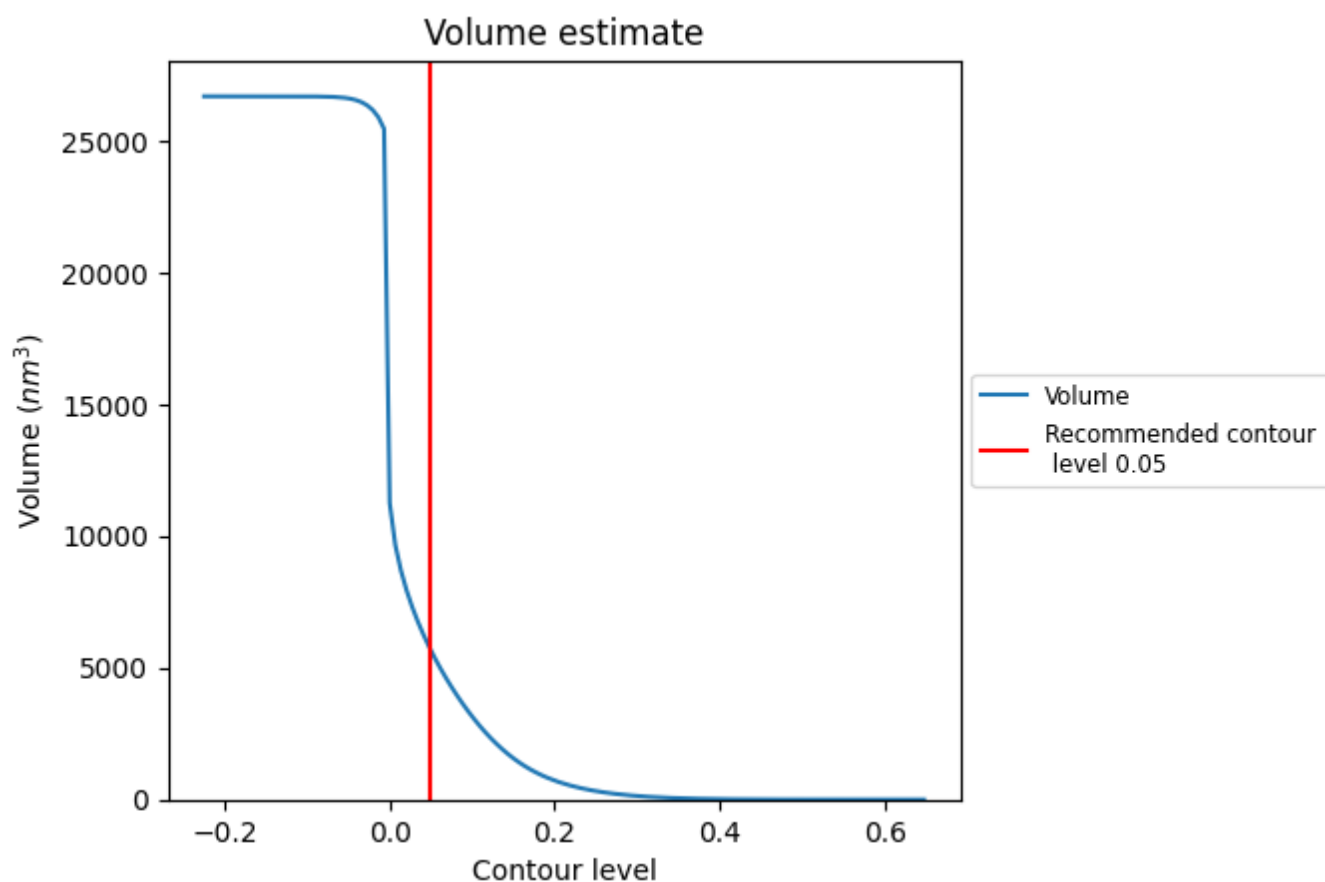
This section contains the results of statistical analysis of the map.

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.

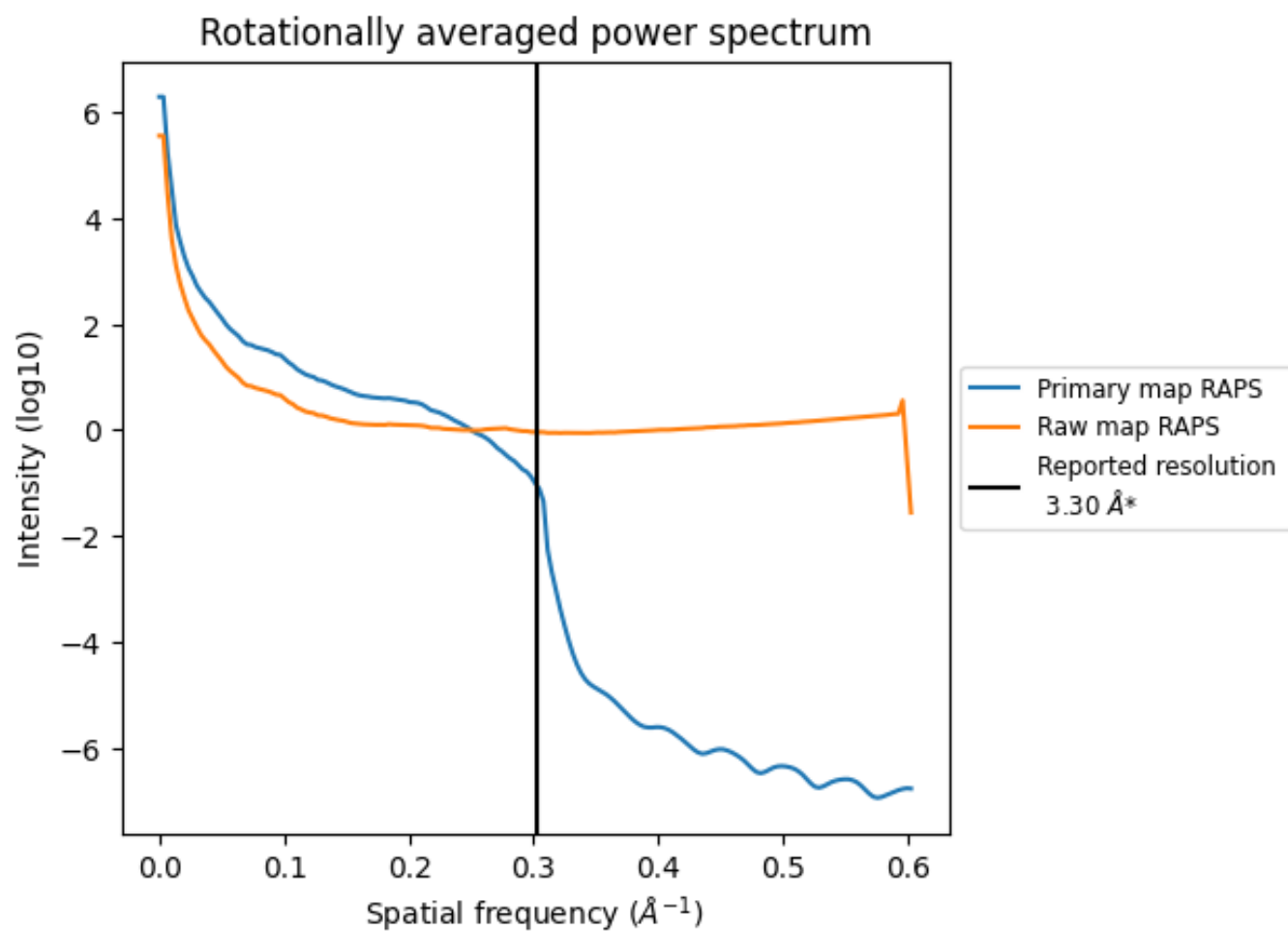
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5668 nm^3 ; this corresponds to an approximate mass of 5120 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 ⓘ

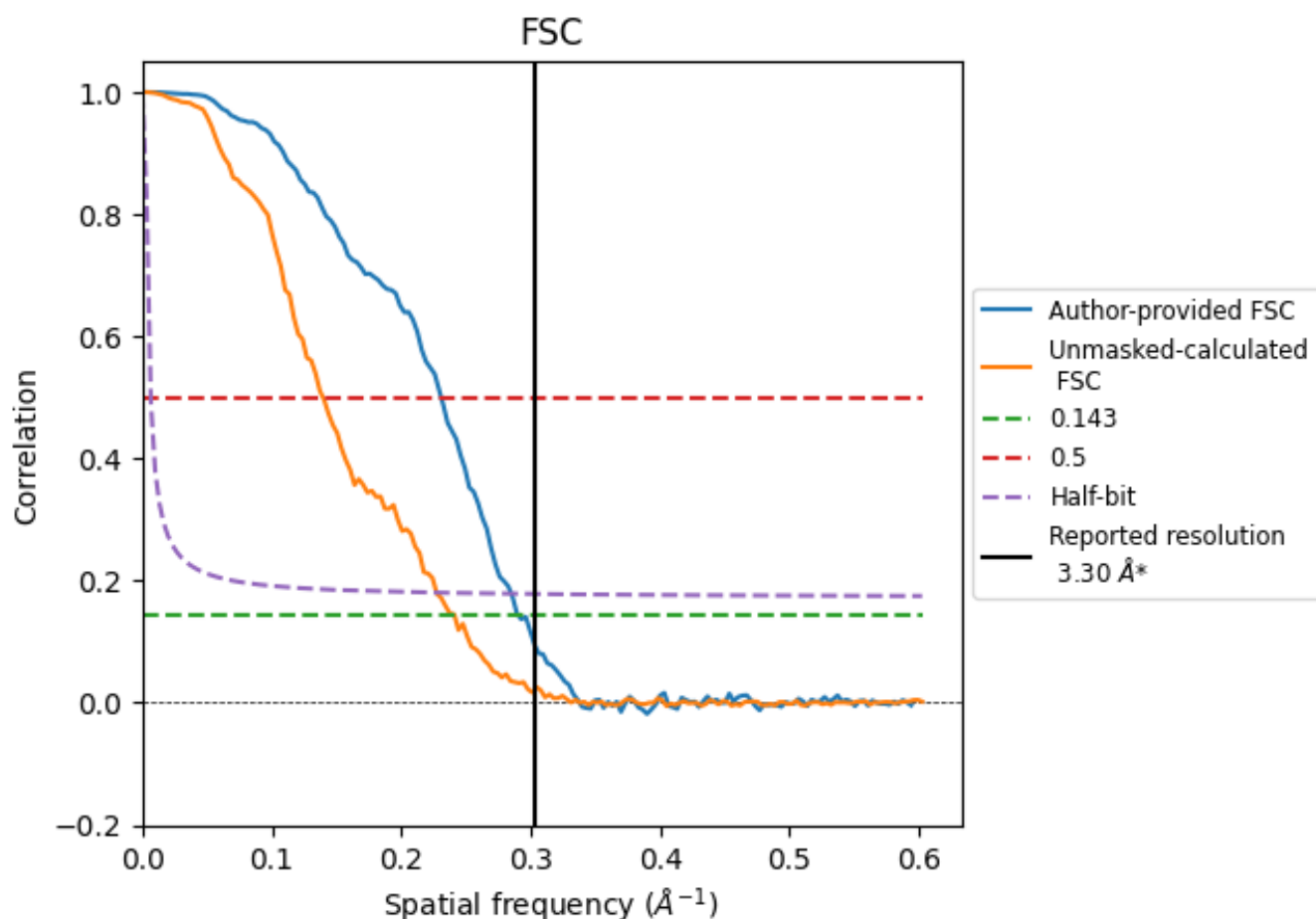


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

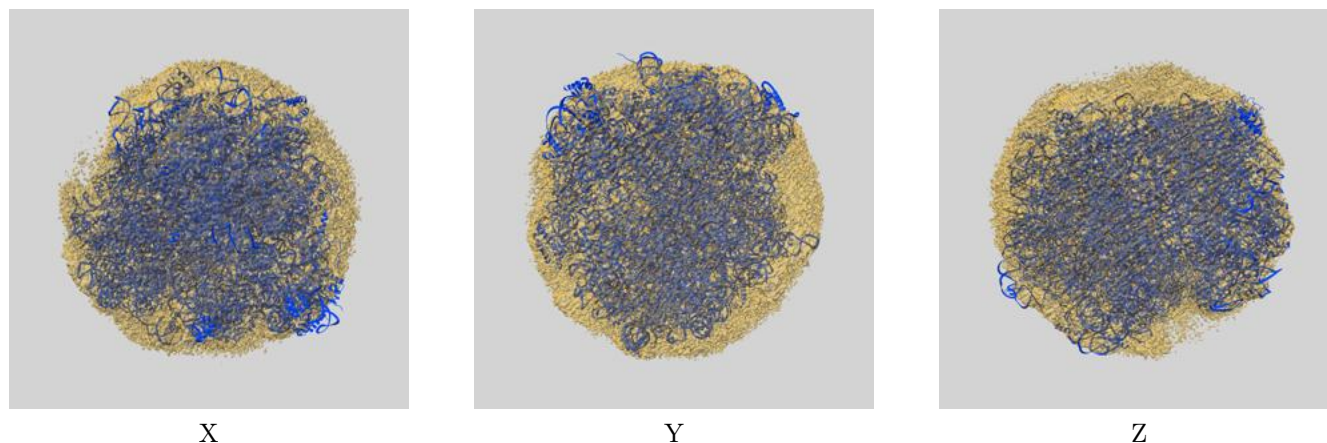
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.44	4.33	3.51
Unmasked-calculated*	4.15	7.16	4.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.15 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

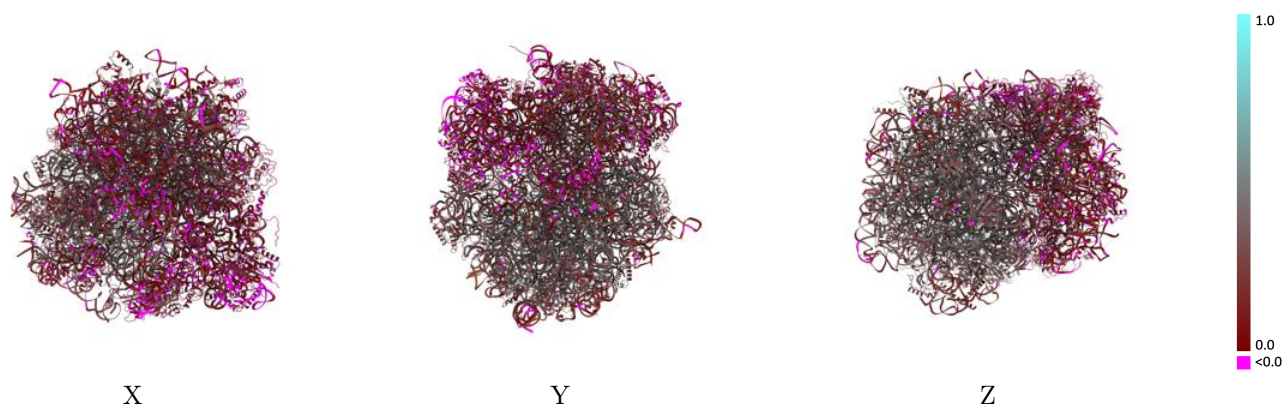
This section contains information regarding the fit between EMDB map EMD-72168 and PDB model 9Q2M. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



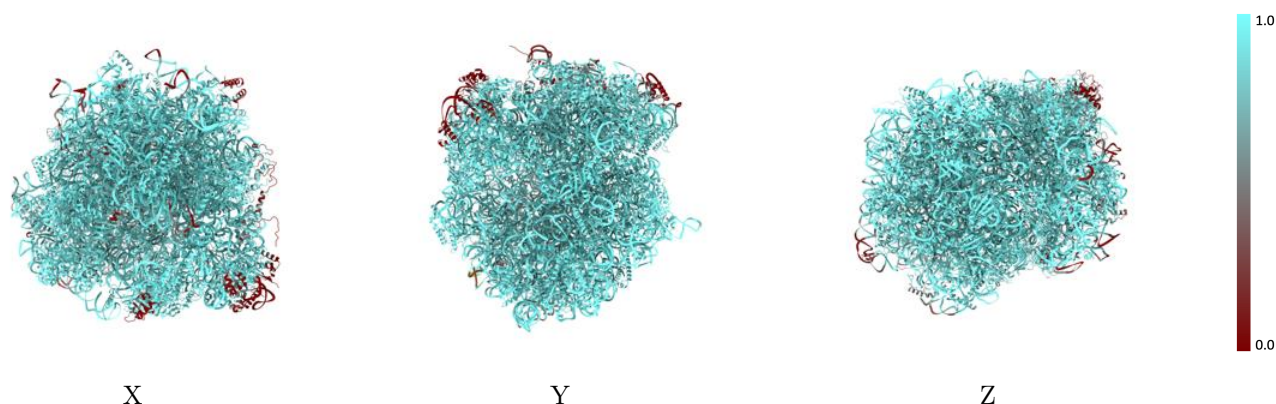
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



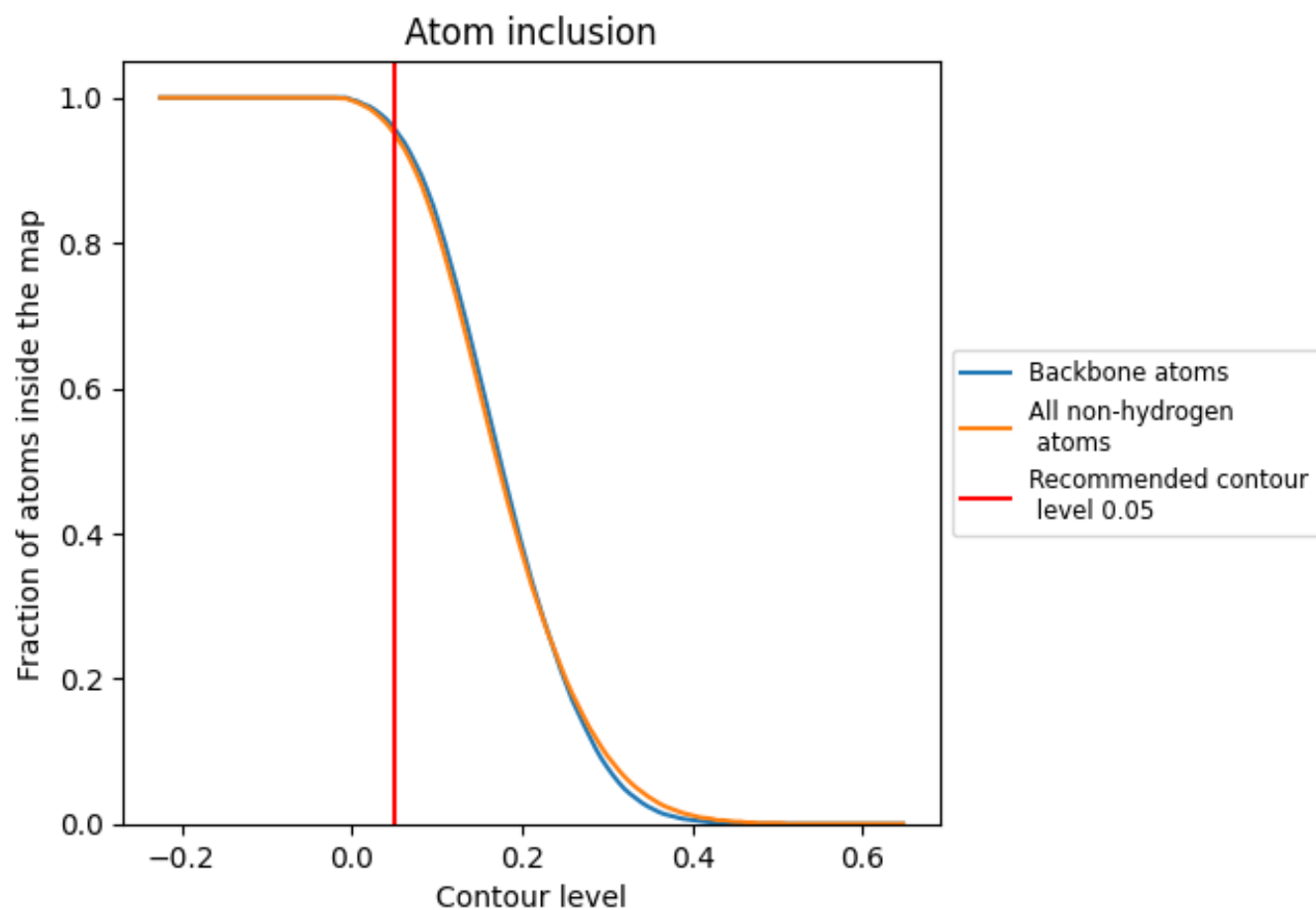
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































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

Chain	Atom inclusion	Q-score
All	 0.9510	 0.2780
1	 0.9430	 0.1730
5	 0.9790	 0.3520
7	 0.9920	 0.3590
8	 0.9950	 0.3710
9	 0.9450	 0.1810
A	 0.9680	 0.3900
AA	 0.8540	 0.1920
B	 0.9700	 0.3820
BB	 0.9760	 0.0870
C	 0.9680	 0.3730
CC	 0.9090	 0.1970
D	 0.9830	 0.3030
DD	 0.8770	 0.1030
E	 0.7700	 0.2930
EE	 0.9460	 0.1610
EF	 0.9390	 0.2080
ET	 0.9420	 0.0930
F	 0.9580	 0.3560
FF	 0.9880	 0.1000
G	 0.9740	 0.3170
GG	 0.8190	 0.1420
H	 0.9340	 0.3240
HH	 0.6760	 0.1420
I	 0.9670	 0.3520
II	 0.9810	 0.1700
J	 0.9570	 0.2690
JJ	 0.9320	 0.1260
KK	 0.9520	 0.0600
L	 0.9580	 0.3490
LL	 0.9810	 0.2480
M	 0.9690	 0.3240
MM	 0.5670	 0.0520
N	 0.9760	 0.3990
NN	 0.9730	 0.1570



















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Chain	Atom inclusion	Q-score
O	 0.9580	 0.3700
OO	 0.9760	 0.1390
P	 0.9810	 0.3960
PP	 0.9630	 0.1520
PT	 0.9490	 0.0930
Q	 0.9720	 0.3850
QQ	 0.7060	 0.1050
R	 0.9530	 0.1800
RR	 0.6030	 0.0970
S	 0.9680	 0.3700
SS	 0.9560	 0.1170
T	 0.9800	 0.3770
TT	 0.6630	 0.0940
U	 0.9850	 0.3120
UU	 0.5890	 0.0670
V	 0.9840	 0.3520
VV	 0.7880	 0.2030
W	 0.9290	 0.1080
WW	 0.9400	 0.2480
X	 0.9750	 0.3660
XX	 0.9330	 0.2070
Y	 0.9650	 0.3500
YY	 0.7850	 0.0730
Z	 0.9910	 0.3350
ZZ	 0.9910	 0.0980
a	 0.9900	 0.3910
aa	 0.9900	 0.2380
b	 0.9390	 0.2990
bb	 0.9830	 0.1560
c	 0.9990	 0.3380
cc	 0.9920	 0.0700
d	 0.9840	 0.4010
dd	 0.9910	 0.1640
e	 0.9820	 0.3950
ee	 0.9270	 0.1400
f	 0.9660	 0.3940
ff	 0.8230	 0.0960
g	 0.9780	 0.3680
h	 0.9600	 0.3200
i	 0.9900	 0.3450
j	 0.9790	 0.4160
k	 0.9710	 0.3150

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Chain	Atom inclusion	Q-score
l	 0.9720	 0.3660
m	 0.9760	 0.3410
n	 0.9730	 0.3070
o	 0.9630	 0.3450
p	 0.9620	 0.3590
r	 0.9350	 0.3420
s	 0.9280	 0.1750
t	 0.8480	 0.1390