



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 09:55 AM EST

PDB ID : 7MDZ  
EMDB ID : EMD-23785  
Title : 80S rabbit ribosome stalled with benzamide-CHX  
Authors : Koga, Y.; Hoang, E.M.; Park, Y.; Keszei, A.F.A.; Murray, J.; Shao, S.; Liao, B.B.  
Deposited on : 2021-04-06  
Resolution : 3.20 Å (reported)  
Based on initial model : 6SGC

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

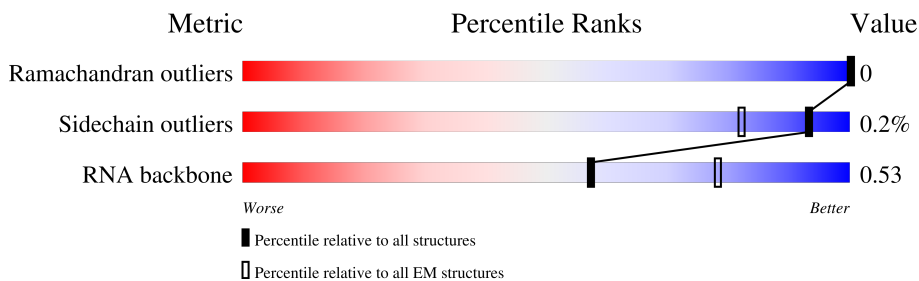
EMDB validation analysis : 0.0.1.dev43  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	A	257	96%
2	B	403	98%
3	C	425	85% 15%
4	D	297	99%
5	E	291	74% 26%
6	F	247	91% 9%
7	G	319	73% 27%
8	H	192	99%

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Mol	Chain	Length	Quality of chain
9	I	214	9% 96%
10	J	178	22% 96%
11	L	211	13% 99%
12	M	218	63% 37%
13	N	204	100%
14	O	203	98%
15	P	184	83% 17%
16	Q	188	99%
17	R	196	19% 91% 8%
18	S	176	99%
19	T	160	10% 98%
20	U	128	16% 77% 23%
21	V	140	11% 99%
22	W	157	40% 60%
23	X	156	12% 76% 24%
24	Y	145	6% 92% 8%
25	Z	136	15% 99%
26	a	148	99%
27	b	245	14% 42% 58%
28	c	115	13% 85% 15%
29	d	125	10% 86% 14%
30	e	135	95% 5%
31	f	110	99%
32	g	116	11% 97%
33	h	123	8% 98%

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Mol	Chain	Length	Quality of chain
34	i	105	21% 97%
35	j	97	89% 11%
36	k	70	37% 97%
37	l	51	96%
38	m	102	6% 51% 49%
39	n	25	8% 100%
40	o	106	12% 98%
41	p	92	9% 99%
42	r	137	91% 9%
43	AA	295	45% 74% 26%
44	BB	264	35% 81% 19%
45	CC	293	26% 75% 25%
46	DD	243	70% 93% 6%
47	EE	263	48% 99%
48	FF	204	60% 91% 9%
49	GG	249	63% 95% 5%
50	HH	194	74% 94% 5%
51	II	208	37% 98%
52	JJ	194	43% 95% 5%
53	KK	165	48% 58% 42%
54	LL	158	22% 90% 9%
55	MM	132	89% 89% 11%
56	NN	151	39% 99%
57	OO	168	22% 81% 19%
58	PP	145	70% 89% 11%

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Mol	Chain	Length	Quality of chain
59	QQ	146	63% 97%
60	RR	135	79% 97%
61	SS	152	66% 94% 5%
62	TT	145	65% 97%
63	UU	119	66% 84% 16%
64	VV	83	61% 100%
65	WW	130	31% 99%
66	XX	143	29% 99%
67	YY	130	47% 95% 5%
68	ZZ	125	48% 60% 40%
69	aa	115	32% 87% 12%
70	bb	84	63% 99%
71	cc	69	59% 87% 10%
72	dd	56	54% 98%
73	ee	133	29% 42% 57%
74	ff	156	42% 43% 56%
75	gg	317	92% 99%
76	5	3603	11% 79% 20%
77	7	120	92% 8%
78	8	156	7% 79% 18%
79	2	76	64% 71% 29%
80	9	1869	19% 72% 19% 9%
81	6	10	70% 50% 50%

## 2 Entry composition [i](#)

There are 84 unique types of molecules in this entry. The entry contains 211192 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ribosomal protein L8.

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

- Molecule 2 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	initiating methionine	UNP G1TL06

- Molecule 3 is a protein called 60S ribosomal protein L4.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called Ribosomal\_L18\_c domain-containing protein.

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

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

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

- Molecule 6 is a protein called 60S ribosomal protein L7.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called 60S ribosomal protein L7a.

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

- Molecule 10 is a protein called 60S ribosomal protein L11.

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

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

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called 60S ribosomal protein L14.

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

- Molecule 13 is a protein called Ribosomal protein L15.



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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called Ribosomal protein L18.

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

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 17 is a protein called Ribosomal protein L19.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called 60S ribosomal protein L18a.

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

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	1	MET	THR	conflict	UNP G1TTY7
S	18	PRO	-	insertion	UNP G1TTY7
S	19	THR	-	insertion	UNP G1TTY7
S	20	PRO	SER	conflict	UNP G1TTY7
S	22	CYS	SER	conflict	UNP G1TTY7
S	23	ARG	PRO	conflict	UNP G1TTY7
S	24	THR	ALA	conflict	UNP G1TTY7
S	49	SER	LEU	conflict	UNP G1TTY7
S	50	GLN	GLU	conflict	UNP G1TTY7
S	95	ARG	HIS	conflict	UNP G1TTY7
S	101	THR	ILE	conflict	UNP G1TTY7
S	102	THR	MET	conflict	UNP G1TTY7
S	104	GLY	SER	conflict	UNP G1TTY7
S	126	ILE	VAL	conflict	UNP G1TTY7
S	132	ILE	MET	conflict	UNP G1TTY7
S	135	SER	ALA	conflict	UNP G1TTY7
S	136	LYS	ARG	conflict	UNP G1TTY7
S	138	ARG	PRO	conflict	UNP G1TTY7
S	149	LYS	ARG	conflict	UNP G1TTY7
S	151	LYS	ARG	conflict	UNP G1TTY7
S	168	THR	TYR	conflict	UNP G1TTY7
S	169	THR	ALA	conflict	UNP G1TTY7
S	176	PHE	-	insertion	UNP G1TTY7

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	T	157	1284	815	250	214	5	0	0

- Molecule 20 is a protein called eL22.

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

There are 11 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
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called Ribosomal protein L23.

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

- Molecule 22 is a protein called 60S ribosomal protein L24.

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

- Molecule 23 is a protein called eL23.

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

- Molecule 24 is a protein called uL24.

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

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

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

- Molecule 26 is a protein called 60S ribosomal protein L27a.

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

- Molecule 27 is a protein called 60S ribosomal protein L29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	113	Total	C	N	O	S	0	0
			897	560	185	146	6		

- Molecule 33 is a protein called eL35.

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

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

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	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 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	49	Total	C	N	O	S	0	0
			438	280	95	62	1		

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called 60s ribosomal protein l41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	AA	217	Total	C	N	O	S	0	0
			1712	1087	300	317	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AA	114	THR	ALA	conflict	UNP G1TLT8

- Molecule 44 is a protein called eS1.

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

- Molecule 45 is a protein called uS5.

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

- Molecule 46 is a protein called Ribosomal protein S3.

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

- Molecule 47 is a protein called 40S ribosomal protein S4.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	25	GLY	SER	conflict	UNP G1TK17
EE	51	ARG	LYS	conflict	UNP G1TK17
EE	78	THR	ALA	conflict	UNP G1TK17
EE	156	VAL	MET	conflict	UNP G1TK17

- Molecule 48 is a protein called uS7.

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

- Molecule 49 is a protein called eS6.

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

- Molecule 50 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	HH	184	Total	C	N	O	S	0	0
			1480	948	269	262	1		

- Molecule 51 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	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 52 is a protein called uS4.

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

- Molecule 53 is a protein called S10\_ plectin domain-containing protein.

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

- Molecule 54 is a protein called uS17.

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

- Molecule 55 is a protein called eS12.



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

- Molecule 56 is a protein called uS15.

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

- Molecule 57 is a protein called uS11.

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

- Molecule 58 is a protein called uS19.

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

- Molecule 59 is a protein called uS9.

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

- Molecule 60 is a protein called eS17.

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

- Molecule 61 is a protein called uS13.

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

- Molecule 62 is a protein called eS19.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 63 is a protein called uS10.

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

- Molecule 64 is a protein called 40S ribosomal protein S21.

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

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 65 is a protein called uS8.

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

- Molecule 66 is a protein called uS12.

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

- Molecule 67 is a protein called 40S ribosomal protein S24.

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

- Molecule 68 is a protein called eS25.

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

- Molecule 69 is a protein called 40S ribosomal protein S26.

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

There are 3 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
aa	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 70 is a protein called eS27.

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

- Molecule 71 is a protein called eS28.

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

- Molecule 72 is a protein called eS29.

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

- Molecule 73 is a protein called eS30.

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

- Molecule 74 is a protein called eS31.

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

- Molecule 75 is a protein called RACK1.

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

- Molecule 76 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
76	5	3541	75929	33814	13902	24672	3541	0	0

- Molecule 77 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
77	7	119	2538	1132	454	834	118	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
7	2	U	N	conflict	GB X06789.1
7	36	C	N	conflict	GB X06789.1
7	102	U	N	conflict	GB X06789.1
7	112	U	N	conflict	GB X06789.1
7	114	U	N	conflict	GB X06789.1
7	119	U	C	conflict	GB X06789.1
7	120	U	N	conflict	GB X06789.1

- Molecule 78 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
78	8	151	3208	1432	564	1062	150	0	0

- Molecule 79 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
79	2	76	1623	723	290	534	76	0	0

- Molecule 80 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
80	9	1697	36229	16171	6507	11855	1696	0	0

- Molecule 81 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
81	6	10	210	94	33	73	10	0	0

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	A	1	Total	Mg	0
			1	1	
82	B	1	Total	Mg	0
			1	1	
82	P	1	Total	Mg	0
			1	1	
82	V	1	Total	Mg	0
			1	1	
82	g	1	Total	Mg	0
			1	1	
82	LL	1	Total	Mg	0
			1	1	
82	5	189	Total	Mg	0
			189	189	
82	7	6	Total	Mg	0
			6	6	
82	8	5	Total	Mg	0
			5	5	

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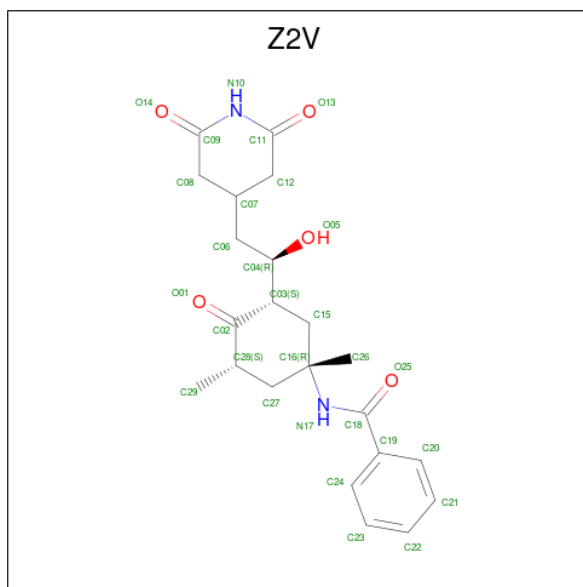
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Mol	Chain	Residues	Atoms		AltConf
82	2	2	Total 2	Mg 2	0
82	9	69	Total 69	Mg 69	0

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 84 is N-[(1R,3S,4R,5S)-3-[(1R)-2-[(2R,4r,6S)-2,6-dihydroxypiperidin-4-yl]-1-hydroxyethyl]-4-hydroxy-1,5-dimethylcyclohexyl]benzamide (three-letter code: Z2V) (formula: C<sub>22</sub>H<sub>28</sub>N<sub>2</sub>O<sub>5</sub>) (labeled as "Ligand of Interest" by depositor).

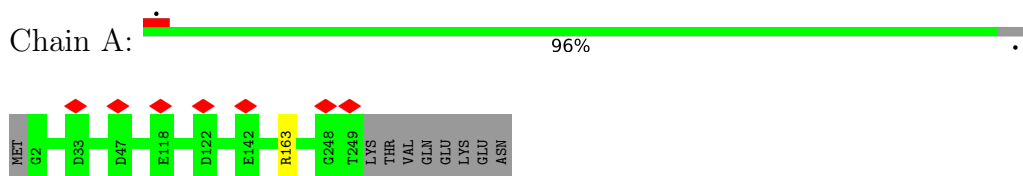


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
84	5	1	29	22	2	5	0

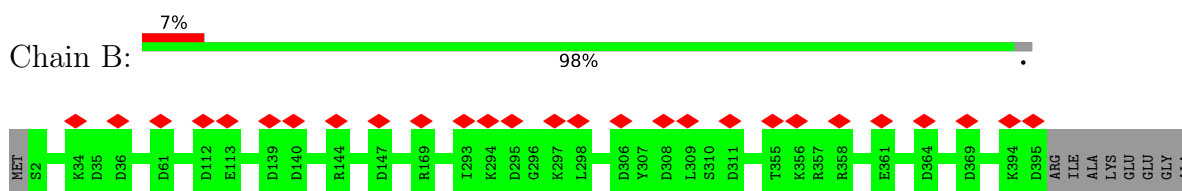
### 3 Residue-property plots [i](#)

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.

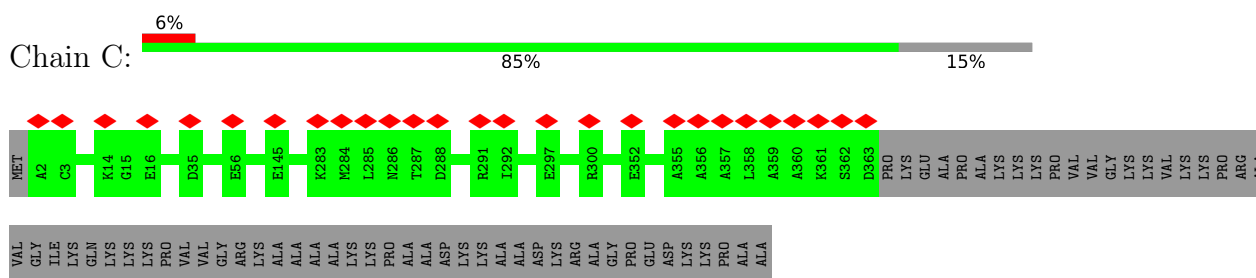
- Molecule 1: Ribosomal protein L8



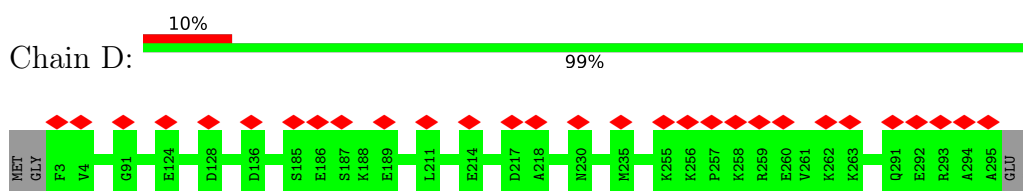
- Molecule 2: uL3



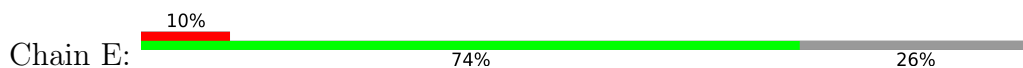
- Molecule 3: 60S ribosomal protein L4



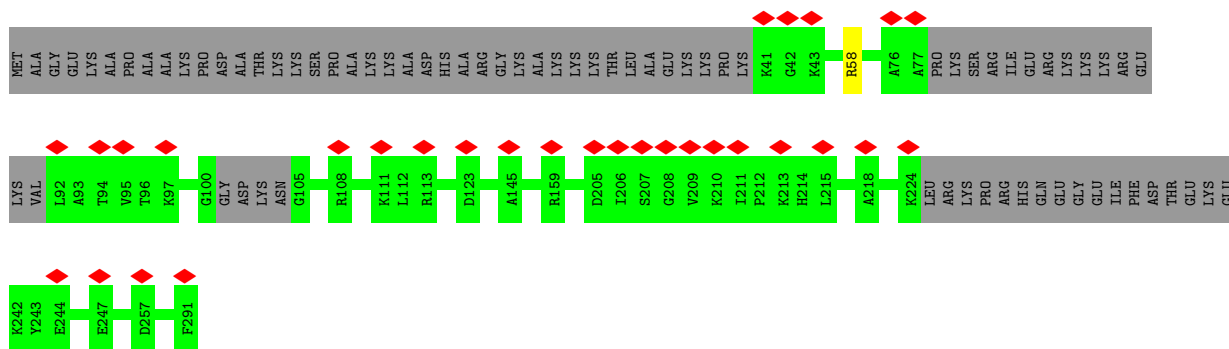
- Molecule 4: Ribosomal\_L18\_c domain-containing protein



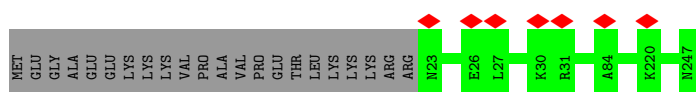
- Molecule 5: 60S ribosomal protein L6



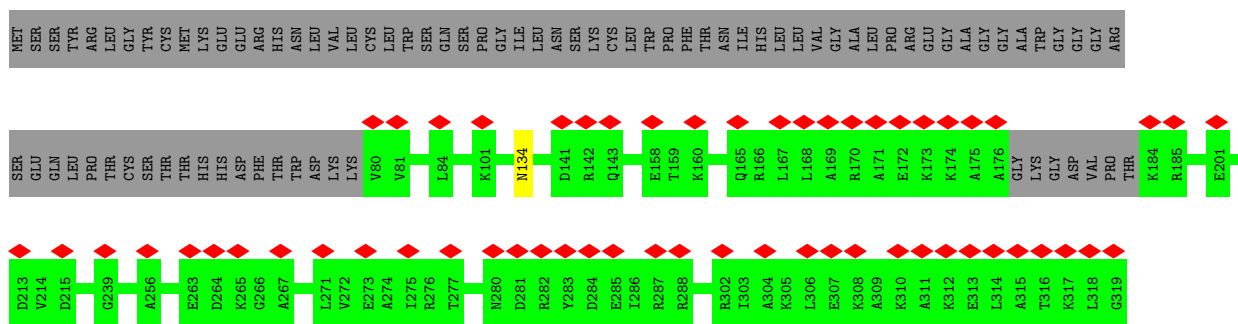
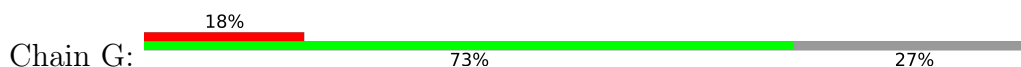




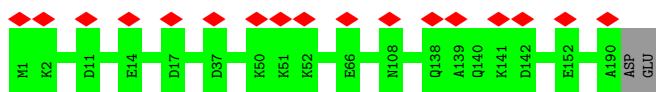
• Molecule 6: 60S ribosomal protein L7



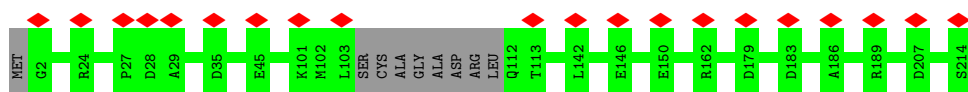
• Molecule 7: 60S ribosomal protein L7a



• Molecule 8: 60S ribosomal protein L9

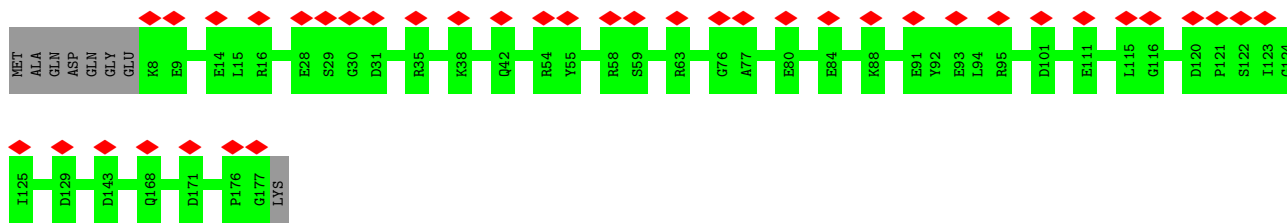


• Molecule 9: 60S ribosomal protein L10

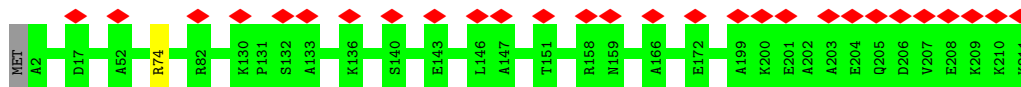


• Molecule 10: 60S ribosomal protein L11

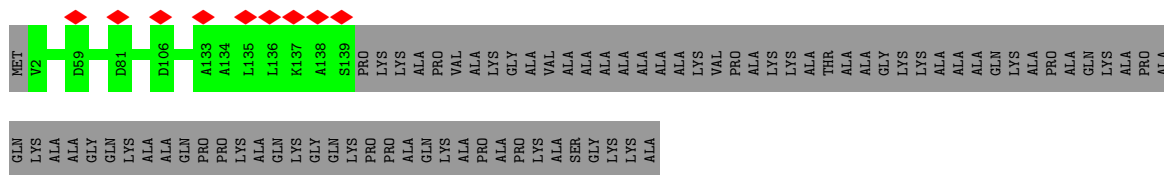




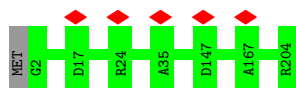
• Molecule 11: 60S ribosomal protein L13



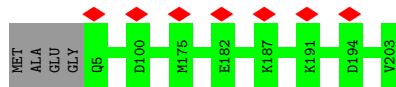
• Molecule 12: 60S ribosomal protein L14



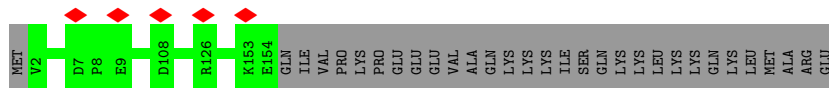
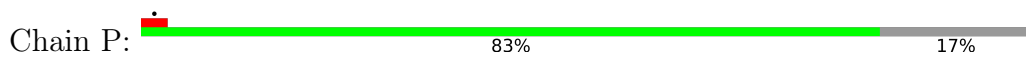
• Molecule 13: Ribosomal protein L15



• Molecule 14: uL13

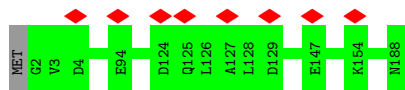


• Molecule 15: uL22

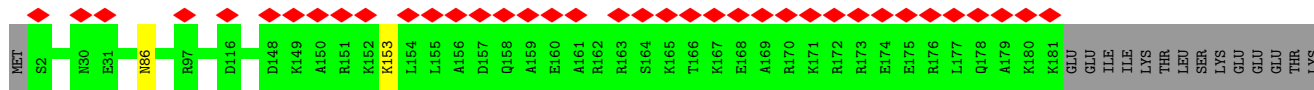
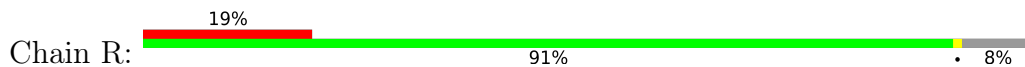


• Molecule 16: Ribosomal protein L18

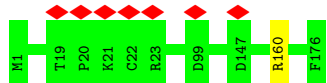




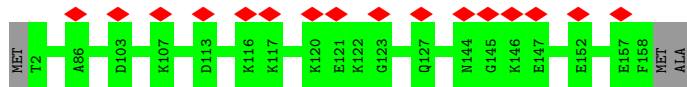
• Molecule 17: Ribosomal protein L19



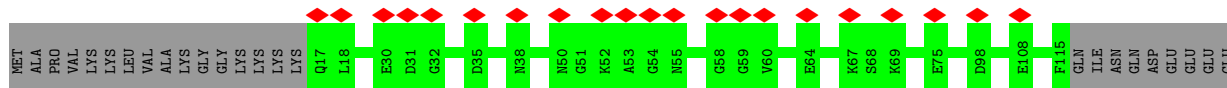
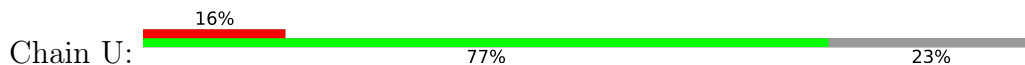
• Molecule 18: 60S ribosomal protein L18a



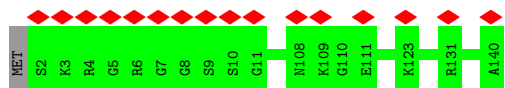
• Molecule 19: eL21



• Molecule 20: eL22

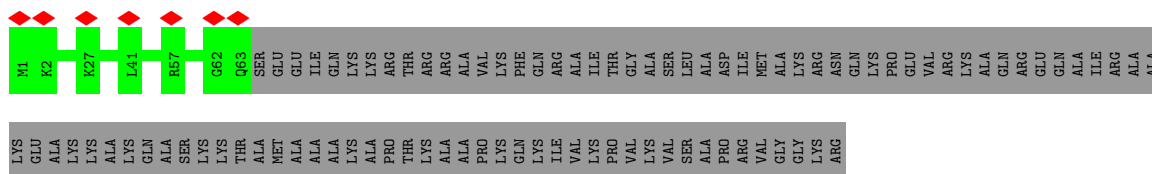


• Molecule 21: Ribosomal protein L23

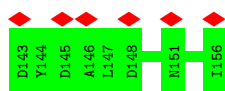
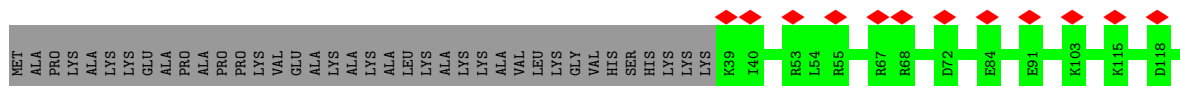
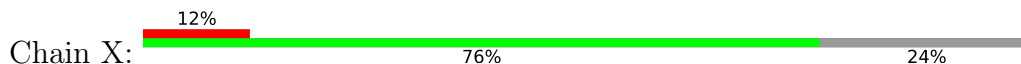


• Molecule 22: 60S ribosomal protein L24

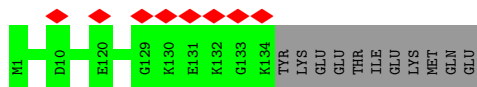




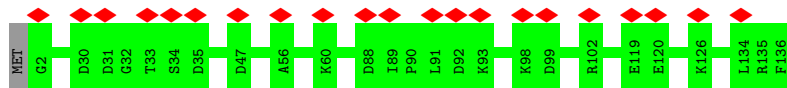
• Molecule 23: eL23



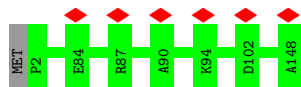
• Molecule 24: uL24



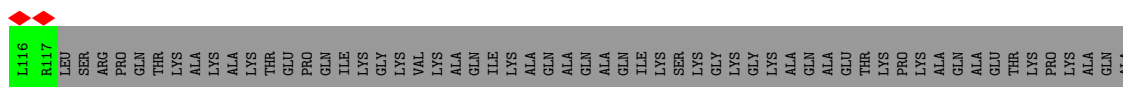
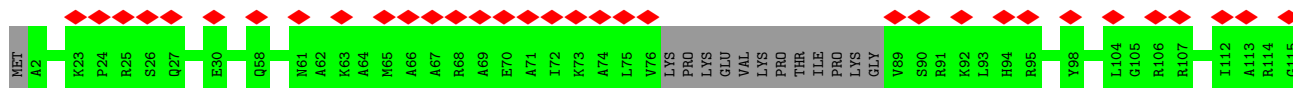
• Molecule 25: 60S ribosomal protein L27



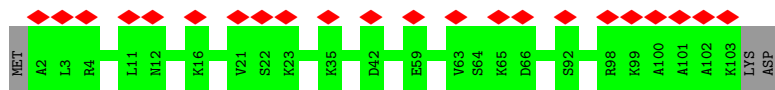
• Molecule 26: 60S ribosomal protein L27a



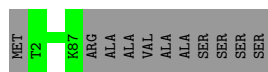
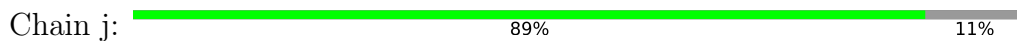
• Molecule 27: 60S ribosomal protein L29



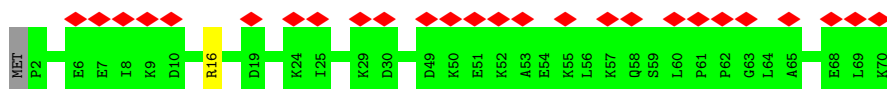




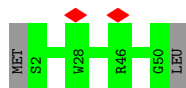
• Molecule 35: Ribosomal protein L37



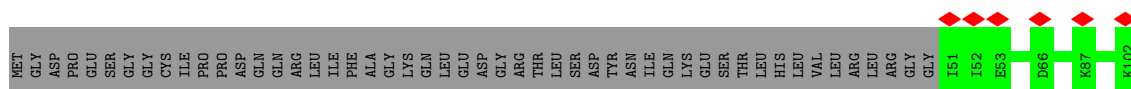
• Molecule 36: 60S ribosomal protein L38



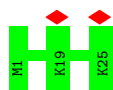
• Molecule 37: eL39



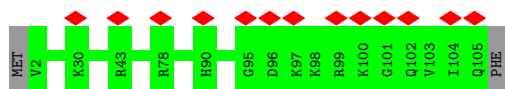
• Molecule 38: eL40



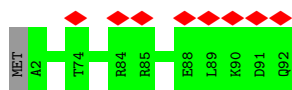
• Molecule 39: 60s ribosomal protein l41



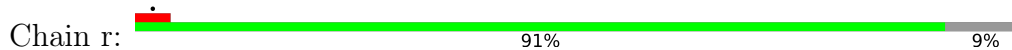
• Molecule 40: eL42



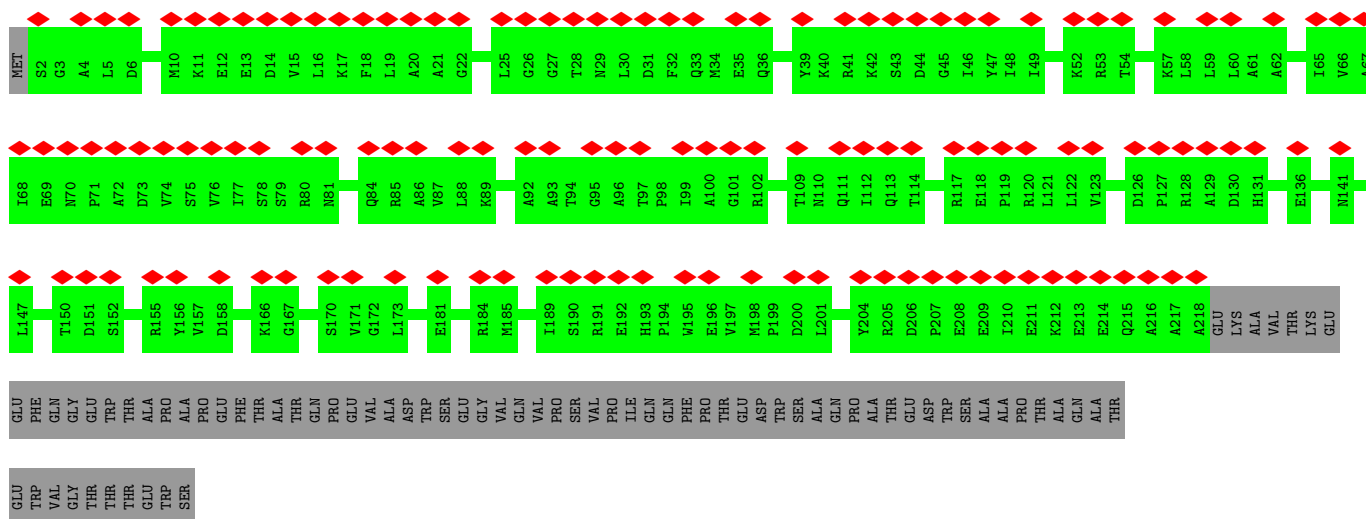
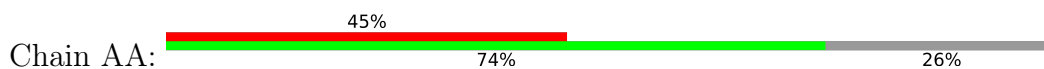
- Molecule 41: eL43



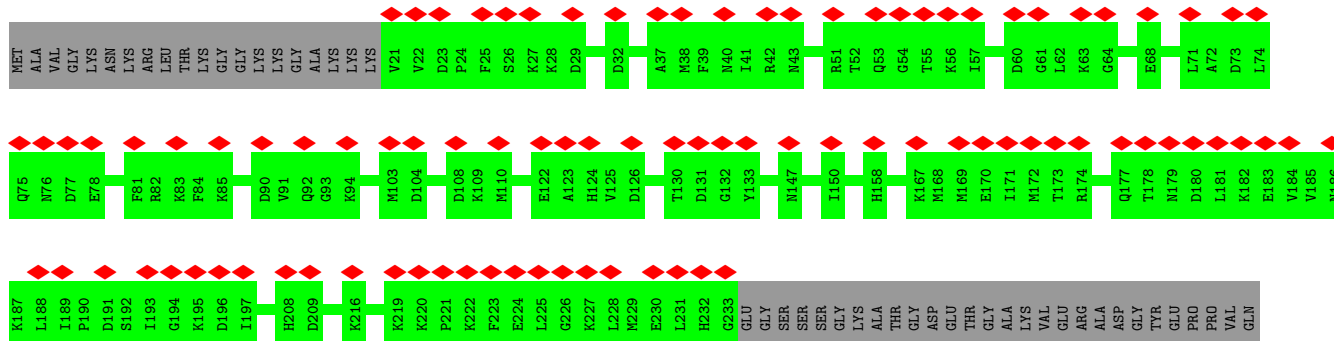
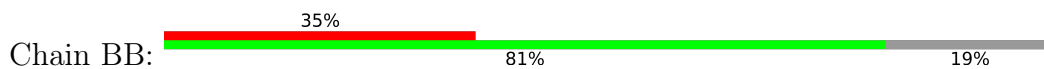
- Molecule 42: eL28



- Molecule 43: 40S ribosomal protein SA

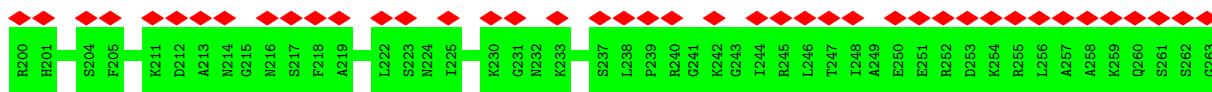


- Molecule 44: eS1

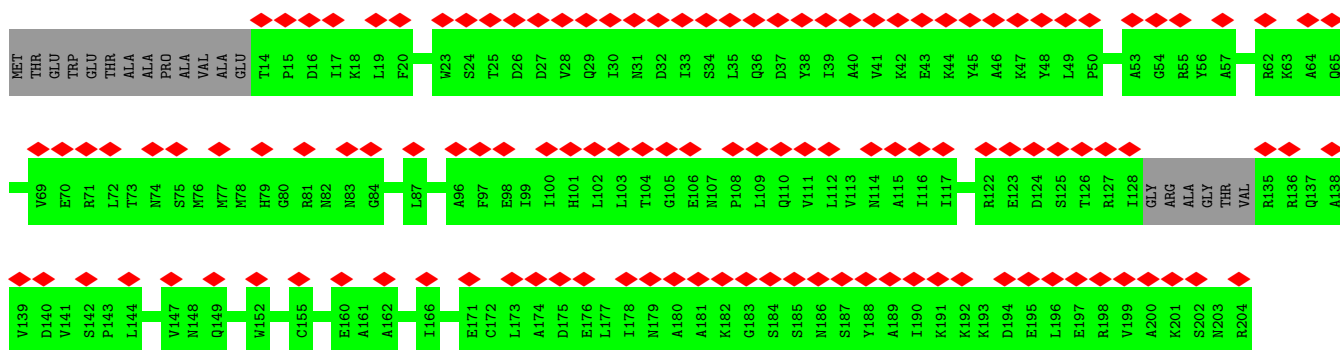
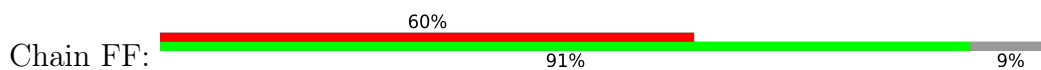




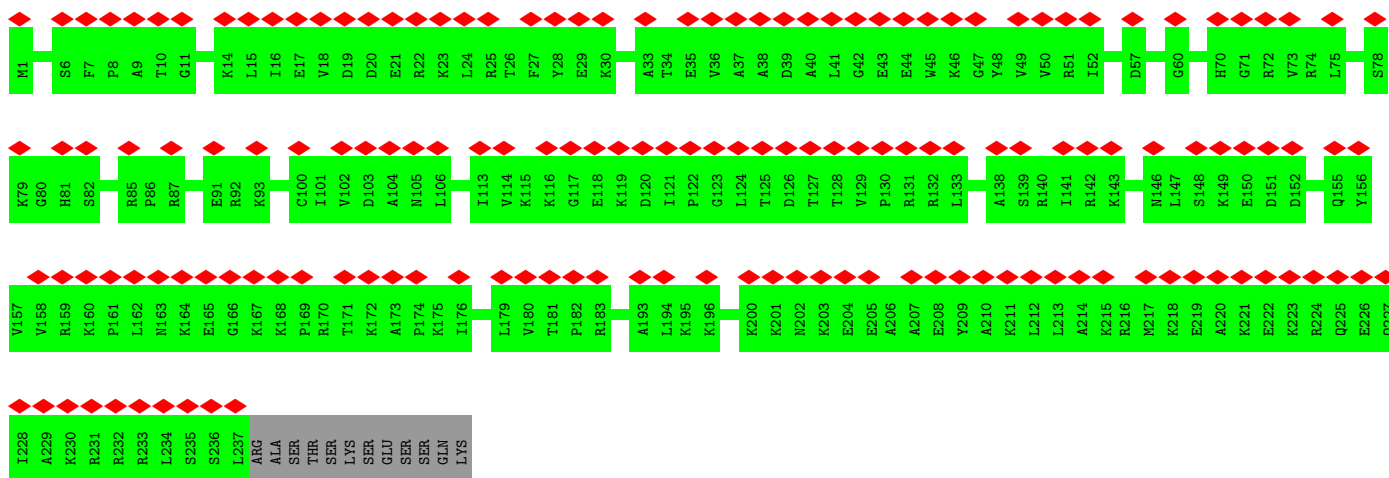




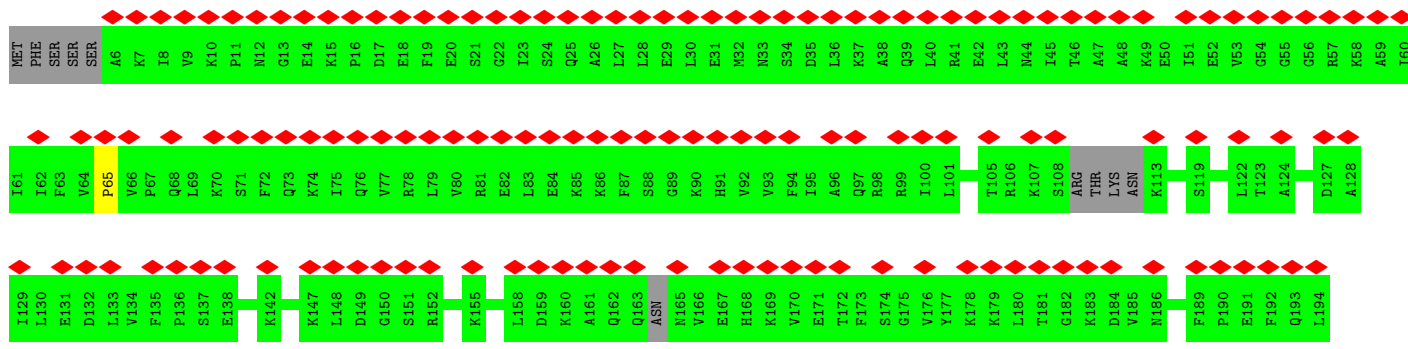
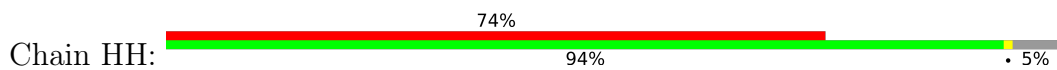
• Molecule 48: uS7



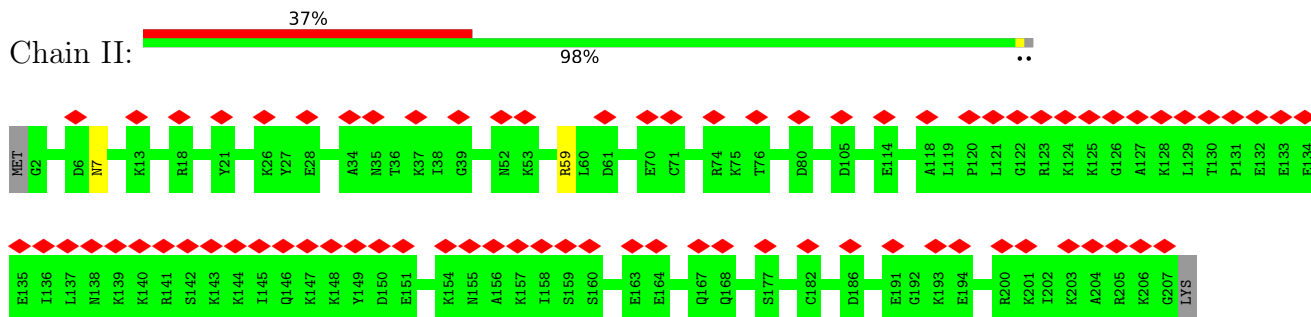
• Molecule 49: eS6



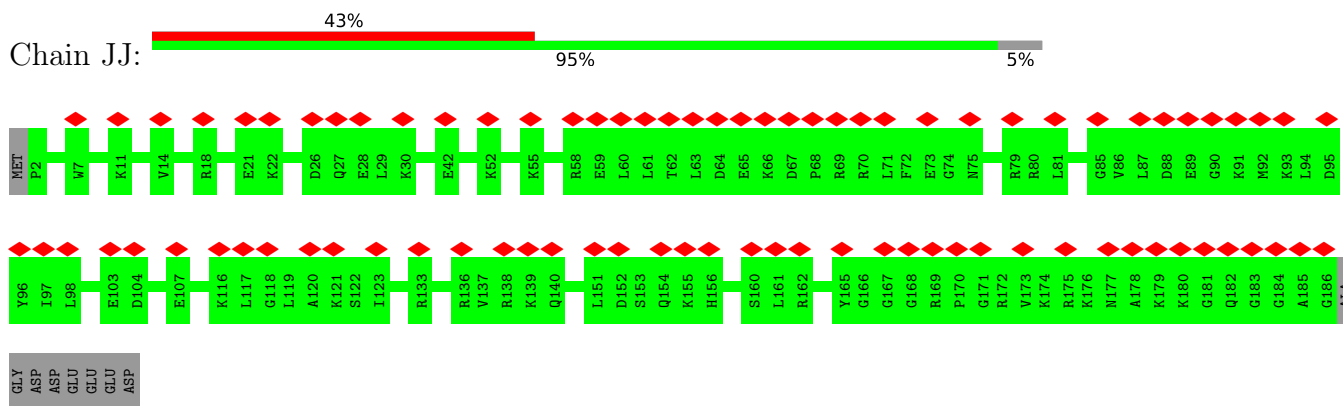
• Molecule 50: eS7



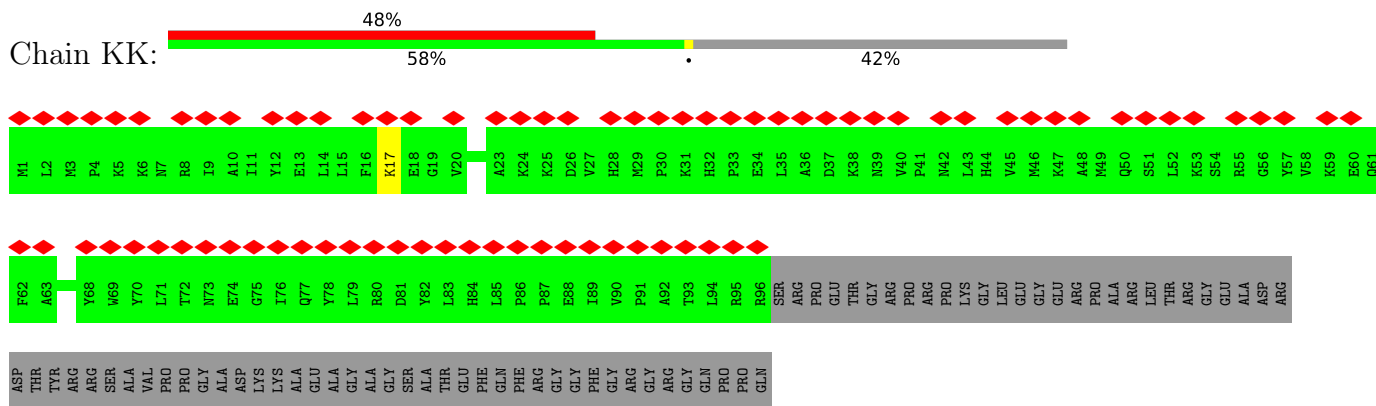
• Molecule 51: eS8



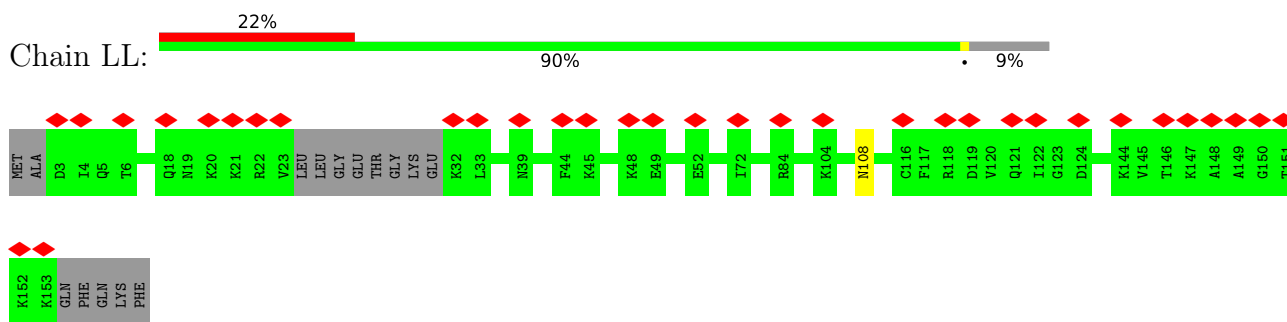
• Molecule 52: uS4



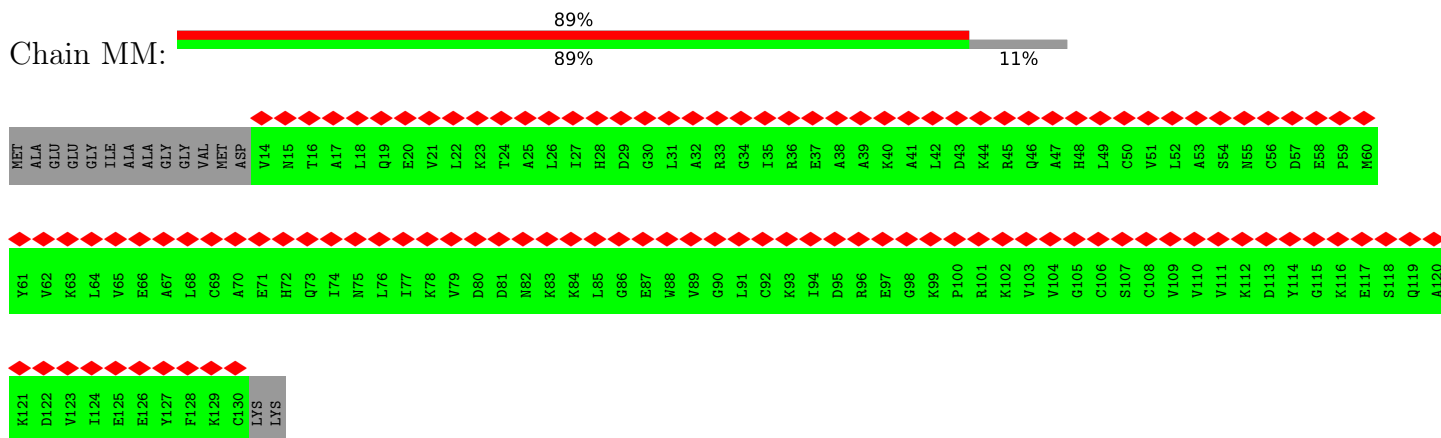
• Molecule 53: S10\_ plectin domain-containing protein



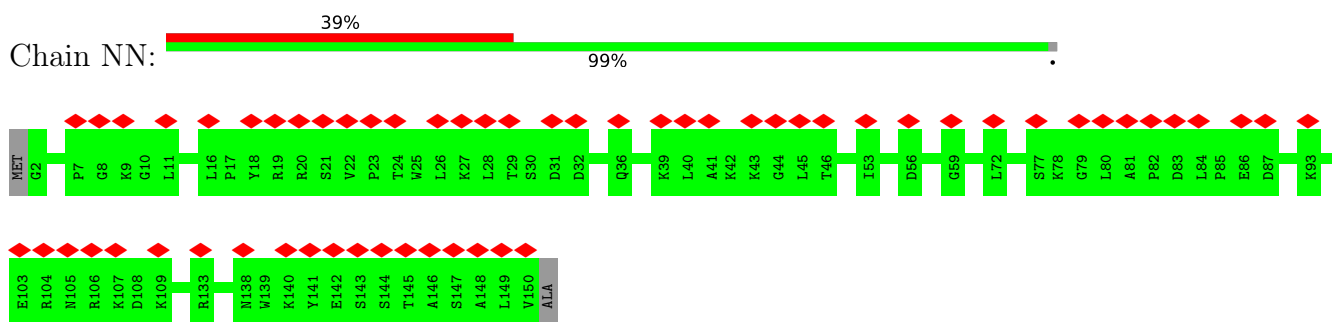
• Molecule 54: uS17



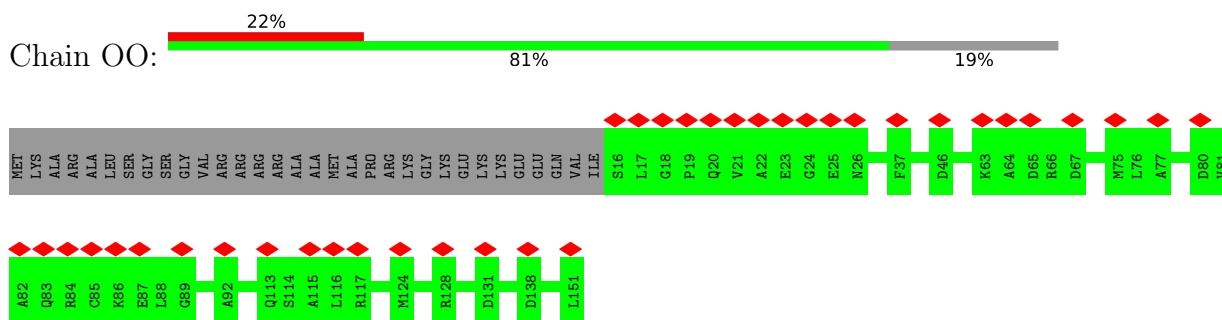
• Molecule 55: eS12



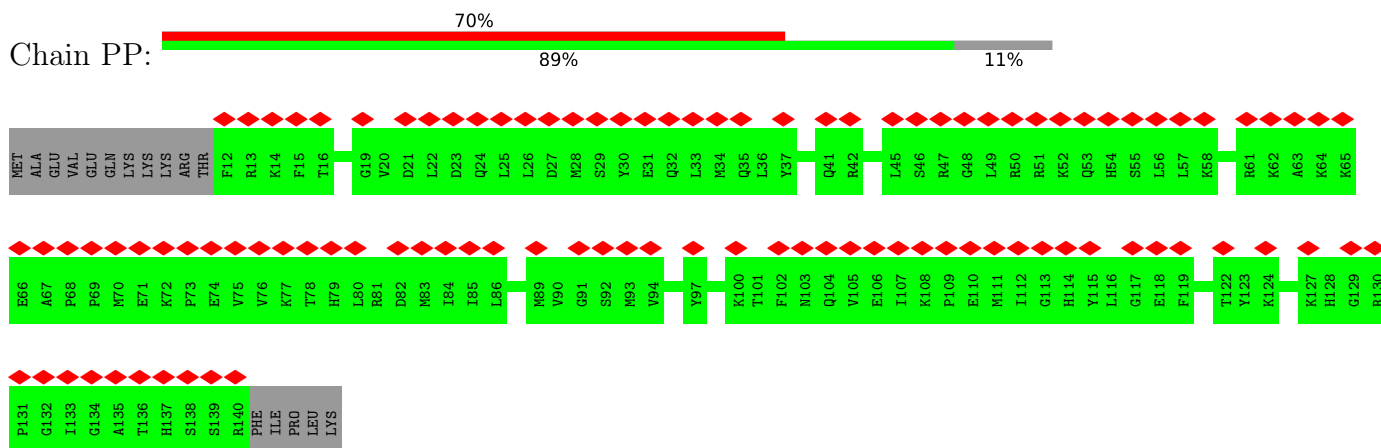
• Molecule 56: uS15



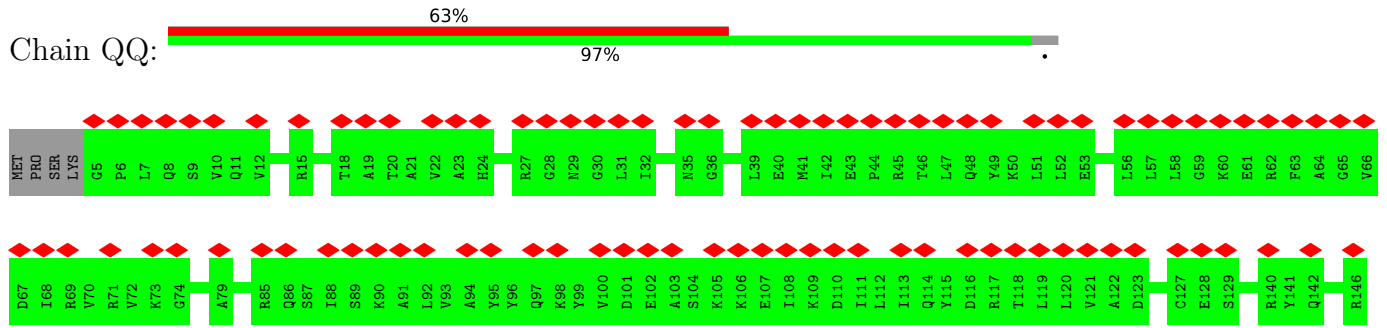
• Molecule 57: uS11



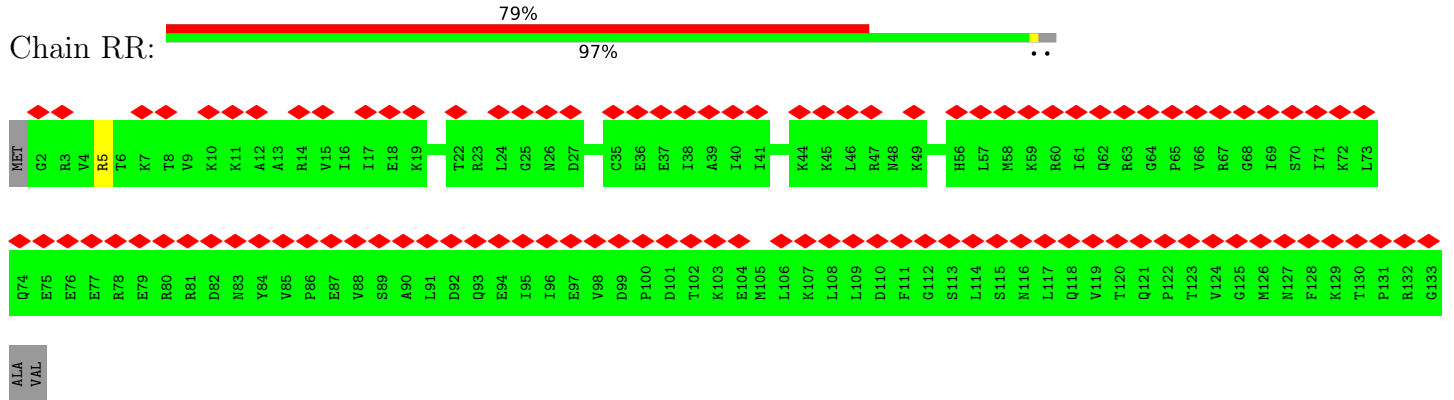
• Molecule 58: uS19



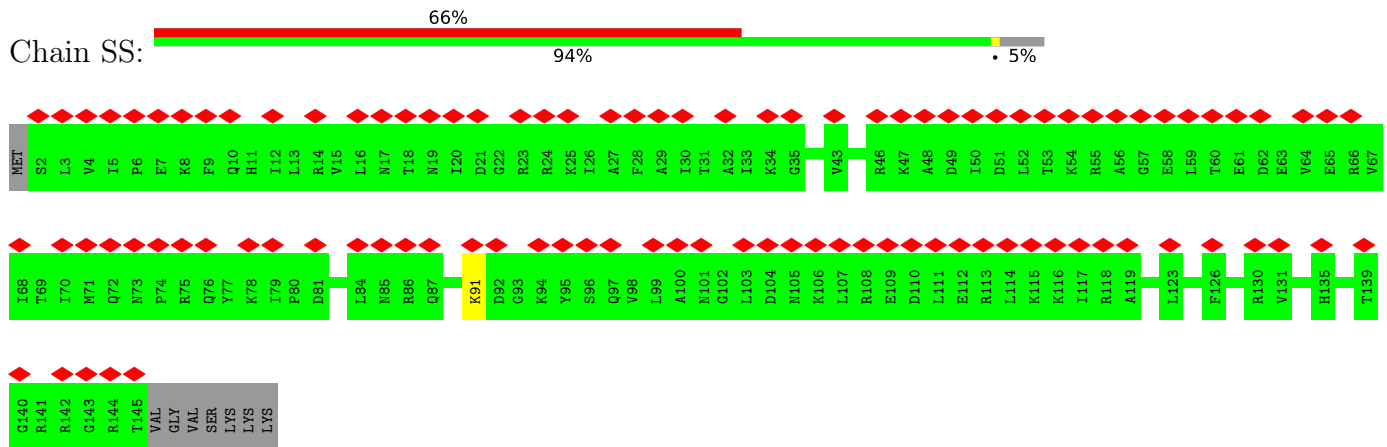
• Molecule 59: uS9



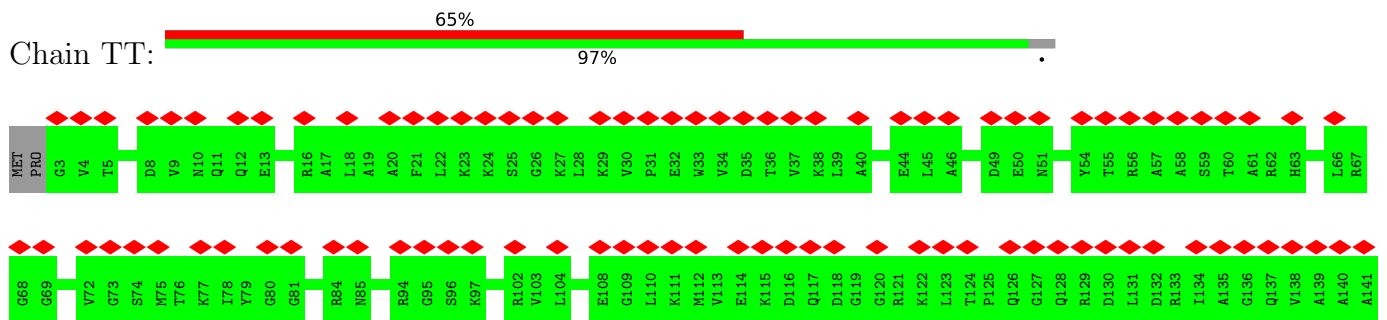
• Molecule 60: eS17



• Molecule 61: uS13

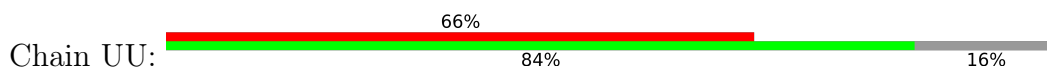


• Molecule 62: eS19

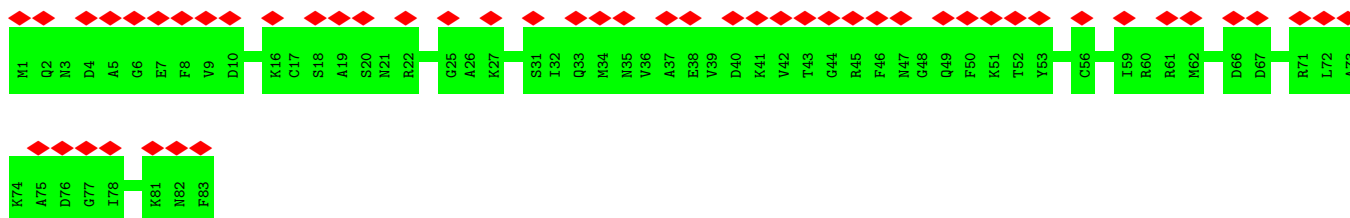




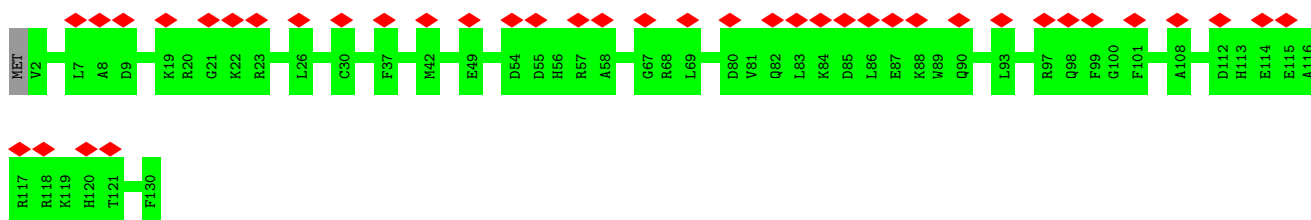
- Molecule 63: uS10



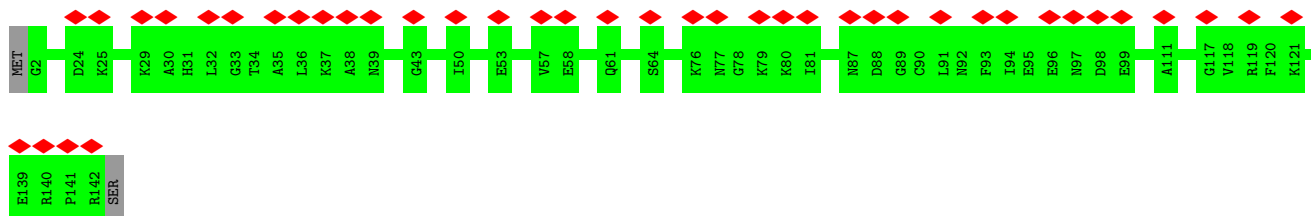
- Molecule 64: 40S ribosomal protein S21



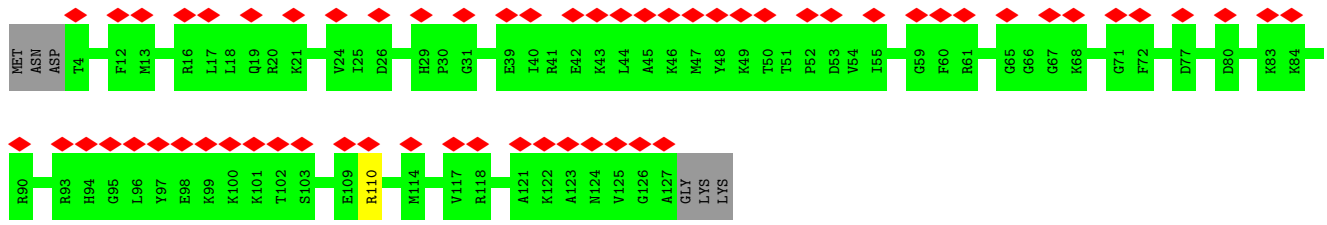
- Molecule 65: uS8



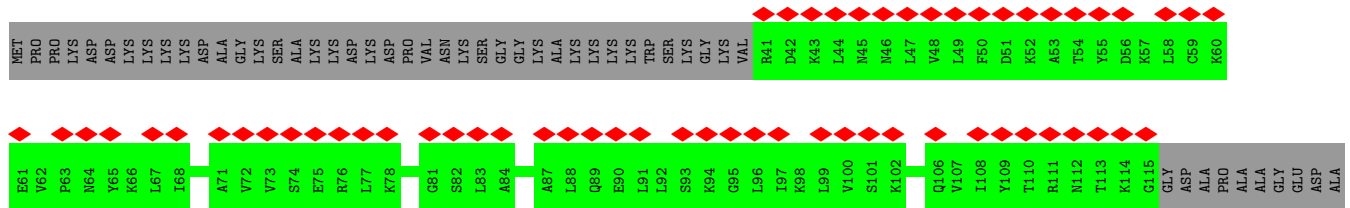
- Molecule 66: uS12



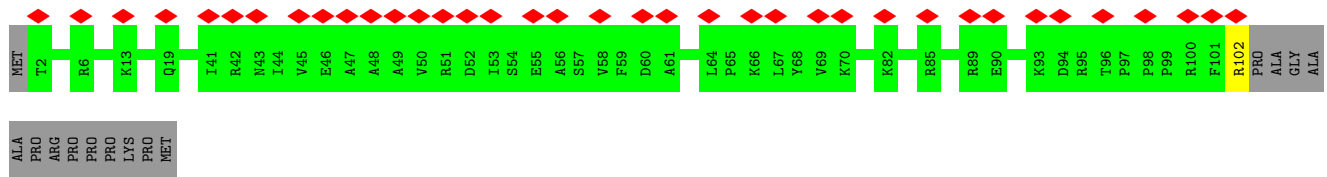
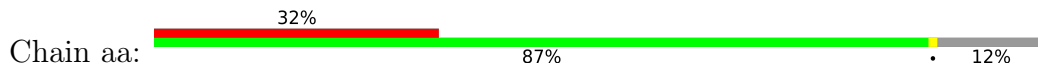
- Molecule 67: 40S ribosomal protein S24



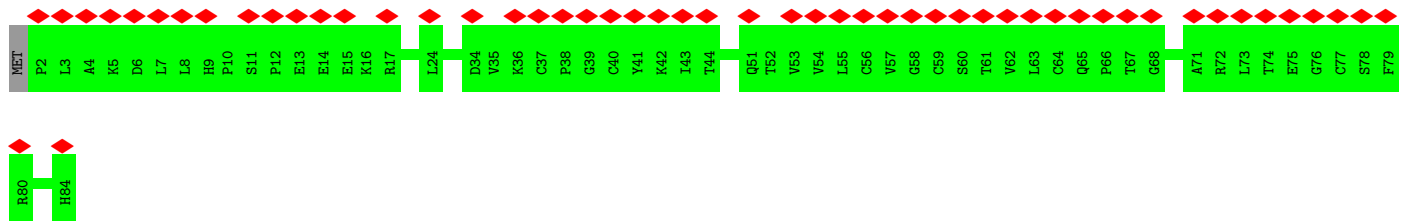
• Molecule 68: eS25



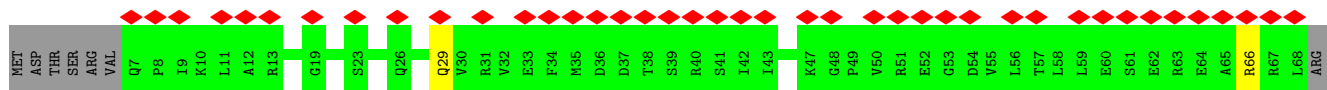
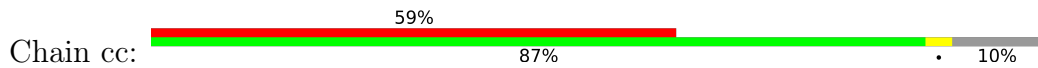
• Molecule 69: 40S ribosomal protein S26



• Molecule 70: eS27



• Molecule 71: eS28

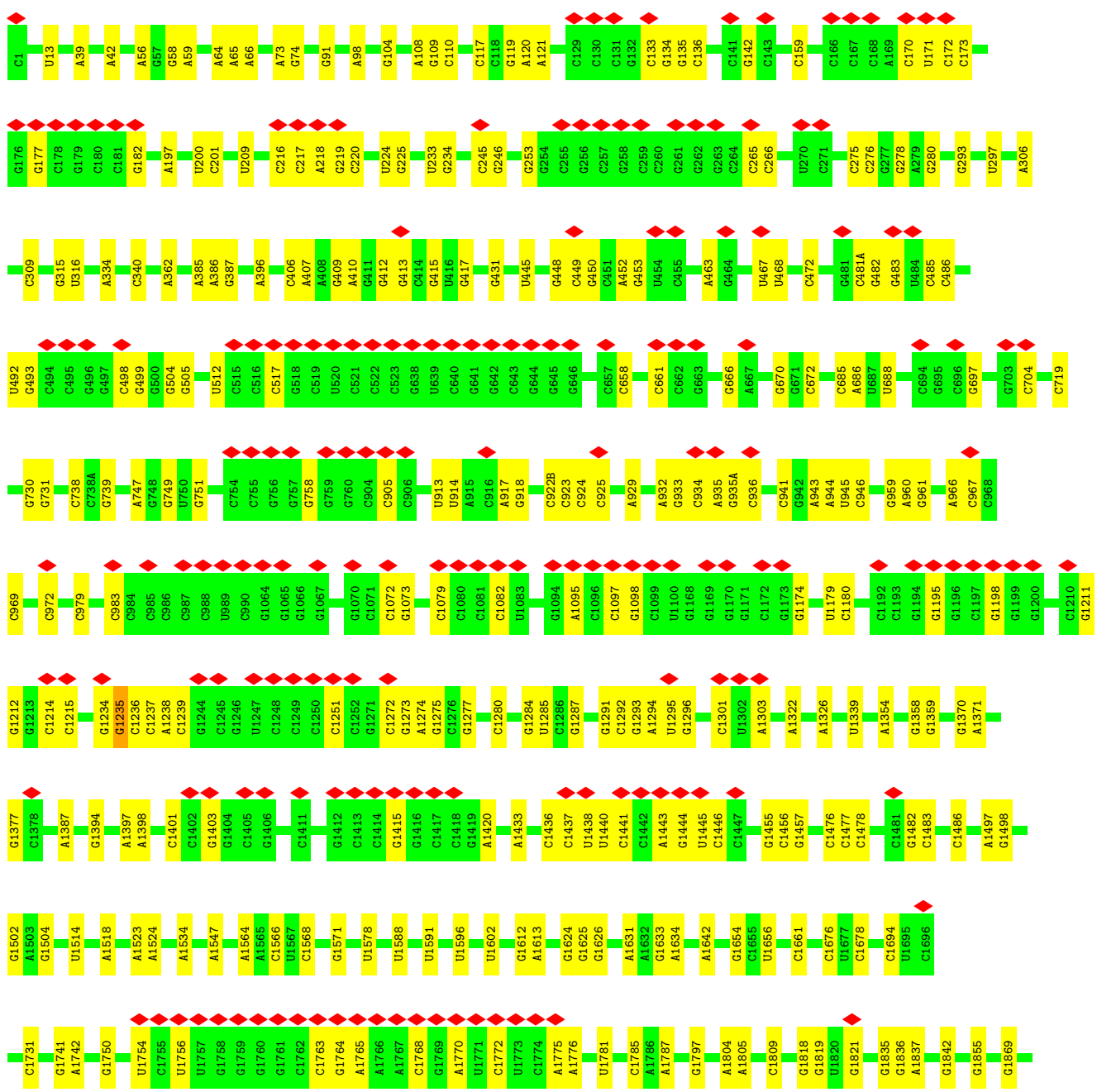
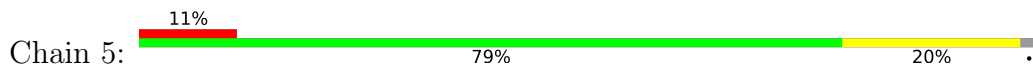


• Molecule 72: eS29

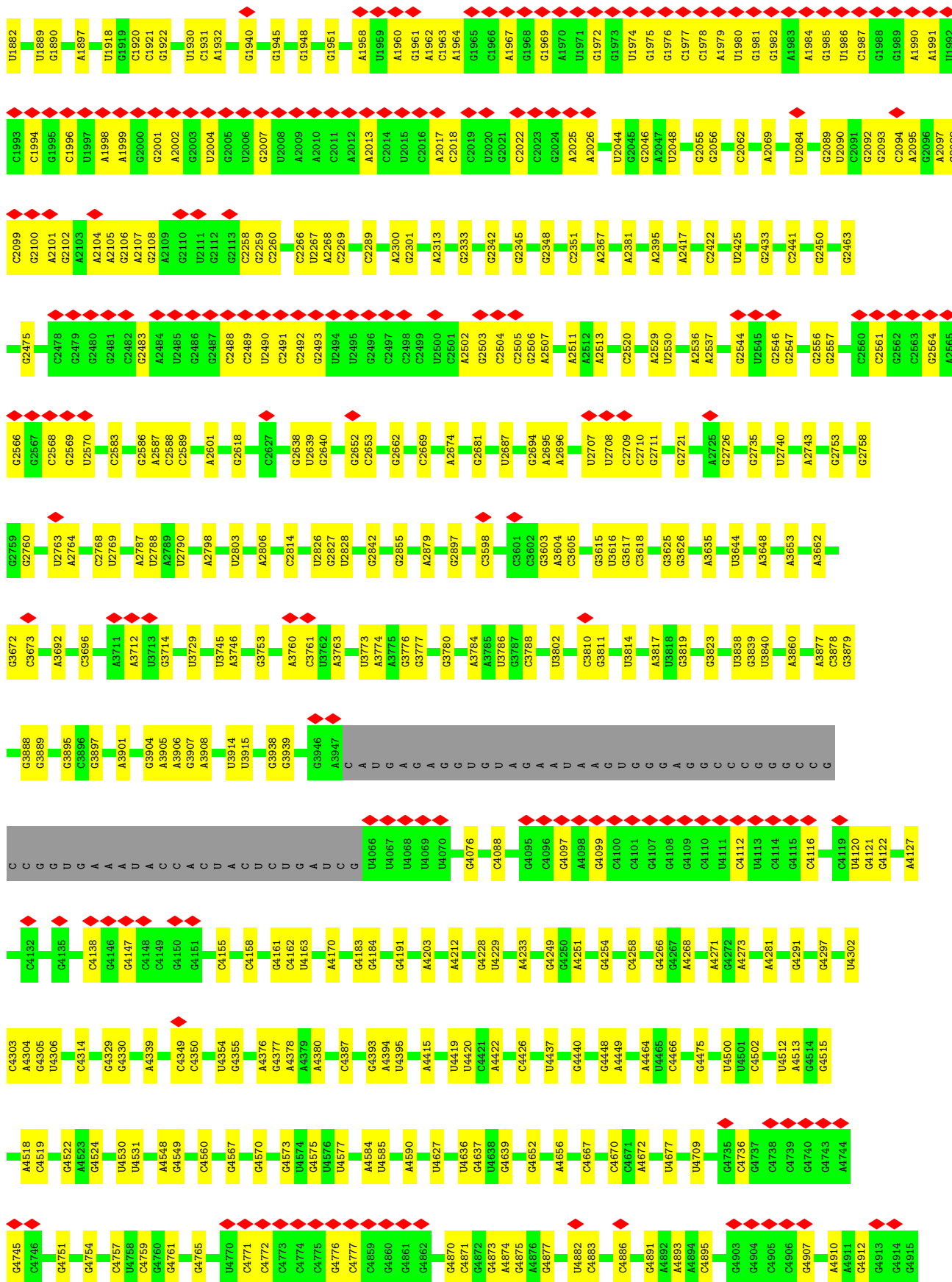


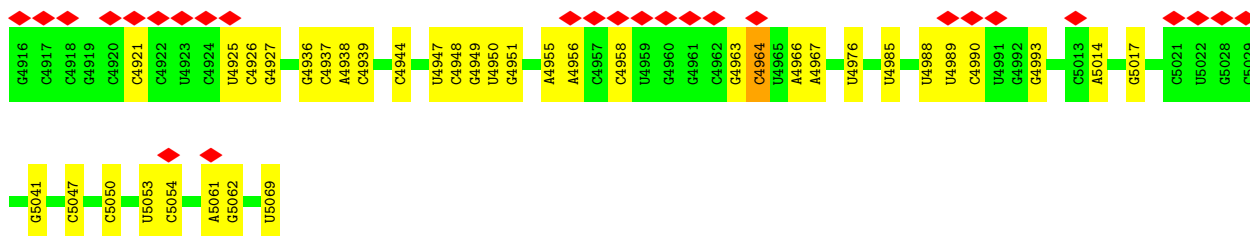


• Molecule 76: 28S rRNA









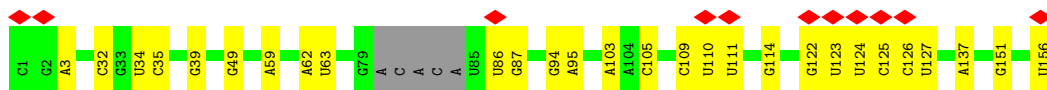
• Molecule 77: 5S rRNA

Chain 7:  92% 8%



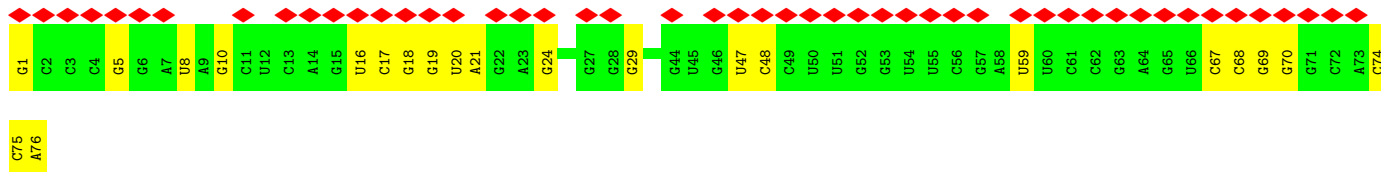
• Molecule 78: 5.8S rRNA

Chain 8:  7% 79% 18%



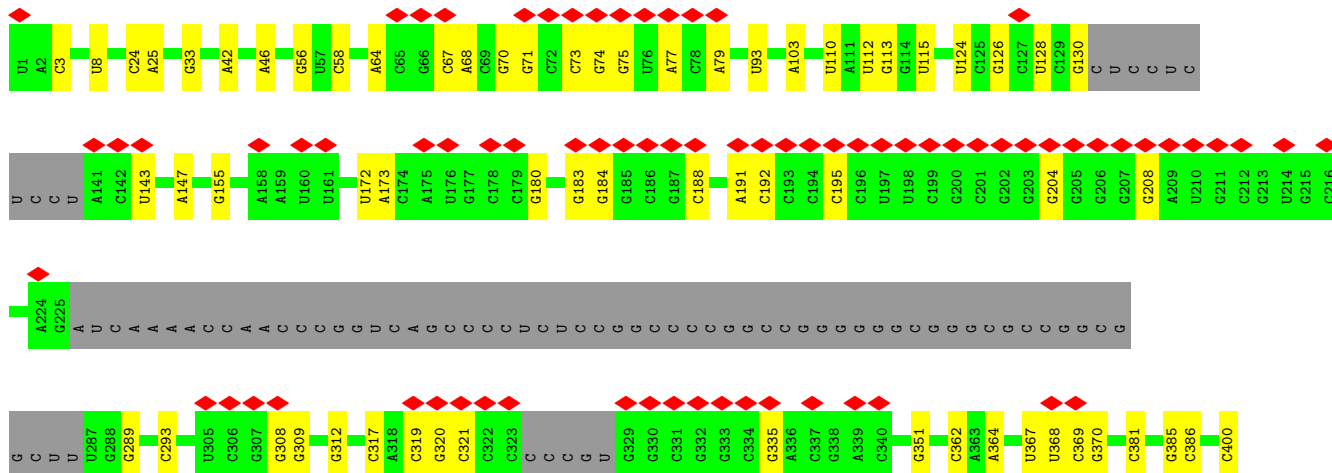
• Molecule 79: P-site tRNA

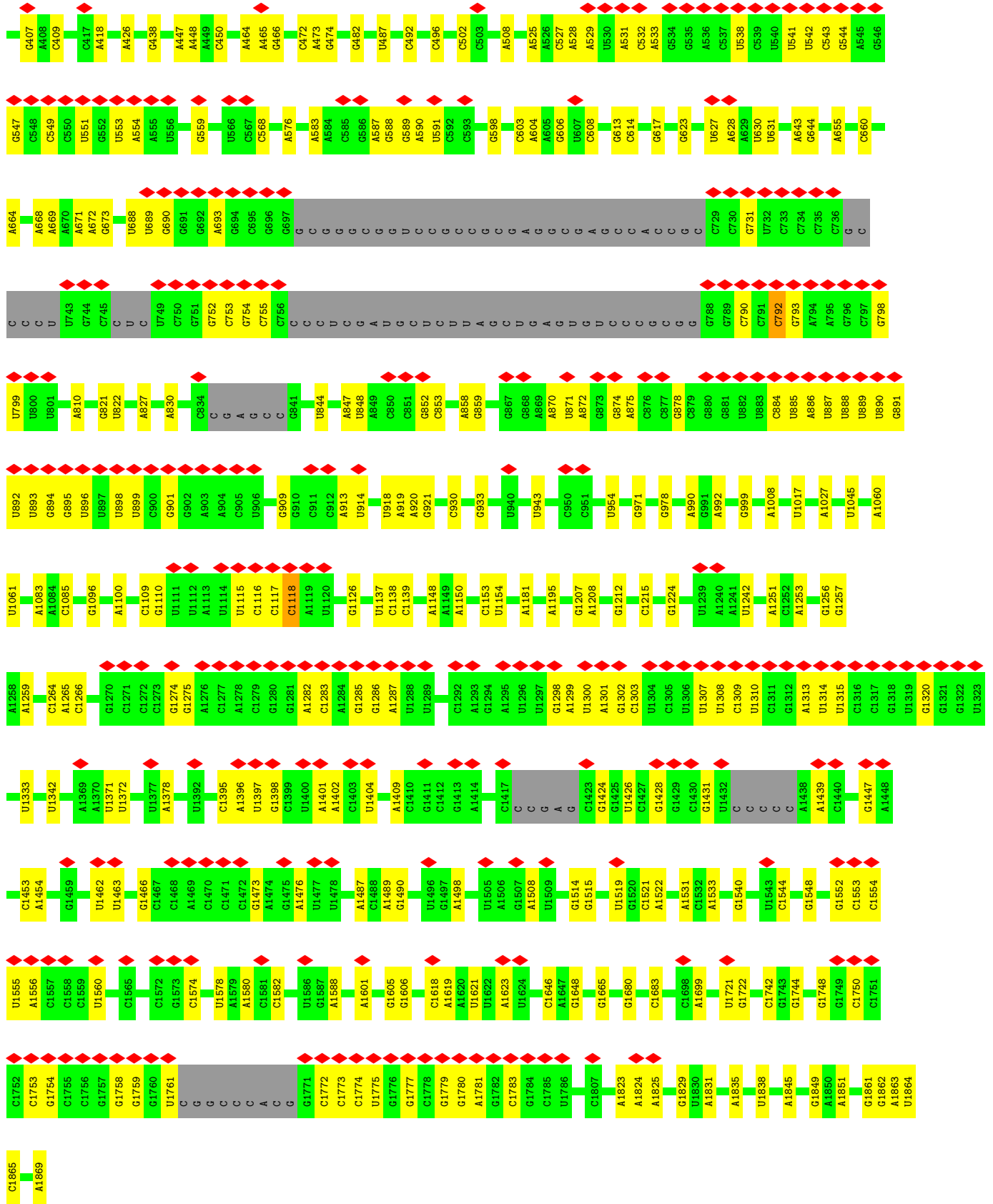
Chain 2:  64% 71% 29%



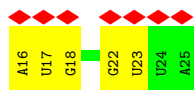
• Molecule 80: 18S rRNA

Chain 9:  19% 72% 19% 9%





• Molecule 81: mRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	34783	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.231	Depositor
Minimum map value	-0.135	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	442.80002, 442.80002, 442.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.23, 1.23	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: Z2V, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.32	0/1936	0.60	0/2596
2	B	0.32	0/3240	0.55	0/4339
3	C	0.30	0/2937	0.58	0/3946
4	D	0.30	0/2437	0.53	0/3264
5	E	0.28	0/1762	0.56	0/2362
6	F	0.32	0/1911	0.55	0/2549
7	G	0.28	0/1910	0.55	0/2569
8	H	0.29	0/1535	0.55	0/2063
9	I	0.30	0/1702	0.55	0/2272
10	J	0.29	0/1385	0.57	0/1852
11	L	0.29	0/1733	0.60	0/2316
12	M	0.29	0/1158	0.55	0/1547
13	N	0.31	0/1746	0.60	0/2338
14	O	0.31	0/1662	0.54	0/2222
15	P	0.31	0/1268	0.55	0/1700
16	Q	0.32	0/1539	0.61	0/2054
17	R	0.27	0/1524	0.60	0/2013
18	S	0.33	0/1501	0.56	0/2012
19	T	0.33	0/1312	0.54	0/1753
20	U	0.29	0/823	0.50	0/1104
21	V	0.31	0/1048	0.56	0/1402
22	W	0.33	0/541	0.56	0/720
23	X	0.29	0/984	0.53	0/1323
24	Y	0.30	0/1132	0.55	0/1504
25	Z	0.31	0/1130	0.56	0/1507
26	a	0.33	0/1191	0.56	0/1590
27	b	0.26	0/861	0.56	0/1138
28	c	0.31	0/771	0.52	0/1034
29	d	0.30	0/903	0.58	0/1216
30	e	0.31	0/1071	0.55	0/1429
31	f	0.34	0/895	0.60	0/1198
32	g	0.30	0/907	0.59	0/1209

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	h	0.27	0/1021	0.56	0/1348
34	i	0.28	0/841	0.57	0/1112
35	j	0.31	0/720	0.62	0/952
36	k	0.29	0/575	0.53	0/761
37	l	0.28	0/450	0.56	0/597
38	m	0.29	0/435	0.55	0/575
39	n	0.28	0/240	0.76	0/305
40	o	0.30	0/864	0.56	0/1140
41	p	0.31	0/718	0.55	0/953
42	r	0.30	0/1010	0.59	0/1354
43	AA	0.26	0/1749	0.53	0/2377
44	BB	0.27	0/1756	0.52	0/2350
45	CC	0.28	0/1753	0.51	0/2369
46	DD	0.28	0/1796	0.56	0/2417
47	EE	0.26	0/2118	0.55	0/2849
48	FF	0.26	0/1492	0.52	0/2005
49	GG	0.27	0/1946	0.57	0/2590
50	HH	0.27	0/1501	0.57	1/2008 (0.0%)
51	II	0.27	0/1715	0.57	0/2287
52	JJ	0.26	0/1550	0.58	0/2069
53	KK	0.28	0/834	0.49	0/1125
54	LL	0.29	0/1195	0.56	0/1597
55	MM	0.24	0/918	0.48	0/1233
56	NN	0.26	0/1226	0.54	0/1649
57	OO	0.28	0/1029	0.59	0/1380
58	PP	0.26	0/1079	0.55	0/1441
59	QQ	0.27	0/1146	0.56	0/1534
60	RR	0.25	0/1082	0.53	0/1452
61	SS	0.26	0/1208	0.59	0/1618
62	TT	0.25	0/1115	0.53	0/1493
63	UU	0.26	0/805	0.62	0/1081
64	VV	0.26	0/643	0.52	0/860
65	WW	0.28	0/1051	0.55	0/1406
66	XX	0.27	0/1116	0.53	0/1490
67	YY	0.27	0/1028	0.57	0/1366
68	ZZ	0.26	0/604	0.53	0/810
69	aa	0.28	0/828	0.59	0/1109
70	bb	0.26	0/665	0.49	0/891
71	cc	0.25	0/490	0.64	0/656
72	dd	0.30	0/470	0.57	0/623
73	ee	0.26	0/462	0.60	0/607
74	ff	0.27	0/567	0.54	0/753
75	gg	0.25	0/2493	0.53	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	5	0.45	0/84931	0.78	6/132457 (0.0%)
77	7	0.43	0/2836	0.76	0/4421
78	8	0.44	0/3581	0.74	0/5577
79	2	0.37	1/1813 (0.1%)	0.80	0/2823
80	9	0.32	0/40509	0.77	9/63128 (0.0%)
81	6	0.30	0/233	0.88	0/360
All	All	0.37	1/226662 (0.0%)	0.70	16/332893 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
79	2	1	G	OP3-P	-10.58	1.48	1.61

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	HH	65	PRO	CA-N-CD	-8.52	99.57	111.50
76	5	658	C	N3-C2-O2	-6.19	117.57	121.90
80	9	792	C	N3-C2-O2	-6.10	117.63	121.90
80	9	1453	C	C2-N1-C1'	5.93	125.33	118.80
80	9	1118	C	C2-N1-C1'	5.86	125.25	118.80

There are no chirality outliers.

There are no planarity outliers.

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

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	246/257 (96%)	231 (94%)	15 (6%)	0	100	100
2	B	392/403 (97%)	364 (93%)	28 (7%)	0	100	100
3	C	360/425 (85%)	327 (91%)	33 (9%)	0	100	100
4	D	291/297 (98%)	281 (97%)	10 (3%)	0	100	100
5	E	208/291 (72%)	192 (92%)	16 (8%)	0	100	100
6	F	223/247 (90%)	210 (94%)	13 (6%)	0	100	100
7	G	229/319 (72%)	215 (94%)	14 (6%)	0	100	100
8	H	188/192 (98%)	181 (96%)	7 (4%)	0	100	100
9	I	201/214 (94%)	190 (94%)	11 (6%)	0	100	100
10	J	168/178 (94%)	165 (98%)	3 (2%)	0	100	100
11	L	208/211 (99%)	195 (94%)	13 (6%)	0	100	100
12	M	136/218 (62%)	129 (95%)	7 (5%)	0	100	100
13	N	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
14	O	197/203 (97%)	188 (95%)	9 (5%)	0	100	100
15	P	151/184 (82%)	144 (95%)	7 (5%)	0	100	100
16	Q	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
17	R	178/196 (91%)	173 (97%)	5 (3%)	0	100	100
18	S	174/176 (99%)	166 (95%)	8 (5%)	0	100	100
19	T	155/160 (97%)	146 (94%)	9 (6%)	0	100	100
20	U	97/128 (76%)	91 (94%)	6 (6%)	0	100	100
21	V	137/140 (98%)	131 (96%)	6 (4%)	0	100	100
22	W	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
23	X	116/156 (74%)	108 (93%)	8 (7%)	0	100	100
24	Y	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
25	Z	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
26	a	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
27	b	100/245 (41%)	95 (95%)	5 (5%)	0	100	100
28	c	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
29	d	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
30	e	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
31	f	107/110 (97%)	104 (97%)	3 (3%)	0	100	100
32	g	111/116 (96%)	109 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	80 (95%)	4 (5%)	0	100	100
36	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l	47/51 (92%)	42 (89%)	5 (11%)	0	100	100
38	m	50/102 (49%)	48 (96%)	2 (4%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	102/106 (96%)	97 (95%)	5 (5%)	0	100	100
41	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
42	r	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
43	AA	215/295 (73%)	203 (94%)	12 (6%)	0	100	100
44	BB	211/264 (80%)	195 (92%)	16 (8%)	0	100	100
45	CC	219/293 (75%)	211 (96%)	8 (4%)	0	100	100
46	DD	226/243 (93%)	214 (95%)	12 (5%)	0	100	100
47	EE	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
48	FF	181/204 (89%)	168 (93%)	13 (7%)	0	100	100
49	GG	235/249 (94%)	222 (94%)	13 (6%)	0	100	100
50	HH	178/194 (92%)	168 (94%)	10 (6%)	0	100	100
51	II	204/208 (98%)	190 (93%)	14 (7%)	0	100	100
52	JJ	183/194 (94%)	177 (97%)	6 (3%)	0	100	100
53	KK	94/165 (57%)	91 (97%)	3 (3%)	0	100	100
54	LL	139/158 (88%)	131 (94%)	8 (6%)	0	100	100
55	MM	115/132 (87%)	105 (91%)	10 (9%)	0	100	100
56	NN	147/151 (97%)	140 (95%)	7 (5%)	0	100	100
57	OO	134/168 (80%)	124 (92%)	10 (8%)	0	100	100
58	PP	127/145 (88%)	119 (94%)	8 (6%)	0	100	100
59	QQ	140/146 (96%)	132 (94%)	8 (6%)	0	100	100
60	RR	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
61	SS	142/152 (93%)	134 (94%)	8 (6%)	0	100	100
62	TT	139/145 (96%)	133 (96%)	6 (4%)	0	100	100
63	UU	98/119 (82%)	93 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	VV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
65	WW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
66	XX	139/143 (97%)	131 (94%)	8 (6%)	0	100	100
67	YY	122/130 (94%)	116 (95%)	6 (5%)	0	100	100
68	ZZ	73/125 (58%)	68 (93%)	5 (7%)	0	100	100
69	aa	99/115 (86%)	95 (96%)	4 (4%)	0	100	100
70	bb	81/84 (96%)	76 (94%)	5 (6%)	0	100	100
71	cc	60/69 (87%)	56 (93%)	4 (7%)	0	100	100
72	dd	53/56 (95%)	50 (94%)	3 (6%)	0	100	100
73	ee	55/133 (41%)	51 (93%)	4 (7%)	0	100	100
74	ff	66/156 (42%)	58 (88%)	8 (12%)	0	100	100
75	gg	311/317 (98%)	279 (90%)	32 (10%)	0	100	100
All	All	11145/12891 (86%)	10516 (94%)	629 (6%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/199 (96%)	189 (100%)	1 (0%)	88	95
2	B	342/348 (98%)	342 (100%)	0	100	100
3	C	302/347 (87%)	302 (100%)	0	100	100
4	D	247/250 (99%)	247 (100%)	0	100	100
5	E	190/251 (76%)	189 (100%)	1 (0%)	88	95
6	F	196/215 (91%)	196 (100%)	0	100	100
7	G	200/272 (74%)	199 (100%)	1 (0%)	88	95
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	175/181 (97%)	175 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	143/149 (96%)	143 (100%)	0	100	100
11	L	175/176 (99%)	174 (99%)	1 (1%)	86	94
12	M	117/161 (73%)	117 (100%)	0	100	100
13	N	171/172 (99%)	171 (100%)	0	100	100
14	O	171/173 (99%)	171 (100%)	0	100	100
15	P	134/163 (82%)	134 (100%)	0	100	100
16	Q	164/165 (99%)	164 (100%)	0	100	100
17	R	159/175 (91%)	157 (99%)	2 (1%)	69	87
18	S	157/157 (100%)	156 (99%)	1 (1%)	86	94
19	T	138/140 (99%)	138 (100%)	0	100	100
20	U	89/114 (78%)	89 (100%)	0	100	100
21	V	106/107 (99%)	106 (100%)	0	100	100
22	W	55/126 (44%)	55 (100%)	0	100	100
23	X	106/134 (79%)	106 (100%)	0	100	100
24	Y	124/135 (92%)	124 (100%)	0	100	100
25	Z	117/118 (99%)	117 (100%)	0	100	100
26	a	119/120 (99%)	119 (100%)	0	100	100
27	b	84/184 (46%)	84 (100%)	0	100	100
28	c	84/98 (86%)	84 (100%)	0	100	100
29	d	98/110 (89%)	98 (100%)	0	100	100
30	e	114/121 (94%)	114 (100%)	0	100	100
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	97/99 (98%)	97 (100%)	0	100	100
33	h	109/110 (99%)	108 (99%)	1 (1%)	78	91
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100
36	k	64/65 (98%)	63 (98%)	1 (2%)	62	84
37	l	46/48 (96%)	46 (100%)	0	100	100
38	m	48/90 (53%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	p	74/75 (99%)	74 (100%)	0	100	100
42	r	108/121 (89%)	108 (100%)	0	100	100
43	AA	181/245 (74%)	181 (100%)	0	100	100
44	BB	194/231 (84%)	194 (100%)	0	100	100
45	CC	187/225 (83%)	187 (100%)	0	100	100
46	DD	190/202 (94%)	189 (100%)	1 (0%)	88	95
47	EE	224/225 (100%)	223 (100%)	1 (0%)	91	95
48	FF	158/170 (93%)	158 (100%)	0	100	100
49	GG	207/218 (95%)	207 (100%)	0	100	100
50	HH	164/174 (94%)	164 (100%)	0	100	100
51	II	178/180 (99%)	176 (99%)	2 (1%)	73	88
52	JJ	161/168 (96%)	161 (100%)	0	100	100
53	KK	87/136 (64%)	86 (99%)	1 (1%)	73	88
54	LL	130/142 (92%)	129 (99%)	1 (1%)	81	93
55	MM	99/108 (92%)	99 (100%)	0	100	100
56	NN	130/131 (99%)	130 (100%)	0	100	100
57	OO	106/130 (82%)	106 (100%)	0	100	100
58	PP	115/130 (88%)	115 (100%)	0	100	100
59	QQ	117/121 (97%)	117 (100%)	0	100	100
60	RR	119/121 (98%)	118 (99%)	1 (1%)	81	93
61	SS	125/132 (95%)	124 (99%)	1 (1%)	81	93
62	TT	111/115 (96%)	111 (100%)	0	100	100
63	UU	92/107 (86%)	92 (100%)	0	100	100
64	VV	67/67 (100%)	67 (100%)	0	100	100
65	WW	112/113 (99%)	112 (100%)	0	100	100
66	XX	113/115 (98%)	113 (100%)	0	100	100
67	YY	107/112 (96%)	106 (99%)	1 (1%)	78	91
68	ZZ	66/103 (64%)	66 (100%)	0	100	100
69	aa	88/98 (90%)	87 (99%)	1 (1%)	73	88
70	bb	75/76 (99%)	75 (100%)	0	100	100
71	cc	55/62 (89%)	53 (96%)	2 (4%)	35	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	dd	48/49 (98%)	48 (100%)	0	100	100
73	ee	47/106 (44%)	46 (98%)	1 (2%)	53	79
74	ff	61/140 (44%)	60 (98%)	1 (2%)	62	84
75	gg	272/275 (99%)	272 (100%)	0	100	100
All	All	9731/10943 (89%)	9708 (100%)	23 (0%)	93	98

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	LL	108	ASN
67	YY	110	ARG
61	SS	91	LYS
69	aa	102	ARG
18	S	160	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	162	ASN
29	d	30	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
76	5	3518/3603 (97%)	675 (19%)	53 (1%)
77	7	118/120 (98%)	9 (7%)	0
78	8	149/156 (95%)	27 (18%)	1 (0%)
79	2	75/76 (98%)	21 (28%)	1 (1%)
80	9	1685/1869 (90%)	344 (20%)	20 (1%)
81	6	10/10 (100%)	4 (40%)	1 (10%)
All	All	5555/5834 (95%)	1080 (19%)	76 (1%)

5 of 1080 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
76	5	13	U
76	5	39	A
76	5	42	A

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Mol	Chain	Res	Type
76	5	56	A
76	5	58	G

5 of 76 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	9	369	C
80	9	1264	C
80	9	527	C
80	9	858	A
81	6	16	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 286 ligands modelled in this entry, 285 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
84	Z2V	5	5288	-	31,31,31	4.13	17 (54%)	30,45,45	4.18	10 (33%)

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
84	Z2V	5	5288	-	-	6/17/47/47	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
84	5	5288	Z2V	O01-C02	11.22	1.39	1.21
84	5	5288	Z2V	C11-N10	8.96	1.52	1.37
84	5	5288	Z2V	C18-N17	7.65	1.49	1.34
84	5	5288	Z2V	O13-C11	7.24	1.38	1.23
84	5	5288	Z2V	O14-C09	7.09	1.37	1.23

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
84	5	5288	Z2V	C11-N10-C09	-10.29	113.30	125.78
84	5	5288	Z2V	O01-C02-C03	-9.62	109.27	123.28
84	5	5288	Z2V	O01-C02-C28	-7.98	110.26	122.15
84	5	5288	Z2V	O13-C11-N10	-7.82	107.89	120.28
84	5	5288	Z2V	O13-C11-C12	-7.60	107.83	122.62

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	5	5288	Z2V	C02-C03-C04-O05
84	5	5288	Z2V	C15-C03-C04-C06
84	5	5288	Z2V	C15-C03-C04-O05
84	5	5288	Z2V	C04-C06-C07-C08
84	5	5288	Z2V	C04-C06-C07-C12

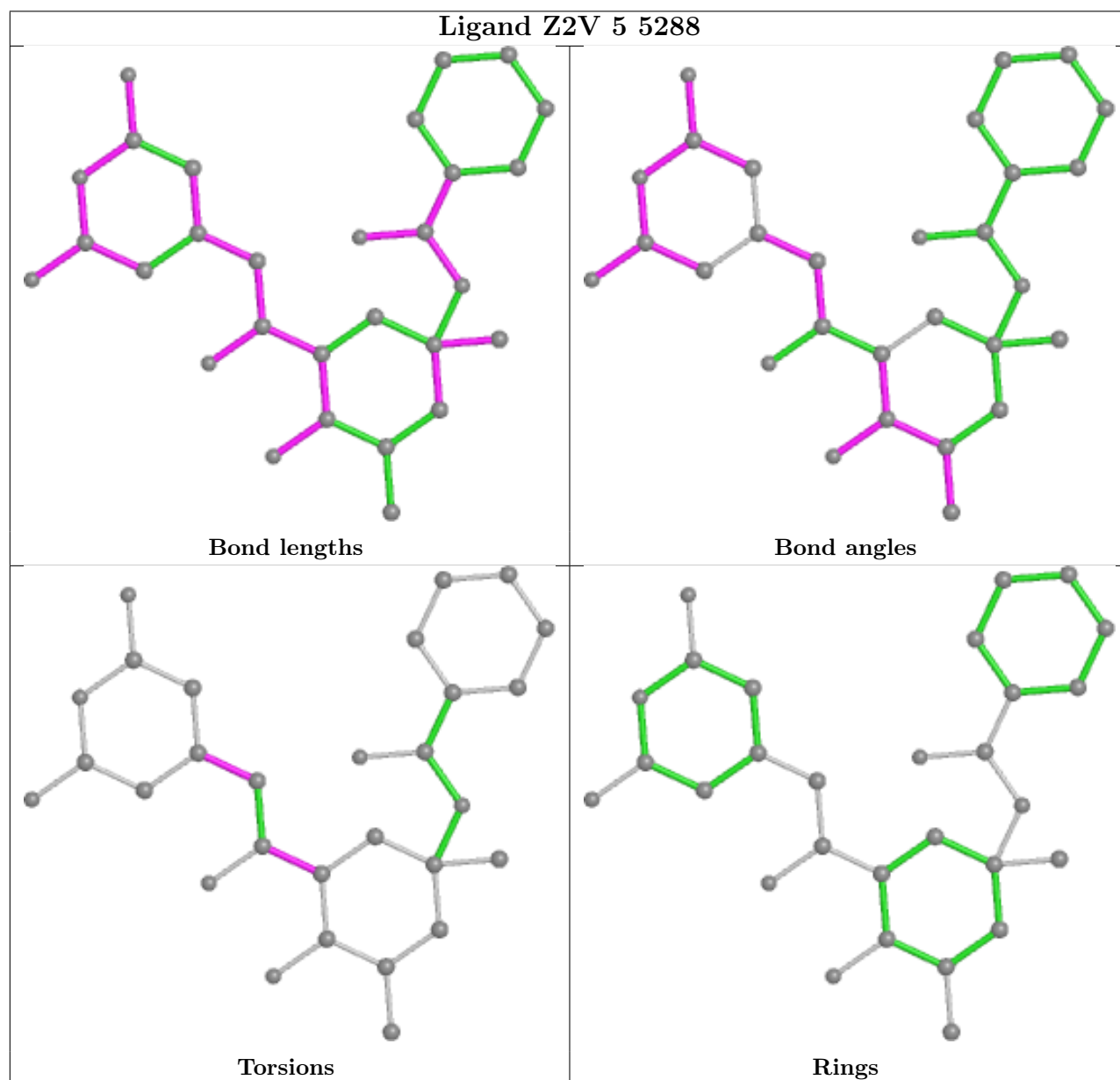
There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.



The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
76	5	23

The worst 5 of 23 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.47
1	5	1252:C	O3'	1271:G	P	36.98
1	5	1219:G	O3'	1233:G	P	19.63
1	5	4138:C	O3'	4146:G	P	17.77
1	5	990:C	O3'	1064:G	P	17.68

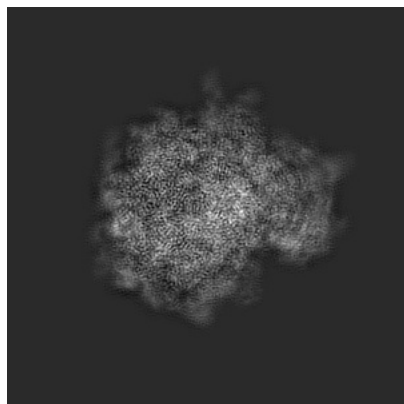
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23785. These allow visual inspection of the internal detail of the map and identification of artifacts.

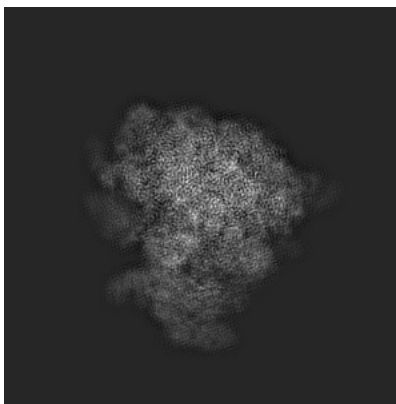
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

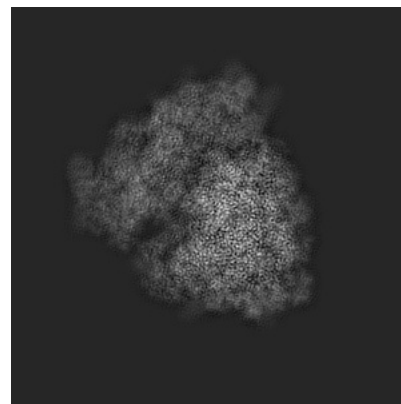
#### 6.1.1 Primary map



X

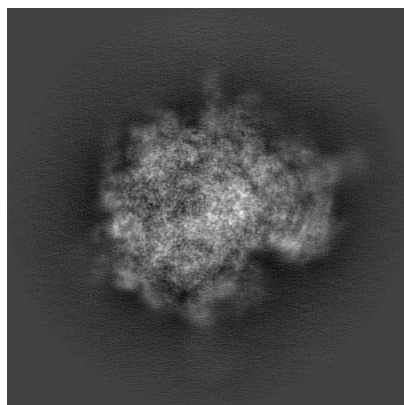


Y

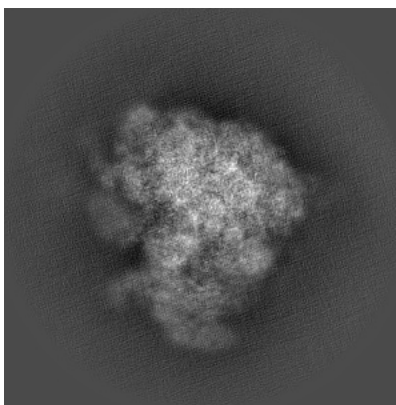


Z

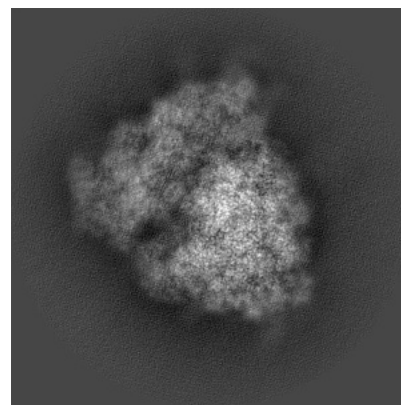
#### 6.1.2 Raw map



X



Y

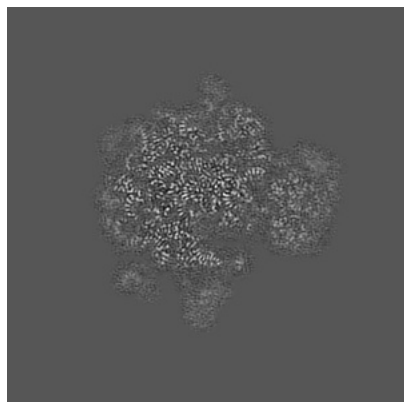


Z

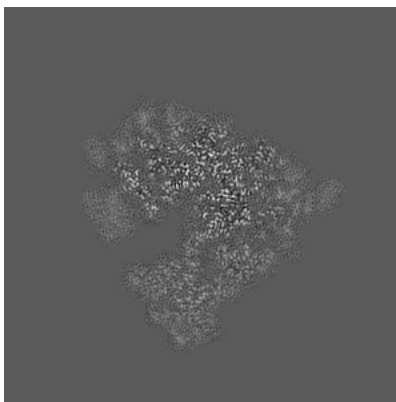
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

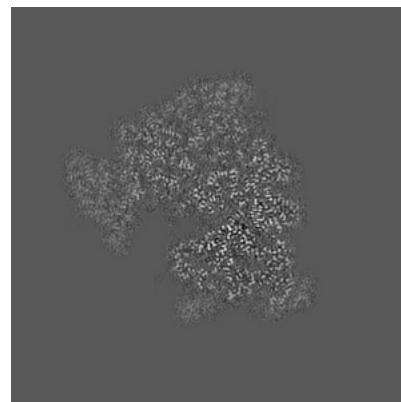
### 6.2.1 Primary map



X Index: 180

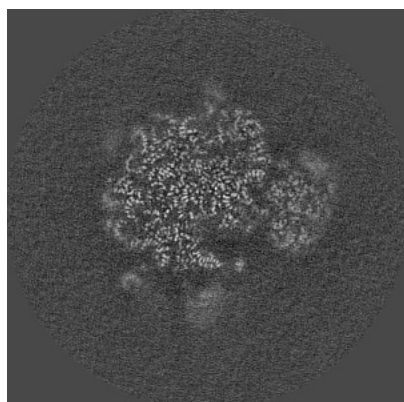


Y Index: 180

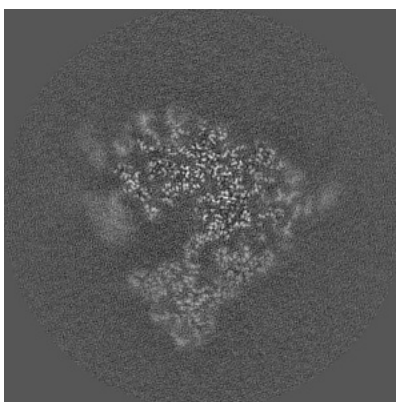


Z Index: 180

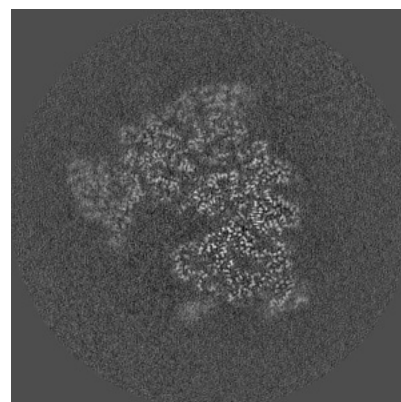
### 6.2.2 Raw map



X Index: 180



Y Index: 180

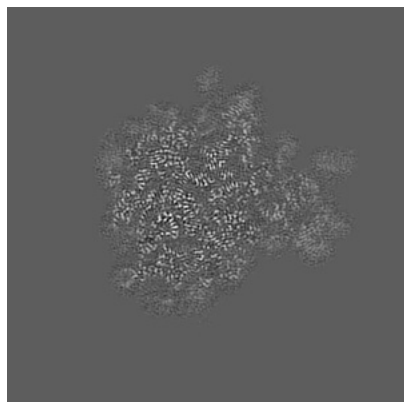


Z Index: 180

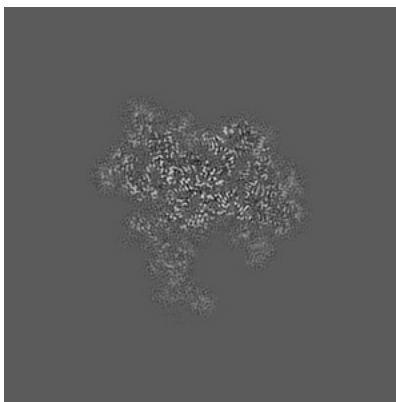
The images above show central slices of the map in three orthogonal directions.

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

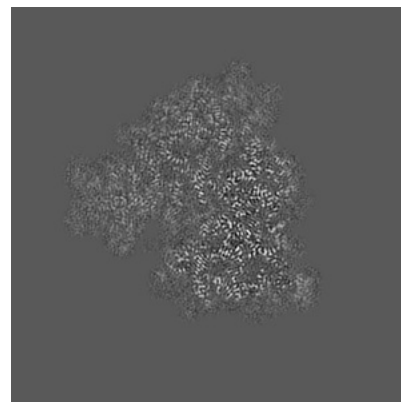
### 6.3.1 Primary map



X Index: 196

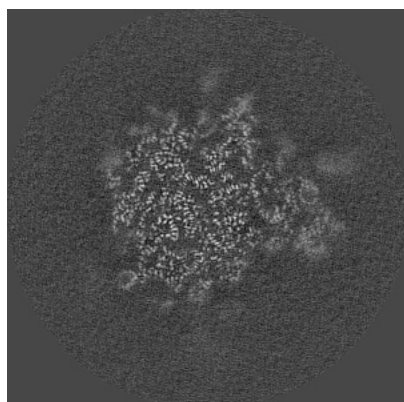


Y Index: 148

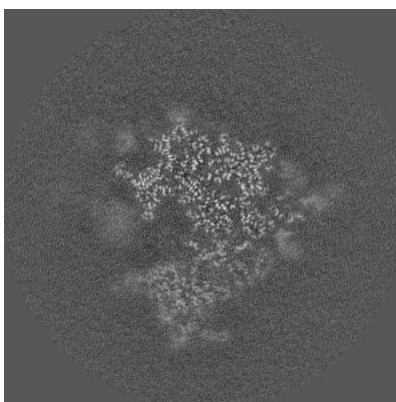


Z Index: 171

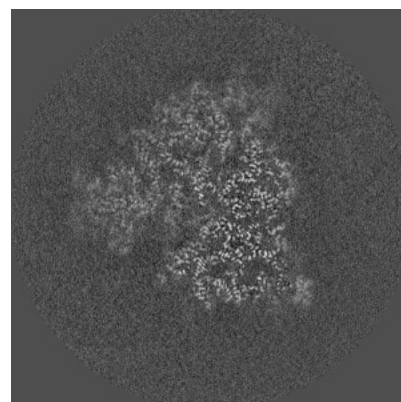
### 6.3.2 Raw map



X Index: 196



Y Index: 188

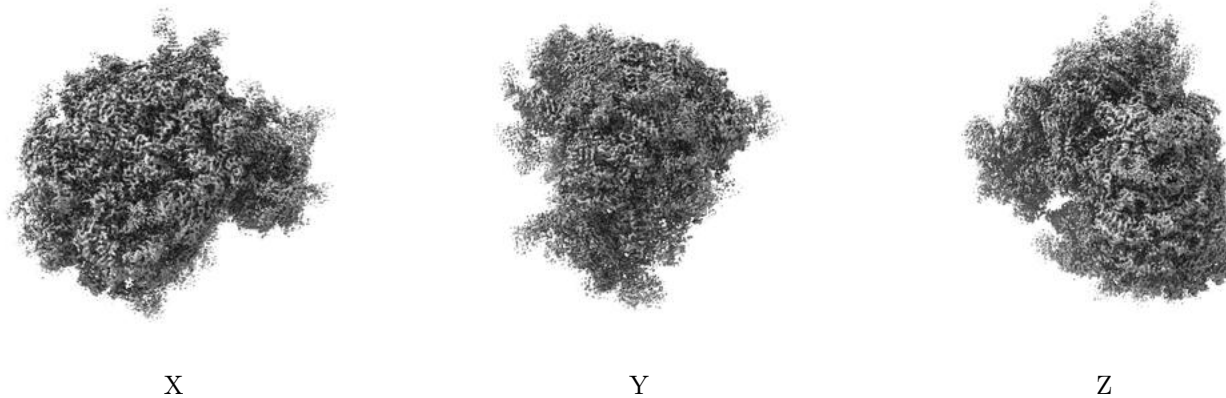


Z Index: 171

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

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

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

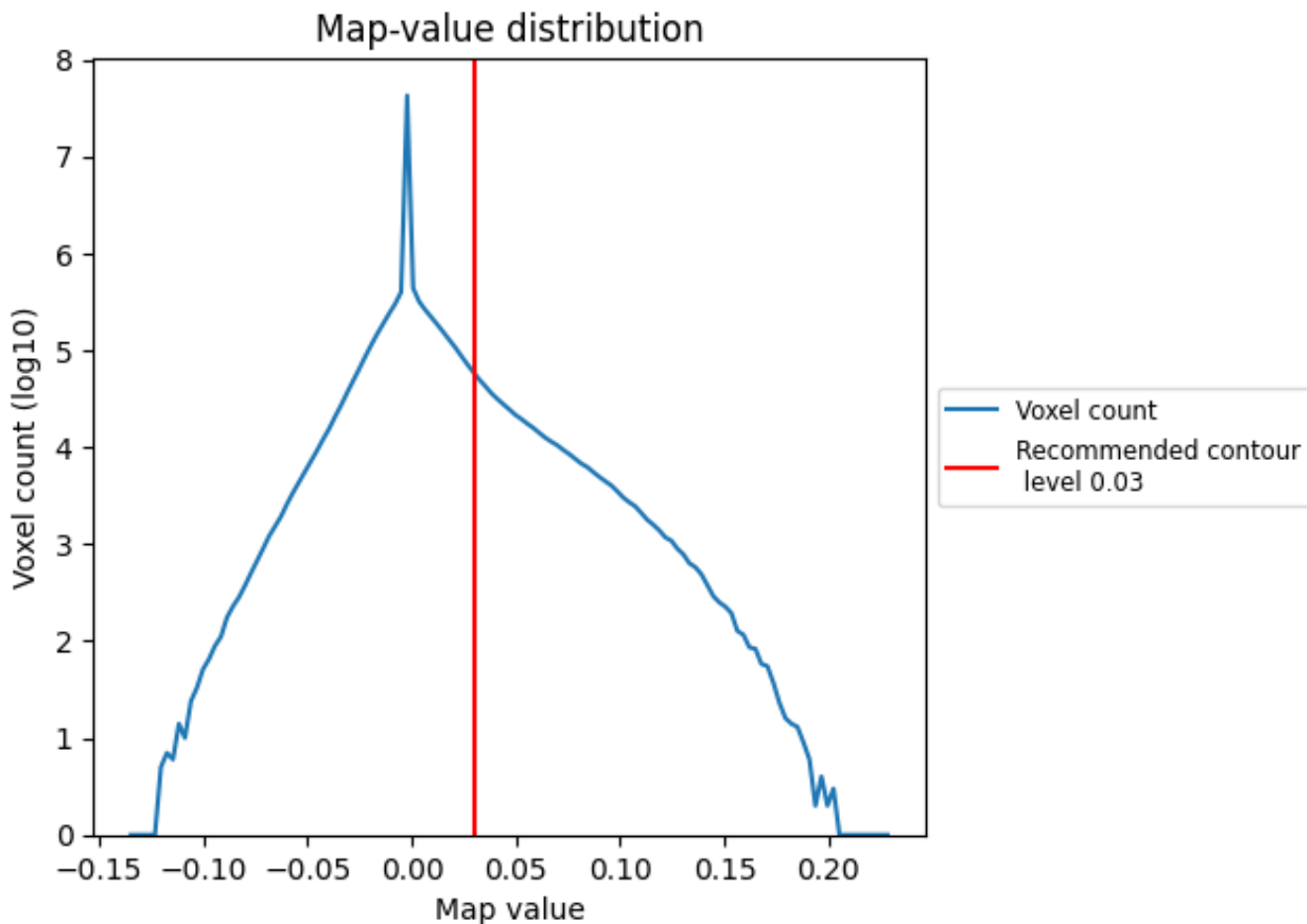
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

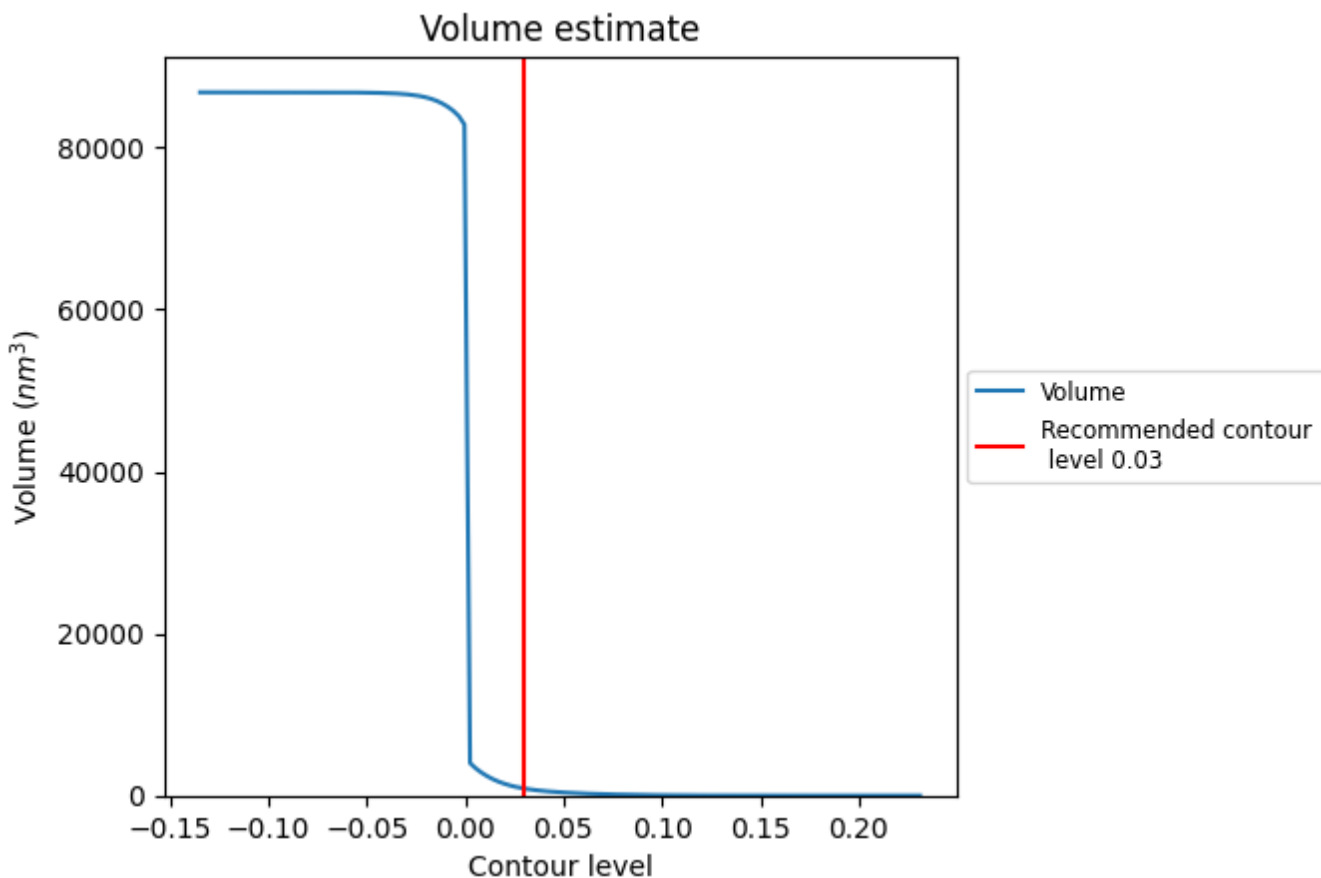
This section contains the results of statistical analysis of the map.

### 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](#)

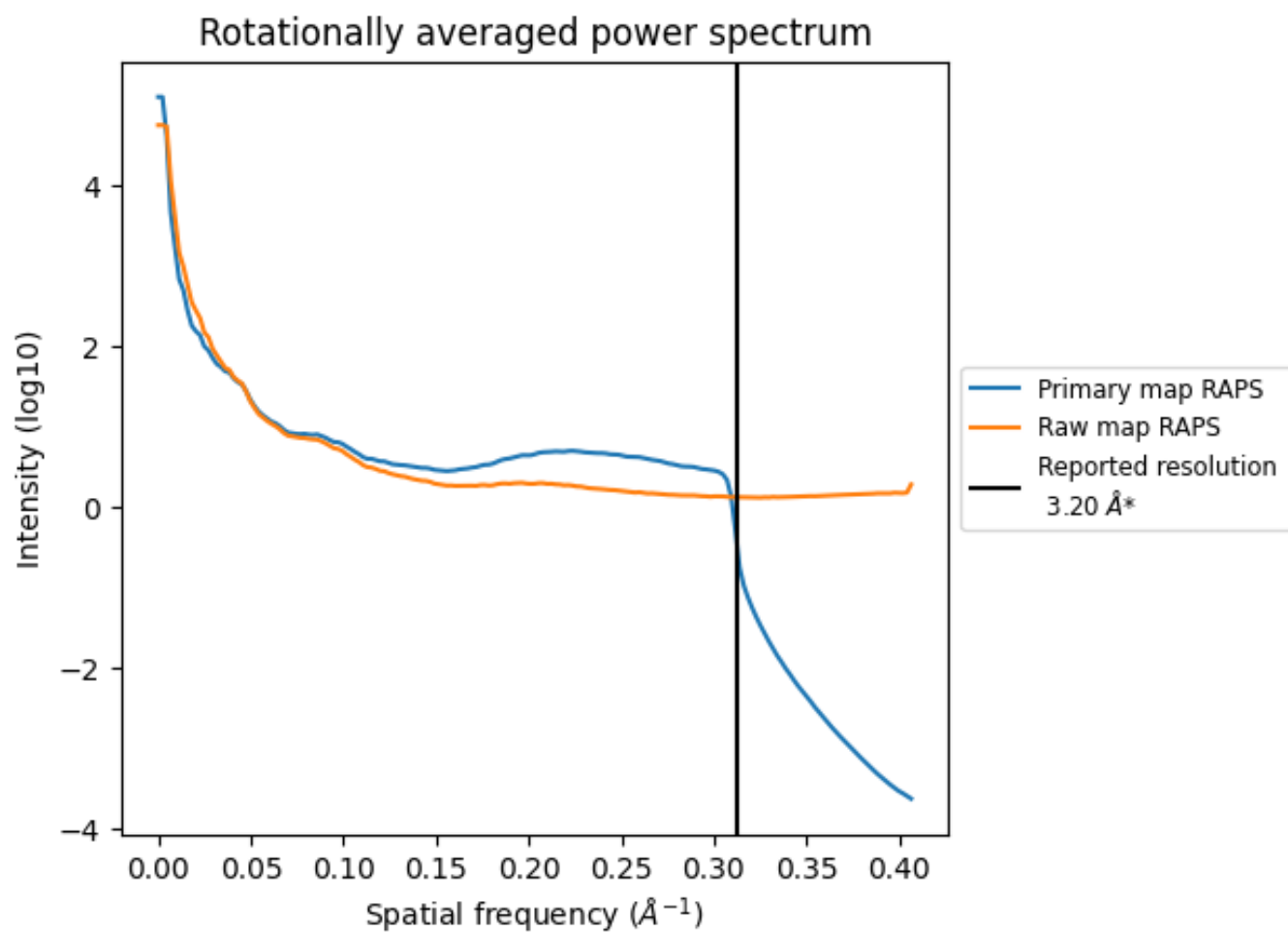


The volume at the recommended contour level is 875  $\text{nm}^3$ ; this corresponds to an approximate mass of 790 kDa.

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 [i](#)

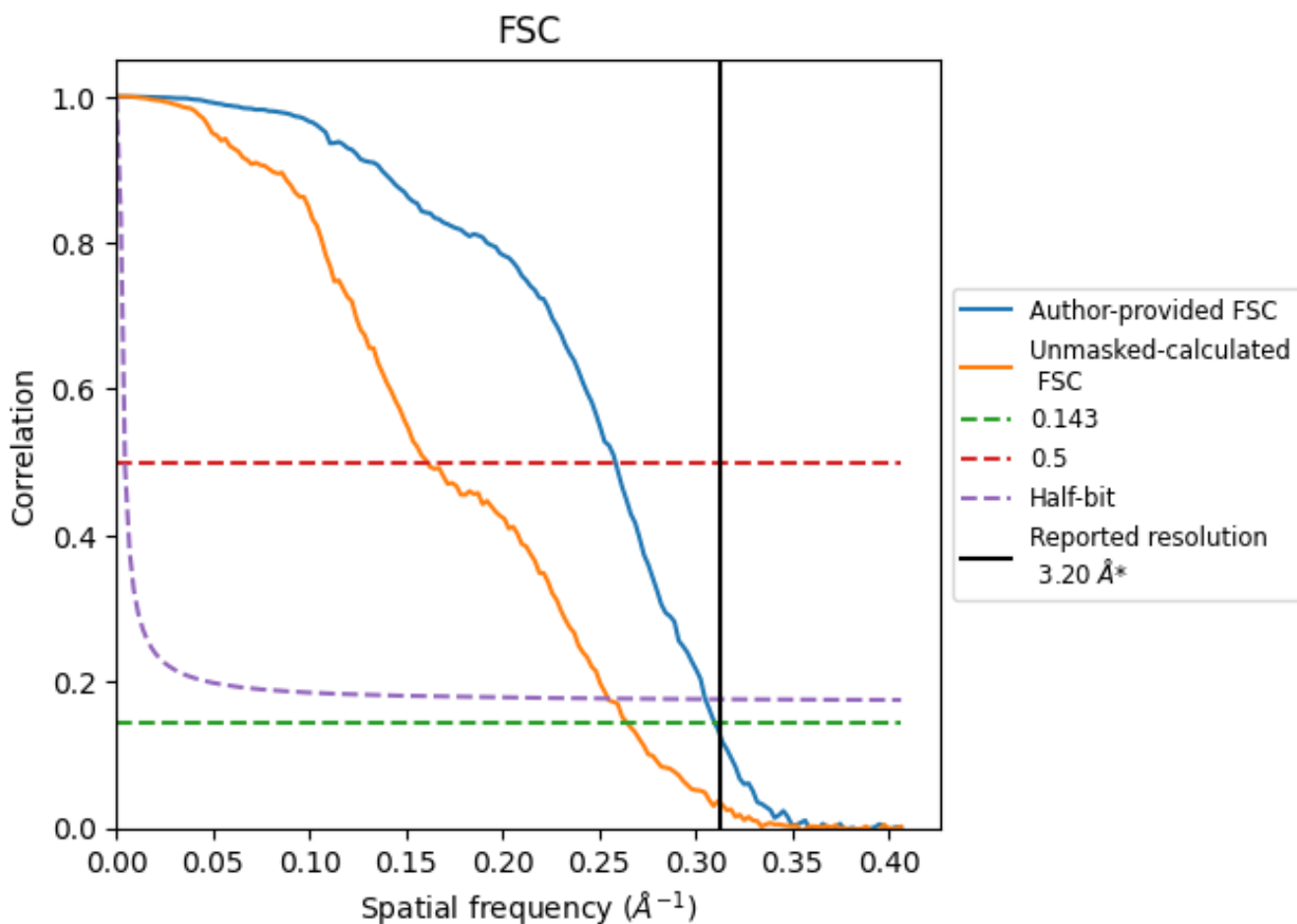


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

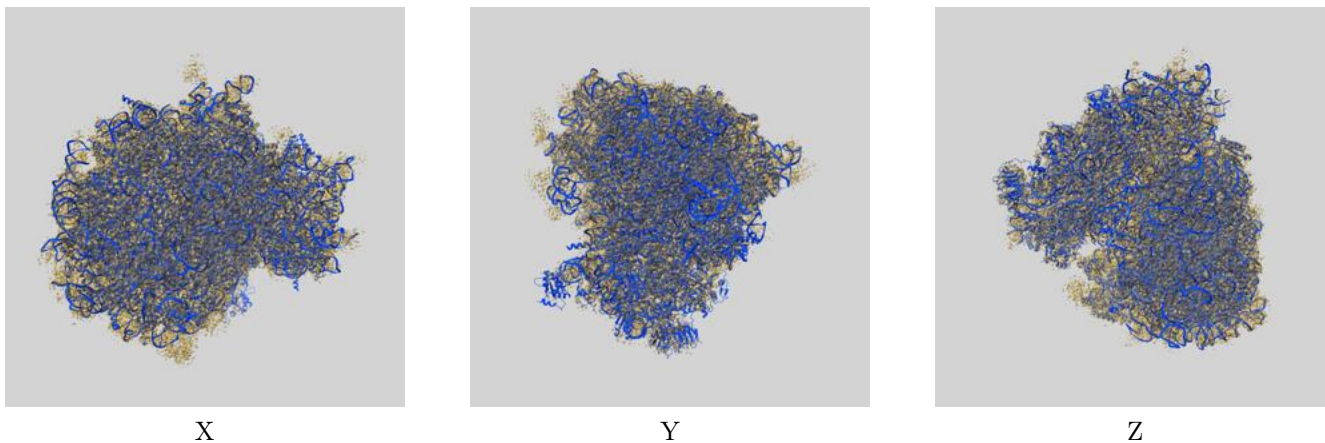
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.87	3.28
Unmasked-calculated*	3.78	6.21	3.93

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 3.2 by more than 10 %

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

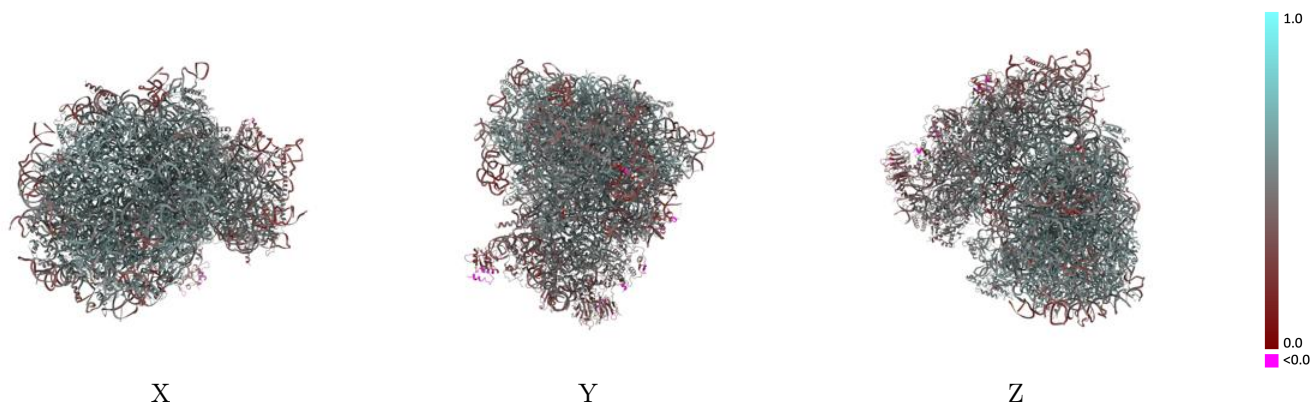
This section contains information regarding the fit between EMDB map EMD-23785 and PDB model 7MDZ. Per-residue inclusion information can be found in section [3](#) on page [24](#).

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



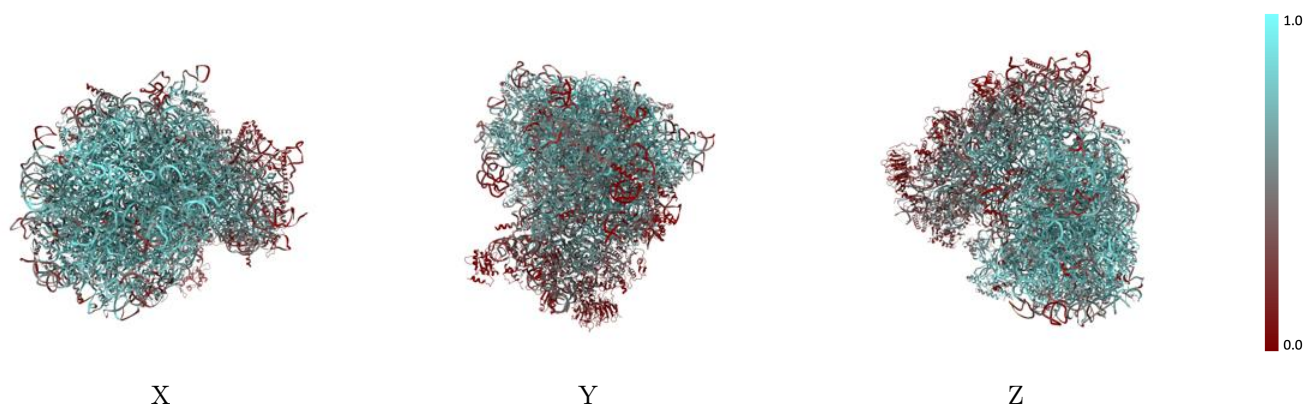
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



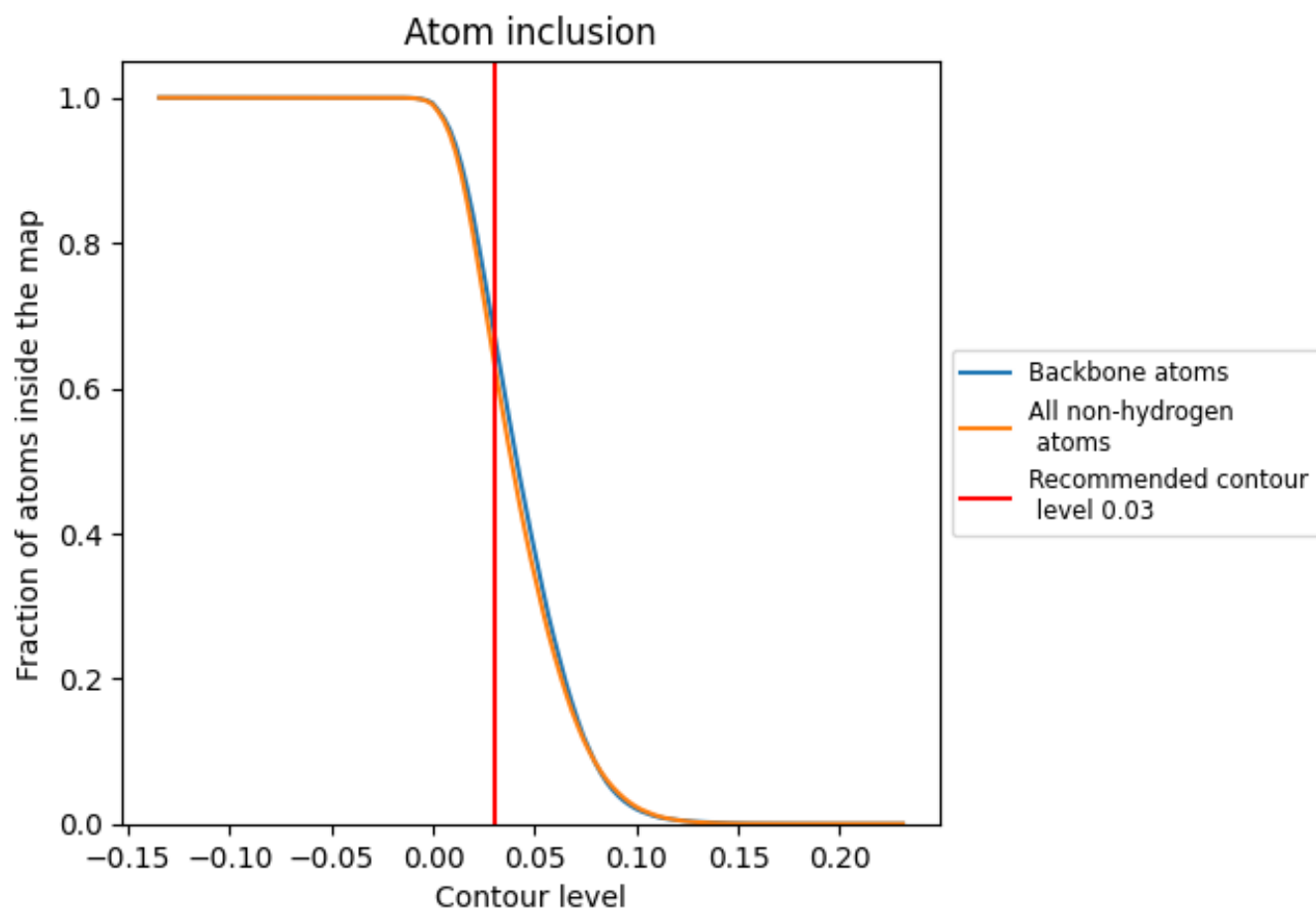
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 64% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6363	 0.5020
2	 0.3508	 0.4190
5	 0.7546	 0.5140
6	 0.2571	 0.4080
7	 0.8526	 0.5500
8	 0.7949	 0.5310
9	 0.5899	 0.4640
A	 0.7413	 0.5700
AA	 0.3351	 0.4510
B	 0.7407	 0.5710
BB	 0.4403	 0.4850
C	 0.7421	 0.5640
CC	 0.4774	 0.4910
D	 0.6809	 0.5290
DD	 0.2539	 0.4250
E	 0.6540	 0.5400
EE	 0.4356	 0.4950
F	 0.7415	 0.5690
FF	 0.3429	 0.4560
G	 0.5556	 0.4930
GG	 0.3213	 0.4230
H	 0.6576	 0.5420
HH	 0.2251	 0.3810
I	 0.7001	 0.5540
II	 0.4849	 0.4850
J	 0.5746	 0.5150
JJ	 0.4532	 0.4990
KK	 0.2354	 0.4120
L	 0.6695	 0.5400
LL	 0.5302	 0.5230
M	 0.7170	 0.5540
MM	 0.0291	 0.2030
N	 0.7920	 0.5820
NN	 0.4640	 0.4940
O	 0.7502	 0.5630



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Chain	Atom inclusion	Q-score
OO	0.5056	0.4960
P	0.7705	0.5780
PP	0.2500	0.4130
Q	0.7497	0.5740
QQ	0.3388	0.4390
R	0.6364	0.5260
RR	0.2168	0.3880
S	0.7436	0.5690
SS	0.3170	0.4360
T	0.6950	0.5510
TT	0.3280	0.4360
U	0.5398	0.5050
UU	0.2377	0.4090
V	0.6789	0.5530
VV	0.3424	0.4520
W	0.7151	0.5710
WW	0.4812	0.4990
X	0.6553	0.5430
XX	0.5444	0.5180
Y	0.7096	0.5590
YY	0.4037	0.4660
Z	0.6337	0.5300
ZZ	0.2487	0.4270
a	0.7926	0.5790
aa	0.4898	0.5110
b	0.5534	0.5090
bb	0.3255	0.4580
c	0.6008	0.5100
cc	0.2957	0.4400
d	0.6908	0.5570
dd	0.3937	0.4790
e	0.7630	0.5760
ee	0.3159	0.4430
f	0.7969	0.5840
ff	0.0628	0.2800
g	0.6729	0.5390
gg	0.1435	0.3550
h	0.6660	0.5440
i	0.6118	0.5210
j	0.8128	0.5770
k	0.5135	0.5040
l	0.7416	0.5740

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Chain	Atom inclusion	Q-score
m	 0.7067	 0.5570
n	 0.6560	 0.5550
o	 0.6949	 0.5780
p	 0.6676	 0.5530
r	 0.7618	 0.5590