



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:16 AM UTC

PDB ID : 6D90 / pdb_00006d90
EMDB ID : EMD-7834
Title : Mammalian 80S ribosome with a double translocated CrPV-IRES, P-site tRNA and eRF1.
Authors : Pisareva, V.P.; Pisarev, A.V.; Fernandez, I.S.
Deposited on : 2018-04-27
Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

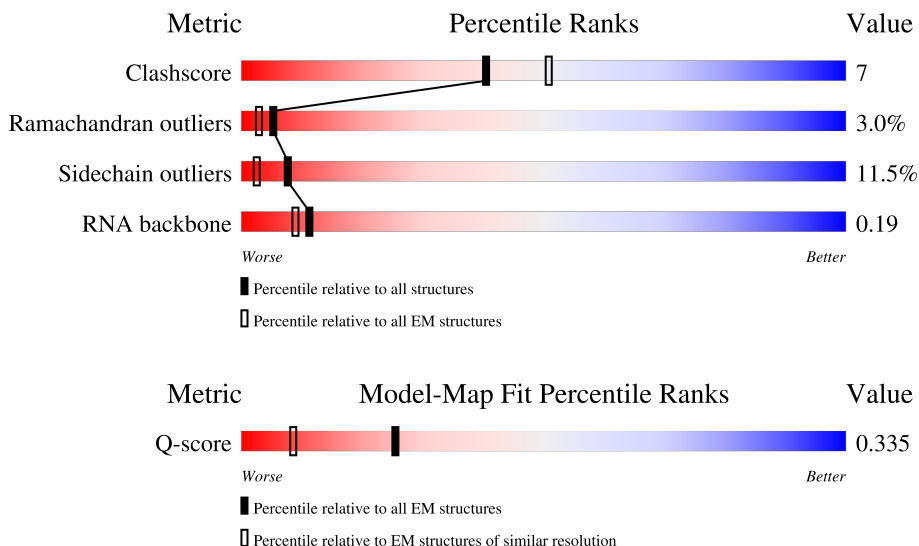
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.20 Å.

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



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

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

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

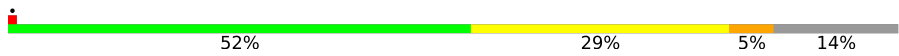
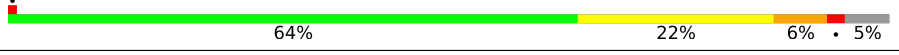

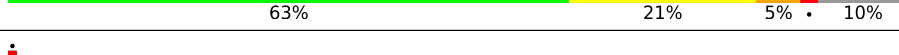
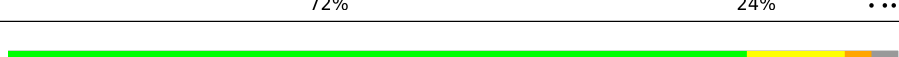
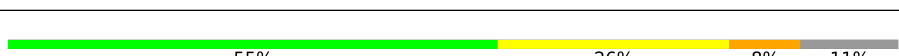



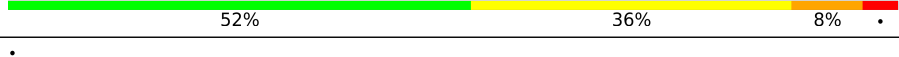




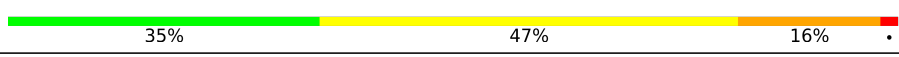



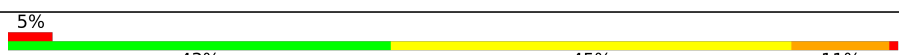
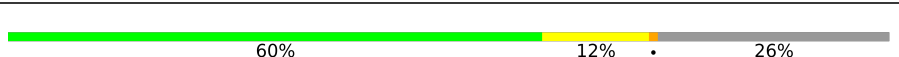

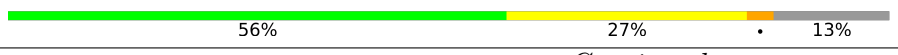



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Mol	Chain	Length	Quality of chain
4	D	297	78% 18% ..
5	E	291	53% 19% • 26%
6	F	249	68% 20% • 10%
7	G	242	80% 15% ..
8	H	192	72% 24% ...
9	I	214	73% 18% • •
10	J	178	82% 11% • •
11	L	211	79% 18% •
12	M	198	51% 13% 5% • 31%
13	N	204	66% 29% ..
14	O	199	62% 32% 6% •
15	P	184	52% 27% 5% 17%
16	Q	188	62% 31% 6% •
17	R	181	71% 20% 9% •
18	S	176	73% 23% ..
19	T	160	74% 23% ..
20	U	128	64% 11% • 23%
21	V	140	64% 23% • • 8%
22	W	157	49% 15% • • 32%
23	X	156	56% 15% • • 24%
24	Y	145	66% 22% • 8%
25	Z	136	69% 25% • •
26	a	148	74% 20% 5% •
27	b	226	39% 5% • 54%
28	c	115	69% 15% • 15%

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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	52	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	303	
44	t	195	
45	5	3594	
46	7	119	
47	8	151	
48	K	217	
49	2	1697	
50	3	87	
51	BB	295	
52	CC	264	
53	DD	255	







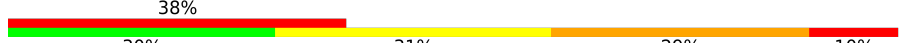
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Mol	Chain	Length	Quality of chain
54	EE	281	63% 17% 19%
55	FF	263	69% 27%
56	GG	204	72% 17% 9%
57	HH	249	72% 20% 5%
58	II	194	58% 29% 8% 5%
59	JJ	208	73% 22%
60	KK	194	69% 23% 5%
61	LL	149	48% 14% 36%
62	MM	158	71% 16% 9%
63	NN	132	64% 73% 14% 11%
64	OO	151	68% 26%
65	PP	151	76% 11% 10%
66	QQ	145	56% 22% 21%
67	RR	172	72% 10% 17%
68	SS	135	80% 17%
69	TT	152	78% 14% 5%
70	UU	145	86% 11%
71	VV	119	59% 24% 16%
72	WW	83	77% 19%
73	XX	130	77% 18%
74	YY	143	63% 29% 6%
75	ZZ	134	69% 22% 7%
76	aa	125	48% 12% 40%
77	bb	115	63% 23% 12%
78	cc	84	75% 24%

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Mol	Chain	Length	Quality of chain
79	dd	69	 81% 9% 10%
80	ee	56	 73% 23% ..
81	ff	133	 5% 28% 12% 57% .
82	gg	156	 17% 35% 8% 56%
83	hh	317	 76% 20% ..
84	jj	437	 43% 78% 16% . 5%
85	4	194	 38% 30% 31% 29% 10%

2 Entry composition i

There are 85 unique types of molecules in this entry. The entry contains 223875 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	239	1777	1110	361	300	6	0	0

- Molecule 2 is a protein called uL3.

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

- Molecule 3 is a protein called Ribosomal protein L4.

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called eL8.

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

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

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

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

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

- Molecule 10 is a protein called Ribosomal protein L11.

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

- Molecule 11 is a protein called eL13.

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

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

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

There are 20 discrepancies between the modelled and reference sequences:

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

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			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	198	1623	1046	318	254	5	0	0

- Molecule 15 is a protein called Large ribosomal subunit protein 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 rL18.

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

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	6	ARG	LEU	conflict	UNP G1TX70
Q	14	ARG	TRP	conflict	UNP G1TX70
Q	23	ILE	MET	conflict	UNP G1TX70
Q	24	TYR	CYS	conflict	UNP G1TX70
Q	38	ARG	HIS	conflict	UNP G1TX70
Q	57	ASN	LYS	conflict	UNP G1TX70
Q	66	MET	VAL	conflict	UNP G1TX70
Q	74	GLY	ASP	conflict	UNP G1TX70
Q	75	ARG	PRO	conflict	UNP G1TX70
Q	86	VAL	ILE	conflict	UNP G1TX70
Q	110	ARG	HIS	conflict	UNP G1TX70
Q	117	GLY	GLU	conflict	UNP G1TX70
Q	124	ASP	HIS	conflict	UNP G1TX70
Q	150	ARG	GLN	conflict	UNP G1TX70
Q	172	ARG	GLY	conflict	UNP G1TX70
Q	184	ARG	TRP	conflict	UNP G1TX70

- 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	159	1298	823	252	217	6	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 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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 21 is a protein called Ribosomal protein L23.

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

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	106	860	538	174	144	4	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 uL15.

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called Ribosomal protein L32.

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

- Molecule 31 is a protein called eL33.

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

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

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

- Molecule 33 is a protein called eL35.

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

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

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called eL38.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	3	ARG	GLN	conflict	UNP G1U3J0
k	38	CYS	TYR	conflict	UNP G1U3J0
k	48	THR	MET	conflict	UNP G1U3J0
k	66	VAL	MET	conflict	UNP G1U3J0

- Molecule 37 is a protein called eL39.

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

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

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

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

- Molecule 41 is a protein called eL43.

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

- Molecule 42 is a protein called eL28.

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

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

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

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
s	262	LEU	ALA	conflict	UNP A0A1U7UFL5
s	?	-	GLU	deletion	UNP A0A1U7UFL5
s	266	THR	ALA	conflict	UNP A0A1U7UFL5
s	267	LEU	PHE	conflict	UNP A0A1U7UFL5
s	269	ILE	ALA	conflict	UNP A0A1U7UFL5
s	270	ILE	ASP	conflict	UNP A0A1U7UFL5
s	?	-	SER	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	PHE	deletion	UNP A0A1U7UFL5
s	?	-	VAL	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5
s	?	-	ALA	deletion	UNP A0A1U7UFL5

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

- Molecule 44 is a protein called Ribosomal protein L12.

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

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

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

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

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

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

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

- Molecule 48 is a protein called Ribosomal protein.

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

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

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

- Molecule 50 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	3	87	1861	829	333	612	87	0	0

- Molecule 51 is a protein called Small ribosomal subunit protein uS2.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BB	114	THR	ALA	conflict	UNP G1TLT8
BB	235	GLU	ALA	conflict	UNP G1TLT8
BB	252	MET	VAL	conflict	UNP G1TLT8
BB	288	MET	VAL	conflict	UNP G1TLT8

- Molecule 52 is a protein called 40S ribosomal protein S3a.

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

- Molecule 53 is a protein called uS5.

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	97	PHE	CYS	conflict	UNP G1SWM1
DD	101	SER	ALA	conflict	UNP G1SWM1
DD	141	VAL	LEU	conflict	UNP G1SWM1
DD	181	PRO	LEU	conflict	UNP G1SWM1
DD	191	VAL	-	insertion	UNP G1SWM1
DD	215	MET	LEU	conflict	UNP G1SWM1
DD	271	ASP	ASN	conflict	UNP G1SWM1
DD	274	VAL	MET	conflict	UNP G1SWM1

- Molecule 54 is a protein called Ribosomal protein S3.

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

- Molecule 55 is a protein called 40S ribosomal protein S4.

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

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 56 is a protein called Ribosomal protein S5.

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

- Molecule 57 is a protein called 40S ribosomal protein S6.

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

- Molecule 58 is a protein called 40S ribosomal protein S7.

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

- Molecule 59 is a protein called 40S ribosomal protein S8.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 60 is a protein called Ribosomal protein S9 (Predicted).

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

- Molecule 61 is a protein called S10_ plectin domain-containing protein.

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

- Molecule 62 is a protein called Ribosomal protein S11.

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

- Molecule 63 is a protein called 40S ribosomal protein S12.

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

- Molecule 64 is a protein called Ribosomal protein S13.

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

- Molecule 65 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called Ribosomal protein S16.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

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

- Molecule 71 is a protein called uS10.

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

- Molecule 72 is a protein called 40S ribosomal protein S21.

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
WW	3	ASN	SER	conflict	UNP G1TM82
WW	4	ASP	ASN	conflict	UNP G1TM82
WW	33	GLN	PRO	conflict	UNP G1TM82
WW	50	PHE	SER	conflict	UNP G1TM82
WW	75	ALA	SER	conflict	UNP G1TM82
WW	76	ASP	HIS	conflict	UNP G1TM82
WW	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called Ribosomal protein S15a.

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

- Molecule 74 is a protein called Ribosomal protein S23.

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

- Molecule 75 is a protein called 40S ribosomal protein S24.

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

- Molecule 76 is a protein called eS25.

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

- Molecule 77 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	bb	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
bb	28	ARG	CYS	conflict	UNP G1TFE8
bb	56	ALA	VAL	conflict	UNP G1TFE8

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called Ribosomal protein S28.

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

- Molecule 80 is a protein called eS29.

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

- Molecule 81 is a protein called 40S ribosomal protein S30.

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

- Molecule 82 is a protein called Ribosomal protein S27a.

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

- Molecule 83 is a protein called RACK1.

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

- Molecule 84 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
84	jj	416	3280	2087	559	623	11	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
jj	183	ALA	GLY	conflict	UNP P62495
jj	184	ALA	GLY	conflict	UNP P62495

- Molecule 85 is a RNA chain called CrPV-IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
85	4	194	4105	1840	704	1367	194	0	0

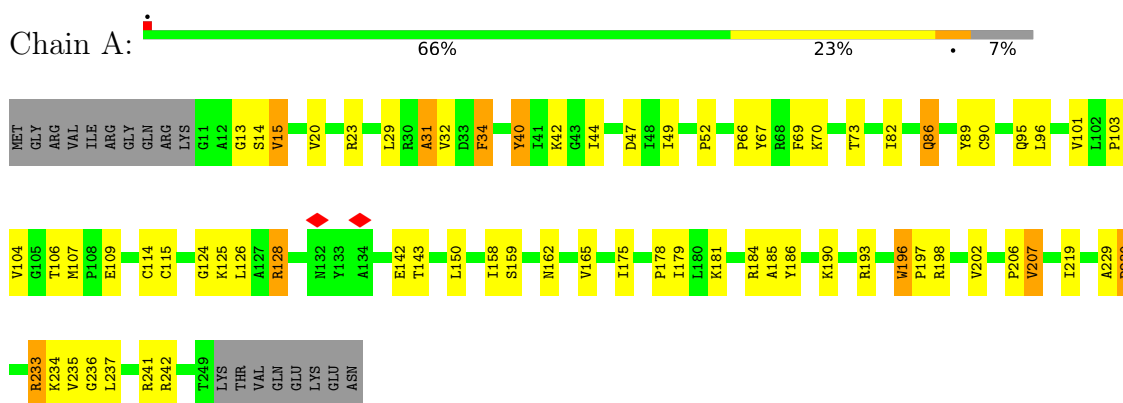
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	?	-	G	deletion	GB KP974707.1
4	6219	C	A	conflict	GB KP974707.1
4	6220	U	C	conflict	GB KP974707.1
4	6222	G	U	conflict	GB KP974707.1

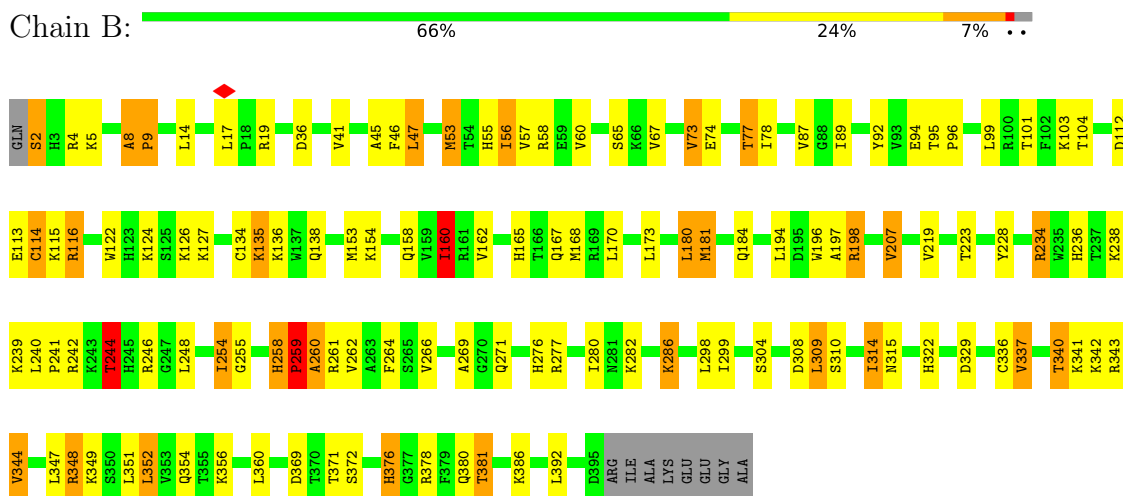
3 Residue-property plots [i](#)

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.

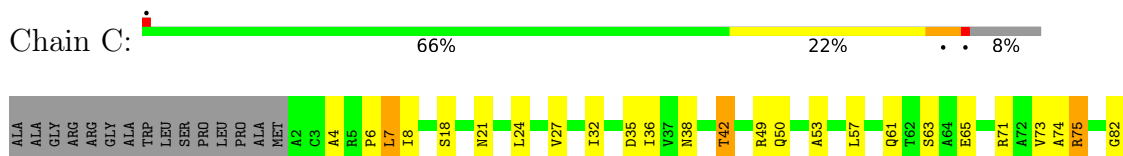
• Molecule 1: Ribosomal protein L8

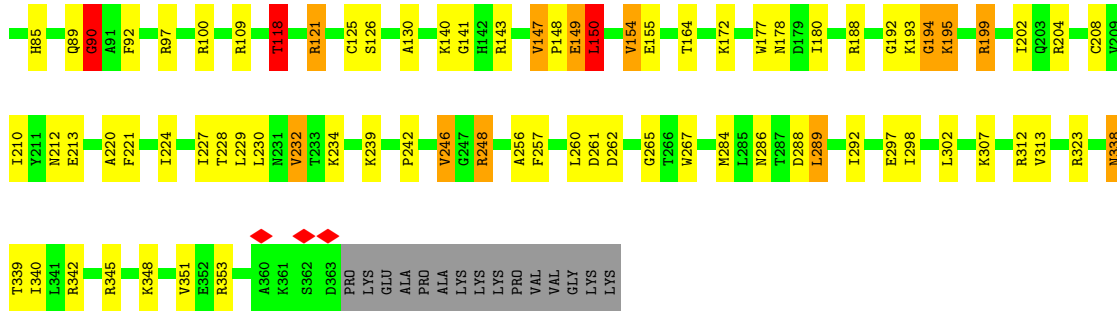


• Molecule 2: uL3

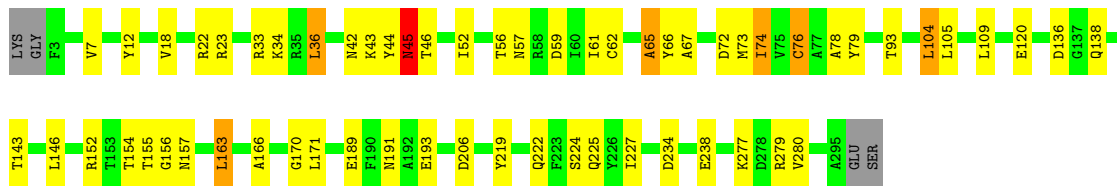
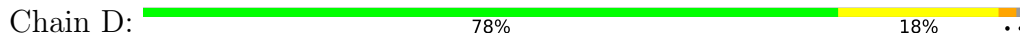


• Molecule 3: Ribosomal protein L4

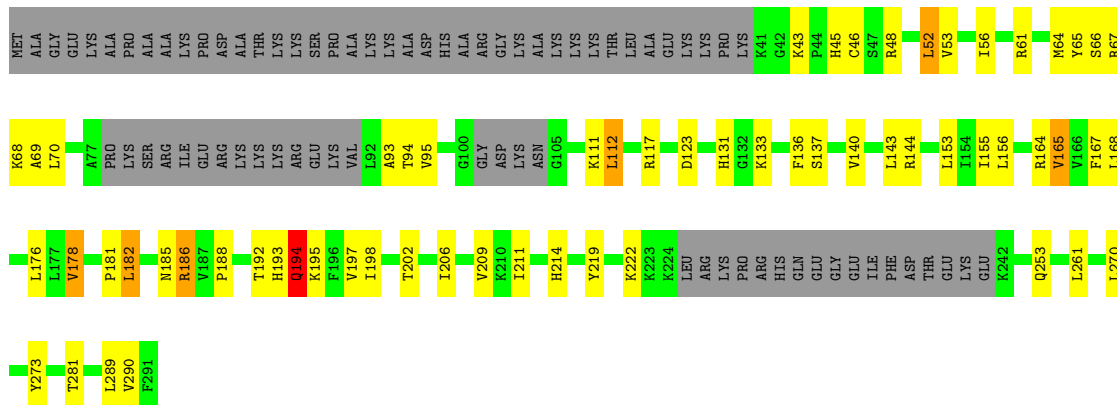




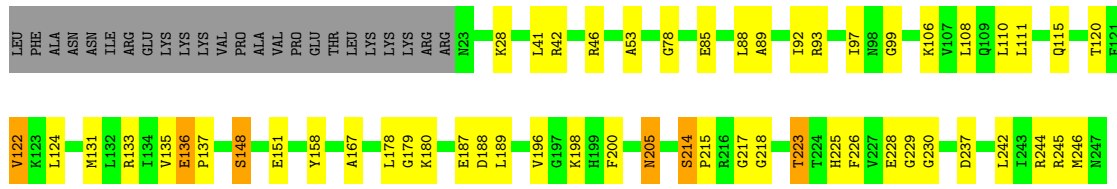
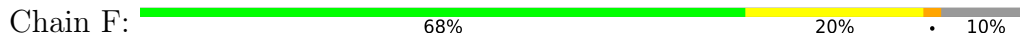
• Molecule 4: Large ribosomal subunit protein uL18



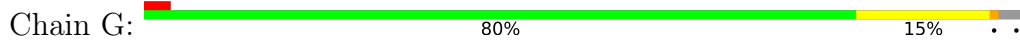
• Molecule 5: 60S ribosomal protein L6

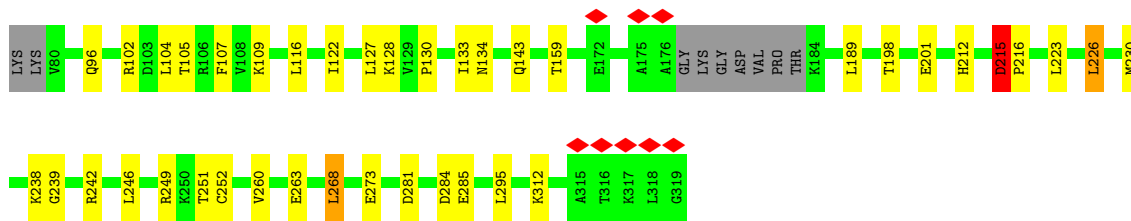


• Molecule 6: uL30

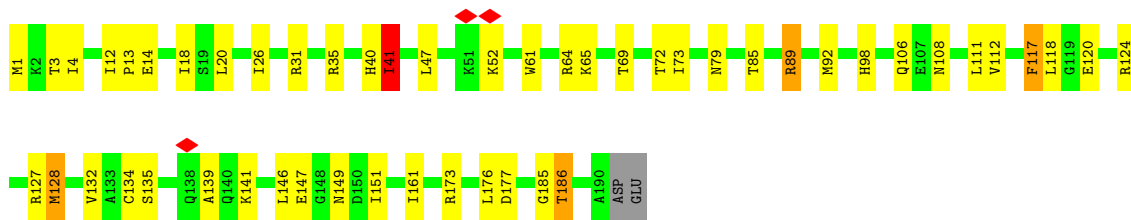


• Molecule 7: eL8

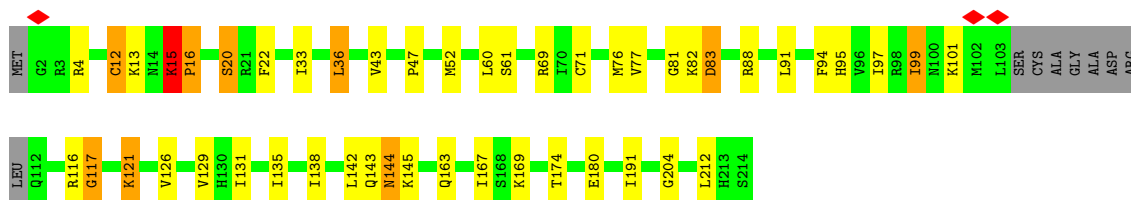




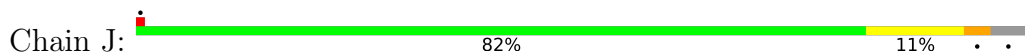
• Molecule 8: 60S ribosomal protein L9



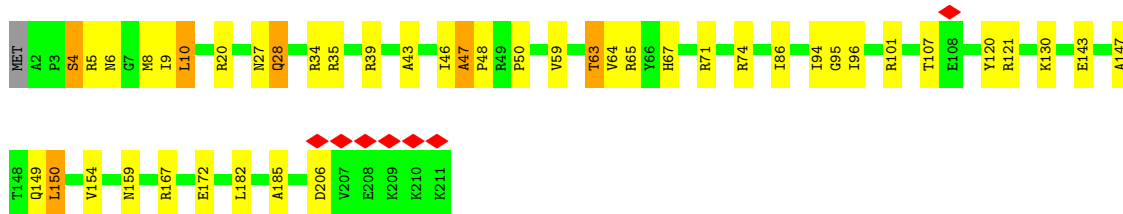
• Molecule 9: 60S ribosomal protein L10



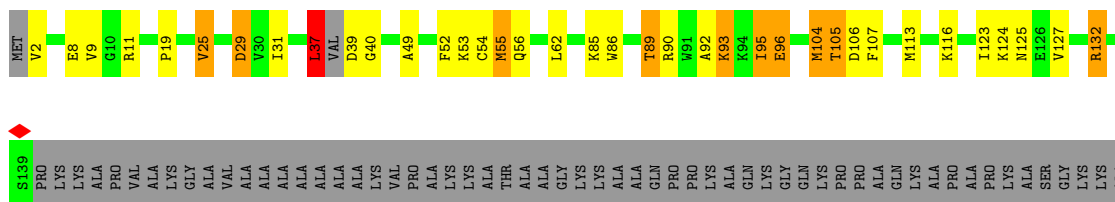
• Molecule 10: Ribosomal protein L11



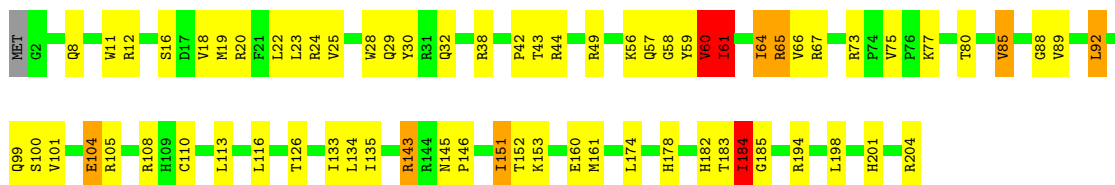
• Molecule 11: eL13



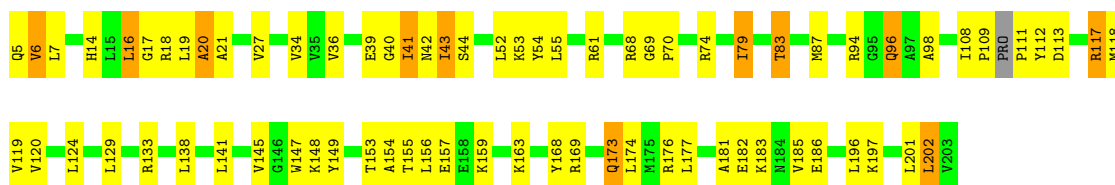
• Molecule 12: Large ribosomal subunit protein eL14



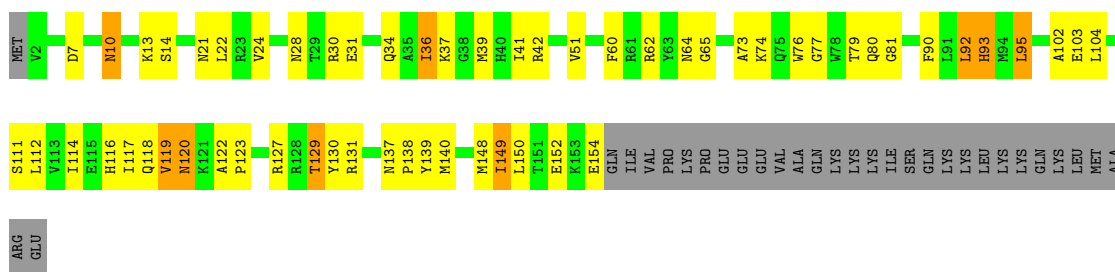
• Molecule 13: Ribosomal protein L15



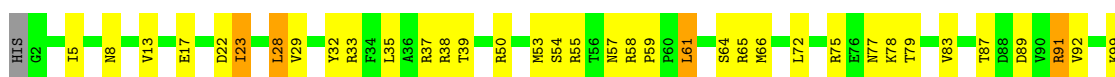
• Molecule 14: uL13



• Molecule 15: Large ribosomal subunit protein uL22



• Molecule 16: rL18

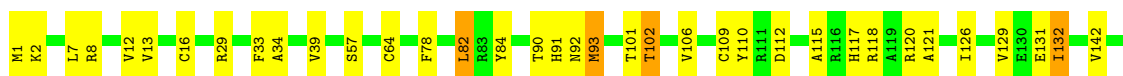




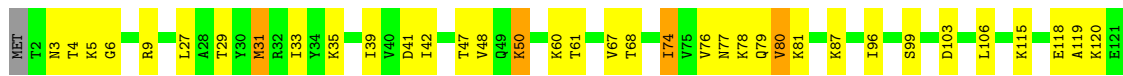
• Molecule 17: Ribosomal protein L19



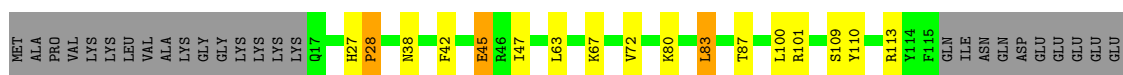
• Molecule 18: 60S ribosomal protein L18a



• Molecule 19: eL21



• Molecule 20: eL22

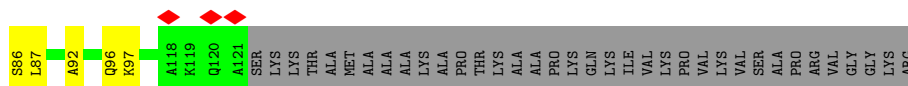


• Molecule 21: Ribosomal protein L23

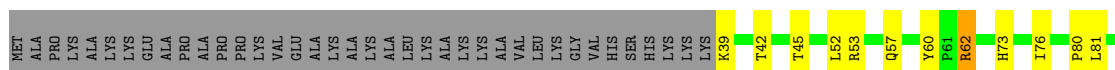




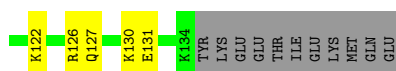
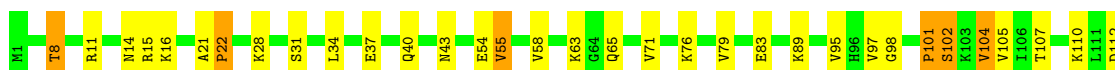
• Molecule 22: eL24



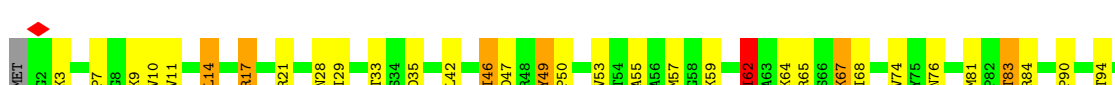
• Molecule 23: eL23



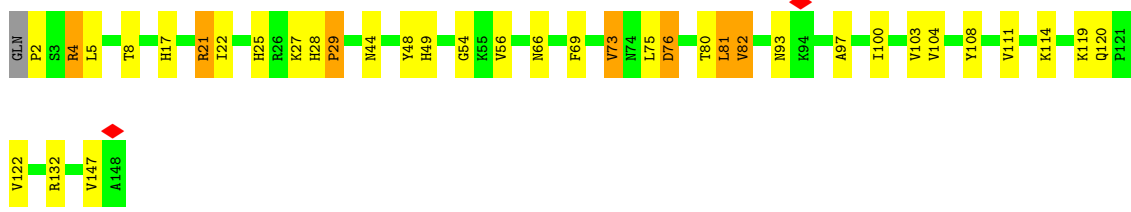
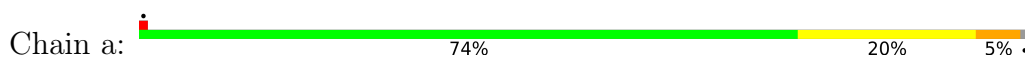
• Molecule 24: uL24



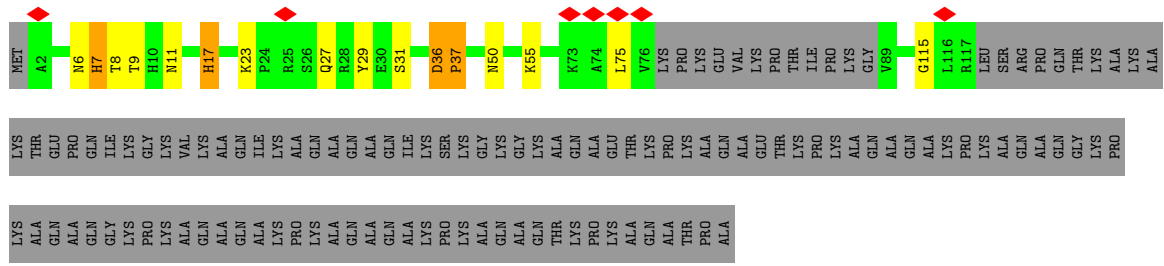
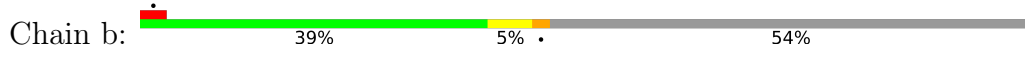
• Molecule 25: 60S ribosomal protein L27



• Molecule 26: uL15



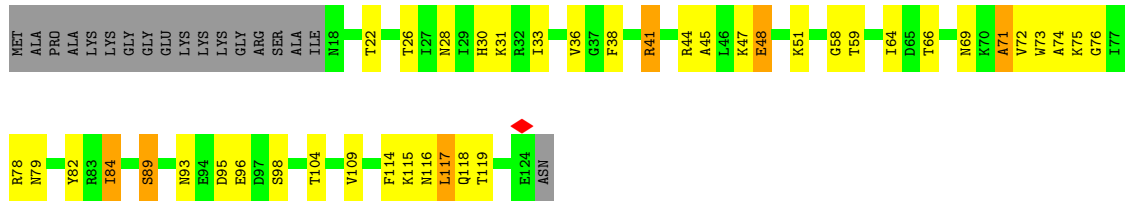
• Molecule 27: eL29



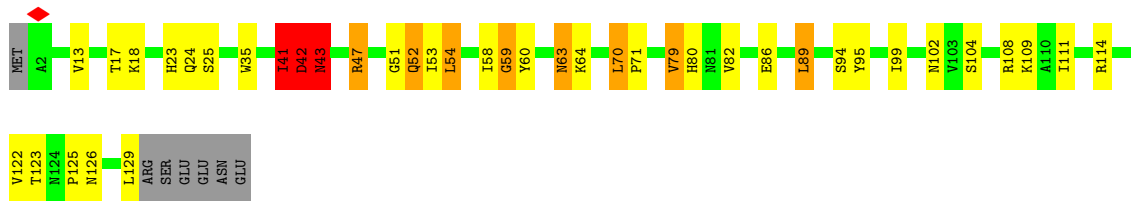
• Molecule 28: eL30



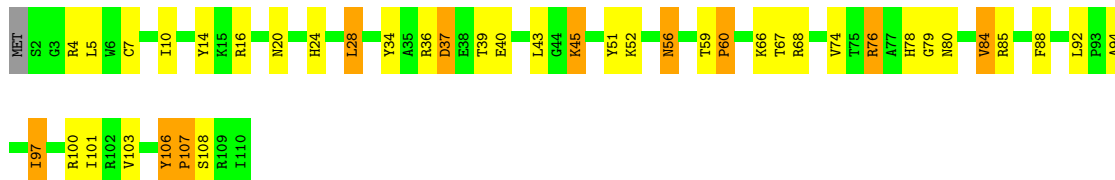
• Molecule 29: eL31



• Molecule 30: Ribosomal protein L32



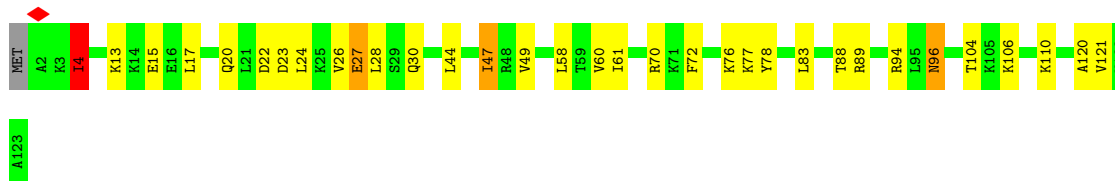
• Molecule 31: eL33



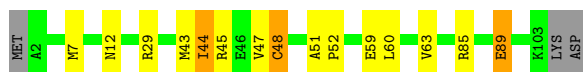
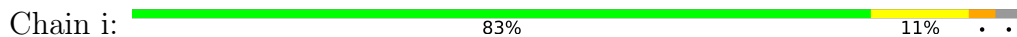
• Molecule 32: Large ribosomal subunit protein eL34



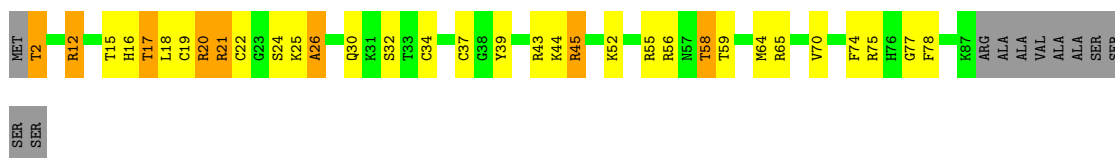
• Molecule 33: eL35



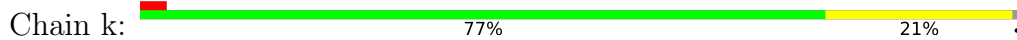
• Molecule 34: 60S ribosomal protein L36



• Molecule 35: Ribosomal protein L37



• Molecule 36: eL38





• Molecule 37: eL39



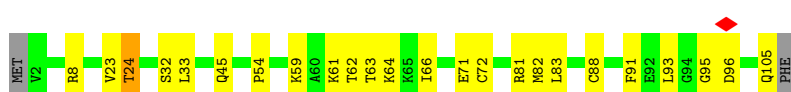
• Molecule 38: eL40



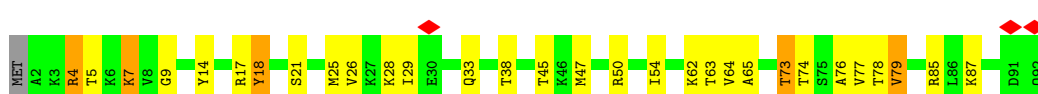
• Molecule 39: eL41



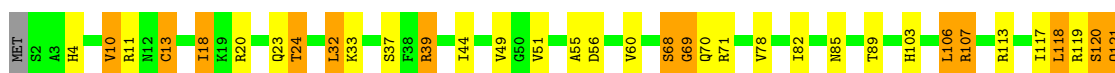
• Molecule 40: Large ribosomal subunit protein eL42

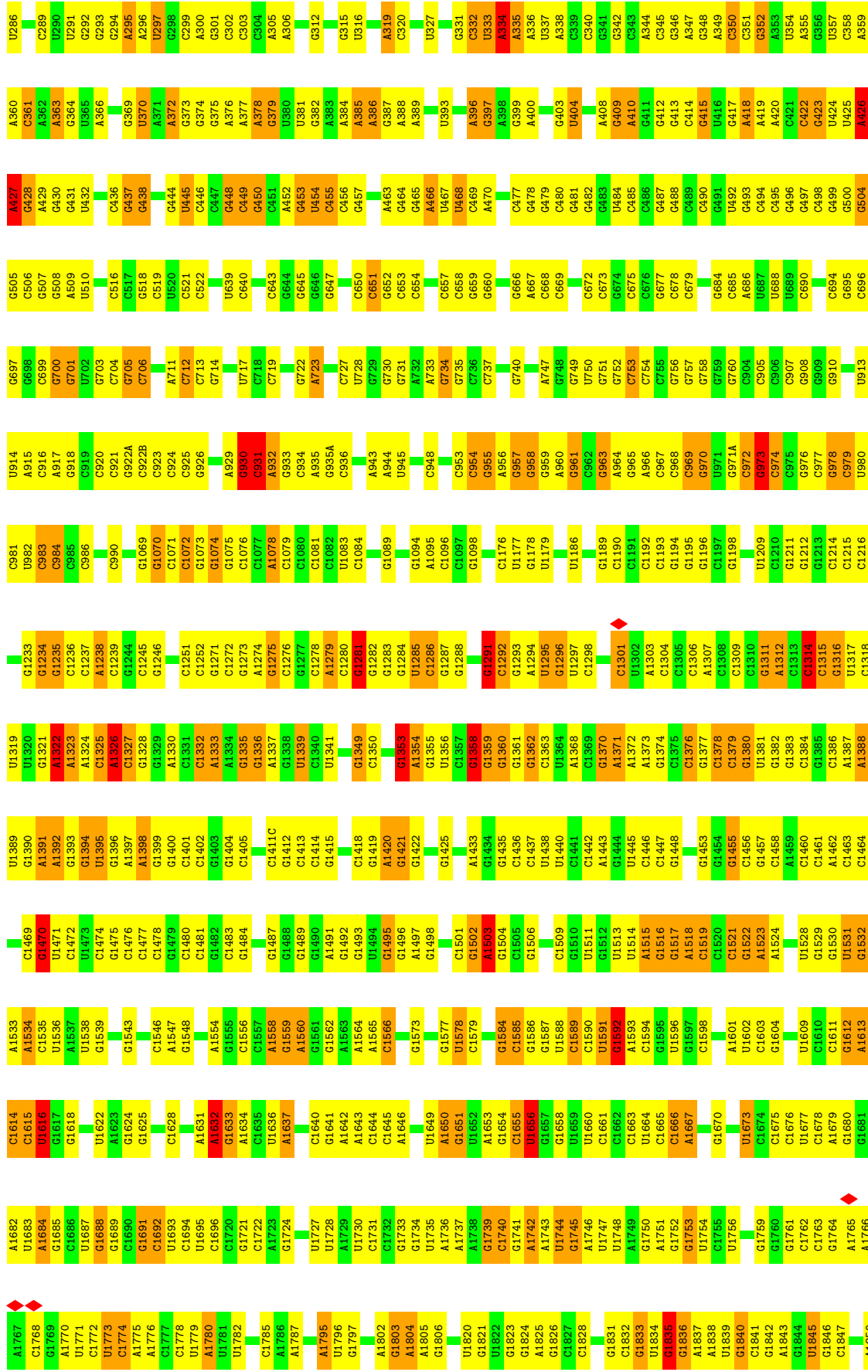


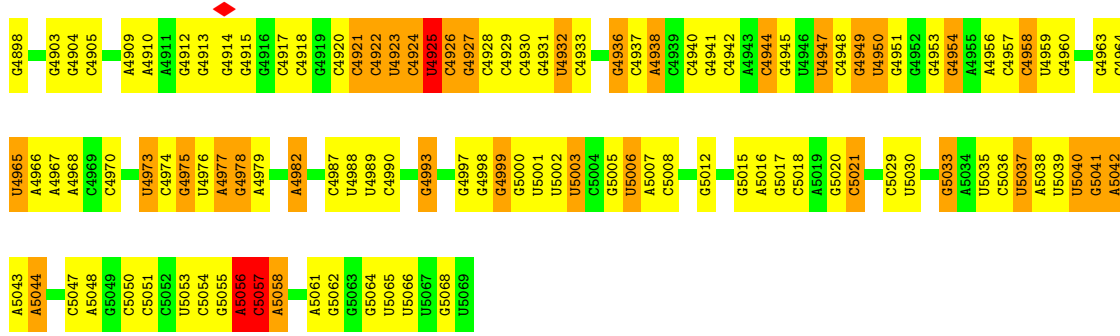
• Molecule 41: eL43



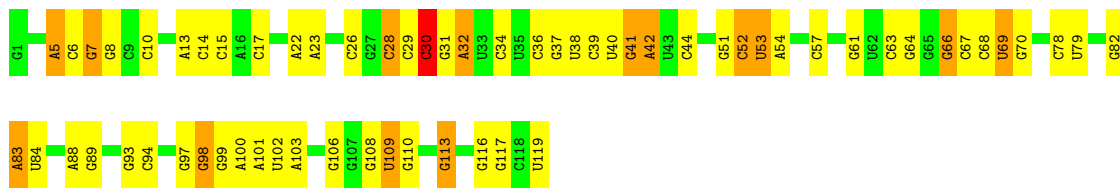
• Molecule 42: eL28



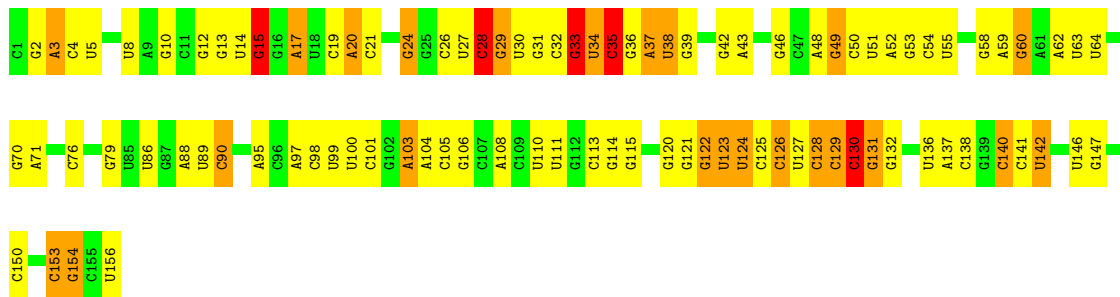




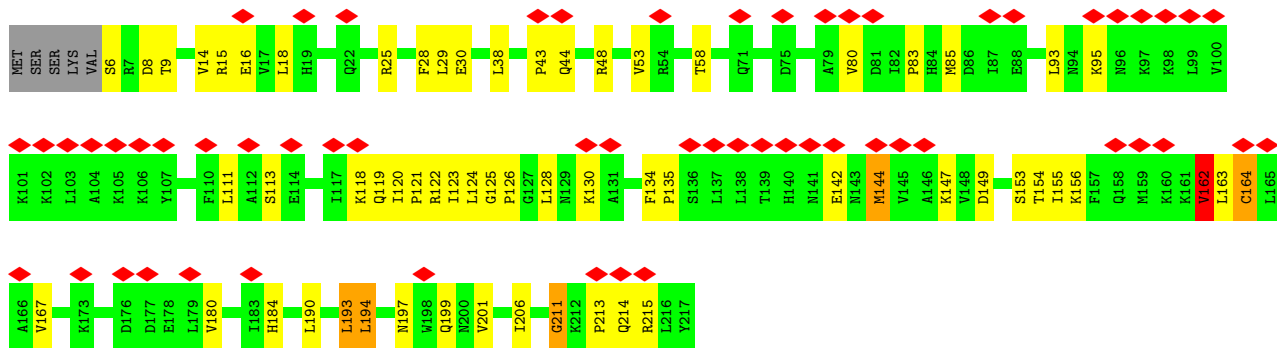
• Molecule 46: 5S rRNA



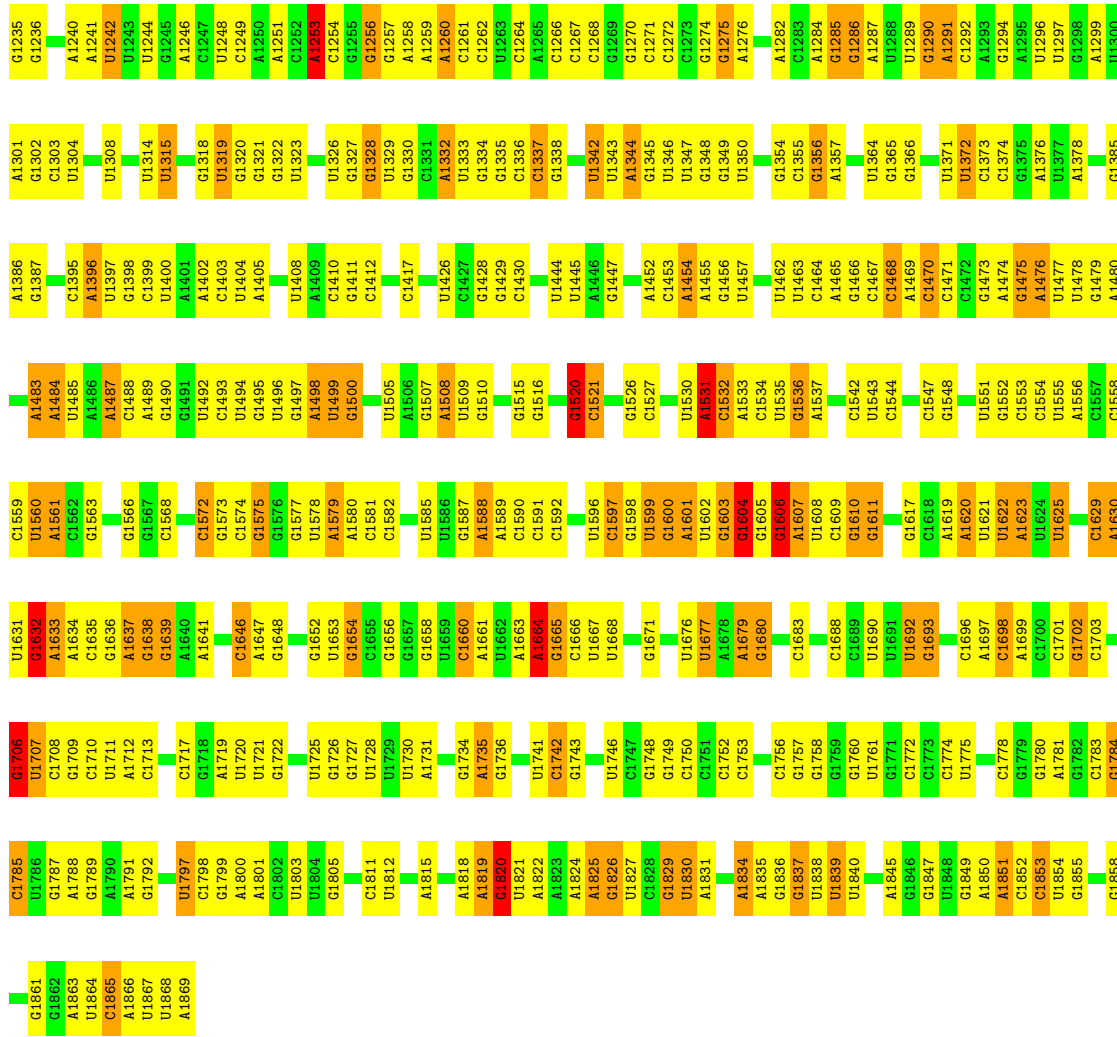
• Molecule 47: 5.8S rRNA

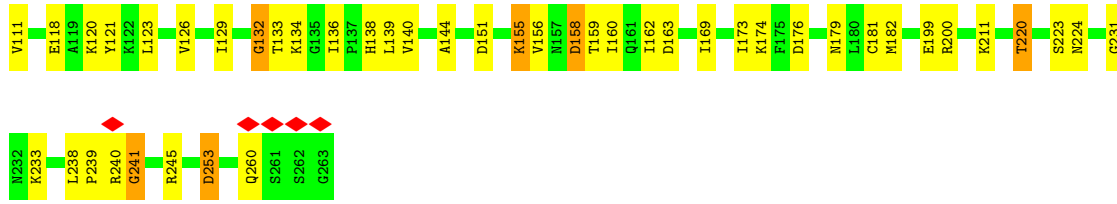


• Molecule 48: Ribosomal protein

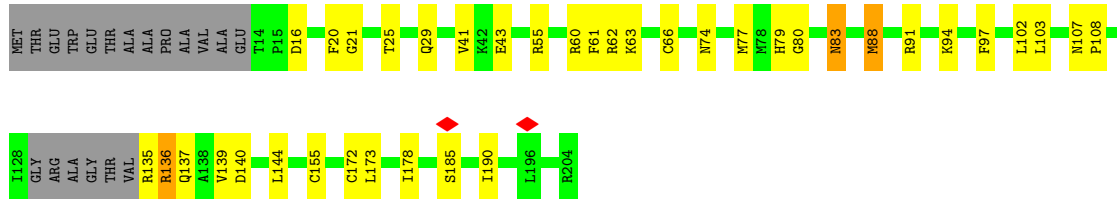
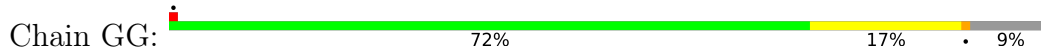


• Molecule 49: 18S rRNA

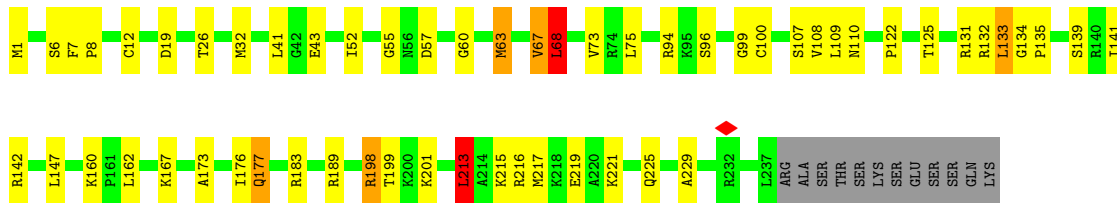
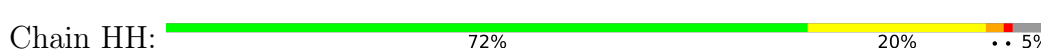




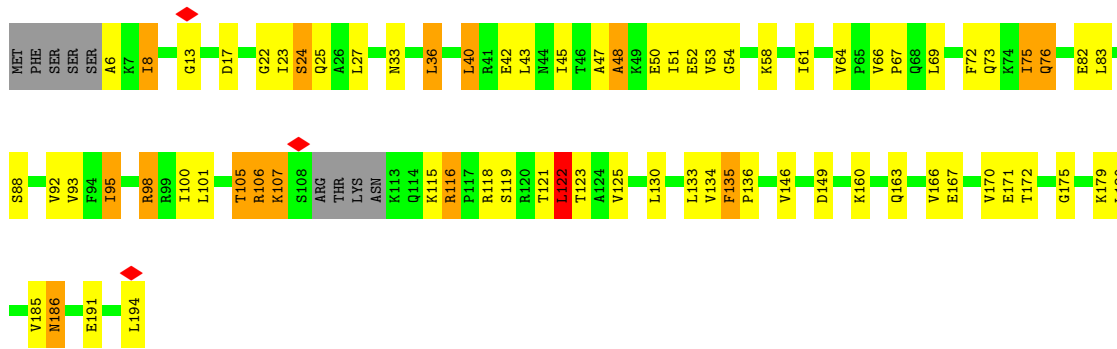
• Molecule 56: Ribosomal protein S5



• Molecule 57: 40S ribosomal protein S6



• Molecule 58: 40S ribosomal protein S7

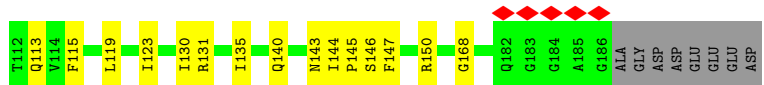


• Molecule 59: 40S ribosomal protein S8

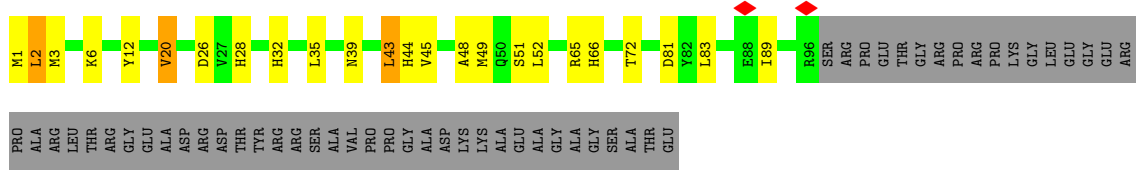




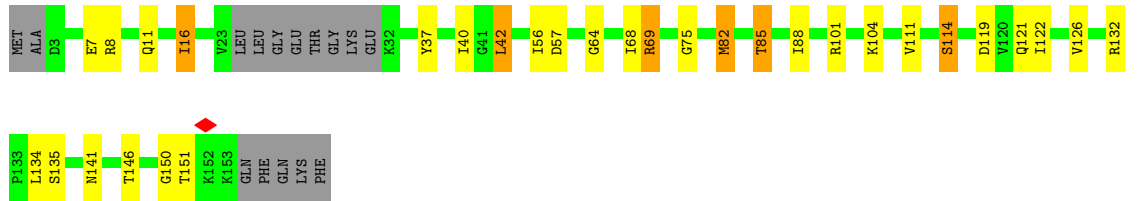
• Molecule 60: Ribosomal protein S9 (Predicted)



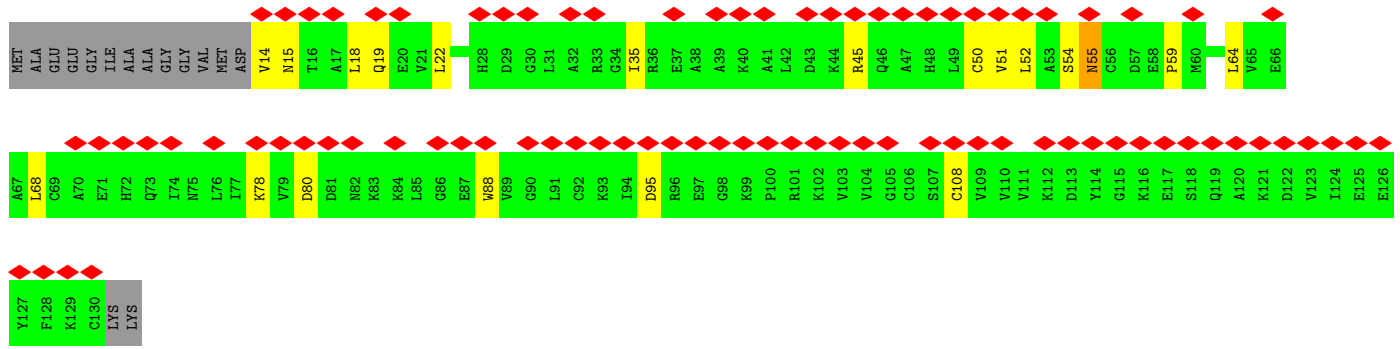
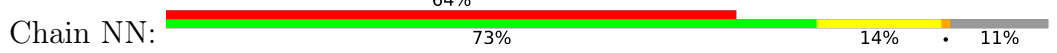
• Molecule 61: S10_ plectin domain-containing protein



• Molecule 62: Ribosomal protein S11

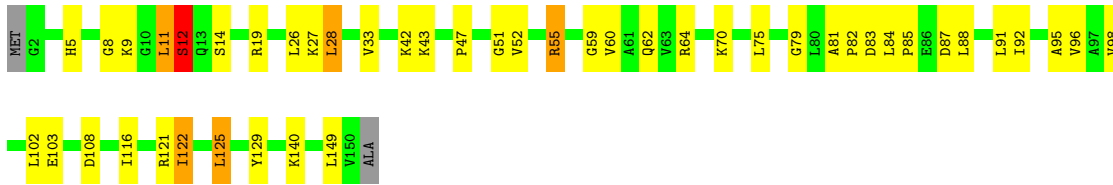


• Molecule 63: 40S ribosomal protein S12




- Molecule 64: Ribosomal protein S13

Chain OO:  68% 26% ...



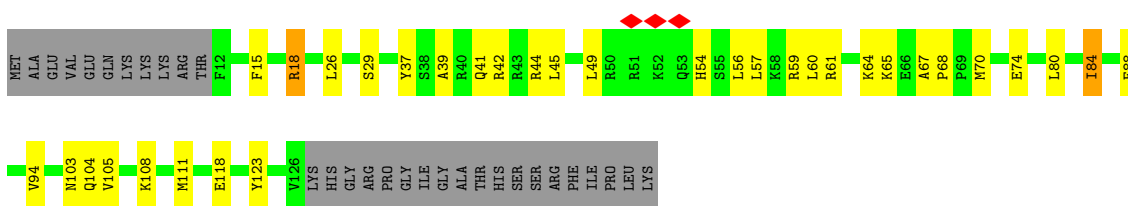
- Molecule 65: Small ribosomal subunit protein uS11

Chain PP:  76% 11% .. 10%



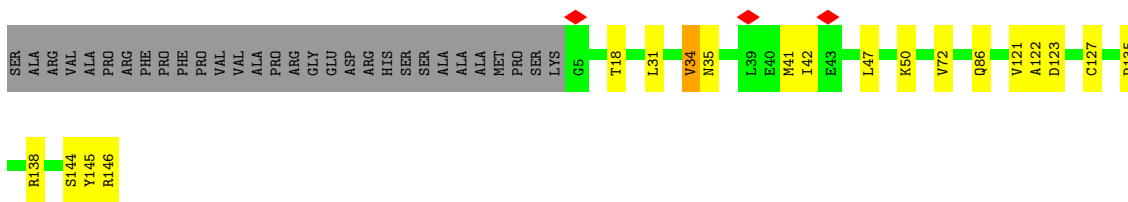
- Molecule 66: uS19

Chain QQ:  56% 22% . 21%




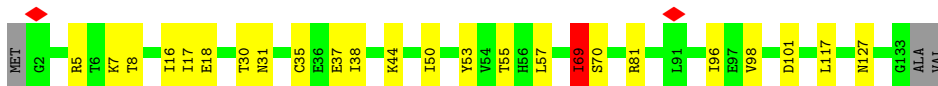
- Molecule 67: Ribosomal protein S16

Chain RR:  72% 10% . 17%




- Molecule 68: eS17

Chain SS:  80% 17% ..

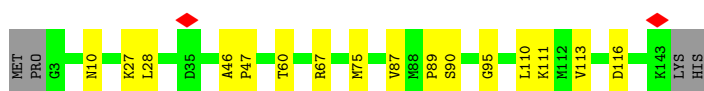
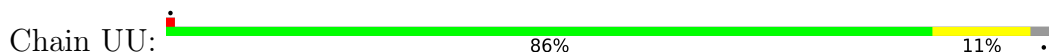


- Molecule 69: uS13

Chain TT:  78% 14% . 5%



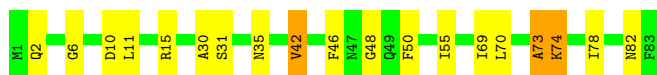
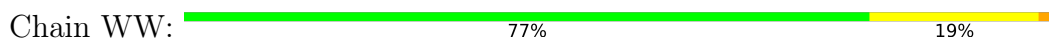
• Molecule 70: eS19



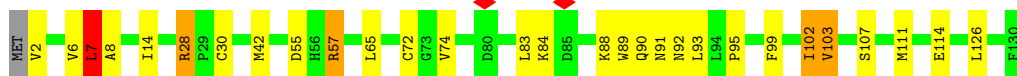
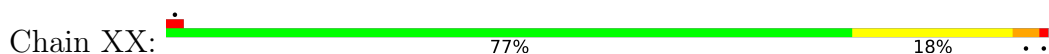
• Molecule 71: uS10



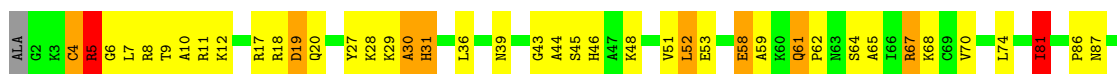
• Molecule 72: 40S ribosomal protein S21



• Molecule 73: Ribosomal protein S15a

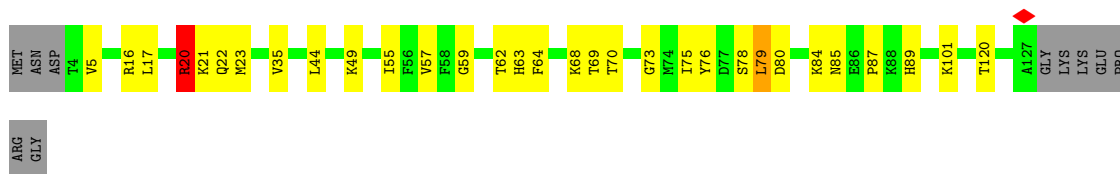


• Molecule 74: Ribosomal protein S23

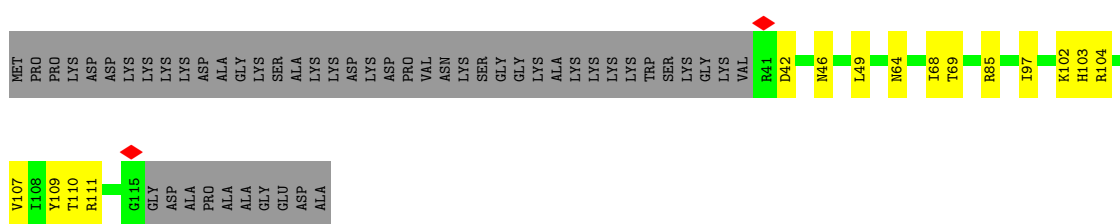


• Molecule 75: 40S ribosomal protein S24

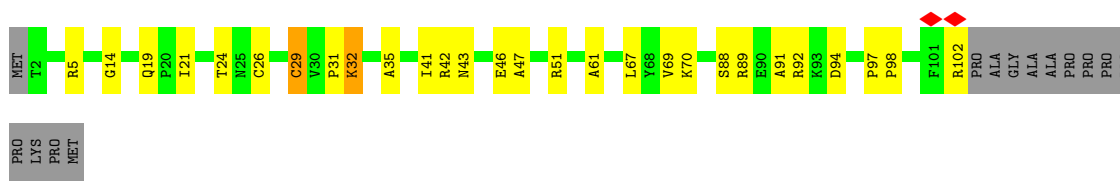




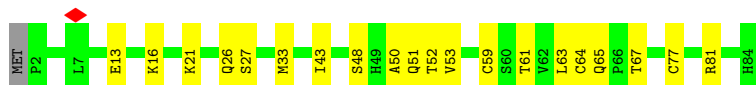
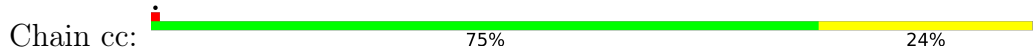
• Molecule 76: eS25



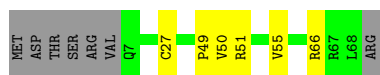
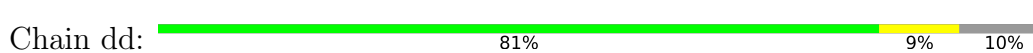
• Molecule 77: 40S ribosomal protein S26



• Molecule 78: 40S ribosomal protein S27



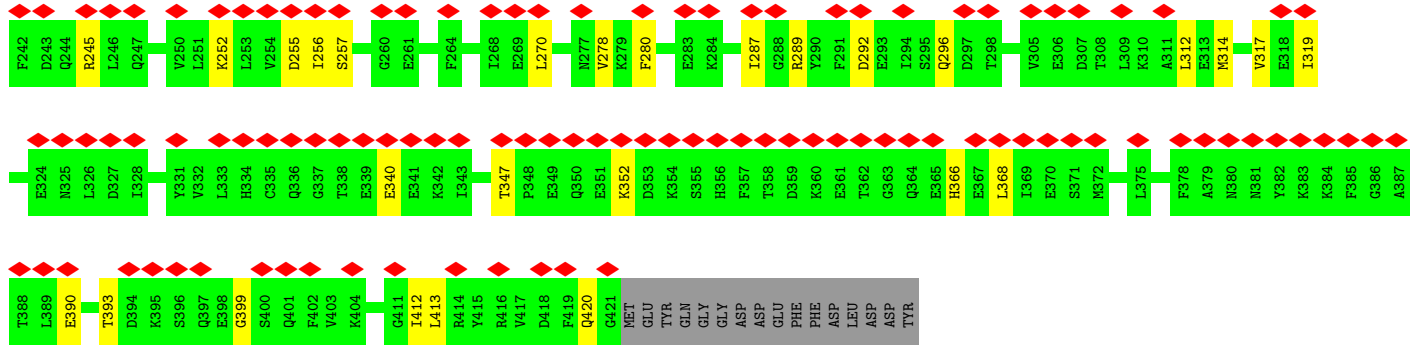
• Molecule 79: Ribosomal protein S28



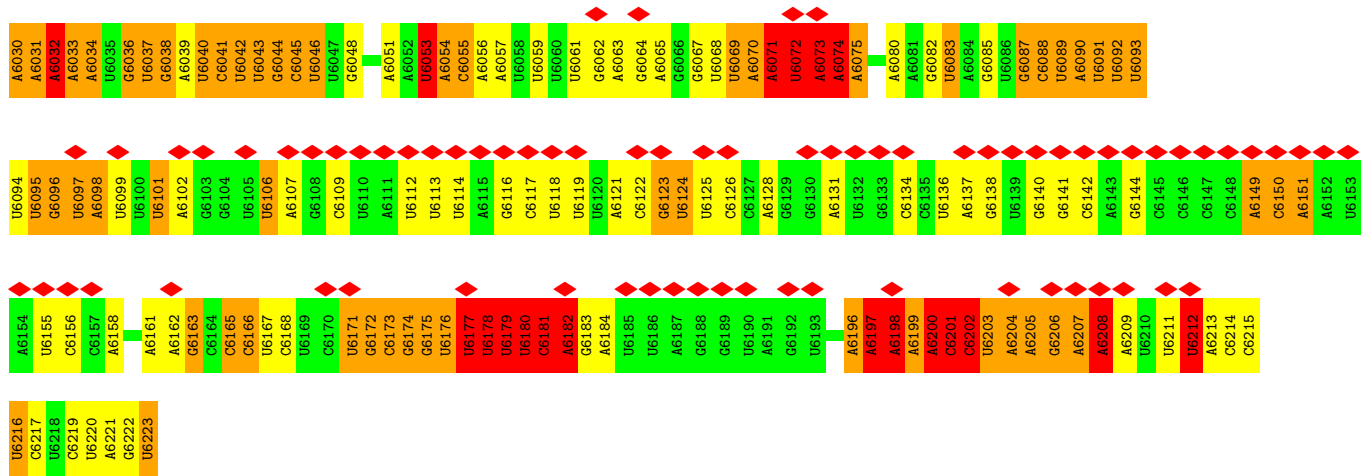
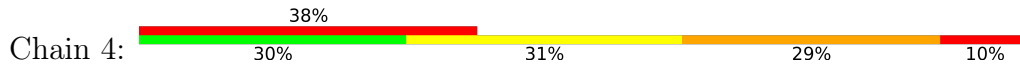
• Molecule 80: eS29



• Molecule 81: 40S ribosomal protein S30



• Molecule 85: CrPV-IRES



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75654	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.144	Depositor
Minimum map value	-0.061	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.025	Depositor
Map size (\AA)	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	Depositor

5 Model quality i

5.1 Standard geometry i

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	1.12	3/1812 (0.2%)	1.17	4/2439 (0.2%)
2	B	1.03	3/3240 (0.1%)	1.21	9/4339 (0.2%)
3	C	1.08	1/2936 (0.0%)	1.18	18/3943 (0.5%)
4	D	0.88	2/2437 (0.1%)	0.97	4/3264 (0.1%)
5	E	0.98	0/1762	1.06	3/2362 (0.1%)
6	F	0.97	1/1911 (0.1%)	1.07	9/2549 (0.4%)
7	G	0.93	0/1910	1.00	3/2569 (0.1%)
8	H	1.01	0/1535	1.09	0/2063
9	I	0.98	2/1702 (0.1%)	1.11	4/2272 (0.2%)
10	J	0.91	0/1385	0.95	3/1852 (0.2%)
11	L	0.96	0/1733	1.03	2/2316 (0.1%)
12	M	1.01	1/1150 (0.1%)	1.07	2/1534 (0.1%)
13	N	1.05	4/1746 (0.2%)	1.23	8/2338 (0.3%)
14	O	1.08	4/1653 (0.2%)	1.15	6/2206 (0.3%)
15	P	1.07	3/1268 (0.2%)	1.15	2/1700 (0.1%)
16	Q	1.05	2/1539 (0.1%)	1.16	9/2054 (0.4%)
17	R	1.00	1/1524 (0.1%)	1.18	2/2013 (0.1%)
18	S	1.03	1/1501 (0.1%)	1.13	4/2012 (0.2%)
19	T	0.99	0/1326	1.06	2/1770 (0.1%)
20	U	0.89	0/823	1.01	2/1104 (0.2%)
21	V	1.08	2/983 (0.2%)	1.24	10/1319 (0.8%)
22	W	0.94	0/873	1.22	5/1158 (0.4%)
23	X	1.05	0/984	1.12	1/1323 (0.1%)
24	Y	0.97	0/1132	1.09	2/1504 (0.1%)
25	Z	0.98	0/1130	1.10	4/1507 (0.3%)
26	a	1.11	2/1191 (0.2%)	1.18	6/1590 (0.4%)
27	b	0.92	0/861	1.03	3/1138 (0.3%)
28	c	0.97	0/771	1.04	0/1034
29	d	1.13	3/903 (0.3%)	1.18	4/1216 (0.3%)
30	e	1.11	3/1071 (0.3%)	1.21	3/1429 (0.2%)
31	f	1.13	0/895	1.25	6/1198 (0.5%)
32	g	1.05	1/916 (0.1%)	1.22	3/1220 (0.2%)
33	h	1.02	1/1021 (0.1%)	1.15	2/1348 (0.1%)
34	i	0.90	0/841	1.04	1/1112 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	1.17	2/720 (0.3%)	1.37	7/952 (0.7%)
36	k	0.91	0/575	1.00	0/761
37	l	1.07	0/459	1.20	2/608 (0.3%)
38	m	1.00	1/435 (0.2%)	1.16	2/575 (0.3%)
39	n	1.12	0/240	1.47	5/305 (1.6%)
40	o	0.91	0/864	0.99	0/1140
41	p	1.05	0/718	1.19	2/953 (0.2%)
42	r	1.06	1/1010 (0.1%)	1.24	5/1354 (0.4%)
43	s	0.92	0/1530	0.85	1/2064 (0.0%)
44	t	0.94	0/1174	0.89	0/1582
45	5	0.62	36/86202 (0.0%)	1.04	604/134412 (0.4%)
46	7	0.54	0/2836	0.92	6/4421 (0.1%)
47	8	0.62	2/3581 (0.1%)	1.02	28/5577 (0.5%)
48	K	0.97	0/1730	0.99	5/2315 (0.2%)
49	2	0.58	7/40502 (0.0%)	0.96	152/63100 (0.2%)
50	3	0.49	0/2079	0.87	5/3238 (0.2%)
51	BB	1.01	2/1747 (0.1%)	0.92	0/2374
52	CC	0.91	1/1756 (0.1%)	1.00	2/2350 (0.1%)
53	DD	0.95	1/1753 (0.1%)	1.15	11/2369 (0.5%)
54	EE	0.90	0/1796	1.04	1/2417 (0.0%)
55	FF	0.95	1/2118 (0.0%)	1.08	1/2849 (0.0%)
56	GG	0.87	0/1492	1.01	1/2005 (0.0%)
57	HH	0.88	0/1946	1.00	3/2590 (0.1%)
58	II	0.95	2/1510 (0.1%)	1.07	2/2022 (0.1%)
59	JJ	0.97	0/1715	1.05	3/2287 (0.1%)
60	KK	0.94	1/1550 (0.1%)	1.07	2/2069 (0.1%)
61	LL	0.98	0/834	1.02	1/1125 (0.1%)
62	MM	1.05	2/1195 (0.2%)	1.13	5/1597 (0.3%)
63	NN	0.82	0/918	0.87	0/1233
64	OO	1.00	1/1226 (0.1%)	1.04	1/1649 (0.1%)
65	PP	0.88	0/1029	0.98	1/1380 (0.1%)
66	QQ	0.89	0/974	1.05	5/1301 (0.4%)
67	RR	0.84	0/1146	0.91	2/1534 (0.1%)
68	SS	0.95	0/1082	0.96	2/1452 (0.1%)
69	TT	0.93	0/1208	0.96	1/1618 (0.1%)
70	UU	0.84	0/1115	0.91	0/1493
71	VV	0.98	1/805 (0.1%)	1.14	3/1081 (0.3%)
72	WW	0.98	0/643	1.04	0/860
73	XX	0.99	0/1051	1.12	2/1406 (0.1%)
74	YY	1.11	0/1116	1.24	9/1490 (0.6%)
75	ZZ	0.89	0/1028	1.07	3/1366 (0.2%)
76	aa	0.90	0/604	0.84	0/810
77	bb	1.03	1/828 (0.1%)	1.09	2/1109 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	cc	0.97	0/665	1.18	4/891 (0.4%)
79	dd	0.92	0/490	0.95	0/656
80	ee	0.87	0/470	0.98	0/623
81	ff	0.89	0/462	1.17	1/607 (0.2%)
82	gg	0.87	0/567	0.89	0/753
83	hh	0.83	0/2492	0.88	4/3391 (0.1%)
84	jj	0.97	0/3333	0.93	2/4483 (0.0%)
85	4	0.54	4/4586 (0.1%)	1.26	65/7136 (0.9%)
All	All	0.78	106/240370 (0.0%)	1.04	1109/352528 (0.3%)

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
1	A	0	4
2	B	0	2
3	C	0	3
12	M	0	1
13	N	0	1
16	Q	0	1
22	W	0	1
23	X	0	1
24	Y	0	1
27	b	0	1
29	d	0	1
30	e	0	1
31	f	0	3
32	g	0	2
35	j	0	1
36	k	0	1
37	l	0	1
40	o	0	1
45	5	0	7
48	K	0	2
49	2	0	3
51	BB	0	1
52	CC	0	1
54	EE	0	1
55	FF	0	3
57	HH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
65	PP	0	2
69	TT	0	1
73	XX	0	2
74	YY	0	1
81	ff	0	1
83	hh	0	1
85	4	1	4
All	All	1	59

The worst 5 of 106 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	BB	12	GLU	CD-OE2	16.54	1.56	1.25
85	4	6182	A	O3'-P	-10.44	1.45	1.61
85	4	6178	U	C1'-N1	9.53	1.61	1.47
45	5	4520	G	O3'-P	8.86	1.74	1.61
49	2	690	G	O5'-C5'	7.83	1.54	1.42

The worst 5 of 1109 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6030	A	O3'-P-O5'	33.43	154.14	104.00
85	4	6030	A	P-O3'-C3'	-26.97	79.75	120.20
85	4	6181	C	C4'-C3'-O3'	-23.70	77.45	113.00
45	5	4520	G	C1'-C2'-O2'	-18.58	80.53	108.40
85	4	6178	U	C1'-C2'-O2'	17.34	137.81	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
85	4	6200	A	C1'

5 of 59 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	162	ASN	Peptide
1	A	178	PRO	Peptide
1	A	196	TRP	Peptide
1	A	31	ALA	Peptide
2	B	2	SER	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1777	0	1819	26	0
2	B	3172	0	3310	54	0
3	C	2883	0	3052	46	0
4	D	2391	0	2424	25	0
5	E	1729	0	1887	37	0
6	F	1875	0	1995	21	0
7	G	1879	0	2025	13	0
8	H	1516	0	1597	20	0
9	I	1664	0	1712	15	0
10	J	1362	0	1399	7	0
11	L	1702	0	1820	25	0
12	M	1130	0	1201	19	0
13	N	1701	0	1749	32	0
14	O	1623	0	1771	39	0
15	P	1242	0	1274	33	0
16	Q	1515	0	1634	30	0
17	R	1508	0	1664	26	0
18	S	1462	0	1508	17	0
19	T	1298	0	1366	15	0
20	U	809	0	833	6	0
21	V	969	0	1031	10	0
22	W	860	0	903	11	0
23	X	967	0	1040	12	0
24	Y	1115	0	1205	11	0
25	Z	1107	0	1182	20	0
26	a	1162	0	1209	23	0
27	b	848	0	920	5	0
28	c	761	0	794	5	0
29	d	888	0	930	18	0
30	e	1053	0	1147	25	0
31	f	876	0	912	17	0
32	g	906	0	1002	14	0
33	h	1013	0	1147	19	0
34	i	830	0	916	8	0
35	j	705	0	741	12	0
36	k	569	0	637	2	0
37	l	447	0	480	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	m	429	0	469	7	0
39	n	239	0	289	5	0
40	o	851	0	924	6	0
41	p	708	0	760	12	0
42	r	994	0	1051	11	0
43	s	1507	0	1564	9	0
44	t	1160	0	1218	10	0
45	5	77073	0	38949	733	0
46	7	2538	0	1286	27	0
47	8	3208	0	1629	50	0
48	K	1705	0	1800	80	0
49	2	36229	0	18306	334	0
50	3	1861	0	939	12	0
51	BB	1710	0	1708	23	0
52	CC	1729	0	1803	12	0
53	DD	1716	0	1806	34	0
54	EE	1768	0	1866	16	0
55	FF	2076	0	2177	26	0
56	GG	1471	0	1522	15	0
57	HH	1923	0	2089	28	0
58	II	1488	0	1582	35	0
59	JJ	1686	0	1772	22	0
60	KK	1525	0	1640	24	0
61	LL	810	0	836	13	0
62	MM	1175	0	1249	10	0
63	NN	908	0	939	7	0
64	OO	1202	0	1289	23	0
65	PP	1016	0	1039	7	0
66	QQ	956	0	1002	15	0
67	RR	1128	0	1195	8	0
68	SS	1068	0	1121	9	0
69	TT	1190	0	1249	13	0
70	UU	1097	0	1130	6	0
71	VV	795	0	862	8	0
72	WW	636	0	637	8	0
73	XX	1034	0	1080	10	0
74	YY	1098	0	1167	22	0
75	ZZ	1011	0	1083	14	0
76	aa	598	0	656	13	0
77	bb	814	0	867	10	0
78	cc	651	0	672	4	0
79	dd	488	0	514	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	ee	459	0	452	6	0
81	ff	457	0	502	16	0
82	gg	555	0	567	3	0
83	hh	2436	0	2392	31	0
84	jj	3280	0	3326	26	0
85	4	4105	0	2053	494	0
All	All	223875	0	167264	2681	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 2681 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
85:4:6181:C:C3'	85:4:6182:A:H2'	1.26	1.62
85:4:6176:U:C4	85:4:6177:U:C5	1.76	1.60
85:4:6181:C:H3'	85:4:6182:A:C2'	1.31	1.60
85:4:6198:A:H2'	85:4:6199:A:C5'	1.25	1.58
85:4:6198:A:C2'	85:4:6199:A:H5'	1.12	1.55

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/257 (92%)	183 (77%)	45 (19%)	9 (4%)	2	18
2	B	392/403 (97%)	327 (83%)	46 (12%)	19 (5%)	2	14
3	C	358/392 (91%)	298 (83%)	48 (13%)	12 (3%)	3	20
4	D	291/297 (98%)	257 (88%)	29 (10%)	5 (2%)	7	35
5	E	208/291 (72%)	173 (83%)	29 (14%)	6 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	223/249 (90%)	193 (86%)	24 (11%)	6 (3%)	4	25
7	G	229/242 (95%)	202 (88%)	25 (11%)	2 (1%)	14	47
8	H	188/192 (98%)	157 (84%)	20 (11%)	11 (6%)	1	10
9	I	201/214 (94%)	171 (85%)	24 (12%)	6 (3%)	3	23
10	J	168/178 (94%)	144 (86%)	20 (12%)	4 (2%)	4	28
11	L	208/211 (99%)	184 (88%)	19 (9%)	5 (2%)	4	28
12	M	133/198 (67%)	108 (81%)	20 (15%)	5 (4%)	2	18
13	N	201/204 (98%)	171 (85%)	25 (12%)	5 (2%)	4	27
14	O	194/199 (98%)	167 (86%)	25 (13%)	2 (1%)	12	45
15	P	151/184 (82%)	123 (82%)	22 (15%)	6 (4%)	2	17
16	Q	185/188 (98%)	154 (83%)	24 (13%)	7 (4%)	2	18
17	R	178/181 (98%)	148 (83%)	24 (14%)	6 (3%)	3	20
18	S	174/176 (99%)	142 (82%)	26 (15%)	6 (3%)	3	20
19	T	157/160 (98%)	128 (82%)	22 (14%)	7 (4%)	2	15
20	U	97/128 (76%)	80 (82%)	14 (14%)	3 (3%)	3	22
21	V	127/140 (91%)	107 (84%)	16 (13%)	4 (3%)	3	22
22	W	102/157 (65%)	87 (85%)	9 (9%)	6 (6%)	1	10
23	X	116/156 (74%)	101 (87%)	11 (10%)	4 (3%)	3	20
24	Y	132/145 (91%)	106 (80%)	23 (17%)	3 (2%)	5	29
25	Z	133/136 (98%)	108 (81%)	21 (16%)	4 (3%)	3	23
26	a	145/148 (98%)	115 (79%)	28 (19%)	2 (1%)	9	39
27	b	100/226 (44%)	86 (86%)	10 (10%)	4 (4%)	2	17
28	c	96/115 (84%)	87 (91%)	9 (9%)	0	100	100
29	d	105/125 (84%)	87 (83%)	13 (12%)	5 (5%)	2	14
30	e	126/135 (93%)	97 (77%)	24 (19%)	5 (4%)	2	17
31	f	107/110 (97%)	91 (85%)	13 (12%)	3 (3%)	4	25
32	g	112/126 (89%)	91 (81%)	14 (12%)	7 (6%)	1	8
33	h	120/123 (98%)	99 (82%)	19 (16%)	2 (2%)	7	35
34	i	100/105 (95%)	90 (90%)	10 (10%)	0	100	100
35	j	84/97 (87%)	67 (80%)	11 (13%)	6 (7%)	1	6
36	k	67/70 (96%)	51 (76%)	12 (18%)	4 (6%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	l	48/51 (94%)	38 (79%)	7 (15%)	3 (6%)	1	8
38	m	50/52 (96%)	42 (84%)	8 (16%)	0	100	100
39	n	23/25 (92%)	17 (74%)	5 (22%)	1 (4%)	2	16
40	o	102/106 (96%)	94 (92%)	6 (6%)	2 (2%)	6	31
41	p	89/92 (97%)	74 (83%)	11 (12%)	4 (4%)	2	15
42	r	122/137 (89%)	95 (78%)	14 (12%)	13 (11%)	0	2
43	s	194/303 (64%)	163 (84%)	27 (14%)	4 (2%)	5	31
44	t	151/195 (77%)	126 (83%)	22 (15%)	3 (2%)	6	31
48	K	204/217 (94%)	143 (70%)	51 (25%)	10 (5%)	1	13
51	BB	215/295 (73%)	193 (90%)	19 (9%)	3 (1%)	9	39
52	CC	211/264 (80%)	174 (82%)	33 (16%)	4 (2%)	6	33
53	DD	219/255 (86%)	185 (84%)	30 (14%)	4 (2%)	6	34
54	EE	226/281 (80%)	187 (83%)	36 (16%)	3 (1%)	9	40
55	FF	260/263 (99%)	212 (82%)	37 (14%)	11 (4%)	2	16
56	GG	181/204 (89%)	153 (84%)	19 (10%)	9 (5%)	1	13
57	HH	235/249 (94%)	197 (84%)	32 (14%)	6 (3%)	4	26
58	II	181/194 (93%)	147 (81%)	22 (12%)	12 (7%)	1	7
59	JJ	204/208 (98%)	173 (85%)	23 (11%)	8 (4%)	2	18
60	KK	183/194 (94%)	155 (85%)	23 (13%)	5 (3%)	4	25
61	LL	94/149 (63%)	84 (89%)	9 (10%)	1 (1%)	11	43
62	MM	139/158 (88%)	120 (86%)	16 (12%)	3 (2%)	5	29
63	NN	115/132 (87%)	91 (79%)	20 (17%)	4 (4%)	3	20
64	OO	147/151 (97%)	118 (80%)	22 (15%)	7 (5%)	2	14
65	PP	134/151 (89%)	116 (87%)	17 (13%)	1 (1%)	18	52
66	QQ	113/145 (78%)	83 (74%)	26 (23%)	4 (4%)	3	20
67	RR	140/172 (81%)	123 (88%)	16 (11%)	1 (1%)	18	52
68	SS	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	50
69	TT	142/152 (93%)	125 (88%)	14 (10%)	3 (2%)	5	31
70	UU	139/145 (96%)	120 (86%)	17 (12%)	2 (1%)	9	39
71	VV	98/119 (82%)	82 (84%)	14 (14%)	2 (2%)	6	31
72	WW	81/83 (98%)	71 (88%)	6 (7%)	4 (5%)	1	13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	XX	127/130 (98%)	107 (84%)	17 (13%)	3 (2%)	4	28
74	YY	139/143 (97%)	112 (81%)	21 (15%)	6 (4%)	2	16
75	ZZ	122/134 (91%)	103 (84%)	17 (14%)	2 (2%)	7	36
76	aa	73/125 (58%)	65 (89%)	7 (10%)	1 (1%)	9	39
77	bb	99/115 (86%)	77 (78%)	16 (16%)	6 (6%)	1	9
78	cc	81/84 (96%)	66 (82%)	13 (16%)	2 (2%)	4	27
79	dd	60/69 (87%)	50 (83%)	9 (15%)	1 (2%)	7	35
80	ee	53/56 (95%)	33 (62%)	18 (34%)	2 (4%)	2	18
81	ff	55/133 (41%)	44 (80%)	9 (16%)	2 (4%)	2	19
82	gg	66/156 (42%)	49 (74%)	16 (24%)	1 (2%)	8	37
83	hh	310/317 (98%)	237 (76%)	69 (22%)	4 (1%)	9	40
84	jj	414/437 (95%)	344 (83%)	65 (16%)	5 (1%)	10	42
All	All	12114/13834 (88%)	10082 (83%)	1668 (14%)	364 (3%)	5	23

5 of 364 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	VAL
1	A	196	TRP
2	B	8	ALA
2	B	9	PRO
2	B	135	LYS

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	172/199 (86%)	146 (85%)	26 (15%)	3	14
2	B	342/348 (98%)	287 (84%)	55 (16%)	2	13
3	C	302/323 (94%)	267 (88%)	35 (12%)	5	24
4	D	247/250 (99%)	221 (90%)	26 (10%)	6	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	190/251 (76%)	170 (90%)	20 (10%)	6	28
6	F	196/218 (90%)	177 (90%)	19 (10%)	8	32
7	G	200/208 (96%)	179 (90%)	21 (10%)	6	28
8	H	169/171 (99%)	154 (91%)	15 (9%)	9	34
9	I	175/181 (97%)	147 (84%)	28 (16%)	2	13
10	J	143/149 (96%)	132 (92%)	11 (8%)	12	41
11	L	175/176 (99%)	158 (90%)	17 (10%)	8	32
12	M	116/151 (77%)	96 (83%)	20 (17%)	2	10
13	N	171/172 (99%)	148 (86%)	23 (14%)	4	19
14	O	170/171 (99%)	141 (83%)	29 (17%)	2	11
15	P	134/163 (82%)	114 (85%)	20 (15%)	3	15
16	Q	164/165 (99%)	140 (85%)	24 (15%)	3	16
17	R	159/160 (99%)	135 (85%)	24 (15%)	3	14
18	S	157/157 (100%)	138 (88%)	19 (12%)	5	22
19	T	139/140 (99%)	124 (89%)	15 (11%)	6	27
20	U	89/114 (78%)	85 (96%)	4 (4%)	24	58
21	V	100/107 (94%)	81 (81%)	19 (19%)	1	9
22	W	86/126 (68%)	77 (90%)	9 (10%)	6	28
23	X	106/134 (79%)	91 (86%)	15 (14%)	3	17
24	Y	124/135 (92%)	98 (79%)	26 (21%)	1	6
25	Z	117/118 (99%)	101 (86%)	16 (14%)	3	18
26	a	119/120 (99%)	109 (92%)	10 (8%)	10	38
27	b	84/172 (49%)	78 (93%)	6 (7%)	13	44
28	c	84/98 (86%)	71 (84%)	13 (16%)	2	14
29	d	98/110 (89%)	91 (93%)	7 (7%)	13	44
30	e	114/121 (94%)	98 (86%)	16 (14%)	3	17
31	f	88/89 (99%)	72 (82%)	16 (18%)	2	9
32	g	98/106 (92%)	85 (87%)	13 (13%)	4	19
33	h	109/110 (99%)	98 (90%)	11 (10%)	7	30
34	i	86/89 (97%)	78 (91%)	8 (9%)	8	33
35	j	73/80 (91%)	65 (89%)	8 (11%)	6	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	k	64/65 (98%)	57 (89%)	7 (11%)	6	26
37	l	47/48 (98%)	38 (81%)	9 (19%)	1	9
38	m	48/48 (100%)	38 (79%)	10 (21%)	1	7
39	n	24/24 (100%)	19 (79%)	5 (21%)	1	7
40	o	92/94 (98%)	79 (86%)	13 (14%)	3	17
41	p	74/75 (99%)	61 (82%)	13 (18%)	2	10
42	r	108/121 (89%)	94 (87%)	14 (13%)	4	20
43	s	164/258 (64%)	160 (98%)	4 (2%)	43	70
44	t	126/163 (77%)	120 (95%)	6 (5%)	23	56
48	K	190/196 (97%)	171 (90%)	19 (10%)	7	30
51	BB	180/246 (73%)	168 (93%)	12 (7%)	15	47
52	CC	194/231 (84%)	178 (92%)	16 (8%)	10	39
53	DD	187/206 (91%)	163 (87%)	24 (13%)	4	20
54	EE	190/232 (82%)	166 (87%)	24 (13%)	4	21
55	FF	224/225 (100%)	193 (86%)	31 (14%)	3	18
56	GG	158/170 (93%)	144 (91%)	14 (9%)	9	34
57	HH	207/218 (95%)	188 (91%)	19 (9%)	8	33
58	II	165/174 (95%)	139 (84%)	26 (16%)	2	13
59	JJ	178/180 (99%)	152 (85%)	26 (15%)	3	16
60	KK	161/168 (96%)	148 (92%)	13 (8%)	11	39
61	LL	87/125 (70%)	80 (92%)	7 (8%)	11	40
62	MM	130/142 (92%)	113 (87%)	17 (13%)	4	19
63	NN	99/108 (92%)	95 (96%)	4 (4%)	28	61
64	OO	130/131 (99%)	112 (86%)	18 (14%)	3	18
65	PP	106/119 (89%)	92 (87%)	14 (13%)	4	19
66	QQ	105/130 (81%)	95 (90%)	10 (10%)	8	32
67	RR	117/140 (84%)	109 (93%)	8 (7%)	14	46
68	SS	119/121 (98%)	106 (89%)	13 (11%)	6	26
69	TT	125/132 (95%)	118 (94%)	7 (6%)	19	52
70	UU	111/116 (96%)	105 (95%)	6 (5%)	20	53
71	VV	92/107 (86%)	80 (87%)	12 (13%)	4	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
72	WW	67/67 (100%)	61 (91%)	6 (9%)	9	34
73	XX	112/113 (99%)	98 (88%)	14 (12%)	4	21
74	YY	113/114 (99%)	96 (85%)	17 (15%)	3	15
75	ZZ	107/115 (93%)	95 (89%)	12 (11%)	6	25
76	aa	66/103 (64%)	64 (97%)	2 (3%)	36	66
77	bb	88/98 (90%)	80 (91%)	8 (9%)	9	34
78	cc	75/76 (99%)	67 (89%)	8 (11%)	6	27
79	dd	55/62 (89%)	53 (96%)	2 (4%)	31	63
80	ee	48/49 (98%)	43 (90%)	5 (10%)	7	28
81	ff	47/106 (44%)	42 (89%)	5 (11%)	6	27
82	gg	61/140 (44%)	54 (88%)	7 (12%)	5	24
83	hh	272/275 (99%)	244 (90%)	28 (10%)	7	28
84	jj	358/376 (95%)	323 (90%)	35 (10%)	7	31
All	All	10567/11789 (90%)	9353 (88%)	1214 (12%)	8	24

5 of 1214 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	JJ	142	SER
82	gg	86	THR
61	LL	43	LEU
59	JJ	139	LYS
69	TT	71	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 226 such sidechains are listed below:

Mol	Chain	Res	Type
38	m	83	ASN
84	jj	67	ASN
52	CC	202	GLN
83	hh	222	ASN
70	UU	10	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3565/3594 (99%)	1667 (46%)	283 (7%)
46	7	118/119 (99%)	40 (33%)	5 (4%)
47	8	149/151 (98%)	63 (42%)	5 (3%)
49	2	1683/1697 (99%)	727 (43%)	107 (6%)
50	3	86/87 (98%)	44 (51%)	5 (5%)
85	4	193/194 (99%)	123 (63%)	28 (14%)
All	All	5794/5842 (99%)	2664 (45%)	433 (7%)

5 of 2664 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
45	5	6	C
45	5	9	C
45	5	10	A
45	5	12	A
45	5	13	U

5 of 433 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
45	5	4447	C
46	7	89	G
49	2	1868	U
45	5	4463	U
45	5	4719	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
45	5	36
49	2	18
48	K	3
47	8	1
50	3	1
83	hh	1
3	C	1

The worst 5 of 61 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	42.98
1	5	1252:C	O3'	1271:G	P	33.33
1	5	1219:G	O3'	1233:G	P	21.96
1	2	697:G	O3'	729:C	P	20.32
1	5	1696:C	O3'	1720:C	P	19.72

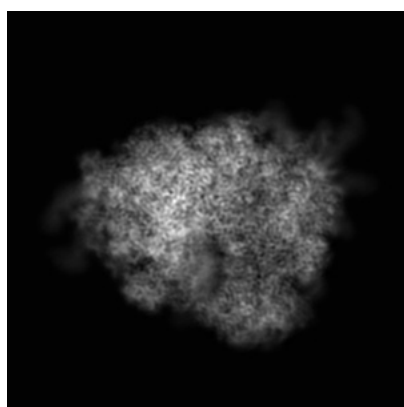
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7834. These allow visual inspection of the internal detail of the map and identification of artifacts.

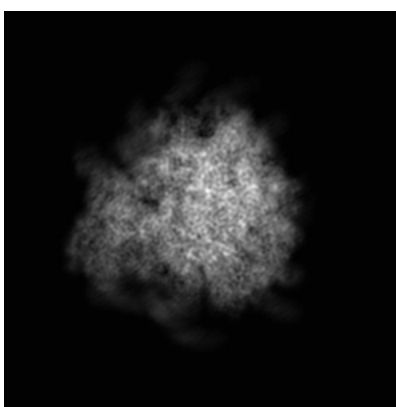
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

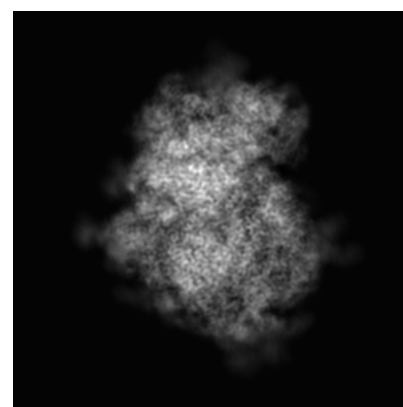
6.1.1 Primary map



X



Y

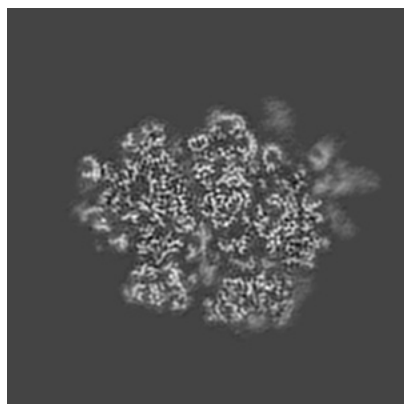


Z

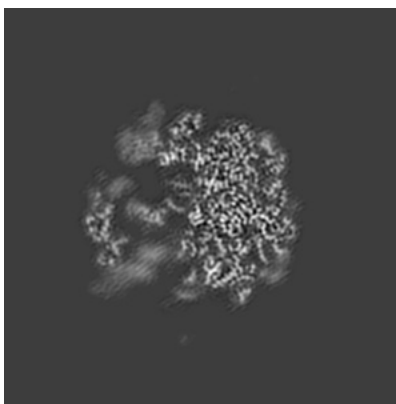
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

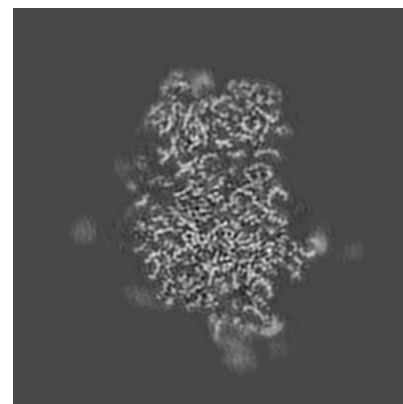
6.2.1 Primary map



X Index: 200



Y Index: 200

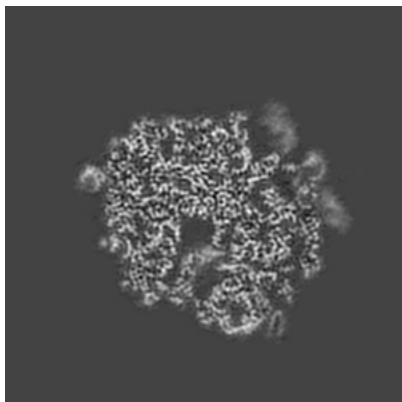


Z Index: 200

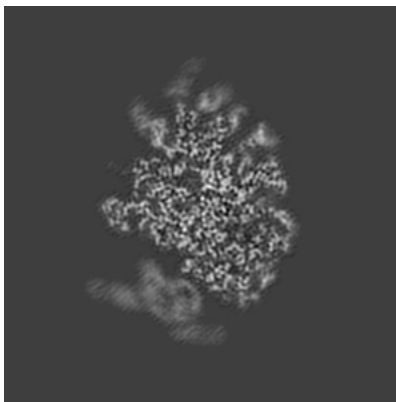
The images above show central slices of the map in three orthogonal directions.

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

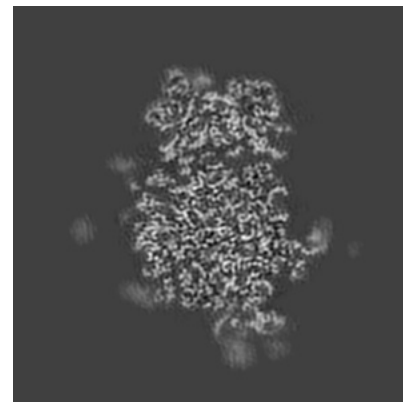
6.3.1 Primary map



X Index: 186



Y Index: 166

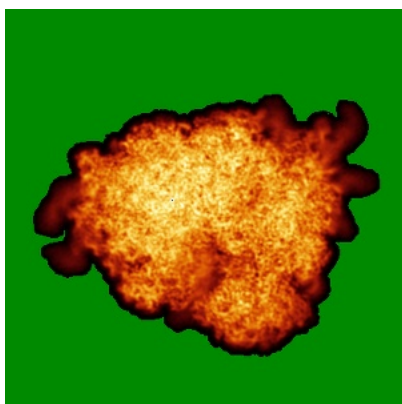


Z Index: 203

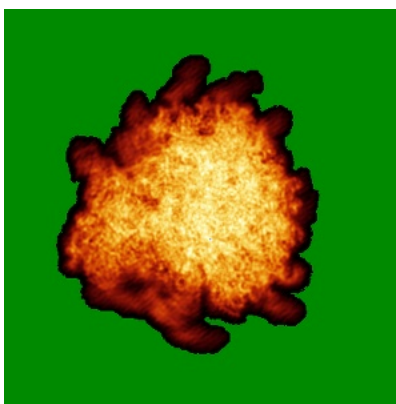
The images above show the largest variance slices of the map in three orthogonal directions.

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

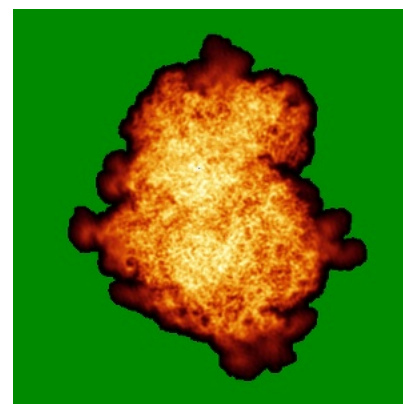
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

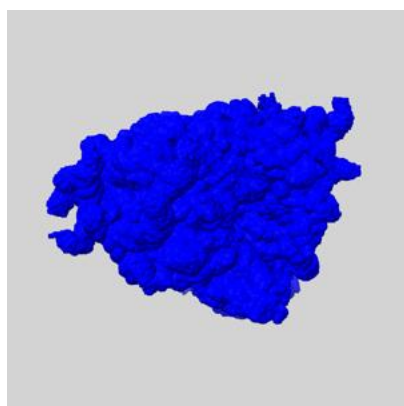
6.6 Mask visualisation [i](#)

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

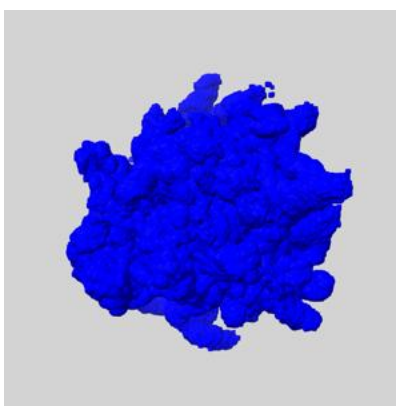
A mask typically either:

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

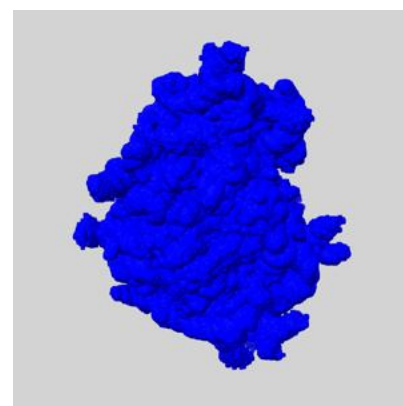
6.6.1 emd_7834_msk_1.map [i](#)



X



Y

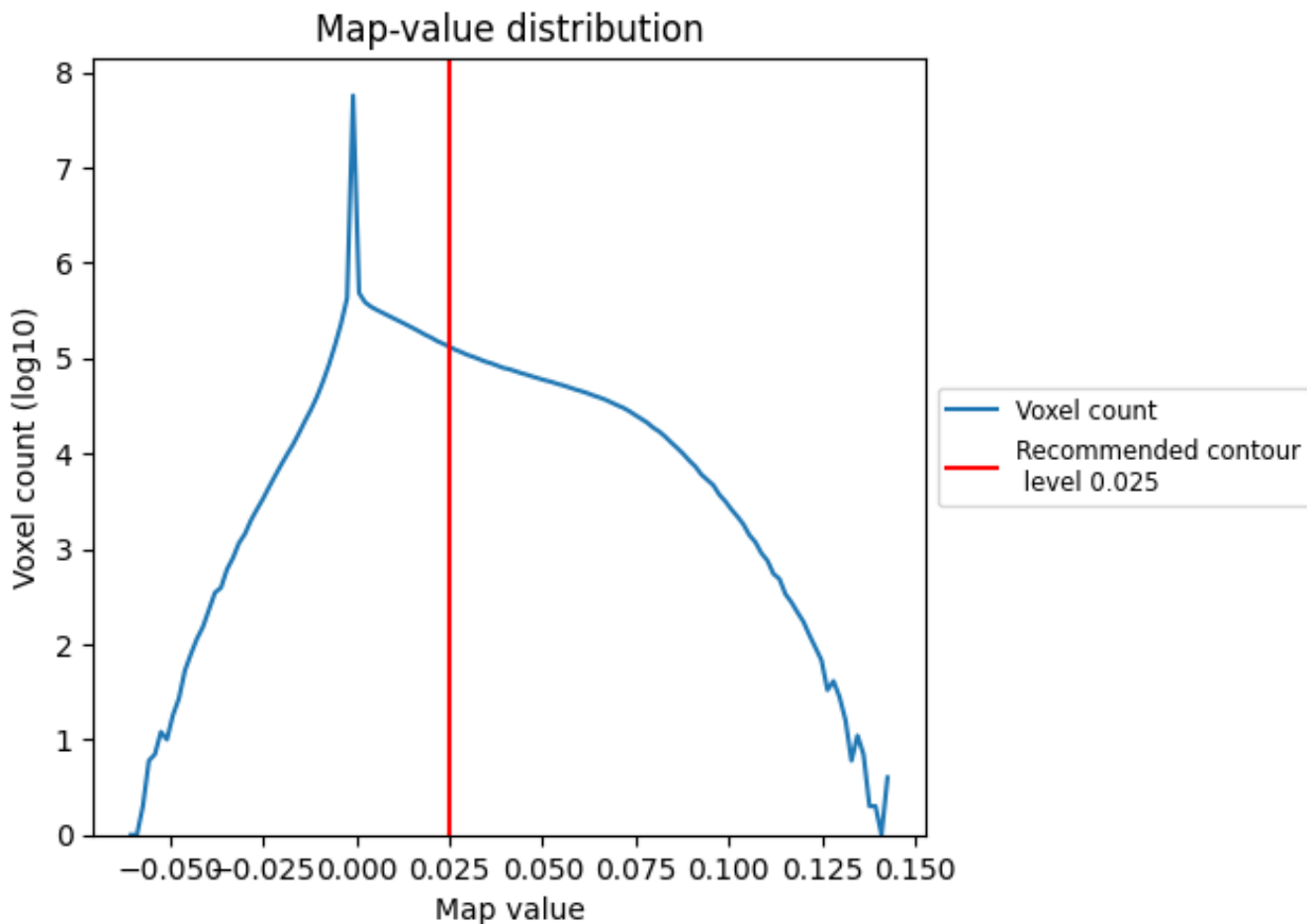


Z

7 Map analysis [i](#)

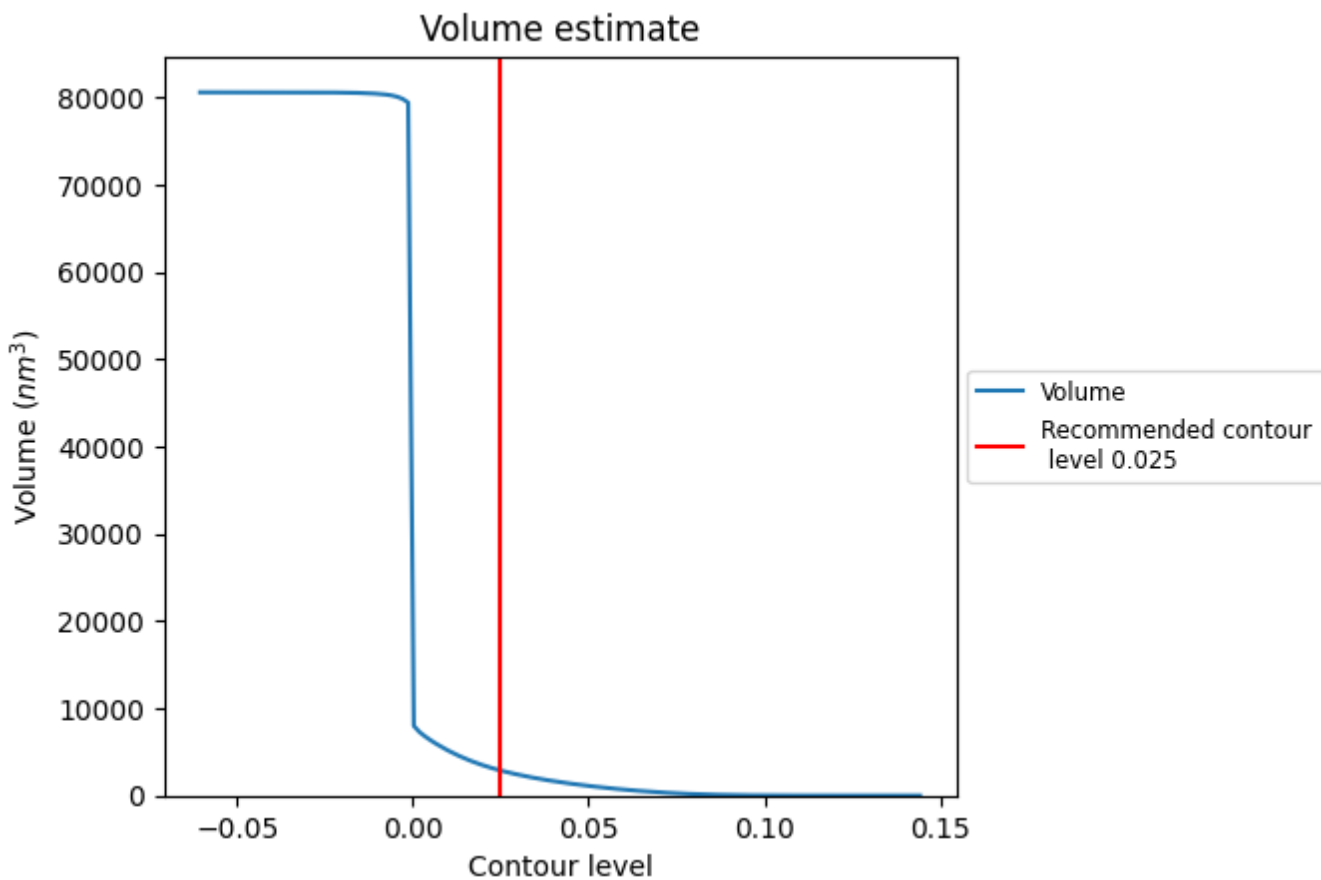
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

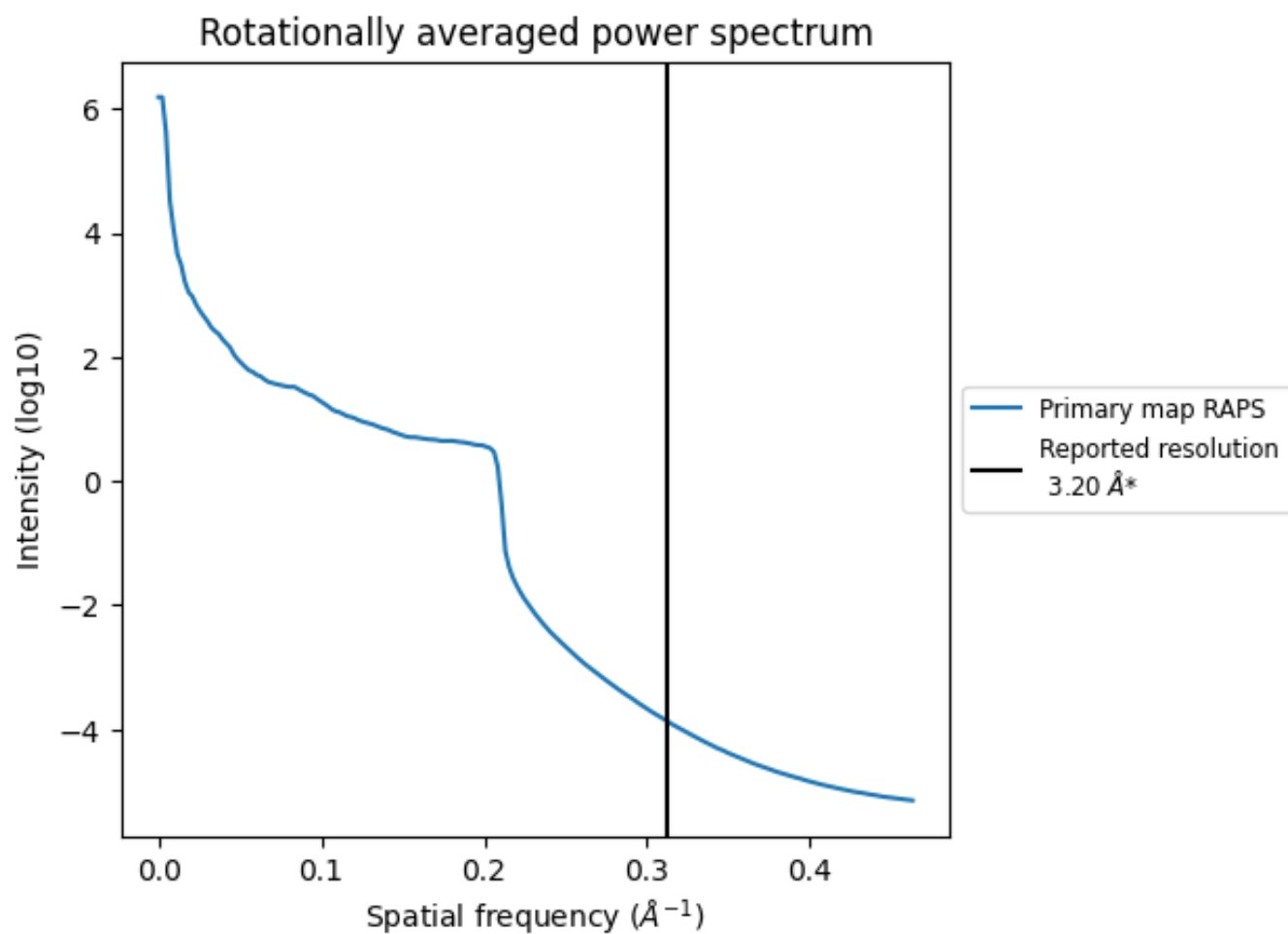
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2873 nm³; this corresponds to an approximate mass of 2595 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](#)

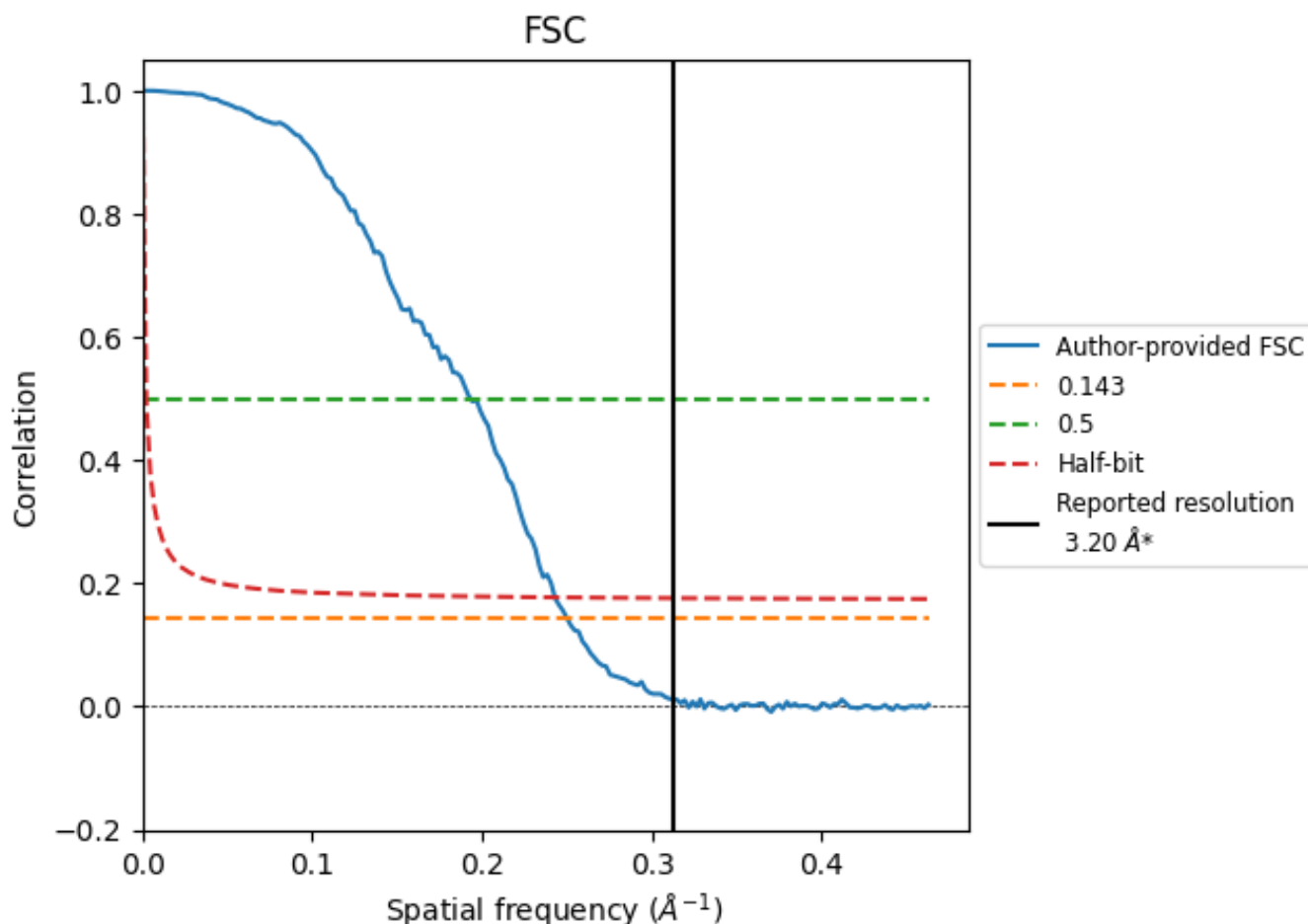


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

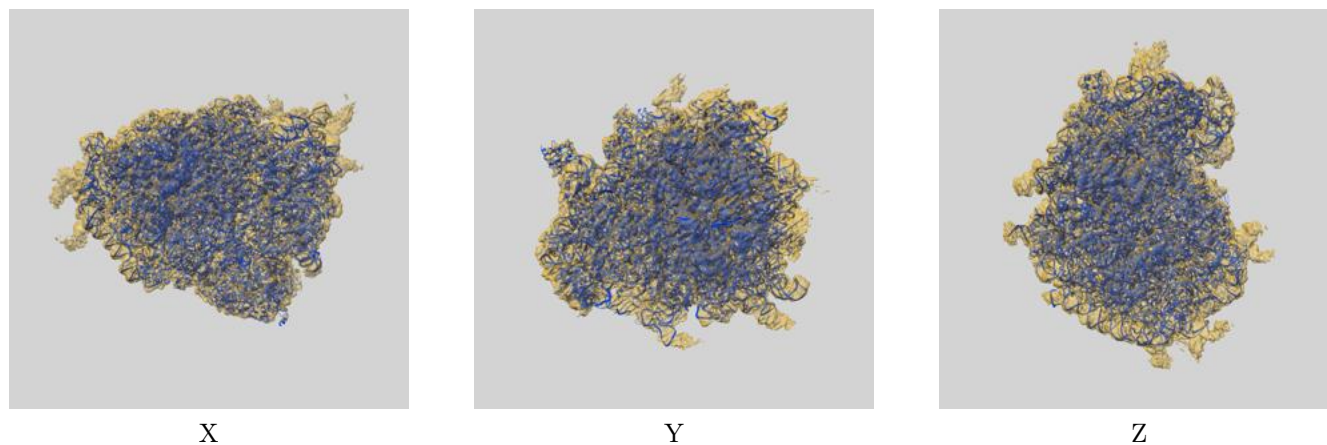
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

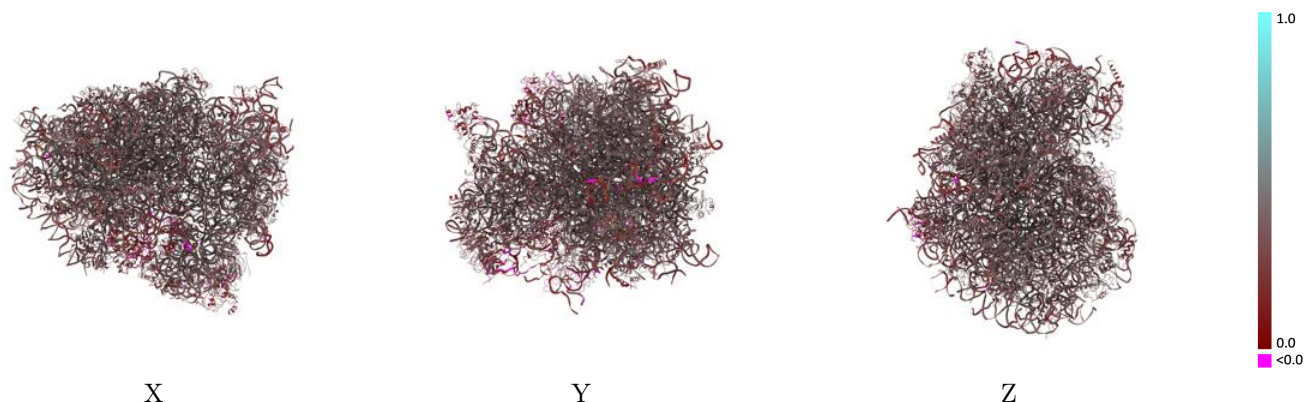
This section contains information regarding the fit between EMDB map EMD-7834 and PDB model 6D90. Per-residue inclusion information can be found in section 3 on page 24.

9.1 Map-model overlay [i](#)



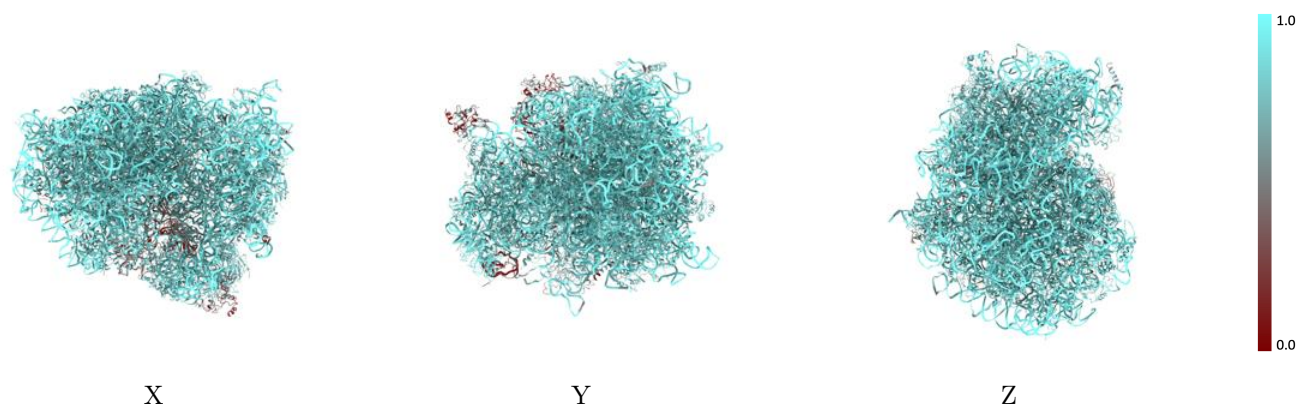
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



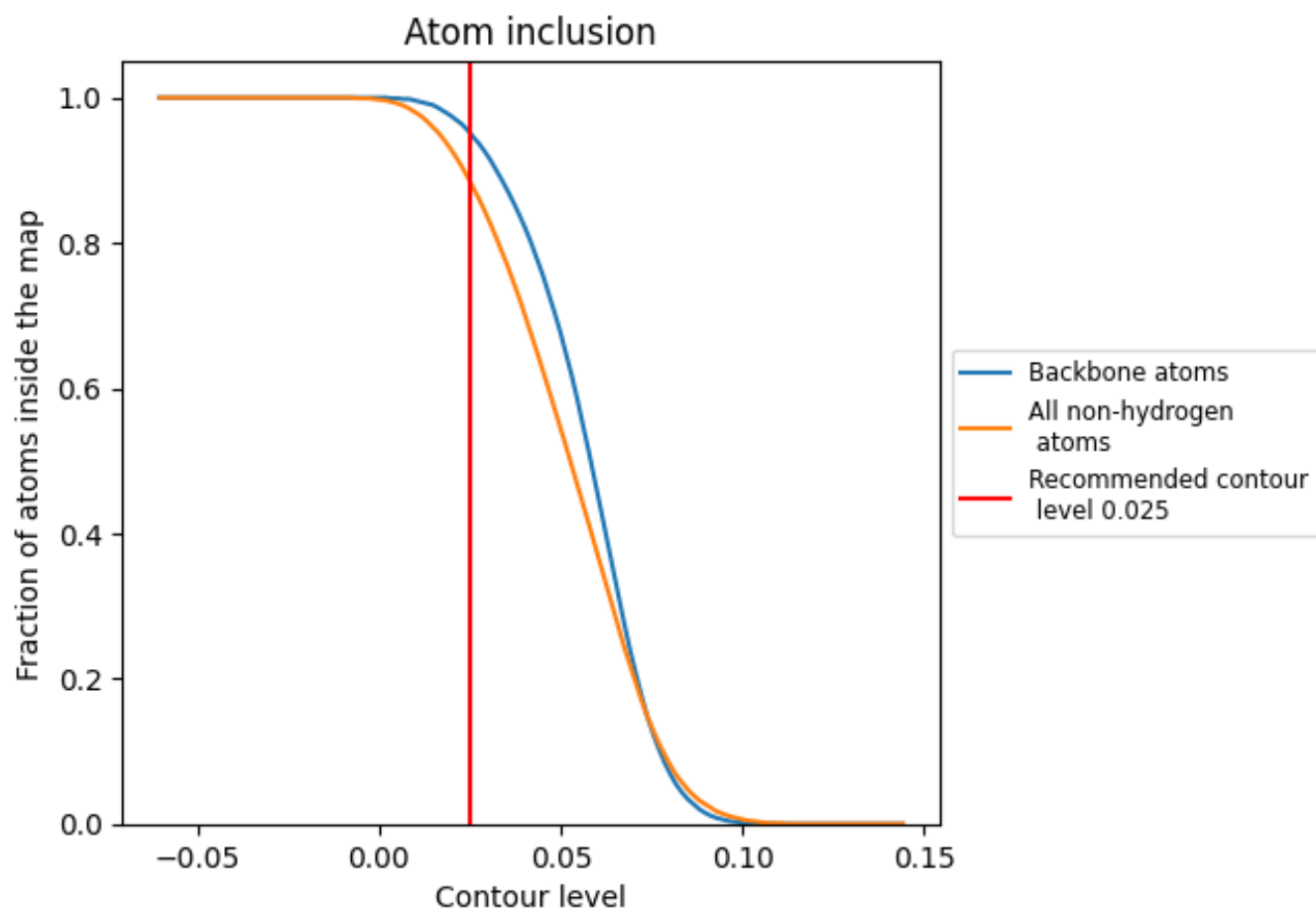
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 88% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8850	 0.3350
2	 0.9740	 0.3550
3	 0.8810	 0.2840
4	 0.5240	 0.1010
5	 0.9720	 0.3540
7	 0.9890	 0.3620
8	 0.9790	 0.3650
A	 0.8190	 0.3560
B	 0.8410	 0.3650
BB	 0.8110	 0.3080
C	 0.8330	 0.3510
CC	 0.8180	 0.3290
D	 0.8500	 0.3110
DD	 0.8350	 0.3540
E	 0.8510	 0.3350
EE	 0.7970	 0.3320
F	 0.8200	 0.3260
FF	 0.8330	 0.3570
G	 0.8020	 0.3200
GG	 0.7860	 0.3000
H	 0.8380	 0.3550
HH	 0.8230	 0.3130
I	 0.8380	 0.3560
II	 0.8120	 0.3140
J	 0.8070	 0.3190
JJ	 0.8180	 0.3150
K	 0.5930	 0.1140
KK	 0.8290	 0.3310
L	 0.8050	 0.3170
LL	 0.7990	 0.2930
M	 0.8430	 0.3310
MM	 0.8250	 0.3550
N	 0.8500	 0.3550
NN	 0.2660	 0.1780
O	 0.8340	 0.3410





















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Chain	Atom inclusion	Q-score
OO	 0.8190	 0.3350
P	 0.8570	 0.3600
PP	 0.8230	 0.3220
Q	 0.8140	 0.3430
QQ	 0.8020	 0.2750
R	 0.8490	 0.3310
RR	 0.8080	 0.2890
S	 0.8450	 0.3550
SS	 0.7650	 0.2940
T	 0.8090	 0.3400
TT	 0.8090	 0.2920
U	 0.8370	 0.3430
UU	 0.8150	 0.2870
V	 0.8210	 0.3610
VV	 0.7750	 0.3300
W	 0.8090	 0.3160
WW	 0.8420	 0.3360
X	 0.8400	 0.3650
XX	 0.8130	 0.3540
Y	 0.8530	 0.3350
YY	 0.8360	 0.3630
Z	 0.8500	 0.3420
ZZ	 0.8510	 0.3390
a	 0.8440	 0.3560
aa	 0.7700	 0.2770
b	 0.7580	 0.2620
bb	 0.8250	 0.3310
c	 0.8250	 0.3320
cc	 0.8190	 0.3460
d	 0.8540	 0.3660
dd	 0.7910	 0.3360
e	 0.8650	 0.3750
ee	 0.8550	 0.3150
f	 0.8610	 0.3680
ff	 0.7390	 0.3160
g	 0.8420	 0.3610
gg	 0.5060	 0.2330
h	 0.8130	 0.3180
hh	 0.8390	 0.3060
i	 0.8320	 0.3300
j	 0.8850	 0.3610
jj	 0.4230	 0.2610

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Chain	Atom inclusion	Q-score
k	 0.8170	 0.3430
l	 0.8340	 0.3440
m	 0.8550	 0.3530
n	 0.8390	 0.3350
o	 0.8170	 0.3380
p	 0.8180	 0.3440
r	 0.8750	 0.3710
s	 0.3510	 0.1620
t	 0.5390	 0.1760