



## wwPDB EM Validation Summary Report ⓘ

Dec 17, 2024 – 04:55 AM EST

PDB ID : 6D90  
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](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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.40

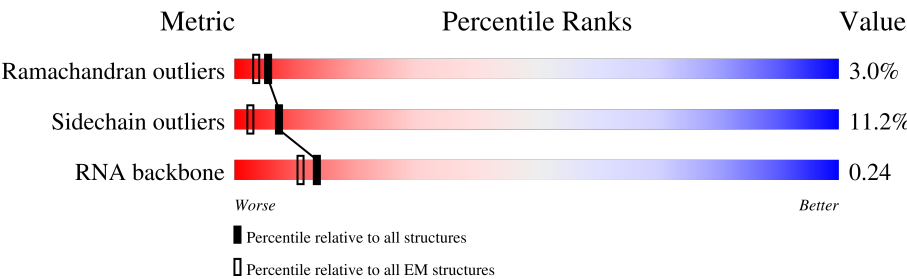
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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.





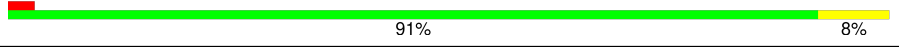



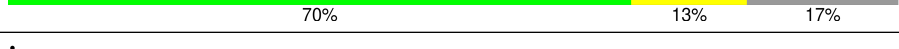
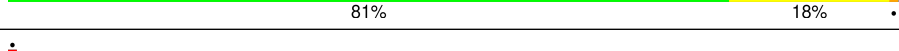
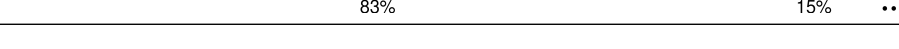
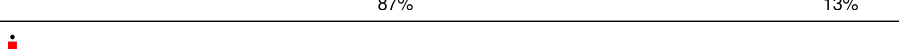
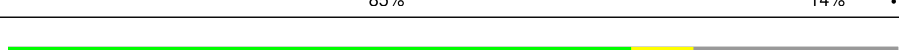

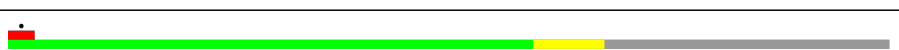

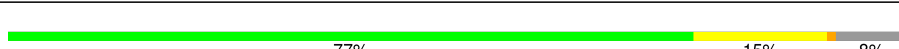





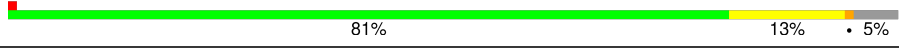
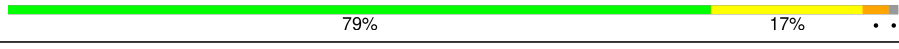



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	
2	B	403	
3	C	392	
4	D	297	
5	E	291	
6	F	249	
7	G	242	
8	H	192	












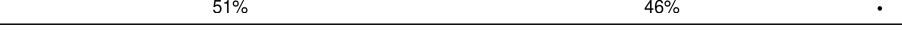







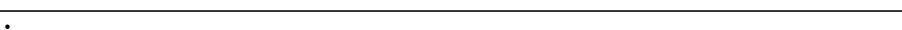

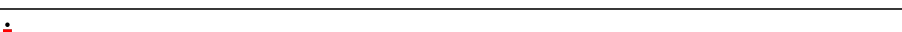
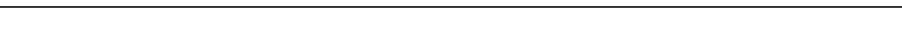


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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	198	
13	N	204	
14	O	199	
15	P	184	
16	Q	188	
17	R	181	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	126	
33	h	123	






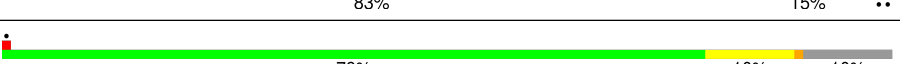
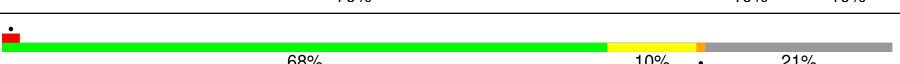
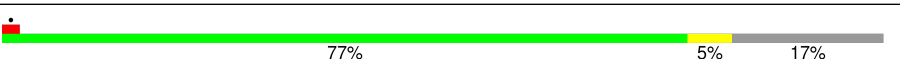


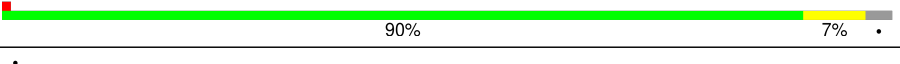
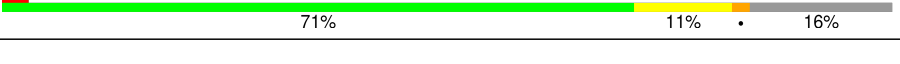

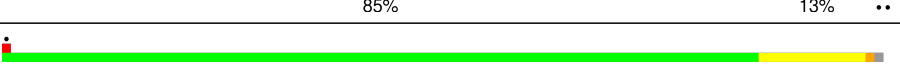
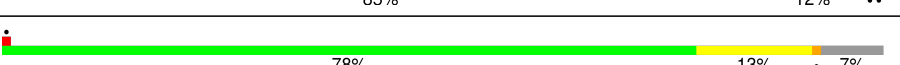










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Mol	Chain	Length	Quality of chain
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	52	
39	n	25	
40	o	106	
41	p	92	
42	r	137	
43	s	303	
44	t	195	
45	5	3594	
46	7	119	
47	8	151	
48	K	217	
49	2	1697	
50	3	87	
51	BB	295	
52	CC	264	
53	DD	255	
54	EE	281	
55	FF	263	
56	GG	204	
57	HH	249	
58	II	194	

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Mol	Chain	Length	Quality of chain
59	JJ	208	
60	KK	194	
61	LL	149	
62	MM	158	
63	NN	132	
64	OO	151	
65	PP	151	
66	QQ	145	
67	RR	172	
68	SS	135	
69	TT	152	
70	UU	145	
71	VV	119	
72	WW	83	
73	XX	130	
74	YY	143	
75	ZZ	134	
76	aa	125	
77	bb	115	
78	cc	84	
79	dd	69	
80	ee	56	
81	ff	133	
82	gg	156	
83	hh	317	

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Mol	Chain	Length	Quality of chain
84	jj	437	<div><div></div><div>43%</div><div>86%</div><div>9%</div><div>5%</div></div>
85	4	194	<div><div></div><div>38%</div><div>34%</div><div>58%</div><div>6%</div></div>

## 2 Entry composition

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
1	A	239	Total	C	N	O	S	0	0
			1777	1110	361	300	6		

- Molecule 2 is a protein called uL3.

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

- Molecule 3 is a protein called Ribosomal protein L4.

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 6 is a protein called uL30.

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

- Molecule 7 is a protein called eL8.

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

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

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

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

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

- Molecule 10 is a protein called Ribosomal protein L11.

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

- Molecule 11 is a protein called 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
13	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

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

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

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

- Molecule 16 is a protein called rL18.

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

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
17	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

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
18	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

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
19	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

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

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
21	V	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called eL23.

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

- Molecule 24 is a protein called uL24.

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

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

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called Ribosomal protein L32.

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

- Molecule 31 is a protein called eL33.

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

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

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

- Molecule 33 is a protein called eL35.

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

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

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

- Molecule 35 is a protein called Ribosomal protein L37.

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

- Molecule 36 is a protein called eL38.

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

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

*Continued on next page...*

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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
44	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

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

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

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

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

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

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



- Molecule 48 is a protein called Ribosomal protein.

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

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

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

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

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

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

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

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
52	CC	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called uS5.

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

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
54	EE	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

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

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

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
56	GG	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

- Molecule 61 is a protein called S10\_ plectin domain-containing protein.

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

- Molecule 62 is a protein called Ribosomal protein S11.

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

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

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

- Molecule 64 is a protein called Ribosomal protein S13.

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

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

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

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called Ribosomal protein S16.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

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

- Molecule 71 is a protein called uS10.

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

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

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

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
73	XX	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called Ribosomal protein S23.

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

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

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

- 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
82	gg	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 83 is a protein called RACK1.

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

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

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

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
85	4	194	Total	C	N	O	P	0	0
			4105	1840	704	1367	194		

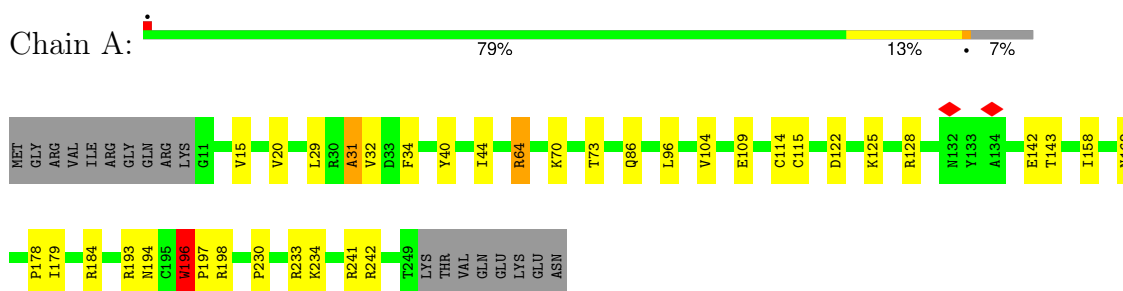
There are 4 discrepancies between the modelled and reference sequences:

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

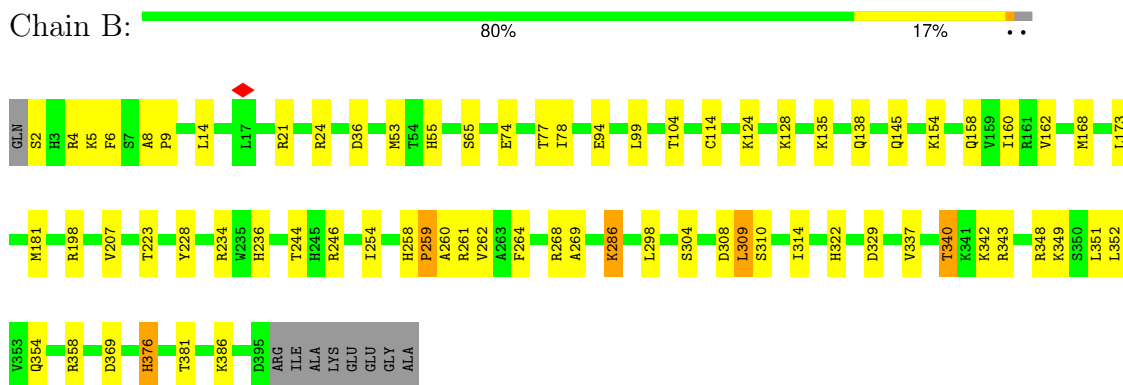
### 3 Residue-property plots [i](#)

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.

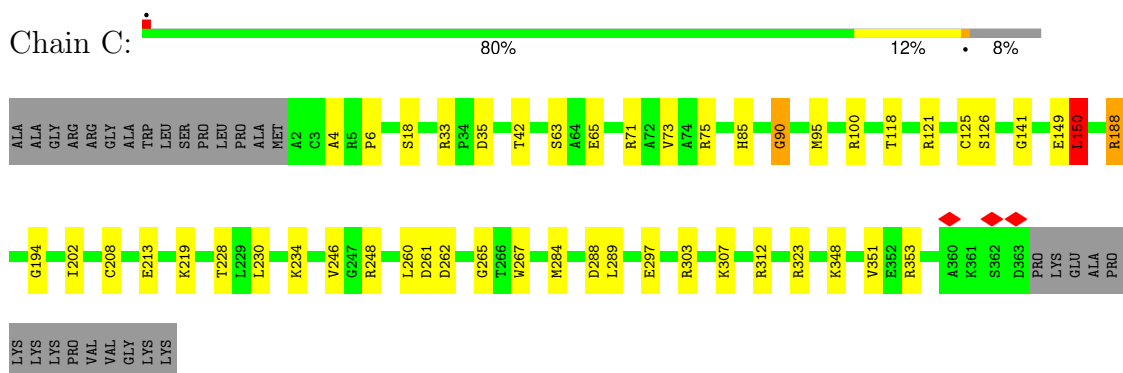
#### • Molecule 1: Ribosomal protein L8



#### • Molecule 2: uL3

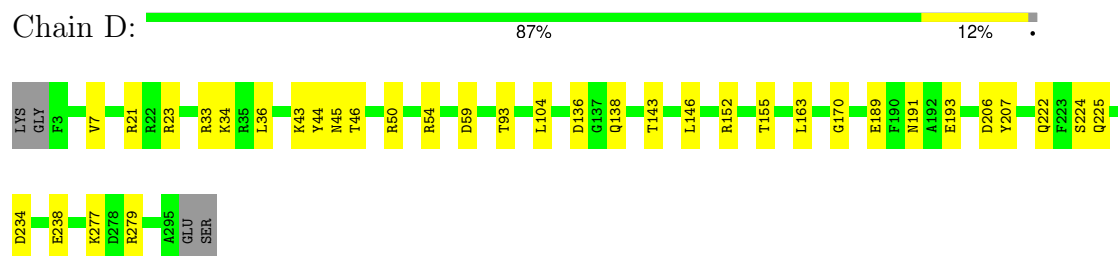


#### • Molecule 3: Ribosomal protein L4

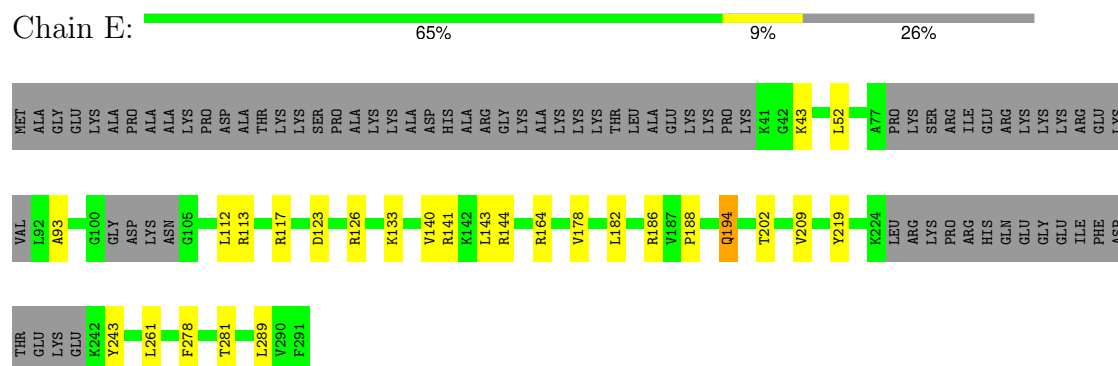




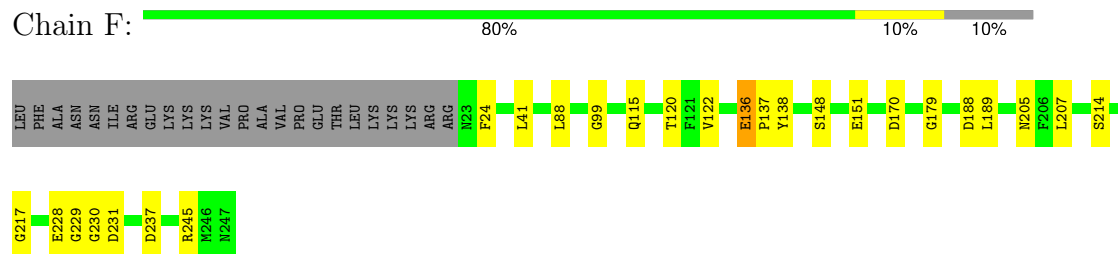
- Molecule 4: Large ribosomal subunit protein uL18



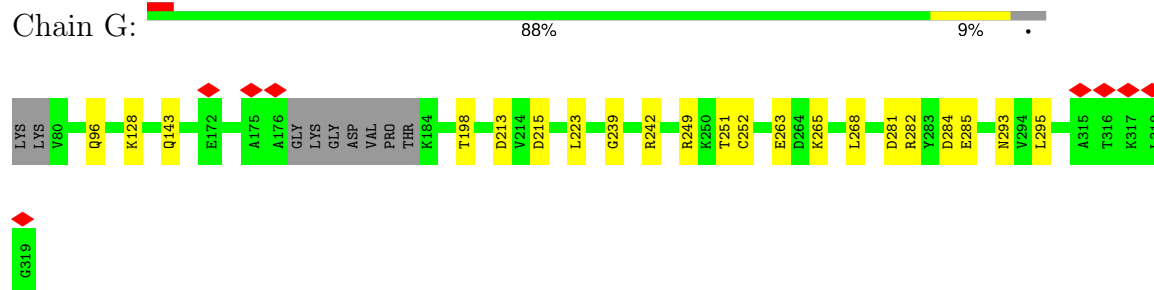
- Molecule 5: 60S ribosomal protein L6



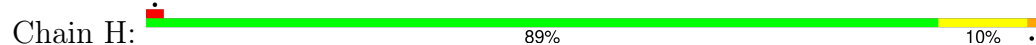
- Molecule 6: uL30

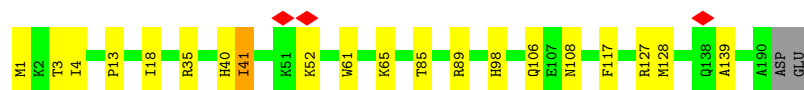


- Molecule 7: eL8

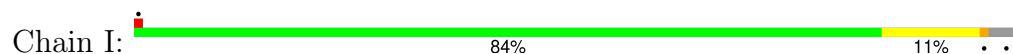


- Molecule 8: 60S ribosomal protein L9

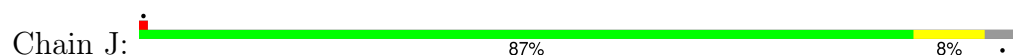




- Molecule 9: 60S ribosomal protein L10



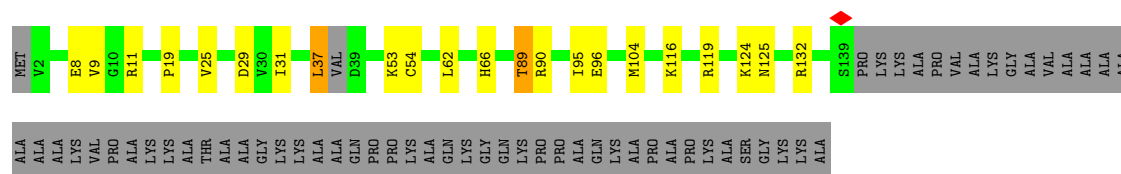
- Molecule 10: Ribosomal protein L11



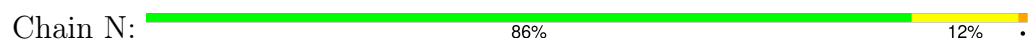
- Molecule 11: eL13



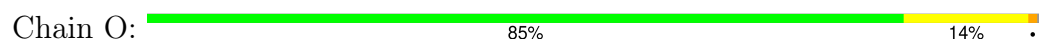
- Molecule 12: Large ribosomal subunit protein eL14

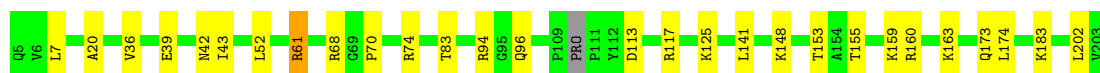


- Molecule 13: Ribosomal protein L15

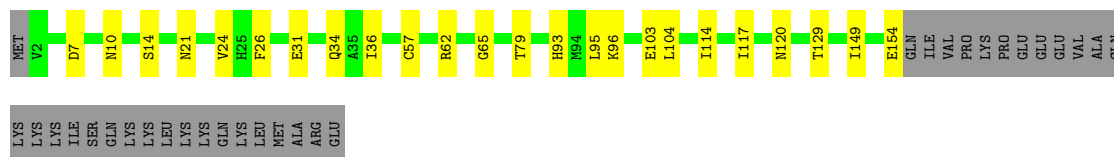


- Molecule 14: uL13

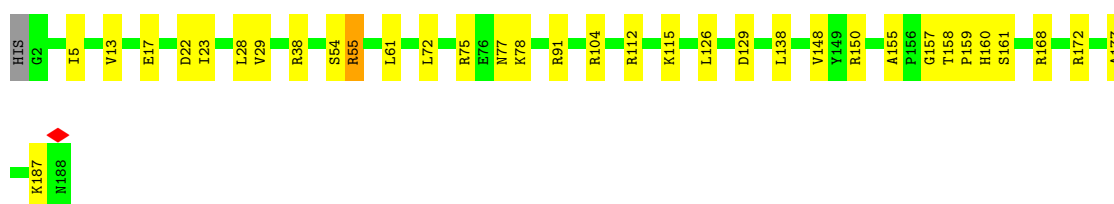
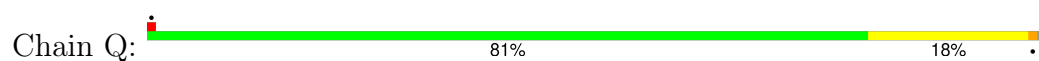




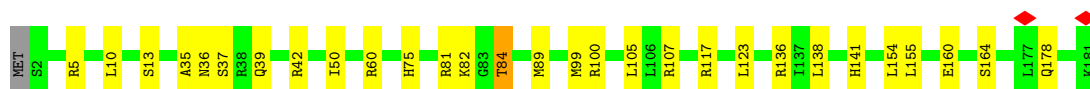
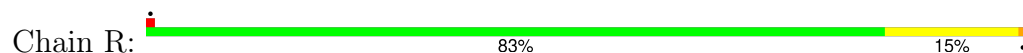
- Molecule 15: Large ribosomal subunit protein uL22



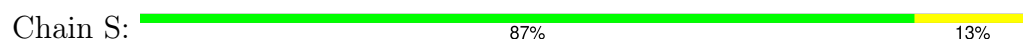
- Molecule 16: rL18



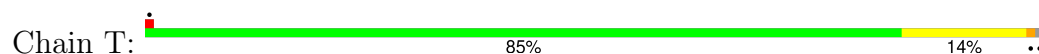
- Molecule 17: Ribosomal protein L19



- Molecule 18: 60S ribosomal protein L18a



- Molecule 19: eL21

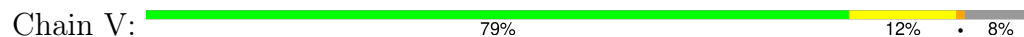


- Molecule 20: eL22

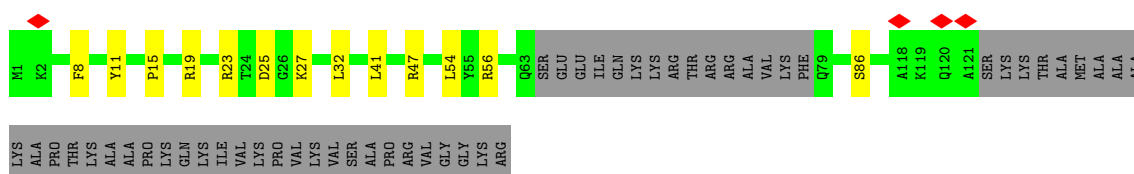




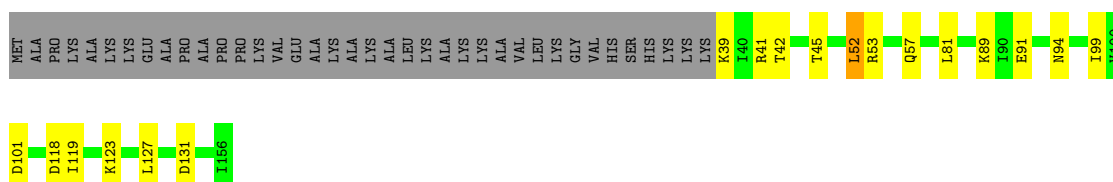
- Molecule 21: Ribosomal protein L23



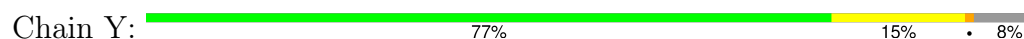
- Molecule 22: eL24



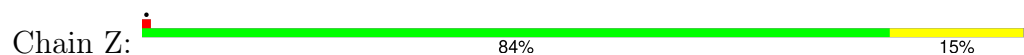
- Molecule 23: eL23



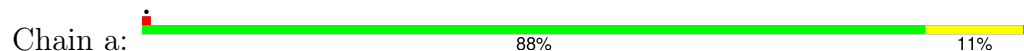
- Molecule 24: uL24



- Molecule 25: 60S ribosomal protein L27

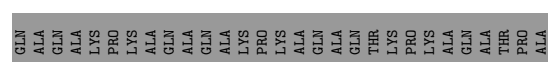
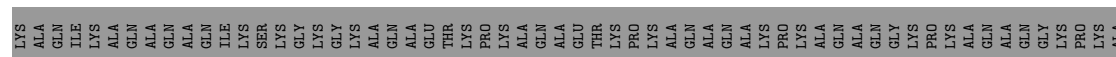
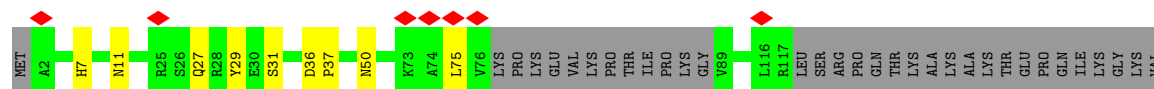


- Molecule 26: uL15





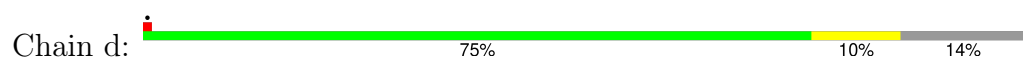
• Molecule 27: eL29



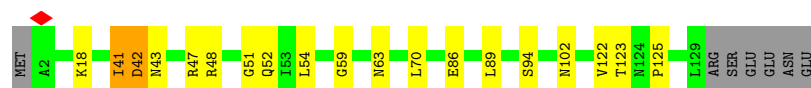
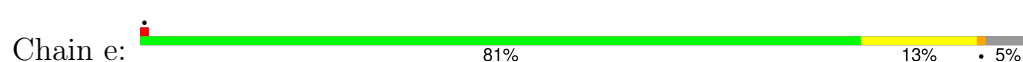
• Molecule 28: eL30



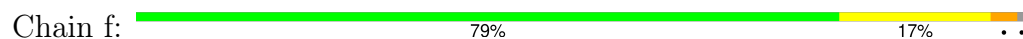
• Molecule 29: eL31



• Molecule 30: Ribosomal protein L32

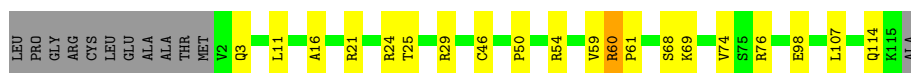


• Molecule 31: eL33

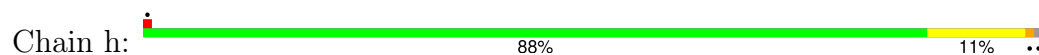


• Molecule 32: Large ribosomal subunit protein eL34

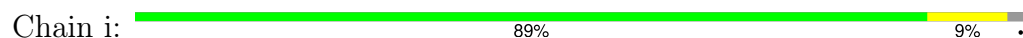




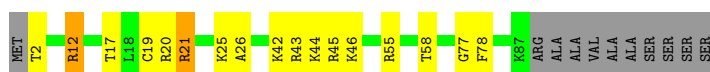
• Molecule 33: eL35



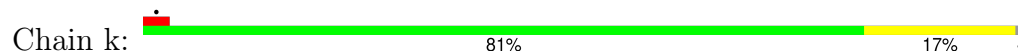
• Molecule 34: 60S ribosomal protein L36



• Molecule 35: Ribosomal protein L37



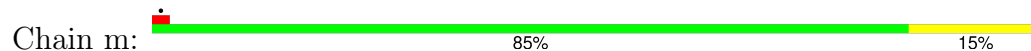
• Molecule 36: eL38



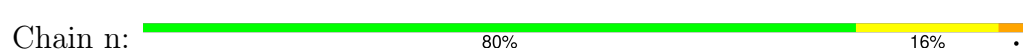
• Molecule 37: eL39

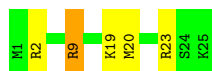


• Molecule 38: eL40

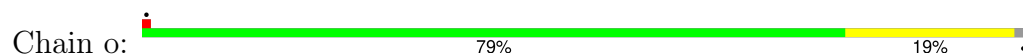


• Molecule 39: eL41

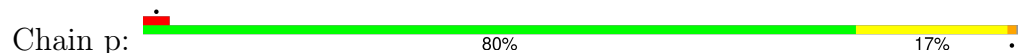




- Molecule 40: Large ribosomal subunit protein eL42



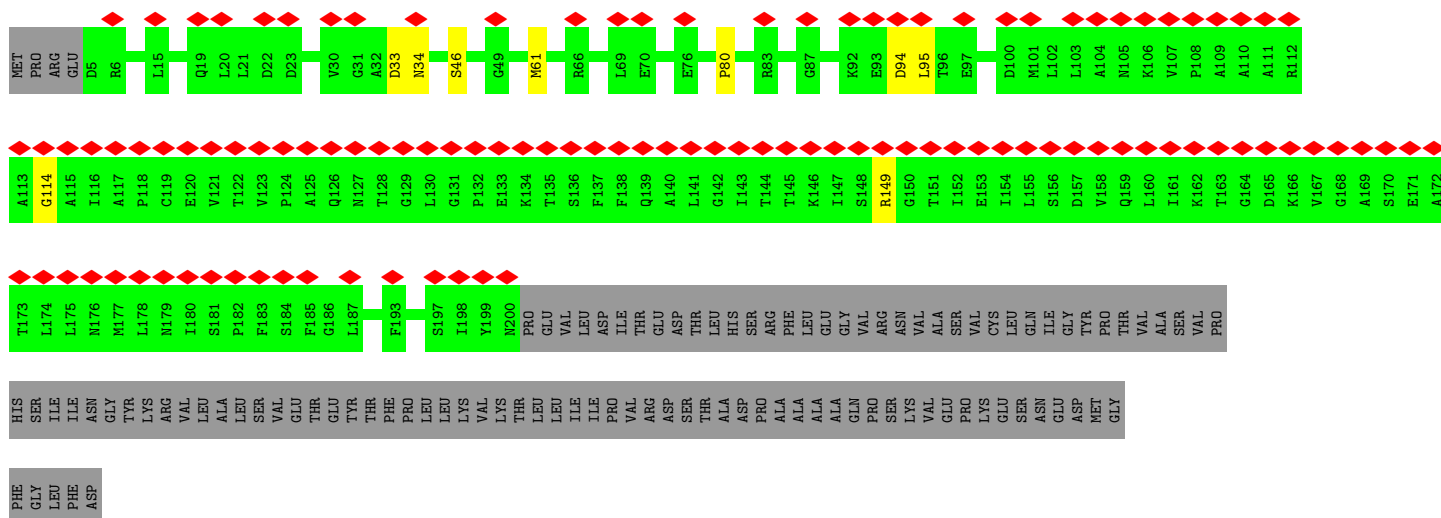
- Molecule 41: eL43



- Molecule 42: eL28

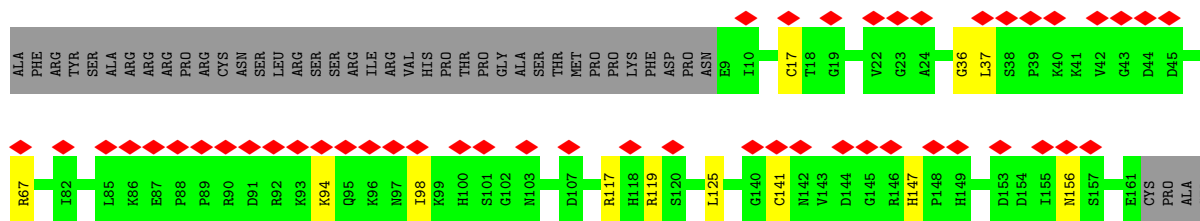


- Molecule 43: 60S acidic ribosomal protein P0



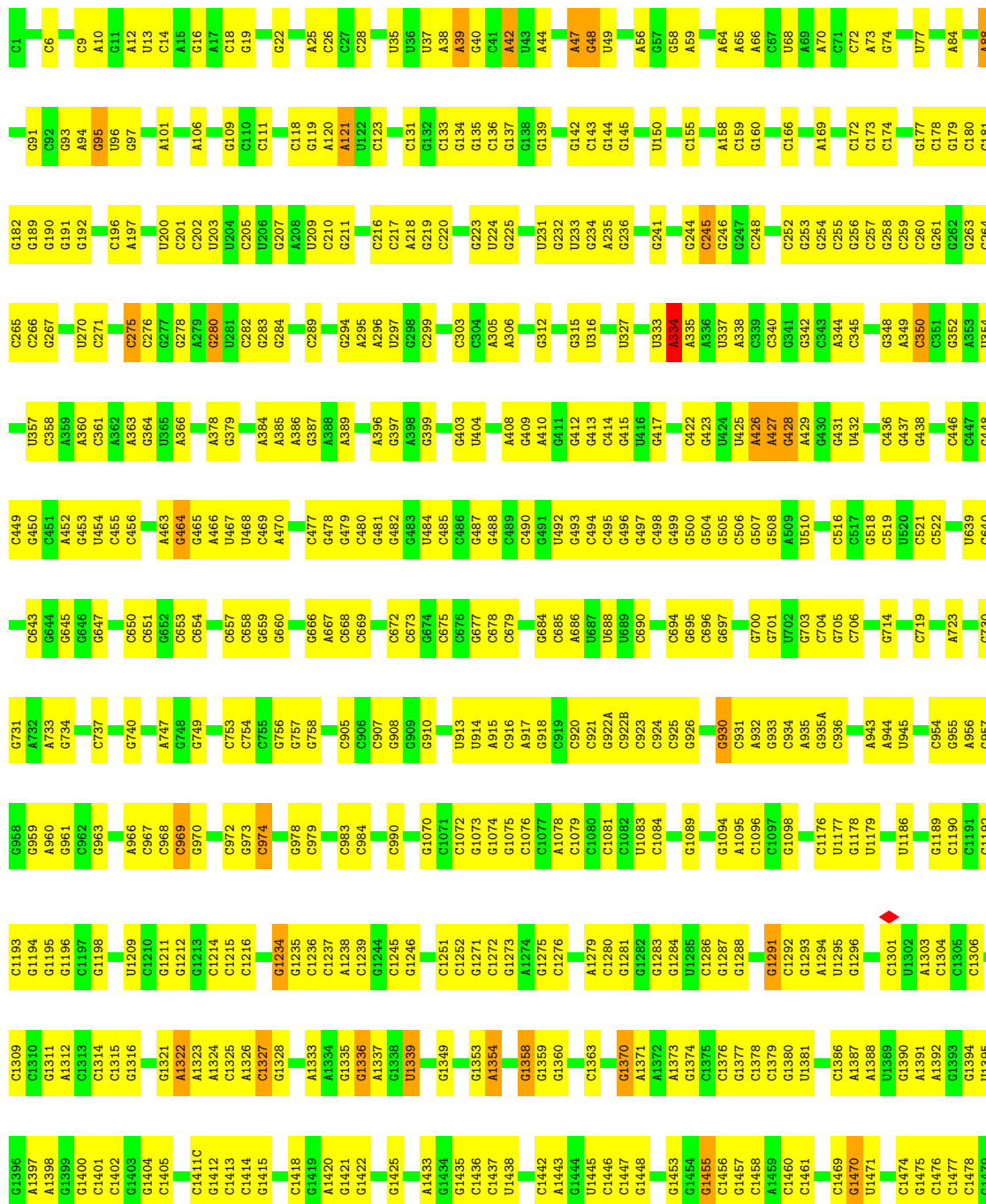
- Molecule 44: Ribosomal protein L12





• Molecule 45: 28S rRNA

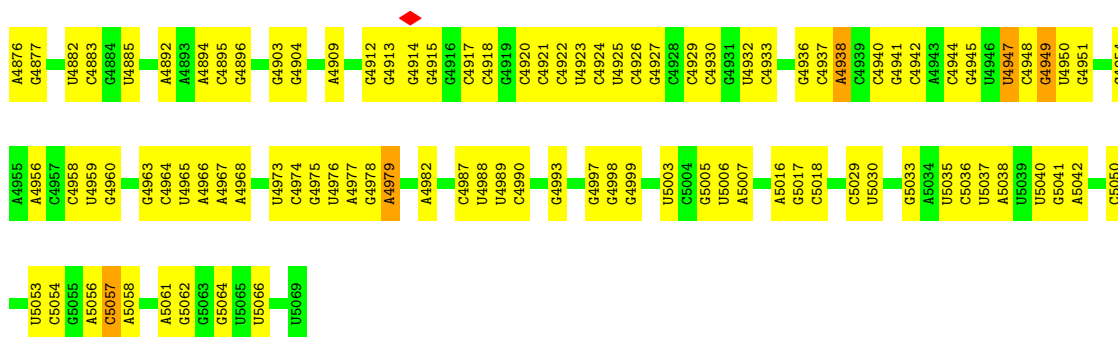
Chain 5: 51% 46%





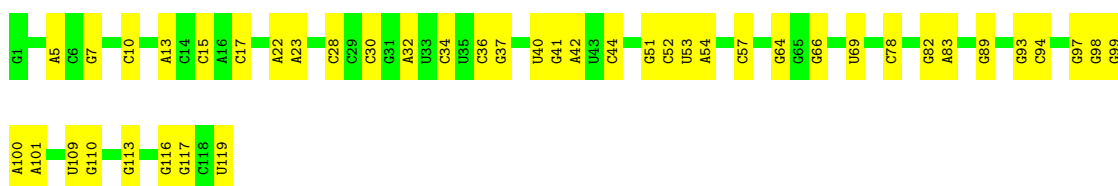
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G2776	C2690	C2690	A2513	U2425	G2332	A2104	A2025	G1856	U1756	U1652	G1562	C1482
G2777	C2693	C2693	A2514	U2426	G2333	A2105	A2026	C1857	C1757	A1653	C1565	C1483
C2780	G2694	C2694	G2515	G2427	G2336	A2106	U2027	A1858	G1762	G1655	A1566	G1484
C2781	A2695	G2596	G2516	A2428	C2337	G2108	A2028	G1869	C1763	U1656	C1573	G1487
G2782	A2697	A2597	A2517	U2432	C2340	A2109	A2029	A1871	G1764	G1657	G1578	G1488
C2785	C2703	A2598	G2521	C2437	C2346	G2259	A2030	C1874	A1765	U1658	U1578	G1489
C2786	G2704	A2600	U2525	A2438	C2347	C2260	A2032	A1875	C1661	C1666	C1585	A1491
A2787	C2705	A2601	C2526	G2439	G2348	G2261	G2034	C1875	C1667	C1666	G1586	G1492
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A2789	G2707	C2611	U2530	C2441	U2350	C2264	C2036	G1881	C1669	C1666	G1588	G1496
U2790	U2708	C2615	C2531	U2444	C2352	G2265	A2041	C1882	C1670	C1666	G1589	A1497
C2791	C2709	C2615	C2532	C2445	U2352	C2266	A2042	U1883	C1671	C1666	G1590	G1498
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C2794	G2712	C2623	C2539	G2450	A2360	C2271	G2045	A1891	C1674	C1666	G1593	G1503
A2795	C2713	G2624	C2540	G2456	G2361	C2277	A2047	A1892	C1675	C1666	G1594	G1504
G2796	G2714	U2625	C2549	C2456	G2362	C2278	U2048	C1893	C1676	C1666	G1595	G1505
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U4703	G4618	A4523	U4450	A4379	G4292	C4204	U4118	G4039	G3904	A3807	A3727	U3641
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		C4453	C4453	A4382	U4295	C4207	C4121	C4041	A3907	C3810	U3730	A2857
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						G4289	C4202	G4115	G3974	A3731		
						G4290	C4203	G4116	G3975	A3732		
						G4291	C4204	G4117	G3976	A3733		
							C4205	U4118	G3977	A3734		
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							C4208	U4121	G3980	A3737		
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							C4218	U4131	G3990	A3747		
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							C4223	U4136	G3995	A3752		
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							C4227	U4140	G3999	A3756		
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							C4231	U4144	G4003	A3760		
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							C4234	U4147	G4006	A3763		
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							C4257	U4170	G4029	A3786		
							C4258	U4171	G4030	A3787		
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							C4262	U4175	G4034	A3791		
							C4263	U4176	G4035	A3792		
							C4264	U4177	G4036	A3793		
							C4265	U4178	G4037	A3794		
							C4266	U4179	G4038	A3795		
							C4267	U4180	G4039	A3796		
							C4268	U4181	G4040	A3797		
							C4269	U4182	G4041	A3798		
							C4270	U4183	G4042	A3799		
							C4271	U4184	G4043	A3800		
							C4272	U4185	G4044	A3801		
							C4273	U4186				



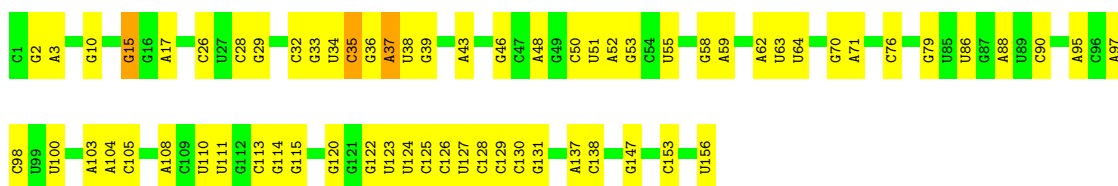
• Molecule 46: 5S rRNA

Chain 7: 64% 36%



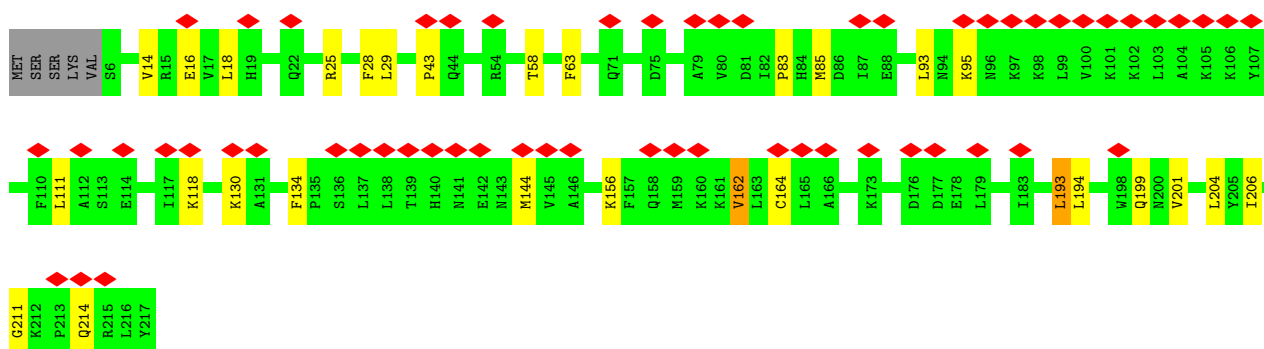
• Molecule 47: 5.8S rRNA

Chain 8: 57% 41%



• Molecule 48: Ribosomal protein

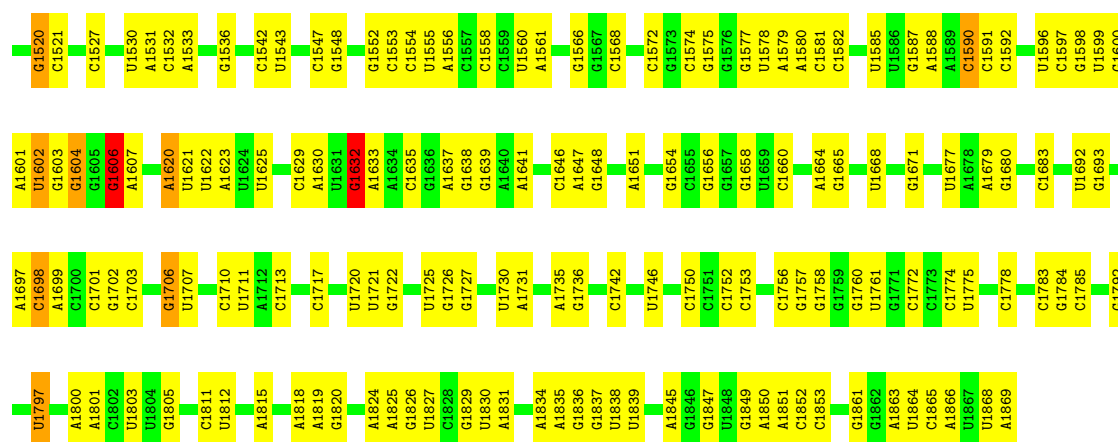
Chain K: 27% 84% 12%



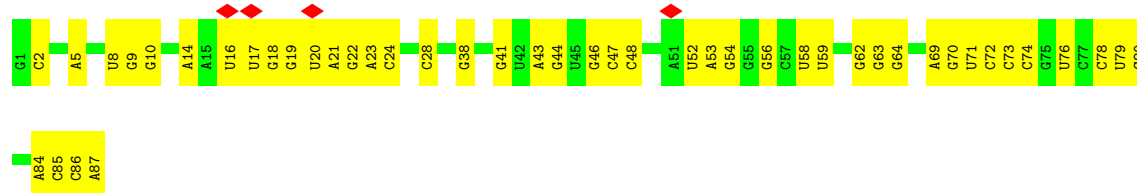
• Molecule 49: 18S rRNA

Chain 2: 55% 43%

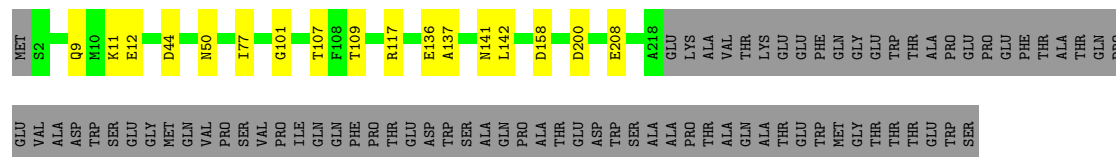
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G1234	G1235	G1236	U1242	U1243	C1249	A1250	A1251	C1252	G1253	C1254	G1255	G1256	G1257	A1258	U1259	U1342	U1343	A1260	C1261	U1262	U1263	U1264	A1265	C1266	C1267	C1268	C1272	C1273	G1274	G1275	A1282	C1283	A1291	C1292	A1293	G1294	A1295	U1296	A1299	U1300	A1301	G1302	G1303	U1304	U1308	U1314	U1315	G1318																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G1134	U1135	U1136	U1137	C1138	C1139	G1140	G1141	A1144	A1148	A1149	A1150	C1153	U1154	U1155	U1156	G1157	U1160	U1161	U1162	C1163	G1164	G1165	U1166	G1167	U1168	C1191	U1192	A1083	C1085	G1086	U1081	A1082	A1083	U1192	G1203	A1204	G1205	G1206	G1207	G1211	C1215	C1216	A1217	G1221	G1224	A1228	G1233																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
U1319	U1323	U1326	U1327	G1328	A1332	U1333	G1334	C1337	U1340	C1341	U1342	U1343	A1344	U1345	U1346	U1347	G1348	G1354	C1355	G1356	U1364	U1365	G1374	G1375	A1376	U1377	A1378	A1386	G1387	C1395	A1396	U1397	A1402	C1403	U1404	A1405	U1408	A1409	C1410	G1411	C1412	U1505	A1506	G1507	A1508	U1509	G1510	G1516																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
G831	G832	U844	G845	G846	A847	U848	C853	C856	U857	A858	G859	G860	A861	U862	U863	A864	U865	U866	A869	A870	U871	A955	U956	G971	U972	C973	C974	C977	G978	A981	G982	A990	G991	A992	A997	U998	G999	U1002	U1003	G1008	A1009	U1016	U1017	G915																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
A672	G673	C676	A679	G684	U688	U689	G690	A693	G696	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	C1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C16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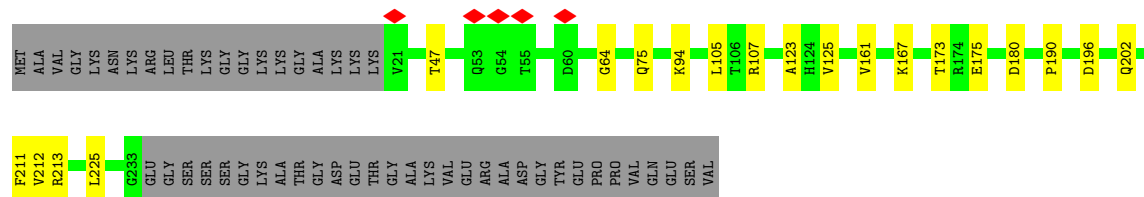
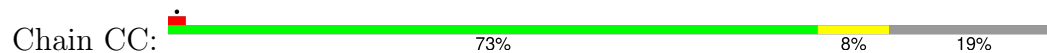
• Molecule 50: P-tRNA



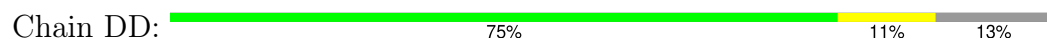
• Molecule 51: Small ribosomal subunit protein uS2



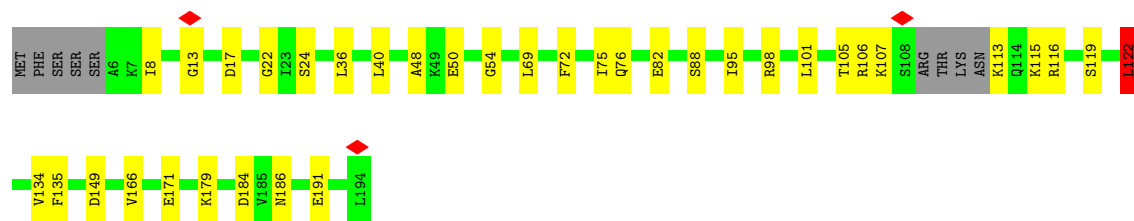
• Molecule 52: 40S ribosomal protein S3a



• Molecule 53: uS5







- Molecule 59: 40S ribosomal protein S8

Chain JJ: 85% 14% .



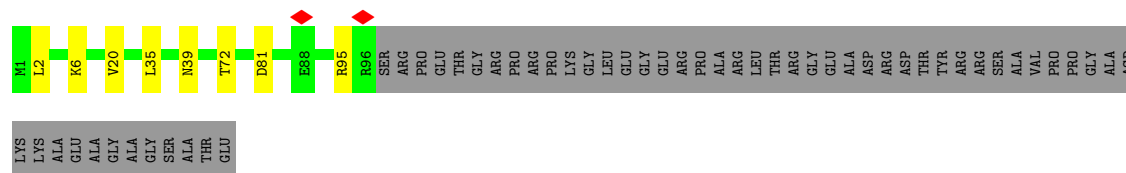
- Molecule 60: Ribosomal protein S9 (Predicted)

Chain KK: 84% 12% 5%



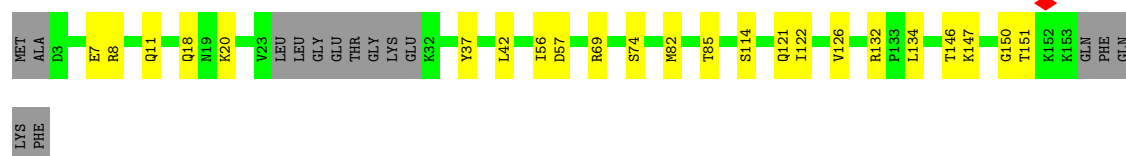
- Molecule 61: S10\_pectin domain-containing protein

Chain LL: 59% 5% 36%



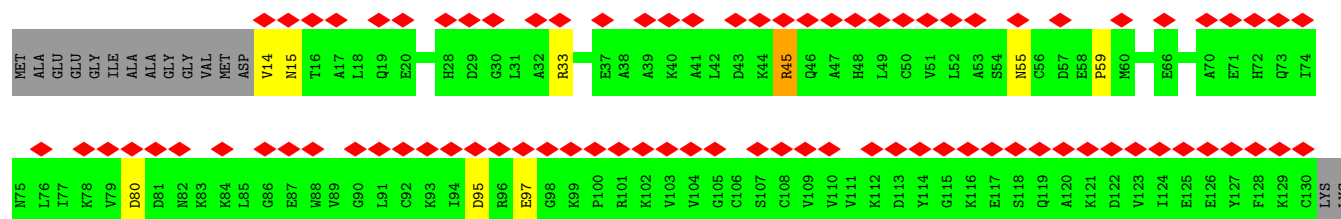
- Molecule 62: Ribosomal protein S11

Chain MM: 76% 15% 9%



- Molecule 63: 40S ribosomal protein S12

Chain NN: 64% 82% 6% 11%



• Molecule 64: Ribosomal protein S13

Chain OO: 83% 15% ..



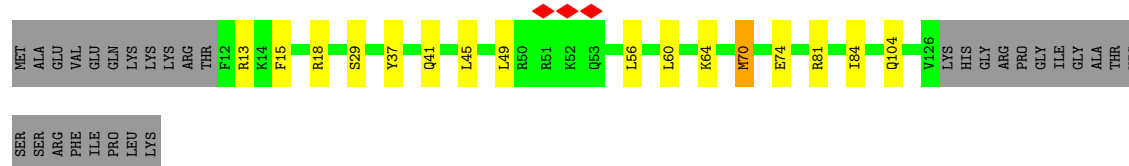
• Molecule 65: Small ribosomal subunit protein uS11

Chain PP: 79% 10% 10%



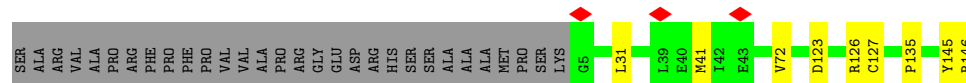
• Molecule 66: uS19

Chain QQ: 68% 10% 21%



• Molecule 67: Ribosomal protein S16

Chain RR: 77% 5% 17%



• Molecule 68: eS17

Chain SS: 89% 9%



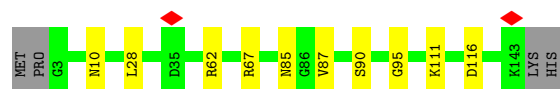
• Molecule 69: uS13

Chain TT: 85% 9% 5%

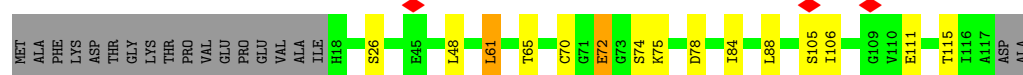




- Molecule 70: eS19



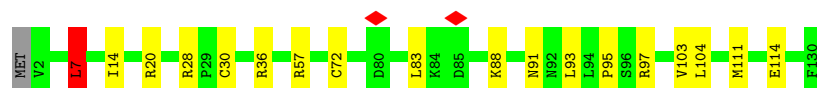
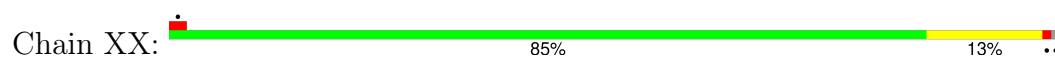
- Molecule 71: uS10



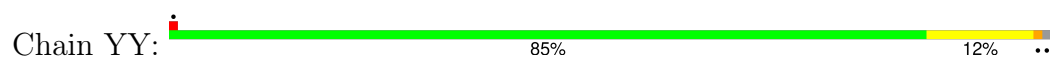
- Molecule 72: 40S ribosomal protein S21



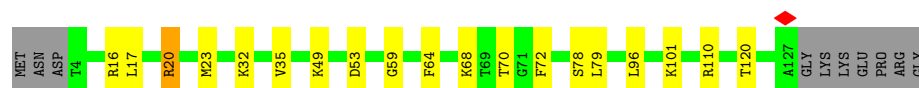
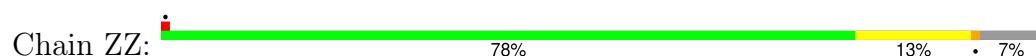
- Molecule 73: Ribosomal protein S15a



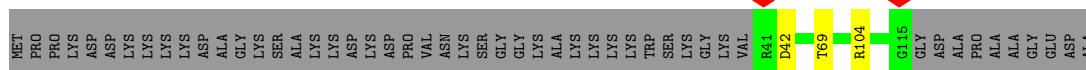
- Molecule 74: Ribosomal protein S23



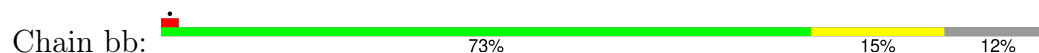
- Molecule 75: 40S ribosomal protein S24



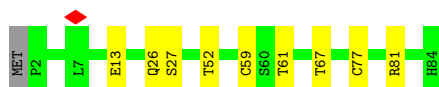
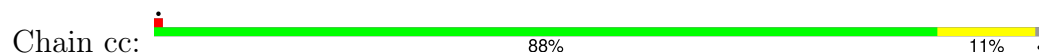
- Molecule 76: eS25



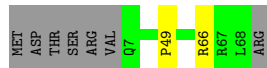
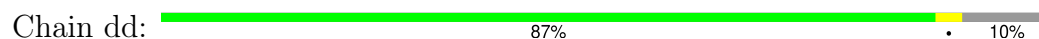
- Molecule 77: 40S ribosomal protein S26



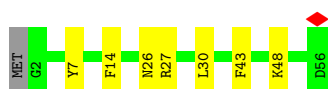
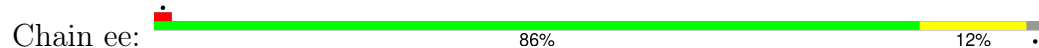
- Molecule 78: 40S ribosomal protein S27



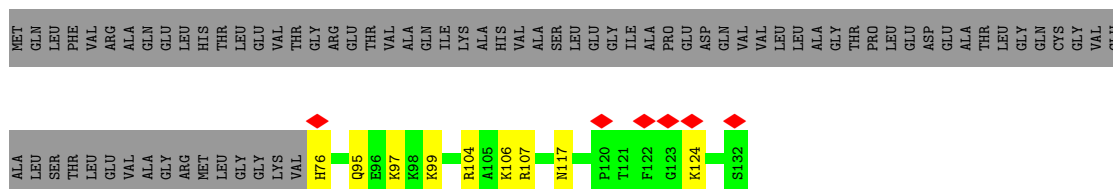
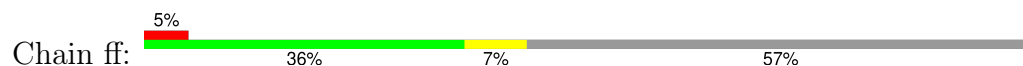
- Molecule 79: Ribosomal protein S28



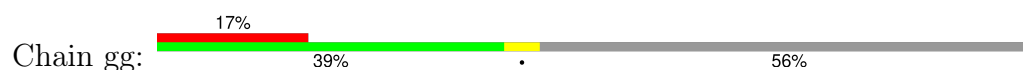
- Molecule 80: eS29

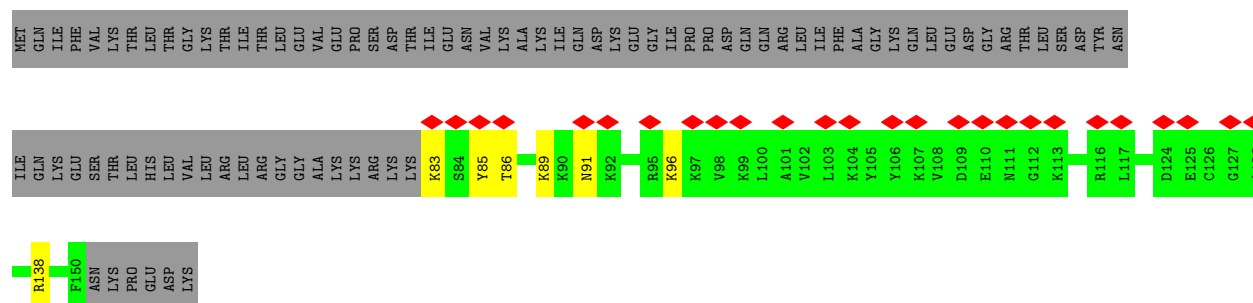


- Molecule 81: 40S ribosomal protein S30

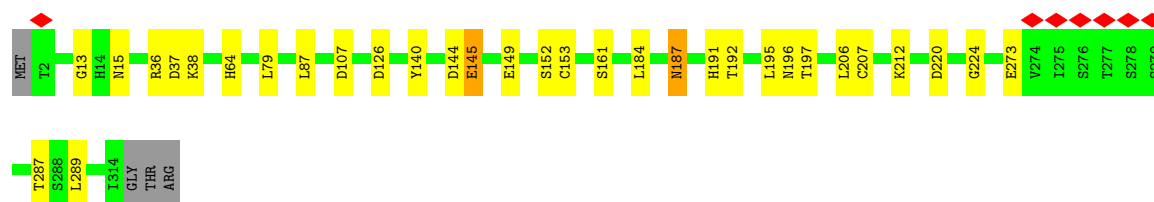


- Molecule 82: Ribosomal protein S27a

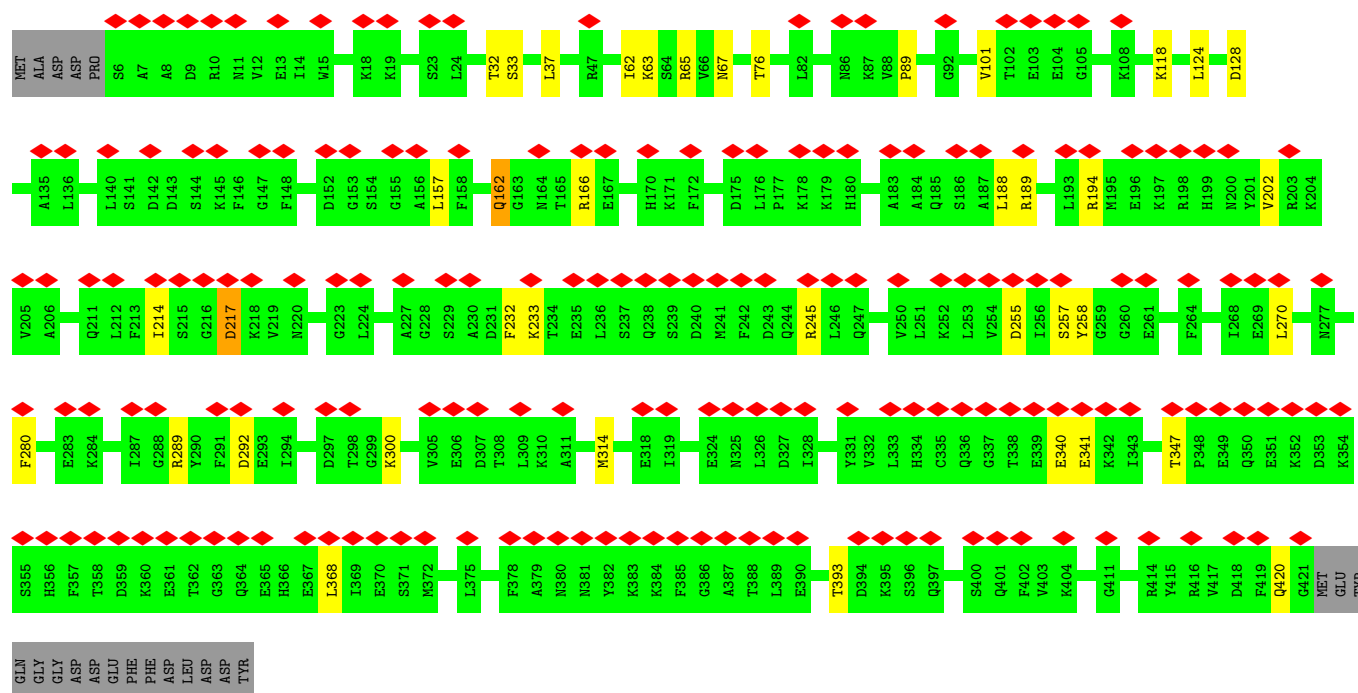
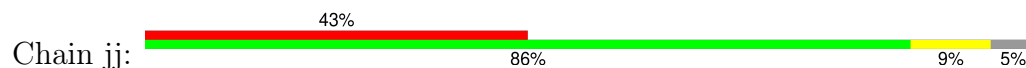




• Molecule 83: RACK1



• Molecule 84: Eukaryotic peptide chain release factor subunit 1



• 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 ( $\text{\AA}$ )	432.00003, 432.00003, 432.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.08, 1.08, 1.08	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	0.73	0/1812	0.95	3/2439 (0.1%)
2	B	0.70	0/3240	0.98	5/4339 (0.1%)
3	C	0.73	0/2936	0.96	3/3943 (0.1%)
4	D	0.59	0/2437	0.77	3/3264 (0.1%)
5	E	0.63	0/1762	0.89	2/2362 (0.1%)
6	F	0.68	1/1911 (0.1%)	0.84	2/2549 (0.1%)
7	G	0.60	0/1910	0.79	0/2569
8	H	0.66	0/1535	0.87	0/2063
9	I	0.67	0/1702	0.89	1/2272 (0.0%)
10	J	0.59	0/1385	0.77	1/1852 (0.1%)
11	L	0.62	0/1733	0.83	0/2316
12	M	0.69	0/1150	0.88	1/1534 (0.1%)
13	N	0.74	0/1746	1.05	5/2338 (0.2%)
14	O	0.73	0/1653	0.95	1/2206 (0.0%)
15	P	0.74	0/1268	0.93	0/1700
16	Q	0.70	0/1539	0.97	0/2054
17	R	0.67	0/1524	0.98	3/2013 (0.1%)
18	S	0.69	0/1501	0.89	0/2012
19	T	0.69	0/1326	0.88	0/1770
20	U	0.67	1/823 (0.1%)	0.80	1/1104 (0.1%)
21	V	0.72	0/983	0.94	0/1319
22	W	0.65	0/873	0.90	1/1158 (0.1%)
23	X	0.70	0/984	0.92	2/1323 (0.2%)
24	Y	0.67	0/1132	0.86	0/1504
25	Z	0.67	0/1130	0.86	2/1507 (0.1%)
26	a	0.76	0/1191	0.94	2/1590 (0.1%)
27	b	0.61	0/861	0.80	0/1138
28	c	0.64	0/771	0.82	0/1034
29	d	0.76	0/903	0.93	0/1216
30	e	0.76	1/1071 (0.1%)	1.02	0/1429
31	f	0.77	0/895	1.04	4/1198 (0.3%)
32	g	0.70	0/916	1.01	0/1220
33	h	0.68	0/1021	0.93	1/1348 (0.1%)
34	i	0.59	0/841	0.82	0/1112

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	j	0.78	0/720	1.09	2/952 (0.2%)
36	k	0.62	0/575	0.81	0/761
37	l	0.71	0/459	1.07	2/608 (0.3%)
38	m	0.67	0/435	0.95	0/575
39	n	0.77	0/240	1.32	2/305 (0.7%)
40	o	0.58	0/864	0.78	1/1140 (0.1%)
41	p	0.73	0/718	0.93	0/953
42	r	0.71	0/1010	0.99	1/1354 (0.1%)
43	s	0.58	0/1530	0.64	0/2064
44	t	0.57	0/1174	0.65	0/1582
45	5	0.62	88/86202 (0.1%)	0.91	151/134412 (0.1%)
46	7	0.50	0/2836	0.79	0/4421
47	8	0.64	5/3581 (0.1%)	0.87	2/5577 (0.0%)
48	K	0.61	0/1730	0.76	1/2315 (0.0%)
49	2	0.55	30/40502 (0.1%)	0.84	23/63100 (0.0%)
50	3	0.39	0/2079	0.77	2/3238 (0.1%)
51	BB	0.95	2/1747 (0.1%)	0.75	2/2374 (0.1%)
52	CC	0.59	0/1756	0.75	0/2350
53	DD	0.64	0/1753	0.87	2/2369 (0.1%)
54	EE	0.60	0/1796	0.82	1/2417 (0.0%)
55	FF	0.62	0/2118	0.88	0/2849
56	GG	0.58	0/1492	0.76	1/2005 (0.0%)
57	HH	0.58	0/1946	0.83	0/2590
58	II	0.60	0/1510	0.81	1/2022 (0.0%)
59	JJ	0.66	0/1715	0.85	0/2287
60	KK	0.64	0/1550	0.88	0/2069
61	LL	0.62	0/834	0.78	0/1125
62	MM	0.71	0/1195	0.89	0/1597
63	NN	0.55	1/918 (0.1%)	0.64	0/1233
64	OO	0.67	0/1226	0.81	0/1649
65	PP	0.57	0/1029	0.79	1/1380 (0.1%)
66	QQ	0.59	0/974	0.83	1/1301 (0.1%)
67	RR	0.55	0/1146	0.71	0/1534
68	SS	0.60	0/1082	0.78	0/1452
69	TT	0.60	0/1208	0.82	0/1618
70	UU	0.56	0/1115	0.68	0/1493
71	VV	0.74	1/805 (0.1%)	0.84	1/1081 (0.1%)
72	WW	0.62	0/643	0.80	0/860
73	XX	0.68	0/1051	0.92	3/1406 (0.2%)
74	YY	0.75	0/1116	0.96	1/1490 (0.1%)
75	ZZ	0.60	0/1028	0.86	1/1366 (0.1%)
76	aa	0.59	0/604	0.70	0/810
77	bb	0.65	0/828	0.86	0/1109

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	cc	0.63	0/665	0.87	0/891
79	dd	0.57	0/490	0.78	0/656
80	ee	0.63	0/470	0.85	0/623
81	ff	0.61	0/462	0.88	0/607
82	gg	0.56	0/567	0.67	0/753
83	hh	0.56	0/2492	0.68	0/3391
84	jj	0.63	1/3333 (0.0%)	0.70	1/4483 (0.0%)
85	4	0.51	6/4586 (0.1%)	1.24	61/7136 (0.9%)
All	All	0.62	137/240370 (0.1%)	0.88	307/352528 (0.1%)

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 137 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	BB	12	GLU	CD-OE2	28.29	1.56	1.25
85	4	6182	A	O3'-P	-13.04	1.45	1.61
45	5	4520	G	O3'-P	11.08	1.74	1.61
51	BB	208	GLU	CD-OE2	10.87	1.37	1.25
71	VV	72	GLU	CD-OE2	10.83	1.37	1.25

The worst 5 of 307 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
85	4	6030	A	P-O3'-C3'	-33.29	79.75	119.70
85	4	6030	A	O3'-P-O5'	26.39	154.14	104.00
85	4	6072	U	N1-C1'-C2'	15.69	134.40	114.00
85	4	6200	A	N9-C1'-C2'	15.45	134.08	114.00
85	4	6181	C	C4'-C3'-O3'	-15.21	77.45	109.40

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 ⓘ

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/257 (92%)	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	21
4	D	291/297 (98%)	257 (88%)	29 (10%)	5 (2%)	7	36
5	E	208/291 (72%)	173 (83%)	29 (14%)	6 (3%)	3	24
6	F	223/249 (90%)	193 (86%)	24 (11%)	6 (3%)	4	26
7	G	229/242 (95%)	202 (88%)	25 (11%)	2 (1%)	14	49
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%)	5	29
11	L	208/211 (99%)	184 (88%)	19 (9%)	5 (2%)	5	29
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	28
14	O	194/199 (98%)	167 (86%)	25 (13%)	2 (1%)	13	47
15	P	151/184 (82%)	123 (82%)	22 (15%)	6 (4%)	2	18
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	21
18	S	174/176 (99%)	142 (82%)	26 (15%)	6 (3%)	3	21
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	21
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	40
27	b	100/226 (44%)	86 (86%)	10 (10%)	4 (4%)	2	18
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	18
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	36
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
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	32
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	32
48	K	204/217 (94%)	143 (70%)	51 (25%)	10 (5%)	2	14
51	BB	215/295 (73%)	193 (90%)	19 (9%)	3 (1%)	9	40
52	CC	211/264 (80%)	174 (82%)	33 (16%)	4 (2%)	6	34
53	DD	219/255 (86%)	185 (84%)	30 (14%)	4 (2%)	7	35
54	EE	226/281 (80%)	187 (83%)	36 (16%)	3 (1%)	10	41
55	FF	260/263 (99%)	212 (82%)	37 (14%)	11 (4%)	2	17
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	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	26
61	LL	94/149 (63%)	84 (89%)	9 (10%)	1 (1%)	12	44
62	MM	139/158 (88%)	120 (86%)	16 (12%)	3 (2%)	5	30
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%)	19	54
66	QQ	113/145 (78%)	83 (74%)	26 (23%)	4 (4%)	3	20
67	RR	140/172 (81%)	123 (88%)	16 (11%)	1 (1%)	19	54
68	SS	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	51
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	40
71	VV	98/119 (82%)	82 (84%)	14 (14%)	2 (2%)	6	32
72	WW	81/83 (98%)	71 (88%)	6 (7%)	4 (5%)	2	14
73	XX	127/130 (98%)	107 (84%)	17 (13%)	3 (2%)	5	29
74	YY	139/143 (97%)	112 (81%)	21 (15%)	6 (4%)	2	16
75	ZZ	122/134 (91%)	103 (84%)	17 (14%)	2 (2%)	8	37
76	aa	73/125 (58%)	65 (89%)	7 (10%)	1 (1%)	9	40
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	28
79	dd	60/69 (87%)	50 (83%)	9 (15%)	1 (2%)	7	36
80	ee	53/56 (95%)	33 (62%)	18 (34%)	2 (4%)	2	18
81	ff	55/133 (41%)	44 (80%)	9 (16%)	2 (4%)	3	20
82	gg	66/156 (42%)	49 (74%)	16 (24%)	1 (2%)	8	38
83	hh	310/317 (98%)	237 (76%)	69 (22%)	4 (1%)	10	41
84	jj	414/437 (95%)	344 (83%)	65 (16%)	5 (1%)	11	43
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

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

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/199 (86%)	146 (85%)	26 (15%)	2	12
2	B	342/348 (98%)	290 (85%)	52 (15%)	2	12
3	C	302/323 (94%)	267 (88%)	35 (12%)	4	21
4	D	247/250 (99%)	220 (89%)	27 (11%)	5	23
5	E	190/251 (76%)	169 (89%)	21 (11%)	5	22
6	F	196/218 (90%)	178 (91%)	18 (9%)	7	29
7	G	200/208 (96%)	181 (90%)	19 (10%)	7	28
8	H	169/171 (99%)	159 (94%)	10 (6%)	16	48
9	I	175/181 (97%)	154 (88%)	21 (12%)	4	19
10	J	143/149 (96%)	133 (93%)	10 (7%)	12	42
11	L	175/176 (99%)	162 (93%)	13 (7%)	11	40
12	M	116/151 (77%)	99 (85%)	17 (15%)	2	12
13	N	171/172 (99%)	150 (88%)	21 (12%)	4	19
14	O	170/171 (99%)	144 (85%)	26 (15%)	2	11
15	P	134/163 (82%)	116 (87%)	18 (13%)	3	15
16	Q	164/165 (99%)	137 (84%)	27 (16%)	2	9
17	R	159/160 (99%)	138 (87%)	21 (13%)	3	16
18	S	157/157 (100%)	140 (89%)	17 (11%)	5	23
19	T	139/140 (99%)	122 (88%)	17 (12%)	4	19
20	U	89/114 (78%)	85 (96%)	4 (4%)	23	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	V	100/107 (94%)	83 (83%)	17 (17%)	1	8
22	W	86/126 (68%)	81 (94%)	5 (6%)	17	49
23	X	106/134 (79%)	94 (89%)	12 (11%)	4	22
24	Y	124/135 (92%)	104 (84%)	20 (16%)	2	9
25	Z	117/118 (99%)	101 (86%)	16 (14%)	3	14
26	a	119/120 (99%)	104 (87%)	15 (13%)	3	18
27	b	84/172 (49%)	80 (95%)	4 (5%)	21	55
28	c	84/98 (86%)	72 (86%)	12 (14%)	2	13
29	d	98/110 (89%)	91 (93%)	7 (7%)	12	42
30	e	114/121 (94%)	100 (88%)	14 (12%)	4	19
31	f	88/89 (99%)	73 (83%)	15 (17%)	1	8
32	g	98/106 (92%)	86 (88%)	12 (12%)	4	19
33	h	109/110 (99%)	97 (89%)	12 (11%)	5	23
34	i	86/89 (97%)	77 (90%)	9 (10%)	5	24
35	j	73/80 (91%)	63 (86%)	10 (14%)	3	14
36	k	64/65 (98%)	57 (89%)	7 (11%)	5	23
37	l	47/48 (98%)	39 (83%)	8 (17%)	1	8
38	m	48/48 (100%)	40 (83%)	8 (17%)	2	9
39	n	24/24 (100%)	21 (88%)	3 (12%)	3	18
40	o	92/94 (98%)	76 (83%)	16 (17%)	1	8
41	p	74/75 (99%)	60 (81%)	14 (19%)	1	6
42	r	108/121 (89%)	96 (89%)	12 (11%)	5	22
43	s	164/258 (64%)	159 (97%)	5 (3%)	36	66
44	t	126/163 (77%)	117 (93%)	9 (7%)	12	42
48	K	190/196 (97%)	172 (90%)	18 (10%)	7	28
51	BB	180/246 (73%)	169 (94%)	11 (6%)	15	47
52	CC	194/231 (84%)	179 (92%)	15 (8%)	10	39
53	DD	187/206 (91%)	164 (88%)	23 (12%)	4	19
54	EE	190/232 (82%)	162 (85%)	28 (15%)	2	12
55	FF	224/225 (100%)	196 (88%)	28 (12%)	3	18
56	GG	158/170 (93%)	141 (89%)	17 (11%)	5	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	HH	207/218 (95%)	189 (91%)	18 (9%)	8	32
58	II	165/174 (95%)	140 (85%)	25 (15%)	2	12
59	JJ	178/180 (99%)	157 (88%)	21 (12%)	4	20
60	KK	161/168 (96%)	143 (89%)	18 (11%)	5	22
61	LL	87/125 (70%)	80 (92%)	7 (8%)	10	37
62	MM	130/142 (92%)	110 (85%)	20 (15%)	2	11
63	NN	99/108 (92%)	94 (95%)	5 (5%)	20	53
64	OO	130/131 (99%)	113 (87%)	17 (13%)	3	16
65	PP	106/119 (89%)	91 (86%)	15 (14%)	2	13
66	QQ	105/130 (81%)	93 (89%)	12 (11%)	4	21
67	RR	117/140 (84%)	109 (93%)	8 (7%)	13	43
68	SS	119/121 (98%)	108 (91%)	11 (9%)	7	29
69	TT	125/132 (95%)	113 (90%)	12 (10%)	7	28
70	UU	111/116 (96%)	103 (93%)	8 (7%)	12	41
71	VV	92/107 (86%)	79 (86%)	13 (14%)	3	14
72	WW	67/67 (100%)	61 (91%)	6 (9%)	8	30
73	XX	112/113 (99%)	100 (89%)	12 (11%)	5	24
74	YY	113/114 (99%)	100 (88%)	13 (12%)	4	21
75	ZZ	107/115 (93%)	90 (84%)	17 (16%)	2	10
76	aa	66/103 (64%)	64 (97%)	2 (3%)	36	66
77	bb	88/98 (90%)	77 (88%)	11 (12%)	3	18
78	cc	75/76 (99%)	68 (91%)	7 (9%)	7	29
79	dd	55/62 (89%)	54 (98%)	1 (2%)	54	77
80	ee	48/49 (98%)	43 (90%)	5 (10%)	5	25
81	ff	47/106 (44%)	41 (87%)	6 (13%)	3	17
82	gg	61/140 (44%)	55 (90%)	6 (10%)	6	27
83	hh	272/275 (99%)	243 (89%)	29 (11%)	5	24
84	jj	358/376 (95%)	323 (90%)	35 (10%)	6	27
All	All	10567/11789 (90%)	9385 (89%)	1182 (11%)	7	22

5 of 1182 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
62	MM	126	VAL
83	hh	289	LEU
65	PP	25	GLU
62	MM	122	ILE
73	XX	30	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
59	JJ	111	GLN
81	ff	88	GLN
61	LL	7	ASN
67	RR	86	GLN
19	T	127	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	5	3562/3594 (99%)	1631 (45%)	283 (7%)
46	7	118/119 (99%)	40 (33%)	5 (4%)
47	8	149/151 (98%)	61 (40%)	5 (3%)
49	2	1681/1697 (99%)	713 (42%)	107 (6%)
50	3	86/87 (98%)	44 (51%)	5 (5%)
85	4	193/194 (99%)	123 (63%)	28 (14%)
All	All	5789/5842 (99%)	2612 (45%)	433 (7%)

5 of 2612 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

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Mol	Chain	Res	Type
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

*Continued on next page...*

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	1696:C	O3'	1720:C	P	19.72

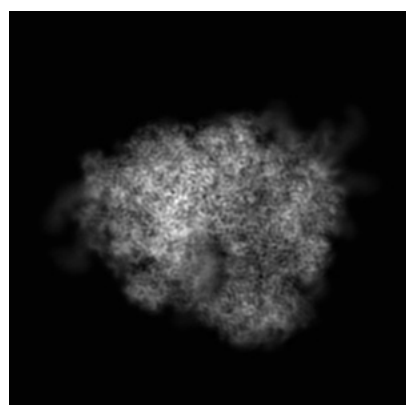
## 6 Map visualisation [i](#)

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.

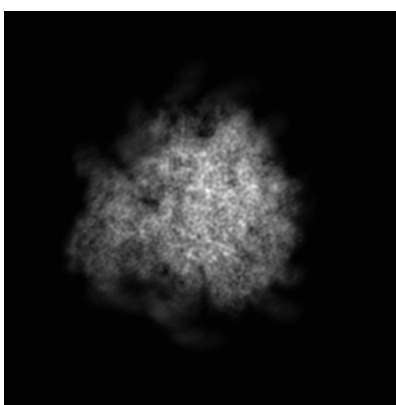
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

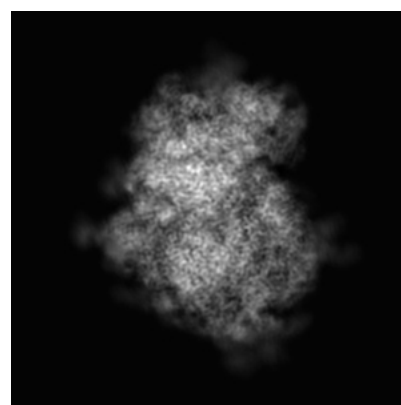
#### 6.1.1 Primary map



X



Y

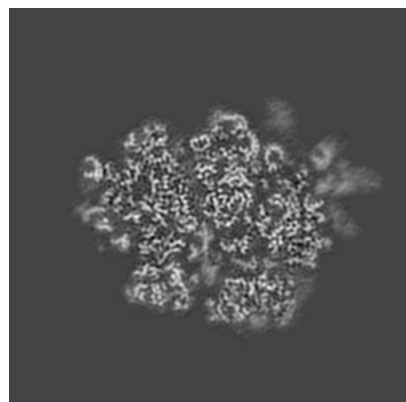


Z

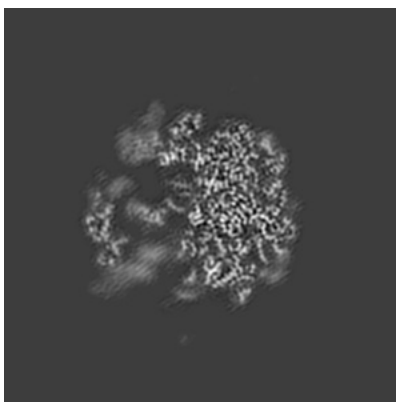
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

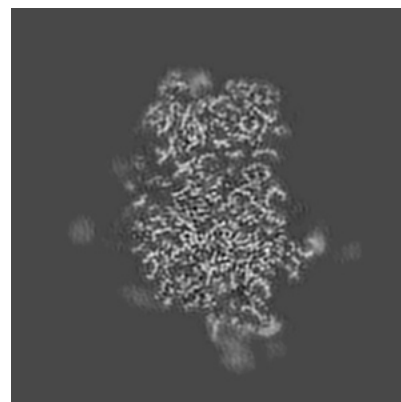
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

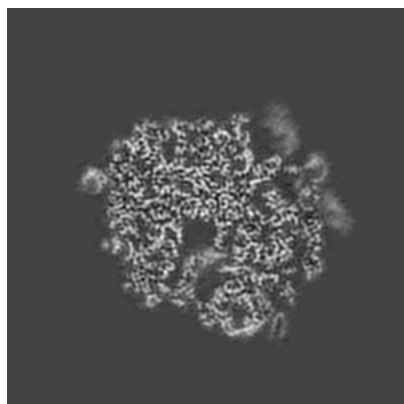


Z Index: 200

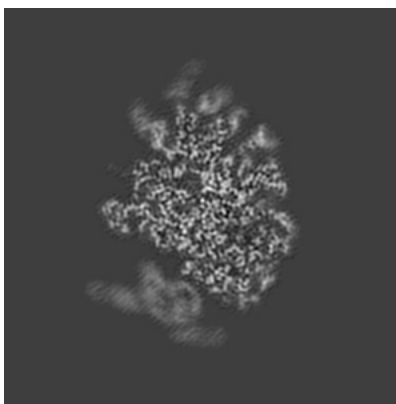
The images above show central slices of the map in three orthogonal directions.

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

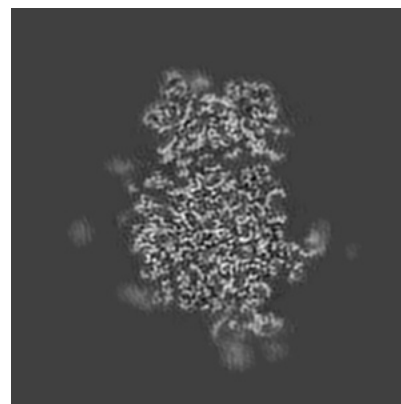
### 6.3.1 Primary map



X Index: 186



Y Index: 166

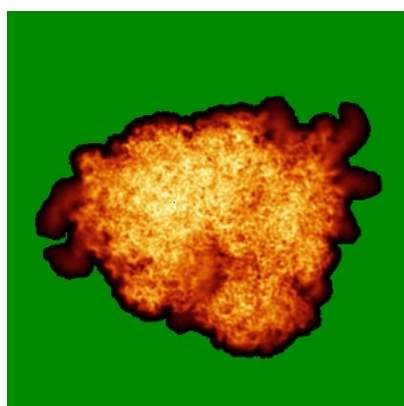


Z Index: 203

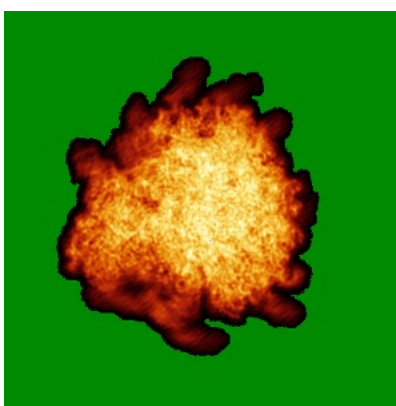
The images above show the largest variance slices of the map in three orthogonal directions.

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

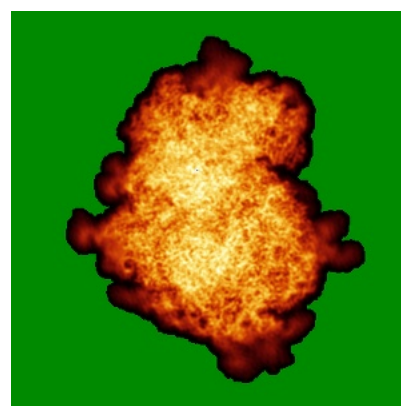
### 6.4.1 Primary map



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.

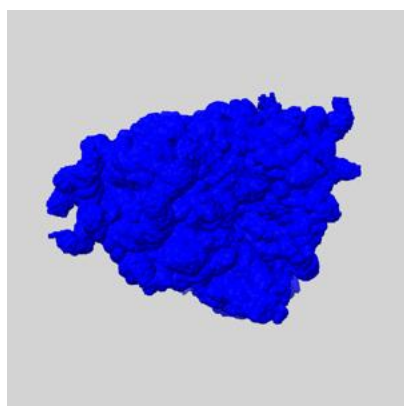
## 6.6 Mask visualisation [i](#)

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

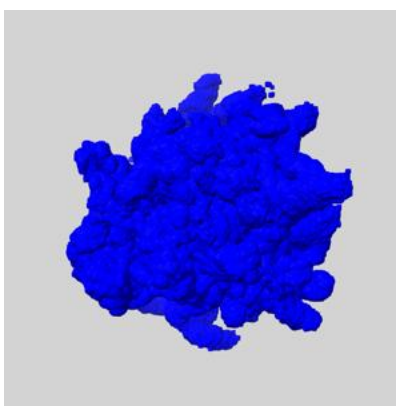
A mask typically either:

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

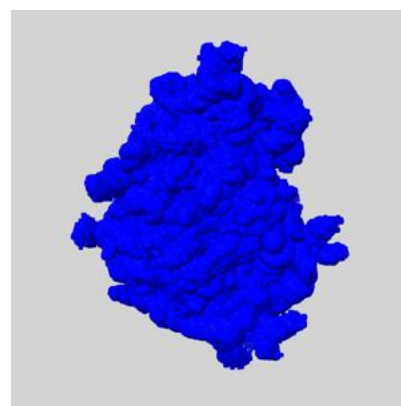
### 6.6.1 emd\_7834\_msk\_1.map [i](#)



X



Y

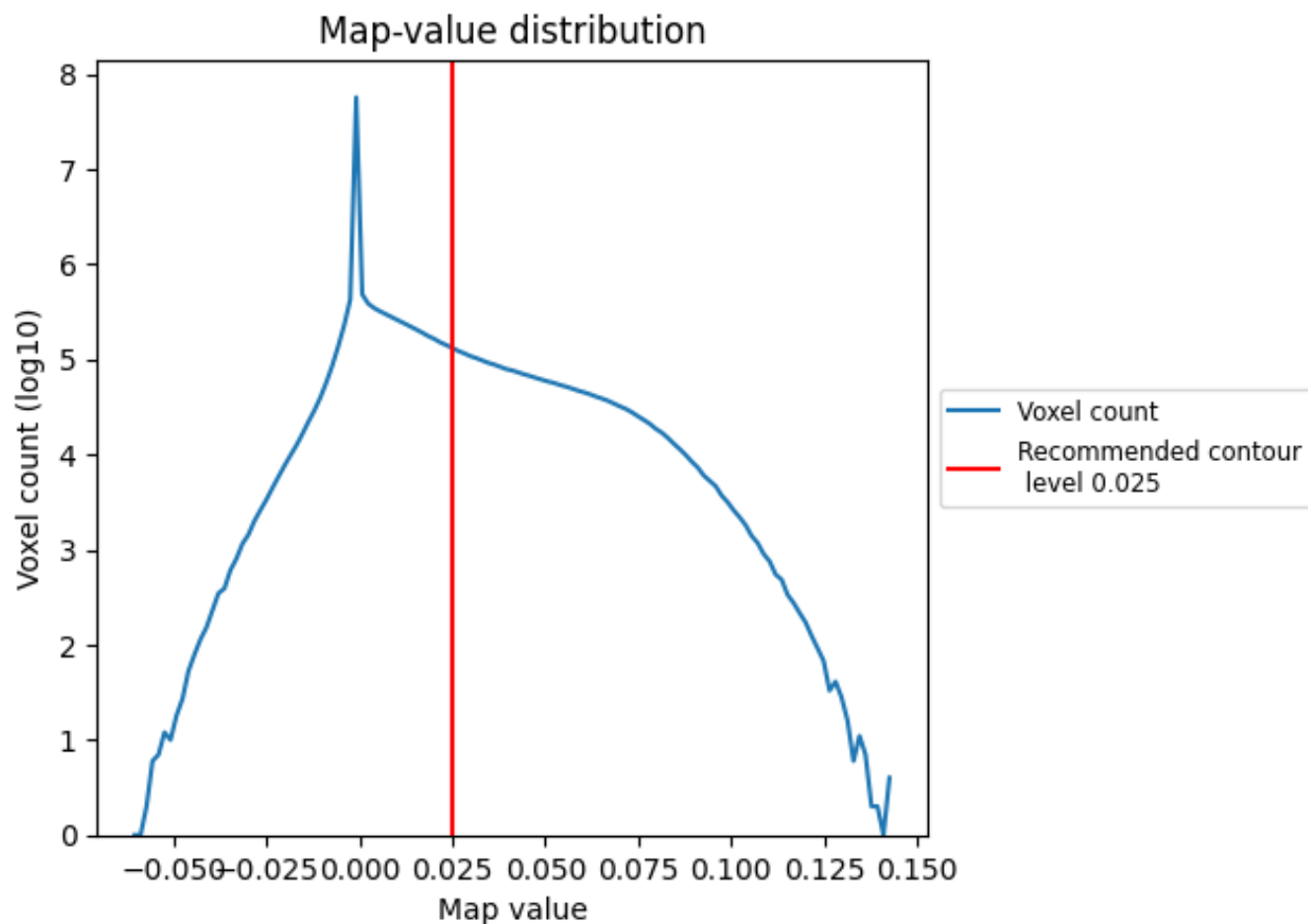


Z

## 7 Map analysis [i](#)

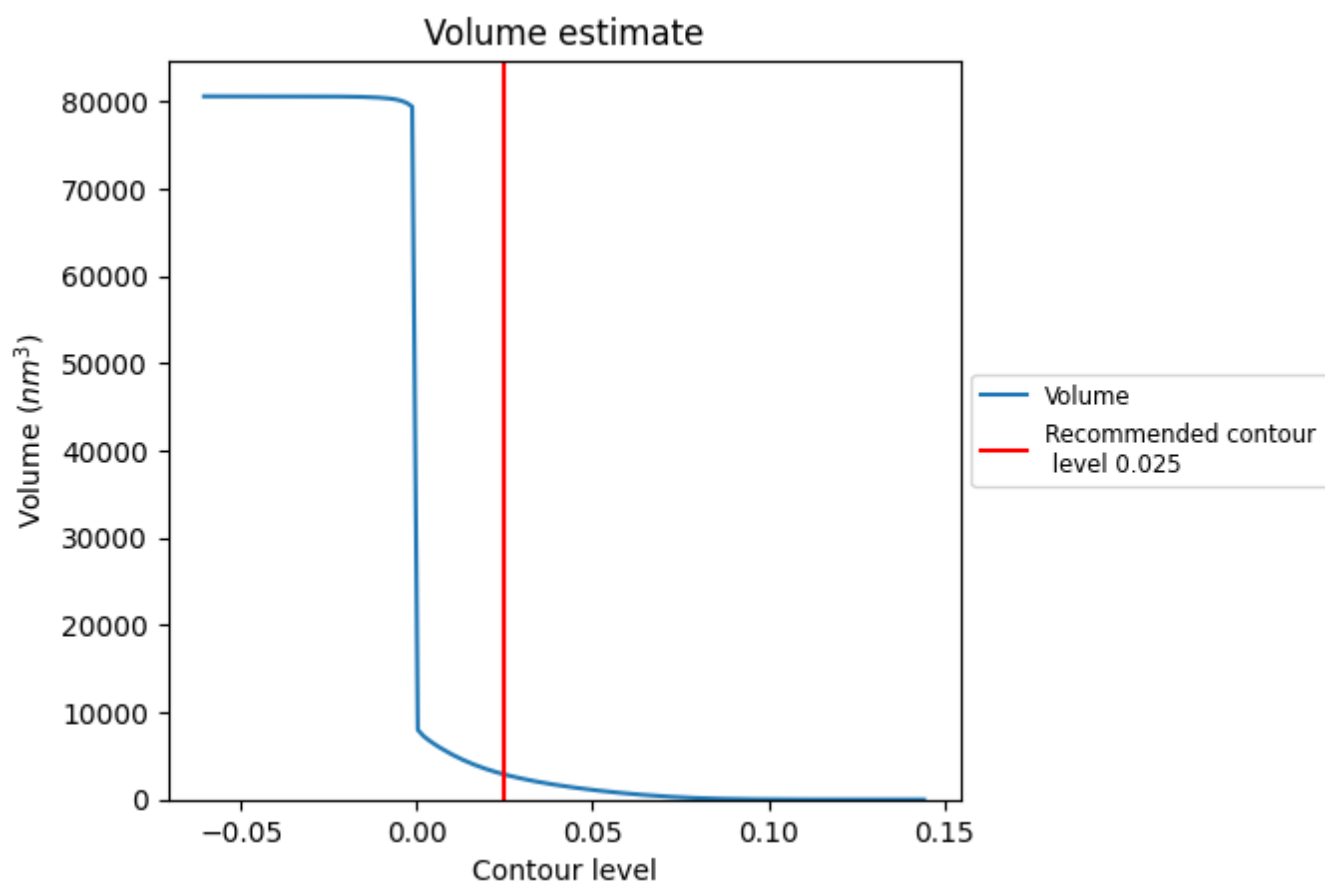
This section contains the results of statistical analysis of the map.

### 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](#)

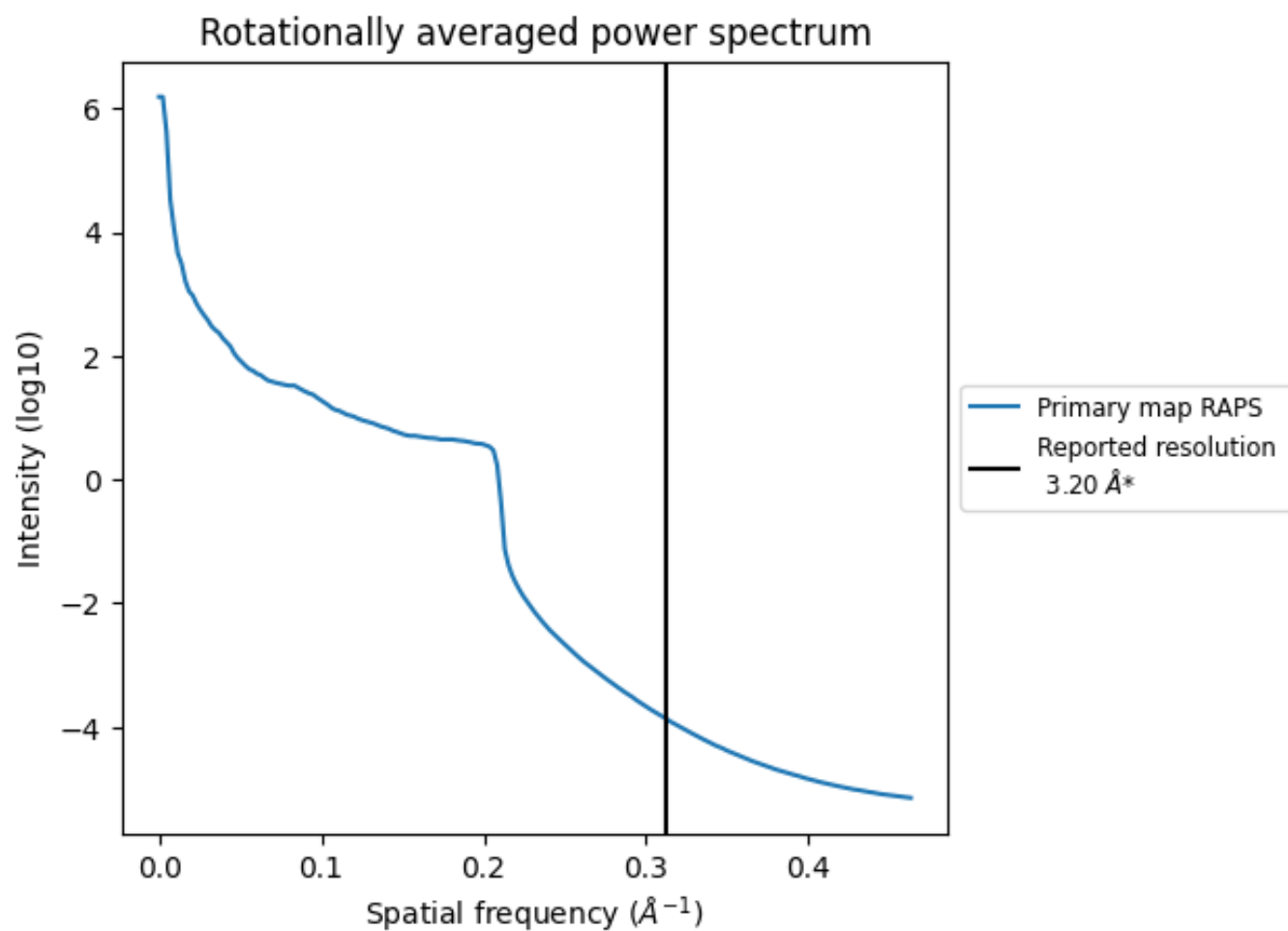


The volume at the recommended contour level is 2873 nm<sup>3</sup>; this corresponds to an approximate mass of 2595 kDa.

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 ⓘ

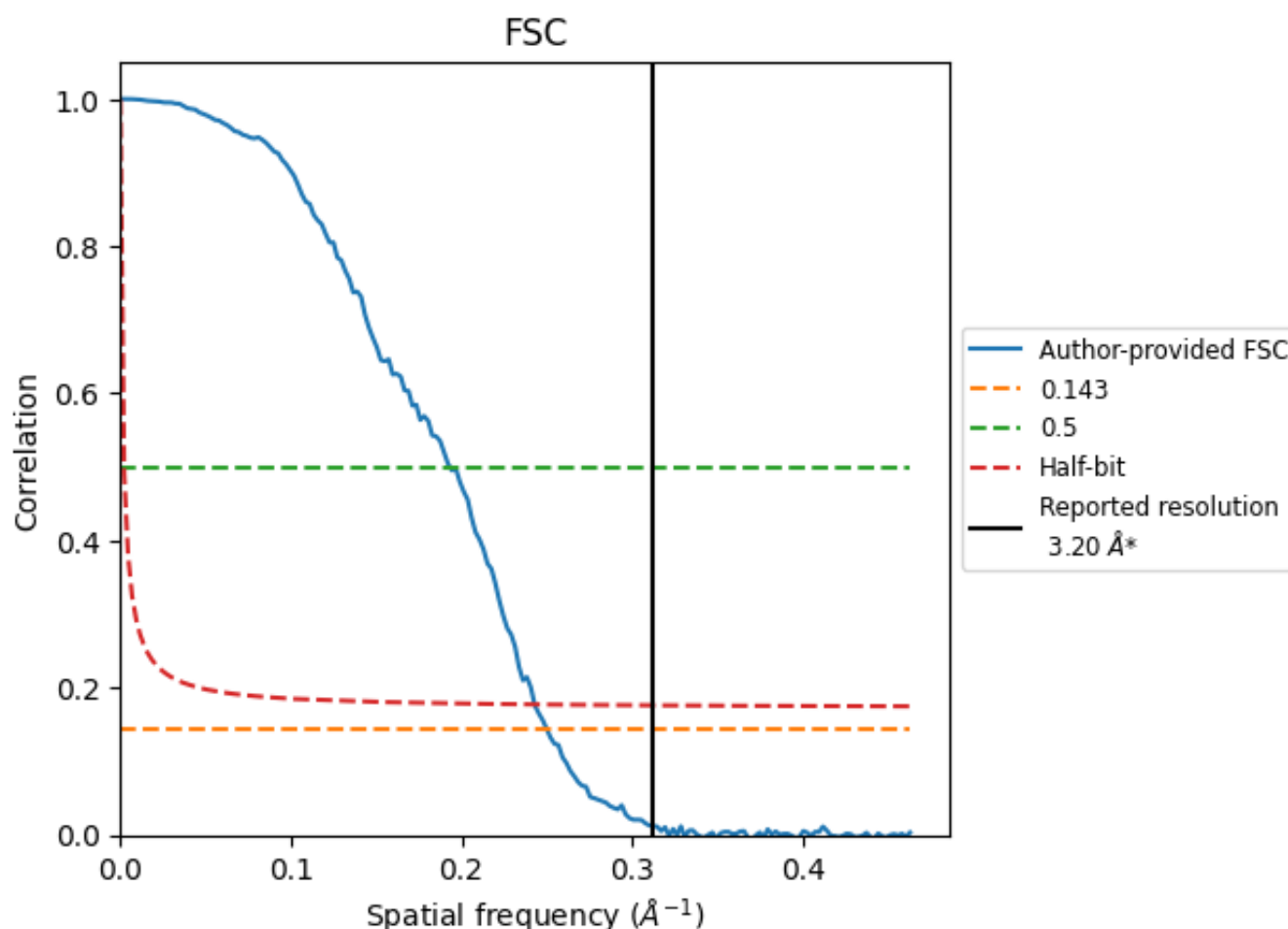


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 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](#)

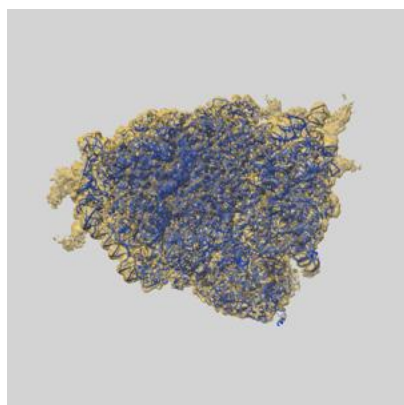
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	4.00	5.17	4.12
Unmasked-calculated*	-	-	-

\*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 %

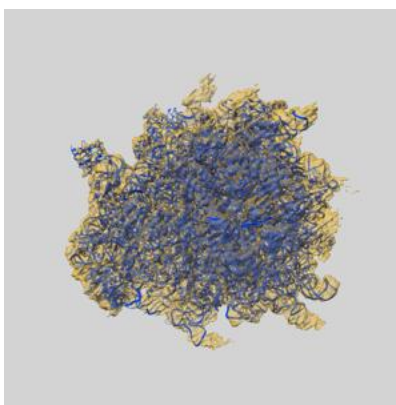
## 9 Map-model fit [i](#)

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](#).

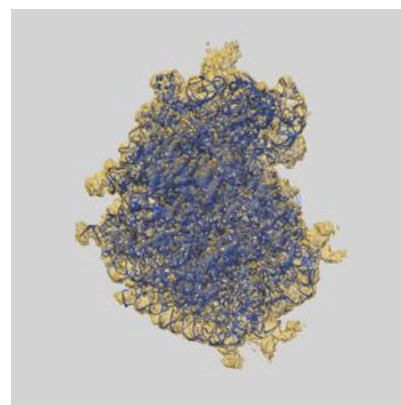
### 9.1 Map-model overlay [i](#)



X



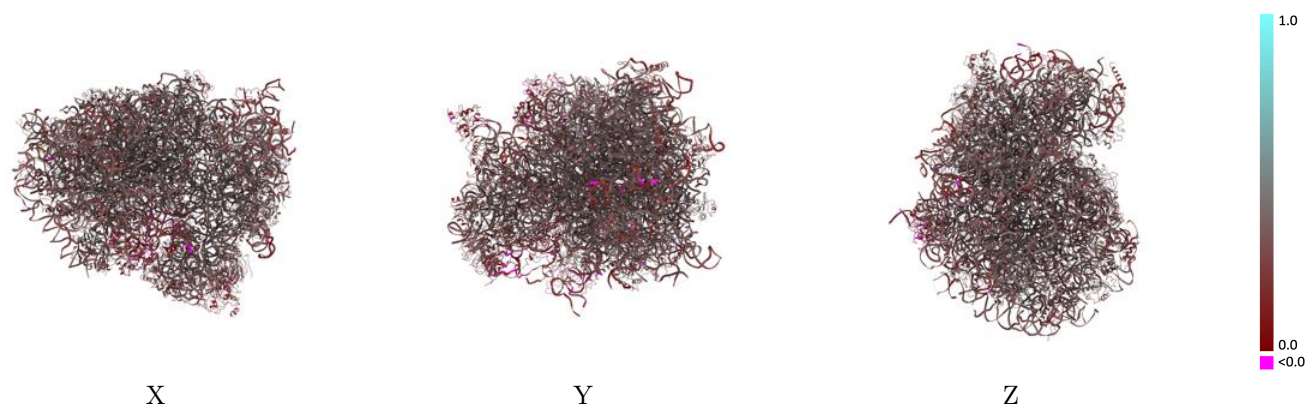
Y



Z

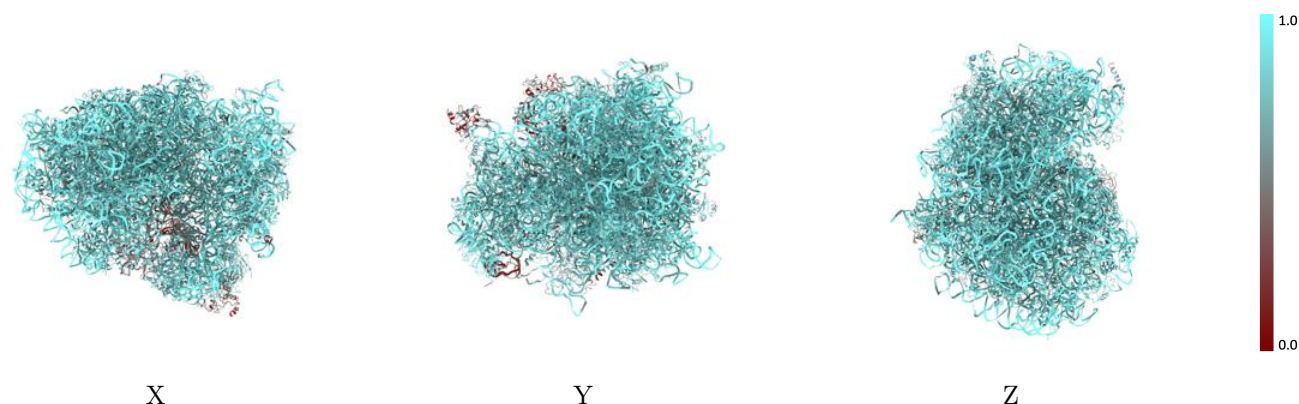
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



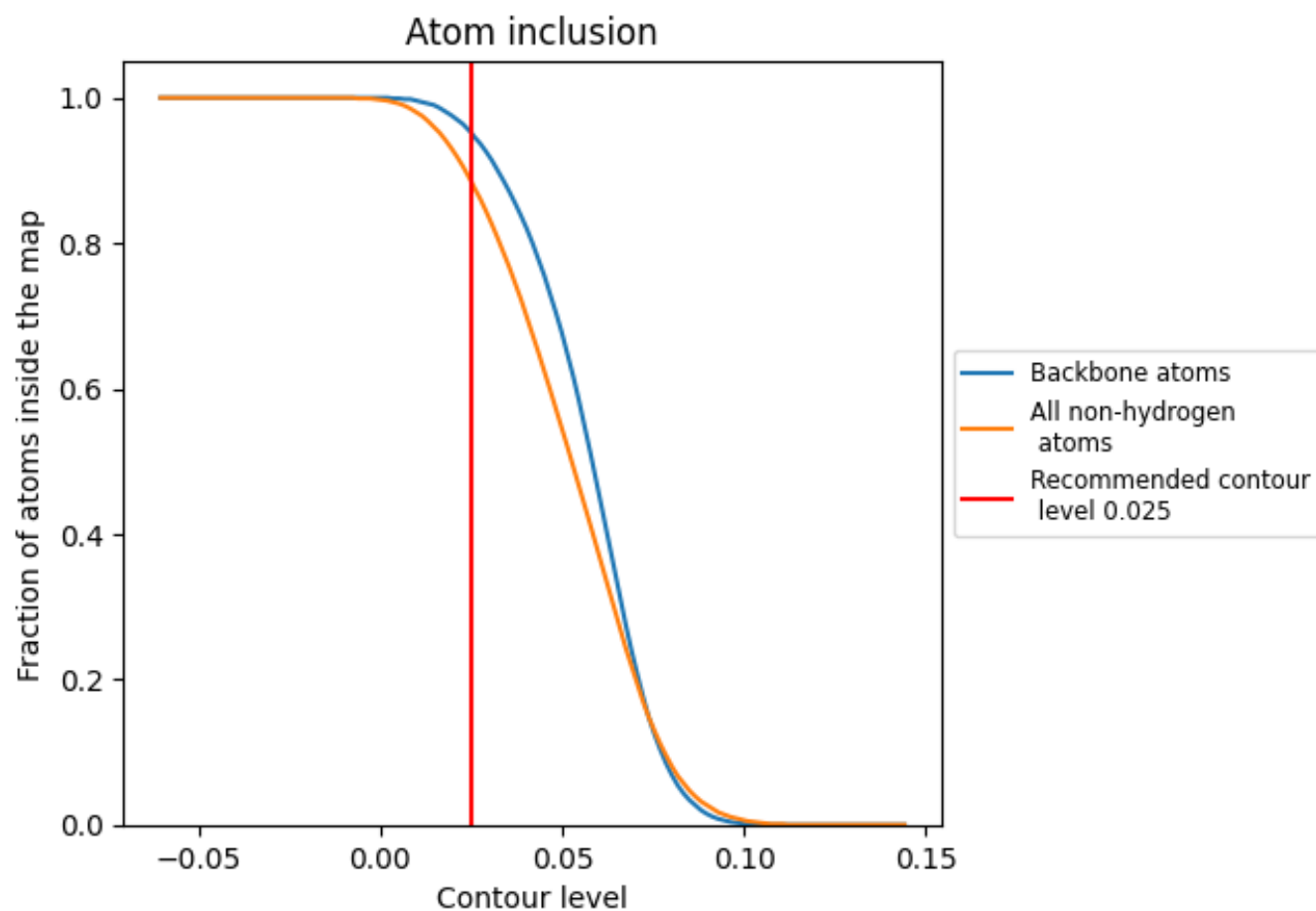
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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