



wwPDB EM Validation Summary Report ⓘ

Dec 19, 2022 – 05:53 am GMT

PDB ID : 7NWI
EMDB ID : EMD-12633
Title : Mammalian pre-termination 80S ribosome with Empty-A site bound by Blasticidin S
Authors : Powers, K.T.; Yadav, S.K.N.; Bufton, J.C.; Schaffitzel, C.
Deposited on : 2021-03-16
Resolution : 3.13 Å(reported)
Based on initial model : 3JAH

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

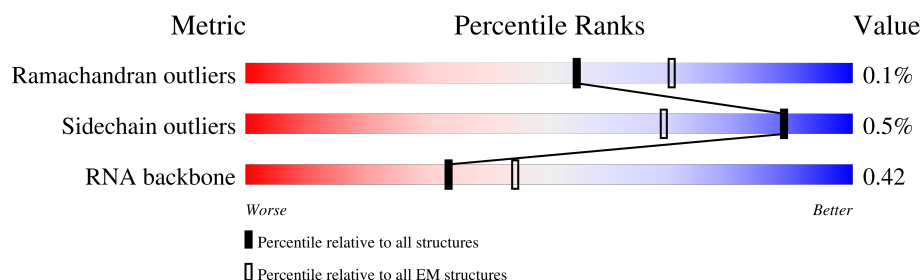
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.13 Å.

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




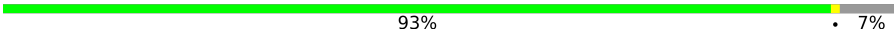
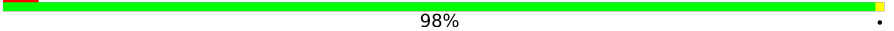

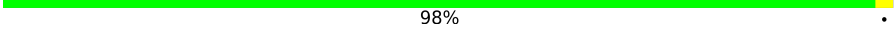
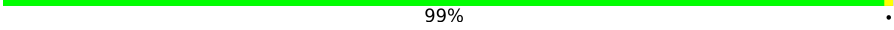
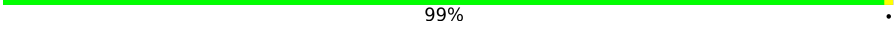
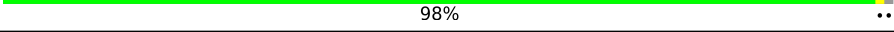

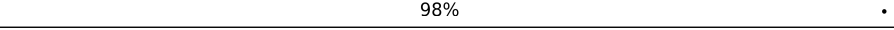
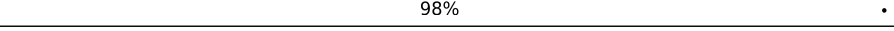
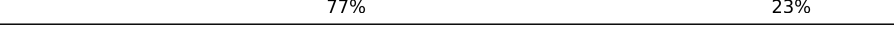
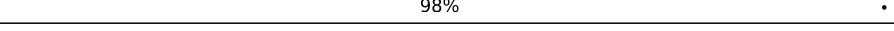


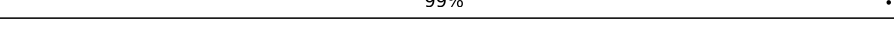
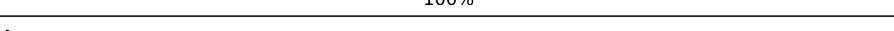


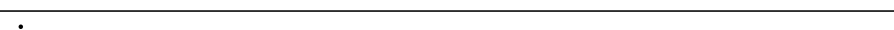

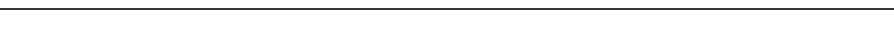
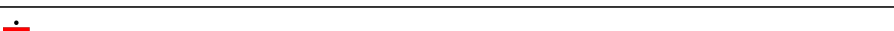


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	244	98%
2	B	403	98%
3	C	425	84%
4	D	297	98%
5	E	291	6%
6	F	249	88%
7	G	241	7%
8	H	190	99%



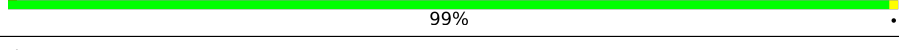
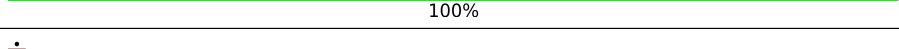
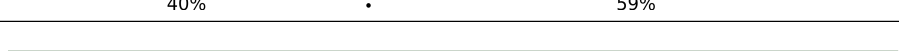
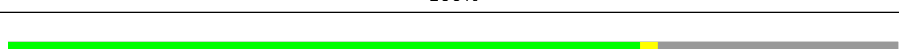
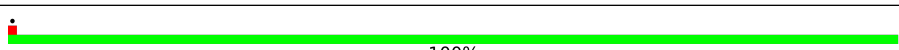


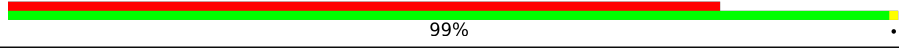

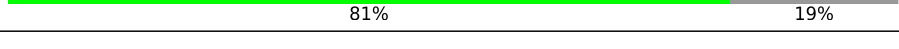
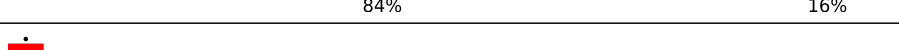

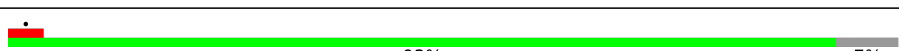

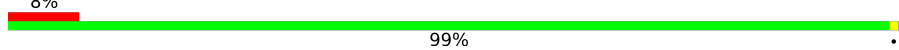
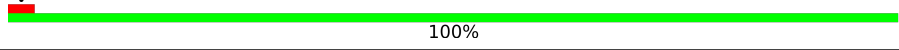
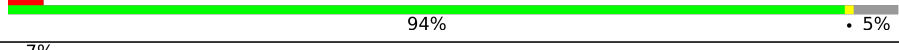
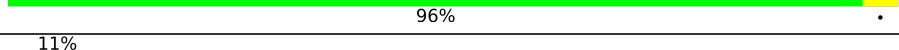
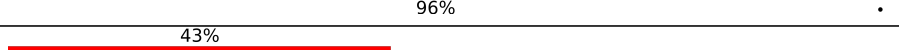
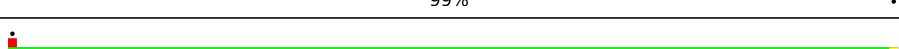



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Mol	Chain	Length	Quality of chain
9	I	214	 94% . 5%
10	J	181	 93% . 7%
11	L	211	 98% .
12	M	218	 62% . 37%
13	N	203	 98% .
14	O	199	 99% .
15	P	153	 99% .
16	Q	188	 98% ..
17	R	196	 90% . 8%
18	S	175	 98% .
19	T	159	 98% .
20	U	128	 77% 23%
21	V	131	 98% .
22	W	134	 46% . 53%
23	X	156	 75% . 24%
24	Y	134	 99% .
25	Z	135	 100%
26	a	160	 89% . 8%
27	b	245	 31% 69%
28	c	115	 81% . 18%
29	d	107	 99% .
30	e	128	 99% .
31	f	109	 99% .
32	g	126	 90% . 10%
33	h	122	 100%




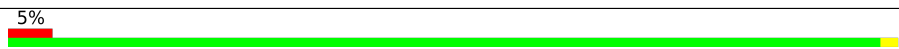
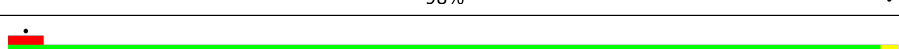
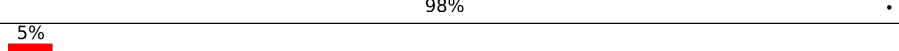
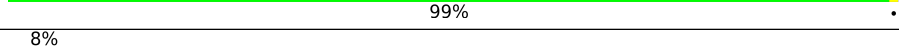
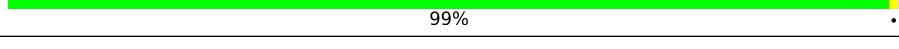
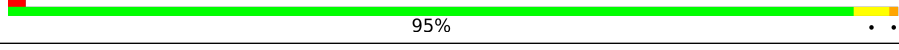
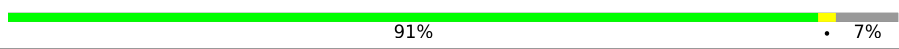
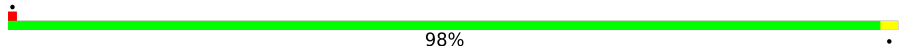

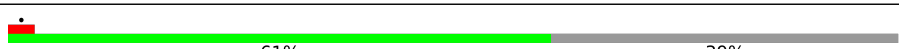


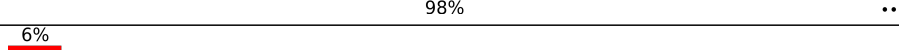

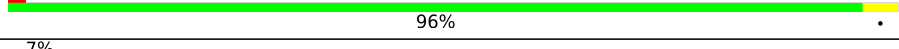

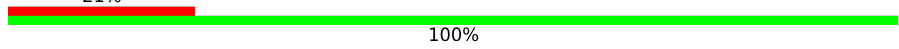
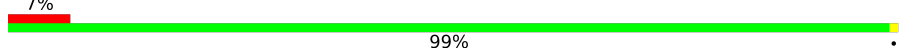
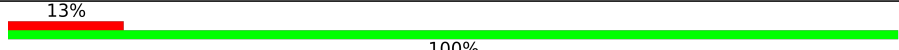


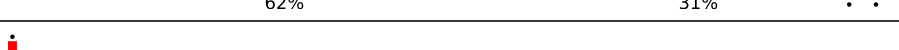
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Mol	Chain	Length	Quality of chain
34	i	117	
35	j	97	
36	k	69	
37	l	50	
38	m	128	
39	n	23	
40	o	142	
41	p	91	
42	r	137	
43	s	318	
44	t	163	
45	AA	295	
46	BB	264	
47	CC	259	
48	DD	281	
49	EE	262	
50	FF	205	
51	GG	262	
52	HH	190	
53	II	206	
54	JJ	194	
55	KK	98	
56	LL	158	
57	MM	124	
58	NN	150	

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Mol	Chain	Length	Quality of chain
59	OO	168	
60	PP	145	
61	QQ	157	
62	RR	129	
63	SS	137	
64	TT	141	
65	UU	104	
66	VV	83	
67	WW	139	
68	XX	141	
69	YY	146	
70	ZZ	123	
71	aa	117	
72	bb	84	
73	cc	69	
74	dd	53	
75	ee	133	
76	ff	62	
77	gg	313	
78	1	15	
79	2	76	
80	5	3788	
81	7	120	
82	8	156	
83	9	1777	

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Mol	Chain	Length	Quality of chain
84	K	10	<div><div></div><div></div><div></div><div></div></div>

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 377740 atoms, of which 160811 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 L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	244	Total	C	H	N	O	S	0	0
			3819	1169	1955	382	307	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	394	Total	C	H	N	O	S	0	0
			6419	2008	3268	591	539	13		

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	361	Total	C	H	N	O	S	0	0
			5924	1808	3049	576	477	14		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	292	Total	C	H	N	O	S	0	0
			4805	1509	2419	437	426	14		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	MET	-	initiating methionine	UNP G1SYJ6

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	236	Total	C	H	N	O	S	0	0
			3931	1215	2033	362	318	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	126	ARG	LYS	conflict	UNP G1SKF7
E	217	GLN	LYS	conflict	UNP G1SKF7

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	225	Total	C	H	N	O	S	0	0
			3862	1202	1992	358	301	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	175	ALA	THR	conflict	UNP G1SV32
F	185	GLY	ASN	conflict	UNP G1SV32
F	202	ARG	HIS	conflict	UNP G1SV32
F	233	GLU	GLY	conflict	UNP G1SV32

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

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	237	Total	C	H	N	O	S	0	0
			3954	1213	2051	365	321	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	191	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	190	Total	C	H	N	O	S	0	0
			3113	954	1597	284	272	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	204	Total	C	H	N	O	S	0	0
			3359	1051	1704	319	272	13		

- Molecule 10 is a protein called Ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	169	Total	C	H	N	O	S	0	0
			2739	855	1386	252	240	6		

- Molecule 11 is a protein called L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	L	210	Total	C	H	N	O	S	0	0
			3521	1065	1818	354	280	4		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	52	SER	ALA	conflict	UNP G1TKB3
L	55	LEU	ILE	conflict	UNP G1TKB3
L	74	ARG	HIS	conflict	UNP G1TKB3
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 12 is a protein called Ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	138	Total	C	H	N	O	S	0	0
			2346	727	1209	221	182	7		

- Molecule 13 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	203	Total	C	H	N	O	S	0	0
			3450	1072	1749	359	266	4		

- Molecule 14 is a protein called L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	199	Total	C	H	N	O	S	0	0
			3415	1056	1777	321	256	5		

- Molecule 15 is a protein called L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	153	Total	C	H	N	O	S	0	0
			2511	776	1269	241	216	9		

- Molecule 16 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	187	Total	C	H	N	O	S	0	0
			3129	941	1623	311	249	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	77	GLY	ASN	conflict	UNP F6QKI9
Q	86	ILE	VAL	conflict	UNP F6QKI9
Q	106	SER	THR	conflict	UNP F6QKI9

- Molecule 17 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	180	Total	C	H	N	O	S	0	0
			3172	933	1664	328	238	9		

- Molecule 18 is a protein called L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	175	Total	C	H	N	O	S	0	0
			2948	925	1494	284	235	10		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	159	Total	C	H	N	O	S	0	0
			2664	823	1366	252	217	6		

- Molecule 20 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	99	Total	C	H	N	O	S	0	0
			1636	518	828	141	147	2		

- Molecule 21 is a protein called eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	131	Total	C	H	N	O	S	0	0
			2018	618	1039	184	172	5		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	63	Total	C	H	N	O	S	0	0
			1069	337	541	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	119	Total	C	H	N	O	S	0	0
			2029	624	1053	183	168	1		

- Molecule 24 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	134	Total	C	H	N	O	S	0	0
			2318	700	1203	226	186	3		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	147	Total	C	H	N	O	S	0	0
			2367	734	1205	239	185	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	75	Total	C	H	N	O	S	0	0
			1259	378	650	130	98	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	c	94	Total	C	H	N	O	S	0	0
			1501	465	769	130	131	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	34	THR	SER	conflict	UNP G1TDL2
c	95	ALA	SER	conflict	UNP G1TDL2

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	107	Total	C	H	N	O	S	0	0
			1818	560	930	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	e	128	Total	C	H	N	O	S	0	0
			2200	667	1147	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	f	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	143	4		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
32	g	114	Total	C	H	N	O	S	0	0
			1907	566	1001	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	h	122	Total	C	H	N	O	S	0	0
			2160	640	1147	204	168	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
34	i	102	Total	C	H	N	O	S	0	0
			1744	520	914	176	129	5		

- Molecule 35 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	j	86	Total	C	H	N	O	S	0	0
			1442	434	737	155	111	5		

- Molecule 36 is a protein called L38.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

- Molecule 37 is a protein called ribosomal protein eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	l	50	Total	C	H	N	O	S	0	0
			927	281	483	98	64	1		

- Molecule 38 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	m	52	Total	C	H	N	O	S	0	0
			894	266	465	90	67	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	54	LEU	ARG	conflict	UNP A0A6P4TG29
m	74	HIS	ARG	conflict	UNP A0A6P4TG29

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

Mol	Chain	Residues	Atoms						AltConf	Trace
39	n	23	Total	C	H	N	O	S	0	0
			486	134	264	61	25	2		

- Molecule 40 is a protein called LOW QUALITY PROTEIN: 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	o	104	Total	C	H	N	O	S	0	0
			1772	533	921	174	138	6		

- Molecule 41 is a protein called ribosomal protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	p	91	Total	C	H	N	O	S	0	0
			1467	445	759	136	120	7		

- Molecule 42 is a protein called eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	r	125	Total	C	H	N	O	S	0	0
			2061	621	1060	206	168	6		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
43	s	198	Total	C	H	N	O	S	0	0
			3098	969	1575	265	280	9		

- Molecule 44 is a protein called L12.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	t	163	Total	C	H	N	O	S	0	0
			2533	773	1295	230	230	5		

- Molecule 45 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	AA	208	Total	C	H	N	O	S	0	0
			3288	1045	1646	289	300	8		

- Molecule 46 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	BB	213	Total	C	H	N	O	S	0	0
			3533	1098	1804	309	308	14		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CC	218	Total	C	H	N	O	S	0	0
			3472	1102	1780	287	296	7		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CC	61	LEU	ILE	conflict	UNP O55214
CC	73	VAL	MET	conflict	UNP O55214
CC	101	ALA	SER	conflict	UNP O55214
CC	119	ALA	GLY	conflict	UNP O55214
CC	142	LYS	GLU	conflict	UNP O55214
CC	215	LEU	MET	conflict	UNP O55214
CC	227	TRP	ARG	conflict	UNP O55214

- Molecule 48 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	DD	227	Total	C	H	N	O	S	0	0
			3622	1124	1858	317	315	8		

- Molecule 49 is a protein called S4.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	EE	262	Total	C	H	N	O	S	0	0
			4248	1323	2175	384	357	9		

- Molecule 50 is a protein called Ribosomal protein S5.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	FF	191	Total	C	H	N	O	S	0	0
			3072	943	1563	286	273	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FF	0	MET	-	initiating methionine	UNP G1TFM5

- Molecule 51 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	GG	237	Total	C	H	N	O	S	0	0
			4010	1200	2087	387	329	7		

- Molecule 52 is a protein called ribosomal protein eS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	HH	189	Total	C	H	N	O	S	0	0
			3137	969	1616	280	271	1		

- Molecule 53 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	II	206	Total	C	H	N	O	S	0	0
			3458	1058	1772	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
II	47	ARG	GLY	variant	UNP G1TJW1

- Molecule 54 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	JJ	185	Total	C	H	N	O	S	0	0
			3165	969	1640	306	248	2		

- Molecule 55 is a protein called S10_pectin domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	KK	98	Total	C	H	N	O	S	0	0
			1682	539	855	148	134	6		

- Molecule 56 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	LL	152	Total	C	H	N	O	S	0	0
			2551	788	1313	232	212	6		

- Molecule 57 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	MM	124	Total	C	H	N	O	S	0	0
			1951	600	993	170	179	9		

- Molecule 58 is a protein called ribosomal protein uS15.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	NN	150	Total	C	H	N	O	S	0	0
			2502	773	1294	229	205	1		

- Molecule 59 is a protein called S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	OO	136	Total	C	H	N	O	S	0	0
			2055	621	1039	199	190	6		

- Molecule 60 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	PP	127	Total	C	H	N	O	S	0	0
			2180	673	1120	201	179	7		

- Molecule 61 is a protein called Rps16 protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	QQ	141	Total	C	H	N	O	S	0	0
			2317	715	1193	212	194	3		

- Molecule 62 is a protein called S17.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	RR	129	Total	C	H	N	O	S	0	0
			2150	658	1103	193	191	5		

- Molecule 63 is a protein called ribosomal protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	SS	137	Total	C	H	N	O	S	0	0
			2330	714	1191	231	193	1		

- Molecule 64 is a protein called S19.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	TT	141	Total	C	H	N	O	S	0	0
			2244	692	1142	212	195	3		

- Molecule 65 is a protein called Ribosomal_S10 domain-containing protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	UU	104	Total	C	H	N	O	S	0	0
			1704	514	883	155	148	4		

- Molecule 66 is a protein called S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	VV	83	Total	C	H	N	O	S	0	0
			1270	394	634	118	119	5		

- Molecule 67 is a protein called Ribosomal protein S15a.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	WW	129	Total	C	H	N	O	S	0	0
			2114	659	1080	193	176	6		

- Molecule 68 is a protein called Ribosomal protein S23.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	XX	141	Total	C	H	N	O	S	0	0
			2265	693	1167	219	183	3		

- Molecule 69 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	YY	126	Total	C	H	N	O	S	0	0
			2113	646	1090	200	172	5		

- Molecule 70 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	ZZ	75	Total	C	H	N	O	S	0	0
			1254	382	656	111	104	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ZZ	3	MET	-	initiating methionine	UNP G1TDB3

- Molecule 71 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	aa	98	Total	C	H	N	O	S	0	0
			1609	486	828	161	129	5		

- Molecule 72 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	bb	83	Total	C	H	N	O	S	0	0
			1323	408	672	121	115	7		

- Molecule 73 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	cc	61	Total	C	H	N	O	S	0	0
			972	290	497	92	91	2		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
cc	5	HIS	ARG	conflict	UNP G1TIB4
cc	18	ILE	LEU	conflict	UNP G1TIB4
cc	20	LYS	ARG	conflict	UNP G1TIB4
cc	40	HIS	ARG	conflict	UNP G1TIB4
cc	42	THR	ILE	conflict	UNP G1TIB4

- Molecule 74 is a protein called ribosomal protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	dd	53	Total	C	H	N	O	S	0	0
			883	278	438	90	72	5		

- Molecule 75 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	ee	57	Total	C	H	N	O	S	0	0
			959	282	502	101	73	1		

- Molecule 76 is a protein called S27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	ff	62	Total	C	H	N	O	S	0	0
			1057	331	537	98	85	6		

- Molecule 77 is a protein called ribosomal protein RACK1.

Mol	Chain	Residues	Atoms						AltConf	Trace
77	gg	313	Total	C	H	N	O	S	0	0
			4830	1535	2394	424	465	12		

- Molecule 78 is a protein called Sec61Beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	1	15	Total	C	H	N	O	S	0	0
			242	82	117	20	22	1		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
79	2	76	Total	C	H	N	O	P	0	0
			2439	723	823	291	527	75		

- Molecule 80 is a RNA chain called 28S ribosomal RNA+BlaS.

Mol	Chain	Residues	Atoms						AltConf	Trace
80	5	3662	Total	C	H	N	O	P	0	0
			118122	34947	39636	14363	25515	3661		

- Molecule 81 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
81	7	120	Total	C	H	N	O	P	0	0
			3854	1141	1296	456	842	119		

- Molecule 82 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
82	8	156	Total	C	H	N	O	P	0	0
			4997	1480	1683	585	1094	155		

- Molecule 83 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
83	9	1719	Total	C	H	N	O	P	0	0
			55209	16371	18529	6586	12005	1718		

- Molecule 84 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	K	10	Total	C	N	O	P	0	0
			217	97	41	69	10		

- Molecule 85 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	B	2	Total	Mg	0
			2	2	
85	P	1	Total	Mg	0
			1	1	
85	V	1	Total	Mg	0
			1	1	
85	g	1	Total	Mg	0
			1	1	
85	j	1	Total	Mg	0
			1	1	
85	5	159	Total	Mg	0
			159	159	
85	7	5	Total	Mg	0
			5	5	
85	8	1	Total	Mg	0
			1	1	
85	9	39	Total	Mg	0
			39	39	

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 87 is BLASTICIDIN S (three-letter code: BLS) (formula: C₁₇H₂₆N₈O₅) (labeled as "Ligand of Interest" by depositor).



3 Residue-property plots

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

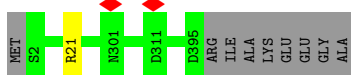
- Molecule 1: L8

Chain A:  98%




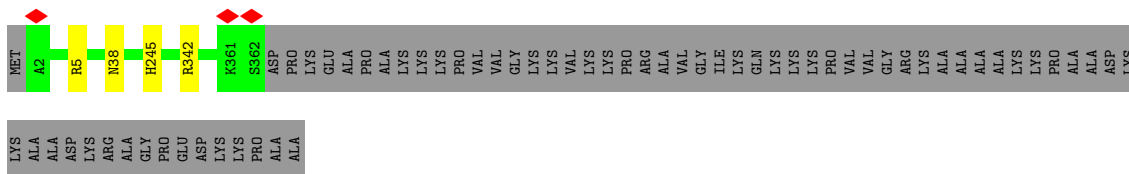
- Molecule 2: uL3

Chain B:  98%



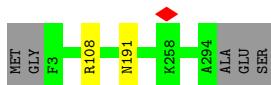
- Molecule 3: 60S ribosomal protein L4

Chain C:  84% 15%




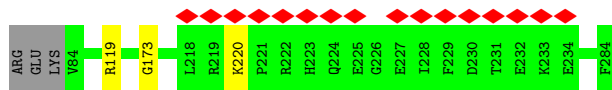
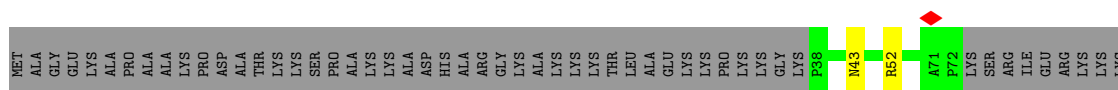
- Molecule 4: 60S ribosomal protein L5

Chain D:  98%



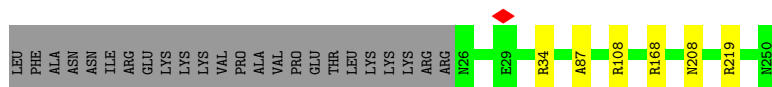
- Molecule 5: 60S ribosomal protein L6

Chain E:  6% 79% 19%



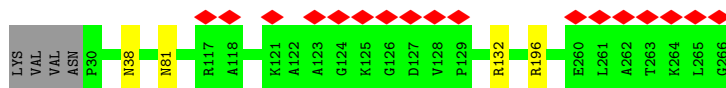
• Molecule 6: uL30

Chain F: 88% 10%



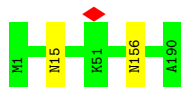
• Molecule 7: 60S ribosomal protein L7a

Chain G: 7% 97% ..



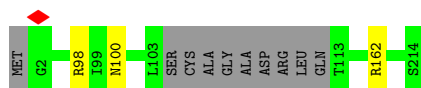
• Molecule 8: L9

Chain H: 99% .



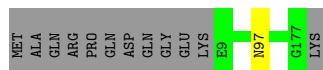
• Molecule 9: 60S ribosomal protein L10

Chain I: 94% . 5%



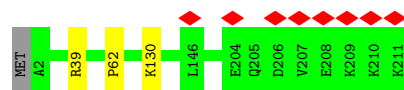
• Molecule 10: Ribosomal protein L11

Chain J: 93% . 7%

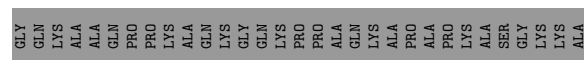
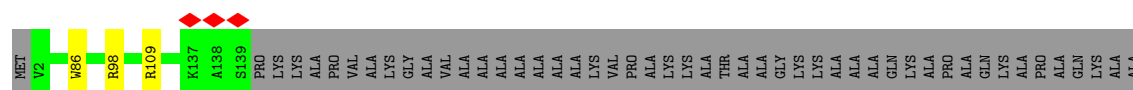


• Molecule 11: L13

Chain L: 98% .



- Molecule 12: Ribosomal protein L14



- Molecule 13: Ribosomal protein L15



- Molecule 14: L13a



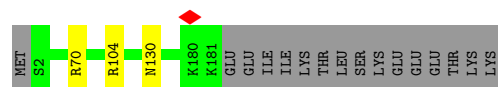
- Molecule 15: L17



- Molecule 16: Ribosomal_L18e/L15P domain-containing protein

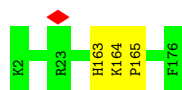


- Molecule 17: 60S ribosomal protein L19



- Molecule 18: L18a

Chain S:  98%





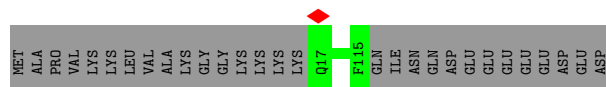
- Molecule 19: eL21

Chain T:  98%



- Molecule 20: 60S ribosomal protein L22

Chain U:  77%  23%



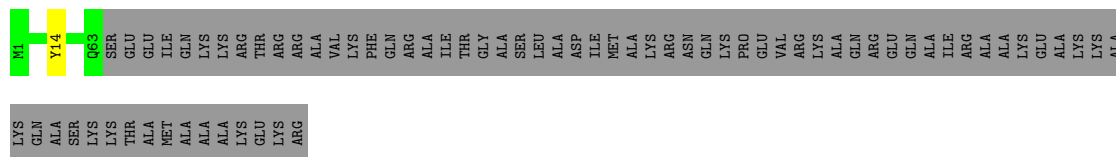
- Molecule 21: eL14

Chain V:  98%





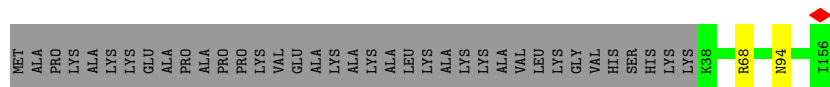
- Molecule 22: 60S ribosomal protein L24-like protein

Chain W:  46%  53%



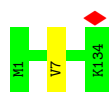
- Molecule 23: uL23

Chain X:  75%  24%



- Molecule 24: Ribosomal protein L26

Chain Y:  99%



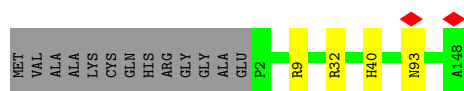
- Molecule 25: 60S ribosomal protein L27

Chain Z: 100%

There are no outlier residues recorded for this chain.

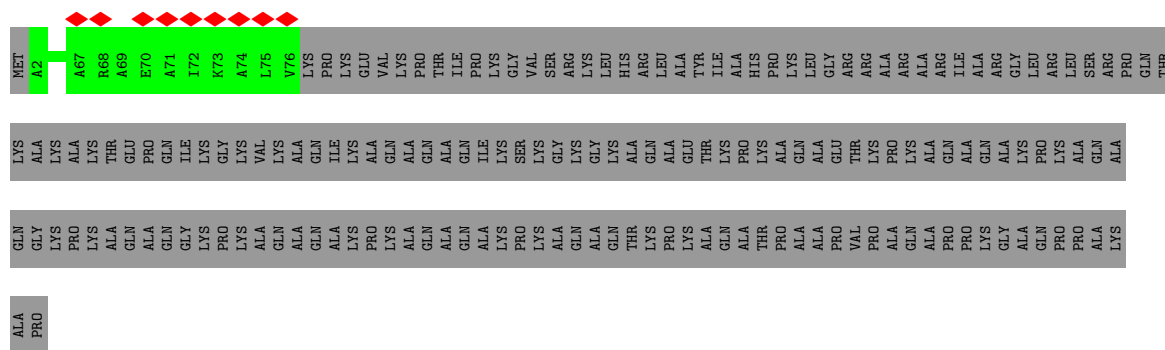
- Molecule 26: uL15

Chain a: 89% 8%



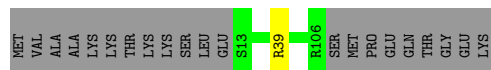
- Molecule 27: 60S ribosomal protein L29

Chain b: 31% 69%



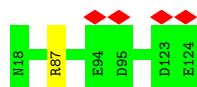
- Molecule 28: eL30

Chain c: 81% 18%



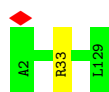
- Molecule 29: eL31

Chain d: 99%



- Molecule 30: eL32

Chain e: 99%



- Molecule 31: eL33

Chain f: 99%



- Molecule 32: 60S ribosomal protein L34

Chain g: 90% 10%



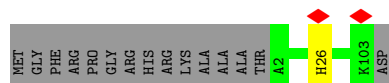
- Molecule 33: uL29

Chain h: 100%



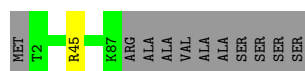
- Molecule 34: 60S ribosomal protein L36

Chain i: 86% 13%



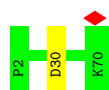
- Molecule 35: Ribosomal protein L37

Chain j: 88% 11%



- Molecule 36: L38

Chain k: 99%



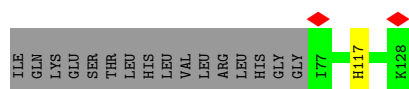
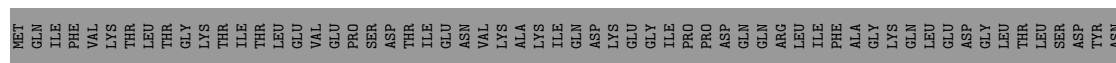
- Molecule 37: ribosomal protein eL39

Chain l:  100%



- Molecule 38: 60S ribosomal protein L40

Chain m:  40% 59%



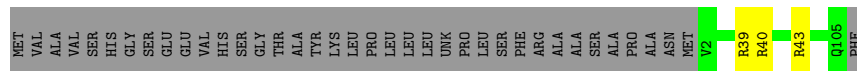
- Molecule 39: 60s ribosomal protein l41

Chain n:  100%

There are no outlier residues recorded for this chain.

- Molecule 40: LOW QUALITY PROTEIN: 60S ribosomal protein L36a

Chain o:  71% 27%



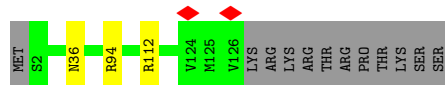
- Molecule 41: ribosomal protein eL43

Chain p:  100%



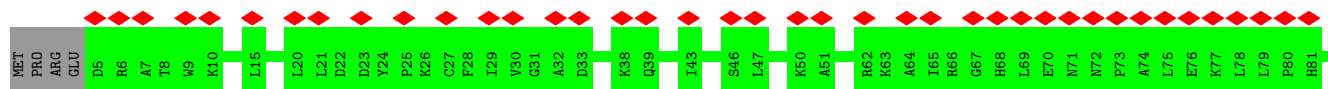
- Molecule 42: eL28

Chain r:  89% 9%

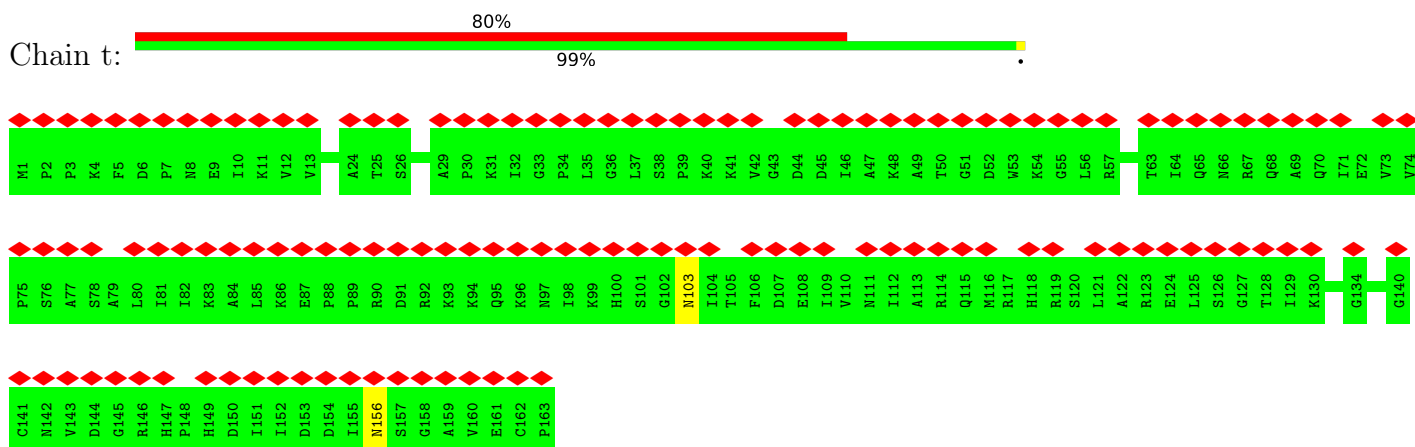


- Molecule 43: 60S acidic ribosomal protein P0

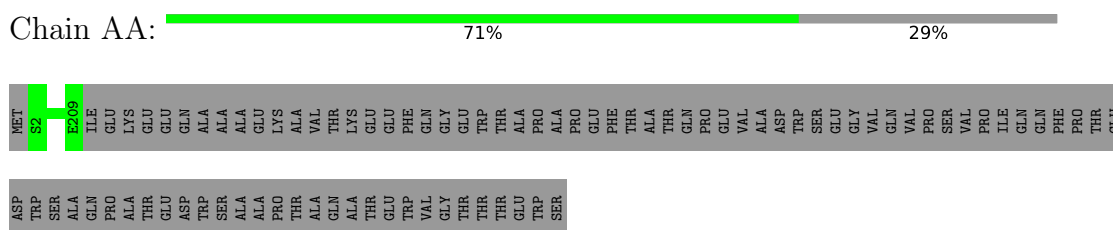
Chain s:  47% 62% 38%



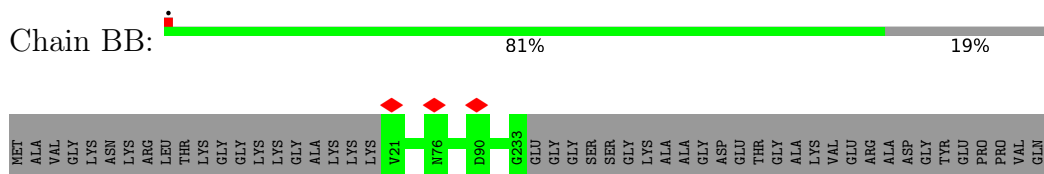
- Molecule 44: L12



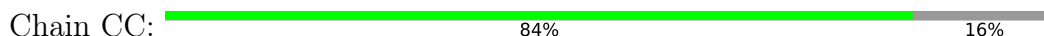
- Molecule 45: 40S ribosomal protein SA

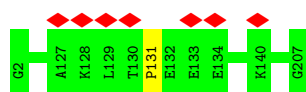


- Molecule 46: 40S ribosomal protein S3a

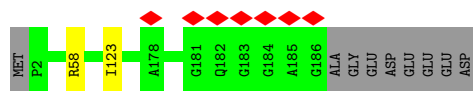


- Molecule 47: 40S ribosomal protein S2

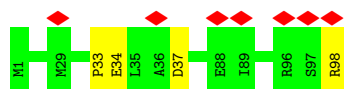




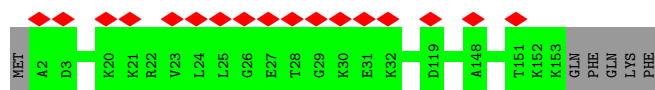
- Molecule 54: 40S ribosomal protein S9



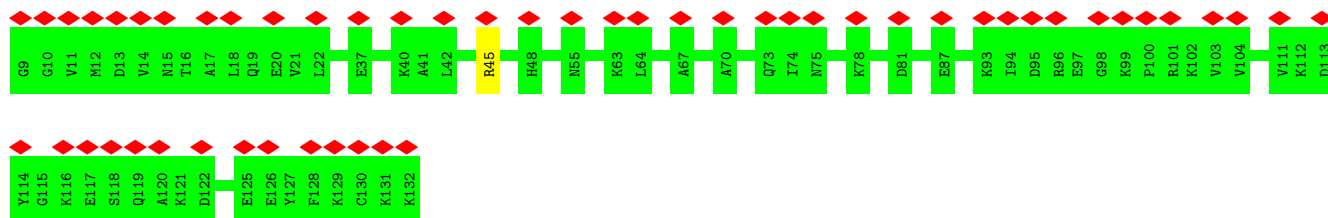
- Molecule 55: S10_pectin domain-containing protein



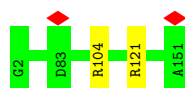
- Molecule 56: 40S ribosomal protein S11



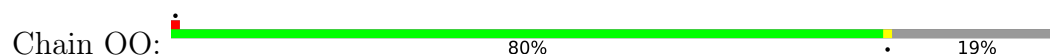
- Molecule 57: 40S ribosomal protein S12

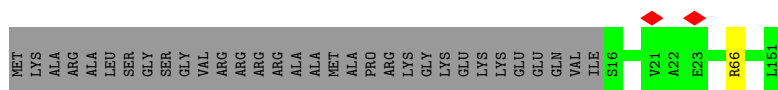


- Molecule 58: ribosomal protein uS15

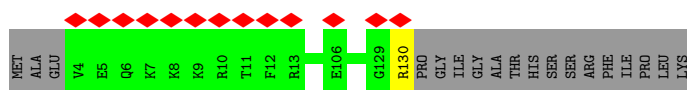
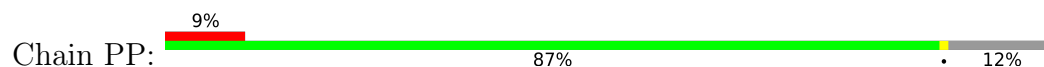


- Molecule 59: S14

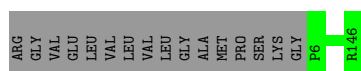




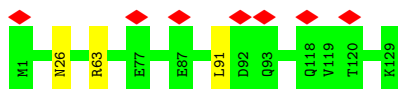
- Molecule 60: 40S ribosomal protein uS19



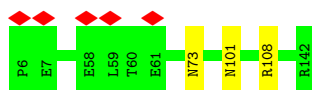
- Molecule 61: Rps16 protein



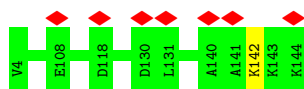
- Molecule 62: S17



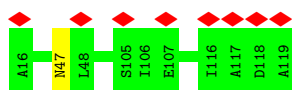
- Molecule 63: ribosomal protein uS13



- Molecule 64: S19



- Molecule 65: Ribosomal_S10 domain-containing protein



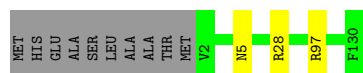
- Molecule 66: S21

Chain VV:  95%



- Molecule 67: Ribosomal protein S15a

Chain WW:  91% 7%




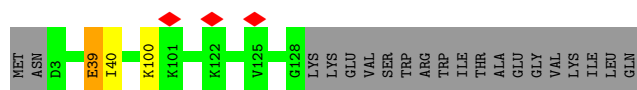
- Molecule 68: Ribosomal protein S23

Chain XX:  98%



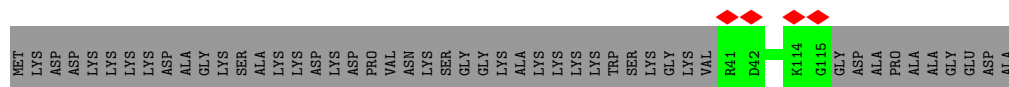
- Molecule 69: 40S ribosomal protein S24

Chain YY:  84% 14%




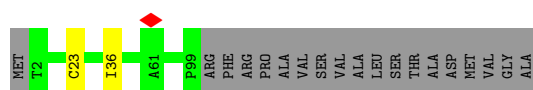
- Molecule 70: 40S ribosomal protein S25

Chain ZZ:  61% 39%



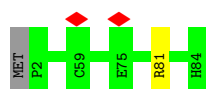
- Molecule 71: 40S ribosomal protein S26

Chain aa:  82% 16%

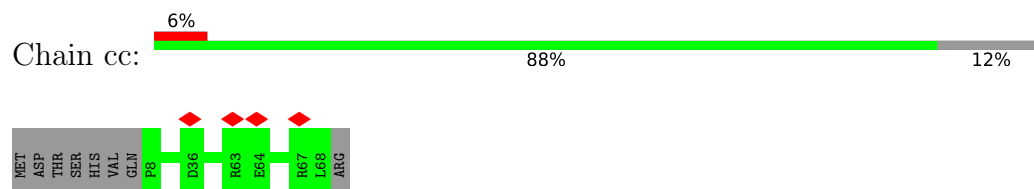


- Molecule 72: 40S ribosomal protein S27

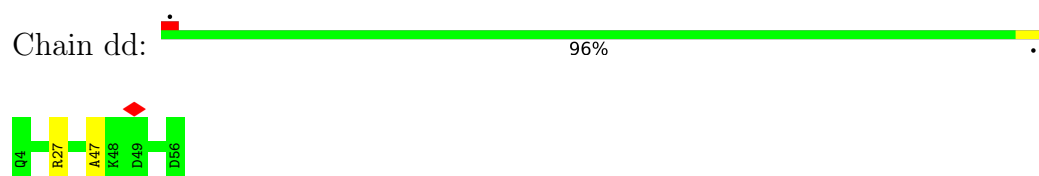
Chain bb:  98%



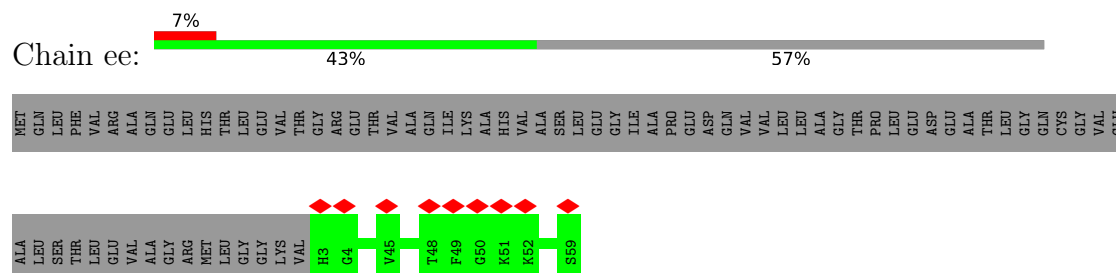
- Molecule 73: 40S ribosomal protein S28



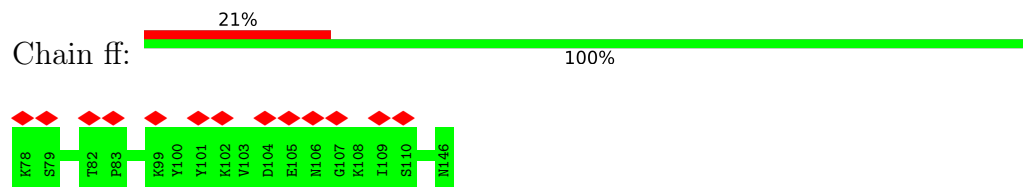
- Molecule 74: ribosomal protein uS14



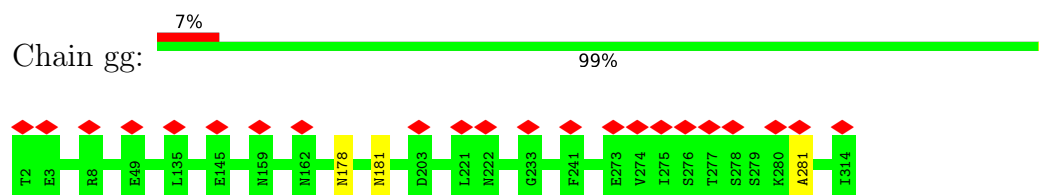
- Molecule 75: 40S ribosomal protein S30



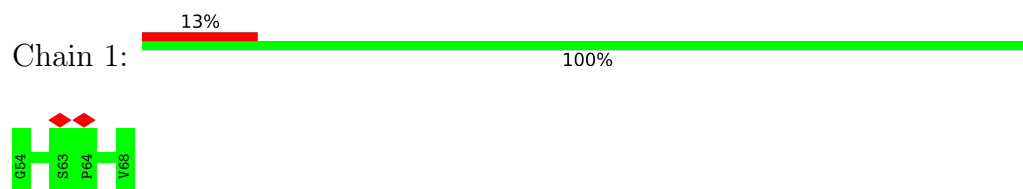
- Molecule 76: S27a



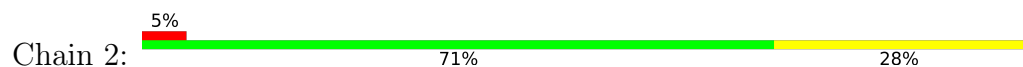
- Molecule 77: ribosomal protein RACK1

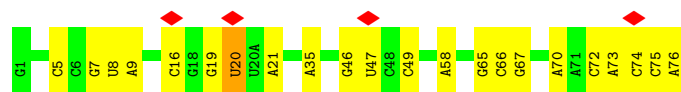


- Molecule 78: Sec61Beta



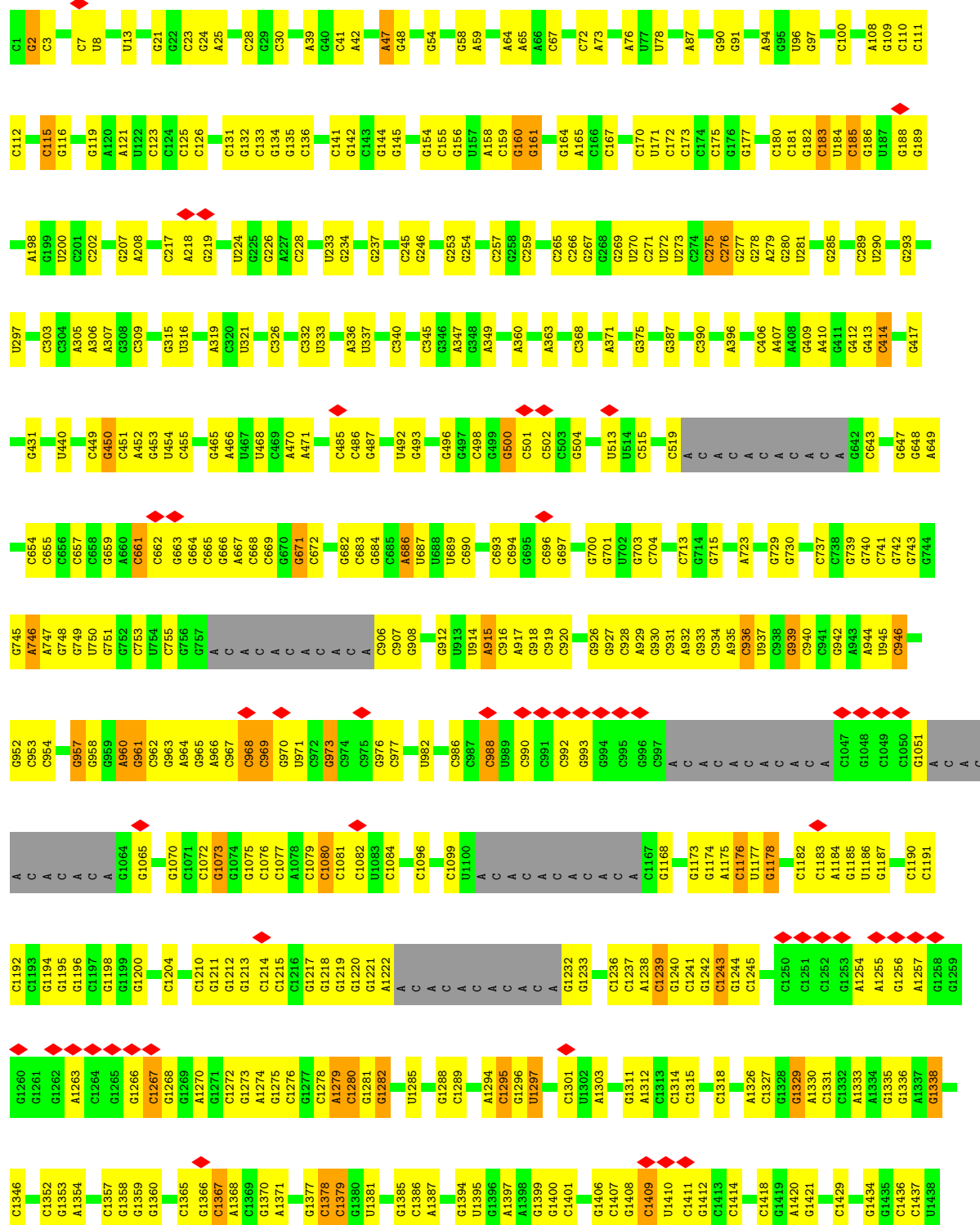
- Molecule 79: P-Site tRNA



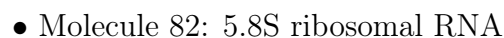


• Molecule 80: 28S ribosomal RNA+BlaS

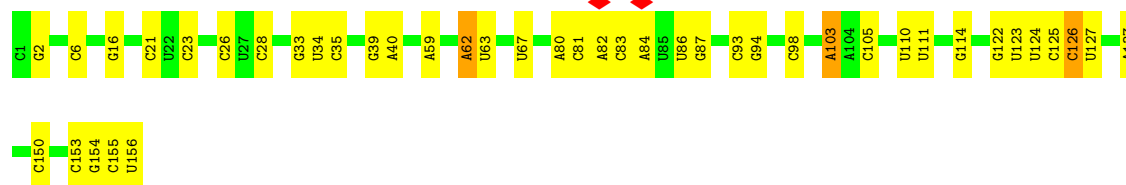
Chain 5: 62% 31%





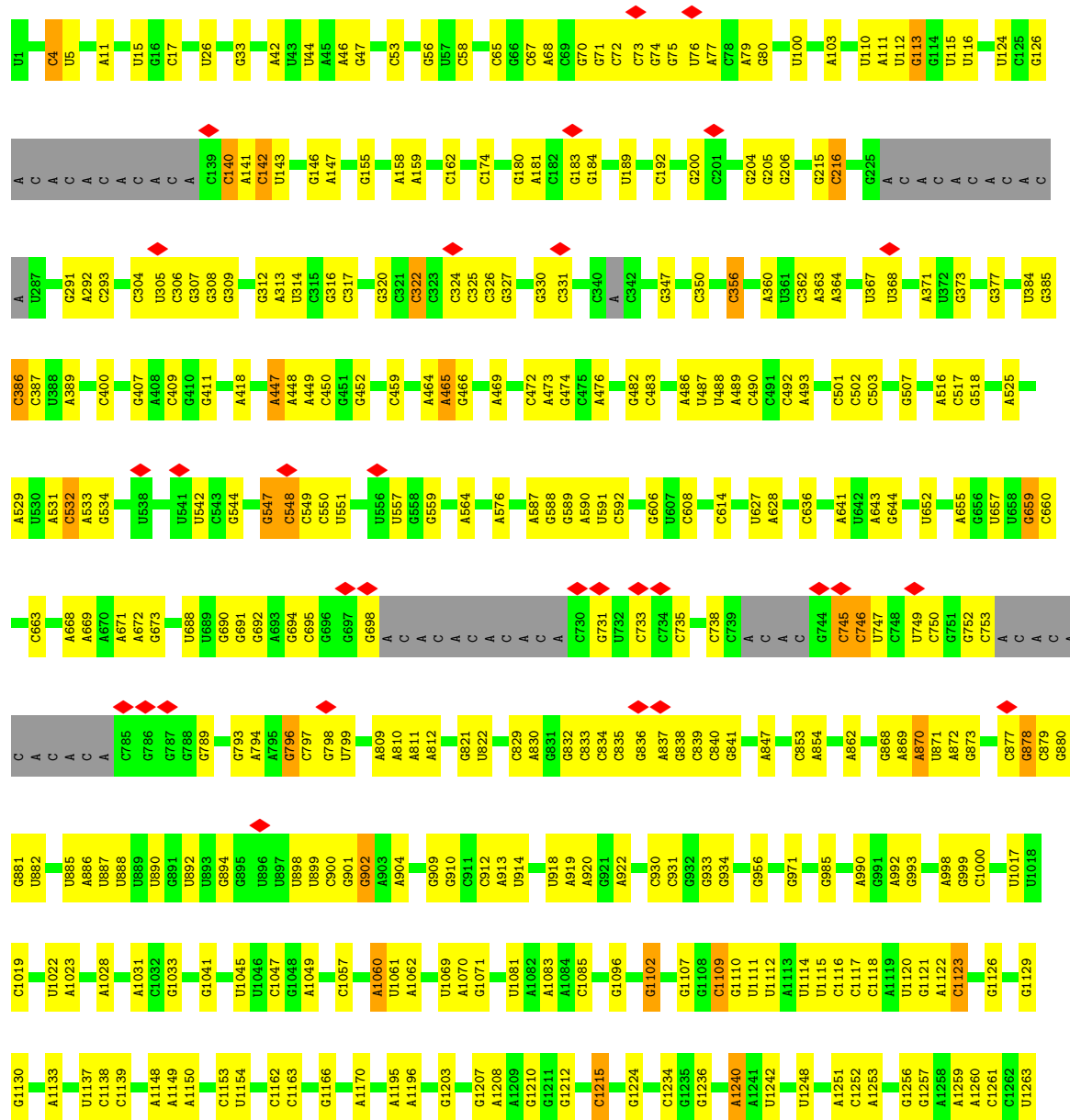


Chain 8:  72% 26%

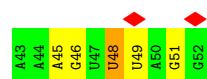


• Molecule 83: 18S ribosomal RNA

Chain 9:  65% 29%



- Molecule 84: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	103842	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.92	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	79000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.078	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.014	Depositor
Map size (Å)	405.0, 405.0, 405.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.82	0/1902	0.75	3/2551 (0.1%)
2	B	0.76	0/3219	0.71	1/4315 (0.0%)
3	C	0.76	0/2929	0.74	2/3935 (0.1%)
4	D	0.65	0/2432	0.64	1/3257 (0.0%)
5	E	0.62	0/1936	0.74	1/2600 (0.0%)
6	F	0.82	1/1905 (0.1%)	0.75	3/2539 (0.1%)
7	G	0.58	0/1936	0.67	1/2604 (0.0%)
8	H	0.59	0/1535	0.64	0/2063
9	I	0.71	0/1693	0.67	1/2260 (0.0%)
10	J	0.51	0/1376	0.66	0/1841
11	L	0.66	0/1734	0.71	1/2317 (0.0%)
12	M	0.73	1/1158 (0.1%)	0.70	2/1547 (0.1%)
13	N	0.87	0/1746	0.77	1/2338 (0.0%)
14	O	0.79	1/1671 (0.1%)	0.72	1/2234 (0.0%)
15	P	0.80	0/1268	0.72	0/1701
16	Q	0.79	1/1530 (0.1%)	0.75	0/2041
17	R	0.63	0/1524	0.70	2/2013 (0.1%)
18	S	0.81	0/1493	0.71	0/2002
19	T	0.77	0/1326	0.70	1/1770 (0.1%)
20	U	0.56	0/822	0.60	0/1103
21	V	0.76	0/993	0.75	2/1332 (0.2%)
22	W	0.74	0/541	0.69	0/720
23	X	0.68	0/993	0.65	0/1334
24	Y	0.70	0/1132	0.72	0/1504
25	Z	0.68	0/1130	0.66	0/1507
26	a	0.81	0/1191	0.73	2/1590 (0.1%)
27	b	0.59	0/619	0.63	0/818
28	c	0.68	0/742	0.64	1/996 (0.1%)
29	d	0.70	0/903	0.73	1/1216 (0.1%)
30	e	0.85	0/1071	0.74	1/1429 (0.1%)
31	f	0.84	0/895	0.81	2/1198 (0.2%)
32	g	0.74	0/916	0.72	1/1220 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.62	0/1021	0.70	0/1348
34	i	0.56	0/841	0.75	0/1112
35	j	0.88	0/720	0.77	1/952 (0.1%)
36	k	0.57	0/575	0.67	1/761 (0.1%)
37	l	0.72	0/454	0.76	0/599
38	m	0.62	0/435	0.71	0/575
39	n	0.62	0/223	0.78	0/284
40	o	0.69	0/864	0.77	3/1140 (0.3%)
41	p	0.77	0/718	0.64	0/953
42	r	0.72	0/1017	0.73	3/1364 (0.2%)
43	s	0.34	0/1547	0.62	0/2088
44	t	0.33	0/1257	0.70	0/1697
45	AA	0.53	0/1679	0.64	0/2283
46	BB	0.59	0/1756	0.64	0/2350
47	CC	0.58	0/1730	0.63	0/2344
48	DD	0.45	0/1792	0.65	1/2412 (0.0%)
49	EE	0.54	0/2115	0.67	0/2843
50	FF	0.47	0/1531	0.61	0/2059
51	GG	0.44	0/1946	0.71	0/2590
52	HH	0.45	0/1544	0.69	0/2068
53	II	0.60	0/1715	0.71	0/2287
54	JJ	0.54	0/1550	0.70	0/2069
55	KK	0.44	0/851	0.63	0/1147
56	LL	0.69	0/1259	0.68	0/1684
57	MM	0.31	0/968	0.62	0/1296
58	NN	0.61	0/1232	0.72	2/1656 (0.1%)
59	OO	0.55	0/1029	0.76	0/1380
60	PP	0.41	0/1079	0.66	0/1437
61	QQ	0.47	0/1142	0.68	0/1528
62	RR	0.46	0/1060	0.60	0/1421
63	SS	0.40	0/1157	0.68	1/1548 (0.1%)
64	TT	0.46	0/1120	0.62	0/1499
65	UU	0.44	0/831	0.68	0/1115
66	VV	0.51	0/645	0.74	0/865
67	WW	0.65	0/1051	0.74	2/1406 (0.1%)
68	XX	0.58	0/1116	0.68	0/1490
69	YY	0.46	0/1040	0.66	0/1382
70	ZZ	0.42	0/604	0.68	0/810
71	aa	0.67	0/794	0.77	1/1065 (0.1%)
72	bb	0.52	0/665	0.66	0/891
73	cc	0.48	0/478	0.74	0/640
74	dd	0.54	0/455	0.78	1/603 (0.2%)
75	ee	0.44	0/462	0.66	0/607

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	ff	0.37	0/531	0.71	0/703
77	gg	0.38	0/2493	0.62	0/3394
78	1	0.63	0/129	0.73	0/173
79	2	0.57	0/1805	1.00	4/2809 (0.1%)
80	5	1.19	47/87794 (0.1%)	1.29	540/136953 (0.4%)
81	7	1.13	0/2858	1.12	4/4455 (0.1%)
82	8	1.19	2/3701 (0.1%)	1.21	12/5766 (0.2%)
83	9	0.93	0/41015	1.15	156/63927 (0.2%)
84	K	0.40	0/243	1.05	2/377 (0.5%)
All	All	0.94	53/232898 (0.0%)	1.07	765/342100 (0.2%)

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
3	C	0	1
5	E	0	1
11	L	0	1
18	S	0	2
19	T	0	2
22	W	0	1
24	Y	0	1
26	a	0	1
34	i	0	1
38	m	0	1
43	s	0	1
48	DD	0	2
50	FF	0	1
52	HH	0	1
55	KK	0	2
62	RR	0	1
66	VV	0	2
68	XX	0	1
69	YY	0	1
77	gg	0	1
All	All	0	25

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	M	86	TRP	CB-CG	-7.04	1.37	1.50
80	5	3911	C	C4-C5	-6.85	1.37	1.43
80	5	4449	A	N9-C4	-6.61	1.33	1.37
80	5	2346	C	N1-C6	-6.30	1.33	1.37
80	5	1279	A	N9-C4	-6.16	1.34	1.37

The worst 5 of 765 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	9	501	C	C2-N1-C1'	11.58	131.54	118.80
80	5	1183	C	N1-C2-O2	11.16	125.60	118.90
83	9	1123	C	C6-N1-C2	-11.11	115.86	120.30
80	5	1183	C	N3-C2-O2	-10.67	114.43	121.90
80	5	4354	U	C2-N1-C1'	10.42	130.20	117.70

There are no chirality outliers.

5 of 25 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	245	HIS	Peptide
5	E	173	GLY	Peptide
11	L	130	LYS	Peptide
18	S	163	HIS	Peptide
18	S	164	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/244 (99%)	218 (90%)	24 (10%)	0	100	100
2	B	392/403 (97%)	352 (90%)	40 (10%)	0	100	100
3	C	359/425 (84%)	315 (88%)	44 (12%)	0	100	100
4	D	290/297 (98%)	268 (92%)	22 (8%)	0	100	100
5	E	232/291 (80%)	194 (84%)	38 (16%)	0	100	100
6	F	223/249 (90%)	198 (89%)	25 (11%)	0	100	100
7	G	235/241 (98%)	209 (89%)	26 (11%)	0	100	100
8	H	188/190 (99%)	175 (93%)	13 (7%)	0	100	100
9	I	200/214 (94%)	176 (88%)	24 (12%)	0	100	100
10	J	167/181 (92%)	159 (95%)	8 (5%)	0	100	100
11	L	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	29	63
12	M	136/218 (62%)	124 (91%)	12 (9%)	0	100	100
13	N	201/203 (99%)	179 (89%)	19 (10%)	3 (2%)	10	37
14	O	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
15	P	151/153 (99%)	140 (93%)	11 (7%)	0	100	100
16	Q	185/188 (98%)	169 (91%)	16 (9%)	0	100	100
17	R	178/196 (91%)	167 (94%)	11 (6%)	0	100	100
18	S	173/175 (99%)	160 (92%)	12 (7%)	1 (1%)	25	59
19	T	157/159 (99%)	138 (88%)	19 (12%)	0	100	100
20	U	97/128 (76%)	89 (92%)	8 (8%)	0	100	100
21	V	129/131 (98%)	115 (89%)	14 (11%)	0	100	100
22	W	61/134 (46%)	55 (90%)	6 (10%)	0	100	100
23	X	117/156 (75%)	109 (93%)	8 (7%)	0	100	100
24	Y	132/134 (98%)	122 (92%)	10 (8%)	0	100	100
25	Z	133/135 (98%)	118 (89%)	15 (11%)	0	100	100
26	a	145/160 (91%)	135 (93%)	10 (7%)	0	100	100
27	b	73/245 (30%)	65 (89%)	8 (11%)	0	100	100
28	c	92/115 (80%)	84 (91%)	8 (9%)	0	100	100
29	d	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
30	e	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
31	f	107/109 (98%)	92 (86%)	15 (14%)	0	100	100
32	g	112/126 (89%)	104 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	h	120/122 (98%)	113 (94%)	7 (6%)	0	100	100
34	i	100/117 (86%)	89 (89%)	11 (11%)	0	100	100
35	j	84/97 (87%)	77 (92%)	7 (8%)	0	100	100
36	k	67/69 (97%)	60 (90%)	7 (10%)	0	100	100
37	l	48/50 (96%)	39 (81%)	9 (19%)	0	100	100
38	m	50/128 (39%)	45 (90%)	5 (10%)	0	100	100
39	n	21/23 (91%)	21 (100%)	0	0	100	100
40	o	102/142 (72%)	90 (88%)	12 (12%)	0	100	100
41	p	89/91 (98%)	77 (86%)	12 (14%)	0	100	100
42	r	123/137 (90%)	109 (89%)	14 (11%)	0	100	100
43	s	196/318 (62%)	160 (82%)	36 (18%)	0	100	100
44	t	161/163 (99%)	122 (76%)	39 (24%)	0	100	100
45	AA	206/295 (70%)	174 (84%)	32 (16%)	0	100	100
46	BB	211/264 (80%)	182 (86%)	29 (14%)	0	100	100
47	CC	216/259 (83%)	188 (87%)	28 (13%)	0	100	100
48	DD	225/281 (80%)	191 (85%)	34 (15%)	0	100	100
49	EE	260/262 (99%)	221 (85%)	39 (15%)	0	100	100
50	FF	189/205 (92%)	165 (87%)	24 (13%)	0	100	100
51	GG	235/262 (90%)	202 (86%)	31 (13%)	2 (1%)	17	50
52	HH	187/190 (98%)	160 (86%)	27 (14%)	0	100	100
53	II	204/206 (99%)	182 (89%)	21 (10%)	1 (0%)	29	63
54	JJ	183/194 (94%)	164 (90%)	18 (10%)	1 (0%)	29	63
55	KK	96/98 (98%)	74 (77%)	21 (22%)	1 (1%)	15	47
56	LL	150/158 (95%)	122 (81%)	28 (19%)	0	100	100
57	MM	122/124 (98%)	96 (79%)	26 (21%)	0	100	100
58	NN	148/150 (99%)	132 (89%)	16 (11%)	0	100	100
59	OO	134/168 (80%)	112 (84%)	22 (16%)	0	100	100
60	PP	125/145 (86%)	111 (89%)	14 (11%)	0	100	100
61	QQ	139/157 (88%)	126 (91%)	13 (9%)	0	100	100
62	RR	127/129 (98%)	110 (87%)	17 (13%)	0	100	100
63	SS	135/137 (98%)	115 (85%)	20 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	TT	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
65	UU	102/104 (98%)	85 (83%)	17 (17%)	0	100	100
66	VV	81/83 (98%)	65 (80%)	13 (16%)	3 (4%)	3	17
67	WW	127/139 (91%)	114 (90%)	13 (10%)	0	100	100
68	XX	139/141 (99%)	115 (83%)	24 (17%)	0	100	100
69	YY	124/146 (85%)	107 (86%)	15 (12%)	2 (2%)	9	35
70	ZZ	73/123 (59%)	65 (89%)	8 (11%)	0	100	100
71	aa	96/117 (82%)	70 (73%)	25 (26%)	1 (1%)	15	47
72	bb	81/84 (96%)	75 (93%)	6 (7%)	0	100	100
73	cc	59/69 (86%)	54 (92%)	5 (8%)	0	100	100
74	dd	51/53 (96%)	42 (82%)	8 (16%)	1 (2%)	7	29
75	ee	55/133 (41%)	48 (87%)	7 (13%)	0	100	100
76	ff	58/62 (94%)	43 (74%)	15 (26%)	0	100	100
77	gg	311/313 (99%)	260 (84%)	51 (16%)	0	100	100
78	1	13/15 (87%)	9 (69%)	4 (31%)	0	100	100
All	All	11505/13109 (88%)	10135 (88%)	1353 (12%)	17 (0%)	54	82

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
69	YY	40	ILE
66	VV	79	VAL
69	YY	39	GLU
13	N	181	HIS
66	VV	11	LEU

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	186/187 (100%)	185 (100%)	1 (0%)	88	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	337/348 (97%)	337 (100%)	0	100	100
3	C	301/347 (87%)	300 (100%)	1 (0%)	92	97
4	D	247/250 (99%)	246 (100%)	1 (0%)	91	96
5	E	208/251 (83%)	205 (99%)	3 (1%)	67	85
6	F	194/217 (89%)	192 (99%)	2 (1%)	76	89
7	G	202/206 (98%)	199 (98%)	3 (2%)	65	84
8	H	169/169 (100%)	167 (99%)	2 (1%)	71	87
9	I	174/181 (96%)	172 (99%)	2 (1%)	73	88
10	J	142/152 (93%)	141 (99%)	1 (1%)	84	93
11	L	176/177 (99%)	176 (100%)	0	100	100
12	M	117/161 (73%)	117 (100%)	0	100	100
13	N	171/171 (100%)	171 (100%)	0	100	100
14	O	171/171 (100%)	171 (100%)	0	100	100
15	P	134/134 (100%)	133 (99%)	1 (1%)	84	93
16	Q	163/164 (99%)	162 (99%)	1 (1%)	86	94
17	R	159/175 (91%)	158 (99%)	1 (1%)	86	94
18	S	156/156 (100%)	156 (100%)	0	100	100
19	T	139/139 (100%)	139 (100%)	0	100	100
20	U	89/114 (78%)	89 (100%)	0	100	100
21	V	101/101 (100%)	101 (100%)	0	100	100
22	W	55/109 (50%)	55 (100%)	0	100	100
23	X	107/134 (80%)	105 (98%)	2 (2%)	57	80
24	Y	124/124 (100%)	124 (100%)	0	100	100
25	Z	117/117 (100%)	117 (100%)	0	100	100
26	a	119/127 (94%)	118 (99%)	1 (1%)	81	92
27	b	62/184 (34%)	62 (100%)	0	100	100
28	c	79/97 (81%)	79 (100%)	0	100	100
29	d	98/98 (100%)	98 (100%)	0	100	100
30	e	114/114 (100%)	114 (100%)	0	100	100
31	f	88/88 (100%)	88 (100%)	0	100	100
32	g	98/106 (92%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	h	109/109 (100%)	109 (100%)	0	100	100
34	i	86/96 (90%)	86 (100%)	0	100	100
35	j	73/80 (91%)	73 (100%)	0	100	100
36	k	64/64 (100%)	64 (100%)	0	100	100
37	l	47/47 (100%)	47 (100%)	0	100	100
38	m	48/116 (41%)	48 (100%)	0	100	100
39	n	22/22 (100%)	22 (100%)	0	100	100
40	o	92/121 (76%)	92 (100%)	0	100	100
41	p	74/74 (100%)	74 (100%)	0	100	100
42	r	109/121 (90%)	108 (99%)	1 (1%)	78	90
43	s	166/258 (64%)	166 (100%)	0	100	100
44	t	136/136 (100%)	134 (98%)	2 (2%)	65	84
45	AA	174/244 (71%)	174 (100%)	0	100	100
46	BB	194/229 (85%)	194 (100%)	0	100	100
47	CC	183/207 (88%)	182 (100%)	1 (0%)	88	95
48	DD	190/232 (82%)	188 (99%)	2 (1%)	73	88
49	EE	223/223 (100%)	223 (100%)	0	100	100
50	FF	161/171 (94%)	161 (100%)	0	100	100
51	GG	207/227 (91%)	205 (99%)	2 (1%)	76	89
52	HH	169/170 (99%)	169 (100%)	0	100	100
53	II	178/178 (100%)	178 (100%)	0	100	100
54	JJ	161/168 (96%)	160 (99%)	1 (1%)	86	94
55	KK	89/89 (100%)	88 (99%)	1 (1%)	73	88
56	LL	136/142 (96%)	136 (100%)	0	100	100
57	MM	104/104 (100%)	103 (99%)	1 (1%)	76	89
58	NN	130/130 (100%)	130 (100%)	0	100	100
59	OO	106/130 (82%)	105 (99%)	1 (1%)	78	90
60	PP	116/130 (89%)	115 (99%)	1 (1%)	78	90
61	QQ	117/129 (91%)	117 (100%)	0	100	100
62	RR	117/117 (100%)	115 (98%)	2 (2%)	60	82
63	SS	119/119 (100%)	117 (98%)	2 (2%)	60	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
64	TT	112/112 (100%)	111 (99%)	1 (1%)	78	90
65	UU	94/94 (100%)	93 (99%)	1 (1%)	73	88
66	VV	67/67 (100%)	67 (100%)	0	100	100
67	WW	112/119 (94%)	111 (99%)	1 (1%)	78	90
68	XX	113/113 (100%)	111 (98%)	2 (2%)	59	81
69	YY	108/126 (86%)	107 (99%)	1 (1%)	78	90
70	ZZ	66/101 (65%)	66 (100%)	0	100	100
71	aa	85/99 (86%)	85 (100%)	0	100	100
72	bb	75/76 (99%)	74 (99%)	1 (1%)	69	86
73	cc	54/62 (87%)	54 (100%)	0	100	100
74	dd	47/47 (100%)	47 (100%)	0	100	100
75	ee	47/106 (44%)	47 (100%)	0	100	100
76	ff	58/58 (100%)	58 (100%)	0	100	100
77	gg	272/272 (100%)	270 (99%)	2 (1%)	84	93
78	1	13/13 (100%)	13 (100%)	0	100	100
All	All	10020/11117 (90%)	9972 (100%)	48 (0%)	89	95

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	GG	56	ASN
62	RR	26	ASN
51	GG	202	ASN
57	MM	45	ARG
63	SS	73	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
52	HH	33	ASN
65	UU	47	ASN
61	QQ	48	GLN
63	SS	85	ASN
68	XX	127	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
79	2	74/76 (97%)	22 (29%)	0
80	5	3648/3788 (96%)	1096 (30%)	73 (2%)
81	7	119/120 (99%)	19 (15%)	0
82	8	155/156 (99%)	38 (24%)	2 (1%)
83	9	1711/1777 (96%)	501 (29%)	23 (1%)
84	K	9/10 (90%)	5 (55%)	0
All	All	5716/5927 (96%)	1681 (29%)	98 (1%)

5 of 1681 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
79	2	5	C
79	2	7	G
79	2	8	U
79	2	9	A
79	2	16	C

5 of 98 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
80	5	3625	G
80	5	5059	C
80	5	3908	A
80	5	4448	G
83	9	70	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 216 ligands modelled in this entry, 215 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
87	BLS	5	5241	-	28,31,31	3.80	14 (50%)	28,43,43	2.15	9 (32%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	BLS	5	5241	-	-	4/21/38/38	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	5	5241	BLS	O5'-C5'	-11.89	1.23	1.43
87	5	5241	BLS	C3'-C2'	7.33	1.55	1.33
87	5	5241	BLS	C4'-C5'	6.62	1.68	1.53
87	5	5241	BLS	C7-N6	4.91	1.44	1.34
87	5	5241	BLS	C1'-C2'	-4.53	1.38	1.49

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	5	5241	BLS	O5'-C1'-C2'	-5.84	109.97	113.13
87	5	5241	BLS	C4-N3-C2	3.49	119.88	116.34
87	5	5241	BLS	C3'-C4'-N6	-3.44	104.28	110.60
87	5	5241	BLS	N4-C4-N3	3.42	121.90	116.49
87	5	5241	BLS	C8-C7-N6	3.15	120.46	116.33

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
87	5	5241	BLS	C11-C10-C9-C8

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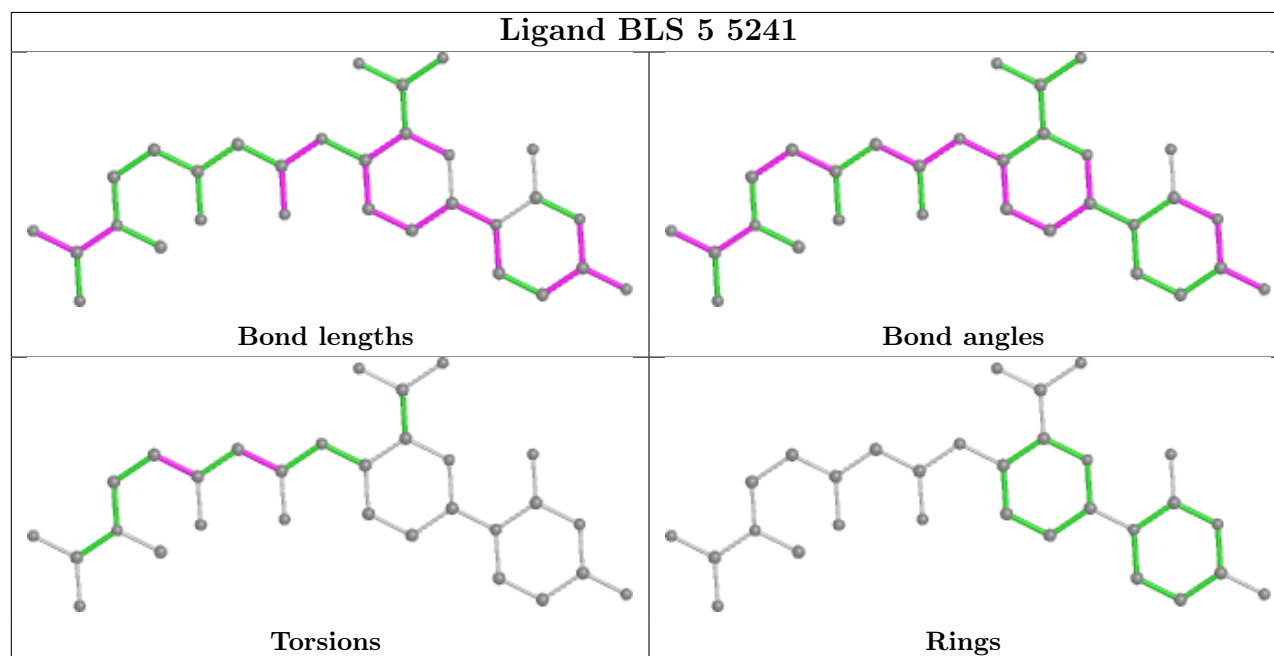
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Mol	Chain	Res	Type	Atoms
87	5	5241	BLS	C11-C10-C9-N9
87	5	5241	BLS	O7-C7-C8-C9
87	5	5241	BLS	N6-C7-C8-C9

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
76	ff	1
80	5	1
79	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	ff	118:SER	C	126:PHE	N	14.56
1	5	2016:C	O3'	2017:A	P	7.36
1	2	16:C	O3'	18:G	P	6.49

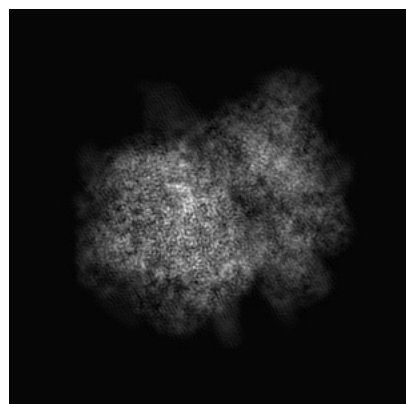
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12633. These allow visual inspection of the internal detail of the map and identification of artifacts.

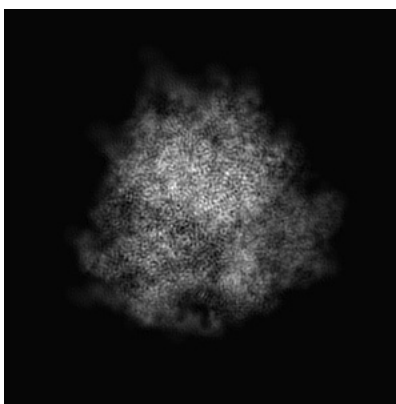
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

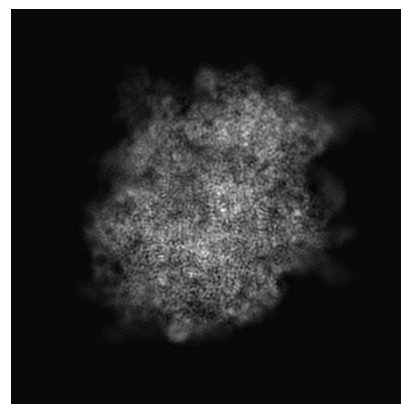
6.1.1 Primary map



X

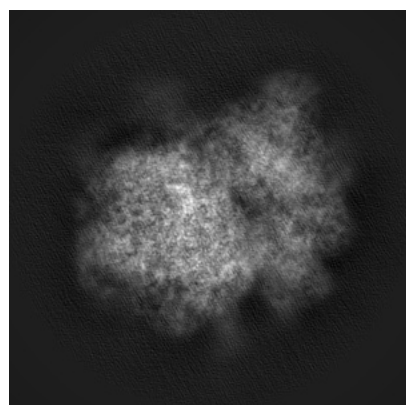


Y

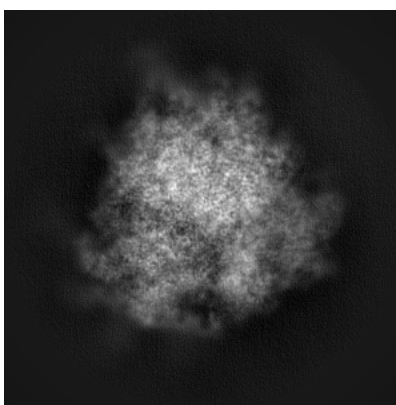


Z

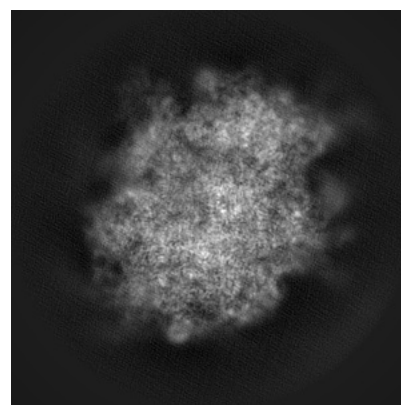
6.1.2 Raw map



X



Y

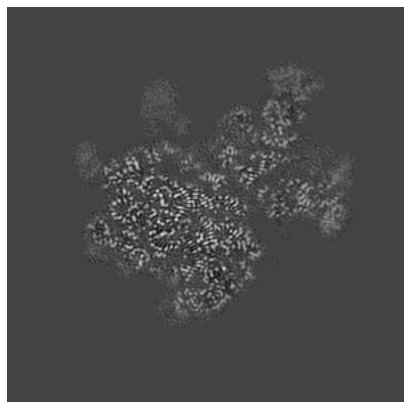


Z

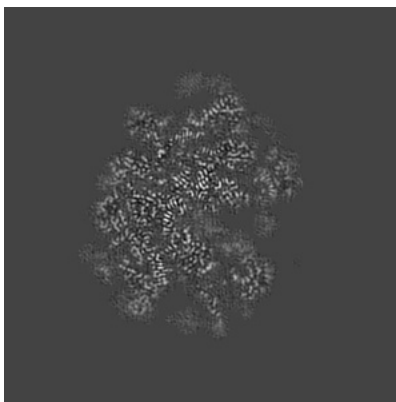
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

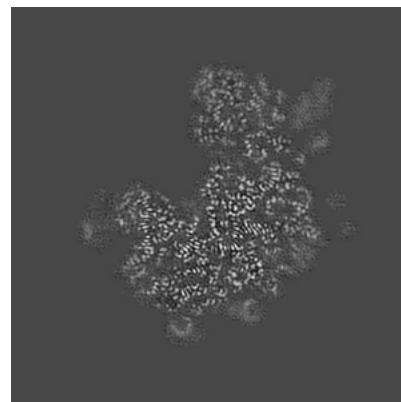
6.2.1 Primary map



X Index: 150

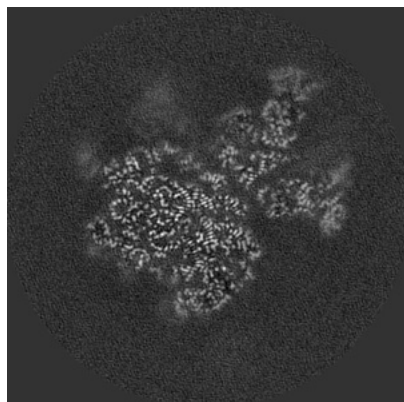


Y Index: 150

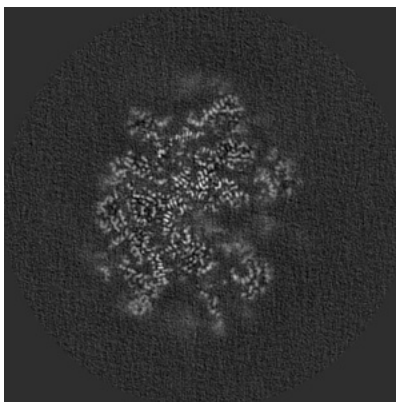


Z Index: 150

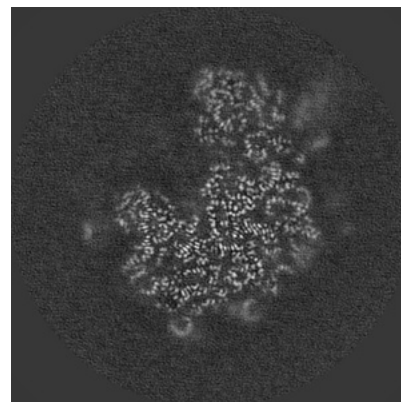
6.2.2 Raw map



X Index: 150



Y Index: 150

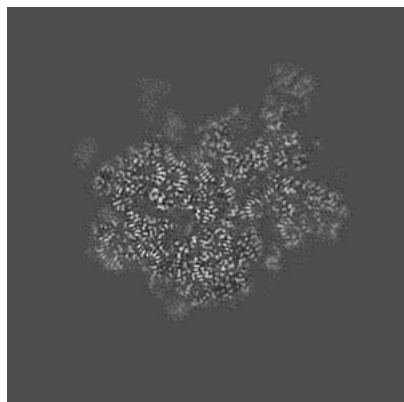


Z Index: 150

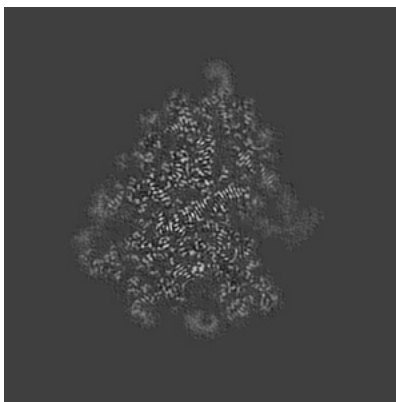
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

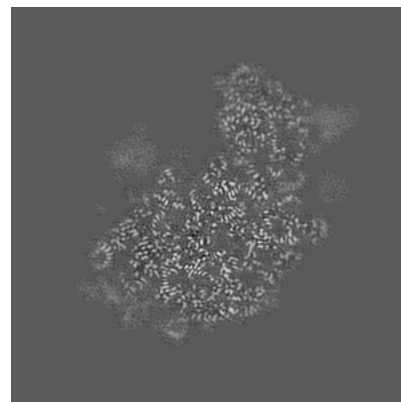
6.3.1 Primary map



X Index: 158

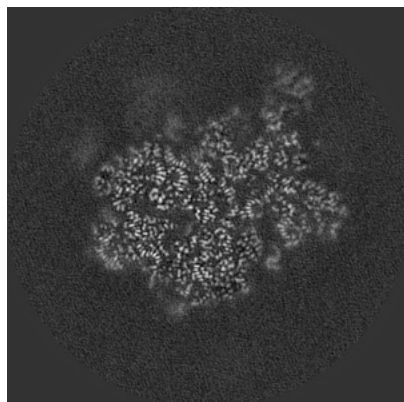


Y Index: 130

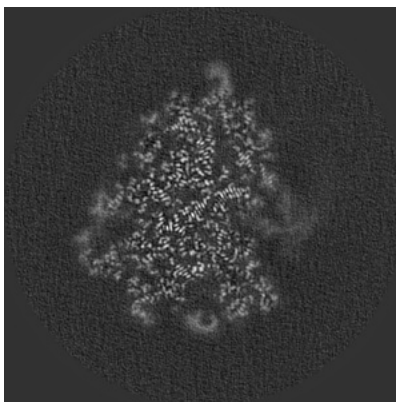


Z Index: 126

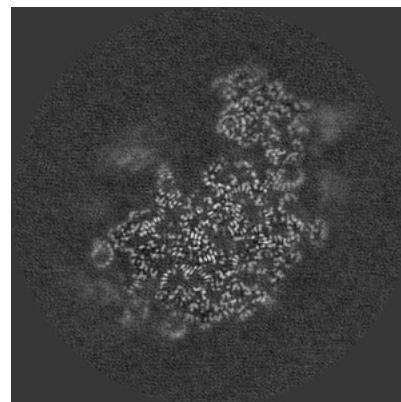
6.3.2 Raw map



X Index: 158



Y Index: 130

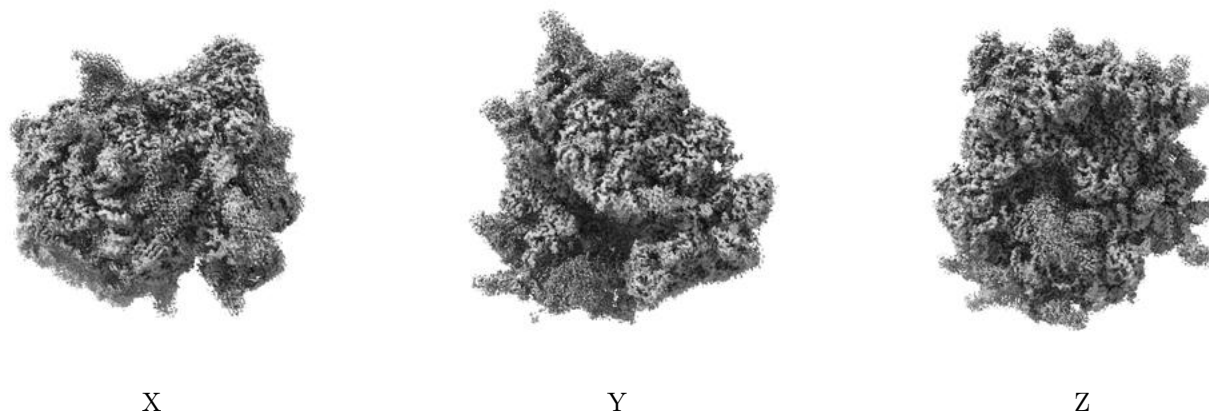


Z Index: 128

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

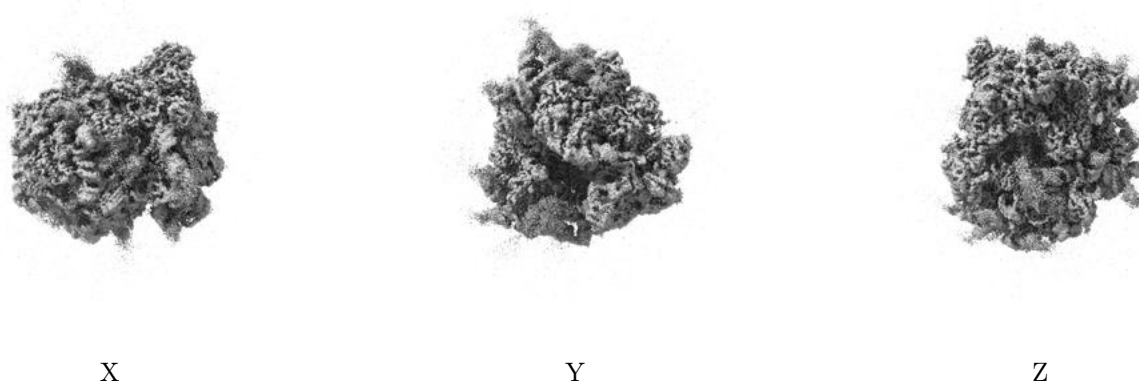
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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

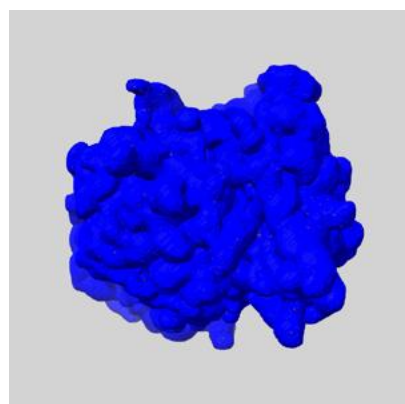
6.5 Mask visualisation [i](#)

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

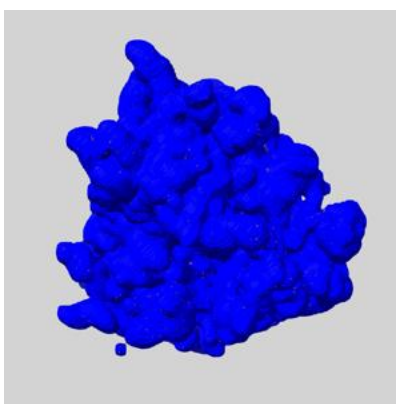
A mask typically either:

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

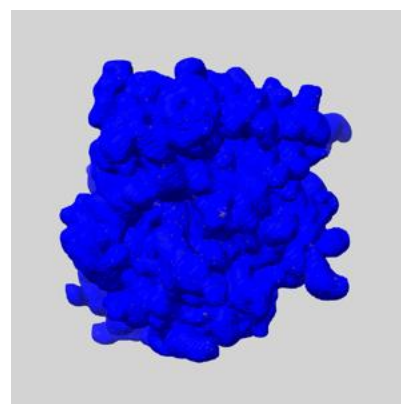
6.5.1 emd_12633_msk_1.map [i](#)



X



Y

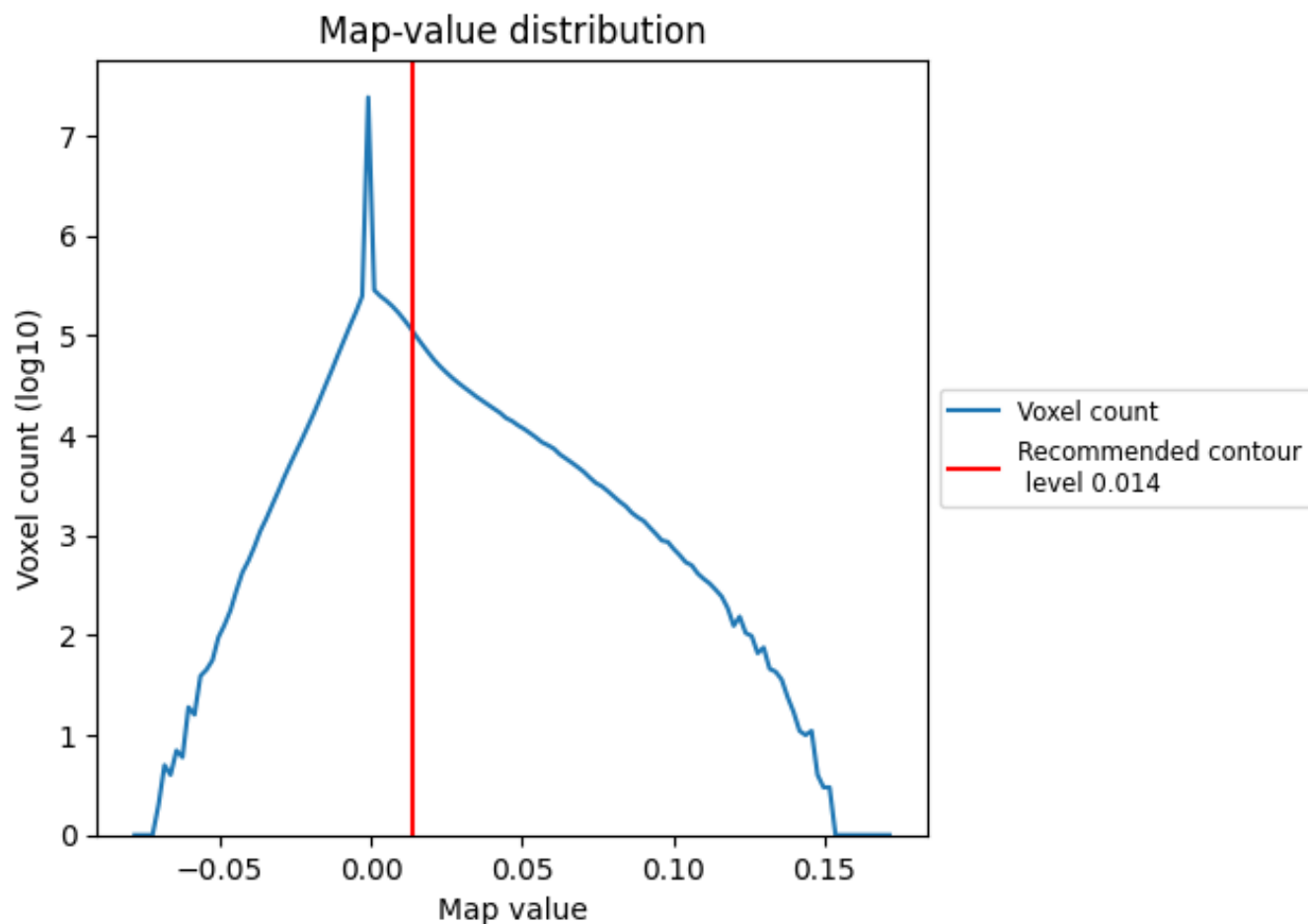


Z

7 Map analysis [i](#)

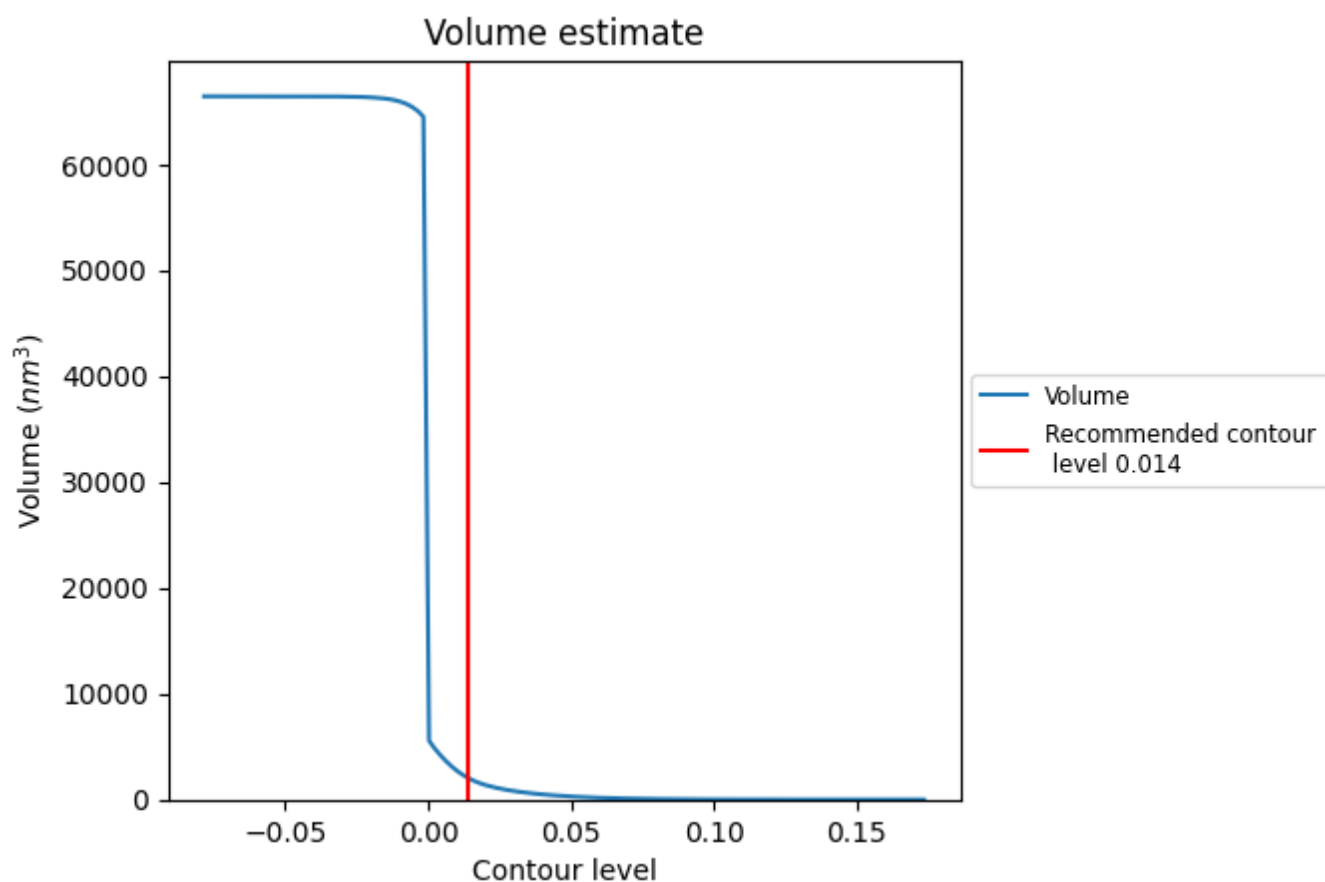
This section contains the results of statistical analysis of the map.

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.

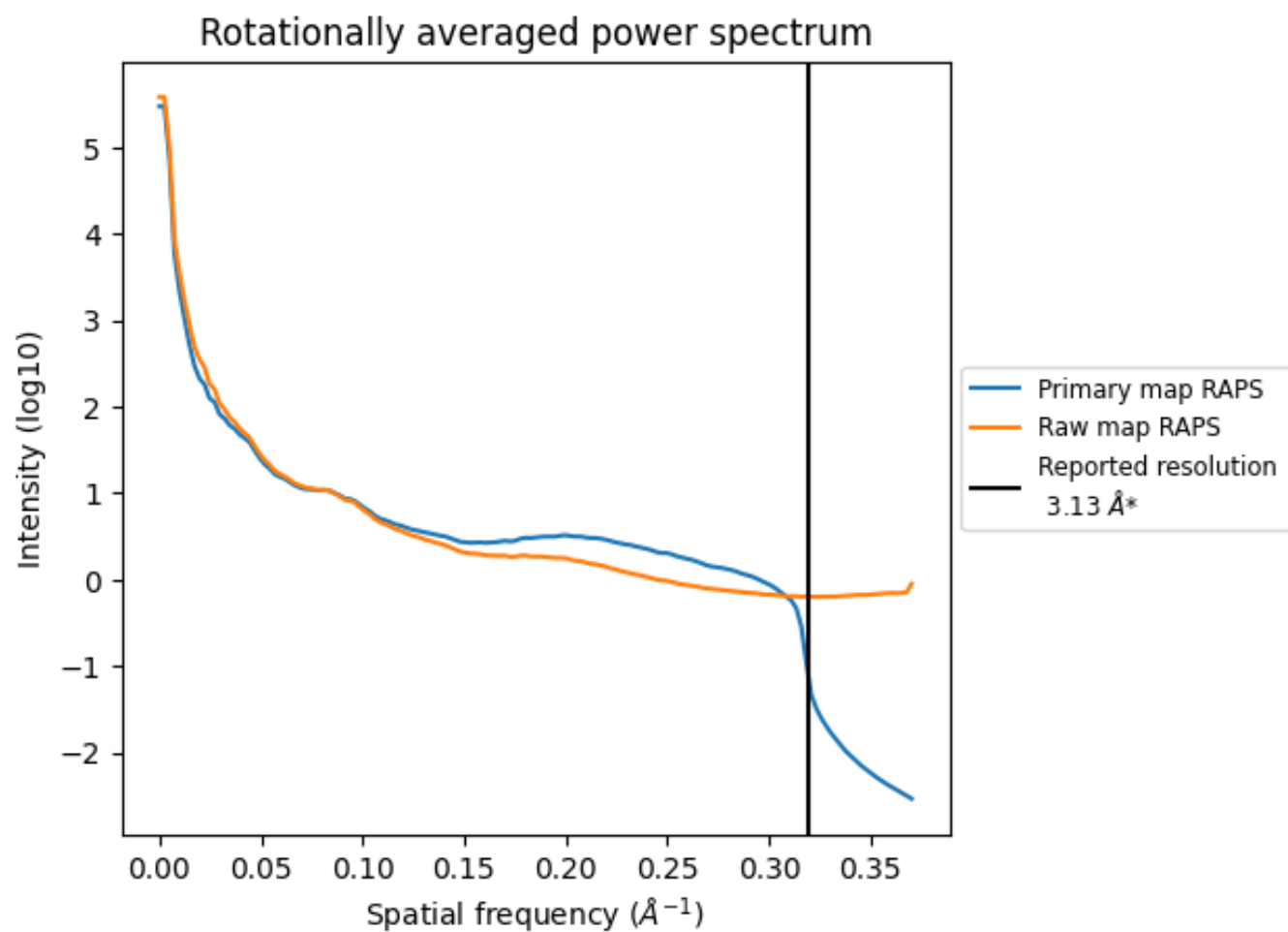
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2047 nm³; this corresponds to an approximate mass of 1850 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 ⓘ

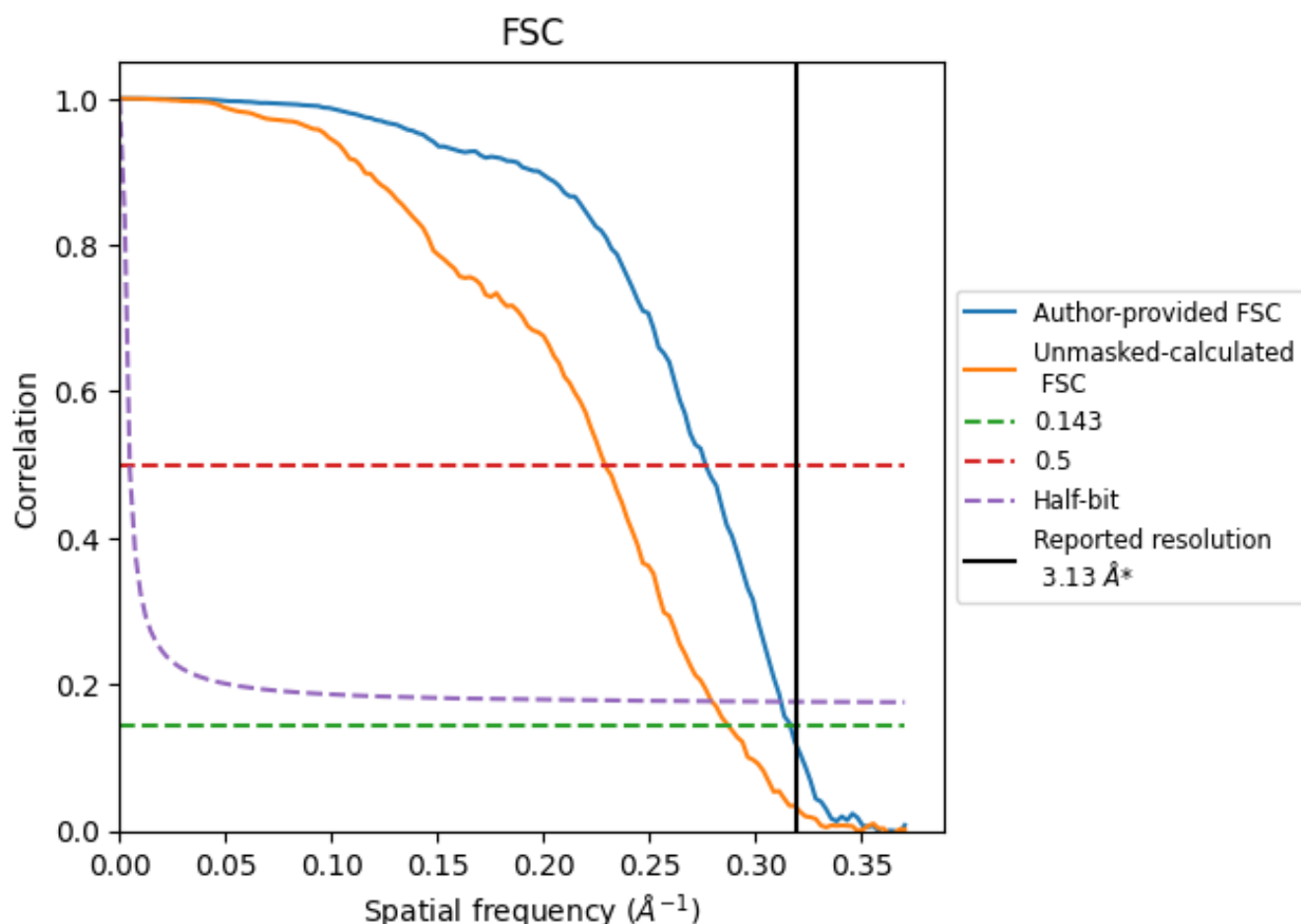


*Reported resolution corresponds to spatial frequency of 0.319 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.319 \AA^{-1}

8.2 Resolution estimates

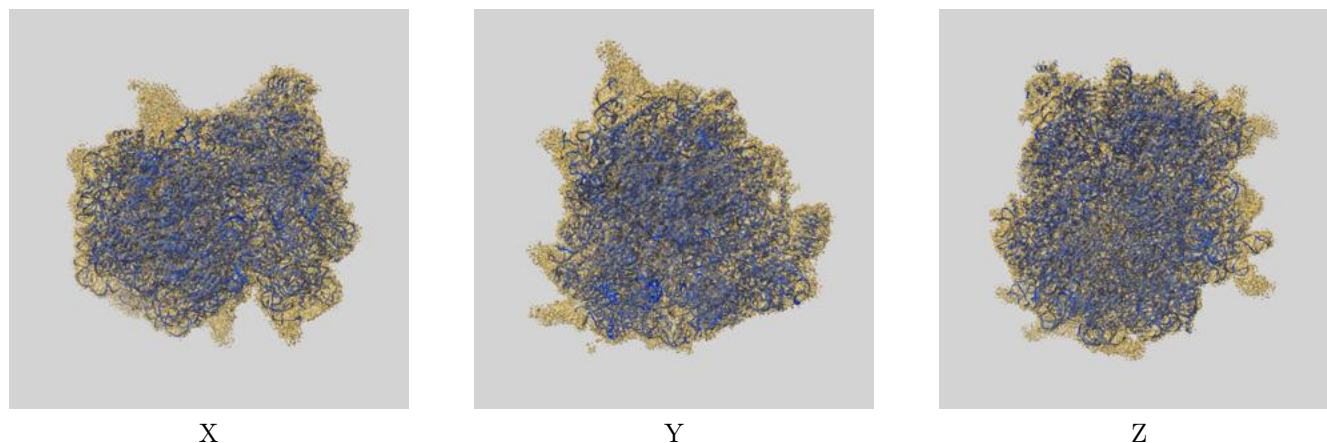
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.13	-	-
Author-provided FSC curve	3.16	3.62	3.21
Unmasked-calculated*	3.48	4.37	3.58

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.48 differs from the reported value 3.13 by more than 10 %

9 Map-model fit [i](#)

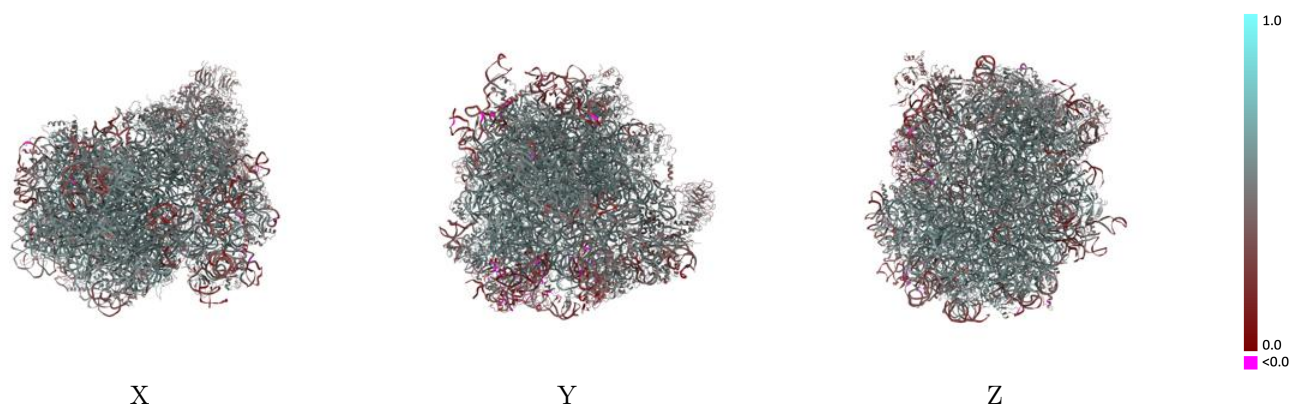
This section contains information regarding the fit between EMDB map EMD-12633 and PDB model 7NWI. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)



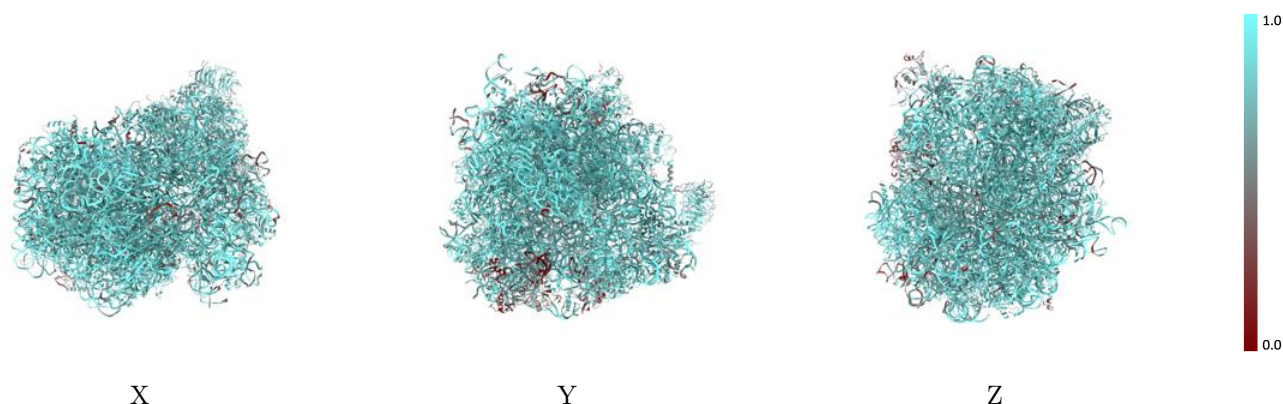
The images above show the 3D surface view of the map at the recommended contour level 0.014 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



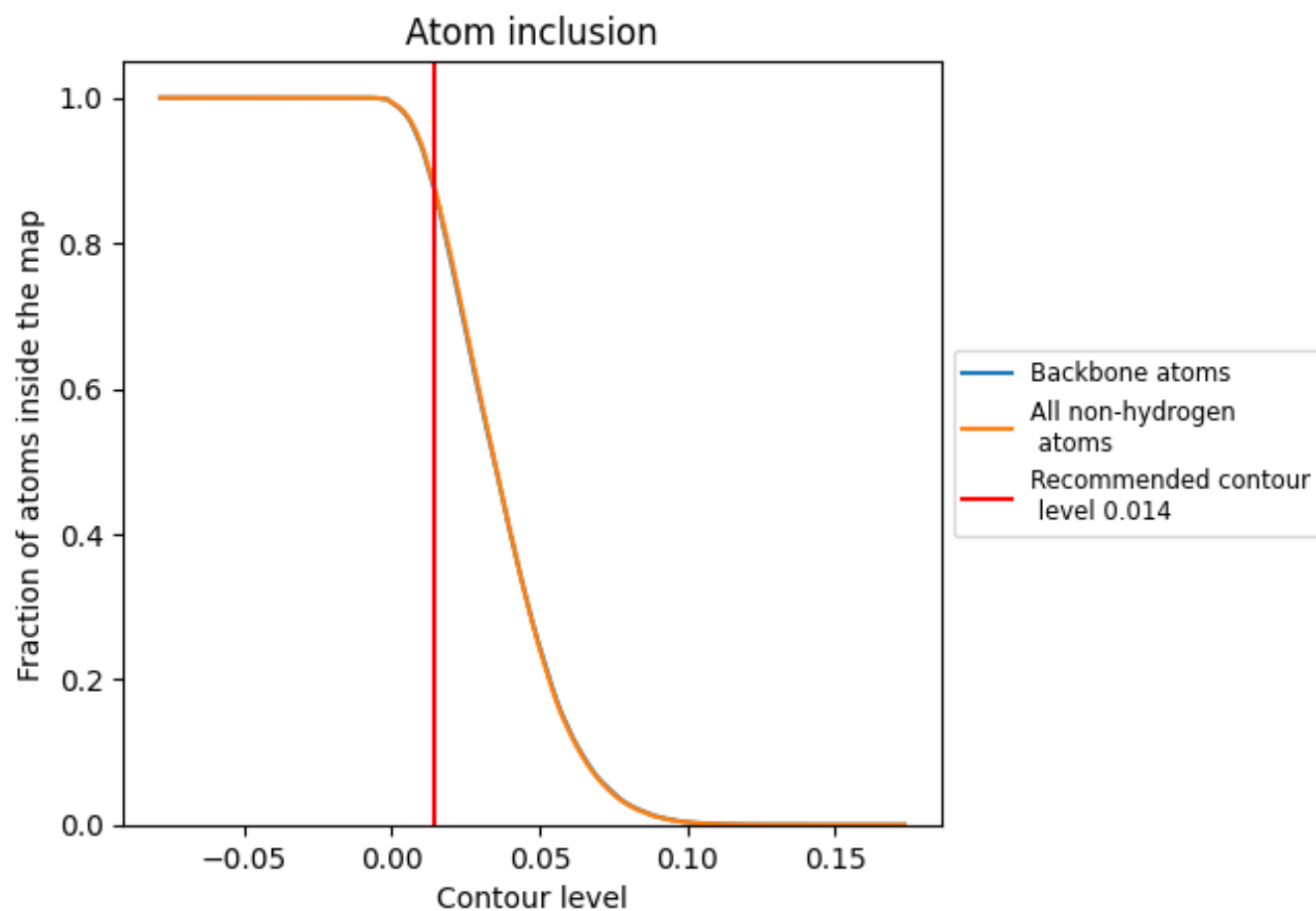
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.014).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 88% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8834	 0.5000
1	 0.7355	 0.4870
2	 0.8280	 0.4300
5	 0.9191	 0.5060
7	 0.9906	 0.5660
8	 0.9587	 0.5380
9	 0.9319	 0.4910
A	 0.9312	 0.5760
AA	 0.8526	 0.4950
B	 0.9162	 0.5500
BB	 0.8440	 0.4880
C	 0.9085	 0.5510
CC	 0.8669	 0.5180
D	 0.8937	 0.5240
DD	 0.7397	 0.4290
E	 0.8328	 0.4990
EE	 0.8592	 0.5120
F	 0.8926	 0.5530
FF	 0.8113	 0.4780
G	 0.8069	 0.4810
GG	 0.7941	 0.4230
H	 0.8829	 0.5350
HH	 0.7460	 0.4360
I	 0.9034	 0.5500
II	 0.8531	 0.5030
J	 0.8712	 0.4990
JJ	 0.8457	 0.4930
K	 0.5714	 0.4100
KK	 0.7814	 0.4160
L	 0.8502	 0.5100
LL	 0.8155	 0.5080
M	 0.8917	 0.5310
MM	 0.4513	 0.2860
N	 0.9327	 0.5700
NN	 0.8549	 0.5060



















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Chain	Atom inclusion	Q-score
O	 0.9071	 0.5570
OO	 0.8470	 0.5040
P	 0.9047	 0.5600
PP	 0.7456	 0.4050
Q	 0.9058	 0.5600
QQ	 0.8428	 0.4680
R	 0.8813	 0.5240
RR	 0.7645	 0.4470
S	 0.9164	 0.5640
SS	 0.8157	 0.4530
T	 0.9026	 0.5400
TT	 0.8340	 0.4640
U	 0.8456	 0.4820
UU	 0.7288	 0.4290
V	 0.9092	 0.5510
VV	 0.8264	 0.4840
W	 0.8900	 0.5310
WW	 0.8851	 0.5300
X	 0.8978	 0.5340
XX	 0.8833	 0.5340
Y	 0.8905	 0.5350
YY	 0.8419	 0.4620
Z	 0.8910	 0.5270
ZZ	 0.7513	 0.4360
a	 0.9211	 0.5690
aa	 0.8830	 0.5220
b	 0.7943	 0.4880
bb	 0.7950	 0.4870
c	 0.8881	 0.5380
cc	 0.7852	 0.4770
d	 0.8728	 0.5300
dd	 0.8923	 0.5080
e	 0.9036	 0.5700
ee	 0.7273	 0.4540
f	 0.9406	 0.5780
ff	 0.6059	 0.2720
g	 0.8898	 0.5400
gg	 0.7549	 0.4120
h	 0.8652	 0.5270
i	 0.8580	 0.5110
j	 0.9436	 0.5730
k	 0.8133	 0.4880

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Chain	Atom inclusion	Q-score
l	 0.9125	 0.5500
m	 0.8846	 0.5480
n	 0.8557	 0.5390
o	 0.8923	 0.5430
p	 0.8694	 0.5470
r	 0.8973	 0.5510
s	 0.2219	 0.1360
t	 0.1842	 0.1670