



wwPDB EM Validation Summary Report ⓘ

Jul 6, 2026 – 02:32 pm BST

PDB ID : 9HIG / pdb_00009hig
EMDB ID : EMD-52192
Title : Cryo-EM composite structure of 70S ribosome of marine cold bacterium *Pseudalteromonas translucida* (P. haloplanktis)TAC125.
Authors : Singh, V.; Godsora, B.K.J.; Emmerich, A.G.; Majumdar, S.; Sanyal, S.
Deposited on : 2024-11-26
Resolution : 2.36 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

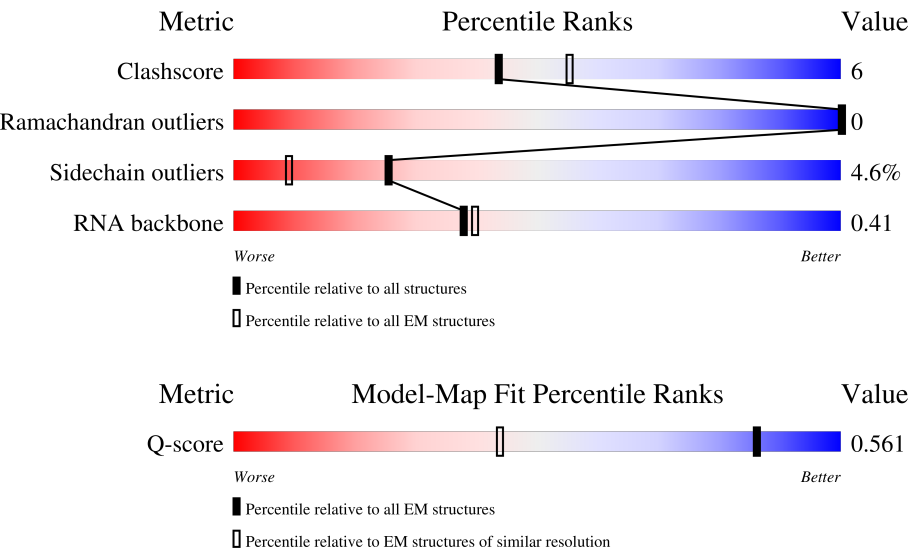
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.36 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4686 (1.86 - 2.86)

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	1528	20% 48% 31% 14% 7%
2	B	242	50% 64% 23% • 12%
3	C	233	50% 52% 33% • 13%

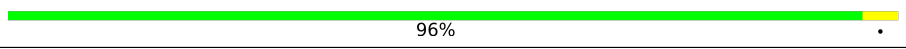
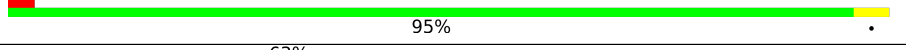
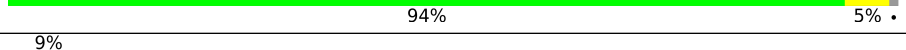
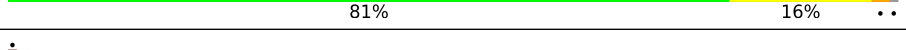
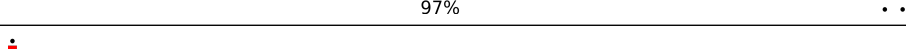
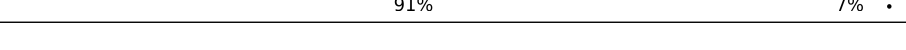
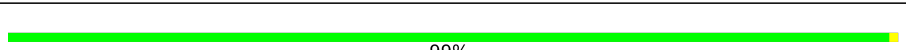
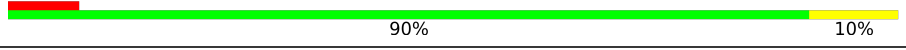
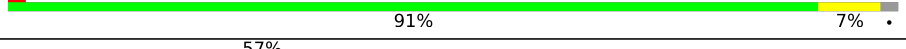
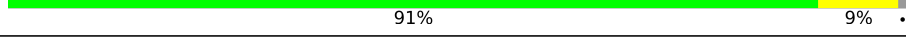
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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	168	
6	F	113	
7	G	156	
8	H	130	
9	I	129	
10	J	103	
11	K	128	
12	L	124	
13	M	118	
14	N	101	
15	O	89	
16	P	82	
17	Q	85	
18	R	75	
19	S	96	
20	T	86	
21	U	71	
22	W	18	
23	X	4	
24	a	2889	
25	b	117	
26	0	51	
27	1	44	
28	2	66	

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Mol	Chain	Length	Quality of chain
29	3	44	
30	c	274	
31	d	211	
32	e	201	
33	g	177	
34	h	150	
35	i	142	
36	j	122	
37	k	144	
38	l	137	
39	m	133	
40	n	116	
41	o	119	
42	p	120	
43	q	103	
44	r	110	
45	s	100	
46	t	104	
47	u	204	
48	v	85	
49	w	95	
50	x	63	
51	y	60	
52	z	56	
53	f	179	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 132798 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 RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1426	Total	C	N	O	P	0	0
			30595	13652	5602	9915	1426		

- Molecule 2 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	214	Total	C	N	O	S	0	0
			1668	1058	297	306	7		

- Molecule 3 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	202	Total	C	N	O	S	0	0
			1553	988	283	279	3		

- Molecule 4 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	154	Total	C	N	O	S	0	0
			1200	759	212	228	1		

- Molecule 5 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	153	Total	C	N	O	S	0	0
			1126	701	213	206	6		

- Molecule 6 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	103	Total	C	N	O	S	0	0
			834	526	149	154	5		

- Molecule 7 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	128	Total	C	N	O	S	0	0
			689	420	136	132	1		

- Molecule 8 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	129	Total	C	N	O	S	0	0
			979	620	176	180	3		

- Molecule 9 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	124	Total	C	N	O	S	0	0
			911	567	178	165	1		

- Molecule 10 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	94	Total	C	N	O	0	0
			602	371	115	116		

- Molecule 11 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	116	Total	C	N	O	S	0	0
			864	533	170	159	2		

- Molecule 12 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	82	Total	C	N	O	S	0	0
			638	395	129	112	2		

- Molecule 13 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	112	Total	C	N	O	S	0	0
			867	535	175	155	2		

- Molecule 14 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	97	Total	C	N	O	S	0	0
			774	480	156	134	4		

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	88	Total	C	N	O	S	0	0
			717	451	138	128			

- Molecule 16 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	79	Total	C	N	O	S	0	0
			634	402	123	108	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	78	Total	C	N	O	S	0	0
			633	402	118	111	2		

- Molecule 18 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	52	Total	C	N	O	0	0
			417	266	75	76		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	79	Total	C	N	O	S	0	0
			586	373	104	105	4		

- Molecule 20 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	79	Total	C	N	O	S	0	0
			622	388	126	106	2		

- Molecule 21 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	42	Total	C	N	O	S	0	0
			267	166	51	49	1		

- Molecule 22 is a RNA chain called P-site tRNA-fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	18	Total	C	N	O	P	0	0
			385	172	71	124	18		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	4	Total	C	N	O	P	0	0
			87	39	17	27	4		

- Molecule 24 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	2708	Total	C	N	O	P	0	0
			58077	25934	10643	18792	2708		

- Molecule 25 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	116	Total	C	N	O	P	0	0
			2476	1107	448	805	116		

- Molecule 26 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	0	51	Total	C	N	O	S	0	0
			420	270	76	71	3		

- Molecule 27 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	44	Total	C	N	O	S	0	0
			356	220	84	50	2		

- Molecule 28 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	65	Total	C	N	O	S	0	0
			531	338	113	77	3		

- Molecule 29 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	38	Total	C	N	O	S	0	0
			298	189	60	46	3		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	253	Total	C	N	O	S	0	0
			1941	1197	396	343	5		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	210	Total	C	N	O	S	0	0
			1551	967	288	292	4		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	201	Total	C	N	O	S	0	0
			1537	969	278	288	2		

- Molecule 33 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	168	Total	C	N	O	S	0	0
			1277	803	231	242	1		

- Molecule 34 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	149	Total	C	N	O	S	0	0
			1072	678	179	214	1		

- Molecule 35 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	141	Total	C	N	O	S	0	0
			1115	714	198	199	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	121	Total	C	N	O	S	0	0
			932	584	179	165	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	144	Total	C	N	O	S	0	0
			1052	653	204	192	3		

- Molecule 38 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	134	Total	C	N	O	S	0	0
			1078	681	212	180	5		

- Molecule 39 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	120	Total	C	N	O	S	0	0
			946	586	191	164	5		

- Molecule 40 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	108	Total	C	N	O	S	0	0
			805	498	158	148	1		

- Molecule 41 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	116	Total	C	N	O		0	0
			908	566	179	163			

- Molecule 42 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	p	118	Total	C	N	O	0	0
			945	599	190	156		

- Molecule 43 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	103	Total	C	N	O	S	0	0
			810	510	152	146	2		

- Molecule 44 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	110	Total	C	N	O	S	0	0
			843	526	158	155	4		

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	97	Total	C	N	O	S	0	0
			759	481	135	142	1		

- Molecule 46 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	103	Total	C	N	O	0	0
			769	482	141	146		

- Molecule 47 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	u	96	Total	C	N	O	0	0
			769	482	138	149		

- Molecule 48 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	v	78	Total	C	N	O	0	0
			595	368	116	111		

- Molecule 49 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	77	Total	C	N	O	S	0	0
			620	385	129	104	2		

- Molecule 50 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	63	Total	C	N	O	S	0	0
			496	303	97	93	3		

- Molecule 51 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	57	Total	C	N	O	S	0	0
			442	274	86	79	3		

- Molecule 52 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	55	Total	C	N	O	S	0	0
			427	255	91	80	1		

- Molecule 53 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	f	178	Total	C	N	O	S	0	0
			987	606	197	183	1		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	47	Total	Mg	0
			47	47	
54	D	1	Total	Mg	0
			1	1	
54	F	1	Total	Mg	0
			1	1	
54	N	1	Total	Mg	0
			1	1	
54	S	1	Total	Mg	0
			1	1	
54	a	230	Total	Mg	0
			230	230	

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Mol	Chain	Residues	Atoms		AltConf
54	b	3	Total 3	Mg 3	0
54	c	3	Total 3	Mg 3	0
54	d	1	Total 1	Mg 1	0
54	e	1	Total 1	Mg 1	0

- Molecule 55 is water.

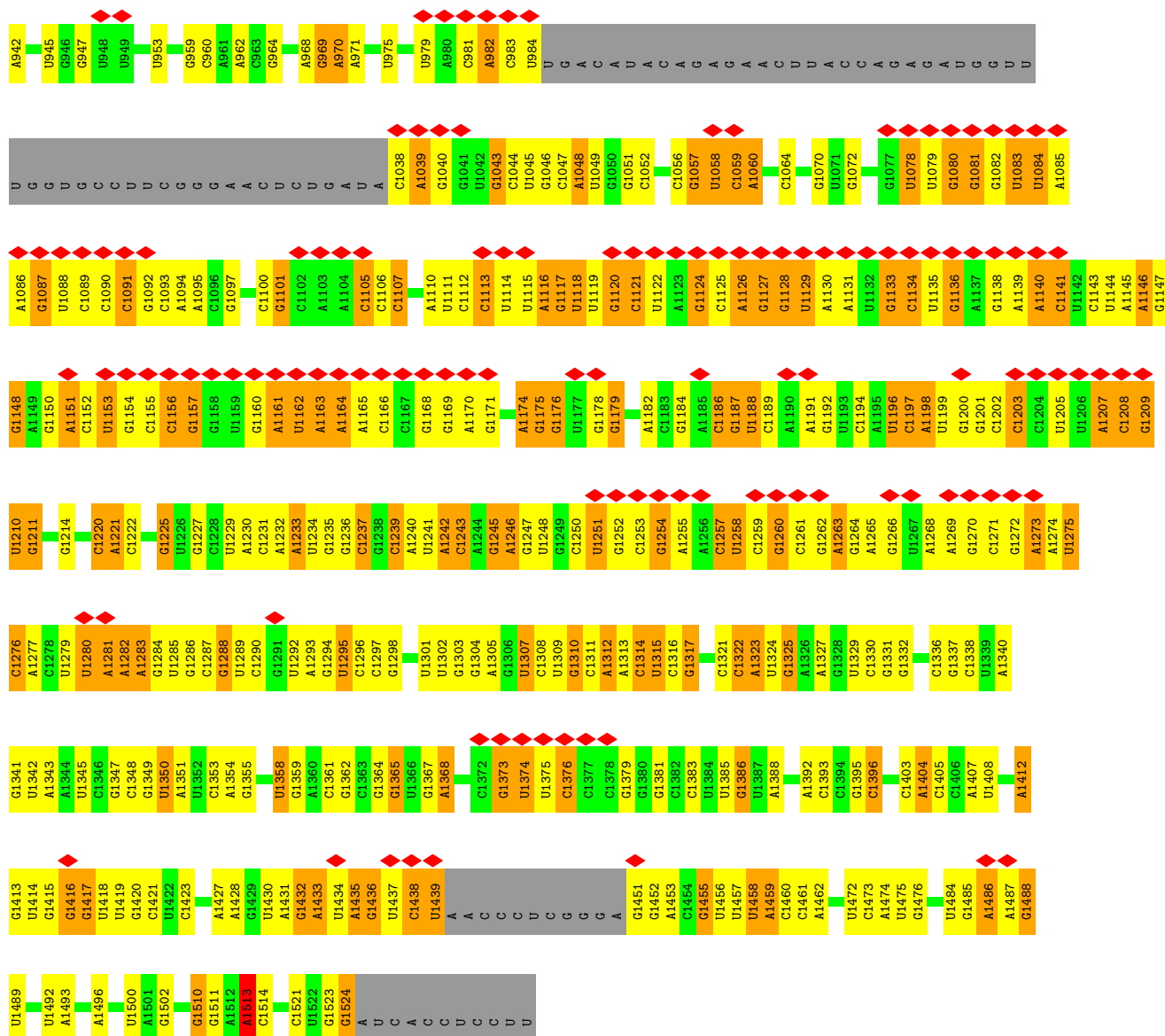
Mol	Chain	Residues	Atoms		AltConf
55	A	2	Total 2	O 2	0
55	a	22	Total 22	O 22	0
55	c	1	Total 1	O 1	0
55	m	1	Total 1	O 1	0
55	z	1	Total 1	O 1	0

3 Residue-property plots

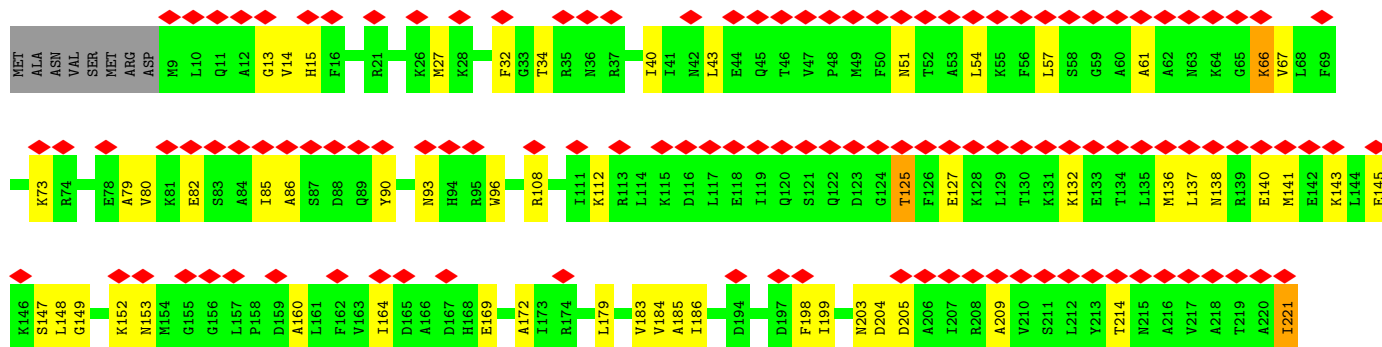
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

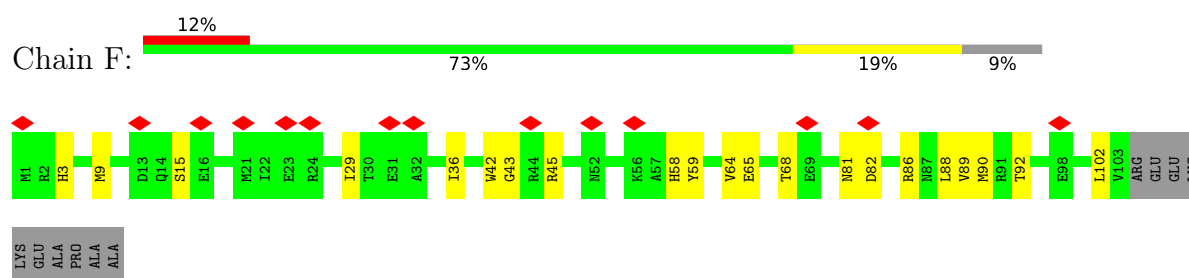
• Molecule 1: 16S rRNA



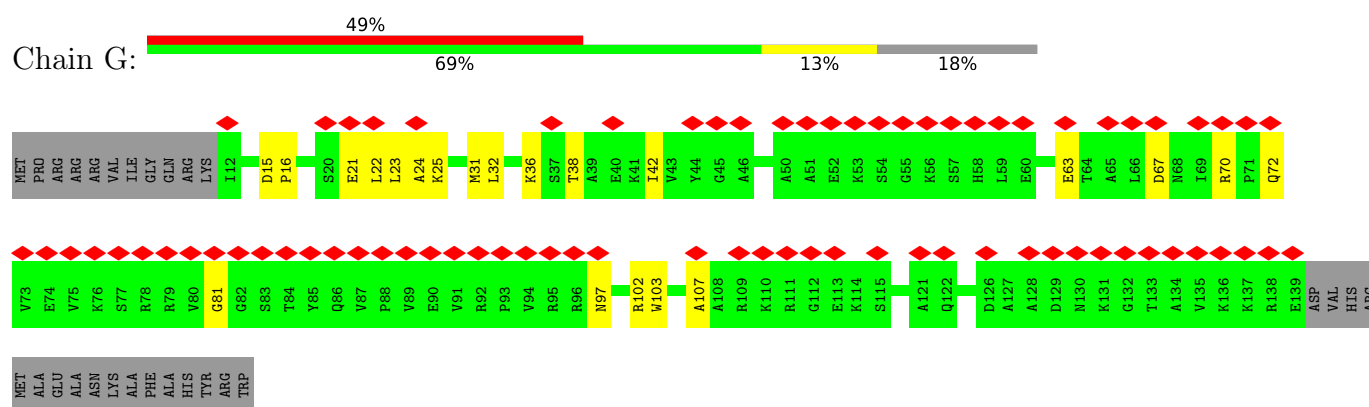


• Molecule 2: Small ribosomal subunit protein uS2

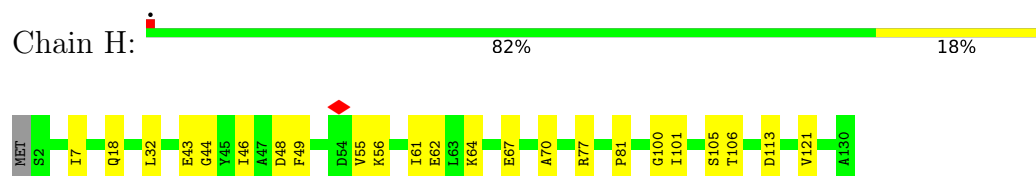




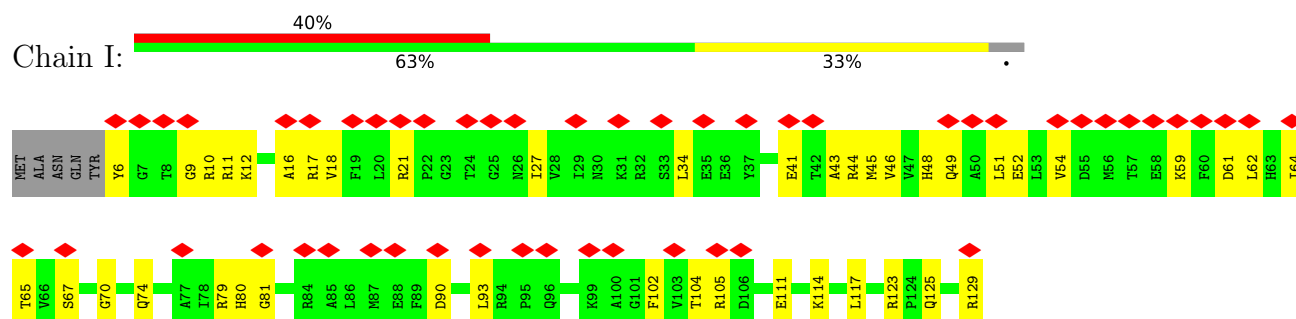
• Molecule 7: Small ribosomal subunit protein uS7



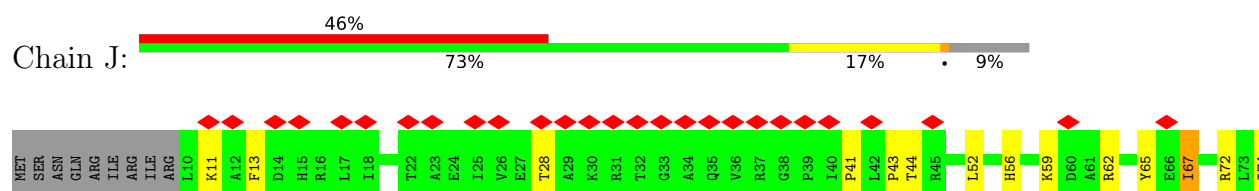
• Molecule 8: Small ribosomal subunit protein uS8

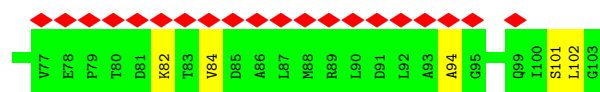


• Molecule 9: Small ribosomal subunit protein uS9

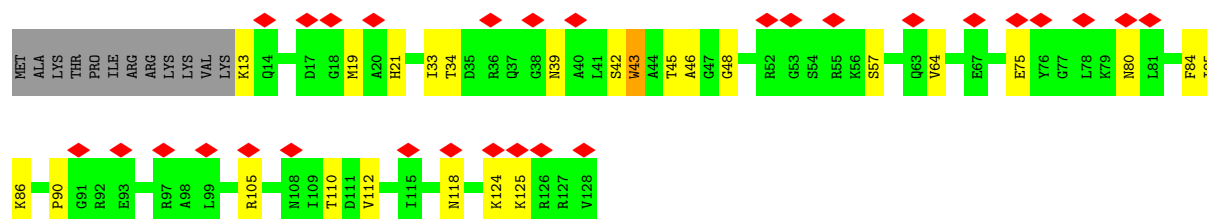


• Molecule 10: Small ribosomal subunit protein uS10

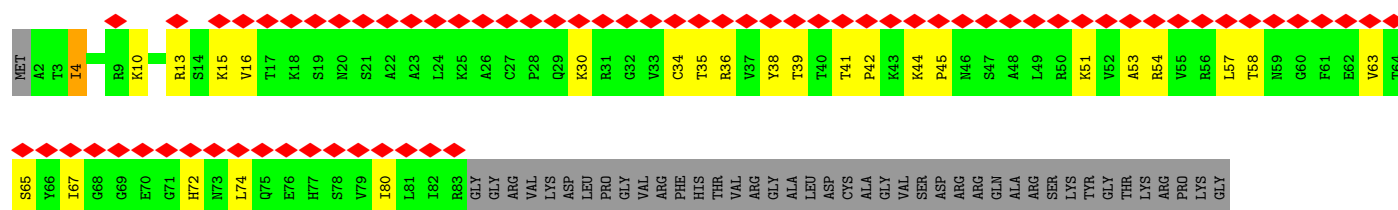




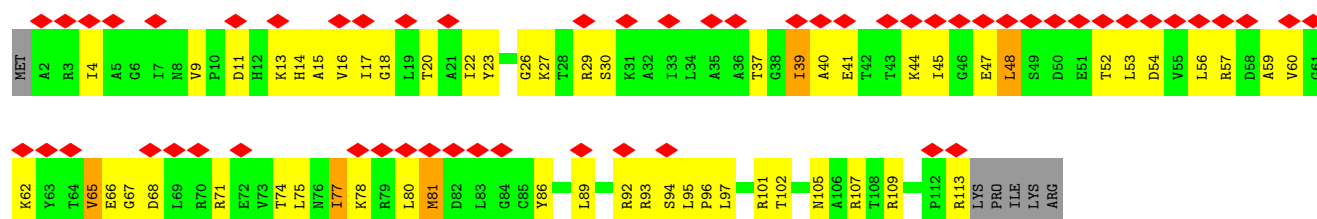
- Molecule 11: Small ribosomal subunit protein uS11



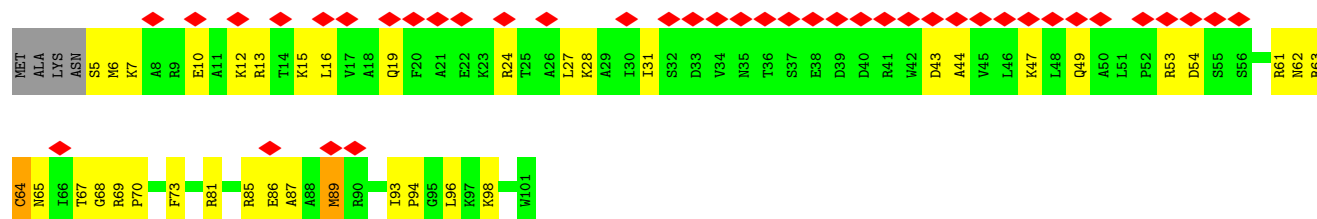
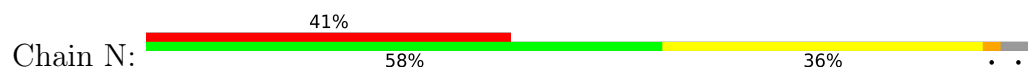
- Molecule 12: Small ribosomal subunit protein uS12



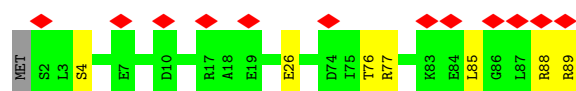
- Molecule 13: Small ribosomal subunit protein uS13



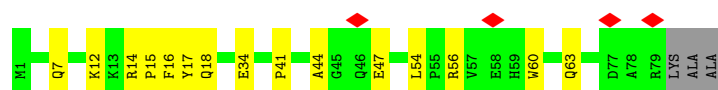
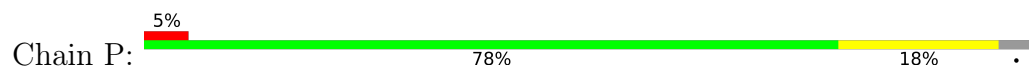
- Molecule 14: Small ribosomal subunit protein uS14



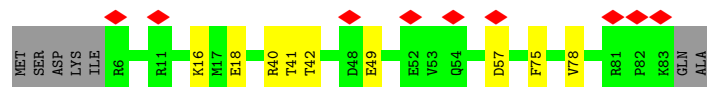
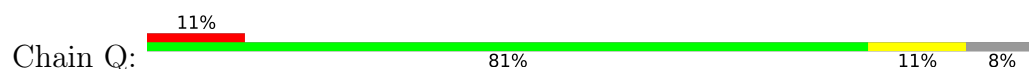
- Molecule 15: Small ribosomal subunit protein uS15



- Molecule 16: Small ribosomal subunit protein bS16



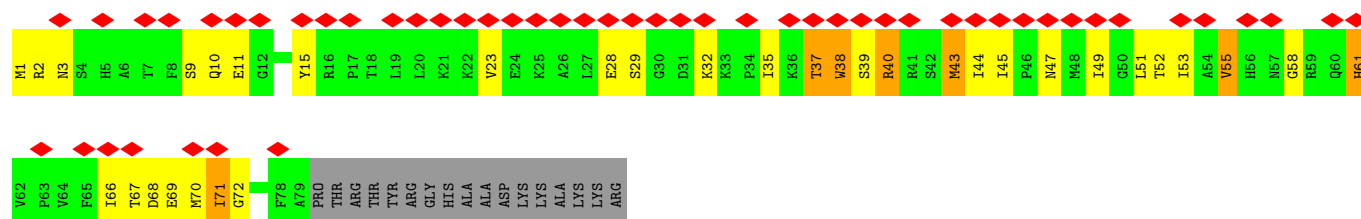
- Molecule 17: Small ribosomal subunit protein uS17



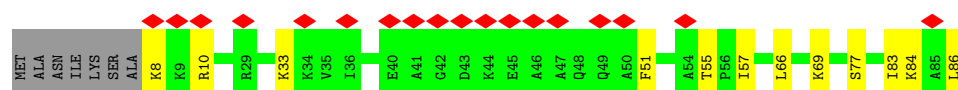
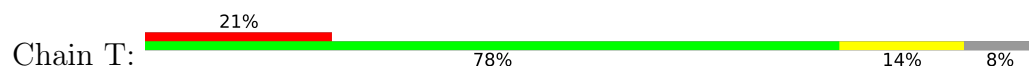
- Molecule 18: Small ribosomal subunit protein bS18



- Molecule 19: Small ribosomal subunit protein uS19

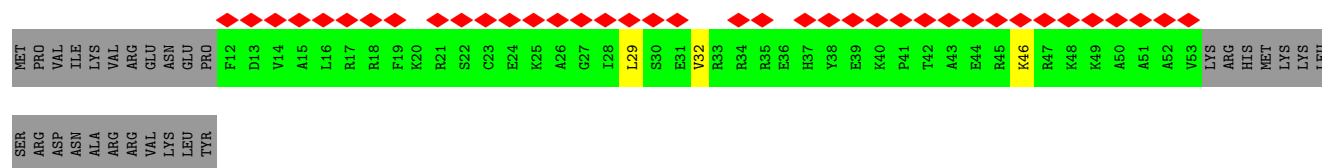


- Molecule 20: Small ribosomal subunit protein bS20

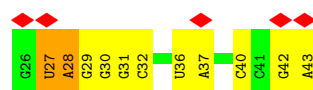
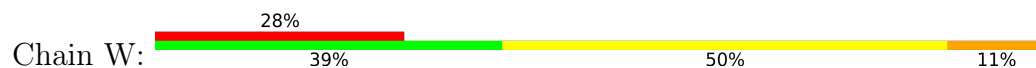


- Molecule 21: Small ribosomal subunit protein bS21





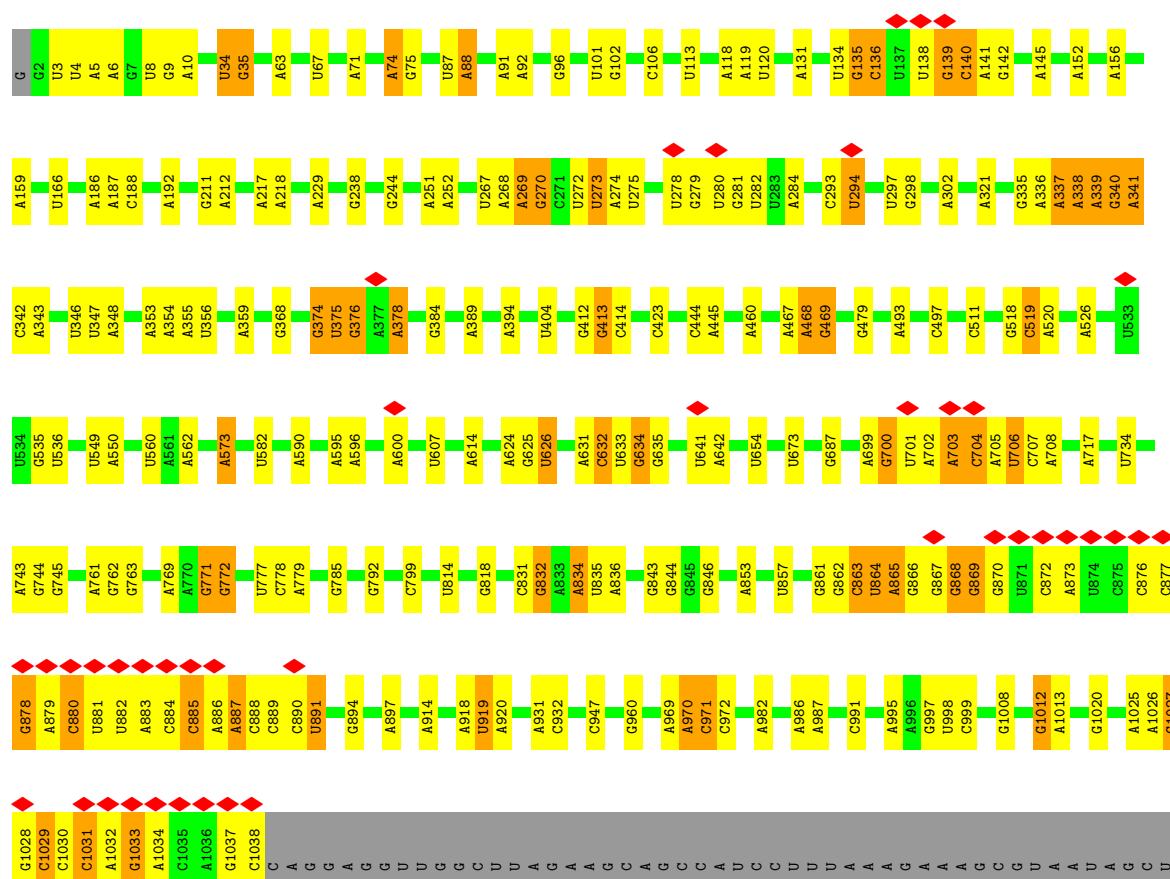
• Molecule 22: P-site tRNA-fMet

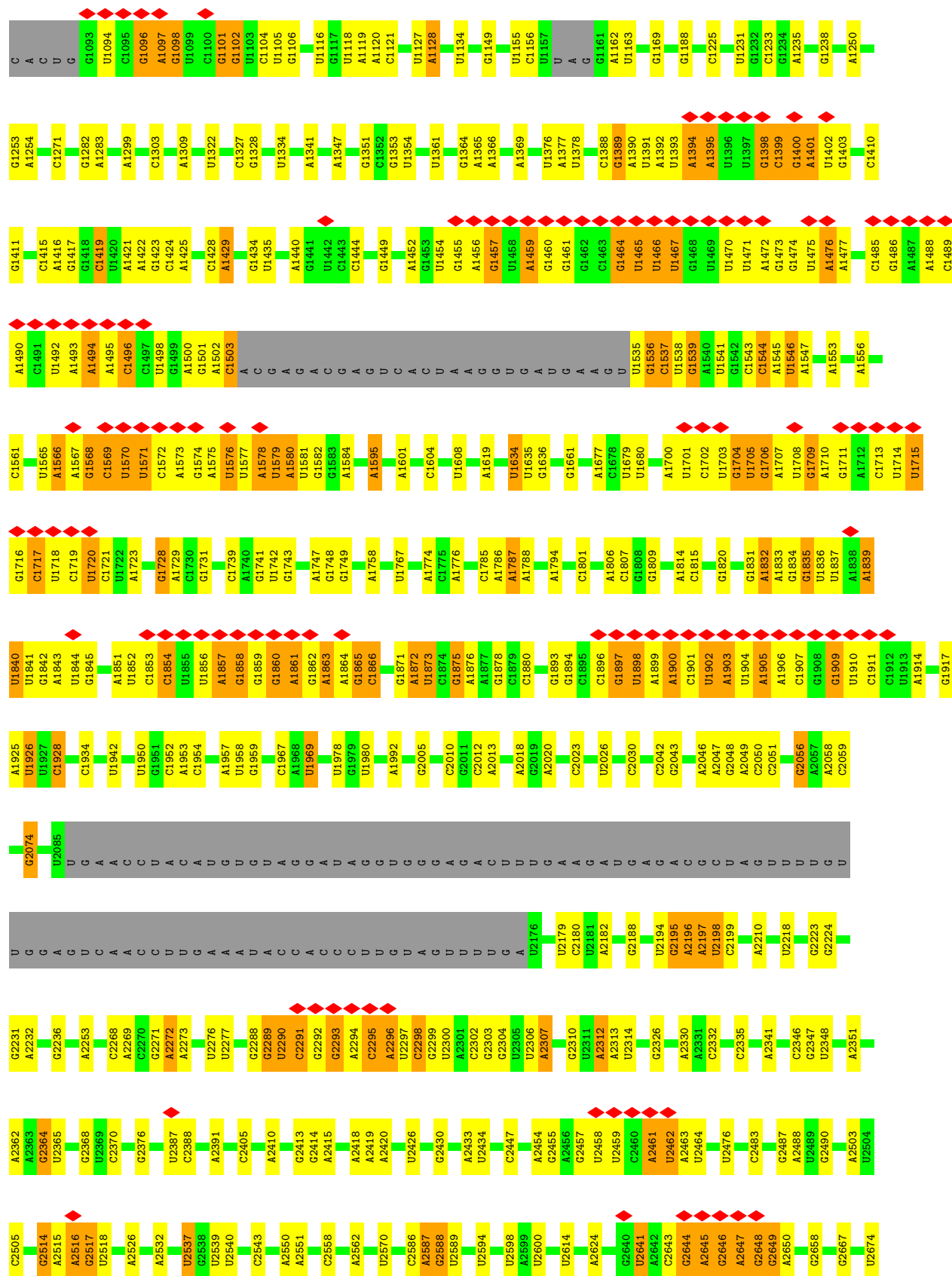


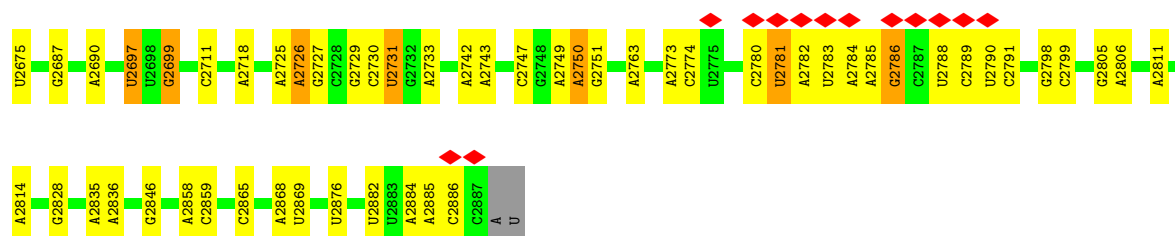
• Molecule 23: mRNA



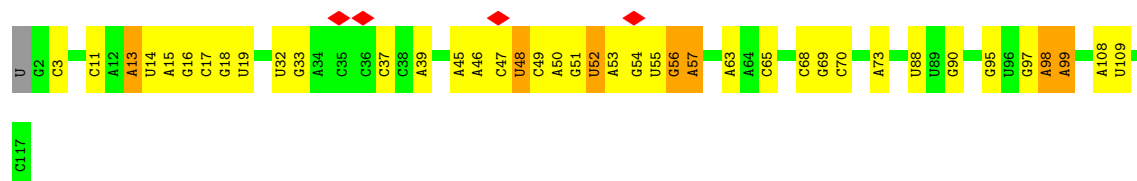
• Molecule 24: 23S rRNA



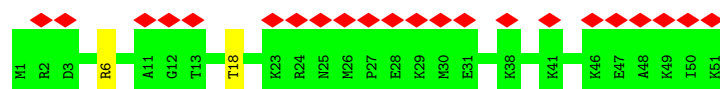
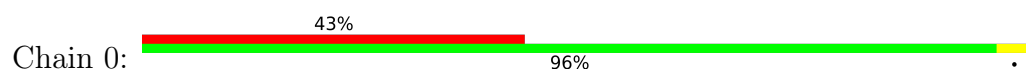




• Molecule 25: 5S rRNA



• Molecule 26: Large ribosomal subunit protein bL33



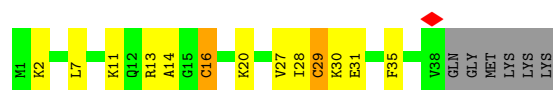
• Molecule 27: Large ribosomal subunit protein bL34



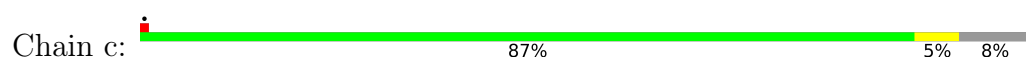
• Molecule 28: Large ribosomal subunit protein bL35



• Molecule 29: Large ribosomal subunit protein bL36



• Molecule 30: Large ribosomal subunit protein uL2

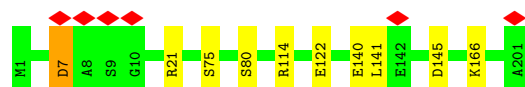




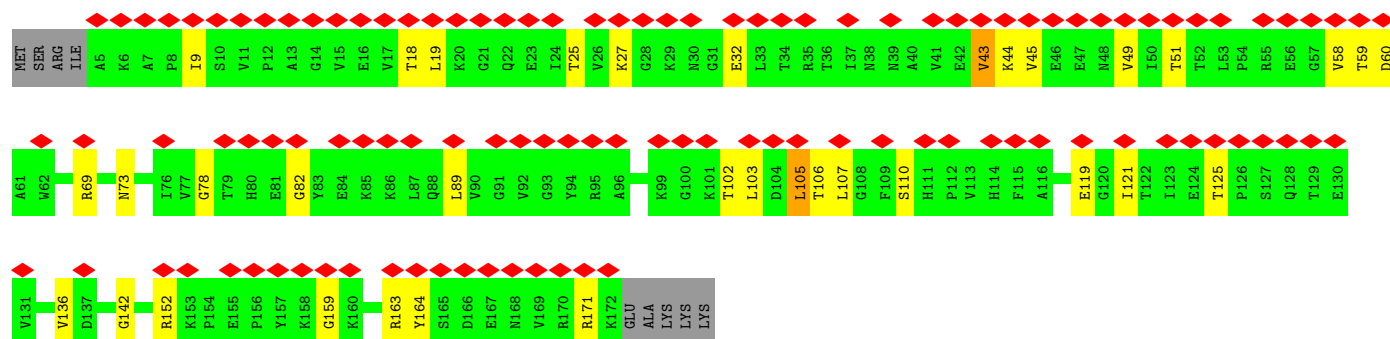
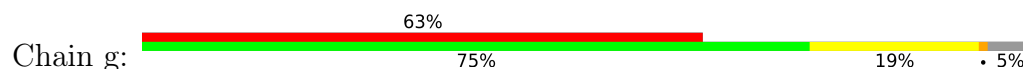
- Molecule 31: Large ribosomal subunit protein uL3



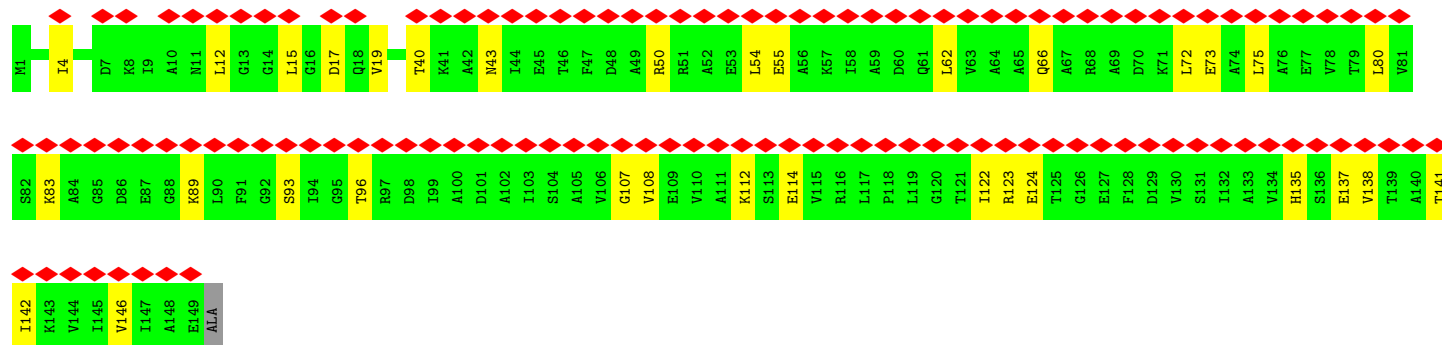
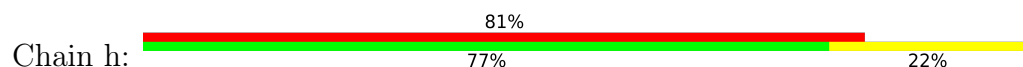
- Molecule 32: Large ribosomal subunit protein uL4



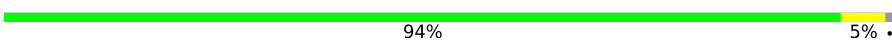
- Molecule 33: Large ribosomal subunit protein uL6



- Molecule 34: Large ribosomal subunit protein bL9



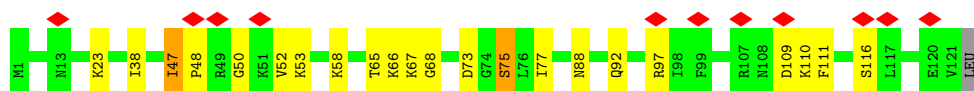
- Molecule 35: Large ribosomal subunit protein uL13

Chain i:  94% 5%

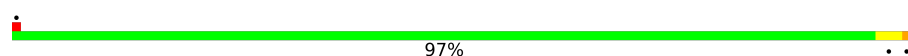


- Molecule 36: Large ribosomal subunit protein uL14

Chain j:  9% 81% 16% ..



- Molecule 37: Large ribosomal subunit protein uL15

Chain k:  97% ..



- Molecule 38: Large ribosomal subunit protein uL16

Chain l:  91% 7% .



- Molecule 39: Large ribosomal subunit protein bL17

Chain m:  84% 5% 10%



- Molecule 40: Large ribosomal subunit protein uL18

Chain n:  73% 19% 7%

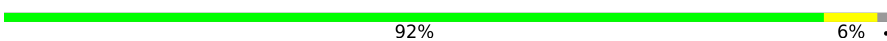


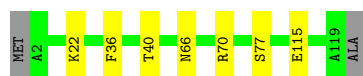
- Molecule 41: Large ribosomal subunit protein bL19

Chain o:  14% 86% 10% ..



- Molecule 42: Large ribosomal subunit protein bL20

Chain p:  92% 6% .

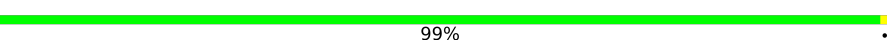


- Molecule 43: Large ribosomal subunit protein bL21

Chain q:  88% 11% .



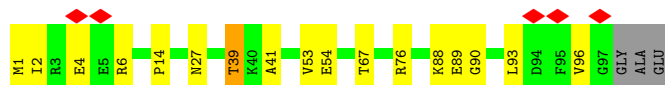
- Molecule 44: Large ribosomal subunit protein uL22

Chain r:  99% .

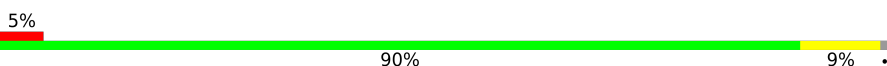


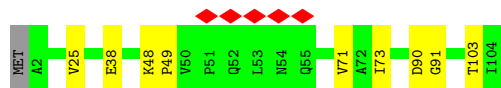
- Molecule 45: Large ribosomal subunit protein uL23

Chain s:  5% 80% 16% ..



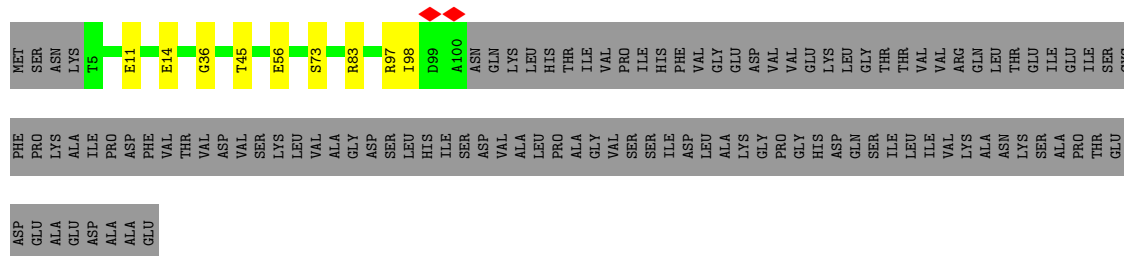
- Molecule 46: Large ribosomal subunit protein uL24

Chain t:  5% 90% 9% .

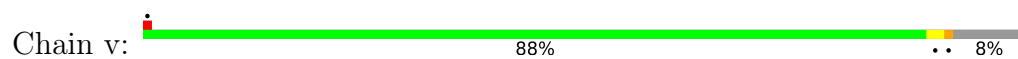


- Molecule 47: Large ribosomal subunit protein bL25

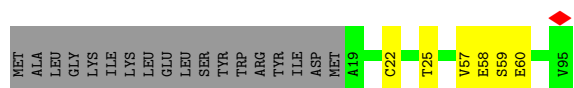
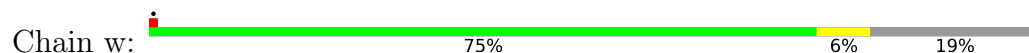
Chain u:  43% 53% .



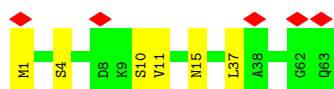
- Molecule 48: Large ribosomal subunit protein bL27



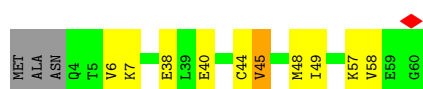
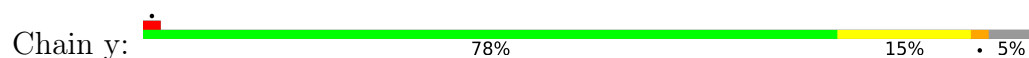
- Molecule 49: Large ribosomal subunit protein bL28



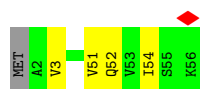
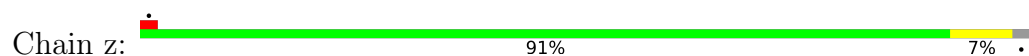
- Molecule 50: Large ribosomal subunit protein uL29



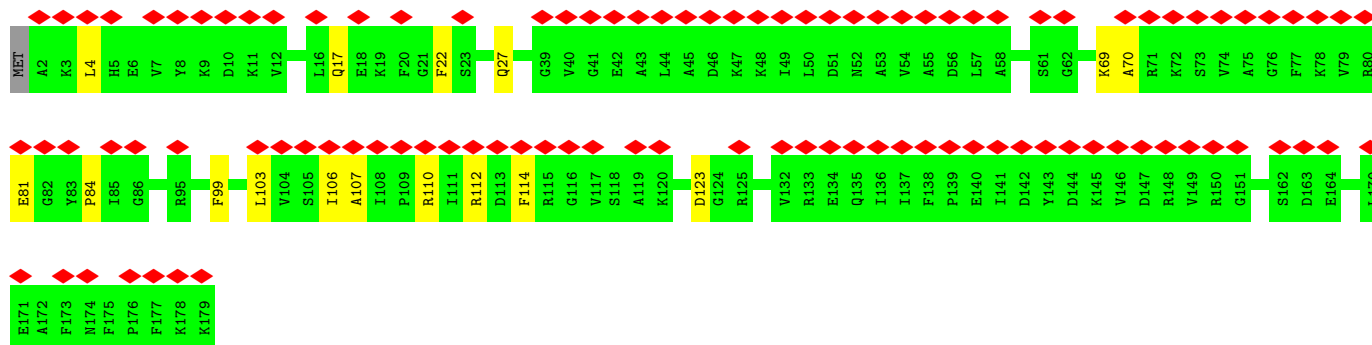
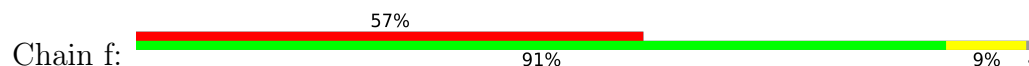
- Molecule 51: Large ribosomal subunit protein uL30



- Molecule 52: Large ribosomal subunit protein bL32



- Molecule 53: Large ribosomal subunit protein uL5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	360324	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	33.362	Depositor
Minimum map value	-7.716	Depositor
Average map value	-0.010	Depositor
Map value standard deviation	1.018	Depositor
Recommended contour level	4.5	Depositor
Map size ($\text{\AA}$)	440.32, 440.32, 440.32	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.86, 0.86, 0.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, OMU, 2MA, 5MC, H2U, 2MG, 5MU, MG, UR3, OMG, G7M, MA6, 4OC

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	0.42	0/34100	0.36	0/53181
2	B	0.23	0/1699	0.38	0/2296
3	C	0.23	0/1580	0.39	0/2134
4	D	0.27	0/1215	0.53	1/1642 (0.1%)
5	E	0.36	0/1138	0.47	1/1530 (0.1%)
6	F	0.33	0/851	0.32	0/1154
7	G	0.23	0/692	0.41	0/953
8	H	0.41	0/990	0.38	0/1327
9	I	0.28	0/923	0.43	0/1239
10	J	0.32	0/611	0.44	0/839
11	K	0.27	0/881	0.45	1/1191 (0.1%)
12	L	0.18	0/646	0.28	0/869
13	M	0.26	0/875	0.51	0/1174
14	N	0.27	0/785	0.43	0/1048
15	O	0.35	0/727	0.26	0/969
16	P	0.42	0/645	0.41	0/863
17	Q	0.36	0/645	0.38	0/868
18	R	0.44	0/423	0.41	0/572
19	S	0.20	0/598	0.38	0/808
20	T	0.34	0/629	0.42	0/837
21	U	0.13	0/270	0.19	0/369
22	W	0.31	0/430	0.38	0/668
23	X	0.44	0/97	0.36	0/149
24	a	0.37	0/64816	0.39	0/101081
25	b	0.29	0/2770	0.33	0/4315
26	0	0.15	0/427	0.35	0/566
27	1	0.33	0/359	0.35	0/471
28	2	0.30	0/542	0.44	0/714
29	3	0.30	0/300	0.54	0/395
30	c	0.29	0/1978	0.39	0/2659
31	d	0.32	0/1573	0.43	0/2116
32	e	0.30	0/1556	0.38	0/2095

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.14	0/1296	0.28	0/1755
34	h	0.15	0/1081	0.38	0/1467
35	i	0.33	0/1139	0.38	0/1535
36	j	0.27	0/941	0.37	0/1262
37	k	0.30	0/1062	0.40	0/1413
38	l	0.31	0/1098	0.39	0/1465
39	m	0.34	0/960	0.42	0/1285
40	n	0.25	0/813	0.46	0/1095
41	o	0.29	0/917	0.36	0/1229
42	p	0.35	0/958	0.32	0/1279
43	q	0.33	0/822	0.45	0/1097
44	r	0.33	0/852	0.38	0/1143
45	s	0.29	0/767	0.45	0/1028
46	t	0.28	0/775	0.43	0/1037
47	u	0.28	0/781	0.37	0/1054
48	v	0.31	0/603	0.45	0/804
49	w	0.30	0/629	0.43	0/842
50	x	0.24	0/497	0.30	0/663
51	y	0.32	0/445	0.45	0/596
52	z	0.31	0/433	0.42	0/577
53	f	0.13	0/997	0.33	0/1373
All	All	0.36	0/143637	0.38	3/215091 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
30	c	0	1
37	k	0	1
All	All	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	59	PRO	CA-N-CD	-7.26	101.83	112.00
11	K	43	TRP	N-CA-CB	-5.23	108.21	114.17
4	D	140	GLU	CA-CB-CG	5.13	124.37	114.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
30	c	232	HIS	Peptide
37	k	27	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	30595	0	15410	430	0
2	B	1668	0	1690	39	0
3	C	1553	0	1609	57	0
4	D	1200	0	1203	57	0
5	E	1126	0	1179	12	0
6	F	834	0	831	10	0
7	G	689	0	440	15	0
8	H	979	0	1039	14	0
9	I	911	0	897	34	0
10	J	602	0	463	12	0
11	K	864	0	864	18	0
12	L	638	0	684	15	0
13	M	867	0	924	42	0
14	N	774	0	814	31	0
15	O	717	0	744	3	0
16	P	634	0	658	14	0
17	Q	633	0	658	7	0
18	R	417	0	440	7	0
19	S	586	0	577	31	0
20	T	622	0	664	9	0
21	U	267	0	210	1	0
22	W	385	0	196	7	0
23	X	87	0	44	0	0
24	a	58077	0	29220	366	0
25	b	2476	0	1251	21	0
26	0	420	0	443	1	0
27	1	356	0	406	1	0
28	2	531	0	585	4	0
29	3	298	0	340	13	0
30	c	1941	0	1995	10	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	d	1551	0	1579	4	0
32	e	1537	0	1602	6	0
33	g	1277	0	1322	17	0
34	h	1072	0	1086	19	0
35	i	1115	0	1154	3	0
36	j	932	0	1005	16	0
37	k	1052	0	1122	2	0
38	l	1078	0	1136	4	0
39	m	946	0	994	3	0
40	n	805	0	827	16	0
41	o	908	0	949	11	0
42	p	945	0	1005	3	0
43	q	810	0	836	8	0
44	r	843	0	894	1	0
45	s	759	0	799	10	0
46	t	769	0	792	3	0
47	u	769	0	771	4	0
48	v	595	0	603	1	0
49	w	620	0	654	4	0
50	x	496	0	525	3	0
51	y	442	0	475	7	0
52	z	427	0	424	1	0
53	f	987	0	597	12	0
54	A	47	0	0	0	0
54	D	1	0	0	0	0
54	F	1	0	0	0	0
54	N	1	0	0	0	0
54	S	1	0	0	0	0
54	a	230	0	0	0	0
54	b	3	0	0	0	0
54	c	3	0	0	0	0
54	d	1	0	0	0	0
54	e	1	0	0	0	0
55	A	2	0	0	0	0
55	a	22	0	0	4	0
55	c	1	0	0	0	0
55	m	1	0	0	0	0
55	z	1	0	0	0	0
All	All	132798	0	87629	1356	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1356 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:a:1926:5MU:C5	24:a:1926:5MU:C4	1.81	1.67
24:a:284:A:N6	24:a:335:G:H1	1.56	1.02
1:A:1298:G:H22	1:A:1329:U:H3	1.06	0.99
1:A:1304:G:H1	1:A:1323:A:H2	1.06	0.98
24:a:1400:G:O6	24:a:1567:A:N1	1.97	0.97

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	212/242 (88%)	192 (91%)	20 (9%)	0	100	100
3	C	200/233 (86%)	182 (91%)	18 (9%)	0	100	100
4	D	152/206 (74%)	128 (84%)	24 (16%)	0	100	100
5	E	151/168 (90%)	144 (95%)	7 (5%)	0	100	100
6	F	101/113 (89%)	97 (96%)	4 (4%)	0	100	100
7	G	126/156 (81%)	114 (90%)	12 (10%)	0	100	100
8	H	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
9	I	122/129 (95%)	104 (85%)	18 (15%)	0	100	100
10	J	92/103 (89%)	77 (84%)	15 (16%)	0	100	100
11	K	114/128 (89%)	99 (87%)	15 (13%)	0	100	100
12	L	80/124 (64%)	76 (95%)	4 (5%)	0	100	100
13	M	110/118 (93%)	95 (86%)	15 (14%)	0	100	100
14	N	95/101 (94%)	87 (92%)	8 (8%)	0	100	100
15	O	86/89 (97%)	83 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	P	77/82 (94%)	73 (95%)	4 (5%)	0	100	100
17	Q	76/85 (89%)	71 (93%)	5 (7%)	0	100	100
18	R	50/75 (67%)	48 (96%)	2 (4%)	0	100	100
19	S	77/96 (80%)	69 (90%)	8 (10%)	0	100	100
20	T	77/86 (90%)	74 (96%)	3 (4%)	0	100	100
21	U	40/71 (56%)	40 (100%)	0	0	100	100
26	0	49/51 (96%)	46 (94%)	3 (6%)	0	100	100
27	1	42/44 (96%)	42 (100%)	0	0	100	100
28	2	63/66 (96%)	59 (94%)	4 (6%)	0	100	100
29	3	36/44 (82%)	30 (83%)	6 (17%)	0	100	100
30	c	251/274 (92%)	239 (95%)	12 (5%)	0	100	100
31	d	208/211 (99%)	196 (94%)	12 (6%)	0	100	100
32	e	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
33	g	166/177 (94%)	156 (94%)	10 (6%)	0	100	100
34	h	147/150 (98%)	131 (89%)	16 (11%)	0	100	100
35	i	139/142 (98%)	139 (100%)	0	0	100	100
36	j	119/122 (98%)	111 (93%)	8 (7%)	0	100	100
37	k	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
38	l	132/137 (96%)	126 (96%)	6 (4%)	0	100	100
39	m	118/133 (89%)	112 (95%)	6 (5%)	0	100	100
40	n	106/116 (91%)	93 (88%)	13 (12%)	0	100	100
41	o	114/119 (96%)	108 (95%)	6 (5%)	0	100	100
42	p	116/120 (97%)	113 (97%)	3 (3%)	0	100	100
43	q	101/103 (98%)	89 (88%)	12 (12%)	0	100	100
44	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
45	s	95/100 (95%)	87 (92%)	8 (8%)	0	100	100
46	t	101/104 (97%)	94 (93%)	7 (7%)	0	100	100
47	u	94/204 (46%)	92 (98%)	2 (2%)	0	100	100
48	v	76/85 (89%)	69 (91%)	7 (9%)	0	100	100
49	w	75/95 (79%)	70 (93%)	5 (7%)	0	100	100
50	x	61/63 (97%)	60 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	y	55/60 (92%)	54 (98%)	1 (2%)	0	100	100
52	z	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
53	f	176/179 (98%)	166 (94%)	10 (6%)	0	100	100
All	All	5307/5945 (89%)	4935 (93%)	372 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	B	177/200 (88%)	168 (95%)	9 (5%)	21	26
3	C	162/191 (85%)	151 (93%)	11 (7%)	14	16
4	D	124/176 (70%)	117 (94%)	7 (6%)	19	23
5	E	117/129 (91%)	110 (94%)	7 (6%)	17	21
6	F	91/98 (93%)	86 (94%)	5 (6%)	19	24
7	G	18/128 (14%)	17 (94%)	1 (6%)	19	23
8	H	104/105 (99%)	99 (95%)	5 (5%)	23	29
9	I	86/106 (81%)	82 (95%)	4 (5%)	23	30
10	J	39/91 (43%)	31 (80%)	8 (20%)	1	1
11	K	86/97 (89%)	83 (96%)	3 (4%)	32	42
12	L	71/103 (69%)	62 (87%)	9 (13%)	4	4
13	M	90/96 (94%)	83 (92%)	7 (8%)	11	12
14	N	81/84 (96%)	77 (95%)	4 (5%)	22	28
15	O	76/77 (99%)	74 (97%)	2 (3%)	40	54
16	P	65/66 (98%)	65 (100%)	0	100	100
17	Q	70/76 (92%)	68 (97%)	2 (3%)	37	49
18	R	44/64 (69%)	40 (91%)	4 (9%)	9	9
19	S	60/82 (73%)	50 (83%)	10 (17%)	2	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	T	62/68 (91%)	60 (97%)	2 (3%)	34	46
21	U	16/63 (25%)	14 (88%)	2 (12%)	4	4
26	0	45/47 (96%)	44 (98%)	1 (2%)	45	59
27	1	35/35 (100%)	35 (100%)	0	100	100
28	2	55/56 (98%)	54 (98%)	1 (2%)	51	66
29	3	33/38 (87%)	30 (91%)	3 (9%)	9	9
30	c	198/216 (92%)	195 (98%)	3 (2%)	57	72
31	d	158/159 (99%)	156 (99%)	2 (1%)	61	76
32	e	159/159 (100%)	155 (98%)	4 (2%)	42	55
33	g	135/143 (94%)	122 (90%)	13 (10%)	8	7
34	h	108/114 (95%)	100 (93%)	8 (7%)	13	14
35	i	118/119 (99%)	116 (98%)	2 (2%)	53	68
36	j	102/103 (99%)	98 (96%)	4 (4%)	28	39
37	k	107/107 (100%)	104 (97%)	3 (3%)	38	51
38	l	110/113 (97%)	107 (97%)	3 (3%)	39	52
39	m	100/110 (91%)	96 (96%)	4 (4%)	28	37
40	n	76/85 (89%)	72 (95%)	4 (5%)	20	25
41	o	95/99 (96%)	90 (95%)	5 (5%)	20	25
42	p	90/91 (99%)	88 (98%)	2 (2%)	45	59
43	q	85/85 (100%)	81 (95%)	4 (5%)	23	30
44	r	89/89 (100%)	89 (100%)	0	100	100
45	s	81/83 (98%)	78 (96%)	3 (4%)	30	40
46	t	80/88 (91%)	76 (95%)	4 (5%)	22	27
47	u	83/175 (47%)	79 (95%)	4 (5%)	23	29
48	v	62/67 (92%)	60 (97%)	2 (3%)	34	46
49	w	66/83 (80%)	66 (100%)	0	100	100
50	x	54/55 (98%)	52 (96%)	2 (4%)	30	40
51	y	50/52 (96%)	47 (94%)	3 (6%)	17	21
52	z	45/47 (96%)	43 (96%)	2 (4%)	25	33
53	f	25/150 (17%)	25 (100%)	0	100	100
All	All	4083/4868 (84%)	3895 (95%)	188 (5%)	25	31

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	e	141	LEU
37	k	5	THR
33	g	51	THR
34	h	17	ASP
39	m	36	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
49	w	40	ASN
49	w	53	HIS
19	S	3	ASN
16	P	63	GLN
51	y	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1422/1528 (93%)	435 (30%)	15 (1%)
22	W	17/18 (94%)	8 (47%)	0
23	X	3/4 (75%)	0	0
24	a	2703/2889 (93%)	515 (19%)	0
25	b	115/117 (98%)	25 (21%)	0
All	All	4260/4556 (93%)	983 (23%)	15 (0%)

5 of 983 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	14	U
1	A	25	C
1	A	26	A
1	A	31	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1057	G
1	A	1418	U

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Mol	Chain	Res	Type
1	A	1092	G
1	A	1488	G
1	A	1413	G

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

15 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	4OC	A	1396	1	20,23,24	2.95	8 (40%)	26,32,35	1.31	4 (15%)
24	OMC	a	2483	24,54	19,22,23	2.88	8 (42%)	26,31,34	0.86	1 (3%)
1	2MG	A	1510	1	23,26,27	2.72	9 (39%)	32,38,41	3.13	11 (34%)
24	2MG	a	1820	24	23,26,27	2.70	9 (39%)	32,38,41	3.14	13 (40%)
24	OMG	a	2236	24	23,26,27	2.33	8 (34%)	33,38,41	2.44	11 (33%)
24	G7M	a	2056	24	23,26,27	2.57	8 (34%)	35,39,42	1.88	8 (22%)
24	H2U	a	2434	24	18,21,22	2.95	5 (27%)	21,30,33	2.27	5 (23%)
1	UR3	A	1492	1	19,22,23	2.92	7 (36%)	26,32,35	1.33	3 (11%)
1	2MG	A	959	1	23,26,27	2.78	9 (39%)	32,38,41	3.56	10 (31%)
1	MA6	A	1513	1	23,26,27	1.41	4 (17%)	34,38,41	4.45	14 (41%)
24	5MU	a	1926	24	19,22,23	7.61	8 (42%)	28,32,35	3.41	10 (35%)
24	2MA	a	2488	24,54	22,25,26	3.72	8 (36%)	33,37,40	2.40	10 (30%)
24	OMU	a	2537	24	19,22,23	3.20	8 (42%)	26,31,34	1.72	5 (19%)
1	5MC	A	960	1	18,22,23	3.71	7 (38%)	26,32,35	0.98	1 (3%)
24	2MG	a	2430	24	23,26,27	2.59	9 (39%)	32,38,41	3.00	14 (43%)

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
1	4OC	A	1396	1	-	4/9/29/30	0/2/2/2
24	OMC	a	2483	24,54	-	0/9/27/28	0/2/2/2
1	2MG	A	1510	1	-	1/9/27/28	0/3/3/3
24	2MG	a	1820	24	-	0/9/27/28	0/3/3/3
24	OMG	a	2236	24	-	0/9/27/28	0/3/3/3
24	G7M	a	2056	24	-	1/7/25/26	0/3/3/3
24	H2U	a	2434	24	-	0/7/38/39	0/2/2/2
1	UR3	A	1492	1	-	0/7/25/26	0/2/2/2
1	2MG	A	959	1	-	2/9/27/28	0/3/3/3
1	MA6	A	1513	1	-	6/11/29/30	0/3/3/3
24	5MU	a	1926	24	-	0/7/25/26	0/2/2/2
24	2MA	a	2488	24,54	-	1/7/25/26	0/3/3/3
24	OMU	a	2537	24	-	2/9/27/28	0/2/2/2
1	5MC	A	960	1	-	0/7/25/26	0/2/2/2
24	2MG	a	2430	24	-	1/9/27/28	0/3/3/3

The worst 5 of 115 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	a	1926	5MU	C4-C5	22.16	1.81	1.44
24	a	1926	5MU	C6-N1	16.30	1.65	1.38
24	a	1926	5MU	C6-C5	-12.61	1.13	1.34
24	a	2488	2MA	C4-N3	11.48	1.48	1.34
24	a	1926	5MU	C4-N3	-11.25	1.18	1.38

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1513	MA6	N1-C6-N6	-15.95	99.64	117.08
1	A	959	2MG	C1'-N9-C8	-12.07	92.35	126.70
1	A	959	2MG	C1'-N9-C4	10.97	159.08	126.50
1	A	1513	MA6	C1'-N9-C8	-10.20	104.11	127.14
24	a	1926	5MU	C5-C4-N3	10.08	123.92	115.31

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	959	2MG	O4'-C1'-N9-C8
1	A	959	2MG	O4'-C1'-N9-C4
1	A	1396	4OC	O4'-C1'-N1-C2
1	A	1396	4OC	O4'-C1'-N1-C6

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Mol	Chain	Res	Type	Atoms
1	A	1513	MA6	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1510	2MG	1	0
1	A	1513	MA6	1	0
24	a	1926	5MU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 289 ligands modelled in this entry, 289 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

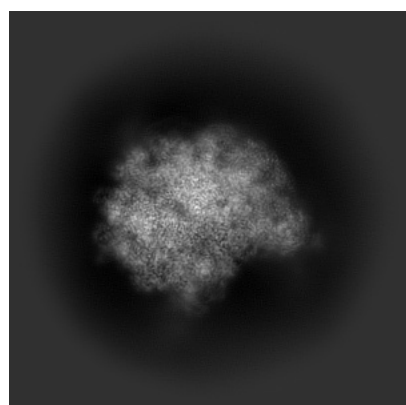
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52192. These allow visual inspection of the internal detail of the map and identification of artifacts.

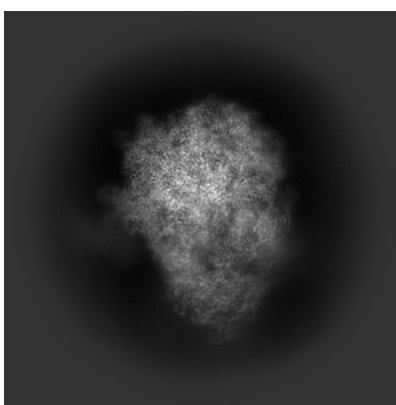
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

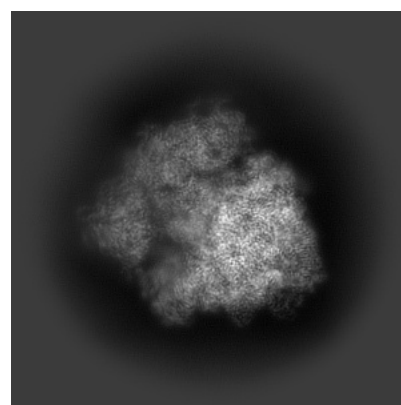
6.1.1 Primary map



X



Y

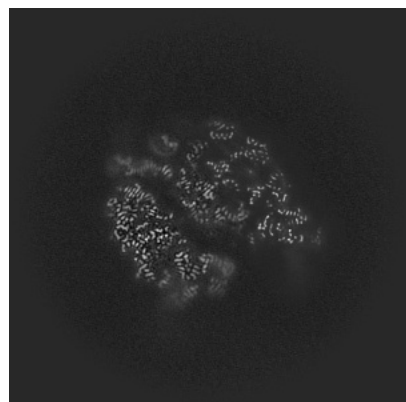


Z

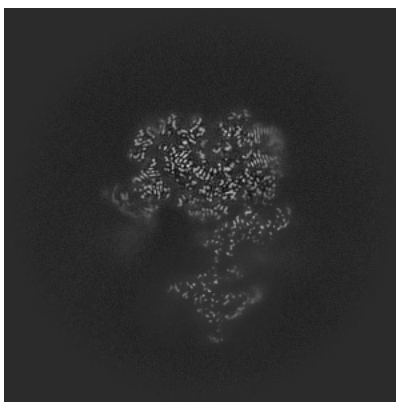
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

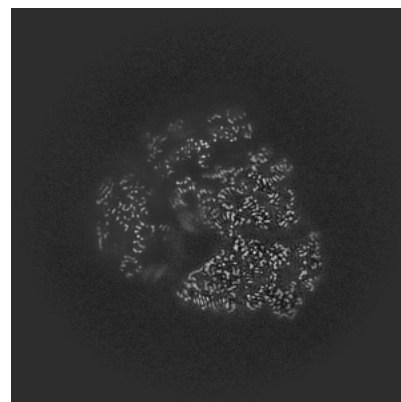
6.2.1 Primary map



X Index: 256



Y Index: 256

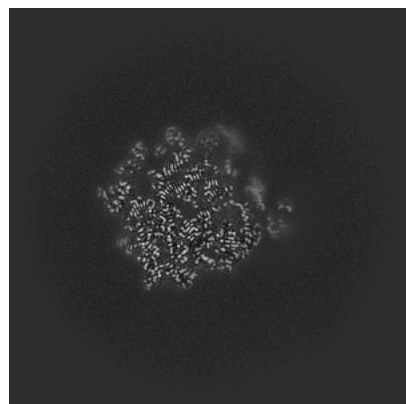


Z Index: 256

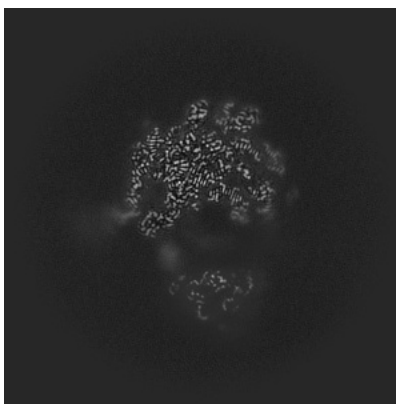
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

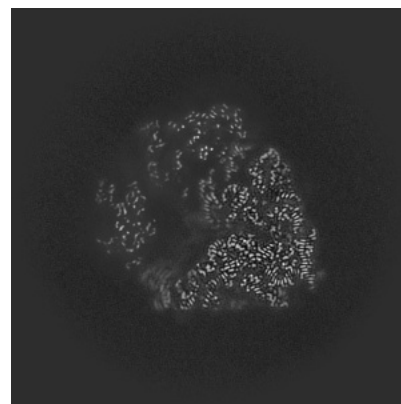
6.3.1 Primary map



X Index: 306



Y Index: 205

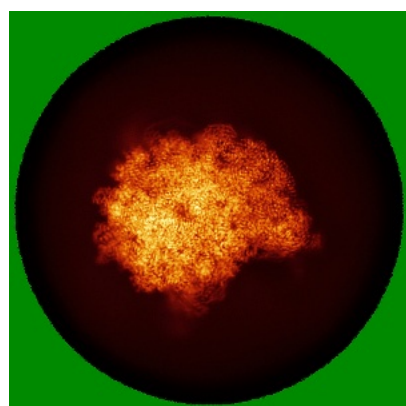


Z Index: 244

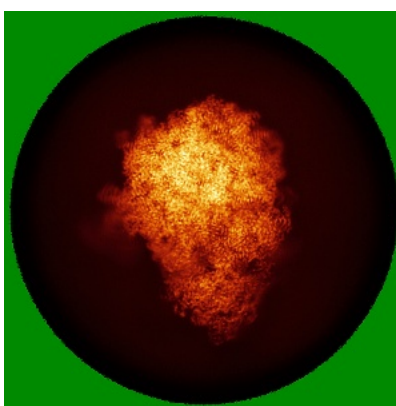
The images above show the largest variance slices of the map in three orthogonal directions.

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

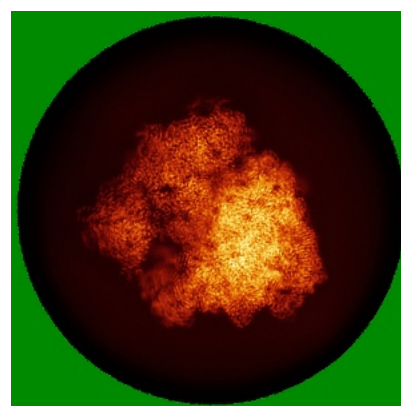
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

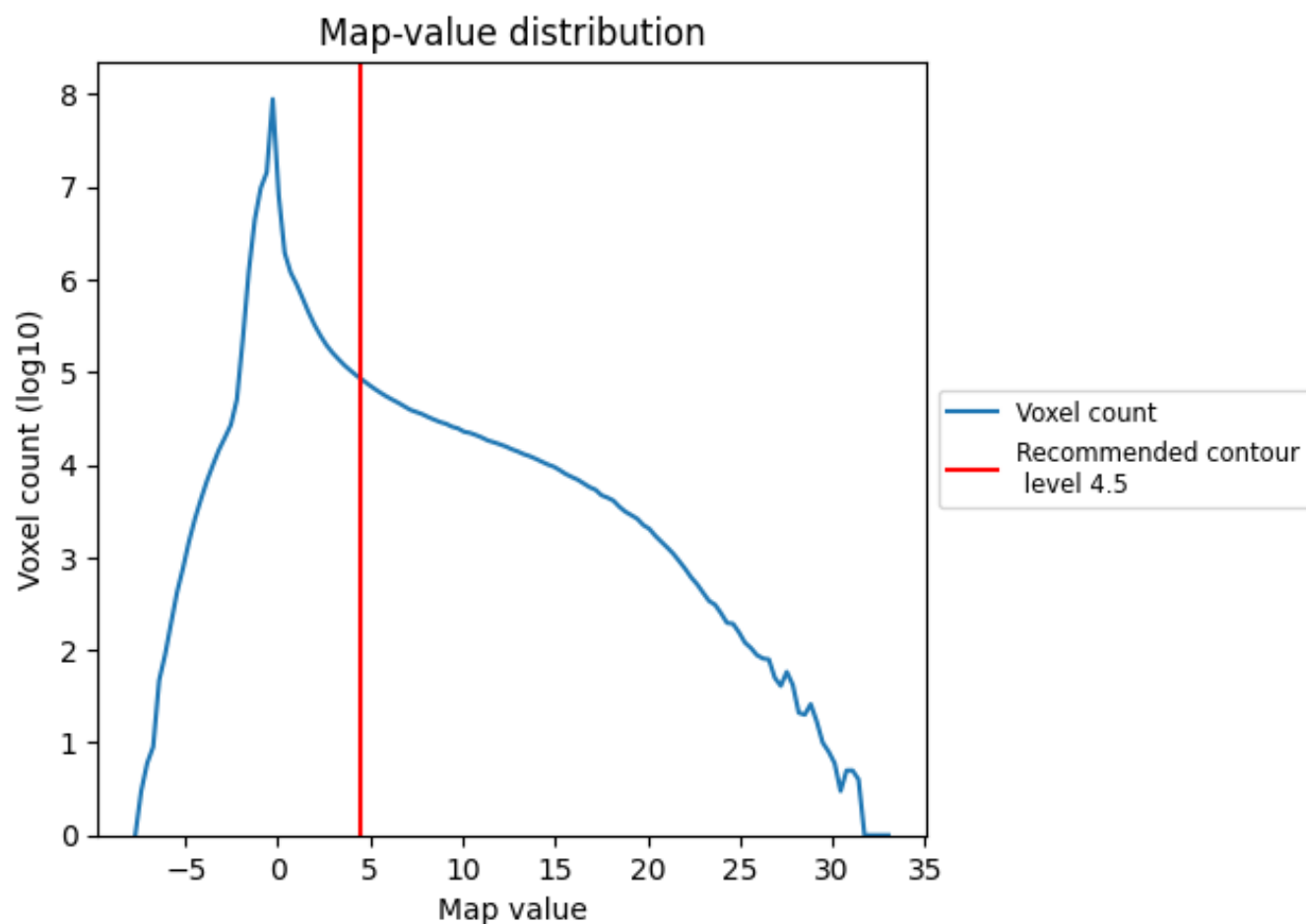
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

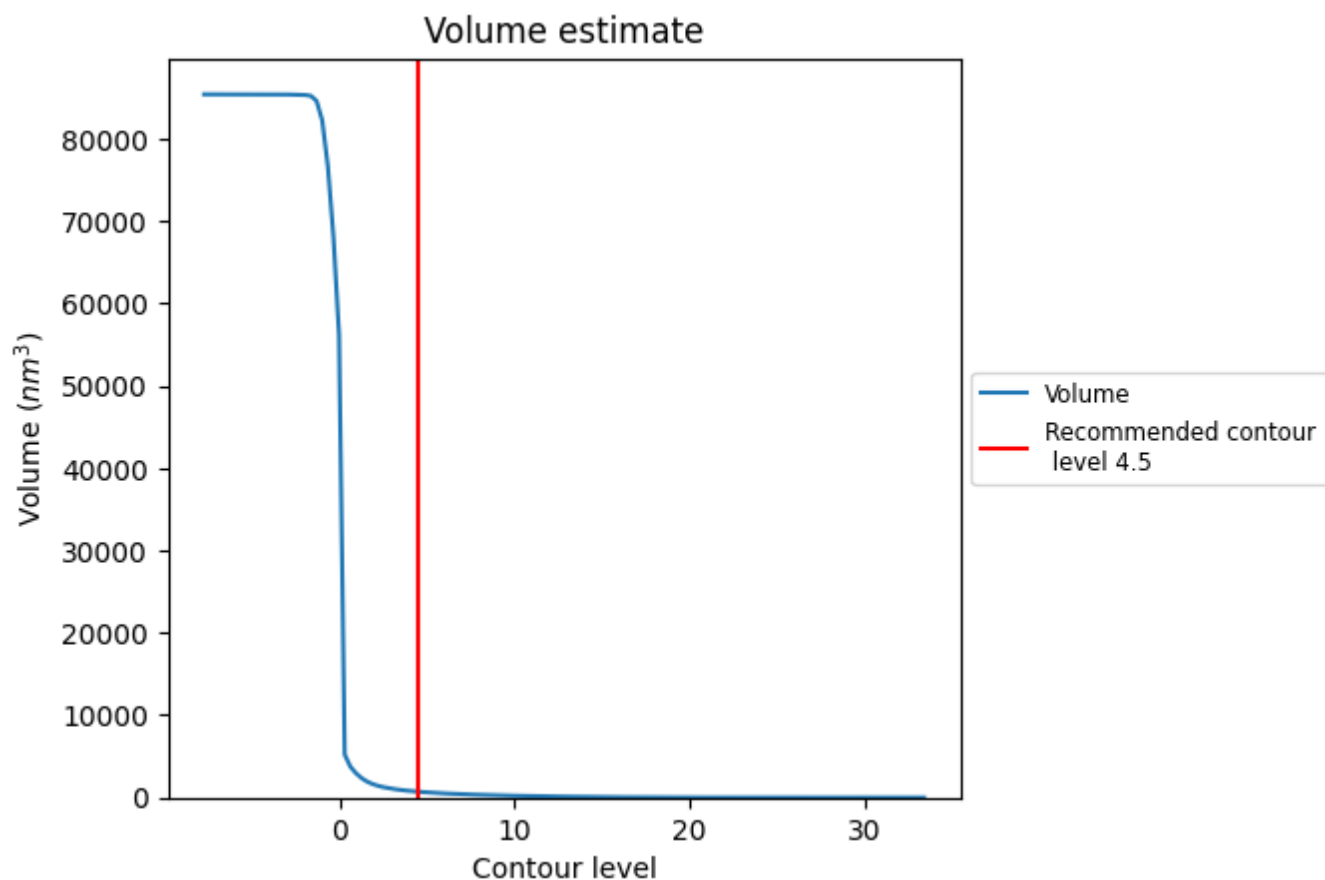
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

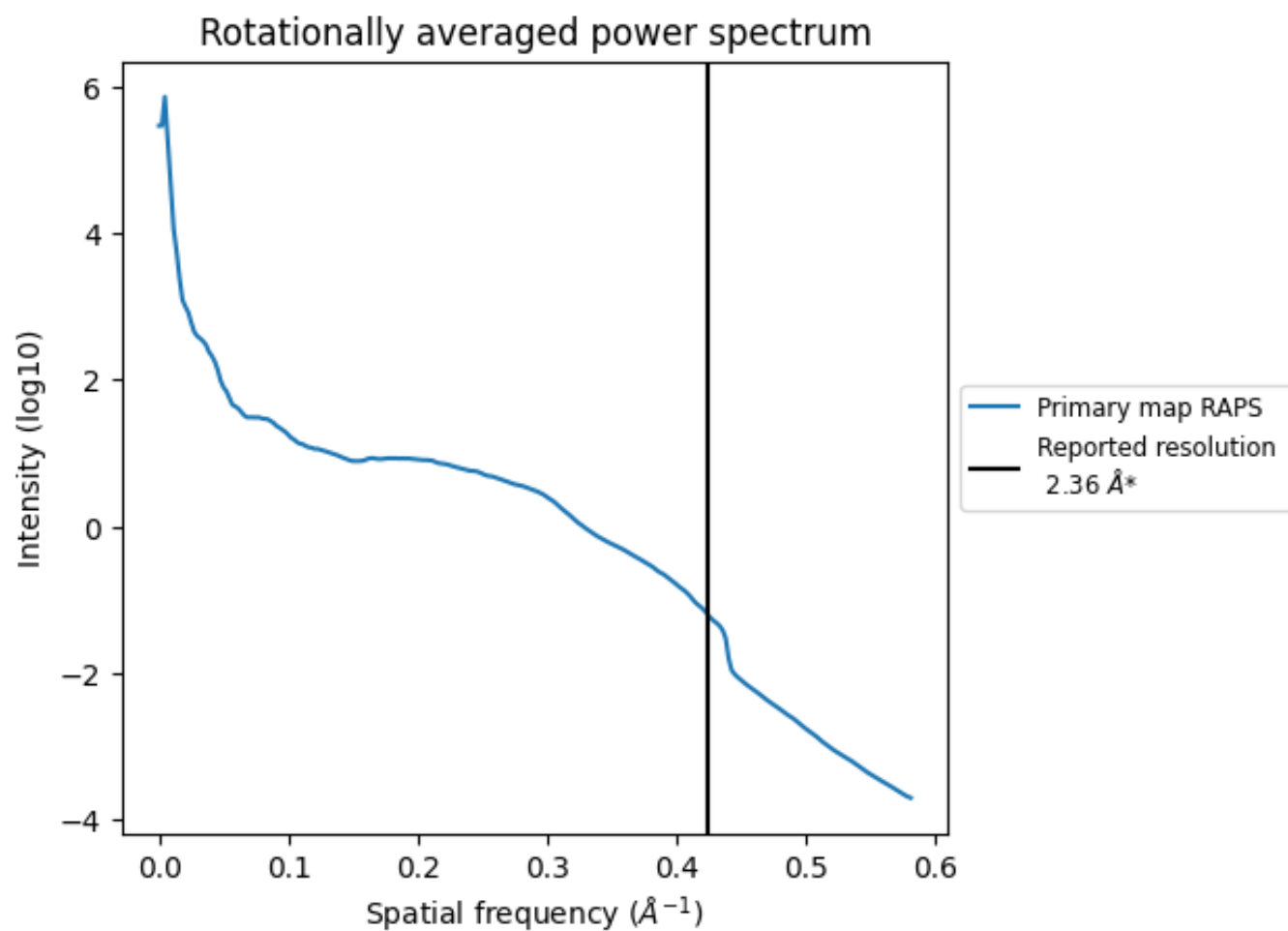
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 710 nm^3 ; this corresponds to an approximate mass of 642 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 0.424 Å⁻¹

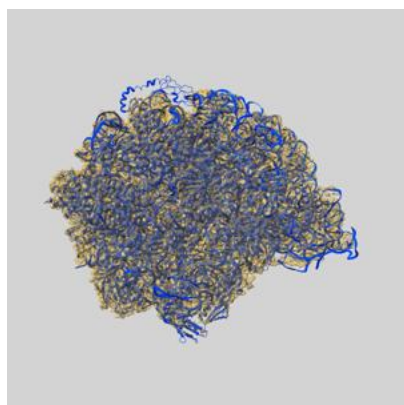
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

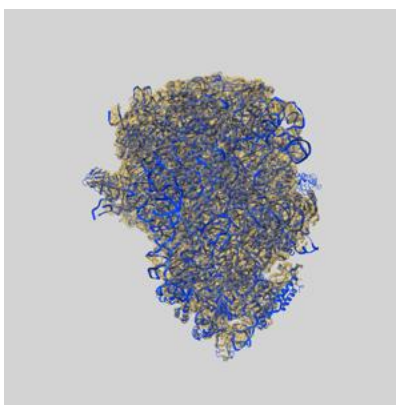
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52192 and PDB model 9HIG. Per-residue inclusion information can be found in section [3](#) on page [14](#).

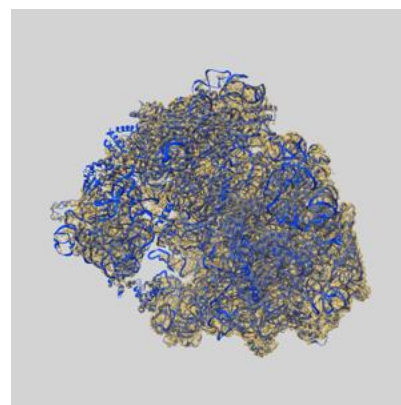
9.1 Map-model overlay [i](#)



X



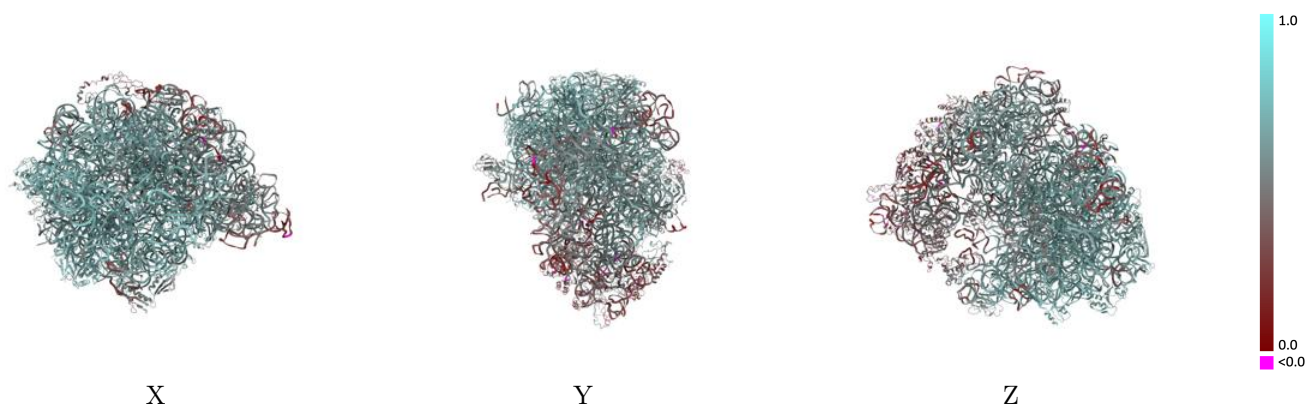
Y



Z

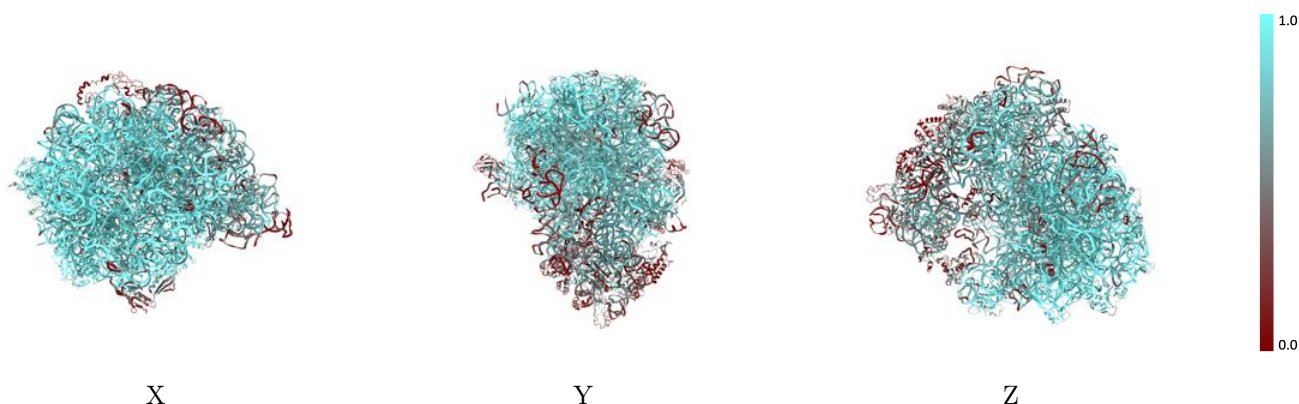
The images above show the 3D surface view of the map at the recommended contour level 4.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



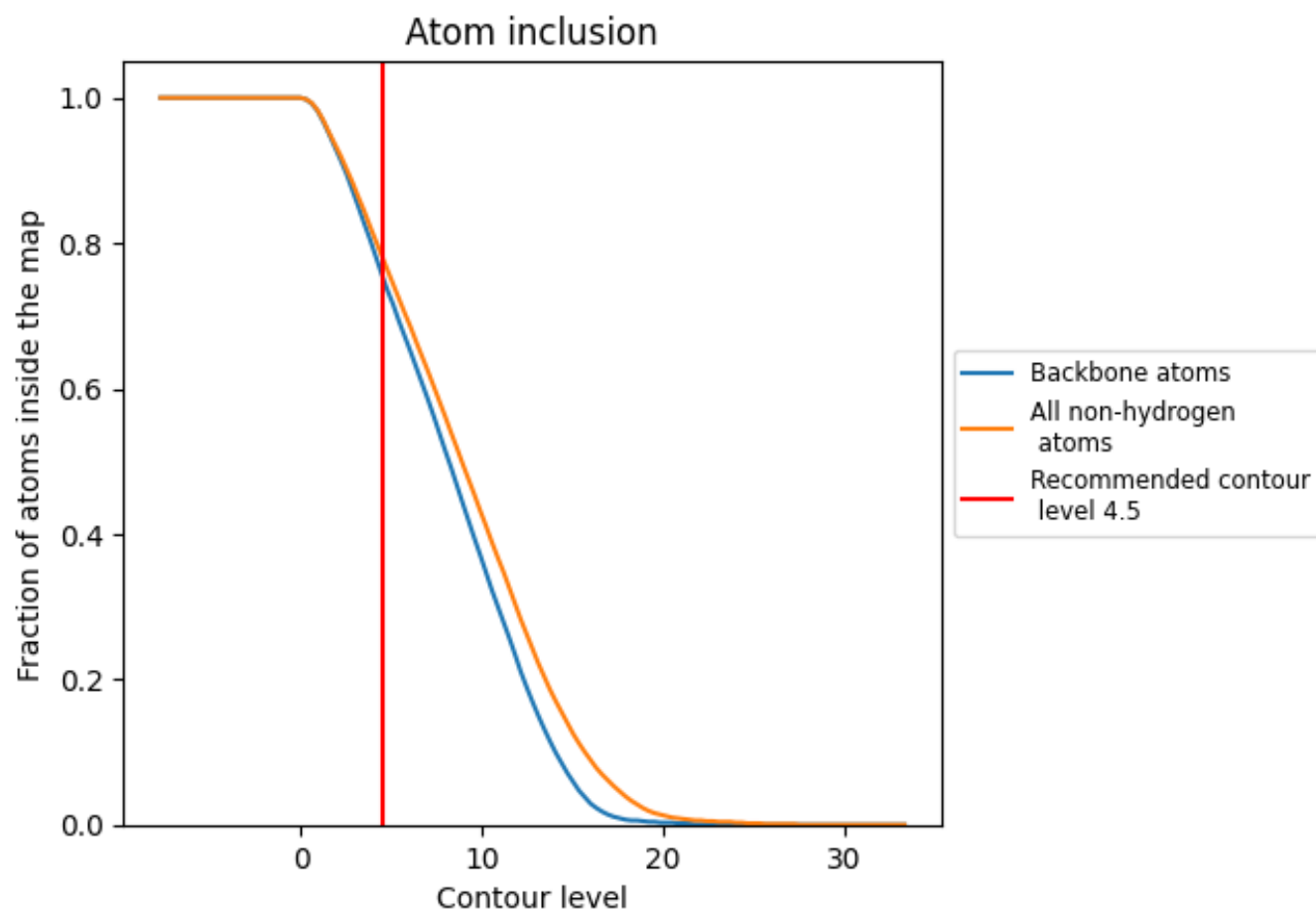
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 78% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7830	 0.5610
0	 0.5080	 0.6220
1	 0.9850	 0.6850
2	 0.9750	 0.6730
3	 0.7930	 0.5430
A	 0.6630	 0.4730
B	 0.3370	 0.4300
C	 0.3330	 0.3640
D	 0.3840	 0.3830
E	 0.6760	 0.5610
F	 0.6190	 0.5450
G	 0.3810	 0.3730
H	 0.7430	 0.5900
I	 0.4880	 0.4080
J	 0.4620	 0.4340
K	 0.5350	 0.4720
L	 0.1360	 0.3620
M	 0.4050	 0.3850
N	 0.4620	 0.3920
O	 0.6430	 0.5660
P	 0.7160	 0.5540
Q	 0.6880	 0.5690
R	 0.7340	 0.5670
S	 0.2970	 0.3120
T	 0.5990	 0.5110
U	 0.1600	 0.4730
W	 0.5560	 0.4840
X	 0.6670	 0.5280
a	 0.9150	 0.6150
b	 0.9230	 0.5620
c	 0.9320	 0.6580
d	 0.9440	 0.6590
e	 0.9070	 0.6490
f	 0.3830	 0.4490
g	 0.3200	 0.4870



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Chain	Atom inclusion	Q-score
h	 0.1710	 0.3980
i	 0.9550	 0.6650
j	 0.8140	 0.6380
k	 0.9420	 0.6570
l	 0.9440	 0.6560
m	 0.9760	 0.6690
n	 0.8200	 0.5550
o	 0.7820	 0.6260
p	 0.9750	 0.6790
q	 0.9170	 0.6420
r	 0.9330	 0.6560
s	 0.8540	 0.6110
t	 0.8520	 0.6190
u	 0.8720	 0.6170
v	 0.9520	 0.6620
w	 0.9460	 0.6510
x	 0.7810	 0.5910
y	 0.9420	 0.6440
z	 0.9490	 0.6590