



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 04:58 AM UTC

PDB ID : 6WNW / pdb_00006wnw
EMDB ID : EMD-21858
Title : Active 70S ribosome without free 5S rRNA and bound with A- and P- tRNA
Authors : Loveland, A.B.; Korostelev, A.A.; Mankin, A.S.; Huang, S.; Aleksashin, N.A.; Klepacki, D.; Reier, K.; Kefi, A.; Szal, A.; Remme, J.; Jaeger, L.; Vazquez-Laslop, N.
Deposited on : 2020-04-23
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

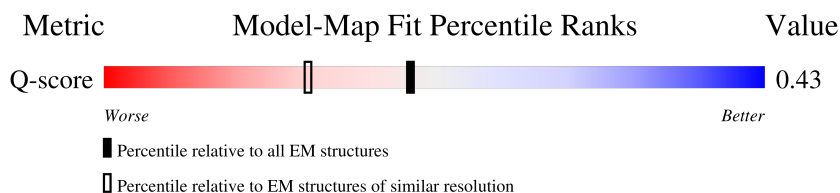
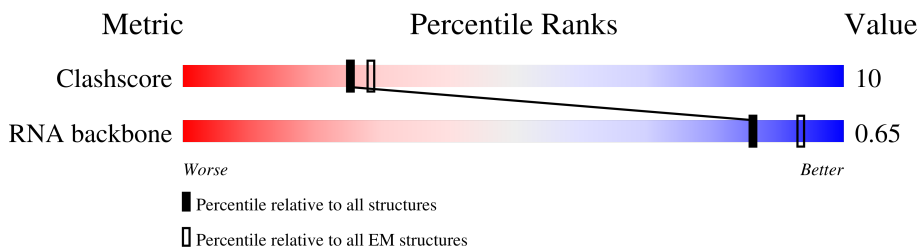
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	b	271	73% 27%
2	c	209	78% 22%
3	d	201	68% 31% .
4	e	177	66% 33% .
5	f	176	66% 33% .

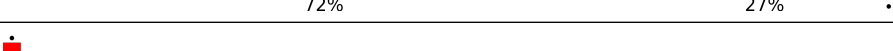
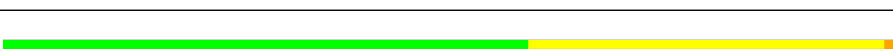
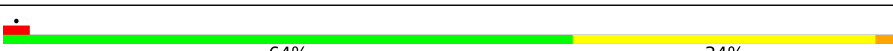
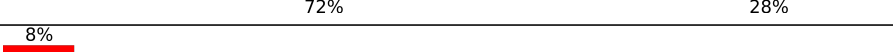
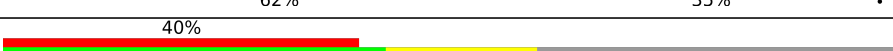
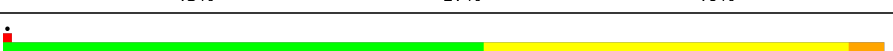
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Mol	Chain	Length	Quality of chain
6	g	149	 68% 28%
7	h	131	 67% 53%
8	i	141	 57% 38%
9	j	142	 70% 28%
10	k	122	 72% 27%
11	l	143	 68% 31%
12	m	136	 74% 26%
13	n	120	 68% 32%
14	o	116	 78% 20%
15	p	114	 77% 23%
16	q	117	 77% 22%
17	r	103	 67% 33%
18	s	110	 83% 16%
19	t	93	 73% 27%
20	u	102	 71% 29%
21	v	94	 72% 27%
22	w	75	 79% 20%
23	x	77	 78% 21%
24	y	63	 67% 33%
25	z	58	 72% 28%
26	A	70	 11% 63% 30% 6%
27	B	56	 71% 29%
28	C	50	 68% 32%
29	D	46	 72% 28%
30	E	64	 81% 19%

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Mol	Chain	Length	Quality of chain
31	F	38	
32	G	225	
33	H	206	
34	I	205	
35	J	157	
36	K	100	
37	L	151	
38	M	129	
39	N	127	
40	O	98	
41	P	116	
42	Q	123	
43	R	114	
44	S	100	
45	T	88	
46	U	82	
47	V	80	
48	W	65	
49	X	79	
50	Y	85	
51	Z	65	
52	a	223	
53	3	1539	
54	4	3031	
55	5	77	

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Mol	Chain	Length	Quality of chain
56	1	10	70% 30%
57	7	76	5% 57% 37% 7%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 149080 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	r	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	s	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	v	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	A	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 27 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 28 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 29 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 30 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 31 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 52 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 54 is a RNA chain called 23s-5s joint ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	3031	Total	C	N	O	P	0	0
			65057	29021	11966	21040	3030		

- Molecule 55 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	1	10	Total	C	N	O	P	0	0
			213	96	39	68	10		

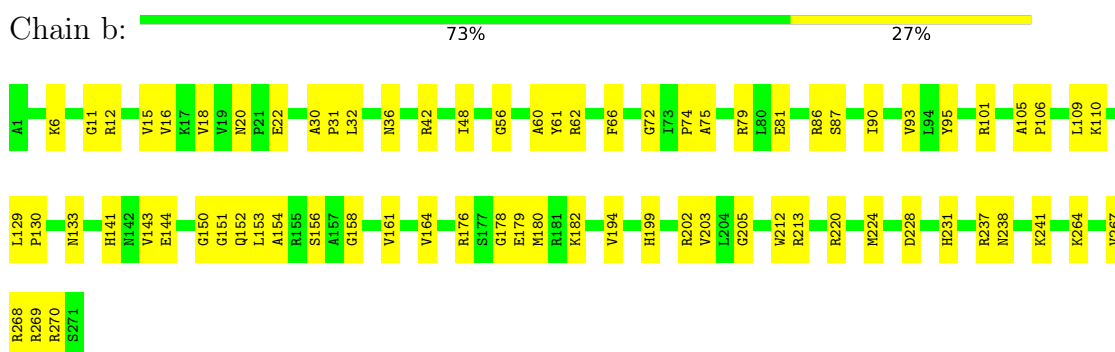
- Molecule 57 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	7	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

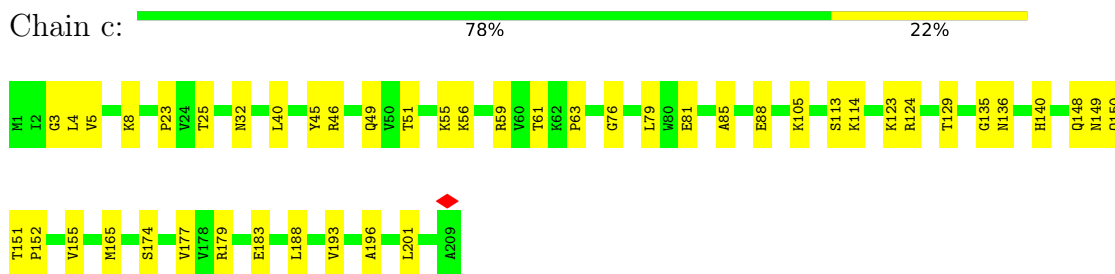
3 Residue-property plots

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.

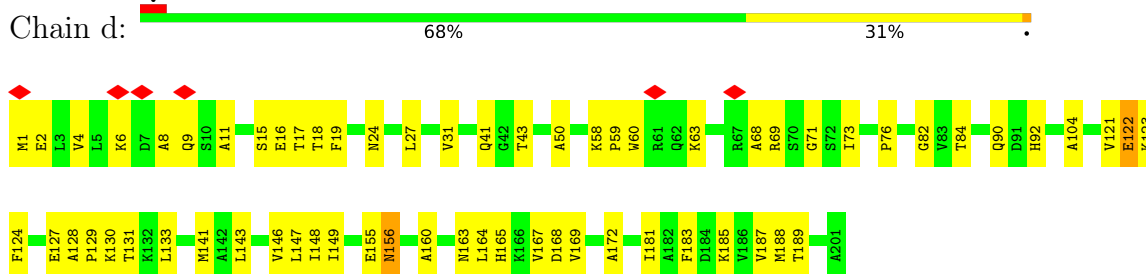
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

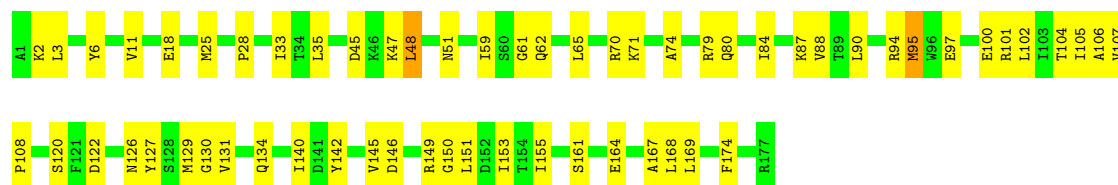


• Molecule 3: 50S ribosomal protein L4



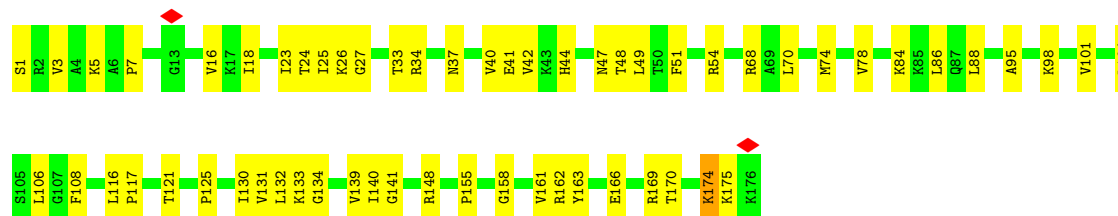
• Molecule 4: 50S ribosomal protein L5





• Molecule 5: 50S ribosomal protein L6

Chain f: 66% 33% .



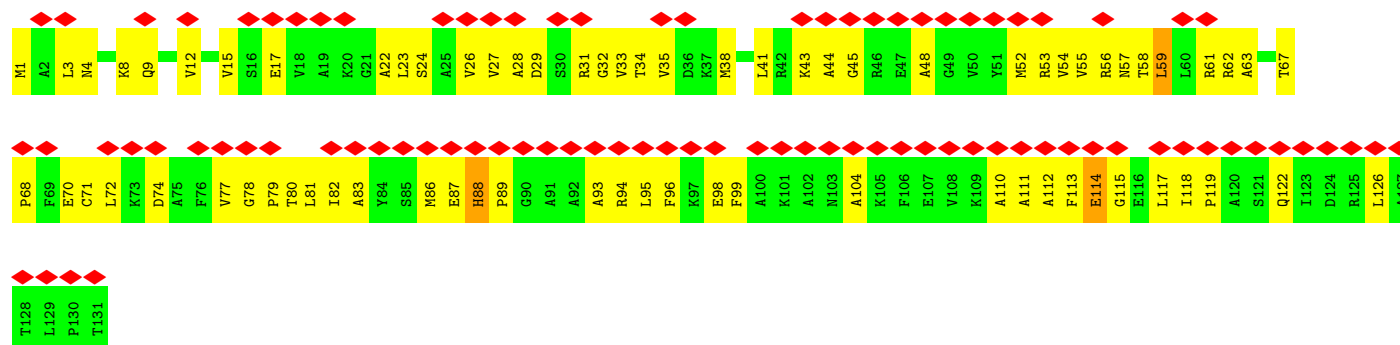
• Molecule 6: 50S ribosomal protein L9

Chain g: 68% 72% 28% .



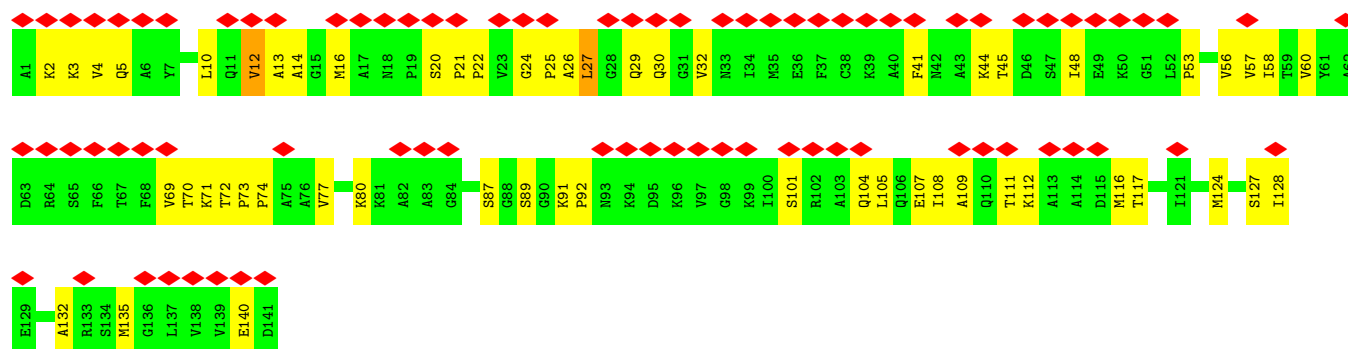
• Molecule 7: 50S ribosomal protein L10

Chain h: 67% 45% 53% .

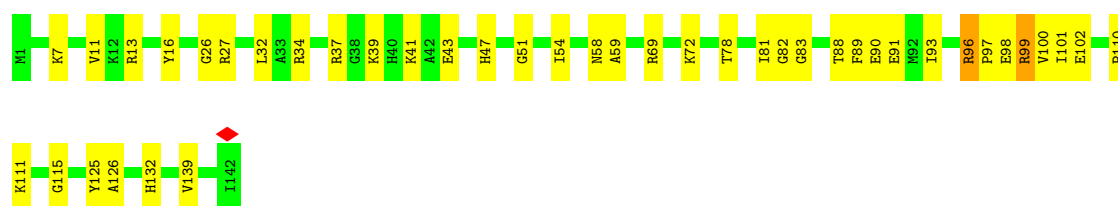


• Molecule 8: 50S ribosomal protein L11

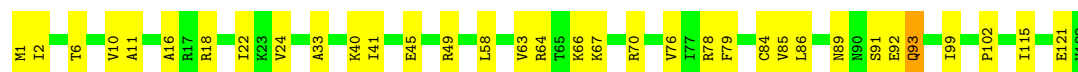
Chain i: 57% 60% 38% .



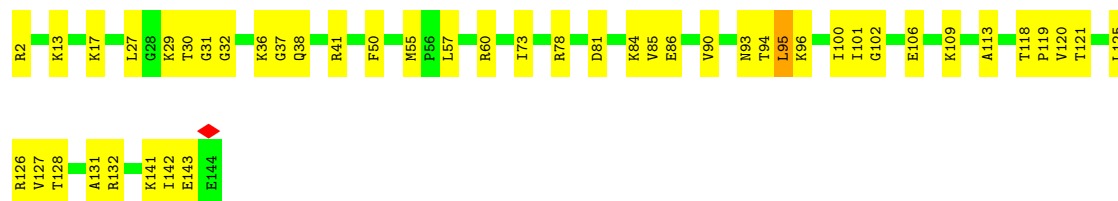
- Molecule 9: 50S ribosomal protein L13



- Molecule 10: 50S ribosomal protein L14



- Molecule 11: 50S ribosomal protein L15

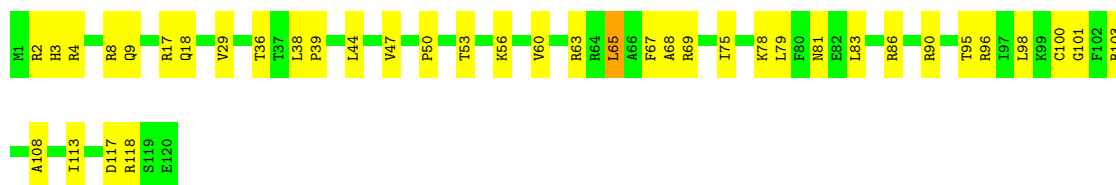


- Molecule 12: 50S ribosomal protein L16



- Molecule 13: 50S ribosomal protein L17





- Molecule 14: 50S ribosomal protein L18

Chain o: 78% 20% .



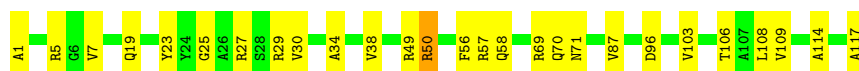
- Molecule 15: 50S ribosomal protein L19

Chain p: 77% 23% .



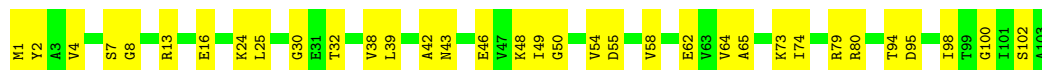
- Molecule 16: 50S ribosomal protein L20

Chain q: 77% 22% .



- Molecule 17: 50S ribosomal protein L21

Chain r: 67% 33% .



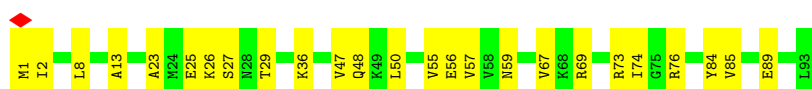
- Molecule 18: 50S ribosomal protein L22

Chain s: 83% 16% .



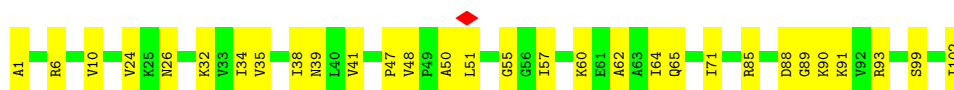
- Molecule 19: 50S ribosomal protein L23

Chain t: 73% 27% .



- Molecule 20: 50S ribosomal protein L24

Chain u:  71% 29%



- Molecule 21: 50S ribosomal protein L25

Chain v:  72% 27%



- Molecule 22: 50S ribosomal protein L27

Chain w:  79% 20%



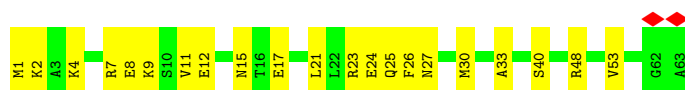
- Molecule 23: 50S ribosomal protein L28

Chain x:  78% 21%



- Molecule 24: 50S ribosomal protein L29

Chain y:  67% 33%



- Molecule 25: 50S ribosomal protein L30

Chain z:  72% 28%



- Molecule 26: 50S ribosomal protein L31

Chain A:  11% 63% 30% 6%



- Molecule 27: 50S ribosomal protein L32



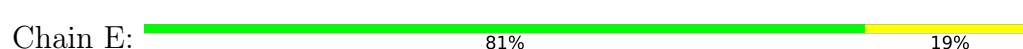
- Molecule 28: 50S ribosomal protein L33



- Molecule 29: 50S ribosomal protein L34



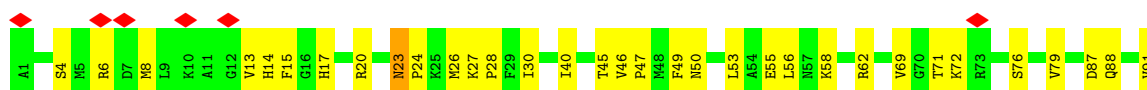
- Molecule 30: 50S ribosomal protein L35

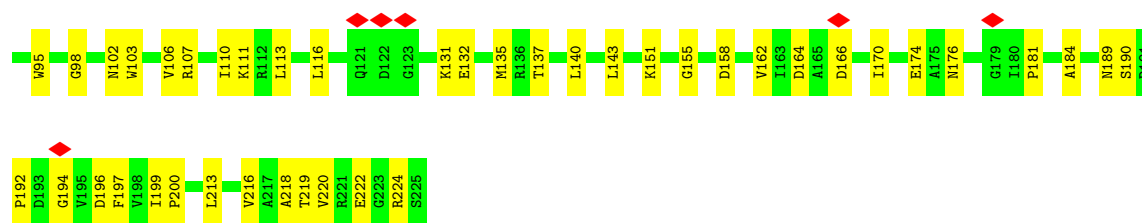


- Molecule 31: 50S ribosomal protein L36

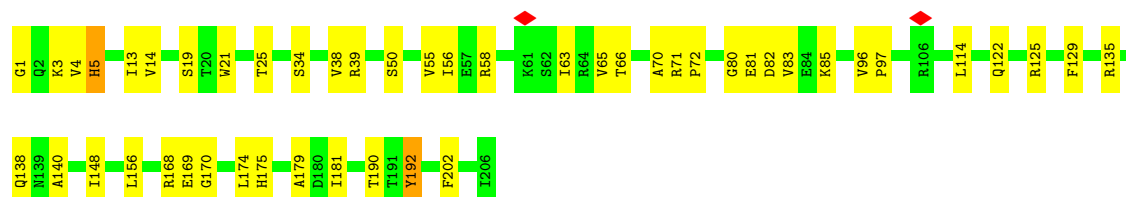
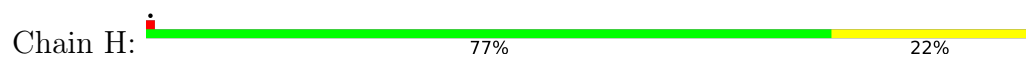


- Molecule 32: 30S ribosomal protein S2





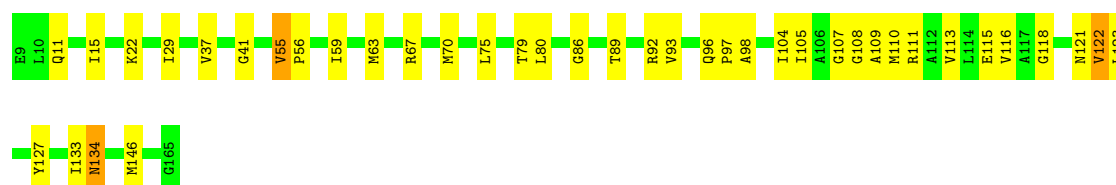
- Molecule 33: 30S ribosomal protein S3



- Molecule 34: 30S ribosomal protein S4



- Molecule 35: 30S ribosomal protein S5

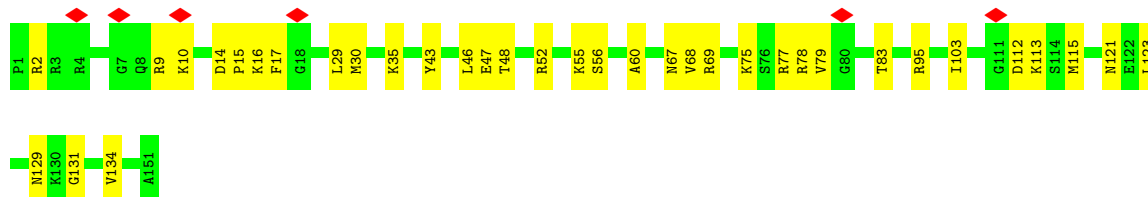
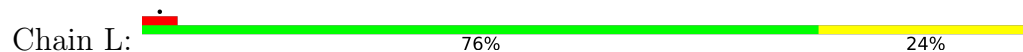


- Molecule 36: 30S ribosomal protein S6

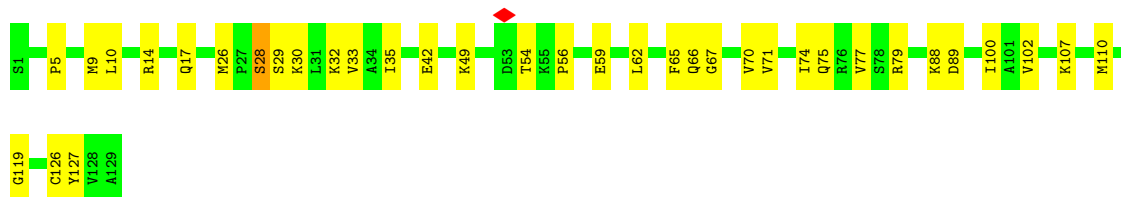




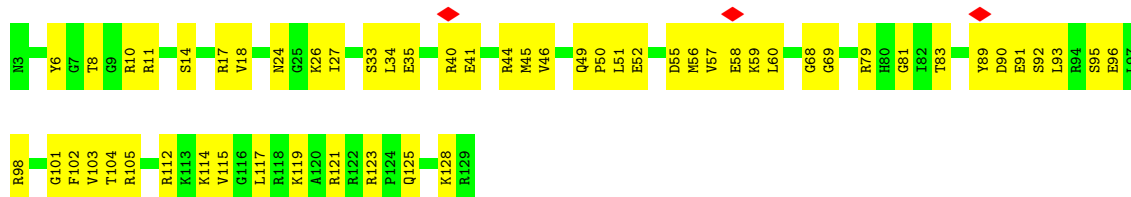
- Molecule 37: 30S ribosomal protein S7



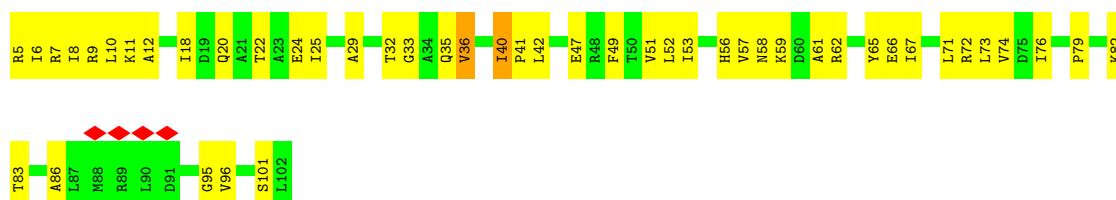
- Molecule 38: 30S ribosomal protein S8



- Molecule 39: 30S ribosomal protein S9

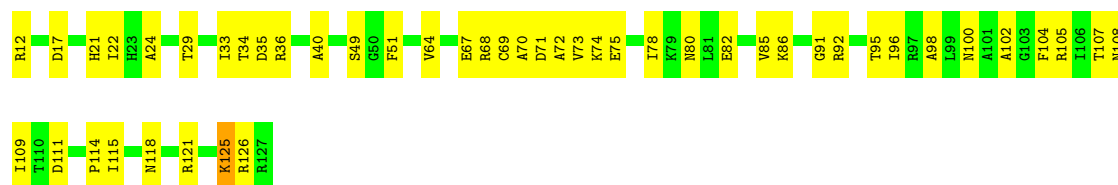


- Molecule 40: 30S ribosomal protein S10

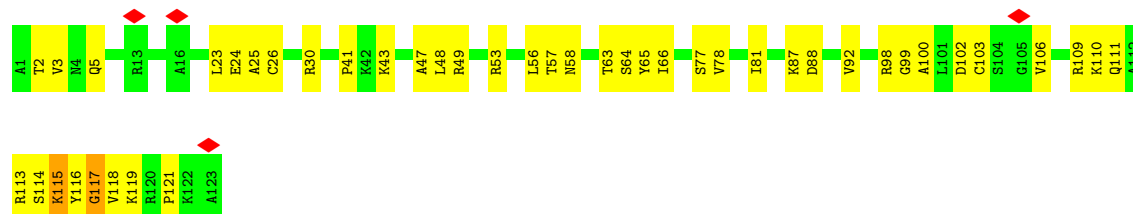


- Molecule 41: 30S ribosomal protein S11





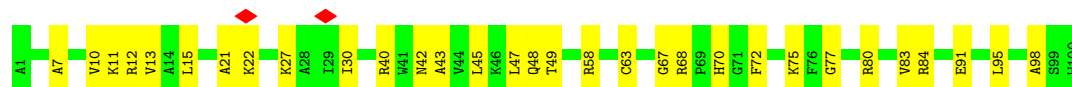
- Molecule 42: 30S ribosomal protein S12



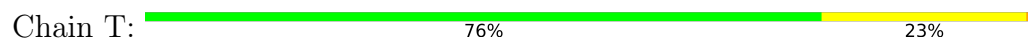
- Molecule 43: 30S ribosomal protein S13



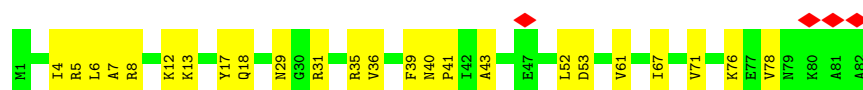
- Molecule 44: 30S ribosomal protein S14



- Molecule 45: 30S ribosomal protein S15



- Molecule 46: 30S ribosomal protein S16



- Molecule 47: 30S ribosomal protein S17

Chain V:  70% 29%



- Molecule 48: 30S ribosomal protein S18

Chain W:  72% 28%



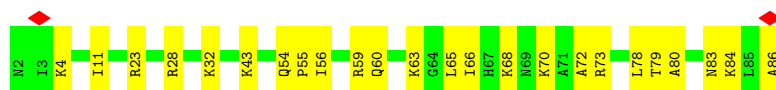
- Molecule 49: 30S ribosomal protein S19

Chain X:  62% 37%



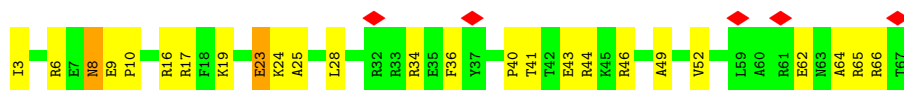
- Molecule 50: 30S ribosomal protein S20

Chain Y:  72% 28%

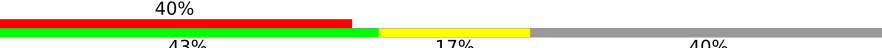


- Molecule 51: 30S ribosomal protein S21

Chain Z:  8% 62% 35%



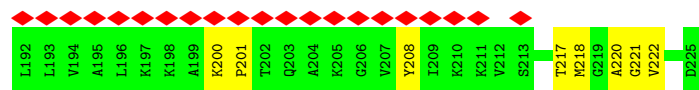
- Molecule 52: 50S ribosomal protein L1

Chain a:  40% 43% 17% 40%

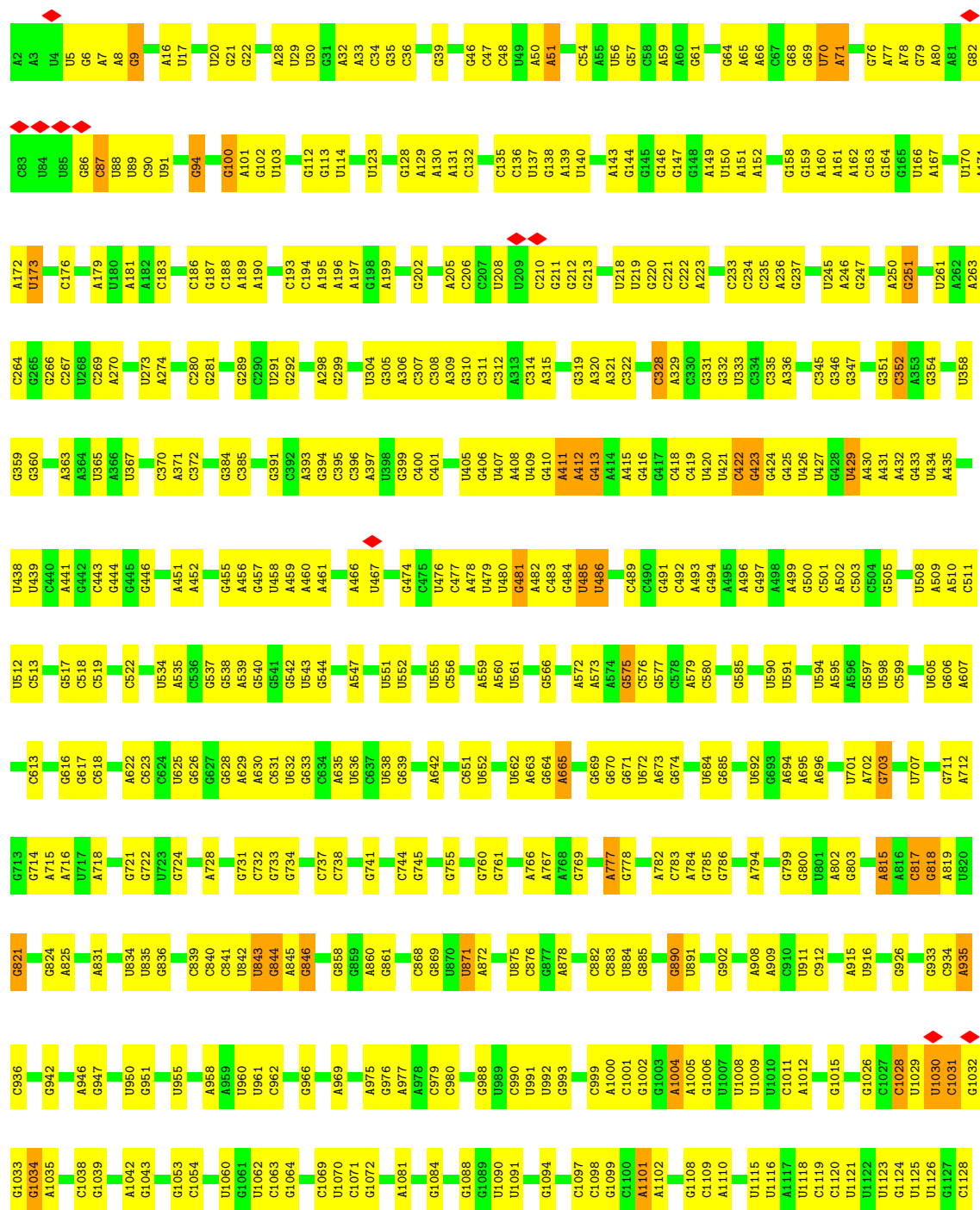


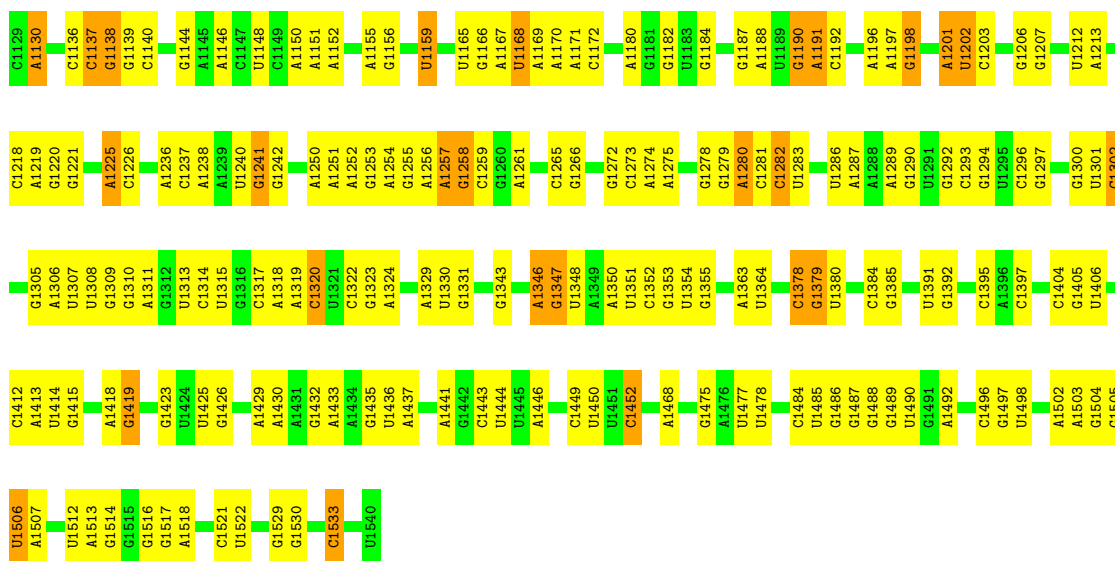
GLY ARG SER VAL ARG VAL VAL ALA VAL PHE THR GLN GLY ALA ASN THR ALA GLU ALA LYS ALA ALA N24 R33 R34 E35 F36 Y37 P40 T41 T42 E43 E44 R45 R46 A49 V52 L59 A60 V61 E62 E63 A64 R65 R66 T67

VAL LEU GLY PRO VAL ARG GLY LEU MET PRO ASN VAL ALA GLU VAL LYS ASN VAL ALA LYS MET LYS ASP LEU ALA Q159 Q160 V161 V162 Y163 R164 R165 D166 K167 N168 G169 I170 I171 H172 T173 T174 I175 G176 F180 D181 A182 D183 K184 L185 K186 E187 N188 L189 E190 A191

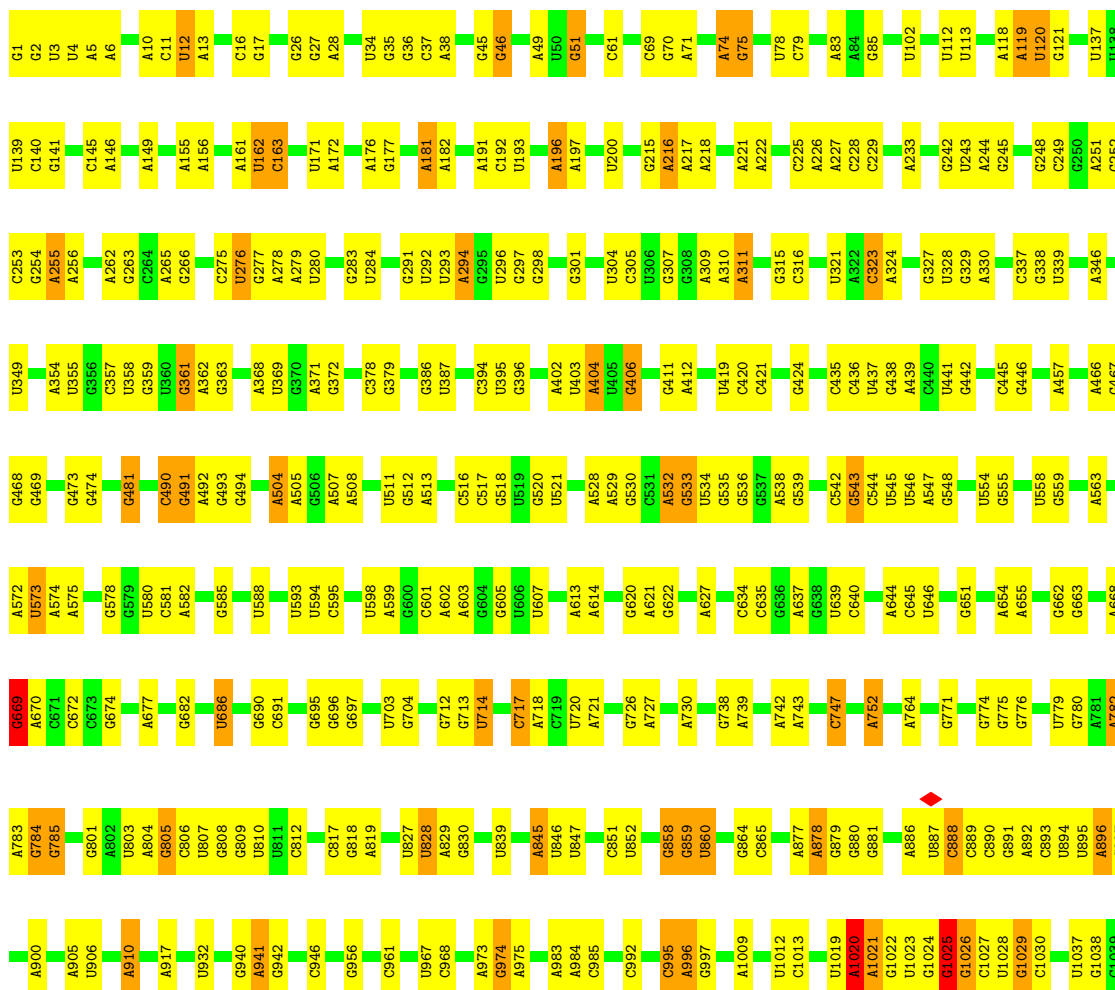


• Molecule 53: 16S ribosomal RNA

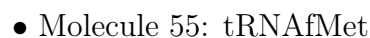




• Molecule 54: 23s-5s joint ribosomal RNA



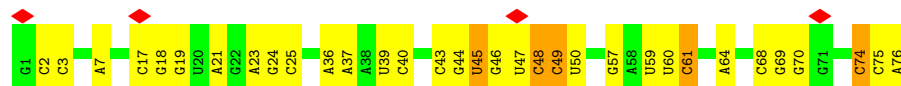
U2322	G2252	C2171	C2062	G1849	U1712	U1613	U1500	G1399	A1283	C1204	A1123	G1040
U2323	G2283	G2176	G2063	G1852	U1717	U1614	A1501	A1400	A1284	A1205	A1041	A1040
G2324	A2254	G2177	A2064	G1853	U1718	U1615	U1507	U1401	G1287	G1206	G1129	G1042
U2325	G2255	A2065	A2066	C1854	A1718	C1616	A1511	A1402	G1288	C1207	G1130	A1043
A2326	G2256	U1955	U1956	C1855	A1725	G1617	A1512	A1403	U1209	U1210	A1132	A1046
U2331	G2257	G1956	A1957	C1856	A1726	G1618	U1513	C1406	G1296	U1211	G1133	G1047
G2332	U2258	A1957	C1965	C1857	G1729	U1622	U1514	G1407	A1297	A1212	G1048	G1048
A2339	U2259	C1965	C1966	U1858	U1730	A1622	A1515	G1408	C1298	A1213	G1049	G1049
A2340	U2260	C1966	C1967	U1859	U1731	G1628	U1516	G1409	A1214	A1214	A1144	A1050
U2341	G2261	C1967	C1968	U1860	A1731	G1629	U1517	U1410	C1300	G1215	A1051	A1051
C2342	U2262	C1968	C1969	U1861	C1734	G1630	U1518	G1411	U1301	G1216	C1052	C1052
C2343	U2263	C1969	C1970	U1862	C1735	A1631	U1519	G1412	U1302	A1217	U1053	U1053
G2344	U2264	C1970	C1971	U1863	A1736	U1632	U1520	A1413	A1303	A1218	G1054	G1054
G2345	U2265	C1971	C1972	U1864	U1737	G1633	U1521	A1414	U1304	A1219	A1057	A1057
G2346	U2266	C1972	C1973	U1865	A1738	G1634	U1522	A1415	U1305	G1220	G1058	G1058
U2347	U2267	C1973	C1974	U1866	C1739	U1635	U1523	A1416	C1306	G1221	G1059	G1059
U2348	G2268	A1974	A1975	U1867	U1740	C1636	U1524	G1417	U1307	U1222	C1060	C1060
U2349	G2269	A1975	A1976	U1868	U1741	C1637	U1525	C1425	U1308	A1223	A1061	A1061
G2350	U2270	A1976	A1977	U1869	C1742	G1638	U1526	G1426	U1309	A1224	U1062	U1062
G2351	U2271	C1977	C1978	U1870	A1754	U1639	U1527	G1427	U1310	U1225	U1063	U1063
A2352	U2272	C1978	C1979	U1871	U1755	C1640	U1528	A1428	U1311	A1226	C1064	C1064
A2353	U2273	U1979	U1980	U1872	A1756	A1643	U1529	A1429	U1312	G1227	G1065	G1065
C2354	U2274	U1980	U1981	U1873	U1757	A1644	U1530	G1430	U1313	C1228	G1066	G1066
U2361	U2275	A2000	A2001	U1874	U1758	U1645	U1531	C1431	G1314	C1229	U1067	U1067
G2362	U2276	C2002	C2003	U1875	A1759	A1646	U1532	U1444	U1315	U1230	G1068	G1068
U2363	U2277	U2003	U2004	U1876	U1760	U1647	U1533	U1445	U1316	A1231	C1069	C1069
G2364	U2278	U2004	U2005	U1877	C1761	U1648	U1534	U1446	U1317	G1232	G1070	G1070
U2365	U2279	U2005	U2006	U1878	A1762	U1649	U1535	U1447	U1318	U1233	C1171	C1171
G2366	U2280	U2006	U2007	U1879	U1763	U1650	U1536	C1448	U1319	G1234	G1072	G1072
G2367	U2281	U2007	U2008	U1880	A1764	A1651	U1537	U1449	U1320	G1235	G1073	G1073
U2368	U2282	U2008	U2009	U1881	U1765	U1652	U1538	A1450	U1321	A1236	A1074	A1074
A2369	U2283	U2009	U2010	U1882	U1766	U1653	U1539	U1451	U1322	G1237	G1075	G1075
G2370	U2284	C2010	C2011	U1883	A1767	U1654	U1540	U1452	U1323	A1238	C1076	C1076
U2371	U2285	U2011	U2012	U1884	U1768	U1655	U1541	U1453	U1324	G1239	C1077	C1077
U2372	U2286	U2012	U2013	U1885	U1769	U1656	U1542	U1454	U1325	A1240	C1078	C1078
G2373	U2287	U2013	U2014	U1886	U1770	U1657	U1543	U1455	U1326	U1241	A1095	A1095
G2374	U2288	U2014	U2015	U1887	U1771	U1658	U1544	A1456	U1327	G1242	C1096	C1096
U2375	U2289	U2015	U2016	U1888	U1772	U1659	U1545	U1457	U1328	U1243	C1097	C1097
G2376	U2290	U2016	U2017	U1889	U1773	U1660	U1546	C1458	U1329	G1253	C1101	C1101
U2377	U2291	U2017	U2018	U1890	U1774	U1661	U1547	U1459	U1330	A1254	C1102	C1102
U2385	U2292	U2018	U2019	U1891	U1775	U1662	U1548	U1471	U1331	G1259	A1105	A1105
C2386	U2293	U2019	U2020	U1892	U1776	U1663	U1549	U1472	U1332	U1260	U1106	U1106
A2394	U2294	U2020	U2021	U1893	U1777	U1664	U1550	U1473	U1333	C1263	G1107	G1107
A2395	U2295	U2021	U2022	U1894	U1778	U1665	U1551	U1474	U1334	U1244	C1108	C1108
A2396	U2296	U2022	U2023	U1895	U1779	U1666	U1552	U1475	U1335	G1245	C1109	C1109
A2405	U2300	U2023	U2024	U1896	U1780	U1667	U1553	U1476	U1336	U1246	G1110	G1110
G2407	A2301	U2024	U2025	U1897	U1781	U1668	U1554	U1477	U1337	G1259	C1113	C1113
G2408	C2302	U2025	U2026	U1898	U1782	U1669	U1555	U1478	U1338	U1260	U1114	U1114
A2409	C2303	U2026	U2027	U1899	U1783	U1670	U1556	U1479	U1339	C1266	G1196	G1196
G2410	A2304	U2027	U2028	U1900	U1784	U1671	U1557	U1480	U1340	G1267	A1197	A1197
G2411	C2305	U2028	U2029	U1901	U1785	U1672	U1558	U1481	U1341	G1268	C1198	C1198
C2412	C2306	U2029	U2030	U1902	U1786	U1673	U1559	U1482	U1342	U1269	U1199	U1199
C2413	C2307	U2030	U2031	U1903	U1787	U1674	U1560	U1483	U1343	A1270	A1195	A1195
C2414	C2308	U2031	U2032	U1904	U1788	U1675	U1561	U1484	U1344	A1271	G1196	G1196
C2415	C2309	U2032	U2033	U1905	U1789	U1676	U1562	U1485	U1345	G1277	A1198	A1198
U2419	U2310	U2033	U2034	U1906	U1790	U1677	U1563	U1486	U1346	C1278	C1200	C1200
	U2311	U2034	U2035	U1907	U1791	U1678	U1564	U1487	U1347	U1279	A1201	A1201
	U2312	U2035	U2036	U1908	U1792	U1679	U1565	U1488	U1348	C1280	C1202	C1202
	U2313	U2036	U2037	U1909	U1793	U1680	U1566	U1489	U1349	G1281	G1203	G1203
	U2314	U2037	U2038	U1910	U1794	U1681	U1567	U1490	U1350	G1282		
	U2315	U2038	U2039	U1911	U1795	U1682	U1568	U1491	U1351			
	U2316	U2039	U2040	U1912	U1796	U1683	U1569	U1492	U1352			
	U2317	U2040	U2041	U1913	U1797	U1684	U1570	U1493	U1353			
	U2318	U2041	U2042	U1914	U1798	U1685	U1571	U1494	U1354			
	U2319	U2042	U2043	U1915	U1799	U1686	U1572	U1495	U1355			
	U2320	U2043	U2044	U1916	U1800	U1687	U1573	U1496	U1356			
	U2321	U2044	U2045	U1917	U1801	U1688	U1574	U1497	U1357			
		U2045	U2046	U1918	U1802	U1689	U1575	U1498	U1358			
		U2046	U2047	U1919	U1803	U1690	U1576	U1499	U1359			
		U2047	U2048	U1920	U1804	U1691	U1577	U1500	U1360			
		U2048	U2049	U1921	U1805	U1692	U1578	U1501	U1361			
		U2049	U2050	U1922	U1806	U1693	U1579	U1502	U1362			
		U2050	U2051	U1923	U1807	U1694	U1580	U1503	U1363			
		U2051	U2052	U1924	U1808	U1695	U1581	U1504	U1364			
		U2052	U2053	U1925	U1809	U1696	U1582	U1505	U1365			
		U2053	U2054	U1926	U1810	U1697	U1583	U1506	U1366			
		U2054	U2055	U1927	U1811	U1698	U1584	U1507	U1367			
		U2055	U2056	U1928	U1812	U1699	U1585	U1508	U1368			
		U2056	U2057	U1929	U1813	U1700	U1586	U1509	U1369			
		U2057	U2058	U1930	U1814	U1701	U1587	U1510	U1370			
		U2058	U2059	U1931	U1815	U1702	U1588	U1511	U1371			
		U2059	U2060	U1932	U1816	U1703	U1589	U1512	U1372			
		U2060	U2061	U1933	U1817	U1704	U1590	U1513	U1373			
		U2061	U2062	U1934	U1818	U1705	U1591	U1514	U1374			
		U2062	U2063	U1935	U1819	U1706	U1592	U1515	U1375			
		U2063	U2064	U1936	U1820	U1707	U1593	U1516	U1376			
		U2064	U2065	U1937	U1821	U1708	U1594	U1517	U1377			
		U2065	U2066	U1938	U1822	U1709	U1595	U1518	U1378			
		U2066	U2067	U1939	U1823	U1710	U1596	U1519	U1379			
		U2067	U2068	U1940	U1824	U1711	U1597	U1520	U1380			
		U2068	U2069	U1941	U1825	U1712	U1598	U1521	U1381			
		U2069	U2070	U1942	U1826	U1713	U1599	U1522	U1382			
		U2070	U2071	U1943	U1827	U1714	U1600	U1523	U1383			
		U2071	U2072	U1944	U1828	U1715	U1601	U1524	U1384			
		U2072	U2073	U1945	U1829	U1716	U1602	U1525	U1385			
		U2073	U2074	U1946	U1830	U1717	U1603	U1526	U1386			
		U2074	U2075	U1947	U1831	U1718	U1604	U1527	U1387			
		U2075	U2076	U1948	U1832	U1719	U1605	U1528	U1388			
		U2076	U2077	U1949	U1833	U1720	U1606	U1529	U1389			
		U2077	U2078	U1950	U1834	U1721	U1607	U1530	U1390			
		U2078	U2079	U1951	U1835	U1722	U1608	U1531	U1391			
		U2079	U2080	U1952	U1836	U1723	U1609	U1532	U1392			
		U2080	U2081	U1953	U1837	U1724	U1610	U1533	U1393			
		U2081	U2082	U1954	U1838	U1725	U1611					



Chain 1: 70% 30%



Chain 7: 5% 57% 37% 7%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26717	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	17.526	Depositor
Minimum map value	-5.137	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.802	Depositor
Recommended contour level	2.5	Depositor
Map size ($\text{\AA}$)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	b	0.33	0/2122	0.93	8/2852 (0.3%)
2	c	0.35	0/1586	0.89	4/2134 (0.2%)
3	d	0.36	0/1571	0.90	4/2113 (0.2%)
4	e	0.39	0/1435	0.91	4/1926 (0.2%)
5	f	0.38	0/1343	0.87	4/1816 (0.2%)
6	g	0.53	0/1122	0.98	5/1515 (0.3%)
7	h	0.56	0/1002	0.99	6/1350 (0.4%)
8	i	0.57	0/1046	1.07	6/1410 (0.4%)
9	j	0.34	0/1152	0.86	4/1551 (0.3%)
10	k	0.35	0/948	0.89	3/1268 (0.2%)
11	l	0.37	0/1054	0.91	1/1403 (0.1%)
12	m	0.35	0/1093	0.86	2/1460 (0.1%)
13	n	0.33	0/974	0.92	4/1301 (0.3%)
14	o	0.34	0/902	1.01	4/1209 (0.3%)
15	p	0.32	0/929	0.82	1/1242 (0.1%)
16	q	0.30	0/960	0.87	4/1278 (0.3%)
17	r	0.35	0/829	0.90	4/1107 (0.4%)
18	s	0.33	0/864	0.88	2/1156 (0.2%)
19	t	0.35	0/745	0.88	1/994 (0.1%)
20	u	0.36	0/788	0.86	0/1051
21	v	0.35	0/766	0.90	2/1025 (0.2%)
22	w	0.30	0/582	0.87	3/769 (0.4%)
23	x	0.31	0/635	0.81	2/848 (0.2%)
24	y	0.34	0/510	0.80	1/677 (0.1%)
25	z	0.35	0/453	0.84	1/605 (0.2%)
26	A	0.44	0/531	1.09	4/709 (0.6%)
27	B	0.33	0/450	0.78	0/599
28	C	0.36	0/417	0.85	1/554 (0.2%)
29	D	0.36	0/380	0.88	0/498
30	E	0.31	0/513	0.82	1/676 (0.1%)
31	F	0.31	0/303	0.90	0/397
32	G	0.42	0/1788	0.92	6/2408 (0.2%)
33	H	0.39	0/1652	0.87	7/2225 (0.3%)
34	I	0.44	0/1665	1.00	10/2227 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	J	0.41	1/1170 (0.1%)	0.88	3/1573 (0.2%)
36	K	0.45	0/836	0.97	3/1128 (0.3%)
37	L	0.42	0/1196	0.98	3/1602 (0.2%)
38	M	0.37	0/989	0.93	3/1326 (0.2%)
39	N	0.41	0/1034	0.96	4/1375 (0.3%)
40	O	0.44	0/797	1.01	5/1077 (0.5%)
41	P	0.40	0/886	1.04	6/1195 (0.5%)
42	Q	0.41	0/969	0.97	5/1300 (0.4%)
43	R	0.41	0/893	0.86	1/1193 (0.1%)
44	S	0.39	0/817	0.88	2/1088 (0.2%)
45	T	0.34	0/722	0.89	3/964 (0.3%)
46	U	0.44	0/659	0.89	1/884 (0.1%)
47	V	0.38	0/658	0.83	1/881 (0.1%)
48	W	0.40	0/545	0.85	0/731
49	X	0.44	0/653	0.94	4/877 (0.5%)
50	Y	0.37	0/671	0.86	1/888 (0.1%)
51	Z	0.49	0/551	1.12	4/728 (0.5%)
52	a	0.57	0/1034	0.91	4/1387 (0.3%)
53	3	0.46	0/36963	0.50	1/57662 (0.0%)
54	4	0.44	0/72860	0.50	5/113668 (0.0%)
55	5	0.48	0/1832	0.45	0/2855
56	1	0.53	0/238	0.46	0/368
57	7	0.51	0/1809	0.49	0/2819
All	All	0.44	1/161892 (0.0%)	0.64	168/241922 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	J	55	VAL	CA-CB	5.42	1.57	1.53

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	t	2	ILE	N-CA-C	-9.03	102.30	111.88
44	S	21	ALA	N-CA-C	-8.89	102.84	114.31
1	b	213	ARG	N-CA-C	-8.81	100.20	112.45
34	I	30	LYS	N-CA-C	-8.77	100.46	113.61
34	I	176	LYS	N-CA-C	-8.68	102.76	112.57

There are no chirality outliers.

There are no planarity outliers.

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	b	2083	0	2157	58	0
2	c	1565	0	1616	30	0
3	d	1552	0	1619	49	0
4	e	1411	0	1447	49	0
5	f	1323	0	1374	37	0
6	g	1111	0	1148	28	0
7	h	989	0	1025	68	0
8	i	1032	0	1088	51	0
9	j	1129	0	1162	31	0
10	k	939	0	1012	25	0
11	l	1045	0	1117	37	0
12	m	1074	0	1157	25	0
13	n	961	0	1000	31	0
14	o	892	0	923	21	0
15	p	917	0	965	21	0
16	q	947	0	1022	21	0
17	r	816	0	839	27	0
18	s	857	0	922	11	0
19	t	739	0	807	17	0
20	u	780	0	834	21	0
21	v	753	0	780	19	0
22	w	575	0	592	10	0
23	x	625	0	655	11	0
24	y	509	0	543	17	0
25	z	449	0	491	9	0
26	A	522	0	524	18	0
27	B	444	0	461	17	0
28	C	410	0	440	9	0
29	D	377	0	418	13	0
30	E	504	0	574	10	0
31	F	302	0	343	13	0
32	G	1757	0	1787	51	0
33	H	1625	0	1699	31	0
34	I	1643	0	1710	70	0
35	J	1157	0	1199	31	0
36	K	818	0	808	36	0
37	L	1182	0	1240	27	0

Continued on next page...

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	M	979	0	1034	28	0
39	N	1022	0	1070	44	0
40	O	787	0	828	42	0
41	P	870	0	878	34	0
42	Q	955	0	1019	38	0
43	R	884	0	944	32	0
44	S	805	0	847	23	0
45	T	714	0	737	13	0
46	U	649	0	666	19	0
47	V	649	0	691	16	0
48	W	536	0	552	18	0
49	X	638	0	665	22	0
50	Y	665	0	714	23	0
51	Z	545	0	579	20	0
52	a	1027	0	1092	31	0
53	3	33012	0	16618	518	0
54	4	65057	0	32732	911	0
55	5	1640	0	837	17	0
56	1	213	0	108	3	0
57	7	1619	0	822	22	0
All	All	149080	0	100931	2588	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 10.

The worst 5 of 2588 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)
54:4:1303:A:H3'	54:4:1304:U:H5'	1.32	1.11
14:o:33:ARG:HG3	54:4:1118:A:H62	1.22	1.05
9:j:100:VAL:HG23	9:j:101:ILE:HD12	1.39	1.04
54:4:45:G:H5''	54:4:46:G:H5'	1.36	1.04
54:4:275:C:H2'	54:4:276:U:H4'	1.41	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	3	1538/1539 (99%)	150 (9%)	1 (0%)
54	4	3030/3031 (99%)	345 (11%)	13 (0%)
55	5	76/77 (98%)	7 (9%)	0
56	1	9/10 (90%)	0	0
57	7	75/76 (98%)	9 (12%)	0
All	All	4728/4733 (99%)	511 (10%)	14 (0%)

5 of 511 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
53	3	6	G
53	3	7	A
53	3	9	G
53	3	22	G
53	3	32	A

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	4	1132	A
54	4	1154	A
54	4	3001	A
54	4	2454	C
54	4	2884	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

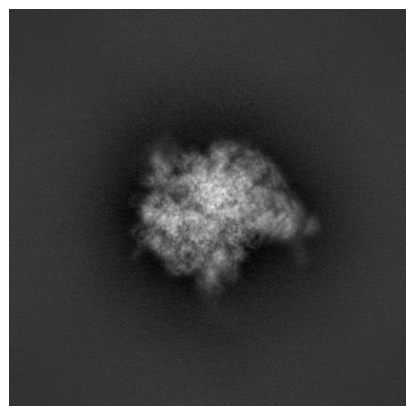
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21858. These allow visual inspection of the internal detail of the map and identification of artifacts.

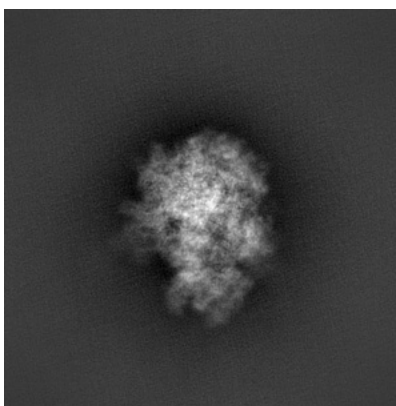
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

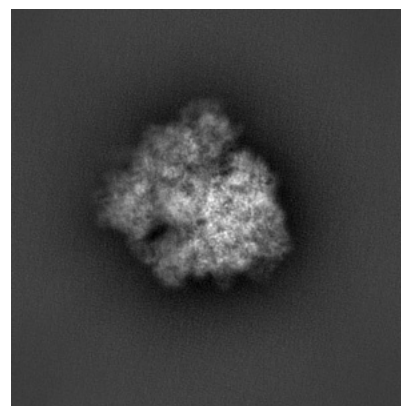
6.1.1 Primary map



X

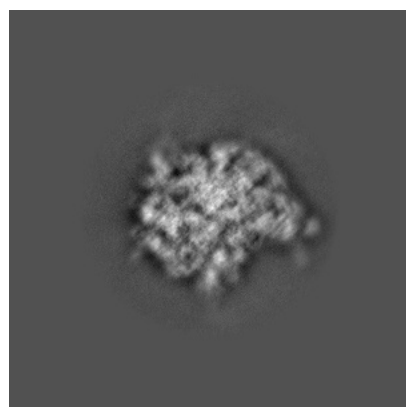


Y

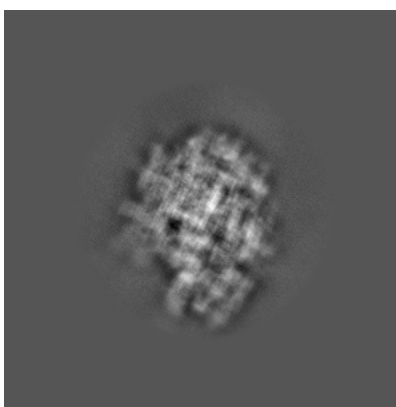


Z

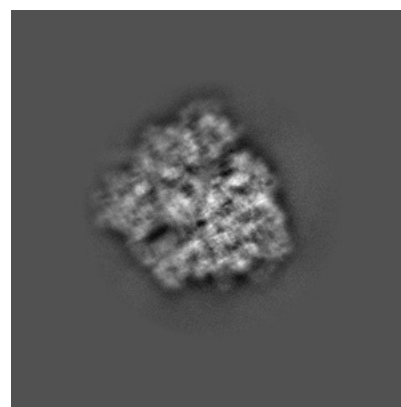
6.1.2 Raw map



X



Y

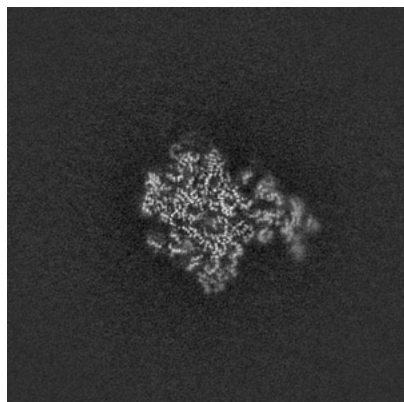


Z

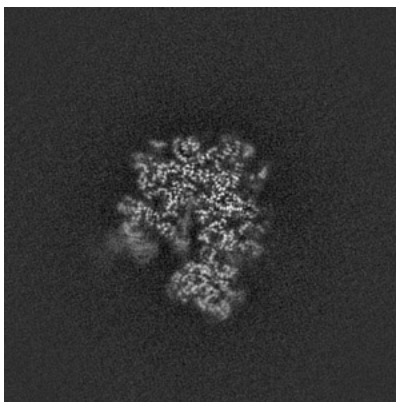
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

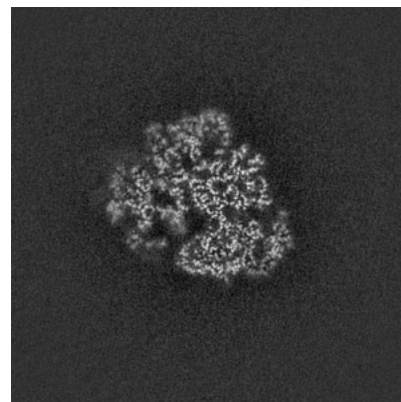
6.2.1 Primary map



X Index: 304

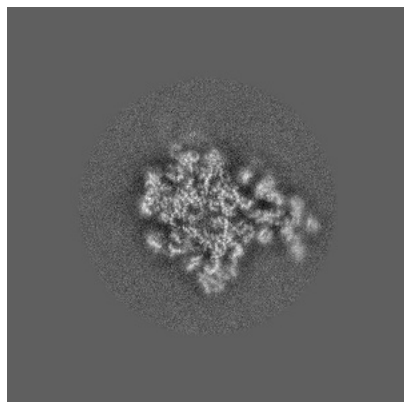


Y Index: 304

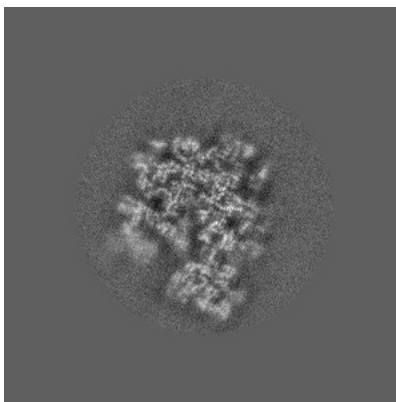


Z Index: 304

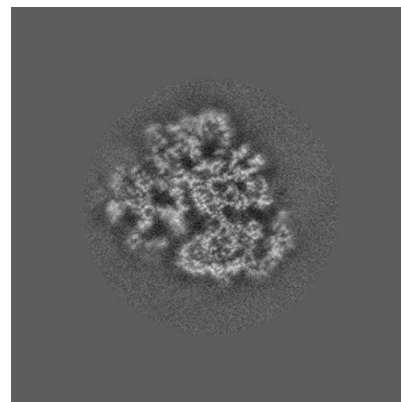
6.2.2 Raw map



X Index: 304



Y Index: 304

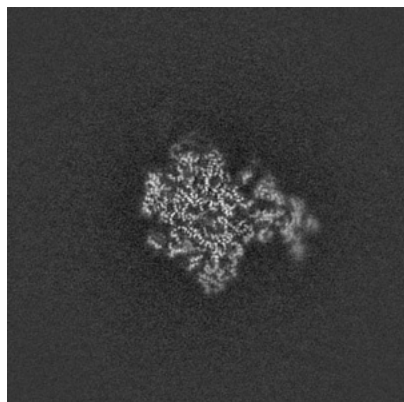


Z Index: 304

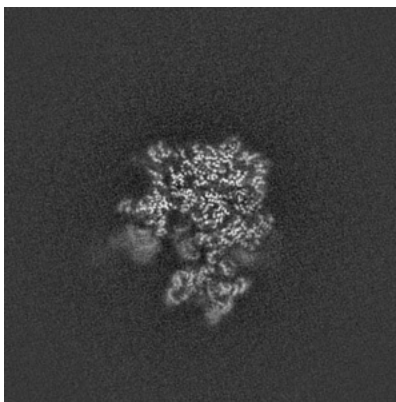
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

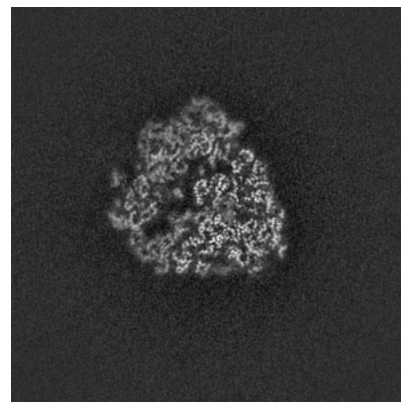
6.3.1 Primary map



X Index: 303

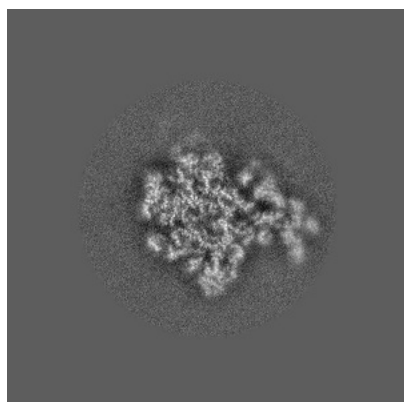


Y Index: 317

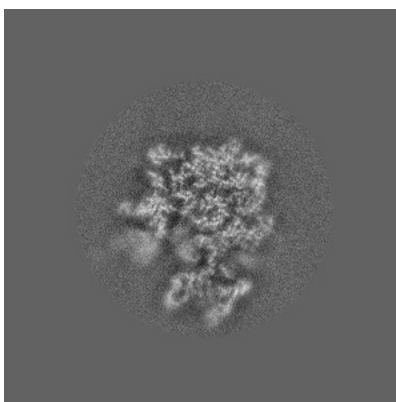


Z Index: 290

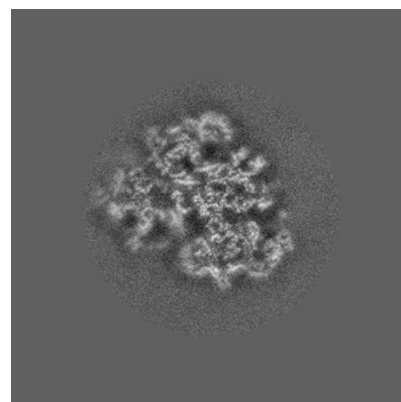
6.3.2 Raw map



X Index: 302



Y Index: 318

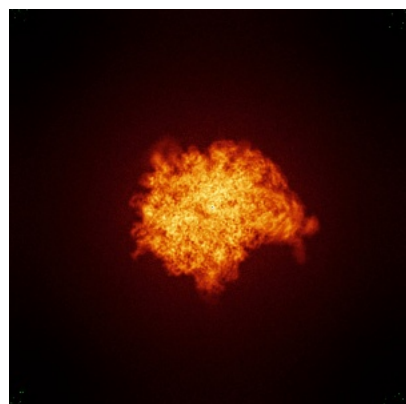


Z Index: 307

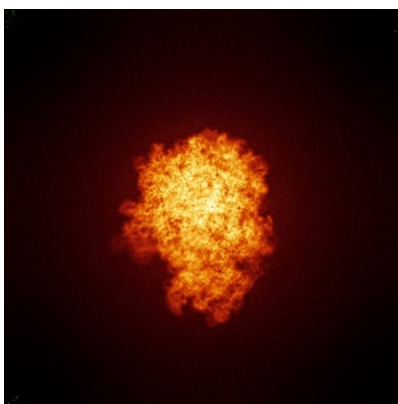
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

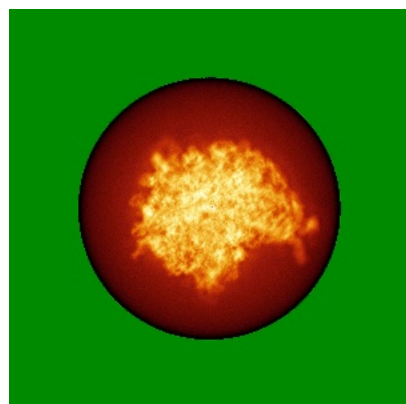


Y

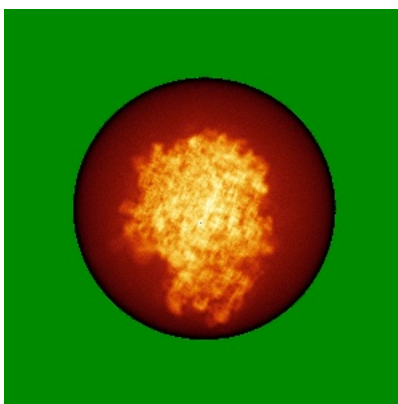


Z

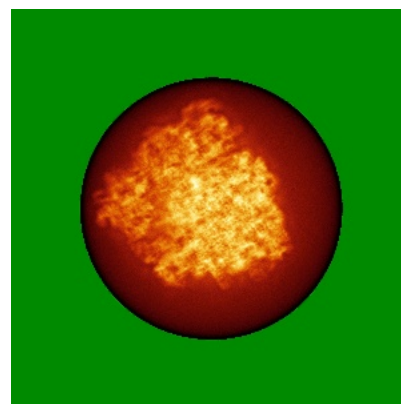
6.4.2 Raw map



X



Y



Z

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

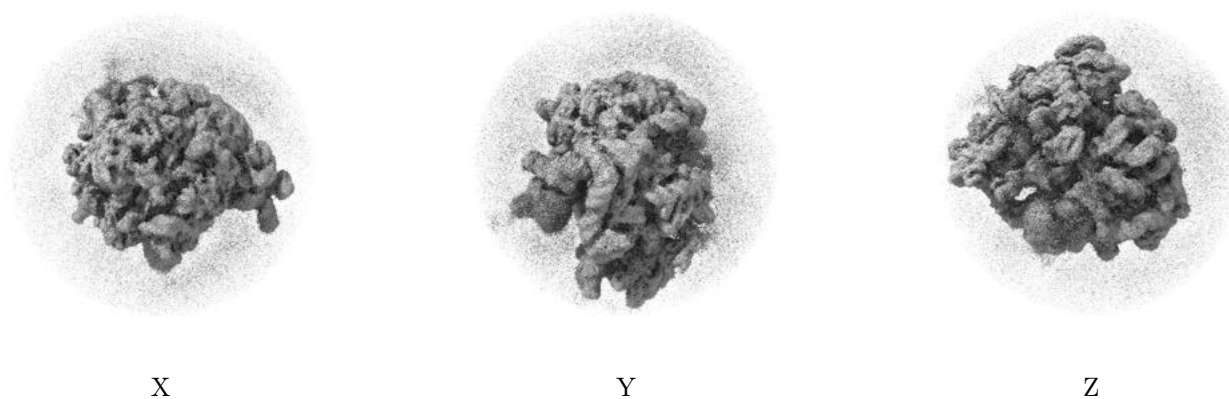
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 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.

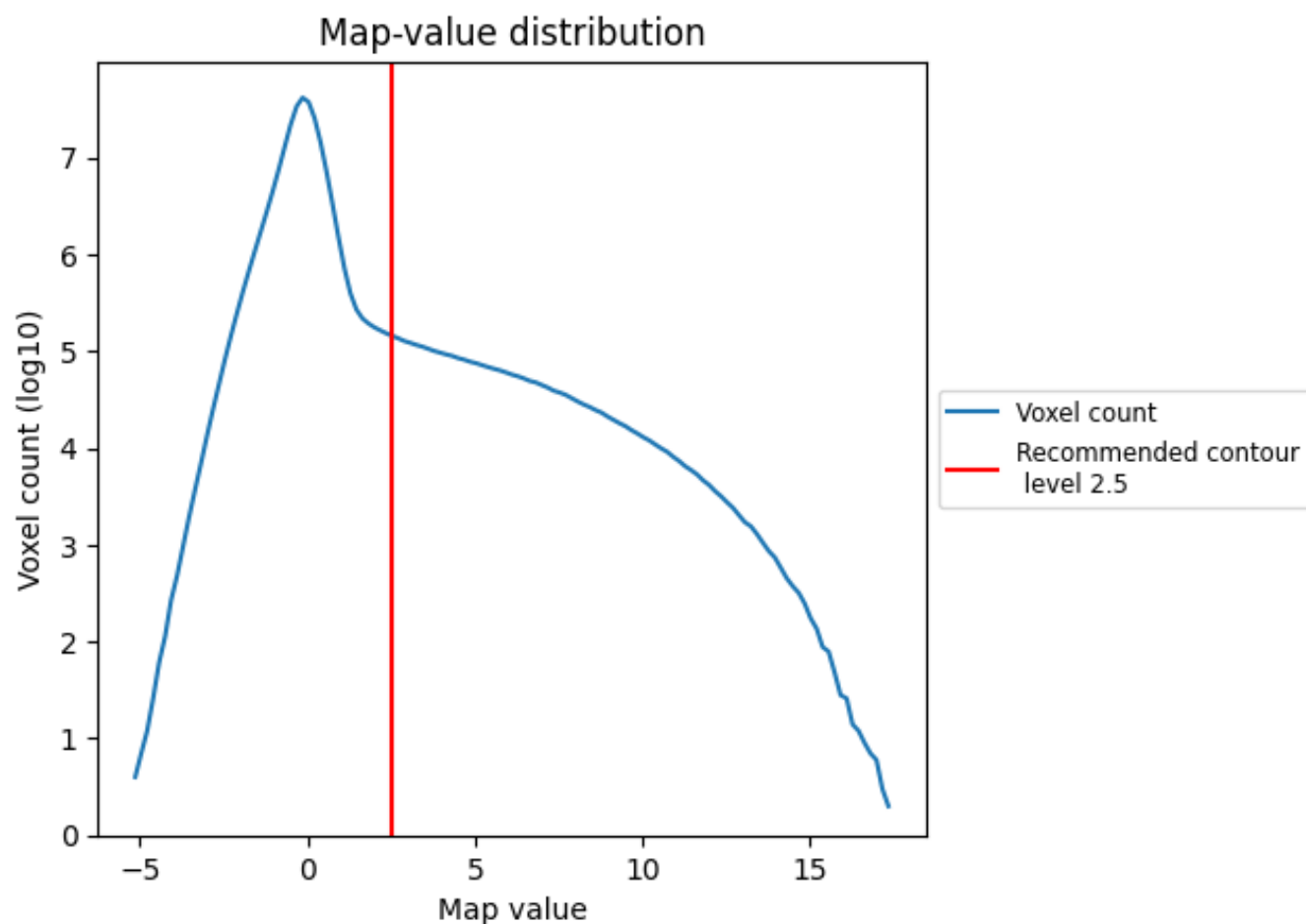
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

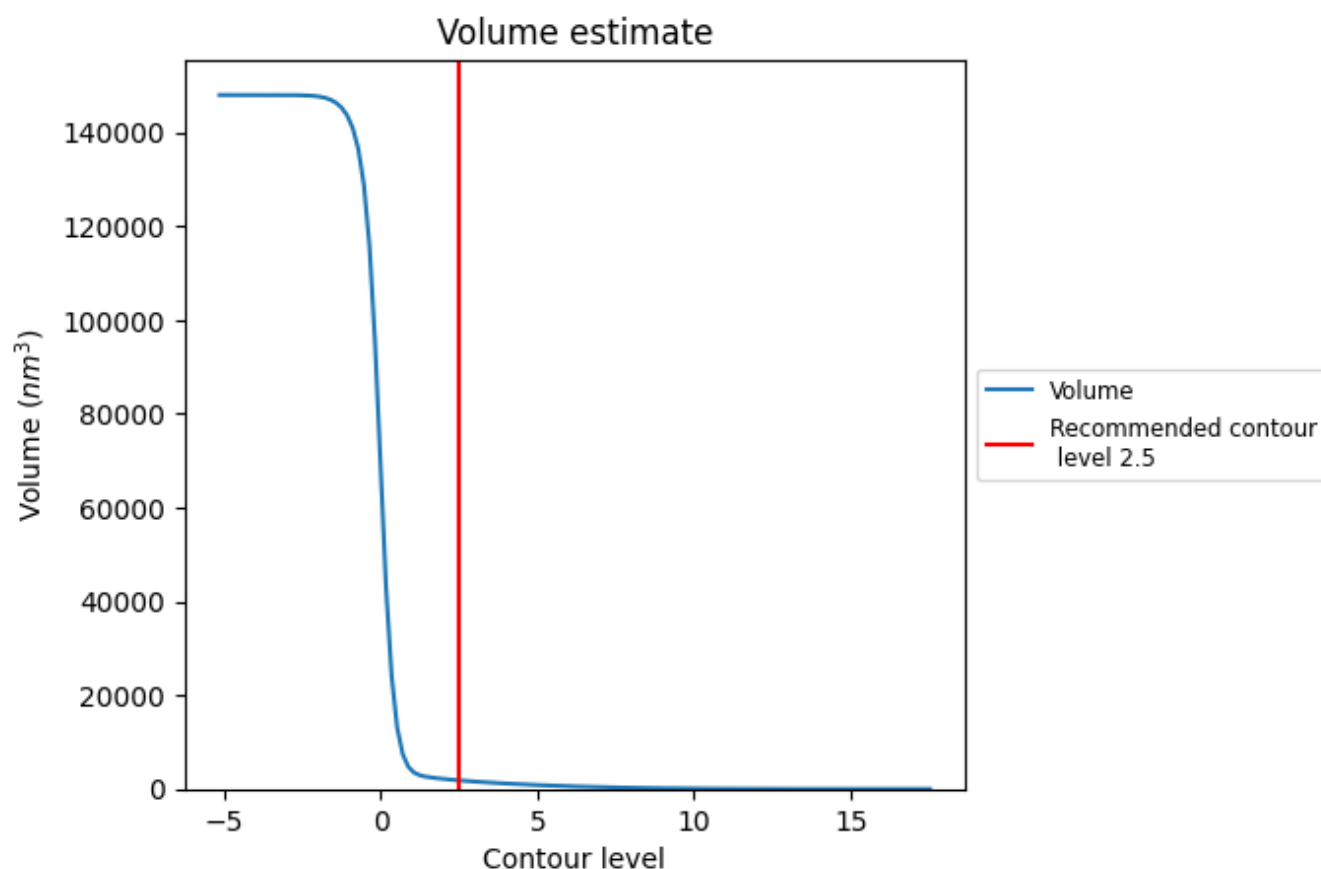
This section contains the results of statistical analysis of the map.

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.

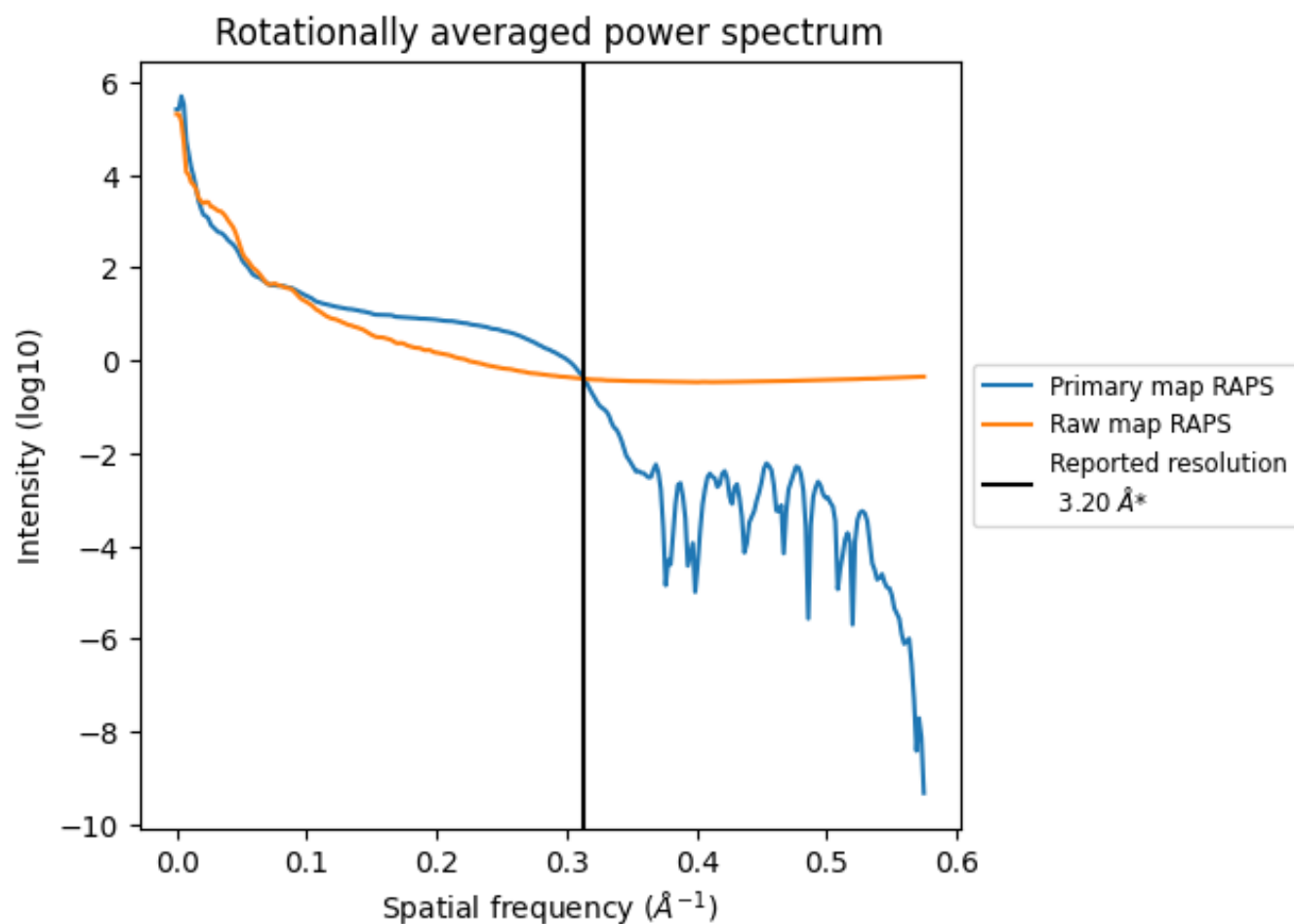
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1831 nm^3 ; this corresponds to an approximate mass of 1654 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

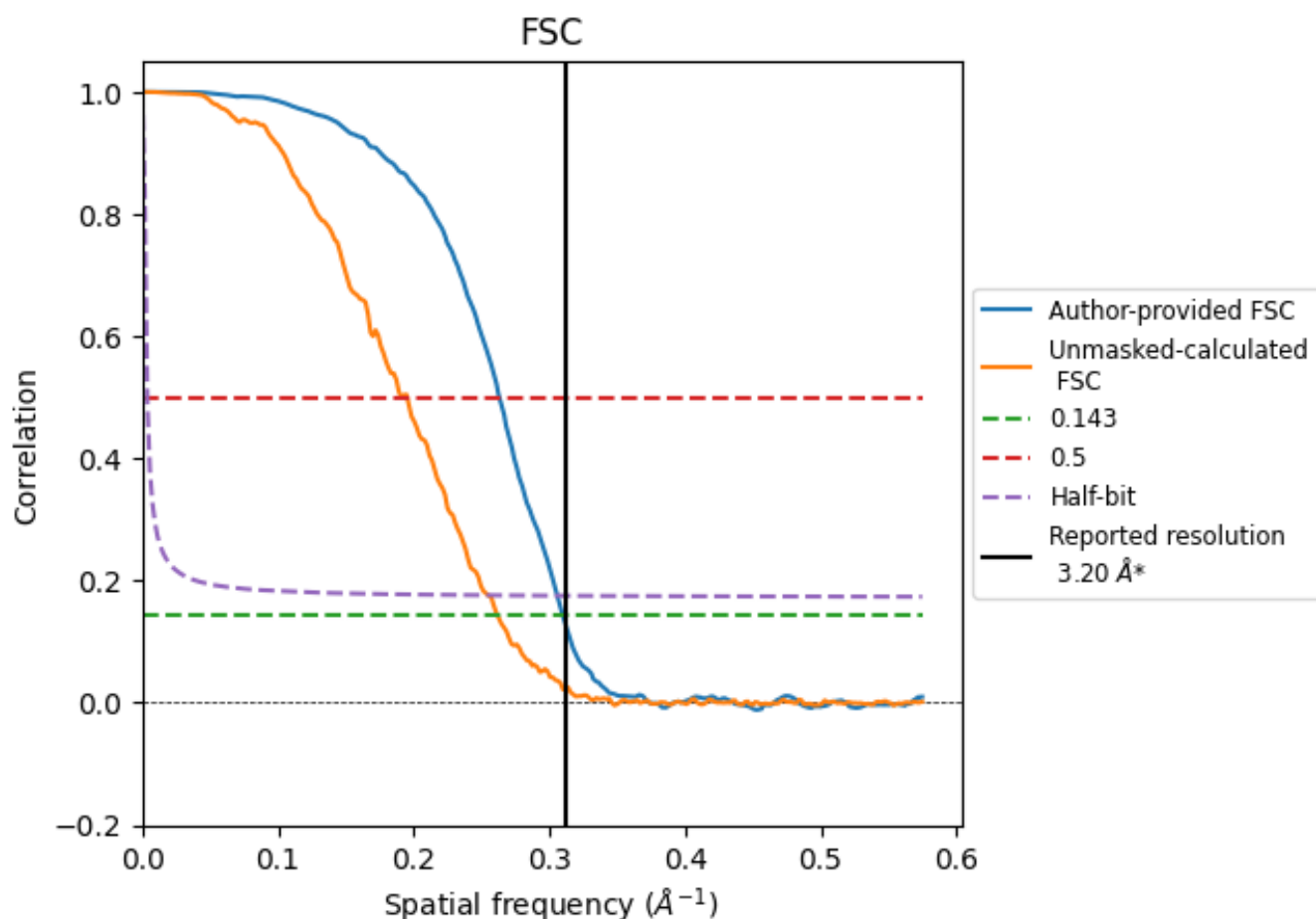


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.23	3.80	3.27
Unmasked-calculated*	3.82	5.24	3.92

*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 3.82 differs from the reported value 3.2 by more than 10 %

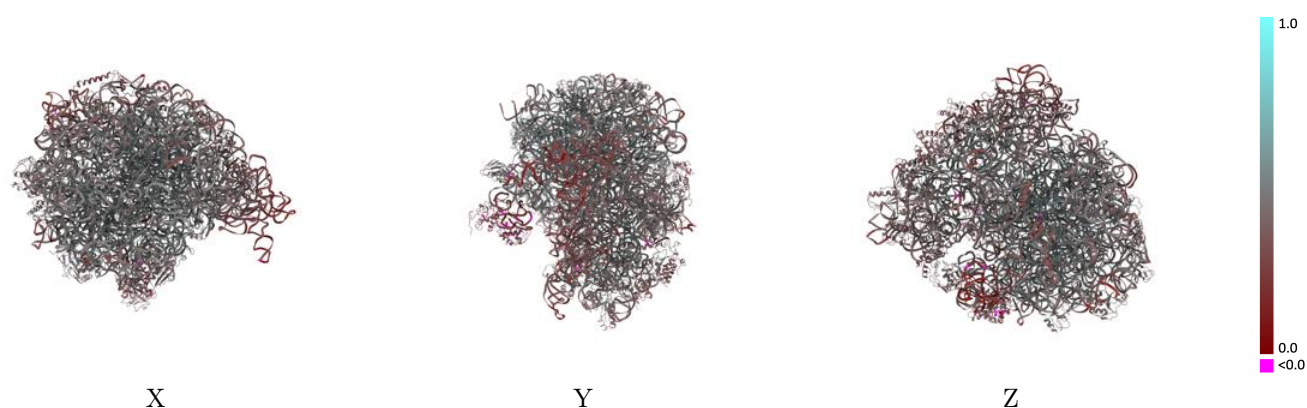
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-21858 and PDB model 6WNW. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

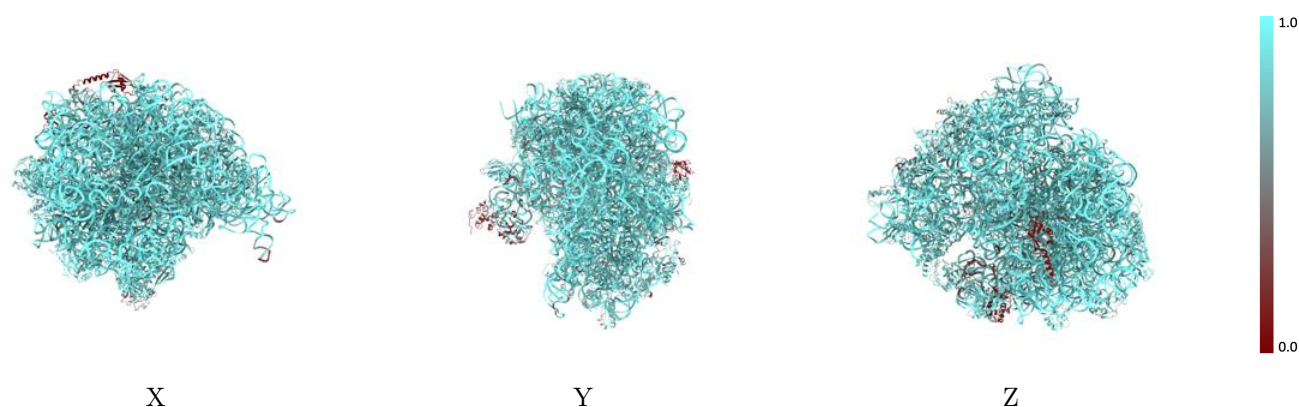
This section was not generated.

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



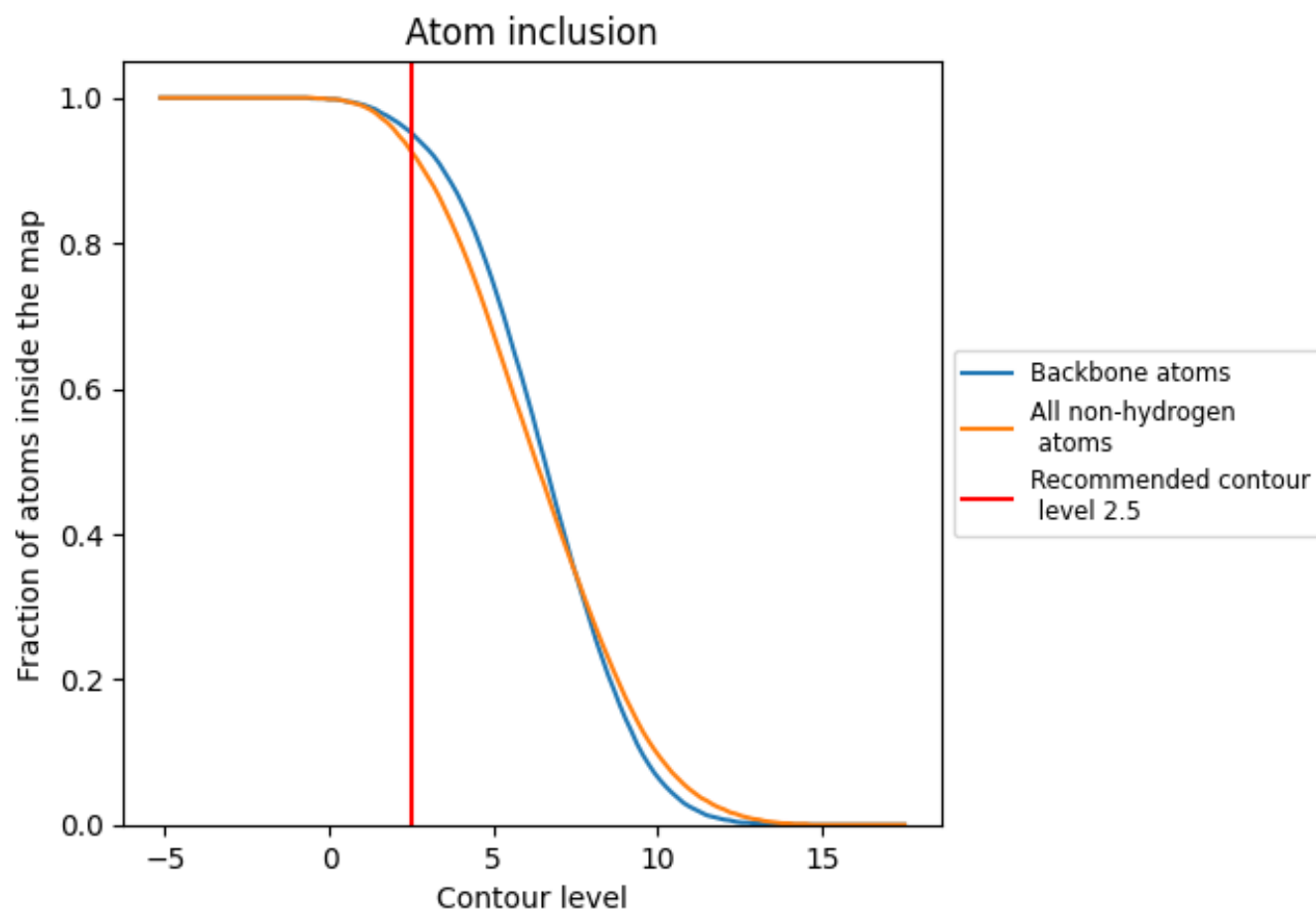
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 93% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9260	 0.4300
1	 0.9440	 0.4570
3	 0.9750	 0.4050
4	 0.9790	 0.4510
5	 0.9450	 0.4090
7	 0.7840	 0.3290
A	 0.7870	 0.3940
B	 0.9160	 0.4750
C	 0.8230	 0.4620
D	 0.9270	 0.5000
E	 0.9450	 0.5130
F	 0.9040	 0.4920
G	 0.7740	 0.3920
H	 0.8320	 0.4340
I	 0.8120	 0.3380
J	 0.8670	 0.4460
K	 0.8720	 0.3990
L	 0.7710	 0.3840
M	 0.8720	 0.4490
N	 0.8690	 0.3890
O	 0.7830	 0.3970
P	 0.9070	 0.4350
Q	 0.8430	 0.4200
R	 0.8780	 0.3930
S	 0.8700	 0.4080
T	 0.9090	 0.4380
U	 0.8490	 0.3730
V	 0.8850	 0.3980
W	 0.8950	 0.4330
X	 0.8910	 0.4110
Y	 0.8650	 0.3600
Z	 0.7160	 0.3550
a	 0.2890	 0.2280
b	 0.9130	 0.5010
c	 0.9170	 0.4930



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Chain	Atom inclusion	Q-score
d	 0.8400	 0.4480
e	 0.8750	 0.4100
f	 0.8950	 0.4240
g	 0.2610	 0.3500
h	 0.3160	 0.2410
i	 0.3940	 0.2430
j	 0.9010	 0.4710
k	 0.8800	 0.4960
l	 0.9150	 0.4780
m	 0.8950	 0.4910
n	 0.9330	 0.4860
o	 0.9150	 0.4420
p	 0.8740	 0.4710
q	 0.9250	 0.4800
r	 0.9030	 0.4750
s	 0.8670	 0.4810
t	 0.8840	 0.4530
u	 0.8890	 0.4360
v	 0.9050	 0.4600
w	 0.9160	 0.5050
x	 0.9150	 0.4850
y	 0.8530	 0.3960
z	 0.8950	 0.4760