



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 02:33 AM UTC

PDB ID : 7JT3 / pdb_00007jt3
EMDB ID : EMD-22472
Title : Rotated 70S ribosome stalled on long mRNA with ArfB-1 and ArfB-2 bound
in the A site (+9-IV)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2020-08-17
Resolution : 3.70 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

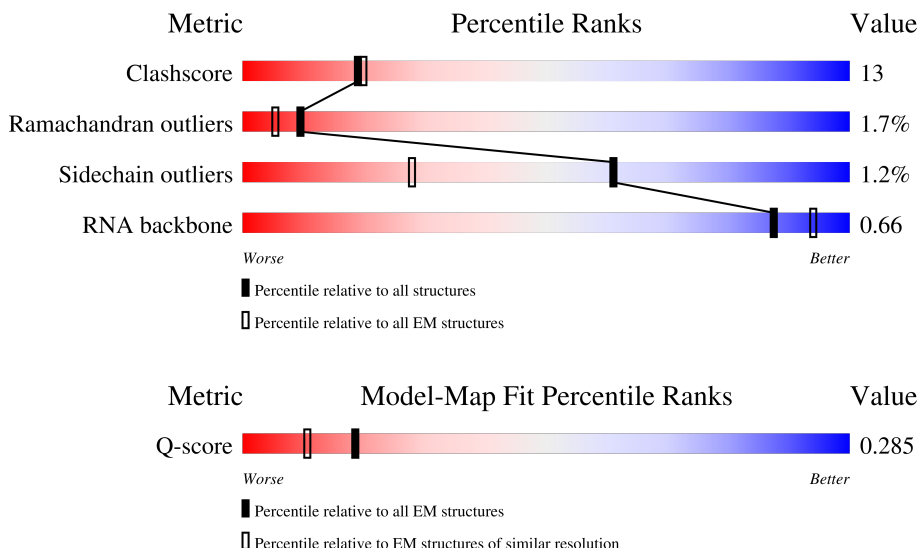
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



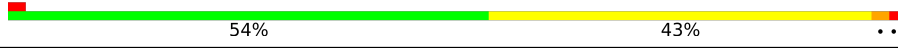
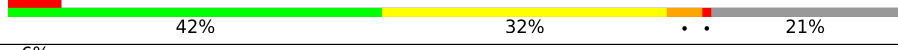
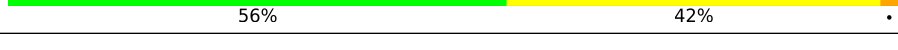
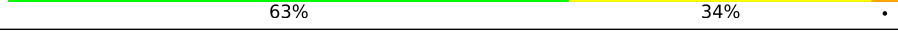
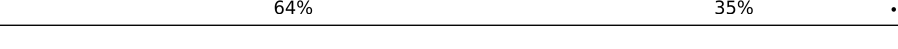
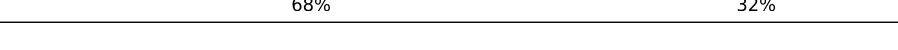
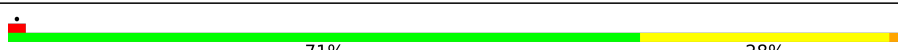
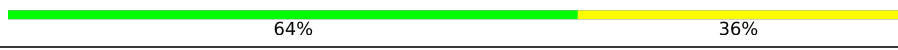
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	
2	c	209	
3	d	201	

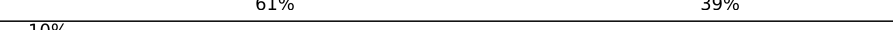
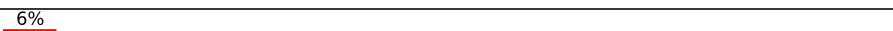
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	165	
8	i	142	
9	j	142	
10	k	122	
11	l	143	
12	m	136	
13	n	120	
14	o	116	
15	p	114	
16	q	117	
17	r	103	
18	s	110	
19	t	93	
20	u	102	
21	v	94	
22	w	75	
23	x	77	
24	y	63	
25	z	58	
26	B	56	
27	C	50	
28	D	46	

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Mol	Chain	Length	Quality of chain
29	E	64	
30	F	38	
31	G	225	
32	H	206	
33	I	205	
34	J	157	
35	K	100	
36	L	151	
37	M	129	
38	N	127	
39	O	98	
40	P	116	
41	Q	123	
42	R	114	
43	S	100	
44	T	88	
45	U	82	
46	V	80	
47	W	65	
48	X	79	
49	Y	85	
50	Z	65	
51	a	234	
52	3	1539	
53	1	2903	

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Mol	Chain	Length	Quality of chain
54	2	120	58%36%7%
55	5	77	38%42%17%
56	4	20	5%40%30%30%
57	8	130	5%45%47%7%
57	9	130	8%37%28%9%25%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 148603 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
			988	625	175	183	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
			917	574	179	163	1	0

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

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

- 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
			816	516	153	145	2	0

- 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
			857	532	166	156	3	0

- 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
			739	466	139	132	2	0

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

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

- 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 L32.

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

- Molecule 27 is a protein called 50S ribosomal protein L33.

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

- Molecule 28 is a protein called 50S ribosomal protein L34.

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

- Molecule 29 is a protein called 50S ribosomal protein L35.

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

- Molecule 30 is a protein called 50S ribosomal protein L36.

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

- Molecule 31 is a protein called 30S ribosomal protein S2.

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

- Molecule 32 is a protein called 30S ribosomal protein S3.

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

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

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

- Molecule 35 is a protein called 30S ribosomal protein S6.

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

- Molecule 36 is a protein called 30S ribosomal protein S7.

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

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

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

- Molecule 40 is a protein called 30S ribosomal protein S11.

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

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

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

- Molecule 43 is a protein called 30S ribosomal protein S14.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18.

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

- Molecule 48 is a protein called 30S ribosomal protein S19.

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- Molecule 50 is a protein called 30S ribosomal protein S21.

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

- Molecule 51 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	1539	Total	C	N	O	P	0	0
			33012	14725	6053	10696	1538		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	1490	C	U	conflict	GB 1789840096

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	1	2903	Total	C	N	O	P	0	0
			62311	27801	11468	20140	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 55 is a RNA chain called tRNAfMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	5	76	Total	C	N	O	P	0	0
			1618	722	292	529	75		

- Molecule 56 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	4	14	Total	C	N	O	P	0	0
			309	138	64	93	14		

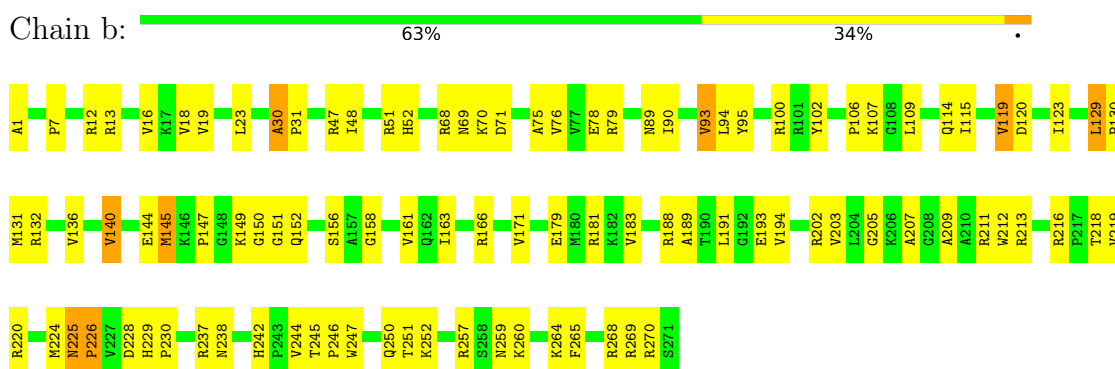
- Molecule 57 is a protein called Peptidyl-tRNA hydrolase ArfB.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	8	130	Total	C	N	O	S	0	0
			1016	627	202	185	2		
57	9	97	Total	C	N	O	S	0	0
			754	471	141	141	1		

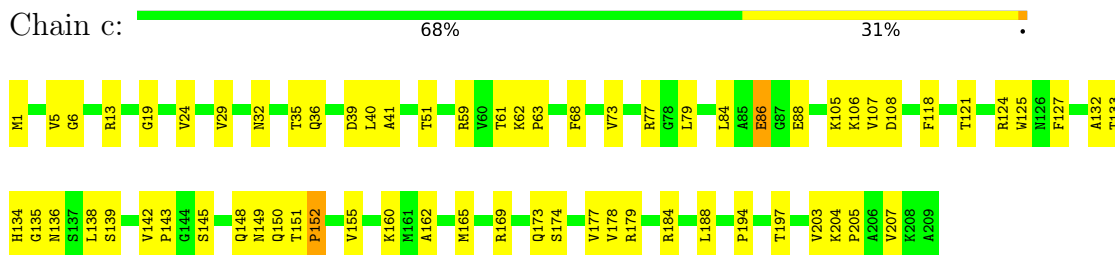
3 Residue-property plots

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.

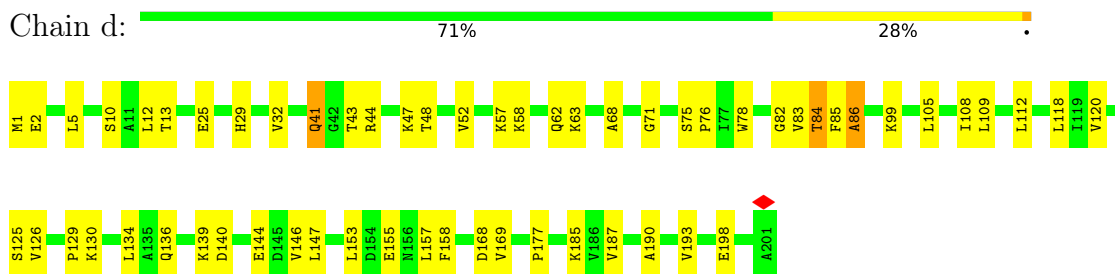
• Molecule 1: 50S ribosomal protein L2



• Molecule 2: 50S ribosomal protein L3

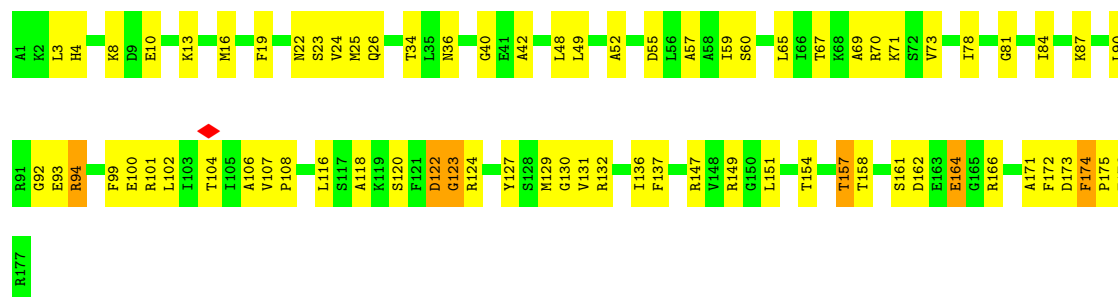


• Molecule 3: 50S ribosomal protein L4

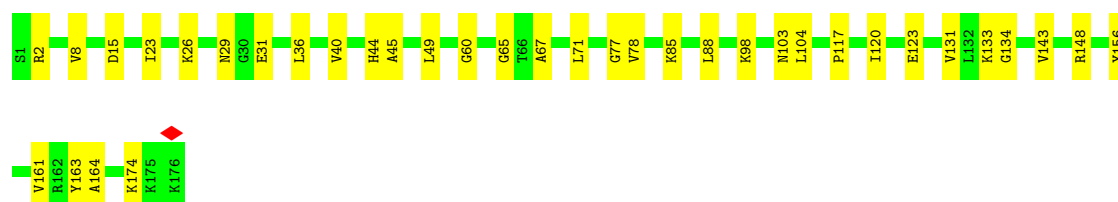
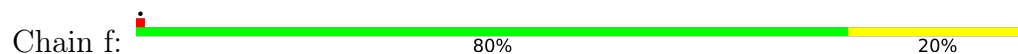


• Molecule 4: 50S ribosomal protein L5

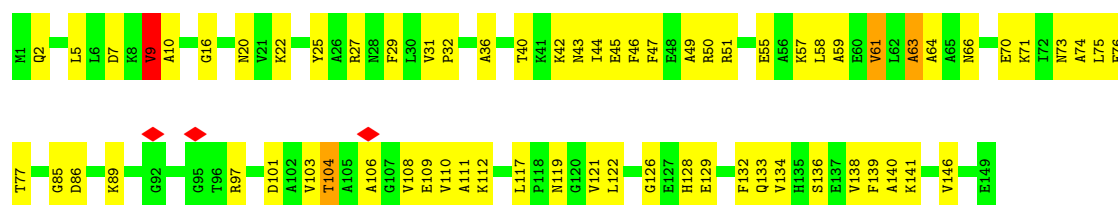




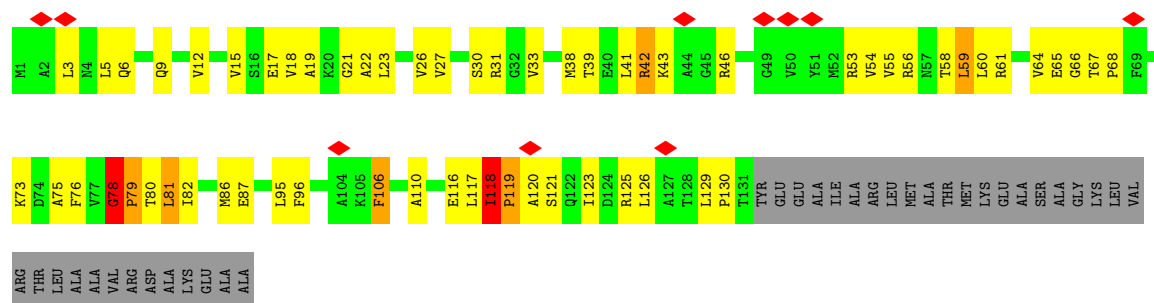
- Molecule 5: 50S ribosomal protein L6



- Molecule 6: 50S ribosomal protein L9

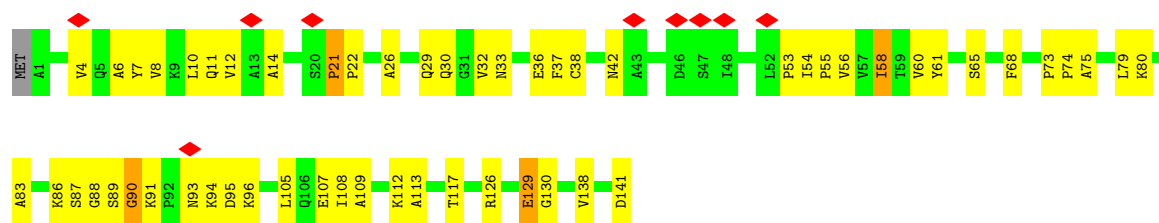


- Molecule 7: 50S ribosomal protein L10



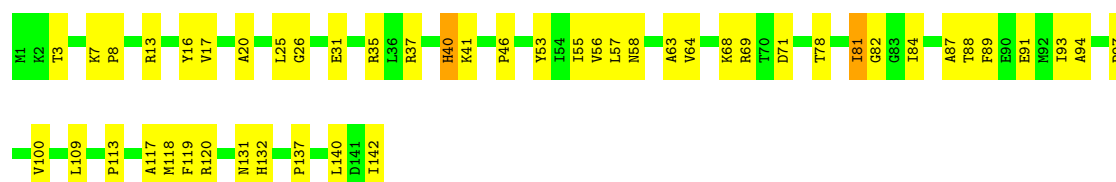
- Molecule 8: 50S ribosomal protein L11





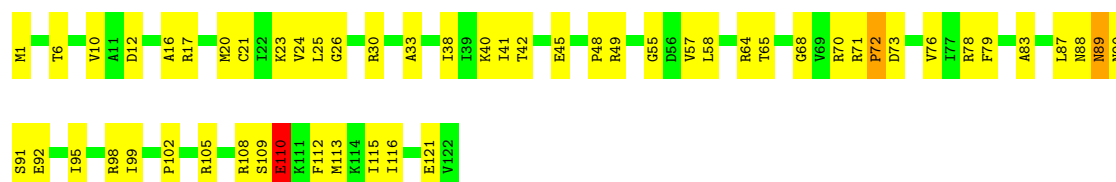
• Molecule 9: 50S ribosomal protein L13

Chain j: 66% 32% .



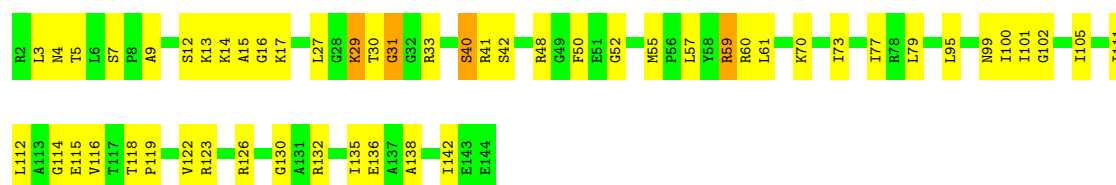
• Molecule 10: 50S ribosomal protein L14

Chain k: 56% 42% . .



• Molecule 11: 50S ribosomal protein L15

Chain l: 63% 34% .



• Molecule 12: 50S ribosomal protein L16

Chain m: 64% 35% .



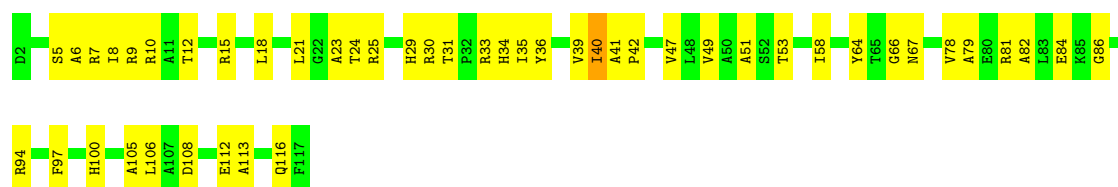
• Molecule 13: 50S ribosomal protein L17

Chain n:  68% 32%



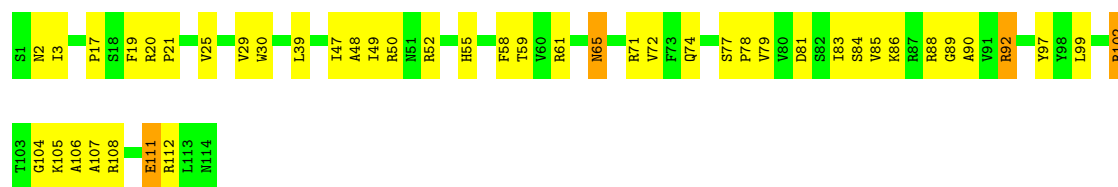
- Molecule 14: 50S ribosomal protein L18

Chain o:  59% 40%



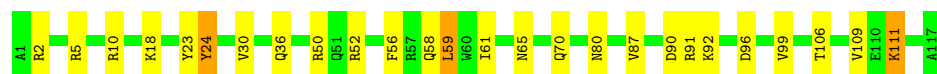
- Molecule 15: 50S ribosomal protein L19

Chain p:  61% 36%



- Molecule 16: 50S ribosomal protein L20

Chain q:  78% 20%



- Molecule 17: 50S ribosomal protein L21

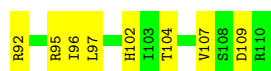
Chain r:  66% 27% 6%



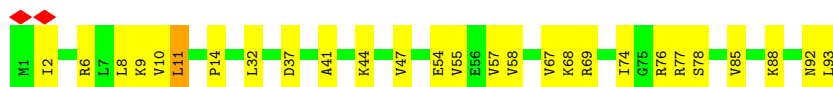
- Molecule 18: 50S ribosomal protein L22

Chain s:  63% 35%

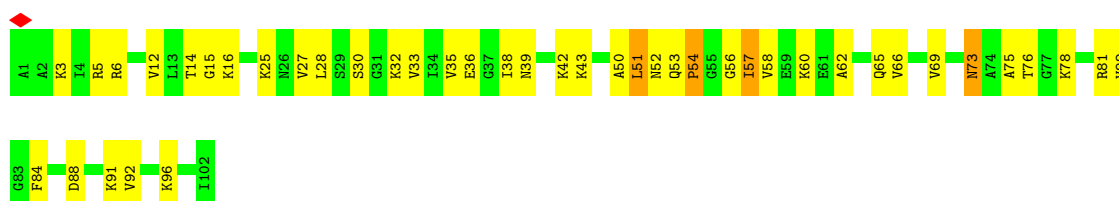




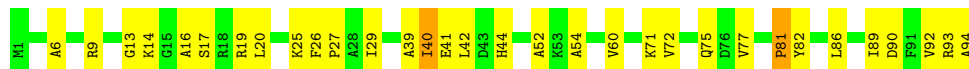
- Molecule 19: 50S ribosomal protein L23



- Molecule 20: 50S ribosomal protein L24



- Molecule 21: 50S ribosomal protein L25



- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28

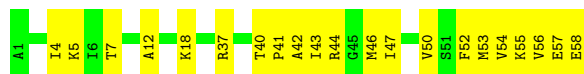


- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30

Chain z:  64% 36%



- Molecule 26: 50S ribosomal protein L32

Chain B:  64% 32% .



- Molecule 27: 50S ribosomal protein L33

Chain C:  76% 24%



- Molecule 28: 50S ribosomal protein L34

Chain D:  61% 35% .



- Molecule 29: 50S ribosomal protein L35

Chain E:  67% 30% .



- Molecule 30: 50S ribosomal protein L36

Chain F:  74% 24% .



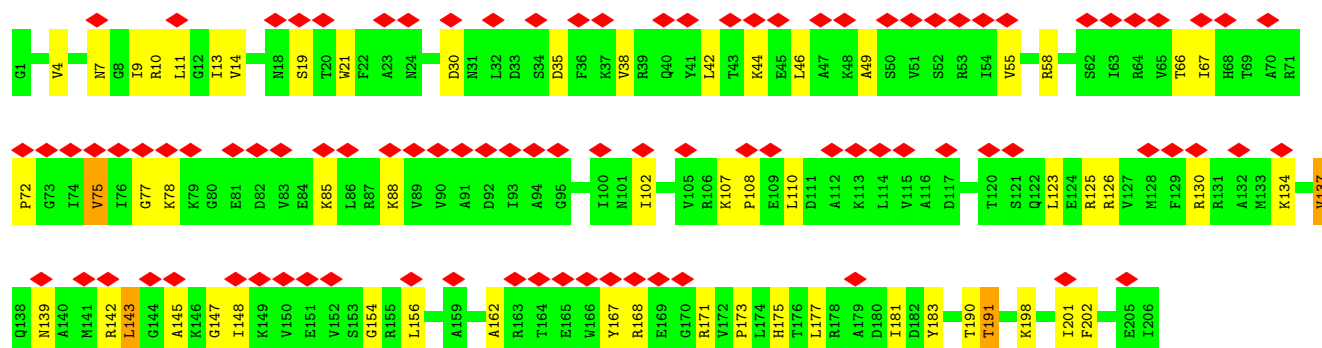
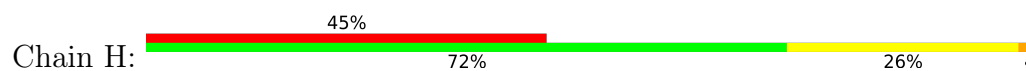
- Molecule 31: 30S ribosomal protein S2

Chain G:  72% 27% .

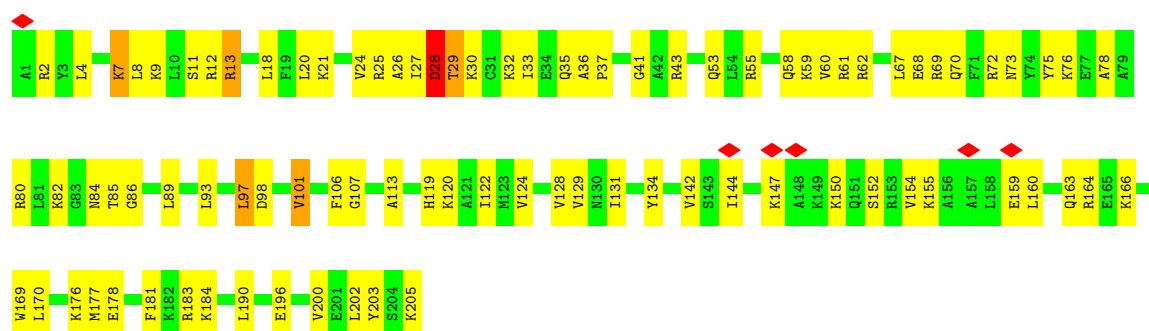




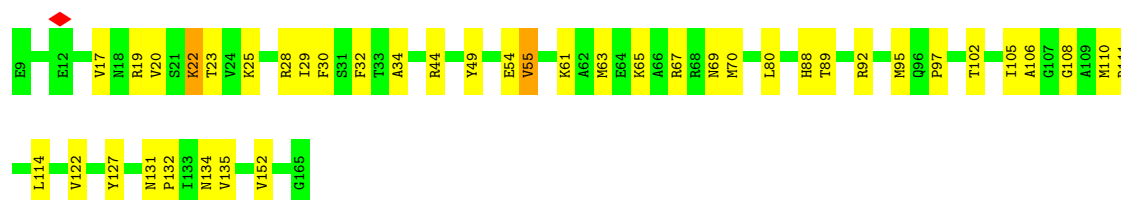
- Molecule 32: 30S ribosomal protein S3



- Molecule 33: 30S ribosomal protein S4

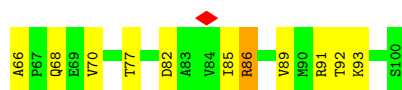


- Molecule 34: 30S ribosomal protein S5



- Molecule 35: 30S ribosomal protein S6

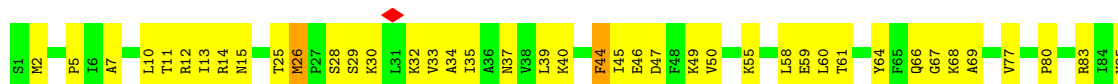




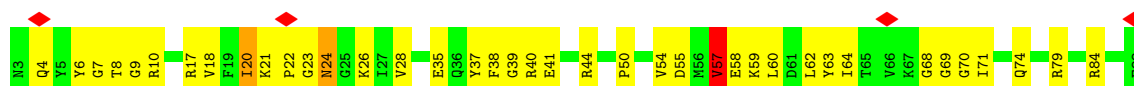
- Molecule 36: 30S ribosomal protein S7



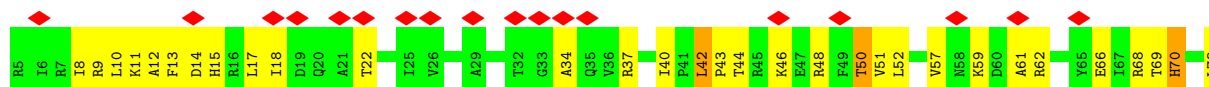
- Molecule 37: 30S ribosomal protein S8



- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10



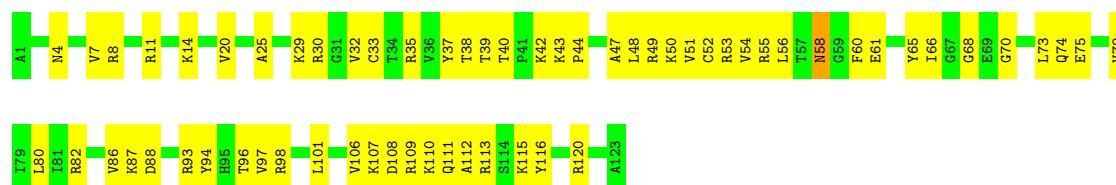
- Molecule 40: 30S ribosomal protein S11

Chain P:  62% 34%



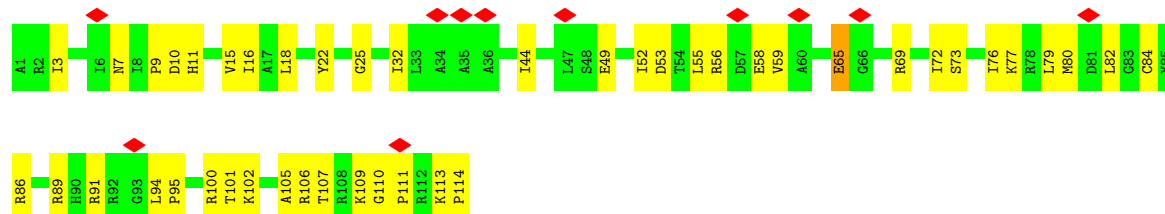
- Molecule 41: 30S ribosomal protein S12

Chain Q:  50% 50%



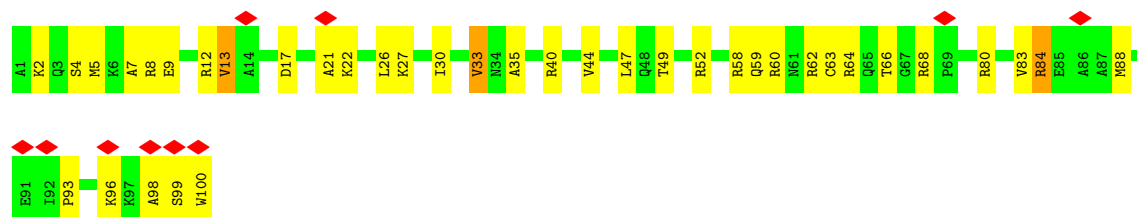
- Molecule 42: 30S ribosomal protein S13

Chain R:  10% 61% 39%



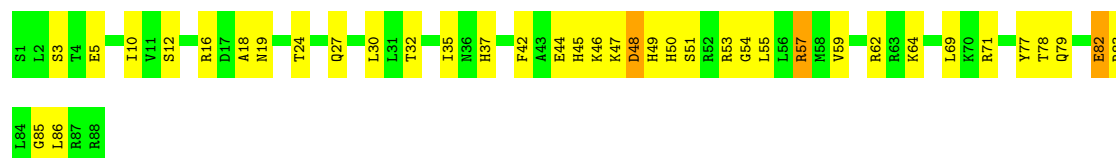
- Molecule 43: 30S ribosomal protein S14

Chain S:  10% 62% 35%

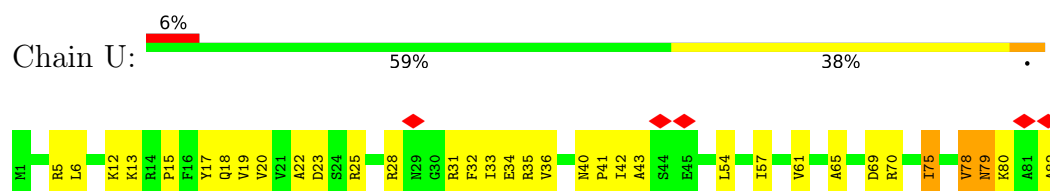


- Molecule 44: 30S ribosomal protein S15

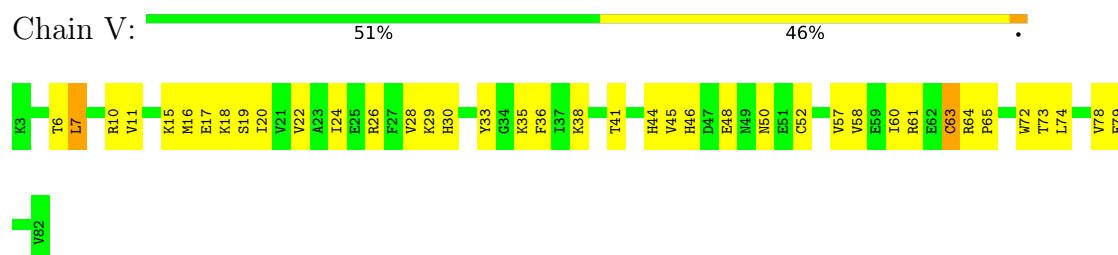
Chain T:  57% 40%



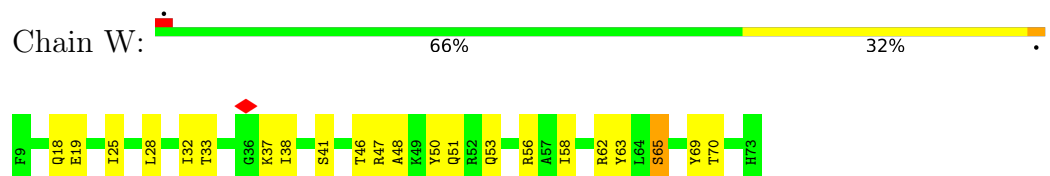
- Molecule 45: 30S ribosomal protein S16



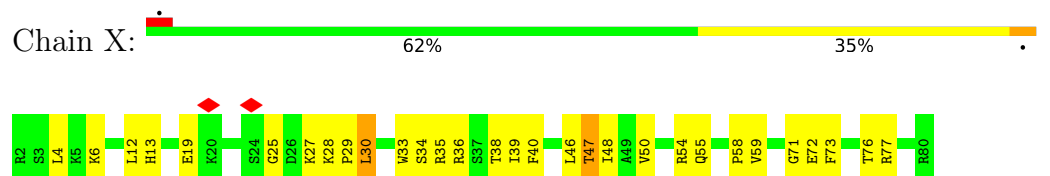
- Molecule 46: 30S ribosomal protein S17



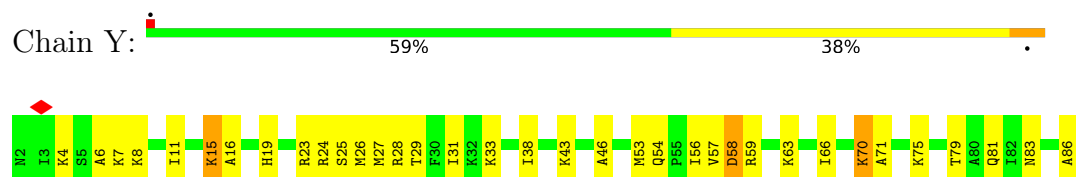
- Molecule 47: 30S ribosomal protein S18



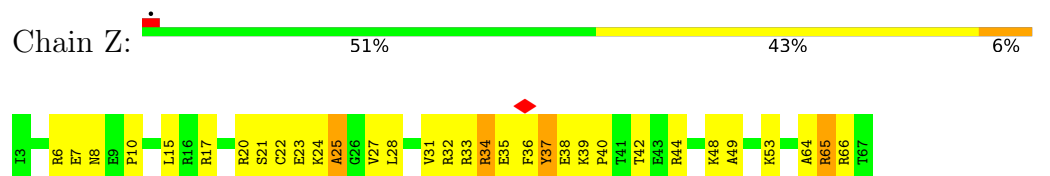
- Molecule 48: 30S ribosomal protein S19



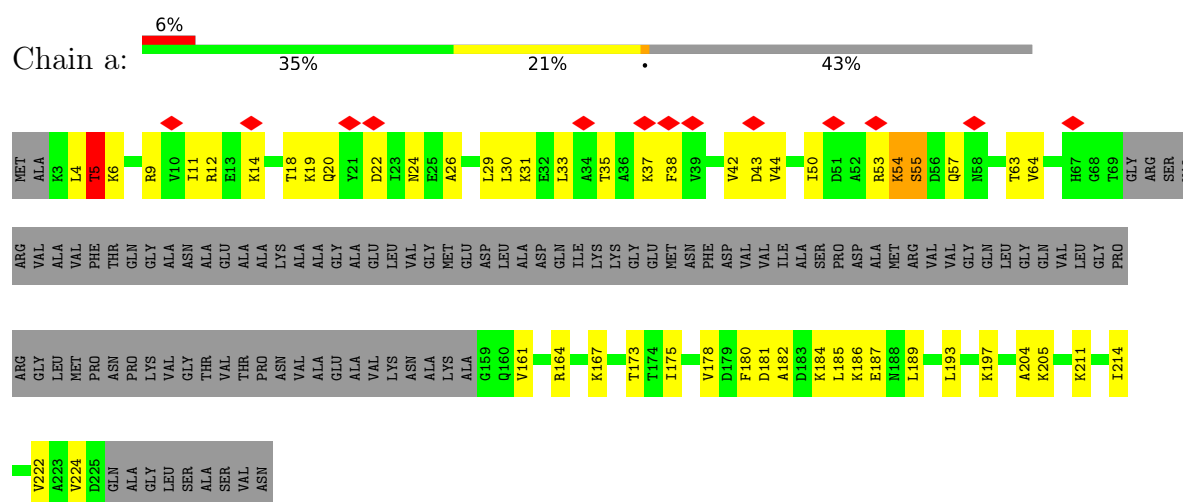
- Molecule 49: 30S ribosomal protein S20



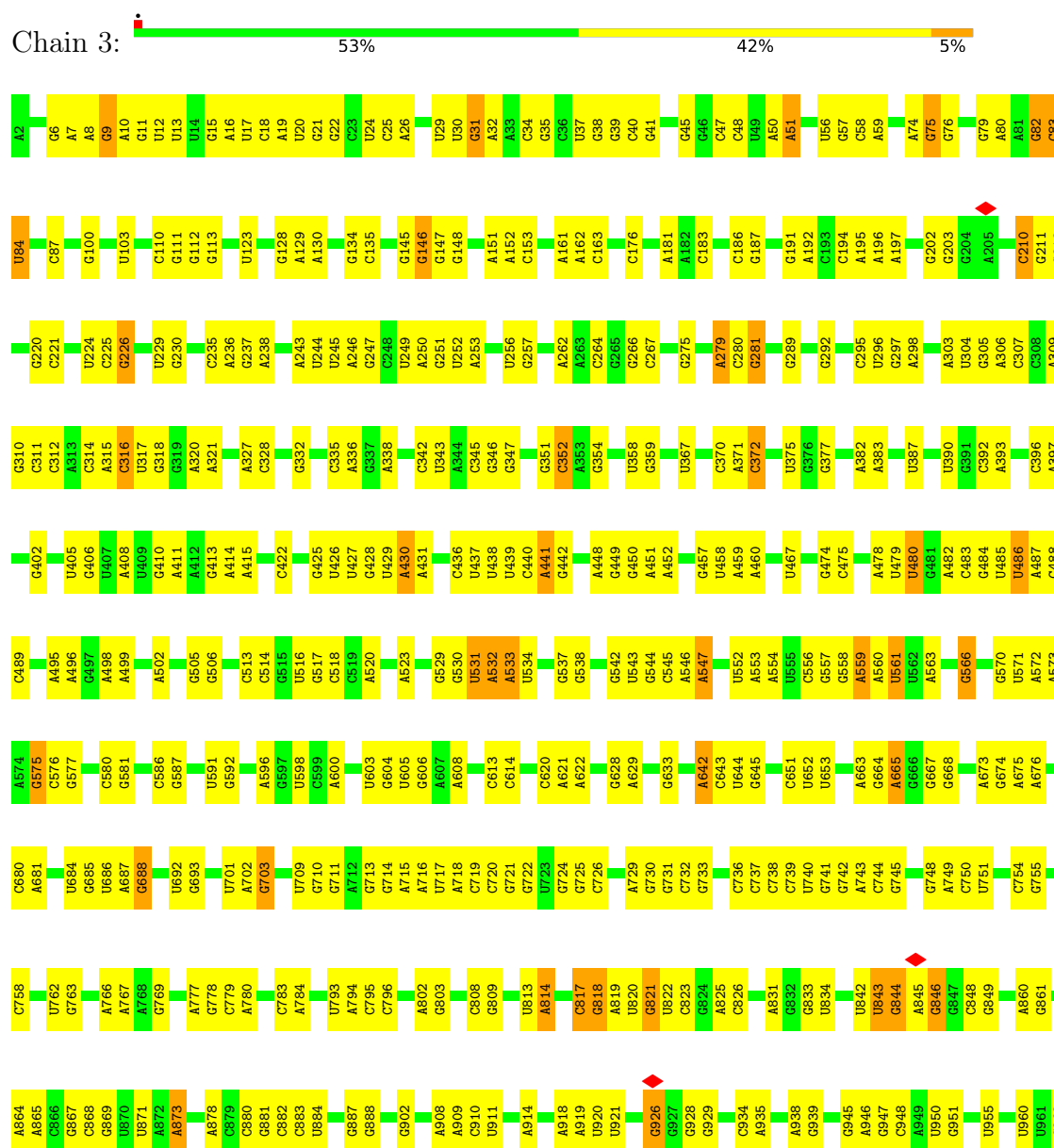
- Molecule 50: 30S ribosomal protein S21



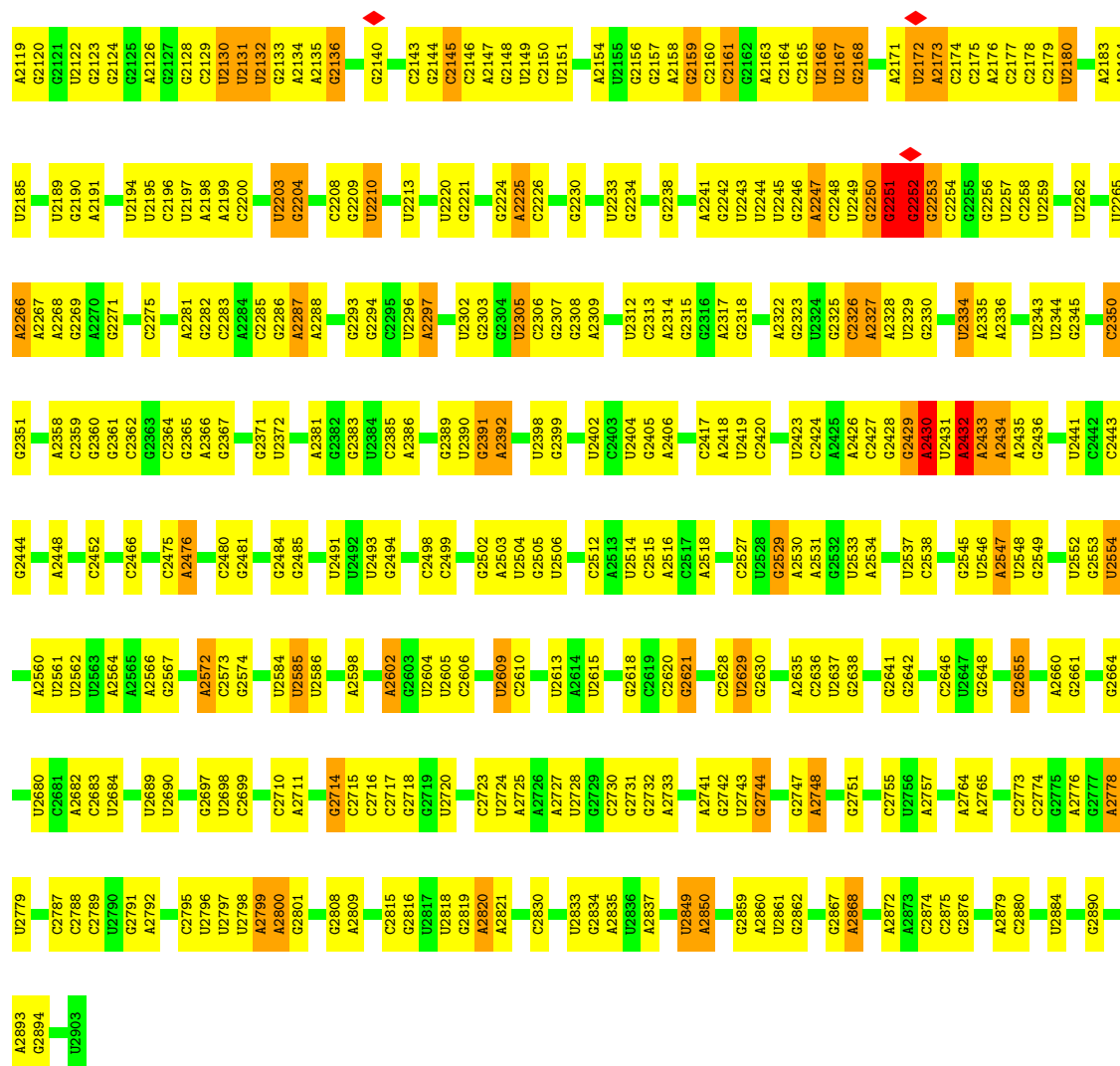
- Molecule 51: 50S ribosomal protein L1



• Molecule 52: 16S ribosomal RNA

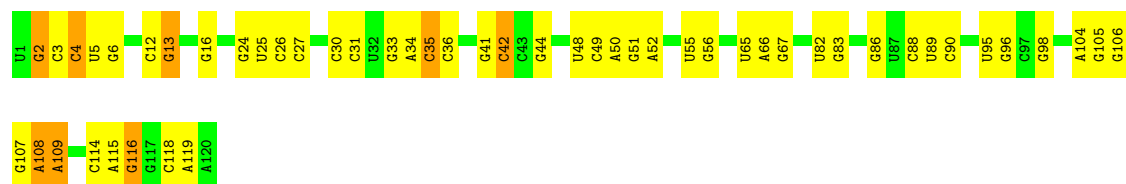


G2040	G1949	C1727	G1510	U1394	A1285	G1182	G1093	C1007	A910	C814	U714	A609
U2041	G1950	C1728	A1515	C1398	A1286	U1183	A1096	A1008	A917	C815	A715	C610
A2042	U1955	U1729	A1523	U1412	C1289	G1185	U1097	A1009	A917	C816	U720	C611
C2043	U1956	C1730	U1524	A1413	C1290	G1186	A1098	A1010	A917	C817	A721	G612
G2049	C1957	G1738	U1525	G1416	C1295	G1187	G1099	G1011	G923	A819	G726	A616
C2050	U1963	A1744	G1526	C1417	G1300	U1203	C1102	C1013	U929	U827	A727	G617
A2051	G1964	A1745	A1528	C1418	A1301	G1204	A1103	A1020	U932	U828	G728	G618
A2052	C1965	U1746	G1527	A1419	G1302	A1205	C1104	A1021	U932	A829	G729	G619
C2055	U1966	U1747	A1528	A1420	C1305	A1206	U1105	G1022	U935	G830	A730	G620
G2056	C1967	C1748	G1529	A1421	C1306	G1210	G1106	U1023	A936	G831	U737	G622
A2060	U1970	U1751	A1535	G1422	A1308	C1211	C1107	C1013	G940	A833	G738	A627
G2061	C1971	C1752	G1536	G1423	A1309	G1212	U1108	G1026	G941	U839	A739	A633
A2062	U1972	G1753	G1537	A1424	C1310	A1213	C1109	A1027	U942	A841	C740	A634
C2066	A1978	A1754	U1542	G1425	C1311	G1219	G1110	A1028	G943	G841	A742	C634
G2067	C1985	U1757	G1543	G1432	C1320	U1222	G1112	A1032	C944	A845	A743	G636
C2068	C1986	U1758	C1550	A1433	U1326	G1223	G1122	U1033	A945	U846	U744	A637
G2069	U1991	C1764	A1551	G1435	A1327	G1225	G1125	G1034	A947	U847	G745	A644
A2070	C1992	C1765	G1555	G1436	U1329	G1225	A1126	U1035	C949	U850	C747	C645
C2071	C1993	A1773	G1555	U1437	C1330	C1229	A1126	G1036	G953	A857	G748	U646
G2072	C1994	C1774	C1558	U1438	G1331	A1230	U1130	C1045	G954	U858	A752	G651
C2073	U1998	U1775	U1559	G1443	G1332	G1236	G1132	A1046	G955	G859	U763	A654
U2074	C1996	G1776	G1560	U1444	G1333	G1236	A1133	G1047	U956	U860	A764	A654
U2075	U1997	A1777	C1563	C1445	G1334	G1245	A1134	A1054	C957	G864	G770	G652
A2077	C1998	U1780	U1563	G1447	G1341	G1246	C1135	G1055	U958	C865	G771	G663
G2078	G1905	U1781	C1564	U1448	A1342	A1247	G1138	U1058	A960	U871	U779	A666
A2080	C1906	U1782	C1565	G1449	G1343	G1248	G1139	G1059	C961	U872	G774	U667
U2081	G1907	A1786	U1566	U1450	A1344	G1250	C1140	U1060	G962	A688	G775	A668
C2082	C1908	U1789	A1569	G1451	C1345	G1251	U1141	U1061	U967	G689	G776	G689
G2083	U1909	C1790	A1570	G1452	U1346	C1261	A1142	G1062	U967	A670	U779	A670
A2084	C1910	A1790	A1571	U1453	A1354	G1263	A1143	G1063	C968	C671	U779	C671
U2086	U1911	U1796	A1583	G1454	G1355	U1263	A1151	C1064	C969	C672	G760	C672
C2087	C1912	G1797	U1584	C1461	G1356	U1265	C1152	U1065	U970	A677	A781	A677
A2090	U1913	U1798	C1585	U1468	G1358	G1266	C1153	A1067	G971	A783	G782	A677
C2091	C1914	U1799	U1589	U1469	G1360	G1267	G1153	G1068	A973	A784	C679	C679
U2092	U1917	C1800	U1594	G1475	C1363	U1268	A1156	U1069	G974	G785	G785	C680
G2093	A1918	A1801	C1595	U1476	A1364	G1269	A1162	A1070	A975	C885	C786	G681
A2094	A1919	A1802	U1596	U1476	A1365	U1269	G1167	C1072	A983	A886	C787	G682
C2095	C1920	A1803	U1599	U1476	A1366	U1269	C1168	G1075	U984	C887	C796	U686
U2096	G1929	C1806	G1601	G1479	A1367	U1269	G1168	C1075	C985	C888	G797	C687
C2097	G1930	G1807	U1602	C1480	A1367	U1270	C1168	C1075	C986	C889	A804	G690
A2098	U1931	A1808	A1603	U1481	G1368	G1271	C1172	C1079	C987	C890	G805	C691
C2099	C1934	A1809	U1608	G1482	C1370	A1272	U1173	A1080	A989	G891	C806	U694
U2099	G1935	G1811	A1609	A1490	G1371	U1272	U1174	U1083	C992	U894	U807	U694
G2100	A1936	C1816	C1611	C1498	U1378	G1277	A1175	U1084	C995	U895	G808	U694
A2101	C1937	U1714	G1615	G1501	U1379	C1278	U1176	A1085	A996	A896	G809	U703
C2102	A1938	G1715	C1616	G1501	U1380	G1279	G1177	A1085	A996	C897	U810	G704
G2103	U1943	U1818	C1617	U1506	A1383	G1280	C1178	A1085	A996	C897	U811	G712
C2104	U1944	U1825	C1617	U1507	C1386	G1281	U1179	A1088	A1000	C898	C812	G713
U2105	C1947	G1826	U1725	A1508	A1387	U1282	U1180	C1092	A1001	A899	U813	G713
G2106	G1948	G1828	C1638	A1509	A1387	A1284	U1181	C1092	A1001	A900	U813	G713



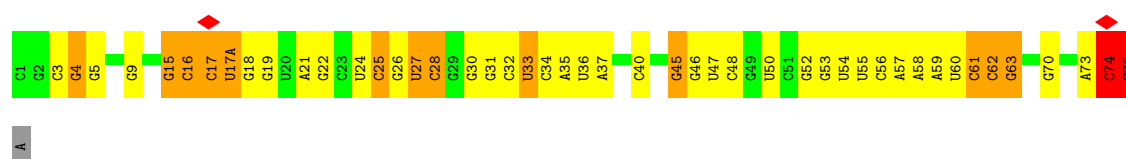
• Molecule 54: 5S ribosomal RNA

Chain 2: 58% 36% 7%

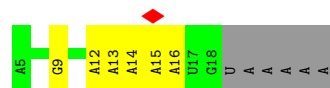


• Molecule 55: tRNA^{fMet}

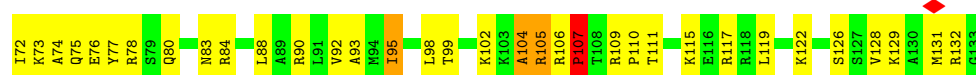
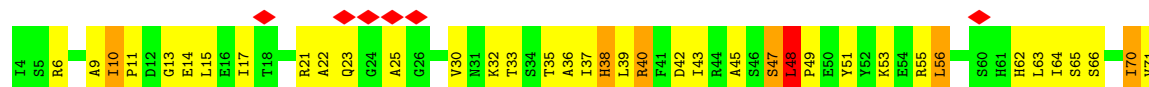
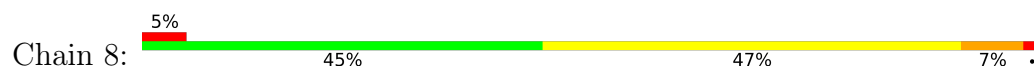
Chain 5: 38% 42% 17%



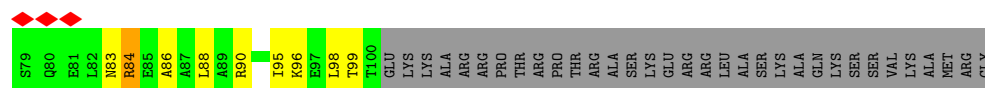
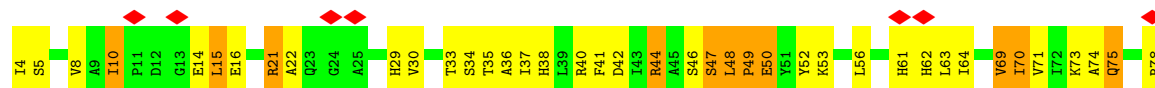
- Molecule 56: mRNA



- Molecule 57: Peptidyl-tRNA hydrolase ArfB



- Molecule 57: Peptidyl-tRNA hydrolase ArfB



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5711	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.467	Depositor
Minimum map value	-5.886	Depositor
Average map value	0.100	Depositor
Map value standard deviation	0.580	Depositor
Recommended contour level	0.75	Depositor
Map size ($\text{\AA}$)	375.12003, 375.12003, 375.12003	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.042, 1.042, 1.042	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	0.30	0/2122	0.96	10/2852 (0.4%)
2	c	0.31	0/1586	0.89	3/2134 (0.1%)
3	d	0.31	0/1571	0.94	4/2113 (0.2%)
4	e	0.34	0/1435	1.06	18/1926 (0.9%)
5	f	0.33	0/1343	0.91	2/1816 (0.1%)
6	g	0.36	0/1122	1.07	10/1515 (0.7%)
7	h	0.38	0/1001	1.19	15/1350 (1.1%)
8	i	0.42	0/1046	1.05	8/1410 (0.6%)
9	j	0.31	0/1152	0.92	4/1551 (0.3%)
10	k	0.30	0/948	0.98	5/1268 (0.4%)
11	l	0.32	0/1054	0.94	4/1403 (0.3%)
12	m	0.32	0/1093	0.90	3/1460 (0.2%)
13	n	0.30	0/974	0.93	3/1301 (0.2%)
14	o	0.31	0/902	0.95	3/1209 (0.2%)
15	p	0.31	0/929	0.91	3/1242 (0.2%)
16	q	0.30	0/960	0.94	4/1278 (0.3%)
17	r	0.34	0/829	0.95	3/1107 (0.3%)
18	s	0.30	0/864	0.88	1/1156 (0.1%)
19	t	0.29	0/745	0.93	3/994 (0.3%)
20	u	0.33	0/788	0.95	5/1051 (0.5%)
21	v	0.34	0/766	0.90	3/1025 (0.3%)
22	w	0.31	0/582	0.97	2/769 (0.3%)
23	x	0.29	0/635	0.87	3/848 (0.4%)
24	y	0.30	0/510	0.96	3/677 (0.4%)
25	z	0.33	0/453	0.79	0/605
26	B	0.32	0/450	0.93	2/599 (0.3%)
27	C	0.35	0/417	0.89	1/554 (0.2%)
28	D	0.33	0/380	0.92	2/498 (0.4%)
29	E	0.31	0/513	0.89	1/676 (0.1%)
30	F	0.29	0/303	0.87	0/397
31	G	0.32	0/1788	0.89	3/2408 (0.1%)
32	H	0.38	0/1652	0.95	6/2225 (0.3%)
33	I	0.34	0/1665	1.04	12/2227 (0.5%)
34	J	0.43	1/1170 (0.1%)	1.07	4/1573 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	K	0.38	0/836	1.10	8/1128 (0.7%)
36	L	0.35	0/1196	0.96	3/1602 (0.2%)
37	M	0.34	0/989	1.01	4/1326 (0.3%)
38	N	0.38	0/1034	1.00	5/1375 (0.4%)
39	O	0.39	0/797	0.99	6/1077 (0.6%)
40	P	0.37	0/886	1.00	4/1195 (0.3%)
41	Q	0.34	0/969	1.02	4/1300 (0.3%)
42	R	0.38	0/893	1.02	2/1193 (0.2%)
43	S	0.34	0/817	1.06	6/1088 (0.6%)
44	T	0.33	0/722	1.03	7/964 (0.7%)
45	U	0.34	0/659	0.90	2/884 (0.2%)
46	V	0.35	0/658	0.91	1/881 (0.1%)
47	W	0.37	0/545	1.00	5/731 (0.7%)
48	X	0.40	0/653	0.92	2/877 (0.2%)
49	Y	0.32	0/671	1.03	3/888 (0.3%)
50	Z	0.36	0/551	0.94	0/728
51	a	0.38	0/1033	1.05	6/1387 (0.4%)
52	3	0.43	0/36963	0.48	2/57662 (0.0%)
53	1	0.42	0/69790	0.48	7/108873 (0.0%)
54	2	0.43	0/2872	0.46	0/4479
55	5	0.53	0/1807	0.62	2/2816 (0.1%)
56	4	0.51	0/348	0.51	0/542
57	8	0.39	0/1028	1.12	11/1378 (0.8%)
57	9	0.38	0/764	1.12	9/1031 (0.9%)
All	All	0.40	1/161229 (0.0%)	0.66	252/240622 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
34	J	0	1
53	1	1	1
All	All	1	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	J	55	VAL	C-N	5.37	1.40	1.34

The worst 5 of 252 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	K	82	ASP	N-CA-C	10.29	122.50	111.28
43	S	21	ALA	N-CA-C	-9.99	101.87	114.56
42	R	107	THR	N-CA-C	-9.57	99.15	112.45
57	9	44	ARG	N-CA-C	9.12	121.30	111.36
57	9	48	LEU	CA-C-N	8.96	131.04	119.84

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
53	1	2251	G	C3'

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	1	2432	A	Sidechain
34	J	88	HIS	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	b	2083	0	2157	81	0
2	c	1565	0	1616	56	0
3	d	1552	0	1619	42	0
4	e	1411	0	1447	58	0
5	f	1323	0	1374	25	0
6	g	1111	0	1148	44	0
7	h	988	0	1025	54	0
8	i	1032	0	1088	38	0
9	j	1129	0	1162	37	0
10	k	939	0	1012	41	0
11	l	1045	0	1117	45	0
12	m	1074	0	1157	39	0
13	n	961	0	1000	31	0
14	o	892	0	923	35	0
15	p	917	0	965	43	0
16	q	947	0	1022	31	0
17	r	816	0	839	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	s	857	0	922	34	0
19	t	739	0	807	24	0
20	u	780	0	834	33	0
21	v	753	0	780	22	0
22	w	575	0	592	14	0
23	x	625	0	655	15	0
24	y	509	0	543	13	0
25	z	449	0	491	16	0
26	B	444	0	461	22	0
27	C	410	0	440	10	0
28	D	377	0	418	16	0
29	E	504	0	574	21	0
30	F	302	0	343	9	0
31	G	1757	0	1787	38	0
32	H	1625	0	1699	60	0
33	I	1643	0	1710	72	0
34	J	1157	0	1199	39	0
35	K	818	0	808	38	0
36	L	1182	0	1240	44	0
37	M	979	0	1034	51	0
38	N	1022	0	1070	74	0
39	O	787	0	828	38	0
40	P	870	0	878	44	0
41	Q	955	0	1019	50	0
42	R	884	0	944	40	0
43	S	805	0	847	38	0
44	T	714	0	737	34	0
45	U	649	0	666	31	0
46	V	649	0	691	40	0
47	W	536	0	552	13	0
48	X	638	0	665	25	0
49	Y	665	0	714	33	0
50	Z	545	0	579	36	0
51	a	1026	0	1092	45	0
52	3	33012	0	16619	739	0
53	1	62311	0	31346	1044	0
54	2	2568	0	1303	41	0
55	5	1618	0	826	85	0
56	4	309	0	153	11	0
57	8	1016	0	1067	84	0
57	9	754	0	773	43	0
All	All	148603	0	101377	3198	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 13.

The worst 5 of 3198 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)
38:N:128:LYS:NZ	55:5:31:G:H5''	1.57	1.17
53:1:2585:U:H4'	53:1:2586:U:H5'	1.22	1.16
55:5:62:C:H2'	55:5:63:G:H5''	1.22	1.12
53:1:2432:A:H1'	55:5:74:C:H2'	1.26	1.11
40:P:126:ARG:HA	52:3:796:C:H5''	1.33	1.09

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	b	269/271 (99%)	231 (86%)	32 (12%)	6 (2%)	5	31
2	c	207/209 (99%)	182 (88%)	23 (11%)	2 (1%)	12	43
3	d	199/201 (99%)	181 (91%)	16 (8%)	2 (1%)	12	43
4	e	175/177 (99%)	154 (88%)	19 (11%)	2 (1%)	11	42
5	f	174/176 (99%)	152 (87%)	19 (11%)	3 (2%)	7	34
6	g	147/149 (99%)	119 (81%)	25 (17%)	3 (2%)	6	32
7	h	129/165 (78%)	99 (77%)	23 (18%)	7 (5%)	1	16
8	i	139/142 (98%)	120 (86%)	18 (13%)	1 (1%)	18	50
9	j	140/142 (99%)	129 (92%)	10 (7%)	1 (1%)	18	50
10	k	120/122 (98%)	102 (85%)	15 (12%)	3 (2%)	4	29
11	l	141/143 (99%)	120 (85%)	18 (13%)	3 (2%)	5	31
12	m	134/136 (98%)	119 (89%)	12 (9%)	3 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	n	118/120 (98%)	102 (86%)	16 (14%)	0	100	100
14	o	114/116 (98%)	103 (90%)	10 (9%)	1 (1%)	14	45
15	p	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	45
16	q	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
17	r	101/103 (98%)	78 (77%)	19 (19%)	4 (4%)	2	21
18	s	108/110 (98%)	96 (89%)	10 (9%)	2 (2%)	6	33
19	t	91/93 (98%)	78 (86%)	13 (14%)	0	100	100
20	u	100/102 (98%)	80 (80%)	17 (17%)	3 (3%)	3	26
21	v	92/94 (98%)	85 (92%)	6 (6%)	1 (1%)	11	42
22	w	73/75 (97%)	63 (86%)	7 (10%)	3 (4%)	2	20
23	x	75/77 (97%)	70 (93%)	4 (5%)	1 (1%)	9	38
24	y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
25	z	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
26	B	54/56 (96%)	48 (89%)	5 (9%)	1 (2%)	6	33
27	C	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
28	D	44/46 (96%)	39 (89%)	3 (7%)	2 (4%)	2	18
29	E	62/64 (97%)	55 (89%)	5 (8%)	2 (3%)	3	25
30	F	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	4	27
31	G	223/225 (99%)	200 (90%)	23 (10%)	0	100	100
32	H	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
33	I	203/205 (99%)	171 (84%)	30 (15%)	2 (1%)	12	43
34	J	155/157 (99%)	135 (87%)	20 (13%)	0	100	100
35	K	98/100 (98%)	79 (81%)	15 (15%)	4 (4%)	2	20
36	L	149/151 (99%)	130 (87%)	18 (12%)	1 (1%)	18	50
37	M	127/129 (98%)	113 (89%)	13 (10%)	1 (1%)	16	48
38	N	125/127 (98%)	94 (75%)	26 (21%)	5 (4%)	2	21
39	O	96/98 (98%)	78 (81%)	16 (17%)	2 (2%)	5	31
40	P	114/116 (98%)	86 (75%)	23 (20%)	5 (4%)	2	19
41	Q	121/123 (98%)	95 (78%)	24 (20%)	2 (2%)	7	34
42	R	112/114 (98%)	96 (86%)	15 (13%)	1 (1%)	14	45
43	S	98/100 (98%)	79 (81%)	17 (17%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	40
45	U	80/82 (98%)	69 (86%)	9 (11%)	2 (2%)	4	29
46	V	78/80 (98%)	65 (83%)	11 (14%)	2 (3%)	4	28
47	W	63/65 (97%)	52 (82%)	11 (18%)	0	100	100
48	X	77/79 (98%)	61 (79%)	15 (20%)	1 (1%)	9	38
49	Y	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
50	Z	63/65 (97%)	45 (71%)	13 (21%)	5 (8%)	1	10
51	a	130/234 (56%)	97 (75%)	30 (23%)	3 (2%)	5	30
57	8	128/130 (98%)	99 (77%)	23 (18%)	6 (5%)	2	18
57	9	95/130 (73%)	71 (75%)	20 (21%)	4 (4%)	2	20
All	All	6142/6418 (96%)	5245 (85%)	790 (13%)	107 (2%)	9	34

5 of 107 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	d	84	THR
4	e	120	SER
6	g	9	VAL
6	g	86	ASP
7	h	79	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	75
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	72
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	147 (99%)	1 (1%)	76	77
5	f	137/137 (100%)	137 (100%)	0	100	100
6	g	114/114 (100%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	h	100/123 (81%)	99 (99%)	1 (1%)	68	74
8	i	109/110 (99%)	106 (97%)	3 (3%)	38	58
9	j	116/116 (100%)	114 (98%)	2 (2%)	53	67
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	74
11	l	102/102 (100%)	102 (100%)	0	100	100
12	m	109/109 (100%)	105 (96%)	4 (4%)	30	54
13	n	100/100 (100%)	100 (100%)	0	100	100
14	o	86/86 (100%)	85 (99%)	1 (1%)	63	72
15	p	99/99 (100%)	98 (99%)	1 (1%)	68	74
16	q	89/89 (100%)	88 (99%)	1 (1%)	65	73
17	r	84/84 (100%)	81 (96%)	3 (4%)	31	54
18	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
19	t	80/80 (100%)	79 (99%)	1 (1%)	61	71
20	u	83/83 (100%)	82 (99%)	1 (1%)	63	72
21	v	78/78 (100%)	78 (100%)	0	100	100
22	w	57/57 (100%)	57 (100%)	0	100	100
23	x	67/67 (100%)	66 (98%)	1 (2%)	57	68
24	y	55/55 (100%)	55 (100%)	0	100	100
25	z	48/48 (100%)	48 (100%)	0	100	100
26	B	47/47 (100%)	46 (98%)	1 (2%)	47	64
27	C	45/45 (100%)	45 (100%)	0	100	100
28	D	38/38 (100%)	38 (100%)	0	100	100
29	E	51/51 (100%)	51 (100%)	0	100	100
30	F	34/34 (100%)	33 (97%)	1 (3%)	37	57
31	G	186/186 (100%)	182 (98%)	4 (2%)	45	63
32	H	170/170 (100%)	169 (99%)	1 (1%)	78	79
33	I	172/172 (100%)	169 (98%)	3 (2%)	53	67
34	J	119/119 (100%)	118 (99%)	1 (1%)	73	76
35	K	87/87 (100%)	85 (98%)	2 (2%)	44	62
36	L	124/124 (100%)	124 (100%)	0	100	100
37	M	104/104 (100%)	103 (99%)	1 (1%)	68	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	N	105/105 (100%)	104 (99%)	1 (1%)	68	74
39	O	86/86 (100%)	84 (98%)	2 (2%)	44	62
40	P	89/89 (100%)	87 (98%)	2 (2%)	45	63
41	Q	103/103 (100%)	102 (99%)	1 (1%)	68	74
42	R	92/92 (100%)	90 (98%)	2 (2%)	45	63
43	S	83/83 (100%)	82 (99%)	1 (1%)	63	72
44	T	76/76 (100%)	76 (100%)	0	100	100
45	U	65/65 (100%)	63 (97%)	2 (3%)	35	57
46	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
47	W	56/56 (100%)	55 (98%)	1 (2%)	51	67
48	X	70/70 (100%)	69 (99%)	1 (1%)	59	70
49	Y	65/65 (100%)	64 (98%)	1 (2%)	57	68
50	Z	55/55 (100%)	54 (98%)	1 (2%)	51	67
51	a	110/181 (61%)	108 (98%)	2 (2%)	51	67
57	8	106/106 (100%)	104 (98%)	2 (2%)	50	65
57	9	79/106 (74%)	77 (98%)	2 (2%)	42	61
All	All	5093/5215 (98%)	5030 (99%)	63 (1%)	61	72

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	F	33	HIS
49	Y	56	ILE
33	I	93	LEU
48	X	47	THR
57	8	48	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 123 such sidechains are listed below:

Mol	Chain	Res	Type
20	u	73	ASN
49	Y	47	GLN
31	G	121	GLN
49	Y	20	ASN
57	8	38	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	1538/1539 (99%)	153 (9%)	1 (0%)
53	1	2902/2903 (99%)	372 (12%)	9 (0%)
54	2	119/120 (99%)	14 (11%)	0
55	5	75/77 (97%)	23 (30%)	0
56	4	13/20 (65%)	1 (7%)	0
All	All	4647/4659 (99%)	563 (12%)	10 (0%)

5 of 563 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	6	G
52	3	9	G
52	3	22	G
52	3	31	G
52	3	32	A

5 of 10 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	1	2391	G
53	1	2430	A
53	1	2433	A
53	1	1475	G
53	1	2250	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

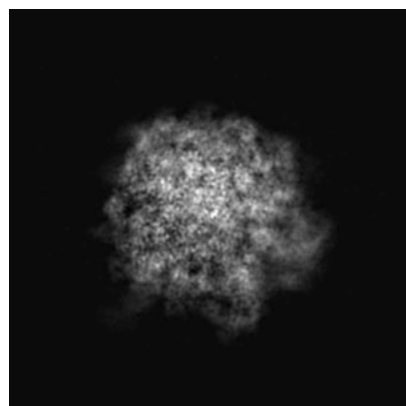
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22472. These allow visual inspection of the internal detail of the map and identification of artifacts.

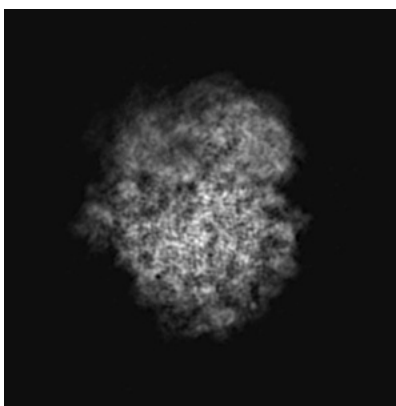
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

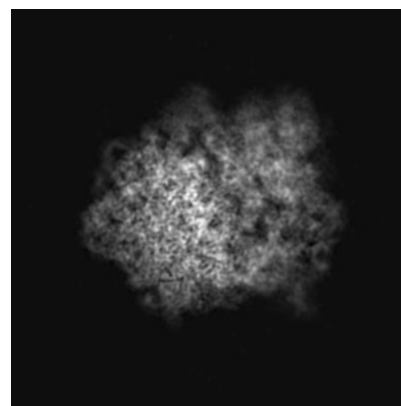
6.1.1 Primary map



X

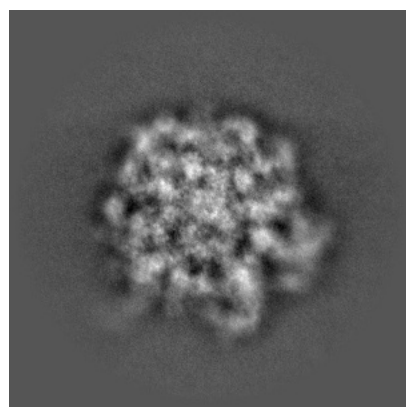


Y

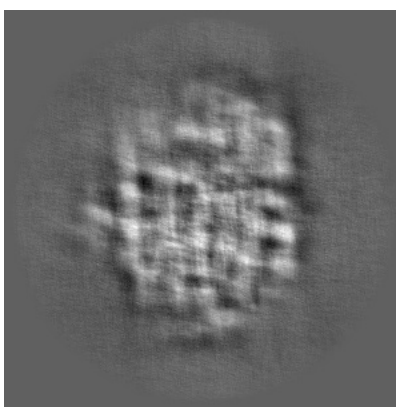


Z

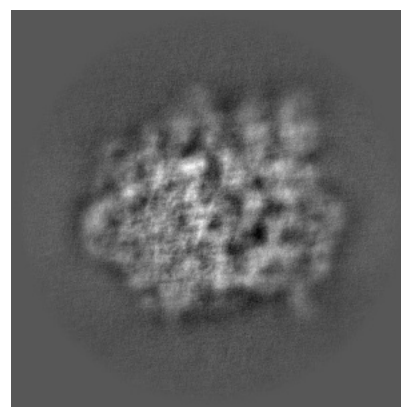
6.1.2 Raw map



X



Y

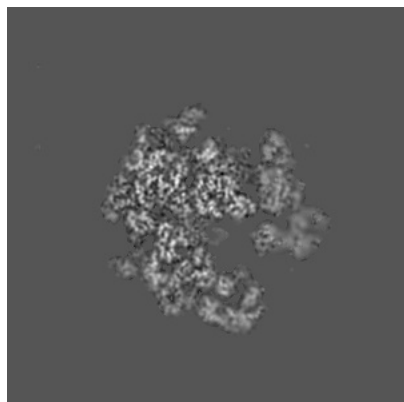


Z

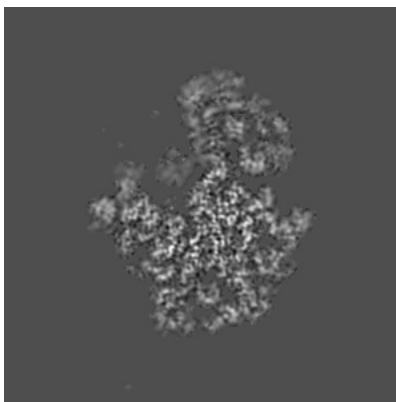
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

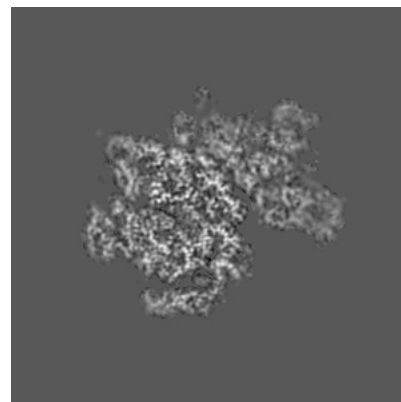
6.2.1 Primary map



X Index: 180

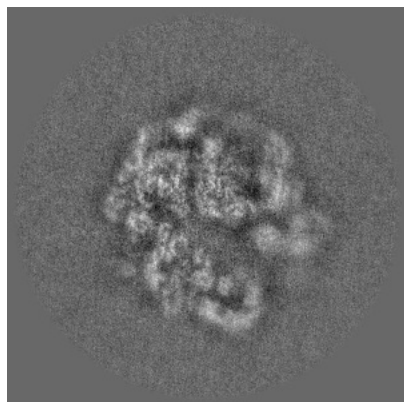


Y Index: 180

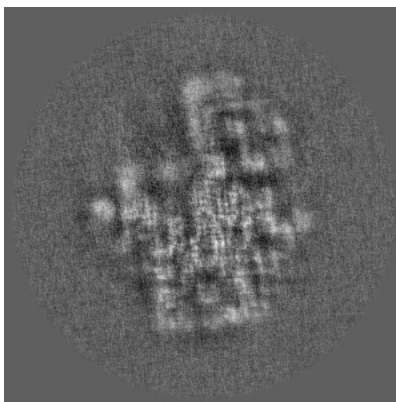


Z Index: 180

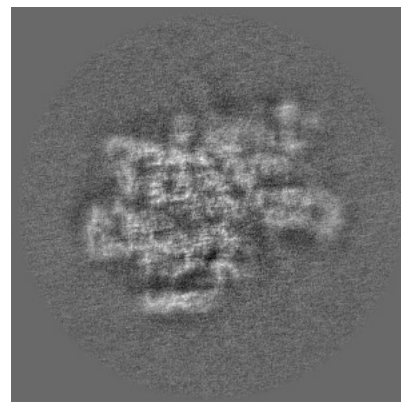
6.2.2 Raw map



X Index: 180



Y Index: 180

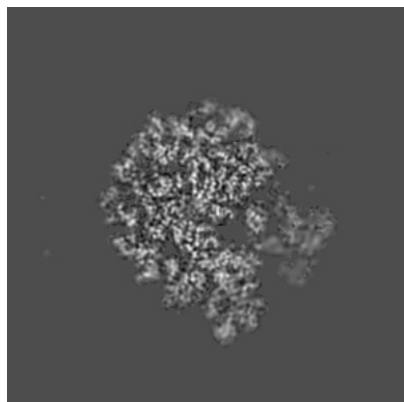


Z Index: 180

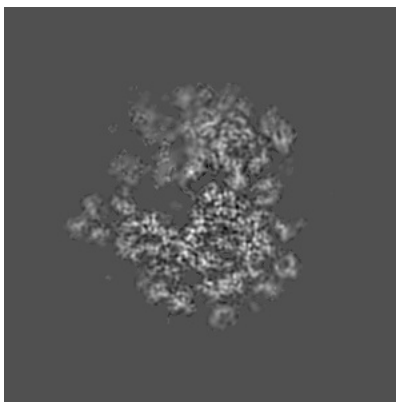
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

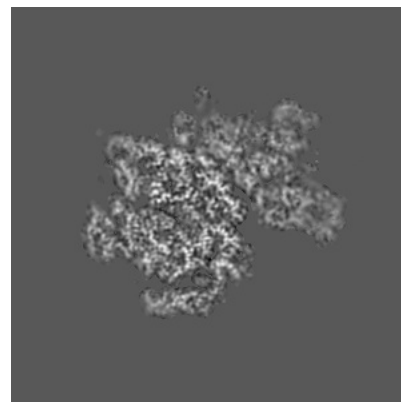
6.3.1 Primary map



X Index: 164

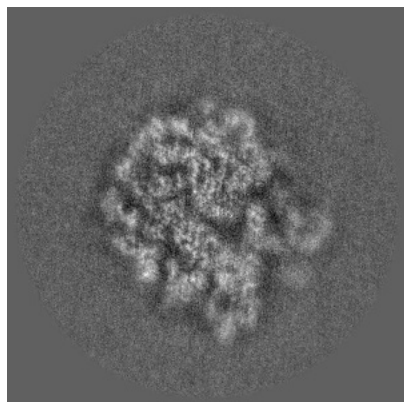


Y Index: 193

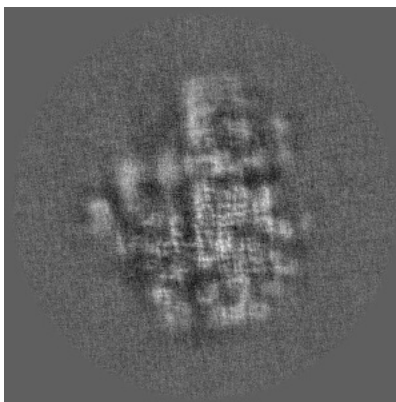


Z Index: 180

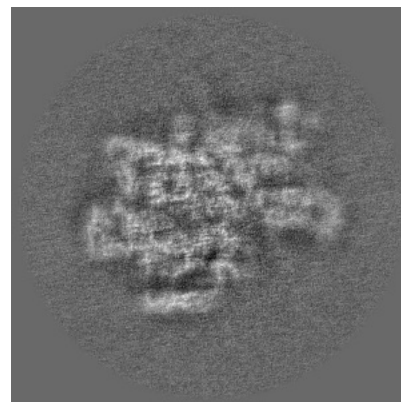
6.3.2 Raw map



X Index: 164



Y Index: 184

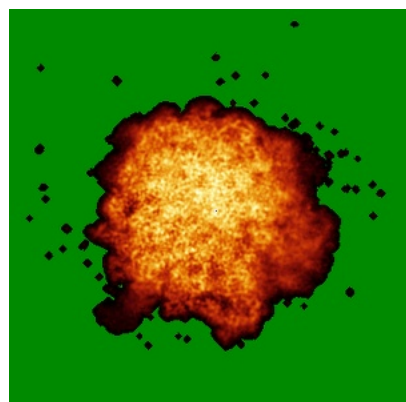


Z Index: 180

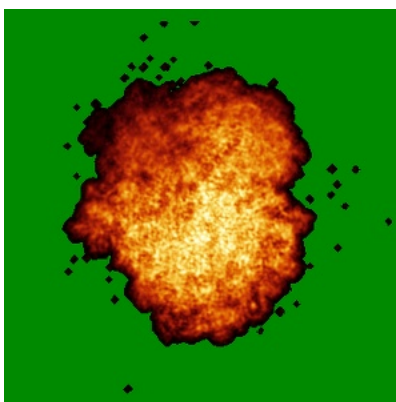
The images above show the largest variance slices of the map in three orthogonal directions.

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

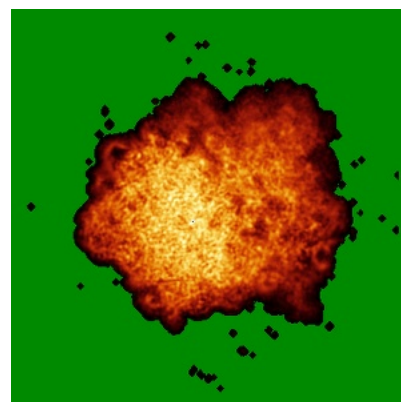
6.4.1 Primary map



X

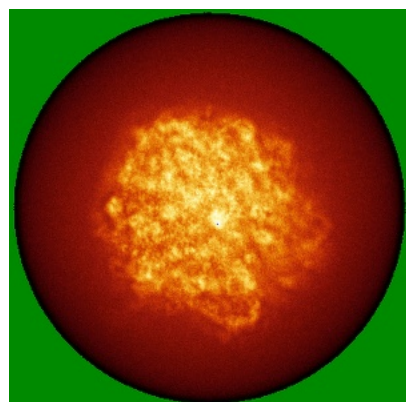


Y

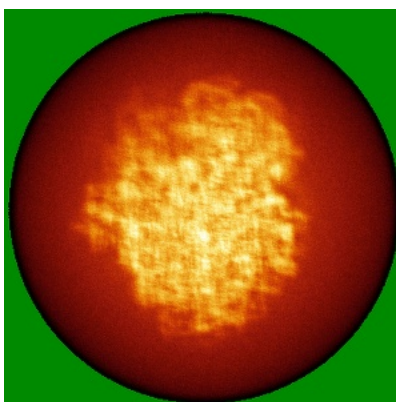


Z

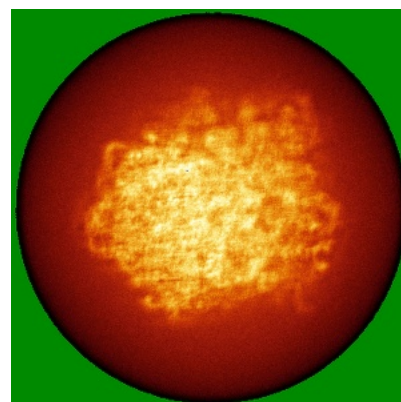
6.4.2 Raw map



X



Y

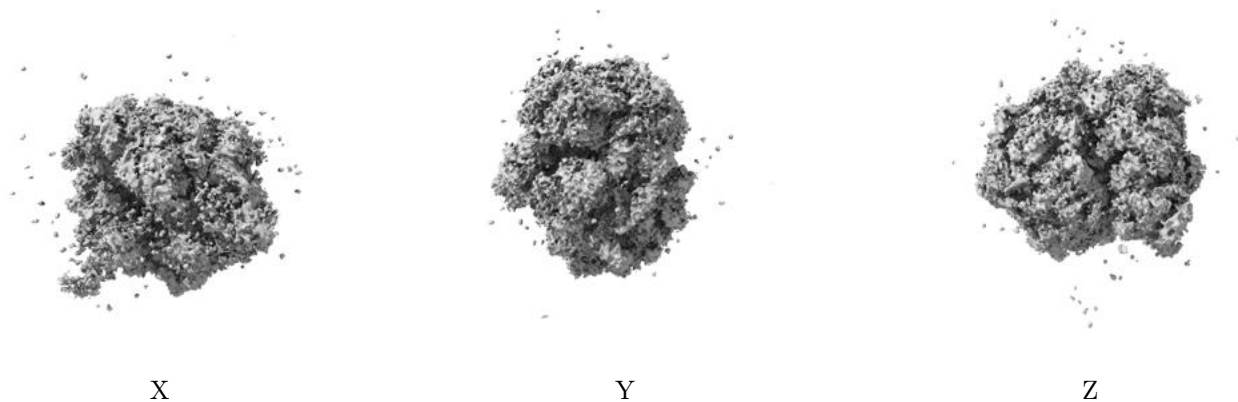


Z

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.

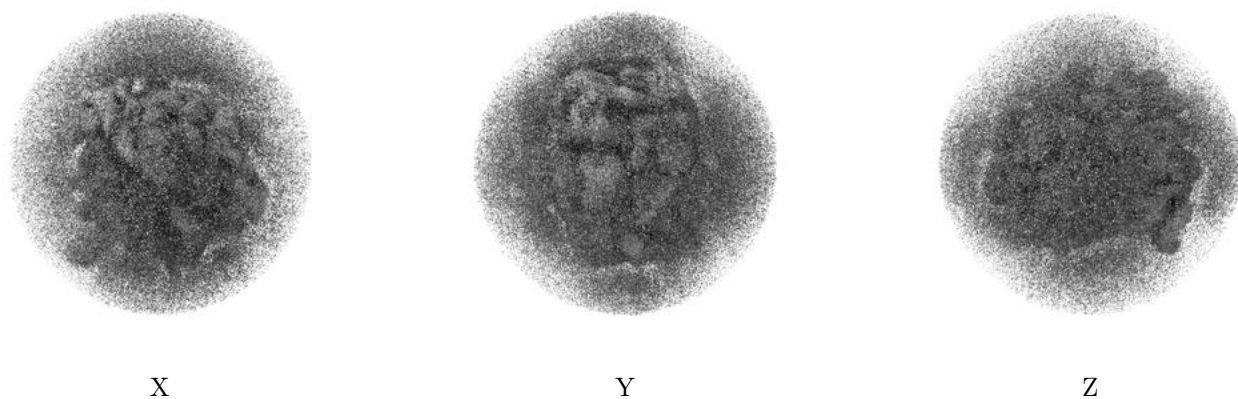
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.75. 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.

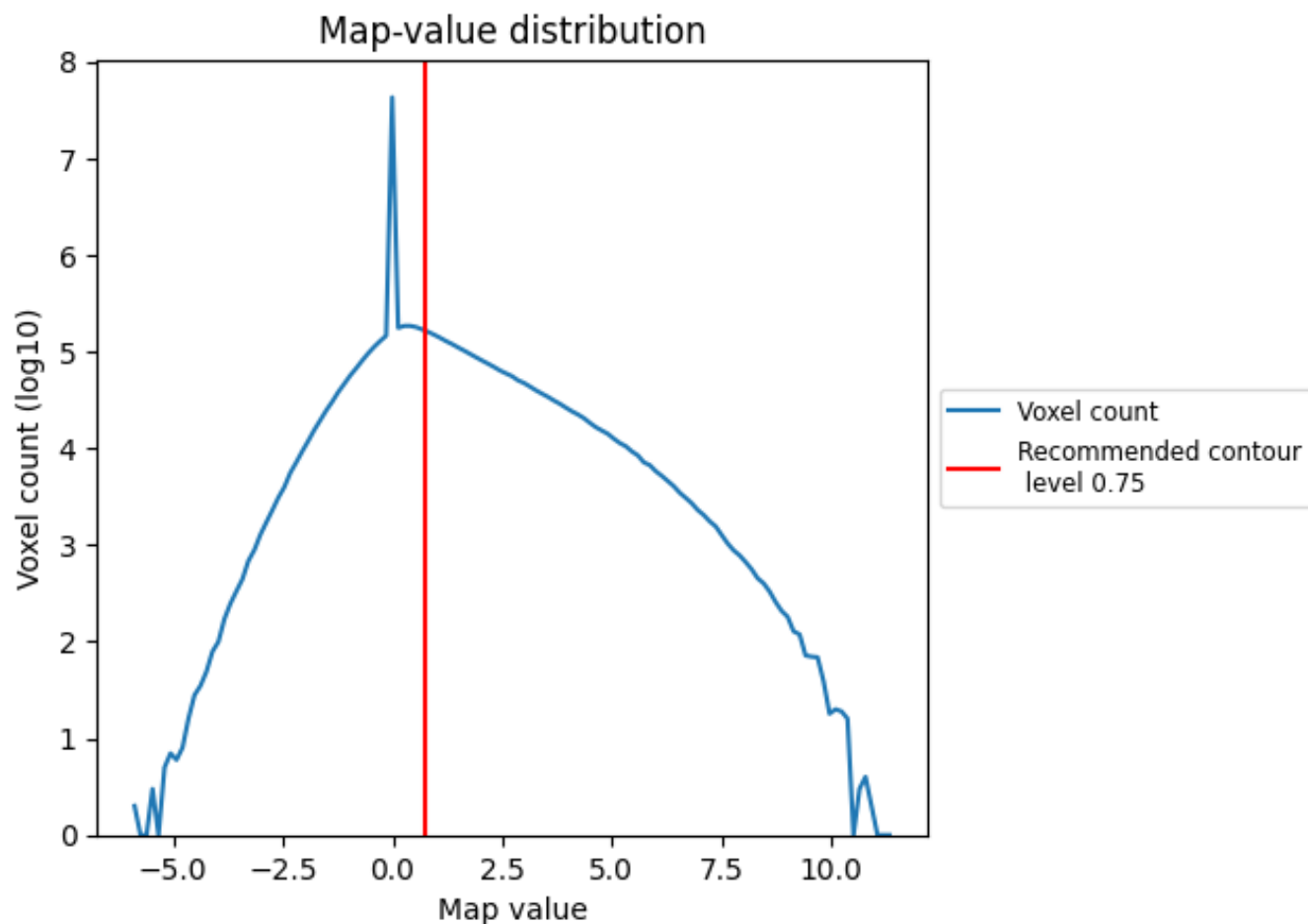
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

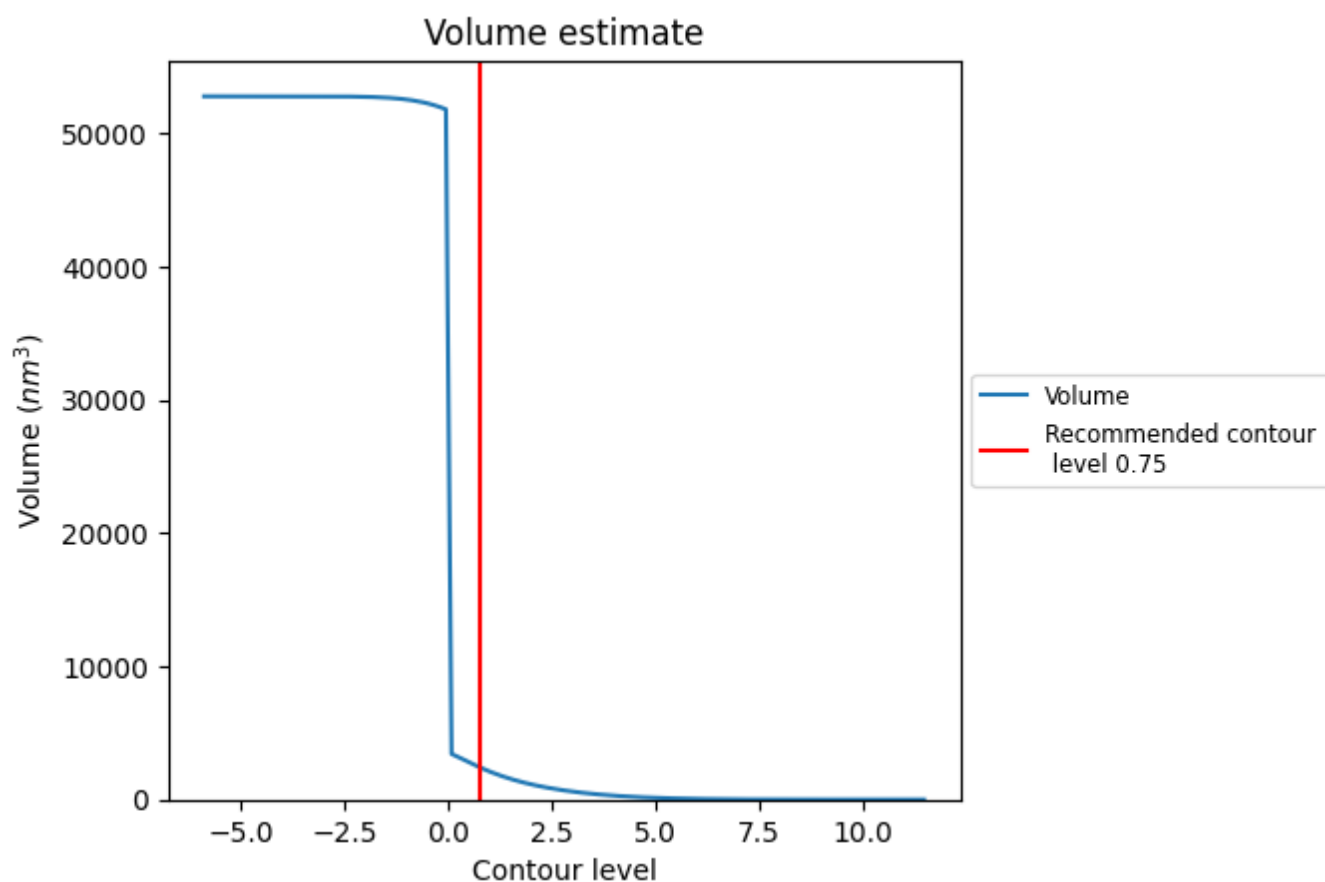
This section contains the results of statistical analysis of the map.

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.

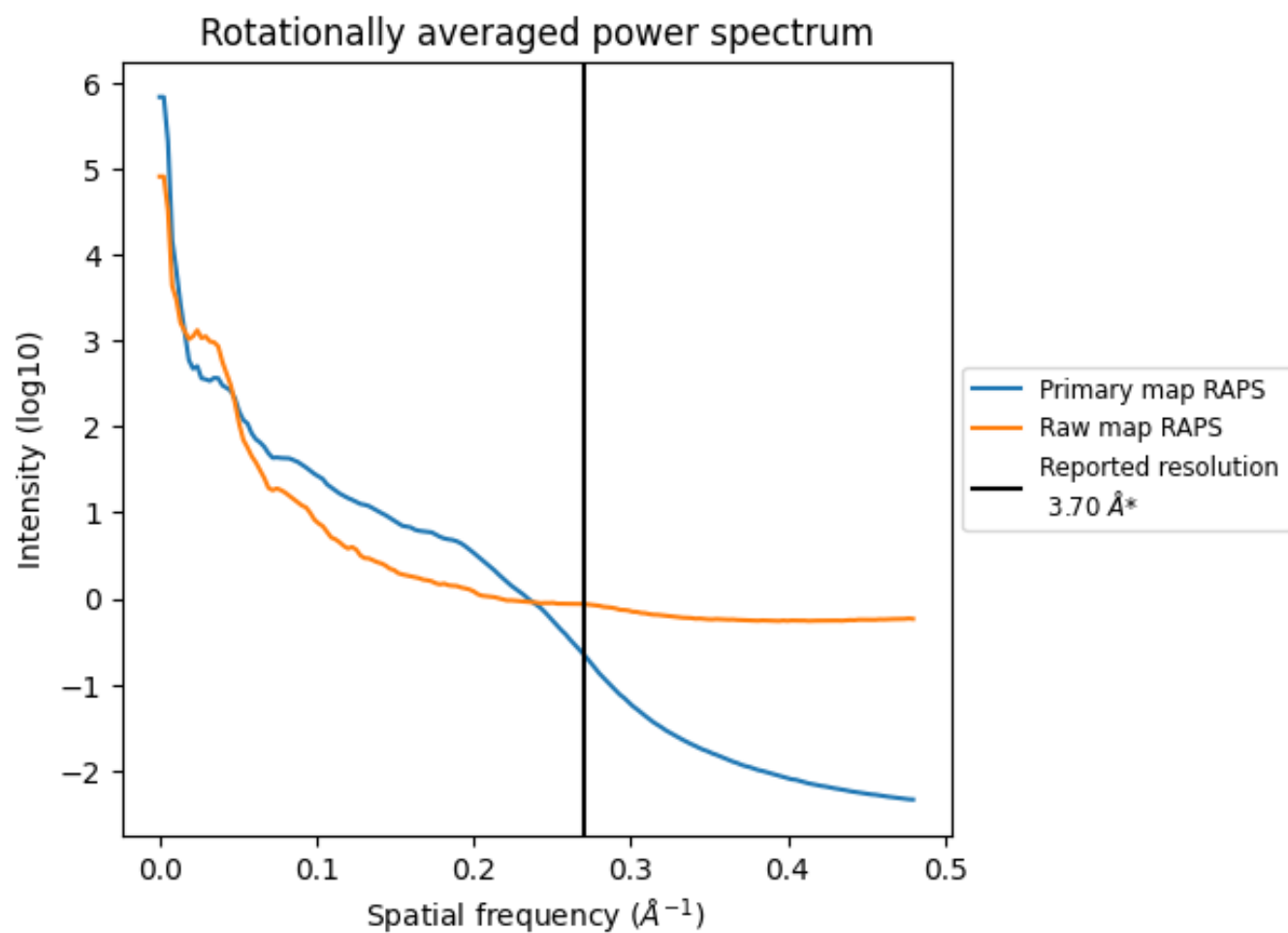
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2431 nm³; this corresponds to an approximate mass of 2196 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 ⓘ

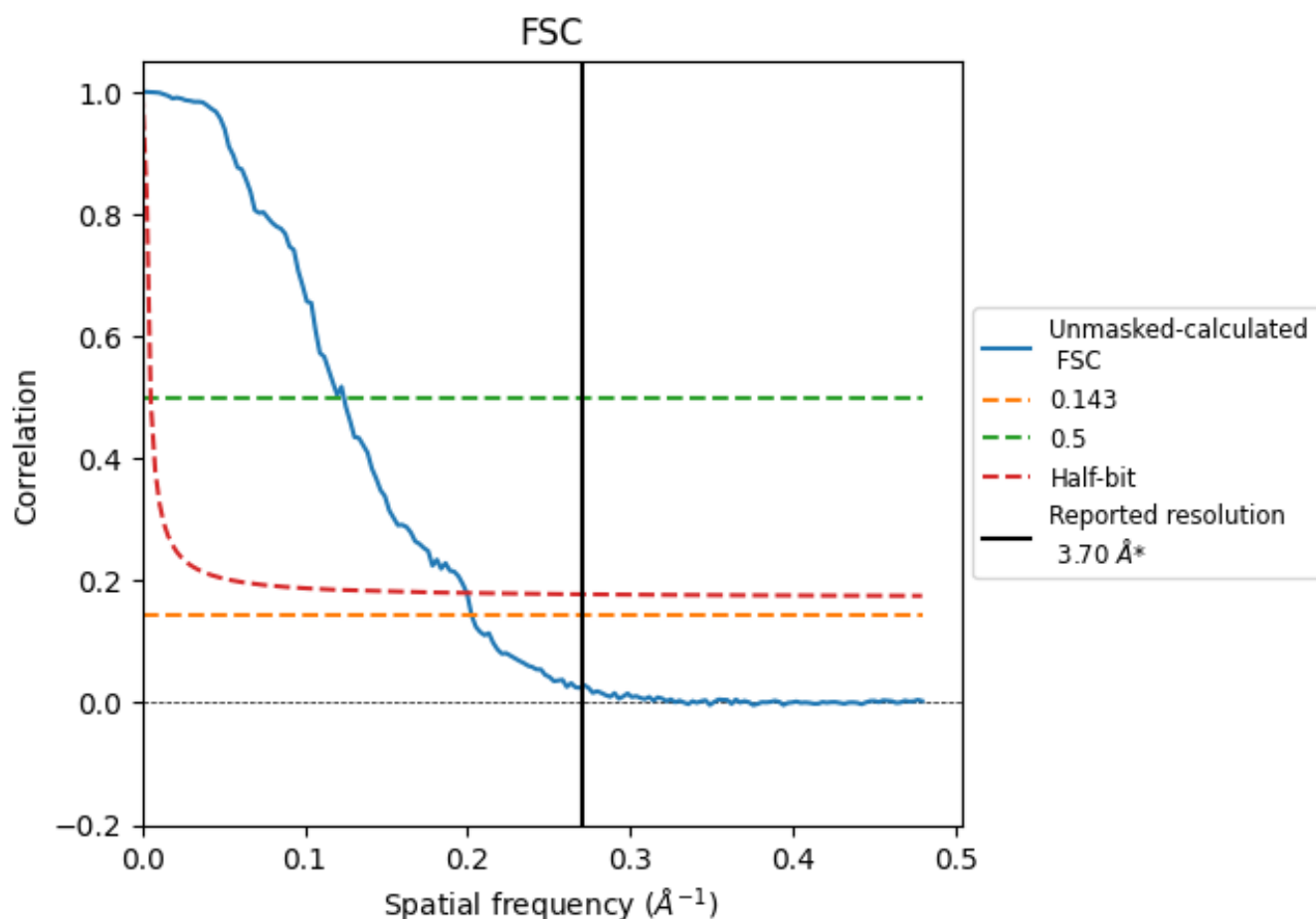


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

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 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

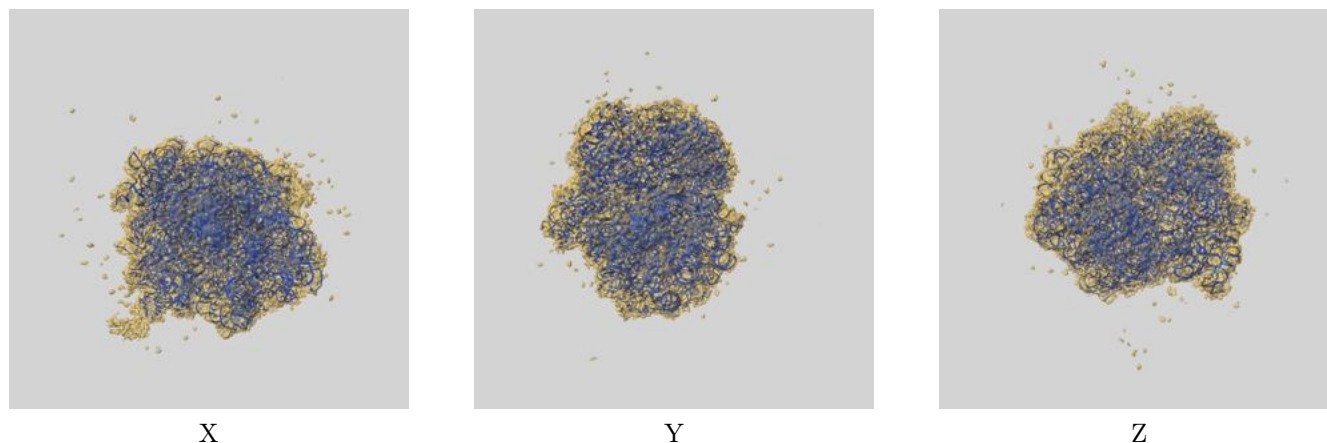
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.94	8.06	5.01

*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 4.94 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

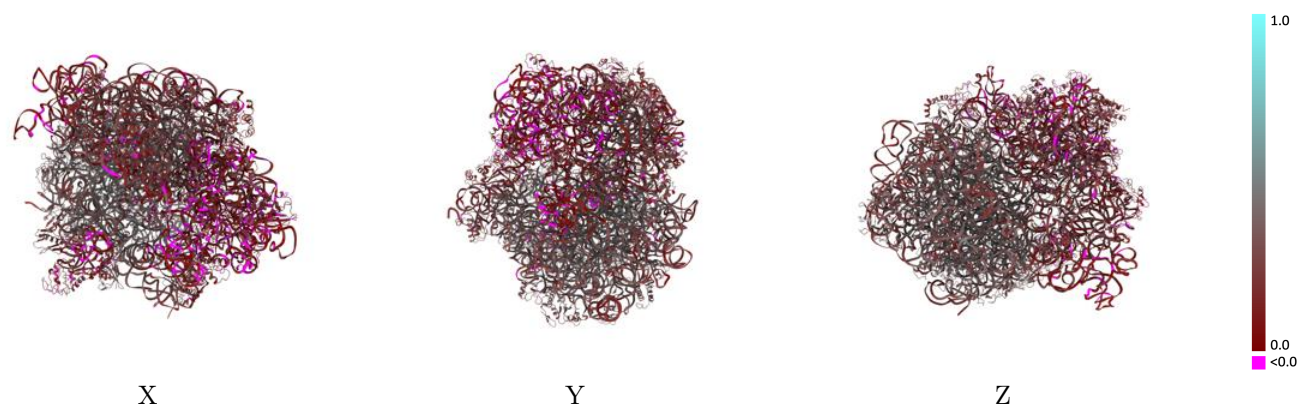
This section contains information regarding the fit between EMDB map EMD-22472 and PDB model 7JT3. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



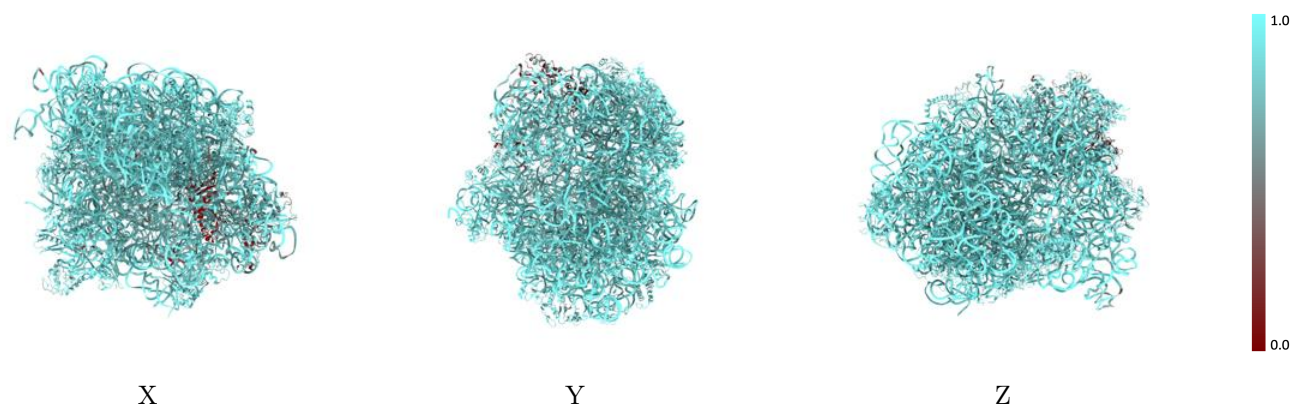
The images above show the 3D surface view of the map at the recommended contour level 0.75 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



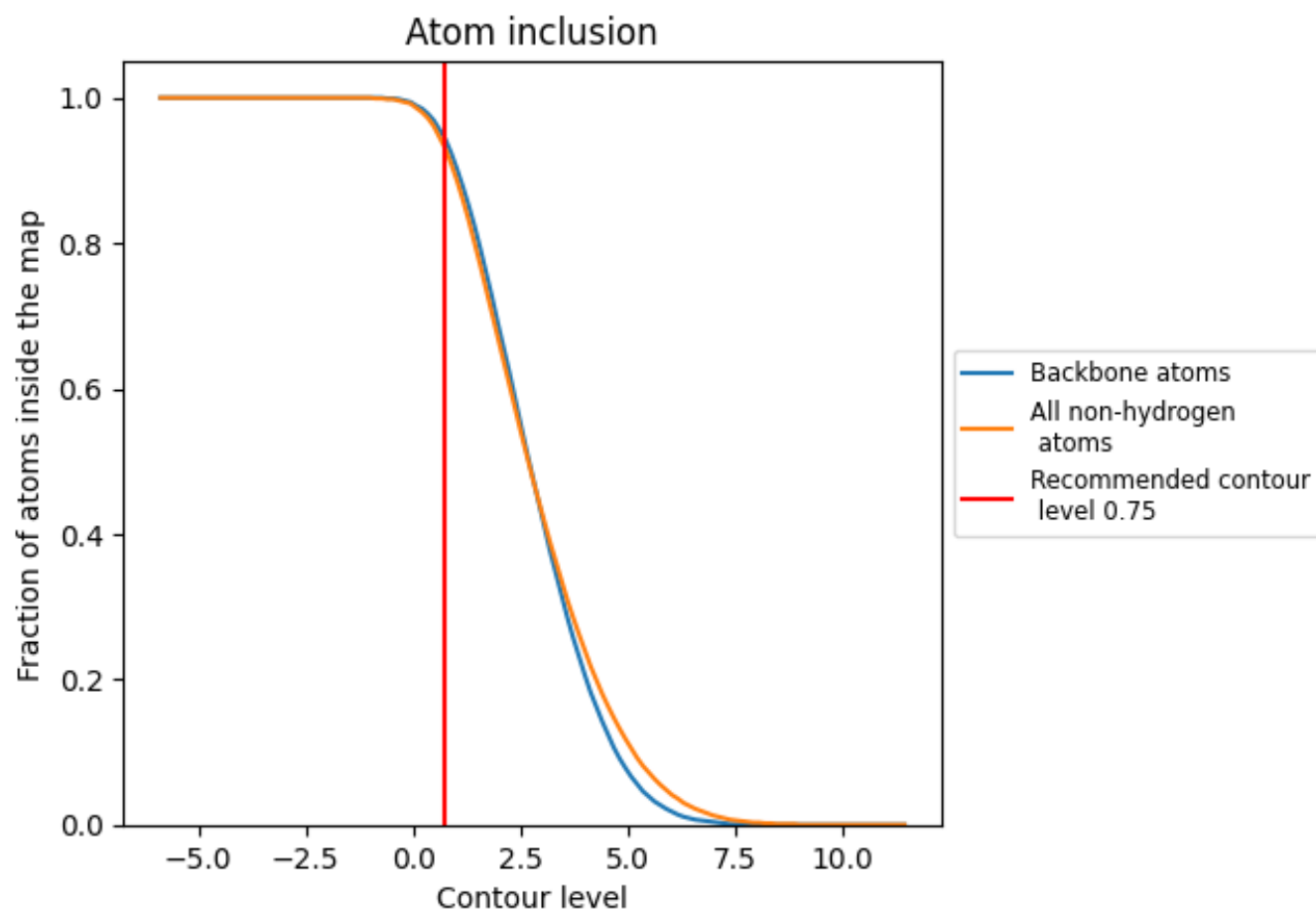
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.75).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% 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 (0.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9310	 0.2850
1	 0.9730	 0.3430
2	 0.9730	 0.2820
3	 0.9200	 0.1850
4	 0.7990	 0.0730
5	 0.8790	 0.1310
8	 0.8640	 0.2250
9	 0.8460	 0.1470
B	 0.9460	 0.3870
C	 0.9400	 0.3490
D	 0.9610	 0.4210
E	 0.9230	 0.4120
F	 0.9310	 0.4010
G	 0.8870	 0.2380
H	 0.4840	 0.1340
I	 0.8620	 0.2090
J	 0.9060	 0.2250
K	 0.9230	 0.2330
L	 0.8040	 0.1920
M	 0.9270	 0.2530
N	 0.7680	 0.1650
O	 0.5490	 0.1370
P	 0.9120	 0.2310
Q	 0.9290	 0.3050
R	 0.7970	 0.1860
S	 0.7970	 0.1500
T	 0.9220	 0.2520
U	 0.8680	 0.2610
V	 0.9340	 0.2610
W	 0.8890	 0.2580
X	 0.8650	 0.1860
Y	 0.9010	 0.2370
Z	 0.8900	 0.2370
a	 0.8050	 0.1690
b	 0.9560	 0.4170



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Chain	Atom inclusion	Q-score
c	 0.9340	 0.4020
d	 0.9240	 0.3540
e	 0.9110	 0.2390
f	 0.9430	 0.3310
g	 0.8910	 0.2550
h	 0.8390	 0.1910
i	 0.8480	 0.1510
j	 0.9470	 0.3990
k	 0.9410	 0.3930
l	 0.9420	 0.3840
m	 0.9440	 0.3860
n	 0.9460	 0.3950
o	 0.9260	 0.3220
p	 0.9570	 0.3780
q	 0.9350	 0.3810
r	 0.9330	 0.3690
s	 0.9230	 0.4010
t	 0.9210	 0.3650
u	 0.9270	 0.3070
v	 0.9470	 0.3620
w	 0.9430	 0.3880
x	 0.9380	 0.3850
y	 0.9340	 0.3080
z	 0.9500	 0.3780