



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:36 PM UTC

PDB ID : 5NJT / pdb_00005njt
EMDB ID : EMD-3656
Title : Structure of the Bacillus subtilis hibernating 100S ribosome reveals the basis for 70S dimerization.
Authors : Beckert, B.; Abdelshahid, M.; Schaefer, H.; Steinchen, W.; Arenz, S.; Berninghausen, O.; Beckmann, R.; Bange, G.; Turgay, K.; Wilson, D.N.
Deposited on : 2017-03-29
Resolution : 3.80 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:

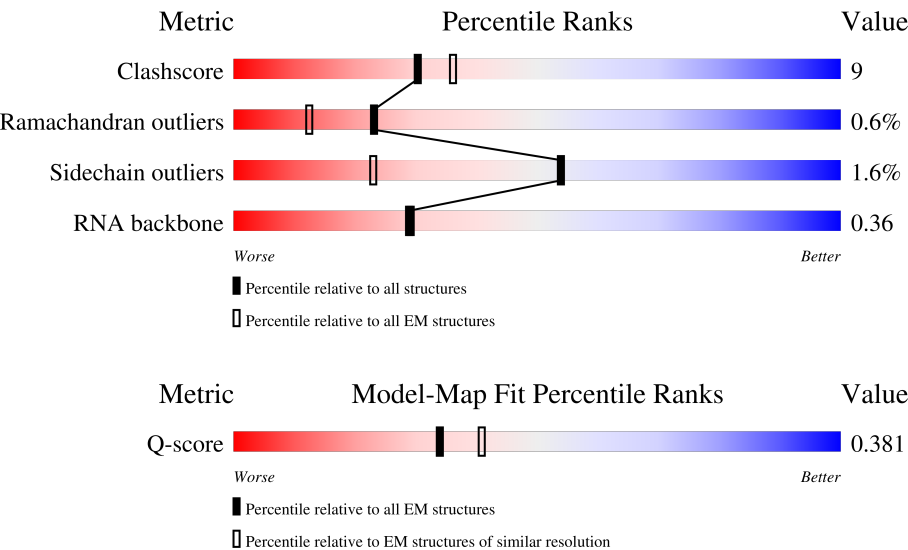
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	A	1544	
2	B	224	
3	C	210	

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Mol	Chain	Length	Quality of chain
4	D	199	
5	E	165	
6	F	95	
7	G	153	
8	H	131	
9	I	130	
10	J	102	
11	K	118	
12	L	137	
13	M	111	
14	N	60	
15	O	88	
16	P	89	
17	Q	86	
18	R	71	
19	S	80	
20	T	86	
21	U	2923	
22	V	112	
23	W	275	
24	X	207	
25	Y	205	
26	Z	178	
27	a	175	
28	b	123	

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Mol	Chain	Length	Quality of chain
29	c	142	
30	d	122	
31	e	146	
32	f	138	
33	g	119	
34	h	120	
35	i	114	
36	j	117	
37	k	101	
38	l	109	
39	m	93	
40	n	100	
41	o	82	
42	p	54	
43	q	48	
44	r	44	
45	s	64	
46	t	36	
47	u	58	
48	v	65	
49	w	58	
50	y	64	
51	x	104	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 133097 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	F	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	G	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	J	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	L	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	111	Total	C	N	O	0	0
			444	222	111	111		

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	80	Total	C	N	O	0	0
			320	160	80	80		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 21 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	1558	C	G	conflict	GB 467326

- Molecule 22 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 23 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 24 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 25 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 26 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 27 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 28 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

- Molecule 29 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 30 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 31 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 32 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 33 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 34 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 35 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	114	Total	C	N	O	S	0	0
			936	595	184	157			

- Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	101	Total	C	N	O	S	0	0
			786	501	139	146			

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 41 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	o	82	Total	C	N	O	0	0
			630	390	123	117		

- Molecule 42 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 43 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 44 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 45 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 46 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 48 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	w	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	64	Total	C	N	O	S	0	0
			503	314	92	92	5		

- Molecule 51 is a protein called Ribosome hibernation promotion factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	104	Total	C	N	O	S	0	0
			866	537	159	167	3		

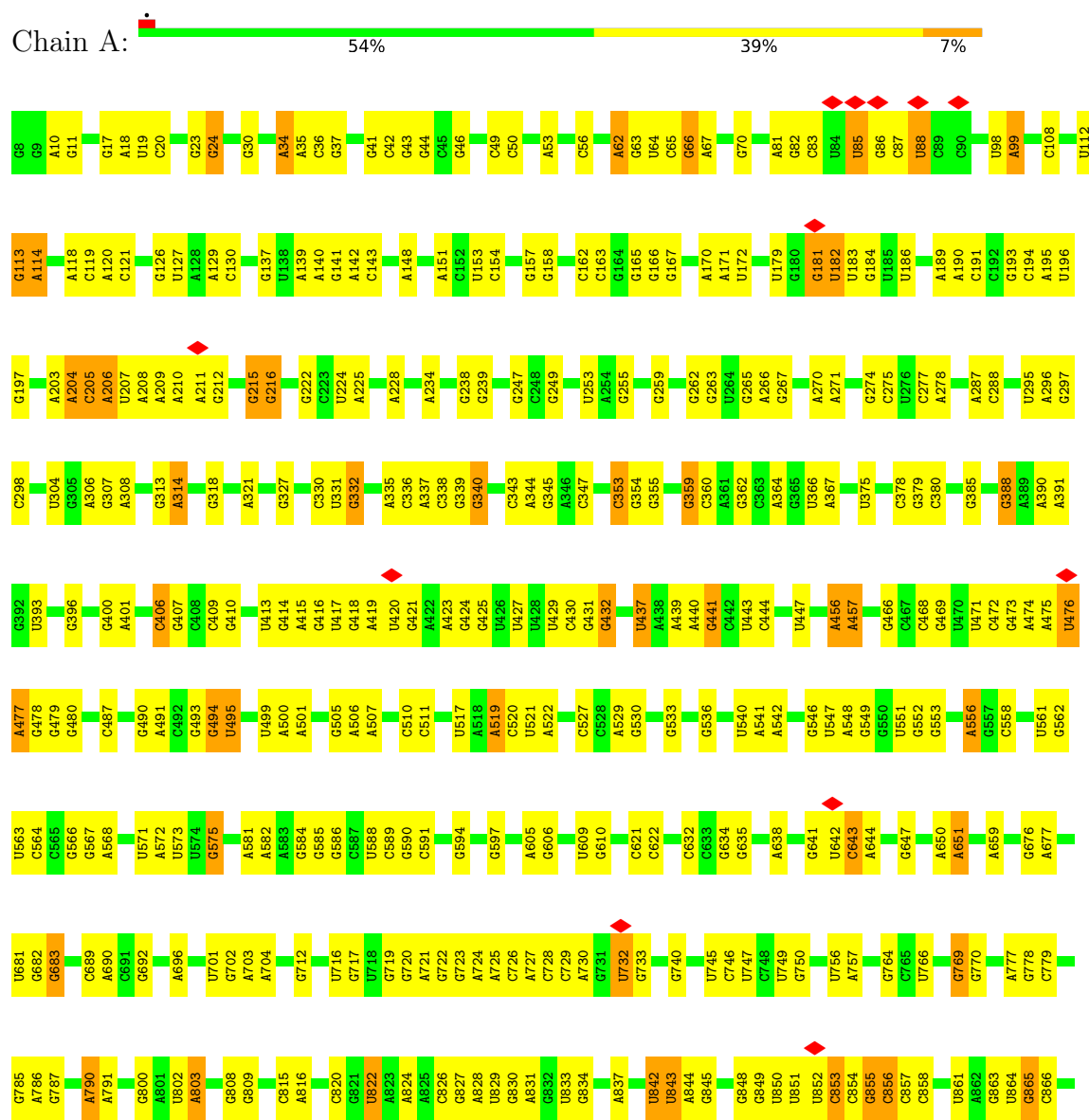
There is a discrepancy between the modelled and reference sequences:

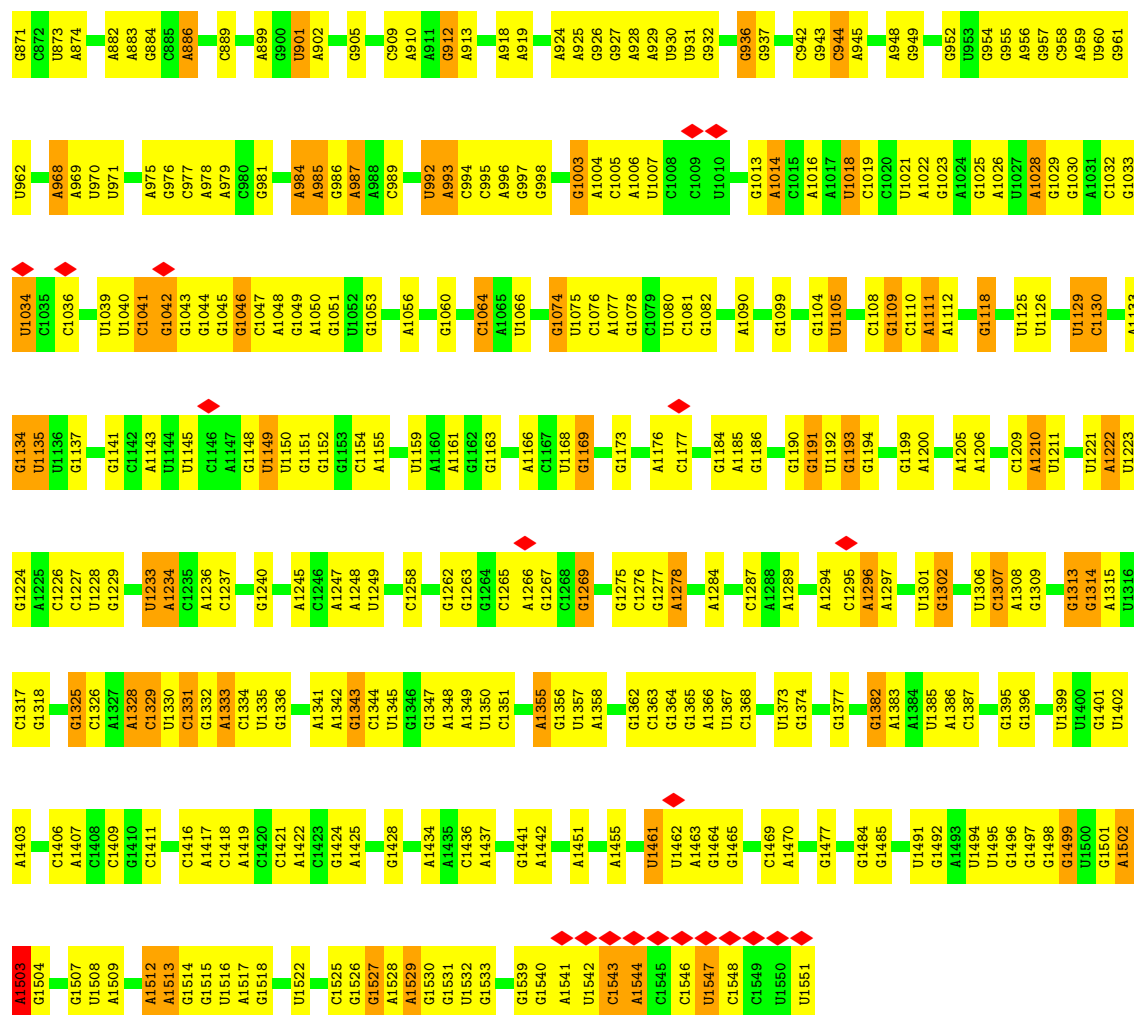
Chain	Residue	Modelled	Actual	Comment	Reference
x	103	GLU	GLY	conflict	UNP P28368

3 Residue-property plots

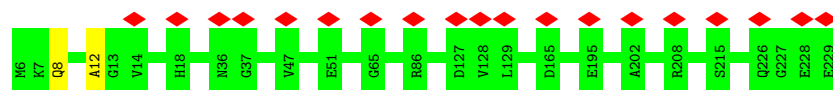
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

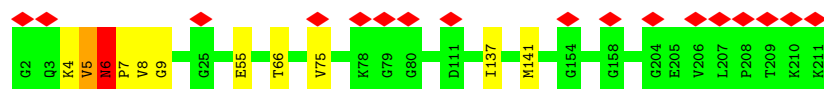




- Molecule 2: 30S ribosomal protein S2

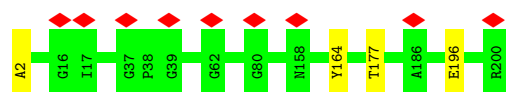


- Molecule 3: 30S ribosomal protein S3

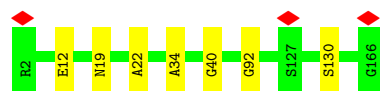


- Molecule 4: 30S ribosomal protein S4

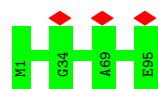




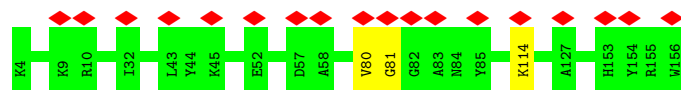
- Molecule 5: 30S ribosomal protein S5



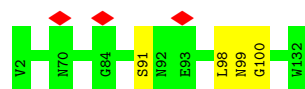
- Molecule 6: 30S ribosomal protein S6



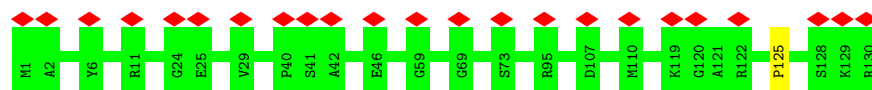
- Molecule 7: 30S ribosomal protein S7



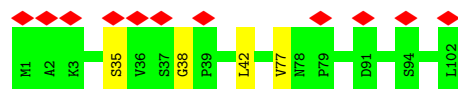
- Molecule 8: 30S ribosomal protein S8



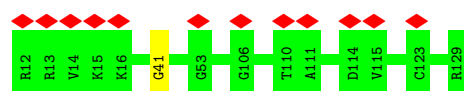
- Molecule 9: 30S ribosomal protein S9



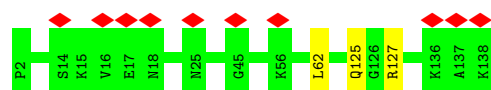
- Molecule 10: 30S ribosomal protein S10



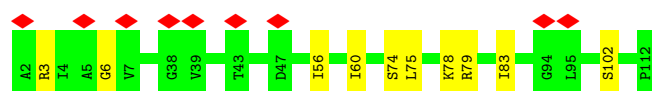
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13

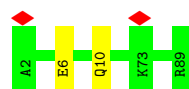


- Molecule 14: 30S ribosomal protein S14

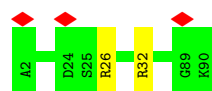


There are no outlier residues recorded for this chain.

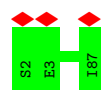
- Molecule 15: 30S ribosomal protein S15



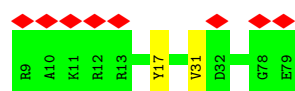
- Molecule 16: 30S ribosomal protein S16



- Molecule 17: 30S ribosomal protein S17



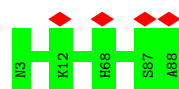
- Molecule 18: 30S ribosomal protein S18



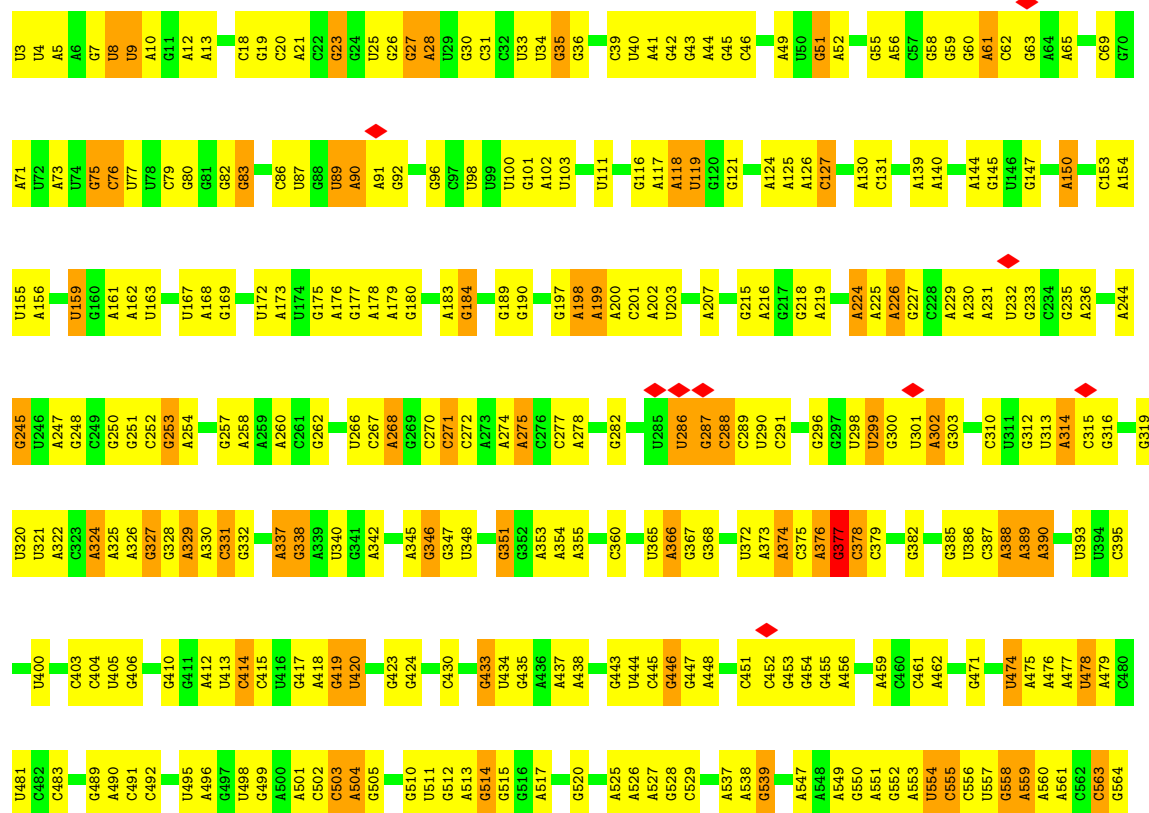
- Molecule 19: 30S ribosomal protein S19



- Molecule 20: 30S ribosomal protein S20

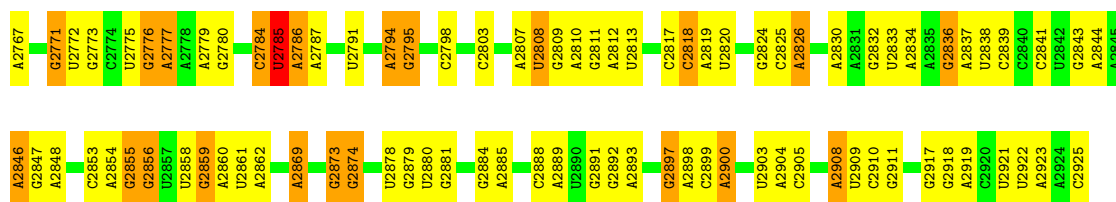


- Molecule 21: 23S ribosomal RNA



U543	C544	C545	G546	A553	U554	A555	U560	C564	U567	G568	A569	U570	G571	G572	C573	G578	A581	U582	A583	U584	A585	G586	U587	A592	A593	G594	U595	U596	U599	G600	A601	U602	C607	C613	A614	A615	G616	A617	A618	A620	U626	G630	A631	G632	G633	U634								
C476	A477	G478	A480	G481	G482	A483	U484	A485	G486	A490	A491	G492	C493	G494	C495	G496	A497	G498	A499	U500	U501	G502	A503	G504	A505	U506	U507	G512	U513	A516	A517	G518	C519	A520	G521	U522	U523	A524	G525	G526	C527	A614	U615	G616	A617	A618	A620							
G1397	A1398	G1311	A1312	A1313	A1314	G1315	A1316	G1317	G1318	G1319	A1326	U1327	C1333	G1334	A1335	G1338	A1339	A1340	A1342	A1343	U1345	A1346	A1347	C1344	U1345	U1351	A1352	C1353	A1360	A1361	G1362	G1363	C1364	U1365	C1366	G1367	U1368	C1369	A1374	G1378	U1379	U1380	A1381	C1384	G1385	A1388	C1389	C1390						
G1476	A1477	G1478	A1480	G1481	G1482	A1483	U1484	A1485	G1486	A1490	A1491	G1492	C1493	G1494	C1495	G1496	G1497	U1498	A1499	U1500	U1501	G1502	G1503	A1504	U1505	U1506	U1507	G1512	U1513	A1516	A1517	G1518	C1519	A1520	G1521	U1522	U1523	A1524	G1525	G1526	C1527	U1528	G1529	G1530	G1531	A1532	A1533	A1534	G1537	G1538	C1539	A1540	A1541	A1542
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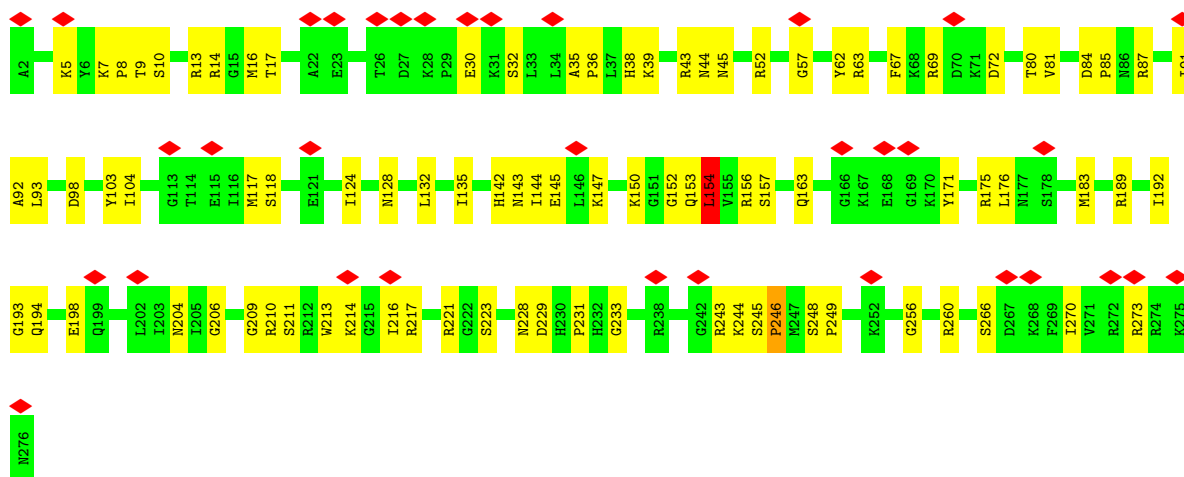




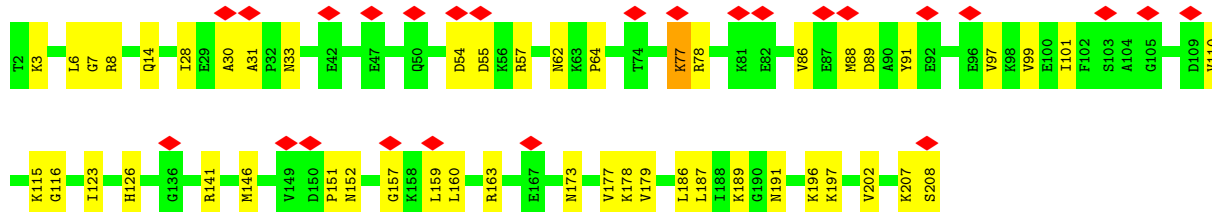
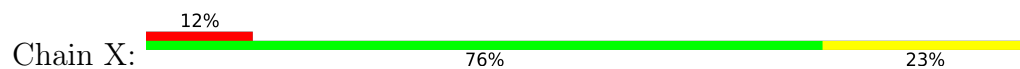
- Molecule 22: 5S ribosomal RNA



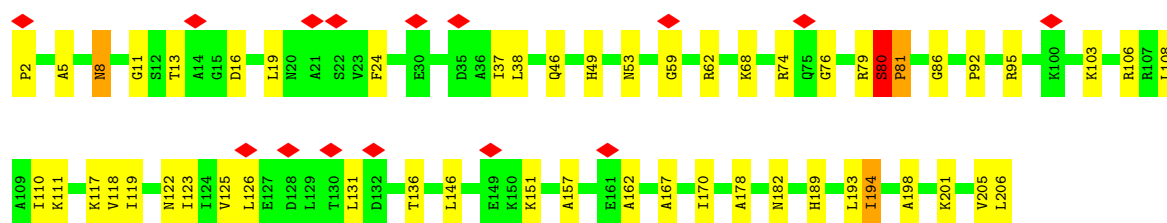
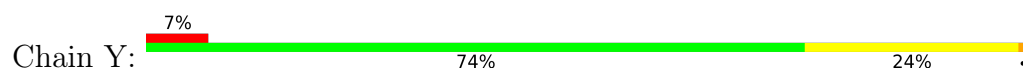
- Molecule 23: 50S ribosomal protein L2



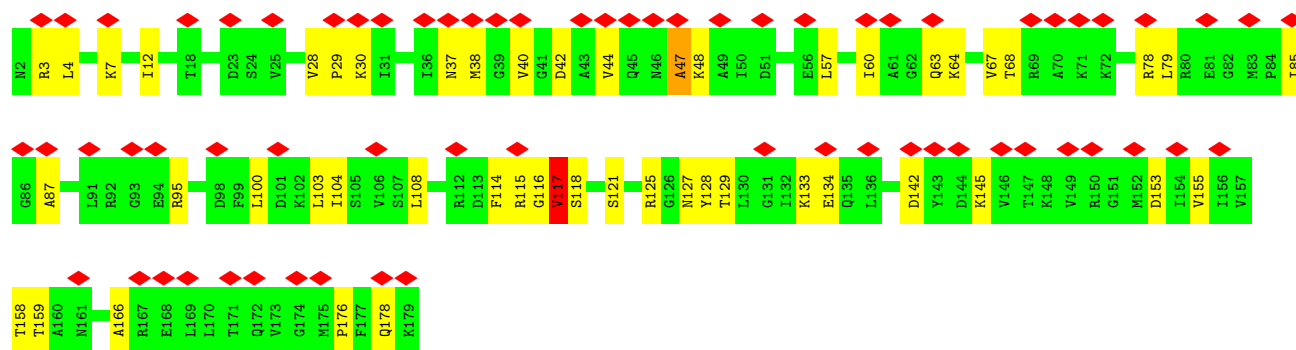
- Molecule 24: 50S ribosomal protein L3



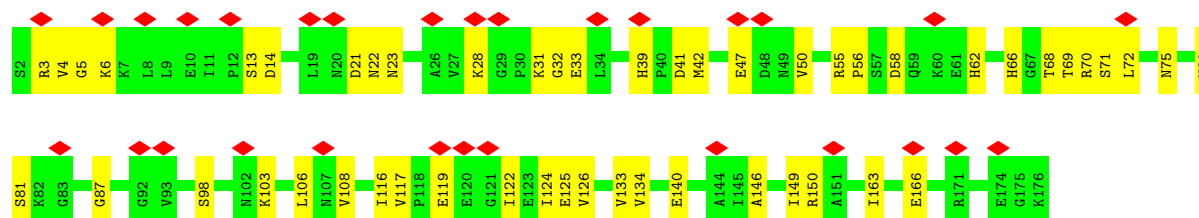
- Molecule 25: 50S ribosomal protein L4



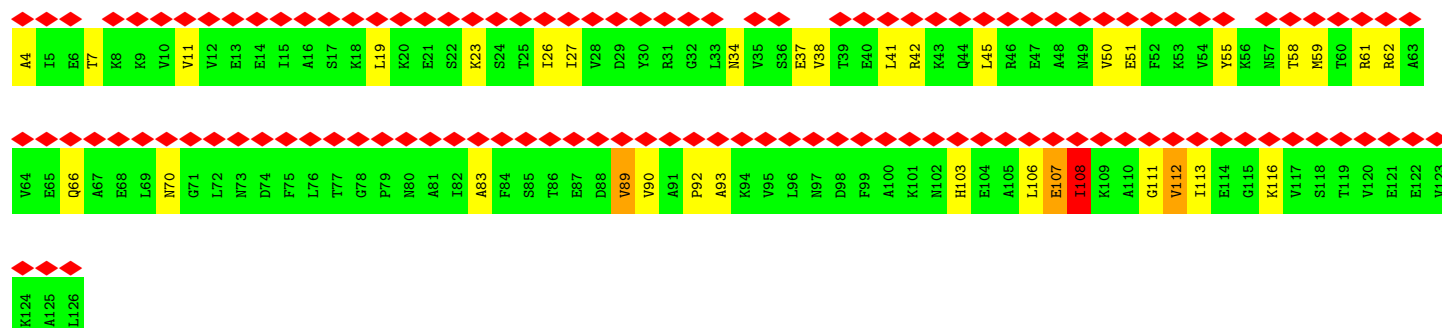
• Molecule 26: 50S ribosomal protein L5



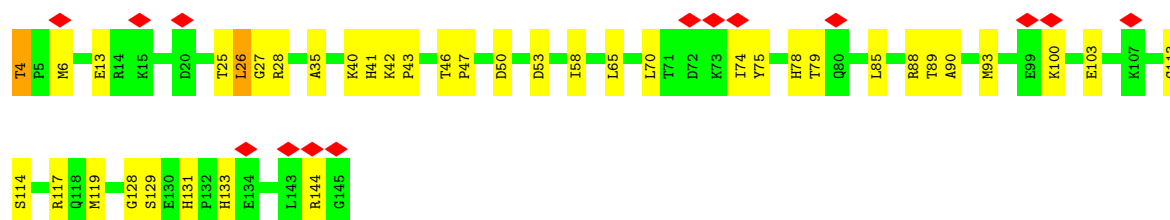
• Molecule 27: 50S ribosomal protein L6



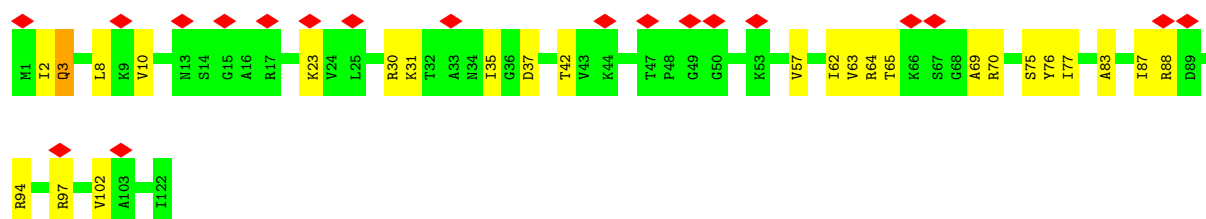
• Molecule 28: 50S ribosomal protein L10



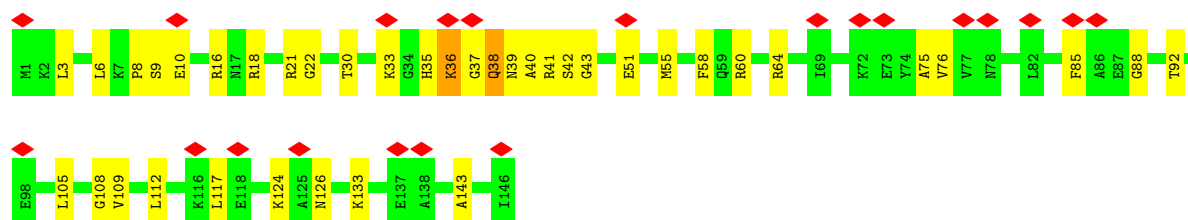
- Molecule 29: 50S ribosomal protein L13



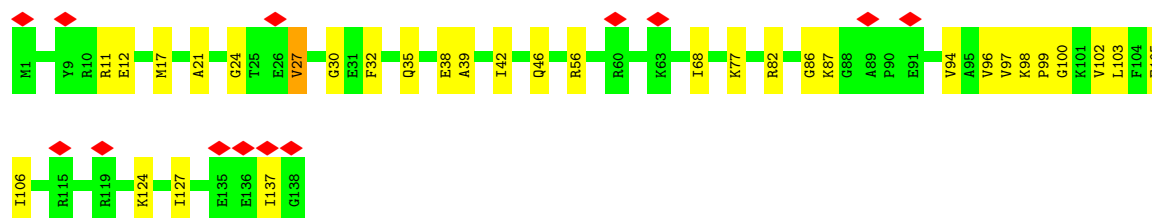
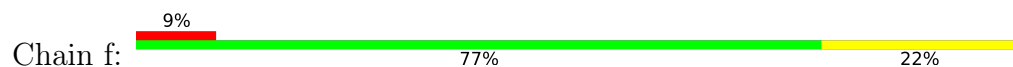
- Molecule 30: 50S ribosomal protein L14



- Molecule 31: 50S ribosomal protein L15

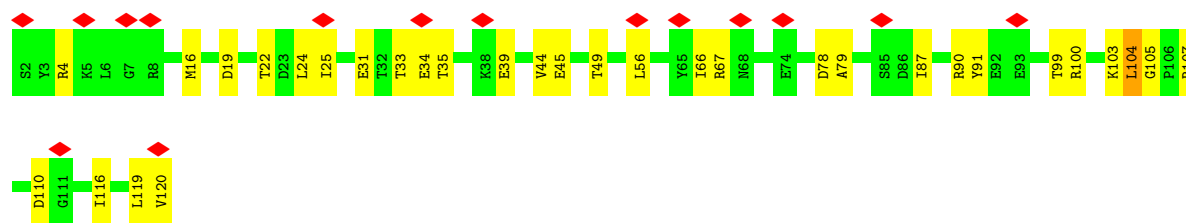


- Molecule 32: 50S ribosomal protein L16

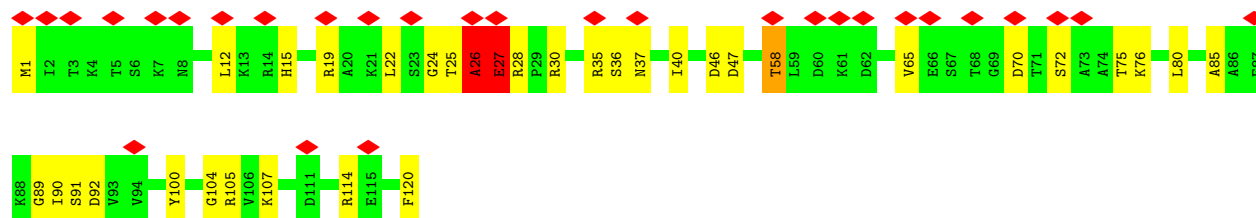


- Molecule 33: 50S ribosomal protein L17

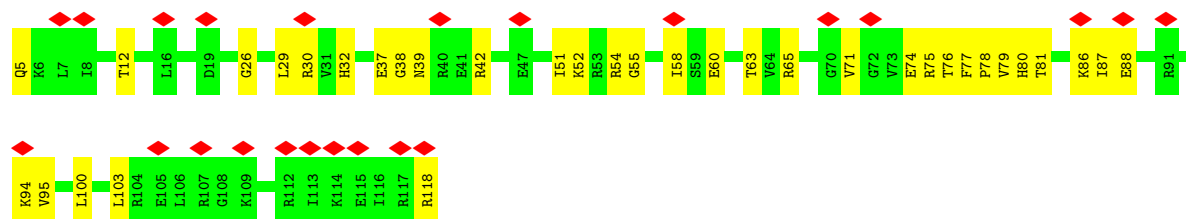




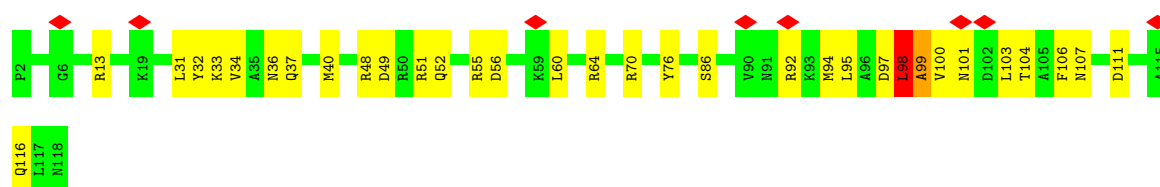
• Molecule 34: 50S ribosomal protein L18



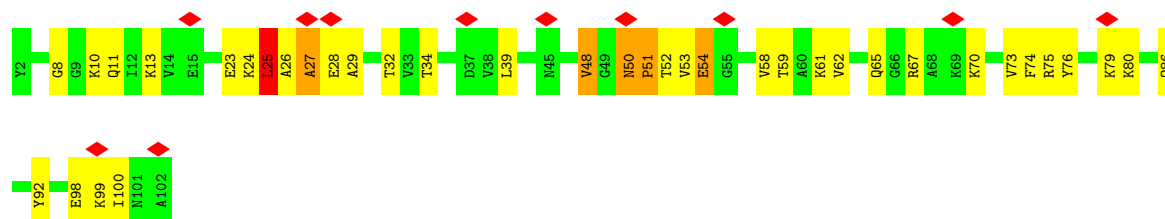
• Molecule 35: 50S ribosomal protein L19



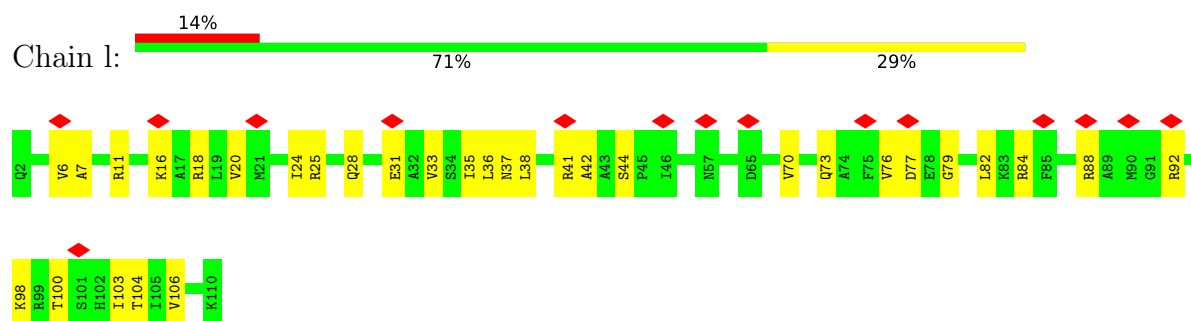
• Molecule 36: 50S ribosomal protein L20



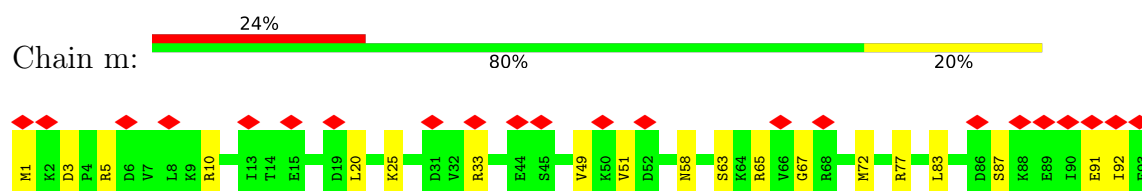
• Molecule 37: 50S ribosomal protein L21



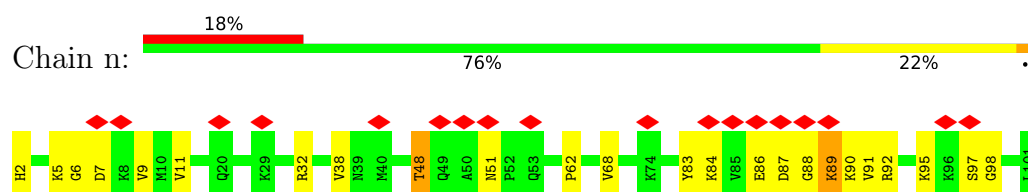
- Molecule 38: 50S ribosomal protein L22



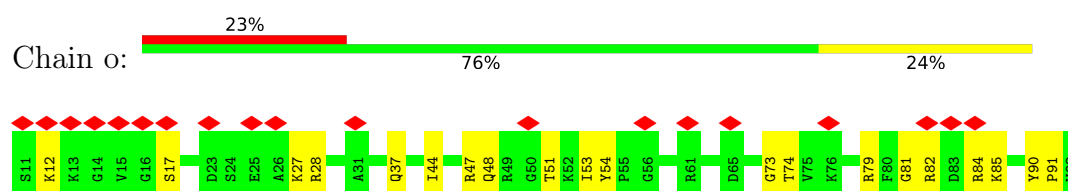
- Molecule 39: 50S ribosomal protein L23



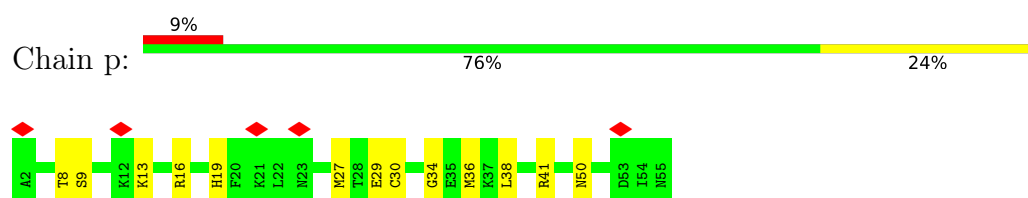
- Molecule 40: 50S ribosomal protein L24



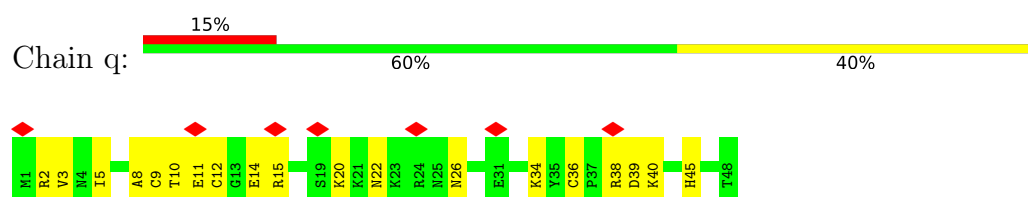
- Molecule 41: 50S ribosomal protein L27



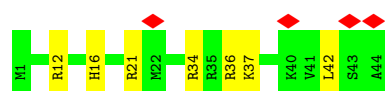
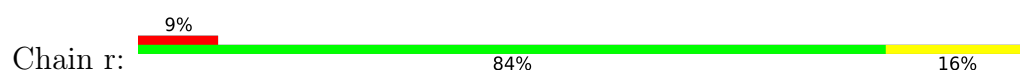
- Molecule 42: 50S ribosomal protein L32



- Molecule 43: 50S ribosomal protein L33 1



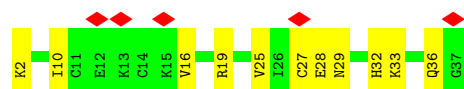
- Molecule 44: 50S ribosomal protein L34



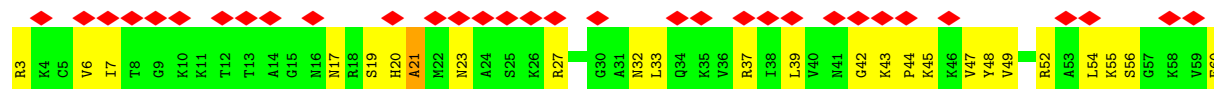
- Molecule 45: 50S ribosomal protein L35



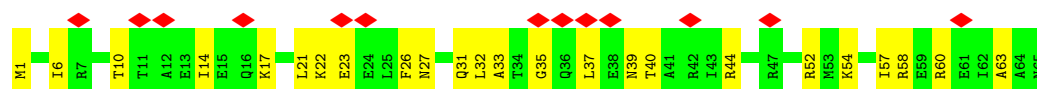
- Molecule 46: 50S ribosomal protein L36



- Molecule 47: 50S ribosomal protein L28



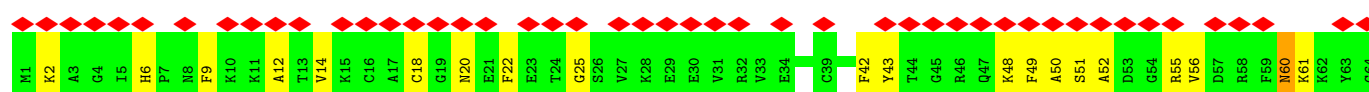
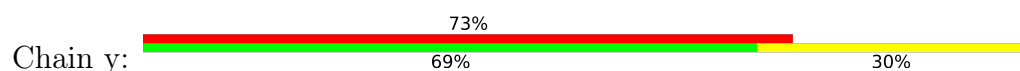
- Molecule 48: 50S ribosomal protein L29



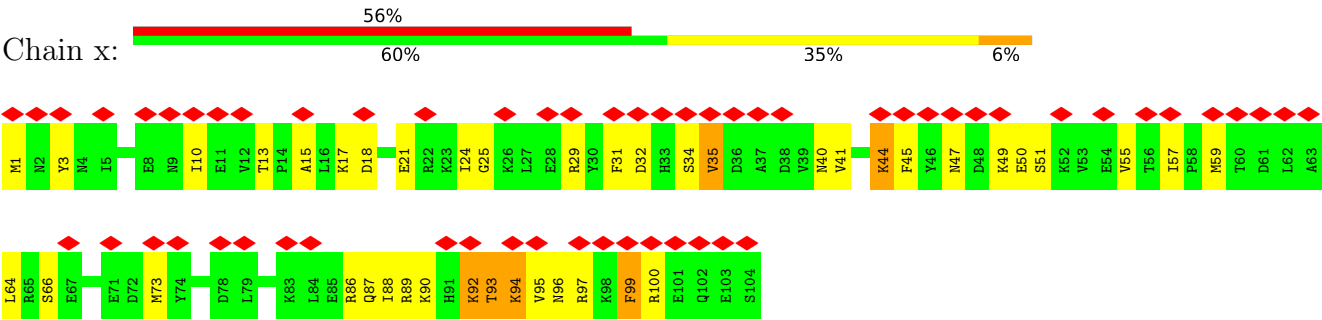
- Molecule 49: 50S ribosomal protein L30



- Molecule 50: 50S ribosomal protein L31



● Molecule 51: Ribosome hibernation promotion factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24546	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	55.100	Depositor
Minimum map value	-33.631	Depositor
Average map value	0.128	Depositor
Map value standard deviation	2.386	Depositor
Recommended contour level	11	Depositor
Map size (Å)	487.8, 487.8, 487.8	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/37074	0.50	5/57834 (0.0%)
2	B	0.23	0/895	0.52	0/1117
3	C	0.84	5/839 (0.6%)	1.10	8/1047 (0.8%)
4	D	0.21	0/796	0.48	0/992
5	E	0.24	0/660	0.50	0/822
6	F	0.26	0/380	0.50	0/472
7	G	0.18	0/612	0.39	0/762
8	H	0.22	0/524	0.47	0/652
9	I	0.22	0/520	0.65	0/647
10	J	0.22	0/408	0.52	0/507
11	K	0.21	0/471	0.46	0/587
12	L	0.24	0/548	0.61	0/682
13	M	0.22	0/443	0.64	0/552
14	N	0.24	0/240	0.55	0/297
15	O	0.19	0/352	0.47	0/437
16	P	0.24	0/356	0.56	0/442
17	Q	0.21	0/344	0.48	0/427
18	R	0.24	0/284	0.76	1/352 (0.3%)
19	S	0.24	0/319	0.62	0/397
20	T	0.22	0/344	0.39	0/427
21	U	0.44	0/70307	0.57	8/109687 (0.0%)
22	V	0.36	0/2678	0.54	0/4174
23	W	0.47	0/2148	0.72	2/2881 (0.1%)
24	X	0.43	0/1597	0.74	0/2140
25	Y	0.43	0/1580	0.76	2/2132 (0.1%)
26	Z	0.33	0/1423	0.83	3/1910 (0.2%)
27	a	0.34	0/1360	0.63	0/1832
28	b	0.32	0/963	0.82	3/1298 (0.2%)
29	c	0.47	0/1146	0.77	2/1542 (0.1%)
30	d	0.44	0/927	0.77	0/1245
31	e	0.42	0/1093	0.82	2/1457 (0.1%)
32	f	0.43	0/1120	0.71	2/1496 (0.1%)
33	g	0.46	0/960	0.71	0/1284
34	h	0.34	0/921	0.86	4/1236 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.42	0/949	0.71	0/1269
36	j	0.49	0/952	0.74	0/1266
37	k	0.45	0/797	0.87	2/1070 (0.2%)
38	l	0.44	0/851	0.81	0/1146
39	m	0.40	0/759	0.72	0/1011
40	n	0.40	0/764	0.87	2/1022 (0.2%)
41	o	0.46	0/638	0.69	0/847
42	p	0.52	0/433	0.81	0/574
43	q	0.36	0/406	0.68	0/540
44	r	0.49	0/370	0.77	0/483
45	s	0.47	0/519	0.79	2/680 (0.3%)
46	t	0.39	0/291	0.65	0/383
47	u	0.42	0/448	1.02	5/596 (0.8%)
48	v	0.34	0/531	0.67	0/707
49	w	0.46	0/457	0.68	0/613
50	y	0.36	0/513	0.75	0/683
51	x	0.41	0/878	0.93	3/1178 (0.3%)
All	All	0.42	5/145188 (0.0%)	0.59	56/217834 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
29	c	0	1
40	n	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	5	VAL	C-O	-13.56	1.07	1.24
3	C	6	ASN	CA-C	10.90	1.66	1.52
3	C	6	ASN	N-CA	10.36	1.60	1.46
3	C	5	VAL	N-CA	9.47	1.58	1.46
3	C	6	ASN	C-O	6.62	1.32	1.24

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6	ASN	CA-C-N	-16.93	98.68	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	6	ASN	C-N-CA	-16.93	98.68	119.84
3	C	5	VAL	N-CA-C	14.49	139.48	109.34
37	k	50	ASN	C-N-CD	-11.29	78.72	125.00
34	h	27	GLU	N-CA-C	-10.80	99.08	112.47

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	c	4	THR	Peptide
40	n	95	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	33115	0	16675	337	0
2	B	896	0	244	1	0
3	C	840	0	241	7	0
4	D	797	0	224	3	0
5	E	661	0	197	4	0
6	F	381	0	104	0	0
7	G	613	0	164	3	0
8	H	525	0	146	1	0
9	I	521	0	155	0	0
10	J	409	0	104	3	0
11	K	472	0	135	1	0
12	L	549	0	157	3	0
13	M	444	0	129	7	0
14	N	241	0	62	0	0
15	O	353	0	94	1	0
16	P	357	0	95	2	0
17	Q	345	0	90	0	0
18	R	285	0	76	0	0
19	S	320	0	89	8	0
20	T	345	0	89	0	0
21	U	62767	0	31584	779	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	V	2395	0	1212	27	0
23	W	2111	0	2200	77	0
24	X	1575	0	1642	36	0
25	Y	1561	0	1647	47	0
26	Z	1404	0	1467	45	0
27	a	1342	0	1388	34	0
28	b	955	0	990	22	0
29	c	1123	0	1162	33	0
30	d	920	0	977	36	0
31	e	1081	0	1132	32	0
32	f	1097	0	1165	21	0
33	g	953	0	983	19	0
34	h	912	0	947	22	0
35	i	936	0	1008	57	0
36	j	940	0	1005	57	0
37	k	786	0	826	37	0
38	l	842	0	899	24	0
39	m	752	0	802	14	0
40	n	754	0	809	15	0
41	o	630	0	644	16	0
42	p	426	0	445	14	0
43	q	401	0	413	18	0
44	r	367	0	410	8	0
45	s	512	0	564	20	0
46	t	288	0	330	8	0
47	u	444	0	487	19	0
48	v	530	0	568	17	0
49	w	455	0	491	14	0
50	y	503	0	494	29	0
51	x	866	0	863	49	0
All	All	133097	0	78824	1780	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 9.

The worst 5 of 1780 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)
36:j:95:LEU:HA	36:j:98:LEU:CD2	1.22	1.57
36:j:95:LEU:CA	36:j:98:LEU:HD21	1.38	1.48
36:j:94:MET:O	36:j:98:LEU:CD2	1.71	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Z:3:ARG:NH1	50:y:22:PHE:HB3	1.33	1.36
21:U:28:A:N6	21:U:558:G:C2	1.94	1.34

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	222/224 (99%)	195 (88%)	27 (12%)	0	100	100
3	C	208/210 (99%)	180 (86%)	25 (12%)	3 (1%)	9	37
4	D	197/199 (99%)	169 (86%)	28 (14%)	0	100	100
5	E	163/165 (99%)	133 (82%)	30 (18%)	0	100	100
6	F	93/95 (98%)	77 (83%)	16 (17%)	0	100	100
7	G	151/153 (99%)	121 (80%)	30 (20%)	0	100	100
8	H	129/131 (98%)	102 (79%)	24 (19%)	3 (2%)	5	30
9	I	128/130 (98%)	95 (74%)	32 (25%)	1 (1%)	16	48
10	J	100/102 (98%)	80 (80%)	20 (20%)	0	100	100
11	K	116/118 (98%)	97 (84%)	19 (16%)	0	100	100
12	L	135/137 (98%)	111 (82%)	24 (18%)	0	100	100
13	M	109/111 (98%)	86 (79%)	23 (21%)	0	100	100
14	N	58/60 (97%)	46 (79%)	12 (21%)	0	100	100
15	O	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
16	P	87/89 (98%)	64 (74%)	23 (26%)	0	100	100
17	Q	84/86 (98%)	72 (86%)	12 (14%)	0	100	100
18	R	69/71 (97%)	54 (78%)	14 (20%)	1 (1%)	9	37
19	S	78/80 (98%)	58 (74%)	20 (26%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	84/86 (98%)	79 (94%)	5 (6%)	0	100	100
23	W	273/275 (99%)	234 (86%)	36 (13%)	3 (1%)	11	41
24	X	205/207 (99%)	188 (92%)	17 (8%)	0	100	100
25	Y	203/205 (99%)	177 (87%)	24 (12%)	2 (1%)	12	43
26	Z	176/178 (99%)	150 (85%)	26 (15%)	0	100	100
27	a	173/175 (99%)	155 (90%)	18 (10%)	0	100	100
28	b	121/123 (98%)	96 (79%)	22 (18%)	3 (2%)	4	28
29	c	140/142 (99%)	125 (89%)	15 (11%)	0	100	100
30	d	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
31	e	144/146 (99%)	128 (89%)	15 (10%)	1 (1%)	18	51
32	f	136/138 (99%)	120 (88%)	16 (12%)	0	100	100
33	g	117/119 (98%)	108 (92%)	9 (8%)	0	100	100
34	h	118/120 (98%)	104 (88%)	13 (11%)	1 (1%)	16	48
35	i	112/114 (98%)	93 (83%)	19 (17%)	0	100	100
36	j	115/117 (98%)	107 (93%)	6 (5%)	2 (2%)	7	34
37	k	99/101 (98%)	72 (73%)	22 (22%)	5 (5%)	1	17
38	l	107/109 (98%)	88 (82%)	18 (17%)	1 (1%)	14	45
39	m	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
40	n	98/100 (98%)	80 (82%)	18 (18%)	0	100	100
41	o	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
42	p	52/54 (96%)	46 (88%)	6 (12%)	0	100	100
43	q	46/48 (96%)	42 (91%)	4 (9%)	0	100	100
44	r	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
45	s	62/64 (97%)	54 (87%)	8 (13%)	0	100	100
46	t	34/36 (94%)	30 (88%)	4 (12%)	0	100	100
47	u	56/58 (97%)	47 (84%)	9 (16%)	0	100	100
48	v	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
49	w	56/58 (97%)	51 (91%)	5 (9%)	0	100	100
50	y	62/64 (97%)	56 (90%)	4 (6%)	2 (3%)	3	24
51	x	102/104 (98%)	79 (78%)	20 (20%)	3 (3%)	3	25
All	All	5500/5596 (98%)	4688 (85%)	781 (14%)	31 (1%)	23	54

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	5	VAL
3	C	6	ASN
8	H	98	LEU
23	W	154	LEU
25	Y	80	SER

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	
23	W	223/223 (100%)	222 (100%)	1 (0%)	84	83
24	X	168/168 (100%)	167 (99%)	1 (1%)	78	79
25	Y	169/169 (100%)	165 (98%)	4 (2%)	43	62
26	Z	153/153 (100%)	151 (99%)	2 (1%)	61	71
27	a	148/148 (100%)	148 (100%)	0	100	100
28	b	105/105 (100%)	100 (95%)	5 (5%)	23	47
29	c	120/120 (100%)	118 (98%)	2 (2%)	53	67
30	d	101/101 (100%)	97 (96%)	4 (4%)	28	52
31	e	110/110 (100%)	108 (98%)	2 (2%)	51	67
32	f	111/111 (100%)	109 (98%)	2 (2%)	51	67
33	g	99/99 (100%)	96 (97%)	3 (3%)	36	57
34	h	93/93 (100%)	90 (97%)	3 (3%)	34	56
35	i	99/99 (100%)	99 (100%)	0	100	100
36	j	96/96 (100%)	95 (99%)	1 (1%)	68	74
37	k	83/83 (100%)	81 (98%)	2 (2%)	43	62
38	l	90/90 (100%)	89 (99%)	1 (1%)	65	73
39	m	84/84 (100%)	84 (100%)	0	100	100
40	n	84/84 (100%)	81 (96%)	3 (4%)	31	54
41	o	64/64 (100%)	63 (98%)	1 (2%)	55	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	p	48/48 (100%)	48 (100%)	0	100	100
43	q	46/46 (100%)	46 (100%)	0	100	100
44	r	39/39 (100%)	39 (100%)	0	100	100
45	s	54/54 (100%)	54 (100%)	0	100	100
46	t	34/34 (100%)	34 (100%)	0	100	100
47	u	47/47 (100%)	46 (98%)	1 (2%)	47	64
48	v	56/56 (100%)	55 (98%)	1 (2%)	51	67
49	w	52/52 (100%)	52 (100%)	0	100	100
50	y	53/53 (100%)	53 (100%)	0	100	100
51	x	97/97 (100%)	93 (96%)	4 (4%)	27	51
All	All	2726/2726 (100%)	2683 (98%)	43 (2%)	54	68

5 of 43 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	h	58	THR
40	n	89	LYS
36	j	98	LEU
38	l	35	ILE
47	u	56	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
36	j	38	GLN
40	n	64	HIS
51	x	96	ASN
37	k	65	GLN
38	l	102	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1543/1544 (99%)	367 (23%)	17 (1%)
21	U	2922/2923 (99%)	1021 (34%)	60 (2%)
22	V	111/112 (99%)	46 (41%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4576/4579 (99%)	1434 (31%)	79 (1%)

5 of 1434 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	G
1	A	18	A
1	A	24	G
1	A	34	A
1	A	41	G

5 of 79 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
21	U	1455	C
21	U	2504	C
21	U	1527	C
21	U	1779	G
21	U	2785	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.

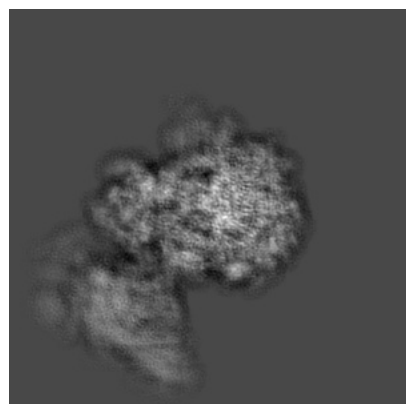
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3656. These allow visual inspection of the internal detail of the map and identification of artifacts.

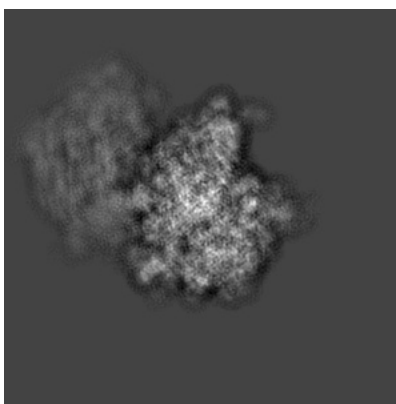
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

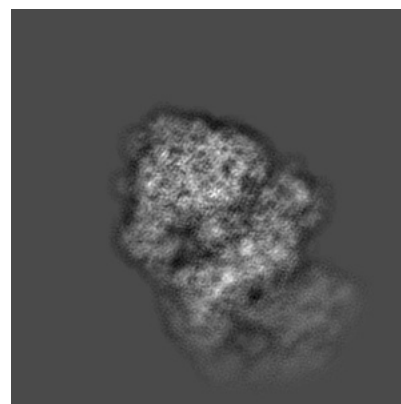
6.1.1 Primary map



X

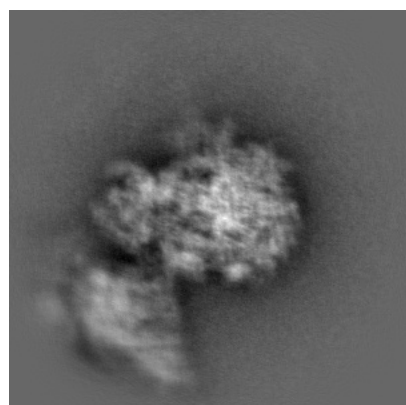


Y

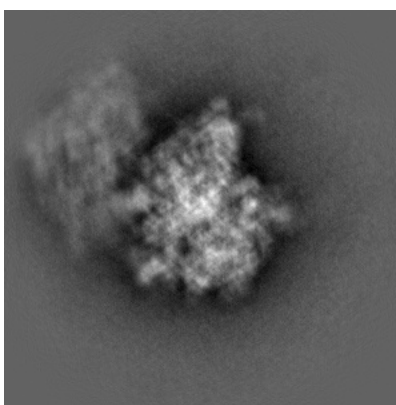


Z

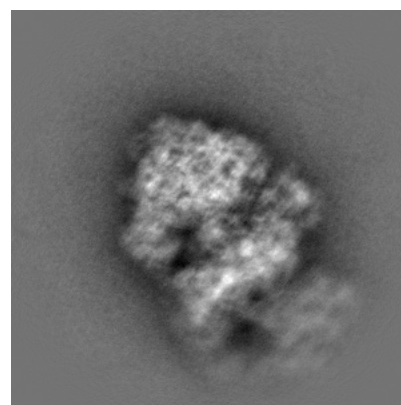
6.1.2 Raw map



X



Y

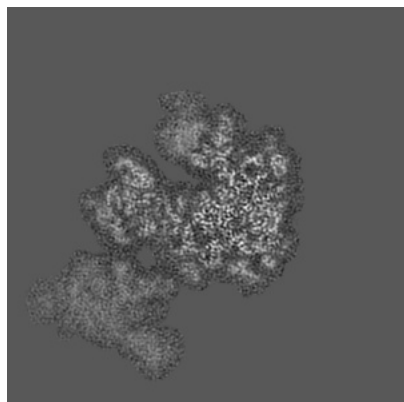


Z

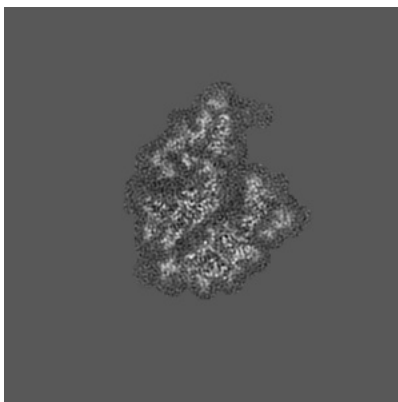
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

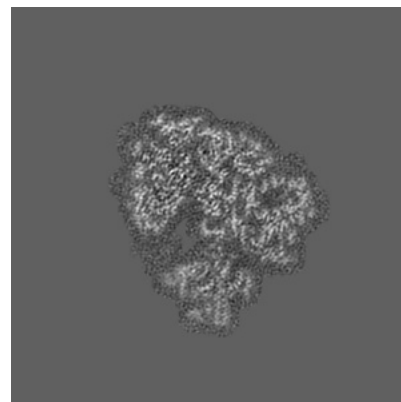
6.2.1 Primary map



X Index: 225

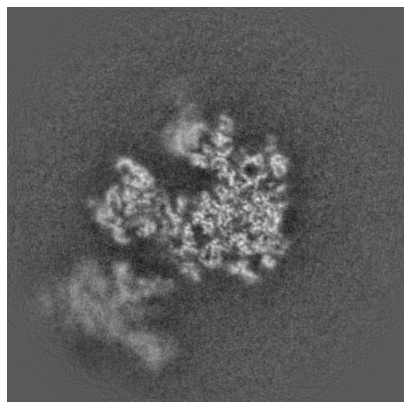


Y Index: 225

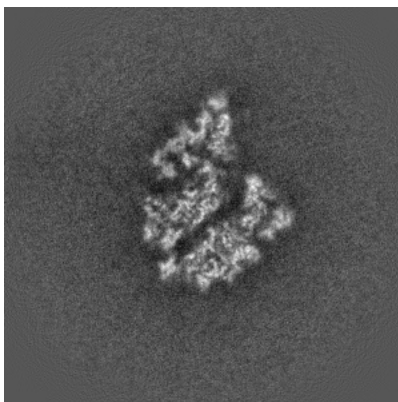


Z Index: 225

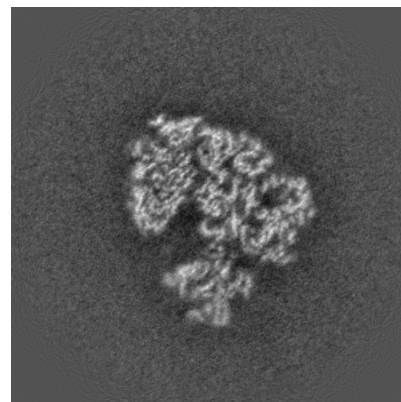
6.2.2 Raw map



X Index: 225



Y Index: 225

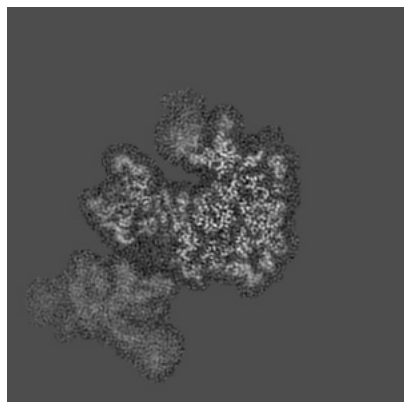


Z Index: 225

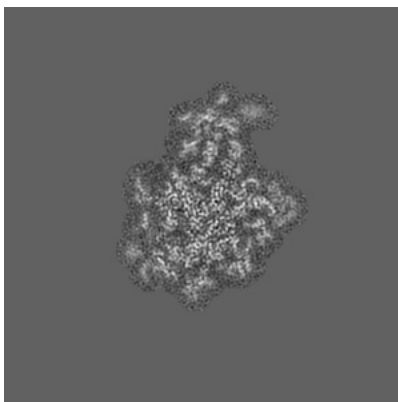
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

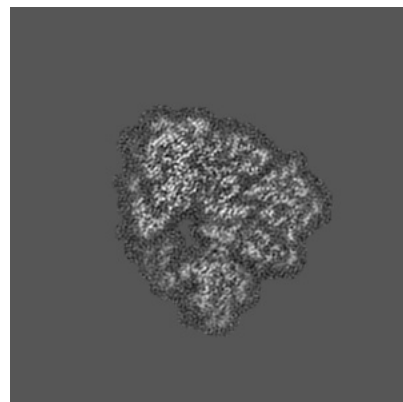
6.3.1 Primary map



X Index: 229

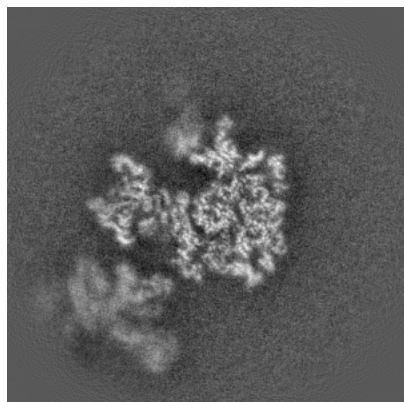


Y Index: 245

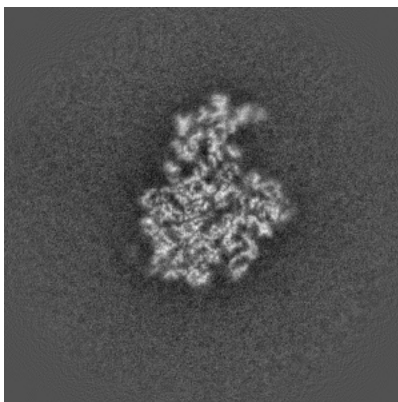


Z Index: 231

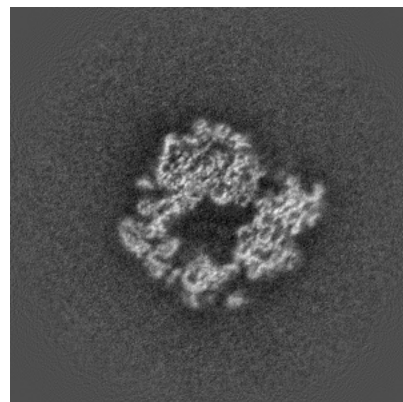
6.3.2 Raw map



X Index: 230



Y Index: 236

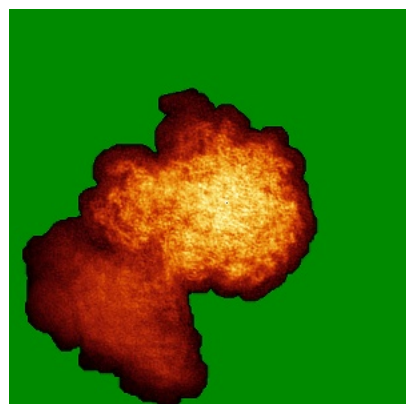


Z Index: 248

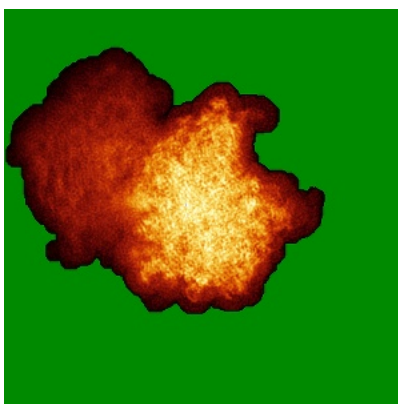
The images above show the largest variance slices of the map in three orthogonal directions.

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

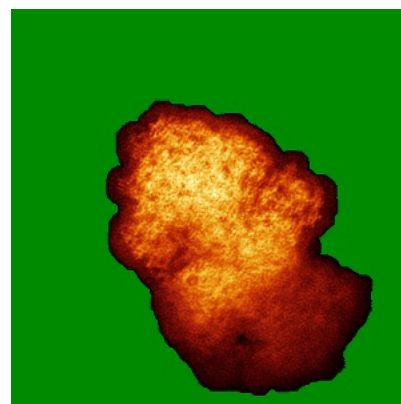
6.4.1 Primary map



X

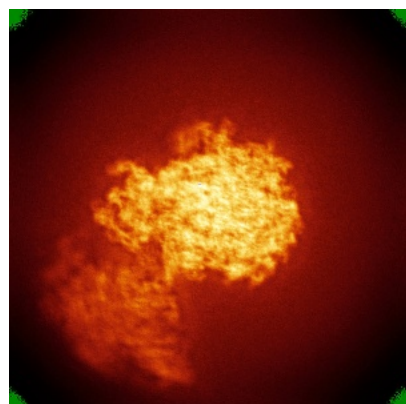


Y

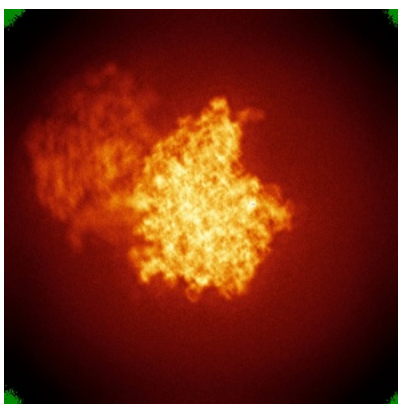


Z

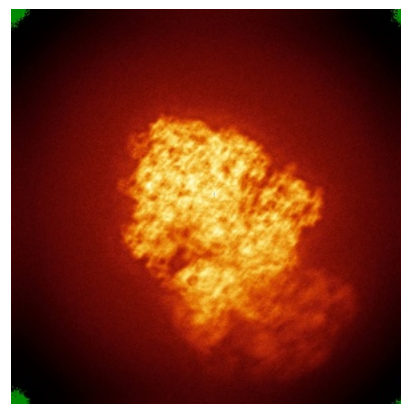
6.4.2 Raw map



X



Y

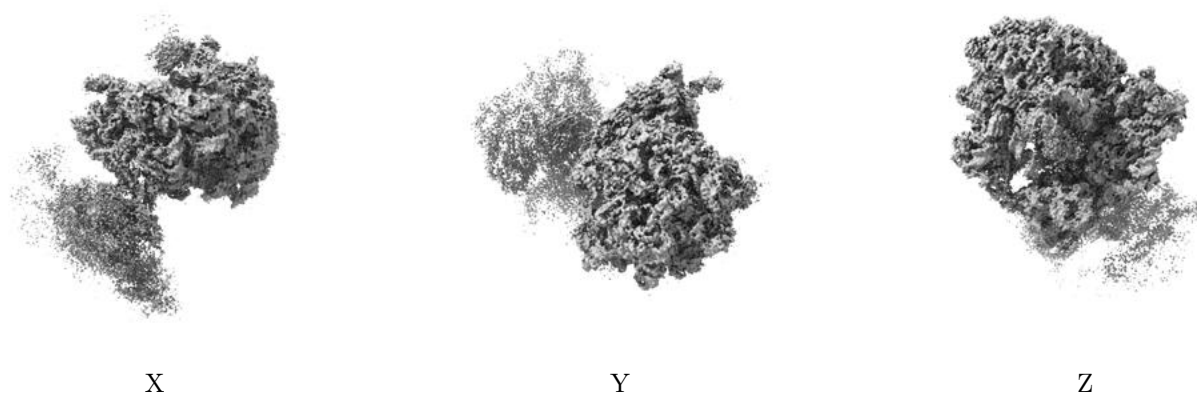


Z

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 11.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

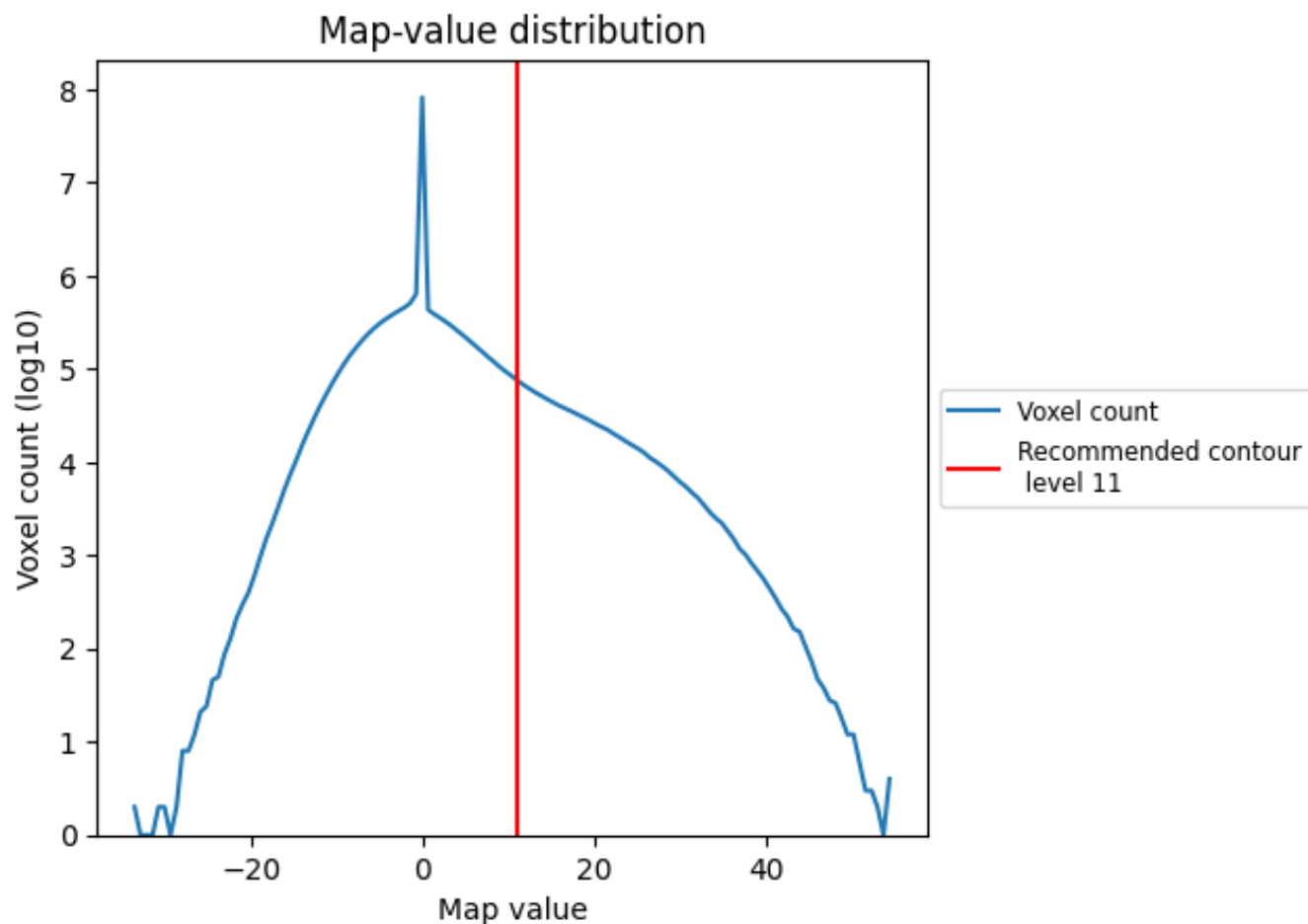
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

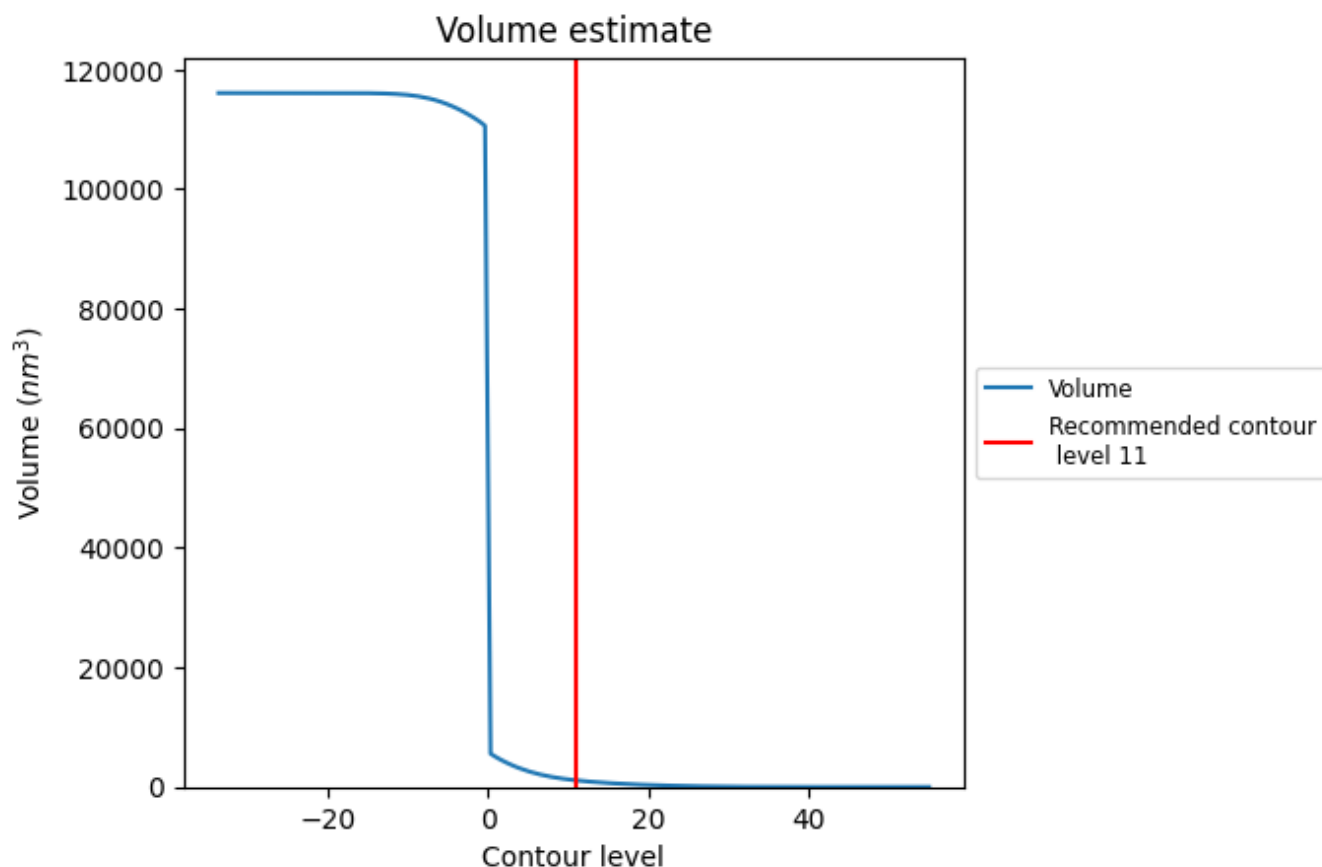
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

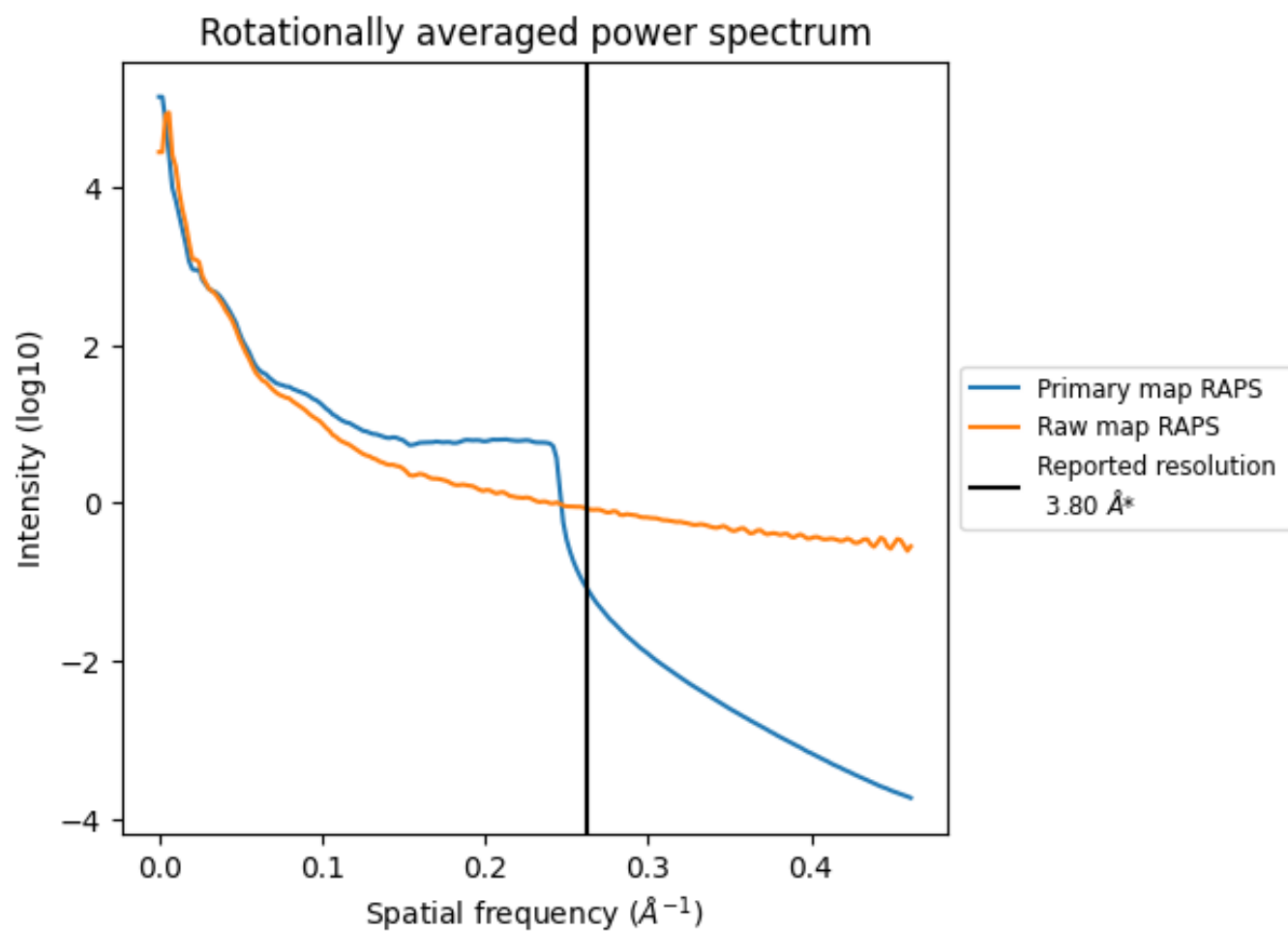
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1108 nm³; this corresponds to an approximate mass of 1001 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 ⓘ

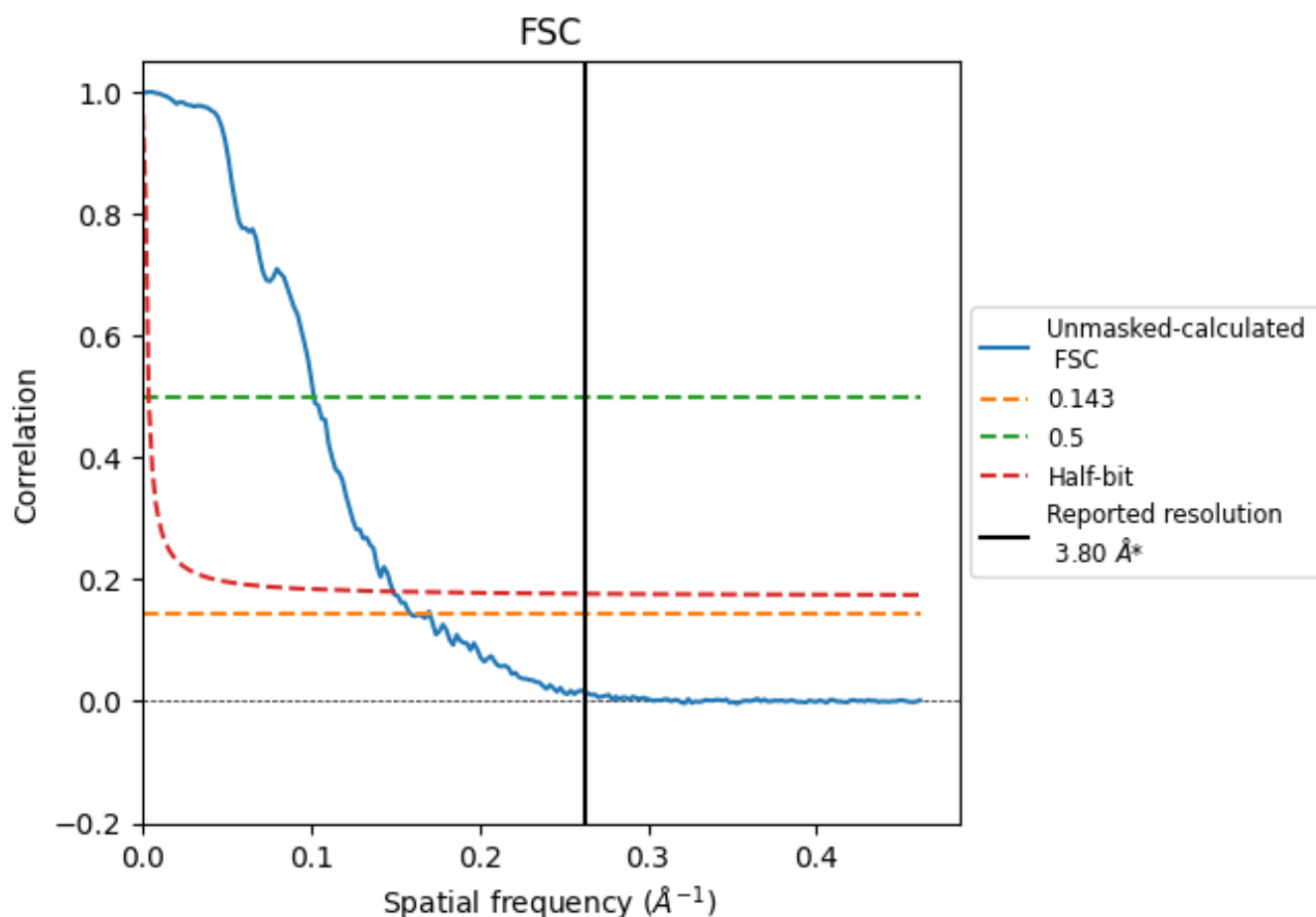


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

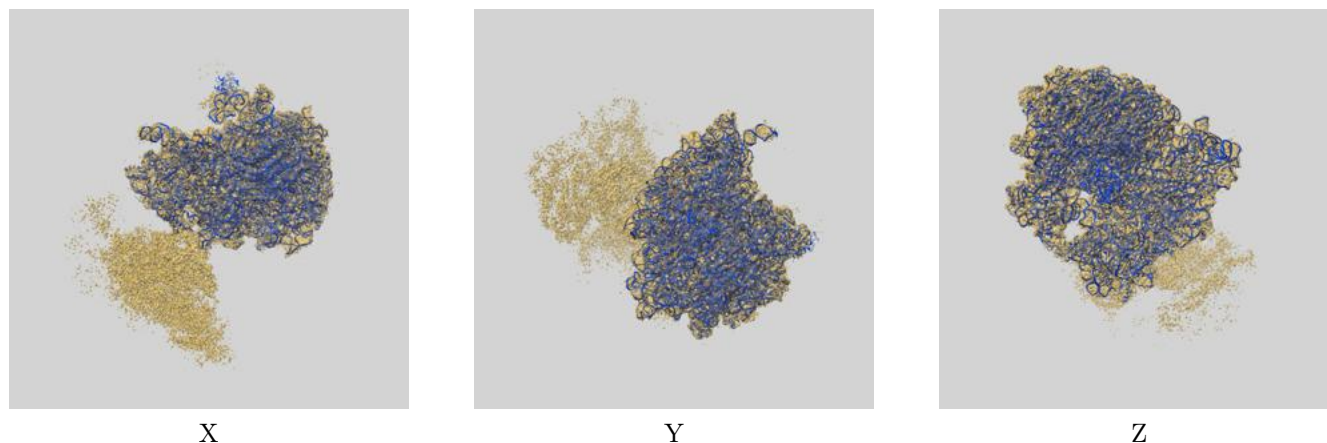
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.27	9.81	6.71

*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 6.27 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

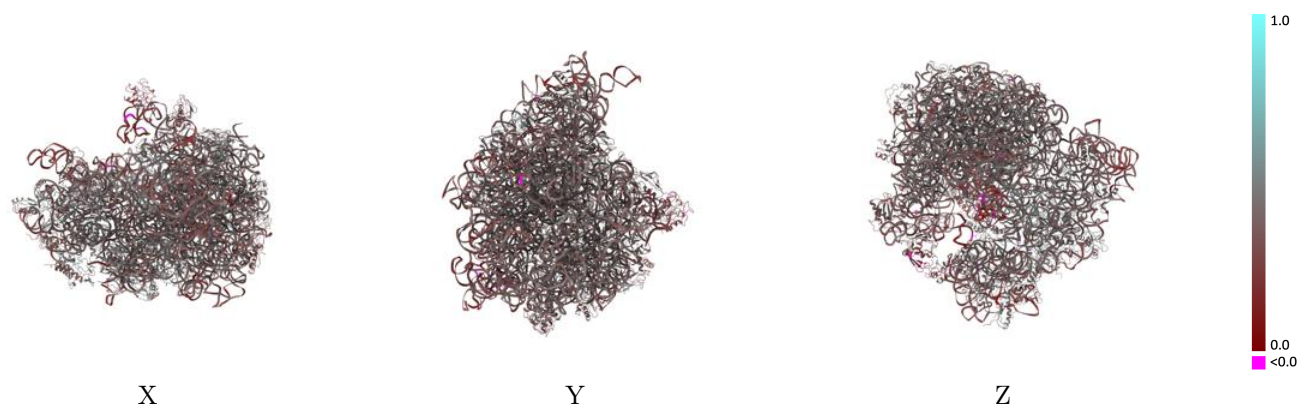
This section contains information regarding the fit between EMDB map EMD-3656 and PDB model 5NJT. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



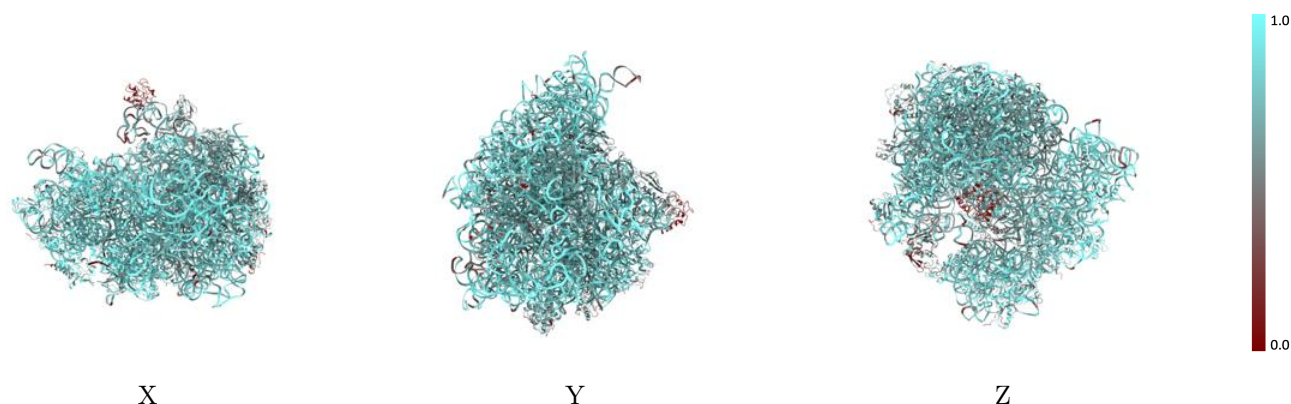
The images above show the 3D surface view of the map at the recommended contour level 11.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



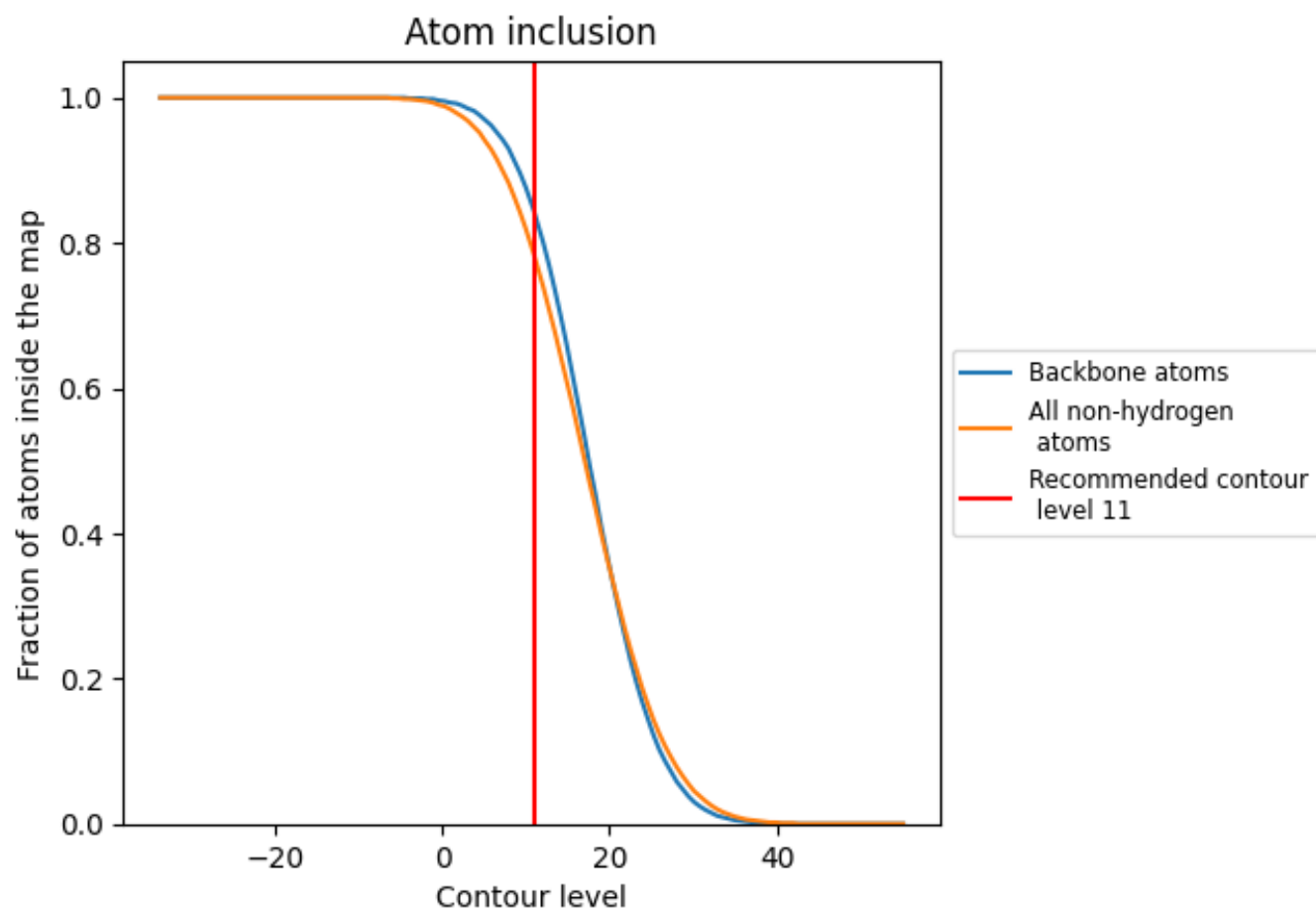
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7840	 0.3810
A	 0.8280	 0.3670
B	 0.8020	 0.4200
C	 0.8240	 0.4520
D	 0.8780	 0.4510
E	 0.8610	 0.4810
F	 0.8840	 0.4740
G	 0.7760	 0.4020
H	 0.8990	 0.4820
I	 0.6770	 0.3890
J	 0.7600	 0.4540
K	 0.8180	 0.4350
L	 0.8600	 0.4900
M	 0.7990	 0.3680
N	 0.8920	 0.4450
O	 0.9090	 0.4310
P	 0.8880	 0.4800
Q	 0.8410	 0.4890
R	 0.7720	 0.4560
S	 0.8660	 0.4170
T	 0.8640	 0.3850
U	 0.8320	 0.3800
V	 0.8610	 0.3620
W	 0.6430	 0.4270
X	 0.6230	 0.4240
Y	 0.6510	 0.4010
Z	 0.4920	 0.3010
a	 0.5830	 0.3550
b	 0.0720	 0.2130
c	 0.6590	 0.4140
d	 0.5920	 0.4290
e	 0.6290	 0.4030
f	 0.6470	 0.4150
g	 0.6250	 0.3870
h	 0.5760	 0.3360



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Chain	Atom inclusion	Q-score
i	 0.5760	 0.3920
j	 0.6800	 0.3950
k	 0.6580	 0.4030
l	 0.6140	 0.4220
m	 0.5550	 0.3880
n	 0.6060	 0.3660
o	 0.6030	 0.4050
p	 0.7000	 0.4330
q	 0.6280	 0.3760
r	 0.6580	 0.4320
s	 0.6310	 0.4270
t	 0.6240	 0.4370
u	 0.3800	 0.3920
v	 0.5560	 0.3260
w	 0.5890	 0.4030
x	 0.3900	 0.3300
y	 0.2520	 0.0930