



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 03:21 PM UTC

PDB ID : 7ASP / pdb_00007asp
EMDB ID : EMD-11903
Title : Staphylococcus aureus 70S after 50 minutes incubation at 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.86 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

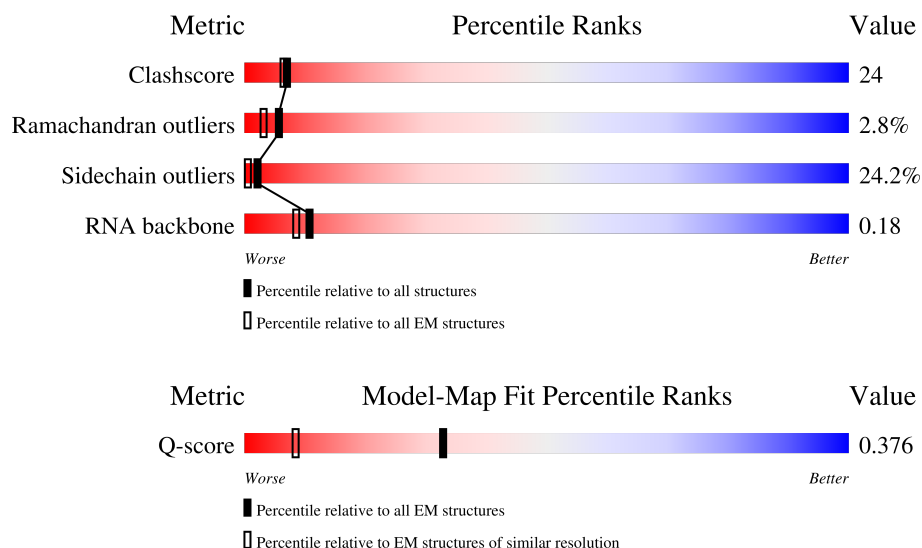
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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.



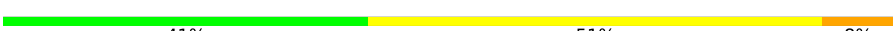
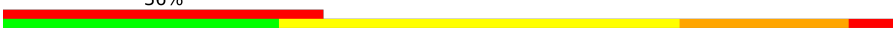
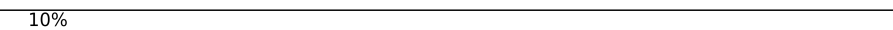
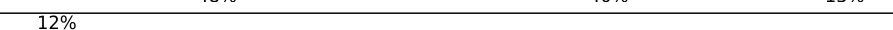
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12017 (2.36 - 3.36)

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	Y	2923	
2	X	1552	
3	3	114	

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Mol	Chain	Length	Quality of chain
4	1	105	
4	A	105	
5	B	43	
6	2	64	
7	4	37	
8	a	80	
9	b	114	
10	c	136	
11	C	274	
12	d	113	
13	D	215	
14	E	206	
15	e	60	
16	f	88	
17	g	83	
18	G	175	
19	H	145	
20	h	80	
21	I	122	
22	i	56	
23	j	78	
24	J	146	
25	k	202	
26	K	137	
27	L	120	

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Mol	Chain	Length	Quality of chain
28	l	198	
29	m	156	
30	M	119	
31	n	95	
32	N	114	
33	o	130	
34	O	116	
35	p	155	
36	P	102	
37	q	127	
38	Q	112	
39	R	89	
40	S	103	
41	T	94	
42	U	79	
43	V	49	
44	W	67	
45	Z	47	
46	F	158	

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 128828 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 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	2723	Total	C	N	O	P	0	0
			58376	26062	10687	18904	2723		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	1447	Total	C	N	O	P	0	0
			31009	13847	5680	10037	1445		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	114	Total	C	N	O	P	0	0
			2430	1086	436	794	114		

- Molecule 4 is a protein called 50S ribosomal protein L33,50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	47	Total	C	N	O	S	0	0
			390	238	78	70	4		
4	1	58	Total	C	N	O		0	0
			449	280	85	84			

- Molecule 5 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 6 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	2	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 7 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

- Molecule 8 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	80	Total	C	N	O	S	0	0
			626	394	116	116			

- Molecule 9 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	114	Total	C	N	O	S	0	0
			826	507	158	159	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	136	Total	C	N	O	S	0	0
			976	611	190	173	2		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	113	Total	C	N	O	S	0	0
			828	510	168	149	1		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	60	Total	C	N	O	S	0	0
			497	314	99	79	5		

- Molecule 16 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	88	Total	C	N	O	S	0	0
			713	441	148	123	1		

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	g	83	Total	C	N	O	S	0	0
			537	335	105	96	1		

- Molecule 18 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	165	Total	C	N	O	S	0	0
			1184	739	226	216	3		

- Molecule 19 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	145	Total	C	N	O	S	0	0
			1143	714	208	218	3		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	h	80	Total	C	N	O	0	0
			520	327	97	96		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 22 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	56	Total	C	N	O	S	0	0
			458	292	88	76	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	j	77	Total	C	N	O	S	0	0
			498	300	99	98	1		

- Molecule 24 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 25 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	k	202	Total	C	N	O	S	0	0
			1551	979	293	278	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 27 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 28 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	198	Total	C	N	O		0	0
			1058	634	211	213			

- Molecule 29 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	156	Total	C	N	O	S	0	0
			1153	727	211	213	2		

- Molecule 30 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	119	Total	C	N	O		0	0
			882	549	174	159			

- Molecule 31 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	n	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	N	114	Total	C	N	O		0	0
			889	563	175	151			

- Molecule 33 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	130	Total	C	N	O	S	0	0
			1007	639	180	184	4		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	154	Total	C	N	O	S	0	0
			1155	719	219	214	3		

- Molecule 36 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	q	127	Total	C	N	O	S	0	0
			975	605	194	175	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	79	Total	C	N	O	0	0
			597	369	117	111		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 45 is a protein called 50S ribosomalprotein L32p.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Z	47	Total	C	N	O	S	0	0
			355	219	76	58	2		

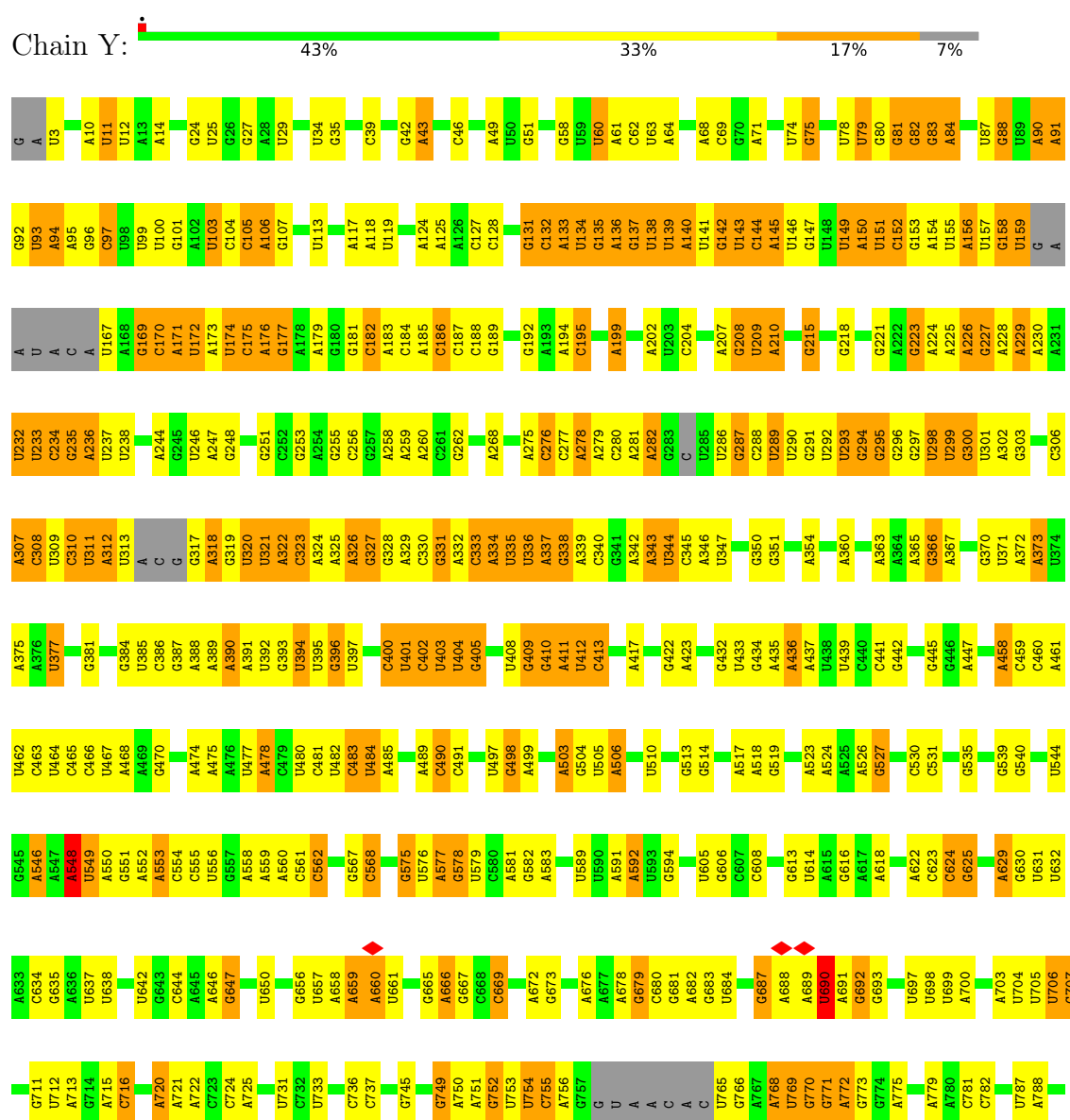
- Molecule 46 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	F	155	Total	C	N	O	0	0
			765	455	155	155		

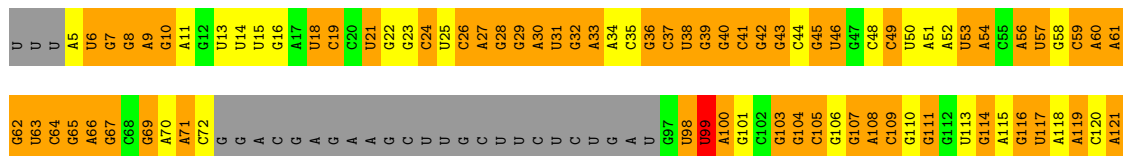
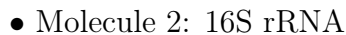
3 Residue-property plots

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: 23S rRNA

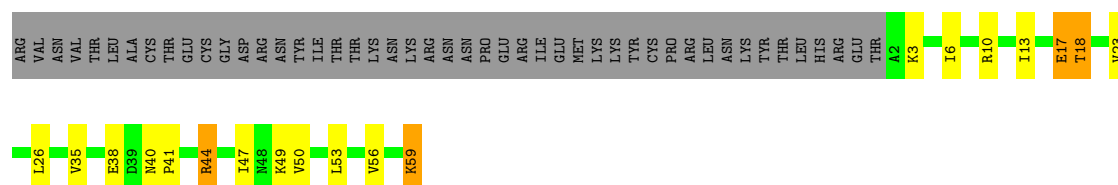






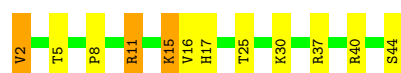


Chain 1:  37% 14% 45%



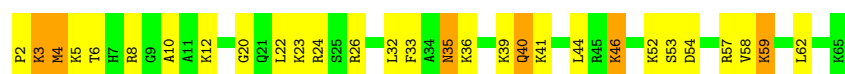
- Molecule 5: 50S ribosomal protein L34

Chain B:  72% 21% 7%



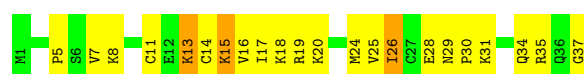
- Molecule 6: 50S ribosomal protein L35

Chain 2:  55% 36% 9%

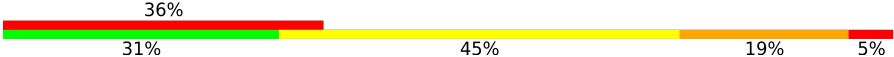


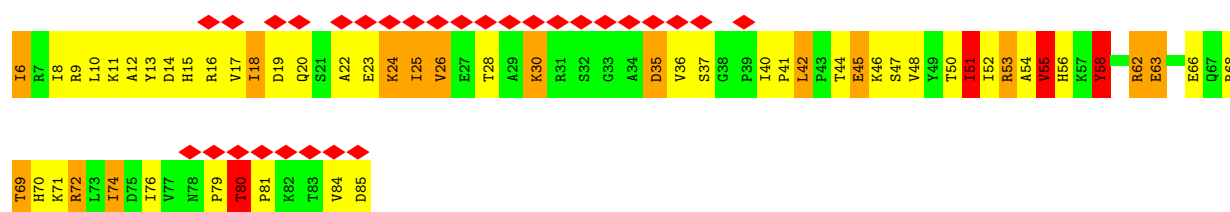
- Molecule 7: 50S ribosomal protein L36

Chain 4:  41% 51% 8%



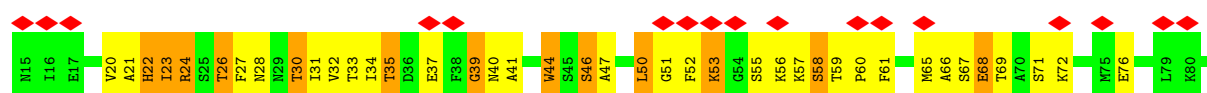
- Molecule 8: 30S ribosomal protein S10

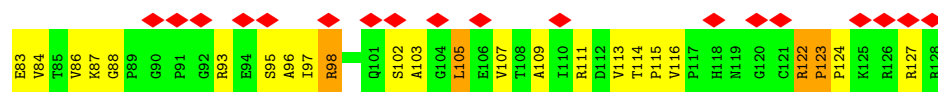
Chain a:  36% 31% 45% 19% 5%



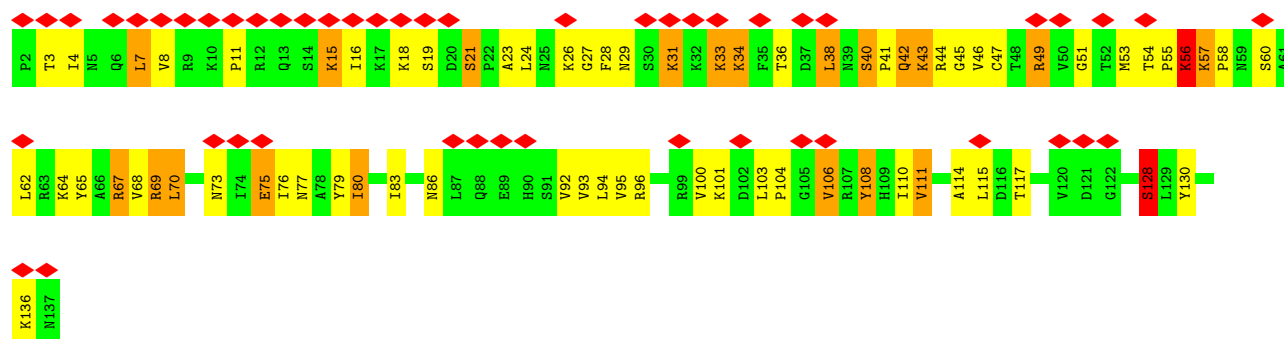
- Molecule 9: 30S ribosomal protein S11

Chain b:  31% 44% 41% 15%

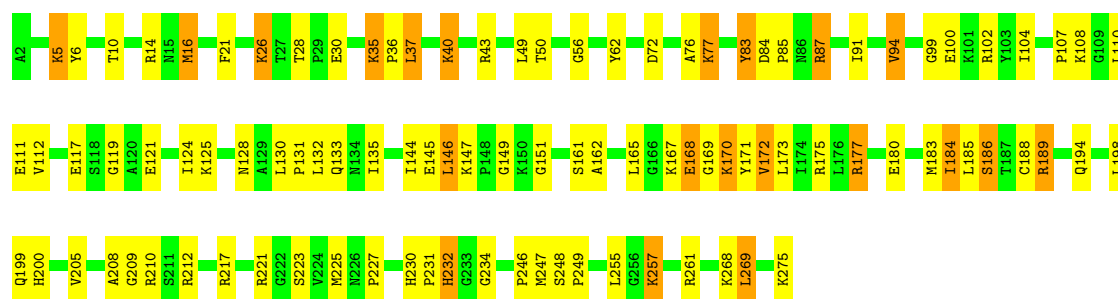




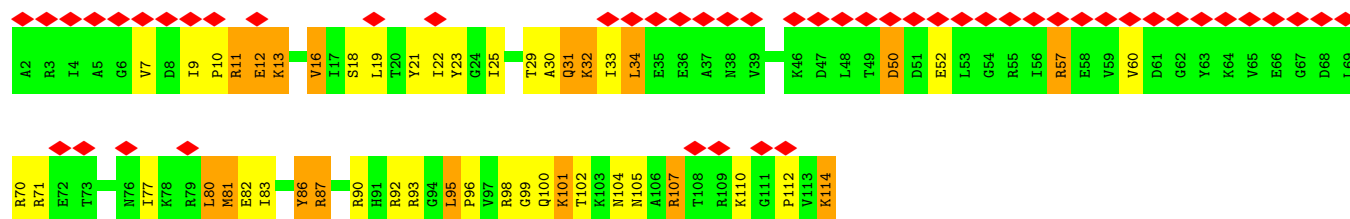
• Molecule 10: 30S ribosomal protein S12



• Molecule 11: 50S ribosomal protein L2



• Molecule 12: 30S ribosomal protein S13

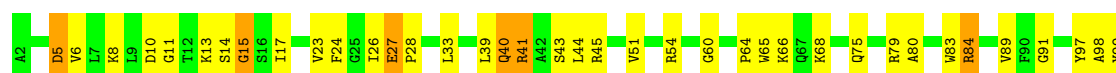


• Molecule 13: 50S ribosomal protein L3





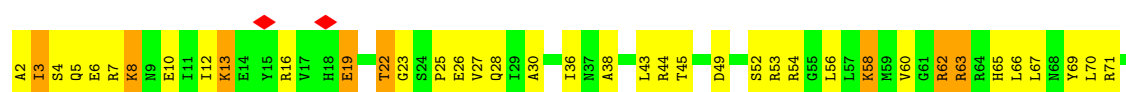
• Molecule 14: 50S ribosomal protein L4



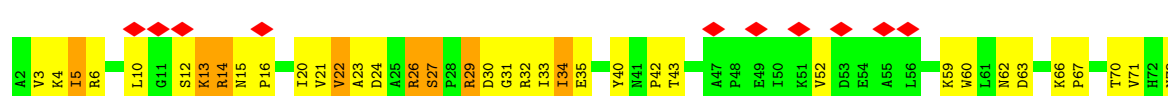
• Molecule 15: 30S ribosomal protein S14 type Z



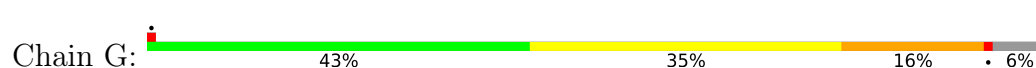
• Molecule 16: 30S ribosomal protein S15

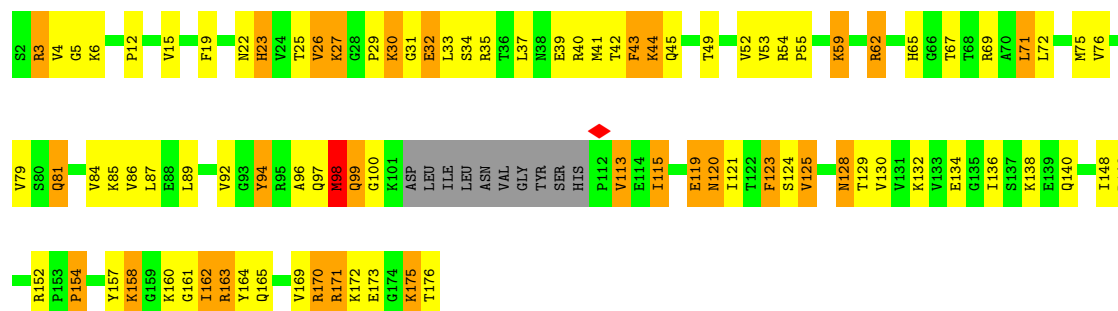


• Molecule 17: 30S ribosomal protein S16

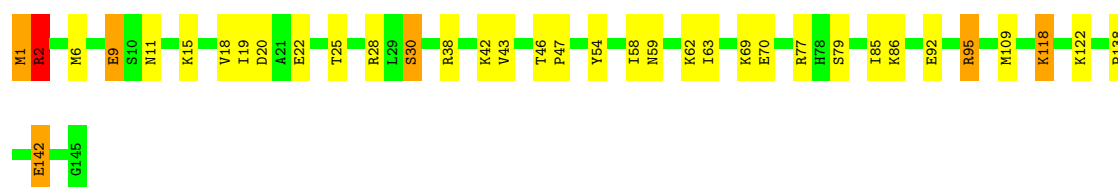
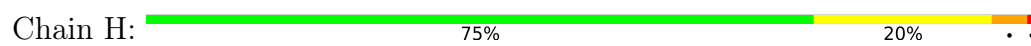


• Molecule 18: 50S ribosomal protein L6

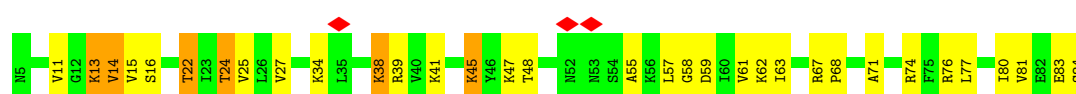




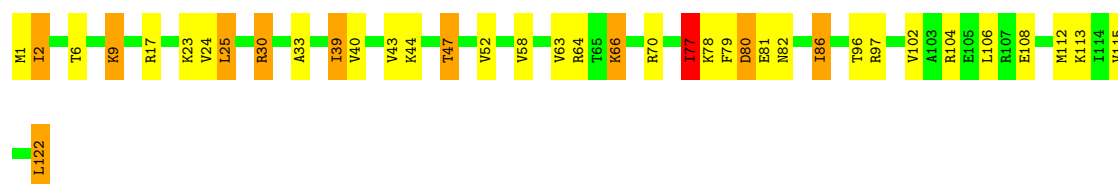
• Molecule 19: 50S ribosomal protein L13



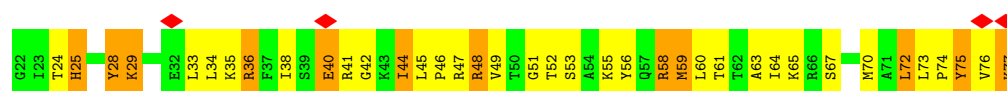
• Molecule 20: 30S ribosomal protein S17



• Molecule 21: 50S ribosomal protein L14



• Molecule 22: 30S ribosomal protein S18

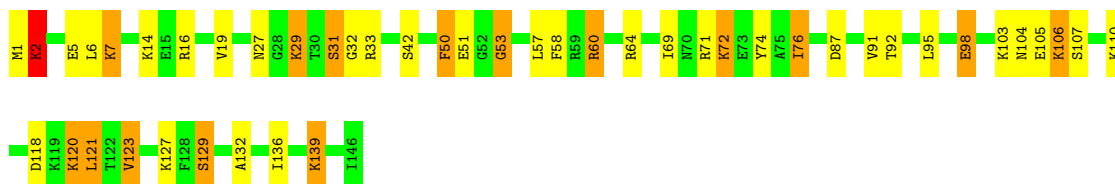


• Molecule 23: 30S ribosomal protein S20

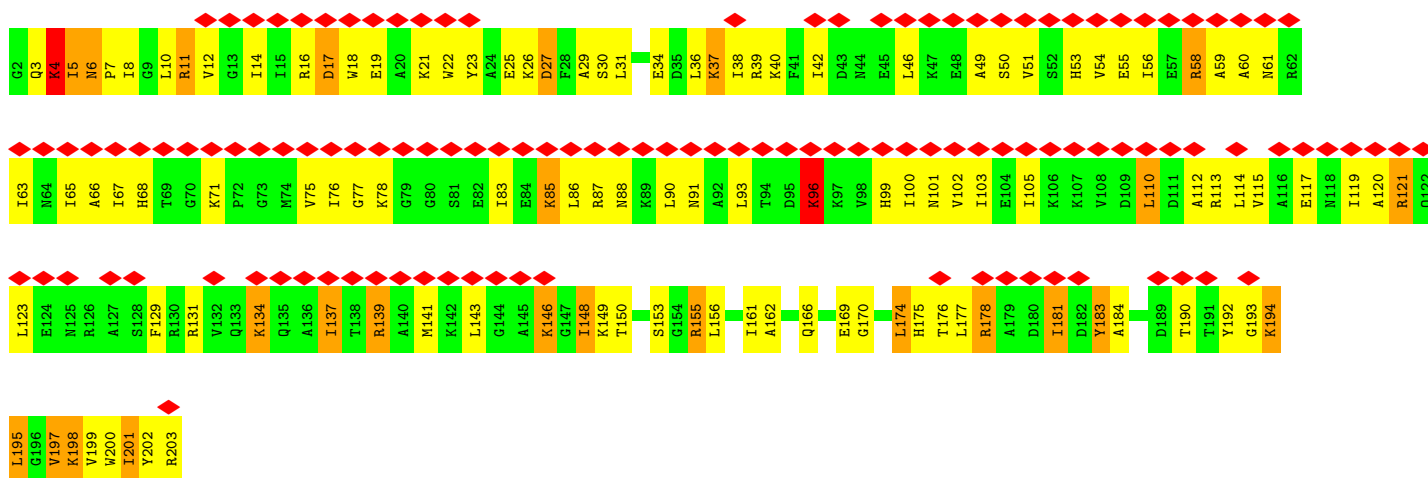




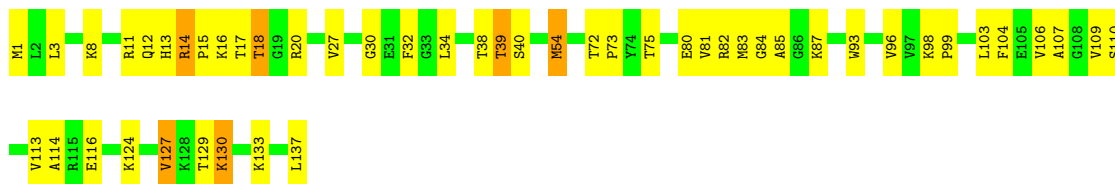
- Molecule 24: 50S ribosomal protein L15



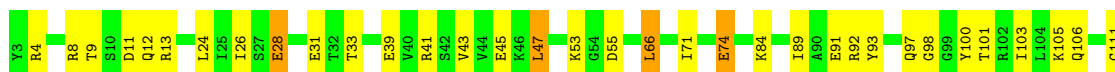
- Molecule 25: 30S ribosomal protein S3



- Molecule 26: 50S ribosomal protein L16

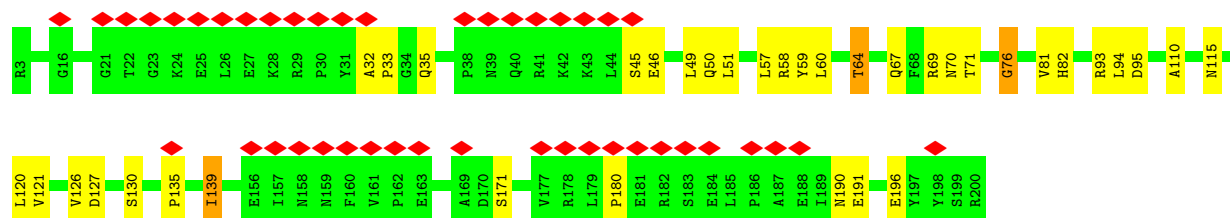
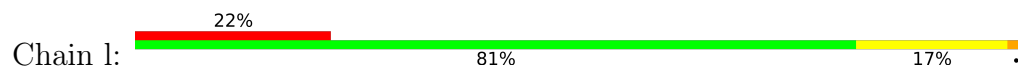


- Molecule 27: 50S ribosomal protein L17

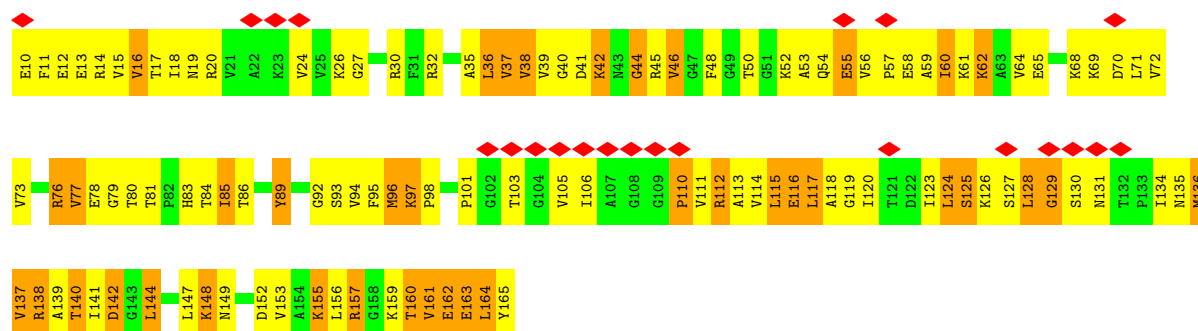




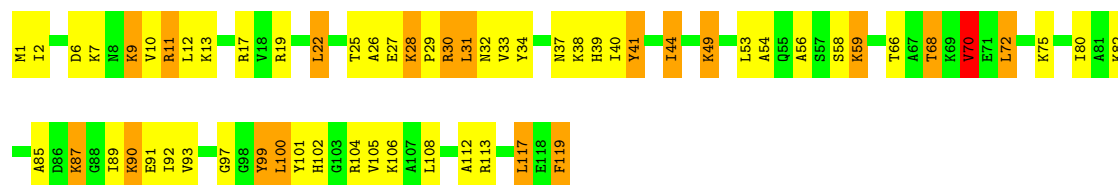
• Molecule 28: 30S ribosomal protein S4



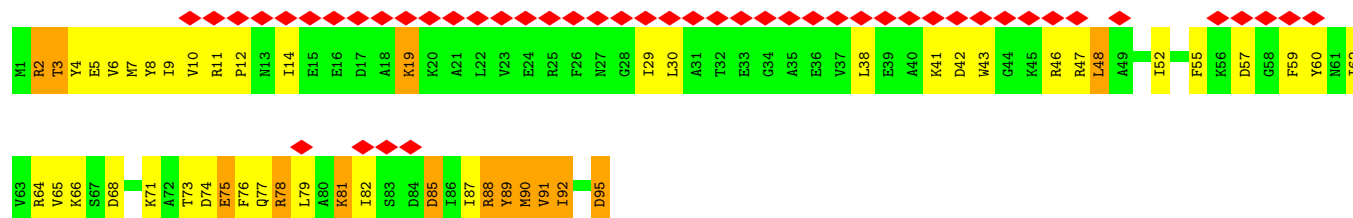
• Molecule 29: 30S ribosomal protein S5



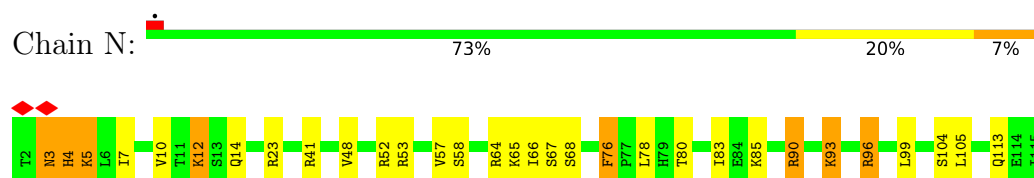
• Molecule 30: 50S ribosomal protein L18



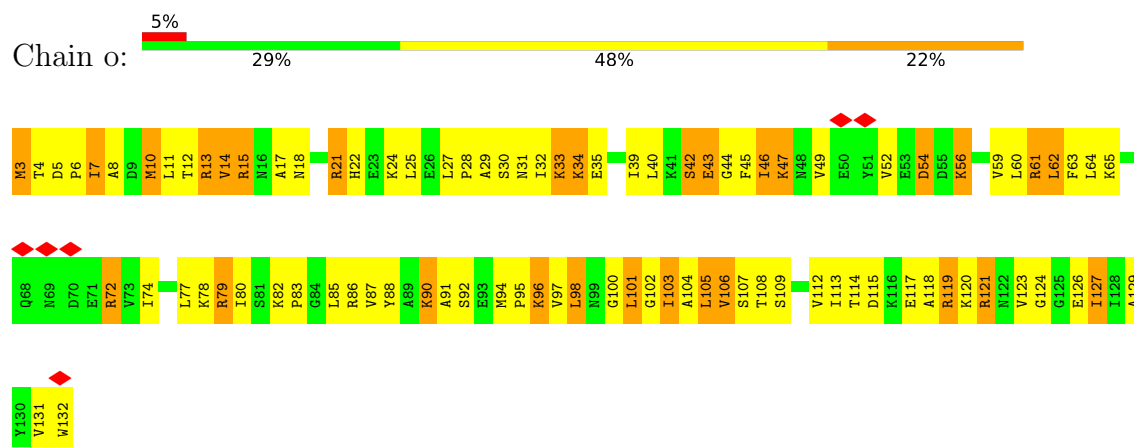
• Molecule 31: 30S ribosomal protein S6



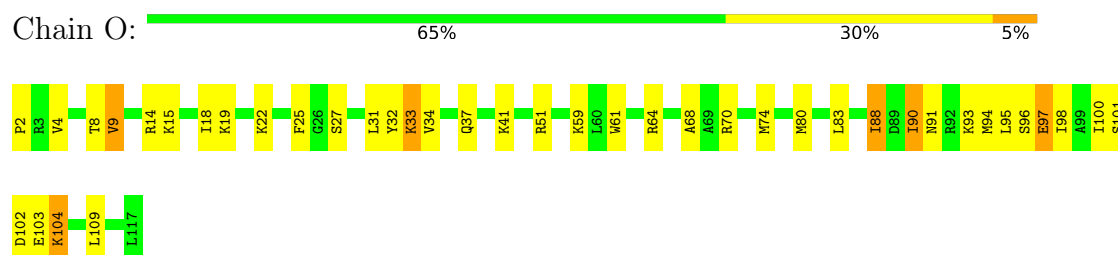
- Molecule 32: 50S ribosomal protein L19



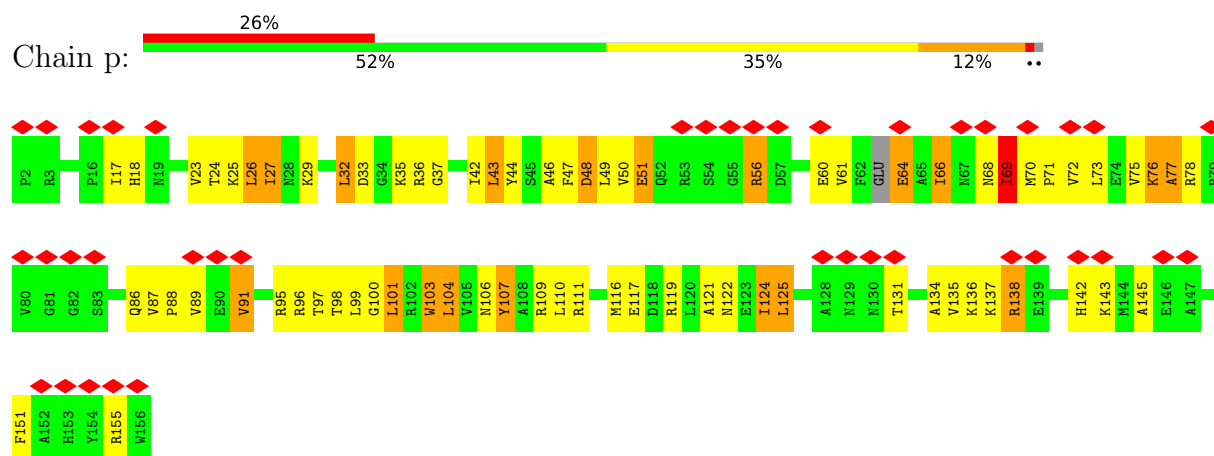
- Molecule 33: 30S ribosomal protein S8



- Molecule 34: 50S ribosomal protein L20

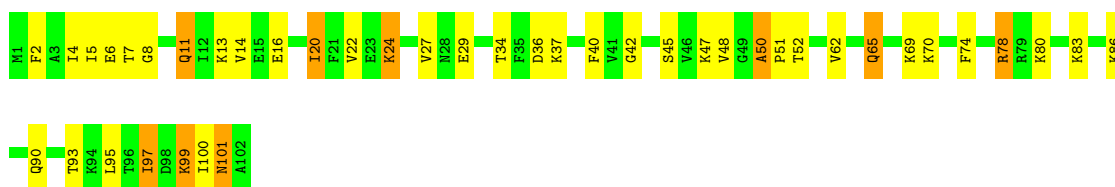


- Molecule 35: 30S ribosomal protein S7



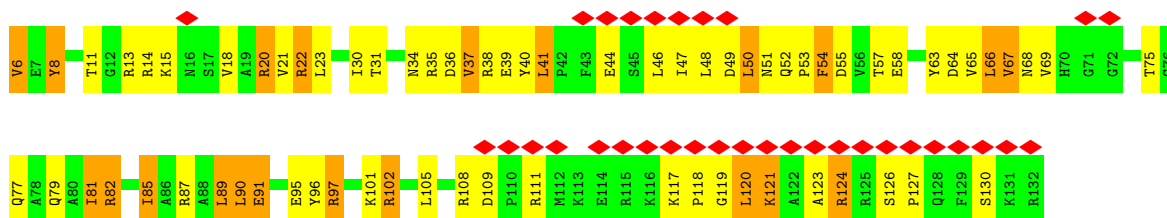
- Molecule 36: 50S ribosomal protein L21

Chain P: 



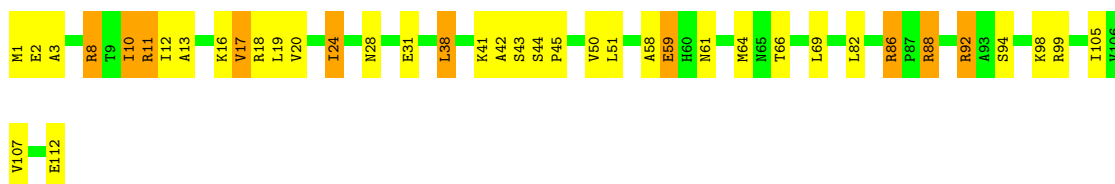
- Molecule 37: 30S ribosomal protein S9

Chain q: 



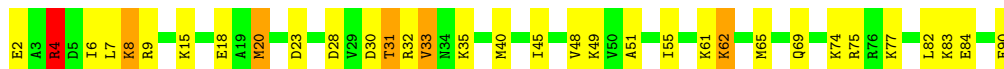
- Molecule 38: 50S ribosomal protein L22

Chain Q: 



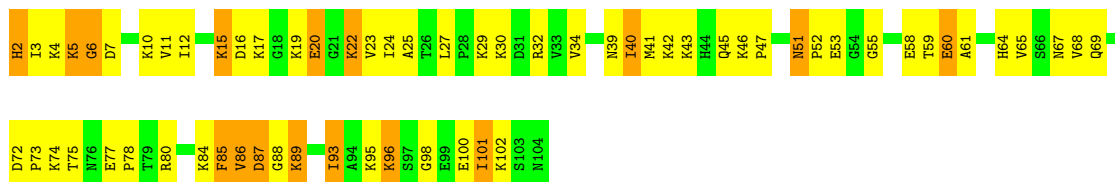
- Molecule 39: 50S ribosomal protein L23

Chain R: 



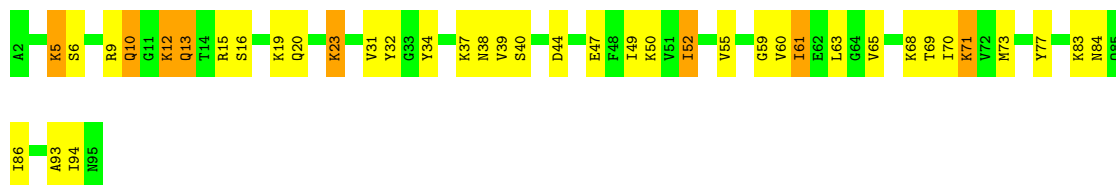
- Molecule 40: 50S ribosomal protein L24

Chain S: 



- Molecule 41: 50S ribosomal protein L25

Chain T:  57% 34% 9%



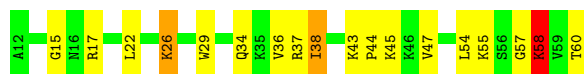
- Molecule 42: 50S ribosomal protein L27

Chain U:  70% 25% . .



- Molecule 43: 50S ribosomal protein L28

Chain V:  63% 31% . .



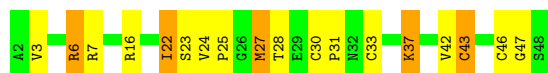
- Molecule 44: 50S ribosomal protein L29

Chain W:  55% 30% 15%



- Molecule 45: 50S ribosomal protein L32p

Chain Z:  62% 28% 11%



- Molecule 46: 50S ribosomal protein L5

Chain F:  78% 18% . .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	192105	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	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	0.076	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0045	Depositor
Map size ($\text{\AA}$)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	Y	0.36	0/65368	0.59	10/101922 (0.0%)
2	X	0.37	0/34716	0.66	25/54120 (0.0%)
3	3	0.37	0/2717	0.64	3/4232 (0.1%)
4	1	1.01	0/451	1.13	0/606
4	A	0.97	0/395	1.04	0/530
5	B	0.93	0/371	1.13	0/484
6	2	0.96	0/526	1.08	0/690
7	4	1.03	0/298	1.01	0/392
8	a	1.04	0/637	1.13	0/865
9	b	1.03	0/840	1.09	0/1137
10	c	1.05	0/991	1.07	0/1337
11	C	1.01	0/2129	1.08	1/2858 (0.0%)
12	d	1.01	0/835	1.14	0/1123
13	D	1.02	0/1651	1.05	0/2215
14	E	1.00	0/1595	1.10	1/2154 (0.0%)
15	e	0.96	0/507	1.08	0/674
16	f	0.98	0/721	1.18	0/964
17	g	1.06	0/541	1.12	0/733
18	G	1.04	0/1199	1.11	0/1621
19	H	0.98	0/1165	1.06	0/1570
20	h	1.12	0/527	1.03	0/721
21	I	1.02	0/925	1.07	0/1242
22	i	0.98	0/465	1.11	0/620
23	j	1.09	0/496	1.33	1/669 (0.1%)
24	J	1.00	0/1100	1.09	0/1467
25	k	1.01	0/1573	1.14	3/2121 (0.1%)
26	K	1.00	0/1095	1.06	0/1472
27	L	0.99	0/936	1.17	1/1253 (0.1%)
28	l	1.20	0/1062	1.27	0/1465
29	m	1.03	0/1167	1.13	1/1576 (0.1%)
30	M	1.02	0/891	1.11	0/1194
31	n	0.97	0/796	1.05	1/1069 (0.1%)
32	N	1.01	0/901	1.03	0/1209
33	o	1.02	0/1019	1.06	0/1371

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	O	0.93	0/954	1.14	0/1264
35	p	1.01	0/1170	1.22	1/1580 (0.1%)
36	P	1.02	0/800	0.98	0/1070
37	q	1.00	0/990	1.11	0/1332
38	Q	1.01	0/862	1.09	0/1161
39	R	0.98	0/723	1.06	0/966
40	S	1.04	0/779	1.07	1/1043 (0.1%)
41	T	1.03	0/730	1.05	0/981
42	U	1.01	0/603	1.02	0/802
43	V	1.00	0/384	1.02	0/515
44	W	0.97	0/542	1.24	1/722 (0.1%)
45	Z	0.97	0/361	1.10	0/482
46	F	1.27	0/763	1.50	4/1059 (0.4%)
All	All	0.61	0/140267	0.77	54/210653 (0.0%)

There are no bond length outliers.

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	1897	U	C2'-C3'-O3'	9.09	123.13	109.50
2	X	99	U	C4'-C3'-O3'	8.88	122.72	109.40
2	X	353	C	C4'-C3'-O3'	8.64	122.37	109.40
1	Y	2591	A	C2'-C3'-O3'	8.34	126.20	113.70
3	3	26	C	C2'-C3'-O3'	8.34	126.20	113.70

There are no chirality outliers.

There are no planarity outliers.

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	Y	58376	0	29353	1341	0
2	X	31009	0	15621	1720	0
3	3	2430	0	1229	92	0
4	1	449	0	491	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	390	0	394	35	0
5	B	367	0	415	13	0
6	2	521	0	586	25	0
7	4	295	0	340	40	0
8	a	626	0	628	141	0
9	b	826	0	817	104	0
10	c	976	0	966	102	0
11	C	2094	0	2205	129	0
12	d	828	0	809	68	0
13	D	1627	0	1667	48	0
14	E	1572	0	1619	66	0
15	e	497	0	512	63	0
16	f	713	0	733	61	0
17	g	537	0	462	66	0
18	G	1184	0	1149	113	0
19	H	1143	0	1134	38	0
20	h	520	0	415	36	0
21	I	918	0	981	38	0
22	i	458	0	496	66	0
23	j	498	0	445	69	0
24	J	1086	0	1125	49	0
25	k	1551	0	1570	178	0
26	K	1071	0	1123	37	0
27	L	932	0	983	19	0
28	l	1058	0	568	34	0
29	m	1153	0	1210	189	0
30	M	882	0	900	62	0
31	n	785	0	781	79	0
32	N	889	0	937	33	0
33	o	1007	0	1050	174	0
34	O	942	0	1014	37	0
35	p	1155	0	1139	71	0
36	P	790	0	830	36	0
37	q	975	0	970	84	0
38	Q	854	0	914	42	0
39	R	715	0	748	21	0
40	S	770	0	809	58	0
41	T	722	0	766	32	0
42	U	597	0	604	23	0
43	V	379	0	400	14	0
44	W	541	0	563	41	0
45	Z	355	0	356	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
46	F	765	0	339	69	0
All	All	128828	0	83166	5018	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 24.

The worst 5 of 5018 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)
33:o:42:SER:HB2	33:o:103:ILE:CD1	1.22	1.58
1:Y:1987:A:H1'	2:X:1429:A:N6	1.33	1.39
2:X:599:U:H5'	33:o:56:LYS:CD	1.54	1.34
8:a:24:LYS:HG2	25:k:59:ALA:CB	1.59	1.33
2:X:682:G:H5''	9:b:115:PRO:CG	1.58	1.32

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	
4	1	56/105 (53%)	51 (91%)	5 (9%)	0	100	100
4	A	45/105 (43%)	41 (91%)	3 (7%)	1 (2%)	5	12
5	B	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
6	2	62/64 (97%)	48 (77%)	13 (21%)	1 (2%)	7	17
7	4	35/37 (95%)	32 (91%)	2 (6%)	1 (3%)	3	8
8	a	78/80 (98%)	51 (65%)	22 (28%)	5 (6%)	1	1
9	b	112/114 (98%)	85 (76%)	22 (20%)	5 (4%)	2	3
10	c	134/136 (98%)	101 (75%)	26 (19%)	7 (5%)	1	2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	C	272/274 (99%)	230 (85%)	38 (14%)	4 (2%)	8	18
12	d	111/113 (98%)	88 (79%)	20 (18%)	3 (3%)	4	9
13	D	213/215 (99%)	179 (84%)	27 (13%)	7 (3%)	3	7
14	E	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	12	25
15	e	58/60 (97%)	44 (76%)	9 (16%)	5 (9%)	0	0
16	f	86/88 (98%)	73 (85%)	12 (14%)	1 (1%)	10	22
17	g	81/83 (98%)	54 (67%)	22 (27%)	5 (6%)	1	2
18	G	161/175 (92%)	126 (78%)	31 (19%)	4 (2%)	4	10
19	H	143/145 (99%)	125 (87%)	15 (10%)	3 (2%)	5	13
20	h	78/80 (98%)	60 (77%)	17 (22%)	1 (1%)	9	21
21	I	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	31
22	i	54/56 (96%)	42 (78%)	10 (18%)	2 (4%)	2	5
23	j	73/78 (94%)	56 (77%)	15 (20%)	2 (3%)	4	9
24	J	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	5	13
25	k	200/202 (99%)	159 (80%)	35 (18%)	6 (3%)	3	8
26	K	135/137 (98%)	119 (88%)	13 (10%)	3 (2%)	5	12
27	L	118/120 (98%)	108 (92%)	9 (8%)	1 (1%)	16	31
28	l	196/198 (99%)	154 (79%)	33 (17%)	9 (5%)	2	3
29	m	154/156 (99%)	116 (75%)	32 (21%)	6 (4%)	2	4
30	M	117/119 (98%)	98 (84%)	15 (13%)	4 (3%)	3	6
31	n	93/95 (98%)	72 (77%)	19 (20%)	2 (2%)	5	12
32	N	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	6	15
33	o	128/130 (98%)	88 (69%)	35 (27%)	5 (4%)	2	4
34	O	114/116 (98%)	108 (95%)	3 (3%)	3 (3%)	4	9
35	p	150/155 (97%)	127 (85%)	20 (13%)	3 (2%)	6	13
36	P	100/102 (98%)	84 (84%)	14 (14%)	2 (2%)	6	13
37	q	125/127 (98%)	98 (78%)	23 (18%)	4 (3%)	3	7
38	Q	110/112 (98%)	96 (87%)	13 (12%)	1 (1%)	14	28
39	R	87/89 (98%)	77 (88%)	8 (9%)	2 (2%)	5	11
40	S	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	2	4
41	T	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	5	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	U	77/79 (98%)	69 (90%)	6 (8%)	2 (3%)	4	9
43	V	47/49 (96%)	39 (83%)	6 (13%)	2 (4%)	2	4
44	W	65/67 (97%)	58 (89%)	6 (9%)	1 (2%)	8	18
45	Z	45/47 (96%)	38 (84%)	5 (11%)	2 (4%)	2	3
46	F	151/158 (96%)	110 (73%)	32 (21%)	9 (6%)	1	2
All	All	4878/5094 (96%)	4016 (82%)	724 (15%)	138 (3%)	6	9

5 of 138 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	a	63	GLU
10	c	57	LYS
12	d	95	LEU
13	D	71	LYS
17	g	66	LYS

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	
4	1	52/97 (54%)	44 (85%)	8 (15%)	2	5
4	A	44/97 (45%)	27 (61%)	17 (39%)	0	0
5	B	39/39 (100%)	32 (82%)	7 (18%)	2	3
6	2	55/55 (100%)	42 (76%)	13 (24%)	1	0
7	4	35/35 (100%)	29 (83%)	6 (17%)	2	3
8	a	67/73 (92%)	42 (63%)	25 (37%)	0	0
9	b	85/90 (94%)	67 (79%)	18 (21%)	1	1
10	c	95/118 (80%)	72 (76%)	23 (24%)	1	0
11	C	221/221 (100%)	189 (86%)	32 (14%)	3	6
12	d	75/97 (77%)	53 (71%)	22 (29%)	0	0
13	D	173/173 (100%)	130 (75%)	43 (25%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	E	168/168 (100%)	136 (81%)	32 (19%)	1	2
15	e	51/52 (98%)	33 (65%)	18 (35%)	0	0
16	f	74/80 (92%)	61 (82%)	13 (18%)	2	3
17	g	36/70 (51%)	19 (53%)	17 (47%)	0	0
18	G	115/153 (75%)	78 (68%)	37 (32%)	0	0
19	H	122/123 (99%)	108 (88%)	14 (12%)	5	10
20	h	35/75 (47%)	24 (69%)	11 (31%)	0	0
21	I	100/100 (100%)	82 (82%)	18 (18%)	2	3
22	i	49/50 (98%)	32 (65%)	17 (35%)	0	0
23	j	37/65 (57%)	19 (51%)	18 (49%)	0	0
24	J	109/112 (97%)	84 (77%)	25 (23%)	1	0
25	k	151/164 (92%)	114 (76%)	37 (24%)	1	0
26	K	108/114 (95%)	91 (84%)	17 (16%)	2	4
27	L	96/101 (95%)	77 (80%)	19 (20%)	1	2
28	l	23/174 (13%)	17 (74%)	6 (26%)	0	0
29	m	120/122 (98%)	73 (61%)	47 (39%)	0	0
30	M	83/95 (87%)	56 (68%)	27 (32%)	0	0
31	n	82/83 (99%)	63 (77%)	19 (23%)	1	0
32	N	93/100 (93%)	73 (78%)	20 (22%)	1	1
33	o	107/111 (96%)	74 (69%)	33 (31%)	0	0
34	O	96/96 (100%)	81 (84%)	15 (16%)	2	4
35	p	114/131 (87%)	83 (73%)	31 (27%)	0	0
36	P	84/86 (98%)	62 (74%)	22 (26%)	0	0
37	q	96/105 (91%)	65 (68%)	31 (32%)	0	0
38	Q	89/91 (98%)	74 (83%)	15 (17%)	2	3
39	R	78/80 (98%)	58 (74%)	20 (26%)	0	0
40	S	81/88 (92%)	59 (73%)	22 (27%)	0	0
41	T	78/82 (95%)	63 (81%)	15 (19%)	1	2
42	U	59/62 (95%)	44 (75%)	15 (25%)	0	0
43	V	39/41 (95%)	32 (82%)	7 (18%)	2	3
44	W	58/60 (97%)	42 (72%)	16 (28%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	Z	35/43 (81%)	29 (83%)	6 (17%)	2	3
All	All	3607/4172 (86%)	2733 (76%)	874 (24%)	2	0

5 of 874 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	K	13	HIS
30	M	90	LYS
40	S	67	ASN
26	K	113	VAL
25	k	203	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
36	P	28	ASN
37	q	16	ASN
41	T	13	GLN
14	E	46	GLN
14	E	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Y	2709/2923 (92%)	1007 (37%)	48 (1%)
2	X	1436/1552 (92%)	1030 (71%)	56 (3%)
3	3	113/114 (99%)	47 (41%)	2 (1%)
All	All	4258/4589 (92%)	2084 (48%)	106 (2%)

5 of 2084 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Y	10	A
1	Y	11	U
1	Y	12	U
1	Y	14	A
1	Y	34	U

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	X	334	G
2	X	730	G
2	X	1431	U
2	X	384	G
2	X	589	G

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.

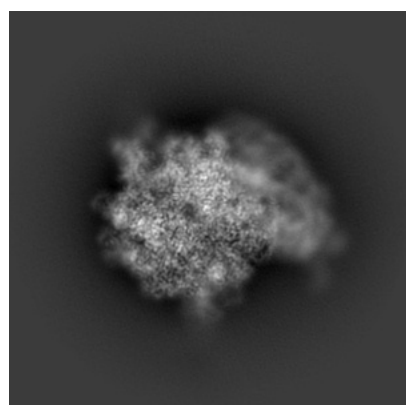
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11903. These allow visual inspection of the internal detail of the map and identification of artifacts.

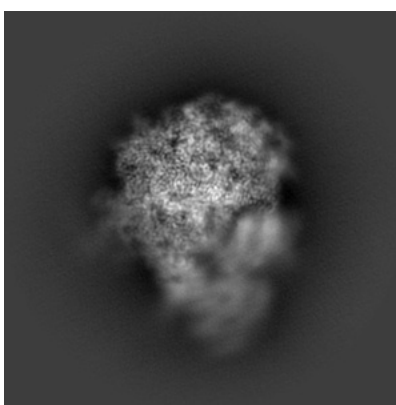
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

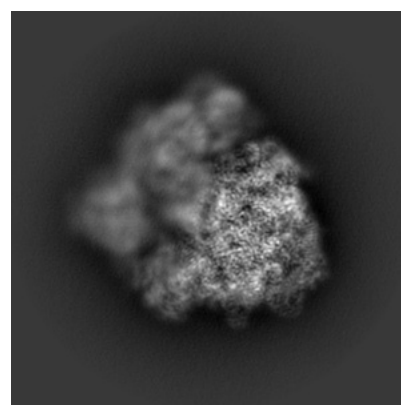
6.1.1 Primary map



X



Y

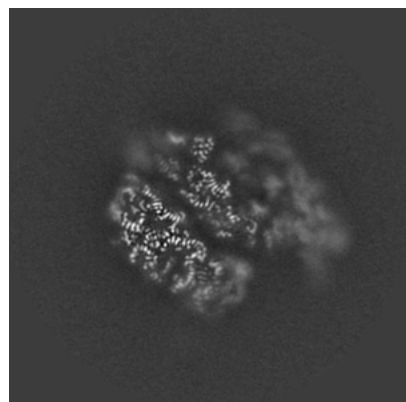


Z

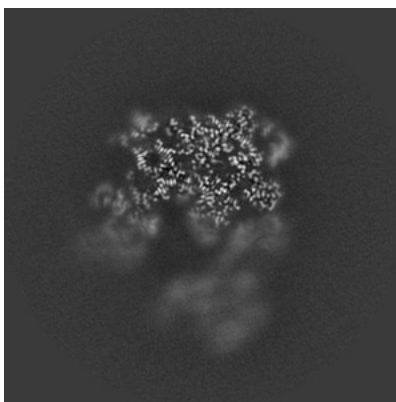
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

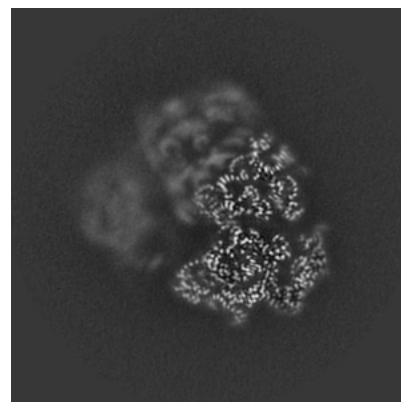
6.2.1 Primary map



X Index: 240



Y Index: 240

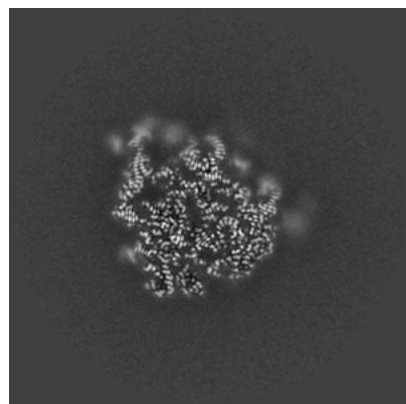


Z Index: 240

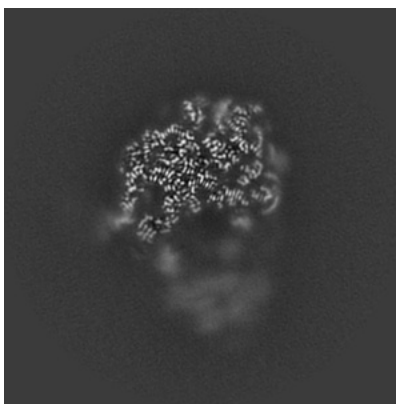
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

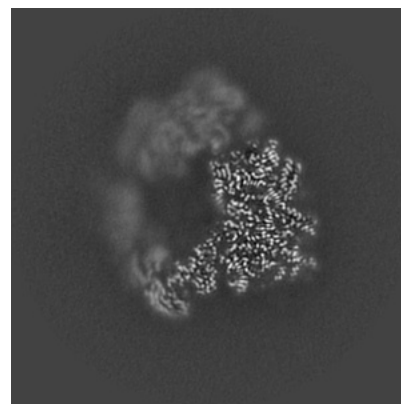
6.3.1 Primary map



X Index: 294



Y Index: 206

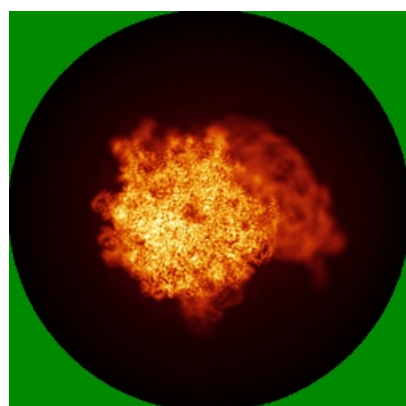


Z Index: 213

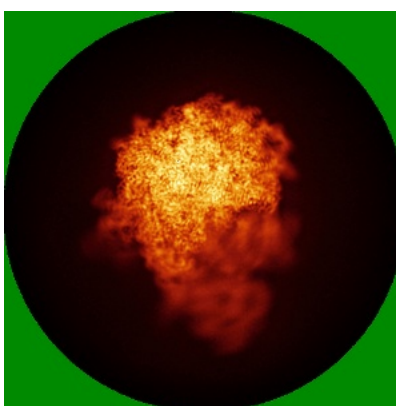
The images above show the largest variance slices of the map in three orthogonal directions.

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

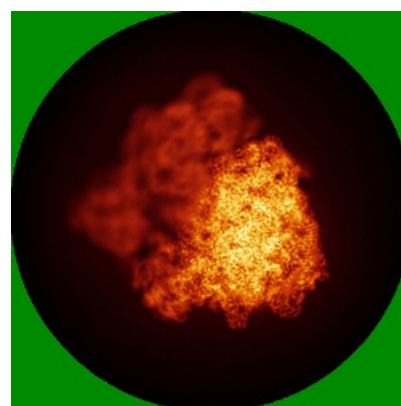
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

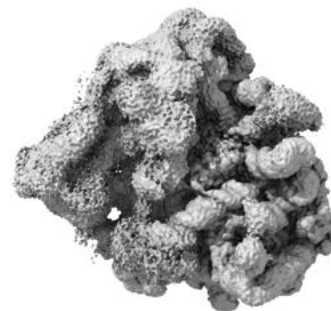
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

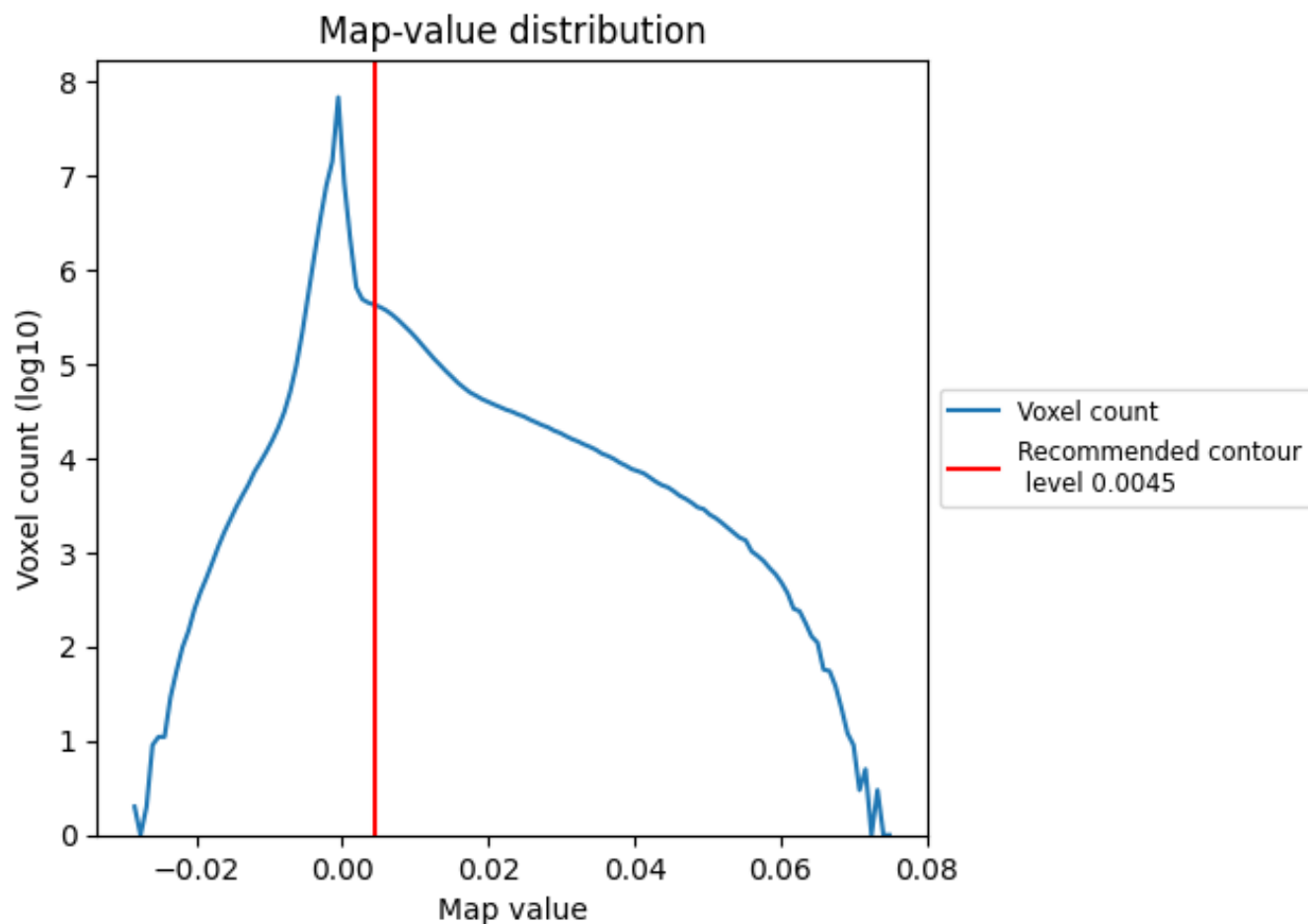
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

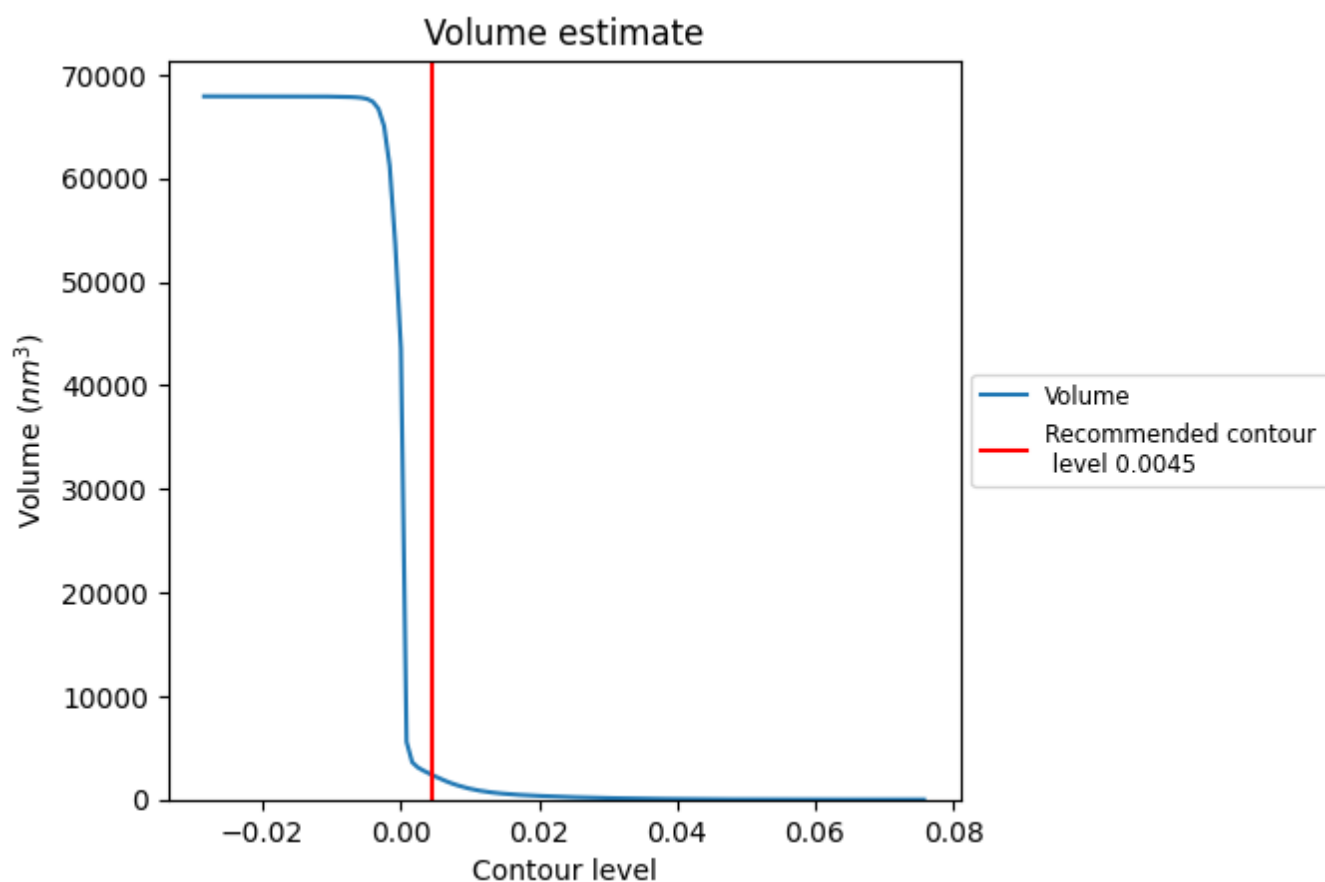
This section contains the results of statistical analysis of the map.

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.

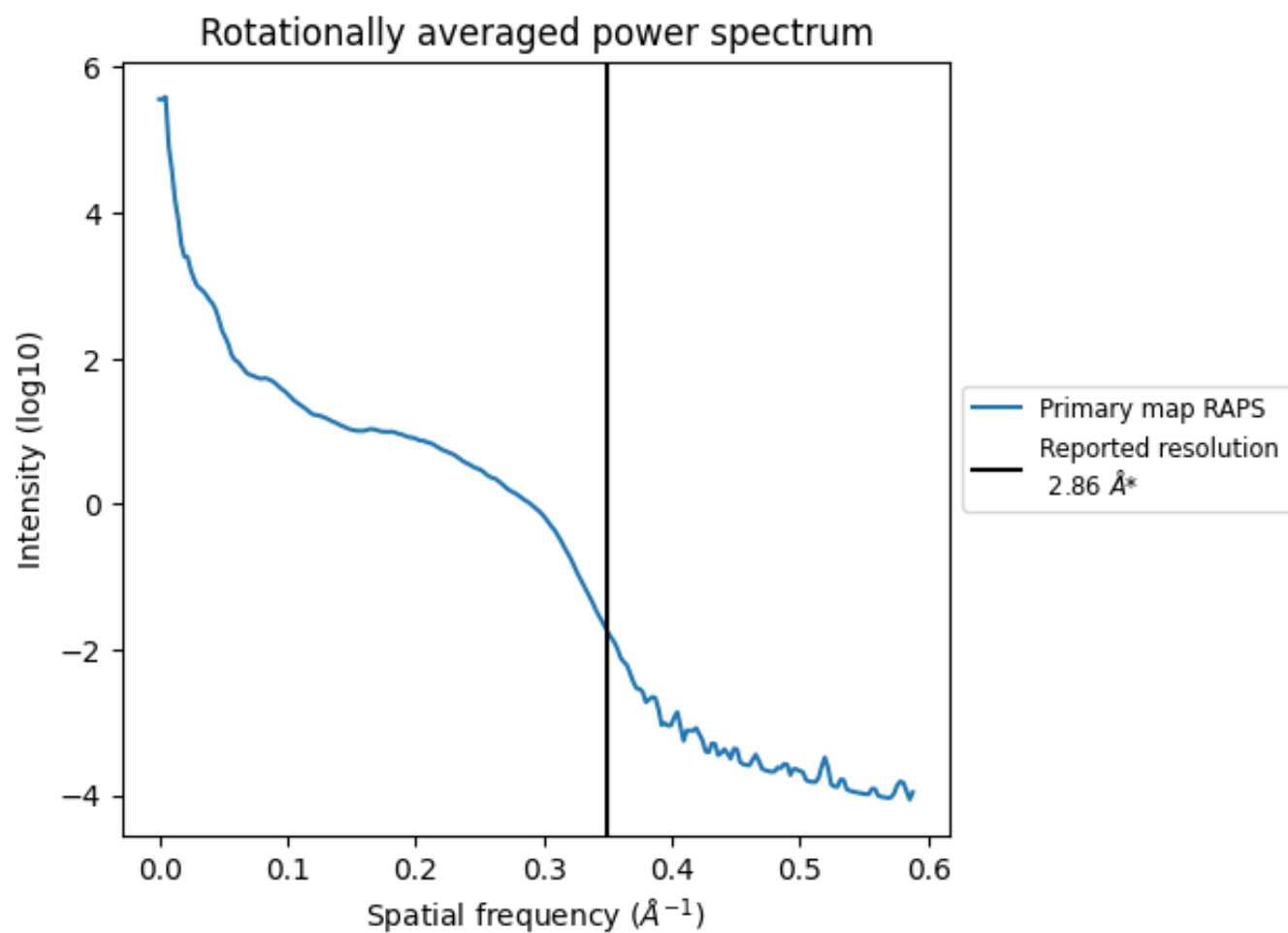
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2394 nm^3 ; this corresponds to an approximate mass of 2163 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 0.350 Å⁻¹

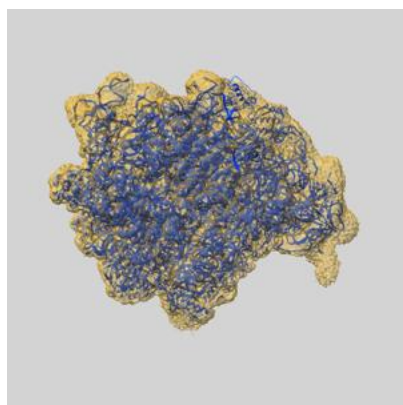
8 Fourier-Shell correlation

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

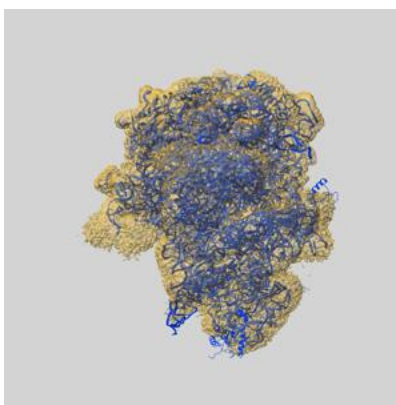
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11903 and PDB model 7ASP. Per-residue inclusion information can be found in section [3](#) on page [12](#).

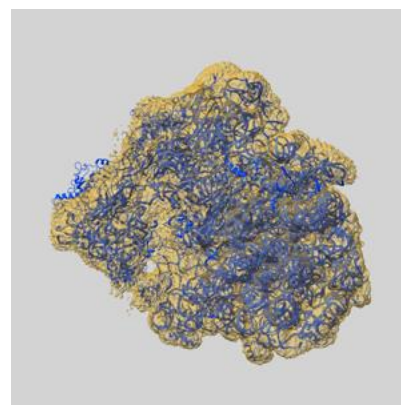
9.1 Map-model overlay [i](#)



X



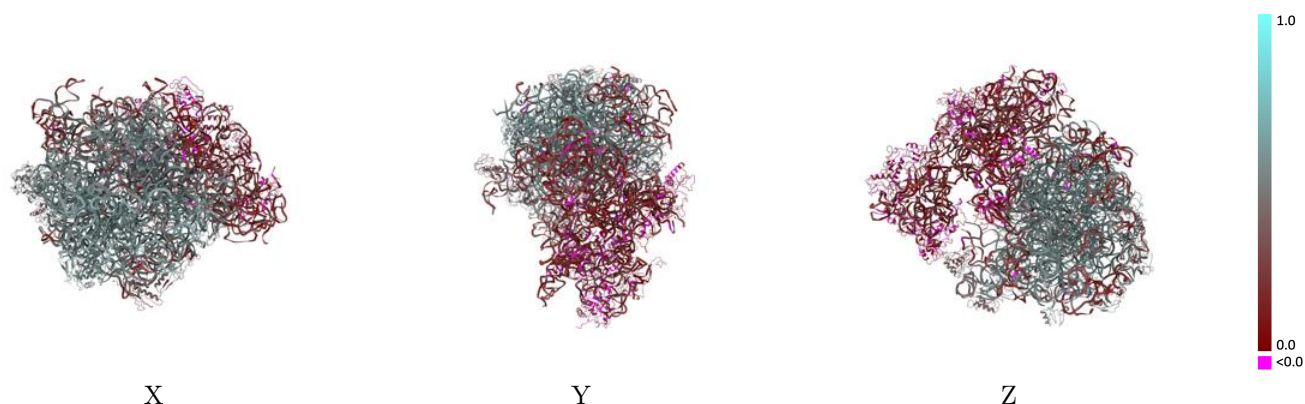
Y



Z

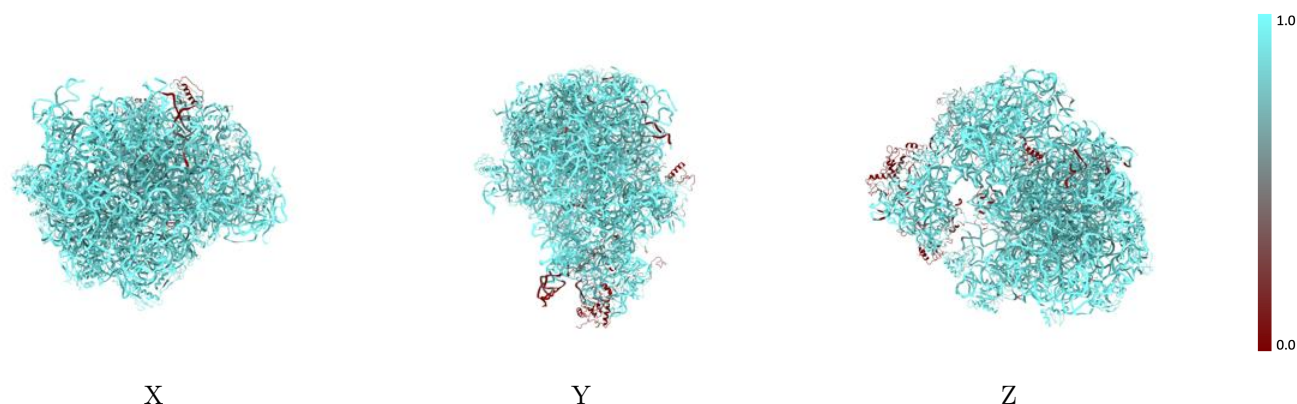
The images above show the 3D surface view of the map at the recommended contour level 0.0045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



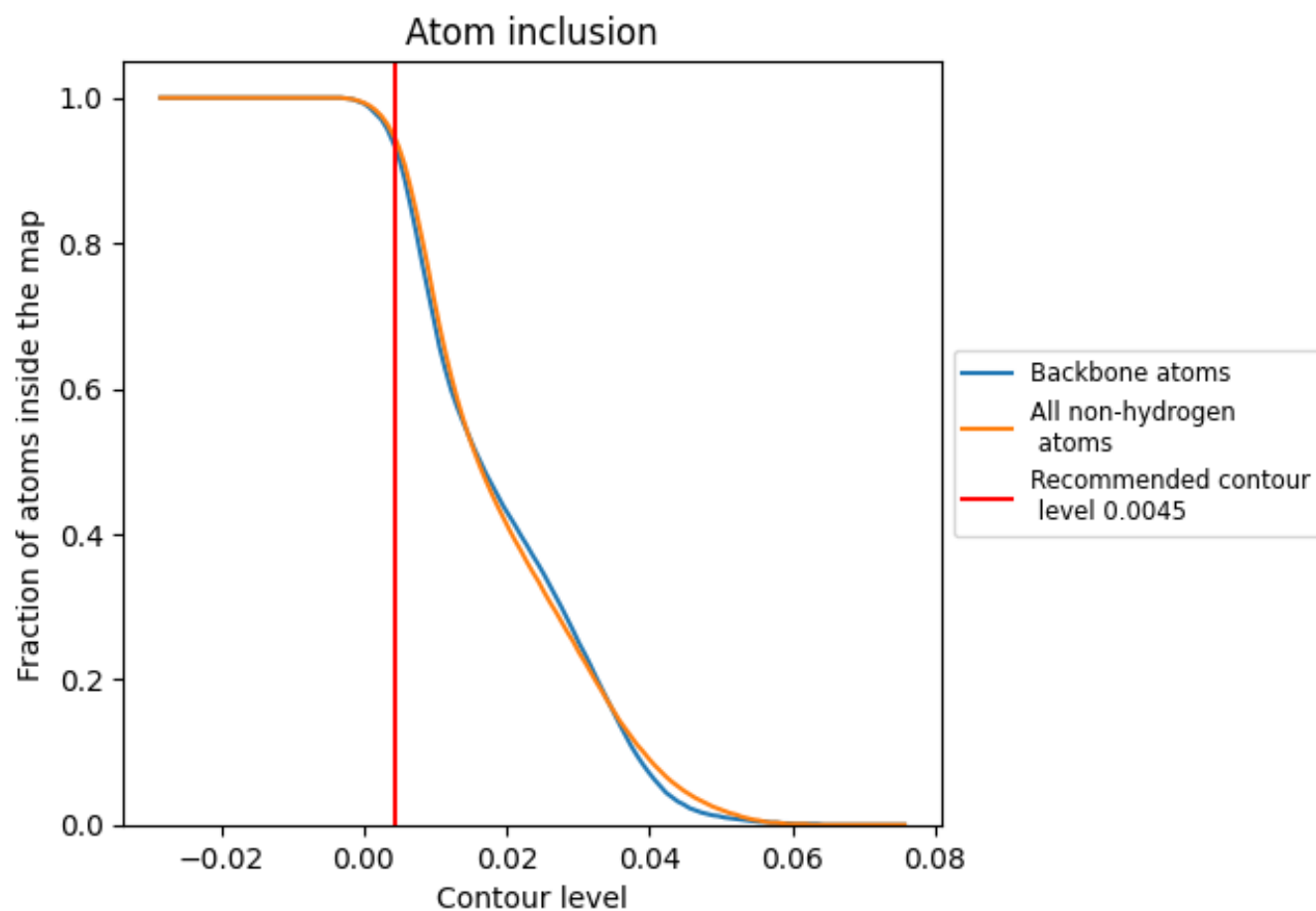
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0045).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.0045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.3760
1	 0.9820	 0.5540
2	 0.9760	 0.5590
3	 0.9980	 0.4340
4	 0.9340	 0.5020
A	 0.8800	 0.4910
B	 0.9830	 0.5810
C	 0.9670	 0.5420
D	 0.9770	 0.5480
E	 0.9810	 0.5310
F	 0.9910	 0.3300
G	 0.9660	 0.2980
H	 0.9810	 0.5560
I	 0.9740	 0.5610
J	 0.9880	 0.5380
K	 0.9800	 0.5410
L	 0.9810	 0.5530
M	 0.9920	 0.4440
N	 0.9620	 0.5490
O	 0.9860	 0.5680
P	 0.9880	 0.5600
Q	 0.9710	 0.5490
R	 0.9830	 0.5250
S	 0.9800	 0.4750
T	 0.9450	 0.4880
U	 0.9670	 0.5580
V	 0.9780	 0.5240
W	 0.9890	 0.4400
X	 0.9560	 0.1800
Y	 0.9810	 0.4900
Z	 0.9850	 0.5060
a	 0.6290	 0.0890
b	 0.6160	 0.0970
c	 0.5690	 0.1800
d	 0.5130	 0.0780



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Chain	Atom inclusion	Q-score
e	 0.4830	 0.0600
f	 0.9010	 0.1860
g	 0.8350	 0.0730
h	 0.9060	 0.1110
i	 0.8730	 0.1350
j	 0.9780	 0.1810
k	 0.4020	 0.0840
l	 0.7630	 0.0860
m	 0.7940	 0.0820
n	 0.4670	 0.0870
o	 0.8880	 0.1140
p	 0.7240	 0.0840
q	 0.7210	 0.1080