



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 05:46 am GMT

PDB ID : 6SWA
EMDB ID : EMD-10321
Title : Mus musculus brain neocortex ribosome 60S bound to Ebp1
Authors : Kraushar, M.L.; Sprink, T.
Deposited on : 2019-09-20
Resolution : 3.10 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

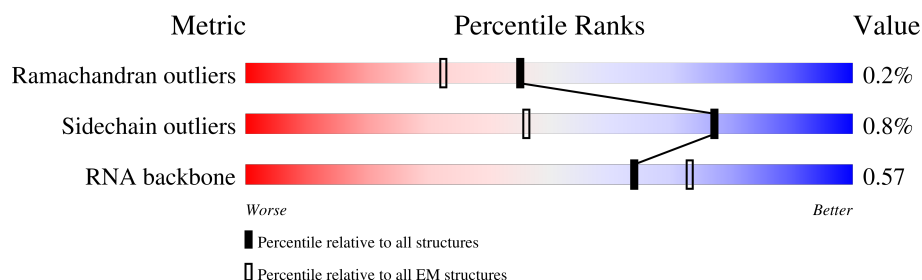
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	252	 7% 99%
2	B	394	 6% 99%
3	C	363	 9% 100%
4	D	294	 11% 100%
5	E	194	 18% 99%
6	F	234	 11% 100%
7	G	234	 18% 99%
8	H	191	 6% 100%

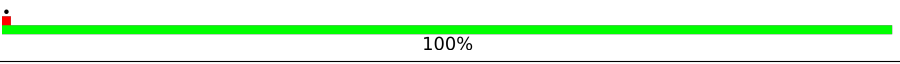
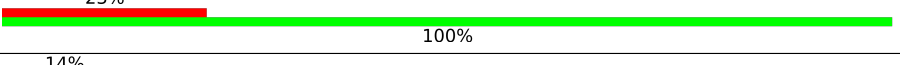
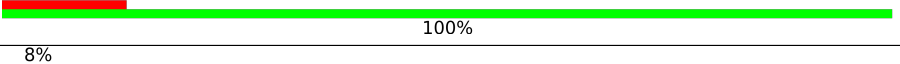
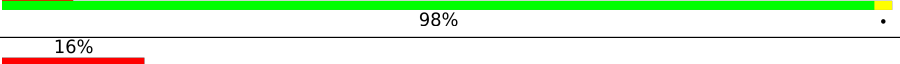
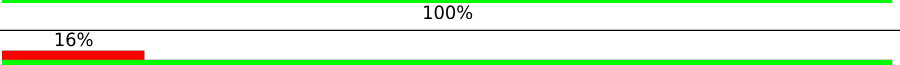
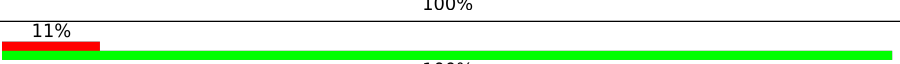
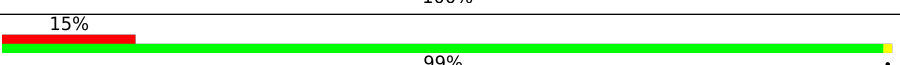
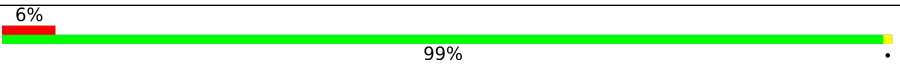
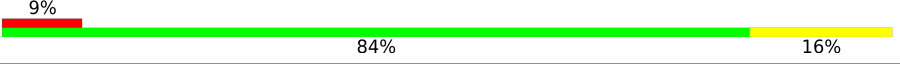
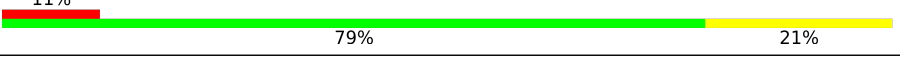
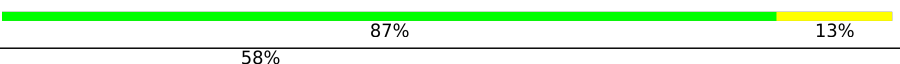
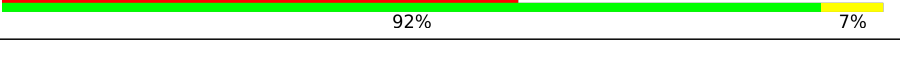

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	211	11% 99%
10	J	169	21% 99%
11	K	205	17% 100%
12	L	139	5% 100%
13	M	203	1% 100%
14	N	195	1% 99%
15	O	153	5% 100%
16	P	185	6% 100%
17	Q	175	1% 99%
18	R	157	6% 99%
19	S	101	17% 99%
20	T	129	6% 99%
21	U	62	11% 100%
22	V	118	12% 98%
23	W	127	5% 99%
24	X	134	10% 98%
25	Y	147	5% 100%
26	Z	68	18% 100%
27	a	97	6% 100%
28	b	106	10% 99%
29	c	129	8% 99%
30	d	109	5% 100%
31	e	114	8% 98%
32	f	122	10% 100%
33	g	98	17% 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	h	84	
35	i	69	
36	j	50	
37	k	50	
38	l	25	
39	m	105	
40	n	91	
41	o	184	
42	p	122	
43	q	3612	
44	r	157	
45	s	119	
46	t	353	

2 Entry composition

There are 48 unique types of molecules in this entry. The entry contains 138160 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	252	Total	C	N	O	S	0	0
			1930	1209	395	320	6		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	394	Total	C	N	O	S	0	0
			3178	2024	597	543	14		

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	363	Total	C	N	O	S	0	0
			2897	1822	578	482	15		

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1509	442	430	14		

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	194	Total	C	N	O	S	0	0
			1576	1008	296	270	2		

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	234	Total	C	N	O	S	0	0
			1947	1251	375	313	8		

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	234	Total	C	N	O	S	0	0
			1879	1197	361	317	4		

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1527	960	285	276	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	205	Total	C	N	O	S	0	0
			1660	1038	342	276	4		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	139	Total	C	N	O	S	0	0
			1143	732	221	183	7		

- Molecule 13 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	195	Total	C	N	O	S	0	0
			1599	1029	314	250	6		

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	185	Total	C	N	O	S	0	0
			1504	941	312	247	4		

- Molecule 17 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	175	Total	C	N	O	S	0	0
			1447	920	283	233	11		

- Molecule 18 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	157	Total	C	N	O	S	0	0
			1284	815	251	213	5		

- Molecule 19 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	101	Total	C	N	O	S	0	0
			826	529	145	150	2		

- Molecule 20 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 21 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	62	Total	C	N	O	S	0	0
			520	332	102	84	2		

- Molecule 22 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	118	Total	C	N	O	S	0	0
			966	618	181	166	1		

- Molecule 23 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 24 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 25 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	68	Total	C	N	O	S	0	0
			558	344	122	90	2		

- Molecule 27 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	97	Total	C	N	O	S	0	0
			753	478	133	135	7		

- Molecule 28 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 29 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 30 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 31 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	98	Total	C	N	O	S	0	0
			802	499	168	130	5		

- Molecule 34 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 36 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 37 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 38 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 39 is a protein called Ribosomal protein L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 40 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 41 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	184	Total	C	N	O	S	0	0
			1542	955	332	246	9		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	122	Total	C	N	O	S	0	0
			980	606	204	165	5		

- Molecule 43 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	3612	Total	C	N	O	P	0	0
			77430	34484	14158	25176	3612		

- Molecule 44 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 45 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 46 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	353	Total	C	N	O	S	0	0
			2739	1729	470	523	17		

- Molecule 47 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
47	B	1	Total	Mg	0
			1	1	
47	K	1	Total	Mg	0
			1	1	
47	M	1	Total	Mg	0
			1	1	
47	P	1	Total	Mg	0
			1	1	
47	W	1	Total	Mg	0
			1	1	
47	b	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
47	c	1	Total 1	Mg 1	0
47	l	1	Total 1	Mg 1	0
47	q	223	Total 223	Mg 223	0
47	r	7	Total 7	Mg 7	0
47	s	9	Total 9	Mg 9	0

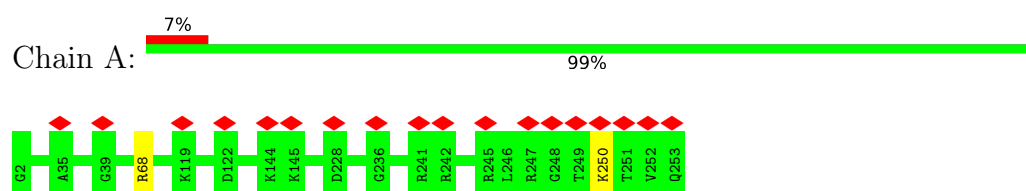
- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
48	h	1	Total 1	Zn 1	0
48	m	1	Total 1	Zn 1	0
48	n	1	Total 1	Zn 1	0

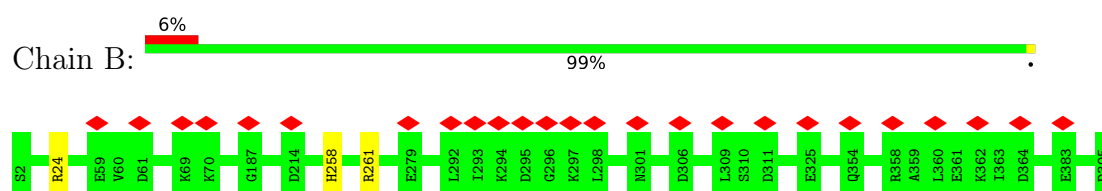
3 Residue-property plots

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

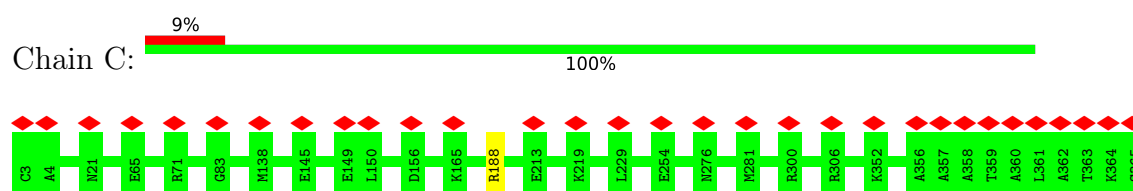
- Molecule 1: 60S ribosomal protein L8



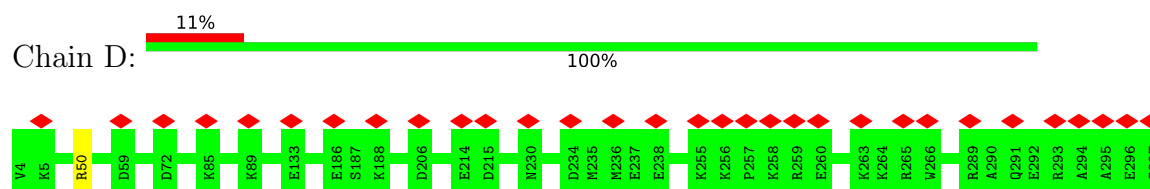
- Molecule 2: 60S ribosomal protein L3



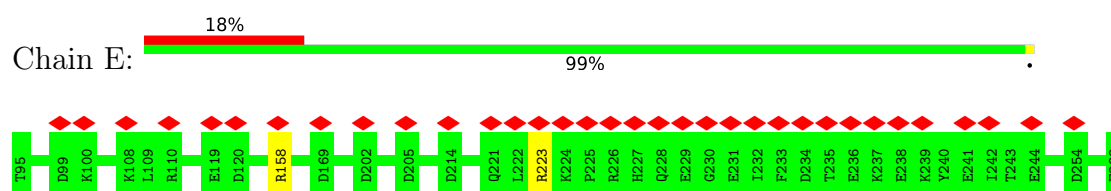
- Molecule 3: 60S ribosomal protein L4



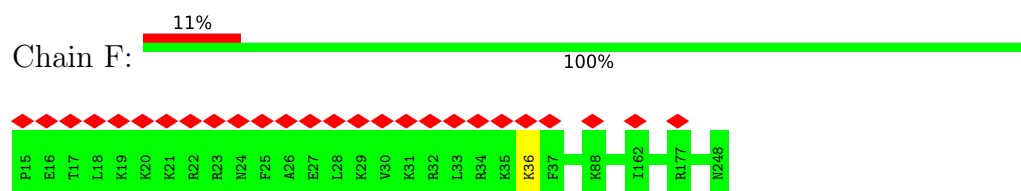
- Molecule 4: 60S ribosomal protein L5



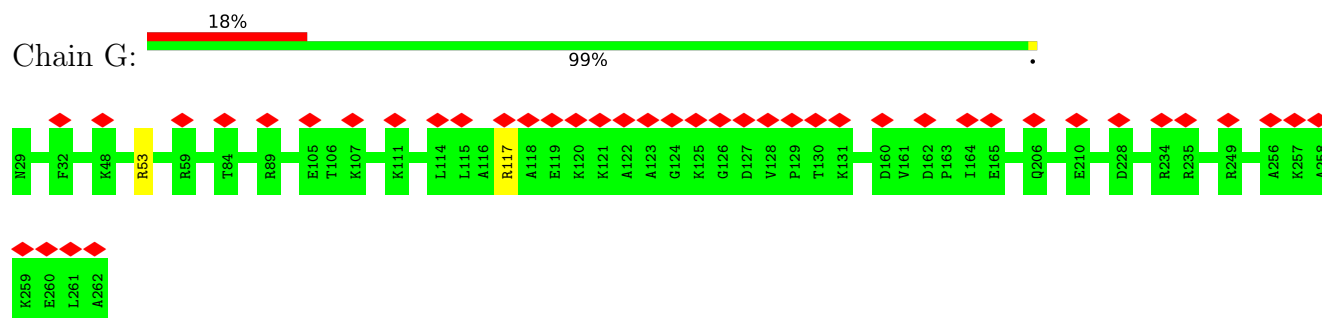
- Molecule 5: 60S ribosomal protein L6



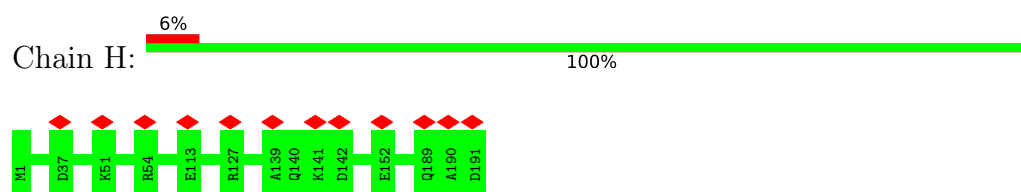
- Molecule 6: 60S ribosomal protein L7



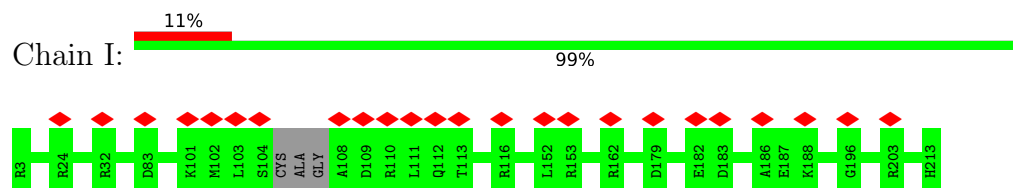
- Molecule 7: 60S ribosomal protein L7a



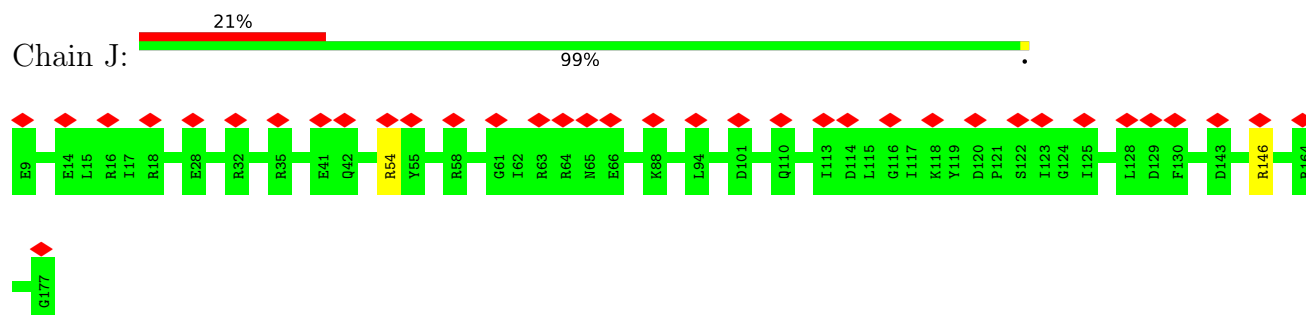
- Molecule 8: 60S ribosomal protein L9



- Molecule 9: 60S ribosomal protein L10

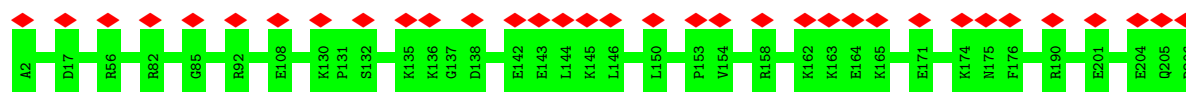


- Molecule 10: 60S ribosomal protein L11

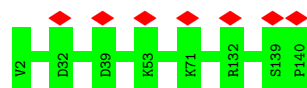


- Molecule 11: 60S ribosomal protein L13

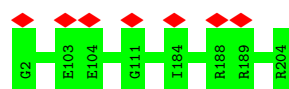




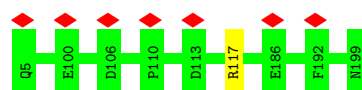
- Molecule 12: 60S ribosomal protein L14



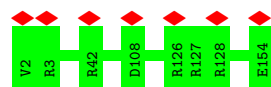
- Molecule 13: 60S ribosomal protein L15



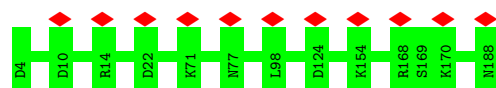
- Molecule 14: 60S ribosomal protein L13a



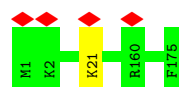
- Molecule 15: 60S ribosomal protein L17



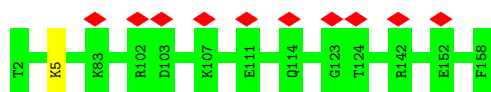
- Molecule 16: 60S ribosomal protein L18



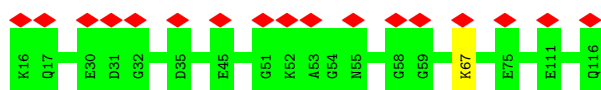
- Molecule 17: 60S ribosomal protein L18a



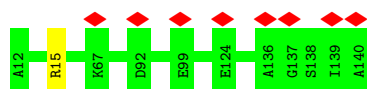
- Molecule 18: 60S ribosomal protein L21



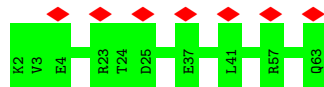
- Molecule 19: 60S ribosomal protein L22



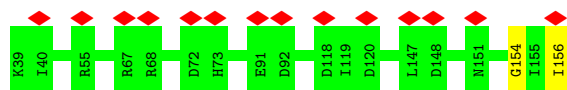
- Molecule 20: 60S ribosomal protein L23



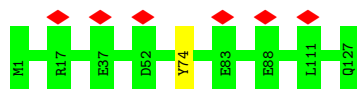
- Molecule 21: 60S ribosomal protein L24



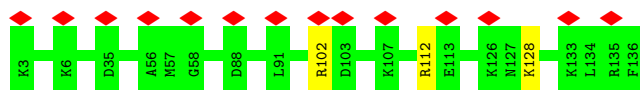
- Molecule 22: 60S ribosomal protein L23a



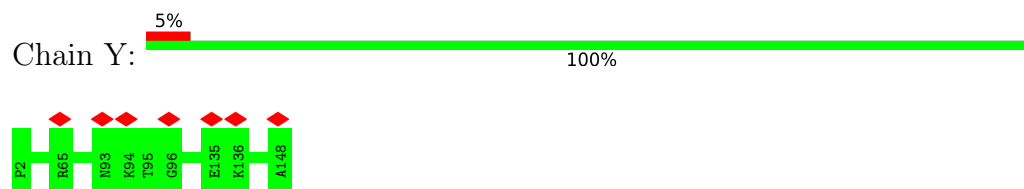
- Molecule 23: Ribosomal protein L26



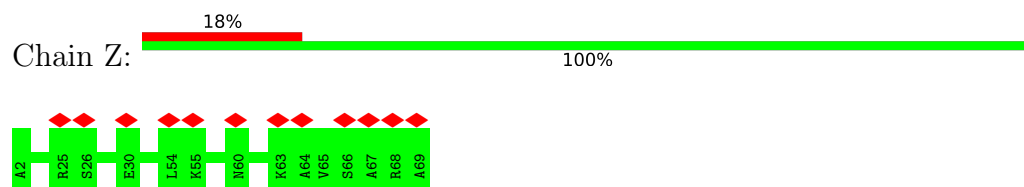
- Molecule 24: 60S ribosomal protein L27



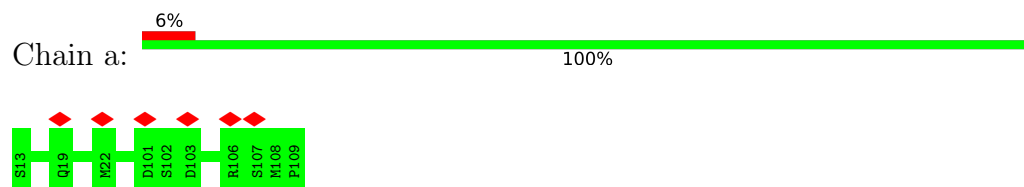
- Molecule 25: 60S ribosomal protein L27a



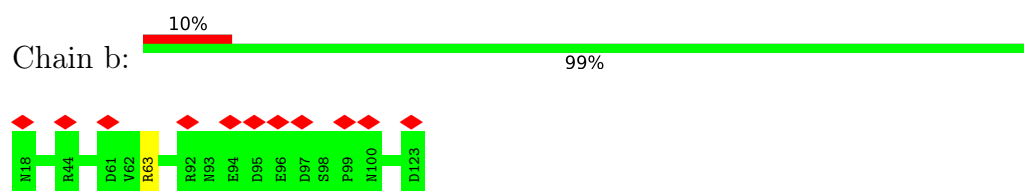
- Molecule 26: 60S ribosomal protein L29



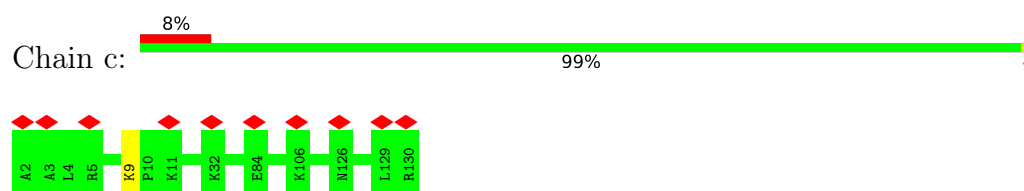
- Molecule 27: 60S ribosomal protein L30



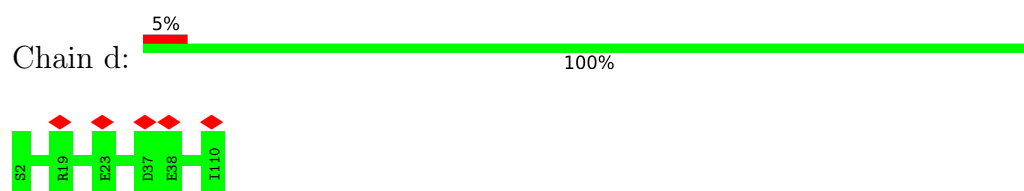
- Molecule 28: 60S ribosomal protein L31



- Molecule 29: 60S ribosomal protein L32

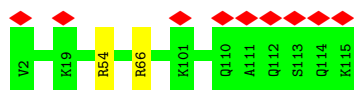


- Molecule 30: 60S ribosomal protein L35a

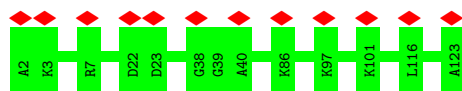


- Molecule 31: 60S ribosomal protein L34

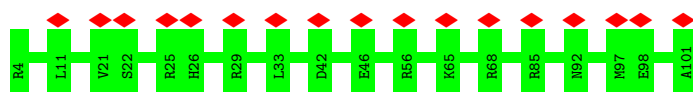




- Molecule 32: 60S ribosomal protein L35



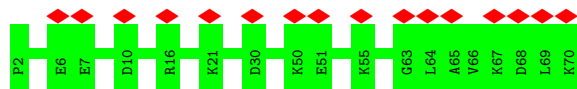
- Molecule 33: 60S ribosomal protein L36



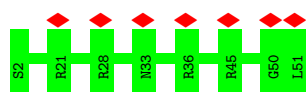
- Molecule 34: 60S ribosomal protein L37



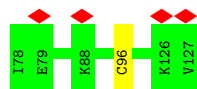
- Molecule 35: 60S ribosomal protein L38



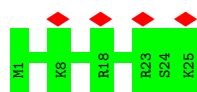
- Molecule 36: Ribosomal protein L39



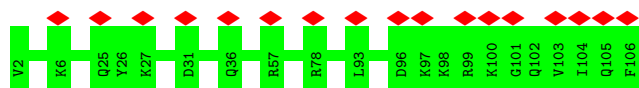
- Molecule 37: 60S ribosomal protein L40



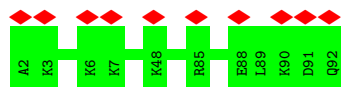
- Molecule 38: 60S ribosomal protein L41



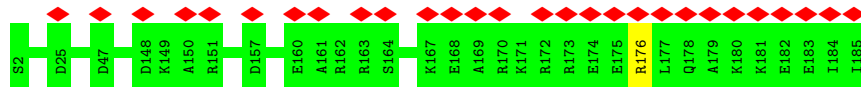
- Molecule 39: Ribosomal protein L36A



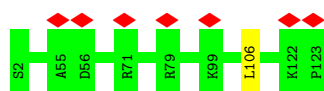
- Molecule 40: Ribosomal protein L37a



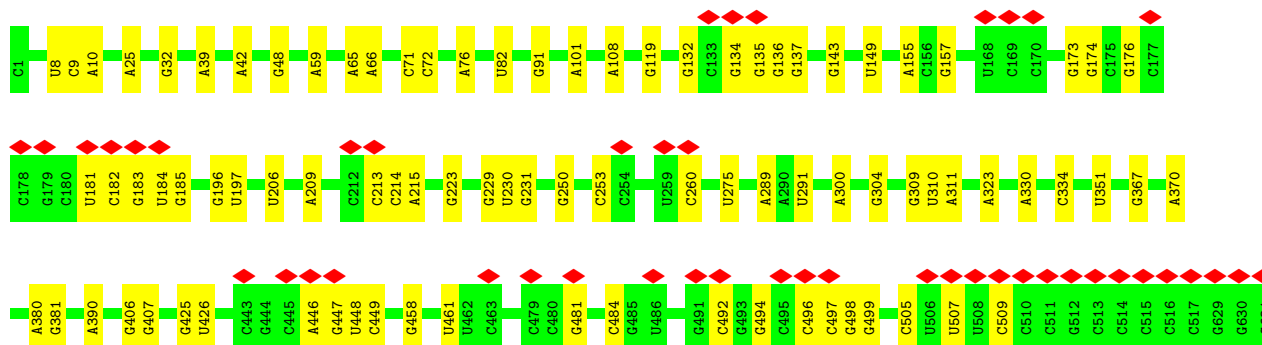
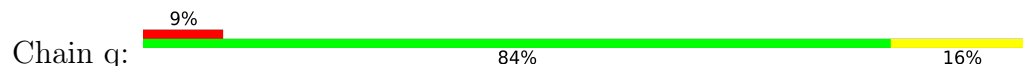
- Molecule 41: 60S ribosomal protein L19

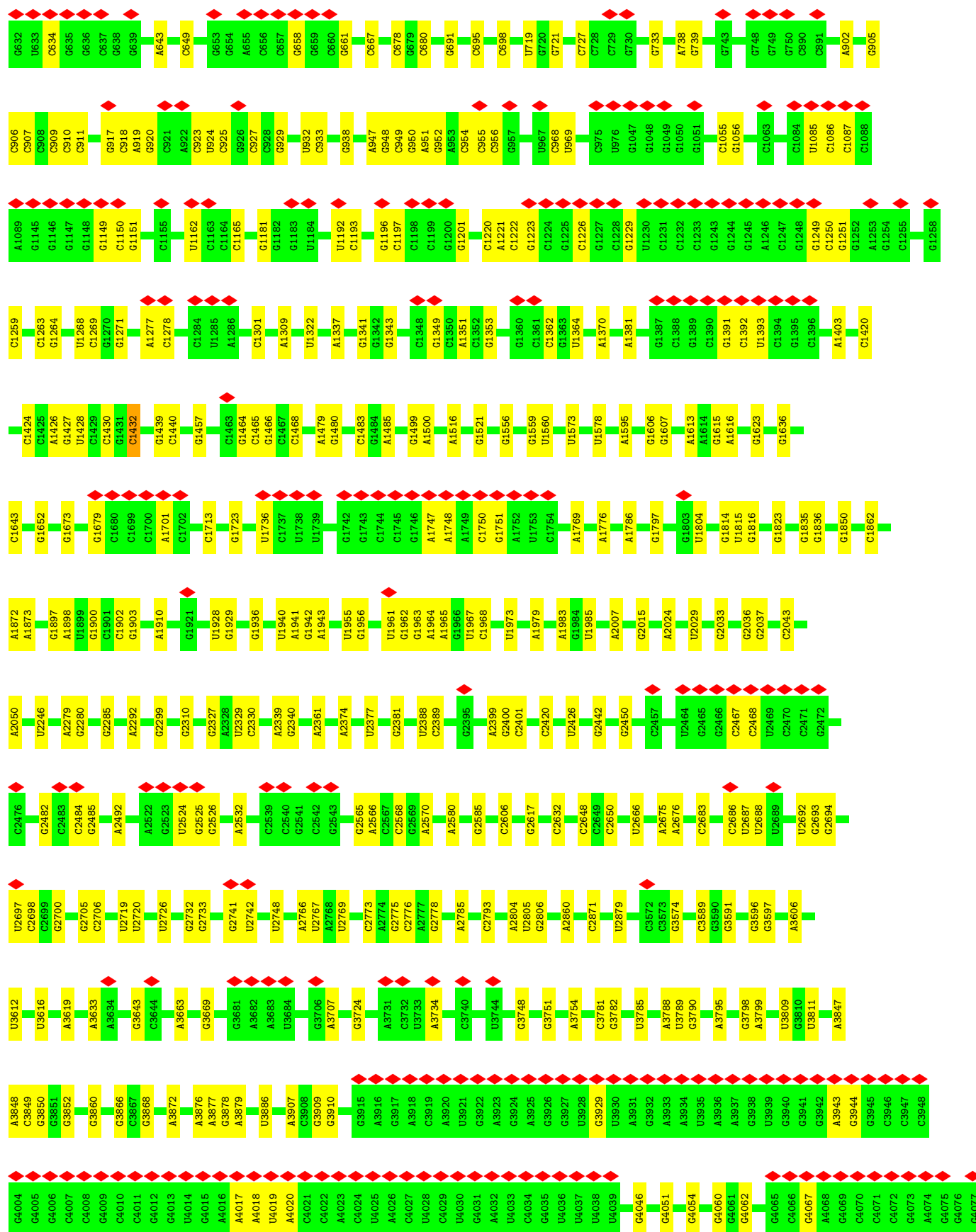


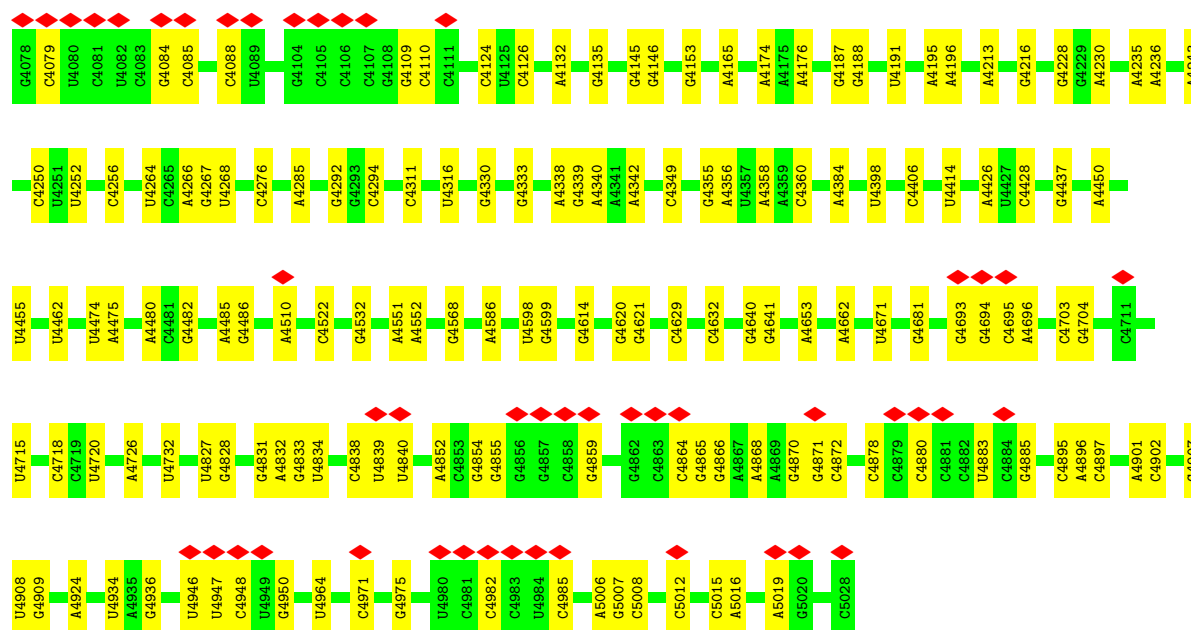
- Molecule 42: 60S ribosomal protein L28



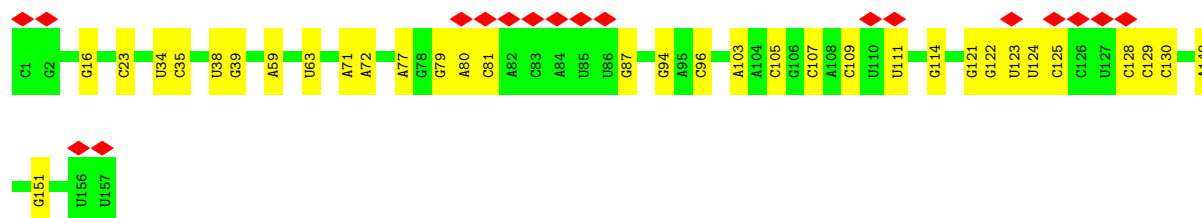
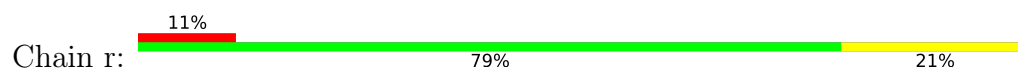
- Molecule 43: 28S ribosomal RNA



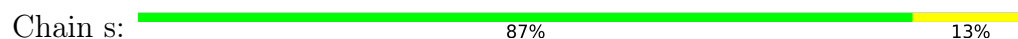




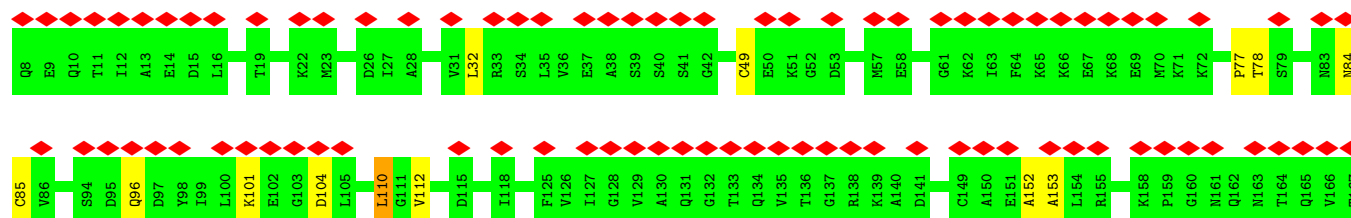
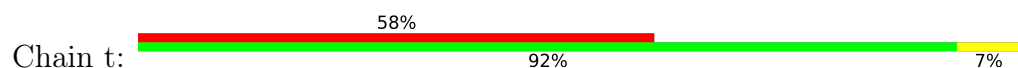
• Molecule 44: 5.8S ribosomal RNA

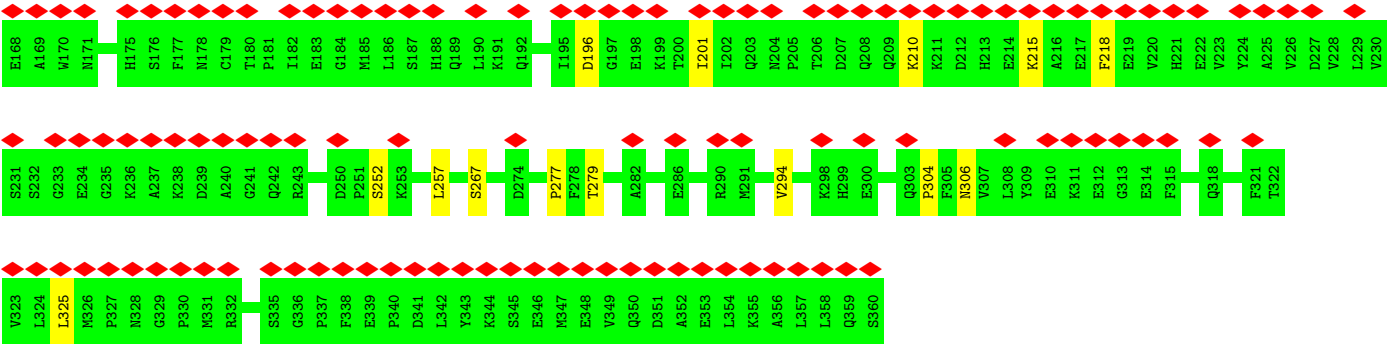


• Molecule 45: 5S ribosomal RNA



• Molecule 46: Proliferation-associated protein 2G4





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	208206	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 ($e^-/\text{\AA}^2$)	31.78	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.986	Depositor
Minimum map value	-10.475	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.898	Depositor
Recommended contour level	4	Depositor
Map size (Å)	477.612, 477.612, 477.612	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3267, 1.3267, 1.3267	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.24	0/1968	0.44	0/2639
2	B	0.24	0/3245	0.42	0/4343
3	C	0.23	0/2951	0.39	0/3961
4	D	0.24	0/2440	0.39	0/3266
5	E	0.24	0/1607	0.43	0/2159
6	F	0.24	0/1983	0.38	0/2641
7	G	0.24	0/1913	0.42	0/2577
8	H	0.25	0/1545	0.44	0/2076
9	I	0.24	0/1730	0.40	0/2311
10	J	0.24	0/1376	0.41	0/1841
11	K	0.24	0/1691	0.41	0/2264
12	L	0.24	0/1165	0.39	0/1558
13	M	0.23	0/1746	0.39	0/2338
14	N	0.24	0/1629	0.39	0/2178
15	O	0.23	0/1268	0.41	0/1700
16	P	0.23	0/1528	0.40	0/2038
17	Q	0.24	0/1486	0.42	0/1994
18	R	0.24	0/1312	0.41	0/1752
19	S	0.25	0/840	0.43	0/1126
20	T	0.25	0/983	0.42	0/1319
21	U	0.24	0/533	0.37	0/710
22	V	0.24	0/983	0.41	0/1323
23	W	0.26	0/1081	0.42	0/1439
24	X	0.25	0/1126	0.39	0/1502
25	Y	0.24	0/1193	0.40	0/1593
26	Z	0.23	0/568	0.37	0/750
27	a	0.24	0/764	0.41	0/1026
28	b	0.23	0/894	0.43	0/1204
29	c	0.23	0/1082	0.40	0/1443
30	d	0.25	0/895	0.43	0/1198
31	e	0.24	0/916	0.42	0/1221
32	f	0.23	0/1023	0.38	0/1350

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.23	0/813	0.38	0/1078
34	h	0.26	0/703	0.44	0/929
35	i	0.24	0/574	0.41	0/760
36	j	0.22	0/453	0.39	0/599
37	k	0.30	0/417	0.46	0/553
38	l	0.21	0/241	0.32	0/305
39	m	0.24	0/877	0.40	0/1156
40	n	0.24	0/718	0.40	0/953
41	o	0.22	0/1558	0.36	0/2059
42	p	0.23	0/995	0.45	1/1333 (0.1%)
43	q	0.17	0/86618	0.74	13/135116 (0.0%)
44	r	0.16	0/3726	0.74	0/5804
45	s	0.19	0/2839	0.76	1/4425 (0.0%)
46	t	0.28	0/2786	0.51	0/3753
All	All	0.20	0/148782	0.65	15/219663 (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
2	B	0	1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	q	909	C	N1-C2-O2	10.02	124.91	118.90
43	q	909	C	N3-C2-O2	-9.96	114.93	121.90
43	q	2650	C	N3-C2-O2	-6.87	117.09	121.90
43	q	667	C	N3-C2-O2	-6.85	117.11	121.90
43	q	2388	U	C2-N1-C1'	6.76	125.81	117.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	258	HIS	Peptide

5.2 Too-close contacts ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	250/252 (99%)	234 (94%)	16 (6%)	0	100	100
2	B	392/394 (100%)	377 (96%)	15 (4%)	0	100	100
3	C	361/363 (99%)	344 (95%)	17 (5%)	0	100	100
4	D	292/294 (99%)	283 (97%)	9 (3%)	0	100	100
5	E	192/194 (99%)	178 (93%)	14 (7%)	0	100	100
6	F	232/234 (99%)	223 (96%)	9 (4%)	0	100	100
7	G	232/234 (99%)	228 (98%)	4 (2%)	0	100	100
8	H	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
9	I	204/211 (97%)	200 (98%)	4 (2%)	0	100	100
10	J	167/169 (99%)	161 (96%)	6 (4%)	0	100	100
11	K	203/205 (99%)	185 (91%)	18 (9%)	0	100	100
12	L	137/139 (99%)	128 (93%)	9 (7%)	0	100	100
13	M	201/203 (99%)	197 (98%)	4 (2%)	0	100	100
14	N	193/195 (99%)	186 (96%)	7 (4%)	0	100	100
15	O	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
16	P	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
17	Q	173/175 (99%)	166 (96%)	7 (4%)	0	100	100
18	R	155/157 (99%)	149 (96%)	6 (4%)	0	100	100
19	S	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
20	T	127/129 (98%)	127 (100%)	0	0	100	100
21	U	60/62 (97%)	60 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	V	116/118 (98%)	113 (97%)	2 (2%)	1 (1%)	14	45
23	W	125/127 (98%)	124 (99%)	1 (1%)	0	100	100
24	X	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
25	Y	145/147 (99%)	140 (97%)	5 (3%)	0	100	100
26	Z	66/68 (97%)	61 (92%)	5 (8%)	0	100	100
27	a	95/97 (98%)	95 (100%)	0	0	100	100
28	b	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
29	c	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
30	d	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
31	e	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
32	f	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
33	g	96/98 (98%)	91 (95%)	5 (5%)	0	100	100
34	h	82/84 (98%)	79 (96%)	3 (4%)	0	100	100
35	i	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
36	j	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
37	k	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
38	l	23/25 (92%)	23 (100%)	0	0	100	100
39	m	103/105 (98%)	95 (92%)	8 (8%)	0	100	100
40	n	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
41	o	182/184 (99%)	181 (100%)	1 (0%)	0	100	100
42	p	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
46	t	351/353 (99%)	296 (84%)	43 (12%)	12 (3%)	3	17
All	All	6651/6742 (99%)	6356 (96%)	282 (4%)	13 (0%)	45	74

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	t	96	GLN
46	t	153	ALA
46	t	294	VAL
46	t	32	LEU
46	t	152	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	194/194 (100%)	192 (99%)	2 (1%)	73	86
2	B	342/342 (100%)	340 (99%)	2 (1%)	84	91
3	C	305/305 (100%)	304 (100%)	1 (0%)	91	95
4	D	247/247 (100%)	246 (100%)	1 (0%)	89	94
5	E	176/176 (100%)	174 (99%)	2 (1%)	70	84
6	F	204/204 (100%)	203 (100%)	1 (0%)	86	92
7	G	199/199 (100%)	197 (99%)	2 (1%)	73	86
8	H	170/170 (100%)	170 (100%)	0	100	100
9	I	178/179 (99%)	178 (100%)	0	100	100
10	J	142/142 (100%)	140 (99%)	2 (1%)	62	81
11	K	172/172 (100%)	172 (100%)	0	100	100
12	L	118/118 (100%)	118 (100%)	0	100	100
13	M	171/171 (100%)	171 (100%)	0	100	100
14	N	168/168 (100%)	167 (99%)	1 (1%)	84	91
15	O	134/134 (100%)	134 (100%)	0	100	100
16	P	163/163 (100%)	163 (100%)	0	100	100
17	Q	155/155 (100%)	154 (99%)	1 (1%)	84	91
18	R	137/137 (100%)	136 (99%)	1 (1%)	81	90
19	S	91/91 (100%)	90 (99%)	1 (1%)	70	84
20	T	100/100 (100%)	99 (99%)	1 (1%)	73	86
21	U	54/54 (100%)	54 (100%)	0	100	100
22	V	106/106 (100%)	105 (99%)	1 (1%)	75	88
23	W	119/119 (100%)	118 (99%)	1 (1%)	79	89
24	X	117/117 (100%)	114 (97%)	3 (3%)	41	68
25	Y	120/120 (100%)	120 (100%)	0	100	100
26	Z	58/58 (100%)	58 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	a	82/82 (100%)	82 (100%)	0	100	100
28	b	97/97 (100%)	96 (99%)	1 (1%)	73	86
29	c	115/115 (100%)	114 (99%)	1 (1%)	75	88
30	d	88/88 (100%)	88 (100%)	0	100	100
31	e	98/98 (100%)	96 (98%)	2 (2%)	50	74
32	f	109/109 (100%)	109 (100%)	0	100	100
33	g	85/85 (100%)	85 (100%)	0	100	100
34	h	71/71 (100%)	71 (100%)	0	100	100
35	i	64/64 (100%)	64 (100%)	0	100	100
36	j	47/47 (100%)	47 (100%)	0	100	100
37	k	46/46 (100%)	45 (98%)	1 (2%)	47	71
38	l	24/24 (100%)	24 (100%)	0	100	100
39	m	93/93 (100%)	93 (100%)	0	100	100
40	n	74/74 (100%)	74 (100%)	0	100	100
41	o	163/163 (100%)	162 (99%)	1 (1%)	84	91
42	p	106/106 (100%)	106 (100%)	0	100	100
46	t	297/302 (98%)	281 (95%)	16 (5%)	18	47
All	All	5799/5805 (100%)	5754 (99%)	45 (1%)	77	89

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	o	176	ARG
46	t	112	VAL
46	t	49	CYS
46	t	101	LYS
46	t	201	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
27	a	51	ASN
42	p	100	ASN
30	d	80	ASN
36	j	25	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
46	t	193	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	q	3600/3612 (99%)	569 (15%)	0
44	r	156/157 (99%)	33 (21%)	0
45	s	118/119 (99%)	15 (12%)	0
All	All	3874/3888 (99%)	617 (15%)	0

5 of 617 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	q	8	U
43	q	9	C
43	q	10	A
43	q	25	A
43	q	32	G

There are no RNA pucker outliers to report.

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](#)

Of 250 ligands modelled in this entry, 250 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
43	q	11

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	4734:C	O3'	4818:G	P	19.70
1	q	3948:C	O3'	4004:G	P	18.35
1	q	1202:G	O3'	1216:G	P	17.70
1	q	517:C	O3'	629:G	P	17.04
1	q	2881:G	O3'	3569:C	P	16.97

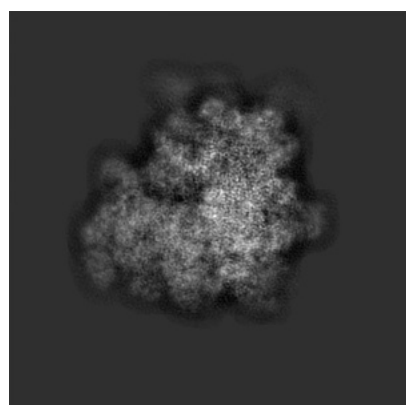
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10321. These allow visual inspection of the internal detail of the map and identification of artifacts.

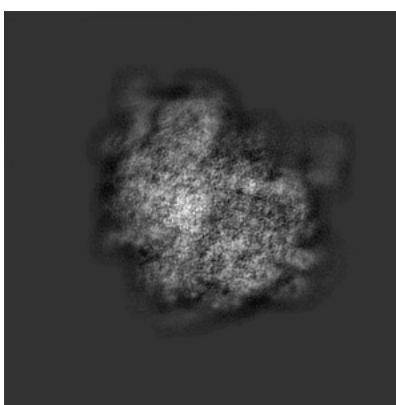
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

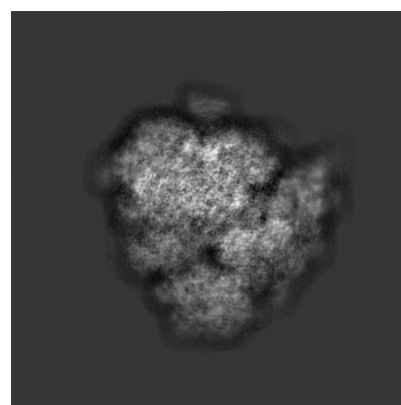
6.1.1 Primary map



X



Y

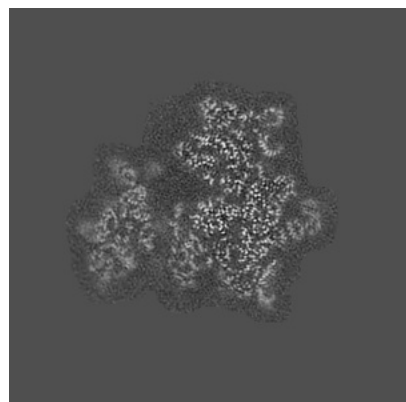


Z

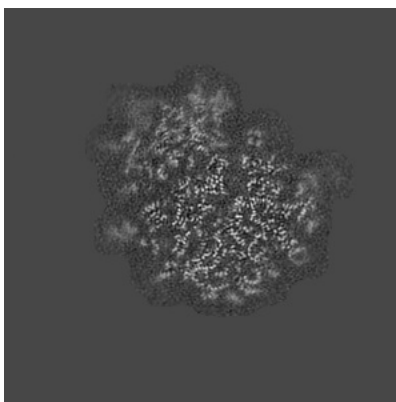
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

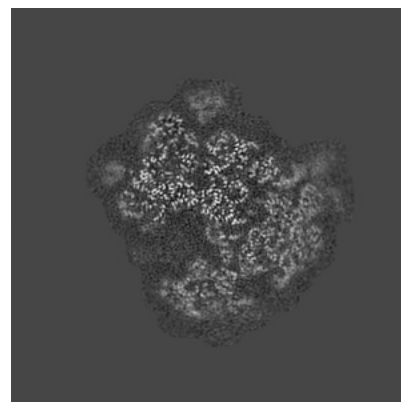
6.2.1 Primary map



X Index: 180



Y Index: 180

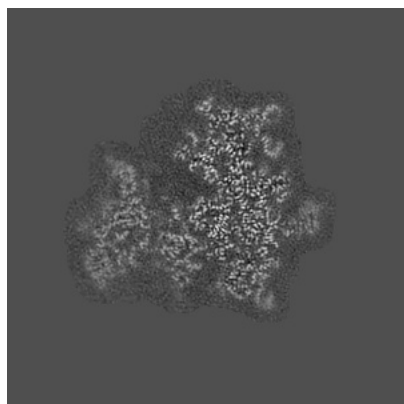


Z Index: 180

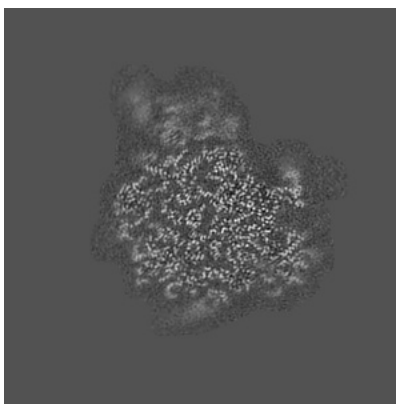
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

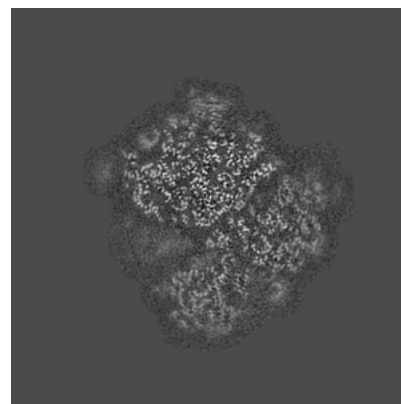
6.3.1 Primary map



X Index: 184



Y Index: 206

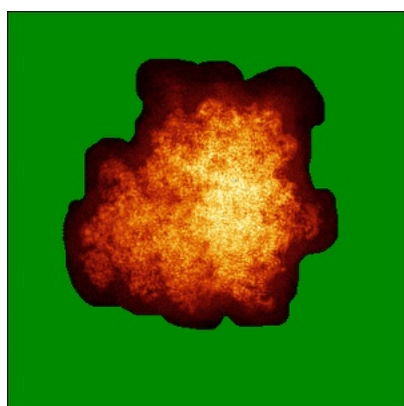


Z Index: 165

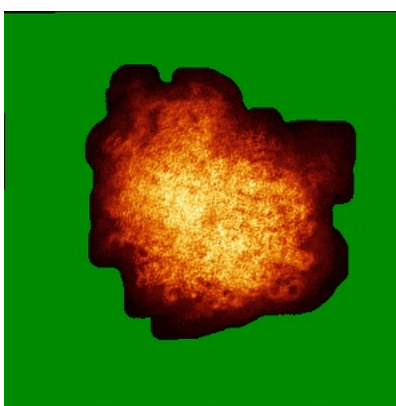
The images above show the largest variance slices of the map in three orthogonal directions.

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

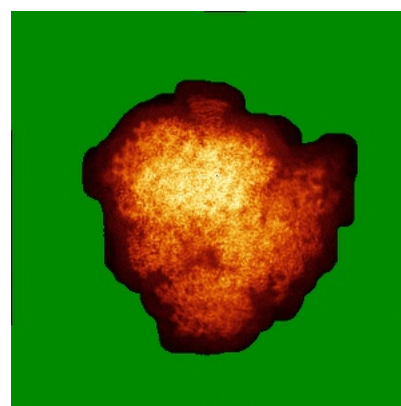
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

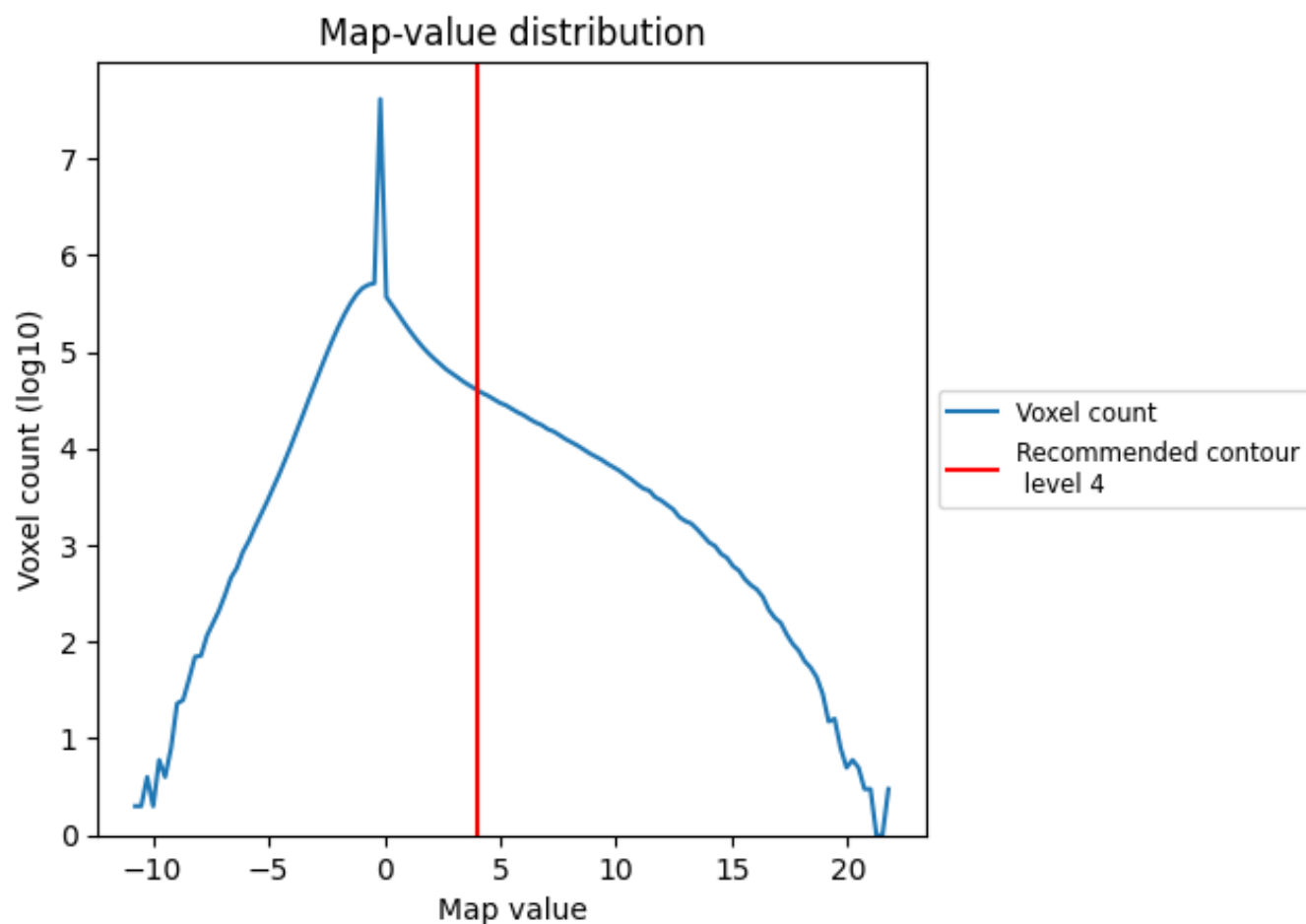
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

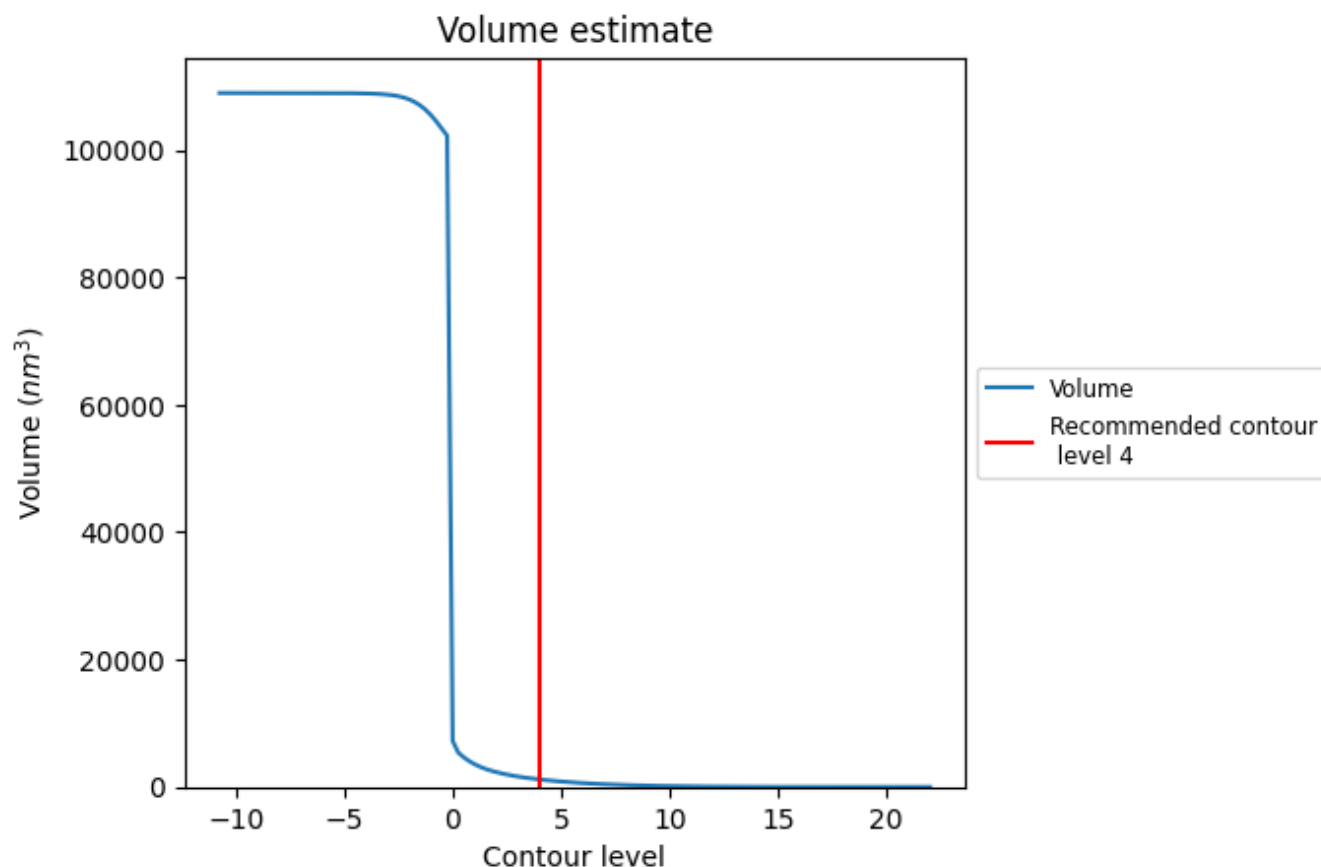
This section contains the results of statistical analysis of the map.

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.

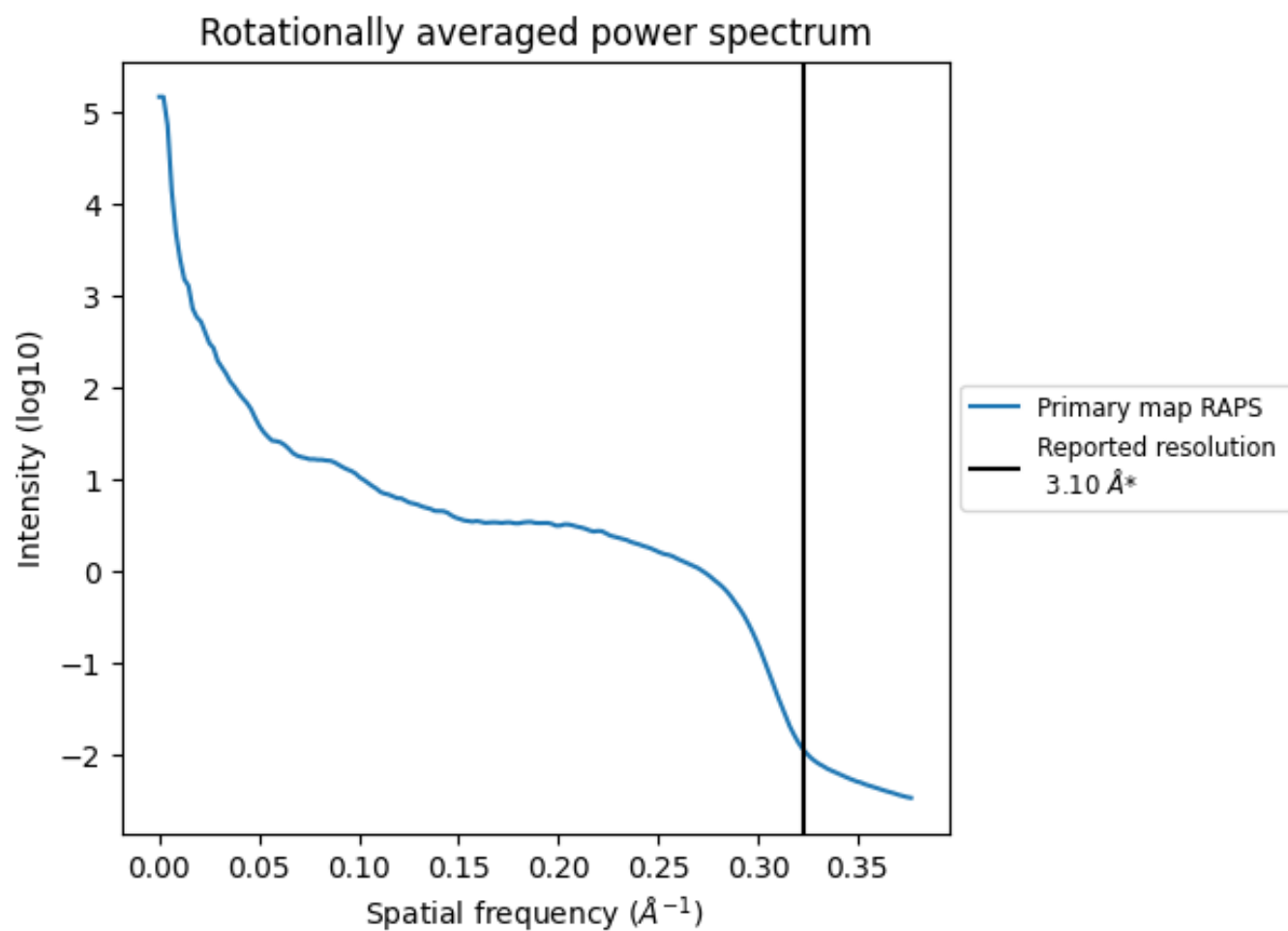
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1181 nm^3 ; this corresponds to an approximate mass of 1066 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 0.323 Å⁻¹

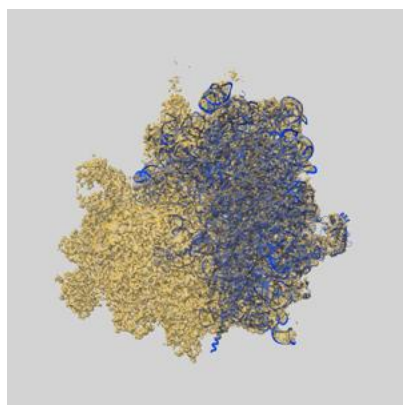
8 Fourier-Shell correlation

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

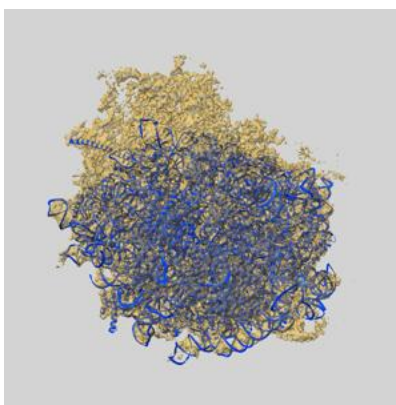
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10321 and PDB model 6SWA. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

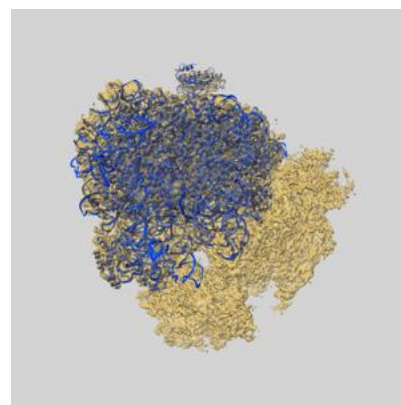
9.1 Map-model overlay [i](#)



X



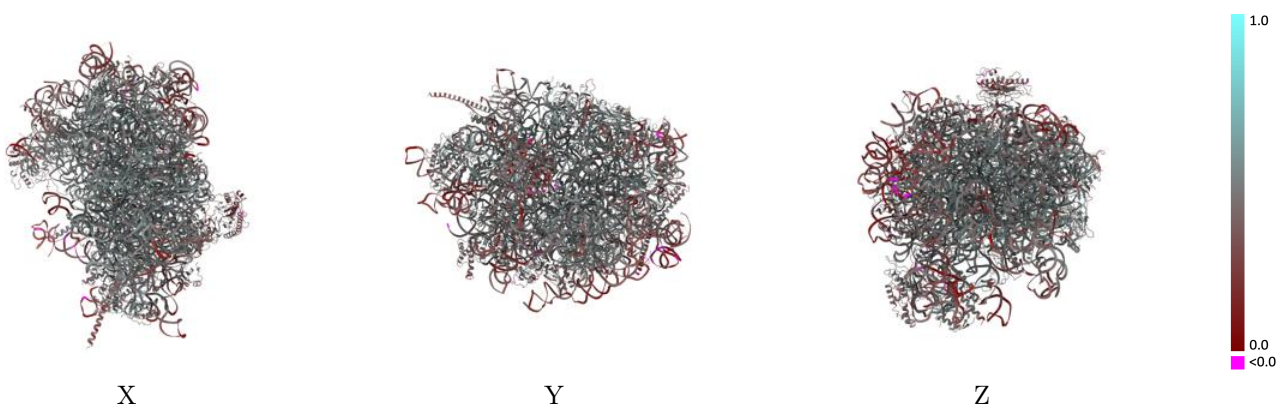
Y



Z

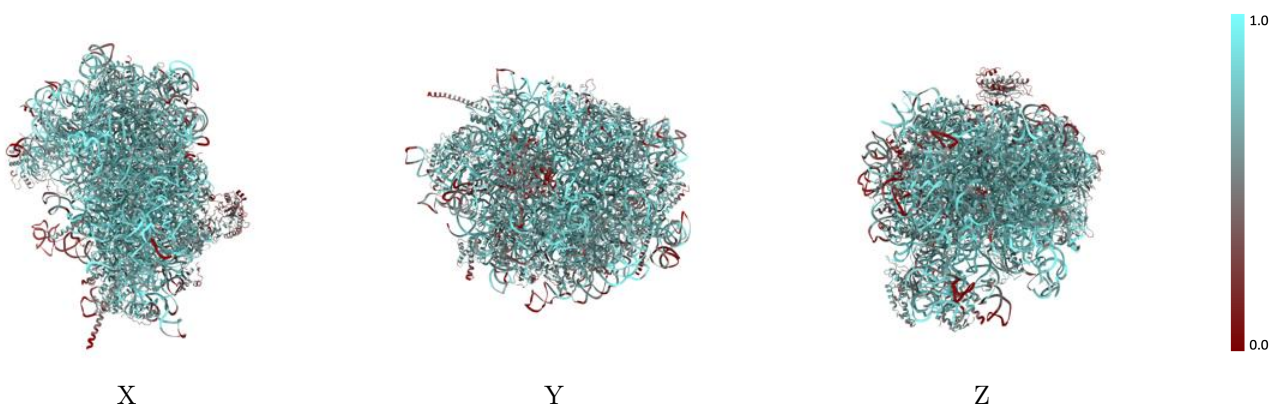
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



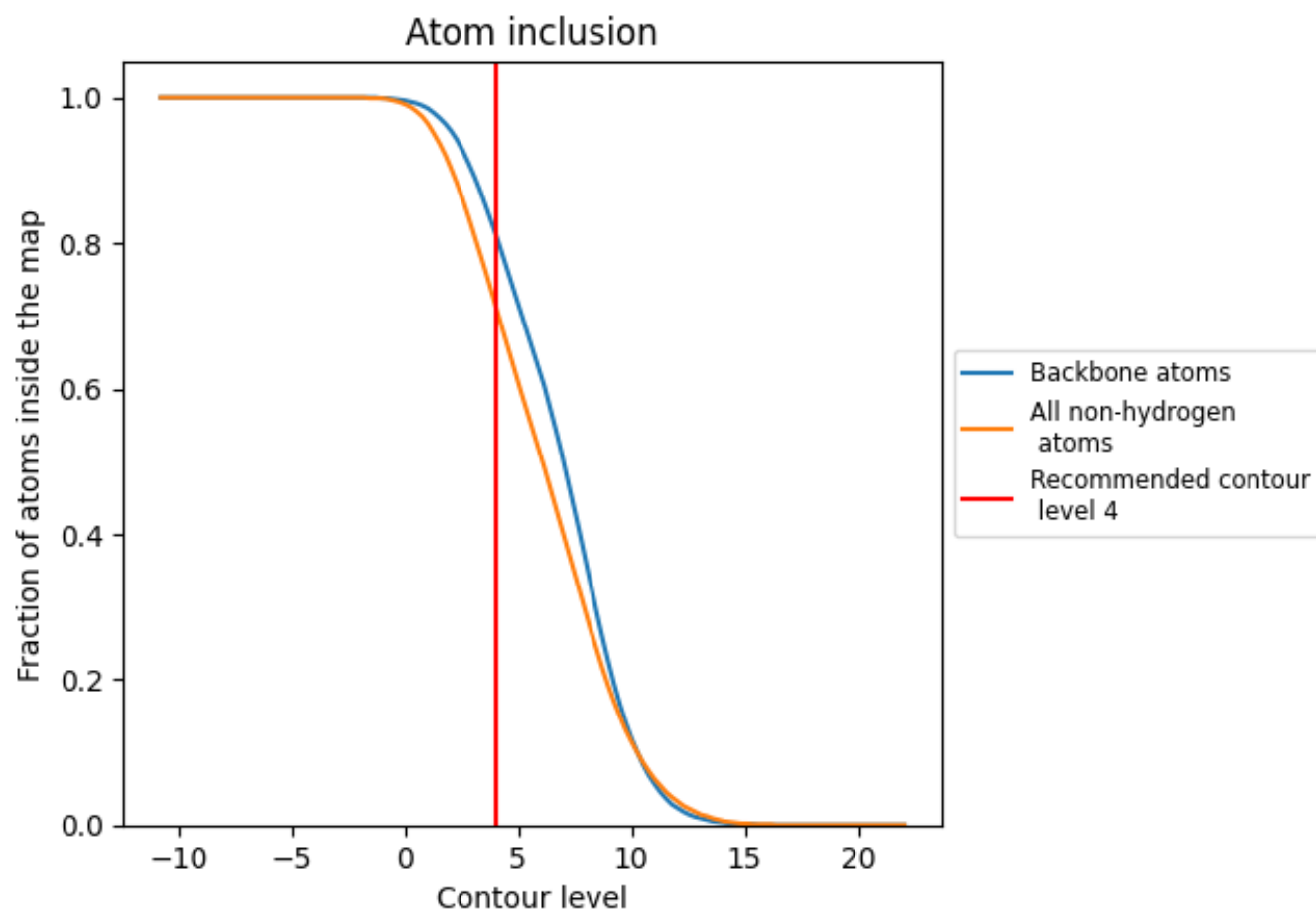
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

























The table lists the average atom inclusion at the recommended contour level (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7150	 0.4490
A	 0.6640	 0.5130
B	 0.6900	 0.4960
C	 0.6600	 0.4890
D	 0.6310	 0.4440
E	 0.5980	 0.4340
F	 0.6440	 0.4610
G	 0.5700	 0.4360
H	 0.6740	 0.4930
I	 0.6630	 0.4830
J	 0.5720	 0.4320
K	 0.6130	 0.4400
L	 0.7090	 0.4760
M	 0.7010	 0.5120
N	 0.7220	 0.5030
O	 0.6950	 0.5040
P	 0.6710	 0.4920
Q	 0.7170	 0.5030
R	 0.6710	 0.4940
S	 0.5740	 0.4270
T	 0.6640	 0.5130
U	 0.6590	 0.5030
V	 0.6290	 0.4860
W	 0.6840	 0.4920
X	 0.6310	 0.4690
Y	 0.6960	 0.4970
Z	 0.5870	 0.4410
a	 0.6520	 0.4680
b	 0.6630	 0.5010
c	 0.6650	 0.5090
d	 0.7400	 0.5250
e	 0.6580	 0.4800
f	 0.6120	 0.4600
g	 0.6070	 0.4410
h	 0.7280	 0.5100



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
i	 0.5360	 0.4350
j	 0.6470	 0.4920
k	 0.6950	 0.5210
l	 0.5590	 0.4800
m	 0.6160	 0.4820
n	 0.6390	 0.4910
o	 0.6180	 0.4670
p	 0.6970	 0.4760
q	 0.7610	 0.4320
r	 0.7550	 0.4330
s	 0.8480	 0.4600
t	 0.3540	 0.3660