



## wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:22 PM UTC

PDB ID : 5IT9 / pdb\_00005it9  
EMDB ID : EMD-8124  
Title : Structure of the yeast *Kluyveromyces lactis* small ribosomal subunit in complex with the cricket paralysis virus IRES.  
Authors : Murray, J.; Savva, C.G.; Shin, B.S.; Dever, T.E.; Ramakrishnan, V.; Fernandez, I.S.  
Deposited on : 2016-03-16  
Resolution : 3.80 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

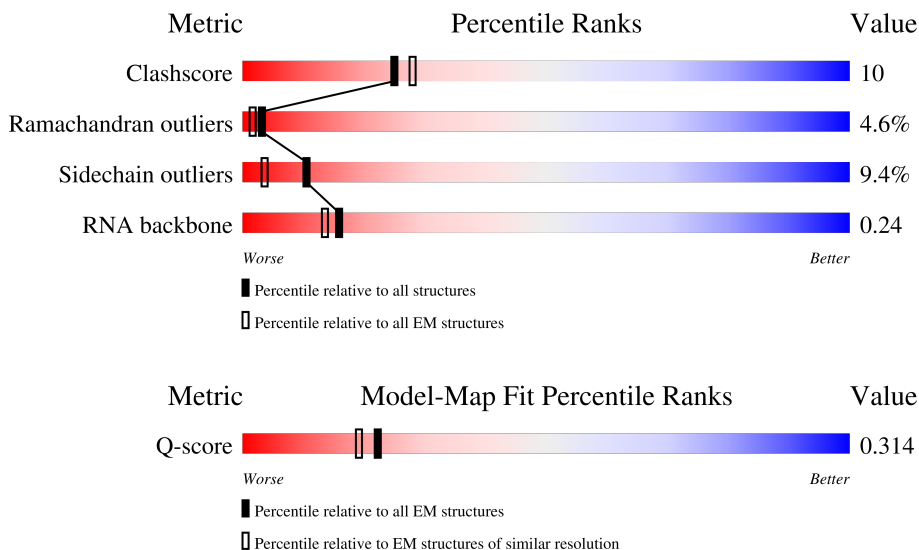
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 ( 3.30 - 4.30 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	206	
2	B	214	
3	C	217	

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Mol	Chain	Length	Quality of chain
4	D	223	10% 87% 13%
5	E	260	5% 90% 10%
6	F	206	14% 77% 20%
7	G	226	28% 78% 18%
8	H	184	9% 84% 15%
9	I	200	24% 72% 16% 6%
10	J	182	7% 72% 21% 7%
11	K	96	19% 77% 22%
12	L	155	14% 87% 10%
13	M	122	60% 83% 15%
14	N	150	12% 83% 13%
15	O	127	84% 15%
16	P	123	28% 76% 20%
17	Q	141	84% 13%
18	R	129	15% 82% 16%
19	S	145	50% 79% 17%
20	T	143	8% 85% 12%
21	U	106	17% 82% 14%
22	V	87	5% 84% 16%
23	W	129	69% 26% 5%
24	X	145	77% 18%
25	Y	134	17% 74% 20%
26	Z	70	29% 56% 33% 10%
27	a	100	8% 70% 22% 5%
28	b	82	13% 89% 11%

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Mol	Chain	Length	Quality of chain
29	c	63	
30	d	53	
31	e	55	
32	f	69	
33	g	324	
34	2	1780	
35	i	192	

## 2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 80144 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 Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	206	1616	1035	285	294	2	0	0

- Molecule 2 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	214	1722	1089	313	317	3	0	0

- Molecule 3 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	217	1629	1041	287	297	4	0	0

- Molecule 4 is a protein called Ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	223	1744	1108	313	318	5	0	0

- Molecule 5 is a protein called Ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	260	2078	1322	393	359	4	0	0

- Molecule 6 is a protein called Ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	206	1609	1008	298	300	3	0	0

- Molecule 7 is a protein called Ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	226	1812	1134	348	326	4	0	0

- Molecule 8 is a protein called Ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	184	1483	950	270	263		0	0

- Molecule 9 is a protein called Ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	188	1493	926	301	265	1	0	0

- Molecule 10 is a protein called Ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	182	1471	929	287	254	1	0	0

- Molecule 11 is a protein called Ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	96	809	533	129	146	1	0	0

- Molecule 12 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	155	1248	798	237	210	3	0	0

- Molecule 13 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	M	122	922	575	167	180	0	0

- Molecule 14 is a protein called Ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	150	Total	C	N	O	S	0	0
			1187	756	223	206	2		

- Molecule 15 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	127	Total	C	N	O	S	0	0
			942	578	188	173	3		

- Molecule 16 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	123	Total	C	N	O	S	0	0
			980	628	179	168	5		

- Molecule 17 is a protein called Ribosomal protein uS9.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	141	Total	C	N	O	0	0
			1105	709	204	192		

- Molecule 18 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	129	Total	C	N	O	S	0	0
			1031	641	193	194	3		

- Molecule 19 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	145	Total	C	N	O	S	0	0
			1193	741	240	210	2		

- Molecule 20 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	143	Total	C	N	O	0	0
			1110	693	210	207		

- Molecule 21 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	106	Total	C	N	O	S	0	0
			845	540	152	152	1		

- Molecule 22 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	87	Total	C	N	O	S	0	0
			687	424	126	135	2		

- Molecule 23 is a protein called Ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	129	Total	C	N	O	S	0	0
			1021	651	187	180	3		

- Molecule 24 is a protein called Ribosomal protein uS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	145	Total	C	N	O	S	0	0
			1127	713	219	192	3		

- Molecule 25 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Y	134	Total	C	N	O	0	0
			1061	665	207	189		

- Molecule 26 is a protein called Ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	70	Total	C	N	O	S	0	0
			558	355	104	98	1		

- Molecule 27 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	100	Total	C	N	O	S	0	0
			798	491	170	131	6		

- Molecule 28 is a protein called Ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	82	Total	C	N	O	S	0	0
			617	384	113	114	6		

- Molecule 29 is a protein called Ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	63	Total	C	N	O	S	0	0
			494	305	98	90	1		

- Molecule 30 is a protein called Ribosomal protein eS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	53	Total	C	N	O	S	0	0
			446	280	89	76	1		

- Molecule 31 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	55	Total	C	N	O	S	0	0
			443	276	90	76	1		

- Molecule 32 is a protein called Ribosomal protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	69	Total	C	N	O	S	0	0
			549	352	102	91	4		

- Molecule 33 is a protein called Ribosomal protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	318	Total	C	N	O	S	0	0
			2466	1561	430	470	5		

- Molecule 34 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2	1780	Total	C	N	O	P	0	0
			37797	16892	6658	12467	1780		

- Molecule 35 is a RNA chain called Cricket paralysis virus IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	i	192	3968	1774	669	1333	192	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
i	6176	C	U	conflict	GB 8895506

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	G	1	Total 1	Mg 1	0
36	N	1	Total 1	Mg 1	0
36	T	1	Total 1	Mg 1	0
36	X	1	Total 1	Mg 1	0
36	2	76	Total 76	Mg 76	0

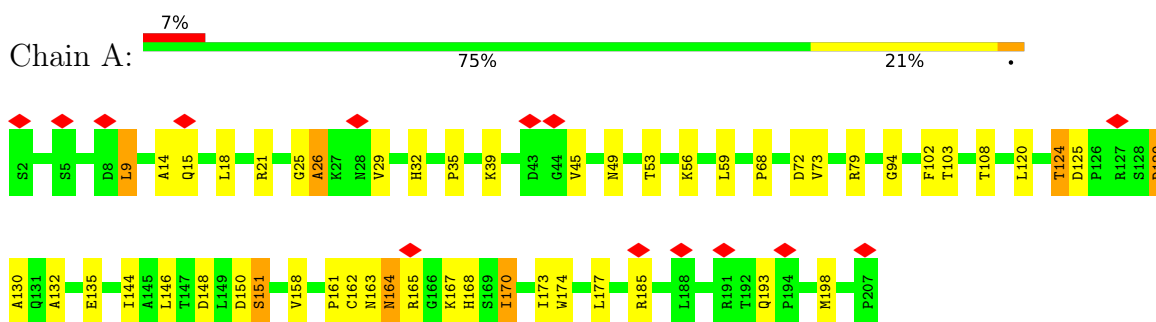
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
37	a	1	Total 1	Zn 1	0
37	b	1	Total 1	Zn 1	0
37	f	1	Total 1	Zn 1	0

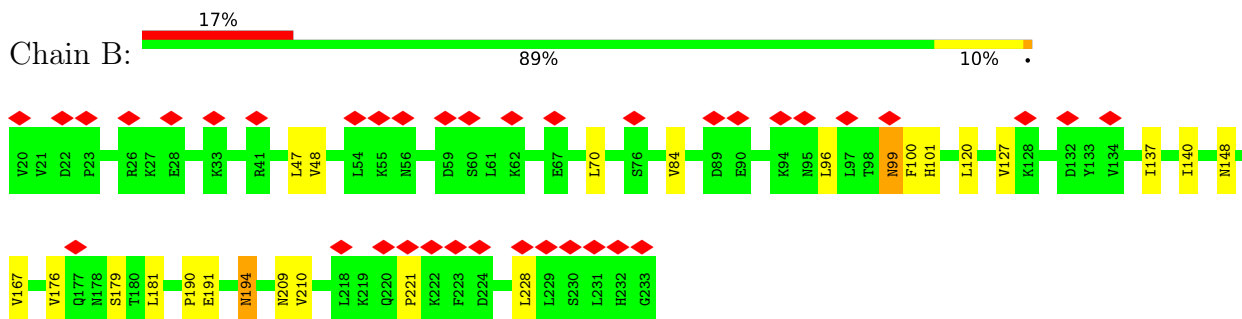
### 3 Residue-property plots [i](#)

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.

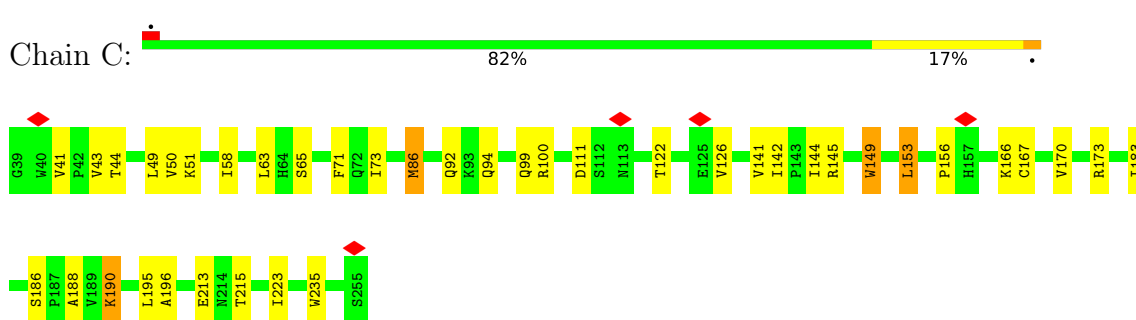
- Molecule 1: Ribosomal protein uS2



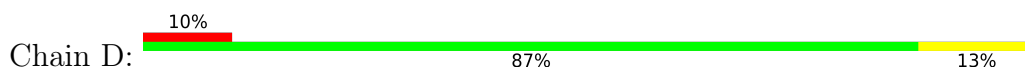
- Molecule 2: Ribosomal protein eS1

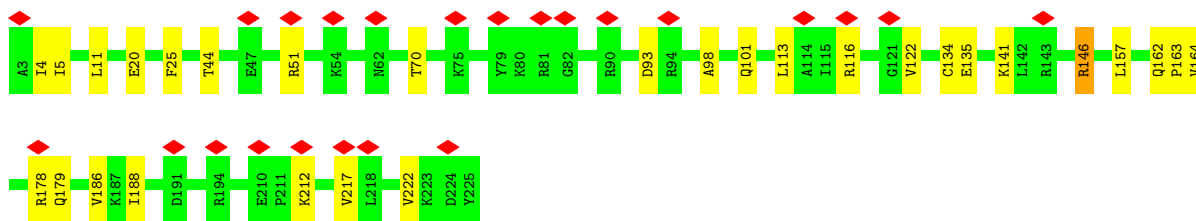


- Molecule 3: Ribosomal protein uS5

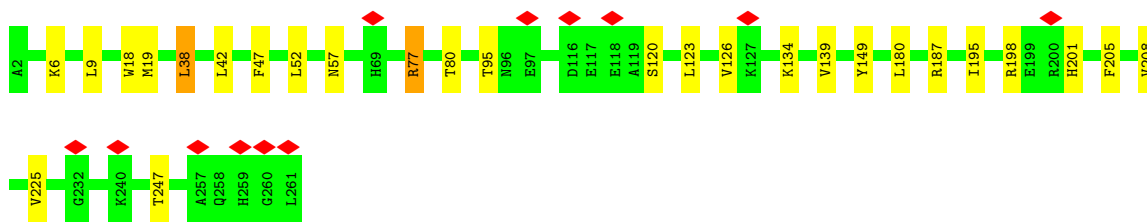
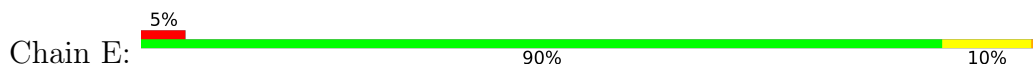


- Molecule 4: Ribosomal protein uS3

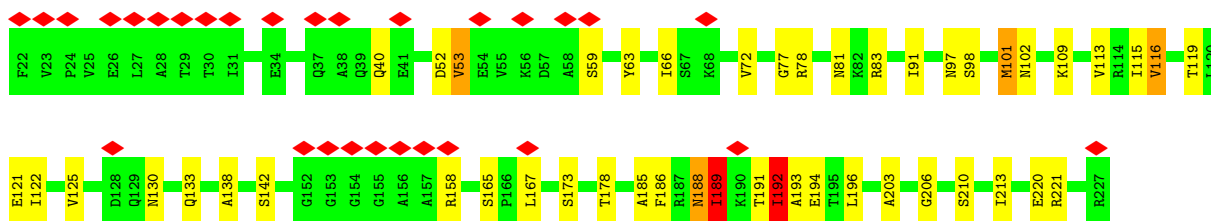
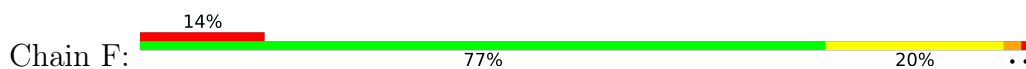




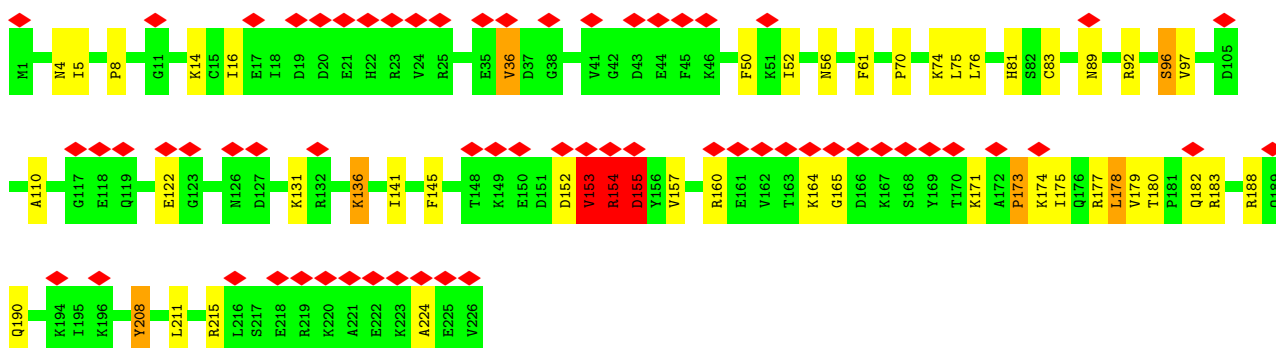
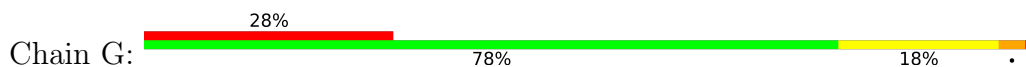
- Molecule 5: Ribosomal protein eS4



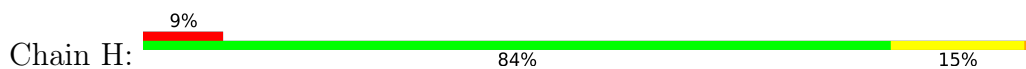
- Molecule 6: Ribosomal protein uS7

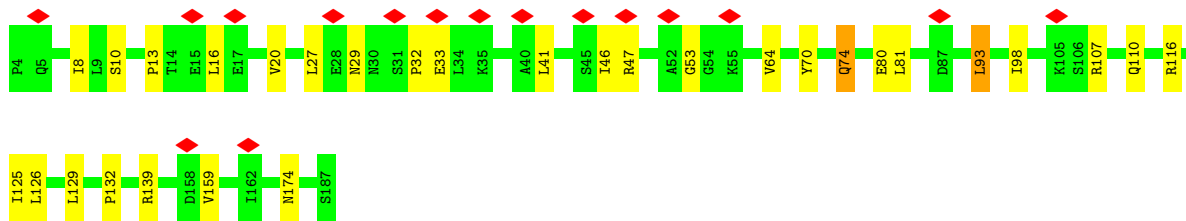


- Molecule 7: Ribosomal protein eS6

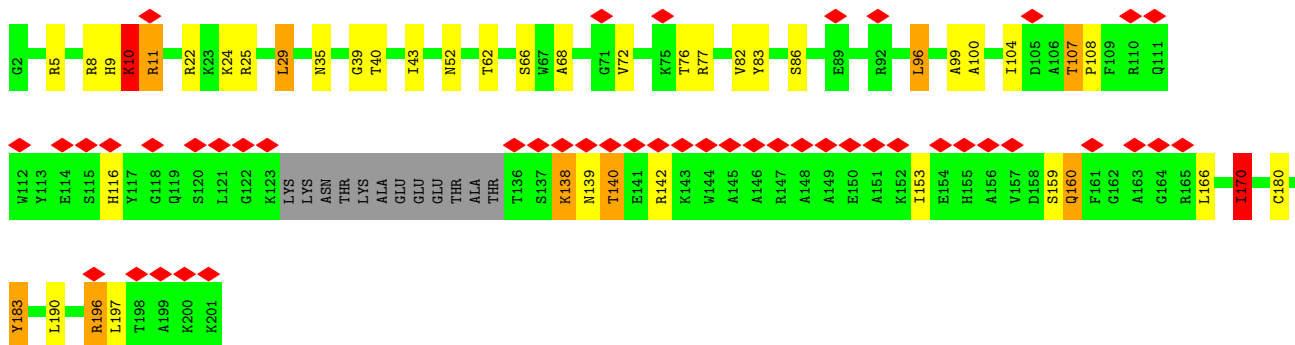


- Molecule 8: Ribosomal protein eS7

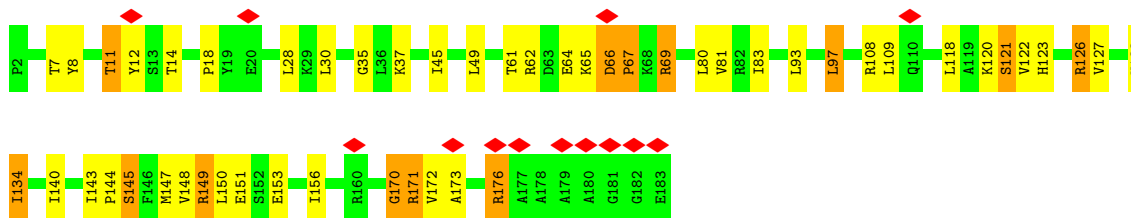




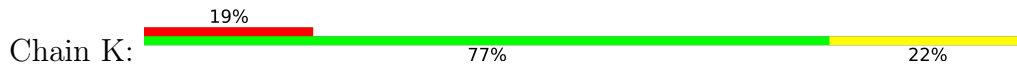
• Molecule 9: Ribosomal protein eS8



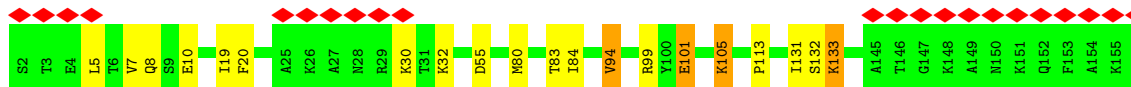
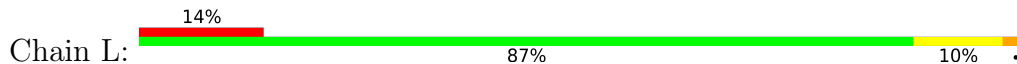
• Molecule 10: Ribosomal protein uS4



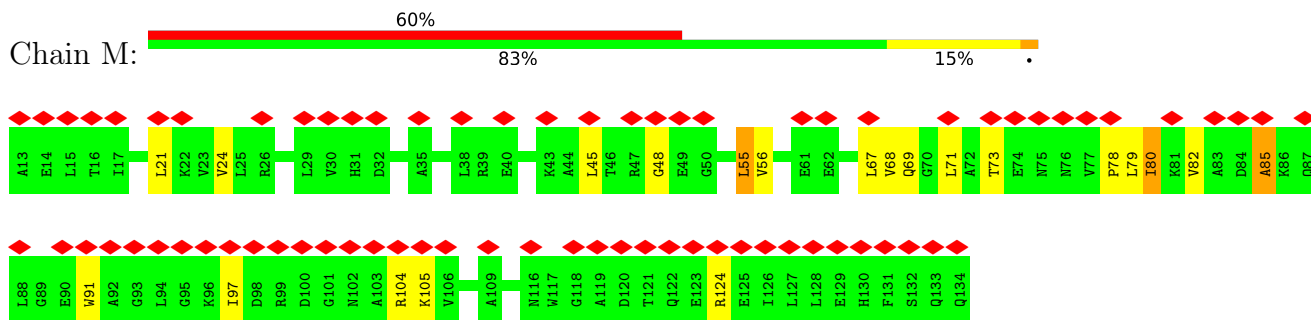
• Molecule 11: Ribosomal protein eS10



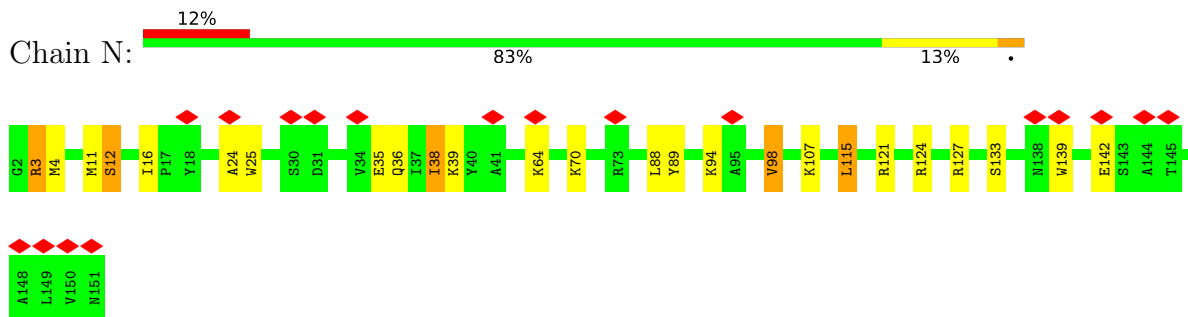
• Molecule 12: Ribosomal protein uS17



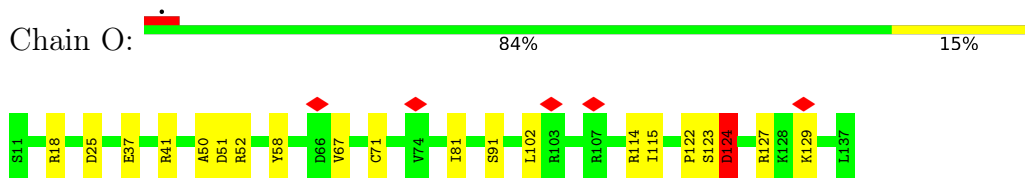
• Molecule 13: Ribosomal protein eS12



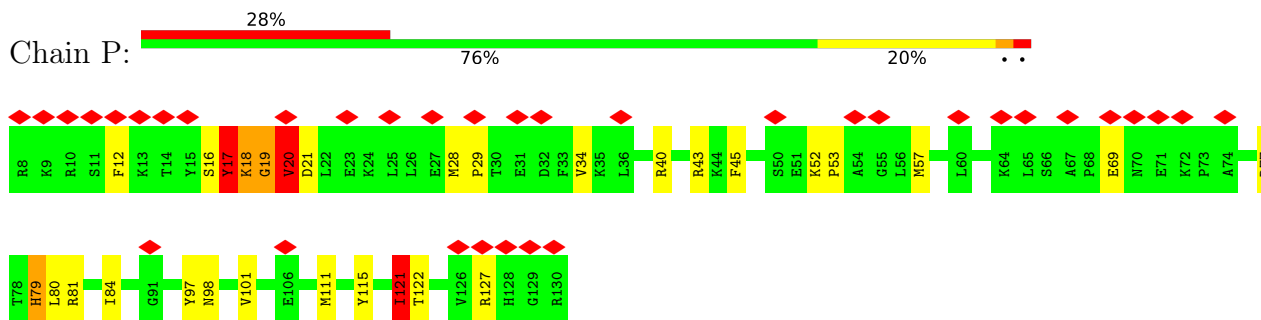
• Molecule 14: Ribosomal protein uS15



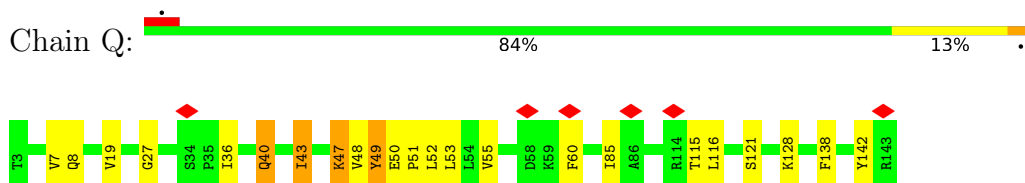
• Molecule 15: Ribosomal protein uS14



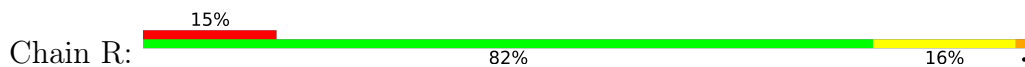
• Molecule 16: Ribosomal protein uS19

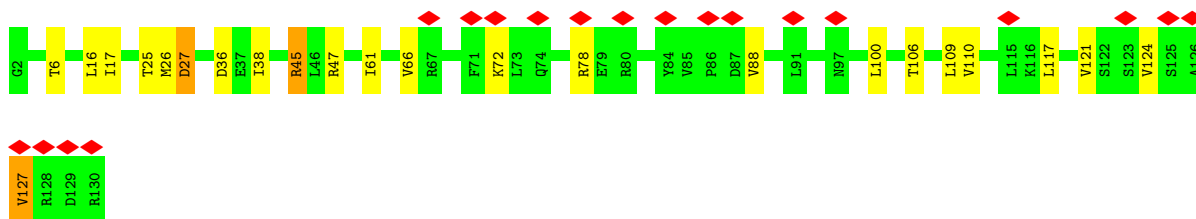


• Molecule 17: Ribosomal protein uS9

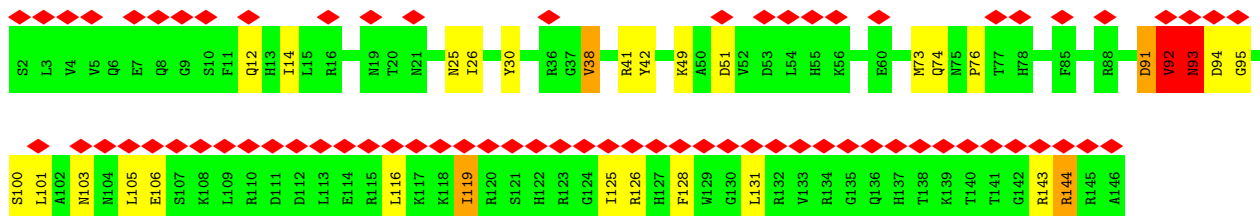
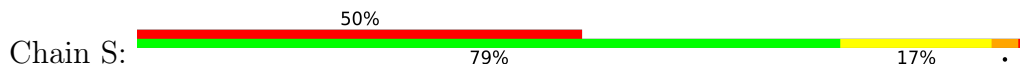


• Molecule 18: Ribosomal protein eS17

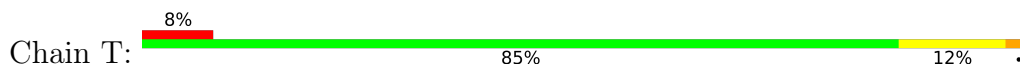




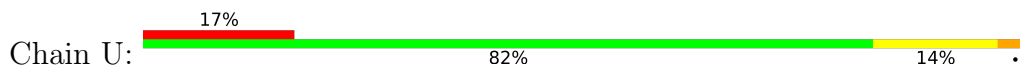
• Molecule 19: Ribosomal protein uS13



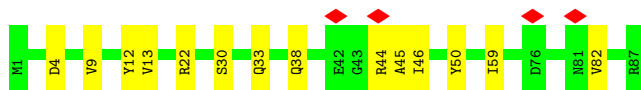
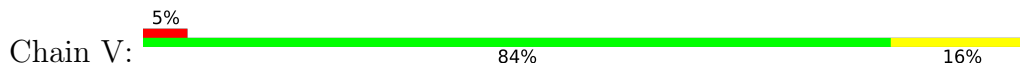
• Molecule 20: Ribosomal protein eS19



• Molecule 21: Ribosomal protein uS10



• Molecule 22: Ribosomal protein eS21

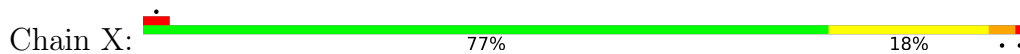


• Molecule 23: Ribosomal protein uS8

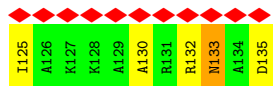
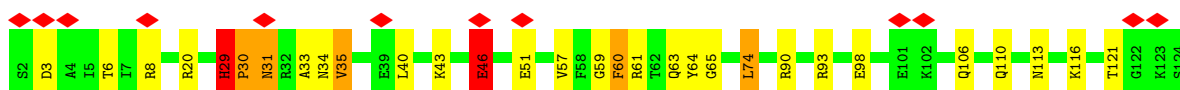
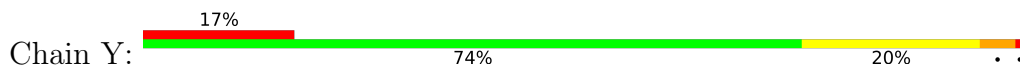




• Molecule 24: Ribosomal protein uS21



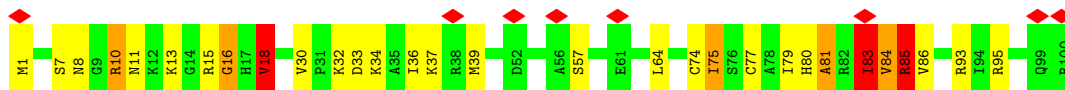
• Molecule 25: Ribosomal protein eS24



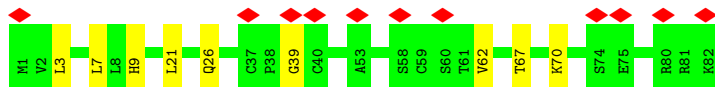
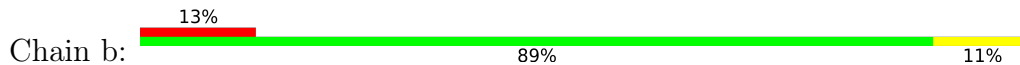
• Molecule 26: Ribosomal protein eS25



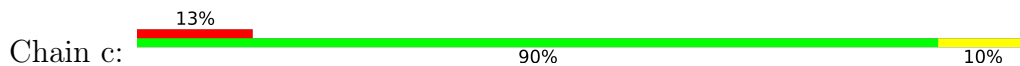
• Molecule 27: Ribosomal protein eS26



• Molecule 28: Ribosomal protein eS27

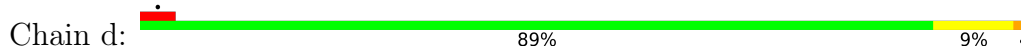


• Molecule 29: Ribosomal protein eS28

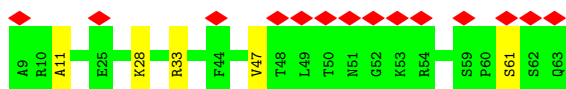




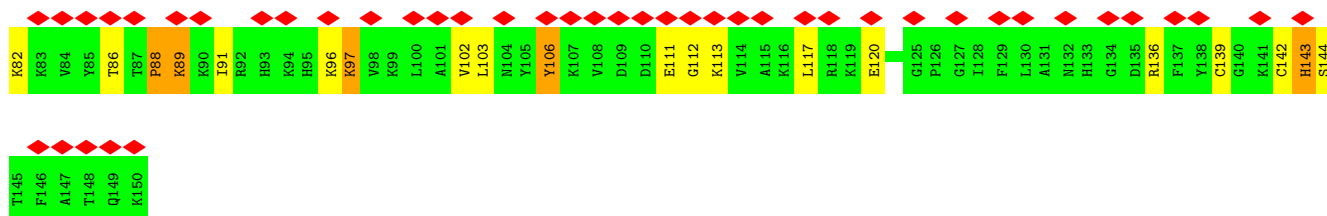
• Molecule 30: Ribosomal protein eS29



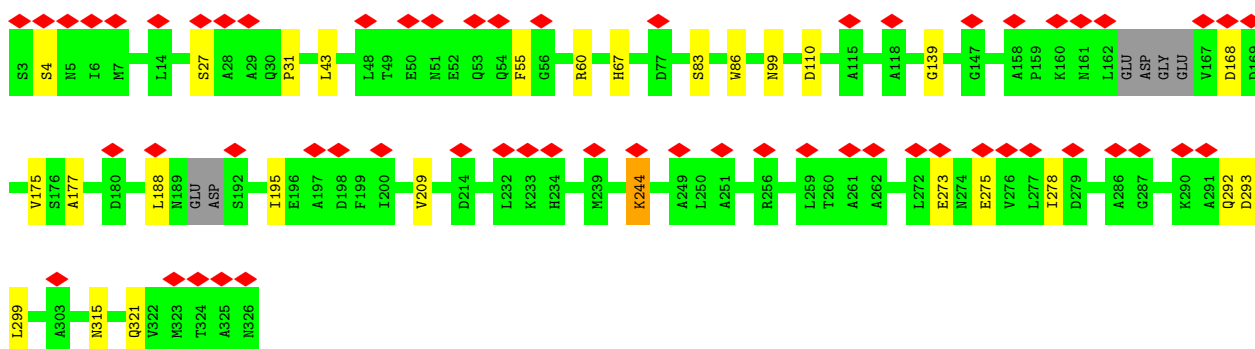
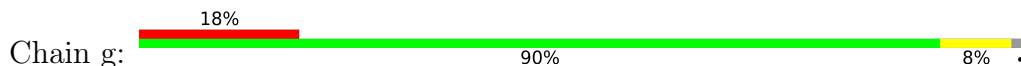
• Molecule 31: Ribosomal protein eS30



• Molecule 32: Ribosomal protein eS31

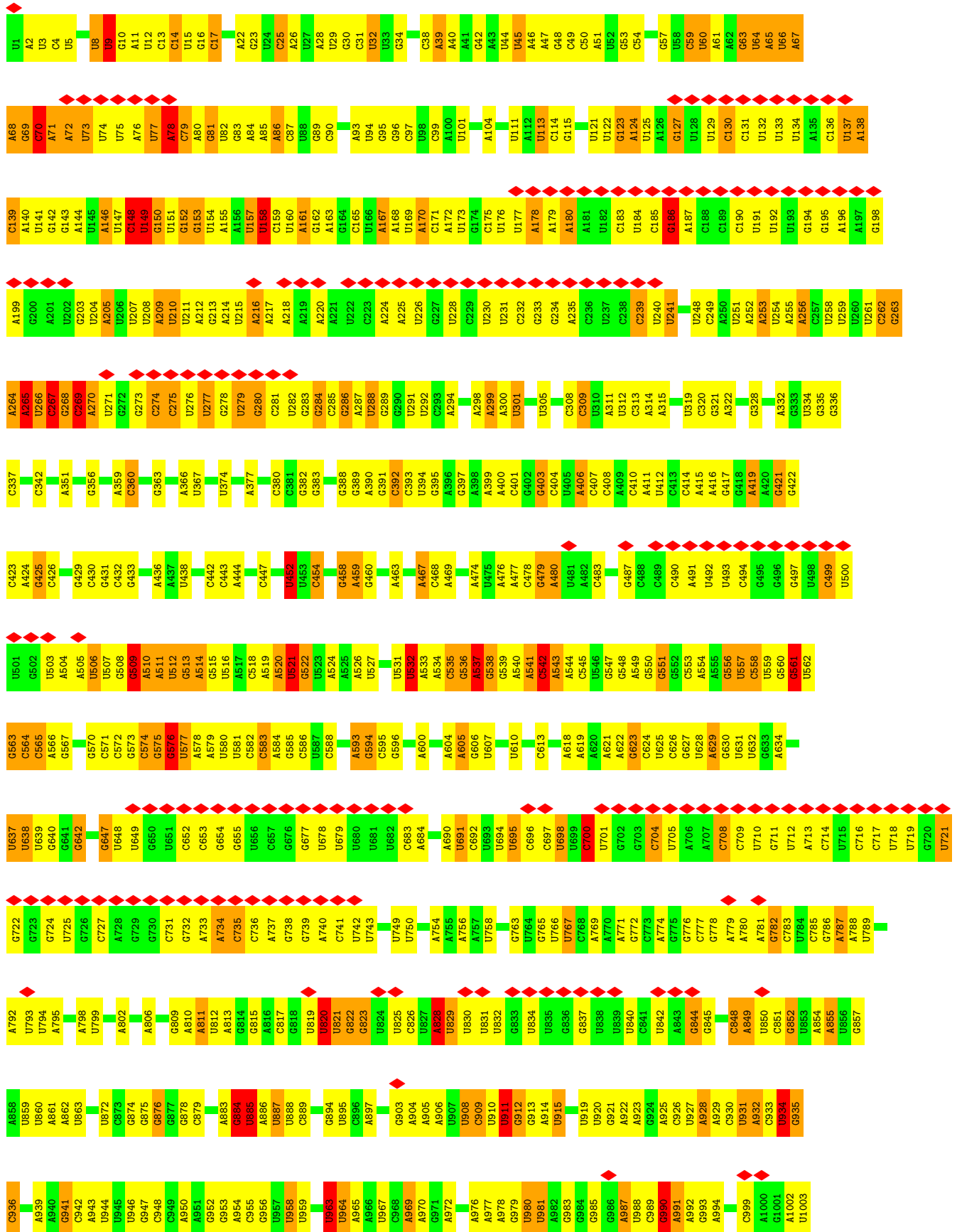


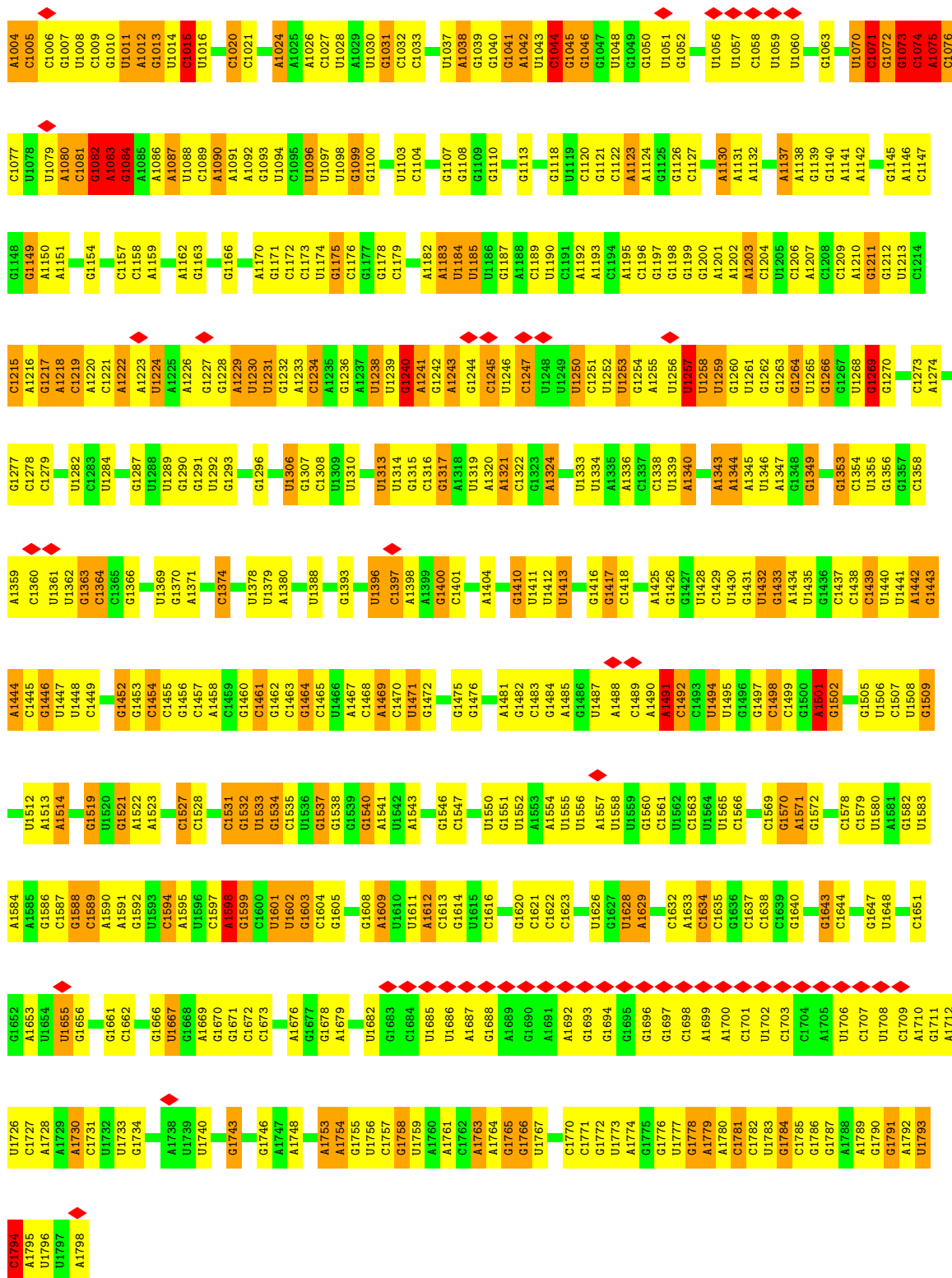
• Molecule 33: Ribosomal protein RACK1



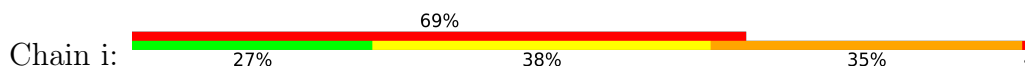
• Molecule 34: 18S ribosomal RNA

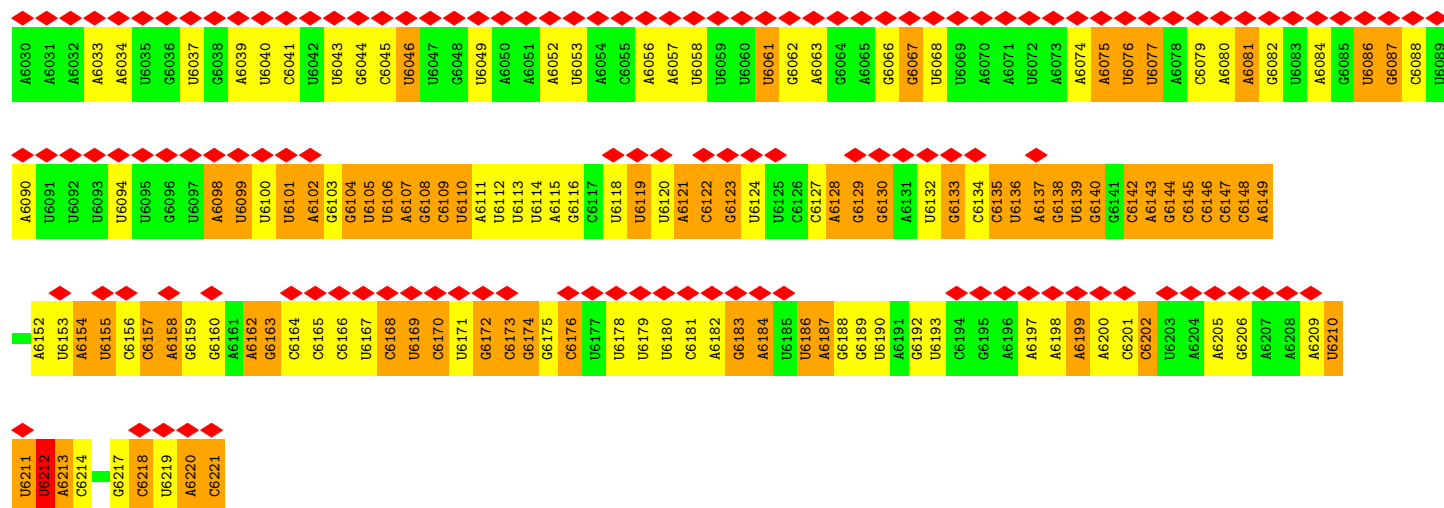






• Molecule 35: Cricket paralysis virus IRES RNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	54481	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.973	Depositor
Minimum map value	-0.641	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.042	Depositor
Recommended contour level	0.1	Depositor
Map size ( $\text{\AA}$ )	375.2, 375.2, 375.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.34, 1.34, 1.34	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	0.56	0/1656	1.06	4/2264 (0.2%)
2	B	0.54	0/1747	0.94	0/2353
3	C	0.50	0/1659	0.98	0/2252
4	D	0.49	0/1769	0.93	1/2378 (0.0%)
5	E	0.52	0/2122	0.84	2/2861 (0.1%)
6	F	0.52	0/1628	1.15	6/2198 (0.3%)
7	G	0.72	3/1835 (0.2%)	1.05	12/2451 (0.5%)
8	H	0.53	0/1507	1.00	0/2028
9	I	0.55	0/1519	1.00	3/2033 (0.1%)
10	J	0.59	1/1495 (0.1%)	1.17	3/2001 (0.1%)
11	K	0.53	0/831	1.05	2/1123 (0.2%)
12	L	0.50	0/1276	0.77	0/1718
13	M	0.56	0/929	1.05	0/1255
14	N	0.54	0/1210	1.17	2/1628 (0.1%)
15	O	0.58	0/953	0.99	0/1279
16	P	0.79	5/1000 (0.5%)	1.05	3/1343 (0.2%)
17	Q	0.53	0/1125	1.04	0/1510
18	R	0.56	0/1042	1.16	1/1399 (0.1%)
19	S	0.68	4/1212 (0.3%)	1.11	4/1629 (0.2%)
20	T	0.47	0/1129	1.09	2/1520 (0.1%)
21	U	0.53	0/857	0.95	1/1158 (0.1%)
22	V	0.51	0/696	0.90	1/938 (0.1%)
23	W	0.52	0/1039	1.12	1/1399 (0.1%)
24	X	0.50	0/1145	0.99	3/1526 (0.2%)
25	Y	0.53	0/1075	1.02	1/1433 (0.1%)
26	Z	0.57	0/567	1.28	4/762 (0.5%)
27	a	0.60	0/810	0.98	3/1084 (0.3%)
28	b	0.48	0/627	0.82	0/847
29	c	0.54	0/496	0.77	0/666
30	d	0.49	0/457	0.80	0/607
31	e	0.48	0/450	0.90	0/599
32	f	0.65	0/562	0.85	0/751

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	g	0.50	0/2521	0.69	0/3431
34	2	0.41	8/42269 (0.0%)	0.83	88/65862 (0.1%)
35	i	0.25	1/4425 (0.0%)	0.35	2/6875 (0.0%)
All	All	0.48	22/85640 (0.0%)	0.89	149/125161 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
7	G	0	1
10	J	0	1
15	O	0	1
17	Q	0	2
22	V	0	1
23	W	0	1
26	Z	0	1
27	a	0	1
34	2	0	7
All	All	0	18

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	G	154	ARG	CA-C	14.08	1.71	1.52
7	G	154	ARG	N-CA	9.13	1.57	1.46
34	2	934	U	O3'-P	-8.14	1.49	1.61
19	S	93	ASN	N-CA	7.88	1.56	1.46
35	i	6109	C	O3'-P	-7.73	1.49	1.61

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	Z	68	ARG	N-CA-C	-19.50	88.93	112.92
34	2	1074	C	C2'-C3'-O3'	13.55	134.03	113.70
34	2	78	A	C4'-C3'-O3'	10.58	128.88	113.00
34	2	1534	G	C2'-C3'-O3'	9.24	123.36	109.50
34	2	1075	A	C4'-C3'-O3'	8.87	122.70	109.40

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	164	ASN	Peptide
1	A	168	HIS	Peptide
7	G	155	ASP	Peptide
10	J	66	ASP	Peptide
15	O	122	PRO	Peptide

## 5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1616	0	1636	18	0
2	B	1722	0	1795	3	0
3	C	1629	0	1710	8	0
4	D	1744	0	1825	22	0
5	E	2078	0	2157	5	0
6	F	1609	0	1679	28	0
7	G	1812	0	1911	58	0
8	H	1483	0	1579	6	0
9	I	1493	0	1515	20	0
10	J	1471	0	1554	39	0
11	K	809	0	810	4	0
12	L	1248	0	1311	6	0
13	M	922	0	953	7	0
14	N	1187	0	1251	6	0
15	O	942	0	979	27	0
16	P	980	0	1026	23	0
17	Q	1105	0	1170	6	0
18	R	1031	0	1082	6	0
19	S	1193	0	1217	22	0
20	T	1110	0	1124	4	0
21	U	845	0	913	5	0
22	V	687	0	682	2	0
23	W	1021	0	1056	12	0
24	X	1127	0	1210	23	0
25	Y	1061	0	1111	15	0
26	Z	558	0	585	77	0
27	a	798	0	855	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	b	617	0	642	1	0
29	c	494	0	534	2	0
30	d	446	0	436	2	0
31	e	443	0	481	1	0
32	f	549	0	564	8	0
33	g	2466	0	2406	2	0
34	2	37797	0	19010	969	0
35	i	3968	0	1986	204	0
36	2	76	0	0	0	0
36	G	1	0	0	0	0
36	N	1	0	0	0	0
36	T	1	0	0	0	0
36	X	1	0	0	0	0
37	a	1	0	0	0	0
37	b	1	0	0	0	0
37	f	1	0	0	0	0
All	All	80144	0	60755	1441	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 1441 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)
4:D:116:ARG:CZ	35:i:6220:A:C2	1.74	1.62
4:D:116:ARG:NH2	35:i:6220:A:C2	1.70	1.49
4:D:116:ARG:CZ	35:i:6220:A:N1	1.70	1.46
26:Z:52:LYS:HA	26:Z:53:GLU:CG	1.47	1.43
34:2:513:G:H1	34:2:542:C:N4	1.27	1.31

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	204/206 (99%)	168 (82%)	25 (12%)	11 (5%)	1	16
2	B	212/214 (99%)	174 (82%)	32 (15%)	6 (3%)	4	26
3	C	215/217 (99%)	187 (87%)	21 (10%)	7 (3%)	3	24
4	D	221/223 (99%)	198 (90%)	17 (8%)	6 (3%)	4	27
5	E	258/260 (99%)	214 (83%)	36 (14%)	8 (3%)	3	25
6	F	204/206 (99%)	174 (85%)	21 (10%)	9 (4%)	2	19
7	G	224/226 (99%)	186 (83%)	29 (13%)	9 (4%)	2	20
8	H	182/184 (99%)	155 (85%)	16 (9%)	11 (6%)	1	14
9	I	184/200 (92%)	154 (84%)	22 (12%)	8 (4%)	2	19
10	J	180/182 (99%)	151 (84%)	17 (9%)	12 (7%)	1	13
11	K	94/96 (98%)	80 (85%)	7 (7%)	7 (7%)	1	11
12	L	153/155 (99%)	129 (84%)	17 (11%)	7 (5%)	2	18
13	M	120/122 (98%)	94 (78%)	21 (18%)	5 (4%)	2	19
14	N	148/150 (99%)	130 (88%)	14 (10%)	4 (3%)	4	27
15	O	125/127 (98%)	108 (86%)	11 (9%)	6 (5%)	2	17
16	P	121/123 (98%)	96 (79%)	16 (13%)	9 (7%)	1	11
17	Q	139/141 (99%)	122 (88%)	12 (9%)	5 (4%)	2	22
18	R	127/129 (98%)	106 (84%)	14 (11%)	7 (6%)	1	16
19	S	143/145 (99%)	119 (83%)	17 (12%)	7 (5%)	1	17
20	T	141/143 (99%)	126 (89%)	10 (7%)	5 (4%)	3	23
21	U	104/106 (98%)	93 (89%)	7 (7%)	4 (4%)	2	21
22	V	85/87 (98%)	69 (81%)	10 (12%)	6 (7%)	1	12
23	W	127/129 (98%)	107 (84%)	14 (11%)	6 (5%)	2	18
24	X	143/145 (99%)	121 (85%)	15 (10%)	7 (5%)	1	17
25	Y	132/134 (98%)	113 (86%)	9 (7%)	10 (8%)	1	11
26	Z	68/70 (97%)	58 (85%)	5 (7%)	5 (7%)	1	11
27	a	98/100 (98%)	74 (76%)	13 (13%)	11 (11%)	0	5
28	b	80/82 (98%)	64 (80%)	12 (15%)	4 (5%)	1	17
29	c	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
30	d	51/53 (96%)	41 (80%)	10 (20%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	e	53/55 (96%)	47 (89%)	3 (6%)	3 (6%)	1	15
32	f	67/69 (97%)	50 (75%)	11 (16%)	6 (9%)	0	8
33	g	312/324 (96%)	261 (84%)	44 (14%)	7 (2%)	5	30
All	All	4776/4866 (98%)	4024 (84%)	534 (11%)	218 (5%)	3	18

5 of 218 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	ALA
2	B	100	PHE
3	C	149	TRP
4	D	164	VAL
6	F	59	SER

### 5.3.2 Protein sidechains [i](#)

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	174/174 (100%)	158 (91%)	16 (9%)	8	31
2	B	196/196 (100%)	181 (92%)	15 (8%)	12	37
3	C	176/176 (100%)	152 (86%)	24 (14%)	3	18
4	D	185/185 (100%)	167 (90%)	18 (10%)	8	29
5	E	223/223 (100%)	210 (94%)	13 (6%)	18	44
6	F	174/174 (100%)	158 (91%)	16 (9%)	8	31
7	G	192/192 (100%)	173 (90%)	19 (10%)	7	28
8	H	164/164 (100%)	152 (93%)	12 (7%)	13	39
9	I	148/158 (94%)	128 (86%)	20 (14%)	4	19
10	J	153/153 (100%)	134 (88%)	19 (12%)	4	21
11	K	88/88 (100%)	79 (90%)	9 (10%)	7	27
12	L	136/136 (100%)	125 (92%)	11 (8%)	11	35
13	M	97/97 (100%)	90 (93%)	7 (7%)	13	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	127/127 (100%)	112 (88%)	15 (12%)	5	22
15	O	96/96 (100%)	90 (94%)	6 (6%)	16	42
16	P	105/106 (99%)	94 (90%)	11 (10%)	6	26
17	Q	117/117 (100%)	106 (91%)	11 (9%)	8	30
18	R	117/117 (100%)	105 (90%)	12 (10%)	7	27
19	S	128/128 (100%)	116 (91%)	12 (9%)	8	30
20	T	117/117 (100%)	106 (91%)	11 (9%)	8	30
21	U	96/96 (100%)	87 (91%)	9 (9%)	8	30
22	V	73/73 (100%)	69 (94%)	4 (6%)	19	45
23	W	110/110 (100%)	93 (84%)	17 (16%)	2	15
24	X	120/120 (100%)	105 (88%)	15 (12%)	4	21
25	Y	108/108 (100%)	93 (86%)	15 (14%)	3	18
26	Z	60/60 (100%)	57 (95%)	3 (5%)	22	47
27	a	85/85 (100%)	72 (85%)	13 (15%)	3	16
28	b	72/72 (100%)	68 (94%)	4 (6%)	19	45
29	c	55/55 (100%)	53 (96%)	2 (4%)	31	54
30	d	46/46 (100%)	43 (94%)	3 (6%)	15	42
31	e	49/49 (100%)	48 (98%)	1 (2%)	48	65
32	f	58/60 (97%)	50 (86%)	8 (14%)	3	18
33	g	265/270 (98%)	248 (94%)	17 (6%)	16	42
All	All	4110/4128 (100%)	3722 (91%)	388 (9%)	10	30

5 of 388 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
17	Q	7	VAL
22	V	12	TYR
17	Q	85	ILE
19	S	100	SER
23	W	47	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
16	P	79	HIS
33	g	292	GLN
19	S	89	GLN
33	g	203	ASN
25	Y	34	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	2	1778/1780 (99%)	772 (43%)	111 (6%)
35	i	183/192 (95%)	106 (57%)	0
All	All	1961/1972 (99%)	878 (44%)	111 (5%)

5 of 878 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	2	2	A
34	2	3	U
34	2	4	C
34	2	5	U
34	2	9	U

5 of 111 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
34	2	710	U
34	2	1791	G
34	2	909	C
34	2	1765	G
34	2	1532	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](#)

Of 83 ligands modelled in this entry, 83 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
34	2	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	657:C	O3'	676:G	P	17.80

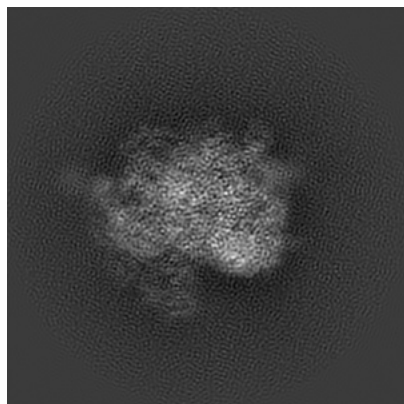
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8124. These allow visual inspection of the internal detail of the map and identification of artifacts.

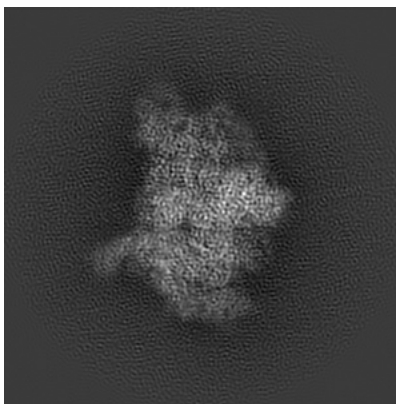
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

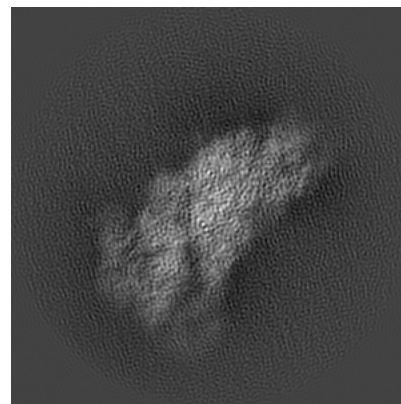
#### 6.1.1 Primary map



X

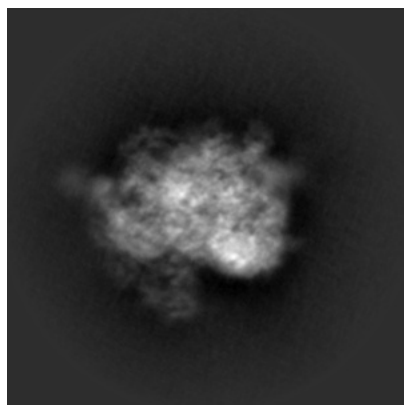


Y

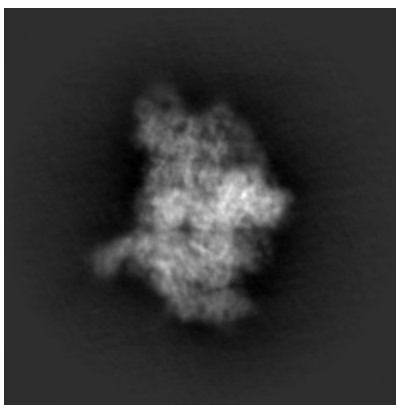


Z

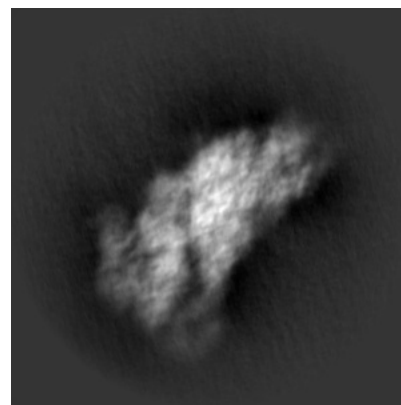
#### 6.1.2 Raw map



X



Y

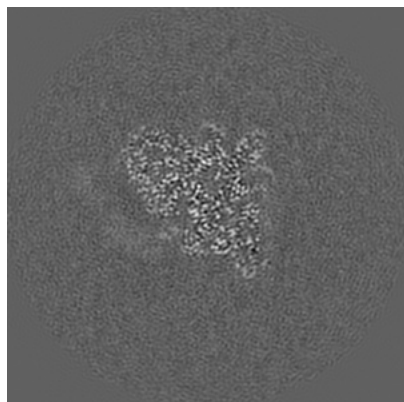


Z

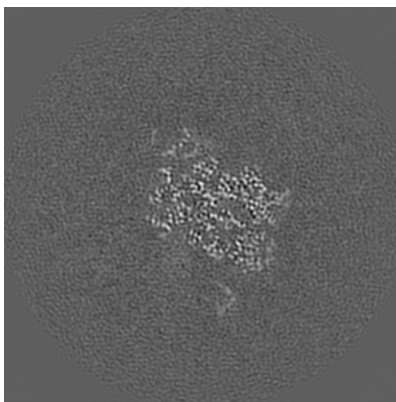
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

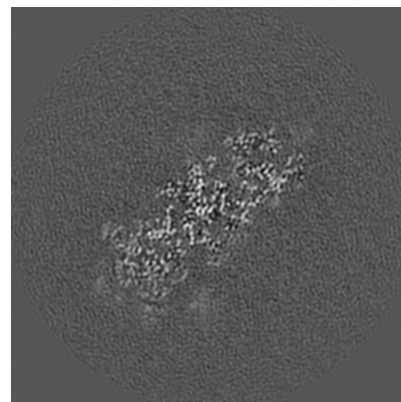
### 6.2.1 Primary map



X Index: 140

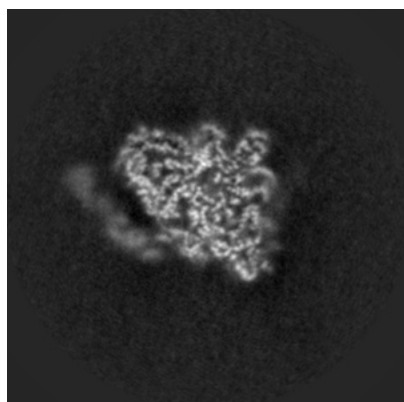


Y Index: 140

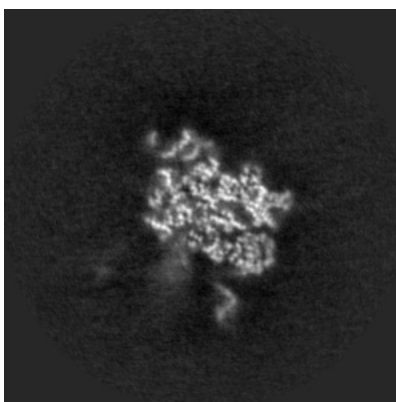


Z Index: 140

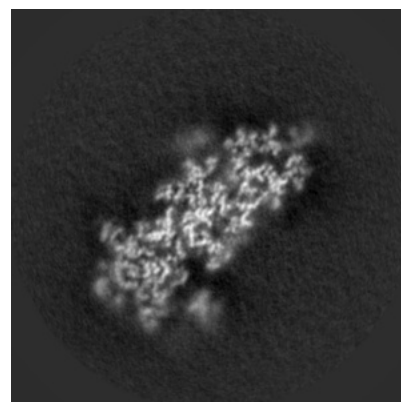
### 6.2.2 Raw map



X Index: 140



Y Index: 140

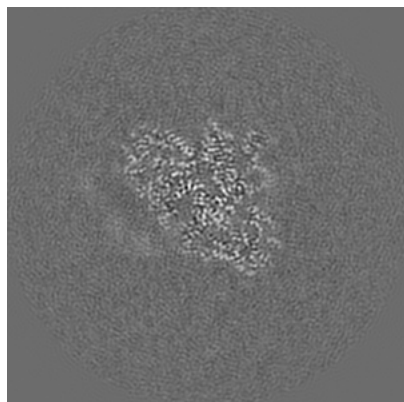


Z Index: 140

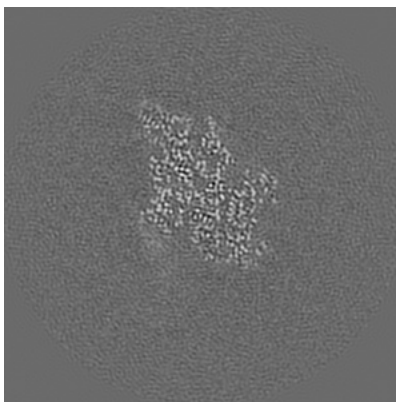
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

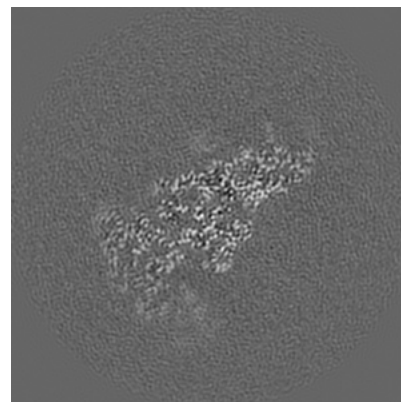
### 6.3.1 Primary map



X Index: 143

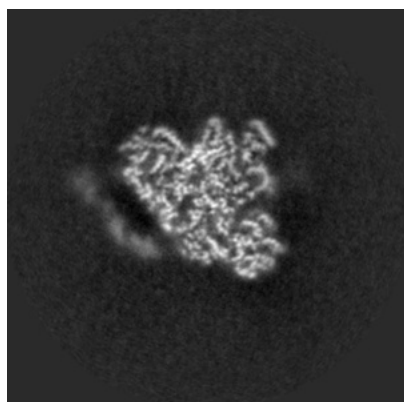


Y Index: 153

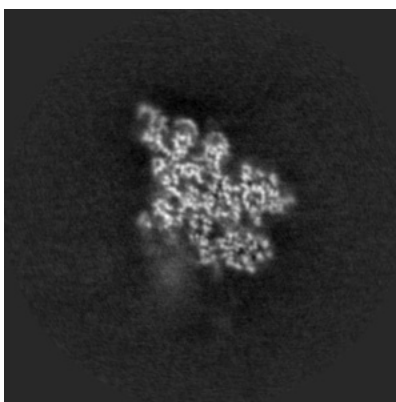


Z Index: 149

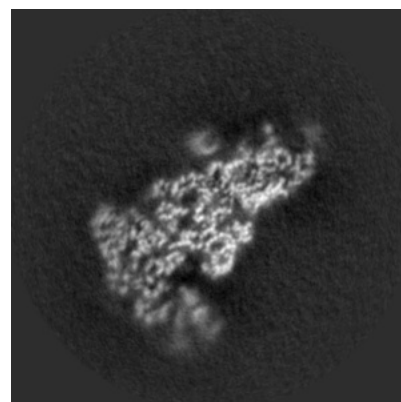
### 6.3.2 Raw map



X Index: 145



Y Index: 148

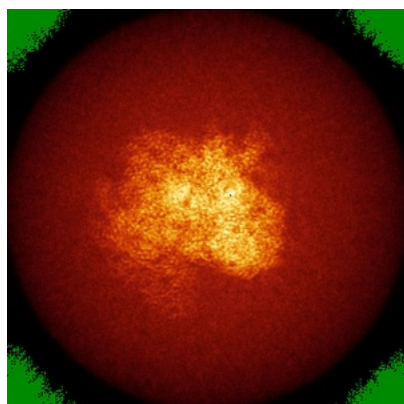


Z Index: 149

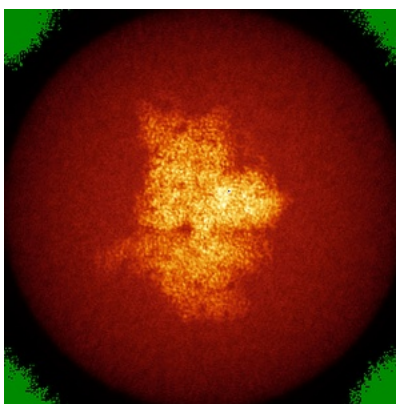
The images above show the largest variance slices of the map in three orthogonal directions.

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

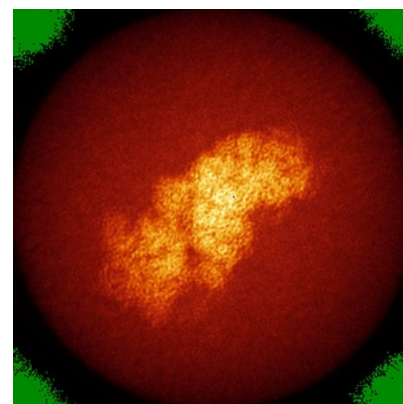
### 6.4.1 Primary map



X

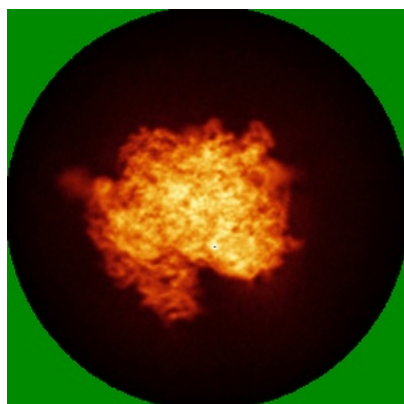


Y

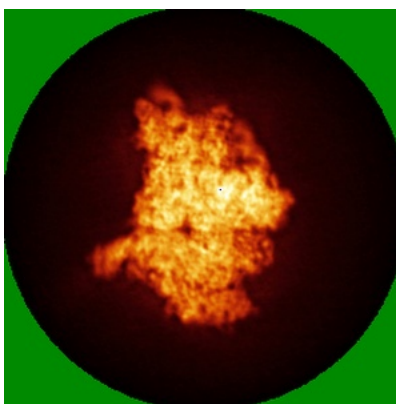


Z

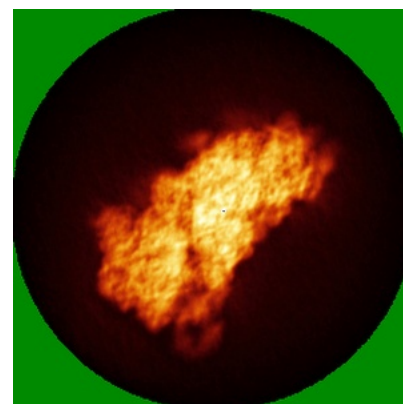
### 6.4.2 Raw map



X



Y

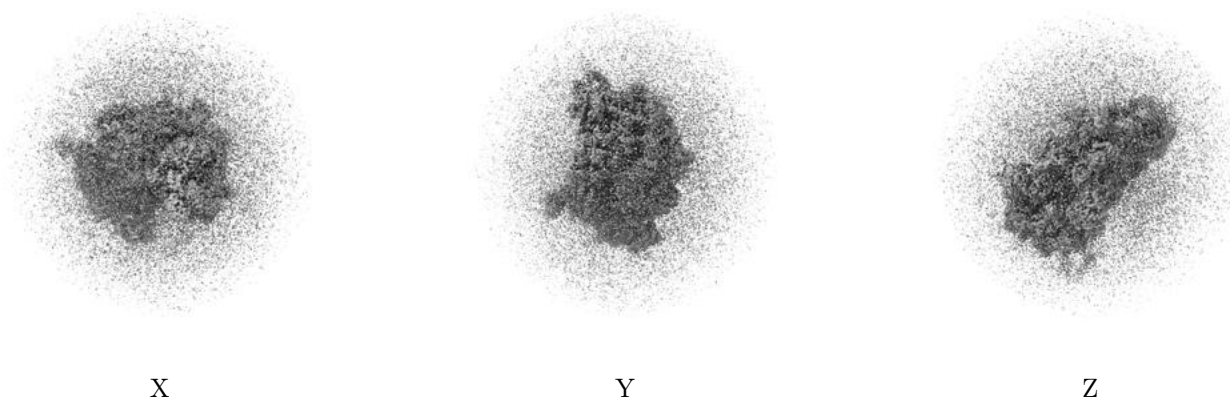


Z

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

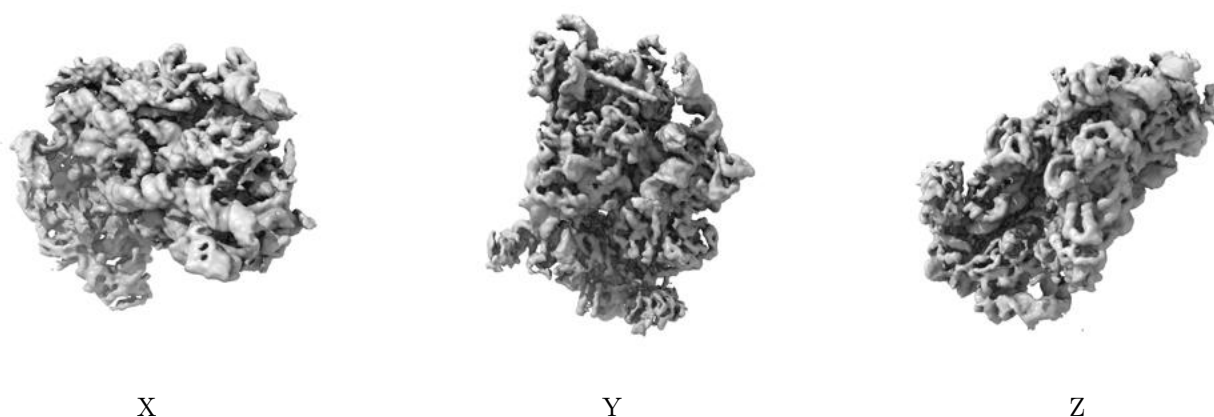
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

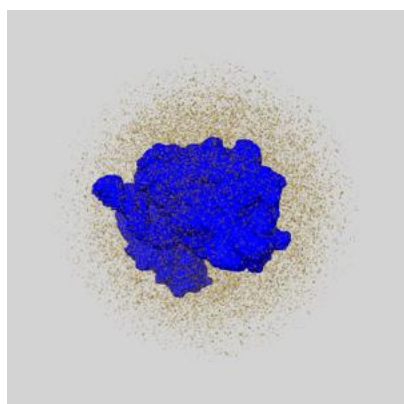
## 6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

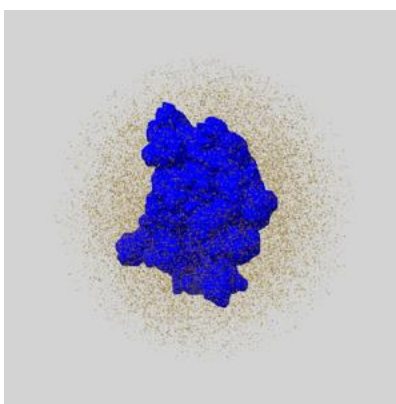
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

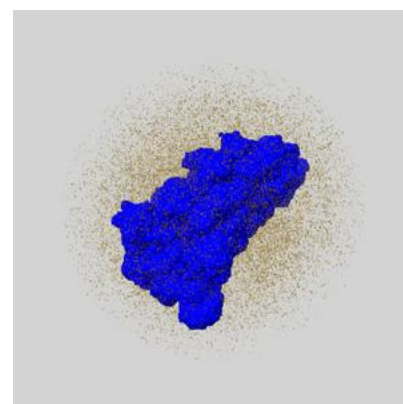
### 6.6.1 emd\_8124\_msk\_1.map [i](#)



X



Y

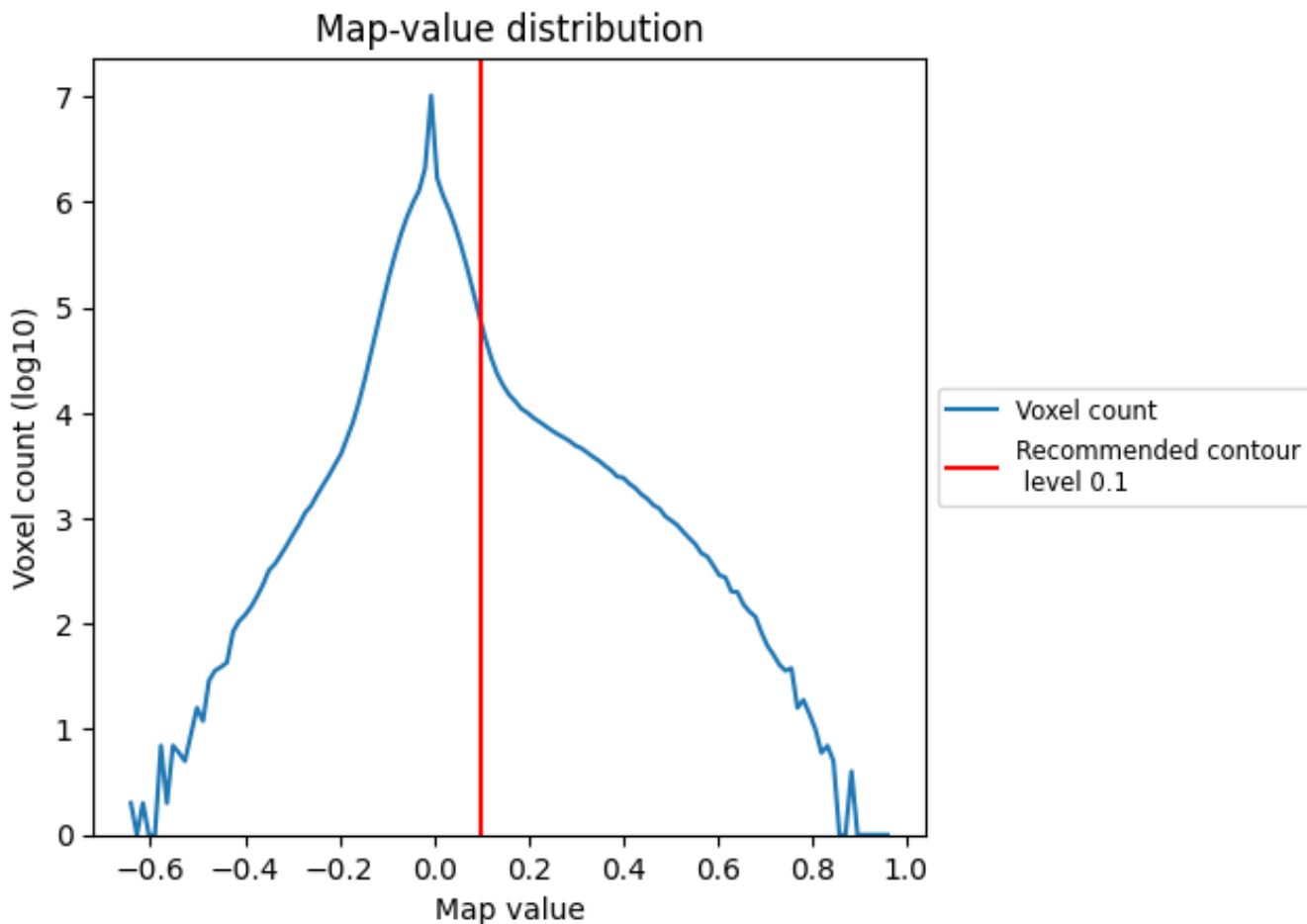


Z

## 7 Map analysis [i](#)

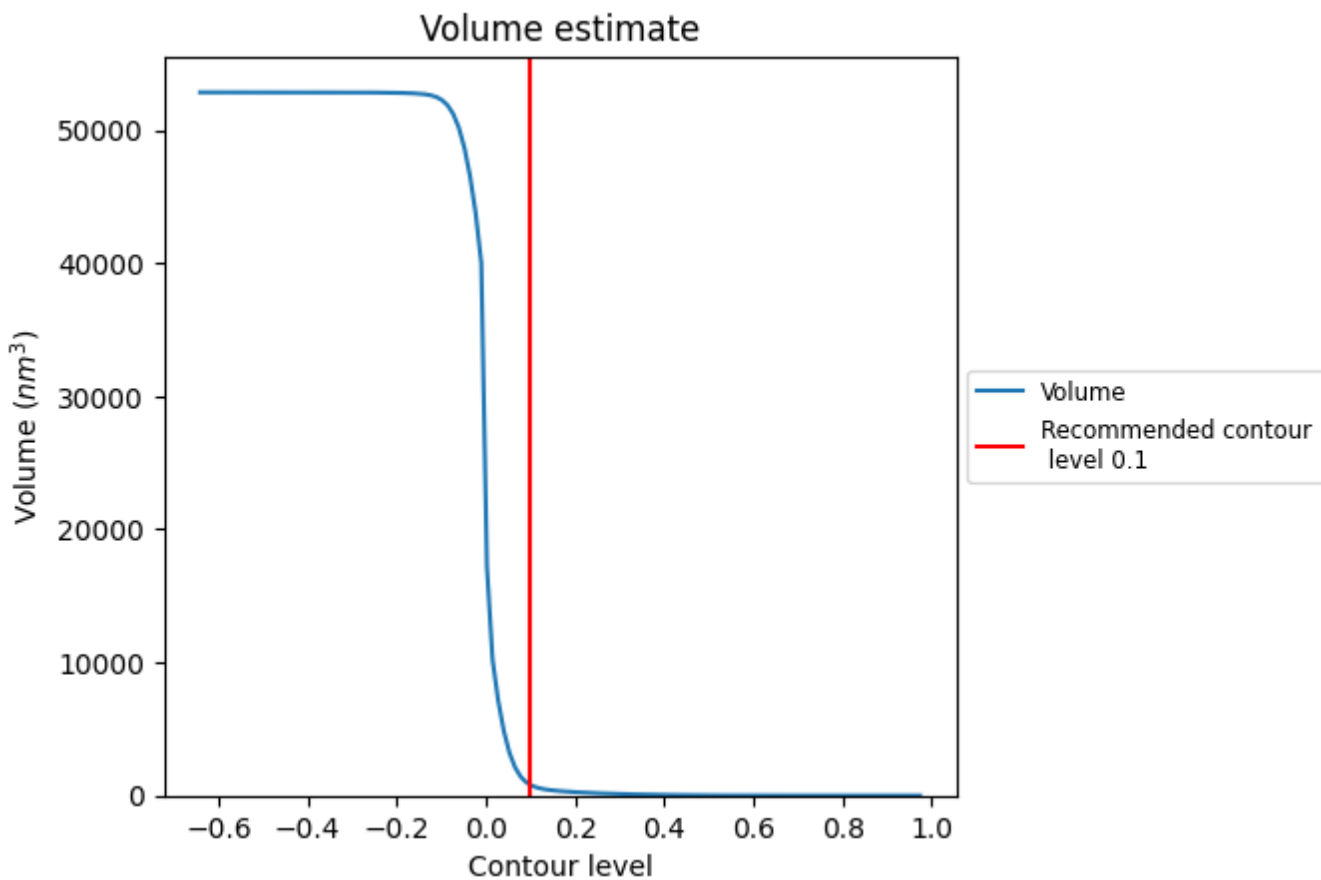
This section contains the results of statistical analysis of the map.

### 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.

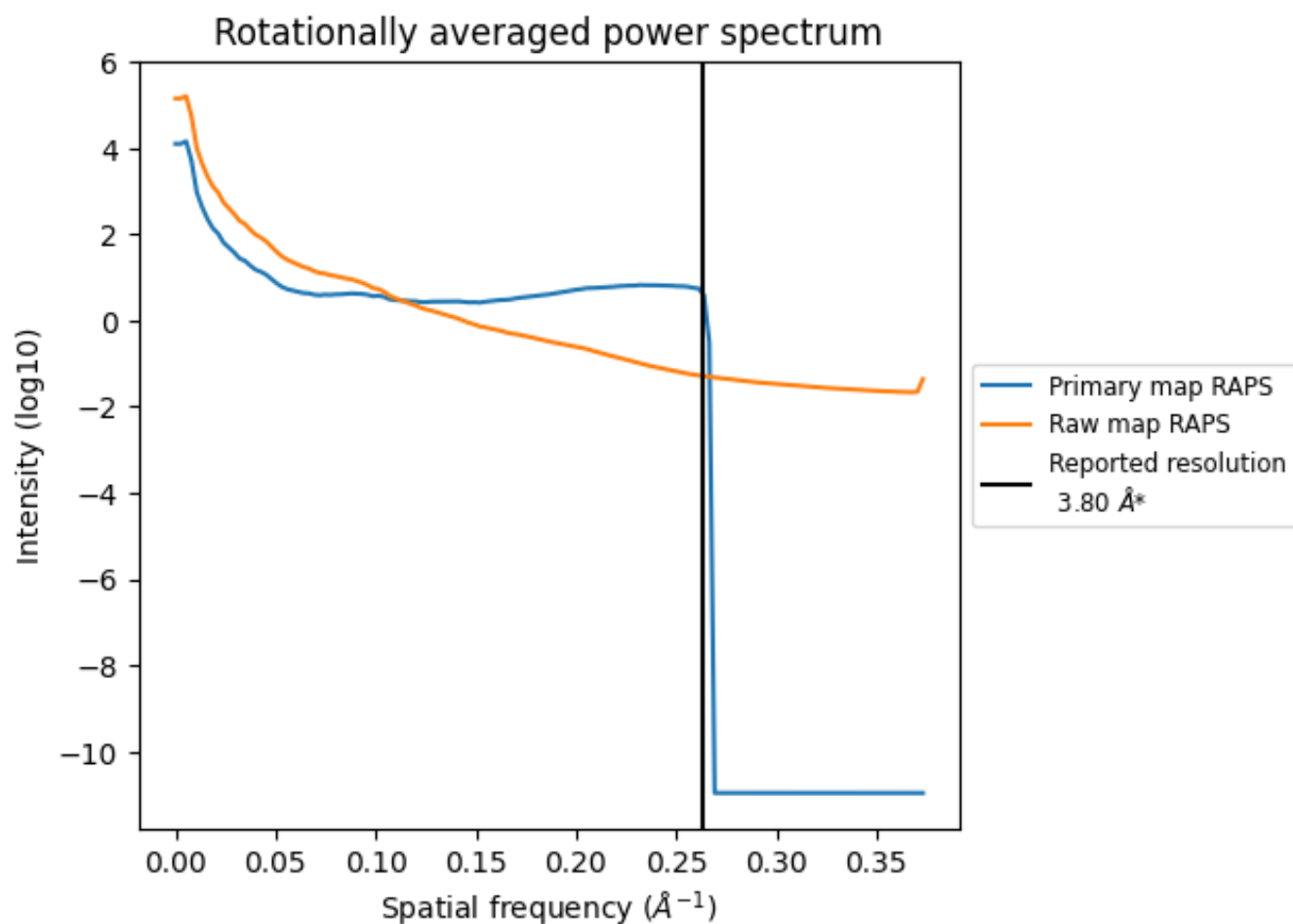
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 800 nm<sup>3</sup>; this corresponds to an approximate mass of 722 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 [i](#)

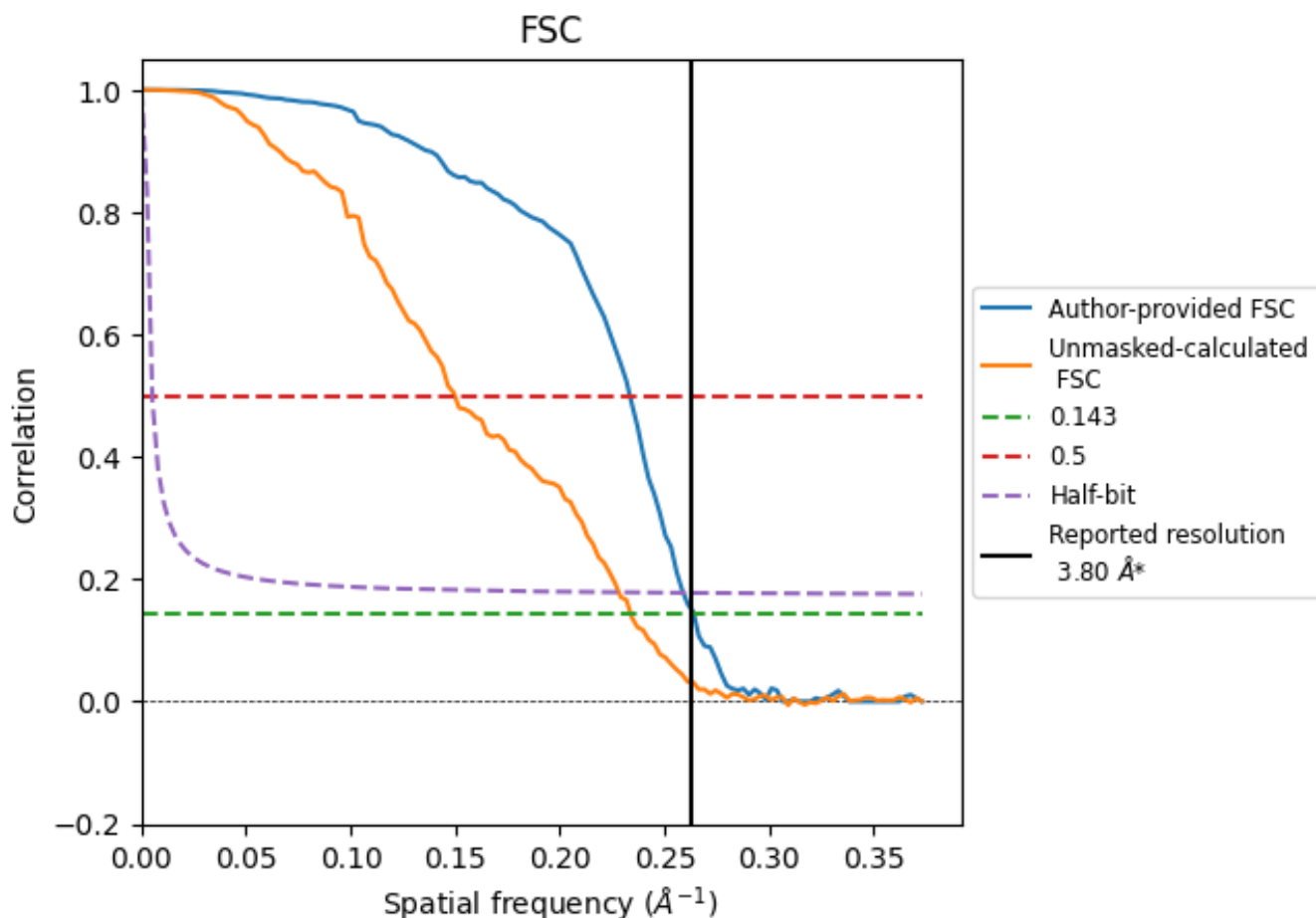


\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

## 8.2 Resolution estimates

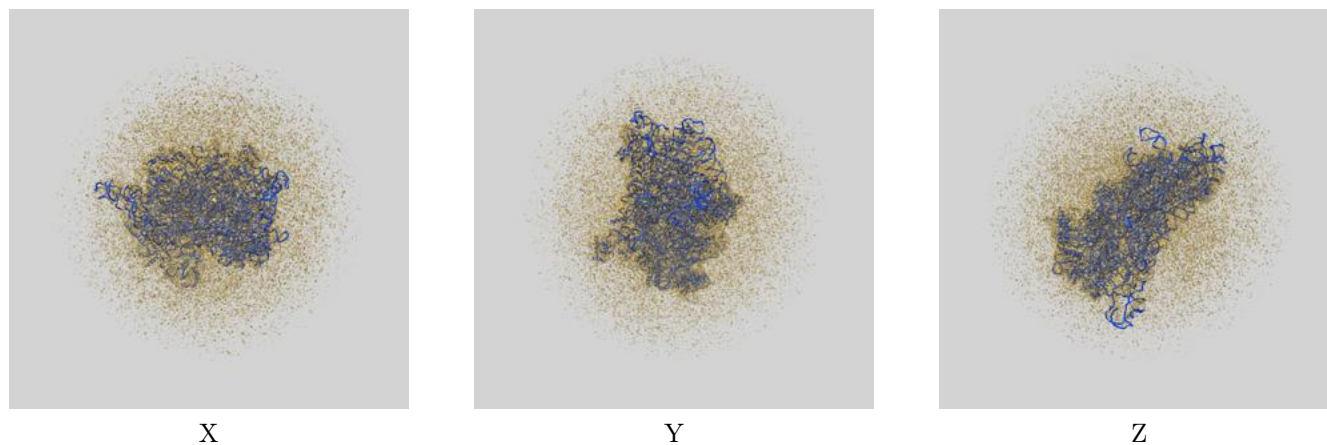
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.79	4.28	3.86
Unmasked-calculated*	4.27	6.68	4.38

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.27 differs from the reported value 3.8 by more than 10 %

## 9 Map-model fit [i](#)

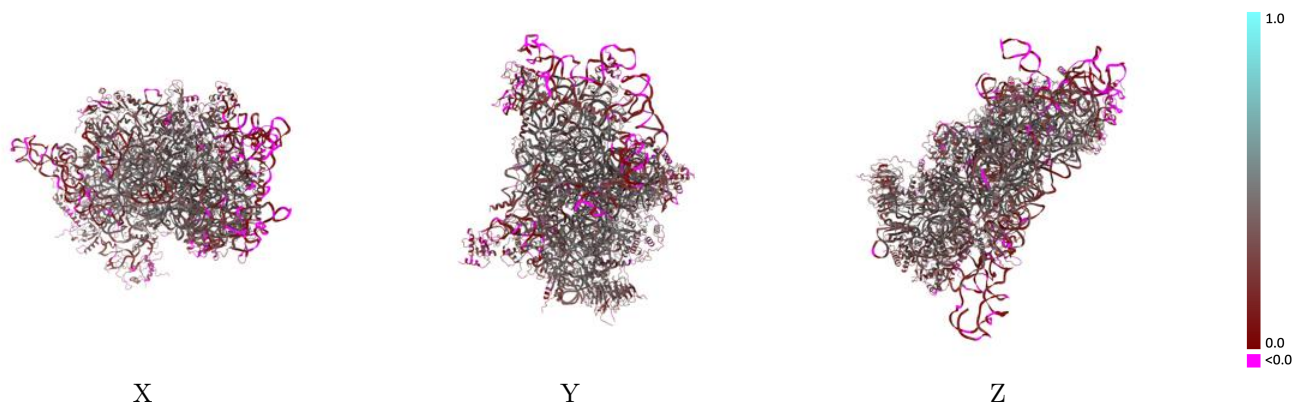
This section contains information regarding the fit between EMDB map EMD-8124 and PDB model 5IT9. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



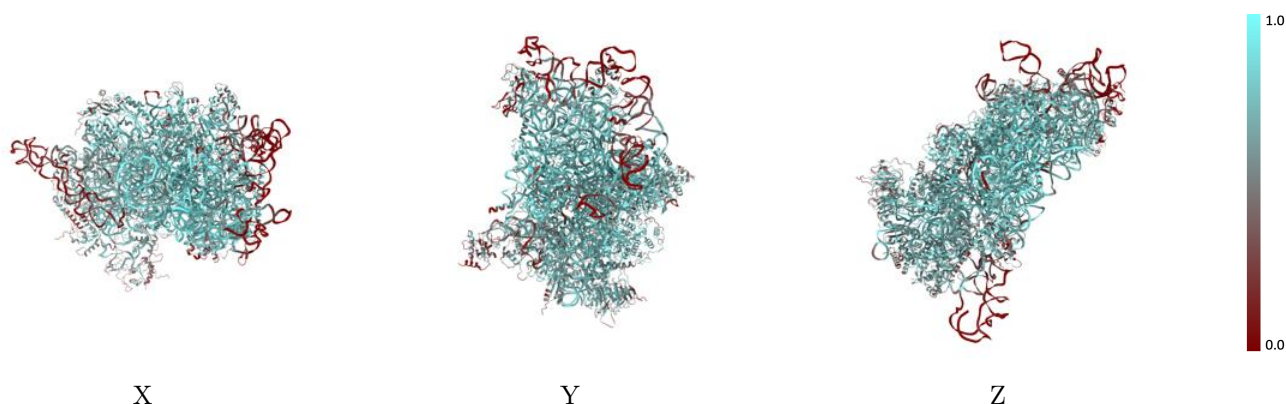
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



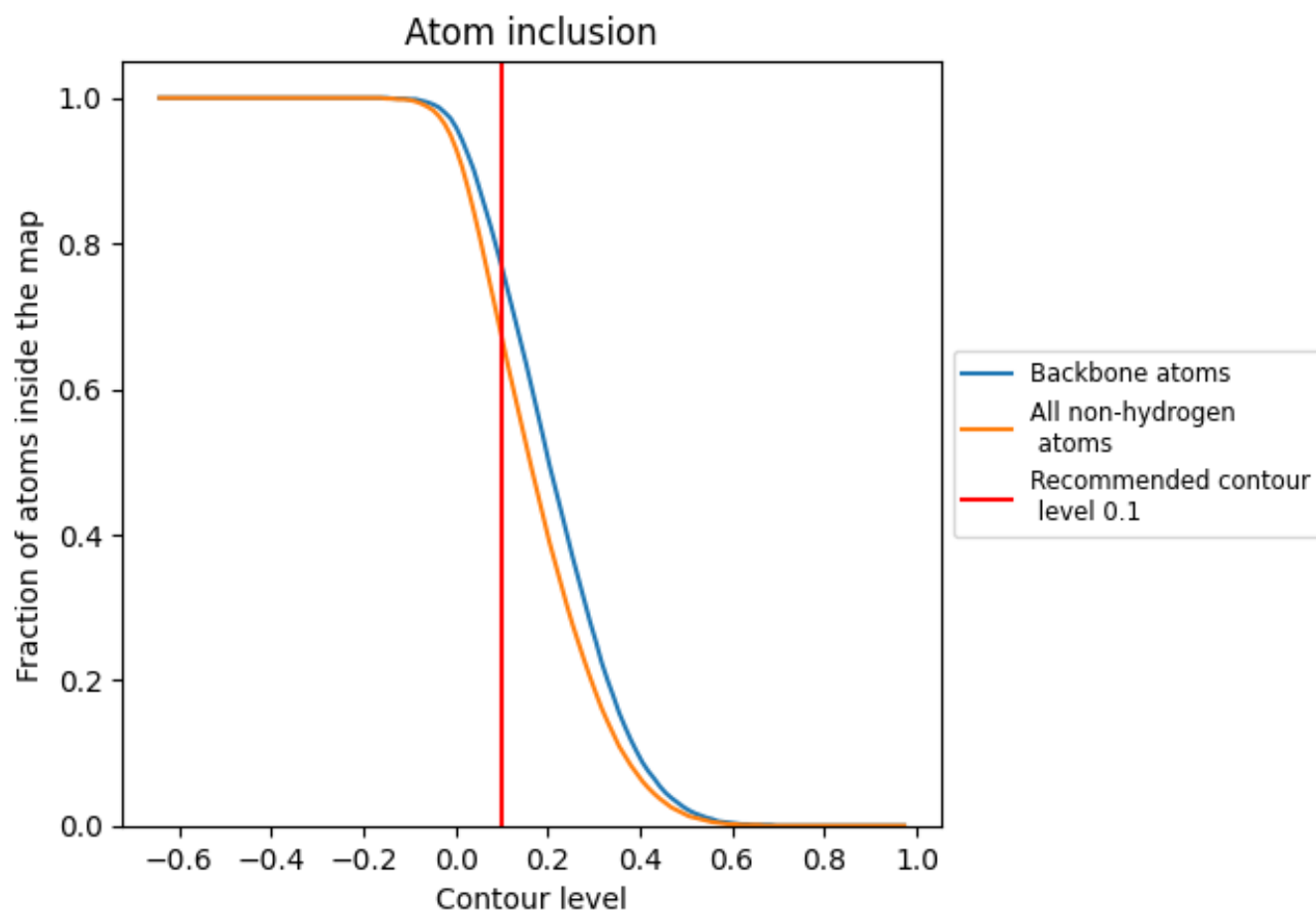
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 67% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.3140
2	 0.7330	 0.3170
A	 0.7340	 0.3460
B	 0.6390	 0.2850
C	 0.7760	 0.4200
D	 0.6470	 0.3370
E	 0.7460	 0.4160
F	 0.6270	 0.3370
G	 0.5480	 0.2380
H	 0.6770	 0.3140
I	 0.6050	 0.2830
J	 0.7470	 0.3750
K	 0.5850	 0.2920
L	 0.7020	 0.3730
M	 0.3190	 0.1150
N	 0.7500	 0.3290
O	 0.7370	 0.3850
P	 0.5350	 0.2530
Q	 0.6930	 0.3620
R	 0.6370	 0.3090
S	 0.3880	 0.1730
T	 0.6580	 0.3360
U	 0.5890	 0.3210
V	 0.7540	 0.3810
W	 0.8200	 0.4430
X	 0.8040	 0.4260
Y	 0.6690	 0.3120
Z	 0.5230	 0.2640
a	 0.7460	 0.3880
b	 0.7020	 0.3450
c	 0.6010	 0.3480
d	 0.7520	 0.4040
e	 0.6290	 0.3100
f	 0.3500	 0.1300
g	 0.5950	 0.3310
i	 0.2960	 0.1530

