



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:08 AM UTC

PDB ID : 8IP9 / pdb_00008ip9
EMDB ID : EMD-35635
Title : Wheat 40S ribosome in complex with a tRNAi
Authors : Yokoyama, T.; Tanaka, M.; Saito, H.; Nishimoto, M.; Tsuda, K.; Sotta, N.;
Shigematsu, H.; Shirouzu, M.; Iwasaki, S.; Ito, T.; Fujiwara, T.
Deposited on : 2023-03-14
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

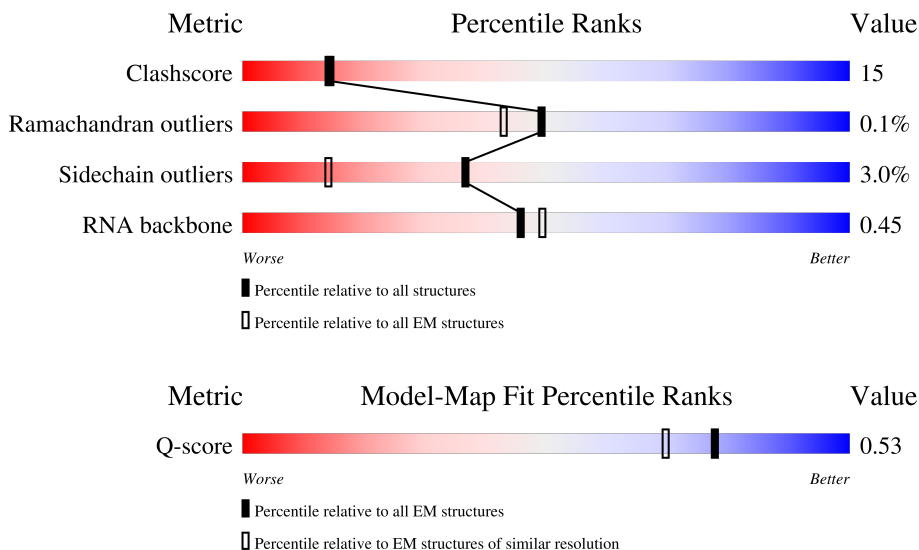
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.00 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	14081 (2.50 - 3.50)

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	aa	1810	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">18%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 18%, orange 45%, yellow 36%, green 12%, grey 6%);"></div> <div style="text-align: center;">45%</div> <div style="text-align: center;">36%</div> <div style="text-align: center;">12%</div> <div style="text-align: center;">6%</div> </div>
2	ba	137	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">36%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 36%, orange 39%, yellow 43%, green 18%, grey 0%);"></div> <div style="text-align: center;">39%</div> <div style="text-align: center;">43%</div> <div style="text-align: center;">18%</div> </div>
3	ca	225	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;">22%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red 22%, orange 52%, yellow 27%, green 21%, grey 0%);"></div> <div style="text-align: center;">52%</div> <div style="text-align: center;">27%</div> <div style="text-align: center;">21%</div> </div>

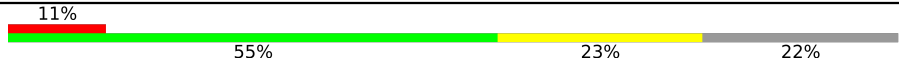
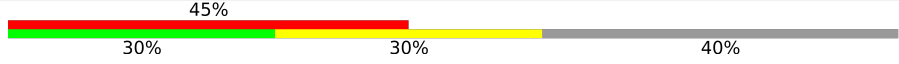

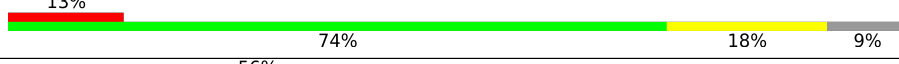
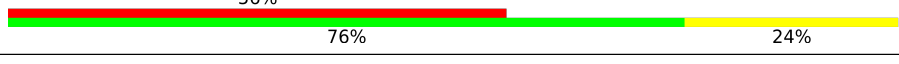

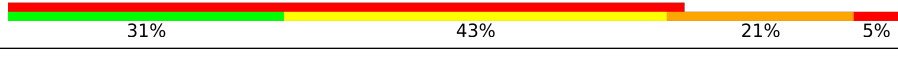
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Mol	Chain	Length	Quality of chain
4	da	188	
5	ga	142	
6	ha	332	
7	ia	227	
8	ja	265	
9	ka	200	
10	la	149	
11	ma	127	
12	na	151	
13	oa	152	
14	pa	151	
15	qa	143	
16	ra	155	
17	sa	154	
18	ta	108	
19	ua	86	
20	va	129	
21	wa	56	
22	xa	86	
23	ya	62	
24	za	308	
25	bb	263	
26	cb	82	
27	db	156	
28	eb	195	

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Mol	Chain	Length	Quality of chain
29	fb	274	
30	gb	250	
31	hb	192	
32	ib	159	
33	IB	25	
34	al	7	
35	cl	75	

2 Entry composition [i](#)

There are 37 unique types of molecules in this entry. The entry contains 73028 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	aa	1695	36156	16155	6463	11845	1693	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
aa	?	-	G	deletion	GB 2123606567
aa	1399	G	C	conflict	GB 2123606567
aa	1411	C	G	conflict	GB 2123606567
aa	1441	C	G	conflict	GB 2123606567
aa	1762	C	G	conflict	GB 2123606567

- Molecule 2 is a protein called 40S ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	ba	113	929	593	178	156	2	0	0

- Molecule 3 is a protein called 40S ribosomal protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	ca	178	1443	891	291	257	4	0	0

- Molecule 4 is a protein called 40S ribosomal protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	da	81	703	461	117	122	3	0	0

- Molecule 5 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	ga	138	Total	C	N	O	S	0	0
			1070	679	207	181	3		

- Molecule 6 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	ha	322	Total	C	N	O	S	0	0
			2473	1555	429	478	11		

- Molecule 7 is a protein called 40S ribosomal protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	ia	213	Total	C	N	O	S	0	0
			1673	1061	303	300	9		

- Molecule 8 is a protein called 40S ribosomal protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	ja	261	Total	C	N	O	S	0	0
			2082	1325	388	362	7		

- Molecule 9 is a protein called 40S ribosomal protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	ka	193	Total	C	N	O	S	0	0
			1516	947	285	277	7		

- Molecule 10 is a protein called 40S ribosomal protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	la	140	Total	C	N	O	S	0	0
			1119	712	215	187	5		

- Molecule 11 is a protein called 40S ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	ma	103	Total	C	N	O	S	0	0
			806	504	147	151	4		

- Molecule 12 is a protein called 40S ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	na	125	Total	C	N	O	S	0	0
			941	579	185	173	4		

- Molecule 13 is a protein called 40S ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	oa	136	Total	C	N	O	S	0	0
			1114	695	220	193	6		

- Molecule 14 is a protein called 40S ribosomal protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	pa	150	Total	C	N	O	S	0	0
			1195	765	224	204	2		

- Molecule 15 is a protein called 40S ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	qa	119	Total	C	N	O	S	0	0
			975	607	185	177	6		

- Molecule 16 is a protein called 40S ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	ra	135	Total	C	N	O	S	0	0
			1065	672	200	189	4		

- Molecule 17 is a protein called 40S ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	sa	100	Total	C	N	O	S	0	0
			807	518	151	133	5		

- Molecule 18 is a protein called 40S ribosomal protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	ta	77	Total	C	N	O	S	0	0
			618	387	116	113	2		

- Molecule 19 is a protein called 40S ribosomal protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	ua	64	Total	C	N	O	S	0	0
			513	314	104	93	2		

- Molecule 20 is a protein called 40S ribosomal protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	va	128	Total	C	N	O	S	0	0
			1039	653	199	182	5		

- Molecule 21 is a protein called 40S ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	wa	39	Total	C	N	O	S	0	0
			314	193	65	50	6		

- Molecule 22 is a protein called 40S ribosomal protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	xa	70	Total	C	N	O	S	0	0
			546	342	101	96	7		

- Molecule 23 is a protein called 40S ribosomal protein eS30.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	ya	39	Total	C	N	O	0	0
			322	199	74	49		

- Molecule 24 is a protein called 40S ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	za	202	Total	C	N	O	S	0	0
			1609	1018	291	289	11		

- Molecule 25 is a protein called 40S ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	bb	211	Total	C	N	O	S	0	0
			1720	1096	311	304	9		

- Molecule 26 is a protein called 40S ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	cb	76	Total	C	N	O	S	0	0
			596	368	111	114	3		

- Molecule 27 is a protein called 40S ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	db	95	Total	C	N	O	S	0	0
			771	472	168	124	7		

- Molecule 28 is a protein called 40S ribosomal protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	eb	181	Total	C	N	O	S	0	0
			1493	945	298	246	4		

- Molecule 29 is a protein called 40S ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	fb	214	Total	C	N	O	S	0	0
			1660	1070	294	287	9		

- Molecule 30 is a protein called 40S ribosomal protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	gb	151	Total	C	N	O	S	0	0
			1199	749	233	209	8		

- Molecule 31 is a protein called 40S ribosomal protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	hb	169	Total	C	N	O	S	0	0
			1389	889	255	243	2		

- Molecule 32 is a protein called 40S ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ib	145	Total	C	N	O	S	0	0
			1166	745	223	192	6		

- Molecule 33 is a protein called 60S ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	IB	25	Total	C	N	O	S	0	0
			237	145	62	27	3		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	al	3	Total	C	N	O	P	0	0
			61	29	12	18	2		

- Molecule 35 is a RNA chain called tRNAi.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	cl	75	Total	C	N	O	P	S	0	0
			1622	730	298	518	75	1		

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

Mol	Chain	Residues	Atoms		AltConf
36	aa	80	Total	Mg	0
			80	80	
36	ja	1	Total	Mg	0
			1	1	
36	al	1	Total	Mg	0
			1	1	
36	cl	2	Total	Mg	0
			2	2	

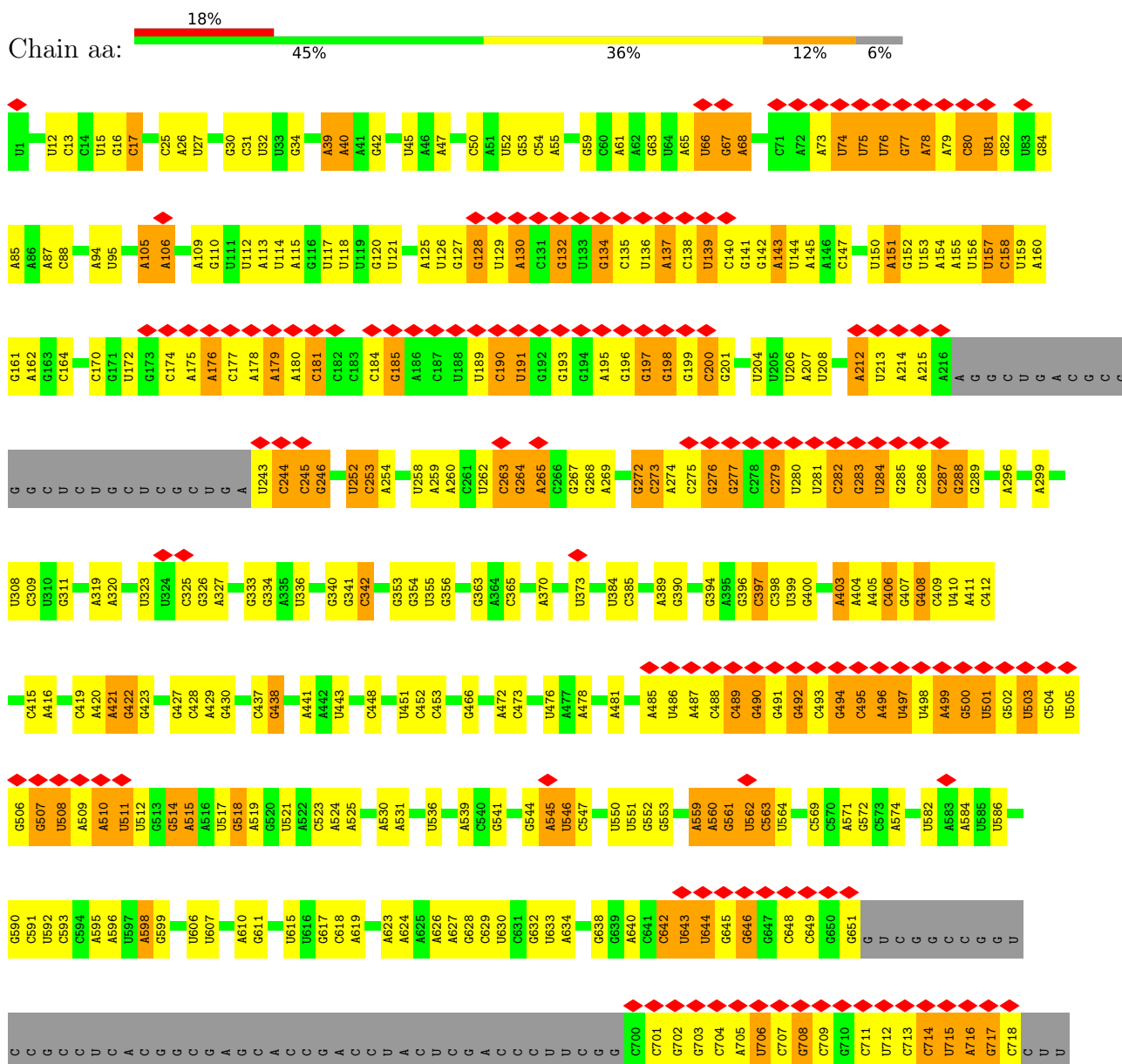
- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

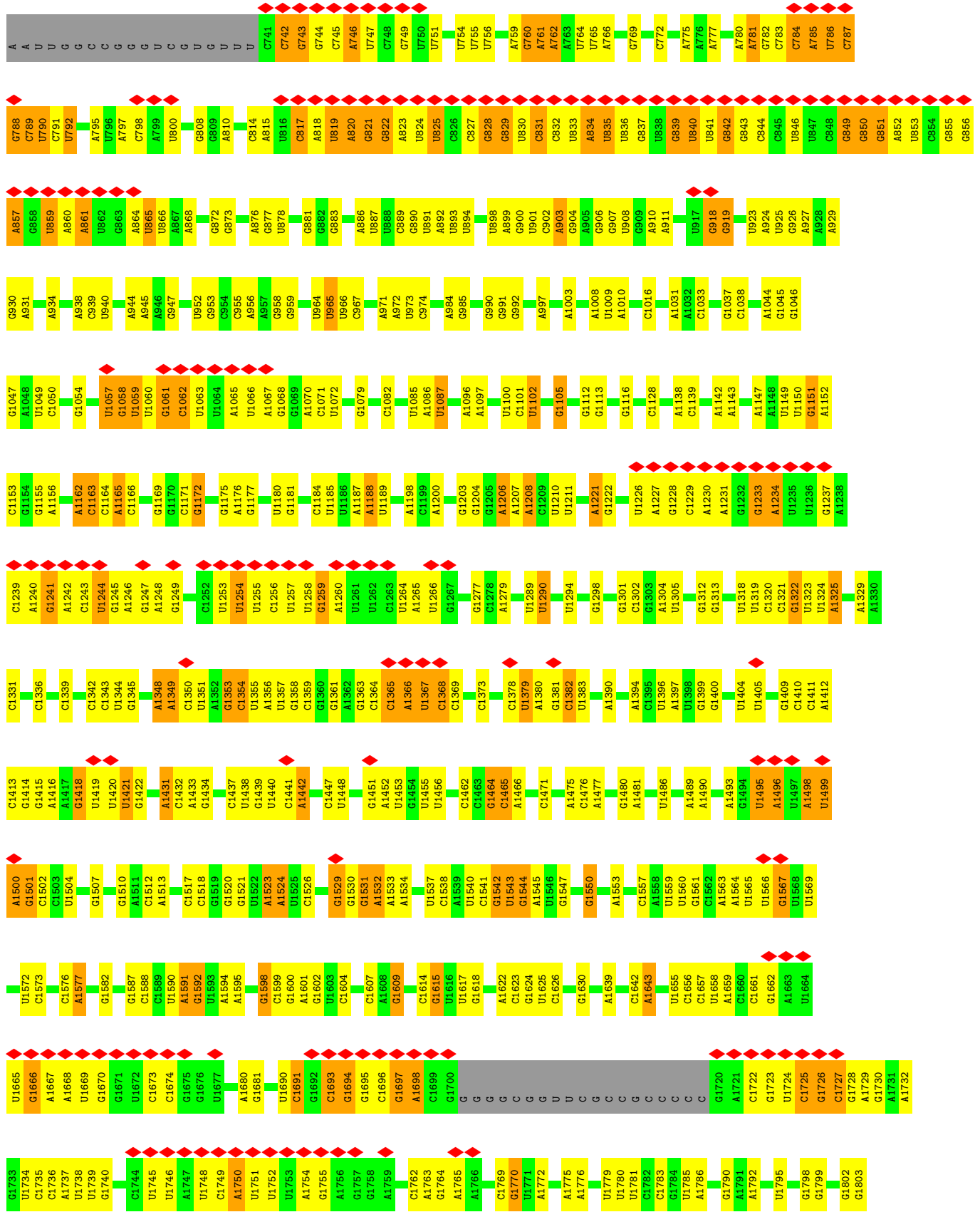
Mol	Chain	Residues	Atoms		AltConf
37	wa	1	Total	Zn	0
			1	1	
37	db	1	Total	Zn	0
			1	1	

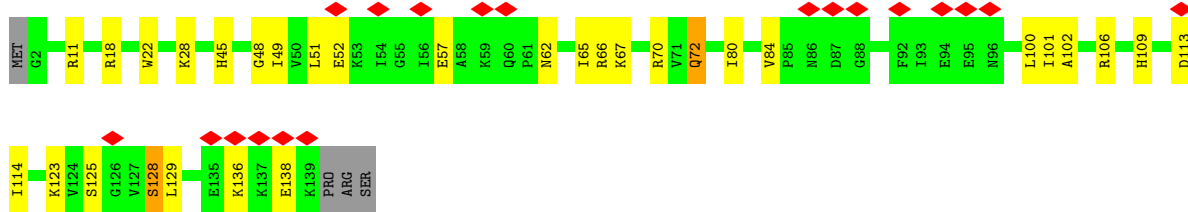
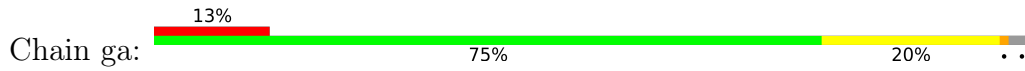
3 Residue-property plots

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

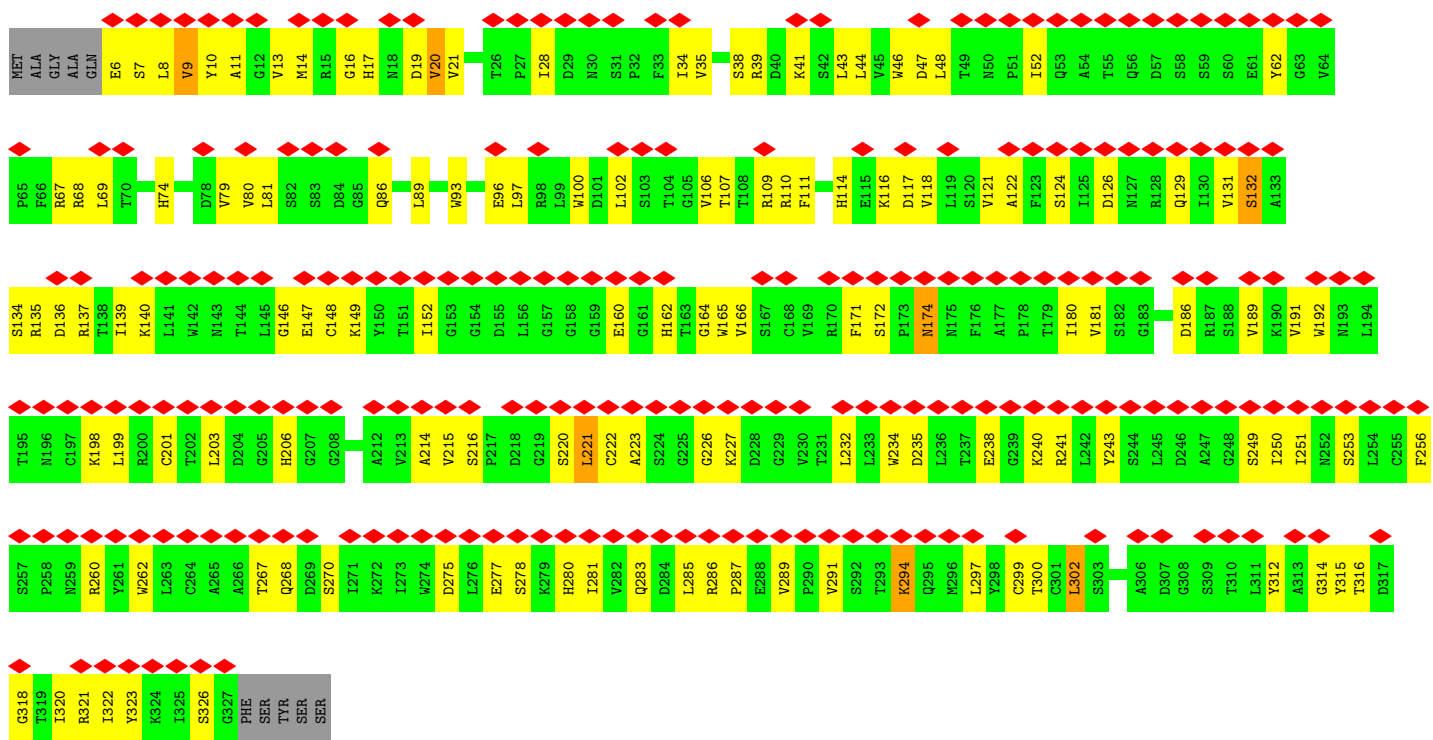
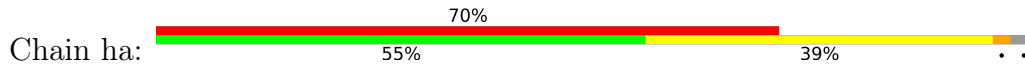
- Molecule 1: 18S ribosomal RNA



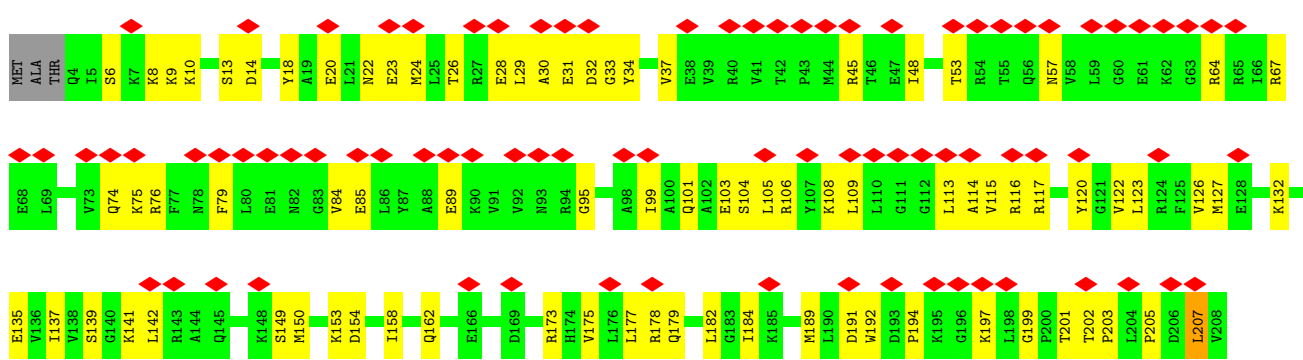
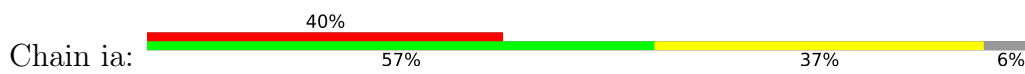


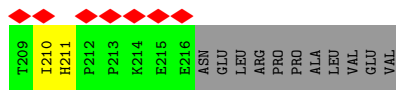


• Molecule 6: RACK1

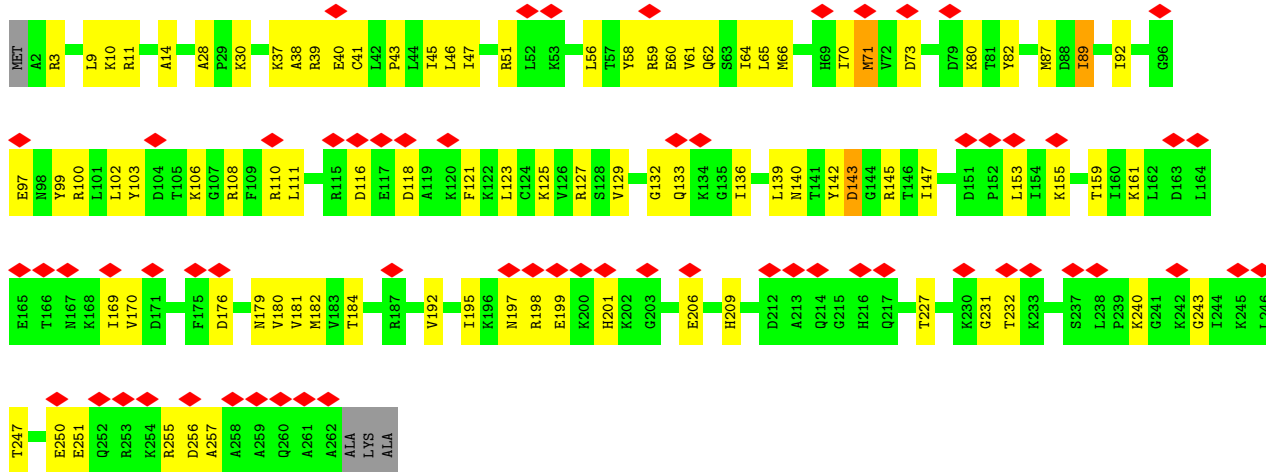


• Molecule 7: 40S ribosomal protein uS3

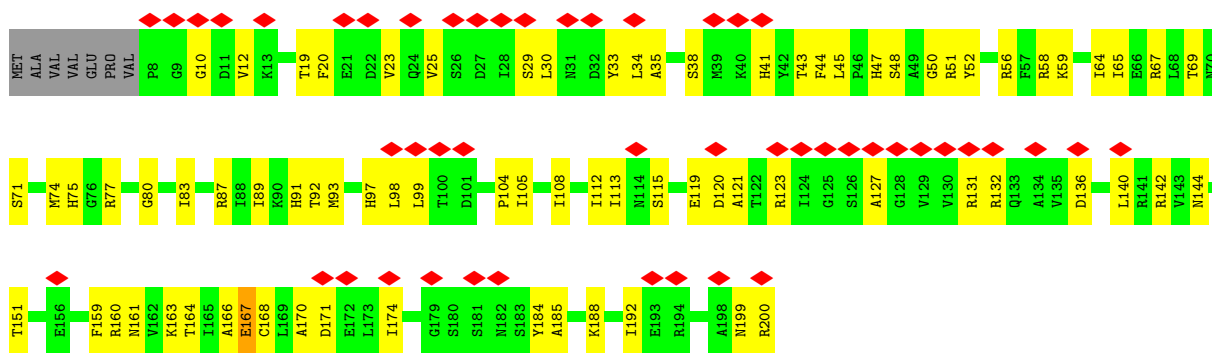




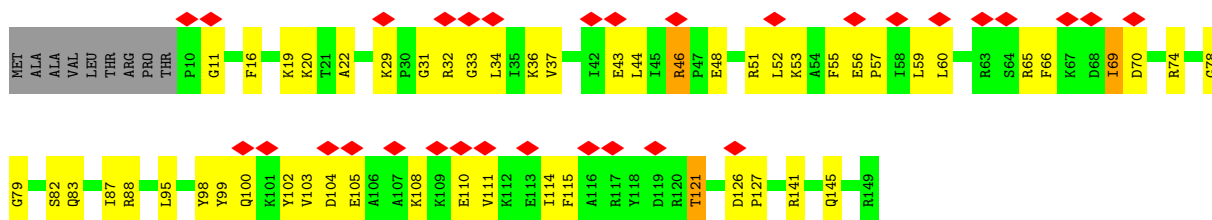
• Molecule 8: 40S ribosomal protein eS4



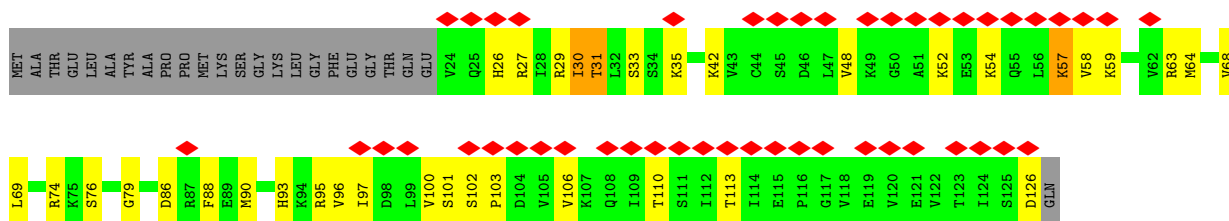
• Molecule 9: 40S ribosomal protein uS7



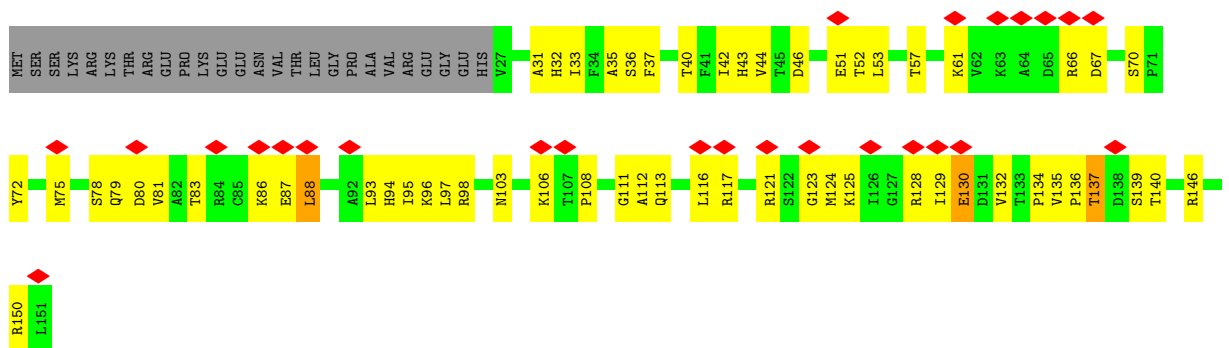
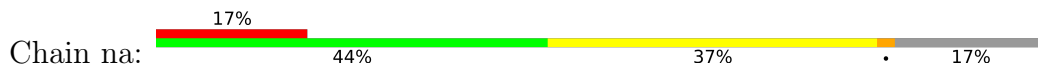
• Molecule 10: 40S ribosomal protein uS9



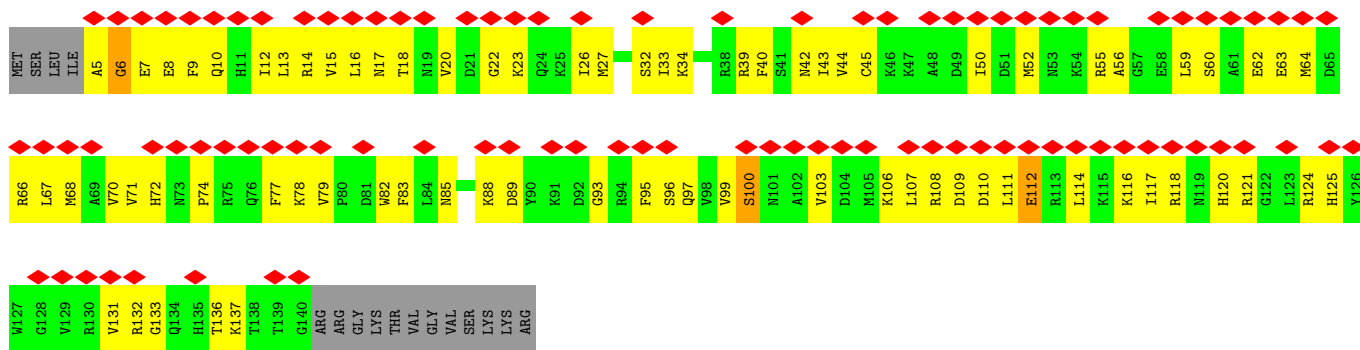
• Molecule 11: 40S ribosomal protein uS10



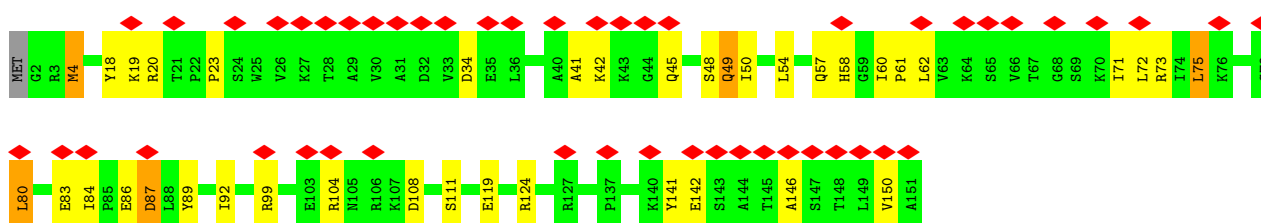
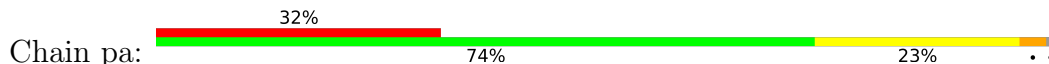
• Molecule 12: 40S ribosomal protein uS11



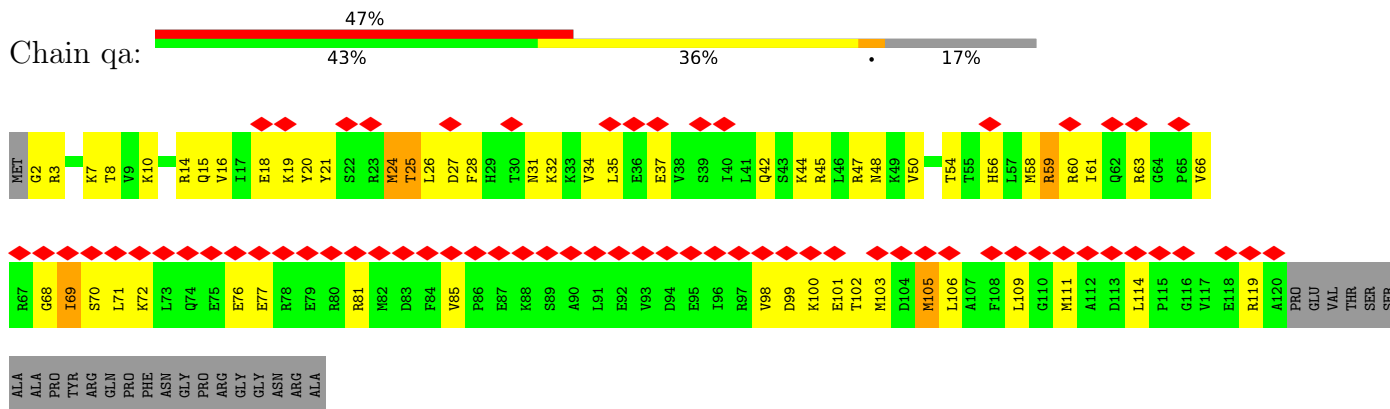
• Molecule 13: 40S ribosomal protein uS13



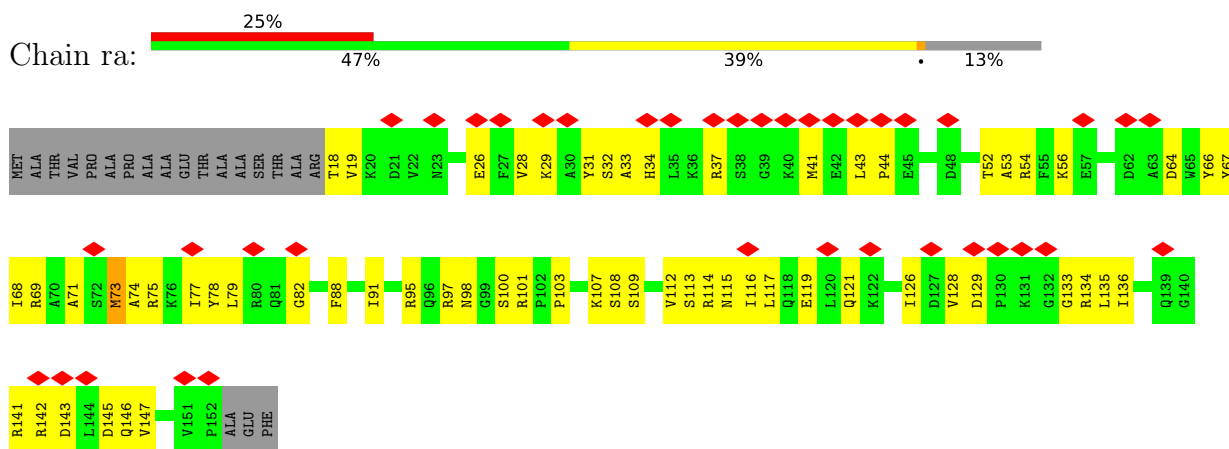
• Molecule 14: 40S ribosomal protein uS15



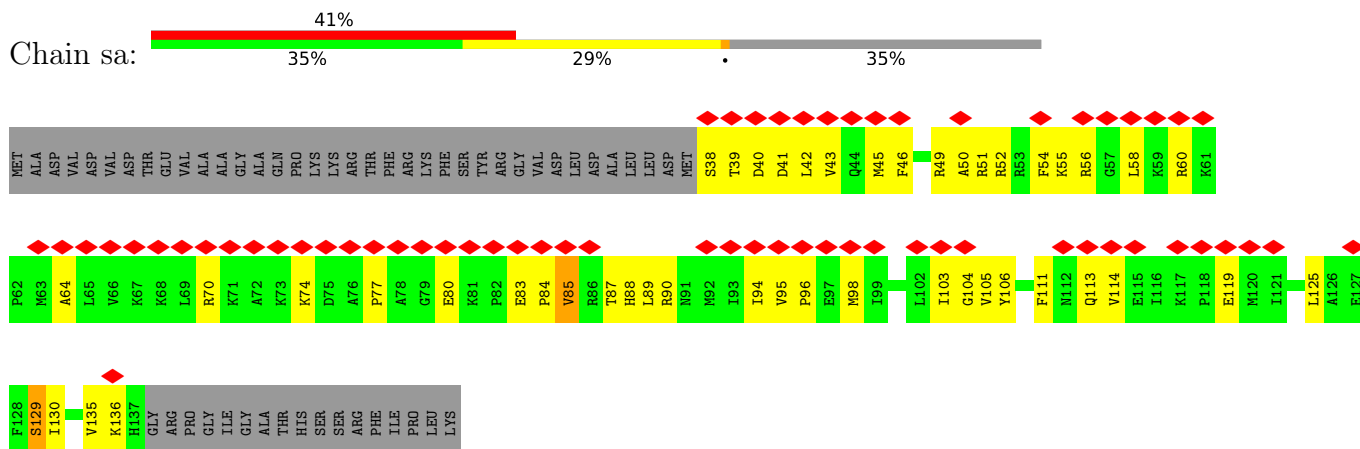
- Molecule 15: 40S ribosomal protein eS17



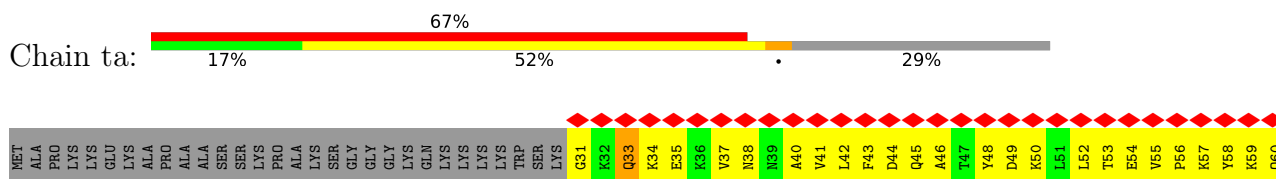
- Molecule 16: 40S ribosomal protein eS19

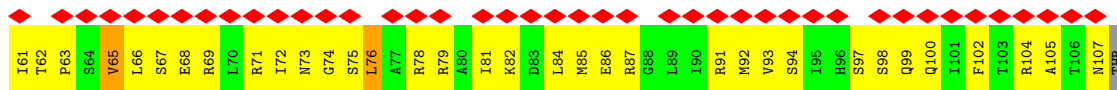


- Molecule 17: 40S ribosomal protein uS19

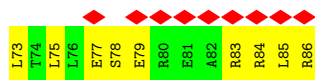


- Molecule 18: 40S ribosomal protein eS25

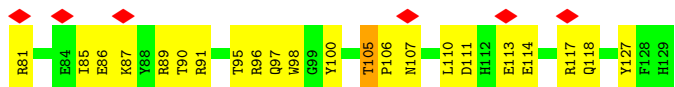
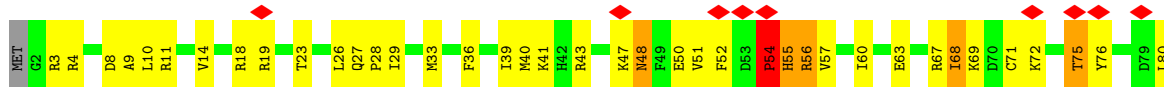




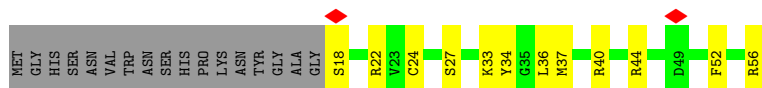
• Molecule 19: 40S ribosomal protein eS28



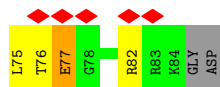
• Molecule 20: 40S ribosomal protein uS8



• Molecule 21: 40S ribosomal protein uS14

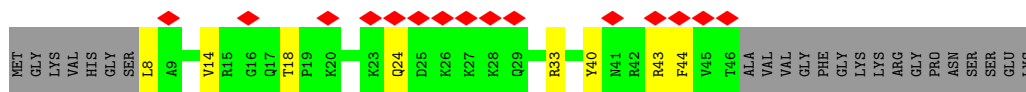


• Molecule 22: 40S ribosomal protein eS27

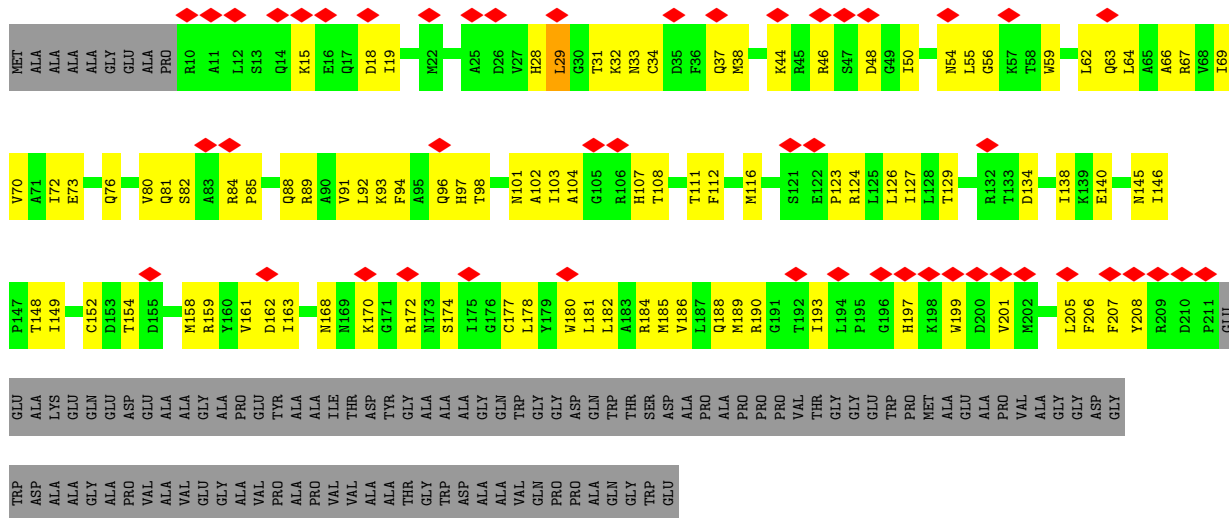


• Molecule 23: 40S ribosomal protein eS30

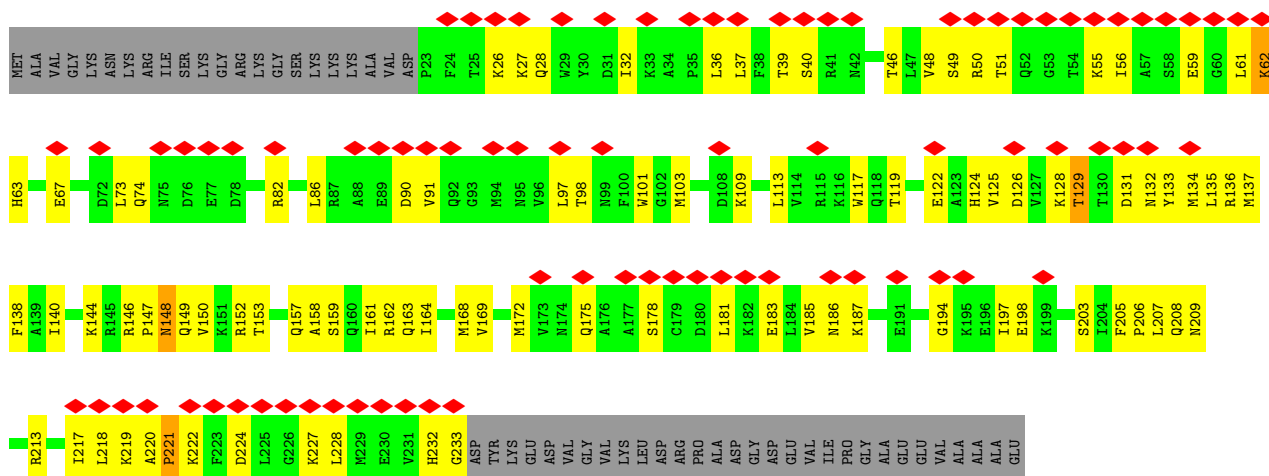




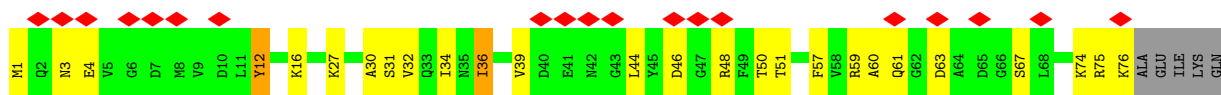
• Molecule 24: 40S ribosomal protein uS2



• Molecule 25: 40S ribosomal protein eS1

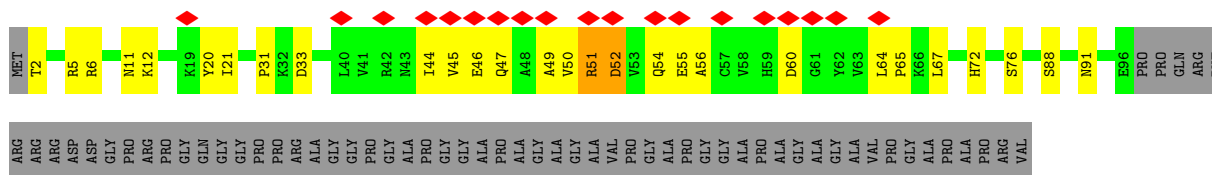


• Molecule 26: 40S ribosomal protein eS21

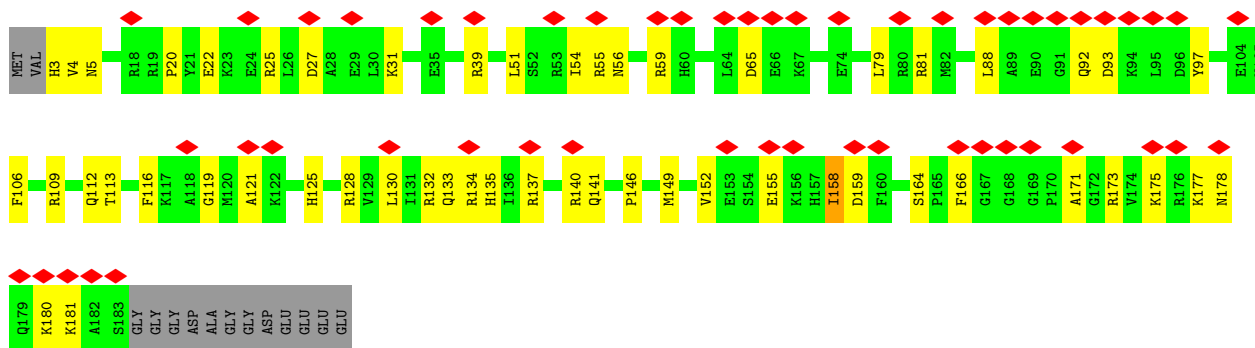


LEU

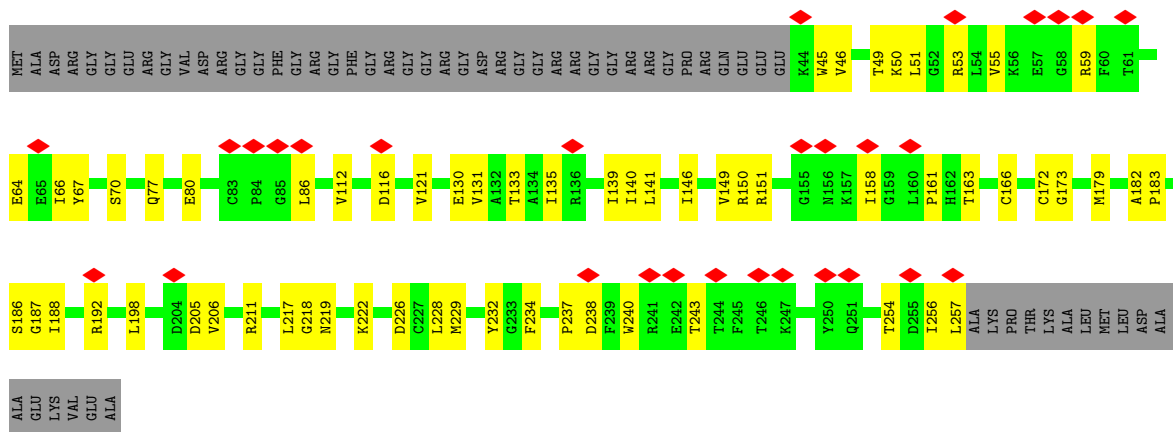
• Molecule 27: 40S ribosomal protein eS26



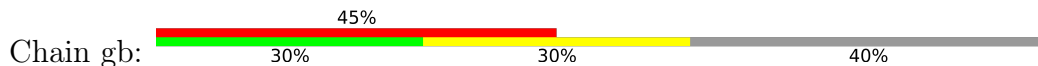
• Molecule 28: 40S ribosomal protein uS4

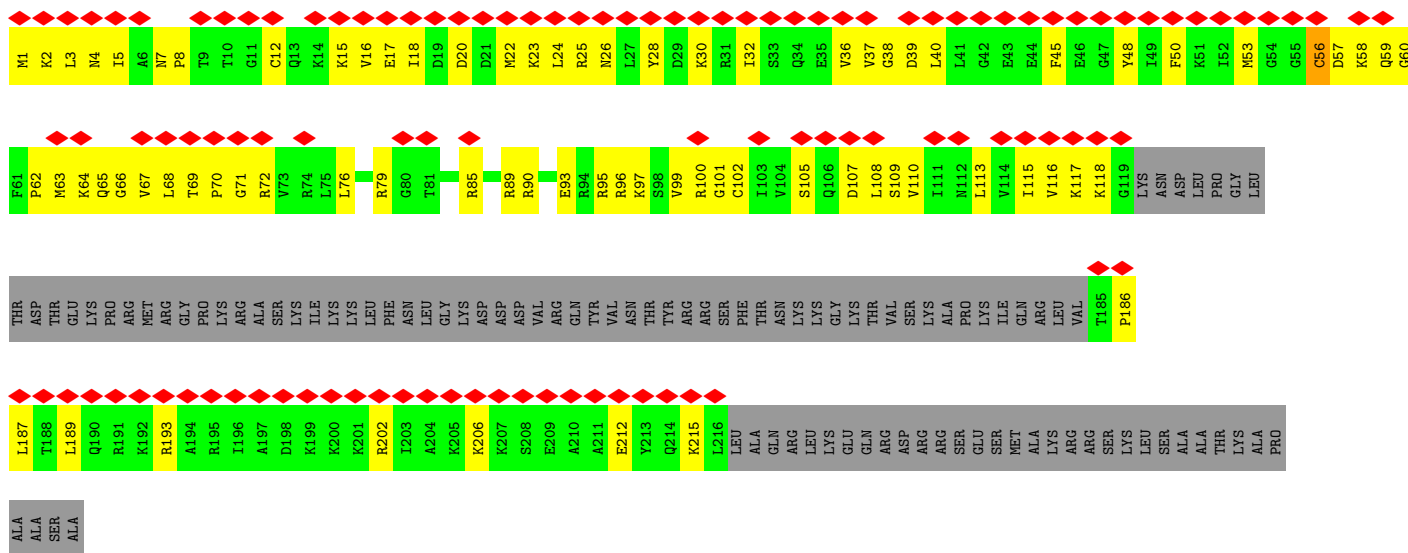


• Molecule 29: 40S ribosomal protein uS5

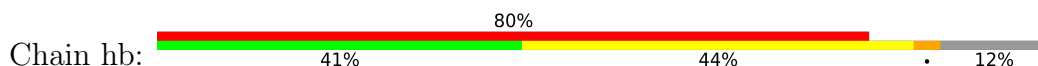


• Molecule 30: 40S ribosomal protein eS6

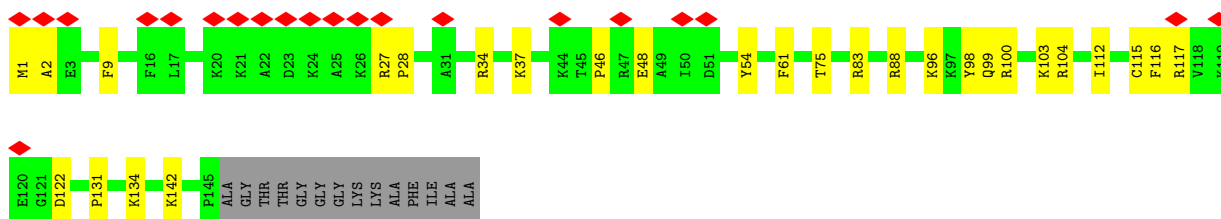
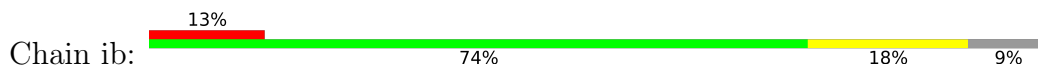




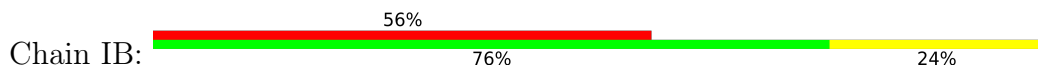
• Molecule 31: 40S ribosomal protein eS7



• Molecule 32: 40S ribosomal protein uS17

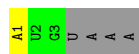


• Molecule 33: 60S ribosomal protein eL41

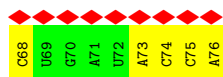
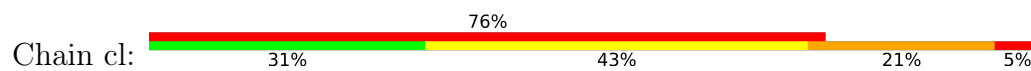




- Molecule 34: mRNA



- Molecule 35: tRNAi



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41361	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.0	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	60000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.068	Depositor
Minimum map value	-0.027	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.013	Depositor
Map size (\AA)	441.28, 441.28, 441.28	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.788, 0.788, 0.788	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, 1MA, MG, H2U, ZN, G7M, MIA, PSU, 2MG, 5MC

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	aa	0.35	0/40441	0.38	0/63026
2	ba	0.31	0/943	0.59	0/1253
3	ca	0.32	0/1464	0.55	0/1957
4	da	0.33	0/722	0.72	0/972
5	ga	0.33	0/1088	0.54	0/1448
6	ha	0.28	0/2530	0.63	0/3443
7	ia	0.31	0/1697	0.55	0/2279
8	ja	0.32	0/2123	0.52	0/2853
9	ka	0.30	0/1538	0.57	0/2070
10	la	0.36	0/1138	0.64	0/1517
11	ma	0.31	0/815	0.53	0/1098
12	na	0.34	0/953	0.63	0/1278
13	oa	0.29	0/1132	0.58	0/1511
14	pa	0.30	0/1219	0.47	0/1638
15	qa	0.30	0/985	0.64	0/1313
16	ra	0.33	0/1088	0.60	1/1463 (0.1%)
17	sa	0.25	0/824	0.56	0/1102
18	ta	0.31	0/624	0.79	0/836
19	ua	0.34	0/514	0.63	0/685
20	va	0.39	0/1057	0.75	3/1421 (0.2%)
21	wa	0.34	0/318	0.45	0/418
22	xa	0.28	0/555	0.47	0/742
23	ya	0.35	0/326	0.53	0/430
24	za	0.33	0/1644	0.55	0/2226
25	bb	0.33	0/1749	0.62	0/2349
26	cb	0.33	0/605	0.57	0/814
27	db	0.36	0/784	0.55	2/1047 (0.2%)
28	eb	0.31	0/1521	0.53	0/2035
29	fb	0.36	0/1696	0.50	0/2292
30	gb	0.30	0/1210	0.70	1/1606 (0.1%)
31	hb	0.27	0/1415	0.62	0/1907
32	ib	0.35	0/1192	0.51	1/1597 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	IB	0.28	0/238	0.54	0/302
34	al	0.36	0/68	0.28	0/105
35	cl	0.22	0/1534	0.36	0/2386
All	All	0.33	0/77750	0.48	8/113419 (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
4	da	0	1
6	ha	0	2
10	la	0	1
12	na	0	1
13	oa	0	1
18	ta	0	2
20	va	0	2
31	hb	0	1
All	All	0	11

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	gb	70	PRO	CA-N-CD	-9.41	98.83	112.00
20	va	55	HIS	N-CA-C	-9.06	91.50	110.80
20	va	54	PRO	CA-C-N	7.53	135.92	121.54
20	va	54	PRO	C-N-CA	7.53	135.92	121.54
32	ib	28	PRO	CA-N-CD	-6.10	103.46	112.00

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	da	63	HIS	Peptide
6	ha	221	LEU	Peptide
6	ha	294	LYS	Peptide
10	la	46	ARG	Peptide
12	na	137	THR	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	aa	36156	0	18230	612	0
2	ba	929	0	992	54	0
3	ca	1443	0	1478	48	0
4	da	703	0	701	53	0
5	ga	1070	0	1133	22	0
6	ha	2473	0	2406	114	0
7	ia	1673	0	1756	68	0
8	ja	2082	0	2171	68	0
9	ka	1516	0	1564	65	0
10	la	1119	0	1190	52	0
11	ma	806	0	863	29	0
12	na	941	0	977	54	0
13	oa	1114	0	1140	67	0
14	pa	1195	0	1287	35	0
15	qa	975	0	1024	55	0
16	ra	1065	0	1083	50	0
17	sa	807	0	863	35	0
18	ta	618	0	654	74	0
19	ua	513	0	551	23	0
20	va	1039	0	1063	66	0
21	wa	314	0	318	11	0
22	xa	546	0	564	16	0
23	ya	322	0	354	10	0
24	za	1609	0	1615	83	0
25	bb	1720	0	1793	72	0
26	cb	596	0	583	26	0
27	db	771	0	789	28	0
28	eb	1493	0	1559	53	0
29	fb	1660	0	1743	51	0
30	gb	1199	0	1287	74	0
31	hb	1389	0	1444	87	0
32	ib	1166	0	1232	18	0
33	IB	237	0	289	3	0
34	al	61	0	31	1	0
35	cl	1622	0	842	33	0
36	aa	80	0	0	0	0
36	al	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	cl	2	0	0	0	0
36	ja	1	0	0	0	0
37	db	1	0	0	0	0
37	wa	1	0	0	0	0
All	All	73028	0	55569	1958	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 15.

The worst 5 of 1958 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)
1:aa:68:A:N6	1:aa:84:G:H1	1.24	1.36
1:aa:782:G:H1	1:aa:790:U:H3	1.11	0.97
1:aa:646:G:H1	1:aa:705:A:H2	1.06	0.95
6:ha:35:VAL:HG11	6:ha:81:LEU:HD21	1.52	0.90
1:aa:67:G:H21	1:aa:147:C:H4'	1.34	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	ba	111/137 (81%)	102 (92%)	9 (8%)	0	100	100
3	ca	174/225 (77%)	165 (95%)	9 (5%)	0	100	100
4	da	79/188 (42%)	66 (84%)	13 (16%)	0	100	100
5	ga	136/142 (96%)	130 (96%)	6 (4%)	0	100	100
6	ha	320/332 (96%)	290 (91%)	30 (9%)	0	100	100
7	ia	211/227 (93%)	196 (93%)	15 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	ja	259/265 (98%)	249 (96%)	10 (4%)	0	100	100
9	ka	191/200 (96%)	177 (93%)	14 (7%)	0	100	100
10	la	138/149 (93%)	124 (90%)	14 (10%)	0	100	100
11	ma	101/127 (80%)	98 (97%)	3 (3%)	0	100	100
12	na	123/151 (82%)	120 (98%)	3 (2%)	0	100	100
13	oa	134/152 (88%)	122 (91%)	12 (9%)	0	100	100
14	pa	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
15	qa	117/143 (82%)	111 (95%)	5 (4%)	1 (1%)	14	48
16	ra	133/155 (86%)	128 (96%)	5 (4%)	0	100	100
17	sa	98/154 (64%)	86 (88%)	12 (12%)	0	100	100
18	ta	75/108 (69%)	53 (71%)	22 (29%)	0	100	100
19	ua	62/86 (72%)	61 (98%)	1 (2%)	0	100	100
20	va	126/129 (98%)	114 (90%)	11 (9%)	1 (1%)	16	50
21	wa	37/56 (66%)	35 (95%)	2 (5%)	0	100	100
22	xa	68/86 (79%)	62 (91%)	6 (9%)	0	100	100
23	ya	37/62 (60%)	35 (95%)	2 (5%)	0	100	100
24	za	200/308 (65%)	195 (98%)	5 (2%)	0	100	100
25	bb	209/263 (80%)	181 (87%)	25 (12%)	3 (1%)	9	36
26	cb	74/82 (90%)	68 (92%)	6 (8%)	0	100	100
27	db	93/156 (60%)	91 (98%)	2 (2%)	0	100	100
28	eb	179/195 (92%)	163 (91%)	16 (9%)	0	100	100
29	fb	212/274 (77%)	202 (95%)	10 (5%)	0	100	100
30	gb	147/250 (59%)	134 (91%)	13 (9%)	0	100	100
31	hb	167/192 (87%)	144 (86%)	22 (13%)	1 (1%)	21	56
32	ib	143/159 (90%)	134 (94%)	9 (6%)	0	100	100
33	IB	23/25 (92%)	23 (100%)	0	0	100	100
All	All	4325/5329 (81%)	4004 (93%)	315 (7%)	6 (0%)	49	80

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	va	56	ARG
15	qa	68	GLY

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Mol	Chain	Res	Type
31	hb	66	PRO
25	bb	55	LYS
25	bb	62	LYS

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
2	ba	99/116 (85%)	96 (97%)	3 (3%)	36 69
3	ca	153/181 (84%)	150 (98%)	3 (2%)	48 76
4	da	77/143 (54%)	74 (96%)	3 (4%)	28 62
5	ga	109/113 (96%)	106 (97%)	3 (3%)	38 70
6	ha	274/281 (98%)	263 (96%)	11 (4%)	28 62
7	ia	180/192 (94%)	175 (97%)	5 (3%)	38 70
8	ja	222/224 (99%)	218 (98%)	4 (2%)	51 77
9	ka	163/169 (96%)	156 (96%)	7 (4%)	26 60
10	la	113/120 (94%)	111 (98%)	2 (2%)	51 77
11	ma	97/115 (84%)	90 (93%)	7 (7%)	13 43
12	na	98/121 (81%)	94 (96%)	4 (4%)	27 61
13	oa	119/133 (90%)	114 (96%)	5 (4%)	26 61
14	pa	129/130 (99%)	121 (94%)	8 (6%)	16 49
15	qa	108/126 (86%)	100 (93%)	8 (7%)	13 42
16	ra	112/124 (90%)	111 (99%)	1 (1%)	70 85
17	sa	87/130 (67%)	85 (98%)	2 (2%)	44 74
18	ta	69/92 (75%)	68 (99%)	1 (1%)	59 80
19	ua	57/78 (73%)	56 (98%)	1 (2%)	51 77
20	va	110/111 (99%)	105 (96%)	5 (4%)	24 59
21	wa	34/47 (72%)	34 (100%)	0	100 100
22	xa	64/78 (82%)	63 (98%)	1 (2%)	55 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	ya	32/49 (65%)	32 (100%)	0	100	100
24	za	172/233 (74%)	169 (98%)	3 (2%)	53	78
25	bb	189/228 (83%)	186 (98%)	3 (2%)	55	79
26	cb	63/68 (93%)	61 (97%)	2 (3%)	34	67
27	db	82/113 (73%)	79 (96%)	3 (4%)	30	64
28	eb	154/162 (95%)	149 (97%)	5 (3%)	34	67
29	fb	181/219 (83%)	178 (98%)	3 (2%)	53	78
30	gb	130/215 (60%)	125 (96%)	5 (4%)	29	63
31	hb	151/171 (88%)	147 (97%)	4 (3%)	40	72
32	ib	126/132 (96%)	124 (98%)	2 (2%)	55	79
33	IB	24/24 (100%)	23 (96%)	1 (4%)	26	61
All	All	3778/4438 (85%)	3663 (97%)	115 (3%)	37	69

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	pa	4	MET
31	hb	137	VAL
15	qa	70	SER
31	hb	84	LEU
28	eb	158	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
24	za	96	GLN
27	db	11	ASN
24	za	97	HIS
25	bb	52	GLN
27	db	73	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	aa	1690/1810 (93%)	431 (25%)	0
34	al	2/7 (28%)	0	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	cl	74/75 (98%)	27 (36%)	0
All	All	1766/1892 (93%)	458 (25%)	0

5 of 458 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	aa	17	C
1	aa	25	C
1	aa	26	A
1	aa	27	U
1	aa	34	G

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

11 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	1MA	cl	58	35	21,25,26	2.93	5 (23%)	30,37,40	2.38	8 (26%)
35	G7M	cl	46	35	23,26,27	2.92	9 (39%)	34,39,42	1.79	9 (26%)
35	1MG	cl	9	35	23,26,27	2.89	8 (34%)	33,39,42	1.77	8 (24%)
35	PSU	cl	55	35	18,21,22	1.21	1 (5%)	21,30,33	1.83	3 (14%)
35	PSU	cl	28	35	18,21,22	1.11	2 (11%)	21,30,33	1.98	5 (23%)
35	H2U	cl	47	35	18,21,22	3.23	5 (27%)	19,30,33	1.43	4 (21%)
35	2MG	cl	10	35	23,26,27	2.90	8 (34%)	33,38,41	2.38	10 (30%)
35	MIA	cl	37	35,36	28,31,32	2.59	6 (21%)	38,44,47	4.99	16 (42%)
35	5MC	cl	49	35	19,22,23	4.10	9 (47%)	26,32,35	1.30	5 (19%)
35	2MG	cl	26	35	23,26,27	2.92	8 (34%)	33,38,41	2.45	10 (30%)
35	5MC	cl	48	35	19,22,23	4.06	9 (47%)	26,32,35	1.14	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	1MA	cl	58	35	-	2/7/25/26	0/3/3/3
35	G7M	cl	46	35	-	2/7/25/26	0/3/3/3
35	1MG	cl	9	35	-	1/7/25/26	0/3/3/3
35	PSU	cl	55	35	-	0/7/25/26	0/2/2/2
35	PSU	cl	28	35	-	0/7/25/26	0/2/2/2
35	H2U	cl	47	35	-	4/7/38/39	0/2/2/2
35	2MG	cl	10	35	-	2/9/27/28	0/3/3/3
35	MIA	cl	37	35,36	-	5/15/33/34	0/3/3/3
35	5MC	cl	49	35	-	4/7/25/26	0/2/2/2
35	2MG	cl	26	35	-	2/9/27/28	0/3/3/3
35	5MC	cl	48	35	-	2/7/25/26	0/2/2/2

The worst 5 of 70 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	cl	47	H2U	C2-N1	10.11	1.49	1.35
35	cl	48	5MC	C6-C5	9.46	1.50	1.34
35	cl	49	5MC	C6-C5	9.38	1.49	1.34
35	cl	58	1MA	C2-N3	9.20	1.47	1.30
35	cl	37	MIA	C6-N6	8.52	1.47	1.34

The worst 5 of 80 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	cl	37	MIA	N6-C6-N1	18.10	142.59	118.33
35	cl	37	MIA	C5-C6-N6	-13.23	96.50	122.03
35	cl	37	MIA	C11-S10-C2	12.34	111.51	102.25
35	cl	37	MIA	C1'-N9-C8	-8.91	107.31	127.09
35	cl	26	2MG	C2-N3-C4	6.96	120.70	112.00

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	cl	26	2MG	O4'-C4'-C5'-O5'
35	cl	37	MIA	C13-C12-N6-C6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
35	cl	37	MIA	N1-C2-S10-C11
35	cl	37	MIA	N3-C2-S10-C11
35	cl	47	H2U	C4'-C5'-O5'-P

There are no ring outliers.

7 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	cl	58	1MA	1	0
35	cl	55	PSU	1	0
35	cl	28	PSU	2	0
35	cl	10	2MG	1	0
35	cl	37	MIA	3	0
35	cl	49	5MC	1	0
35	cl	26	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 86 ligands modelled in this entry, 86 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

There are no chain breaks in this entry.

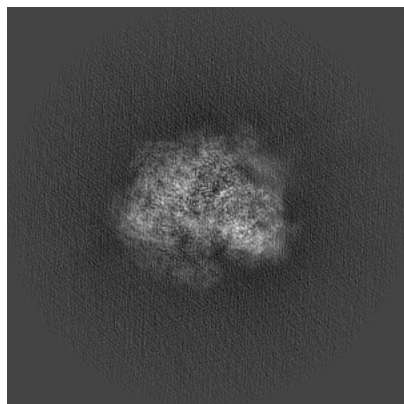
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35635. These allow visual inspection of the internal detail of the map and identification of artifacts.

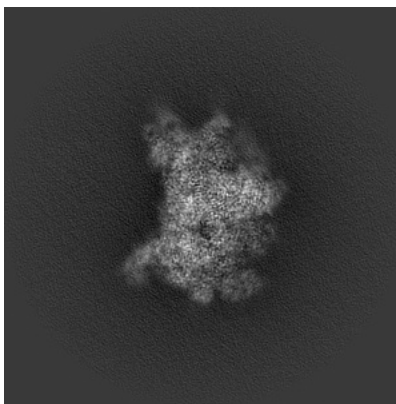
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

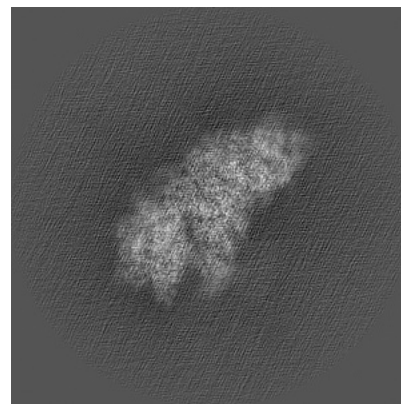
6.1.1 Primary map



X

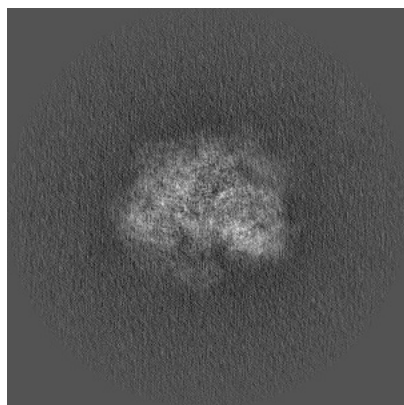


Y

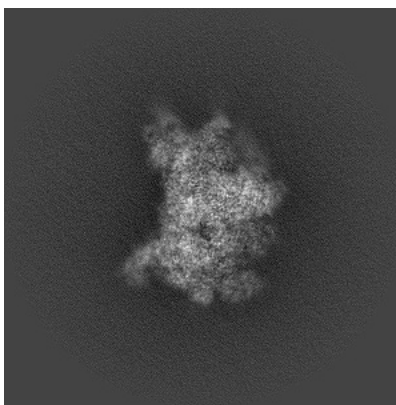


Z

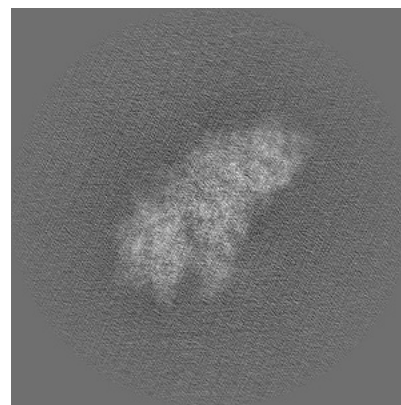
6.1.2 Raw map



X



Y

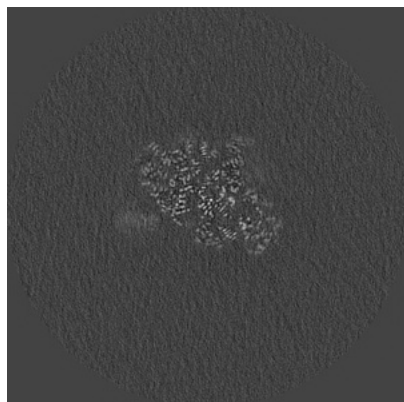


Z

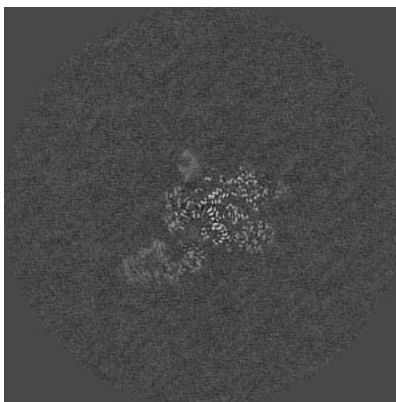
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

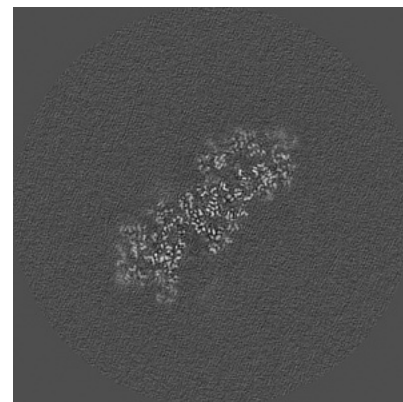
6.2.1 Primary map



X Index: 280

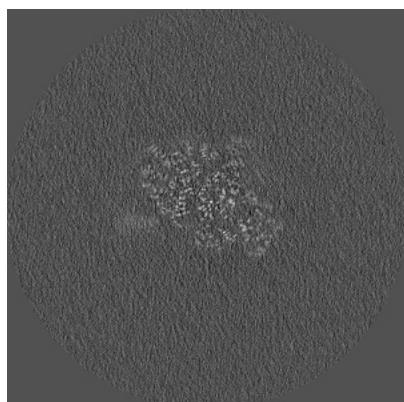


Y Index: 280

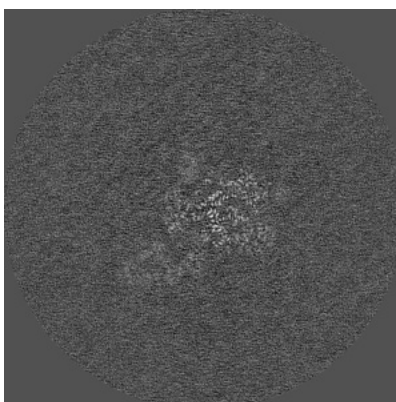


Z Index: 280

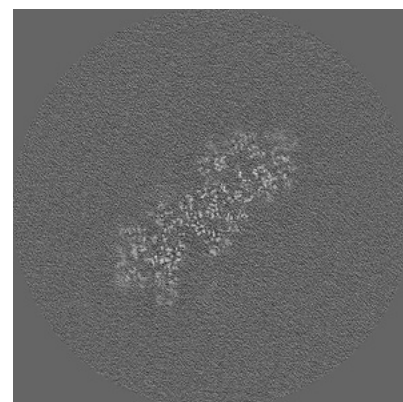
6.2.2 Raw map



X Index: 280



Y Index: 280

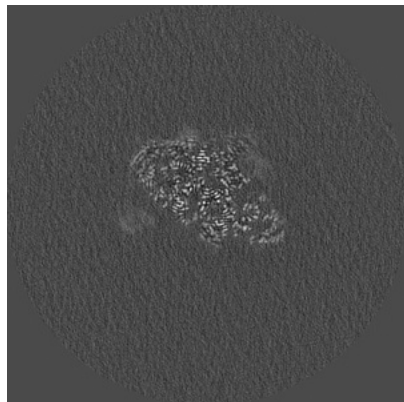


Z Index: 280

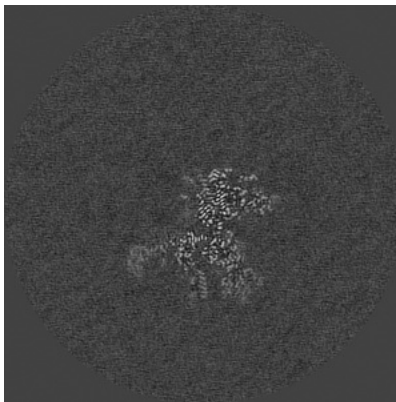
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

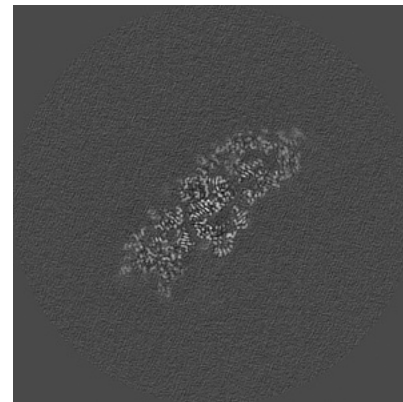
6.3.1 Primary map



X Index: 288

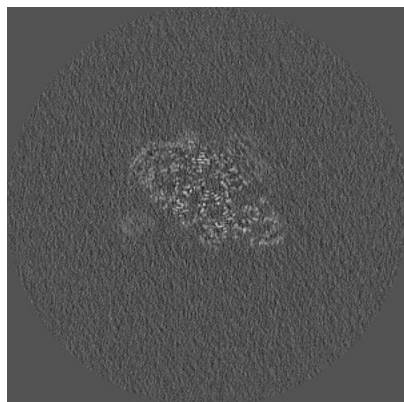


Y Index: 249

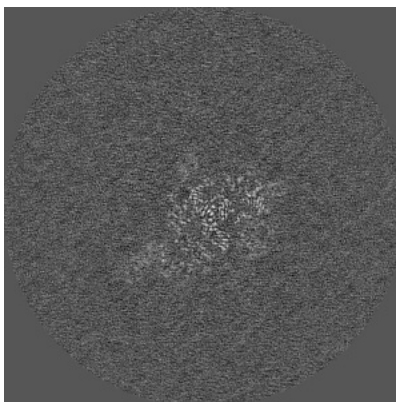


Z Index: 291

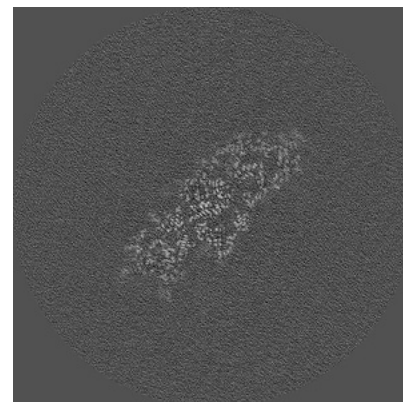
6.3.2 Raw map



X Index: 288



Y Index: 274

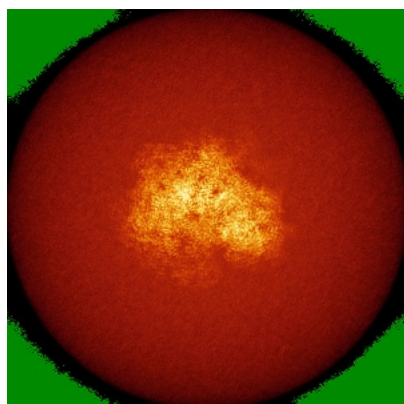


Z Index: 292

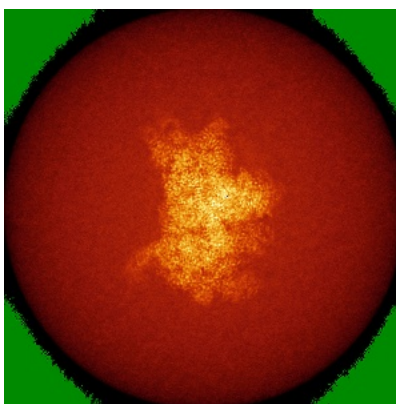
The images above show the largest variance slices of the map in three orthogonal directions.

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

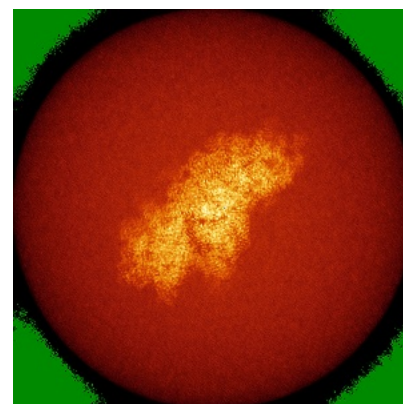
6.4.1 Primary map



X

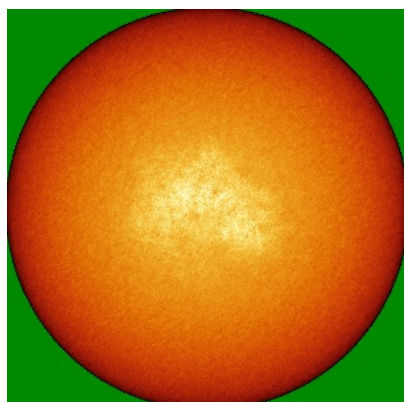


Y

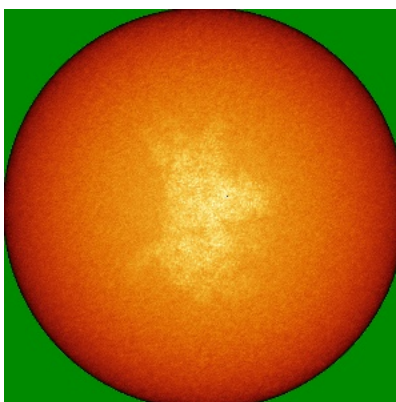


Z

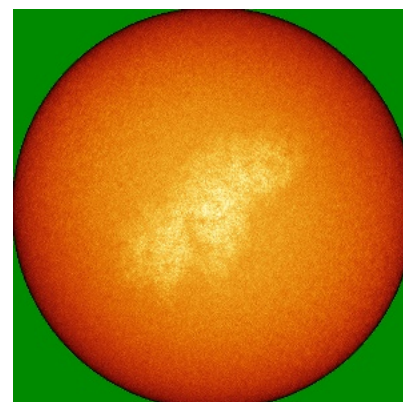
6.4.2 Raw map



X



Y

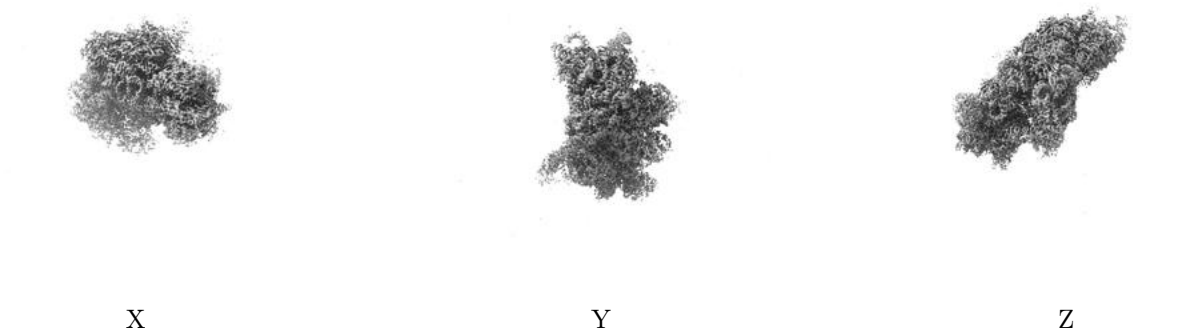


Z

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.

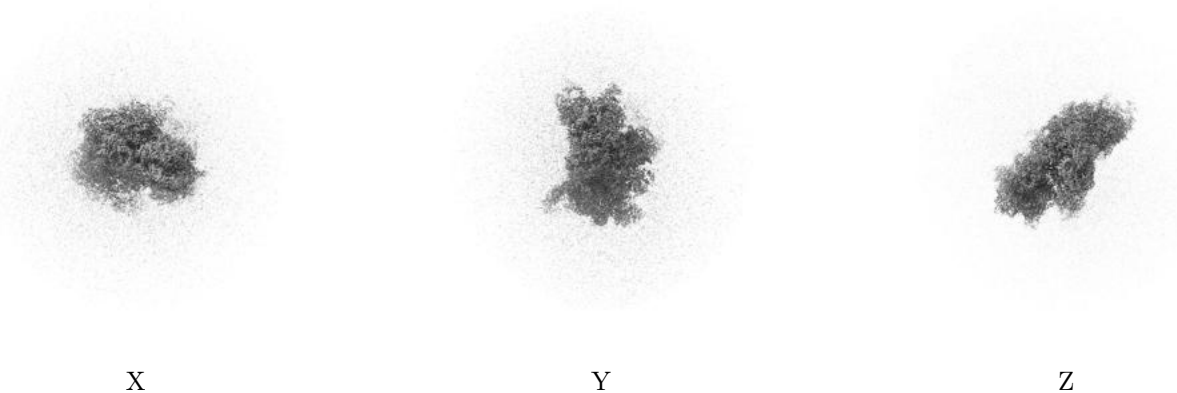
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.013. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

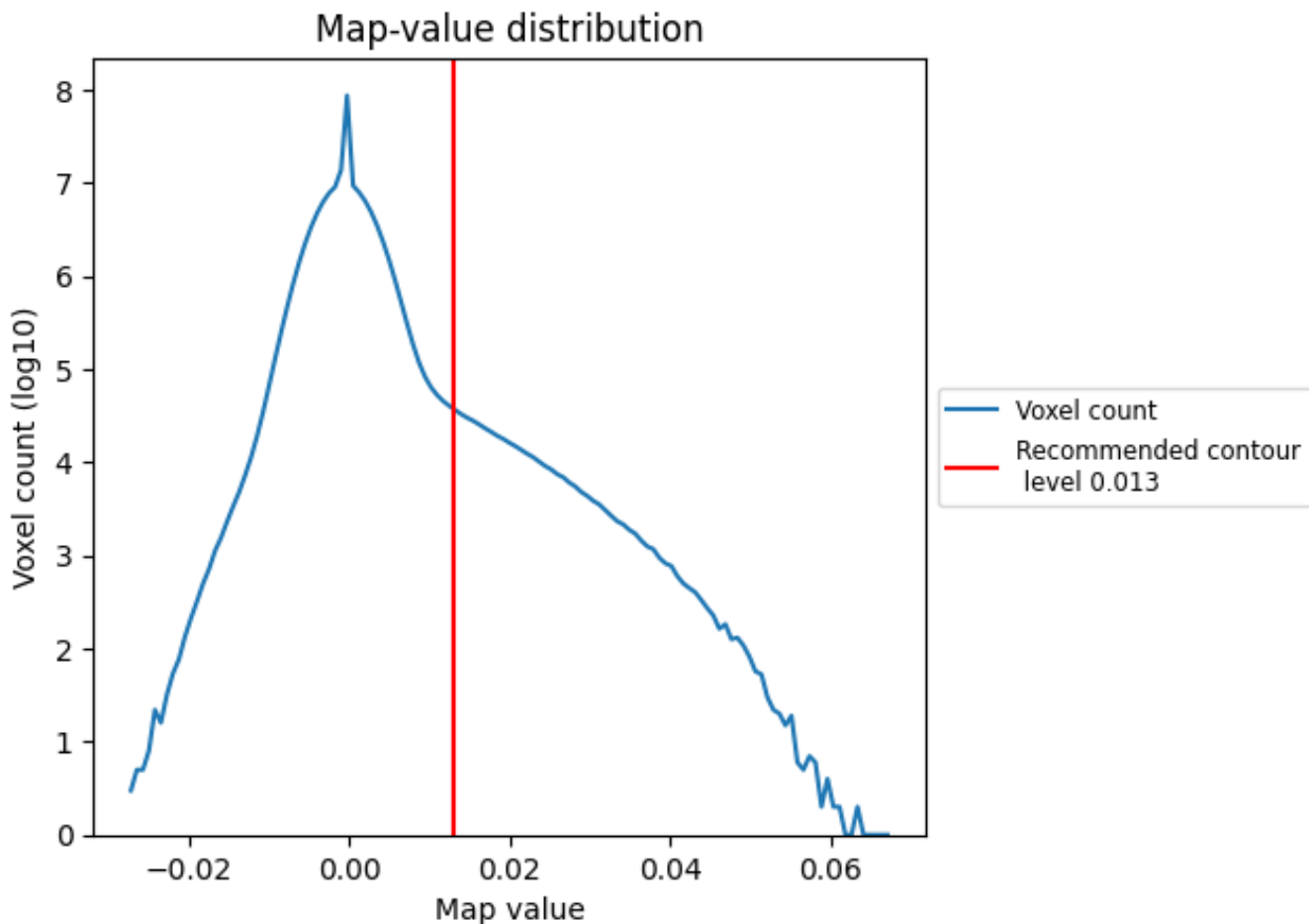
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

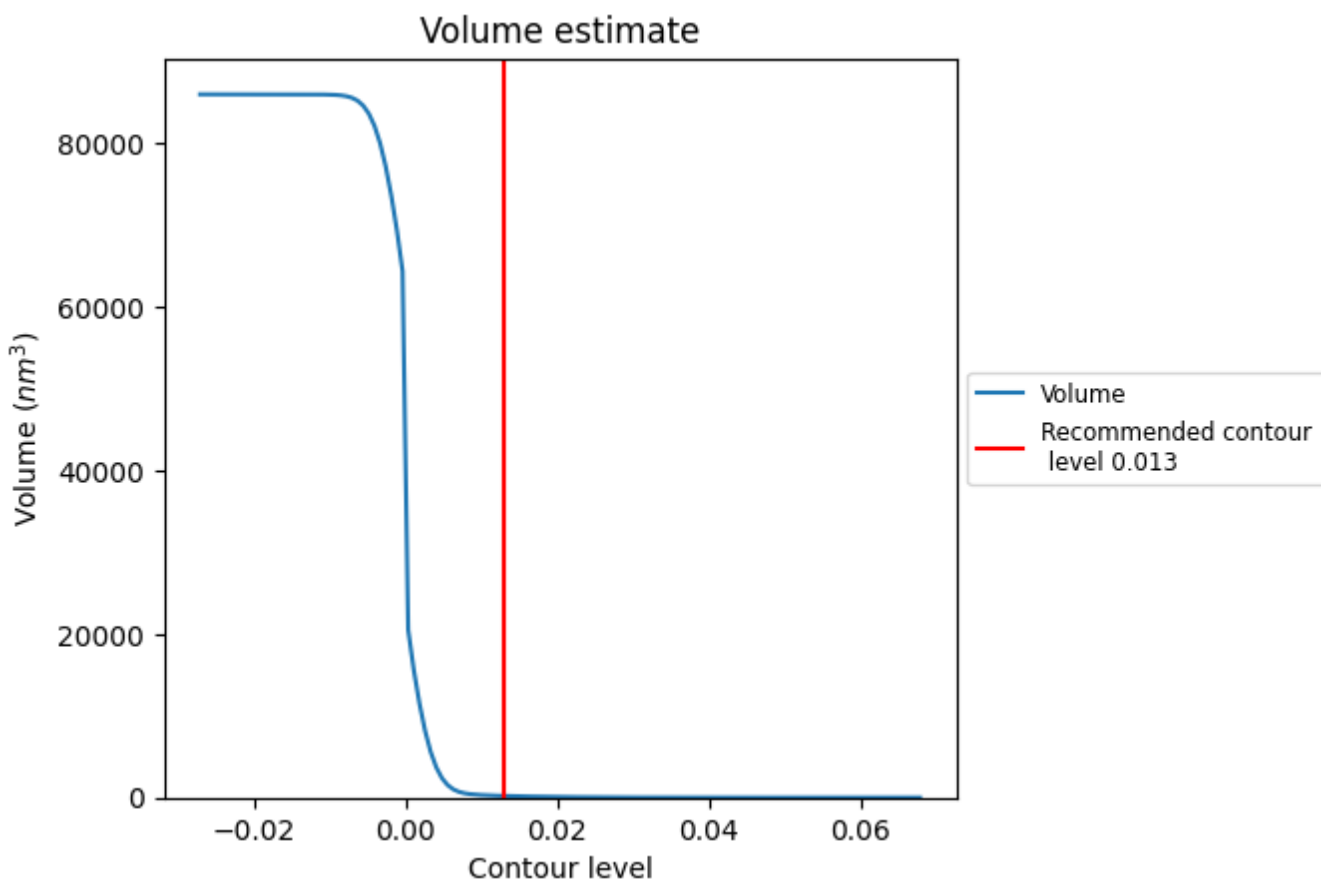
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

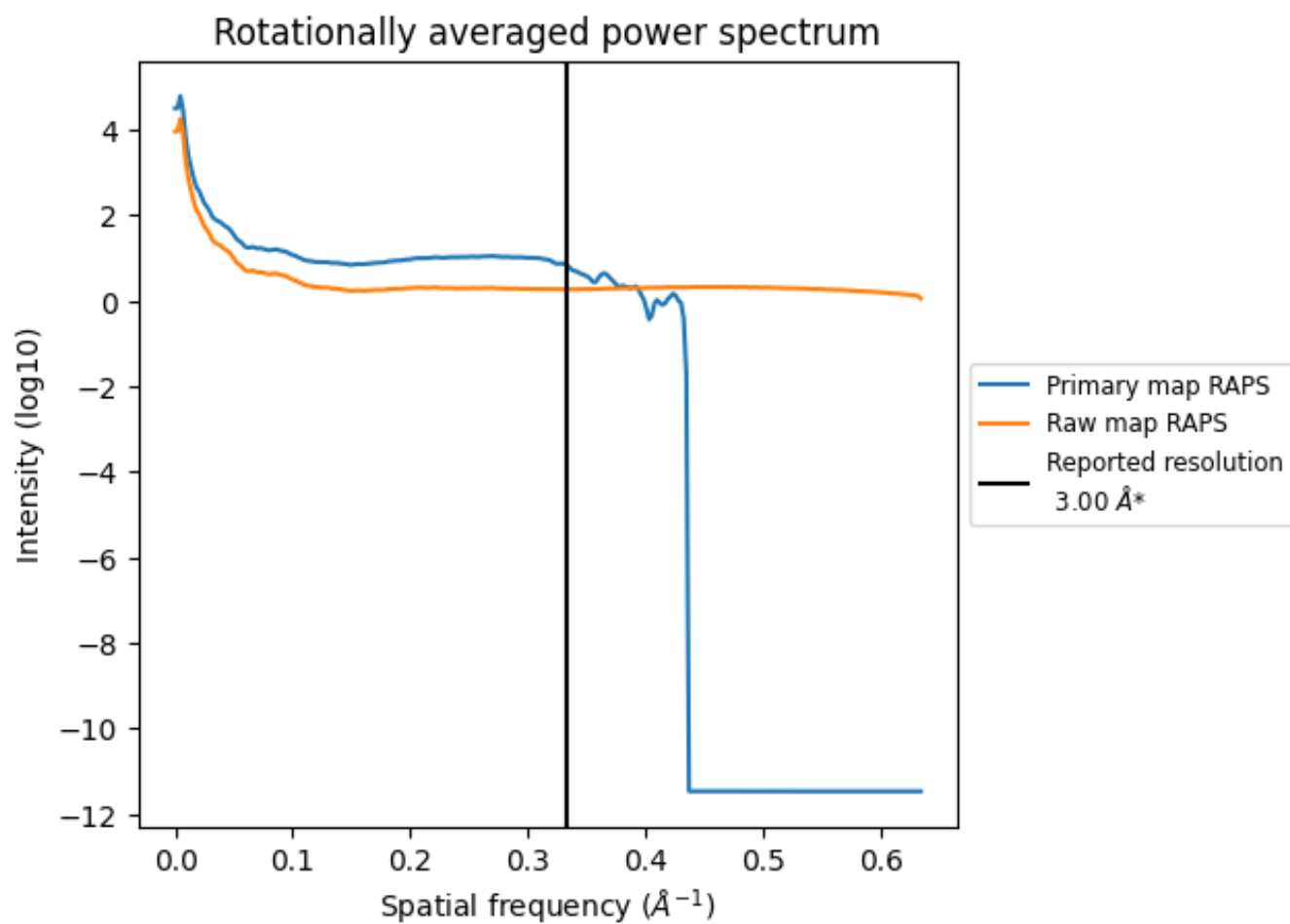
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 201 nm^3 ; this corresponds to an approximate mass of 182 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](#)

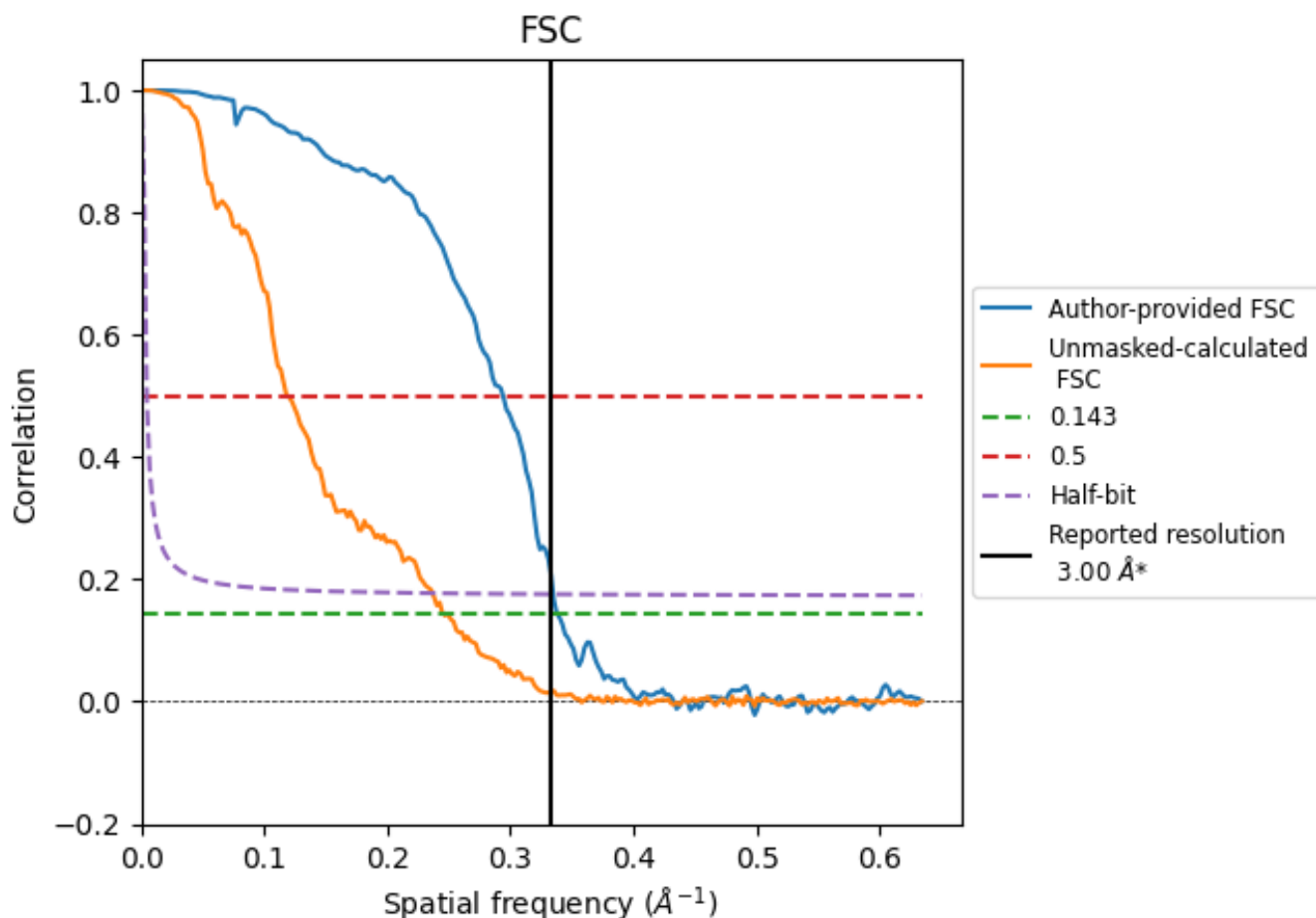


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.40	2.99
Unmasked-calculated*	4.07	8.40	4.22

*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 4.07 differs from the reported value 3.0 by more than 10 %

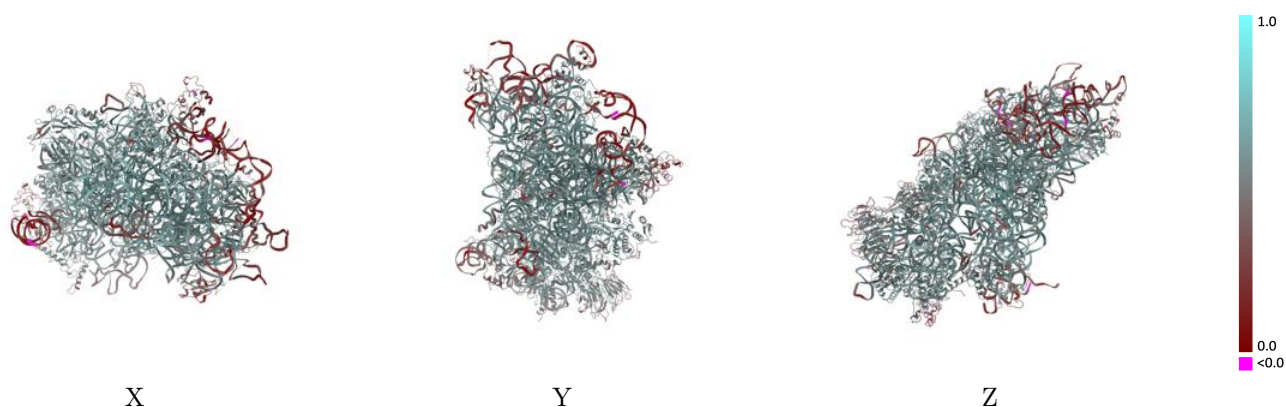
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-35635 and PDB model 8IP9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

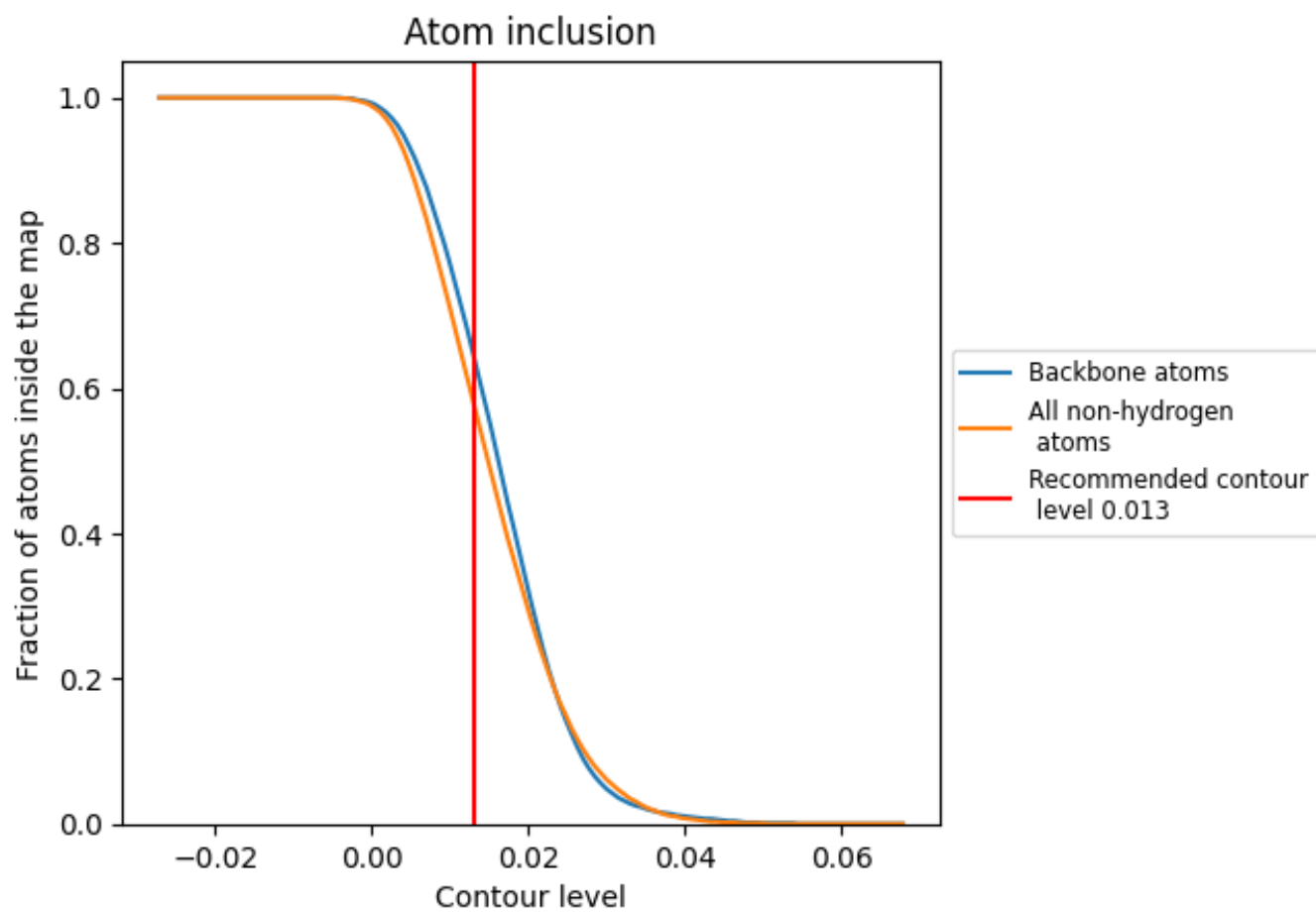


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.









































































9.4 Atom inclusion [i](#)



At the recommended contour level, 65% of all backbone atoms, 58% 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 (0.013) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5790	 0.5300
IB	 0.4040	 0.5110
aa	 0.6950	 0.5390
al	 0.9030	 0.6350
ba	 0.4700	 0.5180
bb	 0.4730	 0.5290
ca	 0.5500	 0.5580
cb	 0.5770	 0.5440
cl	 0.2200	 0.3020
da	 0.3010	 0.4540
db	 0.6600	 0.5900
eb	 0.5480	 0.5660
fb	 0.6520	 0.5990
ga	 0.6430	 0.5990
gb	 0.2670	 0.4230
ha	 0.2840	 0.4590
hb	 0.1200	 0.3860
ia	 0.4280	 0.5380
ib	 0.6390	 0.5980
ja	 0.5520	 0.5680
ka	 0.5370	 0.5540
la	 0.5930	 0.5760
ma	 0.4270	 0.5260
na	 0.5410	 0.5610
oa	 0.3070	 0.5140
pa	 0.5360	 0.5640
qa	 0.3850	 0.5090
ra	 0.5390	 0.5660
sa	 0.3260	 0.4770
ta	 0.1150	 0.2480
ua	 0.4280	 0.5200
va	 0.6400	 0.5720
wa	 0.7280	 0.6050
xa	 0.4440	 0.5210
ya	 0.4850	 0.5740
za	 0.5420	 0.5650

