



Full wwPDB EM Validation Report ⓘ

Feb 13, 2024 – 01:01 PM JST

PDB ID : 8IP9
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 Full wwPDB EM Validation 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:

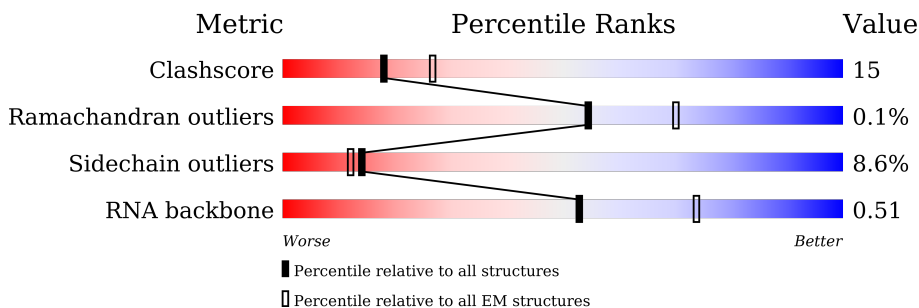
EMDB validation analysis : 0.0.1.dev70
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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;"> 18% 69% 24% • 6% </div>
2	ba	137	<div style="display: flex; justify-content: space-between;"> 36% 75% 7% 18% </div>
3	ca	225	<div style="display: flex; justify-content: space-between;"> 22% 71% 8% 21% </div>
4	da	188	<div style="display: flex; justify-content: space-between;"> 33% 37% 6% 57% </div>
5	ga	142	<div style="display: flex; justify-content: space-between;"> 13% 90% 7% • </div>
6	ha	332	<div style="display: flex; justify-content: space-between;"> 70% 89% 7% • </div>
7	ia	227	<div style="display: flex; justify-content: space-between;"> 40% 88% 6% 6% </div>




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Mol	Chain	Length	Quality of chain
8	ja	265	24% 91% 8%
9	ka	200	24% 90% 6%
10	la	149	21% 89% 5% 6%
11	ma	127	37% 72% 9% 19%
12	na	151	17% 75% 8% 17%
13	oa	152	61% 80% 10% 11%
14	pa	151	32% 96%
15	qa	143	47% 73% 10% 17%
16	ra	155	25% 77% 10% 13%
17	sa	154	41% 60% 5% 35%
18	ta	108	67% 65% 6% 29%
19	ua	86	28% 72% 26%
20	va	129	12% 89% 9%
21	wa	56	64% 5% 30%
22	xa	86	34% 76% 6% 19%
23	ya	62	24% 61% 37%
24	za	308	16% 62% 34%
25	bb	263	32% 71% 9% 20%
26	cb	82	23% 84% 9% 7%
27	db	156	12% 57% 39%
28	eb	195	27% 89% 7%
29	fb	274	11% 73% 5% 22%
30	gb	250	45% 54% 6% 40%
31	hb	192	80% 82% 6% 12%
32	ib	159	13% 84% 8% 9%

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Mol	Chain	Length	Quality of chain
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
			Total	C	N	O	S		
12	na	125	941	579	185	173	4	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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.

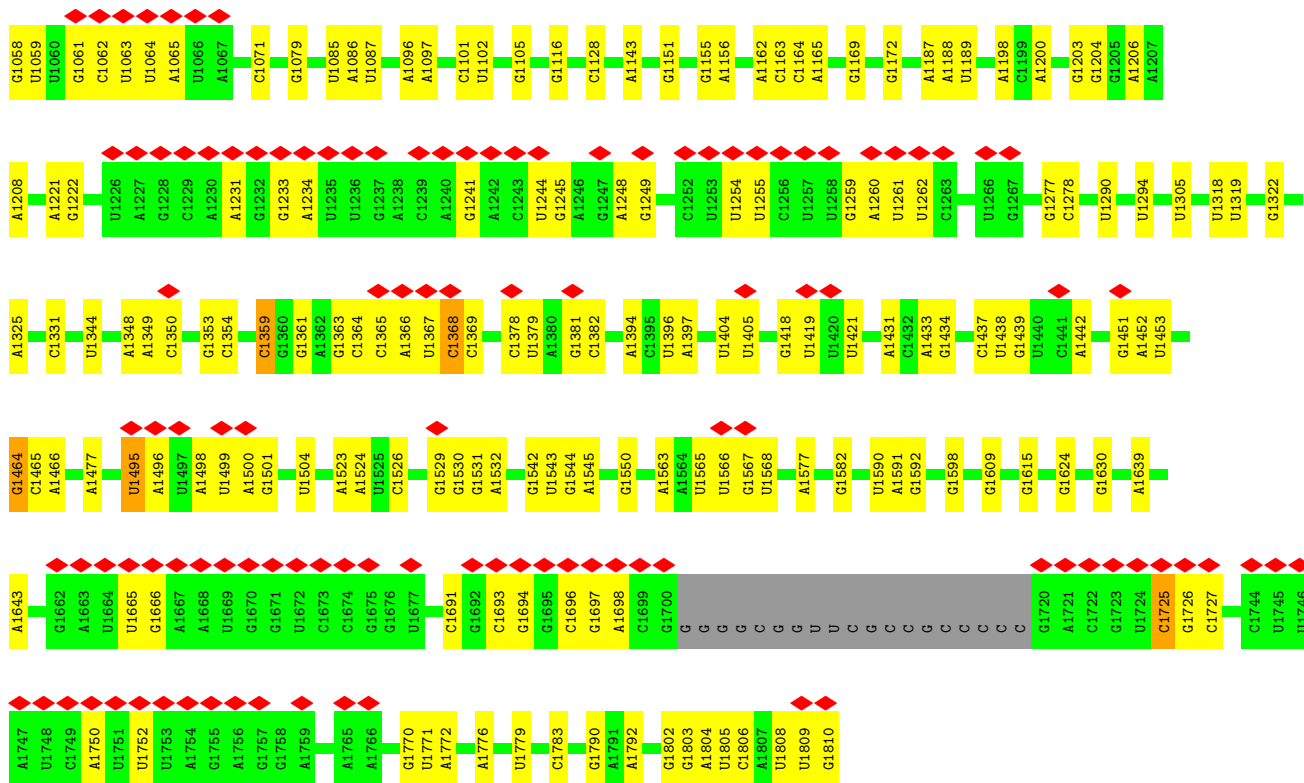
Mol	Chain	Residues	Atoms					AltConf	Trace	
35	cl	75	Total	C	N	O	P	S	0	0
			1622	730	298	518	75	1		

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

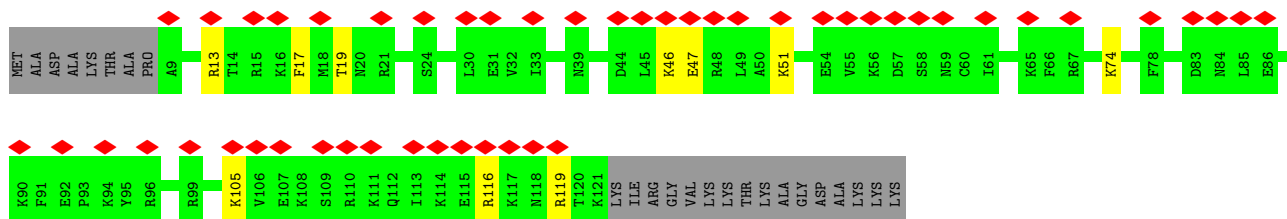
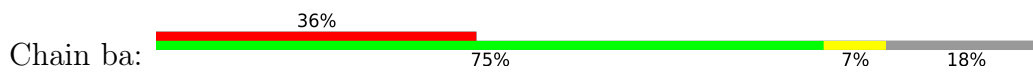
Mol	Chain	Residues	Atoms		AltConf
36	aa	80	Total	Mg	0
			80	80	
36	ja	1	Total	Mg	0
			1	1	
36	al	1	Total	Mg	0
			1	1	
36	cl	2	Total	Mg	0
			2	2	

- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

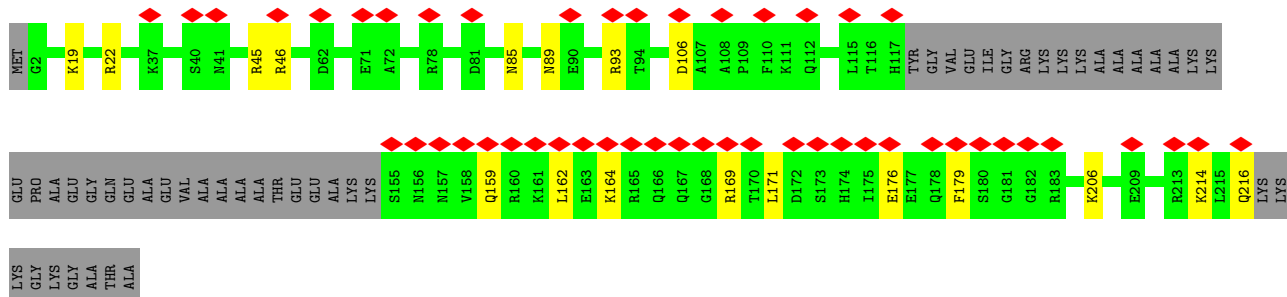
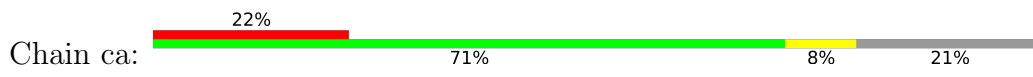
Mol	Chain	Residues	Atoms		AltConf
37	wa	1	Total	Zn	0
			1	1	
37	db	1	Total	Zn	0
			1	1	



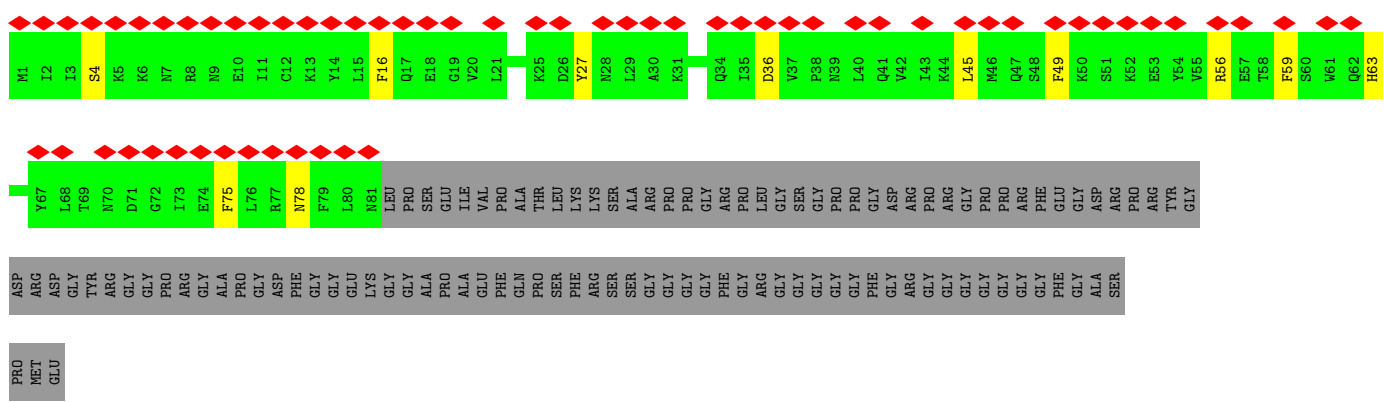
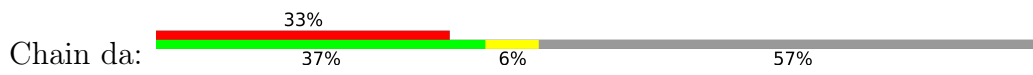
• Molecule 2: 40S ribosomal protein e24



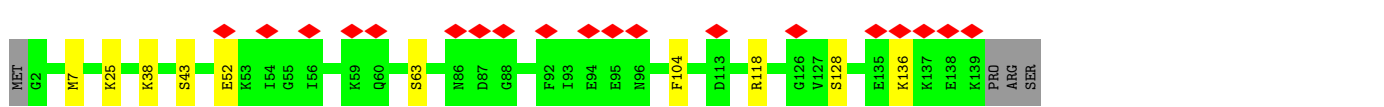
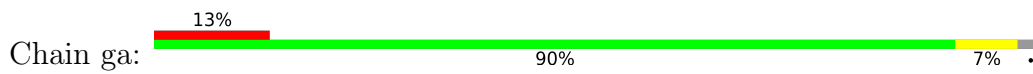
• Molecule 3: 40S ribosomal protein e8



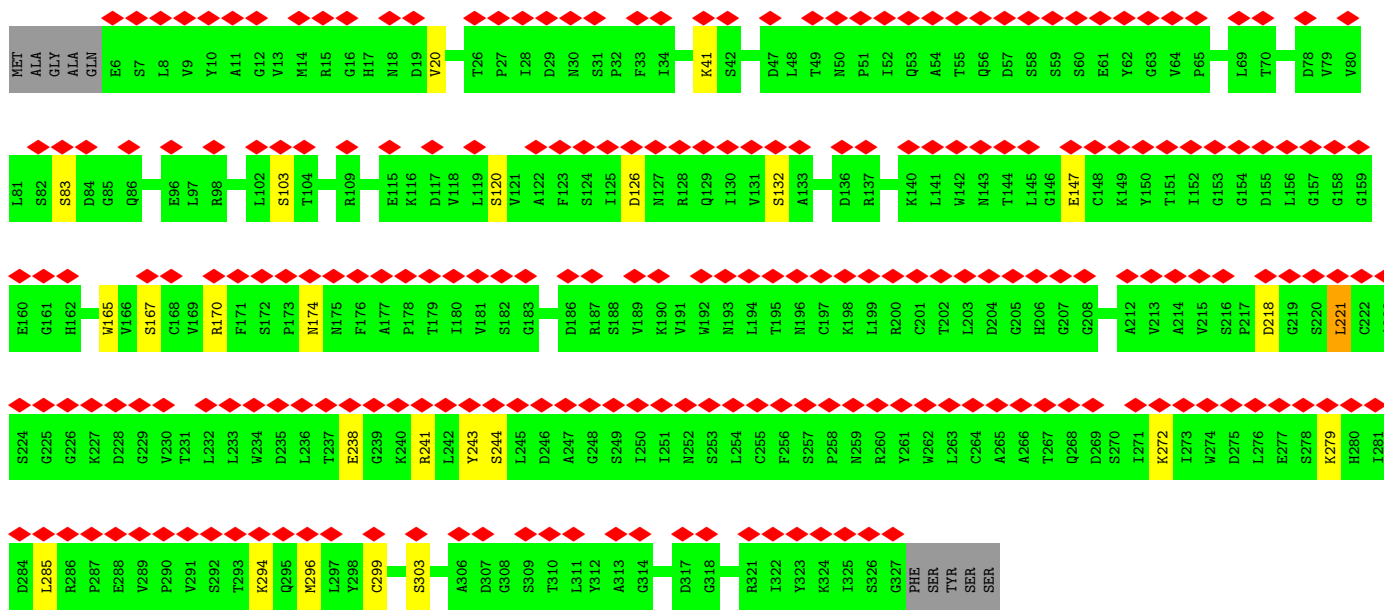
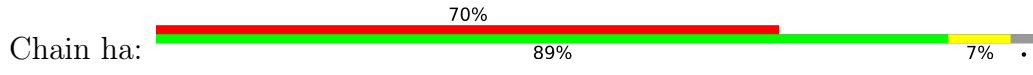
• Molecule 4: 40S ribosomal protein e10



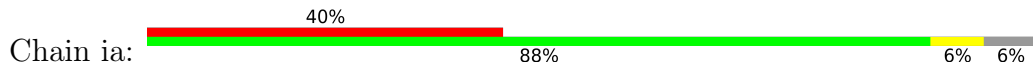
• Molecule 5: 40S ribosomal protein S23

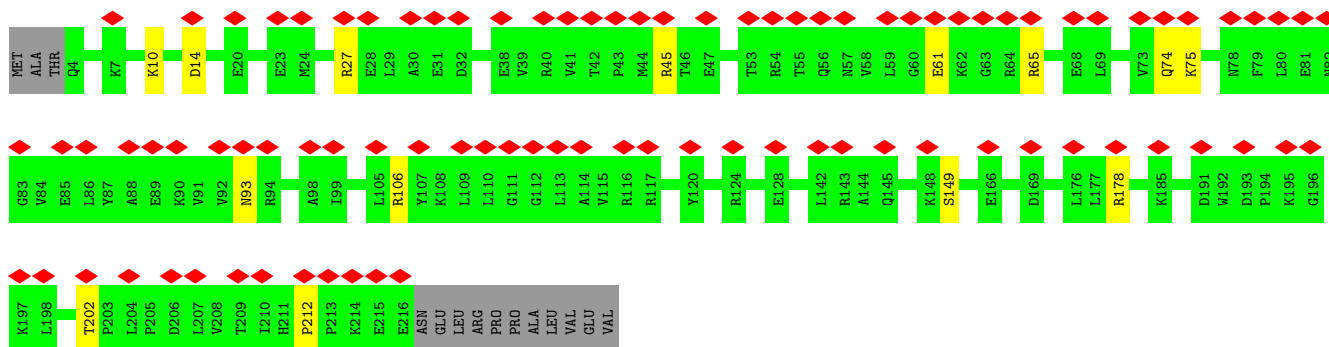


• Molecule 6: RACK1

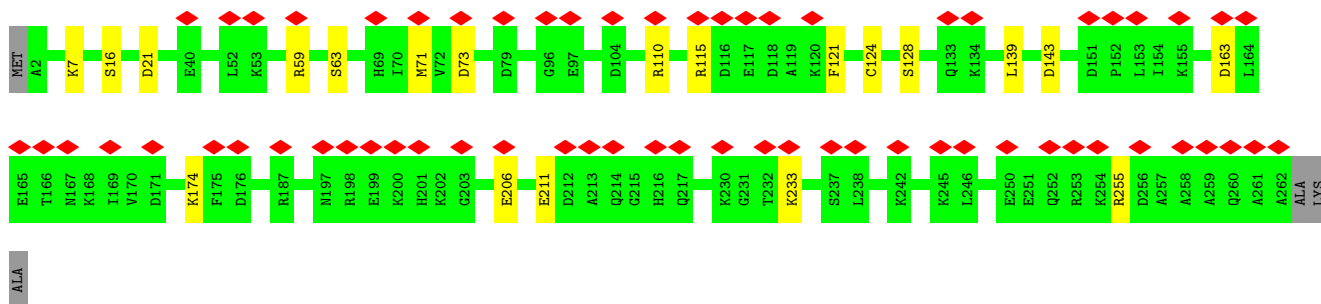
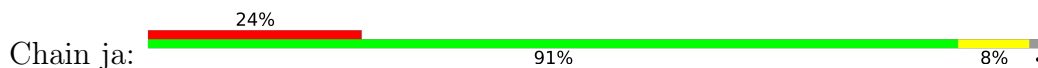


• Molecule 7: 40S ribosomal protein uS3

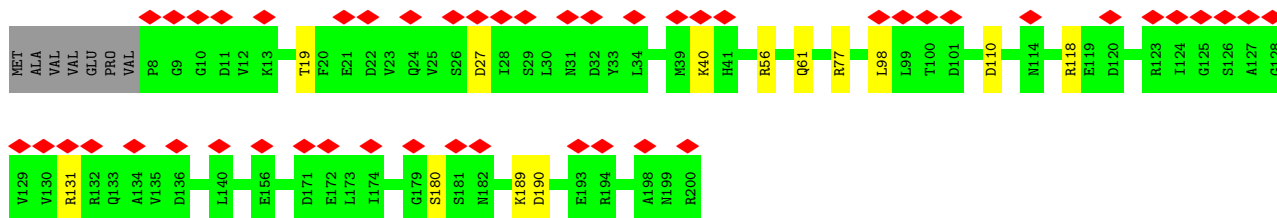
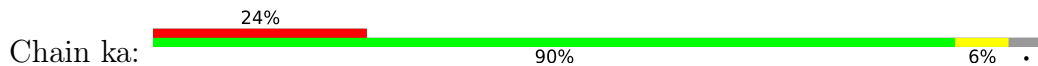




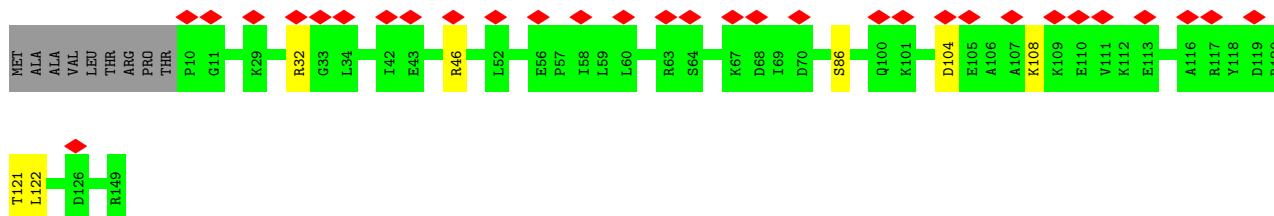
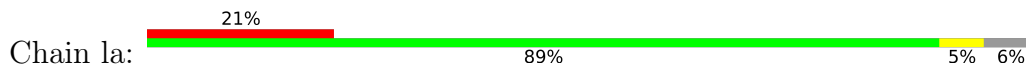
• Molecule 8: 40S ribosomal protein eS4



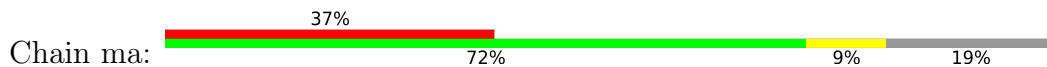
• Molecule 9: 40S ribosomal protein uS7

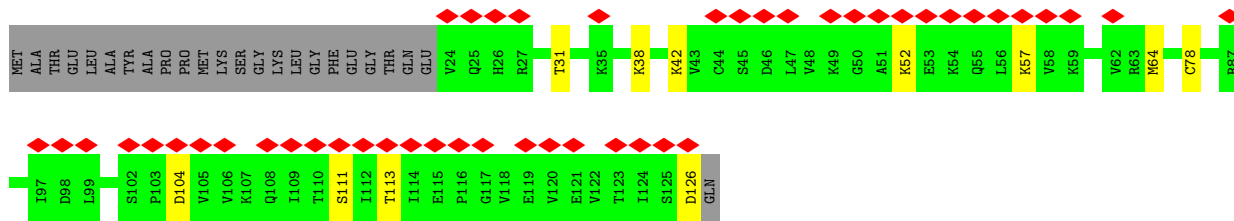


• Molecule 10: 40S ribosomal protein uS9

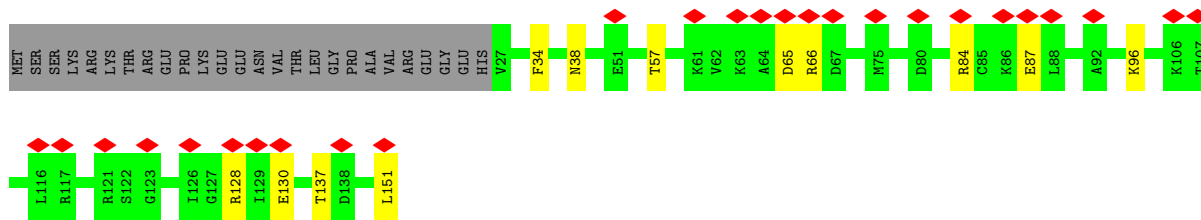
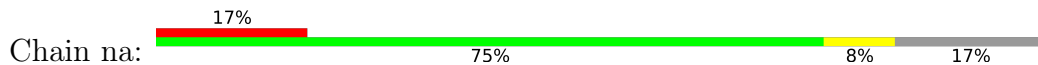


• Molecule 11: 40S ribosomal protein uS10

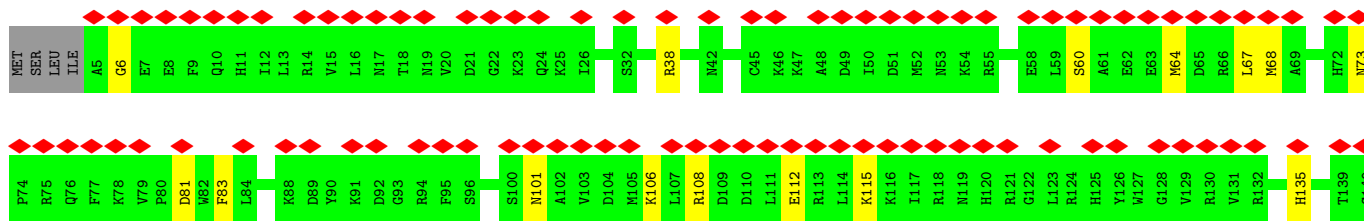
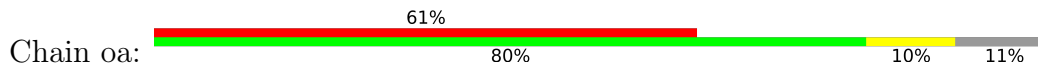




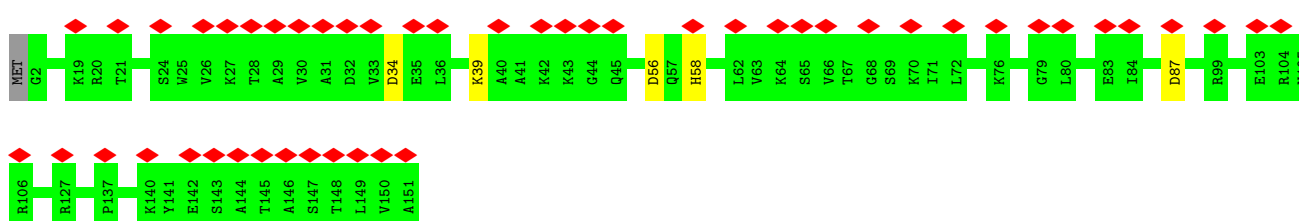
• Molecule 12: 40S ribosomal protein uS11



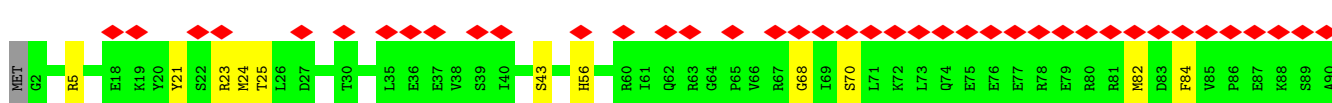
• Molecule 13: 40S ribosomal protein uS13

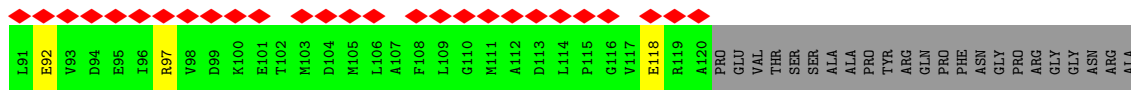


• Molecule 14: 40S ribosomal protein uS15

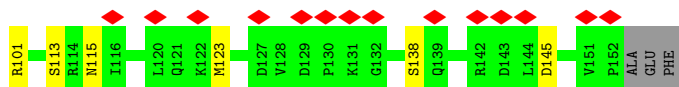
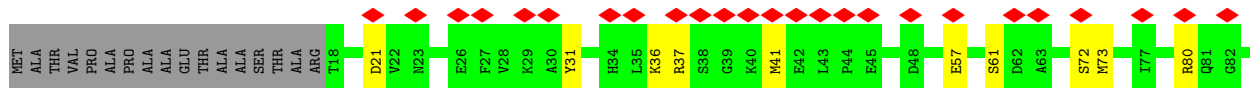
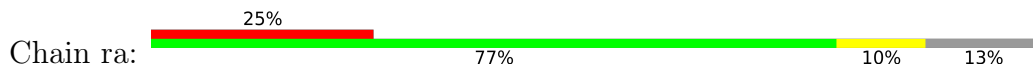


• Molecule 15: 40S ribosomal protein eS17

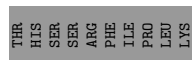
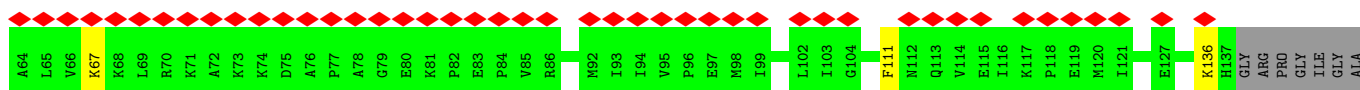
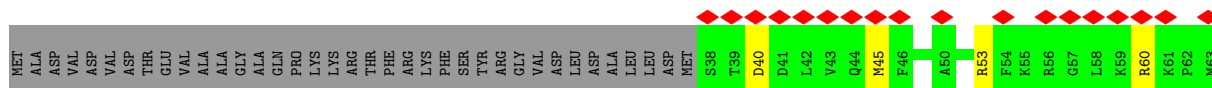
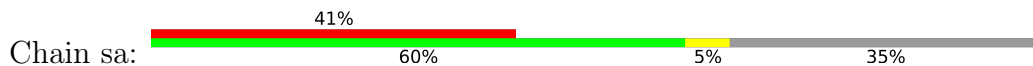




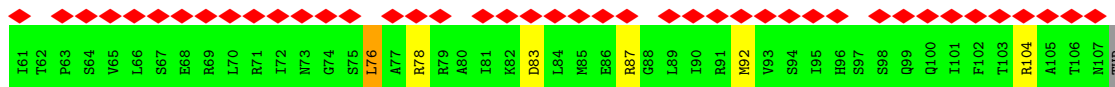
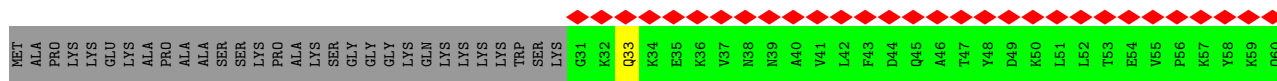
• Molecule 16: 40S ribosomal protein eS19



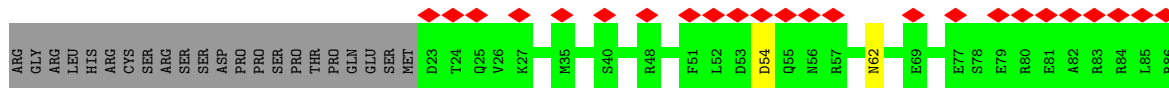
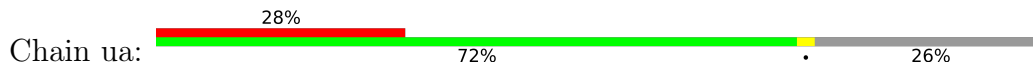
• Molecule 17: 40S ribosomal protein uS19



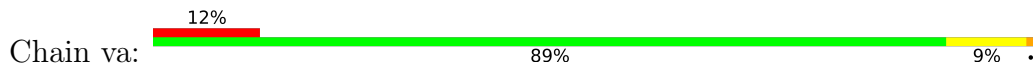
• Molecule 18: 40S ribosomal protein eS25

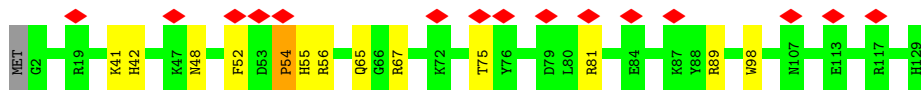


• Molecule 19: 40S ribosomal protein eS28

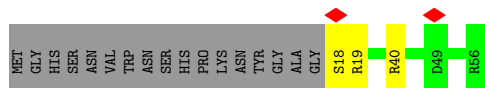


• Molecule 20: 40S ribosomal protein uS8

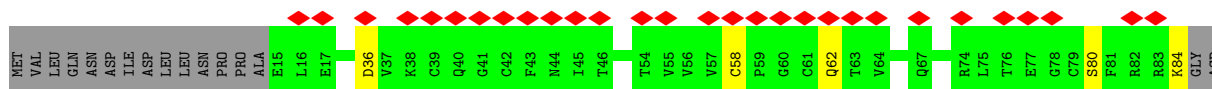
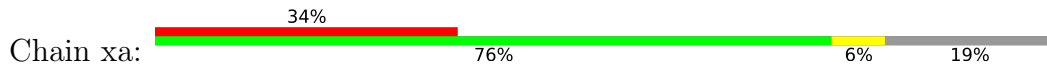




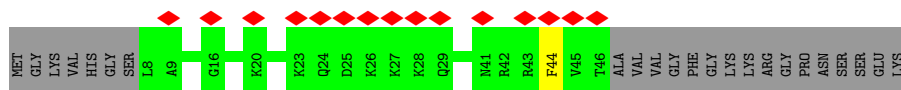
• Molecule 21: 40S ribosomal protein uS14



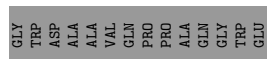
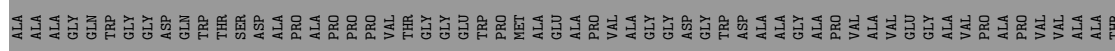
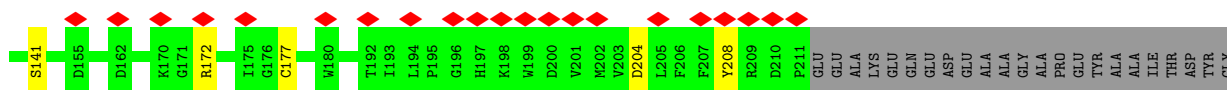
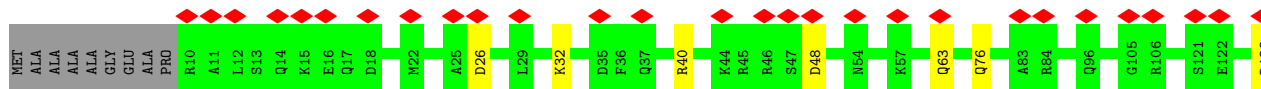
• Molecule 22: 40S ribosomal protein eS27



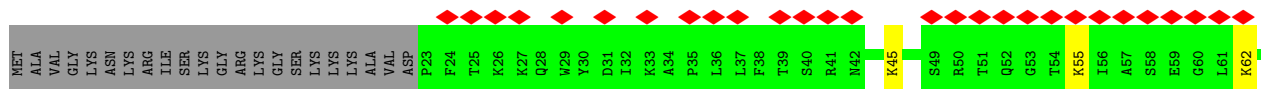
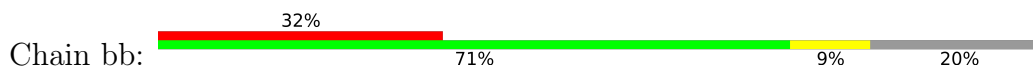
• Molecule 23: 40S ribosomal protein eS30

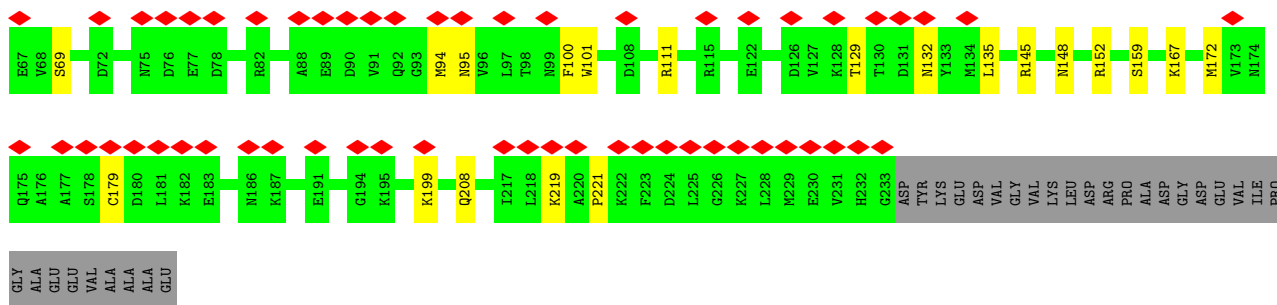


• Molecule 24: 40S ribosomal protein uS2

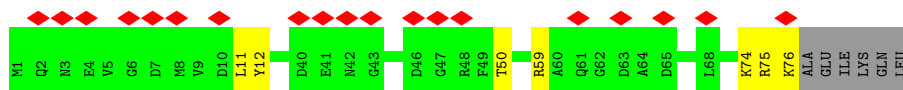
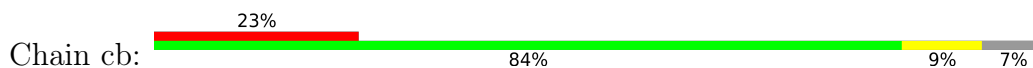


• Molecule 25: 40S ribosomal protein eS1

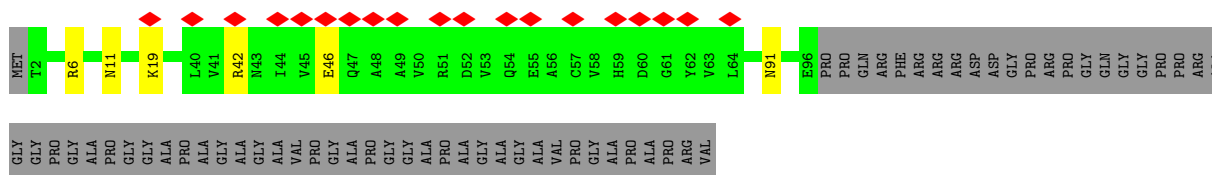




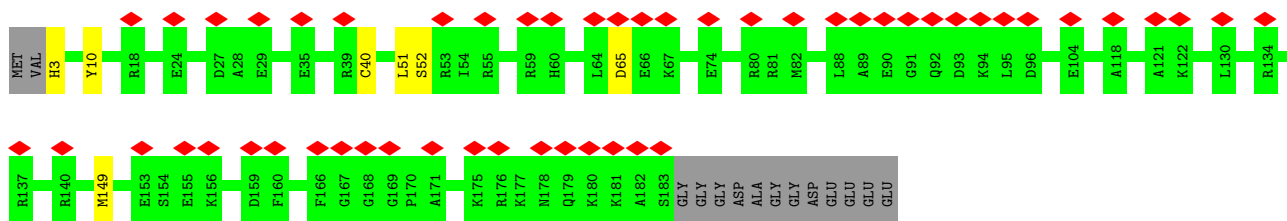
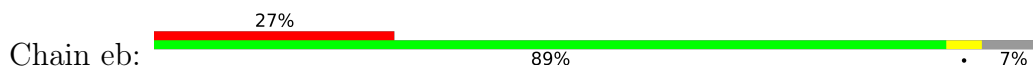
• Molecule 26: 40S ribosomal protein eS21



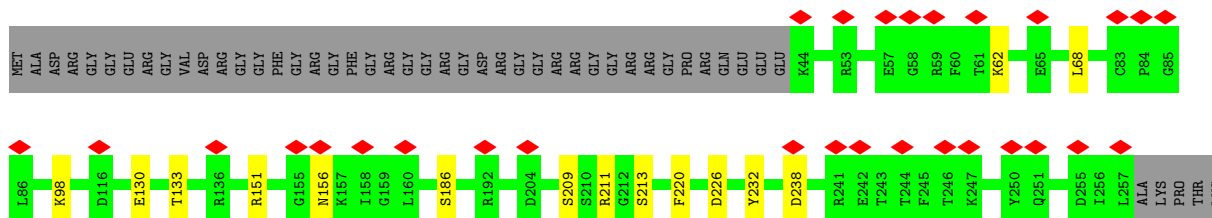
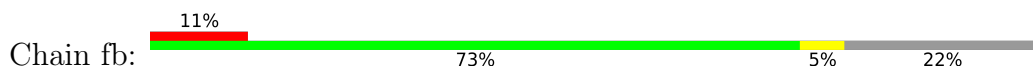
• Molecule 27: 40S ribosomal protein eS26



• Molecule 28: 40S ribosomal protein uS4

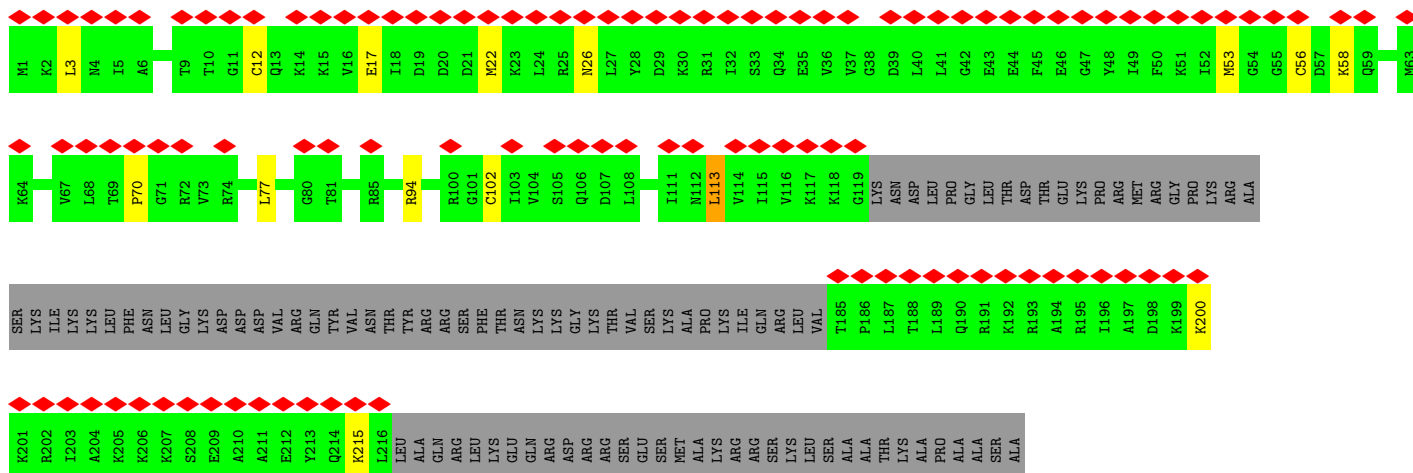


• Molecule 29: 40S ribosomal protein uS5

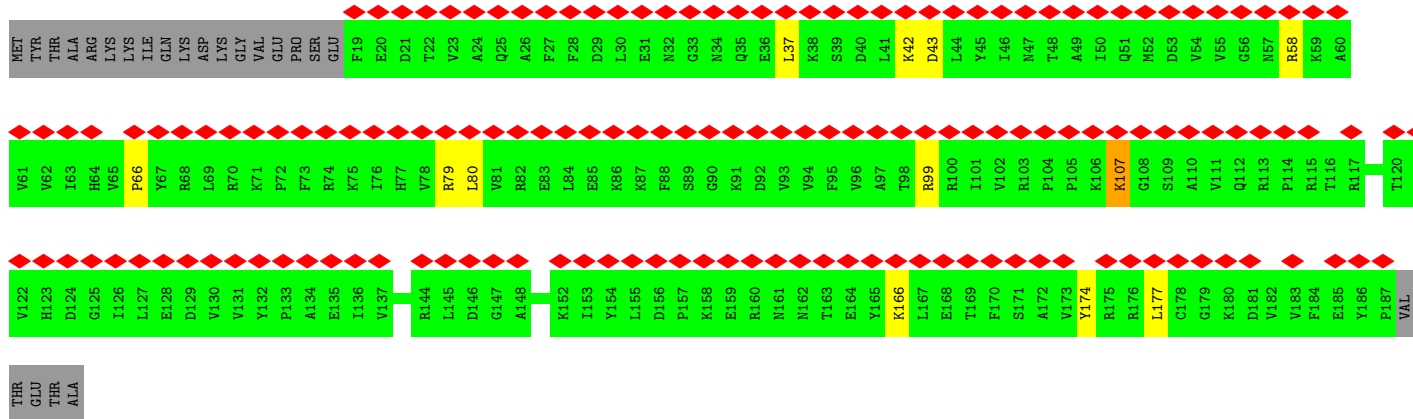
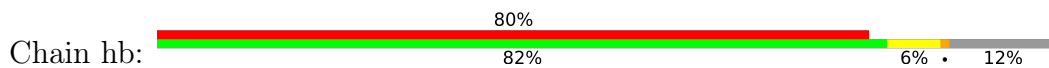


ALA
LEU
MET
LEU
LEU
ASP
ALA
PRO
PRO
ALA
GLU
LYS
VAL
VAL
GLU
ALA

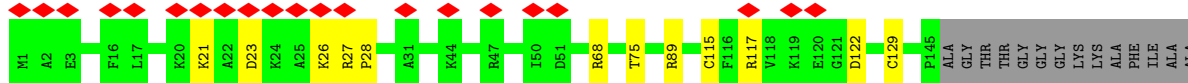
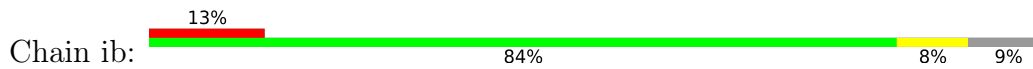
• Molecule 30: 40S ribosomal protein eS6



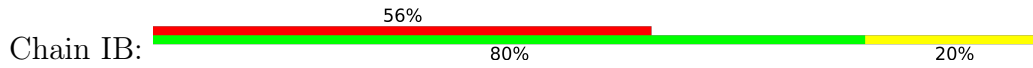
• Molecule 31: 40S ribosomal protein eS7



• Molecule 32: 40S ribosomal protein uS17

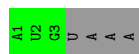


• Molecule 33: 60S ribosomal protein eL41

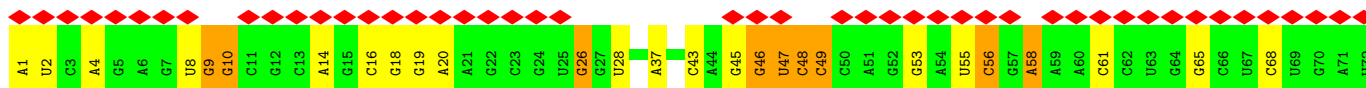




- Molecule 34: mRNA



- 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

5.1 Standard geometry

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

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	0.72	0/40441	0.89	57/63026 (0.1%)
2	ba	0.38	0/943	0.61	0/1253
3	ca	0.40	0/1464	0.57	1/1957 (0.1%)
4	da	0.43	0/722	0.69	1/972 (0.1%)
5	ga	0.40	0/1088	0.59	0/1448
6	ha	0.35	0/2530	0.66	0/3443
7	ia	0.39	0/1697	0.62	1/2279 (0.0%)
8	ja	0.39	0/2123	0.57	1/2853 (0.0%)
9	ka	0.36	0/1538	0.58	1/2070 (0.0%)
10	la	0.43	0/1138	0.64	0/1517
11	ma	0.39	0/815	0.57	0/1098
12	na	0.38	0/953	0.66	0/1278
13	oa	0.35	0/1132	0.59	1/1511 (0.1%)
14	pa	0.36	0/1219	0.55	0/1638
15	qa	0.36	0/985	0.65	0/1313
16	ra	0.39	0/1088	0.61	1/1463 (0.1%)
17	sa	0.36	0/824	0.57	0/1102
18	ta	0.35	0/624	0.70	1/836 (0.1%)
19	ua	0.40	0/514	0.66	0/685
20	va	0.46	0/1057	0.72	2/1421 (0.1%)
21	wa	0.42	0/318	0.52	0/418
22	xa	0.36	0/555	0.56	0/742
23	ya	0.40	0/326	0.54	0/430
24	za	0.38	0/1644	0.60	0/2226
25	bb	0.39	0/1749	0.61	0/2349
26	cb	0.40	0/605	0.63	0/814
27	db	0.43	0/784	0.56	0/1047
28	eb	0.39	0/1521	0.56	0/2035
29	fb	0.44	0/1696	0.57	1/2292 (0.0%)
30	gb	0.36	0/1210	0.72	2/1606 (0.1%)
31	hb	0.36	0/1415	0.64	0/1907
32	ib	0.43	0/1192	0.58	1/1597 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	IB	0.31	0/238	0.60	0/302
34	al	0.80	0/68	0.72	0/105
35	cl	0.53	1/1534 (0.1%)	0.90	1/2386 (0.0%)
All	All	0.59	1/77750 (0.0%)	0.78	72/113419 (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
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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	cl	1	A	OP3-P	-10.59	1.48	1.61

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	aa	457	C	C2-N1-C1'	9.58	129.34	118.80
1	aa	457	C	N1-C2-O2	9.46	124.58	118.90
30	gb	70	PRO	CA-N-CD	-9.05	98.83	111.50
1	aa	742	C	C2-N1-C1'	7.87	127.45	118.80
1	aa	457	C	N3-C2-O2	-7.86	116.40	121.90
1	aa	742	C	N1-C2-O2	7.75	123.55	118.90
20	va	55	HIS	N-CA-C	-7.22	91.50	111.00
4	da	45	LEU	CA-CB-CG	7.19	131.85	115.30
1	aa	643	U	C2-N1-C1'	7.11	126.23	117.70
1	aa	1071	C	N3-C2-O2	-7.10	116.93	121.90
1	aa	457	C	C6-N1-C1'	-7.06	112.33	120.80
1	aa	1359	C	C2-N1-C1'	6.74	126.22	118.80
1	aa	1261	U	C2-N1-C1'	6.37	125.34	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	aa	1278	C	C2-N1-C1'	6.24	125.66	118.80
9	ka	98	LEU	CA-CB-CG	6.23	129.63	115.30
1	aa	643	U	C5-C6-N1	6.23	125.81	122.70
1	aa	970	U	C2-N1-C1'	6.13	125.05	117.70
1	aa	201	G	N3-C4-N9	6.12	129.67	126.00
13	oa	67	LEU	CA-CB-CG	6.10	129.33	115.30
1	aa	1245	G	O4'-C1'-N9	6.05	113.04	108.20
1	aa	67	G	C4-N9-C1'	6.04	134.35	126.50
1	aa	134	G	C4-N9-C1'	-6.02	118.68	126.50
1	aa	201	G	C4-N9-C1'	5.93	134.21	126.50
1	aa	1044	A	O4'-C1'-N9	5.92	112.94	108.20
1	aa	742	C	N3-C2-O2	-5.91	117.76	121.90
1	aa	1071	C	N1-C2-O2	5.91	122.44	118.90
1	aa	643	U	N1-C2-O2	5.88	126.92	122.80
1	aa	67	G	N3-C4-N9	5.86	129.52	126.00
1	aa	1696	C	N1-C2-O2	5.79	122.37	118.90
1	aa	1464	G	C4-N9-C1'	5.75	133.98	126.50
32	ib	28	PRO	CA-N-CD	-5.74	103.46	111.50
1	aa	1771	U	P-O3'-C3'	5.73	126.57	119.70
1	aa	1187	A	N9-C1'-C2'	-5.72	105.71	112.00
20	va	54	PRO	C-N-CA	5.69	135.92	121.70
1	aa	585	U	C2-N1-C1'	5.66	124.49	117.70
1	aa	1368	C	C2-N1-C1'	5.65	125.02	118.80
1	aa	67	G	C8-N9-C1'	-5.64	119.67	127.00
1	aa	964	U	N1-C2-O2	5.62	126.73	122.80
1	aa	742	C	C6-N1-C1'	-5.61	114.06	120.80
1	aa	201	G	C8-N9-C1'	-5.56	119.77	127.00
1	aa	614	G	C4-N9-C1'	5.54	133.71	126.50
1	aa	964	U	N3-C2-O2	-5.54	118.32	122.20
1	aa	801	U	C2-N1-C1'	5.54	124.35	117.70
1	aa	134	G	C8-N9-C1'	5.53	134.19	127.00
1	aa	1294	U	C2-N1-C1'	5.52	124.33	117.70
18	ta	76	LEU	CB-CG-CD2	-5.51	101.63	111.00
1	aa	788	G	P-O3'-C3'	5.49	126.29	119.70
30	gb	113	LEU	CA-CB-CG	5.40	127.72	115.30
1	aa	585	U	N1-C2-O2	5.39	126.57	122.80
1	aa	190	C	P-O3'-C3'	5.31	126.07	119.70
1	aa	201	G	C6-C5-N7	-5.30	127.22	130.40
1	aa	134	G	N3-C4-N9	-5.27	122.84	126.00
1	aa	1278	C	N1-C2-O2	5.19	122.02	118.90
1	aa	1568	U	C2-N1-C1'	5.18	123.92	117.70
1	aa	1262	U	N3-C2-O2	-5.16	118.59	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	aa	834	A	P-O3'-C3'	5.16	125.89	119.70
1	aa	1359	C	C5-C6-N1	5.13	123.56	121.00
1	aa	585	U	N3-C2-O2	-5.13	118.61	122.20
1	aa	614	G	C8-N9-C1'	-5.13	120.33	127.00
1	aa	828	G	P-O3'-C3'	5.11	125.83	119.70
1	aa	1359	C	C6-N1-C1'	-5.10	114.68	120.80
1	aa	1464	G	C8-N9-C1'	-5.10	120.37	127.00
29	fb	68	LEU	CA-CB-CG	5.07	126.95	115.30
3	ca	162	LEU	CA-CB-CG	5.06	126.95	115.30
1	aa	1495	U	OP1-P-O3'	5.06	116.33	105.20
7	ia	14	ASP	CB-CG-OD1	5.05	122.85	118.30
1	aa	1064	U	C2-N1-C1'	5.04	123.74	117.70
1	aa	143	A	O4'-C1'-N9	5.03	112.22	108.20
1	aa	1725	C	OP1-P-O3'	5.01	116.23	105.20
35	cl	56	C	N3-C2-O2	-5.01	118.39	121.90
8	ja	139	LEU	CA-CB-CG	5.01	126.82	115.30
16	ra	73	MET	CB-CG-SD	-5.00	97.39	112.40

There are no chirality outliers.

All (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
31	hb	107	LYS	Peptide
10	la	46	ARG	Peptide
12	na	137	THR	Peptide
13	oa	6	GLY	Peptide
18	ta	33	GLN	Peptide
18	ta	76	LEU	Peptide
20	va	54	PRO	Peptide
20	va	75	THR	Peptide

5.2 Too-close contacts

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	0	0
2	ba	929	0	992	0	0
3	ca	1443	0	1478	0	0
4	da	703	0	701	0	0
5	ga	1070	0	1133	0	0
6	ha	2473	0	2406	0	0
7	ia	1673	0	1756	0	0
8	ja	2082	0	2171	0	0
9	ka	1516	0	1564	0	0
10	la	1119	0	1190	0	0
11	ma	806	0	863	0	0
12	na	941	0	977	0	0
13	oa	1114	0	1140	0	0
14	pa	1195	0	1287	0	0
15	qa	975	0	1024	0	0
16	ra	1065	0	1083	0	0
17	sa	807	0	863	0	0
18	ta	618	0	654	0	0
19	ua	513	0	551	0	0
20	va	1039	0	1063	0	0
21	wa	314	0	318	0	0
22	xa	546	0	564	0	0
23	ya	322	0	354	0	0
24	za	1609	0	1615	0	0
25	bb	1720	0	1793	0	0
26	cb	596	0	583	0	0
27	db	771	0	789	0	0
28	eb	1493	0	1559	0	0
29	fb	1660	0	1743	0	0
30	gb	1199	0	1287	0	0
31	hb	1389	0	1444	0	0
32	ib	1166	0	1232	0	0
33	IB	237	0	289	2	0
34	al	61	0	31	0	0
35	cl	1622	0	842	0	0
36	aa	80	0	0	0	0
36	al	1	0	0	0	0
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	2	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.

All (2) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:IB:12:ARG:HH11	33:IB:12:ARG:HG3	1.60	0.66
33:IB:18:ARG:O	33:IB:22:GLN:HG2	2.02	0.59

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
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%)	17	55
16	ra	133/155 (86%)	128 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	19	57
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%)	11	43
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%)	25	64
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%)	54	85

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	va	56	ARG
15	qa	68	GLY
31	hb	66	PRO
25	bb	55	LYS
25	bb	62	LYS
25	bb	221	PRO

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%)	89 (90%)	10 (10%)	7	29
3	ca	153/181 (84%)	136 (89%)	17 (11%)	6	25
4	da	77/143 (54%)	68 (88%)	9 (12%)	5	22
5	ga	109/113 (96%)	99 (91%)	10 (9%)	9	34
6	ha	274/281 (98%)	250 (91%)	24 (9%)	10	36
7	ia	180/192 (94%)	167 (93%)	13 (7%)	14	45
8	ja	222/224 (99%)	203 (91%)	19 (9%)	10	37
9	ka	163/169 (96%)	151 (93%)	12 (7%)	13	44
10	la	113/120 (94%)	107 (95%)	6 (5%)	22	58
11	ma	97/115 (84%)	86 (89%)	11 (11%)	6	24
12	na	98/121 (81%)	87 (89%)	11 (11%)	6	24
13	oa	119/133 (90%)	106 (89%)	13 (11%)	6	25
14	pa	129/130 (99%)	124 (96%)	5 (4%)	32	69
15	qa	108/126 (86%)	95 (88%)	13 (12%)	5	22
16	ra	112/124 (90%)	97 (87%)	15 (13%)	4	17
17	sa	87/130 (67%)	80 (92%)	7 (8%)	12	40
18	ta	69/92 (75%)	64 (93%)	5 (7%)	14	45
19	ua	57/78 (73%)	55 (96%)	2 (4%)	36	71
20	va	110/111 (99%)	101 (92%)	9 (8%)	11	39
21	wa	34/47 (72%)	31 (91%)	3 (9%)	10	36
22	xa	64/78 (82%)	59 (92%)	5 (8%)	12	42
23	ya	32/49 (65%)	31 (97%)	1 (3%)	40	75
24	za	172/233 (74%)	160 (93%)	12 (7%)	15	47
25	bb	189/228 (83%)	169 (89%)	20 (11%)	6	26
26	cb	63/68 (93%)	56 (89%)	7 (11%)	6	25
27	db	82/113 (73%)	76 (93%)	6 (7%)	14	44
28	eb	154/162 (95%)	147 (96%)	7 (4%)	27	64
29	fb	181/219 (83%)	167 (92%)	14 (8%)	13	42
30	gb	130/215 (60%)	116 (89%)	14 (11%)	6	26
31	hb	151/171 (88%)	140 (93%)	11 (7%)	14	44
32	ib	126/132 (96%)	115 (91%)	11 (9%)	10	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	IB	24/24 (100%)	22 (92%)	2 (8%)	11	39
All	All	3778/4438 (85%)	3454 (91%)	324 (9%)	14	37

All (324) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	ba	13	ARG
2	ba	17	PHE
2	ba	19	THR
2	ba	46	LYS
2	ba	47	GLU
2	ba	51	LYS
2	ba	74	LYS
2	ba	105	LYS
2	ba	116	ARG
2	ba	119	ARG
3	ca	19	LYS
3	ca	22	ARG
3	ca	45	ARG
3	ca	46	ARG
3	ca	85	ASN
3	ca	89	ASN
3	ca	93	ARG
3	ca	106	ASP
3	ca	159	GLN
3	ca	164	LYS
3	ca	169	ARG
3	ca	171	LEU
3	ca	176	GLU
3	ca	179	PHE
3	ca	206	LYS
3	ca	214	LYS
3	ca	216	GLN
4	da	4	SER
4	da	16	PHE
4	da	27	TYR
4	da	36	ASP
4	da	49	PHE
4	da	56	ARG
4	da	59	PHE
4	da	75	PHE
4	da	78	ASN

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Mol	Chain	Res	Type
5	ga	7	MET
5	ga	25	LYS
5	ga	38	LYS
5	ga	43	SER
5	ga	52	GLU
5	ga	63	SER
5	ga	104	PHE
5	ga	118	ARG
5	ga	128	SER
5	ga	136	LYS
6	ha	20	VAL
6	ha	41	LYS
6	ha	83	SER
6	ha	103	SER
6	ha	120	SER
6	ha	126	ASP
6	ha	132	SER
6	ha	147	GLU
6	ha	165	TRP
6	ha	167	SER
6	ha	170	ARG
6	ha	174	ASN
6	ha	218	ASP
6	ha	221	LEU
6	ha	238	GLU
6	ha	241	ARG
6	ha	243	TYR
6	ha	244	SER
6	ha	272	LYS
6	ha	279	LYS
6	ha	285	LEU
6	ha	296	MET
6	ha	299	CYS
6	ha	303	SER
7	ia	10	LYS
7	ia	27	ARG
7	ia	45	ARG
7	ia	61	GLU
7	ia	65	ARG
7	ia	74	GLN
7	ia	75	LYS
7	ia	93	ASN

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Mol	Chain	Res	Type
7	ia	106	ARG
7	ia	149	SER
7	ia	178	ARG
7	ia	202	THR
7	ia	212	PRO
8	ja	7	LYS
8	ja	16	SER
8	ja	21	ASP
8	ja	59	ARG
8	ja	63	SER
8	ja	71	MET
8	ja	73	ASP
8	ja	110	ARG
8	ja	115	ARG
8	ja	121	PHE
8	ja	124	CYS
8	ja	128	SER
8	ja	143	ASP
8	ja	163	ASP
8	ja	174	LYS
8	ja	206	GLU
8	ja	211	GLU
8	ja	233	LYS
8	ja	255	ARG
9	ka	19	THR
9	ka	27	ASP
9	ka	40	LYS
9	ka	56	ARG
9	ka	61	GLN
9	ka	77	ARG
9	ka	110	ASP
9	ka	118	ARG
9	ka	131	ARG
9	ka	180	SER
9	ka	189	LYS
9	ka	190	ASP
10	la	32	ARG
10	la	86	SER
10	la	104	ASP
10	la	108	LYS
10	la	121	THR
10	la	122	LEU

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Mol	Chain	Res	Type
11	ma	31	THR
11	ma	38	LYS
11	ma	42	LYS
11	ma	52	LYS
11	ma	57	LYS
11	ma	64	MET
11	ma	78	CYS
11	ma	104	ASP
11	ma	111	SER
11	ma	113	THR
11	ma	126	ASP
12	na	34	PHE
12	na	38	ASN
12	na	57	THR
12	na	65	ASP
12	na	66	ARG
12	na	84	ARG
12	na	87	GLU
12	na	96	LYS
12	na	128	ARG
12	na	130	GLU
12	na	151	LEU
13	oa	38	ARG
13	oa	60	SER
13	oa	64	MET
13	oa	68	MET
13	oa	73	ASN
13	oa	81	ASP
13	oa	83	PHE
13	oa	101	ASN
13	oa	106	LYS
13	oa	108	ARG
13	oa	112	GLU
13	oa	115	LYS
13	oa	135	HIS
14	pa	34	ASP
14	pa	39	LYS
14	pa	56	ASP
14	pa	58	HIS
14	pa	87	ASP
15	qa	5	ARG
15	qa	21	TYR

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Mol	Chain	Res	Type
15	qa	23	ARG
15	qa	24	MET
15	qa	25	THR
15	qa	43	SER
15	qa	56	HIS
15	qa	70	SER
15	qa	82	MET
15	qa	84	PHE
15	qa	92	GLU
15	qa	97	ARG
15	qa	118	GLU
16	ra	21	ASP
16	ra	31	TYR
16	ra	36	LYS
16	ra	37	ARG
16	ra	41	MET
16	ra	57	GLU
16	ra	61	SER
16	ra	72	SER
16	ra	80	ARG
16	ra	101	ARG
16	ra	113	SER
16	ra	115	ASN
16	ra	123	MET
16	ra	138	SER
16	ra	145	ASP
17	sa	40	ASP
17	sa	45	MET
17	sa	53	ARG
17	sa	60	ARG
17	sa	67	LYS
17	sa	111	PHE
17	sa	136	LYS
18	ta	78	ARG
18	ta	83	ASP
18	ta	87	ARG
18	ta	92	MET
18	ta	104	ARG
19	ua	54	ASP
19	ua	62	ASN
20	va	41	LYS
20	va	42	HIS

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Mol	Chain	Res	Type
20	va	48	ASN
20	va	52	PHE
20	va	65	GLN
20	va	67	ARG
20	va	81	ARG
20	va	89	ARG
20	va	98	TRP
21	wa	18	SER
21	wa	19	ARG
21	wa	40	ARG
22	xa	36	ASP
22	xa	58	CYS
22	xa	62	GLN
22	xa	80	SER
22	xa	84	LYS
23	ya	44	PHE
24	za	26	ASP
24	za	32	LYS
24	za	40	ARG
24	za	48	ASP
24	za	63	GLN
24	za	76	GLN
24	za	132	ARG
24	za	141	SER
24	za	172	ARG
24	za	177	CYS
24	za	204	ASP
24	za	208	TYR
25	bb	45	LYS
25	bb	69	SER
25	bb	94	MET
25	bb	95	ASN
25	bb	100	PHE
25	bb	101	TRP
25	bb	111	ARG
25	bb	129	THR
25	bb	132	ASN
25	bb	135	LEU
25	bb	145	ARG
25	bb	148	ASN
25	bb	152	ARG
25	bb	159	SER

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Mol	Chain	Res	Type
25	bb	167	LYS
25	bb	172	MET
25	bb	179	CYS
25	bb	199	LYS
25	bb	208	GLN
25	bb	219	LYS
26	cb	11	LEU
26	cb	12	TYR
26	cb	50	THR
26	cb	59	ARG
26	cb	74	LYS
26	cb	75	ARG
26	cb	76	LYS
27	db	6	ARG
27	db	11	ASN
27	db	19	LYS
27	db	42	ARG
27	db	46	GLU
27	db	91	ASN
28	eb	3	HIS
28	eb	10	TYR
28	eb	40	CYS
28	eb	51	LEU
28	eb	52	SER
28	eb	65	ASP
28	eb	149	MET
29	fb	62	LYS
29	fb	98	LYS
29	fb	130	GLU
29	fb	133	THR
29	fb	151	ARG
29	fb	156	ASN
29	fb	186	SER
29	fb	209	SER
29	fb	211	ARG
29	fb	213	SER
29	fb	220	PHE
29	fb	226	ASP
29	fb	232	TYR
29	fb	238	ASP
30	gb	3	LEU
30	gb	12	CYS

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Mol	Chain	Res	Type
30	gb	17	GLU
30	gb	22	MET
30	gb	26	ASN
30	gb	53	MET
30	gb	56	CYS
30	gb	58	LYS
30	gb	77	LEU
30	gb	94	ARG
30	gb	102	CYS
30	gb	113	LEU
30	gb	200	LYS
30	gb	215	LYS
31	hb	37	LEU
31	hb	42	LYS
31	hb	43	ASP
31	hb	58	ARG
31	hb	79	ARG
31	hb	80	LEU
31	hb	99	ARG
31	hb	107	LYS
31	hb	166	LYS
31	hb	174	TYR
31	hb	177	LEU
32	ib	21	LYS
32	ib	23	ASP
32	ib	26	LYS
32	ib	27	ARG
32	ib	68	ARG
32	ib	75	THR
32	ib	89	ARG
32	ib	115	CYS
32	ib	117	ARG
32	ib	122	ASP
32	ib	129	CYS
33	IB	11	ARG
33	IB	25	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
4	da	81	ASN
6	ha	206	HIS

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Mol	Chain	Res	Type
6	ha	283	GLN
9	ka	199	ASN
11	ma	26	HIS
12	na	113	GLN
13	oa	97	GLN
16	ra	121	GLN
18	ta	73	ASN
24	za	96	GLN
27	db	11	ASN
27	db	13	HIS
28	eb	112	GLN
28	eb	126	HIS
31	hb	123	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
35	cl	73/75 (97%)	27 (36%)	0
All	All	1765/1892 (93%)	458 (25%)	0

All (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
1	aa	39	A
1	aa	40	A
1	aa	42	G
1	aa	45	U
1	aa	47	A
1	aa	50	C
1	aa	59	G
1	aa	63	G
1	aa	65	A
1	aa	66	U
1	aa	67	G

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Mol	Chain	Res	Type
1	aa	68	A
1	aa	73	A
1	aa	74	U
1	aa	75	U
1	aa	76	U
1	aa	77	G
1	aa	78	A
1	aa	79	A
1	aa	80	C
1	aa	81	U
1	aa	82	G
1	aa	105	A
1	aa	106	A
1	aa	112	U
1	aa	115	A
1	aa	128	G
1	aa	130	A
1	aa	132	G
1	aa	134	G
1	aa	135	C
1	aa	136	U
1	aa	137	A
1	aa	138	C
1	aa	139	U
1	aa	140	C
1	aa	143	A
1	aa	144	U
1	aa	145	A
1	aa	151	A
1	aa	156	U
1	aa	157	U
1	aa	158	C
1	aa	164	C
1	aa	170	C
1	aa	175	A
1	aa	176	A
1	aa	177	C
1	aa	179	A
1	aa	181	C
1	aa	185	G
1	aa	189	U
1	aa	190	C

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Mol	Chain	Res	Type
1	aa	191	U
1	aa	193	G
1	aa	195	A
1	aa	197	G
1	aa	198	G
1	aa	200	C
1	aa	201	G
1	aa	212	A
1	aa	244	C
1	aa	245	C
1	aa	246	G
1	aa	252	U
1	aa	253	C
1	aa	260	A
1	aa	262	U
1	aa	263	C
1	aa	264	G
1	aa	265	A
1	aa	272	G
1	aa	273	C
1	aa	274	A
1	aa	275	C
1	aa	276	G
1	aa	277	G
1	aa	279	C
1	aa	280	U
1	aa	281	U
1	aa	282	C
1	aa	283	G
1	aa	284	U
1	aa	286	C
1	aa	287	C
1	aa	288	G
1	aa	320	A
1	aa	325	C
1	aa	326	G
1	aa	333	G
1	aa	341	G
1	aa	342	C
1	aa	354	G
1	aa	355	U
1	aa	356	G

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Mol	Chain	Res	Type
1	aa	363	G
1	aa	365	C
1	aa	373	U
1	aa	384	U
1	aa	394	G
1	aa	397	C
1	aa	403	A
1	aa	404	A
1	aa	405	A
1	aa	406	C
1	aa	407	G
1	aa	408	G
1	aa	420	A
1	aa	421	A
1	aa	422	G
1	aa	427	G
1	aa	428	C
1	aa	429	A
1	aa	430	G
1	aa	438	G
1	aa	443	U
1	aa	448	C
1	aa	472	A
1	aa	473	C
1	aa	481	A
1	aa	485	A
1	aa	486	U
1	aa	487	A
1	aa	488	C
1	aa	489	C
1	aa	490	G
1	aa	492	G
1	aa	494	G
1	aa	495	C
1	aa	496	A
1	aa	497	U
1	aa	499	A
1	aa	500	G
1	aa	501	U
1	aa	502	G
1	aa	503	U
1	aa	504	C

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Mol	Chain	Res	Type
1	aa	505	U
1	aa	506	G
1	aa	507	G
1	aa	508	U
1	aa	509	A
1	aa	510	A
1	aa	511	U
1	aa	512	U
1	aa	514	G
1	aa	515	A
1	aa	518	G
1	aa	519	A
1	aa	523	C
1	aa	531	A
1	aa	544	G
1	aa	545	A
1	aa	546	U
1	aa	552	G
1	aa	553	G
1	aa	559	A
1	aa	560	A
1	aa	561	G
1	aa	562	U
1	aa	563	C
1	aa	569	C
1	aa	582	U
1	aa	584	A
1	aa	586	U
1	aa	598	A
1	aa	599	G
1	aa	610	A
1	aa	615	U
1	aa	619	A
1	aa	623	A
1	aa	624	A
1	aa	626	A
1	aa	627	A
1	aa	628	G
1	aa	642	C
1	aa	643	U
1	aa	644	U
1	aa	646	G

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Mol	Chain	Res	Type
1	aa	651	G
1	aa	706	U
1	aa	707	C
1	aa	708	G
1	aa	709	C
1	aa	711	C
1	aa	712	U
1	aa	714	C
1	aa	715	U
1	aa	716	A
1	aa	717	G
1	aa	718	C
1	aa	742	C
1	aa	743	G
1	aa	745	C
1	aa	746	A
1	aa	747	U
1	aa	749	G
1	aa	751	U
1	aa	760	G
1	aa	761	A
1	aa	762	A
1	aa	772	C
1	aa	777	A
1	aa	780	A
1	aa	781	A
1	aa	784	C
1	aa	785	A
1	aa	786	U
1	aa	787	C
1	aa	788	G
1	aa	789	C
1	aa	790	U
1	aa	792	U
1	aa	795	A
1	aa	800	U
1	aa	817	C
1	aa	818	A
1	aa	819	U
1	aa	820	A
1	aa	821	G
1	aa	822	G

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Mol	Chain	Res	Type
1	aa	825	U
1	aa	827	C
1	aa	828	G
1	aa	829	G
1	aa	831	C
1	aa	834	A
1	aa	835	U
1	aa	836	U
1	aa	837	G
1	aa	839	G
1	aa	840	U
1	aa	842	G
1	aa	844	C
1	aa	846	U
1	aa	849	G
1	aa	850	G
1	aa	851	G
1	aa	855	G
1	aa	857	A
1	aa	859	U
1	aa	861	A
1	aa	864	A
1	aa	865	U
1	aa	868	A
1	aa	881	G
1	aa	903	A
1	aa	911	A
1	aa	918	G
1	aa	919	G
1	aa	938	A
1	aa	940	U
1	aa	947	G
1	aa	965	U
1	aa	971	A
1	aa	997	A
1	aa	1003	A
1	aa	1008	A
1	aa	1009	U
1	aa	1010	A
1	aa	1016	C
1	aa	1031	A
1	aa	1033	C

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Mol	Chain	Res	Type
1	aa	1037	G
1	aa	1044	A
1	aa	1045	G
1	aa	1057	U
1	aa	1058	G
1	aa	1059	U
1	aa	1061	G
1	aa	1062	C
1	aa	1063	U
1	aa	1065	A
1	aa	1079	G
1	aa	1085	U
1	aa	1086	A
1	aa	1087	U
1	aa	1096	A
1	aa	1097	A
1	aa	1101	C
1	aa	1102	U
1	aa	1105	G
1	aa	1116	G
1	aa	1128	C
1	aa	1143	A
1	aa	1151	G
1	aa	1155	G
1	aa	1156	A
1	aa	1162	A
1	aa	1163	C
1	aa	1164	C
1	aa	1165	A
1	aa	1169	G
1	aa	1172	G
1	aa	1188	A
1	aa	1189	U
1	aa	1198	A
1	aa	1200	A
1	aa	1203	G
1	aa	1204	G
1	aa	1206	A
1	aa	1208	A
1	aa	1221	A
1	aa	1222	G
1	aa	1231	A

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Mol	Chain	Res	Type
1	aa	1233	G
1	aa	1234	A
1	aa	1241	G
1	aa	1244	U
1	aa	1248	A
1	aa	1249	G
1	aa	1254	U
1	aa	1255	U
1	aa	1259	G
1	aa	1260	A
1	aa	1277	G
1	aa	1290	U
1	aa	1305	U
1	aa	1318	U
1	aa	1319	U
1	aa	1322	G
1	aa	1325	A
1	aa	1331	C
1	aa	1344	U
1	aa	1348	A
1	aa	1349	A
1	aa	1350	C
1	aa	1353	G
1	aa	1354	C
1	aa	1359	C
1	aa	1361	G
1	aa	1363	G
1	aa	1364	C
1	aa	1365	C
1	aa	1366	A
1	aa	1367	U
1	aa	1368	C
1	aa	1369	C
1	aa	1378	C
1	aa	1379	U
1	aa	1381	G
1	aa	1382	C
1	aa	1394	A
1	aa	1396	U
1	aa	1397	A
1	aa	1404	U
1	aa	1405	U

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Mol	Chain	Res	Type
1	aa	1418	G
1	aa	1419	U
1	aa	1421	U
1	aa	1431	A
1	aa	1433	A
1	aa	1434	G
1	aa	1437	C
1	aa	1438	U
1	aa	1439	G
1	aa	1442	A
1	aa	1451	G
1	aa	1452	A
1	aa	1453	U
1	aa	1464	G
1	aa	1465	C
1	aa	1466	A
1	aa	1477	A
1	aa	1495	U
1	aa	1496	A
1	aa	1498	A
1	aa	1499	U
1	aa	1500	A
1	aa	1501	G
1	aa	1504	U
1	aa	1523	A
1	aa	1524	A
1	aa	1526	C
1	aa	1529	G
1	aa	1530	G
1	aa	1531	G
1	aa	1532	A
1	aa	1542	G
1	aa	1543	U
1	aa	1544	G
1	aa	1545	A
1	aa	1550	G
1	aa	1563	A
1	aa	1565	U
1	aa	1566	U
1	aa	1567	G
1	aa	1577	A
1	aa	1582	G

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Mol	Chain	Res	Type
1	aa	1590	U
1	aa	1591	A
1	aa	1592	G
1	aa	1598	G
1	aa	1609	G
1	aa	1615	G
1	aa	1624	G
1	aa	1630	G
1	aa	1639	A
1	aa	1643	A
1	aa	1665	U
1	aa	1666	G
1	aa	1691	C
1	aa	1693	C
1	aa	1694	G
1	aa	1697	G
1	aa	1698	A
1	aa	1725	C
1	aa	1726	G
1	aa	1727	C
1	aa	1750	A
1	aa	1752	U
1	aa	1770	G
1	aa	1772	A
1	aa	1776	A
1	aa	1779	U
1	aa	1783	C
1	aa	1790	G
1	aa	1792	A
1	aa	1802	G
1	aa	1803	G
1	aa	1804	A
1	aa	1805	U
1	aa	1806	C
1	aa	1808	U
1	aa	1809	U
1	aa	1810	G
35	cl	2	U
35	cl	4	A
35	cl	8	U
35	cl	9	1MG
35	cl	10	2MG

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Mol	Chain	Res	Type
35	cl	14	A
35	cl	16	C
35	cl	18	G
35	cl	19	G
35	cl	20	A
35	cl	26	2MG
35	cl	43	C
35	cl	45	G
35	cl	46	G7M
35	cl	47	H2U
35	cl	48	5MC
35	cl	49	5MC
35	cl	53	G
35	cl	56	C
35	cl	58	1MA
35	cl	61	C
35	cl	65	G
35	cl	68	C
35	cl	73	A
35	cl	74	C
35	cl	75	C
35	cl	76	A

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	H2U	cl	47	35	18,21,22	3.15	5 (27%)	21,30,33	1.99	5 (23%)
35	PSU	cl	28	35	18,21,22	1.08	2 (11%)	22,30,33	1.83	5 (22%)
35	G7M	cl	46	35	20,26,27	2.83	8 (40%)	17,39,42	1.17	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	1MG	cl	9	35	18,26,27	2.62	5 (27%)	19,39,42	1.45	4 (21%)
35	5MC	cl	49	35	18,22,23	3.82	8 (44%)	26,32,35	1.29	5 (19%)
35	2MG	cl	10	35	18,26,27	2.57	6 (33%)	16,38,41	1.55	4 (25%)
35	5MC	cl	48	35	18,22,23	3.80	8 (44%)	26,32,35	1.15	2 (7%)
35	2MG	cl	26	35	18,26,27	2.61	6 (33%)	16,38,41	1.55	4 (25%)
35	MIA	cl	37	36,35	24,31,32	2.40	3 (12%)	26,44,47	3.40	7 (26%)
35	PSU	cl	55	35	18,21,22	1.16	1 (5%)	22,30,33	1.69	2 (9%)
35	1MA	cl	58	35	16,25,26	4.14	4 (25%)	18,37,40	1.70	3 (16%)

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	H2U	cl	47	35	-	5/7/38/39	0/2/2/2
35	PSU	cl	28	35	-	0/7/25/26	0/2/2/2
35	G7M	cl	46	35	-	1/3/25/26	0/3/3/3
35	1MG	cl	9	35	-	1/3/25/26	0/3/3/3
35	5MC	cl	49	35	-	5/7/25/26	0/2/2/2
35	2MG	cl	10	35	-	2/5/27/28	0/3/3/3
35	5MC	cl	48	35	-	2/7/25/26	0/2/2/2
35	2MG	cl	26	35	-	2/5/27/28	0/3/3/3
35	MIA	cl	37	36,35	-	5/11/33/34	0/3/3/3
35	PSU	cl	55	35	-	0/7/25/26	0/2/2/2
35	1MA	cl	58	35	-	2/3/25/26	0/3/3/3

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	cl	58	1MA	C2-N3	15.07	1.47	1.29
35	cl	47	H2U	C2-N1	9.81	1.49	1.35
35	cl	48	5MC	C6-C5	9.38	1.50	1.34
35	cl	49	5MC	C6-C5	9.31	1.49	1.34
35	cl	37	MIA	C2-S10	7.83	1.82	1.75
35	cl	49	5MC	C4-N3	7.43	1.46	1.34
35	cl	48	5MC	C4-N3	7.40	1.46	1.34
35	cl	37	MIA	C6-N6	7.15	1.47	1.34
35	cl	46	G7M	C2-N2	6.72	1.50	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	cl	49	5MC	C2-N3	6.70	1.49	1.36
35	cl	47	H2U	C2-N3	6.49	1.49	1.38
35	cl	48	5MC	C2-N3	6.44	1.49	1.36
35	cl	9	1MG	C2-N3	6.28	1.46	1.34
35	cl	9	1MG	C2-N2	6.28	1.45	1.34
35	cl	46	G7M	C2-N3	5.74	1.47	1.33
35	cl	26	2MG	C2-N2	5.68	1.46	1.33
35	cl	10	2MG	C2-N2	5.68	1.46	1.33
35	cl	46	G7M	C4-N3	5.24	1.50	1.37
35	cl	48	5MC	C6-N1	5.20	1.46	1.38
35	cl	49	5MC	C6-N1	5.18	1.46	1.38
35	cl	47	H2U	C4-N3	5.11	1.46	1.37
35	cl	26	2MG	C2-N1	5.10	1.44	1.36
35	cl	10	2MG	C4-N3	5.06	1.49	1.37
35	cl	26	2MG	C4-N3	5.00	1.49	1.37
35	cl	10	2MG	C2-N1	4.95	1.44	1.36
35	cl	58	1MA	C2-N1	4.93	1.45	1.35
35	cl	9	1MG	C4-N3	4.76	1.48	1.37
35	cl	49	5MC	C2-N1	4.69	1.50	1.40
35	cl	48	5MC	C2-N1	4.50	1.49	1.40
35	cl	46	G7M	C6-N1	4.42	1.44	1.37
35	cl	48	5MC	C4-N4	4.13	1.44	1.34
35	cl	49	5MC	C4-N4	4.09	1.44	1.34
35	cl	58	1MA	C4-N3	3.84	1.49	1.37
35	cl	55	PSU	C6-C5	3.72	1.39	1.35
35	cl	26	2MG	C6-N1	3.71	1.43	1.37
35	cl	26	2MG	C5-C6	3.56	1.54	1.47
35	cl	37	MIA	C5-C4	-3.53	1.31	1.40
35	cl	10	2MG	C6-N1	3.52	1.43	1.37
35	cl	46	G7M	C5-C6	3.44	1.54	1.45
35	cl	10	2MG	C5-C6	3.44	1.54	1.47
35	cl	28	PSU	C6-C5	3.17	1.39	1.35
35	cl	46	G7M	C2-N1	3.08	1.45	1.37
35	cl	9	1MG	C5-C4	-2.68	1.36	1.43
35	cl	10	2MG	C5-C4	-2.52	1.36	1.43
35	cl	26	2MG	C5-C4	-2.49	1.36	1.43
35	cl	58	1MA	C5-C4	-2.42	1.36	1.43
35	cl	46	G7M	C8-N7	2.25	1.37	1.33
35	cl	46	G7M	O6-C6	-2.23	1.18	1.23
35	cl	48	5MC	CM5-C5	2.22	1.56	1.50
35	cl	49	5MC	CM5-C5	2.20	1.56	1.50
35	cl	47	H2U	O2-C2	-2.19	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	cl	48	5MC	O2-C2	-2.13	1.19	1.23
35	cl	9	1MG	O6-C6	-2.09	1.18	1.22
35	cl	28	PSU	C4-C5	-2.08	1.38	1.44
35	cl	49	5MC	O2-C2	-2.07	1.19	1.23
35	cl	47	H2U	O4-C4	-2.05	1.19	1.23

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	cl	37	MIA	C11-S10-C2	12.38	111.51	102.27
35	cl	37	MIA	C1'-N9-C4	9.22	142.84	126.64
35	cl	47	H2U	C4-N3-C2	-6.90	120.07	125.79
35	cl	58	1MA	N1-C2-N3	-4.79	120.44	126.02
35	cl	55	PSU	C4-N3-C2	-4.62	119.69	126.34
35	cl	28	PSU	N1-C2-N3	4.53	120.27	115.13
35	cl	28	PSU	C4-N3-C2	-4.53	119.81	126.34
35	cl	37	MIA	N3-C2-N1	-4.33	119.02	126.98
35	cl	55	PSU	N1-C2-N3	4.15	119.84	115.13
35	cl	58	1MA	C5-C6-N1	4.07	119.97	113.90
35	cl	9	1MG	C5-C6-N1	3.99	119.90	113.90
35	cl	10	2MG	C5-C6-N1	3.89	120.82	113.95
35	cl	37	MIA	C2-N3-C4	3.59	120.28	115.32
35	cl	26	2MG	C5-C6-N1	3.54	120.21	113.95
35	cl	48	5MC	C5-C6-N1	-3.03	120.22	123.34
35	cl	47	H2U	N3-C2-N1	2.98	119.81	116.65
35	cl	26	2MG	C8-N7-C5	2.95	108.62	102.99
35	cl	47	H2U	C5-C4-N3	2.92	119.93	116.65
35	cl	10	2MG	C8-N7-C5	2.85	108.42	102.99
35	cl	58	1MA	C8-N7-C5	2.84	108.41	102.99
35	cl	28	PSU	O2-C2-N1	-2.80	119.71	122.79
35	cl	26	2MG	CM2-N2-C2	-2.75	117.78	123.86
35	cl	47	H2U	C5-C6-N1	2.74	120.66	111.61
35	cl	46	G7M	C2-N1-C6	-2.69	120.14	125.10
35	cl	9	1MG	C8-N7-C5	2.68	108.09	102.99
35	cl	49	5MC	C5-C6-N1	-2.63	120.63	123.34
35	cl	49	5MC	C1'-N1-C6	-2.63	116.75	121.12
35	cl	49	5MC	CM5-C5-C6	-2.52	119.49	122.85
35	cl	10	2MG	CM2-N2-C2	-2.50	118.35	123.86
35	cl	49	5MC	C1'-N1-C2	2.41	123.79	118.42
35	cl	28	PSU	C6-C5-C4	2.40	119.88	118.20
35	cl	9	1MG	O6-C6-C5	-2.40	119.95	124.19
35	cl	28	PSU	C6-N1-C2	-2.38	120.25	122.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	cl	49	5MC	O2-C2-N3	-2.32	118.56	122.33
35	cl	10	2MG	O6-C6-C5	-2.32	119.84	124.37
35	cl	37	MIA	C4-C5-N7	-2.23	107.08	109.40
35	cl	48	5MC	CM5-C5-C6	-2.21	119.89	122.85
35	cl	46	G7M	N1-C2-N3	-2.19	119.22	123.32
35	cl	37	MIA	S10-C2-N3	2.18	123.67	116.10
35	cl	37	MIA	C16-C14-C15	2.13	119.30	114.60
35	cl	47	H2U	O2-C2-N1	-2.09	120.48	123.11
35	cl	9	1MG	CM1-N1-C6	2.09	120.41	117.55
35	cl	26	2MG	O6-C6-C5	-2.06	120.35	124.37

There are no chirality outliers.

All (25) 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
35	cl	37	MIA	N1-C2-S10-C11
35	cl	37	MIA	N3-C2-S10-C11
35	cl	47	H2U	C4'-C5'-O5'-P
35	cl	47	H2U	C3'-C4'-C5'-O5'
35	cl	49	5MC	O4'-C4'-C5'-O5'
35	cl	49	5MC	C3'-C4'-C5'-O5'
35	cl	26	2MG	C3'-C4'-C5'-O5'
35	cl	58	1MA	O4'-C4'-C5'-O5'
35	cl	10	2MG	O4'-C4'-C5'-O5'
35	cl	37	MIA	O4'-C4'-C5'-O5'
35	cl	58	1MA	C3'-C4'-C5'-O5'
35	cl	10	2MG	C3'-C4'-C5'-O5'
35	cl	47	H2U	O4'-C4'-C5'-O5'
35	cl	48	5MC	C4'-C5'-O5'-P
35	cl	37	MIA	C3'-C4'-C5'-O5'
35	cl	49	5MC	C4'-C5'-O5'-P
35	cl	49	5MC	C2'-C1'-N1-C6
35	cl	46	G7M	C4'-C5'-O5'-P
35	cl	48	5MC	C3'-C4'-C5'-O5'
35	cl	47	H2U	O4'-C1'-N1-C6
35	cl	49	5MC	C2'-C1'-N1-C2
35	cl	9	1MG	C4'-C5'-O5'-P
35	cl	47	H2U	C2'-C1'-N1-C2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

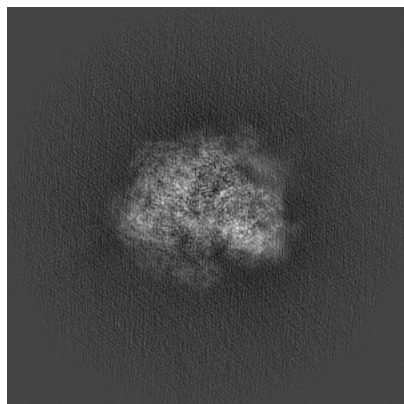
6 Map visualisation [i](#)

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.

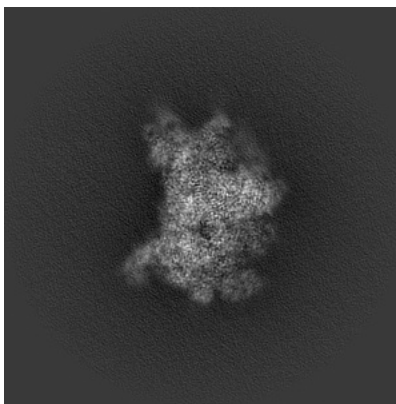
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

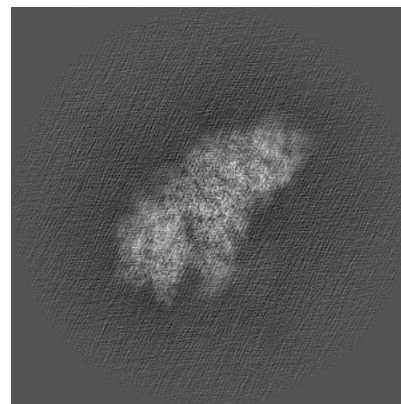
6.1.1 Primary map



X

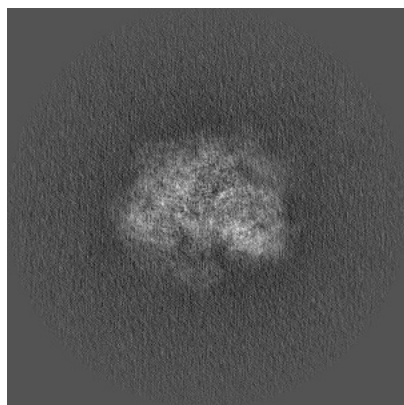


Y

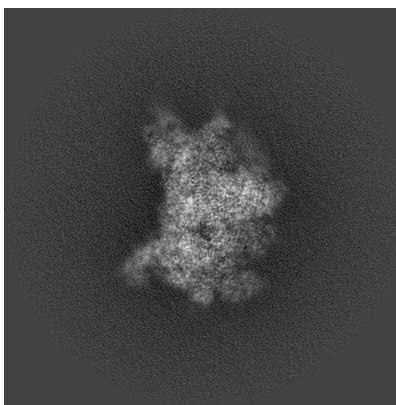


Z

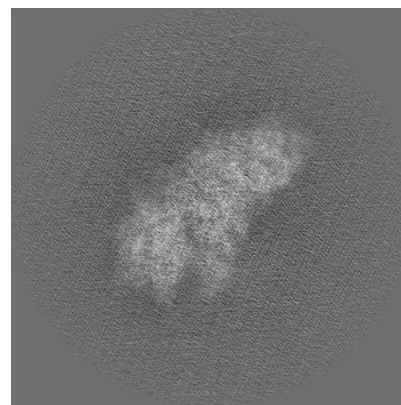
6.1.2 Raw map



X



Y

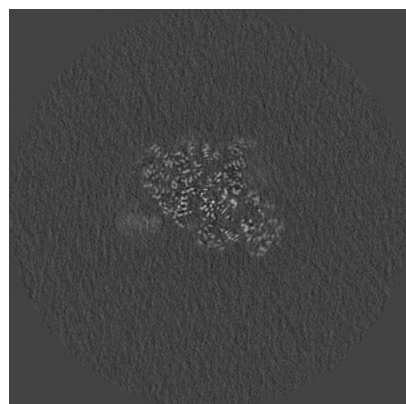


Z

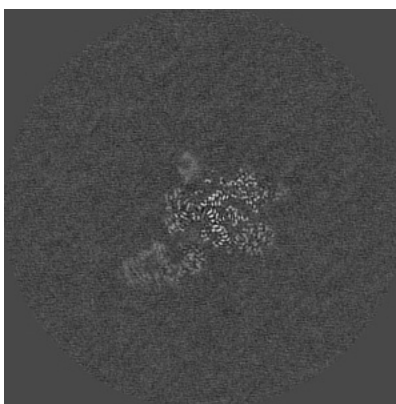
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

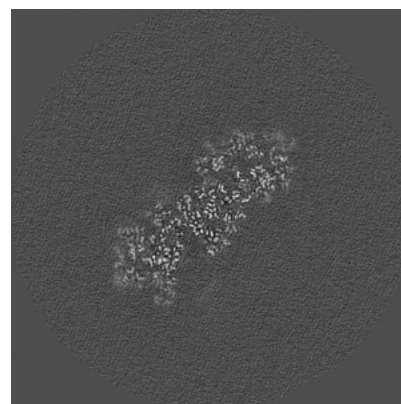
6.2.1 Primary map



X Index: 280

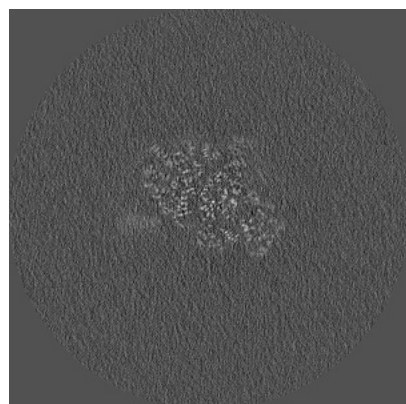


Y Index: 280

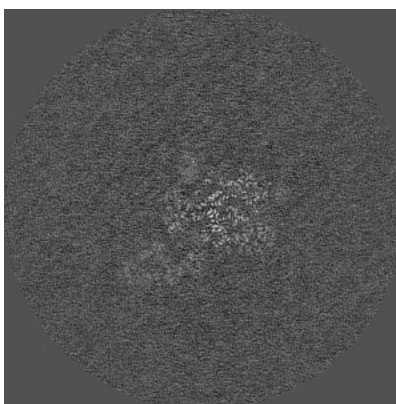


Z Index: 280

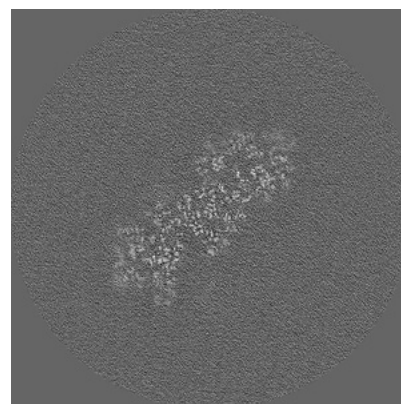
6.2.2 Raw map



X Index: 280



Y Index: 280

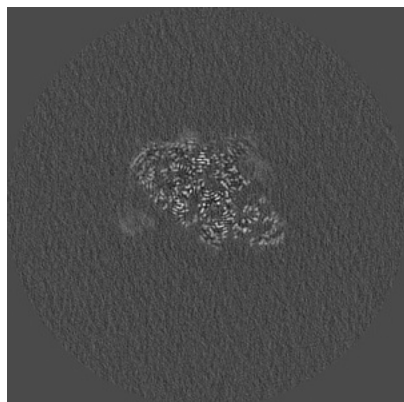


Z Index: 280

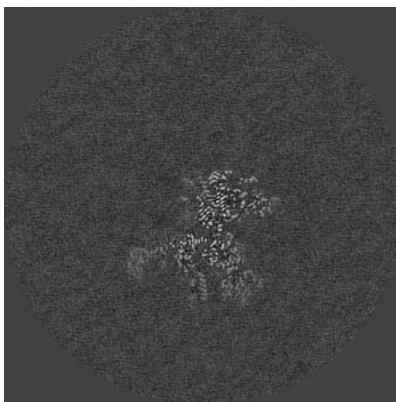
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

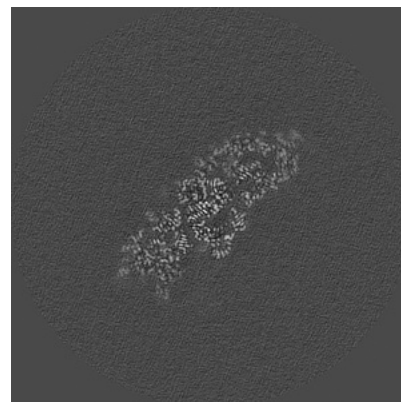
6.3.1 Primary map



X Index: 288

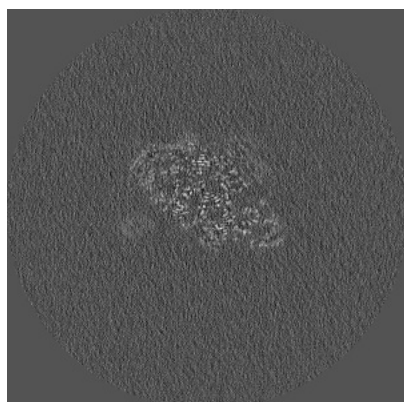


Y Index: 249

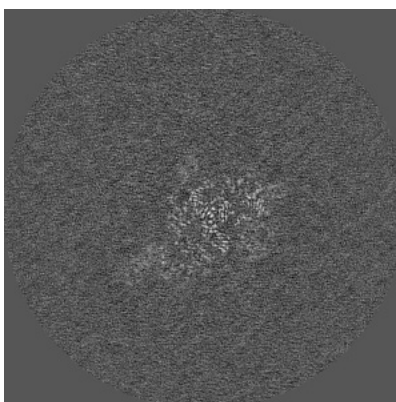


Z Index: 291

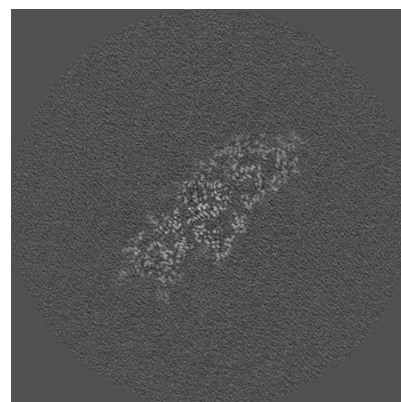
6.3.2 Raw map



X Index: 288



Y Index: 274

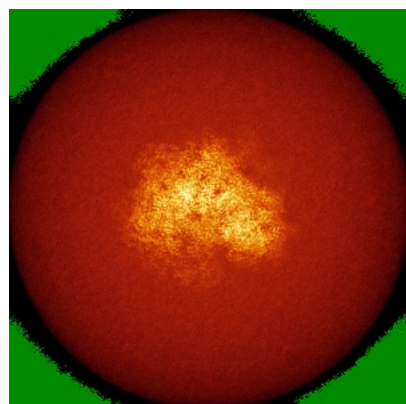


Z Index: 292

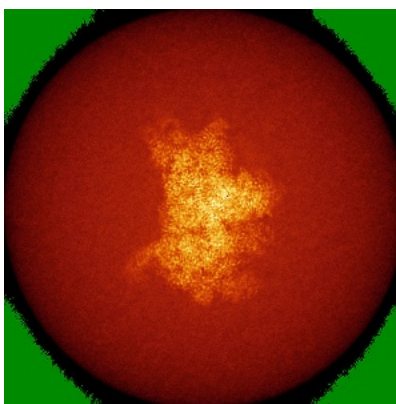
The images above show the largest variance slices of the map in three orthogonal directions.

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

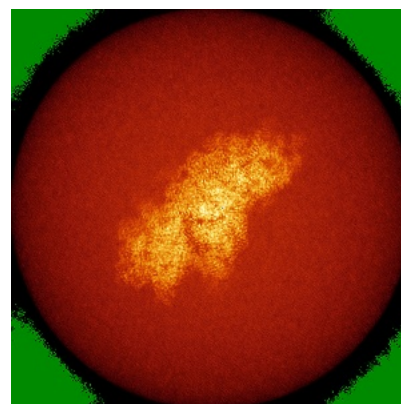
6.4.1 Primary map



X

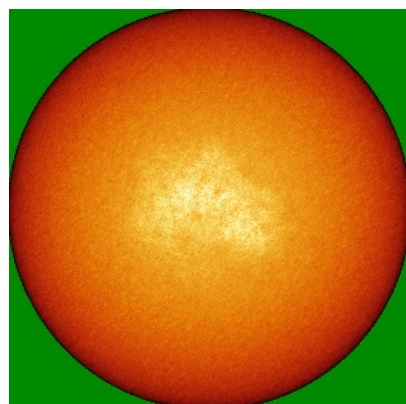


Y

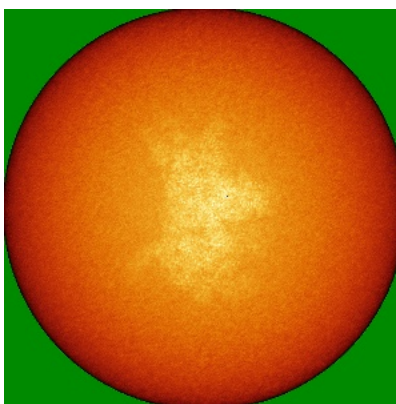


Z

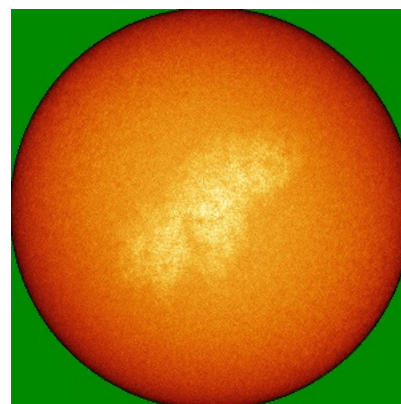
6.4.2 Raw map



X



Y

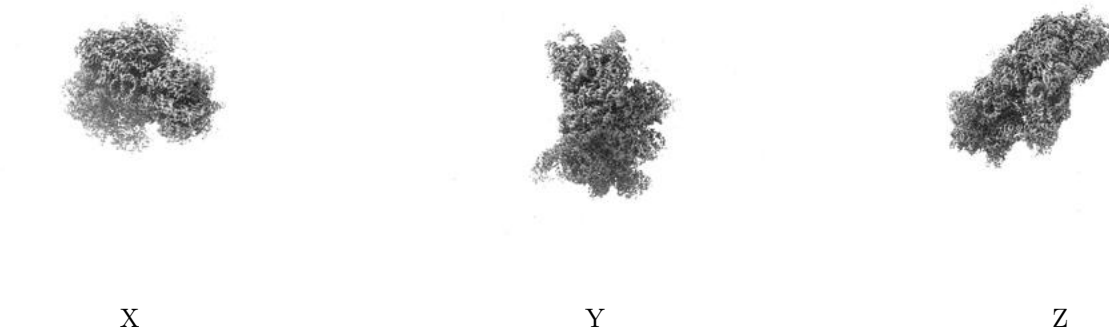


Z

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.

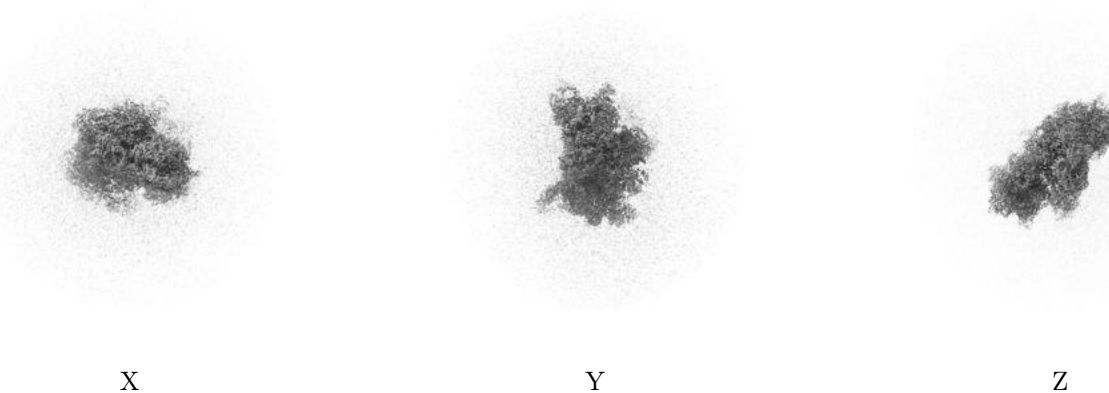
6.5 Orthogonal surface views [i](#)

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.

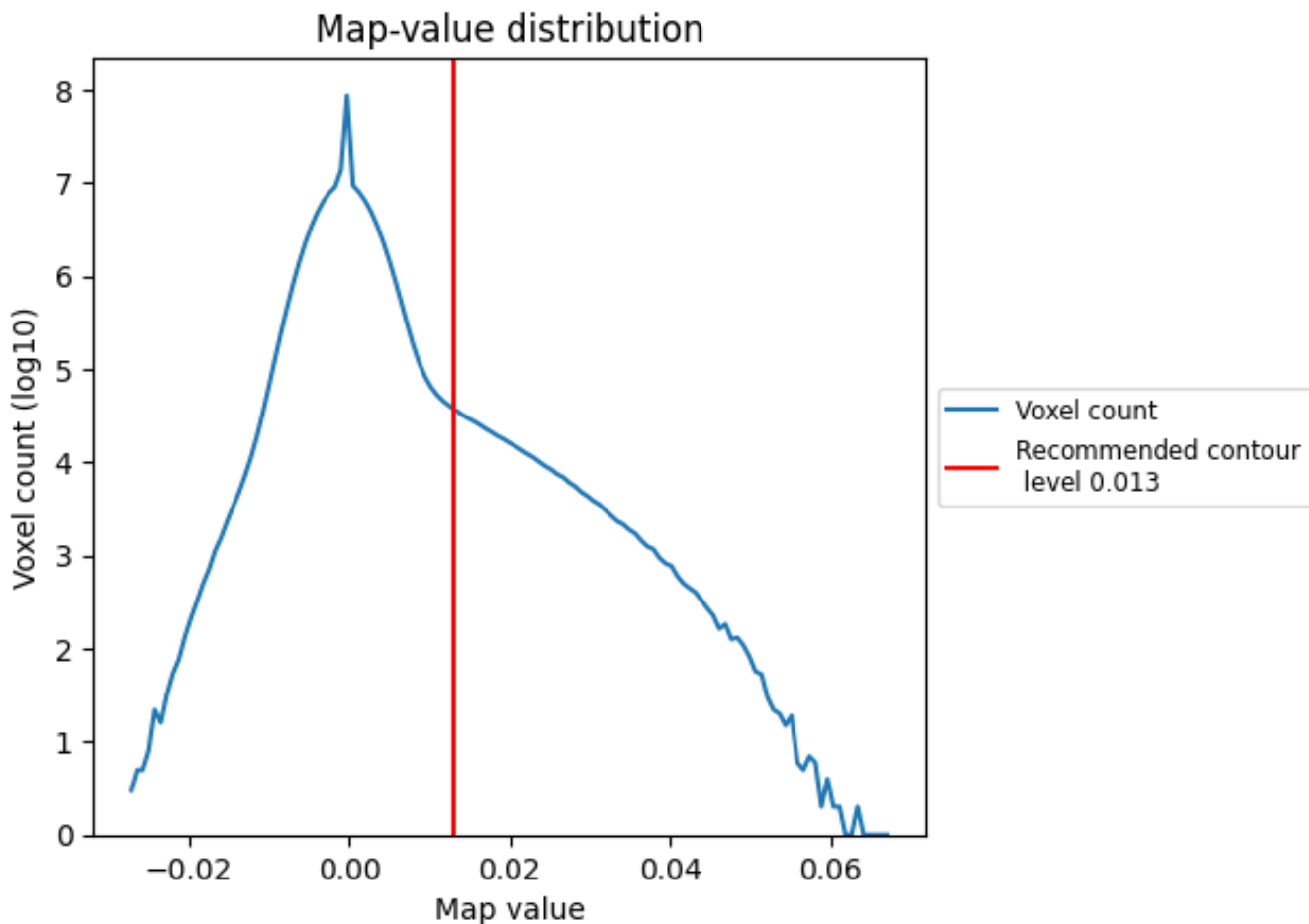
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

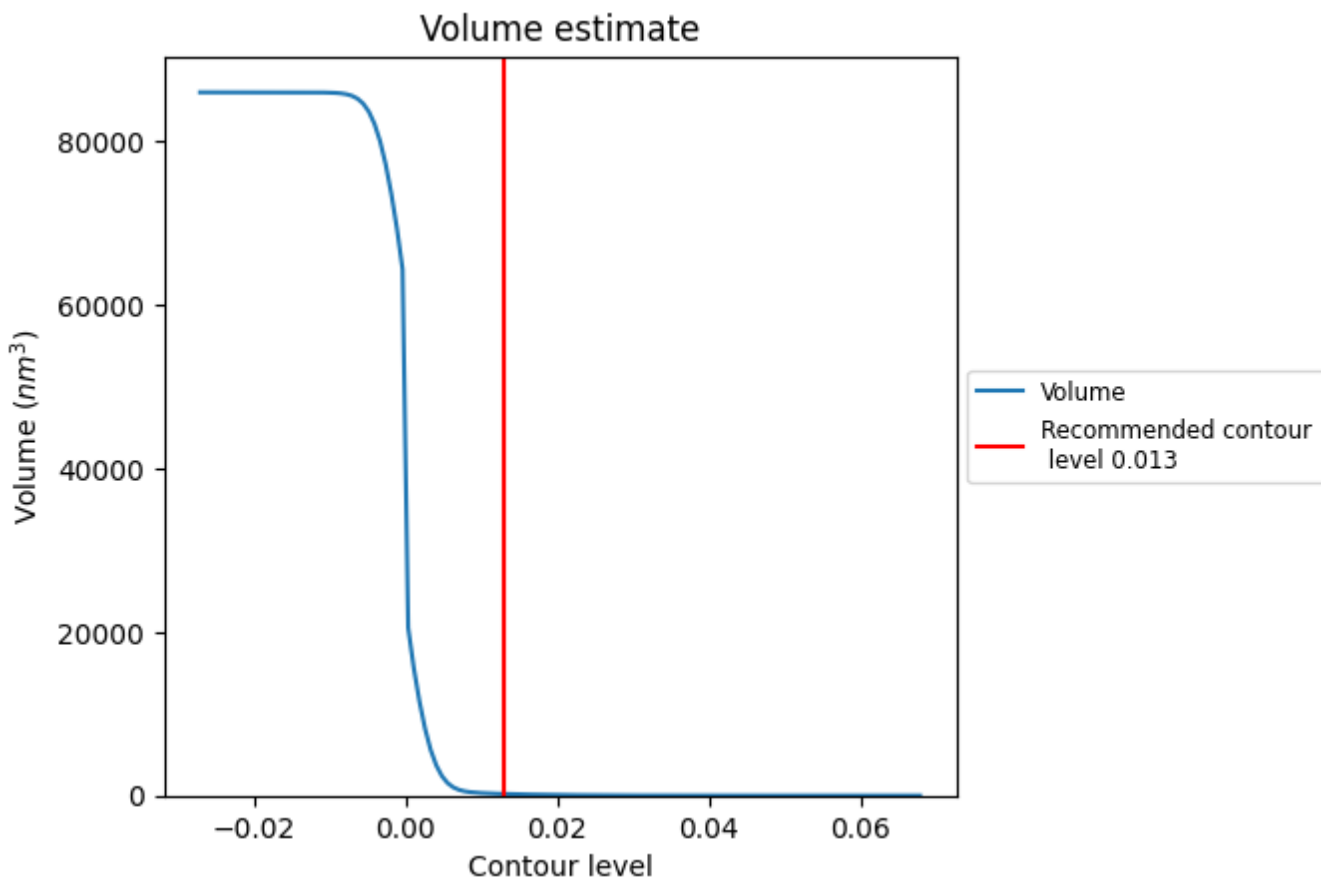
This section contains the results of statistical analysis of the map.

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.

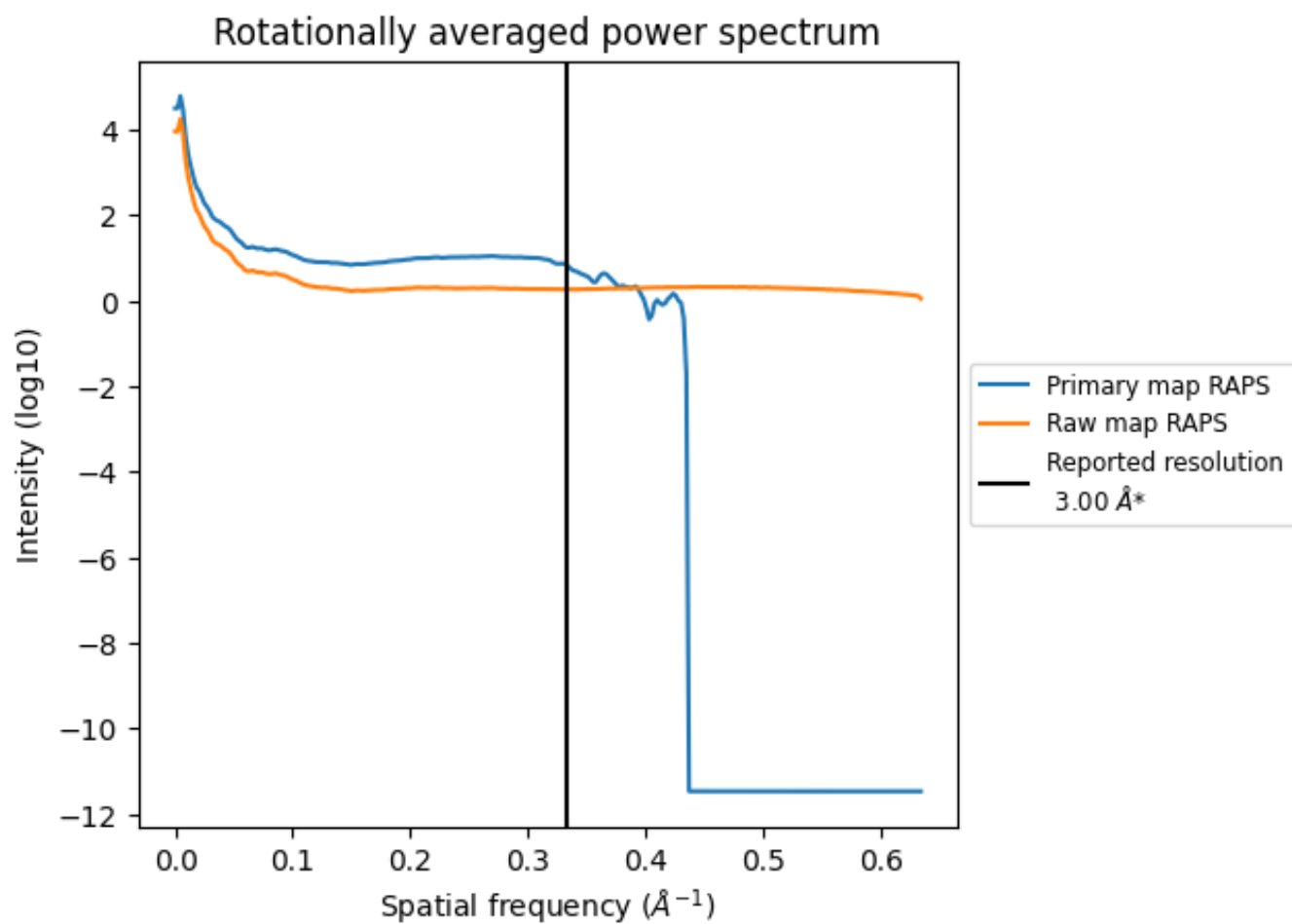
7.2 Volume estimate [i](#)



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](#)

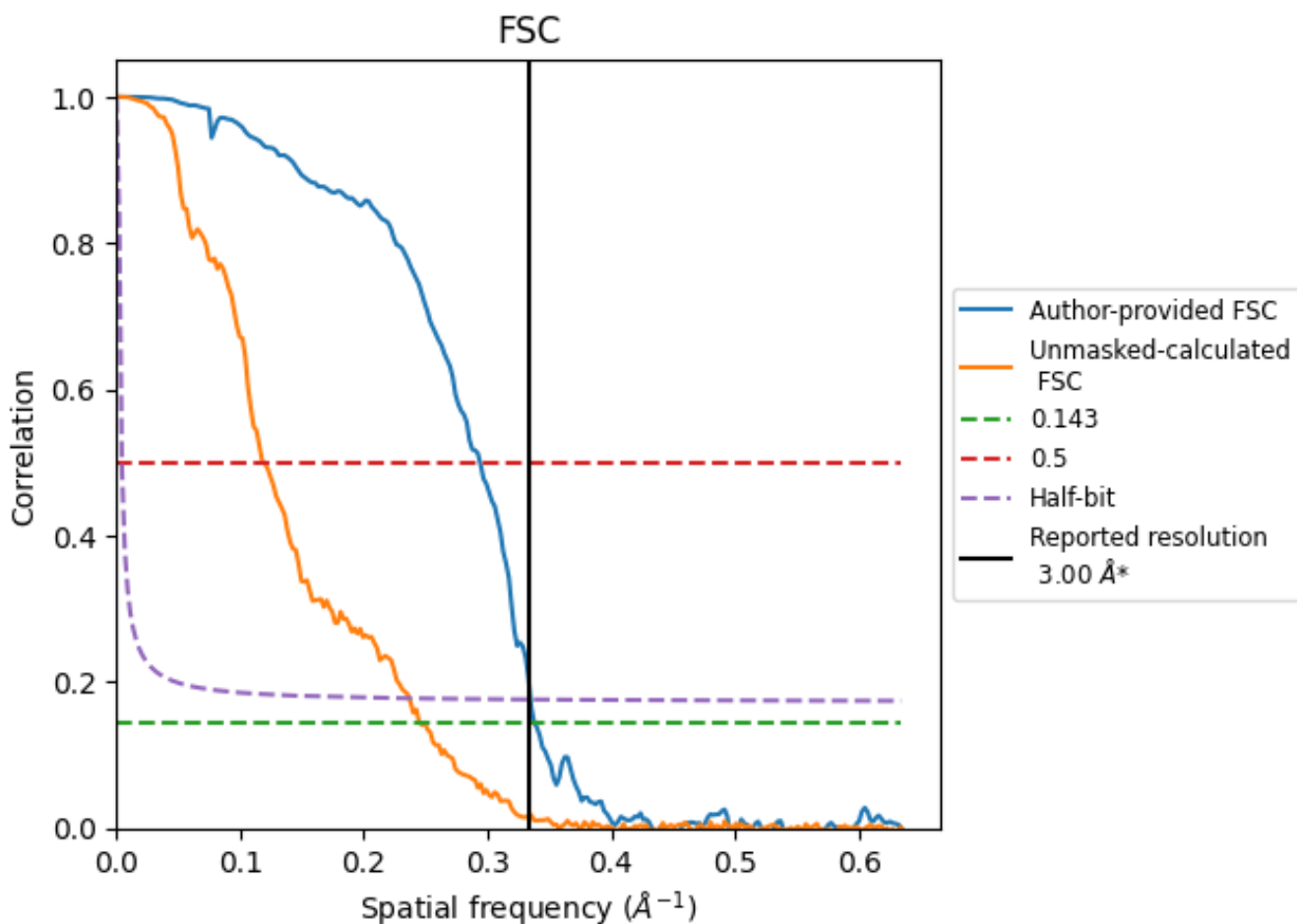


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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](#)

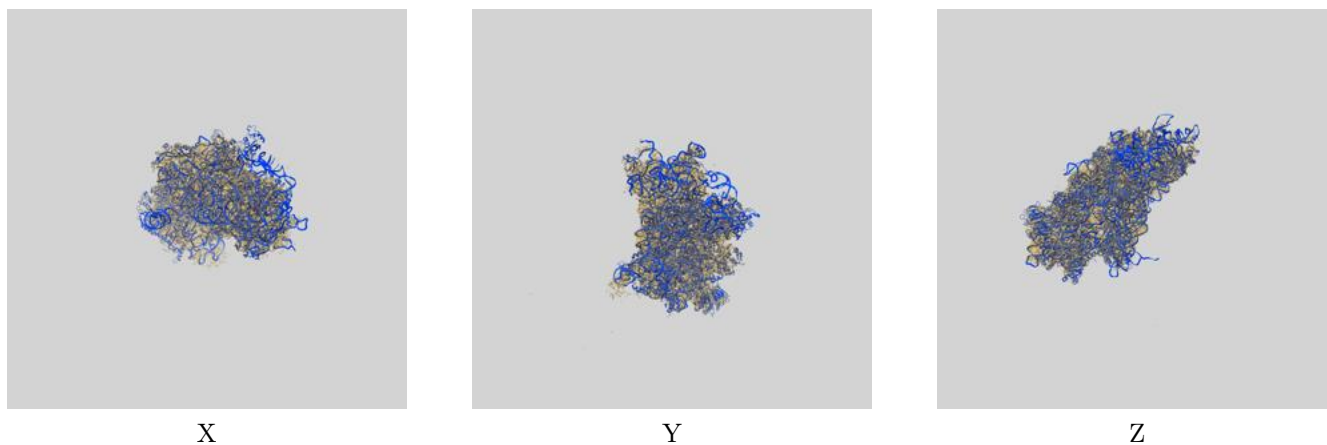
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.96	3.40	2.99
Unmasked-calculated*	4.07	8.40	4.22

*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](#)

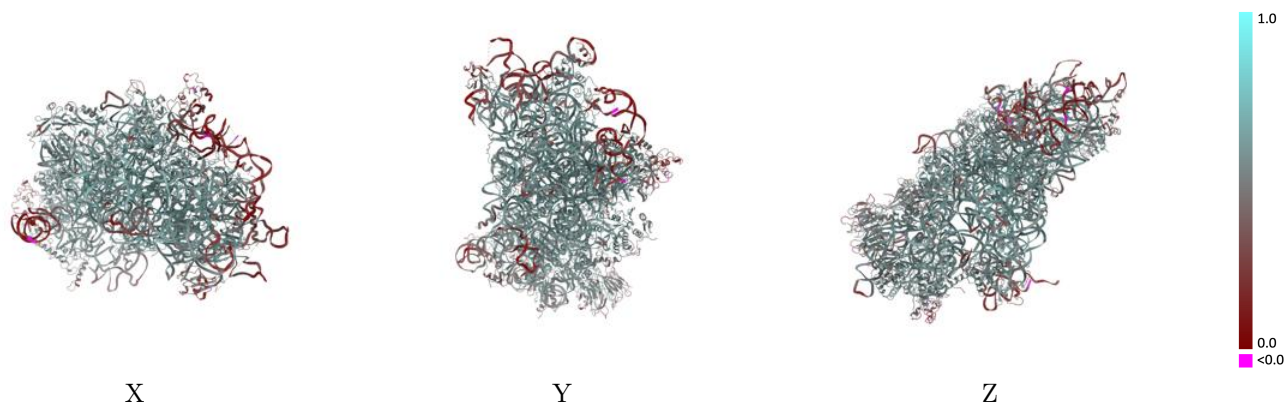
This section contains information regarding the fit between EMDB map EMD-35635 and PDB model 8IP9. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



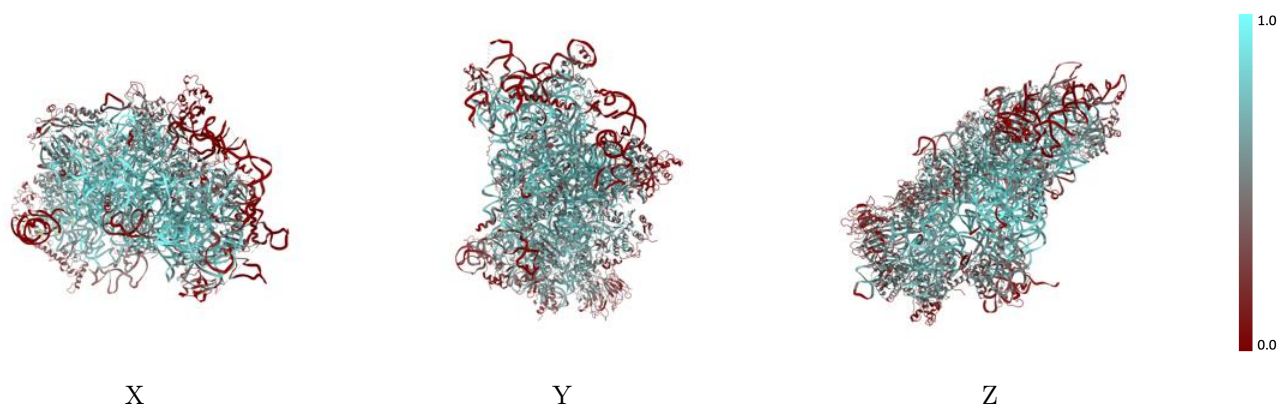
The images above show the 3D surface view of the map at the recommended contour level 0.013 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



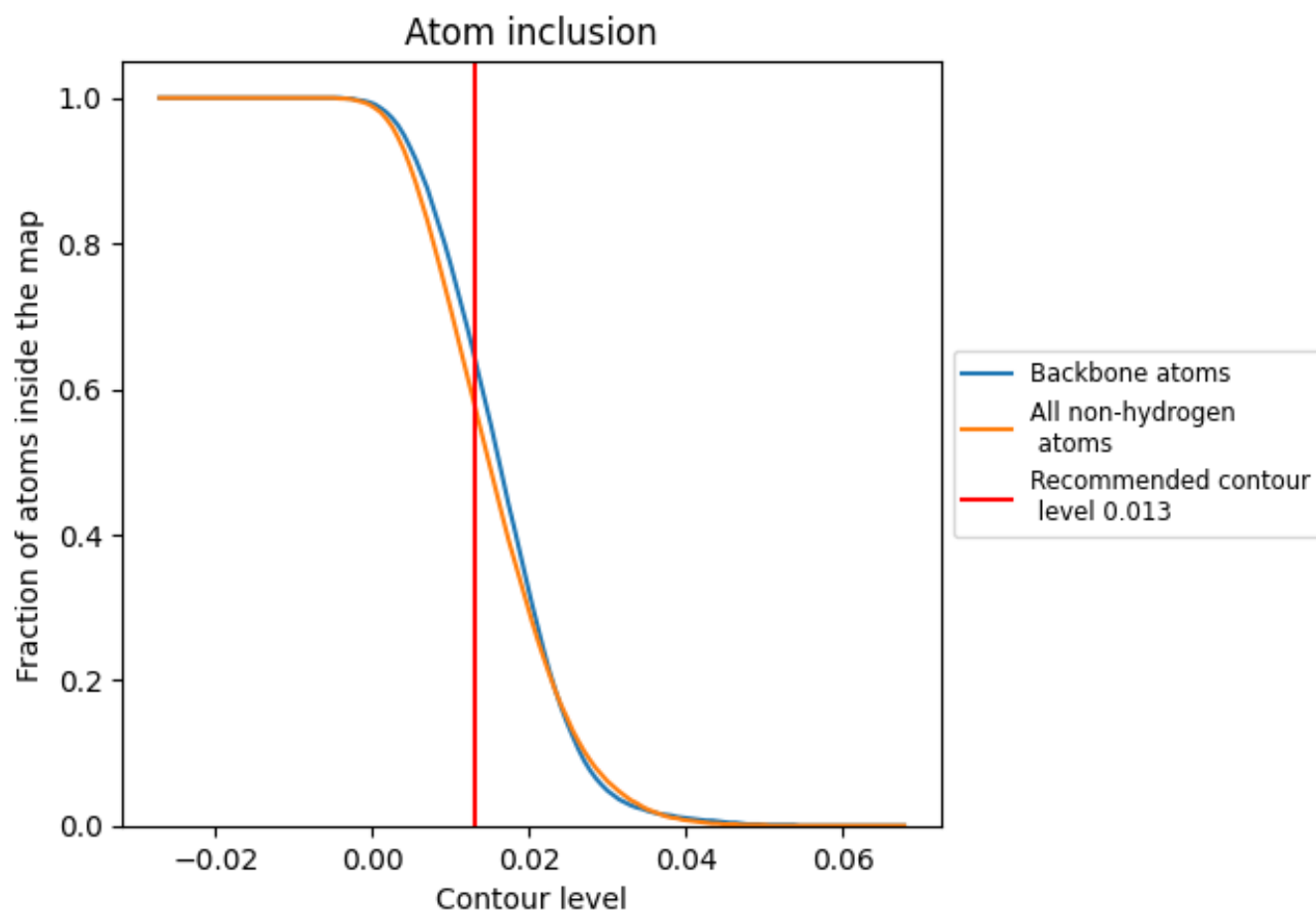
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.013).









































































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

