



Full wwPDB EM Validation Report ⓘ

Dec 11, 2022 – 05:39 am GMT

PDB ID : 4D5L
EMDB ID : EMD-2810
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.
Deposited on : 2014-11-05
Resolution : 9.00 Å (reported)
Based on initial model : 4CXC

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:

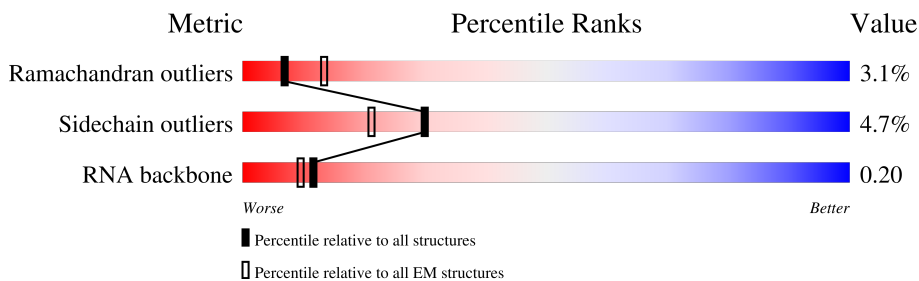
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 9.00 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)
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	1	1869	
2	A	295	
3	B	264	
4	C	293	
5	D	243	
6	E	263	
7	F	204	
8	G	249	

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Mol	Chain	Length	Quality of chain
9	H	194	47% 94% ...
10	I	208	17% 91% 8%
11	J	194	5% 86% 7% 8%
12	K	165	5% 52% 5% 43%
13	L	158	25% 87% 5% 8%
14	M	132	48% 83% 7% 9%
15	N	151	17% 95% ...
16	O	151	17% 85% 5% 9%
17	P	145	14% 75% 6% 19%
18	Q	146	8% 91% 5%
19	R	135	24% 76% 5% 19%
20	S	152	11% 82% 11% 7%
21	T	145	8% 92% 6%
22	U	119	24% 81% 15%
23	V	83	71% 96% .
24	W	130	22% 94% 5%
25	X	142	13% 86% 8% 6%
26	Y	133	7% 84% 8% 8%
27	Z	125	. 55% 6% 39%
28	a	115	21% 74% 9% 17%
29	b	84	29% 90% 5% 5%
30	c	69	19% 83% 7% 10%
31	d	56	5% 88% 7% 5%
32	e	59	31% 81% 5% 14%
33	f	156	14% 37% 61%

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Mol	Chain	Length	Quality of chain
34	g	317	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a red segment on the left labeled '30%', a green segment in the middle labeled '93%', and a yellow segment on the right labeled '5%'. The segments are stacked horizontally, with the red segment starting from the left and the yellow segment ending at the right.</p>

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 75320 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 RRNA 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1742	37159	16589	6665	12164	1741	0	0

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN ES26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	218	1719	1091	301	319	8	0	0

- Molecule 3 is a protein called 40S RIBOSOMAL PROTEIN ES27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	B	213	1729	1098	309	308	14	0	0

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN ES28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	C	222	1724	1114	296	304	10	0	0

- Molecule 5 is a protein called 40S RIBOSOMAL PROTEIN US14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	D	212	1646	1050	299	290	7	0	0

- Molecule 6 is a protein called 40S RIBOSOMAL PROTEIN ES30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	E	257	2031	1298	381	344	8	0	0

- Molecule 7 is a protein called 40S RIBOSOMAL PROTEIN ES31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	F	188	Total	C	N	O	S	0	0
			1486	930	283	266	7		

- Molecule 8 is a protein called 40S RIBOSOMAL PROTEIN RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	G	232	Total	C	N	O	S	0	0
			1884	1176	379	322	7		

- Molecule 9 is a protein called 40S RIBOSOMAL PROTEIN ES7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	H	191	Total	C	N	O	S	0	0
			1535	978	282	274	1		

- Molecule 10 is a protein called 40S RIBOSOMAL PROTEIN ES8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	I	207	Total	C	N	O	S	0	0
			1695	1064	334	292	5		

- Molecule 11 is a protein called 40S RIBOSOMAL PROTEIN US4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	J	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 12 is a protein called 40S RIBOSOMAL PROTEIN ES10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	K	94	Total	C	N	O	S	0	0
			791	519	138	129	5		

- Molecule 13 is a protein called 40S RIBOSOMAL PROTEIN US17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	L	146	Total	C	N	O	S	0	0
			1199	764	224	205	6		

- Molecule 14 is a protein called 40S RIBOSOMAL PROTEIN ES12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	M	120	931	584	164	174	9	0	0

- Molecule 15 is a protein called 40S RIBOSOMAL PROTEIN US15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	N	150	1207	773	229	204	1	0	0

- Molecule 16 is a protein called 40S RIBOSOMAL PROTEIN US11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	O	137	1023	627	200	190	6	0	0

- Molecule 17 is a protein called 40S RIBOSOMAL PROTEIN US19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	P	118	981	625	183	166	7	0	0

- Molecule 18 is a protein called 40S RIBOSOMAL PROTEIN US9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Q	139	1108	704	210	191	3	0	0

- Molecule 19 is a protein called 40S RIBOSOMAL PROTEIN ES17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	R	109	893	561	170	159	3	0	0

- Molecule 20 is a protein called 40S RIBOSOMAL PROTEIN US13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	S	142	1172	736	236	199	1	0	0

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN ES19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	T	143	1112	697	214	198	3	0	0

- Molecule 22 is a protein called 40S RIBOSOMAL PROTEIN US10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	U	101	803	502	153	144	4	0	0

- Molecule 23 is a protein called 40S RIBOSOMAL PROTEIN ES21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	V	83	636	393	117	121	5	0	0

- Molecule 24 is a protein called 40S RIBOSOMAL PROTEIN US8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	W	129	1033	659	193	175	6	0	0

- Molecule 25 is a protein called 40S RIBOSOMAL PROTEIN US12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	X	134	1046	663	205	176	2	0	0

- Molecule 26 is a protein called 40S RIBOSOMAL PROTEIN ES24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Y	122	1002	635	196	166	5	0	0

- Molecule 27 is a protein called 40S RIBOSOMAL PROTEIN ES25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Z	76	605	387	112	105	1	0	0

- Molecule 28 is a protein called 40S RIBOSOMAL PROTEIN US2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 29 is a protein called 40S RIBOSOMAL PROTEIN ES1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	80	Total	C	N	O	S	0	0
			625	391	116	111	7		

- Molecule 30 is a protein called 40S RIBOSOMAL PROTEIN US5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	62	Total	C	N	O	S	0	0
			490	298	99	91	2		

- Molecule 31 is a protein called 40S RIBOSOMAL PROTEIN US3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	53	Total	C	N	O	S	0	0
			444	278	90	71	5		

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN ES4.

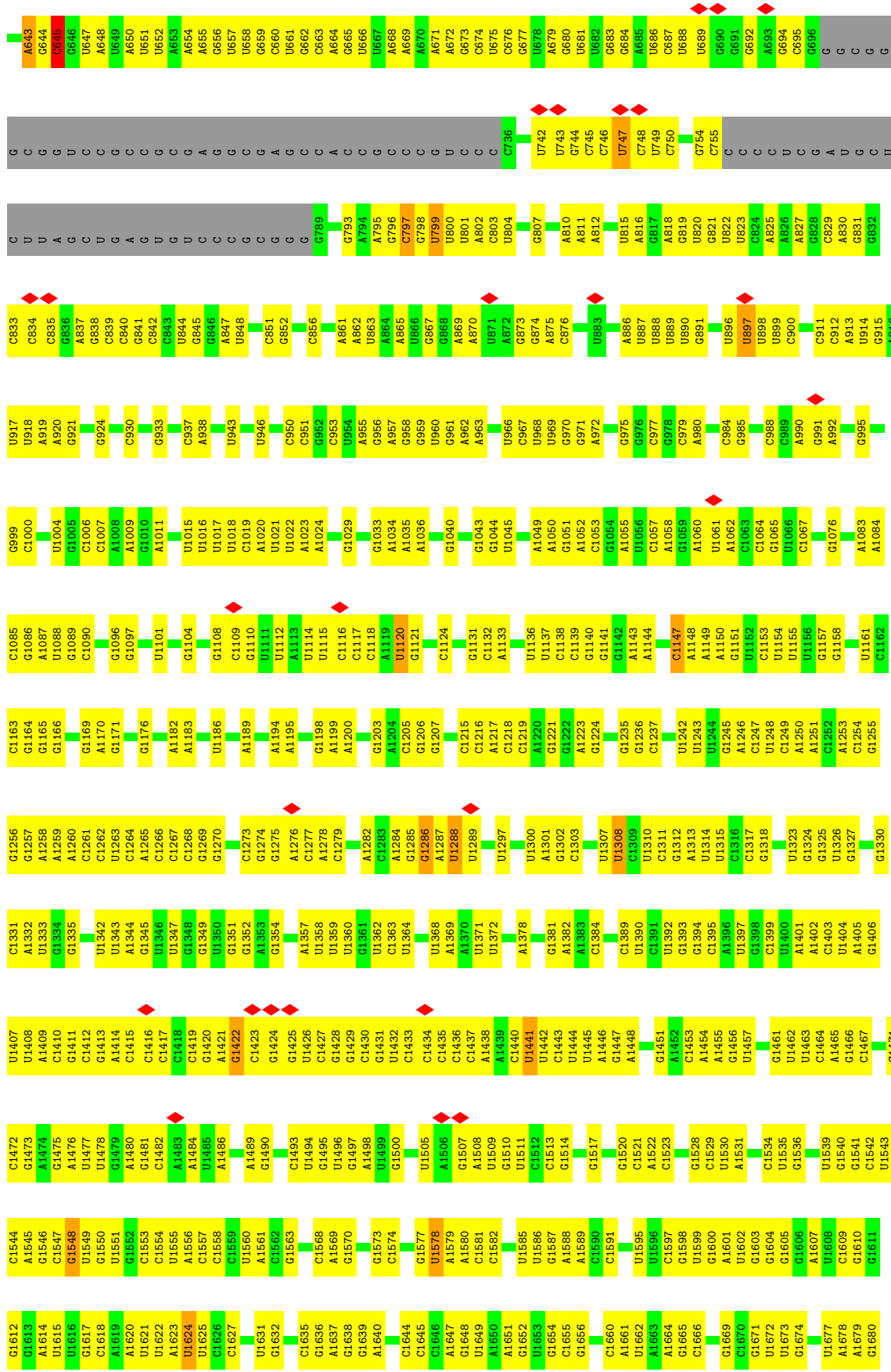
Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	51	Total	C	N	O	S	0	0
			412	258	90	63	1		

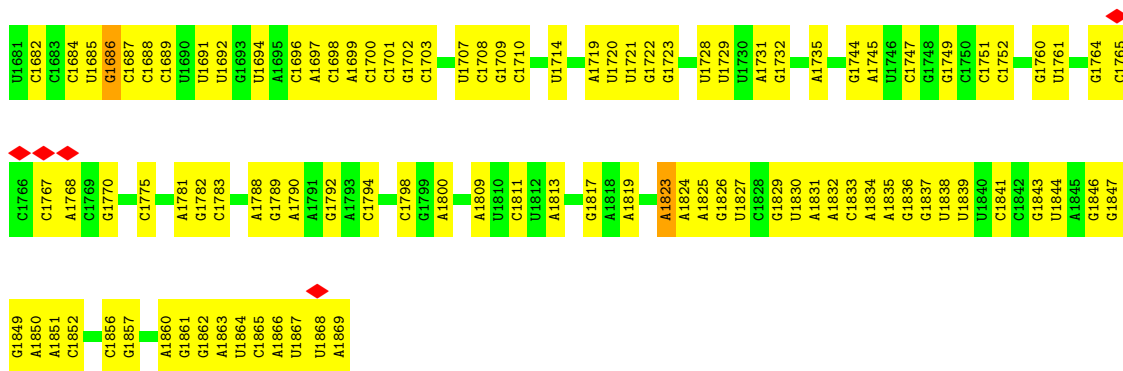
- Molecule 33 is a protein called 40S RIBOSOMAL PROTEIN US7.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	61	Total	C	N	O	S	0	0
			497	312	94	84	7		

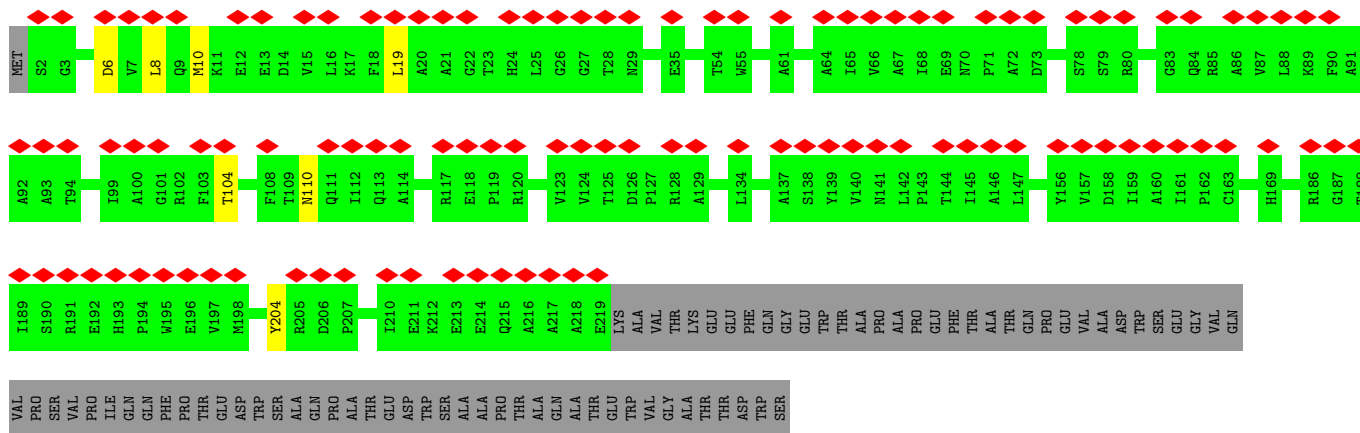
- Molecule 34 is a protein called 40S RIBOSOMAL PROTEIN ES6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	314	Total	C	N	O	S	0	0
			2440	1537	425	466	12		

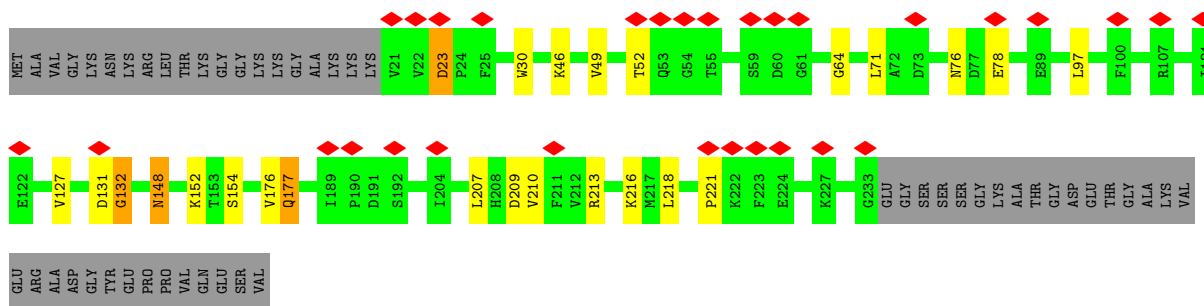




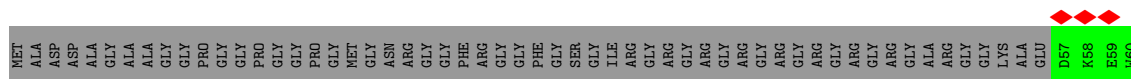
• Molecule 2: 40S RIBOSOMAL PROTEIN ES26

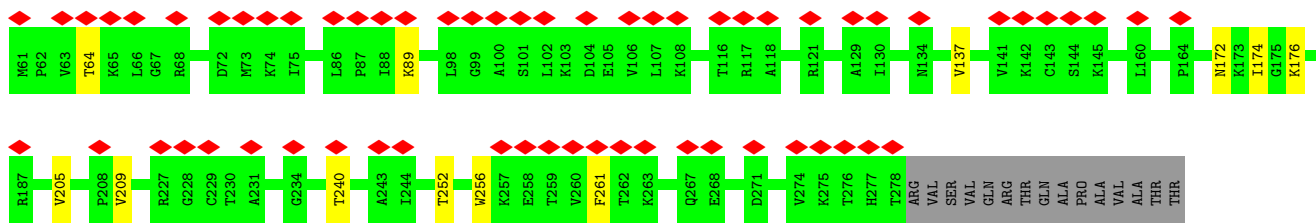


• Molecule 3: 40S RIBOSOMAL PROTEIN ES27

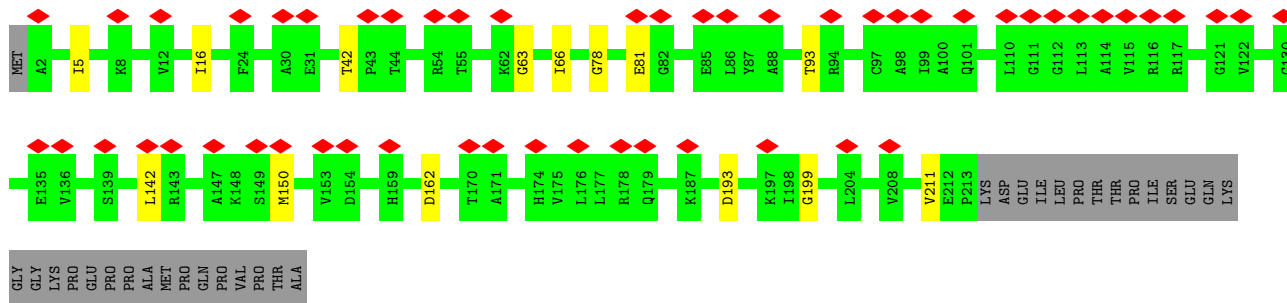
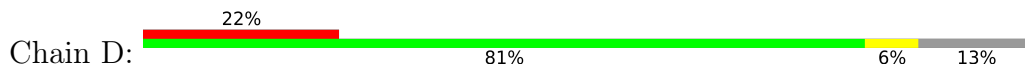


• Molecule 4: 40S RIBOSOMAL PROTEIN ES28

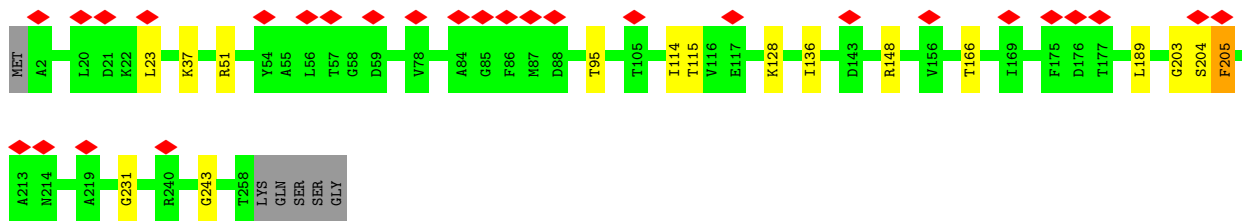
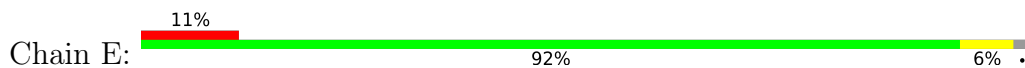




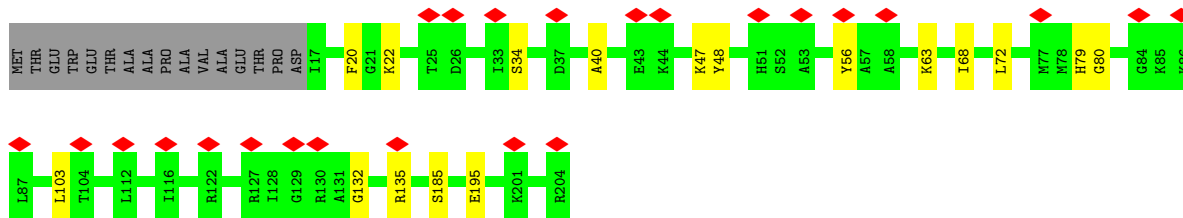
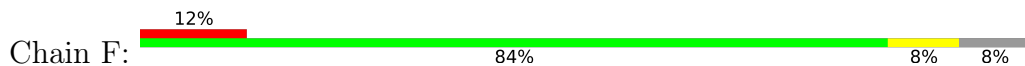
• Molecule 5: 40S RIBOSOMAL PROTEIN US14



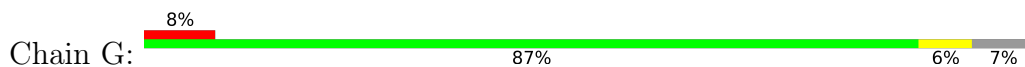
• Molecule 6: 40S RIBOSOMAL PROTEIN ES30

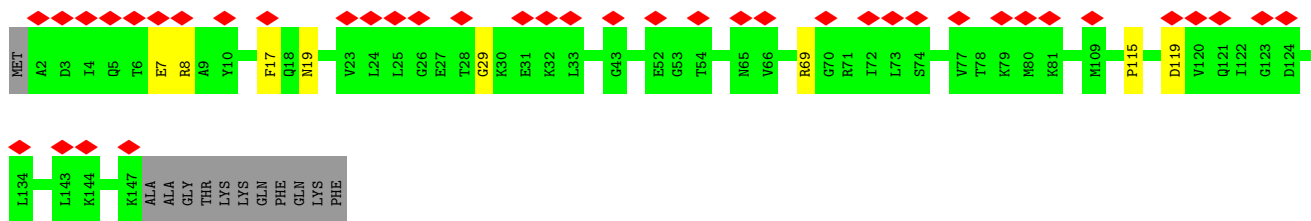


• Molecule 7: 40S RIBOSOMAL PROTEIN ES31

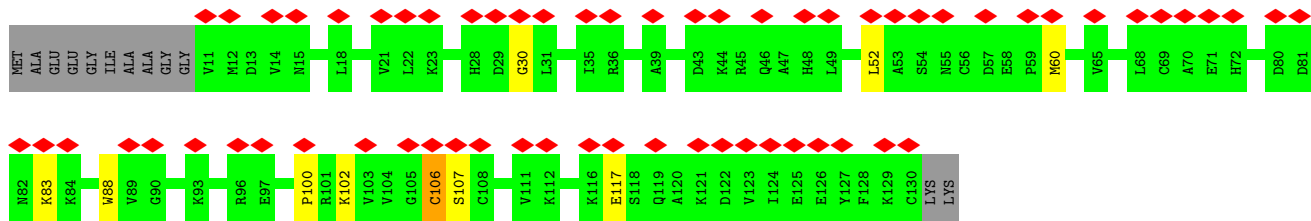
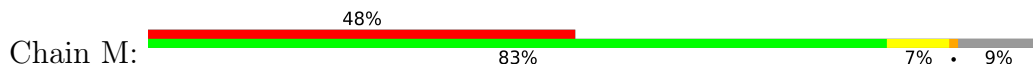


• Molecule 8: 40S RIBOSOMAL PROTEIN RACK1

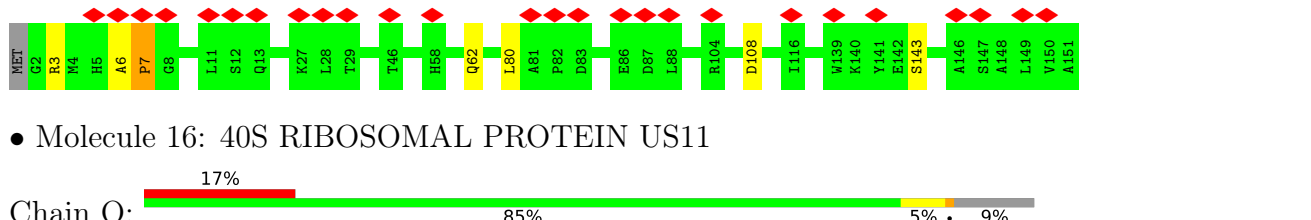
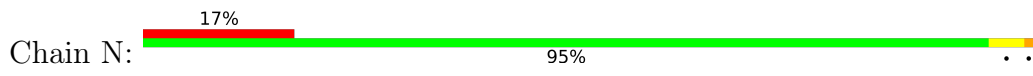




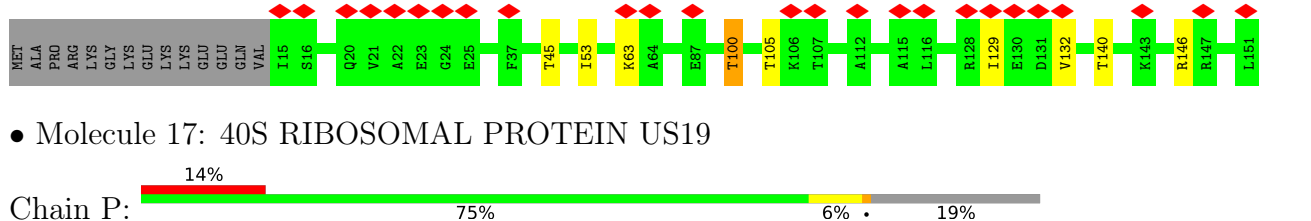
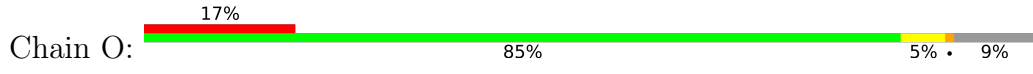
• Molecule 14: 40S RIBOSOMAL PROTEIN ES12



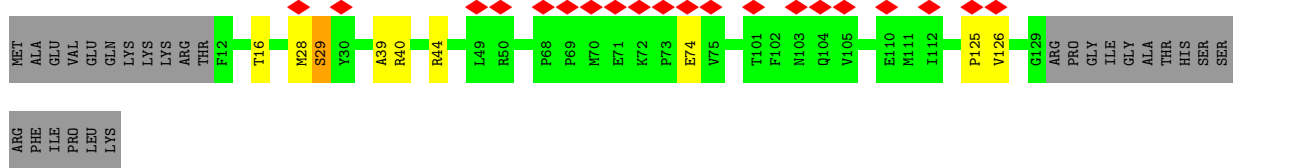
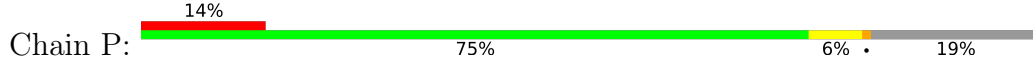
• Molecule 15: 40S RIBOSOMAL PROTEIN US15



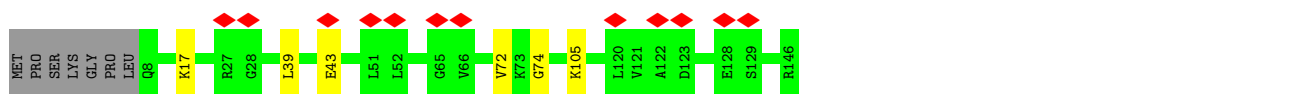
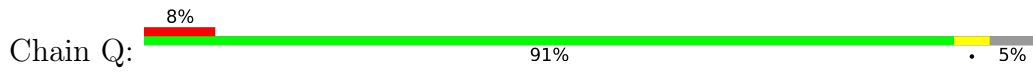
• Molecule 16: 40S RIBOSOMAL PROTEIN US11



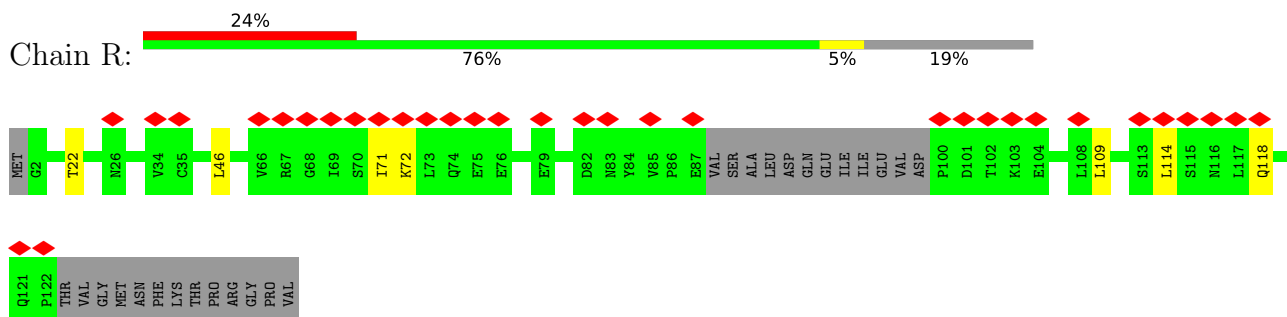
• Molecule 17: 40S RIBOSOMAL PROTEIN US19



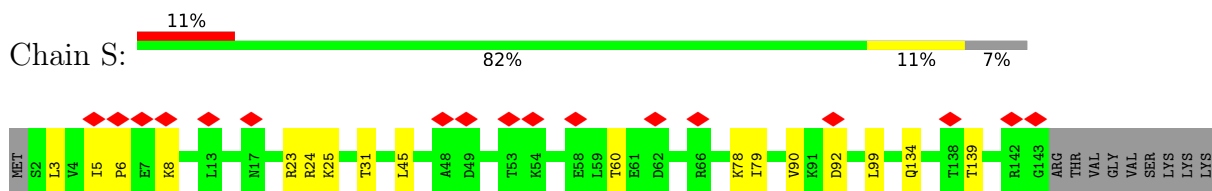
• Molecule 18: 40S RIBOSOMAL PROTEIN US9



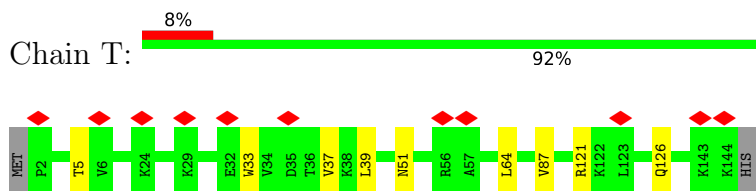
• Molecule 19: 40S RIBOSOMAL PROTEIN ES17



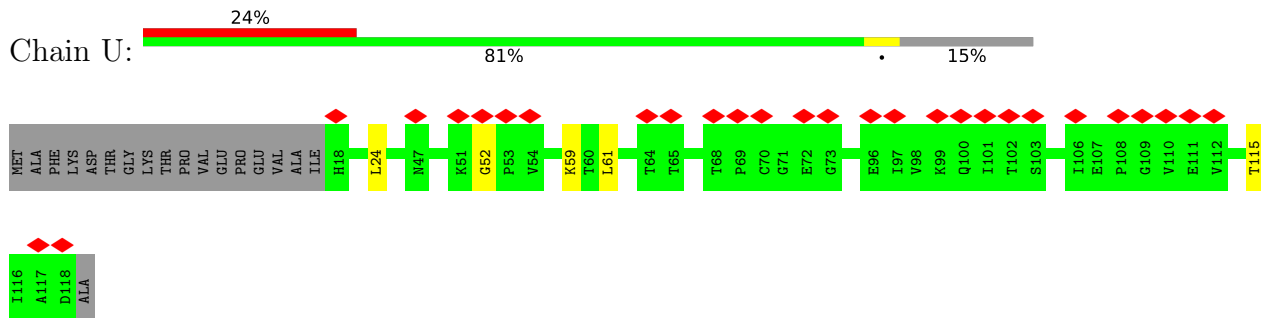
• Molecule 20: 40S RIBOSOMAL PROTEIN US13



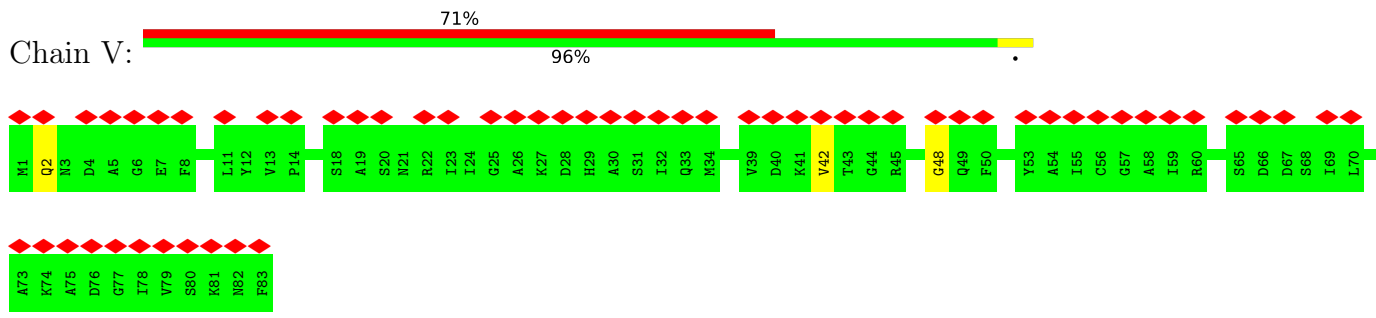
• Molecule 21: 40S RIBOSOMAL PROTEIN ES19



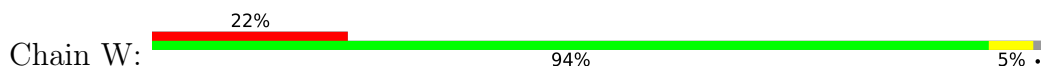
• Molecule 22: 40S RIBOSOMAL PROTEIN US10

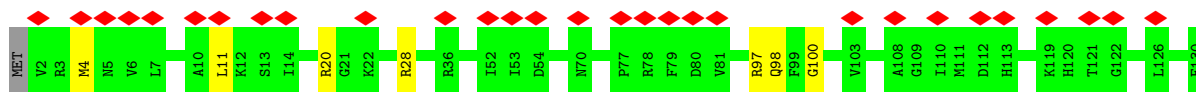


• Molecule 23: 40S RIBOSOMAL PROTEIN ES21

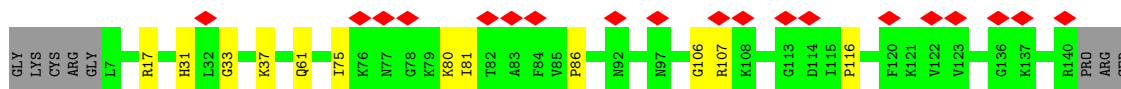
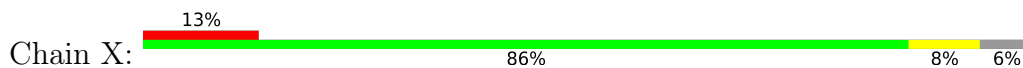


• Molecule 24: 40S RIBOSOMAL PROTEIN US8

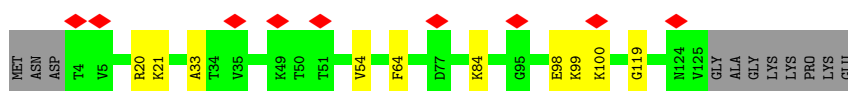
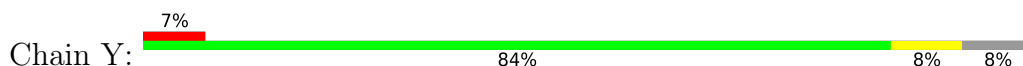




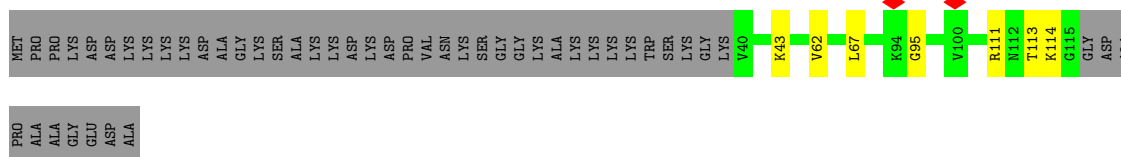
- Molecule 25: 40S RIBOSOMAL PROTEIN US12



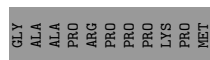
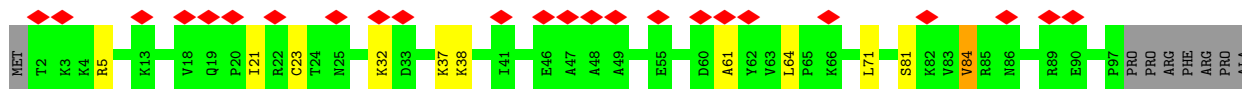
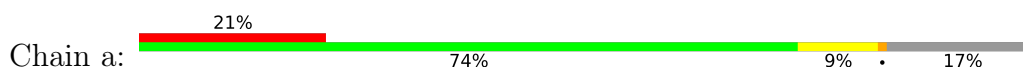
- Molecule 26: 40S RIBOSOMAL PROTEIN ES24



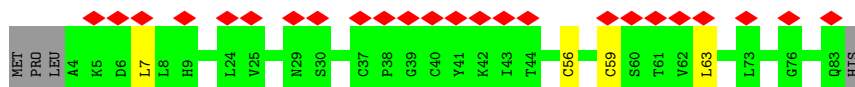
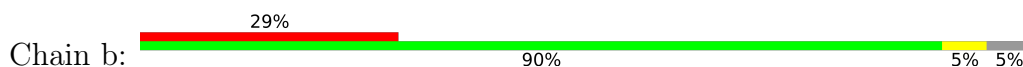
- Molecule 27: 40S RIBOSOMAL PROTEIN ES25



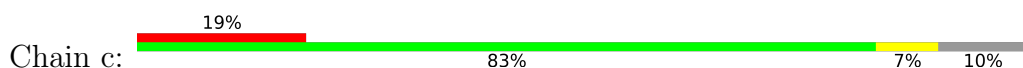
- Molecule 28: 40S RIBOSOMAL PROTEIN US2

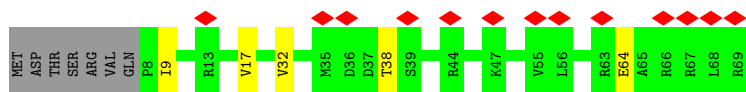


- Molecule 29: 40S RIBOSOMAL PROTEIN ES1

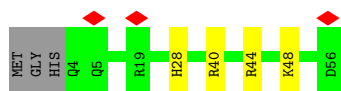
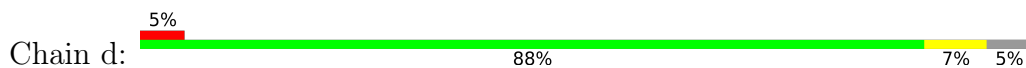


- Molecule 30: 40S RIBOSOMAL PROTEIN US5

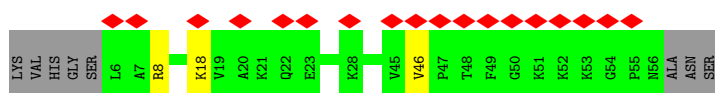
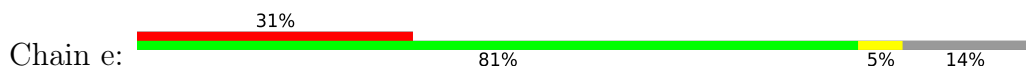




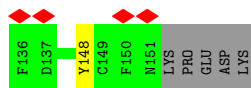
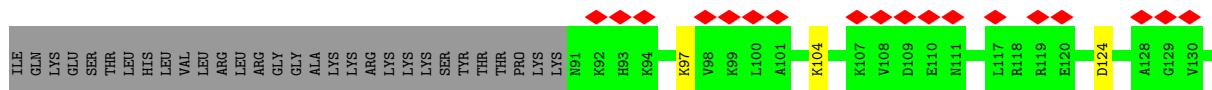
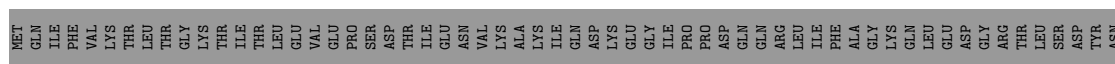
• Molecule 31: 40S RIBOSOMAL PROTEIN US3



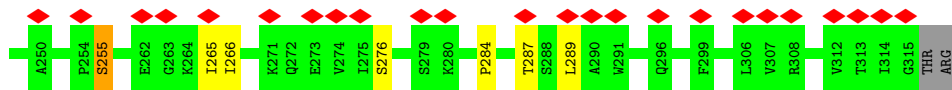
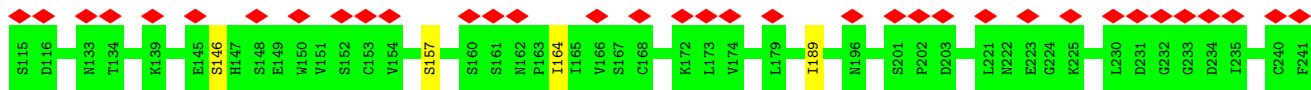
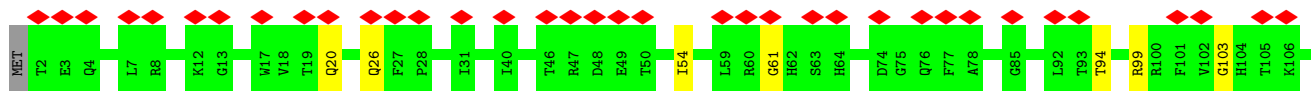
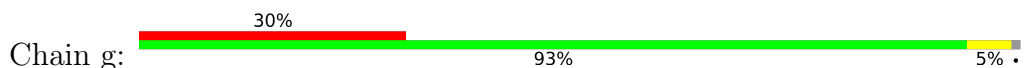
• Molecule 32: 40S RIBOSOMAL PROTEIN ES4



• Molecule 33: 40S RIBOSOMAL PROTEIN US7



• Molecule 34: 40S RIBOSOMAL PROTEIN ES6



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	109596	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	65520	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	12.036	Depositor
Minimum map value	-3.841	Depositor
Average map value	0.203	Depositor
Map value standard deviation	0.880	Depositor
Recommended contour level	2.5	Depositor
Map size (\AA)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.56, 1.56, 1.56	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.37	2/41550 (0.0%)	0.80	6/64763 (0.0%)
2	A	0.51	0/1756	0.68	0/2386
3	B	0.51	0/1756	0.75	1/2350 (0.0%)
4	C	0.42	0/1761	0.65	0/2379
5	D	0.41	0/1672	0.66	0/2250
6	E	0.47	0/2072	0.70	0/2793
7	F	0.43	0/1507	0.74	0/2026
8	G	0.48	0/1907	0.74	0/2538
9	H	0.46	0/1558	0.74	1/2087 (0.0%)
10	I	0.48	0/1724	0.72	0/2298
11	J	0.45	0/1520	0.77	0/2030
12	K	0.48	0/815	0.68	0/1101
13	L	0.45	0/1220	0.72	0/1633
14	M	0.48	0/941	0.72	0/1264
15	N	0.43	0/1231	0.73	1/1656 (0.1%)
16	O	0.46	0/1036	0.71	0/1391
17	P	0.43	0/1000	0.67	0/1335
18	Q	0.43	0/1125	0.66	0/1506
19	R	0.42	0/904	0.67	0/1208
20	S	0.42	0/1190	0.68	0/1594
21	T	0.44	0/1131	0.69	0/1515
22	U	0.50	0/813	0.70	0/1092
23	V	0.47	0/643	0.71	0/860
24	W	0.44	0/1050	0.69	0/1406
25	X	0.46	0/1063	0.70	0/1421
26	Y	0.45	0/1019	0.70	0/1354
27	Z	0.46	0/611	0.71	0/820
28	a	0.48	0/778	0.75	1/1041 (0.1%)
29	b	0.48	0/637	0.68	0/854
30	c	0.46	0/492	0.74	0/657
31	d	0.51	0/454	0.77	0/603
32	e	0.45	0/417	0.69	0/548
33	f	0.53	0/507	0.84	1/673 (0.1%)
34	g	0.45	0/2497	0.67	0/3399

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.42	2/80357 (0.0%)	0.76	11/116831 (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
1	1	0	24

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	992	A	C6-N6	-6.31	1.28	1.33
1	1	1286	G	C2-N2	-5.29	1.29	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	502	C	C3'-C2'-C1'	-6.04	96.66	101.50
1	1	1441	U	C3'-C2'-C1'	-5.56	97.06	101.50
1	1	645	C	C3'-C2'-C1'	-5.51	97.09	101.50
15	N	6	ALA	N-CA-C	-5.40	96.41	111.00
9	H	109	ARG	N-CA-CB	5.26	120.08	110.60
1	1	1422	G	C3'-C2'-C1'	-5.25	97.30	101.50
1	1	797	C	N1-C1'-C2'	-5.24	106.23	112.00
3	B	132	GLY	N-CA-C	5.24	126.20	113.10
33	f	124	ASP	N-CA-C	-5.13	97.14	111.00
1	1	1147	C	C3'-C2'-C1'	-5.06	97.45	101.50
28	a	5	ARG	N-CA-CB	-5.06	101.49	110.60

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	111	A	Sidechain
1	1	1120	U	Sidechain
1	1	1288	U	Sidechain
1	1	1308	U	Sidechain
1	1	1414	A	Sidechain
1	1	1548	G	Sidechain

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Mol	Chain	Res	Type	Group
1	1	1578	U	Sidechain
1	1	1624	U	Sidechain
1	1	1686	G	Sidechain
1	1	1823	A	Sidechain
1	1	216	C	Sidechain
1	1	235	A	Sidechain
1	1	44	U	Sidechain
1	1	570	C	Sidechain
1	1	572	U	Sidechain
1	1	643	A	Sidechain
1	1	645	C	Sidechain
1	1	747	U	Sidechain
1	1	77	A	Sidechain
1	1	799	U	Sidechain
1	1	84	A	Sidechain
1	1	867	G	Sidechain
1	1	88	G	Sidechain
1	1	897	U	Sidechain

5.2 Too-close contacts [i](#)

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

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	A	216/295 (73%)	209 (97%)	5 (2%)	2 (1%)	17	57
3	B	211/264 (80%)	176 (83%)	18 (8%)	17 (8%)	1	12
4	C	220/293 (75%)	213 (97%)	2 (1%)	5 (2%)	6	34
5	D	210/243 (86%)	201 (96%)	4 (2%)	5 (2%)	6	33
6	E	255/263 (97%)	237 (93%)	13 (5%)	5 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	F	186/204 (91%)	163 (88%)	13 (7%)	10 (5%)	2	19
8	G	230/249 (92%)	216 (94%)	5 (2%)	9 (4%)	3	23
9	H	189/194 (97%)	178 (94%)	7 (4%)	4 (2%)	7	36
10	I	205/208 (99%)	184 (90%)	14 (7%)	7 (3%)	3	26
11	J	177/194 (91%)	168 (95%)	6 (3%)	3 (2%)	9	42
12	K	92/165 (56%)	84 (91%)	1 (1%)	7 (8%)	1	13
13	L	144/158 (91%)	133 (92%)	5 (4%)	6 (4%)	3	22
14	M	118/132 (89%)	111 (94%)	1 (1%)	6 (5%)	2	19
15	N	148/151 (98%)	138 (93%)	5 (3%)	5 (3%)	3	26
16	O	135/151 (89%)	129 (96%)	3 (2%)	3 (2%)	6	35
17	P	116/145 (80%)	106 (91%)	5 (4%)	5 (4%)	2	22
18	Q	137/146 (94%)	129 (94%)	6 (4%)	2 (2%)	10	46
19	R	105/135 (78%)	99 (94%)	4 (4%)	2 (2%)	8	38
20	S	140/152 (92%)	125 (89%)	7 (5%)	8 (6%)	1	18
21	T	141/145 (97%)	135 (96%)	4 (3%)	2 (1%)	11	46
22	U	99/119 (83%)	95 (96%)	3 (3%)	1 (1%)	15	55
23	V	81/83 (98%)	78 (96%)	1 (1%)	2 (2%)	5	32
24	W	127/130 (98%)	118 (93%)	7 (6%)	2 (2%)	9	44
25	X	132/142 (93%)	120 (91%)	5 (4%)	7 (5%)	2	19
26	Y	120/133 (90%)	114 (95%)	2 (2%)	4 (3%)	4	26
27	Z	74/125 (59%)	71 (96%)	0	3 (4%)	3	23
28	a	94/115 (82%)	85 (90%)	5 (5%)	4 (4%)	2	22
29	b	78/84 (93%)	70 (90%)	8 (10%)	0	100	100
30	c	60/69 (87%)	57 (95%)	1 (2%)	2 (3%)	4	26
31	d	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
32	e	49/59 (83%)	43 (88%)	5 (10%)	1 (2%)	7	38
33	f	59/156 (38%)	53 (90%)	6 (10%)	0	100	100
34	g	312/317 (98%)	291 (93%)	14 (4%)	7 (2%)	6	35
All	All	4711/5475 (86%)	4373 (93%)	192 (4%)	146 (3%)	7	27

All (146) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	76	ASN
3	B	132	GLY
3	B	148	ASN
3	B	154	SER
3	B	176	VAL
3	B	177	GLN
3	B	207	LEU
3	B	221	PRO
4	C	64	THR
4	C	172	ASN
4	C	176	LYS
5	D	78	GLY
5	D	199	GLY
6	E	204	SER
6	E	205	PHE
7	F	20	PHE
7	F	22	LYS
7	F	40	ALA
7	F	48	TYR
7	F	80	GLY
7	F	132	GLY
7	F	185	SER
8	G	43	GLU
8	G	146	ASN
8	G	147	LEU
8	G	169	PRO
9	H	88	SER
9	H	135	PHE
10	I	123	ARG
10	I	131	PRO
10	I	134	GLU
10	I	142	SER
10	I	159	SER
12	K	30	PRO
12	K	32	HIS
12	K	36	ALA
12	K	84	HIS
12	K	87	PRO
13	L	8	ARG
13	L	19	ASN
15	N	7	PRO
15	N	108	ASP
16	O	100	THR

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Mol	Chain	Res	Type
16	O	146	ARG
17	P	29	SER
17	P	126	VAL
19	R	72	LYS
20	S	78	LYS
20	S	79	ILE
20	S	134	GLN
21	T	37	VAL
22	U	52	GLY
23	V	42	VAL
24	W	100	GLY
25	X	61	GLN
25	X	106	GLY
25	X	107	ARG
25	X	116	PRO
26	Y	33	ALA
26	Y	98	GLU
27	Z	95	GLY
34	g	255	SER
34	g	284	PRO
2	A	6	ASP
3	B	52	THR
3	B	78	GLU
3	B	127	VAL
3	B	209	ASP
4	C	174	ILE
5	D	81	GLU
6	E	231	GLY
6	E	243	GLY
7	F	34	SER
7	F	56	TYR
8	G	87	ARG
8	G	157	VAL
9	H	164	ASN
12	K	64	TRP
13	L	119	ASP
14	M	30	GLY
14	M	60	MET
14	M	106	CYS
14	M	107	SER
15	N	143	SER
19	R	114	LEU

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Mol	Chain	Res	Type
20	S	24	ARG
20	S	31	THR
20	S	90	VAL
20	S	92	ASP
23	V	48	GLY
28	a	61	ALA
34	g	276	SER
3	B	49	VAL
3	B	213	ARG
5	D	142	LEU
6	E	203	GLY
7	F	79	HIS
8	G	91	GLU
8	G	92	ARG
9	H	109	ARG
13	L	7	GLU
14	M	102	LYS
15	N	3	ARG
18	Q	17	LYS
18	Q	74	GLY
25	X	33	GLY
25	X	86	PRO
26	Y	64	PHE
27	Z	113	THR
28	a	81	SER
30	c	38	THR
15	N	62	GLN
17	P	39	ALA
24	W	28	ARG
25	X	75	ILE
26	Y	119	GLY
30	c	64	GLU
34	g	146	SER
4	C	261	PHE
8	G	88	ARG
11	J	138	ARG
11	J	169	ARG
13	L	115	PRO
17	P	28	MET
17	P	125	PRO
21	T	51	ASN
27	Z	114	LYS

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Mol	Chain	Res	Type
28	a	38	LYS
32	e	8	ARG
2	A	104	THR
3	B	23	ASP
3	B	210	VAL
10	I	12	ARG
20	S	6	PRO
28	a	84	VAL
3	B	64	GLY
11	J	170	PRO
12	K	86	PRO
13	L	29	GLY
14	M	100	PRO
34	g	103	GLY
10	I	20	PRO
16	O	53	ILE
34	g	61	GLY
34	g	265	ILE
5	D	63	GLY

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	A	181/243 (74%)	176 (97%)	5 (3%)	43	65
3	B	194/231 (84%)	183 (94%)	11 (6%)	20	45
4	C	188/225 (84%)	181 (96%)	7 (4%)	34	58
5	D	175/202 (87%)	166 (95%)	9 (5%)	24	48
6	E	220/225 (98%)	208 (94%)	12 (6%)	21	47
7	F	158/170 (93%)	151 (96%)	7 (4%)	28	53
8	G	202/218 (93%)	195 (96%)	7 (4%)	36	59
9	H	171/174 (98%)	167 (98%)	4 (2%)	50	70
10	I	179/180 (99%)	167 (93%)	12 (7%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	J	160/168 (95%)	150 (94%)	10 (6%)	18	43
12	K	85/136 (62%)	82 (96%)	3 (4%)	36	59
13	L	133/142 (94%)	131 (98%)	2 (2%)	65	80
14	M	102/108 (94%)	97 (95%)	5 (5%)	25	50
15	N	130/131 (99%)	128 (98%)	2 (2%)	65	80
16	O	107/119 (90%)	100 (94%)	7 (6%)	17	42
17	P	107/130 (82%)	102 (95%)	5 (5%)	26	51
18	Q	115/121 (95%)	111 (96%)	4 (4%)	36	59
19	R	99/122 (81%)	94 (95%)	5 (5%)	24	48
20	S	123/132 (93%)	114 (93%)	9 (7%)	14	39
21	T	113/115 (98%)	106 (94%)	7 (6%)	18	43
22	U	93/107 (87%)	89 (96%)	4 (4%)	29	53
23	V	67/67 (100%)	66 (98%)	1 (2%)	65	80
24	W	112/113 (99%)	107 (96%)	5 (4%)	27	52
25	X	108/114 (95%)	103 (95%)	5 (5%)	27	52
26	Y	107/115 (93%)	101 (94%)	6 (6%)	21	46
27	Z	67/103 (65%)	63 (94%)	4 (6%)	19	44
28	a	83/98 (85%)	76 (92%)	7 (8%)	11	33
29	b	72/76 (95%)	68 (94%)	4 (6%)	21	46
30	c	55/62 (89%)	52 (94%)	3 (6%)	21	47
31	d	47/49 (96%)	43 (92%)	4 (8%)	10	33
32	e	42/48 (88%)	40 (95%)	2 (5%)	25	51
33	f	54/140 (39%)	51 (94%)	3 (6%)	21	46
34	g	272/275 (99%)	260 (96%)	12 (4%)	28	53
All	All	4121/4659 (88%)	3928 (95%)	193 (5%)	30	51

All (193) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	8	LEU
2	A	10	MET
2	A	19	LEU
2	A	110	ASN
2	A	204	TYR

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Mol	Chain	Res	Type
3	B	23	ASP
3	B	30	TRP
3	B	46	LYS
3	B	71	LEU
3	B	97	LEU
3	B	131	ASP
3	B	148	ASN
3	B	152	LYS
3	B	177	GLN
3	B	216	LYS
3	B	218	LEU
4	C	89	LYS
4	C	137	VAL
4	C	205	VAL
4	C	209	VAL
4	C	240	THR
4	C	252	THR
4	C	256	TRP
5	D	5	ILE
5	D	16	ILE
5	D	42	THR
5	D	66	ILE
5	D	93	THR
5	D	150	MET
5	D	162	ASP
5	D	193	ASP
5	D	211	VAL
6	E	23	LEU
6	E	37	LYS
6	E	51	ARG
6	E	95	THR
6	E	114	ILE
6	E	115	THR
6	E	128	LYS
6	E	136	ILE
6	E	148	ARG
6	E	166	THR
6	E	189	LEU
6	E	205	PHE
7	F	47	LYS
7	F	63	LYS
7	F	68	ILE

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Mol	Chain	Res	Type
7	F	72	LEU
7	F	103	LEU
7	F	135	ARG
7	F	195	GLU
8	G	24	LEU
8	G	29	GLU
8	G	34	THR
8	G	87	ARG
8	G	160	LYS
8	G	176	ILE
8	G	195	LYS
9	H	111	LYS
9	H	116	ARG
9	H	118	ARG
9	H	152	ARG
10	I	19	LYS
10	I	21	TYR
10	I	29	LEU
10	I	48	VAL
10	I	55	TYR
10	I	62	VAL
10	I	78	ILE
10	I	93	THR
10	I	131	PRO
10	I	136	ILE
10	I	137	LEU
10	I	144	LYS
11	J	8	VAL
11	J	12	THR
11	J	30	LYS
11	J	41	ARG
11	J	47	LYS
11	J	78	LEU
11	J	128	VAL
11	J	130	ILE
11	J	147	PHE
11	J	163	SER
12	K	15	LEU
12	K	70	TYR
12	K	84	HIS
13	L	17	PHE
13	L	69	ARG

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Mol	Chain	Res	Type
14	M	52	LEU
14	M	83	LYS
14	M	88	TRP
14	M	106	CYS
14	M	117	GLU
15	N	7	PRO
15	N	80	LEU
16	O	45	THR
16	O	63	LYS
16	O	100	THR
16	O	105	THR
16	O	129	ILE
16	O	132	VAL
16	O	140	THR
17	P	16	THR
17	P	29	SER
17	P	40	ARG
17	P	44	ARG
17	P	74	GLU
18	Q	39	LEU
18	Q	43	GLU
18	Q	72	VAL
18	Q	105	LYS
19	R	22	THR
19	R	46	LEU
19	R	71	ILE
19	R	109	LEU
19	R	118	GLN
20	S	3	LEU
20	S	5	ILE
20	S	8	LYS
20	S	23	ARG
20	S	25	LYS
20	S	45	LEU
20	S	60	THR
20	S	99	LEU
20	S	139	THR
21	T	5	THR
21	T	33	TRP
21	T	39	LEU
21	T	64	LEU
21	T	87	VAL

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Mol	Chain	Res	Type
21	T	121	ARG
21	T	126	GLN
22	U	24	LEU
22	U	59	LYS
22	U	61	LEU
22	U	115	THR
23	V	2	GLN
24	W	4	MET
24	W	11	LEU
24	W	20	ARG
24	W	97	ARG
24	W	98	GLN
25	X	17	ARG
25	X	31	HIS
25	X	37	LYS
25	X	80	LYS
25	X	81	ILE
26	Y	20	ARG
26	Y	21	LYS
26	Y	54	VAL
26	Y	84	LYS
26	Y	99	LYS
26	Y	100	LYS
27	Z	43	LYS
27	Z	62	VAL
27	Z	67	LEU
27	Z	111	ARG
28	a	21	ILE
28	a	23	CYS
28	a	32	LYS
28	a	37	LYS
28	a	64	LEU
28	a	71	LEU
28	a	84	VAL
29	b	7	LEU
29	b	56	CYS
29	b	59	CYS
29	b	63	LEU
30	c	9	ILE
30	c	17	VAL
30	c	32	VAL
31	d	28	HIS

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Mol	Chain	Res	Type
31	d	40	ARG
31	d	44	ARG
31	d	48	LYS
32	e	18	LYS
32	e	46	VAL
33	f	97	LYS
33	f	104	LYS
33	f	148	TYR
34	g	20	GLN
34	g	26	GLN
34	g	54	ILE
34	g	94	THR
34	g	99	ARG
34	g	157	SER
34	g	164	ILE
34	g	189	ILE
34	g	255	SER
34	g	266	ILE
34	g	287	THR
34	g	289	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (86) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	50	ASN
2	A	110	ASN
2	A	215	GLN
3	B	40	ASN
3	B	53	GLN
3	B	149	GLN
3	B	157	GLN
3	B	160	GLN
3	B	177	GLN
4	C	267	GLN
5	D	4	GLN
5	D	56	GLN
5	D	57	ASN
5	D	101	GLN
5	D	179	GLN
6	E	36	HIS
6	E	138	HIS
6	E	188	ASN

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Mol	Chain	Res	Type
6	E	216	ASN
6	E	230	ASN
7	F	29	GLN
7	F	82	ASN
7	F	95	HIS
7	F	107	ASN
7	F	110	GLN
7	F	114	ASN
7	F	165	ASN
7	F	203	ASN
8	G	65	GLN
8	G	81	HIS
8	G	105	ASN
9	H	25	GLN
9	H	76	GLN
9	H	97	GLN
9	H	112	ASN
10	I	22	HIS
11	J	124	HIS
11	J	143	ASN
12	K	44	HIS
12	K	84	HIS
13	L	5	GLN
13	L	112	HIS
14	M	19	GLN
15	N	105	ASN
16	O	32	HIS
16	O	43	HIS
17	P	35	GLN
17	P	104	GLN
18	Q	11	GLN
18	Q	48	GLN
18	Q	80	GLN
18	Q	86	GLN
19	R	62	GLN
20	S	19	ASN
20	S	73	ASN
20	S	85	ASN
20	S	87	GLN
21	T	63	HIS
21	T	126	GLN
22	U	100	GLN

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Mol	Chain	Res	Type
23	V	2	GLN
24	W	24	GLN
24	W	82	GLN
24	W	113	HIS
25	X	61	GLN
25	X	73	GLN
25	X	77	ASN
26	Y	19	GLN
26	Y	22	GLN
26	Y	29	HIS
27	Z	103	HIS
28	a	19	GLN
29	b	49	HIS
30	c	45	ASN
31	d	5	GLN
31	d	16	GLN
31	d	26	ASN
31	d	41	GLN
32	e	22	GLN
32	e	44	ASN
34	g	20	GLN
34	g	26	GLN
34	g	56	GLN
34	g	64	HIS
34	g	117	ASN
34	g	196	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1738/1869 (92%)	1037 (59%)	152 (8%)

All (1037) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	A
1	1	3	C
1	1	4	C
1	1	5	U
1	1	6	G
1	1	7	G

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Mol	Chain	Res	Type
1	1	8	U
1	1	9	U
1	1	15	U
1	1	16	G
1	1	17	C
1	1	21	U
1	1	22	A
1	1	24	C
1	1	25	A
1	1	26	U
1	1	30	C
1	1	33	G
1	1	39	A
1	1	40	A
1	1	41	G
1	1	44	U
1	1	45	A
1	1	46	A
1	1	47	G
1	1	48	C
1	1	50	A
1	1	55	U
1	1	56	G
1	1	59	U
1	1	60	A
1	1	61	A
1	1	62	G
1	1	63	U
1	1	64	A
1	1	65	C
1	1	66	G
1	1	67	C
1	1	68	A
1	1	69	C
1	1	70	G
1	1	71	G
1	1	72	C
1	1	74	G
1	1	75	G
1	1	76	U
1	1	77	A
1	1	78	C

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Mol	Chain	Res	Type
1	1	79	A
1	1	80	G
1	1	81	U
1	1	82	G
1	1	83	A
1	1	84	A
1	1	87	U
1	1	98	C
1	1	99	A
1	1	101	U
1	1	103	A
1	1	104	A
1	1	105	U
1	1	106	C
1	1	109	U
1	1	110	U
1	1	111	A
1	1	112	U
1	1	113	G
1	1	114	G
1	1	115	U
1	1	116	U
1	1	117	C
1	1	118	C
1	1	120	U
1	1	121	U
1	1	122	G
1	1	123	G
1	1	124	U
1	1	125	C
1	1	126	G
1	1	127	C
1	1	128	U
1	1	129	C
1	1	130	G
1	1	131	C
1	1	132	U
1	1	133	C
1	1	134	C
1	1	135	U
1	1	136	C
1	1	137	U

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Mol	Chain	Res	Type
1	1	138	C
1	1	139	C
1	1	140	C
1	1	141	A
1	1	142	C
1	1	143	U
1	1	144	U
1	1	145	G
1	1	146	G
1	1	147	A
1	1	150	A
1	1	151	C
1	1	152	U
1	1	153	G
1	1	158	A
1	1	160	U
1	1	161	U
1	1	162	C
1	1	163	U
1	1	164	A
1	1	166	A
1	1	167	G
1	1	168	C
1	1	169	U
1	1	171	A
1	1	173	A
1	1	174	C
1	1	176	U
1	1	179	C
1	1	180	G
1	1	181	A
1	1	182	C
1	1	183	G
1	1	184	G
1	1	185	G
1	1	187	G
1	1	193	C
1	1	198	U
1	1	199	C
1	1	200	G
1	1	201	C
1	1	202	G

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Mol	Chain	Res	Type
1	1	204	G
1	1	205	G
1	1	207	G
1	1	208	G
1	1	209	A
1	1	210	U
1	1	211	G
1	1	213	G
1	1	214	U
1	1	215	G
1	1	216	C
1	1	217	A
1	1	218	U
1	1	219	U
1	1	220	U
1	1	225	G
1	1	226	A
1	1	227	U
1	1	228	C
1	1	229	A
1	1	230	A
1	1	233	C
1	1	234	C
1	1	235	A
1	1	236	A
1	1	237	C
1	1	238	C
1	1	239	C
1	1	298	G
1	1	301	A
1	1	303	C
1	1	304	C
1	1	305	U
1	1	306	C
1	1	307	G
1	1	308	G
1	1	309	G
1	1	310	C
1	1	311	C
1	1	312	G
1	1	313	A
1	1	314	U

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Mol	Chain	Res	Type
1	1	315	C
1	1	317	C
1	1	318	A
1	1	319	C
1	1	320	G
1	1	321	C
1	1	327	G
1	1	328	U
1	1	329	G
1	1	330	G
1	1	332	G
1	1	333	G
1	1	337	C
1	1	338	G
1	1	339	A
1	1	343	A
1	1	344	U
1	1	345	U
1	1	346	C
1	1	347	G
1	1	350	C
1	1	352	U
1	1	353	C
1	1	354	U
1	1	356	C
1	1	357	C
1	1	358	C
1	1	359	U
1	1	362	C
1	1	363	A
1	1	364	A
1	1	368	U
1	1	369	C
1	1	371	A
1	1	372	U
1	1	375	U
1	1	376	A
1	1	378	U
1	1	379	C
1	1	380	G
1	1	381	C
1	1	382	C

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Mol	Chain	Res	Type
1	1	383	G
1	1	384	U
1	1	386	C
1	1	389	A
1	1	395	G
1	1	399	C
1	1	400	C
1	1	407	G
1	1	408	A
1	1	409	C
1	1	410	G
1	1	412	G
1	1	416	U
1	1	421	G
1	1	422	U
1	1	423	U
1	1	424	C
1	1	426	A
1	1	427	U
1	1	429	C
1	1	431	G
1	1	433	A
1	1	435	A
1	1	436	G
1	1	438	G
1	1	440	G
1	1	441	C
1	1	442	C
1	1	443	U
1	1	445	A
1	1	447	A
1	1	448	A
1	1	449	A
1	1	450	C
1	1	451	G
1	1	452	G
1	1	454	U
1	1	459	C
1	1	460	A
1	1	463	C
1	1	464	A
1	1	465	A

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Mol	Chain	Res	Type
1	1	466	G
1	1	467	G
1	1	468	A
1	1	472	C
1	1	473	A
1	1	474	G
1	1	475	C
1	1	476	A
1	1	477	G
1	1	480	G
1	1	482	G
1	1	485	A
1	1	487	U
1	1	488	U
1	1	489	A
1	1	491	C
1	1	492	C
1	1	493	A
1	1	495	U
1	1	496	C
1	1	497	C
1	1	499	G
1	1	500	A
1	1	501	C
1	1	502	C
1	1	503	C
1	1	504	G
1	1	506	G
1	1	507	G
1	1	509	G
1	1	510	G
1	1	512	A
1	1	516	A
1	1	517	C
1	1	518	G
1	1	523	A
1	1	525	A
1	1	526	A
1	1	527	C
1	1	529	A
1	1	530	U
1	1	533	A

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Mol	Chain	Res	Type
1	1	535	G
1	1	536	A
1	1	537	C
1	1	538	U
1	1	539	C
1	1	541	U
1	1	542	U
1	1	543	C
1	1	544	G
1	1	545	A
1	1	546	G
1	1	547	G
1	1	548	C
1	1	549	C
1	1	550	C
1	1	553	U
1	1	554	A
1	1	555	A
1	1	559	G
1	1	560	A
1	1	562	U
1	1	564	A
1	1	565	G
1	1	566	U
1	1	568	C
1	1	570	C
1	1	571	U
1	1	572	U
1	1	573	U
1	1	574	A
1	1	575	A
1	1	576	A
1	1	577	U
1	1	578	C
1	1	579	C
1	1	580	U
1	1	582	U
1	1	586	G
1	1	587	A
1	1	588	G
1	1	589	G
1	1	590	A

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Mol	Chain	Res	Type
1	1	591	U
1	1	592	C
1	1	593	C
1	1	594	A
1	1	595	U
1	1	596	U
1	1	597	G
1	1	599	A
1	1	600	G
1	1	603	C
1	1	604	A
1	1	605	A
1	1	606	G
1	1	607	U
1	1	608	C
1	1	609	U
1	1	612	U
1	1	613	G
1	1	614	C
1	1	617	G
1	1	619	A
1	1	620	G
1	1	621	C
1	1	623	G
1	1	624	C
1	1	627	U
1	1	628	A
1	1	629	A
1	1	630	U
1	1	631	U
1	1	634	A
1	1	638	C
1	1	643	A
1	1	644	G
1	1	645	C
1	1	647	U
1	1	648	A
1	1	650	A
1	1	651	U
1	1	652	U
1	1	654	A
1	1	655	A

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Mol	Chain	Res	Type
1	1	656	G
1	1	657	U
1	1	658	U
1	1	659	G
1	1	660	C
1	1	661	U
1	1	663	C
1	1	664	A
1	1	665	G
1	1	666	U
1	1	668	A
1	1	669	A
1	1	671	A
1	1	672	A
1	1	673	G
1	1	674	C
1	1	675	U
1	1	676	C
1	1	677	G
1	1	679	A
1	1	680	G
1	1	681	U
1	1	683	G
1	1	684	G
1	1	686	U
1	1	688	U
1	1	689	U
1	1	692	G
1	1	694	G
1	1	695	C
1	1	742	U
1	1	743	U
1	1	744	G
1	1	745	C
1	1	746	C
1	1	747	U
1	1	748	C
1	1	749	U
1	1	750	C
1	1	754	G
1	1	755	C
1	1	793	G

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Mol	Chain	Res	Type
1	1	795	A
1	1	796	G
1	1	797	C
1	1	798	G
1	1	799	U
1	1	800	U
1	1	801	U
1	1	802	A
1	1	803	C
1	1	804	U
1	1	807	G
1	1	810	A
1	1	812	A
1	1	815	U
1	1	816	A
1	1	818	A
1	1	819	G
1	1	820	U
1	1	821	G
1	1	822	U
1	1	823	U
1	1	825	A
1	1	827	A
1	1	829	C
1	1	830	A
1	1	831	G
1	1	834	C
1	1	835	C
1	1	837	A
1	1	838	G
1	1	839	C
1	1	840	C
1	1	841	G
1	1	842	C
1	1	844	U
1	1	845	G
1	1	847	A
1	1	848	U
1	1	851	C
1	1	852	G
1	1	856	C
1	1	861	A

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Mol	Chain	Res	Type
1	1	862	A
1	1	863	U
1	1	865	A
1	1	869	A
1	1	870	A
1	1	873	G
1	1	874	G
1	1	875	A
1	1	876	C
1	1	886	A
1	1	887	U
1	1	888	U
1	1	889	U
1	1	890	U
1	1	891	G
1	1	896	U
1	1	897	U
1	1	898	U
1	1	899	U
1	1	900	C
1	1	911	C
1	1	912	C
1	1	913	A
1	1	914	U
1	1	915	G
1	1	917	U
1	1	918	U
1	1	919	A
1	1	920	A
1	1	921	G
1	1	924	G
1	1	930	C
1	1	933	G
1	1	937	C
1	1	938	A
1	1	943	U
1	1	946	U
1	1	950	C
1	1	951	C
1	1	953	C
1	1	955	A
1	1	956	G

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Mol	Chain	Res	Type
1	1	957	A
1	1	958	G
1	1	959	G
1	1	960	U
1	1	961	G
1	1	962	A
1	1	963	A
1	1	966	U
1	1	967	C
1	1	968	U
1	1	969	U
1	1	970	G
1	1	971	G
1	1	972	A
1	1	975	G
1	1	977	C
1	1	979	C
1	1	980	A
1	1	984	C
1	1	985	G
1	1	988	C
1	1	990	A
1	1	991	G
1	1	995	G
1	1	999	G
1	1	1000	C
1	1	1004	U
1	1	1006	C
1	1	1007	C
1	1	1009	A
1	1	1011	A
1	1	1015	U
1	1	1016	U
1	1	1017	U
1	1	1018	U
1	1	1019	C
1	1	1020	A
1	1	1021	U
1	1	1022	U
1	1	1023	A
1	1	1024	A
1	1	1029	G

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Mol	Chain	Res	Type
1	1	1033	G
1	1	1034	A
1	1	1035	A
1	1	1036	A
1	1	1040	G
1	1	1044	G
1	1	1045	U
1	1	1049	A
1	1	1050	A
1	1	1051	G
1	1	1052	A
1	1	1053	C
1	1	1055	A
1	1	1057	C
1	1	1058	A
1	1	1060	A
1	1	1061	U
1	1	1062	A
1	1	1064	C
1	1	1065	G
1	1	1067	C
1	1	1076	G
1	1	1083	A
1	1	1084	A
1	1	1085	C
1	1	1086	G
1	1	1087	A
1	1	1088	U
1	1	1089	G
1	1	1090	C
1	1	1096	G
1	1	1097	G
1	1	1101	U
1	1	1104	G
1	1	1108	G
1	1	1109	C
1	1	1110	G
1	1	1112	U
1	1	1115	U
1	1	1116	C
1	1	1117	C
1	1	1118	C

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Mol	Chain	Res	Type
1	1	1120	U
1	1	1121	G
1	1	1124	C
1	1	1131	G
1	1	1132	C
1	1	1133	A
1	1	1136	U
1	1	1137	U
1	1	1139	C
1	1	1140	G
1	1	1141	G
1	1	1143	A
1	1	1144	A
1	1	1147	C
1	1	1148	A
1	1	1149	A
1	1	1150	A
1	1	1151	G
1	1	1153	C
1	1	1154	U
1	1	1155	U
1	1	1157	G
1	1	1158	G
1	1	1161	U
1	1	1163	C
1	1	1164	G
1	1	1165	G
1	1	1166	G
1	1	1169	G
1	1	1170	A
1	1	1171	G
1	1	1176	G
1	1	1182	A
1	1	1183	A
1	1	1186	U
1	1	1189	A
1	1	1194	A
1	1	1195	A
1	1	1198	G
1	1	1199	A
1	1	1200	A
1	1	1203	G

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Mol	Chain	Res	Type
1	1	1205	C
1	1	1206	G
1	1	1207	G
1	1	1215	C
1	1	1216	C
1	1	1217	A
1	1	1218	C
1	1	1219	C
1	1	1221	G
1	1	1223	A
1	1	1224	G
1	1	1235	G
1	1	1236	G
1	1	1237	C
1	1	1242	U
1	1	1243	U
1	1	1245	G
1	1	1246	A
1	1	1247	C
1	1	1248	U
1	1	1249	C
1	1	1251	A
1	1	1253	A
1	1	1254	C
1	1	1255	G
1	1	1256	G
1	1	1257	G
1	1	1258	A
1	1	1259	A
1	1	1260	A
1	1	1261	C
1	1	1262	C
1	1	1263	U
1	1	1264	C
1	1	1265	A
1	1	1266	C
1	1	1267	C
1	1	1268	C
1	1	1269	G
1	1	1270	G
1	1	1273	C
1	1	1274	G

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Mol	Chain	Res	Type
1	1	1275	G
1	1	1276	A
1	1	1277	C
1	1	1278	A
1	1	1279	C
1	1	1282	A
1	1	1284	A
1	1	1285	G
1	1	1286	G
1	1	1287	A
1	1	1288	U
1	1	1289	U
1	1	1297	U
1	1	1300	U
1	1	1301	A
1	1	1302	G
1	1	1303	C
1	1	1307	U
1	1	1308	U
1	1	1310	U
1	1	1311	C
1	1	1312	G
1	1	1313	A
1	1	1314	U
1	1	1315	U
1	1	1317	C
1	1	1318	G
1	1	1323	U
1	1	1324	G
1	1	1325	G
1	1	1326	U
1	1	1327	G
1	1	1330	G
1	1	1331	C
1	1	1332	A
1	1	1333	U
1	1	1335	G
1	1	1343	U
1	1	1344	A
1	1	1345	G
1	1	1347	U
1	1	1349	G

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Mol	Chain	Res	Type
1	1	1351	G
1	1	1352	G
1	1	1354	G
1	1	1357	A
1	1	1358	U
1	1	1359	U
1	1	1360	U
1	1	1363	C
1	1	1364	U
1	1	1368	U
1	1	1369	A
1	1	1371	U
1	1	1372	U
1	1	1378	A
1	1	1381	G
1	1	1382	A
1	1	1384	C
1	1	1389	C
1	1	1390	U
1	1	1392	U
1	1	1393	G
1	1	1394	G
1	1	1395	C
1	1	1397	U
1	1	1399	C
1	1	1401	A
1	1	1402	A
1	1	1403	C
1	1	1404	U
1	1	1405	A
1	1	1406	G
1	1	1407	U
1	1	1408	U
1	1	1409	A
1	1	1410	C
1	1	1411	G
1	1	1412	C
1	1	1413	G
1	1	1415	C
1	1	1416	C
1	1	1417	C
1	1	1419	C

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Mol	Chain	Res	Type
1	1	1420	G
1	1	1421	A
1	1	1422	G
1	1	1423	C
1	1	1424	G
1	1	1425	G
1	1	1426	U
1	1	1427	C
1	1	1428	G
1	1	1429	G
1	1	1430	C
1	1	1431	G
1	1	1432	U
1	1	1433	C
1	1	1434	C
1	1	1435	C
1	1	1436	C
1	1	1437	C
1	1	1438	A
1	1	1440	C
1	1	1441	U
1	1	1442	U
1	1	1443	C
1	1	1444	U
1	1	1445	U
1	1	1446	A
1	1	1447	G
1	1	1448	A
1	1	1451	G
1	1	1453	C
1	1	1454	A
1	1	1455	A
1	1	1456	G
1	1	1457	U
1	1	1461	G
1	1	1462	U
1	1	1463	U
1	1	1464	C
1	1	1465	A
1	1	1466	G
1	1	1467	C
1	1	1471	C

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Mol	Chain	Res	Type
1	1	1472	C
1	1	1473	G
1	1	1475	G
1	1	1476	A
1	1	1477	U
1	1	1478	U
1	1	1480	A
1	1	1481	G
1	1	1482	C
1	1	1484	A
1	1	1486	A
1	1	1489	A
1	1	1490	G
1	1	1493	C
1	1	1494	U
1	1	1495	G
1	1	1496	U
1	1	1498	A
1	1	1500	G
1	1	1505	U
1	1	1507	G
1	1	1508	A
1	1	1509	U
1	1	1510	G
1	1	1511	U
1	1	1513	C
1	1	1514	G
1	1	1517	G
1	1	1520	G
1	1	1521	C
1	1	1522	A
1	1	1523	C
1	1	1528	G
1	1	1529	C
1	1	1530	U
1	1	1531	A
1	1	1535	U
1	1	1536	G
1	1	1539	U
1	1	1540	G
1	1	1541	G
1	1	1542	C

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Mol	Chain	Res	Type
1	1	1543	U
1	1	1544	C
1	1	1545	A
1	1	1546	G
1	1	1547	C
1	1	1548	G
1	1	1549	U
1	1	1550	G
1	1	1551	U
1	1	1553	C
1	1	1554	C
1	1	1555	U
1	1	1556	A
1	1	1557	C
1	1	1558	C
1	1	1560	U
1	1	1561	A
1	1	1563	G
1	1	1568	C
1	1	1569	A
1	1	1570	G
1	1	1573	G
1	1	1574	C
1	1	1577	G
1	1	1578	U
1	1	1579	A
1	1	1580	A
1	1	1581	C
1	1	1582	C
1	1	1585	U
1	1	1586	U
1	1	1587	G
1	1	1588	A
1	1	1589	A
1	1	1591	C
1	1	1595	U
1	1	1597	C
1	1	1598	G
1	1	1599	U
1	1	1600	G
1	1	1601	A
1	1	1602	U

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Mol	Chain	Res	Type
1	1	1603	G
1	1	1604	G
1	1	1605	G
1	1	1607	A
1	1	1609	C
1	1	1610	G
1	1	1612	G
1	1	1614	A
1	1	1615	U
1	1	1617	G
1	1	1618	C
1	1	1620	A
1	1	1621	U
1	1	1622	U
1	1	1623	A
1	1	1624	U
1	1	1625	U
1	1	1627	C
1	1	1631	U
1	1	1632	G
1	1	1635	C
1	1	1636	G
1	1	1637	A
1	1	1638	G
1	1	1639	G
1	1	1640	A
1	1	1644	C
1	1	1645	C
1	1	1647	A
1	1	1648	G
1	1	1649	U
1	1	1651	A
1	1	1652	G
1	1	1654	G
1	1	1655	C
1	1	1656	G
1	1	1660	C
1	1	1661	A
1	1	1662	U
1	1	1664	A
1	1	1665	G
1	1	1666	C

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Mol	Chain	Res	Type
1	1	1669	G
1	1	1671	G
1	1	1672	U
1	1	1673	U
1	1	1674	G
1	1	1677	U
1	1	1678	A
1	1	1679	A
1	1	1680	G
1	1	1682	C
1	1	1684	C
1	1	1685	U
1	1	1686	G
1	1	1687	C
1	1	1688	C
1	1	1689	C
1	1	1691	U
1	1	1692	U
1	1	1694	U
1	1	1696	C
1	1	1697	A
1	1	1698	C
1	1	1699	A
1	1	1700	C
1	1	1701	C
1	1	1702	G
1	1	1703	C
1	1	1707	U
1	1	1708	C
1	1	1709	G
1	1	1710	C
1	1	1714	U
1	1	1719	A
1	1	1720	U
1	1	1721	U
1	1	1722	G
1	1	1723	G
1	1	1728	U
1	1	1729	U
1	1	1731	A
1	1	1732	G
1	1	1735	A

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Mol	Chain	Res	Type
1	1	1744	G
1	1	1745	A
1	1	1747	C
1	1	1749	G
1	1	1751	C
1	1	1752	C
1	1	1760	G
1	1	1761	U
1	1	1764	G
1	1	1765	C
1	1	1767	C
1	1	1768	A
1	1	1770	G
1	1	1775	C
1	1	1781	A
1	1	1782	G
1	1	1783	C
1	1	1788	A
1	1	1789	G
1	1	1790	A
1	1	1792	G
1	1	1794	C
1	1	1798	C
1	1	1800	A
1	1	1809	A
1	1	1811	C
1	1	1813	A
1	1	1817	G
1	1	1819	A
1	1	1823	A
1	1	1824	A
1	1	1825	A
1	1	1826	G
1	1	1827	U
1	1	1829	G
1	1	1831	A
1	1	1832	A
1	1	1833	C
1	1	1834	A
1	1	1835	A
1	1	1836	G
1	1	1837	G

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Mol	Chain	Res	Type
1	1	1838	U
1	1	1839	U
1	1	1841	C
1	1	1843	G
1	1	1844	U
1	1	1846	G
1	1	1847	G
1	1	1849	G
1	1	1850	A
1	1	1851	A
1	1	1852	C
1	1	1856	C
1	1	1857	G
1	1	1860	A
1	1	1861	G
1	1	1862	G
1	1	1863	A
1	1	1864	U
1	1	1865	C
1	1	1866	A
1	1	1867	U
1	1	1868	U
1	1	1869	A

All (152) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	24	C
1	1	44	U
1	1	61	A
1	1	64	A
1	1	66	G
1	1	68	A
1	1	77	A
1	1	78	C
1	1	102	A
1	1	111	A
1	1	113	G
1	1	124	U
1	1	131	C
1	1	136	C
1	1	139	C

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Mol	Chain	Res	Type
1	1	140	C
1	1	147	A
1	1	162	C
1	1	181	A
1	1	183	G
1	1	199	C
1	1	200	G
1	1	207	G
1	1	209	A
1	1	227	U
1	1	304	C
1	1	307	G
1	1	308	G
1	1	310	C
1	1	312	G
1	1	317	C
1	1	319	C
1	1	332	G
1	1	338	G
1	1	356	C
1	1	363	A
1	1	368	U
1	1	370	G
1	1	383	G
1	1	399	C
1	1	428	U
1	1	448	A
1	1	465	A
1	1	475	C
1	1	486	A
1	1	487	U
1	1	501	C
1	1	517	C
1	1	544	G
1	1	546	G
1	1	547	G
1	1	558	G
1	1	577	U
1	1	578	C
1	1	589	G
1	1	590	A
1	1	593	C

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Mol	Chain	Res	Type
1	1	604	A
1	1	656	G
1	1	662	G
1	1	671	A
1	1	687	C
1	1	743	U
1	1	799	U
1	1	811	A
1	1	821	G
1	1	822	U
1	1	833	C
1	1	834	C
1	1	840	C
1	1	899	U
1	1	913	A
1	1	970	G
1	1	971	G
1	1	1015	U
1	1	1016	U
1	1	1020	A
1	1	1021	U
1	1	1043	G
1	1	1060	A
1	1	1088	U
1	1	1108	G
1	1	1114	U
1	1	1115	U
1	1	1138	C
1	1	1150	A
1	1	1164	G
1	1	1198	G
1	1	1215	C
1	1	1242	U
1	1	1247	C
1	1	1250	A
1	1	1253	A
1	1	1257	G
1	1	1259	A
1	1	1261	C
1	1	1264	C
1	1	1277	C
1	1	1285	G

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Mol	Chain	Res	Type
1	1	1301	A
1	1	1307	U
1	1	1308	U
1	1	1311	C
1	1	1313	A
1	1	1326	U
1	1	1342	U
1	1	1351	G
1	1	1362	U
1	1	1401	A
1	1	1404	U
1	1	1406	G
1	1	1411	G
1	1	1456	G
1	1	1476	A
1	1	1477	U
1	1	1494	U
1	1	1497	G
1	1	1508	A
1	1	1520	G
1	1	1534	C
1	1	1542	C
1	1	1543	U
1	1	1555	U
1	1	1556	A
1	1	1578	U
1	1	1586	U
1	1	1603	G
1	1	1624	U
1	1	1631	U
1	1	1635	C
1	1	1637	A
1	1	1638	G
1	1	1644	C
1	1	1648	G
1	1	1654	G
1	1	1655	C
1	1	1673	U
1	1	1697	A
1	1	1698	C
1	1	1700	C
1	1	1721	U

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Mol	Chain	Res	Type
1	1	1781	A
1	1	1823	A
1	1	1824	A
1	1	1830	U
1	1	1833	C
1	1	1834	A
1	1	1836	G
1	1	1848	U
1	1	1860	A
1	1	1862	G
1	1	1867	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

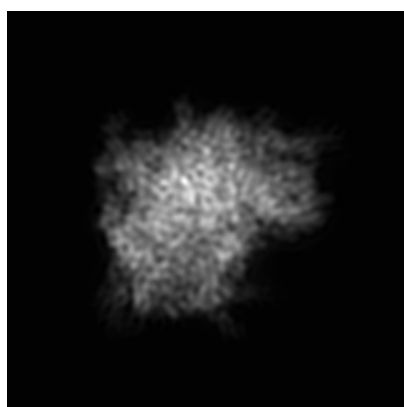
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2810. These allow visual inspection of the internal detail of the map and identification of artifacts.

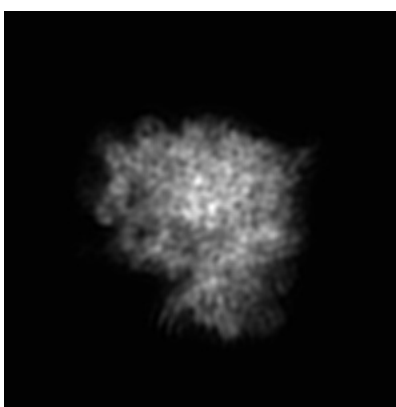
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

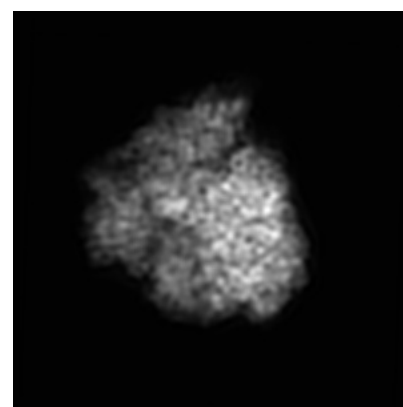
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 150



Y Index: 150

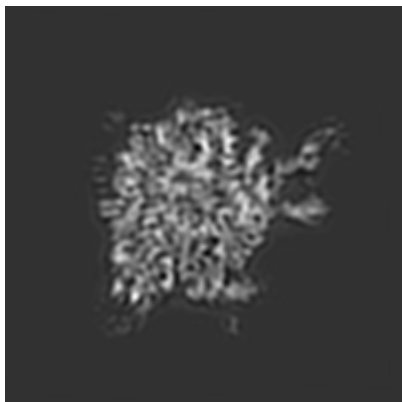


Z Index: 150

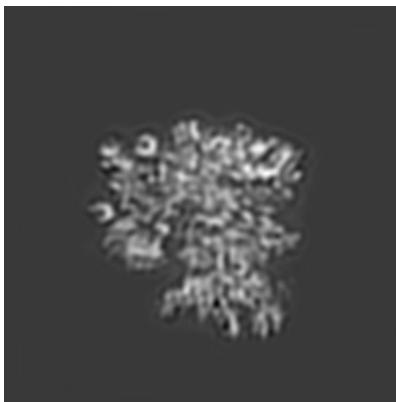
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

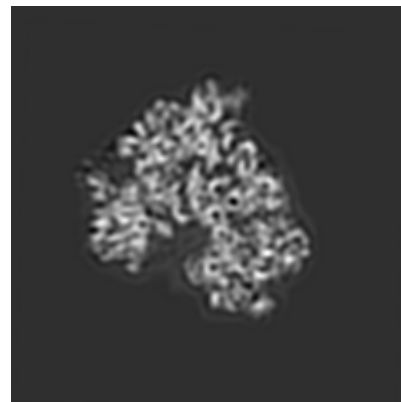
6.3.1 Primary map



X Index: 173



Y Index: 149

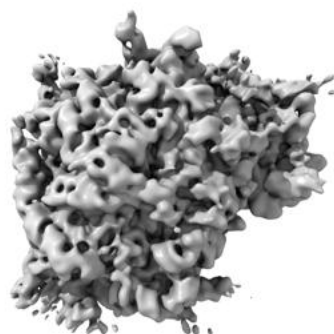


Z Index: 154

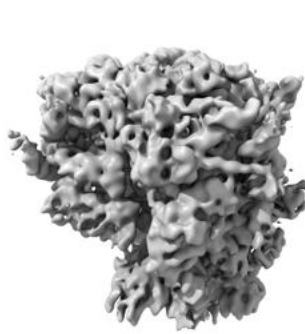
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

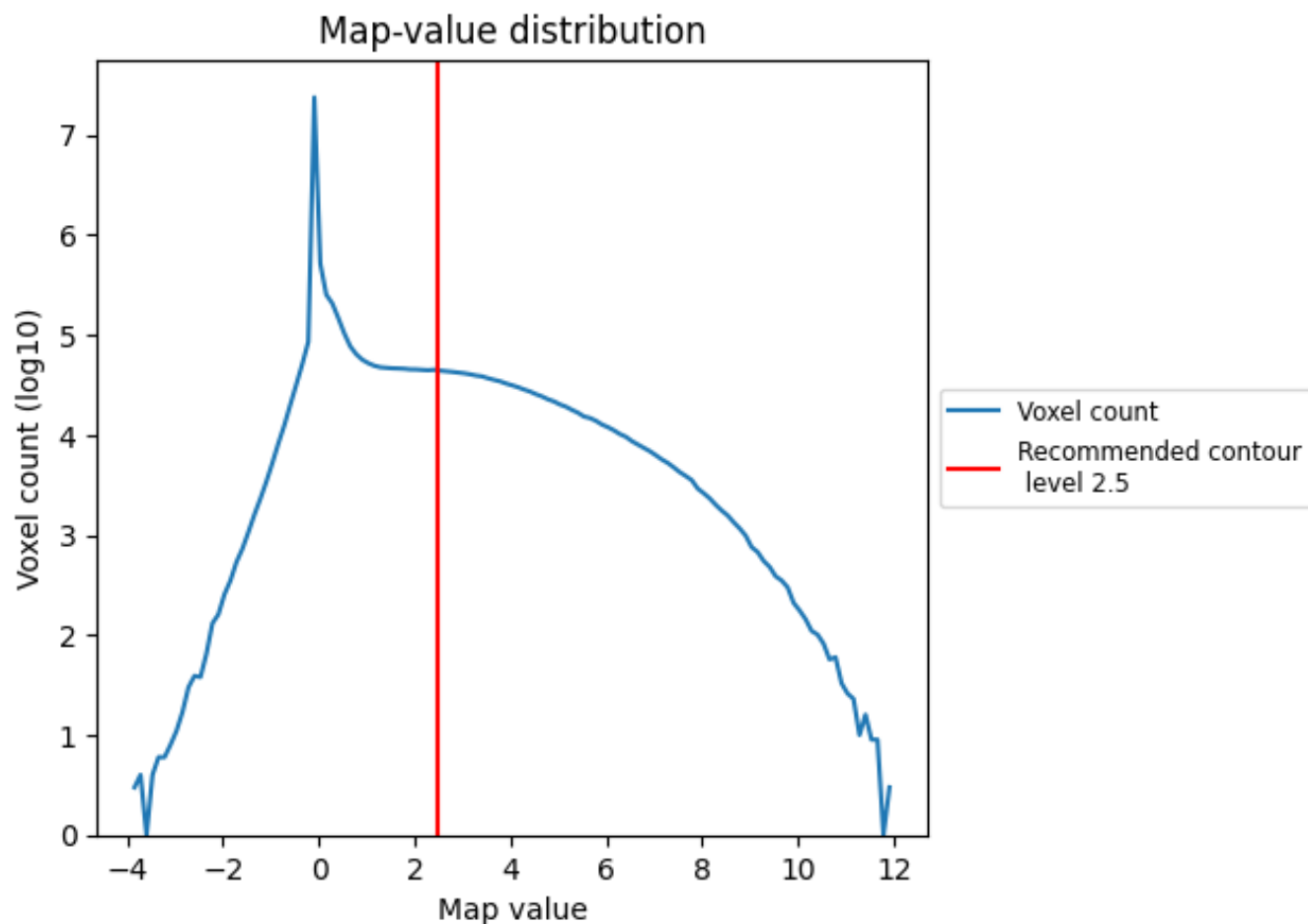
6.5 Mask visualisation

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

7 Map analysis [i](#)

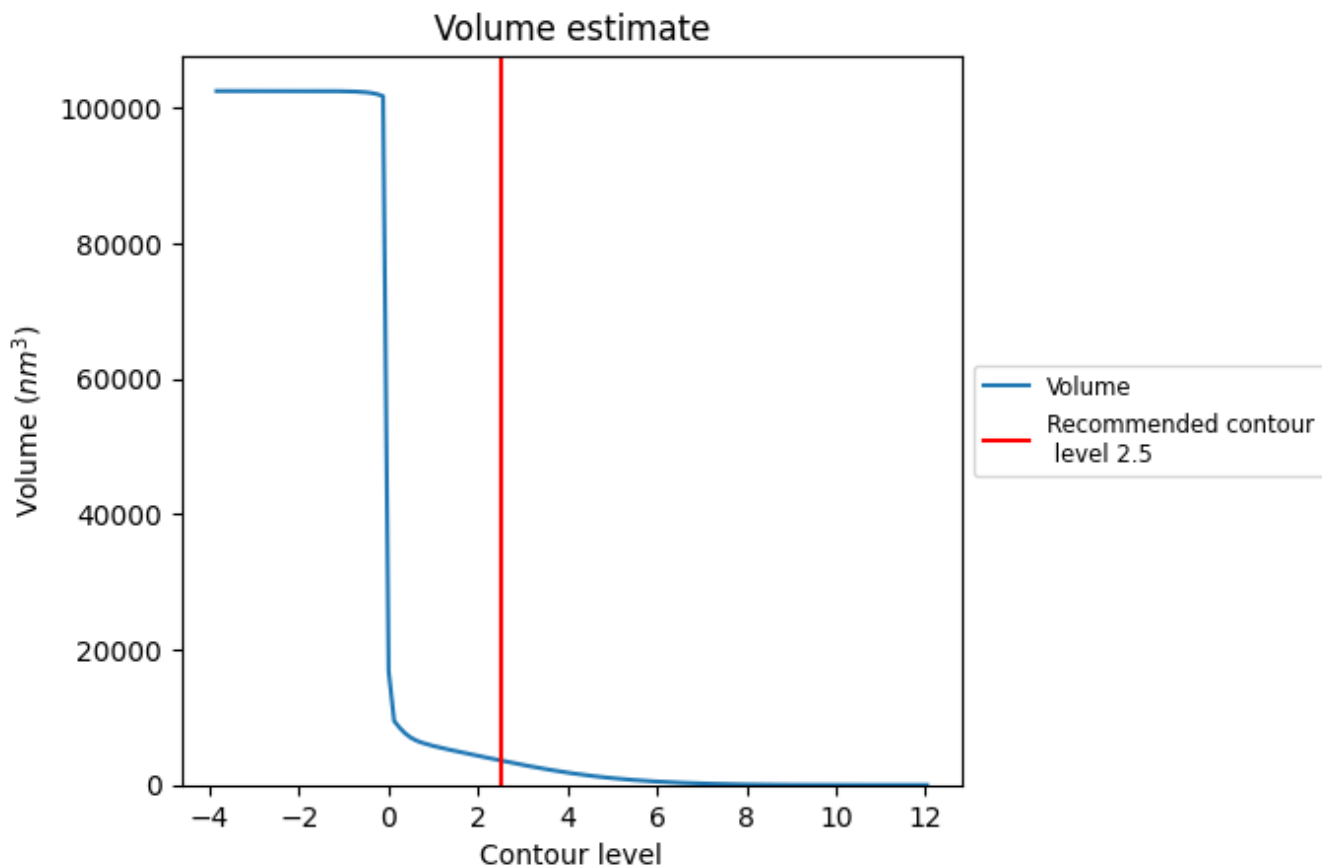
This section contains the results of statistical analysis of the map.

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.

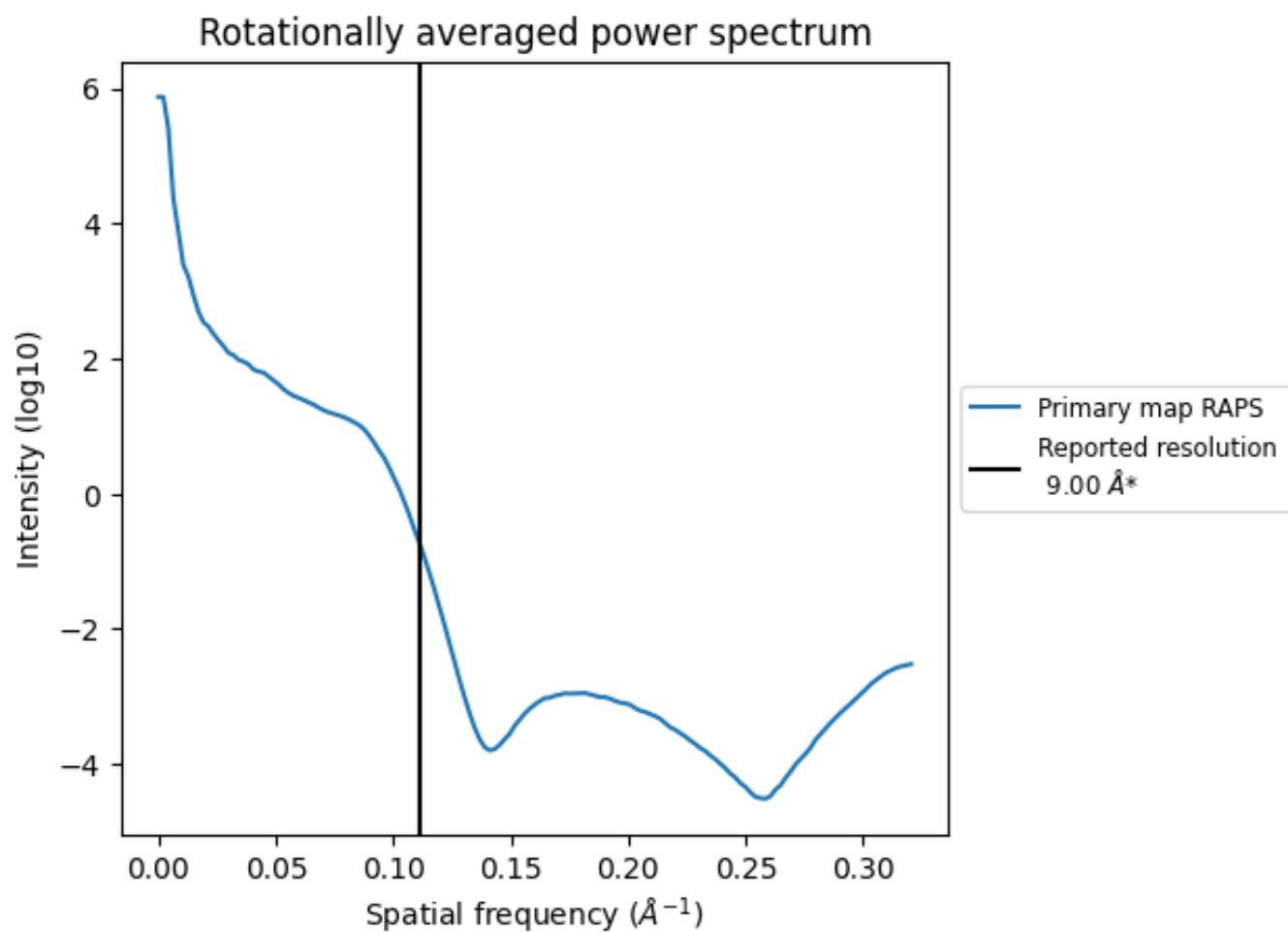
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3628 nm³; this corresponds to an approximate mass of 3277 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 0.111 Å⁻¹

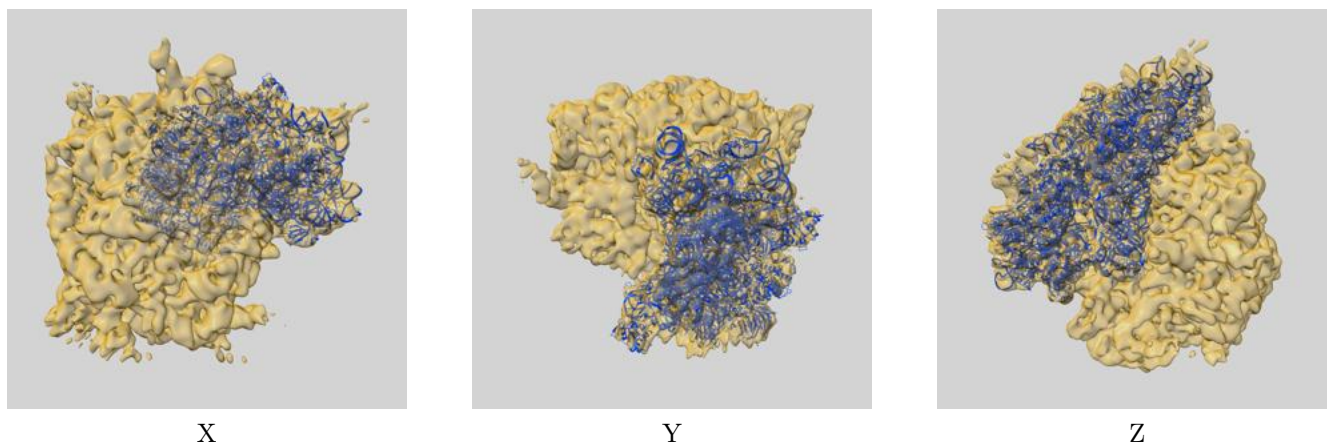
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

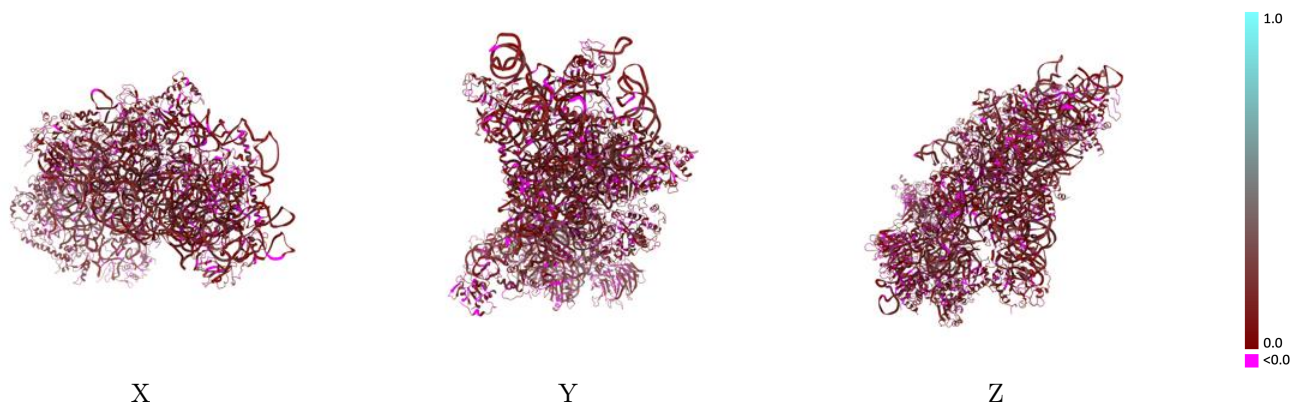
This section contains information regarding the fit between EMDB map EMD-2810 and PDB model 4D5L. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



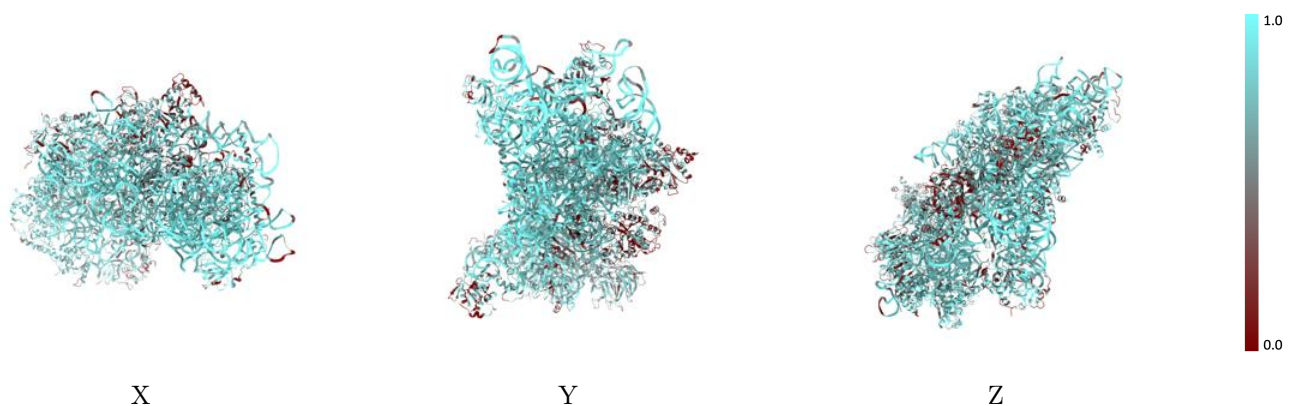
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



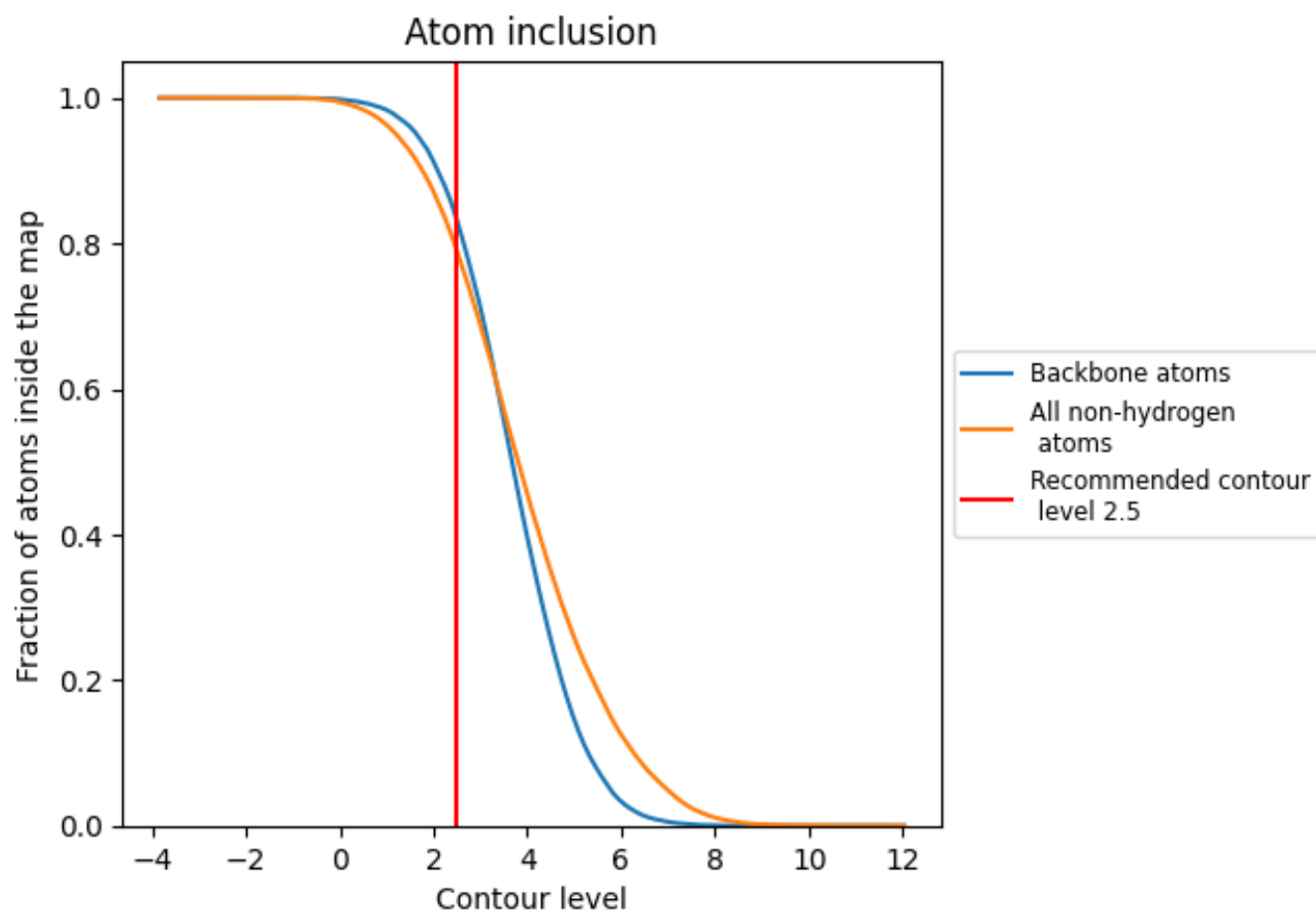
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 83% of all backbone atoms, 79% 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 (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7895	 0.1090
1	 0.9134	 0.1300
A	 0.4631	 0.0870
B	 0.7134	 0.1180
C	 0.5851	 0.1000
D	 0.6494	 0.0960
E	 0.7455	 0.0850
F	 0.7592	 0.1020
G	 0.8003	 0.0860
H	 0.4124	 0.0890
I	 0.6993	 0.0840
J	 0.7902	 0.0940
K	 0.7736	 0.0990
L	 0.6186	 0.0850
M	 0.4351	 0.0490
N	 0.6892	 0.1010
O	 0.6841	 0.0880
P	 0.7298	 0.1050
Q	 0.7808	 0.0790
R	 0.5803	 0.0950
S	 0.7635	 0.0980
T	 0.7911	 0.0900
U	 0.6138	 0.0550
V	 0.3071	 0.0670
W	 0.6501	 0.0720
X	 0.6989	 0.0900
Y	 0.8117	 0.0920
Z	 0.8356	 0.1260
a	 0.6585	 0.0570
b	 0.6183	 0.0960
c	 0.6851	 0.0880
d	 0.8099	 0.0640
e	 0.5945	 0.0640
f	 0.5507	 0.0420
g	 0.6046	 0.0890

