Full wwPDB EM Validation Report

Nov 6, 2022 – 01:59 PM EST

PDB ID	:	6C0F
EMDB ID	:	EMD-7324
Title	:	Yeast nucleolar pre-60S ribosomal subunit (state 2)
Authors	:	Sanghai, Z.A.; Miller, L.; Barandun, J.; Hunziker, M.; Chaker-Margot, M.; Klinge, S.
Deposited on	:	2017-12-29
Resolution	:	3.70 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:

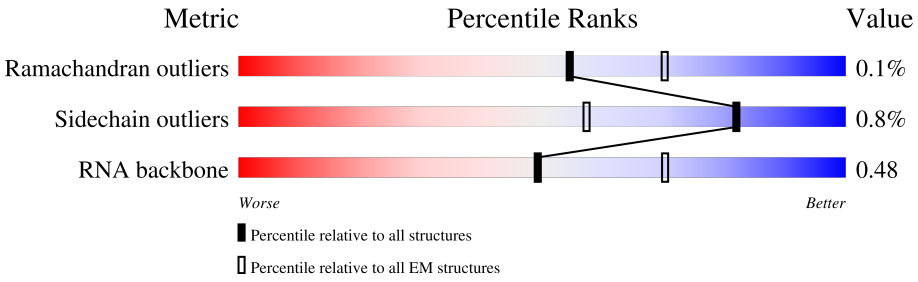
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 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 <=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	3395	28% 11% 60%
2	2	158	73% 25%
3	6	232	16% 16% 5% 62%
4	A	463	85% 15%
5	B	387	14% 83% 16%
6	C	362	85% 13%
7	D	306	61% 38%
8	E	176	96%

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Mol	Chain	Length	Quality of chain
9	F	244	98%
10	G	256	5% 71% 27%
11	I	295	97%
12	K	376	69% 31%
13	L	199	51% 47%
14	M	138	93% 7%
15	N	204	6% 85% 14%
16	O	199	91% 8%
17	P	184	67% 33%
18	Q	186	70% 29%
19	S	172	9% 97%
20	V	137	59% 89% 11%
21	W	647	14% 14% 85%
22	Y	127	98%
23	7	231	7% 67% 32%
24	8	434	11% 23% 77%
25	b	291	82% 17%
26	e	130	12% 88% 12%
27	f	107	99%
28	h	120	6% 97%
29	i	100	6% 84% 16%
30	j	88	5% 81% 18%
31	x	28	100%
32	m	74	9% 100%
33	n	605	56% 44%

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Mol	Chain	Length	Quality of chain
34	o	220	60% 40%
35	p	505	14% 86% 13%
36	q	285	100% 100%
37	s	807	19% 81%
38	t	322	75% 23%
39	u	199	37% 63% 35%
40	v	453	28% 49% 50%
41	w	250	18% 28% 72%
42	y	245	55% 92% 8%
43	z	278	87% 13%

2 Entry composition (i)

There are 44 unique types of molecules in this entry. The entry contains 91742 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 Saccharomyces cerevisiae S288c 35S pre-ribosomal RNA miscRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1357	29055	12970	5242	9486	1357	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	U	deletion	GB 259147931

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	6	87	1838	823	309	619	87	0	0

- Molecule 4 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	394	3126	1997	525	593	11	0	0

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	324	2577	1635	478	458	6	0	0

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	314	Total	C	N	O	S	0	0
			2418	1531	454	430	3		

- Molecule 7 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	190	Total	C	N	O	S	0	0
			1578	996	297	275	10		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	170	Total	C	N	O	S	0	0
			1366	882	244	239	1		

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	242	Total	C	N	O	S	0	0
			1941	1249	352	339	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	187	Total	C	N	O	S	0	0
			1453	934	253	264	2		

- Molecule 11 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	288	Total	C	N	O	S	0	0
			2429	1544	439	442	4		

- Molecule 12 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	260	Total	C	N	O	S	0	0
			2099	1352	346	398	3		

- Molecule 13 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	106	Total	C	N	O	0	0
			845	531	174	140		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	128	Total	C	N	O	S	0	0
			997	641	190	164	2		

- Molecule 15 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	176	Total	C	N	O	S	0	0
			1509	946	319	243	1		

- Molecule 16 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	184	Total	C	N	O	S	0	0
			1451	936	268	246	1		

- Molecule 17 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	124	Total	C	N	O	0	0
			975	612	184	179		

- Molecule 18 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	132	Total	C	N	O	S	0	0
			1015	648	191	175	1		

- Molecule 19 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	122	Total	C	N	O	S	0	0
			903	567	169	160	7		

- Molecule 21 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	98	Total	C	N	O	S	0	0
			806	509	132	164	1		

- Molecule 22 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	Y	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 23 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	7	156	Total	C	N	O	S	0	0
			1295	813	250	228	4		

- Molecule 24 is a protein called Ribosomal RNA-processing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	8	98	Total	C	N	O	S	0	0
			836	515	165	154	2		

- Molecule 25 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	242	Total	C	N	O	S	0	0
			1919	1221	344	350	4		

- Molecule 26 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	e	114	Total	C	N	O	S	0	0
			914	580	181	152	1		

- Molecule 27 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 28 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	h	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 29 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	i	84	Total	C	N	O	S	0	0
			665	413	136	114	2		

- Molecule 30 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	72	Total	C	N	O	S	0	0
			575	350	125	95	5		

- Molecule 31 is a protein called Brx1-associated peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	x	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 32 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	m	74	Total	C	N	O	0	0
			370	222	74	74		

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	341	Total	C	N	O	S	0	0
			2794	1823	470	492	9		

- Molecule 34 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	133	Total	C	N	O	S	0	0
			1107	716	198	189	4		

- Molecule 35 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	437	Total	C	N	O	S	0	0
			3486	2247	600	627	12		

- Molecule 36 is a protein called Protein MAK11.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	q	285	Total	C	N	O	0	0
			1409	839	285	285		

- Molecule 37 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	157	Total	C	N	O	S	0	0
			1069	672	203	191	3		

- Molecule 38 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	t	248	Total	C	N	O	S	0	0
			1965	1254	350	358	3		

- Molecule 39 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	129	Total	C	N	O	S	0	0
			1088	682	220	178	8		

- Molecule 40 is a protein called Ribosome biogenesis protein SSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	225	Total	C	N	O	S	0	0
			1795	1142	320	324	9		

- Molecule 41 is a protein called Ribosomal RNA-processing protein 15.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	w	70	Total 562	C 357	N 96	O 109	0	0

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	226	Total 1709	C 1060	N 296	O 346	S 7	0	0

- Molecule 43 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	z	243	Total 2058	C 1334	N 353	O 366	S 5	0	0

- Molecule 44 is ZINC ION (three-letter code: ZN) (formula: Zn).

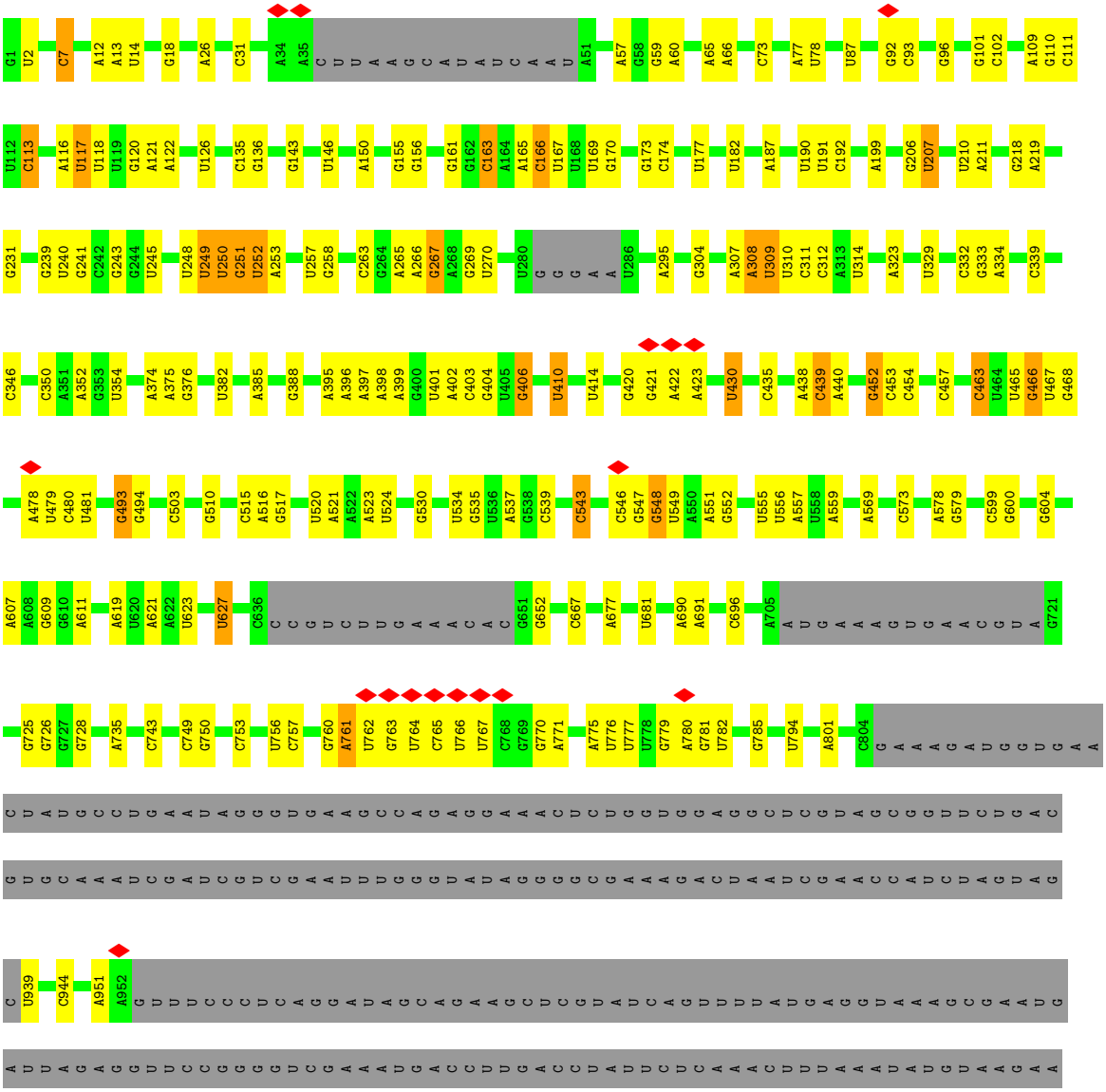
Mol	Chain	Residues	Atoms		AltConf
44	D	1	Total 1	Zn 1	0
44	j	1	Total 1	Zn 1	0
44	u	1	Total 1	Zn 1	0

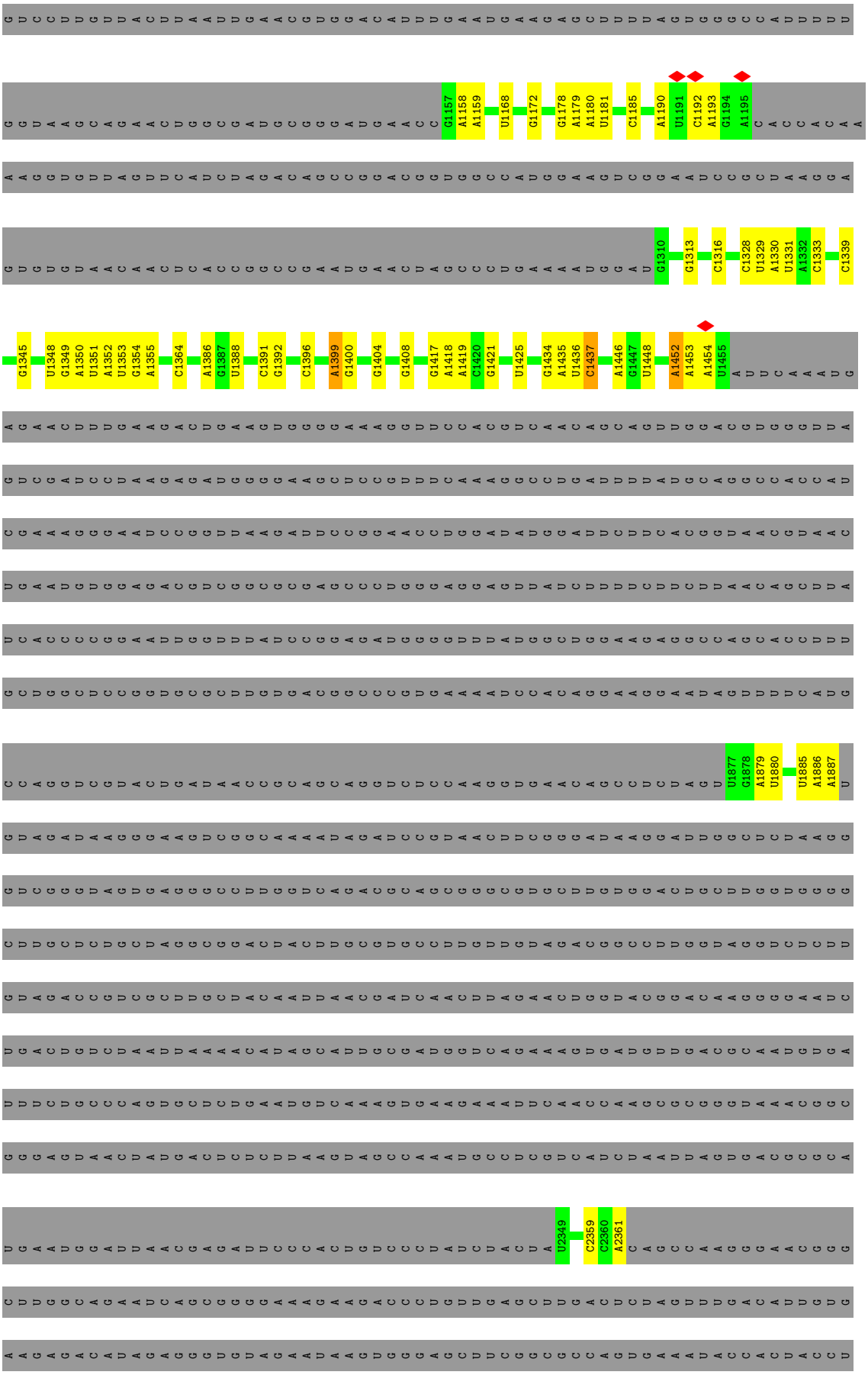
3 Residue-property plots (i)

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

- Molecule 1: Saccharomyces cerevisiae S288c 35S pre-ribosomal RNA miscRNA

Chain 1:




G1157
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U1168
G1172
G1178
A1179
A1180
U1181
C1185
A1190
U1191
C1192
A1193
G1194
A1195
G1310
G1313
C1316
C1328
U1329
A1330
U1331
A1332
C1333
C1339
G1345
U1348
G1349
A1350
U1351
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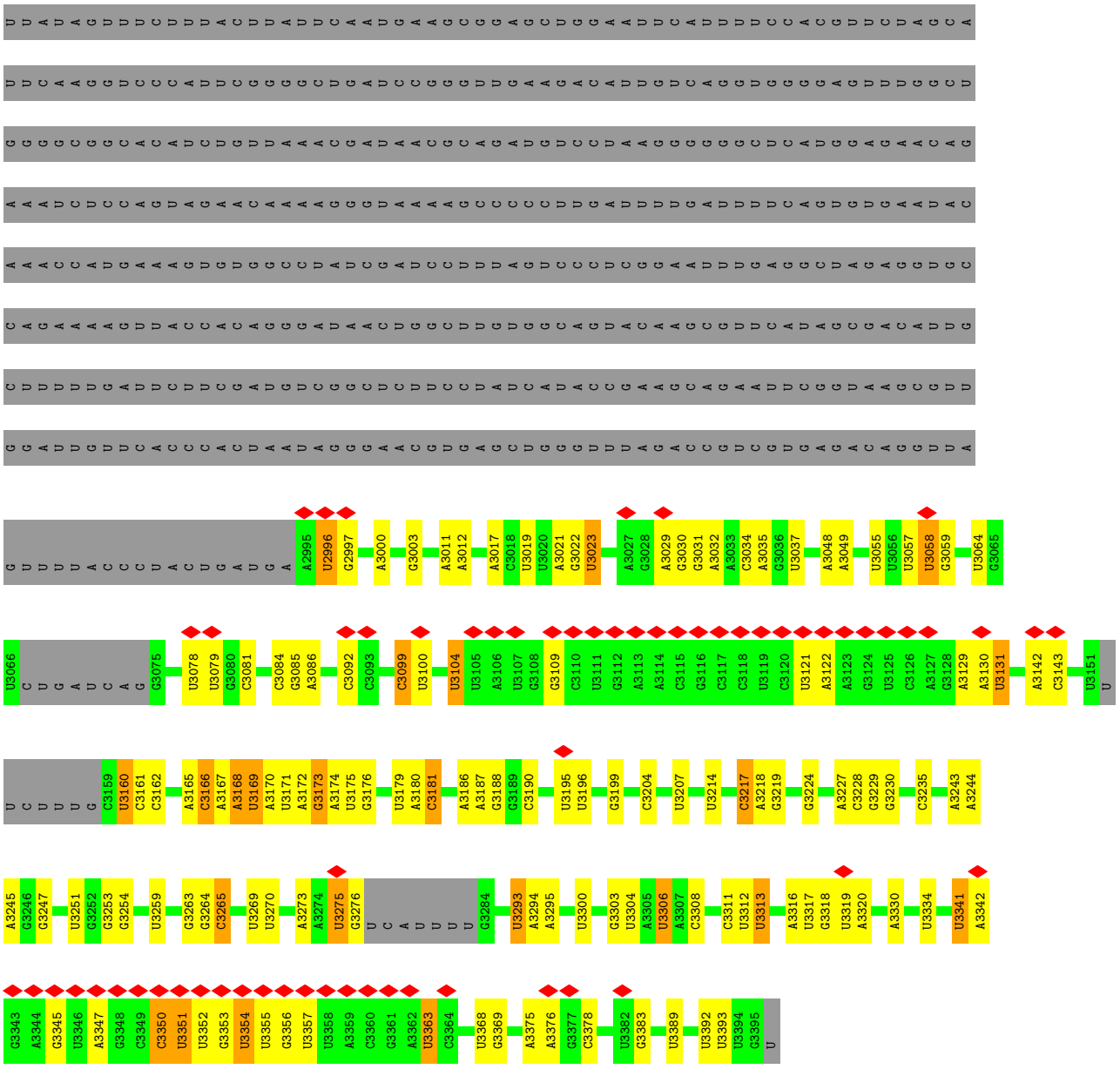
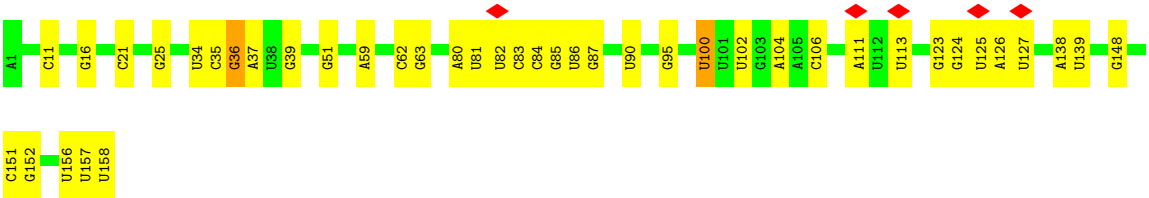
C2360
A2361



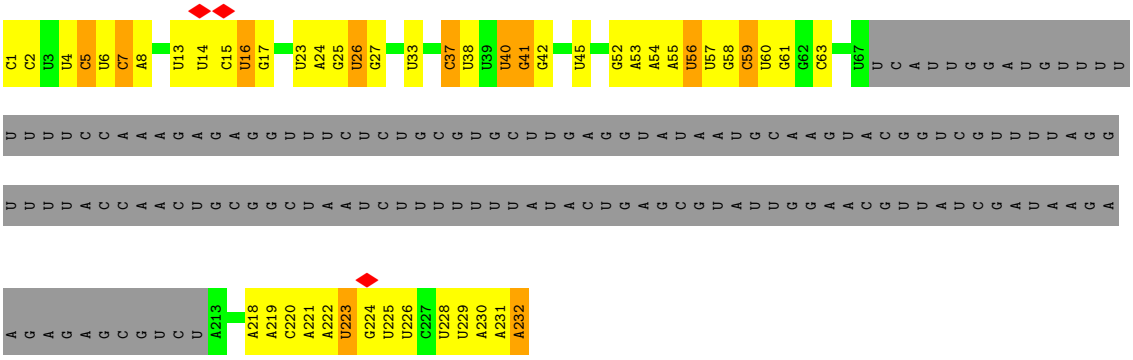
• Molecule 2: 5.8S rRNA

Chain 2:



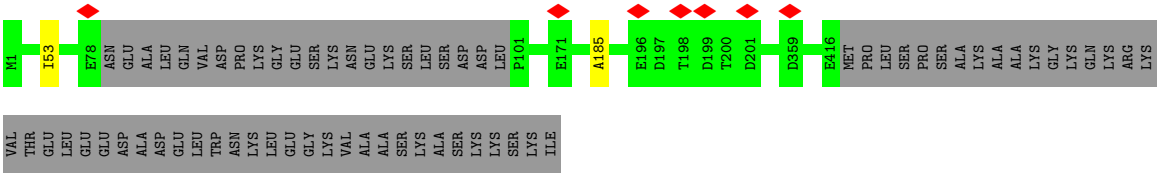
• Molecule 3: ITS2

Chain 6:



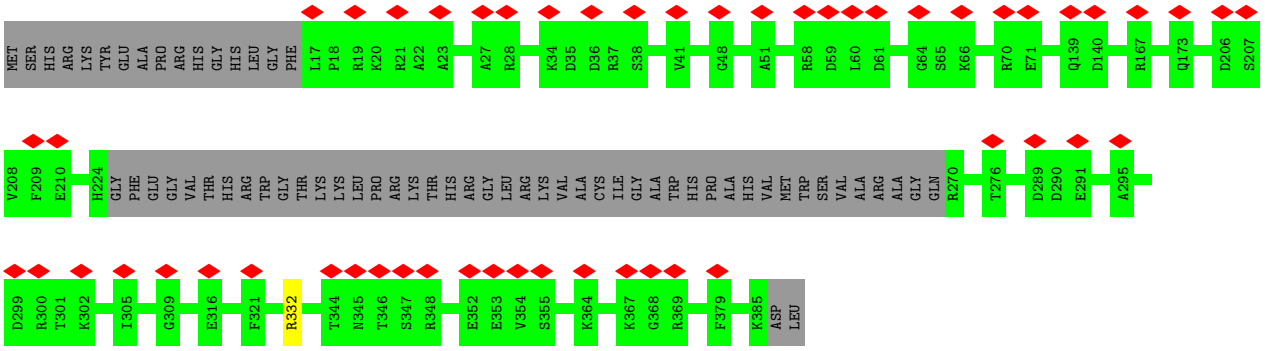
• Molecule 4: Ribosome biogenesis protein NSA1

Chain A:



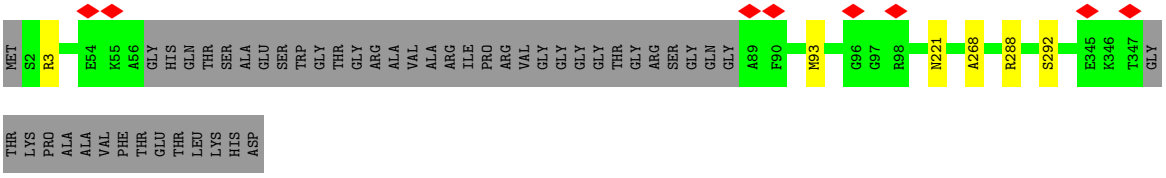
• Molecule 5: 60S ribosomal protein L3

Chain B:



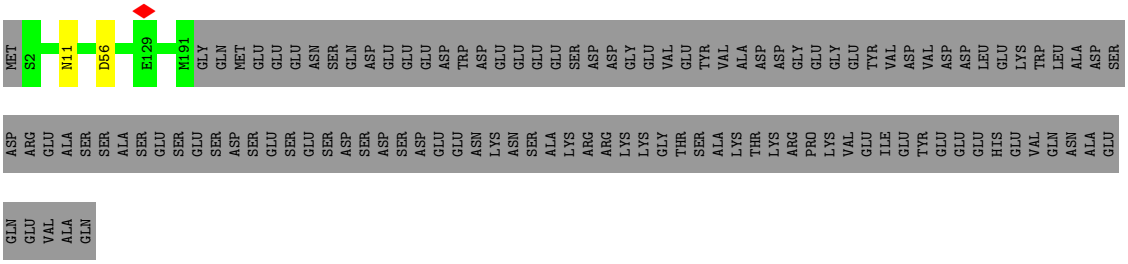
• Molecule 6: 60S ribosomal protein L4-A

Chain C:

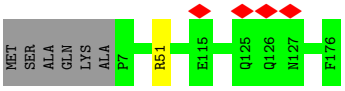


• Molecule 7: Protein MAK16

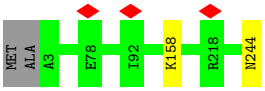
Chain D:



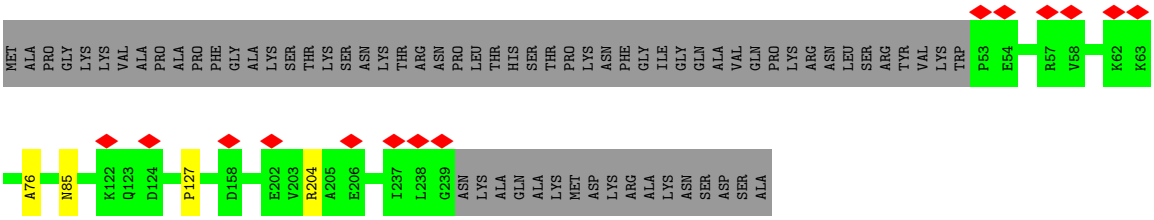
• Molecule 8: 60S ribosomal protein L6-A



• Molecule 9: 60S ribosomal protein L7-A

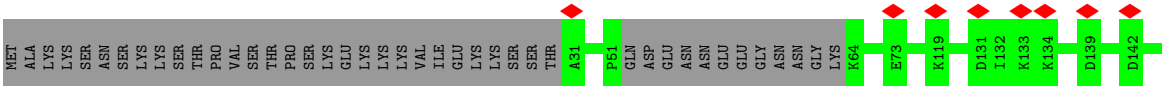


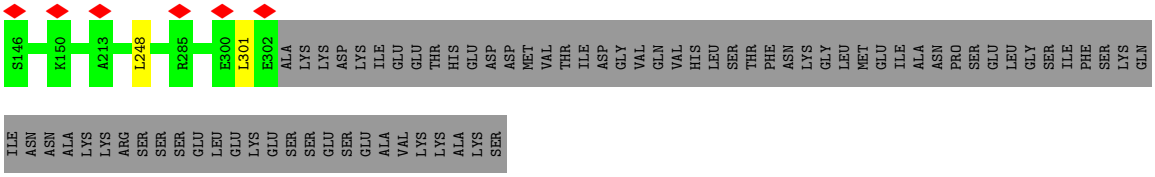
• Molecule 10: 60S ribosomal protein L8-A



• Molecule 11: Ribosome production factor 1

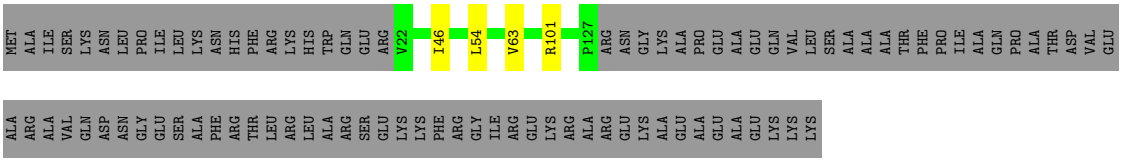
• Molecule 12: Proteasome-interacting protein CIC1





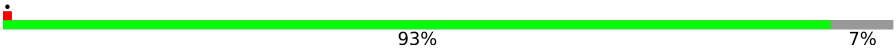
• Molecule 13: 60S ribosomal protein L13-A

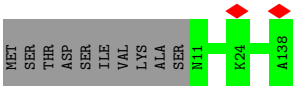
Chain L:



• Molecule 14: 60S ribosomal protein L14-A

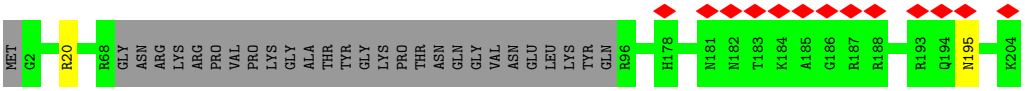
Chain M:





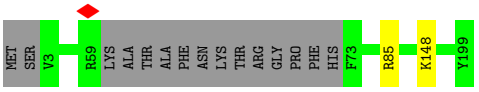
• Molecule 15: 60S ribosomal protein L15-A

Chain N:



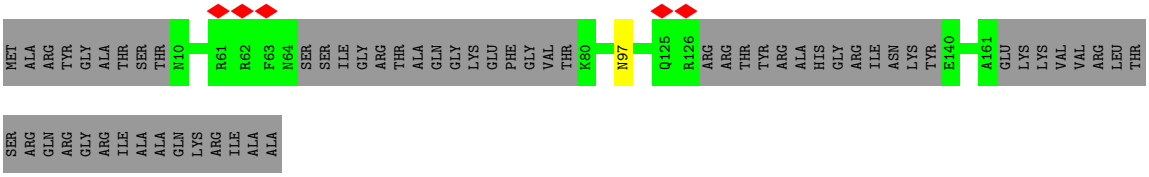
• Molecule 16: 60S ribosomal protein L16-A

Chain O:



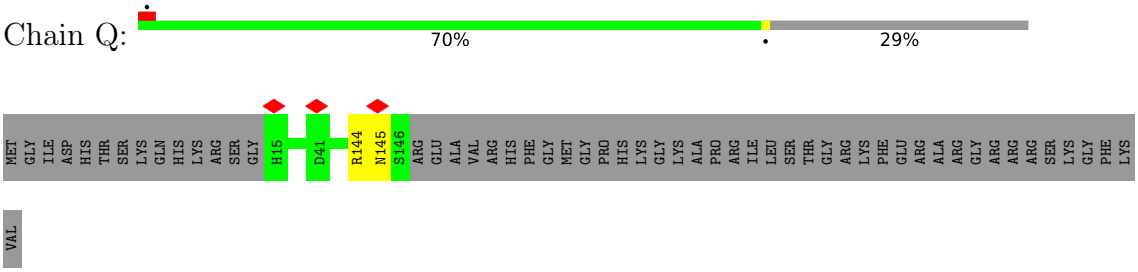
• Molecule 17: 60S ribosomal protein L17-A

Chain P:



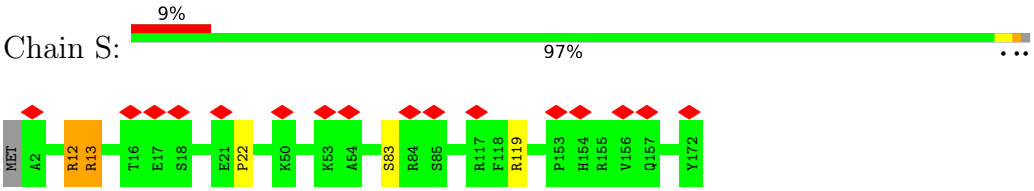
• Molecule 18: 60S ribosomal protein L18-A

Chain Q:



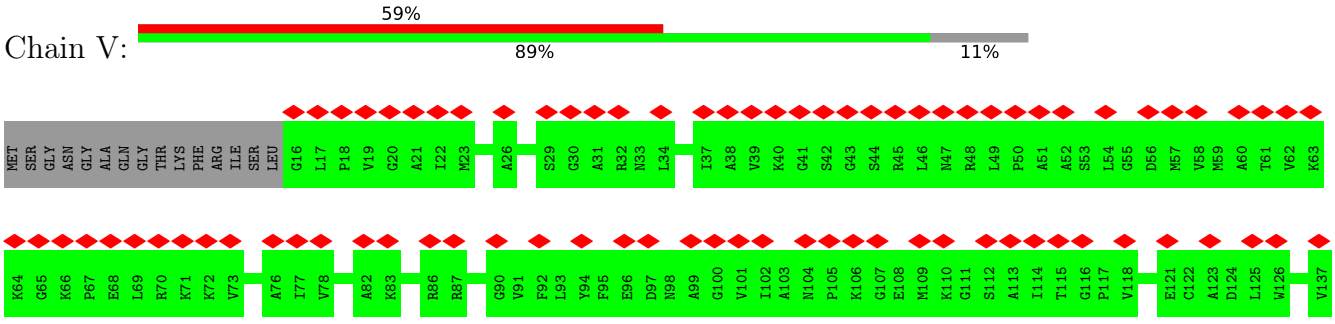
• Molecule 19: 60S ribosomal protein L20-A

Chain S:



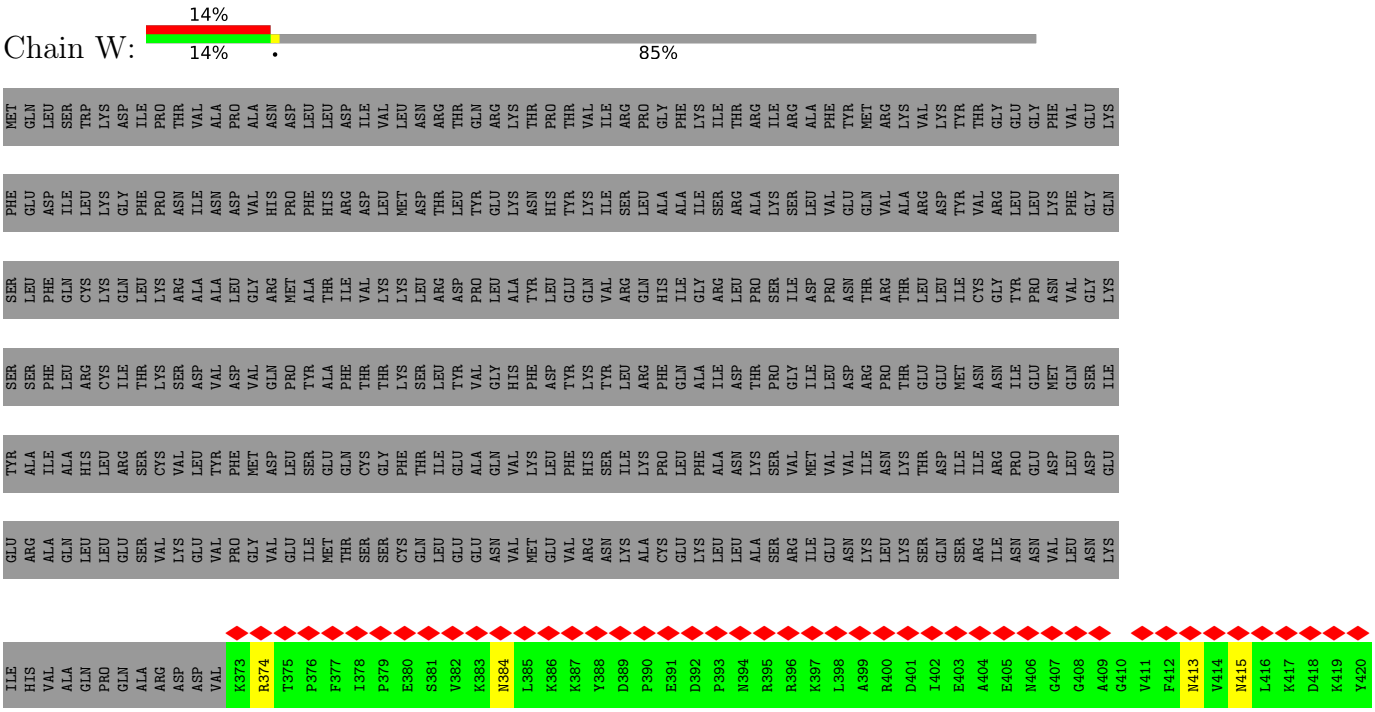
• Molecule 20: 60S ribosomal protein L23-A

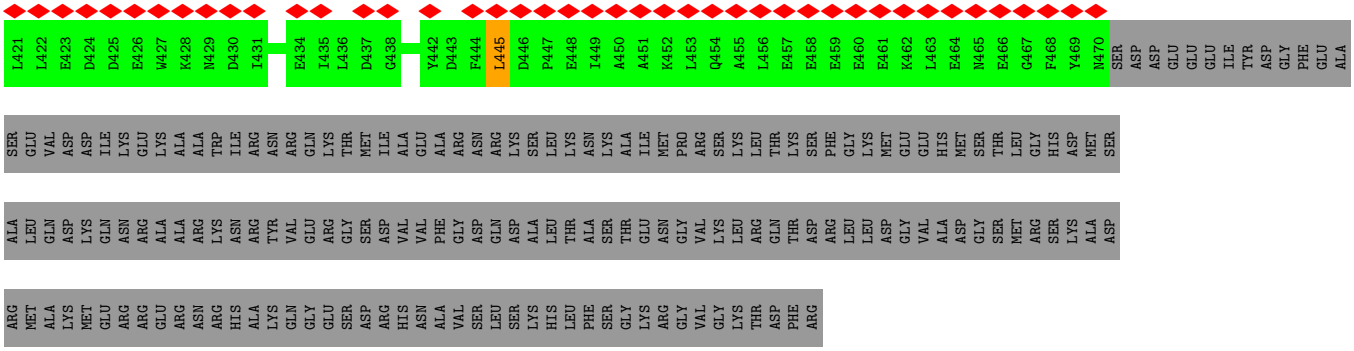
Chain V:



• Molecule 21: Nucleolar GTP-binding protein 1

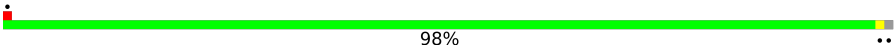
Chain W:

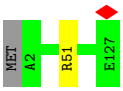




• Molecule 22: 60S ribosomal protein L26-A

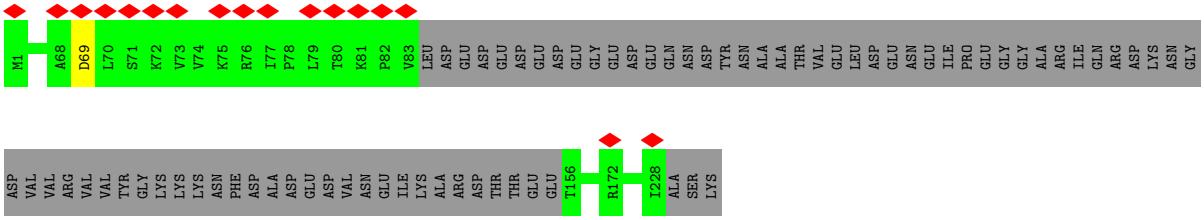
Chain Y:





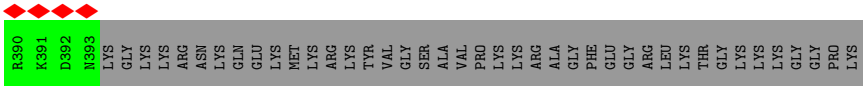
• Molecule 23: Nucleolar protein 16

Chain 7:



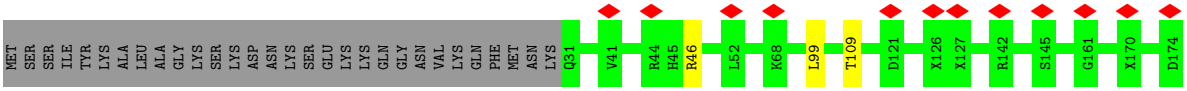
• Molecule 24: Ribosomal RNA-processing protein 14

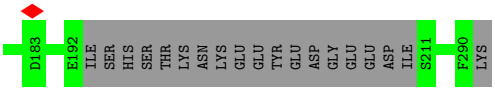
Chain 8:



• Molecule 25: Ribosome biogenesis protein BRX1

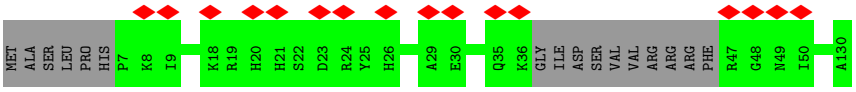
Chain b:





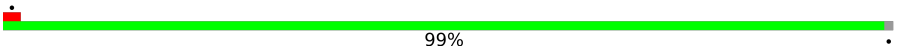
• Molecule 26: 60S ribosomal protein L32

Chain e:



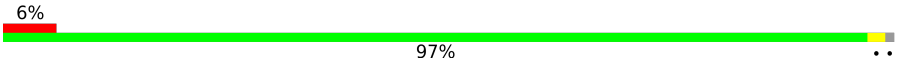
• Molecule 27: 60S ribosomal protein L33-A

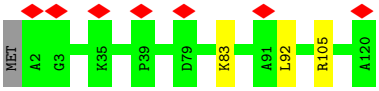
Chain f:



• Molecule 28: 60S ribosomal protein L35-A

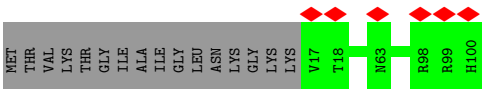
Chain h:





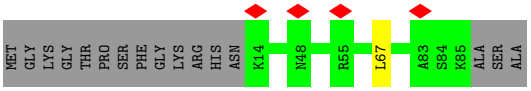
• Molecule 29: 60S ribosomal protein L36-A

Chain i:



• Molecule 30: 60S ribosomal protein L37-A

Chain j:

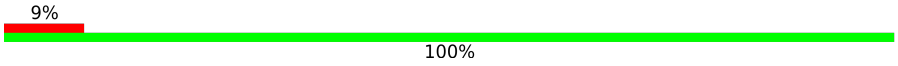


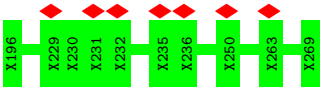
• Molecule 31: Brx1-associated peptide

Chain x: 

There are no outlier residues recorded for this chain.

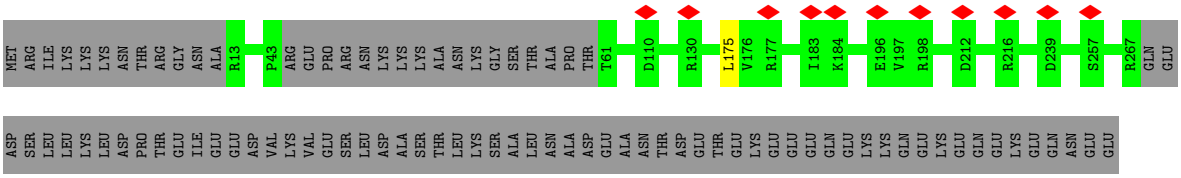
• Molecule 32: rRNA-processing protein EBP2

Chain m: 



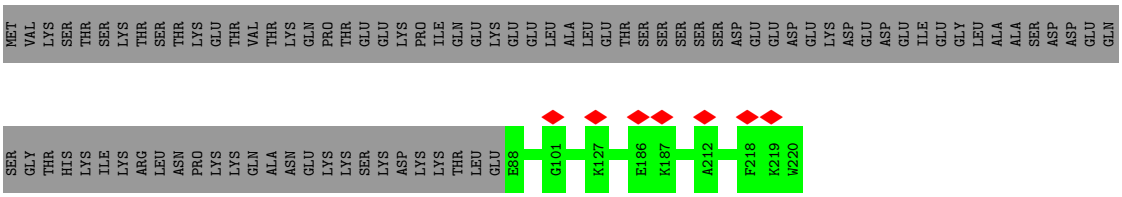
• Molecule 33: Pescadillo homolog

Chain n: 



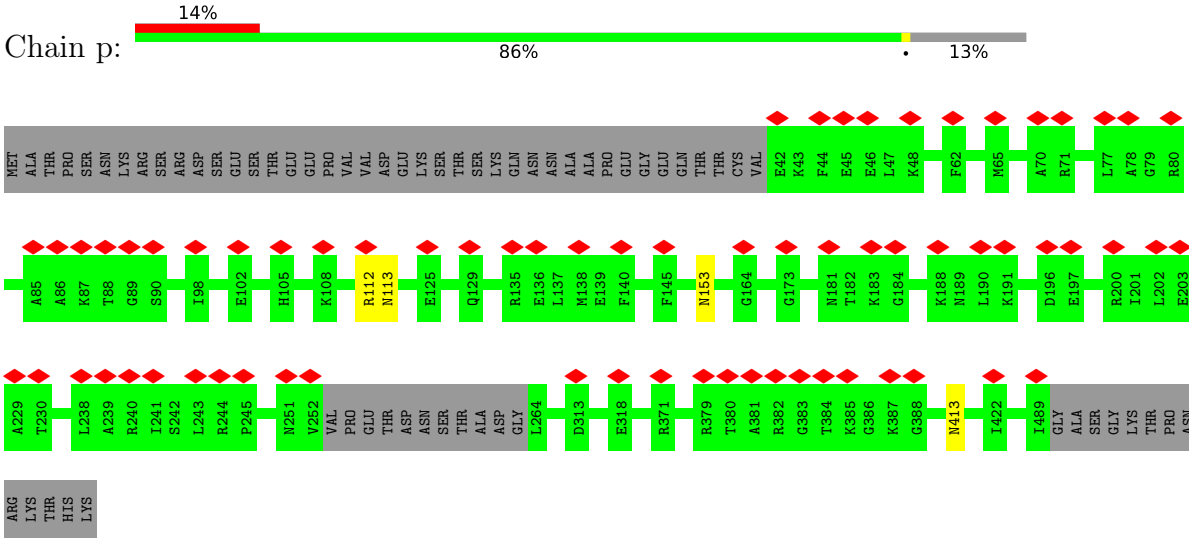
• Molecule 34: Ribosome biogenesis protein 15

Chain o: 



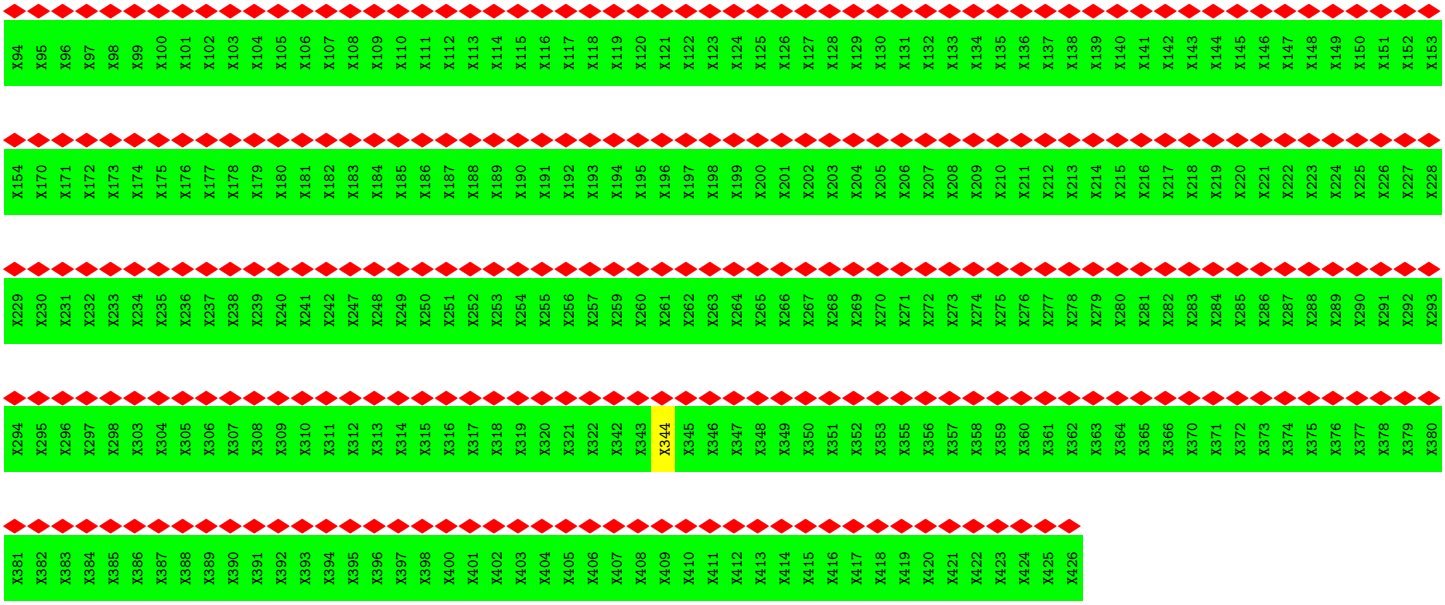
• Molecule 35: ATP-dependent RNA helicase HAS1

Chain p:



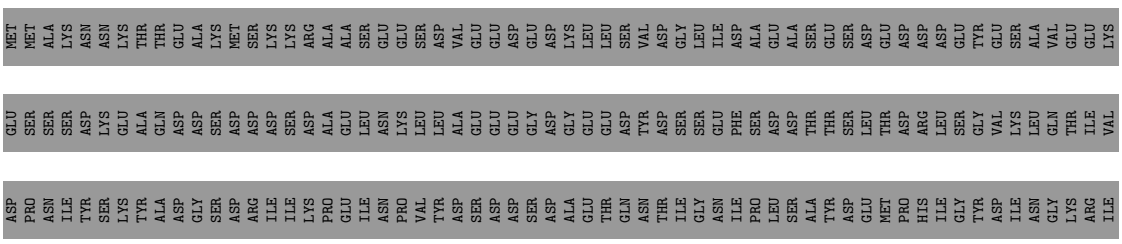
• Molecule 36: Protein MAK11

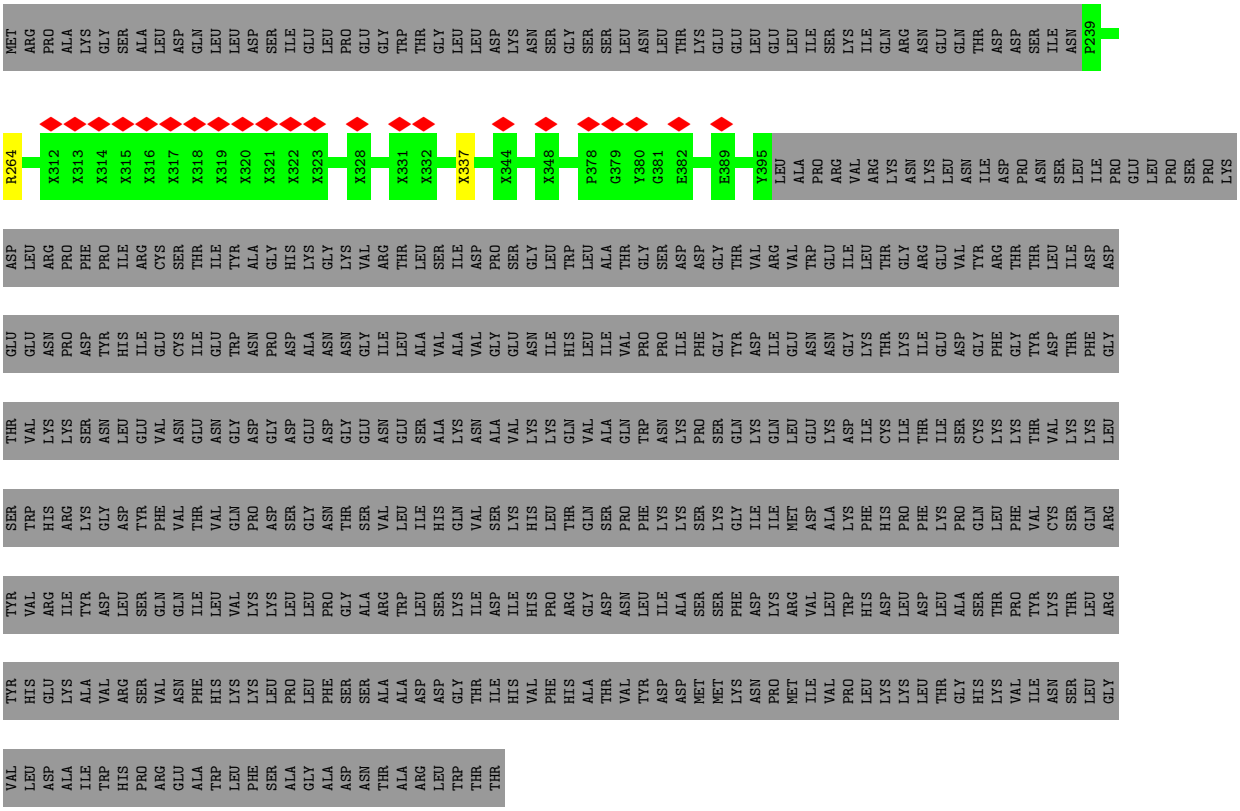
Chain q:



• Molecule 37: Ribosome biogenesis protein ERB1

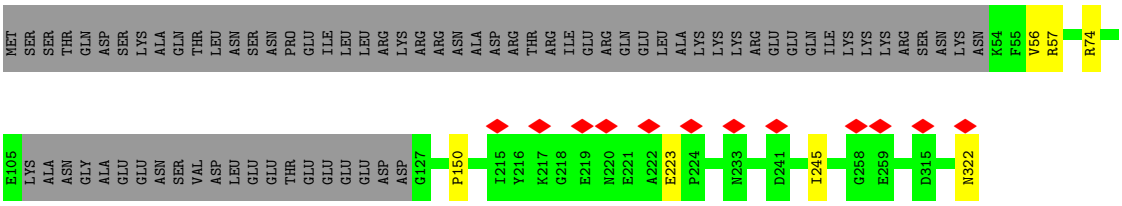
Chain s:





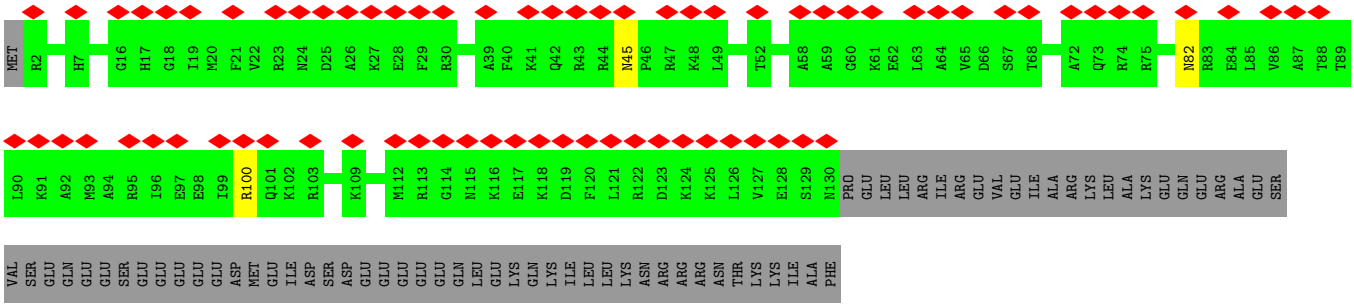
• Molecule 38: Ribosome biogenesis protein RLP7

Chain t:



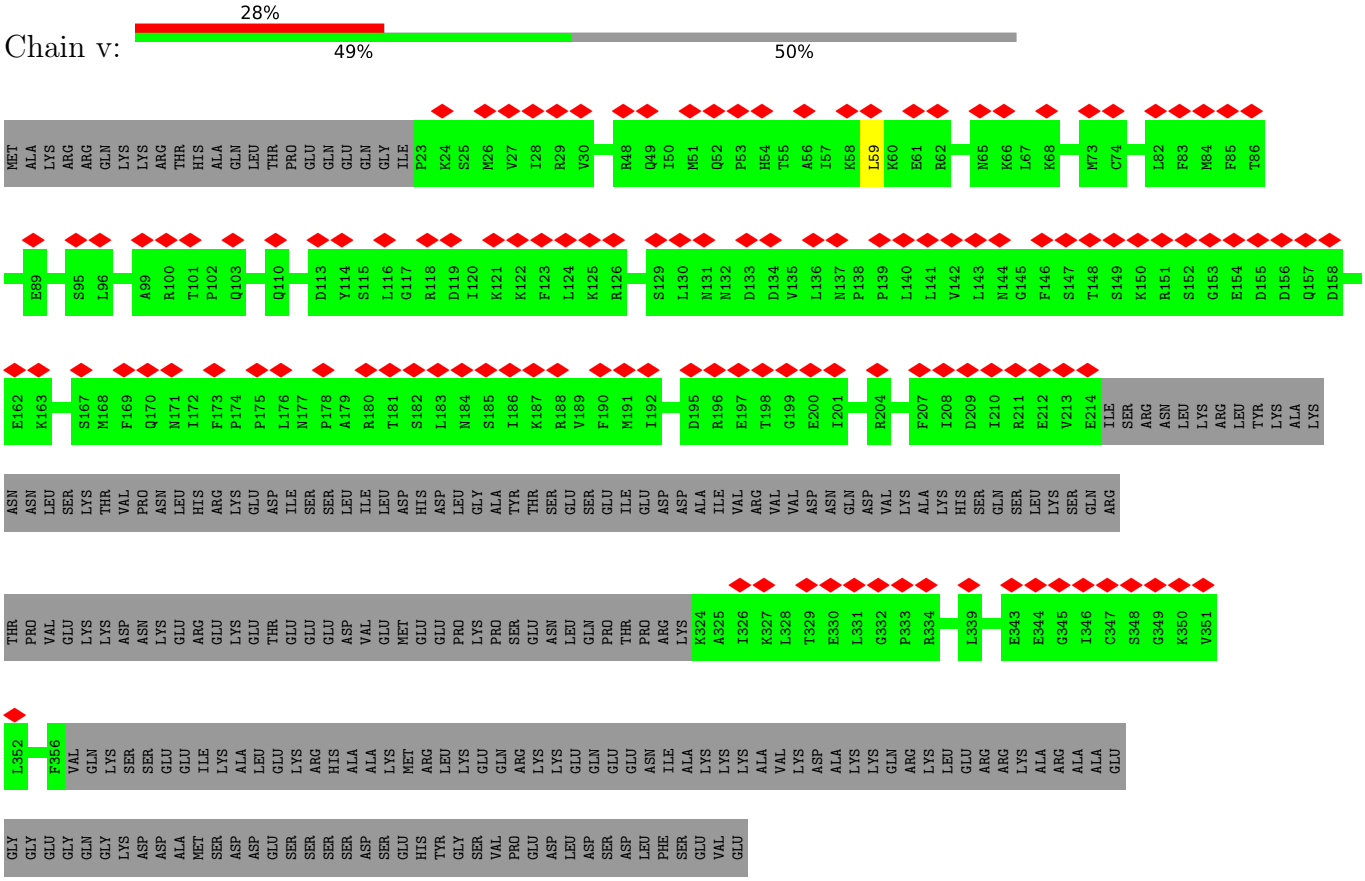
• Molecule 39: Ribosome biogenesis protein RLP24

Chain u:



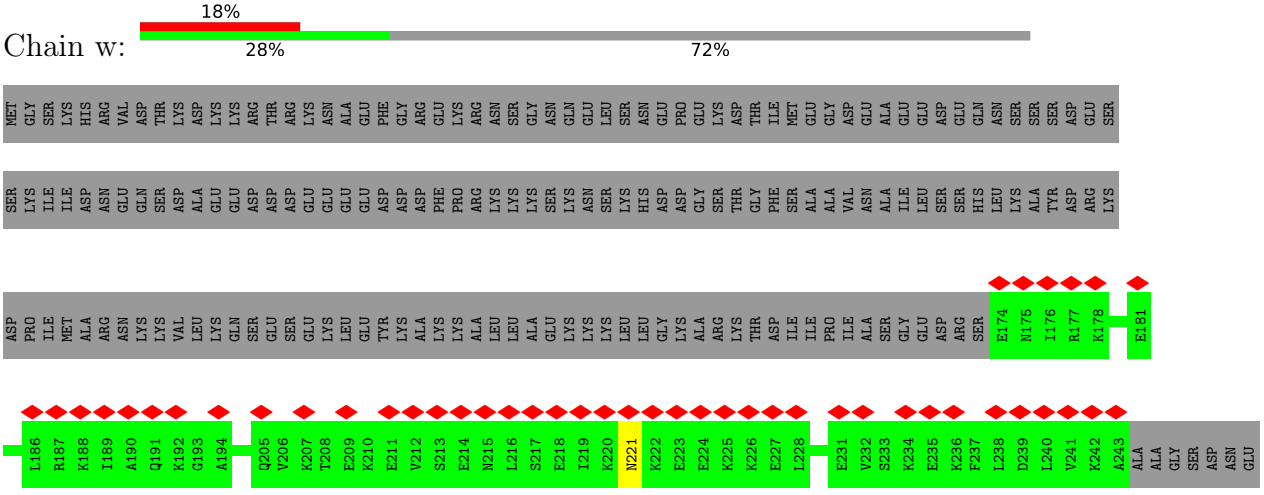
• Molecule 40: Ribosome biogenesis protein SSF1

Chain v:



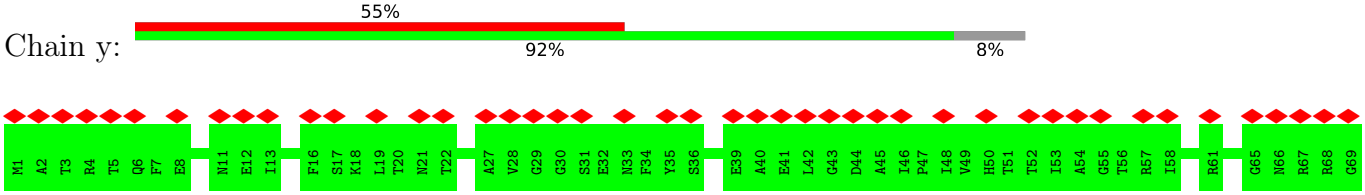
• Molecule 41: Ribosomal RNA-processing protein 15

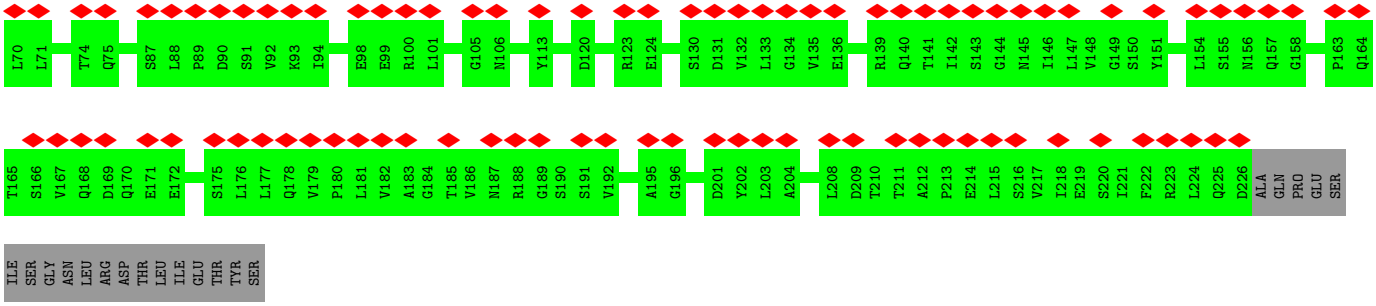
Chain w:



• Molecule 42: Eukaryotic translation initiation factor 6

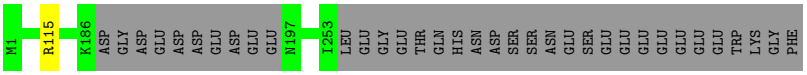
Chain y:





• Molecule 43: Ribosomal RNA-processing protein 1

Chain z:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	201114	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	1.56	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.173	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	624.0, 624.0, 624.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0.72	0/32512	1.16	224/50669 (0.4%)
2	2	0.71	0/3746	1.09	13/5832 (0.2%)
3	6	0.63	0/2050	1.33	34/3186 (1.1%)
4	A	0.39	0/3182	0.59	0/4288
5	B	0.34	0/2628	0.58	0/3529
6	C	0.41	0/2462	0.60	0/3333
7	D	0.44	0/1609	0.55	0/2157
8	E	0.39	0/1390	0.56	0/1866
9	F	0.37	0/1979	0.58	0/2661
10	G	0.39	0/1477	0.67	0/1994
11	I	0.41	0/2476	0.58	0/3323
12	K	0.35	0/2133	0.59	1/2879 (0.0%)
13	L	0.42	0/858	0.64	2/1154 (0.2%)
14	M	0.36	0/1012	0.53	0/1362
15	N	0.42	0/1540	0.55	0/2060
16	O	0.37	0/1476	0.52	0/1980
17	P	0.35	0/991	0.50	0/1334
18	Q	0.39	0/1030	0.59	0/1393
19	S	0.37	0/1473	0.57	1/1980 (0.1%)
20	V	0.29	0/917	0.50	0/1235
21	W	0.32	0/821	0.51	1/1106 (0.1%)
22	Y	0.40	0/1004	0.60	0/1341
23	7	0.40	0/1312	0.62	1/1744 (0.1%)
24	8	0.28	0/840	0.42	0/1105
25	b	0.36	0/1868	0.58	0/2522
26	e	0.36	0/931	0.53	0/1243
27	f	0.42	0/868	0.57	0/1168
28	h	0.36	0/978	0.62	1/1301 (0.1%)
29	i	0.34	0/672	0.57	0/894
30	j	0.34	0/587	0.54	0/778
33	n	0.36	0/2862	0.56	0/3870
34	o	0.37	0/1129	0.54	0/1502

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
35	p	0.37	0/3552	0.61	0/4789
37	s	0.40	0/720	0.55	0/964
38	t	0.36	0/1991	0.61	0/2679
39	u	0.34	0/1109	0.50	0/1474
40	v	0.31	0/1825	0.62	1/2453 (0.0%)
41	w	0.29	0/563	0.51	0/748
42	y	0.31	0/1730	0.58	0/2354
43	z	0.40	0/2104	0.55	0/2832
All	All	0.54	0/94407	0.88	279/135082 (0.2%)

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	A	0	2
7	D	0	1
9	F	0	1
10	G	0	1
19	S	0	4
28	h	0	1
33	n	0	1
36	q	0	1
37	s	0	1
38	t	0	3
All	All	0	16

There are no bond length outliers.

All (279) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	3217	C	N1-C2-O2	13.30	126.88	118.90
1	1	3217	C	N3-C2-O2	-10.79	114.35	121.90
1	1	3217	C	C2-N1-C1'	10.48	130.33	118.80
1	1	406	G	O4'-C1'-N9	9.94	116.15	108.20
1	1	3058	U	N1-C2-O2	9.91	129.74	122.80
1	1	117	U	N1-C2-O2	9.83	129.68	122.80
1	1	117	U	C2-N1-C1'	9.77	129.42	117.70
1	1	102	C	N1-C2-O2	9.69	124.71	118.90
1	1	117	U	N3-C2-O2	-9.58	115.49	122.20
1	1	3162	C	N1-C2-O2	9.40	124.54	118.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	6	223	U	C2-N1-C1'	9.15	128.68	117.70
1	1	3162	C	N3-C2-O2	-9.00	115.60	121.90
1	1	312	C	N3-C2-O2	-8.73	115.79	121.90
1	1	3181	C	C2-N1-C1'	8.58	128.24	118.80
1	1	463	C	N1-C2-O2	8.49	123.99	118.90
3	6	223	U	N3-C2-O2	-8.40	116.32	122.20
1	1	1364	C	N1-C2-O2	8.39	123.93	118.90
1	1	250	U	N1-C2-O2	8.37	128.66	122.80
3	6	223	U	N1-C2-O2	8.36	128.65	122.80
1	1	249	U	C2-N1-C1'	8.33	127.69	117.70
1	1	249	U	N1-C2-O2	8.33	128.63	122.80
1	1	270	U	N3-C2-O2	-8.33	116.37	122.20
1	1	3037	U	N3-C2-O2	-8.29	116.40	122.20
1	1	102	C	N3-C2-O2	-8.27	116.11	121.90
1	1	466	G	N3-C4-N9	8.25	130.95	126.00
1	1	457	C	N3-C2-O2	-8.14	116.20	121.90
1	1	3293	U	N1-C2-O2	8.10	128.47	122.80
1	1	3058	U	N3-C2-O2	-8.02	116.58	122.20
1	1	270	U	N1-C2-O2	7.97	128.38	122.80
1	1	3023	U	N3-C2-O2	-7.85	116.71	122.20
1	1	166	C	N1-C2-O2	7.83	123.60	118.90
1	1	3181	C	N1-C2-O2	7.81	123.59	118.90
1	1	3235	C	N1-C2-O2	7.81	123.59	118.90
1	1	3214	U	N3-C2-O2	-7.79	116.75	122.20
1	1	78	U	N3-C2-O2	-7.72	116.80	122.20
1	1	466	G	C4-N9-C1'	7.55	136.32	126.50
1	1	250	U	N3-C2-O2	-7.53	116.93	122.20
3	6	38	U	N3-C2-O2	-7.46	116.98	122.20
1	1	3058	U	C2-N1-C1'	7.43	126.61	117.70
1	1	667	C	C2-N1-C1'	7.41	126.95	118.80
1	1	250	U	C2-N1-C1'	7.41	126.59	117.70
1	1	3023	U	C2-N1-C1'	7.36	126.53	117.70
3	6	38	U	N1-C2-O2	7.35	127.95	122.80
3	6	40	U	N1-C2-O2	7.34	127.94	122.80
1	1	3217	C	C6-N1-C1'	-7.31	112.03	120.80
1	1	1328	C	N1-C2-O2	7.28	123.27	118.90
1	1	1364	C	N3-C2-O2	-7.25	116.82	121.90
1	1	439	C	N1-C2-O2	7.23	123.24	118.90
1	1	7	C	N1-C2-O2	7.22	123.23	118.90
1	1	251	G	N3-C4-N9	7.17	130.30	126.00
3	6	37	C	N1-C2-O2	7.14	123.19	118.90
1	1	3037	U	N1-C2-O2	7.12	127.78	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	3019	U	C2-N1-C1'	7.10	126.22	117.70
1	1	3019	U	N3-C2-O2	-7.06	117.26	122.20
1	1	3162	C	C6-N1-C2	-7.05	117.48	120.30
1	1	439	C	C2-N1-C1'	7.02	126.52	118.80
1	1	3214	U	C2-N1-C1'	7.01	126.11	117.70
1	1	3214	U	N1-C2-O2	7.00	127.70	122.80
1	1	1425	U	N3-C2-O2	-6.99	117.30	122.20
1	1	1328	C	N3-C2-O2	-6.98	117.01	121.90
12	K	301	LEU	CA-CB-CG	6.97	131.33	115.30
1	1	3293	U	N3-C2-O2	-6.92	117.36	122.20
3	6	37	C	C6-N1-C2	-6.90	117.54	120.30
1	1	3217	C	C6-N1-C2	-6.86	117.56	120.30
2	2	21	C	N1-C2-O2	6.86	123.02	118.90
1	1	3393	U	N3-C2-O2	-6.78	117.45	122.20
1	1	549	U	N1-C2-O2	6.76	127.53	122.80
1	1	3169	U	OP1-P-O3'	6.75	120.06	105.20
3	6	232	A	O4'-C1'-N9	6.73	113.58	108.20
1	1	249	U	N3-C2-O2	-6.72	117.50	122.20
3	6	7	C	O4'-C1'-N1	6.71	113.57	108.20
1	1	7	C	C2-N1-C1'	6.71	126.18	118.80
1	1	667	C	C6-N1-C2	-6.70	117.62	120.30
1	1	251	G	N9-C4-C5	-6.68	102.73	105.40
1	1	3169	U	P-O3'-C3'	6.65	127.68	119.70
1	1	463	C	C2-N1-C1'	6.64	126.10	118.80
1	1	439	C	N3-C2-O2	-6.63	117.26	121.90
1	1	7	C	N3-C2-O2	-6.63	117.26	121.90
3	6	16	U	P-O3'-C3'	6.60	127.62	119.70
1	1	113	C	C2-N1-C1'	6.59	126.05	118.80
1	1	760	G	O4'-C1'-N9	6.59	113.48	108.20
19	S	13	ARG	C-N-CA	6.59	138.17	121.70
1	1	3023	U	N1-C2-O2	6.58	127.40	122.80
1	1	539	C	C5-C6-N1	6.55	124.28	121.00
1	1	549	U	N3-C2-O2	-6.53	117.63	122.20
1	1	466	G	N3-C4-C5	-6.51	125.34	128.60
1	1	1364	C	C2-N1-C1'	6.50	125.95	118.80
1	1	466	G	C6-C5-N7	-6.47	126.52	130.40
1	1	466	G	C8-N9-C1'	-6.46	118.60	127.00
1	1	117	U	C6-N1-C1'	-6.45	112.18	121.20
1	1	3341	U	P-O3'-C3'	6.44	127.43	119.70
1	1	3275	U	OP1-P-O3'	6.44	119.37	105.20
3	6	1	C	N1-C2-O2	6.44	122.76	118.90
1	1	78	U	N1-C2-O2	6.43	127.30	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	410	U	N3-C2-O2	-6.42	117.70	122.20
1	1	3168	A	OP2-P-O3'	6.37	119.20	105.20
1	1	466	G	C4-C5-N7	6.36	113.34	110.80
1	1	1339	C	N3-C2-O2	-6.35	117.45	121.90
3	6	41	G	N3-C4-N9	6.34	129.81	126.00
1	1	3181	C	C6-N1-C1'	-6.32	113.21	120.80
1	1	3235	C	N3-C2-O2	-6.32	117.48	121.90
3	6	56	U	C2-N1-C1'	6.30	125.26	117.70
1	1	257	U	N3-C2-O2	-6.30	117.79	122.20
1	1	743	C	C6-N1-C2	-6.26	117.79	120.30
1	1	270	U	C2-N1-C1'	6.26	125.21	117.70
1	1	480	C	N1-C2-O2	6.25	122.65	118.90
1	1	250	U	C6-N1-C1'	-6.23	112.47	121.20
3	6	16	U	C2-N1-C1'	6.21	125.15	117.70
1	1	1168	U	N1-C2-O2	6.21	127.14	122.80
1	1	3181	C	N3-C2-O2	-6.19	117.57	121.90
1	1	3313	U	N1-C2-O2	6.18	127.12	122.80
1	1	524	U	N1-C2-O2	6.18	127.12	122.80
2	2	21	C	N3-C2-O2	-6.16	117.59	121.90
1	1	245	U	N1-C2-O2	6.14	127.10	122.80
1	1	249	U	C6-N1-C1'	-6.14	112.61	121.20
1	1	1425	U	N1-C2-O2	6.11	127.08	122.80
23	7	69	ASP	CB-CG-OD1	6.11	123.80	118.30
1	1	3306	U	C2-N1-C1'	6.10	125.03	117.70
1	1	3393	U	N1-C2-O2	6.10	127.07	122.80
1	1	1437	C	C6-N1-C2	-6.09	117.86	120.30
1	1	3392	U	N3-C2-O2	-6.08	117.94	122.20
3	6	40	U	N3-C2-O2	-6.08	117.95	122.20
1	1	3300	U	N3-C2-O2	-6.06	117.96	122.20
1	1	667	C	N1-C2-O2	6.05	122.53	118.90
3	6	45	U	N1-C2-O2	6.04	127.03	122.80
3	6	45	U	N3-C2-O2	-6.04	117.97	122.20
1	1	1339	C	N1-C2-O2	6.01	122.51	118.90
3	6	37	C	C5-C6-N1	6.01	124.00	121.00
3	6	59	C	N1-C2-O2	6.00	122.50	118.90
1	1	573	C	C5-C6-N1	5.99	124.00	121.00
2	2	156	U	C2-N1-C1'	5.97	124.86	117.70
1	1	463	C	N3-C2-O2	-5.96	117.73	121.90
2	2	36	G	N7-C8-N9	5.96	116.08	113.10
1	1	308	A	C4-N9-C1'	5.95	137.02	126.30
3	6	26	U	O4'-C1'-N1	5.94	112.95	108.20
1	1	3313	U	C2-N1-C1'	5.92	124.80	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	794	U	N1-C2-O2	5.92	126.94	122.80
1	1	3168	A	P-O3'-C3'	5.91	126.79	119.70
1	1	166	C	C2-N1-C1'	5.90	125.29	118.80
1	1	3162	C	C2-N1-C1'	5.89	125.28	118.80
1	1	3166	C	P-O3'-C3'	5.87	126.74	119.70
1	1	3306	U	N3-C2-O2	-5.86	118.09	122.20
1	1	3392	U	N1-C2-O2	5.86	126.90	122.80
1	1	3293	U	C2-N1-C1'	5.85	124.72	117.70
1	1	163	C	C6-N1-C2	-5.83	117.97	120.30
1	1	761	A	P-O3'-C3'	5.81	126.67	119.70
1	1	251	G	C8-N9-C1'	-5.77	119.50	127.00
3	6	223	U	C6-N1-C1'	-5.75	113.15	121.20
1	1	267	G	O4'-C1'-N9	-5.75	103.60	108.20
1	1	3311	C	N3-C2-O2	-5.73	117.89	121.90
3	6	37	C	N3-C2-O2	-5.73	117.89	121.90
40	v	59	LEU	CA-CB-CG	5.70	128.42	115.30
1	1	312	C	C5-C4-N4	5.67	124.17	120.20
1	1	623	U	N3-C2-O2	-5.67	118.23	122.20
1	1	1399	A	C4-N9-C1'	5.66	136.49	126.30
1	1	263	C	C2-N1-C1'	5.65	125.01	118.80
1	1	537	A	C5-C6-N6	-5.64	119.18	123.70
1	1	1388	U	N3-C2-O2	-5.64	118.25	122.20
1	1	1190	A	C2-N3-C4	5.64	113.42	110.60
1	1	3160	U	N1-C2-O2	5.64	126.75	122.80
2	2	157	U	N3-C2-O2	-5.64	118.25	122.20
1	1	87	U	N1-C2-O2	5.63	126.74	122.80
3	6	229	U	N3-C2-O2	-5.62	118.27	122.20
1	1	87	U	N3-C2-O2	-5.58	118.29	122.20
1	1	312	C	N3-C4-N4	-5.58	114.09	118.00
1	1	182	U	N1-C2-O2	5.58	126.70	122.80
1	1	3037	U	C2-N1-C1'	5.58	124.39	117.70
1	1	537	A	N9-C4-C5	-5.56	103.58	105.80
1	1	166	C	N3-C2-O2	-5.55	118.01	121.90
1	1	1168	U	N3-C2-O2	-5.55	118.31	122.20
1	1	549	U	C2-N1-C1'	5.54	124.35	117.70
3	6	41	G	C5-C6-O6	-5.53	125.28	128.60
1	1	257	U	N1-C2-O2	5.53	126.67	122.80
1	1	430	U	N3-C2-O2	-5.51	118.34	122.20
2	2	100	U	N1-C2-O2	5.47	126.63	122.80
2	2	36	G	C4-C5-N7	5.46	112.99	110.80
3	6	56	U	N1-C2-O2	5.46	126.62	122.80
1	1	3131	U	N1-C2-O2	5.46	126.62	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	21	C	C2-N1-C1'	5.44	124.79	118.80
1	1	3313	U	N3-C2-O2	-5.44	118.39	122.20
1	1	782	U	C2-N1-C1'	5.43	124.22	117.70
1	1	252	U	C5-C6-N1	5.43	125.41	122.70
1	1	2996	U	C2-N1-C1'	5.42	124.20	117.70
1	1	7	C	C6-N1-C2	-5.41	118.14	120.30
1	1	3350	C	C6-N1-C2	-5.41	118.14	120.30
1	1	207	U	N1-C2-O2	5.40	126.58	122.80
1	1	667	C	C5-C6-N1	5.39	123.70	121.00
1	1	1190	A	N3-C4-N9	5.39	131.71	127.40
3	6	16	U	N1-C2-O2	5.39	126.57	122.80
1	1	3160	U	N3-C2-O2	-5.38	118.43	122.20
1	1	3354	U	C2-N1-C1'	5.38	124.15	117.70
1	1	3313	U	C5-C6-N1	5.37	125.39	122.70
3	6	59	C	C2-N1-C1'	5.37	124.70	118.80
1	1	696	C	N3-C2-O2	-5.37	118.14	121.90
1	1	166	C	C5-C6-N1	5.36	123.68	121.00
2	2	11	C	N1-C2-O2	5.36	122.12	118.90
3	6	229	U	N1-C2-O2	5.35	126.55	122.80
1	1	174	C	N1-C2-O2	5.35	122.11	118.90
2	2	102	U	N3-C2-O2	-5.35	118.45	122.20
1	1	3190	C	C5-C6-N1	5.34	123.67	121.00
1	1	457	C	C6-N1-C2	-5.34	118.17	120.30
1	1	753	C	C6-N1-C2	-5.33	118.17	120.30
1	1	382	U	N3-C2-O2	-5.33	118.47	122.20
1	1	3019	U	N1-C2-O2	5.33	126.53	122.80
1	1	308	A	N7-C8-N9	5.32	116.46	113.80
1	1	1190	A	C4-N9-C1'	5.31	135.85	126.30
1	1	1437	C	C5-C6-N1	5.30	123.65	121.00
2	2	36	G	C5-N7-C8	-5.30	101.65	104.30
3	6	223	U	C5-C6-N1	5.30	125.35	122.70
1	1	102	C	C2-N1-C1'	5.29	124.62	118.80
1	1	463	C	C5-C6-N1	5.29	123.64	121.00
1	1	3350	C	N1-C2-O2	5.29	122.07	118.90
1	1	480	C	C6-N1-C2	-5.29	118.19	120.30
1	1	548	G	N1-C6-O6	5.28	123.07	119.90
3	6	1	C	N3-C2-O2	-5.28	118.20	121.90
1	1	466	G	C5-C6-O6	-5.28	125.43	128.60
1	1	3173	G	N3-C4-N9	5.26	129.16	126.00
1	1	452	G	C4-C5-N7	5.26	112.90	110.80
1	1	939	U	N1-C2-O2	5.26	126.48	122.80
1	1	430	U	N1-C2-O2	5.25	126.47	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	1399	A	C8-N9-C1'	-5.24	118.27	127.70
1	1	493	G	P-O3'-C3'	5.22	125.97	119.70
2	2	139	U	N3-C2-O2	-5.22	118.55	122.20
1	1	304	G	C5-C6-O6	5.22	131.73	128.60
1	1	1452	A	N3-C4-N9	5.21	131.57	127.40
1	1	1399	A	N3-C4-N9	5.21	131.57	127.40
2	2	102	U	N1-C2-O2	5.20	126.44	122.80
1	1	251	G	C4-C5-N7	5.20	112.88	110.80
1	1	3104	U	N3-C2-O2	-5.20	118.56	122.20
1	1	308	A	C8-N9-C1'	-5.20	118.34	127.70
1	1	480	C	N3-C2-O2	-5.20	118.26	121.90
1	1	539	C	C6-N1-C2	-5.19	118.22	120.30
1	1	3300	U	N1-C2-O2	5.19	126.43	122.80
1	1	753	C	C5-C6-N1	5.19	123.59	121.00
3	6	56	U	N3-C2-O2	-5.19	118.57	122.20
1	1	101	G	C4-N9-C1'	5.18	133.23	126.50
1	1	2359	C	C5-C6-N1	5.18	123.59	121.00
1	1	113	C	C5-C6-N1	5.17	123.58	121.00
1	1	3350	C	P-O3'-C3'	5.16	125.89	119.70
1	1	1452	A	N9-C4-C5	-5.14	103.74	105.80
1	1	3131	U	C2-N1-C1'	5.14	123.87	117.70
13	L	46	ILE	CG1-CB-CG2	-5.14	100.10	111.40
1	1	743	C	N3-C2-O2	-5.13	118.31	121.90
1	1	3131	U	C5-C6-N1	5.13	125.27	122.70
1	1	113	C	N1-C2-O2	5.13	121.98	118.90
1	1	3081	C	N1-C2-O2	5.13	121.98	118.90
1	1	543	C	C5-C6-N1	5.12	123.56	121.00
1	1	414	U	C5-C6-N1	5.12	125.26	122.70
1	1	126	U	N3-C2-O2	-5.12	118.62	122.20
3	6	5	C	C2-N1-C1'	5.11	124.42	118.80
1	1	782	U	C5-C6-N1	5.11	125.25	122.70
1	1	3265	C	C2-N1-C1'	5.09	124.40	118.80
1	1	3055	U	C5-C6-N1	5.09	125.24	122.70
1	1	3363	U	N3-C2-O2	-5.09	118.64	122.20
28	h	92	LEU	CA-CB-CG	5.08	126.99	115.30
3	6	41	G	N3-C4-C5	-5.08	126.06	128.60
13	L	54	LEU	CA-CB-CG	5.08	126.98	115.30
1	1	439	C	C6-N1-C1'	-5.07	114.72	120.80
1	1	3251	U	N1-C2-O2	5.07	126.35	122.80
1	1	251	G	C4-N9-C1'	5.07	133.09	126.50
1	1	463	C	C6-N1-C2	-5.06	118.28	120.30
1	1	627	U	N3-C2-O2	-5.06	118.66	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	515	C	C6-N1-C2	-5.05	118.28	120.30
1	1	1333	C	C2-N1-C1'	5.05	124.35	118.80
1	1	3099	C	C6-N1-C2	-5.04	118.28	120.30
1	1	3181	C	O4'-C1'-N1	5.04	112.24	108.20
1	1	177	U	C5-C6-N1	5.04	125.22	122.70
1	1	794	U	N3-C2-O2	-5.04	118.67	122.20
1	1	3058	U	C6-N1-C1'	-5.04	114.15	121.20
1	1	251	G	C6-C5-N7	-5.04	127.38	130.40
1	1	435	C	N3-C2-O2	-5.04	118.38	121.90
1	1	3173	G	C4-N9-C1'	5.02	133.03	126.50
1	1	309	U	P-O3'-C3'	5.02	125.72	119.70
1	1	1396	C	N1-C2-O2	5.01	121.91	118.90
1	1	3217	C	C5-C6-N1	5.01	123.50	121.00
1	1	3351	U	P-O3'-C3'	5.01	125.71	119.70
1	1	466	G	N7-C8-N9	5.01	115.60	113.10
1	1	3306	U	N1-C2-O2	5.00	126.30	122.80
21	W	445	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	185	ALA	Peptide
4	A	53	ILE	Peptide
7	D	56	ASP	Peptide
9	F	158	LYS	Peptide
10	G	76	ALA	Peptide
19	S	12	ARG	Peptide
19	S	13	ARG	Peptide
19	S	22	PRO	Peptide
19	S	83	SER	Peptide
28	h	83	LYS	Peptide
33	n	175	LEU	Peptide
36	q	344	UNK	Peptide
37	s	337	UNK	Peptide
38	t	150	PRO	Peptide
38	t	223	GLU	Peptide
38	t	245	ILE	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	390/463 (84%)	368 (94%)	22 (6%)	0	100	100
5	B	320/387 (83%)	302 (94%)	18 (6%)	0	100	100
6	C	310/362 (86%)	285 (92%)	23 (7%)	2 (1%)	25	62
7	D	188/306 (61%)	177 (94%)	11 (6%)	0	100	100
8	E	168/176 (96%)	158 (94%)	10 (6%)	0	100	100
9	F	240/244 (98%)	225 (94%)	15 (6%)	0	100	100
10	G	185/256 (72%)	170 (92%)	14 (8%)	1 (0%)	29	66
11	I	286/295 (97%)	272 (95%)	14 (5%)	0	100	100
12	K	256/376 (68%)	243 (95%)	13 (5%)	0	100	100
13	L	104/199 (52%)	96 (92%)	7 (7%)	1 (1%)	15	51
14	M	126/138 (91%)	123 (98%)	3 (2%)	0	100	100
15	N	172/204 (84%)	162 (94%)	10 (6%)	0	100	100
16	O	180/199 (90%)	173 (96%)	7 (4%)	0	100	100
17	P	118/184 (64%)	113 (96%)	5 (4%)	0	100	100
18	Q	130/186 (70%)	128 (98%)	2 (2%)	0	100	100
19	S	169/172 (98%)	154 (91%)	15 (9%)	0	100	100
20	V	120/137 (88%)	115 (96%)	5 (4%)	0	100	100
21	W	96/647 (15%)	94 (98%)	2 (2%)	0	100	100
22	Y	124/127 (98%)	118 (95%)	6 (5%)	0	100	100
23	7	152/231 (66%)	137 (90%)	15 (10%)	0	100	100
24	8	96/434 (22%)	96 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	b	220/291 (76%)	207 (94%)	13 (6%)	0	100	100
26	e	110/130 (85%)	106 (96%)	4 (4%)	0	100	100
27	f	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
28	h	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
29	i	82/100 (82%)	78 (95%)	4 (5%)	0	100	100
30	j	70/88 (80%)	66 (94%)	4 (6%)	0	100	100
33	n	333/605 (55%)	322 (97%)	11 (3%)	0	100	100
34	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
35	p	433/505 (86%)	422 (98%)	11 (2%)	0	100	100
37	s	82/807 (10%)	77 (94%)	5 (6%)	0	100	100
38	t	244/322 (76%)	220 (90%)	23 (9%)	1 (0%)	34	69
39	u	127/199 (64%)	127 (100%)	0	0	100	100
40	v	221/453 (49%)	207 (94%)	14 (6%)	0	100	100
41	w	68/250 (27%)	64 (94%)	4 (6%)	0	100	100
42	y	224/245 (91%)	214 (96%)	10 (4%)	0	100	100
43	z	239/278 (86%)	228 (95%)	11 (5%)	0	100	100
All	All	6735/10443 (64%)	6380 (95%)	350 (5%)	5 (0%)	54	83

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	268	ALA
6	C	292	SER
13	L	63	VAL
10	G	127	PRO
38	t	56	VAL

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	
4	A	352/410 (86%)	352 (100%)	0	100	100
5	B	272/323 (84%)	271 (100%)	1 (0%)	91	95
6	C	257/289 (89%)	253 (98%)	4 (2%)	62	80
7	D	171/274 (62%)	170 (99%)	1 (1%)	86	93
8	E	149/153 (97%)	148 (99%)	1 (1%)	84	91
9	F	204/205 (100%)	203 (100%)	1 (0%)	88	94
10	G	152/208 (73%)	150 (99%)	2 (1%)	69	83
11	I	271/276 (98%)	268 (99%)	3 (1%)	73	85
12	K	241/346 (70%)	240 (100%)	1 (0%)	91	95
13	L	85/159 (54%)	84 (99%)	1 (1%)	71	84
14	M	100/109 (92%)	100 (100%)	0	100	100
15	N	153/176 (87%)	151 (99%)	2 (1%)	69	83
16	O	150/162 (93%)	148 (99%)	2 (1%)	69	83
17	P	100/146 (68%)	99 (99%)	1 (1%)	76	86
18	Q	108/151 (72%)	106 (98%)	2 (2%)	57	76
19	S	155/156 (99%)	153 (99%)	2 (1%)	69	83
20	V	94/105 (90%)	94 (100%)	0	100	100
21	W	87/573 (15%)	82 (94%)	5 (6%)	20	52
22	Y	109/110 (99%)	108 (99%)	1 (1%)	78	88
23	7	141/205 (69%)	141 (100%)	0	100	100
24	8	90/388 (23%)	90 (100%)	0	100	100
25	b	203/247 (82%)	200 (98%)	3 (2%)	65	81
26	e	97/111 (87%)	97 (100%)	0	100	100
27	f	90/91 (99%)	90 (100%)	0	100	100
28	h	104/105 (99%)	103 (99%)	1 (1%)	76	86
29	i	70/82 (85%)	70 (100%)	0	100	100
30	j	60/71 (84%)	59 (98%)	1 (2%)	60	79
33	n	309/548 (56%)	308 (100%)	1 (0%)	92	96
34	o	118/199 (59%)	118 (100%)	0	100	100
35	p	381/440 (87%)	377 (99%)	4 (1%)	76	86
37	s	77/653 (12%)	76 (99%)	1 (1%)	69	83
38	t	219/287 (76%)	216 (99%)	3 (1%)	67	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	u	114/180 (63%)	111 (97%)	3 (3%)	46 69
40	v	208/413 (50%)	208 (100%)	0	100 100
41	w	63/219 (29%)	62 (98%)	1 (2%)	62 80
42	y	194/211 (92%)	194 (100%)	0	100 100
43	z	225/257 (88%)	224 (100%)	1 (0%)	91 95
All	All	5973/9038 (66%)	5924 (99%)	49 (1%)	82 89

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	332	ARG
6	C	3	ARG
6	C	93	MET
6	C	221	ASN
6	C	288	ARG
7	D	11	ASN
8	E	51	ARG
9	F	244	ASN
10	G	85	ASN
10	G	204	ARG
11	I	30	ARG
11	I	82	MET
11	I	88	ASN
12	K	248	LEU
13	L	101	ARG
15	N	20	ARG
15	N	195	ASN
16	O	85	ARG
16	O	148	LYS
17	P	97	ASN
18	Q	144	ARG
18	Q	145	ASN
19	S	12	ARG
19	S	119	ARG
21	W	374	ARG
21	W	384	ASN
21	W	413	ASN
21	W	415	ASN
21	W	445	LEU
22	Y	51	ARG

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Mol	Chain	Res	Type
25	b	46	ARG
25	b	99	LEU
25	b	109	THR
28	h	105	ARG
30	j	67	LEU
33	n	445	ASN
35	p	112	ARG
35	p	113	ASN
35	p	153	ASN
35	p	413	ASN
37	s	264	ARG
38	t	57	ARG
38	t	74	ARG
38	t	322	ASN
39	u	45	ASN
39	u	82	ASN
39	u	100	ARG
41	w	221	ASN
43	z	115	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (93) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	34	HIS
4	A	75	HIS
4	A	152	ASN
4	A	332	ASN
5	B	173	GLN
6	C	45	ASN
6	C	48	GLN
6	C	110	ASN
6	C	114	ASN
6	C	307	GLN
7	D	11	ASN
7	D	96	HIS
7	D	110	GLN
8	E	57	HIS
9	F	37	ASN
9	F	61	ASN
9	F	172	ASN
9	F	244	ASN
10	G	59	GLN

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Mol	Chain	Res	Type
10	G	95	ASN
10	G	137	ASN
11	I	55	ASN
11	I	88	ASN
11	I	100	ASN
11	I	102	ASN
11	I	164	HIS
11	I	228	GLN
12	K	245	ASN
12	K	295	GLN
13	L	37	ASN
14	M	105	GLN
15	N	37	HIS
15	N	194	GLN
15	N	195	ASN
16	O	29	ASN
16	O	50	ASN
16	O	55	HIS
17	P	10	ASN
17	P	45	GLN
17	P	54	HIS
17	P	97	ASN
18	Q	145	ASN
19	S	8	GLN
19	S	74	ASN
19	S	89	ASN
21	W	384	ASN
21	W	413	ASN
21	W	415	ASN
22	Y	120	GLN
23	7	48	GLN
23	7	49	ASN
23	7	209	GLN
24	8	322	GLN
25	b	45	HIS
25	b	75	ASN
25	b	82	ASN
25	b	118	HIS
25	b	158	HIS
25	b	175	HIS
26	e	52	GLN
27	f	42	GLN

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Mol	Chain	Res	Type
28	h	59	ASN
29	i	91	ASN
29	i	92	ASN
33	n	160	GLN
33	n	189	GLN
33	n	445	ASN
34	o	199	ASN
35	p	69	GLN
35	p	141	HIS
35	p	153	ASN
35	p	166	ASN
35	p	266	GLN
35	p	287	ASN
35	p	330	ASN
35	p	397	ASN
35	p	413	ASN
35	p	441	GLN
39	u	45	ASN
39	u	73	GLN
39	u	82	ASN
40	v	38	HIS
40	v	137	ASN
40	v	171	ASN
41	w	221	ASN
42	y	79	GLN
42	y	106	ASN
42	y	162	HIS
42	y	178	GLN
43	z	13	ASN
43	z	20	ASN
43	z	43	ASN
43	z	63	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1343/3395 (39%)	352 (26%)	28 (2%)
2	2	157/158 (99%)	35 (22%)	3 (1%)
3	6	85/232 (36%)	44 (51%)	5 (5%)
All	All	1585/3785 (41%)	431 (27%)	36 (2%)

All (431) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	U
1	1	7	C
1	1	12	A
1	1	13	A
1	1	14	U
1	1	18	G
1	1	26	A
1	1	31	C
1	1	57	A
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	73	C
1	1	77	A
1	1	92	G
1	1	93	C
1	1	96	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	113	C
1	1	116	A
1	1	117	U
1	1	118	U
1	1	120	G
1	1	121	A
1	1	122	A
1	1	135	C
1	1	136	G
1	1	143	G
1	1	146	U
1	1	150	A
1	1	155	G
1	1	156	G
1	1	161	G
1	1	163	C
1	1	165	A
1	1	166	C
1	1	167	U
1	1	169	U
1	1	170	G
1	1	173	G

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Mol	Chain	Res	Type
1	1	187	A
1	1	190	U
1	1	191	U
1	1	192	C
1	1	199	A
1	1	206	G
1	1	207	U
1	1	210	U
1	1	211	A
1	1	218	G
1	1	219	A
1	1	231	G
1	1	240	U
1	1	241	G
1	1	243	G
1	1	248	U
1	1	249	U
1	1	250	U
1	1	251	G
1	1	252	U
1	1	253	A
1	1	258	G
1	1	265	A
1	1	266	A
1	1	267	G
1	1	269	G
1	1	295	A
1	1	307	A
1	1	308	A
1	1	309	U
1	1	310	U
1	1	311	C
1	1	314	U
1	1	323	A
1	1	329	U
1	1	332	C
1	1	333	G
1	1	334	A
1	1	339	C
1	1	346	C
1	1	350	C
1	1	352	A

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Mol	Chain	Res	Type
1	1	354	U
1	1	374	A
1	1	375	A
1	1	376	G
1	1	385	A
1	1	388	G
1	1	395	A
1	1	396	A
1	1	397	A
1	1	398	A
1	1	399	A
1	1	401	U
1	1	402	A
1	1	403	C
1	1	404	G
1	1	410	U
1	1	421	G
1	1	422	A
1	1	423	A
1	1	430	U
1	1	438	A
1	1	439	C
1	1	440	A
1	1	453	C
1	1	454	C
1	1	463	C
1	1	465	U
1	1	466	G
1	1	467	U
1	1	468	G
1	1	478	A
1	1	479	U
1	1	481	U
1	1	494	G
1	1	503	C
1	1	510	G
1	1	516	A
1	1	517	G
1	1	520	U
1	1	521	A
1	1	523	A
1	1	530	G

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Mol	Chain	Res	Type
1	1	534	U
1	1	535	G
1	1	543	C
1	1	546	C
1	1	547	G
1	1	548	G
1	1	551	A
1	1	552	G
1	1	555	U
1	1	556	U
1	1	557	A
1	1	559	A
1	1	569	A
1	1	578	A
1	1	579	G
1	1	599	C
1	1	600	G
1	1	604	G
1	1	607	A
1	1	609	G
1	1	611	A
1	1	619	A
1	1	621	A
1	1	627	U
1	1	652	G
1	1	677	A
1	1	681	U
1	1	690	A
1	1	691	A
1	1	725	G
1	1	726	G
1	1	728	G
1	1	735	A
1	1	749	C
1	1	750	G
1	1	756	U
1	1	757	C
1	1	762	U
1	1	763	G
1	1	764	U
1	1	765	C
1	1	766	U

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Mol	Chain	Res	Type
1	1	767	U
1	1	770	G
1	1	771	A
1	1	775	A
1	1	776	U
1	1	777	U
1	1	779	G
1	1	780	A
1	1	781	G
1	1	785	G
1	1	801	A
1	1	944	C
1	1	951	A
1	1	1158	A
1	1	1159	A
1	1	1172	G
1	1	1178	G
1	1	1179	A
1	1	1180	A
1	1	1181	U
1	1	1185	C
1	1	1192	C
1	1	1193	A
1	1	1313	G
1	1	1316	C
1	1	1330	A
1	1	1331	U
1	1	1345	G
1	1	1348	U
1	1	1349	G
1	1	1350	A
1	1	1351	U
1	1	1352	A
1	1	1353	U
1	1	1354	G
1	1	1355	A
1	1	1386	A
1	1	1391	C
1	1	1392	G
1	1	1399	A
1	1	1400	G
1	1	1404	G

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Mol	Chain	Res	Type
1	1	1408	G
1	1	1417	G
1	1	1418	A
1	1	1419	A
1	1	1421	G
1	1	1434	G
1	1	1435	A
1	1	1436	U
1	1	1437	C
1	1	1446	A
1	1	1448	U
1	1	1452	A
1	1	1453	A
1	1	1454	A
1	1	1879	A
1	1	1880	U
1	1	1885	U
1	1	1887	A
1	1	2361	A
1	1	2996	U
1	1	2997	G
1	1	3000	A
1	1	3003	G
1	1	3011	A
1	1	3012	A
1	1	3017	A
1	1	3021	A
1	1	3022	G
1	1	3023	U
1	1	3029	A
1	1	3030	G
1	1	3031	G
1	1	3032	A
1	1	3034	C
1	1	3035	A
1	1	3048	A
1	1	3049	A
1	1	3057	U
1	1	3058	U
1	1	3059	G
1	1	3064	U
1	1	3078	U

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Mol	Chain	Res	Type
1	1	3079	U
1	1	3084	C
1	1	3085	G
1	1	3086	A
1	1	3092	C
1	1	3099	C
1	1	3100	U
1	1	3104	U
1	1	3109	G
1	1	3122	A
1	1	3129	A
1	1	3130	A
1	1	3131	U
1	1	3142	A
1	1	3143	C
1	1	3160	U
1	1	3161	C
1	1	3165	A
1	1	3166	C
1	1	3167	A
1	1	3168	A
1	1	3169	U
1	1	3170	A
1	1	3171	U
1	1	3172	A
1	1	3173	G
1	1	3174	A
1	1	3175	U
1	1	3176	G
1	1	3179	U
1	1	3180	A
1	1	3181	C
1	1	3186	A
1	1	3187	A
1	1	3188	G
1	1	3195	U
1	1	3196	U
1	1	3199	G
1	1	3204	C
1	1	3207	U
1	1	3217	C
1	1	3218	A

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Mol	Chain	Res	Type
1	1	3219	G
1	1	3224	G
1	1	3227	A
1	1	3228	C
1	1	3229	G
1	1	3230	G
1	1	3243	A
1	1	3244	A
1	1	3245	A
1	1	3247	G
1	1	3253	G
1	1	3254	G
1	1	3259	U
1	1	3263	G
1	1	3264	G
1	1	3265	C
1	1	3269	U
1	1	3270	U
1	1	3273	A
1	1	3275	U
1	1	3276	G
1	1	3293	U
1	1	3294	A
1	1	3295	A
1	1	3303	G
1	1	3304	U
1	1	3306	U
1	1	3308	C
1	1	3312	U
1	1	3313	U
1	1	3316	A
1	1	3317	U
1	1	3318	G
1	1	3319	U
1	1	3320	A
1	1	3330	A
1	1	3334	U
1	1	3341	U
1	1	3342	A
1	1	3345	G
1	1	3347	A
1	1	3350	C

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Mol	Chain	Res	Type
1	1	3351	U
1	1	3352	U
1	1	3353	G
1	1	3354	U
1	1	3355	U
1	1	3356	G
1	1	3357	U
1	1	3363	U
1	1	3368	U
1	1	3369	G
1	1	3375	A
1	1	3376	A
1	1	3378	C
1	1	3383	G
1	1	3389	U
2	2	16	G
2	2	25	G
2	2	34	U
2	2	35	C
2	2	36	G
2	2	37	A
2	2	39	G
2	2	51	G
2	2	59	A
2	2	62	C
2	2	63	G
2	2	80	A
2	2	81	U
2	2	82	U
2	2	83	C
2	2	84	C
2	2	85	G
2	2	86	U
2	2	87	G
2	2	90	U
2	2	95	G
2	2	100	U
2	2	104	A
2	2	106	C
2	2	111	A
2	2	113	U
2	2	124	G

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Mol	Chain	Res	Type
2	2	125	U
2	2	126	A
2	2	127	U
2	2	138	A
2	2	148	G
2	2	151	C
2	2	152	G
2	2	158	U
3	6	2	C
3	6	4	U
3	6	5	C
3	6	6	U
3	6	7	C
3	6	8	A
3	6	13	U
3	6	14	U
3	6	15	C
3	6	16	U
3	6	17	G
3	6	23	U
3	6	24	A
3	6	25	G
3	6	26	U
3	6	27	G
3	6	33	U
3	6	37	C
3	6	40	U
3	6	41	G
3	6	42	G
3	6	52	G
3	6	53	A
3	6	54	A
3	6	55	A
3	6	56	U
3	6	57	U
3	6	58	G
3	6	59	C
3	6	60	U
3	6	61	G
3	6	63	C
3	6	218	A
3	6	219	A

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Mol	Chain	Res	Type
3	6	220	C
3	6	221	A
3	6	223	U
3	6	224	G
3	6	225	U
3	6	226	U
3	6	228	U
3	6	230	A
3	6	231	A
3	6	232	A

All (36) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	13	A
1	1	239	G
1	1	250	U
1	1	307	A
1	1	309	U
1	1	406	G
1	1	420	G
1	1	452	G
1	1	465	U
1	1	493	G
1	1	761	A
1	1	765	C
1	1	1329	U
1	1	1886	A
1	1	3030	G
1	1	3078	U
1	1	3121	U
1	1	3166	C
1	1	3168	A
1	1	3169	U
1	1	3218	A
1	1	3228	C
1	1	3269	U
1	1	3293	U
1	1	3316	A
1	1	3341	U
1	1	3350	C
1	1	3351	U

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Mol	Chain	Res	Type
2	2	36	G
2	2	123	G
2	2	126	A
3	6	16	U
3	6	25	G
3	6	60	U
3	6	222	A
3	6	225	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)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	q	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	398:UNK	C	400:UNK	N	14.84
1	q	136:UNK	C	137:UNK	N	9.43
1	q	114:UNK	C	115:UNK	N	7.34
1	q	257:UNK	C	259:UNK	N	6.77
1	q	242:UNK	C	247:UNK	N	4.06

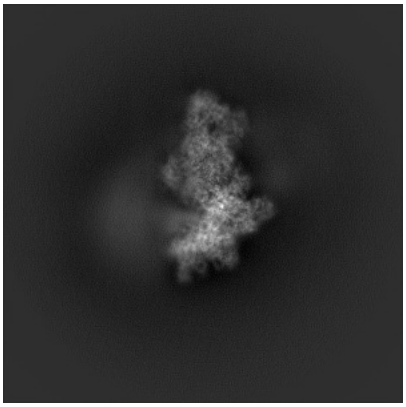
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-7324. These allow visual inspection of the internal detail of the map and identification of artifacts.

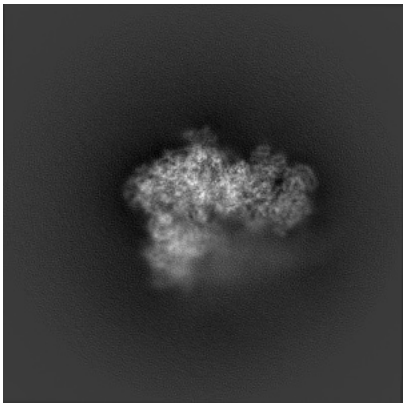
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

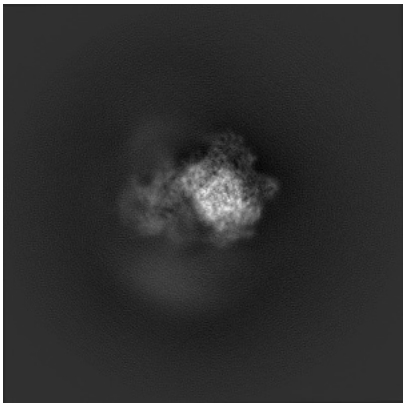
6.1.1 Primary map



X



Y

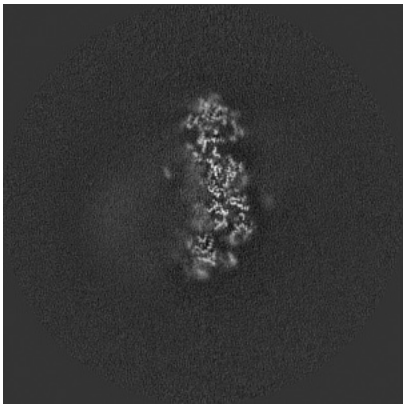


Z

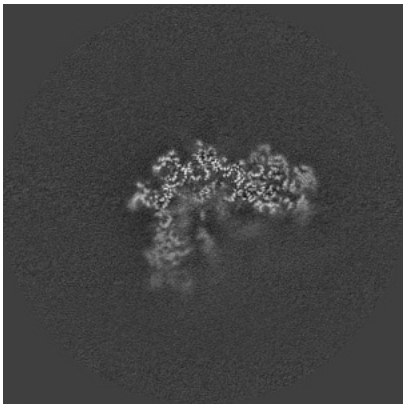
The images above show the map projected in three orthogonal directions.

6.2 Central slices

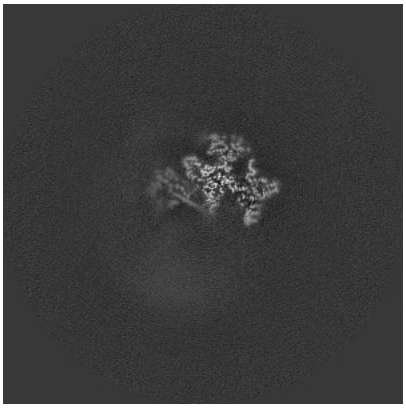
6.2.1 Primary map



X Index: 240



Y Index: 240

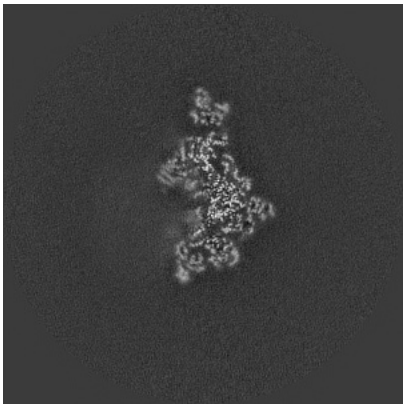


Z Index: 240

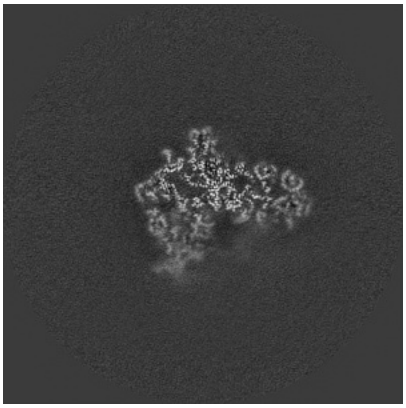
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

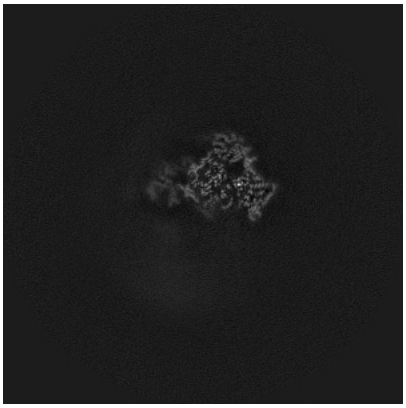
6.3.1 Primary map



X Index: 264



Y Index: 257

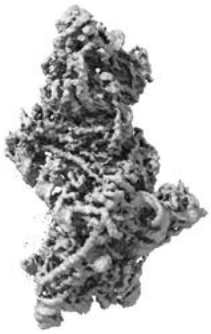


Z Index: 235

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

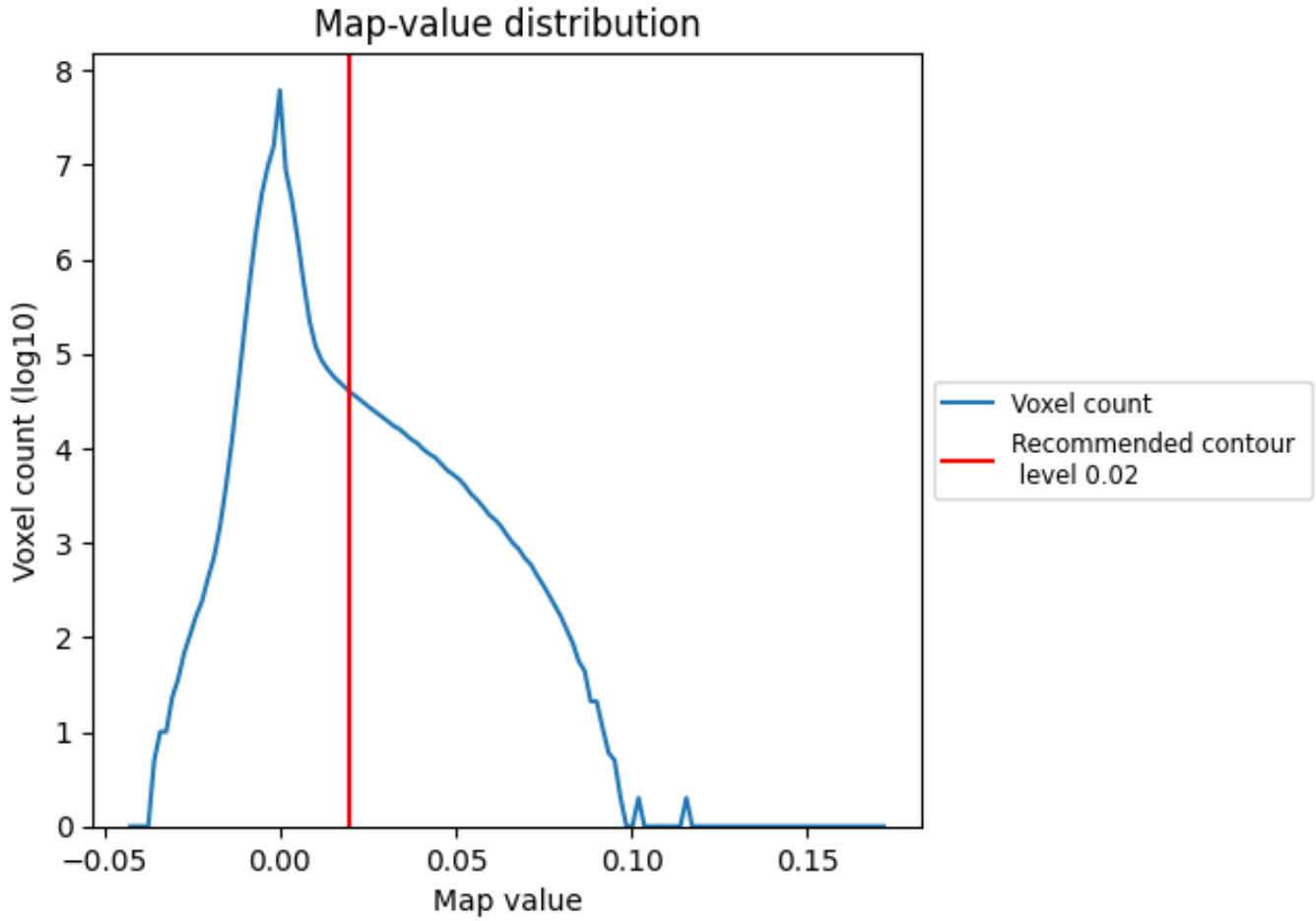
6.5 Mask visualisation (i)

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

7 Map analysis

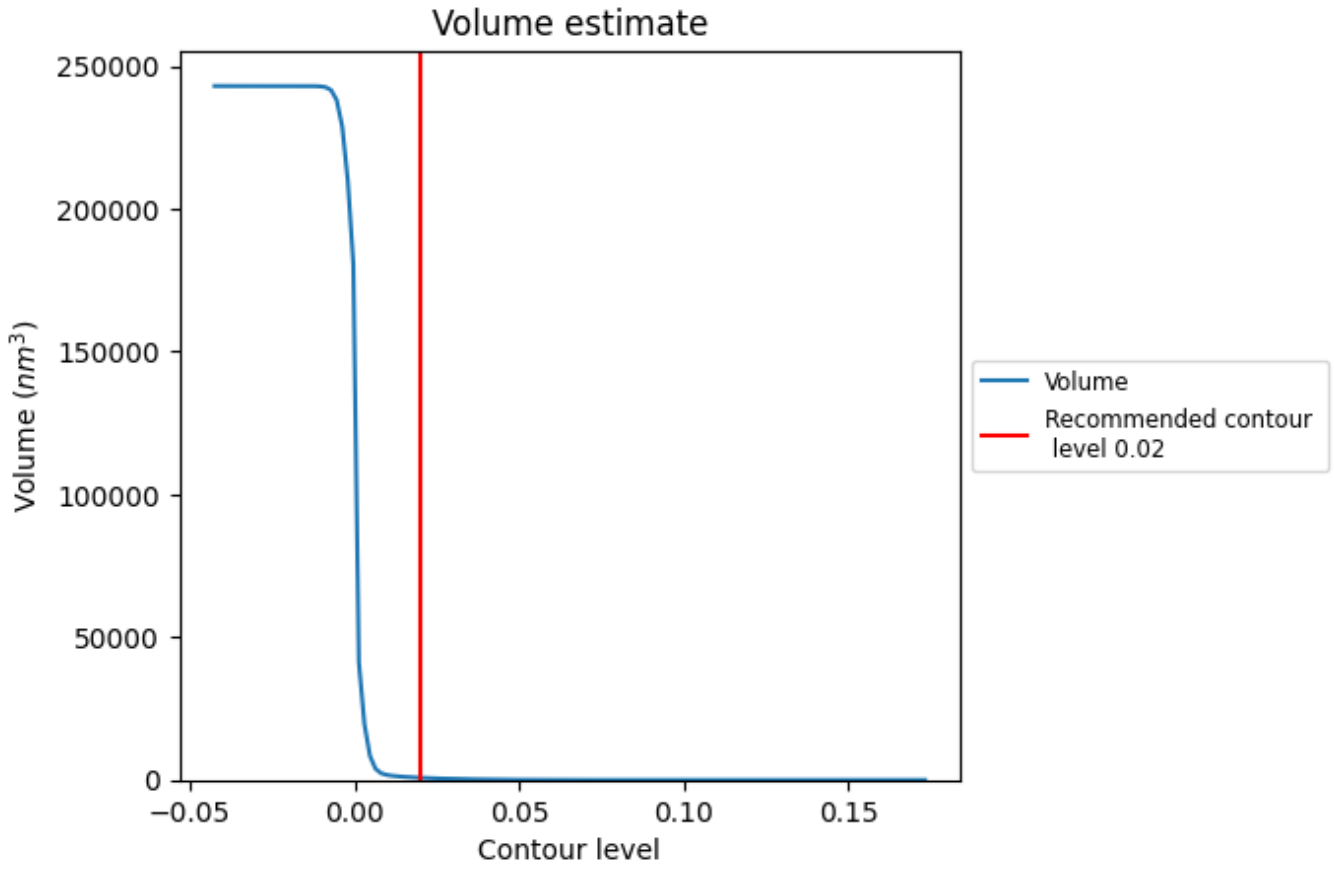
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

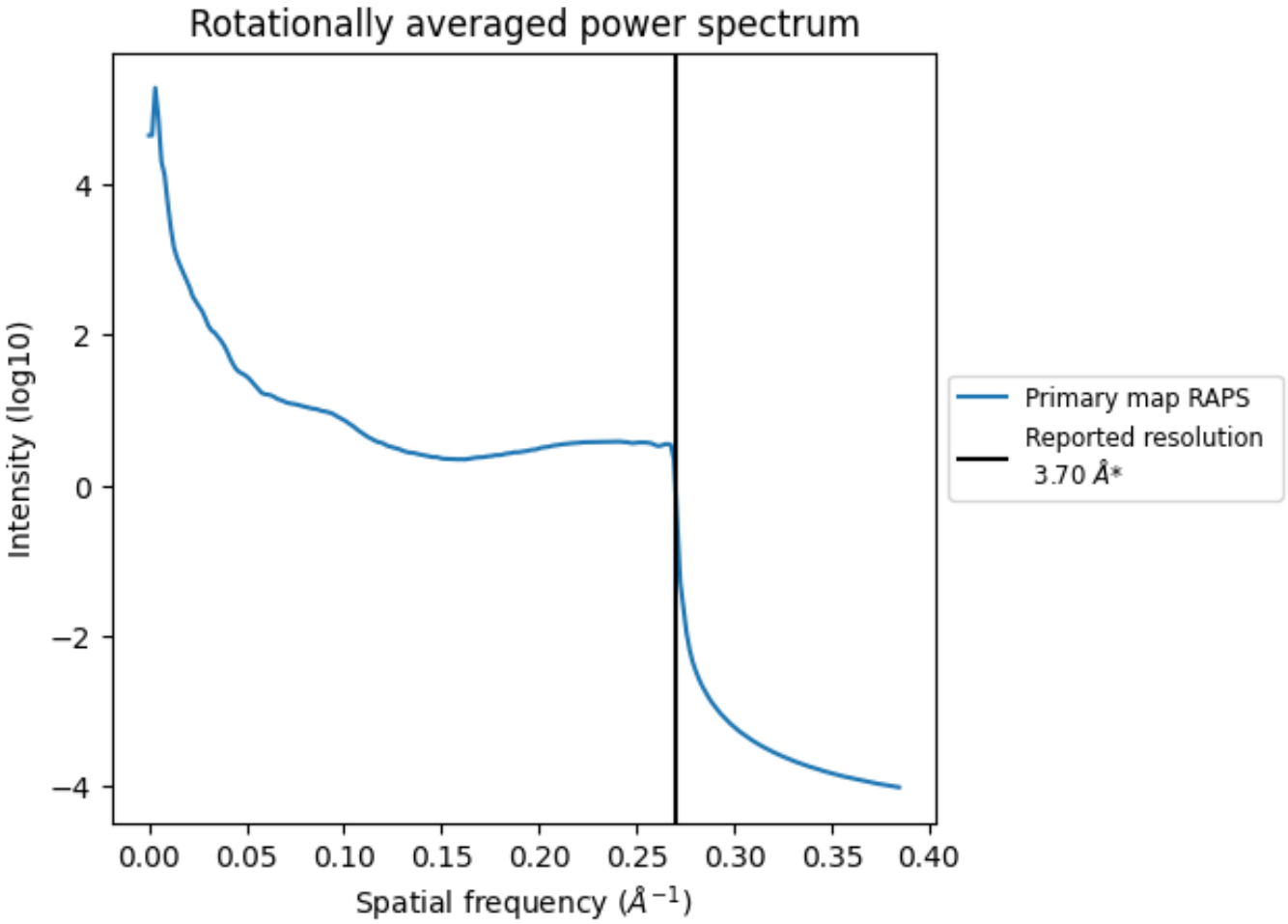
7.2 Volume estimate



The volume at the recommended contour level is 766 nm^3; this corresponds to an approximate mass of 692 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 0.270 Å^{-1}

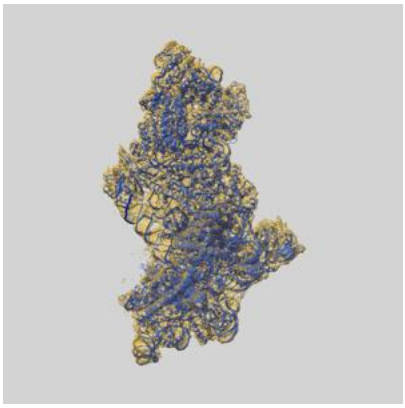
8 Fourier-Shell correlation

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

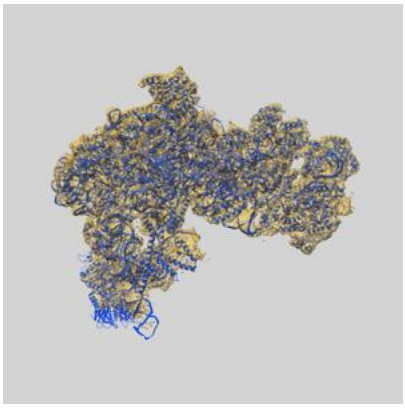
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-7324 and PDB model 6C0F. Per-residue inclusion information can be found in section 3 on page 12.

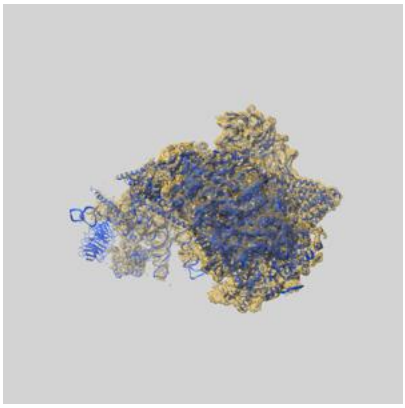
9.1 Map-model overlay



X



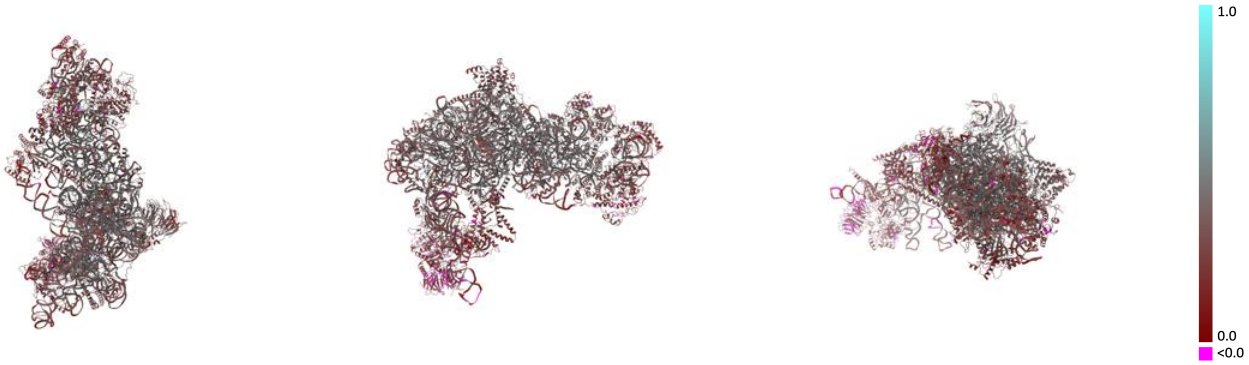
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 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.

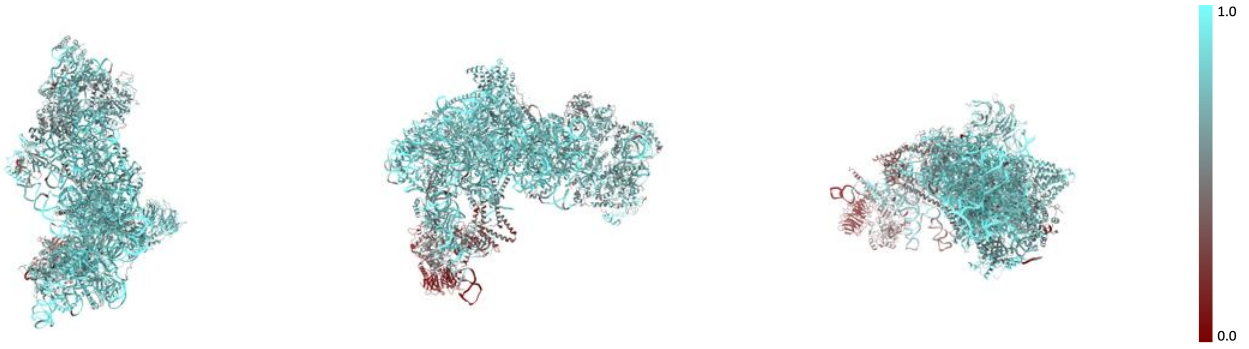
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

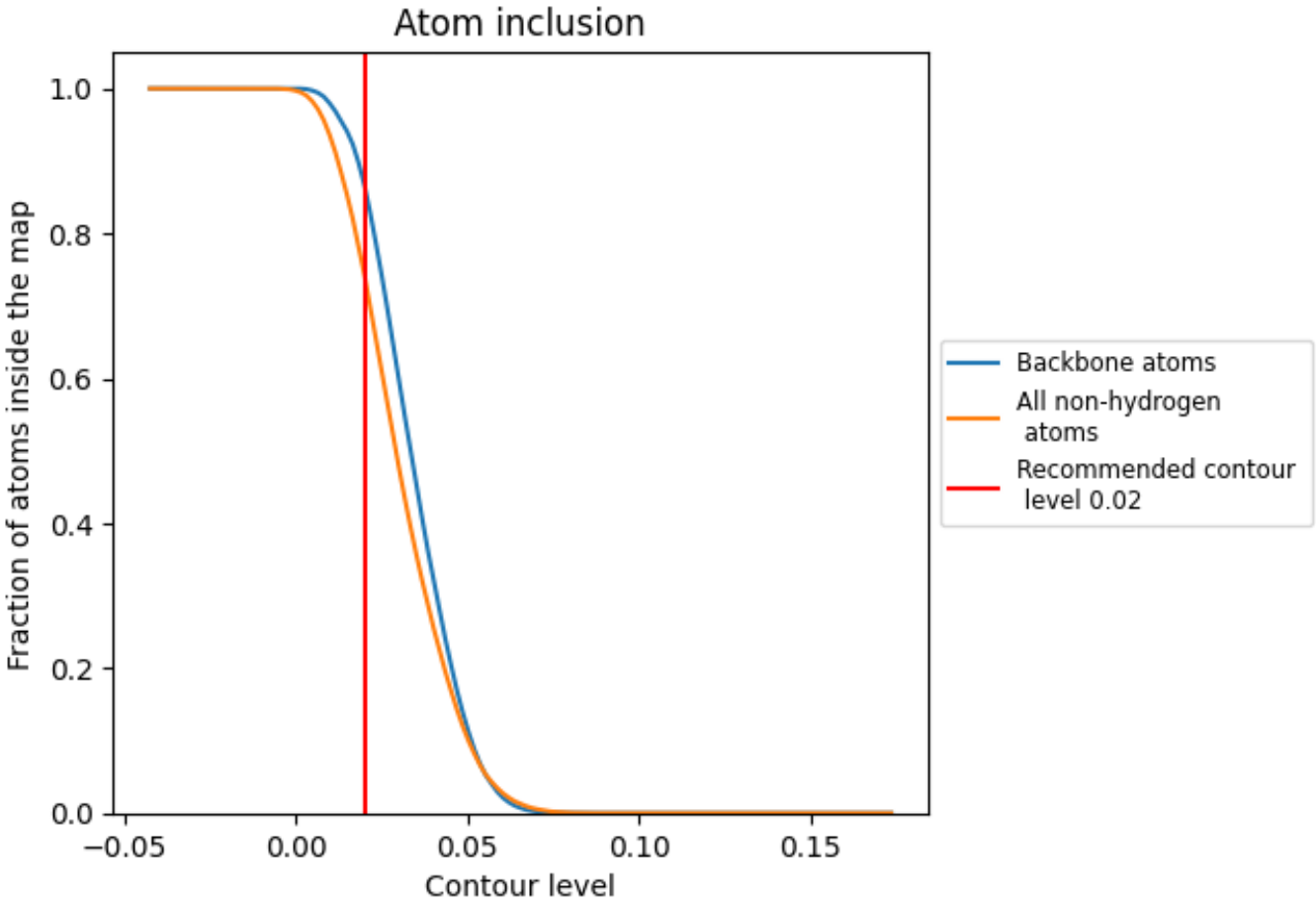
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 86% of all backbone atoms, 74% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7407	0.3390
1	0.8834	0.3610
2	0.8974	0.3760
6	0.9053	0.3320
7	0.6837	0.3700
8	0.3978	0.2320
A	0.7579	0.3680
B	0.6191	0.3050
C	0.8038	0.4470
D	0.8066	0.4120
E	0.7672	0.3790
F	0.7615	0.3610
G	0.7075	0.3880
I	0.7414	0.3890
K	0.6773	0.2960
L	0.8325	0.4340
M	0.7691	0.3460
N	0.7528	0.4110
O	0.7670	0.3700
P	0.7002	0.4030
Q	0.7988	0.4310
S	0.6836	0.2910
V	0.3042	0.2010
W	0.1450	0.1650
Y	0.7888	0.4300
b	0.6940	0.3020
e	0.6756	0.4540
f	0.8112	0.4470
h	0.7010	0.3560
i	0.7042	0.3450
j	0.7591	0.4070
m	0.8541	0.2610
n	0.6678	0.2740
o	0.6848	0.2810
p	0.6211	0.3030

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Chain	Atom inclusion	Q-score
q	0.0021	0.0870
s	0.7210	0.3360
t	0.6751	0.2990
u	0.3824	0.1740
v	0.3599	0.2200
w	0.2849	0.1910
x	0.8786	0.3140
y	0.3613	0.1580
z	0.7754	0.3490