Full wwPDB EM Validation Report (i)

Nov 8, 2022 – 08:32 AM JST

PDB ID	:	5Z3G
EMDB ID	:	EMD-6878
Title	:	Cryo-EM structure of a nucleolar pre-60S ribosome (Rpf1-TAP)
Authors	:	Zhu, X.; Zhou, D.; Ye, K.
Deposited on	:	2018-01-06
Resolution	:	3.65 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 (i) 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 (i)) were used in the production of this report:

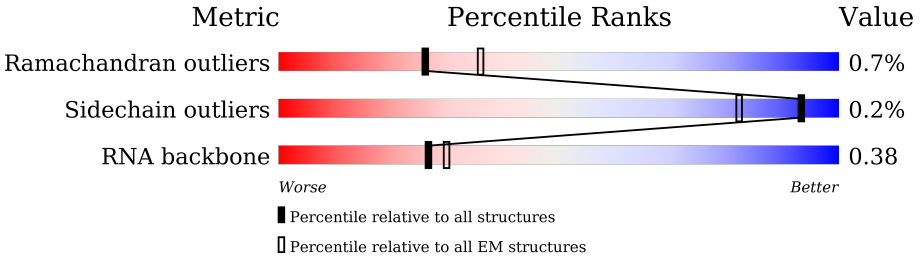
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.65 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	A	3396	7%; 23%; 18%; •; 56%
2	B	158	13%; 54%; 41%; • •
3	C	232	11%; 13%; 14%; •; 72%
4	D	322	55%; 75%; • •; 23%
5	E	220	41%; 60%; •; 40%
6	F	387	49%; 86%; •; 13%
7	G	362	6%; 98%; •
8	H	376	54%; 67%; •; 32%

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Mol	Chain	Length	Quality of chain
9	I	176	85% 15%
10	J	244	94%
11	K	256	14% 63% 37%
12	L	191	94% 98%
13	M	605	55% 60% 39%
14	N	245	90% 92% 8%
15	O	295	9% 62% 36%
16	P	199	52% 46%
17	Q	138	9% 98%
18	R	204	7% 85% 14%
19	S	199	10% 98%
20	T	184	38% 74% 26%
21	U	186	5% 72% 28%
22	V	463	26% 84% 15%
23	W	172	13% 97%
24	X	278	71% 27%
25	Y	505	72% 84% 13%
26	Z	306	53% 45%
27	a	291	70% 72% 27%
28	b	427	19% 19% 81%
29	c	127	96%
30	d	154	38% 99%
31	i	130	94% 5%
32	j	107	99%
33	l	120	18% 95%

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Mol	Chain	Length	Quality of chain
34	m	100	33% 67% 33%
35	n	88	81% 18%

2 Entry composition (i)

There are 35 unique types of molecules in this entry. The entry contains 85899 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 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1501	32146	14349	5813	10483	1501	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	156	3313	1482	582	1093	156	0	0

- Molecule 3 is a RNA chain called ITS2 RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	65	1370	614	228	463	65	0	0

- Molecule 4 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	247	1956	1248	348	357	3	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	336	2670	1696	493	475	6	0	0

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	361	2749	1730	522	494	3	0	0

- Molecule 8 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	256	2063	1332	341	387	3	0	0

- Molecule 9 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	150	1198	775	214	208	1	0	0

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	239	1918	1235	348	334	1	0	0

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	162	1247	804	212	229	2	0	0

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	191	1518	963	274	277	4	0	0

- Molecule 13 is a protein called Nucleolar protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	371	3030	1963	523	534	10	0	0

- Molecule 14 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 15 is a protein called Ribosome production factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	O	190	1591	1031	277	281	2	0	0

- Molecule 16 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	P	108	867	543	182	142	0	0

- Molecule 17 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	137	1059	678	200	179	2	0	0

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	175	1498	940	315	242	1	0	0

- Molecule 19 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	197	1555	1003	289	262	1	0	0

- Molecule 20 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	T	136	1057	663	197	197	0	0

- Molecule 21 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	134	1035	659	196	179	1	0	0

- Molecule 22 is a protein called Ribosome biogenesis protein NSA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	392	3096	1982	522	581	11	0	0

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	W	170	1425	916	265	241	3	0	0

- Molecule 24 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	202	1718	1121	298	295	4	0	0

- Molecule 25 is a protein called ATP-dependent RNA helicase HAS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Y	438	3486	2245	600	629	12	0	0

- Molecule 26 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Z	169	1410	887	269	245	9	0	0

- Molecule 27 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	a	212	1747	1125	309	307	6	0	0

- Molecule 28 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	b	82	689	437	122	129	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	c	125	984	620	191	173	0	0

- Molecule 30 is a protein called Unassigned.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	d	154	770	462	154	154	0	0

- Molecule 31 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	i	124	1001	635	202	163	1	0	0

- Molecule 32 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	l	117	959	609	184	165	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	m	67	533	329	111	92	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L37-A.

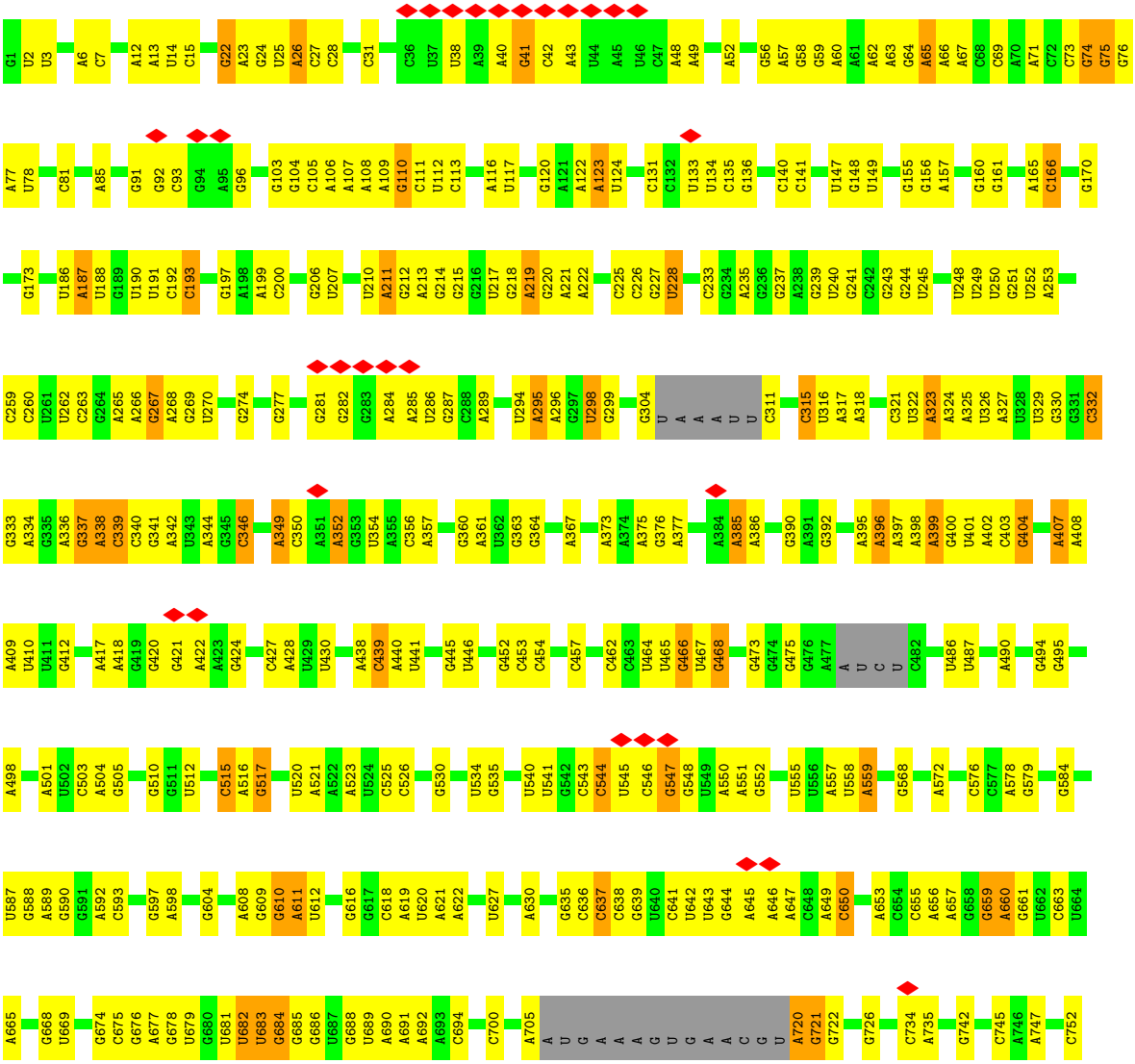
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	n	72	575	350	125	95	5	0	0

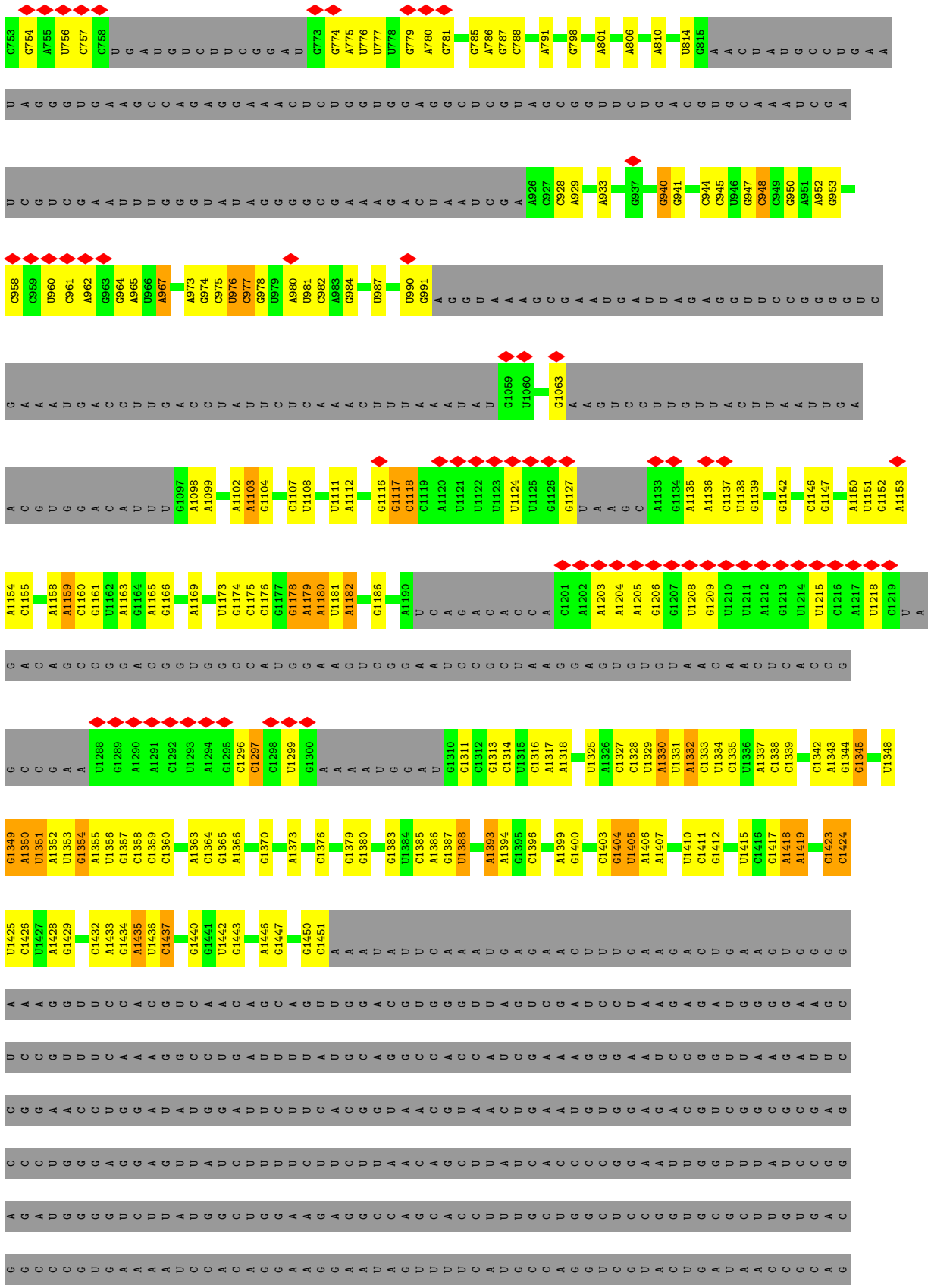
3 Residue-property plots (i)

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: 25S rRNA

Chain A:

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G A A A A U G A C U U G A C C U A U U C U C A A A C U U U A U A G G U C C U G A
A C G U G G A C A U U G A C C U A U U C U C A A A C U U U A U A G G U C C U G A G1059 U1060 G1063 A A G U U C C U U G U U A G A G G U U C A C U U A A U U G A
A C G U G G A C A U U U G1097 A1098 A1099 A1102 A1103 G1104 C1107 U1108 U1111 A1112 G1116 G1117 C1118 C1119 A1120 U1121 U1122 U1123 U1124 U1125 G1126 G1127 U A A G C A1133 G1134 A1135 A1136 C1137 U1138 G1139 G1142 C1146 G1147 A1150 U1151 G1152 A1153
A1154 C1155 A1158 A1159 C1160 G1161 U1162 A1163 G1164 A1165 G1166 A1169 U1173 G1174 C1175 C1176 G1177 G1178 A1179 A1180 U1181 A1182 G1186 A1190 U C A G A C A C C A C1201 A1202 A1203 A1204 A1205 G1206 G1207 U1208 G1209 U1210 U1211 A1212 G1213 U1214 U1215 C1216 A1217 U1218 C1219 U A
G A C A G C C G G A U G G A A G U C G G A A U C C U U G G A G G A G U G U G U A A C A A C A C U C A C C G
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G1349 A1350 U1351 A1352 U1353 G1354 A1355 U1356 G1357 C1358 C1359 C1360 A1363 C1364 G1365 A1366 G1370 A1373 C1376 G1379 G1380 G1383 U1384 C1385 A1386 G1387 U1388 A1393 A1394 G1395 C1396 A1399 G1400 C1403 G1404 U1405 A1406 A1407 U1410 C1411 G1412 U1415 C1416 G1417 A1418 A1419 C1423 C1424
U1425 C1426 U1427 A1428 G1429 C1432 A1433 G1434 A1435 U1436 C1437 G1440 G1441 U1442 G1443 A1446 G1447 G1450 C1451 A A A U A U U C U U C A A A U G G A A G G A A C U U U G A A A C C U G A A G G G G
A A A G U U C U C C A C U C A A A G C A G U U U U U G A A A U A A A G A A U C C U G A A G A U G G G A A G
U C C G U U U C C A U C C U U U U U C A A U U U A A U C C C C G G G G A U U C
C U U G G A C C U U U U U C A C U U A A C A G C U U A U C U U C C U G G A G
C C C G A A C C U G G G G U U U U C A A U C C U U A A U C A C C C C G G G G U C
A G A U G G G G G U C A A U G G G A A G G C A C U U U G G C U C C A A G G G A A G G C U C G G A C
G G C C C U G G A A A A U C C C A A G G G A A U U U C A A U G C C A G G G U C G U A A C U G G A U A A A C C G G C A G
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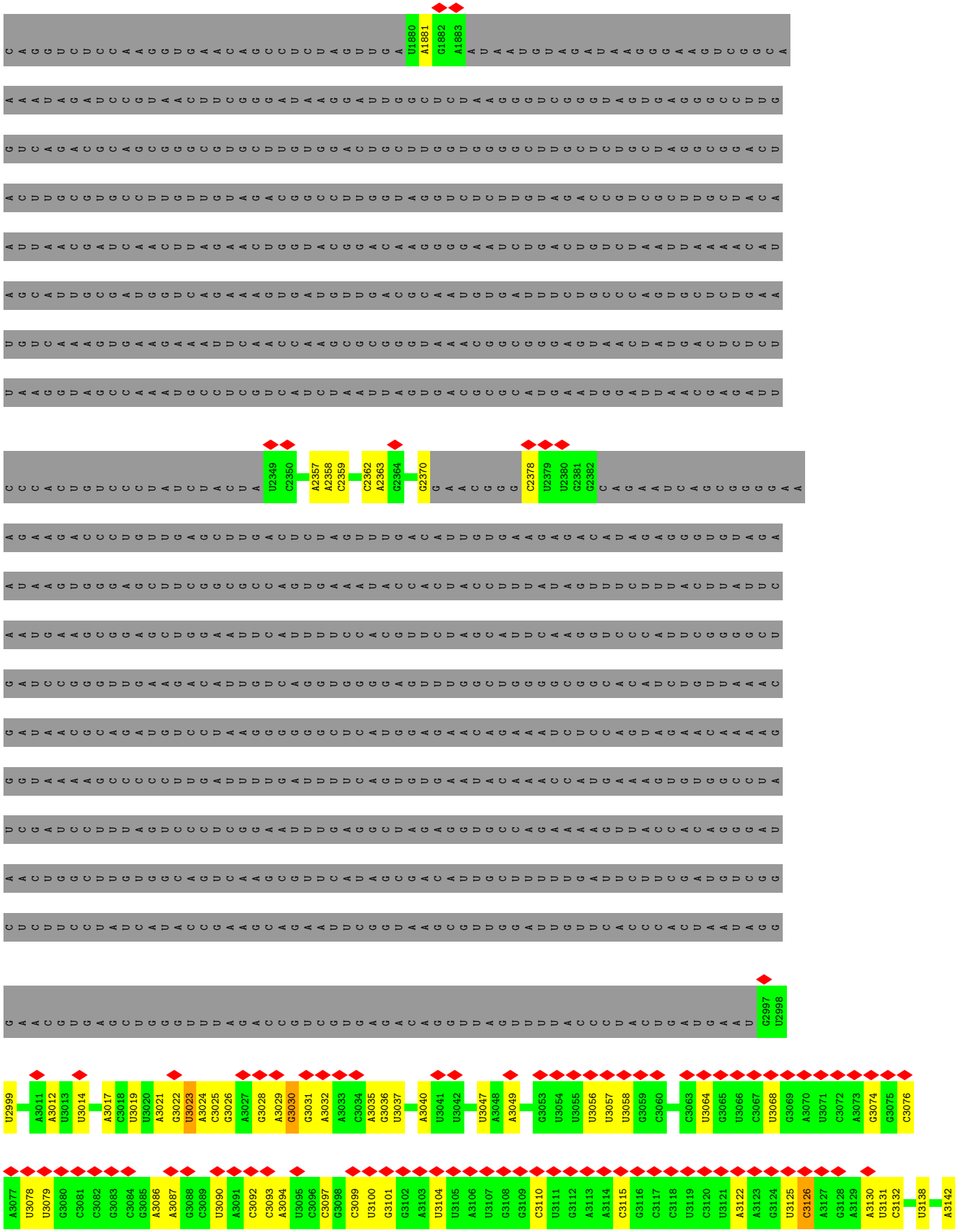
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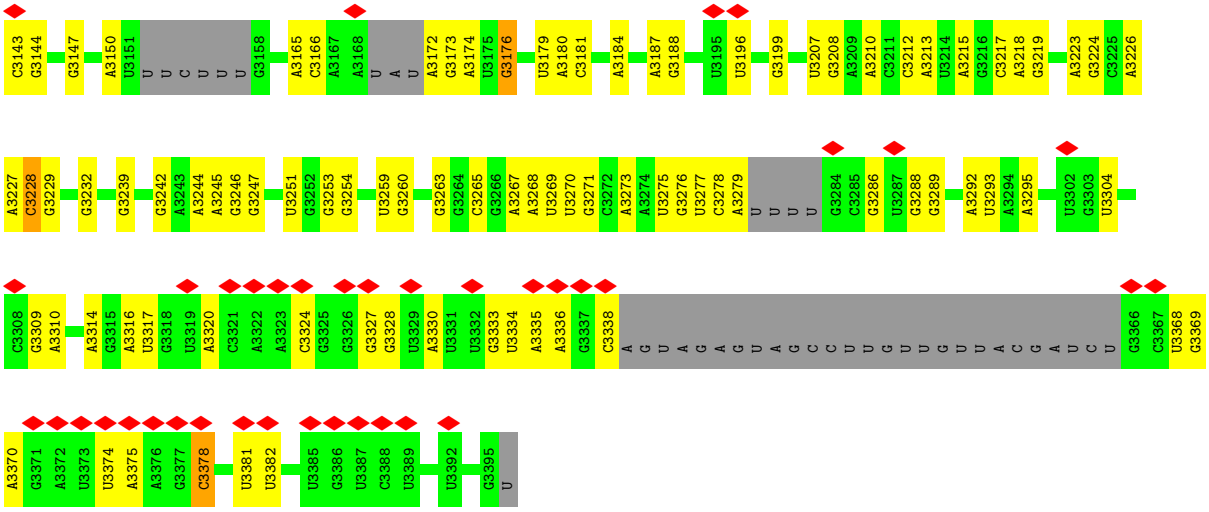
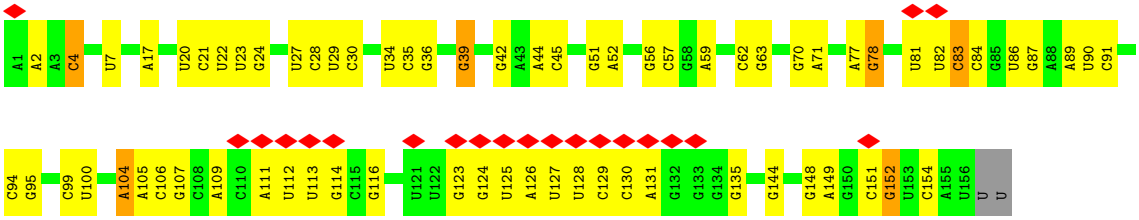


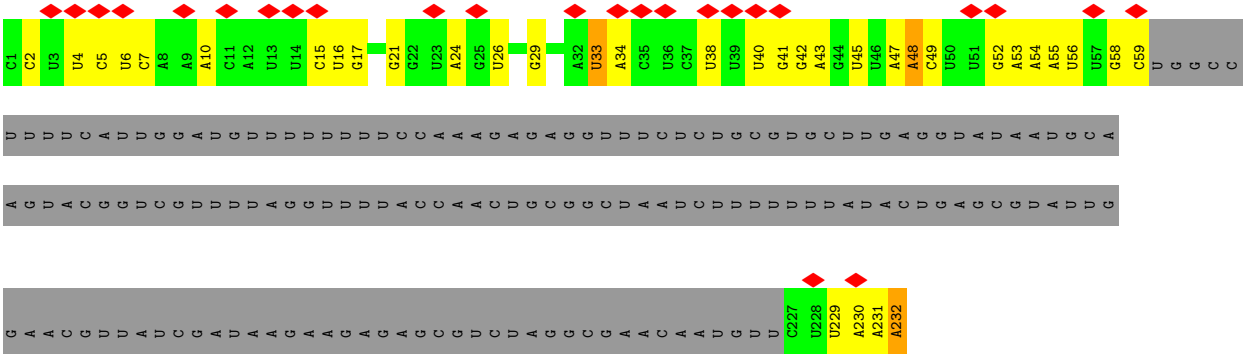
- Molecule 2: 5.8S rRNA

Chain B:



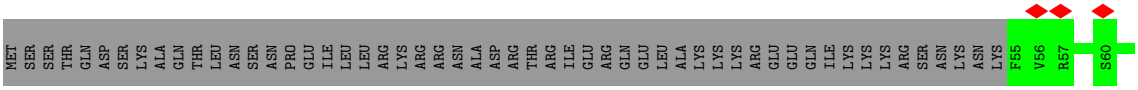
- Molecule 3: ITS2 RNA

Chain C:



- Molecule 4: Ribosome biogenesis protein RLP7

Chain D:



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L128 I129 R130 E131 K132 T133 T134 Y135 D136 G137 K138 P139 A140 L141 L142 F143 I144 V145 R146 V147 R148 L151 K161 T162 L163 S164 L165 L166 R167 L168 V169 E170 T173 G174 V175 F176 V177 K178 L179 T180 L186 L187 K188 V189 I190 V195 I196 G197 K198 P199 S200 S203 I204 R205

S206 L207 I208 Q209 K210 R211 G212 R213 I214 I215 Y216 K217 G218 E219 N220 E221 A222 E223 P224 H225 E226 I227 V228 L229 N230 D231 N232 N233 I234 V235 E236 E237 Q238 L239 G240 D241 H242 G243 I244 I245 C246 V247 E248 D249 I250 I251 H252 E253 I254 A255 T256 M257 G258 E259 S260 F261 S262 V263 C264 N265

F266 P267 L268 Q269 P270 F271 K272 L273 N274 R275 E276 G279 S282 L283 N284 R287 K288 I289 K290 Q291 R292 E293 A294 E295 S296 R297 T298 R299 Q300 F301 S302 N303 A304 A305 T306 A307 I310 E311 V312 D313 I314 D315 S316 L317 L318 A319 K320 L321 N322

- Molecule 5: Ribosome biogenesis protein 15

Chain E:

MET VAL LYS SER THR SER LYS THR SER THR LYS GLU THR VAL THR LYS GLN PRO THR GLU GLU LYS PRO ILE GLN GLU LYS GLU GLU LEU ALA LEU GLU THR SER SER SER SER SER ASP GLU GLU ASP GLU LYS ASP GLU ASP GLU ILE GLU GLY LEU ALA ALA SER ASP ASP GLU GLN

SER GLY THR HIS LYS ILE LYS ARG LEU ASN PRO LYS LYS GLN ALA ASN GLU LYS LYS SER LYS ASP LYS LYS THR LEU GLU E88 Y89 I92 I93 Y94 L98 P99 H100 G101 F102 H103 E104 K105 E106 L107 S108 K109 Y110 F111 A112 Q113 F114 G115 D116 L117 K118 E119 V120 R121 K126

K127 T128 G129 N130 S131 R132 G135 E138 F139 V140 N141 K142 E143 D144 A145 M146 I147 A148 Q149 E150 S151 L156 R165 P168 K169 G170 A171 K172 I173 E174 K180 K181 R182 V183 L184 V185 E186 K187 G188 I189 T190 K191 P192 Y193 K194 Q195 L196 K197 D198 N199 M200 K201 Q202 K203

H204 E205 E206 R207 I208 K209 K210 L211 A212 K213 S214 G215 I216 E217 F218 K219 W220

- Molecule 6: 60S ribosomal protein L3

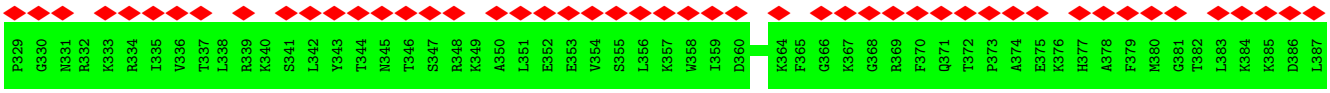
Chain F:

MET SER HIS ARG LYS TYR GLU ALA PRO ARG HIS G12 H13 L14 G15 F16 L17 P18 R19 K20 R21 A22 A23 S24 I25 R26 A27 R28 V29 K30 K34 D35 D36 R37 L43 T44 S45 F46 L47 K50 A51 G52 M53 T54 T55 I56 V57 R58 D59 L60 D61 R62 P63 G64 S65 K66 F67

R70 E71 V72 V73 E74 A75 V76 V79 D80 V84 V85 V86 V87 W106 A107 E108 H109 L110 S111 D112 E113 K124 S125 K126 S134 A138 Q139 D140 G141 I144 E147 S156 L161 I166 R167 K168 T169 P170 L171 A172 Q173 L178 A179 E180 I181 S187

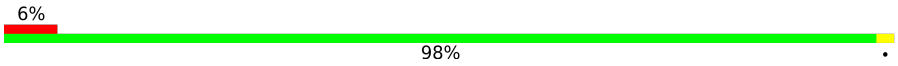
E190 E197 H198 F199 E200 K201 T202 V203 A204 V205 D206 S207 V208 F209 E210 Q211 N212 E213 A217 G223 F226 E227 GLY VAL THR HIS ARG TRP GLY THR LYS LYS LEU PRO ARG LYS THR HIS ARG GLY LEU ARG LYS VAL ALA CYS ILE GLY ALA TRP HIS PRO ALA HIS VAL

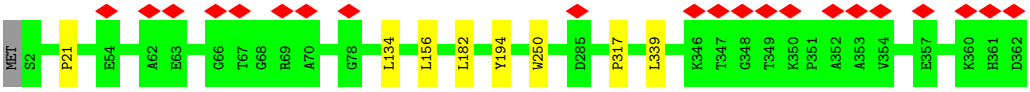
MET TRP SER VAL ALA ARG ALA G268 Q269 R270 G271 S274 R275 T276 S277 I278 N279 H280 K281 I282 Y283 R284 K287 G288 D289 D290 E291 A292 N293 G294 A295 T296 S297 F298 D299 R300 T301 K302 K303 T304 I305 T306 P307 M308 G309 G310 F311 V312 H313 Y314 G315 E316 I317 D320 F321 I322



- Molecule 7: 60S ribosomal protein L4-A

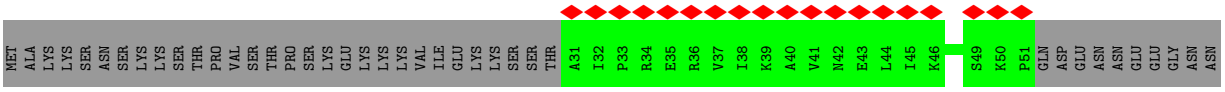
Chain G:

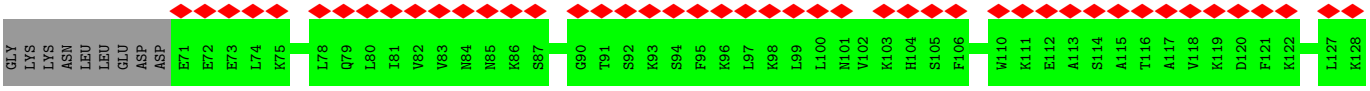


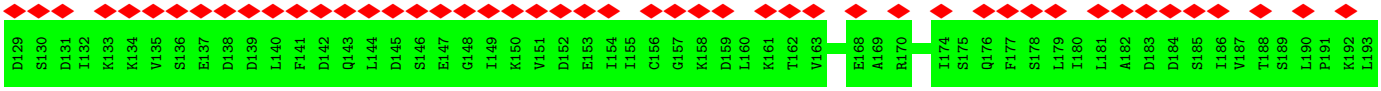


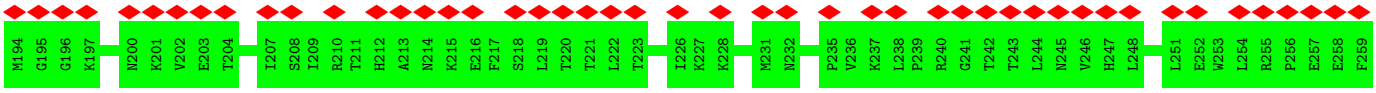
- Molecule 8: Proteasome-interacting protein CIC1

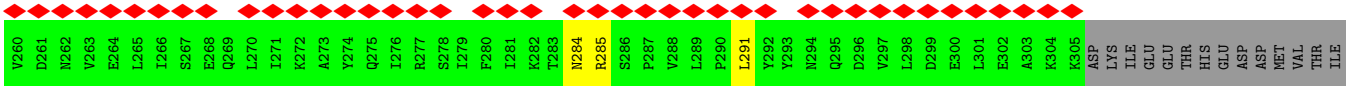
Chain H:





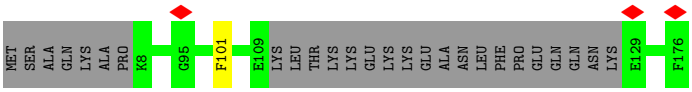






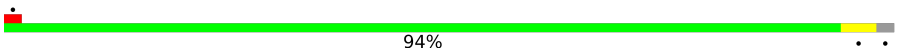
- Molecule 9: 60S ribosomal protein L6-A

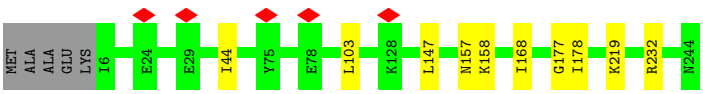
Chain I:



- Molecule 10: 60S ribosomal protein L7-A

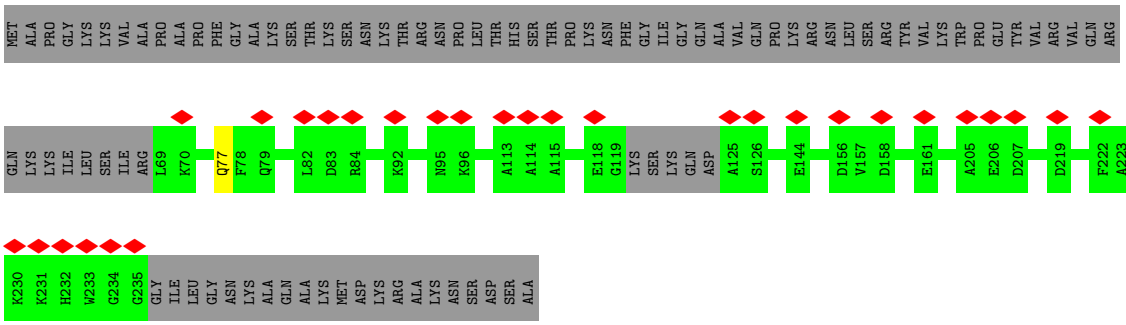
Chain J:





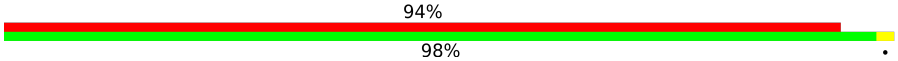
- Molecule 11: 60S ribosomal protein L8-A

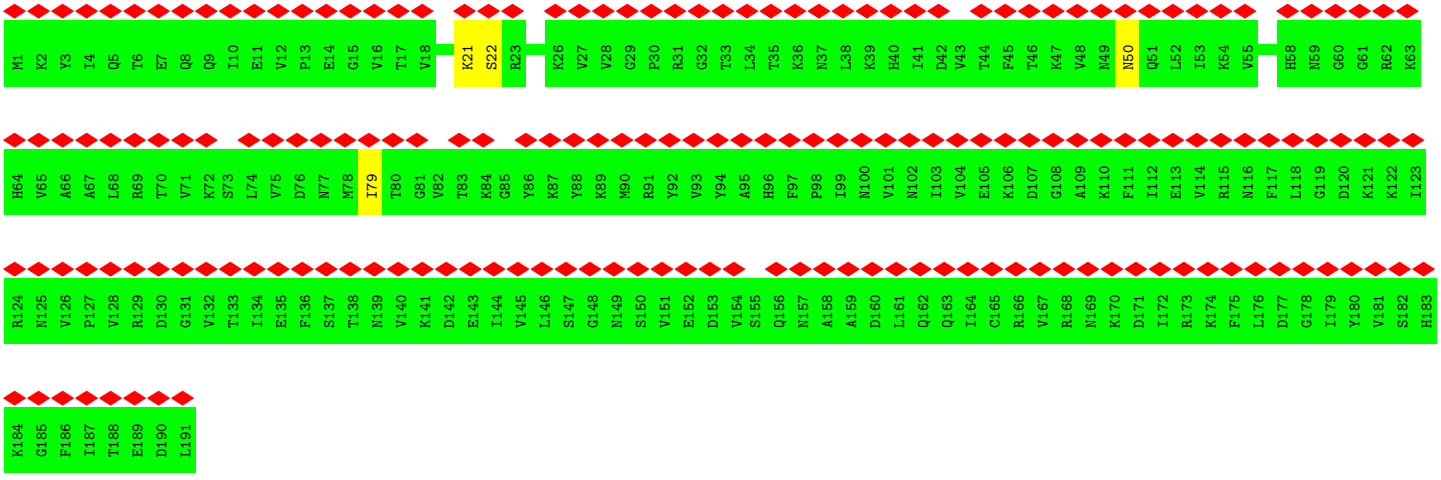
Chain K:



- Molecule 12: 60S ribosomal protein L9-A

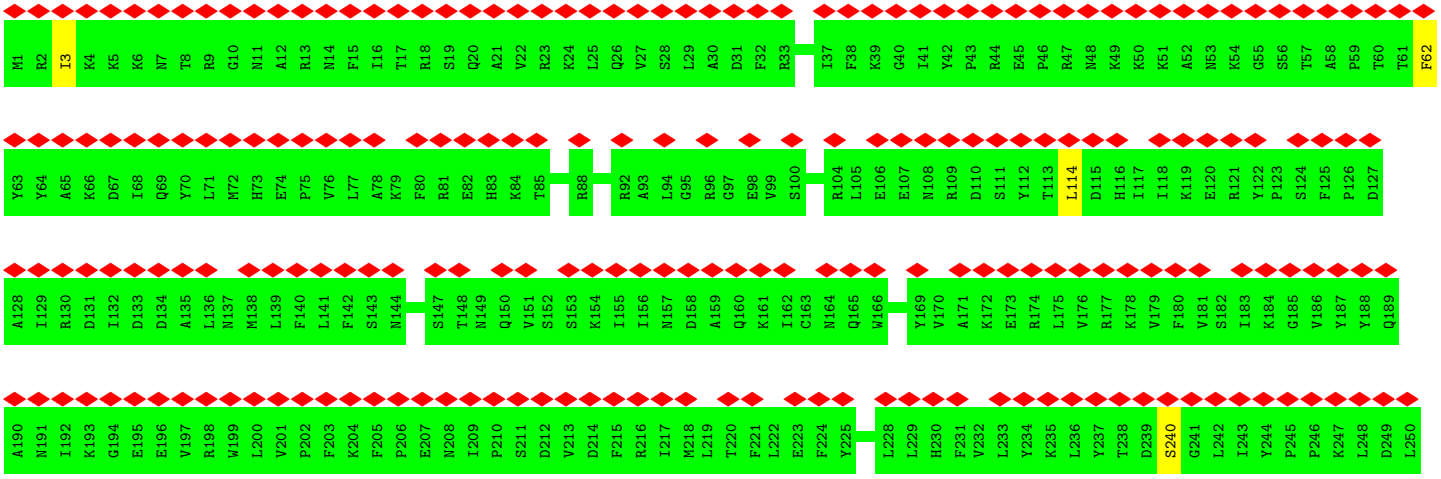
Chain L:

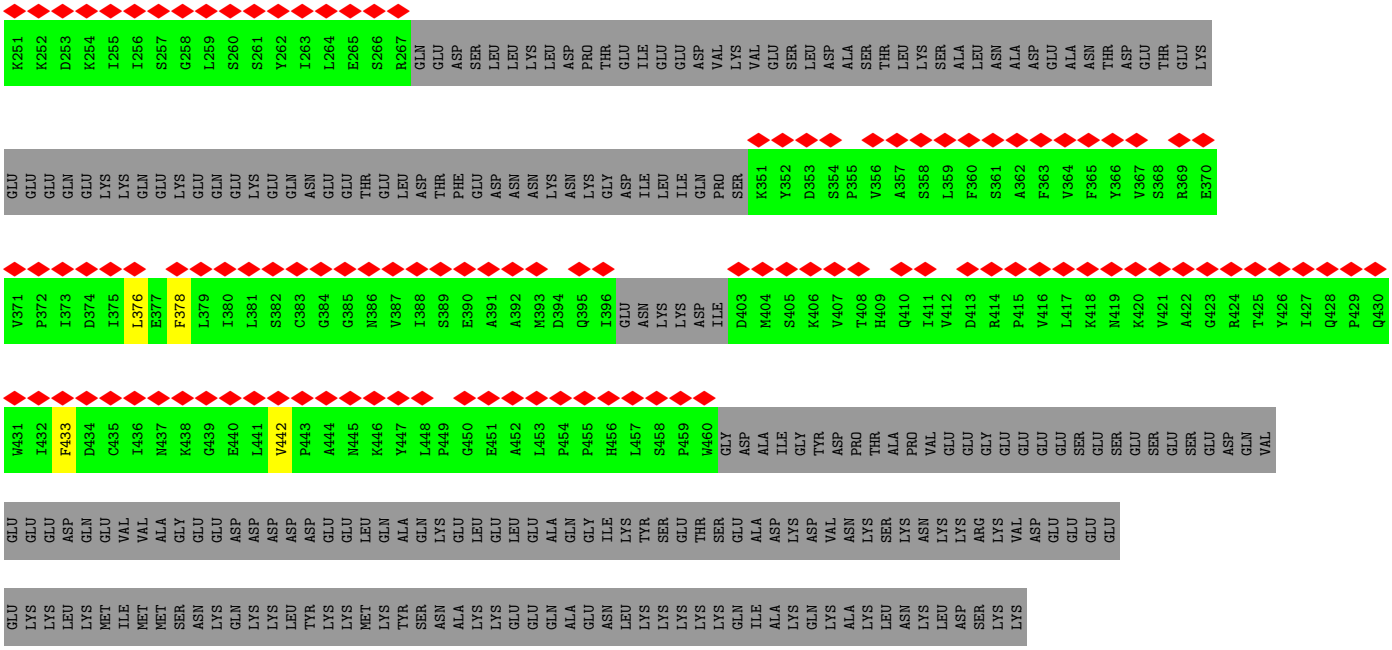




- Molecule 13: Nucleolar protein 7

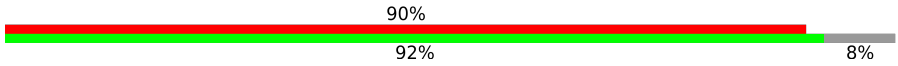
Chain M:

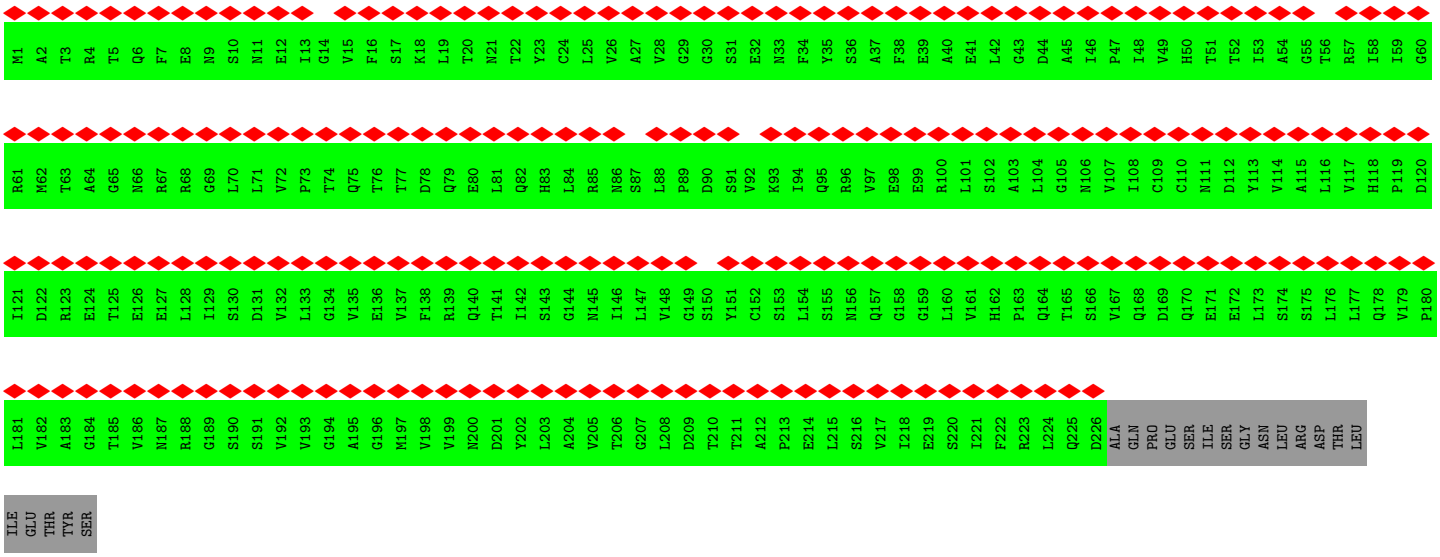




- Molecule 14: Eukaryotic translation initiation factor 6

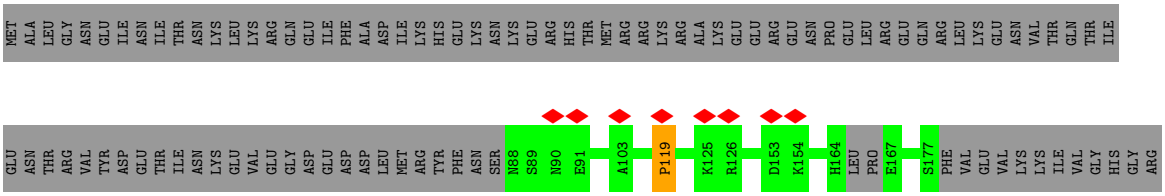
Chain N:

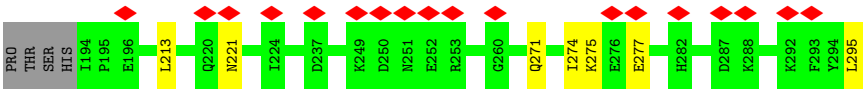




- Molecule 15: Ribosome production factor 1

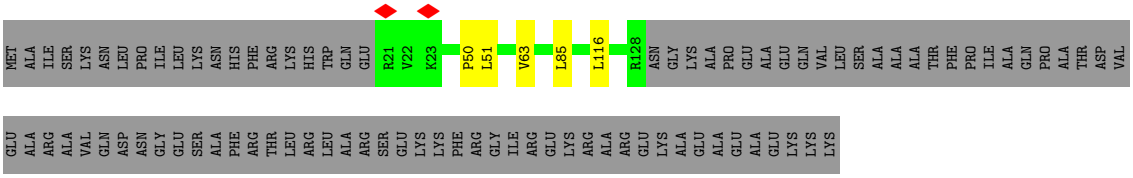
Chain O:





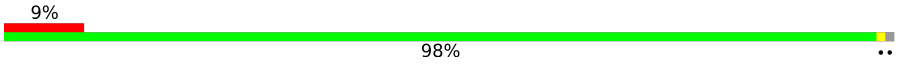
• Molecule 16: 60S ribosomal protein L13-A

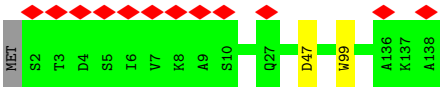
Chain P:



• Molecule 17: 60S ribosomal protein L14-A

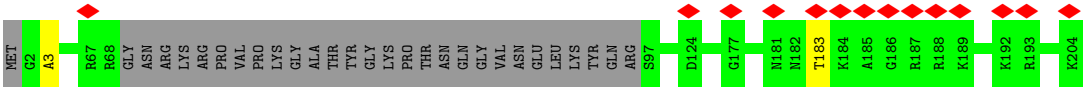
Chain Q:





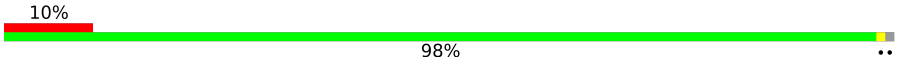
• Molecule 18: 60S ribosomal protein L15-A

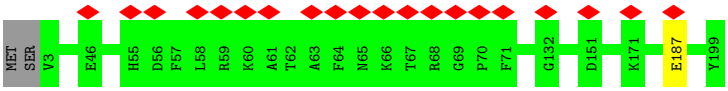
Chain R:



• Molecule 19: 60S ribosomal protein L16-A

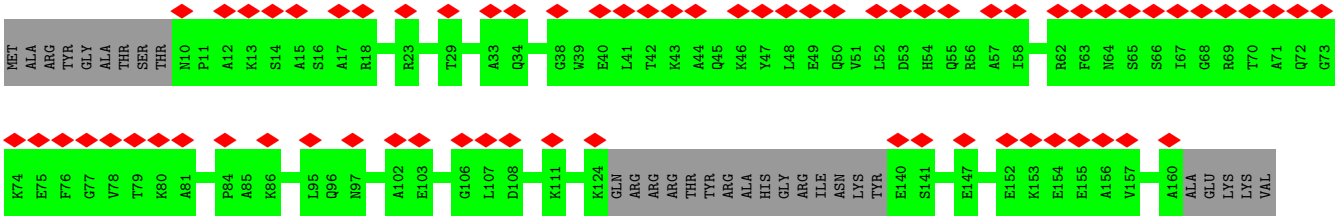
Chain S:





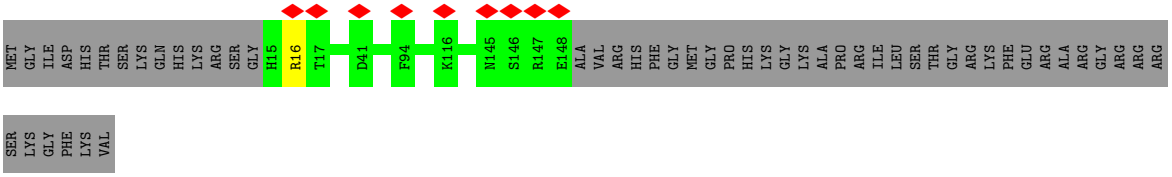
• Molecule 20: 60S ribosomal protein L17-A

Chain T:



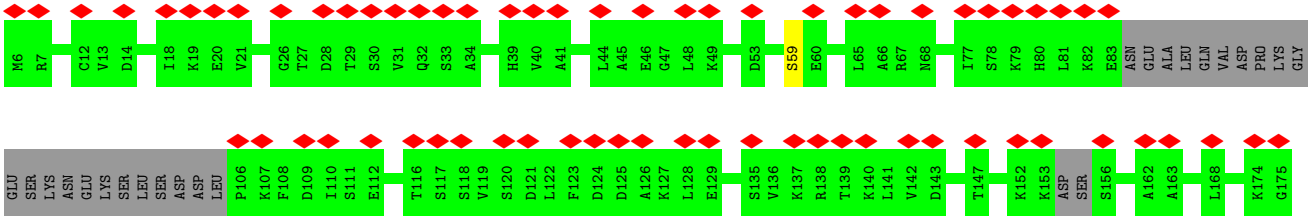
• Molecule 21: 60S ribosomal protein L18-A

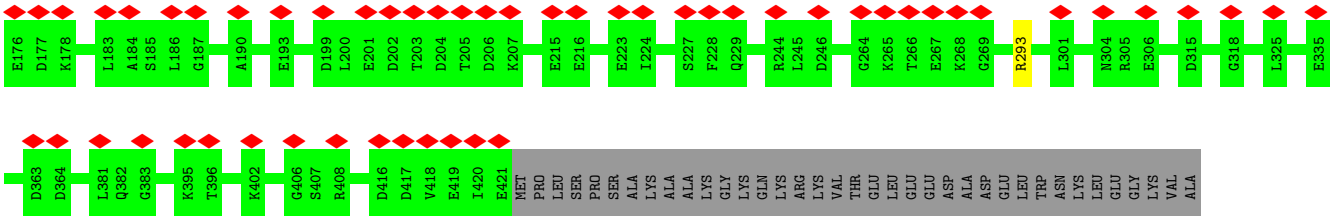
Chain U:

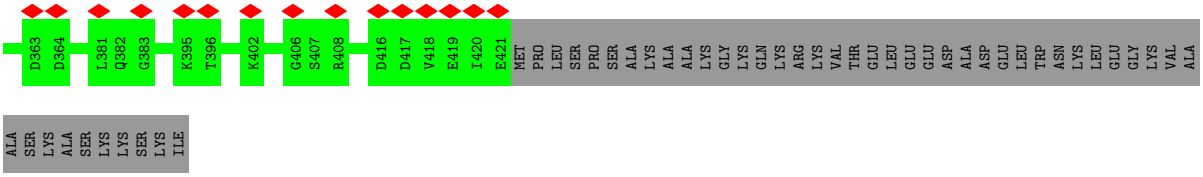


• Molecule 22: Ribosome biogenesis protein NSA1

Chain V:

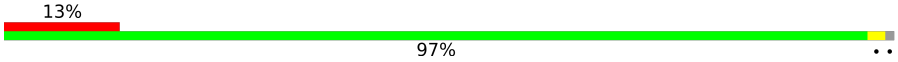


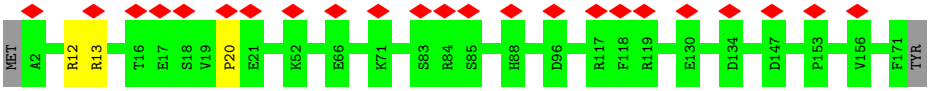




• Molecule 23: 60S ribosomal protein L20-A

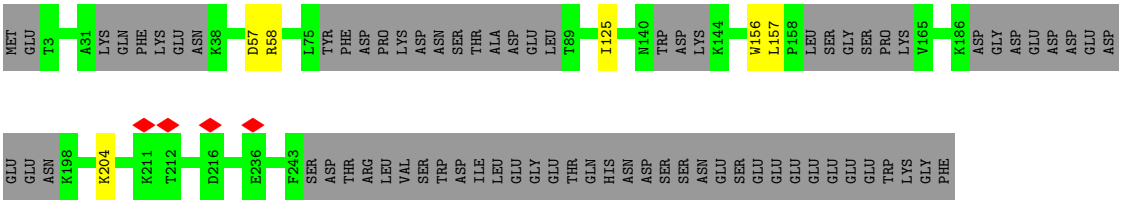
Chain W:





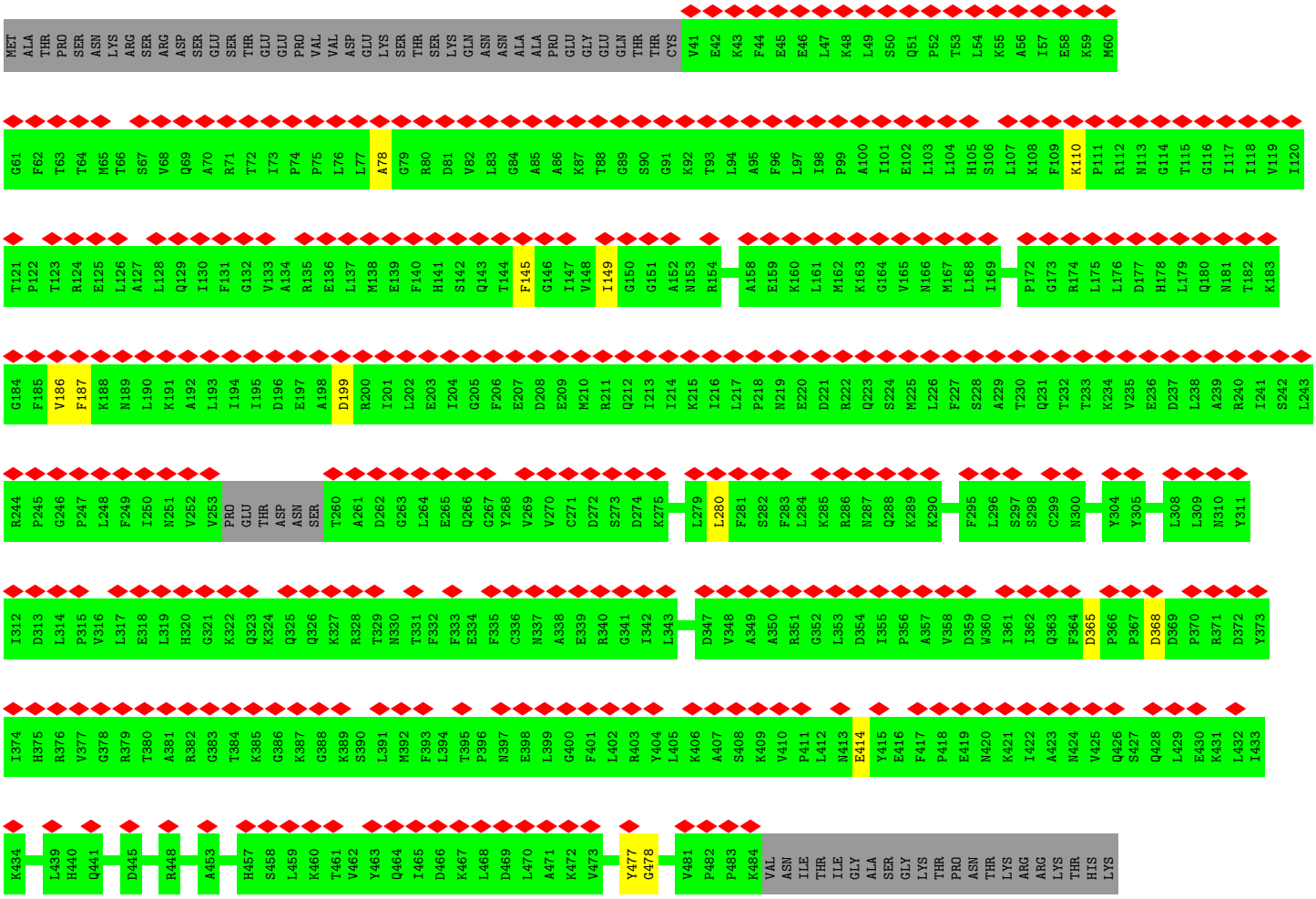
• Molecule 24: Ribosomal RNA-processing protein 1

Chain X:



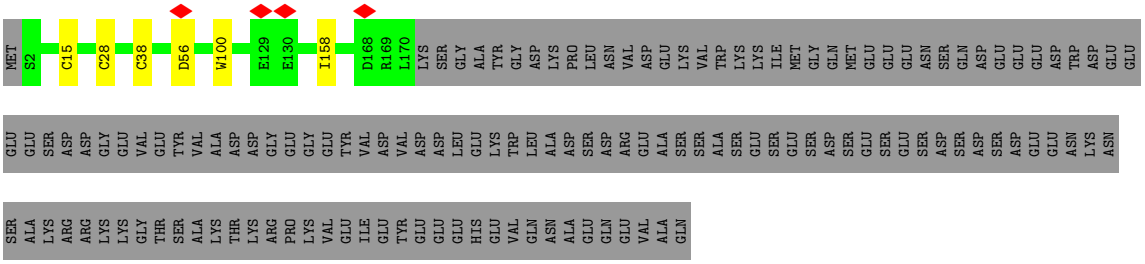
• Molecule 25: ATP-dependent RNA helicase HAS1

Chain Y:



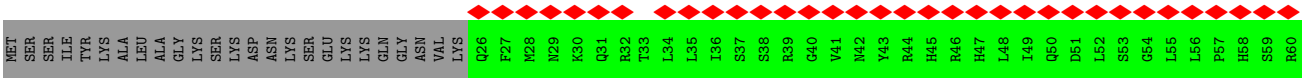
- Molecule 26: Protein MAK16

Chain Z:



- Molecule 27: Ribosome biogenesis protein BRX1

Chain a:



K61 E62 P63 K64 L65 ASP THR LYS LYS D70 L71 Q72 Q73 L74 N75 A78 E79 L80 Y81 N82 C83 N84 N85 V86 L87 F88 F89 E90 A91 R92 K93 H94 Q95 D96 L97 Y98 L99 W100 L101 S102 K103 P104 P105 N106 G107 P108 T109 I110 K111 F112 Y113 I114 Q115 N116 L117 H118 T119 M120 D121

E122 L123 N124 F125 T126 G127 N128 C129 L130 K131 G132 S133 R134 P135 V136 L137 S138 F139 D140 Q141 R142 F143 E144 S145 S146 P147 H148 Y149 Q150 L151 T152 K153 E154 L155 L156 V157 H158 N159 F160 G161 V162 P163 P164 N165 A166 R167 K168 S169 K170 P171 F172 I173 D174 H175 V176 M177 S178 F179 S180 I181

V182 D183 D184 K185 I186 W187 V188 R189 T190 Y191 E192 I193 S194 H195 SER THR LYS ASN LYS GLU GLU TYR GLU ASP GLY GLU GLU ASP I210 S211 L212 V213 E214 I215 G216 P217 R218 F219 V220 M221 T222 V223 I224 L225 I226 L227 E228 G229 S230 F231 G232 G233 P234 K235 I236 Y237 E238 N239 K240 Q241

Y242 V243 S244 P245 N246 V247 V248 R249 A250 Q251 I252 K253 Q254 Q255 ALA ALA GLU GLU ALA LYS SER ARG ALA GLU ALA ALA VAL GLU ARG LYS ILE LYS ARG ARG GLU ASN VAL LEU ALA ALA ASP PRO LEU SER ASN ASP ALA LEU PHE LYS

- Molecule 28: rRNA-processing protein EBP2

Chain b:

MET ALA LYS GLY PHE LYS LEU LYS GLU LEU LEU SER HIS GLN LYS GLU ILE GLU LYS ALA GLU LYS LEU GLU ASN ASP LEU LYS LYS LYS LYS SER GLN GLU GLU LEU LYS LYS GLU GLU PRO THR ILE VAL THR ALA SER ASN LEU LYS LYS LYS LEU GLU LYS LYS ALA ASP VAL

LYS LYS GLU VAL ALA ALA ASP THR GLU GLU TYR GLN SER GLN ALA LEU SER LYS LYS GLU LYS ARG LYS LEU LYS LYS GLU LEU LYS LYS MET GLN GLU GLN ASP ALA THR GLU ALA GLN LYS HIS MET SER GLY ASP GLU ASP GLU SER GLY ASP ASP ARG GLU GLU GLU GLU GLU

GLU GLU GLU GLU GLY ARG LEU ASP LEU GLU LYS LEU ALA LYS SER ASP SER GLU SER GLU ASP ASP SER GLU SER GLU ASN ASP SER GLU GLU ASP GLU ASP VAL VAL ALA LYS GLU GLU SER GLU GLU LYS GLU GLU GLN GLU GLU GLU GLN ASP VAL PRO LEU SER ASP VAL GLU

PHE ASP SER ASP ALA ASP VAL VAL PRO HIS HIS LYS LEU THR V195 N196 N197 T198 K199 A200 M201 K202 H203 A204 L205 E206 R207 V208 Q209 L210 P211 W212 K213 K214 H215 S216 F217 Q218 E219 H220 Q221 S222 V223 T224 S225 E226 T227 N228 T229 D230 E231 H232 I233 K234 D235 I236 Y237 D238 D239 T240

E241 R242 E243 L244 A245 F246 Y247 K248 Q249 S250 L251 D252 A253 V254 L255 V256 A257 R258 D259 E260 L261 K262 R263 L264 K265 V266 P267 F268 K269 R270 P271 L272 D273 Y274 F275 A276 GLU MET VAL LYS SER ASP GLU HIS MET ASP LYS ILE LYS GLY LYS LEU ILE GLU GLU ALA SER ASP LYS LYS

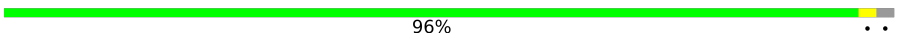
ALA ARG GLU GLU ALA ARG ARG GLN ARG GLN LEU LYS LYS PHE GLY LYS GLN VAL GLN ASN ALA THR LEU GLN LYS ARG GLU THR LEU GLU LYS ILE LYS SER LEU LYS ASN LYS ARG LYS HIS ASN GLU ILE ASP HIS SER GLU PHE ASN VAL GLY VAL GLU GLU

GLU VAL GLU GLY LYS ARG PHE ASP ARG GLY ARG PRO ASN GLY LYS ARG ALA ALA LYS ASN ALA LYS TYR GLY GLN GLY GLY MET LYS ARG PHE LYS ARG LYS ASN ASP ALA THR SER SER ALA ASP VAL SER GLY PHE SER SER ARG LYS MET LYS GLY LYS THR ASN ARG PRO GLY LYS

SER ARG ARG ALA ARG ARG PHE

- Molecule 29: 60S ribosomal protein L26-A

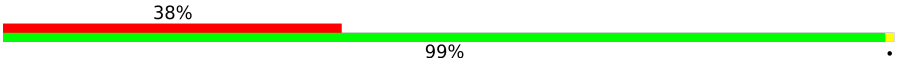
Chain c:

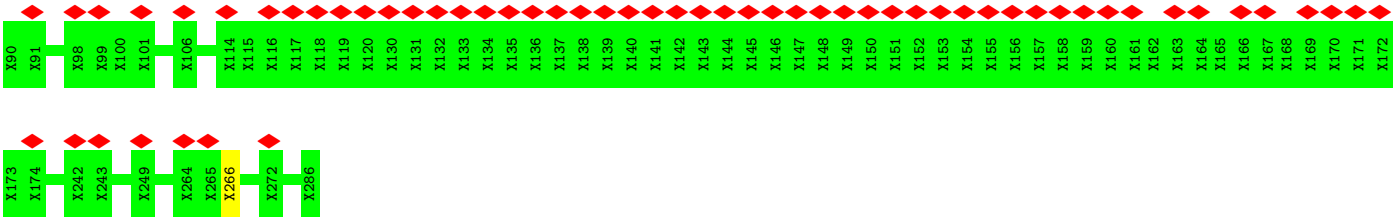


MET A2 K14 I45 L126 GLU

- Molecule 30: Unassigned

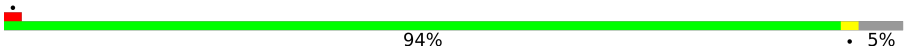
Chain d:

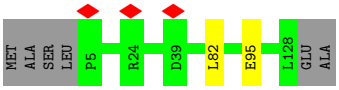




- Molecule 31: 60S ribosomal protein L32

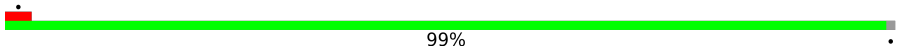
Chain i:

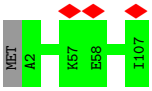




- Molecule 32: 60S ribosomal protein L33-A

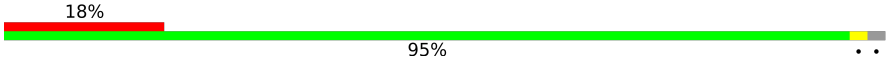
Chain j:

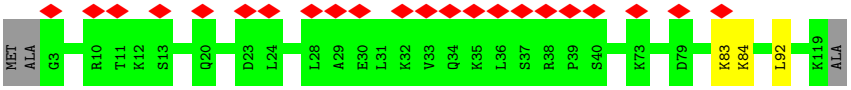




- Molecule 33: 60S ribosomal protein L35-A

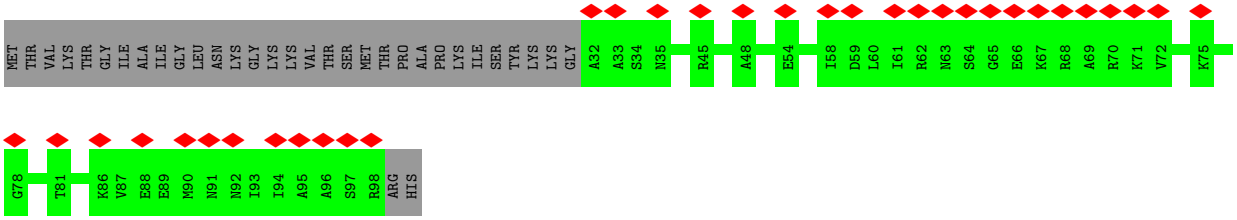
Chain l:





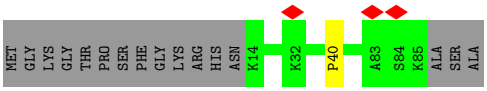
- Molecule 34: 60S ribosomal protein L36-A

Chain m:



- Molecule 35: 60S ribosomal protein L37-A

Chain n:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98155	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.564	Depositor
Minimum map value	-0.265	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	496.8, 496.8, 496.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	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	A	1.49	246/35968 (0.7%)	1.31	241/56046 (0.4%)
2	B	1.50	18/3702 (0.5%)	1.32	22/5764 (0.4%)
3	C	0.79	0/1527	1.11	6/2371 (0.3%)
4	D	0.42	0/1982	0.65	2/2668 (0.1%)
5	E	0.47	0/1129	0.62	0/1502
6	F	0.47	0/2724	0.66	0/3659
7	G	0.94	2/2801 (0.1%)	0.83	4/3792 (0.1%)
8	H	0.44	0/2097	0.65	1/2828 (0.0%)
9	I	0.77	0/1218	0.69	0/1637
10	J	0.81	0/1956	0.75	1/2631 (0.0%)
11	K	0.65	0/1268	0.71	0/1716
12	L	0.42	0/1539	0.62	0/2073
13	M	0.40	0/3101	0.64	1/4187 (0.0%)
14	N	0.36	0/1730	0.65	0/2354
15	O	0.67	0/1623	0.73	1/2178 (0.0%)
16	P	0.87	0/880	0.77	1/1182 (0.1%)
17	Q	0.73	1/1074 (0.1%)	0.69	0/1446
18	R	0.83	0/1529	0.71	0/2046
19	S	0.80	0/1585	0.69	0/2128
20	T	0.53	0/1075	0.65	0/1448
21	U	0.86	0/1050	0.82	2/1419 (0.1%)
22	V	0.58	0/3151	0.68	0/4244
23	W	0.67	0/1460	0.66	0/1962
24	X	0.79	1/1751 (0.1%)	0.79	2/2348 (0.1%)
25	Y	0.46	0/3552	0.69	1/4789 (0.0%)
26	Z	1.02	3/1437 (0.2%)	0.84	0/1927
27	a	0.43	0/1790	0.64	1/2418 (0.0%)
28	b	0.45	0/704	0.62	0/949
29	c	0.74	0/995	0.73	1/1329 (0.1%)
31	i	0.88	0/1022	0.76	1/1367 (0.1%)
32	j	1.12	0/868	0.79	0/1168
33	l	0.64	0/968	0.68	1/1287 (0.1%)
34	m	0.51	0/536	0.64	0/711
35	n	0.90	0/587	0.77	0/778

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
All	All	1.11	271/90379 (0.3%)	1.04	289/130352 (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	D	0	2
6	F	0	1
8	H	0	1
10	J	0	3
11	K	0	1
13	M	0	4
15	O	0	3
17	Q	0	1
18	R	0	2
22	V	0	1
23	W	0	3
24	X	0	2
25	Y	0	7
26	Z	0	1
27	a	0	1
28	b	0	3
30	d	0	1
31	i	0	1
33	l	0	1
All	All	0	39

All (271) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1366	A	N9-C4	-8.81	1.32	1.37
1	A	1354	G	N9-C4	-8.31	1.31	1.38
1	A	219	A	N9-C4	-7.89	1.33	1.37
1	A	340	C	N1-C6	-7.84	1.32	1.37
1	A	63	A	N9-C4	-7.55	1.33	1.37
1	A	346	C	N1-C6	-7.53	1.32	1.37
1	A	1354	G	N3-C4	-7.48	1.30	1.35
1	A	1330	A	N9-C4	-7.43	1.33	1.37
1	A	324	A	N9-C4	-7.34	1.33	1.37
1	A	27	C	N1-C6	-7.16	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1407	A	N9-C4	-7.12	1.33	1.37
1	A	657	A	N3-C4	-7.06	1.30	1.34
1	A	228	U	N1-C2	-7.03	1.32	1.38
1	A	1403	C	N1-C6	-7.02	1.32	1.37
1	A	945	C	N1-C6	-7.00	1.32	1.37
1	A	1147	G	N9-C8	-6.93	1.32	1.37
1	A	324	A	N3-C4	-6.87	1.30	1.34
1	A	941	G	N9-C8	-6.85	1.33	1.37
1	A	1376	C	N1-C6	-6.79	1.33	1.37
1	A	74	G	N9-C4	-6.79	1.32	1.38
1	A	334	A	N9-C4	-6.76	1.33	1.37
1	A	77	A	N9-C4	-6.68	1.33	1.37
1	A	1180	A	N9-C4	-6.67	1.33	1.37
1	A	1146	C	N1-C6	-6.67	1.33	1.37
7	G	194	TYR	CD2-CE2	-6.65	1.29	1.39
1	A	1387	G	C5-C4	-6.62	1.33	1.38
1	A	516	A	N9-C4	-6.61	1.33	1.37
1	A	296	A	N9-C4	-6.60	1.33	1.37
1	A	690	A	N9-C4	-6.60	1.33	1.37
1	A	1158	A	N9-C4	-6.59	1.33	1.37
1	A	199	A	N9-C4	-6.58	1.33	1.37
1	A	341	G	C6-N1	-6.58	1.34	1.39
1	A	504	A	N9-C4	-6.55	1.33	1.37
2	B	35	C	N1-C6	-6.54	1.33	1.37
1	A	327	A	N9-C4	-6.54	1.33	1.37
1	A	630	A	N9-C4	-6.53	1.33	1.37
1	A	123	A	N9-C4	-6.50	1.33	1.37
1	A	219	A	N7-C5	-6.47	1.35	1.39
24	X	156	TRP	CB-CG	-6.47	1.38	1.50
1	A	219	A	N3-C4	-6.43	1.30	1.34
1	A	409	A	N9-C8	-6.38	1.32	1.37
1	A	1388	U	N1-C2	-6.32	1.32	1.38
1	A	340	C	N3-C4	-6.32	1.29	1.33
1	A	367	A	N9-C4	-6.31	1.34	1.37
26	Z	28	CYS	CB-SG	-6.27	1.71	1.82
1	A	1433	A	N9-C4	-6.26	1.34	1.37
1	A	396	A	N9-C4	-6.25	1.34	1.37
1	A	1169	A	N7-C5	-6.25	1.35	1.39
1	A	1159	A	N9-C4	-6.22	1.34	1.37
1	A	399	A	N3-C4	-6.21	1.31	1.34
1	A	407	A	N9-C4	-6.19	1.34	1.37
1	A	3172	A	N9-C4	-6.18	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	215	G	N3-C4	-6.17	1.31	1.35
1	A	685	G	N7-C5	-6.17	1.35	1.39
1	A	323	A	N9-C4	-6.16	1.34	1.37
1	A	1418	A	C5-C4	-6.16	1.34	1.38
1	A	1335	C	N1-C6	-6.14	1.33	1.37
1	A	1404	G	C5-C4	-6.14	1.34	1.38
1	A	373	A	N9-C4	-6.12	1.34	1.37
1	A	1161	G	C5-C4	-6.12	1.34	1.38
1	A	584	G	C5-C4	-6.11	1.34	1.38
1	A	1405	U	N1-C2	-6.11	1.33	1.38
2	B	28	C	N1-C6	-6.10	1.33	1.37
1	A	62	A	N9-C4	-6.09	1.34	1.37
1	A	1419	A	C6-N1	-6.07	1.31	1.35
1	A	77	A	N3-C4	-6.06	1.31	1.34
1	A	215	G	C5-C4	-6.04	1.34	1.38
1	A	657	A	N7-C5	-6.02	1.35	1.39
2	B	36	G	C5-C4	-6.01	1.34	1.38
2	B	36	G	N7-C5	-6.00	1.35	1.39
1	A	325	A	N9-C4	-6.00	1.34	1.37
1	A	199	A	N3-C4	-6.00	1.31	1.34
1	A	24	G	N9-C4	-5.99	1.33	1.38
1	A	409	A	N7-C5	-5.99	1.35	1.39
1	A	107	A	C5-C4	-5.98	1.34	1.38
1	A	656	A	N3-C4	-5.97	1.31	1.34
1	A	317	A	N9-C4	-5.96	1.34	1.37
2	B	105	A	N7-C5	-5.95	1.35	1.39
1	A	1327	C	N1-C6	-5.95	1.33	1.37
1	A	1330	A	N3-C4	-5.94	1.31	1.34
1	A	1380	G	C5-C4	-5.91	1.34	1.38
1	A	589	A	N7-C5	-5.91	1.35	1.39
1	A	235	A	N9-C4	-5.89	1.34	1.37
1	A	1426	C	N1-C6	-5.89	1.33	1.37
1	A	941	G	N7-C5	-5.89	1.35	1.39
1	A	341	G	N7-C5	-5.89	1.35	1.39
1	A	318	A	N9-C4	-5.88	1.34	1.37
26	Z	15	CYS	CB-SG	-5.88	1.72	1.81
1	A	1166	G	C5-C4	-5.87	1.34	1.38
2	B	24	G	C6-N1	-5.87	1.35	1.39
1	A	197	G	N9-C4	-5.86	1.33	1.38
1	A	339	C	N1-C6	-5.84	1.33	1.37
1	A	22	G	N7-C5	-5.83	1.35	1.39
1	A	327	A	N3-C4	-5.82	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	788	C	N1-C6	-5.82	1.33	1.37
1	A	267	G	N3-C4	-5.82	1.31	1.35
1	A	929	A	N3-C4	-5.81	1.31	1.34
1	A	321	C	N1-C6	-5.80	1.33	1.37
1	A	65	A	C5-C4	-5.80	1.34	1.38
1	A	350	C	N1-C6	-5.79	1.33	1.37
1	A	1437	C	N1-C6	-5.78	1.33	1.37
1	A	211	A	N9-C4	-5.77	1.34	1.37
1	A	1393	A	C5-C6	-5.76	1.35	1.41
1	A	344	A	N7-C5	-5.75	1.35	1.39
1	A	1317	A	N9-C4	-5.75	1.34	1.37
1	A	1342	C	N1-C6	-5.74	1.33	1.37
1	A	341	G	C5-C6	-5.74	1.36	1.42
1	A	656	A	N7-C5	-5.74	1.35	1.39
1	A	1433	A	C5-C4	-5.73	1.34	1.38
1	A	1332	A	N7-C5	-5.73	1.35	1.39
1	A	342	A	N3-C4	-5.73	1.31	1.34
1	A	1366	A	N3-C4	-5.72	1.31	1.34
1	A	1388	U	C2-N3	-5.71	1.33	1.37
1	A	665	A	N9-C4	-5.70	1.34	1.37
2	B	45	C	N1-C6	-5.70	1.33	1.37
1	A	657	A	C5-C4	-5.70	1.34	1.38
1	A	589	A	C5-C4	-5.68	1.34	1.38
17	Q	99	TRP	CB-CG	-5.68	1.40	1.50
1	A	1158	A	N3-C4	-5.68	1.31	1.34
1	A	342	A	C5-C4	-5.67	1.34	1.38
1	A	504	A	N3-C4	-5.66	1.31	1.34
1	A	64	G	N9-C8	-5.66	1.33	1.37
1	A	1424	C	N1-C6	-5.65	1.33	1.37
1	A	26	A	N7-C5	-5.65	1.35	1.39
1	A	610	G	N9-C8	-5.61	1.33	1.37
1	A	344	A	C5-C4	-5.60	1.34	1.38
1	A	952	A	N9-C4	-5.60	1.34	1.37
1	A	327	A	C5-C4	-5.59	1.34	1.38
1	A	1418	A	N3-C4	-5.59	1.31	1.34
1	A	349	A	N9-C4	-5.57	1.34	1.37
1	A	1176	C	N1-C2	-5.56	1.34	1.40
1	A	657	A	N9-C4	-5.56	1.34	1.37
1	A	103	G	N7-C5	-5.54	1.35	1.39
1	A	214	G	C6-N1	-5.54	1.35	1.39
1	A	576	C	N1-C6	-5.53	1.33	1.37
1	A	1175	C	N1-C6	-5.53	1.33	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1161	G	N3-C4	-5.50	1.31	1.35
1	A	1423	C	N1-C6	-5.50	1.33	1.37
1	A	610	G	C6-N1	-5.49	1.35	1.39
1	A	213	A	N7-C5	-5.49	1.35	1.39
1	A	57	A	N9-C4	-5.49	1.34	1.37
1	A	678	G	N7-C5	-5.48	1.35	1.39
1	A	611	A	N9-C4	-5.47	1.34	1.37
1	A	678	G	C6-N1	-5.47	1.35	1.39
1	A	344	A	N9-C4	-5.46	1.34	1.37
1	A	1365	G	N3-C4	-5.46	1.31	1.35
1	A	339	C	N3-C4	-5.45	1.30	1.33
1	A	674	G	N9-C8	-5.44	1.34	1.37
2	B	78	G	N9-C4	-5.43	1.33	1.38
1	A	1383	G	C5-C4	-5.43	1.34	1.38
1	A	1379	G	C6-N1	-5.43	1.35	1.39
1	A	1425	U	N1-C2	-5.42	1.33	1.38
1	A	1158	A	N7-C5	-5.42	1.35	1.39
2	B	17	A	N3-C4	-5.42	1.31	1.34
1	A	1173	U	N1-C2	-5.41	1.33	1.38
1	A	338	A	N7-C5	-5.41	1.36	1.39
1	A	1418	A	C6-N1	-5.41	1.31	1.35
1	A	1163	A	N9-C4	-5.40	1.34	1.37
1	A	1176	C	N1-C6	-5.40	1.33	1.37
1	A	1328	C	N1-C6	-5.39	1.33	1.37
1	A	219	A	C5-C6	-5.39	1.36	1.41
1	A	692	A	N7-C5	-5.39	1.36	1.39
1	A	1165	A	C5-C4	-5.39	1.34	1.38
1	A	296	A	N3-C4	-5.39	1.31	1.34
1	A	1343	A	N9-C4	-5.38	1.34	1.37
1	A	1412	G	C5-C4	-5.38	1.34	1.38
1	A	655	C	N1-C6	-5.37	1.33	1.37
1	A	1419	A	C5-C4	-5.37	1.34	1.38
1	A	1432	C	N1-C6	-5.37	1.33	1.37
1	A	1342	C	N3-C4	-5.37	1.30	1.33
1	A	1180	A	C5-C4	-5.36	1.35	1.38
1	A	65	A	N3-C4	-5.36	1.31	1.34
1	A	1345	G	N3-C4	-5.35	1.31	1.35
1	A	653	A	N3-C4	-5.35	1.31	1.34
1	A	657	A	C6-N1	-5.35	1.31	1.35
1	A	23	A	N9-C4	-5.35	1.34	1.37
1	A	63	A	N3-C4	-5.35	1.31	1.34
1	A	787	G	C6-N1	-5.34	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1344	G	N3-C4	-5.34	1.31	1.35
1	A	1364	C	N1-C6	-5.34	1.33	1.37
1	A	611	A	N7-C5	-5.33	1.36	1.39
1	A	1415	U	N1-C2	-5.33	1.33	1.38
1	A	193	C	N1-C6	-5.32	1.33	1.37
1	A	377	A	N9-C4	-5.32	1.34	1.37
1	A	407	A	N3-C4	-5.31	1.31	1.34
1	A	947	G	N7-C5	-5.29	1.36	1.39
1	A	1179	A	N9-C4	-5.28	1.34	1.37
1	A	653	A	N9-C4	-5.28	1.34	1.37
1	A	1180	A	N9-C8	-5.26	1.33	1.37
1	A	1339	C	N1-C6	-5.26	1.33	1.37
1	A	324	A	C6-N1	-5.26	1.31	1.35
1	A	503	C	N1-C6	-5.26	1.33	1.37
1	A	31	C	N1-C6	-5.26	1.33	1.37
1	A	67	A	N9-C4	-5.25	1.34	1.37
1	A	427	C	C4-C5	-5.25	1.38	1.43
2	B	39	G	N3-C4	-5.25	1.31	1.35
1	A	336	A	N7-C5	-5.24	1.36	1.39
1	A	1396	C	N1-C6	-5.24	1.34	1.37
1	A	222	A	C5-C6	-5.23	1.36	1.41
1	A	660	A	C5-C4	-5.23	1.35	1.38
1	A	1147	G	C5-C4	-5.23	1.34	1.38
1	A	1411	C	N1-C6	-5.21	1.34	1.37
1	A	332	C	N1-C6	-5.21	1.34	1.37
2	B	39	G	C5-C4	-5.21	1.34	1.38
1	A	342	A	C6-N1	-5.20	1.31	1.35
1	A	1158	A	C5-C6	-5.20	1.36	1.41
1	A	187	A	N9-C4	-5.20	1.34	1.37
2	B	17	A	N7-C5	-5.20	1.36	1.39
1	A	598	A	N9-C4	-5.19	1.34	1.37
1	A	801	A	C6-N1	-5.19	1.31	1.35
2	B	44	A	C5-C6	-5.19	1.36	1.41
1	A	338	A	N3-C4	-5.19	1.31	1.34
2	B	30	C	N1-C6	-5.18	1.34	1.37
1	A	559	A	N9-C4	-5.18	1.34	1.37
1	A	660	A	N9-C4	-5.18	1.34	1.37
1	A	791	A	N3-C4	-5.18	1.31	1.34
1	A	1419	A	N3-C4	-5.18	1.31	1.34
1	A	1379	G	N9-C8	-5.18	1.34	1.37
1	A	399	A	N9-C4	-5.17	1.34	1.37
1	A	466	G	C5-C4	-5.15	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	36	G	N9-C8	-5.15	1.34	1.37
1	A	1333	C	N1-C6	-5.15	1.34	1.37
26	Z	100	TRP	CB-CG	-5.15	1.41	1.50
1	A	22	G	N3-C4	-5.15	1.31	1.35
1	A	395	A	N9-C4	-5.14	1.34	1.37
1	A	639	G	C5-C4	-5.14	1.34	1.38
1	A	1182	A	N9-C4	-5.14	1.34	1.37
1	A	408	A	N3-C4	-5.13	1.31	1.34
1	A	1417	G	N7-C5	-5.13	1.36	1.39
1	A	105	C	N1-C6	-5.13	1.34	1.37
1	A	357	A	C5-C4	-5.13	1.35	1.38
1	A	197	G	N3-C4	-5.12	1.31	1.35
1	A	1419	A	N9-C4	-5.12	1.34	1.37
1	A	690	A	N3-C4	-5.12	1.31	1.34
1	A	1334	U	N1-C6	-5.12	1.33	1.38
1	A	228	U	C2-N3	-5.12	1.34	1.37
1	A	295	A	N9-C4	-5.12	1.34	1.37
1	A	52	A	N9-C4	-5.12	1.34	1.37
1	A	1350	A	N3-C4	-5.11	1.31	1.34
1	A	1380	G	N3-C4	-5.11	1.31	1.35
1	A	363	G	N9-C8	-5.10	1.34	1.37
7	G	250	TRP	CB-CG	-5.10	1.41	1.50
2	B	27	U	N1-C6	-5.09	1.33	1.38
1	A	222	A	N7-C5	-5.09	1.36	1.39
2	B	44	A	C5-C4	-5.09	1.35	1.38
1	A	940	G	N7-C5	-5.08	1.36	1.39
1	A	3215	A	N9-C4	-5.08	1.34	1.37
1	A	1365	G	C5-C4	-5.08	1.34	1.38
1	A	1406	A	N9-C4	-5.08	1.34	1.37
1	A	787	G	N7-C5	-5.07	1.36	1.39
1	A	1363	A	N7-C5	-5.07	1.36	1.39
1	A	810	A	N9-C4	-5.07	1.34	1.37
1	A	1365	G	N9-C4	-5.07	1.33	1.38
1	A	333	G	N9-C8	-5.07	1.34	1.37
1	A	322	U	N1-C2	-5.07	1.33	1.38
1	A	1415	U	C2-N3	-5.06	1.34	1.37
1	A	656	A	C6-N1	-5.05	1.32	1.35
1	A	1423	C	C4-C5	-5.05	1.39	1.43
1	A	952	A	N3-C4	-5.05	1.31	1.34
1	A	334	A	N3-C4	-5.04	1.31	1.34
1	A	610	G	N7-C5	-5.04	1.36	1.39
1	A	1358	C	N1-C6	-5.04	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	663	C	N1-C6	-5.03	1.34	1.37
1	A	1344	G	C5-C4	-5.03	1.34	1.38
1	A	791	A	N7-C5	-5.03	1.36	1.39
2	B	104	A	N3-C4	-5.02	1.31	1.34
1	A	683	U	N1-C2	-5.01	1.34	1.38
1	A	1165	A	N3-C4	-5.01	1.31	1.34
1	A	346	C	C4-C5	-5.01	1.39	1.43
1	A	3147	G	N9-C4	-5.00	1.33	1.38
1	A	289	A	N9-C4	-5.00	1.34	1.37

All (289) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	544	C	N1-C2-O2	-11.10	112.24	118.90
1	A	1354	G	O4'-C1'-N9	-10.44	99.84	108.20
1	A	544	C	C2-N3-C4	-9.76	115.02	119.90
1	A	1423	C	C6-N1-C2	-8.66	116.84	120.30
1	A	544	C	C2-N1-C1'	-8.63	109.31	118.80
1	A	1354	G	C2-N3-C4	-8.59	107.61	111.90
1	A	547	G	N3-C2-N2	-8.58	113.89	119.90
1	A	638	C	C6-N1-C2	-8.21	117.02	120.30
1	A	544	C	C6-N1-C1'	8.11	130.53	120.80
1	A	1108	U	C2-N1-C1'	7.99	127.28	117.70
1	A	141	C	N3-C2-O2	-7.95	116.34	121.90
1	A	340	C	N3-C2-O2	-7.95	116.34	121.90
1	A	74	G	N3-C4-N9	-7.93	121.24	126.00
1	A	544	C	N1-C2-N3	7.85	124.70	119.20
1	A	660	A	O5'-P-OP1	-7.76	98.72	105.70
1	A	1354	G	N3-C4-N9	-7.68	121.39	126.00
1	A	1349	G	C2-N3-C4	-7.67	108.07	111.90
1	A	228	U	C2-N1-C1'	-7.65	108.52	117.70
1	A	341	G	C6-C5-N7	-7.63	125.82	130.40
7	G	21	PRO	C-N-CA	-7.57	102.77	121.70
1	A	1103	A	C8-N9-C4	7.49	108.80	105.80
1	A	57	A	C2-N3-C4	-7.42	106.89	110.60
1	A	1435	A	O5'-P-OP1	-7.39	99.04	105.70
3	C	33	U	N1-C2-O2	7.33	127.93	122.80
1	A	74	G	N3-C4-C5	7.29	132.25	128.60
1	A	1354	G	N3-C4-C5	7.28	132.24	128.60
1	A	400	G	C8-N9-C4	7.26	109.31	106.40
1	A	220	G	C8-N9-C1'	-7.24	117.58	127.00
1	A	75	G	C4-N9-C1'	7.20	135.86	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	39	G	O4'-C1'-N9	7.07	113.86	108.20
24	X	157	LEU	CA-CB-CG	6.99	131.38	115.30
2	B	78	G	N3-C4-C5	6.97	132.09	128.60
1	A	333	G	C8-N9-C1'	-6.94	117.97	127.00
15	O	119	PRO	N-CA-CB	6.94	111.63	103.30
3	C	33	U	C2-N1-C1'	6.88	125.96	117.70
7	G	134	LEU	CA-CB-CG	-6.88	99.48	115.30
1	A	140	C	N3-C2-O2	-6.87	117.09	121.90
1	A	641	C	C2-N1-C1'	-6.86	111.25	118.80
1	A	547	G	N9-C4-C5	6.86	108.14	105.40
1	A	678	G	C4-N9-C1'	6.86	135.42	126.50
2	B	152	G	N3-C4-N9	-6.83	121.90	126.00
3	C	48	A	O4'-C1'-N9	6.81	113.65	108.20
1	A	1351	U	C2-N1-C1'	6.78	125.84	117.70
1	A	404	G	N9-C4-C5	-6.78	102.69	105.40
1	A	1415	U	C5-C6-N1	-6.78	119.31	122.70
1	A	56	G	C8-N9-C4	-6.75	103.70	106.40
21	U	16	ARG	NE-CZ-NH2	-6.75	116.93	120.30
2	B	94	C	C6-N1-C2	6.74	123.00	120.30
1	A	588	G	N3-C4-C5	-6.73	125.24	128.60
1	A	439	C	C2-N1-C1'	6.70	126.17	118.80
1	A	333	G	C4-N9-C1'	6.70	135.20	126.50
1	A	678	G	C6-C5-N7	-6.66	126.40	130.40
1	A	352	A	O5'-P-OP2	-6.64	99.72	105.70
1	A	439	C	C6-N1-C1'	-6.64	112.83	120.80
1	A	694	C	C6-N1-C2	-6.62	117.65	120.30
3	C	33	U	N3-C2-O2	-6.60	117.58	122.20
2	B	78	G	N3-C4-N9	-6.59	122.05	126.00
1	A	75	G	C8-N9-C1'	-6.59	118.44	127.00
2	B	56	G	N1-C6-O6	-6.57	115.96	119.90
2	B	152	G	N3-C4-C5	6.56	131.88	128.60
1	A	1118	C	N1-C2-O2	-6.50	115.00	118.90
1	A	656	A	N1-C2-N3	6.49	132.54	129.30
1	A	1358	C	C5-C6-N1	-6.48	117.76	121.00
1	A	721	G	N9-C4-C5	-6.47	102.81	105.40
1	A	220	G	C4-N9-C1'	6.46	134.90	126.50
1	A	678	G	N3-C4-N9	6.45	129.87	126.00
1	A	700	C	N1-C2-O2	6.42	122.75	118.90
1	A	682	U	C2-N1-C1'	-6.42	110.00	117.70
29	c	126	LEU	CA-CB-CG	6.41	130.03	115.30
1	A	976	U	C5-C6-N1	6.39	125.90	122.70
1	A	228	U	C6-N1-C1'	6.37	130.12	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	57	C	N3-C2-O2	-6.36	117.45	121.90
2	B	24	G	C5-C6-O6	6.36	132.41	128.60
1	A	515	C	C2-N1-C1'	6.35	125.78	118.80
1	A	1415	U	C2-N1-C1'	-6.29	110.15	117.70
1	A	953	G	N3-C4-C5	6.29	131.75	128.60
1	A	2378	C	C2-N1-C1'	6.28	125.70	118.80
1	A	266	A	C8-N9-C4	-6.27	103.29	105.80
1	A	385	A	N1-C6-N6	6.22	122.33	118.60
1	A	678	G	N3-C4-C5	-6.21	125.50	128.60
1	A	547	G	N3-C4-N9	-6.19	122.28	126.00
1	A	334	A	C6-N1-C2	-6.17	114.90	118.60
1	A	1338	C	C6-N1-C2	-6.16	117.84	120.30
1	A	3126	C	N1-C2-O2	6.12	122.57	118.90
1	A	439	C	N1-C2-O2	6.12	122.57	118.90
1	A	1118	C	C2-N1-C1'	-6.11	112.08	118.80
1	A	1366	A	C8-N9-C4	6.09	108.24	105.80
1	A	630	A	C2-N3-C4	-6.09	107.56	110.60
1	A	637	C	O4'-C1'-N1	6.08	113.07	108.20
1	A	220	G	N3-C4-N9	6.07	129.64	126.00
1	A	700	C	N3-C2-O2	-6.06	117.66	121.90
1	A	197	G	N3-C4-N9	-6.05	122.37	126.00
1	A	656	A	C8-N9-C4	-6.04	103.38	105.80
1	A	462	C	C6-N1-C1'	6.01	128.01	120.80
21	U	16	ARG	CG-CD-NE	-6.01	99.19	111.80
1	A	457	C	N1-C2-O2	5.99	122.50	118.90
1	A	341	G	C4-N9-C1'	5.98	134.27	126.50
1	A	263	C	N3-C2-O2	-5.97	117.72	121.90
7	G	182	LEU	CA-CB-CG	5.97	129.03	115.30
1	A	1108	U	C5-C6-N1	5.96	125.68	122.70
1	A	948	C	C6-N1-C2	-5.94	117.92	120.30
1	A	267	G	C2-N3-C4	-5.94	108.93	111.90
1	A	141	C	N1-C2-O2	5.94	122.46	118.90
7	G	156	LEU	CA-CB-CG	5.94	128.95	115.30
1	A	685	G	C6-C5-N7	-5.93	126.84	130.40
1	A	641	C	C6-N1-C1'	5.92	127.91	120.80
1	A	1425	U	C2-N3-C4	-5.92	123.45	127.00
1	A	74	G	C2-N3-C4	-5.91	108.94	111.90
1	A	207	U	C2-N1-C1'	5.90	124.78	117.70
1	A	260	C	C6-N1-C2	5.90	122.66	120.30
1	A	1117	G	N3-C4-N9	-5.89	122.47	126.00
4	D	224	PRO	N-CA-C	-5.87	96.84	112.10
1	A	641	C	N1-C2-O2	-5.85	115.39	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1118	C	C6-N1-C1'	5.85	127.82	120.80
1	A	1435	A	N7-C8-N9	5.84	116.72	113.80
1	A	940	G	O5'-P-OP1	-5.83	100.45	105.70
1	A	360	G	C8-N9-C4	5.82	108.73	106.40
1	A	267	G	N3-C4-C5	5.82	131.51	128.60
1	A	682	U	C5-C6-N1	-5.81	119.80	122.70
1	A	3239	G	N1-C6-O6	-5.81	116.42	119.90
1	A	590	G	C4-C5-N7	5.81	113.12	110.80
2	B	127	U	N1-C2-O2	5.79	126.85	122.80
1	A	1435	A	C5-N7-C8	-5.76	101.02	103.90
1	A	41	G	C4-N9-C1'	5.76	133.99	126.50
1	A	63	A	C2-N3-C4	-5.76	107.72	110.60
1	A	404	G	C8-N9-C4	5.76	108.70	106.40
1	A	547	G	C4-C5-N7	-5.76	108.50	110.80
1	A	294	U	O5'-P-OP1	-5.76	100.52	105.70
1	A	215	G	N3-C4-N9	-5.75	122.55	126.00
1	A	399	A	O5'-P-OP2	-5.74	100.53	105.70
2	B	39	G	N9-C4-C5	5.74	107.70	105.40
1	A	24	G	N3-C4-C5	5.74	131.47	128.60
2	B	29	U	N1-C2-O2	-5.73	118.79	122.80
10	J	103	LEU	CA-CB-CG	-5.68	102.23	115.30
1	A	678	G	C8-N9-C1'	-5.68	119.61	127.00
1	A	960	U	N1-C2-O2	5.67	126.77	122.80
1	A	3147	G	N3-C4-C5	5.67	131.43	128.60
1	A	227	G	C4-N9-C1'	5.66	133.86	126.50
1	A	227	G	C6-C5-N7	-5.66	127.00	130.40
1	A	315	C	N3-C2-O2	-5.66	117.94	121.90
1	A	745	C	N1-C2-O2	-5.66	115.51	118.90
1	A	3023	U	C2-N1-C1'	5.64	124.47	117.70
1	A	1338	C	C6-N1-C1'	5.63	127.56	120.80
1	A	544	C	C5-C6-N1	-5.62	118.19	121.00
3	C	21	G	N1-C6-O6	-5.61	116.53	119.90
1	A	407	A	O4'-C1'-N9	-5.61	103.71	108.20
24	X	125	ILE	CG1-CB-CG2	-5.61	99.06	111.40
1	A	428	A	C6-N1-C2	-5.59	115.25	118.60
1	A	3247	G	N3-C4-N9	-5.59	122.65	126.00
1	A	515	C	N1-C2-O2	5.59	122.25	118.90
1	A	1124	U	C2-N1-C1'	5.58	124.40	117.70
2	B	4	C	C2-N1-C1'	5.58	124.94	118.80
2	B	39	G	N3-C2-N2	-5.58	116.00	119.90
1	A	430	U	C5-C6-N1	5.58	125.49	122.70
1	A	24	G	N3-C4-N9	-5.56	122.66	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	656	A	C6-N1-C2	-5.56	115.27	118.60
1	A	1297	C	C6-N1-C2	-5.56	118.08	120.30
1	A	1328	C	C2-N3-C4	-5.55	117.12	119.90
1	A	457	C	C4-C5-C6	-5.55	114.62	117.40
4	D	163	LEU	CB-CG-CD2	-5.55	101.56	111.00
1	A	3019	U	N3-C2-O2	-5.54	118.32	122.20
1	A	588	G	C6-N1-C2	-5.54	121.78	125.10
1	A	1159	A	O5'-P-OP2	-5.53	100.72	105.70
1	A	950	G	C6-C5-N7	-5.52	127.09	130.40
13	M	376	LEU	CA-CB-CG	5.52	127.99	115.30
2	B	83	C	C6-N1-C2	5.50	122.50	120.30
1	A	3126	C	N3-C2-O2	-5.50	118.05	121.90
1	A	58	G	C5-C6-O6	5.50	131.90	128.60
1	A	75	G	C6-C5-N7	-5.49	127.10	130.40
1	A	1107	C	N1-C2-O2	-5.49	115.60	118.90
1	A	341	G	C8-N9-C1'	-5.49	119.87	127.00
1	A	547	G	C8-N9-C1'	5.48	134.13	127.00
1	A	612	U	C2-N3-C4	-5.47	123.72	127.00
1	A	266	A	C4-C5-C6	5.46	119.73	117.00
1	A	341	G	N1-C2-N2	-5.46	111.28	116.20
1	A	274	G	C8-N9-C4	5.46	108.58	106.40
1	A	445	G	C4-C5-N7	5.45	112.98	110.80
1	A	1103	A	N7-C8-N9	-5.44	111.08	113.80
1	A	361	A	C6-C5-N7	-5.44	128.49	132.30
1	A	515	C	C6-N1-C1'	-5.44	114.27	120.80
1	A	110	G	N3-C4-C5	-5.43	125.88	128.60
1	A	638	C	C5-C6-N1	5.43	123.72	121.00
1	A	140	C	C6-N1-C2	-5.43	118.13	120.30
1	A	1349	G	N3-C4-C5	5.43	131.31	128.60
1	A	1415	U	C6-N1-C2	5.42	124.25	121.00
1	A	27	C	N3-C2-O2	-5.41	118.11	121.90
1	A	311	C	N1-C2-O2	5.41	122.14	118.90
1	A	526	C	C6-N1-C2	5.40	122.46	120.30
25	Y	280	LEU	CA-CB-CG	5.40	127.71	115.30
1	A	967	A	C5-N7-C8	-5.40	101.20	103.90
1	A	721	G	C4-C5-N7	5.39	112.95	110.80
1	A	364	G	C6-C5-N7	-5.38	127.17	130.40
1	A	457	C	C5-C6-N1	5.38	123.69	121.00
1	A	3023	U	N3-C2-O2	-5.38	118.44	122.20
1	A	217	U	C2-N1-C1'	-5.38	111.25	117.70
1	A	110	G	N3-C4-N9	5.37	129.22	126.00
1	A	1349	G	N1-C6-O6	5.36	123.11	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	3176	G	C4-N9-C1'	5.36	133.47	126.50
1	A	1165	A	C6-N1-C2	-5.34	115.39	118.60
1	A	977	C	N1-C2-O2	5.34	122.10	118.90
1	A	684	G	C4-C5-N7	5.34	112.94	110.80
1	A	81	C	C6-N1-C2	-5.33	118.17	120.30
1	A	41	G	N3-C4-N9	5.33	129.20	126.00
1	A	341	G	N3-C4-N9	5.33	129.20	126.00
1	A	337	G	N3-C4-N9	-5.32	122.81	126.00
1	A	166	C	C5-C6-N1	5.32	123.66	121.00
1	A	517	G	C4-C5-N7	5.32	112.93	110.80
2	B	91	C	C6-N1-C2	-5.31	118.17	120.30
1	A	418	A	C8-N9-C4	-5.30	103.68	105.80
1	A	341	G	C4-C5-N7	5.30	112.92	110.80
2	B	56	G	C5-C6-O6	5.30	131.78	128.60
1	A	650	C	C5-C6-N1	5.30	123.65	121.00
16	P	116	LEU	CB-CG-CD2	-5.30	101.99	111.00
1	A	547	G	C6-N1-C2	-5.29	121.92	125.10
1	A	1103	A	OP1-P-O3'	5.29	116.84	105.20
1	A	950	G	C8-N9-C1'	-5.29	120.13	127.00
1	A	950	G	N9-C4-C5	-5.29	103.29	105.40
1	A	928	C	N3-C2-O2	-5.28	118.21	121.90
1	A	3030	G	P-O3'-C3'	5.27	126.03	119.70
1	A	427	C	N3-C4-C5	5.27	124.01	121.90
8	H	291	LEU	CA-CB-CG	5.26	127.41	115.30
1	A	3378	C	N1-C2-O2	5.26	122.06	118.90
1	A	360	G	N9-C4-C5	-5.26	103.30	105.40
31	i	82	LEU	CA-CB-CG	5.25	127.38	115.30
1	A	298	U	C2-N1-C1'	5.25	124.00	117.70
1	A	404	G	N3-C4-N9	5.25	129.15	126.00
1	A	977	C	C2-N1-C1'	5.24	124.56	118.80
1	A	222	A	C6-C5-N7	-5.24	128.63	132.30
1	A	262	U	C2-N1-C1'	5.23	123.98	117.70
1	A	468	G	O5'-P-OP1	-5.23	100.99	105.70
1	A	3147	G	N3-C4-N9	-5.23	122.86	126.00
1	A	1169	A	C6-C5-N7	-5.23	128.64	132.30
1	A	1108	U	N1-C2-O2	5.22	126.45	122.80
1	A	1176	C	C6-N1-C2	5.22	122.39	120.30
27	a	186	ILE	CG1-CB-CG2	-5.22	99.92	111.40
1	A	1137	C	C2-N1-C1'	5.21	124.54	118.80
1	A	1388	U	C2-N3-C4	-5.21	123.87	127.00
1	A	340	C	N1-C2-O2	5.21	122.03	118.90
1	A	1108	U	N3-C2-O2	-5.21	118.55	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	333	G	C6-C5-N7	-5.19	127.28	130.40
1	A	409	A	N7-C8-N9	5.19	116.39	113.80
1	A	948	C	C5-C6-N1	5.19	123.59	121.00
1	A	1425	U	C6-N1-C2	5.18	124.11	121.00
2	B	135	G	N3-C4-C5	5.18	131.19	128.60
1	A	188	U	C2-N1-C1'	-5.17	111.49	117.70
1	A	222	A	C4-C5-N7	5.17	113.29	110.70
1	A	430	U	C2-N1-C1'	5.17	123.91	117.70
1	A	217	U	N1-C2-N3	5.17	118.00	114.90
1	A	1365	G	O4'-C1'-N9	-5.17	104.07	108.20
1	A	1379	G	N3-C4-C5	-5.16	126.02	128.60
33	l	92	LEU	CA-CB-CG	5.16	127.16	115.30
1	A	1358	C	C2-N3-C4	-5.15	117.32	119.90
1	A	454	C	N1-C2-O2	5.15	121.99	118.90
1	A	659	G	OP2-P-O3'	5.14	116.52	105.20
1	A	544	C	O4'-C1'-N1	5.14	112.31	108.20
1	A	798	G	N9-C4-C5	5.12	107.45	105.40
1	A	505	G	C4-N9-C1'	5.12	133.16	126.50
1	A	56	G	N9-C4-C5	5.12	107.45	105.40
1	A	1351	U	C6-N1-C1'	-5.11	114.04	121.20
1	A	1379	G	N1-C6-O6	-5.11	116.84	119.90
2	B	107	G	C4-C5-N7	5.11	112.84	110.80
1	A	612	U	C5-C6-N1	-5.09	120.16	122.70
1	A	650	C	C6-N1-C2	-5.09	118.27	120.30
1	A	1174	G	C4-C5-N7	5.09	112.83	110.80
1	A	517	G	C6-C5-N7	-5.08	127.35	130.40
1	A	3076	C	C5-C6-N1	5.08	123.54	121.00
1	A	404	G	C4-C5-N7	5.08	112.83	110.80
1	A	720	A	P-O3'-C3'	5.08	125.80	119.70
1	A	1180	A	C8-N9-C4	5.07	107.83	105.80
3	C	232	A	N1-C2-N3	5.07	131.84	129.30
1	A	227	G	C8-N9-C1'	-5.06	120.42	127.00
1	A	1328	C	C5-C6-N1	-5.06	118.47	121.00
1	A	1354	G	C5-N7-C8	-5.05	101.77	104.30
1	A	1108	U	C6-N1-C1'	-5.05	114.14	121.20
1	A	1159	A	N1-C6-N6	5.05	121.63	118.60
1	A	454	C	C6-N1-C1'	-5.04	114.75	120.80
1	A	547	G	C4-N9-C1'	-5.04	119.95	126.50
2	B	135	G	N3-C4-N9	-5.04	122.98	126.00
1	A	3228	C	P-O3'-C3'	5.03	125.74	119.70
1	A	267	G	C4-C5-N7	5.03	112.81	110.80
1	A	587	U	N3-C2-O2	5.03	125.72	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	94	C	C5-C6-N1	-5.03	118.49	121.00
1	A	1311	G	C6-C5-N7	-5.02	127.39	130.40
1	A	1178	G	N3-C4-N9	5.02	129.01	126.00
1	A	517	G	N1-C6-O6	5.02	122.91	119.90
1	A	294	U	C2-N1-C1'	-5.01	111.68	117.70
1	A	186	U	C5-C6-N1	-5.01	120.20	122.70
1	A	3288	G	N3-C4-C5	5.00	131.10	128.60
2	B	70	G	N3-C4-N9	-5.00	123.00	126.00

There are no chirality outliers.

All (39) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	245	ILE	Peptide
4	D	270	PRO	Peptide
6	F	187	SER	Peptide
8	H	285	ARG	Peptide
10	J	177	GLY	Peptide
10	J	219	LYS	Peptide
10	J	232	ARG	Peptide
11	K	77	GLN	Peptide
13	M	114	LEU	Peptide
13	M	240	SER	Peptide
13	M	3	ILE	Peptide
13	M	62	PHE	Peptide
15	O	221	ASN	Peptide
15	O	271	GLN	Peptide
15	O	275	LYS	Peptide
17	Q	47	ASP	Peptide
18	R	183	THR	Peptide
18	R	3	ALA	Peptide
22	V	59	SER	Peptide
23	W	12	ARG	Peptide
23	W	13	ARG	Peptide
23	W	20	PRO	Peptide
24	X	57	ASP	Peptide
24	X	58	ARG	Peptide
25	Y	110	LYS	Peptide
25	Y	186	VAL	Peptide
25	Y	187	PHE	Peptide
25	Y	365	ASP	Peptide
25	Y	368	ASP	Peptide

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Mol	Chain	Res	Type	Group
25	Y	414	GLU	Peptide
25	Y	478	GLY	Peptide
26	Z	56	ASP	Peptide
27	a	185	LYS	Peptide
28	b	261	LEU	Peptide
28	b	265	LYS	Peptide
28	b	268	PHE	Peptide
30	d	266	UNK	Peptide
31	i	95	GLU	Peptide
33	l	83	LYS	Peptide

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
4	D	243/322 (76%)	198 (82%)	41 (17%)	4 (2%)	9 43
5	E	131/220 (60%)	109 (83%)	20 (15%)	2 (2%)	10 44
6	F	332/387 (86%)	290 (87%)	40 (12%)	2 (1%)	25 62
7	G	359/362 (99%)	317 (88%)	40 (11%)	2 (1%)	25 62
8	H	252/376 (67%)	218 (86%)	33 (13%)	1 (0%)	34 69
9	I	146/176 (83%)	133 (91%)	13 (9%)	0	100 100
10	J	237/244 (97%)	212 (90%)	20 (8%)	5 (2%)	7 38
11	K	158/256 (62%)	132 (84%)	26 (16%)	0	100 100
12	L	189/191 (99%)	167 (88%)	18 (10%)	4 (2%)	7 38
13	M	365/605 (60%)	305 (84%)	58 (16%)	2 (0%)	29 66
14	N	224/245 (91%)	199 (89%)	25 (11%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	O	184/295 (62%)	152 (83%)	29 (16%)	3 (2%)	9	43
16	P	106/199 (53%)	84 (79%)	19 (18%)	3 (3%)	5	33
17	Q	135/138 (98%)	113 (84%)	22 (16%)	0	100	100
18	R	171/204 (84%)	148 (86%)	23 (14%)	0	100	100
19	S	195/199 (98%)	179 (92%)	15 (8%)	1 (0%)	29	66
20	T	132/184 (72%)	116 (88%)	16 (12%)	0	100	100
21	U	132/186 (71%)	121 (92%)	11 (8%)	0	100	100
22	V	386/463 (83%)	362 (94%)	24 (6%)	0	100	100
23	W	168/172 (98%)	145 (86%)	23 (14%)	0	100	100
24	X	190/278 (68%)	160 (84%)	29 (15%)	1 (0%)	29	66
25	Y	434/505 (86%)	372 (86%)	59 (14%)	3 (1%)	22	59
26	Z	167/306 (55%)	144 (86%)	22 (13%)	1 (1%)	25	62
27	a	206/291 (71%)	191 (93%)	14 (7%)	1 (0%)	29	66
28	b	80/427 (19%)	70 (88%)	10 (12%)	0	100	100
29	c	123/127 (97%)	115 (94%)	6 (5%)	2 (2%)	9	43
31	i	122/130 (94%)	111 (91%)	11 (9%)	0	100	100
32	j	104/107 (97%)	94 (90%)	10 (10%)	0	100	100
33	l	115/120 (96%)	104 (90%)	10 (9%)	1 (1%)	17	54
34	m	65/100 (65%)	58 (89%)	7 (11%)	0	100	100
35	n	70/88 (80%)	65 (93%)	4 (6%)	1 (1%)	11	45
All	All	5921/7903 (75%)	5184 (88%)	698 (12%)	39 (1%)	26	59

All (39) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	339	LEU
15	O	119	PRO
8	H	284	ASN
26	Z	158	ILE
6	F	34	LYS
12	L	22	SER
12	L	50	ASN
16	P	51	LEU
25	Y	477	TYR
29	c	45	ILE

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Mol	Chain	Res	Type
4	D	224	PRO
5	E	194	LYS
13	M	378	PHE
16	P	63	VAL
19	S	187	GLU
24	X	204	LYS
33	l	84	LYS
4	D	260	SER
6	F	35	ASP
10	J	147	LEU
10	J	157	ASN
10	J	158	LYS
13	M	433	PHE
25	Y	78	ALA
25	Y	199	ASP
27	a	228	GLU
4	D	270	PRO
12	L	21	LYS
15	O	213	LEU
29	c	14	LYS
35	n	40	PRO
10	J	168	ILE
16	P	50	PRO
5	E	147	ILE
7	G	317	PRO
10	J	178	ILE
15	O	274	ILE
4	D	235	VAL
12	L	79	ILE

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	D	218/287 (76%)	218 (100%)	0	100	100
5	E	118/199 (59%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	282/323 (87%)	281 (100%)	1 (0%)	91	95
7	G	288/289 (100%)	288 (100%)	0	100	100
8	H	236/346 (68%)	236 (100%)	0	100	100
9	I	130/153 (85%)	129 (99%)	1 (1%)	81	89
10	J	202/205 (98%)	201 (100%)	1 (0%)	88	94
11	K	129/208 (62%)	129 (100%)	0	100	100
12	L	171/171 (100%)	171 (100%)	0	100	100
13	M	334/548 (61%)	333 (100%)	1 (0%)	92	96
14	N	194/211 (92%)	194 (100%)	0	100	100
15	O	176/276 (64%)	174 (99%)	2 (1%)	73	85
16	P	87/159 (55%)	86 (99%)	1 (1%)	73	85
17	Q	108/109 (99%)	108 (100%)	0	100	100
18	R	152/176 (86%)	152 (100%)	0	100	100
19	S	160/162 (99%)	160 (100%)	0	100	100
20	T	109/146 (75%)	109 (100%)	0	100	100
21	U	110/151 (73%)	110 (100%)	0	100	100
22	V	345/410 (84%)	344 (100%)	1 (0%)	92	96
23	W	154/156 (99%)	154 (100%)	0	100	100
24	X	186/257 (72%)	186 (100%)	0	100	100
25	Y	380/440 (86%)	378 (100%)	2 (0%)	88	94
26	Z	153/274 (56%)	152 (99%)	1 (1%)	84	91
27	a	198/263 (75%)	198 (100%)	0	100	100
28	b	76/383 (20%)	76 (100%)	0	100	100
29	c	108/110 (98%)	108 (100%)	0	100	100
31	i	107/111 (96%)	107 (100%)	0	100	100
32	j	90/91 (99%)	90 (100%)	0	100	100
33	l	104/105 (99%)	104 (100%)	0	100	100
34	m	55/82 (67%)	55 (100%)	0	100	100
35	n	60/71 (84%)	60 (100%)	0	100	100
All	All	5220/6872 (76%)	5209 (100%)	11 (0%)	93	97

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	85	VAL
9	I	101	PHE
10	J	44	ILE
13	M	442	VAL
15	O	277	GLU
15	O	295	LEU
16	P	85	LEU
22	V	293	ARG
25	Y	145	PHE
25	Y	149	ILE
26	Z	38	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (95) such sidechains are listed below:

Mol	Chain	Res	Type
4	D	242	HIS
4	D	291	GLN
5	E	100	HIS
5	E	113	GLN
5	E	130	ASN
6	F	211	GLN
6	F	212	ASN
6	F	273	HIS
6	F	293	ASN
6	F	319	ASN
7	G	5	GLN
7	G	48	GLN
7	G	59	GLN
7	G	114	ASN
7	G	320	ASN
8	H	84	ASN
8	H	101	ASN
8	H	212	HIS
8	H	245	ASN
8	H	295	GLN
9	I	57	HIS
10	J	52	GLN
10	J	64	GLN
11	K	137	ASN
11	K	138	HIS
11	K	155	ASN
11	K	232	HIS
12	L	9	GLN

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Mol	Chain	Res	Type
12	L	50	ASN
12	L	163	GLN
13	M	11	ASN
13	M	14	ASN
13	M	20	GLN
13	M	53	ASN
13	M	189	GLN
14	N	178	GLN
15	O	200	ASN
15	O	201	ASN
15	O	220	GLN
15	O	221	ASN
15	O	233	HIS
15	O	235	GLN
15	O	262	GLN
16	P	25	HIS
16	P	106	GLN
18	R	15	GLN
18	R	23	GLN
18	R	37	HIS
18	R	117	ASN
18	R	138	GLN
18	R	139	HIS
19	S	42	ASN
19	S	50	ASN
20	T	97	ASN
20	T	118	GLN
21	U	45	ASN
22	V	24	ASN
22	V	233	GLN
22	V	283	HIS
22	V	290	GLN
22	V	298	GLN
22	V	310	GLN
22	V	337	ASN
22	V	375	HIS
23	W	3	HIS
23	W	46	GLN
23	W	62	ASN
23	W	74	ASN
24	X	73	HIS
24	X	172	HIS

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Mol	Chain	Res	Type
24	X	229	ASN
24	X	230	ASN
25	Y	51	GLN
25	Y	178	HIS
25	Y	266	GLN
25	Y	288	GLN
25	Y	300	ASN
25	Y	330	ASN
25	Y	363	GLN
25	Y	397	ASN
26	Z	47	ASN
26	Z	110	GLN
27	a	85	ASN
27	a	115	GLN
27	a	141	GLN
27	a	195	HIS
28	b	197	ASN
28	b	209	GLN
28	b	215	HIS
28	b	221	GLN
29	c	120	GLN
32	j	42	GLN
32	j	75	HIS
32	j	88	ASN
34	m	35	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1482/3396 (43%)	506 (34%)	38 (2%)
2	B	155/158 (98%)	50 (32%)	3 (1%)
3	C	63/232 (27%)	34 (53%)	0
All	All	1700/3786 (44%)	590 (34%)	41 (2%)

All (590) RNA backbone outliers are listed below:

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

Continued on next page...

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Mol	Chain	Res	Type
1	A	12	A
1	A	13	A
1	A	14	U
1	A	15	C
1	A	22	G
1	A	25	U
1	A	26	A
1	A	28	C
1	A	38	U
1	A	40	A
1	A	41	G
1	A	42	C
1	A	43	A
1	A	48	A
1	A	49	A
1	A	59	G
1	A	60	A
1	A	65	A
1	A	66	A
1	A	69	C
1	A	71	A
1	A	73	C
1	A	74	G
1	A	76	G
1	A	78	U
1	A	85	A
1	A	91	G
1	A	92	G
1	A	93	C
1	A	96	G
1	A	104	G
1	A	106	A
1	A	108	A
1	A	109	A
1	A	110	G
1	A	111	C
1	A	112	U
1	A	113	C
1	A	116	A
1	A	117	U
1	A	120	G
1	A	122	A

Continued on next page...

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Mol	Chain	Res	Type
1	A	123	A
1	A	124	U
1	A	131	C
1	A	133	U
1	A	134	U
1	A	135	C
1	A	136	G
1	A	147	U
1	A	148	G
1	A	149	U
1	A	155	G
1	A	156	G
1	A	157	A
1	A	161	G
1	A	165	A
1	A	166	C
1	A	170	G
1	A	173	G
1	A	187	A
1	A	190	U
1	A	191	U
1	A	192	C
1	A	193	C
1	A	200	C
1	A	206	G
1	A	210	U
1	A	211	A
1	A	212	G
1	A	218	G
1	A	219	A
1	A	221	A
1	A	225	C
1	A	226	C
1	A	228	U
1	A	233	C
1	A	237	G
1	A	240	U
1	A	241	G
1	A	243	G
1	A	244	G
1	A	245	U
1	A	248	U

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Mol	Chain	Res	Type
1	A	249	U
1	A	250	U
1	A	251	G
1	A	252	U
1	A	253	A
1	A	259	C
1	A	265	A
1	A	267	G
1	A	268	A
1	A	269	G
1	A	270	U
1	A	277	G
1	A	281	G
1	A	282	G
1	A	284	A
1	A	285	A
1	A	286	U
1	A	287	G
1	A	295	A
1	A	298	U
1	A	299	G
1	A	304	G
1	A	316	U
1	A	323	A
1	A	326	U
1	A	329	U
1	A	330	G
1	A	332	C
1	A	337	G
1	A	338	A
1	A	339	C
1	A	346	C
1	A	349	A
1	A	352	A
1	A	354	U
1	A	356	C
1	A	375	A
1	A	376	G
1	A	386	A
1	A	390	G
1	A	392	G
1	A	396	A

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Mol	Chain	Res	Type
1	A	397	A
1	A	398	A
1	A	399	A
1	A	401	U
1	A	402	A
1	A	403	C
1	A	404	G
1	A	407	A
1	A	410	U
1	A	412	G
1	A	417	A
1	A	421	G
1	A	422	A
1	A	424	G
1	A	438	A
1	A	439	C
1	A	440	A
1	A	441	U
1	A	446	U
1	A	453	C
1	A	464	U
1	A	465	U
1	A	466	G
1	A	467	U
1	A	468	G
1	A	473	G
1	A	475	G
1	A	487	U
1	A	490	A
1	A	494	G
1	A	495	G
1	A	498	A
1	A	501	A
1	A	510	G
1	A	512	U
1	A	515	C
1	A	517	G
1	A	520	U
1	A	521	A
1	A	523	A
1	A	525	C
1	A	530	G

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Mol	Chain	Res	Type
1	A	534	U
1	A	535	G
1	A	540	U
1	A	541	U
1	A	543	C
1	A	544	C
1	A	545	U
1	A	546	C
1	A	547	G
1	A	548	G
1	A	550	A
1	A	551	A
1	A	552	G
1	A	555	U
1	A	557	A
1	A	558	U
1	A	559	A
1	A	568	G
1	A	572	A
1	A	578	A
1	A	579	G
1	A	592	A
1	A	593	C
1	A	597	G
1	A	604	G
1	A	608	A
1	A	609	G
1	A	610	G
1	A	611	A
1	A	616	G
1	A	619	A
1	A	620	U
1	A	621	A
1	A	622	A
1	A	627	U
1	A	635	G
1	A	636	C
1	A	637	C
1	A	642	U
1	A	643	U
1	A	644	G
1	A	645	A

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Mol	Chain	Res	Type
1	A	646	A
1	A	647	A
1	A	649	A
1	A	650	C
1	A	659	G
1	A	660	A
1	A	661	G
1	A	668	G
1	A	669	U
1	A	675	C
1	A	676	G
1	A	677	A
1	A	679	U
1	A	681	U
1	A	682	U
1	A	683	U
1	A	684	G
1	A	686	G
1	A	688	G
1	A	689	U
1	A	691	A
1	A	705	A
1	A	721	G
1	A	722	G
1	A	726	G
1	A	734	C
1	A	735	A
1	A	742	G
1	A	747	A
1	A	752	C
1	A	754	G
1	A	756	U
1	A	757	C
1	A	774	G
1	A	775	A
1	A	776	U
1	A	777	U
1	A	779	G
1	A	780	A
1	A	781	G
1	A	785	G
1	A	786	A

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Mol	Chain	Res	Type
1	A	806	A
1	A	814	U
1	A	933	A
1	A	940	G
1	A	944	C
1	A	948	C
1	A	958	C
1	A	961	C
1	A	962	A
1	A	964	G
1	A	965	A
1	A	967	A
1	A	973	A
1	A	974	G
1	A	975	C
1	A	976	U
1	A	977	C
1	A	978	G
1	A	980	A
1	A	981	U
1	A	982	C
1	A	984	G
1	A	987	U
1	A	990	U
1	A	991	G
1	A	1063	G
1	A	1098	A
1	A	1099	A
1	A	1103	A
1	A	1104	G
1	A	1111	U
1	A	1112	A
1	A	1116	G
1	A	1117	G
1	A	1118	C
1	A	1127	G
1	A	1135	A
1	A	1136	A
1	A	1138	U
1	A	1139	G
1	A	1142	G
1	A	1150	A

Continued on next page...

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Mol	Chain	Res	Type
1	A	1151	U
1	A	1153	A
1	A	1155	C
1	A	1159	A
1	A	1160	C
1	A	1178	G
1	A	1179	A
1	A	1180	A
1	A	1181	U
1	A	1182	A
1	A	1186	G
1	A	1204	A
1	A	1206	G
1	A	1208	U
1	A	1209	G
1	A	1215	U
1	A	1218	U
1	A	1296	C
1	A	1297	C
1	A	1299	U
1	A	1313	G
1	A	1314	C
1	A	1316	C
1	A	1318	A
1	A	1325	U
1	A	1330	A
1	A	1331	U
1	A	1332	A
1	A	1337	A
1	A	1345	G
1	A	1348	U
1	A	1349	G
1	A	1350	A
1	A	1351	U
1	A	1352	A
1	A	1353	U
1	A	1354	G
1	A	1355	A
1	A	1356	U
1	A	1357	G
1	A	1359	C
1	A	1360	C

Continued on next page...

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Mol	Chain	Res	Type
1	A	1370	G
1	A	1373	A
1	A	1385	C
1	A	1386	A
1	A	1388	U
1	A	1393	A
1	A	1394	A
1	A	1399	A
1	A	1400	G
1	A	1404	G
1	A	1405	U
1	A	1410	U
1	A	1418	A
1	A	1419	A
1	A	1423	C
1	A	1424	C
1	A	1428	A
1	A	1429	G
1	A	1434	G
1	A	1435	A
1	A	1436	U
1	A	1437	C
1	A	1440	G
1	A	1442	U
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1450	G
1	A	1451	C
1	A	1881	A
1	A	2357	A
1	A	2358	A
1	A	2359	C
1	A	2362	C
1	A	2363	A
1	A	2370	G
1	A	2999	U
1	A	3012	A
1	A	3014	U
1	A	3017	A
1	A	3021	A
1	A	3022	G

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Mol	Chain	Res	Type
1	A	3023	U
1	A	3024	A
1	A	3025	C
1	A	3026	G
1	A	3028	G
1	A	3029	A
1	A	3031	G
1	A	3032	A
1	A	3035	A
1	A	3036	G
1	A	3037	U
1	A	3040	A
1	A	3047	U
1	A	3049	A
1	A	3056	U
1	A	3057	U
1	A	3058	U
1	A	3064	U
1	A	3068	U
1	A	3074	G
1	A	3078	U
1	A	3079	U
1	A	3086	A
1	A	3087	A
1	A	3090	U
1	A	3092	C
1	A	3093	C
1	A	3094	A
1	A	3097	C
1	A	3099	C
1	A	3100	U
1	A	3101	G
1	A	3104	U
1	A	3110	C
1	A	3115	C
1	A	3122	A
1	A	3125	U
1	A	3126	C
1	A	3130	A
1	A	3131	U
1	A	3132	C
1	A	3138	U

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Mol	Chain	Res	Type
1	A	3142	A
1	A	3143	C
1	A	3144	G
1	A	3150	A
1	A	3165	A
1	A	3166	C
1	A	3173	G
1	A	3174	A
1	A	3176	G
1	A	3179	U
1	A	3180	A
1	A	3181	C
1	A	3184	A
1	A	3187	A
1	A	3188	G
1	A	3196	U
1	A	3199	G
1	A	3207	U
1	A	3208	G
1	A	3210	A
1	A	3212	C
1	A	3213	A
1	A	3217	C
1	A	3218	A
1	A	3219	G
1	A	3223	A
1	A	3224	G
1	A	3226	A
1	A	3227	A
1	A	3229	G
1	A	3232	G
1	A	3242	G
1	A	3244	A
1	A	3245	A
1	A	3246	G
1	A	3251	U
1	A	3253	G
1	A	3254	G
1	A	3259	U
1	A	3260	G
1	A	3263	G
1	A	3265	C

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Mol	Chain	Res	Type
1	A	3267	A
1	A	3268	A
1	A	3269	U
1	A	3270	U
1	A	3271	G
1	A	3273	A
1	A	3275	U
1	A	3276	G
1	A	3277	U
1	A	3278	C
1	A	3279	A
1	A	3286	G
1	A	3289	G
1	A	3292	A
1	A	3293	U
1	A	3295	A
1	A	3304	U
1	A	3309	G
1	A	3310	A
1	A	3314	A
1	A	3316	A
1	A	3317	U
1	A	3320	A
1	A	3324	C
1	A	3327	G
1	A	3328	G
1	A	3330	A
1	A	3333	G
1	A	3334	U
1	A	3335	A
1	A	3336	A
1	A	3338	C
1	A	3368	U
1	A	3369	G
1	A	3370	A
1	A	3374	U
1	A	3375	A
1	A	3378	C
1	A	3381	U
1	A	3382	U
2	B	2	A
2	B	4	C

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Mol	Chain	Res	Type
2	B	7	U
2	B	20	U
2	B	22	U
2	B	23	U
2	B	34	U
2	B	39	G
2	B	42	G
2	B	51	G
2	B	52	A
2	B	59	A
2	B	62	C
2	B	63	G
2	B	71	A
2	B	77	A
2	B	78	G
2	B	81	U
2	B	82	U
2	B	83	C
2	B	84	C
2	B	86	U
2	B	87	G
2	B	89	A
2	B	90	U
2	B	95	G
2	B	99	C
2	B	100	U
2	B	104	A
2	B	106	C
2	B	109	A
2	B	111	A
2	B	112	U
2	B	113	U
2	B	114	G
2	B	116	G
2	B	123	G
2	B	124	G
2	B	125	U
2	B	126	A
2	B	128	U
2	B	129	C
2	B	130	C
2	B	131	A

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Mol	Chain	Res	Type
2	B	144	G
2	B	148	G
2	B	149	A
2	B	151	C
2	B	152	G
2	B	154	C
3	C	2	C
3	C	4	U
3	C	5	C
3	C	6	U
3	C	7	C
3	C	10	A
3	C	15	C
3	C	16	U
3	C	17	G
3	C	24	A
3	C	26	U
3	C	29	G
3	C	33	U
3	C	34	A
3	C	38	U
3	C	40	U
3	C	41	G
3	C	42	G
3	C	43	A
3	C	45	U
3	C	47	A
3	C	48	A
3	C	49	C
3	C	52	G
3	C	53	A
3	C	54	A
3	C	55	A
3	C	56	U
3	C	58	G
3	C	59	C
3	C	229	U
3	C	230	A
3	C	231	A
3	C	232	A

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2	U
1	A	13	A
1	A	75	G
1	A	160	G
1	A	239	G
1	A	250	U
1	A	315	C
1	A	385	A
1	A	420	G
1	A	452	G
1	A	486	U
1	A	618	C
1	A	621	A
1	A	645	A
1	A	646	A
1	A	649	A
1	A	661	G
1	A	720	A
1	A	976	U
1	A	1102	A
1	A	1103	A
1	A	1152	G
1	A	1154	A
1	A	1159	A
1	A	1203	A
1	A	1205	A
1	A	1329	U
1	A	1351	U
1	A	2362	C
1	A	3030	G
1	A	3035	A
1	A	3078	U
1	A	3218	A
1	A	3228	C
1	A	3269	U
1	A	3276	G
1	A	3292	A
1	A	3316	A
2	B	21	C
2	B	123	G
2	B	151	C

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	d	6

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	174:UNK	C	180:UNK	N	119.43
1	d	120:UNK	C	130:UNK	N	51.93
1	d	233:UNK	C	240:UNK	N	39.23
1	d	213:UNK	C	220:UNK	N	26.40
1	d	250:UNK	C	259:UNK	N	16.25
1	d	190:UNK	C	200:UNK	N	13.74

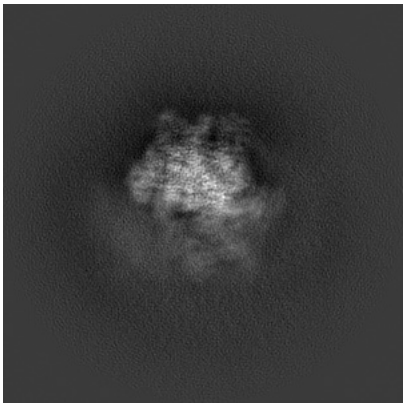
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-6878. These allow visual inspection of the internal detail of the map and identification of artifacts.

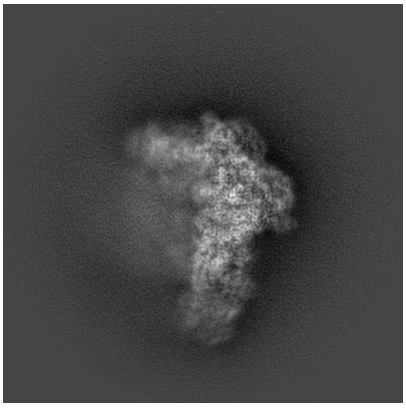
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

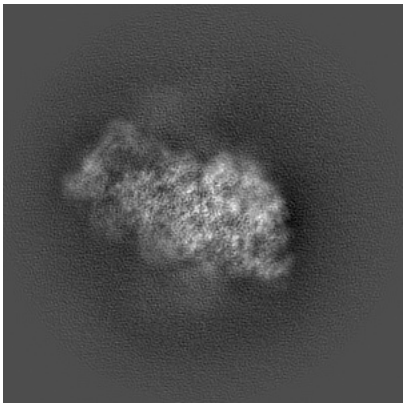
6.1.1 Primary map



X



Y

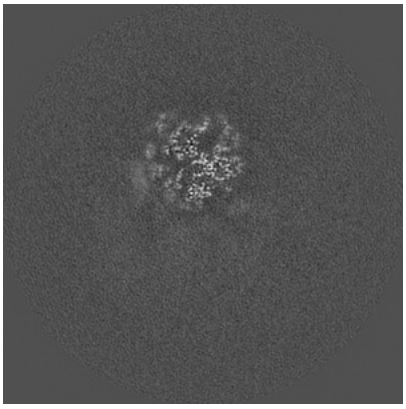


Z

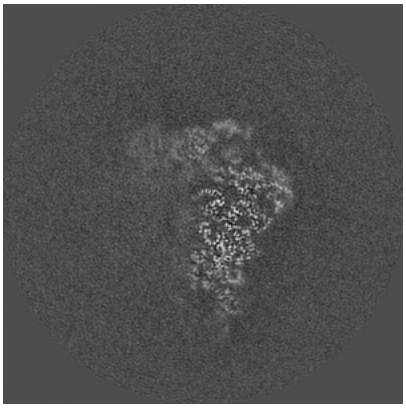
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

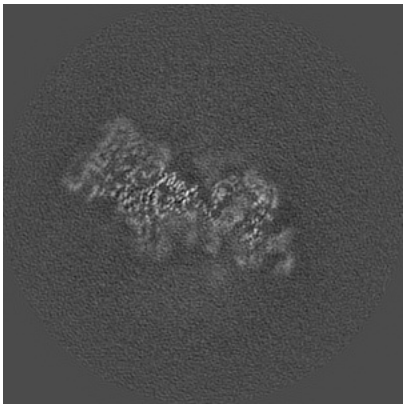
6.2.1 Primary map



X Index: 180



Y Index: 180

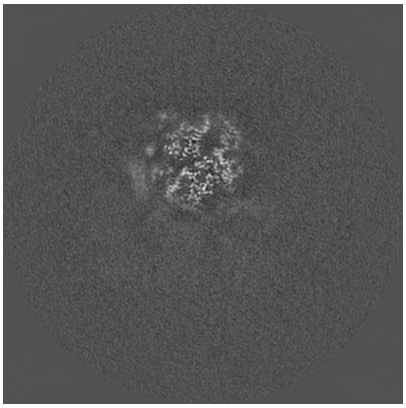


Z Index: 180

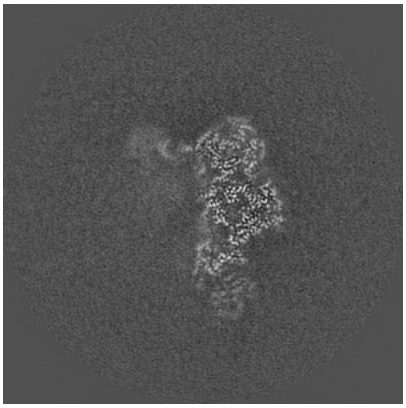
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

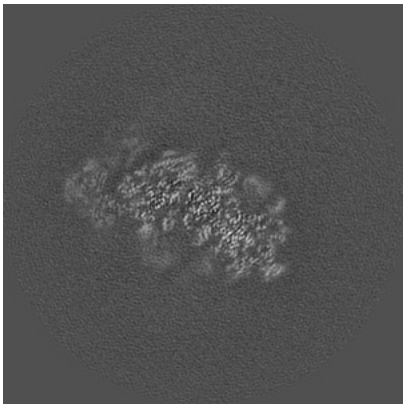
6.3.1 Primary map



X Index: 182



Y Index: 168



Z Index: 195

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

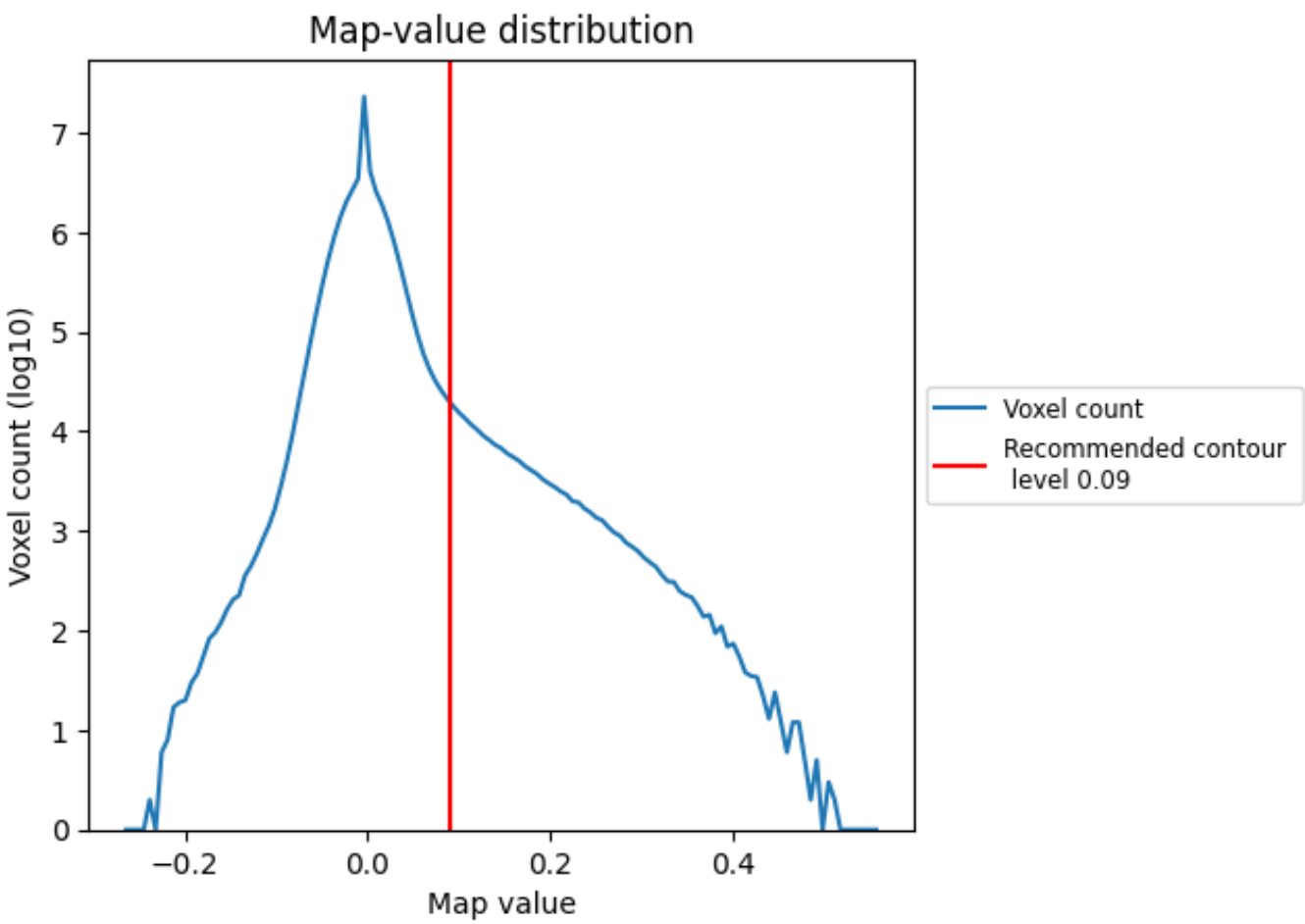
6.5 Mask visualisation (i)

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

7 Map analysis (i)

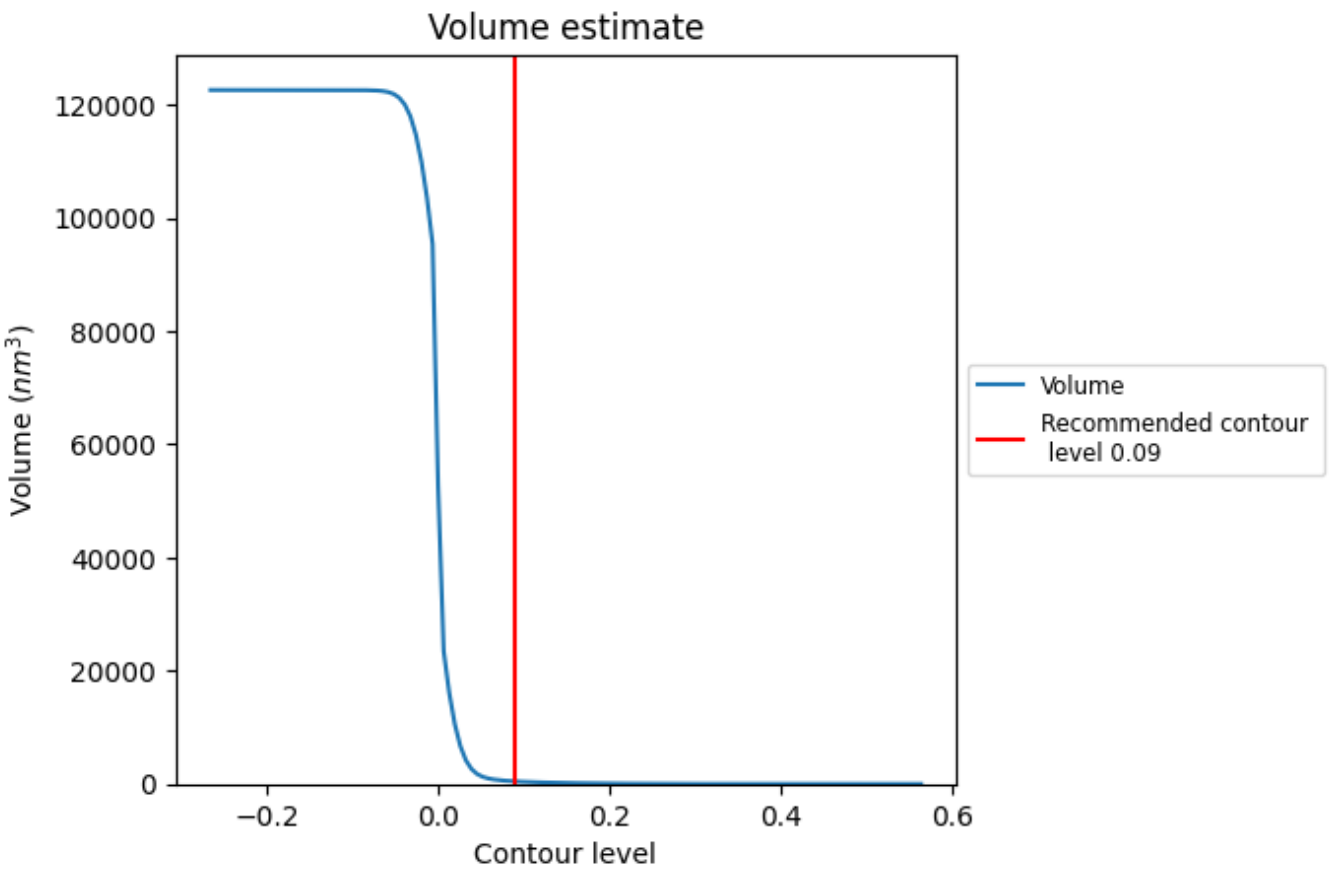
This section contains the results of statistical analysis of the map.

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.

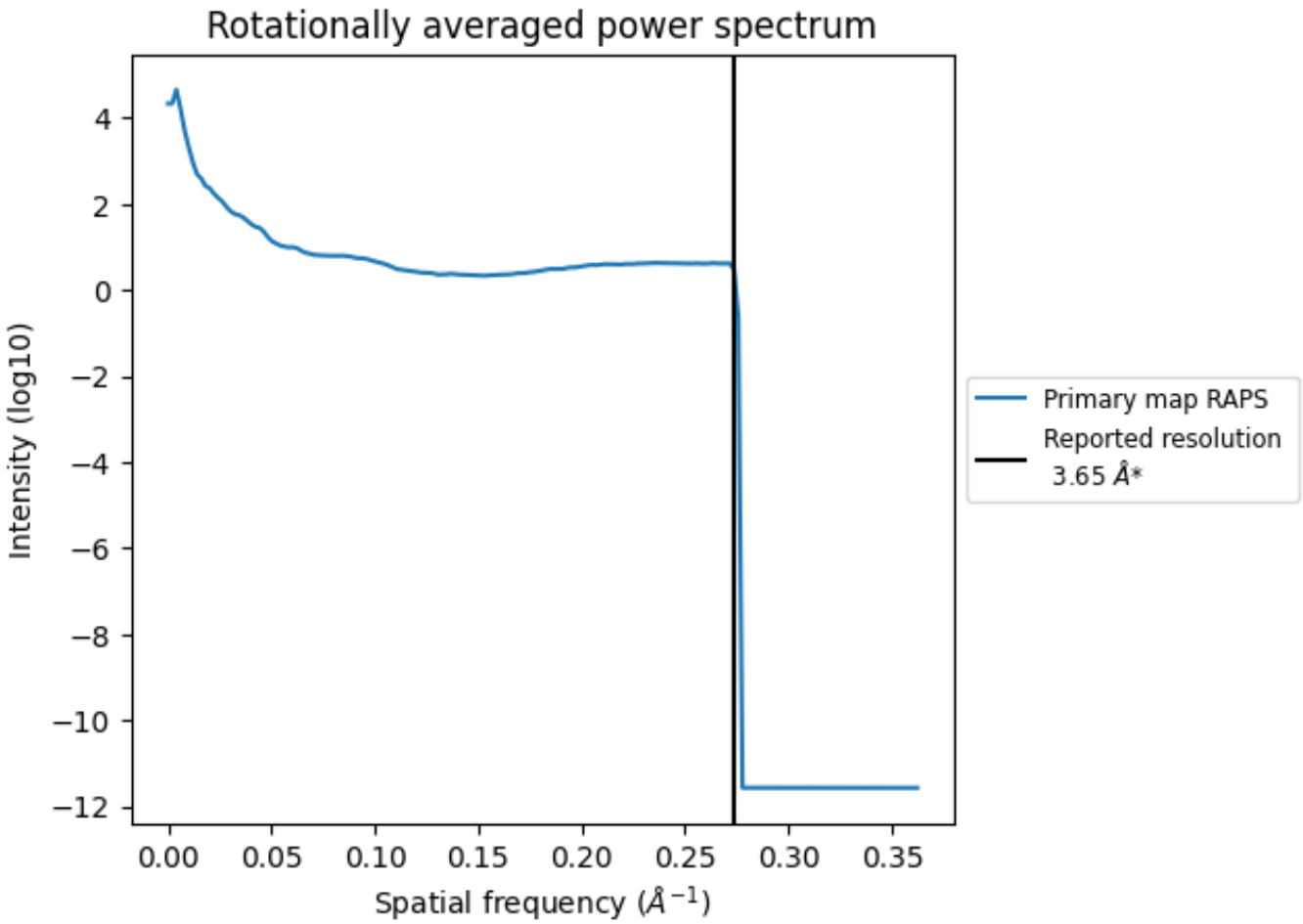
7.2 Volume estimate (i)



The volume at the recommended contour level is 459 nm^3; this corresponds to an approximate mass of 415 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)

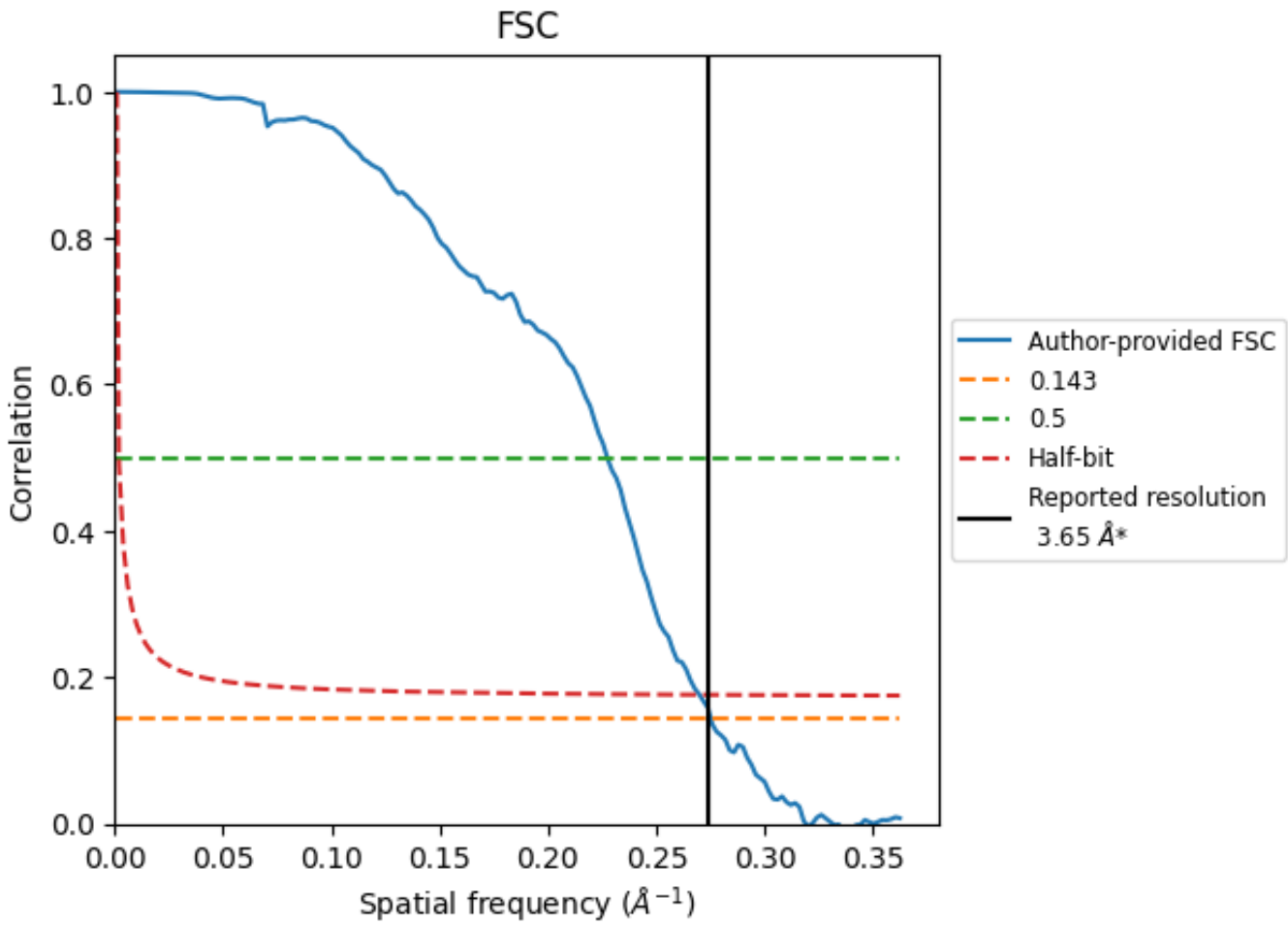


*Reported resolution corresponds to spatial frequency of 0.274 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.274 Å^{-1}

8.2 Resolution estimates (i)

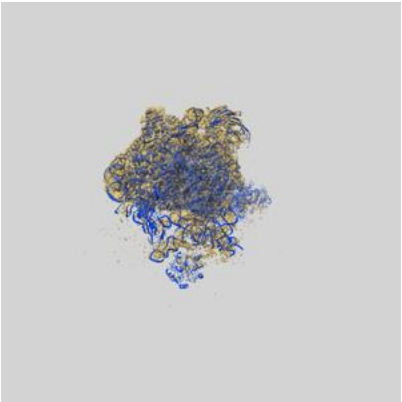
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.65	-	-
Author-provided FSC curve	3.64	4.40	3.71
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

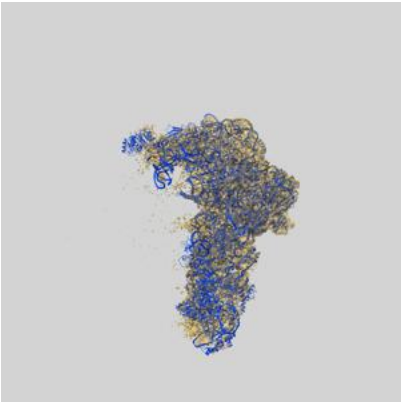
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-6878 and PDB model 5Z3G. Per-residue inclusion information can be found in section 3 on page 11.

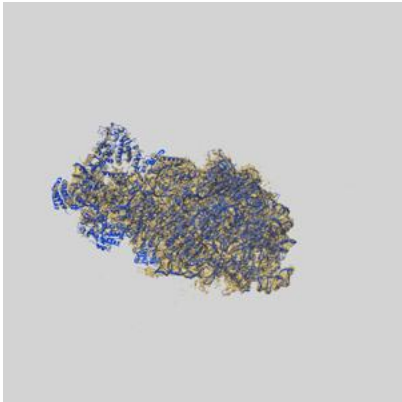
9.1 Map-model overlay (i)



X



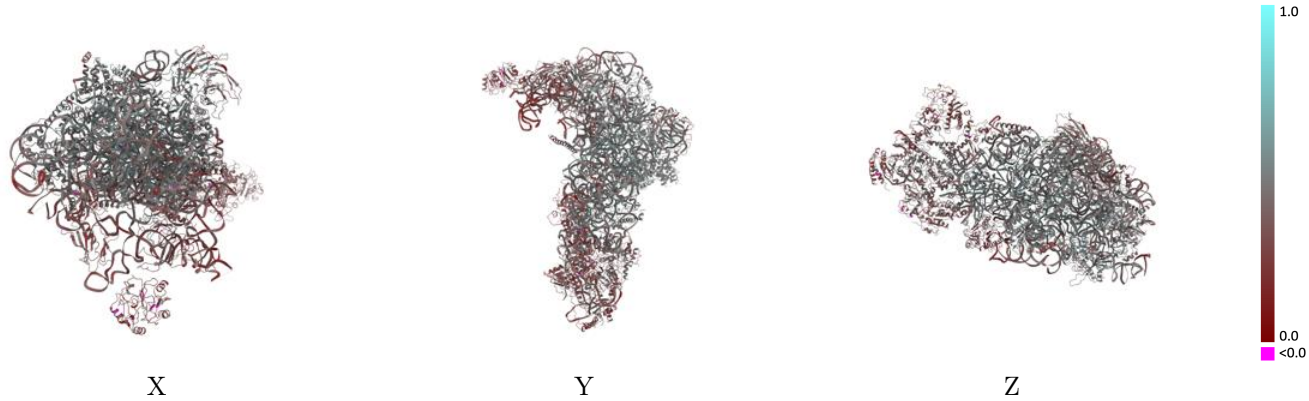
Y



Z

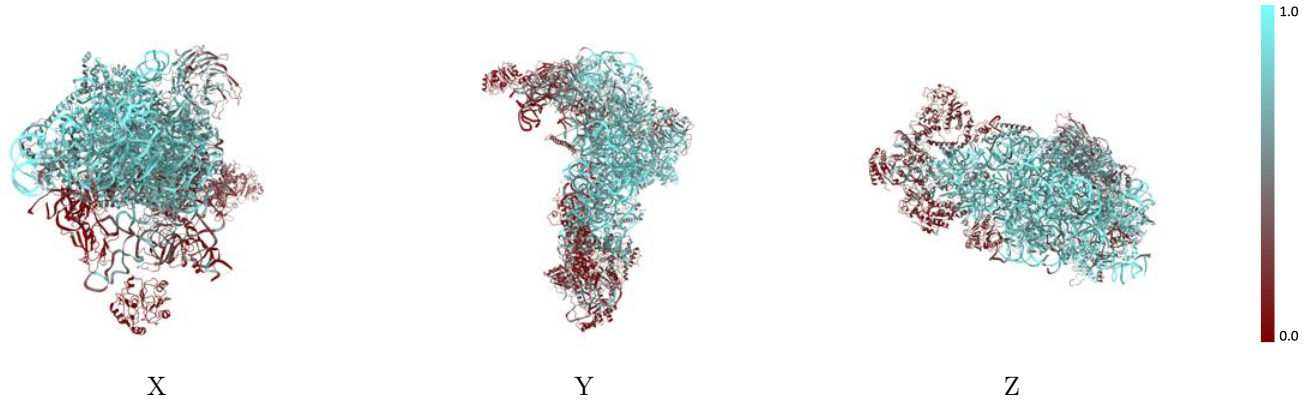
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



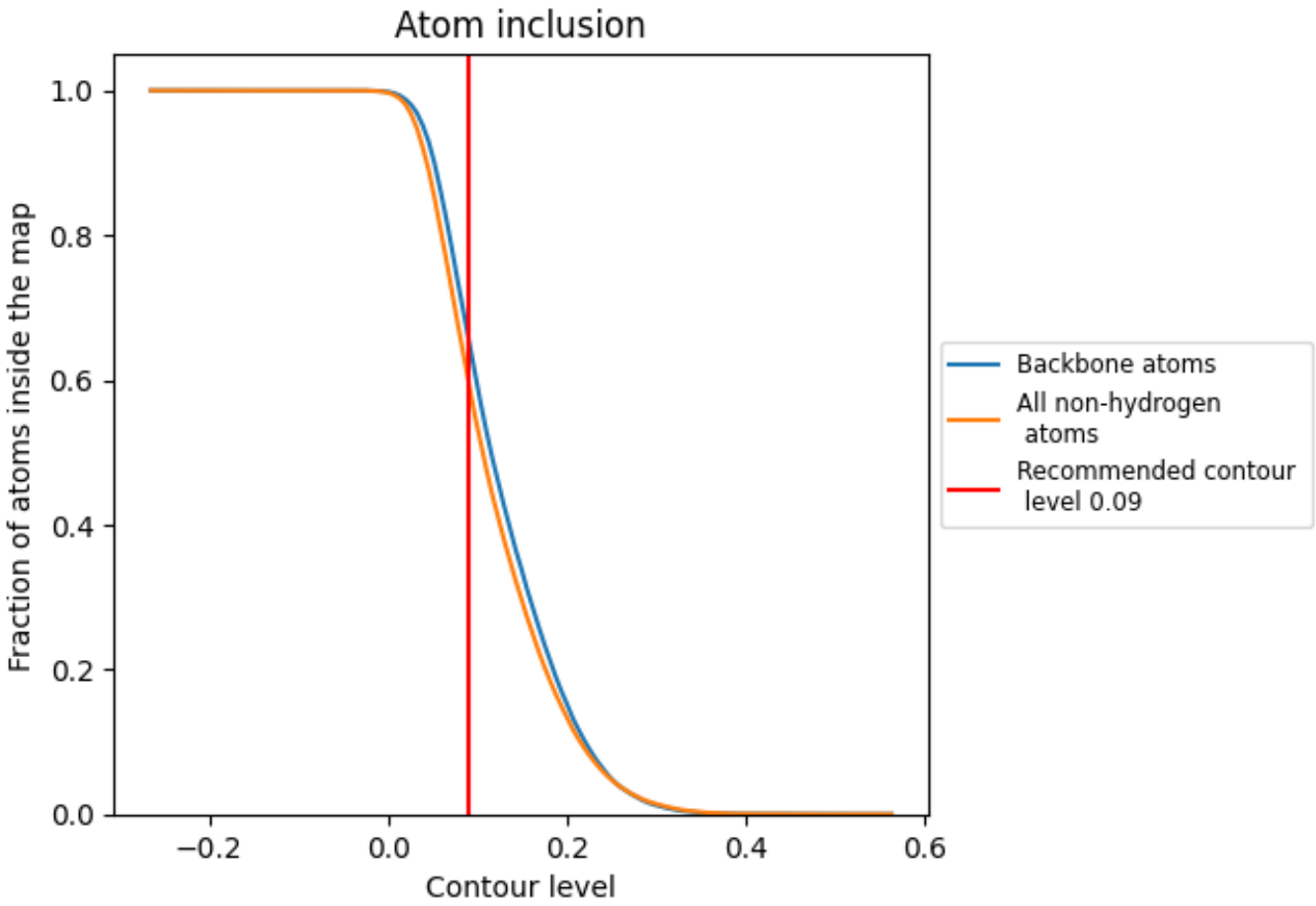
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion (i)



At the recommended contour level, 66% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6007	0.4220
A	0.7607	0.4290
B	0.7797	0.4320
C	0.5095	0.3770
D	0.2748	0.3480
E	0.2922	0.3550
F	0.3700	0.3670
G	0.7678	0.5190
H	0.2450	0.3530
I	0.7654	0.4890
J	0.7788	0.4920
K	0.5772	0.4550
L	0.0987	0.3730
M	0.1376	0.2980
N	0.0458	0.2850
O	0.6263	0.4490
P	0.7687	0.4960
Q	0.7374	0.4630
R	0.6894	0.4930
S	0.7160	0.4770
T	0.4006	0.4380
U	0.7378	0.4870
V	0.5215	0.4380
W	0.6500	0.4530
X	0.7729	0.4610
Y	0.1908	0.3440
Z	0.7962	0.4920
a	0.1033	0.3090
b	0.0119	0.2690
c	0.7534	0.4970
d	0.5727	0.4430
i	0.7538	0.5340
j	0.8173	0.5310
l	0.5981	0.4430
m	0.4627	0.4030
n	0.8040	0.5170