Full wwPDB EM Validation Report (i)

Nov 21, 2022 – 02:25 PM EST

PDB ID	:	8ETI
EMDB ID	:	EMD-24395
Title	:	Fkbp39 associated 60S nascent ribosome State 1
Authors	:	Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on	:	2022-10-17
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 (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:

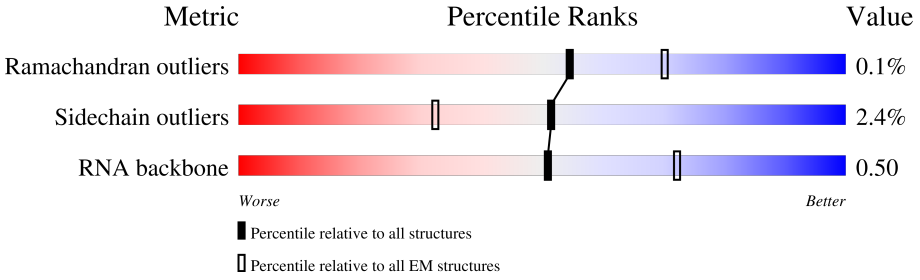
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.70 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	3497	6% 33% 12% 55%
2	2	165	7% 70% 22% 8%
3	3	302	58% 62% • 37%
4	4	217	96% 94% • •
5	5	387	88% 87% • 12%
6	6	300	27% 15% 12% 73%
7	A	295	85% 85% • 14%
8	B	388	30% 84% • 14%

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Mol	Chain	Length	Quality of chain
9	C	363	89% 10%
10	D	578	67% 68% 32%
11	E	195	38% 84% 13%
12	F	250	14% 95%
13	G	259	41% 70% 28%
14	H	190	43% 96%
15	J	333	34% 34% 66%
16	K	373	64% 64% 36%
17	L	208	6% 55% 45%
18	M	134	16% 90% 7%
19	N	201	10% 82% 17%
20	O	197	12% 97%
21	P	187	43% 77% 21%
22	Q	187	9% 72% 27%
23	S	176	12% 90% 5% 5%
24	V	139	73% 91% 9%
25	W	241	58% 72% 28%
26	X	141	32% 87% 13%
27	Y	126	6% 98%
28	b	642	48% 61% 39%
29	d	113	48% 86% 14%
30	e	127	10% 96%
31	f	108	6% 94%
32	h	122	11% 96%
33	i	99	36% 84% 14%

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Mol	Chain	Length	Quality of chain
34	j	91	76% 22%
35	m	740	16% 16% 84%
36	n	607	61% 60% 39%
37	o	276	49% 49% 51%
38	r	260	51% 64% 36%
39	t	249	90% 90% 10%
40	u	192	40% 57% 43%
41	v	209	75% 76% 23%
42	x	306	99% 97%
43	y	244	67% 92% 8%
44	z	117	20% 30% 70%
45	T	160	8% 14% 86%

2 Entry composition (i)

There are 46 unique types of molecules in this entry. The entry contains 90456 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 RNA (1564-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1579	33816	15104	6144	10989	1579	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	501	G	U	conflict	GB 157310483
1	503	U	G	conflict	GB 157310483
1	2930	U	C	conflict	GB 157310483

- Molecule 2 is a RNA chain called RNA (152-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	152	3229	1445	568	1064	152	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	190	1576	999	299	272	6	0	0

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	209	1762	1149	301	304	8	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein nsa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	340	2686	1716	468	491	11	0	0

- Molecule 6 is a RNA chain called RNA (125-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	81	1717	770	296	570	81	0	0

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A	254	1427	856	285	285	1	0	0

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	B	332	2641	1676	488	468	9	0	0

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	328	2571	1631	486	450	4	0	0

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	D	391	1931	1149	391	391	0	0

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	170	1328	854	243	228	3	0	0

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	239	1939	1247	355	334	3	0	0

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	186	1464	938	264	260	2	0	0

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	H	183	902	536	183	183	0	0

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	J	113	564	338	113	113	0	0

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	K	240	1190	710	240	240	0	0

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	L	115	938	590	197	150	1	0	0

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	M	125	1007	644	191	168	4	0	0

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	N	166	1401	877	291	230	3	0	0

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	196	1557	999	297	257	4	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	P	147	1154	733	209	209	3	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Q	136	1057	664	205	187	1	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	S	167	1395	900	262	228	5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	V	127	624	369	127	128	0	0

- Molecule 25 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	W	173	850	504	173	173	0	0

- Molecule 26 is a protein called 60S ribosomal protein L25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	X	122	750	457	153	140	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Y	125	998	622	201	173	2	0	0

- Molecule 28 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	b	391	1939	1157	391	391	0	0

- Molecule 29 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	d	97	483	289	97	97	0	0

- Molecule 30 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	123	986	616	201	164	5	0	0

- Molecule 31 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	106	839	534	162	140	3	0	0

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	h	120	994	626	193	175	0	0

- Molecule 33 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	i	85	696	431	148	116	1	0	0

- Molecule 34 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	j	71	563	346	121	90	6	0	0

- Molecule 35 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	m	121	859	529	163	167	0	0

- Molecule 36 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	n	369	2215	1369	430	415	1	0	0

- Molecule 37 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	o	134	666	398	134	134	0	0

- Molecule 38 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
38	r	166	823	490	166	167	0	0

- Molecule 39 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
39	t	225	1115	664	225	226	0	0

- Molecule 40 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	u	110	546	326	110	110	0	0

- Molecule 41 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	v	161	1299	818	243	235	3	0	0

- Molecule 42 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	x	303	2503	1570	460	465	8	0	0

- Molecule 43 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	y	225	1107	657	225	225	0	0

- Molecule 44 is a protein called UPF0642 protein C32H8.05.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
44	z	35	173	103	35	35	0	0

- Molecule 45 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	T	23	175	111	31	33	0	0

- Molecule 46 is ZINC ION (three-letter code: ZN) (formula: Zn).

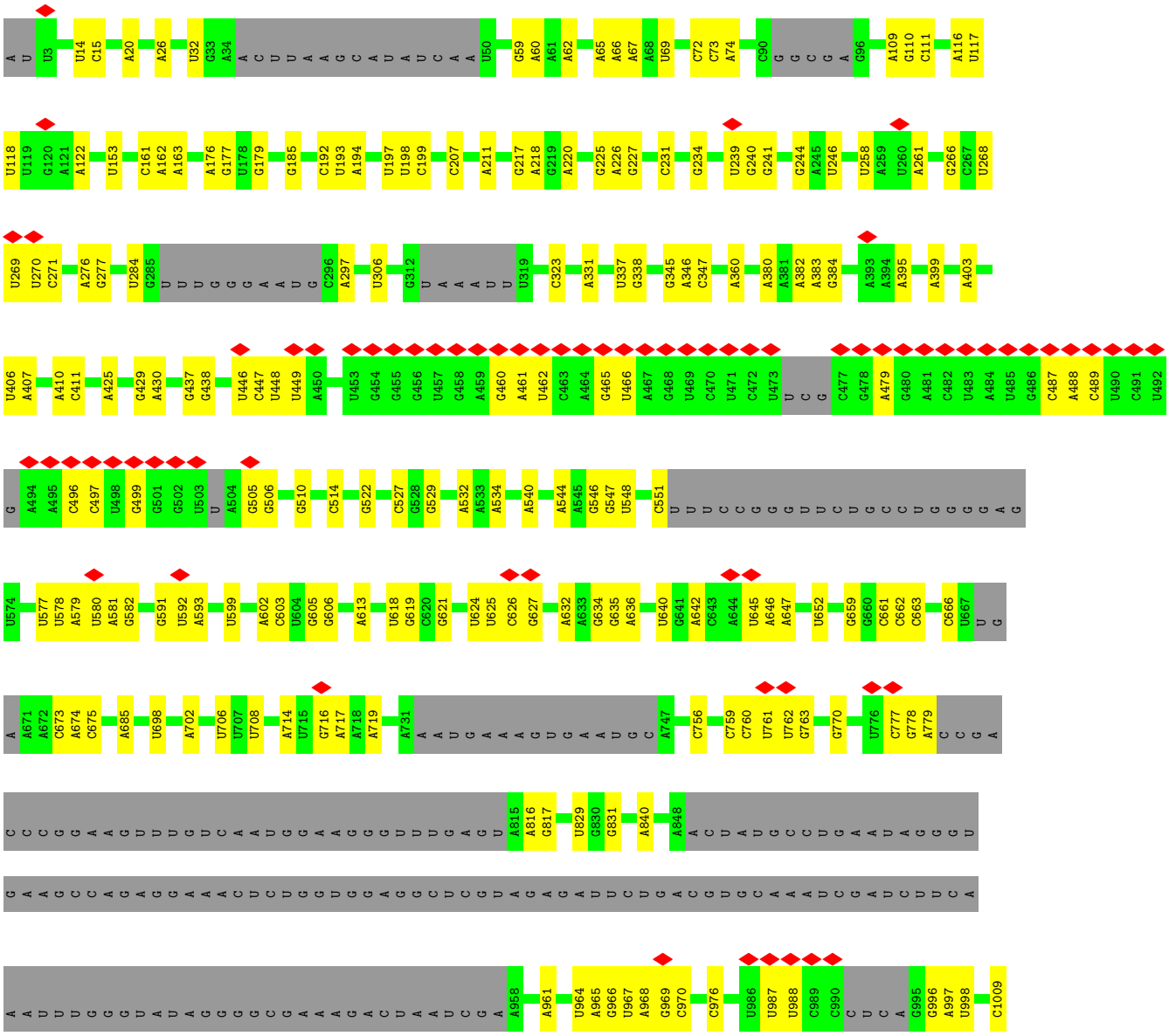
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
46	j	1	1	1	0

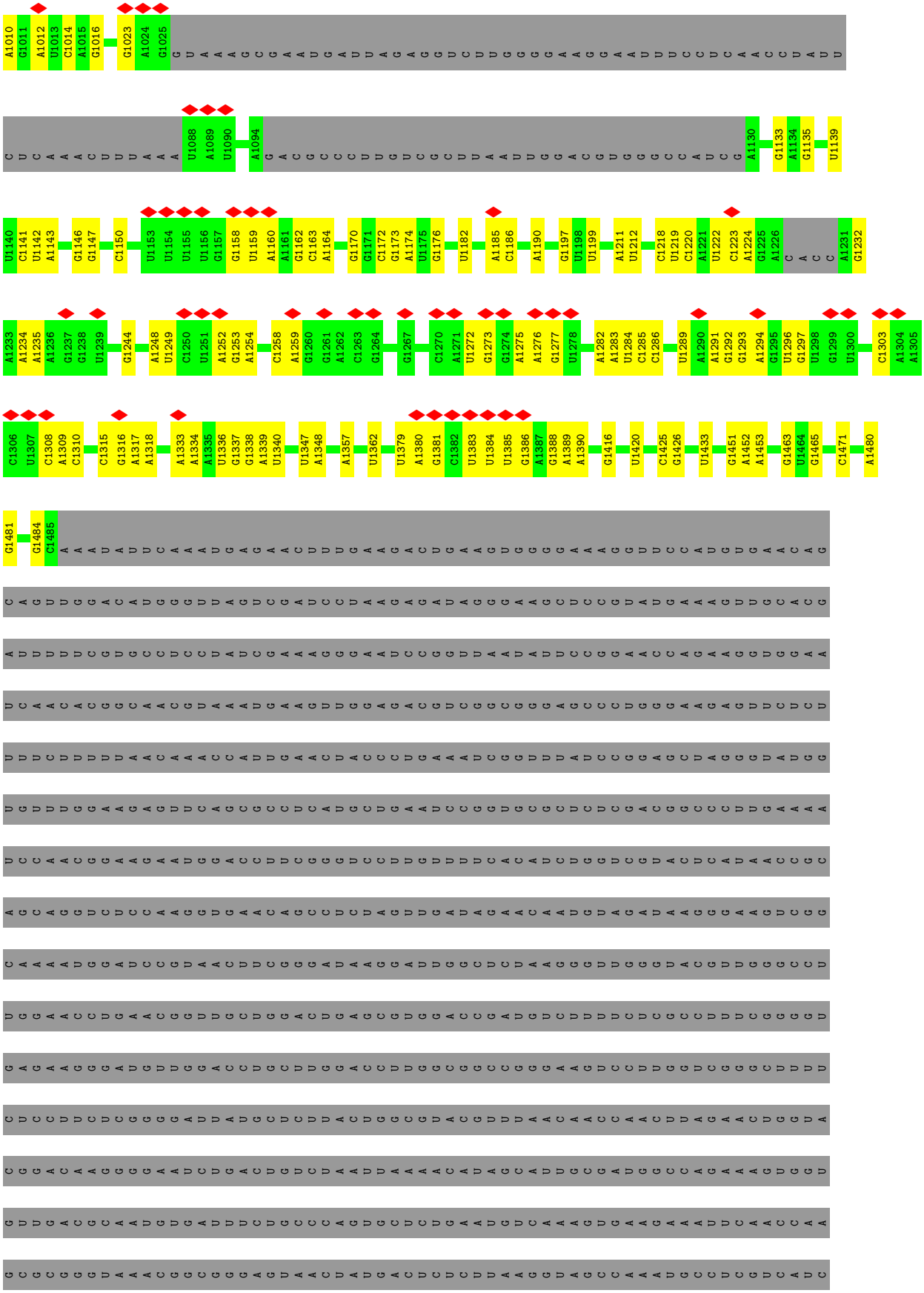
3 Residue-property plots (i)

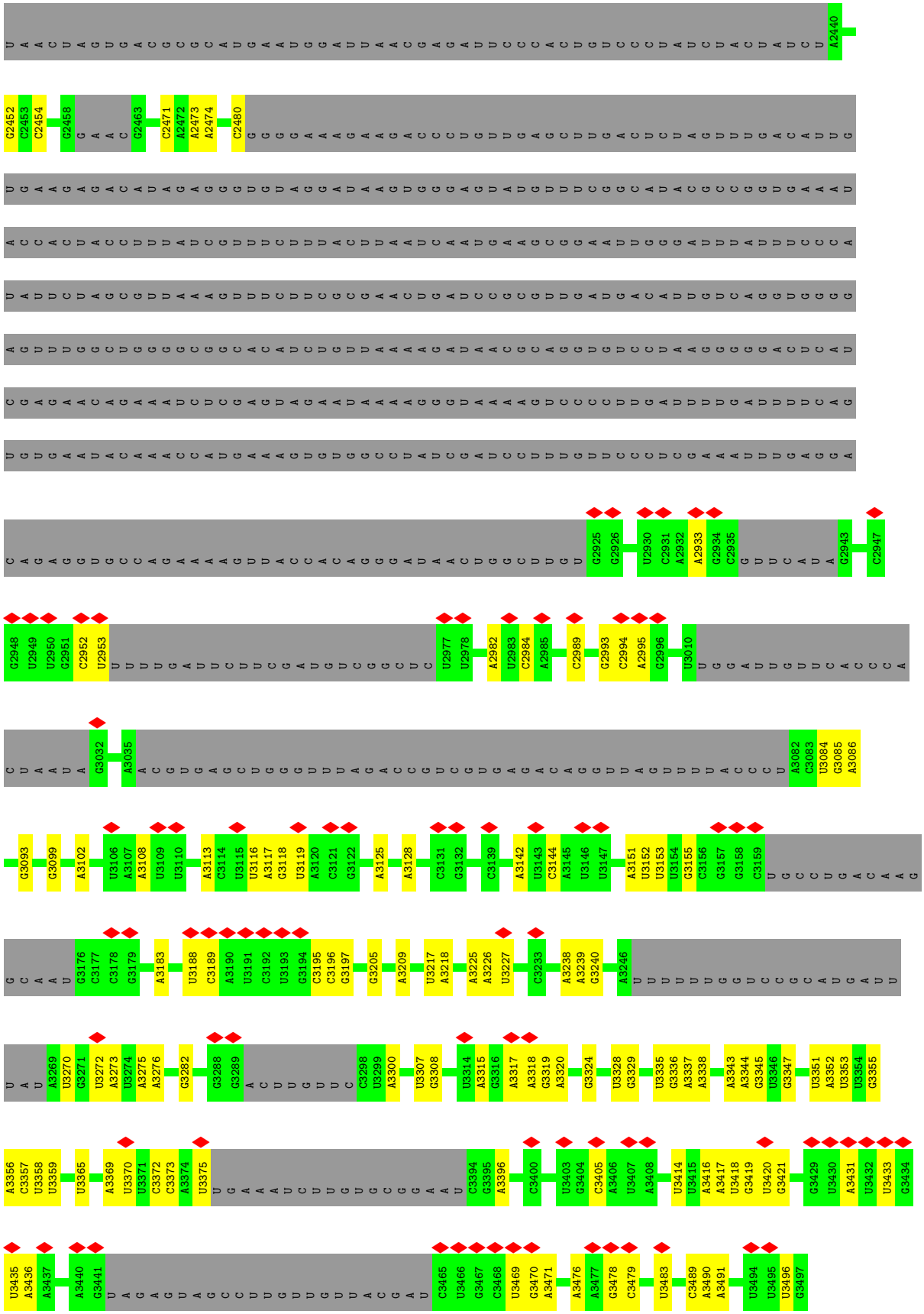
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (1564-MER)

Chain 1:

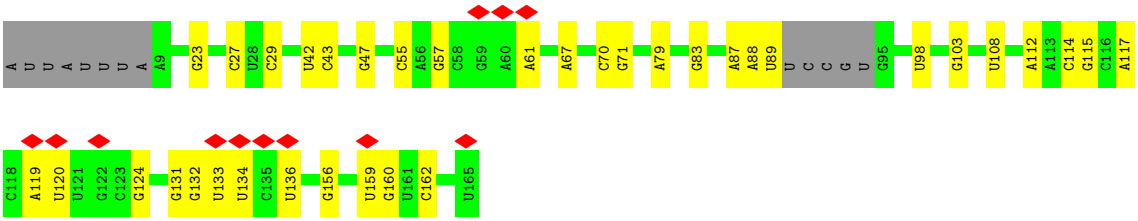



A1010 G1011 A1012 U1013 C1014 A1015 G1016 G1023 A1024 G1025
U1088 A1089 U1090 A1094 A1130 G1133 A1134 G1135 U1139
U1140 C1141 U1142 A1143 G1146 G1147 C1150 U1153 U1154 U1155 U1156 G1157 G1158 U1159 A1160 A1161 G1162 C1163 A1164 G1170 C1171 C1172 G1173 A1174 U1175 G1176 U1182 A1185 C1186 A1190 G1197 U1198 U1199 A1211 U1212 C1218 U1219 C1220 A1221 U1222 C1223 A1224 G1225 A1226 A1231 G1232
A1233 A1234 A1235 A1236 G1237 G1238 U1239 G1244 A1248 U1249 C1250 U1251 A1252 G1253 A1254 C1258 A1259 G1260 G1261 A1262 C1263 G1264 G1267 C1270 A1271 U1272 G1273 G1274 A1275 A1276 G1277 U1278 A1282 A1283 U1284 C1285 C1286 U1289 A1290 A1291 G1292 G1293 A1294 G1295 U1296 G1297 U1298 G1299 U1300 C1303 A1304 A1305
C1306 U1307 C1308 A1309 C1310 C1315 G1316 A1317 A1318 A1333 A1334 A1335 U1336 G1337 G1338 A1339 U1340 U1347 A1348 A1357 U1362 U1379 A1380 G1381 C1382 U1383 U1384 U1385 G1386 A1387 G1388 A1389 A1390 G1416 U1420 C1425 G1426 U1433 G1451 A1452 A1453 G1463 U1464 G1465 C1471 A1480
G1481 G1484 C1485



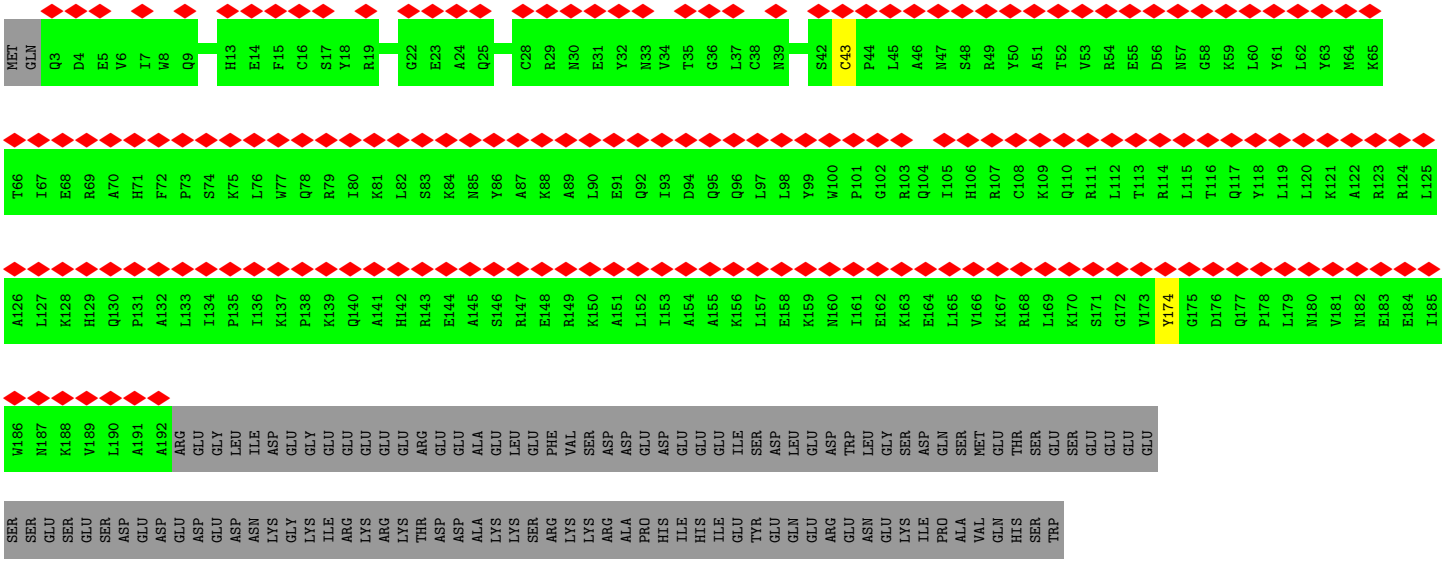
• Molecule 2: RNA (152-MER)

Chain 2:



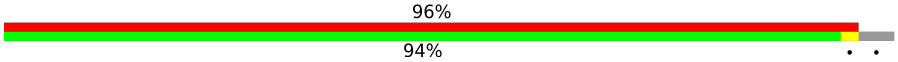
- Molecule 3: Protein mak16

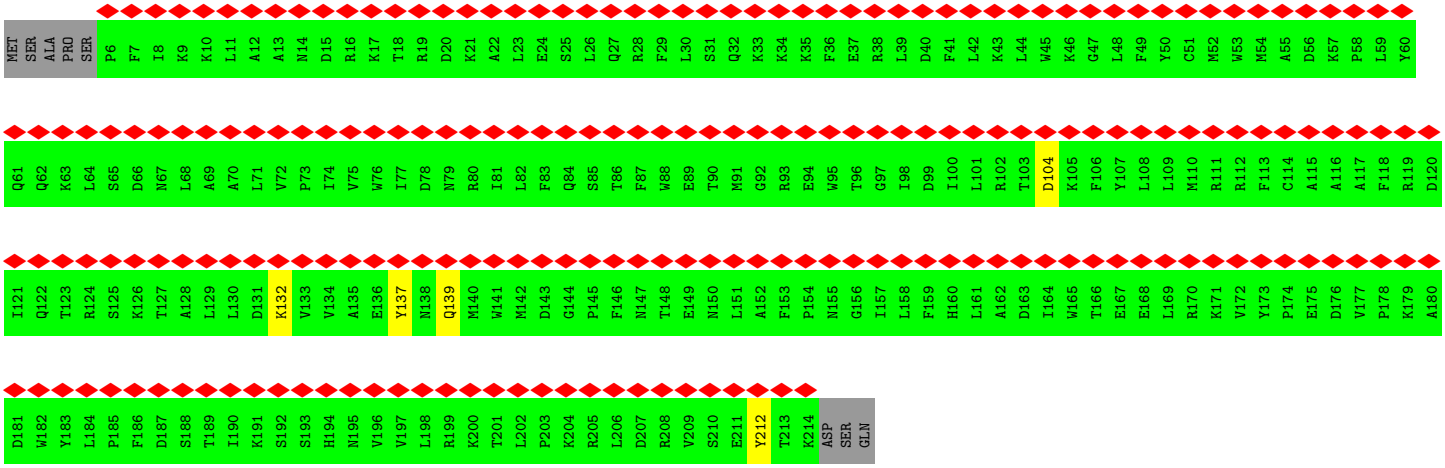
Chain 3:



- Molecule 4: Ribosomal RNA-processing protein 1 homolog

Chain 4:





- Molecule 5: Ribosome biogenesis protein nsa1

Chain 5: 88% 87% 12%

M1 K2 L3 L4 L5 G6 D7 E8 I9 G10 Q11 L12 K13 F14 I15 E16 I17 K18 K19 G20 T21 D22 T23 S24 N25 P26 E27 S28 E29 A30 P31 V32 I33 Q34 K35 F36 G37 E38 L39 D40 R41 E42 K43 G44 V45 L46 F47 M48 L49 K50 H51 E52 M53 N54 V55 F56 V57 A58 R59 K60

N61 G62 T63 I64 E65 C66 W67 N68 V69 N70 Q71 E72 P73 P74 I75 L76 S77 S78 L79 W80 Q81 L82 D83 S84 S85 L86 L87 E88 T89 A90 S91 I92 V93 S94 M95 K96 Y97 S98 N99 G100 W101 L102 M103 L104 A105 L106 S107 D108 G109 N110 L111 L112 F113 R114 H115 I116 E117 S118 S119 K120

L121 R122 K123 L124 Q125 L126 H127 G128 P129 L130 S131 A132 V133 E134 L135 H136 P137 R138 L139 P140 G141 I142 I143 A144 A145 G146 G147 K148 E149 N150 D151 V152 C153 L154 Y155 S156 C157 N158 P159 T160 C161 K162 S163 N164 I165 D166 E167 L168 E169 L170 W171 R172 T173 E174 N175 V176 V177 K178 V179 F180

Q181 G182 K183 N184 V185 K186 N187 D188 S189 L190 N191 L192 R193 V194 R195 V196 W197 I198 T199 G200 I201 V202 F203 T204 E205 D206 I207 I208 ASN VAL ILE ASP GLY LYS SER GLU ASP D218 E219 S220 L221 C222 F223 H224 F225 A226 T227 I228 T229 H230 Y231 G232 Q233 L234 R235 F236 Y237 D238 T239 K240

H241 G242 R243 R244 P245 V246 S247 T248 F249 D250 V251 S252 T253 S254 P255 L256 S257 H258 V259 G260 L261 L262 P263 S264 I265 K266 L267 L268 Y269 F270 A271 D272 K273 R274 A275 Q276 I277 S278 I279 F280 D281 H282 S283 K284 K285 K286 V287 I288 G289 R290 F291 Q292 G293 V294 K295 G296 A297 P298 S299 S300

I301 H302 C303 L304 G305 N306 V307 V308 A309 I310 T311 G312 L313 D314 R315 N316 V317 R318 I319 F320 D321 A322 D323 R324 K325 P326 L327 A328 N329 A330 Y331 I332 K333 A334 L335 P336 T337 S338 I339 I340 V341 I342 N343 E344 R345 D346 A347 E348 I349 ILE LYS LYS GLU GLU GLU LEU GLU ALA ALA LYS

GLU GLU GLU GLU GLU ILE TRP ARG ASN MET GLU GLN LEU GLU ASP THR GLU ASP LYS LYS PRO SER LYS ARG ILE LYS LEU

- Molecule 6: RNA (125-MER)

Chain 6: 27% 15% 12% 73%

A1 C2 A3 A4 U5 C6 U7 U8 C9 U10 C11 A12 C13 A A A A A A U G U U U U U U U U U U A A A A U A U U U U U G A41 U42 G43 A44 G45 G46 U47 G48 U49 U50 G51 A52 A53 C54 G55 A56 A57 A58 A59

U60 U61 U62 G U U U U U U U U U U U A A A A U A U U81 A82 A83 U84 U85 U86 A87 G88 U89 U90 U91 G92 A93 A94 A95 U96 C97 G98 A99 U100 U101 G102 G103 U104 G105 A106 A107 A108 A109 C110 A A A A G G G A A G

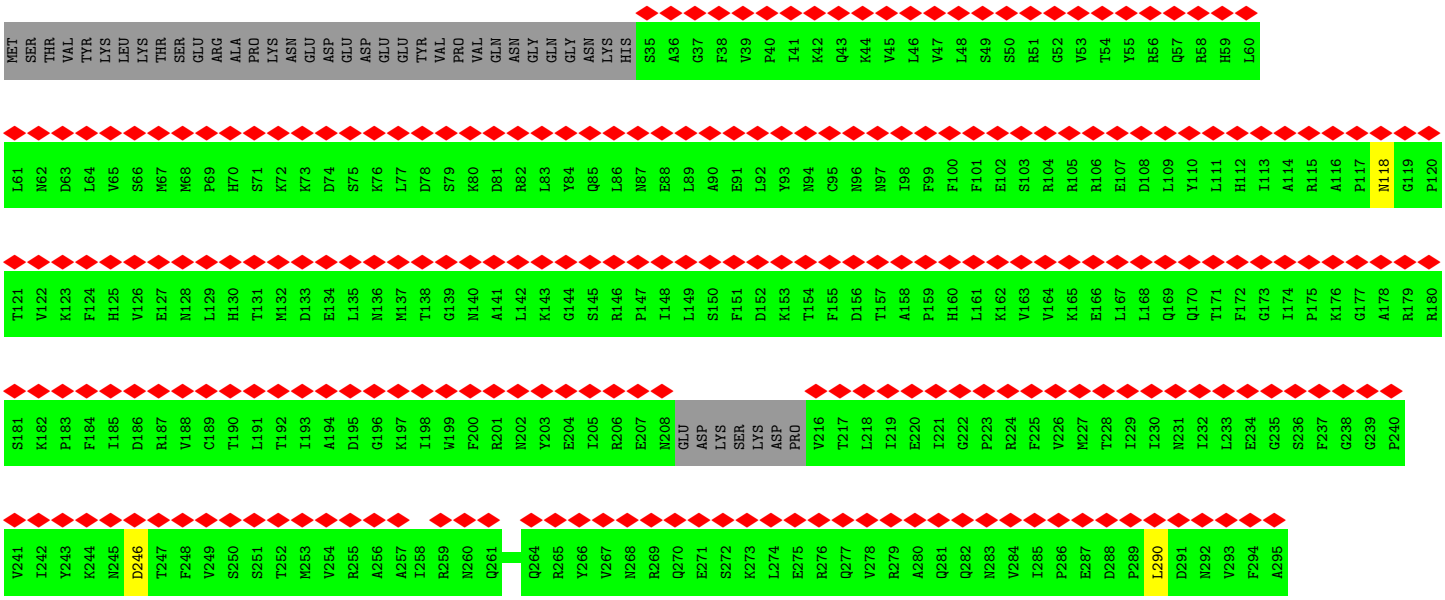
A U U G A A A U U U A U U U U U U C U U A A U G G C C U U U U U U U U U U U U C U A A U U G A A C G U A A U A G174 G175 U176 U177 U178 U179 A180

C181 C182 A183 C184 U185 U186 U187 G188 U189 U U G A U A G A A A A A A A A G A A A A U U A G G G A A A G A A A A A A U A A C U A A A A A G U U U U U A A U C

U C U U U U A U A U U U G A A A C C U U A A A C G A A A A A A A A A G U U A U U U U U U U U U U C A C A G U A C C U U U U U A

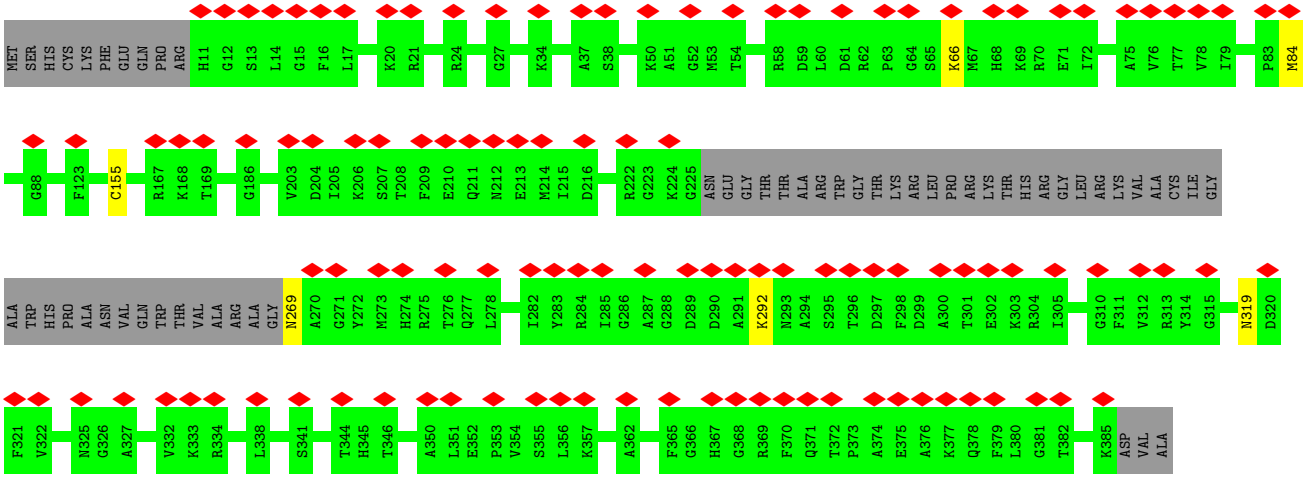
- Molecule 7: Ribosome biogenesis protein brx1

Chain A: 85% 85% 14%



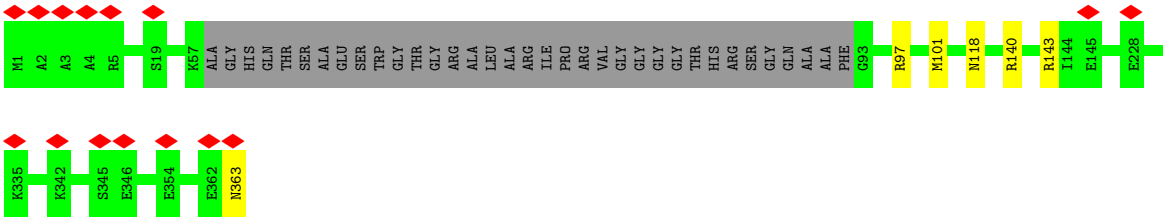
• Molecule 8: 60S ribosomal protein L3-A

Chain B:



• Molecule 9: 60S ribosomal protein L4-B

Chain C:



• Molecule 10: ATP-dependent RNA helicase has1

Chain D: 67% 68% 32%

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

GLU SER GLU GLU LEU ASP ASN GLU ASN GLU ASP GLU ARG VAL GLN LYS SER VAL ASN LEU ASN ALA SER SER THR SER ASP ILE GLU LYS PHE SER ASP LEU GLN L96 S97 E98 N99 I100 Q101 K102 A103 I104 K105 E106 M107 G108 F109 E110 T111 M112 T113 E114 I115 Q116 K117 R118 S119 I120

P121 P122 L123 L124 A125 G126 R127 D128 V129 L130 G131 A132 A133 K134 T135 G136 S137 G138 K139 T140 L141 A142 F143 L144 I145 P146 T147 I148 E149 M150 L151 Y152 A153 L154 K155 F156 K157 P158 R159 N160 G161 T162 G163 V164 I165 I166 I167 S168 P169 T170 R171 E172 L173 A174 L175 Q176 I177 F178 G179 V180

A181 K182 E183 L184 L185 K186 Y187 H188 H189 Q190 T191 F192 G193 I194 V195 I196 G197 G198 A199 N200 R201 R202 A203 E204 A205 D206 K207 L208 V209 K210 G211 V212 N213 L214 L215 V216 A217 T218 P219 G220 R221 L222 L223 D224 H225 L226 Q227 N228 T229 K230 G231 F232 V233 F234 R235 N236 L237 R238 S239 L240

V241 I242 D243 E244 A245 D246 R247 I248 L249 E250 I251 G252 F253 E254 D255 E256 M257 R258 Q259 I260 M261 K262 I263 L264 P265 S266 E267 N268 R269 Q270 T271 L272 LEU PHE SER ALA THR GLN THR THR LYS VAL GLU ASP LEU ALA ARG ILE SER LEU LYS PRO GLY PRO LEU TYR VAL ASN VAL ASP

SER GLY LYS PRO THR SER THR VAL GLU GLY LEU E312 Q313 G314 Y315 V316 V317 V318 D319 S320 D321 K322 R323 F324 L325 L326 L327 F328 S329 F330 L331 K332 R333 N334 L335 K336 K337 K338 V339 I340 V341 F342 M343 S344 S345 C346 A347 S348 V349 K350 Y351 M352 A353 E354 L355 L356 N357 Y358 I359 D360

L361 P362 V363 L364 D365 L366 H367 G368 K369 Q370 K371 Q372 Q373 R374 R375 T376 N377 T378 F379 F380 E381 F382 C383 N384 A385 E386 K387 G388 I389 L390 L391 C392 T393 N394 V395 A396 A397 R398 G399 L400 D401 I402 P403 A404 V405 D406 W407 I408 V409 Q410 Y411 D412 P413 P414 D415 D416 P417 R418 D419 Y420

I421 H422 R423 V424 G425 ARG THR ALA ARG GLY THR LYS GLY THR G435 K436 S437 L438 M439 F440 L441 A442 P443 S444 E445 L446 G447 F448 L449 R450 Y451 L452 K453 T454 A455 K456 V457 S458 L459 N460 E461 F462 E463 F464 P465 A466 N467 K468 V469 A470 N471 V472 Q473 S474 Q475 L476 E477 K478 L479 V480

S481 K482 N483 Y484 Y485 L486 Q487 Q488 S489 A490 K491 D492 G493 Y494 R495 S496 Y497 L498 Q499 A500 Y501 A502 S503 Y504 S505 L506 K507 S508 I509 F510 D511 I512 N513 K514 L515 D516 L517 A518 K519 V520 A521 K522 S523 F524 G525 F526 A527 H528 P529 P530 N531 V532 N533 I534 THR ILE GLY ALA SER GLY

ARG THR ASP LYS LYS GLU ARG ARG ALA GLY TYR ASN LYS LYS ASN HIS VAL ASP VAL TYR SER LYS GLN ARG SER SER ALA ILE SER GLN ASP LYS GLU ARG GLY TRP SER ARG

- Molecule 11: 60S ribosomal protein L6

Chain E: 38% 84% • 13%

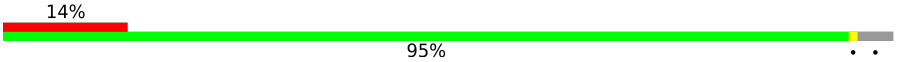
MET SER THR VAL LYS VAL ASN GLY ALA LYS ASN GLY GLY GLU ARG MET VAL LEU PRO ALA GLY GLU ALA ALA ALA K26 Y27 Y28 P29 A30 Y31 R32 E33 N34 V35 K38 R44 K47 L52 G55 G63 L73 E77 D78 T79 L80 V81 V82 T83 G84 G90

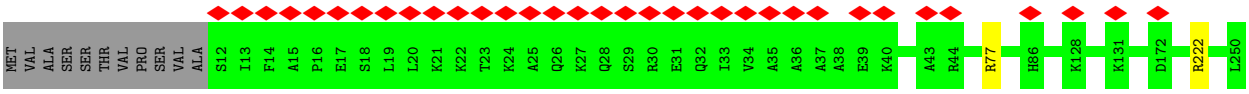
I93 R94 A106 I109 D110 V111 S112 G113 V114 S115 K118 K121 A122 K126 Q127 K128 R129 S130 G131 P132 V133 K134 K135 D136 E137 A138 F139 F140 A141 E142 N143 A144 P145 K146 M147 A148 L149 P150 A151 E152 R153 I154 Q157 K158 D161 A162 K163 L164 I168 I171

M174 K175 E176 Y177 L178 A179 N186 R189 F195

- Molecule 12: 60S ribosomal protein L7-B

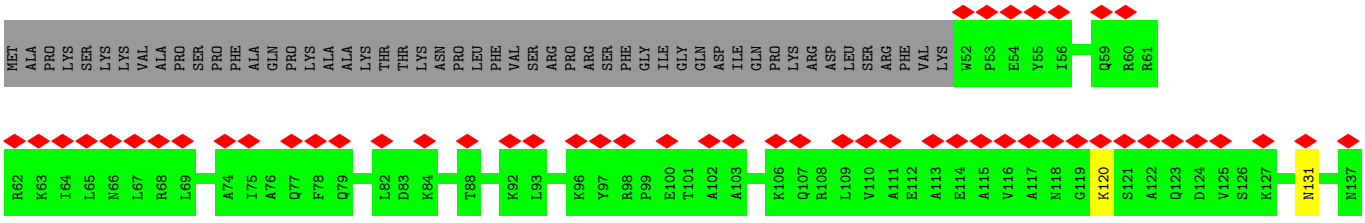
Chain F:

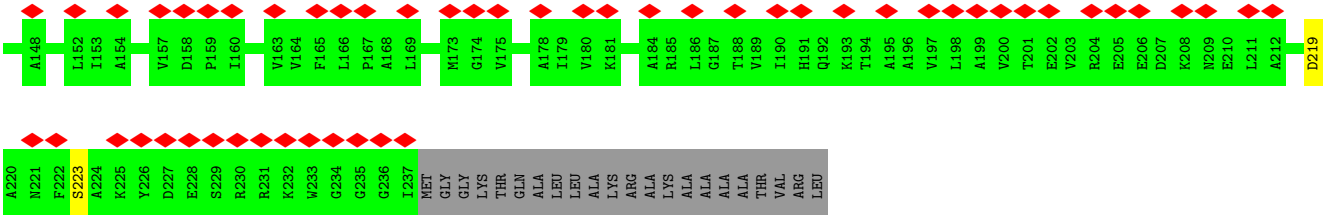




- Molecule 13: 60S ribosomal protein L8

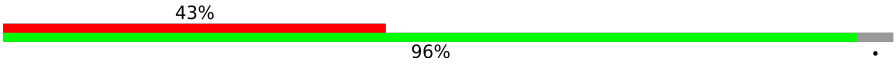
Chain G:

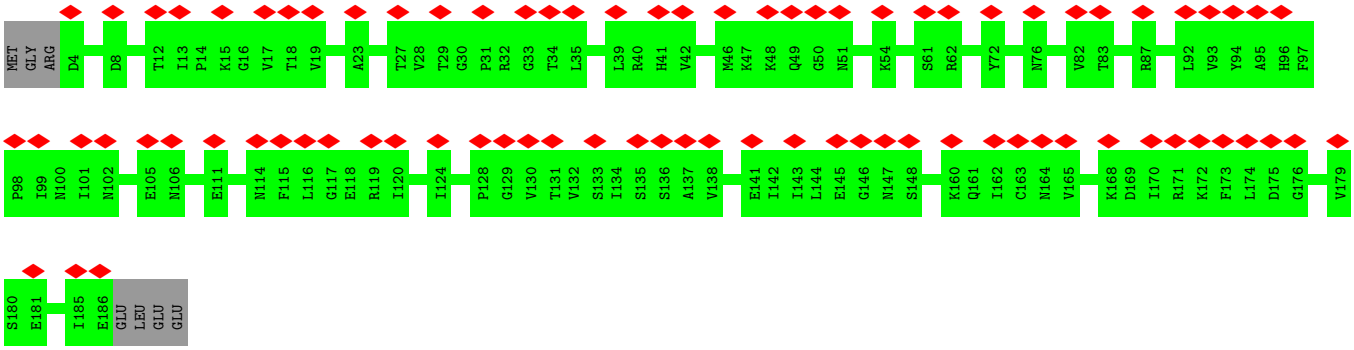




- Molecule 14: 60S ribosomal protein L9-A

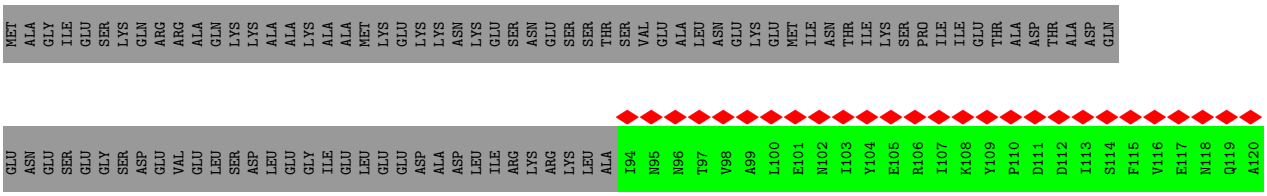
Chain H:





- Molecule 15: Probable rRNA-processing protein ebp2

Chain J:



V121 T122 T123 K124 E125 P126 I127 I128 I129 E130 N131 V132 E133 D134 D135 L136 A137 R138 E139 L140 A141 F142 Y143 K144 Q145 G146 V147 S148 S149 V150 K151 A152 A153 F154 A155 K156 L157 R158 E159 A160 N161 V162 L163 I164 S165 R166 P167 H168 D169 Y170 F171 A172 E173 M174 L175 K176 S177 D178 D179 H180

M181 E182 K183 V184 R185 Q186 E187 L188 I189 K190 E191 A192 T193 A194 K195 K196 L197 S198 Q199 Q200 A201 K202 K203 Q204 R205 E206 LEU LYS LYS PHE GLY LYS GLN VAL GLN LEU ALA LYS GLN GLU GLU ARG GLN ARG GLU LYS LYS GLU THR LEU GLU LYS ILE ASN LEU LEU LYS ARG LYS HIS

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

LEU ASP SER LEU ALA ALA THR GLU PHE GLY ARG LYS GLY LEU LYS ASN ILE LYS SER LYS LYS ARG PRO GLY LYS ALA ARG ARG GLU LYS ALA ARG LYS

- Molecule 16: Putative ribosome biogenesis protein C8F11.04

Chain K: 64% 64% 36%

MET ALA LEU LYS E5 L6 L7 G8 S9 D10 A11 P12 L13 E14 K15 V16 C17 S18 A19 L20 L21 E22 Y23 E24 S25 K26 R27 K28 S29 SER GLU ASN ILE ASP SER GLU SER LYS LYS THR ASN LEU LEU GLU ASP GLU GLN ASP ASP ILE GLU P52 V53 W54 L55 Q56 L57 A58 T59 L60

K61 F62 I63 G64 N65 N66 R67 K68 L69 I70 P71 Y72 K73 I74 A75 I76 K77 N78 P79 V80 I81 P82 S83 S84 S85 E86 A87 C88 L89 I90 V91 K92 D93 P94 Q95 R96 V97 Y98 K99 D100 L101 V102 N103 E104 A105 G106 L107 S108 K109 V110 V111 T112 R113 V114 I115 G116 L117 S118 K119 L120

K121 A122 K123 W124 N125 S126 Y127 E128 Q129 K130 R131 Q132 L133 R134 D135 Q136 F137 D138 I139 F140 L141 A142 D143 D144 R145 V146 I147 P148 M149 L150 P151 R152 I153 L154 G155 K156 T157 F158 Y159 Q160 K161 S162 K163 V164 P165 V166 P167 V168 K169 I170 S171 K172 G173 T174 A175 E176 Q177 L178 K179 R180

E181 V182 V183 S184 A185 Y186 G187 A188 T189 Y190 F191 N192 S193 A194 P195 C196 S197 S198 F199 M200 I201 K202 C203 G204 H205 V206 S207 N208 T209 S210 T211 E212 L213 A214 E215 N216 V217 E218 S219 I220 L221 Q222 F223 V224 S225 K226 H227 I228 V229 P230 D231 G232 A233 K234 G235 I236 A237 S238 I239 H240

L241 K242 T243 S244 Q245 S246 I247 A248 I249 P250 L251 W252 N253 N254 P255 N256 L257 K258 E259 L260 I261 A262 S263 S264 R265 K266 VAL VAL THR LYS GLU THR ALA SER SER LYS ARG LYS SER ASP GLU GLU SER LEU PRO SER GLN LYS LYS GLN LYS LYS VAL GLU VAL ALA LYS GLU SER LYS

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

ILE LYS LYS VAL ALA LYS GLY LYS ASN LYS VAL LYS HIS

- Molecule 17: 60S ribosomal protein L13

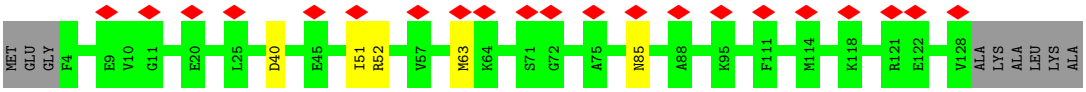
Chain L: 6% 55% 45%

MET ALA ILE HIS VAL LYS GLY GLN LEU PRO ASN ALA HIS PHE HIS LYS ASP TRP GLN ARG Y21 A47 L80 A83 E107 Q110 K129 A130 G131 Q132 P133 K134 K135 GLY ASP ALA THR ASP VAL SER GLY ALA GLU GLN THR ASP VAL ALA ALA VAL LEU PRO ILE THR

GLN GLU ALA VAL GLU GLU ALA LYS PRO ILE THR GLU GLU ALA LYS ASN PHE ASN ALA PHE SER THR LEU SER ASN GLU ARG ALA TYR ALA ARG TYR ALA GLY ALA ARG ALA ALA PHE GLN LYS LYS ARG ALA GLU GLU ALA GLU ALA LYS LYS LYS

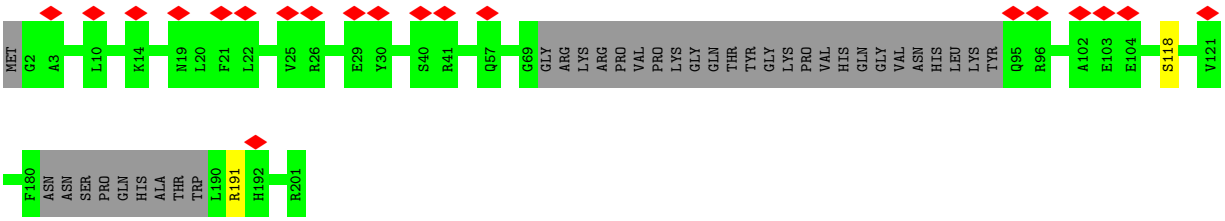
- Molecule 18: 60S ribosomal protein L14

Chain M: 16% 90% 7%



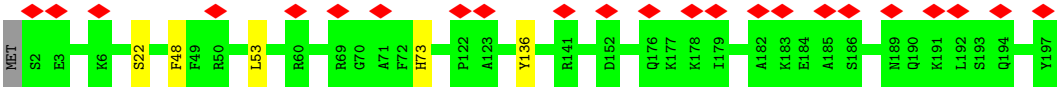
• Molecule 19: 60S ribosomal protein L15-A

Chain N: 10% 82% 17%



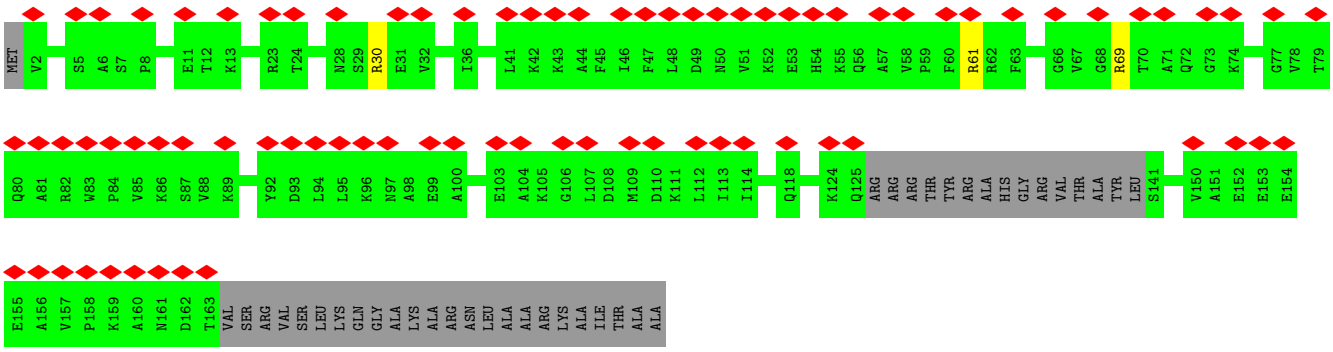
• Molecule 20: 60S ribosomal protein L16-B

Chain O: 12% 97%



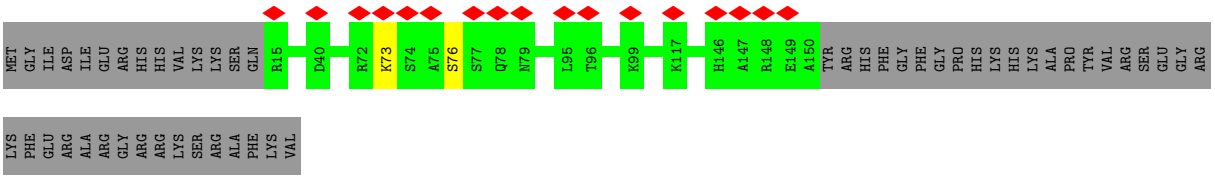
• Molecule 21: 60S ribosomal protein L17-A

Chain P: 43% 77% 21%



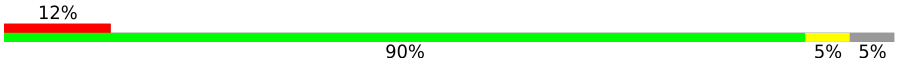
• Molecule 22: 60S ribosomal protein L18-A

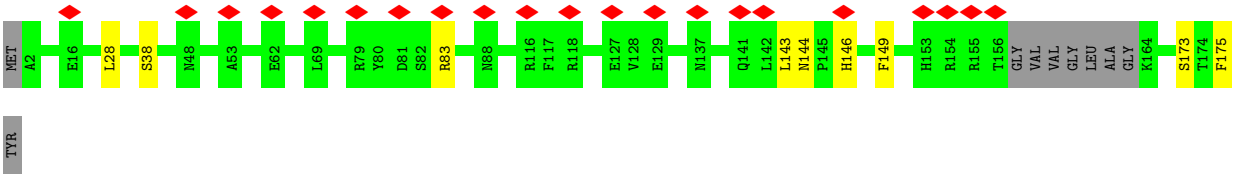
Chain Q: 9% 72% 27%



• Molecule 23: 60S ribosomal protein L20-A

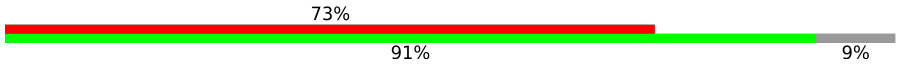
Chain S:

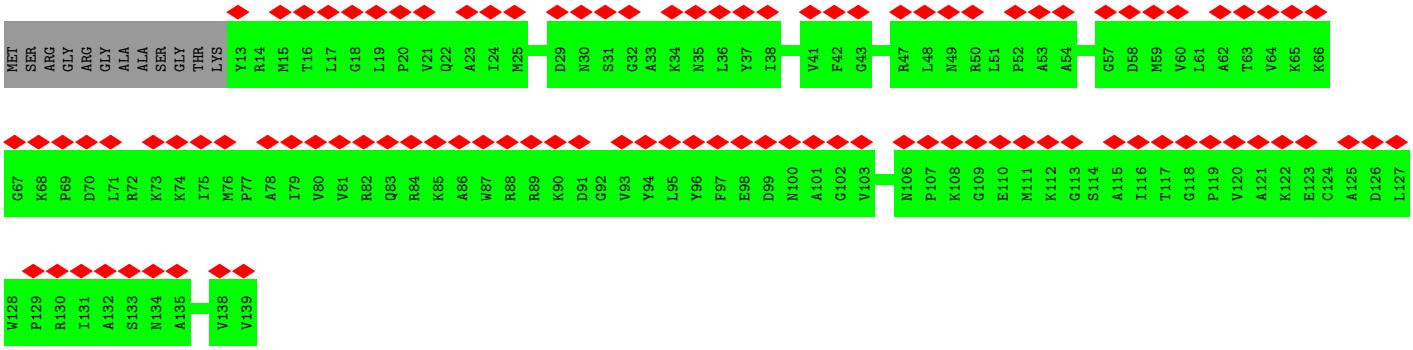




- Molecule 24: 60S ribosomal protein L23-A

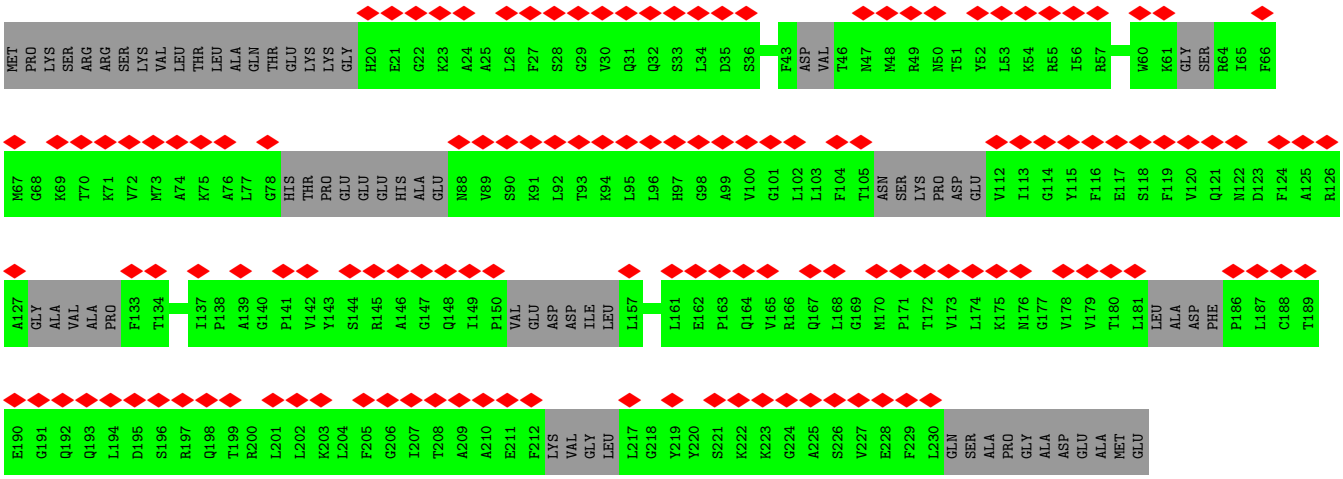
Chain V:





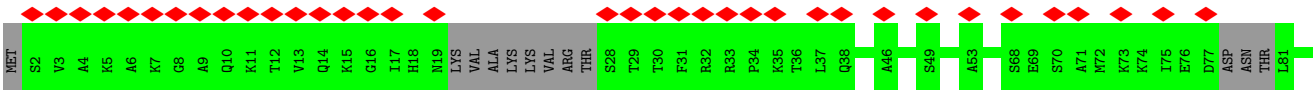
- Molecule 25: Ribosome assembly factor mrt4

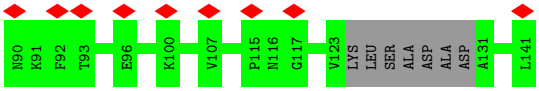
Chain W:



- Molecule 26: 60S ribosomal protein L25-A

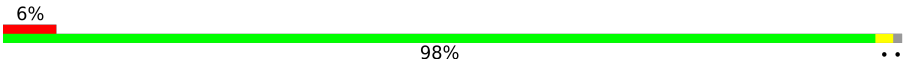
Chain X:

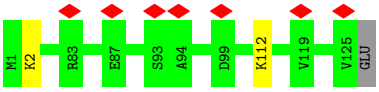




• Molecule 27: 60S ribosomal protein L26

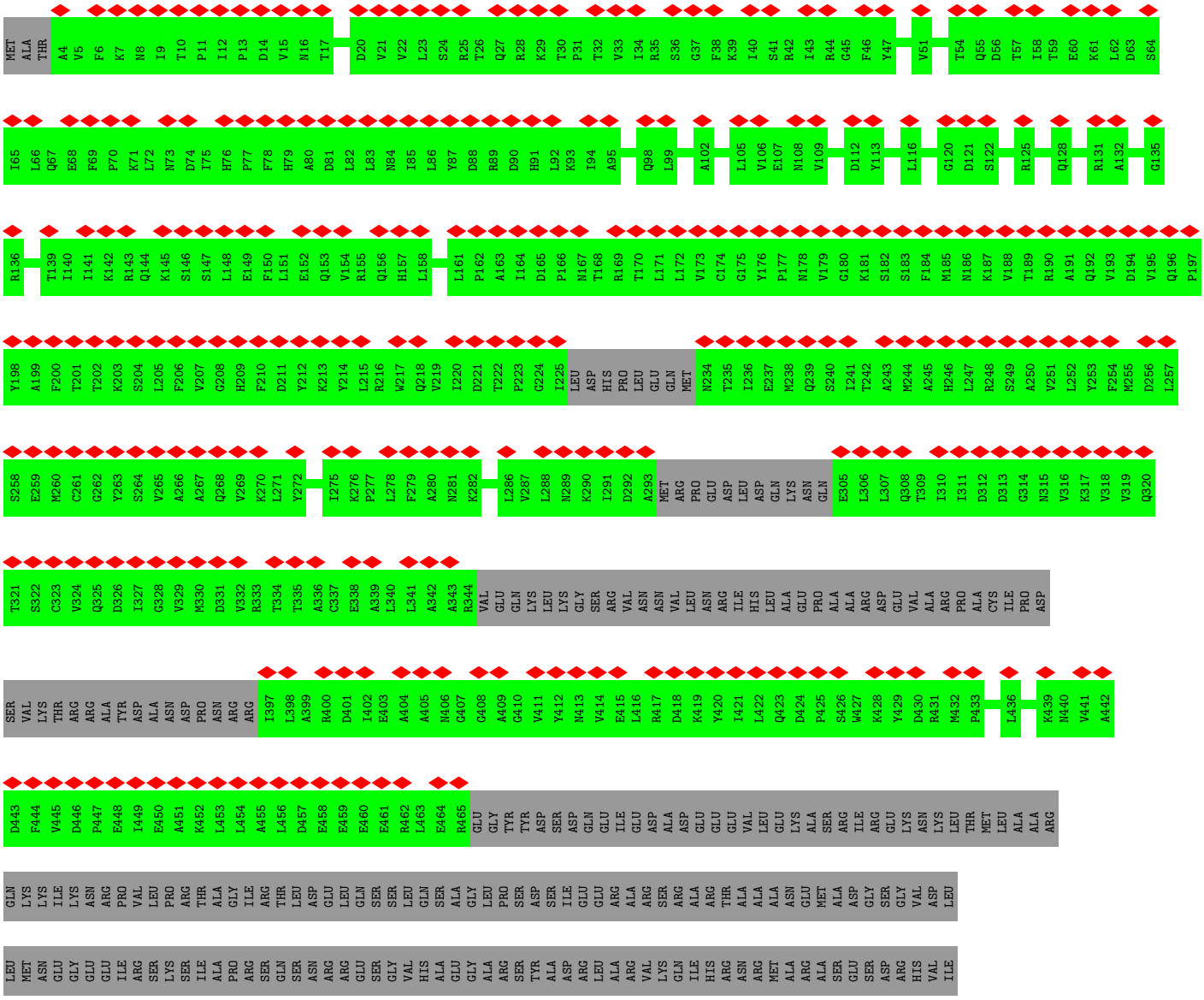
Chain Y:





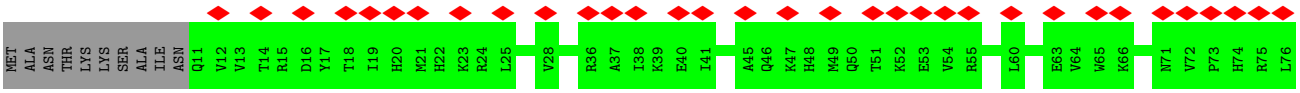
• Molecule 28: Probable nucleolar GTP-binding protein 1

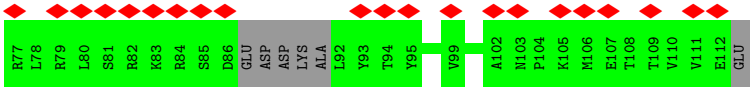
Chain b:



- Molecule 29: 60S ribosomal protein L31

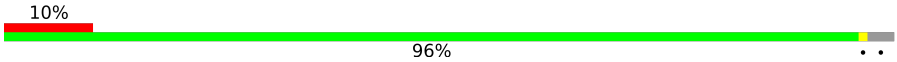
Chain d:

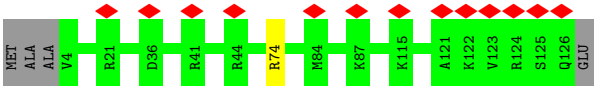




- Molecule 30: 60S ribosomal protein L32-A

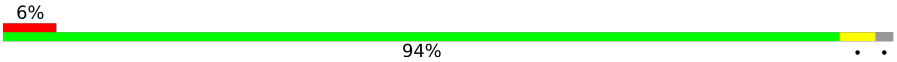
Chain e:

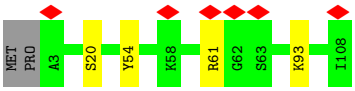




- Molecule 31: 60S ribosomal protein L33-B

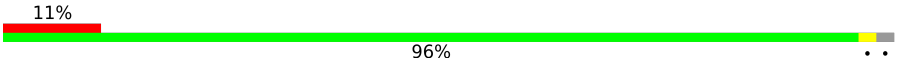
Chain f:





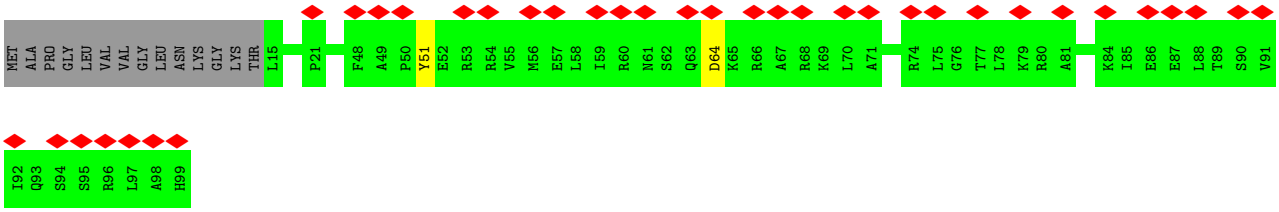
- Molecule 32: 60S ribosomal protein L35

Chain h:



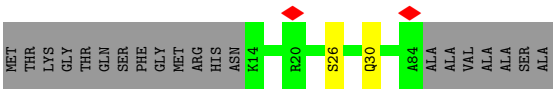
- Molecule 33: 60S ribosomal protein L36-B

Chain i:



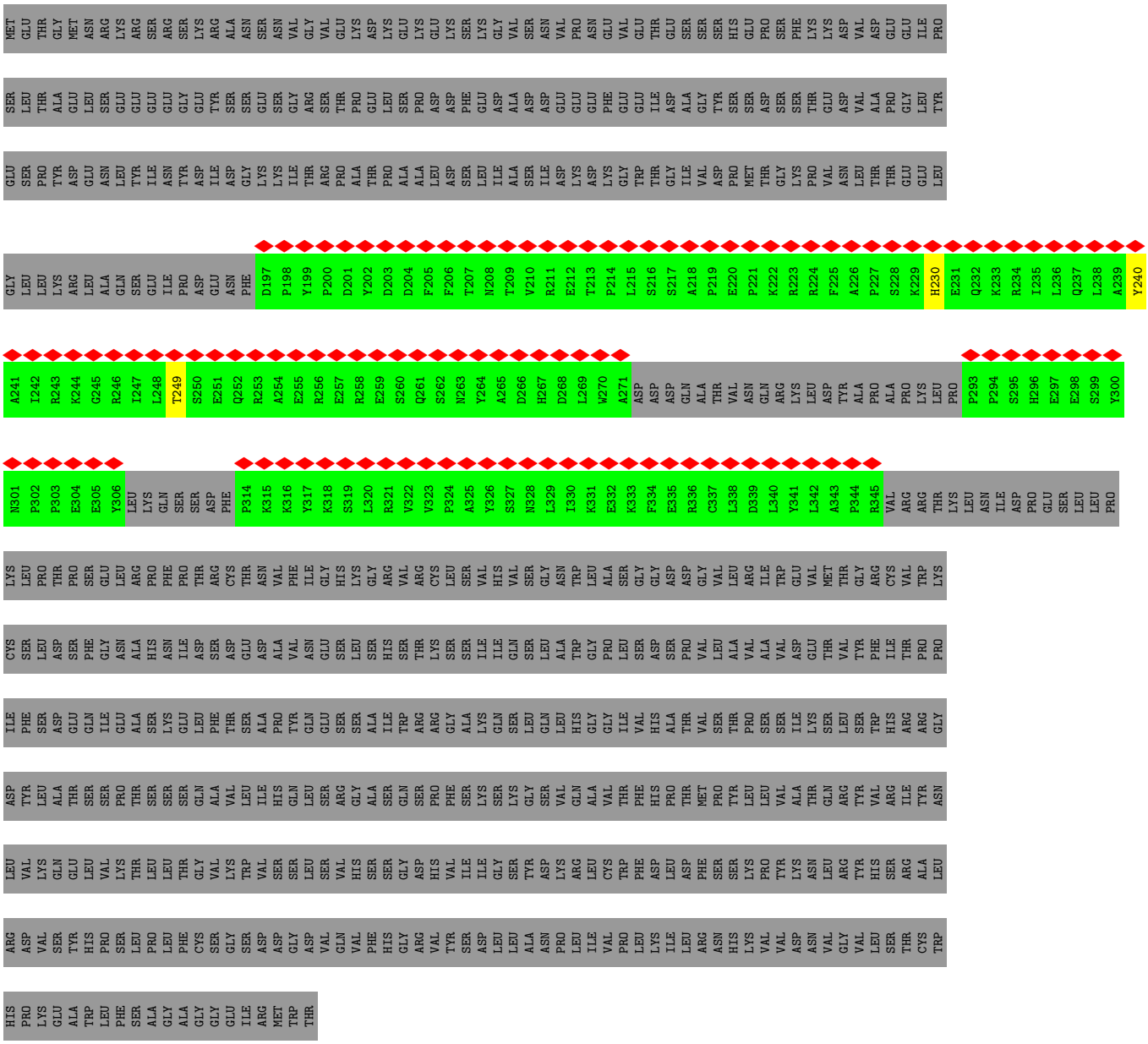
- Molecule 34: 60S ribosomal protein L37-B

Chain j:



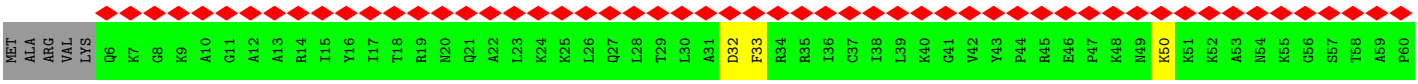
- Molecule 35: Ribosome biogenesis protein erb1

Chain m:



- Molecule 36: Pescadillo homolog

Chain n:



V61 T62 F63 Y64 Y65 T66 K67 D68 I69 Q70 Y71 L72 L73 H74 E75 P76 I77 V78 Q79 K80 F81 R82 E83 Y84 K85 V86 F87 A88 R89 K90 L91 S92 K93 A94 L95 G96 K97 G98 E99 L100 E101 T102 A103 K104 R105 L106 E107 A108 R109 K110 P111 T112 Y113 S114 L115 D116 H117 I118 I119 K120

E121 R122 Y123 P124 T125 F126 H127 D128 A129 L130 K131 D132 I133 D134 D135 A136 L137 S138 M139 L140 F141 L142 F143 S144 T145 M146 P147 V148 T149 D150 K151 I152 G153 A154 A155 T156 V157 A158 N159 C160 E161 R162 L163 C164 A165 E166 F167 Q168 H169 Y170 V171 I172 R173 S174 N175 S176 L177 R178 K179 A180

F181 L182 S183 I184 K185 G186 I187 Y188 Y189 Q190 A191 E192 I193 F194 G195 E196 Q197 I198 T199 W200 I201 V202 P203 Y204 K205 F206 A207 Q208 S209 V210 P211 T212 D213 V214 D215 F216 R217 I218 M219 H220 T221 F222 L223 E224 F225 Y226 Q227 A228 L229 M230 G231 F232 V233 N234 F235 K236 L237 Y238 N239 T240

L241 G242 L243 R244 Y245 P246 P247 K248 I249 D250 V251 A252 K253 S254 E255 S256 A257 A258 G259 L260 A261 A262 Y263 E264 L265 E266 E267 S268 SER SER LEU PRO ALA ILE VAL HIS GLY ASN ASN LYS ASN ALA ARG LYS ASN ILE ALA THR LEU LYS SER LYS ILE ARG ASP ILE VAL ASN SER ASP

ALA ASN VAL VAL GLU GLN SER GLU LYS THR THR GLU ASP ALA ASP GLU GLU PRO GLU THR GLU GLU ASN LEU ASP GLU PHE LYS PRO ALA ASP GLY ALA ASP ASN GLU ASP SER LYS SER LEU VAL SER HIS ILE SER SER SER N349 T350 S351 L352 F353 S354 N355 F356 T357 F358 F359 L360

S361 R362 E363 V364 P365 R366 F367 S368 L369 E370 F371 V372 I373 R374 A375 F376 G377 G378 K379 V380 G381 W382 D383 P384 I385 L386 G387 S388 G389 S390 P391 F392 S393 E394 S395 D396 P397 V398 I399 T400 H401 H402 I403 C404 D405 R406 P407 H408 I409 S410 Q411 K412 Y413 E414 G415 R416 I417 Y418 I419 Q420

P421 Q422 W423 V424 Y425 D426 S427 I428 N429 K430 G431 I432 L433 E434 R435 T436 D437 L438 Y439 A440 C441 G442 A443 T444 L445 P446 P447 H448 L449 S450 P451 F452 V453 K454 VAL GLY GLU ASN ASP TYR ASP PRO GLU ALA GLU LEU SER ALA GLU GLU ASN ASP ASP VAL SER GLU ALA LEU ASP ASP

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

LYS ARG GLN ARG ASP THR LEU THR ALA GLU GLU LYS GLU GLU LYS GLU ALA LYS GLU LEU SER LYS MET MET MET SER ASN LYS GLN ARG LYS LEU TYR SER LYS LEU LYS ASN GLU ASN SER LYS ASN GLU ASN TYR ASN ASN ALA LEU ARG ASN ARG LYS ARG ASP ILE GLU LYS ARG

LYS LYS LEU LYS VAL GLU ASN

- Molecule 37: Uncharacterized RNA-binding protein C1827.05c

Chain o: 49% 49% 51%

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

SER ASP ASP ASP GLU GLU ASP SER PRO ASN ALA LEU VAL ASN THR SER ARG GLN ILE MET ASP LEU GLY GLU GLY ASP ALA GLU LYS THR ILE LYS LYS LYS VAL SER GLU ASN LYS LYS ASN LEU GLN LYS LYS LYS G105 V106 L107 Y108 V109 G110 R111 L112 P113 H114 G115 F116 Y117 E118 K119 Q120

M121 R122 M123 Y124 F125 S126 Q127 F128 G129 P130 V131 L132 R133 L134 R135 M136 S137 R138 N139 K140 K141 T142 G143 S144 S145 K146 H147 Y148 A149 F150 I151 E152 F153 E154 S155 L156 D157 V158 A159 N160 V161 V162 A163 E164 T165 M166 H167 M168 Y169 L170 L171 Y172 G173 K174 L175 L176 Q177 C178 K179 V180

I181 P182 E183 D184 Q185 V186 H187 E188 N189 M190 F191 K192 G193 A194 D195 V196 P197 F198 K199 R200 I201 P202 H203 A204 T205 I206 A207 R208 L209 Q210 H211 E212 K213 P214 L215 S216 K217 E218 K219 A220 D221 K222 L223 I224 T225 R226 H227 N228 R229 K230 L231 K232 L233 K234 K235 R236 K237 L238 LYS GLU

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

• Molecule 38: Ribosome biogenesis protein nsa2

Chain r: 51% 64% 36%

MET P2 Q3 N4 E5 Y6 E9 R12 K13 H14 G15 R16 R17 F18 D19 H20 E21 E22 K26 K27 A28 A29 R30 E31 A32 H33 D34 A35 S36 L37 Y38 K41 T42 K46 A47 Y50 Q51 E52 K53 R54 E57 K58 I59 Q60 M61 T64 I65 H68 E69 E70 R71

N72 A73 THR GLN ARG GLY SER ASP ALA GLN THR GLN GLY ALA VAL PRO THR TYR LEU LEU ASP ARG GLU GLN GLU SER GLN ALA LYS MET LEU SER SER ALA VAL LYS GLN LYS ARG LYS GLU LYS ALA ALA LYS TYR SER VAL PRO LEU PRO GLN VAL ARG GLY VAL ALA GLU GLU GLU

MET PHE LYS VAL ILE ARG THR GLY LYS SER LYS LYS ASN SER TRP K147 R148 M149 I150 T151 K152 A153 T154 F155 V156 GLY ASP GLY PHE THR ARG ARG PRO VAL K166 Y167 E168 R169 F170 I171 R172 P173 M174 A175 L176 R177 Q178 K179 K180 A181 N182 V183 T184 H185 K186 E187 L188 G189 V190 T191

M192 Q193 L194 P195 I196 I197 G198 V199 K200 K201 N202 P203 P206 T207 Y208 T209 Q210 L211 G212 V213 L214 T215 K216 G217 T218 V219 I220 E221 V222 N223 V224 S225 E226 L227 GLY LEU VAL THR SER GLY GLY LYS VAL VAL TRP G239 K240 Y241 A242 Q243 I244 T245 N246 N247 P248 E249 L250 D251 G252

C253 V254 N255 A256 L257 L258 L259 T260

• Molecule 39: 60S ribosomal protein L7-A

Chain t: 90% 90% 10%

MET ALA GLU ASP ALA PRO VAL VAL GLN GLN THR MET LEU GLU PRO GLU VAL LEU LEU LYS LYS ARG LYS VAL N25 E26 R27 T28 R29 K30 E31 R32 V33 E34 Q35 A36 I37 A38 K39 K40 E41 A42 Q43 K44 K45 N46 R47 K48 E49 T50 F51 K52 R53 A54 E55 T56 F57 I58 N59 N60

Y61 R62 Q63 R64 E65 R66 E67 R68 I69 R70 L71 N72 R73 S74 A75 K76 N77 K78 G79 D80 I81 F82 V83 P84 D85 E86 T87 K88 L89 L90 F91 V92 I93 R94 I95 A96 G97 V98 K99 N100 M101 P102 P103 K104 I105 R106 K107 V108 L109 R110 L111 L112 R113 L114 S115 R116 I117 N118 N119 A120

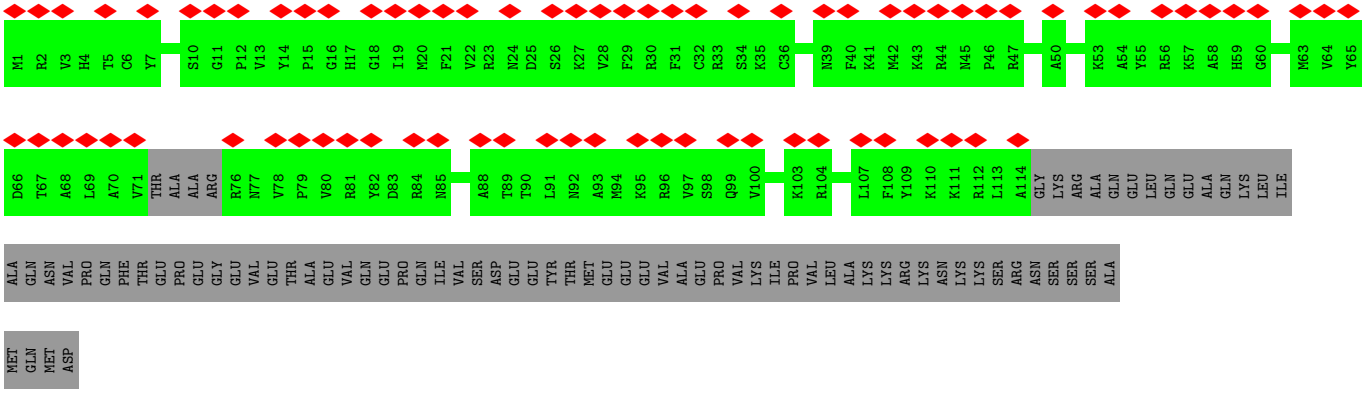
V121 F122 V123 R124 N125 N126 K127 A128 V129 A130 Q131 M132 L133 R134 I135 V136 E137 P138 Y139 V140 M141 Y142 G143 I144 P145 N146 L147 H148 S149 V150 R151 E152 L153 I154 Y155 K156 R157 G158 F159 G160 K161 I162 N163 G164 Q165 R166 I167 A168 L169 S170 D171 N172 A173 L174 I175 E176 E177 A178 L179 G180

K181 Y182 D183 V184 I185 S186 I187 E188 D189 I190 I191 H192 E193 I194 Y195 N196 V197 G198 S199 H200 F201 K202 E203 V204 T205 K206 F207 L208 W209 P210 F211 T212 L213 T214 P215 V216 K217 H218 S219 L220 M221 E222 K223 K224 V225 K226 H227 F228 N229 E230 G231 R232 K233 A234 G235 Y236 C237 G238 E239 E240

I241 N242 E243 L244 I245 K246 K247 Q248 V249

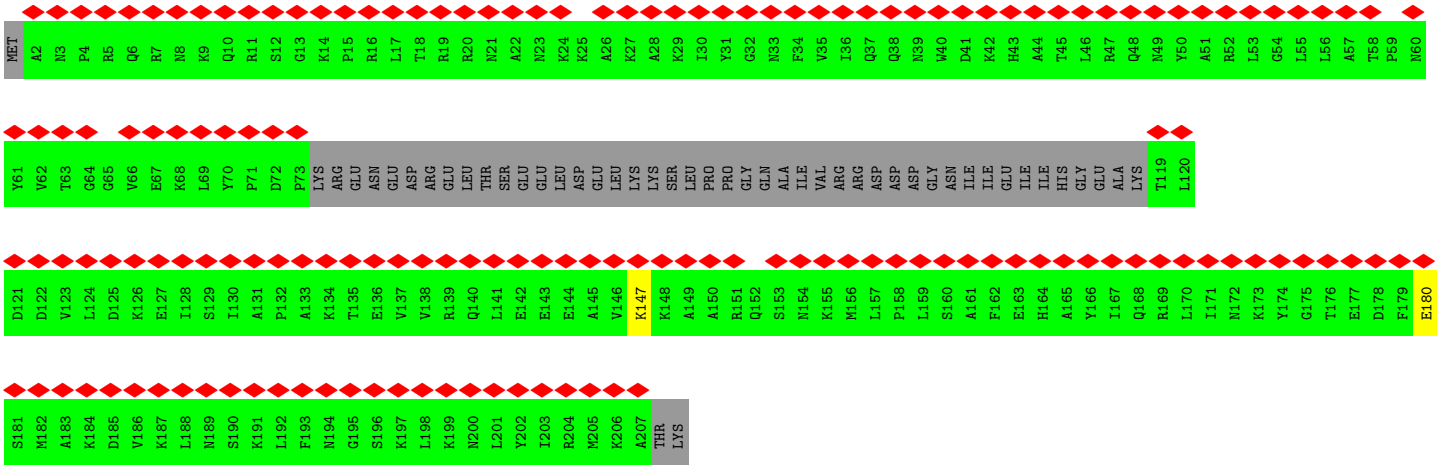
• Molecule 40: Ribosome biogenesis protein rlp24

Chain u: 40% 57% 43%



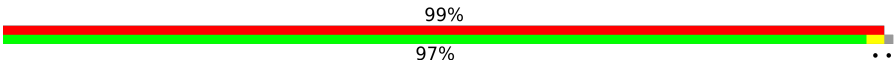
- Molecule 41: Nucleolar protein 16

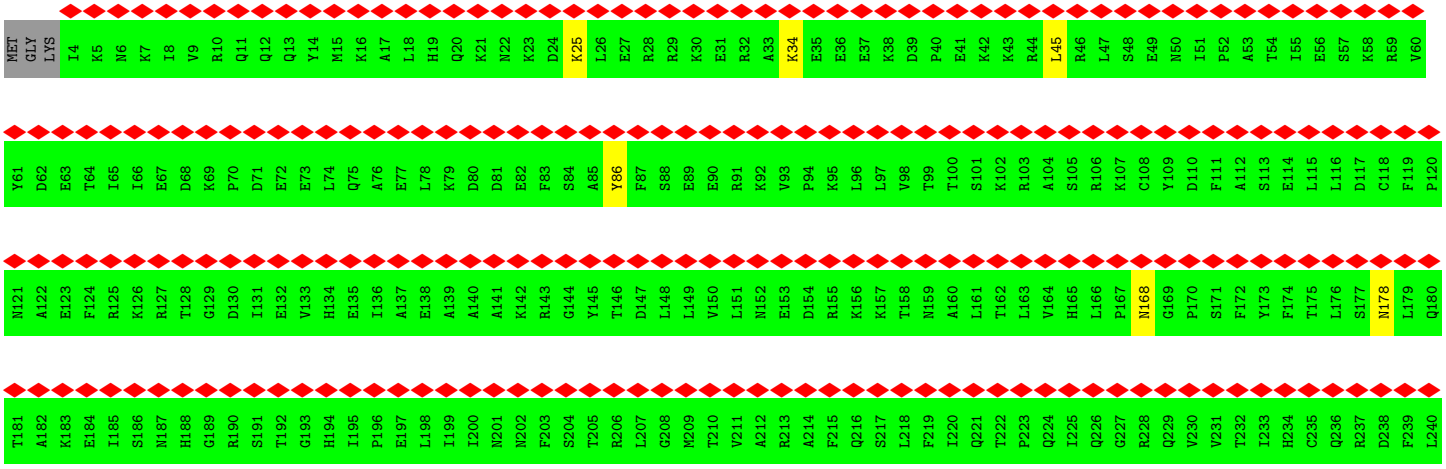
Chain v:

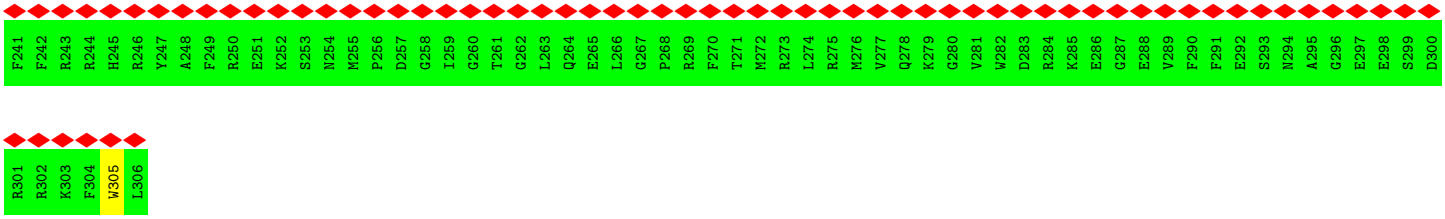


- Molecule 42: Brix domain-containing protein C4F8.04

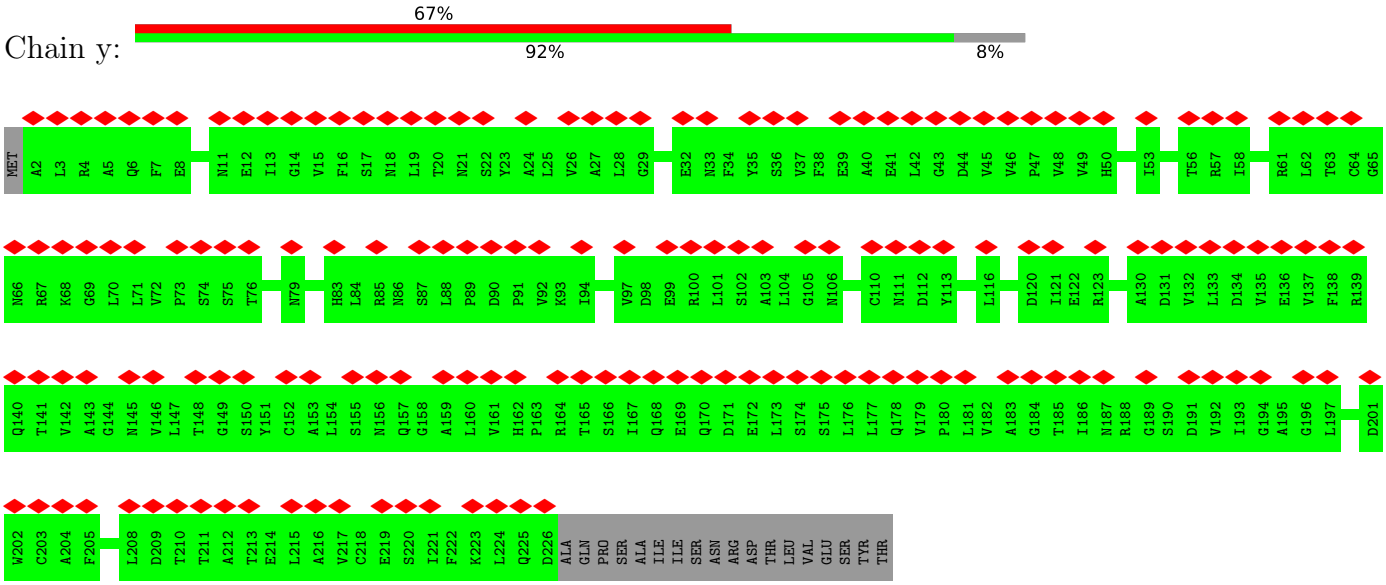
Chain x:



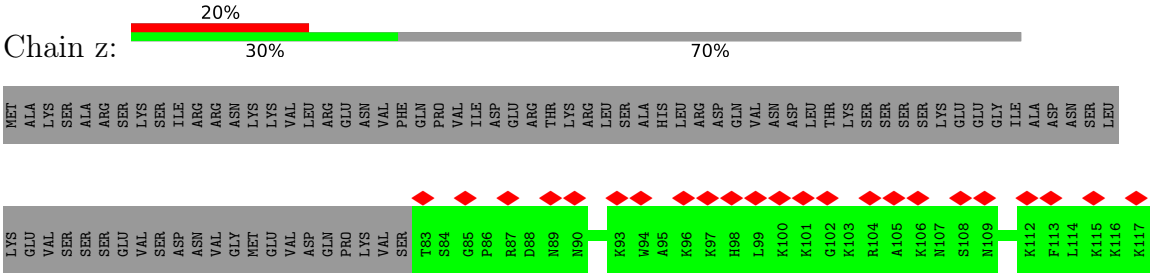




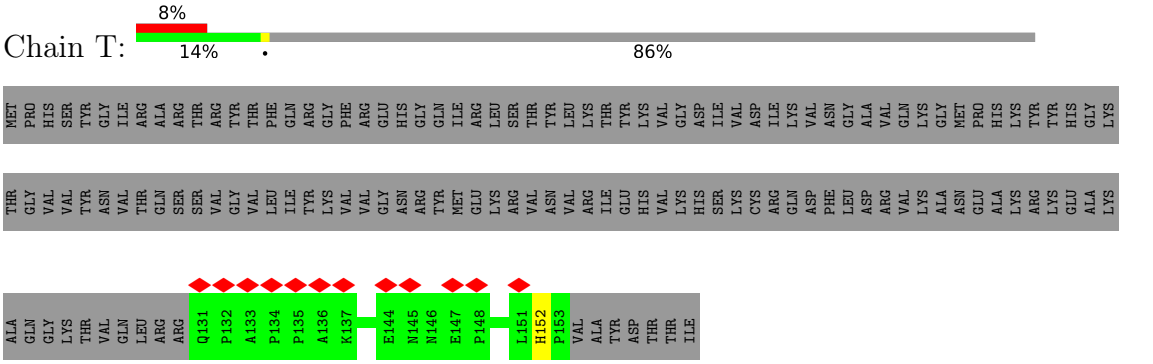
• Molecule 43: Eukaryotic translation initiation factor 6



• Molecule 44: UPF0642 protein C32H8.05



• Molecule 45: 60S ribosomal protein L21-A



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.491	Depositor
Minimum map value	-0.210	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.43	0/37838	0.75	0/58935
2	2	0.44	0/3608	0.73	0/5615
3	3	0.36	0/1607	0.54	0/2162
4	4	0.30	0/1809	0.54	0/2443
5	5	0.28	0/2739	0.56	0/3702
6	6	0.24	0/1916	0.86	0/2973
7	A	0.27	0/1431	0.54	0/1971
8	B	0.28	0/2694	0.58	0/3619
9	C	0.38	0/2617	0.59	0/3529
10	D	0.24	0/1928	0.41	0/2680
11	E	0.32	0/1356	0.60	0/1829
12	F	0.32	0/1977	0.53	0/2651
13	G	0.32	0/1487	0.56	0/2007
14	H	0.25	0/901	0.45	0/1252
15	J	0.23	0/563	0.35	0/786
16	K	0.24	0/1188	0.41	0/1654
17	L	0.39	0/956	0.67	0/1283
18	M	0.28	0/1024	0.59	0/1375
19	N	0.39	0/1429	0.61	0/1909
20	O	0.31	0/1588	0.57	0/2128
21	P	0.32	0/1176	0.54	0/1580
22	Q	0.32	0/1068	0.60	0/1434
23	S	0.30	0/1430	0.64	0/1921
24	V	0.25	0/623	0.44	0/862
25	W	0.24	0/841	0.44	0/1154
26	X	0.30	0/753	0.52	0/1021
27	Y	0.32	0/1008	0.64	0/1341
28	b	0.23	0/1935	0.38	0/2693
29	d	0.24	0/481	0.41	0/669
30	e	0.38	0/1000	0.63	0/1333
31	f	0.35	0/859	0.58	0/1152
32	h	0.33	0/1003	0.62	0/1333

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	i	0.32	0/703	0.66	0/931
34	j	0.35	0/575	0.62	0/761
35	m	0.30	0/873	0.60	0/1188
36	n	0.29	0/2233	0.52	0/3054
37	o	0.25	0/665	0.43	0/925
38	r	0.23	0/819	0.40	0/1134
39	t	0.23	0/1114	0.40	0/1550
40	u	0.24	0/544	0.40	0/756
41	v	0.29	0/1319	0.56	0/1769
42	x	0.30	0/2549	0.57	0/3416
43	y	0.24	0/1106	0.45	0/1536
44	z	0.23	0/172	0.36	0/238
45	T	0.27	0/182	0.48	0/252
All	All	0.36	0/95687	0.66	0/138506

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	
3	3	188/302 (62%)	177 (94%)	11 (6%)	0	100	100
4	4	207/217 (95%)	198 (96%)	9 (4%)	0	100	100
5	5	336/387 (87%)	301 (90%)	35 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	A	250/295 (85%)	237 (95%)	12 (5%)	1 (0%)	34	69
8	B	328/388 (84%)	314 (96%)	14 (4%)	0	100	100
9	C	324/363 (89%)	302 (93%)	22 (7%)	0	100	100
10	D	385/578 (67%)	364 (94%)	21 (6%)	0	100	100
11	E	168/195 (86%)	144 (86%)	23 (14%)	1 (1%)	25	62
12	F	237/250 (95%)	217 (92%)	19 (8%)	1 (0%)	34	69
13	G	184/259 (71%)	175 (95%)	9 (5%)	0	100	100
14	H	181/190 (95%)	175 (97%)	6 (3%)	0	100	100
15	J	111/333 (33%)	106 (96%)	5 (4%)	0	100	100
16	K	236/373 (63%)	228 (97%)	8 (3%)	0	100	100
17	L	113/208 (54%)	106 (94%)	7 (6%)	0	100	100
18	M	123/134 (92%)	115 (94%)	8 (6%)	0	100	100
19	N	160/201 (80%)	154 (96%)	6 (4%)	0	100	100
20	O	194/197 (98%)	186 (96%)	8 (4%)	0	100	100
21	P	143/187 (76%)	134 (94%)	9 (6%)	0	100	100
22	Q	134/187 (72%)	121 (90%)	12 (9%)	1 (1%)	22	59
23	S	163/176 (93%)	149 (91%)	14 (9%)	0	100	100
24	V	125/139 (90%)	120 (96%)	5 (4%)	0	100	100
25	W	155/241 (64%)	147 (95%)	8 (5%)	0	100	100
26	X	114/141 (81%)	104 (91%)	10 (9%)	0	100	100
27	Y	123/126 (98%)	120 (98%)	3 (2%)	0	100	100
28	b	383/642 (60%)	374 (98%)	9 (2%)	0	100	100
29	d	93/113 (82%)	91 (98%)	2 (2%)	0	100	100
30	e	121/127 (95%)	111 (92%)	10 (8%)	0	100	100
31	f	104/108 (96%)	93 (89%)	11 (11%)	0	100	100
32	h	118/122 (97%)	110 (93%)	8 (7%)	0	100	100
33	i	83/99 (84%)	81 (98%)	2 (2%)	0	100	100
34	j	69/91 (76%)	64 (93%)	5 (7%)	0	100	100
35	m	115/740 (16%)	107 (93%)	8 (7%)	0	100	100
36	n	365/607 (60%)	353 (97%)	12 (3%)	0	100	100
37	o	132/276 (48%)	132 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	r	158/260 (61%)	153 (97%)	5 (3%)	0	100	100
39	t	223/249 (90%)	215 (96%)	8 (4%)	0	100	100
40	u	106/192 (55%)	104 (98%)	2 (2%)	0	100	100
41	v	157/209 (75%)	141 (90%)	16 (10%)	0	100	100
42	x	301/306 (98%)	289 (96%)	12 (4%)	0	100	100
43	y	223/244 (91%)	219 (98%)	4 (2%)	0	100	100
44	z	33/117 (28%)	32 (97%)	1 (3%)	0	100	100
45	T	21/160 (13%)	18 (86%)	3 (14%)	0	100	100
All	All	7487/10729 (70%)	7081 (95%)	402 (5%)	4 (0%)	54	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	118	ASN
11	E	136	ASP
22	Q	76	SER
12	F	222	ARG

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	
3	3	167/271 (62%)	165 (99%)	2 (1%)	71	84
4	4	190/197 (96%)	185 (97%)	5 (3%)	46	69
5	5	301/345 (87%)	297 (99%)	4 (1%)	69	83
7	A	47/266 (18%)	45 (96%)	2 (4%)	29	58
8	B	282/326 (86%)	276 (98%)	6 (2%)	53	74
9	C	276/297 (93%)	270 (98%)	6 (2%)	52	72
11	E	139/155 (90%)	133 (96%)	6 (4%)	29	58
12	F	201/210 (96%)	200 (100%)	1 (0%)	88	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	G	155/212 (73%)	151 (97%)	4 (3%)	46	69
17	L	97/167 (58%)	97 (100%)	0	100	100
18	M	108/113 (96%)	103 (95%)	5 (5%)	27	57
19	N	146/176 (83%)	144 (99%)	2 (1%)	67	82
20	O	161/162 (99%)	156 (97%)	5 (3%)	40	65
21	P	120/149 (80%)	117 (98%)	3 (2%)	47	70
22	Q	116/159 (73%)	115 (99%)	1 (1%)	78	88
23	S	149/154 (97%)	140 (94%)	9 (6%)	19	50
26	X	41/122 (34%)	41 (100%)	0	100	100
27	Y	110/111 (99%)	108 (98%)	2 (2%)	59	77
30	e	105/107 (98%)	104 (99%)	1 (1%)	76	86
31	f	89/91 (98%)	85 (96%)	4 (4%)	27	57
32	h	106/107 (99%)	103 (97%)	3 (3%)	43	67
33	i	74/84 (88%)	72 (97%)	2 (3%)	44	68
34	j	58/71 (82%)	56 (97%)	2 (3%)	37	64
35	m	67/659 (10%)	64 (96%)	3 (4%)	27	57
36	n	102/532 (19%)	98 (96%)	4 (4%)	32	60
37	o	1/246 (0%)	1 (100%)	0	100	100
41	v	138/181 (76%)	136 (99%)	2 (1%)	67	82
42	x	271/273 (99%)	264 (97%)	7 (3%)	46	69
45	T	20/139 (14%)	19 (95%)	1 (5%)	24	55
All	All	3837/6082 (63%)	3745 (98%)	92 (2%)	51	71

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	43	CYS
3	3	174	TYR
4	4	104	ASP
4	4	132	LYS
4	4	137	TYR
4	4	139	GLN
4	4	212	TYR
5	5	18	LYS
5	5	127	HIS

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Mol	Chain	Res	Type
5	5	218	ASP
5	5	345	ARG
7	A	246	ASP
7	A	290	LEU
8	B	66	LYS
8	B	84	MET
8	B	155	CYS
8	B	269	ASN
8	B	292	LYS
8	B	319	ASN
9	C	97	ARG
9	C	101	MET
9	C	118	ASN
9	C	140	ARG
9	C	143	ARG
9	C	363	ASN
11	E	44	ARG
11	E	112	SER
11	E	137	GLU
11	E	139	PHE
11	E	176	GLU
11	E	189	ARG
12	F	77	ARG
13	G	120	LYS
13	G	131	ASN
13	G	219	ASP
13	G	223	SER
18	M	40	ASP
18	M	51	ILE
18	M	52	ARG
18	M	63	MET
18	M	85	ASN
19	N	118	SER
19	N	191	ARG
20	O	22	SER
20	O	48	PHE
20	O	53	LEU
20	O	73	HIS
20	O	136	TYR
21	P	30	ARG
21	P	61	ARG
21	P	69	ARG

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Mol	Chain	Res	Type
22	Q	73	LYS
23	S	28	LEU
23	S	38	SER
23	S	83	ARG
23	S	143	LEU
23	S	144	ASN
23	S	146	HIS
23	S	149	PHE
23	S	173	SER
23	S	175	PHE
27	Y	2	LYS
27	Y	112	LYS
30	e	74	ARG
31	f	20	SER
31	f	54	TYR
31	f	61	ARG
31	f	93	LYS
32	h	6	PHE
32	h	18	GLU
32	h	42	LYS
33	i	51	TYR
33	i	64	ASP
34	j	26	SER
34	j	30	GLN
35	m	230	HIS
35	m	240	TYR
35	m	249	THR
36	n	32	ASP
36	n	33	PHE
36	n	50	LYS
36	n	122	ARG
41	v	147	LYS
41	v	180	GLU
42	x	25	LYS
42	x	34	LYS
42	x	45	LEU
42	x	86	TYR
42	x	168	ASN
42	x	178	ASN
42	x	305	TRP
45	T	152	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14)

such sidechains are listed below:

Mol	Chain	Res	Type
3	3	30	ASN
5	5	68	ASN
5	5	71	GLN
5	5	230	HIS
8	B	277	GLN
9	C	50	GLN
12	F	243	ASN
19	N	57	GLN
21	P	64	ASN
21	P	80	GLN
36	n	70	GLN
42	x	165	HIS
42	x	202	ASN
42	x	234	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1550/3497 (44%)	407 (26%)	25 (1%)
2	2	150/165 (90%)	35 (23%)	1 (0%)
6	6	77/300 (25%)	37 (48%)	0
All	All	1777/3962 (44%)	479 (26%)	26 (1%)

All (479) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	14	U
1	1	15	C
1	1	20	A
1	1	26	A
1	1	32	U
1	1	59	G
1	1	60	A
1	1	62	A
1	1	65	A
1	1	66	A
1	1	67	A
1	1	69	U
1	1	72	C
1	1	73	C
1	1	74	A

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Mol	Chain	Res	Type
1	1	109	A
1	1	110	G
1	1	111	C
1	1	117	U
1	1	118	U
1	1	122	A
1	1	153	U
1	1	161	C
1	1	162	A
1	1	163	A
1	1	176	A
1	1	177	G
1	1	179	G
1	1	185	G
1	1	192	C
1	1	193	U
1	1	194	A
1	1	197	U
1	1	198	U
1	1	199	C
1	1	207	C
1	1	211	A
1	1	217	G
1	1	218	A
1	1	220	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	231	C
1	1	234	G
1	1	239	U
1	1	240	G
1	1	241	G
1	1	244	G
1	1	246	U
1	1	258	U
1	1	261	A
1	1	266	G
1	1	268	U
1	1	269	U
1	1	271	C
1	1	276	A

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Mol	Chain	Res	Type
1	1	277	G
1	1	284	U
1	1	297	A
1	1	306	U
1	1	323	C
1	1	331	A
1	1	337	U
1	1	338	G
1	1	345	G
1	1	346	A
1	1	347	C
1	1	360	A
1	1	380	A
1	1	383	A
1	1	384	G
1	1	395	A
1	1	399	A
1	1	403	A
1	1	406	U
1	1	407	A
1	1	410	A
1	1	411	C
1	1	425	A
1	1	429	G
1	1	430	A
1	1	437	G
1	1	438	G
1	1	446	U
1	1	447	C
1	1	448	U
1	1	449	U
1	1	461	A
1	1	462	U
1	1	465	G
1	1	466	U
1	1	479	A
1	1	488	A
1	1	489	C
1	1	497	C
1	1	499	G
1	1	505	G
1	1	506	G

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Mol	Chain	Res	Type
1	1	510	G
1	1	514	C
1	1	522	G
1	1	527	C
1	1	529	G
1	1	532	A
1	1	534	A
1	1	540	A
1	1	544	A
1	1	546	G
1	1	547	G
1	1	548	U
1	1	551	C
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	591	G
1	1	592	U
1	1	593	A
1	1	599	U
1	1	602	A
1	1	603	C
1	1	605	G
1	1	606	G
1	1	613	A
1	1	618	U
1	1	619	G
1	1	621	G
1	1	624	U
1	1	625	U
1	1	626	C
1	1	627	G
1	1	632	A
1	1	634	G
1	1	635	G
1	1	636	A
1	1	640	U
1	1	642	A
1	1	645	U

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Mol	Chain	Res	Type
1	1	646	A
1	1	647	A
1	1	652	U
1	1	659	G
1	1	661	C
1	1	662	C
1	1	663	C
1	1	666	C
1	1	673	C
1	1	674	A
1	1	675	C
1	1	685	A
1	1	698	U
1	1	702	A
1	1	706	U
1	1	708	U
1	1	714	A
1	1	716	G
1	1	717	A
1	1	719	A
1	1	756	C
1	1	759	C
1	1	760	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	770	G
1	1	777	C
1	1	778	G
1	1	779	A
1	1	816	A
1	1	817	G
1	1	829	U
1	1	831	G
1	1	840	A
1	1	961	A
1	1	964	U
1	1	965	A
1	1	966	G
1	1	967	U
1	1	968	A
1	1	969	G

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Mol	Chain	Res	Type
1	1	970	C
1	1	976	C
1	1	987	U
1	1	988	U
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1009	C
1	1	1010	A
1	1	1012	A
1	1	1014	C
1	1	1016	G
1	1	1023	G
1	1	1133	G
1	1	1135	G
1	1	1139	U
1	1	1141	C
1	1	1142	U
1	1	1143	A
1	1	1146	G
1	1	1147	G
1	1	1150	C
1	1	1158	G
1	1	1160	A
1	1	1162	G
1	1	1163	C
1	1	1164	A
1	1	1170	G
1	1	1172	C
1	1	1173	G
1	1	1174	A
1	1	1176	G
1	1	1182	U
1	1	1185	A
1	1	1186	C
1	1	1190	A
1	1	1197	G
1	1	1199	U
1	1	1211	A
1	1	1212	U
1	1	1218	C
1	1	1219	U

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Mol	Chain	Res	Type
1	1	1220	C
1	1	1222	U
1	1	1223	C
1	1	1224	A
1	1	1232	G
1	1	1235	A
1	1	1244	G
1	1	1248	A
1	1	1249	U
1	1	1252	A
1	1	1253	G
1	1	1254	A
1	1	1258	C
1	1	1259	A
1	1	1273	G
1	1	1275	A
1	1	1276	A
1	1	1277	G
1	1	1282	A
1	1	1283	A
1	1	1284	U
1	1	1285	C
1	1	1286	C
1	1	1289	U
1	1	1291	A
1	1	1292	G
1	1	1293	G
1	1	1294	A
1	1	1296	U
1	1	1297	G
1	1	1303	C
1	1	1308	C
1	1	1309	A
1	1	1310	C
1	1	1315	C
1	1	1316	G
1	1	1317	A
1	1	1318	A
1	1	1334	A
1	1	1336	U
1	1	1337	G
1	1	1338	G

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Mol	Chain	Res	Type
1	1	1339	A
1	1	1340	U
1	1	1347	U
1	1	1348	A
1	1	1357	A
1	1	1362	U
1	1	1379	U
1	1	1380	A
1	1	1381	G
1	1	1383	U
1	1	1384	U
1	1	1386	G
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1416	G
1	1	1420	U
1	1	1425	C
1	1	1426	G
1	1	1433	U
1	1	1451	G
1	1	1452	A
1	1	1453	A
1	1	1463	G
1	1	1465	G
1	1	1471	C
1	1	1480	A
1	1	1481	G
1	1	1484	G
1	1	2452	G
1	1	2454	C
1	1	2471	C
1	1	2473	A
1	1	2474	A
1	1	2480	C
1	1	2933	A
1	1	2952	C
1	1	2953	U
1	1	2982	A
1	1	2984	C
1	1	2989	C
1	1	2993	G

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Mol	Chain	Res	Type
1	1	2994	C
1	1	2995	A
1	1	3084	U
1	1	3085	G
1	1	3086	A
1	1	3093	G
1	1	3099	G
1	1	3102	A
1	1	3108	A
1	1	3113	A
1	1	3116	U
1	1	3117	A
1	1	3118	G
1	1	3119	U
1	1	3125	A
1	1	3128	A
1	1	3142	A
1	1	3144	C
1	1	3151	A
1	1	3152	U
1	1	3153	U
1	1	3155	G
1	1	3183	A
1	1	3188	U
1	1	3189	C
1	1	3195	C
1	1	3196	C
1	1	3197	G
1	1	3205	G
1	1	3209	A
1	1	3218	A
1	1	3225	A
1	1	3226	A
1	1	3227	U
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3270	U
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A

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Mol	Chain	Res	Type
1	1	3282	G
1	1	3300	A
1	1	3307	U
1	1	3308	G
1	1	3315	A
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3320	A
1	1	3324	G
1	1	3329	G
1	1	3335	U
1	1	3336	G
1	1	3337	A
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3347	G
1	1	3351	U
1	1	3352	A
1	1	3353	U
1	1	3355	G
1	1	3356	A
1	1	3357	C
1	1	3358	U
1	1	3359	U
1	1	3365	U
1	1	3369	A
1	1	3370	U
1	1	3372	C
1	1	3373	C
1	1	3375	U
1	1	3396	A
1	1	3405	C
1	1	3414	U
1	1	3417	A
1	1	3418	U
1	1	3419	G
1	1	3420	U
1	1	3421	G
1	1	3431	A

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Mol	Chain	Res	Type
1	1	3433	U
1	1	3435	U
1	1	3436	A
1	1	3469	U
1	1	3470	G
1	1	3471	A
1	1	3476	A
1	1	3478	G
1	1	3479	C
1	1	3483	U
1	1	3489	C
1	1	3490	A
1	1	3491	A
1	1	3496	U
2	2	23	G
2	2	27	C
2	2	29	C
2	2	42	U
2	2	43	C
2	2	47	G
2	2	55	C
2	2	57	G
2	2	61	A
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	83	G
2	2	87	A
2	2	88	A
2	2	89	U
2	2	98	U
2	2	103	G
2	2	108	U
2	2	112	A
2	2	114	C
2	2	115	G
2	2	117	A
2	2	119	A
2	2	120	U
2	2	124	G
2	2	132	G

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Mol	Chain	Res	Type
2	2	133	U
2	2	134	U
2	2	136	U
2	2	156	G
2	2	159	U
2	2	160	G
2	2	162	C
6	6	5	U
6	6	6	C
6	6	8	U
6	6	9	C
6	6	12	A
6	6	43	G
6	6	45	G
6	6	46	G
6	6	47	U
6	6	48	G
6	6	49	U
6	6	50	U
6	6	51	G
6	6	57	A
6	6	60	U
6	6	84	U
6	6	87	A
6	6	89	U
6	6	90	U
6	6	91	U
6	6	93	A
6	6	94	A
6	6	96	U
6	6	97	C
6	6	99	A
6	6	101	U
6	6	102	G
6	6	105	G
6	6	106	A
6	6	108	A
6	6	178	U
6	6	181	C
6	6	182	C
6	6	184	C
6	6	186	U

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Mol	Chain	Res	Type
6	6	187	U
6	6	188	G

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	116	A
1	1	270	U
1	1	382	A
1	1	460	G
1	1	487	C
1	1	496	C
1	1	626	C
1	1	661	C
1	1	674	A
1	1	759	C
1	1	760	C
1	1	761	U
1	1	997	A
1	1	1159	U
1	1	1234	A
1	1	1272	U
1	1	1333	A
1	1	1338	G
1	1	1385	U
1	1	2952	C
1	1	3217	U
1	1	3318	A
1	1	3328	U
1	1	3337	A
1	1	3416	A
2	2	131	G

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 1 ligands modelled in this entry, 1 is 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)

There are no chain breaks in this entry.

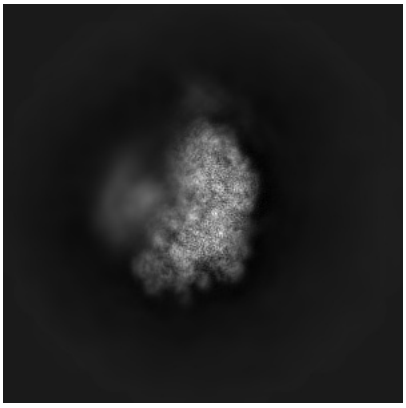
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-24395. These allow visual inspection of the internal detail of the map and identification of artifacts.

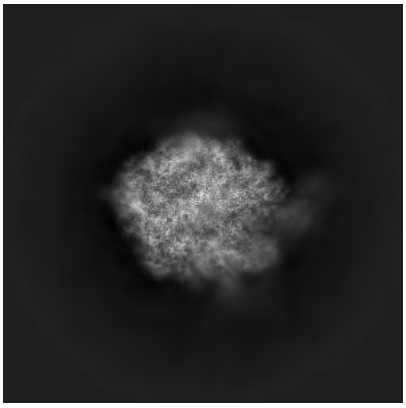
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

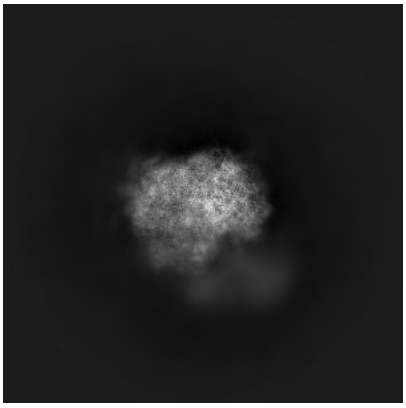
6.1.1 Primary map



X



Y

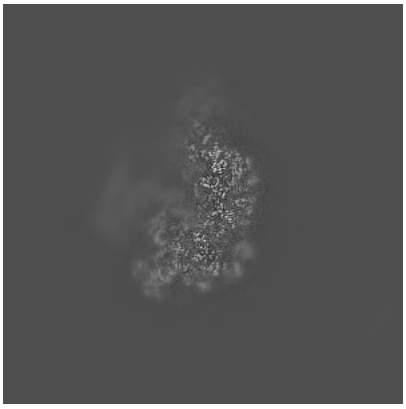


Z

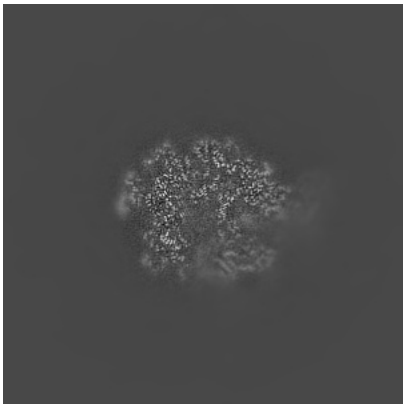
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

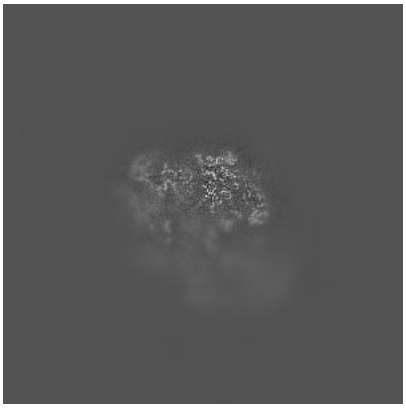
6.2.1 Primary map



X Index: 256



Y Index: 256

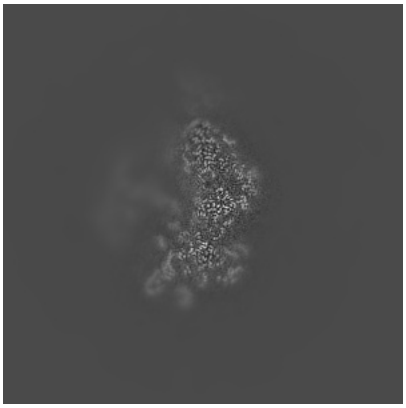


Z Index: 256

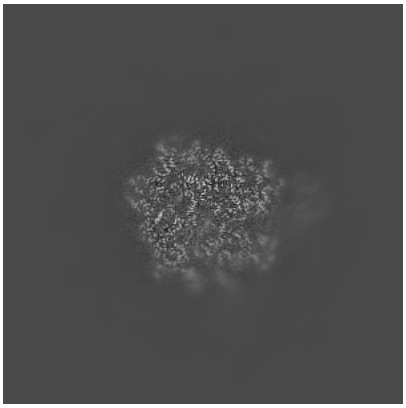
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

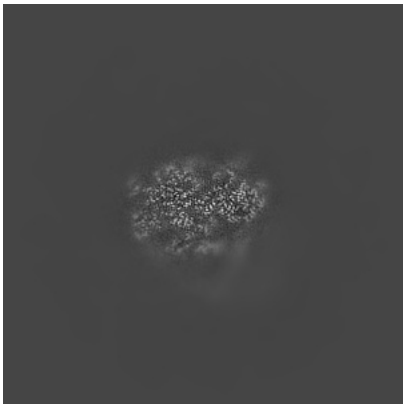
6.3.1 Primary map



X Index: 267



Y Index: 272



Z Index: 208

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

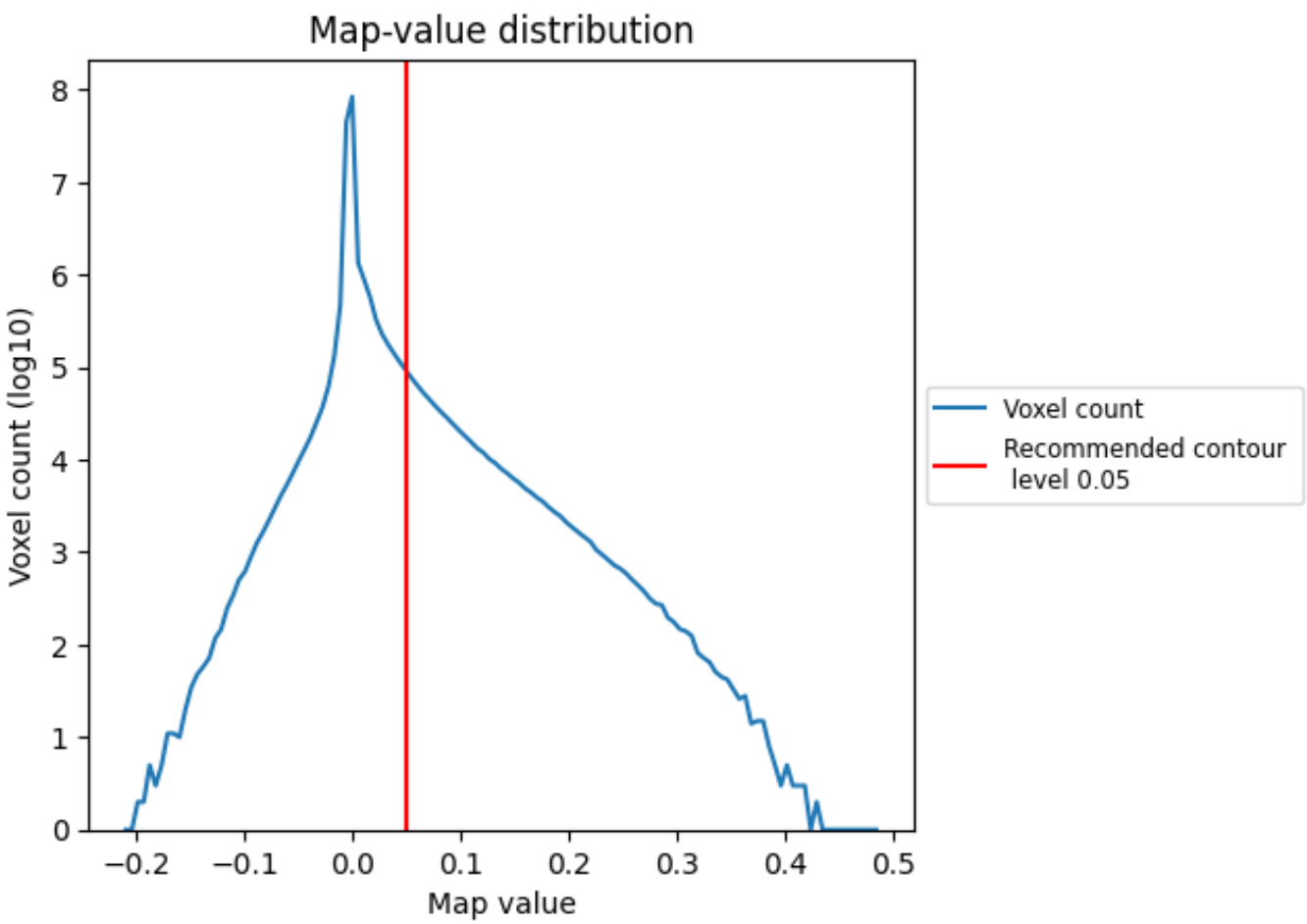
6.5 Mask visualisation (i)

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

7 Map analysis (i)

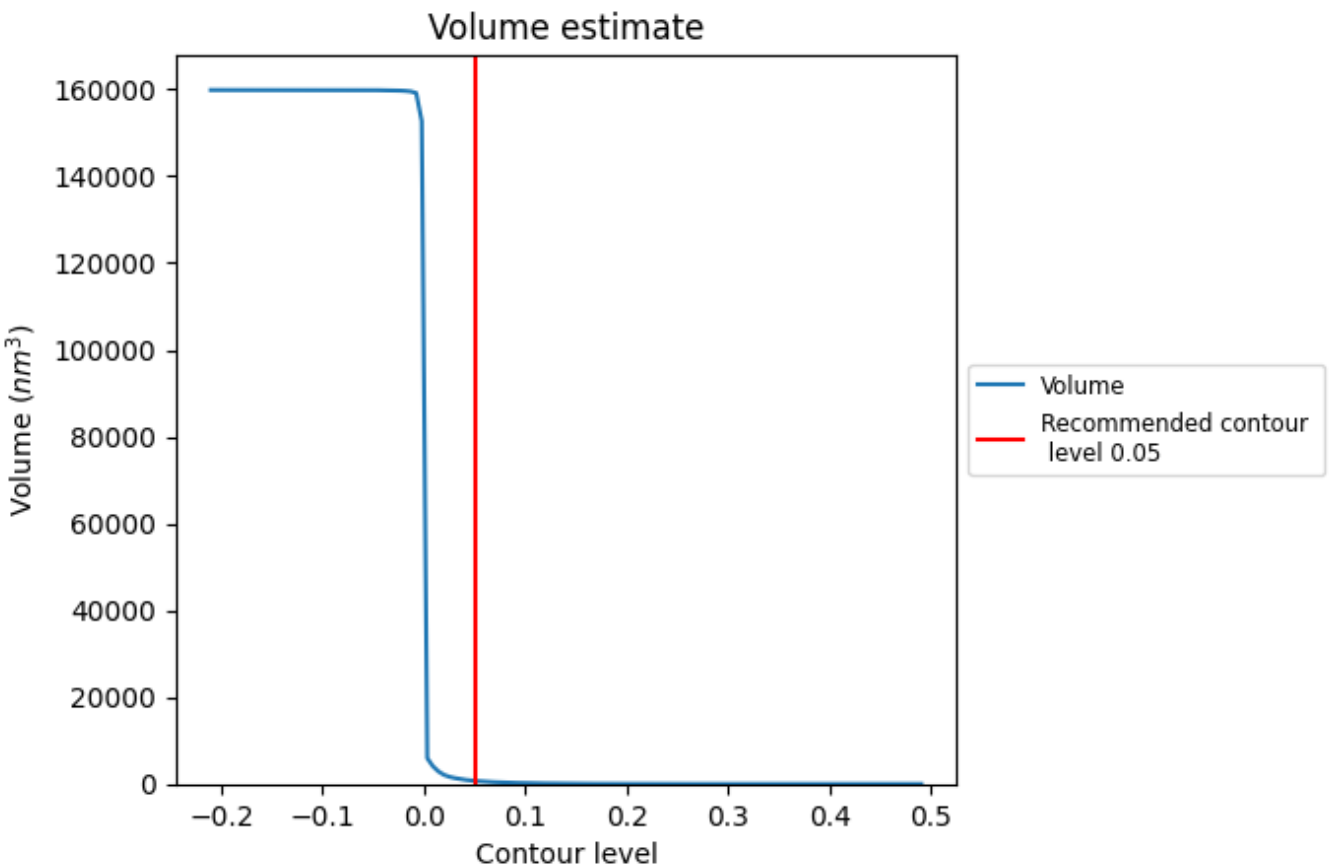
This section contains the results of statistical analysis of the map.

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.

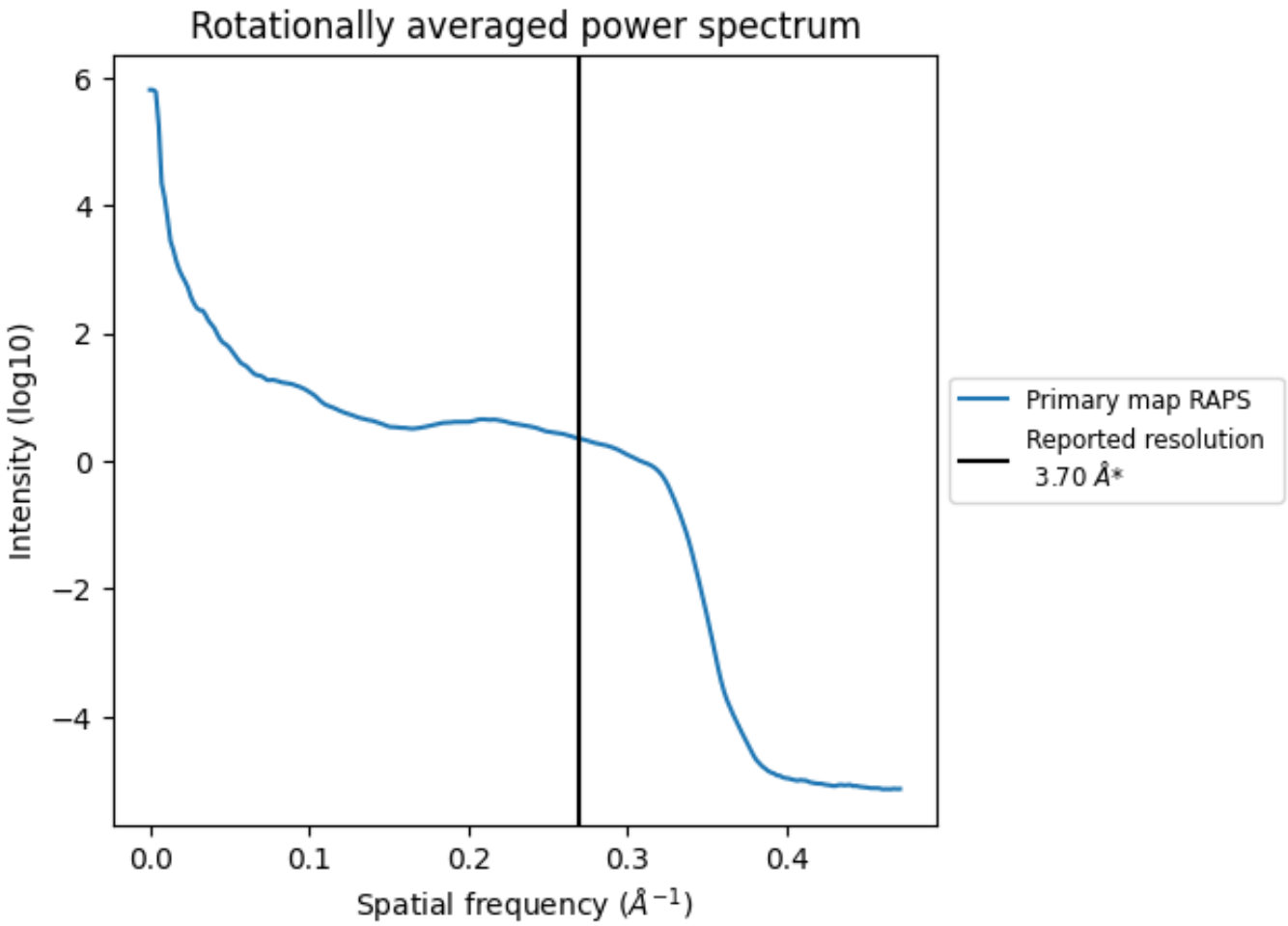
7.2 Volume estimate (i)



The volume at the recommended contour level is 724 nm^3; this corresponds to an approximate mass of 654 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}

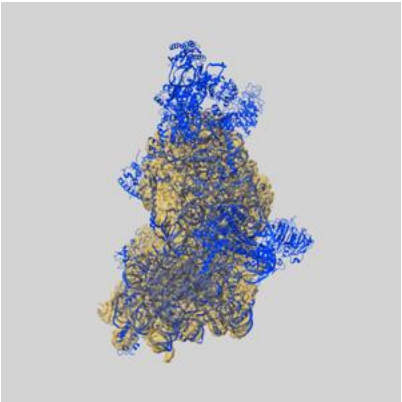
8 Fourier-Shell correlation (i)

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

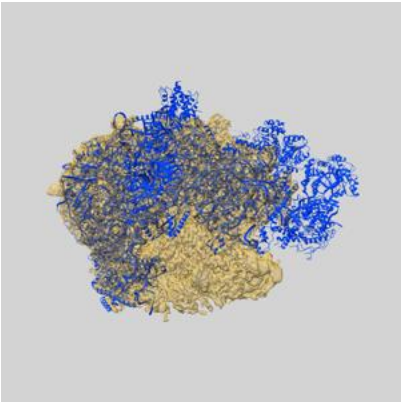
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-24395 and PDB model 8ETI. Per-residue inclusion information can be found in section 3 on page 12.

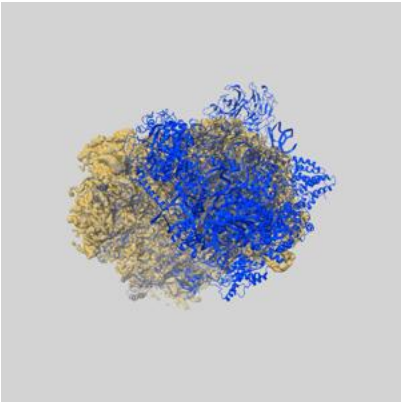
9.1 Map-model overlay (i)



X



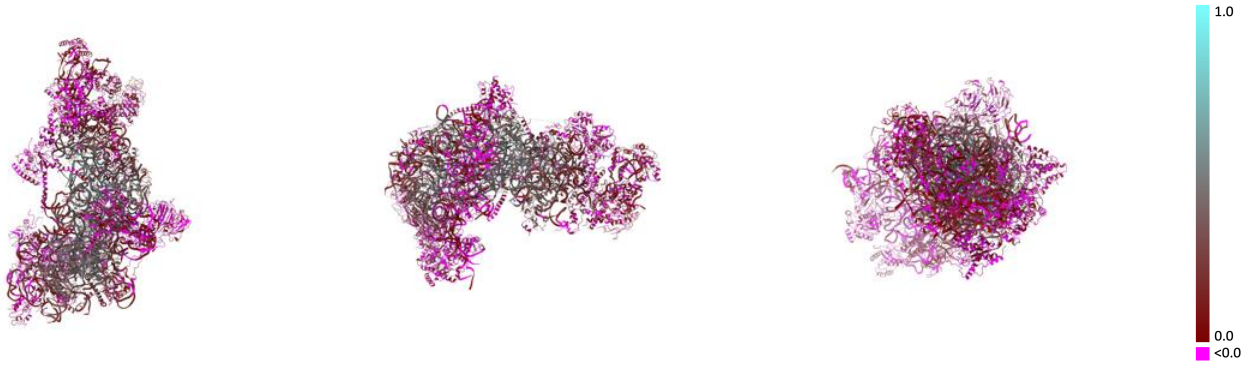
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

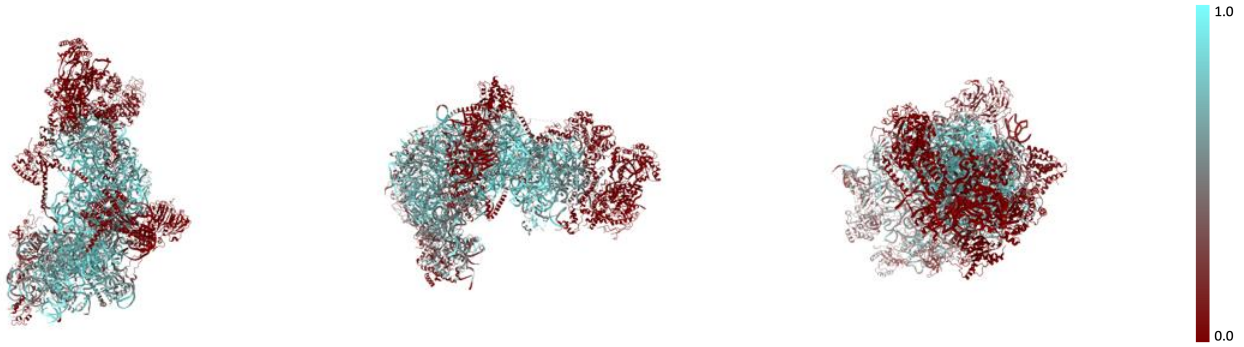
9.2 Q-score mapped to coordinate model (i)



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.

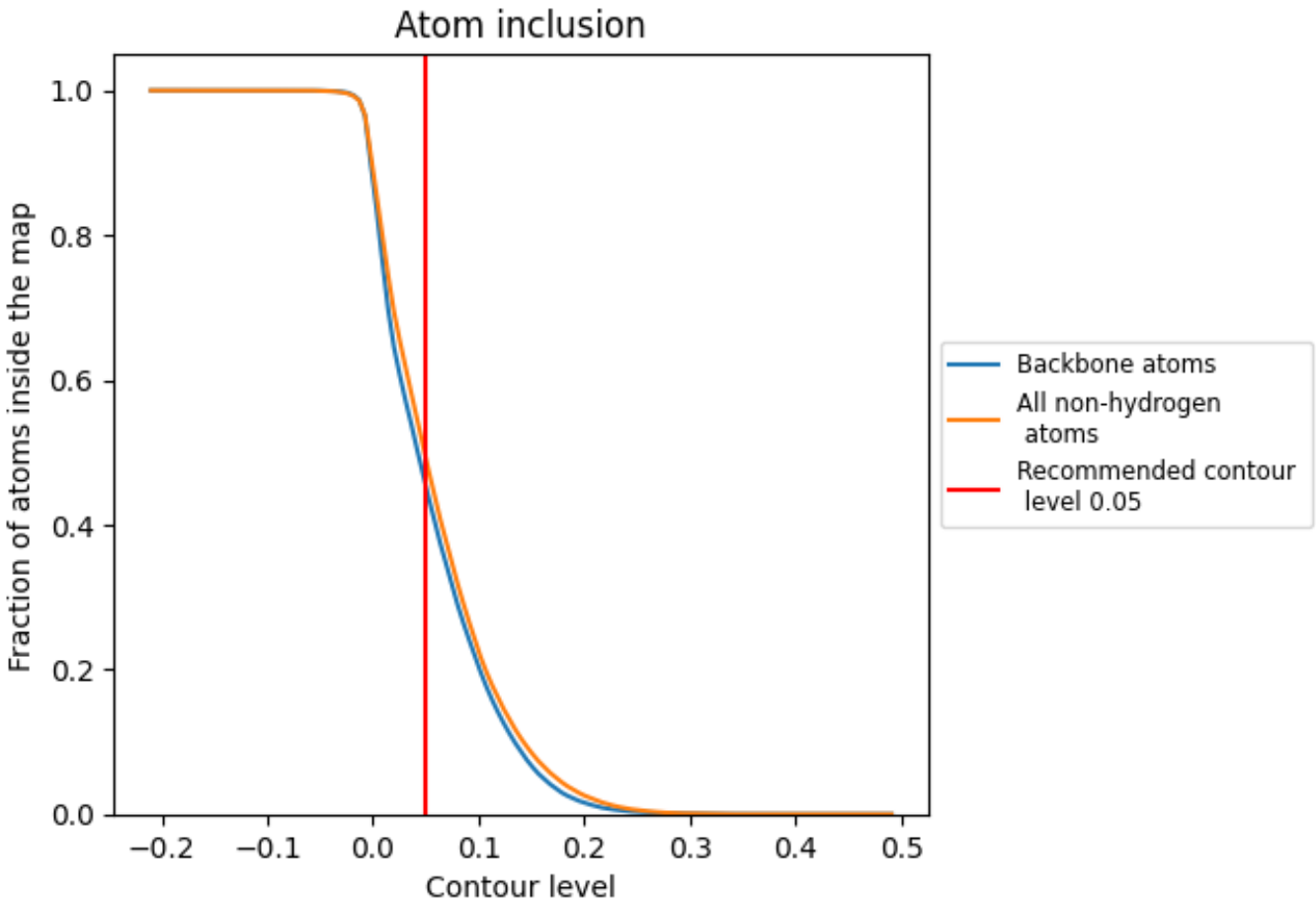
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 45% of all backbone atoms, 49% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4908	0.1930
1	0.7234	0.2640
2	0.7739	0.3030
3	0.0948	0.0660
4	0.0006	0.0230
5	0.0000	-0.0020
6	0.0000	0.0910
A	0.0269	-0.0030
B	0.5031	0.1290
C	0.7533	0.4280
D	0.0062	-0.0100
E	0.4448	0.1270
F	0.6640	0.3560
G	0.3654	0.0980
H	0.5177	0.1110
J	0.0000	-0.0180
K	0.0000	0.0750
L	0.7121	0.3730
M	0.6151	0.2320
N	0.6614	0.2970
O	0.6950	0.3370
P	0.3915	0.0530
Q	0.6839	0.3500
S	0.6119	0.2970
T	0.3371	0.2730
V	0.2516	-0.0370
W	0.2141	0.0360
X	0.4926	0.1990
Y	0.7464	0.3550
b	0.2388	0.0380
d	0.4679	0.0530
e	0.6937	0.3750
f	0.7706	0.4090
h	0.6420	0.2830
i	0.4361	0.1280

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Chain	Atom inclusion	Q-score
j	0.7593	0.4040
m	0.0012	0.0230
n	0.0027	0.0640
o	0.0000	0.0840
r	0.2394	0.0300
t	0.0000	0.0550
u	0.3205	0.0090
v	0.0276	0.0140
x	0.0078	-0.0010
y	0.2909	-0.0090
z	0.3584	0.0840