wwPDB EM Validation Summary Report

Mar 13, 2024 – 07:19 PM JST

PDB ID	:	5H4P
EMDB ID	:	EMD-9569
Title	:	Structural snapshot of cytoplasmic pre-60S ribosomal particles bound with Nmd3, Lsg1, Tif6 and Reh1
Authors	:	Ma, C.; Wu, S.; Li, N.; Chen, Y.; Yan, K.; Li, Z.; Zheng, L.; Lei, J.; Woolford, J.L.; Gao, N.
Deposited on	:	2016-11-01
Resolution	:	3.07 Å(reported)

This is a wwPDB EM Validation Summary 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:

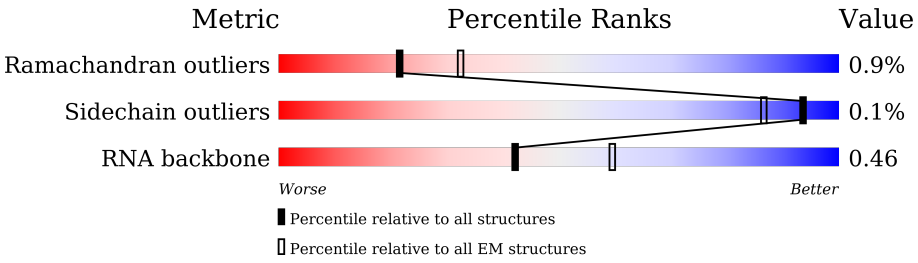
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.07 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	3396	44% 68% 22% · 9%
2	3	121	77% 83% 17%
3	4	158	40% 75% 25%
4	A	246	59% 100%
5	B	387	60% 98% ·
6	C	361	73% 99% ·
7	D	297	93% 98% ·
8	E	176	81% 87% · 11%

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Mol	Chain	Length	Quality of chain
9	F	244	73% 91% 9%
10	G	256	70% 89% 9%
11	H	191	92% 99%
12	J	174	96% 94%
13	L	199	71% 94%
14	M	138	82% 96%
15	N	204	65% 99%
16	O	199	60% 97%
17	P	184	66% 99%
18	Q	186	83% 99%
19	R	189	57% 81% 17%
20	S	172	87% 97%
21	T	160	81% 99%
22	U	121	74% 81% 17%
23	V	137	64% 99%
24	W	155	32% 41% 59%
25	X	142	57% 85% 15%
26	Y	127	73% 98%
27	Z	136	82% 97%
28	a	149	67% 97%
29	b	59	92% 98%
30	c	105	81% 92% 8%
31	d	113	64% 95%
32	e	130	75% 96%
33	f	107	61% 99%

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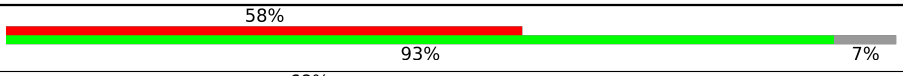
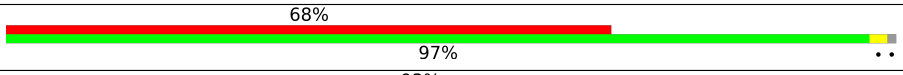
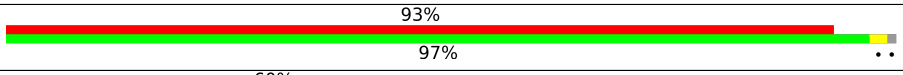
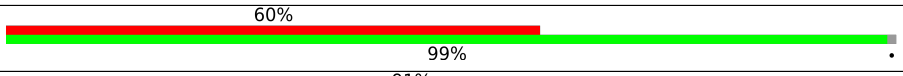
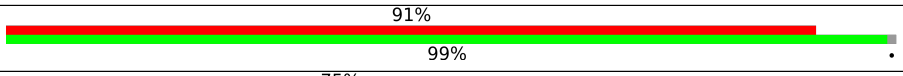
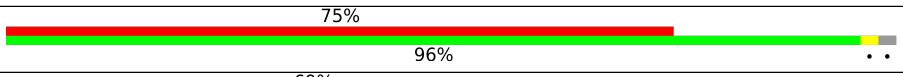
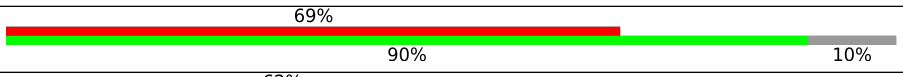
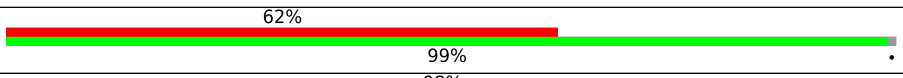
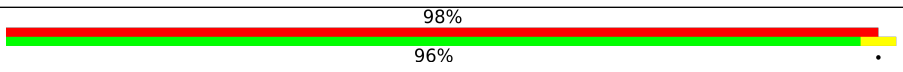
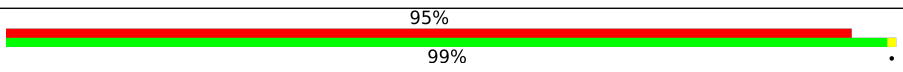
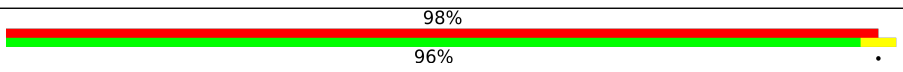
Mol	Chain	Length	Quality of chain
34	g	121	
35	h	120	
36	i	100	
37	j	88	
38	k	78	
39	l	51	
40	o	106	
41	p	92	
42	w	248	
43	y	227	
44	z	56	

2 Entry composition (i)

There are 44 unique types of molecules in this entry. The entry contains 122929 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	3091	66124	29535	11927	21571	3091	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	3	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	246	1874	1168	380	325	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	386	3075	1950	584	533	8	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	361	2748	1729	522	494	3	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	L	193	Total	C	N	O	0	0
			1543	962	315	266		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

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

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

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	183	Total	C	N	O	0	0
			1442	896	287	259		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 19 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	R	156	Total	C	N	O	0	0
			1258	781	265	212		

- Molecule 20 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 21 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 22 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 23 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 24 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	64	Total	C	N	O	S	0	0
			528	340	103	84	1		

- Molecule 25 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 26 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 27 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Z	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 28 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	b	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 31 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 34 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 35 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 37 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 38 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 40 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	95	Total	C	N	O	S	0	0
			765	481	154	125	5		

- Molecule 41 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 42 is a protein called 60S ribosomal export protein NMD3.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	w	248	Total	C	N	O	S	0	0
			1894	1208	318	361	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	227	Total	C	N	O	S	0	0
			1699	1054	296	342	7		

- Molecule 44 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1.

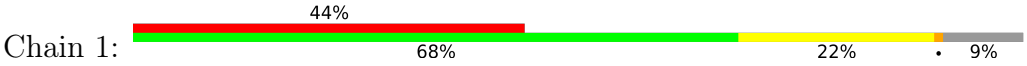
Mol	Chain	Residues	Atoms					AltConf	Trace
44	z	56	Total	C	N	O	S	0	0
			469	289	92	85	3		

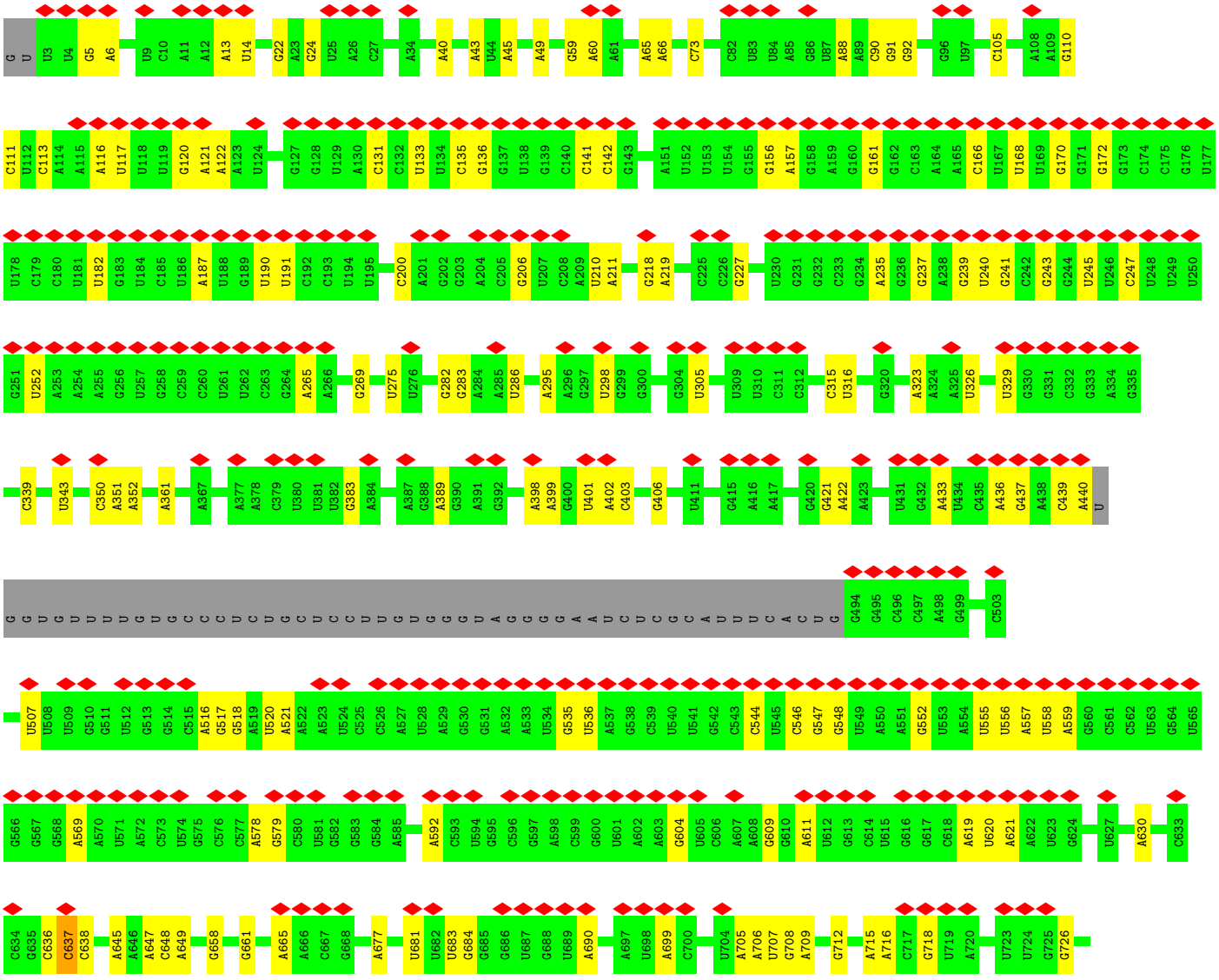
3 Residue-property plots (i)

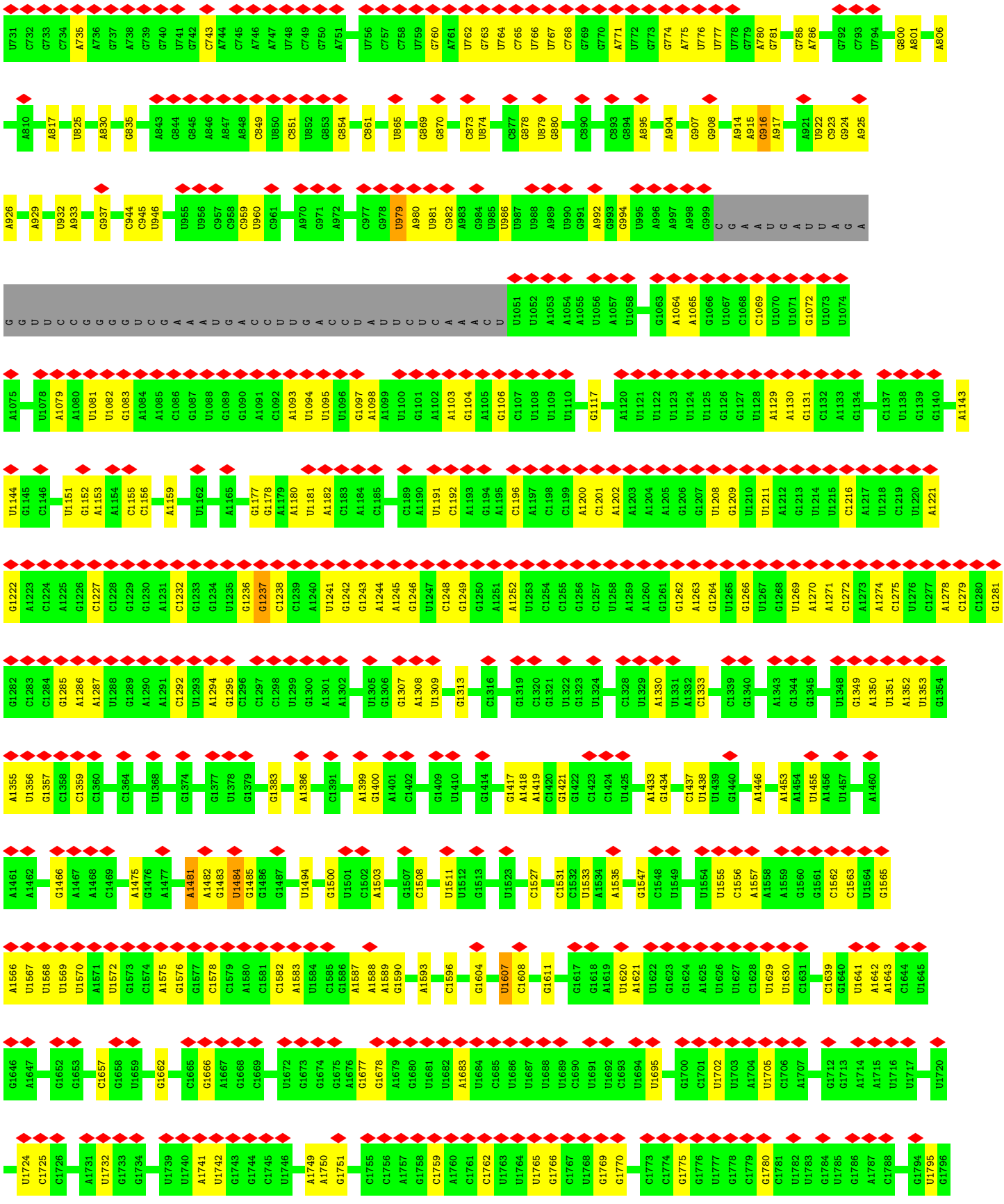
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

Chain 1:






U731 C732 G733 C734 A735 A736 G737 A738 G739 G740 U741 U742 C743 A744 C745 A746 A747 U748 C749 G750 A751 U756 C757 C758 U759 G760 A761 U762 G763 U764 C765 U766 U767 C768 G769 G770 A771 U772 G773 G774 A775 U776 U777 U778 G779 A780 G781 G785 A786 G792 C793 U794 G800 A801 A806
A810 A817 U825 A830 G835 A843 G844 G845 A846 A847 A848 C849 U850 C851 U852 C853 G854 C861 U865 G869 G870 C873 U874 C877 G878 U879 G880 C890 C893 C894 A895 A904 G907 G908 A914 A915 G916 A917 A921 U922 C923 G924 A925
A926 A929 U932 A933 G937 C944 C945 U946 U955 U956 C957 C958 C959 U960 C961 A970 G971 A972 C977 G978 U979 A980 U981 C982 A983 G984 U985 U986 U987 U988 A989 U990 G991 A992 G993 G994 U995 A996 A997 A998 G999 C G A A U G A U U A G A
G G U U C C G G G G U C G A A A U U G A C C C U U U G A C C C U A A U U C U C A A A A C U U1051 U1052 A1053 A1054 A1055 U1056 A1057 U1058 G1063 A1064 A1065 G1066 U1067 C1068 C1069 U1070 U1071 G1072 U1073 U1074
A1075 U1078 A1079 A1080 U1081 U1082 G1083 A1084 A1085 C1086 G1087 U1088 G1089 G1090 A1091 C1092 A1093 U1094 U1095 U1096 G1097 A1098 A1099 U1100 G1101 A1102 A1103 G1104 A1105 G1106 C1107 U1108 U1109 U1110 G1117 A1120 U1121 U1122 U1123 U1124 U1125 G1126 G1127 U1128 A1129 A1130 G1131 C1132 A1133 G1134 C1137 U1138 G1139 G1140 A1143
U1144 G1145 C1146 U1151 G1152 A1153 A1154 C1155 C1156 A1159 U1162 A1165 G1177 G1178 A1179 A1180 U1181 A1182 C1183 A1184 C1185 C1189 A1190 U1191 C1192 A1193 G1194 A1195 C1196 A1197 C1198 C1199 A1200 C1201 A1202 A1203 A1204 A1205 G1206 G1207 U1208 G1209 U1210 U1211 A1212 G1213 U1214 U1215 C1216 A1217 U1218 C1219 U1220 A1221
G1222 A1223 C1224 A1225 G1226 C1227 C1228 G1229 G1230 A1231 C1232 G1233 G1234 U1235 G1236 G1237 C1238 C1239 A1240 U1241 G1242 G1243 A1244 A1245 G1246 U1247 C1248 G1249 G1250 A1251 A1252 U1253 C1254 C1255 G1256 C1257 U1258 A1259 A1260 G1261 G1262 A1263 G1264 U1265 G1266 U1267 G1268 U1269 A1270 A1271 C1272 A1273 A1274 C1275 U1276 C1277 A1278 C1279 C1280 G1281
G1282 C1283 C1284 G1285 A1286 A1287 U1288 G1289 A1290 A1291 C1292 U1293 A1294 G1295 C1296 C1297 G1298 U1299 G1300 A1301 A1302 U1305 G1306 G1307 A1308 U1309 G1313 C1316 G1319 C1320 G1321 U1322 G1323 U1324 C1328 U1329 A1330 U1331 A1332 C1333 C1339 G1340 A1343 G1344 G1345 U1348 G1349 A1350 U1351 A1352 U1353 G1354
A1355 U1356 G1357 C1358 C1359 C1360 C1364 U1368 G1374 G1377 U1378 G1379 G1383 A1386 C1391 A1399 G1400 A1401 C1402 G1409 U1410 G1414 G1417 A1418 A1419 C1420 G1421 G1422 C1423 C1424 U1425 A1433 G1434 C1437 U1438 U1439 G1440 A1446 A1453 A1454 U1455 A1456 U1457 A1460
A1461 A1462 G1466 A1467 A1468 C1469 A1475 G1476 A1477 A1481 A1482 G1483 U1484 G1485 G1486 G1487 U1494 G1500 U1501 C1502 A1503 G1507 C1508 U1511 U1512 G1513 U1523 C1527 C1531 C1532 U1533 A1534 A1535 G1547 C1548 U1549 U1554 U1555 C1556 A1557 A1558 A1559 G1560 G1561 C1562 C1563 U1564 G1565
A1566 U1567 U1568 U1569 U1570 A1571 U1572 G1573 C1574 A1575 G1576 G1577 C1578 C1579 A1580 C1581 C1582 A1583 U1584 C1585 G1586 A1587 A1588 A1589 G1590 A1593 C1596 G1604 U1607 C1608 G1611 G1617 G1618 A1619 U1620 A1621 U1622 G1623 A1624 A1625 U1626 U1627 C1628 U1629 U1630 C1631 C1639 G1640 U1641 A1642 A1643 C1644 U1645
G1646 A1647 G1652 G1653 C1657 G1658 U1659 G1662 C1665 G1666 A1667 G1668 C1669 U1672 G1673 G1674 G1675 A1676 G1677 G1678 A1679 G1680 U1681 U1682 A1683 U1684 C1685 U1686 U1687 U1688 U1689 C1690 U1691 U1692 C1693 U1694 U1695 G1700 C1701 U1702 U1703 A1704 U1705 C1706 A1707 G1712 G1713 A1714 A1715 U1716 U1717 U1720
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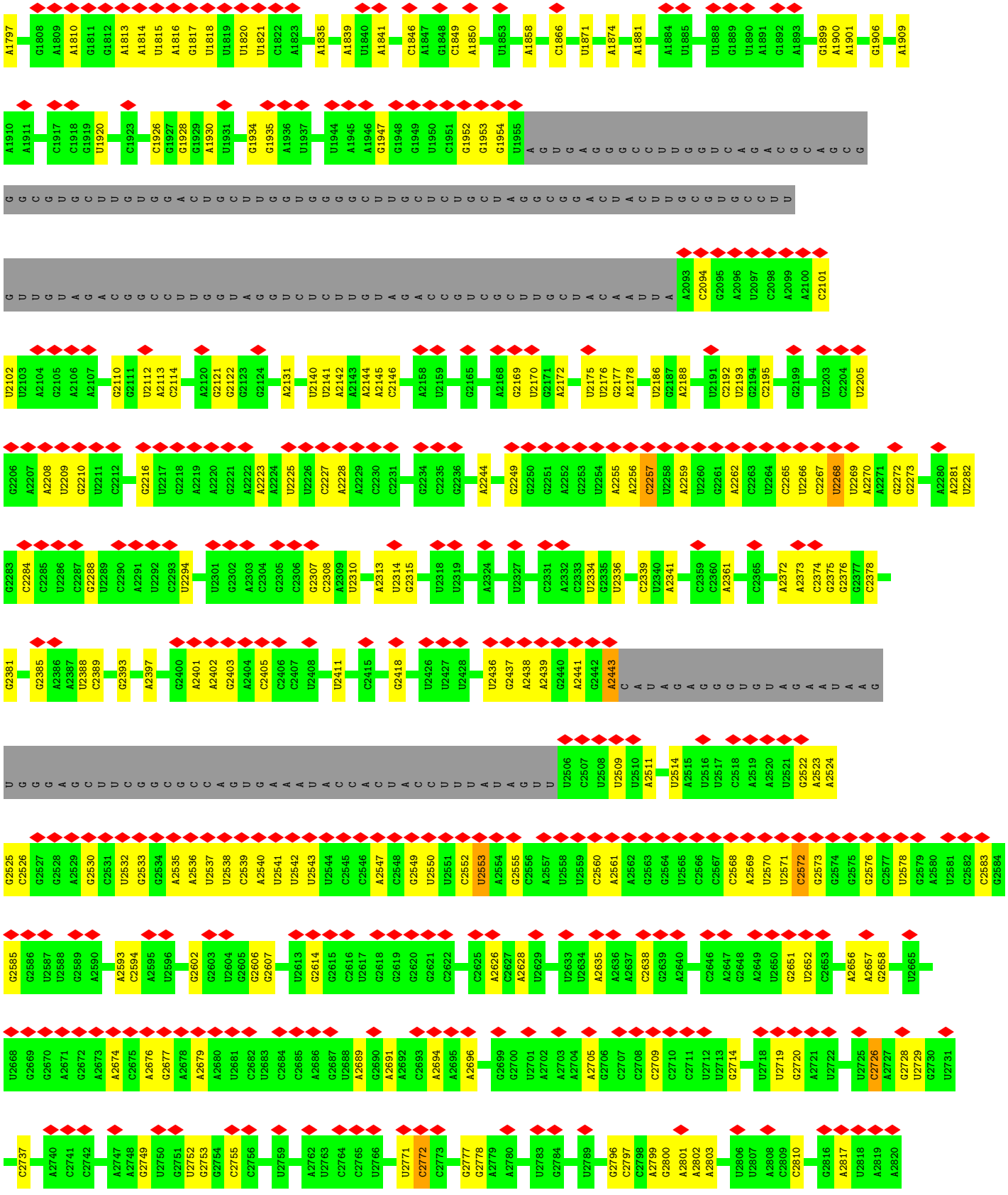
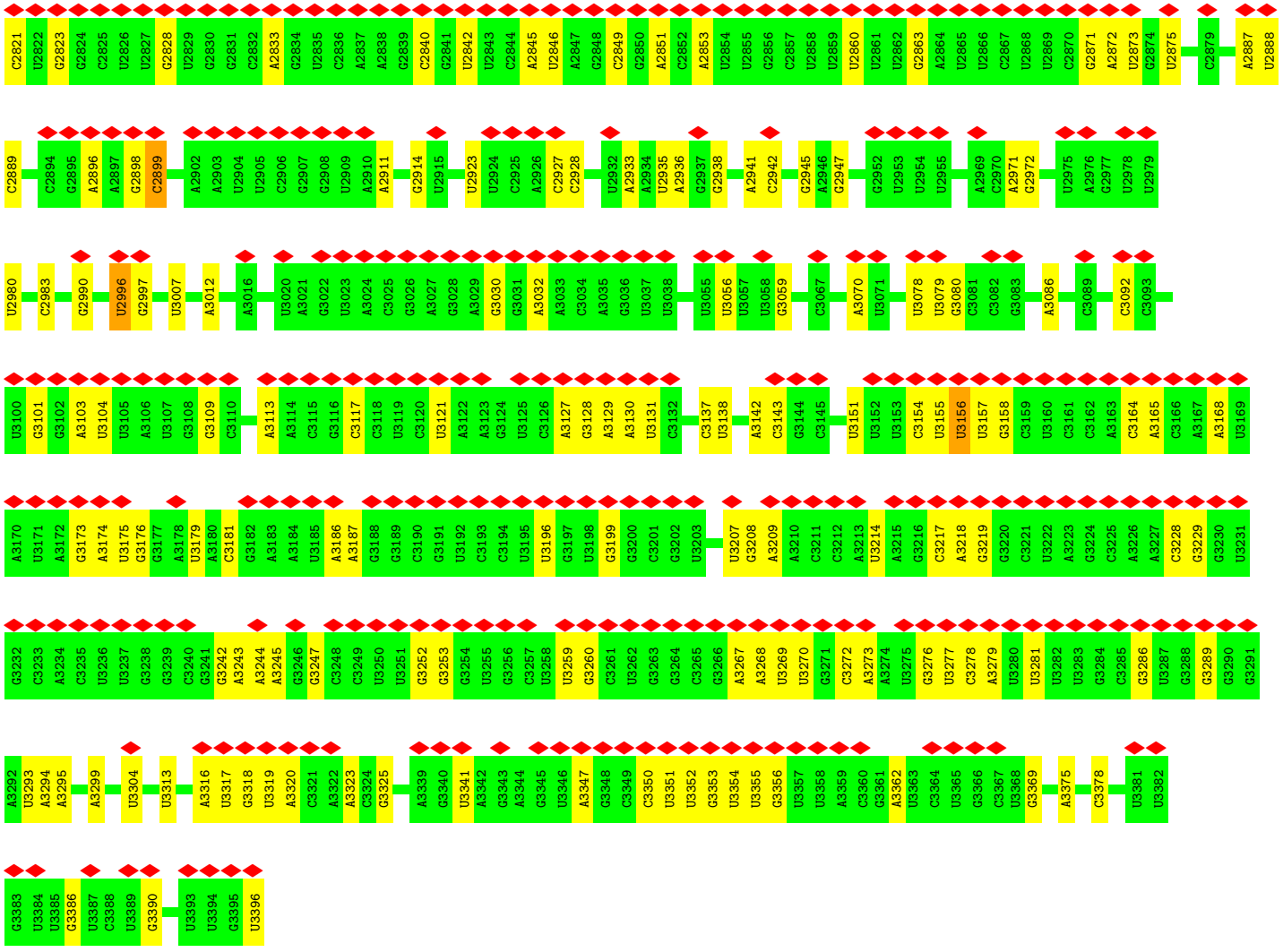
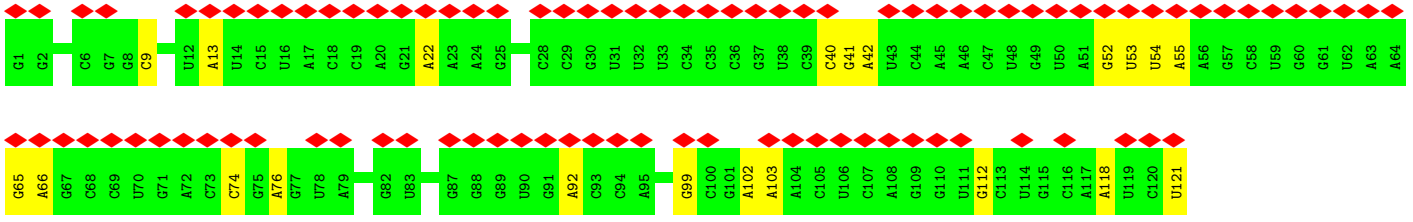




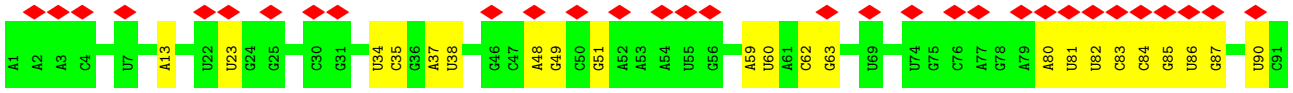
• Molecule 2: 5S ribosomal RNA

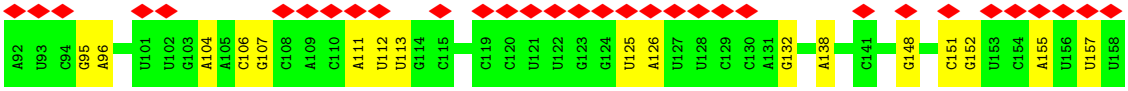
Chain 3:



• Molecule 3: 5.8S ribosomal RNA

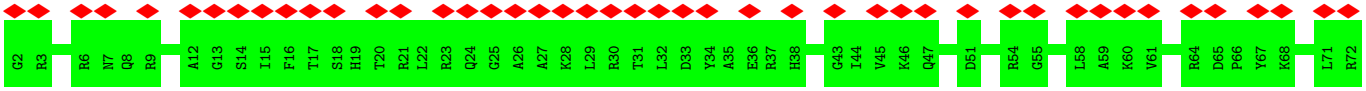
Chain 4:

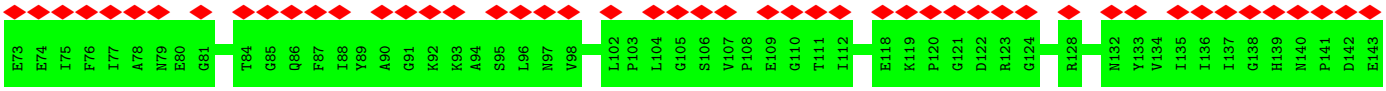


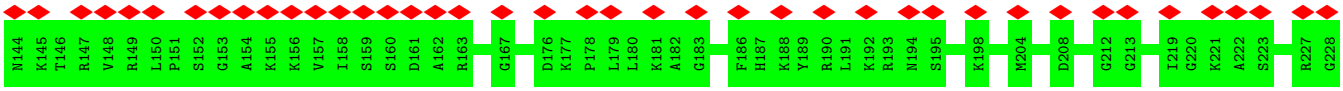


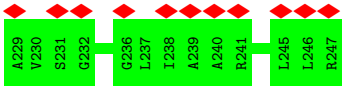
• Molecule 4: 60S ribosomal protein L2-A

Chain A:



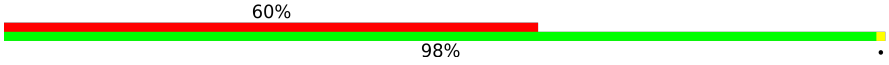


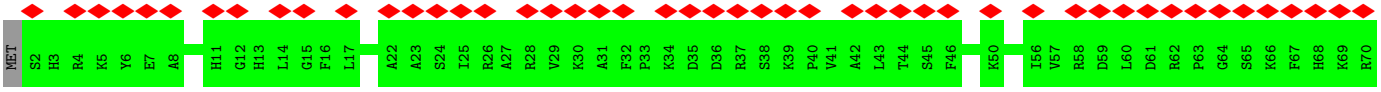


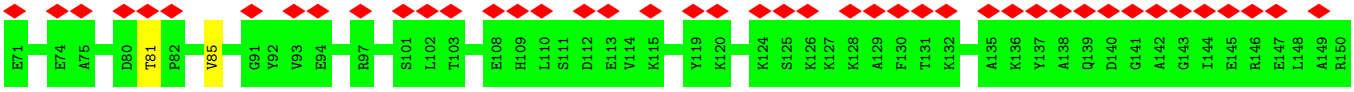


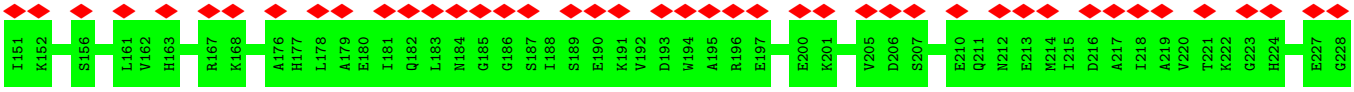
• Molecule 5: 60S ribosomal protein L3

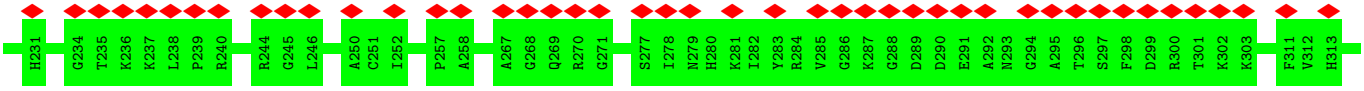
Chain B:

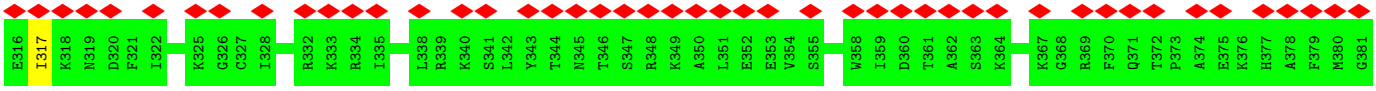


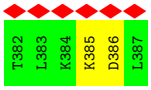






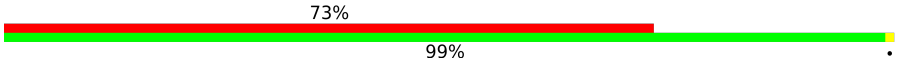


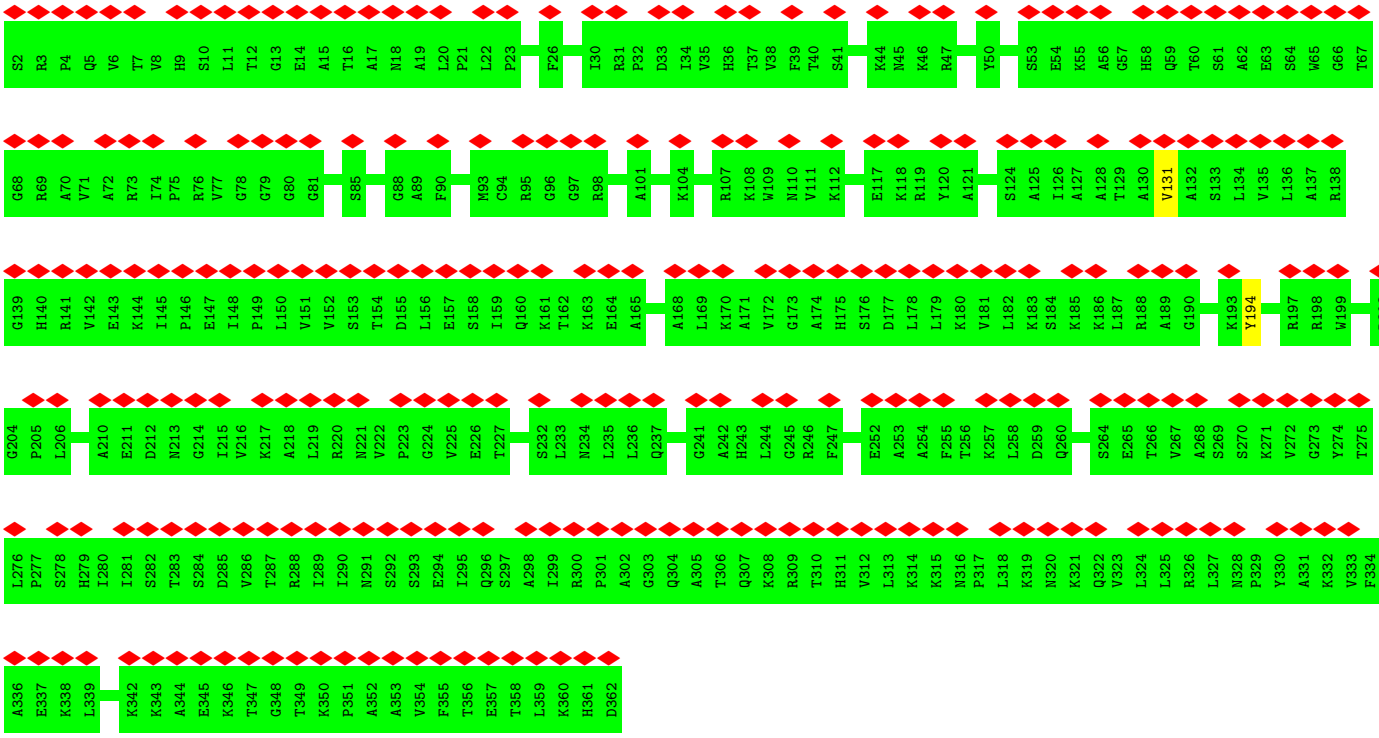




• Molecule 6: 60S ribosomal protein L4-A

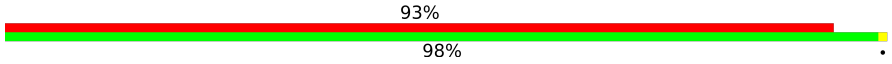
Chain C:

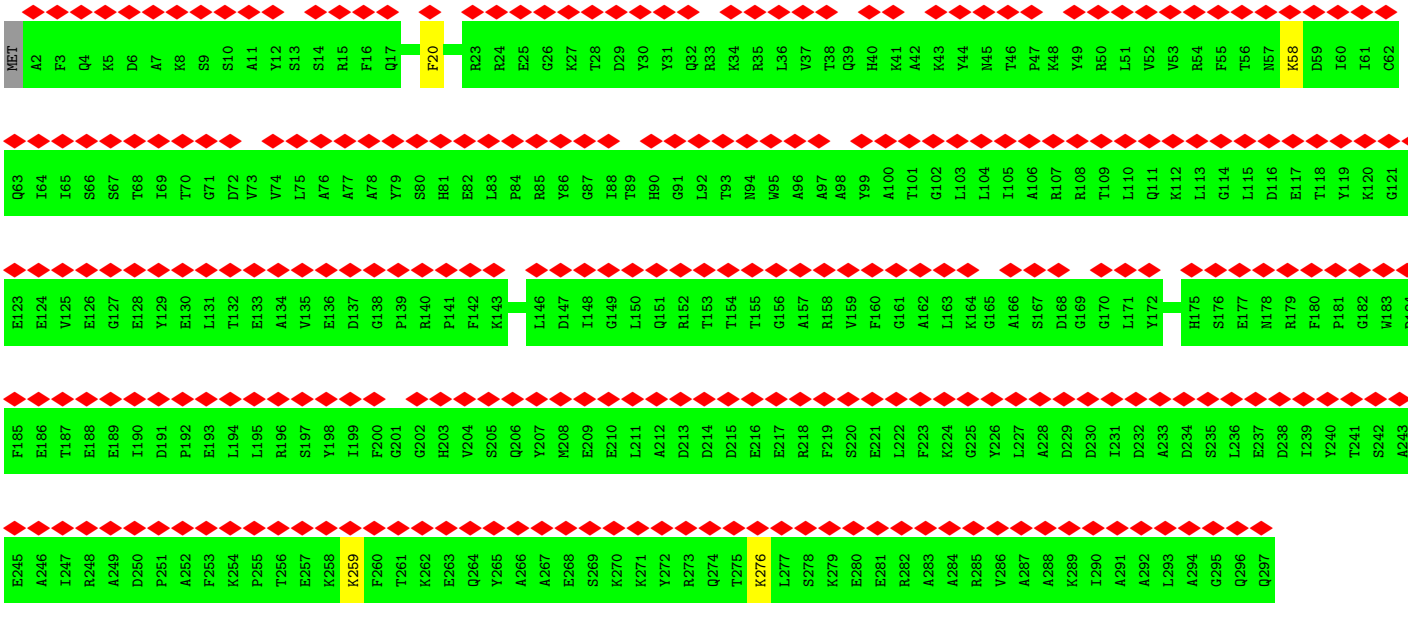




• Molecule 7: 60S ribosomal protein L5

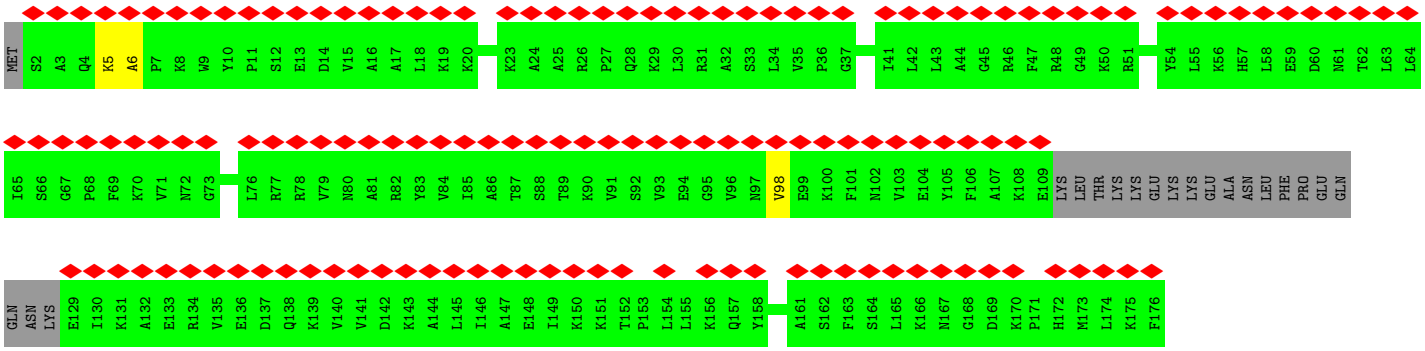
Chain D:





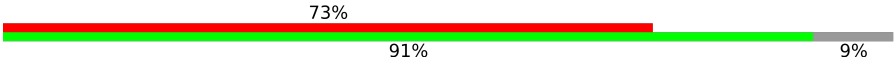
• Molecule 8: 60S ribosomal protein L6-A

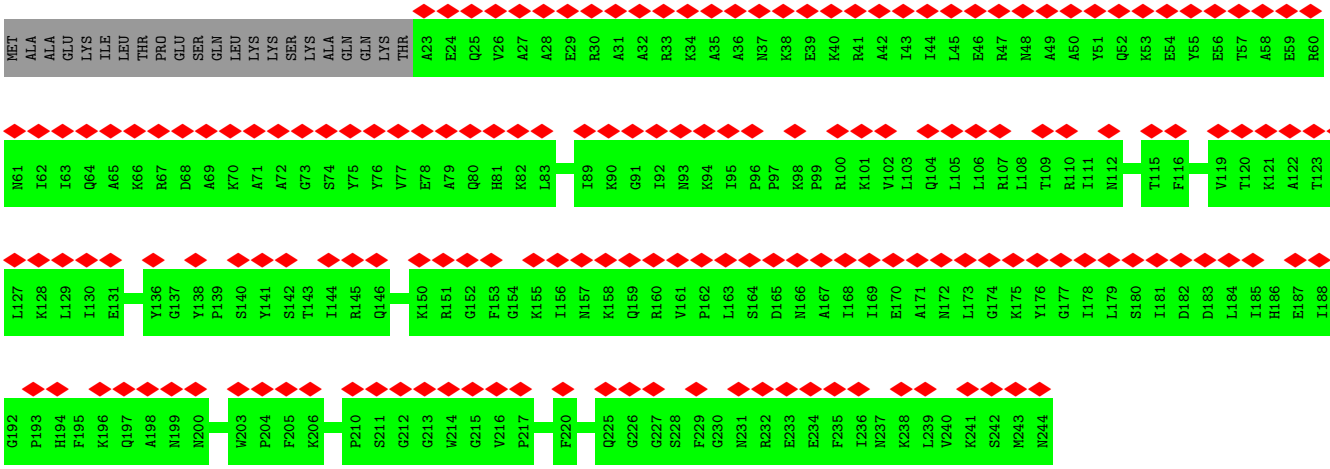
Chain E:



• Molecule 9: 60S ribosomal protein L7-A

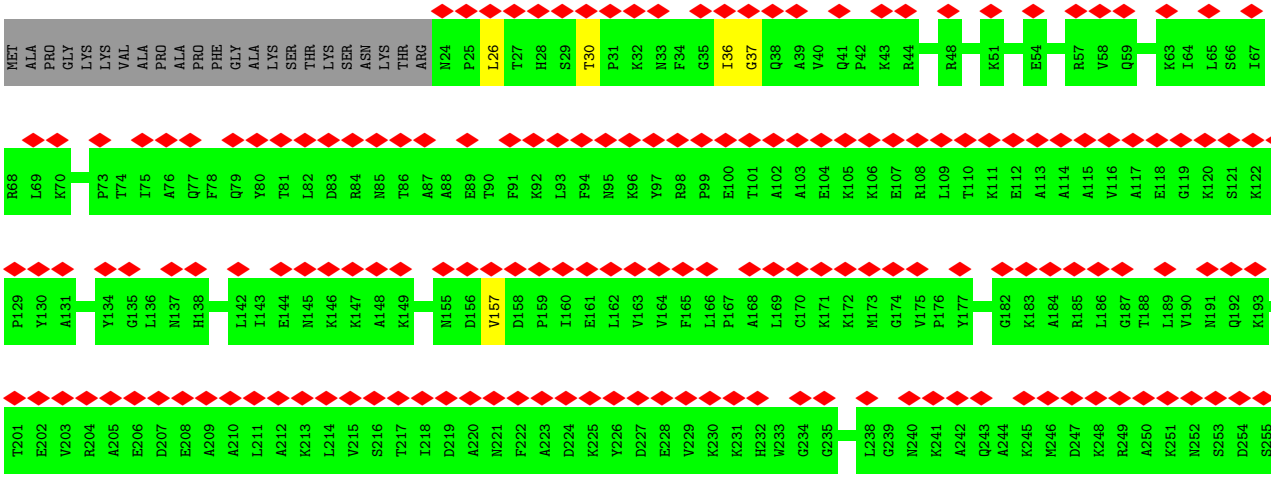
Chain F:





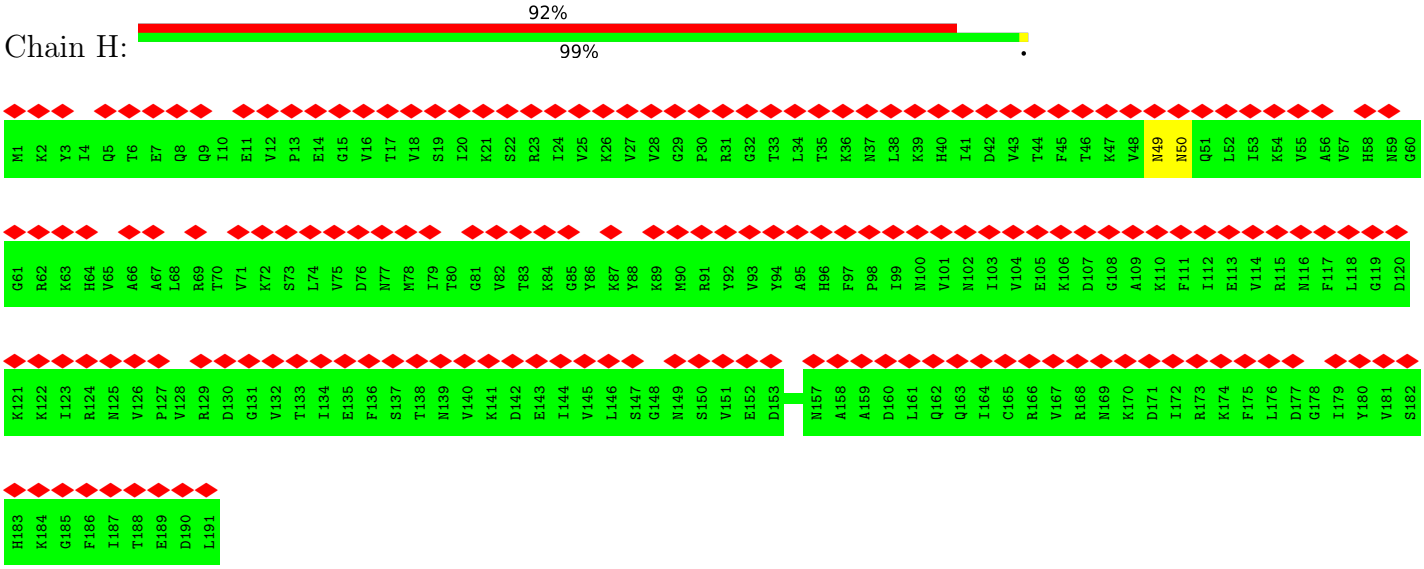
• Molecule 10: 60S ribosomal protein L8-A

Chain G:



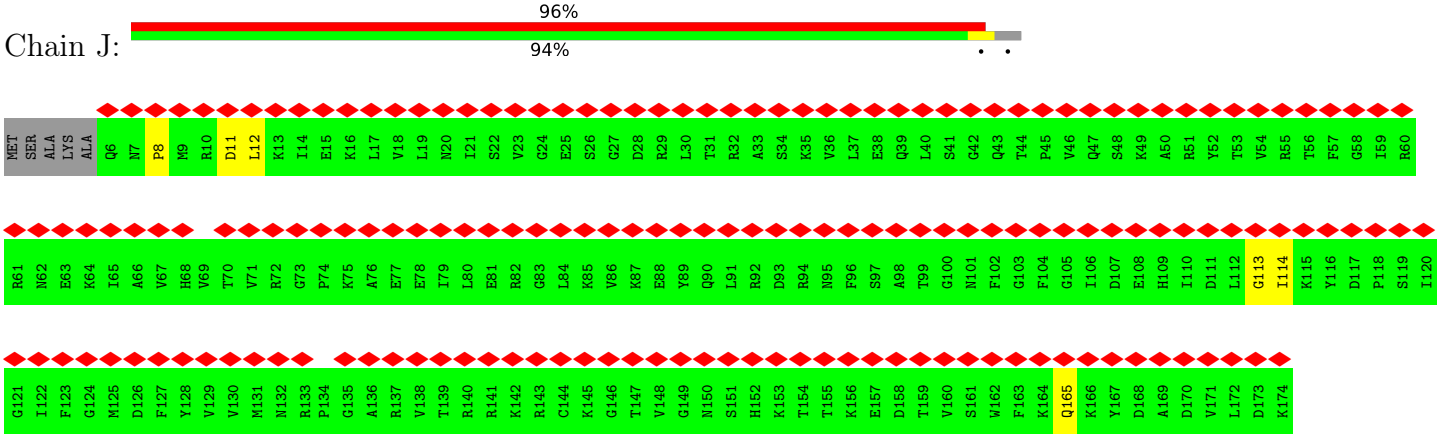
• Molecule 11: 60S ribosomal protein L9-A

Chain H:



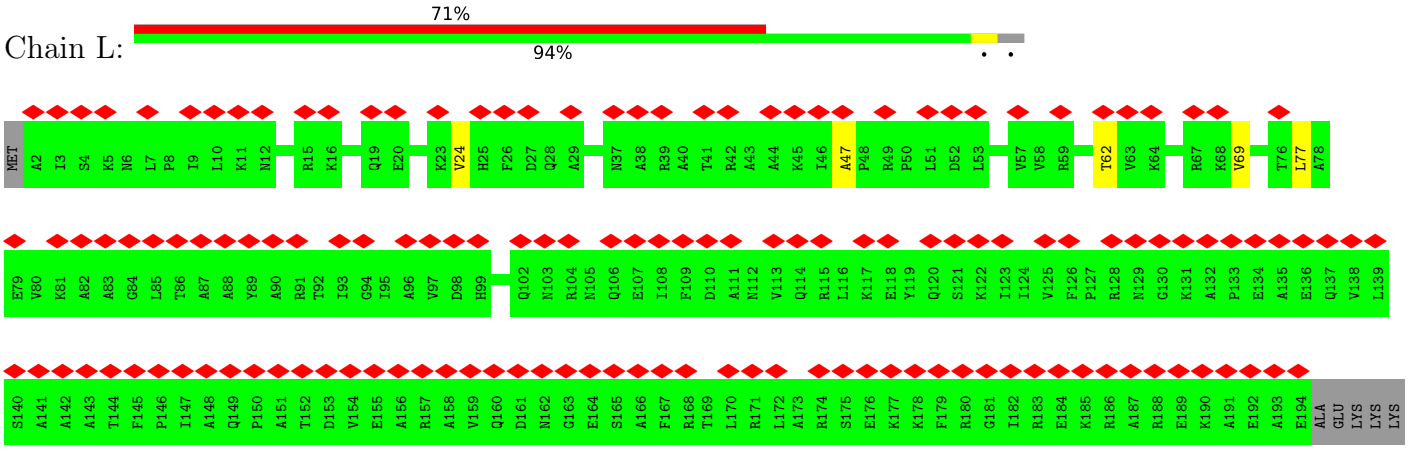
• Molecule 12: 60S ribosomal protein L11-A

Chain J:



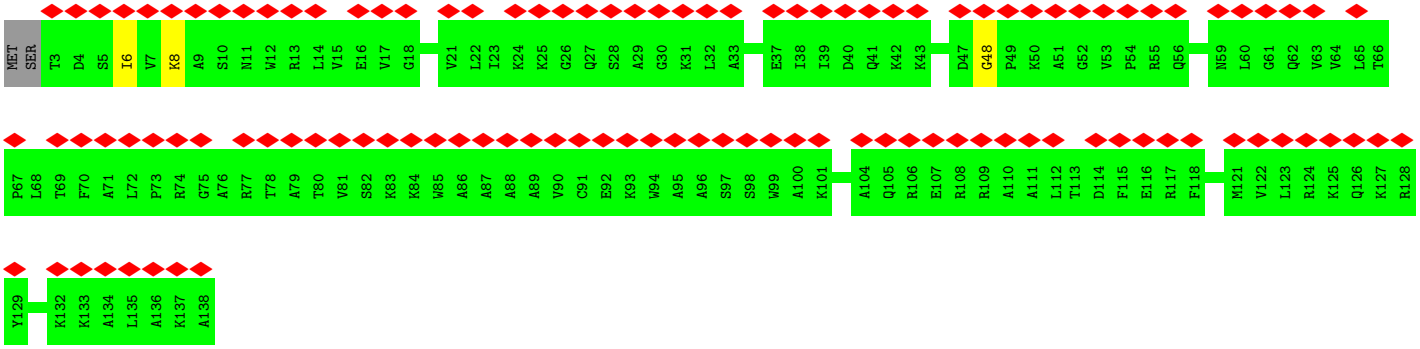
• Molecule 13: 60S ribosomal protein L13-A

Chain L:



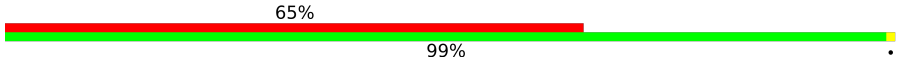
• Molecule 14: 60S ribosomal protein L14-A

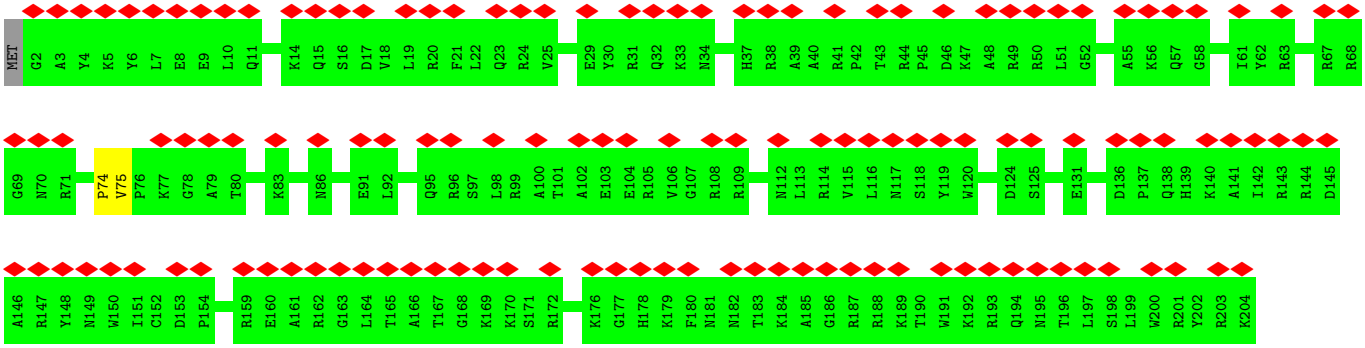
Chain M:



• Molecule 15: 60S ribosomal protein L15-A

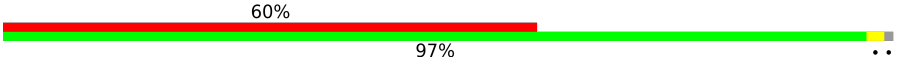
Chain N:

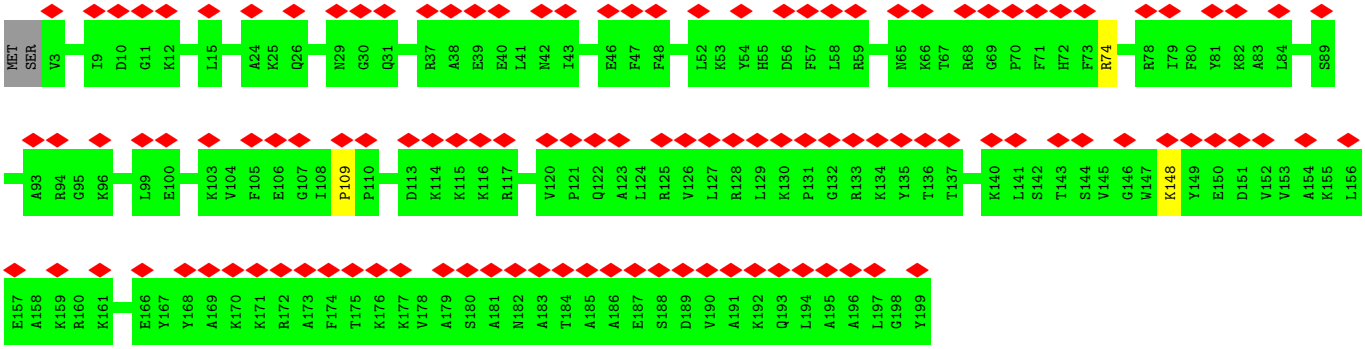




• Molecule 16: 60S ribosomal protein L16-A

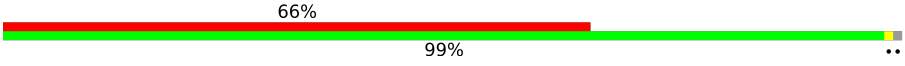
Chain O:

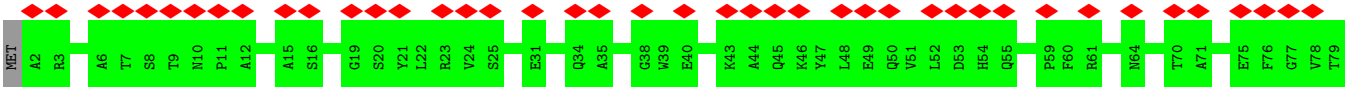


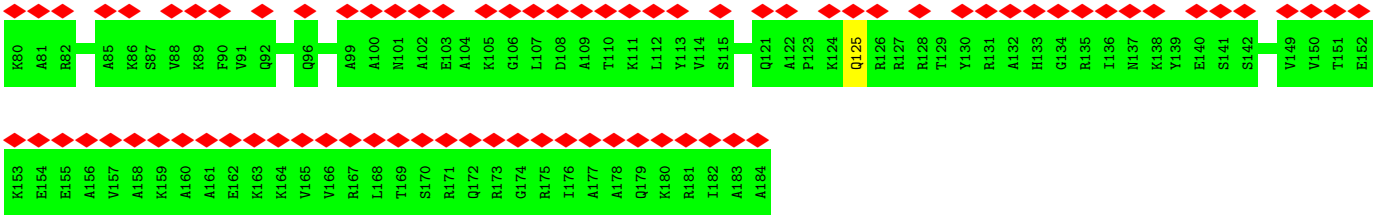


• Molecule 17: 60S ribosomal protein L17-A

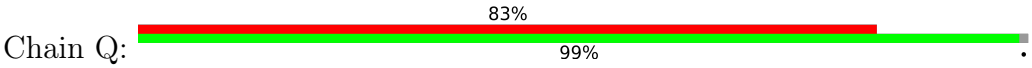
Chain P:

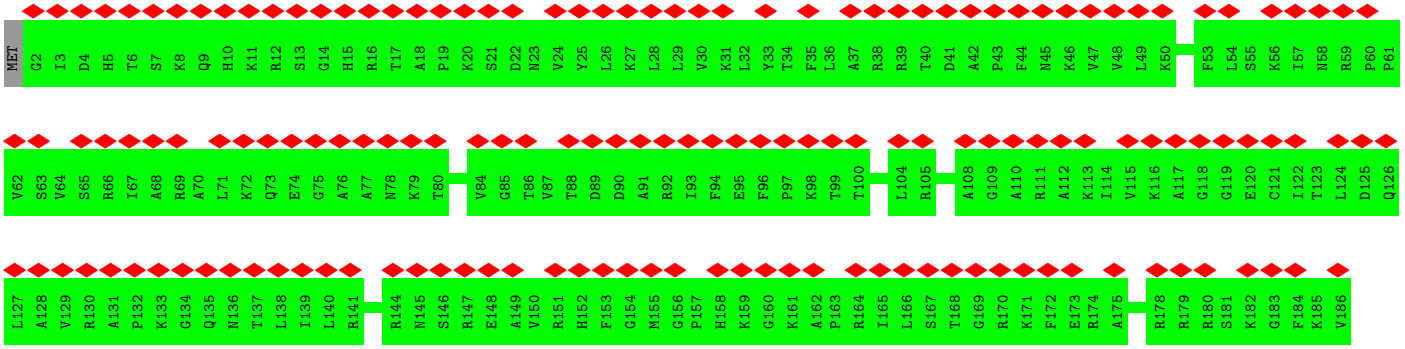




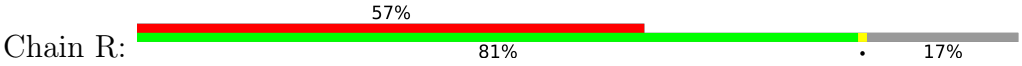


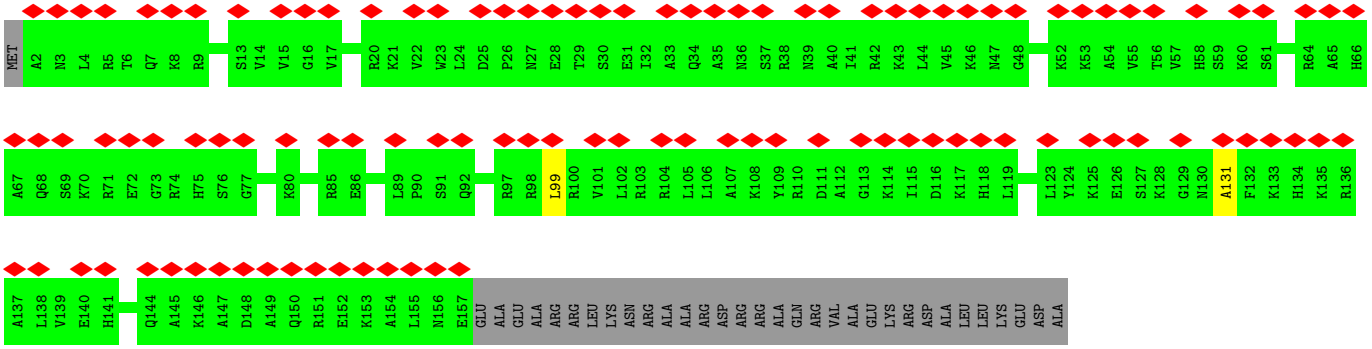
• Molecule 18: 60S ribosomal protein L18-A



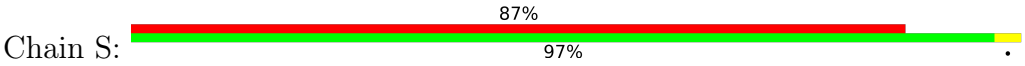


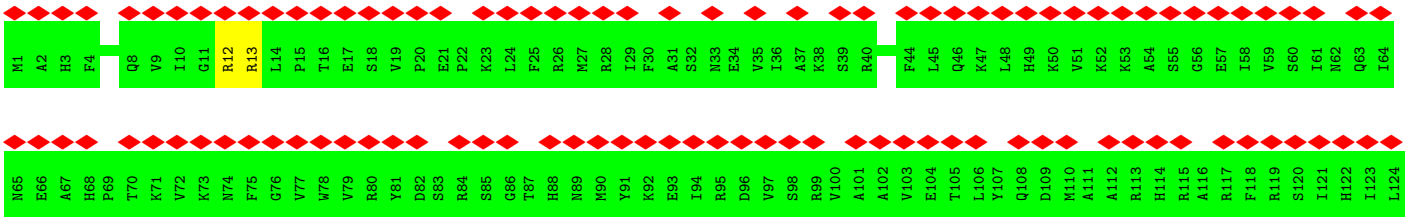
• Molecule 19: 60S ribosomal protein L19-A

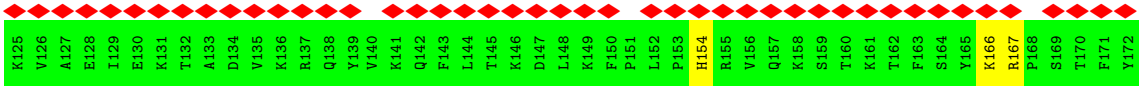




• Molecule 20: 60S ribosomal protein L20-A

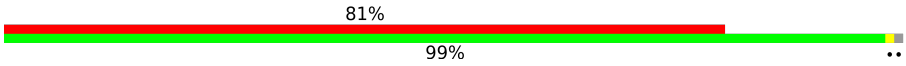


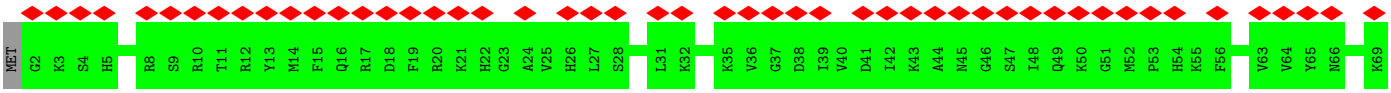


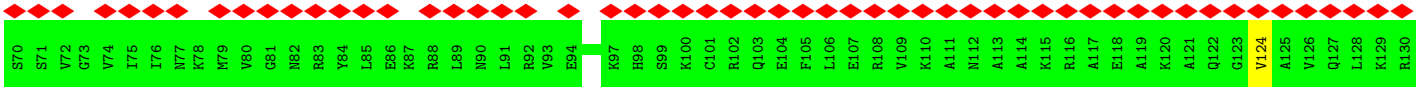


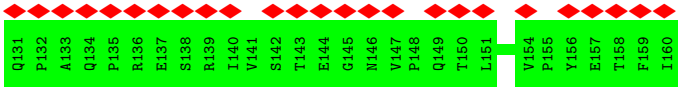
• Molecule 21: 60S ribosomal protein L21-A

Chain T:



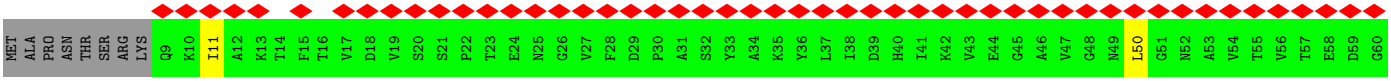


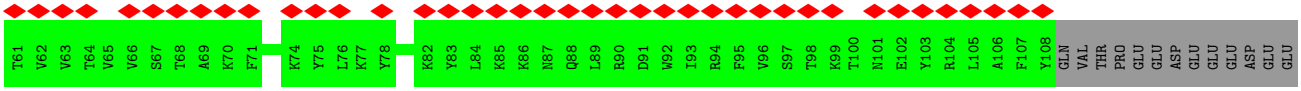




• Molecule 22: 60S ribosomal protein L22-A

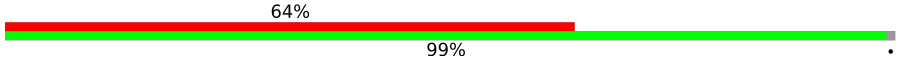
Chain U:

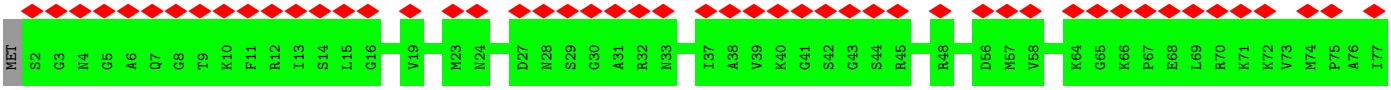


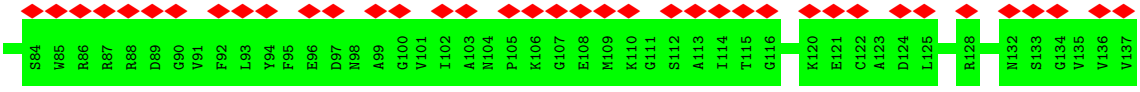


• Molecule 23: 60S ribosomal protein L23-A

Chain V:

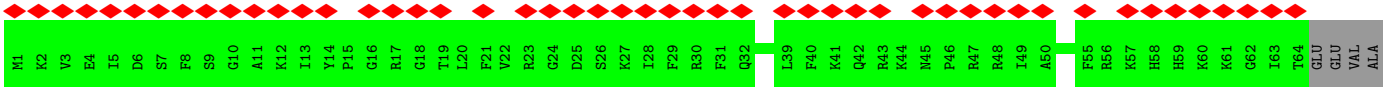


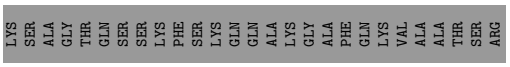




• Molecule 24: 60S ribosomal protein L24-A

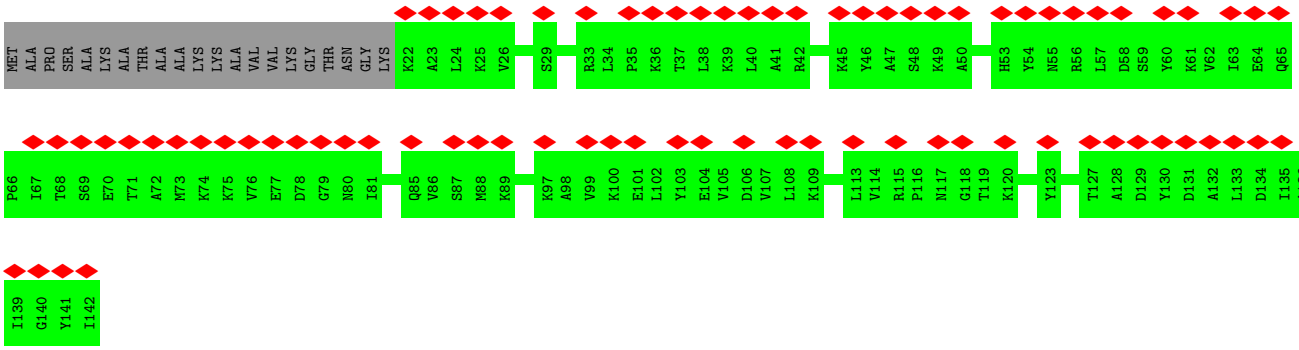
Chain W:





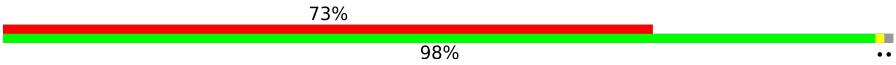
• Molecule 25: 60S ribosomal protein L25

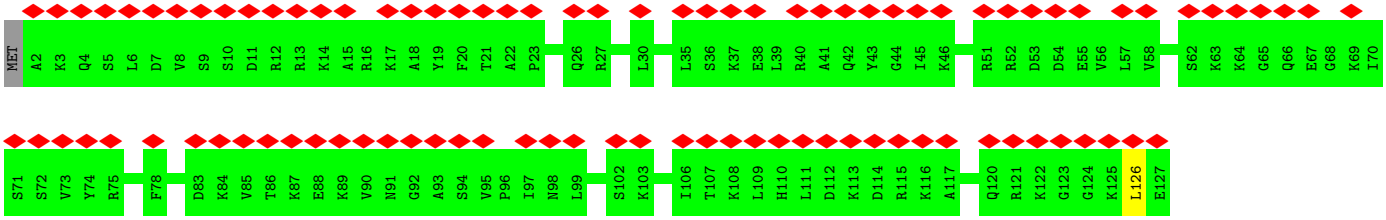
Chain X:



• Molecule 26: 60S ribosomal protein L26-A

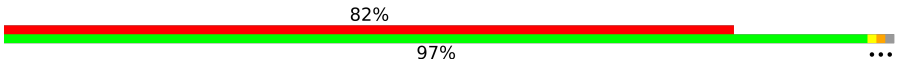
Chain Y:

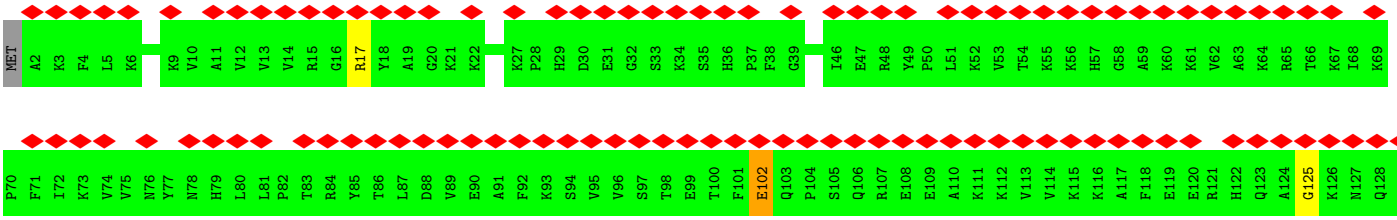




• Molecule 27: 60S ribosomal protein L27-A

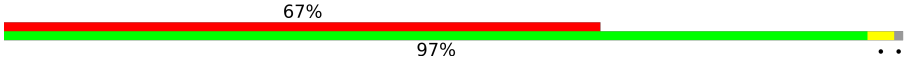
Chain Z:

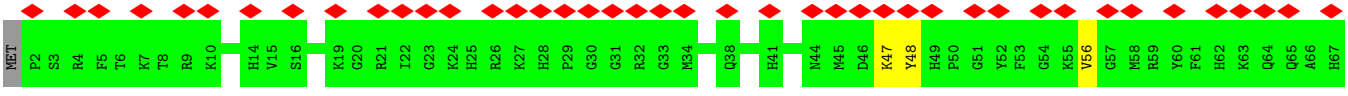


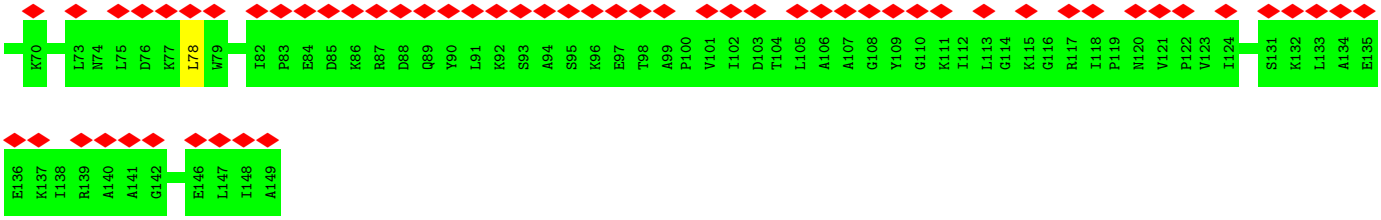


• Molecule 28: 60S ribosomal protein L28

Chain a:

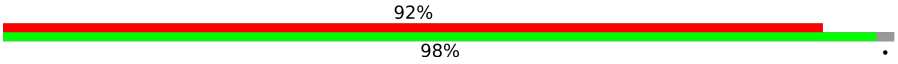


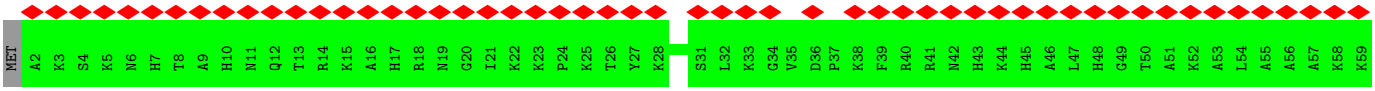




• Molecule 29: 60S ribosomal protein L29

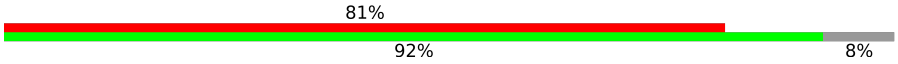
Chain b:

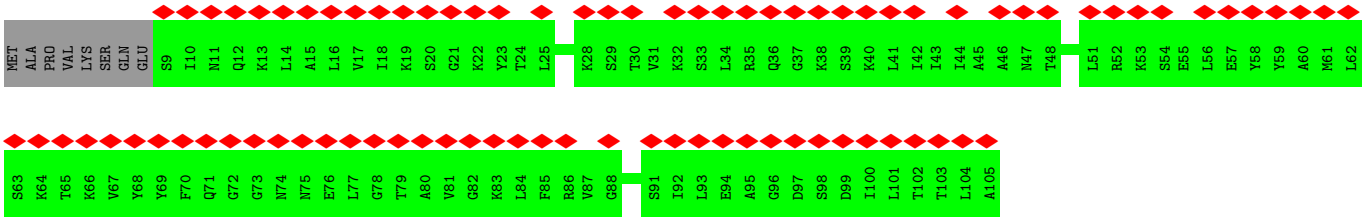




• Molecule 30: 60S ribosomal protein L30

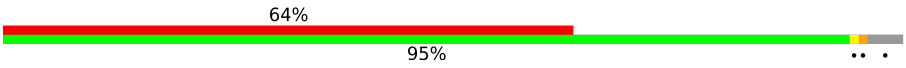
Chain c:

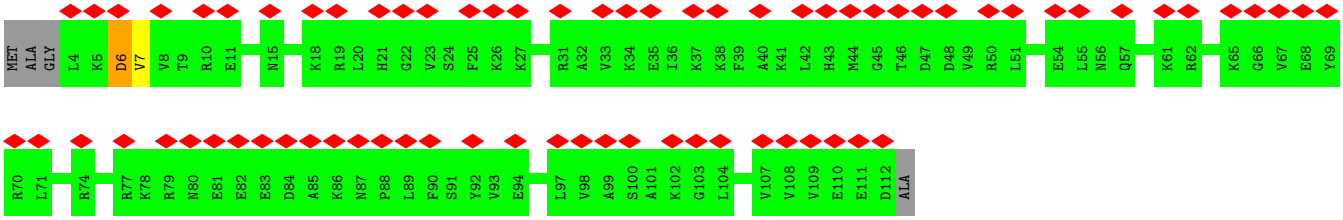




• Molecule 31: 60S ribosomal protein L31-A

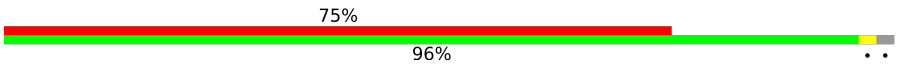
Chain d:

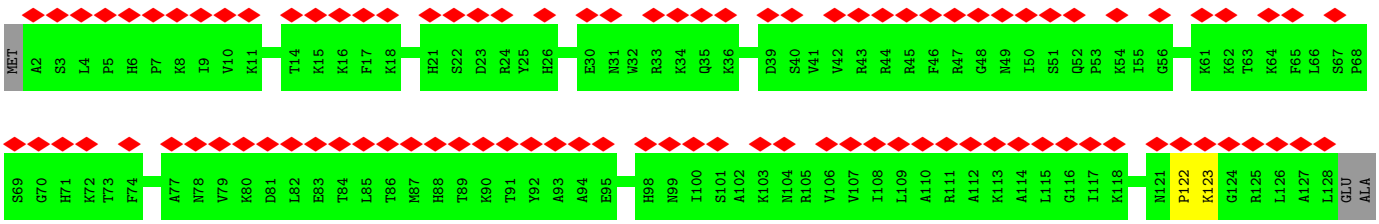




• Molecule 32: 60S ribosomal protein L32

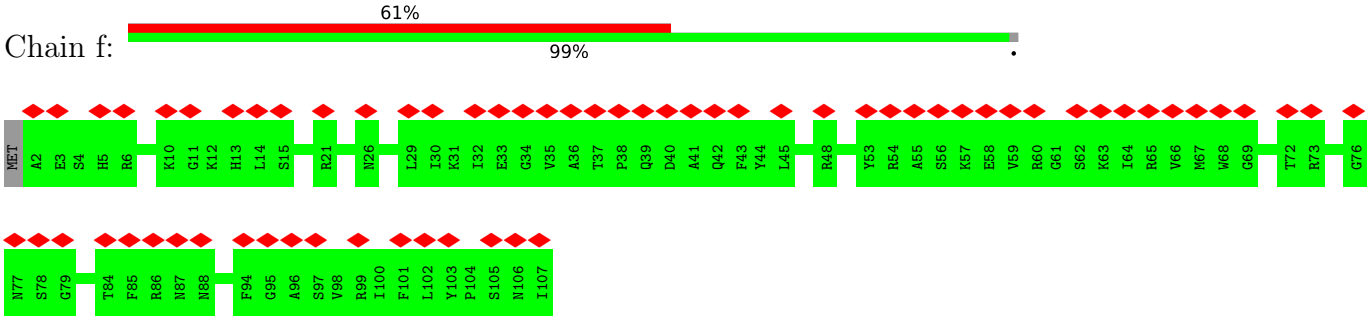
Chain e:





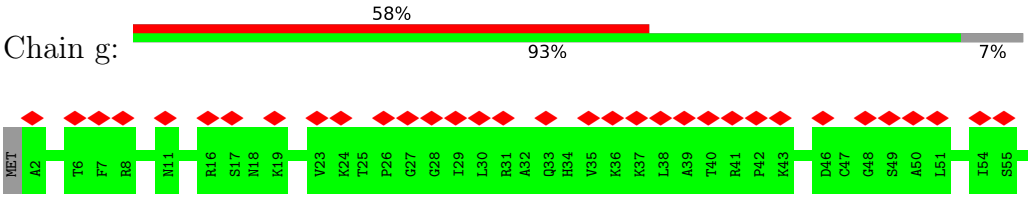
• Molecule 33: 60S ribosomal protein L33-A

Chain f:



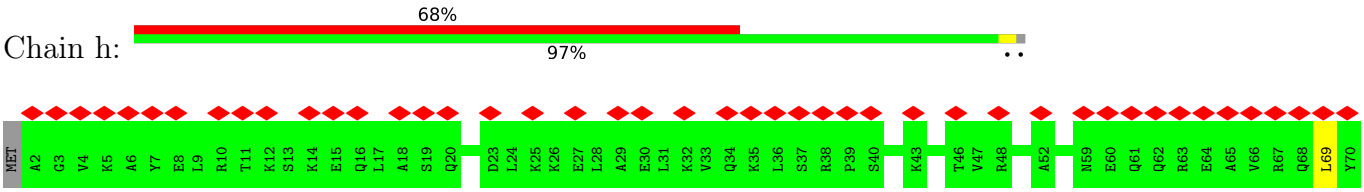
• Molecule 34: 60S ribosomal protein L34-A

Chain g:



• Molecule 35: 60S ribosomal protein L35-A

Chain h:

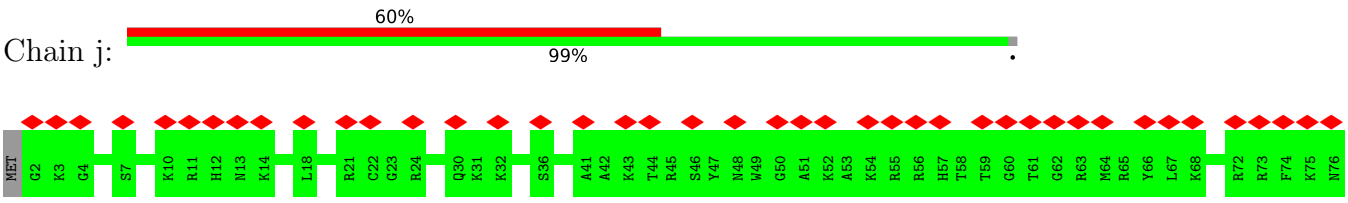


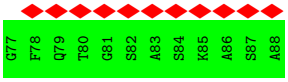
• Molecule 36: 60S ribosomal protein L36-A

Chain i:

• Molecule 37: 60S ribosomal protein L37-A

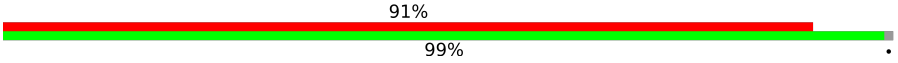
Chain j:

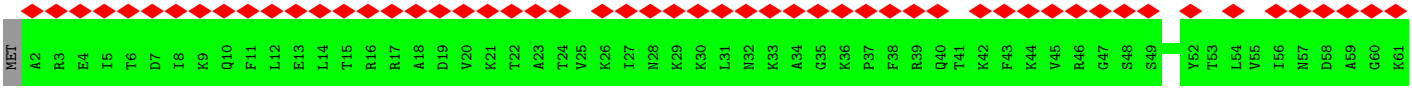


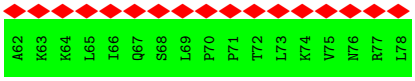


• Molecule 38: 60S ribosomal protein L38

Chain k:

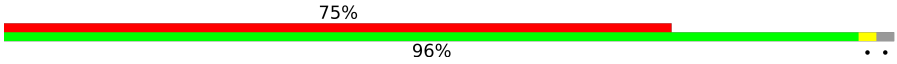


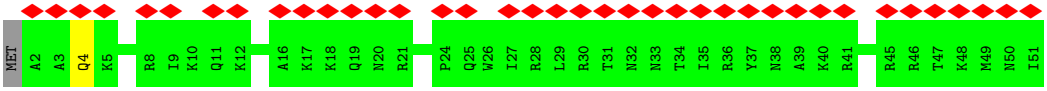




• Molecule 39: 60S ribosomal protein L39

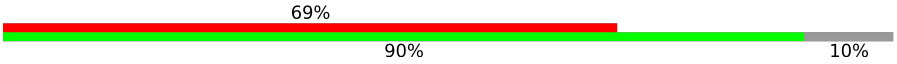
Chain l:

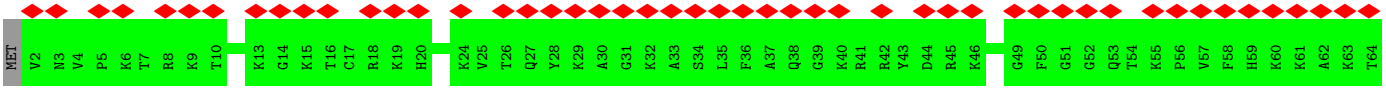


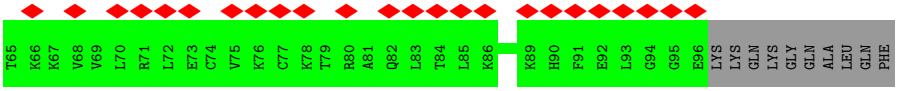


• Molecule 40: 60S ribosomal protein L42-A

Chain o:

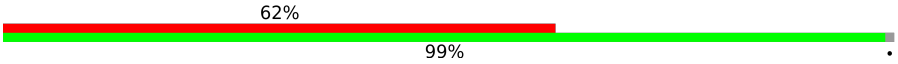


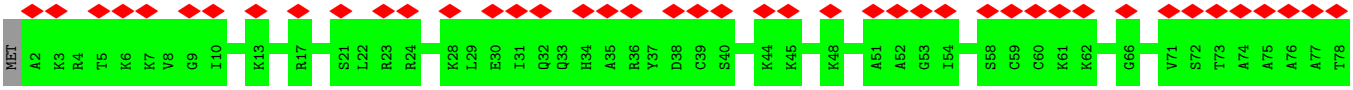


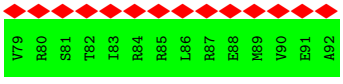


• Molecule 41: 60S ribosomal protein L43-A

Chain p:

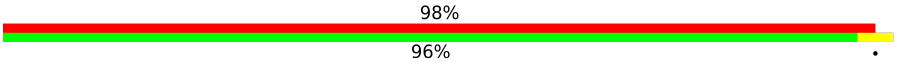






• Molecule 42: 60S ribosomal export protein NMD3

Chain w:



W155 R156 A157 T158 V159 Q160 I161 R162 Q163 K164 V165 P166 H167 K168 R169 T170 F171 L172 F173 L174 E175 Q176 L177 I178 L179 K180 H181 N182 A183 H184 V185 D186 T187 I188 S189 I190 S191 E192 A193 K194 D195 G196 L197 D198 F199 F200 Y201 A202 Q203 K204 N205 H206 A207 V208 K209 M210 I211 D212 F213 L214

N215 A216 V217 Y218 P219 I220 K221 H222 K223 K224 S225 E226 E227 L228 I229 S230 Q231 D232 T233 H234 T235 G236 A237 S238 T239 Y240 K241 F242 S243 Y244 S245 V246 E247 I248 V249 P250 I251 C252 K253 D254 D255 L256 V257 Y258 L259 P260 K261 K262 L263 A264 K265 S266 M267 G268 N269 I270 S271 Q272 F273 V274

L275 C276 S277 K278 I279 S280 N281 T282 V283 Q284 F285 M286 D287 P288 T289 T290 L291 Q292 T293 A294 D295 L296 S297 P298 S299 V300 Y301 W302 R303 A304 P305 F306 N307 A308 L309 A310 D311 V312 T313 Q314 L315 V316 E317 F318 I319 V320 L321 D322 V323 D324 S325 T326 G327 I328 S329 R330 G331 N332 R333 V334

L335 A336 D337 I338 T339 V340 A341 R342 T343 S344 D345 L346 G347 V348 N349 D350 Q351 V352 Y353 Y354 V355 R356 S357 H358 L359 G360 G361 I362 C363 H364 A365 G366 D367 S368 V369 M370 G371 Y372 F373 I374 A375 N376 S377 N378 Y379 N380 S381 D382 L383 F384 D385 G386 L387 N388 I389 D390 Y391 V392 P393 D394

V395 V396 L397 V398 K399 K400 L401 Y402

• Molecule 43: Eukaryotic translation initiation factor 6

Chain y: 95% 99%

M1 A2 T3 R4 T5 Q6 F7 E8 N9 S10 N11 E12 I13 G14 V15 K18 L19 T20 N21 T22 Y23 C24 L25 V28 G29 G30 S31 E32 N33 F34 Y35 S36 A37 F38 E39 A40 E41 L42 G43 D44 A45 I46 P47 I48 V49 H50 T51 A54 G55 T56 R57 I58 I59 G60 R61 M62 T63

A64 G65 N66 R67 R68 G69 L70 L71 V72 P73 T74 Q75 T76 T77 D78 Q79 E80 L81 Q82 H83 L84 R85 N86 S87 L88 P89 D90 S91 V92 K93 I94 Q95 R96 V97 E98 E99 R100 L101 S102 A103 L104 G105 N106 V107 I108 C109 C110 N111 D112 Y113 V114 A115 L116 V117 H118 P119 D120 I121 D122 R123

E124 T125 E126 E127 L128 I129 S130 D131 V132 L133 G134 V135 E136 V137 F138 R139 Q140 T141 I142 S143 G144 N145 I146 L147 V148 G149 S150 Y151 C152 S153 L154 S155 N156 Q157 G158 G159 L160 V161 H162 P163 Q164 T165 S166 V167 Q168 D169 Q170 E171 E172 L173 S174 S175 L176 L177 Q178 V179 P180 L181 V182 A183

G184 T185 V186 N187 R188 G189 S190 S191 V192 V193 G194 A195 G196 M197 V198 V199 N200 D201 Y202 L203 A204 V205 T206 G207 L208 D209 T210 T211 A212 P213 E214 L215 S216 V217 I218 E219 S220 I221 F222 R223 L224 Q225 D226 A227

• Molecule 44: Cytoplasmic 60S subunit biogenesis factor REH1

Chain z: 98% 96%

T377 I378 T379 A380 A381 D382 R383 R384 M385 V386 S387 G388 V389 T390 E391 K392 Q393 Y394 K395 K396 G397 M398 K399 K400 M401 Q402 Q403 L404 E405 K406 N407 A408 I409 N410 T411 Q412 I413 R414 R415 E416 I417 K418 R419 V420 N421 F422 Q423 T424 H425 Y426 R427 D428 E429 L430 L431 Q432

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84240	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.483	Depositor
Minimum map value	-0.325	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.143	Depositor
Map size (Å)	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

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	0.88	0/74017	0.89	34/115398 (0.0%)
2	3	0.73	0/2883	0.83	0/4491
3	4	0.94	0/3746	0.86	0/5832
4	A	0.50	0/1908	0.61	0/2564
5	B	0.52	0/3146	0.61	0/4228
6	C	0.46	0/2800	0.61	0/3790
7	D	0.39	0/2425	0.55	0/3271
8	E	0.41	0/1260	0.57	0/1694
9	F	0.46	0/1821	0.57	0/2451
10	G	0.43	0/1836	0.59	0/2481
11	H	0.40	0/1539	0.57	0/2073
12	J	0.34	0/1374	0.55	0/1842
13	L	0.44	0/1568	0.63	0/2106
14	M	0.43	0/1068	0.55	0/1438
15	N	0.52	0/1757	0.63	0/2354
16	O	0.51	1/1585 (0.1%)	0.58	0/2128
17	P	0.48	0/1465	0.61	0/1968
18	Q	0.44	0/1465	0.62	0/1965
19	R	0.42	0/1275	0.57	1/1702 (0.1%)
20	S	0.48	0/1481	0.57	0/1990
21	T	0.44	0/1300	0.56	0/1743
22	U	0.40	0/812	0.58	0/1099
23	V	0.46	0/1018	0.64	0/1369
24	W	0.44	0/540	0.56	0/717
25	X	0.46	0/979	0.61	0/1321
26	Y	0.42	0/1004	0.62	1/1341 (0.1%)
27	Z	0.46	0/1118	0.60	0/1497
28	a	0.46	0/1204	0.63	0/1612
29	b	0.35	0/473	0.50	0/629
30	c	0.46	0/751	0.53	0/1008
31	d	0.47	0/890	0.55	0/1196
32	e	0.45	0/1041	0.58	0/1394
33	f	0.52	0/868	0.56	0/1168
34	g	0.48	0/890	0.57	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	h	0.40	0/978	0.55	1/1301 (0.1%)
36	i	0.40	0/778	0.61	0/1034
37	j	0.48	0/696	0.62	0/923
38	k	0.38	0/618	0.58	0/826
39	l	0.47	0/443	0.58	0/588
40	o	0.46	0/777	0.61	0/1028
41	p	0.53	0/701	0.58	0/934
42	w	0.51	2/1931 (0.1%)	0.64	2/2629 (0.1%)
43	y	0.38	0/1720	0.56	0/2341
44	z	0.37	0/472	0.56	0/626
All	All	0.74	3/132421 (0.0%)	0.79	39/195279 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	B	0	2
7	D	0	1
10	G	0	1
11	H	0	1
12	J	0	1
13	L	0	1
14	M	0	1
16	O	0	2
17	P	0	1
20	S	0	2
22	U	0	1
27	Z	0	1
31	d	0	1
32	e	0	1
35	h	0	1
39	l	0	1
42	w	0	1
43	y	0	1
All	All	0	21

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	186	ASP	C-N	11.11	1.59	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	w	165	VAL	C-N	7.19	1.48	1.34
16	O	74	ARG	C-N	-5.12	1.22	1.34

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	2572	C	N1-C2-O2	8.73	124.14	118.90
42	w	165	VAL	O-C-N	8.29	136.85	121.10
1	1	2572	C	C2-N1-C1'	7.83	127.42	118.80
1	1	1269	U	C2-N1-C1'	7.74	126.99	117.70
26	Y	126	LEU	CA-CB-CG	6.84	131.03	115.30

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	B	385	LYS	Peptide
5	B	81	THR	Peptide
7	D	58	LYS	Peptide
10	G	30	THR	Peptide
11	H	49	ASN	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	A	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
5	B	384/387 (99%)	357 (93%)	25 (6%)	2 (0%)	29	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
6	C	359/361 (99%)	329 (92%)	29 (8%)	1 (0%)	41 71
7	D	294/297 (99%)	267 (91%)	24 (8%)	3 (1%)	15 47
8	E	152/176 (86%)	143 (94%)	6 (4%)	3 (2%)	7 29
9	F	220/244 (90%)	205 (93%)	15 (7%)	0	100 100
10	G	231/256 (90%)	208 (90%)	20 (9%)	3 (1%)	12 40
11	H	189/191 (99%)	174 (92%)	14 (7%)	1 (0%)	29 61
12	J	167/174 (96%)	144 (86%)	18 (11%)	5 (3%)	4 21
13	L	191/199 (96%)	172 (90%)	16 (8%)	3 (2%)	9 35
14	M	134/138 (97%)	123 (92%)	9 (7%)	2 (2%)	10 37
15	N	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	15 47
16	O	195/199 (98%)	193 (99%)	2 (1%)	0	100 100
17	P	181/184 (98%)	178 (98%)	3 (2%)	0	100 100
18	Q	183/186 (98%)	172 (94%)	11 (6%)	0	100 100
19	R	154/189 (82%)	147 (96%)	6 (4%)	1 (1%)	25 57
20	S	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	8 32
21	T	157/160 (98%)	148 (94%)	8 (5%)	1 (1%)	25 57
22	U	98/121 (81%)	86 (88%)	11 (11%)	1 (1%)	15 47
23	V	134/137 (98%)	130 (97%)	4 (3%)	0	100 100
24	W	62/155 (40%)	60 (97%)	2 (3%)	0	100 100
25	X	119/142 (84%)	113 (95%)	6 (5%)	0	100 100
26	Y	124/127 (98%)	115 (93%)	9 (7%)	0	100 100
27	Z	133/136 (98%)	124 (93%)	6 (4%)	3 (2%)	6 26
28	a	146/149 (98%)	131 (90%)	11 (8%)	4 (3%)	5 23
29	b	56/59 (95%)	51 (91%)	5 (9%)	0	100 100
30	c	95/105 (90%)	92 (97%)	3 (3%)	0	100 100
31	d	107/113 (95%)	101 (94%)	4 (4%)	2 (2%)	8 31
32	e	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	19 52
33	f	104/107 (97%)	98 (94%)	6 (6%)	0	100 100
34	g	110/121 (91%)	105 (96%)	5 (4%)	0	100 100
35	h	117/120 (98%)	110 (94%)	6 (5%)	1 (1%)	17 49
36	i	97/100 (97%)	82 (84%)	13 (13%)	2 (2%)	7 28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	j	85/88 (97%)	77 (91%)	8 (9%)	0	100	100
38	k	75/78 (96%)	70 (93%)	5 (7%)	0	100	100
39	l	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
40	o	93/106 (88%)	84 (90%)	9 (10%)	0	100	100
41	p	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
42	w	246/248 (99%)	220 (89%)	19 (8%)	7 (3%)	5	23
43	y	225/227 (99%)	220 (98%)	4 (2%)	1 (0%)	34	66
44	z	54/56 (96%)	47 (87%)	5 (9%)	2 (4%)	3	17
All	All	6348/6731 (94%)	5900 (93%)	394 (6%)	54 (1%)	21	49

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	E	98	VAL
10	G	36	ILE
28	a	78	LEU
32	e	123	LYS
42	w	328	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	A	189/189 (100%)	189 (100%)	0	100	100
5	B	318/323 (98%)	317 (100%)	1 (0%)	92	96
6	C	288/288 (100%)	287 (100%)	1 (0%)	92	96
7	D	244/245 (100%)	244 (100%)	0	100	100
8	E	134/153 (88%)	134 (100%)	0	100	100
9	F	186/205 (91%)	186 (100%)	0	100	100
10	G	187/208 (90%)	186 (100%)	1 (0%)	88	94
11	H	171/171 (100%)	171 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	J	147/150 (98%)	147 (100%)	0	100	100
13	L	154/159 (97%)	153 (99%)	1 (1%)	86	93
14	M	107/109 (98%)	107 (100%)	0	100	100
15	N	175/176 (99%)	175 (100%)	0	100	100
16	O	160/162 (99%)	160 (100%)	0	100	100
17	P	145/146 (99%)	145 (100%)	0	100	100
18	Q	150/151 (99%)	150 (100%)	0	100	100
19	R	129/154 (84%)	129 (100%)	0	100	100
20	S	156/156 (100%)	156 (100%)	0	100	100
21	T	136/137 (99%)	136 (100%)	0	100	100
22	U	87/107 (81%)	87 (100%)	0	100	100
23	V	104/105 (99%)	104 (100%)	0	100	100
24	W	56/129 (43%)	56 (100%)	0	100	100
25	X	104/118 (88%)	104 (100%)	0	100	100
26	Y	109/110 (99%)	109 (100%)	0	100	100
27	Z	115/116 (99%)	115 (100%)	0	100	100
28	a	118/119 (99%)	118 (100%)	0	100	100
29	b	46/47 (98%)	46 (100%)	0	100	100
30	c	81/88 (92%)	81 (100%)	0	100	100
31	d	92/97 (95%)	92 (100%)	0	100	100
32	e	109/111 (98%)	109 (100%)	0	100	100
33	f	90/91 (99%)	90 (100%)	0	100	100
34	g	95/103 (92%)	95 (100%)	0	100	100
35	h	104/105 (99%)	104 (100%)	0	100	100
36	i	81/82 (99%)	81 (100%)	0	100	100
37	j	70/71 (99%)	70 (100%)	0	100	100
38	k	68/69 (99%)	68 (100%)	0	100	100
39	l	45/46 (98%)	45 (100%)	0	100	100
40	o	82/91 (90%)	82 (100%)	0	100	100
41	p	71/72 (99%)	71 (100%)	0	100	100
42	w	205/221 (93%)	203 (99%)	2 (1%)	76	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
43	y	189/194 (97%)	189 (100%)	0	100 100
44	z	51/51 (100%)	51 (100%)	0	100 100
All	All	5348/5625 (95%)	5342 (100%)	6 (0%)	93 97

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	L	24	VAL
42	w	328	ILE
42	w	330	ARG
6	C	194	TYR
5	B	85	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
41	p	34	HIS
42	w	332	ASN
17	P	133	HIS
16	O	90	HIS
43	y	86	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3086/3396 (90%)	747 (24%)	47 (1%)
2	3	120/121 (99%)	20 (16%)	1 (0%)
3	4	157/158 (99%)	39 (24%)	2 (1%)
All	All	3363/3675 (91%)	806 (23%)	50 (1%)

5 of 806 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	6	A
1	1	14	U
1	1	22	G
1	1	24	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2227	C
1	1	2771	U
3	4	85	G
1	1	2372	A
1	1	2537	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

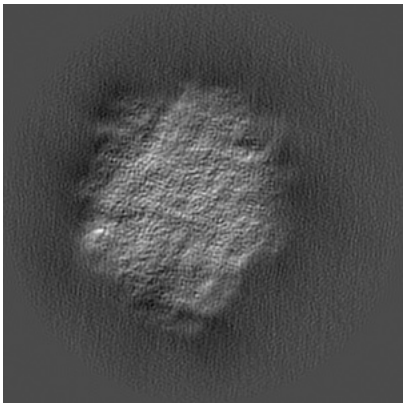
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-9569. These allow visual inspection of the internal detail of the map and identification of artifacts.

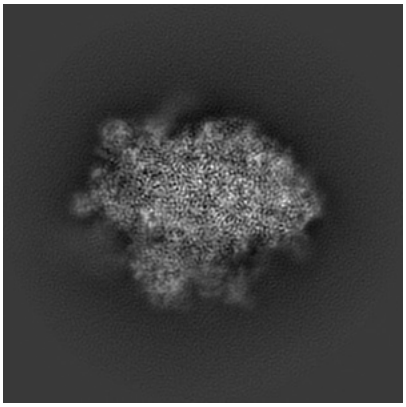
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

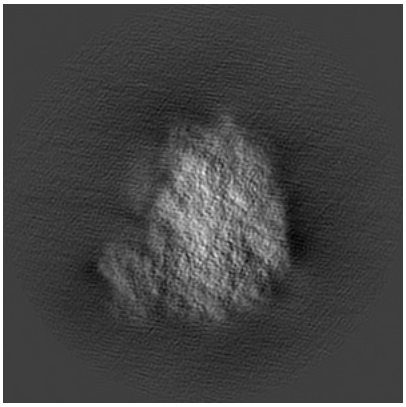
6.1.1 Primary map



X



Y

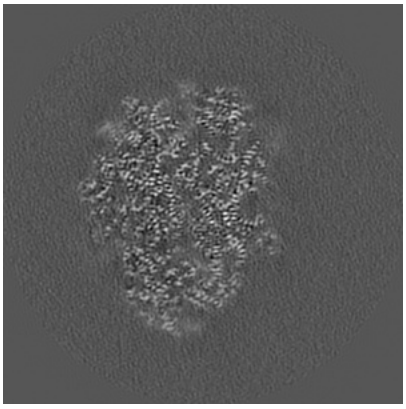


Z

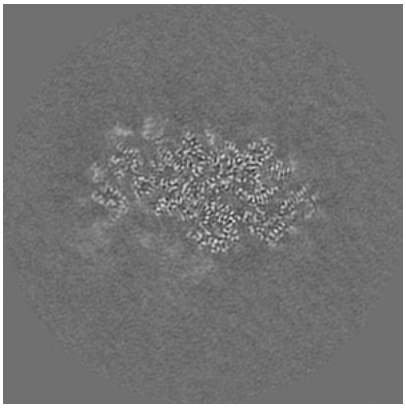
The images above show the map projected in three orthogonal directions.

6.2 Central slices

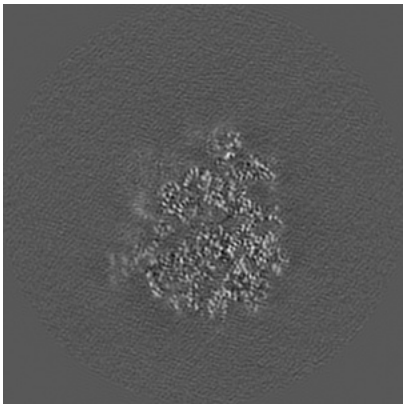
6.2.1 Primary map



X Index: 180



Y Index: 180

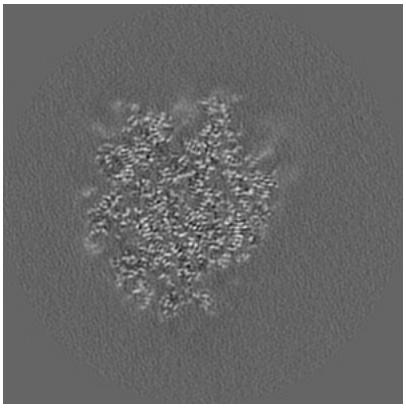


Z Index: 180

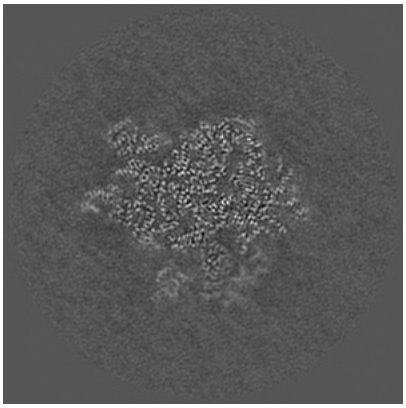
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

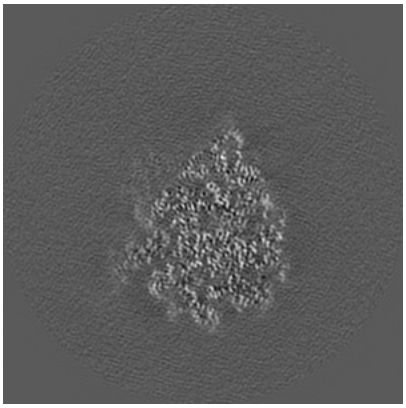
6.3.1 Primary map



X Index: 193



Y Index: 133

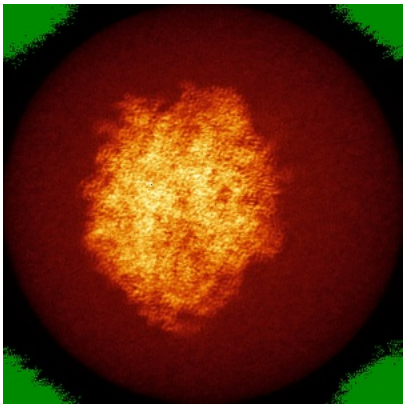


Z Index: 188

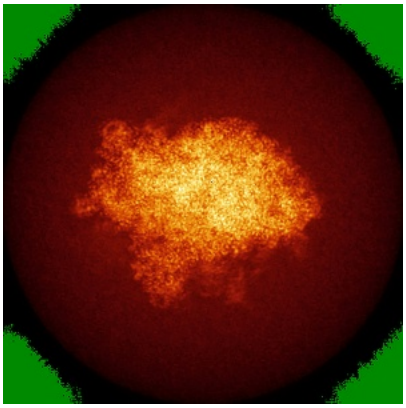
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

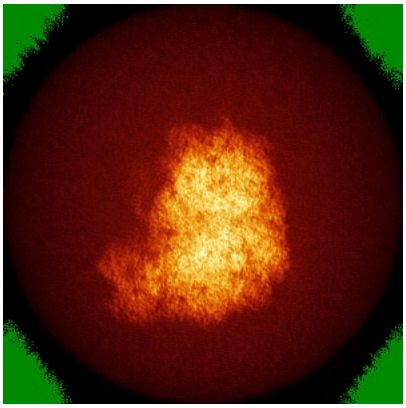
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.143. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

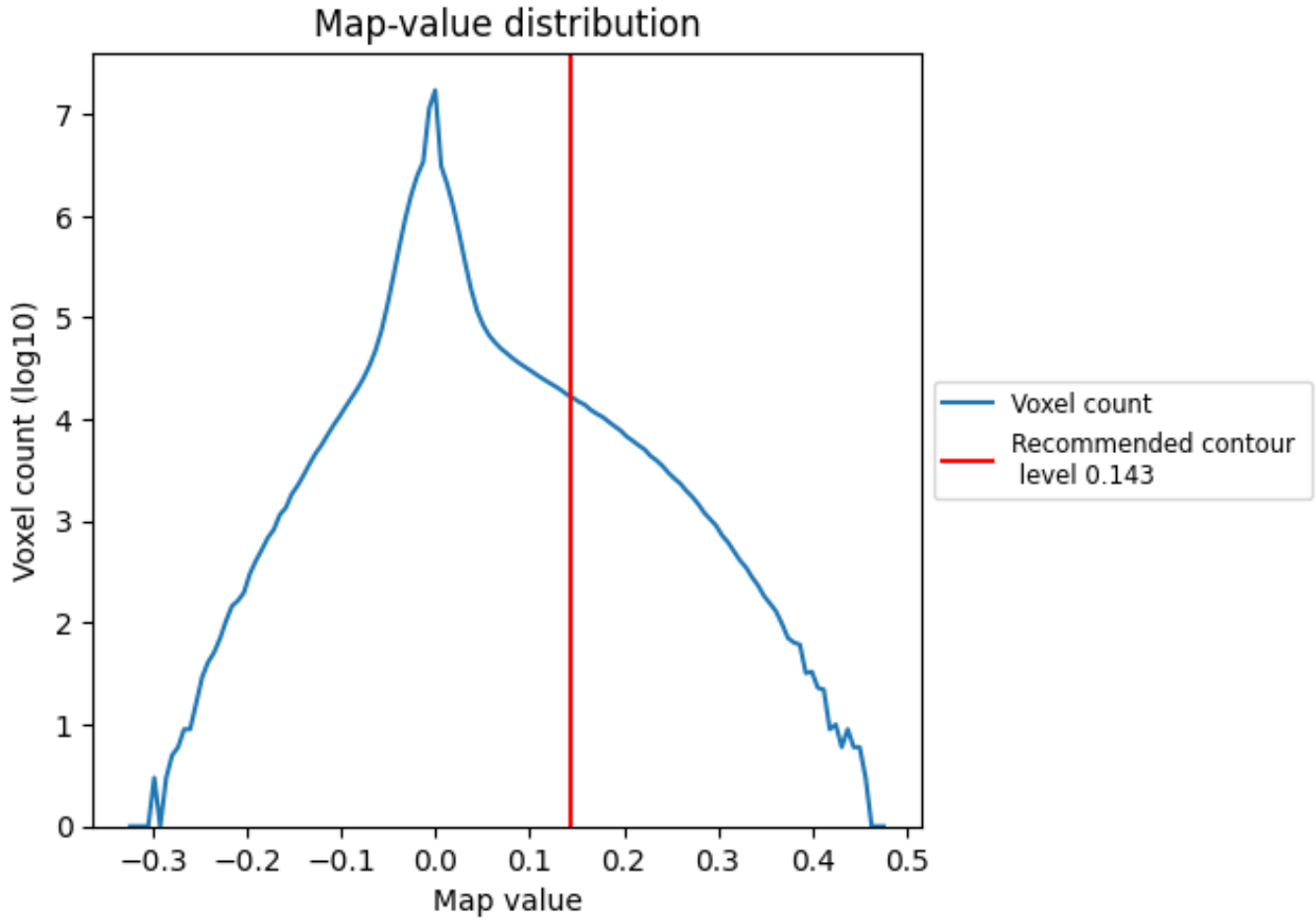
6.6 Mask visualisation (i)

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

7 Map analysis

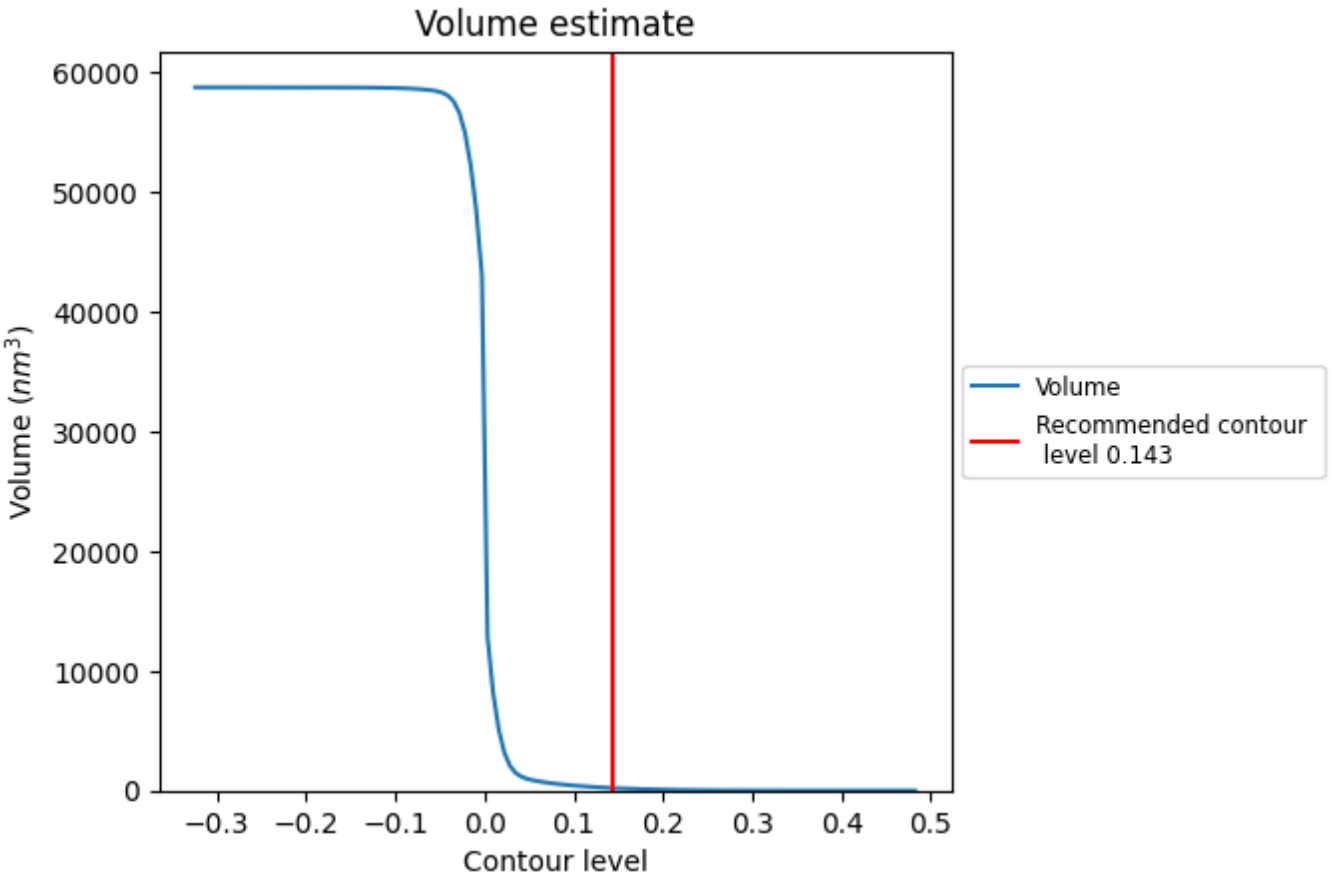
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

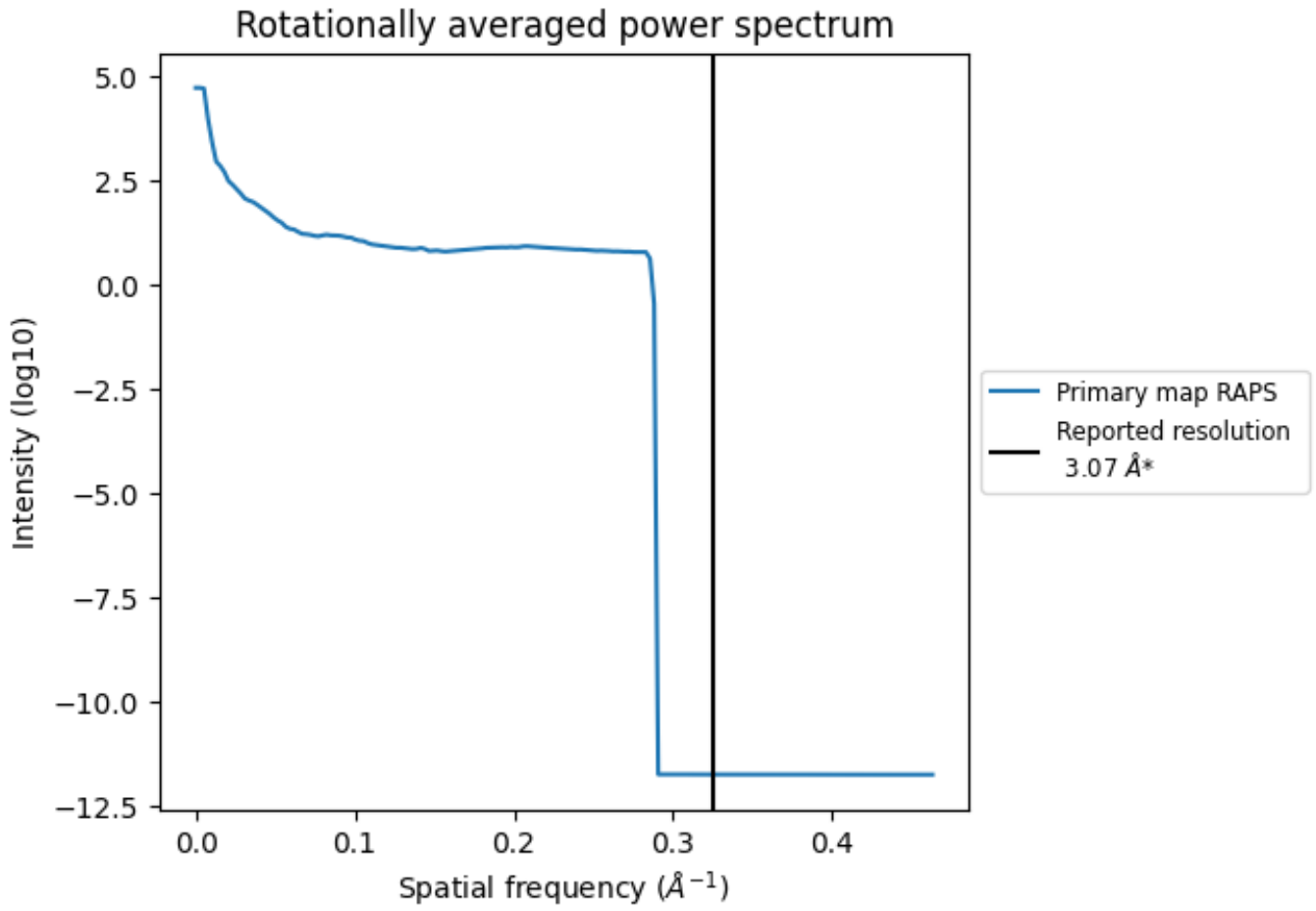
7.2 Volume estimate (i)



The volume at the recommended contour level is 212 nm^3; this corresponds to an approximate mass of 192 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 0.326 Å^{-1}

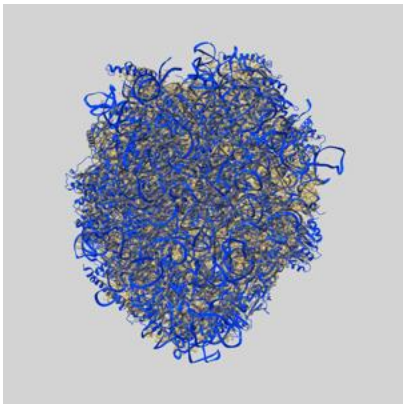
8 Fourier-Shell correlation (i)

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

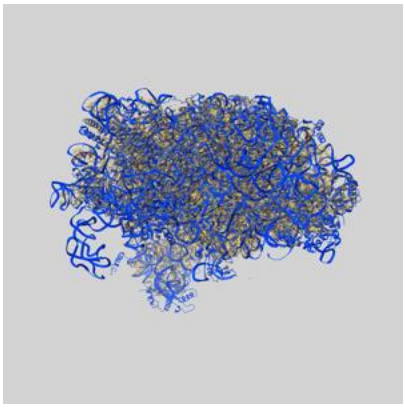
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-9569 and PDB model 5H4P. Per-residue inclusion information can be found in section 3 on page 12.

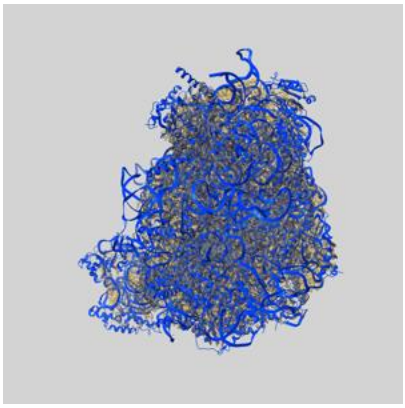
9.1 Map-model overlay



X



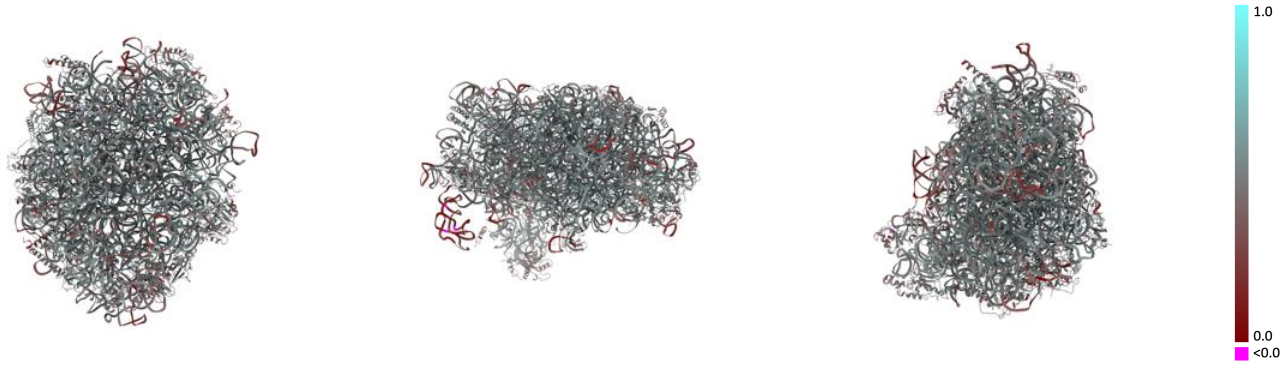
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.143 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.

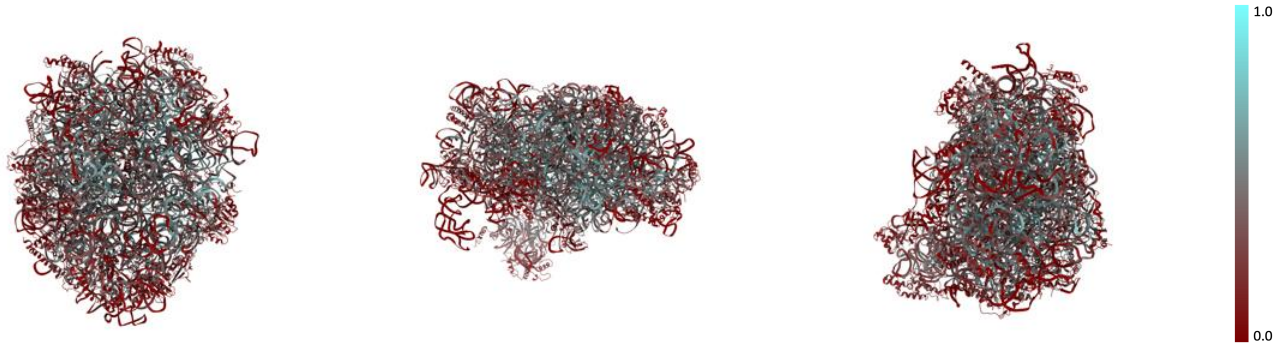
9.2 Q-score mapped to coordinate model



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.

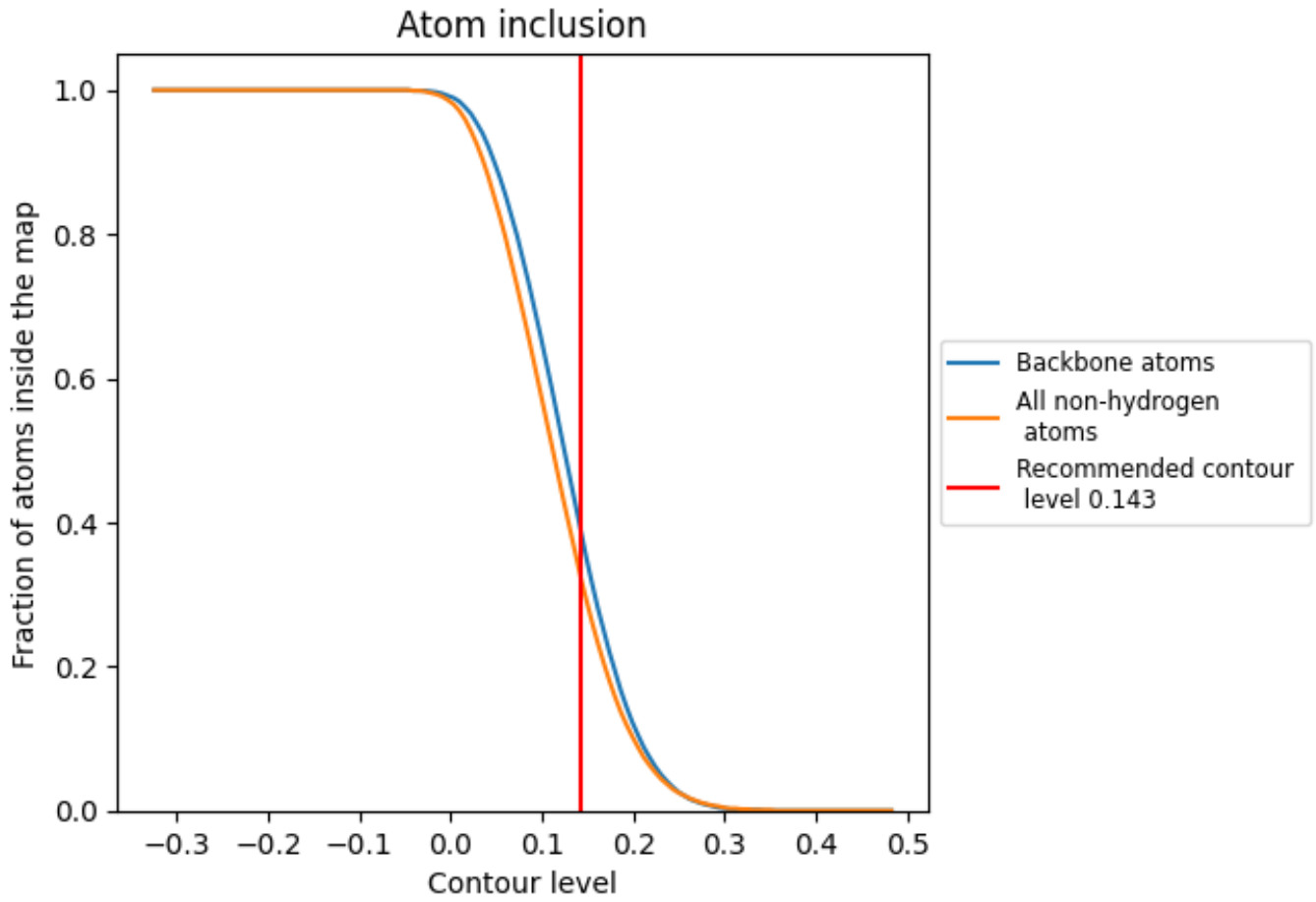
9.3 Atom inclusion mapped to coordinate model



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 (0.143).

9.4 Atom inclusion (i)



At the recommended contour level, 38% of all backbone atoms, 32% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.143) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3200	0.4830
1	0.3760	0.4820
3	0.2740	0.4830
4	0.4380	0.5040
A	0.3590	0.5090
B	0.3570	0.5000
C	0.2730	0.4980
D	0.1030	0.4330
E	0.1390	0.4730
F	0.2700	0.5000
G	0.2380	0.4730
H	0.1360	0.4590
J	0.0590	0.4070
L	0.2540	0.4830
M	0.2220	0.4870
N	0.3560	0.5130
O	0.3360	0.5110
P	0.3080	0.4810
Q	0.2250	0.4990
R	0.3040	0.4830
S	0.2070	0.4840
T	0.1990	0.4760
U	0.1390	0.4490
V	0.3060	0.5020
W	0.2380	0.4910
X	0.3140	0.4980
Y	0.2610	0.4990
Z	0.2100	0.4720
a	0.3010	0.5060
b	0.1240	0.4470
c	0.1750	0.4550
d	0.3070	0.4890
e	0.2760	0.5100
f	0.3460	0.5150
g	0.3350	0.4920

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Chain	Atom inclusion	Q-score
h	0.2850	0.4870
i	0.1440	0.4550
j	0.3770	0.5170
k	0.1200	0.4530
l	0.3280	0.5160
o	0.2780	0.4800
p	0.3170	0.4830
w	0.0840	0.4590
y	0.1050	0.4390
z	0.0610	0.4690