wwPDB EM Validation Summary Report (i)

Mar 20, 2026 – 04:54 PM UTC

PDB ID	:	7PAT / pdb_00007pat
EMDB ID	:	EMD-13285
Title	:	free 50S in untreated Mycoplasma pneumoniae cells
Authors	:	Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on	:	2021-07-30
Resolution	:	9.20 Å(reported)
Based on initial model	:	7OOD

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:

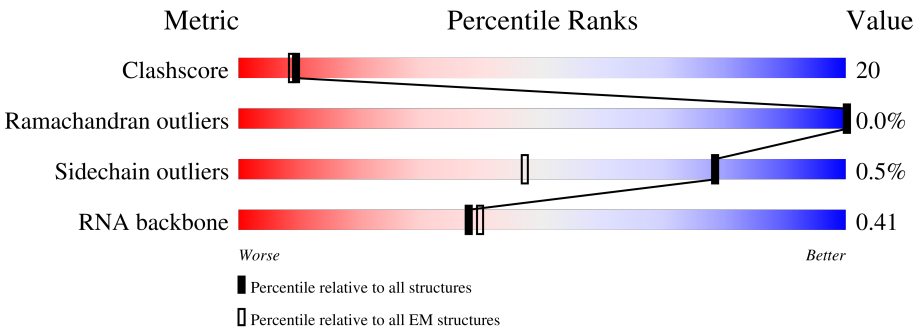
EMDB validation analysis	:	0.0.1.dev132
MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

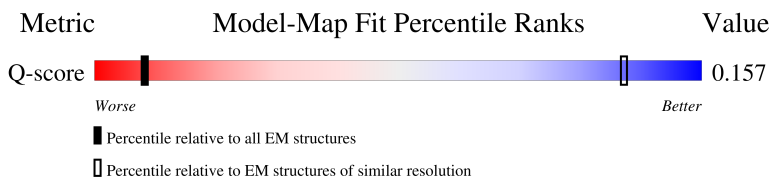
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 9.20 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	239 (8.70 - 9.70)

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	0	48	46% 52% .
2	1	59	51% 49%
3	2	37	51% 49%

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Mol	Chain	Length	Quality of chain
4	a	287	60% 39%
5	b	287	52% 28% 20%
6	c	212	66% 33%
7	d	180	17% 67% 31%
8	e	184	20% 64% 32%
9	f	149	32% 68% 29%
10	g	161	31% 63% 15% 22%
11	h	137	54% 88% 6% 7%
12	i	146	60% 38%
13	j	122	64% 36%
14	k	151	61% 37%
15	l	139	52% 45%
16	m	124	64% 32%
17	n	116	5% 62% 34%
18	o	119	59% 38%
19	p	127	51% 39% 10%
20	q	100	66% 33%
21	r	159	57% 31% 13%
22	s	237	25% 14% 61%
23	t	111	6% 77% 23%
24	u	104	52% 31% 17%
25	v	65	57% 40%
26	w	111	58% 32% 10%
27	x	97	20% 35% 10% 55%
28	y	57	58% 35% 5%

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Mol	Chain	Length	Quality of chain
29	z	53	68% 26% 6%
30	3	2907	21% 58% 19%
31	4	108	27% 47% 23%

2 Entry composition (i)

There are 31 unique types of molecules in this entry. The entry contains 91293 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 protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	47	380	236	81	61	2	0	0

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	59	477	300	99	77	1	0	0

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	37	304	189	65	46	4	0	0

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	a	285	2225	1385	437	397	6	0	0

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	b	229	1762	1119	318	318	7	0	0

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	c	210	1644	1047	297	297	3	0	0

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	d	175	1388	893	245	246	4	0	0

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	e	176	1396	899	247	250	0	0

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	f	145	1160	746	204	207	3	0	0

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	g	126	960	612	167	178	3	0	0

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	h	128	959	616	160	177	6	0	0

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	i	144	1164	737	213	209	5	0	0

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	j	122	944	595	178	167	4	0	0

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	k	148	1153	731	226	196	0	0

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	l	136	1079	694	196	182	7	0	0

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	m	119	958	609	175	171	3	0	0

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	n	112	889	557	175	155	2	0	0

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	o	115	938	592	180	165	1	0	0

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	p	114	947	603	188	154	2	0	0

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	q	99	811	525	148	134	4	0	0

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	r	139	1068	663	207	191	7	0	0

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	s	92	720	475	122	122	1	0	0

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	t	111	872	550	166	153	3	0	0

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	u	86	657	409	130	117	1	0	0

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	v	63	513	317	108	87	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	w	100	818	517	153	148	0	0

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	x	44	344	221	55	64	4	0	0

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	y	56	452	274	98	75	5	0	0

- Molecule 29 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	z	50	408	255	81	68	4	0	0

- Molecule 30 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
30	3	2878	61664	27558	11236	19995	2875	0	0

- Molecule 31 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
31	4	105	2239	1003	409	724	103	0	0

3 Residue-property plots (i)

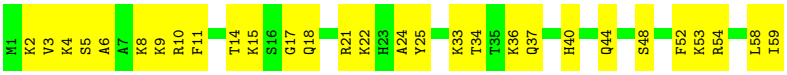
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 50S ribosomal protein L34

Chain 0:

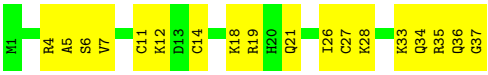
- Molecule 2: 50S ribosomal protein L35

Chain 1:



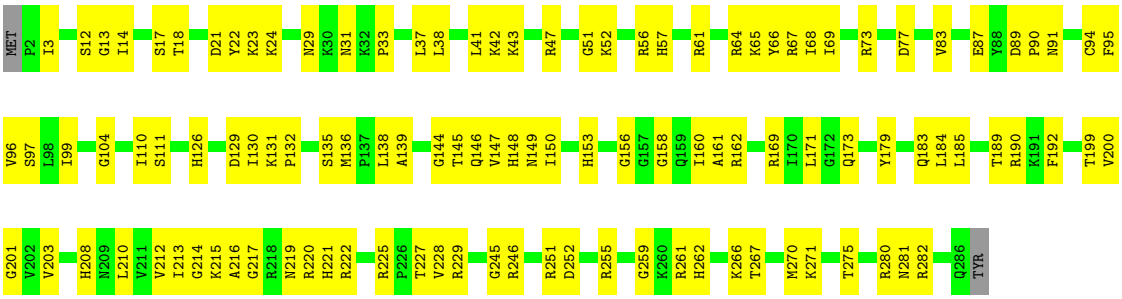
- Molecule 3: 50S ribosomal protein L36

Chain 2:



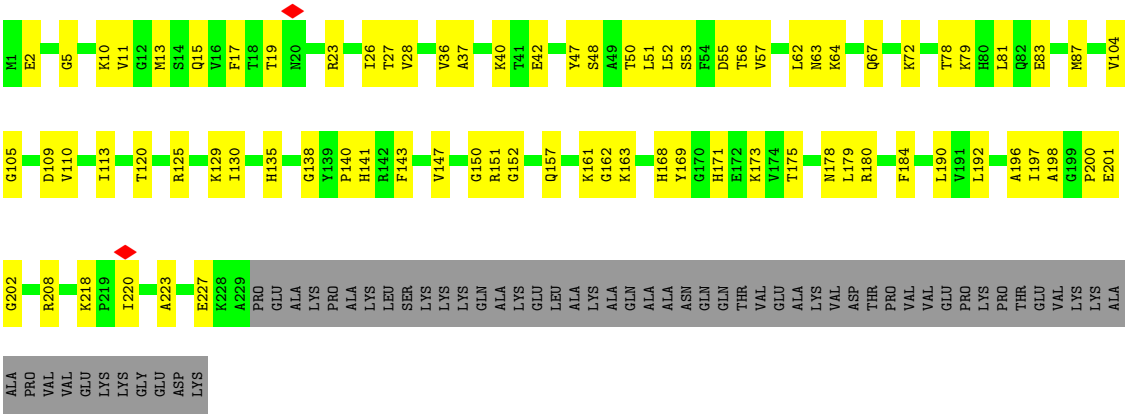
- Molecule 4: 50S ribosomal protein L2

Chain a:



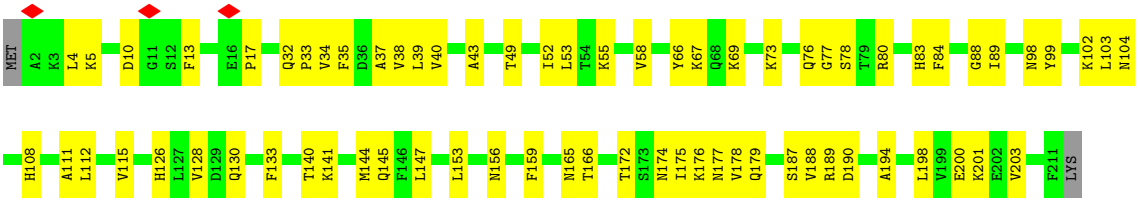
- Molecule 5: 50S ribosomal protein L3

Chain b:



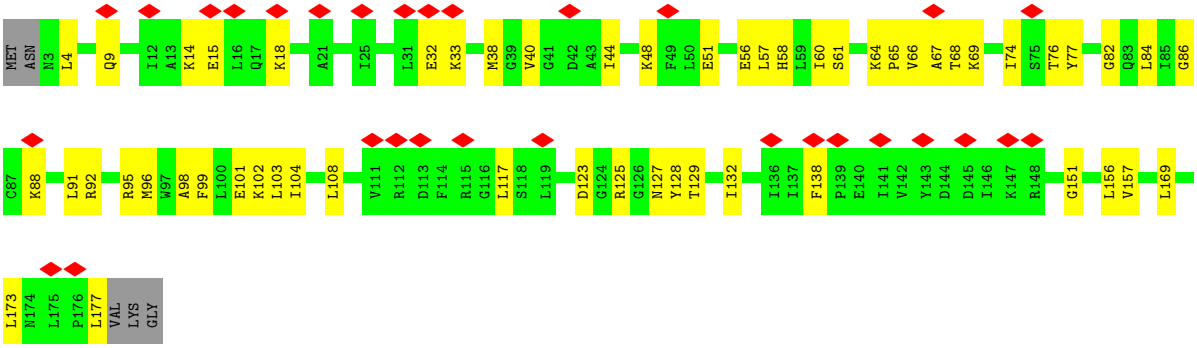
- Molecule 6: 50S ribosomal protein L4

Chain c:



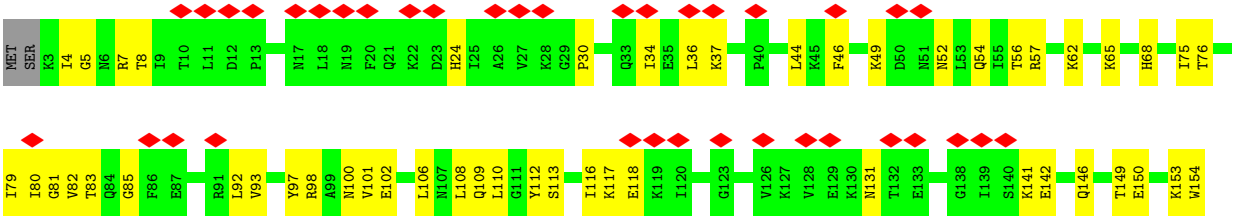
- Molecule 7: 50S ribosomal protein L5

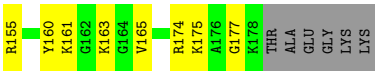
Chain d:



- Molecule 8: 50S ribosomal protein L6

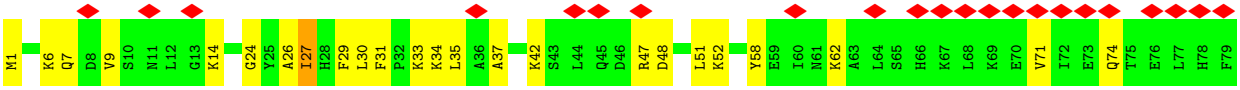
Chain e:

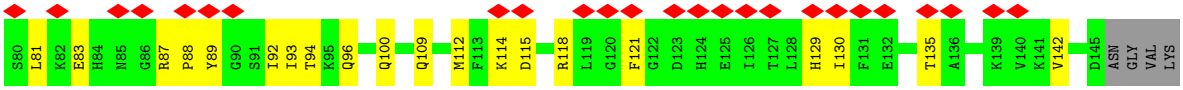




• Molecule 9: 50S ribosomal protein L9

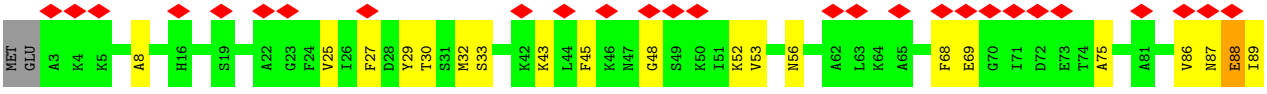
Chain f:

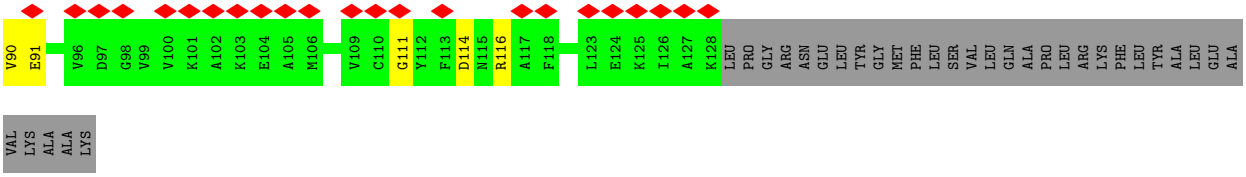




• Molecule 10: 50S ribosomal protein L10

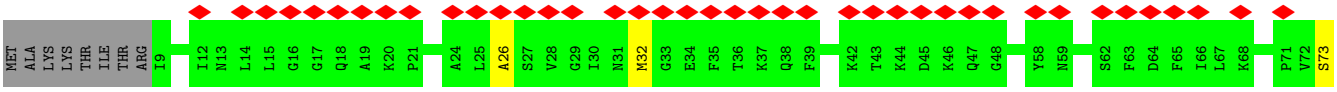
Chain g:

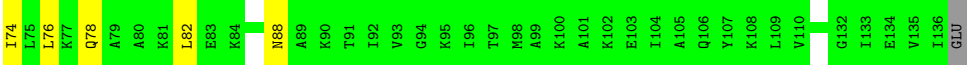




• Molecule 11: 50S ribosomal protein L11

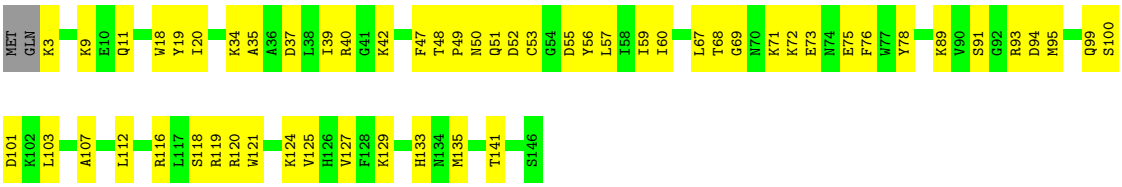
Chain h:





• Molecule 12: 50S ribosomal protein L13

Chain i:



• Molecule 13: 50S ribosomal protein L14

Chain j: 64% 36%

M1 V2 S3 T6 R7 A11 T14 Q18 V19 G20 I21 I22 K23 V24 L25 G26 S27 K30 R31 G36 D37 V38 V39 V40 V41 S42 V43 L58 R64 K67 Q70 R71 K72 D73 H76 L77 A83 L86 I87 K88 K91 S92 P93 R94 G95

P101 V102 E105 L106 R109 G110 Y111 I114 V122

• Molecule 14: 50S ribosomal protein L15

Chain k: 61% 37%

MET GLU L3 N4 Q5 L6 K7 A12 R13 N14 H15 K18 T19 L20 S32 G33 R34 G35 Q36 K37 G38 Q39 K40 A41 R42 K43 R48 P49 G50 F51 R61 L62 P63 K64 R69 F72 L73 K74 W77 V78 L82 N83 K84 I85 D91 K92 L98 K101

Q102 V103 I104 S105 L110 P111 I112 G116 K119 L120 E121 H125 H129 K133 Q134 A135 L136 K137 A138 V139 E140 S145 L149 E150 LYS

• Molecule 15: 50S ribosomal protein L16

Chain l: 52% 45%

M1 P4 K5 R6 T7 K8 Y9 R10 K11 P12 H13 N14 V15 A21 K22 G23 N24 S25 Y26 V27 A28 F29 G30 E31 L34 V35 G39 N40 W41 I42 D43 A44 R45 A46 I47 E48 I52 K56 G62 K63 M64 W65 I66 R67 I68 T75 K76 K77 R82 S85

G86 K87 G88 V94 A95 V96 V97 K98 V102 E105 V106 A107 N108 I109 P110 E111 M114 I115 K116 A117 L118 T119 R120 A121 G122 L125 W129 K130 I131 R134 E135 E136 VAL SER ALA

• Molecule 16: 50S ribosomal protein L17

Chain m: 64% 32%

MET S2 K9 T10 W13 R14 R19 Q20 Q21 V22 V25 L35 A38 R44 I49 T50 L51 A52 K53 N58 N59 R60 R61 Q62 V63 L67 N71 L72 F73 D74 V75 L78 M79 D80 H81 L82 F83 S84 K85 V86 P94 S98 R99 V100 L101 K102

L103 R107 G108 D109 L116 D120 ALA LYS TYR LYS

• Molecule 17: 50S ribosomal protein L18

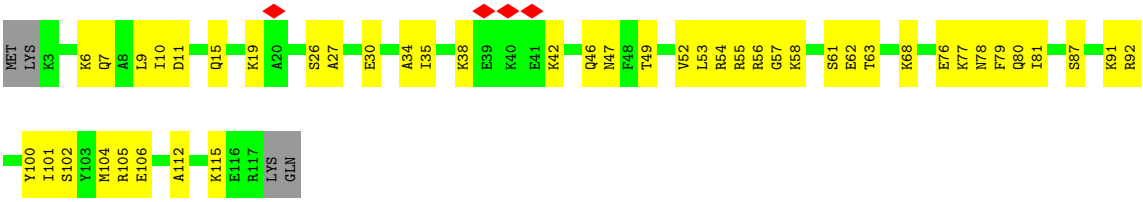
Chain n: 5% 62% 34%

M1 K2 T3 R4 T5 E6 Q7 L10 R11 H12 K13 R14 I15 V16 D25 N26 R27 V28 M31 V32 I33 K34 H38 I39 S40 V41 D45 F46 S47 Q48 N49 L52 A53 S56 S57 N64 GLY ASN LYS ASP N69 L72 Q75 D76 I77 A78 D79 K80 L81 V82

K83 N88 D92 T93 G94 R101 I102 A108 A109 R110 E111 R112 F116

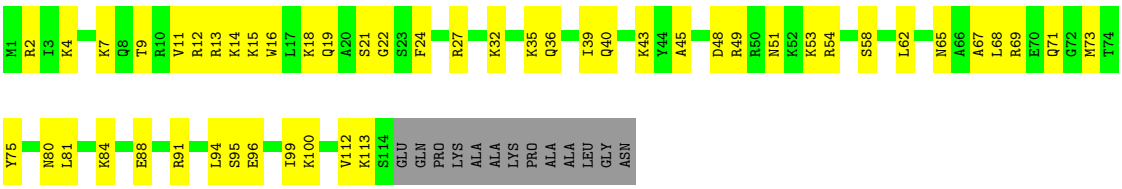
- Molecule 18: 50S ribosomal protein L19

Chain o:



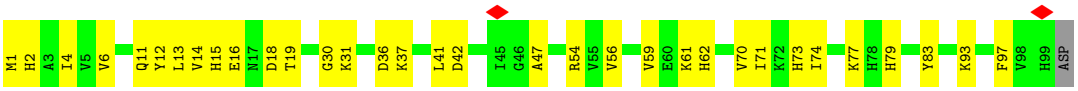
- Molecule 19: 50S ribosomal protein L20

Chain p:



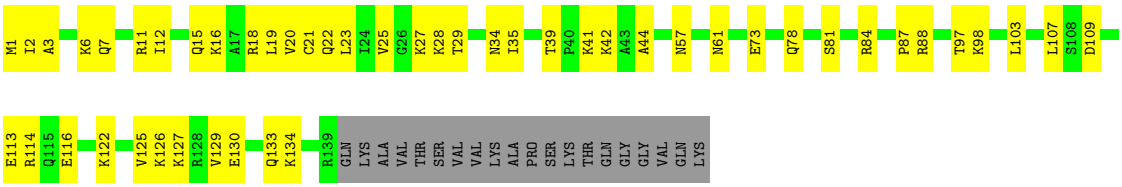
- Molecule 20: 50S ribosomal protein L21

Chain q:



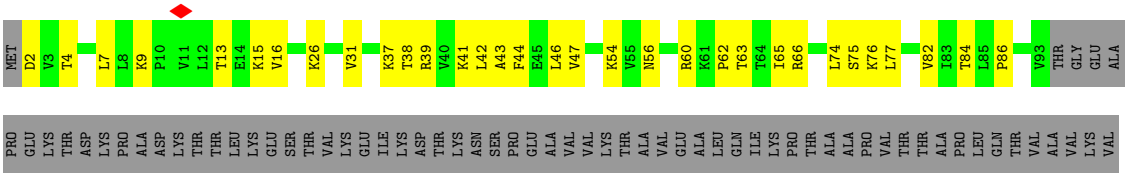
- Molecule 21: 50S ribosomal protein L22

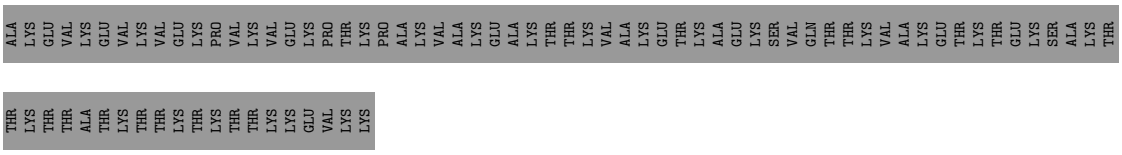
Chain r:



- Molecule 22: 50S ribosomal protein L23

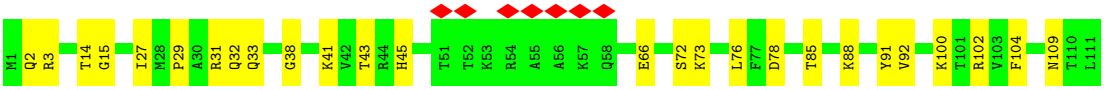
Chain s:





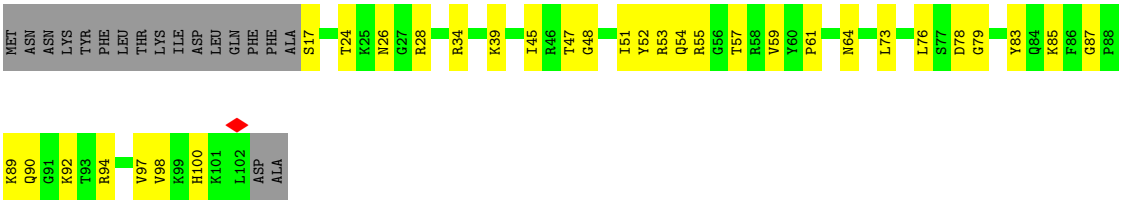
- Molecule 23: 50S ribosomal protein L24

Chain t:



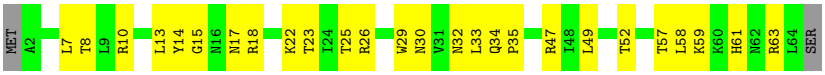
- Molecule 24: 50S ribosomal protein L27

Chain u:



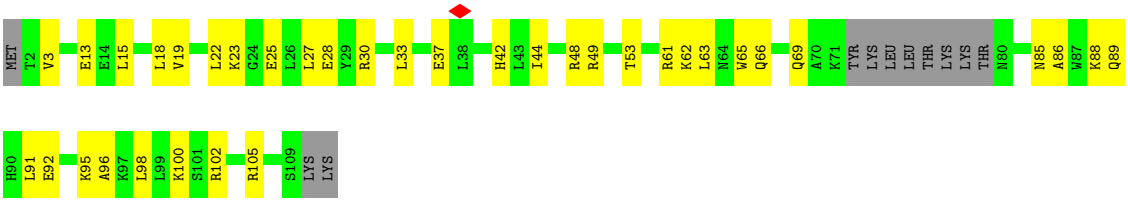
- Molecule 25: 50S ribosomal protein L28

Chain v:



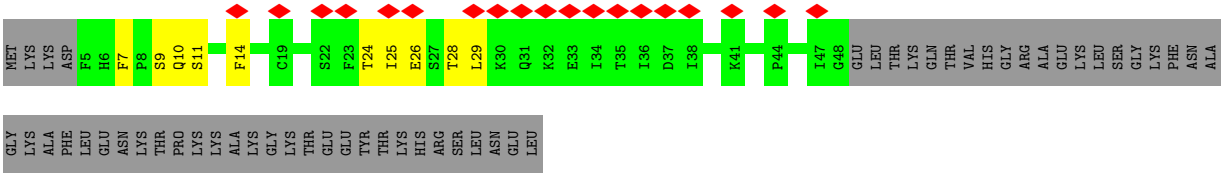
- Molecule 26: 50S ribosomal protein L29

Chain w:



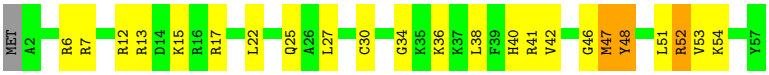
- Molecule 27: 50S ribosomal protein L31

Chain x:



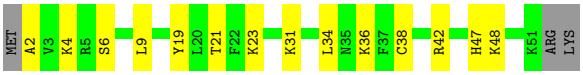
- Molecule 28: 50S ribosomal protein L32

Chain y:



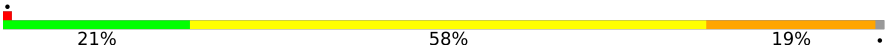
- Molecule 29: 50S ribosomal protein L33 1

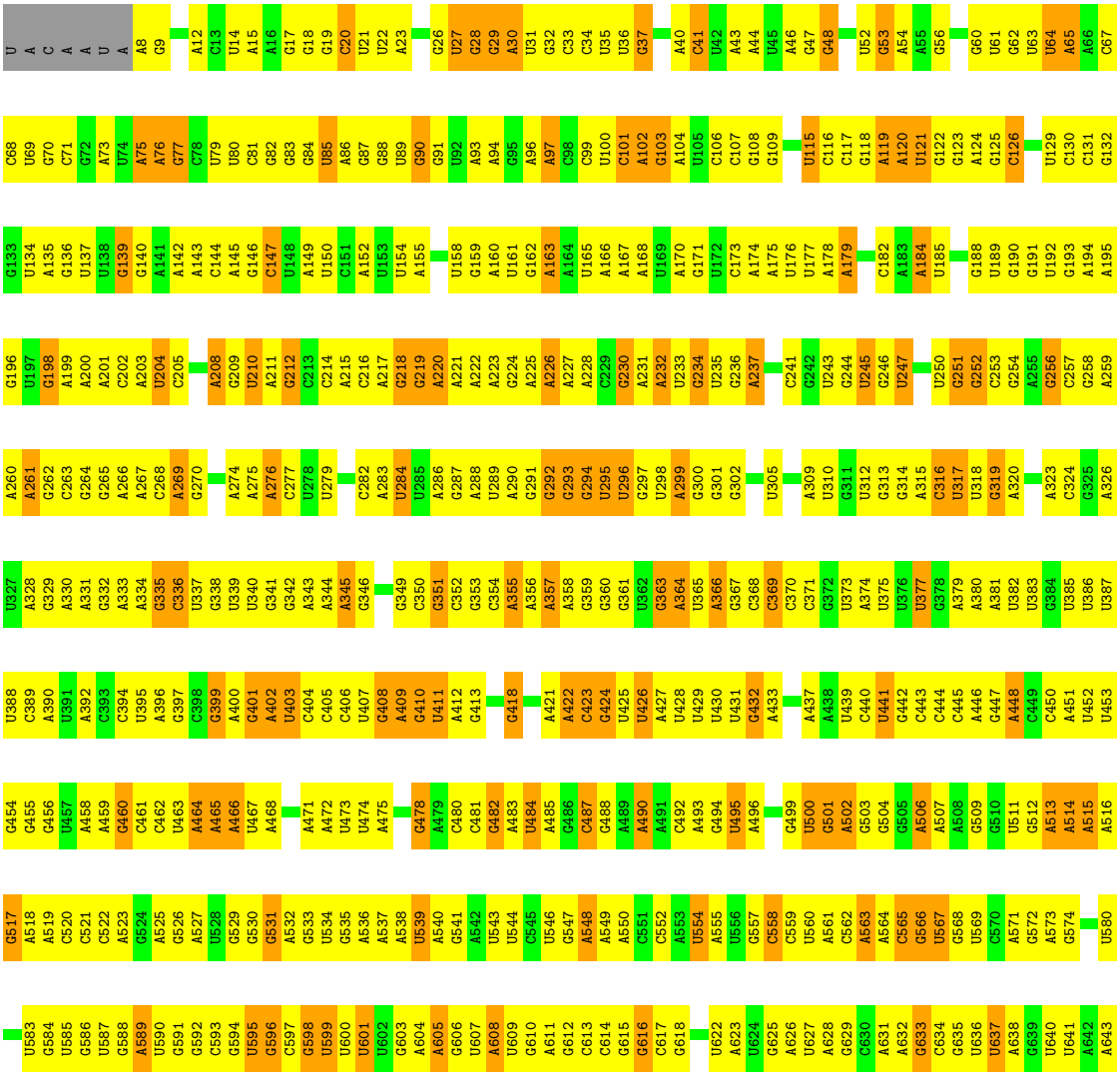
Chain z:

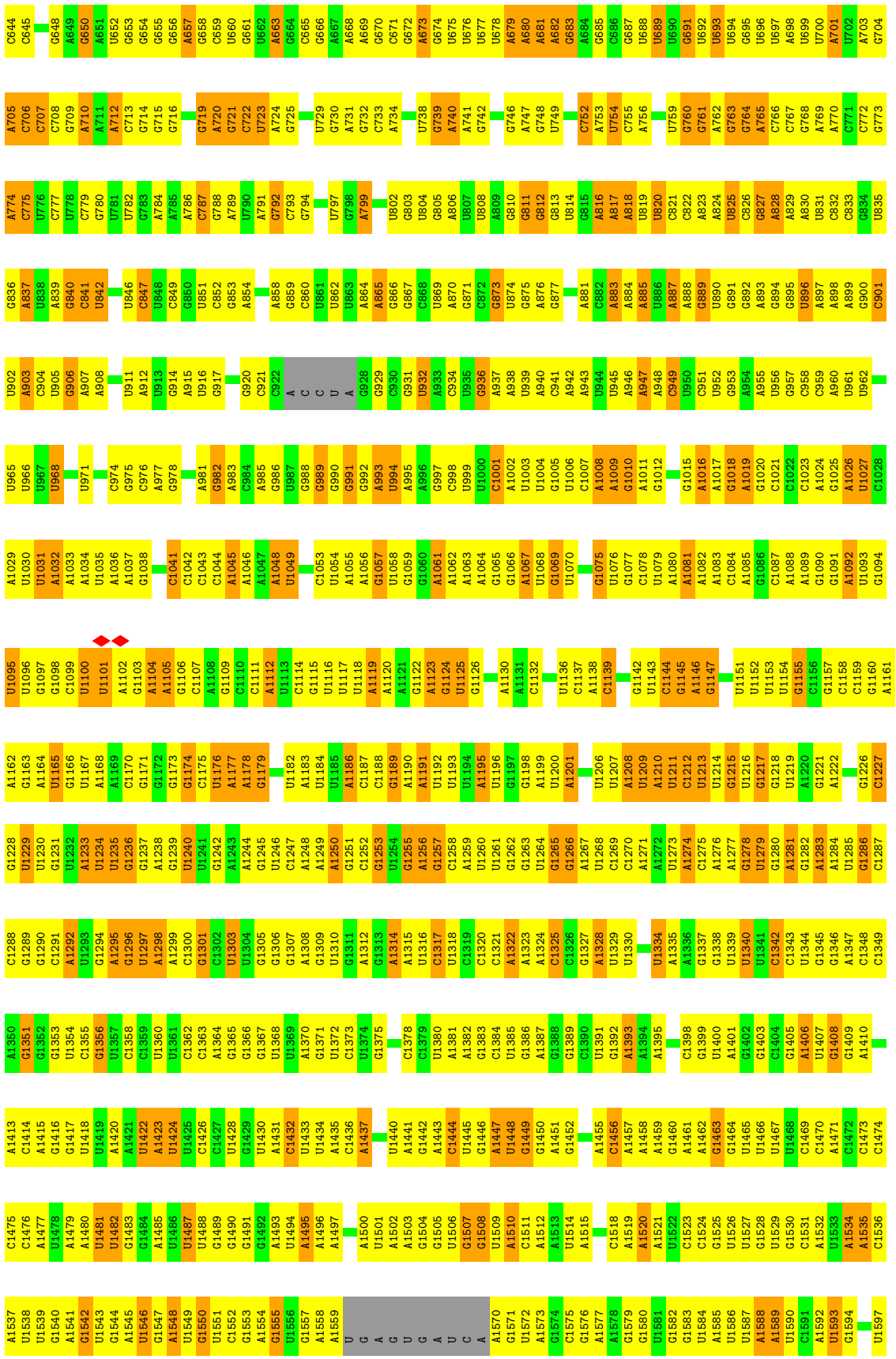


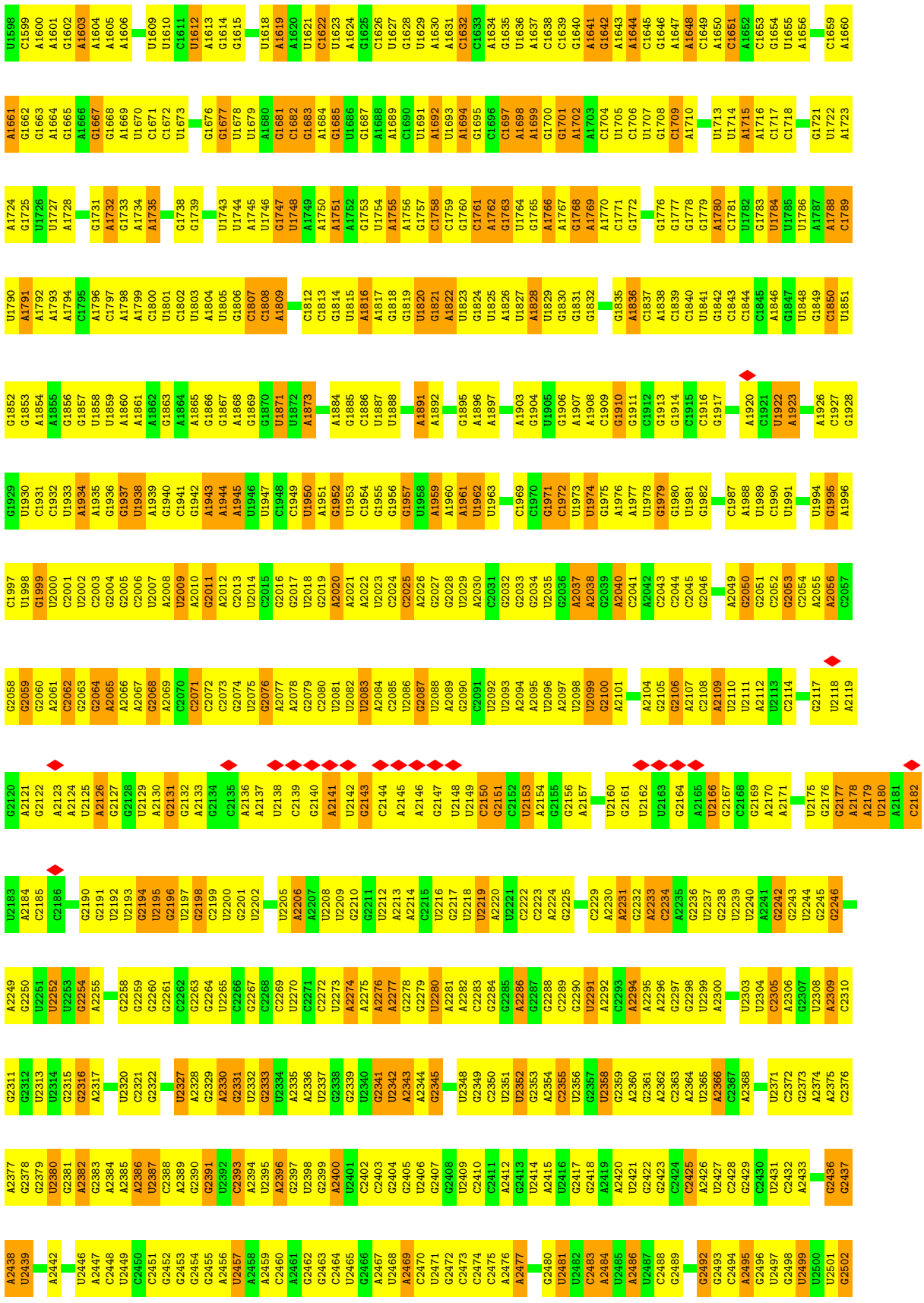
- Molecule 30: 23S ribosomal RNA

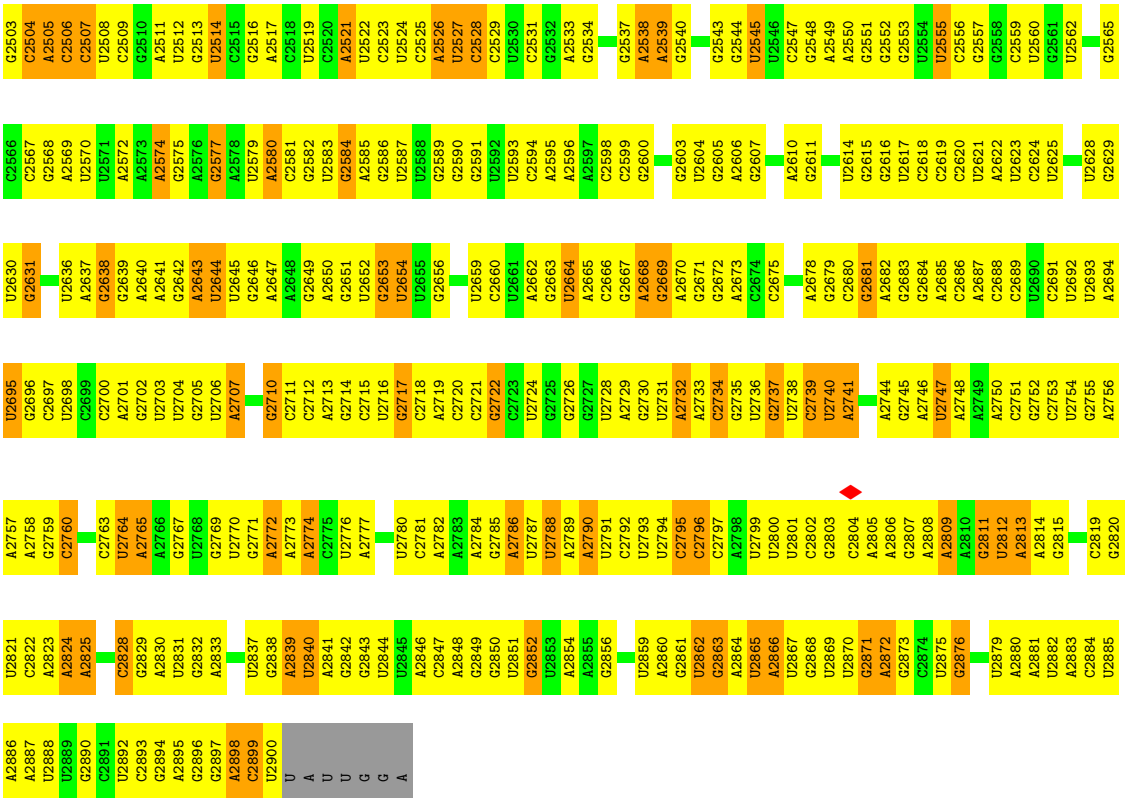
Chain 3:





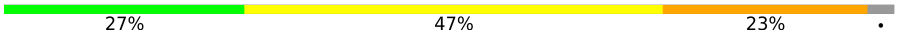

C644 C645 G648 A649 G650 A651 U652 G653 G654 G655 G656 A657 G658 C659 U660 G661 U662 A663 G664 C665 G666 A667 A668 A669 G670 C671 G672 A673 G674 U675 U676 U677 U678 A679 A680 A681 A682 G683 A684 G685 C686 G687 U688 U689 U690 G691 U692 U693 U694 G695 U696 U697 A698 U699 U700 A701 U702 A703 G704
A705 C706 C707 C708 G709 A710 A711 A712 C713 G714 G715 G716 G719 A720 G721 C722 U723 A724 G725 U729 G730 A731 G732 C733 A734 U738 G739 A740 A741 G742 G746 A747 G748 U749 C752 A753 U754 C755 A756 U759 G760 G761 A762 G763 G764 A765 C766 C767 G768 A769 A770 C771 G772 G773
A774 C775 U776 C777 U778 C779 G780 U781 U782 G783 A784 A785 A786 C787 G788 A789 U790 A791 G792 C793 G794 U797 G798 A799 U802 G803 U804 G805 A806 U807 U808 A809 G810 G811 G812 G813 U814 G815 A816 A817 A818 U819 U820 C821 C822 A823 A824 U825 C826 G827 A828 A829 A830 U831 C832 C833 G834 U835
G836 A837 U838 A839 G840 C841 U842 U846 C847 U848 C849 G850 U851 C852 G853 A854 A858 G859 C860 U861 U862 U863 A864 A865 G866 G867 C868 U869 A870 G871 C872 G873 U874 G875 A876 G877 A881 C882 A883 A884 A885 U886 A887 A888 G889 U890 G891 G892 A893 G894 G895 U896 A897 A898 G899 G900 C901
U902 A903 C904 U905 G906 A907 A908 U911 A912 U913 G914 A915 U916 G917 G920 C921 C922 A C C U A G928 G929 C930 G931 U932 A933 C934 U935 G936 A937 A938 U939 A940 C941 A942 A943 U944 U945 A946 A947 A948 C949 U950 C951 U952 G953 A954 A955 U956 G957 C958 C959 A960 U961 U962
U965 U966 U967 U968 U971 C974 G975 C976 A977 G978 A981 G982 A983 C984 A985 G986 U987 G988 G989 G990 G991 G992 A993 U994 A995 A996 G997 C998 U999 U1000 C1001 A1002 U1003 U1004 G1005 U1006 C1007 A1008 A1009 A1010 A1011 G1012 G1015 A1016 A1017 G1018 A1019 G1020 C1021 C1022 C1023 A1024 G1025 A1026 U1027 C1028
A1029 U1030 U1031 A1032 A1033 A1034 U1035 A1036 A1037 G1038 C1041 C1042 C1043 C1044 A1045 A1046 A1047 A1048 U1049 C1053 U1054 A1055 A1056 G1057 U1058 G1059 G1060 A1061 A1062 A1063 A1064 G1065 G1066 A1067 U1068 G1069 U1070 G1075 U1076 G1077 C1078 U1079 A1080 A1081 A1082 A1083 C1084 A1085 G1086 C1087 A1088 A1089 G1090 G1091 A1092 U1093 G1094
U1095 U1096 G1097 G1098 C1099 U1100 U1101 A1102 G1103 A1104 A1105 G1106 C1107 A1108 G1109 C1110 C1111 A1112 U1113 C1114 G1115 U1116 U1117 U1118 A1119 A1120 A1121 G1122 A1123 G1124 U1125 G1126 A1130 A1131 C1132 U1136 C1137 A1138 C1139 G1142 U1143 C1144 G1145 A1146 G1147 U1151 U1152 U1153 U1154 G1155 C1156 G1157 C1158 C1159 G1160 A1161
A1162 G1163 A1164 U1165 G1166 U1167 A1168 A1169 C1170 G1171 G1172 G1173 G1174 C1175 U1176 A1177 A1178 G1179 U1182 A1183 U1184 U1185 A1186 C1187 C1188 G1189 A1190 A1191 U1192 U1193 U1194 A1195 U1196 G1197 G1198 A1199 U1200 A1201 U1206 U1207 A1208 U1209 A1210 U1211 C1212 U1213 U1214 G1215 U1216 G1217 G1218 U1219 A1220 G1221 A1222 G1226 C1227
G1228 U1229 U1230 G1231 U1232 A1233 U1234 U1235 G1236 G1237 A1238 G1239 U1240 U1241 G1242 A1243 A1244 G1245 U1246 C1247 A1248 A1249 A1250 G1251 C1252 G1253 U1254 G1255 A1256 G1257 C1258 A1259 U1260 U1261 G1262 G1263 U1264 G1265 G1266 A1267 U1268 C1269 C1270 A1271 A1272 U1273 A1274 C1275 A1276 A1277 G1278 U1279 G1280 A1281 G1282 A1283 A1284 U1285 G1286 C1287
C1288 G1289 G1290 C1291 A1292 U1293 G1294 A1295 G1296 U1297 A1298 A1299 C1300 G1301 C1302 U1303 U1304 G1305 G1306 G1307 A1308 G1309 U1310 G1311 A1312 G1313 A1314 A1315 U1316 C1317 U1318 C1319 C1320 C1321 A1322 A1323 A1324 C1325 C1326 G1327 A1328 U1329 U1330 U1334 A1335 A1336 G1337 G1338 U1339 U1340 U1341 C1342 C1343 U1344 G1345 G1346 A1347 C1348 C1349
A1350 G1351 G1352 G1353 U1354 C1355 G1356 U1357 C1358 C1359 U1360 U1361 C1362 C1363 A1364 G1365 G1366 G1367 U1368 U1369 A1370 G1371 U1372 C1373 U1374 G1375 C1378 C1379 U1380 A1381 A1382 G1383 C1384 U1385 G1386 A1387 G1388 G1389 C1390 U1391 G1392 A1393 A1394 A1395 C1398 G1399 U1400 A1401 G1402 G1403 C1404 G1405 A1406 U1407 G1408 G1409 A1410
A1413 C1414 A1415 G1416 G1417 U1418 U1419 A1420 A1421 U1422 A1423 U1424 U1425 C1426 C1427 U1428 G1429 U1430 A1431 C1432 U1433 U1434 A1435 C1436 A1437 U1440 A1441 U1442 A1443 C1444 U1445 G1446 A1447 U1448 G1449 G1450 A1451 G1452 A1455 C1456 A1457 A1458 A1459 G1460 A1461 A1462 G1463 G1464 U1465 U1466 U1467 U1468 C1469 C1470 A1471 C1472 C1473 C1474
C1475 C1476 A1477 U1478 A1479 A1480 U1481 U1482 G1483 G1484 A1485 U1486 U1487 U1488 G1489 G1490 G1491 G1492 A1493 U1494 A1495 A1496 A1497 A1500 U1501 A1502 A1503 G1504 G1505 U1506 G1507 G1508 U1509 A1510 C1511 A1512 A1513 U1514 A1515 C1518 A1519 A1520 A1521 U1522 C1523 C1524 G1525 U1526 U1527 G1528 U1529 G1530 C1531 A1532 U1533 A1534 A1535 C1536
A1537 U1538 U1539 G1540 A1541 G1542 U1543 G1544 A1545 U1546 G1547 A1548 U1549 G1550 U1551 C1552 G1553 A1554 G1555 U1556 G1557 A1558 A1559 U G A G U G A U C A A1570 G1571 U1572 A1573 G1574 C1575 G1576 A1577 A1578 G1579 G1580 U1581 G1582 G1583 U1584 A1585 U1586 U1587 A1588 A1589 U1590 C1591 A1592 U1593 G1594 U1597

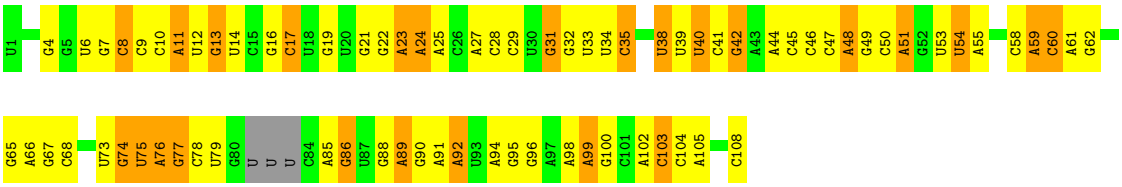




- Molecule 31: 5S ribosomal RNA

Chain 4:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	15954	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.419	Depositor
Minimum map value	-0.423	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.100	Depositor
Recommended contour level	0.41	Depositor
Map size (Å)	480.00003, 480.00003, 480.00003	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.4, 2.4, 2.4	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	0	0.12	0/383	0.40	0/504
2	1	0.12	0/484	0.39	0/637
3	2	0.12	0/306	0.42	0/401
4	a	0.15	0/2267	0.41	0/3044
5	b	0.14	0/1795	0.42	0/2412
6	c	0.13	0/1671	0.38	0/2246
7	d	0.15	0/1409	0.43	0/1894
8	e	0.14	0/1420	0.39	0/1912
9	f	0.15	0/1183	0.47	1/1587 (0.1%)
10	g	0.51	0/969	0.78	0/1295
11	h	0.14	0/968	0.43	1/1298 (0.1%)
12	i	0.12	0/1186	0.40	0/1592
13	j	0.13	0/953	0.39	0/1275
14	k	0.15	0/1170	0.42	0/1559
15	l	0.15	0/1104	0.42	0/1481
16	m	0.12	0/973	0.41	0/1309
17	n	0.13	0/897	0.44	0/1198
18	o	0.15	0/948	0.42	0/1262
19	p	0.16	0/961	0.41	0/1278
20	q	0.15	0/828	0.42	0/1111
21	r	0.13	0/1077	0.37	0/1441
22	s	0.12	0/732	0.40	0/988
23	t	0.14	0/879	0.39	0/1165
24	u	0.15	0/665	0.47	0/884
25	v	0.14	0/519	0.41	0/695
26	w	0.14	0/826	0.40	0/1104
27	x	0.11	0/353	0.37	0/474
28	y	0.32	0/457	0.68	1/601 (0.2%)
29	z	0.13	0/412	0.38	0/547
30	3	0.10	0/69073	0.25	0/107710
31	4	0.10	0/2505	0.27	0/3902
All	All	0.12	0/99373	0.31	3/148806 (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
15	l	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	y	48	TYR	N-CA-C	-5.89	104.78	111.14
11	h	74	ILE	N-CA-C	-5.52	107.43	111.90
9	f	27	ILE	N-CA-C	-5.10	108.30	113.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	l	14	ASN	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	24	0
2	1	477	0	530	27	0
3	2	304	0	350	19	0
4	a	2225	0	2301	104	0
5	b	1762	0	1808	67	0
6	c	1644	0	1731	56	0
7	d	1388	0	1469	41	0
8	e	1396	0	1481	42	0
9	f	1160	0	1172	31	0
10	g	960	0	1014	9	0
11	h	959	0	1039	4	0
12	i	1164	0	1192	43	0
13	j	944	0	1019	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	k	1153	0	1256	55	0
15	l	1079	0	1134	49	0
16	m	958	0	1011	34	0
17	n	889	0	952	28	0
18	o	938	0	1008	45	0
19	p	947	0	1028	44	0
20	q	811	0	858	26	0
21	r	1068	0	1150	48	0
22	s	720	0	803	28	0
23	t	872	0	972	19	0
24	u	657	0	695	28	0
25	v	513	0	560	24	0
26	w	818	0	870	28	0
27	x	344	0	333	7	0
28	y	452	0	472	24	0
29	z	408	0	440	13	0
30	3	61664	0	30954	2141	0
31	4	2239	0	1137	54	0
All	All	91293	0	61168	2838	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

The worst 5 of 2838 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:3:535:G:C2	30:3:540:A:N6	2.14	1.15
30:3:341:G:N2	30:3:364:A:H61	1.44	1.13
30:3:341:G:H21	30:3:364:A:N6	1.51	1.08
30:3:1807:C:H42	30:3:1824:G:N2	1.49	1.07
30:3:2108:C:N4	30:3:2109:A:N6	2.01	1.06

There are no symmetry-related clashes.

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	
1	0	45/48 (94%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	54 (95%)	3 (5%)	0	100	100
3	2	35/37 (95%)	35 (100%)	0	0	100	100
4	a	283/287 (99%)	260 (92%)	23 (8%)	0	100	100
5	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100
6	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
7	d	173/180 (96%)	161 (93%)	12 (7%)	0	100	100
8	e	174/184 (95%)	164 (94%)	10 (6%)	0	100	100
9	f	143/149 (96%)	130 (91%)	13 (9%)	0	100	100
10	g	124/161 (77%)	114 (92%)	9 (7%)	1 (1%)	16	54
11	h	126/137 (92%)	121 (96%)	5 (4%)	0	100	100
12	i	142/146 (97%)	130 (92%)	12 (8%)	0	100	100
13	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
14	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
15	l	134/139 (96%)	122 (91%)	12 (9%)	0	100	100
16	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
17	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
18	o	113/119 (95%)	104 (92%)	9 (8%)	0	100	100
19	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
20	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
21	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
22	s	90/237 (38%)	85 (94%)	5 (6%)	0	100	100
23	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
24	u	84/104 (81%)	77 (92%)	7 (8%)	0	100	100
25	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
26	w	96/111 (86%)	88 (92%)	8 (8%)	0	100	100
27	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
28	y	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
29	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	3405/3879 (88%)	3183 (94%)	221 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	g	32	MET

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	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	a	241/243 (99%)	241 (100%)	0	100	100
5	b	186/233 (80%)	186 (100%)	0	100	100
6	c	182/184 (99%)	182 (100%)	0	100	100
7	d	150/154 (97%)	150 (100%)	0	100	100
8	e	153/159 (96%)	153 (100%)	0	100	100
9	f	123/134 (92%)	123 (100%)	0	100	100
10	g	101/129 (78%)	88 (87%)	13 (13%)	4	15
11	h	102/110 (93%)	102 (100%)	0	100	100
12	i	126/128 (98%)	126 (100%)	0	100	100
13	j	103/103 (100%)	103 (100%)	0	100	100
14	k	123/126 (98%)	123 (100%)	0	100	100
15	l	113/115 (98%)	113 (100%)	0	100	100
16	m	105/109 (96%)	105 (100%)	0	100	100
17	n	96/99 (97%)	96 (100%)	0	100	100
18	o	101/105 (96%)	101 (100%)	0	100	100
19	p	100/108 (93%)	100 (100%)	0	100	100
20	q	90/91 (99%)	90 (100%)	0	100	100
21	r	116/132 (88%)	116 (100%)	0	100	100
22	s	82/208 (39%)	82 (100%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	t	96/96 (100%)	96 (100%)	0	100	100
24	u	69/85 (81%)	69 (100%)	0	100	100
25	v	58/60 (97%)	58 (100%)	0	100	100
26	w	87/98 (89%)	87 (100%)	0	100	100
27	x	41/86 (48%)	41 (100%)	0	100	100
28	y	48/49 (98%)	45 (94%)	3 (6%)	16	37
29	z	47/50 (94%)	47 (100%)	0	100	100
All	All	2965/3321 (89%)	2949 (100%)	16 (0%)	78	83

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	y	51	LEU
28	y	47	MET
10	g	88	GLU
10	g	116	ARG
10	g	86	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
23	t	17	ASN
24	u	54	GLN
25	v	34	GLN
8	e	21	GLN
8	e	6	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	3	2875/2907 (98%)	844 (29%)	34 (1%)
31	4	103/108 (95%)	42 (40%)	3 (2%)
All	All	2978/3015 (98%)	886 (29%)	37 (1%)

5 of 886 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	3	12	A
30	3	14	U
30	3	15	A
30	3	20	C
30	3	27	U

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	3	2506	C
31	4	54	U
30	3	2668	A
30	3	2862	U
30	3	1048	A

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

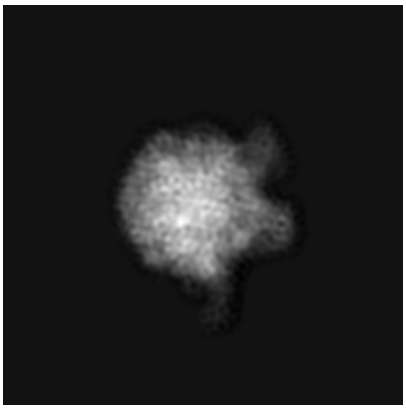
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13285. These allow visual inspection of the internal detail of the map and identification of artifacts.

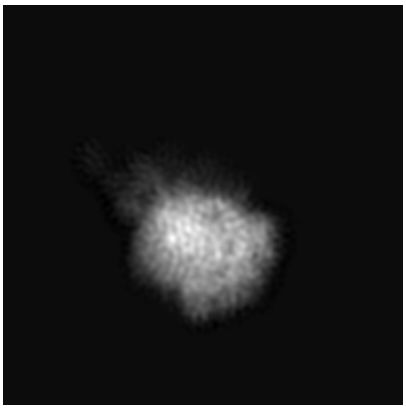
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

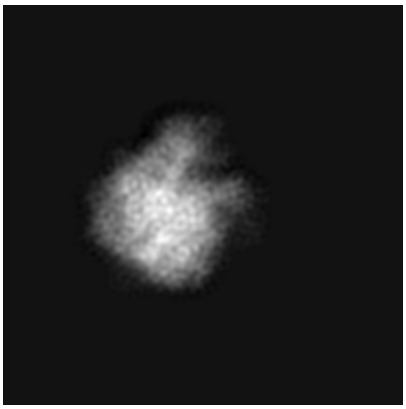
6.1.1 Primary map



X

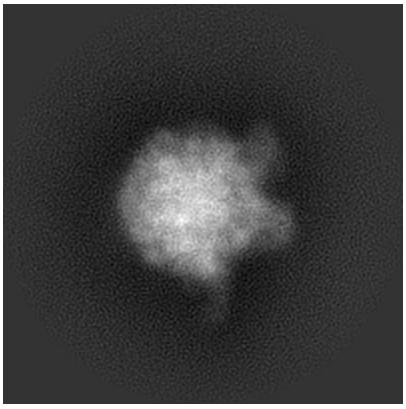


Y

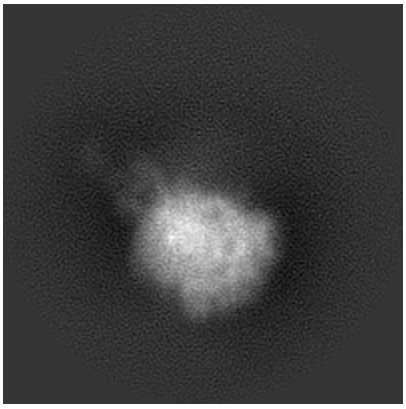


Z

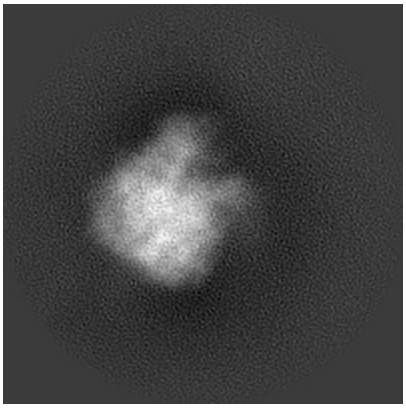
6.1.2 Raw map



X



Y

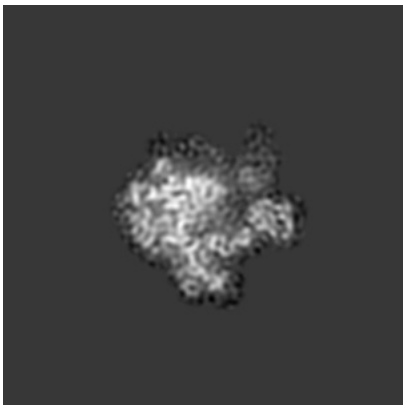


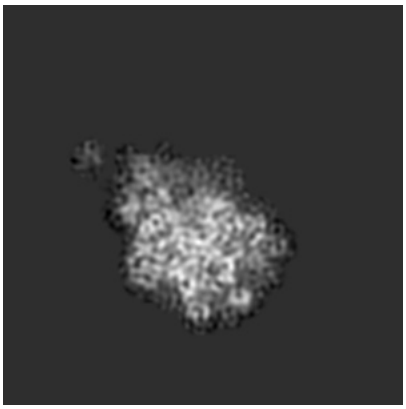
Z

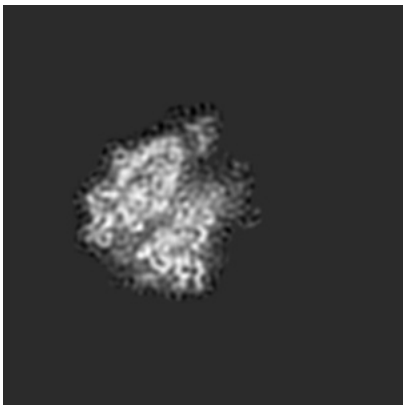
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

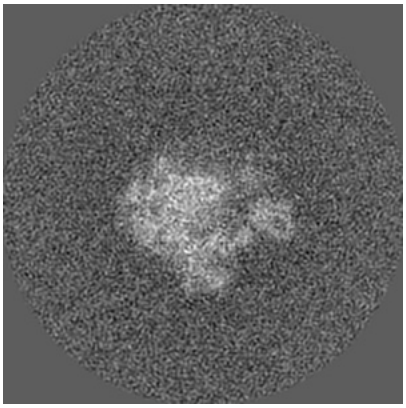
6.2.1 Primary map

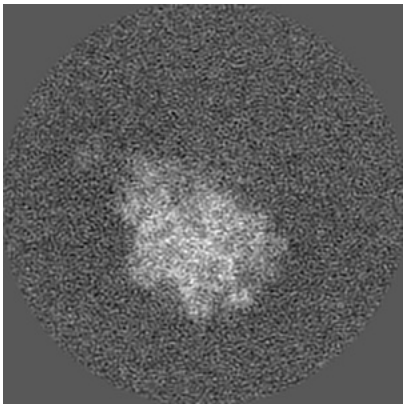

X Index: 100

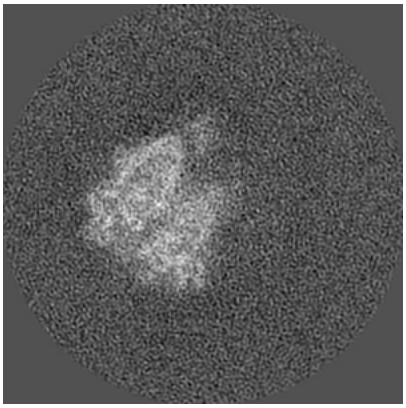

Y Index: 100


Z Index: 100

6.2.2 Raw map


X Index: 100

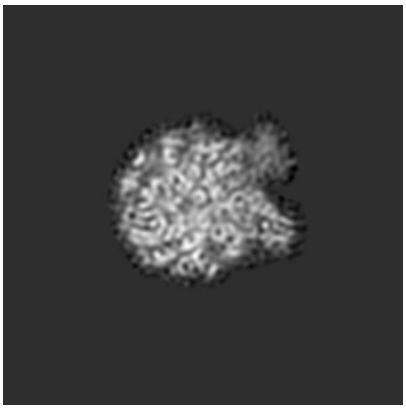

Y Index: 100


Z Index: 100

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

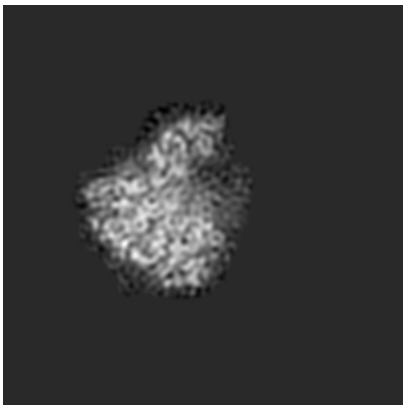
6.3 Largest variance slices (i)

6.3.1 Primary map



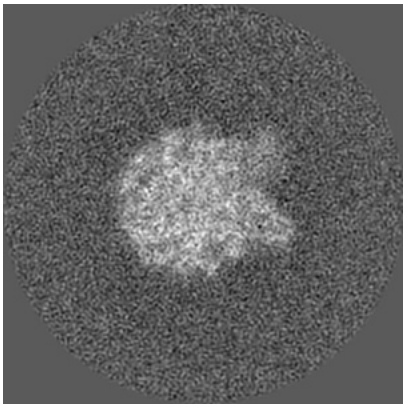
X Index: 83

Y Index: 89

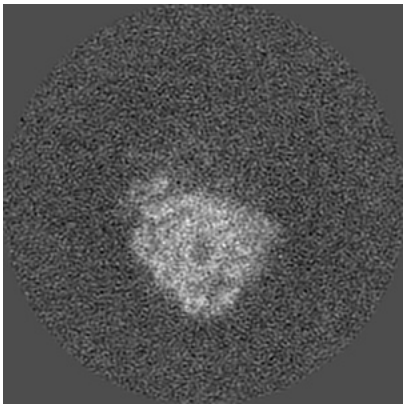


Z Index: 94

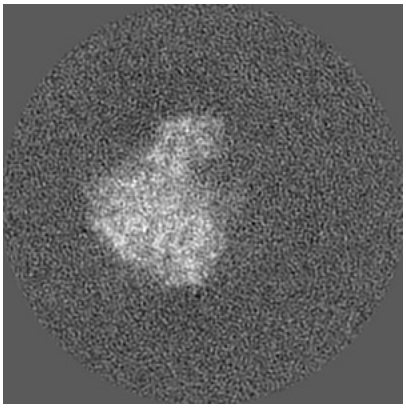
6.3.2 Raw map



X Index: 83



Y Index: 89



Z Index: 93

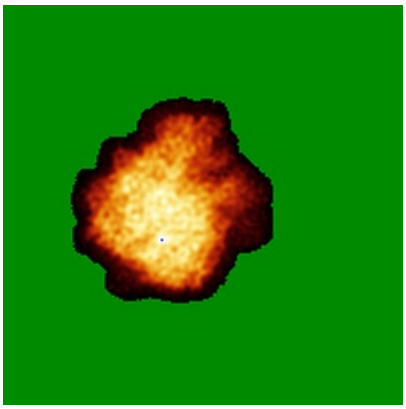
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map

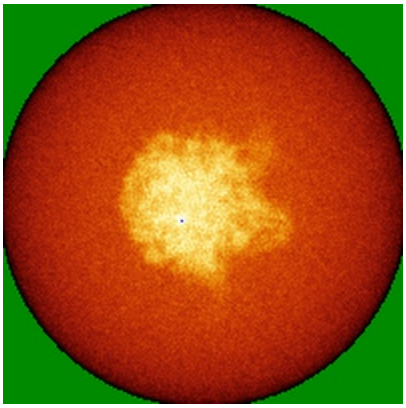
X

Y

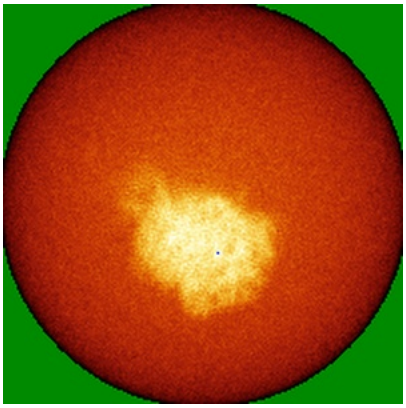


Z

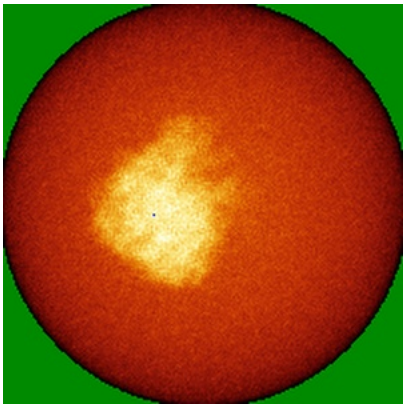
6.4.2 Raw map



X



Y

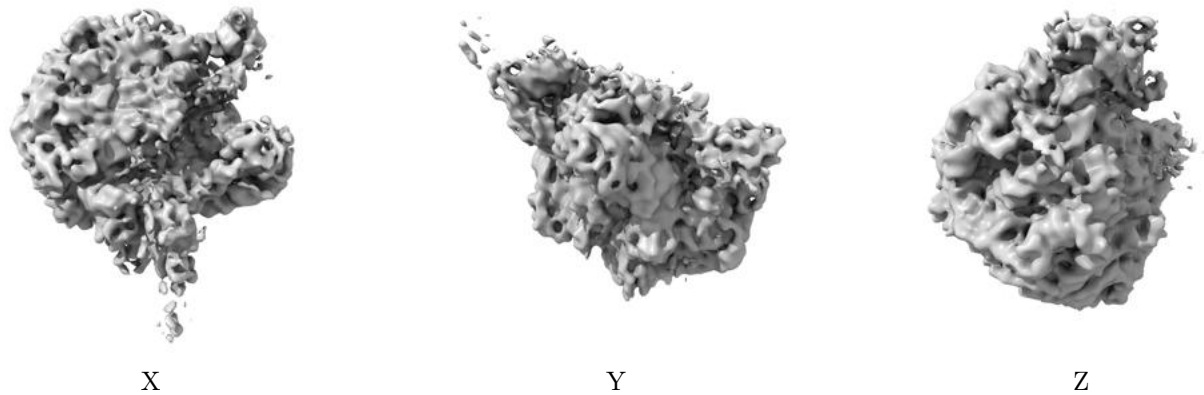


Z

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.

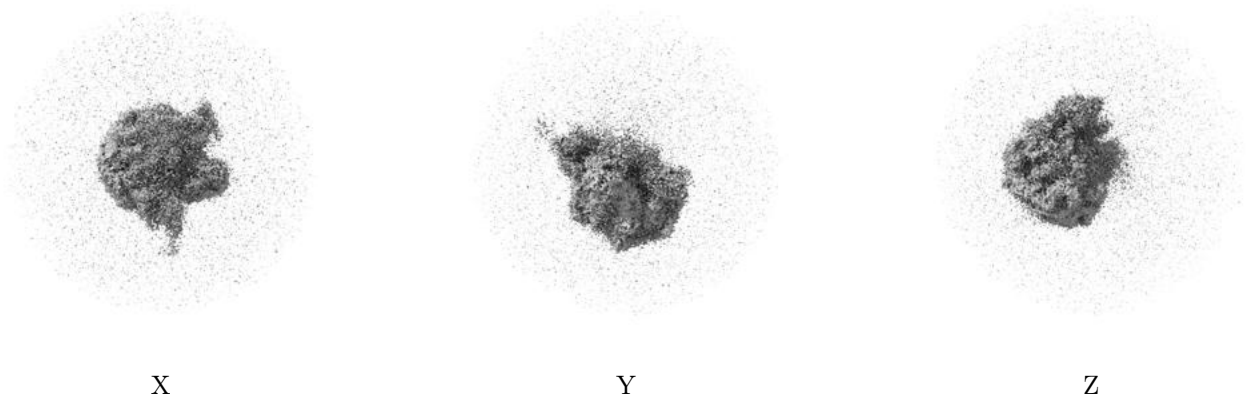
6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.41. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

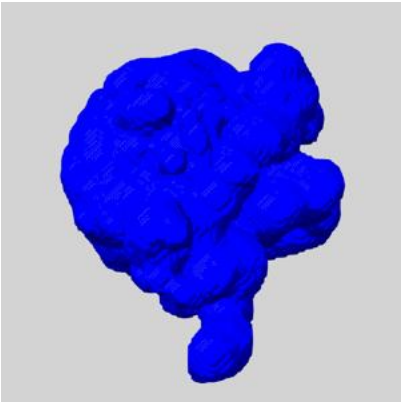
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

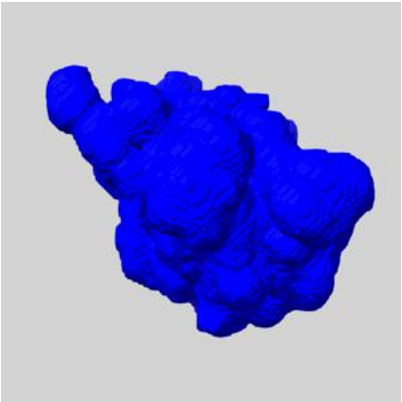
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

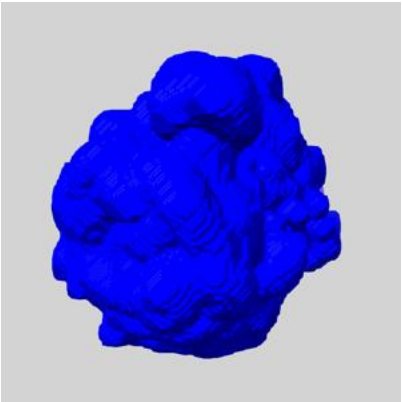
6.6.1 emd_13285_msk_1.map (i)



X



Y

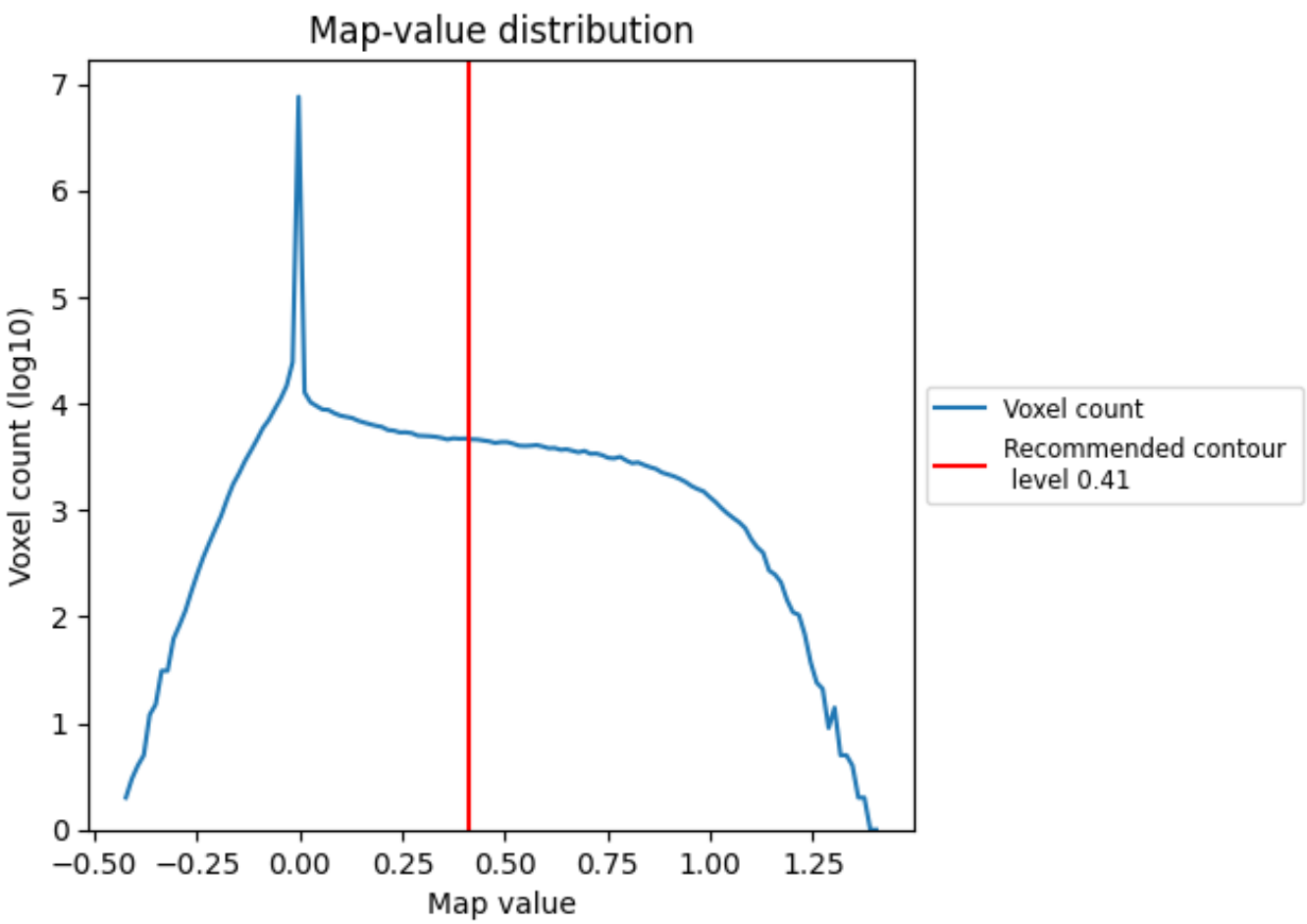


Z

7 Map analysis (i)

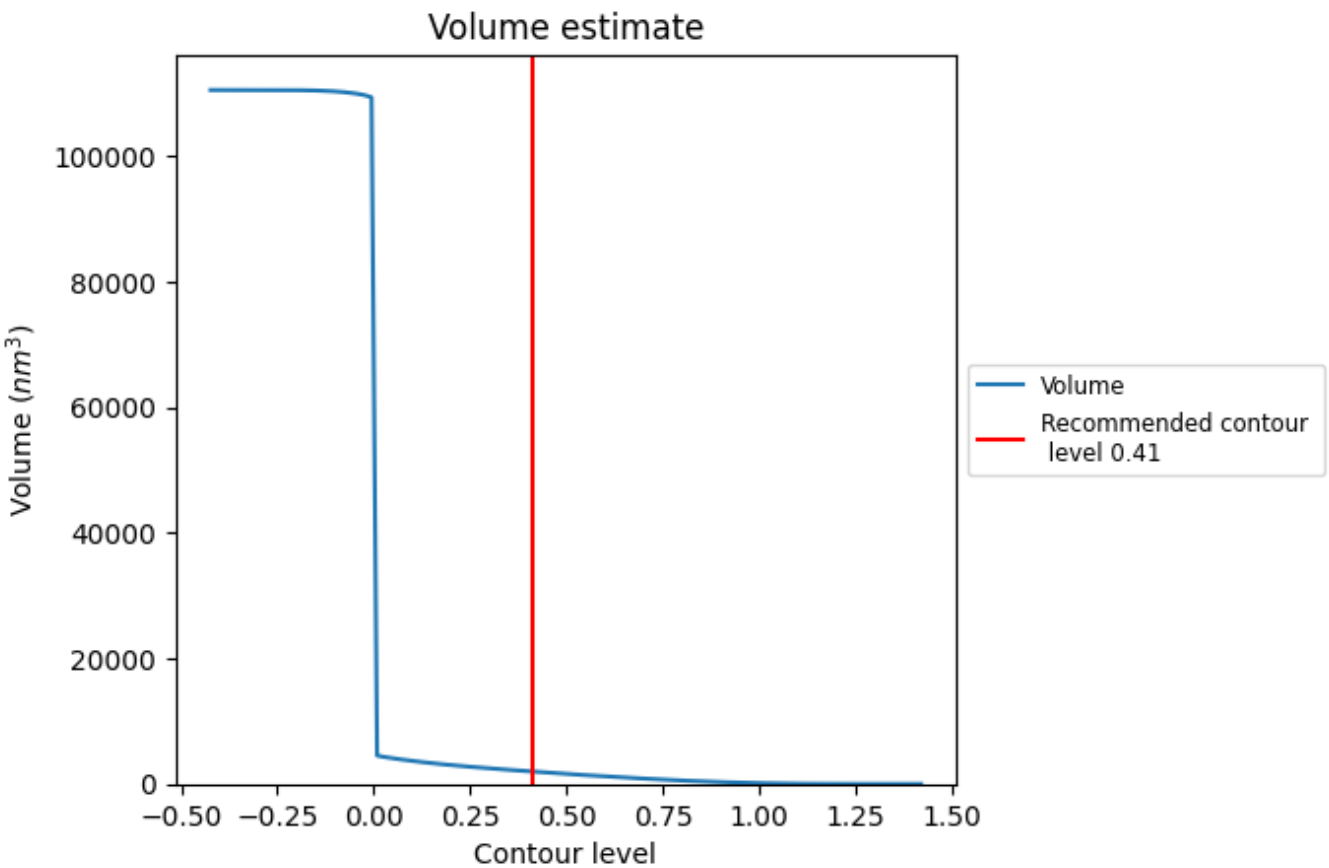
This section contains the results of statistical analysis of the map.

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.

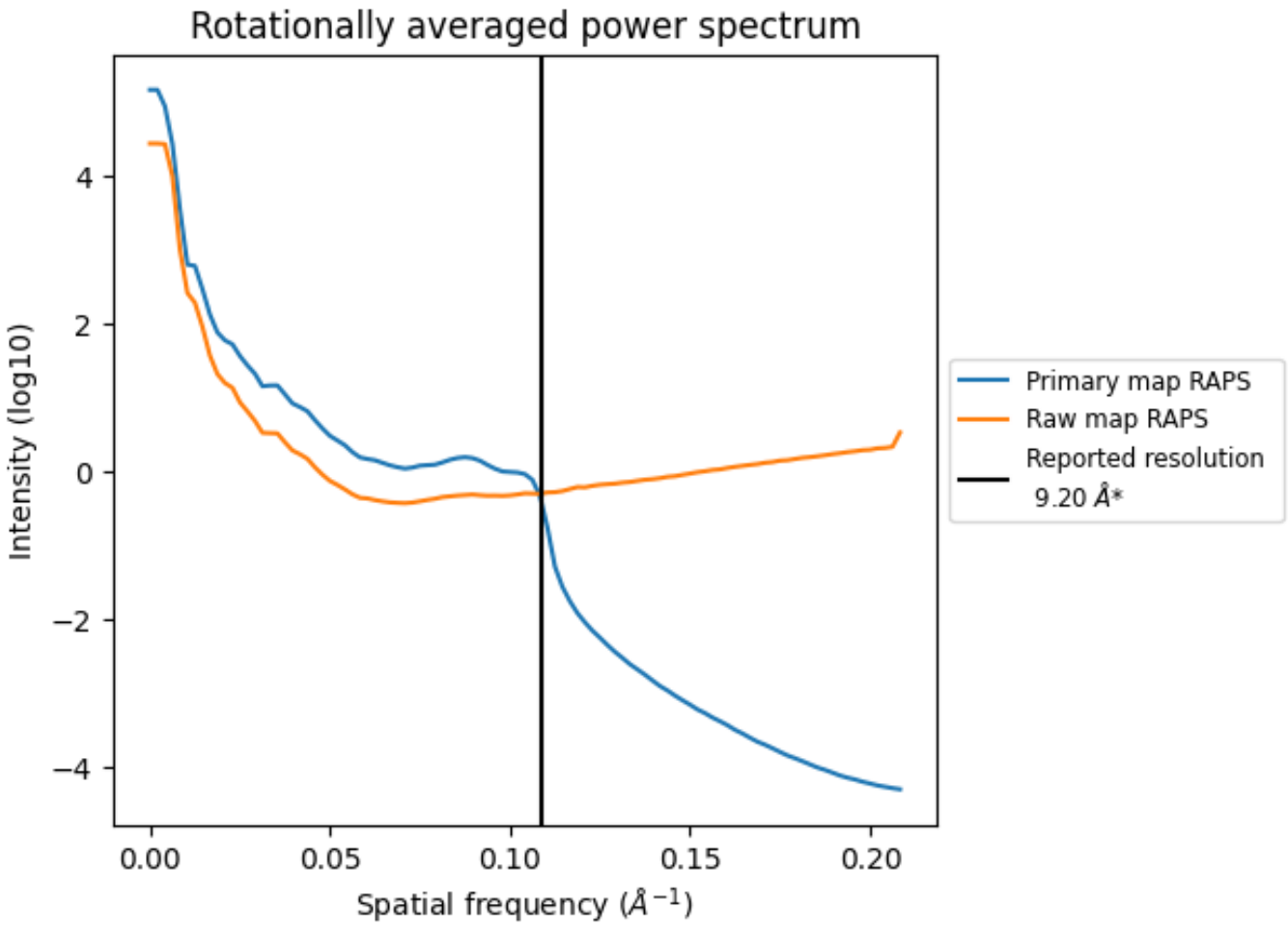
7.2 Volume estimate (i)



The volume at the recommended contour level is 1985 nm^3; this corresponds to an approximate mass of 1793 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)

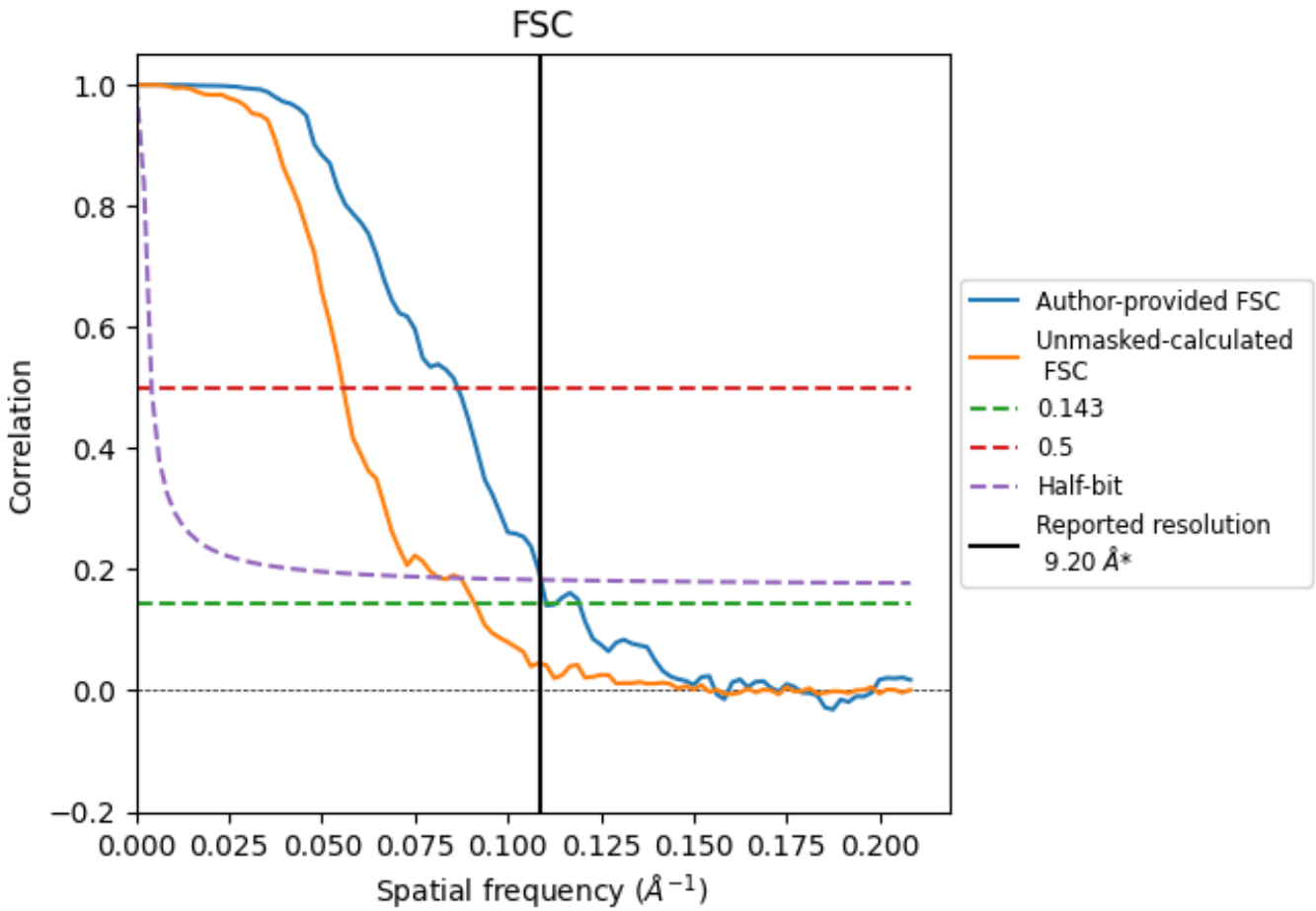


*Reported resolution corresponds to spatial frequency of 0.109 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.109 Å^{-1}

8.2 Resolution estimates (i)

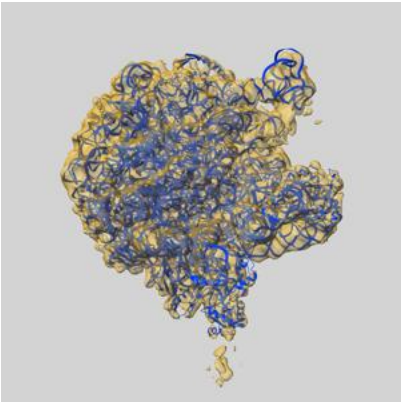
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.20	-	-
Author-provided FSC curve	9.07	11.56	9.18
Unmasked-calculated*	10.98	17.95	12.29

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 10.98 differs from the reported value 9.2 by more than 10 %

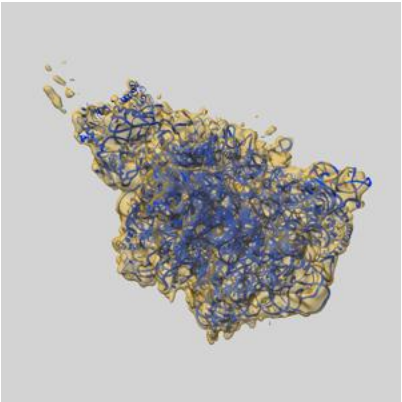
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-13285 and PDB model 7PAT. Per-residue inclusion information can be found in section 3 on page 10.

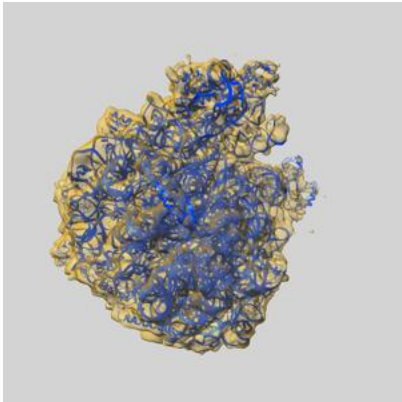
9.1 Map-model overlay (i)



X



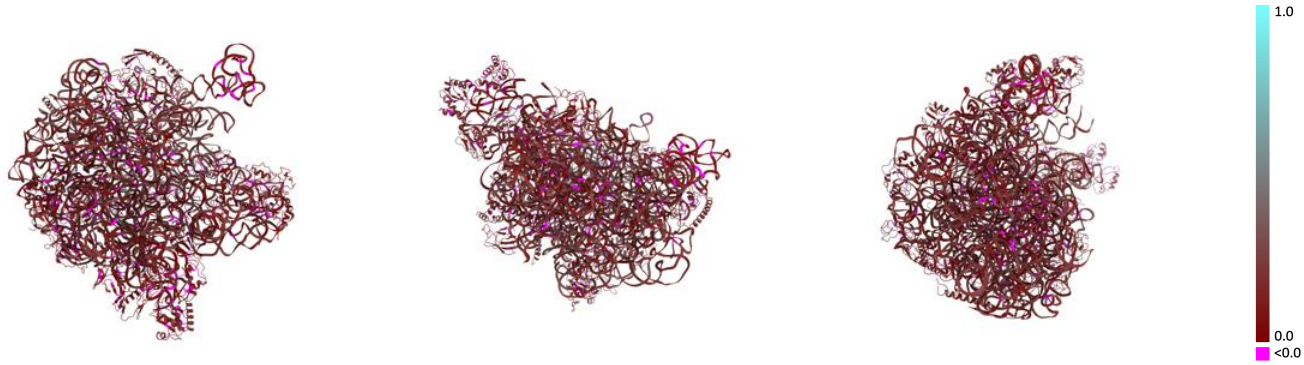
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.41 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.

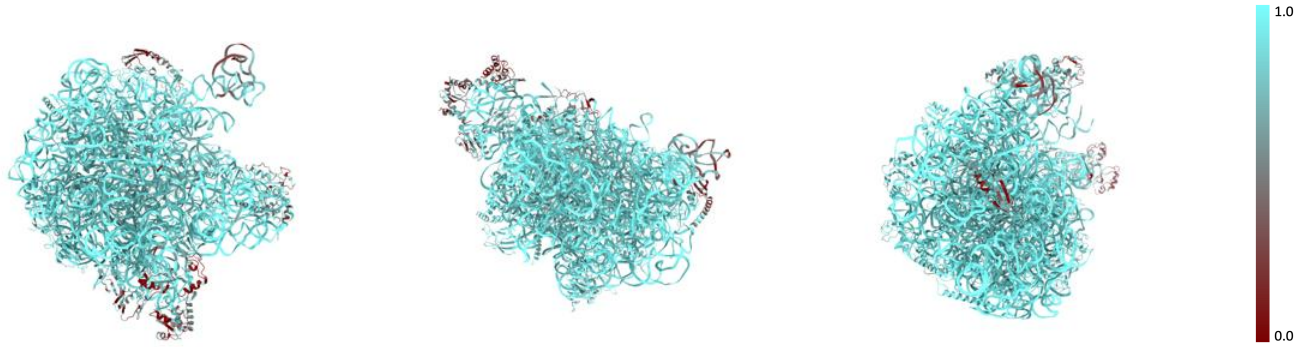
9.2 Q-score mapped to coordinate model (i)



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.

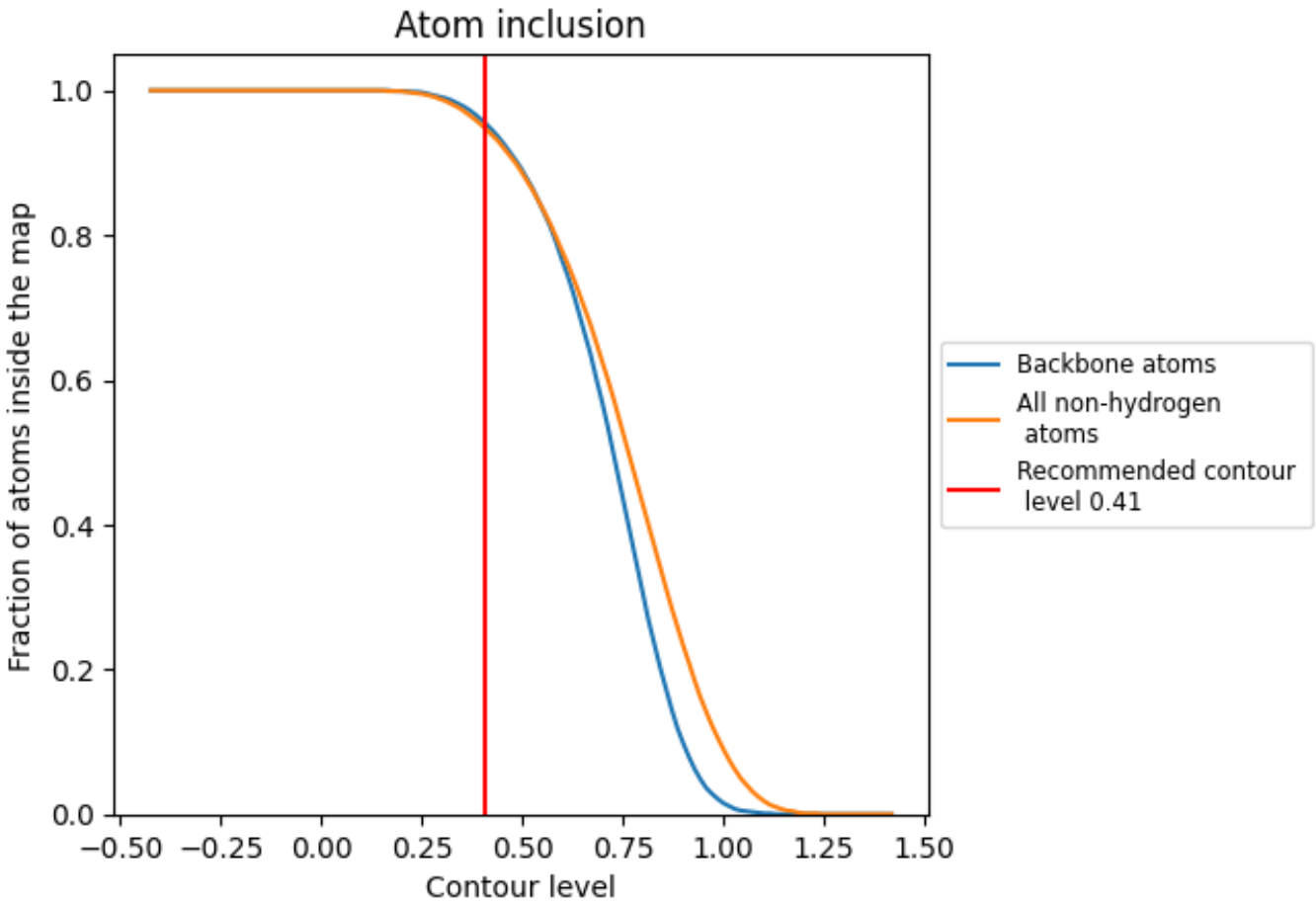
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.41).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 95% 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 (0.41) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9470	0.1570
0	0.9950	0.1330
1	0.9850	0.1160
2	0.9560	0.0860
3	0.9830	0.1680
4	0.9640	0.1800
a	0.9840	0.1170
b	0.9490	0.1070
c	0.9320	0.1350
d	0.7000	0.1380
e	0.6600	0.1340
f	0.5750	0.1350
g	0.4890	0.1510
h	0.3630	0.1220
i	0.9740	0.1400
j	0.9460	0.1300
k	0.9580	0.1280
l	0.9370	0.1280
m	0.9750	0.1290
n	0.8130	0.1410
o	0.9000	0.1440
p	0.9650	0.1200
q	0.9260	0.1390
r	0.9890	0.1490
s	0.9790	0.1430
t	0.8750	0.1210
u	0.9560	0.1070
v	0.9980	0.1150
w	0.9300	0.1780
x	0.4900	0.1520
y	0.9860	0.1100
z	0.9850	0.1180