Full wwPDB EM Validation Report

Oct 8, 2024 – 01:03 PM EDT

PDB ID	:	9AXU
EMDB ID	:	EMD-43973
Title	:	Non-translating S. pombe ribosome large subunit
Authors	:	Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.
Deposited on	:	2024-03-06
Resolution	:	1.94 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

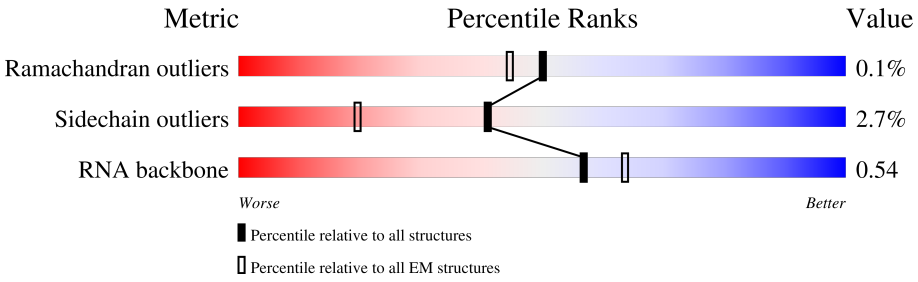
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 1.94 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	106	20% 84% · 12%
2	1	94	10% 98% ··
3	2	3498	21% 71% 19% · 8%
4	3	246	· 41% 6% · 52%
5	4	165	10% 79% 16% · 5%
6	N	253	· 96% ··
7	O	388	5% 97% ··
8	P	363	5% 96% ·

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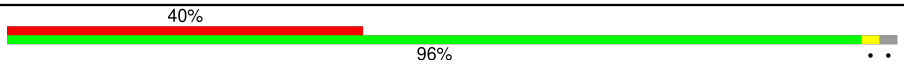
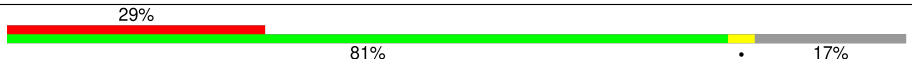
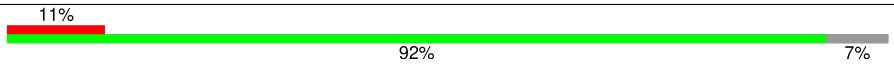
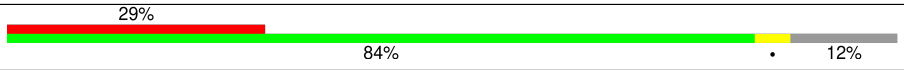
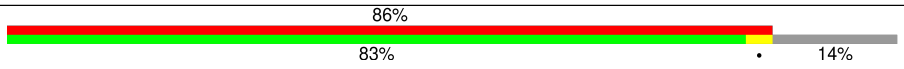
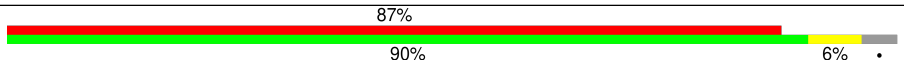
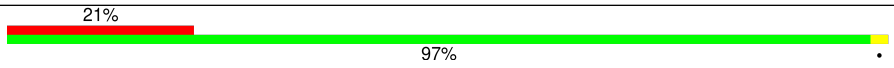
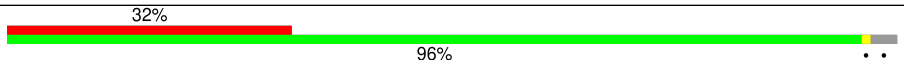
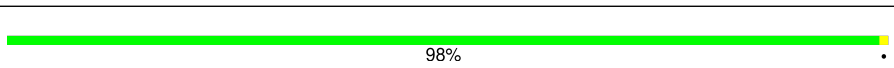
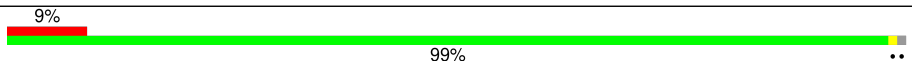
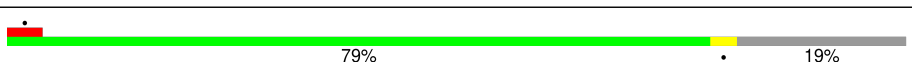
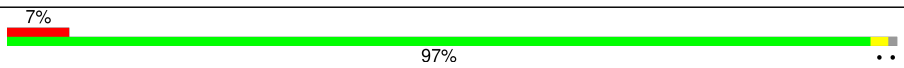
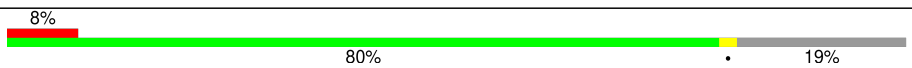
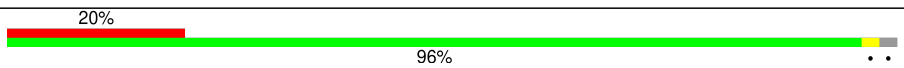
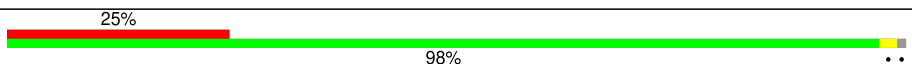
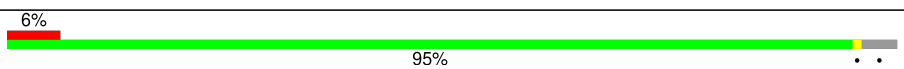
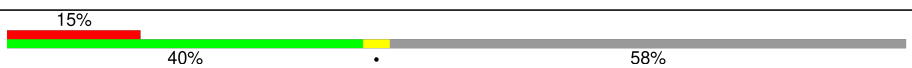
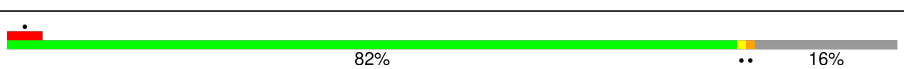
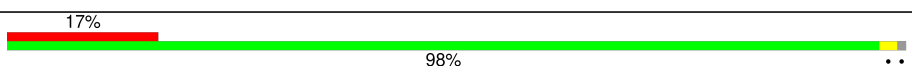
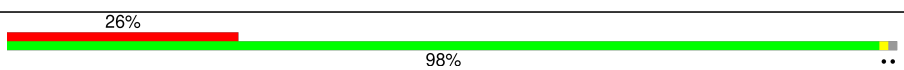
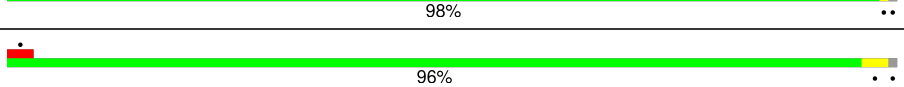
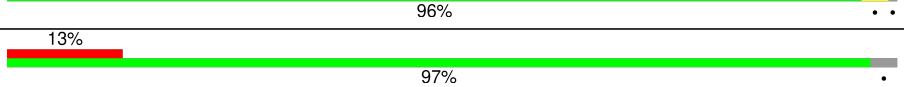
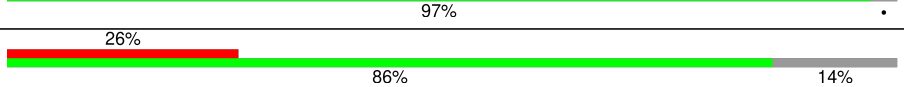
Mol	Chain	Length	Quality of chain
9	Q	294	
10	R	195	
11	S	251	
12	T	259	
13	U	189	
14	V	221	
15	W	174	
16	X	208	
17	Y	134	
18	Z	201	
19	a	197	
20	b	187	
21	c	187	
22	d	193	
23	e	176	
24	f	160	
25	g	117	
26	h	139	
27	i	149	
28	j	141	
29	k	126	
30	l	136	
31	m	148	
32	n	61	
33	o	109	

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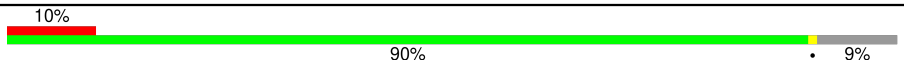
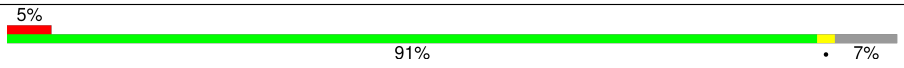
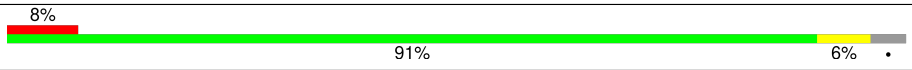
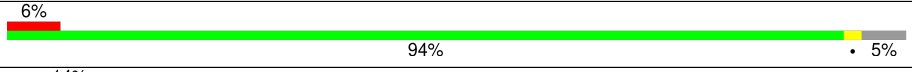
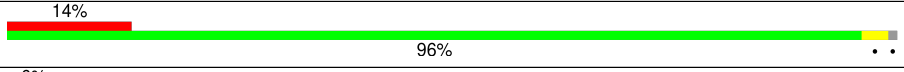
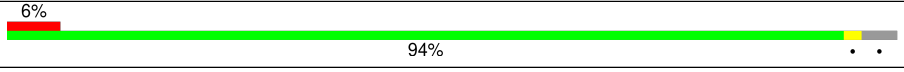
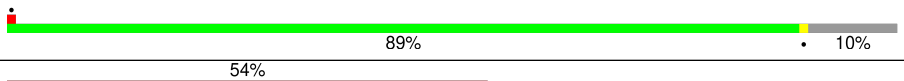
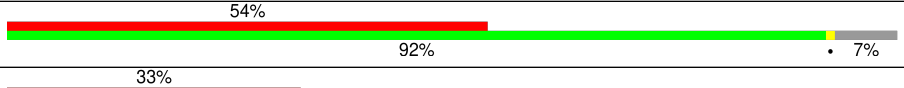
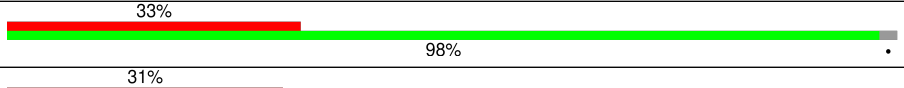
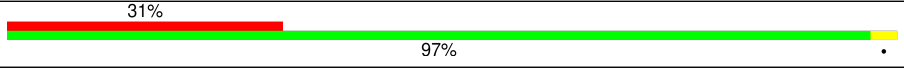
Mol	Chain	Length	Quality of chain
34	p	113	
35	q	127	
36	r	108	
37	s	111	
38	t	122	
39	u	99	
40	v	91	
41	w	74	
42	x	51	
43	y	134	

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 123561 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 Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	93	758	479	152	122	5	0	0

- Molecule 2 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	93	718	442	147	123	6	0	0

- Molecule 3 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	3212	68676	30687	12377	22400	3212	0	0

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	3	119	2539	1133	454	833	119	0	0

- Molecule 5 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	4	157	3332	1491	583	1101	157	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	N	248	1872	1166	377	324	5	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	384	Total	C	N	O	S	0	0
			3050	1929	576	535	10		

- Molecule 8 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	362	Total	C	N	O	S	0	0
			2799	1768	538	490	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	287	Total	C	N	O	S	0	0
			2312	1461	410	437	4		

- Molecule 10 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	R	162	Total	C	N	O	S	0	0
			1251	802	231	215	3		

- Molecule 11 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	S	233	Total	C	N	O	S	0	0
			1897	1211	349	334	3		

- Molecule 12 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	T	229	Total	C	N	O	S	0	0
			1772	1135	325	309	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	U	168	Total	C	N	O	S	0	0
			1319	828	244	242	5		

- Molecule 14 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	V	191	Total	C	N	O	S	0	0
			1549	982	291	270	6		

- Molecule 15 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	W	167	Total	C	N	O	S	0	0
			1346	854	252	235	5		

- Molecule 16 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	X	207	Total	C	N	O	S	0	0
			1654	1034	329	290	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Y	130	Total	C	N	O	S	0	0
			1038	662	198	174	4		

- Molecule 18 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Z	200	Total	C	N	O	S	0	0
			1676	1050	348	275	3		

- Molecule 19 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	a	196	Total	C	N	O	S	0	0
			1545	991	294	256	4		

- Molecule 20 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	b	152	Total	C	N	O	S	0	0
			1212	770	229	210	3		

- Molecule 21 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	c	186	Total	C	N	O	0	0
			1487	937	300	250		

- Molecule 22 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	157	Total	C	N	O	S	0	0
			1301	809	275	212	5		

- Molecule 23 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	e	173	Total	C	N	O	S	0	0
			1423	916	268	234	5		

- Molecule 24 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	f	159	Total	C	N	O	S	0	0
			1286	810	247	226	3		

- Molecule 25 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	g	99	Total	C	N	O	0	0
			798	518	138	142		

- Molecule 26 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	h	134	Total	C	N	O	S	0	0
			999	630	184	177	8		

- Molecule 27 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	63	Total	C	N	O	S	0	0
			523	336	102	82	3		

- Molecule 28 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	118	Total 947	C 605	N 175	O 166	S 1	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 30 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	l	135	Total 1078	C 698	N 200	O 178	S 2	0	0

- Molecule 31 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	m	147	Total 1171	C 740	N 235	O 194	S 2	0	0

- Molecule 32 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	n	59	Total 495	C 299	N 112	O 84	0	0

- Molecule 33 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	94	Total 705	C 450	N 121	O 130	S 4	0	0

- Molecule 34 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	p	103	Total 857	C 538	N 167	O 149	S 3	0	0

- Molecule 35 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	q	118	Total	C	N	O	S	0	0
			944	591	191	157	5		

- Molecule 36 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	r	104	Total	C	N	O	S	0	0
			831	531	160	137	3		

- Molecule 37 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	s	106	Total	C	N	O	S	0	0
			858	538	176	142	2		

- Molecule 38 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	t	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 39 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	u	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 40 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	v	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 41 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	w	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 42 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	x	50	Total	C	N	O	S	0	0
			436	273	98	64	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	y	134	Total	C	N	O	S	0	0
			1039	646	204	187	2		

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

Mol	Chain	Residues	Atoms		AltConf
44	0	1	Total	Zn	0
			1	1	
44	1	1	Total	Zn	0
			1	1	
44	v	1	Total	Zn	0
			1	1	

- Molecule 45 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

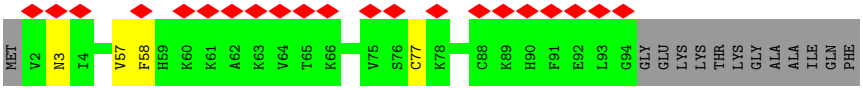
Mol	Chain	Residues	Atoms		AltConf
45	2	91	Total	Mg	0
			91	91	
45	3	2	Total	Mg	0
			2	2	
45	4	1	Total	Mg	0
			1	1	
45	b	1	Total	Mg	0
			1	1	
45	h	1	Total	Mg	0
			1	1	
45	q	1	Total	Mg	0
			1	1	

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.

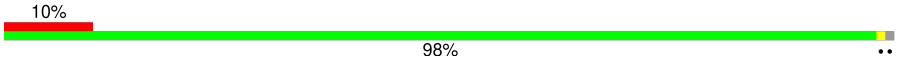
• Molecule 1: Large ribosomal subunit protein eL42

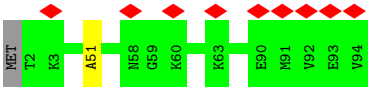
Chain 0:



• Molecule 2: Large ribosomal subunit protein eL43A

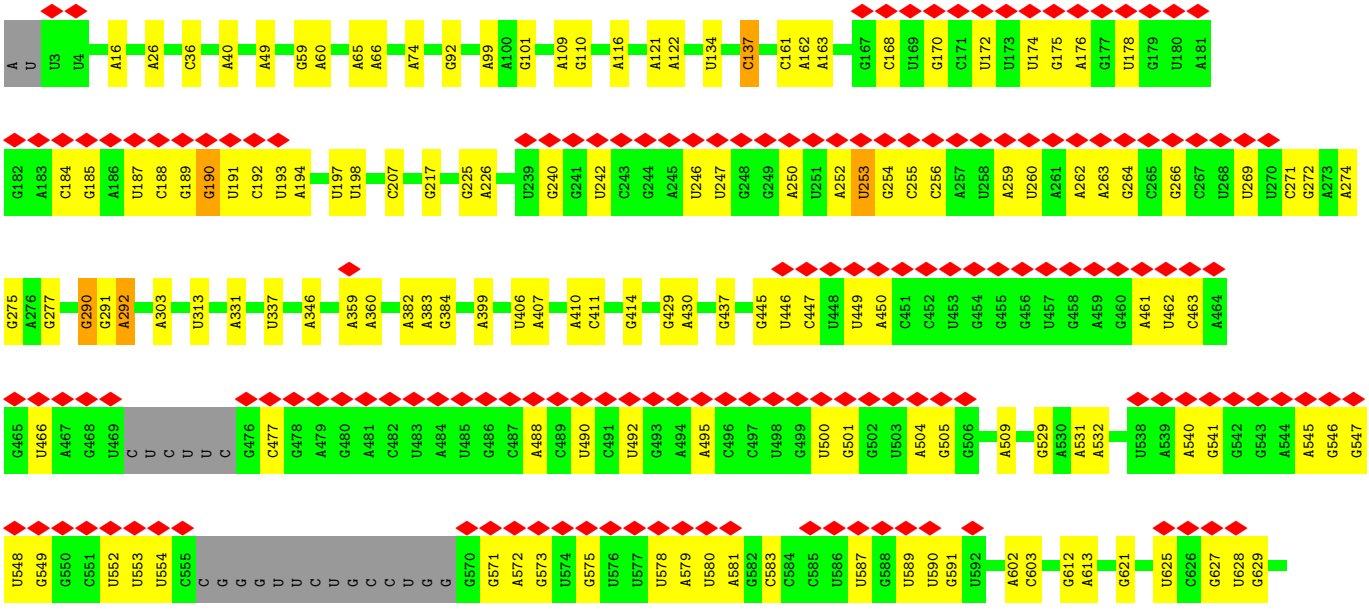
Chain 1:

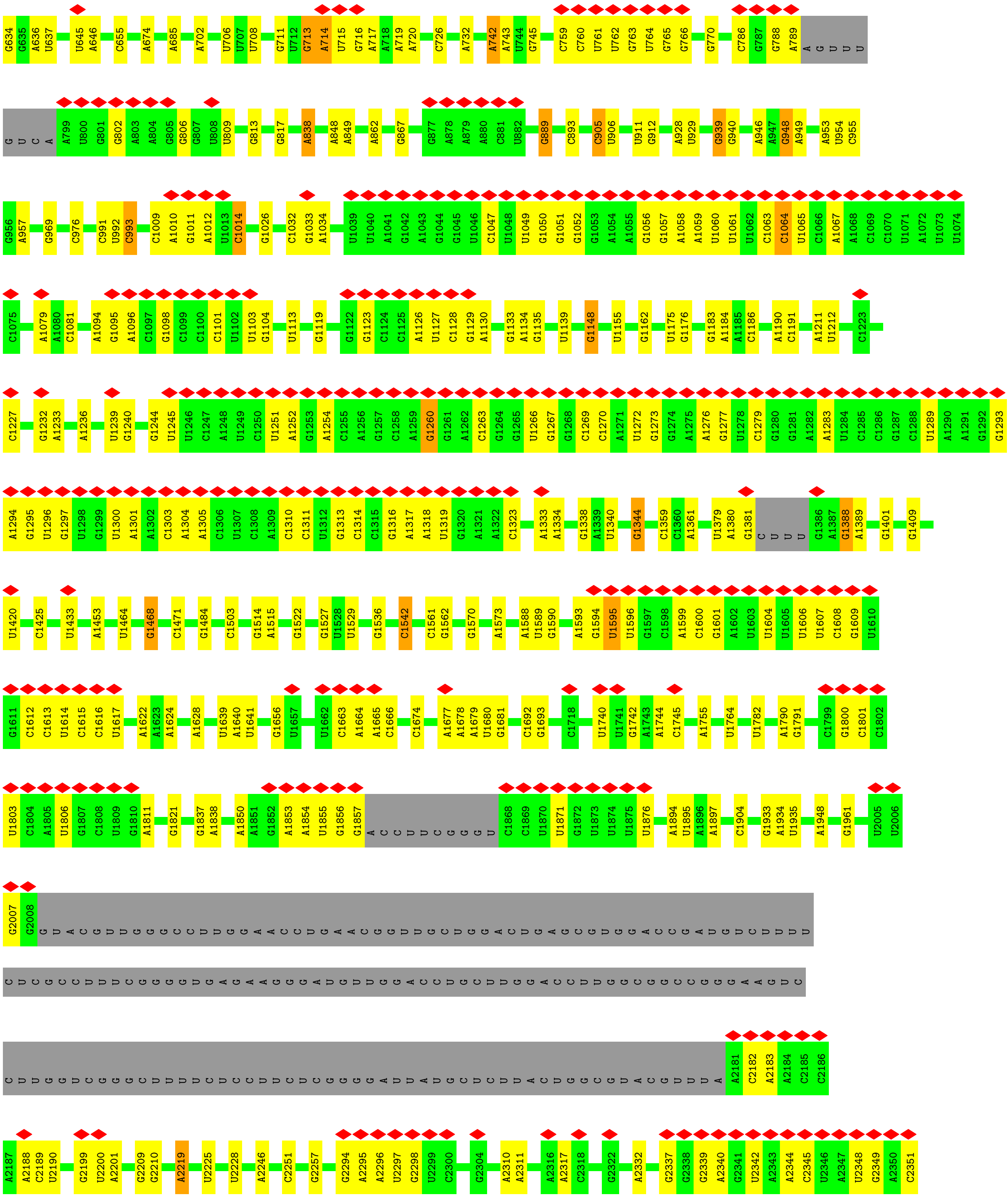


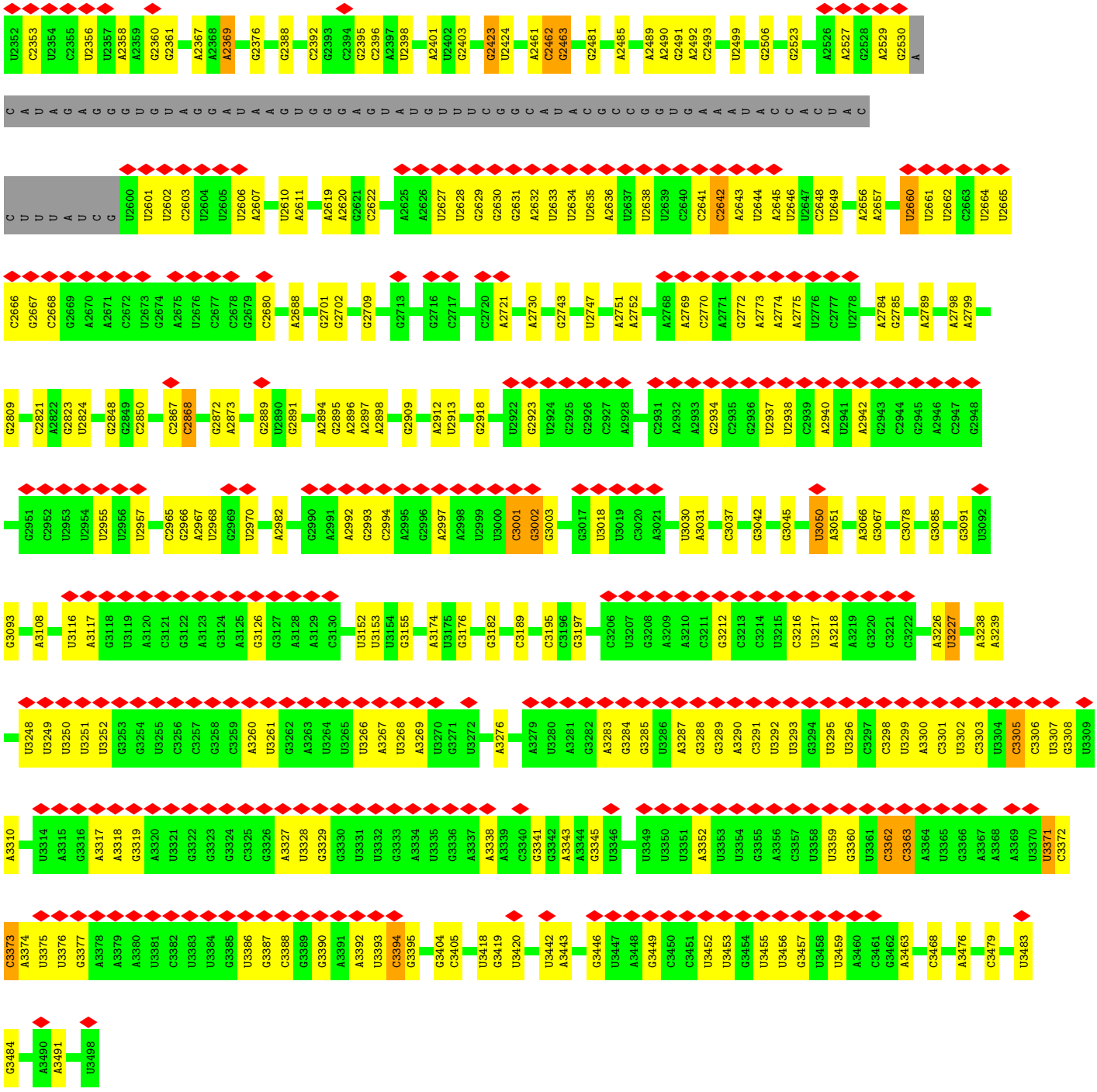


• Molecule 3: 28S ribosomal RNA

Chain 2:

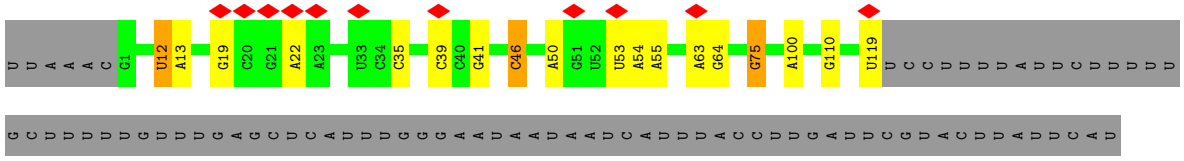



G634 G635 A636 U637 U645 A646 C655 A674 A685 A702 U706 U707 U708 G711 U712 G713 A714 U715 G716 A717 A718 A719 A720 C726 A732 A742 A743 U744 G745 C759 C760 U761 U762 G763 U764 G765 G766 G770 C786 G787 G788 A789 A G U U U
G U C A A799 U800 G801 G802 A803 A804 G805 G806 G807 U808 U809 G813 G817 A838 A848 A849 A862 G867 G877 A878 A879 A880 C881 U882 G889 C893 C905 U906 U911 G912 A928 U929 G939 G940 A946 A947 G948 A949 A953 U954 C955
G956 A957 G969 C976 C991 U992 C993 C1009 A1010 G1011 A1012 U1013 C1014 G1026 C1032 G1033 A1034 U1039 U1040 A1041 G1042 A1043 G1044 G1045 U1046 C1047 U1048 U1049 G1050 G1051 C1052 G1053 A1054 A1055 G1056 G1057 A1058 A1059 U1060 U1061 U1062 C1063 C1064 U1065 C1066 A1067 A1068 C1069 C1070 U1071 A1072 U1073 U1074
C1075 A1079 A1080 C1081 A1094 G1095 A1096 C1097 G1098 C1099 C1100 C1101 U1102 U1103 G1104 U1113 G1119 G1122 G1123 C1124 C1125 A1126 U1127 C1128 G1129 A1130 G1133 A1134 G1135 U1139 G1148 U1155 G1162 U1175 G1176 G1183 A1184 A1185 C1186 A1190 C1191 A1211 U1212 C1223
C1227 G1232 A1233 A1236 U1239 G1240 G1244 U1245 U1246 C1247 A1248 U1249 C1250 U1251 A1252 G1253 A1254 C1255 A1256 G1257 C1258 A1259 G1260 G1261 A1262 C1263 G1264 G1265 U1266 G1267 G1268 C1269 C1270 A1271 U1272 G1273 G1274 A1275 A1276 G1277 U1278 C1279 G1280 G1281 A1282 A1283 U1284 C1285 C1286 G1287 C1288 U1289 A1290 A1291 G1292 G1293
A1294 G1295 U1296 G1297 U1298 G1299 U1300 A1301 A1302 C1303 A1304 A1305 C1306 U1307 C1308 A1309 C1310 C1311 U1312 G1313 C1314 C1315 G1316 A1317 A1318 U1319 G1320 A1321 A1322 C1323 A1333 A1334 G1338 A1339 U1340 G1344 C1359 C1360 A1361 U1379 A1380 G1381 C U U U G1386 A1387 G1388 A1389 G1401 G1409
U1420 C1425 U1433 A1453 U1464 G1468 C1471 G1484 C1503 G1514 A1515 G1522 G1527 U1528 U1529 G1536 C1542 C1561 G1562 G1570 A1573 A1588 U1589 G1590 A1593 G1594 U1595 U1596 G1597 C1598 A1599 C1600 G1601 A1602 U1603 U1604 U1605 U1606 U1607 C1608 G1609 U1610
G1611 C1612 C1613 U1614 C1615 C1616 U1617 A1622 A1623 A1624 A1628 U1639 A1640 U1641 G1656 U1657 U1662 C1663 A1664 A1665 C1666 C1674 A1677 A1678 A1679 U1680 G1681 C1692 G1693 C1718 U1740 U1741 G1742 A1743 A1744 C1745 A1755 U1764 U1782 A1790 G1791 C1799 G1800 C1801 C1802
U1803 C1804 A1805 U1806 G1807 C1808 U1809 G1810 A1811 G1821 G1837 A1838 A1850 A1851 G1852 A1853 A1854 U1855 G1856 G1857 A C C U U C G G G U C1868 C1869 U1870 U1871 G1872 U1873 U1874 U1875 U1876 A1894 U1895 A1896 A1897 C1904 G1933 A1934 U1935 A1948 G1961 U2005 U2006
G2007 G2008 G U A C G U U G G G C C U U G G A A C C U G A A C G G U U G C U G G A C U G A G C G U G G A C C G A U G G U C U U U U
C U C G C C U U U C G G G G U G A G A A G G G A U G U U G G A C C U G C U U G G A C C U U G G C G G C C G G G A A G U C
C U U G G U C G G G C U U U U C U C C U U C U C G G G G A U U A U G C U C U U A C U G G C G U A C G U U U A A2181 C2182 A2183 A2184 C2185 C2186
A2187 A2188 C2189 U2190 G2199 U2200 A2201 G2209 G2210 A2219 U2225 U2228 A2246 C2251 G2257 G2294 A2295 A2296 U2297 G2298 U2299 C2300 G2304 A2310 A2311 A2316 A2317 C2318 G2322 A2332 G2337 G2338 G2339 A2340 G2341 U2342 A2343 A2344 C2345 U2346 A2347 U2348 G2349 A2350 C2351



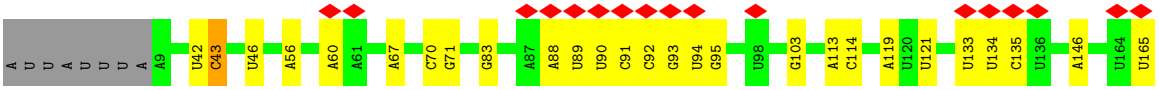
• Molecule 4: 5S ribosomal RNA

Chain 3:



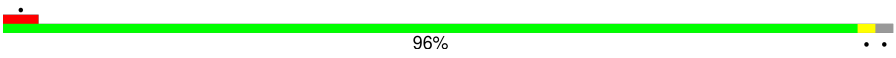
• Molecule 5: 5.8S ribosomal RNA

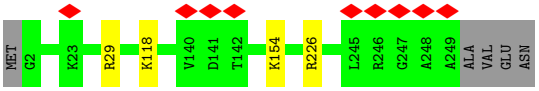
Chain 4:



• Molecule 6: Large ribosomal subunit protein uL2C

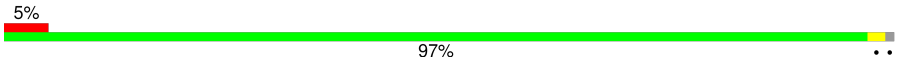
Chain N:





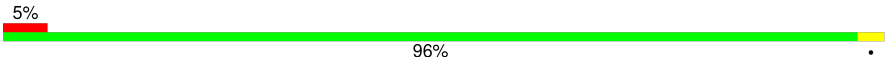
• Molecule 7: Large ribosomal subunit protein uL3A

Chain O:



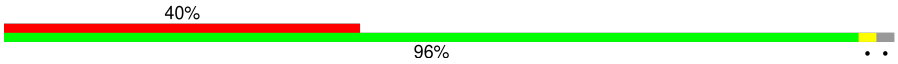
• Molecule 8: Large ribosomal subunit protein uL4A

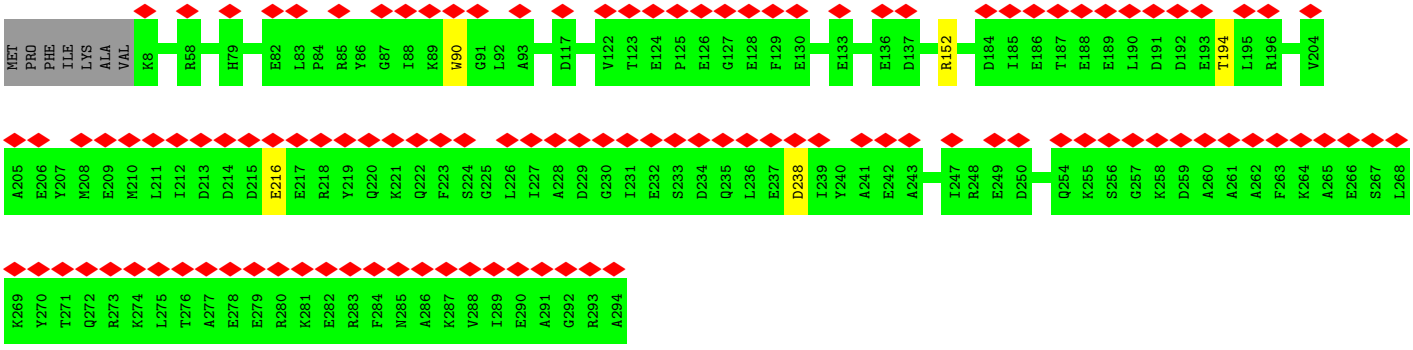
Chain P:



• Molecule 9: Large ribosomal subunit protein uL18B

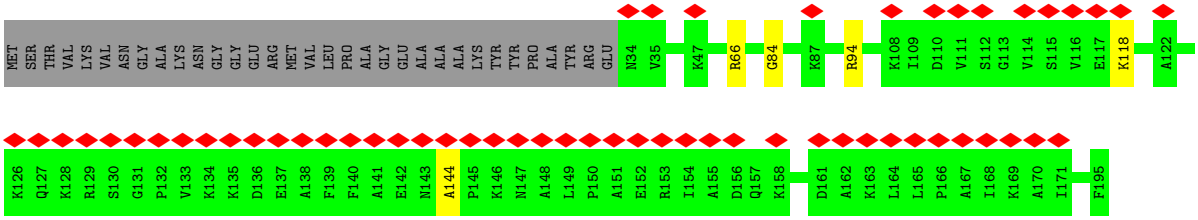
Chain Q:





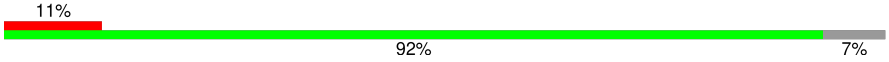
• Molecule 10: Large ribosomal subunit protein eL6

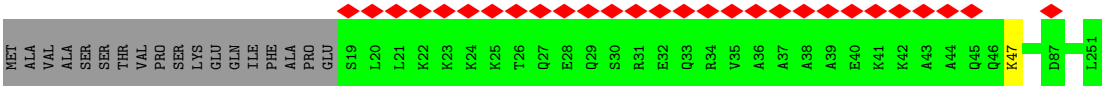
Chain R:



• Molecule 11: Large ribosomal subunit protein uL30C

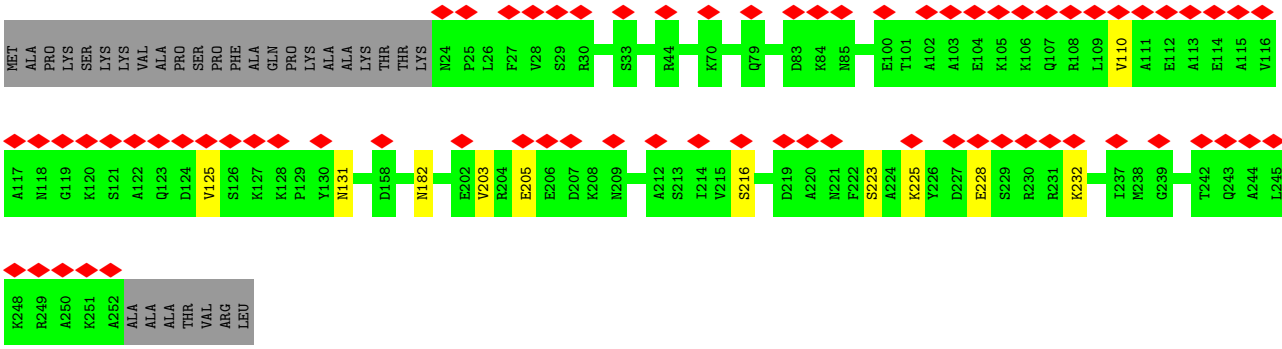
Chain S:





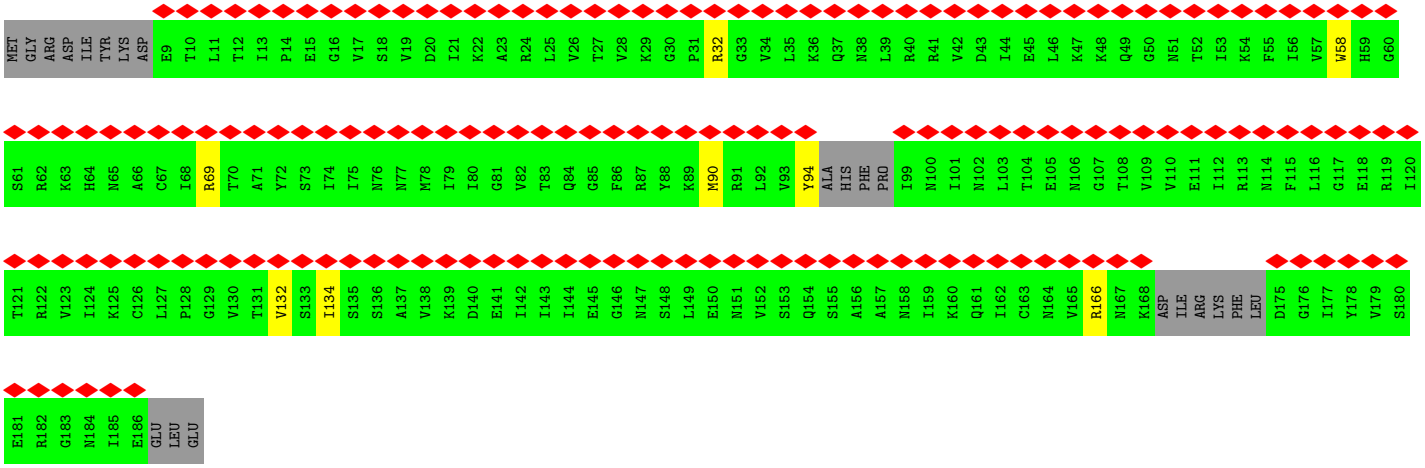
• Molecule 12: Large ribosomal subunit protein eL8

Chain T:



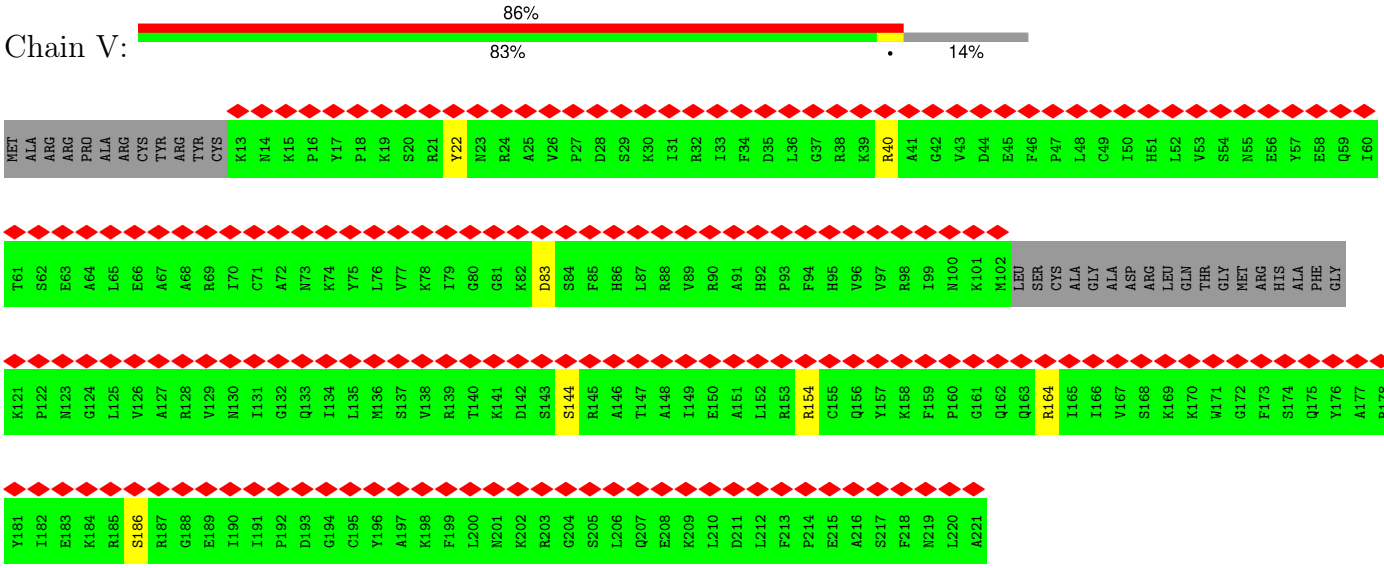
• Molecule 13: Large ribosomal subunit protein uL6B

Chain U:



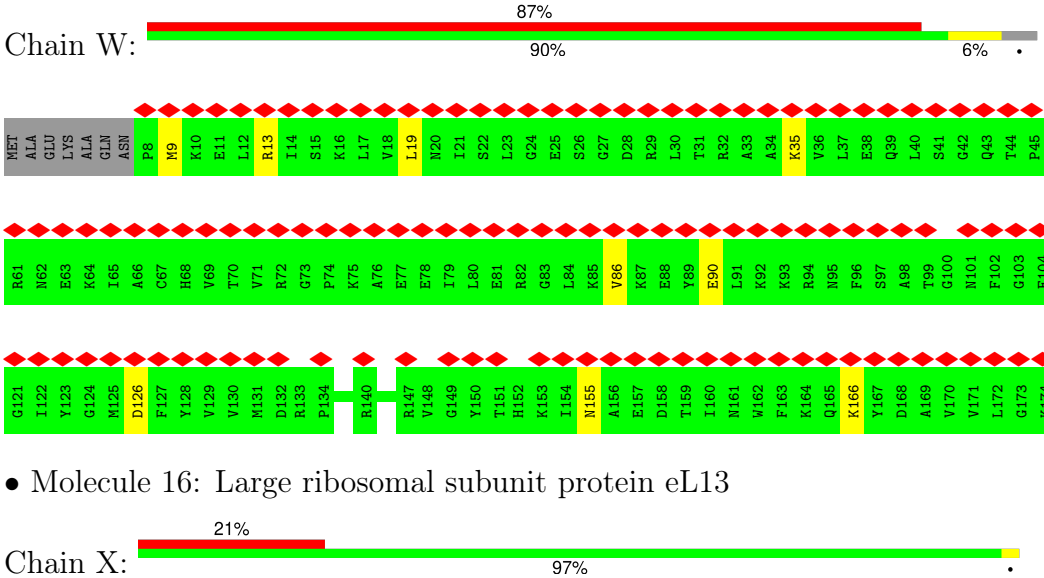
• Molecule 14: Large ribosomal subunit protein uL16A

Chain V:



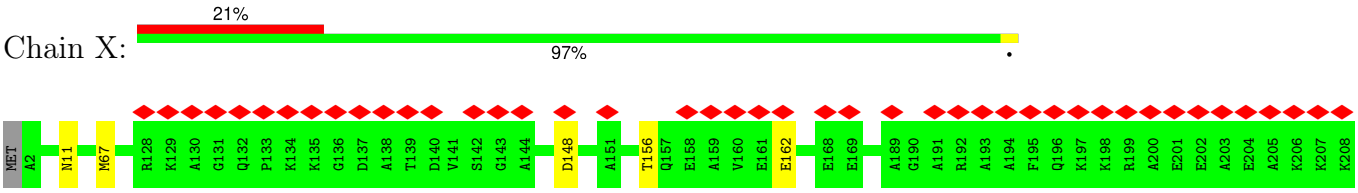
• Molecule 15: Large ribosomal subunit protein uL5A

Chain W:



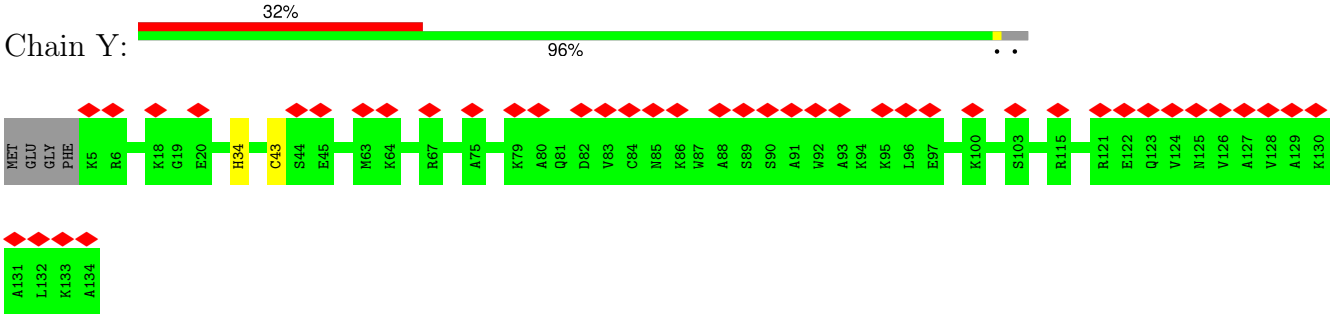
• Molecule 16: Large ribosomal subunit protein eL13

Chain X:



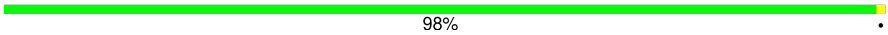
• Molecule 17: Large ribosomal subunit protein eL14

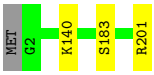
Chain Y:



• Molecule 18: Large ribosomal subunit protein eL15B

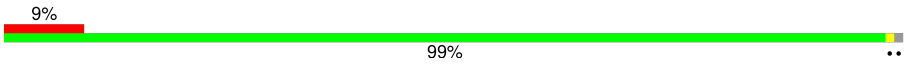
Chain Z:

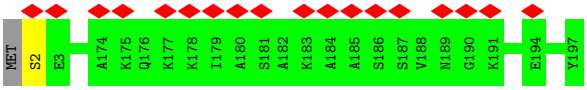




• Molecule 19: Large ribosomal subunit protein uL13A

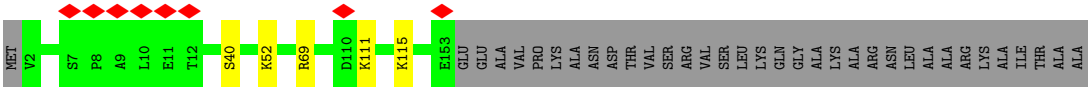
Chain a:





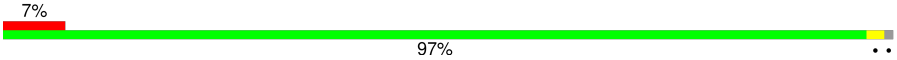
• Molecule 20: Large ribosomal subunit protein uL22A

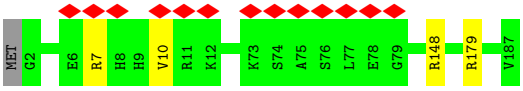
Chain b:



• Molecule 21: Large ribosomal subunit protein eL18B

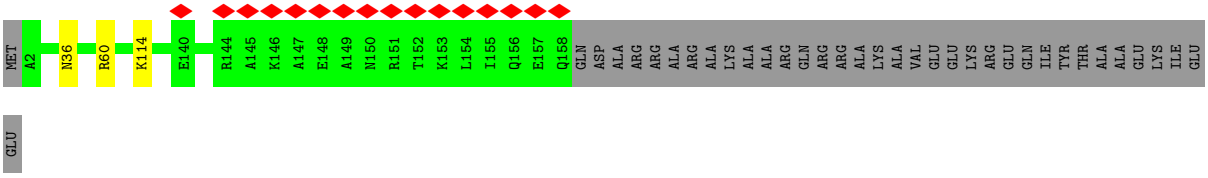
Chain c:





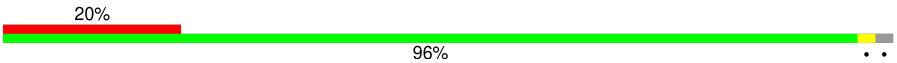
• Molecule 22: Large ribosomal subunit protein eL19B

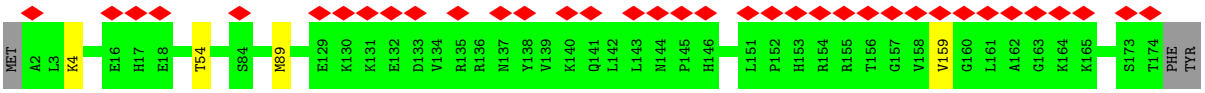
Chain d:



• Molecule 23: Large ribosomal subunit protein eL20A

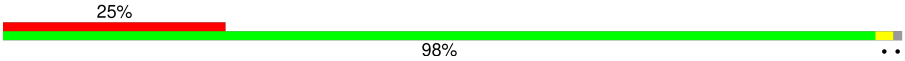
Chain e:

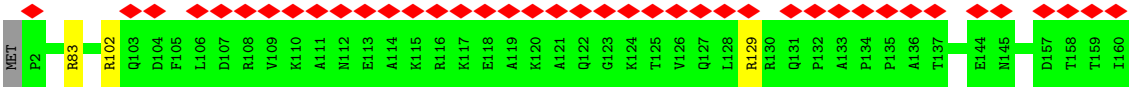




• Molecule 24: Large ribosomal subunit protein eL21B

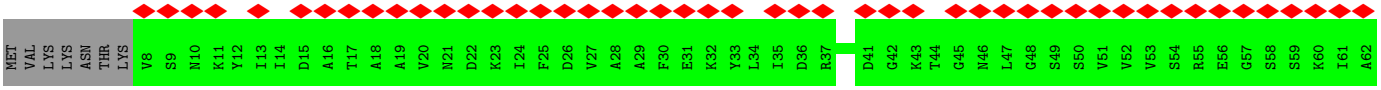
Chain f:

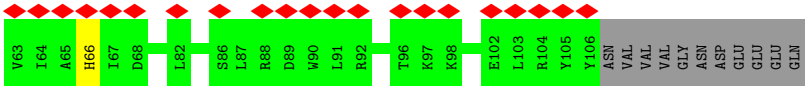




• Molecule 25: Large ribosomal subunit protein eL22

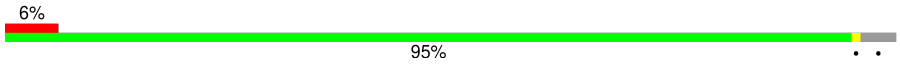
Chain g:

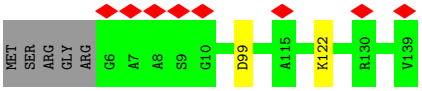




• Molecule 26: Large ribosomal subunit protein uL14B

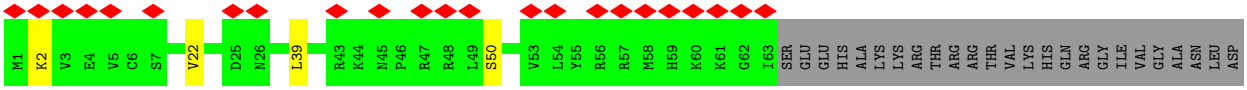
Chain h:





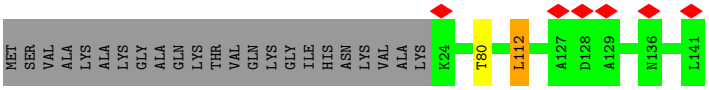
• Molecule 27: Large ribosomal subunit protein eL24B

Chain i:



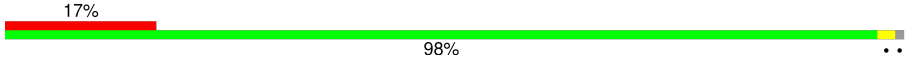
• Molecule 28: Large ribosomal subunit protein uL23A

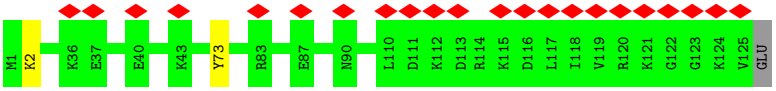
Chain j:



• Molecule 29: Large ribosomal subunit protein uL24

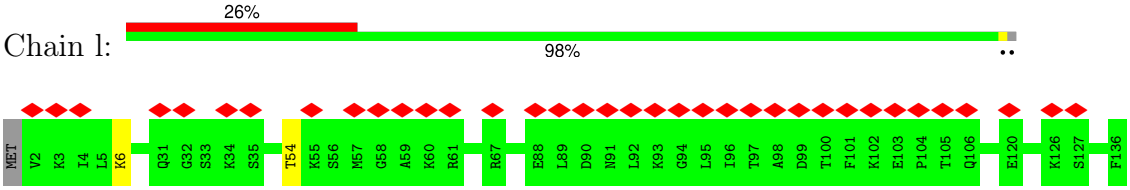
Chain k:





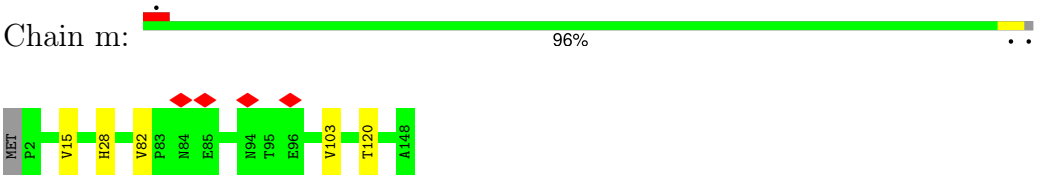
• Molecule 30: Large ribosomal subunit protein eL27A

Chain l:



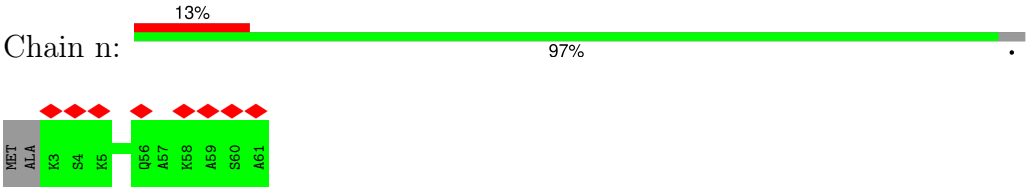
• Molecule 31: Large ribosomal subunit protein uL15B

Chain m:



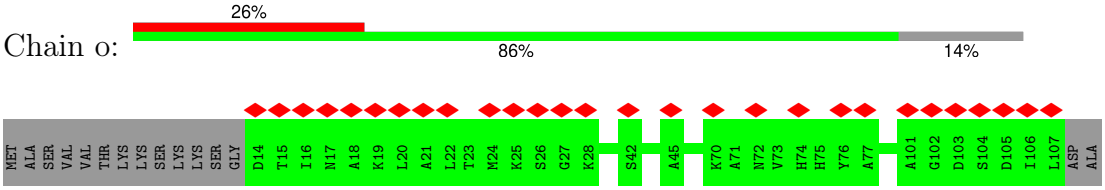
• Molecule 32: Large ribosomal subunit protein eL29

Chain n:



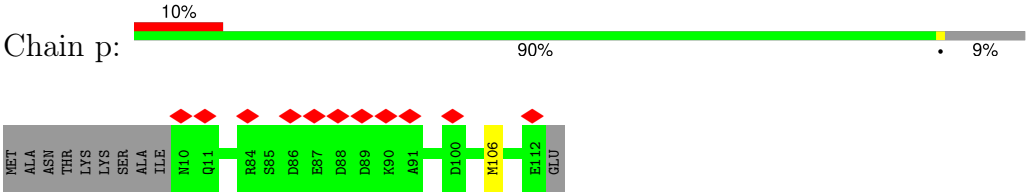
• Molecule 33: Large ribosomal subunit protein eL30A

Chain o:



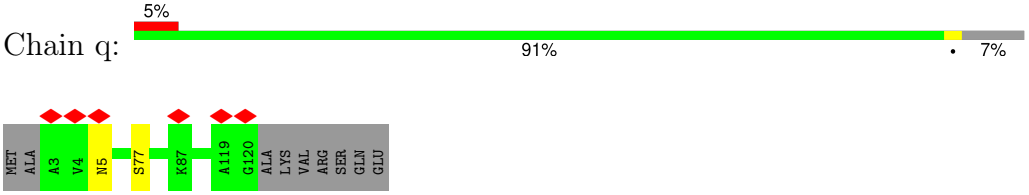
• Molecule 34: Large ribosomal subunit protein eL31

Chain p:



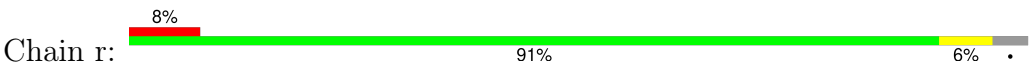
• Molecule 35: Large ribosomal subunit protein eL32A

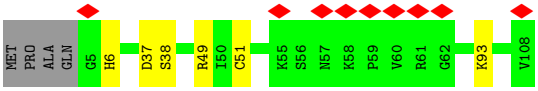
Chain q:



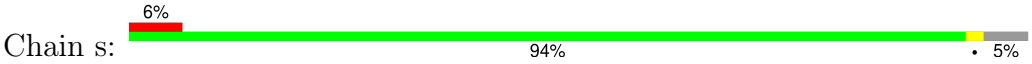
• Molecule 36: Large ribosomal subunit protein eL33A

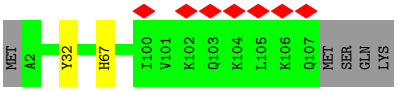
Chain r:



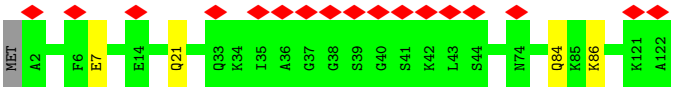


• Molecule 37: Large ribosomal subunit protein eL34B

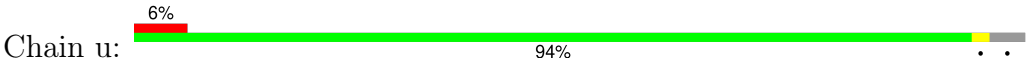


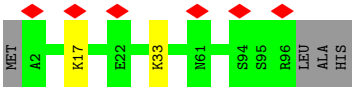


• Molecule 38: Large ribosomal subunit protein uL29

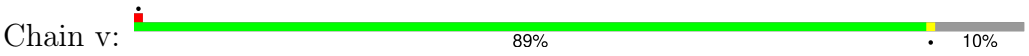


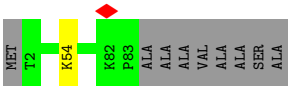
• Molecule 39: Large ribosomal subunit protein eL36B



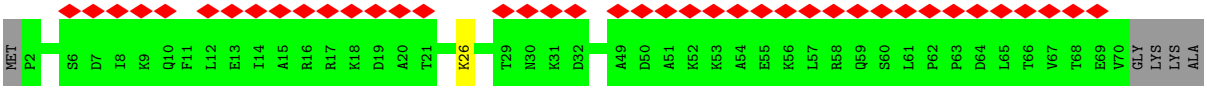


• Molecule 40: Large ribosomal subunit protein eL37B

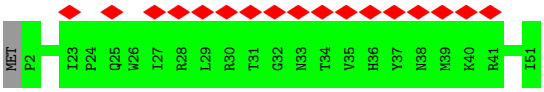




• Molecule 41: Large ribosomal subunit protein eL38A

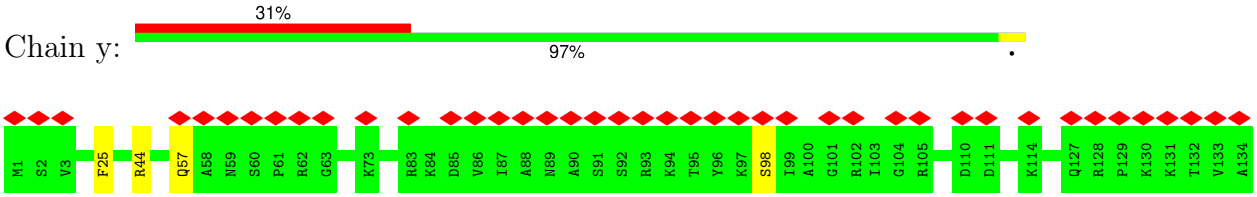


• Molecule 42: Large ribosomal subunit protein eL39



• Molecule 43: Large ribosomal subunit protein eL28

Chain y:


31%
97%
M1
S2
V3
F25
R44
Q57
A58
N59
S60
P61
R62
G63
K73
R83
K84
D85
V86
I87
A88
N89
A90
S91
S92
R93
K94
T95
Y96
K97
S98
I99
A100
G101
R102
I103
G104
R105
D110
D111
K114
Q127
R128
P129
K130
K131
T132
V133
A134

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	820453	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	3.551	Depositor
Minimum map value	-1.428	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.38	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.36	0/772	0.59	0/1025
2	1	0.35	0/727	0.63	0/973
3	2	0.79	2/76871 (0.0%)	1.02	131/119827 (0.1%)
4	3	0.66	0/2838	0.93	5/4422 (0.1%)
5	4	0.79	0/3723	0.96	3/5796 (0.1%)
6	N	0.38	0/1910	0.62	0/2575
7	O	0.38	0/3116	0.61	0/4190
8	P	0.38	0/2852	0.60	0/3850
9	Q	0.37	0/2361	0.56	0/3173
10	R	0.34	0/1275	0.55	0/1719
11	S	0.37	0/1929	0.55	0/2583
12	T	0.34	0/1801	0.55	0/2430
13	U	0.27	0/1330	0.54	0/1789
14	V	0.29	0/1579	0.55	0/2115
15	W	0.29	0/1369	0.57	0/1830
16	X	0.35	0/1686	0.58	0/2267
17	Y	0.32	0/1054	0.56	0/1413
18	Z	0.43	0/1717	0.67	0/2306
19	a	0.38	0/1575	0.56	0/2109
20	b	0.38	0/1237	0.58	0/1661
21	c	0.36	0/1511	0.64	0/2021
22	d	0.30	0/1320	0.56	0/1757
23	e	0.37	0/1458	0.57	0/1961
24	f	0.40	0/1314	0.57	0/1771
25	g	0.32	0/812	0.54	0/1090
26	h	0.36	0/1015	0.61	0/1369
27	i	0.36	0/534	0.60	0/709
28	j	0.35	0/963	0.59	1/1296 (0.1%)
29	k	0.34	0/1008	0.62	0/1341
30	l	0.33	0/1101	0.55	0/1477
31	m	0.38	0/1200	0.65	0/1611
32	n	0.34	0/503	0.58	0/664

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	o	0.36	0/714	0.55	0/961
34	p	0.38	0/872	0.64	0/1172
35	q	0.38	0/958	0.65	0/1278
36	r	0.40	0/853	0.60	0/1146
37	s	0.37	0/870	0.63	0/1165
38	t	0.34	0/1008	0.60	0/1340
39	u	0.34	0/766	0.61	0/1017
40	v	0.40	0/666	0.66	0/881
41	w	0.33	0/566	0.55	0/757
42	x	0.32	0/447	0.64	0/597
43	y	0.34	0/1053	0.61	0/1414
All	All	0.66	2/133234 (0.0%)	0.90	140/196848 (0.1%)

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
2	1	0	1
10	R	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	2730	A	N9-C4	-8.13	1.32	1.37
3	2	2730	A	N3-C4	-5.12	1.31	1.34

All (140) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2	1542	C	O5'-P-OP1	-12.46	94.48	105.70
3	2	3363	C	OP1-P-OP2	12.29	138.03	119.60
3	2	3362	C	OP2-P-O3'	-11.73	79.40	105.20
3	2	414	G	O4'-C1'-N9	11.50	117.40	108.20
3	2	1464	U	N3-C2-O2	-10.07	115.15	122.20
3	2	3362	C	OP1-P-O3'	-9.75	83.75	105.20
3	2	1311	C	N3-C2-O2	-9.29	115.39	121.90
3	2	2730	A	C2-N3-C4	-9.15	106.02	110.60
3	2	1639	U	N3-C2-O2	-9.03	115.88	122.20
3	2	2423	G	O5'-P-OP2	-9.00	97.60	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2	3394	C	C2-N1-C1'	8.49	128.14	118.80
3	2	1311	C	N1-C2-O2	7.93	123.66	118.90
3	2	2642	C	C2-N1-C1'	-7.86	110.16	118.80
3	2	256	C	N1-C2-O2	7.67	123.50	118.90
3	2	256	C	N3-C2-O2	-7.62	116.57	121.90
3	2	1895	U	C2-N3-C4	-7.62	122.43	127.00
3	2	2821	C	C6-N1-C2	-7.59	117.26	120.30
3	2	3394	C	N3-C2-O2	-7.48	116.66	121.90
3	2	1425	C	N1-C2-O2	7.44	123.37	118.90
3	2	3305	C	N1-C2-O2	7.41	123.35	118.90
3	2	1639	U	N1-C2-O2	7.38	127.97	122.80
3	2	867	G	O4'-C1'-N9	7.28	114.02	108.20
3	2	1464	U	N1-C2-O2	7.22	127.85	122.80
3	2	3394	C	N1-C2-O2	7.18	123.21	118.90
3	2	3002	G	C8-N9-C1'	-7.03	117.86	127.00
3	2	954	U	N1-C2-N3	6.95	119.07	114.90
3	2	1639	U	C2-N1-C1'	6.90	125.98	117.70
3	2	3002	G	C4-N9-C1'	6.90	135.47	126.50
3	2	1425	C	N3-C2-O2	-6.88	117.08	121.90
3	2	2821	C	N3-C2-O2	-6.87	117.09	121.90
3	2	1527	G	O4'-C1'-N9	6.82	113.66	108.20
28	j	112	LEU	CA-CB-CG	6.82	130.98	115.30
3	2	1782	U	N3-C2-O2	-6.81	117.43	122.20
3	2	2642	C	C6-N1-C1'	6.68	128.82	120.80
3	2	1148	G	O5'-P-OP1	-6.63	99.73	105.70
3	2	2463	G	O4'-C1'-N9	6.56	113.45	108.20
3	2	137	C	C6-N1-C2	-6.54	117.68	120.30
3	2	2199	G	C5-C6-O6	-6.53	124.68	128.60
3	2	275	G	O4'-C1'-N9	-6.49	103.01	108.20
3	2	954	U	C5-C6-N1	-6.47	119.46	122.70
3	2	253	U	C2-N1-C1'	6.41	125.39	117.70
3	2	3002	G	N3-C4-N9	6.40	129.84	126.00
3	2	954	U	C4-C5-C6	6.39	123.54	119.70
3	2	2730	A	N3-C4-C5	6.38	131.27	126.80
3	2	2462	C	O5'-P-OP2	-6.35	99.99	105.70
5	4	46	U	C5-C6-N1	-6.35	119.53	122.70
3	2	2369	A	O4'-C1'-N9	6.30	113.24	108.20
3	2	290	G	P-O3'-C3'	6.29	127.24	119.70
3	2	3394	C	C6-N1-C1'	-6.24	113.31	120.80
3	2	742	A	O5'-P-OP2	-6.22	100.10	105.70
3	2	2225	U	O4'-C1'-N1	6.19	113.15	108.20
3	2	3305	C	N3-C2-O2	-6.16	117.59	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2	2730	A	O4'-C1'-N9	6.16	113.12	108.20
3	2	2642	C	N3-C4-N4	-6.14	113.70	118.00
4	3	46	C	C2-N1-C1'	6.10	125.51	118.80
3	2	3045	G	O4'-C1'-N9	6.09	113.08	108.20
3	2	3305	C	C2-N1-C1'	6.09	125.50	118.80
3	2	1344	G	O5'-P-OP2	-6.09	100.22	105.70
3	2	1617	U	N3-C2-O2	-6.07	117.95	122.20
3	2	3002	G	C6-C5-N7	-6.07	126.76	130.40
3	2	292	A	O5'-P-OP2	-6.07	100.24	105.70
3	2	714	A	O4'-C1'-N9	6.00	113.00	108.20
3	2	2730	A	C5-C6-N1	-5.96	114.72	117.70
5	4	46	U	C4-C5-C6	5.94	123.26	119.70
3	2	3227	U	C2-N1-C1'	5.91	124.79	117.70
3	2	137	C	C2-N1-C1'	5.91	125.30	118.80
4	3	75	G	C5-N7-C8	-5.89	101.36	104.30
3	2	2730	A	N3-C4-N9	-5.88	122.69	127.40
3	2	137	C	N3-C2-O2	-5.87	117.79	121.90
3	2	583	C	C2-N1-C1'	5.86	125.25	118.80
3	2	1388	G	C2-N3-C4	5.86	114.83	111.90
3	2	1425	C	C2-N1-C1'	5.86	125.25	118.80
3	2	3002	G	N9-C4-C5	-5.85	103.06	105.40
3	2	1064	C	N3-C2-O2	-5.82	117.83	121.90
3	2	939	G	O4'-C1'-N9	5.74	112.80	108.20
3	2	1536	G	C2-N3-C4	-5.69	109.06	111.90
3	2	2506	G	N9-C4-C5	-5.69	103.12	105.40
3	2	889	G	O4'-C1'-N9	5.65	112.72	108.20
3	2	2642	C	C5-C4-N4	5.61	124.13	120.20
3	2	3371	U	C2-N1-C1'	5.61	124.43	117.70
3	2	1183	G	N3-C4-C5	5.61	131.40	128.60
3	2	1529	U	O4'-C1'-N1	5.60	112.68	108.20
3	2	2219	A	N9-C1'-C2'	-5.60	105.84	112.00
3	2	2506	G	C6-C5-N7	-5.59	127.05	130.40
3	2	1468	G	O5'-P-OP1	5.58	117.40	110.70
3	2	912	G	O4'-C1'-N9	5.58	112.66	108.20
3	2	3002	G	C4-C5-N7	5.57	113.03	110.80
5	4	43	C	N1-C2-O2	-5.55	115.57	118.90
3	2	134	U	N3-C2-O2	-5.55	118.31	122.20
3	2	2506	G	C4-C5-N7	5.54	113.01	110.80
3	2	1014	C	C6-N1-C2	-5.53	118.09	120.30
3	2	3305	C	C6-N1-C2	-5.52	118.09	120.30
3	2	2388	G	N1-C6-O6	-5.51	116.59	119.90
3	2	2493	C	C6-N1-C2	-5.50	118.10	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2	2660	U	N3-C2-O2	-5.48	118.37	122.20
3	2	713	G	N3-C4-C5	5.47	131.34	128.60
3	2	2821	C	N1-C2-N3	5.44	123.01	119.20
3	2	3373	C	N3-C2-O2	-5.44	118.09	121.90
3	2	1401	G	C2-N3-C4	5.43	114.62	111.90
3	2	838	A	O5'-P-OP1	-5.41	100.83	105.70
3	2	1409	G	N9-C4-C5	-5.41	103.24	105.40
3	2	2251	C	C2-N1-C1'	-5.41	112.85	118.80
3	2	742	A	O4'-C1'-N9	5.39	112.51	108.20
3	2	36	C	C6-N1-C2	-5.38	118.15	120.30
3	2	1639	U	C6-N1-C2	-5.38	117.77	121.00
3	2	2506	G	C8-N9-C1'	-5.35	120.04	127.00
3	2	905	C	P-O3'-C3'	5.35	126.12	119.70
3	2	1595	U	O4'-C1'-N1	5.35	112.48	108.20
3	2	2660	U	N1-C2-O2	5.33	126.53	122.80
4	3	75	G	C4-C5-N7	5.32	112.93	110.80
3	2	948	G	P-O3'-C3'	5.30	126.06	119.70
3	2	190	G	N3-C4-N9	-5.28	122.83	126.00
3	2	713	G	N3-C4-N9	-5.27	122.84	126.00
3	2	1359	C	C6-N1-C2	-5.25	118.20	120.30
3	2	253	U	N1-C2-O2	5.25	126.47	122.80
3	2	3463	A	C2-N3-C4	-5.25	107.98	110.60
3	2	993	C	C6-N1-C2	-5.24	118.20	120.30
3	2	3001	C	P-O3'-C3'	5.23	125.97	119.70
3	2	3050	U	P-O3'-C3'	5.21	125.95	119.70
3	2	2506	G	C4-N9-C1'	5.21	133.28	126.50
3	2	583	C	N1-C2-O2	5.21	122.03	118.90
3	2	726	C	C5-C6-N1	5.21	123.60	121.00
3	2	1514	G	O4'-C1'-N9	5.20	112.36	108.20
3	2	2730	A	C5-N7-C8	-5.18	101.31	103.90
3	2	490	U	C2-N1-C1'	5.17	123.91	117.70
3	2	655	C	C6-N1-C2	-5.16	118.24	120.30
4	3	75	G	N7-C8-N9	5.15	115.68	113.10
3	2	745	G	O4'-C1'-N9	5.15	112.32	108.20
4	3	12	U	OP2-P-O3'	5.15	116.52	105.20
3	2	726	C	C6-N1-C2	-5.14	118.24	120.30
3	2	101	G	O4'-C1'-N9	5.11	112.29	108.20
3	2	2868	C	C6-N1-C2	-5.10	118.26	120.30
3	2	1311	C	C6-N1-C2	-5.07	118.27	120.30
3	2	2199	G	C6-N1-C2	-5.04	122.08	125.10
3	2	3373	C	C2-N1-C1'	5.04	124.34	118.80
3	2	529	G	O4'-C1'-N9	5.03	112.23	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	2	2821	C	C4-C5-C6	5.03	119.91	117.40
3	2	1260	G	N3-C4-N9	5.02	129.01	126.00
3	2	2965	C	C6-N1-C1'	5.02	126.82	120.80
3	2	1522	G	C5-C6-N1	5.01	114.01	111.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	51	ALA	Peptide
10	R	84	GLY	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	
1	0	91/106 (86%)	86 (94%)	5 (6%)	0	100	100
2	1	91/94 (97%)	83 (91%)	8 (9%)	0	100	100
6	N	246/253 (97%)	233 (95%)	12 (5%)	1 (0%)	30	22
7	O	382/388 (98%)	371 (97%)	10 (3%)	1 (0%)	37	30
8	P	360/363 (99%)	347 (96%)	13 (4%)	0	100	100
9	Q	285/294 (97%)	277 (97%)	8 (3%)	0	100	100
10	R	160/195 (82%)	148 (92%)	11 (7%)	1 (1%)	22	12
11	S	231/251 (92%)	228 (99%)	3 (1%)	0	100	100
12	T	227/259 (88%)	213 (94%)	14 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
13	U	162/189 (86%)	153 (94%)	8 (5%)	1 (1%)	22 12
14	V	187/221 (85%)	179 (96%)	8 (4%)	0	100 100
15	W	165/174 (95%)	158 (96%)	7 (4%)	0	100 100
16	X	205/208 (99%)	200 (98%)	5 (2%)	0	100 100
17	Y	128/134 (96%)	126 (98%)	2 (2%)	0	100 100
18	Z	198/201 (98%)	188 (95%)	9 (4%)	1 (0%)	25 15
19	a	194/197 (98%)	191 (98%)	3 (2%)	0	100 100
20	b	150/187 (80%)	145 (97%)	5 (3%)	0	100 100
21	c	184/187 (98%)	174 (95%)	10 (5%)	0	100 100
22	d	155/193 (80%)	152 (98%)	3 (2%)	0	100 100
23	e	171/176 (97%)	164 (96%)	6 (4%)	1 (1%)	22 12
24	f	157/160 (98%)	149 (95%)	8 (5%)	0	100 100
25	g	97/117 (83%)	83 (86%)	14 (14%)	0	100 100
26	h	132/139 (95%)	123 (93%)	9 (7%)	0	100 100
27	i	61/149 (41%)	60 (98%)	1 (2%)	0	100 100
28	j	116/141 (82%)	111 (96%)	5 (4%)	0	100 100
29	k	123/126 (98%)	120 (98%)	3 (2%)	0	100 100
30	l	133/136 (98%)	119 (90%)	14 (10%)	0	100 100
31	m	145/148 (98%)	140 (97%)	4 (3%)	1 (1%)	19 9
32	n	57/61 (93%)	55 (96%)	2 (4%)	0	100 100
33	o	92/109 (84%)	91 (99%)	1 (1%)	0	100 100
34	p	101/113 (89%)	99 (98%)	2 (2%)	0	100 100
35	q	116/127 (91%)	110 (95%)	6 (5%)	0	100 100
36	r	102/108 (94%)	100 (98%)	2 (2%)	0	100 100
37	s	104/111 (94%)	102 (98%)	2 (2%)	0	100 100
38	t	119/122 (98%)	115 (97%)	3 (2%)	1 (1%)	16 7
39	u	93/99 (94%)	90 (97%)	3 (3%)	0	100 100
40	v	80/91 (88%)	77 (96%)	3 (4%)	0	100 100
41	w	67/74 (90%)	65 (97%)	2 (3%)	0	100 100
42	x	48/51 (94%)	43 (90%)	5 (10%)	0	100 100
43	y	132/134 (98%)	121 (92%)	11 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6047/6586 (92%)	5789 (96%)	250 (4%)	8 (0%)	50 41

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	N	29	ARG
10	R	144	ALA
13	U	134	ILE
18	Z	183	SER
23	e	159	VAL
7	O	187	SER
38	t	86	LYS
31	m	28	HIS

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	84/93 (90%)	80 (95%)	4 (5%)	21 8
2	1	74/75 (99%)	74 (100%)	0	100 100
6	N	188/192 (98%)	185 (98%)	3 (2%)	58 49
7	O	318/326 (98%)	311 (98%)	7 (2%)	47 35
8	P	293/294 (100%)	281 (96%)	12 (4%)	26 12
9	Q	235/241 (98%)	230 (98%)	5 (2%)	48 36
10	R	132/155 (85%)	129 (98%)	3 (2%)	45 33
11	S	198/213 (93%)	197 (100%)	1 (0%)	86 86
12	T	182/212 (86%)	171 (94%)	11 (6%)	16 5
13	U	149/168 (89%)	142 (95%)	7 (5%)	22 9
14	V	165/187 (88%)	158 (96%)	7 (4%)	25 12
15	W	141/146 (97%)	131 (93%)	10 (7%)	12 3
16	X	166/167 (99%)	161 (97%)	5 (3%)	36 23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	Y	110/113 (97%)	108 (98%)	2 (2%)	54 43
18	Z	175/176 (99%)	173 (99%)	2 (1%)	70 64
19	a	159/160 (99%)	158 (99%)	1 (1%)	84 83
20	b	124/149 (83%)	119 (96%)	5 (4%)	27 13
21	c	157/158 (99%)	153 (98%)	4 (2%)	42 30
22	d	136/163 (83%)	133 (98%)	3 (2%)	47 35
23	e	151/154 (98%)	148 (98%)	3 (2%)	50 38
24	f	138/139 (99%)	135 (98%)	3 (2%)	47 35
25	g	86/103 (84%)	85 (99%)	1 (1%)	67 61
26	h	103/107 (96%)	101 (98%)	2 (2%)	52 41
27	i	57/121 (47%)	53 (93%)	4 (7%)	12 3
28	j	105/122 (86%)	103 (98%)	2 (2%)	52 41
29	k	110/111 (99%)	108 (98%)	2 (2%)	54 43
30	l	114/115 (99%)	112 (98%)	2 (2%)	54 43
31	m	122/123 (99%)	118 (97%)	4 (3%)	33 20
32	n	50/51 (98%)	50 (100%)	0	100 100
33	o	75/87 (86%)	75 (100%)	0	100 100
34	p	94/102 (92%)	93 (99%)	1 (1%)	70 64
35	q	100/107 (94%)	98 (98%)	2 (2%)	50 38
36	r	91/94 (97%)	85 (93%)	6 (7%)	14 4
37	s	91/96 (95%)	89 (98%)	2 (2%)	47 35
38	t	106/107 (99%)	103 (97%)	3 (3%)	38 25
39	u	81/84 (96%)	79 (98%)	2 (2%)	42 30
40	v	68/71 (96%)	67 (98%)	1 (2%)	60 52
41	w	63/66 (96%)	62 (98%)	1 (2%)	58 49
42	x	46/47 (98%)	46 (100%)	0	100 100
43	y	113/113 (100%)	109 (96%)	4 (4%)	31 18
All	All	5150/5508 (94%)	5013 (97%)	137 (3%)	41 26

All (137) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	3	ASN

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Mol	Chain	Res	Type
1	0	57	VAL
1	0	58	PHE
1	0	77	CYS
6	N	118	LYS
6	N	154	LYS
6	N	226	ARG
7	O	59	ASP
7	O	123	PHE
7	O	142	GLN
7	O	147	GLU
7	O	167	ARG
7	O	255	TRP
7	O	276	THR
8	P	5	ARG
8	P	13	LYS
8	P	48	LYS
8	P	55	SER
8	P	62	THR
8	P	71	ARG
8	P	122	TYR
8	P	178	ARG
8	P	262	SER
8	P	291	ARG
8	P	309	ARG
8	P	327	LEU
9	Q	90	TRP
9	Q	152	ARG
9	Q	194	THR
9	Q	216	GLU
9	Q	238	ASP
10	R	66	ARG
10	R	94	ARG
10	R	118	LYS
11	S	47	LYS
12	T	110	VAL
12	T	125	VAL
12	T	131	ASN
12	T	182	ASN
12	T	203	VAL
12	T	205	GLU
12	T	216	SER
12	T	223	SER

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Mol	Chain	Res	Type
12	T	225	LYS
12	T	228	GLU
12	T	232	LYS
13	U	32	ARG
13	U	58	TRP
13	U	69	ARG
13	U	90	MET
13	U	94	TYR
13	U	132	VAL
13	U	166	ARG
14	V	22	TYR
14	V	40	ARG
14	V	83	ASP
14	V	144	SER
14	V	154	ARG
14	V	164	ARG
14	V	186	SER
15	W	9	MET
15	W	13	ARG
15	W	19	LEU
15	W	35	LYS
15	W	57	PHE
15	W	86	VAL
15	W	90	GLU
15	W	126	ASP
15	W	155	ASN
15	W	166	LYS
16	X	11	ASN
16	X	67	MET
16	X	148	ASP
16	X	156	THR
16	X	162	GLU
17	Y	34	HIS
17	Y	43	CYS
18	Z	140	LYS
18	Z	201	ARG
19	a	2	SER
20	b	40	SER
20	b	52	LYS
20	b	69	ARG
20	b	111	LYS
20	b	115	LYS

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Mol	Chain	Res	Type
21	c	7	ARG
21	c	10	VAL
21	c	148	ARG
21	c	179	ARG
22	d	36	ASN
22	d	60	ARG
22	d	114	LYS
23	e	4	LYS
23	e	54	THR
23	e	89	MET
24	f	83	ARG
24	f	102	ARG
24	f	129	ARG
25	g	66	HIS
26	h	99	ASP
26	h	122	LYS
27	i	2	LYS
27	i	22	VAL
27	i	39	LEU
27	i	50	SER
28	j	80	THR
28	j	112	LEU
29	k	2	LYS
29	k	73	TYR
30	l	6	LYS
30	l	54	THR
31	m	15	VAL
31	m	82	VAL
31	m	103	VAL
31	m	120	THR
34	p	106	MET
35	q	5	ASN
35	q	77	SER
36	r	6	HIS
36	r	37	ASP
36	r	38	SER
36	r	49	ARG
36	r	51	CYS
36	r	93	LYS
37	s	32	TYR
37	s	67	HIS
38	t	7	GLU

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Mol	Chain	Res	Type
38	t	21	GLN
38	t	84	GLN
39	u	17	LYS
39	u	33	LYS
40	v	54	LYS
41	w	26	LYS
43	y	25	PHE
43	y	44	ARG
43	y	57	GLN
43	y	98	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	0	3	ASN
1	0	27	GLN
6	N	217	HIS
7	O	198	HIS
7	O	293	ASN
7	O	319	ASN
8	P	245	HIS
10	R	157	GLN
10	R	186	ASN
11	S	27	GLN
12	T	192	GLN
13	U	77	ASN
13	U	161	GLN
15	W	152	HIS
16	X	11	ASN
18	Z	19	ASN
18	Z	153	ASN
19	a	5	GLN
19	a	47	HIS
21	c	14	GLN
22	d	34	ASN
22	d	36	ASN
23	e	87	HIS
24	f	3	HIS
24	f	152	HIS
26	h	35	ASN
26	h	134	ASN
28	j	86	HIS

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Mol	Chain	Res	Type
29	k	54	GLN
30	l	123	GLN
31	m	105	GLN
31	m	139	GLN
32	n	6	ASN
33	o	74	HIS
35	q	86	ASN
36	r	6	HIS
37	s	107	GLN
38	t	15	ASN
38	t	21	GLN
39	u	30	HIS
41	w	28	ASN
42	x	19	GLN
43	y	15	ASN
43	y	89	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	3204/3498 (91%)	656 (20%)	49 (1%)
4	3	118/246 (47%)	18 (15%)	1 (0%)
5	4	156/165 (94%)	26 (16%)	1 (0%)
All	All	3478/3909 (88%)	700 (20%)	51 (1%)

All (700) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	2	16	A
3	2	26	A
3	2	40	A
3	2	49	A
3	2	59	G
3	2	60	A
3	2	65	A
3	2	66	A
3	2	74	A
3	2	92	G
3	2	99	A
3	2	109	A
3	2	110	G

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Mol	Chain	Res	Type
3	2	116	A
3	2	121	A
3	2	122	A
3	2	137	C
3	2	161	C
3	2	162	A
3	2	163	A
3	2	168	C
3	2	170	G
3	2	172	U
3	2	174	U
3	2	175	G
3	2	176	A
3	2	178	U
3	2	184	C
3	2	185	G
3	2	187	U
3	2	188	C
3	2	189	G
3	2	190	G
3	2	191	U
3	2	192	C
3	2	193	U
3	2	194	A
3	2	197	U
3	2	198	U
3	2	207	C
3	2	217	G
3	2	225	G
3	2	226	A
3	2	240	G
3	2	242	U
3	2	246	U
3	2	247	U
3	2	250	A
3	2	252	A
3	2	253	U
3	2	254	G
3	2	255	C
3	2	259	A
3	2	260	U
3	2	262	A

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Mol	Chain	Res	Type
3	2	263	A
3	2	264	G
3	2	266	G
3	2	269	U
3	2	271	C
3	2	272	G
3	2	274	A
3	2	277	G
3	2	291	G
3	2	292	A
3	2	303	A
3	2	313	U
3	2	331	A
3	2	337	U
3	2	346	A
3	2	359	A
3	2	360	A
3	2	383	A
3	2	384	G
3	2	399	A
3	2	406	U
3	2	407	A
3	2	410	A
3	2	411	C
3	2	429	G
3	2	430	A
3	2	437	G
3	2	445	G
3	2	446	U
3	2	447	C
3	2	449	U
3	2	450	A
3	2	461	A
3	2	462	U
3	2	463	C
3	2	466	U
3	2	477	C
3	2	488	A
3	2	492	U
3	2	495	A
3	2	500	U
3	2	501	G

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Mol	Chain	Res	Type
3	2	504	A
3	2	505	G
3	2	509	A
3	2	531	A
3	2	532	A
3	2	540	A
3	2	541	G
3	2	545	A
3	2	546	G
3	2	547	G
3	2	548	U
3	2	549	G
3	2	552	U
3	2	553	U
3	2	554	U
3	2	571	G
3	2	572	A
3	2	573	G
3	2	575	G
3	2	578	U
3	2	579	A
3	2	580	U
3	2	581	A
3	2	587	U
3	2	590	U
3	2	591	G
3	2	602	A
3	2	603	C
3	2	613	A
3	2	621	G
3	2	625	U
3	2	627	G
3	2	628	U
3	2	629	G
3	2	634	G
3	2	636	A
3	2	637	U
3	2	645	U
3	2	646	A
3	2	674	A
3	2	685	A
3	2	702	A

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Mol	Chain	Res	Type
3	2	706	U
3	2	708	U
3	2	711	G
3	2	713	G
3	2	714	A
3	2	715	U
3	2	716	G
3	2	717	A
3	2	720	A
3	2	732	A
3	2	742	A
3	2	743	A
3	2	759	C
3	2	760	C
3	2	761	U
3	2	762	U
3	2	763	G
3	2	764	U
3	2	765	G
3	2	766	G
3	2	770	G
3	2	786	C
3	2	788	G
3	2	789	A
3	2	802	G
3	2	806	G
3	2	809	U
3	2	813	G
3	2	817	G
3	2	838	A
3	2	849	A
3	2	862	A
3	2	889	G
3	2	893	C
3	2	906	U
3	2	911	U
3	2	928	A
3	2	929	U
3	2	939	G
3	2	940	G
3	2	946	A
3	2	948	G

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Mol	Chain	Res	Type
3	2	949	A
3	2	953	A
3	2	955	C
3	2	957	A
3	2	969	G
3	2	976	C
3	2	991	C
3	2	992	U
3	2	993	C
3	2	1009	C
3	2	1010	A
3	2	1011	G
3	2	1012	A
3	2	1014	C
3	2	1026	G
3	2	1032	C
3	2	1033	G
3	2	1034	A
3	2	1047	C
3	2	1049	U
3	2	1050	G
3	2	1051	G
3	2	1052	G
3	2	1056	G
3	2	1057	G
3	2	1058	A
3	2	1059	A
3	2	1060	U
3	2	1061	U
3	2	1063	C
3	2	1064	C
3	2	1065	U
3	2	1067	A
3	2	1079	A
3	2	1081	C
3	2	1095	G
3	2	1096	A
3	2	1098	G
3	2	1101	C
3	2	1104	G
3	2	1113	U
3	2	1119	G

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Mol	Chain	Res	Type
3	2	1123	G
3	2	1126	A
3	2	1127	U
3	2	1128	C
3	2	1129	G
3	2	1130	A
3	2	1134	A
3	2	1135	G
3	2	1139	U
3	2	1148	G
3	2	1155	U
3	2	1162	G
3	2	1175	U
3	2	1176	G
3	2	1184	A
3	2	1186	C
3	2	1190	A
3	2	1191	C
3	2	1211	A
3	2	1212	U
3	2	1227	C
3	2	1232	G
3	2	1233	A
3	2	1236	A
3	2	1239	U
3	2	1240	G
3	2	1245	U
3	2	1251	U
3	2	1252	A
3	2	1254	A
3	2	1260	G
3	2	1263	C
3	2	1266	U
3	2	1267	G
3	2	1269	C
3	2	1270	C
3	2	1272	U
3	2	1273	G
3	2	1276	A
3	2	1277	G
3	2	1279	C
3	2	1283	A

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Mol	Chain	Res	Type
3	2	1289	U
3	2	1293	G
3	2	1294	A
3	2	1295	G
3	2	1296	U
3	2	1297	G
3	2	1300	U
3	2	1301	A
3	2	1303	C
3	2	1304	A
3	2	1305	A
3	2	1310	C
3	2	1313	G
3	2	1314	C
3	2	1316	G
3	2	1317	A
3	2	1318	A
3	2	1319	U
3	2	1323	C
3	2	1333	A
3	2	1334	A
3	2	1338	G
3	2	1340	U
3	2	1344	G
3	2	1361	A
3	2	1379	U
3	2	1380	A
3	2	1381	G
3	2	1388	G
3	2	1389	A
3	2	1420	U
3	2	1433	U
3	2	1453	A
3	2	1468	G
3	2	1471	C
3	2	1484	G
3	2	1503	C
3	2	1515	A
3	2	1542	C
3	2	1561	C
3	2	1562	G
3	2	1570	G

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Mol	Chain	Res	Type
3	2	1573	A
3	2	1588	A
3	2	1589	U
3	2	1590	G
3	2	1593	A
3	2	1594	G
3	2	1595	U
3	2	1596	U
3	2	1599	A
3	2	1600	C
3	2	1601	G
3	2	1604	U
3	2	1606	U
3	2	1607	U
3	2	1608	C
3	2	1609	G
3	2	1612	C
3	2	1613	C
3	2	1614	U
3	2	1615	C
3	2	1616	C
3	2	1622	A
3	2	1624	A
3	2	1628	A
3	2	1640	A
3	2	1641	U
3	2	1656	G
3	2	1663	C
3	2	1664	A
3	2	1665	A
3	2	1666	C
3	2	1674	C
3	2	1677	A
3	2	1678	A
3	2	1679	A
3	2	1680	U
3	2	1681	G
3	2	1692	C
3	2	1693	G
3	2	1740	U
3	2	1742	G
3	2	1744	A

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Mol	Chain	Res	Type
3	2	1745	C
3	2	1755	A
3	2	1764	U
3	2	1790	A
3	2	1791	G
3	2	1800	G
3	2	1801	C
3	2	1803	U
3	2	1806	U
3	2	1811	A
3	2	1821	G
3	2	1837	G
3	2	1838	A
3	2	1850	A
3	2	1853	A
3	2	1854	A
3	2	1855	U
3	2	1856	G
3	2	1857	G
3	2	1871	U
3	2	1876	U
3	2	1894	A
3	2	1897	A
3	2	1904	C
3	2	1933	G
3	2	1934	A
3	2	1935	U
3	2	1948	A
3	2	1961	G
3	2	2007	G
3	2	2182	C
3	2	2183	A
3	2	2188	A
3	2	2189	C
3	2	2190	U
3	2	2200	U
3	2	2201	A
3	2	2209	G
3	2	2210	G
3	2	2219	A
3	2	2228	U
3	2	2246	A

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Mol	Chain	Res	Type
3	2	2257	G
3	2	2294	G
3	2	2295	A
3	2	2296	A
3	2	2297	U
3	2	2298	G
3	2	2310	A
3	2	2311	A
3	2	2317	A
3	2	2332	A
3	2	2337	G
3	2	2339	G
3	2	2340	A
3	2	2342	U
3	2	2344	A
3	2	2345	C
3	2	2348	U
3	2	2349	G
3	2	2351	C
3	2	2353	C
3	2	2356	U
3	2	2358	A
3	2	2360	G
3	2	2361	G
3	2	2367	A
3	2	2369	A
3	2	2376	G
3	2	2392	C
3	2	2395	G
3	2	2396	C
3	2	2398	U
3	2	2401	A
3	2	2403	G
3	2	2423	G
3	2	2424	U
3	2	2461	A
3	2	2462	C
3	2	2463	G
3	2	2481	G
3	2	2485	A
3	2	2489	A
3	2	2490	A

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Mol	Chain	Res	Type
3	2	2491	G
3	2	2492	A
3	2	2499	U
3	2	2523	G
3	2	2527	A
3	2	2529	A
3	2	2530	G
3	2	2601	U
3	2	2602	U
3	2	2603	C
3	2	2606	U
3	2	2607	A
3	2	2610	U
3	2	2611	A
3	2	2619	A
3	2	2620	A
3	2	2622	C
3	2	2627	U
3	2	2628	U
3	2	2629	G
3	2	2630	G
3	2	2631	G
3	2	2632	A
3	2	2633	U
3	2	2634	U
3	2	2635	U
3	2	2636	A
3	2	2638	U
3	2	2641	C
3	2	2642	C
3	2	2643	A
3	2	2644	U
3	2	2645	A
3	2	2646	U
3	2	2648	C
3	2	2649	U
3	2	2656	A
3	2	2657	A
3	2	2660	U
3	2	2661	U
3	2	2662	U
3	2	2664	U

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Mol	Chain	Res	Type
3	2	2665	U
3	2	2666	C
3	2	2667	G
3	2	2668	C
3	2	2680	C
3	2	2688	A
3	2	2701	G
3	2	2702	G
3	2	2709	G
3	2	2721	A
3	2	2743	G
3	2	2747	U
3	2	2751	A
3	2	2752	A
3	2	2769	A
3	2	2770	C
3	2	2772	G
3	2	2773	A
3	2	2774	A
3	2	2775	A
3	2	2784	A
3	2	2785	G
3	2	2789	A
3	2	2798	A
3	2	2799	A
3	2	2809	G
3	2	2823	G
3	2	2824	U
3	2	2848	G
3	2	2850	C
3	2	2868	C
3	2	2872	G
3	2	2873	A
3	2	2889	G
3	2	2891	G
3	2	2894	A
3	2	2895	G
3	2	2896	A
3	2	2897	A
3	2	2898	A
3	2	2909	G
3	2	2912	A

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Mol	Chain	Res	Type
3	2	2913	U
3	2	2918	G
3	2	2923	G
3	2	2934	G
3	2	2937	U
3	2	2938	U
3	2	2940	A
3	2	2942	A
3	2	2955	U
3	2	2957	U
3	2	2966	G
3	2	2967	A
3	2	2968	U
3	2	2970	U
3	2	2982	A
3	2	2992	A
3	2	2993	G
3	2	2994	C
3	2	2997	A
3	2	3001	C
3	2	3002	G
3	2	3003	G
3	2	3018	U
3	2	3030	U
3	2	3031	A
3	2	3037	C
3	2	3042	G
3	2	3050	U
3	2	3051	A
3	2	3066	A
3	2	3067	G
3	2	3078	C
3	2	3085	G
3	2	3091	G
3	2	3093	G
3	2	3108	A
3	2	3116	U
3	2	3117	A
3	2	3126	G
3	2	3153	U
3	2	3155	G
3	2	3174	A

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Mol	Chain	Res	Type
3	2	3176	G
3	2	3182	G
3	2	3189	C
3	2	3195	C
3	2	3197	G
3	2	3212	G
3	2	3216	C
3	2	3218	A
3	2	3226	A
3	2	3227	U
3	2	3238	A
3	2	3239	A
3	2	3248	U
3	2	3249	U
3	2	3250	U
3	2	3251	U
3	2	3252	U
3	2	3260	A
3	2	3261	U
3	2	3266	U
3	2	3268	U
3	2	3269	A
3	2	3276	A
3	2	3283	A
3	2	3284	G
3	2	3285	G
3	2	3287	A
3	2	3288	G
3	2	3289	G
3	2	3290	A
3	2	3291	C
3	2	3292	U
3	2	3293	U
3	2	3295	U
3	2	3296	U
3	2	3298	C
3	2	3299	U
3	2	3300	A
3	2	3301	C
3	2	3302	U
3	2	3303	C
3	2	3305	C

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Mol	Chain	Res	Type
3	2	3306	C
3	2	3307	U
3	2	3308	G
3	2	3310	A
3	2	3317	A
3	2	3318	A
3	2	3319	G
3	2	3327	A
3	2	3328	U
3	2	3329	G
3	2	3338	A
3	2	3341	G
3	2	3343	A
3	2	3345	G
3	2	3352	A
3	2	3359	U
3	2	3360	G
3	2	3362	C
3	2	3363	C
3	2	3371	U
3	2	3372	C
3	2	3373	C
3	2	3374	A
3	2	3375	U
3	2	3376	U
3	2	3377	G
3	2	3386	U
3	2	3387	G
3	2	3388	C
3	2	3390	G
3	2	3392	A
3	2	3393	U
3	2	3394	C
3	2	3395	G
3	2	3404	G
3	2	3405	C
3	2	3418	U
3	2	3419	G
3	2	3420	U
3	2	3442	U
3	2	3443	A
3	2	3446	G

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Mol	Chain	Res	Type
3	2	3449	G
3	2	3452	U
3	2	3453	U
3	2	3455	U
3	2	3456	U
3	2	3457	G
3	2	3459	U
3	2	3468	C
3	2	3476	A
3	2	3479	C
3	2	3483	U
3	2	3484	G
3	2	3491	A
4	3	12	U
4	3	13	A
4	3	19	G
4	3	22	A
4	3	35	C
4	3	39	C
4	3	41	G
4	3	46	C
4	3	50	A
4	3	53	U
4	3	54	A
4	3	55	A
4	3	63	A
4	3	64	G
4	3	75	G
4	3	100	A
4	3	110	G
4	3	119	U
5	4	42	U
5	4	43	C
5	4	56	A
5	4	60	A
5	4	67	A
5	4	70	C
5	4	71	G
5	4	83	G
5	4	88	A
5	4	89	U
5	4	90	U

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Mol	Chain	Res	Type
5	4	91	C
5	4	92	C
5	4	93	G
5	4	94	U
5	4	95	G
5	4	103	G
5	4	113	A
5	4	114	C
5	4	119	A
5	4	121	U
5	4	133	U
5	4	134	U
5	4	135	C
5	4	146	A
5	4	165	U

All (51) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	137	C
3	2	191	U
3	2	290	G
3	2	382	A
3	2	446	U
3	2	572	A
3	2	589	U
3	2	612	G
3	2	719	A
3	2	762	U
3	2	764	U
3	2	848	A
3	2	905	C
3	2	928	A
3	2	948	G
3	2	992	U
3	2	1059	A
3	2	1094	A
3	2	1103	U
3	2	1133	G
3	2	1190	A
3	2	1244	G
3	2	1272	U

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Mol	Chain	Res	Type
3	2	1380	A
3	2	1608	C
3	2	1640	A
3	2	1665	A
3	2	1854	A
3	2	1897	A
3	2	2200	U
3	2	2369	A
3	2	2823	G
3	2	2867	C
3	2	2896	A
3	2	2913	U
3	2	2993	G
3	2	3001	C
3	2	3152	U
3	2	3217	U
3	2	3249	U
3	2	3260	A
3	2	3267	A
3	2	3292	U
3	2	3298	C
3	2	3328	U
3	2	3373	C
3	2	3404	G
3	2	3418	U
3	2	3456	U
4	3	12	U
5	4	88	A

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 100 ligands modelled in this entry, 100 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

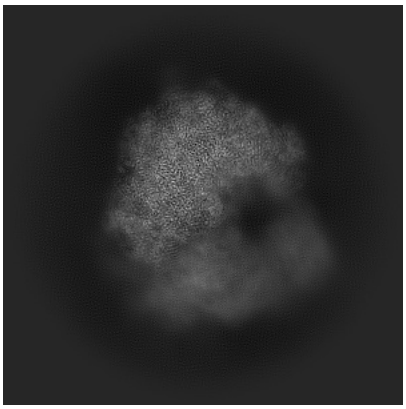
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-43973. These allow visual inspection of the internal detail of the map and identification of artifacts.

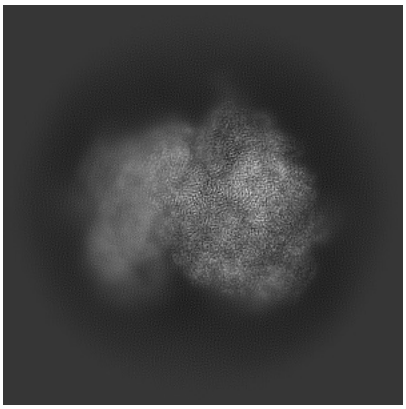
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

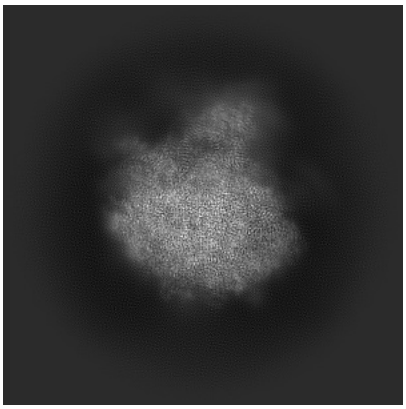
6.1.1 Primary map



X

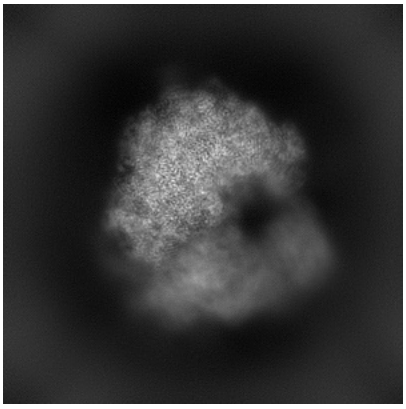


Y

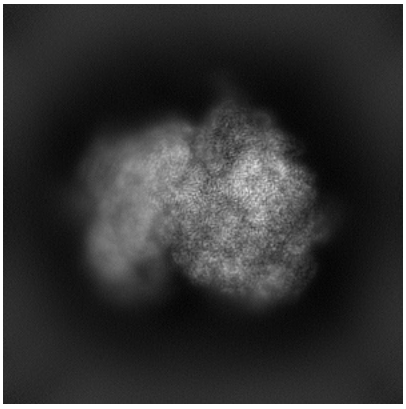


Z

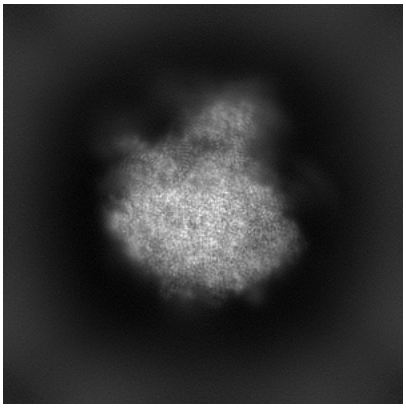
6.1.2 Raw map



X



Y

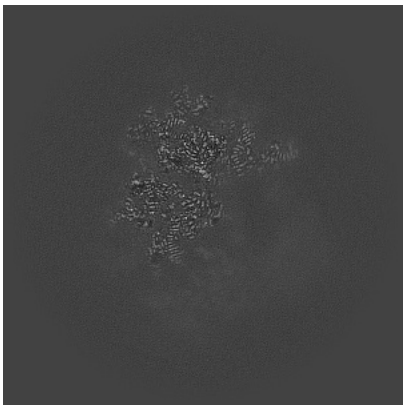


Z

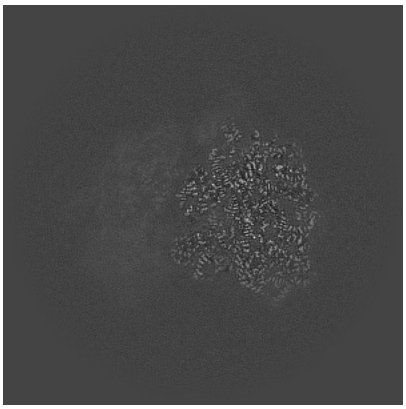
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

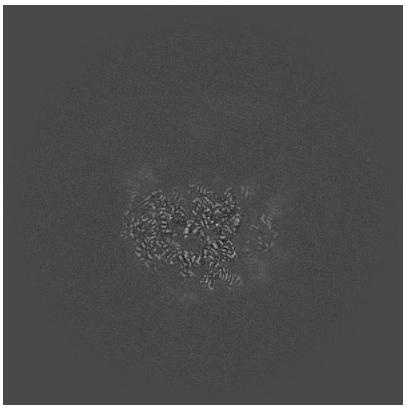
6.2.1 Primary map



X Index: 256

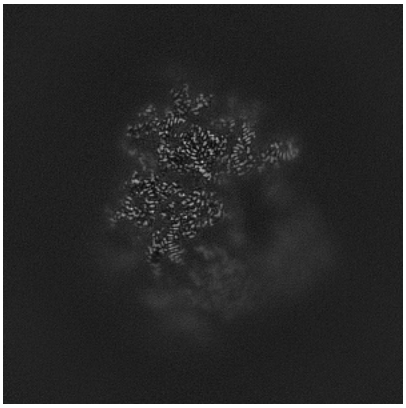


Y Index: 256

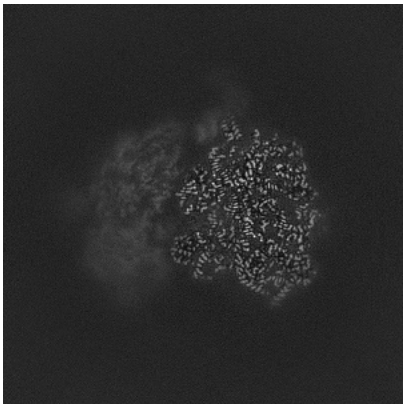


Z Index: 256

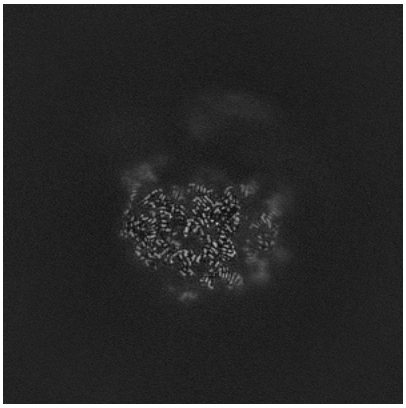
6.2.2 Raw map



X Index: 256



Y Index: 256

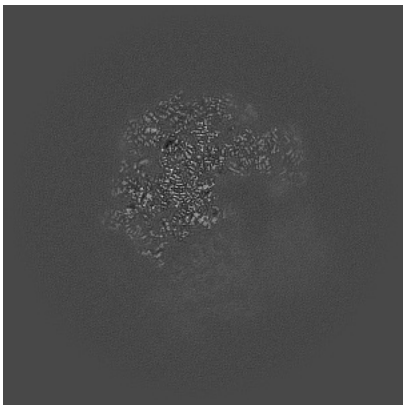


Z Index: 256

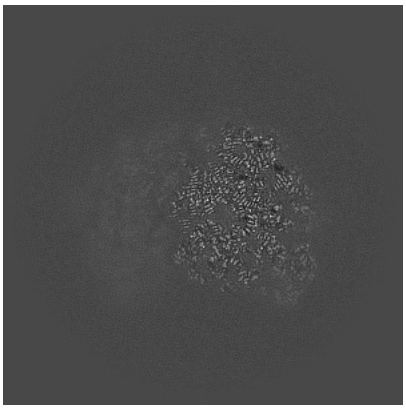
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

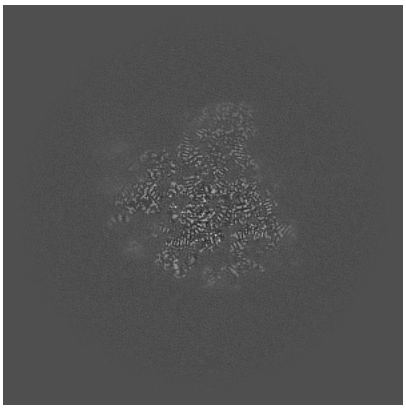
6.3.1 Primary map



X Index: 275

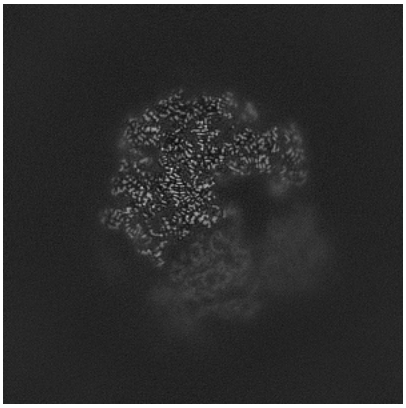


Y Index: 246

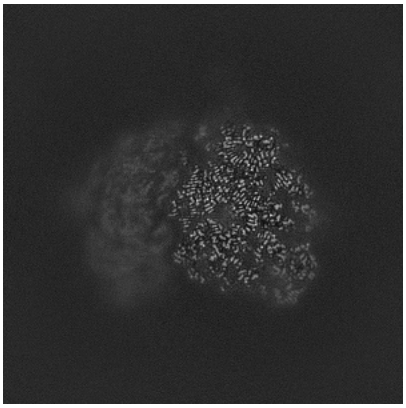


Z Index: 324

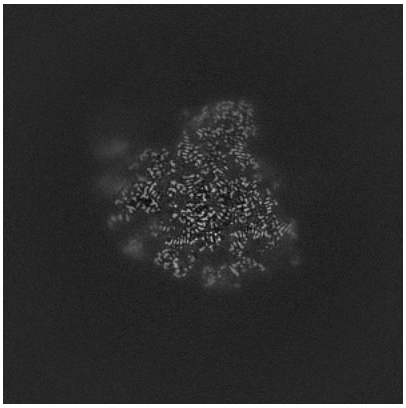
6.3.2 Raw map



X Index: 275



Y Index: 246

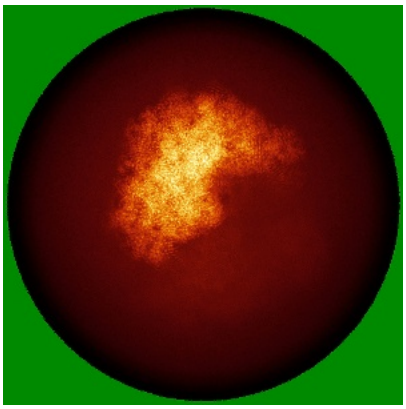


Z Index: 324

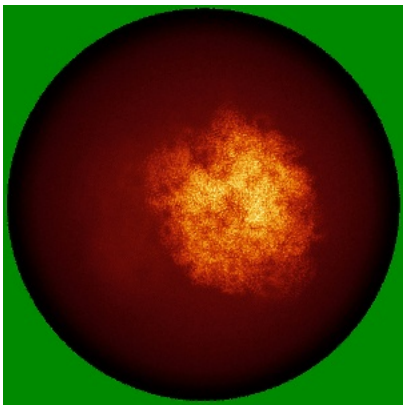
The images above show the largest variance slices of the map in three orthogonal directions.

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

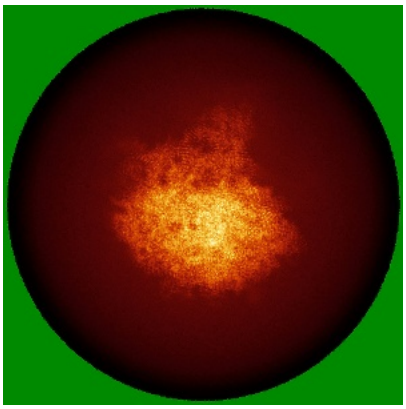
6.4.1 Primary map



X

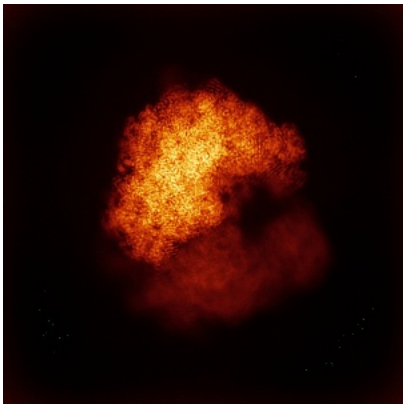


Y

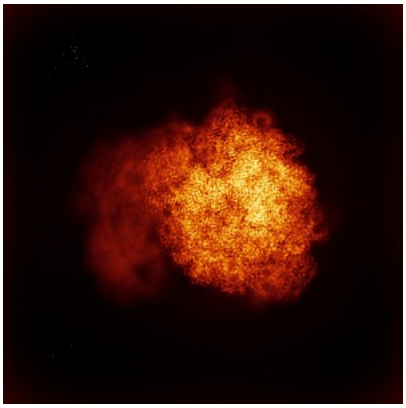


Z

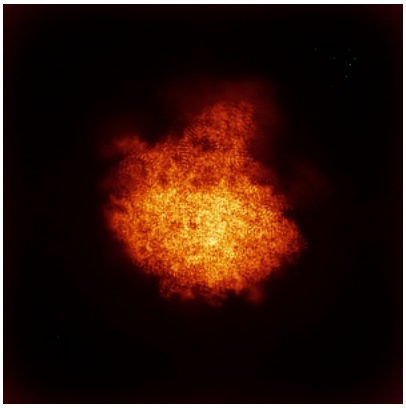
6.4.2 Raw map



X



Y

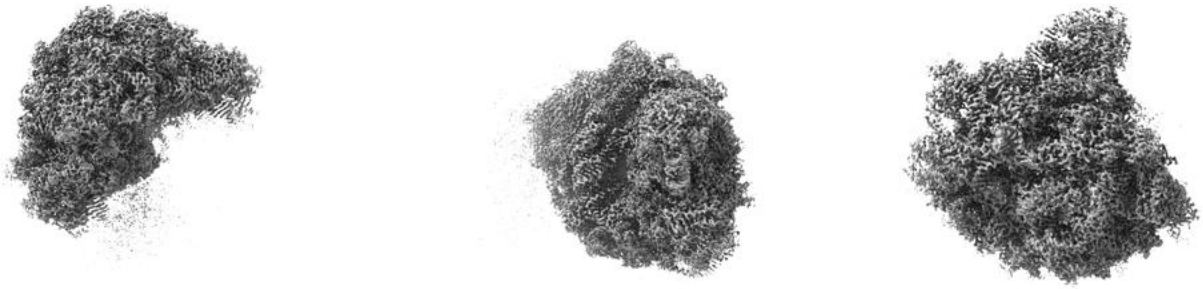


Z

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)

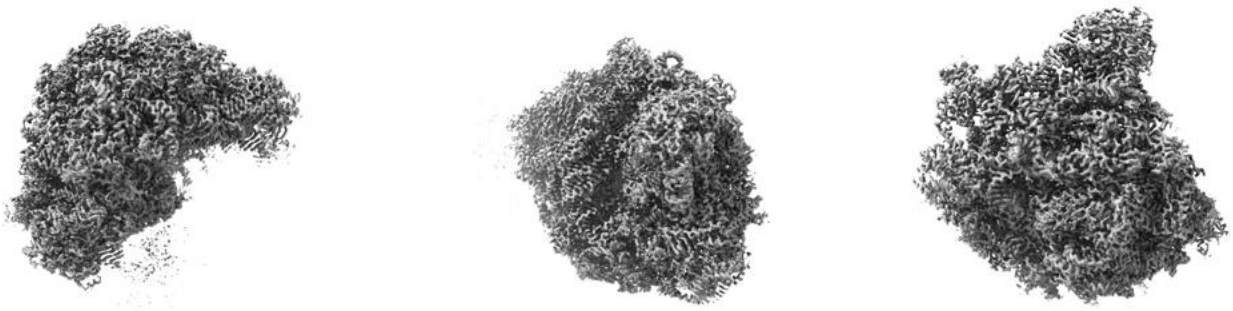
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.38. 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



X Y Z

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.

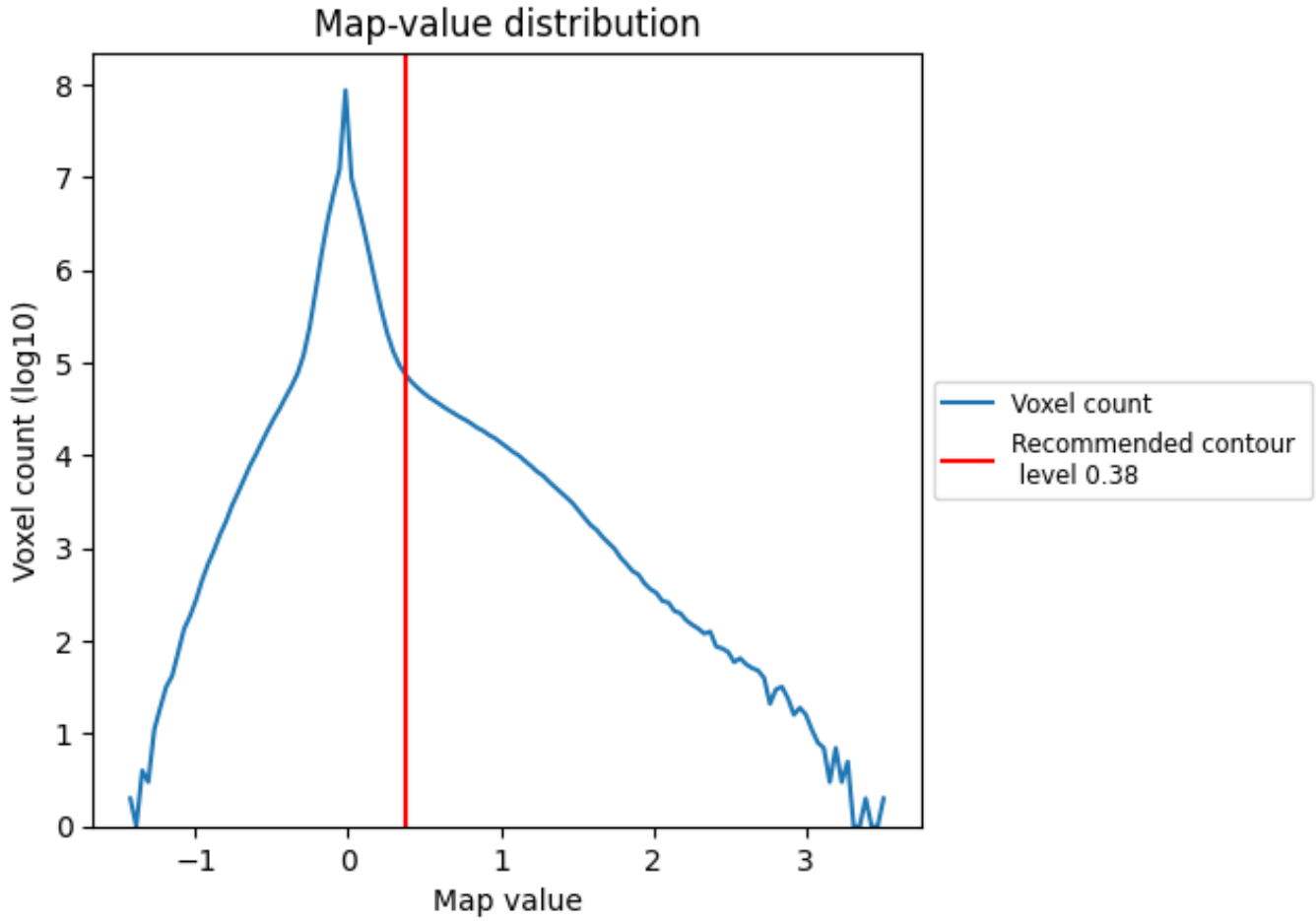
6.6 Mask visualisation (i)

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

7 Map analysis

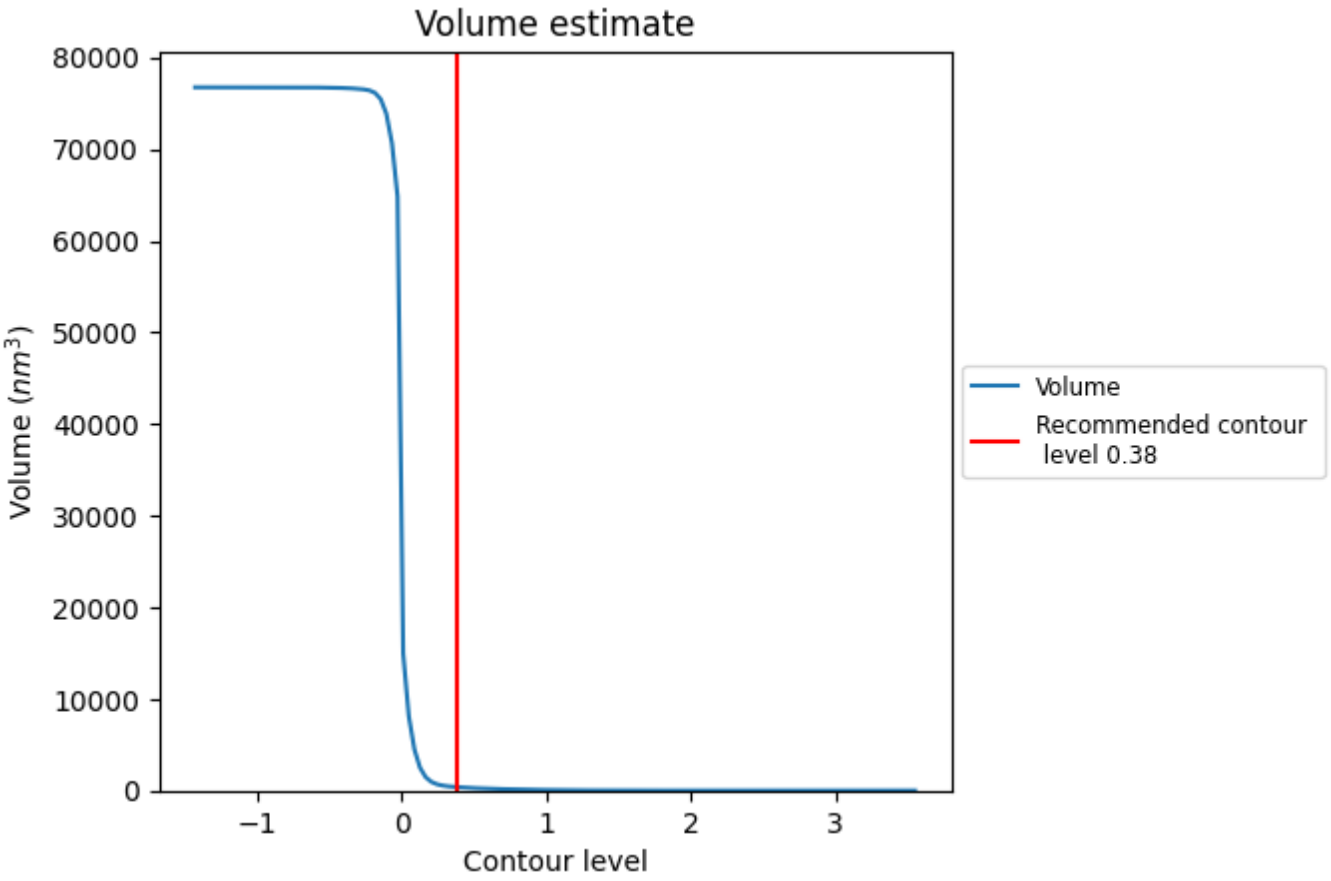
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

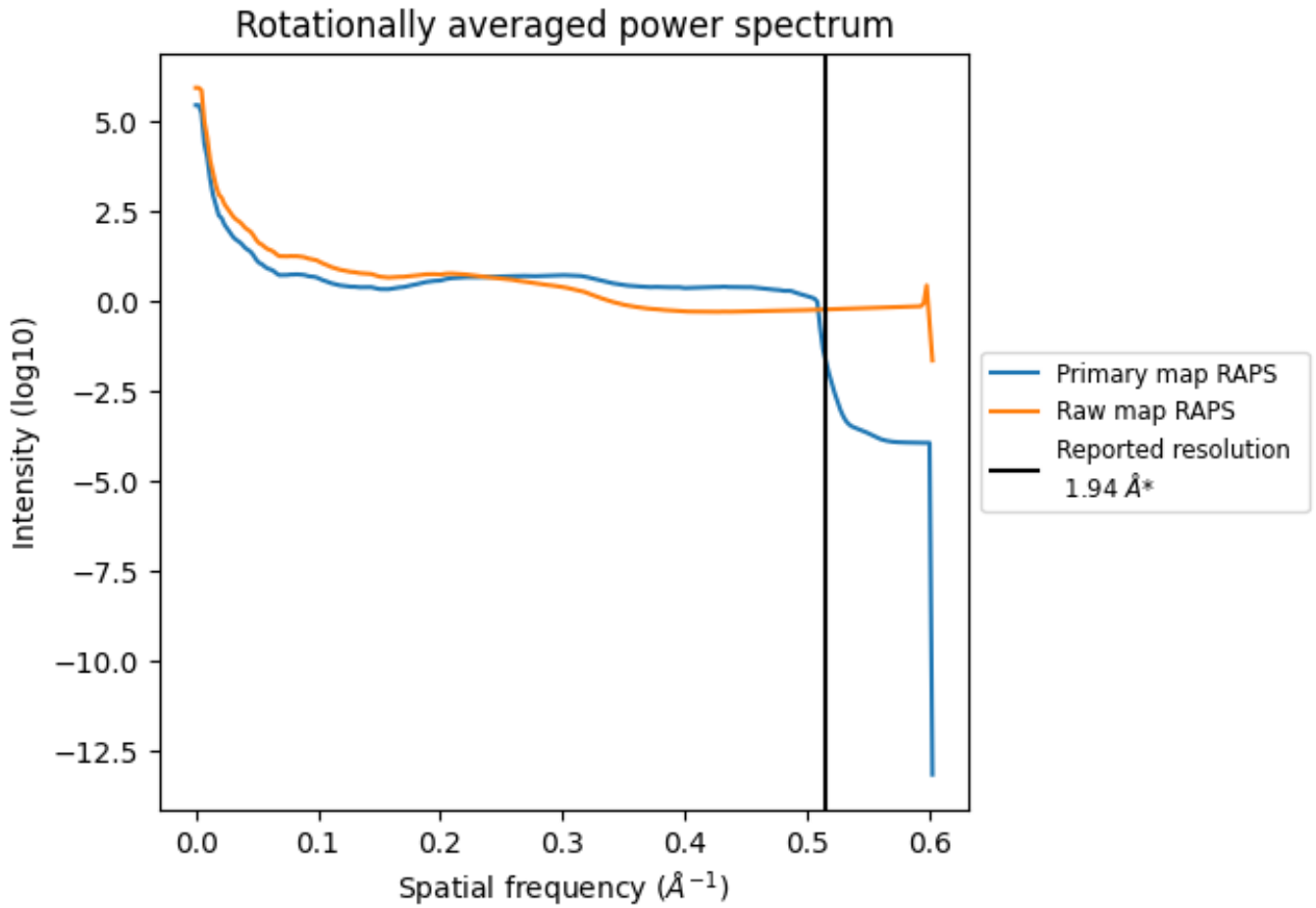
7.2 Volume estimate



The volume at the recommended contour level is 381 nm^3; this corresponds to an approximate mass of 344 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)

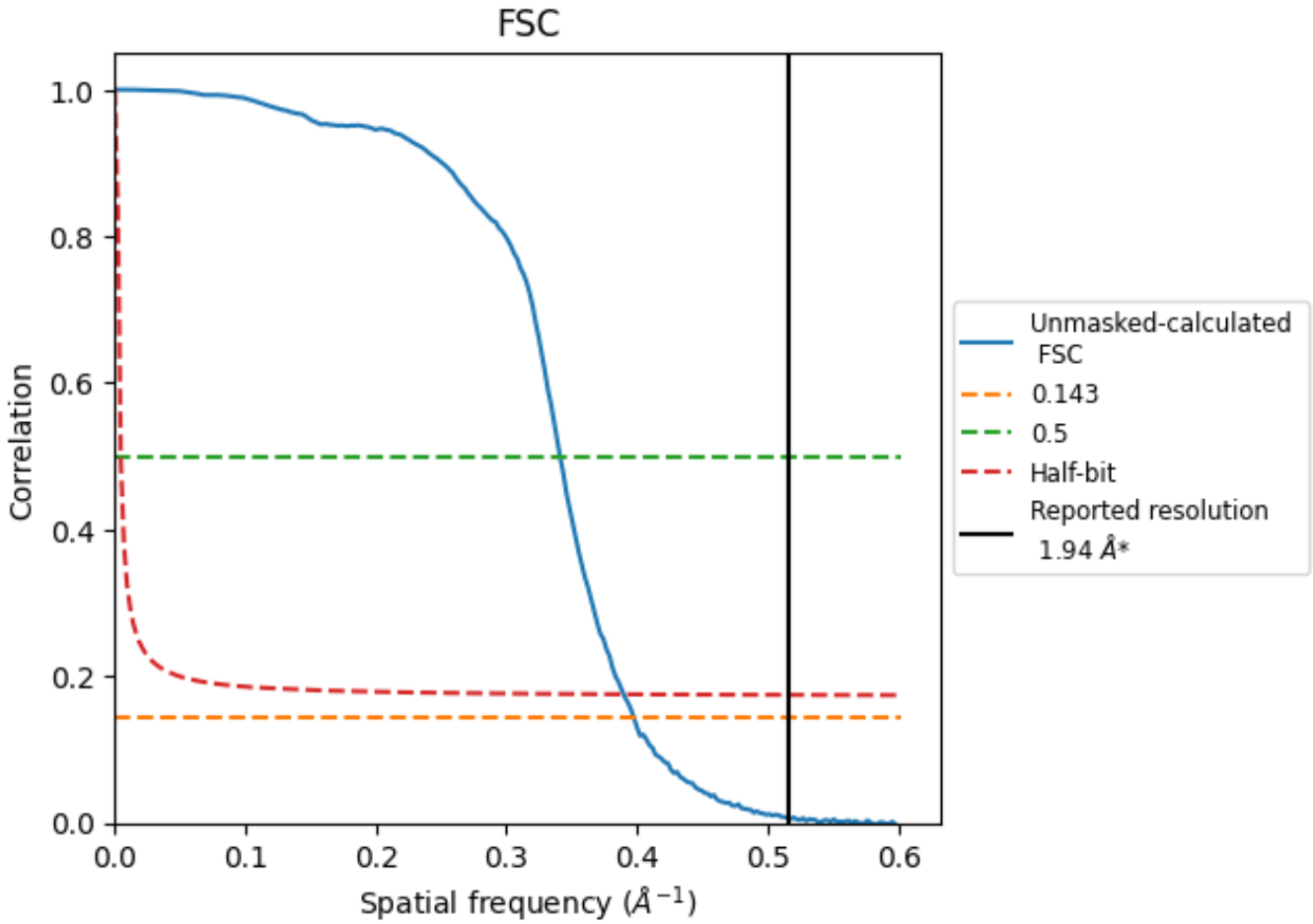


*Reported resolution corresponds to spatial frequency of 0.515 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.515 Å^{-1}

8.2 Resolution estimates (i)

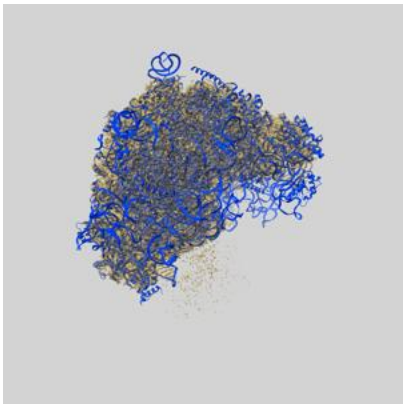
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	1.94	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.52	2.93	2.57

*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 2.52 differs from the reported value 1.94 by more than 10 %

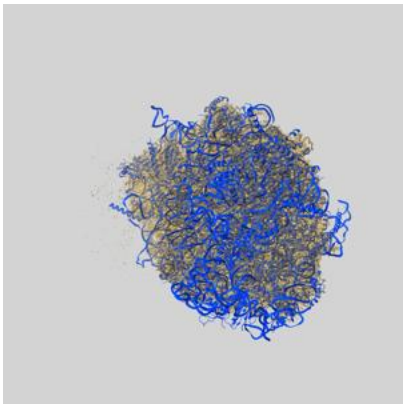
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-43973 and PDB model 9AXU. Per-residue inclusion information can be found in section 3 on page 12.

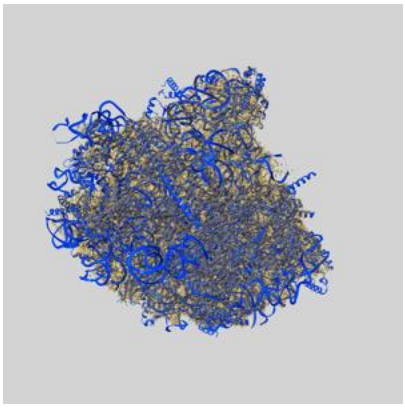
9.1 Map-model overlay



X



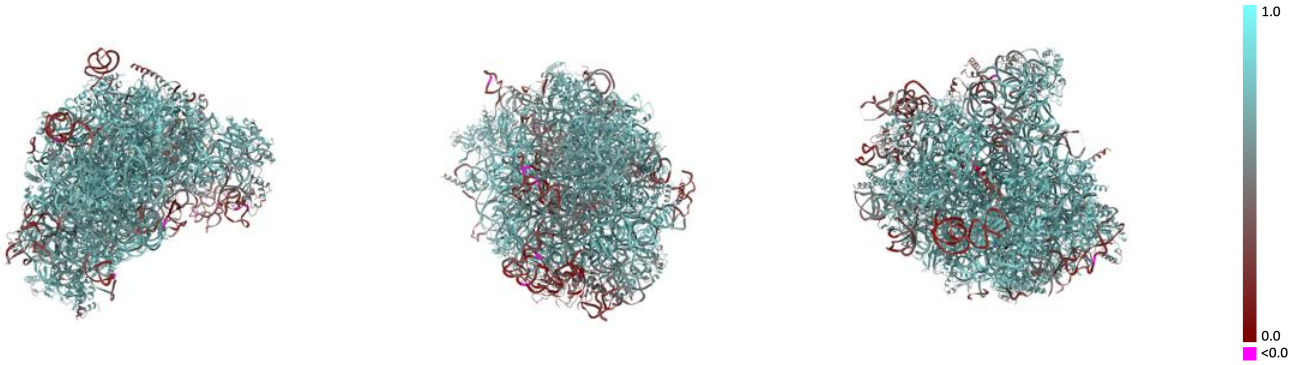
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.38 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.

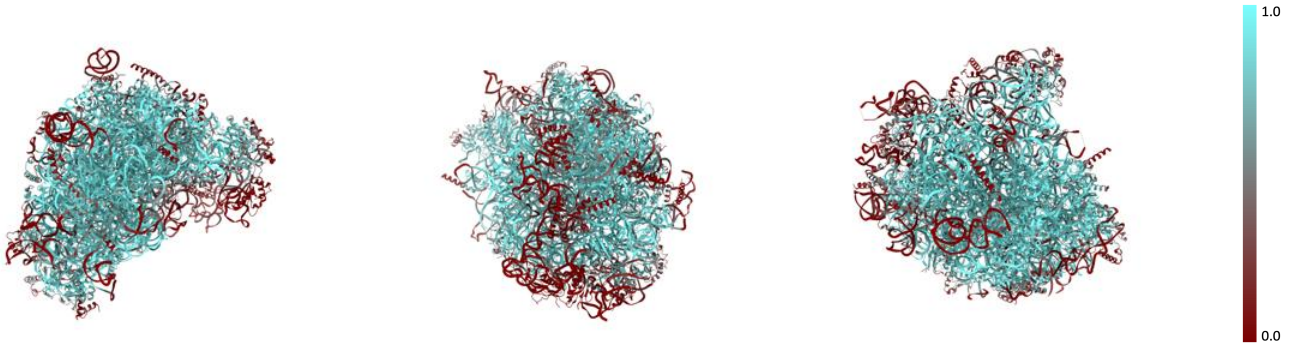
9.2 Q-score mapped to coordinate model (i)



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.

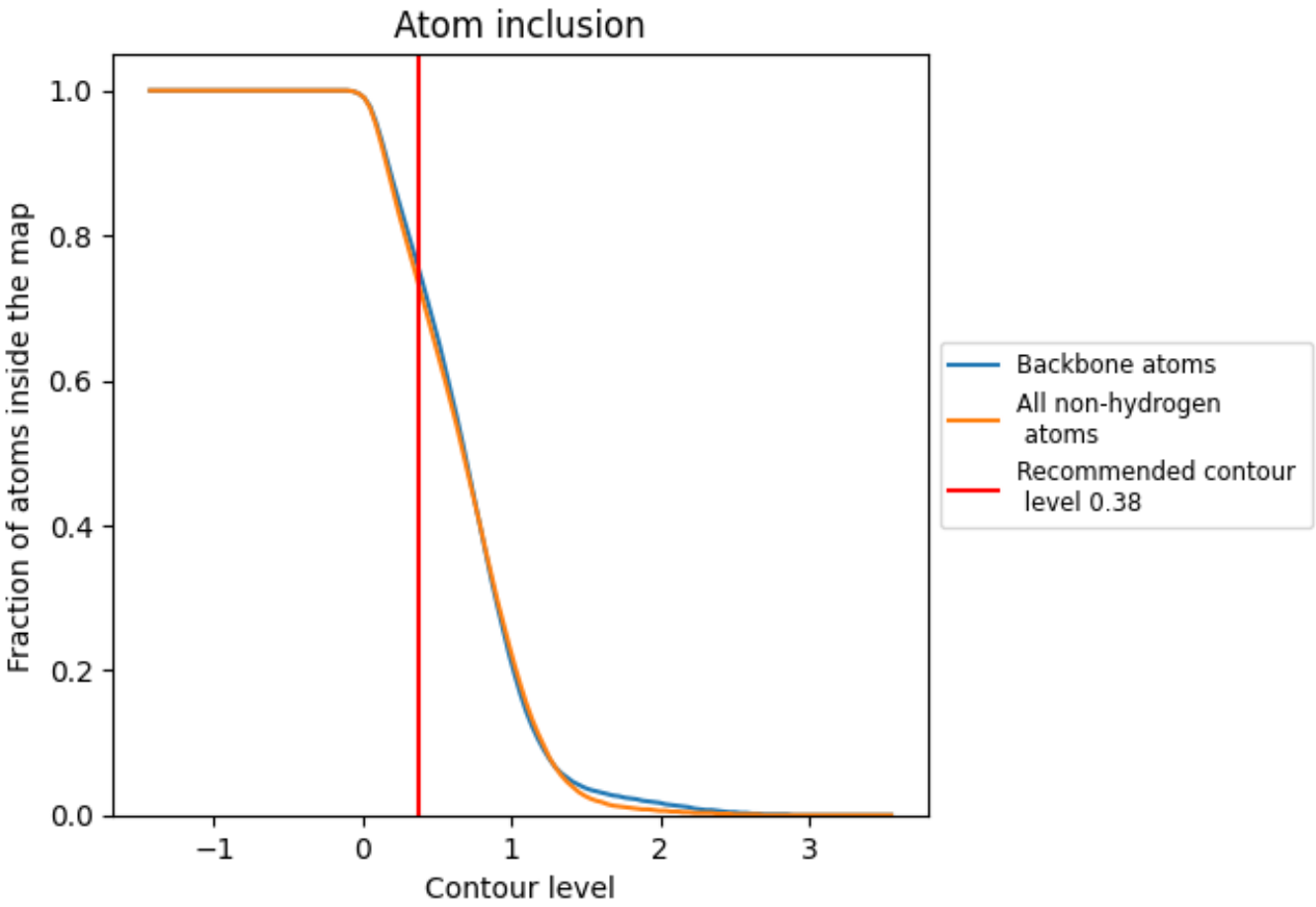
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.38).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 73% 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 (0.38) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7290	0.6610
0	0.6590	0.6920
1	0.7990	0.7110
2	0.7360	0.6390
3	0.7530	0.6620
4	0.8300	0.6840
N	0.9360	0.7670
O	0.8860	0.7510
P	0.8990	0.7550
Q	0.5560	0.6430
R	0.5680	0.6300
S	0.8200	0.7180
T	0.6350	0.6780
U	0.0030	0.3280
V	0.0340	0.4920
W	0.0980	0.4460
X	0.7390	0.7060
Y	0.5390	0.6550
Z	0.9830	0.7810
a	0.8620	0.7510
b	0.8970	0.7610
c	0.8850	0.7540
d	0.8380	0.7280
e	0.7350	0.6940
f	0.7040	0.6870
g	0.3370	0.5810
h	0.8410	0.7390
i	0.5790	0.6840
j	0.8320	0.7330
k	0.7390	0.7150
l	0.6230	0.6720
m	0.9330	0.7690
n	0.7860	0.7160
o	0.6120	0.6610
p	0.8230	0.7190

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Chain	Atom inclusion	Q-score
q	0.8980	0.7610
r	0.8770	0.7450
s	0.8980	0.7490
t	0.7550	0.7170
u	0.7950	0.7210
v	0.9510	0.7790
w	0.3970	0.5910
x	0.6240	0.6430
y	0.5960	0.6890