



wwPDB EM Validation Summary Report ⓘ

Oct 28, 2024 – 03:24 am GMT

PDB ID : 6YLX
EMDB ID : EMD-10841
Title : pre-60S State NE1 (TAP-Flag-Nop53)
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 3.90 Å(reported)
Based on initial models : 6N8J, 3JCT, 6ELZ

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 ⓘ 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 ⓘ](#)) were used in the production of this report:

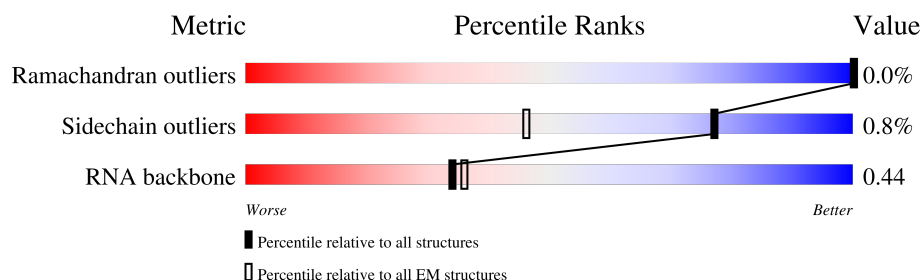
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) :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

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.90 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 $\leq 5\%$. 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	B	387	<div> <div>13%</div> <div>92%</div> <div>8%</div> </div>
2	C	362	<div> <div>90%</div> <div>9%</div> </div>
3	E	176	<div> <div>5%</div> <div>85%</div> <div>11%</div> </div>
4	F	244	<div> <div>84%</div> <div>7%</div> <div>9%</div> </div>
5	G	256	<div> <div>10%</div> <div>69%</div> <div>5%</div> <div>25%</div> </div>
6	H	191	<div> <div>8%</div> <div>94%</div> <div>6%</div> </div>
7	K	376	<div> <div>46%</div> <div>68%</div> <div>32%</div> </div>
8	L	199	<div> <div>15%</div> <div>84%</div> <div>10%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
9	M	138	
10	N	204	
11	O	199	
12	P	184	
13	Q	186	
14	R	189	
15	S	172	
16	T	160	
17	U	121	
18	V	137	
19	W	236	
20	X	142	
21	Y	127	
22	Z	136	
23	a	149	
24	b	647	
25	c	105	
26	d	113	
27	e	130	
28	f	107	
29	g	121	
30	h	120	
31	i	100	
32	j	88	
33	k	78	

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Mol	Chain	Length	Quality of chain
34	l	51	
35	n	605	
36	o	220	
37	q	455	
38	r	261	
39	s	520	
40	t	322	
41	u	199	
42	y	245	
43	z	106	
44	1	3396	
45	2	158	
46	6	232	
47	w	841	

2 Entry composition

There are 47 unique types of molecules in this entry. The entry contains 118882 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 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	386	Total	C	N	O	S	0	0
			3081	1956	584	533	8		

- Molecule 2 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 3 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 4 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	192	Total	C	N	O	S	0	0
			1515	974	267	272	2		

- Molecule 6 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 7 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 8 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	187	Total	C	N	O	S	0	0
			1499	934	307	258			

- Molecule 9 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	180	Total	C	N	O	S	0	0
			1543	968	325	249	1		

- Molecule 11 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 12 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	P	176	Total	C	N	O	S	0	0
			1397	868	279	250			

- Molecule 13 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 14 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 16 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	56	Total	C	N	O	S	0	0
			434	268	86	79	1		

- Molecule 17 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	U	106	Total	C	N	O	0	0
			844	545	138	161		

- Molecule 18 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 19 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	234	Total	C	N	O	S	0	0
			1885	1194	323	362	6		

- Molecule 20 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

- Molecule 21 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	a	93	Total	C	N	O	S	0	0
			735	479	130	125	1		

- Molecule 24 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	b	470	Total	C	N	O	S	0	0
			3814	2424	663	709	18		

- Molecule 25 is a protein called 60S ribosomal protein L30.

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

- Molecule 26 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 27 is a protein called 60S ribosomal protein L32.

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

- Molecule 28 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 30 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L38.

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

- Molecule 34 is a protein called 60S ribosomal protein L39.

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

- Molecule 35 is a protein called Pescadillo homolog.

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

- Molecule 36 is a protein called Ribosome biogenesis protein 15.

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

- Molecule 37 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	q	87	Total	C	N	O	S	0	0
			723	450	129	143	1		

- Molecule 38 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	r	217	Total	C	N	O	S	0	0
			1760	1110	334	309	7		

- Molecule 39 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

- Molecule 40 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 41 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	u	123	Total	C	N	O	S	0	0
			1040	652	211	168	9		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	y	244	Total	C	N	O	S	0	0
			1849	1146	319	377	7		

- Molecule 43 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	z	55	Total	C	N	O	0	0
			444	273	88	83		

- Molecule 44 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1	2534	Total	C	N	O	P	0	0
			54232	24220	9799	17679	2534		

- Molecule 45 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	2	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 46 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

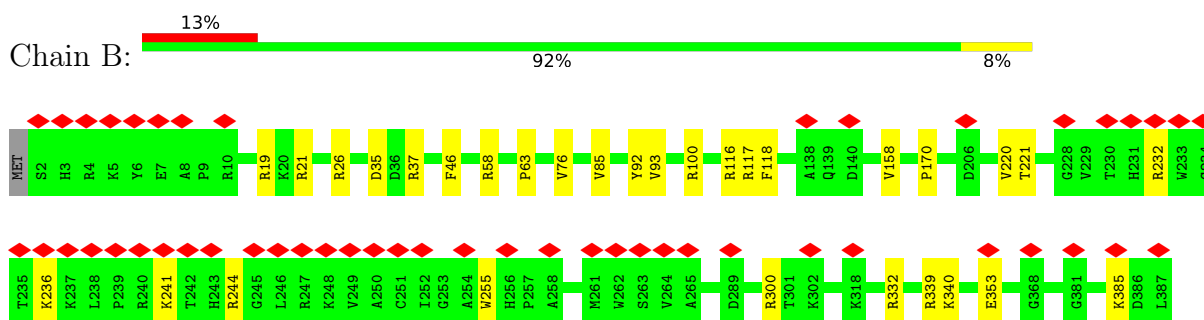
- Molecule 47 is a protein called 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	360	Total	C	N	O	S	0	0
			2898	1860	507	516	15		

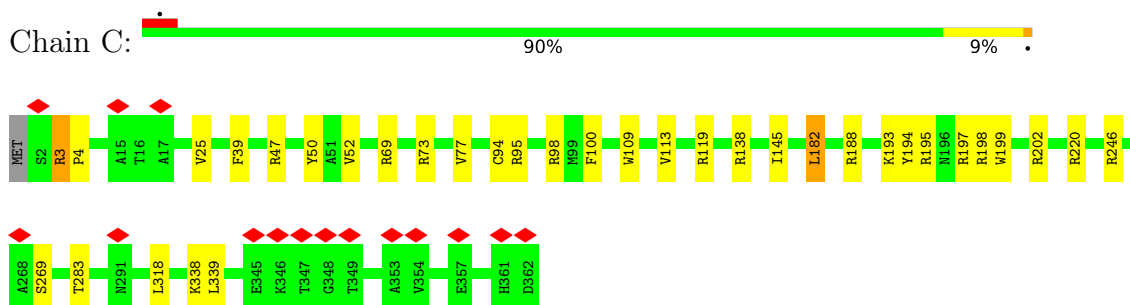
3 Residue-property plots [i](#)

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.

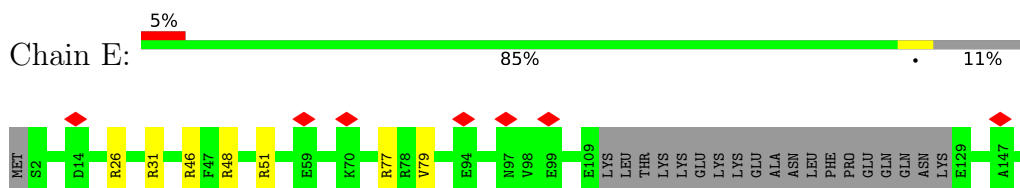
- Molecule 1: 60S ribosomal protein L3



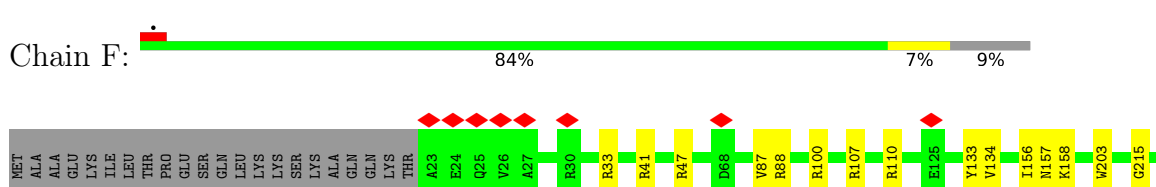
- Molecule 2: 60S ribosomal protein L4-A

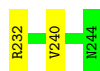


- Molecule 3: 60S ribosomal protein L6-A

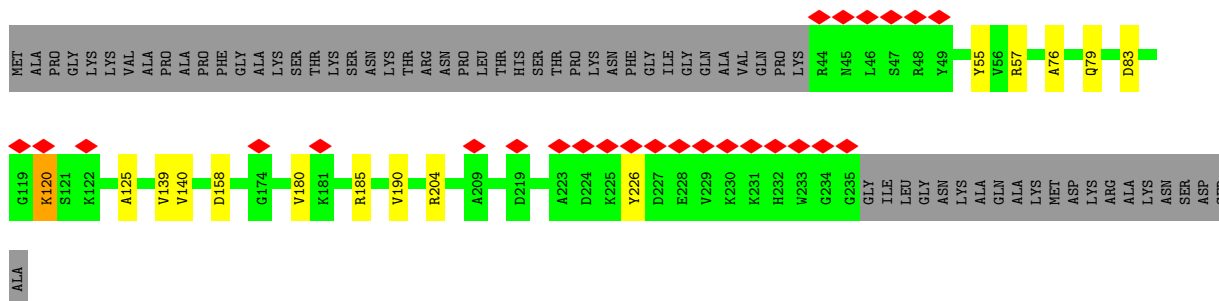


- Molecule 4: 60S ribosomal protein L7-A

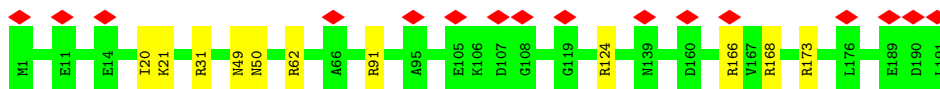




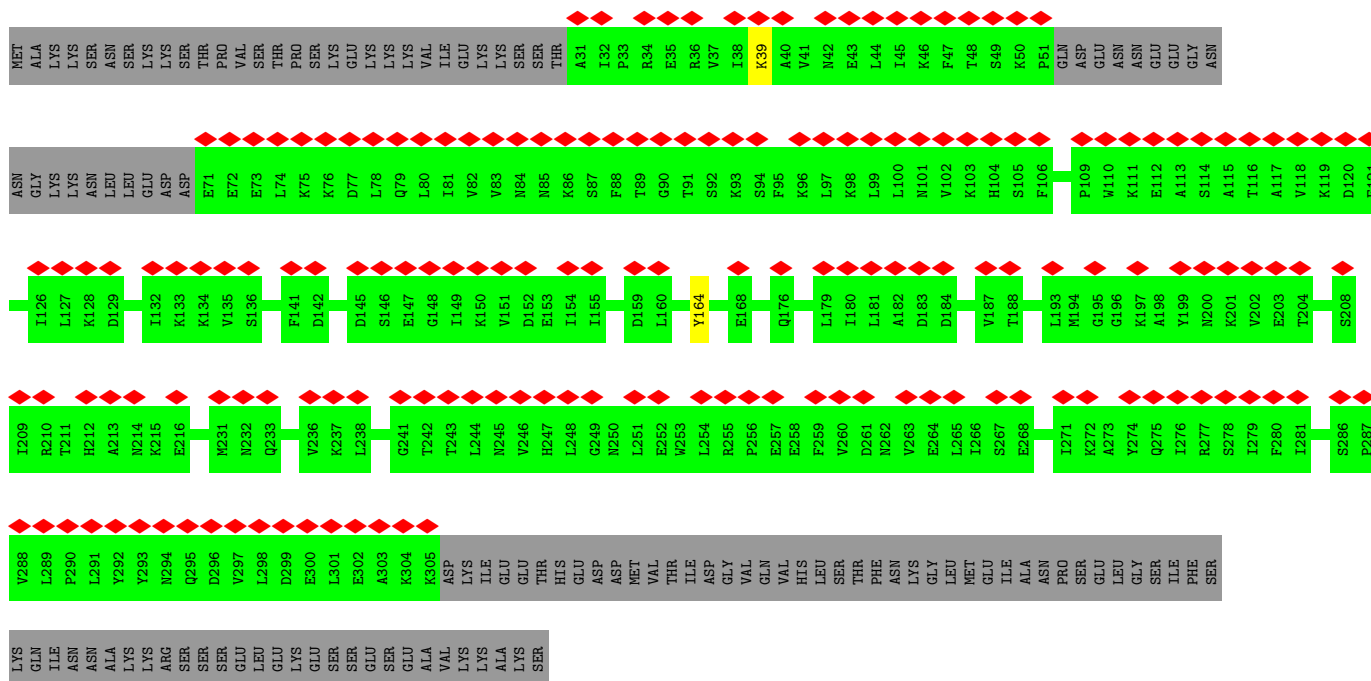
- Molecule 5: 60S ribosomal protein L8-A



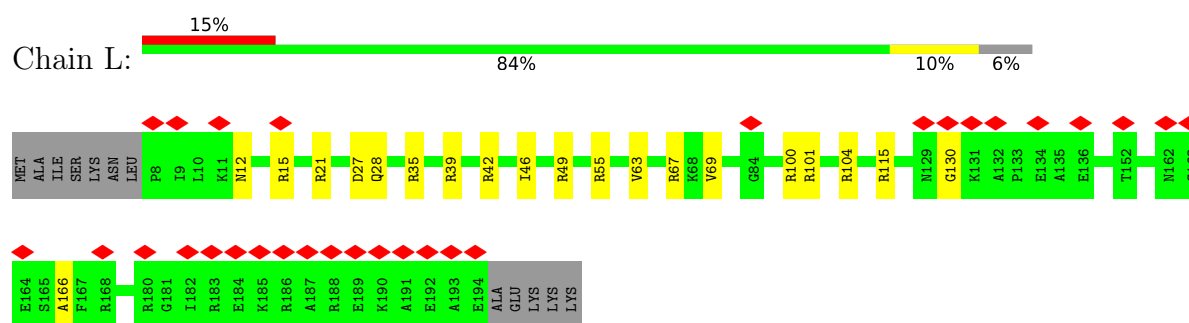
- Molecule 6: 60S ribosomal protein L9-A



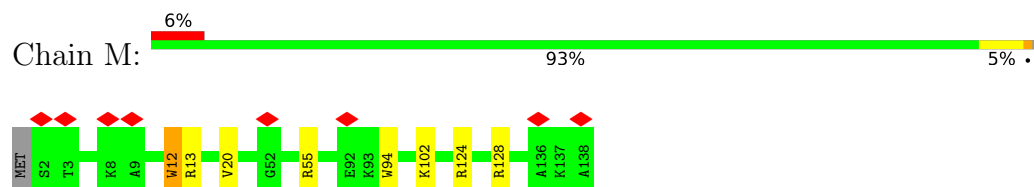
- Molecule 7: Proteasome-interacting protein CIC1



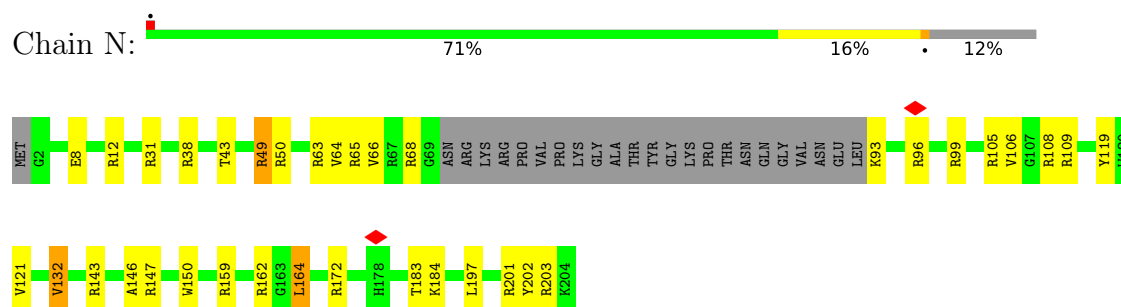
- Molecule 8: 60S ribosomal protein L13-A



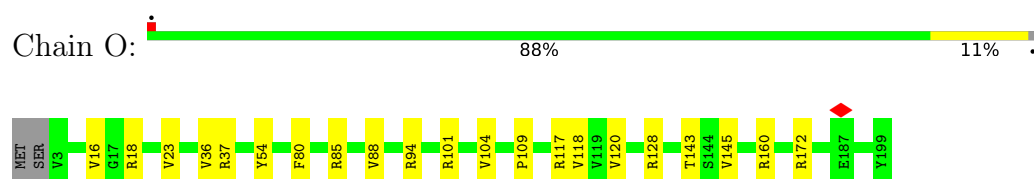
- Molecule 9: 60S ribosomal protein L14-A



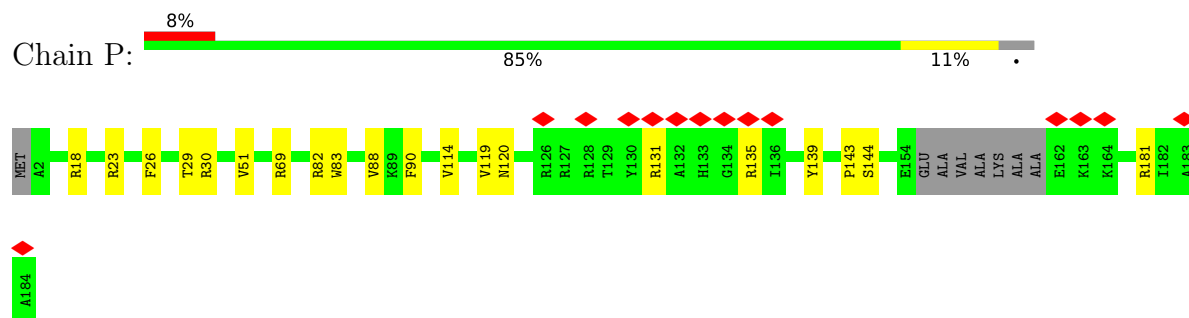
- Molecule 10: 60S ribosomal protein L15-A



- Molecule 11: 60S ribosomal protein L16-A

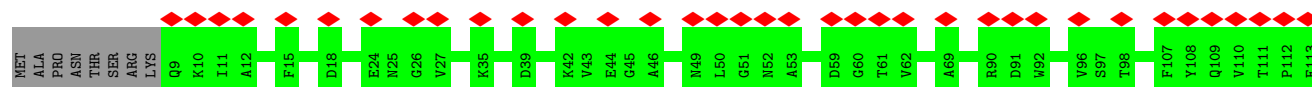


- Molecule 12: 60S ribosomal protein L17-A



- Molecule 13: 60S ribosomal protein L18-A

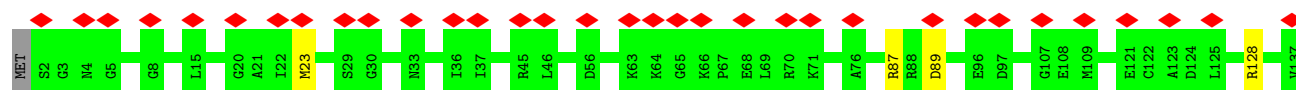






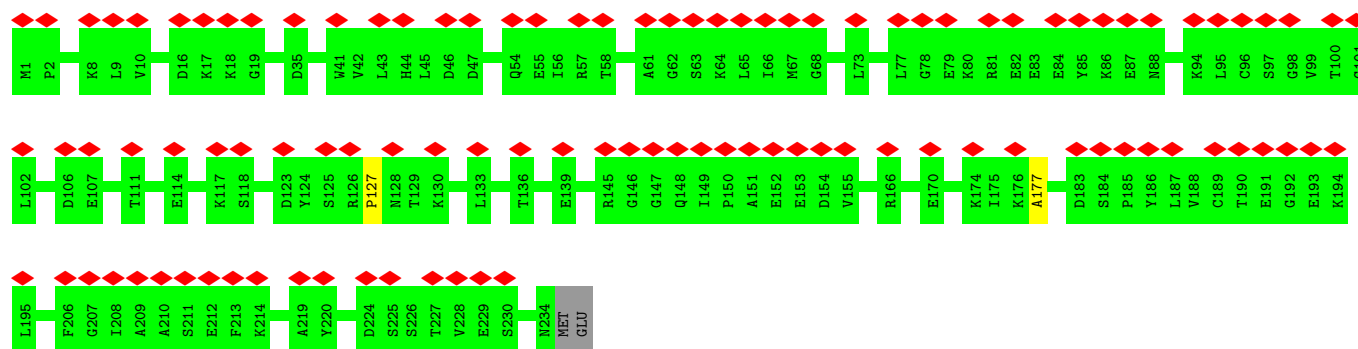
- Molecule 18: 60S ribosomal protein L23-A

Chain V: 24% 96%



- Molecule 19: Ribosome assembly factor MRT4

Chain W: 44% 98%



- Molecule 20: 60S ribosomal protein L25

Chain X: 11% 94% 5%



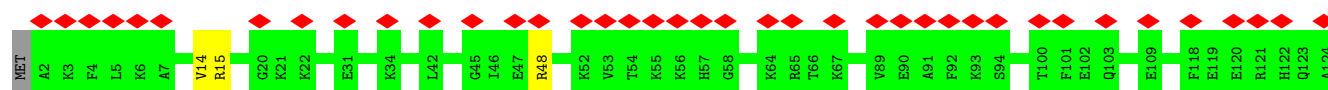
- Molecule 21: 60S ribosomal protein L26-A

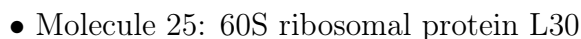
Chain Y: 94% 6%

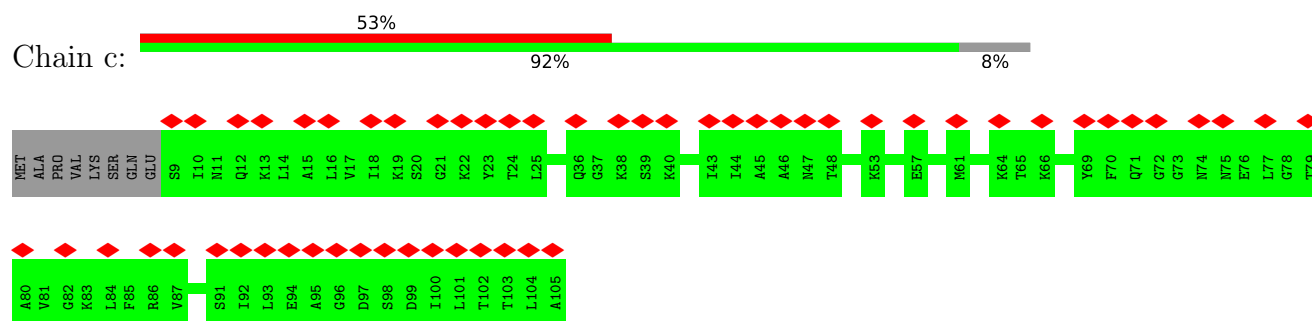


- Molecule 22: 60S ribosomal protein L27-A

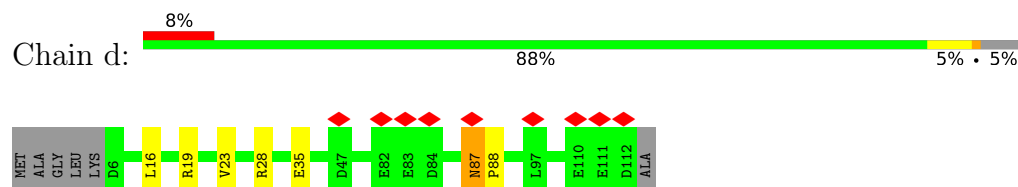
Chain Z: 29% 97%



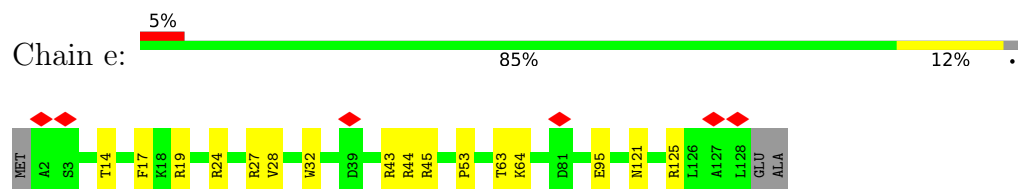




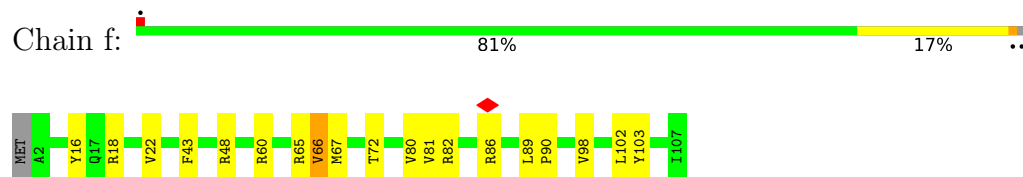
- Molecule 26: 60S ribosomal protein L31-A



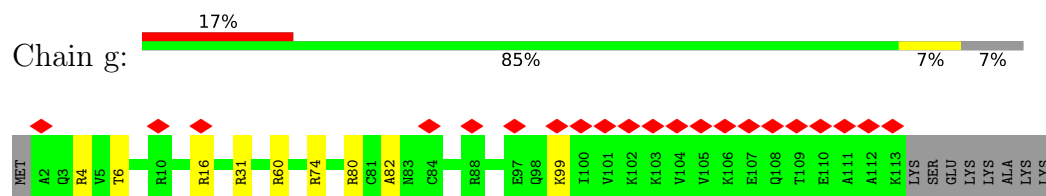
- Molecule 27: 60S ribosomal protein L32



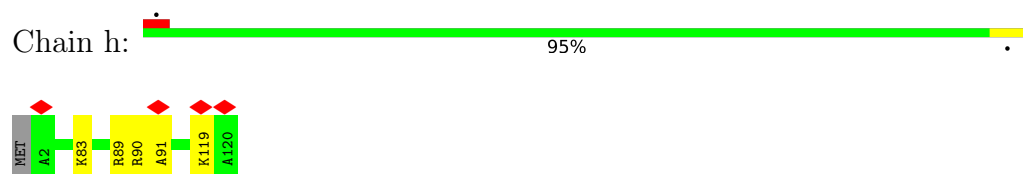
- Molecule 28: 60S ribosomal protein L33-A



- Molecule 29: 60S ribosomal protein L34-A

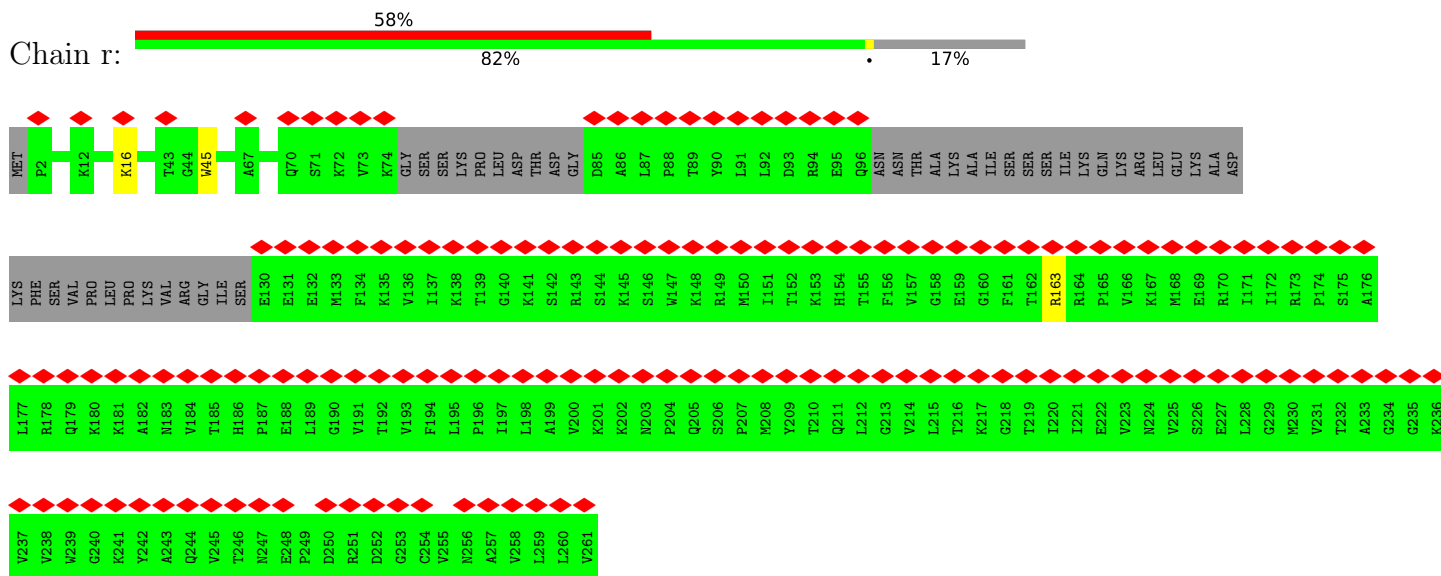


- Molecule 30: 60S ribosomal protein L35-A

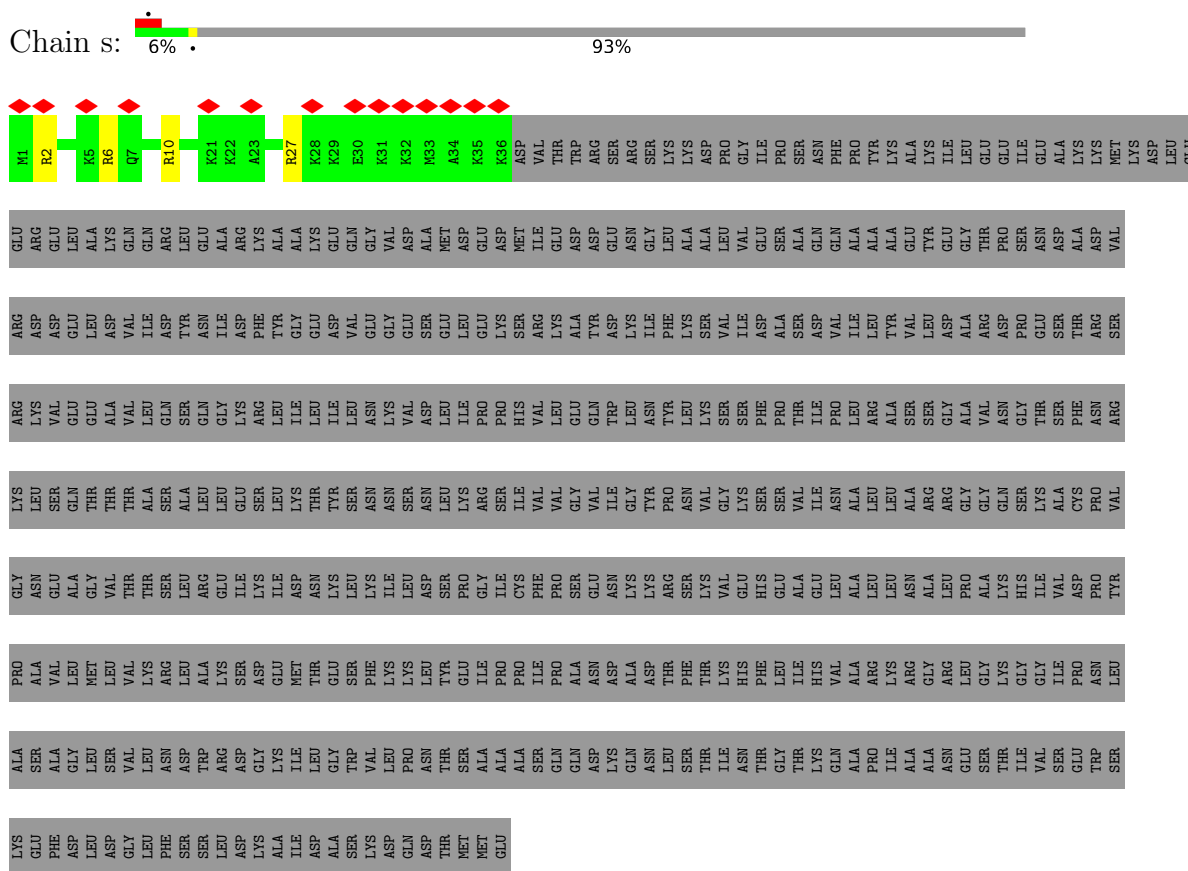


- Molecule 31: 60S ribosomal protein L36-A

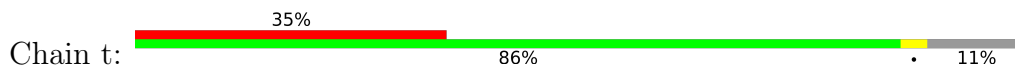




- Molecule 39: Nuclear GTP-binding protein NUG1

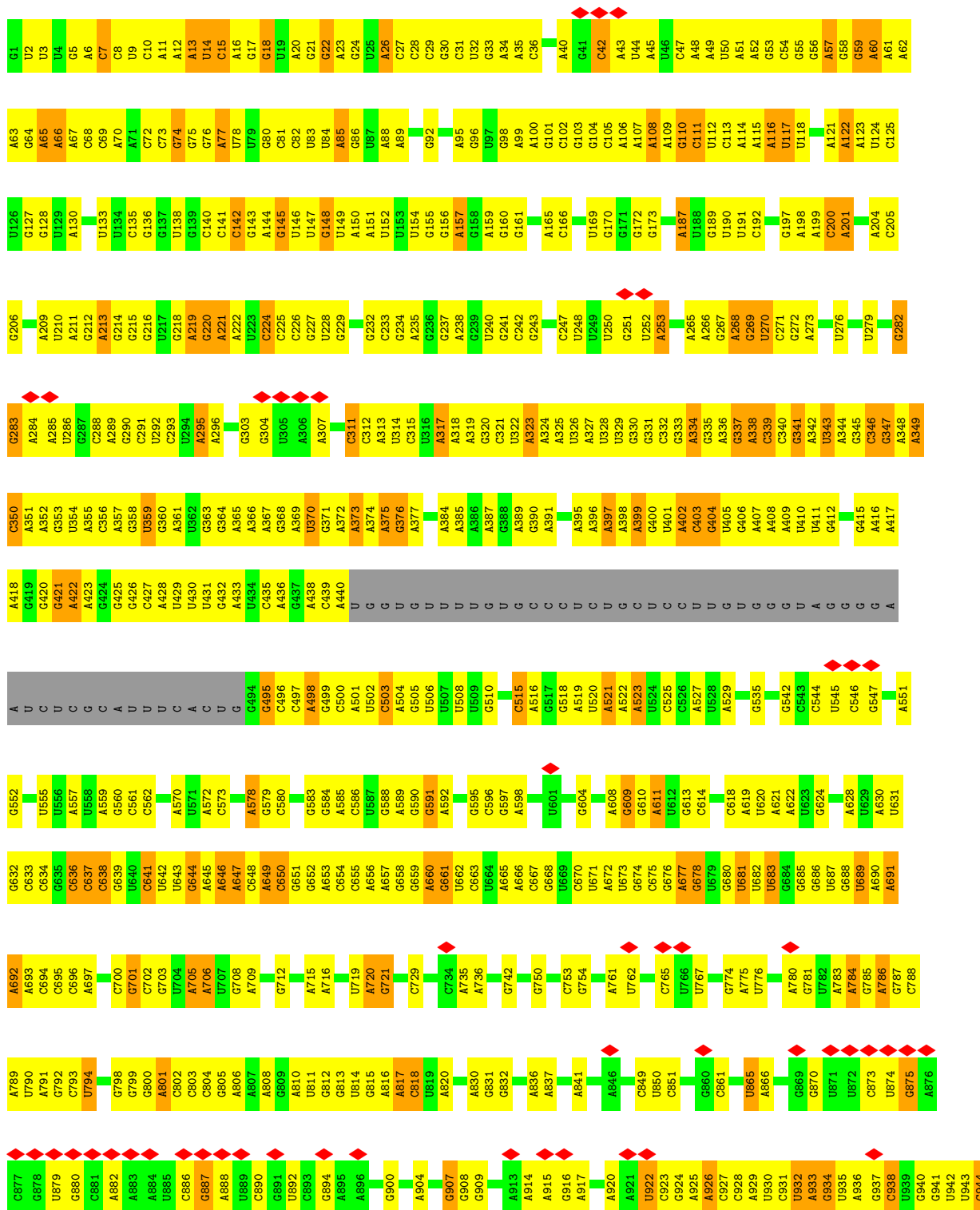
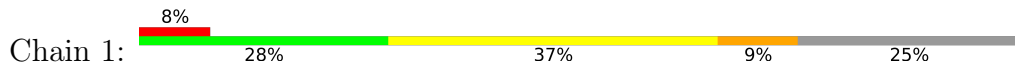


- Molecule 40: Ribosome biogenesis protein RLP7

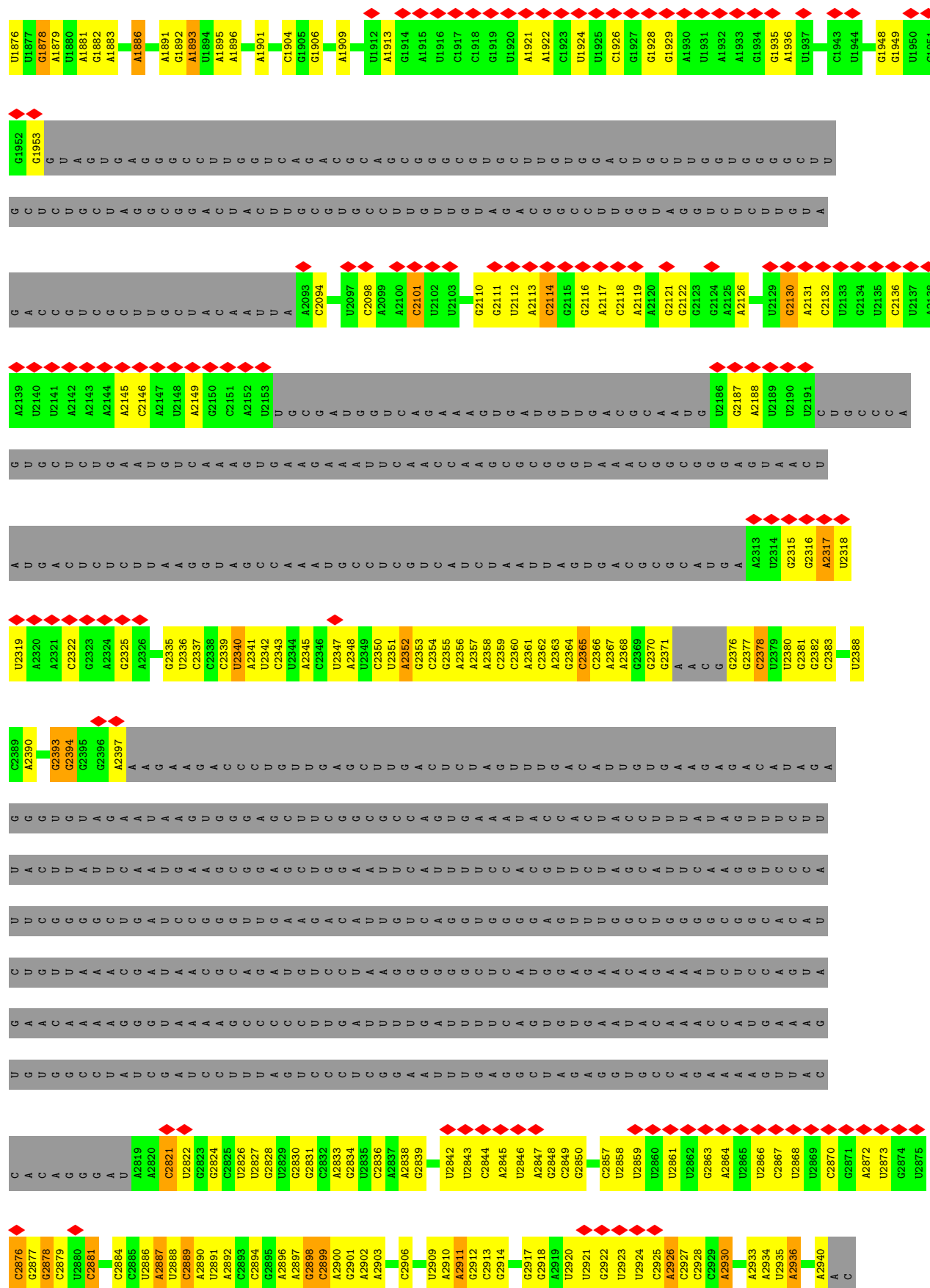


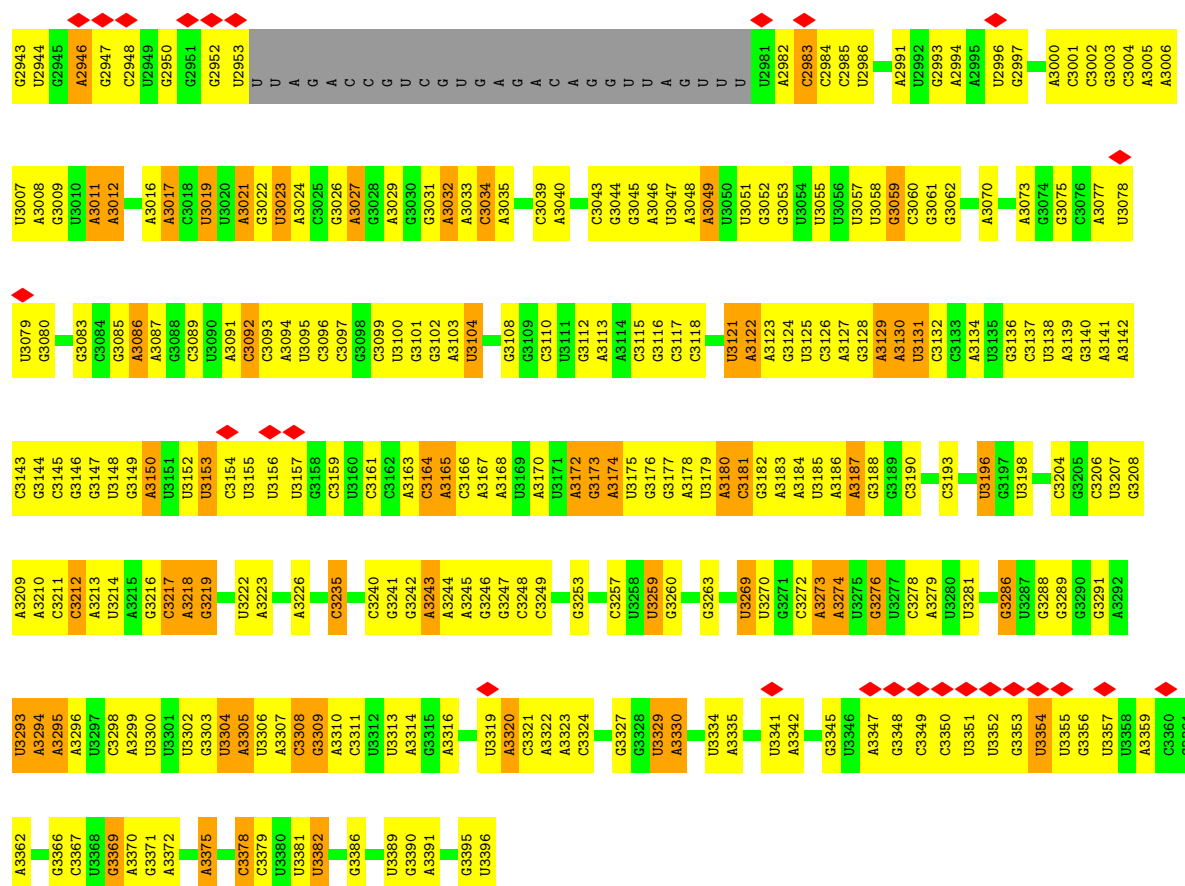
HIS
THR
TYR
LYS
LYS
ALA
LYS
LEU
MET
LYS
GLN
SER
LYS
LYS
THR
SER
PHE
THR
ARG
PHE

● Molecule 44: 25S rRNA

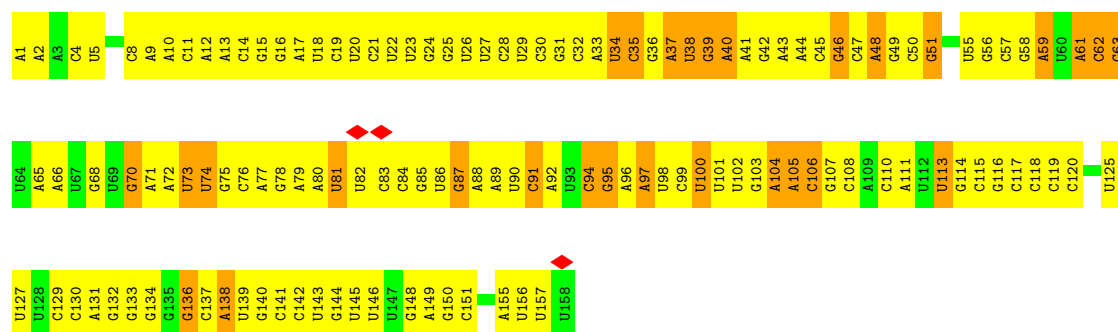


U1801	C1802	A1696	G1599	C1831	A1462	C1402	U1341	C1279	A1200	G1140	U	G	C945
C1803	A1602	C1532	U1463	C1403	U1463	C1403	C1342	C1280	C1201	C1141	U	G	U946
A1804	A1603	U1533	G1465	G1404	G1465	G1404	G1281	G1281	A1202	A1142	A	U	G947
C1805	G1604	A1534	G1466	U1405	G1466	U1405	G1282	G1282	A1203	A1143	C	U	C948
A1806	A1605	A1535	G1467	A1406	G1467	A1406	C1283	C1283	A1204	U1144	U	C	C949
A1810	A1606	G1536	U1468	A1407	U1468	A1407	G1284	G1284	A1205	G1145	U	C	G950
G1811	U1607	A1537	C1469	G1408	U1469	G1408	G1285	G1285	G1206	C1146	A	G	A951
A1812	C1608	G1538	U1470	U1409	U1470	U1409	A1286	A1286	G1207	G1147	U	G	A952
C1813	U1609	U1539	U1471	A1410	U1471	A1410	A1287	A1287	U1208	G1148	U	G	G953
A1814	A1610	G1540	U1472	C1411	U1472	C1411	A1290	A1290	G1209	G1149	U	G	U954
U1815	A1611	G1541	G1473	G1412	G1473	G1412	A1291	A1291	U1210	U1151	A	C	C959
A1816	A1612	G1542	U1474	U1413	U1474	U1413	A1292	A1292	U1211	U1152	A	C	U960
U1819	C1614	A1543	A1475	U1414	A1475	U1414	U1293	U1293	G1212	A1153	C	A	C961
U1820	A1615	U1476	U1476	C1415	U1476	C1415	A1355	A1355	A1222	C1154	U	A	A962
U1821	C1616	C1477	C1477	G1417	C1477	G1417	A1356	A1356	A1223	C1155	U	A	A965
A1822	G1617	A1478	C1478	A1418	C1478	A1418	G1357	G1357	G1226	G1156	G	U	G968
U1823	U1618	U1482	G1482	A1419	U1482	A1419	C1297	C1297	C1227	G1157	U	U	C969
G1824	A1619	G1483	G1483	C1420	G1483	C1420	C1358	C1358	U1226	A1158	U	A	A970
A1825	U1620	U1487	U1487	G1421	U1487	G1421	C1359	C1359	C1227	G1159	U	C	A971
A1828	A1621	C1487	C1487	C1423	C1487	C1423	U1361	U1361	A1231	G1161	U	U	A972
G1829	A1625	A1556	A1488	C1424	A1488	C1424	A1363	A1363	C1233	A1162	U	U	A973
C1832	U1629	A1557	A1489	U1425	A1489	U1425	C1364	C1364	G1234	G1163	U	G	A974
A1833	U1630	A1558	A1490	C1426	A1490	C1426	G1365	G1365	U1234	A1164	A	A	C975
U1834	A1631	A1559	A1491	U1427	A1491	U1427	A1366	A1366	G1237	A1165	U	C	U976
A1835	C1632	G1561	G1492	A1428	G1492	A1428	C1367	C1367	C1238	G1166	U	C	C977
C1836	A1633	C1562	U1493	G1429	U1493	G1429	A1368	A1368	C1239	G1167	U	U	G978
A1837	U1634	U1564	U1494	A1430	U1494	A1430	A1369	A1369	A1240	A1168	U	U	A979
U1838	G1635	G1565	C1495	G1431	C1495	G1431	G1370	G1370	A1241	A1169	U	U	A980
A1839	A1638	A1566	C1497	A1433	A1497	A1433	G1371	G1371	A1244	G1170	U	U	U981
U1840	C1639	A1567	A1498	G1434	A1498	G1434	C1372	C1372	A1245	A1171	U	C	C982
A1841	G1640	U1568	C1499	U1435	C1499	U1435	A1373	A1373	A1246	A1172	U	C	A983
U1842	U1641	U1569	C1502	U1436	U1569	U1436	G1374	G1374	U1247	G1173	A	A	U984
C1843	A1642	A1570	A1503	C1437	A1570	C1437	C1375	C1375	C1248	C1174	U	C	U985
U1844	U1643	A1571	A1504	U1438	A1571	U1438	G1376	G1376	G1249	G1175	U	U	U986
G1845	U1644	U1574	C1505	U1439	U1574	U1439	U1377	U1377	C1254	G1176	U	U	A1047
A1846	U1645	A1575	A1506	G1440	A1575	G1440	G1378	G1378	C1255	G1177	U	U	C1048
U1847	A1647	C1574	C1507	U1442	C1507	U1442	G1380	G1380	C1256	G1178	U	U	C1049
C1848	A1654	C1579	C1508	G1443	C1508	G1443	A1381	A1381	U1258	A1179	U	U	U1050
U1849	G1655	A1580	A1509	U1444	A1580	U1444	G1382	G1382	U1259	A1180	U	U	U1051
A1850	C1656	C1581	U1510	U1445	C1581	U1445	G1383	G1383	A1261	G1181	U	U	U1052
G1851	A1657	C1582	U1511	A1446	C1582	A1446	U1384	U1384	G1262	G1182	U	U	U1053
U1854	C1663	C1583	U1512	G1447	C1583	G1447	C1385	C1385	A1263	G1183	U	U	A1054
C1855	G1664	A1584	G1513	U1448	A1584	U1448	A1386	A1386	G1264	G1184	U	U	A1055
U1856	U1665	U1584	G1514	A1449	U1584	A1449	G1387	G1387	U1265	C1185	U	U	G993
A1857	G1666	U1585	U1515	G1450	U1585	G1450	U1388	U1388	G1266	G1186	U	U	G994
U1858	C1667	C1586	A1516	C1451	C1586	C1451	G1389	G1389	U1267	U1187	U	U	U995
A1859	A1668	A1587	U1522	A1452	A1587	A1452	A1390	A1390	G1268	G1188	U	U	A996
G1863	U1669	U1588	U1523	A1453	U1588	A1453	U1391	U1391	U1269	G1189	U	U	A997
U1864	C1670	A1589	A1524	U1454	A1589	U1454	C1392	C1392	A1270	A1190	U	U	A998
A1865	U1671	G1590	G1525	U1455	G1590	U1455	A1393	A1393	G1271	G1191	U	U	G999
U1866	G1680	U1593	U1526	A1456	U1593	A1456	A1394	A1394	A1272	C1192	U	U	C1000
G1867	A1683	A1594	G1527	U1457	A1594	U1457	U1395	U1395	C1273	G1193	U	U	G1001
U1868	U1684	U1595	U1528	U1458	U1595	U1458	G1396	G1396	A1274	G1194	U	U	G1002
A1869	C1685	C1596	A1529	A1459	C1596	A1459	C1397	C1397	C1277	A1195	U	U	A1003
U1870	U1686	U1597	U1530	U1460	U1597	U1460	U1398	U1398	A1278	G1196	U	U	G1065
G1871	A1800	G1598	U1531	A1461	G1598	A1461	A1401	A1401	C1279	C1197	U	U	G1066
U1872	U1801	U1599	U1532	U1462	U1599	U1462	U1399	U1399	C1277	C1198	U	U	U1067
A1873	C1802	C1532	U1463	U1463	C1532	U1463	G1400	G1400	A1278	C1199	U	U	C1068
U1874	A1803	A1602	G1465	G1404	A1602	G1404	A1401	A1401	C1277	C1199	U	U	G
C1875	A1804	A1603	U1466	U1405	A1603	U1405	U1399	U1399	C1277	C1199	U	U	A
U1876	A1805	G1604	G1467	A1406	A1805	A1406	U1399	U1399	C1277	C1199	U	U	G
A1877	A1806	A1605	U1468	A1407	A1806	A1407	U1399	U1399	C1277	C1199	U	U	A
U1878	G1807	A1606	C1469	G1408	G1807	G1408	U1399	U1399	C1277	C1199	U	U	G
A1879	A1808	U1607	U1470	U1409	A1808	U1409	U1399	U1399	C1277	C1199	U	U	A
U1880	C1809	C1608	U1471	A1410	C1809	A1410	U1399	U1399	C1277	C1199	U	U	G
A1881	A1810	G1609	U1472	C1411	A1810	C1411	U1399	U1399	C1277	C1199	U	U	A
U1882	A1811	U1610	U1473	G1412	A1811	G1412	U1399	U1399	C1277	C1199	U	U	G
A1883	A1812	G1611	G1474	U1413	A1812	U1413	U1399	U1399	C1277	C1199	U	U	A
U1884	A1813	G1612	A1475	U1414	A1813	A1475	U1399	U1399	C1277	C1199	U	U	G
A1885	A1814	A1613	U1476	U1415	A1814	U1415	U1399	U1399	C1277	C1199	U	U	A
U1886	U1815	C1614	U1477	C1416	U1815	C1416	U1399	U1399	C1277	C1199	U	U	G
A1887	U1816	A1615	C1478	A1417	A1887	A1417	U1399	U1399	C1277	C1199	U	U	A
U1888	U1817	U1616	U1479	A1418	U1817	A1418	U1399	U1399	C1277	C1199	U	U	G
A1889	A1818	G1617	C1482	A1419	A1818	A1419	U1399	U1399	C1277	C1199	U	U	A
U1890	U1819	U1618	G1483	C1420	U1819	C1420	U1399	U1399	C1277	C1199	U	U	G
A1891	U1820	U1619	U1487	G1421	A1891	G1421	U1399	U1399	C1277	C1199	U	U	A
C1892	U1821	A1620	C1487	C1423	C1892	C1423	U1399	U1399	C1277	C1199	U	U	G
U1893	A1822	A1621	A1556	A1488	U1893	A1488	U1399	U1399	C1277	C1199	U	U	A
A1894	U1823	A1625	A1557	A1489	A1894	A1489	U1399	U1399	C1277	C1199	U	U	G
U1895	G1824	U1629	A1558	A1490	U1895	A1490	U1399	U1399	C1277	C1199	U	U	A
A1896	A1825	U1630	A1559	A1491	A1896	A1491	U1399	U1399	C1277	C1199	U	U	G
U1897	U1826	C1631	G1561	G1492	U1897	G1492	U1399	U1399	C1277	C1199	U	U	A
A1898	A1827	A1632	C1562	U1493	A1898	U1493	U1399	U1399	C1277	C1199	U	U	G
U1899	U1828	C1633	U1564	A1494	U1899	A1494	U1399	U1399	C1277	C1199	U	U	A
A1900	G1829	U1634	G1565	C1495	A1900	C1495	U1399	U1399	C1277	C1199	U	U	G
U1901	A1830	A1635	A1497	A1433	U1901	A1433	U1399	U1399	C1277	C1199	U	U	A
C1902	U1831	U1638	C1498	G1434	C1902	G1434	U1399	U1399	C1277	C1199	U	U	G
A1903	A1832	A1639	A1498	U1435	A1903	U1435	U1399	U1399	C1277	C1199	U	U	A
U1904	U1833	G1640	U1567	U1436	U1904	U1436	U1399	U1399	C1277	C1199	U	U	G
A1905	A1834	U1641	U1568	U1437	A1905	U1437	U1399	U1399	C1277	C1199	U	U	A
U1906	U1835	A1642	U1569	U1438	U1906	U1438	U1399	U1399	C1277	C1199	U	U	G
C1907	A1836	U1643	U1570	U1439	C1907	U1439	U1399	U1399	C1277	C1199	U	U	A
A1908	U1837	U1644	U1574	C1440	A1908	C1440	U1399	U1399	C1277	C1199	U	U	G
U1909	G1838	U1645	C1507	U1442	U1909	U1442	U1399	U1399	C1277	C1199	U	U	A
A1910	A1839	A1647	C1508	G1443	A1910	G1443	U1399	U1399	C1277	C1199	U	U	G
U1911	U1840	A1654	A1509	U1444	U1911	U1444	U1399	U1399	C1277	C1199	U	U	A
C1912	A1841	G1655	U1510	U1445	C1912	U1445	U1399	U1399	C1277	C1199	U	U	G
A1913	U1842	C1656	U1511	A1446	A1913	A1446	U1399	U1399</					

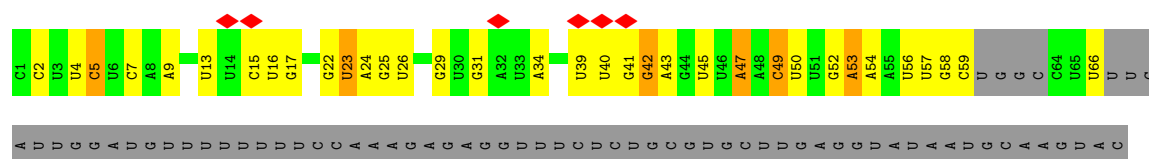




• Molecule 45: 5.8S rRNA

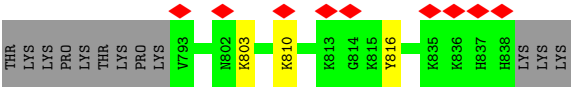


• Molecule 46: ITS2



- Molecule 47: 27S pre-rRNA (guanosine(2922)-2'-O)-methyltransferase





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29163	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.483	Depositor
Minimum map value	-0.257	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.055	Depositor
Map size (\AA)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	B	1.10	6/3152 (0.2%)	1.05	15/4239 (0.4%)
2	C	1.33	14/2801 (0.5%)	1.10	22/3792 (0.6%)
3	E	0.95	0/1260	0.96	9/1694 (0.5%)
4	F	1.23	5/1821 (0.3%)	1.00	10/2451 (0.4%)
5	G	0.91	5/1542 (0.3%)	0.92	3/2083 (0.1%)
6	H	0.86	0/1539	0.95	8/2073 (0.4%)
7	K	0.47	0/2098	0.75	0/2830
8	L	1.08	2/1524 (0.1%)	1.12	13/2046 (0.6%)
9	M	1.04	3/1074 (0.3%)	0.98	6/1446 (0.4%)
10	N	1.49	12/1575 (0.8%)	1.28	29/2106 (1.4%)
11	O	1.51	13/1585 (0.8%)	1.11	13/2128 (0.6%)
12	P	1.35	12/1419 (0.8%)	1.06	9/1904 (0.5%)
13	Q	1.10	1/1050 (0.1%)	1.06	8/1419 (0.6%)
14	R	0.69	0/1275	0.91	7/1702 (0.4%)
15	S	1.01	1/1473 (0.1%)	1.01	9/1980 (0.5%)
16	T	0.44	0/440	0.93	2/594 (0.3%)
17	U	0.56	0/861	0.73	0/1167
18	V	0.68	0/1018	0.89	2/1369 (0.1%)
19	W	0.50	0/1918	0.81	0/2586
20	X	1.18	3/1116 (0.3%)	0.93	4/1503 (0.3%)
21	Y	1.17	2/1004 (0.2%)	1.06	7/1341 (0.5%)
22	Z	0.54	0/1118	0.78	2/1497 (0.1%)
23	a	0.80	0/751	0.96	3/1013 (0.3%)
24	b	0.57	1/3885 (0.0%)	0.85	6/5242 (0.1%)
25	c	0.43	0/751	0.72	0/1008
26	d	1.00	1/887 (0.1%)	0.98	4/1191 (0.3%)
27	e	1.40	7/1041 (0.7%)	1.09	10/1394 (0.7%)
28	f	1.72	7/868 (0.8%)	1.25	12/1168 (1.0%)
29	g	0.80	0/891	1.07	8/1191 (0.7%)
30	h	1.12	0/978	1.03	2/1301 (0.2%)
31	i	0.73	0/778	0.91	2/1034 (0.2%)
32	j	1.49	8/696 (1.1%)	1.34	10/923 (1.1%)
33	k	0.64	0/618	0.89	0/826
34	l	0.69	0/443	1.12	4/588 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	n	0.74	0/3101	0.91	12/4187 (0.3%)
36	o	0.55	0/1129	0.84	0/1502
37	q	0.47	0/733	0.90	4/977 (0.4%)
38	r	0.63	0/1789	0.91	3/2389 (0.1%)
39	s	0.70	0/301	1.15	3/386 (0.8%)
40	t	0.54	0/2333	0.89	3/3128 (0.1%)
41	u	0.72	0/1061	0.99	6/1410 (0.4%)
42	y	0.52	0/1872	0.79	2/2548 (0.1%)
43	z	0.58	0/445	0.89	0/585
44	1	1.93	1801/60703 (3.0%)	1.96	3153/94630 (3.3%)
45	2	2.45	221/3746 (5.9%)	2.31	330/5832 (5.7%)
46	6	0.96	1/1527 (0.1%)	1.50	26/2371 (1.1%)
47	w	0.46	0/2952	0.76	0/3965
All	All	1.55	2126/126942 (1.7%)	1.61	3781/184739 (2.0%)

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
1	B	0	7
2	C	0	6
4	F	0	2
5	G	0	5
6	H	0	3
7	K	0	1
8	L	0	5
9	M	0	1
10	N	0	1
12	P	0	1
14	R	0	1
15	S	0	2
18	V	0	1
19	W	0	2
20	X	0	1
23	a	0	2
24	b	0	3
26	d	0	1
27	e	0	1
28	f	0	2
29	g	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	h	0	3
31	i	0	2
33	k	0	2
35	n	0	11
36	o	0	5
37	q	0	1
38	r	0	1
39	s	0	1
40	t	0	5
41	u	0	2
42	y	0	1
47	w	0	2
All	All	0	86

The worst 5 of 2126 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	1	346	C	N1-C6	-13.06	1.29	1.37
44	1	945	C	C4-C5	-12.55	1.32	1.43
44	1	1437	C	C4-C5	-12.42	1.33	1.43
44	1	1332	A	N7-C5	-12.41	1.31	1.39
44	1	407	A	N9-C4	-12.35	1.30	1.37

The worst 5 of 3781 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	1	630	A	N1-C6-N6	17.03	128.82	118.60
44	1	630	A	C5-C6-N6	-16.99	110.11	123.70
44	1	1363	A	C5-C6-N6	-16.56	110.45	123.70
44	1	630	A	C4-C5-N7	16.19	118.79	110.70
44	1	1159	A	C5-C6-N6	-15.59	111.23	123.70

There are no chirality outliers.

5 of 86 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	170	PRO	Peptide
1	B	221	THR	Peptide
1	B	241	LYS	Peptide
1	B	35	ASP	Peptide
1	B	37	ARG	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	B	384/387 (99%)	363 (94%)	21 (6%)	0	100	100
2	C	359/362 (99%)	338 (94%)	20 (6%)	1 (0%)	37	70
3	E	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
4	F	220/244 (90%)	206 (94%)	14 (6%)	0	100	100
5	G	190/256 (74%)	183 (96%)	7 (4%)	0	100	100
6	H	189/191 (99%)	182 (96%)	6 (3%)	1 (0%)	25	60
7	K	252/376 (67%)	242 (96%)	10 (4%)	0	100	100
8	L	185/199 (93%)	176 (95%)	8 (4%)	1 (0%)	25	60
9	M	135/138 (98%)	133 (98%)	2 (2%)	0	100	100
10	N	176/204 (86%)	167 (95%)	9 (5%)	0	100	100
11	O	195/199 (98%)	191 (98%)	4 (2%)	0	100	100
12	P	172/184 (94%)	167 (97%)	5 (3%)	0	100	100
13	Q	132/186 (71%)	132 (100%)	0	0	100	100
14	R	154/189 (82%)	152 (99%)	2 (1%)	0	100	100
15	S	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
16	T	54/160 (34%)	53 (98%)	1 (2%)	0	100	100
17	U	104/121 (86%)	103 (99%)	1 (1%)	0	100	100
18	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
19	W	232/236 (98%)	229 (99%)	3 (1%)	0	100	100
20	X	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
21	Y	124/127 (98%)	122 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	Z	133/136 (98%)	132 (99%)	1 (1%)	0	100	100
23	a	91/149 (61%)	87 (96%)	4 (4%)	0	100	100
24	b	468/647 (72%)	451 (96%)	17 (4%)	0	100	100
25	c	95/105 (90%)	95 (100%)	0	0	100	100
26	d	105/113 (93%)	103 (98%)	2 (2%)	0	100	100
27	e	125/130 (96%)	123 (98%)	2 (2%)	0	100	100
28	f	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
29	g	110/121 (91%)	107 (97%)	3 (3%)	0	100	100
30	h	117/120 (98%)	110 (94%)	7 (6%)	0	100	100
31	i	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
32	j	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
33	k	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
34	l	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
35	n	365/605 (60%)	339 (93%)	26 (7%)	0	100	100
36	o	131/220 (60%)	123 (94%)	8 (6%)	0	100	100
37	q	83/455 (18%)	80 (96%)	3 (4%)	0	100	100
38	r	211/261 (81%)	200 (95%)	11 (5%)	0	100	100
39	s	34/520 (6%)	31 (91%)	3 (9%)	0	100	100
40	t	283/322 (88%)	267 (94%)	16 (6%)	0	100	100
41	u	121/199 (61%)	115 (95%)	6 (5%)	0	100	100
42	y	242/245 (99%)	240 (99%)	2 (1%)	0	100	100
43	z	53/106 (50%)	52 (98%)	1 (2%)	0	100	100
47	w	350/841 (42%)	347 (99%)	3 (1%)	0	100	100
All	All	7377/10105 (73%)	7124 (97%)	250 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	339	LEU
8	L	63	VAL
6	H	50	ASN

5.3.2 Protein sidechains ⓘ

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	B	322/323 (100%)	316 (98%)	6 (2%)	52	70
2	C	288/289 (100%)	286 (99%)	2 (1%)	81	86
3	E	134/153 (88%)	133 (99%)	1 (1%)	81	86
4	F	186/205 (91%)	186 (100%)	0	100	100
5	G	159/208 (76%)	156 (98%)	3 (2%)	52	70
6	H	171/171 (100%)	171 (100%)	0	100	100
7	K	236/346 (68%)	235 (100%)	1 (0%)	89	91
8	L	149/159 (94%)	148 (99%)	1 (1%)	81	86
9	M	108/109 (99%)	107 (99%)	1 (1%)	75	83
10	N	156/176 (89%)	151 (97%)	5 (3%)	34	56
11	O	160/162 (99%)	159 (99%)	1 (1%)	84	88
12	P	142/146 (97%)	141 (99%)	1 (1%)	81	86
13	Q	110/151 (73%)	110 (100%)	0	100	100
14	R	129/154 (84%)	128 (99%)	1 (1%)	79	84
15	S	155/156 (99%)	155 (100%)	0	100	100
16	T	45/137 (33%)	45 (100%)	0	100	100
17	U	93/107 (87%)	93 (100%)	0	100	100
18	V	104/105 (99%)	103 (99%)	1 (1%)	73	81
19	W	211/213 (99%)	211 (100%)	0	100	100
20	X	117/118 (99%)	117 (100%)	0	100	100
21	Y	109/110 (99%)	108 (99%)	1 (1%)	75	83
22	Z	115/116 (99%)	114 (99%)	1 (1%)	75	83
23	a	76/119 (64%)	75 (99%)	1 (1%)	65	76
24	b	424/573 (74%)	423 (100%)	1 (0%)	92	94
25	c	81/88 (92%)	81 (100%)	0	100	100
26	d	94/97 (97%)	92 (98%)	2 (2%)	48	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	e	109/111 (98%)	107 (98%)	2 (2%)	54	71
28	f	90/91 (99%)	89 (99%)	1 (1%)	70	79
29	g	95/103 (92%)	94 (99%)	1 (1%)	70	79
30	h	104/105 (99%)	104 (100%)	0	100	100
31	i	81/82 (99%)	81 (100%)	0	100	100
32	j	70/71 (99%)	69 (99%)	1 (1%)	62	75
33	k	68/69 (99%)	68 (100%)	0	100	100
34	l	45/46 (98%)	44 (98%)	1 (2%)	47	65
35	n	334/548 (61%)	333 (100%)	1 (0%)	91	92
36	o	118/199 (59%)	116 (98%)	2 (2%)	56	72
37	q	80/420 (19%)	80 (100%)	0	100	100
38	r	191/229 (83%)	191 (100%)	0	100	100
39	s	32/445 (7%)	32 (100%)	0	100	100
40	t	256/287 (89%)	253 (99%)	3 (1%)	67	78
41	u	108/180 (60%)	107 (99%)	1 (1%)	75	83
42	y	210/211 (100%)	210 (100%)	0	100	100
43	z	48/95 (50%)	48 (100%)	0	100	100
47	w	319/745 (43%)	311 (98%)	8 (2%)	42	62
All	All	6432/8728 (74%)	6381 (99%)	51 (1%)	77	84

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	d	16	LEU
34	l	41	ARG
47	w	810	LYS
26	d	23	VAL
28	f	72	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
24	b	454	GLN
42	y	82	GLN
30	h	59	ASN

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Mol	Chain	Res	Type
41	u	110	ASN
27	e	121	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	1	2523/3396 (74%)	688 (27%)	34 (1%)
45	2	157/158 (99%)	46 (29%)	3 (1%)
46	6	63/232 (27%)	29 (46%)	0
All	All	2743/3786 (72%)	763 (27%)	37 (1%)

5 of 763 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	1	2	U
44	1	3	U
44	1	7	C
44	1	13	A
44	1	14	U

5 of 37 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	1	2317	A
45	2	73	U
44	1	2920	U
44	1	3350	C
44	1	761	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 [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
28	f	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	f	102:LEU	C	103:TYR	N	1.16

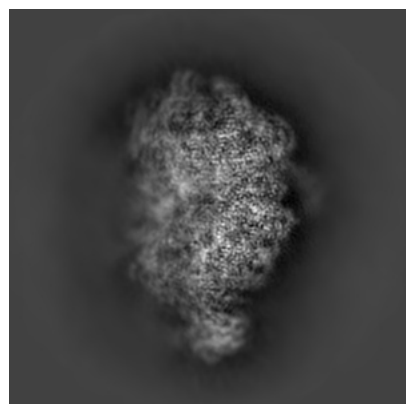
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10841. These allow visual inspection of the internal detail of the map and identification of artifacts.

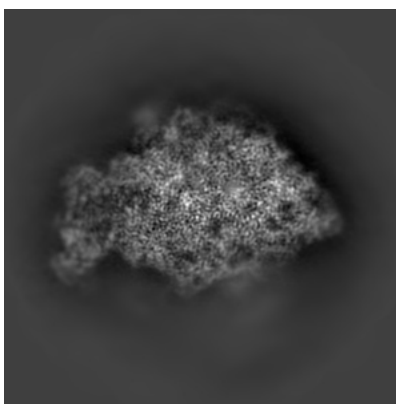
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

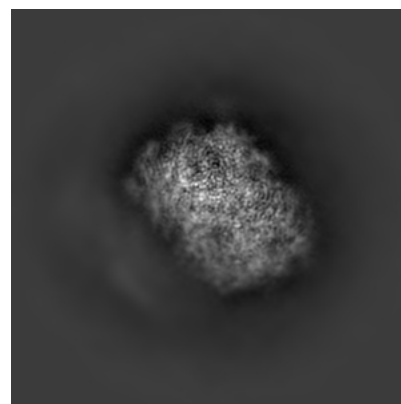
6.1.1 Primary map



X

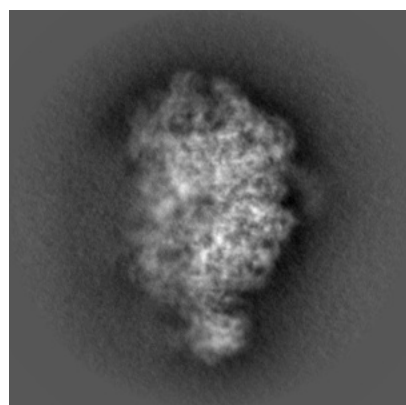


Y

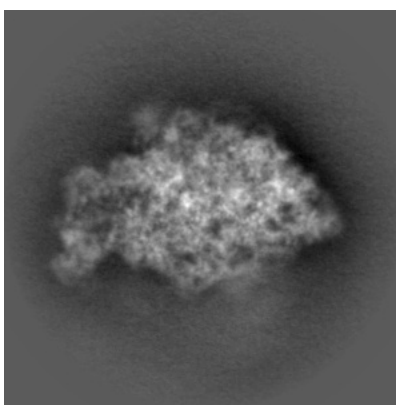


Z

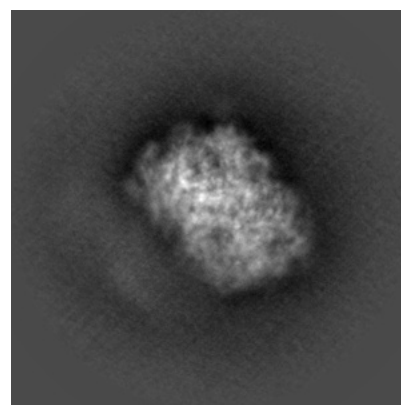
6.1.2 Raw map



X



Y

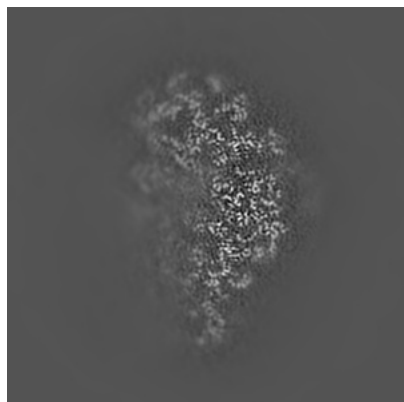


Z

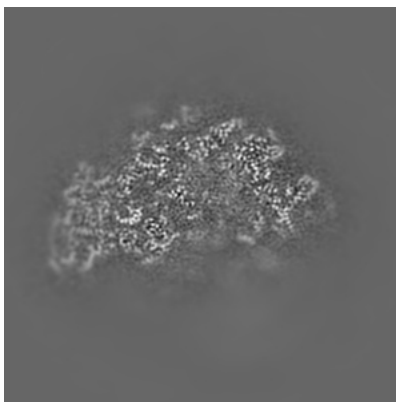
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

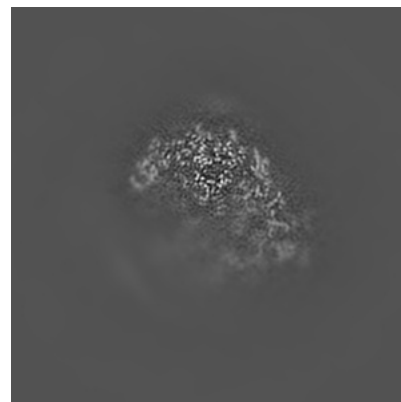
6.2.1 Primary map



X Index: 192

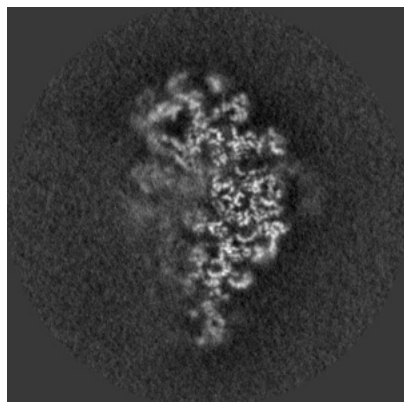


Y Index: 192

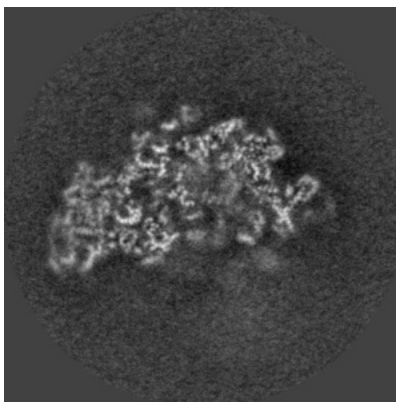


Z Index: 192

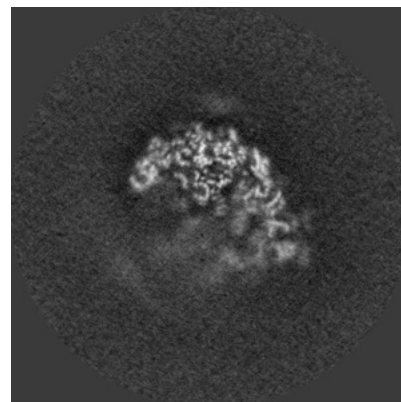
6.2.2 Raw map



X Index: 192



Y Index: 192

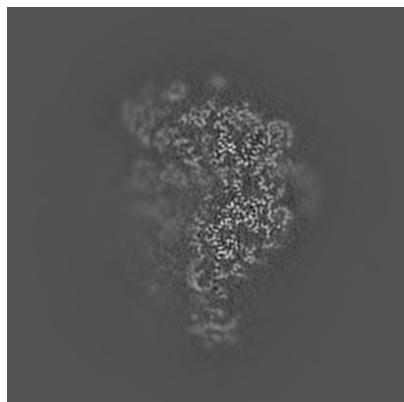


Z Index: 192

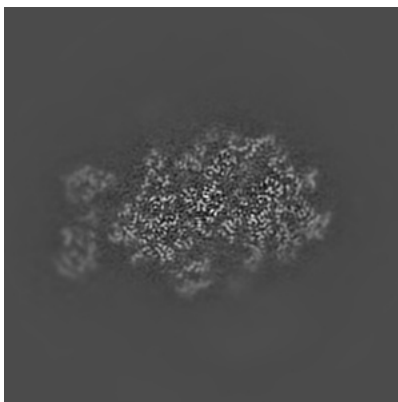
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

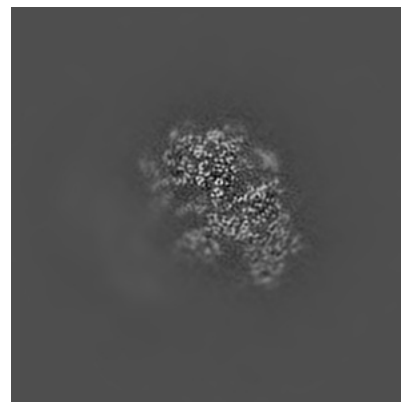
6.3.1 Primary map



X Index: 201

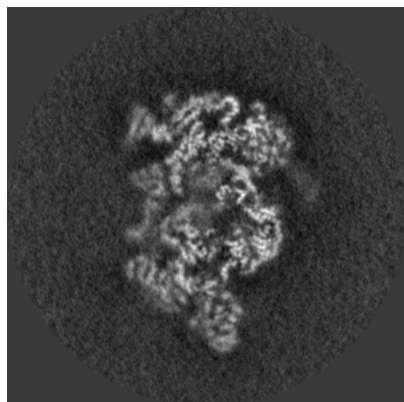


Y Index: 216

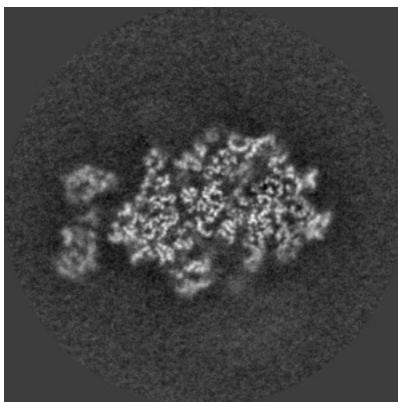


Z Index: 245

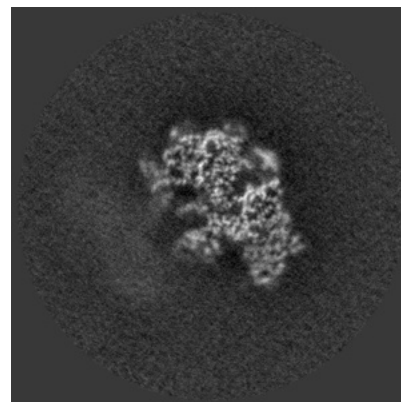
6.3.2 Raw map



X Index: 217



Y Index: 216

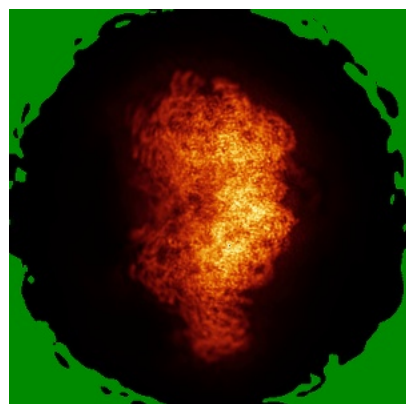


Z Index: 244

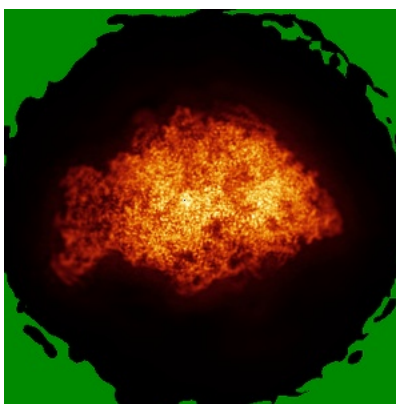
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

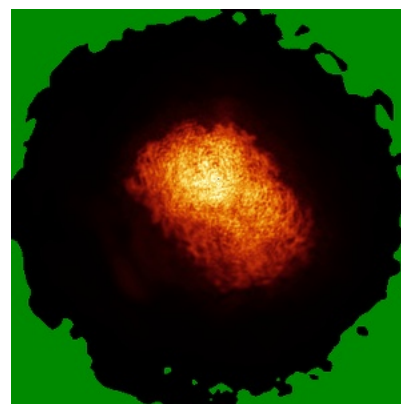
6.4.1 Primary map



X

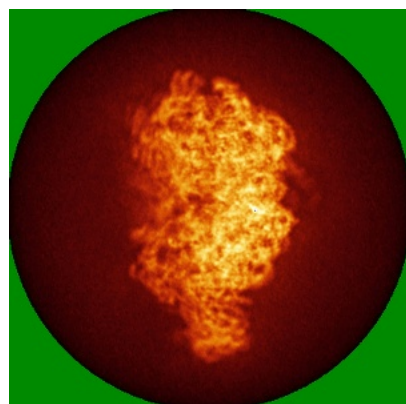


Y

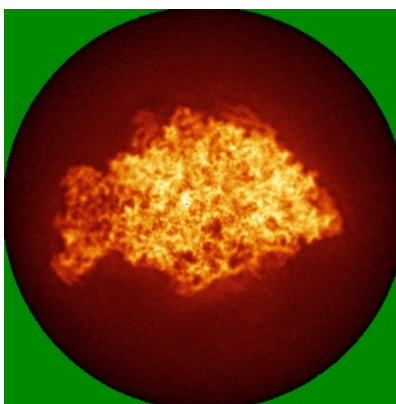


Z

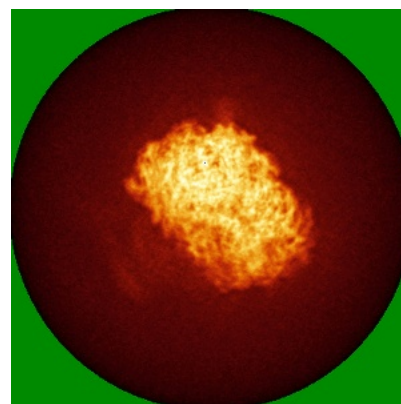
6.4.2 Raw map



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 0.055. 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.

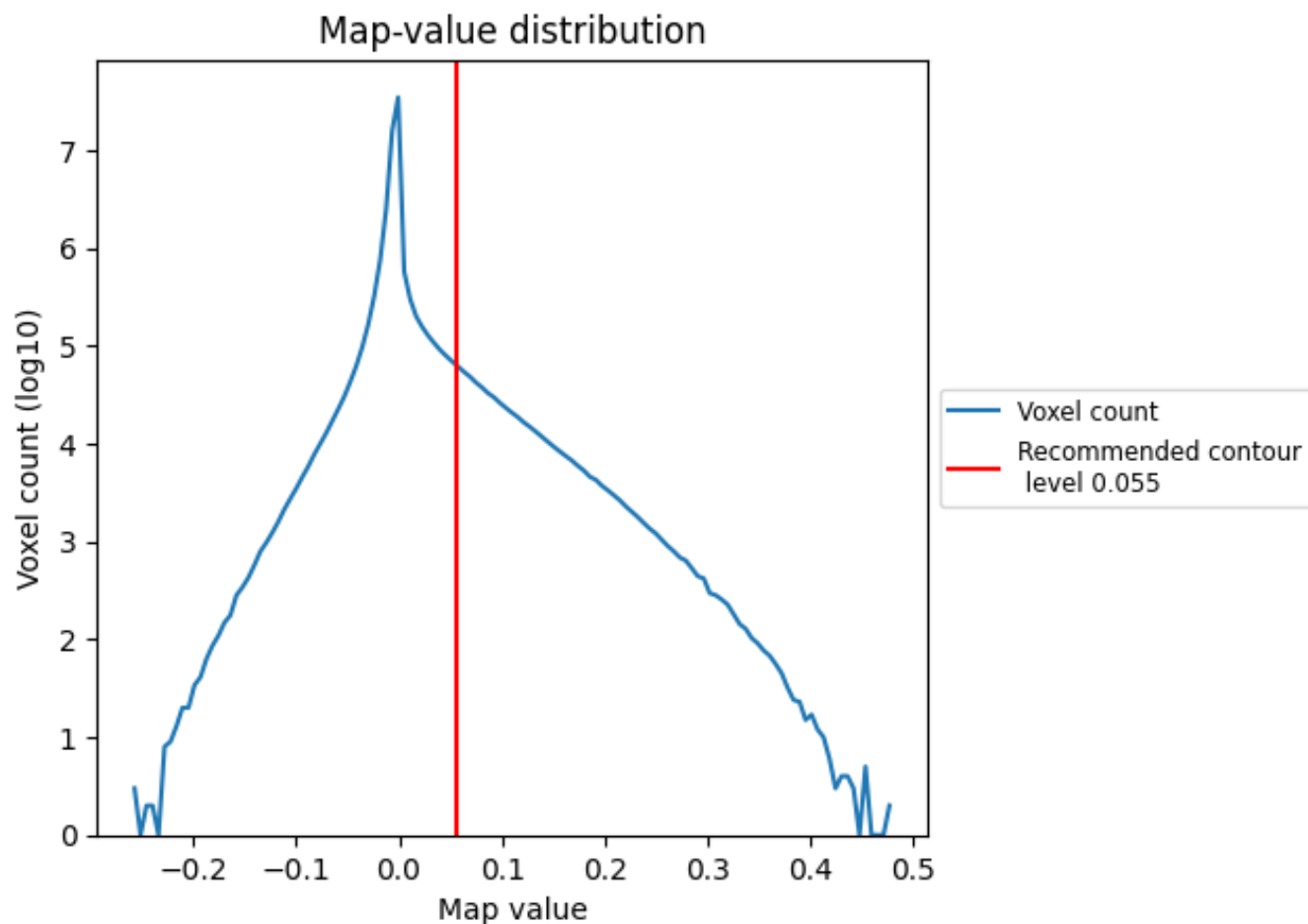
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

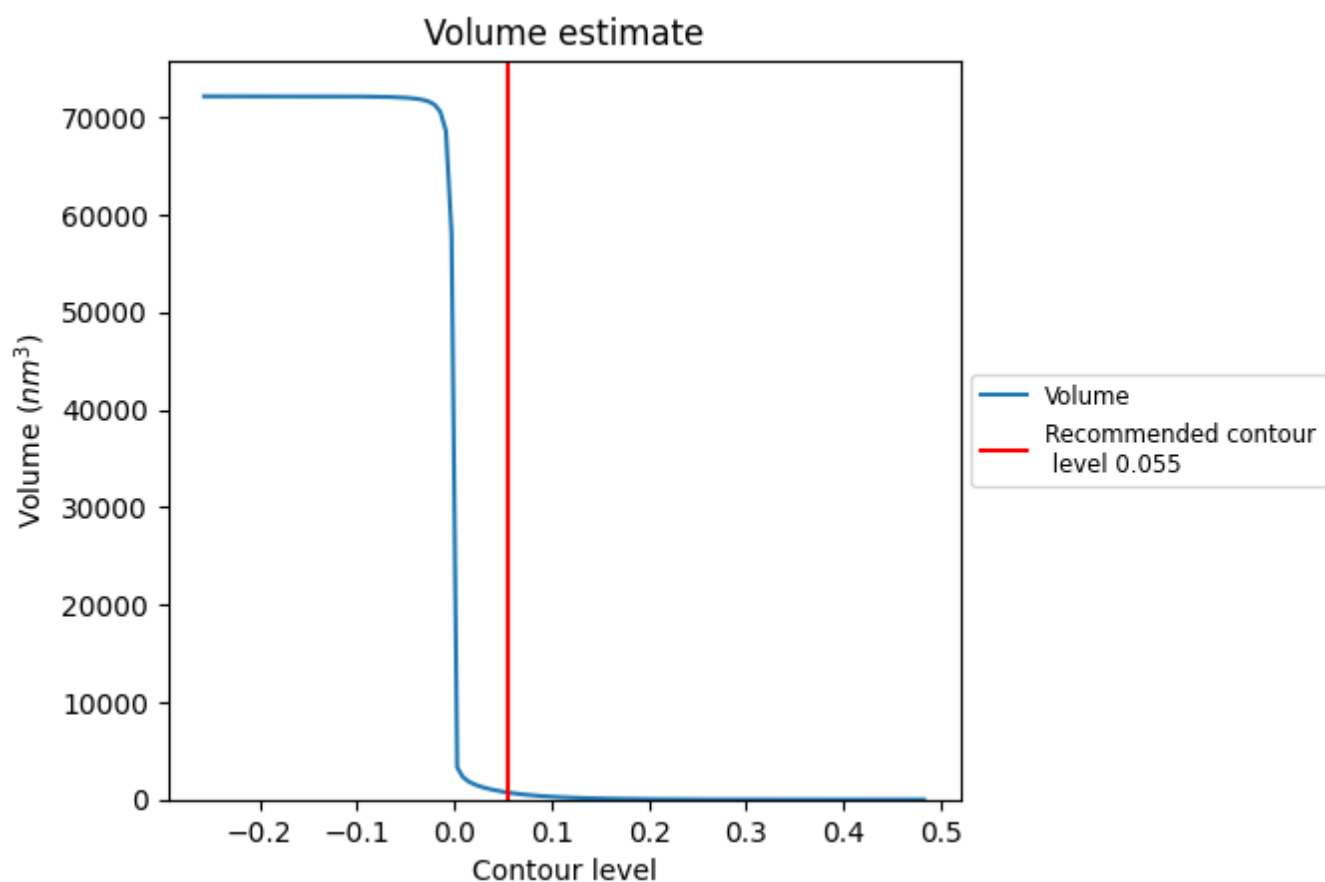
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

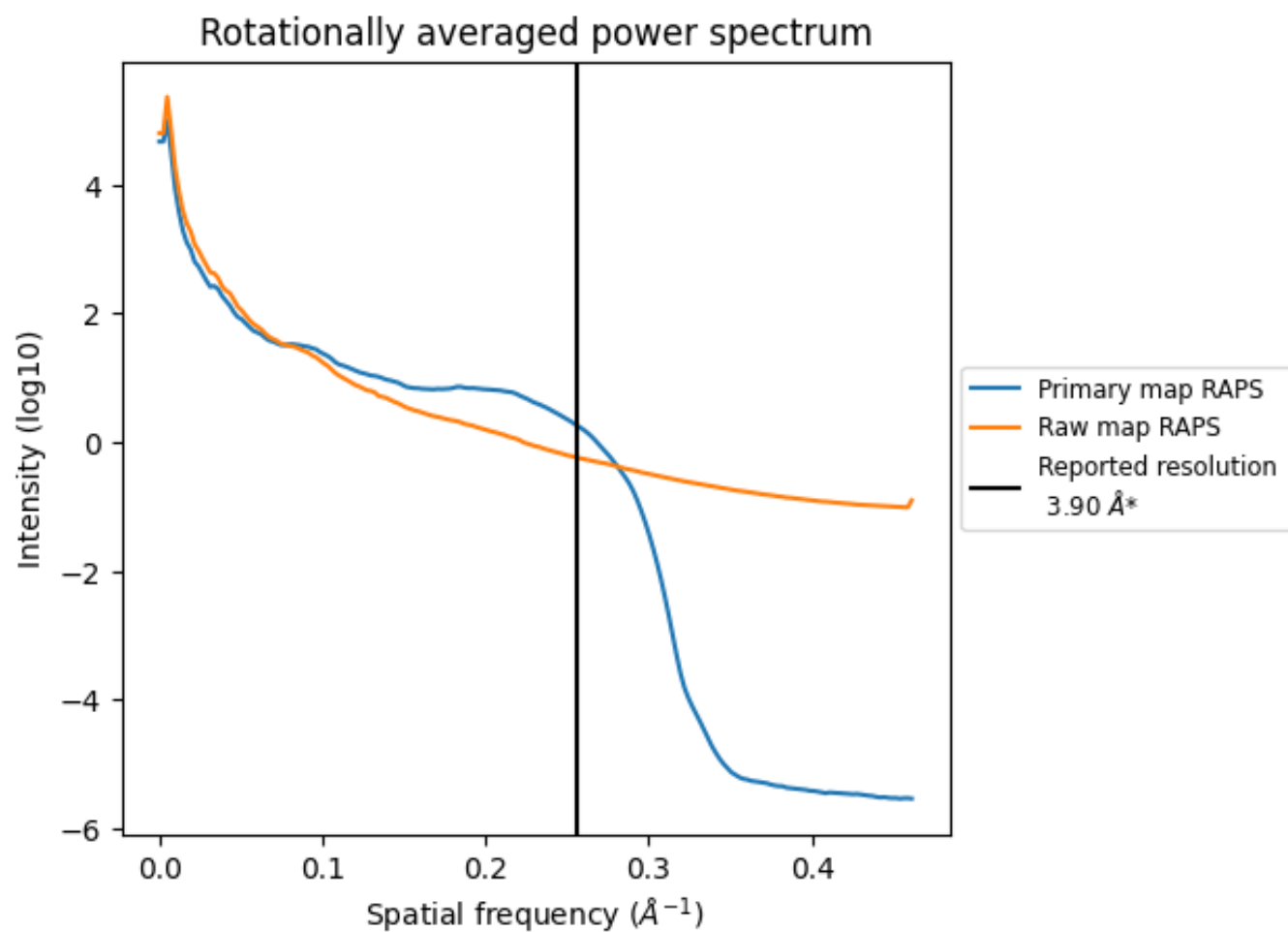
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 727 nm³; this corresponds to an approximate mass of 656 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 ⓘ

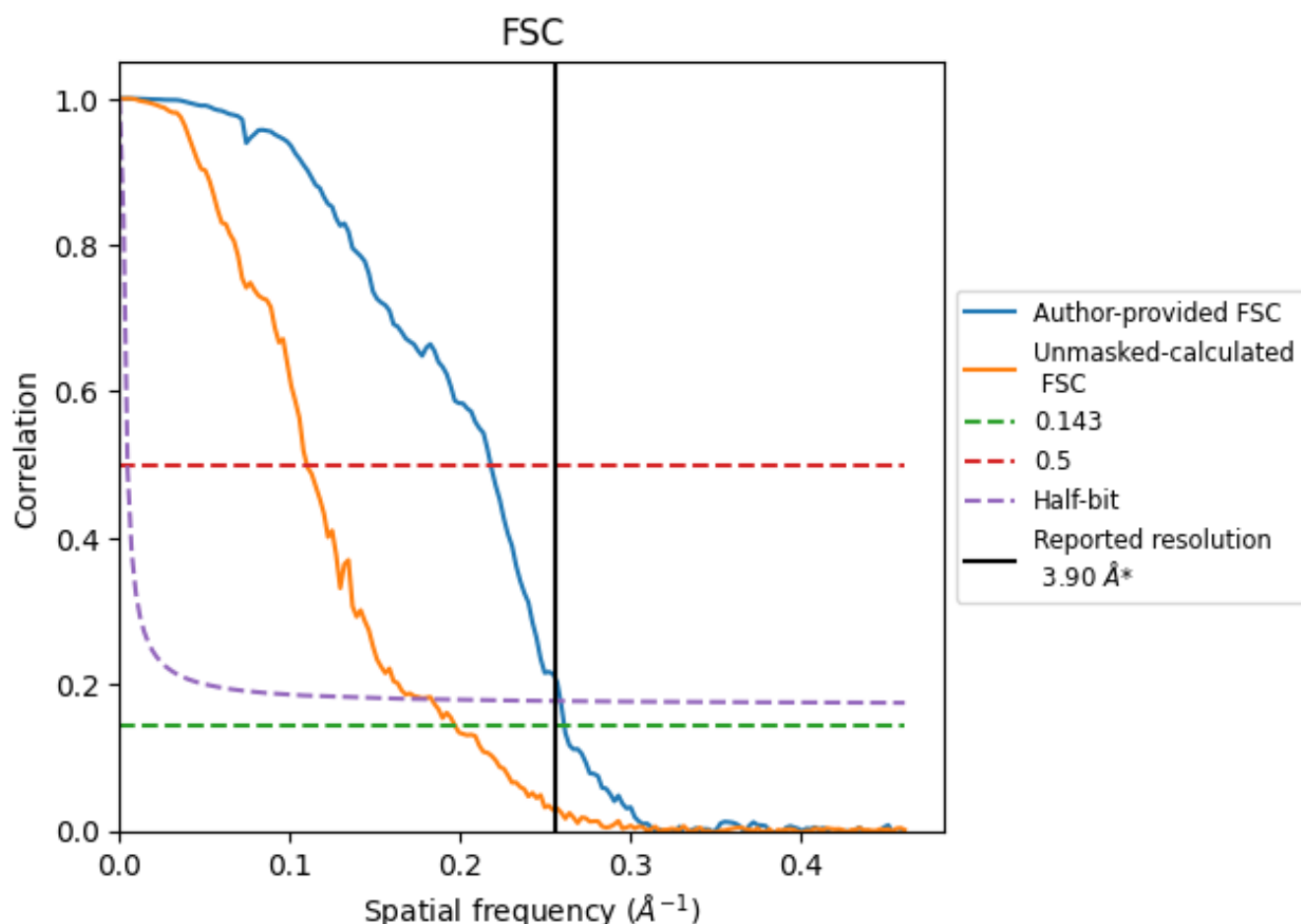


*Reported resolution corresponds to spatial frequency of 0.256 \AA^{-1}

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

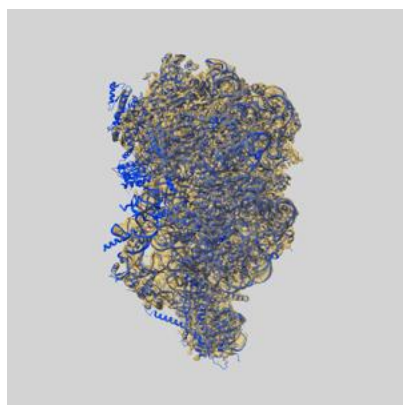
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.83	4.59	3.86
Unmasked-calculated*	5.07	9.08	5.45

*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 5.07 differs from the reported value 3.9 by more than 10 %

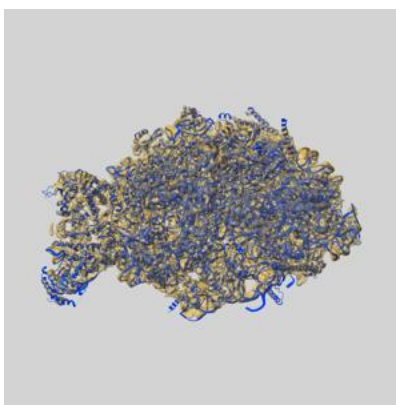
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10841 and PDB model 6YLX. Per-residue inclusion information can be found in section 3 on page 12.

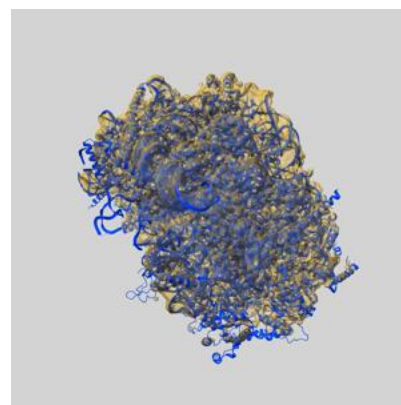
9.1 Map-model overlay [i](#)



X



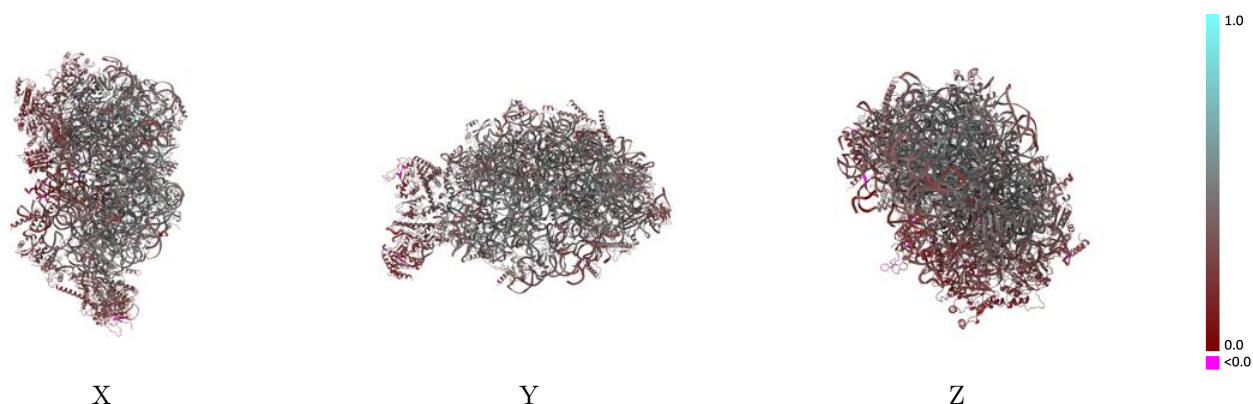
Y



Z

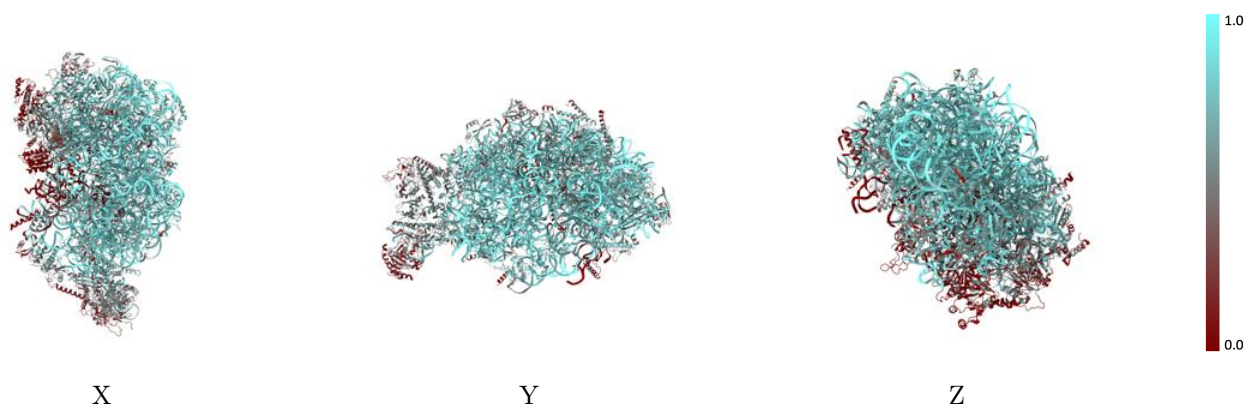
The images above show the 3D surface view of the map at the recommended contour level 0.055 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



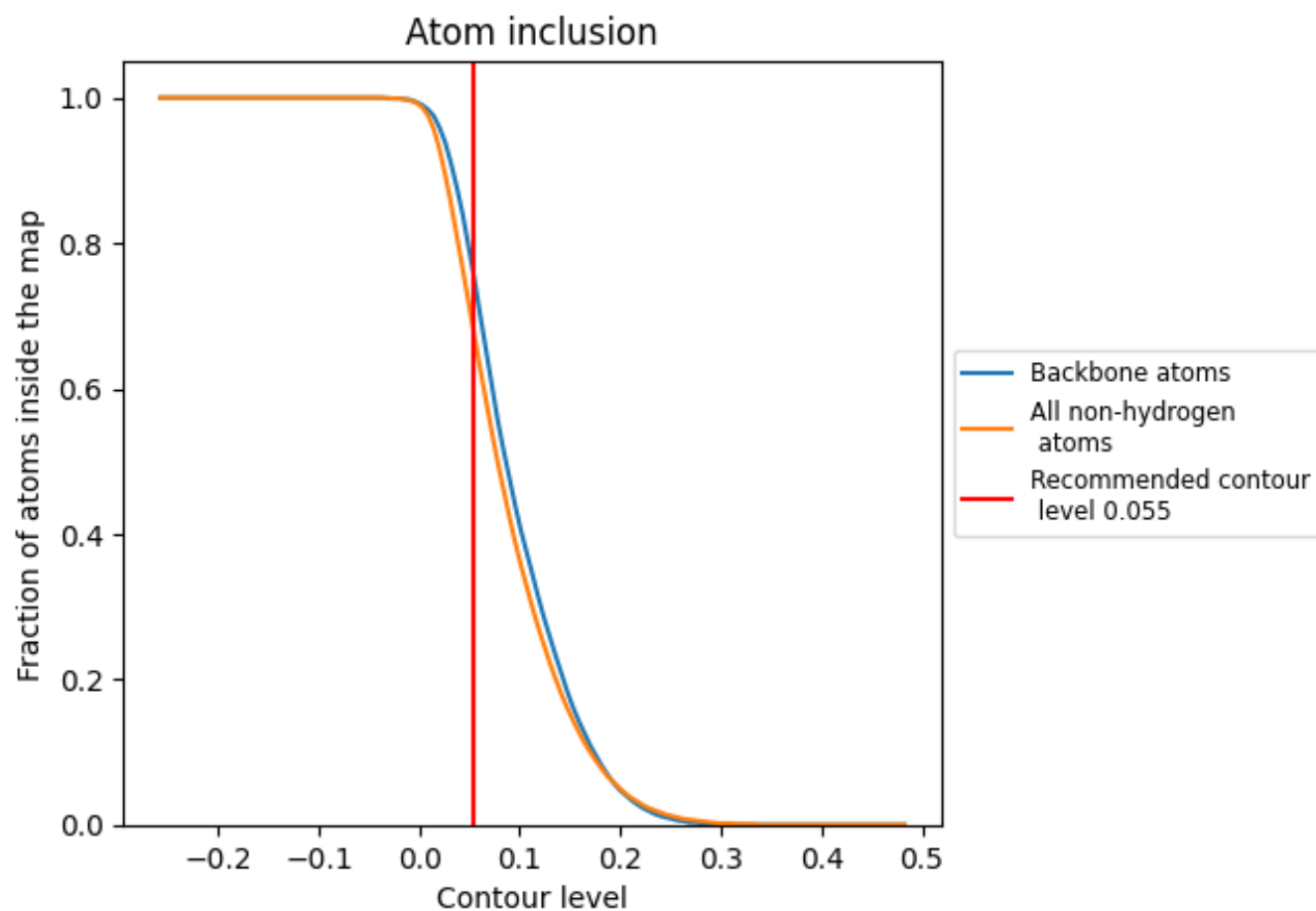
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.055).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 67% 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 (0.055) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6730	 0.3840
1	 0.7890	 0.3960
2	 0.8920	 0.4560
6	 0.6830	 0.3070
B	 0.6810	 0.4290
C	 0.7750	 0.4690
E	 0.7250	 0.4280
F	 0.7770	 0.4300
G	 0.6420	 0.3890
H	 0.6870	 0.4150
K	 0.2690	 0.2150
L	 0.6910	 0.4310
M	 0.7610	 0.4410
N	 0.8020	 0.4900
O	 0.8060	 0.4790
P	 0.7620	 0.4590
Q	 0.7510	 0.4440
R	 0.4550	 0.3430
S	 0.7070	 0.4280
T	 0.1880	 0.3110
U	 0.4610	 0.3320
V	 0.5390	 0.3800
W	 0.4070	 0.2770
X	 0.7080	 0.4430
Y	 0.7800	 0.4720
Z	 0.5030	 0.3200
a	 0.6190	 0.3960
b	 0.3230	 0.2730
c	 0.3410	 0.2580
d	 0.7040	 0.4430
e	 0.8010	 0.4980
f	 0.8390	 0.5110
g	 0.5810	 0.3980
h	 0.7410	 0.4570
i	 0.5930	 0.3700



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Chain	Atom inclusion	Q-score
j	 0.7500	 0.4660
k	 0.5410	 0.3910
l	 0.2800	 0.3650
n	 0.5320	 0.3380
o	 0.3760	 0.2480
q	 0.1930	 0.2420
r	 0.2480	 0.2720
s	 0.4770	 0.4100
t	 0.4620	 0.3010
u	 0.5330	 0.3480
w	 0.1110	 0.2630
y	 0.4430	 0.2890
z	 0.4560	 0.3770