



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 05:06 am BST

PDB ID : 6YSU / pdb_00006ysu
EMDB ID : EMD-10908
Title : Structure of the P+0 ArfB-ribosome complex in the post-hydrolysis state
Authors : Chan, K.-H.; Petrychenko, V.; Mueller, C.; Maracci, C.; Holtkamp, W.; Wilson, D.N.; Fischer, N.; Rodnina, M.V.
Deposited on : 2020-04-23
Resolution : 3.70 Å(reported)
Based on initial models : 5O2R, 5AFI, 4V95, 4RB7

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:

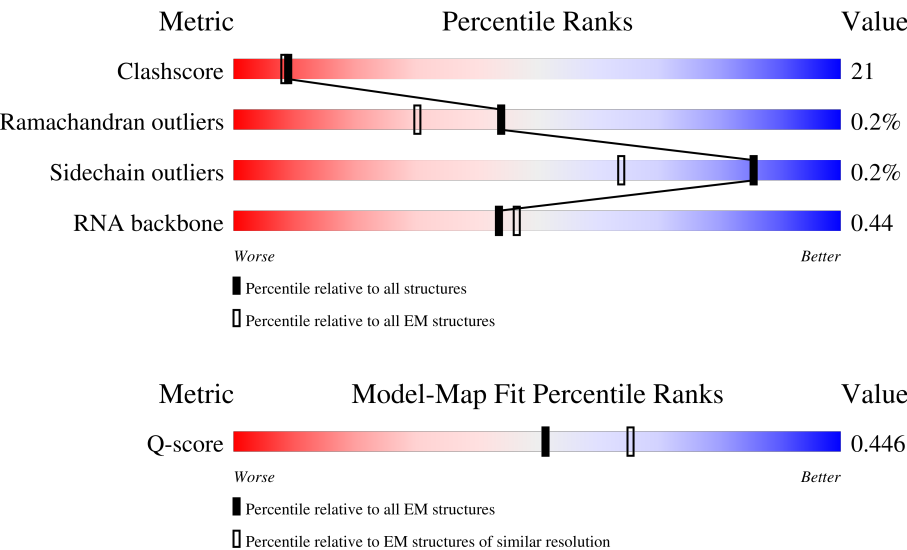
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



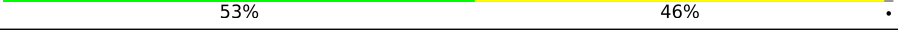
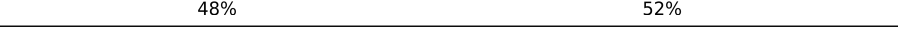
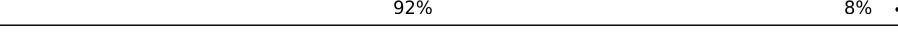
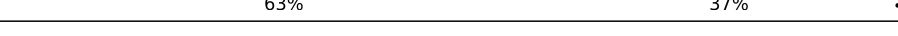
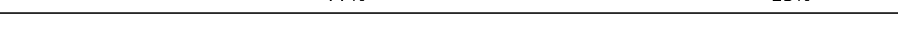
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	0	57	60%37%. .
2	1	55	60%31%9%
3	2	46	61%39%

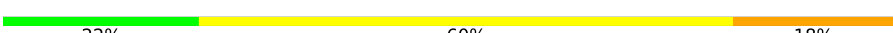
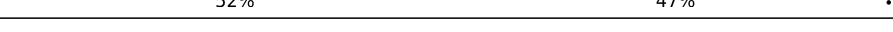
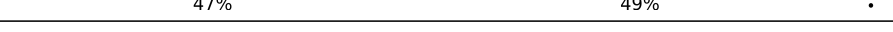
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	65	
5	4	38	
6	5	165	
7	A	2903	
8	B	120	
9	C	273	
10	D	209	
11	E	201	
12	F	179	
13	G	177	
14	H	149	
15	I	142	
16	J	142	
17	K	123	
18	L	144	
19	M	136	
20	N	127	
21	O	117	
22	P	115	
23	Q	118	
24	R	103	
25	S	110	
26	T	100	
27	U	104	
28	V	94	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	W	85	
30	X	78	
31	Y	63	
32	Z	59	
33	a	1542	
34	b	240	
35	c	233	
36	d	206	
37	e	167	
38	f	135	
39	g	179	
40	h	130	
41	i	130	
42	j	103	
43	k	129	
44	l	124	
45	m	118	
46	n	102	
47	o	89	
48	p	82	
49	q	84	
50	r	75	
51	s	92	
52	t	87	
53	u	71	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	v	14	64% 36%
55	w	76	16% 49% 29% 7%
56	x	15	20% 20% 60%
57	y	140	62% 37% .

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 146398 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62336	27815	11468	20150	2903		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 15 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 19 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 22 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 23 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 24 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	U	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 28 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 30 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 33 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	r	56	Total	C	N	O	0	0
			464	293	88	83		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 54 is a protein called Api137.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	v	14	Total	C	N	O	0	0
			121	80	25	16		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
v	10	ARG	GLN	engineered mutation	UNP Q8WSY8

- Molecule 55 is a RNA chain called P-site tRNAPhe.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 56 is a RNA chain called RNA (5'-R(P*AP*UP*GP*UP*UP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	6	Total	C	N	O	P	0	0
			125	56	19	44	6		

- Molecule 57 is a protein called Alternative stalled-ribosome rescue factor B.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	139	Total	C	N	O	S	0	0
			1078	666	215	195	2		

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
58	0	2	Total	Mg	0
			2	2	
58	3	1	Total	Mg	0
			1	1	
58	A	244	Total	Mg	0
			244	244	
58	B	5	Total	Mg	0
			5	5	
58	C	2	Total	Mg	0
			2	2	
58	D	2	Total	Mg	0
			2	2	
58	L	1	Total	Mg	0
			1	1	
58	X	1	Total	Mg	0
			1	1	
58	a	93	Total	Mg	0
			93	93	
58	m	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
58	w	4	Total	Mg	0
			4	4	

- Molecule 59 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
59	4	1	Total	Zn	0
			1	1	

- Molecule 60 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
60	A	1	Total	Na	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: 50S ribosomal protein L32

Chain 0: 



- Molecule 2: 50S ribosomal protein L33

Chain 1: 



- Molecule 3: 50S ribosomal protein L34

Chain 2: 



- Molecule 4: 50S ribosomal protein L35

Chain 3: 



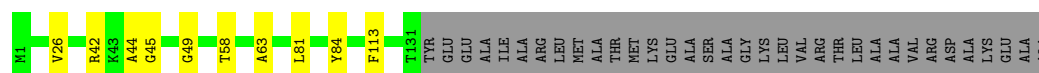
- Molecule 5: 50S ribosomal protein L36

Chain 4: 

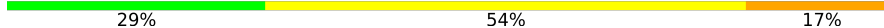


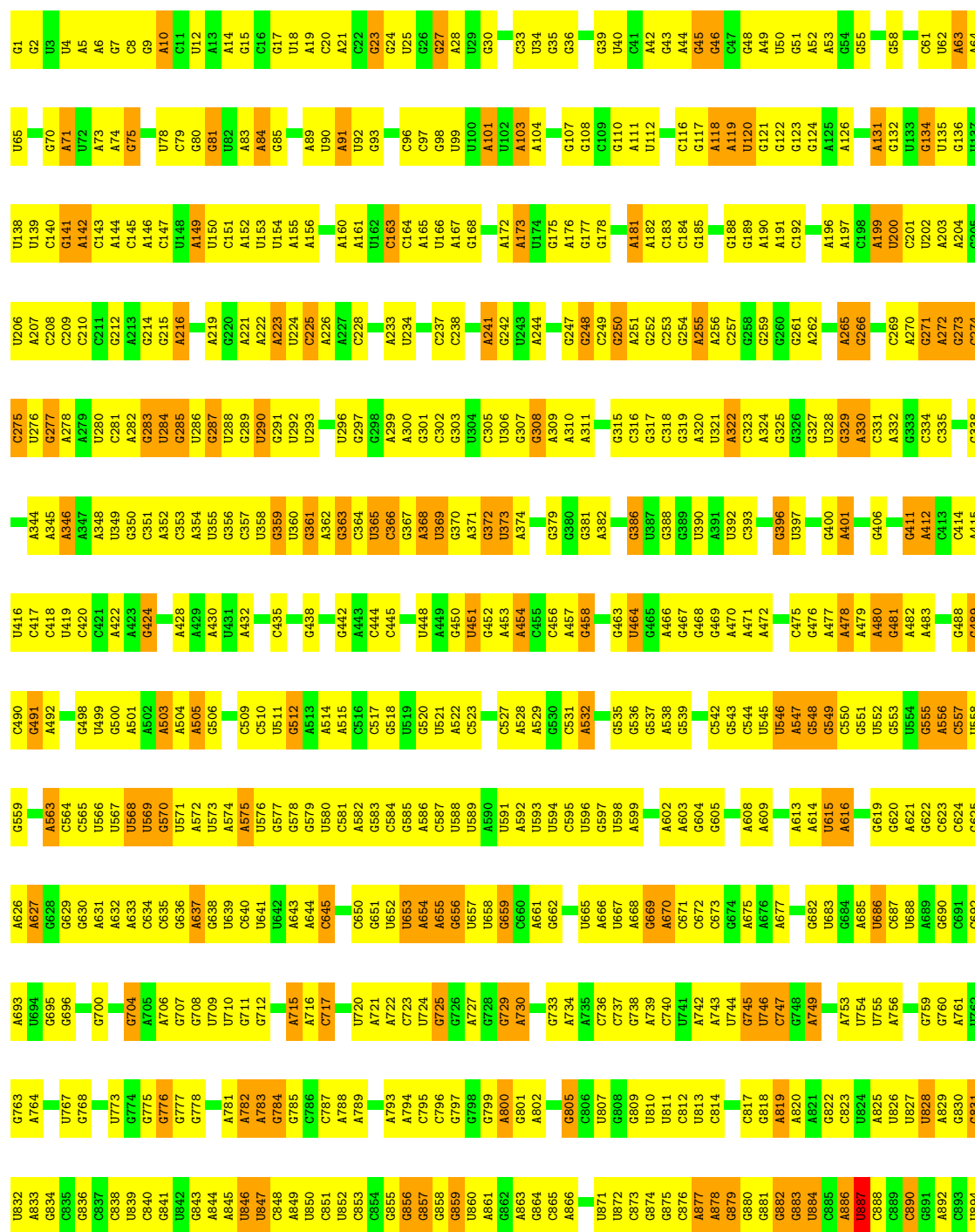
- Molecule 6: 50S ribosomal protein L10

Chain 5:  73% 6% 21%



● Molecule 7: 23S ribosomal RNA

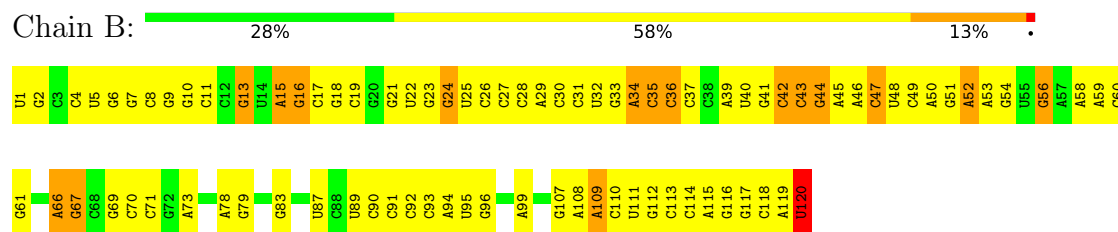
Chain A:  29% 54% 17%



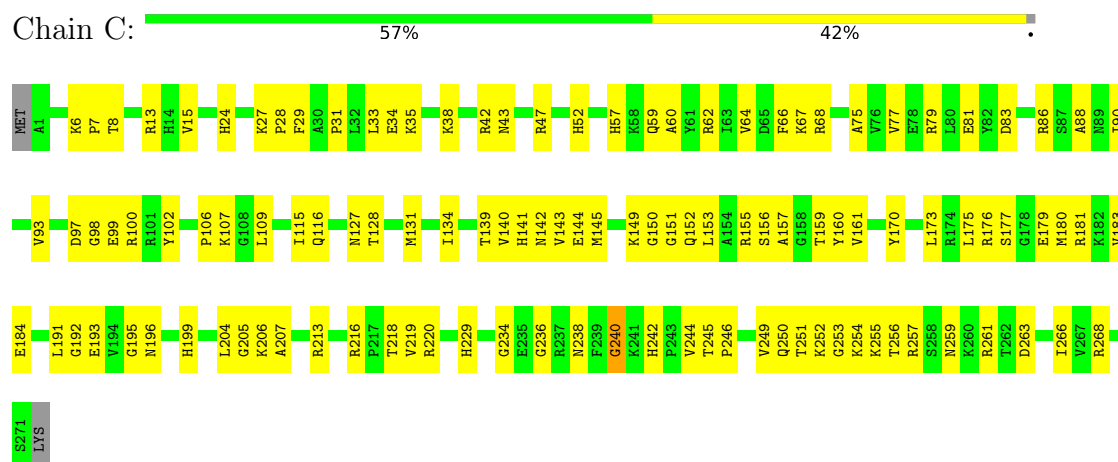
G1847	A1796	G1721	C1658	G1588	C1518	G1445	G1381	U1234	C1167	U1097	G1034	U896
A1848	A1787	A1722	G1659	U1589	G1519	C1446	A1308	G1235	A1168	A1098	U1035	A896
G1849	C1788	G1723	G1659	A1590	U1520	C1447	A1383	G1236	A1169	G1099	G1036	C897
	A1789	G1724	G1663	A1591	G1521	G1448	G1310	A1237	A1170	C1100	G1037	C898
A1853	C1790		A1664	C1592	A1522		A1385	A1237	G1171	U1101	G1038	A899
A1854	A1791	U1729	A1665	A1593	U1523		C1386	A1244	C1172	C1102	A1039	A900
U1855		C1730	G1666	U1594	G1524		A1387	G1245	U1173	A1103	A1040	C901
U1856	A1794	G1731	G1667	C1595				A1453	U1174	C1104	G1041	C902
G1857	C1795	G1732	A1668	A1596	A1528		A1392	G1246	A1175	U1105	G1042	C903
A1858	U1796	G1733	C1669	A1597	G1529		A1393	G1248	U1176	G1106		G904
U1859	G1797	G1734	A1670	A1598	G1530		U1394	U1249	G1177	U1107	C1045	
G1860	U1798	A1735	U1671	A1598	C1531		A1395	G1250	C1178	U1108	A1046	
G1861	U1736	U1736	A1672	U1602	G1532		U1396	C1251	C1179	C1109	G1047	G907
G1862	C1800	G1737	G1673	A1603	U1533		A1397	G1252	A1180	A984	A1110	A910
G1863	A1801	G1738	G1674	C1604	U1534		C1398	A1253	U1181	G1111	A1048	A911
U1864	A1802	A1739	C1675	C1605	A1535		C1399	A1254	G1112	C1112	C1062	C912
A1803	A1803	G1740	A1676	C1606	C1536		U1400	U1255	U1183	U1113	C1063	U913
A1865	A1803	G1740	A1676	C1606	C1536		U1400	G1256	U1184	C1114	A1054	G914
A1866	G1804	C1741	A1677	C1607	G1537		G1401	G1256		A988		
	A1805	U1742	A1678	A1608	U1538		U1402	C1257	G1185	G1115	G1055	
G1869	C1806	G1743	A1679	A1609	U1539		A1403	C1258	A1186	A990	G1056	
C1870	A1807	A1744	U1680	A1610	G1540		A1328	G1259	G1187	G1116	G1057	A920
A1871	G1807	A1745	G1681		C1541		U1405		U1188	U1119	U1058	
A1872	A1809	U1746	U1682	G1613	U1542		U1406	A1262	A1189	G1120	C1059	G923
G1873	A1810	U1747	U1683	A1614	G1543		G1407	A1262	G1190	C1121	U1060	G924
	C1811	C1748	G1684		A1544		U1408	A1265		C1122	U1061	A925
A1876	U1812	A1749	C1685	A1618	U1545		U1409	G1266	C1196		G1062	A927
A1877	G1813	G1750	C1686	G1619	A1546		G1410	U1267	G1197	G1128	G1063	A928
G1878	G1814	U1751	G1687	G1620	C1547		U1411	A1268	U1198	A1129	C1064	U929
C1879	A1815	C1752	U1688	U1621	G1547		U1412	A1269	U1199	U1130	U1065	G930
U1880	C1816	G1753	A1689	G1622	A1548		A1413	C1270	C1200	G1131	U1066	U931
C1881	A1817	A1754	A1690		U1550		U1414	G1271	U1201	U1132	A1067	U932
U1882	U1818	G1755	C1691	A1626			U1415	A1272	C1202	A1133	G1068	A933
A1883	A1819	G1756	U1692	U1629	G1554		G1416	U1273	A1134	G1003	U1069	U934
G1884	U1820	A1757	U1693	A1630	C1555		C1417	A1274	U1203	A1335	A1070	C935
A1885	A1821	U1758	C1694	G1630	C1556		G1418	A1275	A1204	U1004	C936	
U1886	G1822	A1759	G1695	C1631	C1557		A1419	A1275	A1205	C1005	A936	
C1887	C1823	C1760	G1696	A1632	C1558		A1420		G1206	C1072	C937	
G1888	G1824	C1761	A1697	G1633	U1559		G1421	C1278	C1207	G1139	G938	
A1889	U1825	A1762	A1698	A1634	G1560		G1422	G1279	U1208	C1140	G1074	G939
G1890	G1635	G1763	C1699	A1635	C1560		G1423	G1280	U1209	C1075	A1010	
U1827	G1764	C1764	A1700	U1636			A1494	A1281	A1142	G1076	G1011	A941
G1891	U1827	G1765	A1700	A1495	U1563		G1424	U1282	A1143	U1012		
	G1828	U1765	C1701	A1637	C1564		G1425	G1283		C1013	U1078	A945
G1896	A1829	G1766	G1702	U1638	C1565			A1284	A1214	C1079	C1014	C946
G1897	C1830		G1703	C1639	A1566		C1428	G1279	G1215	A1080	U1015	C947
	G1831	U1769	C1704	A1640	G1567		G1429	A1286	G1149	C948	G1016	
A1900	C1832	G1770	A1705		U1568		C1430	A1287	C1150	U1081		G949
	C1833		C1706	G1643	A1569		A1431	G1288	U1219		U1019	
G1904	U1834	A1773	G1707	C1644	A1570		A1365		G1220	U1083		G953
	C1835	C1774	C1708	G1645	A1571		A1366		C1221	A1084	A1020	G954
G1907	C1836	U1775	U1709	C1646	U1571		C1362	C1291	U1222	C1153	A1095	
C1908	C1837	G1776	G1710	U1647	C1577		C1363	G1292	G1154	C1086	U1022	
G1909	C1838	U1777	A1711	G1648	U1578		G1364	C1293	U1224	G1087	G1023	G956
G1910	C1839	U1778	U1712	U1649	A1579		A1365	U1294	G1225	A1088	G1024	C957
U1911	G1840	U1779	A1713	A1650	A1579		A1366	C1295	A1296	U1089	G1025	U958
A1912	U1841	U1780	U1714	G1651			A1372	G1296	G1227	A1090	G1026	A959
A1913	G1842	U1781	G1715	A1583	C1582		A1439	C1297	G1228	C1161	A1091	A960
C1914	C1843	U1782	U1716	U1584	A1583		C1376	C1297	C1229	C1092	C1092	C961
	C1844	A1783	A1717	A1655	U1584		A1441	G1300	A1230	G1093	A1028	G962
	G1845	A1784	A1717	C1656	A1586		A1442	G1300	G1163	U1094	A1029	
A1916	C1846	A1785	C1657	U1657	C1587		U1379	A1301	G1232	A1165	A1032	G969
		G1786	U1700	C1657	C1587		C1444	A1302	C1232	C1163	U1032	U970

G2869	A2809	U2746	G2677	C2610	A2478	G2409	G2341	A2267	C2196	A2135	G2061	U1918
G2870	A2810	G2747	C2678	C2611	U2479	G2410	C2342	A2268	U2197	G2136	A2062	A1919
G2871	G2811	A2748	U2679	G2612	C2480	A2411	C2343	G2269	A2198	U2137	C2063	G1922
A2872	G2812	A2749	U2680	U2613	G2481	A2412	G2345	G2270	A2199	G2138	G2064	U1923
G2873	A2813	A2750	G2681	G2614	A2482	G2413	A2346	G2271	G2201	U2139	C2065	U1924
G2874	G2814	G2751	C2682	U2615	C2483	G2414	C2347	U2272	G2202	G2140	U2075	C1925
G2875	C2815	C2752	C2683	C2616	G2484	G2415	U2348	A2278	U2203	G2141	G2069	C1926
G2876	G2816	U2753	U2684	C2620	G2485	G2416	G2349	A2279	U2204	A2142	A2070	U1926
G2877	U2817	U2754	G2685	G2621	C2486	C2417	C2350	G2282	G2205	G2143	A2071	A1927
U2878	G2818	C2755	U2686	U2622	G2487	U2418	G2351	G2283	A2206	C2144	C2072	A1928
A2879	U2819	U2756	U2687	G2623	G2488	U2419	A2352	A2284	G2207	G2145	C2073	G1929
G2880	G2820	A2757	G2688	G2624	U2490	C2420	G2353	A2285	U2210	C2146	U2074	U1930
A2881	A2821	A2758	U2689	G2625	U2491	C2421	C2354	A2286	A2211	G2147	U2075	U1931
A2882	G2822	G2759	C2690	G2626	U2492	G2422	U2355	G2288	G2212	G2148	U2076	A1932
A2883	A2823	C2760	A2691	G2627	U2493	A2423	U2356	A2289	U2213	U2149		G1933
G2884	G2824	G2761	U2692	C2628	G2494	G2424	G2357	A2290	G2214	U2151	U2080	A1936
G2885	A2825	G2762	U2693	U2629	G2495	A2425	G2358	G2291	C2215	G2152	U2081	A1937
A2886	G2826	G2763	U2694	G2630	G2496	G2426	G2359	G2292	G2216	C2153	A2082	A1938
G2887	C2827	U2764	A2695	C2631	C2498	G2427	G2360	U2293	U2219	A2155	G2093	U1940
G2888	G2828	A2765	A2696	A2634	U2499	G2428	C2361	U2294	U2220	G2156	A2094	A1941
G2889	A2829	U2766	U2697	A2635	U2500	A2429	C2362	G2295	G2221	G2157	A2095	C1942
G2890	G2830	G2767	G2701	C2636	C2501	G2430	G2363	U2296	G2222	U2158	C2096	U1943
U2891	G2831	G2770	G2702	U2637	G2502	G2431	G2364	A2297	G2223		A2097	U1944
G2892	U2832		A2705	G2638	A2503	G2432	G2365	A2298	C2224		C2098	G1945
A2893	G2833	C2773	G2706	A2639	U2504	U2433	G2370	A2299	G2225	C2161	U2098	G1946
G2894	A2834	C2774	U2707	G2640	U2505	U2441	G2371	U2305	U2228	A2163	G2100	U1947
G2895	U2835	G2775	G2710	G2641	U2506	C2442	C2374	C2306	G2229	C2165	G2101	U2026
U2897	A2837	A2776	U2711	G2642	G2507	G2443	C2375	G2307	U2231	C2166	G2102	G2027
G2898	G2838	G2777	G2712	G2643	G2508	G2444	A2376	G2308	U2232	U2167	C2103	U2028
U2899	U2839	U2778	U2713	G2644	C2512	G2445	A2377	A2309	C2232	G2168	U2105	A1952
A2900	G2840	G2780	C2714	G2645	U2513	G2446	A2378	C2310	U2233	A2169	U2106	A1953
C2901	C2841	A2781	G2715	G2646	U2514	A2447	G2379	C2311	G2234	A2170	G2107	G1954
G2902	G2842	G2782	U2716	U2647	G2515	A2448	C2380	A2311	G2235	C2171	A2108	U1955
U2903	U2843	U2783	G2717	G2648	A2516	U2449	A2381	U2312	U2236	A2172	U2109	G1956
	G2844	G2784	G2718	C2649	G2517	G2450	G2382	C2313	U2237	C2173	G2110	G1957
	U2845	C2785	U2719	U2650	C2518	A2451	G2383	A2314	G2238	C2174	G2111	C1958
	G2846	U2786	U2720	C2651	U2519	G2452	U2384	G2315	G2239		G2112	C1962
	U2847	U2787	C2652	C2652	C2520	G2453	C2385	G2316	U2240	C2175	U2113	U1963
G2848	A2848	C2788	U2721	G2653	G2521	G2454	A2388		A2241	C2176	A2114	U1964
U2849	U2849	U2789	G2722	A2654	U2522	G2455	G2389	U2320	G2242	C2177	G2115	C1965
	A2850	U2790	U2723	G2655	G2523	U2456	U2390	U2321	U2243	C2178	G2116	A1966
	G2851	A2791	A2725	U2656	G2524	U2457	G2391	A2322	U2244	C2179	A2117	C1967
G2852	C2852	A2792	U2726	A2657	C2525	A2460	U2392	G2323	U2245	U2180	G2043	G1968
C2853	G2853	C2793	G2658	C2659	U2526	A2461	U2393	U2324	A2246	U2181	U2118	A1969
G2854	U2854	C2794	C2660	G2660	G2527	G2462	C2394	G2325	G2247	A2183	G2120	A1970
C2855	C2855	C2795	U2596	A2661	A2530	G2463	C2395	G2326	C2248	A2184	G2121	G1972
	A2856	U2796	G2597	G2662	A2531	C2464	G2396	U2327	C2249	U2185		G2046
G2857	G2857	U2797	G2732	G2663	G2532	C2465	U2397	A2328	G2251	U2187	G2047	G2048
G2858	C2858	U2798	A2733	G2664	G2533	C2466	G2398	U2329	G2126	U2188	G2049	C2050
	A2860	A2800	G2737	A2665	G2534	U2467	U2399	G2330	G2127	A2051		G1975
U2861	U2861	G2801	U2738	C2666	U2535	A2468	G2400	G2331	G2128	A2052		A1978
G2862	G2862	G2802	U2739		U2536	A2469	G2401	G2332	G2129	G2055		U1982
C2863	G2863	A2740	G2803	G2671	C2537	U2470	U2402	G2333	C2260	A2191	C2056	G1983
G2864	U2864	U2804	U2741	U2672	C2538	U2471	G2405	A2334	C2261	U2192		C2055
U2865	U2865	C2805	G2742	G2673	A2542	U2472	A2406	U2335	U2262	U2193		G2056
G2866	U2866	G2806	U2743	G2674	G2543	C2475	A2407	U2336	C2263	U2194		A1987
G2867	G2867	U2807	G2744	A2675	G2544	A2476	A2408	A2336	A2266	U2195		A2059
A2868	A2868	C2745	C2745	C2676	G2545	U2477	U2408					G1988

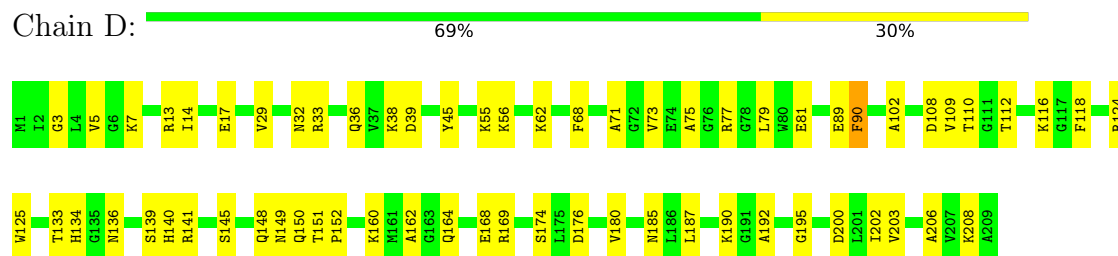
• Molecule 8: 5S ribosomal RNA



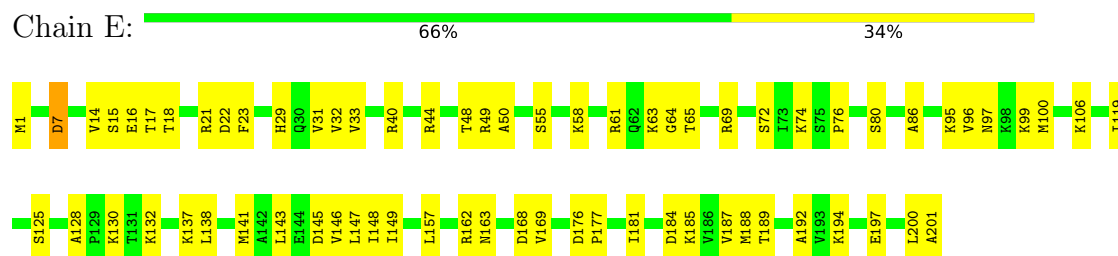
• Molecule 9: 50S ribosomal protein L2



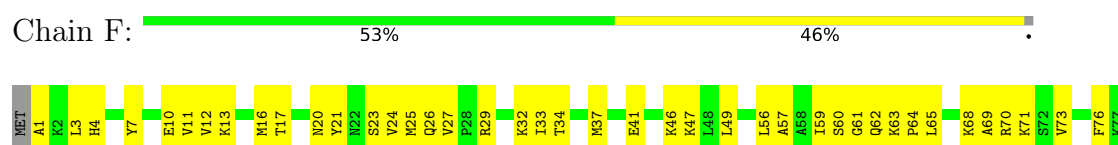
• Molecule 10: 50S ribosomal protein L3

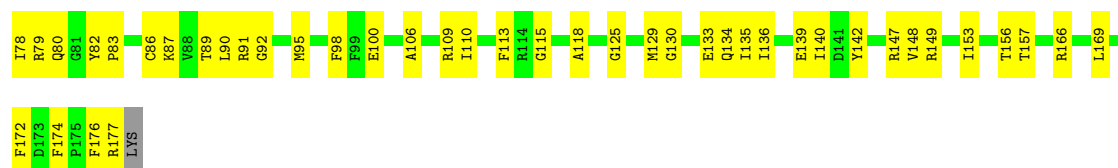


• Molecule 11: 50S ribosomal protein L4



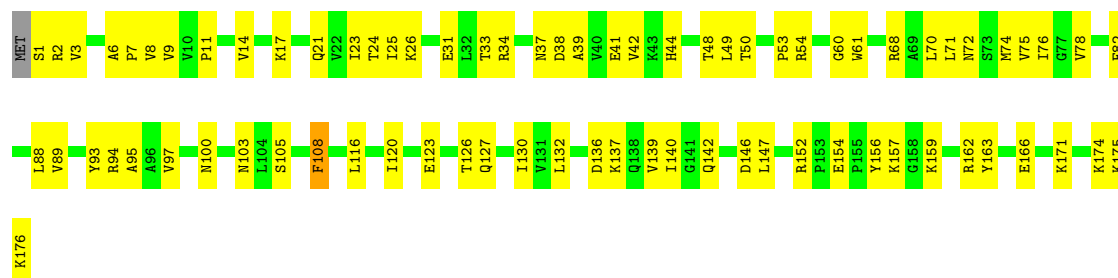
• Molecule 12: 50S ribosomal protein L5





- Molecule 13: 50S ribosomal protein L6

Chain G: 56% 42%



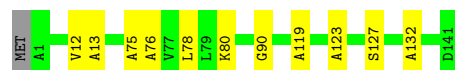
- Molecule 14: 50S ribosomal protein L9

Chain H: 48% 52%



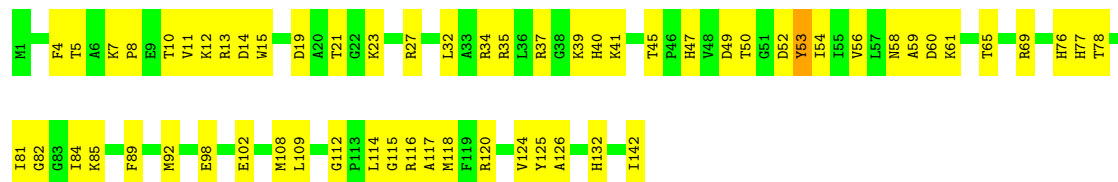
- Molecule 15: 50S ribosomal protein L11

Chain I: 92% 8%



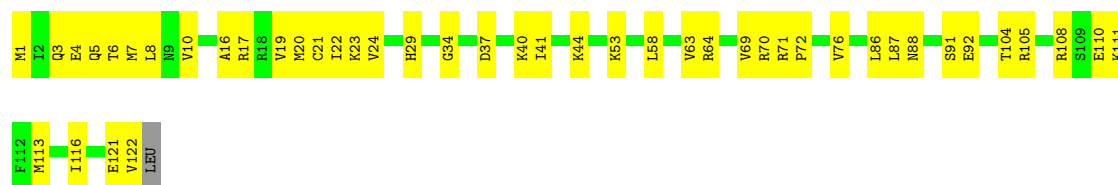
- Molecule 16: 50S ribosomal protein L13

Chain J: 58% 42%



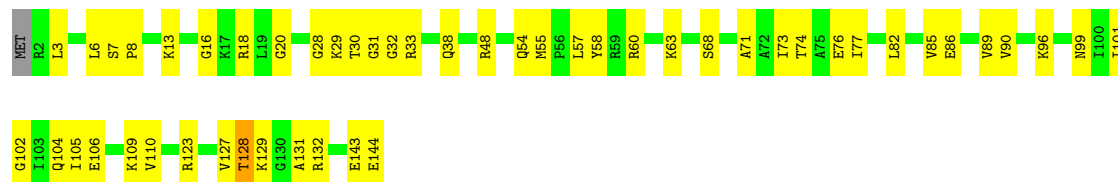
- Molecule 17: 50S ribosomal protein L14

Chain K: 63% 37%



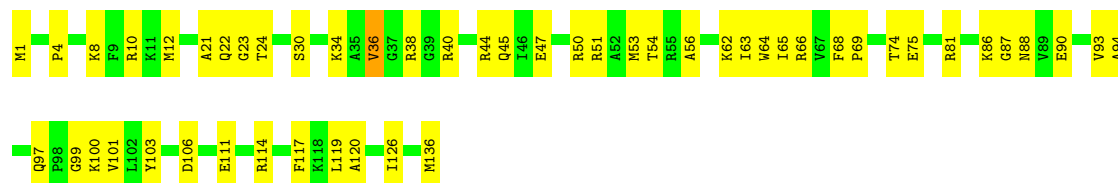
- Molecule 18: 50S ribosomal protein L15

Chain L: 65% 34% ..



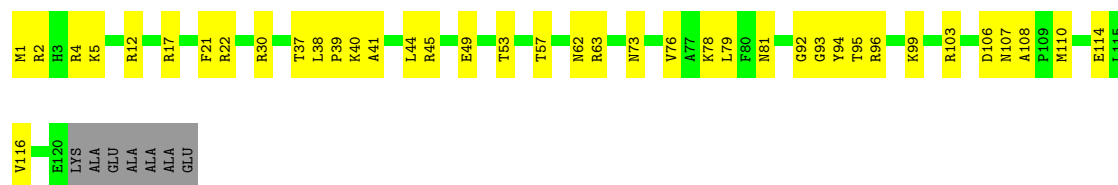
- Molecule 19: 50S ribosomal protein L16

Chain M: 63% 37% .



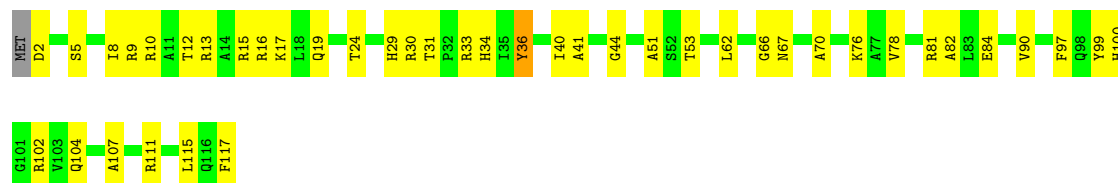
- Molecule 20: 50S ribosomal protein L17

Chain N: 64% 31% 6%



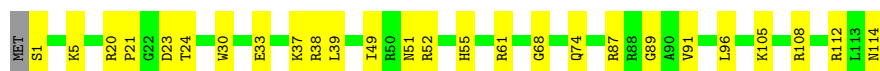
- Molecule 21: 50S ribosomal protein L18

Chain O: 63% 35% ..



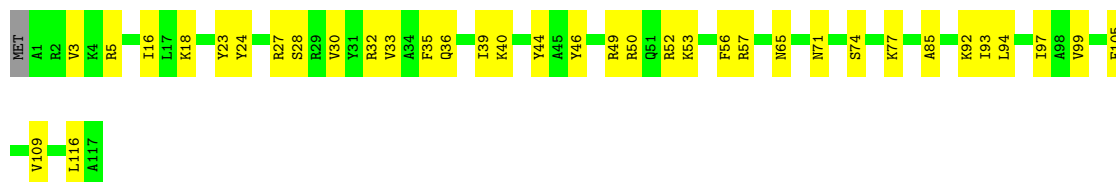
- Molecule 22: 50S ribosomal protein L19

Chain P: 77% 23% .



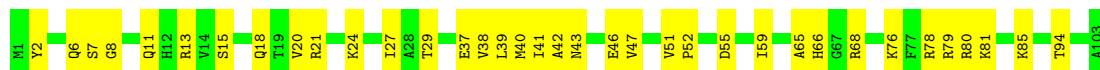
- Molecule 23: 50S ribosomal protein L20

Chain Q: 69% 31%



- Molecule 24: 50S ribosomal protein L21

Chain R: 65% 35%



- Molecule 25: 50S ribosomal protein L22

Chain S: 69% 31%



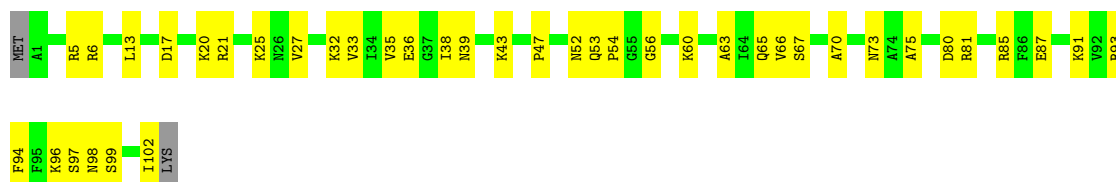
- Molecule 26: 50S ribosomal protein L23

Chain T: 61% 32% 7%



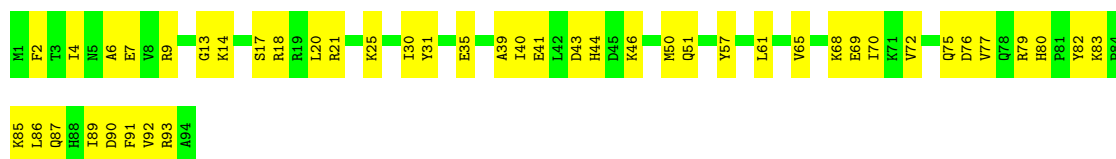
- Molecule 27: 50S ribosomal protein L24

Chain U: 60% 38%



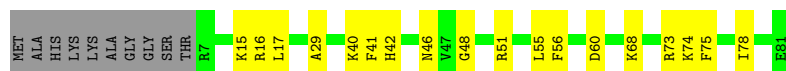
- Molecule 28: 50S ribosomal protein L25

Chain V: 52% 48%



- Molecule 29: 50S ribosomal protein L27

Chain W: 67% 21% 12%



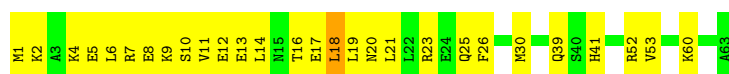
- Molecule 30: 50S ribosomal protein L28

Chain X: 62% 37%



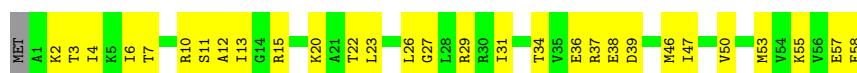
- Molecule 31: 50S ribosomal protein L29

Chain Y: 56% 43%



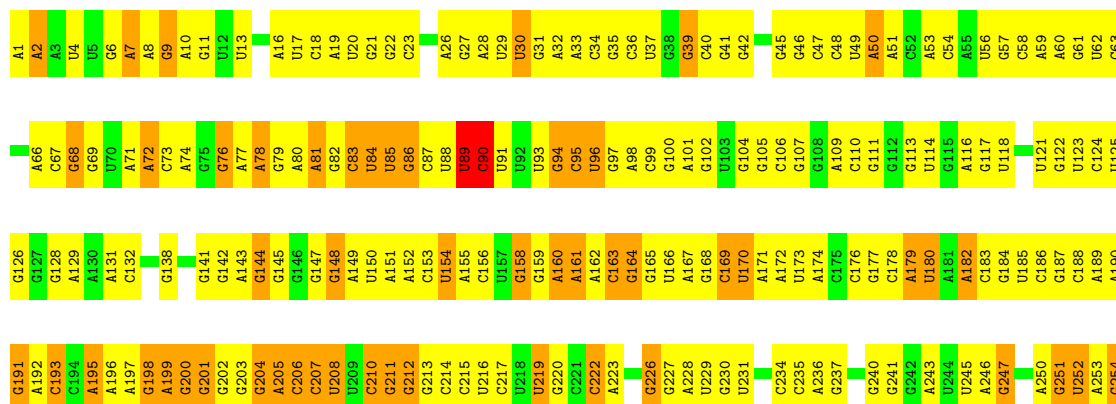
- Molecule 32: 50S ribosomal protein L30

Chain Z: 49% 49%

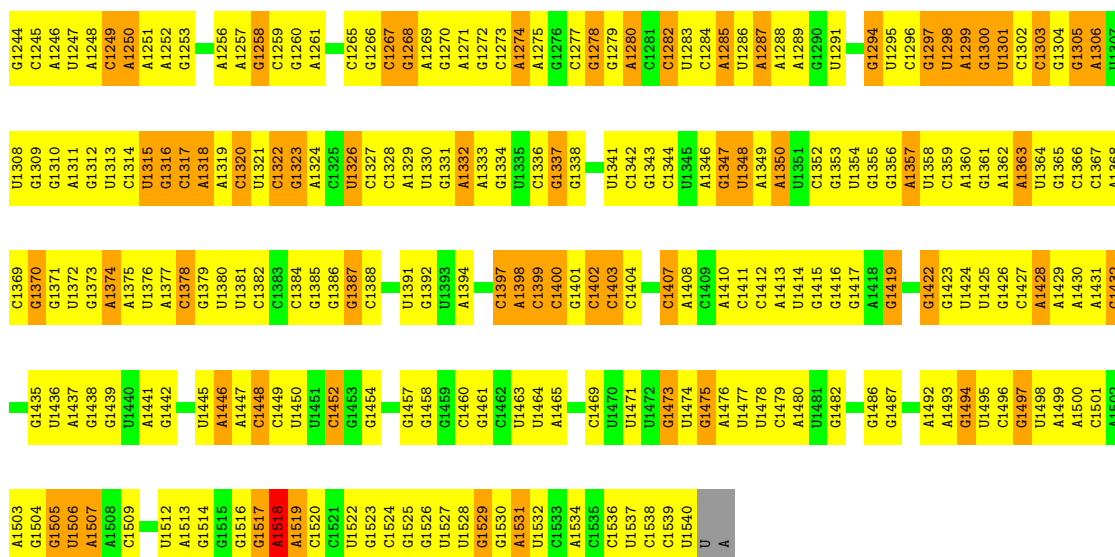


- Molecule 33: 16S ribosomal RNA

Chain a: 22% 60% 18%

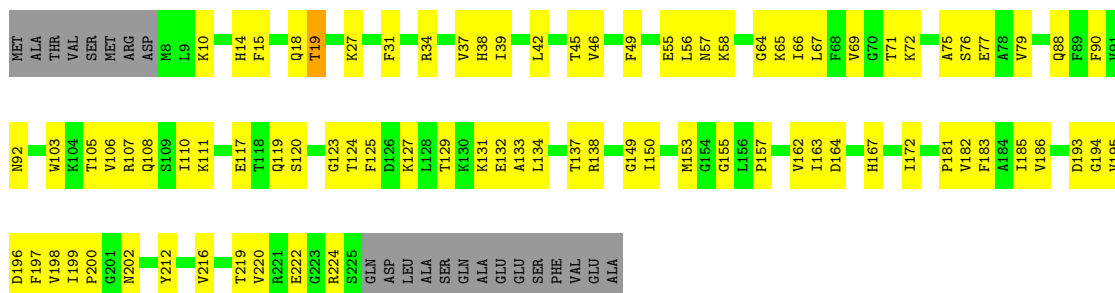


G178	A1179	A1180	G1181	G1182	G1183	G1184	G1185	G1186	G1187	G1188	G1189	G1190	G1191	G1192	G1193	A1196	A1197	G1198	G1199	C1200	A1204	U1205	G1206	G1207	A1212	A1213	G1214	G1215	A1216	C1217	A1218	A1219	G1220	G1221	G1222	G1223	A1224	A1225	G1226	A1227	C1228	A1229	C1230	G1231	U1232	G1233	C1234	U1235	A1236	C1237	A1238	A1239	U1240	G1241	G1242	C1243				
A1111	C1114	G1050	C1051	U1052	G1053	C1054	A1055	U1056	U1057	G1058	G1059	U1060	G1061	U1062	C1063	G1064	U1065	C1066	A1067	G1068	C1069	G1070	C1071	G1072	U1073	G1074	G1075	U1076	G1077	G1078	G1079	A1080	A1081	U1082	U1083	G1084	U1085	U1086	G1087	G1088	G1089	U1090	U1091	A1092	A1093	G1094	U1095	C1096	C1097	G1098	G1099	A1100	A1101	G1106	C1107	G1108	C1109	A1110		
U981	U982	A983	C984	C985	U986	G987	G988	U991	U992	U993	G994	A994	C995	A996	G1002	G1003	A1004	A1005	G1006	U1007	U1008	A938	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1017	G1018	A1019	G1020	A1021	A1022	U1023	G1024	U1025	G1026	C1027	U1030	C1031	G1032	G1033	G1034	A1035	A1036	C1037	C1038	G1039	U1040	A1041	A1042	G1043	A1044	C1045	A1046		
A913	A914	G915	G916	G917	A918	A919	U920	U921	G922	A923	G924	U925	G926	G927	C932	G933	C934	A935	C936	A937	A938	G939	C940	U941	C942	G943	A944	A945	A946	A947	A948	A949	U950	G951	G954	U955	A956	A959	U960	U961	U962	G963	A964	U965	G966	C967	A968	A969	C970	G971	C972	G973	A974	A975	G976	A977	A978	C979	C980	
U843	G844	A845	G846	G847	A848	G849	U850	G851	U852	A853	G854	C855	C856	C857	C858	A859	C860	G861	A864	C867	C868	U869	G870	U871	A872	A873	G874	U875	C876	C877	A878	C879	C883	A884	C885	A886	A889	G890	U891	G892	G893	A894	A900	A901	G902	G903	U904	U905	A906	A907	A908	A909	C910	C841	C990					
A780	A781	A782	C783	A784	G785	G786	A787	U788	A789	U790	G791	A792	U793	U794	C795	C796	C797	U798	G799	G800	A801	A802	G803	U804	C805	C806	A807	C808	G809	C810	C811	G812	U813	A814	A815	A816	C817	G818	A819	U820	C821	U822	C823	G824	A825	C826	U827	U828	G829	U834	U835	G836	U837	G838	C839	C840	C911	U842		
C719	C720	G721	G722	U723	G724	G725	G726	G727	A728	A729	G730	G731	G732	G733	C734	C735	G736	A737	C738	C739	G740	G741	G742	A743	C744	G745	U746	G747	A748	G749	G750	U751	G752	A753	C754	G755	G756	U757	C758	A759	G760	G763	C764	G765	A766	A767	A768	G769	C770	G771	U772	G773	G774	G775	G776	A777	G778	C779		
U780	A781	A782	C783	A784	G785	G786	A787	U788	A789	U790	G791	A792	U793	U794	C795	C796	C797	U798	G799	G800	A801	A802	G803	U804	C805	C806	A807	C808	G809	C810	C811	G812	U813	A814	A815	A816	C817	G818	A819	U820	C821	U822	C823	G824	A825	C826	U827	U828	G829	U834	U835	G836	U837	G838	C839	C840	C911	U842		
U843	G844	A845	G846	G847	A848	G849	U850	G851	U852	A853	G854	C855	C856	C857	C858	A859	C860	G861	A864	C867	C868	U869	G870	U871	A872	A873	G874	U875	C876	C877	A878	C879	C883	A884	C885	A886	A889	G890	U891	G892	G893	A894	A900	A901	G902	G903	U904	U905	A906	A907	A908	A909	C910	C841	C990					
G912	A913	A914	G915	G916	G917	A918	A919	U920	U921	G922	A923	G924	U925	G926	G927	C932	G933	C934	A935	C936	A937	A938	G939	C940	U941	C942	G943	A944	A945	A946	A947	A948	A949	U950	G951	G954	U955	A956	A959	U960	U961	U962	G963	A964	U965	G966	C967	A968	A969	C970	G971	C972	G973	A974	A975	G976	A977	A978	C979	C980
U981	U982	A983	C984	C985	U986	G987	G988	U991	U992	U993	G994	A994	C995	A996	G1002	G1003	A1004	A1005	G1006	U1007	U1008	A938	U1009	U1010	C1011	A1012	G1013	A1014	G1015	A1016	U1017	G1018	A1019	G1020	A1021	A1022	U1023	G1024	U1025	G1026	C1027	U1030	C1031	G1032	G1033	G1034	A1035	A1036	C1037	C1038	G1039	U1040	A1041	A1042	G1043	A1044	C1045	A1046		
G1047	G1050	C1051	U1052	G1053	C1054	A1055	U1056	U1057	G1058	G1059	U1060	G1061	U1062	C1063	G1064	U1065	C1066	A1067	G1068	C1069	G1070	C1071	G1072	U1073	G1074	U1075	U1076	G1077	G1078	G1079	A1080	A1081	U1082	U1083	G1084	U1085	U1086	G1087	G1088	G1089	U1090	U1091	A1092	A1093	G1094	U1095	C1096	C1097	G1098	G1099	A1100	A1101	G1106	C1107	G1108	C1109	A1110			
A1111	C1114	G1050	C1051	U1052	G1053	C1054	A1055	U1056	U1057	G1058	G1059	U1060	G1061	U1062	C1063	G1064	U1065	C1066	A1067	G1068	C1069	G1070	C1071	G1072	U1073	G1074	U1075	U1076	G1077	G1078	G1079	A1080	A1081	U1082	U1083	G1084	U1085	U1086	G1087	G1088	G1089	U1090	U1091	A1092	A1093	G1094	U1095	C1096	C1097	G1098	G1099	A1100	A1101	G1106	C1107	G1108	C1109	A1110		
A1157	C1158	G1159	G1160	C1161	C1162	A1163	G1166	A1167	U1168	A1169	A1170	A1171	C1172	U1173	G1174	G1175	A1176	C1177	G1178	G1179	A1180	A1181	A1182	A1183	A1184	A1185	A1186	A1187	A1188	A1189	A1190	A1191	A1192	A1193	A1194	A1195	A1196	A1197	A1198	A1199	A1200	A1201	A1202	A1203	A1204	A1205	A1206	A1207												
G255	U256	G257	G258	G259	G260	U261	A262	A263	C264	G265	G266	C267	U268	C269	A270	C271	G272	U273	A274	G275	G276	C277	G278	A279	C280	G281	A282	U283	C284	C285	C286	U287	A288	G289	G293	U294	C295	U296	G297	A298	G299	A300	G301	G302	A303	U304	G305	A306	C307	C308	A309	G310	C316	U317	G318	C381	A382			



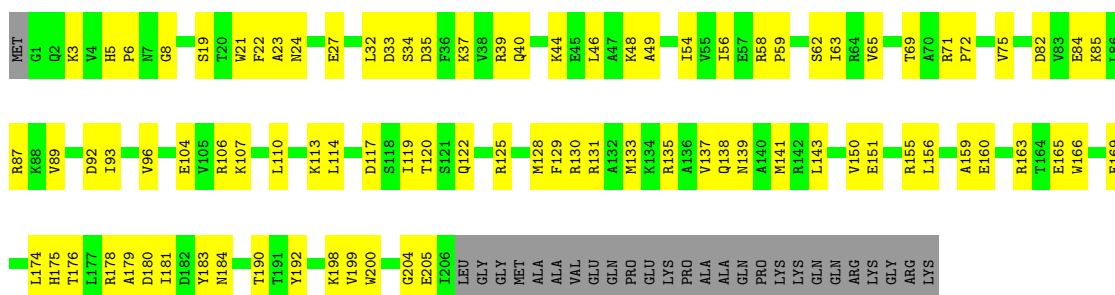
• Molecule 34: 30S ribosomal protein S2

Chain b: 56% 35% 9%



• Molecule 35: 30S ribosomal protein S3

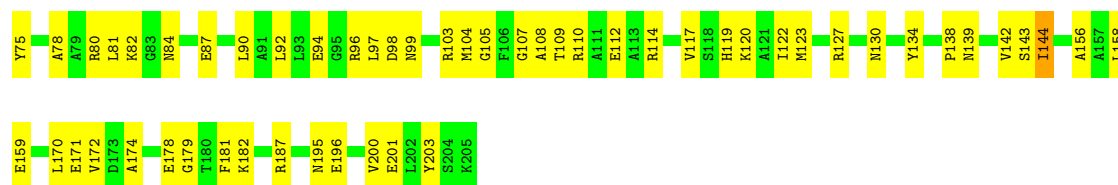
Chain c: 51% 38% 12%



• Molecule 36: 30S ribosomal protein S4

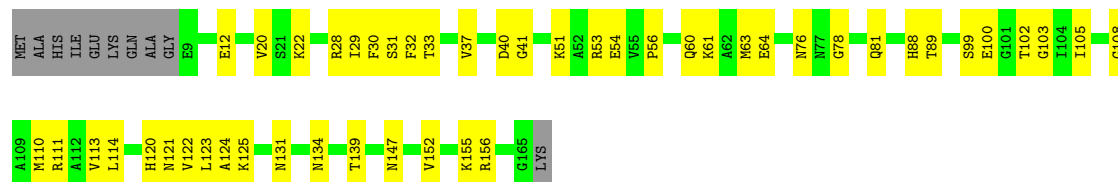
Chain d: 52% 46%





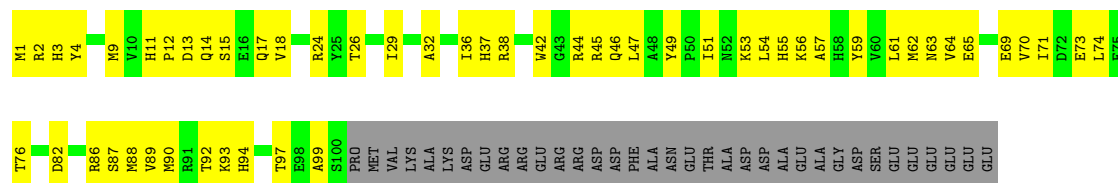
• Molecule 37: 30S ribosomal protein S5

Chain e: 65% 29% 6%



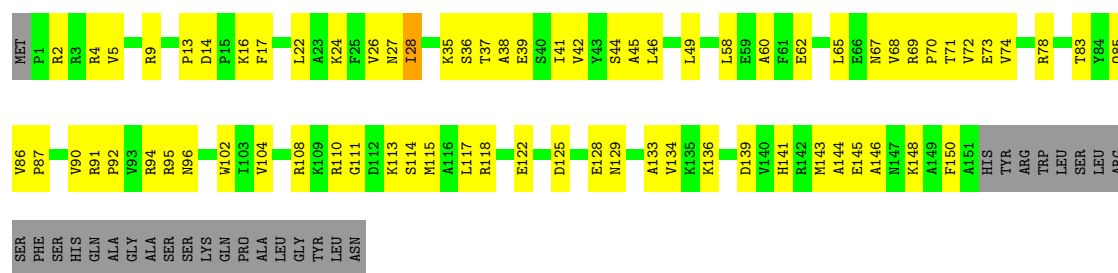
• Molecule 38: 30S ribosomal protein S6

Chain f: 34% 40% 26%



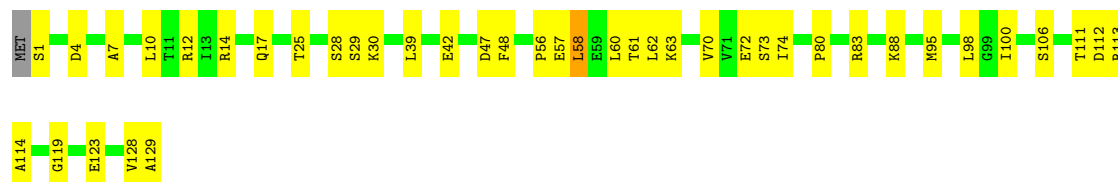
• Molecule 39: 30S ribosomal protein S7

Chain g: 44% 40% 16%



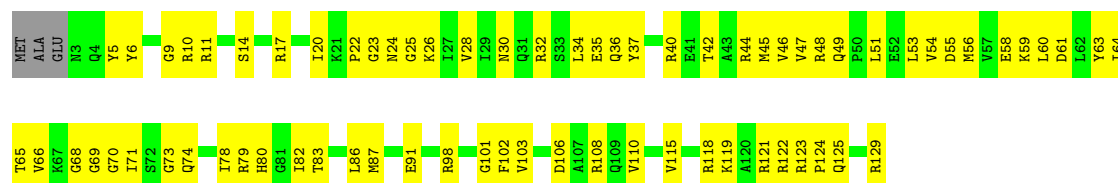
• Molecule 40: 30S ribosomal protein S8

Chain h: 68% 31% 1%

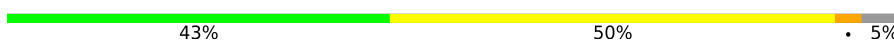


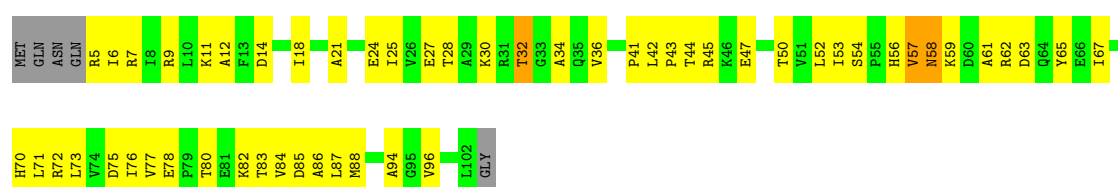
- Molecule 41: 30S ribosomal protein S9

Chain i: 



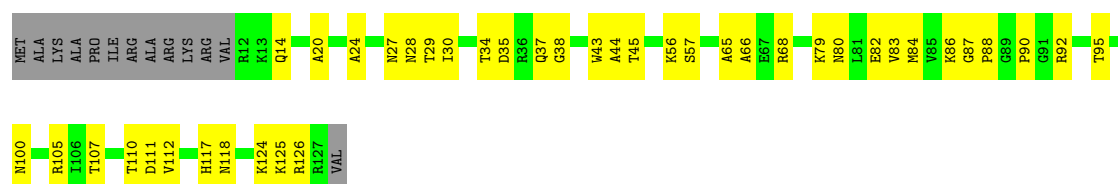
- Molecule 42: 30S ribosomal protein S10

Chain j: 



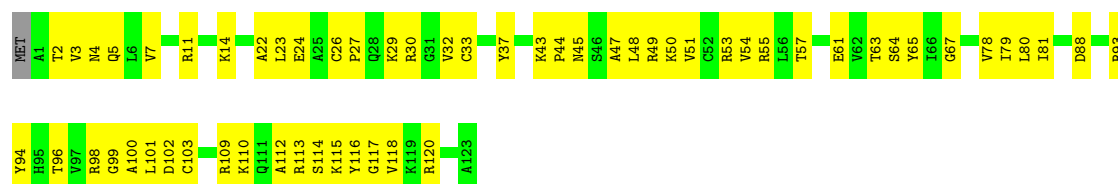
- Molecule 43: 30S ribosomal protein S11

Chain k: 



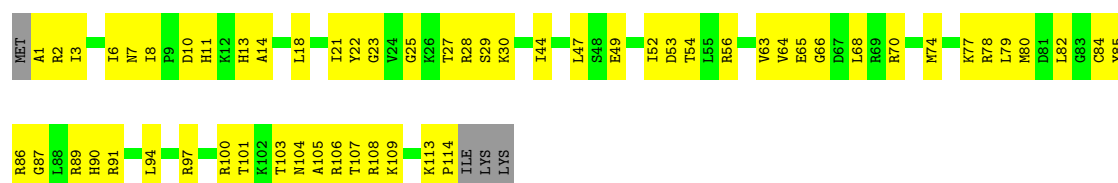
- Molecule 44: 30S ribosomal protein S12

Chain l: 

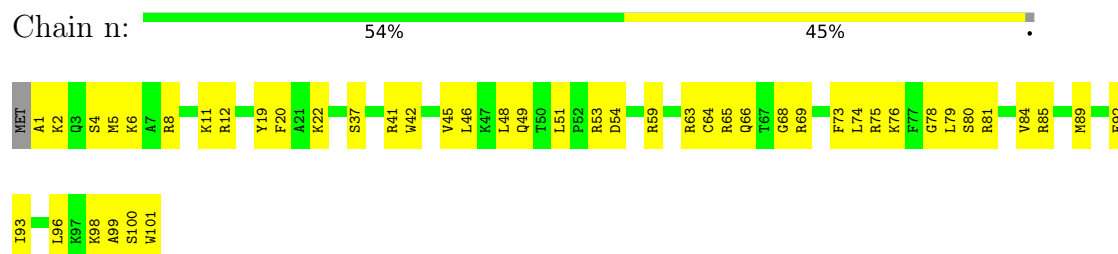


- Molecule 45: 30S ribosomal protein S13

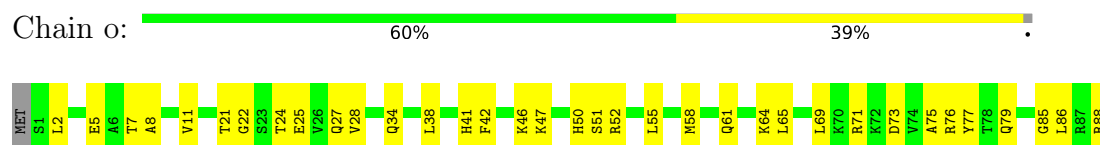
Chain m: 



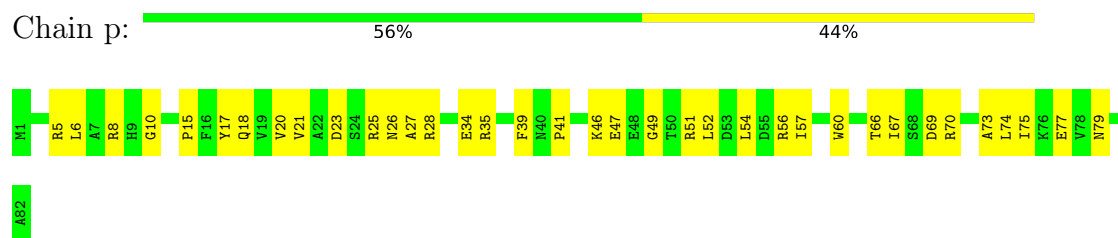
- Molecule 46: 30S ribosomal protein S14



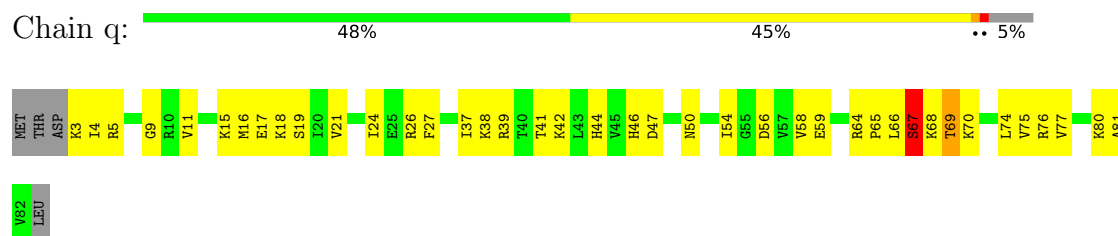
- Molecule 47: 30S ribosomal protein S15



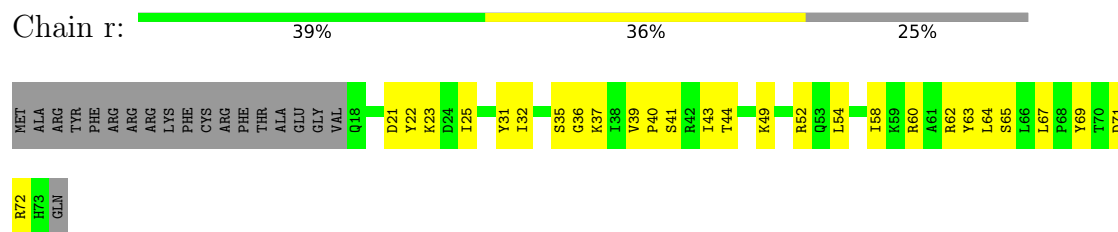
- Molecule 48: 30S ribosomal protein S16



- Molecule 49: 30S ribosomal protein S17



- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19





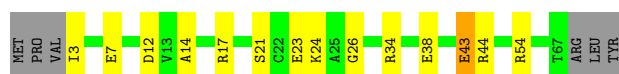
- Molecule 52: 30S ribosomal protein S20

Chain t: 68% 30% .



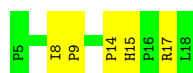
- Molecule 53: 30S ribosomal protein S21

Chain u: 72% 18% 8% .



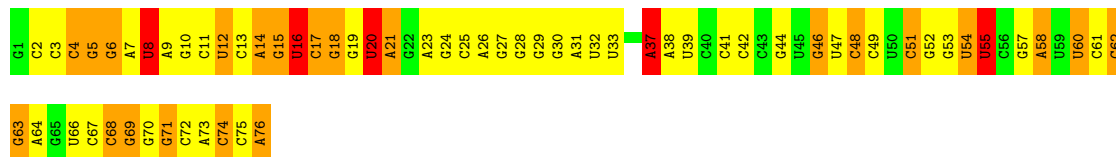
- Molecule 54: Api137

Chain v: 64% 36%



- Molecule 55: P-site tRNA^{Phe}

Chain w: 16% 49% 29% 7%



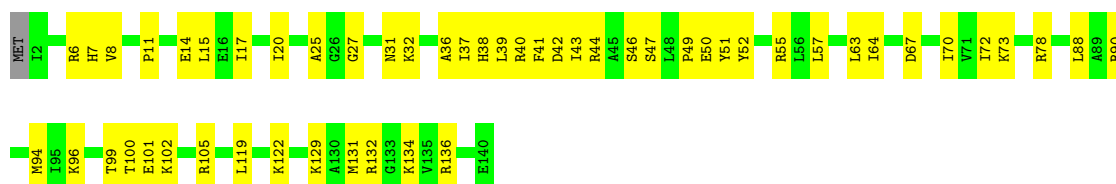
- Molecule 56: RNA (5'-R(P*AP*UP*GP*UP*UP*C)-3')

Chain x: 20% 20% 60%



- Molecule 57: Alternative stalled-ribosome rescue factor B

Chain y: 62% 37% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	60692	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	14.417	Depositor
Minimum map value	-7.317	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	347.328, 347.328, 347.328	wwPDB
Map dimensions	324, 324, 324	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 6MZ, 5MC, MG, 3TD, ZN, 5MU, MIA, 4OC, UR3, MA6, 2MA, 1MG, G7M, PSU, OMC, OMU, NA, 4SU, 2MG, OMG

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	0.38	0/450	0.66	2/599 (0.3%)
2	1	0.32	0/416	0.44	0/554
3	2	0.39	0/380	0.51	0/498
4	3	0.37	0/513	0.59	0/676
5	4	0.36	0/303	0.50	0/397
6	5	0.18	0/646	0.52	0/898
7	A	0.39	4/69263 (0.0%)	0.38	2/108050 (0.0%)
8	B	0.32	1/2873 (0.0%)	0.34	0/4478
9	C	0.40	0/2121	0.53	0/2852
10	D	0.38	0/1586	0.51	0/2134
11	E	0.34	0/1571	0.45	0/2113
12	F	0.22	0/1434	0.46	0/1926
13	G	0.28	0/1343	0.44	0/1816
14	H	0.29	0/1122	0.59	0/1515
15	I	0.17	0/692	0.53	0/960
16	J	0.37	0/1152	0.43	0/1551
17	K	0.38	0/947	0.51	0/1268
18	L	0.37	0/1054	0.53	0/1403
19	M	0.36	0/1093	0.50	1/1460 (0.1%)
20	N	0.37	0/973	0.52	0/1301
21	O	0.28	0/902	0.47	0/1209
22	P	0.34	0/929	0.43	0/1242
23	Q	0.42	0/960	0.49	0/1278
24	R	0.34	0/829	0.49	0/1107
25	S	0.37	0/864	0.47	0/1156
26	T	0.32	0/744	0.51	0/994
27	U	0.30	0/787	0.44	0/1051
28	V	0.32	0/766	0.46	0/1025
29	W	0.37	0/582	0.43	0/769
30	X	0.36	0/635	0.48	0/848
31	Y	0.36	0/510	0.63	1/677 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Z	0.38	0/453	0.49	0/605
33	a	0.32	1/36725 (0.0%)	0.36	2/57285 (0.0%)
34	b	0.25	0/1735	0.50	2/2338 (0.1%)
35	c	0.27	0/1651	0.42	0/2225
36	d	0.45	4/1665 (0.2%)	0.63	3/2227 (0.1%)
37	e	0.33	0/1154	0.47	0/1554
38	f	0.28	0/835	0.48	0/1128
39	g	0.25	0/1195	0.50	0/1602
40	h	0.30	0/989	0.43	0/1326
41	i	0.24	0/1034	0.48	0/1375
42	j	0.26	0/796	0.56	0/1077
43	k	0.27	0/885	0.42	0/1195
44	l	0.32	0/969	0.50	0/1300
45	m	0.23	0/892	0.46	0/1193
46	n	0.27	0/811	0.48	0/1081
47	o	0.28	0/722	0.43	0/964
48	p	0.29	0/659	0.46	0/884
49	q	0.38	1/657 (0.2%)	0.54	0/881
50	r	0.28	0/471	0.42	0/633
51	s	0.23	0/675	0.44	0/908
52	t	0.27	0/671	0.43	0/888
53	u	0.22	0/512	0.54	0/683
54	v	0.24	0/128	0.39	0/175
55	w	0.57	7/1650 (0.4%)	0.37	0/2569
56	x	0.31	0/138	0.35	0/212
57	y	0.23	0/1090	0.46	0/1461
All	All	0.36	18/157602 (0.0%)	0.41	13/235574 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
36	d	0	2

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	d	71	PHE	C-O	-7.80	1.14	1.24
55	w	16	U	C5-C6	7.58	1.49	1.34
55	w	20	U	C5-C6	7.53	1.49	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	w	20	U	N1-C2	7.40	1.53	1.38
55	w	16	U	N1-C2	7.32	1.53	1.38

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	d	71	PHE	N-CA-C	-11.32	86.68	110.80
1	0	5	ASN	CA-C-N	-7.83	109.61	121.83
1	0	5	ASN	C-N-CA	-7.83	109.61	121.83
36	d	70	GLN	CA-C-N	-7.02	108.14	121.54
36	d	70	GLN	C-N-CA	-7.02	108.14	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
36	d	70	GLN	Mainchain
36	d	71	PHE	Mainchain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	19	0
2	1	409	0	440	15	0
3	2	377	0	418	17	0
4	3	504	0	574	24	0
5	4	302	0	340	12	0
6	5	647	0	336	8	0
7	A	62336	0	31366	1981	0
8	B	2570	0	1301	96	0
9	C	2082	0	2157	98	0
10	D	1565	0	1616	65	0
11	E	1552	0	1619	59	0
12	F	1410	0	1447	65	0
13	G	1323	0	1374	51	0
14	H	1111	0	1148	67	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
15	I	693	0	347	11	0
16	J	1129	0	1162	45	0
17	K	938	0	1012	35	0
18	L	1045	0	1117	45	0
19	M	1074	0	1156	42	0
20	N	960	0	1000	33	0
21	O	892	0	923	34	0
22	P	917	0	965	25	0
23	Q	947	0	1022	36	0
24	R	816	0	839	30	0
25	S	857	0	922	25	0
26	T	738	0	807	31	0
27	U	779	0	834	30	0
28	V	753	0	780	34	0
29	W	575	0	592	17	0
30	X	625	0	655	25	0
31	Y	509	0	543	27	0
32	Z	449	0	491	20	0
33	a	33050	0	16650	1396	0
34	b	1704	0	1732	57	0
35	c	1624	0	1699	66	0
36	d	1643	0	1710	94	0
37	e	1141	0	1170	40	0
38	f	817	0	808	48	0
39	g	1181	0	1240	68	0
40	h	979	0	1034	35	0
41	i	1022	0	1070	77	0
42	j	786	0	828	58	0
43	k	869	0	878	34	0
44	l	955	0	1019	53	0
45	m	883	0	944	56	0
46	n	799	0	841	42	0
47	o	714	0	737	28	0
48	p	649	0	666	34	0
49	q	648	0	691	36	0
50	r	464	0	486	27	0
51	s	658	0	685	30	0
52	t	665	0	714	29	0
53	u	506	0	502	11	0
54	v	121	0	128	7	0
55	w	1631	0	837	53	0
56	x	125	0	64	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	y	1078	0	1134	48	0
58	0	2	0	0	0	0
58	3	1	0	0	0	0
58	A	244	0	0	0	0
58	B	5	0	0	0	0
58	C	2	0	0	0	0
58	D	2	0	0	0	0
58	L	1	0	0	0	0
58	X	1	0	0	0	0
58	a	93	0	0	0	0
58	m	1	0	0	0	0
58	w	4	0	0	0	0
59	4	1	0	0	0	0
60	A	1	0	0	0	0
All	All	146398	0	98031	4936	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

The worst 5 of 4936 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:d:61:ARG:HG3	36:d:71:PHE:CE2	1.47	1.48
33:a:153:C:C2	33:a:169:C:N4	1.83	1.44
36:d:61:ARG:CG	36:d:71:PHE:HE2	1.38	1.36
33:a:207:C:H1'	33:a:213:G:C6	1.70	1.25
36:d:61:ARG:CG	36:d:71:PHE:CE2	2.13	1.25

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	47 (87%)	7 (13%)	0	100	100
2	1	48/55 (87%)	46 (96%)	2 (4%)	0	100	100
3	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
4	3	62/65 (95%)	52 (84%)	8 (13%)	2 (3%)	3	25
5	4	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
6	5	129/165 (78%)	104 (81%)	25 (19%)	0	100	100
9	C	269/273 (98%)	237 (88%)	31 (12%)	1 (0%)	30	60
10	D	207/209 (99%)	182 (88%)	25 (12%)	0	100	100
11	E	199/201 (99%)	181 (91%)	18 (9%)	0	100	100
12	F	175/179 (98%)	152 (87%)	23 (13%)	0	100	100
13	G	174/177 (98%)	159 (91%)	14 (8%)	1 (1%)	21	52
14	H	147/149 (99%)	115 (78%)	32 (22%)	0	100	100
15	I	139/142 (98%)	110 (79%)	29 (21%)	0	100	100
16	J	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
17	K	120/123 (98%)	102 (85%)	18 (15%)	0	100	100
18	L	141/144 (98%)	117 (83%)	23 (16%)	1 (1%)	18	50
19	M	134/136 (98%)	107 (80%)	27 (20%)	0	100	100
20	N	118/127 (93%)	106 (90%)	12 (10%)	0	100	100
21	O	114/117 (97%)	105 (92%)	9 (8%)	0	100	100
22	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
23	Q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
24	R	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
25	S	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
26	T	91/100 (91%)	74 (81%)	17 (19%)	0	100	100
27	U	100/104 (96%)	87 (87%)	13 (13%)	0	100	100
28	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
29	W	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
30	X	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
31	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
32	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
34	b	216/240 (90%)	188 (87%)	27 (12%)	1 (0%)	24	56
35	c	204/233 (88%)	188 (92%)	16 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	d	203/206 (98%)	170 (84%)	32 (16%)	1 (0%)	24	56
37	e	155/167 (93%)	141 (91%)	14 (9%)	0	100	100
38	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
39	g	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
40	h	127/130 (98%)	114 (90%)	13 (10%)	0	100	100
41	i	125/130 (96%)	105 (84%)	20 (16%)	0	100	100
42	j	96/103 (93%)	72 (75%)	22 (23%)	2 (2%)	5	31
43	k	114/129 (88%)	101 (89%)	13 (11%)	0	100	100
44	l	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
45	m	112/118 (95%)	94 (84%)	18 (16%)	0	100	100
46	n	99/102 (97%)	87 (88%)	12 (12%)	0	100	100
47	o	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
48	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
49	q	78/84 (93%)	60 (77%)	16 (20%)	2 (3%)	4	28
50	r	54/75 (72%)	48 (89%)	6 (11%)	0	100	100
51	s	80/92 (87%)	73 (91%)	7 (9%)	0	100	100
52	t	83/87 (95%)	79 (95%)	4 (5%)	0	100	100
53	u	63/71 (89%)	53 (84%)	10 (16%)	0	100	100
54	v	12/14 (86%)	8 (67%)	4 (33%)	0	100	100
57	y	137/140 (98%)	132 (96%)	5 (4%)	0	100	100
All	All	5926/6304 (94%)	5198 (88%)	717 (12%)	11 (0%)	44	72

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	3	31	ILE
49	q	67	SER
4	3	32	LEU
18	L	128	THR
49	q	69	THR

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	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	51 (100%)	0	100	100
5	4	34/34 (100%)	34 (100%)	0	100	100
9	C	216/218 (99%)	216 (100%)	0	100	100
10	D	164/164 (100%)	163 (99%)	1 (1%)	78	79
11	E	165/165 (100%)	164 (99%)	1 (1%)	78	79
12	F	148/150 (99%)	148 (100%)	0	100	100
13	G	137/138 (99%)	137 (100%)	0	100	100
14	H	114/114 (100%)	114 (100%)	0	100	100
16	J	116/116 (100%)	115 (99%)	1 (1%)	70	75
17	K	103/104 (99%)	103 (100%)	0	100	100
18	L	102/103 (99%)	102 (100%)	0	100	100
19	M	109/109 (100%)	109 (100%)	0	100	100
20	N	100/103 (97%)	100 (100%)	0	100	100
21	O	86/87 (99%)	85 (99%)	1 (1%)	63	72
22	P	99/100 (99%)	99 (100%)	0	100	100
23	Q	89/90 (99%)	89 (100%)	0	100	100
24	R	84/84 (100%)	84 (100%)	0	100	100
25	S	93/93 (100%)	93 (100%)	0	100	100
26	T	80/84 (95%)	80 (100%)	0	100	100
27	U	83/85 (98%)	83 (100%)	0	100	100
28	V	78/78 (100%)	78 (100%)	0	100	100
29	W	57/63 (90%)	57 (100%)	0	100	100
30	X	67/68 (98%)	67 (100%)	0	100	100
31	Y	55/55 (100%)	55 (100%)	0	100	100
32	Z	48/49 (98%)	48 (100%)	0	100	100
34	b	180/198 (91%)	180 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	c	170/190 (90%)	170 (100%)	0	100	100
36	d	172/173 (99%)	172 (100%)	0	100	100
37	e	114/126 (90%)	114 (100%)	0	100	100
38	f	87/116 (75%)	87 (100%)	0	100	100
39	g	124/147 (84%)	123 (99%)	1 (1%)	73	76
40	h	104/105 (99%)	103 (99%)	1 (1%)	68	74
41	i	105/107 (98%)	105 (100%)	0	100	100
42	j	86/90 (96%)	85 (99%)	1 (1%)	63	72
43	k	89/99 (90%)	89 (100%)	0	100	100
44	l	103/104 (99%)	103 (100%)	0	100	100
45	m	92/96 (96%)	92 (100%)	0	100	100
46	n	79/84 (94%)	79 (100%)	0	100	100
47	o	76/77 (99%)	76 (100%)	0	100	100
48	p	65/65 (100%)	65 (100%)	0	100	100
49	q	74/78 (95%)	74 (100%)	0	100	100
50	r	49/65 (75%)	49 (100%)	0	100	100
51	s	72/79 (91%)	72 (100%)	0	100	100
52	t	65/66 (98%)	65 (100%)	0	100	100
53	u	46/61 (75%)	45 (98%)	1 (2%)	45	63
54	v	14/14 (100%)	14 (100%)	0	100	100
57	y	112/115 (97%)	112 (100%)	0	100	100
All	All	4686/4896 (96%)	4678 (100%)	8 (0%)	85	86

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	u	43	GLU
42	j	32	THR
39	g	28	ILE
21	O	36	TYR
40	h	58	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
41	i	49	GLN
51	s	56	HIS
41	i	125	GLN
46	n	71	HIS
57	y	28	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
33	a	1539/1542 (99%)	398 (25%)	0
55	w	75/76 (98%)	38 (50%)	0
56	x	5/15 (33%)	1 (20%)	0
7	A	2902/2903 (99%)	712 (24%)	49 (1%)
8	B	119/120 (99%)	23 (19%)	1 (0%)
All	All	4640/4656 (99%)	1172 (25%)	50 (1%)

5 of 1172 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	2	G
7	A	10	A
7	A	14	A
7	A	15	G
7	A	23	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1877	A
7	A	2185	U
8	B	34	A
7	A	1941	C
7	A	2128	G

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

41 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	OMG	A	2251	55,58,7	23,26,27	2.39	9 (39%)	33,38,41	2.90	9 (27%)
7	6MZ	A	1618	7	22,25,26	2.34	6 (27%)	30,36,39	2.43	10 (33%)
7	1MG	A	745	7	22,26,27	2.61	7 (31%)	33,39,42	1.72	5 (15%)
7	PSU	A	2604	7	18,21,22	1.34	2 (11%)	22,30,33	1.94	4 (18%)
33	MA6	a	1518	33	23,26,27	1.57	2 (8%)	34,38,41	3.10	11 (32%)
7	3TD	A	1915	7	18,22,23	4.43	7 (38%)	22,32,35	1.74	4 (18%)
55	PSU	w	55	55	18,21,22	1.11	1 (5%)	22,30,33	1.82	5 (22%)
7	2MA	A	2503	58,7	22,25,26	3.73	8 (36%)	33,37,40	1.99	8 (24%)
33	UR3	a	1498	33	19,22,23	2.69	6 (31%)	26,32,35	1.59	4 (15%)
7	PSU	A	746	58,7	18,21,22	1.05	2 (11%)	22,30,33	1.70	3 (13%)
55	MIA	w	37	55	28,31,32	2.58	7 (25%)	40,44,47	3.00	17 (42%)
33	2MG	a	1516	33	23,26,27	2.76	9 (39%)	32,38,41	2.17	11 (34%)
7	PSU	A	955	7	18,21,22	1.07	3 (16%)	22,30,33	1.67	4 (18%)
55	4SU	w	8	55	18,21,22	3.70	8 (44%)	26,30,33	2.20	4 (15%)
7	6MZ	A	2030	7	22,25,26	2.38	8 (36%)	30,36,39	2.49	12 (40%)
55	PSU	w	39	55	18,21,22	1.03	1 (5%)	22,30,33	1.70	2 (9%)
7	PSU	A	1917	7	18,21,22	1.08	1 (5%)	22,30,33	1.90	4 (18%)
33	5MC	a	1407	33	18,22,23	3.54	7 (38%)	26,32,35	1.06	2 (7%)
7	5MU	A	1939	58,7	19,22,23	4.59	7 (36%)	28,32,35	3.81	10 (35%)
7	PSU	A	2605	7	18,21,22	1.05	2 (11%)	22,30,33	1.87	5 (22%)
7	PSU	A	2457	7	18,21,22	0.98	2 (11%)	22,30,33	1.75	4 (18%)
33	5MC	a	967	33	18,22,23	3.52	7 (38%)	26,32,35	1.03	1 (3%)
7	5MC	A	747	7	18,22,23	3.40	7 (38%)	26,32,35	1.17	3 (11%)
7	PSU	A	2504	7	18,21,22	1.09	2 (11%)	22,30,33	1.80	4 (18%)
33	4OC	a	1402	33	20,23,24	3.17	8 (40%)	26,32,35	0.89	1 (3%)
33	MA6	a	1519	33	23,26,27	1.59	2 (8%)	34,38,41	3.23	11 (32%)
7	OMU	A	2552	58,7	19,22,23	2.85	7 (36%)	26,31,34	1.83	4 (15%)
7	OMC	A	2498	58,7	19,22,23	2.78	7 (36%)	26,31,34	0.93	2 (7%)
55	5MU	w	54	55	19,22,23	4.84	7 (36%)	28,32,35	3.64	8 (28%)
55	G7M	w	46	55	23,26,27	2.24	7 (30%)	35,39,42	3.18	10 (28%)
33	PSU	a	516	33,58	18,21,22	1.03	2 (11%)	22,30,33	1.71	5 (22%)
7	G7M	A	2069	7	23,26,27	3.39	10 (43%)	35,39,42	1.68	7 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
33	2MG	a	1207	33	23,26,27	2.83	9 (39%)	32,38,41	2.25	11 (34%)
7	2MG	A	1835	7	23,26,27	2.74	7 (30%)	32,38,41	2.23	9 (28%)
7	PSU	A	2580	7	18,21,22	1.11	3 (16%)	22,30,33	1.93	6 (27%)
7	PSU	A	1911	7	18,21,22	1.05	1 (5%)	22,30,33	1.84	5 (22%)
55	PSU	w	32	55	18,21,22	1.47	3 (16%)	22,30,33	1.94	4 (18%)
7	5MC	A	1962	7	18,22,23	3.46	7 (38%)	26,32,35	1.12	1 (3%)
7	2MG	A	2445	7	23,26,27	2.73	9 (39%)	32,38,41	2.12	11 (34%)
33	2MG	a	966	33	23,26,27	2.76	9 (39%)	32,38,41	2.13	9 (28%)
33	G7M	a	527	33	23,26,27	3.52	11 (47%)	35,39,42	1.65	7 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	OMG	A	2251	55,58,7	-	0/9/27/28	0/3/3/3
7	6MZ	A	1618	7	-	3/9/27/28	0/3/3/3
7	1MG	A	745	7	-	0/7/25/26	0/3/3/3
7	PSU	A	2604	7	-	2/7/25/26	0/2/2/2
33	MA6	a	1518	33	-	2/11/29/30	0/3/3/3
7	3TD	A	1915	7	-	2/7/25/26	0/2/2/2
55	PSU	w	55	55	-	5/7/25/26	0/2/2/2
7	2MA	A	2503	58,7	-	2/7/25/26	0/3/3/3
33	UR3	a	1498	33	-	4/7/25/26	0/2/2/2
7	PSU	A	746	58,7	-	3/7/25/26	0/2/2/2
55	MIA	w	37	55	-	4/15/33/34	0/3/3/3
33	2MG	a	1516	33	-	0/9/27/28	0/3/3/3
7	PSU	A	955	7	-	0/7/25/26	0/2/2/2
55	4SU	w	8	55	-	2/7/25/26	0/2/2/2
7	6MZ	A	2030	7	-	5/9/27/28	0/3/3/3
55	PSU	w	39	55	-	3/7/25/26	0/2/2/2
7	PSU	A	1917	7	-	0/7/25/26	0/2/2/2
33	5MC	a	1407	33	-	0/7/25/26	0/2/2/2
7	5MU	A	1939	58,7	-	2/7/25/26	0/2/2/2
7	PSU	A	2605	7	-	0/7/25/26	0/2/2/2
7	PSU	A	2457	7	-	0/7/25/26	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	5MC	a	967	33	-	2/7/25/26	0/2/2/2
7	5MC	A	747	7	-	3/7/25/26	0/2/2/2
7	PSU	A	2504	7	-	2/7/25/26	0/2/2/2
33	4OC	a	1402	33	-	1/9/29/30	0/2/2/2
33	MA6	a	1519	33	-	2/11/29/30	0/3/3/3
7	OMU	A	2552	58,7	-	5/9/27/28	0/2/2/2
7	OMC	A	2498	58,7	-	4/9/27/28	0/2/2/2
55	5MU	w	54	55	-	3/7/25/26	0/2/2/2
55	G7M	w	46	55	-	3/7/25/26	0/3/3/3
33	PSU	a	516	33,58	-	0/7/25/26	0/2/2/2
7	G7M	A	2069	7	-	1/7/25/26	0/3/3/3
33	2MG	a	1207	33	-	0/9/27/28	0/3/3/3
7	2MG	A	1835	7	-	2/9/27/28	0/3/3/3
7	PSU	A	2580	7	-	0/7/25/26	0/2/2/2
7	PSU	A	1911	7	-	0/7/25/26	0/2/2/2
55	PSU	w	32	55	-	2/7/25/26	0/2/2/2
7	5MC	A	1962	7	-	4/7/25/26	0/2/2/2
7	2MG	A	2445	7	-	2/9/27/28	0/3/3/3
33	2MG	a	966	33	-	0/9/27/28	0/3/3/3
33	G7M	a	527	33	-	3/7/25/26	0/3/3/3

The worst 5 of 230 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1915	3TD	C6-C5	14.14	1.51	1.35
7	A	2503	2MA	C4-N3	11.31	1.48	1.34
55	w	54	5MU	C2-N1	11.21	1.56	1.38
55	w	54	5MU	C6-N1	10.36	1.55	1.38
55	w	54	5MU	C4-C5	10.11	1.61	1.44

The worst 5 of 257 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1519	MA6	N1-C6-N6	-12.62	103.29	117.08
7	A	1939	5MU	C5-C4-N3	12.43	125.92	115.31
55	w	54	5MU	C5-C4-N3	12.17	125.70	115.31
33	a	1518	MA6	N1-C6-N6	-12.06	103.89	117.08
7	A	1939	5MU	C5-C6-N1	-11.04	111.99	123.34

There are no chirality outliers.

5 of 78 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	746	PSU	C2'-C1'-C5-C6
7	A	747	5MC	C3'-C4'-C5'-O5'
7	A	1618	6MZ	N1-C6-N6-C9
7	A	1915	3TD	O4'-C1'-C5-C4
7	A	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

21 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	2251	OMG	1	0
7	A	745	1MG	1	0
7	A	2604	PSU	1	0
33	a	1518	MA6	4	0
7	A	1915	3TD	5	0
55	w	55	PSU	1	0
7	A	2503	2MA	2	0
7	A	746	PSU	1	0
55	w	37	MIA	1	0
7	A	955	PSU	1	0
55	w	8	4SU	2	0
7	A	2030	6MZ	2	0
33	a	1407	5MC	1	0
7	A	2457	PSU	3	0
7	A	2504	PSU	1	0
33	a	1402	4OC	2	0
7	A	2552	OMU	2	0
7	A	2498	OMC	1	0
33	a	516	PSU	1	0
7	A	2580	PSU	1	0
7	A	2445	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 358 ligands modelled in this entry, 358 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.

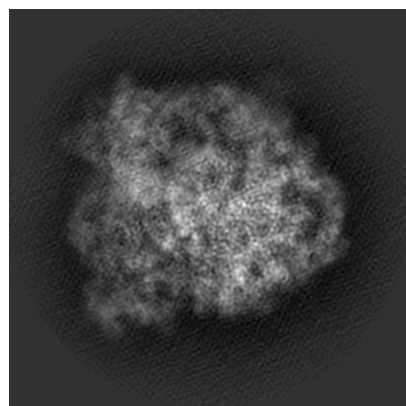
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10908. These allow visual inspection of the internal detail of the map and identification of artifacts.

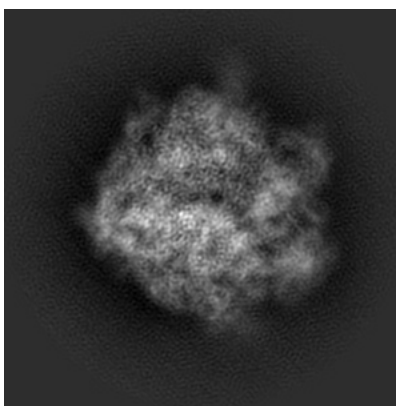
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

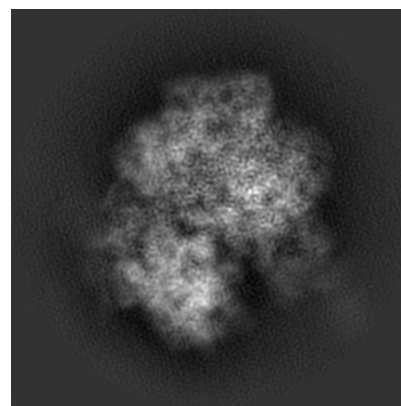
6.1.1 Primary map



X

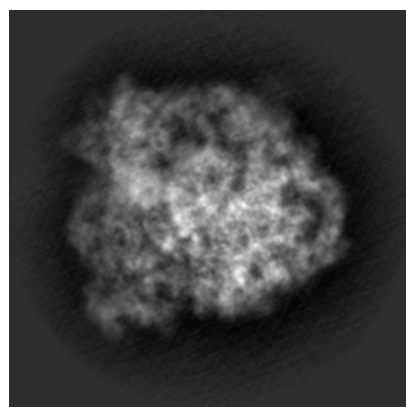


Y

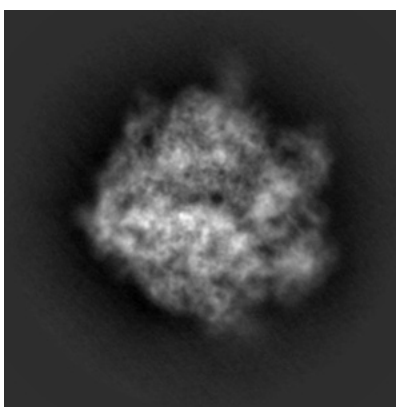


Z

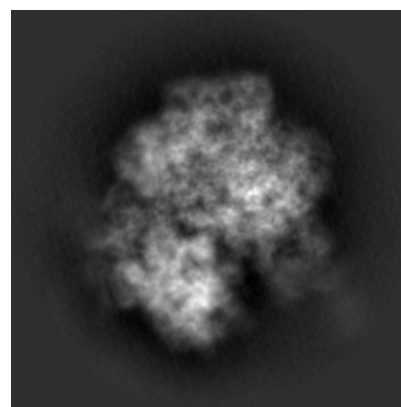
6.1.2 Raw map



X



Y

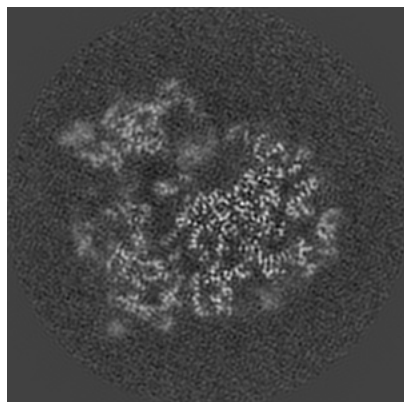


Z

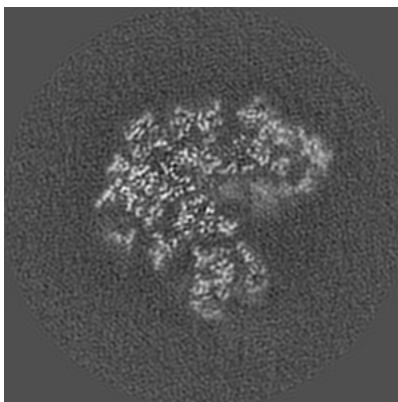
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

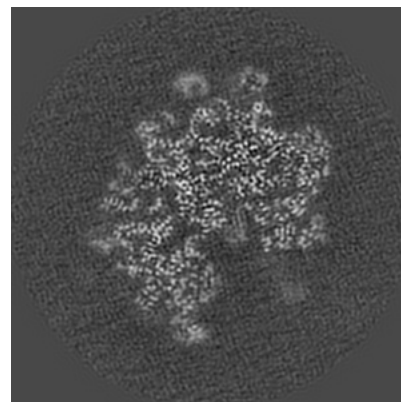
6.2.1 Primary map



X Index: 162

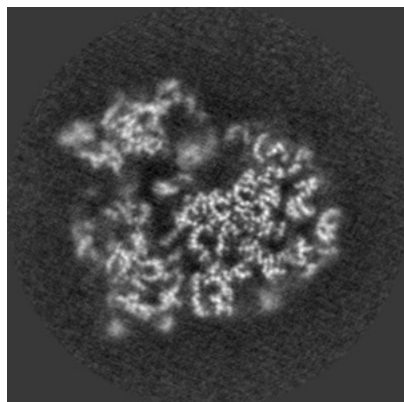


Y Index: 162

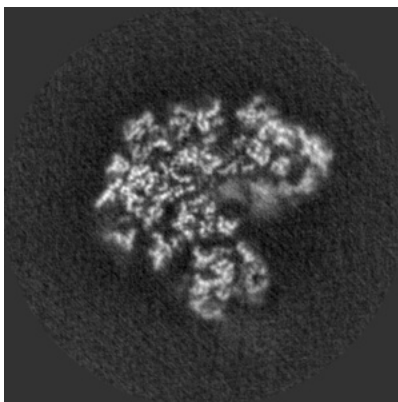


Z Index: 162

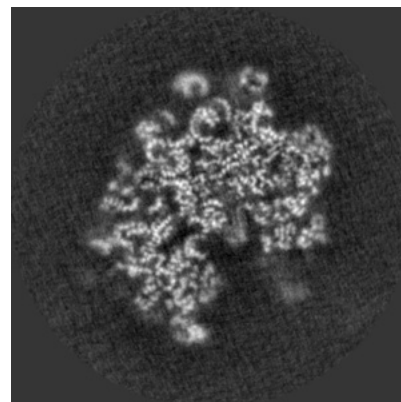
6.2.2 Raw map



X Index: 162



Y Index: 162

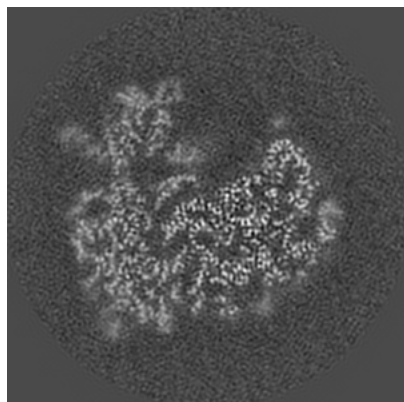


Z Index: 162

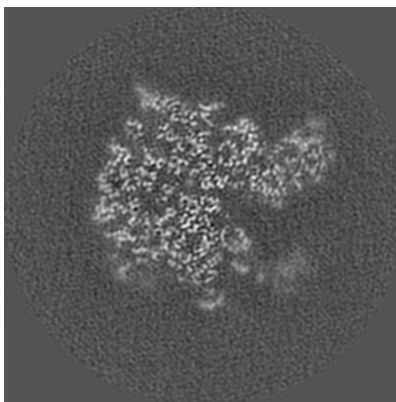
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

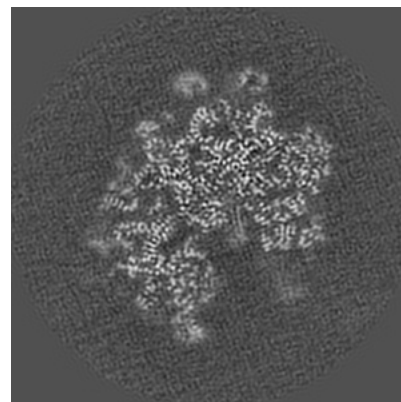
6.3.1 Primary map



X Index: 156

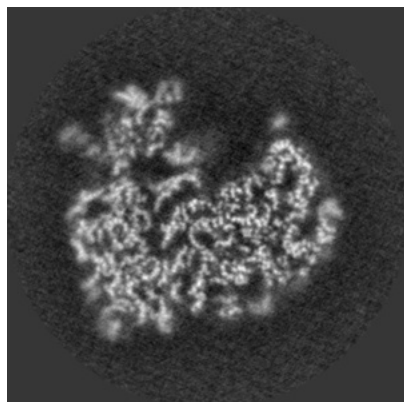


Y Index: 180

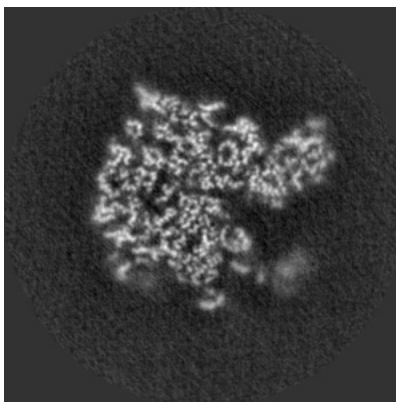


Z Index: 163

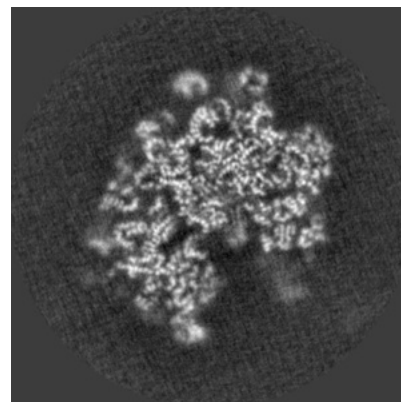
6.3.2 Raw map



X Index: 155



Y Index: 180

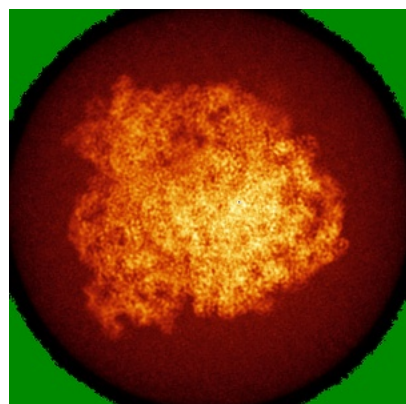


Z Index: 163

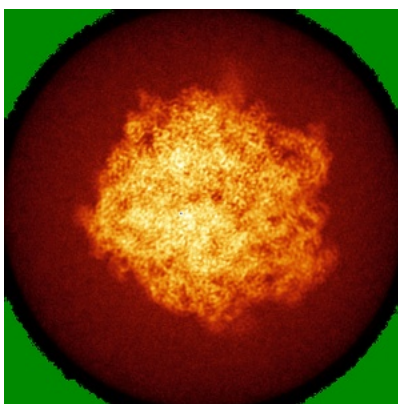
The images above show the largest variance slices of the map in three orthogonal directions.

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

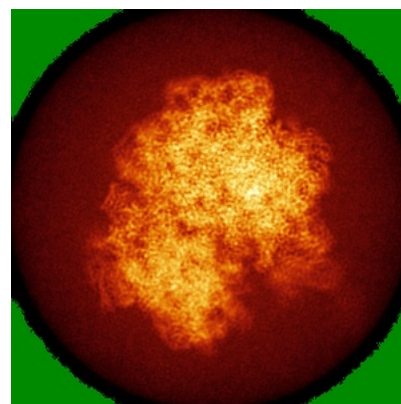
6.4.1 Primary map



X

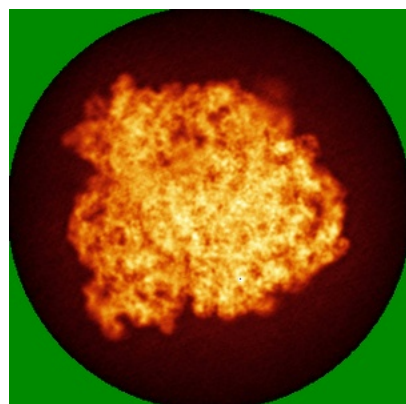


Y

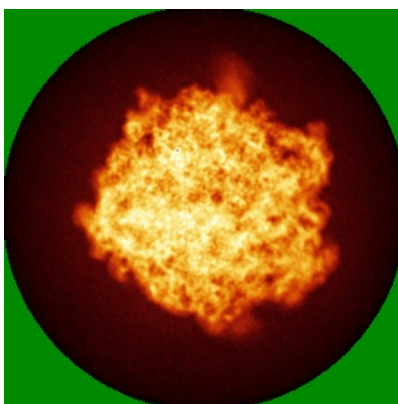


Z

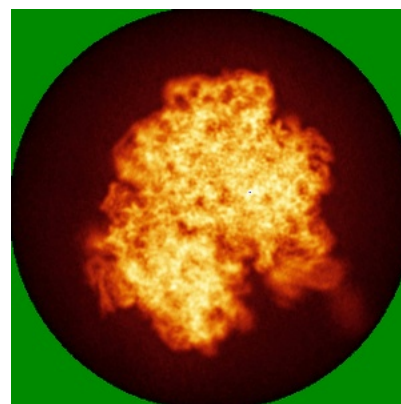
6.4.2 Raw map



X



Y

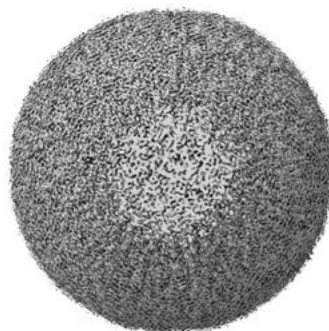


Z

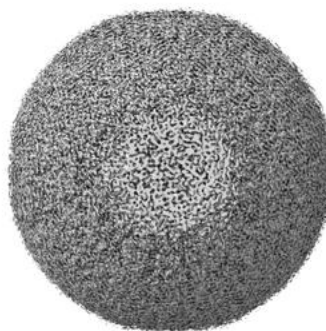
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

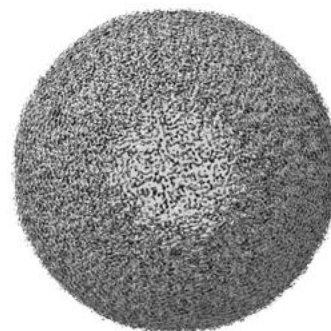
6.5.1 Primary map



X



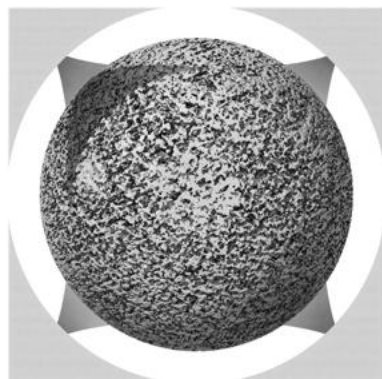
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

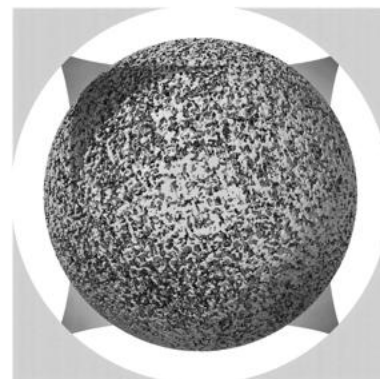
6.5.2 Raw map



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.

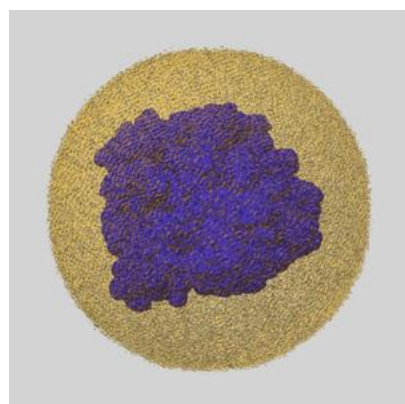
6.6 Mask visualisation [i](#)

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

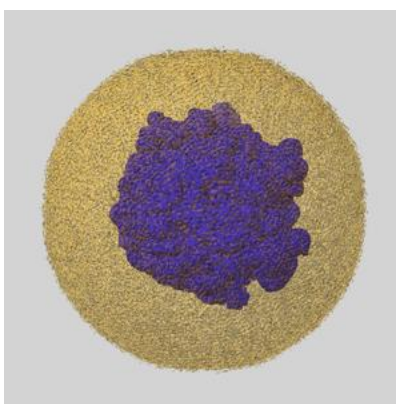
A mask typically either:

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

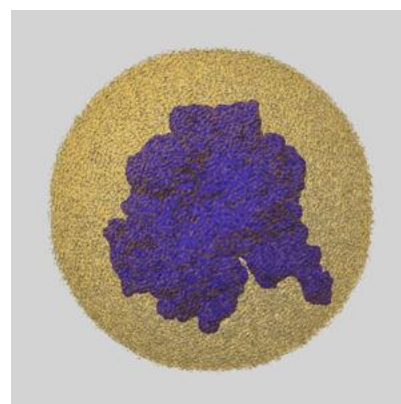
6.6.1 emd_10908_msk_1.map [i](#)



X



Y

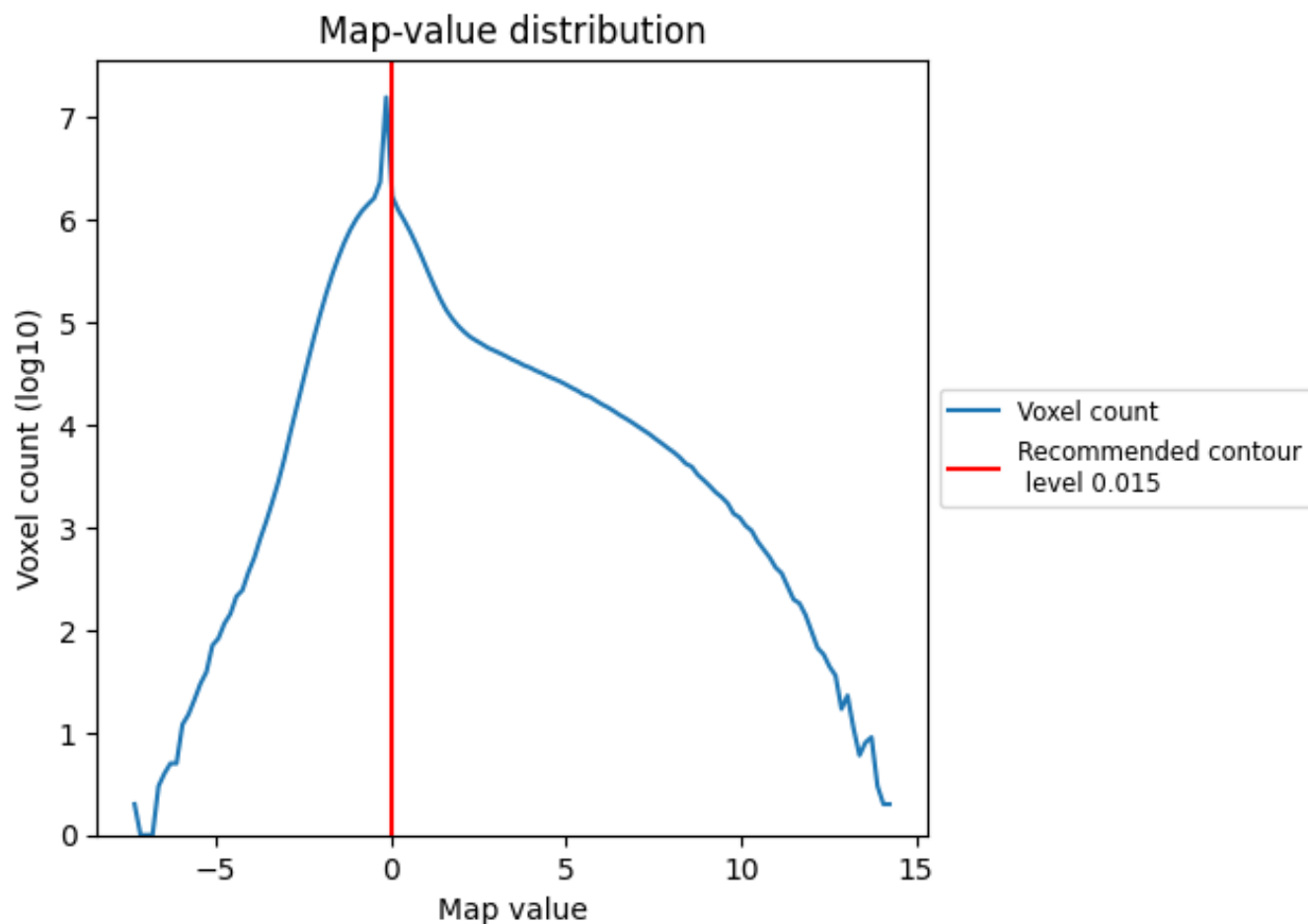


Z

7 Map analysis [i](#)

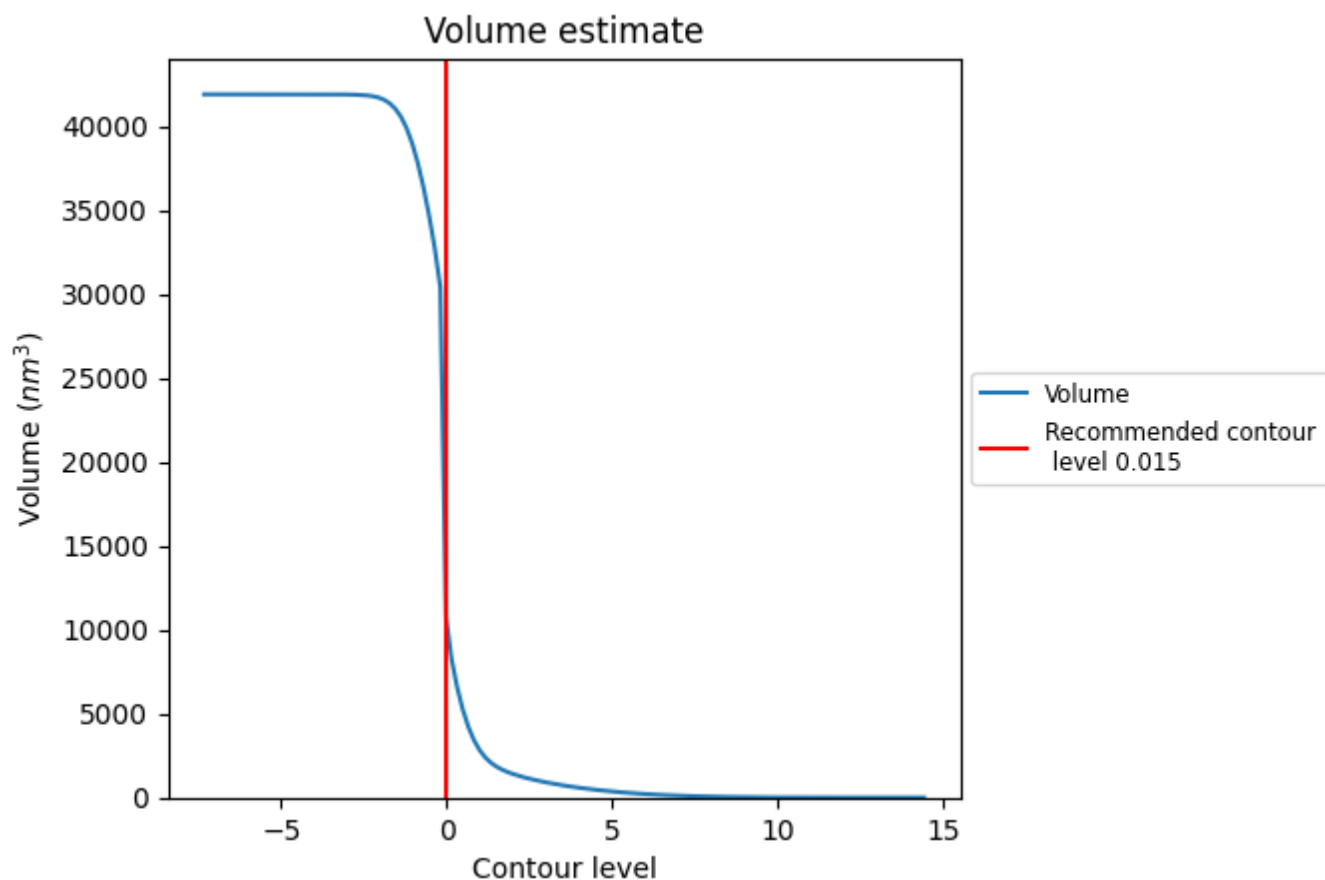
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

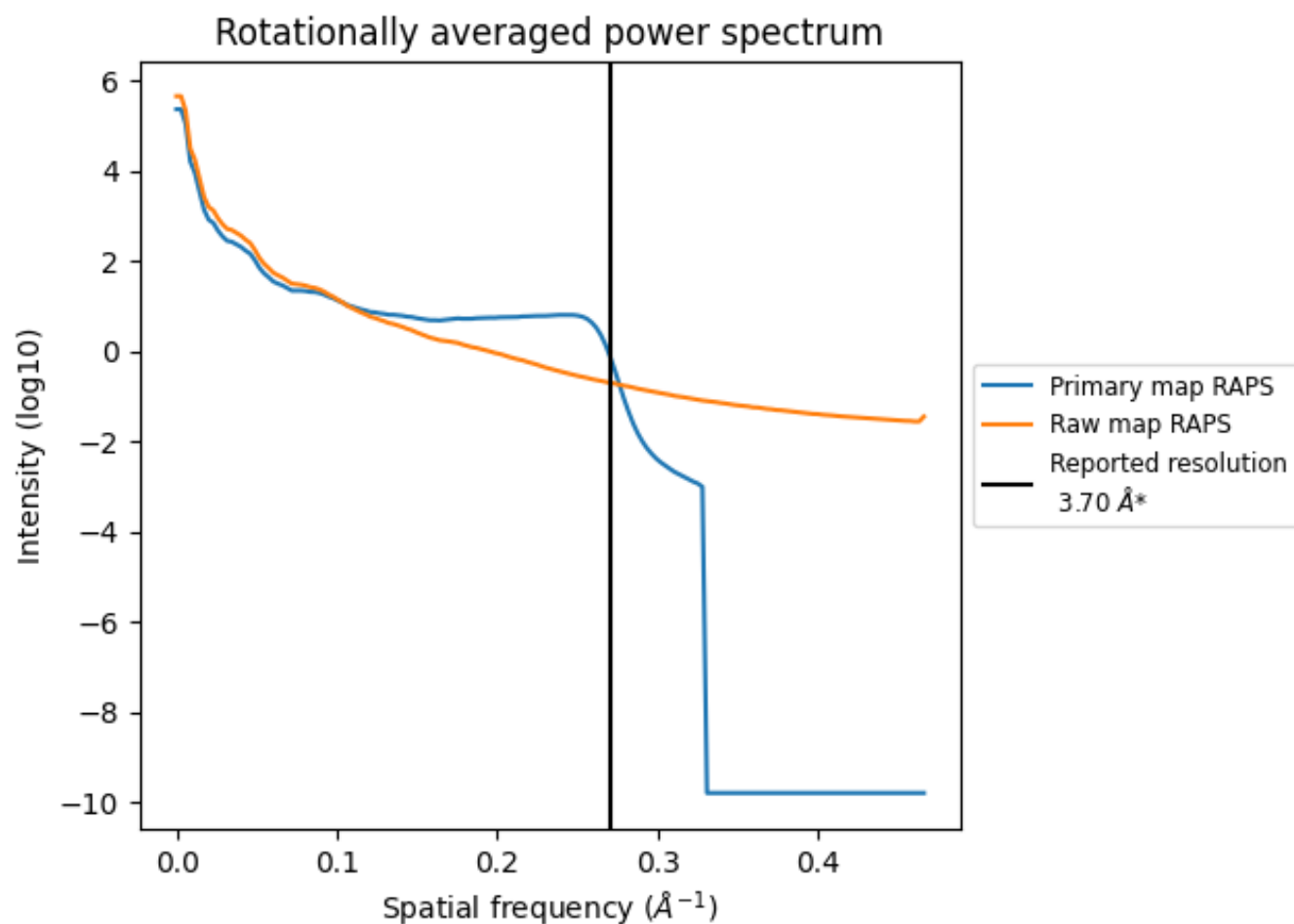
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 10367 nm³; this corresponds to an approximate mass of 9365 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 ⓘ

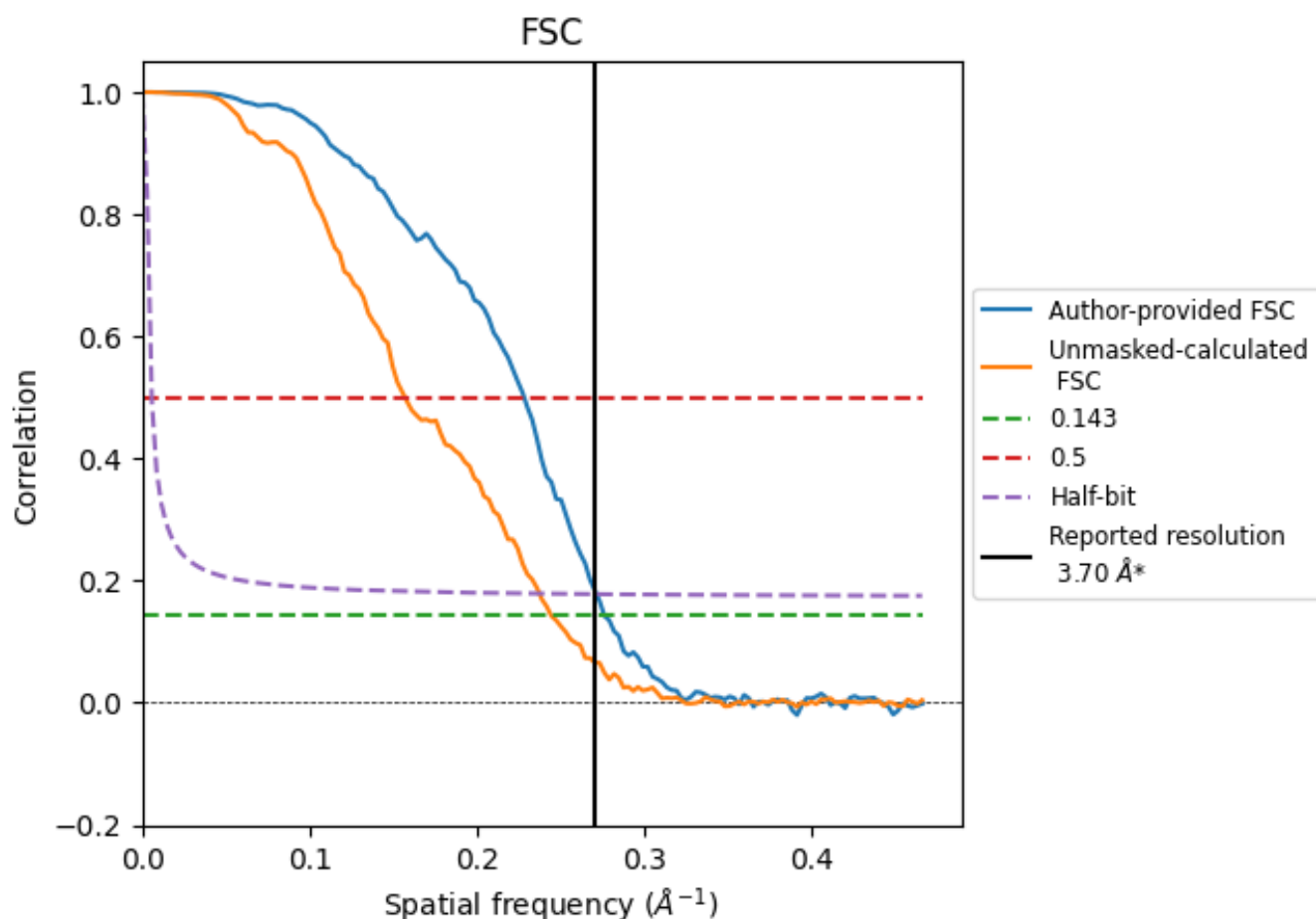


*Reported resolution corresponds to spatial frequency of $0.270 \text{ \AA}^{-1}$

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 0.270 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

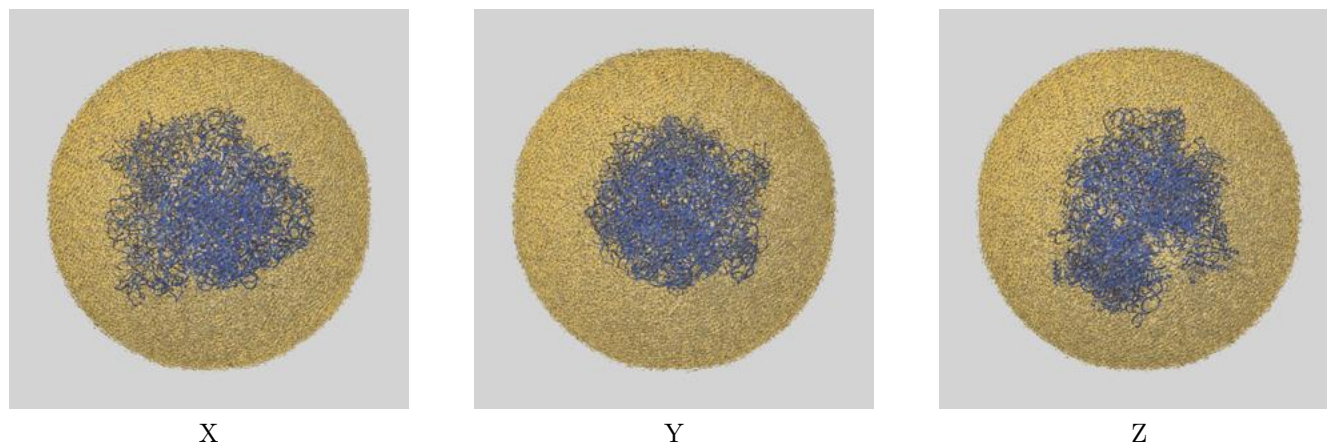
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.62	4.38	3.68
Unmasked-calculated*	4.09	6.37	4.21

*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 4.09 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

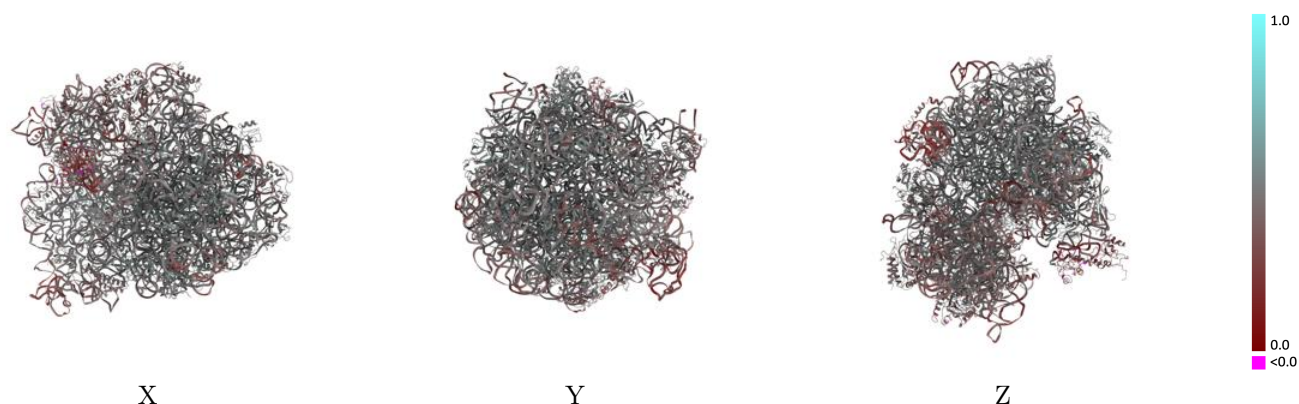
This section contains information regarding the fit between EMDB map EMD-10908 and PDB model 6YSU. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



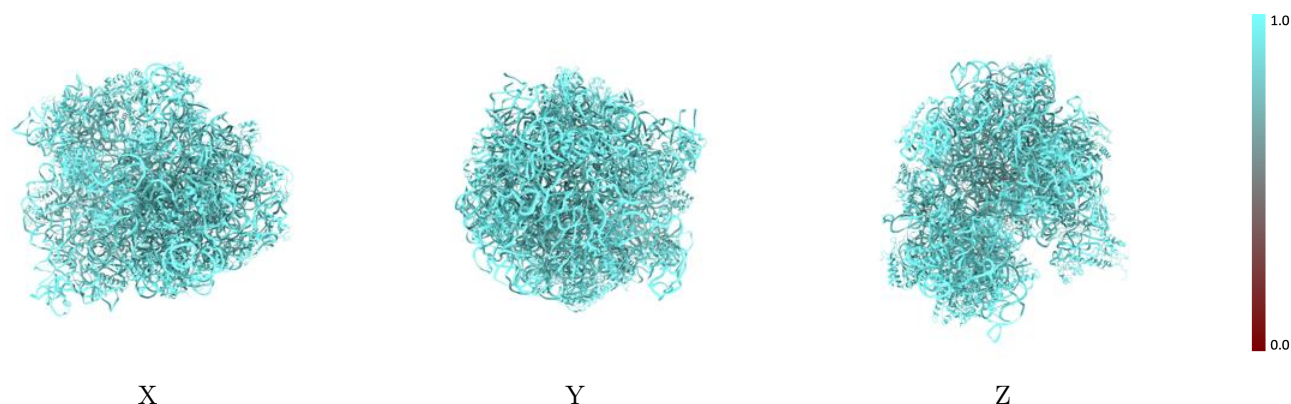
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



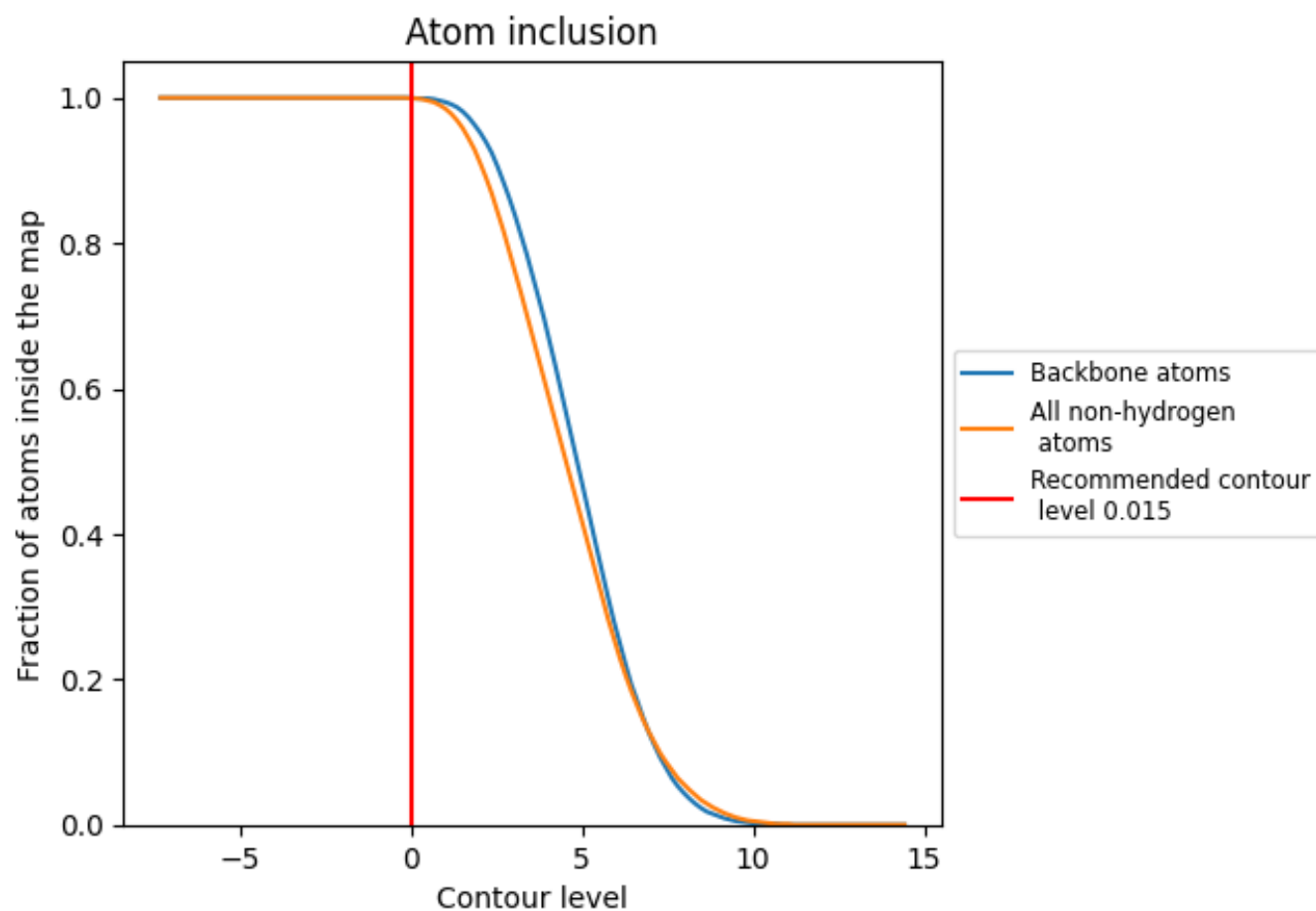
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9990	 0.4460
0	 1.0000	 0.5050
1	 0.9950	 0.4970
2	 0.9970	 0.5250
3	 0.9980	 0.5170
4	 1.0000	 0.5120
5	 1.0000	 0.2850
A	 1.0000	 0.4500
B	 1.0000	 0.4160
C	 0.9980	 0.5170
D	 0.9990	 0.5070
E	 1.0000	 0.4880
F	 1.0000	 0.3980
G	 1.0000	 0.4570
H	 0.9980	 0.3960
I	 0.9970	 0.2800
J	 0.9980	 0.5100
K	 0.9990	 0.5110
L	 0.9970	 0.4980
M	 0.9970	 0.5030
N	 0.9990	 0.5050
O	 1.0000	 0.4360
P	 1.0000	 0.5050
Q	 1.0000	 0.5010
R	 1.0000	 0.5000
S	 0.9980	 0.5050
T	 1.0000	 0.4930
U	 0.9990	 0.4640
V	 0.9990	 0.4740
W	 1.0000	 0.5200
X	 0.9950	 0.4990
Y	 1.0000	 0.4320
Z	 1.0000	 0.4980
a	 1.0000	 0.4270
b	 0.9960	 0.4300



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	 0.9980	 0.4500
d	 0.9990	 0.4480
e	 0.9980	 0.4820
f	 0.9990	 0.4410
g	 0.9990	 0.3910
h	 0.9990	 0.4810
i	 0.9980	 0.4130
j	 0.9960	 0.4000
k	 0.9980	 0.4630
l	 0.9980	 0.4920
m	 1.0000	 0.4030
n	 1.0000	 0.4340
o	 1.0000	 0.4570
p	 1.0000	 0.4610
q	 0.9980	 0.4560
r	 1.0000	 0.4780
s	 1.0000	 0.4230
t	 0.9990	 0.4400
u	 1.0000	 0.4180
v	 1.0000	 0.4260
w	 0.9950	 0.3300
x	 1.0000	 0.4530
y	 0.9880	 0.4320