



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:47 AM UTC

PDB ID : 7P6Z / pdb_00007p6z
EMDB ID : EMD-13234
Title : Mycoplasma pneumoniae 70S ribosome in untreated cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-18
Resolution : 3.50 Å (reported)
Based on initial models : 3J9W, 7OOD, 7OOC, 4V7C

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
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

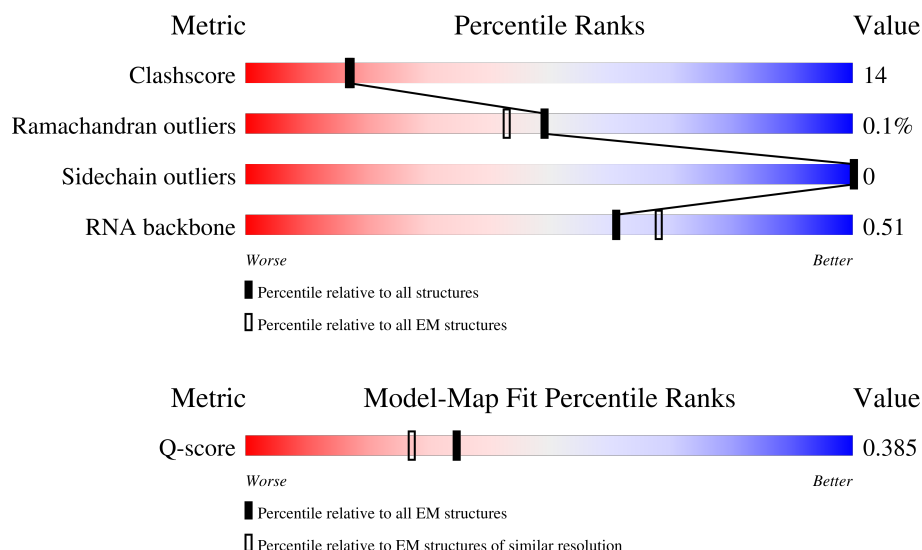
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	3	2907	
2	4	108	
3	w	111	

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Mol	Chain	Length	Quality of chain
4	a	287	
5	c	212	
6	e	184	
7	k	151	
8	i	146	
9	m	124	
10	q	100	
11	u	104	
12	y	57	
13	0	48	
14	2	37	
15	1	59	
16	o	119	
17	s	237	
18	v	65	
19	x	97	
20	z	53	
21	d	180	
22	b	287	
23	l	139	
24	p	127	
25	j	122	
26	n	116	
27	t	111	
28	r	159	

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Mol	Chain	Length	Quality of chain
29	B	273	
30	D	219	
31	F	155	
32	A	294	
33	H	132	
34	J	121	
35	C	205	
36	S	87	
37	O	94	
38	K	139	
39	M	61	
40	I	108	
41	L	124	
42	N	86	
43	R	87	
44	T	60	
45	G	142	
46	Q	104	
47	E	215	
48	P	85	
49	5	1520	
50	Z	5	
51	7	76	
52	Y	9	
53	f	149	

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Mol	Chain	Length	Quality of chain
54	h	137	93% 88% 5% • 7%
55	g	161	77% 71% 5% • 22%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 142534 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	2879	Total	C	N	O	P	0	0
			61690	27566	11236	20009	2879		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	4	105	Total	C	N	O	P	0	0
			2245	1003	409	728	105		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	w	99	Total	C	N	O	0	0
			798	505	149	144		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	a	285	Total	C	N	O	S	0	0
			2199	1370	433	390	6		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	210	Total	C	N	O	S	0	0
			1613	1026	294	290	3		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	e	176	Total	C	N	O	0	0
			1349	867	240	242		

- Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	148	Total	C	N	O	0	0
			1138	722	223	193		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	144	Total	C	N	O	S	0	0
			1158	733	212	208	5		

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	m	119	Total	C	N	O	S	0	0
			957	609	175	170	3		

- Molecule 10 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	q	99	Total	C	N	O	S	0	0
			809	525	148	133	3		

- Molecule 11 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	u	86	Total	C	N	O	S	0	0
			641	397	127	116	1		

- Molecule 12 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	y	56	Total	C	N	O	S	0	0
			436	262	96	73	5		

- Molecule 13 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	0	47	Total	C	N	O	S	0	0
			377	234	81	61	1		

- Molecule 14 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	2	37	Total	C	N	O	S	0	0
			303	189	65	45	4		

- Molecule 15 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	o	115	Total	C	N	O	S	0	0
			895	568	169	157	1		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	92	Total	C	N	O	S	0	0
			714	470	121	122	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	v	63	Total	C	N	O	S	0	0
			504	312	107	84	1		

- Molecule 19 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	x	44	Total	C	N	O	0	0
			218	130	44	44		

- Molecule 20 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 21 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	d	175	Total	C	N	O	S	0	0
			1244	797	214	229	4		

- Molecule 22 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	229	Total	C	N	O	S	0	0
			1758	1116	317	318	7		

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	l	136	Total	C	N	O	S	0	0
			1057	680	193	177	7		

- Molecule 24 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	p	114	Total	C	N	O	S	0	0
			941	600	185	154	2		

- Molecule 25 is a protein called 50S ribosomal protein L14.

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

- Molecule 26 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	n	112	Total	C	N	O	S	0	0
			853	534	169	149	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	t	96	Total	C	N	O	S	0	0
			706	449	132	122	3		

- Molecule 28 is a protein called 50S ribosomal protein L22.

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

- Molecule 29 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B	215	Total	C	N	O	S	0	0
			1682	1063	308	306	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	D	153	Total	C	N	O	S	0	0
			1153	731	222	197	3		

- Molecule 31 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	F	154	Total	C	N	O	S	0	0
			1231	777	234	215	5		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A	249	Total	C	N	O	S	0	0
			1917	1224	331	355	7		

- Molecule 33 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	H	128	Total	C	N	O	S	0	0
			993	634	184	174	1		

- Molecule 34 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	J	114	Total	C	N	O	S	0	0
			828	514	153	155	6		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	C	203	Total	C	N	O	S	0	0
			1605	1015	306	280	4		

- Molecule 36 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 37 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	87	Total	C	N	O	S	0	0
			690	445	128	115	2		

- Molecule 38 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	K	136	Total	C	N	O	S	0	0
			1055	667	209	177	2		

- Molecule 39 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	M	60	Total	C	N	O	S	0	0
			473	302	96	71	4		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	I	101	Total	C	N	O	S	0	0
			803	518	141	143	1		

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	L	118	Total	C	N	O		0	0
			922	576	186	160			

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	N	83	Total	C	N	O	0	0
			673	428	125	120		

- Molecule 43 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	R	84	Total	C	N	O	S	0	0
			654	419	119	114	2		

- Molecule 44 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	T	53	Total	C	N	O	S	0	0
			439	275	93	70	1		

- Molecule 45 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	G	141	Total	C	N	O	S	0	0
			1103	720	192	189	2		

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 47 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	E	167	Total	C	N	O	S	0	0
			1211	762	219	229	1		

- Molecule 48 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	P	83	Total	C	N	O	0	0
			675	425	135	115		

- Molecule 49 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5	1493	Total	C	N	O	P	0	0
			31952	14279	5792	10388	1493		

- Molecule 50 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	Z	5	Total	C	N	O	0	0
			26	15	5	6		

- Molecule 51 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

- Molecule 52 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Y	9	Total	C	N	O	P	0	0
			177	81	18	70	8		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	f	144	Total	C	N	O	0	0
			713	425	144	144		

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	h	128	Total	C	N	O	0	0
			630	374	128	128		

- Molecule 55 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	g	125	Total	C	N	O	0	0
			617	367	125	125		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	3	24	Total 24	Mg 24	0
56	y	1	Total 1	Mg 1	0

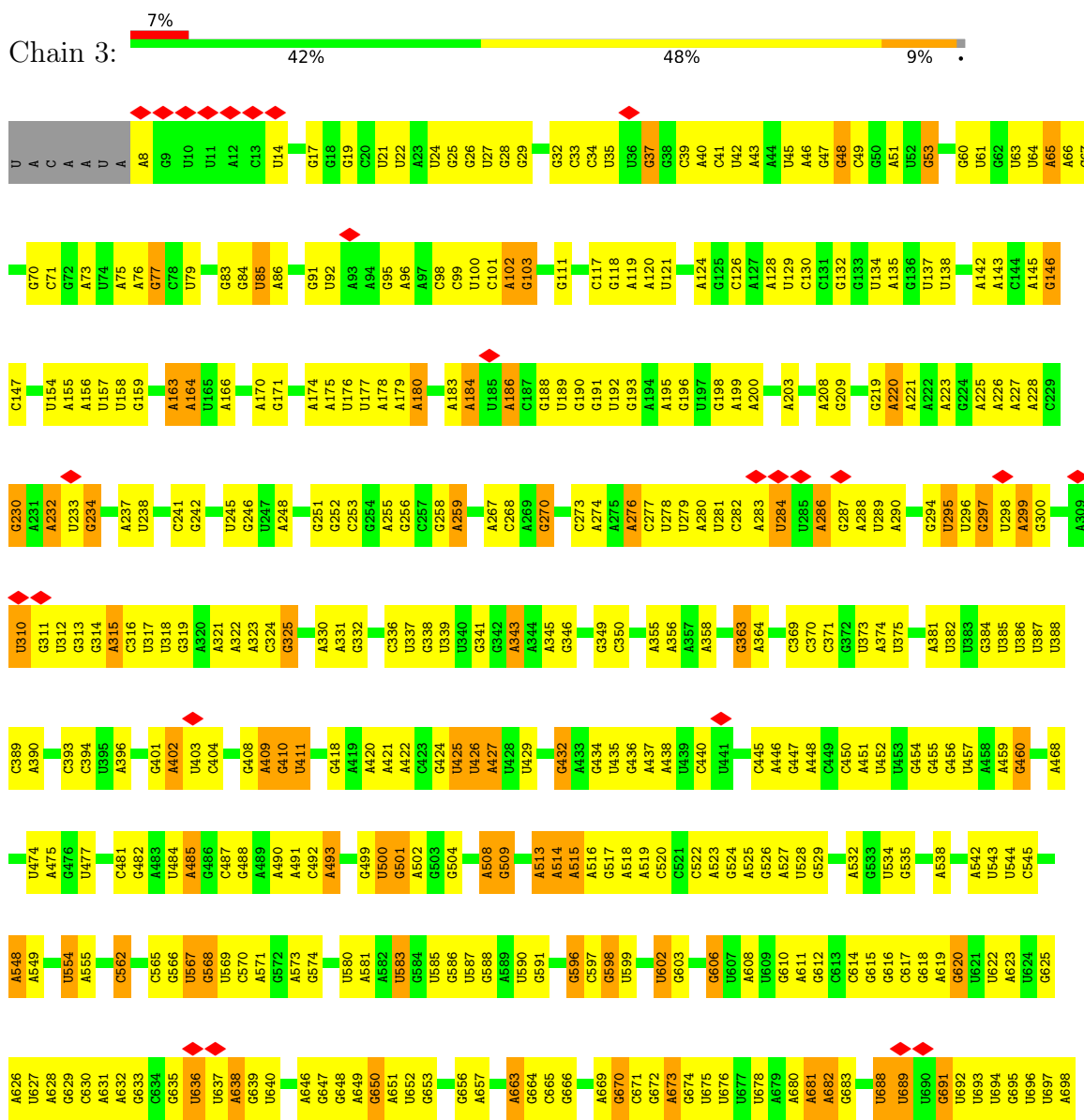
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	y	1	Total 1	Zn 1	0
57	2	1	Total 1	Zn 1	0
57	z	1	Total 1	Zn 1	0
57	M	1	Total 1	Zn 1	0
57	Q	1	Total 1	Zn 1	0

3 Residue-property plots

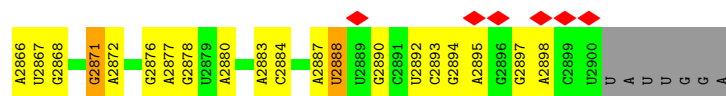
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 23S ribosomal RNA

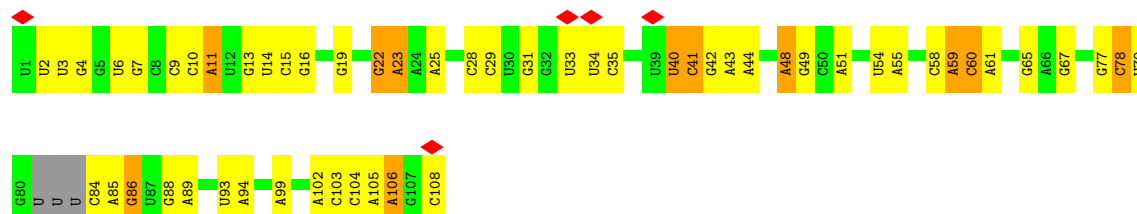


A1680	G1681	A1682	A1688	U1691	A1692	A1693	A1694	A1695	A1696	A1697	G1700	G1701	U1706	U1707	G1708	U1709	A1710	A1711	A1712	A1716	C1717	G1720	G1721	U1722	U1727	A1734	G1741	G1742	U1743	U1744	U1748	A1749	A1750	A1751	U1754	A1755	A1756	G1761	U1764	G1765	A1766	A1767	G1768	A1769	A1770	C1771													
G1602	A1603	A1604	A1605	A1606	U1612	A1613	G1614	A1615	A1616	A1617	A1618	A1619	A1620	C1621	A1622	U1623	A1624	G1625	A1626	A1627	G1628	A1629	G1633	A1634	G1635	U1636	A1637	A1638	G1639	G1640	A1641	U1642	A1643	A1644	A1645	A1646	A1647	A1648	A1649	A1650	C1651	A1652	C1653	G1662	G1663	U1668	A1669	C1670	A1671	C1672	G1676	A1677	A1678	A1679	A1700	A1701			
U1533	A1534	A1535	U1536	A1537	U1538	U1539	U1540	A1541	A1545	U1546	G1547	U1548	U1549	C1552	G1553	A1554	U1555	A1556	G1557	A1558	A1559	U	G	A	G	U	U	A	U	C	A	A1570	G1571	U1572	A1573	A1577	U1578	G1579	U1580	U1581	G1582	U1583	A1584	U1585	U1586	U1587	A1588	A1589	C1595	U1596	U1597	U1598	C1599	A1600	A1601				
A1462	G1463	A1464	U1465	A1466	U1467	U1468	C1469	A1470	A1471	C1472	C1473	C1474	C1475	C1476	A1477	U1480	A1481	U1482	G1483	A1484	A1485	U1486	U1487	U1488	A1493	A1497	U1498	A1499	A1500	U1501	A1502	A1503	G1504	G1507	G1508	U1509	A1510	A1511	A1512	A1513	U1514	A1515	G1516	G1517	C1518	A1519	A1520	A1521	U1522	C1523	U1529	G1530	C1531	A1532					
U1391	G1392	A1393	U1394	U1395	U1400	A1401	G1402	A1406	U1407	A1412	A1413	C1414	A1415	U1416	A1417	U1418	U1419	A1420	A1421	A1422	A1423	A1424	A1425	C1426	A1427	U1428	G1429	U1430	A1431	U1432	A1433	A1434	A1435	C1436	A1437	U1438	U1439	U1440	A1441	A1442	A1443	A1444	U1445	A1446	A1447	U1448	G1449	U1450	A1451	U1452	A1455	A1456	A1457	A1458	A1459	A1460	A1461		
G1306	G1307	A1308	A1309	U1310	A1314	A1315	U1316	A1323	A1324	A1325	A1326	G1327	A1328	U1329	U1330	G1331	A1332	C1333	A1334	A1335	A1336	G1337	U1341	C1342	A1343	U1344	G1345	A1346	A1347	A1348	A1349	A1350	G1353	U1354	C1355	U1356	A1357	C1358	A1364	G1367	U1368	U1369	U1380	A1381	A1382	G1383	U1384	U1385	G1388	G1389	C1390								
U1232	A1233	U1234	U1235	U1236	U1237	A1238	U1239	G1242	U1245	A1246	C1247	A1248	A1249	A1250	G1251	G1255	U1261	A1262	A1263	U1264	A1265	A1266	A1267	U1268	A1269	C1270	C1275	A1276	A1277	A1281	A1282	A1283	U1284	U1285	A1286	A1287	C1288	A1289	A1292	U1293	A1294	A1295	A1296	U1297	A1298	U1299	A1300	A1301	C1302	U1303	A1304	G1305							
U1153	U1154	G1155	U1156	A1161	A1164	U1165	G1166	A1168	A1169	C1170	G1171	G1174	C1175	U1176	A1177	A1178	A1186	C1187	G1188	G1189	U1192	U1193	C1194	G1195	U1197	U1200	A1201	A1202	G1203	A1204	U1205	A1206	U1207	A1208	U1209	A1210	U1211	C1212	U1213	U1214	G1217	A1218	U1219	A1220	G1221	G1224	C1227	U1228	U1229	U1230	G1231								
U1093	G1094	U1095	U1096	G1097	G1098	C1099	U1100	U1101	A1102	G1103	A1104	A1105	G1106	C1107	A1108	G1109	C1110	C1111	A1112	U1113	C1114	G1115	U1116	U1117	U1118	U1119	A1120	A1121	G1122	A1123	U1124	U1125	G1126	A1127	G1128	U1129	A1130	A1131	C1132	A1133	G1134	U1135	U1136	C1137	A1138	C1139	U1140	G1141	U1142	U1143	C1144	G1145	A1146	G1147	U1148	U1149	U1150	U1151	U1152
A1008	A1009	G1010	A1016	A1019	G1020	A1026	U1027	A1028	A1029	A1032	A1036	A1037	G1038	G1039	C1043	A1048	U1049	U1054	A1055	A1056	G1057	U1058	A1061	A1062	A1063	A1064	U1068	G1069	U1070	G1071	A1072	A1073	A1074	G1075	U1076	G1077	C1078	U1079	U1094	A1080	A1081	A1082	A1083	C1084	A1085	A1086	C1087	A1088	A1092										
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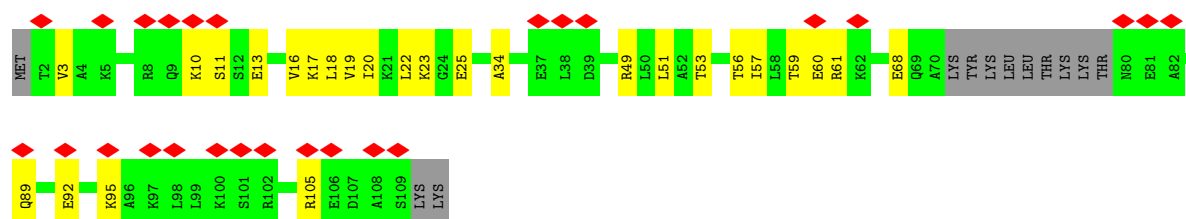
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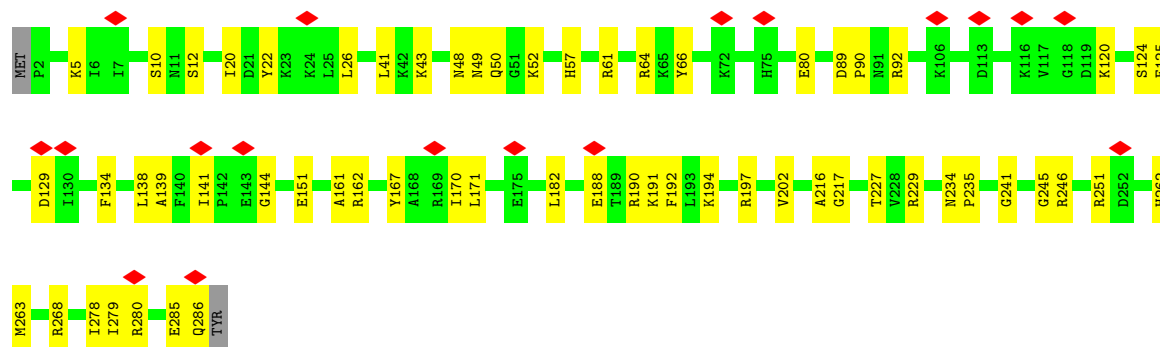
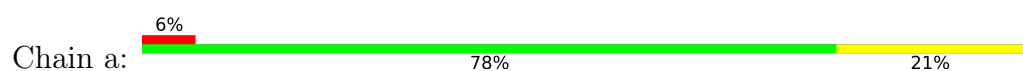
• Molecule 2: 5S ribosomal RNA



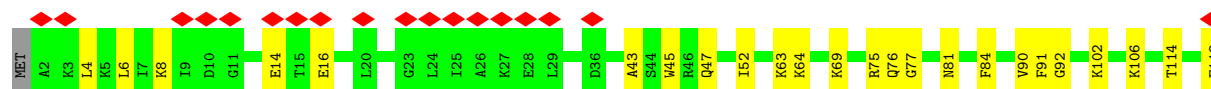
• Molecule 3: 50S ribosomal protein L29

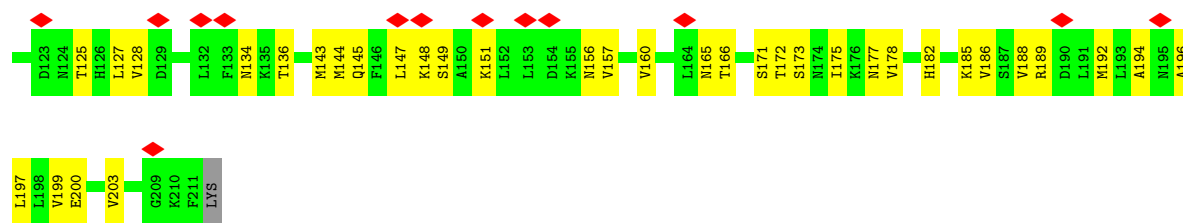


• Molecule 4: 50S ribosomal protein L2

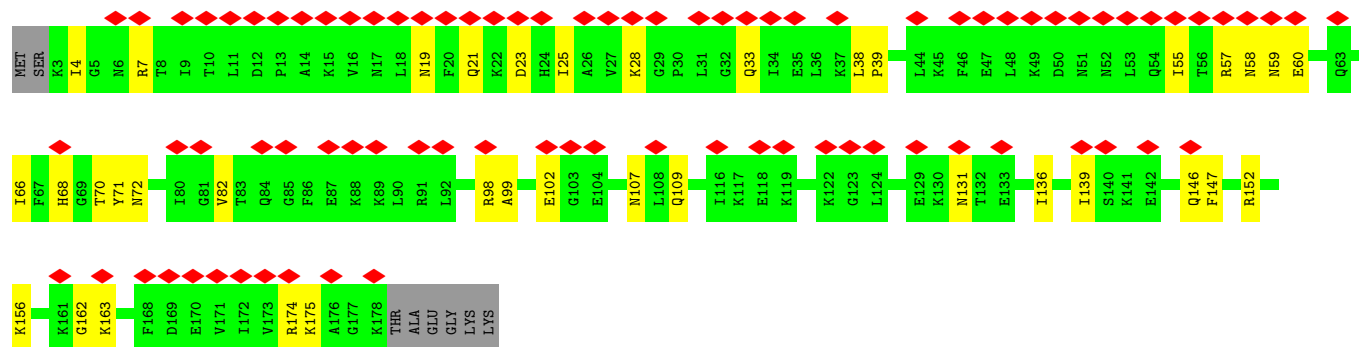
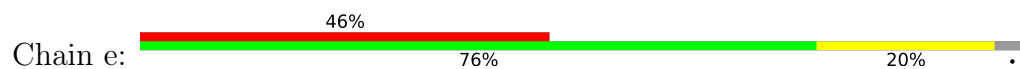


• Molecule 5: 50S ribosomal protein L4

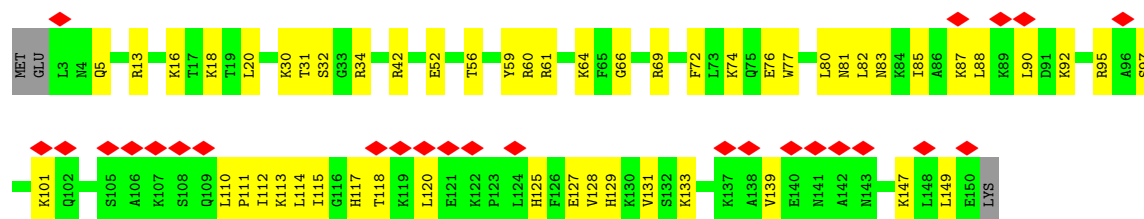




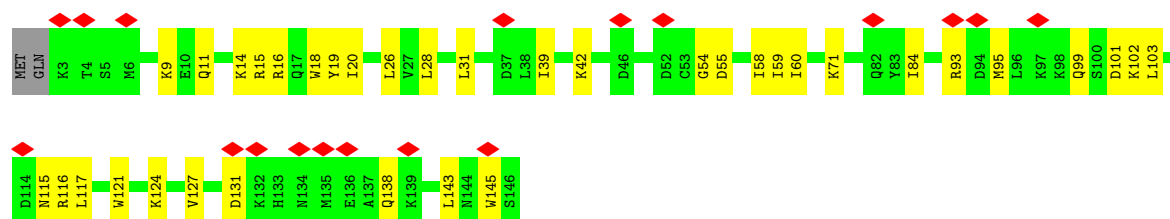
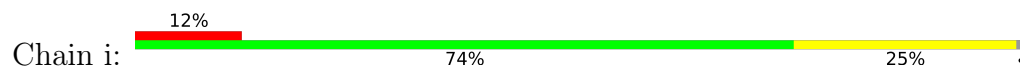
• Molecule 6: 50S ribosomal protein L6



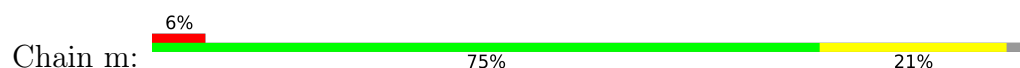
• Molecule 7: 50S ribosomal protein L15

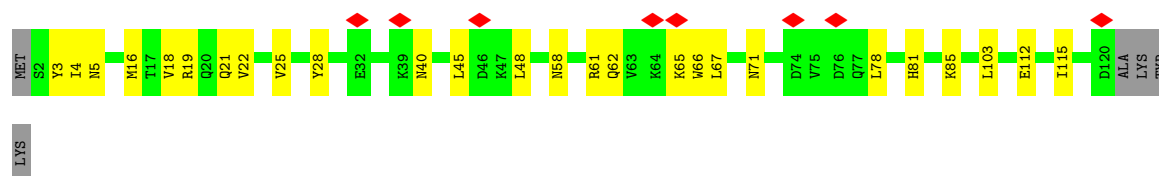


• Molecule 8: 50S ribosomal protein L13

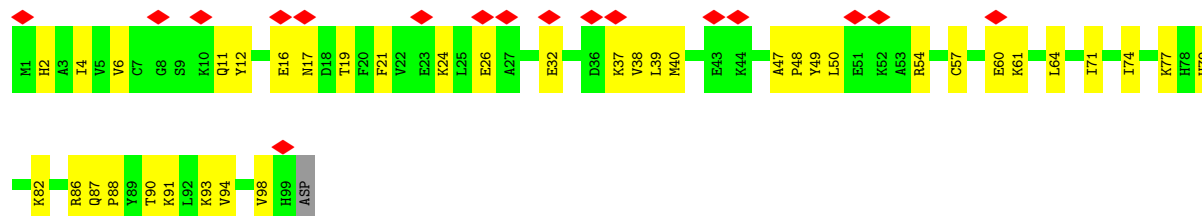


• Molecule 9: 50S ribosomal protein L17

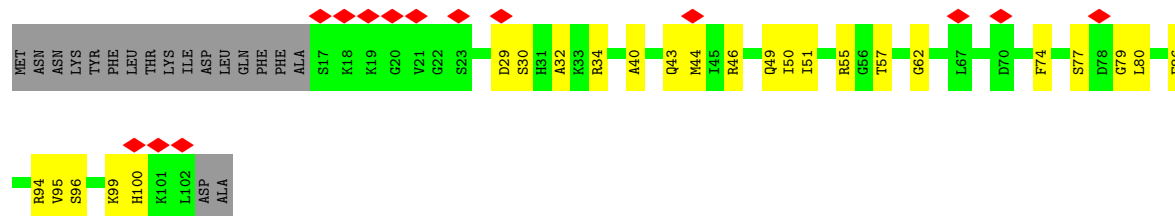




- Molecule 10: 50S ribosomal protein L21



- Molecule 11: 50S ribosomal protein L27



- Molecule 12: 50S ribosomal protein L32



- Molecule 13: 50S ribosomal protein L34

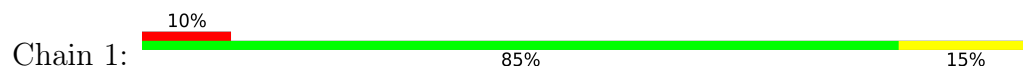


- Molecule 14: 50S ribosomal protein L36

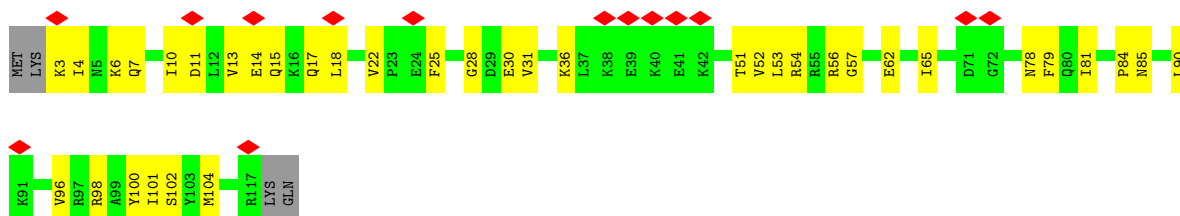




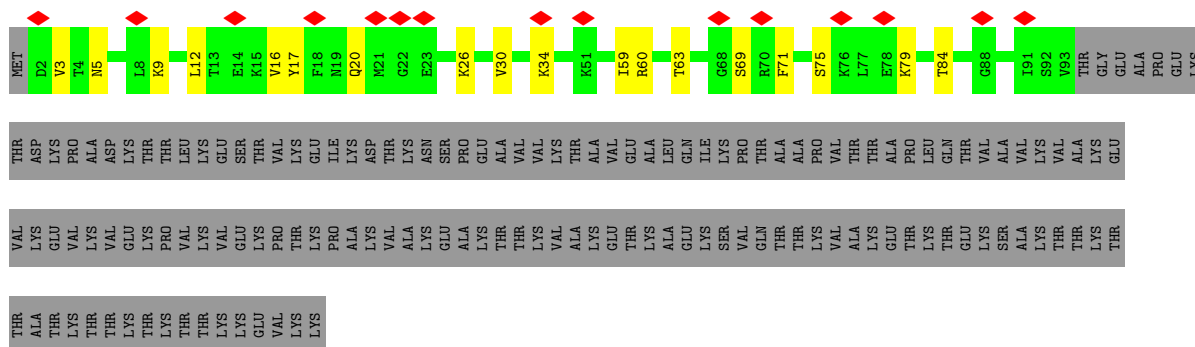
- Molecule 15: 50S ribosomal protein L35



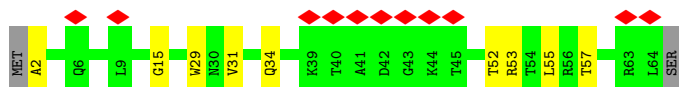
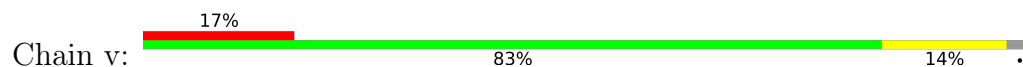
- Molecule 16: 50S ribosomal protein L19



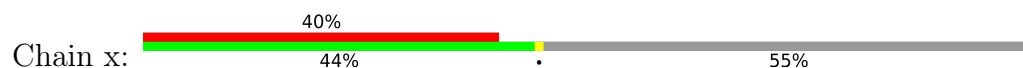
- Molecule 17: 50S ribosomal protein L23

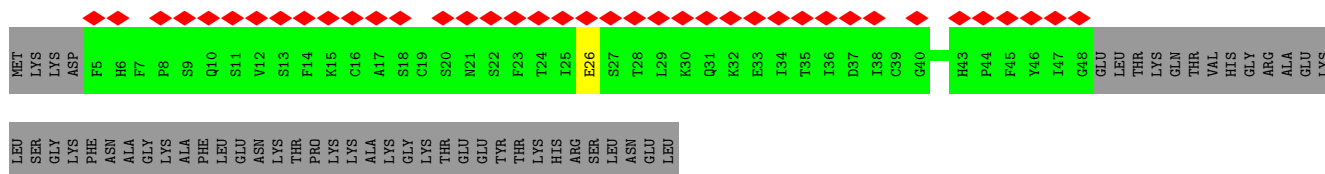


- Molecule 18: 50S ribosomal protein L28

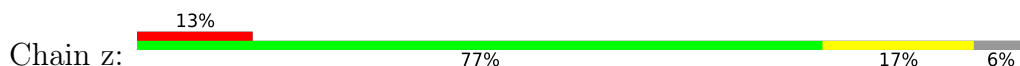


- Molecule 19: 50S ribosomal protein L31

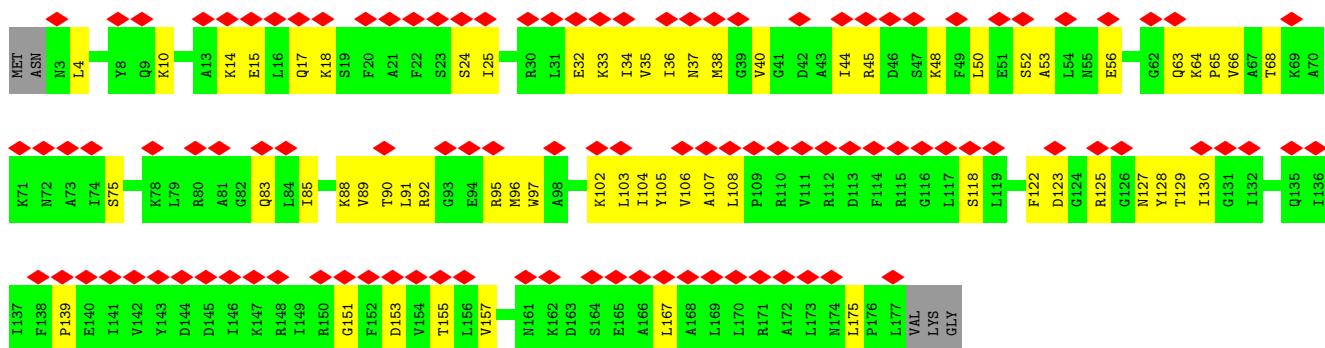




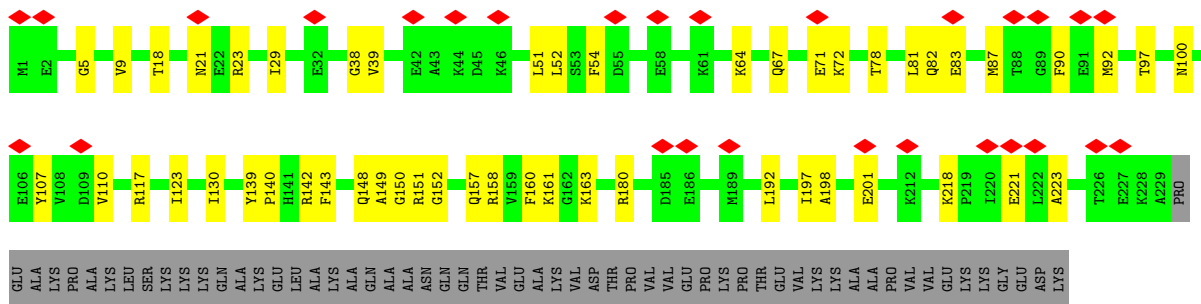
• Molecule 20: 50S ribosomal protein L33 1



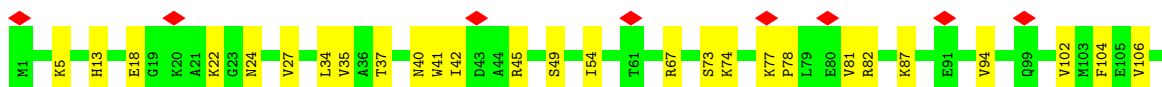
• Molecule 21: 50S ribosomal protein L5



• Molecule 22: 50S ribosomal protein L3

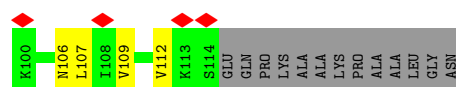


• Molecule 23: 50S ribosomal protein L16

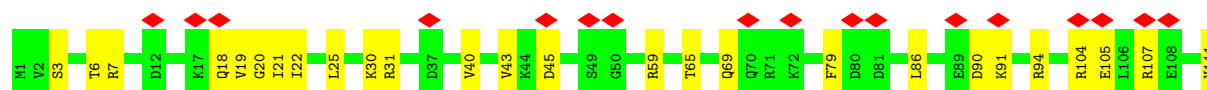
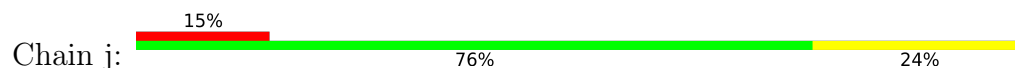




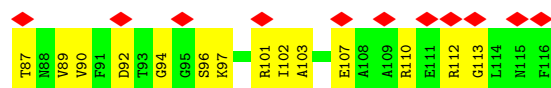
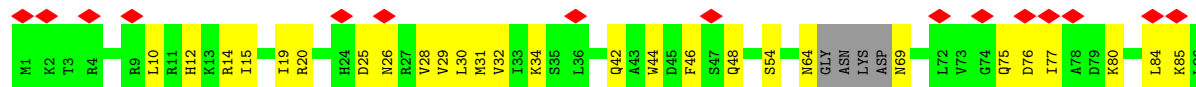
- Molecule 24: 50S ribosomal protein L20



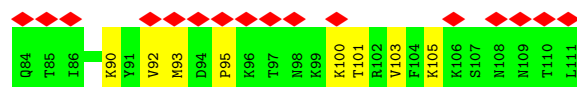
- Molecule 25: 50S ribosomal protein L14



- Molecule 26: 50S ribosomal protein L18

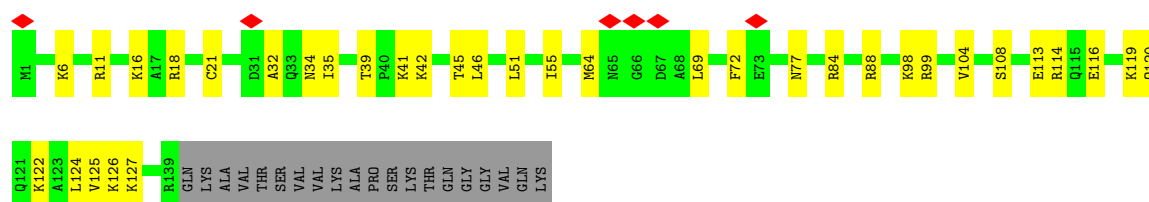


- Molecule 27: 50S ribosomal protein L24



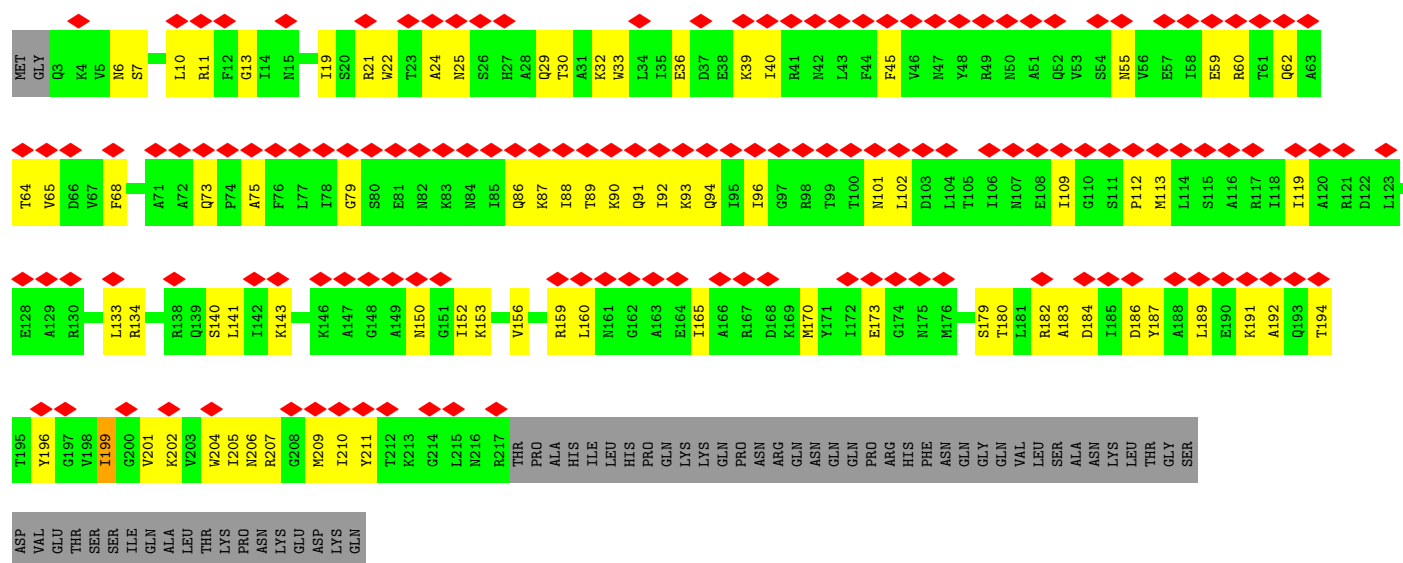
- Molecule 28: 50S ribosomal protein L22

Chain r: 



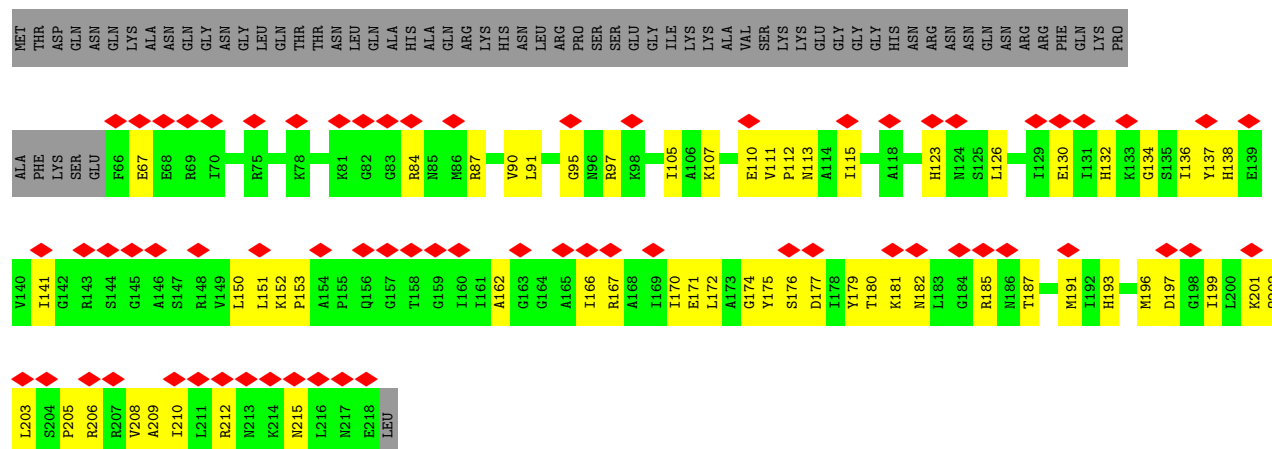
• Molecule 29: 30S ribosomal protein S3

Chain B: 

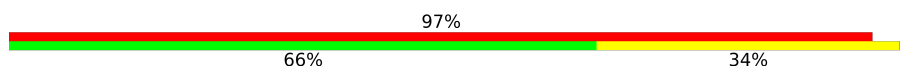


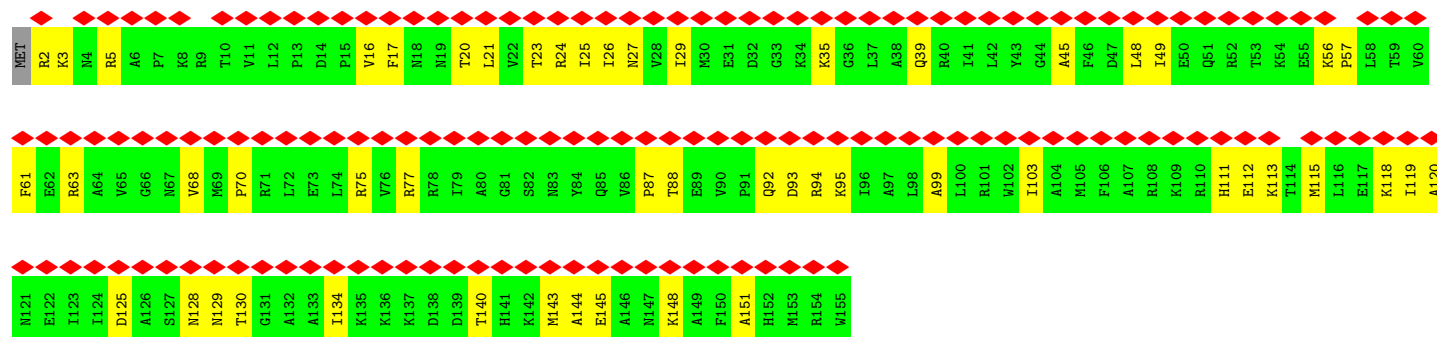
• Molecule 30: 30S ribosomal protein S5

Chain D: 

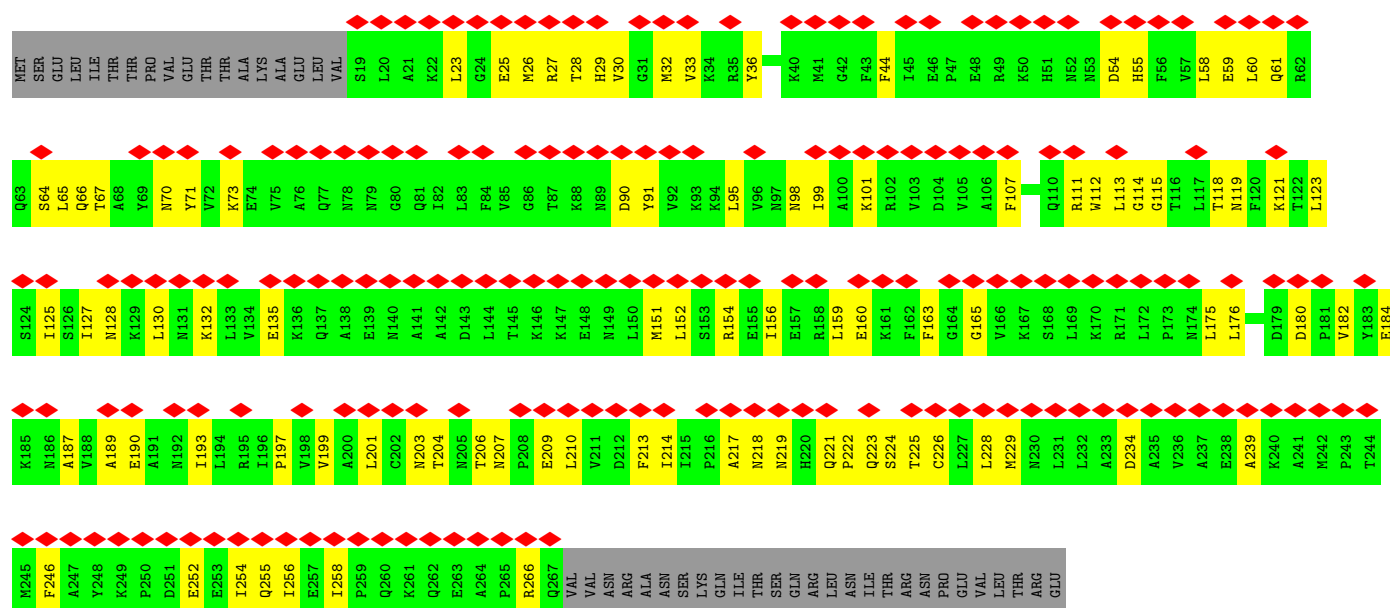


• Molecule 31: 30S ribosomal protein S7

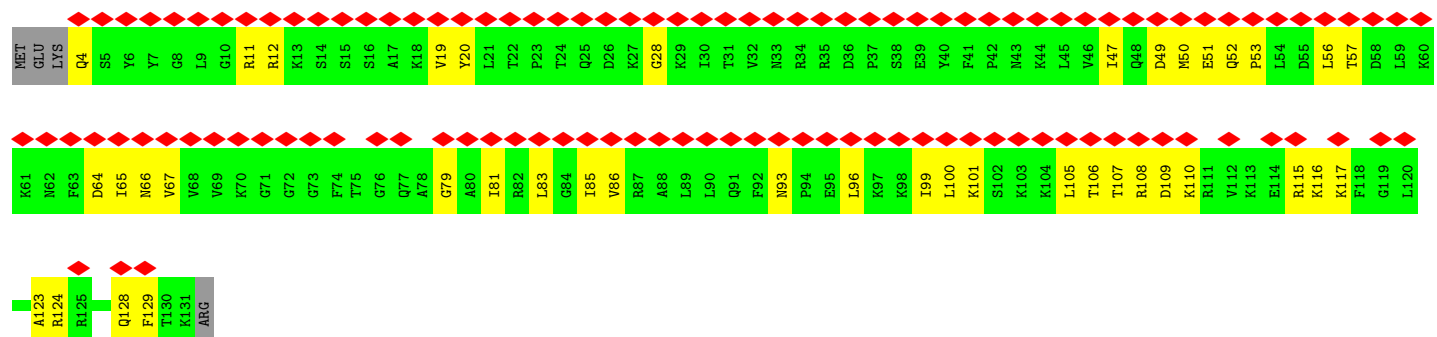
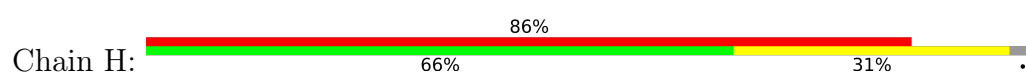
Chain F: 



• Molecule 32: 30S ribosomal protein S2

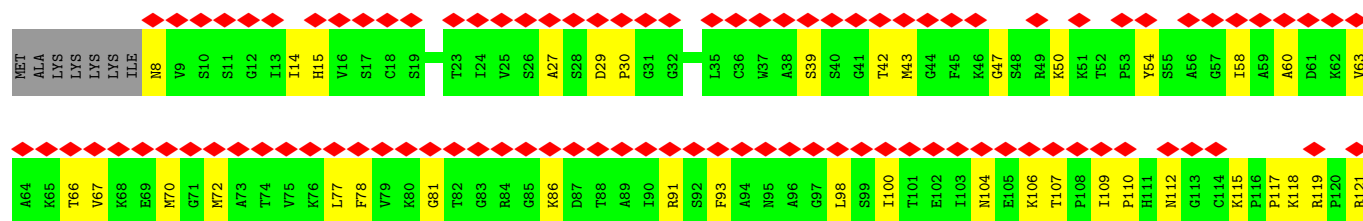


• Molecule 33: 30S ribosomal protein S9

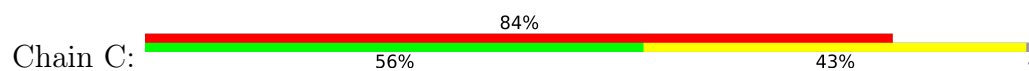


• Molecule 34: 30S ribosomal protein S11

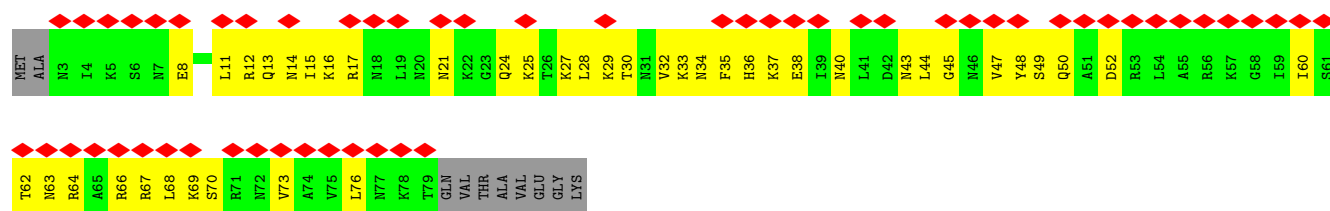




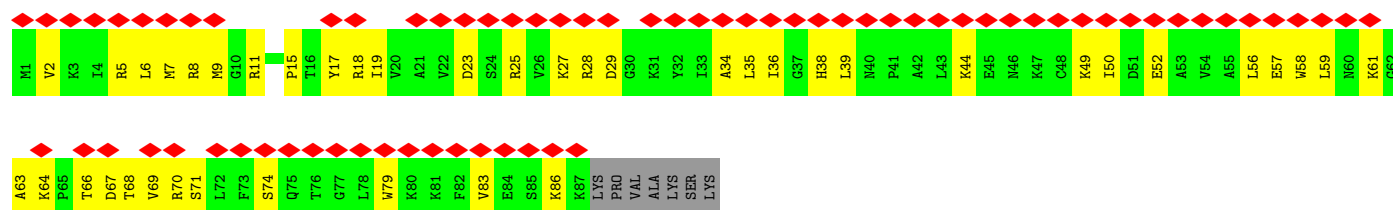
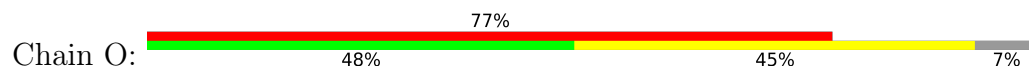
• Molecule 35: 30S ribosomal protein S4



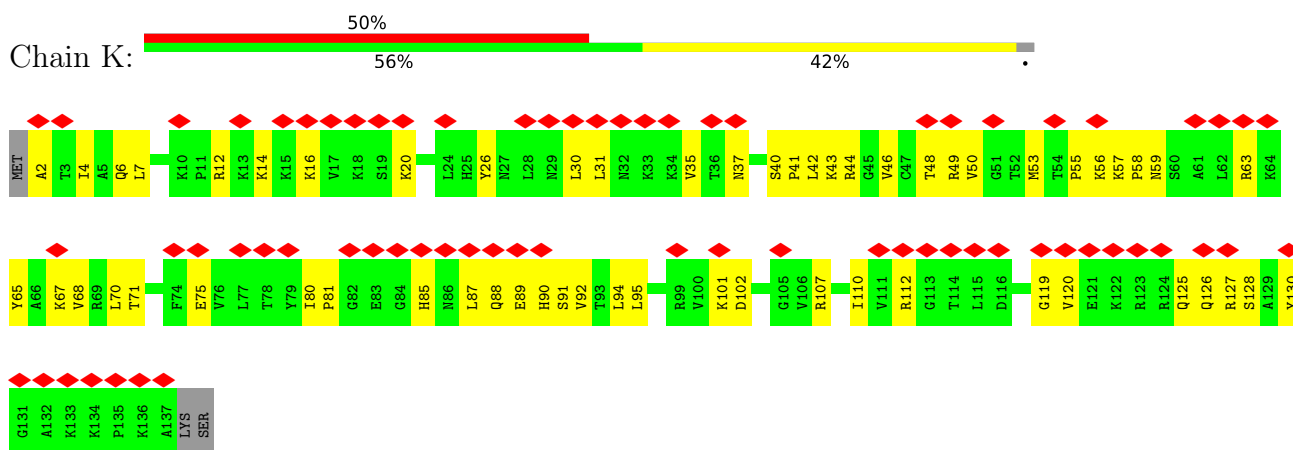
• Molecule 36: 30S ribosomal protein S20



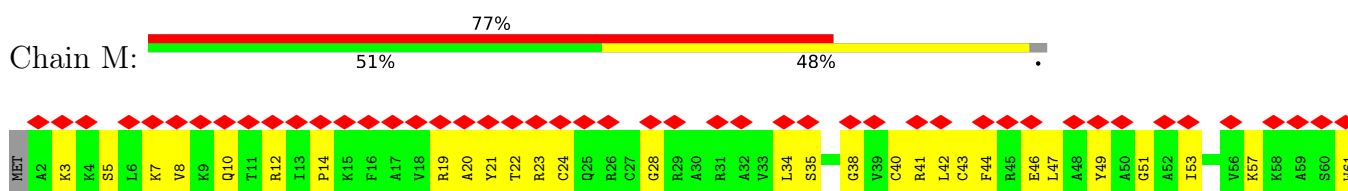
• Molecule 37: 30S ribosomal protein S16



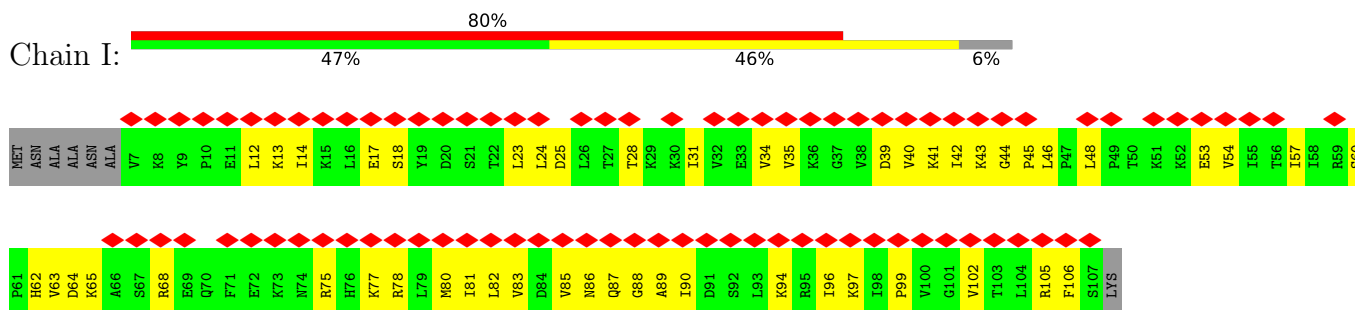
• Molecule 38: 30S ribosomal protein S12



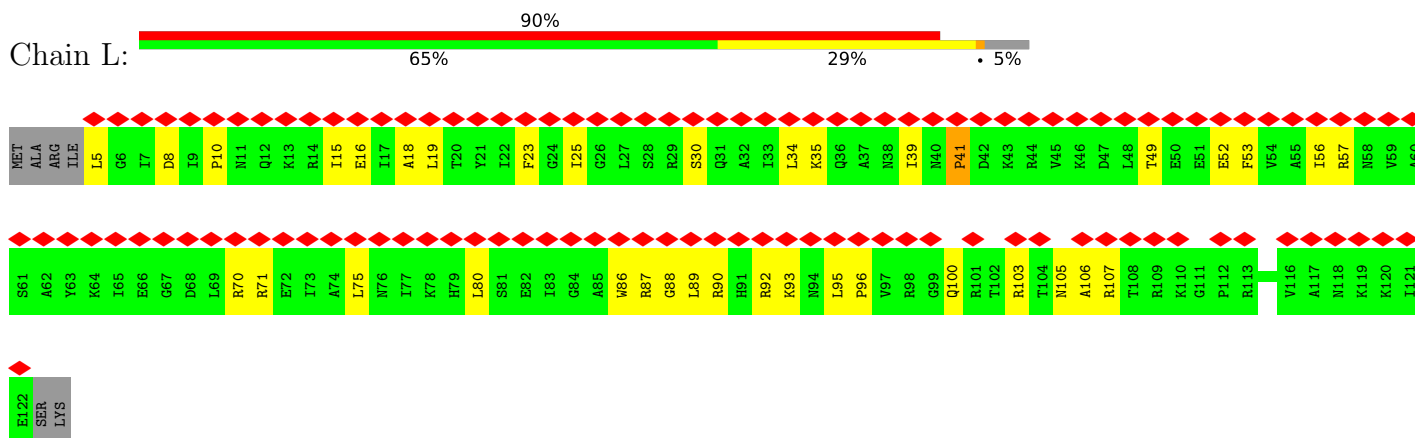
- Molecule 39: 30S ribosomal protein S14 type Z



- Molecule 40: 30S ribosomal protein S10

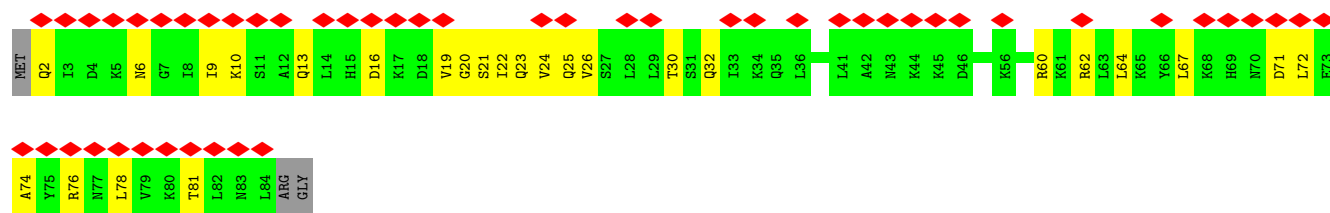


- Molecule 41: 30S ribosomal protein S13

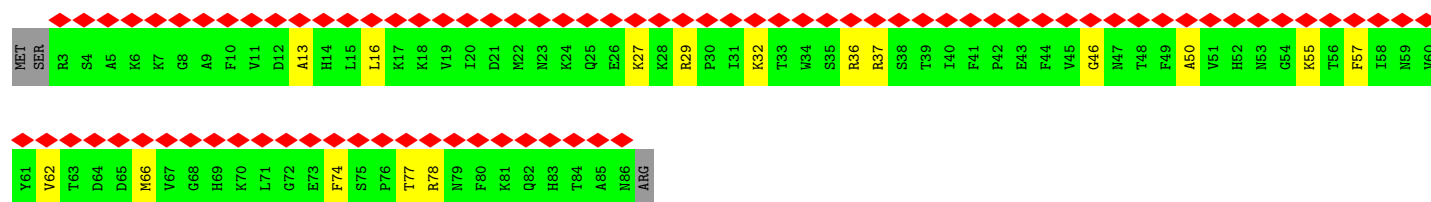
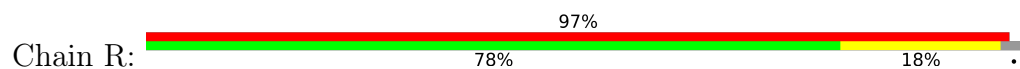


- Molecule 42: 30S ribosomal protein S15

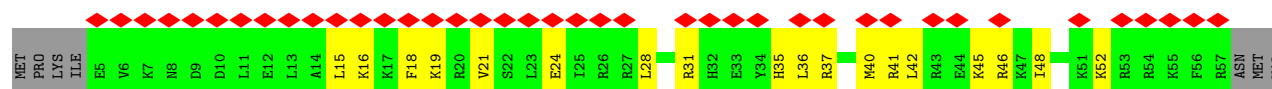




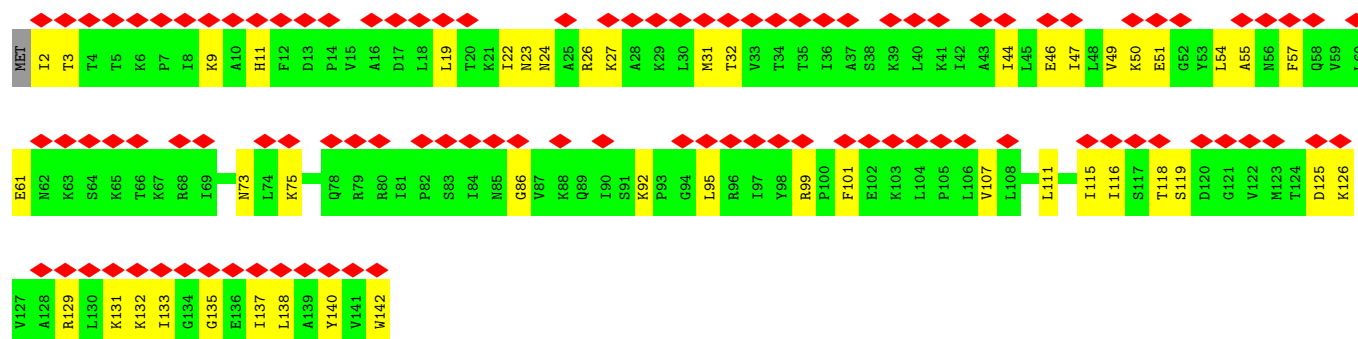
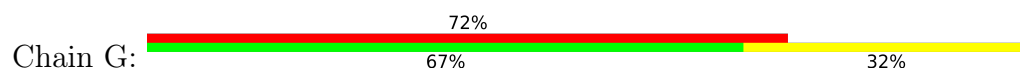
• Molecule 43: 30S ribosomal protein S19



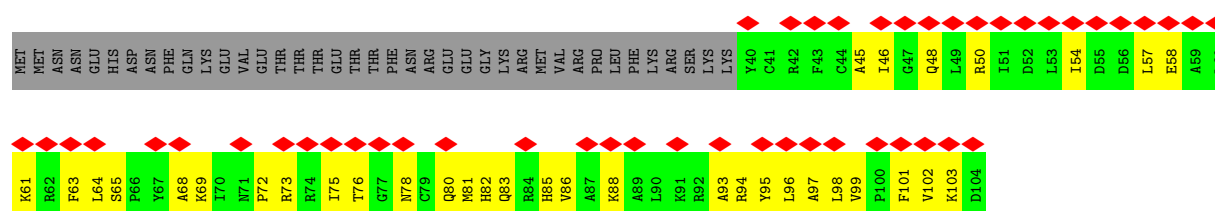
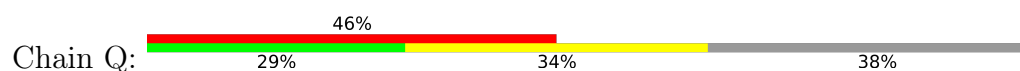
• Molecule 44: 30S ribosomal protein S21



• Molecule 45: 30S ribosomal protein S8

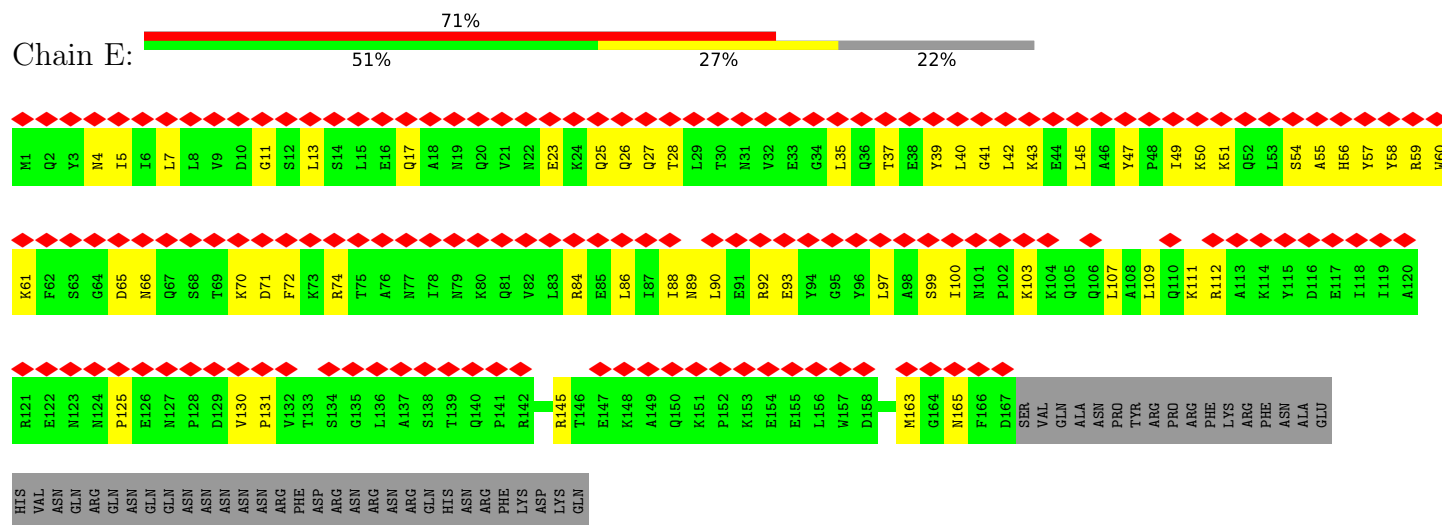


• Molecule 46: 30S ribosomal protein S18



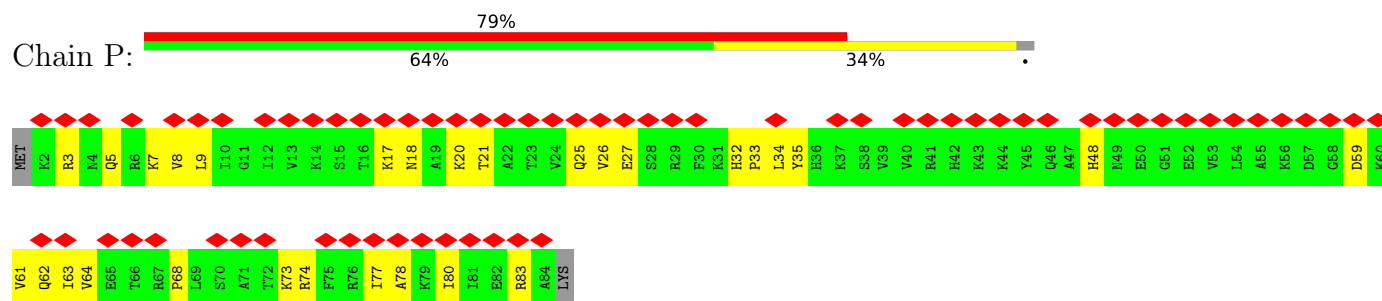
- Molecule 47: 30S ribosomal protein S6

Chain E:



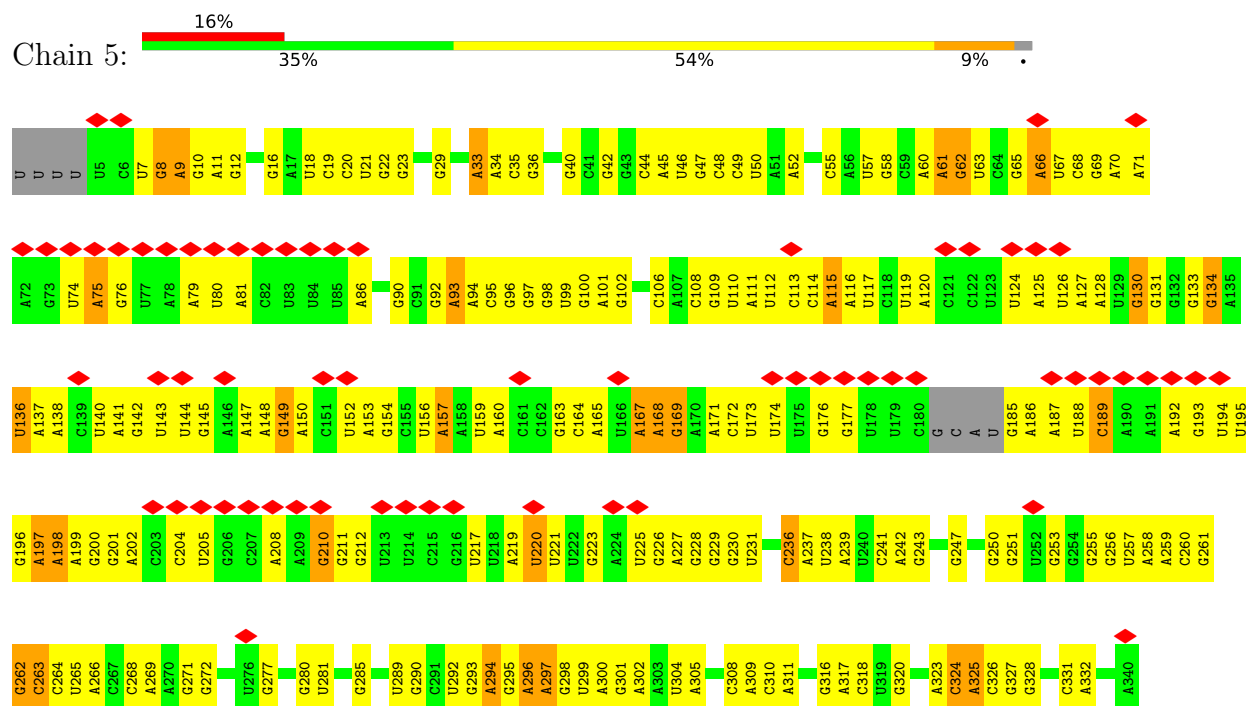
- Molecule 48: 30S ribosomal protein S17

Chain P:



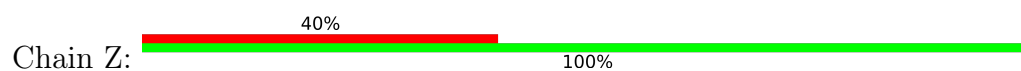
- Molecule 49: 16S ribosomal RNA

Chain 5:

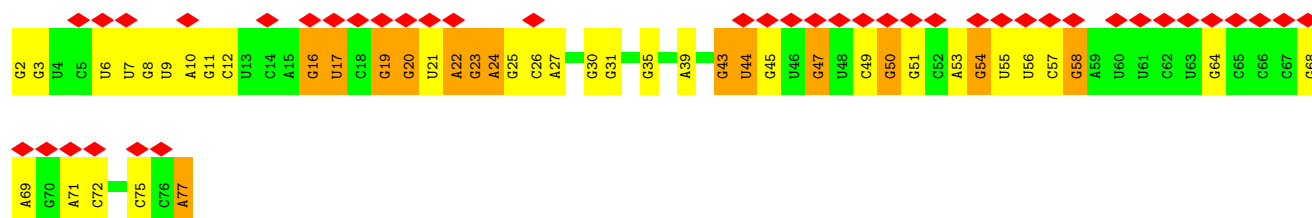




- Molecule 50: nascent peptide



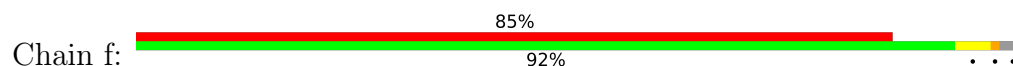
- Molecule 51: tRNA-Phe

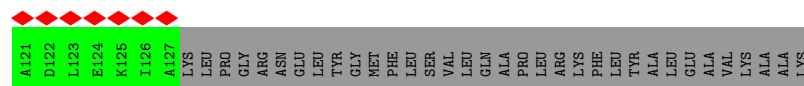


- Molecule 52: mRNA



- Molecule 53: 50S ribosomal protein L9





4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	77539	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.009	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0024	Depositor
Map size (Å)	571.368, 571.368, 571.368	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7004999, 1.7004999, 1.7004999	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	3	0.14	0/69100	0.30	9/107749 (0.0%)
2	4	0.12	0/2511	0.29	0/3910
3	w	0.17	0/806	0.47	0/1080
4	a	0.15	0/2241	0.38	0/3013
5	c	0.16	0/1639	0.47	0/2209
6	e	0.13	0/1373	0.32	0/1854
7	k	0.25	0/1155	0.47	0/1541
8	i	0.15	0/1180	0.38	0/1585
9	m	0.14	0/972	0.39	0/1308
10	q	0.16	0/826	0.45	0/1109
11	u	0.16	0/649	0.42	0/867
12	y	0.16	0/440	0.47	0/582
13	0	0.14	0/380	0.36	0/501
14	2	0.18	0/305	0.40	0/401
15	1	0.14	0/484	0.39	0/637
16	o	0.18	0/905	0.43	0/1211
17	s	0.15	0/726	0.40	0/981
18	v	0.14	0/510	0.39	0/684
19	x	0.14	0/217	0.31	0/301
20	z	0.14	0/412	0.42	0/547
21	d	0.18	0/1264	0.48	0/1719
22	b	0.14	0/1791	0.39	0/2408
23	l	0.17	0/1082	0.41	0/1456
24	p	0.15	0/955	0.38	0/1271
25	j	0.16	0/953	0.49	0/1275
26	n	0.18	0/861	0.45	0/1156
27	t	0.14	0/712	0.38	0/954
28	r	0.16	0/1077	0.39	0/1441
29	B	0.29	1/1705 (0.1%)	0.45	0/2304
30	D	0.16	0/1168	0.43	0/1568
31	F	0.19	0/1250	0.51	0/1682
32	A	0.17	0/1951	0.44	0/2652

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	H	0.16	0/1009	0.46	0/1354
34	J	0.23	0/843	0.49	2/1136 (0.2%)
35	C	0.19	0/1635	0.48	0/2202
36	S	0.24	0/631	0.63	0/838
37	O	0.15	0/703	0.41	0/945
38	K	0.17	0/1073	0.51	0/1445
39	M	0.16	0/482	0.40	0/643
40	I	0.18	0/814	0.48	0/1096
41	L	0.24	0/933	0.61	2/1254 (0.2%)
42	N	0.16	0/679	0.36	0/907
43	R	0.17	0/670	0.44	0/904
44	T	0.29	0/442	0.58	0/582
45	G	0.16	0/1119	0.45	0/1508
46	Q	0.19	0/545	0.46	0/730
47	E	0.20	0/1229	0.44	0/1670
48	P	0.14	0/684	0.43	0/913
49	5	0.12	0/35777	0.26	0/55776
51	7	0.13	0/1808	0.33	0/2817
52	Y	0.83	3/194 (1.5%)	0.42	0/298
53	f	0.66	0/711	1.06	1/988 (0.1%)
54	h	1.01	0/629	1.69	2/873 (0.2%)
55	g	1.21	0/616	1.76	7/856 (0.8%)
All	All	0.18	4/154826 (0.0%)	0.37	23/231691 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	B	199	ILE	C-N	9.42	1.38	1.33
52	Y	2	U	C1'-N1	6.67	1.58	1.48
52	Y	9	U	C1'-N1	6.40	1.58	1.48
52	Y	1	U	C1'-N1	6.21	1.57	1.48

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	L	41	PRO	CA-N-CD	-9.17	99.16	112.00
1	3	1211	U	C2'-C3'-O3'	7.98	125.67	113.70
41	L	41	PRO	N-CD-CG	-7.66	91.71	103.20
1	3	1209	U	C2'-C3'-O3'	7.29	120.44	109.50
53	f	117	VAL	N-CA-C	6.91	117.96	108.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3	61690	0	30961	1261	0
2	4	2245	0	1135	33	0
3	w	798	0	838	19	0
4	a	2199	0	2248	52	0
5	c	1613	0	1676	46	0
6	e	1349	0	1373	29	0
7	k	1138	0	1223	43	0
8	i	1158	0	1176	31	0
9	m	957	0	1008	19	0
10	q	809	0	852	31	0
11	u	641	0	650	19	0
12	y	436	0	441	17	0
13	0	377	0	422	12	0
14	2	303	0	347	9	0
15	1	477	0	530	12	0
16	o	895	0	932	33	0
17	s	714	0	785	12	0
18	v	504	0	542	9	0
19	x	218	0	90	1	0
20	z	408	0	436	6	0
21	d	1244	0	1160	50	0
22	b	1758	0	1797	47	0
23	l	1057	0	1088	31	0
24	p	941	0	1017	27	0
25	j	944	0	1019	24	0
26	n	853	0	873	28	0
27	t	706	0	726	18	0
28	r	1068	0	1150	27	0
29	B	1682	0	1733	59	0
30	D	1153	0	1231	42	0
31	F	1231	0	1285	41	0
32	A	1917	0	1894	69	0
33	H	993	0	1023	35	0
34	J	828	0	855	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	C	1605	0	1603	75	0
36	S	629	0	681	39	0
37	O	690	0	726	35	0
38	K	1055	0	1124	48	0
39	M	473	0	505	31	0
40	I	803	0	876	44	0
41	L	922	0	957	28	0
42	N	673	0	730	20	0
43	R	654	0	629	14	0
44	T	439	0	467	13	0
45	G	1103	0	1218	34	0
46	Q	535	0	559	37	0
47	E	1211	0	1108	49	0
48	P	675	0	728	25	0
49	5	31952	0	16055	835	0
50	Z	26	0	8	0	0
51	7	1618	0	821	38	0
52	Y	177	0	92	5	0
53	f	713	0	313	3	0
54	h	630	0	309	12	0
55	g	617	0	308	7	0
56	3	24	0	0	0	0
56	y	1	0	0	0	0
57	2	1	0	0	0	0
57	M	1	0	0	0	0
57	Q	1	0	0	0	0
57	y	1	0	0	0	0
57	z	1	0	0	0	0
All	All	142534	0	94333	3200	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 14.

The worst 5 of 3200 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)
51:7:35:G:H1	52:Y:5:U:H3	1.00	1.00
1:3:1095:U:OP2	54:h:72:VAL:N	1.95	0.98
49:5:940:G:H1	49:5:1211:A:N6	1.60	0.98
49:5:612:G:H1	49:5:624:U:H3	1.08	0.98
49:5:1138:U:H3	49:5:1149:G:H1	1.03	0.97

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	
3	w	95/111 (86%)	91 (96%)	4 (4%)	0	100	100
4	a	283/287 (99%)	265 (94%)	18 (6%)	0	100	100
5	c	208/212 (98%)	190 (91%)	18 (9%)	0	100	100
6	e	174/184 (95%)	168 (97%)	6 (3%)	0	100	100
7	k	146/151 (97%)	126 (86%)	20 (14%)	0	100	100
8	i	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
9	m	117/124 (94%)	113 (97%)	4 (3%)	0	100	100
10	q	97/100 (97%)	88 (91%)	9 (9%)	0	100	100
11	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
12	y	54/57 (95%)	49 (91%)	5 (9%)	0	100	100
13	0	45/48 (94%)	44 (98%)	1 (2%)	0	100	100
14	2	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
15	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
16	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
17	s	90/237 (38%)	84 (93%)	6 (7%)	0	100	100
18	v	61/65 (94%)	58 (95%)	3 (5%)	0	100	100
19	x	42/97 (43%)	38 (90%)	4 (10%)	0	100	100
20	z	48/53 (91%)	46 (96%)	2 (4%)	0	100	100
21	d	173/180 (96%)	156 (90%)	17 (10%)	0	100	100
22	b	227/287 (79%)	217 (96%)	10 (4%)	0	100	100
23	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
24	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	j	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
26	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
27	t	92/111 (83%)	83 (90%)	9 (10%)	0	100	100
28	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
29	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
30	D	151/219 (69%)	142 (94%)	9 (6%)	0	100	100
31	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
32	A	247/294 (84%)	228 (92%)	19 (8%)	0	100	100
33	H	126/132 (96%)	104 (82%)	22 (18%)	0	100	100
34	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
35	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
36	S	75/87 (86%)	72 (96%)	3 (4%)	0	100	100
37	O	85/94 (90%)	79 (93%)	6 (7%)	0	100	100
38	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
39	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
40	I	99/108 (92%)	87 (88%)	12 (12%)	0	100	100
41	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
42	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
43	R	82/87 (94%)	77 (94%)	5 (6%)	0	100	100
44	T	51/60 (85%)	44 (86%)	7 (14%)	0	100	100
45	G	139/142 (98%)	122 (88%)	17 (12%)	0	100	100
46	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
47	E	165/215 (77%)	148 (90%)	17 (10%)	0	100	100
48	P	81/85 (95%)	75 (93%)	6 (7%)	0	100	100
53	f	140/149 (94%)	124 (89%)	15 (11%)	1 (1%)	18	51
54	h	126/137 (92%)	116 (92%)	8 (6%)	2 (2%)	7	36
55	g	123/161 (76%)	115 (94%)	4 (3%)	4 (3%)	3	23
All	All	5814/6670 (87%)	5364 (92%)	443 (8%)	7 (0%)	49	79

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
53	f	115	ASP

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Mol	Chain	Res	Type
54	h	20	LYS
55	g	45	PHE
55	g	110	CYS
54	h	23	PRO

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	
3	w	83/98 (85%)	83 (100%)	0	100	100
4	a	233/243 (96%)	233 (100%)	0	100	100
5	c	174/184 (95%)	174 (100%)	0	100	100
6	e	138/159 (87%)	138 (100%)	0	100	100
7	k	118/126 (94%)	118 (100%)	0	100	100
8	i	124/128 (97%)	124 (100%)	0	100	100
9	m	104/109 (95%)	104 (100%)	0	100	100
10	q	88/91 (97%)	88 (100%)	0	100	100
11	u	64/85 (75%)	64 (100%)	0	100	100
12	y	45/49 (92%)	45 (100%)	0	100	100
13	0	39/41 (95%)	39 (100%)	0	100	100
14	2	35/35 (100%)	35 (100%)	0	100	100
15	1	51/51 (100%)	51 (100%)	0	100	100
16	o	91/105 (87%)	91 (100%)	0	100	100
17	s	80/208 (38%)	80 (100%)	0	100	100
18	v	55/60 (92%)	55 (100%)	0	100	100
20	z	47/50 (94%)	47 (100%)	0	100	100
21	d	111/154 (72%)	111 (100%)	0	100	100
22	b	185/233 (79%)	185 (100%)	0	100	100
23	l	107/115 (93%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	p	99/108 (92%)	99 (100%)	0	100	100
25	j	103/103 (100%)	103 (100%)	0	100	100
26	n	85/99 (86%)	85 (100%)	0	100	100
27	t	69/96 (72%)	69 (100%)	0	100	100
28	r	116/132 (88%)	116 (100%)	0	100	100
29	B	176/232 (76%)	176 (100%)	0	100	100
30	D	117/178 (66%)	117 (100%)	0	100	100
31	F	128/132 (97%)	128 (100%)	0	100	100
32	A	200/262 (76%)	200 (100%)	0	100	100
33	H	101/115 (88%)	101 (100%)	0	100	100
34	J	91/97 (94%)	91 (100%)	0	100	100
35	C	164/183 (90%)	164 (100%)	0	100	100
36	S	70/77 (91%)	70 (100%)	0	100	100
37	O	71/82 (87%)	71 (100%)	0	100	100
38	K	111/120 (92%)	111 (100%)	0	100	100
39	M	47/48 (98%)	47 (100%)	0	100	100
40	I	93/99 (94%)	93 (100%)	0	100	100
41	L	92/105 (88%)	92 (100%)	0	100	100
42	N	76/78 (97%)	76 (100%)	0	100	100
43	R	66/77 (86%)	66 (100%)	0	100	100
44	T	43/56 (77%)	43 (100%)	0	100	100
45	G	121/124 (98%)	121 (100%)	0	100	100
46	Q	56/94 (60%)	56 (100%)	0	100	100
47	E	107/196 (55%)	107 (100%)	0	100	100
48	P	73/75 (97%)	73 (100%)	0	100	100
All	All	4447/5292 (84%)	4447 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
26	n	26	ASN

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Mol	Chain	Res	Type
41	L	91	HIS
29	B	94	GLN
41	L	76	ASN
46	Q	83	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	2877/2907 (98%)	532 (18%)	37 (1%)
2	4	103/108 (95%)	28 (27%)	2 (1%)
49	5	1490/1520 (98%)	274 (18%)	6 (0%)
51	7	75/76 (98%)	20 (26%)	1 (1%)
52	Y	8/9 (88%)	0	0
All	All	4553/4620 (98%)	854 (18%)	46 (1%)

5 of 854 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	17	G
1	3	37	G
1	3	48	G
1	3	53	G
1	3	64	U

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	1588	A
1	3	2764	U
1	3	1618	U
1	3	2506	C
2	4	54	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 30 ligands modelled in this entry, 30 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

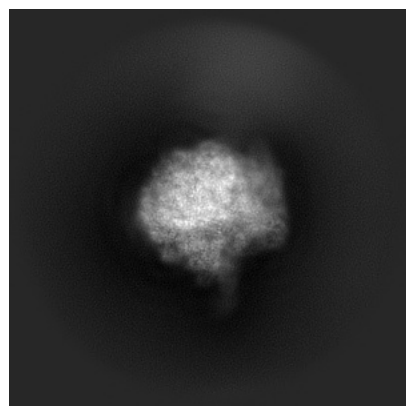
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13234. These allow visual inspection of the internal detail of the map and identification of artifacts.

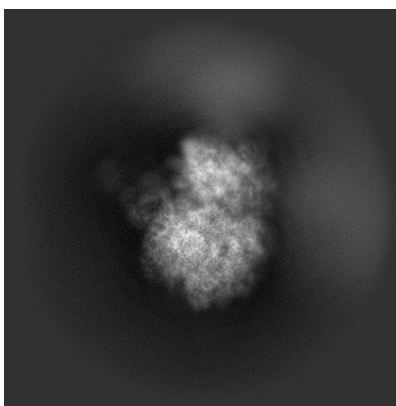
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

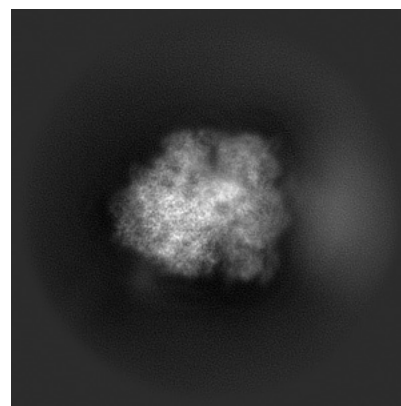
6.1.1 Primary map



X

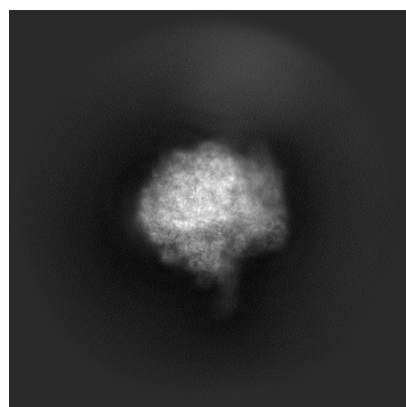


Y

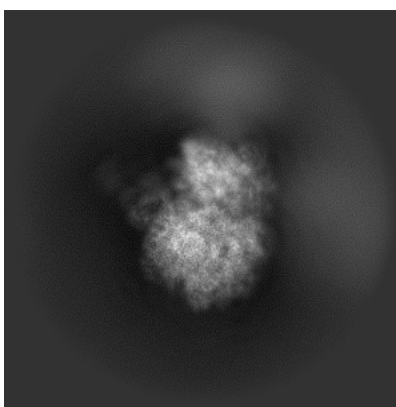


Z

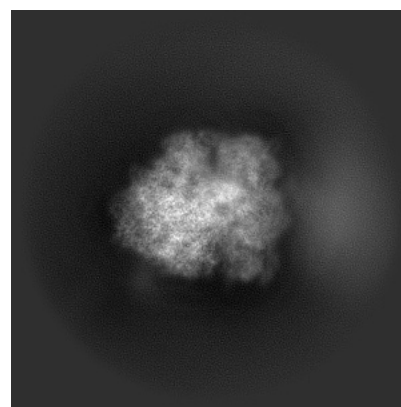
6.1.2 Raw map



X



Y

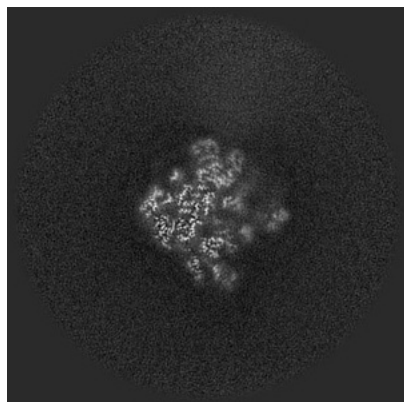


Z

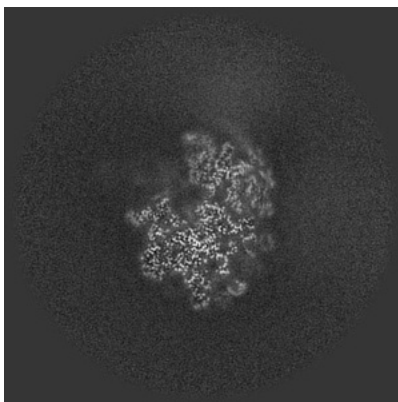
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

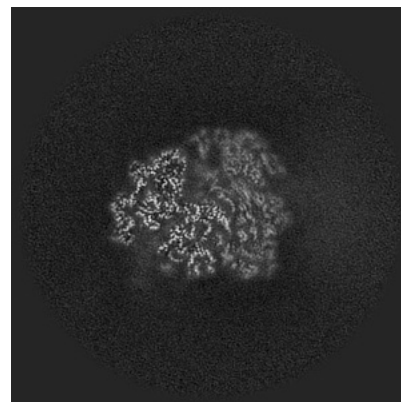
6.2.1 Primary map



X Index: 168

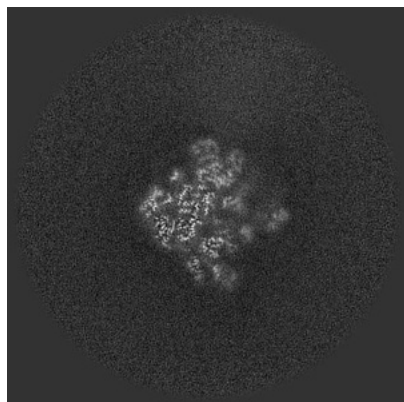


Y Index: 168

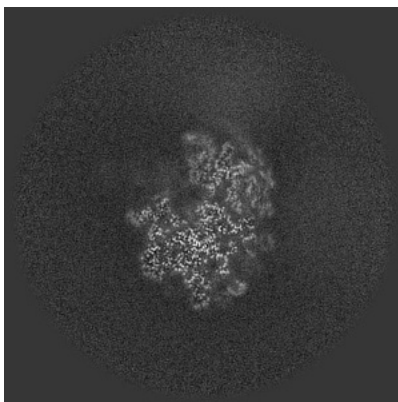


Z Index: 168

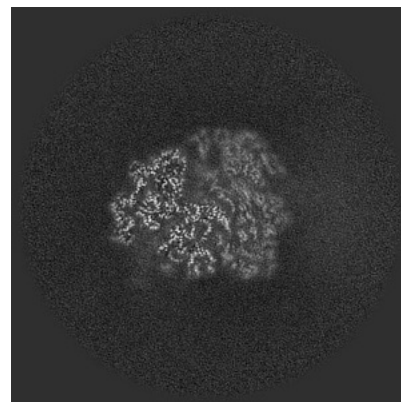
6.2.2 Raw map



X Index: 168



Y Index: 168

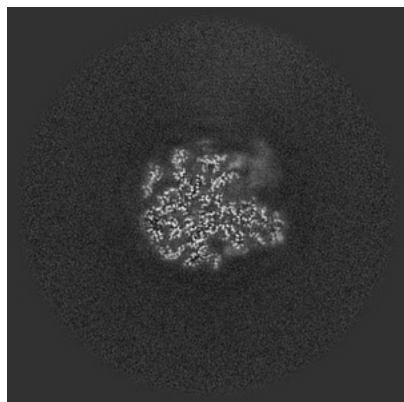


Z Index: 168

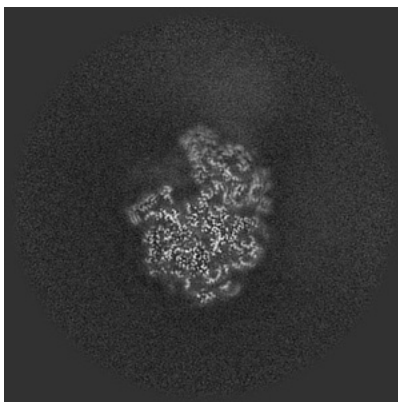
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

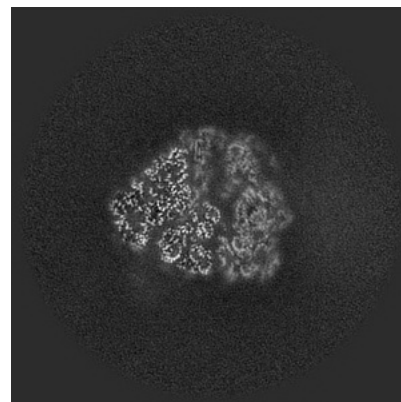
6.3.1 Primary map



X Index: 142

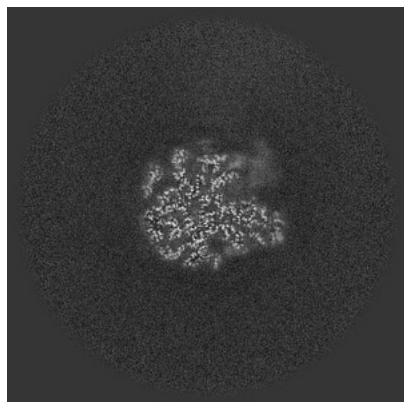


Y Index: 160

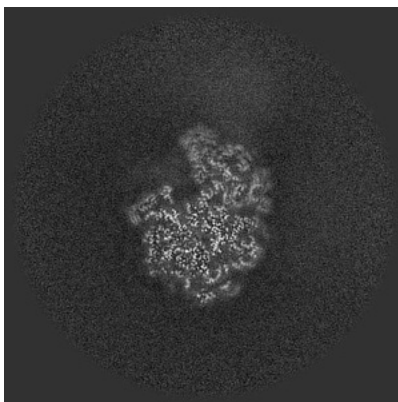


Z Index: 163

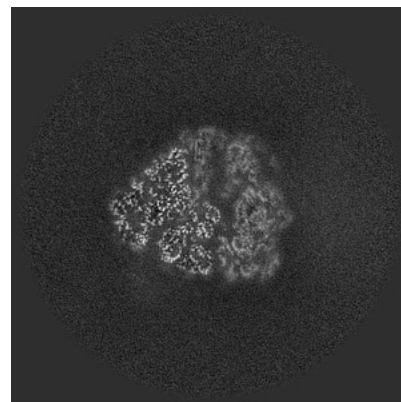
6.3.2 Raw map



X Index: 142



Y Index: 160

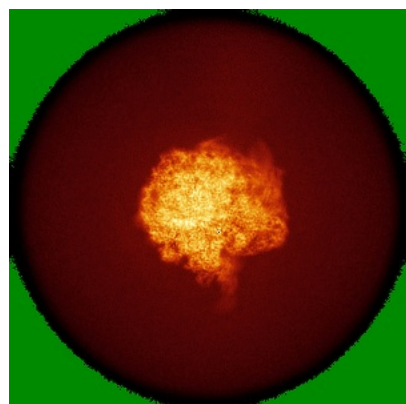


Z Index: 163

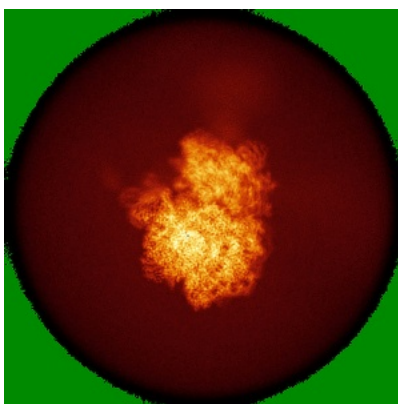
The images above show the largest variance slices of the map in three orthogonal directions.

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

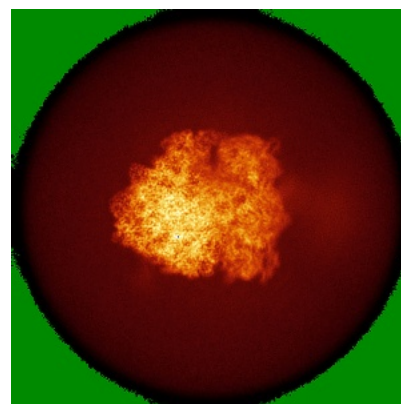
6.4.1 Primary map



X

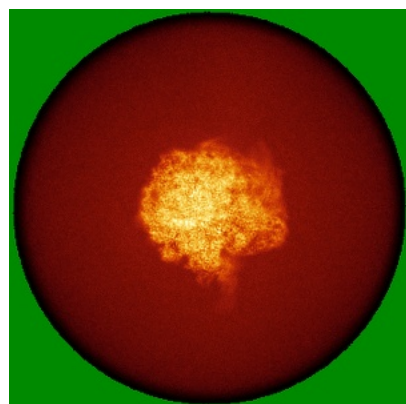


Y

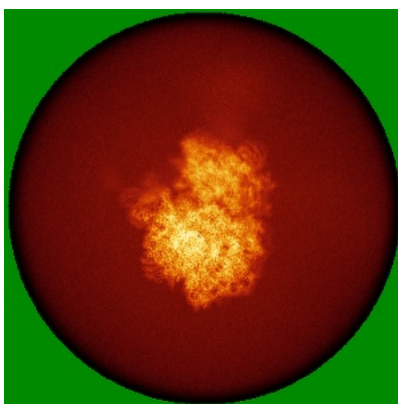


Z

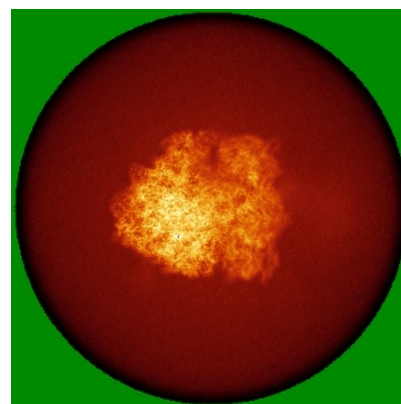
6.4.2 Raw map



X



Y



Z

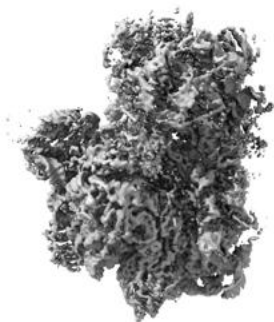
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



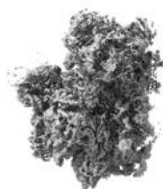
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0024. 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.

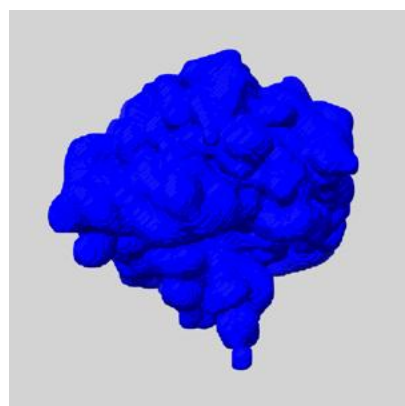
6.6 Mask visualisation [i](#)

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

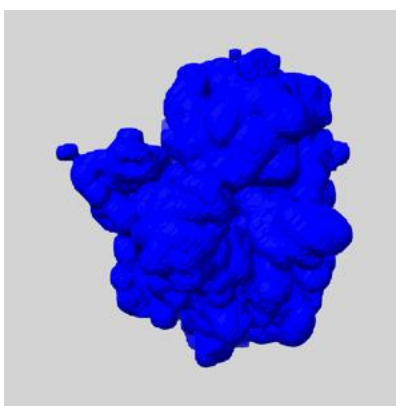
A mask typically either:

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

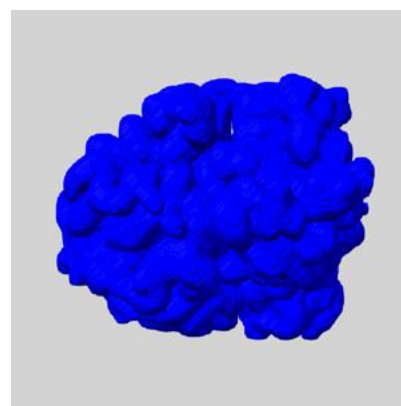
6.6.1 emd_13234_msk_1.map [i](#)



X



Y

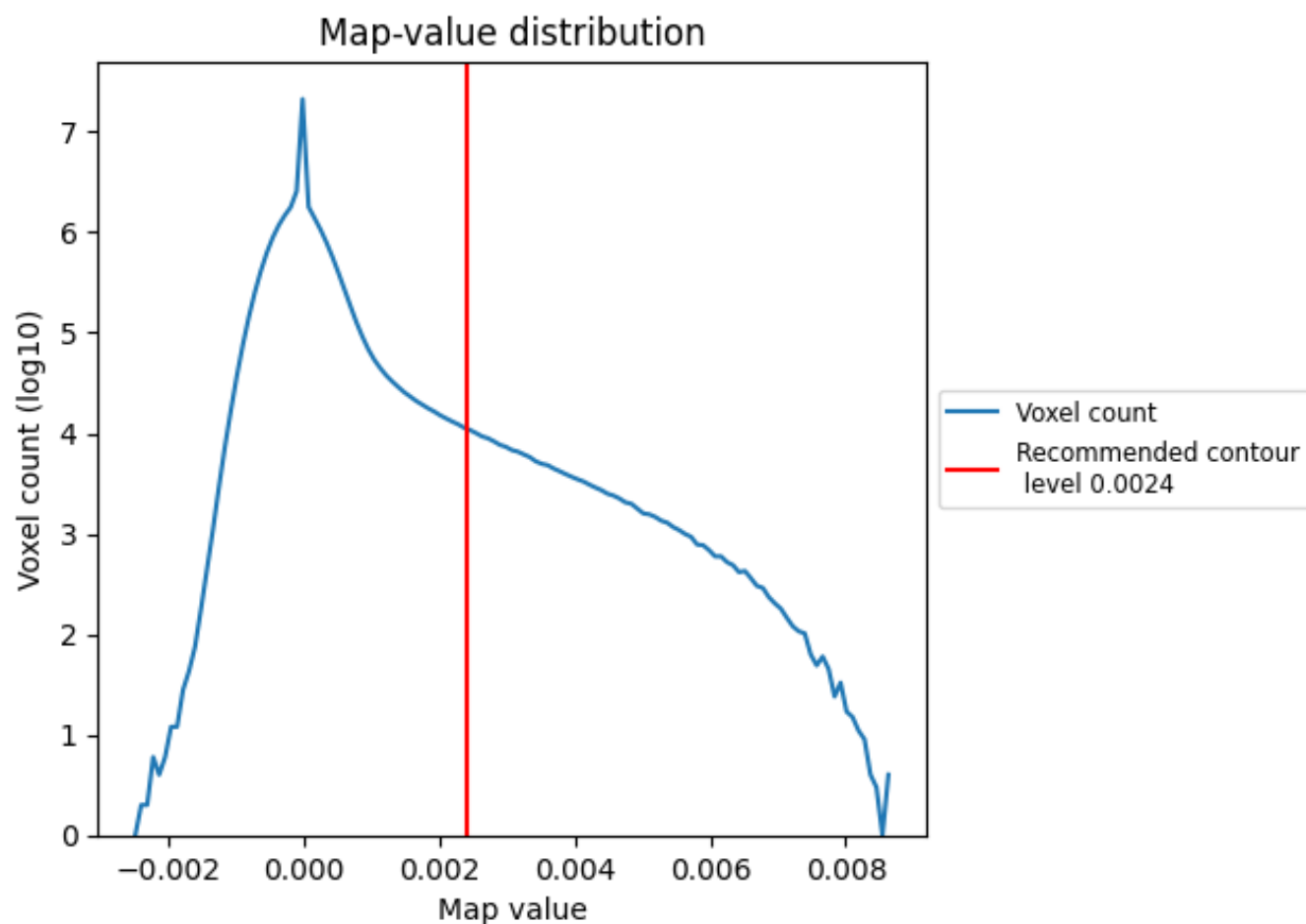


Z

7 Map analysis [i](#)

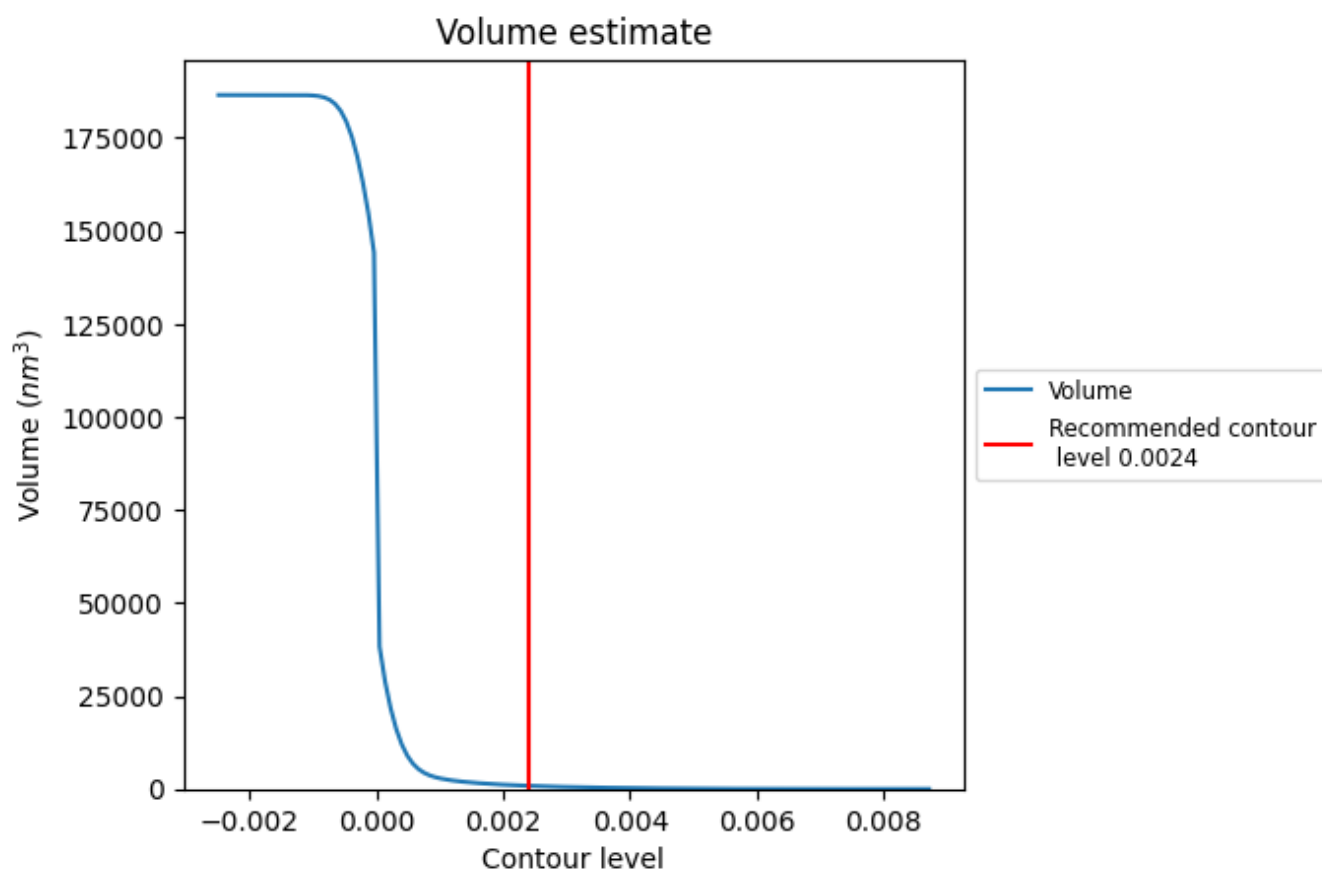
This section contains the results of statistical analysis of the map.

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.

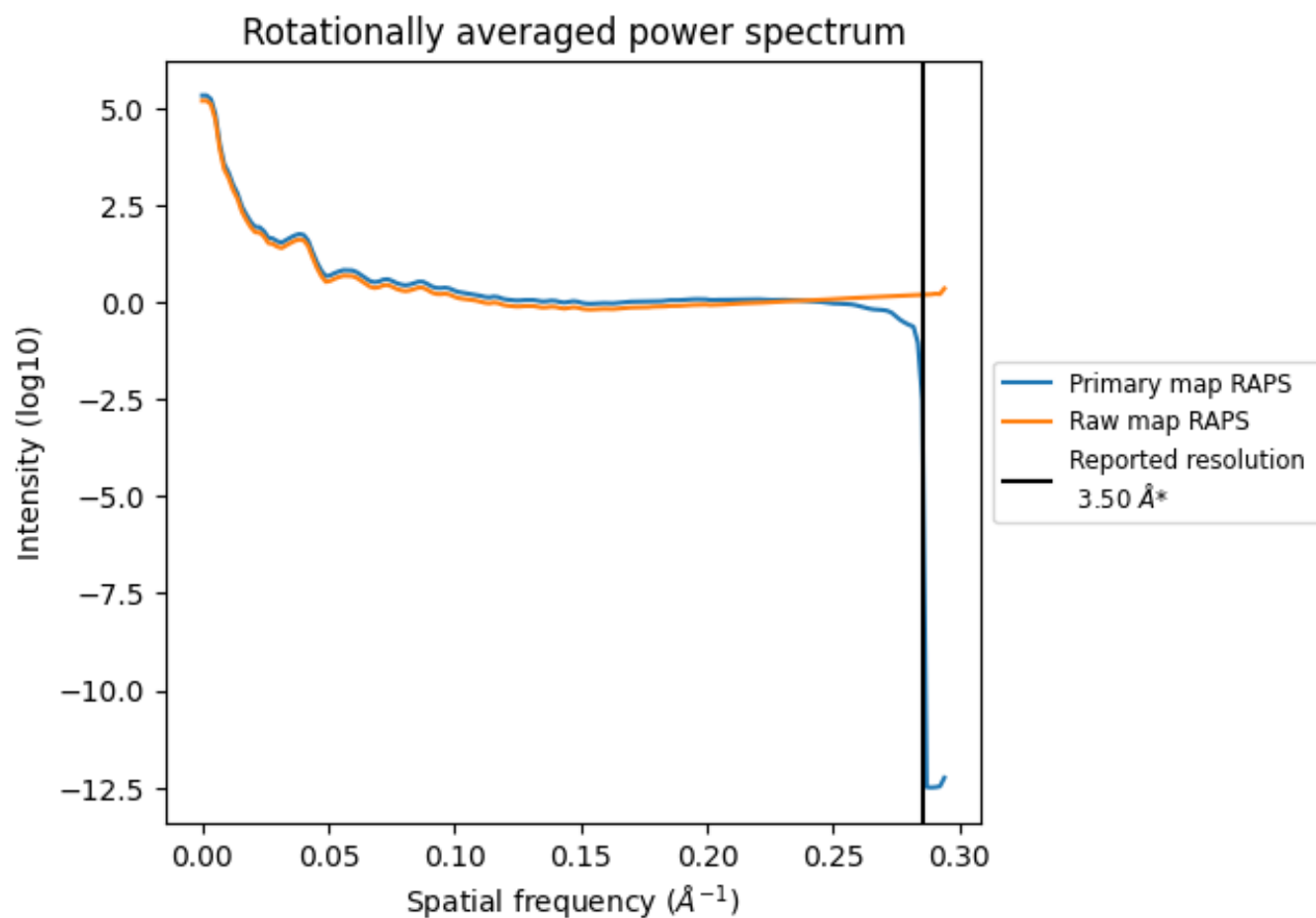
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 852 nm³; this corresponds to an approximate mass of 770 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 ⓘ

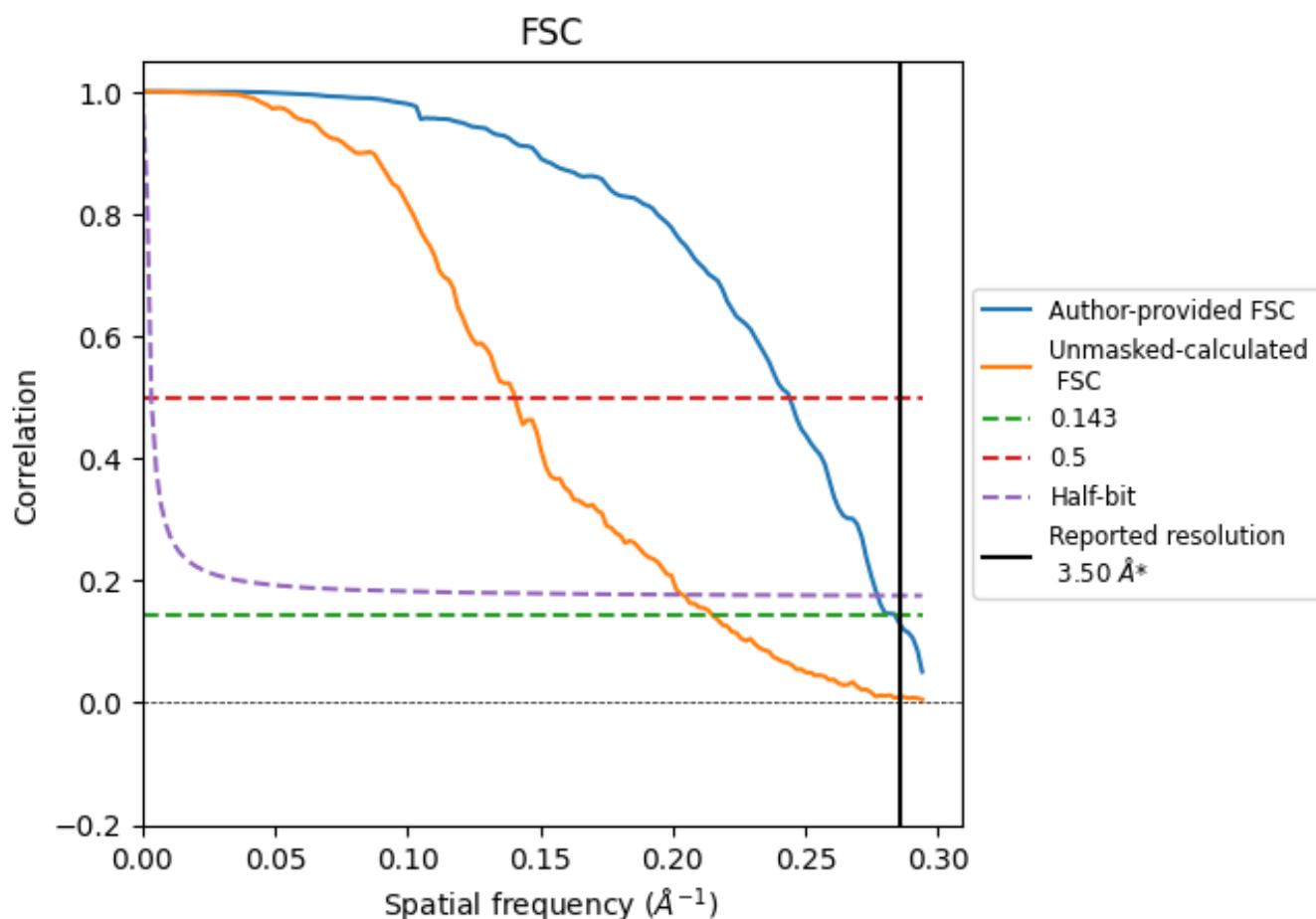


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.52	4.10	3.61
Unmasked-calculated*	4.65	7.12	4.91

*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 4.65 differs from the reported value 3.5 by more than 10 %

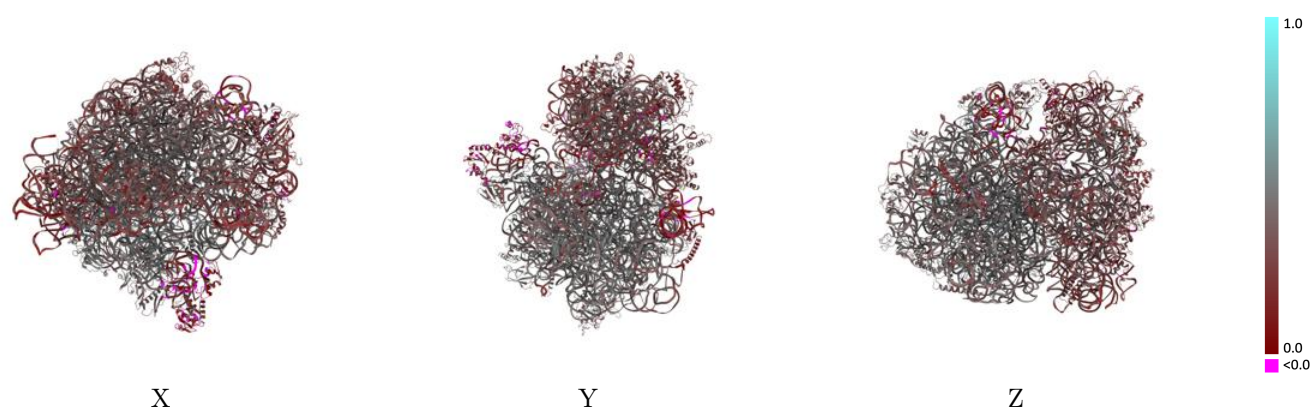
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13234 and PDB model 7P6Z. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)

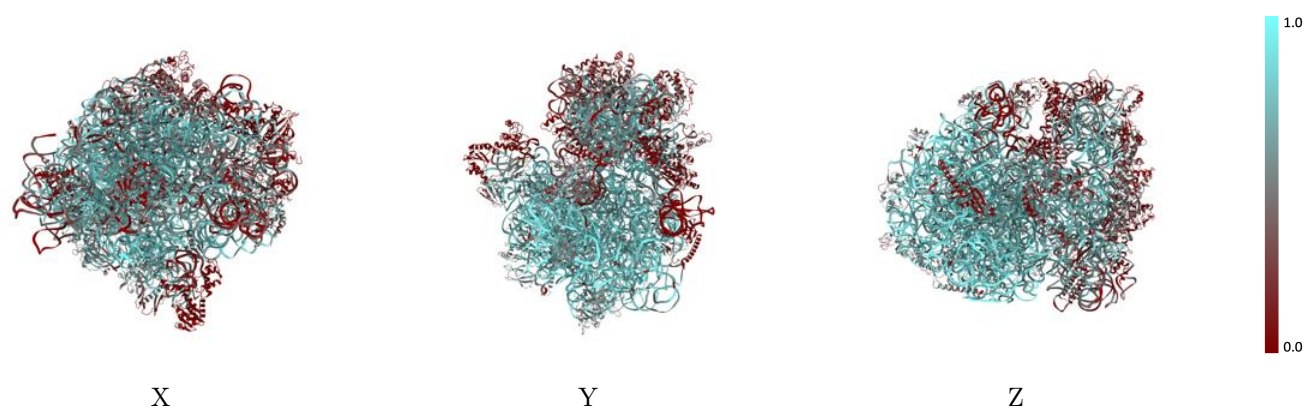
This section was not generated.

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



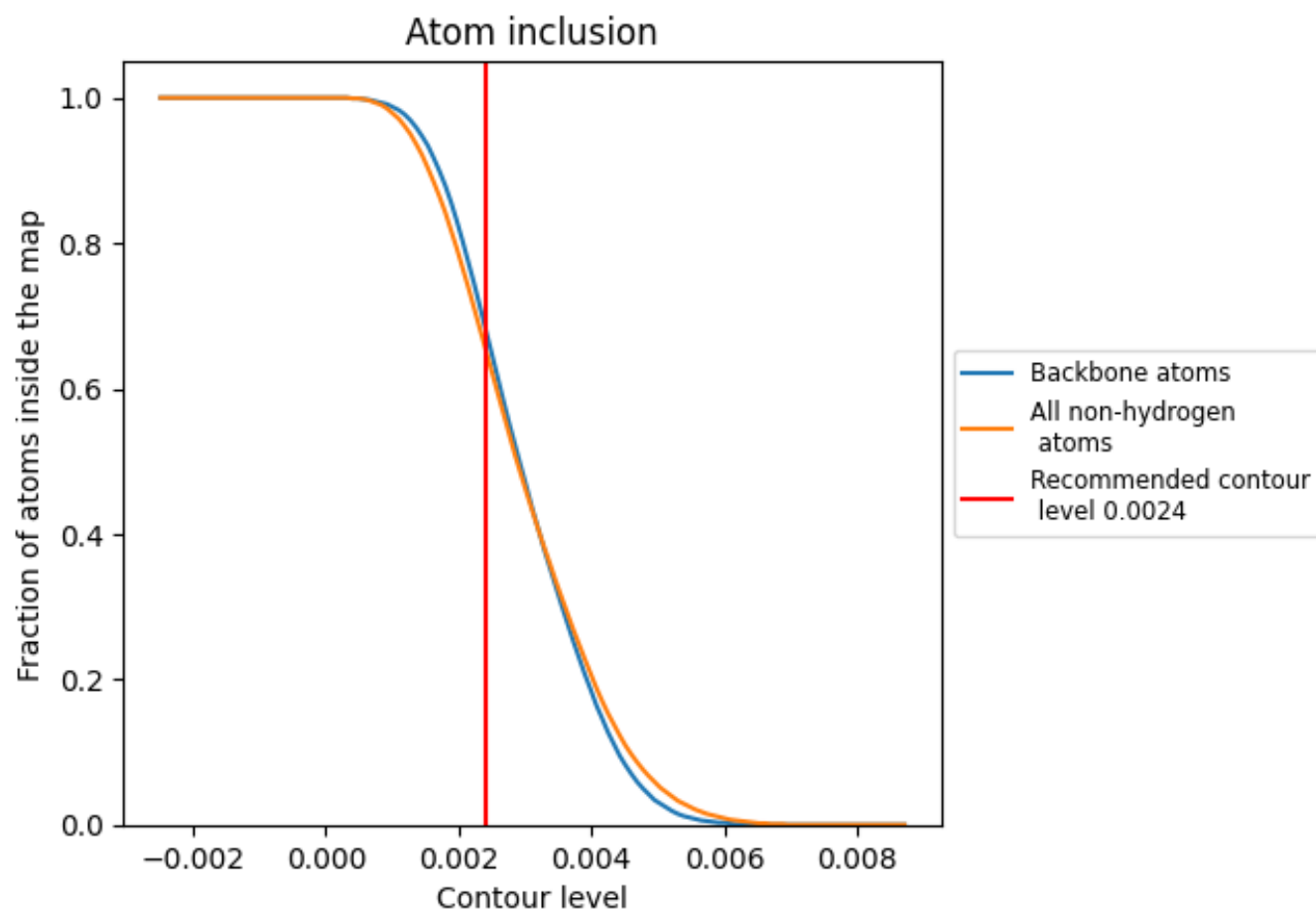
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0024).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 66% 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 (0.0024) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6560	 0.3850
0	 0.7400	 0.4890
1	 0.6250	 0.4890
2	 0.6550	 0.4960
3	 0.8260	 0.4190
4	 0.7900	 0.3920
5	 0.6650	 0.3330
7	 0.4130	 0.2870
A	 0.2560	 0.3130
B	 0.3260	 0.3640
C	 0.1810	 0.2840
D	 0.4440	 0.3790
E	 0.1370	 0.2990
F	 0.0730	 0.2520
G	 0.2910	 0.3320
H	 0.1410	 0.2910
I	 0.1610	 0.3110
J	 0.1810	 0.3320
K	 0.3930	 0.3910
L	 0.0730	 0.2260
M	 0.2420	 0.3610
N	 0.3160	 0.2880
O	 0.1970	 0.3180
P	 0.1890	 0.2940
Q	 0.2520	 0.3370
R	 0.0330	 0.2340
S	 0.2770	 0.2470
T	 0.3010	 0.3340
Y	 0.7680	 0.4050
Z	 0.4620	 0.4520
a	 0.6720	 0.4760
b	 0.6260	 0.4640
c	 0.6010	 0.4470
d	 0.3720	 0.3530
e	 0.4140	 0.4210



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.1360	 0.2600
g	 0.0150	 0.1680
h	 0.0000	 0.0500
i	 0.6360	 0.4600
j	 0.5840	 0.4740
k	 0.6070	 0.4570
l	 0.6540	 0.4710
m	 0.6380	 0.4660
n	 0.5490	 0.4160
o	 0.6020	 0.4660
p	 0.6540	 0.4630
q	 0.6110	 0.4780
r	 0.6660	 0.4580
s	 0.5760	 0.4550
t	 0.4690	 0.4420
u	 0.6070	 0.4830
v	 0.6210	 0.4680
w	 0.5150	 0.3970
x	 0.2290	 0.3570
y	 0.7030	 0.4800
z	 0.6010	 0.4670