



## wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 05:23 PM UTC

PDB ID : 7PAS / pdb\_00007pas  
EMDB ID : EMD-13282  
Title : 70S ribosome with P/E-site tRNA in Mycoplasma pneumoniae cells  
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.  
Deposited on : 2021-07-30  
Resolution : 16.00 Å (reported)  
Based on initial models : 4V7C, 7OOC, 7OOD

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

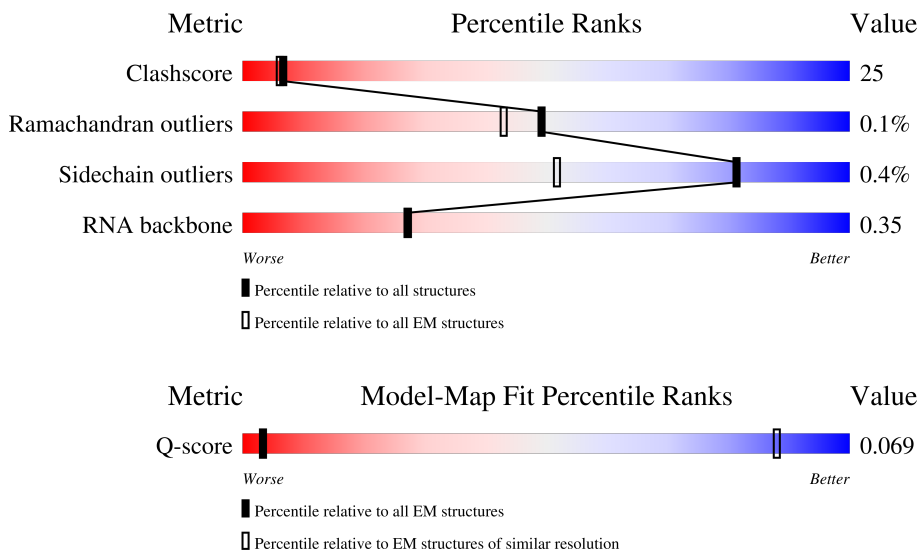
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 16.00 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	41 ( 15.50 - 16.50 )

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  $\geq 3$ , 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	48	
2	1	59	
3	2	37	

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Mol	Chain	Length	Quality of chain
4	A	294	
5	B	273	
6	C	205	
7	D	219	
8	E	215	
9	F	155	
10	G	142	
11	H	132	
12	I	108	
13	J	121	
14	K	139	
15	L	124	
16	M	61	
17	N	86	
18	O	94	
19	P	85	
20	Q	104	
21	R	87	
22	S	87	
23	T	60	
24	a	287	
25	b	287	
26	c	212	
27	d	180	
28	e	184	

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Mol	Chain	Length	Quality of chain
29	f	149	54% 64% 34%
30	g	161	38% 60% 18% 22%
31	h	137	53% 85% 8% 7%
32	i	146	8% 65% 34%
33	j	122	7% 63% 37%
34	k	151	65% 33%
35	l	139	53% 45%
36	m	124	61% 35%
37	n	116	7% 53% 43%
38	o	119	13% 54% 43%
39	p	127	9% 54% 35% 10%
40	q	100	18% 51% 48%
41	r	159	53% 34% 13%
42	s	237	22% 17% 61%
43	t	111	31% 73% 27%
44	u	104	56% 27% 17%
45	v	65	57% 40%
46	w	111	14% 59% 32% 10%
47	x	97	29% 42% 55%
48	y	57	7% 54% 37% 7%
49	z	53	57% 38% 6%
50	3	2907	17% 58% 24%
51	4	108	18% 56% 24%
52	5	1520	16% 60% 22%
53	8	76	25% 49% 22%

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 144440 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

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

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

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

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

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

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	240	1921	1226	334	352	9	0	0

- Molecule 5 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	B	215	1698	1073	313	307	5	0	0

- Molecule 6 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	C	203	1660	1051	314	290	5	0	0

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	D	153	1173	742	226	202	3	0	0

- Molecule 8 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	E	167	1362	857	240	263	2	0	0

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	F	154	1246	785	239	216	6	0	0

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	G	141	1110	723	193	192	2	0	0

- Molecule 11 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	H	128	1028	655	191	181	1	0	0

- Molecule 12 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	I	101	809	523	142	143	1	0	0

- Molecule 13 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	J	114	829	514	153	156	6	0	0

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	K	136	1076	680	213	181	2	0	0

- Molecule 15 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	L	118	951	594	191	166		0	0

- Molecule 16 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	M	60	474	302	96	72	4	0	0

- Molecule 17 is a protein called 30S ribosomal protein S15.

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

- Molecule 18 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	O	80	646	414	119	111	2	0	0

- Molecule 19 is a protein called 30S ribosomal protein S17.

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

- Molecule 20 is a protein called 30S ribosomal protein S18.

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

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 22 is a protein called 30S ribosomal protein S20.

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

- Molecule 23 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 24 is a protein called 50S ribosomal protein L2.

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

- Molecule 25 is a protein called 50S ribosomal protein L3.

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

- Molecule 26 is a protein called 50S ribosomal protein L4.

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

- Molecule 27 is a protein called 50S ribosomal protein L5.

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

- Molecule 28 is a protein called 50S ribosomal protein L6.

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

- Molecule 29 is a protein called 50S ribosomal protein L9.

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

- Molecule 30 is a protein called 50S ribosomal protein L10.

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

- Molecule 31 is a protein called 50S ribosomal protein L11.

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

- Molecule 32 is a protein called 50S ribosomal protein L13.

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

- Molecule 33 is a protein called 50S ribosomal protein L14.

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

- Molecule 34 is a protein called 50S ribosomal protein L15.

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

- Molecule 35 is a protein called 50S ribosomal protein L16.

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

- Molecule 36 is a protein called 50S ribosomal protein L17.

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

- Molecule 37 is a protein called 50S ribosomal protein L18.

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

- Molecule 38 is a protein called 50S ribosomal protein L19.

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

- Molecule 39 is a protein called 50S ribosomal protein L20.

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

- Molecule 40 is a protein called 50S ribosomal protein L21.

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

- Molecule 41 is a protein called 50S ribosomal protein L22.

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

- Molecule 42 is a protein called 50S ribosomal protein L23.

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

- Molecule 43 is a protein called 50S ribosomal protein L24.

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

- Molecule 44 is a protein called 50S ribosomal protein L27.

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

- Molecule 45 is a protein called 50S ribosomal protein L28.

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

- Molecule 46 is a protein called 50S ribosomal protein L29.

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

- Molecule 47 is a protein called 50S ribosomal protein L31.

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

- Molecule 48 is a protein called 50S ribosomal protein L32.

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

- Molecule 49 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 50 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

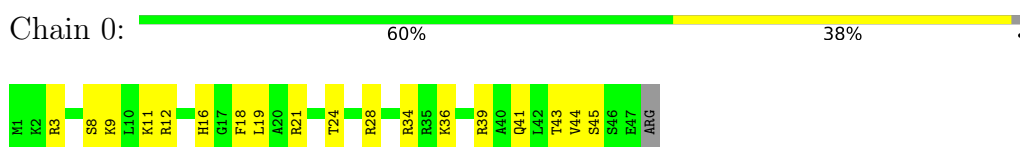
- Molecule 53 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	8	73	Total	C	N	O	P	0	0
			1556	695	278	511	72		

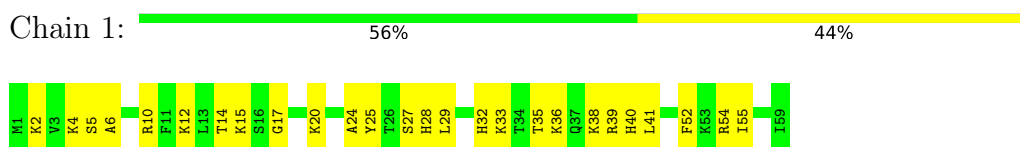
### 3 Residue-property plots

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.

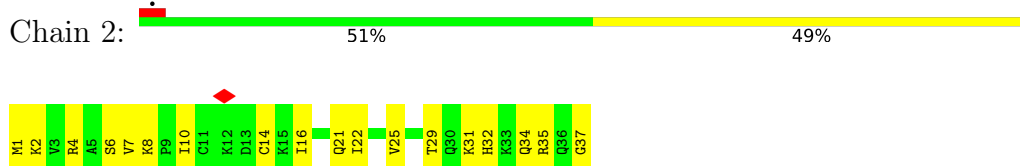
- Molecule 1: 50S ribosomal protein L34



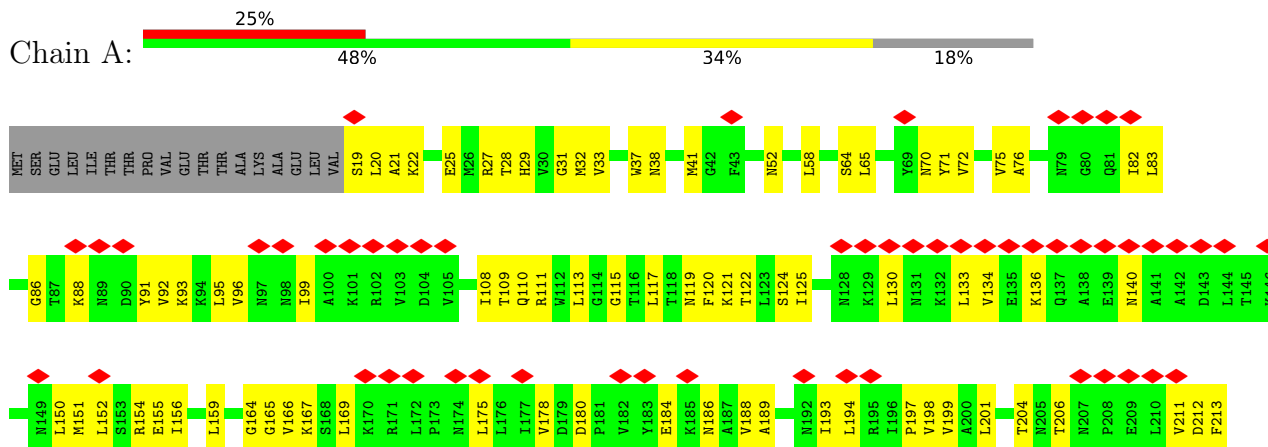
- Molecule 2: 50S ribosomal protein L35

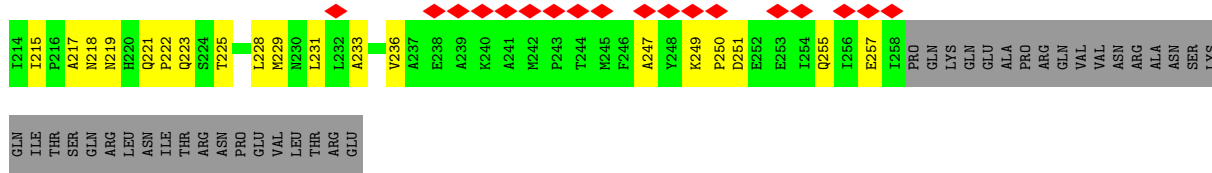


- Molecule 3: 50S ribosomal protein L36

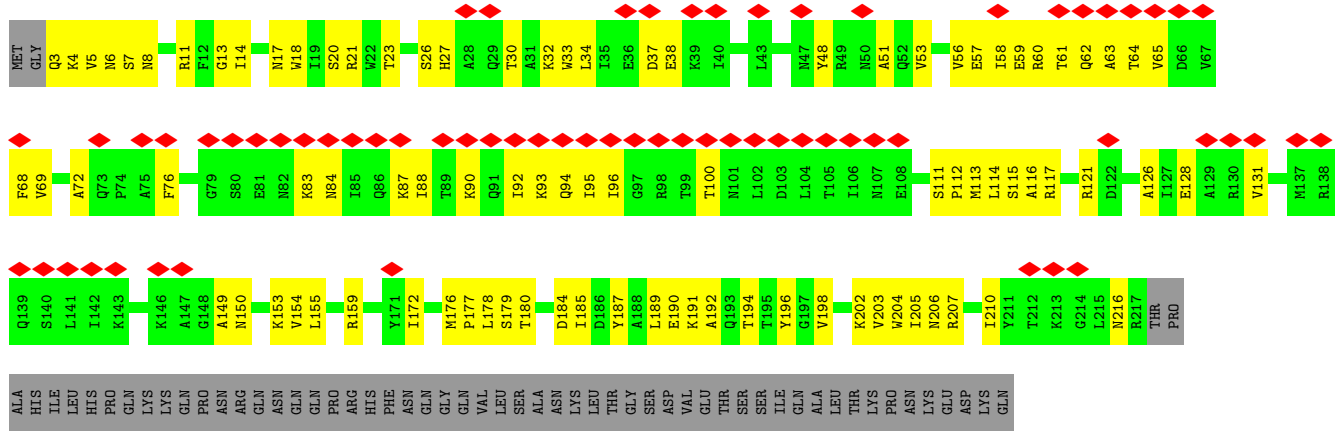


- Molecule 4: 30S ribosomal protein S2

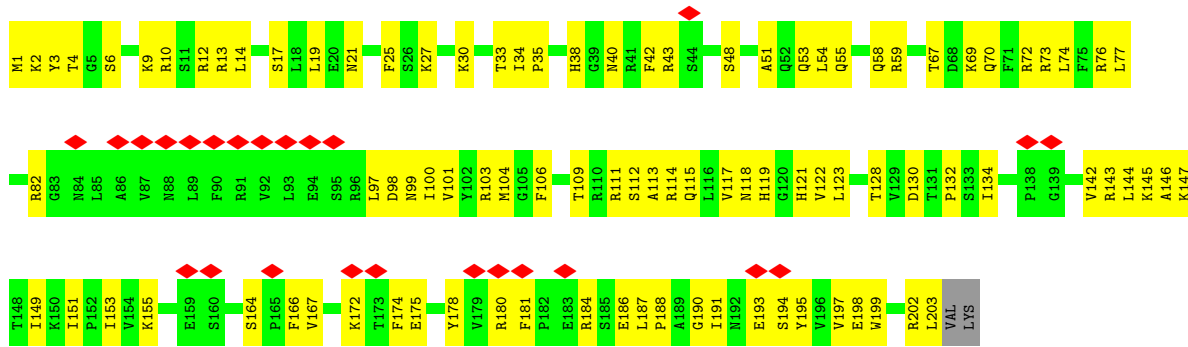




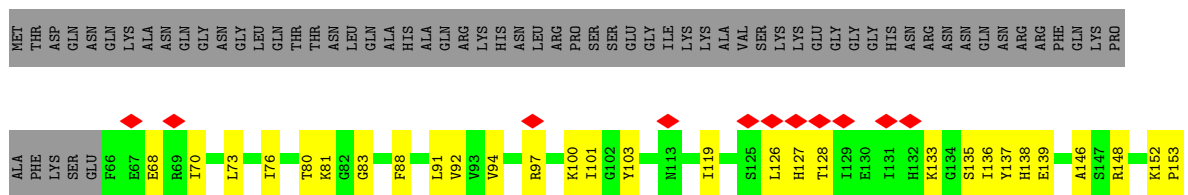
• Molecule 5: 30S ribosomal protein S3

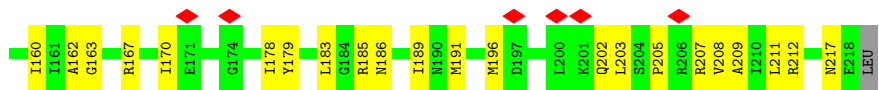


• Molecule 6: 30S ribosomal protein S4



• Molecule 7: 30S ribosomal protein S5

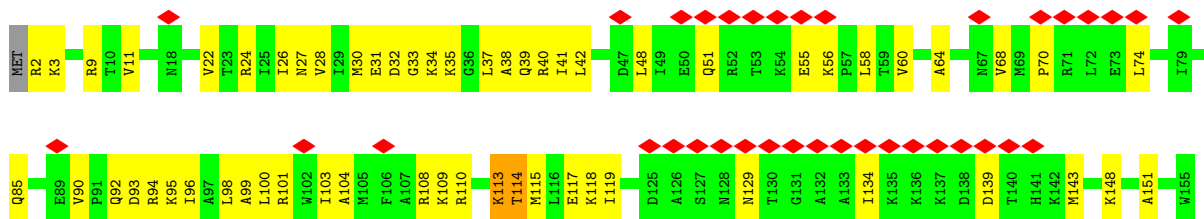




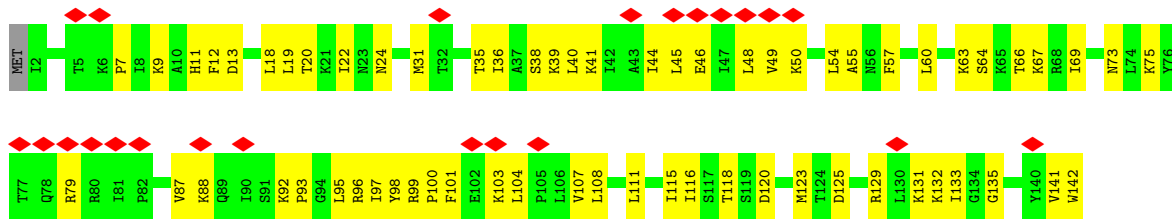
• Molecule 8: 30S ribosomal protein S6



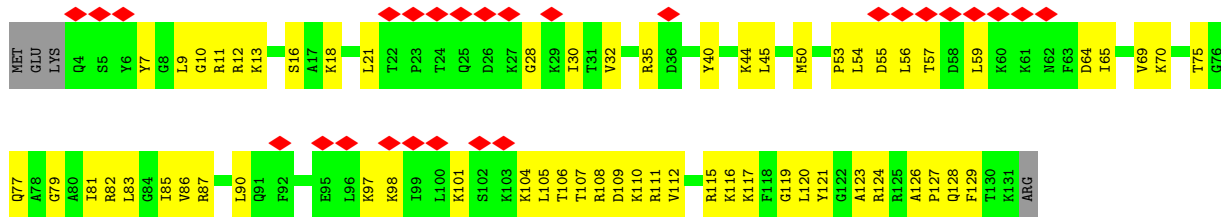
• Molecule 9: 30S ribosomal protein S7



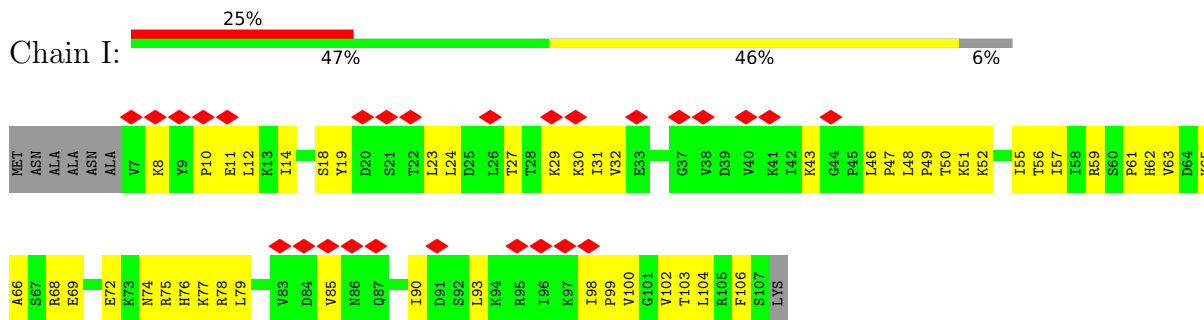
• Molecule 10: 30S ribosomal protein S8



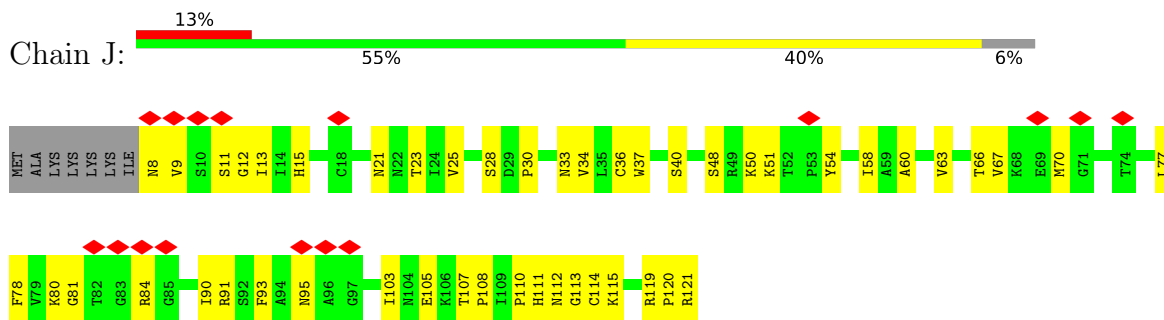
• Molecule 11: 30S ribosomal protein S9



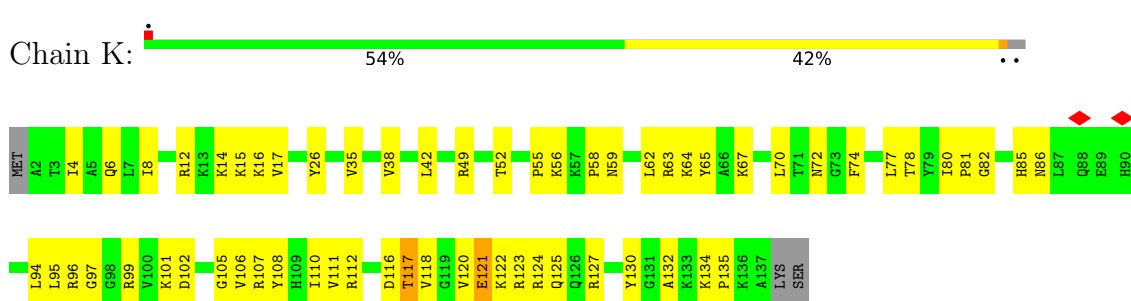
• Molecule 12: 30S ribosomal protein S10



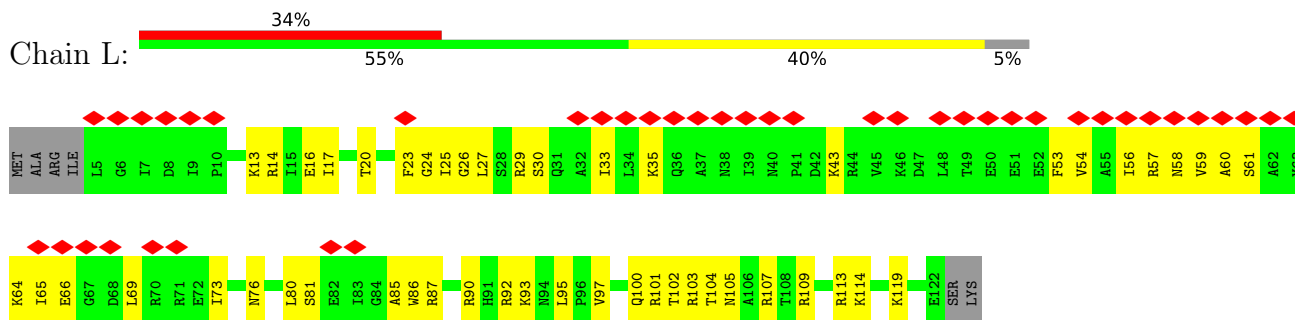
• Molecule 13: 30S ribosomal protein S11



• Molecule 14: 30S ribosomal protein S12



• Molecule 15: 30S ribosomal protein S13

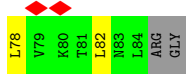
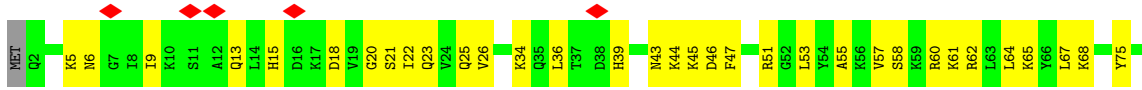


• Molecule 16: 30S ribosomal protein S14 type Z

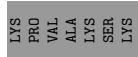
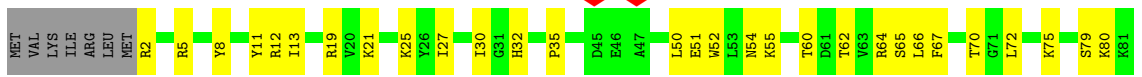




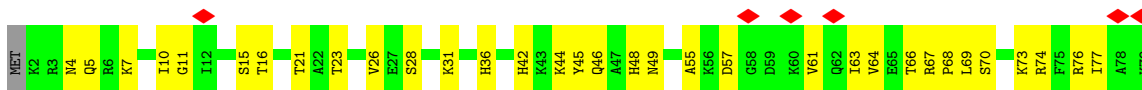
• Molecule 17: 30S ribosomal protein S15



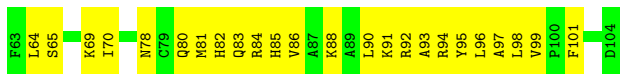
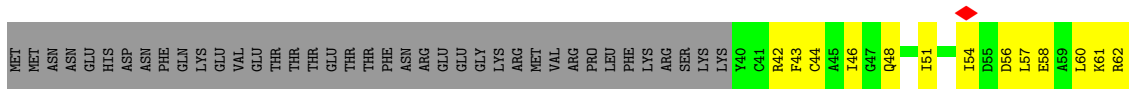
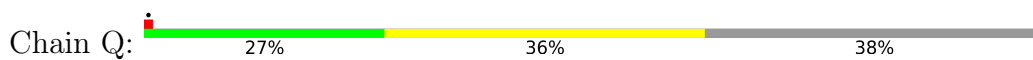
• Molecule 18: 30S ribosomal protein S16



• Molecule 19: 30S ribosomal protein S17



• Molecule 20: 30S ribosomal protein S18

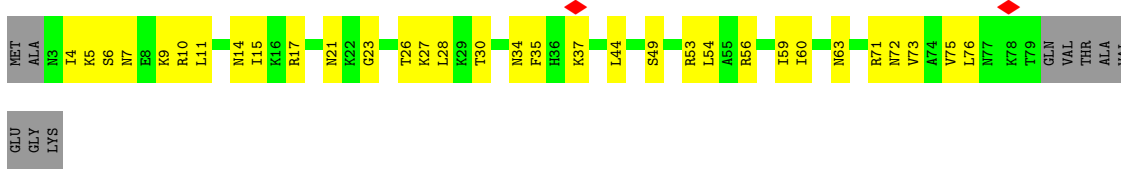


• Molecule 21: 30S ribosomal protein S19

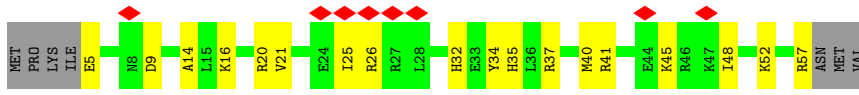




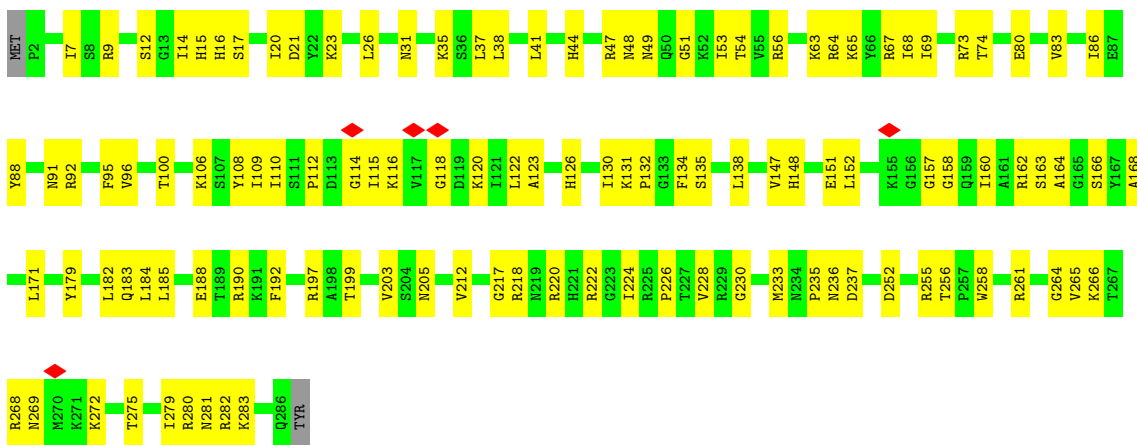
• Molecule 22: 30S ribosomal protein S20



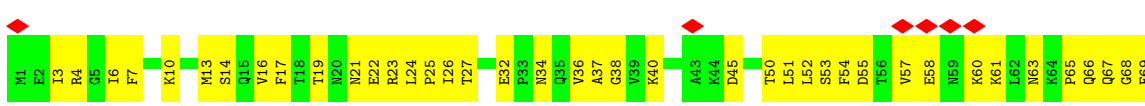
• Molecule 23: 30S ribosomal protein S21

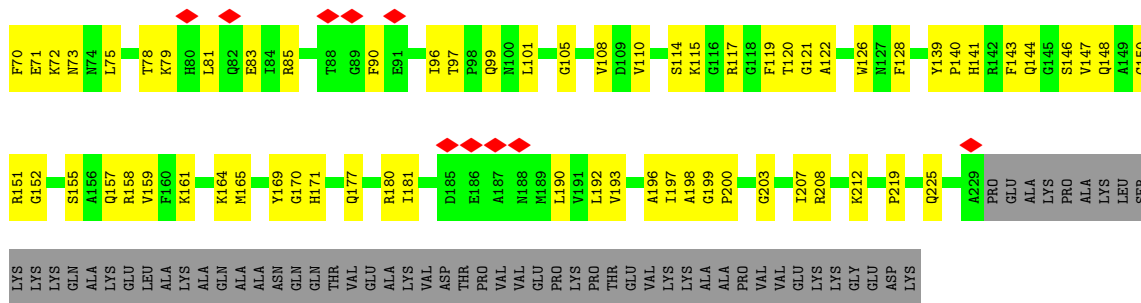


• Molecule 24: 50S ribosomal protein L2

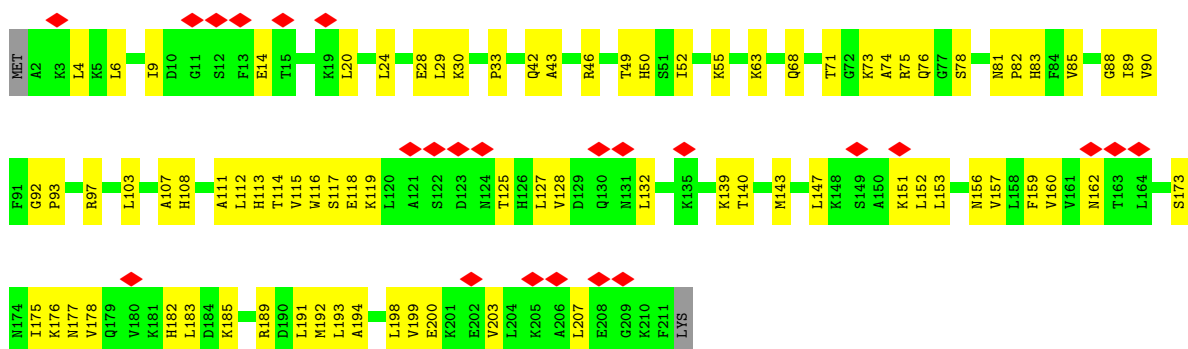


• Molecule 25: 50S ribosomal protein L3

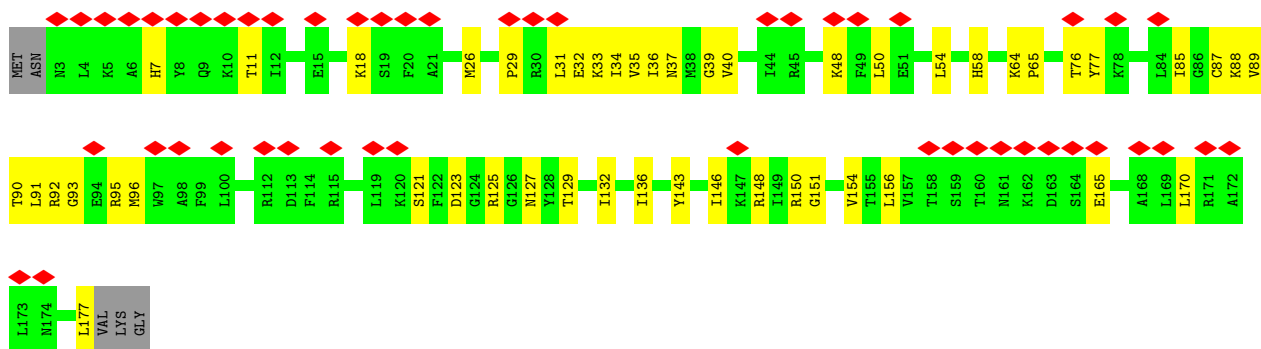




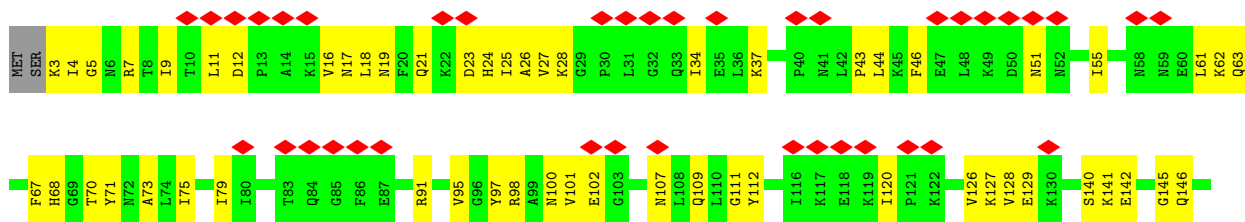
• Molecule 26: 50S ribosomal protein L4

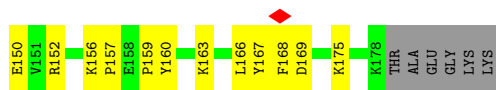


• Molecule 27: 50S ribosomal protein L5

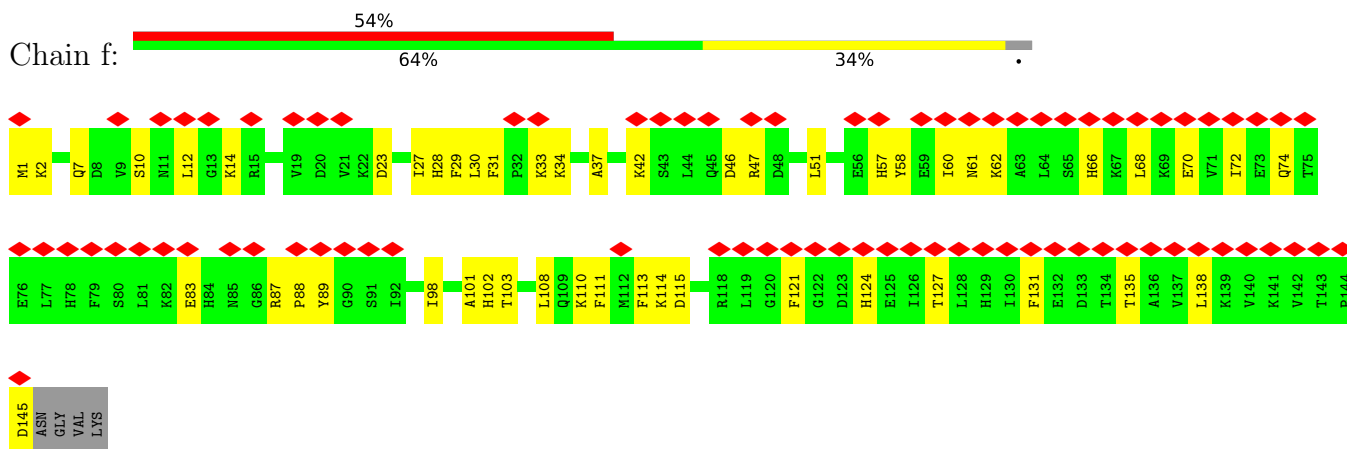


• Molecule 28: 50S ribosomal protein L6

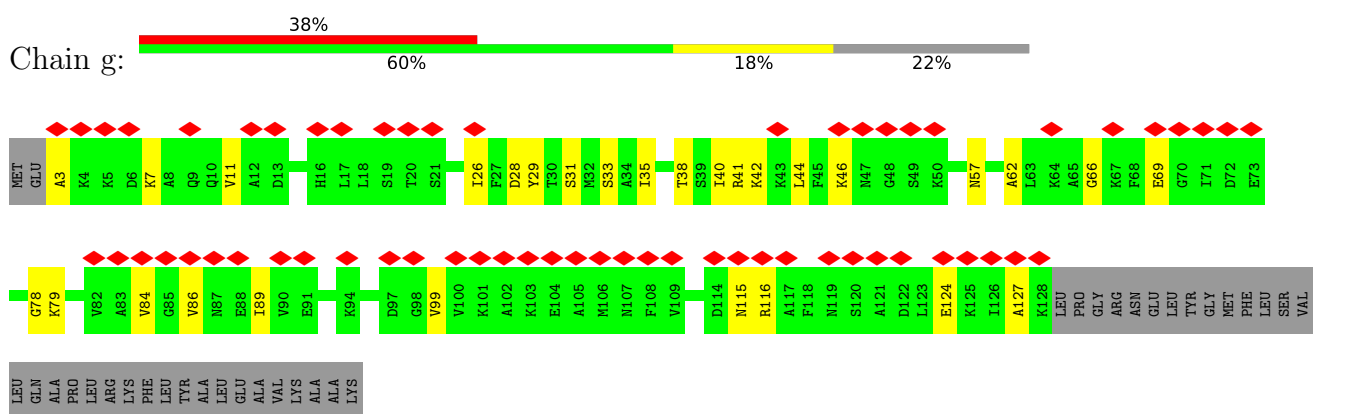




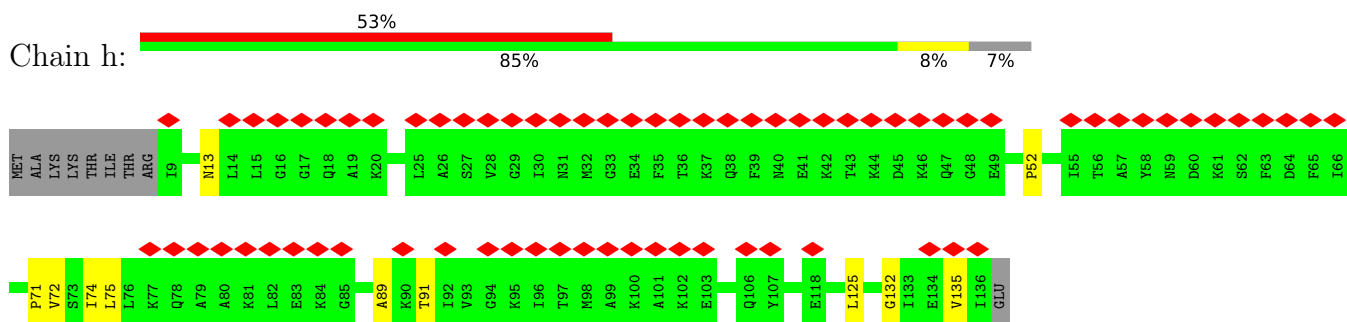
• Molecule 29: 50S ribosomal protein L9



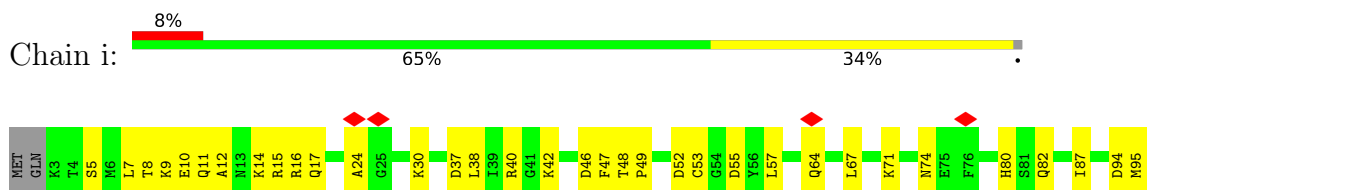
• Molecule 30: 50S ribosomal protein L10



• Molecule 31: 50S ribosomal protein L11

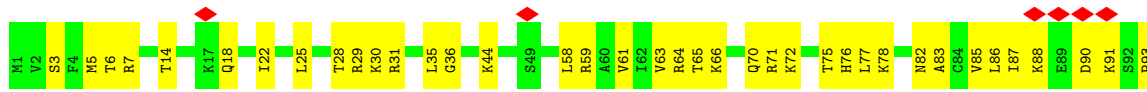


• Molecule 32: 50S ribosomal protein L13

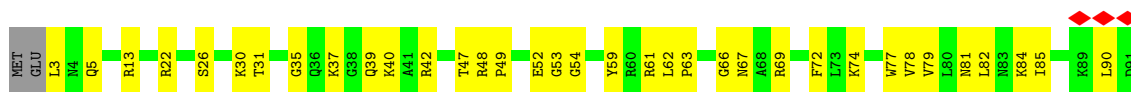




- Molecule 33: 50S ribosomal protein L14



- Molecule 34: 50S ribosomal protein L15



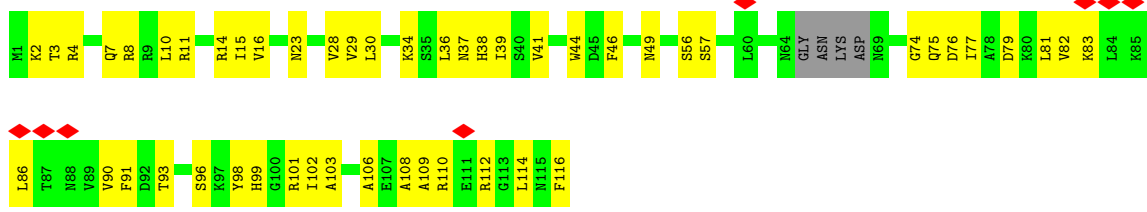
- Molecule 35: 50S ribosomal protein L16



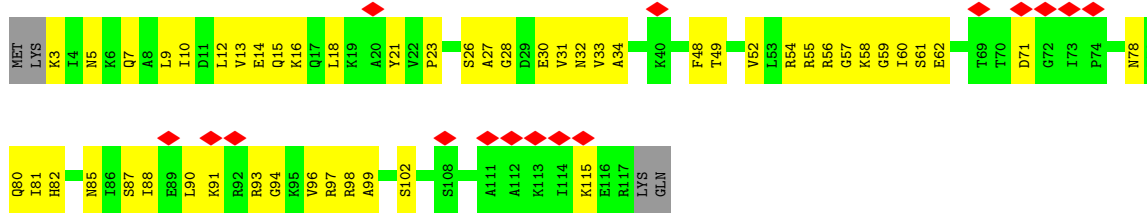
- Molecule 36: 50S ribosomal protein L17



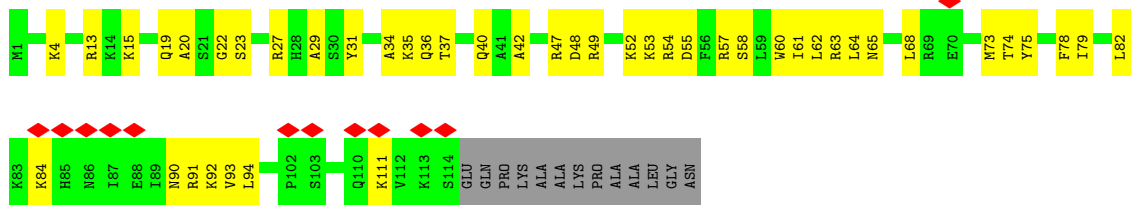
- Molecule 37: 50S ribosomal protein L18



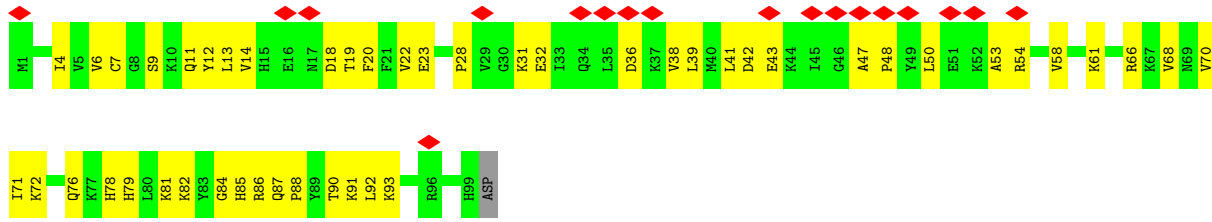
• Molecule 38: 50S ribosomal protein L19



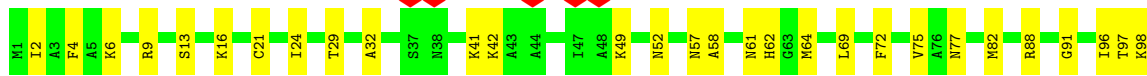
• Molecule 39: 50S ribosomal protein L20



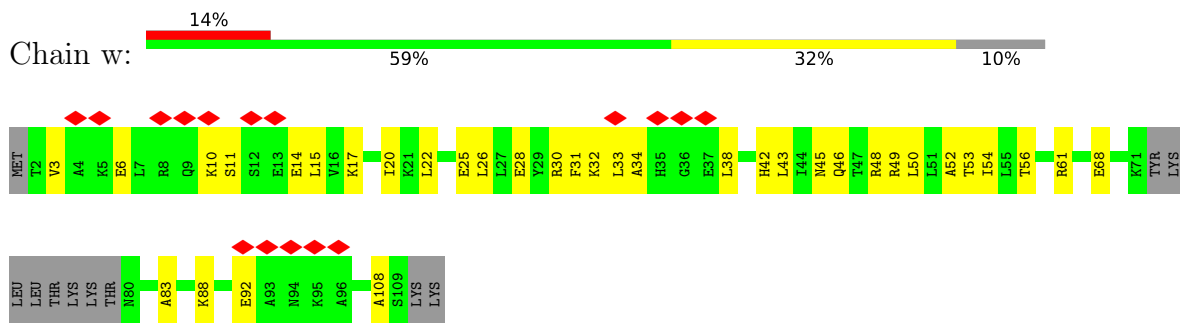
• Molecule 40: 50S ribosomal protein L21



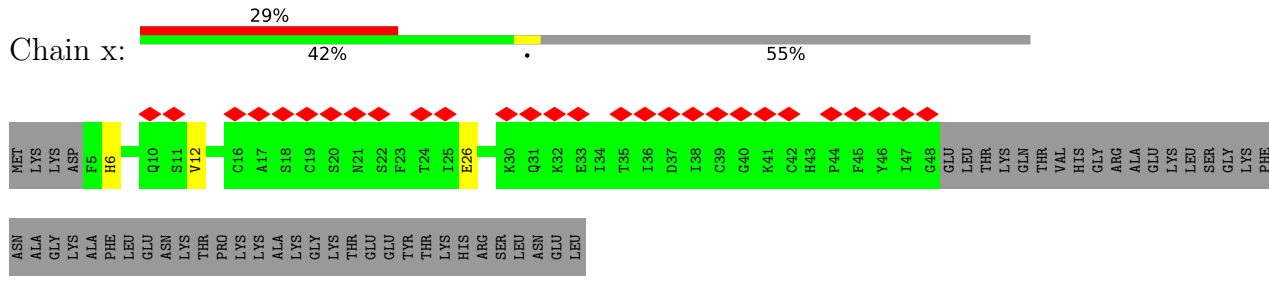
• Molecule 41: 50S ribosomal protein L22



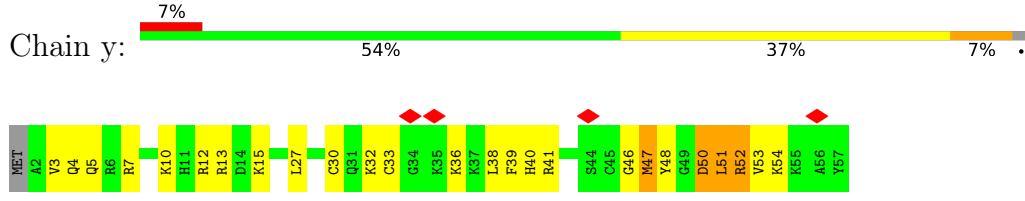




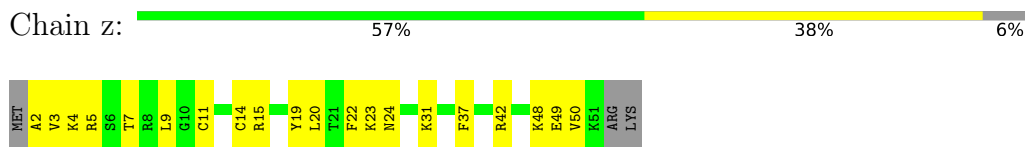
• Molecule 47: 50S ribosomal protein L31



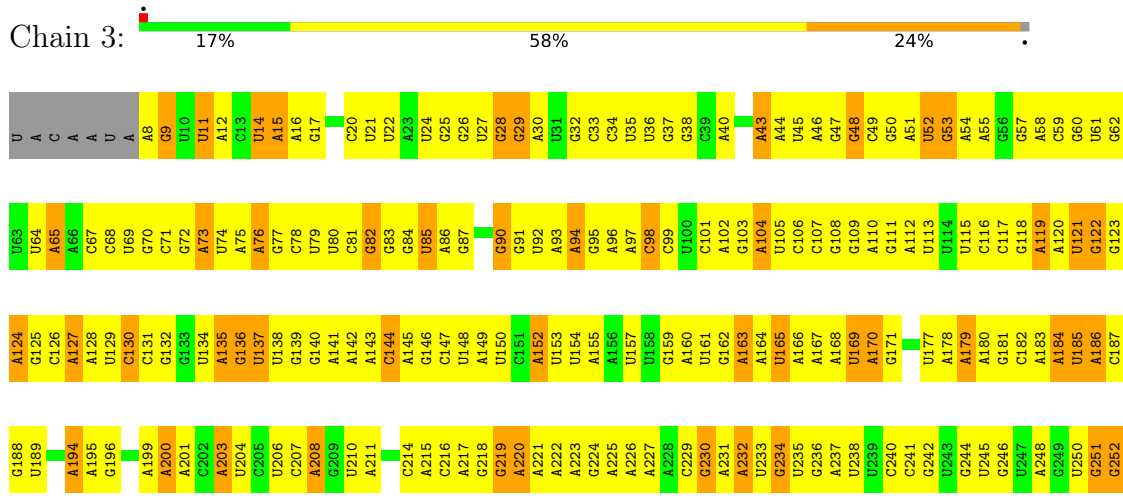
• Molecule 48: 50S ribosomal protein L32



• Molecule 49: 50S ribosomal protein L33 1



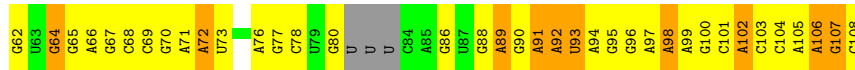
• Molecule 50: 23S ribosomal RNA



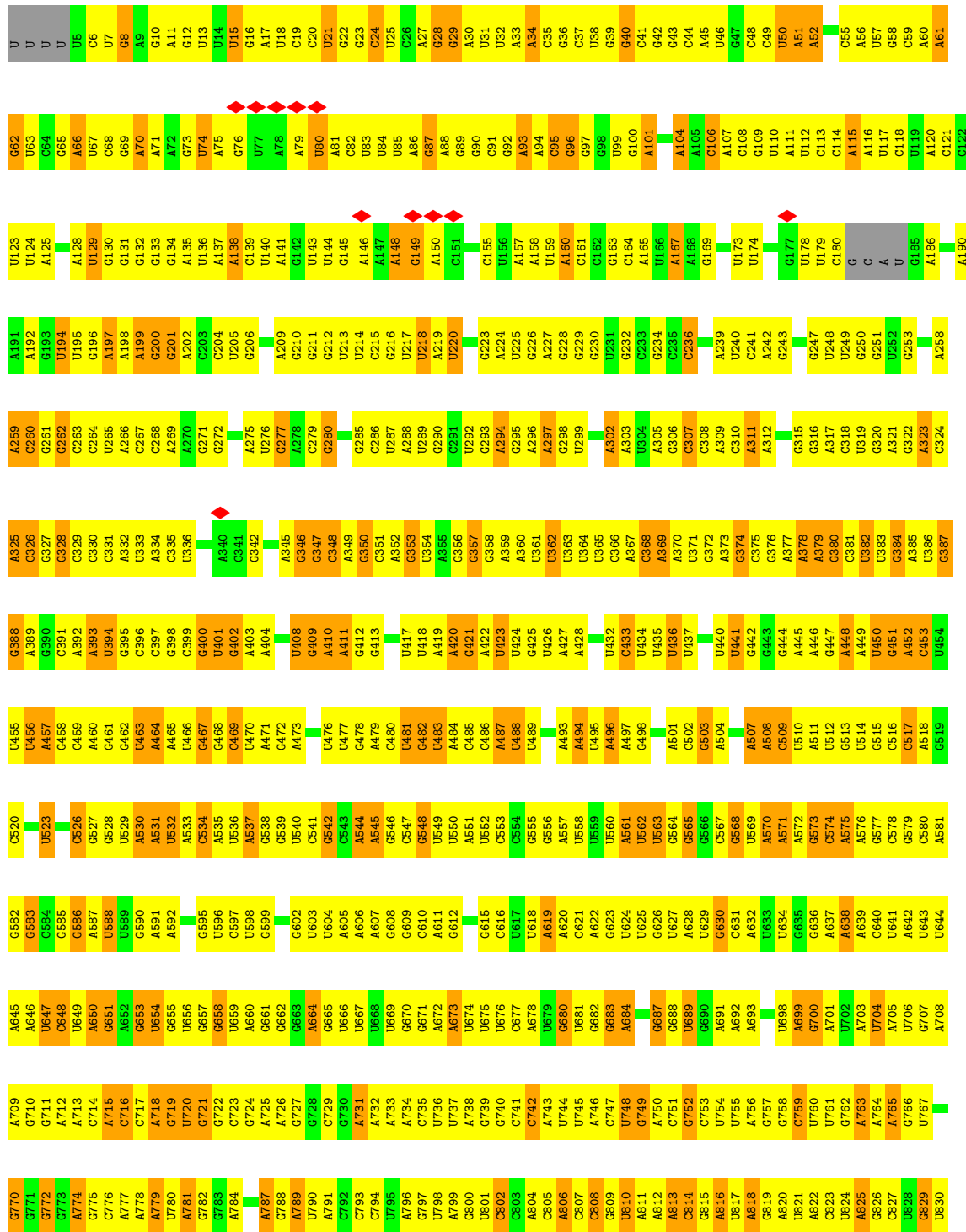
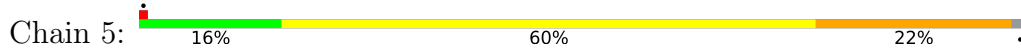


U2093	A2030	C1969	A1903	U1841	G1779	U1714	C1849	U1586	U1522	A1455	C1390	U1330	G1266	G1203
A2094	C2031	C1970	G1904	G1842	A1780	A1715	A1650	U1587	C1523	C1456	U1391	G1331	A1267	A1204
U2096	G2032	G1971	U1905	C1844	C1781	C1716	A1651	A1588	G1524	A1457	G1392	G1332	C1268	A1208
A2097	G2033	C1972	G1906	C1844	A1652	C1717	A1652	A1589	G1525	A1458	A1393	C1333	C1269	U1209
U2098	G2034	U1973	C1907	C1845	G1783	G1718	G1654	U1590	U1526	A1459	A1396	U1334	U1210	U1210
U2099	U2035	U1974	A1908	A1846	U1784	G1720	U1655	C1591	U1527	G1460	A1397	A1335	U1211	U1211
G2100	G2036	G1975	C1909	G1847	U1785	G1721	U1655	A1592	U1528	A1461	C1398	A1336	C1275	U1212
A2101	A2037	A1976	G1910	U1848	U1786	A1722	A1656	U1593	U1529	A1462	G1399	G1337	A1276	C1213
U2102	A2038	A1977	G1911	G1849	U1787	A1723	G1657	G1594	G1530	A1463	U1399	G1338	A1277	U1213
C2103	G2039	U1978	C1912	C1850	A1724	G1724	U1658	C1595	C1531	G1464	U1340	U1339	G1278	G1214
A2104	C2041	U1979	G1913	U1851	C1789	G1725	C1659	U1596	A1532	G1465	A1401	U1340	U1279	U1215
C2105	A2042	G1982	C1914	G1852	U1790	U1726	A1660	U1597	U1533	U1466	G1402	U1341	G1280	G1216
G2106	C2043	U1983	C1915	G1853	A1791	U1727	A1661	U1598	A1534	U1467	G1403	C1342	A1281	U1217
A2107	C2044	A1884	C1916	A1854	A1792	G1728	G1662	C1599	A1535	U1468	C1343	C1343	G1282	G1218
A2109	C2045	A1885	G1917	A1855	A1793	G1729	G1663	A1600	C1536	A1469	A1406	U1344	A1283	U1219
U2110	G2046	G1986	U1918	G1856	A1794	C1730	A1666	A1601	U1537	C1470	U1407	U1345	A1284	A1220
U2111	A2049	A1987	A1920	G1857	C1795	G1731	G1667	G1602	U1538	C1471	G1408	U1346	U1285	G1221
A2112	G2050	U1988	C1921	A1859	C1797	G1733	G1668	A1604	G1540	U1478	A1412	A1347	G1286	A1222
U2113	C2051	A1860	A1735	A1861	A1798	A1734	A1669	A1605	A1541	A1479	A1413	C1348	C1287	C1223
C2114	U1924	A1862	U1736	G1862	U1801	G1736	U1670	A1606	A1542	U1478	A1414	C1349	C1288	G1224
A2115	A1925	A1863	G1737	G1863	C1802	G1737	C1671	G1607	U1543	U1481	A1415	G1351	G1290	C1227
U2116	G2052	A1864	G1738	C1864	U1803	G1738	C1672	C1608	G1544	U1482	G1416	U1352	C1291	G1228
A2055	A2055	A1865	A1804	A1865	A1804	G1746	A1673	U1609	A1545	G1483	G1417	U1353	A1292	U1229
A2056	G1928	G1866	U1805	G1866	U1805	G1747	A1674	U1610	U1546	G1484	U1426	U1361	U1293	U1230
C2057	C1932	A1867	U1806	G1867	U1806	U1748	G1675	U1611	U1547	A1485	A1420	C1362	G1294	G1231
U2058	U1868	A1868	C1807	G1868	C1807	U1742	G1676	U1612	A1548	U1486	A1421	U1366	A1295	U1232
G2059	A1935	A1869	U1808	G1869	U1808	U1744	G1677	A1613	U1549	U1487	A1422	U1367	A1296	A1233
G2060	U1936	G1870	A1909	G1870	A1909	U1745	A1680	G1614	U1550	U1488	A1423	U1358	U1297	U1234
A2061	G1937	U1871	U1871	G1871	U1871	U1746	A1681	G1615	G1551	G1489	A1424	U1359	A1298	U1235
C2062	U1938	U1872	U1872	G1872	C1812	G1747	C1682	U1616	C1552	G1490	U1425	U1360	U1299	U1236
G2063	C2003	A1873	G1814	G1873	C1813	U1748	G1683	U1618	U1554	G1492	C1427	U1362	G1301	G1237
A2065	A1939	A1874	U1815	A1874	U1815	U1752	A1684	A1620	A1556	U1493	G1428	U1363	G1302	A1238
A2066	G1940	A1875	U1816	G1875	U1816	G1753	U1685	A1621	U1557	A1495	G1429	U1364	U1303	U1240
A2067	C1941	A1876	U1817	G1876	U1817	U1754	U1686	U1622	G1557	A1496	U1430	G1365	U1304	U1241
G2068	A1944	A1877	U1818	G1877	U1818	A1755	A1688	C1623	A1558	A1497	A1431	U1366	G1305	G1242
A2069	U1879	A1878	G1819	A1878	U1819	U1756	A1689	U1623	A1559	U1498	C1432	U1367	G1306	A1243
U2070	U1945	G1880	U1820	G1880	U1820	G1757	A1690	C1626	U	C1499	U1433	U1368	G1307	A1244
A2071	U1946	C1881	G1821	G1881	G1821	C1758	C1690	U1627	G	C1500	U1434	U1369	A1308	G1245
G2072	C1948	A1883	U1822	G1883	U1822	C1759	A1692	G1628	A	A1500	A1435	A1370	G1309	U1246
A2136	C1949	A1884	U1823	G1884	U1823	G1760	U1693	U1629	C	U1501	C1436	G1371	U1310	C1247
C2013	G1952	G1885	G1824	G1885	U1824	C1761	A1694	U1632	U	A1502	A1437	U1372	G1311	A1248
U2075	U1953	C1886	U1825	G1886	U1825	A1762	G1695	C1632	A	A1503	G1438	C1373	A1312	A1249
G2076	C1954	U1887	A1826	G1887	A1826	U1763	C1696	C1633	U	G1504	U1439	U1374	G1313	A1250
A2077	U1955	U1888	U1827	G1888	U1827	U1764	C1697	A1634	C	G1505	U1440	G1375	C1314	A1251
A2078	G1956	U1889	U1828	G1889	U1828	G1765	A1698	U1637	A	U1506	G1442	G1376	C1317	G1253
G2079	U1958	A1890	U1829	G1890	U1829	A1766	A1699	A1643	U	G1507	A1443	A1377	U1318	U1254
C2080	A1959	A1891	G1830	G1891	U1830	A1767	A1700	A1644	C	U1509	G1444	C1378	C1319	G1255
U2081	A1892	A1892	G1831	G1892	U1831	G1768	G1701	C1638	G1571	U1510	U1445	U1380	C1320	A1256
A2021	A1960	C1893	U1832	G1893	U1832	A1769	A1702	C1639	U	A1511	G1446	U1381	G1321	G1257
A2022	A1961	U1894	G1833	G1894	U1833	A1770	A1703	A1641	G1577	A1513	U1447	A1382	A1322	C1258
U2023	U1962	G1895	U1834	G1895	U1834	C1771	A1706	G1642	A1578	U1514	U1448	G1383	A1323	A1259
C2024	U1963	A1896	G1835	G1896	U1835	G1774	U1707	A1643	G1580	G1517	G1449	U1384	A1324	U1260
G2025	C1964	C1897	A1836	G1897	U1836	G1775	G1708	A1644	U1581	G1518	G1450	U1385	C1325	U1261
A2026	C1965	C1899	C1837	G1899	U1837	G1776	C1709	G1645	U1581	C1518	A1451	G1386	C1326	G1262
G2027	U1966	A1900	C1838	G1900	U1838	G1777	C1709	G1646	U1584	A1519	G1452	U1387	G1327	U1263
G2028	U1967	C1901	C1839	G1901	U1839	G1778	C1710	A1647	A1585	A1521	U1453	G1388	A1328	U1264
U2029	C1968	C1902	C1840	G1902	U1840	G1778	U1713	A1648	U1585	A1521	G1454	U1389	U1329	G1265





• Molecule 52: 16S ribosomal RNA





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	675	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	0.831	Depositor
Minimum map value	-0.134	Depositor
Average map value	0.024	Depositor
Map value standard deviation	0.100	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	0	0.13	0/383	0.40	0/504
2	1	0.13	0/484	0.39	0/637
3	2	0.16	0/306	0.42	0/401
4	A	0.15	0/1954	0.42	0/2642
5	B	0.14	0/1721	0.40	1/2323 (0.0%)
6	C	0.15	0/1691	0.44	0/2267
7	D	0.15	0/1188	0.44	0/1593
8	E	0.15	0/1384	0.43	0/1867
9	F	0.15	0/1266	0.48	0/1700
10	G	0.16	0/1126	0.44	0/1517
11	H	0.16	0/1044	0.50	0/1395
12	I	0.17	0/820	0.43	0/1103
13	J	0.17	0/844	0.46	0/1136
14	K	0.31	0/1094	0.56	0/1468
15	L	0.16	0/962	0.45	0/1289
16	M	0.16	0/483	0.45	0/643
17	N	0.15	0/679	0.43	0/907
18	O	0.16	0/659	0.49	0/885
19	P	0.14	0/684	0.44	0/913
20	Q	0.13	0/545	0.45	0/730
21	R	0.17	0/698	0.48	0/936
22	S	0.15	0/631	0.40	0/838
23	T	0.12	0/475	0.36	0/621
24	a	0.16	0/2267	0.44	0/3044
25	b	0.15	0/1795	0.42	0/2412
26	c	0.13	0/1671	0.44	2/2246 (0.1%)
27	d	0.14	0/1409	0.43	0/1894
28	e	0.16	0/1420	0.42	0/1912
29	f	0.18	0/1183	0.45	0/1587
30	g	0.53	0/969	0.86	0/1295
31	h	0.17	0/968	0.56	1/1298 (0.1%)
32	i	0.13	0/1186	0.36	0/1592
33	j	0.13	0/953	0.38	0/1275
34	k	0.13	0/1170	0.40	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	l	0.16	0/1104	0.45	0/1481
36	m	0.13	0/973	0.40	0/1309
37	n	0.15	0/897	0.51	0/1198
38	o	0.15	0/948	0.42	0/1262
39	p	0.14	0/961	0.40	0/1278
40	q	0.17	0/828	0.48	0/1111
41	r	0.14	0/1077	0.44	0/1441
42	s	0.14	0/732	0.45	0/988
43	t	0.16	0/879	0.42	0/1165
44	u	0.15	0/665	0.42	0/884
45	v	0.14	0/519	0.41	0/695
46	w	0.13	0/826	0.40	0/1104
47	x	0.12	0/353	0.37	0/474
48	y	0.31	0/457	0.73	1/601 (0.2%)
49	z	0.16	0/412	0.41	0/547
50	3	0.11	0/69073	0.28	0/107710
51	4	0.11	0/2505	0.31	0/3902
52	5	0.11	0/35768	0.28	0/55764
53	8	0.12	0/1739	0.30	0/2710
All	All	0.13	0/156828	0.34	5/234053 (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
6	C	0	1
9	F	0	1
21	R	0	1
37	n	0	1
All	All	0	4

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	h	74	ILE	N-CA-C	-8.33	105.80	113.71
48	y	50	ASP	CA-CB-CG	-7.14	105.46	112.60
26	c	63	LYS	CA-C-N	-6.54	112.52	121.61
26	c	63	LYS	C-N-CA	-6.54	112.52	121.61
5	B	14	ILE	N-CA-C	-5.24	108.73	113.71

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	19	LEU	Peptide
9	F	113	LYS	Peptide
21	R	25	GLN	Peptide
37	n	90	VAL	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	380	0	429	24	0
2	1	477	0	530	25	0
3	2	304	0	350	19	0
4	A	1921	0	1973	70	0
5	B	1698	0	1768	85	0
6	C	1660	0	1719	94	0
7	D	1173	0	1267	45	0
8	E	1362	0	1377	41	0
9	F	1246	0	1308	54	0
10	G	1110	0	1226	61	0
11	H	1028	0	1094	64	0
12	I	809	0	894	53	0
13	J	829	0	855	51	0
14	K	1076	0	1170	61	0
15	L	951	0	1014	64	0
16	M	474	0	509	50	0
17	N	673	0	730	38	0
18	O	646	0	677	30	0
19	P	675	0	728	28	0
20	Q	535	0	562	41	0
21	R	682	0	691	38	0
22	S	629	0	681	32	0
23	T	471	0	522	17	0
24	a	2225	0	2301	104	0
25	b	1762	0	1808	103	0
26	c	1644	0	1731	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	d	1388	0	1469	37	0
28	e	1396	0	1481	61	0
29	f	1160	0	1172	42	0
30	g	960	0	1014	13	0
31	h	959	0	1039	8	0
32	i	1164	0	1192	54	0
33	j	944	0	1019	50	0
34	k	1153	0	1256	59	0
35	l	1079	0	1134	56	0
36	m	958	0	1011	39	0
37	n	889	0	952	46	0
38	o	938	0	1008	53	0
39	p	947	0	1028	54	0
40	q	811	0	858	45	0
41	r	1068	0	1150	57	0
42	s	720	0	803	43	0
43	t	872	0	972	26	0
44	u	657	0	695	26	0
45	v	513	0	560	24	0
46	w	818	0	870	31	0
47	x	344	0	333	2	0
48	y	452	0	472	28	0
49	z	408	0	440	21	0
50	3	61664	0	30954	2662	0
51	4	2239	0	1137	88	0
52	5	31943	0	16058	1559	0
53	8	1556	0	788	34	0
All	All	144440	0	98779	5664	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 25.

The worst 5 of 5664 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)
50:3:314:G:H1	50:3:392:A:N6	1.37	1.21
52:5:684:A:H62	52:5:700:G:N2	1.49	1.11
50:3:496:A:H62	50:3:505:G:N2	1.49	1.10
50:3:1798:A:N6	50:3:1835:G:C2	2.19	1.09
52:5:661:G:H1	52:5:738:A:N6	1.50	1.09

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	45/48 (94%)	41 (91%)	4 (9%)	0	100	100
2	1	57/59 (97%)	55 (96%)	2 (4%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	A	238/294 (81%)	216 (91%)	22 (9%)	0	100	100
5	B	213/273 (78%)	201 (94%)	12 (6%)	0	100	100
6	C	201/205 (98%)	182 (90%)	18 (9%)	1 (0%)	24	63
7	D	151/219 (69%)	140 (93%)	11 (7%)	0	100	100
8	E	165/215 (77%)	149 (90%)	16 (10%)	0	100	100
9	F	152/155 (98%)	134 (88%)	16 (10%)	2 (1%)	9	42
10	G	139/142 (98%)	128 (92%)	11 (8%)	0	100	100
11	H	126/132 (96%)	110 (87%)	16 (13%)	0	100	100
12	I	99/108 (92%)	82 (83%)	17 (17%)	0	100	100
13	J	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
14	K	134/139 (96%)	118 (88%)	16 (12%)	0	100	100
15	L	116/124 (94%)	107 (92%)	9 (8%)	0	100	100
16	M	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
17	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
18	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100
19	P	81/85 (95%)	74 (91%)	7 (9%)	0	100	100
20	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
21	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
22	S	75/87 (86%)	73 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	257 (91%)	26 (9%)	0	100	100
25	b	227/287 (79%)	203 (89%)	24 (11%)	0	100	100
26	c	208/212 (98%)	194 (93%)	14 (7%)	0	100	100
27	d	173/180 (96%)	164 (95%)	9 (5%)	0	100	100
28	e	174/184 (95%)	167 (96%)	7 (4%)	0	100	100
29	f	143/149 (96%)	127 (89%)	16 (11%)	0	100	100
30	g	124/161 (77%)	114 (92%)	10 (8%)	0	100	100
31	h	126/137 (92%)	119 (94%)	7 (6%)	0	100	100
32	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
33	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
34	k	146/151 (97%)	133 (91%)	13 (9%)	0	100	100
35	l	134/139 (96%)	126 (94%)	8 (6%)	0	100	100
36	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
37	n	108/116 (93%)	100 (93%)	8 (7%)	0	100	100
38	o	113/119 (95%)	109 (96%)	4 (4%)	0	100	100
39	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
40	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
41	r	137/159 (86%)	128 (93%)	9 (7%)	0	100	100
42	s	90/237 (38%)	83 (92%)	7 (8%)	0	100	100
43	t	109/111 (98%)	102 (94%)	7 (6%)	0	100	100
44	u	84/104 (81%)	75 (89%)	9 (11%)	0	100	100
45	v	61/65 (94%)	59 (97%)	2 (3%)	0	100	100
46	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
47	x	42/97 (43%)	37 (88%)	5 (12%)	0	100	100
48	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
49	z	48/53 (91%)	44 (92%)	4 (8%)	0	100	100
All	All	5820/6670 (87%)	5357 (92%)	460 (8%)	3 (0%)	49	83

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	F	113	LYS

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Mol	Chain	Res	Type
6	C	146	ALA
9	F	114	THR

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	34 (97%)	1 (3%)	37	58
4	A	212/262 (81%)	212 (100%)	0	100	100
5	B	180/232 (78%)	180 (100%)	0	100	100
6	C	181/183 (99%)	181 (100%)	0	100	100
7	D	123/178 (69%)	123 (100%)	0	100	100
8	E	150/196 (76%)	150 (100%)	0	100	100
9	F	131/132 (99%)	131 (100%)	0	100	100
10	G	123/124 (99%)	123 (100%)	0	100	100
11	H	111/115 (96%)	111 (100%)	0	100	100
12	I	95/99 (96%)	95 (100%)	0	100	100
13	J	91/97 (94%)	91 (100%)	0	100	100
14	K	117/120 (98%)	112 (96%)	5 (4%)	26	47
15	L	100/105 (95%)	100 (100%)	0	100	100
16	M	47/48 (98%)	47 (100%)	0	100	100
17	N	76/78 (97%)	76 (100%)	0	100	100
18	O	69/82 (84%)	69 (100%)	0	100	100
19	P	73/75 (97%)	72 (99%)	1 (1%)	59	72
20	Q	56/94 (60%)	56 (100%)	0	100	100
21	R	74/77 (96%)	74 (100%)	0	100	100
22	S	70/77 (91%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	T	49/56 (88%)	49 (100%)	0	100	100
24	a	241/243 (99%)	241 (100%)	0	100	100
25	b	186/233 (80%)	186 (100%)	0	100	100
26	c	182/184 (99%)	182 (100%)	0	100	100
27	d	150/154 (97%)	150 (100%)	0	100	100
28	e	153/159 (96%)	153 (100%)	0	100	100
29	f	123/134 (92%)	123 (100%)	0	100	100
30	g	101/129 (78%)	90 (89%)	11 (11%)	6	21
31	h	102/110 (93%)	102 (100%)	0	100	100
32	i	126/128 (98%)	126 (100%)	0	100	100
33	j	103/103 (100%)	103 (100%)	0	100	100
34	k	123/126 (98%)	123 (100%)	0	100	100
35	l	113/115 (98%)	113 (100%)	0	100	100
36	m	105/109 (96%)	105 (100%)	0	100	100
37	n	96/99 (97%)	96 (100%)	0	100	100
38	o	101/105 (96%)	101 (100%)	0	100	100
39	p	100/108 (93%)	100 (100%)	0	100	100
40	q	90/91 (99%)	90 (100%)	0	100	100
41	r	116/132 (88%)	116 (100%)	0	100	100
42	s	82/208 (39%)	82 (100%)	0	100	100
43	t	96/96 (100%)	96 (100%)	0	100	100
44	u	69/85 (81%)	69 (100%)	0	100	100
45	v	58/60 (97%)	58 (100%)	0	100	100
46	w	87/98 (89%)	87 (100%)	0	100	100
47	x	41/86 (48%)	41 (100%)	0	100	100
48	y	48/49 (98%)	44 (92%)	4 (8%)	10	30
49	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5093/5751 (89%)	5071 (100%)	22 (0%)	81	84

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	g	86	VAL

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Mol	Chain	Res	Type
30	g	116	ARG
30	g	115	ASN
48	y	47	MET
19	P	5	GLN

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

Mol	Chain	Res	Type
29	f	61	ASN
41	r	121	GLN
32	i	74	ASN
36	m	58	ASN
44	u	31	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2875/2907 (98%)	934 (32%)	32 (1%)
51	4	103/108 (95%)	40 (38%)	1 (0%)
52	5	1490/1520 (98%)	459 (30%)	10 (0%)
53	8	72/76 (94%)	34 (47%)	2 (2%)
All	All	4540/4611 (98%)	1467 (32%)	45 (0%)

5 of 1467 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	9	G
50	3	11	U
50	3	12	A
50	3	14	U
50	3	15	A

5 of 45 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2668	A
52	5	529	U
50	3	2764	U
51	4	54	U
52	5	748	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 [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

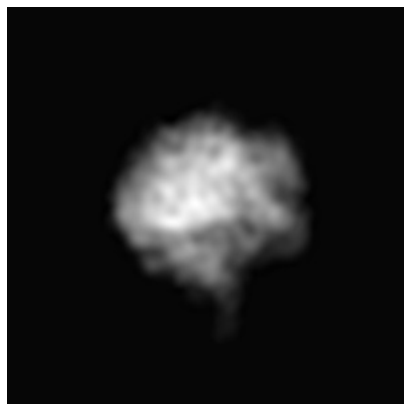
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13282. These allow visual inspection of the internal detail of the map and identification of artifacts.

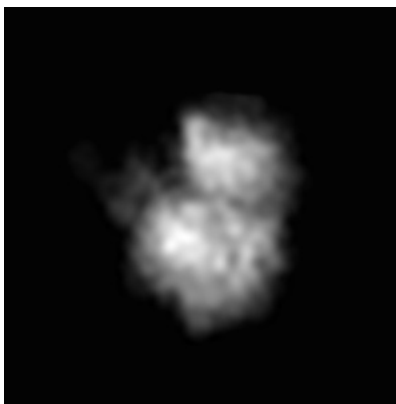
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

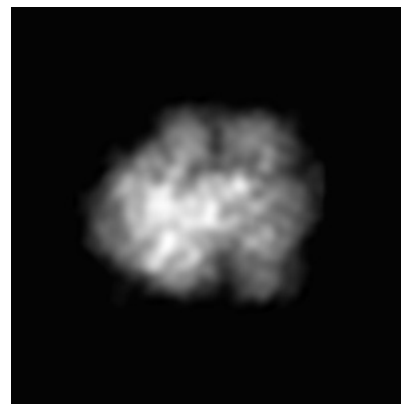
#### 6.1.1 Primary map



X

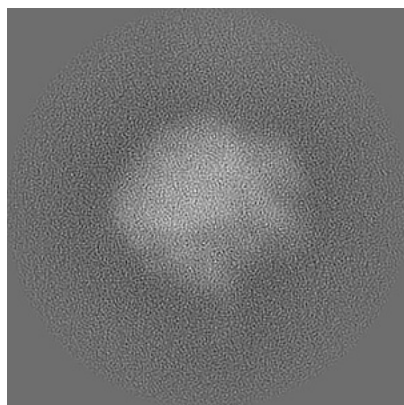


Y

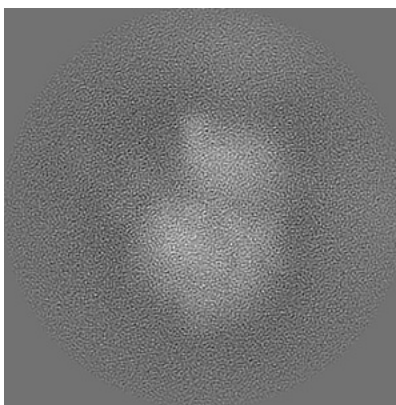


Z

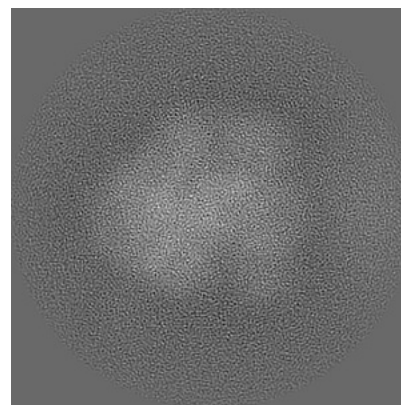
#### 6.1.2 Raw map



X



Y

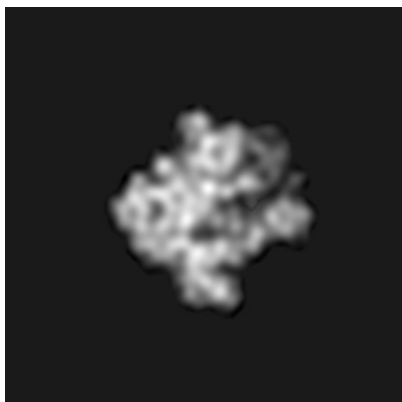


Z

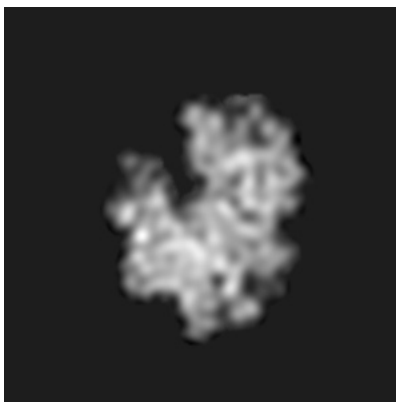
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

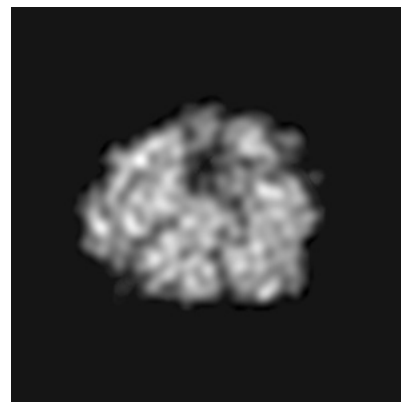
### 6.2.1 Primary map



X Index: 128

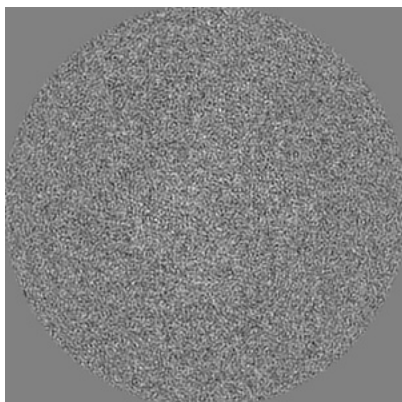


Y Index: 128

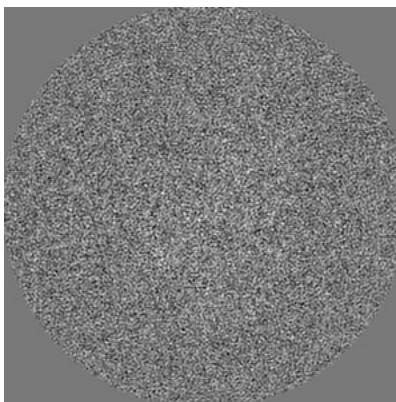


Z Index: 128

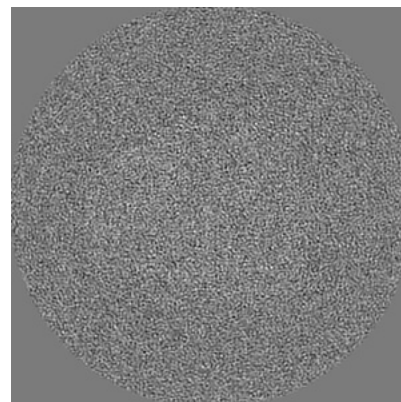
### 6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

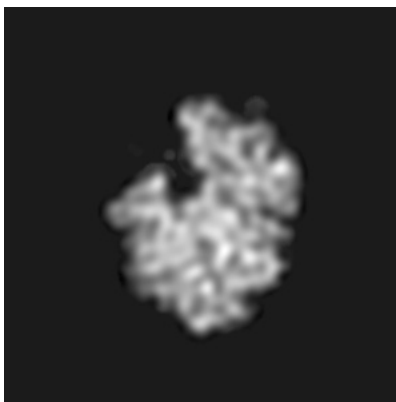
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

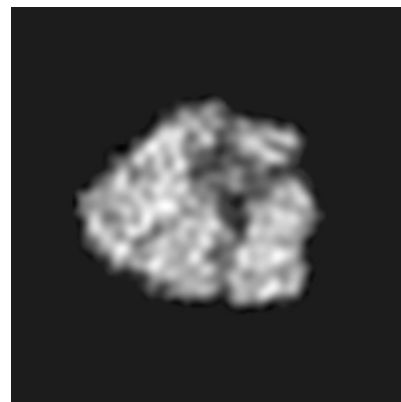
### 6.3.1 Primary map



X Index: 100

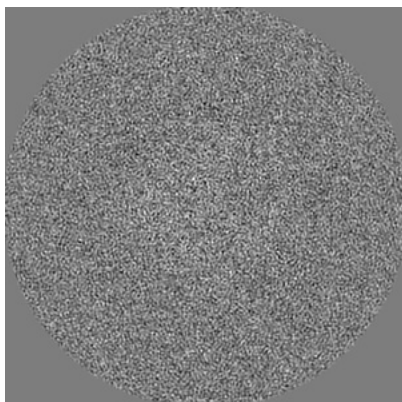


Y Index: 119

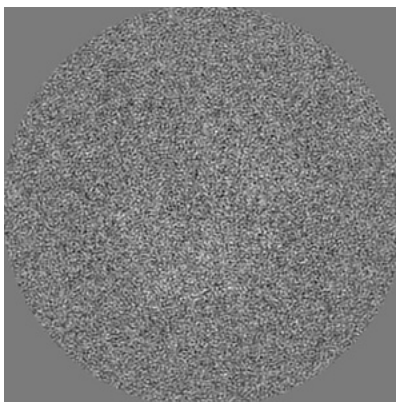


Z Index: 123

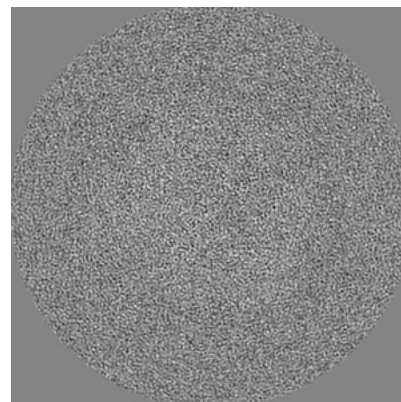
### 6.3.2 Raw map



X Index: 127



Y Index: 129



Z Index: 122

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

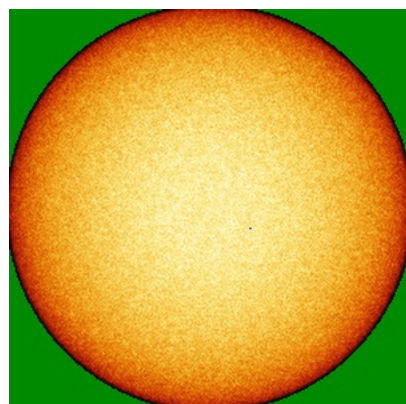


Y

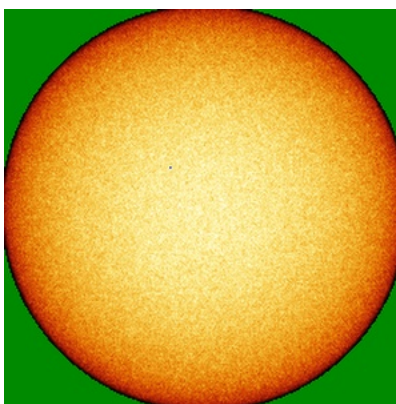


Z

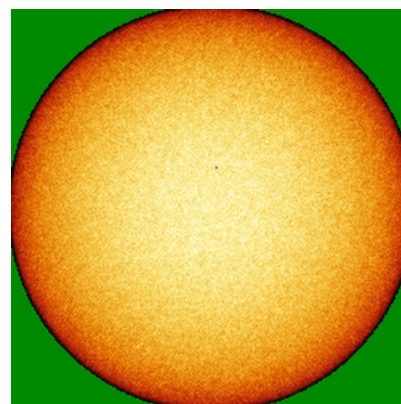
### 6.4.2 Raw map



X



Y

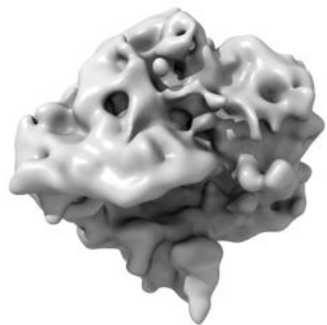


Z

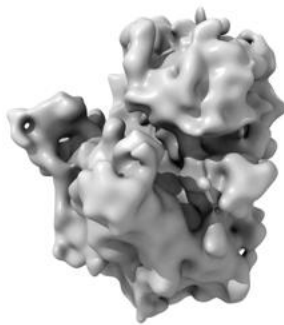
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

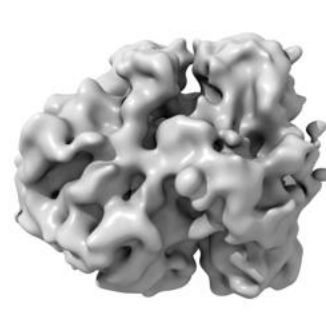
### 6.5.1 Primary map



X



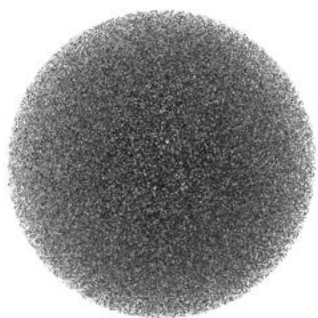
Y



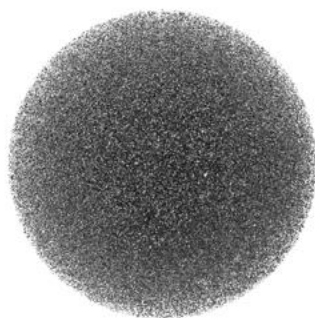
Z

The images above show the 3D surface view of the map at the recommended contour level 0.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

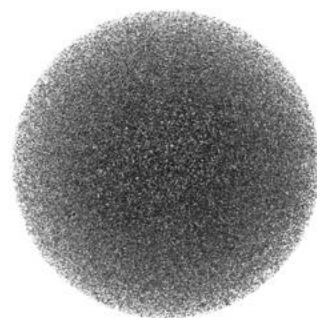
### 6.5.2 Raw map



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.

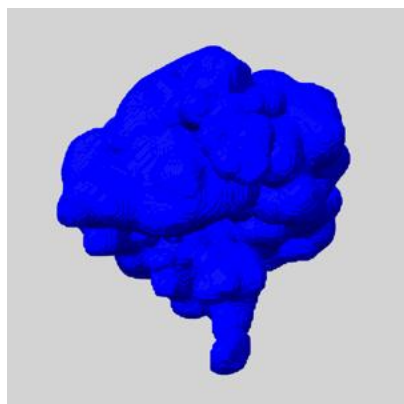
## 6.6 Mask visualisation [i](#)

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

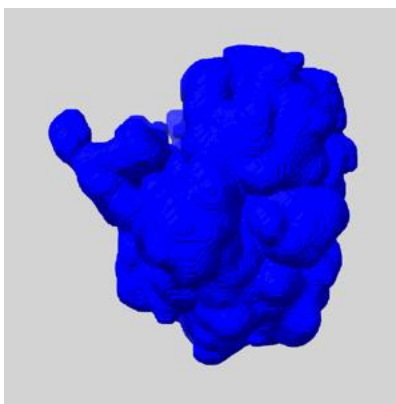
A mask typically either:

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

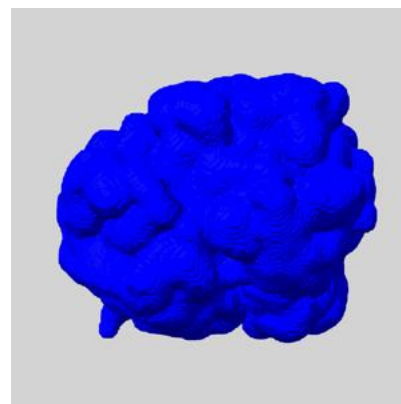
### 6.6.1 emd\_13282\_msk\_1.map [i](#)



X



Y

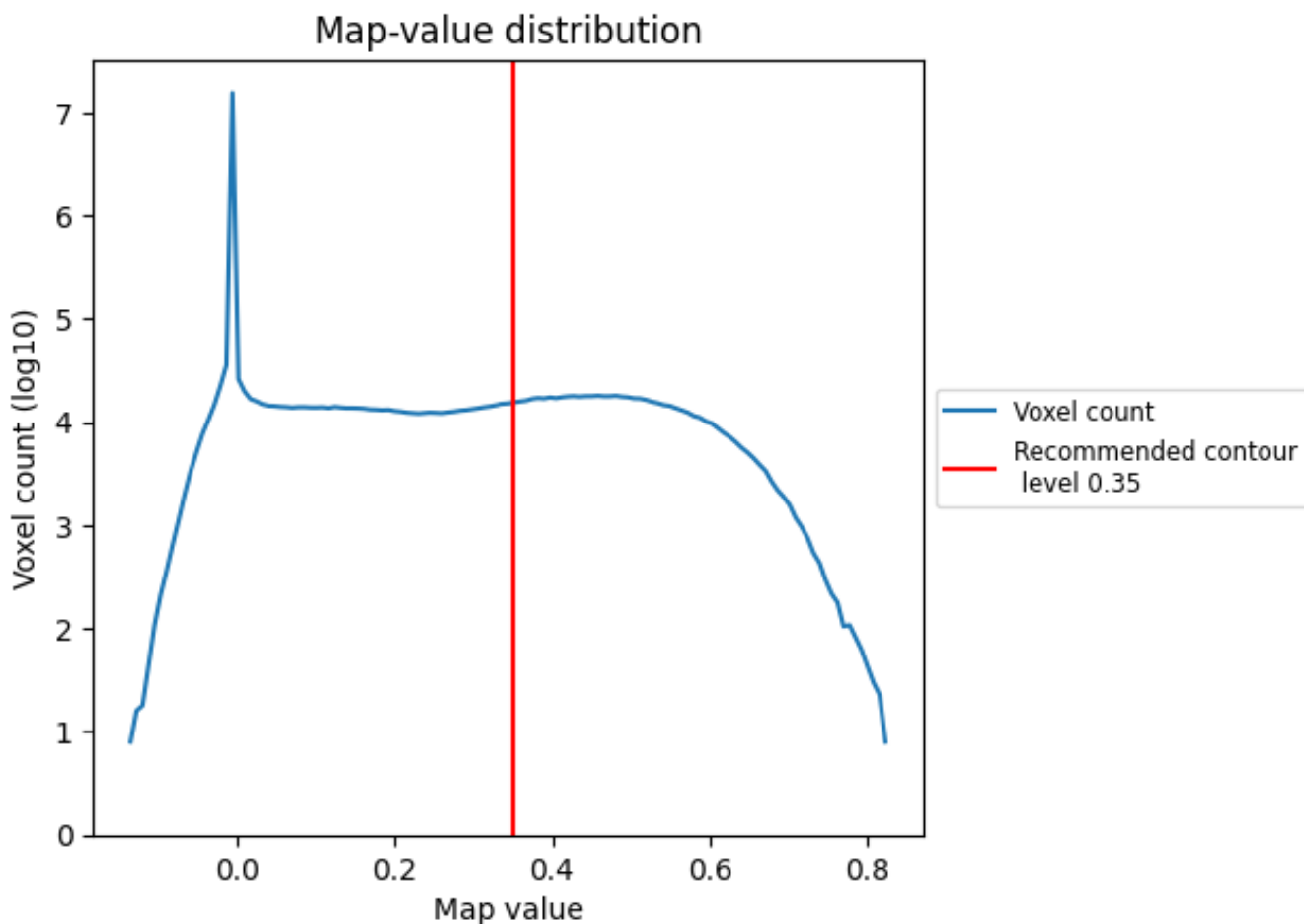


Z

## 7 Map analysis [i](#)

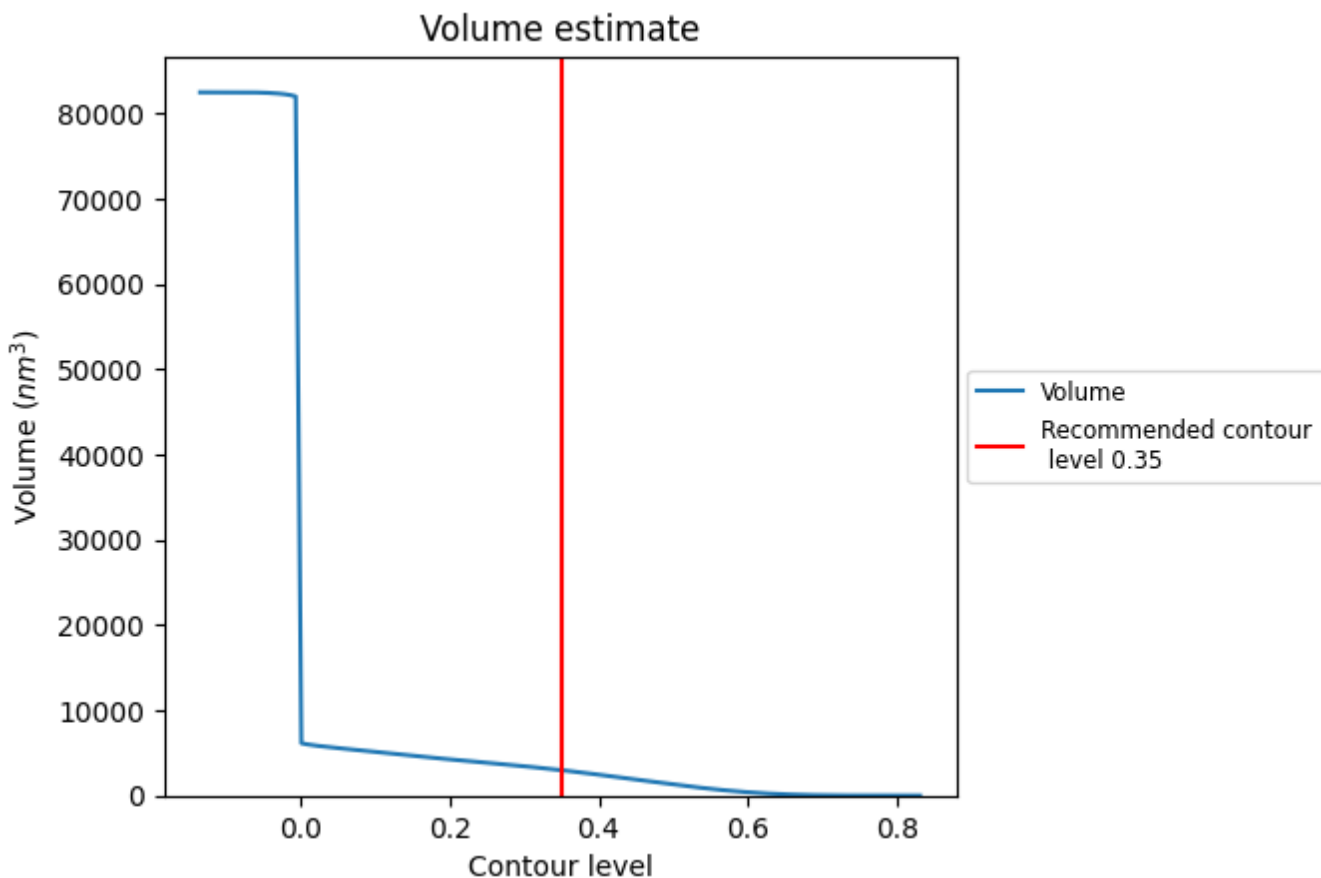
This section contains the results of statistical analysis of the map.

### 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.

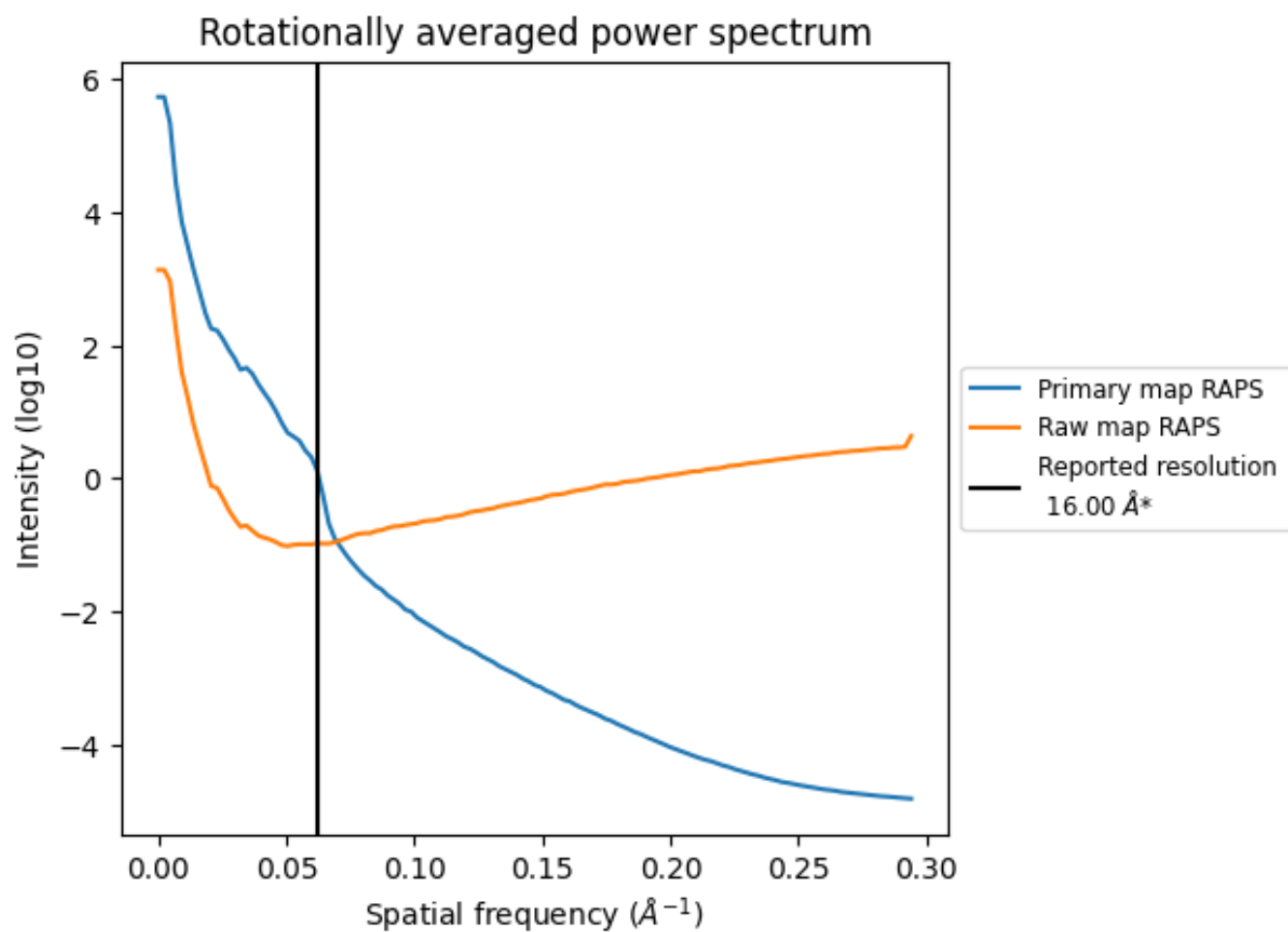
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2979  $\text{nm}^3$ ; this corresponds to an approximate mass of 2691 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

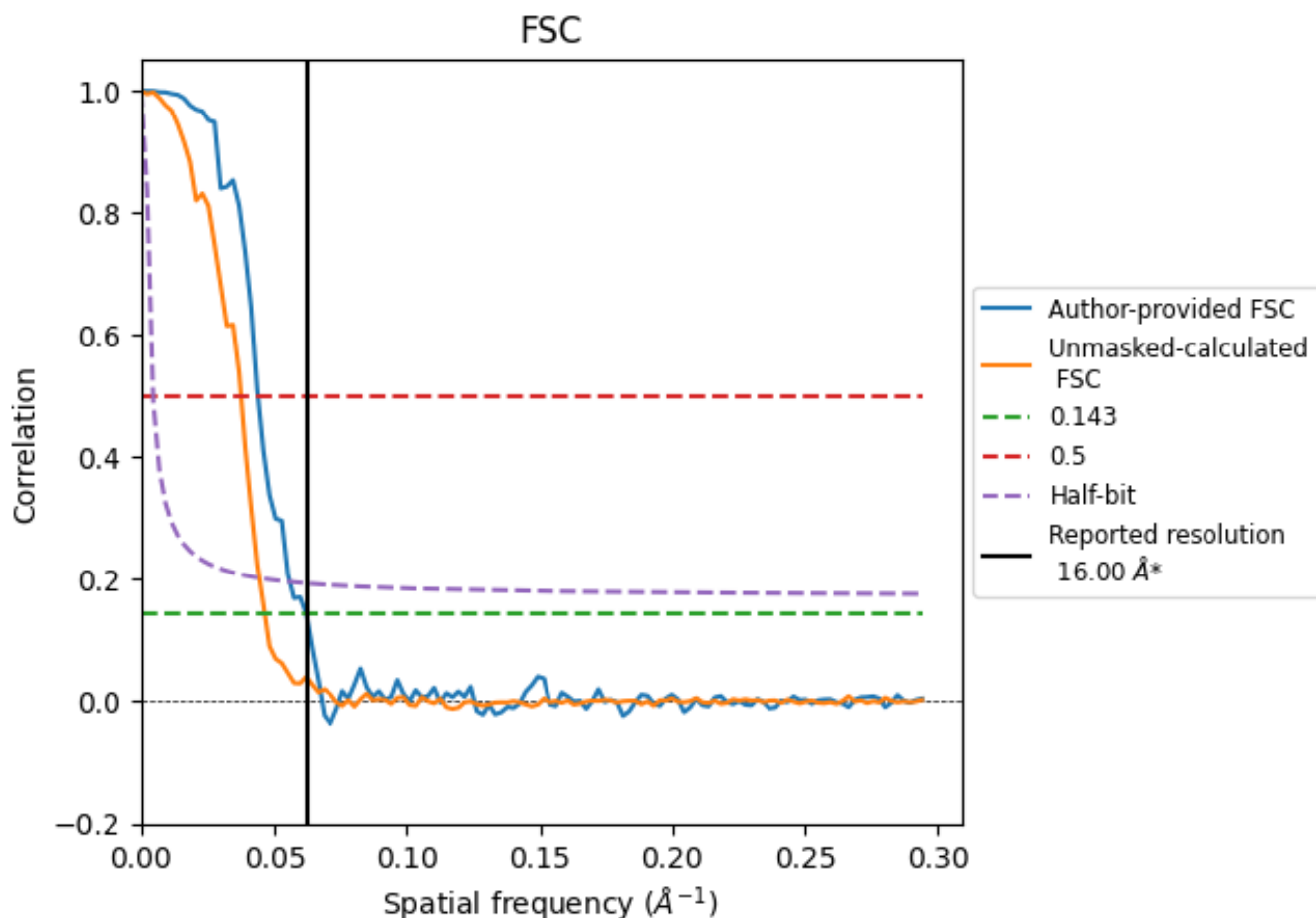


\*Reported resolution corresponds to spatial frequency of 0.062 Å<sup>-1</sup>

## 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 0.062 Å<sup>-1</sup>

## 8.2 Resolution estimates

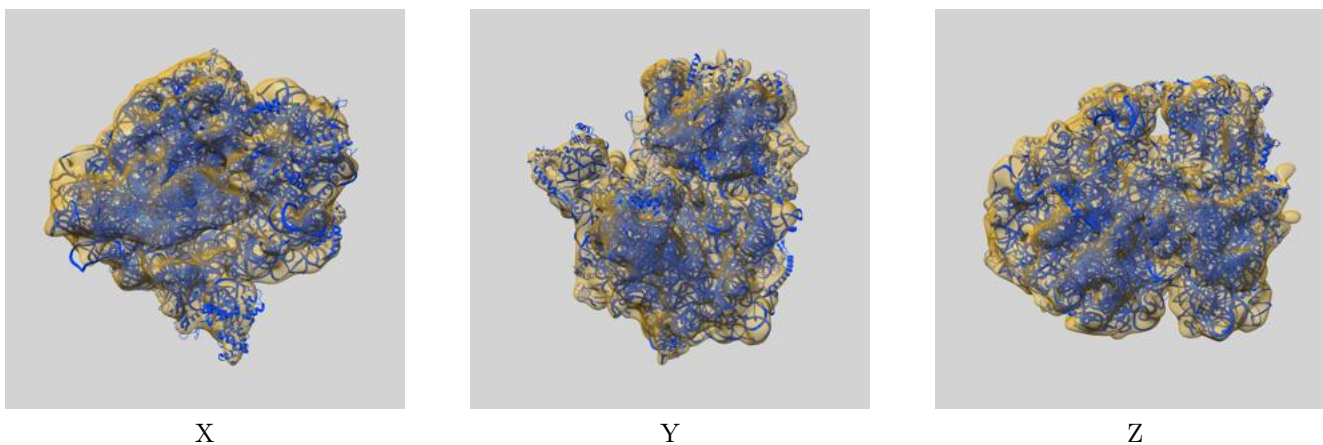
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	16.00	-	-
Author-provided FSC curve	16.10	22.78	17.89
Unmasked-calculated*	21.51	26.67	22.52

\*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 21.51 differs from the reported value 16.0 by more than 10 %

## 9 Map-model fit [i](#)

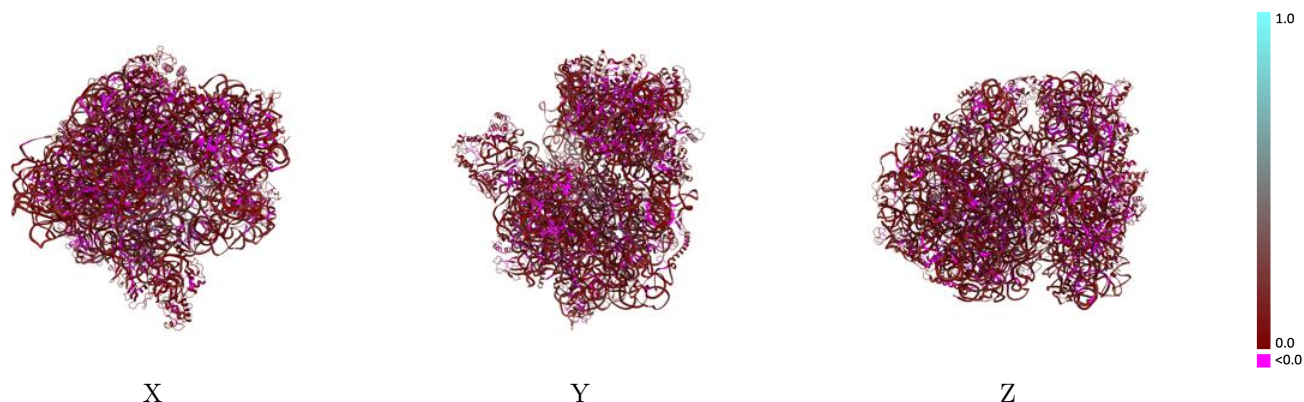
This section contains information regarding the fit between EMDB map EMD-13282 and PDB model 7PAS. Per-residue inclusion information can be found in section 3 on page 13.

### 9.1 Map-model overlay [i](#)



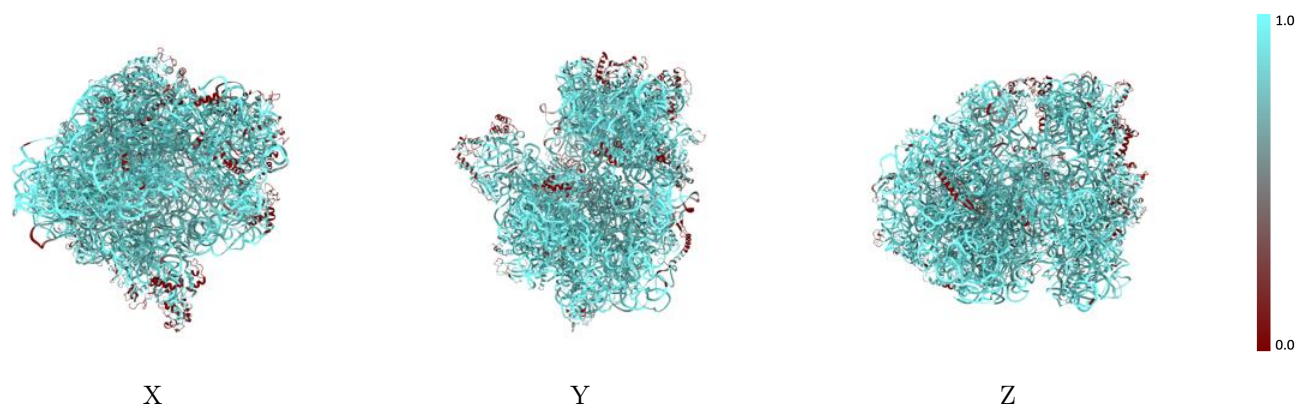
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



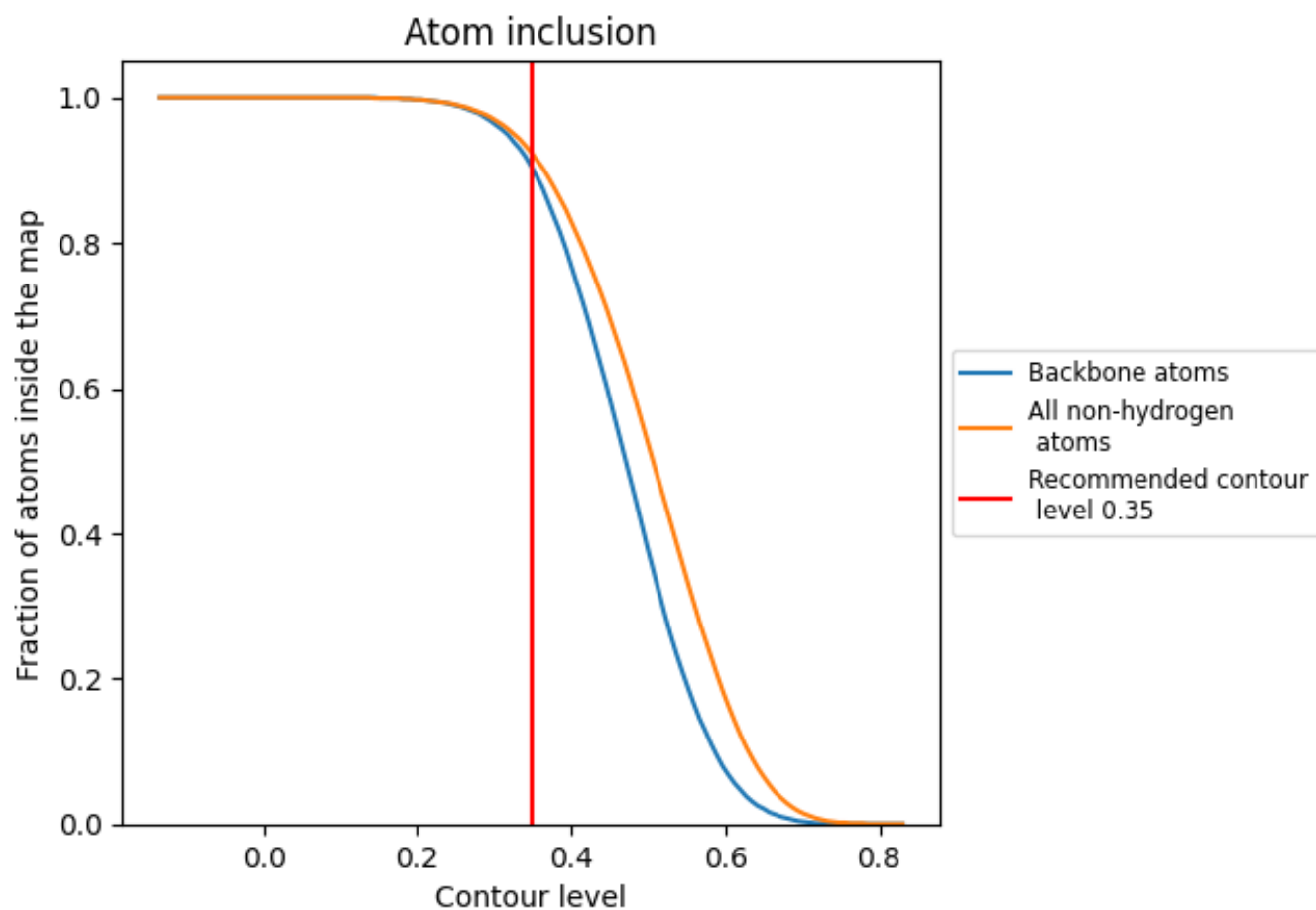
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 92% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.0690
0	 1.0000	 0.0170
1	 0.9980	 -0.0070
2	 0.9760	 -0.0040
3	 0.9810	 0.0810
4	 0.9680	 0.0870
5	 0.9720	 0.0790
8	 0.9040	 0.0960
A	 0.6370	 0.0660
B	 0.6700	 0.0430
C	 0.8310	 0.0380
D	 0.8540	 0.0470
E	 0.7020	 0.0820
F	 0.7380	 0.0690
G	 0.7710	 0.0490
H	 0.7590	 0.0530
I	 0.6870	 0.0310
J	 0.8210	 0.0360
K	 0.9650	 0.0310
L	 0.6400	 0.0550
M	 0.9580	 0.0350
N	 0.8910	 0.0570
O	 0.9670	 0.0150
P	 0.8620	 0.0570
Q	 0.9830	 0.0510
R	 0.8630	 0.0550
S	 0.9610	 0.0260
T	 0.7920	 0.0260
a	 0.9690	 0.0320
b	 0.8860	 0.0290
c	 0.8760	 0.0510
d	 0.6580	 0.0580
e	 0.7030	 0.0550
f	 0.4190	 0.0600
g	 0.5290	 0.0730



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Chain	Atom inclusion	Q-score
h	 0.3770	 0.0690
i	 0.9090	 0.0240
j	 0.8900	 0.0310
k	 0.9350	 0.0220
l	 0.9450	 0.0400
m	 0.9630	 0.0060
n	 0.9020	 0.0280
o	 0.8260	 0.0430
p	 0.8800	 0.0110
q	 0.8010	 0.0620
r	 0.9420	 0.0490
s	 0.9630	 0.0250
t	 0.6280	 0.0520
u	 0.9700	 0.0190
v	 0.9620	 0.0080
w	 0.8000	 0.0620
x	 0.3940	 0.1020
y	 0.8890	 0.0230
z	 1.0000	 0.0840