



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 01:53 AM UTC

PDB ID : 7PAK / pdb_00007pak
EMDB ID : EMD-13275
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 5.30 Å (reported)
Based on initial models : 4V5L, 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:

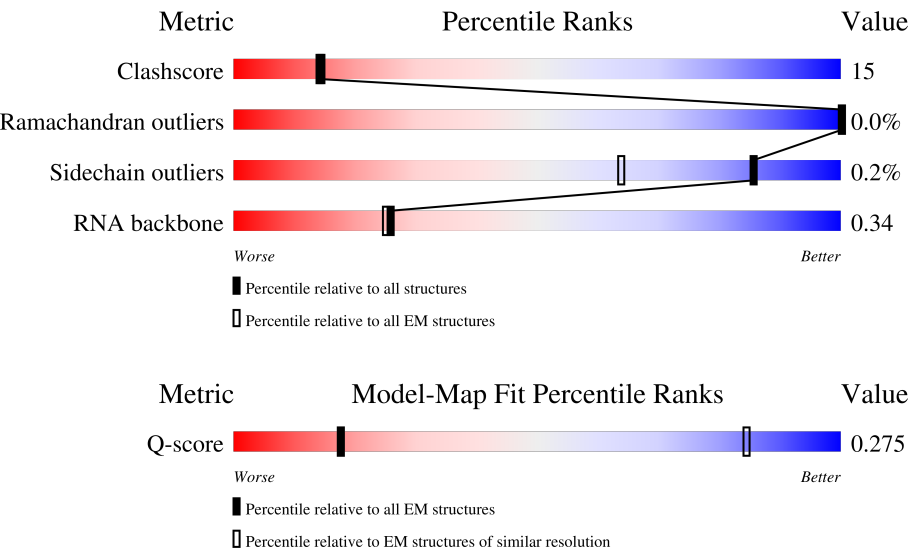
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.30 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	625 (4.80 - 5.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	48	58% 40%
2	1	59	73% 27%
3	2	37	8% 54% 46%

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Mol	Chain	Length	Quality of chain
4	9	394	
5	A	294	
6	B	273	
7	C	205	
8	D	219	
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	

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Mol	Chain	Length	Quality of chain
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	

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Mol	Chain	Length	Quality of chain
54	6	76	33% 38% 45% 17%
54	7	76	41% 42% 17%

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149141 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
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

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

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

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

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

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	393	Total	C	N	O	S	0	0
			3021	1892	533	583	13		

- Molecule 5 is a protein called 30S ribosomal protein S2.

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

- Molecule 6 is a protein called 30S ribosomal protein S3.

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

- Molecule 7 is a protein called 30S ribosomal protein S4.

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

- Molecule 8 is a protein called 30S ribosomal protein S5.

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

- Molecule 9 is a protein called 30S ribosomal protein S6.

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

- Molecule 10 is a protein called 30S ribosomal protein S7.

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

- Molecule 11 is a protein called 30S ribosomal protein S8.

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

- Molecule 12 is a protein called 30S ribosomal protein S9.

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

- Molecule 13 is a protein called 30S ribosomal protein S10.

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

- Molecule 14 is a protein called 30S ribosomal protein S11.

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

- Molecule 15 is a protein called 30S ribosomal protein S12.

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

- Molecule 16 is a protein called 30S ribosomal protein S13.

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

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 18 is a protein called 30S ribosomal protein S15.

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

- Molecule 19 is a protein called 30S ribosomal protein S16.

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

- Molecule 20 is a protein called 30S ribosomal protein S17.

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

- Molecule 21 is a protein called 30S ribosomal protein S18.

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

- Molecule 22 is a protein called 30S ribosomal protein S19.

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

- Molecule 23 is a protein called 30S ribosomal protein S20.

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

- Molecule 24 is a protein called 30S ribosomal protein S21.

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

- Molecule 25 is a protein called 50S ribosomal protein L2.

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

- Molecule 26 is a protein called 50S ribosomal protein L3.

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

- Molecule 27 is a protein called 50S ribosomal protein L4.

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

- Molecule 28 is a protein called 50S ribosomal protein L5.

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

- Molecule 29 is a protein called 50S ribosomal protein L6.

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

- Molecule 30 is a protein called 50S ribosomal protein L9.

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

- Molecule 31 is a protein called 50S ribosomal protein L10.

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

- Molecule 32 is a protein called 50S ribosomal protein L11.

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

- Molecule 33 is a protein called 50S ribosomal protein L13.

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

- Molecule 34 is a protein called 50S ribosomal protein L14.

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

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

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

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

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

- Molecule 39 is a protein called 50S ribosomal protein L19.

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

- Molecule 40 is a protein called 50S ribosomal protein L20.

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

- Molecule 41 is a protein called 50S ribosomal protein L21.

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

- Molecule 42 is a protein called 50S ribosomal protein L22.

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

- Molecule 43 is a protein called 50S ribosomal protein L23.

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

- Molecule 44 is a protein called 50S ribosomal protein L24.

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

- Molecule 45 is a protein called 50S ribosomal protein L27.

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

- Molecule 46 is a protein called 50S ribosomal protein L28.

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

- Molecule 47 is a protein called 50S ribosomal protein L29.

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

- Molecule 48 is a protein called 50S ribosomal protein L31.

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

- Molecule 49 is a protein called 50S ribosomal protein L32.

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

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

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

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

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

Chain 0: 



- Molecule 2: 50S ribosomal protein L35

Chain 1: 



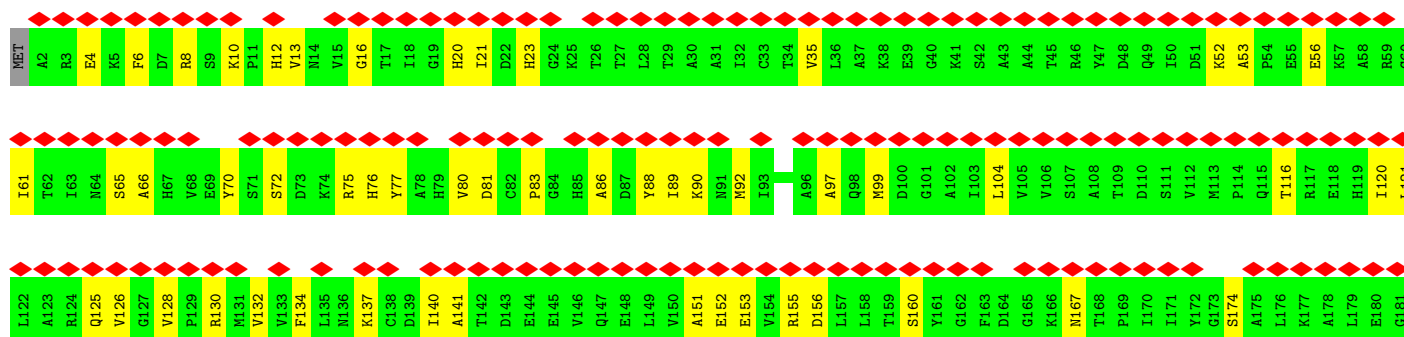
- Molecule 3: 50S ribosomal protein L36

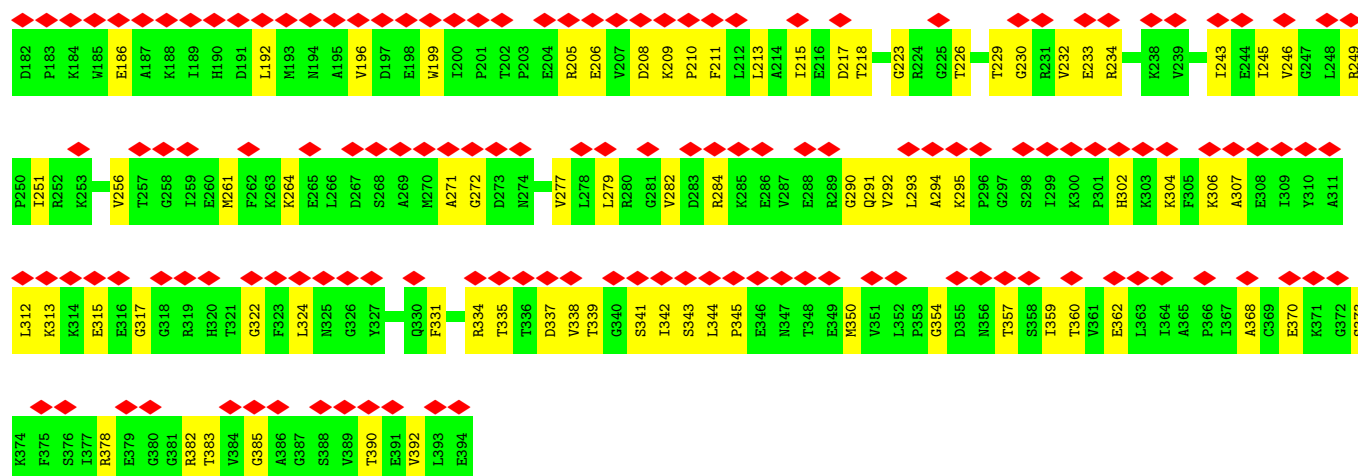
Chain 2: 



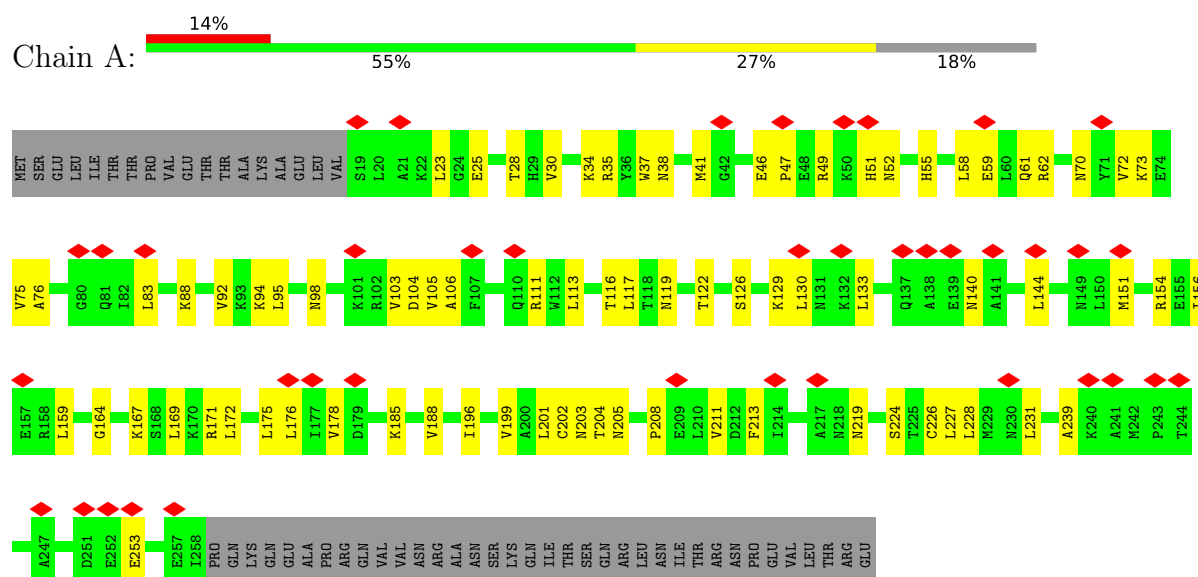
- Molecule 4: Elongation factor Tu

Chain 9: 

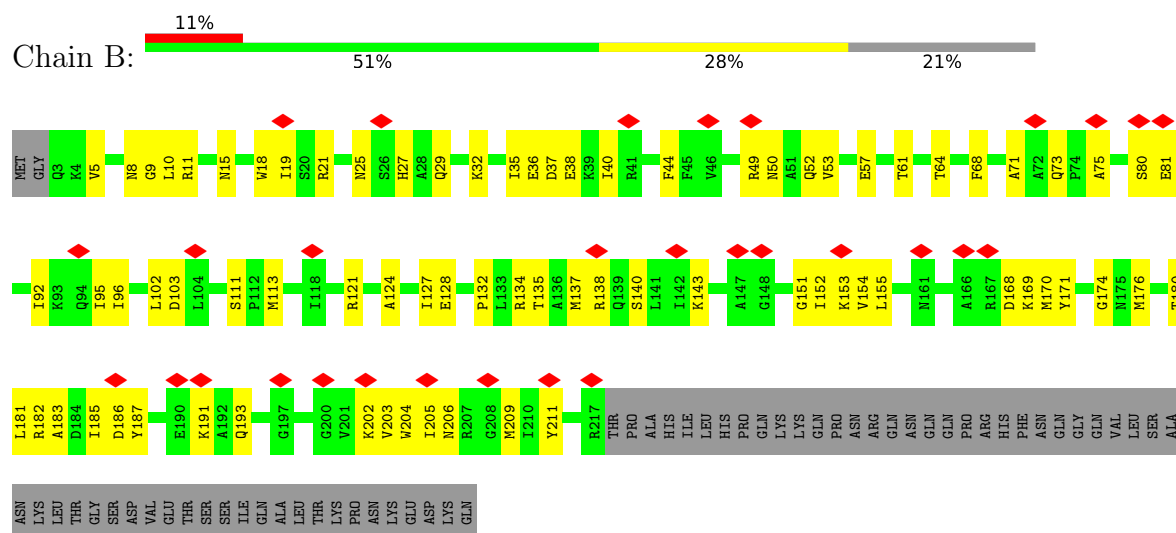




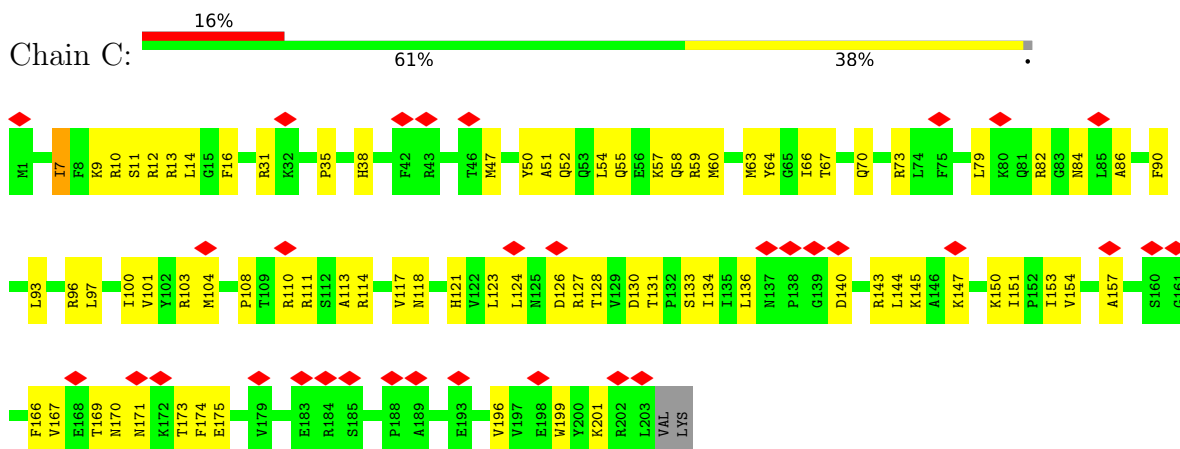
• Molecule 5: 30S ribosomal protein S2



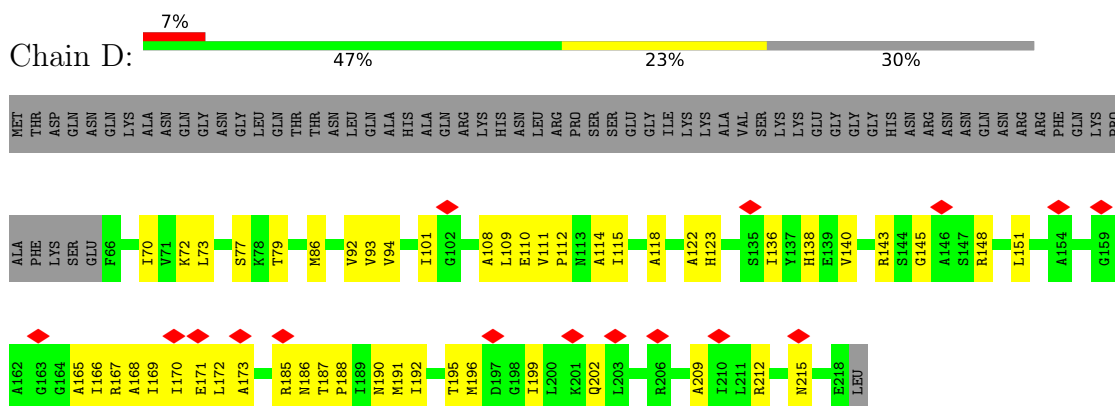
• Molecule 6: 30S ribosomal protein S3



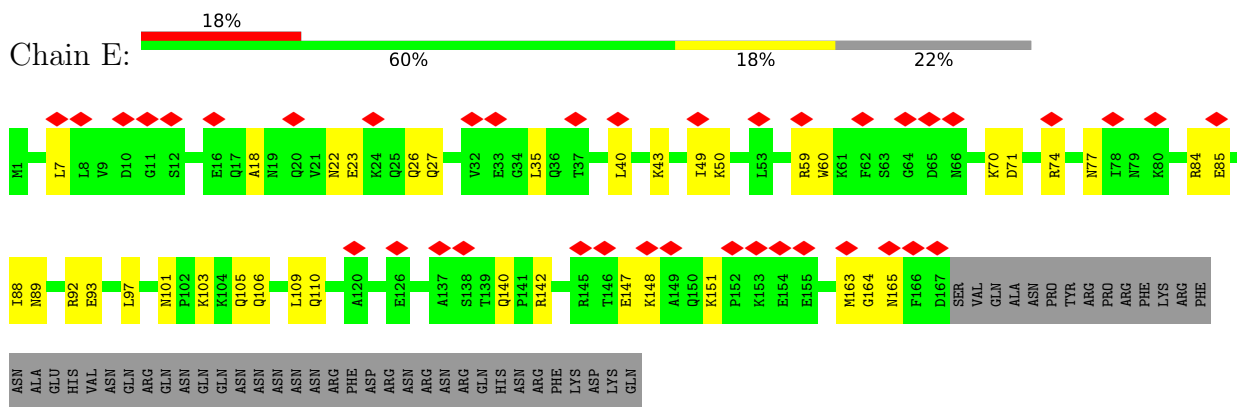
- Molecule 7: 30S ribosomal protein S4



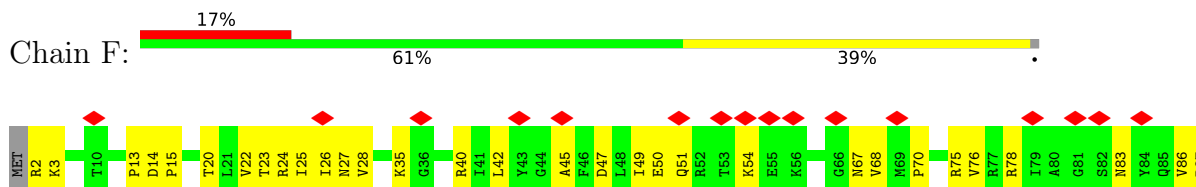
- Molecule 8: 30S ribosomal protein S5



- Molecule 9: 30S ribosomal protein S6

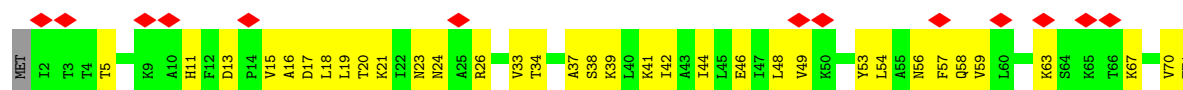


- Molecule 10: 30S ribosomal protein S7

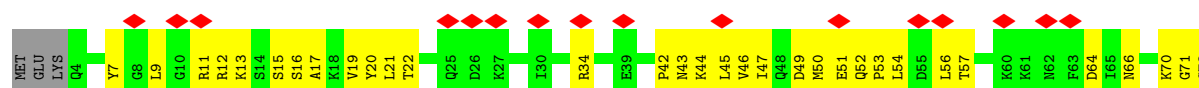




- Molecule 11: 30S ribosomal protein S8



- Molecule 12: 30S ribosomal protein S9



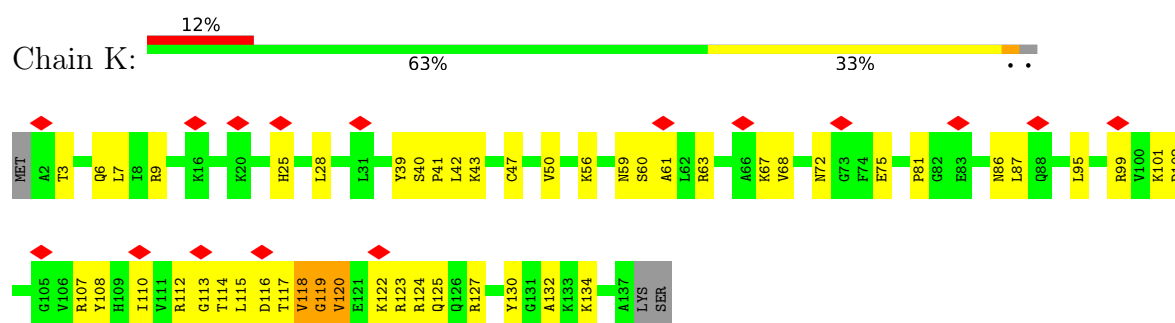
- Molecule 13: 30S ribosomal protein S10



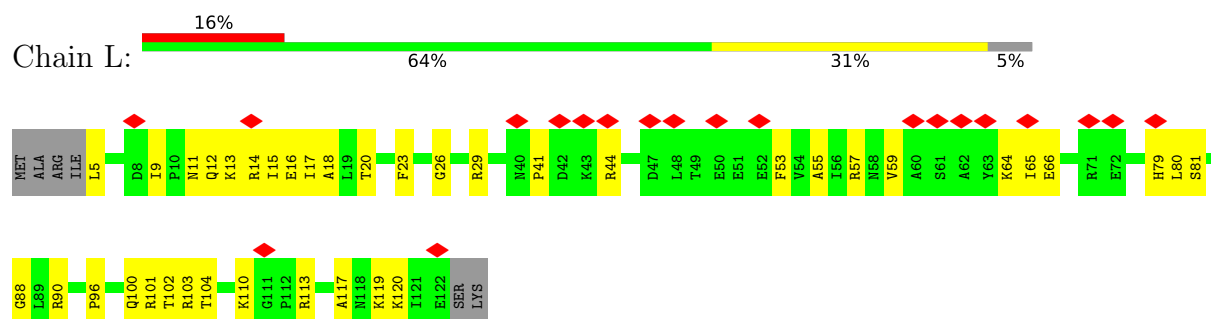
- Molecule 14: 30S ribosomal protein S11



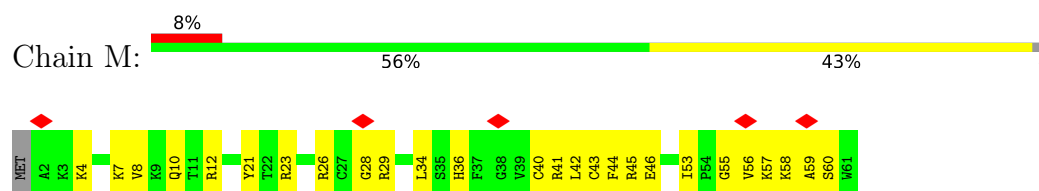
- Molecule 15: 30S ribosomal protein S12



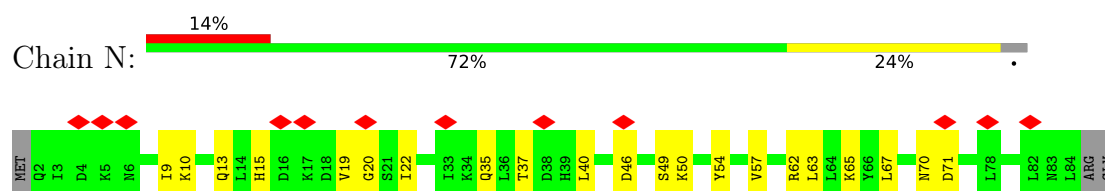
- Molecule 16: 30S ribosomal protein S13



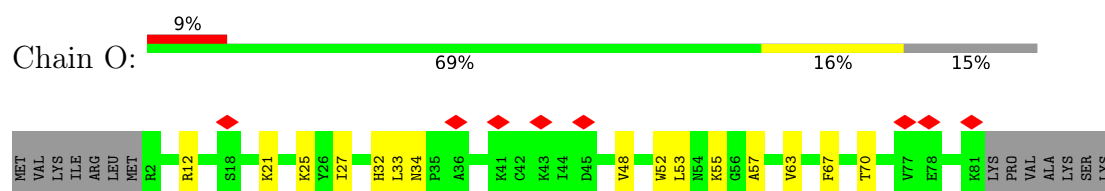
- Molecule 17: 30S ribosomal protein S14 type Z



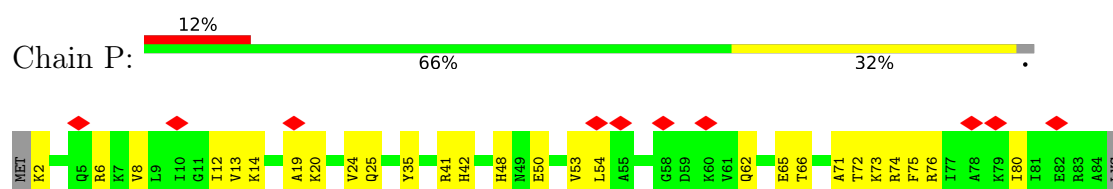
- Molecule 18: 30S ribosomal protein S15



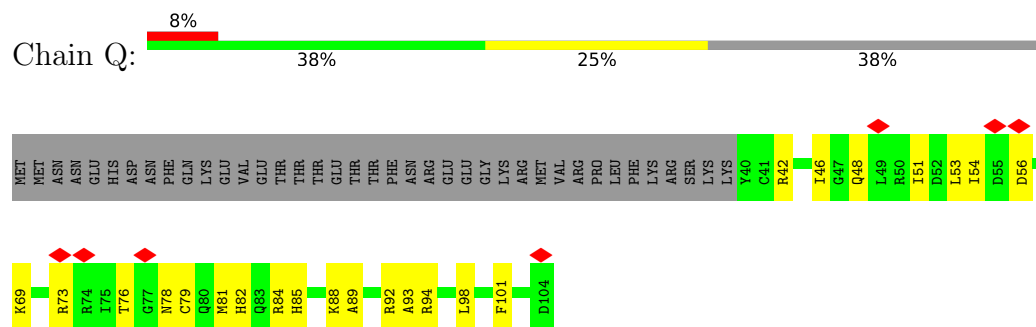
- Molecule 19: 30S ribosomal protein S16



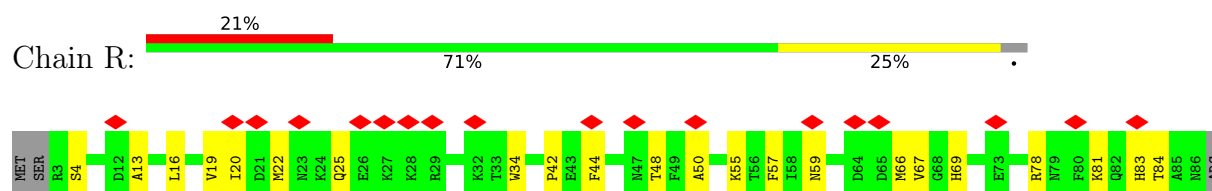
- Molecule 20: 30S ribosomal protein S17



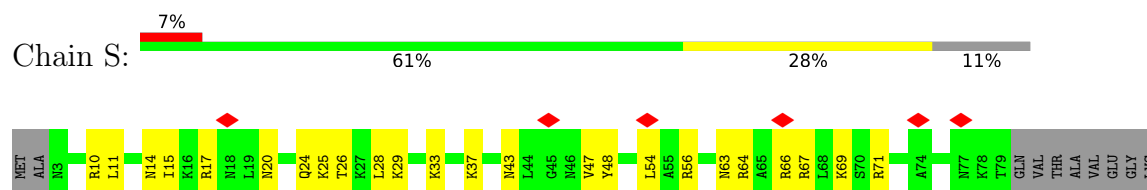
- Molecule 21: 30S ribosomal protein S18



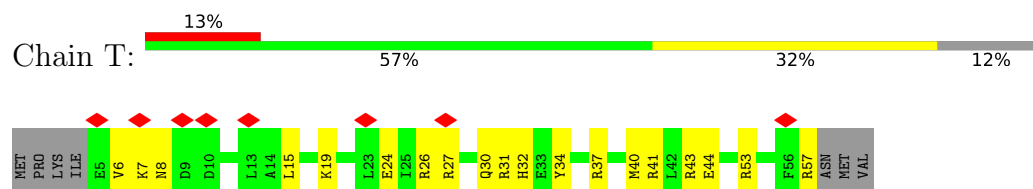
- Molecule 22: 30S ribosomal protein S19



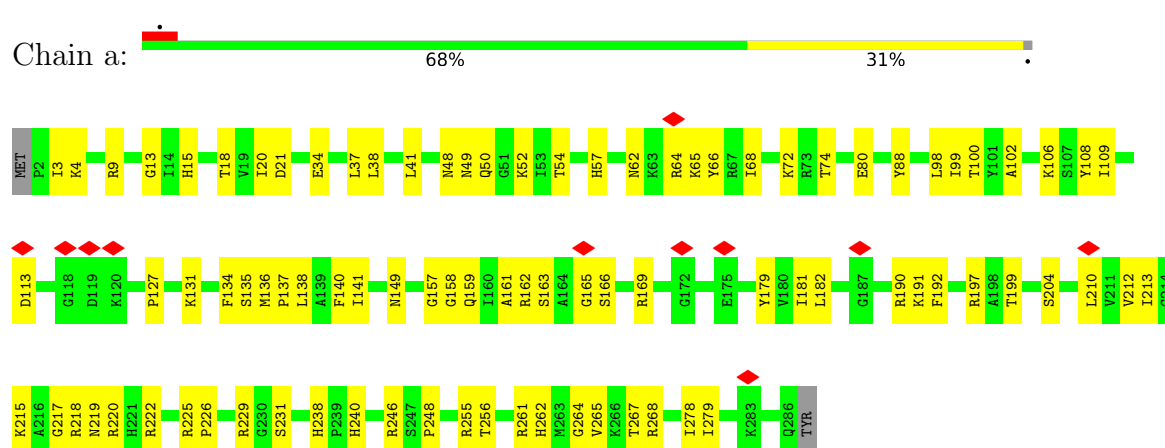
- Molecule 23: 30S ribosomal protein S20



- Molecule 24: 30S ribosomal protein S21



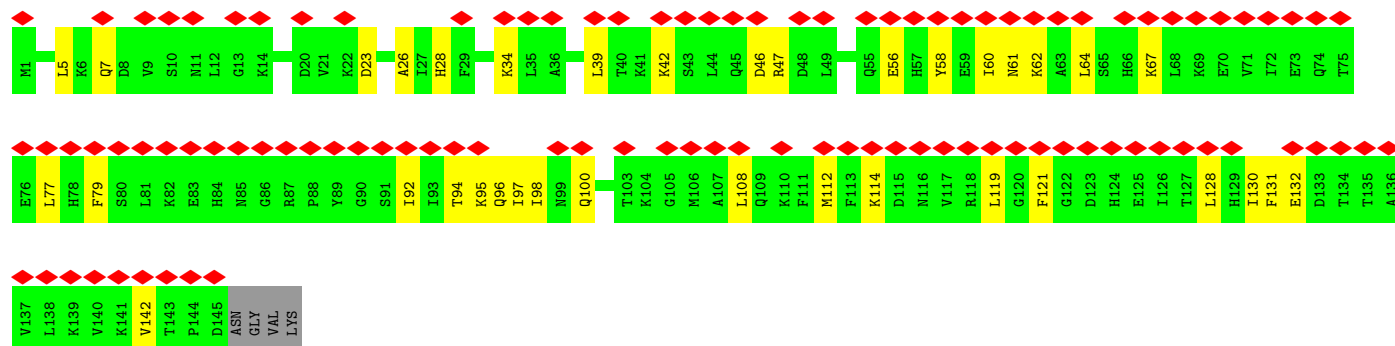
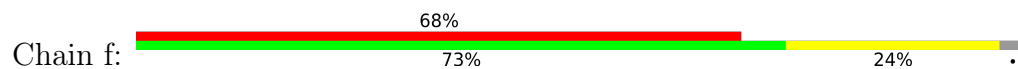
- Molecule 25: 50S ribosomal protein L2



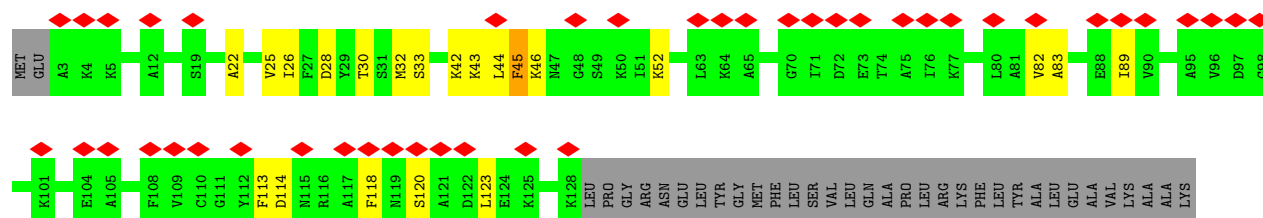
- Molecule 26: 50S ribosomal protein L3



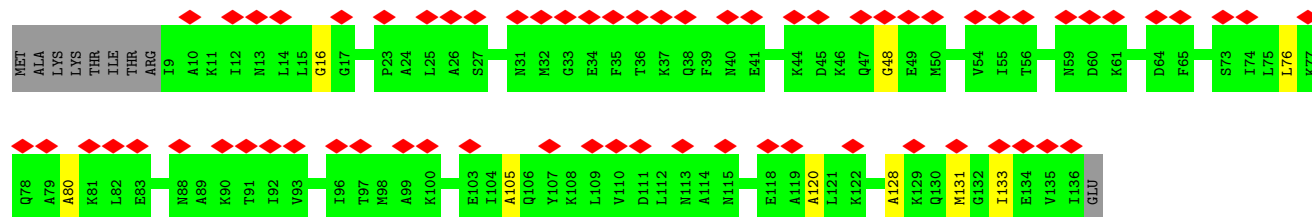
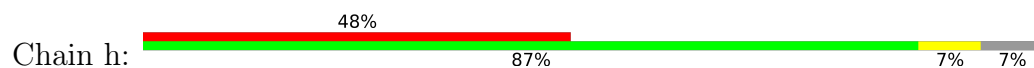
• Molecule 30: 50S ribosomal protein L9



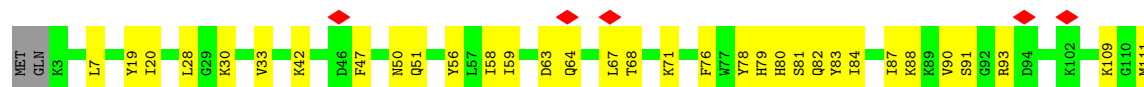
• Molecule 31: 50S ribosomal protein L10

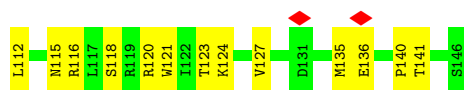


• Molecule 32: 50S ribosomal protein L11

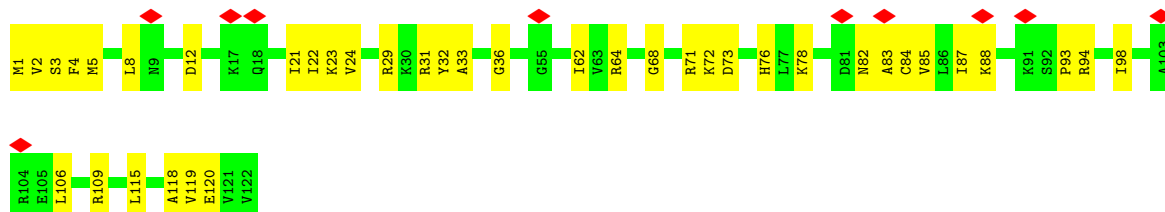


• Molecule 33: 50S ribosomal protein L13

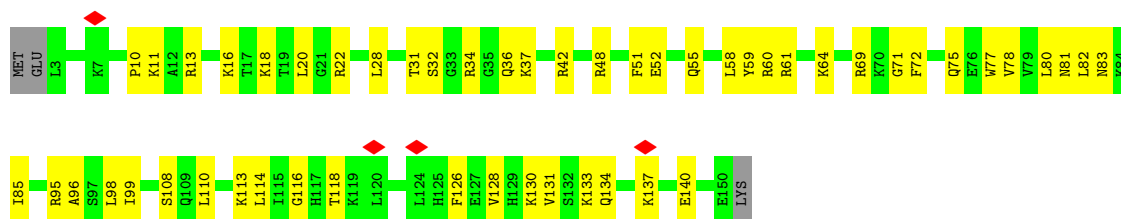




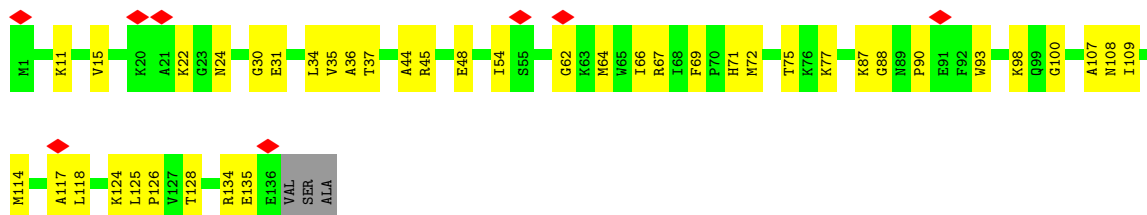
- Molecule 34: 50S ribosomal protein L14



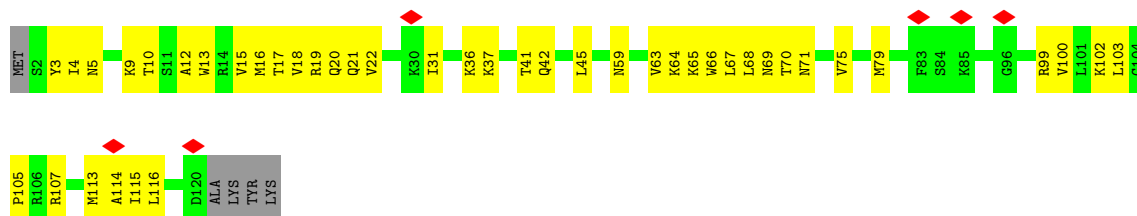
- Molecule 35: 50S ribosomal protein L15



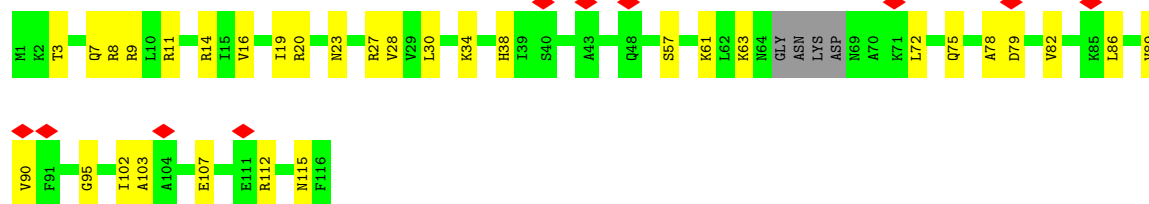
- Molecule 36: 50S ribosomal protein L16



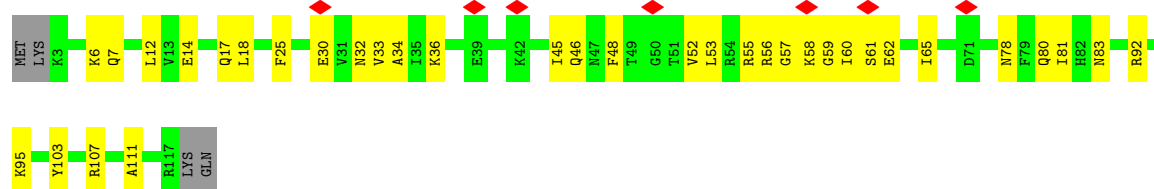
- Molecule 37: 50S ribosomal protein L17



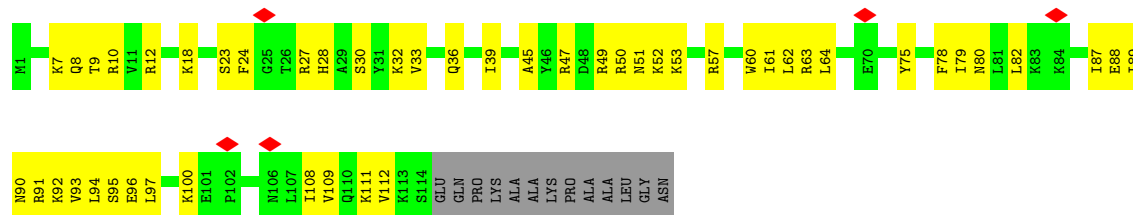
- Molecule 38: 50S ribosomal protein L18



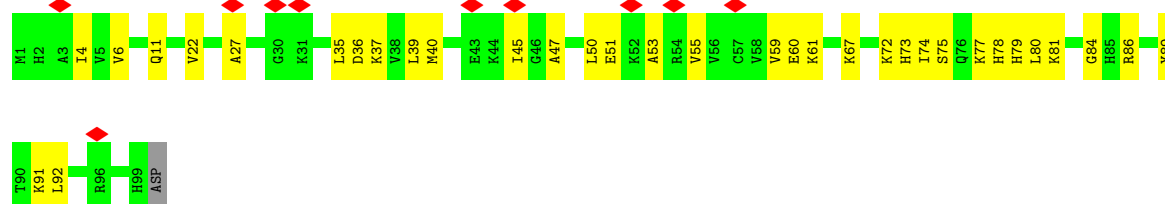
- Molecule 39: 50S ribosomal protein L19



- Molecule 40: 50S ribosomal protein L20



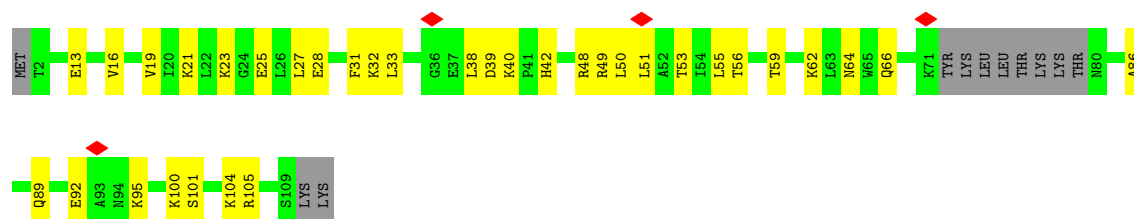
- Molecule 41: 50S ribosomal protein L21



- Molecule 42: 50S ribosomal protein L22

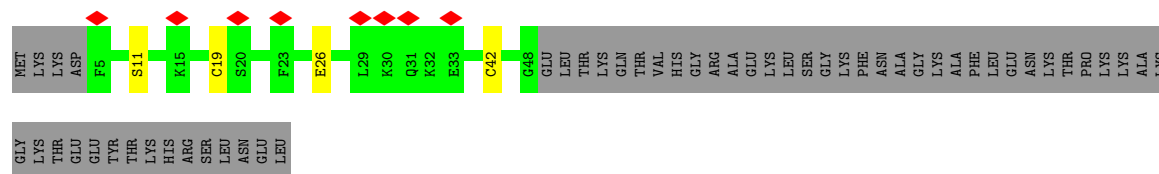


Chain w:  59% 31% 10%



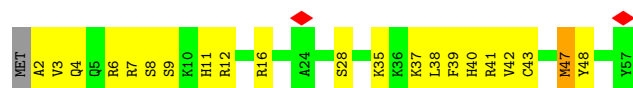
- Molecule 48: 50S ribosomal protein L31

Chain x:  8% 41% 55%



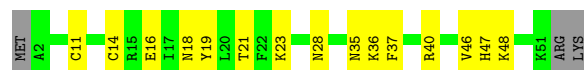
- Molecule 49: 50S ribosomal protein L32

Chain y:  61% 35% 4%

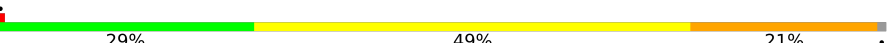


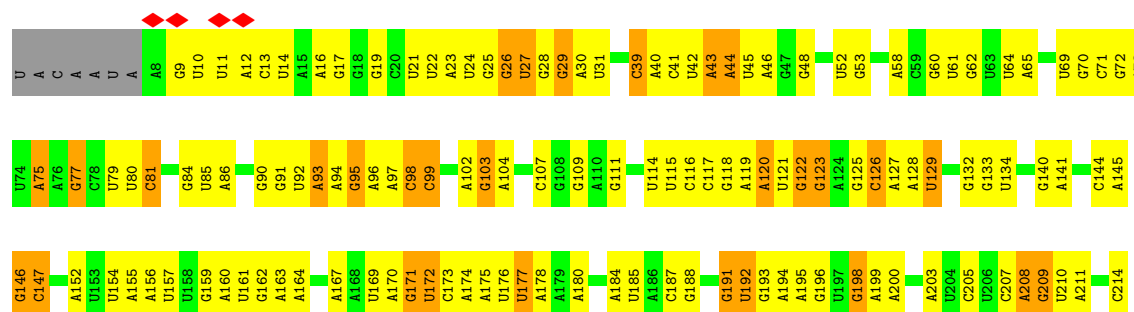
- Molecule 50: 50S ribosomal protein L33 1

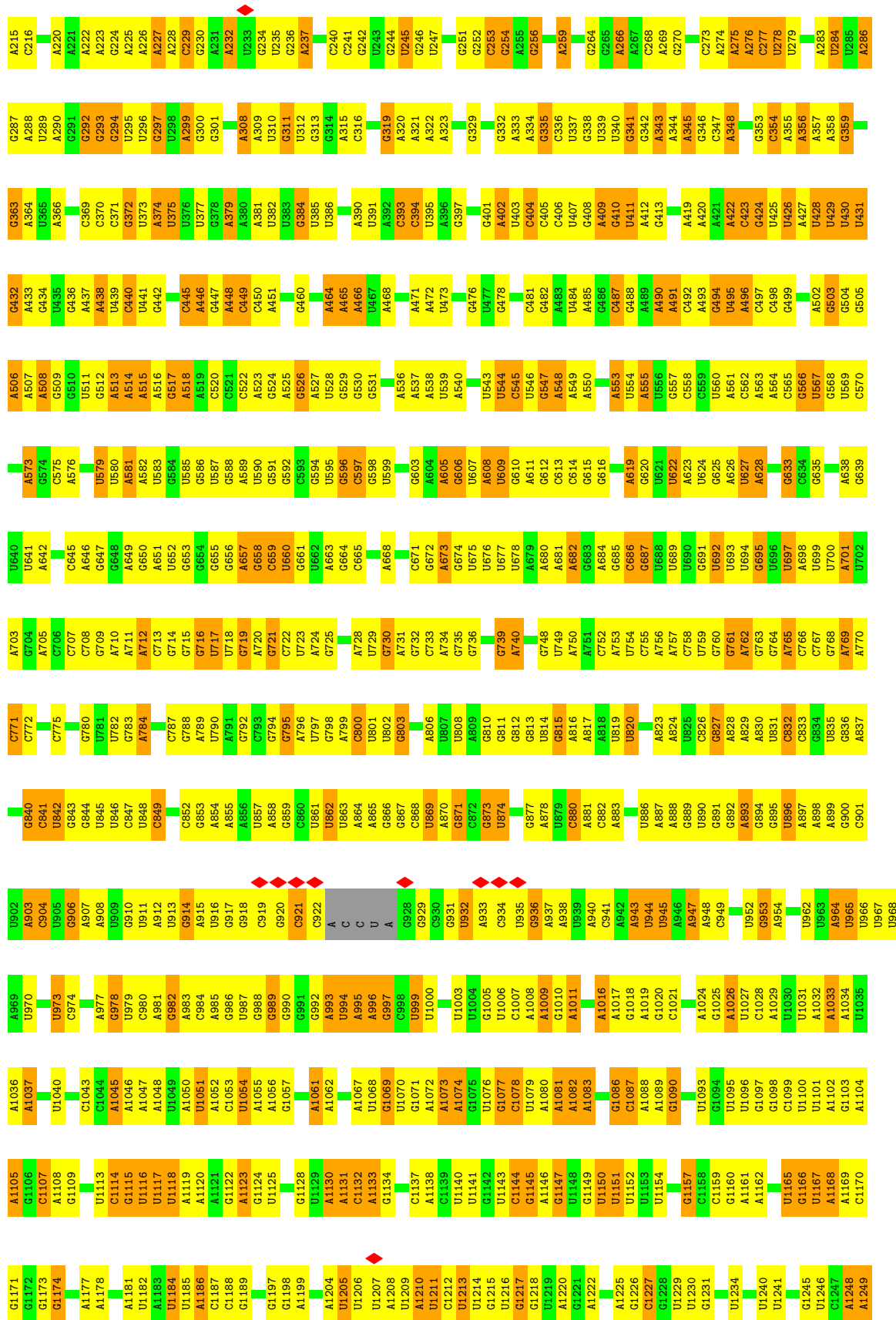
Chain z:  66% 28% 6%



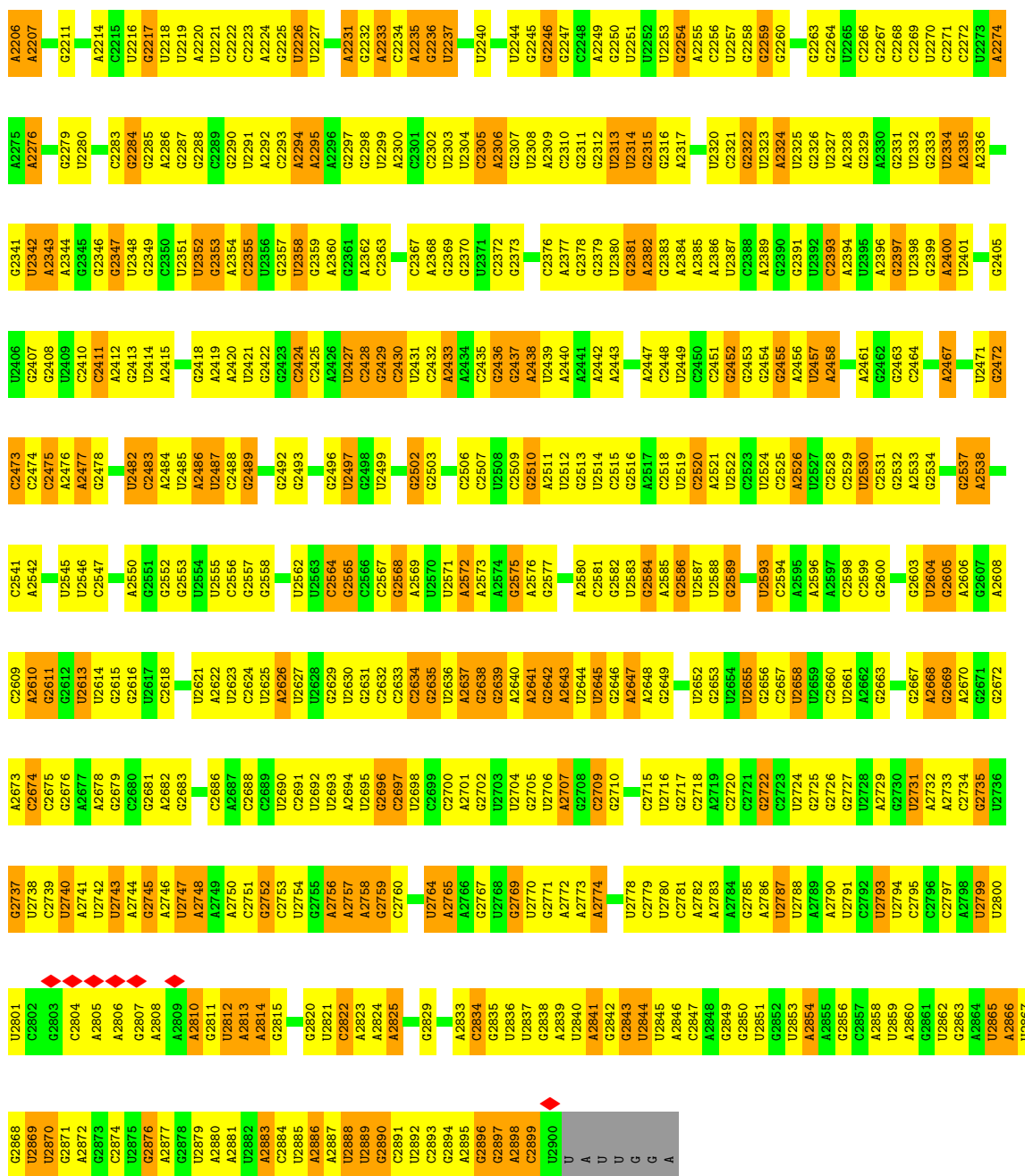
- Molecule 51: 23S ribosomal RNA

Chain 3:  29% 49% 21%

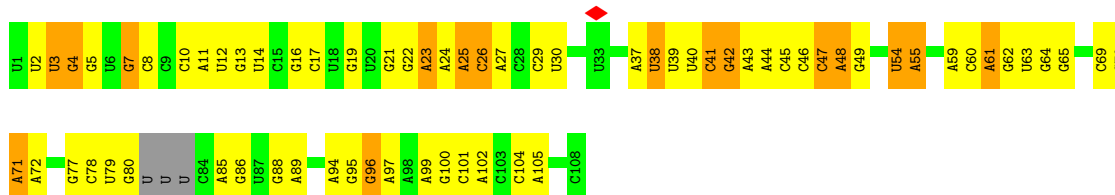
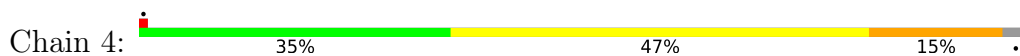




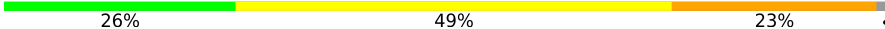
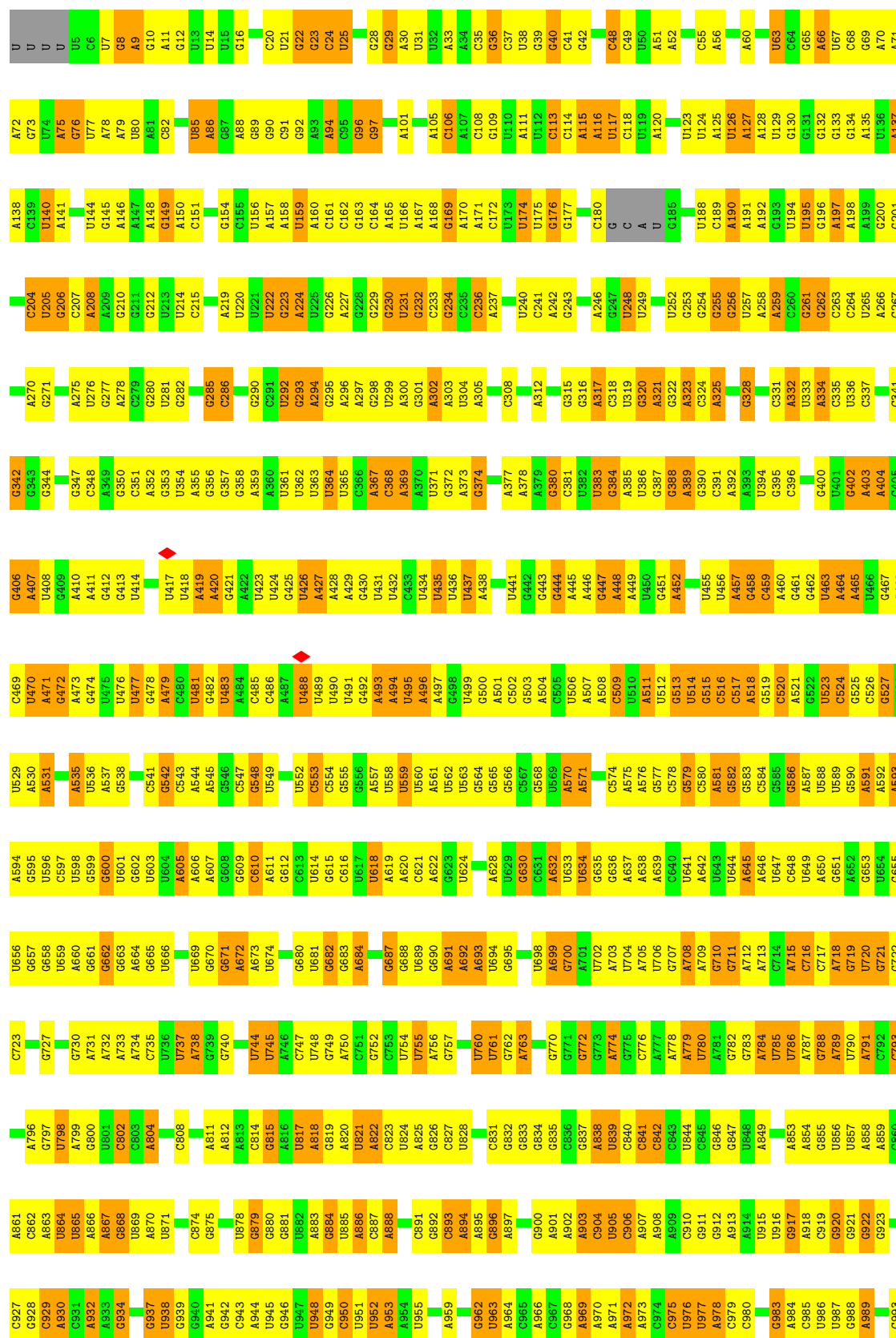
C2144	A2078	A2010	G1942	G1869	G1800	G1730	G1663	U1598	A1535	G1464	A1393	A1250
A2145	G2079	G2011	A1943	U1801	U1801	G1731	A1664	C1536	C1536	U1465	A1394	G1253
A2146	C2080	A2012	A1944	U1802	C1802	A1734	A1665	A1601	U1537	U1466	A1395	U1254
G2147	U2082	C2013	A1945	G1876	A1803	G1735	A1666	G1603	U1538	U1467	A1396	G1255
U2148	U2083	C2015	U1946	G1877	A1804	G1736	G1667	A1604	G1540	C1470	C1398	A1256
C2149	C2084	G2016	U1947	A1805	G1806	G1736	A1668	A1604	U1541	A1471	G1399	G1257
C2151	C2085	G2017	C1948	A1806	C1807	G1741	A1669	A1605	A1542	C1472	U1400	C1258
C2152	U2086	U2018	C1949	A1807	C1808	U1745	U1670	A1606	U1543	C1473	A1401	U1259
U2153	G2087	G2019	U1950	G1881	C1809	A1746	C1671	A1607	U1544	C1474	G1402	U1260
U2154	U2088	A2020	A1951	G1882	C1810	U1747	C1672	G1608	A1545	C1475	G1403	U1261
G2155	A2089	A2021	G1954	G1883	U1814	A1748	U1673	U1609	A1546	C1476	C1404	G1262
G2156	U2092	U2022	G1955	A1884	U1815	G1747	U1677	U1610	U1547	C1477	G1405	G1263
A2157	U2093	U2023	U1956	G1885	A1816	U1748	U1678	C1611	A1548	U1478	A1406	U1264
U2158	C2094	C2024	G1957	C1886	U1817	A1749	U1679	U1612	U1549	U1479	U1407	G1265
U2159	A2095	G2025	U1958	U1887	G1818	A1750	U1680	A1613	G1550	A1480	G1338	G1266
C2160	U2096	A2026	A1959	U1888	U1819	A1751	G1681	G1614	U1551	U1409	U1339	A1267
U2161	U2097	G2027	U1962	U1889	G1820	G1753	G1682	G1615	C1552	U1482	U1340	U1268
G2161	A2098	A2030	U1963	U1890	A1822	U1754	G1683	U1616	G1553	G1483	U1341	A1276
U2162	U2099	C2031	U1964	A1891	U1823	A1755	A1684	U1617	U1556	U1487	C1342	A1277
U2163	G2100	G2032	C1965	U1887	G1824	A1756	G1685	A1618	G1557	U1488	C1343	G1278
U2164	A2101	G2033	U1966	U1894	A1825	U1766	U1686	A1619	A1558	U1489	U1344	U1279
A2165	U2102	G2034	U1967	U1895	A1826	G1761	G1687	U1620	U1559	U1494	G1345	G1280
G2166	U2103	U2035	U1968	A1897	U1827	G1762	A1688	U1621	U	A1495	G1346	A1281
A2167	A2104	G2036	U1969	U1898	U1828	G1763	U1689	G1622	G	A1496	G1348	G1282
C2168	G2105	A2037	C1970	C1901	U1829	U1764	U1691	U1623	A	U1497	C1349	A1283
G2169	U2110	G2038	G1971	C1902	G1830	G1765	U1692	A1624	A	A1498	A1350	A1284
A2170	U2111	G2039	U1972	A1903	G1831	A1766	U1693	G1625	G	U1499	G1351	U1285
A2171	G2112	A2040	U1973	G1906	G1832	G1767	A1694	G1628	U	A1500	G1352	U1286
A2172	U2113	C2041	U1974	A1907	U1834	A1769	C1696	U1629	C	U1501	G1353	G1289
G2173	U2114	G2042	U1975	U1910	G1835	A1770	C1697	C1633	A	A1502	U1430	G1290
U2174	A2115	C2043	U1976	G1913	A1836	G1772	A1698	A1634	U1570	U1503	A1431	U1293
G2175	U2116	G2050	U1977	U1914	C1837	G1775	A1699	G1635	G1571	U1506	U1432	G1294
G2176	G2117	C2051	G1978	G1915	A1838	G1776	G1700	U1636	U1572	U1507	U1434	A1295
A2177	U2118	G2052	U1979	G1916	U1841	G1777	G1701	A1637	A1573	G1508	A1435	G1296
U2178	A2119	G2053	U1983	C1917	G1842	G1778	U1706	G1640	A1577	U1509	A1437	U1297
U2180	G2120	A2054	U1986	U1918	C1845	G1779	U1707	A1641	U1578	A1510	A1440	A1298
C2181	A2121	G2055	C1987	A1919	A1846	A1780	G1708	G1642	G1579	C1511	U1440	A1299
C2182	G2122	C2057	U1988	A1920	G1847	C1781	G1709	A1643	U1580	A1512	G1444	C1300
U2183	A2123	G2058	U1989	U1924	U1848	U1782	A1710	A1644	G1581	U1513	U1445	G1301
A2184	G2124	C2059	C1990	A1925	G1849	G1783	U1713	G1645	G1582	U1514	G1446	C1302
C2185	U2125	A2061	U1991	A1926	C1850	U1784	U1714	G1646	G1583	A1515	U1446	U1303
G2186	A2126	G2062	C1992	C1927	G1851	U1785	A1715	A1647	U1584	G1516	G1449	U1304
C2187	G2127	G2063	U1996	U1930	G1854	A1787	A1716	A1648	A1585	G1517	A1451	G1307
U2188	C2128	A2064	C1997	C1931	A1854	U1788	C1717	G1651	U1586	C1523	G1450	A1308
U2189	G2132	A2065	U1998	U1932	A1855	U1789	U1720	A1652	U1587	C1524	A1451	G1309
G2190	A2133	G2066	U1999	U1933	U1859	A1790	G1721	G1653	A1588	U1526	G1452	G1375
U2191	C2134	U2067	U2000	A1934	U1862	A1791	U1722	G1654	U1589	U1527	U1453	G1372
U2192	C2135	A2068	U2001	U1935	G1863	U1792	U1723	A1655	C1590	G1528	A1456	A1382
G2193	U2136	G2069	C2003	A1936	A1724	A1793	G1725	A1656	U1591	U1529	A1457	G1313
U2194	A2137	U2070	G2004	G1937	U1864	C1794	G1726	G1657	U1592	G1530	A1458	A1314
U2195	U2138	G2071	G2005	U1938	A1865	A1795	U1727	C1658	U1593	C1531	A1459	A1315
G2196	C2139	U2072	G2006	U1939	G1866	C1797	U1728	C1659	G1594	A1532	G1460	U1316
U2197	A2140	G2073	A2008	A1940	G1867	A1798	A1728	A1661	U1595	U1533	A1461	G1388
G2198	U2141	U2074	U2009	C1941	A1868	A1799	G1729	G1662	U1597	A1534	A1462	C1389
C2199	U2142	U2075	U2010	U2011	U2012	U2013	U2014	U2015	U2016	U2017	U2018	U2019
U2200	U2143	U2076	U2011	U2012	U2013	U2014	U2015	U2016	U2017	U2018	U2019	U2202



• Molecule 52: 5S ribosomal RNA



• Molecule 53: 16S ribosomal RNA

Chain 5:  26% 49% 23%

4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	12464	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	2.467	Depositor
Minimum map value	-0.851	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.139	Depositor
Recommended contour level	0.53	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	0.22	0/383	0.55	0/504
2	1	0.13	0/484	0.45	0/637
3	2	0.21	0/306	0.60	0/401
4	9	0.16	0/3071	0.45	0/4147
5	A	0.17	0/1954	0.47	0/2642
6	B	0.16	0/1721	0.47	0/2323
7	C	0.22	0/1691	0.57	1/2267 (0.0%)
8	D	0.19	0/1188	0.47	0/1593
9	E	0.18	0/1384	0.48	0/1867
10	F	0.17	0/1266	0.51	0/1700
11	G	0.18	0/1126	0.46	0/1517
12	H	0.17	0/1044	0.50	0/1395
13	I	0.16	0/820	0.57	0/1103
14	J	0.21	0/844	0.51	0/1136
15	K	0.27	0/1094	0.66	3/1468 (0.2%)
16	L	0.15	0/962	0.43	0/1289
17	M	0.16	0/483	0.49	0/643
18	N	0.18	0/679	0.49	1/907 (0.1%)
19	O	0.13	0/659	0.43	0/885
20	P	0.15	0/684	0.45	0/913
21	Q	0.16	0/545	0.50	0/730
22	R	0.14	0/698	0.44	0/936
23	S	0.14	0/631	0.37	0/838
24	T	0.22	0/475	0.56	0/621
25	a	0.16	0/2267	0.44	0/3044
26	b	0.16	0/1795	0.47	0/2412
27	c	0.17	0/1671	0.51	0/2246
28	d	0.17	0/1409	0.47	0/1894
29	e	0.15	0/1420	0.42	0/1912
30	f	0.17	0/1183	0.46	0/1587
31	g	0.38	0/969	0.72	0/1295
32	h	0.15	0/968	0.44	0/1298
33	i	0.16	0/1186	0.42	0/1592
34	j	0.16	0/953	0.43	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.15	0/1170	0.43	0/1559
36	l	0.18	0/1104	0.51	2/1481 (0.1%)
37	m	0.18	0/973	0.52	0/1309
38	n	0.28	0/897	0.61	0/1198
39	o	0.17	0/948	0.46	0/1262
40	p	0.17	0/961	0.44	0/1278
41	q	0.19	0/828	0.58	0/1111
42	r	0.16	0/1077	0.45	0/1441
43	s	0.15	0/732	0.47	0/988
44	t	0.18	0/879	0.45	0/1165
45	u	0.16	0/665	0.44	0/884
46	v	0.16	0/519	0.45	0/695
47	w	0.14	0/826	0.43	0/1104
48	x	0.14	0/353	0.42	0/474
49	y	0.33	0/457	0.68	0/601
50	z	0.17	0/412	0.46	0/547
51	3	0.10	0/69073	0.26	0/107710
52	4	0.09	0/2505	0.26	0/3902
53	5	0.10	0/35768	0.26	0/55764
54	6	0.10	0/1808	0.25	0/2817
54	7	0.10	0/1808	0.25	0/2817
All	All	0.13	0/161776	0.34	7/241124 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	7	ILE	N-CA-C	-7.83	105.13	112.96
15	K	119	GLY	CA-C-N	-7.44	110.43	122.33
15	K	119	GLY	C-N-CA	-7.44	110.43	122.33
15	K	120	VAL	N-CA-C	7.43	118.46	108.27
18	N	19	VAL	N-CA-C	-5.83	108.17	113.71

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	0	380	0	429	22	0
2	1	477	0	530	15	0
3	2	304	0	350	21	0
4	9	3021	0	3050	99	0
5	A	1921	0	1973	54	0
6	B	1698	0	1768	62	0
7	C	1660	0	1719	61	0
8	D	1173	0	1267	36	0
9	E	1362	0	1377	38	0
10	F	1246	0	1308	49	0
11	G	1110	0	1226	42	0
12	H	1028	0	1094	55	0
13	I	809	0	894	44	0
14	J	829	0	855	32	0
15	K	1076	0	1170	47	0
16	L	951	0	1014	32	0
17	M	474	0	509	29	0
18	N	673	0	730	16	0
19	O	646	0	677	12	0
20	P	675	0	728	20	0
21	Q	535	0	562	33	0
22	R	682	0	691	18	0
23	S	629	0	681	22	0
24	T	471	0	522	16	0
25	a	2225	0	2301	76	0
26	b	1762	0	1808	53	0
27	c	1644	0	1731	52	0
28	d	1388	0	1469	45	0
29	e	1396	0	1481	30	0
30	f	1160	0	1172	33	0
31	g	960	0	1014	7	0
32	h	959	0	1039	5	0
33	i	1164	0	1192	35	0
34	j	944	0	1019	30	0
35	k	1153	0	1256	48	0
36	l	1079	0	1134	31	0
37	m	958	0	1011	39	0
38	n	889	0	952	21	0
39	o	938	0	1008	31	0
40	p	947	0	1028	53	0
41	q	811	0	858	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	r	1068	0	1150	32	0
43	s	720	0	803	27	0
44	t	872	0	972	15	0
45	u	657	0	695	19	0
46	v	513	0	560	21	0
47	w	818	0	870	27	0
48	x	344	0	333	2	0
49	y	452	0	472	24	0
50	z	408	0	440	14	0
51	3	61664	0	30954	1471	0
52	4	2239	0	1137	36	0
53	5	31943	0	16058	864	0
54	6	1618	0	821	35	0
54	7	1618	0	821	33	0
All	All	149141	0	102683	3653	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 15.

The worst 5 of 3653 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)
53:5:887:C:N4	53:5:888:A:N6	1.83	1.26
53:5:580:C:H42	53:5:756:A:N6	1.47	1.10
53:5:580:C:N4	53:5:756:A:H62	1.50	1.09
51:3:573:A:N6	51:3:588:G:H21	1.53	1.06
51:3:573:A:H62	51:3:588:G:N2	1.55	1.04

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%)	44 (98%)	1 (2%)	0	100	100
2	1	57/59 (97%)	52 (91%)	5 (9%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	391/394 (99%)	368 (94%)	23 (6%)	0	100	100
5	A	238/294 (81%)	222 (93%)	16 (7%)	0	100	100
6	B	213/273 (78%)	193 (91%)	20 (9%)	0	100	100
7	C	201/205 (98%)	189 (94%)	12 (6%)	0	100	100
8	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
9	E	165/215 (77%)	141 (86%)	23 (14%)	1 (1%)	21	58
10	F	152/155 (98%)	135 (89%)	17 (11%)	0	100	100
11	G	139/142 (98%)	125 (90%)	14 (10%)	0	100	100
12	H	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
13	I	99/108 (92%)	91 (92%)	8 (8%)	0	100	100
14	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
15	K	134/139 (96%)	123 (92%)	11 (8%)	0	100	100
16	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
17	M	58/61 (95%)	54 (93%)	4 (7%)	0	100	100
18	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
19	O	78/94 (83%)	74 (95%)	4 (5%)	0	100	100
20	P	81/85 (95%)	76 (94%)	5 (6%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	78 (95%)	4 (5%)	0	100	100
23	S	75/87 (86%)	73 (97%)	2 (3%)	0	100	100
24	T	51/60 (85%)	46 (90%)	5 (10%)	0	100	100
25	a	283/287 (99%)	270 (95%)	13 (5%)	0	100	100
26	b	227/287 (79%)	210 (92%)	17 (8%)	0	100	100
27	c	208/212 (98%)	192 (92%)	16 (8%)	0	100	100
28	d	173/180 (96%)	159 (92%)	14 (8%)	0	100	100
29	e	174/184 (95%)	168 (97%)	6 (3%)	0	100	100
30	f	143/149 (96%)	127 (89%)	16 (11%)	0	100	100
31	g	124/161 (77%)	116 (94%)	7 (6%)	1 (1%)	16	52
32	h	126/137 (92%)	116 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	i	142/146 (97%)	128 (90%)	14 (10%)	0	100	100
34	j	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
35	k	146/151 (97%)	130 (89%)	16 (11%)	0	100	100
36	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
37	m	117/124 (94%)	108 (92%)	9 (8%)	0	100	100
38	n	108/116 (93%)	102 (94%)	6 (6%)	0	100	100
39	o	113/119 (95%)	101 (89%)	12 (11%)	0	100	100
40	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
41	q	97/100 (97%)	87 (90%)	10 (10%)	0	100	100
42	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
43	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
44	t	109/111 (98%)	99 (91%)	10 (9%)	0	100	100
45	u	84/104 (81%)	76 (90%)	8 (10%)	0	100	100
46	v	61/65 (94%)	54 (88%)	7 (12%)	0	100	100
47	w	96/111 (86%)	88 (92%)	8 (8%)	0	100	100
48	x	42/97 (43%)	39 (93%)	3 (7%)	0	100	100
49	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6211/7064 (88%)	5755 (93%)	454 (7%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	g	45	PHE
9	E	164	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	324/325 (100%)	324 (100%)	0	100	100
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	123 (100%)	0	100	100
9	E	150/196 (76%)	150 (100%)	0	100	100
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	123 (100%)	0	100	100
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	95 (100%)	0	100	100
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	115 (98%)	2 (2%)	53	67
16	L	100/105 (95%)	100 (100%)	0	100	100
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	241 (100%)	0	100	100
26	b	186/233 (80%)	186 (100%)	0	100	100
27	c	182/184 (99%)	182 (100%)	0	100	100
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	123/134 (92%)	123 (100%)	0	100	100
31	g	101/129 (78%)	93 (92%)	8 (8%)	11	31
32	h	102/110 (93%)	102 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	103 (100%)	0	100	100
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	105 (100%)	0	100	100
38	n	96/99 (97%)	94 (98%)	2 (2%)	47	64
39	o	101/105 (96%)	101 (100%)	0	100	100
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	116 (100%)	0	100	100
43	s	82/208 (39%)	82 (100%)	0	100	100
44	t	96/96 (100%)	96 (100%)	0	100	100
45	u	69/85 (81%)	69 (100%)	0	100	100
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	41 (100%)	0	100	100
49	y	48/49 (98%)	47 (98%)	1 (2%)	47	64
50	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5417/6076 (89%)	5404 (100%)	13 (0%)	85	85

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	g	43	LYS
31	g	46	LYS
49	y	47	MET
38	n	61	LYS
38	n	63	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
39	o	15	GLN
47	w	85	ASN
39	o	80	GLN

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Mol	Chain	Res	Type
41	q	99	HIS
12	H	93	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	1067 (37%)	77 (2%)
52	4	103/108 (95%)	41 (39%)	1 (0%)
53	5	1490/1520 (98%)	564 (37%)	35 (2%)
54	6	75/76 (98%)	26 (34%)	0
54	7	75/76 (98%)	26 (34%)	0
All	All	4618/4687 (98%)	1724 (37%)	113 (2%)

5 of 1724 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	11	U
51	3	12	A
51	3	13	C
51	3	16	A
51	3	26	G

5 of 113 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	2097	A
53	5	1445	G
51	3	2604	U
53	5	1401	A
53	5	921	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

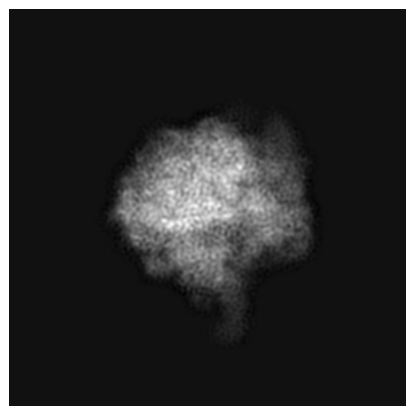
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13275. These allow visual inspection of the internal detail of the map and identification of artifacts.

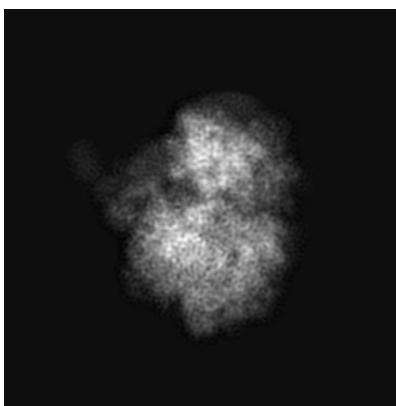
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

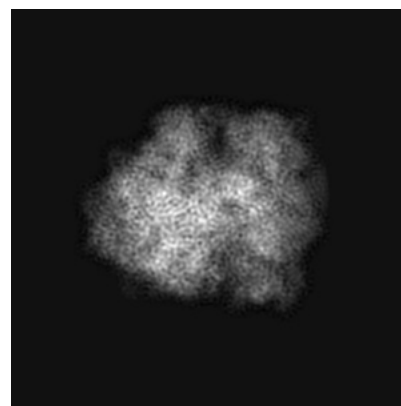
6.1.1 Primary map



X

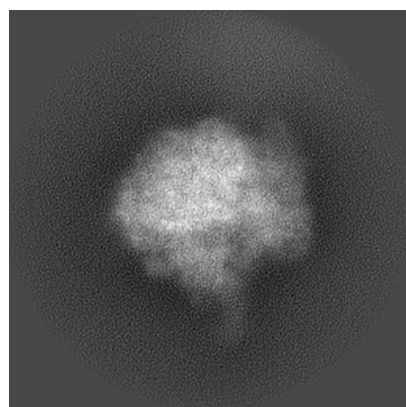


Y

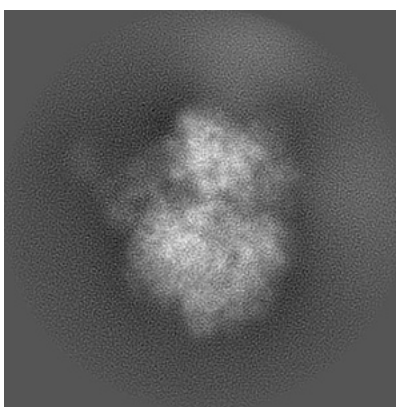


Z

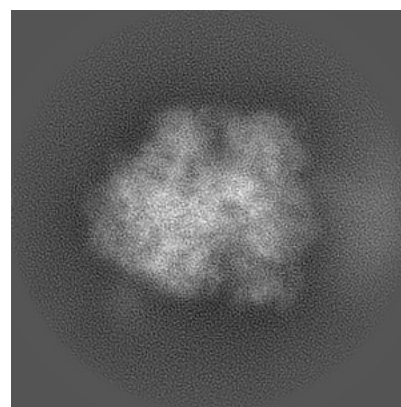
6.1.2 Raw map



X



Y

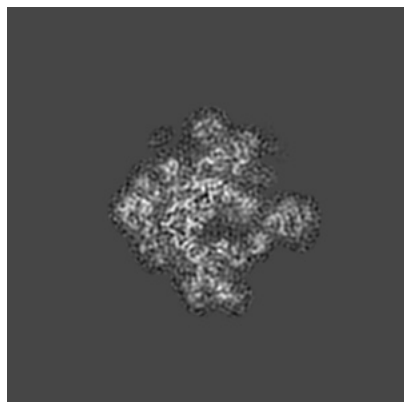


Z

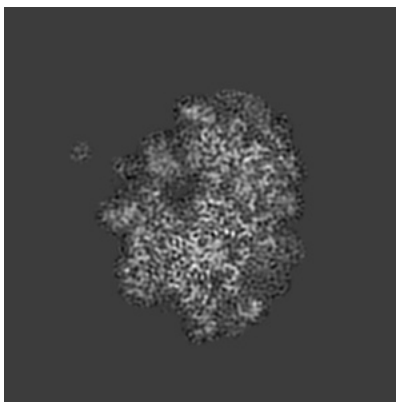
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

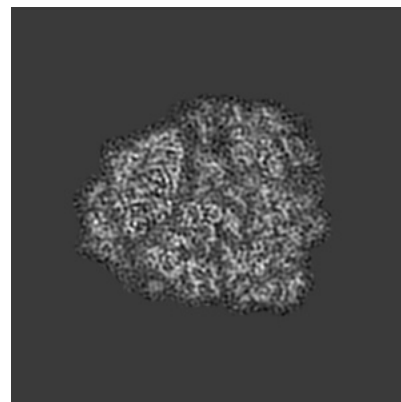
6.2.1 Primary map



X Index: 128

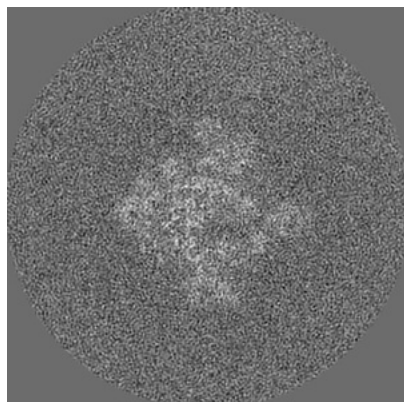


Y Index: 128

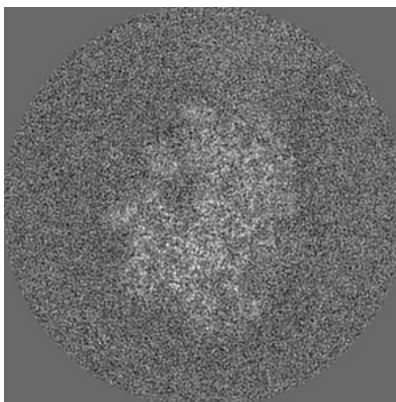


Z Index: 128

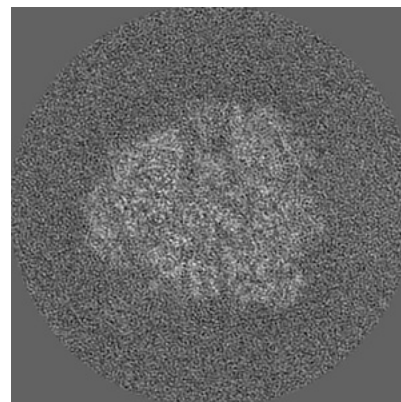
6.2.2 Raw map



X Index: 128



Y Index: 128

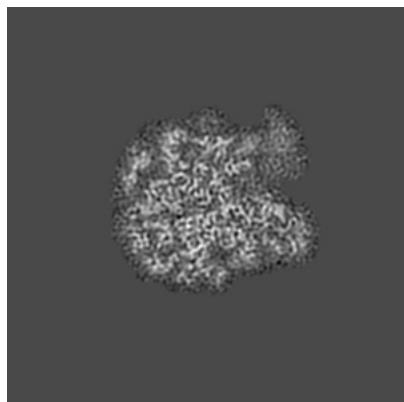


Z Index: 128

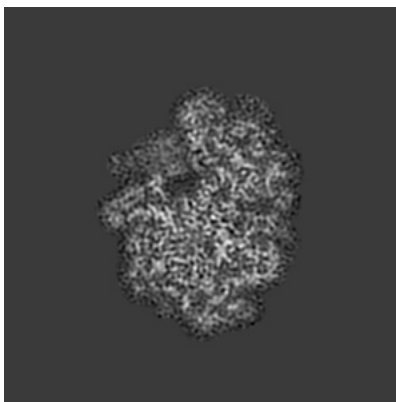
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

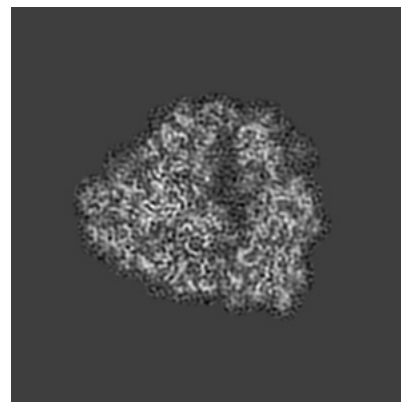
6.3.1 Primary map



X Index: 104

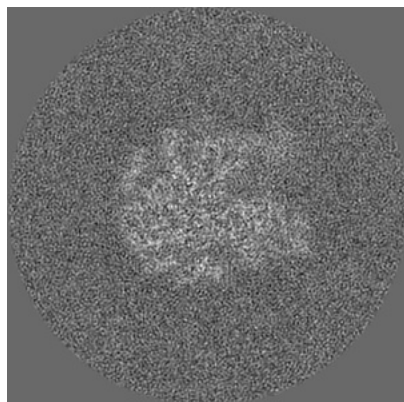


Y Index: 120

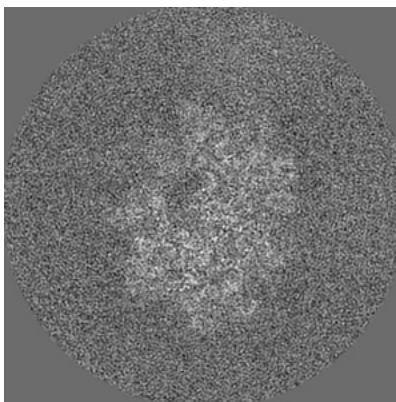


Z Index: 122

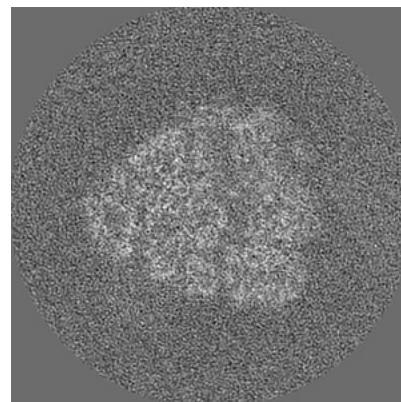
6.3.2 Raw map



X Index: 106



Y Index: 125

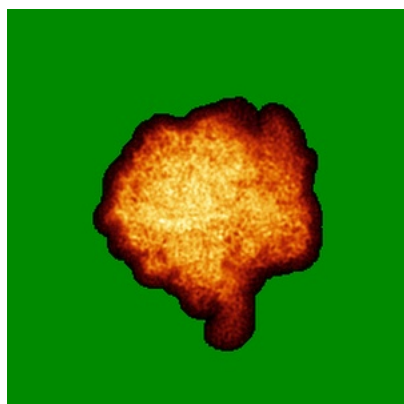


Z Index: 125

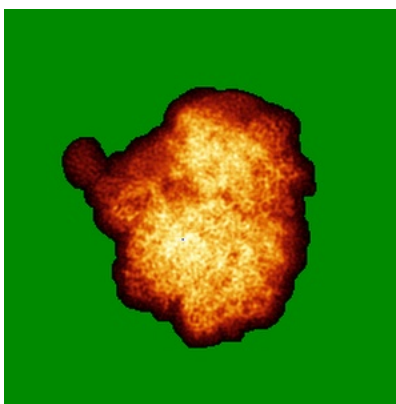
The images above show the largest variance slices of the map in three orthogonal directions.

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

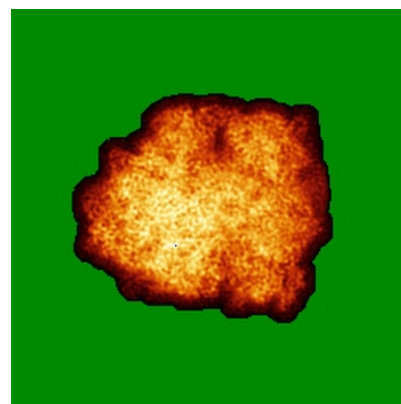
6.4.1 Primary map



X

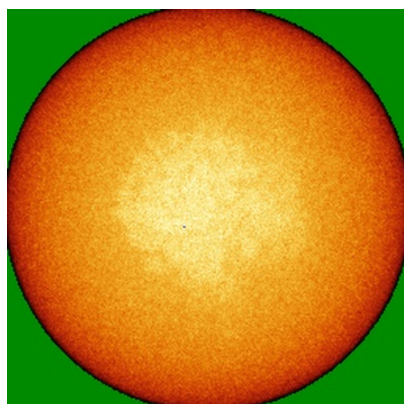


Y

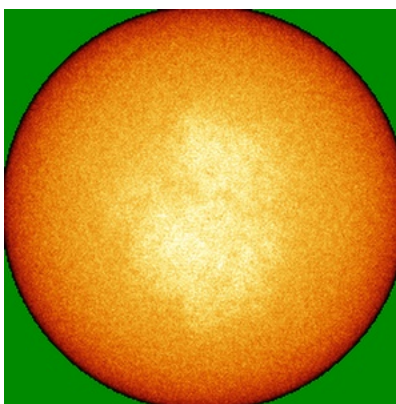


Z

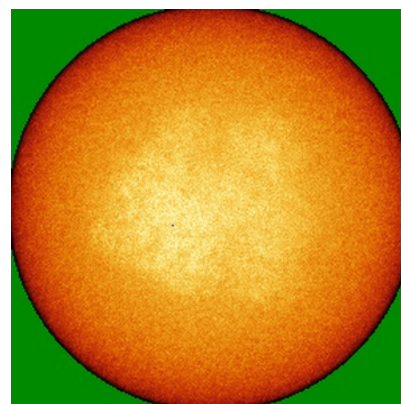
6.4.2 Raw map



X



Y



Z

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

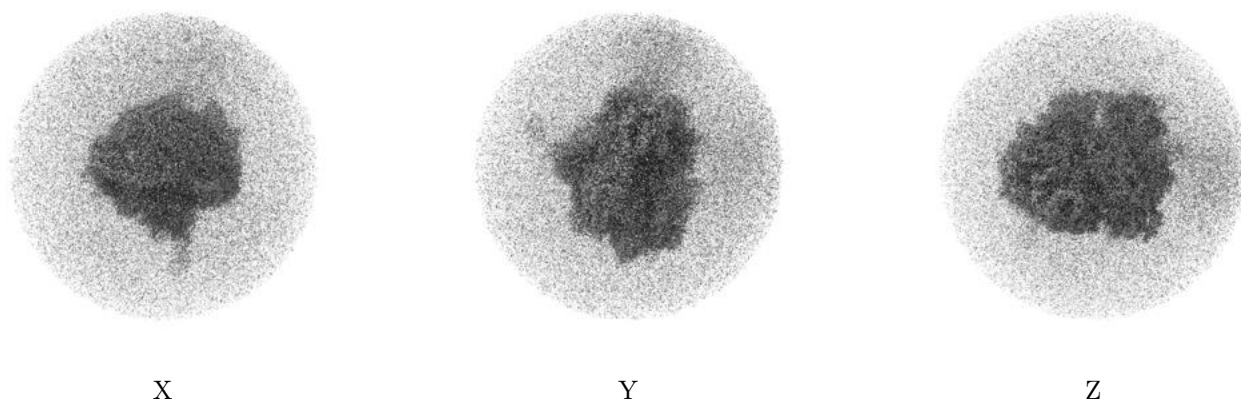
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.53. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

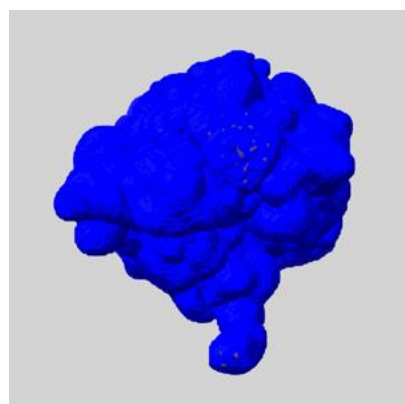
6.6 Mask visualisation [i](#)

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

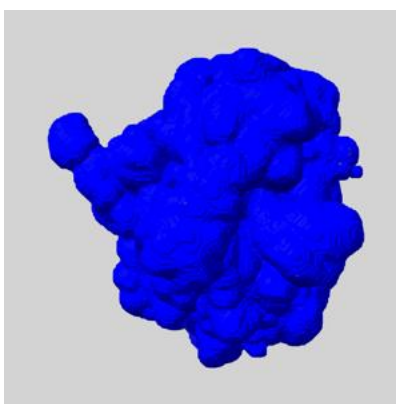
A mask typically either:

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

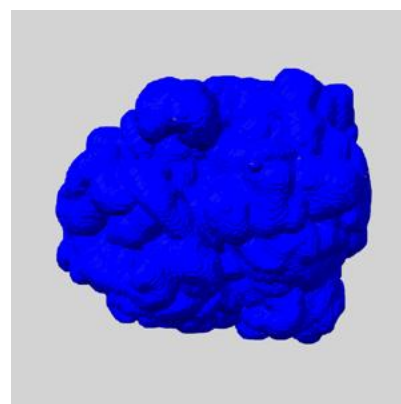
6.6.1 emd_13275_msk_1.map [i](#)



X



Y

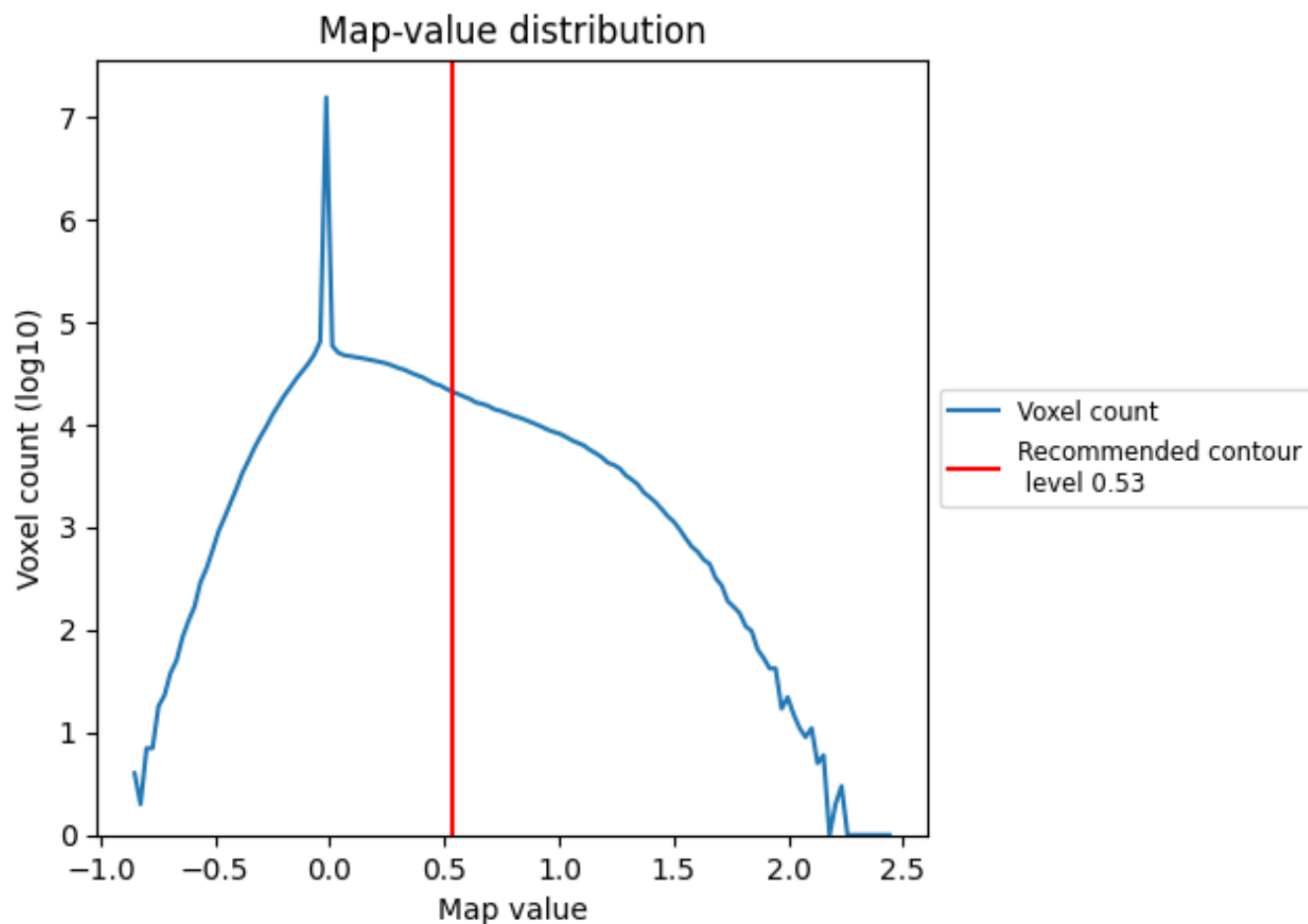


Z

7 Map analysis [i](#)

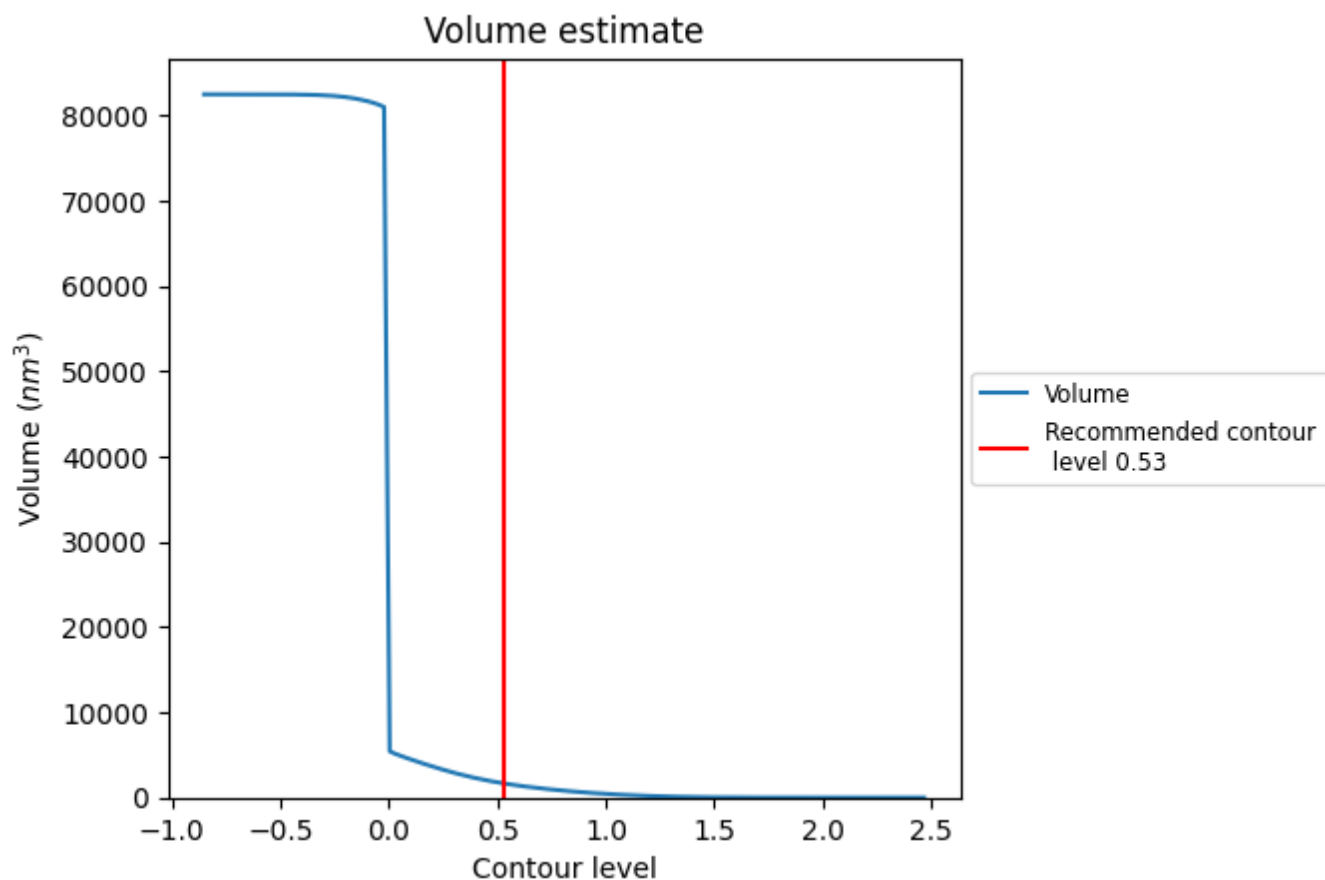
This section contains the results of statistical analysis of the map.

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.

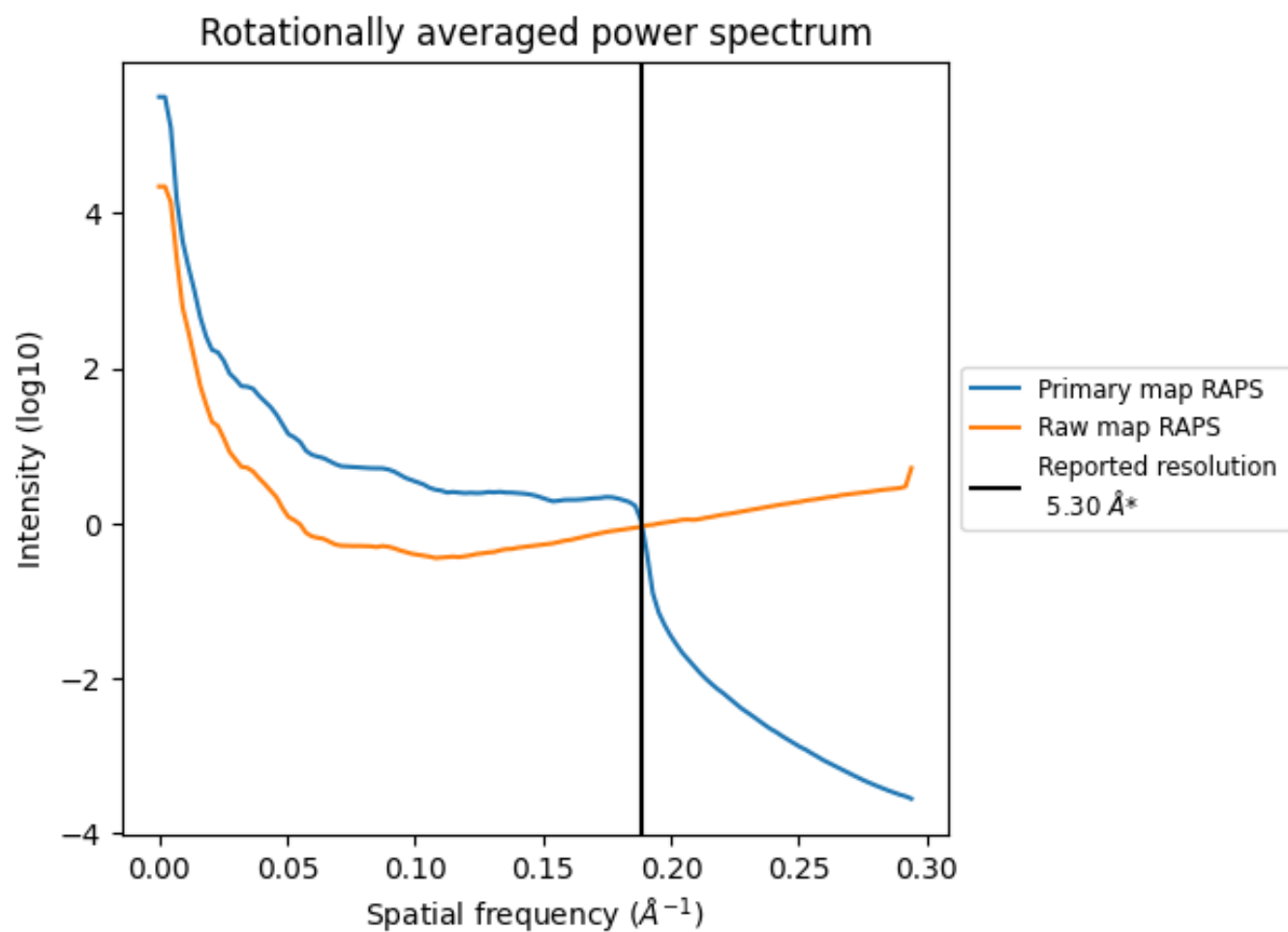
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1661 nm³; this corresponds to an approximate mass of 1501 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 ⓘ

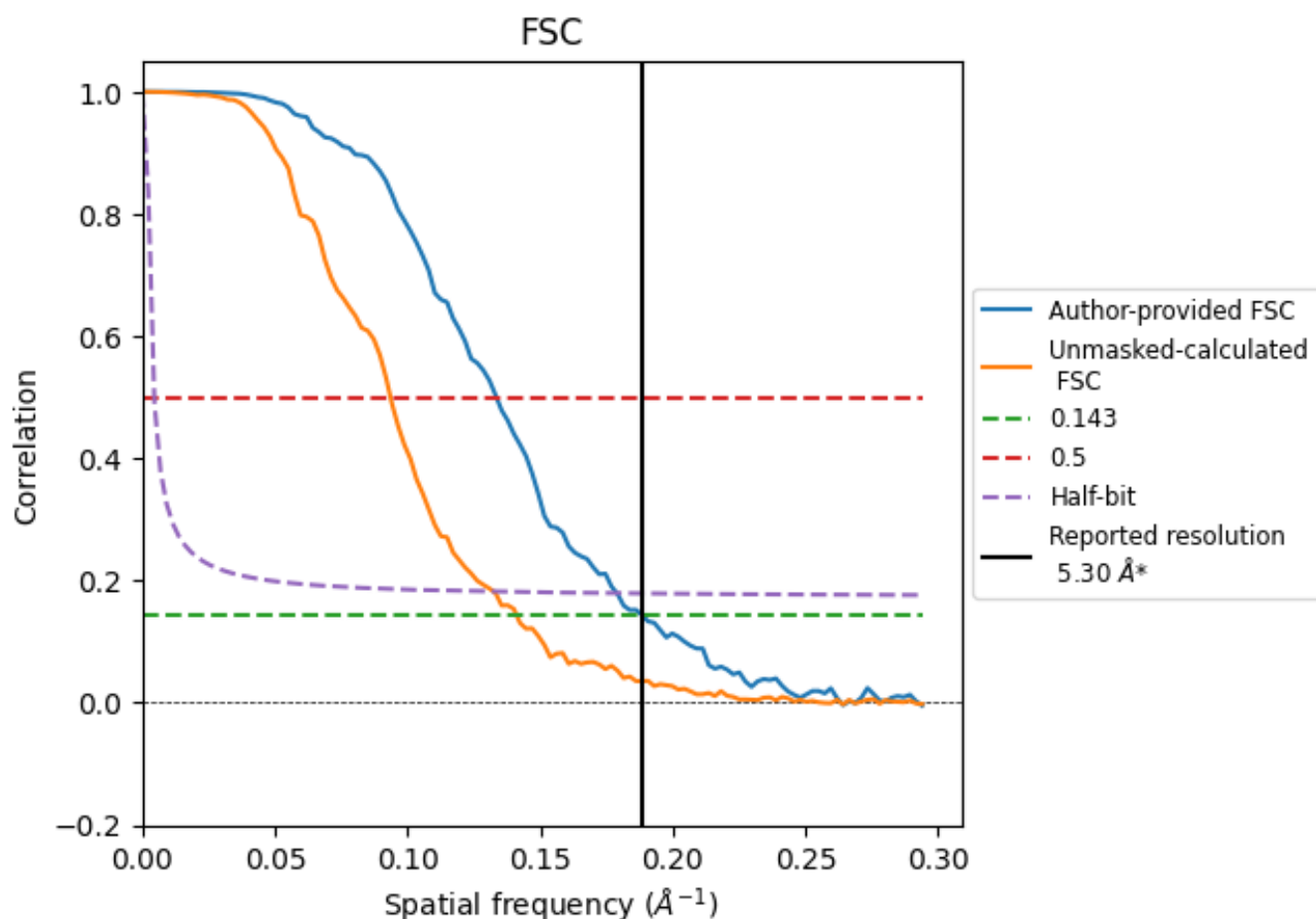


*Reported resolution corresponds to spatial frequency of 0.189 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.189 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

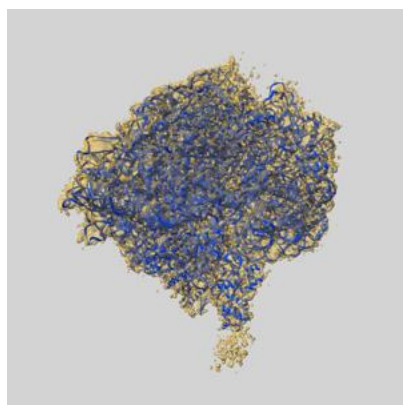
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.30	-	-
Author-provided FSC curve	5.31	7.49	5.59
Unmasked-calculated*	7.08	10.68	7.55

*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 7.08 differs from the reported value 5.3 by more than 10 %

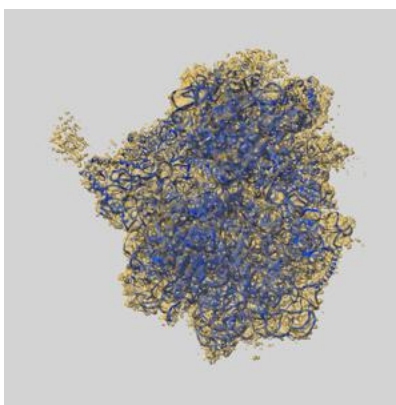
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13275 and PDB model 7PAK. Per-residue inclusion information can be found in section [3](#) on page [14](#).

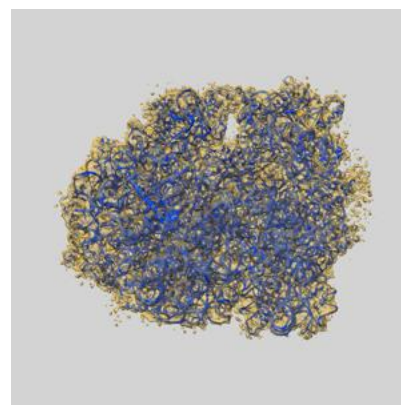
9.1 Map-model overlay [i](#)



X



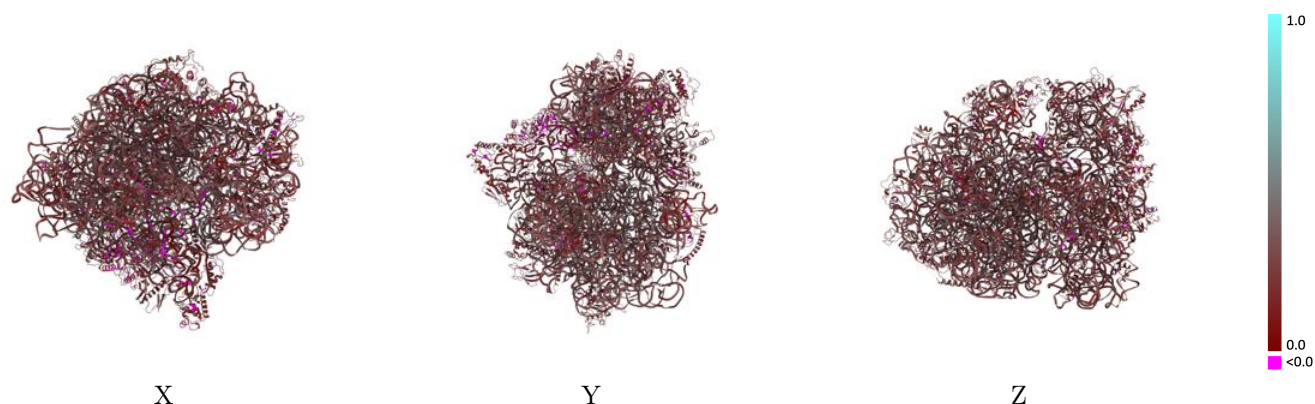
Y



Z

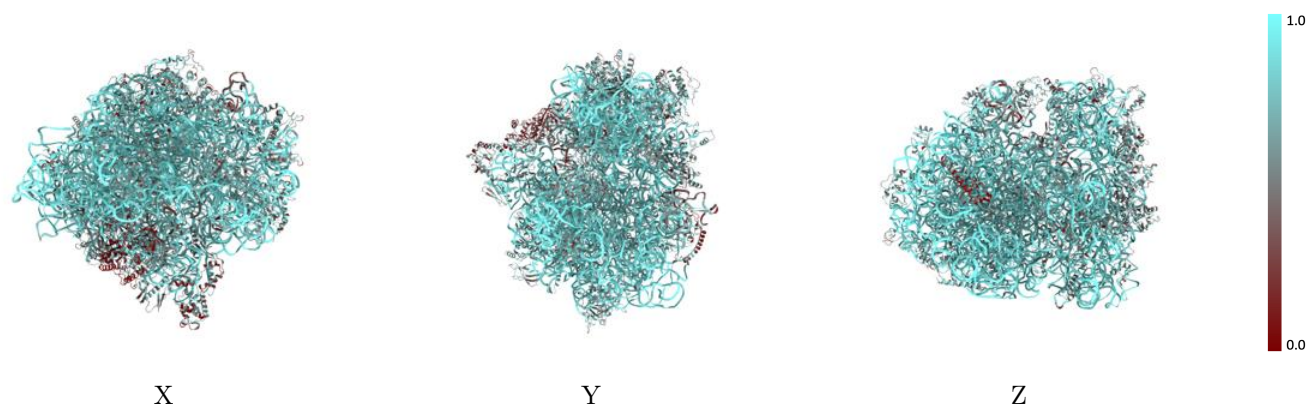
The images above show the 3D surface view of the map at the recommended contour level 0.53 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



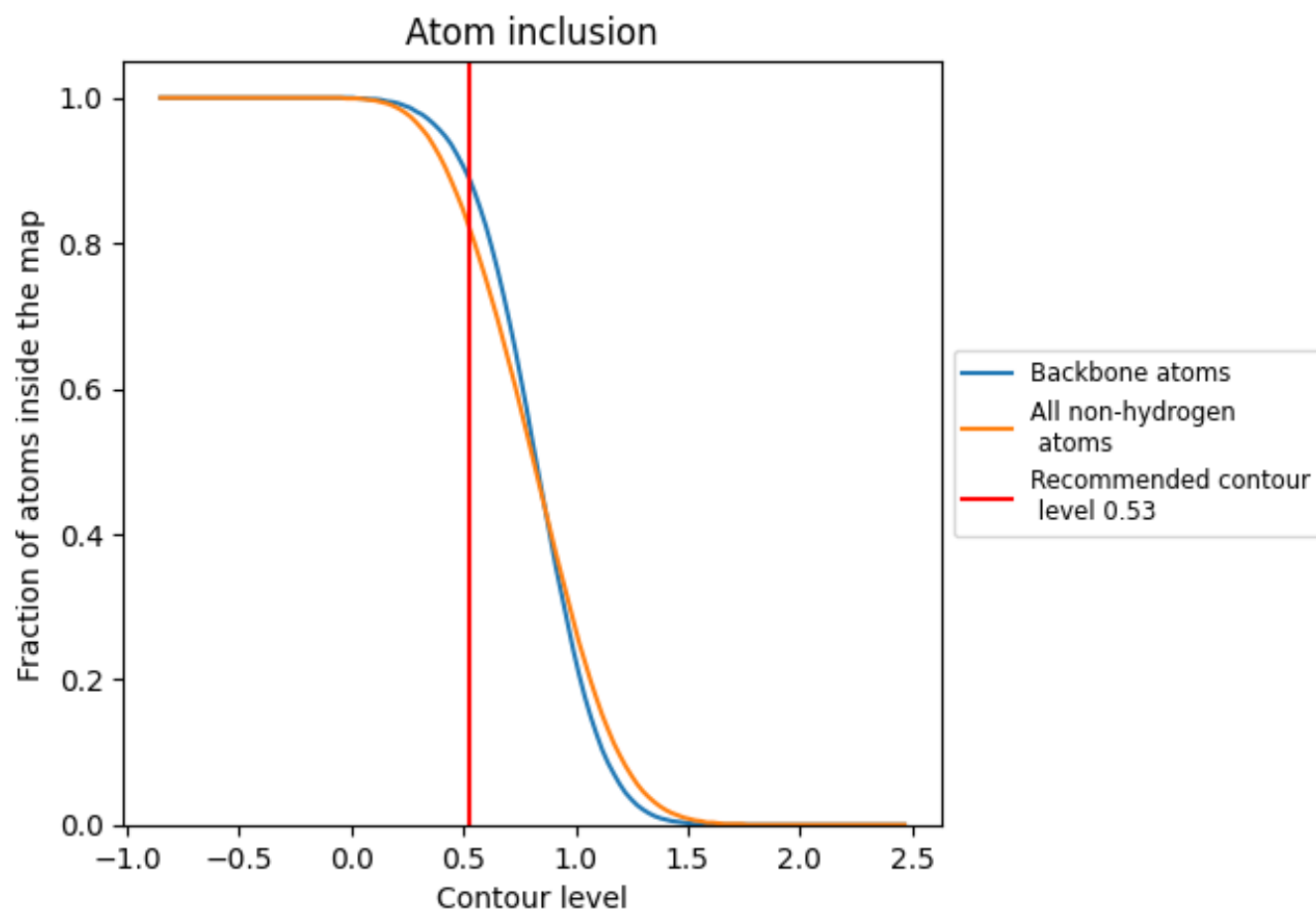
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.53).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 82% 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 (0.53) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.2750
0	 0.7970	 0.2880
1	 0.7340	 0.2870
2	 0.7160	 0.2640
3	 0.9210	 0.2920
4	 0.9270	 0.2910
5	 0.9240	 0.2830
6	 0.5180	 0.0740
7	 0.8380	 0.2340
9	 0.2150	 0.1850
A	 0.6080	 0.2560
B	 0.6330	 0.2560
C	 0.6170	 0.2390
D	 0.6600	 0.2570
E	 0.5830	 0.2700
F	 0.6080	 0.2550
G	 0.6380	 0.2430
H	 0.6260	 0.2360
I	 0.5990	 0.2410
J	 0.6760	 0.2590
K	 0.6940	 0.2810
L	 0.6390	 0.2540
M	 0.6950	 0.2570
N	 0.6330	 0.2380
O	 0.7010	 0.2820
P	 0.6730	 0.2480
Q	 0.6820	 0.2590
R	 0.6370	 0.2470
S	 0.7100	 0.2520
T	 0.6120	 0.2330
a	 0.7320	 0.2860
b	 0.7050	 0.2670
c	 0.6730	 0.2730
d	 0.6140	 0.2260
e	 0.6070	 0.2740



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Chain	Atom inclusion	Q-score
f	 0.2590	 0.1870
g	 0.4790	 0.2030
h	 0.3890	 0.1950
i	 0.7210	 0.2710
j	 0.6810	 0.2930
k	 0.7260	 0.2840
l	 0.7240	 0.2880
m	 0.7180	 0.2680
n	 0.6640	 0.2550
o	 0.6920	 0.2860
p	 0.7310	 0.2490
q	 0.6830	 0.2860
r	 0.7230	 0.2700
s	 0.6980	 0.2920
t	 0.5660	 0.2680
u	 0.7230	 0.2790
v	 0.7390	 0.2790
w	 0.6920	 0.2640
x	 0.6120	 0.2650
y	 0.7740	 0.2980
z	 0.7610	 0.2920