



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 03:42 PM UTC

PDB ID : 7PAM / pdb_00007pam
EMDB ID : EMD-13277
Title : 70S ribosome with A*- and P/E-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 6.80 Å(reported)
Based on initial models : 7OOC, 7OOD, 4V7C

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

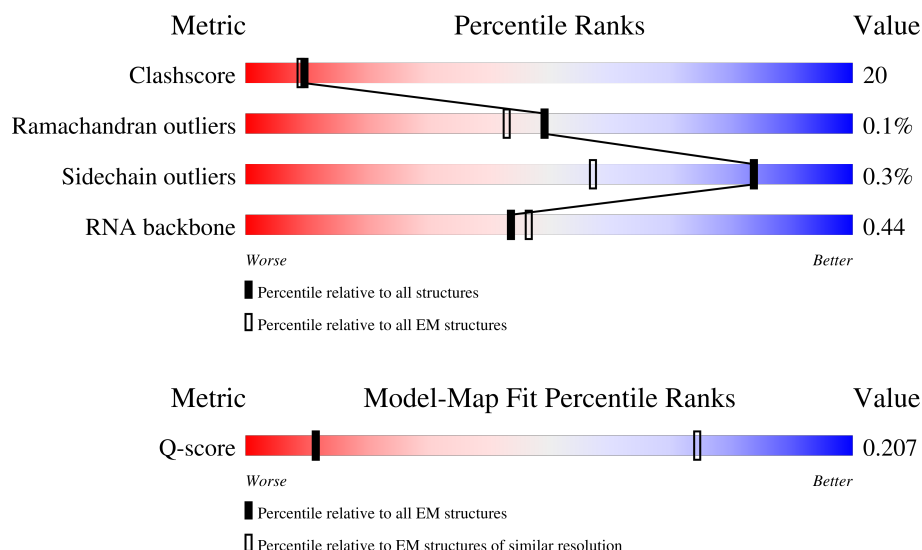
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.80 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	503 (6.30 - 7.30)

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	
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	
30	g	161	
31	h	137	
32	i	146	
33	j	122	
34	k	151	
35	l	139	
36	m	124	
37	n	116	
38	o	119	
39	p	127	
40	q	100	
41	r	159	
42	s	237	
43	t	111	
44	u	104	
45	v	65	
46	w	111	
47	x	97	
48	y	57	
49	z	53	
50	3	2907	
51	4	108	
52	5	1520	
53	6	76	

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Mol	Chain	Length	Quality of chain
53	8	76	25% 51% 22%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146120 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 30S ribosomal protein S2.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			1160	746	204	207	3	0

- 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
			960	612	167	178	3	0

- 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
			959	616	160	177	6	0

- 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
			1164	737	213	209	5	0

- 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
			944	595	178	167	4	0

- 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	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
53	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

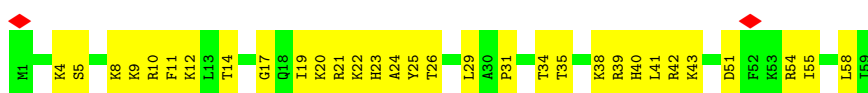
- Molecule 1: 50S ribosomal protein L34

Chain 0: 



- Molecule 2: 50S ribosomal protein L35

Chain 1: 

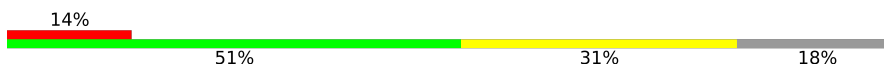


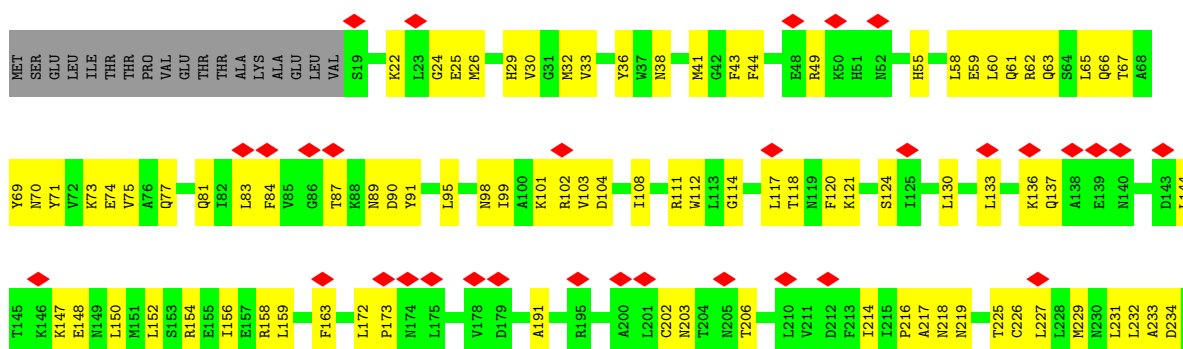
- Molecule 3: 50S ribosomal protein L36

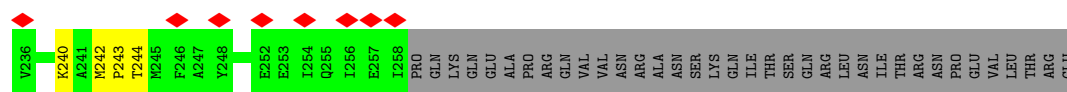
Chain 2: 



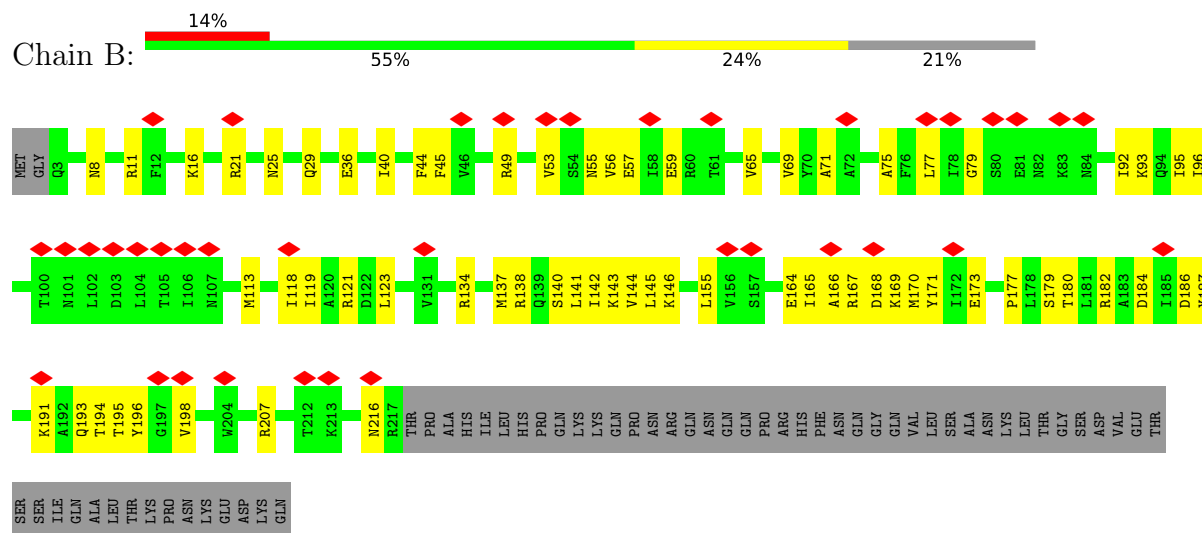
- Molecule 4: 30S ribosomal protein S2

Chain A: 

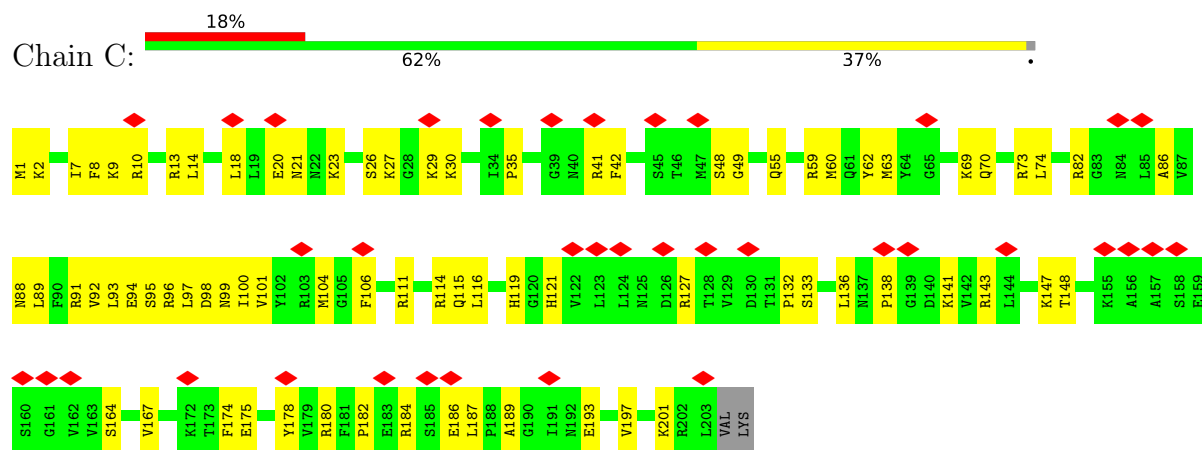




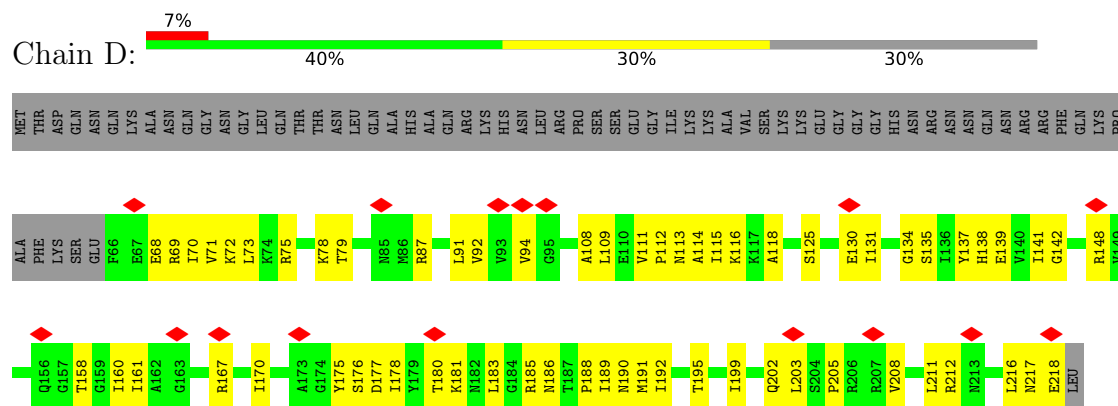
• Molecule 5: 30S ribosomal protein S3



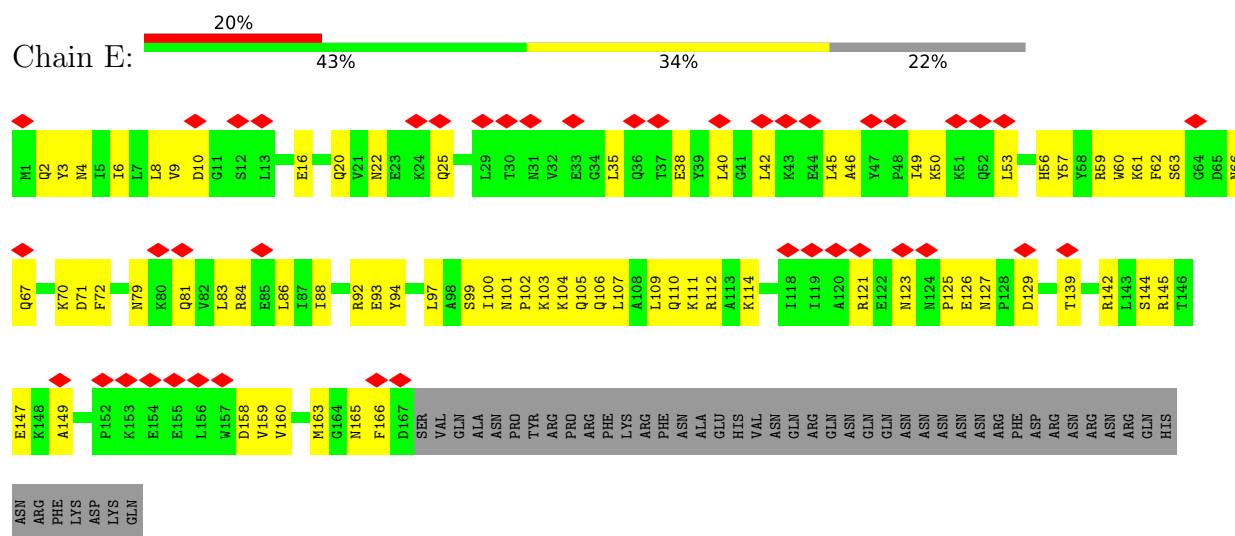
• Molecule 6: 30S ribosomal protein S4



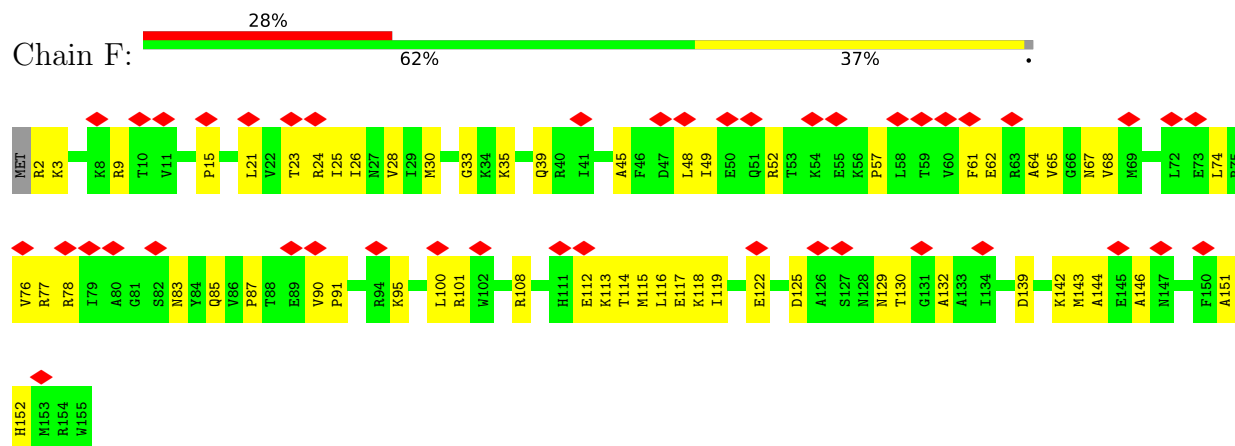
• Molecule 7: 30S ribosomal protein S5



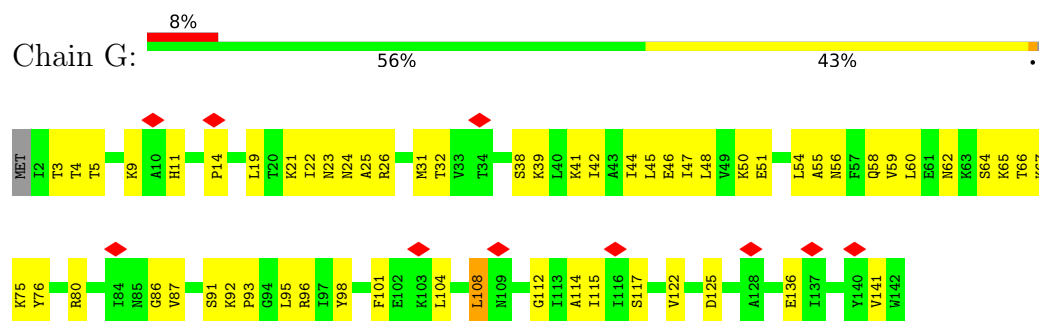
• Molecule 8: 30S ribosomal protein S6



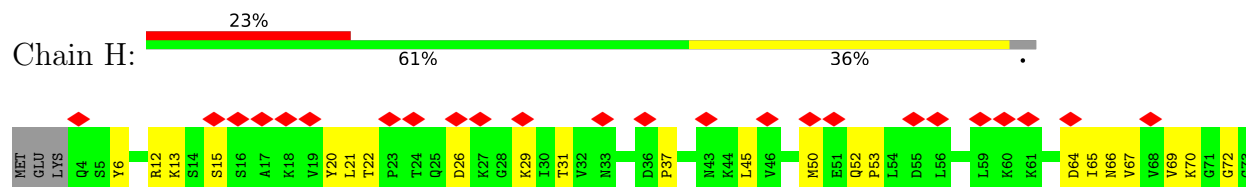
• Molecule 9: 30S ribosomal protein S7

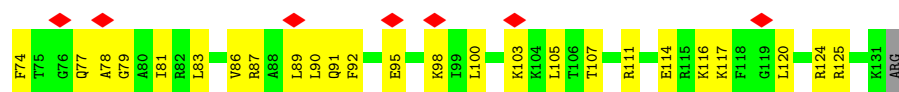


• Molecule 10: 30S ribosomal protein S8

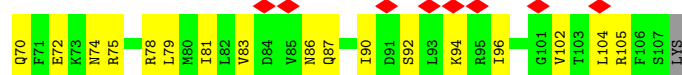


• Molecule 11: 30S ribosomal protein S9

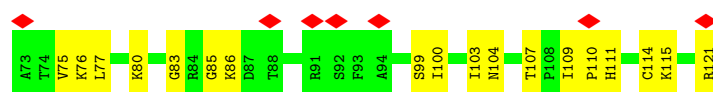
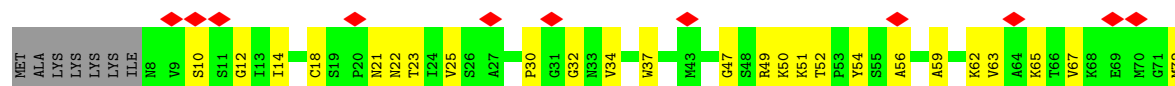




- Molecule 12: 30S ribosomal protein S10



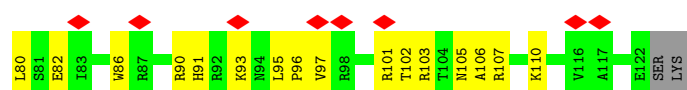
- Molecule 13: 30S ribosomal protein S11



- Molecule 14: 30S ribosomal protein S12



- Molecule 15: 30S ribosomal protein S13



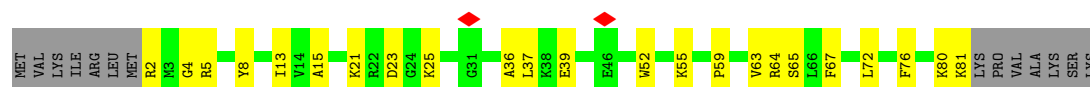
- Molecule 16: 30S ribosomal protein S14 type Z



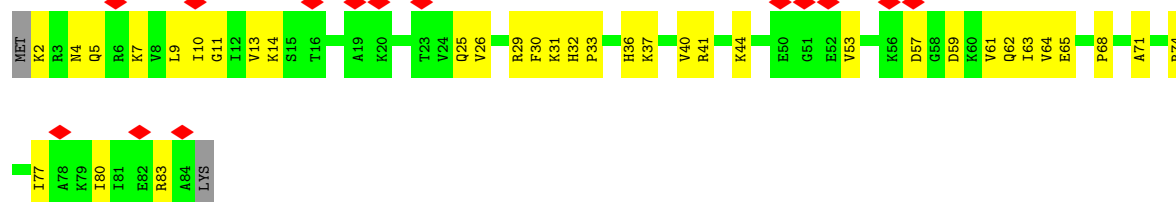
- Molecule 17: 30S ribosomal protein S15



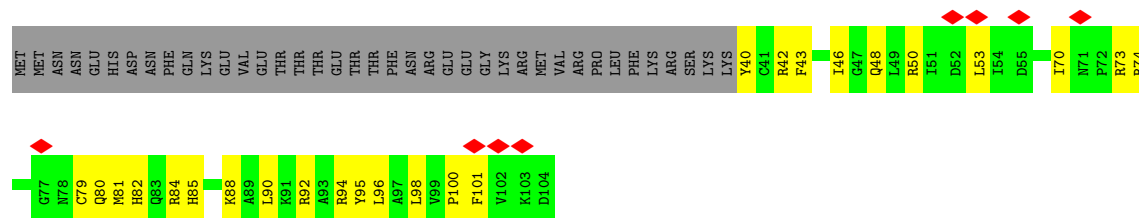
- Molecule 18: 30S ribosomal protein S16



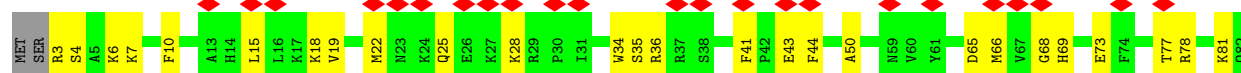
- Molecule 19: 30S ribosomal protein S17

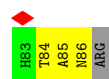


- Molecule 20: 30S ribosomal protein S18

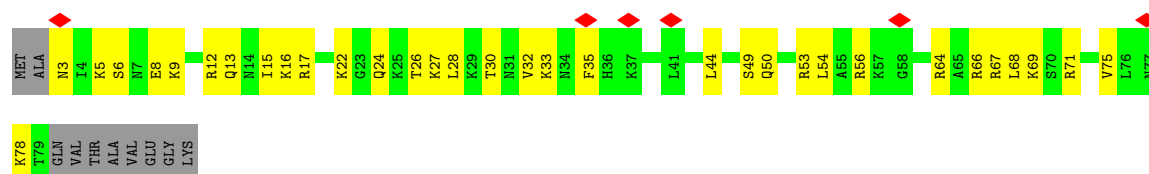


- Molecule 21: 30S ribosomal protein S19





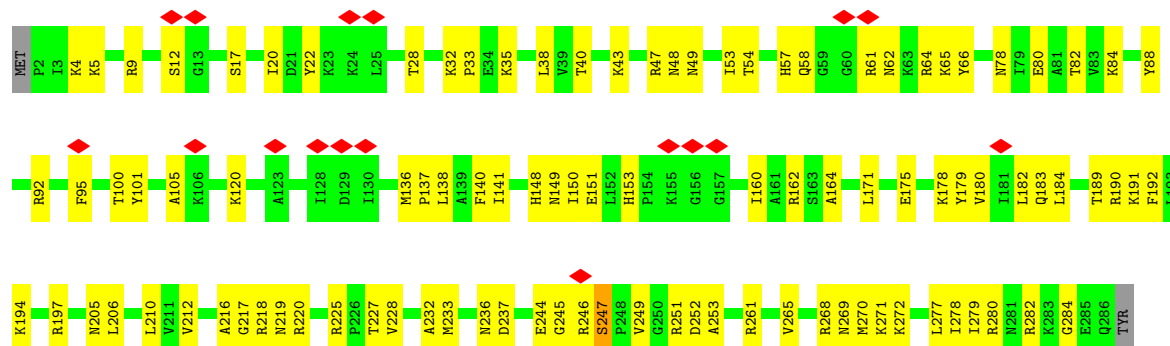
• Molecule 22: 30S ribosomal protein S20



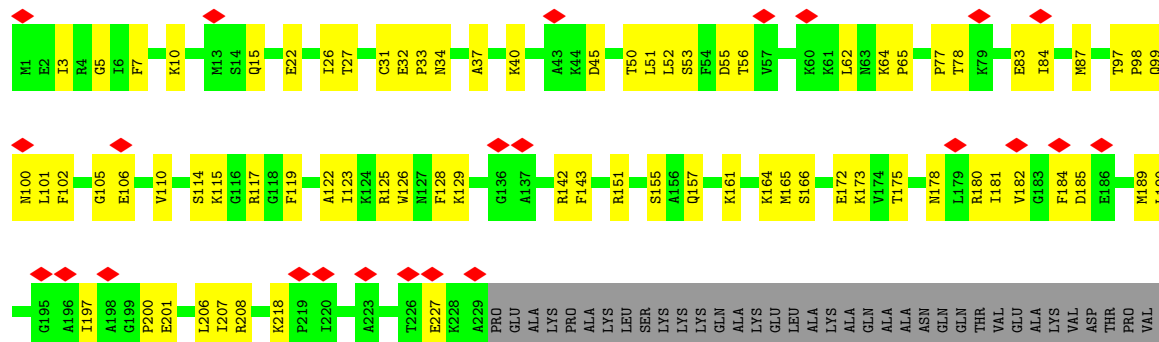
• Molecule 23: 30S ribosomal protein S21



• Molecule 24: 50S ribosomal protein L2



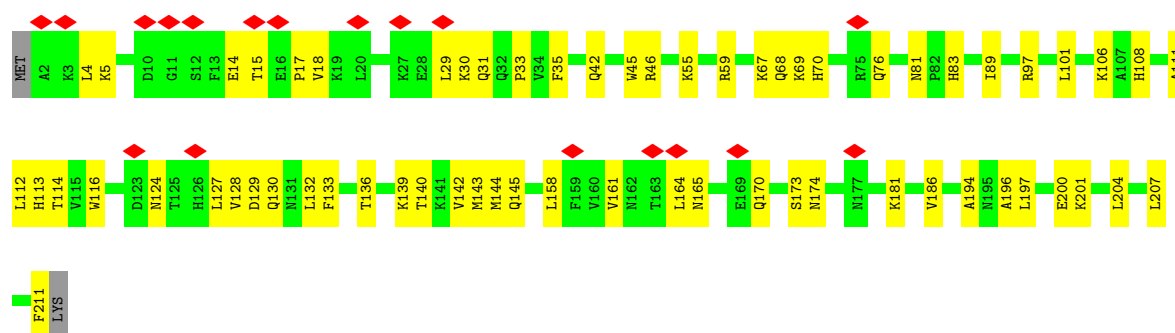
• Molecule 25: 50S ribosomal protein L3



GLU
PRO
LYS
PRO
THR
GLU
VAL
LYS
LYS
ALA
ALA
PRO
VAL
VAL
GLU
LYS
GLY
GLU
ASP
LYS

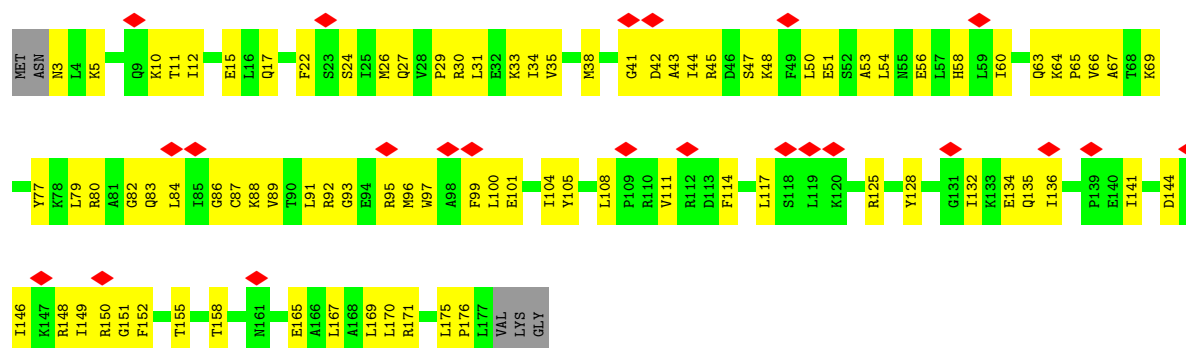
• Molecule 26: 50S ribosomal protein L4

Chain c:  8% 69% 30%



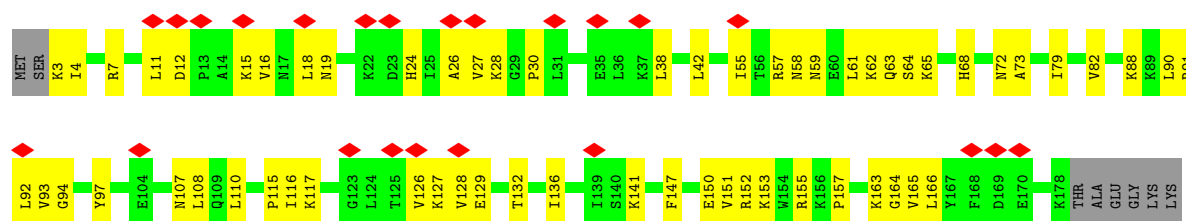
• Molecule 27: 50S ribosomal protein L5

Chain d:  13% 49% 48%



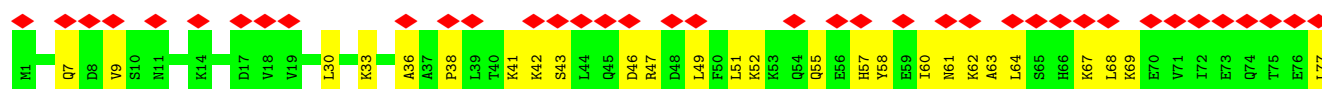
• Molecule 28: 50S ribosomal protein L6

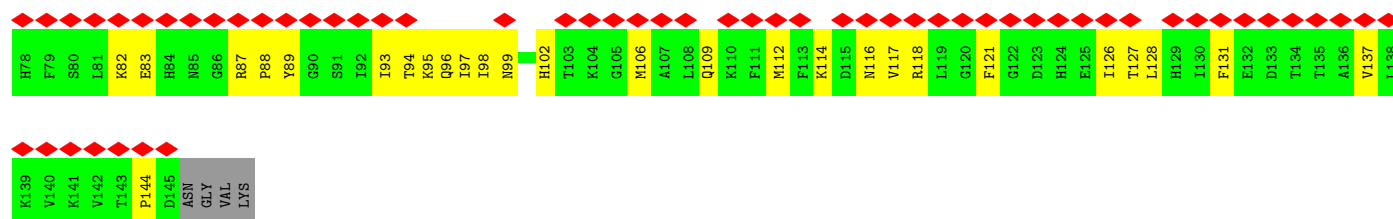
Chain e:  12% 62% 33%



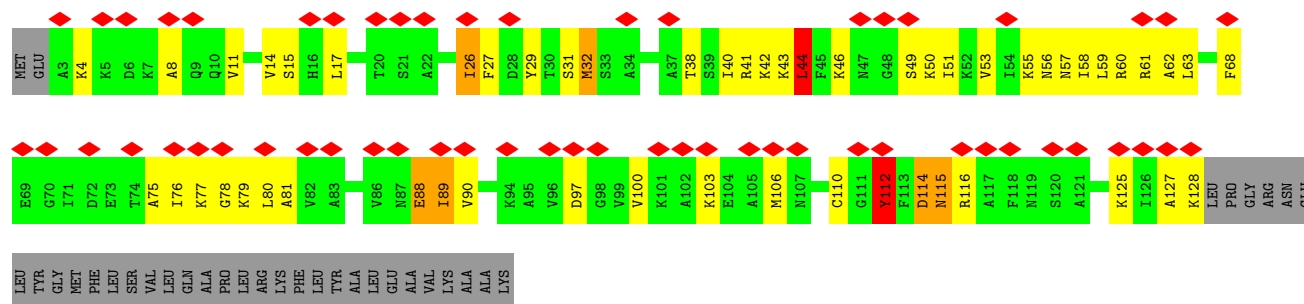
• Molecule 29: 50S ribosomal protein L9

Chain f:  64% 62% 36%

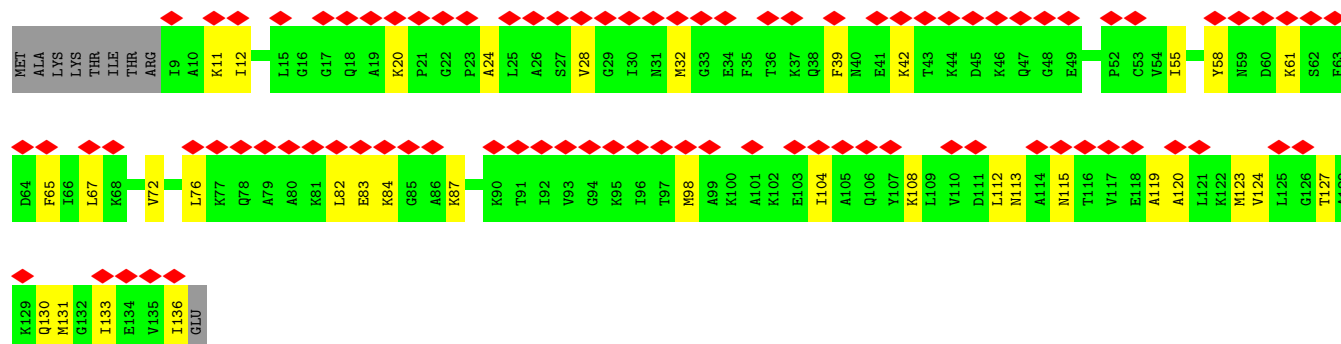




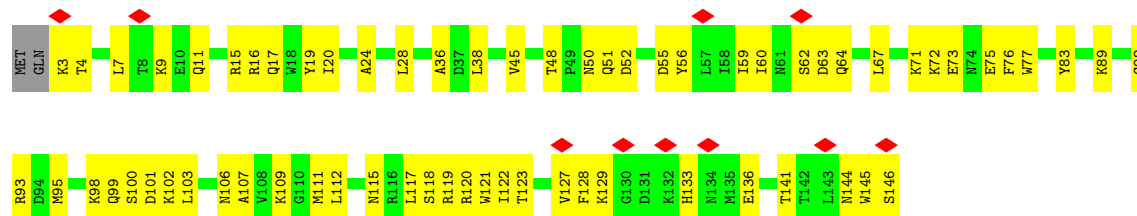
• Molecule 30: 50S ribosomal protein L10



• Molecule 31: 50S ribosomal protein L11

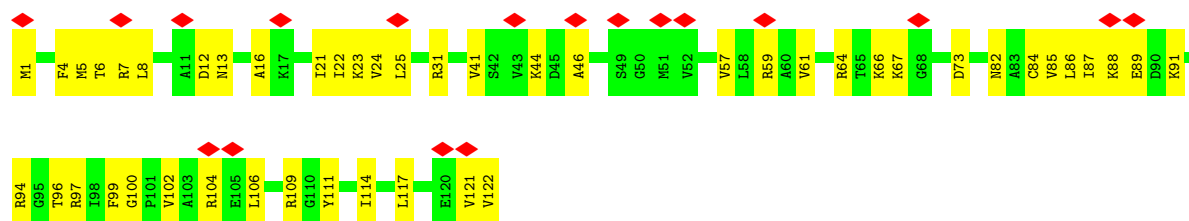


• Molecule 32: 50S ribosomal protein L13

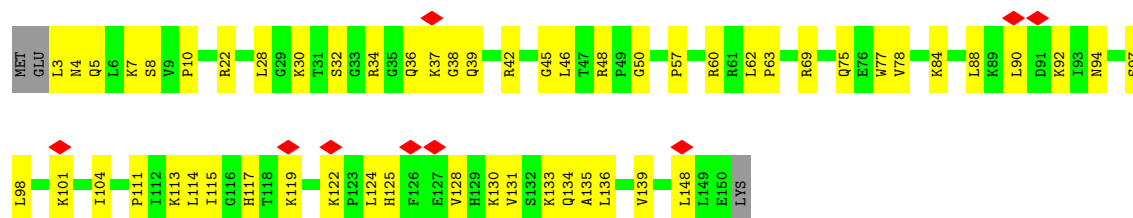


• Molecule 33: 50S ribosomal protein L14

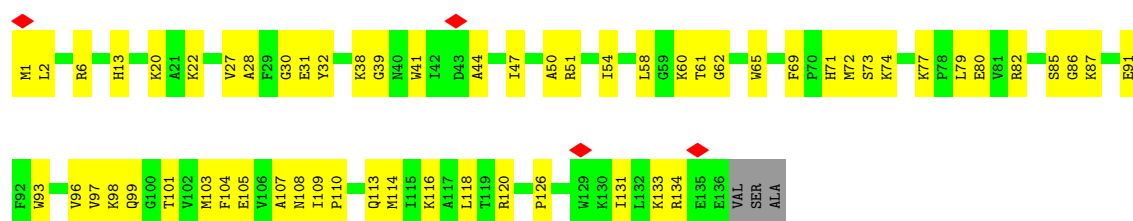




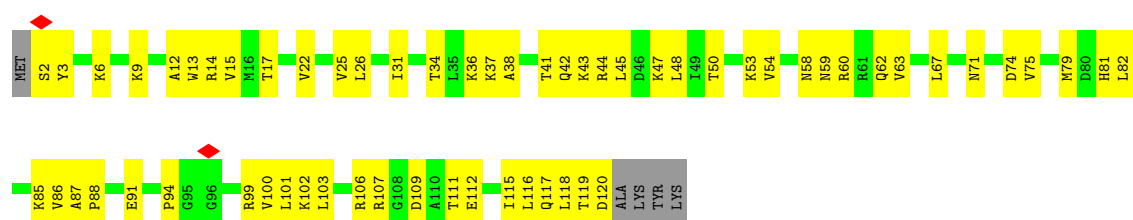
• Molecule 34: 50S ribosomal protein L15



• Molecule 35: 50S ribosomal protein L16



• Molecule 36: 50S ribosomal protein L17

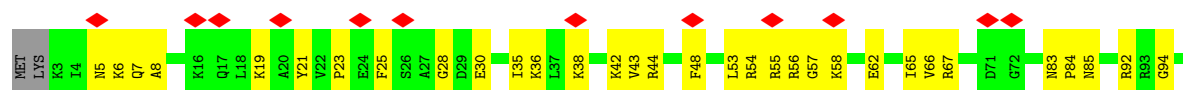


• Molecule 37: 50S ribosomal protein L18





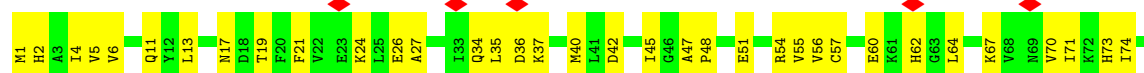
- Molecule 38: 50S ribosomal protein L19



- Molecule 39: 50S ribosomal protein L20



- Molecule 40: 50S ribosomal protein L21



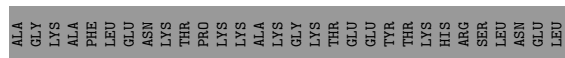
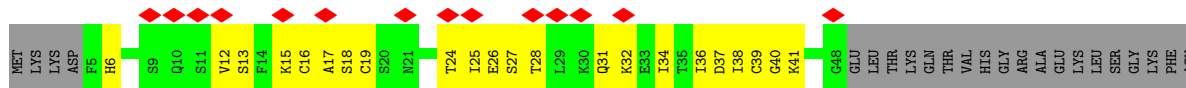
- Molecule 41: 50S ribosomal protein L22



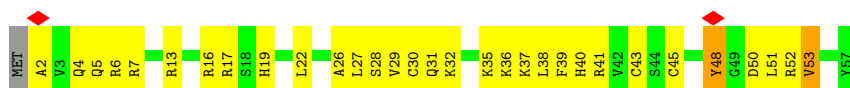
- Molecule 42: 50S ribosomal protein L23



- Molecule 47: 50S ribosomal protein L31



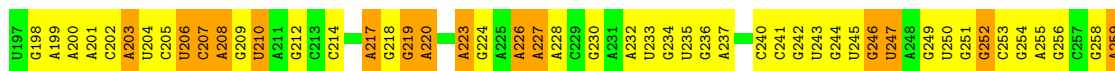
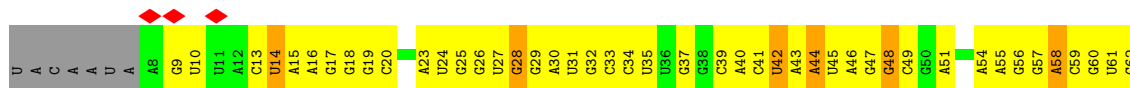
- Molecule 48: 50S ribosomal protein L32

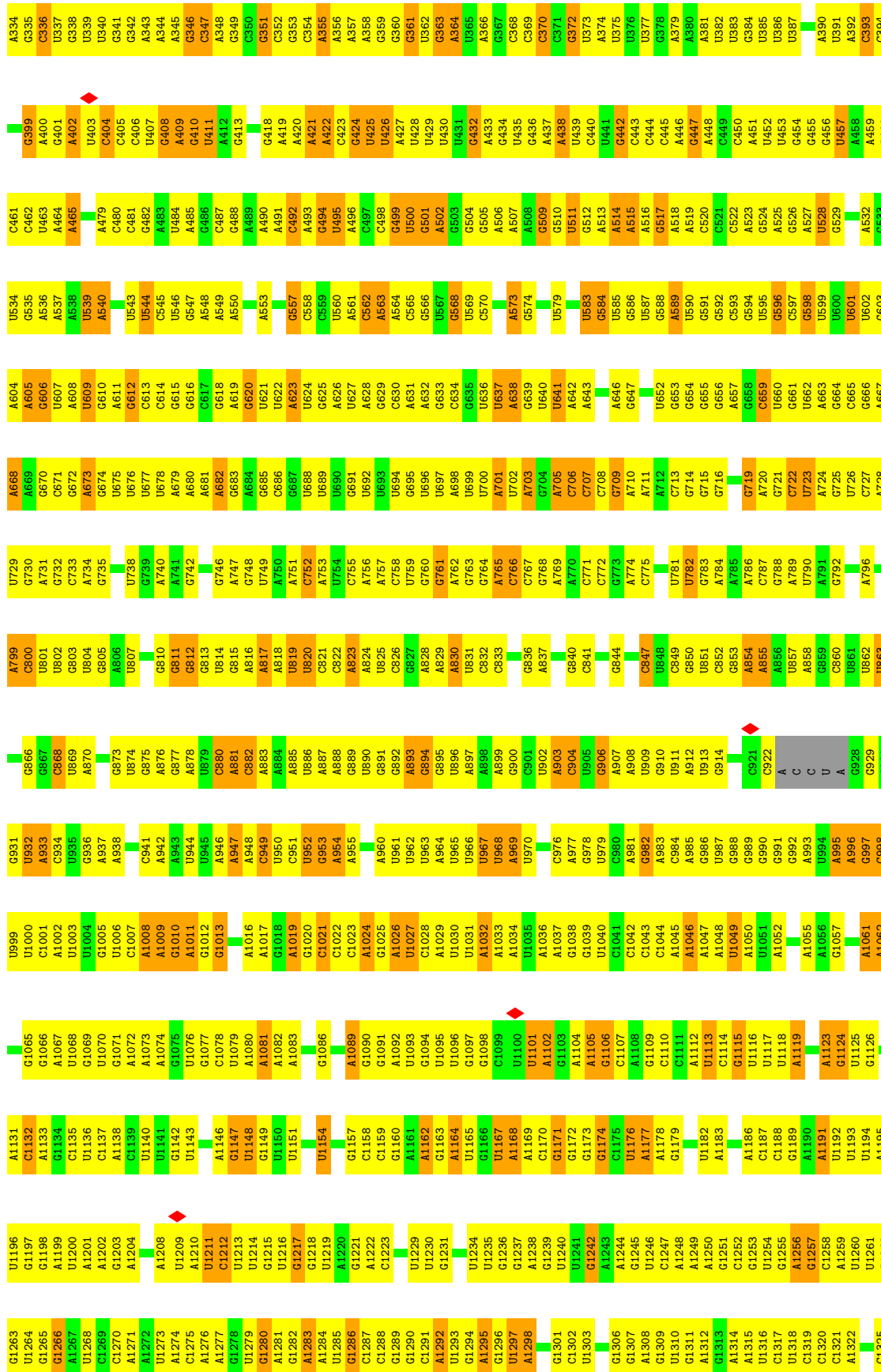


- Molecule 49: 50S ribosomal protein L33 1



- Molecule 50: 23S ribosomal RNA

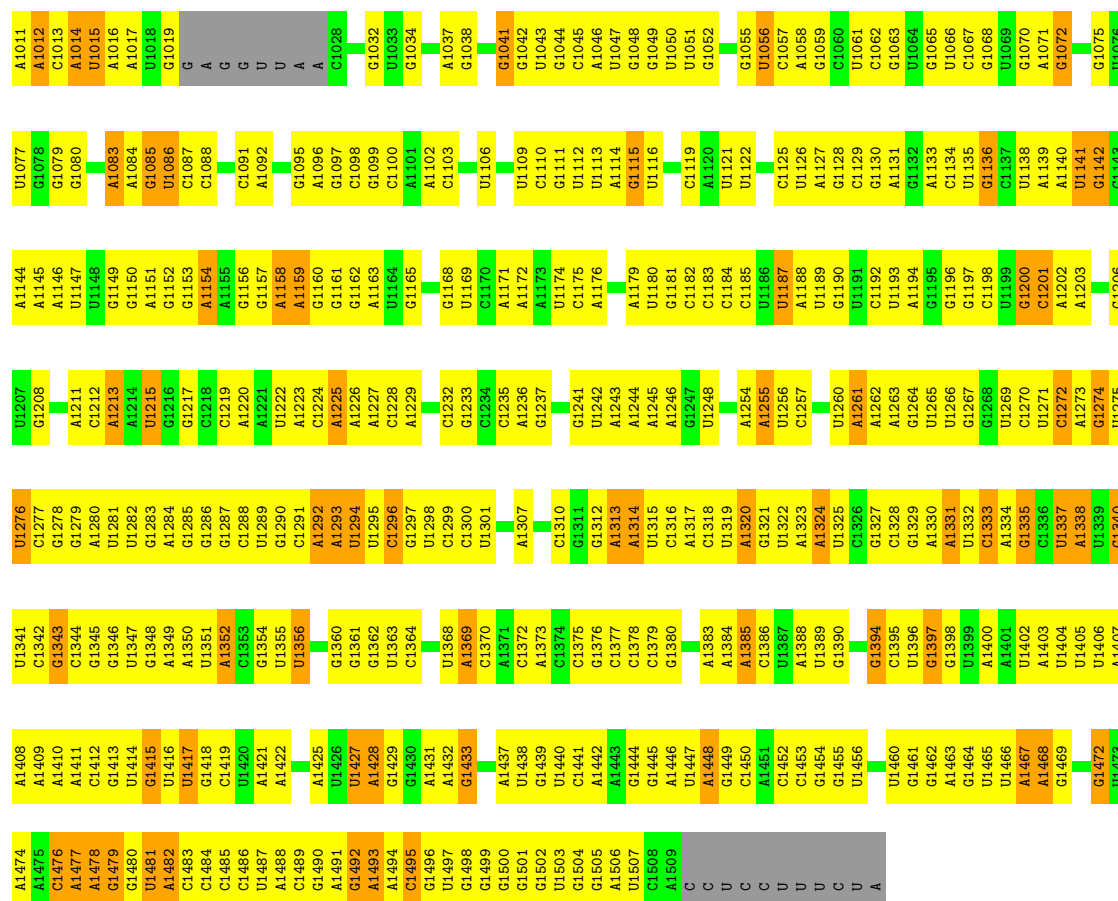




U2208	G1326	C1398	A1461	G1530	A1603	G1681	U1748	G1814	G1876	A1946	A2008	C2072	C2139	U2208
U2209	G1327	G1399	A1462	C1531	A1604	G1682	A1749	A1815	C1877	U1947	U2009	C2073	G2140	U2209
G2210	U1328	A1400	G1463	U1532	A1605	G1683	A1750	A1816	A1878	U1948	G2010	G2074	A2141	G2210
U2211	U1329	A1401	G1464	U1533	G1684	G1685	A1751	A1817	A1879	C1948	G2011	U2075	G2142	G2211
A2212	U1330	G1404	U1465	A1534	U1609	U1610	A1752	G1881	G1880	C1949	A2012	G2076	G2143	U2212
A2213	G1331	G1405	U1466	A1535	U1611	U1612	A1753	G1882	G1882	U1950	C2013	A2077	G2144	A2213
A2214	A1332	G1406	U1467	C1536	C1611	U1613	U1754	U1820	G1882	A1951	U2014	A2078	U2149	A2214
G2215	A1335	A1407	C1470	A1537	U1612	A1613	A1755	G1821	A1883	G1952	C2015	G2079	G2150	G2215
G2216	A1336	U1407	A1471	A1538	U1613	A1614	A1756	A1822	A1884	U1953	G2016	C2080	C2151	G2216
G2217	G1337	G1408	A1471	U1539	G1614	U1615	G1757	U1823	G1885	C1954	G2017	U2081	C2152	G2217
U2218	G1337	G1409	G1474	G1540	G1615	U1616	G1758	U1824	G1886	G1955	U2018	U2082	U2153	U2218
U2219	U1338	A1410	C1474	A1541	G1616	U1617	C1759	U1825	U1887	G1956	G2019	U2083	U2154	U2219
G2220	G1339	C1411	C1475	A1541	U1617	U1618	G1760	U1826	U1888	G1957	A2020	A2084	G2155	G2220
U2221	U1340	A1412	C1476	A1541	U1618	U1619	C1761	U1827	U1889	U1958	A2021	C2085	G2156	U2221
C2222	U1341	A1413	A1477	U1546	U1619	A1620	A1762	U1828	U1890	A1959	A2022	G2085	G2157	C2222
C2223	C1342	C1414	A1548	G1547	A1620	U1621	G1763	A1829	U1891	A1960	U2023	U2088	A2157	C2223
A2224	C1343	A1415	A1480	U1549	U1623	U1624	U1764	G1830	G1898	U1961	C2024	A2089	C2158	A2224
G2225	U1344	A1416	U1481	G1550	U1624	G1625	G1765	G1831	G1899	U1962	G2025	U2090	U2160	G2225
U2226	G1345	G1417	U1482	G1551	A1624	C1626	A1766	G1832	C1899	U1963	A2026	U2092	G2161	U2226
U2227	G1346	U1418	U1483	G1551	G1626	C1627	A1767	G1833	C1900	C1964	G2027	G2092	U2162	U2227
U2228	C1349	A1421	U1484	A1554	C1627	C1628	U1768	U1834	C1901	U1965	G2028	U2096	U2163	U2228
C2229	U1422	U1427	U1485	G1555	U1640	U1641	G1769	U1835	C1902	C1969	U2029	A2097	G2164	C2229
A2230	G1350	A1422	U1486	G1556	A1641	U1642	C1709	A1836	G1906	U1970	A2030	U2098	G2165	A2230
A2231	G1351	A1423	U1487	G1557	A1642	U1643	G1710	U1837	U1905	C1970	G2031	U2100	U2166	A2231
G2232	G1352	U1424	U1488	A1558	A1643	U1644	C1711	U1838	G1906	U1971	G2032	G2100	G2166	G2232
A2233	G1353	G1427	U1488	A1559	A1644	U1645	C1712	C1839	A1907	U1972	G2033	A2101	G2169	A2233
G2236	U1354	G1428	G1491	U	U1645	U1646	A1715	G1840	A1908	U1973	G2034	G2105	A2170	G2236
U2237	C1355	U1428	G1492	G	A1646	U1647	A1716	G1841	C1909	U1974	U2035	G2106	A2171	U2237
G2238	G1356	G1429	G1493	A	U1647	U1648	C1717	G1842	G1910	G1975	G2036	A2107	A2172	U2238
U2239	U1357	U1430	U1494	U	U1648	U1649	C1718	G1843	G1911	A1976	A2037	U2108	G2173	U2239
U2240	C1360	A1431	A1495	U	U1649	U1650	U1722	G1844	G1912	U1977	G2038	C2108	G2174	U2240
A2241	U1361	U1432	G1499	G	U1650	U1651	U1723	C1845	G1913	U1978	G2039	A2109	G2175	U2241
G2242	U1362	U1433	U1500	A	U1651	U1652	U1724	U1846	G1914	G1979	A2040	U2110	U2176	G2242
C2246	C1363	U1434	A1501	U	U1652	U1653	U1725	G1847	C1915	U1980	G2041	U2111	A2180	C2246
A2249	U1364	U1435	A1502	C	U1653	U1654	U1726	U1848	G1916	G1981	C2042	U2112	U2181	C2249
G2250	G1365	A1437	A1503	A	U1654	U1655	U1727	G1849	U1917	U1982	A2043	U2113	A2184	G2250
U2253	G1366	U1438	G1504	G1571	U1655	U1656	U1728	C1850	U1918	A1983	C2044	U2114	G2187	U2253
G2254	A1370	U1440	G1507	G1574	U1656	U1657	U1729	U1851	A1919	A1984	C2045	C2114	U2188	G2254
A2255	U1372	A1441	G1508	C1575	U1657	U1658	U1730	U1852	A1920	C1986	G2046	U2115	U2189	A2255
C2256	C1378	U1442	G1509	G1576	U1658	U1659	U1731	U1853	A1921	C1987	U2048	U2116	G2190	C2256
G2258	C1379	U1443	A1510	A1577	U1659	U1660	U1732	U1854	U1922	U1988	G2049	U2117	G2191	G2258
G2259	U1380	U1444	A1511	A1577	U1660	U1661	U1733	U1855	U1923	U1989	G2050	U2118	G2192	G2259
G2260	C1379	U1445	A1512	A1577	U1661	U1662	U1734	U1856	U1924	C1990	C2054	U2119	G2193	G2260
G2263	U1387	U1446	A1515	A1577	U1662	U1663	U1735	U1857	U1925	U1991	A2055	U2120	U2194	G2263
G2264	A1382	U1447	A1515	A1577	U1663	U1664	U1736	U1858	U1926	U1992	G2056	U2121	G2195	G2264
U2265	G1383	U1448	A1518	U1584	U1664	U1665	U1737	U1859	U1927	C1993	A2057	U2122	G2196	U2265
C2266	C1384	U1449	A1519	U1584	U1665	U1666	U1738	U1860	U1928	U1994	G2058	U2123	U2197	C2266
G2267	U1385	U1450	A1520	U1587	U1666	U1667	U1739	U1861	U1929	U1995	G2059	U2124	U2198	G2267
C2268	G1386	U1451	A1521	U1588	U1667	U1668	U1740	U1862	U1930	A1996	A2060	U2125	G2199	C2268
U2201	A1392	U1452	U1522	A1589	U1668	U1669	U1741	U1863	U1931	U1997	G2061	U2126	G2200	U2201
G2202	A1393	U1453	A1523	U1590	U1669	U1670	U1742	U1864	U1932	C1998	A2062	U2127	G2201	G2202
A1394	A1455	U1454	A1524	C1591	U1670	U1671	U1743	U1865	U1933	U1999	G2063	A2130	U2205	A1394
A1395	U1527	U1455	A1525	U1593	U1671	U1672	U1744	U1866	U1934	U2000	G2064	G2131	U2206	A1395
A1396	U1528	U1456	A1526	U1593	U1672	U1673	U1745	U1867	U1935	U2001	G2065	G2132	U2207	A1396
G1460	U1529	U1457	U1527	A1600	U1673	U1674	U1746	U1868	U1936	U2002	G2066	G2133	U2208	G1460
					U1674	U1675	U1747	U1869	U1937	U2003	G2067	G2134	U2209	
					U1675	U1676	U1748	U1870	U1938	U2004	G2068	G2135	U2210	
					U1676	U1677	U1749	U1871	U1939	U2005	G2069	A2136	U2211	
					U1677	U1678	U1750	U1872	U1940	U2006	G2070	A2137	U2212	
					U1678	U1679	U1751	U1873	U1941	U2007	G2071	U2138	U2213	



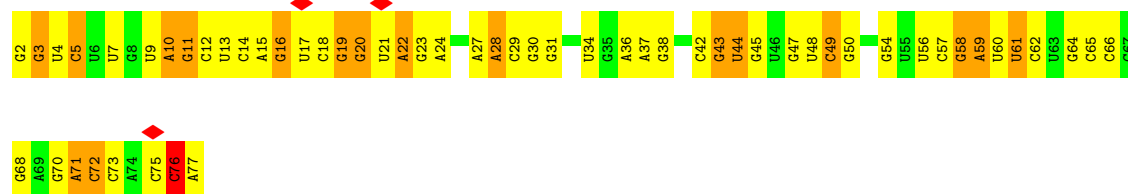




• Molecule 53: tRNA-Phe



• Molecule 53: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	6587	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	1.866	Depositor
Minimum map value	-0.639	Depositor
Average map value	0.025	Depositor
Map value standard deviation	0.126	Depositor
Recommended contour level	0.47	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.15	0/383	0.50	0/504
2	1	0.18	0/484	0.50	0/637
3	2	0.20	0/306	0.46	0/401
4	A	0.18	0/1954	0.50	0/2642
5	B	0.18	0/1721	0.49	1/2323 (0.0%)
6	C	0.15	0/1691	0.47	0/2267
7	D	0.16	0/1188	0.47	0/1593
8	E	0.18	0/1384	0.47	0/1867
9	F	0.19	0/1266	0.50	0/1700
10	G	0.23	0/1126	0.69	0/1517
11	H	0.19	0/1044	0.52	0/1395
12	I	0.15	0/820	0.45	0/1103
13	J	0.54	2/844 (0.2%)	0.79	4/1136 (0.4%)
14	K	0.31	0/1094	0.70	1/1468 (0.1%)
15	L	0.18	0/962	0.53	0/1289
16	M	0.15	0/483	0.45	0/643
17	N	0.16	0/679	0.46	0/907
18	O	0.15	0/659	0.41	0/885
19	P	0.18	0/684	0.46	0/913
20	Q	0.15	0/545	0.50	0/730
21	R	0.14	0/698	0.46	0/936
22	S	0.16	0/631	0.39	0/838
23	T	0.18	0/475	0.52	0/621
24	a	0.17	0/2267	0.49	0/3044
25	b	0.17	0/1795	0.47	0/2412
26	c	0.16	0/1671	0.48	0/2246
27	d	0.17	0/1409	0.50	0/1894
28	e	0.15	0/1420	0.39	0/1912
29	f	0.16	0/1183	0.50	0/1587
30	g	2.16	8/969 (0.8%)	1.26	8/1295 (0.6%)
31	h	0.16	0/968	0.44	0/1298
32	i	0.25	0/1186	0.55	0/1592
33	j	0.18	0/953	0.53	0/1275
34	k	0.21	0/1170	0.56	0/1559

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	l	0.18	0/1104	0.56	0/1481
36	m	0.18	0/973	0.50	0/1309
37	n	0.22	0/897	0.59	0/1198
38	o	0.17	0/948	0.49	0/1262
39	p	0.18	0/961	0.48	0/1278
40	q	0.19	0/828	0.55	0/1111
41	r	0.17	0/1077	0.47	0/1441
42	s	0.17	0/732	0.51	0/988
43	t	0.18	0/879	0.49	0/1165
44	u	0.15	0/665	0.50	0/884
45	v	0.17	0/519	0.47	0/695
46	w	0.18	0/826	0.49	0/1104
47	x	0.17	0/353	0.40	0/474
48	y	0.34	0/457	0.76	0/601
49	z	0.22	0/412	0.62	0/547
50	3	0.25	6/69073 (0.0%)	0.25	0/107710
51	4	0.10	0/2505	0.26	0/3902
52	5	0.10	0/35768	0.24	0/55764
53	6	0.67	3/1808 (0.2%)	0.55	8/2817 (0.3%)
53	8	0.67	3/1808 (0.2%)	0.55	8/2817 (0.3%)
All	All	0.28	22/158705 (0.0%)	0.36	30/236977 (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
10	G	0	1
24	a	0	1
30	g	0	1
44	u	0	1
All	All	0	4

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	g	112	TYR	CD1-CE1	33.77	2.40	1.38
30	g	112	TYR	CD2-CE2	27.95	2.22	1.38
50	3	2440	A	C5-C6	27.28	1.95	1.41
50	3	2440	A	C2-N3	25.90	1.85	1.33
50	3	2440	A	N3-C4	25.78	1.86	1.34

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	g	114	ASP	CA-C-N	23.26	165.97	121.54
30	g	114	ASP	C-N-CA	23.26	165.97	121.54
13	J	110	PRO	N-CD-CG	-14.43	81.55	103.20
53	6	76	C	C6-N1-C2	-12.71	82.08	120.20
53	8	76	C	C6-N1-C2	-12.70	82.09	120.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	G	108	LEU	Peptide
24	a	247	SER	Peptide
30	g	112	TYR	Peptide
44	u	24	THR	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	20	0
2	1	477	0	530	31	0
3	2	304	0	350	10	0
4	A	1921	0	1973	79	0
5	B	1698	0	1768	53	0
6	C	1660	0	1719	74	0
7	D	1173	0	1267	51	0
8	E	1362	0	1377	69	0
9	F	1246	0	1308	45	0
10	G	1110	0	1226	64	0
11	H	1028	0	1094	33	0
12	I	809	0	894	41	0
13	J	829	0	855	36	0
14	K	1076	0	1170	57	0
15	L	951	0	1014	43	0
16	M	474	0	509	26	0
17	N	673	0	730	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	O	646	0	677	22	0
19	P	675	0	728	31	0
20	Q	535	0	562	22	0
21	R	682	0	691	25	0
22	S	629	0	681	31	0
23	T	471	0	522	17	0
24	a	2225	0	2301	81	0
25	b	1762	0	1808	65	0
26	c	1644	0	1731	52	0
27	d	1388	0	1469	72	0
28	e	1396	0	1481	41	0
29	f	1160	0	1172	43	0
30	g	960	0	1014	83	0
31	h	959	0	1039	30	0
32	i	1164	0	1192	62	0
33	j	944	0	1019	38	0
34	k	1153	0	1256	50	0
35	l	1079	0	1134	52	0
36	m	958	0	1011	66	0
37	n	889	0	952	37	0
38	o	938	0	1008	35	0
39	p	947	0	1028	55	0
40	q	811	0	858	41	0
41	r	1068	0	1150	35	0
42	s	720	0	803	27	0
43	t	872	0	972	40	0
44	u	657	0	695	17	0
45	v	513	0	560	31	0
46	w	818	0	870	34	0
47	x	344	0	333	19	0
48	y	452	0	472	30	0
49	z	408	0	440	16	0
50	3	61664	0	30954	1959	0
51	4	2239	0	1137	52	0
52	5	31943	0	16058	1044	0
53	6	1618	0	821	38	0
53	8	1618	0	821	74	0
All	All	146120	0	99633	4618	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 20.

The worst 5 of 4618 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)
30:g:112:TYR:CG	30:g:112:TYR:CD1	1.78	1.71
30:g:112:TYR:CG	30:g:112:TYR:CD2	1.78	1.66
30:g:112:TYR:CZ	30:g:112:TYR:CE2	1.89	1.58
50:3:2440:A:C5	53:8:76:C:H1'	1.36	1.56
30:g:112:TYR:CZ	30:g:112:TYR:CE1	1.94	1.55

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%)	40 (89%)	5 (11%)	0	100	100
2	1	57/59 (97%)	49 (86%)	8 (14%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	A	238/294 (81%)	215 (90%)	23 (10%)	0	100	100
5	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
6	C	201/205 (98%)	192 (96%)	9 (4%)	0	100	100
7	D	151/219 (69%)	146 (97%)	5 (3%)	0	100	100
8	E	165/215 (77%)	153 (93%)	12 (7%)	0	100	100
9	F	152/155 (98%)	142 (93%)	10 (7%)	0	100	100
10	G	139/142 (98%)	121 (87%)	18 (13%)	0	100	100
11	H	126/132 (96%)	113 (90%)	13 (10%)	0	100	100
12	I	99/108 (92%)	89 (90%)	10 (10%)	0	100	100
13	J	112/121 (93%)	105 (94%)	7 (6%)	0	100	100
14	K	134/139 (96%)	119 (89%)	14 (10%)	1 (1%)	18	56
15	L	116/124 (94%)	105 (90%)	11 (10%)	0	100	100
16	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	N	81/86 (94%)	79 (98%)	2 (2%)	0	100	100
18	O	78/94 (83%)	72 (92%)	6 (8%)	0	100	100
19	P	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
20	Q	63/104 (61%)	58 (92%)	5 (8%)	0	100	100
21	R	82/87 (94%)	75 (92%)	7 (8%)	0	100	100
22	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
23	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
24	a	283/287 (99%)	256 (90%)	27 (10%)	0	100	100
25	b	227/287 (79%)	213 (94%)	14 (6%)	0	100	100
26	c	208/212 (98%)	197 (95%)	11 (5%)	0	100	100
27	d	173/180 (96%)	161 (93%)	12 (7%)	0	100	100
28	e	174/184 (95%)	165 (95%)	9 (5%)	0	100	100
29	f	143/149 (96%)	136 (95%)	7 (5%)	0	100	100
30	g	124/161 (77%)	114 (92%)	9 (7%)	1 (1%)	16	54
31	h	126/137 (92%)	114 (90%)	12 (10%)	0	100	100
32	i	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
33	j	120/122 (98%)	110 (92%)	10 (8%)	0	100	100
34	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
35	l	134/139 (96%)	124 (92%)	10 (8%)	0	100	100
36	m	117/124 (94%)	109 (93%)	8 (7%)	0	100	100
37	n	108/116 (93%)	97 (90%)	11 (10%)	0	100	100
38	o	113/119 (95%)	106 (94%)	7 (6%)	0	100	100
39	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
40	q	97/100 (97%)	82 (84%)	15 (16%)	0	100	100
41	r	137/159 (86%)	127 (93%)	10 (7%)	0	100	100
42	s	90/237 (38%)	87 (97%)	3 (3%)	0	100	100
43	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
44	u	84/104 (81%)	78 (93%)	6 (7%)	0	100	100
45	v	61/65 (94%)	55 (90%)	6 (10%)	0	100	100
46	w	96/111 (86%)	92 (96%)	3 (3%)	1 (1%)	12	48
47	x	42/97 (43%)	40 (95%)	2 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	y	54/57 (95%)	49 (91%)	4 (7%)	1 (2%)	6	32
49	z	48/53 (91%)	48 (100%)	0	0	100	100
All	All	5820/6670 (87%)	5397 (93%)	419 (7%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	K	116	ASP
30	g	88	GLU
46	w	39	ASP
48	y	53	VAL

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	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%)	114 (97%)	3 (3%)	40	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	73 (100%)	0	100	100
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
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%)	93 (92%)	8 (8%)	11	32
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%)	68 (99%)	1 (1%)	59	72
45	v	58/60 (97%)	58 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	45 (94%)	3 (6%)	16	37
49	z	47/50 (94%)	46 (98%)	1 (2%)	47	65
All	All	5093/5751 (89%)	5077 (100%)	16 (0%)	84	86

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	y	52	ARG
48	y	48	TYR
30	g	88	GLU
48	y	19	HIS
30	g	46	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
31	h	130	GLN
38	o	85	ASN
32	i	82	GLN
35	l	14	ASN
40	q	34	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	2876/2907 (98%)	774 (26%)	34 (1%)
51	4	103/108 (95%)	36 (34%)	3 (2%)
52	5	1490/1520 (98%)	353 (23%)	5 (0%)
53	6	75/76 (98%)	29 (38%)	4 (5%)
53	8	75/76 (98%)	29 (38%)	4 (5%)
All	All	4619/4687 (98%)	1221 (26%)	50 (1%)

5 of 1221 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	14	U

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Mol	Chain	Res	Type
50	3	15	A
50	3	16	A
50	3	28	G
50	3	37	G

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	3	2604	U
51	4	54	U
53	8	58	G
50	3	2635	G
50	3	2823	A

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.

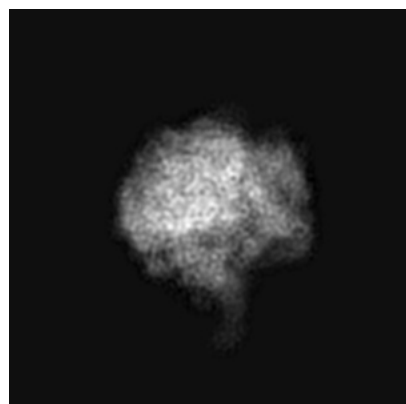
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13277. These allow visual inspection of the internal detail of the map and identification of artifacts.

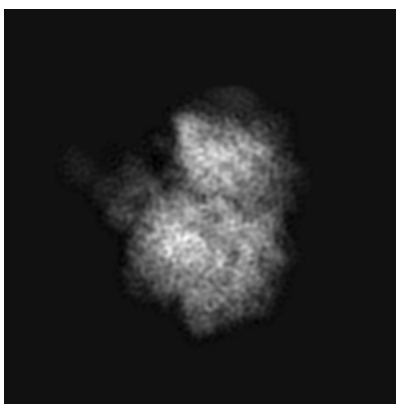
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

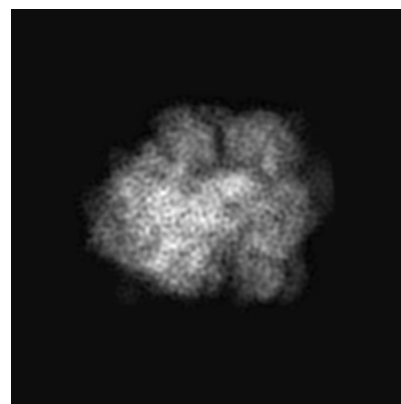
6.1.1 Primary map



X

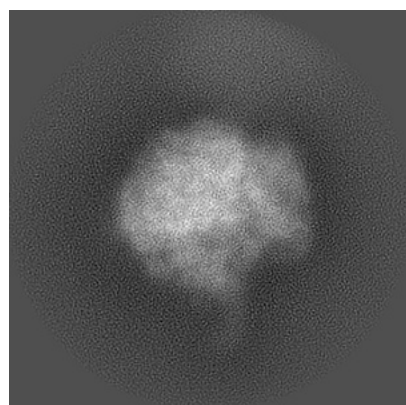


Y

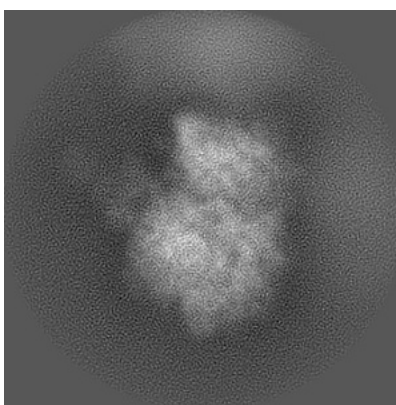


Z

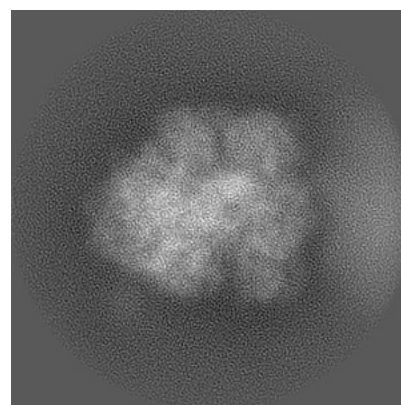
6.1.2 Raw map



X



Y

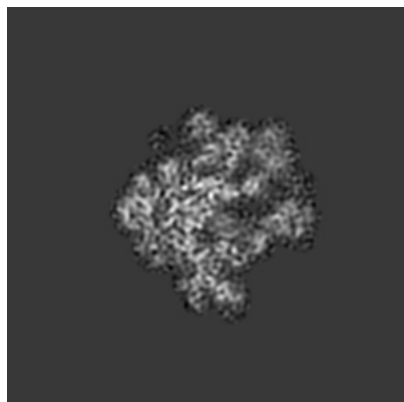


Z

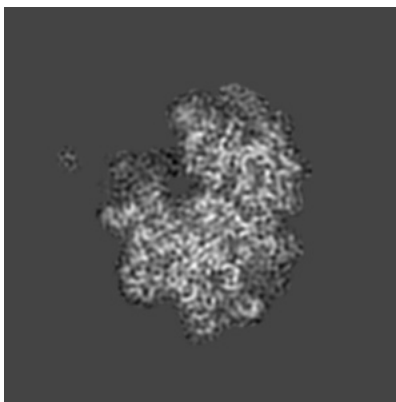
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

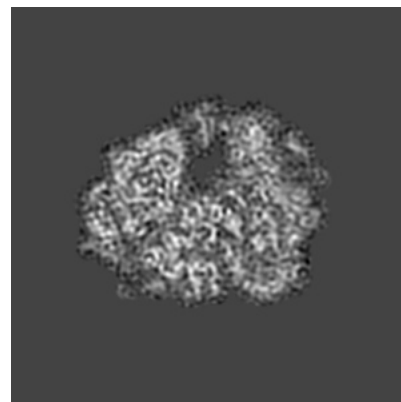
6.2.1 Primary map



X Index: 128

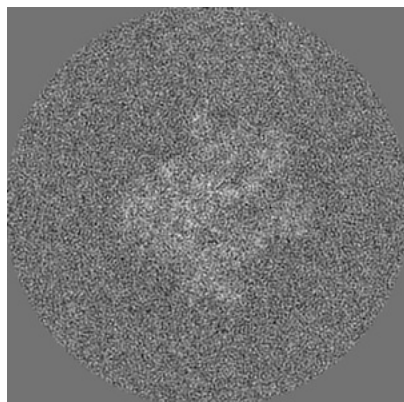


Y Index: 128

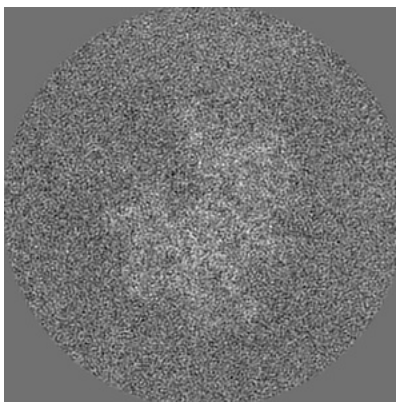


Z Index: 128

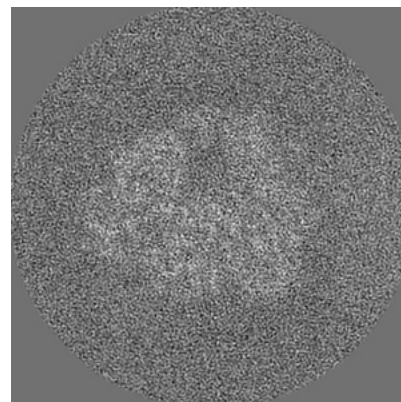
6.2.2 Raw map



X Index: 128



Y Index: 128

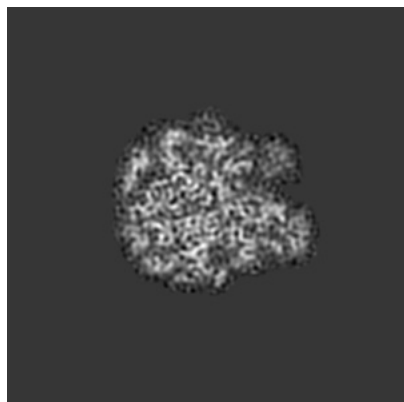


Z Index: 128

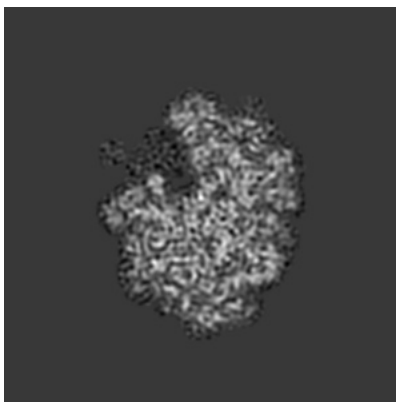
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

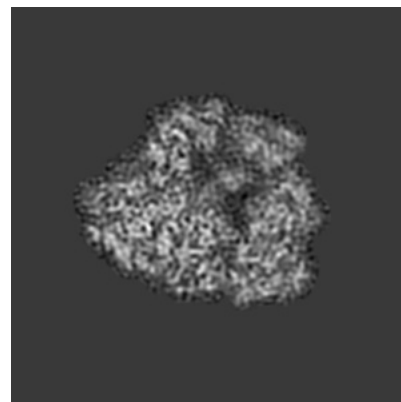
6.3.1 Primary map



X Index: 104

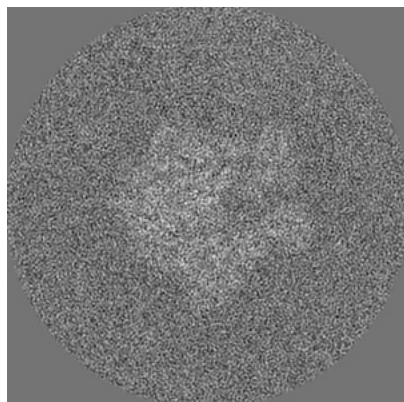


Y Index: 120

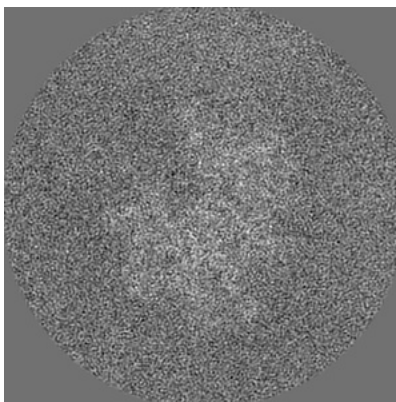


Z Index: 120

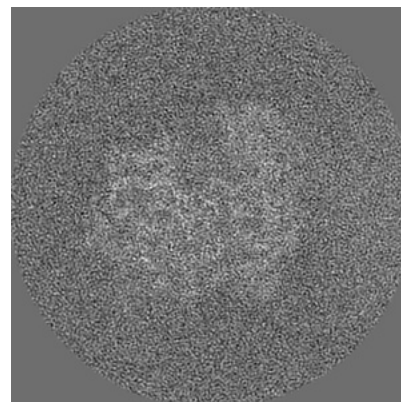
6.3.2 Raw map



X Index: 120



Y Index: 128

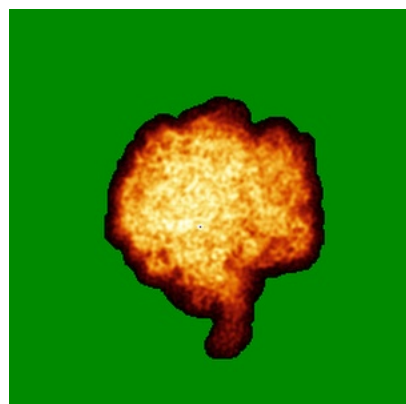


Z Index: 135

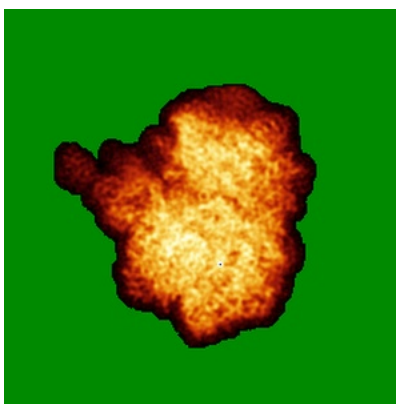
The images above show the largest variance slices of the map in three orthogonal directions.

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

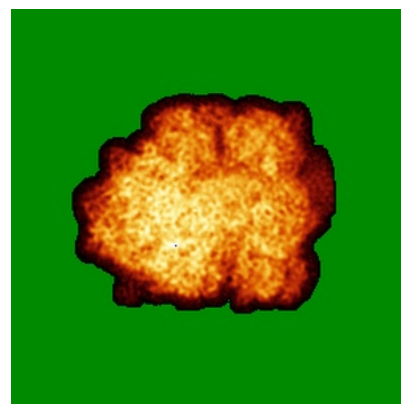
6.4.1 Primary map



X

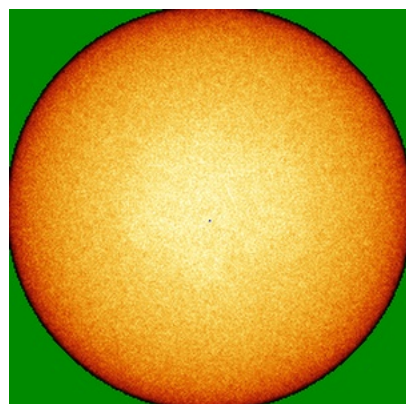


Y

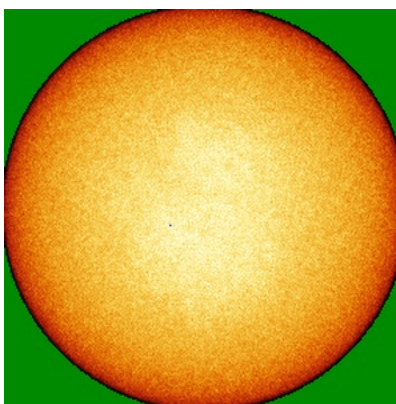


Z

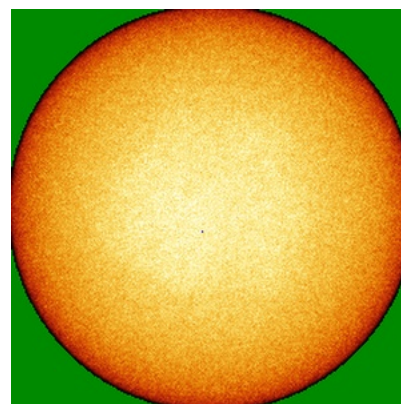
6.4.2 Raw map



X



Y

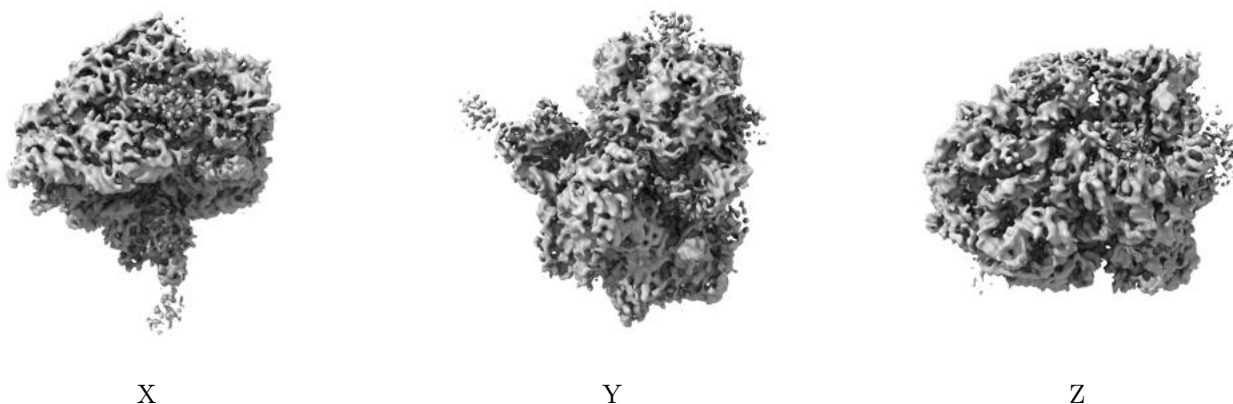


Z

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.

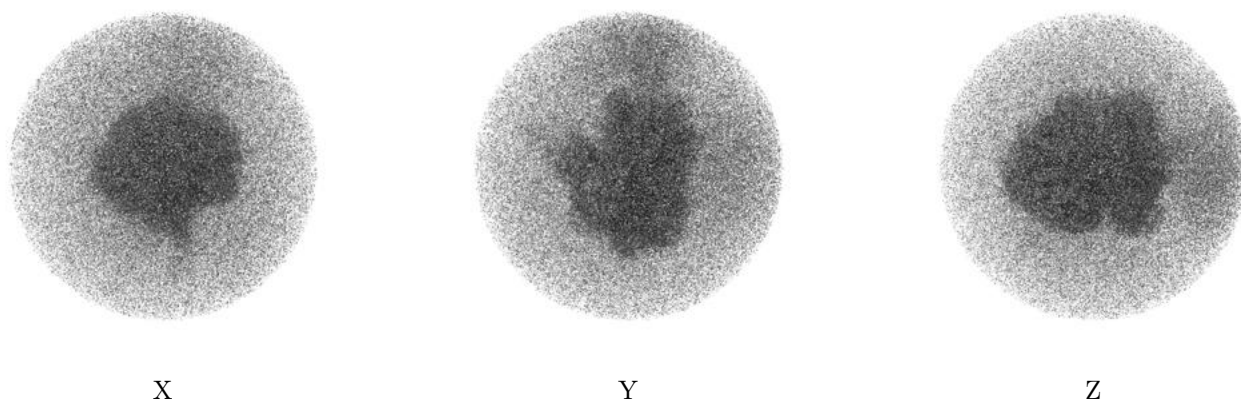
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.47. 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.

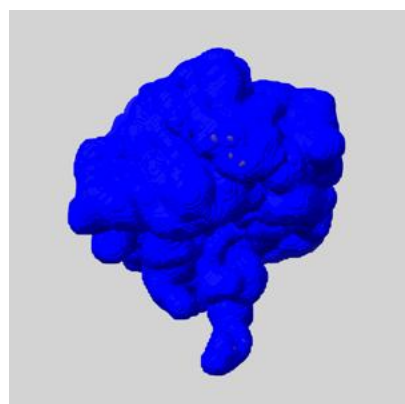
6.6 Mask visualisation [i](#)

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

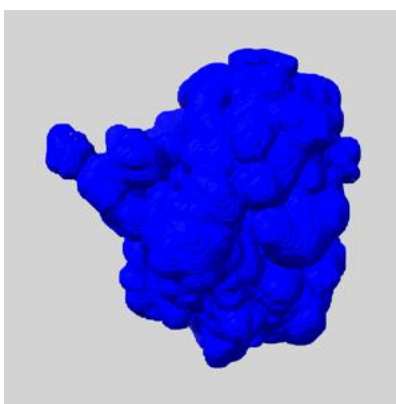
A mask typically either:

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

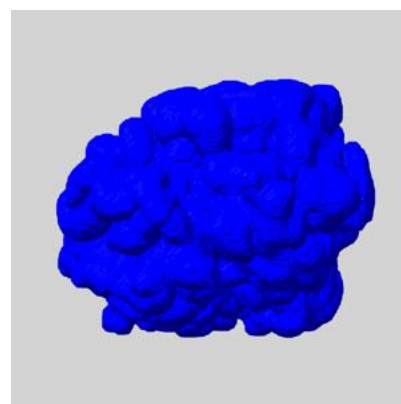
6.6.1 emd_13277_msk_1.map [i](#)



X



Y

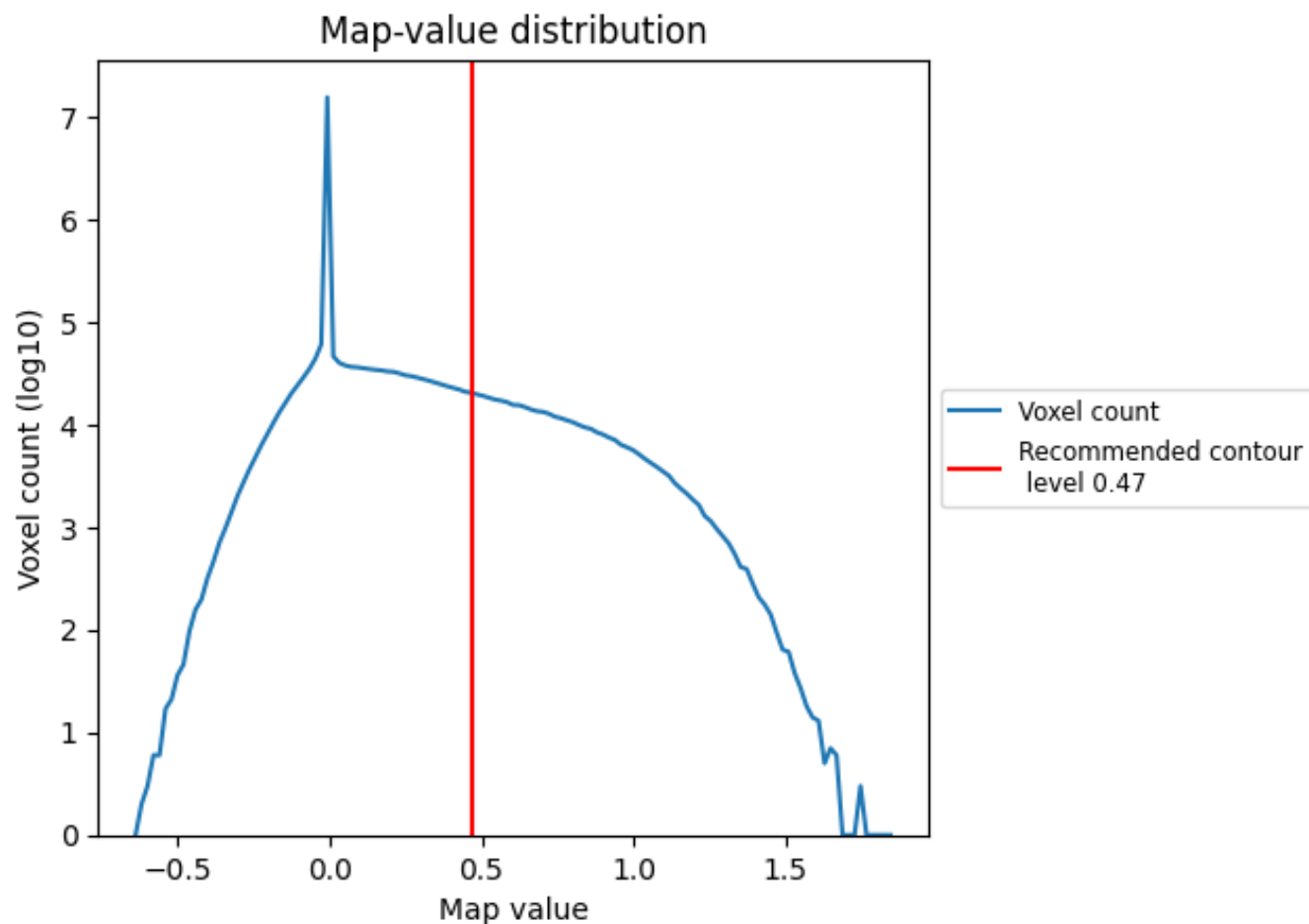


Z

7 Map analysis [i](#)

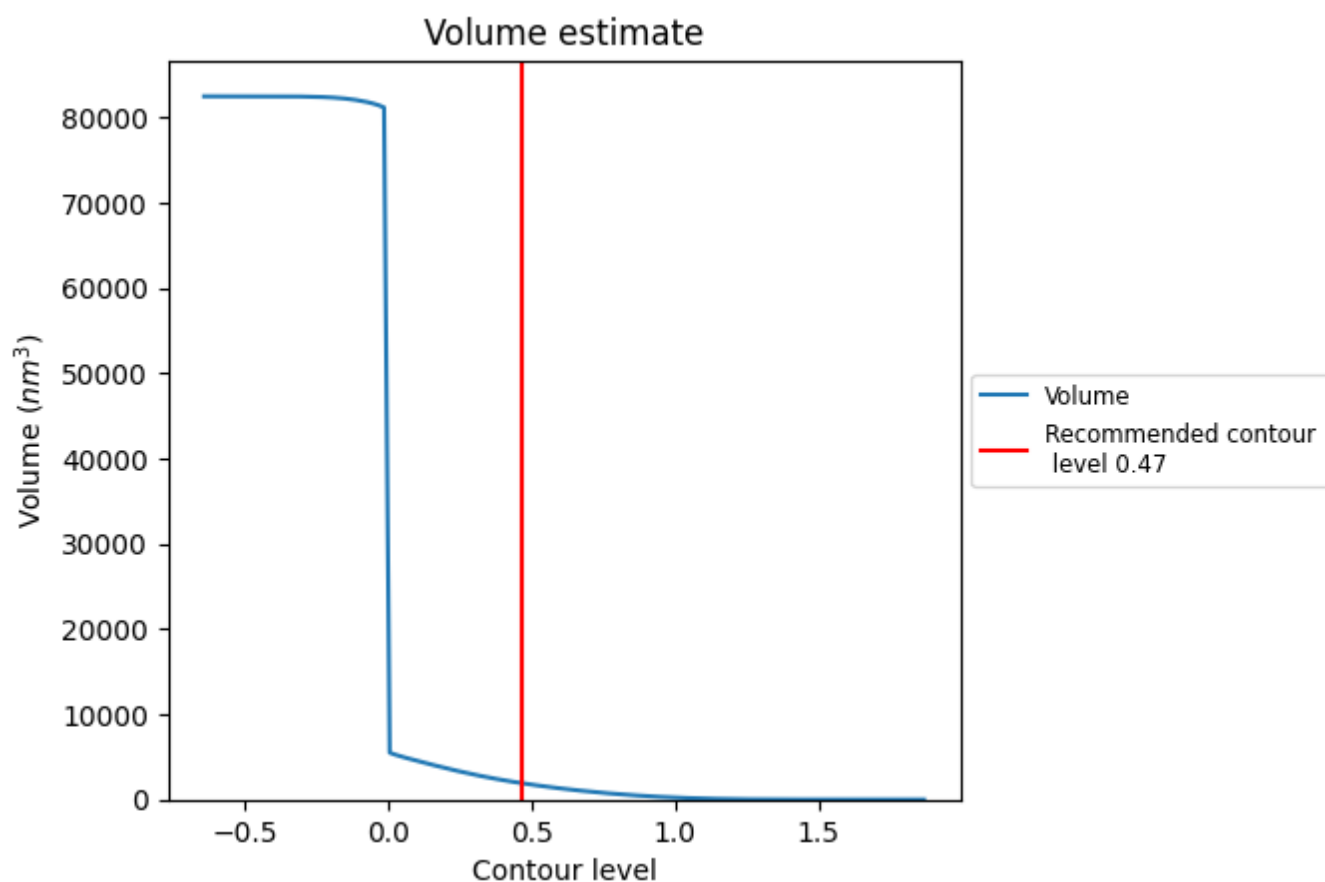
This section contains the results of statistical analysis of the map.

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.

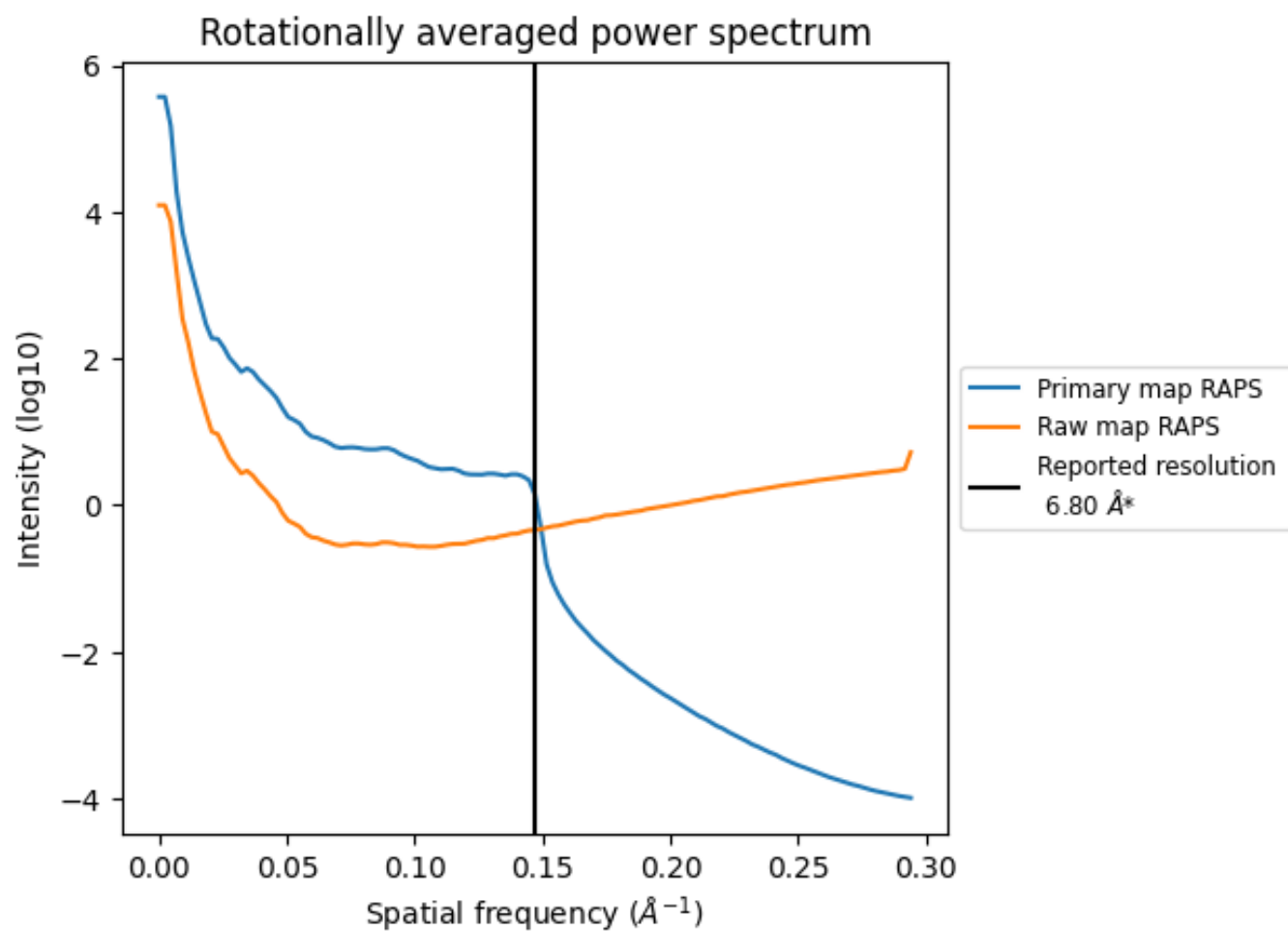
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1905 nm^3 ; this corresponds to an approximate mass of 1721 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 ⓘ

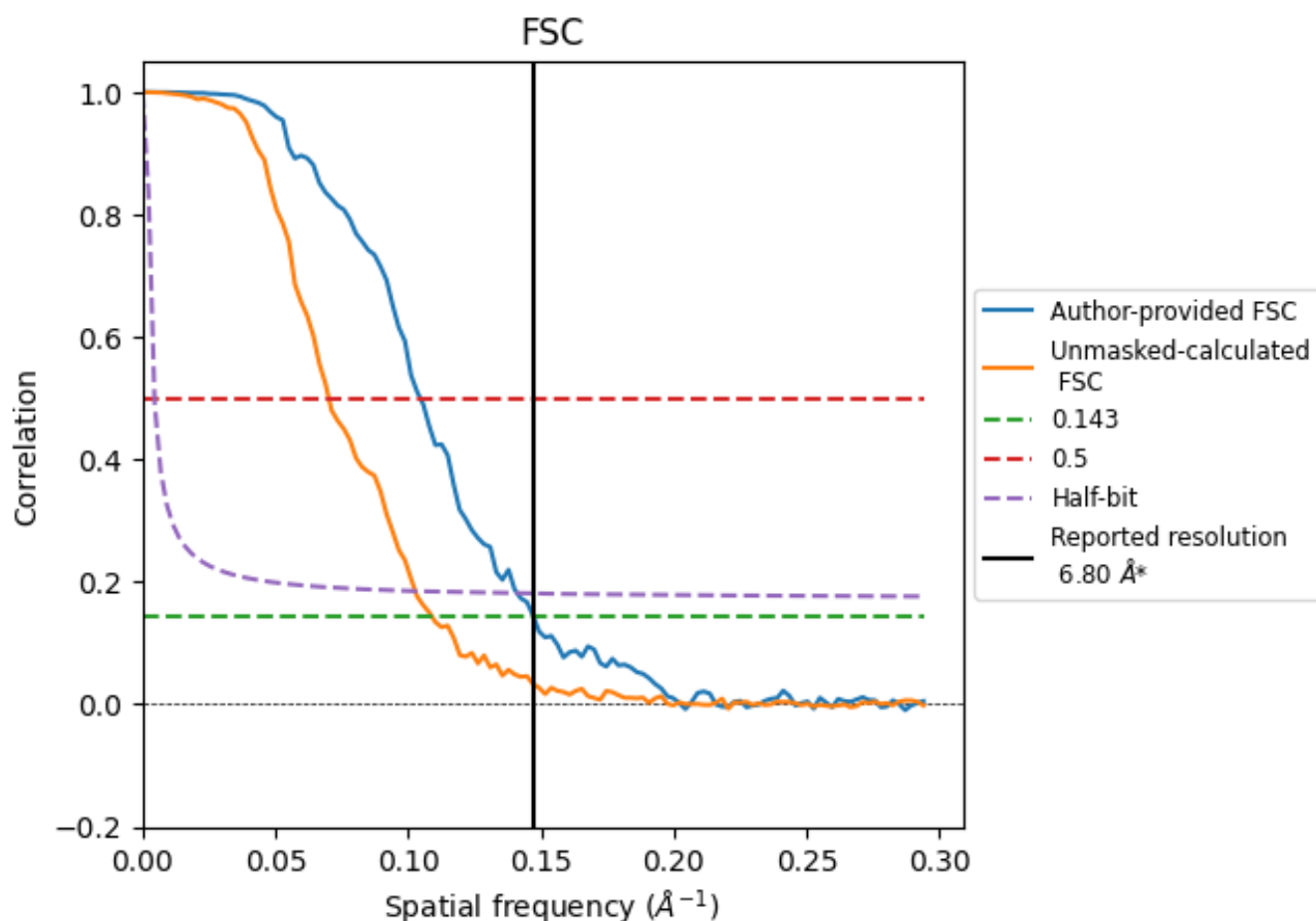


*Reported resolution corresponds to spatial frequency of 0.147 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.147 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

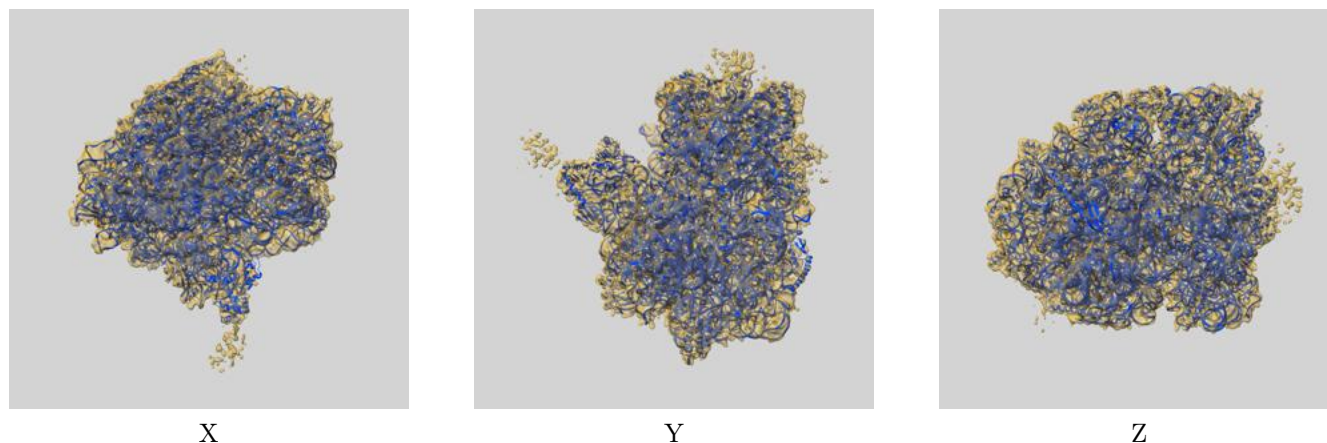
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.80	-	-
Author-provided FSC curve	6.79	9.57	7.09
Unmasked-calculated*	9.17	14.27	9.74

*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 9.17 differs from the reported value 6.8 by more than 10 %

9 Map-model fit [i](#)

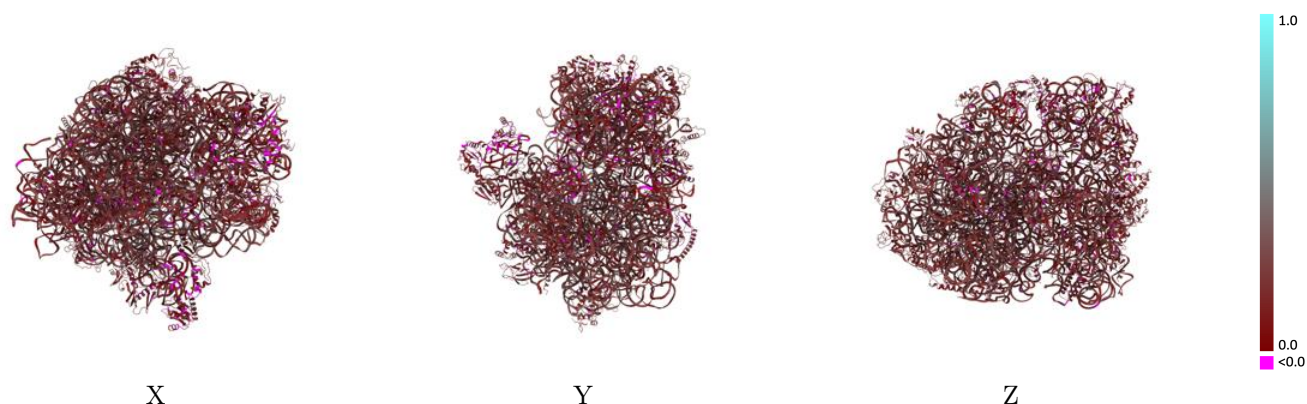
This section contains information regarding the fit between EMDB map EMD-13277 and PDB model 7PAM. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



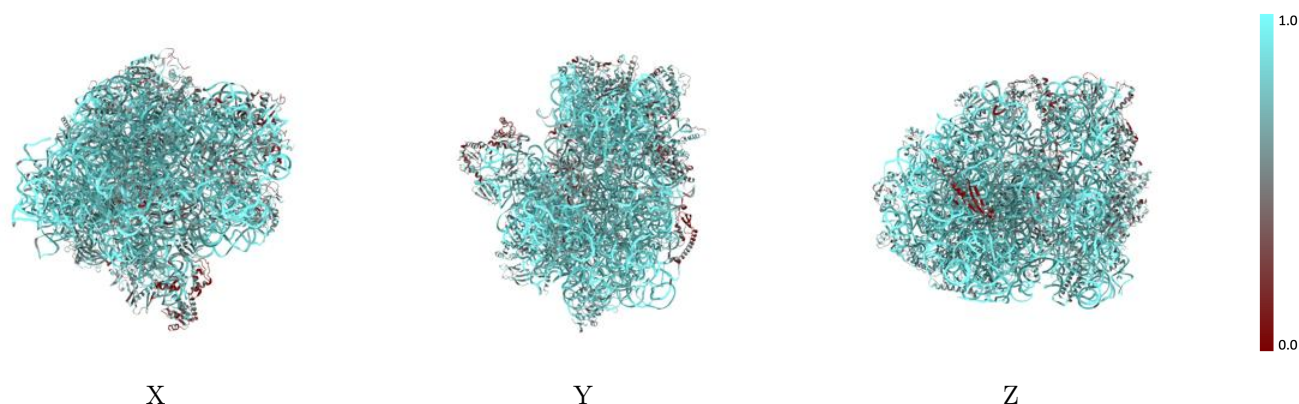
The images above show the 3D surface view of the map at the recommended contour level 0.47 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



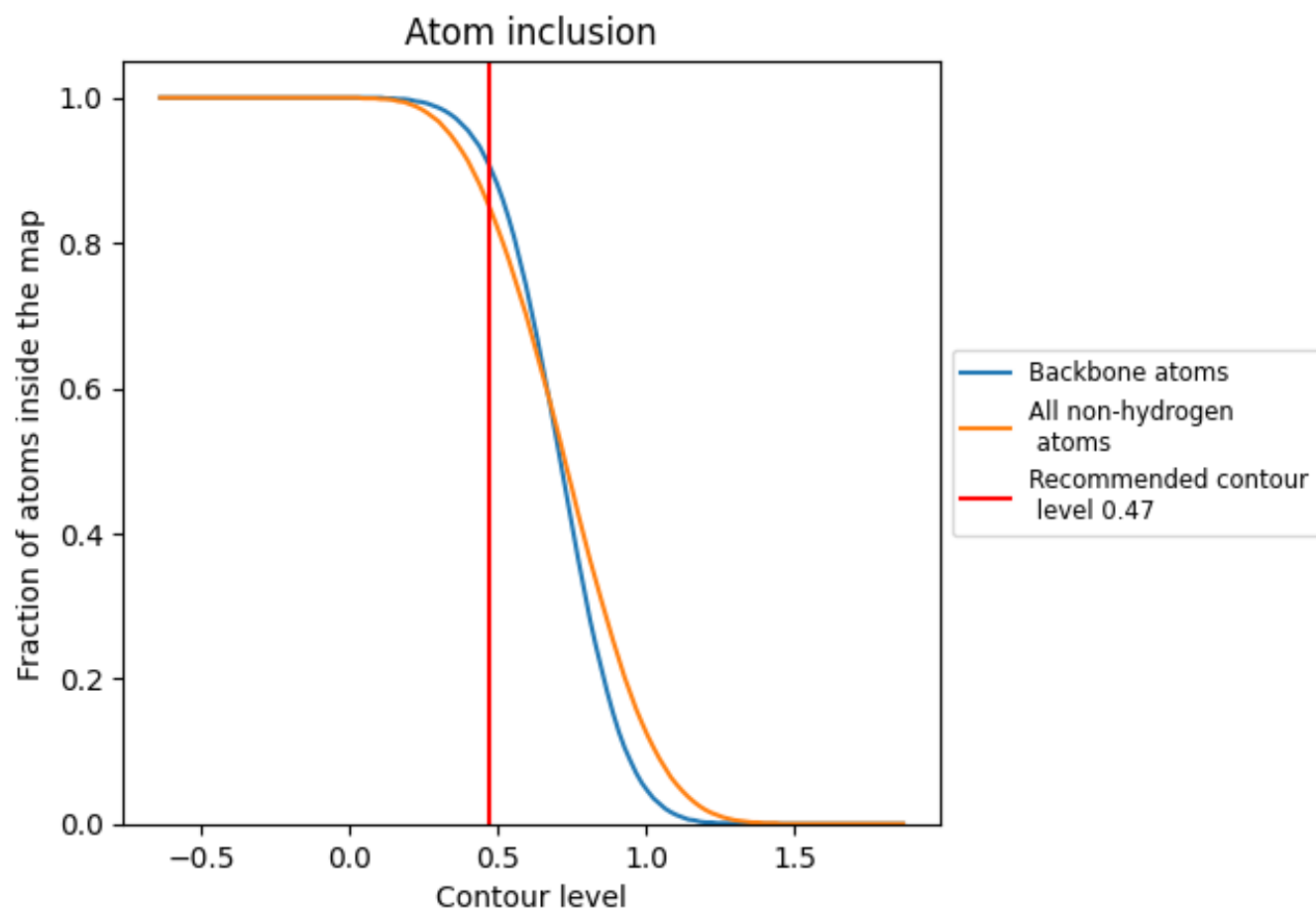
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.47).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.47) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8500	 0.2070
0	 0.7780	 0.2020
1	 0.7360	 0.1820
2	 0.7740	 0.1920
3	 0.9510	 0.2250
4	 0.9400	 0.2230
5	 0.9430	 0.2100
6	 0.5790	 0.0940
8	 0.8780	 0.1940
A	 0.6320	 0.2010
B	 0.6220	 0.1920
C	 0.6310	 0.1730
D	 0.6790	 0.1900
E	 0.5970	 0.1960
F	 0.5620	 0.1730
G	 0.6620	 0.1780
H	 0.6080	 0.1660
I	 0.5900	 0.1650
J	 0.6780	 0.1820
K	 0.7140	 0.1950
L	 0.5620	 0.1710
M	 0.6860	 0.1500
N	 0.6370	 0.1840
O	 0.7680	 0.1960
P	 0.6930	 0.1740
Q	 0.6800	 0.1850
R	 0.5880	 0.1280
S	 0.7160	 0.1710
T	 0.6900	 0.1930
a	 0.7530	 0.1910
b	 0.6940	 0.1780
c	 0.7020	 0.2030
d	 0.6350	 0.1710
e	 0.6430	 0.2010
f	 0.2820	 0.1690



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Chain	Atom inclusion	Q-score
g	 0.4810	 0.1440
h	 0.3030	 0.1390
i	 0.7400	 0.1920
j	 0.6390	 0.1800
k	 0.7420	 0.1980
l	 0.7550	 0.2050
m	 0.7670	 0.1890
n	 0.7070	 0.2000
o	 0.6830	 0.2000
p	 0.7490	 0.1670
q	 0.7000	 0.1990
r	 0.7380	 0.2000
s	 0.7150	 0.2000
t	 0.5690	 0.1720
u	 0.6860	 0.1560
v	 0.7560	 0.1780
w	 0.6900	 0.2060
x	 0.5630	 0.1940
y	 0.7880	 0.2140
z	 0.7330	 0.1960