



wwPDB EM Validation Summary Report ⓘ

Oct 13, 2022 – 05:30 am BST

PDB ID : 7PIS
EMDB ID : EMD-13449
Title : 70S ribosome with EF-G, A*- and P/E-site tRNAs in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 15.00 Å (reported)
Based on initial models : 4V7D, 7OOC, 4V7C, 7OOD

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:

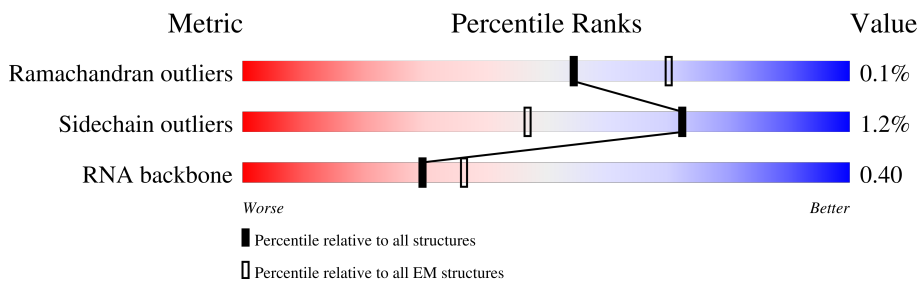
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 15.00 Å.

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




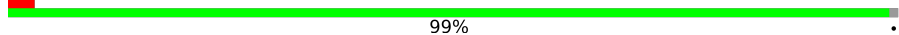
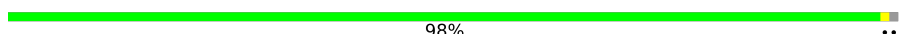
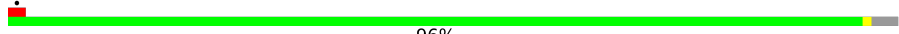


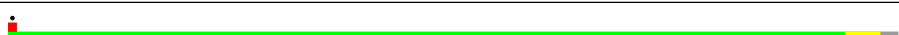
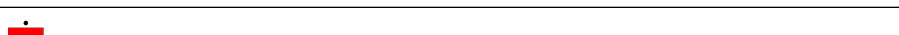
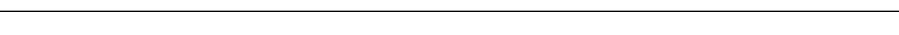
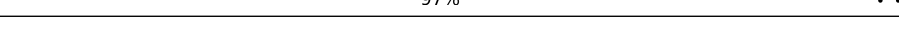
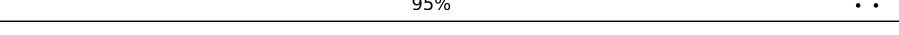
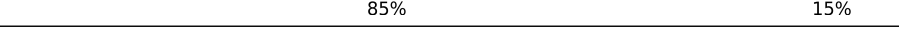
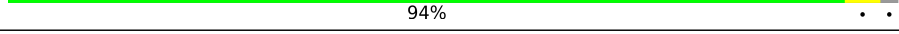

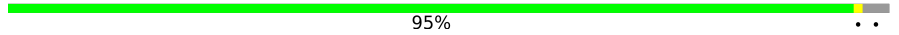








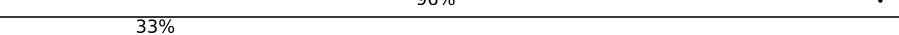
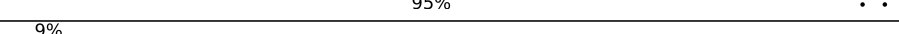
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
4	9	688	
5	A	294	
6	B	273	
7	C	205	
8	D	219	

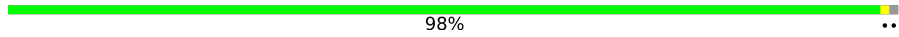
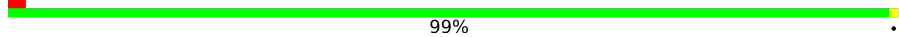
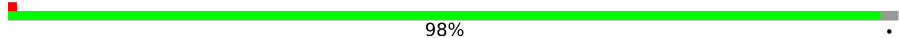
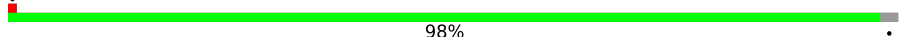

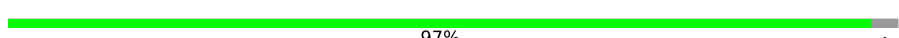







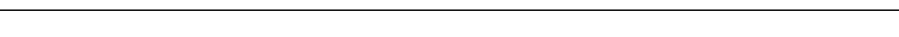
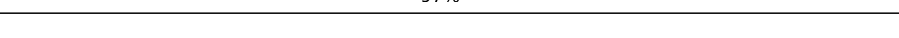
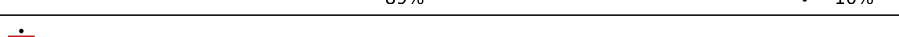

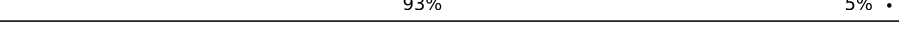
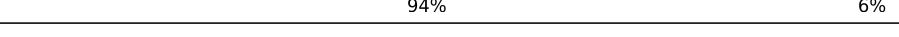
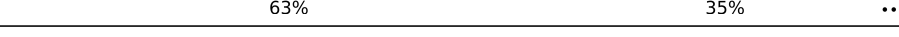


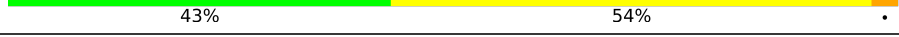
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Mol	Chain	Length	Quality of chain
9	E	215	 76% 22%
10	F	155	 99%
11	G	142	 98%
12	H	132	 96%
13	I	108	 93% 6%
14	J	121	 94% 6%
15	K	139	 94%
16	L	124	 94% 5%
17	M	61	 97%
18	N	86	 95%
19	O	94	 85% 15%
20	P	85	 94%
21	Q	104	 62% 38%
22	R	87	 95%
23	S	87	 87% 11%
24	T	60	 88% 12%
25	W	122	 44% 56% 43%
26	a	287	 99%
27	b	287	 79% 20%
28	c	212	 99%
29	d	180	 96%
30	e	184	 96%
31	f	149	 33% 95%
32	g	161	 9% 68% 10% 22%
33	h	137	 15% 92% 7%

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Mol	Chain	Length	Quality of chain
34	i	146	 98%
35	j	122	 99%
36	k	151	 98%
37	l	139	 98%
38	m	124	 95%
39	n	116	 97%
40	o	119	 97%
41	p	127	 89% 10%
42	q	100	 96%
43	r	159	 87% 13%
44	s	237	 39% 61%
45	t	111	 100%
46	u	104	 82% 17%
47	v	65	 97%
48	w	111	 89% 10%
49	x	97	 45% 55%
50	y	57	 93% 5%
51	z	53	 94% 6%
52	3	2907	 63% 35%
53	4	108	 56% 40%
54	5	1520	 65% 33%
55	6	76	 43% 54%
55	8	76	 43% 54%

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 151980 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

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

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

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

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

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	9	682	5326	3369	911	1021	25	0	0

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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	S	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	S	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	S	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 L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	69	Total	C	N	O	S	0	0
			534	342	87	103	2		

- Molecule 26 is a protein called 50S ribosomal protein L2.

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

- Molecule 27 is a protein called 50S ribosomal protein L3.

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

- Molecule 28 is a protein called 50S ribosomal protein L4.

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

- Molecule 29 is a protein called 50S ribosomal protein L5.

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

- Molecule 30 is a protein called 50S ribosomal protein L6.

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

- Molecule 31 is a protein called 50S ribosomal protein L9.

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

- Molecule 32 is a protein called 50S ribosomal protein L10.

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

- Molecule 33 is a protein called 50S ribosomal protein L11.

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

- Molecule 34 is a protein called 50S ribosomal protein L13.

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

- Molecule 35 is a protein called 50S ribosomal protein L14.

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

- Molecule 36 is a protein called 50S ribosomal protein L15.

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

- Molecule 37 is a protein called 50S ribosomal protein L16.

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

- Molecule 38 is a protein called 50S ribosomal protein L17.

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

- Molecule 39 is a protein called 50S ribosomal protein L18.

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

- Molecule 40 is a protein called 50S ribosomal protein L19.

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

- Molecule 41 is a protein called 50S ribosomal protein L20.

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

- Molecule 42 is a protein called 50S ribosomal protein L21.

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

- Molecule 43 is a protein called 50S ribosomal protein L22.

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

- Molecule 44 is a protein called 50S ribosomal protein L23.

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

- Molecule 45 is a protein called 50S ribosomal protein L24.

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

- Molecule 46 is a protein called 50S ribosomal protein L27.

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

- Molecule 47 is a protein called 50S ribosomal protein L28.

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

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L31.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L33 1.

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

- Molecule 52 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 53 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 54 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

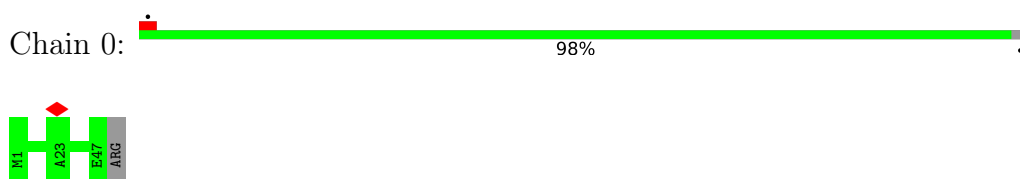
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
55	8	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

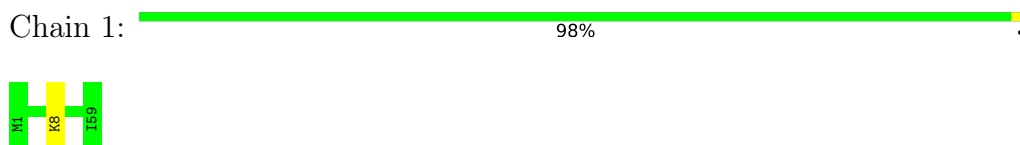
3 Residue-property plots [i](#)

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



- Molecule 2: 50S ribosomal protein L35

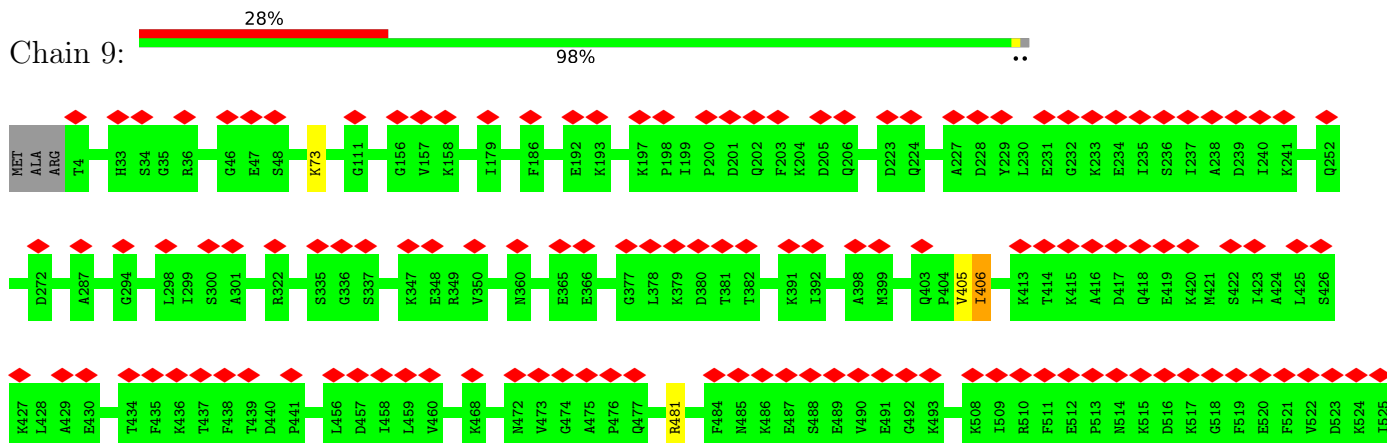


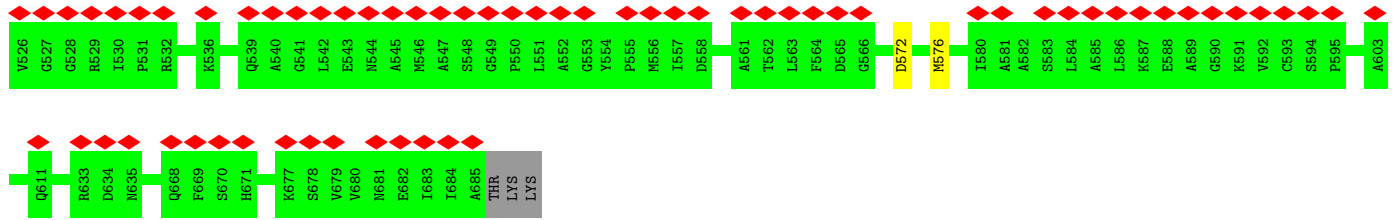
- Molecule 3: 50S ribosomal protein L36



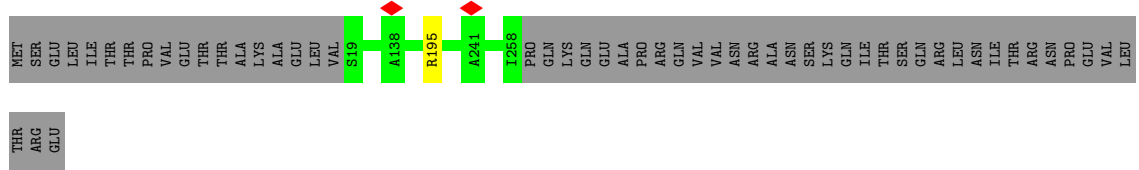
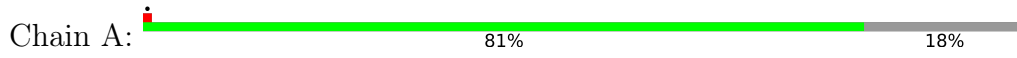
There are no outlier residues recorded for this chain.

- Molecule 4: Elongation factor G

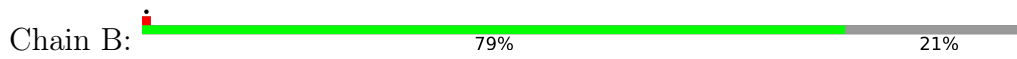




• Molecule 5: 30S ribosomal protein S2



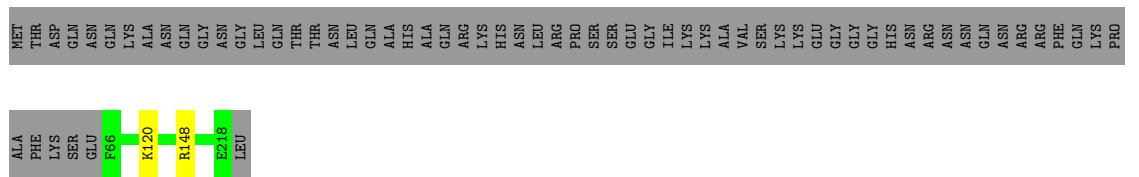
• Molecule 6: 30S ribosomal protein S3



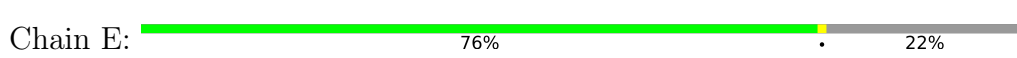
• Molecule 7: 30S ribosomal protein S4

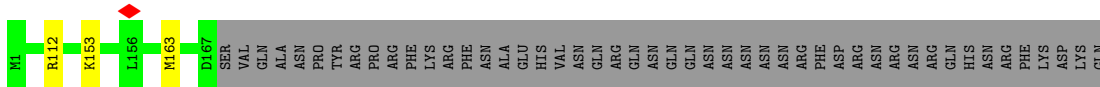


• Molecule 8: 30S ribosomal protein S5

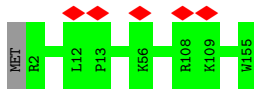


• Molecule 9: 30S ribosomal protein S6





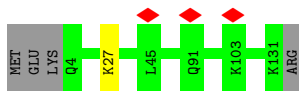
- Molecule 10: 30S ribosomal protein S7



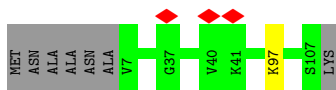
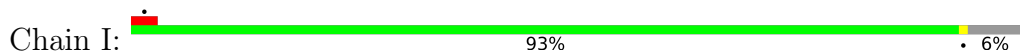
- Molecule 11: 30S ribosomal protein S8



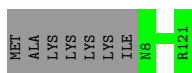
- Molecule 12: 30S ribosomal protein S9



- Molecule 13: 30S ribosomal protein S10



- Molecule 14: 30S ribosomal protein S11

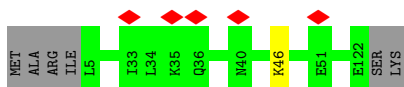


- Molecule 15: 30S ribosomal protein S12



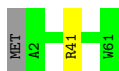
- Molecule 16: 30S ribosomal protein S13

Chain L:  94% 5%



- Molecule 17: 30S ribosomal protein S14 type Z

Chain M:  97%




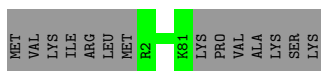
- Molecule 18: 30S ribosomal protein S15

Chain N:  95%



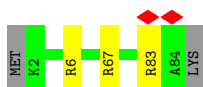
- Molecule 19: 30S ribosomal protein S16

Chain O:  85% 15%



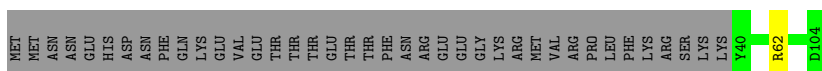
- Molecule 20: 30S ribosomal protein S17

Chain P:  94%



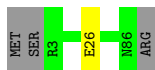
- Molecule 21: 30S ribosomal protein S18

Chain Q:  62% 38%

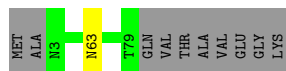
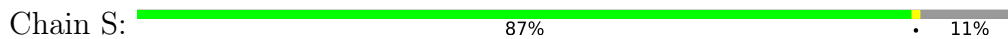


- Molecule 22: 30S ribosomal protein S19

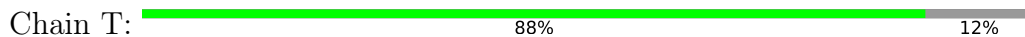
Chain R:  95%



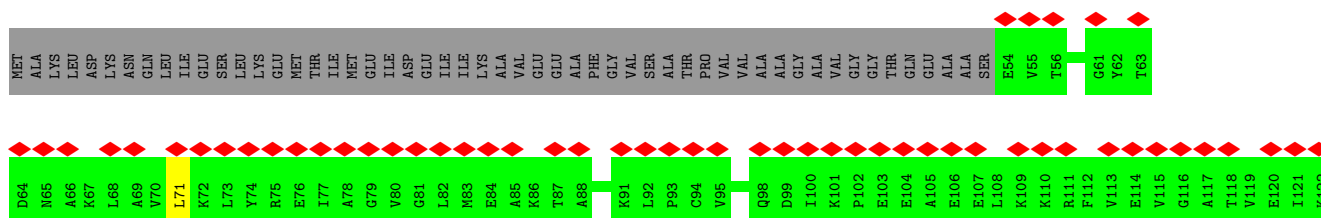
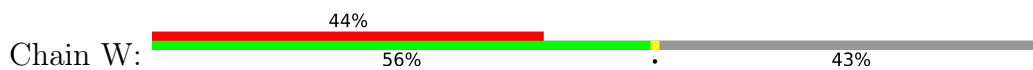
- Molecule 23: 30S ribosomal protein S20



- Molecule 24: 30S ribosomal protein S21



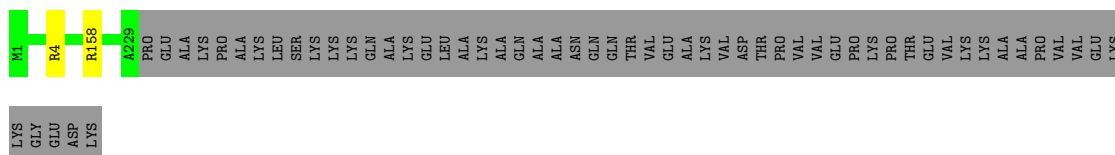
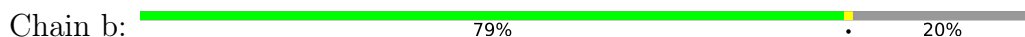
- Molecule 25: 50S ribosomal protein L7/L12



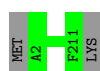
- Molecule 26: 50S ribosomal protein L2



- Molecule 27: 50S ribosomal protein L3

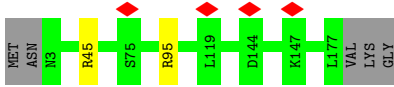


- Molecule 28: 50S ribosomal protein L4



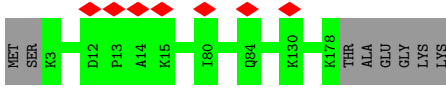
- Molecule 29: 50S ribosomal protein L5





- Molecule 30: 50S ribosomal protein L6

Chain e: 96%



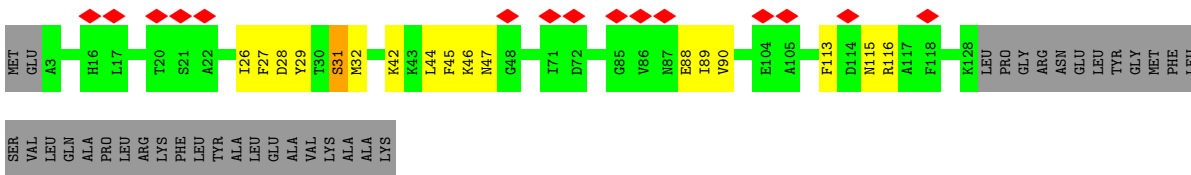
- Molecule 31: 50S ribosomal protein L9

Chain f: 33% 95%



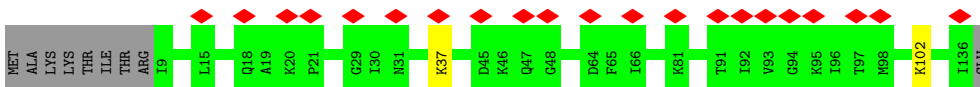
- Molecule 32: 50S ribosomal protein L10

Chain g: 9% 68% 10% 22%



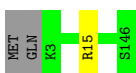
- Molecule 33: 50S ribosomal protein L11

Chain h: 15% 92% 7%



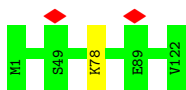
- Molecule 34: 50S ribosomal protein L13

Chain i: 98%

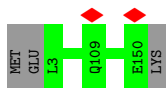


- Molecule 35: 50S ribosomal protein L14

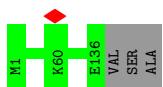
Chain j: 99%



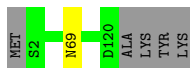
- Molecule 36: 50S ribosomal protein L15



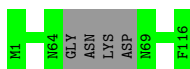
- Molecule 37: 50S ribosomal protein L16



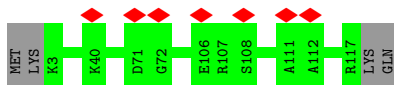
- Molecule 38: 50S ribosomal protein L17



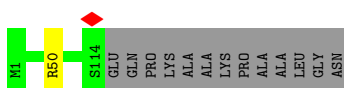
- Molecule 39: 50S ribosomal protein L18



- Molecule 40: 50S ribosomal protein L19

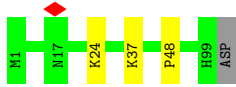


- Molecule 41: 50S ribosomal protein L20




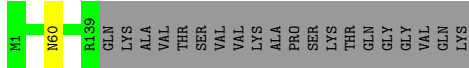
- Molecule 42: 50S ribosomal protein L21

Chain q:  96%



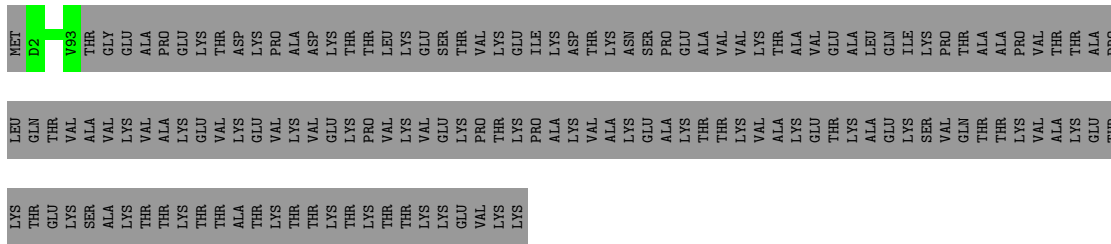
- Molecule 43: 50S ribosomal protein L22

Chain r:  87% 13%



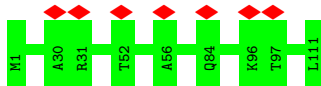
- Molecule 44: 50S ribosomal protein L23

Chain s:  39% 61%




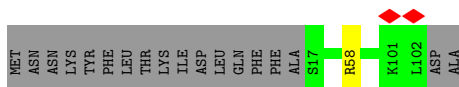
- Molecule 45: 50S ribosomal protein L24

Chain t:  6% 100%



- Molecule 46: 50S ribosomal protein L27

Chain u:  82% 17%

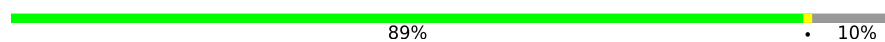


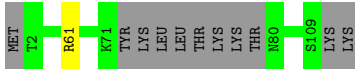
- Molecule 47: 50S ribosomal protein L28

Chain v:  97%

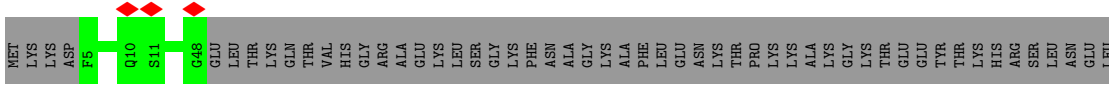


- Molecule 48: 50S ribosomal protein L29

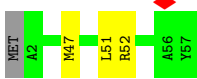
Chain w:  89% 10%



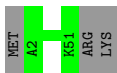
- Molecule 49: 50S ribosomal protein L31



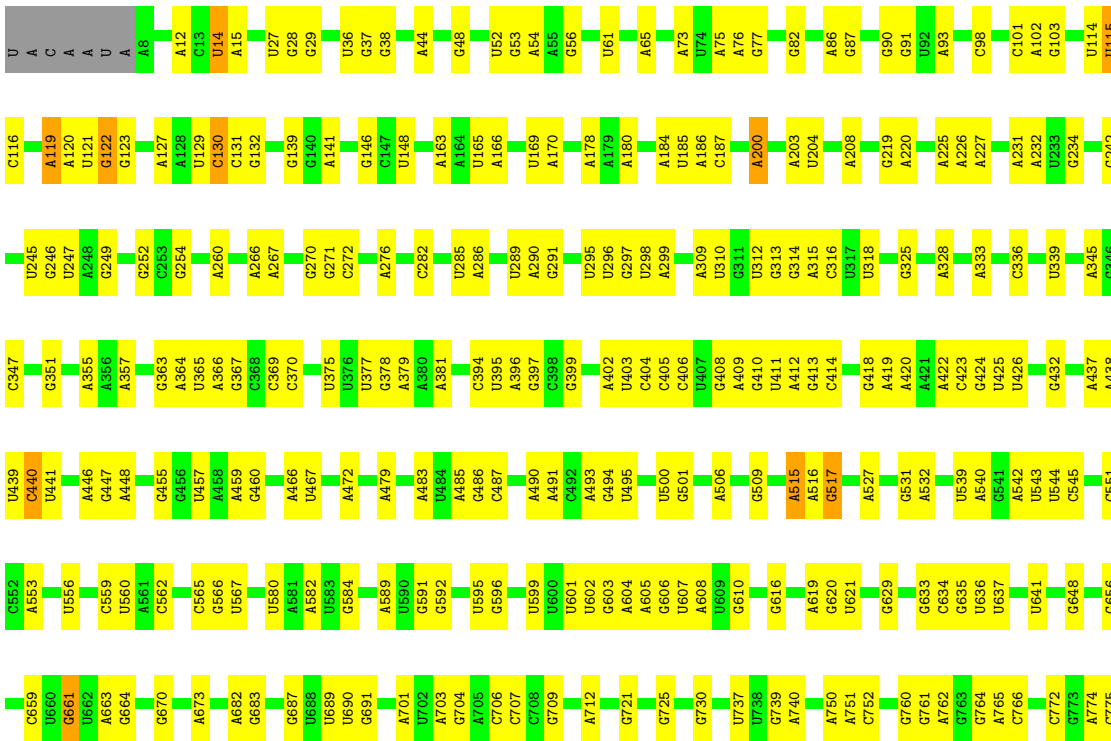
- Molecule 50: 50S ribosomal protein L32



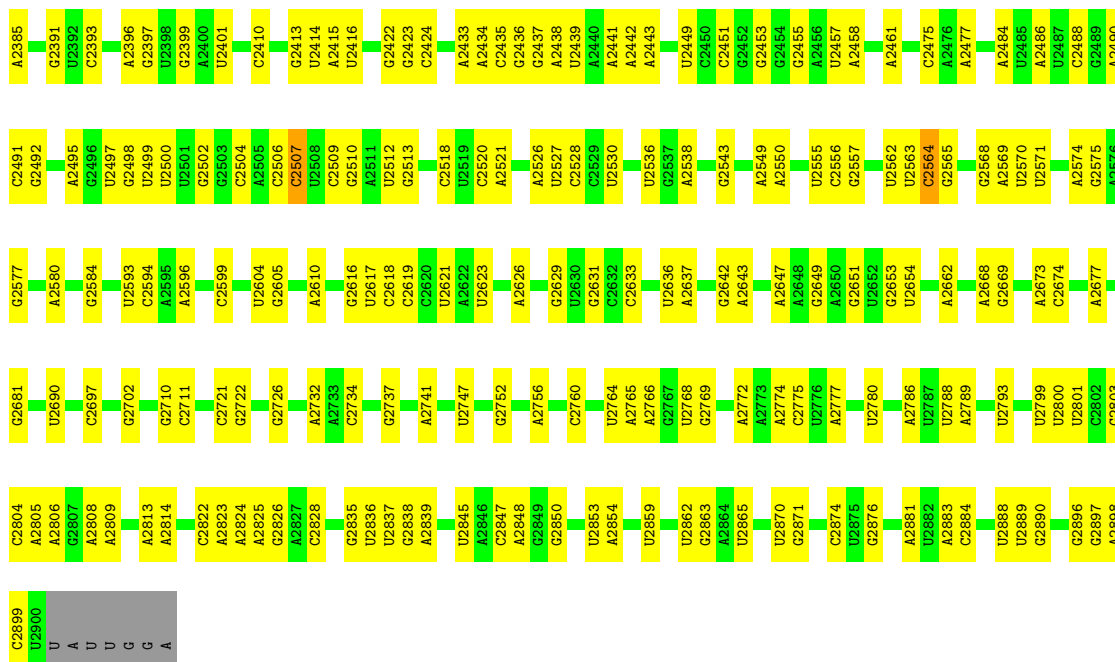
- Molecule 51: 50S ribosomal protein L33 1



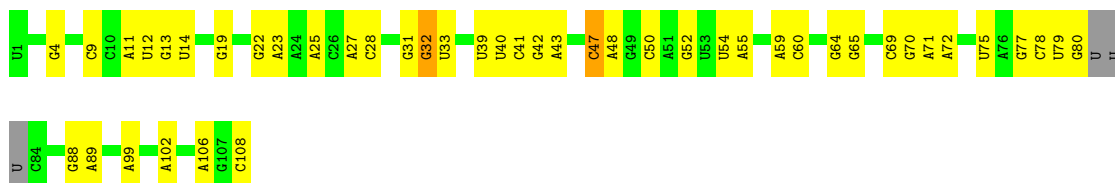
- Molecule 52: 23S ribosomal RNA



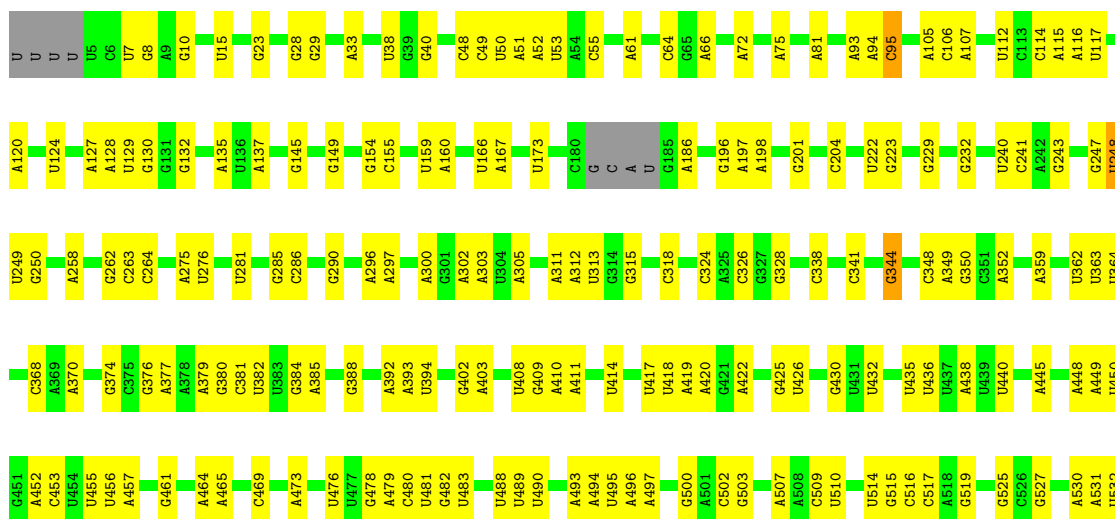
G2284	G2285	U2291	C2293	A2294	A2295	A2300	U2304	C2305	U2308	G2311	G2312	U2313	U2314	G2315	A2316	A2317	A2318	A2319	U2320	U2322	U2323	U2327	U2328	C2329	A2330	U2331	G2332	C2333	U2334	G2341	U2342	A2343	G2345	U2348	U2352	A2353	C2354	G2355	C2356	G2357	U2358	A2362	G2369	C2370	U2380	G2381	C2383			
G1975	A1976	U1977	U1978	G1979	G1982	U1993	C1997	G1998	U1999	U2000	C2003	G2004	A2010	G2011	A2012	A2020	G2027	G2028	U2029	A2030	C2031	A2038	C2039	A2040	C2041	A2042	C2043	C2044	G2050	C2058	G2059	C2062	G2063	A2066	A2067	G2068	A2069	C2070	G2076	A2084	C2085	U2086	G2087	G2090						
C2091	U2098	U2099	G2100	G2106	A2107	U2110	U2111	A2112	A2115	U2116	A2123	A2124	U2125	A2126	G2127	G2132	A2133	G2134	A2137	U2138	C2139	G2140	A2141	U2142	G2143	A2144	A2145	G2152	G2155	U2163	A2170	A2171	G2174	U2175	G2176	G2177	A2178	U2179	U2180	A2184	C2187	G2190								
U2183	G2194	U2195	G2196	U2197	G2198	C2199	U2200	G2201	U2202	U2203	C2204	U2205	A2206	U2208	G2211	U2212	U2219	A2220	U2221	C2222	C2223	U2227	U2228	C2229	A2230	U2231	G2232	A2233	C2234	G2246	G2247	U2251	U2257	G2260	C2261	C2262	G2267	C2271	C2272	U2273	A2274	A2275	A2276	U2277	G2278	A2281	A2282	C2283		
G1807	A1808	C1809	U1810	A1811	U1815	A1816	U1820	G1821	C1822	A1823	U1826	U1827	A1828	A1836	C1837	U1838	A1839	G1842	C1843	U1844	A1845	U1846	A1951	G1956	U1957	A1959	U1960	U1961	U1962	U1963	U1964	C1965	G1966	U1967	A1864	U1865	G1866	U1867	U1871	U1874										
U1872	A1873	G1874	G1885	U1890	A1891	A1892	A1896	A1903	G1906	A1907	G1910	G1913	G1914	C1915	A1919	A1920	C1921	C1927	A1934	U1935	G1936	U1937	U1938	A1943	A1944	A1945	U1946	A1951	G1956	U1957	U1958	A1959	C1962	G1963	A1864	U1865	G1866	U1867	U1871	U1874										
A1643	A1644	C1645	A1648	A1660	A1661	G1665	U1670	U1673	A1674	U1679	A1680	G1681	C1682	G1683	U1686	G1687	A1694	G1695	A1702	A1703	C1706	U1707	G1708	C1709	A1710	U1714	A1715	A1716	U1727	A1728	G1729	G1730	A1732	G1733	A1734	A1735	G1741	U1748	A1749	A1750	A1751	G1753								
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U1316	C1317	C1325	A1328	U1329	U1330	G1331	G1338	U1341	C1342	C1343	A1347	G1353	U1354	C1355	G1356	U1357	C1358	C1359	U1360	U1361	A1364	U1365	U1366	U1369	A1370	G1371	U1372	C1373	U1374	G1375	C1378	G1388	A1393	U1400	U1404	G1405	A1406	U1407	A1410	A1413	U1414	A1415								
U1213	U1214	G1215	U1216	G1217	G1226	C1227	U1234	G1235	U1236	U1240	G1241	G1242	U1246	A1250	G1251	C1252	G1253	U1254	U1255	A1256	G1257	C1258	A1259	G1265	G1266	A1267	U1268	A1272	U1273	A1274	C1275	A1276	A1277	G1278	U1279	G1280	A1281	G1282	U1283	U1284	U1285	G1286	G1289	U1297	A1298	A1299	C1300	G1301	C1302	U1303
C1110	C1111	A1112	U1113	U1118	A1119	A1120	A1121	G1122	A1123	G1124	U1125	G1126	U1129	A1130	A1131	C1132	C1144	G1147	U1148	U1150	U1151	A1162	G1163	A1164	U1165	G1166	U1167	A1168	A1169	C1170	G1171	U1176	A1177	G1178	G1179	A1186	U1192	U1193	U1199	A1199	U1200	A1204	U1207	A1208	G1209	G1210	U1211	C1212		
A1008	A1009	G1010	A1016	A1019	G1025	A1026	U1027	U1031	A1032	G1039	A1040	C1041	A1046	A1047	A1048	U1049	A1055	A1056	G1057	U1058	G1059	G1060	A1061	G840	C841	G844	C847	A854	U862	U863	A864	A865	C880	A881	C882	A883	A884	A885	U896	C901	U902	A903	C904	U905	G906					
G914	G917	G920	C921	C922	A	C	C	U	A	G928	G931	U932	A933	G936	A937	A938	U939	A940	A943	U944	U945	A946	A947	C948	C949	U950	C951	U952	G953	A964	U968	A969	U970	A977	A981	G982	A983	G989	G990	U994	A995	A996	A1001							

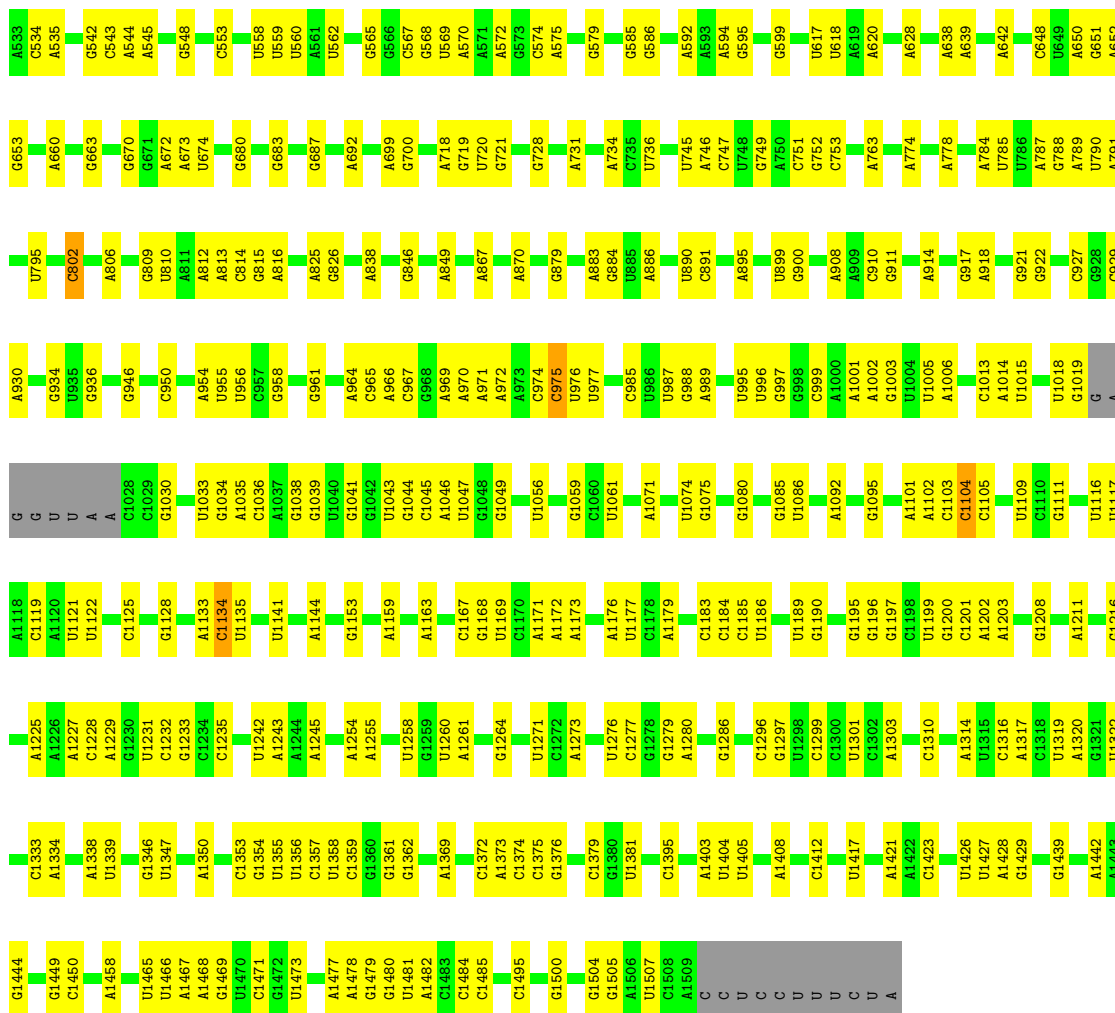


• Molecule 53: 5S ribosomal RNA

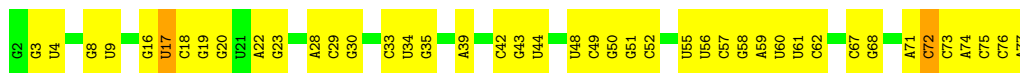


• Molecule 54: 16S ribosomal RNA

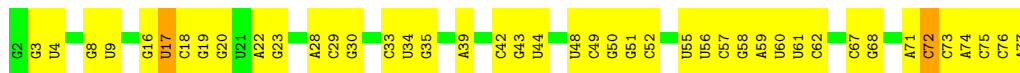




● Molecule 55: tRNA-Phe



● Molecule 55: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	627	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.988	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.098	Depositor
Recommended contour level	0.22	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	0.34	0/383	0.54	0/504
2	1	0.23	0/484	0.44	0/637
3	2	0.22	0/306	0.45	0/401
4	9	0.27	0/5419	0.51	1/7307 (0.0%)
5	A	0.26	0/1954	0.47	0/2642
6	B	0.24	0/1721	0.45	0/2323
7	C	0.27	0/1691	0.46	0/2267
8	D	0.24	0/1188	0.47	0/1593
9	E	0.26	0/1384	0.51	1/1867 (0.1%)
10	F	0.25	0/1266	0.46	0/1700
11	G	0.26	0/1126	0.46	0/1517
12	H	0.25	0/1044	0.47	0/1395
13	I	0.24	0/820	0.47	0/1103
14	J	0.26	0/844	0.49	0/1136
15	K	0.31	0/1094	0.55	0/1468
16	L	0.23	0/962	0.46	0/1289
17	M	0.26	0/483	0.45	0/643
18	N	0.23	0/679	0.42	0/907
19	O	0.24	0/659	0.48	0/885
20	P	0.23	0/684	0.47	0/913
21	Q	0.31	0/545	0.61	0/730
22	R	0.26	0/698	0.52	0/936
23	S	0.24	0/631	0.41	0/838
24	T	0.30	0/475	0.45	0/621
25	W	0.27	0/538	0.58	1/722 (0.1%)
26	a	0.23	0/2267	0.47	0/3044
27	b	0.25	0/1795	0.50	0/2412
28	c	0.26	0/1671	0.50	0/2246
29	d	0.25	0/1409	0.48	0/1894
30	e	0.25	0/1420	0.50	0/1912
31	f	0.30	0/1183	0.54	0/1587
32	g	0.39	0/969	0.61	0/1295
33	h	0.26	0/968	0.50	0/1298
34	i	0.24	0/1186	0.45	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.25	0/953	0.50	0/1275
36	k	0.24	0/1170	0.45	0/1559
37	l	0.29	0/1104	0.50	0/1481
38	m	0.24	0/973	0.47	0/1309
39	n	0.28	0/897	0.51	0/1198
40	o	0.29	0/948	0.53	0/1262
41	p	0.24	0/961	0.43	0/1278
42	q	0.26	0/828	0.54	0/1111
43	r	0.26	0/1077	0.47	0/1441
44	s	0.25	0/732	0.50	0/988
45	t	0.24	0/879	0.51	0/1165
46	u	0.25	0/665	0.44	0/884
47	v	0.23	0/519	0.48	0/695
48	w	0.23	0/826	0.43	0/1104
49	x	0.26	0/353	0.47	0/474
50	y	0.31	0/457	0.49	0/601
51	z	0.30	0/412	0.52	0/547
52	3	0.24	0/69073	0.88	75/107710 (0.1%)
53	4	0.23	0/2505	0.91	5/3902 (0.1%)
54	5	0.24	0/35768	0.87	25/55764 (0.0%)
55	6	0.31	0/1808	1.08	9/2817 (0.3%)
55	8	0.31	0/1808	1.08	9/2817 (0.3%)
All	All	0.25	0/164662	0.79	126/245006 (0.1%)

There are no bond length outliers.

The worst 5 of 126 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	131	C	N3-C2-O2	-10.59	114.48	121.90
52	3	1111	C	N3-C2-O2	-10.39	114.63	121.90
52	3	131	C	N1-C2-O2	9.73	124.74	118.90
52	3	1672	C	N3-C2-O2	-9.27	115.41	121.90
52	3	1111	C	N1-C2-O2	9.21	124.43	118.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	45 (100%)	0	0	100	100
2	1	57/59 (97%)	50 (88%)	7 (12%)	0	100	100
3	2	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
4	9	680/688 (99%)	620 (91%)	58 (8%)	2 (0%)	41	77
5	A	238/294 (81%)	221 (93%)	17 (7%)	0	100	100
6	B	213/273 (78%)	205 (96%)	8 (4%)	0	100	100
7	C	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
8	D	151/219 (69%)	138 (91%)	13 (9%)	0	100	100
9	E	165/215 (77%)	139 (84%)	26 (16%)	0	100	100
10	F	152/155 (98%)	137 (90%)	15 (10%)	0	100	100
11	G	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
12	H	126/132 (96%)	121 (96%)	5 (4%)	0	100	100
13	I	99/108 (92%)	93 (94%)	6 (6%)	0	100	100
14	J	112/121 (93%)	108 (96%)	4 (4%)	0	100	100
15	K	134/139 (96%)	109 (81%)	25 (19%)	0	100	100
16	L	116/124 (94%)	103 (89%)	13 (11%)	0	100	100
17	M	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
18	N	81/86 (94%)	78 (96%)	3 (4%)	0	100	100
19	O	78/94 (83%)	67 (86%)	11 (14%)	0	100	100
20	P	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
21	Q	63/104 (61%)	56 (89%)	7 (11%)	0	100	100
22	R	82/87 (94%)	63 (77%)	19 (23%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	61 (91%)	6 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	283/287 (99%)	257 (91%)	26 (9%)	0	100	100
27	b	227/287 (79%)	199 (88%)	28 (12%)	0	100	100
28	c	208/212 (98%)	193 (93%)	15 (7%)	0	100	100
29	d	173/180 (96%)	154 (89%)	19 (11%)	0	100	100
30	e	174/184 (95%)	166 (95%)	8 (5%)	0	100	100
31	f	143/149 (96%)	133 (93%)	8 (6%)	2 (1%)	11	46
32	g	124/161 (77%)	109 (88%)	13 (10%)	2 (2%)	9	44
33	h	126/137 (92%)	113 (90%)	13 (10%)	0	100	100
34	i	142/146 (97%)	132 (93%)	10 (7%)	0	100	100
35	j	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
36	k	146/151 (97%)	131 (90%)	15 (10%)	0	100	100
37	l	134/139 (96%)	127 (95%)	7 (5%)	0	100	100
38	m	117/124 (94%)	103 (88%)	14 (12%)	0	100	100
39	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
40	o	113/119 (95%)	100 (88%)	13 (12%)	0	100	100
41	p	112/127 (88%)	106 (95%)	6 (5%)	0	100	100
42	q	97/100 (97%)	88 (91%)	8 (8%)	1 (1%)	15	55
43	r	137/159 (86%)	126 (92%)	11 (8%)	0	100	100
44	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
45	t	109/111 (98%)	98 (90%)	11 (10%)	0	100	100
46	u	84/104 (81%)	79 (94%)	5 (6%)	0	100	100
47	v	61/65 (94%)	52 (85%)	9 (15%)	0	100	100
48	w	96/111 (86%)	84 (88%)	12 (12%)	0	100	100
49	x	42/97 (43%)	39 (93%)	3 (7%)	0	100	100
50	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
51	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100
All	All	6567/7480 (88%)	6003 (91%)	557 (8%)	7 (0%)	54	86

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	9	406	ILE
4	9	572	ASP

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Mol	Chain	Res	Type
32	g	31	SER
31	f	18	VAL
32	g	116	ARG

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	50 (98%)	1 (2%)	55	74
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	579/584 (99%)	575 (99%)	4 (1%)	84	90
5	A	212/262 (81%)	211 (100%)	1 (0%)	88	93
6	B	180/232 (78%)	180 (100%)	0	100	100
7	C	181/183 (99%)	180 (99%)	1 (1%)	86	92
8	D	123/178 (69%)	121 (98%)	2 (2%)	62	79
9	E	150/196 (76%)	148 (99%)	2 (1%)	69	81
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	121 (98%)	2 (2%)	62	79
12	H	111/115 (96%)	110 (99%)	1 (1%)	78	87
13	I	95/99 (96%)	94 (99%)	1 (1%)	73	84
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	111 (95%)	6 (5%)	24	48
16	L	100/105 (95%)	99 (99%)	1 (1%)	76	86
17	M	47/48 (98%)	46 (98%)	1 (2%)	53	72
18	N	76/78 (97%)	75 (99%)	1 (1%)	69	81
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	70 (96%)	3 (4%)	30	55
21	Q	56/94 (60%)	55 (98%)	1 (2%)	59	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	R	74/77 (96%)	73 (99%)	1 (1%)	67	80
23	S	70/77 (91%)	69 (99%)	1 (1%)	67	80
24	T	49/56 (88%)	49 (100%)	0	100	100
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	240 (100%)	1 (0%)	91	94
27	b	186/233 (80%)	184 (99%)	2 (1%)	73	84
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	148 (99%)	2 (1%)	69	81
30	e	153/159 (96%)	153 (100%)	0	100	100
31	f	123/134 (92%)	122 (99%)	1 (1%)	81	89
32	g	101/129 (78%)	85 (84%)	16 (16%)	2	13
33	h	102/110 (93%)	100 (98%)	2 (2%)	55	74
34	i	126/128 (98%)	125 (99%)	1 (1%)	81	89
35	j	103/103 (100%)	102 (99%)	1 (1%)	76	86
36	k	123/126 (98%)	123 (100%)	0	100	100
37	l	113/115 (98%)	113 (100%)	0	100	100
38	m	105/109 (96%)	104 (99%)	1 (1%)	76	86
39	n	96/99 (97%)	96 (100%)	0	100	100
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	99 (99%)	1 (1%)	76	86
42	q	90/91 (99%)	88 (98%)	2 (2%)	52	71
43	r	116/132 (88%)	115 (99%)	1 (1%)	78	87
44	s	82/208 (39%)	82 (100%)	0	100	100
45	t	96/96 (100%)	96 (100%)	0	100	100
46	u	69/85 (81%)	68 (99%)	1 (1%)	67	80
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	86 (99%)	1 (1%)	73	84
49	x	41/86 (48%)	41 (100%)	0	100	100
50	y	48/49 (98%)	45 (94%)	3 (6%)	18	43
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5664 (99%)	66 (1%)	72	83

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	p	50	ARG
42	q	37	LYS
50	y	52	ARG
20	P	6	ARG
18	N	70	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
26	a	269	ASN
36	k	36	GLN
27	b	35	GLN
32	g	47	ASN
39	n	88	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	1011 (35%)	30 (1%)
53	4	103/108 (95%)	41 (39%)	4 (3%)
54	5	1490/1520 (98%)	492 (33%)	10 (0%)
55	6	75/76 (98%)	40 (53%)	4 (5%)
55	8	75/76 (98%)	40 (53%)	4 (5%)
All	All	4618/4687 (98%)	1624 (35%)	52 (1%)

5 of 1624 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	12	A
52	3	14	U
52	3	15	A
52	3	28	G
52	3	29	G

5 of 52 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	3	2721	C
54	5	166	U

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Mol	Chain	Res	Type
55	8	18	C
52	3	2897	G
53	4	59	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 monosaccharides 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-13449. These allow visual inspection of the internal detail of the map and identification of artifacts.

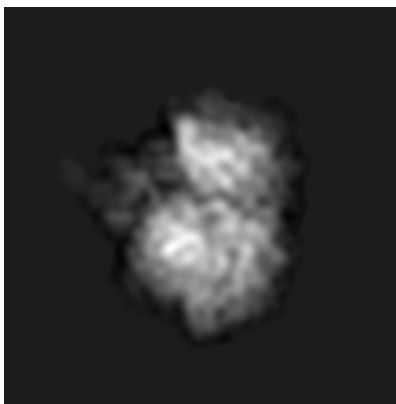
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X

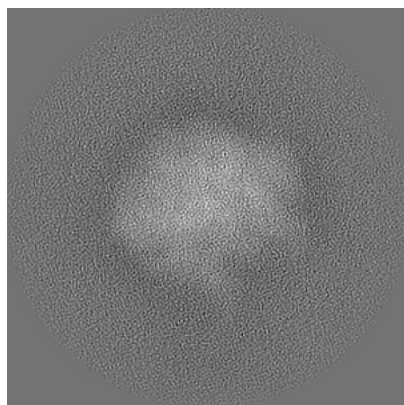


Y

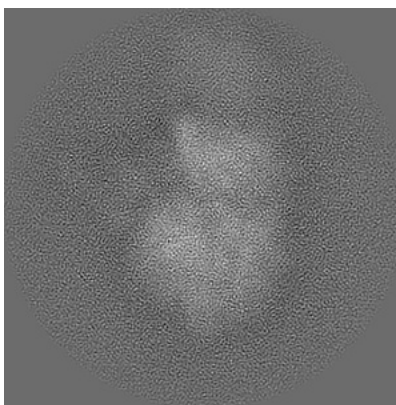


Z

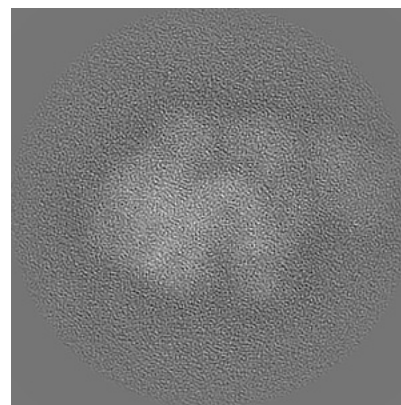
6.1.2 Raw map



X



Y

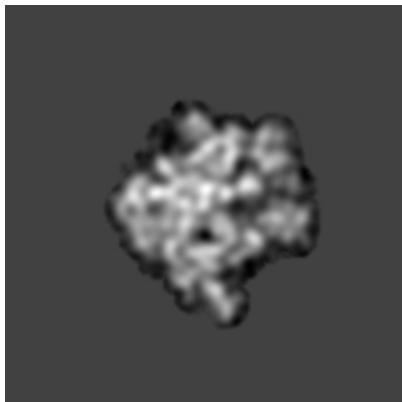


Z

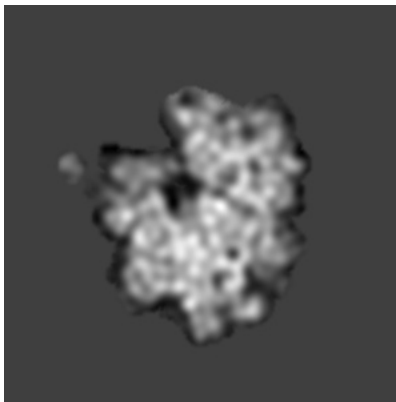
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

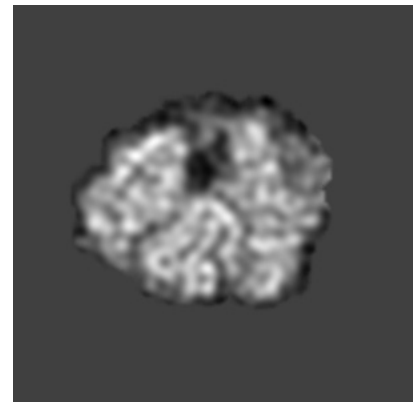
6.2.1 Primary map



X Index: 128

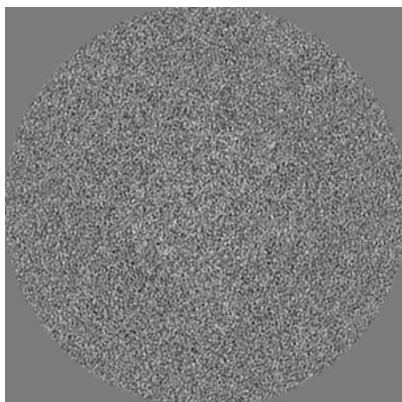


Y Index: 128

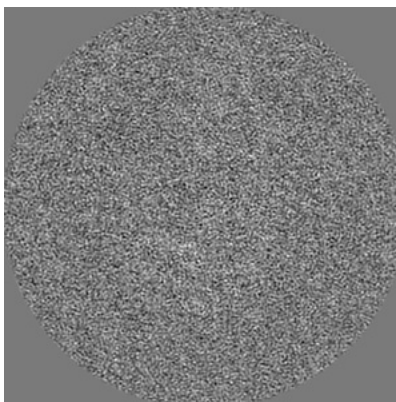


Z Index: 128

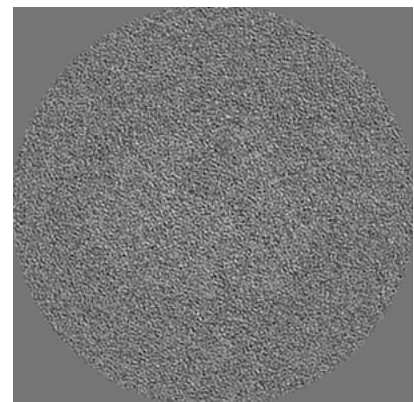
6.2.2 Raw map



X Index: 128



Y Index: 128



Z Index: 128

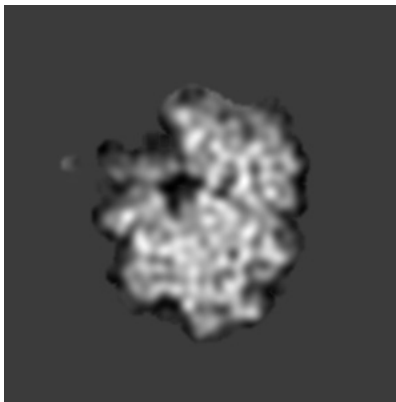
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

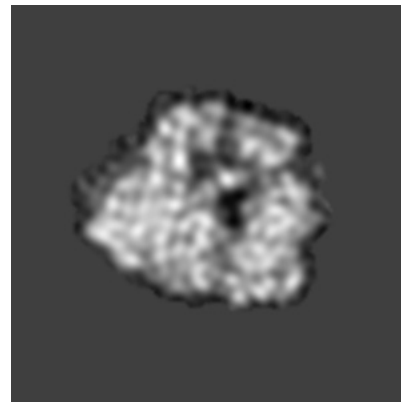
6.3.1 Primary map



X Index: 102

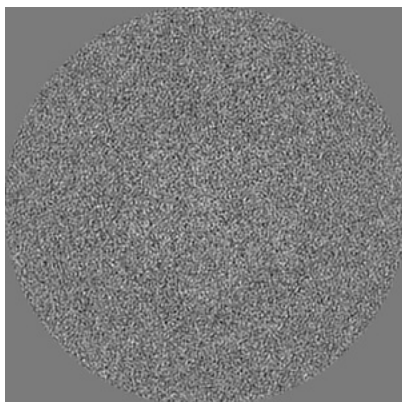


Y Index: 125

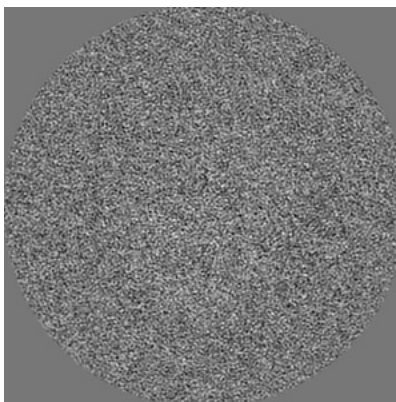


Z Index: 119

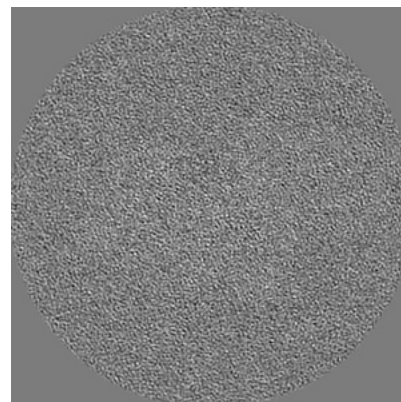
6.3.2 Raw map



X Index: 118



Y Index: 118

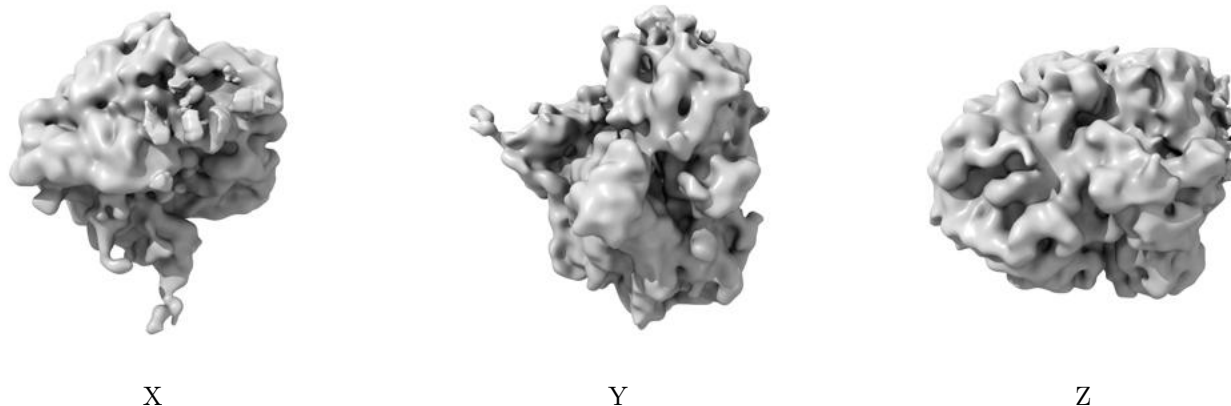


Z Index: 130

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

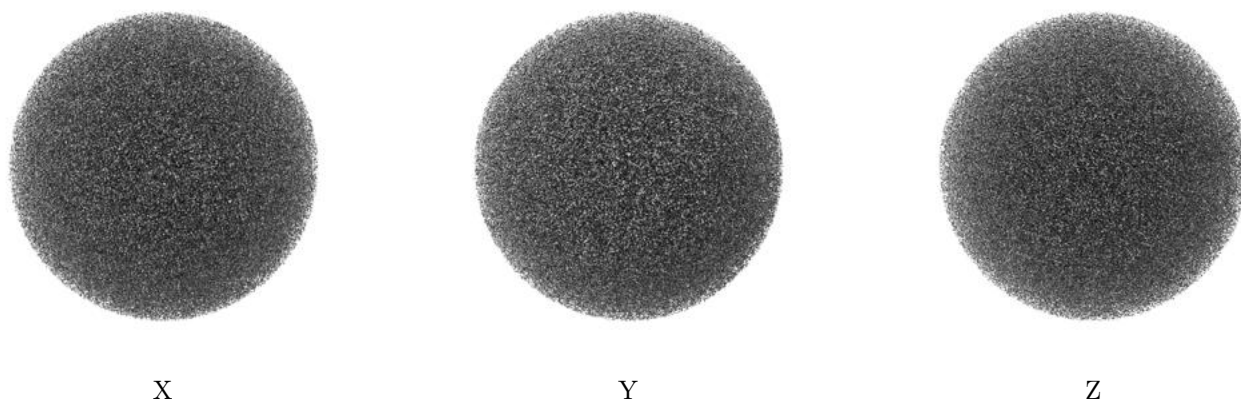
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.22. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

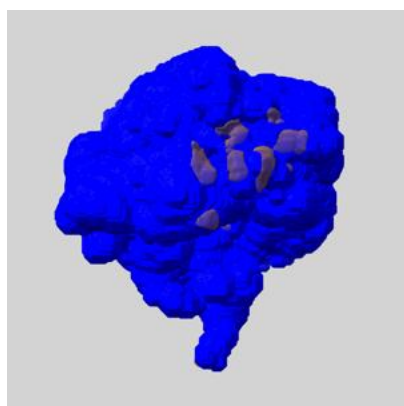
6.5 Mask visualisation [i](#)

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

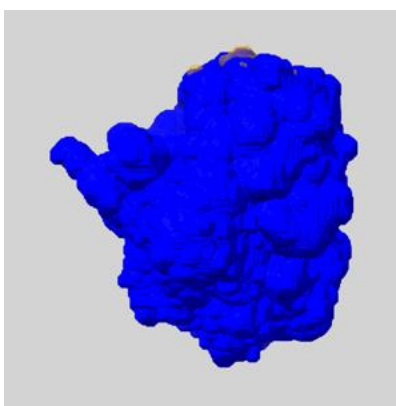
A mask typically either:

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

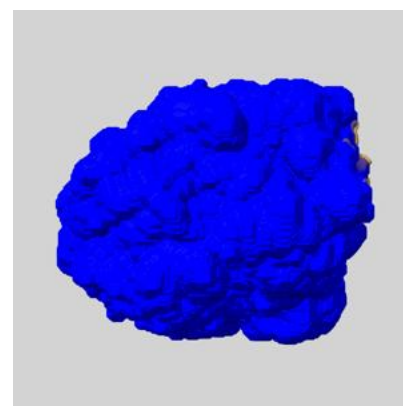
6.5.1 emd_13449_msk_1.map [i](#)



X



Y

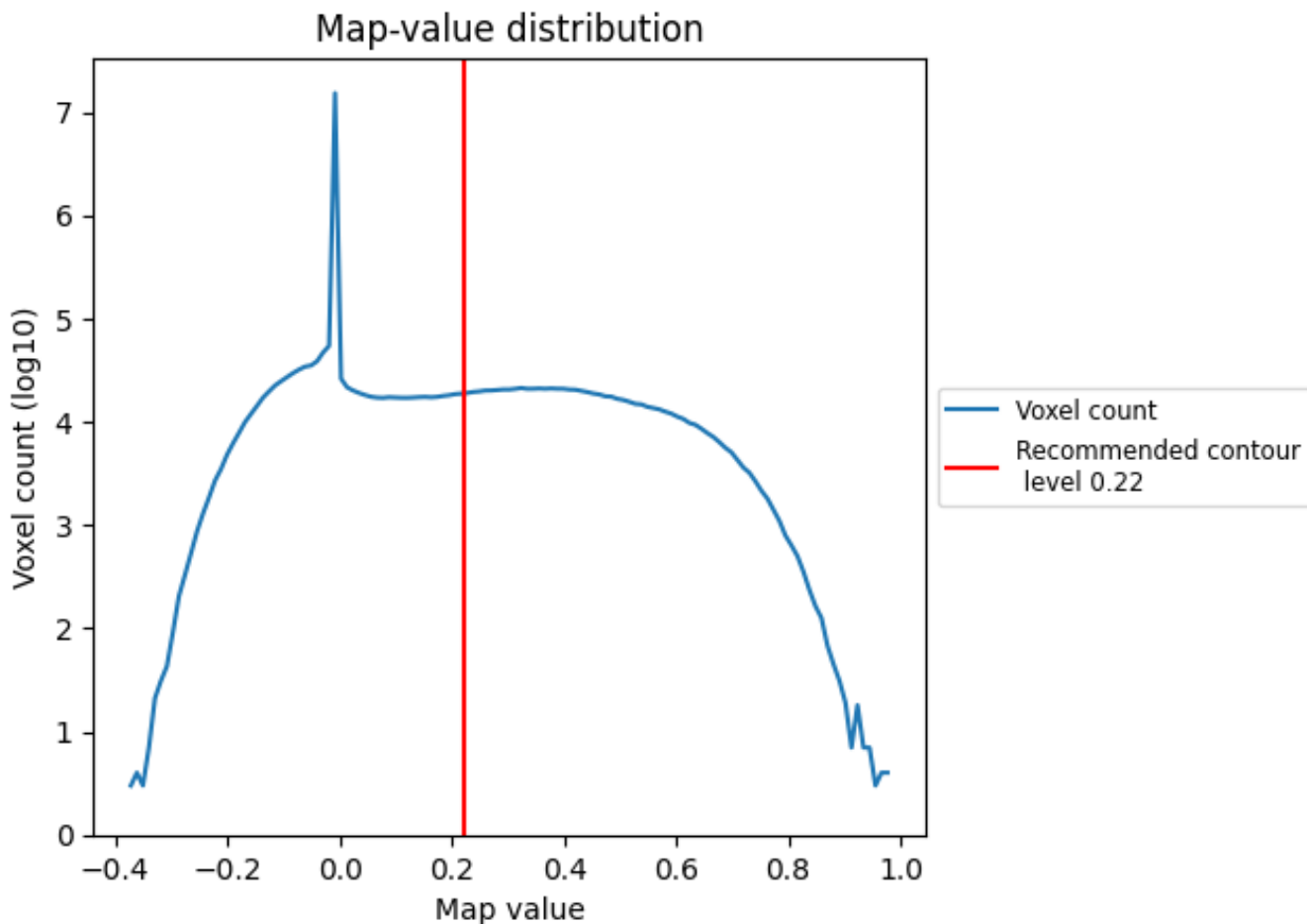


Z

7 Map analysis [i](#)

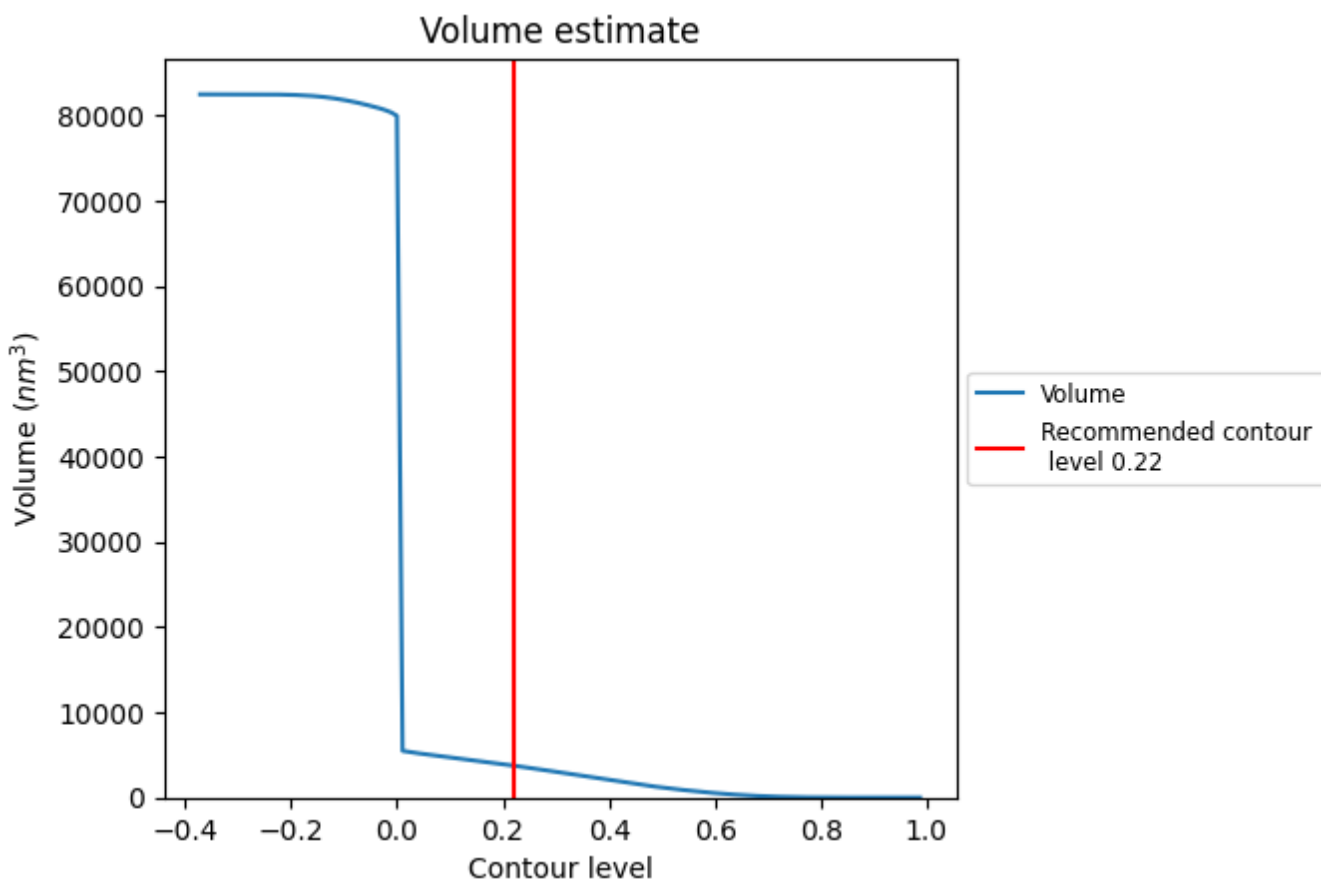
This section contains the results of statistical analysis of the map.

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.

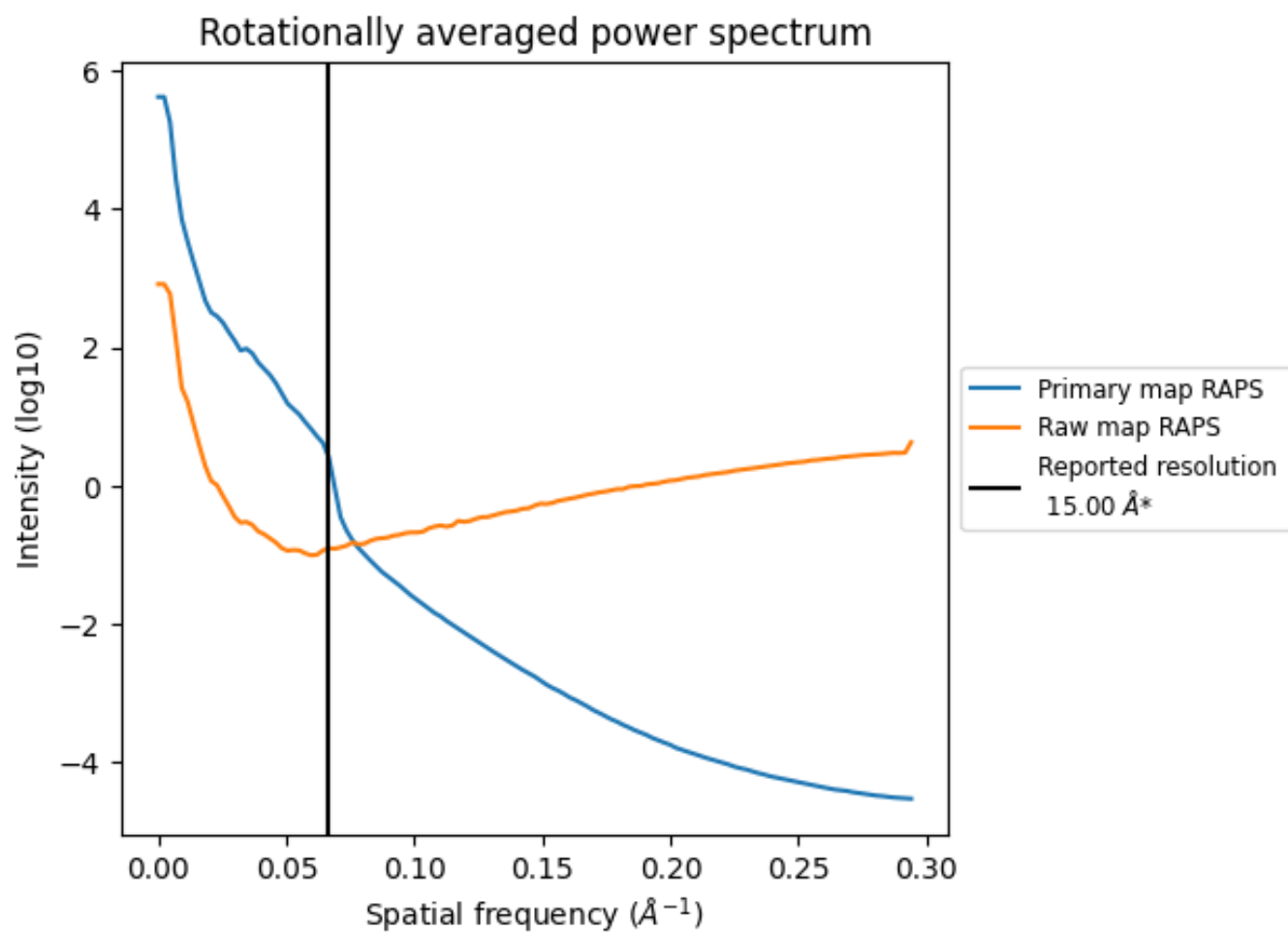
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3746 nm³; this corresponds to an approximate mass of 3384 kDa.

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

7.3 Rotationally averaged power spectrum i

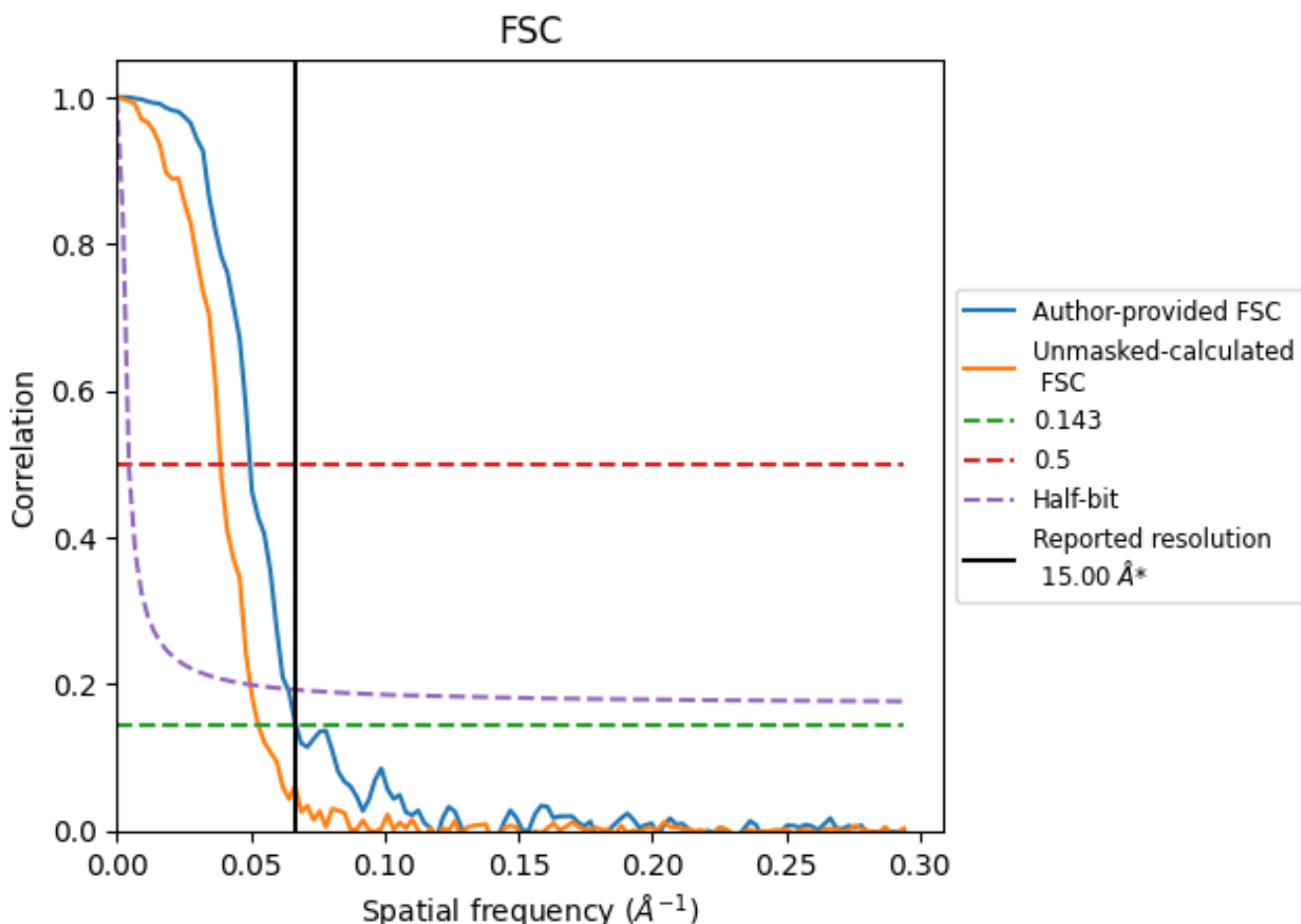


*Reported resolution corresponds to spatial frequency of 0.067 Å⁻¹

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 0.067 Å⁻¹

8.2 Resolution estimates

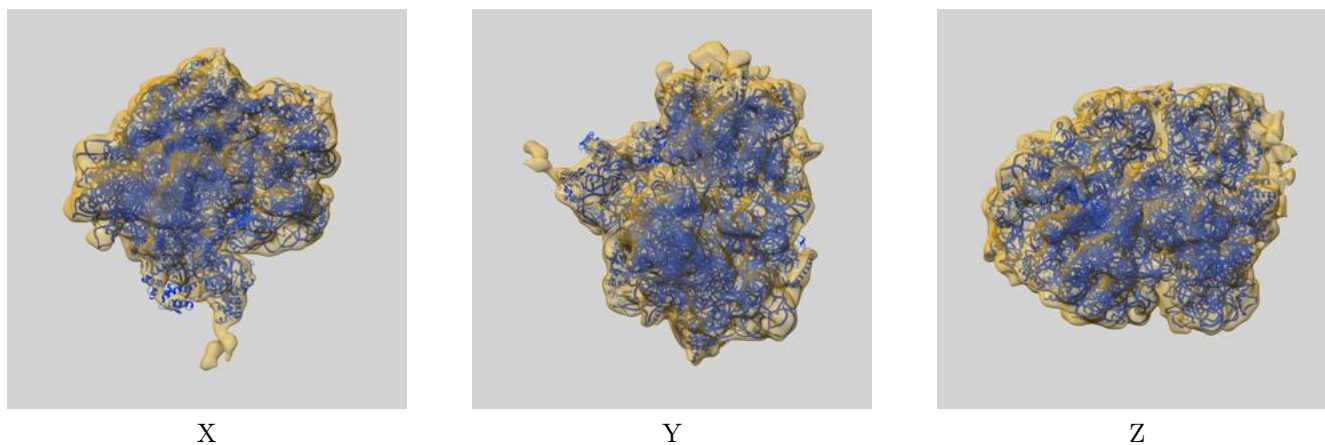
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	15.00	-	-
Author-provided FSC curve	14.95	20.08	15.62
Unmasked-calculated*	18.90	25.84	20.04

*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 18.90 differs from the reported value 15.0 by more than 10 %

9 Map-model fit [i](#)

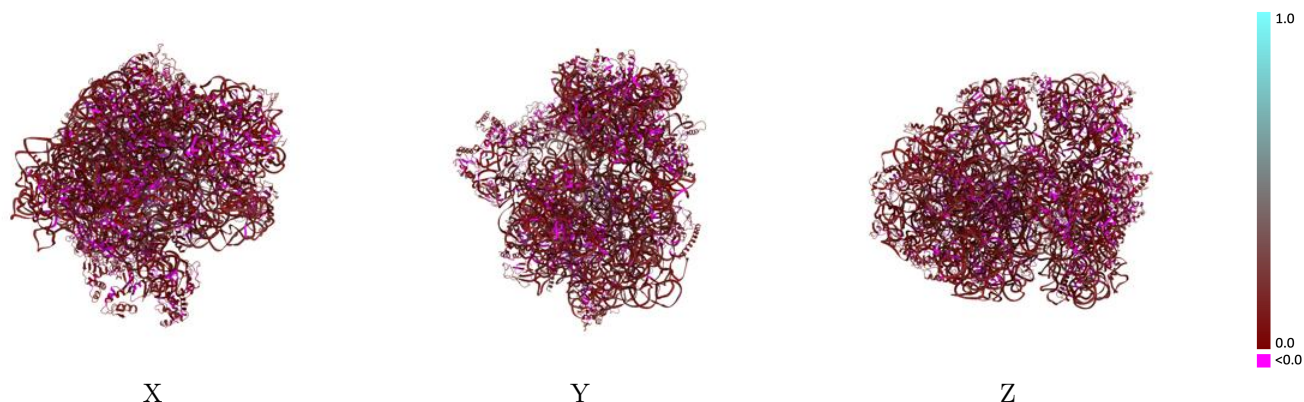
This section contains information regarding the fit between EMDB map EMD-13449 and PDB model 7PIS. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



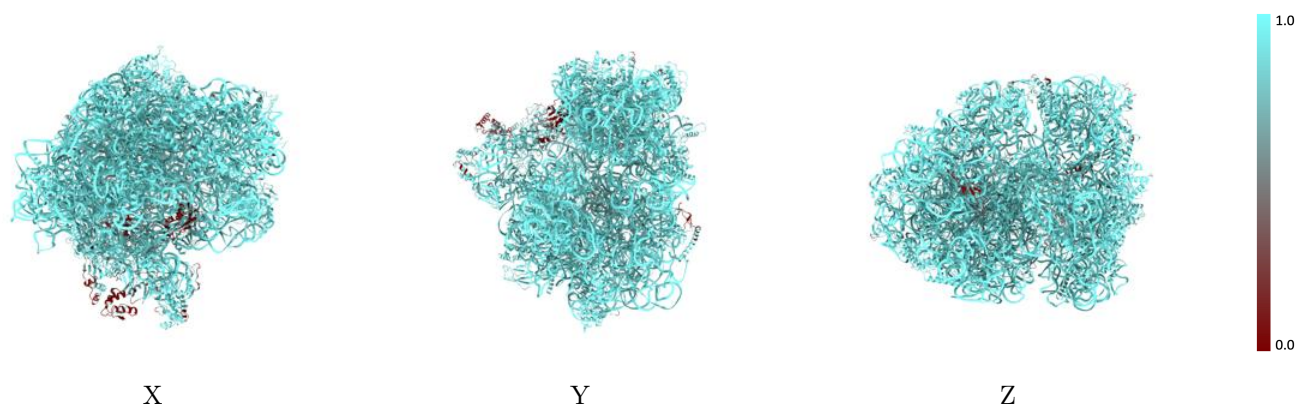
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



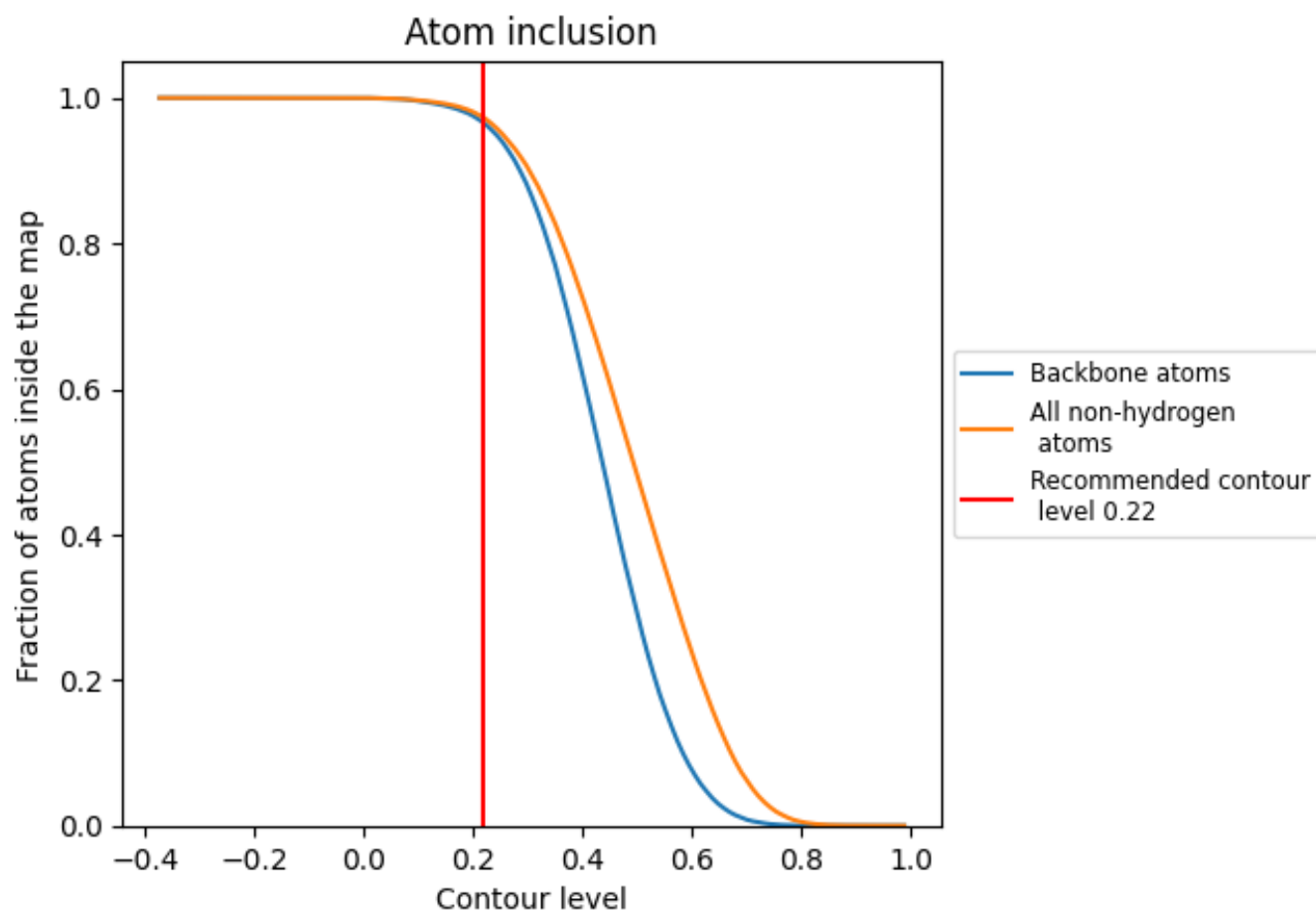
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.22).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9728	 0.0820
0	 0.9918	 0.0050
1	 1.0000	 0.0320
2	 1.0000	 0.0070
3	 0.9986	 0.0970
4	 0.9996	 0.1040
5	 0.9977	 0.1000
6	 0.9876	 0.0950
8	 0.9839	 0.0790
9	 0.6775	 0.0620
A	 0.9831	 0.0770
B	 0.9771	 0.0530
C	 0.9876	 0.0340
D	 0.9904	 0.0530
E	 0.9633	 0.0830
F	 0.9504	 0.0770
G	 0.9991	 0.0570
H	 0.9451	 0.0480
I	 0.9484	 0.0380
J	 0.9890	 0.0460
K	 0.9875	 0.0270
L	 0.9085	 0.0510
M	 1.0000	 0.0280
N	 0.9940	 0.0500
O	 1.0000	 0.0400
P	 0.9574	 0.0600
Q	 0.9845	 0.0700
R	 0.9940	 0.0610
S	 0.9951	 0.0440
T	 0.9888	 0.0700
W	 0.1686	 0.0900
a	 0.9995	 0.0280
b	 0.9925	 0.0380
c	 0.9963	 0.0580
d	 0.9632	 0.0700



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Chain	Atom inclusion	Q-score
e	 0.9295	 0.0580
f	 0.6118	 0.0700
g	 0.8337	 0.0780
h	 0.7952	 0.0770
i	 0.9939	 0.0450
j	 0.9761	 0.0240
k	 0.9815	 0.0370
l	 0.9896	 0.0490
m	 0.9936	 0.0260
n	 0.9862	 0.0590
o	 0.9308	 0.0400
p	 0.9803	 0.0390
q	 0.9474	 0.0690
r	 0.9981	 0.0510
s	 1.0000	 0.0370
t	 0.9175	 0.0620
u	 0.9750	 0.0320
v	 1.0000	 0.0320
w	 0.9875	 0.0950
x	 0.9009	 0.1130
y	 0.9885	 0.0720
z	 1.0000	 0.0290