



wwPDB EM Validation Summary Report

Oct 13, 2024 – 01:44 am BST


PDB ID : 7PAQ
EMDB ID : EMD-13280
Title : 70S ribosome with EF-G, A/P- and P/E-site tRNAs in Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-07-30
Resolution : 8.90 Å (reported)
Based on initial models : 4V7D, 4V7C, 7OOD, 7OOC

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:

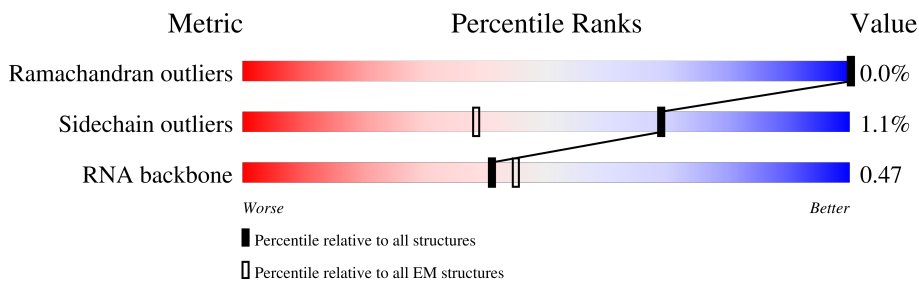
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance i

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

The reported resolution of this entry is 8.90 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	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	10% (red), 98% (green), 2% (grey)
2	1	59	7% (red), 98% (green), 3% (grey)
3	2	37	14% (red), 97% (green), 9% (grey)
4	9	688	53% (red), 98% (green), 4% (grey)
5	A	294	19% (red), 81% (green), 18% (grey)
6	B	273	19% (red), 79% (green), 21% (grey)
7	C	205	15% (red), 98% (green), 7% (grey)
8	D	219	8% (red), 69% (green), 23% (grey)

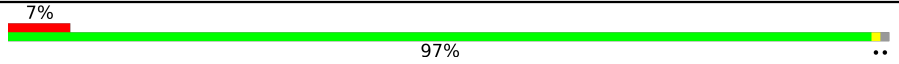
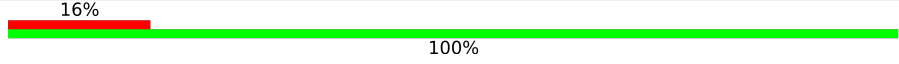
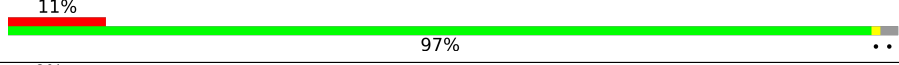
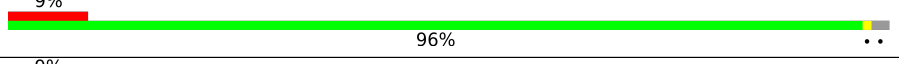
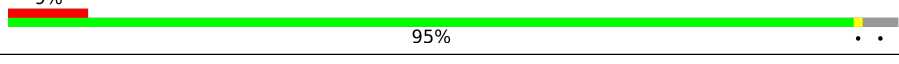
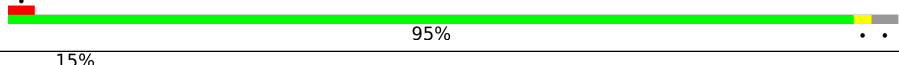
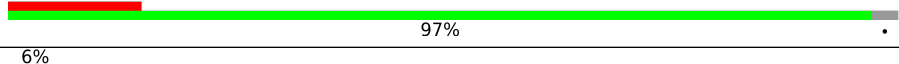
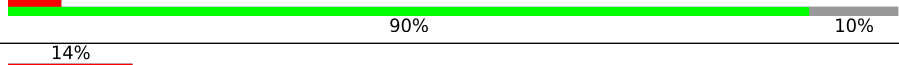
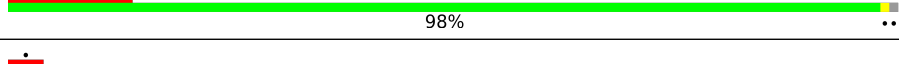


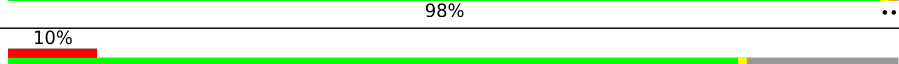

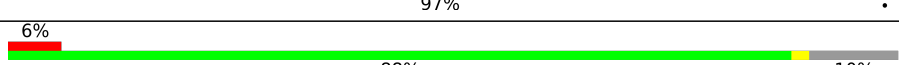
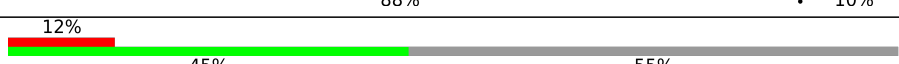
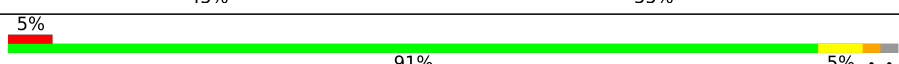
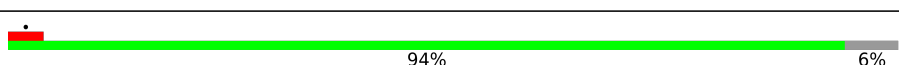
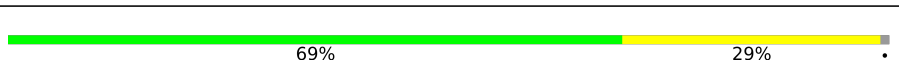
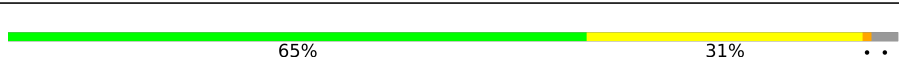




Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	E	215	17% 75% 22%
10	F	155	31% 98% ..
11	G	142	8% 98% ..
12	H	132	22% 97% .
13	I	108	27% 92% 6%
14	J	121	16% 93% 6%
15	K	139	11% 95% ..
16	L	124	27% 94% 5%
17	M	61	13% 98% .
18	N	86	10% 97% .
19	O	94	. 85% 15%
20	P	85	15% 96% ..
21	Q	104	10% 62% 38%
22	R	87	26% 97% .
23	S	87	6% 89% 11%
24	T	60	7% 88% 12%
25	W	122	51% 57% 43%
26	a	287	8% 99% .
27	b	287	8% 79% 20%
28	c	212	11% 99% .
29	d	180	15% 97% ..
30	e	184	22% 95% ..
31	f	149	60% 97% ..
32	g	161	24% 72% 6% 22%
33	h	137	43% 93% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	i	146	 7% 97% ..
35	j	122	 16% 100%
36	k	151	 11% 97% ..
37	l	139	 9% 96% ..
38	m	124	 9% 95% ..
39	n	116	 95% ..
40	o	119	 15% 97% .
41	p	127	 6% 90% 10%
42	q	100	 14% 98% ..
43	r	159	 87% . 13%
44	s	237	 39% 61%
45	t	111	 16% 98% ..
46	u	104	 10% 82% 17%
47	v	65	 18% 97% .
48	w	111	 6% 88% 10%
49	x	97	 12% 45% 55%
50	y	57	 5% 91% 5% ..
51	z	53	 94% 6%
52	3	2907	 69% 29% .
53	4	108	 65% 31% ..
54	5	1520	 72% 25% .
55	7	76	 14% 67% 32% .
55	8	76	 67% 32% .

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	1660	1051	314	290	5	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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		

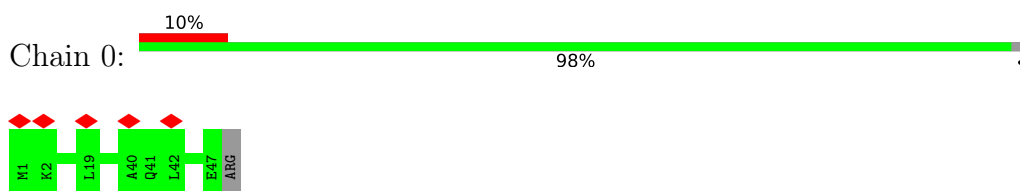
- Molecule 55 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	7	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		

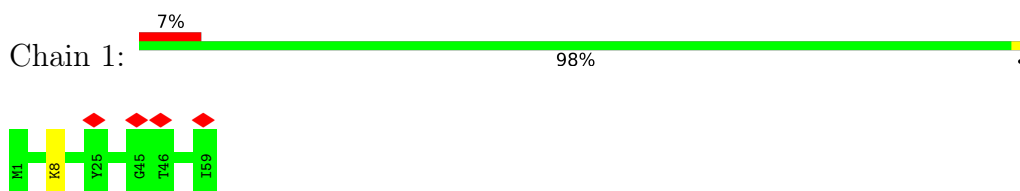
3 Residue-property plots [i](#)

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.

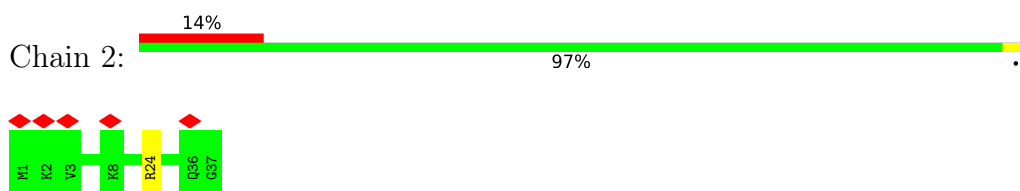
- Molecule 1: 50S ribosomal protein L34



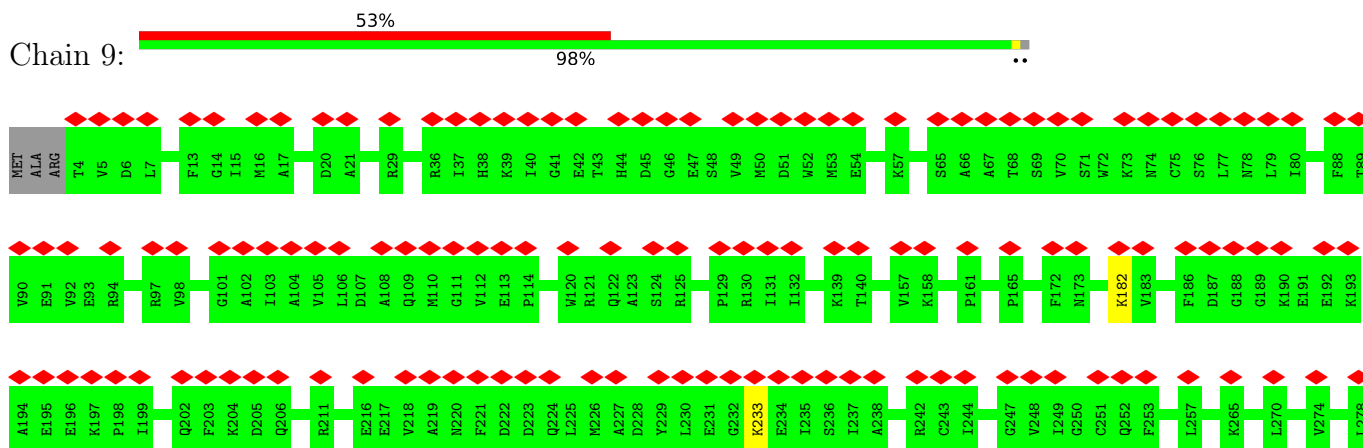
- Molecule 2: 50S ribosomal protein L35

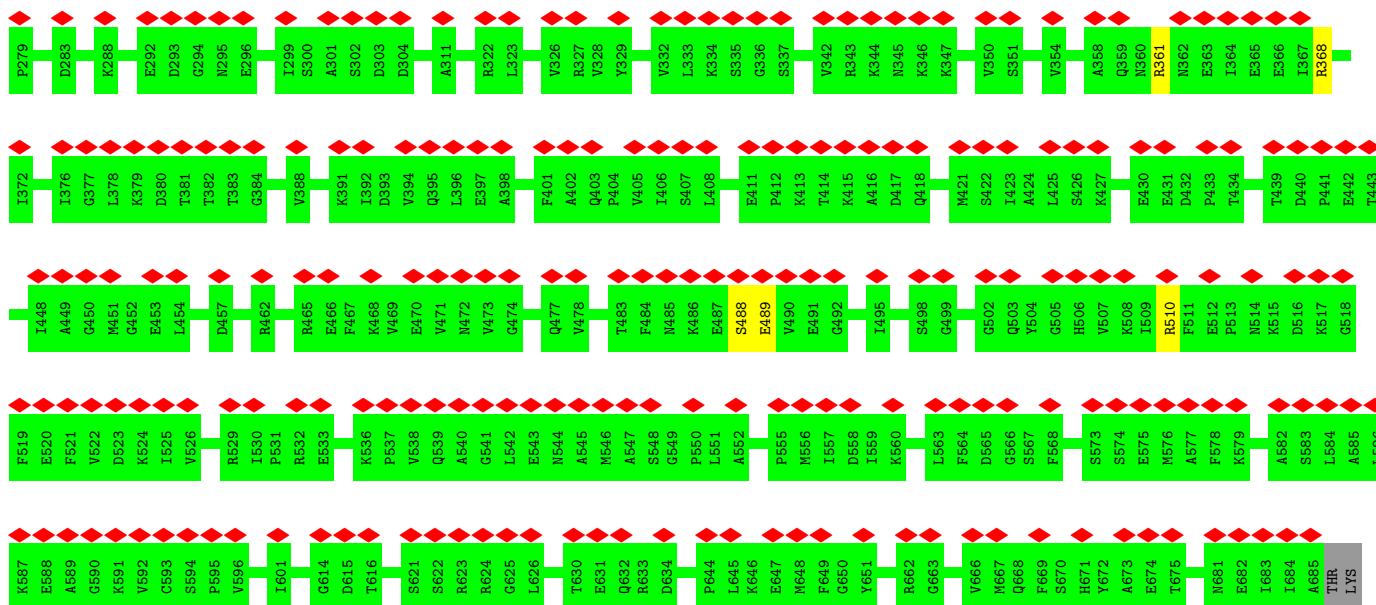


- Molecule 3: 50S ribosomal protein L36



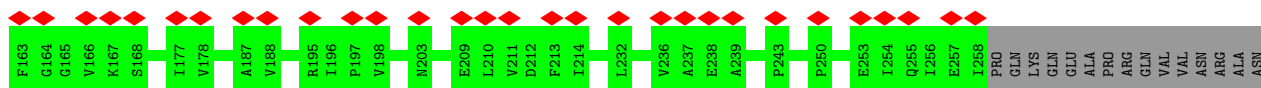
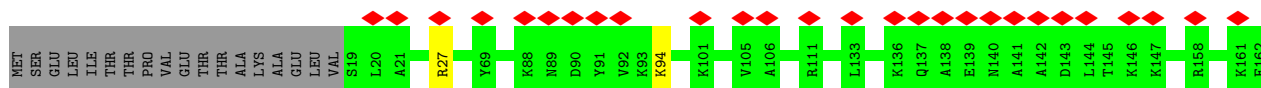
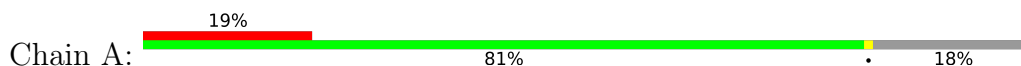
- Molecule 4: Elongation factor G





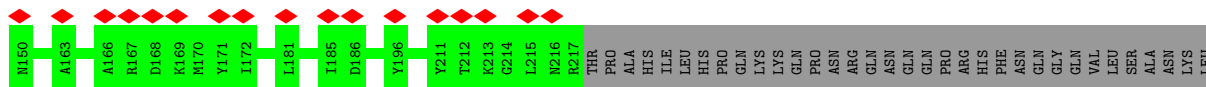
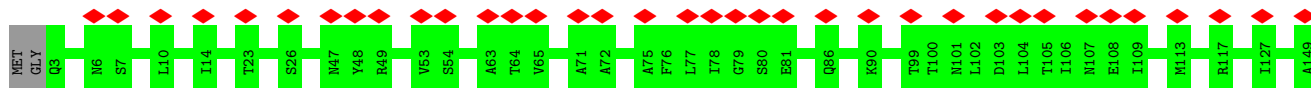
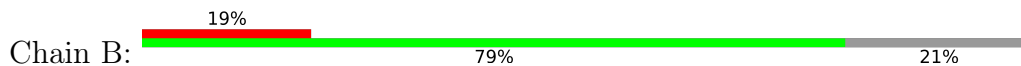
LYS

• Molecule 5: 30S ribosomal protein S2



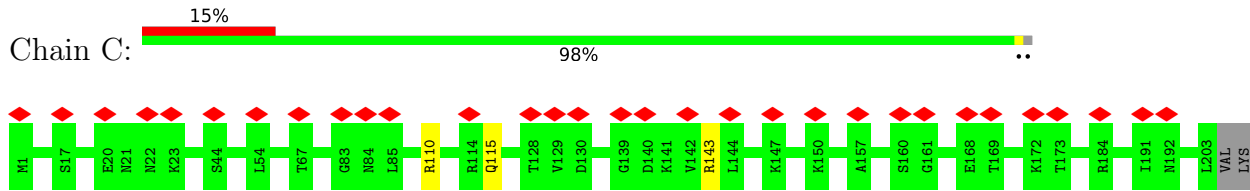
LYS
GLN
ILE
THR
SER
GLM
ARG
LEU
ASN
ILE
THR
ARG
ASN
PRO
VAL
GLU
THR
THR
VAL

• Molecule 6: 30S ribosomal protein S3

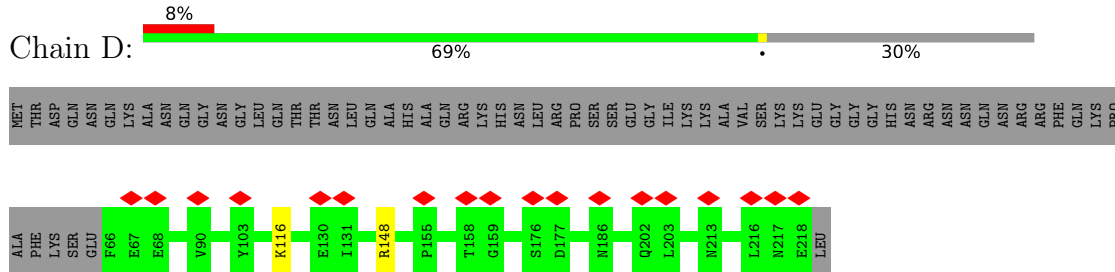


THR
GLY
SER
ASP
VAL
GLU
THR
THR
SER
SER
ILE
GLN
ALA
LEU
THR
LYS
PRO
ASN
LYS
GLU
ASP
LYS
GLN

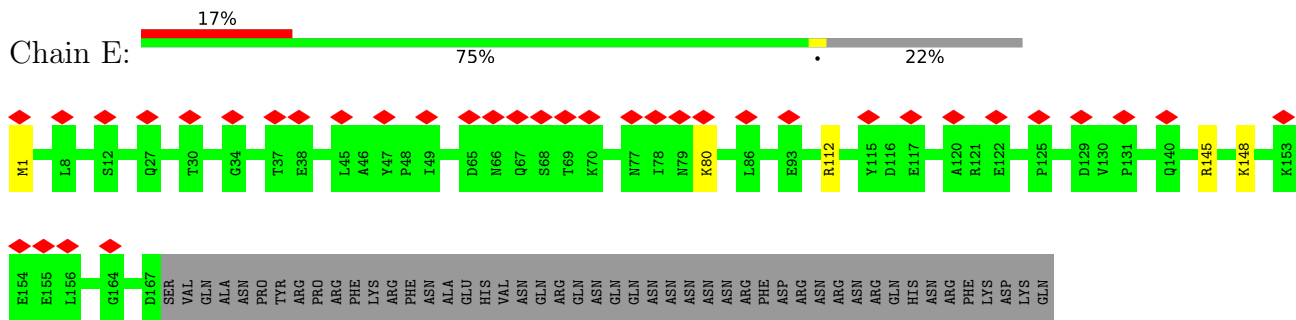
• Molecule 7: 30S ribosomal protein S4



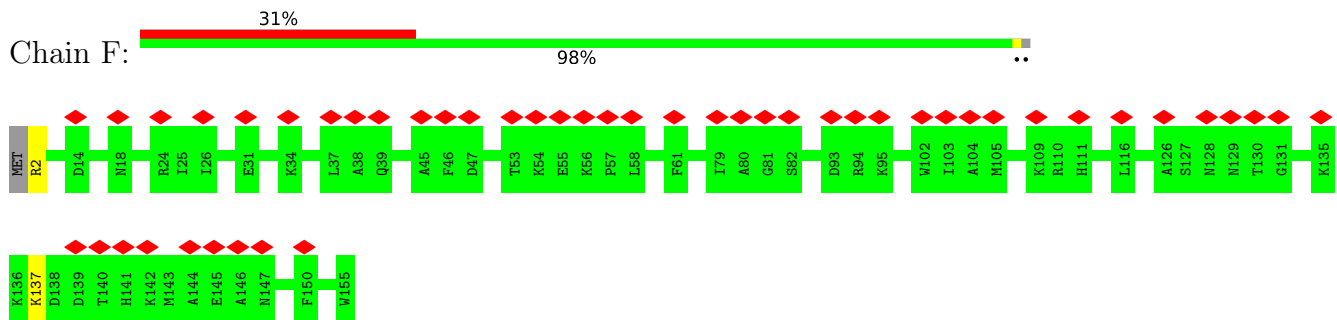
- Molecule 8: 30S ribosomal protein S5



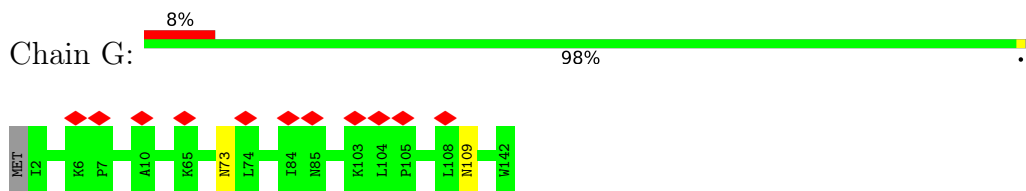
- Molecule 9: 30S ribosomal protein S6



- Molecule 10: 30S ribosomal protein S7

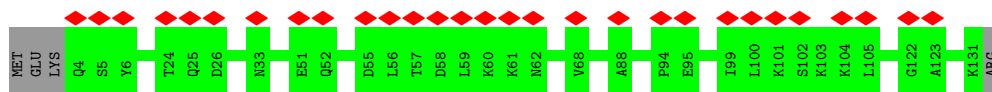


- Molecule 11: 30S ribosomal protein S8

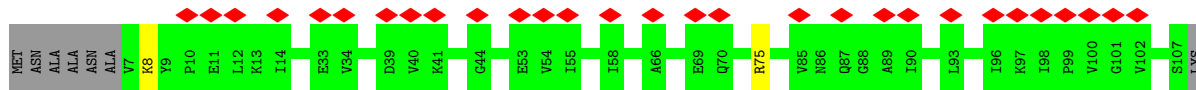
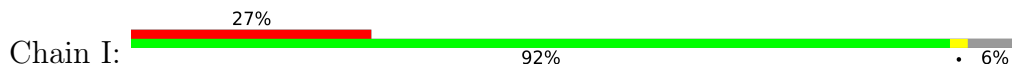


- Molecule 12: 30S ribosomal protein S9

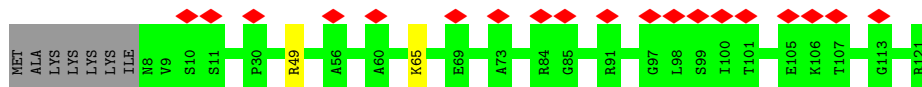
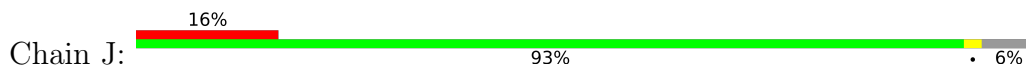




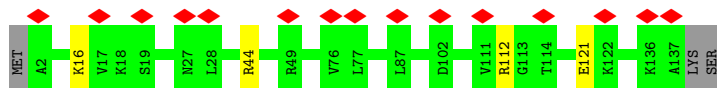
- Molecule 13: 30S ribosomal protein S10



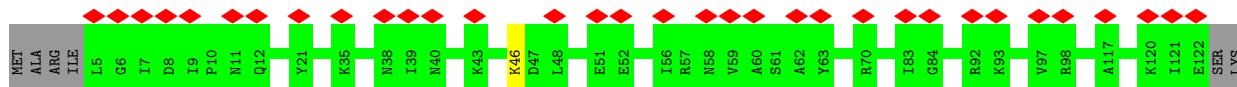
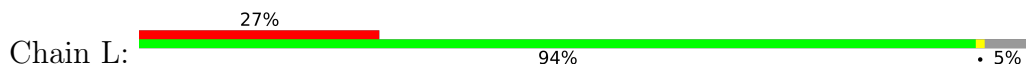
- Molecule 14: 30S ribosomal protein S11



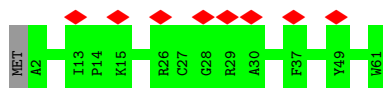
- Molecule 15: 30S ribosomal protein S12



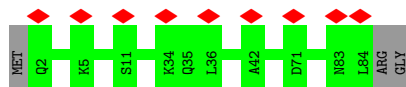
- Molecule 16: 30S ribosomal protein S13



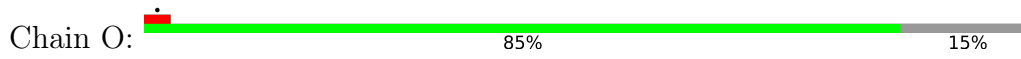
- Molecule 17: 30S ribosomal protein S14 type Z



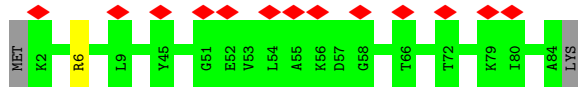
- Molecule 18: 30S ribosomal protein S15



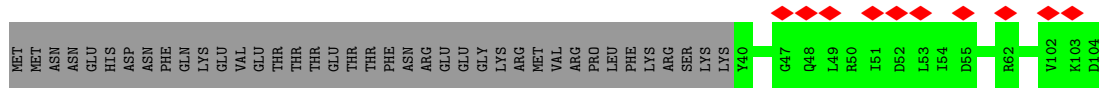
- Molecule 19: 30S ribosomal protein S16



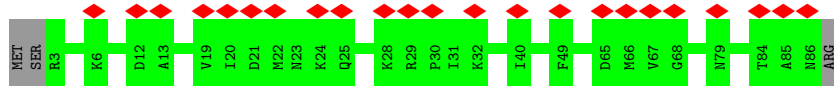
• Molecule 20: 30S ribosomal protein S17



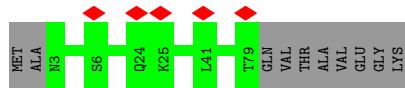
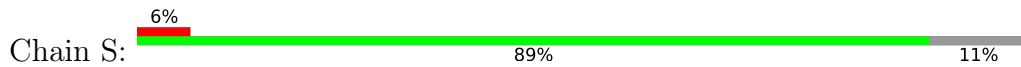
• Molecule 21: 30S ribosomal protein S18



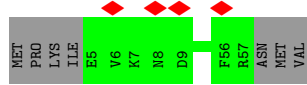
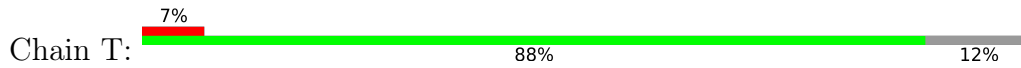
• Molecule 22: 30S ribosomal protein S19



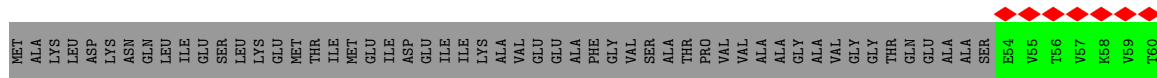
• Molecule 23: 30S ribosomal protein S20



• Molecule 24: 30S ribosomal protein S21

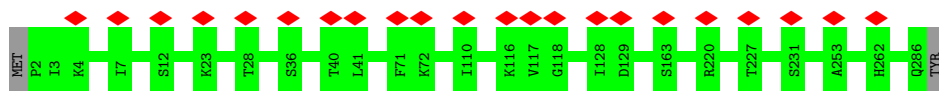


• Molecule 25: 50S ribosomal protein L7/L12

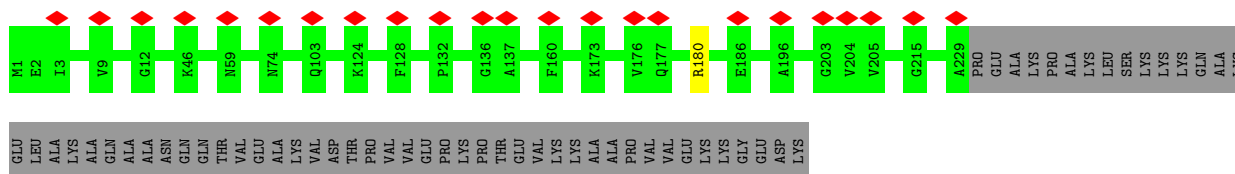
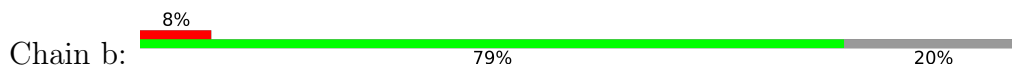




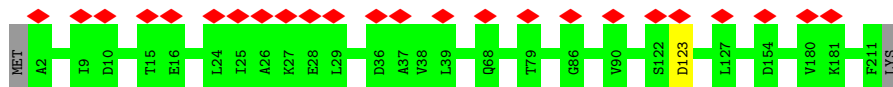
- Molecule 26: 50S ribosomal protein L2



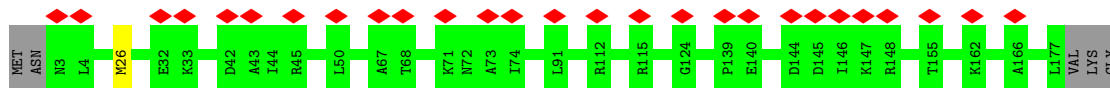
- Molecule 27: 50S ribosomal protein L3



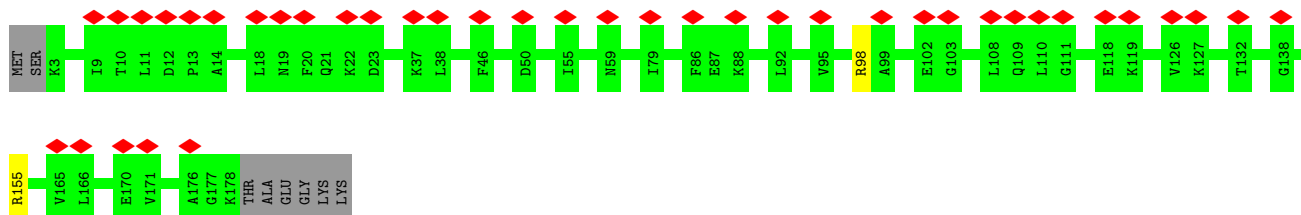
- Molecule 28: 50S ribosomal protein L4



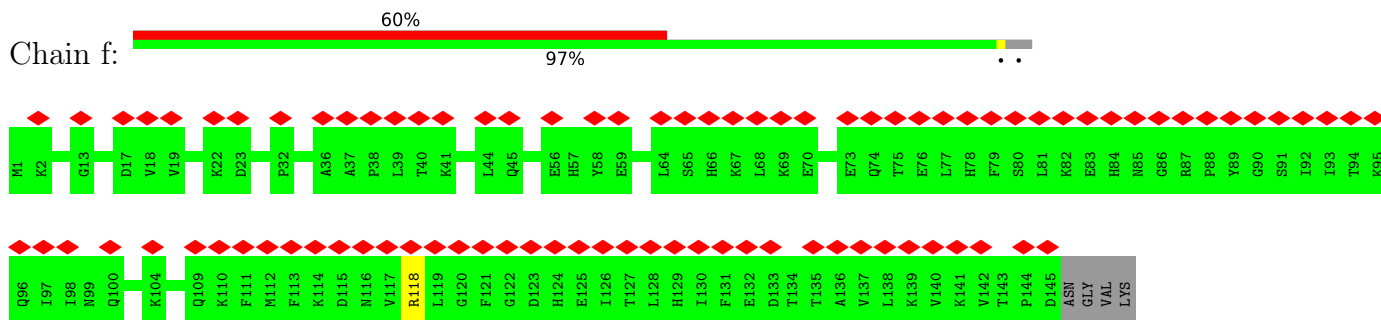
- Molecule 29: 50S ribosomal protein L5



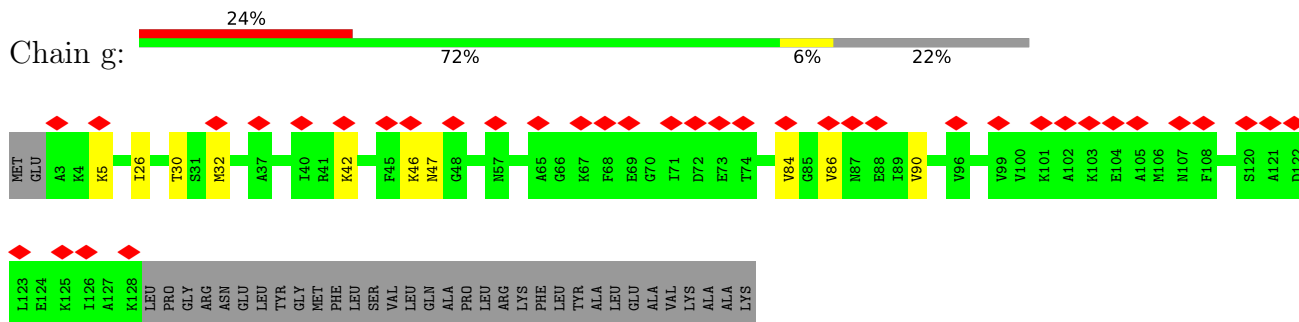
- Molecule 30: 50S ribosomal protein L6



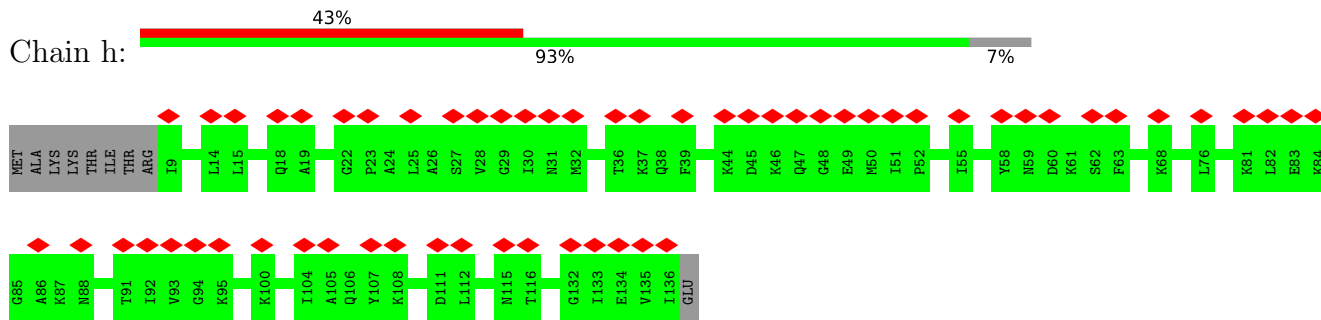
- Molecule 31: 50S ribosomal protein L9



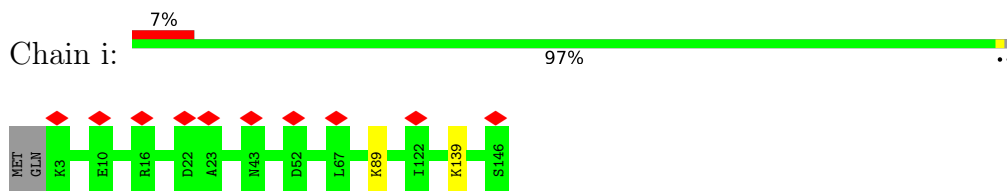
• Molecule 32: 50S ribosomal protein L10



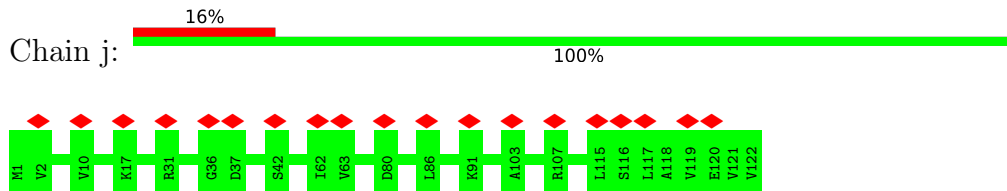
• Molecule 33: 50S ribosomal protein L11



• Molecule 34: 50S ribosomal protein L13

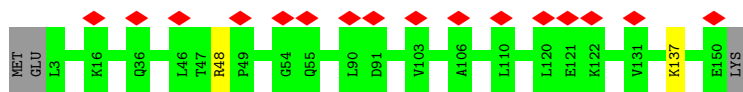


• Molecule 35: 50S ribosomal protein L14

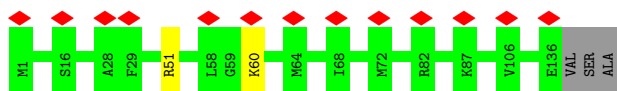


• Molecule 36: 50S ribosomal protein L15

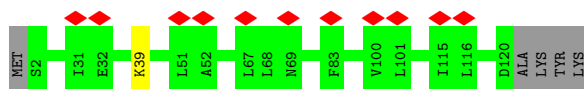




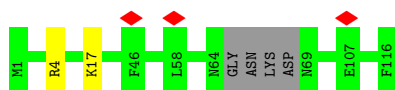
- Molecule 37: 50S ribosomal protein L16



- Molecule 38: 50S ribosomal protein L17



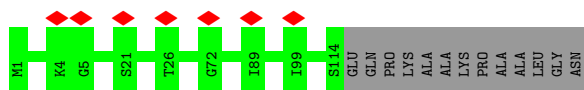
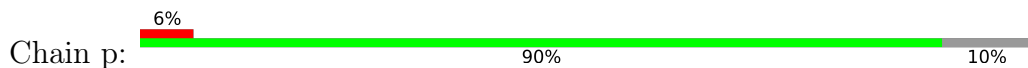
- Molecule 39: 50S ribosomal protein L18



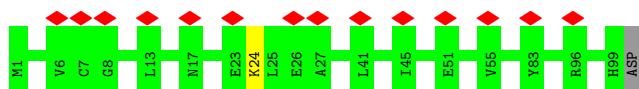
- Molecule 40: 50S ribosomal protein L19



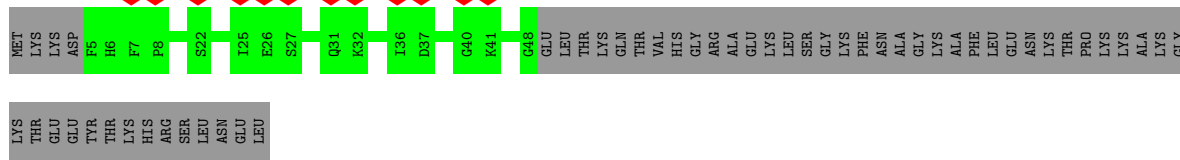
- Molecule 41: 50S ribosomal protein L20



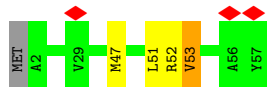
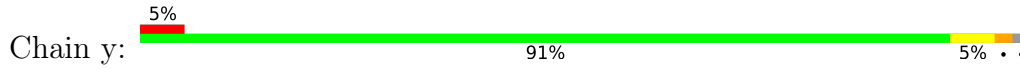
- Molecule 42: 50S ribosomal protein L21



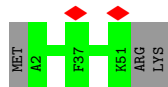
- Molecule 43: 50S ribosomal protein L22



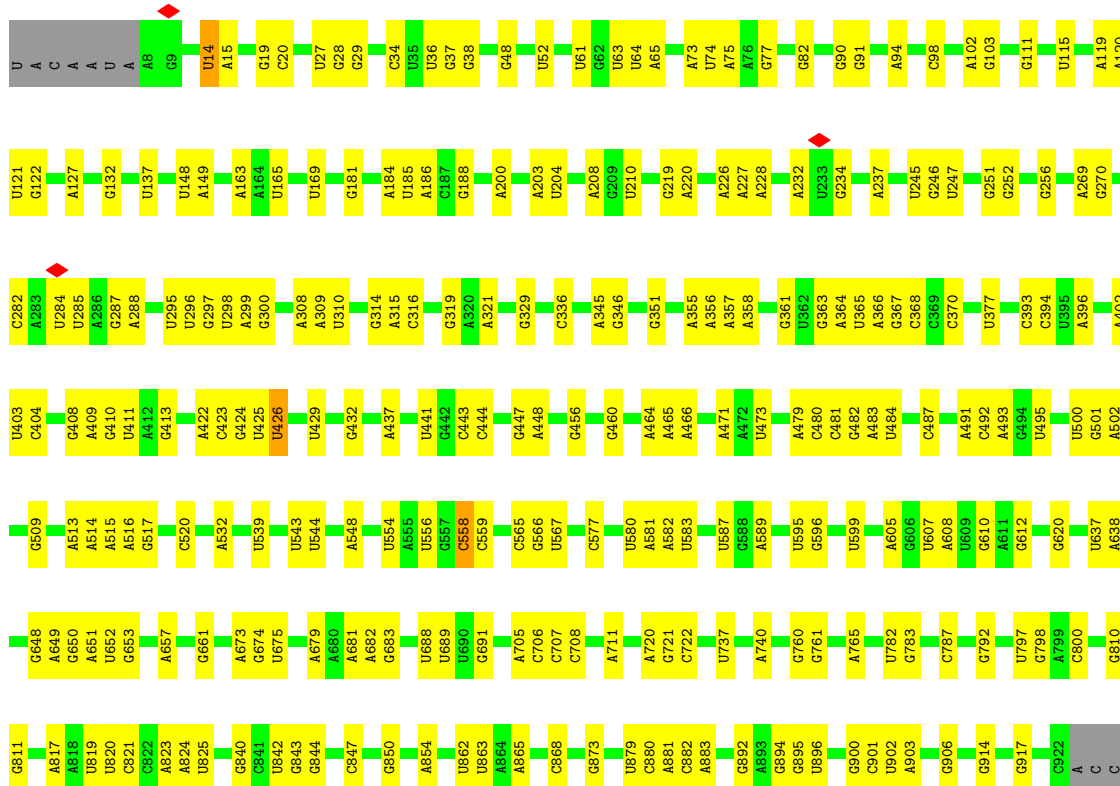
- Molecule 50: 50S ribosomal protein L32



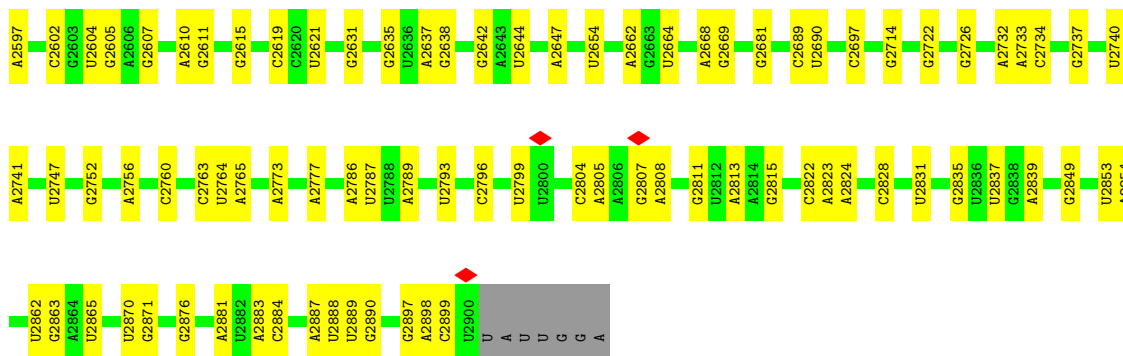
- Molecule 51: 50S ribosomal protein L33 1



- Molecule 52: 23S ribosomal RNA



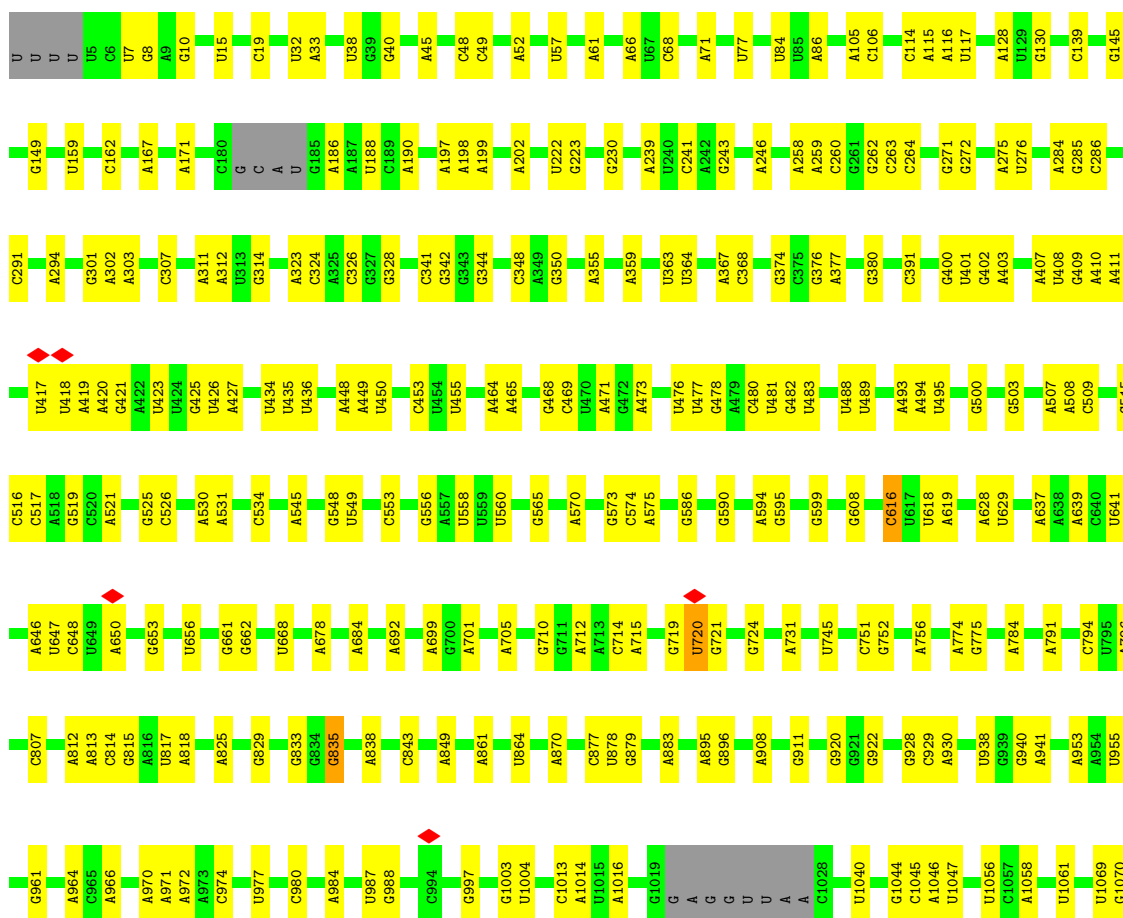
A2484	A2485	A2486	G2492	A2495	G2496	U2497	G2498	U2499	A2505	C2506	C2507	U2508	G2510	A2511	G2512	G2513	U2514	A2517	C2520	A2521	U2524	C2525	A2526	U2527	C2528	A2538	A2539	G2543	G2561	U2571	A2572	G2573	G2574	G2575	G2577	C2581	G2582	U2583	G2584	A2585	G2586	C2594	A2595	A2596			
A2336	G2341	U2342	A2343	G2344	G2345	C2355	U2358	G2359	U2365	U2380	U2387	G2391	U2392	C2393	C2402	C2410	U2414	A2415	U2416	C2424	C2425	C2430	U2431	A2433	A2434	C2435	G2436	G2437	A2438	U2439	A2442	A2443	U2449	C2450	G2454	A2319	G2455	A2456	U2457	A2477	U2481						
G2194	U2195	G2196	U2197	G2198	U2200	U2202	U2205	A2206	U2212	U2219	A2220	U2221	C2222	A2231	G2232	A2233	C2234	A2235	G2242	G2246	G2247	A2275	A2276	A2277	A2281	U2291	A2294	A2295	U2299	C2305	G2312	U2313	G2316	A2317	A2318	U2319	C2320	C2321	G2322	A2330	G2333						
U1974	A1977	U1978	G1979	U1982	U1983	A1984	U1998	G1999	U2000	C2001	U2002	C2003	G2004	G2005	U2009	A2010	C2013	A2020	C2025	U2028	G2029	A2037	A2038	G2039	A2040	C2041	G2050	G2053	C2054	A2055	C2057	G2058	G2059	C2062	G2063	G2064	A2065	A2066	G2067	G2068	C2070	C2071	C2072	U2075			
G2076	A2084	G2087	U2089	G2100	A2101	G2106	A2107	U2110	U2111	A2112	U2113	C2114	G2117	A2123	A2124	U2125	A2126	G2127	A2133	A2136	A2137	U2138	C2139	G2140	C2144	A2145	C2152	U2153	A2154	A2157	A2165	U2166	A2171	U2180	A2184	C2185	C2186	C2187	U2188	U2189	U2192	U2193					
U1874	A1877	U1878	G1879	U1882	U1883	A1884	U1889	U1889	U1889	U1889	A1891	A1892	C1900	C1901	C1902	G1906	A1907	A1908	C1909	G1910	G1913	G1914	A1920	C1921	C1922	U1930	A1934	A1935	G1936	G1937	U1938	A1943	U1946	U1947	C2062	G2063	G2064	A2065	A2066	A2067	G2068	C2070	C2071	C2072	U2075		
A1603	U1612	G1615	U1618	A1619	G1625	A1637	G1642	A1643	A1644	C1645	A1648	C1649	A1650	C1651	A1652	C1653	G1654	U1655	A1656	A1660	G1668	U1679	A1680	G1681	C1682	G1685	U1686	G1687	A1688	U1692	U1693	A1694	G1695	C1696	C1697	A1698	U1699	G1700	G1708	C1709	U1713	U1714	U1715	A1716			
C1720	U1727	A1728	G1733	U1737	G1748	A1751	A1752	C1758	C1761	A1762	G1763	U1764	G1765	A1766	A1767	G1768	A1769	A1770	C1771	A1780	U1784	A1787	A1788	C1789	U1790	A1793	C1807	C1808	U1815	U1820	G1821	A1822	U1823	G1824	U1825	A1826	U1827	A1836	U1962	U1963	C1840	U1841	G1842	G1853			
U1658	A1665	A1673	U1676	A1684	G1685	U1688	U1689	U1689	A1691	C1902	G1906	A1907	A1908	C1909	G1910	G1913	G1914	A1920	C1921	C1922	U1930	A1934	A1935	G1936	G1937	U1938	A1943	U1946	U1947	C2062	G2063	G2064	A2065	A2066	A2067	G2068	C2070	C2071	C2072	U2075							
U1509	A1510	C1518	A1519	A1520	C1523	G1528	A1532	U1533	A1534	A1541	G1542	U1543	U1546	G1547	A1548	U1549	G1550	G1557	A1558	A1559	U	G	A	C	U	G	A	U	C	A	A1570	G1571	U1572	G1579	U1581	G1582	U1583	A1584	A1585	U1586	U1587	A1588	A1589	A1592	U1593	G1594	A1600
C1359	U1360	C1363	U1369	A1370	U1371	C1372	U1373	U1380	A1393	A1406	U1407	A1412	A1413	A1420	U1424	U1425	C1426	A1435	C1436	C1444	U1445	G1446	A1447	U1448	A1455	C1456	A1457	G1463	U1466	A1479	A1480	U1481	U1482	A1483	G1484	A1485	U1486	U1487	A1495	A1502	G1507	G1508					
C1252	G1253	U1254	G1255	A1256	G1257	U1260	G1266	U1268	G1276	U1279	G1280	A1281	G1282	A1283	G1286	C1287	A1292	U1297	A1298	C1302	A1308	A1314	A1315	C1316	C1317	A1322	A1323	C1326	G1327	A1328	U1329	C1333	U1340	U1341	U1341	C1342	C1349	A1350	G1351	G1352	G1353	U1354	G1355	G1356			
U1140	G1145	A1146	G1147	U1151	G1157	C1158	A1163	A1164	U1165	U1167	A1168	A1169	C1170	G1171	A1177	A1178	G1179	A1186	A1191	U1196	G1203	A1208	G1209	A1210	G1215	U1216	G1217	G1218	G1221	G1226	U1229	U1234	U1235	G1236	G1237	G1238	A1238	G1239	U1240	U1241	G1242	A1250	G1251				
A1026	U1027	U1031	A1032	A1033	A1034	U1035	C1041	A1046	A1047	A1048	U1049	A1055	A1056	G1057	A1061	A1062	U1068	G1075	A1080	A1081	A1082	C984	G989	G990	G991	A995	A996	G997	C1001	A1100	A1101	G1103	A1104	A1105	G1106	C1107	A1108	C1111	U1112	U1113	G1114	G1115	G1122	A1123	G1124	U1125	C1132
U	A	G928	U932	A933	G936	U944	A947	A948	C949	U952	G953	U968	U971	U973	A977	G978	A981	G982	A983	C984	G989	G990	G991	A995	A996	G997	C1001	A1005	A1008	A1009	G1010	G1014	G1015	A1016	A1017	G1018	A1019	G1020	C1021	C1022	C1023	G1025					



• Molecule 53: 5S ribosomal RNA

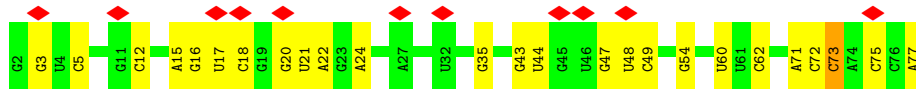


• Molecule 54: 16S ribosomal RNA





• 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	1479	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	1.530	Depositor
Minimum map value	-0.551	Depositor
Average map value	0.027	Depositor
Map value standard deviation	0.125	Depositor
Recommended contour level	0.45	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	0.24	0/383	0.42	0/504
2	1	0.25	0/484	0.47	0/637
3	2	0.22	0/306	0.46	0/401
4	9	0.25	0/5419	0.47	0/7307
5	A	0.25	0/1954	0.43	0/2642
6	B	0.24	0/1721	0.45	0/2323
7	C	0.24	0/1691	0.44	0/2267
8	D	0.23	0/1188	0.45	0/1593
9	E	0.25	0/1384	0.45	0/1867
10	F	0.23	0/1266	0.43	0/1700
11	G	0.24	0/1126	0.48	0/1517
12	H	0.25	0/1044	0.47	0/1395
13	I	0.23	0/820	0.47	0/1103
14	J	0.25	0/844	0.44	0/1136
15	K	0.28	0/1094	0.51	0/1468
16	L	0.24	0/962	0.44	0/1289
17	M	0.24	0/483	0.42	0/643
18	N	0.23	0/679	0.44	0/907
19	O	0.23	0/659	0.44	0/885
20	P	0.25	0/684	0.46	0/913
21	Q	0.24	0/545	0.44	0/730
22	R	0.25	0/698	0.48	0/936
23	S	0.23	0/631	0.40	0/838
24	T	0.22	0/475	0.42	0/621
25	W	0.23	0/538	0.43	0/722
26	a	0.24	0/2267	0.46	0/3044
27	b	0.25	0/1795	0.45	0/2412
28	c	0.24	0/1671	0.47	1/2246 (0.0%)
29	d	0.24	0/1409	0.45	0/1894
30	e	0.25	0/1420	0.47	0/1912
31	f	0.25	0/1183	0.45	0/1587
32	g	0.35	0/969	0.55	0/1295
33	h	0.25	0/968	0.46	0/1298
34	i	0.24	0/1186	0.44	0/1592

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.24	0/953	0.47	0/1275
36	k	0.24	0/1170	0.47	0/1559
37	l	0.25	0/1104	0.46	0/1481
38	m	0.23	0/973	0.41	0/1309
39	n	0.23	0/897	0.43	0/1198
40	o	0.25	0/948	0.46	0/1262
41	p	0.24	0/961	0.38	0/1278
42	q	0.26	0/828	0.49	0/1111
43	r	0.24	0/1077	0.44	0/1441
44	s	0.25	0/732	0.51	0/988
45	t	0.25	0/879	0.55	0/1165
46	u	0.25	0/665	0.49	0/884
47	v	0.23	0/519	0.50	0/695
48	w	0.24	0/826	0.51	1/1104 (0.1%)
49	x	0.25	0/353	0.43	0/474
50	y	0.34	0/457	0.58	0/601
51	z	0.24	0/412	0.44	0/547
52	3	0.21	0/69073	0.84	82/107710 (0.1%)
53	4	0.21	0/2505	0.83	6/3902 (0.2%)
54	5	0.20	0/35768	0.79	21/55764 (0.0%)
55	7	0.21	0/1808	0.85	1/2817 (0.0%)
55	8	0.21	0/1808	0.85	1/2817 (0.0%)
All	All	0.22	0/164662	0.74	113/245006 (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
4	9	0	2
11	G	0	1
45	t	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
52	3	1033	A	O5'-P-OP2	-30.62	73.95	110.70
52	3	1033	A	OP1-P-OP2	-26.78	79.43	119.60
52	3	1033	A	O5'-P-OP1	17.55	131.76	110.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	3	1032	A	OP1-P-O3'	-13.65	75.18	105.20
52	3	1032	A	OP2-P-O3'	13.64	135.22	105.20

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	9	488	SER	Peptide
4	9	489	GLU	Peptide
11	G	109	ASN	Peptide
45	t	80	LYS	Peptide
45	t	81	ALA	Peptide

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 [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%)	42 (93%)	3 (7%)	0	100	100
2	1	57/59 (97%)	48 (84%)	9 (16%)	0	100	100
3	2	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
4	9	680/688 (99%)	630 (93%)	50 (7%)	0	100	100
5	A	238/294 (81%)	218 (92%)	20 (8%)	0	100	100
6	B	213/273 (78%)	193 (91%)	20 (9%)	0	100	100
7	C	201/205 (98%)	190 (94%)	11 (6%)	0	100	100
8	D	151/219 (69%)	145 (96%)	6 (4%)	0	100	100
9	E	165/215 (77%)	147 (89%)	18 (11%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	F	152/155 (98%)	147 (97%)	5 (3%)	0	100	100
11	G	139/142 (98%)	124 (89%)	15 (11%)	0	100	100
12	H	126/132 (96%)	111 (88%)	15 (12%)	0	100	100
13	I	99/108 (92%)	92 (93%)	7 (7%)	0	100	100
14	J	112/121 (93%)	107 (96%)	5 (4%)	0	100	100
15	K	134/139 (96%)	113 (84%)	21 (16%)	0	100	100
16	L	116/124 (94%)	106 (91%)	10 (9%)	0	100	100
17	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	74 (95%)	4 (5%)	0	100	100
20	P	81/85 (95%)	78 (96%)	3 (4%)	0	100	100
21	Q	63/104 (61%)	57 (90%)	6 (10%)	0	100	100
22	R	82/87 (94%)	71 (87%)	11 (13%)	0	100	100
23	S	75/87 (86%)	74 (99%)	1 (1%)	0	100	100
24	T	51/60 (85%)	50 (98%)	1 (2%)	0	100	100
25	W	67/122 (55%)	65 (97%)	2 (3%)	0	100	100
26	a	283/287 (99%)	245 (87%)	38 (13%)	0	100	100
27	b	227/287 (79%)	211 (93%)	16 (7%)	0	100	100
28	c	208/212 (98%)	199 (96%)	9 (4%)	0	100	100
29	d	173/180 (96%)	159 (92%)	14 (8%)	0	100	100
30	e	174/184 (95%)	163 (94%)	11 (6%)	0	100	100
31	f	143/149 (96%)	134 (94%)	9 (6%)	0	100	100
32	g	124/161 (77%)	115 (93%)	9 (7%)	0	100	100
33	h	126/137 (92%)	116 (92%)	10 (8%)	0	100	100
34	i	142/146 (97%)	135 (95%)	7 (5%)	0	100	100
35	j	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
36	k	146/151 (97%)	135 (92%)	11 (8%)	0	100	100
37	l	134/139 (96%)	129 (96%)	5 (4%)	0	100	100
38	m	117/124 (94%)	112 (96%)	5 (4%)	0	100	100
39	n	108/116 (93%)	99 (92%)	9 (8%)	0	100	100
40	o	113/119 (95%)	107 (95%)	6 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	p	112/127 (88%)	110 (98%)	2 (2%)	0	100	100
42	q	97/100 (97%)	83 (86%)	14 (14%)	0	100	100
43	r	137/159 (86%)	125 (91%)	12 (9%)	0	100	100
44	s	90/237 (38%)	79 (88%)	11 (12%)	0	100	100
45	t	109/111 (98%)	95 (87%)	13 (12%)	1 (1%)	14	52
46	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
47	v	61/65 (94%)	55 (90%)	6 (10%)	0	100	100
48	w	96/111 (86%)	87 (91%)	8 (8%)	1 (1%)	13	49
49	x	42/97 (43%)	40 (95%)	2 (5%)	0	100	100
50	y	54/57 (95%)	48 (89%)	5 (9%)	1 (2%)	6	32
51	z	48/53 (91%)	45 (94%)	3 (6%)	0	100	100
All	All	6567/7480 (88%)	6073 (92%)	491 (8%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
45	t	81	ALA
50	y	53	VAL
48	w	39	ASP

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%)	50	68
3	2	35/35 (100%)	34 (97%)	1 (3%)	37	56
4	9	579/584 (99%)	574 (99%)	5 (1%)	75	83
5	A	212/262 (81%)	210 (99%)	2 (1%)	75	83
6	B	180/232 (78%)	180 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	C	181/183 (99%)	178 (98%)	3 (2%)	56	72
8	D	123/178 (69%)	121 (98%)	2 (2%)	58	73
9	E	150/196 (76%)	145 (97%)	5 (3%)	33	52
10	F	131/132 (99%)	129 (98%)	2 (2%)	60	75
11	G	123/124 (99%)	122 (99%)	1 (1%)	79	85
12	H	111/115 (96%)	111 (100%)	0	100	100
13	I	95/99 (96%)	93 (98%)	2 (2%)	48	66
14	J	91/97 (94%)	89 (98%)	2 (2%)	47	65
15	K	117/120 (98%)	113 (97%)	4 (3%)	32	51
16	L	100/105 (95%)	99 (99%)	1 (1%)	73	82
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	72 (99%)	1 (1%)	62	75
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	70 (100%)	0	100	100
24	T	49/56 (88%)	49 (100%)	0	100	100
25	W	58/98 (59%)	58 (100%)	0	100	100
26	a	241/243 (99%)	241 (100%)	0	100	100
27	b	186/233 (80%)	185 (100%)	1 (0%)	86	89
28	c	182/184 (99%)	182 (100%)	0	100	100
29	d	150/154 (97%)	149 (99%)	1 (1%)	81	87
30	e	153/159 (96%)	151 (99%)	2 (1%)	65	77
31	f	123/134 (92%)	122 (99%)	1 (1%)	79	85
32	g	101/129 (78%)	91 (90%)	10 (10%)	6	21
33	h	102/110 (93%)	102 (100%)	0	100	100
34	i	126/128 (98%)	124 (98%)	2 (2%)	58	73
35	j	103/103 (100%)	103 (100%)	0	100	100
36	k	123/126 (98%)	121 (98%)	2 (2%)	58	73
37	l	113/115 (98%)	111 (98%)	2 (2%)	54	71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	m	105/109 (96%)	104 (99%)	1 (1%)	73	82
39	n	96/99 (97%)	94 (98%)	2 (2%)	48	66
40	o	101/105 (96%)	101 (100%)	0	100	100
41	p	100/108 (93%)	100 (100%)	0	100	100
42	q	90/91 (99%)	89 (99%)	1 (1%)	70	80
43	r	116/132 (88%)	115 (99%)	1 (1%)	75	83
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%)	62	75
47	v	58/60 (97%)	58 (100%)	0	100	100
48	w	87/98 (89%)	87 (100%)	0	100	100
49	x	41/86 (48%)	41 (100%)	0	100	100
50	y	48/49 (98%)	44 (92%)	4 (8%)	9	27
51	z	47/50 (94%)	47 (100%)	0	100	100
All	All	5730/6433 (89%)	5667 (99%)	63 (1%)	69	80

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
15	K	112	ARG
39	n	17	LYS
30	e	155	ARG
39	n	4	ARG
50	y	47	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
31	f	57	HIS
35	j	9	ASN
43	r	15	GLN
32	g	47	ASN
35	j	18	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	3	2875/2907 (98%)	826 (28%)	28 (0%)
53	4	103/108 (95%)	31 (30%)	2 (1%)
54	5	1490/1520 (98%)	387 (25%)	1 (0%)
55	7	75/76 (98%)	25 (33%)	1 (1%)
55	8	75/76 (98%)	25 (33%)	1 (1%)
All	All	4618/4687 (98%)	1294 (28%)	33 (0%)

5 of 1294 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
52	3	14	U
52	3	15	A
52	3	27	U
52	3	28	G
52	3	29	G

5 of 33 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	4	54	U
53	4	59	A
55	8	16	G
52	3	1209	U
52	3	1104	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

There are no chain breaks in this entry.

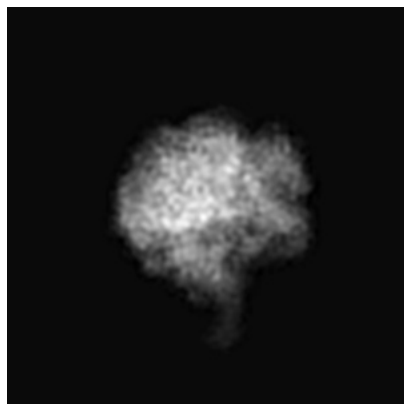
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13280. These allow visual inspection of the internal detail of the map and identification of artifacts.

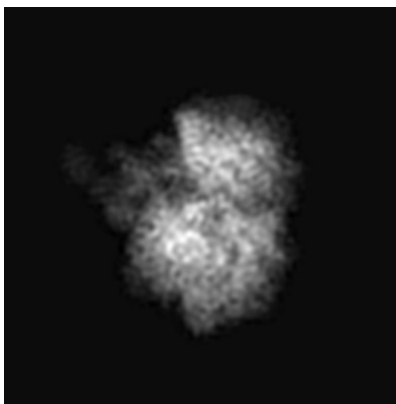
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

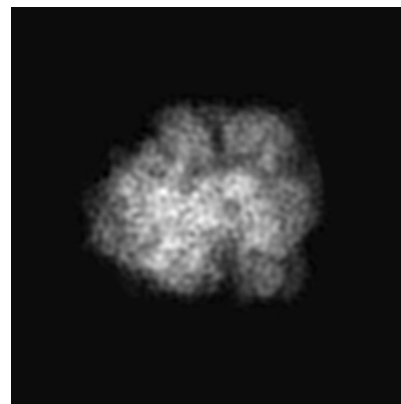
6.1.1 Primary map



X

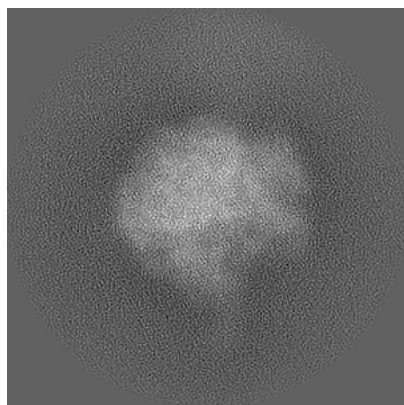


Y

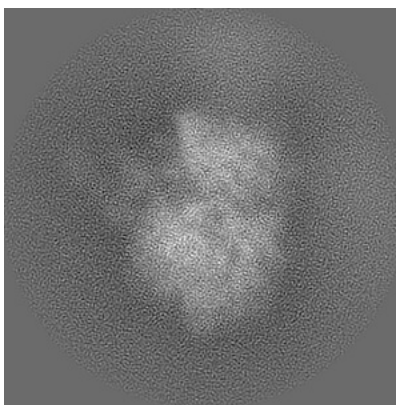


Z

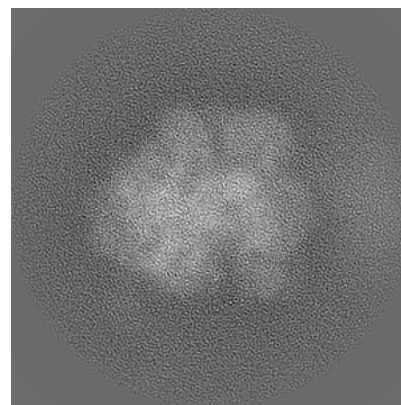
6.1.2 Raw map



X



Y

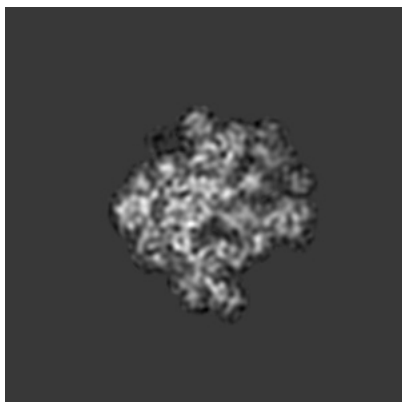


Z

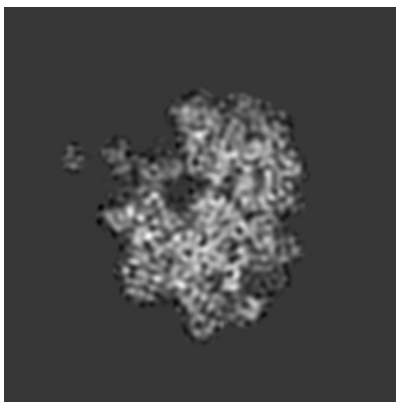
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

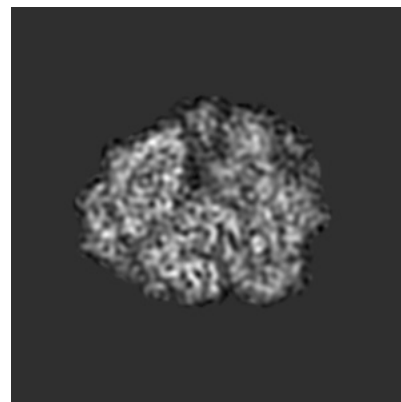
6.2.1 Primary map



X Index: 128

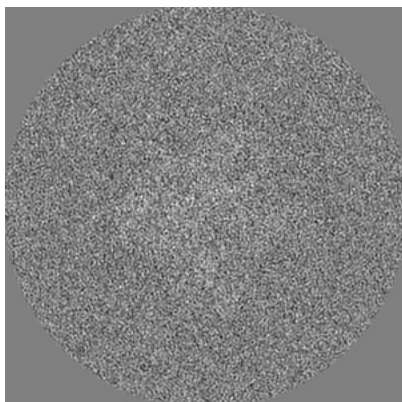


Y Index: 128

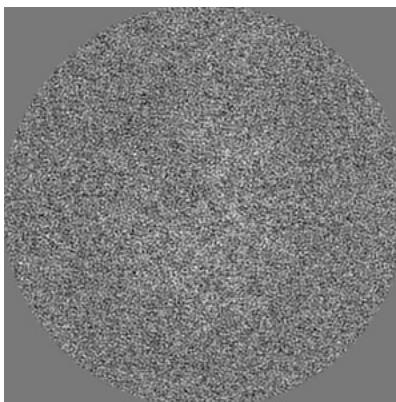


Z Index: 128

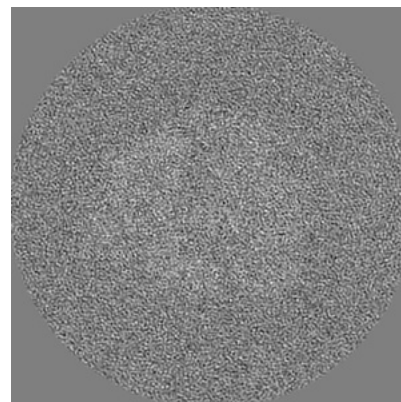
6.2.2 Raw map



X Index: 128



Y Index: 128

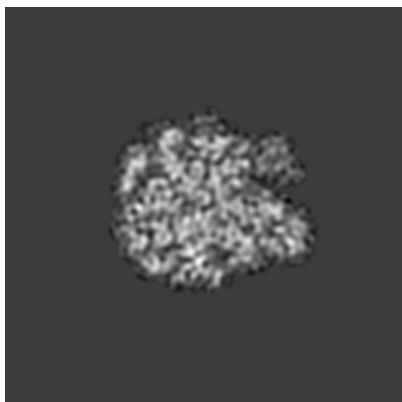


Z Index: 128

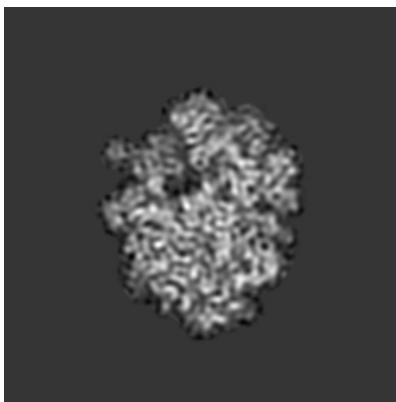
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 104

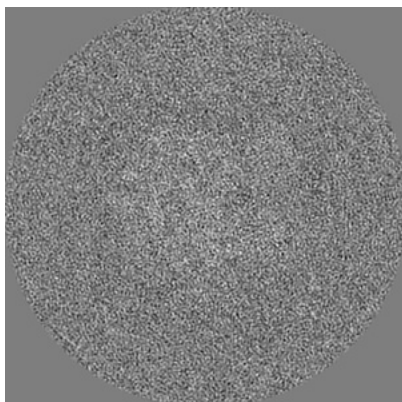


Y Index: 119

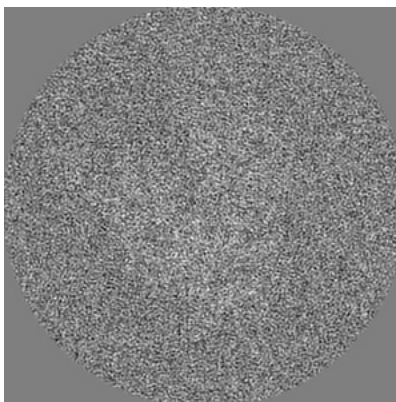


Z Index: 121

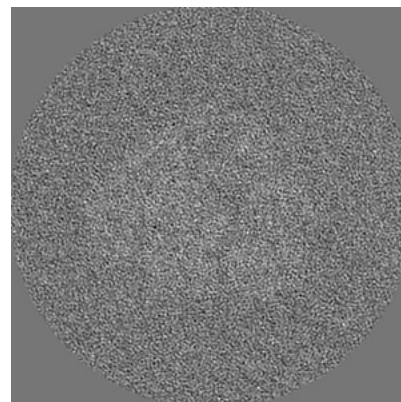
6.3.2 Raw map



X Index: 118



Y Index: 136



Z Index: 125

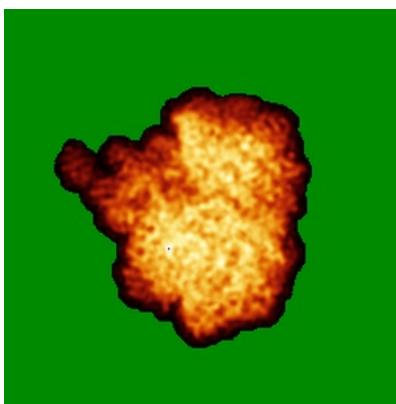
The images above show the largest variance slices of the map in three orthogonal directions.

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

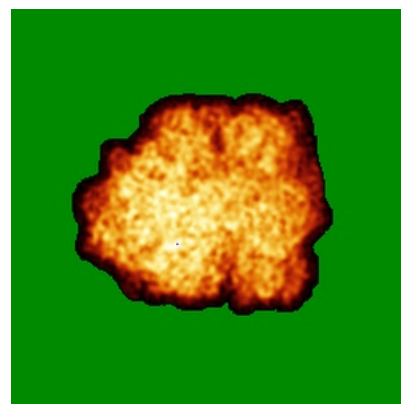
6.4.1 Primary map



X

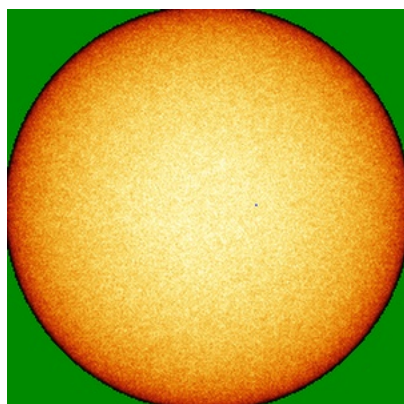


Y

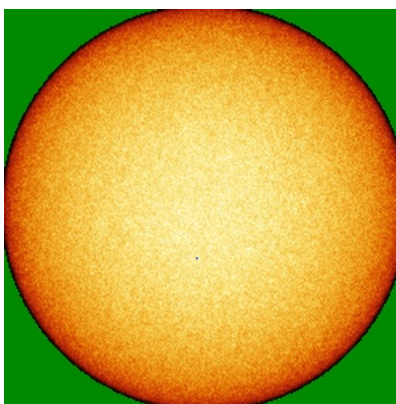


Z

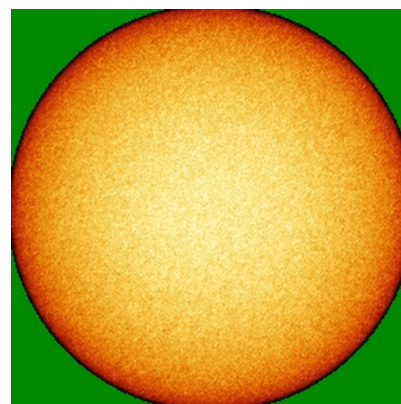
6.4.2 Raw map



X



Y

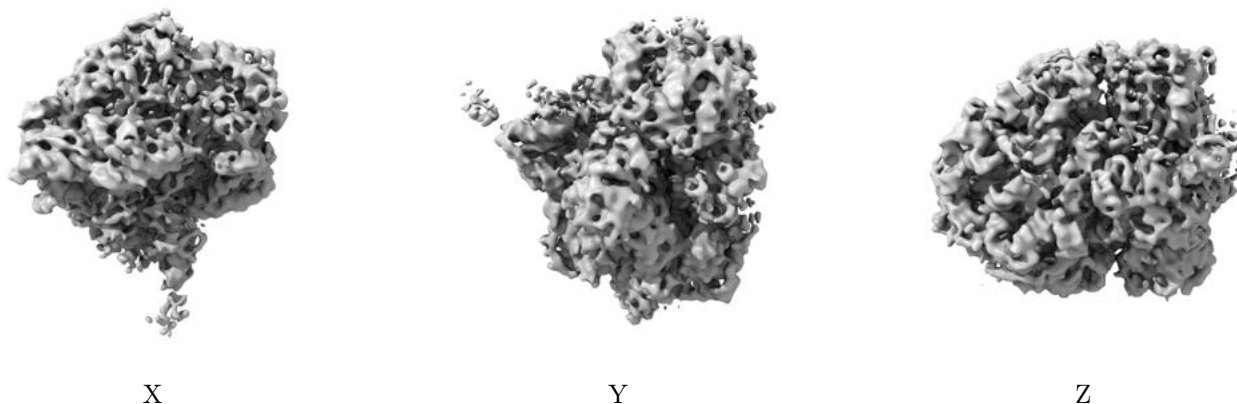


Z

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

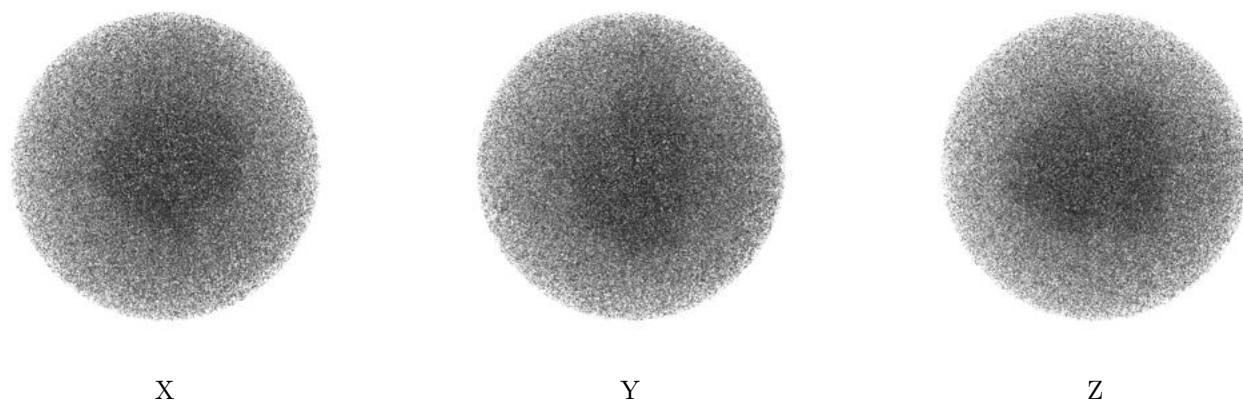
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.45. 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.

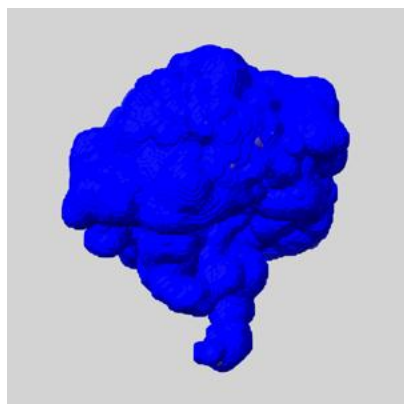
6.6 Mask visualisation [i](#)

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

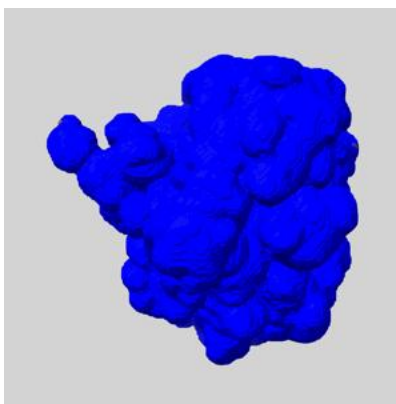
A mask typically either:

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

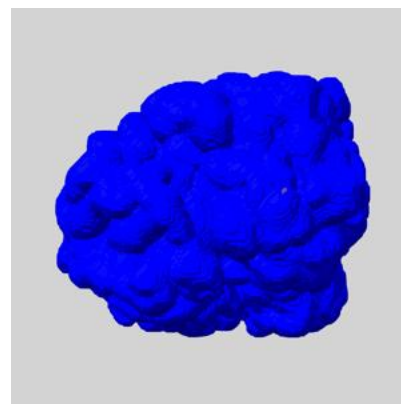
6.6.1 emd_13280_msk_1.map [i](#)



X



Y

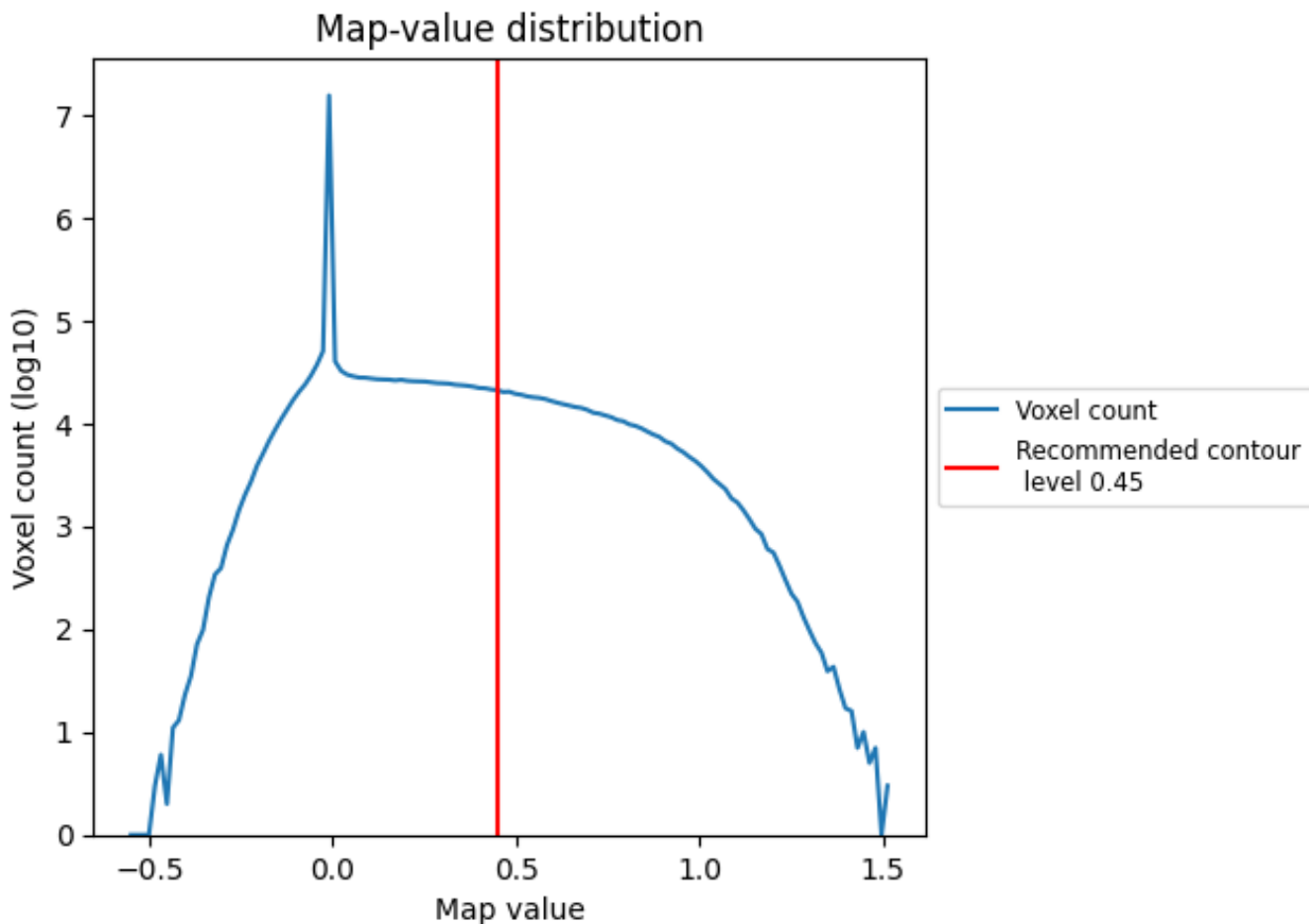


Z

7 Map analysis [i](#)

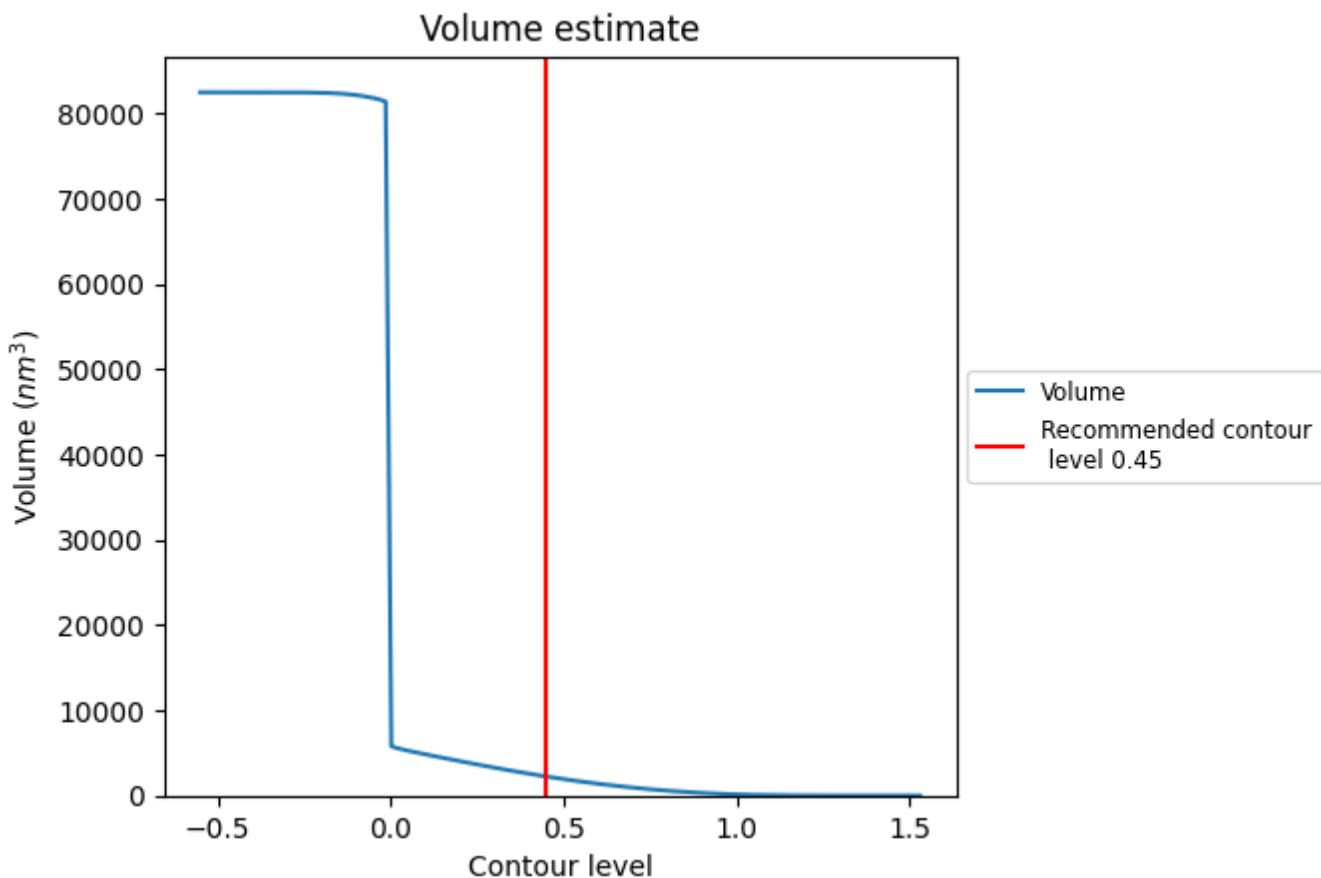
This section contains the results of statistical analysis of the map.

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.

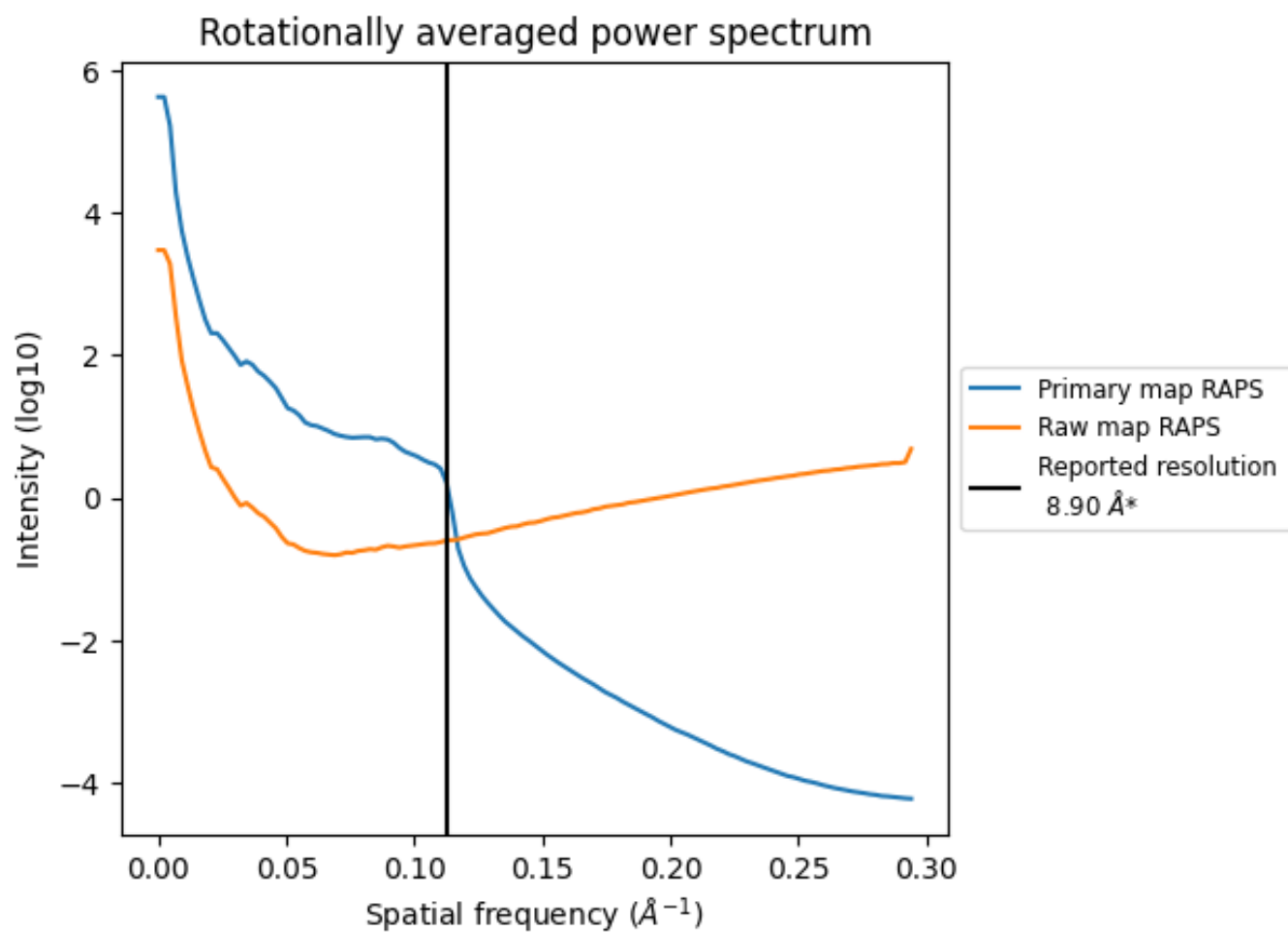
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2232 nm³; this corresponds to an approximate mass of 2016 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](#)

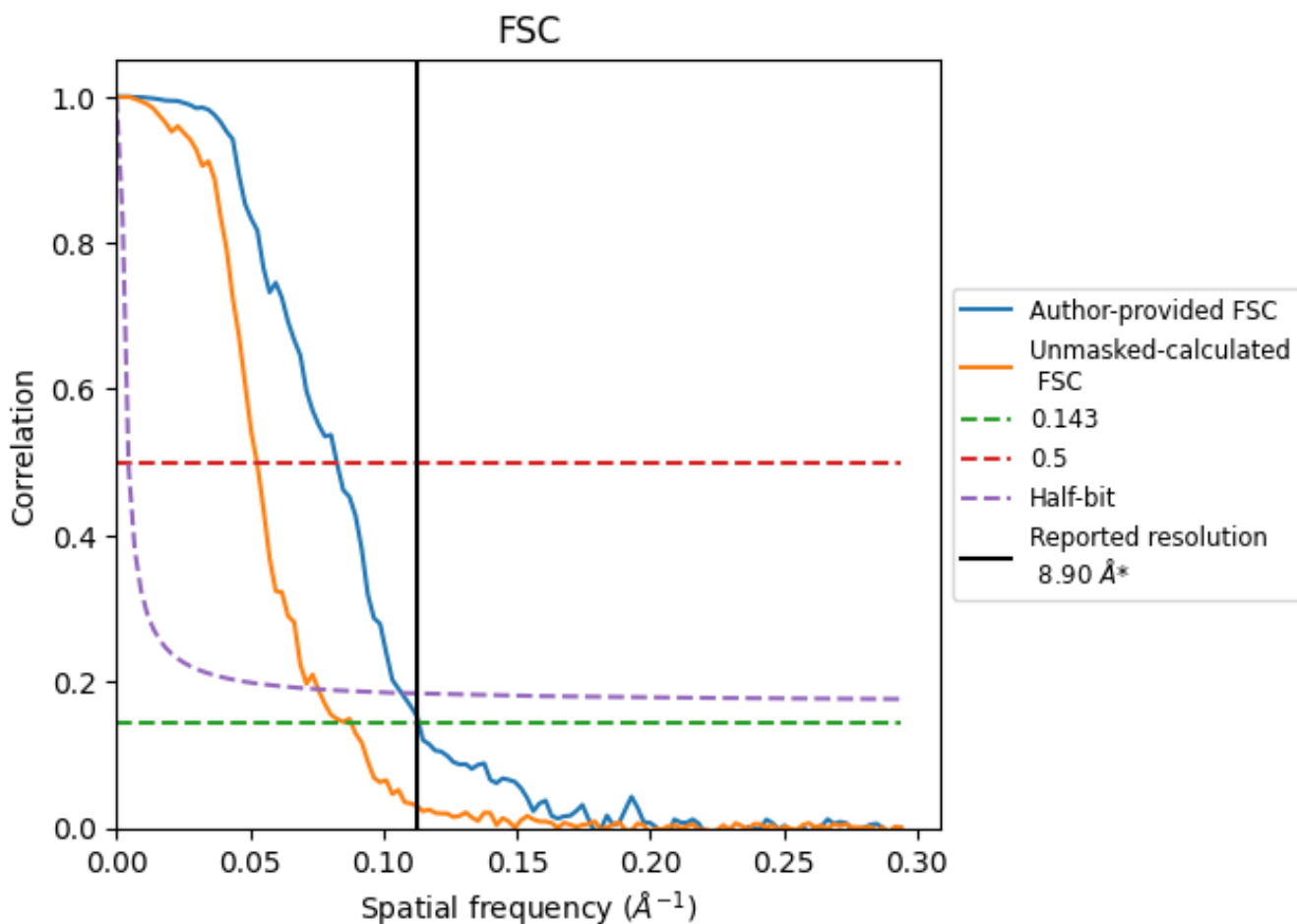


*Reported resolution corresponds to spatial frequency of 0.112 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.112 Å⁻¹

8.2 Resolution estimates [i](#)

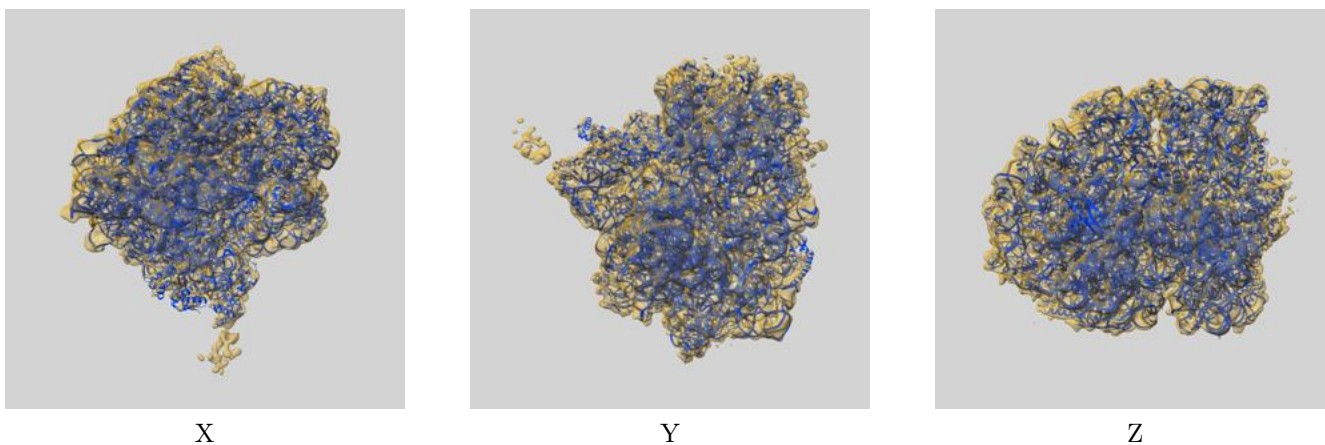
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.90	-	-
Author-provided FSC curve	8.83	12.12	9.36
Unmasked-calculated*	11.36	18.98	13.23

*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 11.36 differs from the reported value 8.9 by more than 10 %

9 Map-model fit [i](#)

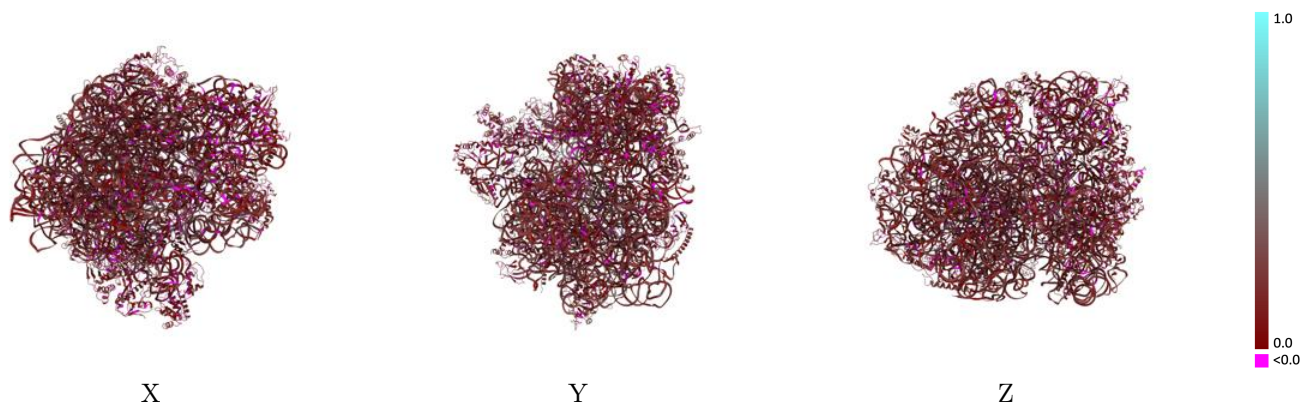
This section contains information regarding the fit between EMDB map EMD-13280 and PDB model 7PAQ. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



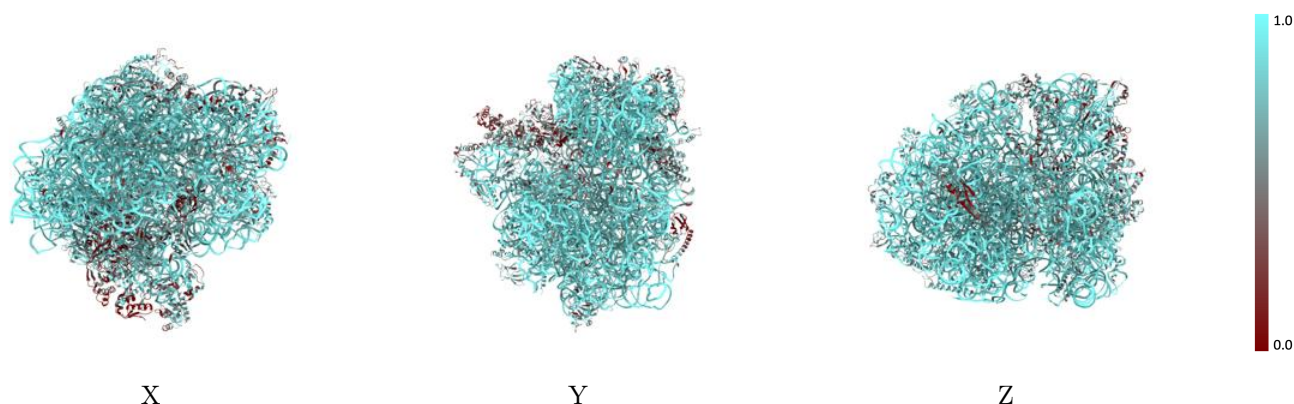
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



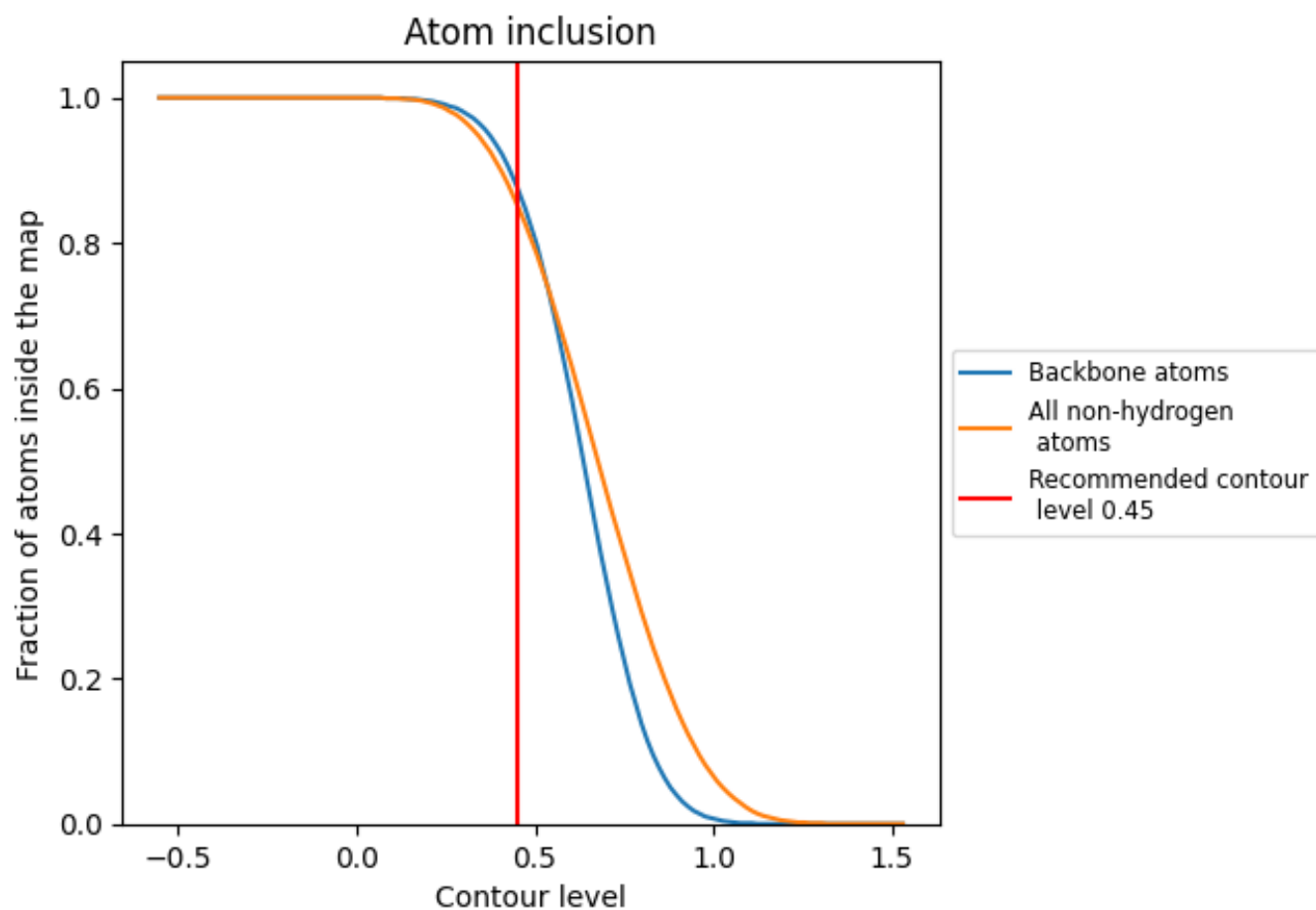
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.1570
0	 0.7780	 0.1250
1	 0.7720	 0.1190
2	 0.7670	 0.1010
3	 0.9620	 0.1720
4	 0.9740	 0.1830
5	 0.9560	 0.1660
7	 0.7210	 0.1000
8	 0.9180	 0.1630
9	 0.3870	 0.1310
A	 0.6140	 0.1520
B	 0.6360	 0.1370
C	 0.7230	 0.1250
D	 0.7090	 0.1260
E	 0.6450	 0.1560
F	 0.5860	 0.1220
G	 0.7160	 0.1490
H	 0.6650	 0.1120
I	 0.6150	 0.1030
J	 0.6660	 0.1340
K	 0.7260	 0.1480
L	 0.5900	 0.1010
M	 0.7060	 0.0620
N	 0.7190	 0.1570
O	 0.7960	 0.1540
P	 0.7090	 0.1360
Q	 0.7040	 0.1270
R	 0.6630	 0.0920
S	 0.7740	 0.1490
T	 0.7080	 0.1570
W	 0.1140	 0.1060
a	 0.7850	 0.1190
b	 0.7240	 0.1210
c	 0.7270	 0.1530
d	 0.6920	 0.1440



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	 0.6580	 0.1410
f	 0.3120	 0.1430
g	 0.5850	 0.1270
h	 0.4740	 0.1320
i	 0.7550	 0.1460
j	 0.6730	 0.1370
k	 0.7550	 0.1270
l	 0.7510	 0.1220
m	 0.7640	 0.1380
n	 0.7830	 0.1490
o	 0.7100	 0.1490
p	 0.7990	 0.1320
q	 0.7560	 0.1500
r	 0.8050	 0.1560
s	 0.7690	 0.1490
t	 0.6500	 0.1390
u	 0.7770	 0.1090
v	 0.7250	 0.1080
w	 0.7640	 0.1860
x	 0.6120	 0.1390
y	 0.8300	 0.1250
z	 0.8620	 0.1350