



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2026 – 03:16 pm BST

PDB ID : 9SY6 / pdb_00009sy6
EMDB ID : EMD-55345
Title : Structural characterization of hibernating ribosomes in the Gram-negative pathogen *Pseudomonas aeruginosa*
Authors : Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G.
Deposited on : 2025-10-10
Resolution : 2.60 Å (reported)
Based on initial model : 7UNW

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:

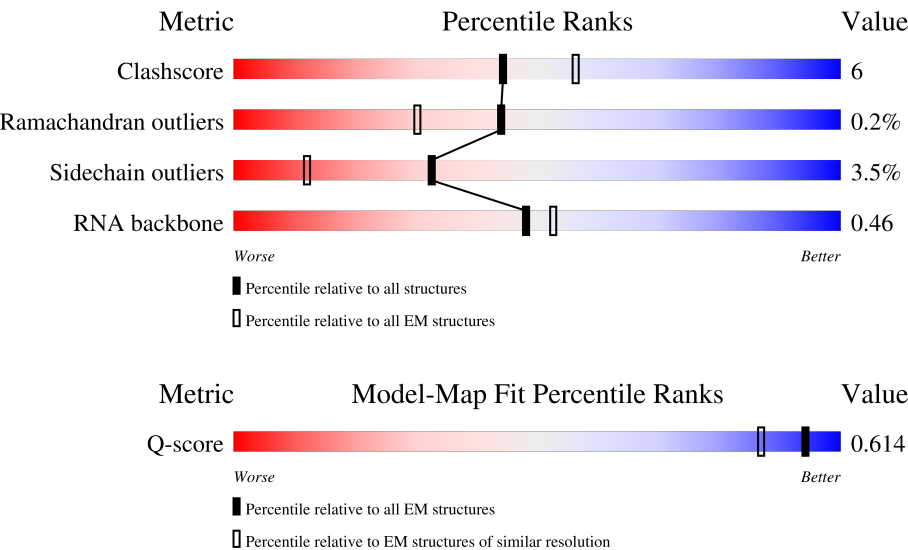
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.2
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.51

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 2.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

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	51	35% 73% 27%
2	1	44	5% 86% 9% 5%
3	2	64	92% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	38	
5	4	71	
6	A	1536	
7	B	246	
8	C	228	
9	D	206	
10	E	166	
11	F	139	
12	G	156	
13	H	130	
14	I	130	
15	J	103	
16	K	129	
17	L	123	
18	M	118	
19	N	101	
20	O	89	
21	P	83	
22	Q	88	
23	R	76	
24	S	91	
25	T	91	
26	W	15	
27	X	102	
28	a	2891	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	b	120	
30	c	273	
31	d	211	
32	e	200	
33	f	179	
34	g	177	
35	h	148	
36	i	142	
37	j	122	
38	k	144	
39	l	137	
40	m	129	
41	n	116	
42	o	116	
43	p	118	
44	q	103	
45	r	110	
46	s	99	
47	t	104	
48	u	204	
49	v	85	
50	w	78	
51	x	63	
52	y	58	
53	z	60	

2 Entry composition

There are 56 unique types of molecules in this entry. The entry contains 143096 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 Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	68	Total	C	N	O	S	0	0
			531	334	95	96	6		

- Molecule 6 is a RNA chain called 16S rRNA (1535-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1535	Total	C	N	O	P	0	0
			32945	14701	6039	10670	1535		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	224	Total	C	N	O	S	0	0
			1763	1112	322	319	10		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	208	Total	C	N	O	S	0	0
			1664	1052	315	292	5		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	205	Total	C	N	O	S	0	0
			1627	1003	316	303	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	154	Total	C	N	O	S	0	0
			1134	711	210	207	6		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	106	Total	C	N	O	S	0	0
			868	539	159	164	6		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	153	Total	C	N	O	S	0	0
			1199	752	232	210	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	129	Total	C	N	O	S	0	0
			982	618	173	185	6		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	127	Total	C	N	O	S	0	0
			1010	625	203	181	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	99	Total	C	N	O	S	0	0
			793	496	150	146	1		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	119	Total	C	N	O	S	0	0
			881	546	171	162	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP E2RXU4

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			961	589	198	169	5		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	113	Total	C	N	O	S	0	0
			883	541	178	160	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	100	Total	C	N	O	S	0	0
			804	496	167	138	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	88	Total	C	N	O	S	0	0
			703	434	139	129	1		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	81	Total	C	N	O	S	0	0
			637	398	125	113	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	80	Total	C	N	O	S	0	0
			645	404	124	115	2		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	62	Total	C	N	O	0	0
			494	316	86	92		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	83	Total	C	N	O	S	0	0
			663	422	129	109	3		

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	87	Total	C	N	O	S	0	0
			671	414	138	117	2		

- Molecule 26 is a RNA chain called non-STOP mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	10	Total	C	N	O	P	0	0
			219	97	41	71	10		

- Molecule 27 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	98	Total	C	N	O	S	0	0
			796	498	143	152	3		

- Molecule 28 is a RNA chain called 23S rRNA (2890-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	2890	Total	C	N	O	P	0	0
			62019	27677	11363	20089	2890		

- Molecule 29 is a RNA chain called 5S rRNA (117-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	117	Total	C	N	O	P	0	0
			2495	1114	448	816	117		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	272	Total	C	N	O	S	0	0
			2072	1276	426	364	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	211	Total	C	N	O	S	0	0
			1589	982	304	297	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	200	Total	C	N	O	S	0	0
			1524	956	283	282	3		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	177	Total	C	N	O	S	0	0
			1418	905	253	256	4		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	175	Total	C	N	O	S	0	0
			1326	835	244	245	2		

- Molecule 35 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	72	Total	C	N	O	S	0	0
			533	334	98	100	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	137	Total	C	N	O	S	0	0
			1086	689	211	181	5		

- Molecule 40 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	120	Total	C	N	O	S	0	0
			959	600	192	162	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 42 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	114	Total	C	N	O	S	0	0
			902	568	171	162	1		

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			936	592	196	148			

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	103	Total	C	N	O	S	0	0
			822	521	156	143	2		

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	94	Total	C	N	O	S	0	0
			739	472	134	132	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	103	Total	C	N	O	S	0	0
			800	503	152	143	2		

- Molecule 48 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	190	Total	C	N	O	S	0	0
			1446	915	262	266	3		

- Molecule 49 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	76	Total	C	N	O		0	0
			575	364	111	100			

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 51 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	57	Total	C	N	O	S	0	0
			445	277	87	79	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	55	Total	C	N	O	S	0	0
			440	264	93	82	1		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	
54	4	1	Total	Zn	0
			1	1	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	A	94	Total 94	Mg 94	0
55	X	1	Total 1	Mg 1	0
55	a	249	Total 249	Mg 249	0
55	b	5	Total 5	Mg 5	0
55	c	1	Total 1	Mg 1	0
55	p	2	Total 2	Mg 2	0
55	v	1	Total 1	Mg 1	0
55	z	1	Total 1	Mg 1	0

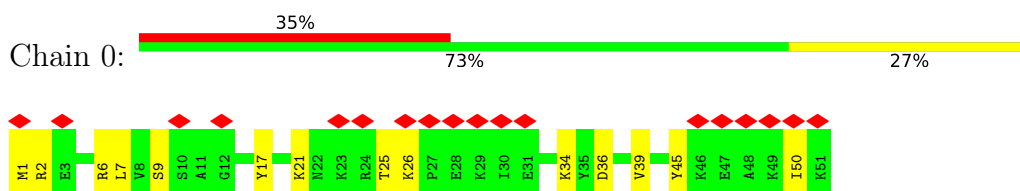
- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
56	A	48	Total 48	K 48	0
56	X	1	Total 1	K 1	0
56	a	113	Total 113	K 113	0
56	b	1	Total 1	K 1	0
56	c	4	Total 4	K 4	0
56	e	1	Total 1	K 1	0
56	f	1	Total 1	K 1	0

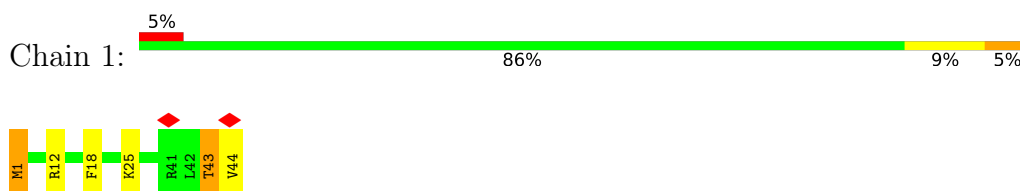
3 Residue-property plots [i](#)

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.

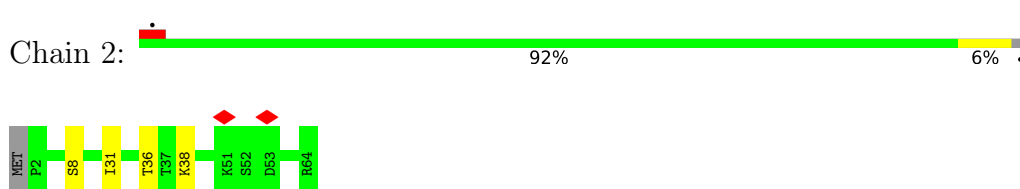
- Molecule 1: Large ribosomal subunit protein bL33



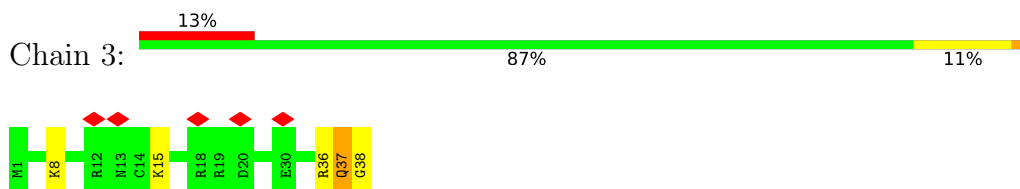
- Molecule 2: Large ribosomal subunit protein bL34



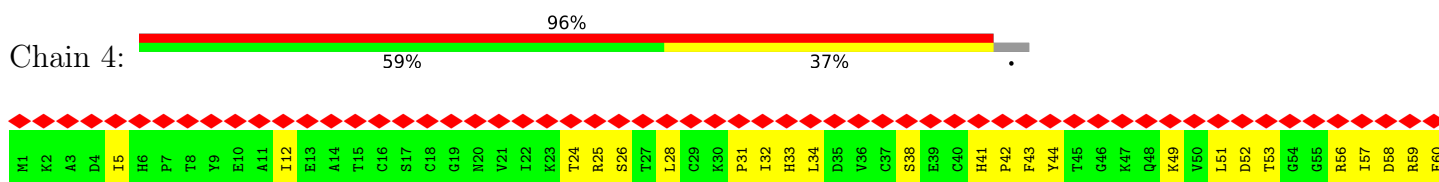
- Molecule 3: Large ribosomal subunit protein bL35



- Molecule 4: Large ribosomal subunit protein bL36

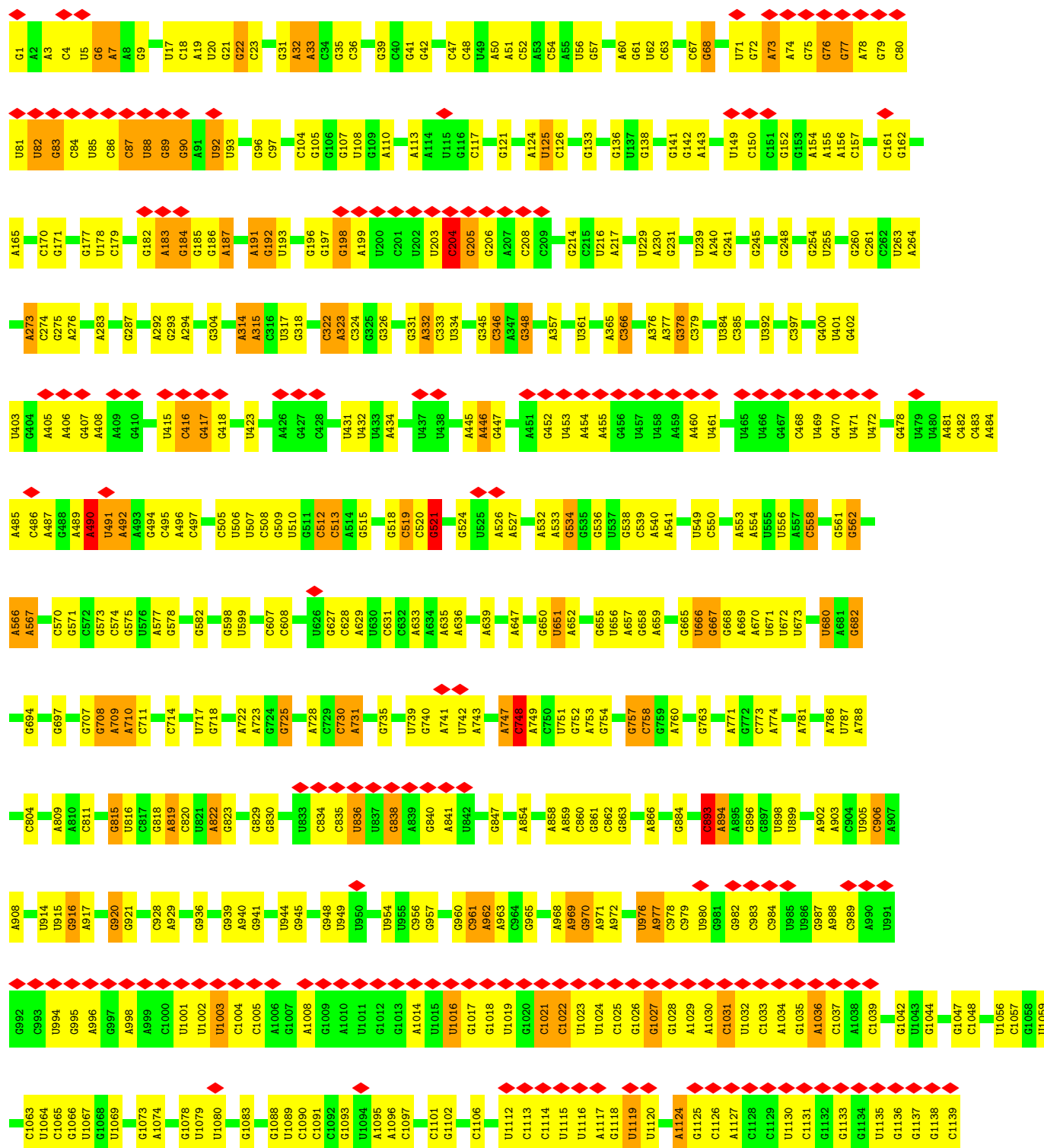


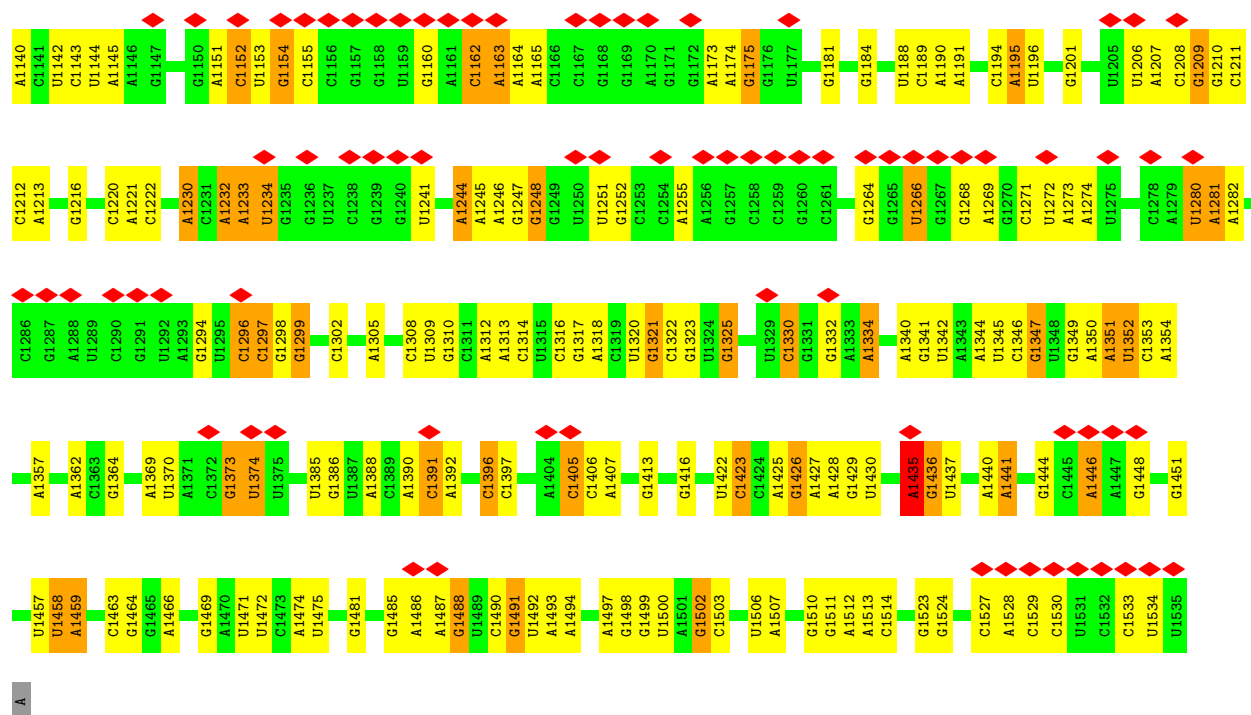
- Molecule 5: Large ribosomal subunit protein bL31

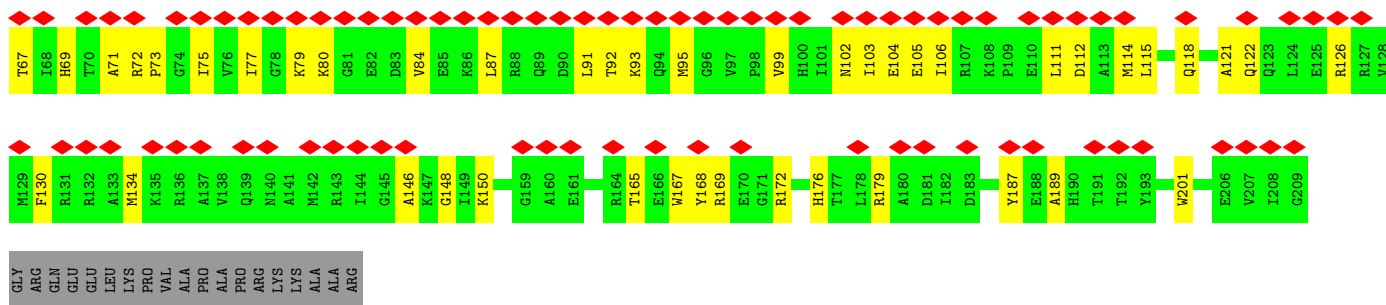




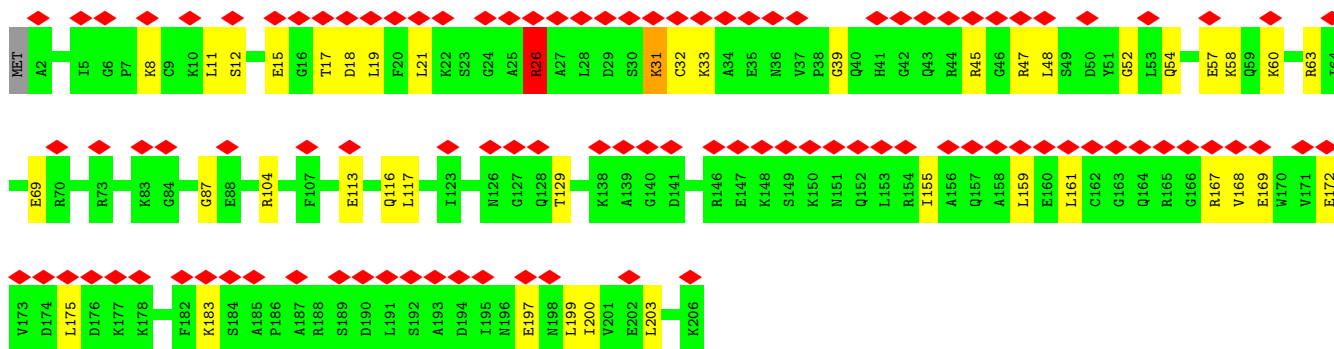
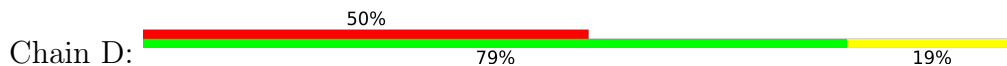
• Molecule 6: 16S rRNA (1535-MER)



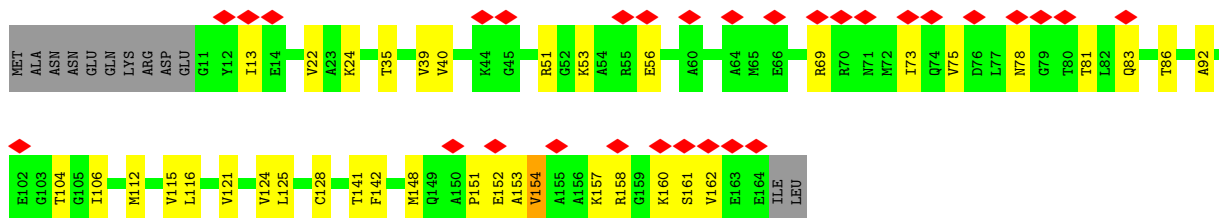




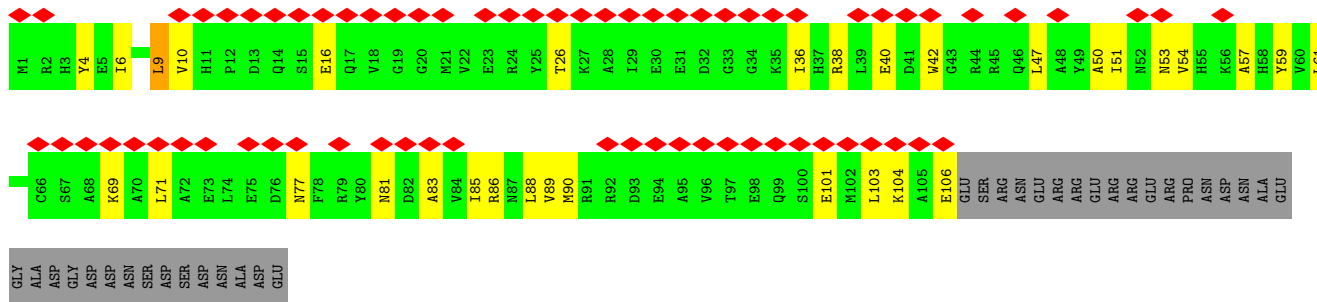
• Molecule 9: Small ribosomal subunit protein uS4



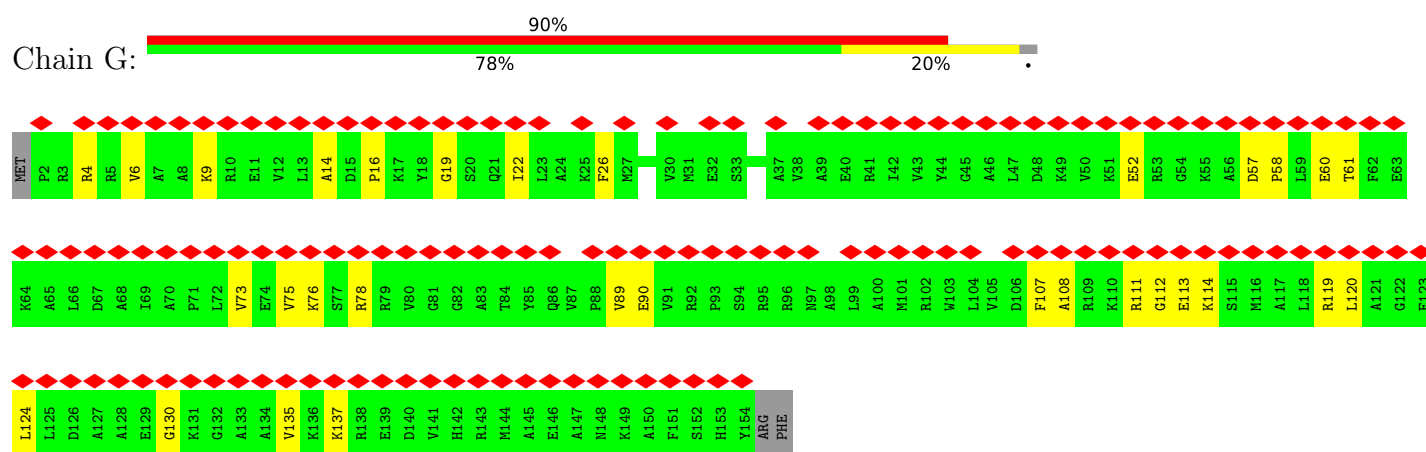
• Molecule 10: Small ribosomal subunit protein uS5



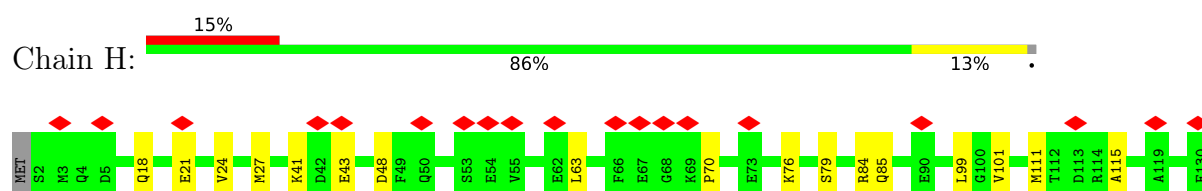
• Molecule 11: Small ribosomal subunit protein bS6



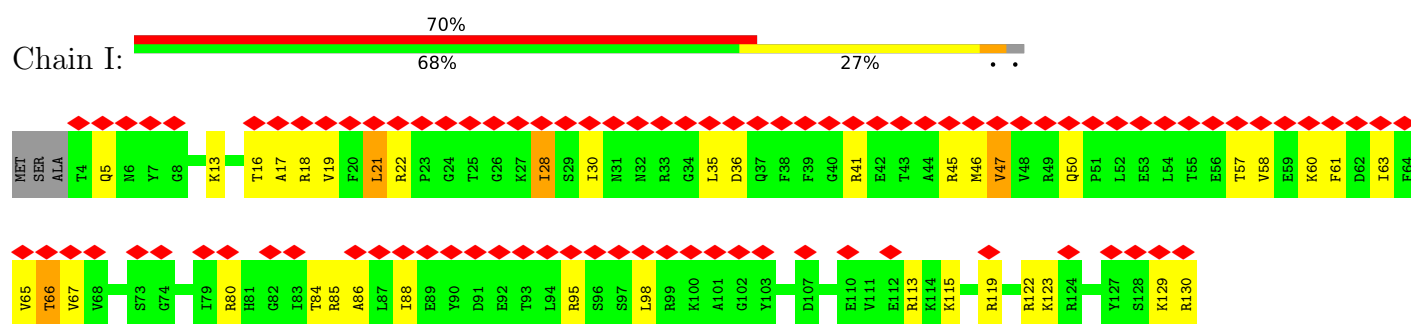
• Molecule 12: Small ribosomal subunit protein uS7



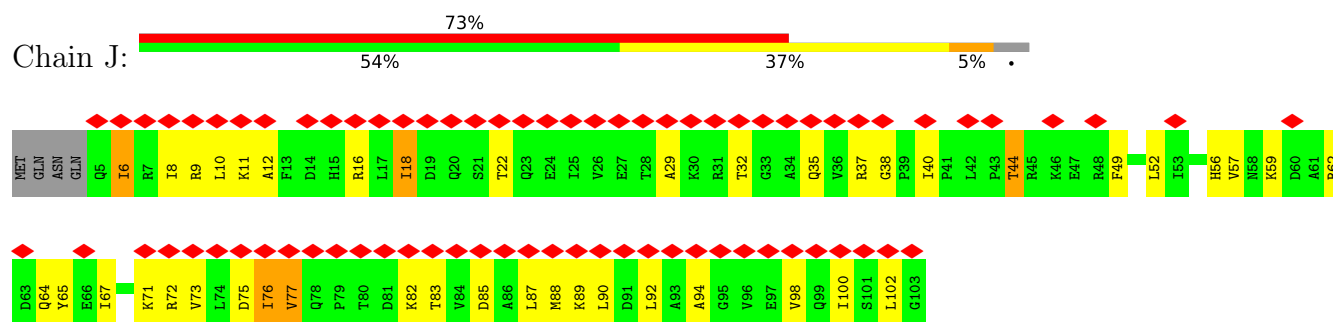
- Molecule 13: Small ribosomal subunit protein uS8



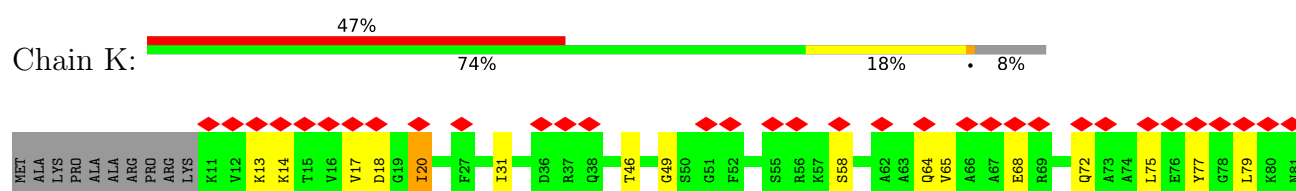
- Molecule 14: Small ribosomal subunit protein uS9

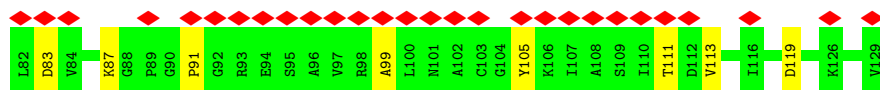


- Molecule 15: Small ribosomal subunit protein uS10



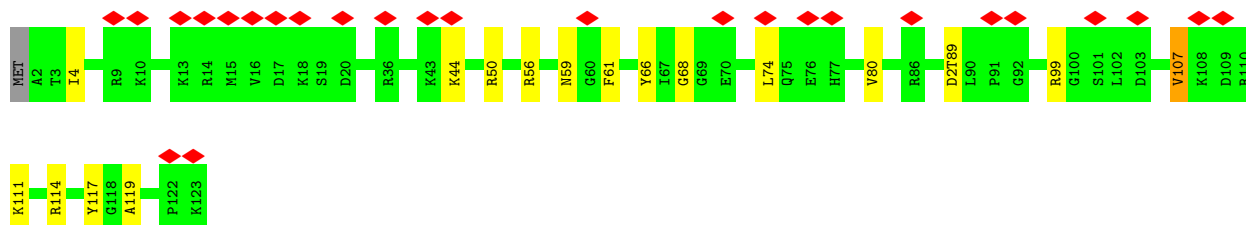
- Molecule 16: Small ribosomal subunit protein uS11





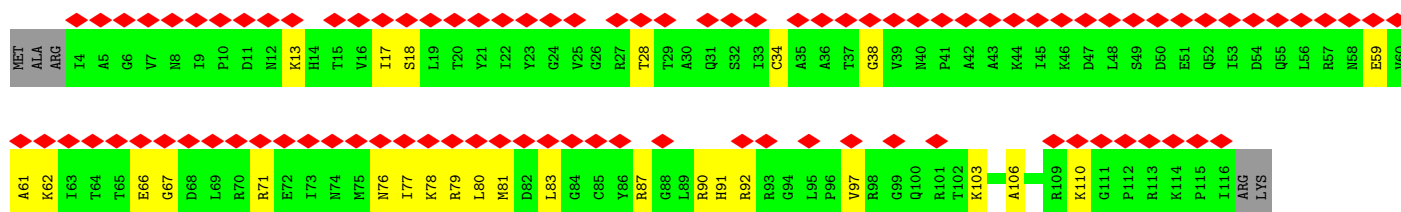
- Molecule 17: Small ribosomal subunit protein uS12

Chain L: 21% 85% 13% ..



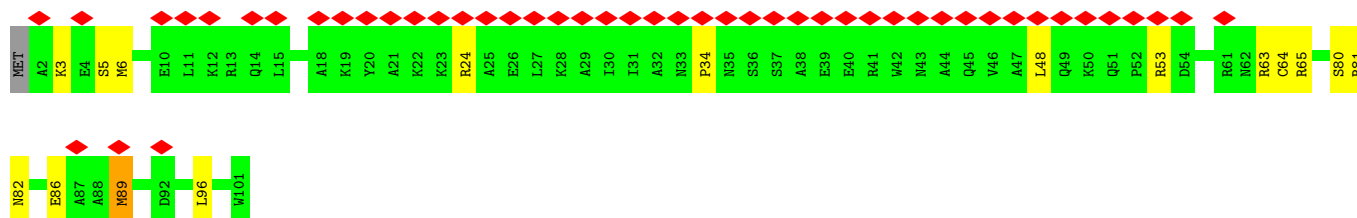
- Molecule 18: Small ribosomal subunit protein uS13

Chain M: 80% 73% 23% .



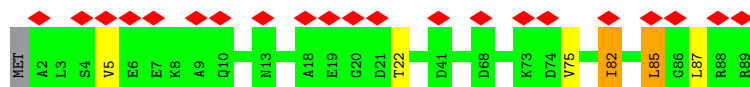
- Molecule 19: Small ribosomal subunit protein uS14

Chain N: 48% 83% 15% ..



- Molecule 20: Small ribosomal subunit protein uS15

Chain O: 24% 92% 14% ..

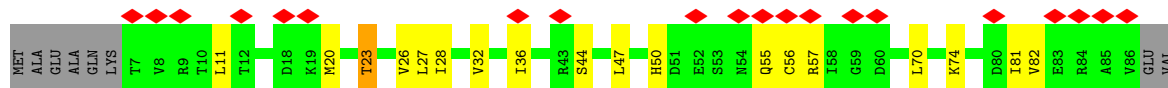


- Molecule 21: Small ribosomal subunit protein bS16

Chain P: 14% 83% 14% .



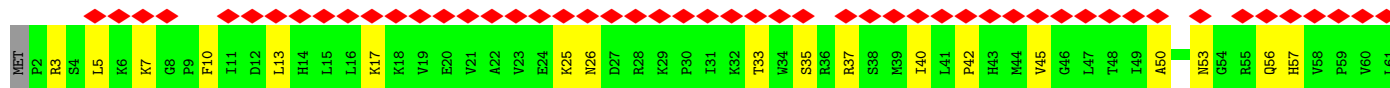
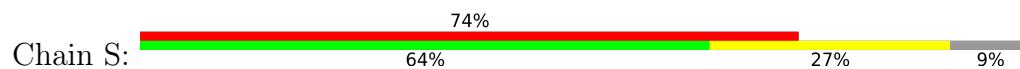
- Molecule 22: Small ribosomal subunit protein uS17



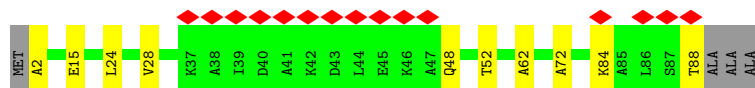
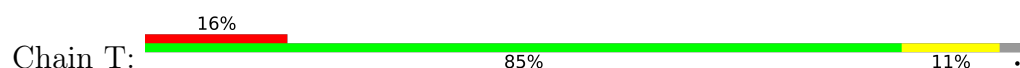
- Molecule 23: Small ribosomal subunit protein bS18



- Molecule 24: Small ribosomal subunit protein uS19



- Molecule 25: Small ribosomal subunit protein bS20



- Molecule 26: non-STOP mRNA

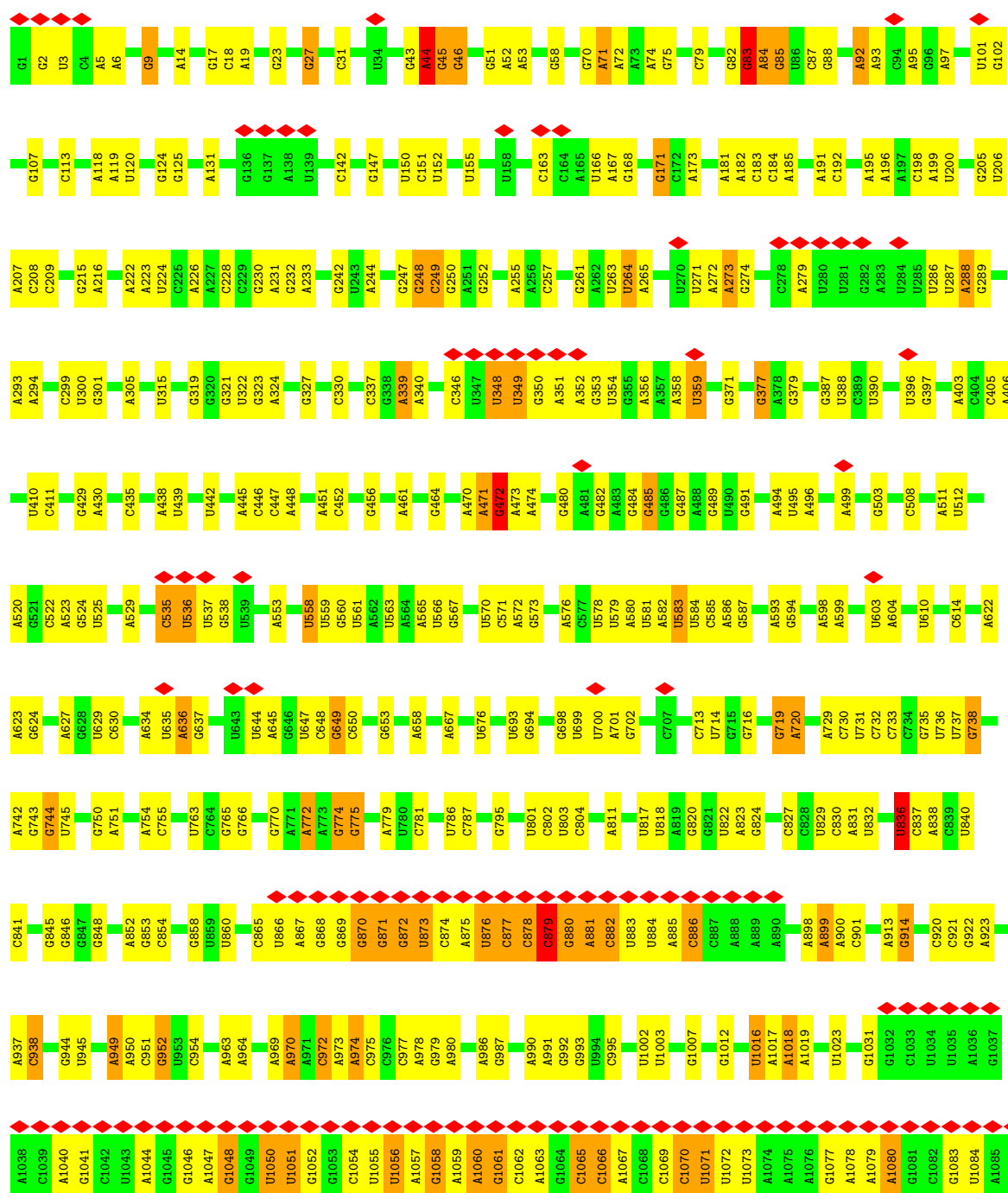


- Molecule 27: Ribosome hibernation promoting factor

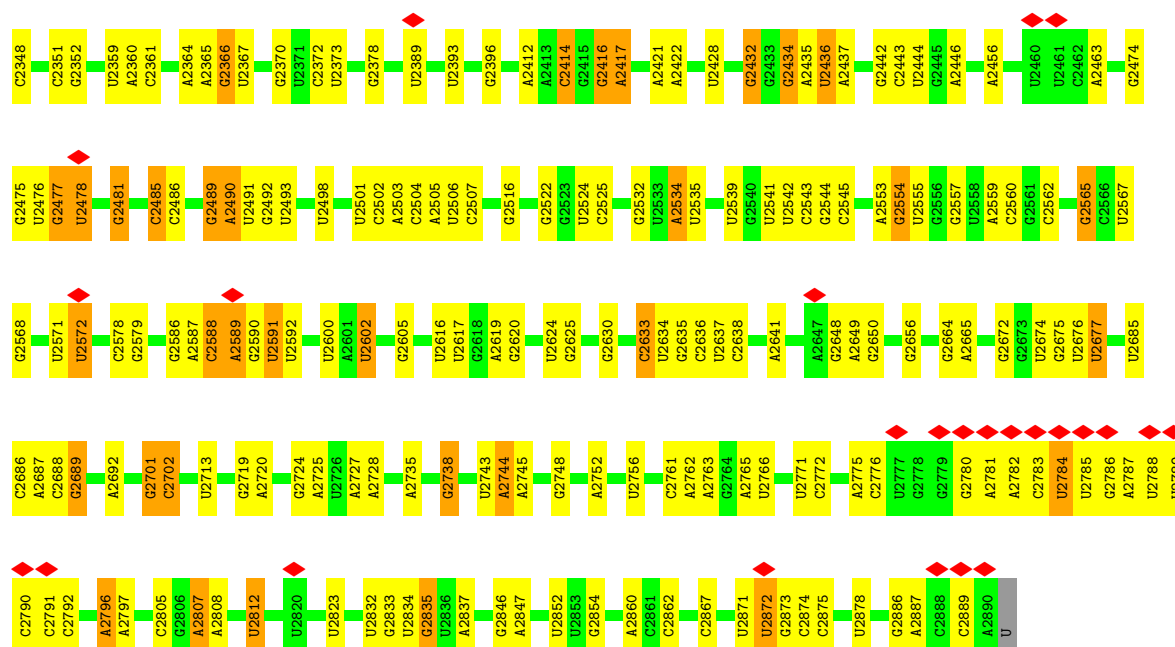




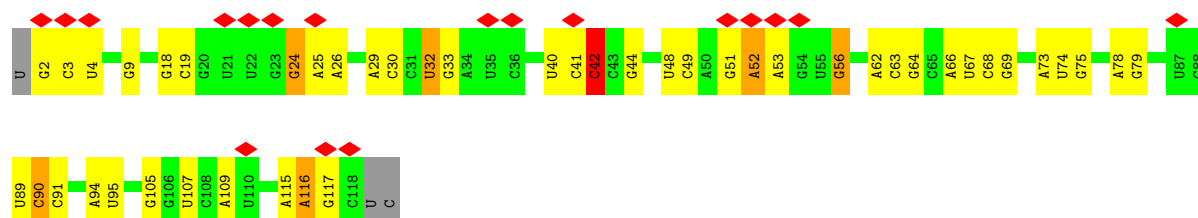
• Molecule 28: 23S rRNA (2890-MER)



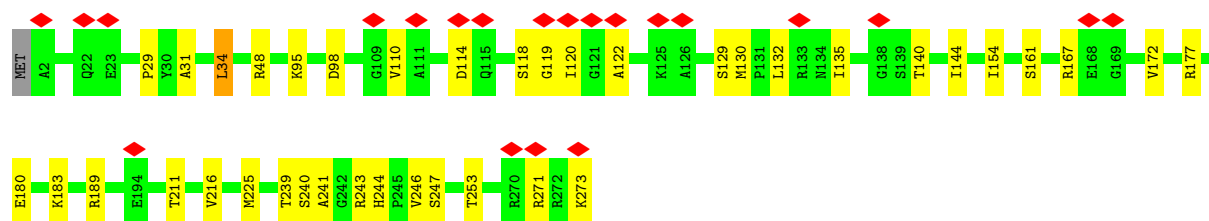
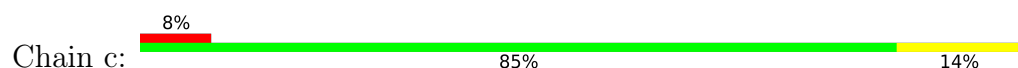
A2265	U2270	A2274	A2275	U2278	G2279	C2282	U2283	A2284	A2285	G2286	A2287	C2288	C2289	G2290	C2291	U2292	C2293	G2294	G2295	A2296	A2297	U2298	U2299	G2302	U2303	C2304	G2305	U2306	A2307	A2308	A2309	A2312	U2313	A2314	A2315	A2316	G2317	A2321	A2322	A2323	U2330	U2331	G2332	A2333	C2334	C2337	A2343	G2344																																																		
U2167	G2168	G2169	C2170	A2171	U2172	G2173	C2174	U2175	U2176	G2177	A2178	U2179	G2180	U2181	U2182	C2183	U2184	A2185	A2186	C2187	G2191	C2194	C2195	G2198	U2200	C2201	C2202	G2203	G2204	A2212	U2220	G2221	G2225	G2226	C2227	A2228	G2229	U2230	U2231	A2234	C2235	C2236	A2238	U2239	A2260	A2261																																																				
G2107	G2108	U2109	G2110	G2111	G2112	A2113	G2114	G2115	G2116	U2117	U2118	U2119	G2120	A2121	A2122	G2123	C2124	G2125	U2126	G2127	G2128	G2129	C2132	C2133	A2134	G2135	U2136	U2137	C2138	G2139	C2140	G2141	U2142	G2143	G2144	A2145	G2146	C2147	C2148	A2149	U2150	C2151	C2152	U2153	U2154	G2155	A2156	A2157	U2158	U2159	A2160	C2161	C2162	A2163	C2164	C2165	C2166																																									
C1912	A1915	G1916	G1917	A1924	A1925	U1926	U1927	C1928	U1933	C1934	A1939	U1942	C1945	C1949	U1950	G1951	C1954	A1957	U1958	G1959	G1967	C1977	U1978	G1979	U1980	C1984	A2001	A2002	A2008	U2009	C2010	G2011	C2012	U2013	G2014	U2015	G2016	A2017	A2018	C2019	A2020	U2021	G2022	C2023	A2024	G2025	U2026	G2027	U2030	G2031	C2032	U2038	A2039	G2040	A2041	C2042	G2043	A2047	G2048	A2049	C2050	C2051	C2052	G2053	U2055	G2056	A2057	A2058	C2059	U2060	U2061	U2062	G2067	G2080	C2083	U2084	U2085	U2086	G2087	A2088	G2089	C2090	C2091	U2092	G2093	C2094	U2095	U2096	G2097	U2098	G2099	U2100	A2101	G2102	G2103	A2104	U2105	A2106
U1814	A1815	A1816	G1822	A1834	A1835	A1841	U1842	U1843	G1844	A1845	U1846	G1849	G1850	U1851	U1852	C1855	G1856	C1857	A1858	A1859	G1860	C1861	G1862	G1865	G1866	U1867	C1868	U1870	G1871	A1876	A1877	G1893	G1894	C1895	C1896	G1897	U1898	A1899	A1900	C1901	3TD1902	A1903	U1904	A1905	A1906	G1909	U1910	C1911																																																		
U1720	C1721	C1722	G1723	U1724	A1725	G1733	C1734	U1738	U1739	G1740	A1741	G1743	A1744	U1745	G1750	G1751	A1760	C1761	U1762	G1763	U1766	U1769	A1770	A1771	A1772	A1773	A1774	C1775	A1776	C1777	A1778	A1781	C1782	U1783	C1784	C1787	A1788	A1789	A1790	A1795	A1796	A1797	G1798	C1803	U1807	G1811																																																				
G1616	A1624	A1625	A1626	A1627	C1628	C1629	C1634	G1635	U1636	U1637	U1638	G1639	A1640	G1641	A1642	G1643	G1650	G1657	G1664	C1665	U1670	G1671	G1672	C1673	A1674	C1685	G1686	A1690	G1693	U1694	C1702	U1703	U1708	G1709	A1710	A1711	G1712	G1713	A1714	U1715	U1716	U1717	A1718	C1719																																																						
G1519	U1520	C1521	U1522	G1523	U1524	U1525	A1526	G1527	A1528	U1529	G1530	A1531	C1532	G1538	U1539	U1540	U1541	G1542	A1548	U1549	C1551	U1552	U1553	C1554	C1555	A1556	A1557	G1558	A1559	A1560	C1567	U1568	G1571	C1572	U1573	U1574	C1575	A1576	G1577	G1578	U1579	A1580	A1581	C1582	C1583	C1587	A1598	A1608	G1612	C1615																																																
A1421	G1422	G1423	C1424	U1425	A1426	G1427	G1428	C1429	C1433	U1434	U1435	C1438	G1439	U1445	G1446	U1447	A1450	A1451	A1456	A1457	U1468	G1469	A1470	A1471	A1472	U1473	C1474	U1475	U1476	A1477	U1480	A1481	A1482	A1483	U1484	G1490	U1491	U1492	U1493	C1494	A1495	A1496	G1497	A1502	U1510	G1511	U1517	C1518																																																		
U1339	A1340	A1341	C1344	G1345	A1346	G1347	G1348	C1349	A1352	A1353	A1354	A1355	G1356	C1357	G1358	G1361	U1366	A1370	A1371	A1372	C1373	G1375	G1376	U1377	U1378	A1379	A1382	U1392	U1393	C1394	U1395	G1396	G1397	U1398	U1399	A1400	C1401	U1402	G1403	C1404	U1407	G1408	A1414	C1415	G1416	G1417	A1418	G1419	A1420																																																	
U1198	G1199	A1200	A1201	A1214	G1223	A1224	G1225	A1233	A1234	G1237	C1238	G1239	A1240	U1241	U1242	G1243	A1249	U1250	G1251	A1252	G1253	G1258	A1259	C1260	A1261	U1263	G1270	A1271	A1272	U1275	C1276	A1277	C1278	A1287	A1288	U1300	C1301	G1304	C1307	A1308	U1316	G1334																																																								
U1098	C1099	G1100	A1101	G1102	U1103	C1104	G1105	G1112	G1115	A1116	A1117	G1118	A1119	U1120	G1121	U1122	A1123	A1124	C1125	G1126	G1127	G1128	G1129	A1133	A1140	C1141	C1144	G1145	A1146	A1147	G1148	G1157	U1158	G1162	U1163	A1164	A1165	G1166	U1167	U1175	A1178	G1184	U1185	U1186	C1187	U1190	G1193																																																			



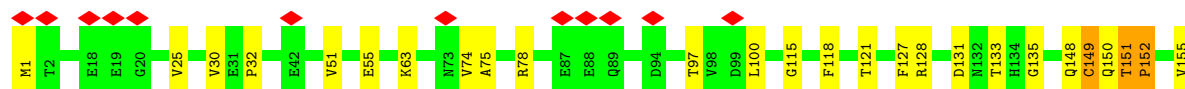
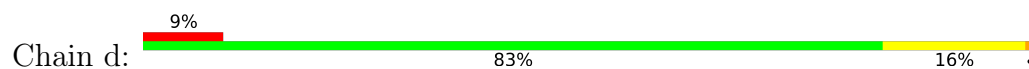
• Molecule 29: 5S rRNA (117-MER)

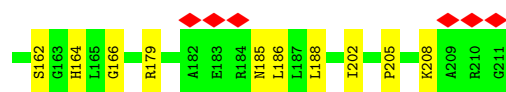


• Molecule 30: Large ribosomal subunit protein uL2

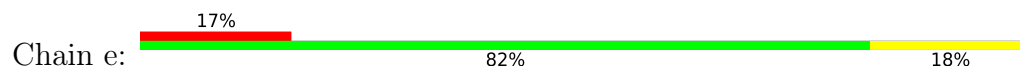


• Molecule 31: Large ribosomal subunit protein uL3

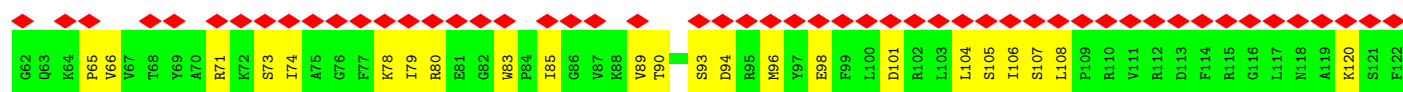
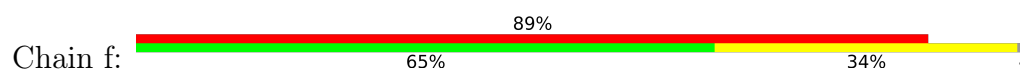




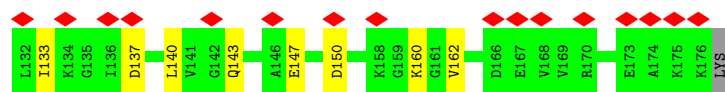
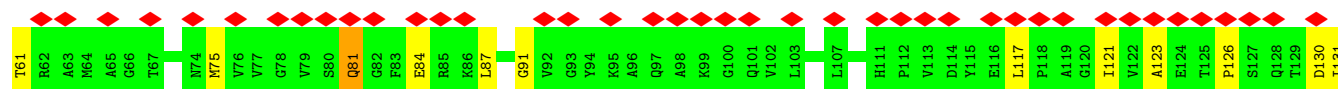
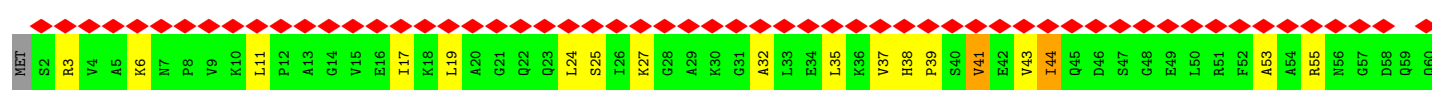
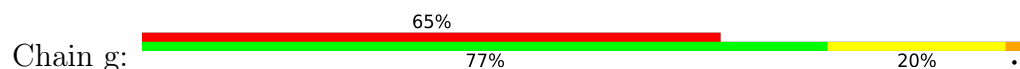
- Molecule 32: Large ribosomal subunit protein uL4



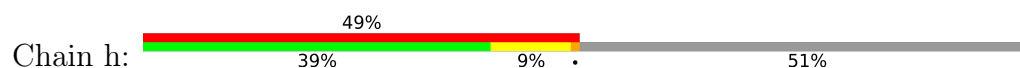
- Molecule 33: Large ribosomal subunit protein uL5

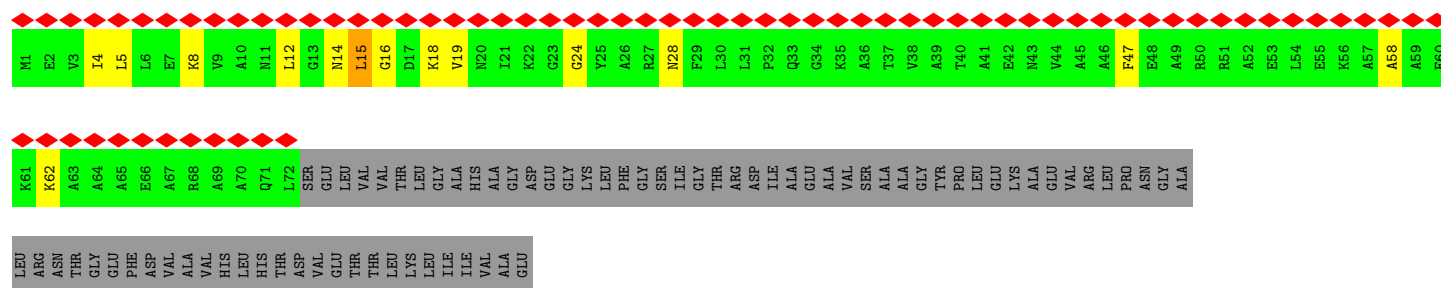


- Molecule 34: Large ribosomal subunit protein uL6

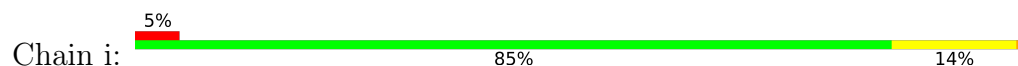


- Molecule 35: Large ribosomal subunit protein bL9

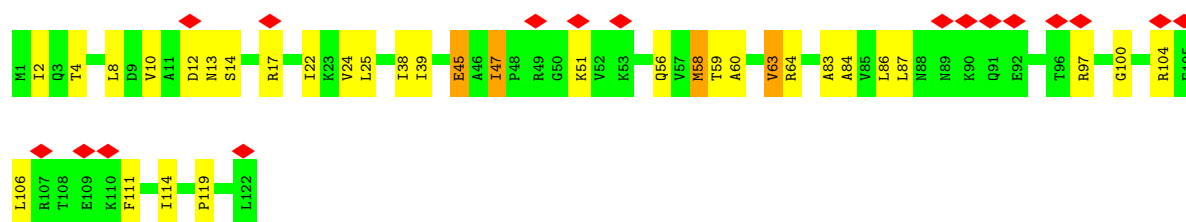




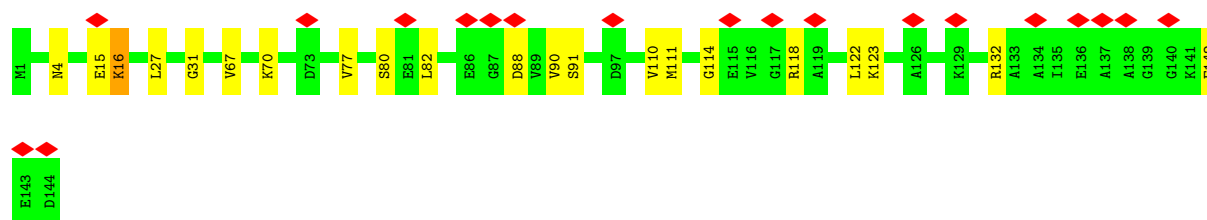
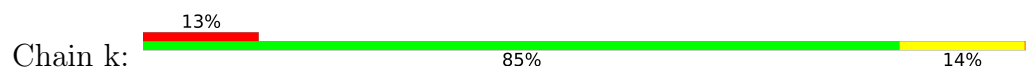
- Molecule 36: Large ribosomal subunit protein uL13



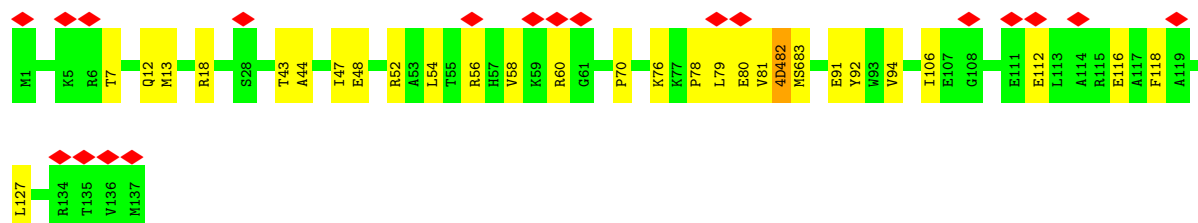
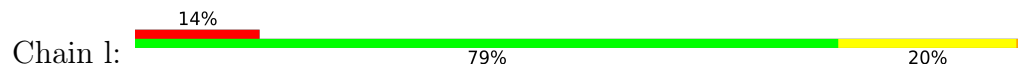
- Molecule 37: Large ribosomal subunit protein uL14



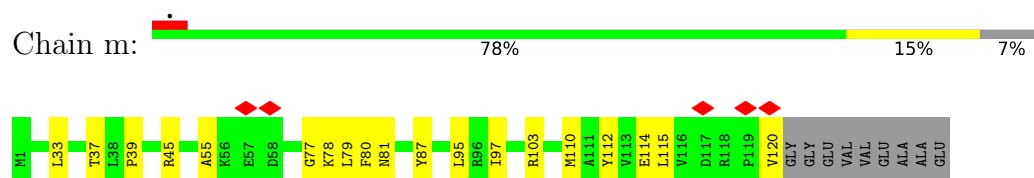
- Molecule 38: Large ribosomal subunit protein uL15



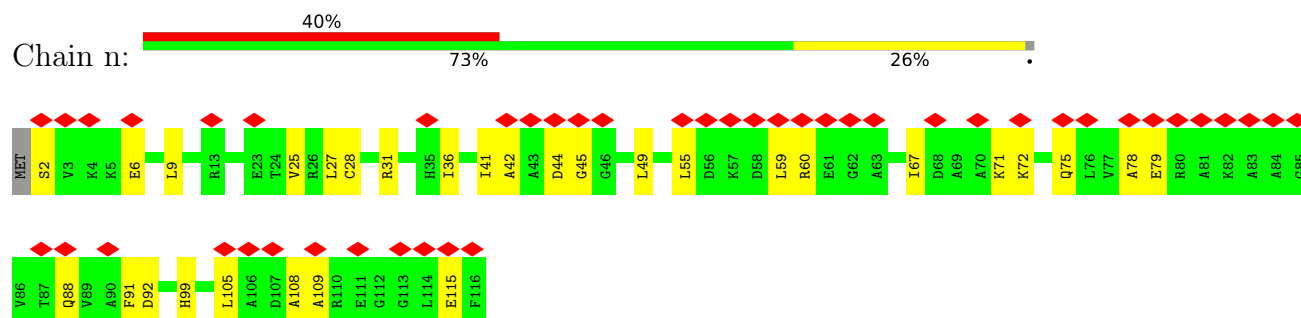
- Molecule 39: Large ribosomal subunit protein uL16



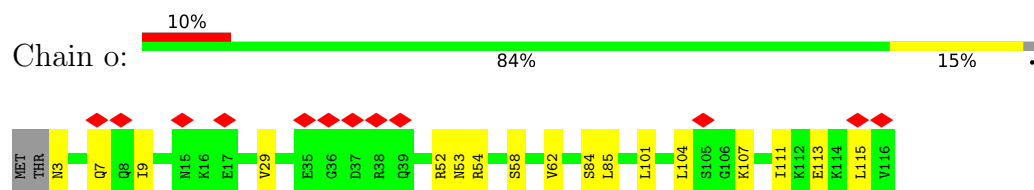
- Molecule 40: Large ribosomal subunit protein bL17



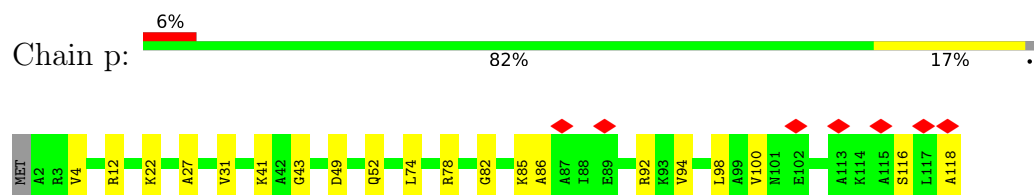
- Molecule 41: Large ribosomal subunit protein uL18



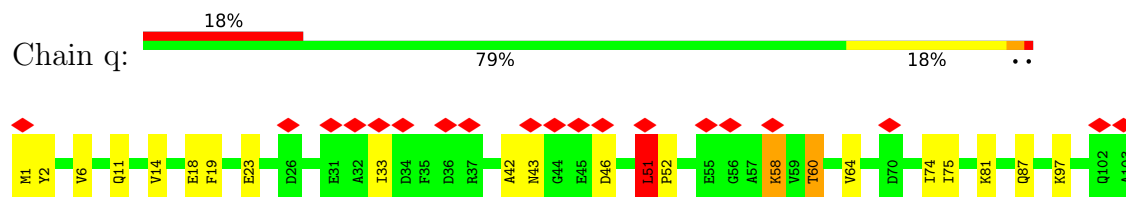
- Molecule 42: Large ribosomal subunit protein bL19



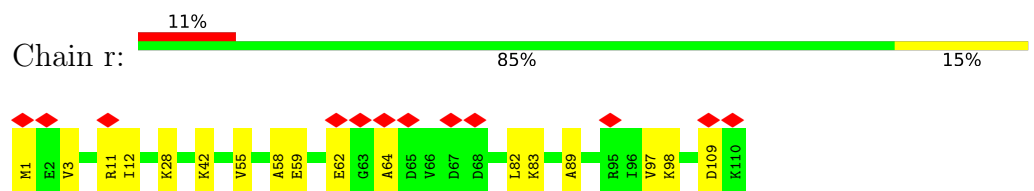
- Molecule 43: Large ribosomal subunit protein bL20



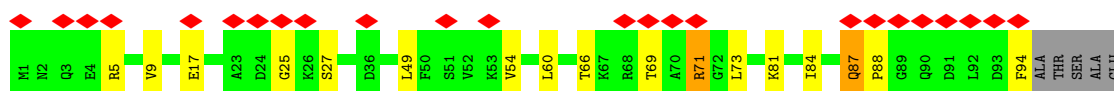
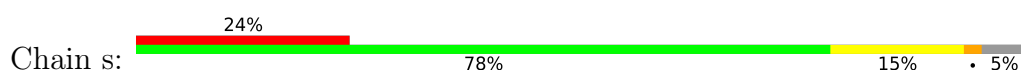
- Molecule 44: Large ribosomal subunit protein bL21



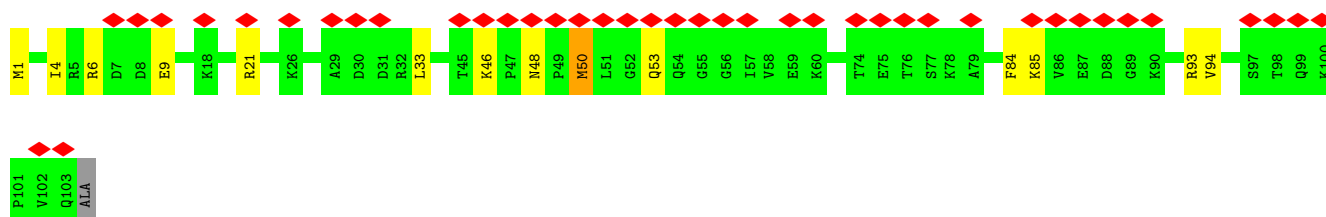
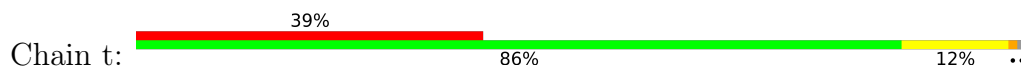
- Molecule 45: Large ribosomal subunit protein uL22



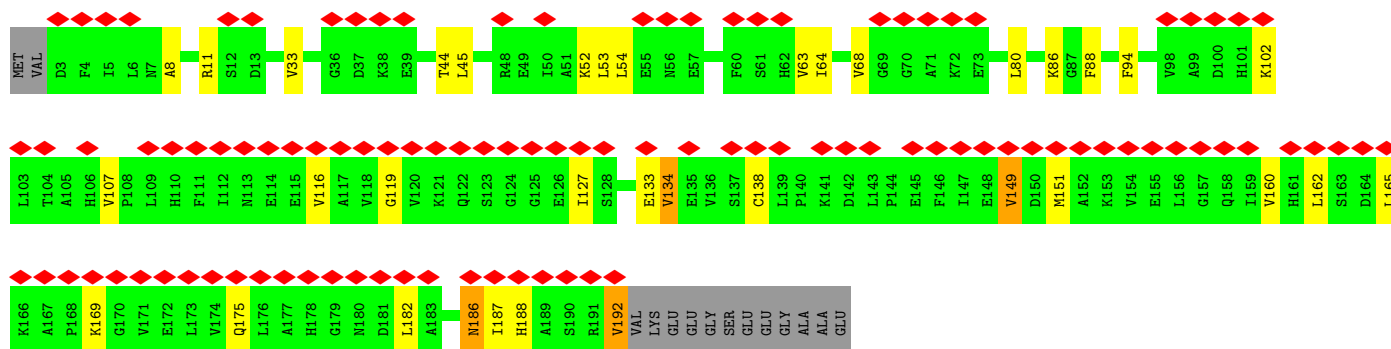
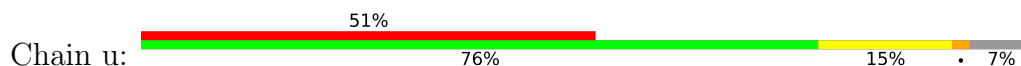
- Molecule 46: Large ribosomal subunit protein uL23



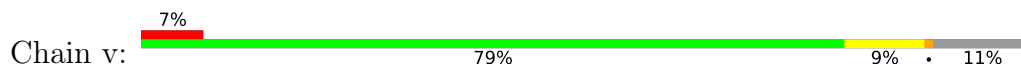
- Molecule 47: Large ribosomal subunit protein uL24



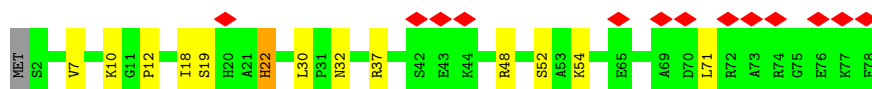
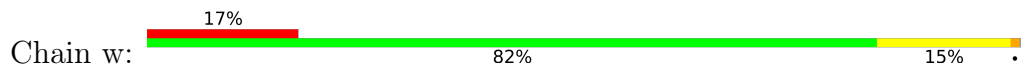
- Molecule 48: Large ribosomal subunit protein bL25



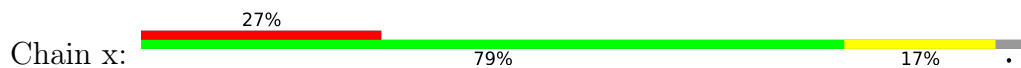
- Molecule 49: Large ribosomal subunit protein bL27

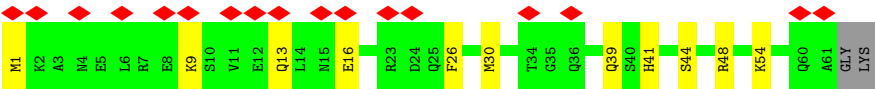


- Molecule 50: Large ribosomal subunit protein bL28

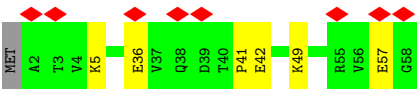
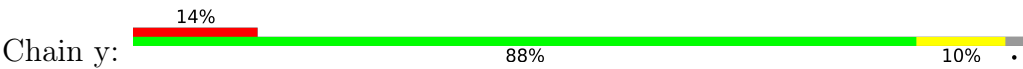


- Molecule 51: Large ribosomal subunit protein uL29

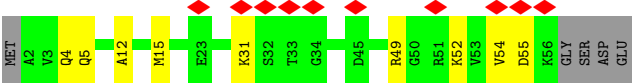
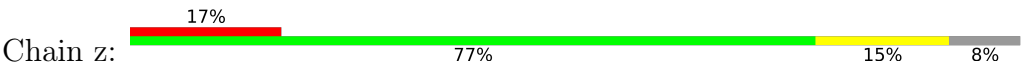




• Molecule 52: Large ribosomal subunit protein uL30



• Molecule 53: Large ribosomal subunit protein bL32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	131785	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.134	Depositor
Minimum map value	-1.499	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: H2U, MEQ, 1MG, MG, IAS, 6MZ, ZN, 2MG, D2T, MS6, 4D4, G7M, 2MA, OMU, K, 3TD, 5MU, OMG, MA6, 5MC, UR3, PSU, OMC, 4OC

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	0.28	0/433	0.41	0/576
2	1	0.40	0/368	0.44	0/482
3	2	0.33	0/511	0.38	0/668
4	3	0.35	0/308	0.40	0/404
5	4	0.18	0/542	0.45	0/728
6	A	0.78	0/36632	0.85	21/57140 (0.0%)
7	B	0.20	0/1791	0.41	0/2405
8	C	0.26	0/1693	0.38	0/2279
9	D	0.26	0/1646	0.47	2/2201 (0.1%)
10	E	0.31	0/1148	0.48	0/1544
11	F	0.25	0/882	0.41	0/1186
12	G	0.21	0/1217	0.36	0/1627
13	H	0.30	0/993	0.39	0/1332
14	I	0.24	0/1022	0.41	0/1365
15	J	0.27	0/803	0.45	0/1083
16	K	0.26	0/889	0.33	0/1199
17	L	0.31	0/964	0.39	0/1289
18	M	0.22	0/892	0.42	0/1199
19	N	0.25	0/816	0.39	1/1087 (0.1%)
20	O	0.29	0/710	0.27	0/947
21	P	0.31	0/648	0.43	0/872
22	Q	0.29	0/653	0.43	0/881
23	R	0.26	0/502	0.32	0/677
24	S	0.22	0/678	0.34	0/912
25	T	0.31	0/678	0.33	0/904
26	W	0.50	0/245	0.86	0/381
27	X	0.24	0/803	0.42	0/1075
28	a	0.94	0/68901	0.88	50/107478 (0.0%)
29	b	0.72	0/2789	0.78	1/4345 (0.0%)
30	c	0.39	0/2108	0.43	0/2831
31	d	0.39	0/1601	0.46	0/2152

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.35	0/1544	0.37	0/2079
33	f	0.24	0/1439	0.42	0/1932
34	g	0.24	0/1344	0.40	0/1809
35	h	0.16	0/536	0.34	0/719
36	i	0.35	0/1156	0.42	0/1559
37	j	0.35	0/947	0.40	0/1268
38	k	0.34	0/1078	0.43	0/1436
39	l	0.34	0/1085	0.42	0/1449
40	m	0.38	0/975	0.41	0/1304
41	n	0.29	0/888	0.38	0/1183
42	o	0.35	0/911	0.39	0/1218
43	p	0.39	0/946	0.38	0/1257
44	q	0.33	0/835	0.43	0/1117
45	r	0.34	0/837	0.38	0/1114
46	s	0.33	0/749	0.42	0/1002
47	t	0.28	0/808	0.38	0/1079
48	u	0.26	0/1469	0.34	0/1988
49	v	0.38	0/583	0.45	0/774
50	w	0.34	0/641	0.35	0/854
51	x	0.28	0/491	0.36	0/654
52	y	0.32	0/449	0.40	0/602
53	z	0.38	0/446	0.45	0/594
All	All	0.76	0/154023	0.78	75/230240 (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
31	d	0	1
44	q	0	1
46	s	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	a	2087	G	OP1-P-O3'	-10.67	76.00	108.00
28	a	2087	G	OP2-P-O3'	-10.46	76.62	108.00
28	a	503	G	O4'-C1'-N9	9.10	115.48	108.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	a	879	C	O4'-C1'-N1	8.58	114.51	108.50
9	D	26	ARG	CA-C-N	-8.02	112.90	122.44

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	d	151	THR	Peptide
44	q	51	LEU	Peptide
46	s	25	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	0	457	10	0
2	1	365	0	409	4	0
3	2	506	0	569	1	0
4	3	307	0	342	4	0
5	4	531	0	528	23	0
6	A	32945	0	16588	354	0
7	B	1763	0	1811	44	0
8	C	1664	0	1723	40	0
9	D	1627	0	1665	25	0
10	E	1134	0	1181	27	0
11	F	868	0	846	23	0
12	G	1199	0	1253	18	0
13	H	982	0	1036	9	0
14	I	1010	0	1052	33	0
15	J	793	0	833	30	0
16	K	881	0	897	11	0
17	L	961	0	1010	9	0
18	M	883	0	929	21	0
19	N	804	0	841	15	0
20	O	703	0	727	3	0
21	P	637	0	648	7	0
22	Q	645	0	689	11	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	R	494	0	514	9	0
24	S	663	0	697	23	0
25	T	671	0	722	5	0
26	W	219	0	108	4	0
27	X	796	0	818	8	0
28	a	62019	0	31188	522	0
29	b	2495	0	1263	21	0
30	c	2072	0	2152	28	0
31	d	1589	0	1605	20	0
32	e	1524	0	1582	24	0
33	f	1418	0	1486	45	0
34	g	1326	0	1388	23	0
35	h	533	0	560	8	0
36	i	1130	0	1160	14	0
37	j	938	0	1012	17	0
38	k	1066	0	1112	13	0
39	l	1086	0	1145	19	0
40	m	959	0	1005	11	0
41	n	881	0	920	18	0
42	o	902	0	960	12	0
43	p	936	0	1025	13	0
44	q	822	0	858	15	0
45	r	833	0	897	9	0
46	s	739	0	788	9	0
47	t	800	0	863	9	0
48	u	1446	0	1486	19	0
49	v	575	0	598	5	0
50	w	630	0	653	8	0
51	x	490	0	520	8	0
52	y	445	0	472	4	0
53	z	440	0	437	9	0
54	3	1	0	0	0	0
54	4	1	0	0	0	0
55	A	94	0	0	0	0
55	X	1	0	0	0	0
55	a	249	0	0	0	0
55	b	5	0	0	0	0
55	c	1	0	0	0	0
55	p	2	0	0	0	0
55	v	1	0	0	0	0
55	z	1	0	0	0	0
56	A	48	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	X	1	0	0	0	0
56	a	113	0	0	0	0
56	b	1	0	0	0	0
56	c	4	0	0	0	0
56	e	1	0	0	0	0
56	f	1	0	0	0	0
All	All	143096	0	96028	1534	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1534 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:74:A:H62	6:A:89:G:N2	1.47	1.12
28:a:2126:U:H3	28:a:2139:G:H1	1.04	1.03
6:A:74:A:N6	6:A:89:G:H21	1.56	1.01
10:E:83:GLN:H	10:E:148:MET:HE1	1.36	0.91
28:a:1834:A:HO2'	28:a:1835:A:H8	0.92	0.90

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/51 (96%)	49 (100%)	0	0	100	100
2	1	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
3	2	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
4	3	36/38 (95%)	34 (94%)	1 (3%)	1 (3%)	4	6
5	4	66/71 (93%)	55 (83%)	10 (15%)	1 (2%)	8	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	B	222/246 (90%)	198 (89%)	23 (10%)	1 (0%)	24	46
8	C	206/228 (90%)	186 (90%)	20 (10%)	0	100	100
9	D	203/206 (98%)	188 (93%)	15 (7%)	0	100	100
10	E	152/166 (92%)	139 (91%)	13 (9%)	0	100	100
11	F	104/139 (75%)	100 (96%)	3 (3%)	1 (1%)	12	28
12	G	151/156 (97%)	141 (93%)	10 (7%)	0	100	100
13	H	127/130 (98%)	118 (93%)	8 (6%)	1 (1%)	16	34
14	I	125/130 (96%)	115 (92%)	9 (7%)	1 (1%)	16	34
15	J	97/103 (94%)	88 (91%)	9 (9%)	0	100	100
16	K	115/129 (89%)	108 (94%)	6 (5%)	1 (1%)	14	30
17	L	119/123 (97%)	110 (92%)	9 (8%)	0	100	100
18	M	111/118 (94%)	100 (90%)	11 (10%)	0	100	100
19	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
20	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
21	P	79/83 (95%)	79 (100%)	0	0	100	100
22	Q	78/88 (89%)	77 (99%)	1 (1%)	0	100	100
23	R	60/76 (79%)	55 (92%)	5 (8%)	0	100	100
24	S	81/91 (89%)	78 (96%)	3 (4%)	0	100	100
25	T	85/91 (93%)	85 (100%)	0	0	100	100
27	X	96/102 (94%)	92 (96%)	4 (4%)	0	100	100
30	c	270/273 (99%)	258 (96%)	12 (4%)	0	100	100
31	d	208/211 (99%)	192 (92%)	13 (6%)	3 (1%)	9	19
32	e	198/200 (99%)	186 (94%)	11 (6%)	1 (0%)	24	46
33	f	175/179 (98%)	154 (88%)	20 (11%)	1 (1%)	21	42
34	g	173/177 (98%)	159 (92%)	14 (8%)	0	100	100
35	h	70/148 (47%)	63 (90%)	7 (10%)	0	100	100
36	i	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
37	j	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
38	k	142/144 (99%)	132 (93%)	9 (6%)	1 (1%)	18	38
39	l	133/137 (97%)	129 (97%)	4 (3%)	0	100	100
40	m	118/129 (92%)	113 (96%)	5 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	n	113/116 (97%)	103 (91%)	10 (9%)	0	100	100
42	o	112/116 (97%)	103 (92%)	9 (8%)	0	100	100
43	p	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
44	q	101/103 (98%)	100 (99%)	0	1 (1%)	12	28
45	r	108/110 (98%)	107 (99%)	1 (1%)	0	100	100
46	s	92/99 (93%)	85 (92%)	7 (8%)	0	100	100
47	t	101/104 (97%)	93 (92%)	8 (8%)	0	100	100
48	u	188/204 (92%)	184 (98%)	4 (2%)	0	100	100
49	v	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
50	w	75/78 (96%)	75 (100%)	0	0	100	100
51	x	59/63 (94%)	59 (100%)	0	0	100	100
52	y	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
53	z	53/60 (88%)	51 (96%)	2 (4%)	0	100	100
All	All	5642/6039 (93%)	5314 (94%)	314 (6%)	14 (0%)	44	66

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	d	152	PRO
38	k	16	LYS
44	q	52	PRO
4	3	37	GLN
7	B	126	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/47 (100%)	47 (100%)	0	100	100
2	1	37/37 (100%)	35 (95%)	2 (5%)	20	42
3	2	54/55 (98%)	52 (96%)	2 (4%)	30	57

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	59/61 (97%)	57 (97%)	2 (3%)	32	60
7	B	187/202 (93%)	177 (95%)	10 (5%)	20	43
8	C	172/187 (92%)	169 (98%)	3 (2%)	53	78
9	D	173/174 (99%)	164 (95%)	9 (5%)	21	44
10	E	113/124 (91%)	107 (95%)	6 (5%)	20	43
11	F	91/119 (76%)	89 (98%)	2 (2%)	45	72
12	G	119/122 (98%)	112 (94%)	7 (6%)	18	38
13	H	108/109 (99%)	106 (98%)	2 (2%)	50	75
14	I	104/106 (98%)	99 (95%)	5 (5%)	23	47
15	J	88/92 (96%)	79 (90%)	9 (10%)	7	15
16	K	90/97 (93%)	87 (97%)	3 (3%)	33	61
17	L	105/106 (99%)	102 (97%)	3 (3%)	37	65
18	M	95/99 (96%)	93 (98%)	2 (2%)	47	73
19	N	81/82 (99%)	79 (98%)	2 (2%)	42	69
20	O	74/75 (99%)	70 (95%)	4 (5%)	20	42
21	P	64/65 (98%)	63 (98%)	1 (2%)	55	79
22	Q	73/79 (92%)	69 (94%)	4 (6%)	19	41
23	R	52/64 (81%)	50 (96%)	2 (4%)	29	56
24	S	72/78 (92%)	72 (100%)	0	100	100
25	T	69/70 (99%)	68 (99%)	1 (1%)	59	81
27	X	86/88 (98%)	82 (95%)	4 (5%)	23	48
30	c	212/213 (100%)	210 (99%)	2 (1%)	70	87
31	d	161/161 (100%)	151 (94%)	10 (6%)	16	36
32	e	158/158 (100%)	156 (99%)	2 (1%)	61	82
33	f	151/153 (99%)	145 (96%)	6 (4%)	28	55
34	g	139/141 (99%)	134 (96%)	5 (4%)	31	58
35	h	49/107 (46%)	47 (96%)	2 (4%)	27	54
36	i	119/119 (100%)	114 (96%)	5 (4%)	26	52
37	j	102/102 (100%)	96 (94%)	6 (6%)	18	38
38	k	106/106 (100%)	105 (99%)	1 (1%)	70	87

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	l	108/108 (100%)	104 (96%)	4 (4%)	30	57
40	m	99/104 (95%)	97 (98%)	2 (2%)	48	74
41	n	86/87 (99%)	84 (98%)	2 (2%)	44	71
42	o	96/98 (98%)	94 (98%)	2 (2%)	47	73
43	p	87/88 (99%)	85 (98%)	2 (2%)	44	71
44	q	86/86 (100%)	80 (93%)	6 (7%)	14	31
45	r	87/87 (100%)	85 (98%)	2 (2%)	44	71
46	s	79/82 (96%)	75 (95%)	4 (5%)	21	45
47	t	88/88 (100%)	87 (99%)	1 (1%)	65	84
48	u	155/165 (94%)	146 (94%)	9 (6%)	18	39
49	v	56/61 (92%)	53 (95%)	3 (5%)	20	42
50	w	66/67 (98%)	63 (96%)	3 (4%)	24	50
51	x	54/55 (98%)	54 (100%)	0	100	100
52	y	48/49 (98%)	48 (100%)	0	100	100
53	z	48/52 (92%)	48 (100%)	0	100	100
All	All	4687/4909 (96%)	4523 (96%)	164 (4%)	32	59

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	i	101	ILE
45	r	62	GLU
37	j	51	LYS
41	n	44	ASP
48	u	63	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
30	c	134	ASN
50	w	22	HIS
32	e	172	GLN
48	u	67	ASN
51	x	39	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	W	9/15 (60%)	1 (11%)	0
28	a	2889/2891 (99%)	604 (20%)	0
29	b	116/120 (96%)	22 (18%)	0
6	A	1534/1536 (99%)	324 (21%)	22 (1%)
All	All	4548/4562 (99%)	951 (20%)	22 (0%)

5 of 951 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	3	A
6	A	4	C
6	A	5	U
6	A	6	G
6	A	7	A

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	976	U
6	A	1164	A
6	A	1162	C
6	A	1195	A
6	A	322	C

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

38 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
28	PSU	a	2591	28	18,21,22	2.25	8 (44%)	22,30,33	1.84	4 (18%)
28	PSU	a	2567	56,28	18,21,22	2.30	9 (50%)	22,30,33	1.93	4 (18%)
28	PSU	a	1904	28	18,21,22	2.08	7 (38%)	22,30,33	1.77	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
28	5MC	a	1949	56,28	18,22,23	1.94	6 (33%)	26,32,35	1.23	2 (7%)
6	2MG	A	1201	6,56	23,26,27	2.56	6 (26%)	32,38,41	2.10	11 (34%)
6	2MG	A	1510	6,56	23,26,27	2.59	6 (26%)	32,38,41	2.18	10 (31%)
28	OMG	a	2238	56,28	23,26,27	2.40	6 (26%)	33,38,41	1.80	8 (24%)
28	PSU	a	2592	28	18,21,22	2.24	8 (44%)	22,30,33	1.89	3 (13%)
6	MA6	A	1512	6	23,26,27	1.28	3 (13%)	34,38,41	2.28	9 (26%)
28	6MZ	a	2017	28	22,25,26	2.37	3 (13%)	30,36,39	2.49	10 (33%)
28	OMU	a	2539	56,28	19,22,23	2.71	7 (36%)	26,31,34	1.76	5 (19%)
28	5MU	a	1926	56,28	19,22,23	2.65	7 (36%)	28,32,35	3.86	9 (32%)
28	PSU	a	2444	28	18,21,22	2.37	8 (44%)	22,30,33	1.85	3 (13%)
28	OMC	a	2485	28,55	19,22,23	1.83	5 (26%)	26,31,34	1.05	2 (7%)
6	MA6	A	1513	6	23,26,27	1.26	3 (13%)	34,38,41	2.27	9 (26%)
28	2MG	a	2432	28	23,26,27	2.57	7 (30%)	32,38,41	2.19	11 (34%)
6	4OC	A	1396	6	20,23,24	2.15	4 (20%)	26,32,35	1.04	3 (11%)
31	MEQ	d	150	31	8,9,10	0.90	0	5,10,12	0.66	0
28	6MZ	a	1608	28	22,25,26	2.41	4 (18%)	30,36,39	2.21	10 (33%)
28	PSU	a	1898	28	18,21,22	2.00	7 (38%)	22,30,33	1.85	3 (13%)
28	1MG	a	735	28	22,26,27	2.51	6 (27%)	33,39,42	2.00	8 (24%)
16	IAS	K	119	16	5,6,8	1.86	1 (20%)	3,6,10	3.52	1 (33%)
28	PSU	a	736	28,55	18,21,22	2.20	9 (50%)	22,30,33	1.93	4 (18%)
28	PSU	a	945	28	18,21,22	2.29	8 (44%)	22,30,33	1.96	4 (18%)
28	H2U	a	2436	28	18,21,22	4.04	5 (27%)	21,30,33	4.63	6 (28%)
6	2MG	A	960	6	23,26,27	2.58	5 (21%)	32,38,41	2.15	9 (28%)
28	3TD	a	1902	28	18,22,23	2.73	7 (38%)	22,32,35	1.75	2 (9%)
17	D2T	L	89	17	7,9,10	1.35	1 (14%)	6,11,13	1.41	1 (16%)
28	G7M	a	2056	56,28	23,26,27	2.22	5 (21%)	35,39,42	1.84	8 (22%)
28	PSU	a	2491	56,28	18,21,22	2.23	7 (38%)	22,30,33	1.87	3 (13%)
6	G7M	A	521	6,56	23,26,27	2.17	5 (21%)	35,39,42	1.89	7 (20%)
6	UR3	A	1492	6	19,22,23	2.54	5 (26%)	26,32,35	1.39	2 (7%)
39	4D4	l	82	39	9,11,12	0.80	0	8,13,15	1.70	2 (25%)
28	2MA	a	2490	56,28,55	22,25,26	1.37	4 (18%)	33,37,40	2.08	7 (21%)
6	5MC	A	961	6	18,22,23	1.91	6 (33%)	26,32,35	1.33	3 (11%)
28	2MG	a	1822	28	23,26,27	2.59	7 (30%)	32,38,41	2.01	8 (25%)
39	MS6	l	83	39	5,7,8	0.64	0	2,7,9	1.53	1 (50%)
6	PSU	A	510	6,56,55	18,21,22	2.10	9 (50%)	22,30,33	1.81	5 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	PSU	a	2591	28	-	0/7/25/26	0/2/2/2
28	PSU	a	2567	56,28	-	0/7/25/26	0/2/2/2
28	PSU	a	1904	28	-	0/7/25/26	0/2/2/2
28	5MC	a	1949	56,28	-	0/7/25/26	0/2/2/2
6	2MG	A	1201	6,56	-	0/9/27/28	0/3/3/3
6	2MG	A	1510	6,56	-	0/9/27/28	0/3/3/3
28	OMG	a	2238	56,28	-	3/9/27/28	0/3/3/3
28	PSU	a	2592	28	-	0/7/25/26	0/2/2/2
6	MA6	A	1512	6	-	0/11/29/30	0/3/3/3
28	6MZ	a	2017	28	-	2/9/27/28	0/3/3/3
28	OMU	a	2539	56,28	-	0/9/27/28	0/2/2/2
28	5MU	a	1926	56,28	-	0/7/25/26	0/2/2/2
28	PSU	a	2444	28	-	0/7/25/26	0/2/2/2
28	OMC	a	2485	28,55	-	1/9/27/28	0/2/2/2
6	MA6	A	1513	6	-	2/11/29/30	0/3/3/3
28	2MG	a	2432	28	-	2/9/27/28	0/3/3/3
6	4OC	A	1396	6	-	1/9/29/30	0/2/2/2
31	MEQ	d	150	31	-	4/8/9/11	-
28	6MZ	a	1608	28	-	0/9/27/28	0/3/3/3
28	PSU	a	1898	28	-	0/7/25/26	0/2/2/2
28	1MG	a	735	28	-	0/7/25/26	0/3/3/3
16	IAS	K	119	16	-	1/3/5/8	-
28	PSU	a	736	28,55	-	1/7/25/26	0/2/2/2
28	PSU	a	945	28	-	0/7/25/26	0/2/2/2
28	H2U	a	2436	28	-	1/7/38/39	0/2/2/2
6	2MG	A	960	6	-	0/9/27/28	0/3/3/3
28	3TD	a	1902	28	-	3/7/25/26	0/2/2/2
17	D2T	L	89	17	-	4/7/12/14	-
28	G7M	a	2056	56,28	-	2/7/25/26	0/3/3/3
28	PSU	a	2491	56,28	-	2/7/25/26	0/2/2/2
6	G7M	A	521	6,56	-	3/7/25/26	0/3/3/3
6	UR3	A	1492	6	-	0/7/25/26	0/2/2/2
39	4D4	l	82	39	-	1/11/12/14	-
28	2MA	a	2490	56,28,55	-	2/7/25/26	0/3/3/3
6	5MC	A	961	6	-	0/7/25/26	0/2/2/2
28	2MG	a	1822	28	-	0/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	MS6	1	83	39	-	2/4/6/8	-
6	PSU	A	510	6,56,55	-	0/7/25/26	0/2/2/2

The worst 5 of 204 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	2436	H2U	O4-C4	9.71	1.43	1.23
28	a	1608	6MZ	C6-N6	9.65	1.44	1.34
28	a	2017	6MZ	C6-N6	9.27	1.44	1.34
6	A	1201	2MG	O6-C6	9.00	1.40	1.23
6	A	1510	2MG	O6-C6	8.96	1.40	1.23

The worst 5 of 201 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	a	2436	H2U	C4-N3-C2	-12.41	115.49	125.79
28	a	2436	H2U	O2-C2-N1	-10.48	109.95	123.11
28	a	1926	5MU	C4-N3-C2	-8.63	116.17	127.35
28	a	1926	5MU	N3-C2-N1	8.63	126.34	114.89
28	a	1926	5MU	C5M-C5-C4	8.44	128.06	118.77

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	521	G7M	C3'-C4'-C5'-O5'
17	L	89	D2T	CA-CB-CG-OD1
17	L	89	D2T	CA-CB-CG-OD2
17	L	89	D2T	SB-CB-CG-OD2
31	d	150	MEQ	O-C-CA-CB

There are no ring outliers.

9 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	a	2591	PSU	1	0
28	a	2238	OMG	1	0
28	a	2017	6MZ	3	0
6	A	1396	4OC	2	0
31	d	150	MEQ	2	0
6	A	521	G7M	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	l	82	4D4	1	0
28	a	2490	2MA	1	0
6	A	961	5MC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 525 ligands modelled in this entry, 525 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

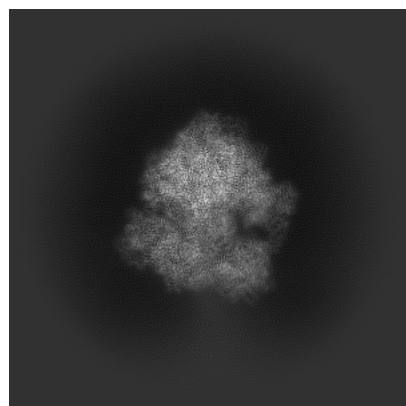
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55345. These allow visual inspection of the internal detail of the map and identification of artifacts.

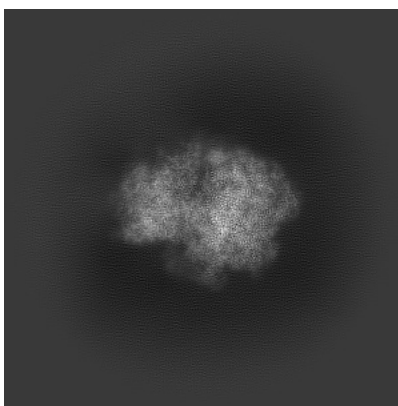
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

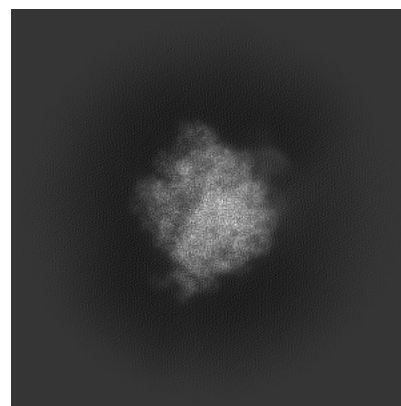
6.1.1 Primary map



X

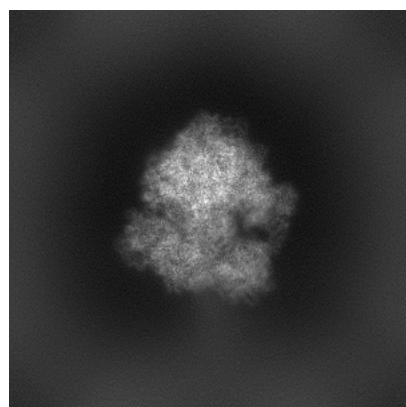


Y

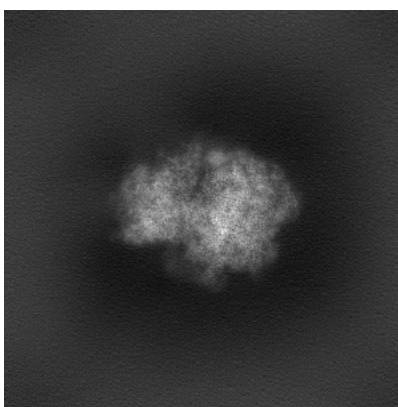


Z

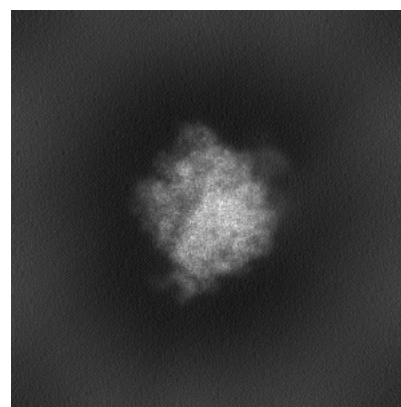
6.1.2 Raw map



X



Y

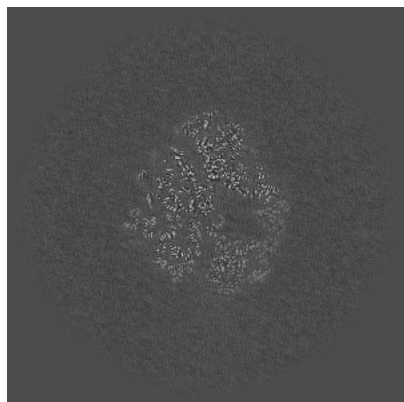


Z

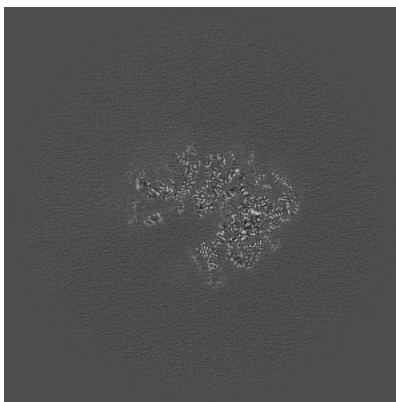
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

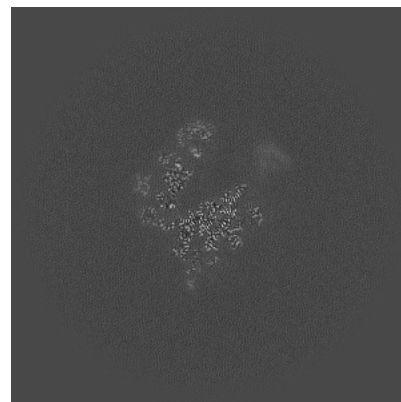
6.2.1 Primary map



X Index: 256

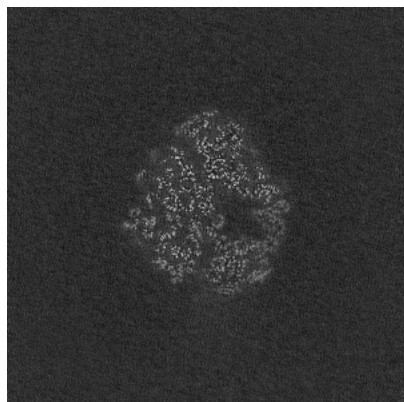


Y Index: 256

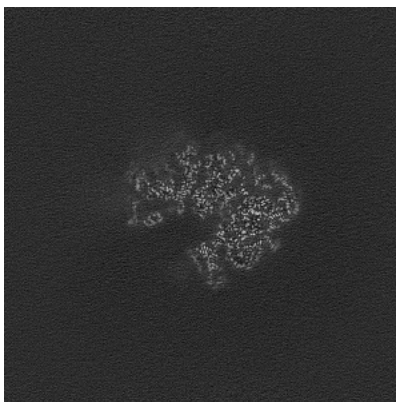


Z Index: 256

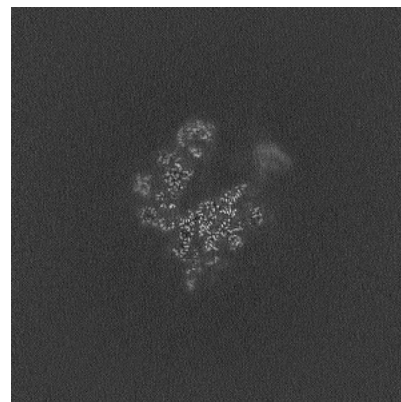
6.2.2 Raw map



X Index: 256



Y Index: 256

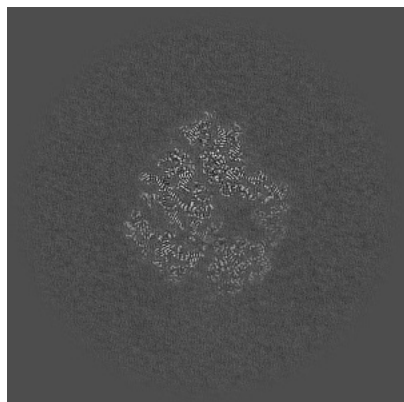


Z Index: 256

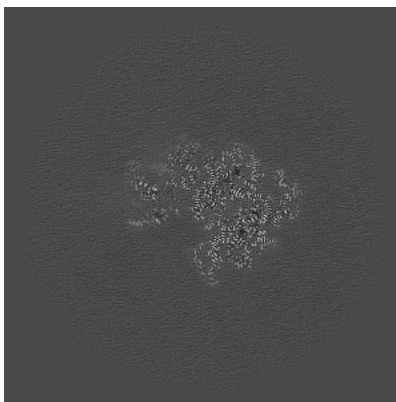
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

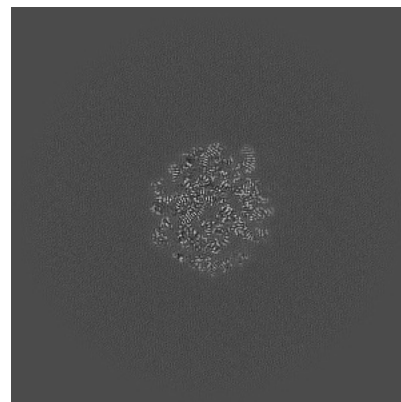
6.3.1 Primary map



X Index: 252

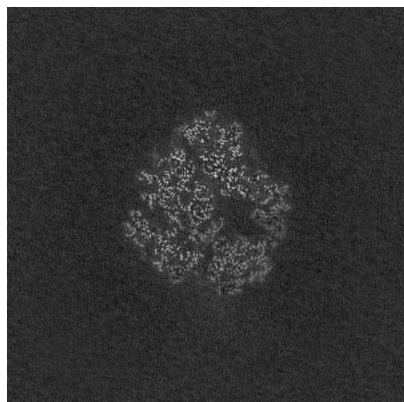


Y Index: 251

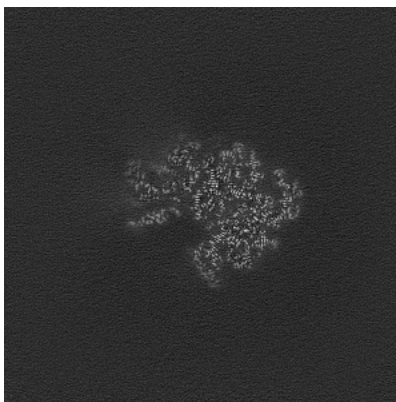


Z Index: 295

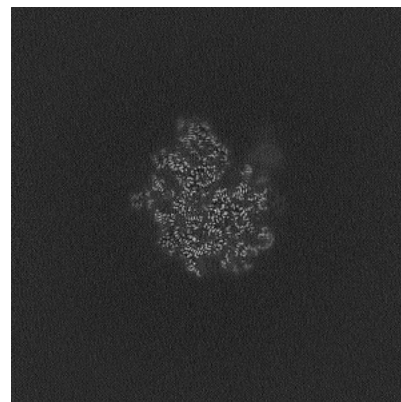
6.3.2 Raw map



X Index: 253



Y Index: 252

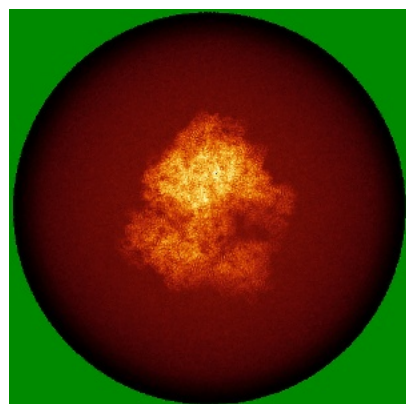


Z Index: 278

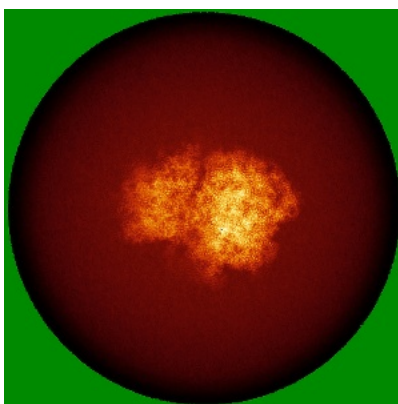
The images above show the largest variance slices of the map in three orthogonal directions.

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

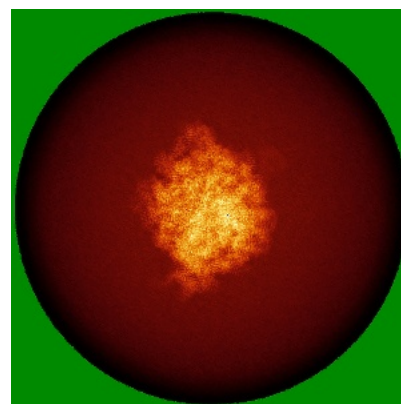
6.4.1 Primary map



X

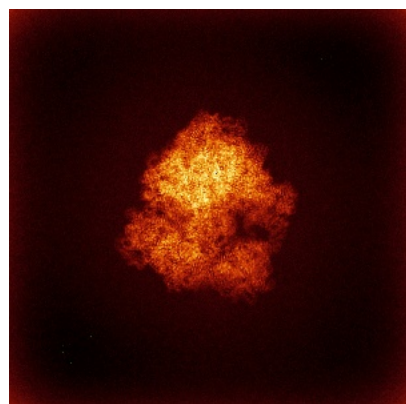


Y

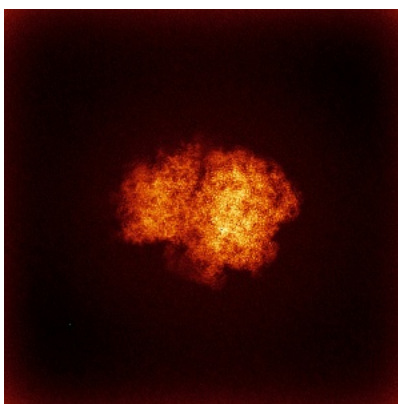


Z

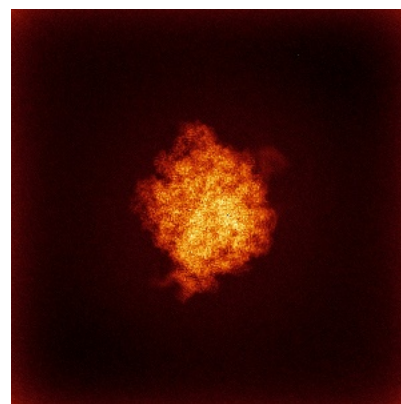
6.4.2 Raw map



X



Y

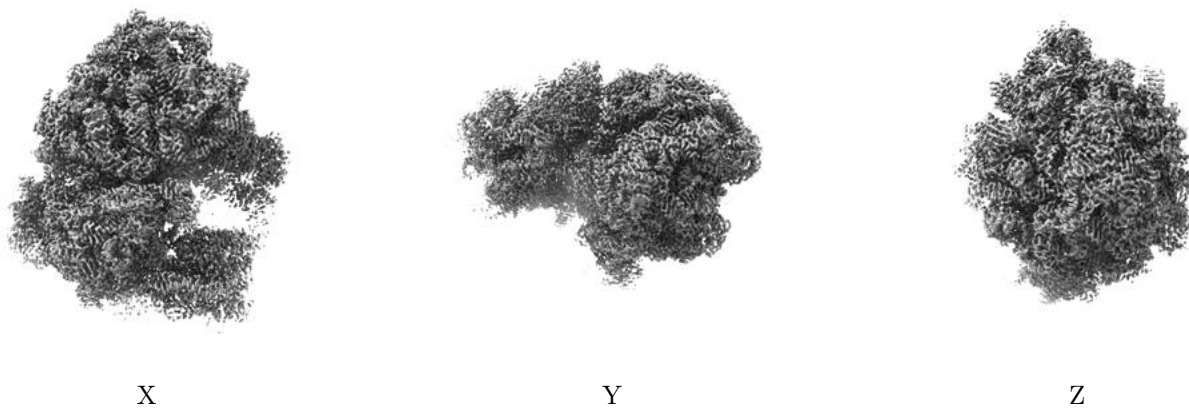


Z

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.

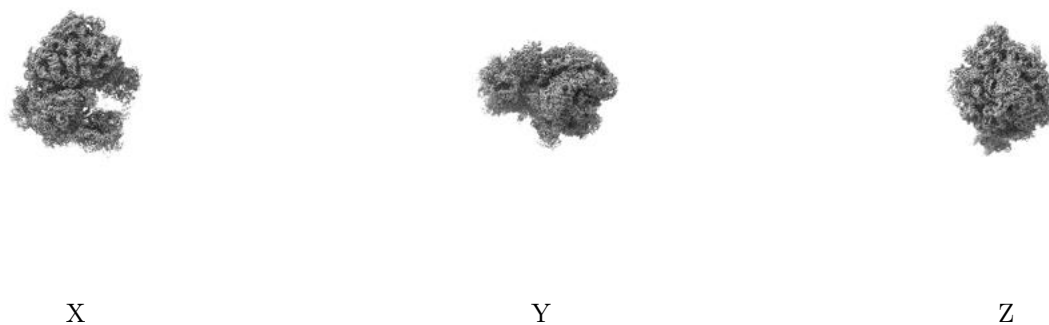
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. 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.

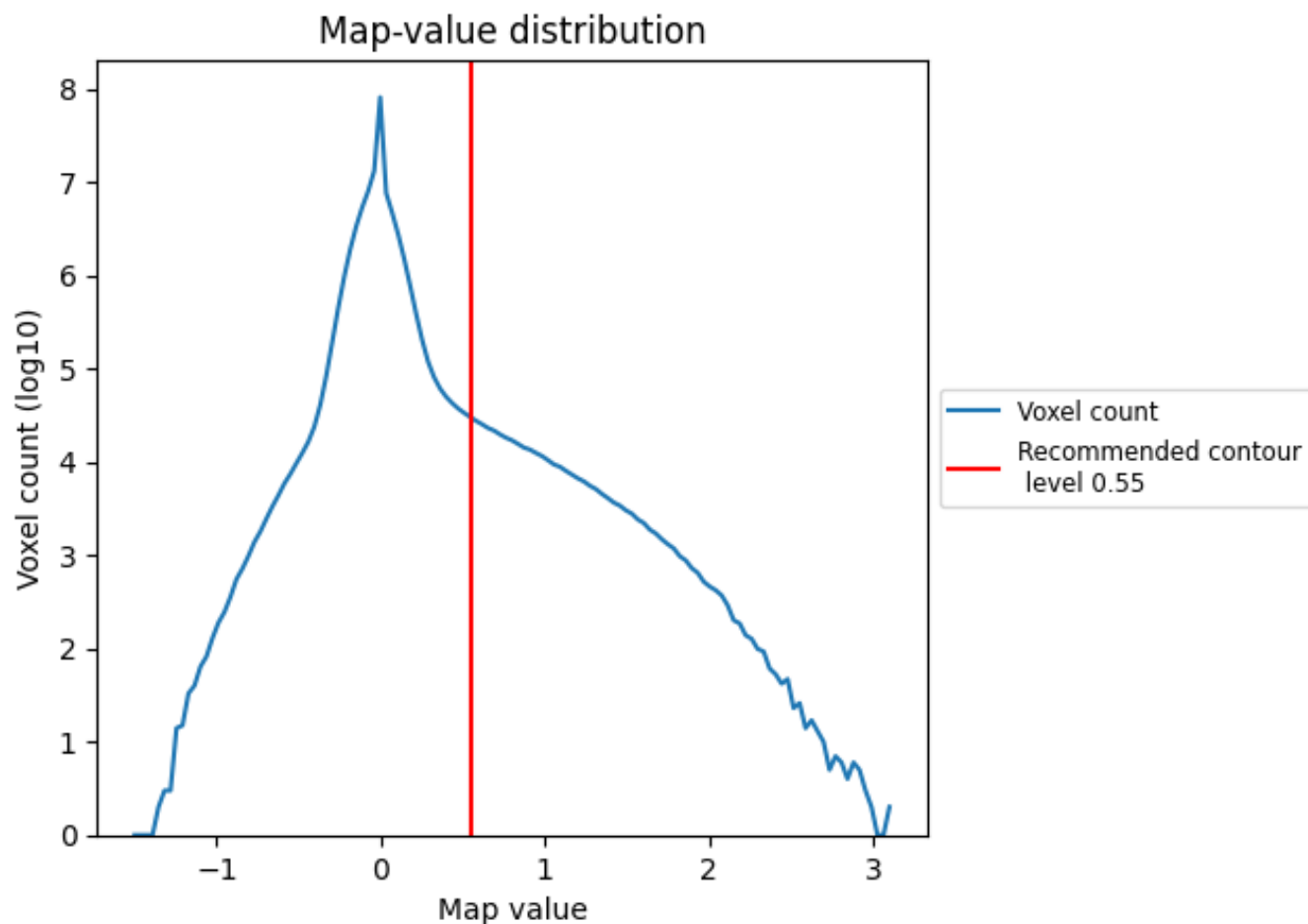
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

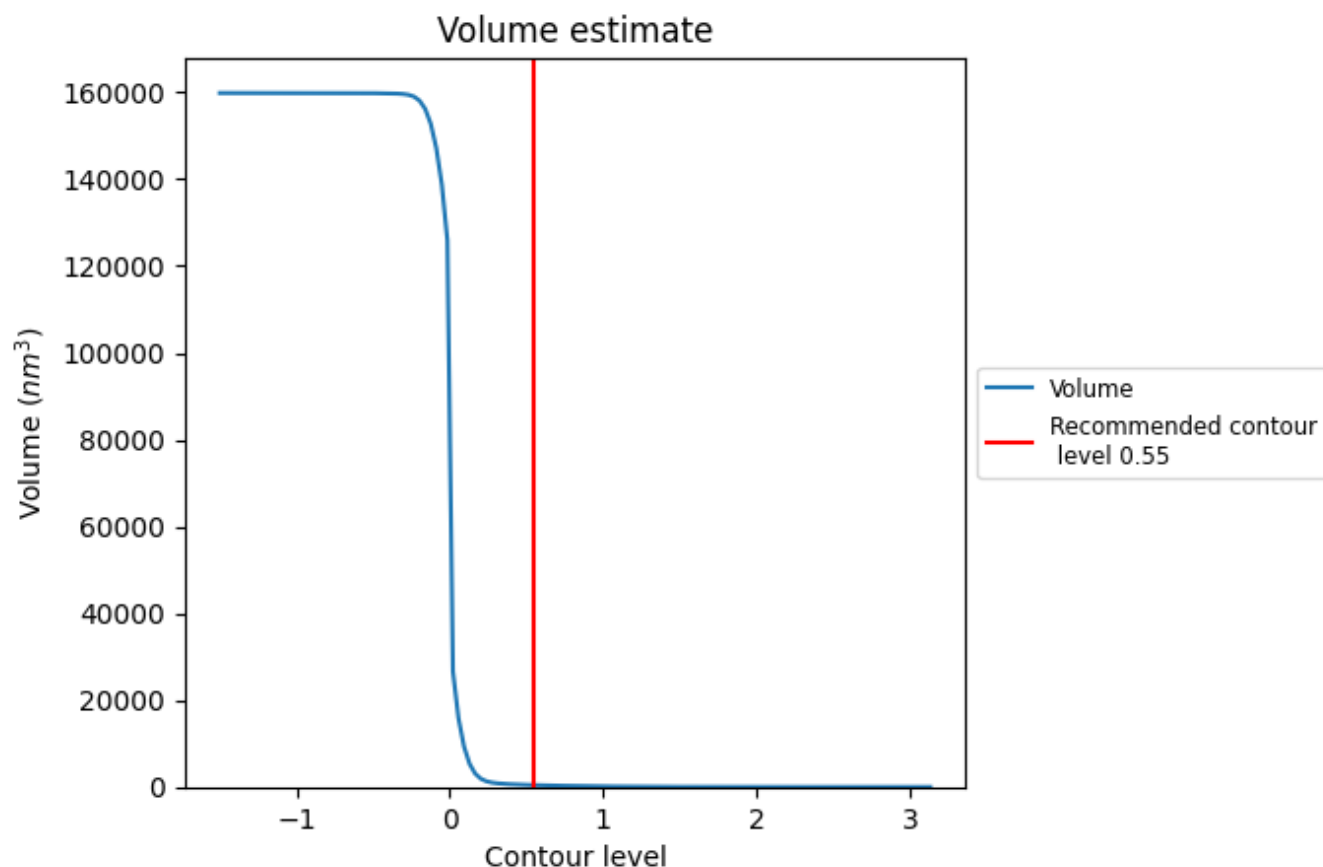
This section contains the results of statistical analysis of the map.

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.

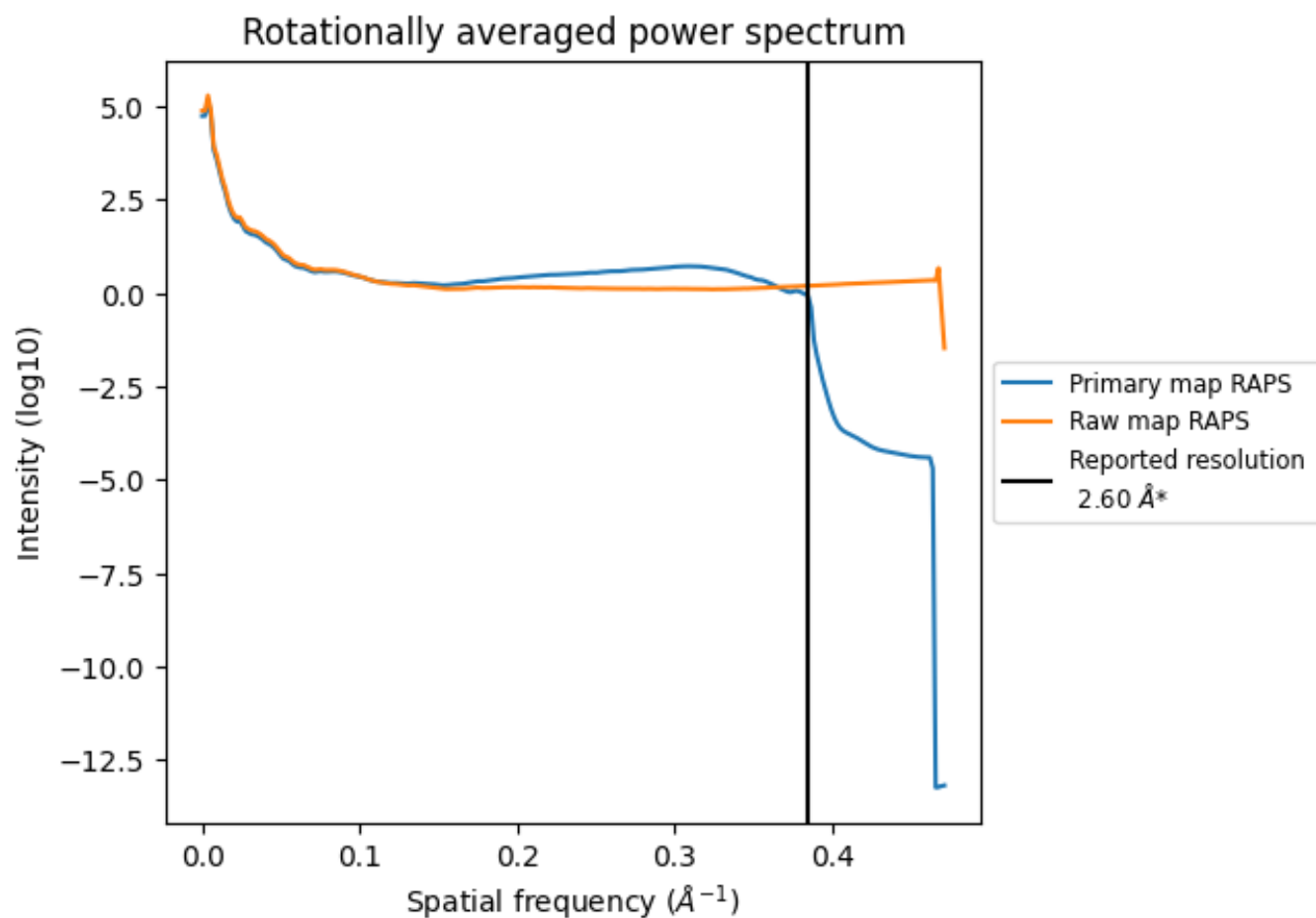
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 422 nm³; this corresponds to an approximate mass of 381 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

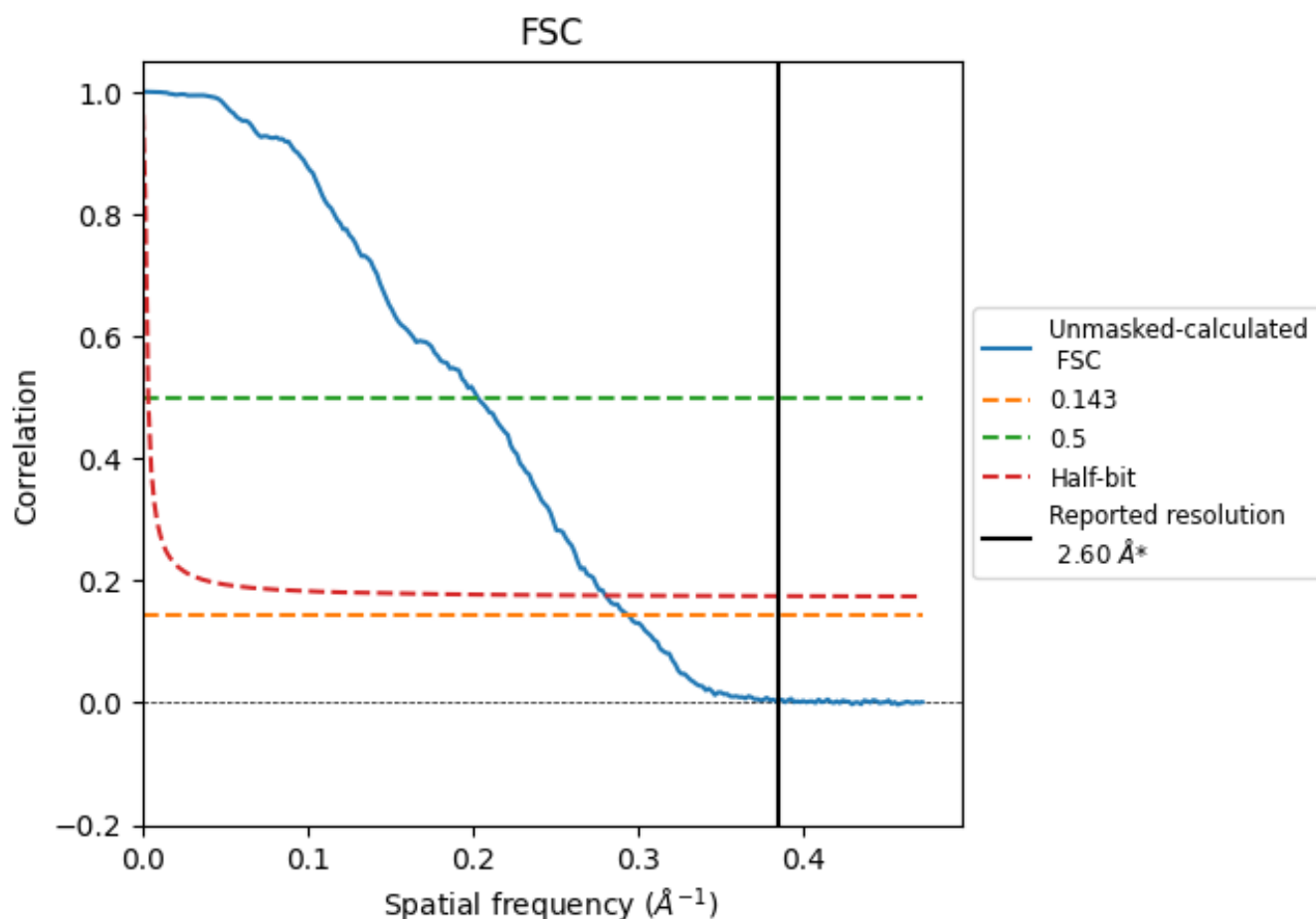


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

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 0.385 Å⁻¹

8.2 Resolution estimates [i](#)

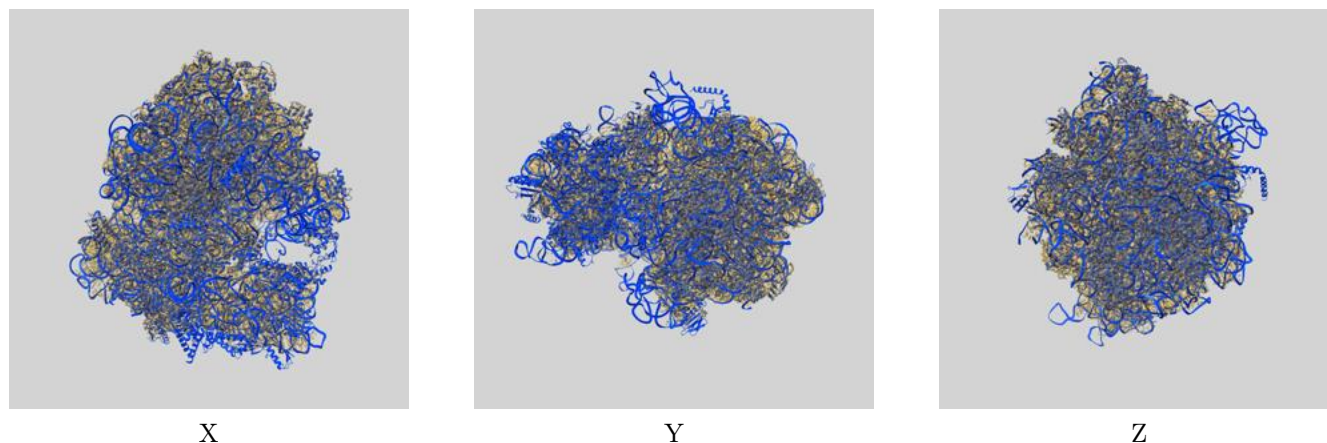
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.40	4.93	3.57

*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 3.40 differs from the reported value 2.6 by more than 10 %

9 Map-model fit [i](#)

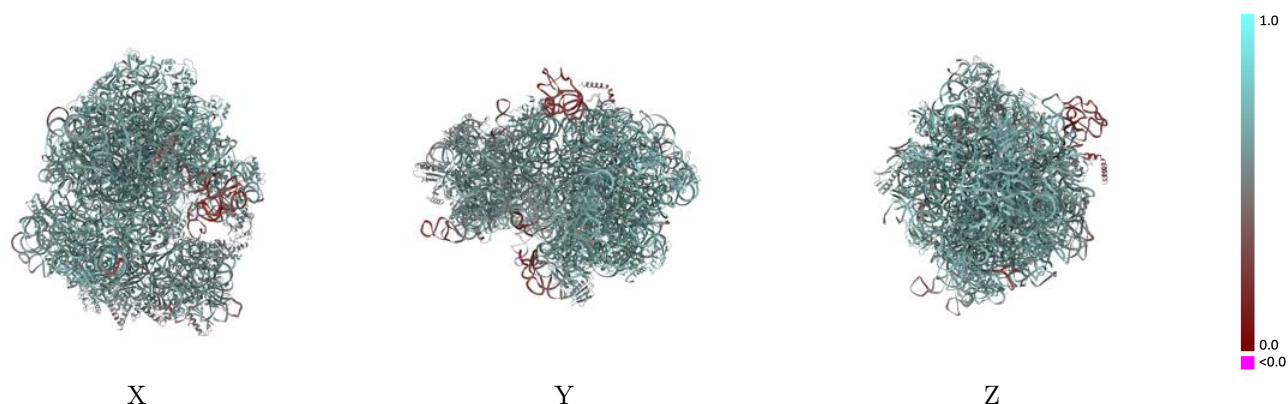
This section contains information regarding the fit between EMDB map EMD-55345 and PDB model 9SY6. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



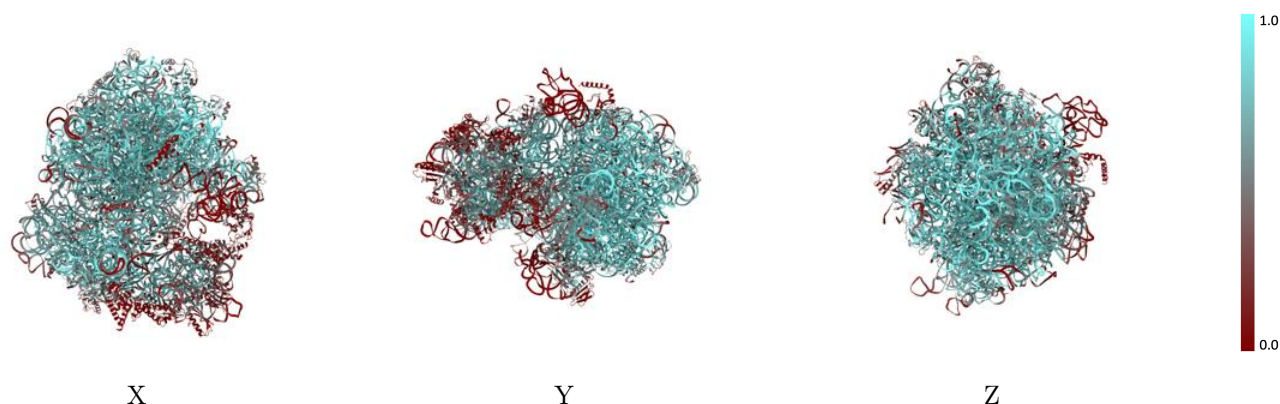
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



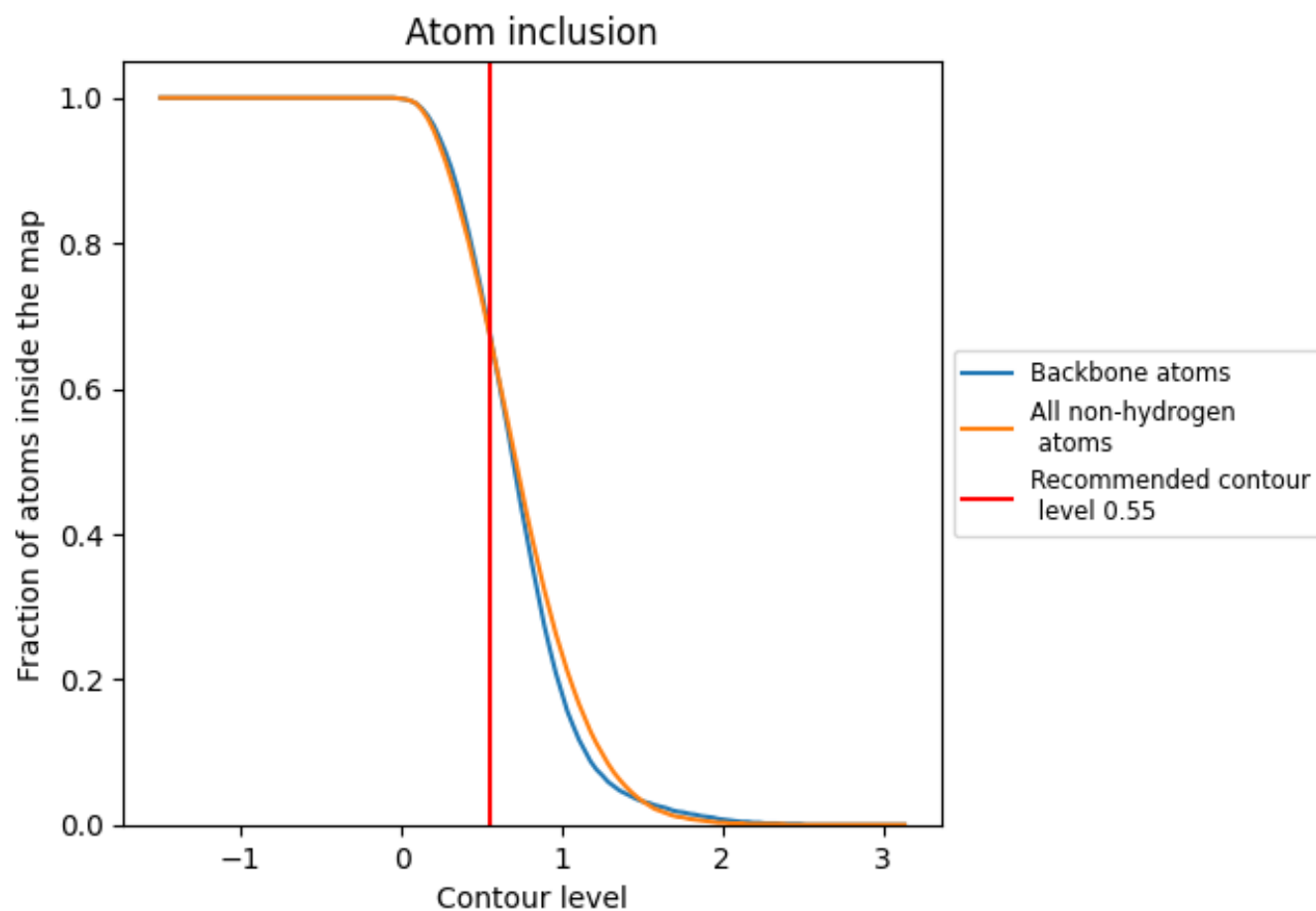
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 68% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6750	 0.6140
0	 0.4890	 0.6190
1	 0.8460	 0.6640
2	 0.8040	 0.6660
3	 0.6910	 0.6480
4	 0.0380	 0.4780
A	 0.6870	 0.6090
B	 0.0460	 0.5070
C	 0.3690	 0.5900
D	 0.4150	 0.6050
E	 0.5980	 0.6230
F	 0.3200	 0.5770
G	 0.1470	 0.5500
H	 0.6130	 0.6340
I	 0.2700	 0.5690
J	 0.2280	 0.5220
K	 0.4210	 0.5990
L	 0.6080	 0.6350
M	 0.2030	 0.5630
N	 0.3870	 0.5850
O	 0.5840	 0.6270
P	 0.6660	 0.6400
Q	 0.5480	 0.6240
R	 0.4530	 0.5900
S	 0.1930	 0.5520
T	 0.6060	 0.6310
W	 0.1280	 0.4930
X	 0.3190	 0.6010
a	 0.7890	 0.6190
b	 0.6490	 0.6090
c	 0.7690	 0.6600
d	 0.7740	 0.6520
e	 0.6920	 0.6430
f	 0.1660	 0.5450
g	 0.2980	 0.5790



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
h	 0.0020	 0.4060
i	 0.7600	 0.6530
j	 0.6930	 0.6470
k	 0.7240	 0.6500
l	 0.6850	 0.6500
m	 0.8070	 0.6550
n	 0.4780	 0.6090
o	 0.6890	 0.6510
p	 0.8000	 0.6620
q	 0.6590	 0.6470
r	 0.7300	 0.6550
s	 0.6010	 0.6270
t	 0.4820	 0.5980
u	 0.3880	 0.6100
v	 0.7460	 0.6540
w	 0.7040	 0.6500
x	 0.5580	 0.6180
y	 0.7140	 0.6490
z	 0.7110	 0.6420