



wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 03:28 pm GMT

PDB ID : 7ASP
EMDB ID : EMD-11903
Title : Staphylococcus aureus 70S after 50 minutes incubation at 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.86 Å(reported)

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

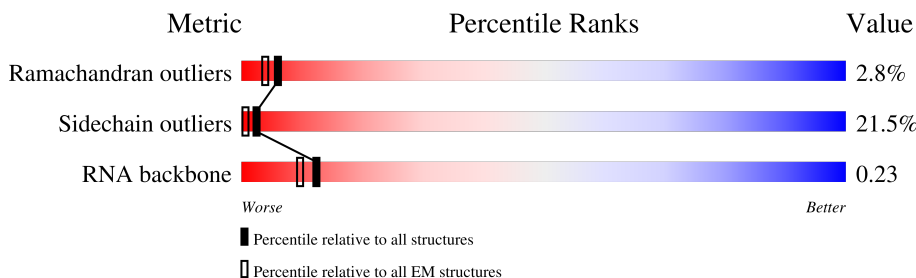
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.86 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	Y	2923	
2	X	1552	
3	3	114	
4	1	105	
4	A	105	
5	B	43	
6	2	64	
7	4	37	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	a	80	
9	b	114	
10	c	136	
11	C	274	
12	d	113	
13	D	215	
14	E	206	
15	e	60	
16	f	88	
17	g	83	
18	G	175	
19	H	145	
20	h	80	
21	I	122	
22	i	56	
23	j	78	
24	J	146	
25	k	202	
26	K	137	
27	L	120	
28	l	198	
29	m	156	
30	M	119	
31	n	95	
32	N	114	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
33	o	130	 5% 76% 22% .
34	O	116	 88% 12%
35	p	155	 26% 78% 21% ..
36	P	102	 78% 21% .
37	q	127	 26% 75% 24% .
38	Q	112	 90% 10%
39	R	89	 81% 18% .
40	S	103	 83% 17%
41	T	94	 82% 18%
42	U	79	 82% 16% .
43	V	49	 82% 16% .
44	W	67	 78% 22%
45	Z	47	 83% 17%
46	F	158	 92% 6% .

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 128828 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 RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Y	2723	Total	C	N	O	P	0	0
			58376	26062	10687	18904	2723		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	X	1447	Total	C	N	O	P	0	0
			31009	13847	5680	10037	1445		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	114	Total	C	N	O	P	0	0
			2430	1086	436	794	114		

- Molecule 4 is a protein called 50S ribosomal protein L33,50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	47	Total	C	N	O	S	0	0
			390	238	78	70	4		
4	1	58	Total	C	N	O		0	0
			449	280	85	84			

- Molecule 5 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 6 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	2	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 7 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	4	37	Total	C	N	O	S	0	0
			295	186	60	44	5		

- Molecule 8 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	a	80	Total	C	N	O	S	0	0
			626	394	116	116			

- Molecule 9 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	b	114	Total	C	N	O	S	0	0
			826	507	158	159	2		

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	c	136	Total	C	N	O	S	0	0
			976	611	190	173	2		

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	C	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	d	113	Total	C	N	O	S	0	0
			828	510	168	149	1		

- Molecule 13 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 14 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	e	60	Total	C	N	O	S	0	0
			497	314	99	79	5		

- Molecule 16 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	f	88	Total	C	N	O	S	0	0
			713	441	148	123	1		

- Molecule 17 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	g	83	Total	C	N	O	S	0	0
			537	335	105	96	1		

- Molecule 18 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	G	165	Total	C	N	O	S	0	0
			1184	739	226	216	3		

- Molecule 19 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	H	145	Total	C	N	O	S	0	0
			1143	714	208	218	3		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	h	80	Total	C	N	O		
			520	327	97	96	0	0

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	I	122	Total	C	N	O	S		
			918	572	174	168	4	0	0

- Molecule 22 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	i	56	Total	C	N	O	S		
			458	292	88	76	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	j	77	Total	C	N	O	S		
			498	300	99	98	1	0	0

- Molecule 24 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	J	146	Total	C	N	O	S		
			1086	674	214	197	1	0	0

- Molecule 25 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	k	202	Total	C	N	O	S		
			1551	979	293	278	1	0	0

- Molecule 26 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	K	137	Total	C	N	O	S		
			1071	689	203	175	4	0	0

- Molecule 27 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	L	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 28 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	l	198	Total	C	N	O		0	0
			1058	634	211	213			

- Molecule 29 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	m	156	Total	C	N	O	S	0	0
			1153	727	211	213	2		

- Molecule 30 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	119	Total	C	N	O		0	0
			882	549	174	159			

- Molecule 31 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	n	95	Total	C	N	O	S	0	0
			785	496	138	149	2		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	N	114	Total	C	N	O		0	0
			889	563	175	151			

- Molecule 33 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	o	130	Total	C	N	O	S	0	0
			1007	639	180	184	4		

- Molecule 34 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	p	154	Total	C	N	O	S	0	0
			1155	719	219	214	3		

- Molecule 36 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	q	127	Total	C	N	O	S	0	0
			975	605	194	175	1		

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	U	79	Total	C	N	O	0	0
			597	369	117	111		

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	W	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 45 is a protein called 50S ribosomalprotein L32p.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Z	47	Total	C	N	O	S	0	0
			355	219	76	58	2		

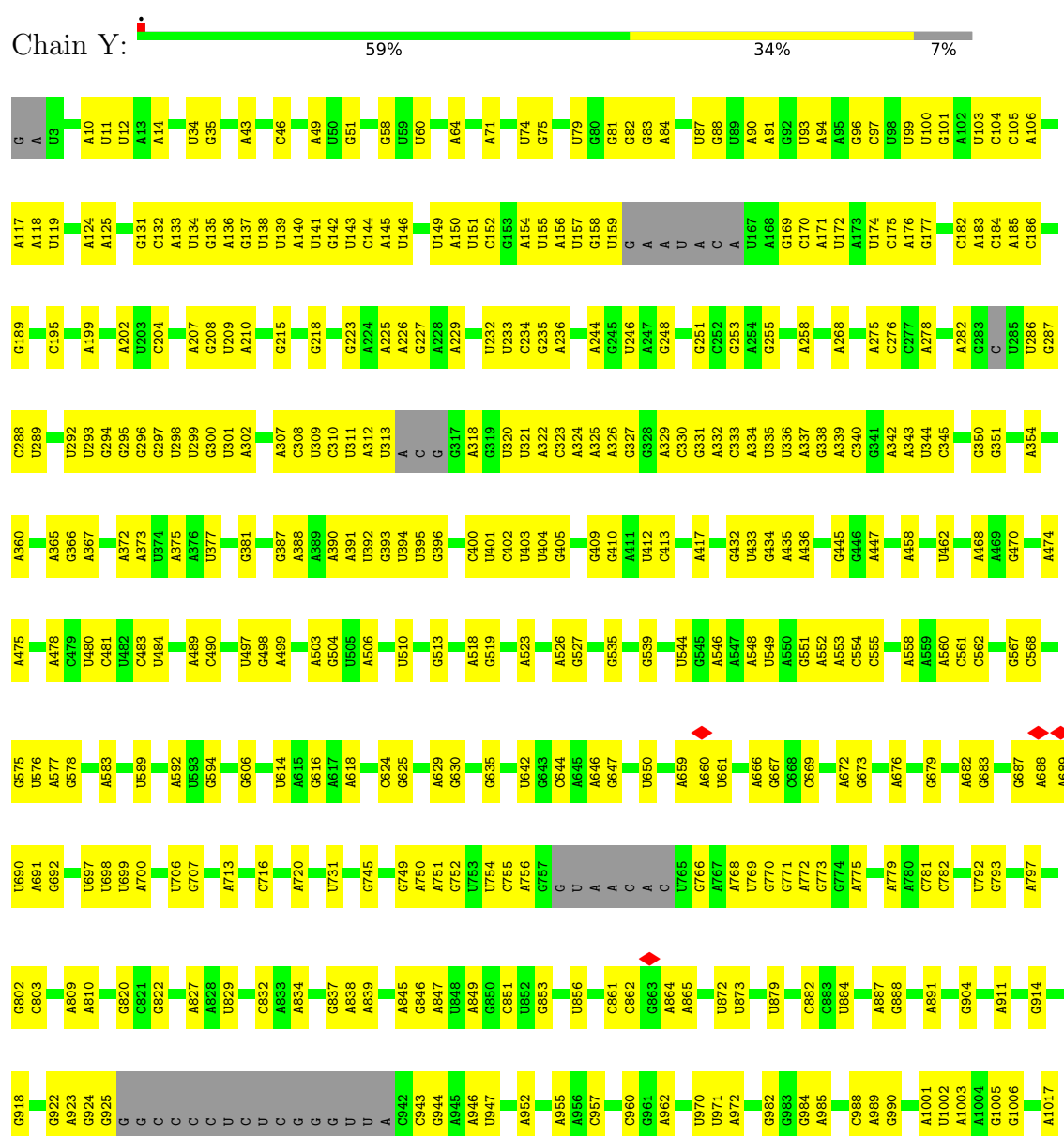
- Molecule 46 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	F	155	Total	C	N	O	0	0
			765	455	155	155		

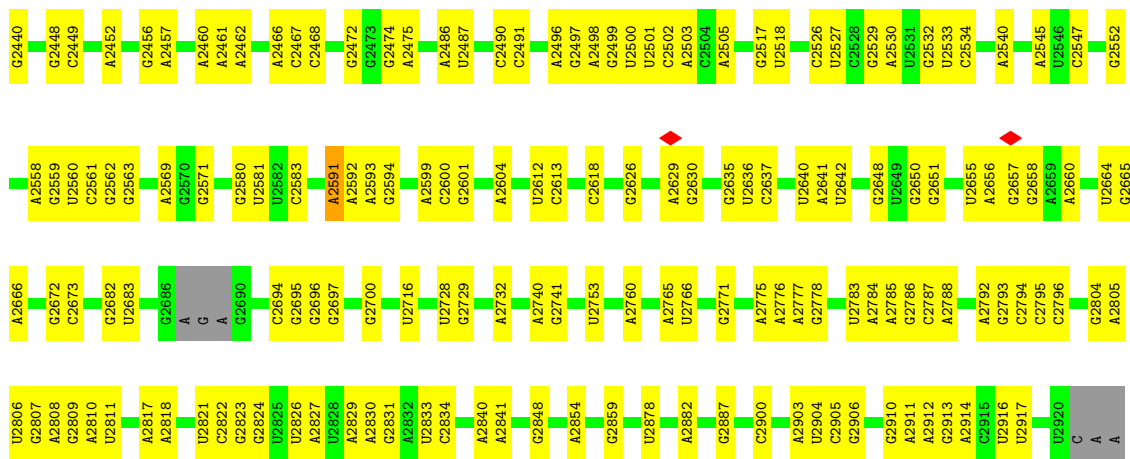
3 Residue-property plots

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

• Molecule 1: 23S rRNA

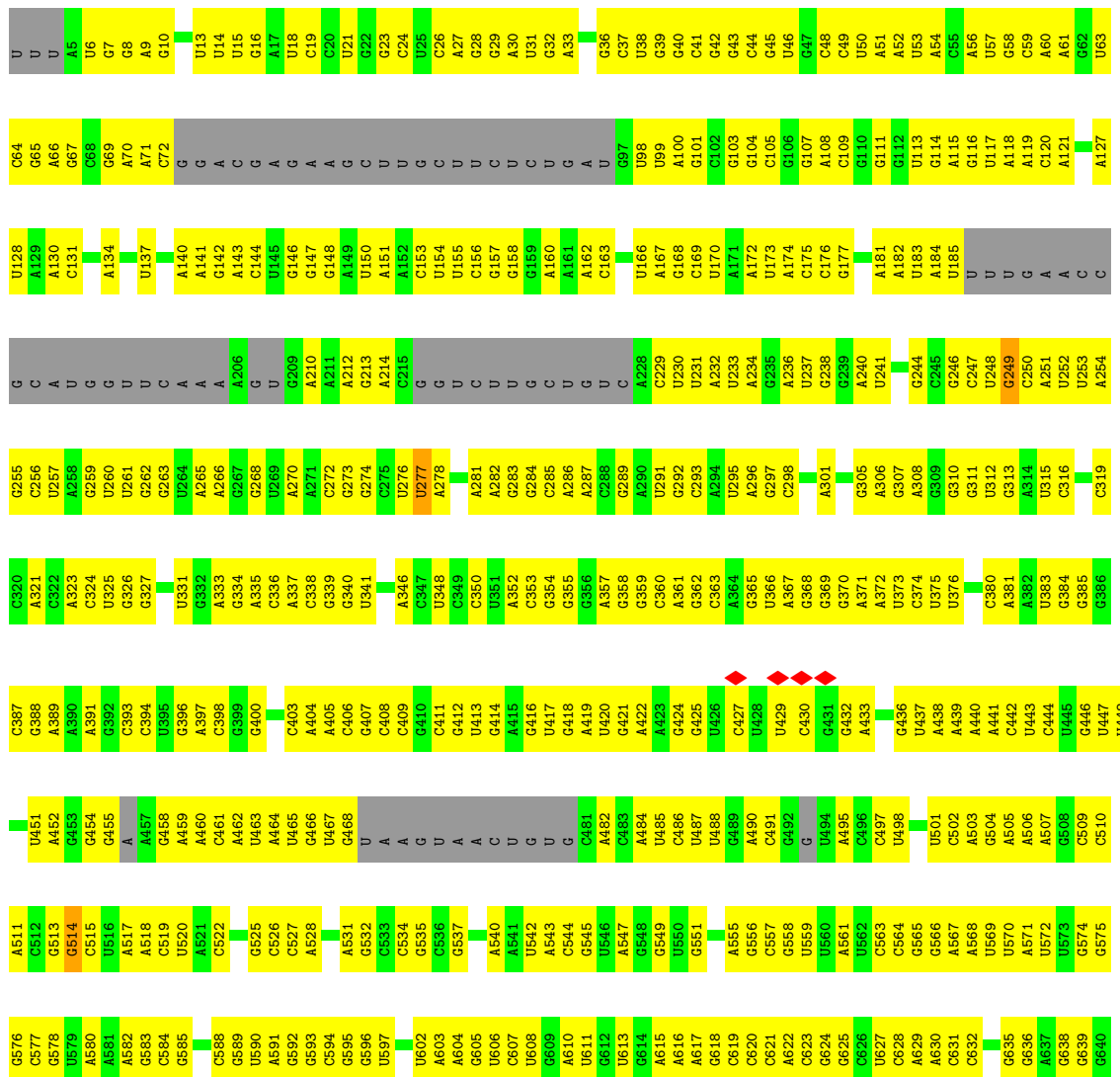


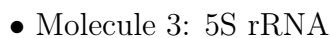
A2325	G2326	U2329	G2330	G2331	U2332	U2333	A2208	G2209	G2210	G2334	A2335	A2336	A2337	A2338	U2339	C2340	A2345	U2346	A2347	G2348	U2224	A2225	A2226	C2231	A2232	U2361	U2362	C2374	C2377	A2381	G2242	U2243	G2244	G2245	U2246	G2247	A2252	G2265	G2266	G2269	A2295	U2400	C2401	G2410	C2412	U2413	U2417	G2306	A2419	U2425	C2433	A2434	G2437						
C	U	A	C	C	C	U	G	U	A	G	C	G	A	G	U	C	C	A	A	U	C	A	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C					
A1018	A1027	G1028	C1029	C1030	G1031	A1032	G1033	A1034	C1035	A1040	U1043	A1052	A1053	A1054	U1055	U1056	A1057	U1060	G1061	U1062	G1066	U1067	G1068	G1069	A1070	U1077	G1078	C1082	G1083	G1086	C1089	A1090	G1091	A1092	C1093	A1095	C1096	U1097	A1098	G1099	G	A	U	G	U	U	G	A	A1172										
	U1176	A1177	C1178	C1179	G1180	G1181	C1342	U1343	U1185	U1186	G1357	A1358	A1359	G1360	G1361	U1363	U1366	C1367	G1207	A1208	C1214	U1217	G1218	G1219	C1220	C1221	G1229	G1245	A1263	A1267	A1275	G1276	C1277	G1278	C1422	C1423	U1280	A1285	A1291	U1292	U1293	G1294	U1446	A1447	U1448	A1449	A1450	U1451	A1314	C1315	G1453								
	A1321	A1337	U1338	U1339	U1339	G1181	C1342	U1343	U1185	U1186	G1357	A1358	A1359	G1360	G1361	U1363	U1366	C1367	G1207	A1208	C1214	U1217	G1218	G1219	C1220	C1221	G1229	G1245	A1263	A1267	A1275	G1276	C1277	G1278	C1422	C1423	U1280	A1285	A1291	U1292	U1293	G1294	U1446	A1447	U1448	A1449	A1450	U1451	A1314	C1315	G1453								
U	U	U	U	A	A1459	U1460	C1461	A1462	U1464	G1465	G1468	A1471	C1472	G1473	C1474	U1477	A1478	G1479	A1481	U1482	A1483	G1484	G1485	G1486	G1487	A1488	A1489	G1490	C1491	G1492	U1493	G1494	C1495	G1496	A1497	U1498	U1499	G1500	G1501	A1502	U1503	U1504	G1505	C1506	C1508	G1509	U1510	C1511	U1512	A1513	A1514	G1515	C1516						
A1517	G1518	U1519	A1520	A1521	G1522	G1523	U1524	U1525	G1526	A1527	G1528	U1529	A1530	U	U	A	G	G	C	C	A	U1600	U1601	U1602	U1603	C1604	A1607	C1608	U1609	G1610	C1611	C1612	G1613	A1614	G1615	A1616	A1626	G1627	A1628	U1629	A1630	G1631	A1635	U1636	A1637	G1638	G1639	U1640	G1641	C1642	C1643	C1651	G1659	G1670	A1652	A1653	A1654	U1806	A1807
C1579	A	U	U	G	A	U1586	C1587	U1588	U1589	C1590	G1591	A1592	G1593	U1594	C1595	G1596	U1597	U1598	G1599	A1600	U1601	U1602	U1603	C1604	A1607	C1608	U1609	G1610	C1611	C1612	G1613	A1614	G1615	A1616	A1626	G1627	A1628	U1629	A1630	G1631	A1635	U1636	A1637	G1638	G1639	U1640	G1641	C1642	C1643	C1651	G1659	G1670	A1652	A1653	A1654	U1806	A1807		
A1660	C1661	A1662	G1677	A1678	U1683	A1690	G1691	C1692	G1693	A1709	G1718	A1721	C1738	G1739	G1740	G1748	U1755	U1756	U1757	A1758	G1759	G1760	G1761	U1762	A1765	G1766	G1767	C1768	C1769	C1770	A1771	G1772	A1773	A1774	G1775	G1785	U1788	A1789	G1790	G1791	A1796	A1800	U1806	A1807	A1912														
A1811	A1814	A1818	C1827	U1828	A1829	G1839	A1842	U1843	G1844	A1856	G1866	C1870	U1871	A1874	A1875	G1876	U1877	U1878	U1879	A1880	A1881	G1882	A1883	G1884	G1885	A1886	G1887	U1888	G1889	U1891	U1892	A1893	G1894	C1895	C1896	C1897	C1898	U1899	G1900	C1901	G1902	A1903	A1904	U1907	A1908	A1912													
G1915	A1916	A1917	G1918	C1919	C1920	C1921	C1922	A1923	G1924	A1928	G1933	G1934	C1935	G1936	G1937	U1938	C1941	U1942	A1943	U1944	A1945	C1947	G1948	G1949	U1950	C1951	U1953	A1954	A1955	G1956	G1957	U1958	A1959	G1960	A1965	U1966	U1967	U1978	U1982	C1990	G1991	C1992	A1993	C1994	A1997	A1998	G1999												
G2002	U2003	A2004	U2011	G2012	G2013	G2014	C2015	A2016	C2017	G2018	G2019	U2020	A2024	C2033	A2050	G2054	A2058	G2059	A2060	C2063	C2070	C2077	C2082	G2083	A2087	G2088	A2089	G2096	U2103	G2120	U2124	U2125	C2126	G2127	G2128	A2132	U2135	U	G	U	U	U	U	U	U	U	C												
A	G	G	A	U	A	G	U	G	G	G	G	G	C	U	U	G	A	C	U	U	C	C	U	G	U	U	C	C	C	C	G	G	G	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C								
C	U	A	C	C	C	U	G	G	G	G	G	G	C	U	U	G	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C							
A2325	G2326	U2329	G2330	G2331	U2332	U2333	A2208	G2209	G2210	G2334	A2335	A2336	A2337	A2338	U2339	C2340	A2345	U2346	A2347	G2348	U2224	A2225	A2226	C2231	A2232	U2361	U2362	C2374	C2377	A2381	G2242	U2243	G2244	G2245	U2246	G2247	A2252	G2265	G2266	G2269	A2295	U2400	C2401	G2410	C2412	U2413	U2417	G2306	A2419	U2425	C2433	A2434	G2437						



• Molecule 2: 16S rRNA

Chain X: 26% 66% 7%




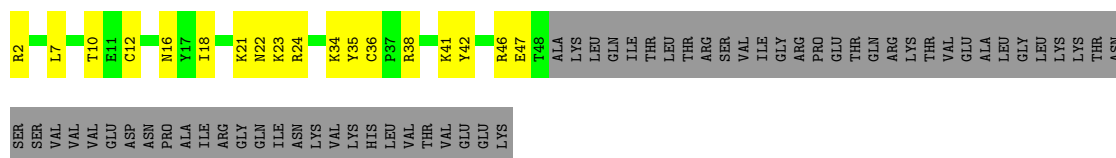


Chain 3:  59% 40%



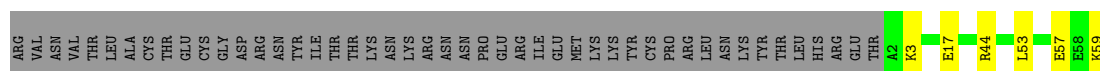
- Molecule 4: 50S ribosomal protein L33, 50S ribosomal protein L30

Chain A:  28% 17% 55%




- Molecule 4: 50S ribosomal protein L33, 50S ribosomal protein L30

Chain 1:  50% 6% 45%



- Molecule 5: 50S ribosomal protein L34

Chain B:  88% 12%




- Molecule 6: 50S ribosomal protein L35

Chain 2:  86% 14%



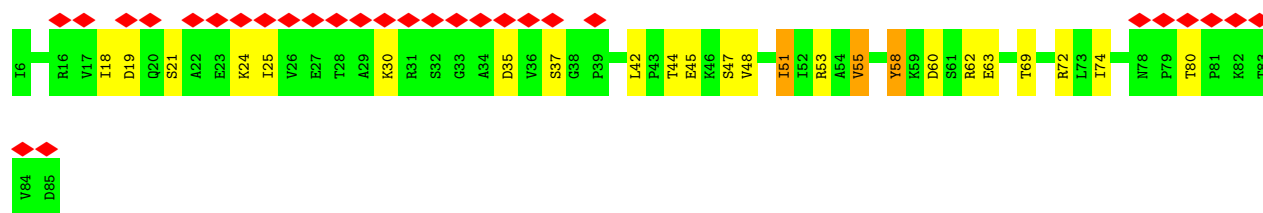
- Molecule 7: 50S ribosomal protein L36

Chain 4:  81% 19%

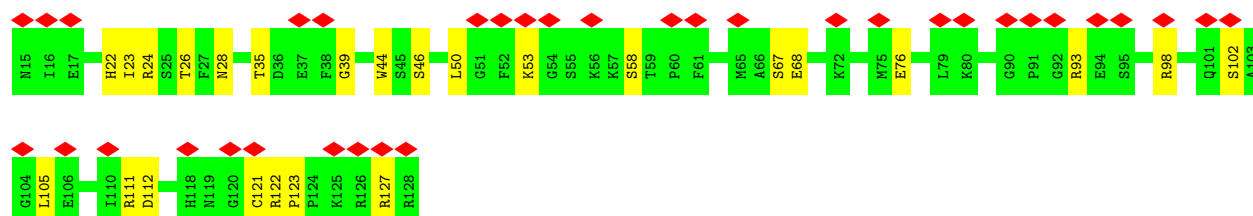
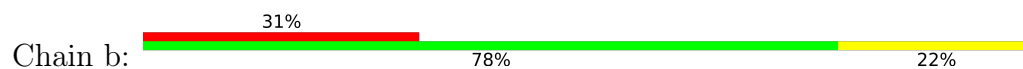


- Molecule 8: 30S ribosomal protein S10

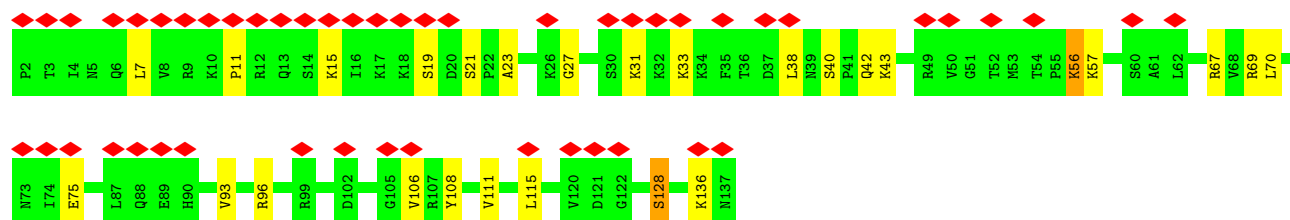
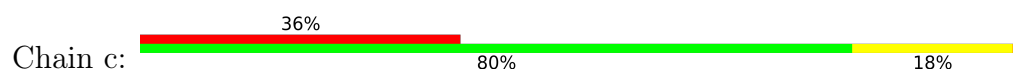
Chain a:  36% 70% 26%



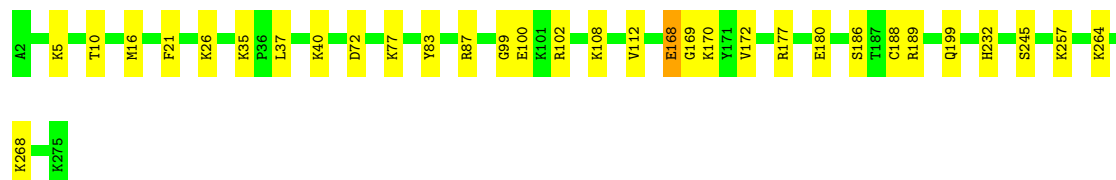
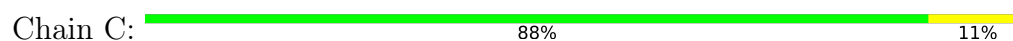
• Molecule 9: 30S ribosomal protein S11



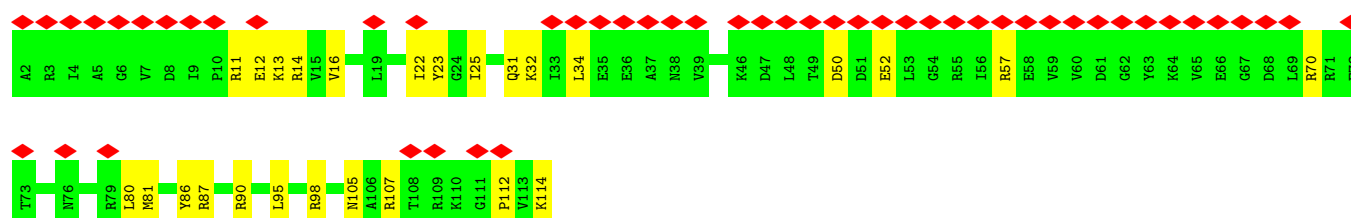
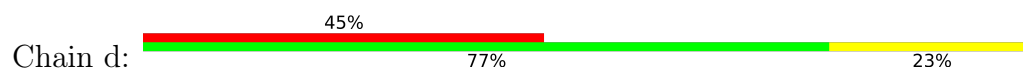
• Molecule 10: 30S ribosomal protein S12



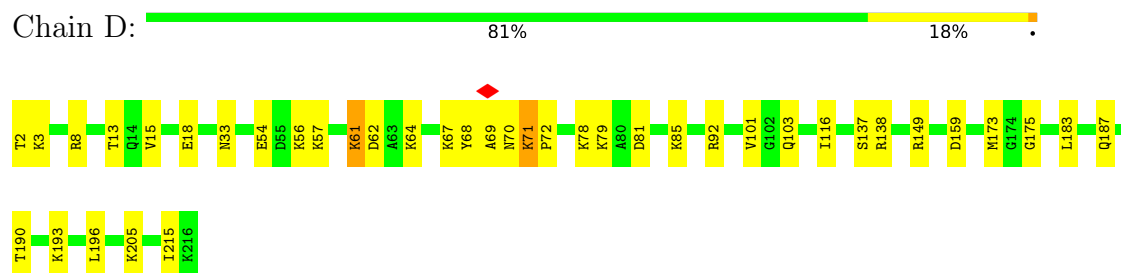
• Molecule 11: 50S ribosomal protein L2



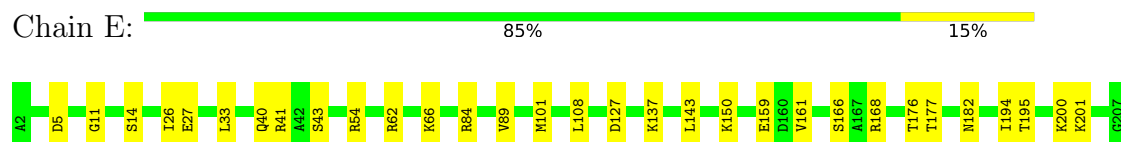
• Molecule 12: 30S ribosomal protein S13



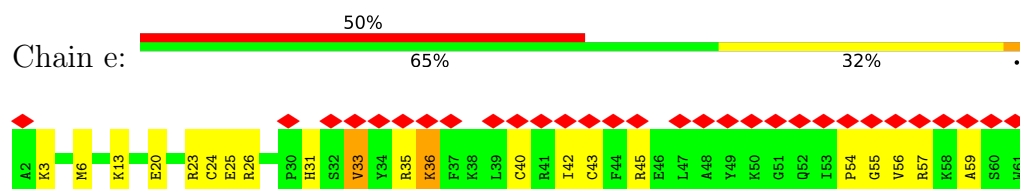
- Molecule 13: 50S ribosomal protein L3



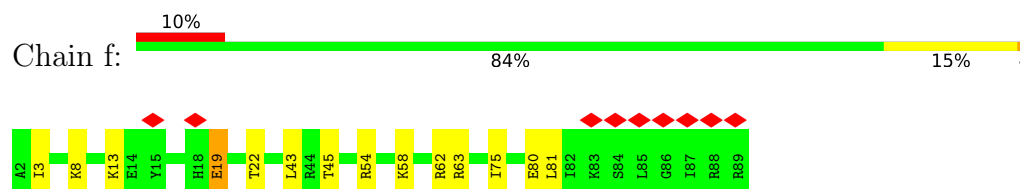
- Molecule 14: 50S ribosomal protein L4



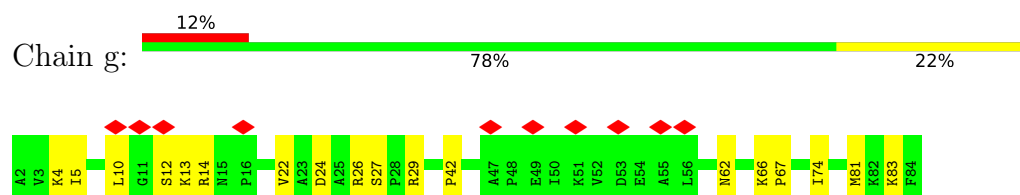
- Molecule 15: 30S ribosomal protein S14 type Z



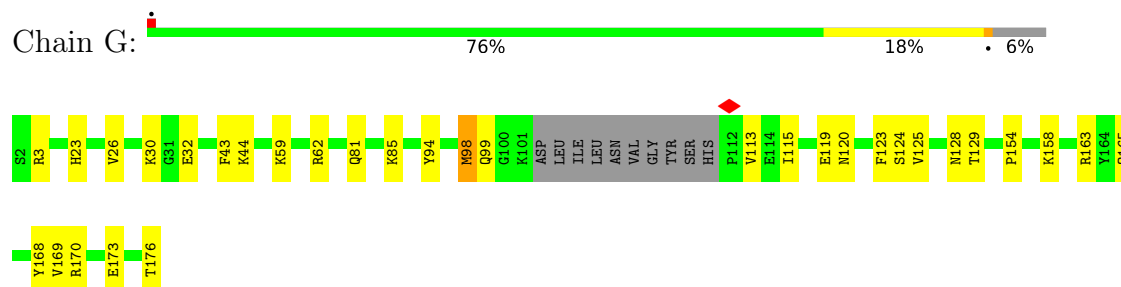
- Molecule 16: 30S ribosomal protein S15



- Molecule 17: 30S ribosomal protein S16

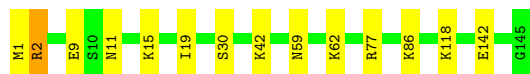


- Molecule 18: 50S ribosomal protein L6




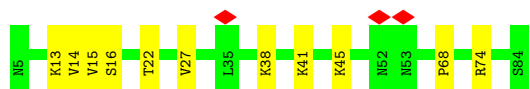
- Molecule 19: 50S ribosomal protein L13

Chain H:  90% 9% .




- Molecule 20: 30S ribosomal protein S17

Chain h:  86% 14% .



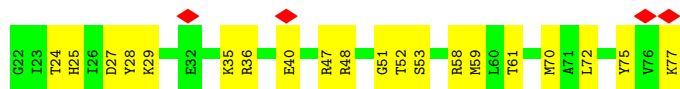
- Molecule 21: 50S ribosomal protein L14

Chain I:  86% 13% .



- Molecule 22: 30S ribosomal protein S18

Chain i:  7% 64% 36%




- Molecule 23: 30S ribosomal protein S20

Chain j:  74% 23% ..




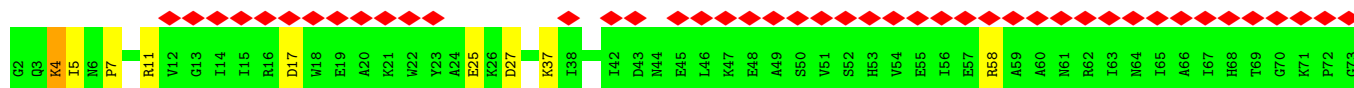
- Molecule 24: 50S ribosomal protein L15

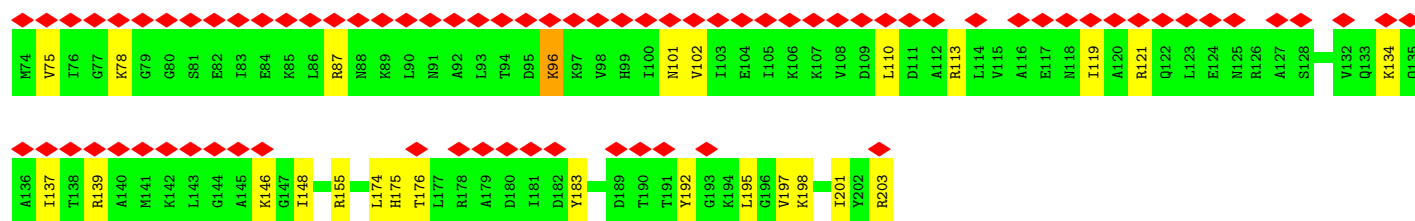
Chain J:  85% 14% .



- Molecule 25: 30S ribosomal protein S3

Chain k:  60% 83% 16% .





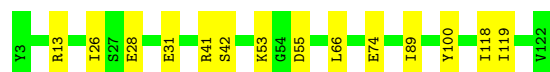
- Molecule 26: 50S ribosomal protein L16

Chain K: 86% 14%



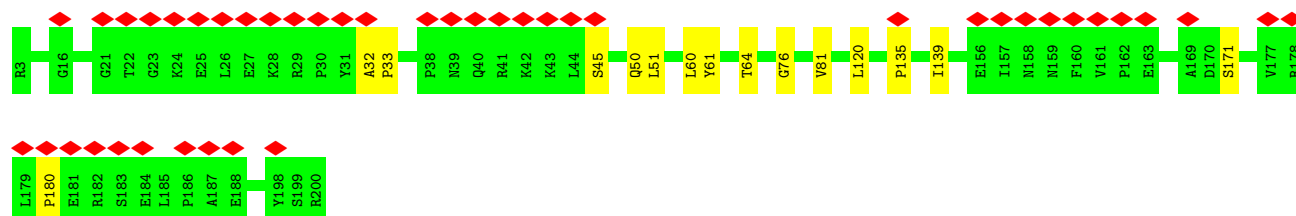
- Molecule 27: 50S ribosomal protein L17

Chain L: 88% 12%



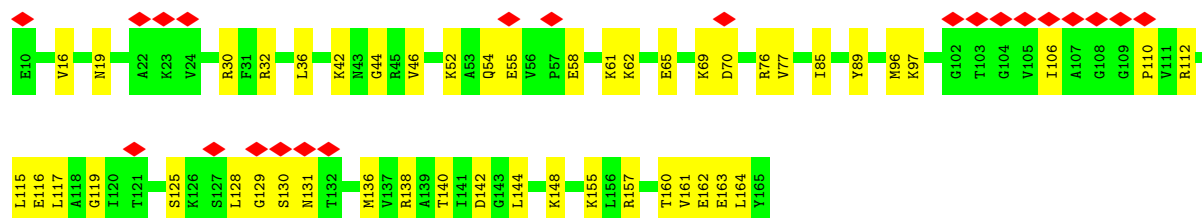
- Molecule 28: 30S ribosomal protein S4

Chain l: 22% 92% 8%



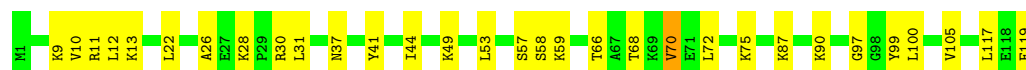
- Molecule 29: 30S ribosomal protein S5

Chain m: 14% 69% 31%

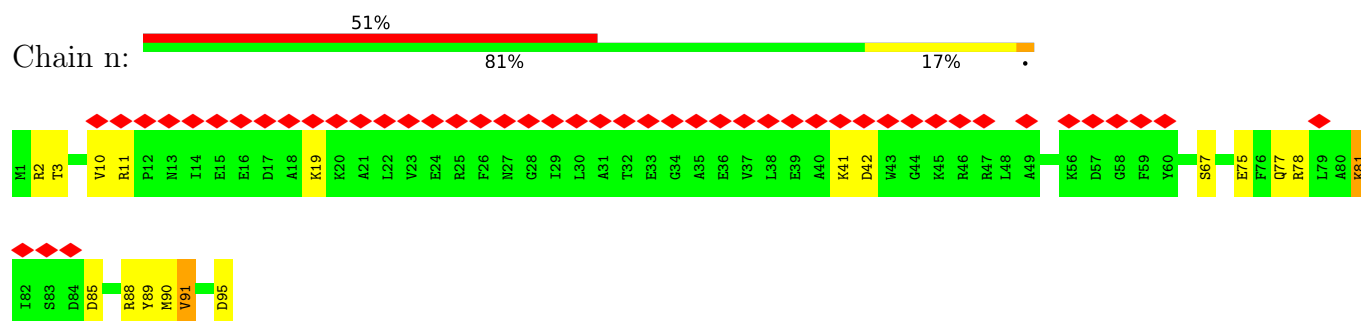


- Molecule 30: 50S ribosomal protein L18

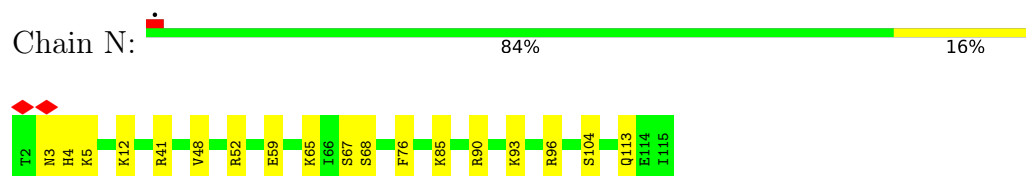
Chain M: 74% 25%



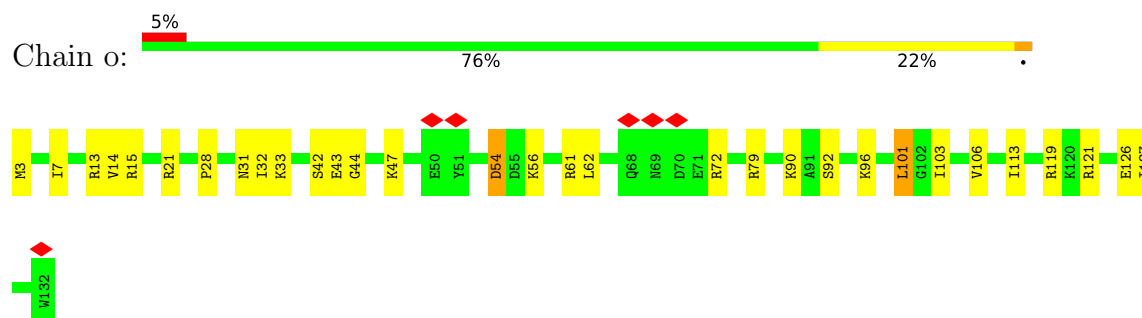
- Molecule 31: 30S ribosomal protein S6



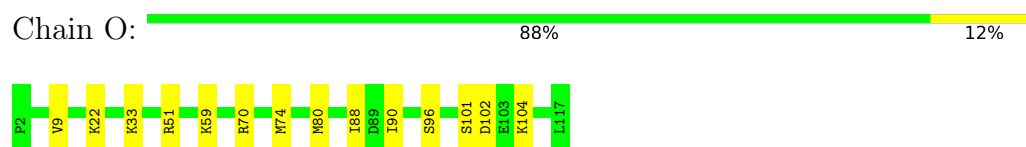
- Molecule 32: 50S ribosomal protein L19



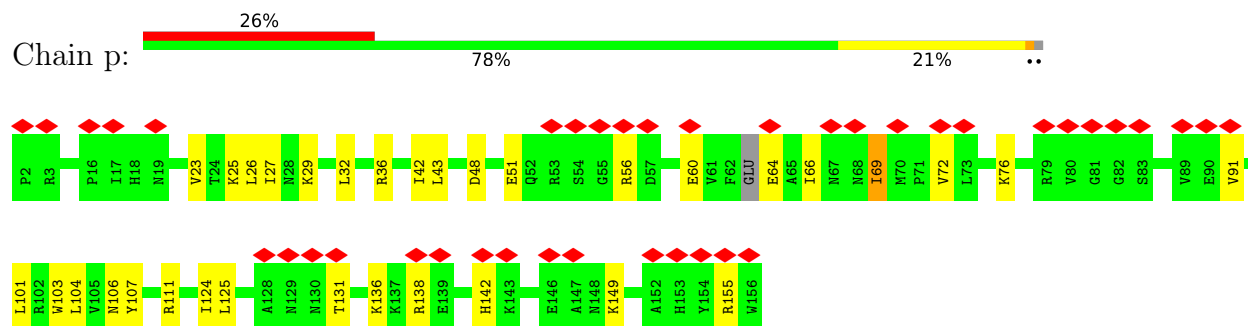
- Molecule 33: 30S ribosomal protein S8




- Molecule 34: 50S ribosomal protein L20



- Molecule 35: 30S ribosomal protein S7




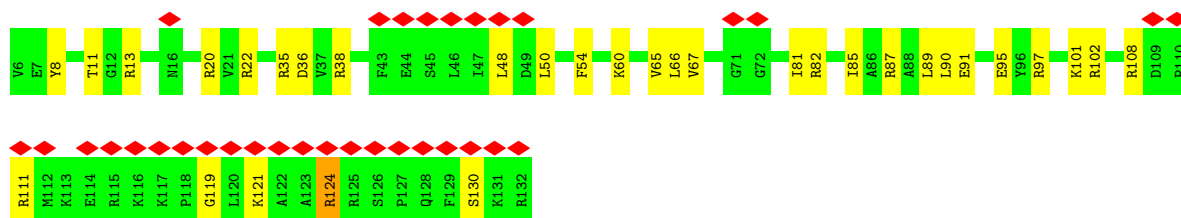
- Molecule 36: 50S ribosomal protein L21

Chain P:  78% 21% .




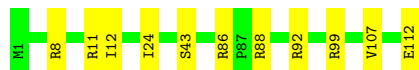
- Molecule 37: 30S ribosomal protein S9

Chain q:  26% 75% 24% .




- Molecule 38: 50S ribosomal protein L22

Chain Q:  90% 10% .




- Molecule 39: 50S ribosomal protein L23

Chain R:  81% 18% .




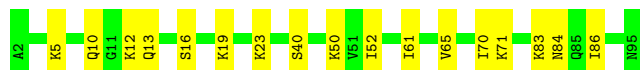
- Molecule 40: 50S ribosomal protein L24

Chain S:  83% 17% .




- Molecule 41: 50S ribosomal protein L25

Chain T:  82% 18% .

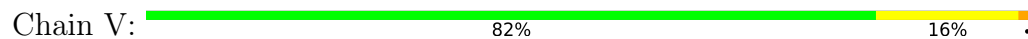


- Molecule 42: 50S ribosomal protein L27

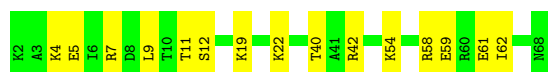
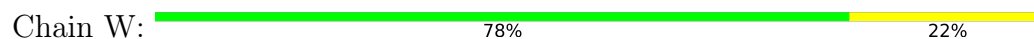
Chain U:  82% 16% .



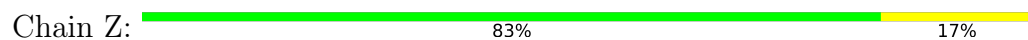
- Molecule 43: 50S ribosomal protein L28



- Molecule 44: 50S ribosomal protein L29



- Molecule 45: 50S ribosomal protein L32p



- Molecule 46: 50S ribosomal protein L5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	192105	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.076	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0045	Depositor
Map size (Å)	408.0, 408.0, 408.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	Y	0.21	0/65368	0.63	2/101922 (0.0%)
2	X	0.20	0/34716	0.64	6/54120 (0.0%)
3	3	0.21	0/2717	0.64	1/4232 (0.0%)
4	1	0.65	0/451	0.57	0/606
4	A	0.62	0/395	0.57	0/530
5	B	0.61	0/371	0.56	0/484
6	2	0.62	0/526	0.57	0/690
7	4	0.64	0/298	0.57	0/392
8	a	0.67	0/637	0.62	0/865
9	b	0.67	0/840	0.60	0/1137
10	c	0.68	0/991	0.60	0/1337
11	C	0.64	0/2129	0.60	0/2858
12	d	0.68	0/835	0.59	0/1123
13	D	0.65	0/1651	0.59	0/2215
14	E	0.64	0/1595	0.57	0/2154
15	e	0.63	0/507	0.58	0/674
16	f	0.65	0/721	0.56	0/964
17	g	0.71	0/541	0.62	0/733
18	G	0.69	0/1199	0.62	0/1621
19	H	0.64	0/1165	0.57	0/1570
20	h	0.72	0/527	0.60	0/721
21	I	0.65	0/925	0.58	0/1242
22	i	0.64	0/465	0.56	0/620
23	j	0.72	0/496	0.71	0/669
24	J	0.65	0/1100	0.59	0/1467
25	k	0.66	0/1573	0.59	0/2121
26	K	0.64	0/1095	0.58	0/1472
27	L	0.65	0/936	0.57	0/1253
28	l	0.78	0/1062	0.64	0/1465
29	m	0.67	0/1167	0.61	0/1576
30	M	0.66	0/891	0.59	0/1194
31	n	0.64	0/796	0.56	0/1069
32	N	0.64	0/901	0.56	0/1209
33	o	0.66	0/1019	0.59	0/1371

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	O	0.62	0/954	0.55	0/1264
35	p	0.67	0/1170	0.65	0/1580
36	P	0.64	0/800	0.57	0/1070
37	q	0.65	0/990	0.60	0/1332
38	Q	0.64	0/862	0.57	0/1161
39	R	0.64	0/723	0.56	0/966
40	S	0.66	0/779	0.59	0/1043
41	T	0.67	0/730	0.59	0/981
42	U	0.65	0/603	0.58	0/802
43	V	0.65	0/384	0.58	0/515
44	W	0.65	0/542	0.55	0/722
45	Z	0.65	0/361	0.59	0/482
46	F	0.84	0/763	0.83	0/1059
All	All	0.39	0/140267	0.62	9/210653 (0.0%)

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Y	2591	A	C2'-C3'-O3'	7.59	126.20	109.50
3	3	26	C	C2'-C3'-O3'	7.59	126.20	109.50
2	X	1431	U	C2'-C3'-O3'	7.43	125.85	109.50
2	X	514	G	C2'-C3'-O3'	6.51	124.11	113.70
2	X	277	U	C2'-C3'-O3'	6.34	123.84	113.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [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	
4	1	56/105 (53%)	51 (91%)	5 (9%)	0	100	100
4	A	45/105 (43%)	41 (91%)	3 (7%)	1 (2%)	5	12
5	B	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
6	2	62/64 (97%)	48 (77%)	13 (21%)	1 (2%)	8	18
7	4	35/37 (95%)	32 (91%)	2 (6%)	1 (3%)	3	8
8	a	78/80 (98%)	51 (65%)	22 (28%)	5 (6%)	1	1
9	b	112/114 (98%)	85 (76%)	22 (20%)	5 (4%)	2	3
10	c	134/136 (98%)	101 (75%)	26 (19%)	7 (5%)	1	2
11	C	272/274 (99%)	230 (85%)	38 (14%)	4 (2%)	8	19
12	d	111/113 (98%)	88 (79%)	20 (18%)	3 (3%)	4	10
13	D	213/215 (99%)	179 (84%)	27 (13%)	7 (3%)	3	7
14	E	204/206 (99%)	181 (89%)	21 (10%)	2 (1%)	13	26
15	e	58/60 (97%)	44 (76%)	9 (16%)	5 (9%)	0	1
16	f	86/88 (98%)	73 (85%)	12 (14%)	1 (1%)	11	23
17	g	81/83 (98%)	54 (67%)	22 (27%)	5 (6%)	1	2
18	G	161/175 (92%)	126 (78%)	31 (19%)	4 (2%)	4	10
19	H	143/145 (99%)	125 (87%)	15 (10%)	3 (2%)	5	13
20	h	78/80 (98%)	60 (77%)	17 (22%)	1 (1%)	10	22
21	I	120/122 (98%)	105 (88%)	14 (12%)	1 (1%)	16	32
22	i	54/56 (96%)	42 (78%)	10 (18%)	2 (4%)	2	5
23	j	73/78 (94%)	56 (77%)	15 (20%)	2 (3%)	4	10
24	J	144/146 (99%)	123 (85%)	18 (12%)	3 (2%)	5	13
25	k	200/202 (99%)	159 (80%)	35 (18%)	6 (3%)	3	8
26	K	135/137 (98%)	119 (88%)	13 (10%)	3 (2%)	5	12
27	L	118/120 (98%)	108 (92%)	9 (8%)	1 (1%)	16	32
28	l	196/198 (99%)	154 (79%)	33 (17%)	9 (5%)	2	3
29	m	154/156 (99%)	116 (75%)	32 (21%)	6 (4%)	2	5
30	M	117/119 (98%)	98 (84%)	15 (13%)	4 (3%)	3	6
31	n	93/95 (98%)	72 (77%)	19 (20%)	2 (2%)	5	12
32	N	112/114 (98%)	100 (89%)	10 (9%)	2 (2%)	7	16

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
33	o	128/130 (98%)	88 (69%)	35 (27%)	5 (4%)	2	5
34	O	114/116 (98%)	108 (95%)	3 (3%)	3 (3%)	4	10
35	p	150/155 (97%)	127 (85%)	20 (13%)	3 (2%)	6	14
36	P	100/102 (98%)	84 (84%)	14 (14%)	2 (2%)	6	14
37	q	125/127 (98%)	98 (78%)	23 (18%)	4 (3%)	3	7
38	Q	110/112 (98%)	96 (87%)	13 (12%)	1 (1%)	14	29
39	R	87/89 (98%)	77 (88%)	8 (9%)	2 (2%)	5	11
40	S	101/103 (98%)	83 (82%)	14 (14%)	4 (4%)	2	4
41	T	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	5	12
42	U	77/79 (98%)	69 (90%)	6 (8%)	2 (3%)	4	10
43	V	47/49 (96%)	39 (83%)	6 (13%)	2 (4%)	2	4
44	W	65/67 (97%)	58 (89%)	6 (9%)	1 (2%)	8	19
45	Z	45/47 (96%)	38 (84%)	5 (11%)	2 (4%)	2	4
46	F	151/158 (96%)	110 (73%)	32 (21%)	9 (6%)	1	2
All	All	4878/5094 (96%)	4016 (82%)	724 (15%)	138 (3%)	6	9

5 of 138 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	a	63	GLU
10	c	57	LYS
12	d	95	LEU
13	D	71	LYS
17	g	66	LYS

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	
4	1	52/97 (54%)	46 (88%)	6 (12%)	4	8
4	A	44/97 (45%)	27 (61%)	17 (39%)	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	39/39 (100%)	34 (87%)	5 (13%)	3	6
6	2	55/55 (100%)	47 (86%)	8 (14%)	2	4
7	4	35/35 (100%)	29 (83%)	6 (17%)	1	2
8	a	67/73 (92%)	45 (67%)	22 (33%)	0	0
9	b	85/90 (94%)	65 (76%)	20 (24%)	0	0
10	c	95/118 (80%)	73 (77%)	22 (23%)	0	0
11	C	221/221 (100%)	192 (87%)	29 (13%)	3	6
12	d	75/97 (77%)	52 (69%)	23 (31%)	0	0
13	D	173/173 (100%)	138 (80%)	35 (20%)	1	1
14	E	168/168 (100%)	139 (83%)	29 (17%)	1	2
15	e	51/52 (98%)	33 (65%)	18 (35%)	0	0
16	f	74/80 (92%)	60 (81%)	14 (19%)	1	1
17	g	36/70 (51%)	23 (64%)	13 (36%)	0	0
18	G	115/153 (75%)	86 (75%)	29 (25%)	0	0
19	H	122/123 (99%)	110 (90%)	12 (10%)	6	13
20	h	35/75 (47%)	25 (71%)	10 (29%)	0	0
21	I	100/100 (100%)	83 (83%)	17 (17%)	1	2
22	i	49/50 (98%)	31 (63%)	18 (37%)	0	0
23	j	37/65 (57%)	19 (51%)	18 (49%)	0	0
24	J	109/112 (97%)	89 (82%)	20 (18%)	1	1
25	k	151/164 (92%)	120 (80%)	31 (20%)	1	1
26	K	108/114 (95%)	92 (85%)	16 (15%)	2	4
27	L	96/101 (95%)	83 (86%)	13 (14%)	3	5
28	l	23/174 (13%)	17 (74%)	6 (26%)	0	0
29	m	120/122 (98%)	78 (65%)	42 (35%)	0	0
30	M	83/95 (87%)	55 (66%)	28 (34%)	0	0
31	n	82/83 (99%)	64 (78%)	18 (22%)	1	0
32	N	93/100 (93%)	77 (83%)	16 (17%)	1	2
33	o	107/111 (96%)	79 (74%)	28 (26%)	0	0
34	O	96/96 (100%)	85 (88%)	11 (12%)	4	8
35	p	114/131 (87%)	83 (73%)	31 (27%)	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	P	84/86 (98%)	63 (75%)	21 (25%)	0	0
37	q	96/105 (91%)	67 (70%)	29 (30%)	0	0
38	Q	89/91 (98%)	79 (89%)	10 (11%)	5	9
39	R	78/80 (98%)	62 (80%)	16 (20%)	1	1
40	S	81/88 (92%)	67 (83%)	14 (17%)	1	2
41	T	78/82 (95%)	63 (81%)	15 (19%)	1	1
42	U	59/62 (95%)	46 (78%)	13 (22%)	1	0
43	V	39/41 (95%)	31 (80%)	8 (20%)	1	1
44	W	58/60 (97%)	44 (76%)	14 (24%)	0	0
45	Z	35/43 (81%)	29 (83%)	6 (17%)	1	2
All	All	3607/4172 (86%)	2830 (78%)	777 (22%)	2	0

5 of 777 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	m	62	LYS
33	o	92	SER
29	m	117	LEU
29	m	61	LYS
30	M	119	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
32	N	14	GLN
41	T	13	GLN
32	N	31	HIS
34	O	91	ASN
41	T	84	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	Y	2709/2923 (92%)	1004 (37%)	48 (1%)
2	X	1436/1552 (92%)	1029 (71%)	56 (3%)
3	3	113/114 (99%)	47 (41%)	2 (1%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	4258/4589 (92%)	2080 (48%)	106 (2%)

5 of 2080 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	Y	10	A
1	Y	11	U
1	Y	12	U
1	Y	14	A
1	Y	34	U

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	X	334	G
2	X	730	G
2	X	1431	U
2	X	384	G
2	X	589	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

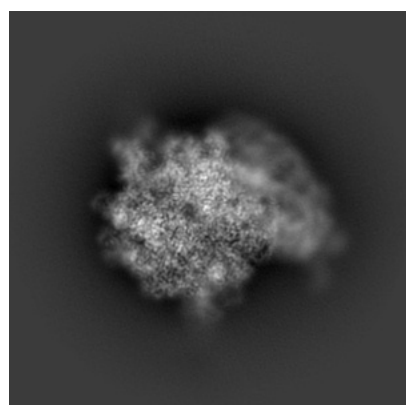
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11903. These allow visual inspection of the internal detail of the map and identification of artifacts.

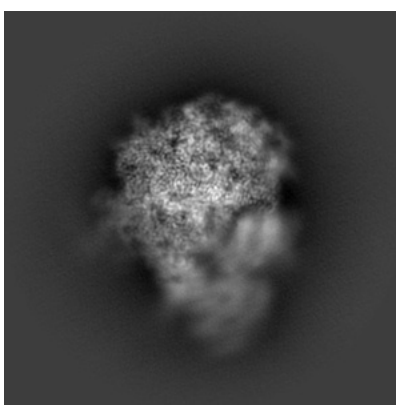
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

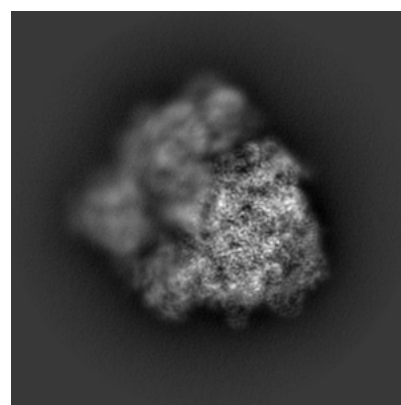
6.1.1 Primary map



X



Y

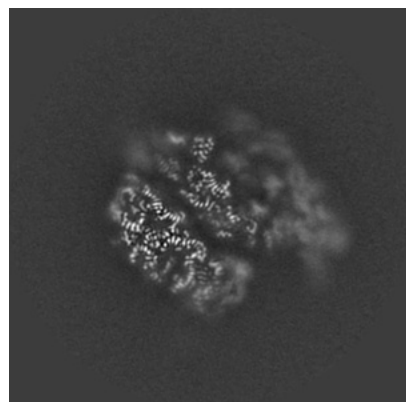


Z

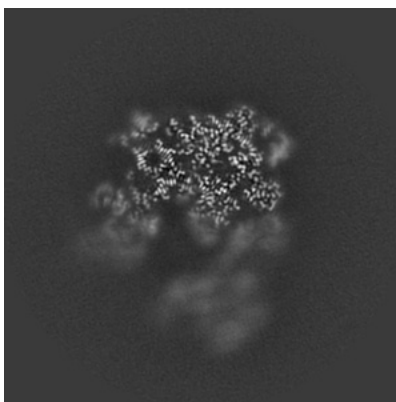
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

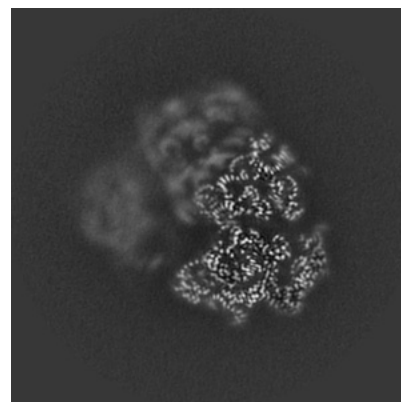
6.2.1 Primary map



X Index: 240



Y Index: 240

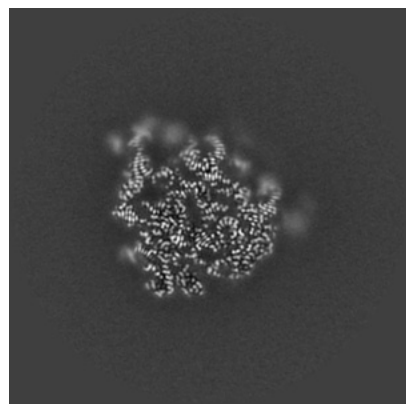


Z Index: 240

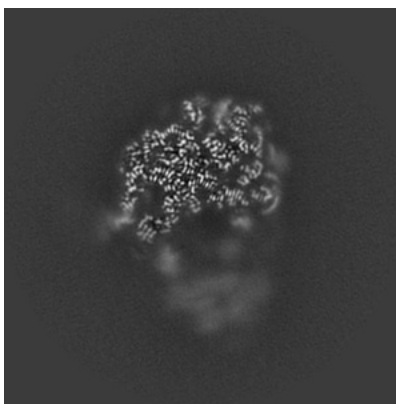
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

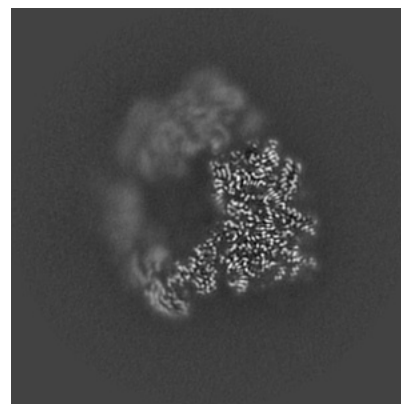
6.3.1 Primary map



X Index: 294



Y Index: 206

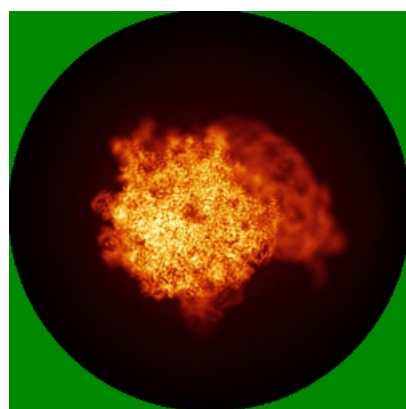


Z Index: 213

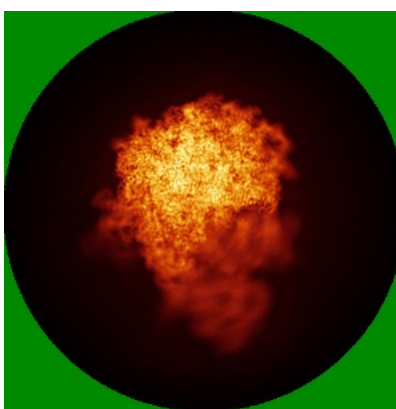
The images above show the largest variance slices of the map in three orthogonal directions.

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

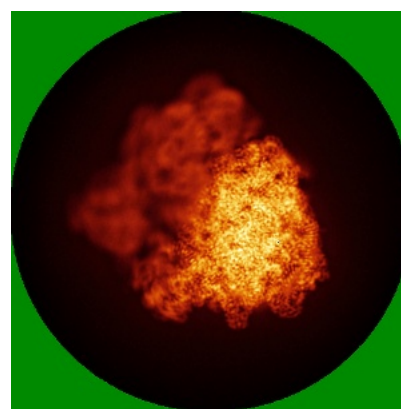
6.4.1 Primary map



X



Y



Z

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](#)

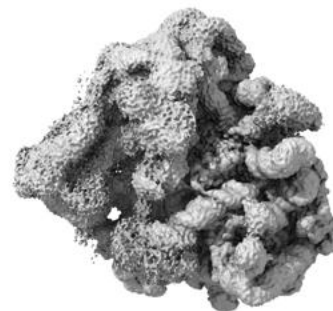
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

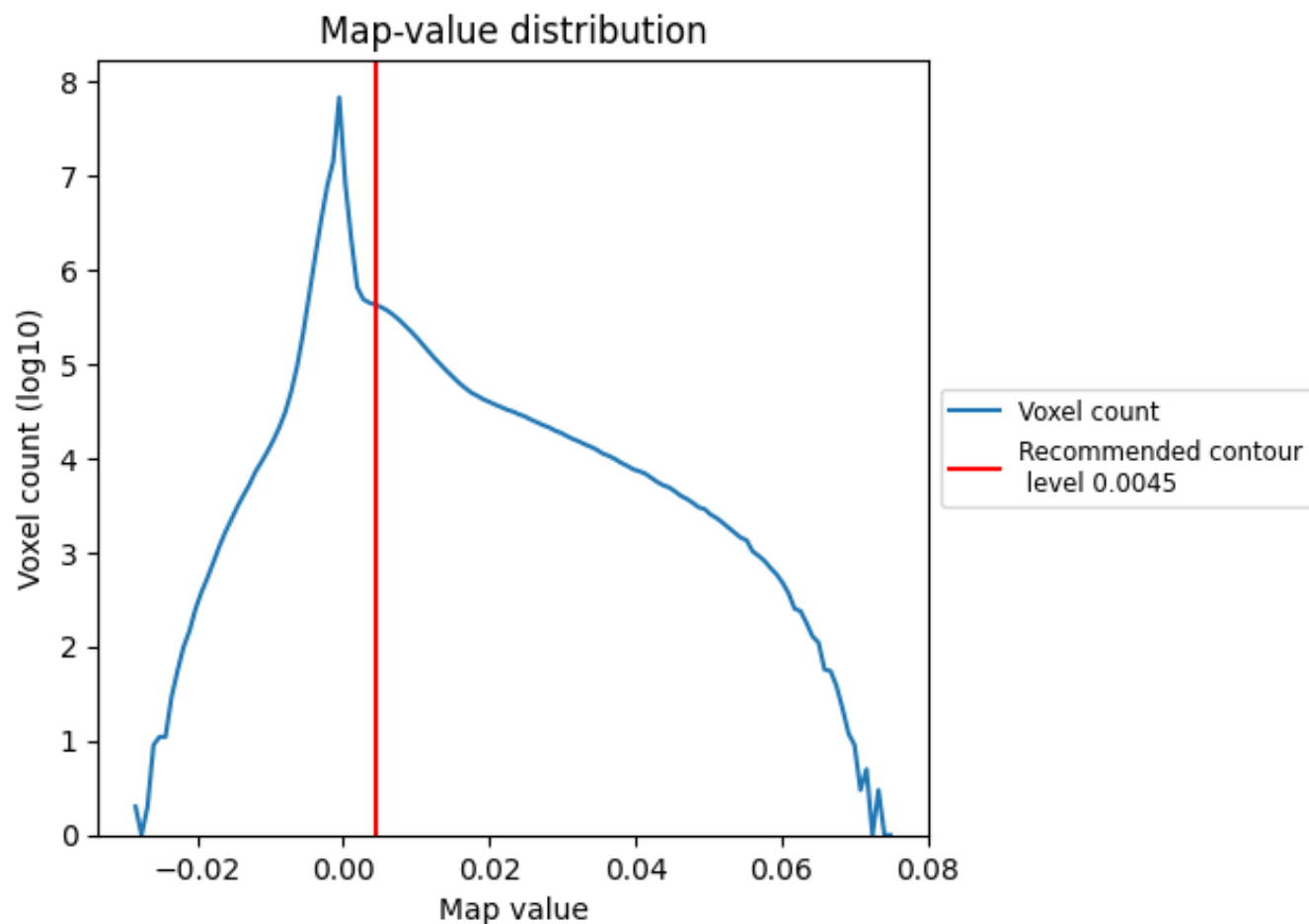
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

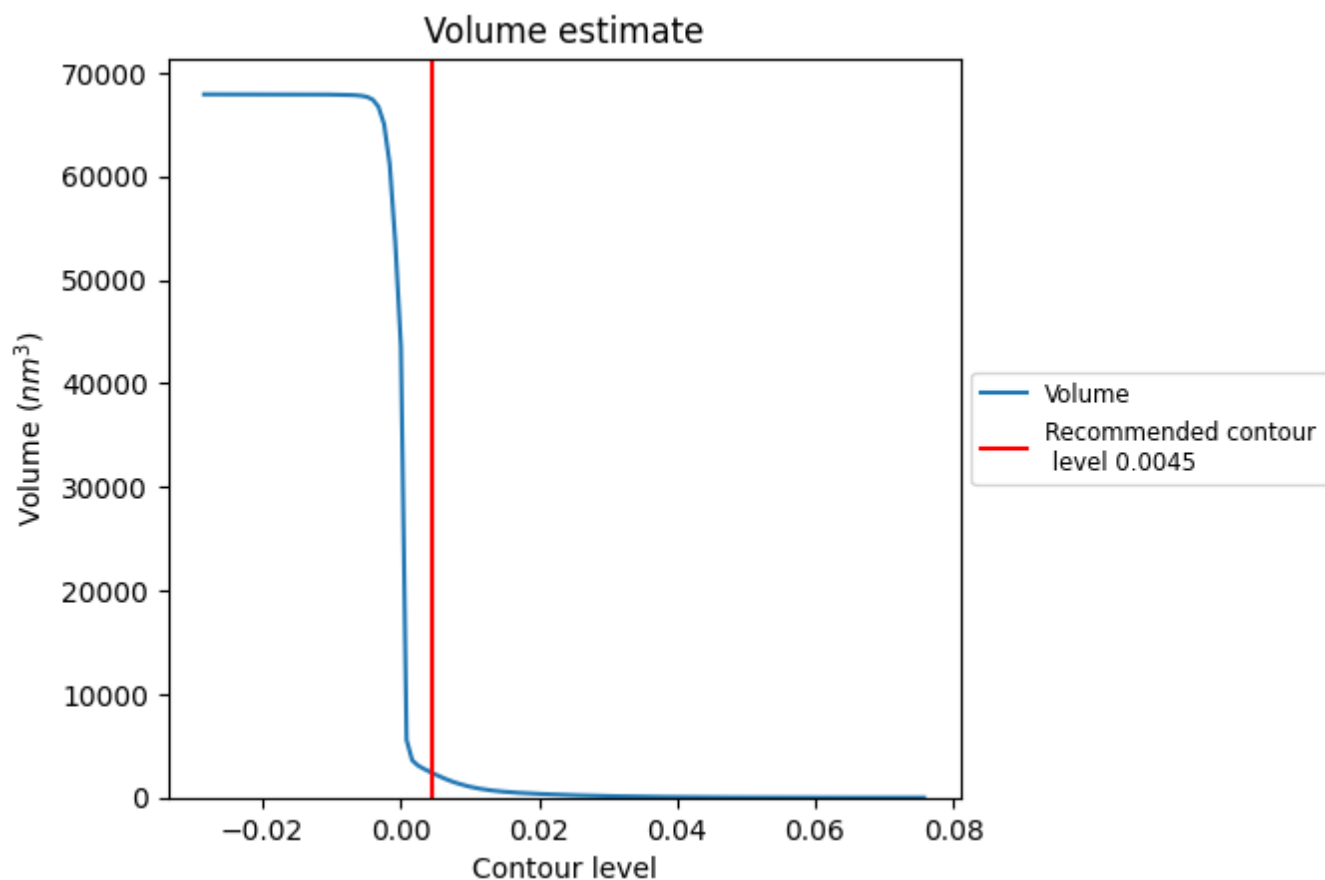
This section contains the results of statistical analysis of the map.

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.

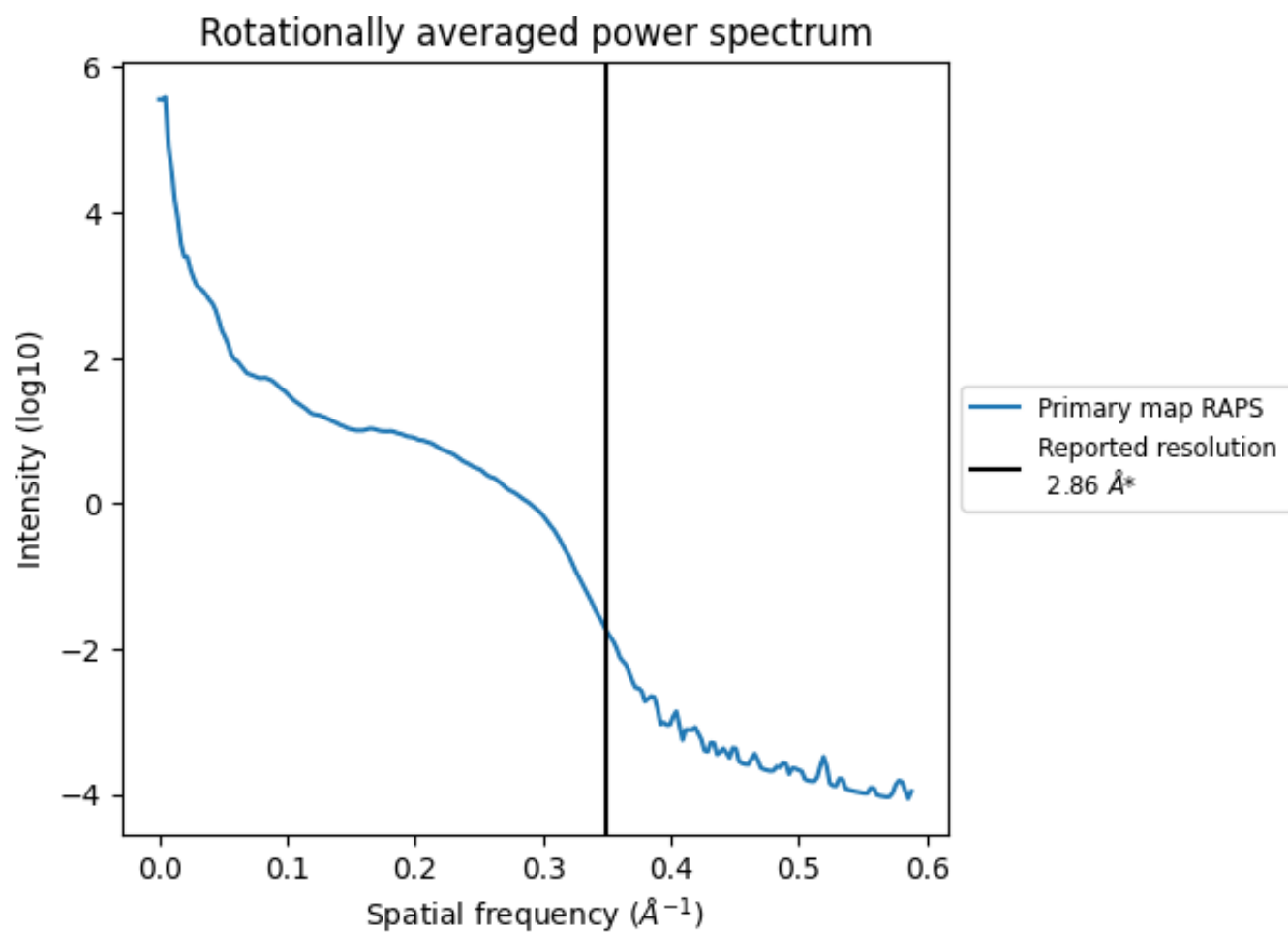
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2394 nm^3 ; this corresponds to an approximate mass of 2163 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 0.350 \AA^{-1}

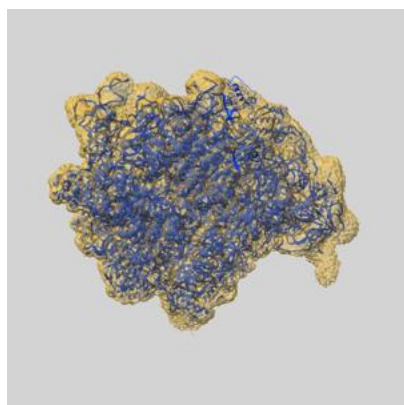
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

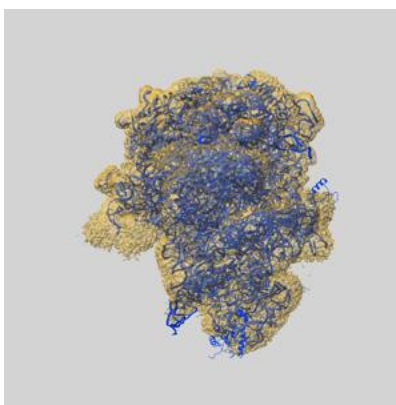
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11903 and PDB model 7ASP. Per-residue inclusion information can be found in section [3](#) on page [12](#).

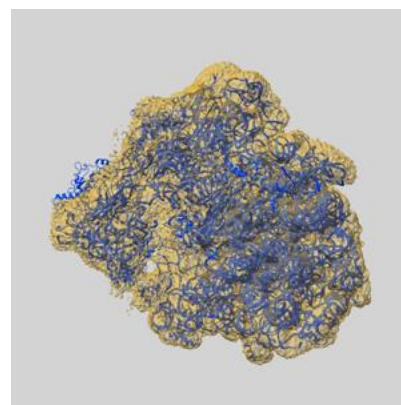
9.1 Map-model overlay [i](#)



X



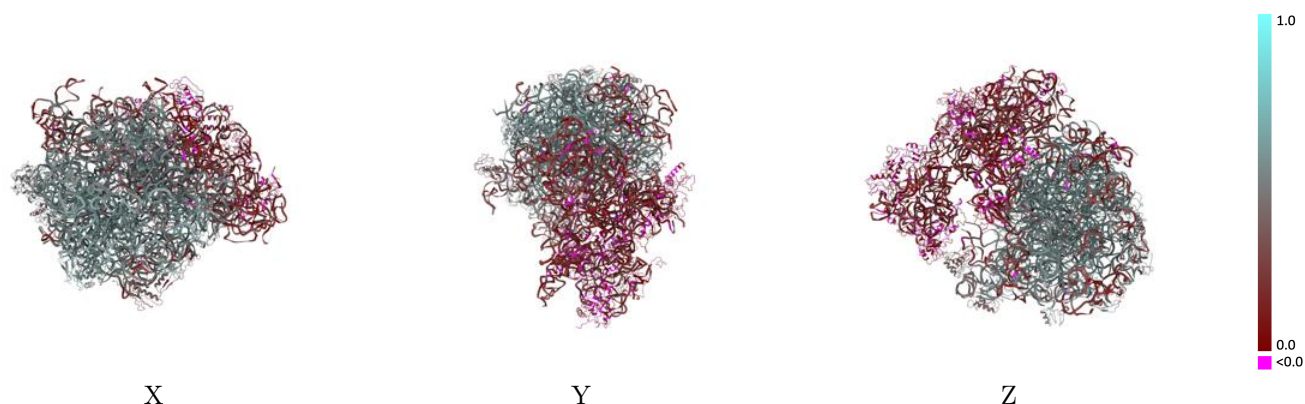
Y



Z

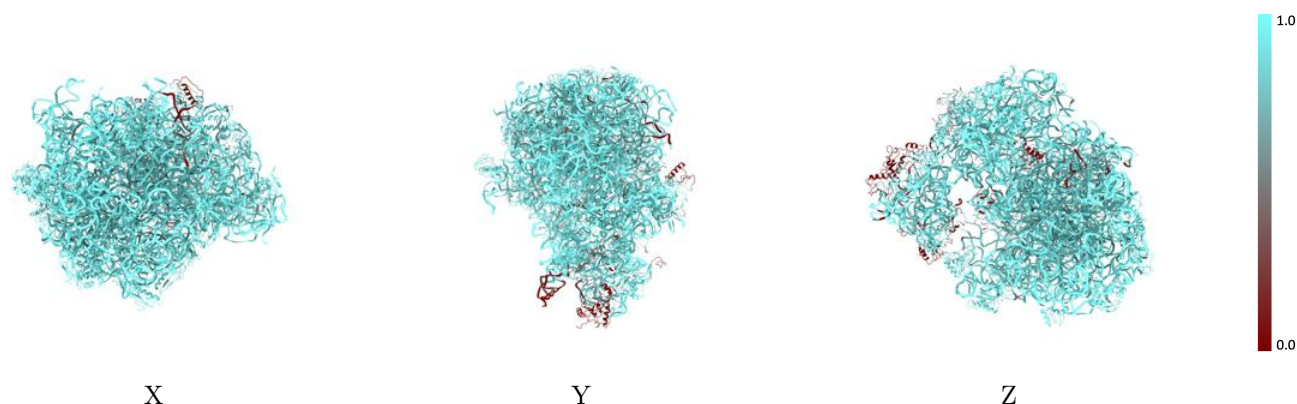
The images above show the 3D surface view of the map at the recommended contour level 0.0045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



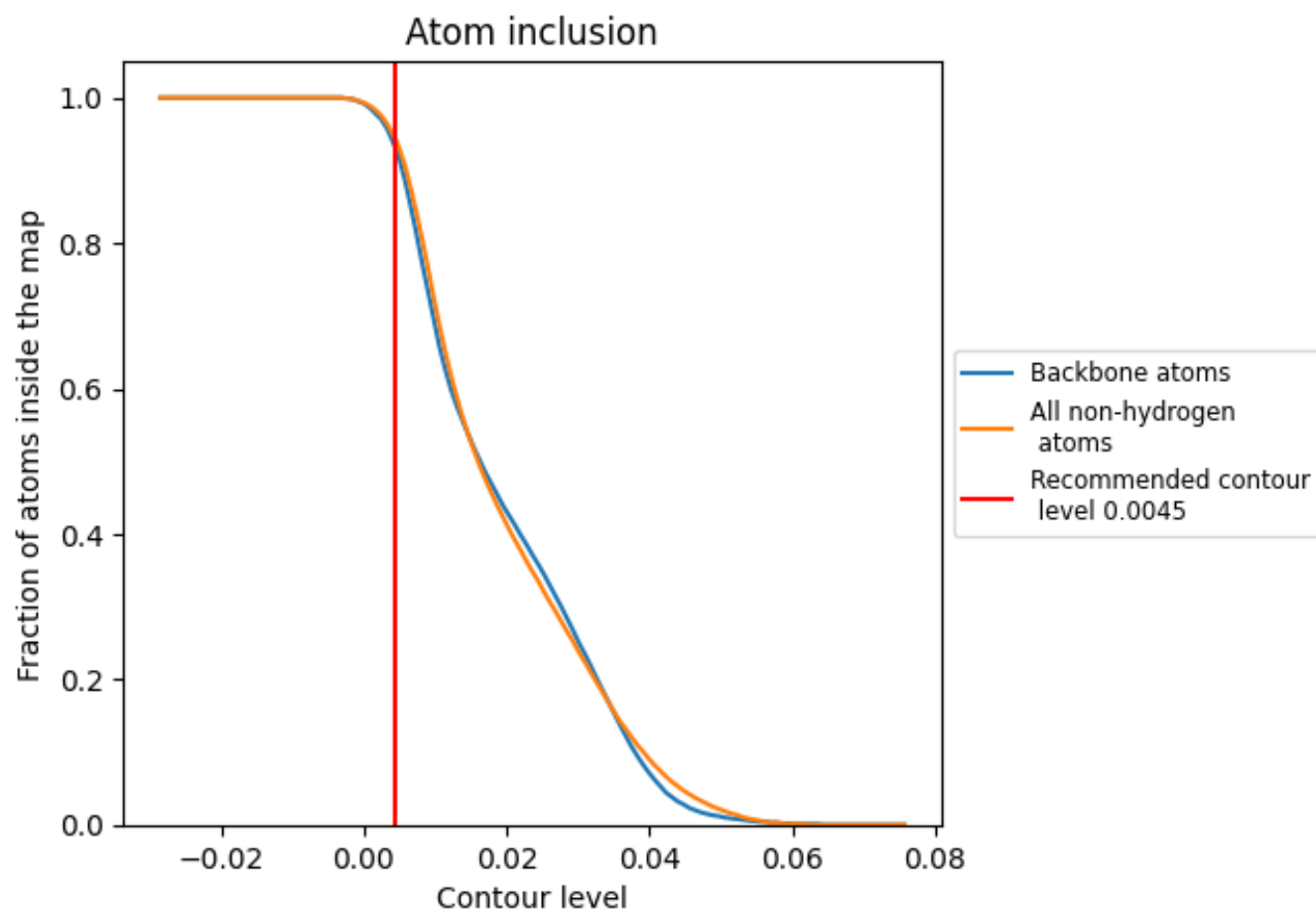
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0045).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 94% 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 (0.0045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.3760
1	 0.9820	 0.5540
2	 0.9760	 0.5590
3	 0.9980	 0.4340
4	 0.9340	 0.5020
A	 0.8800	 0.4910
B	 0.9830	 0.5810
C	 0.9670	 0.5420
D	 0.9770	 0.5480
E	 0.9810	 0.5310
F	 0.9910	 0.3300
G	 0.9660	 0.2980
H	 0.9810	 0.5560
I	 0.9740	 0.5610
J	 0.9880	 0.5380
K	 0.9800	 0.5410
L	 0.9810	 0.5530
M	 0.9920	 0.4440
N	 0.9620	 0.5490
O	 0.9860	 0.5680
P	 0.9880	 0.5600
Q	 0.9710	 0.5490
R	 0.9830	 0.5250
S	 0.9800	 0.4750
T	 0.9450	 0.4880
U	 0.9670	 0.5580
V	 0.9780	 0.5240
W	 0.9890	 0.4400
X	 0.9560	 0.1800
Y	 0.9810	 0.4900
Z	 0.9850	 0.5060
a	 0.6290	 0.0890
b	 0.6160	 0.0970
c	 0.5690	 0.1800
d	 0.5130	 0.0780



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
e	 0.4830	 0.0600
f	 0.9010	 0.1860
g	 0.8350	 0.0730
h	 0.9060	 0.1110
i	 0.8730	 0.1350
j	 0.9780	 0.1810
k	 0.4020	 0.0840
l	 0.7630	 0.0860
m	 0.7940	 0.0820
n	 0.4670	 0.0870
o	 0.8880	 0.1140
p	 0.7240	 0.0840
q	 0.7210	 0.1080