wwPDB EM Validation Summary Report

Nov 19, 2022 – 04:08 pm GMT

PDB ID	:	5ND9
EMDB ID	:	EMD-3625
Title	:	Hibernating ribosome from Staphylococcus aureus (Rotated state)
Authors	:	Khusainov, I.; Vicens, Q.; Ayupov, R.; Usachev, K.; Myasnikov, A.; Simonetti, A.; Validov, S.; Kieffer, B.; Yusupova, G.; Yusupov, M.; Hashem, Y.
Deposited on	:	2017-03-07
Resolution	:	3.70 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:

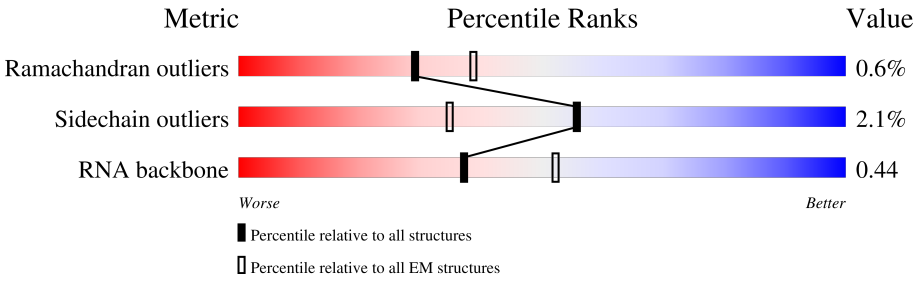
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.70 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	a	1556	5% 70% 27%
2	b	255	63% 84% 13%
3	c	217	74% 91% 6%
4	d	200	46% 97%
5	e	166	40% 92%
6	f	98	60% 93%
7	g	156	74% 84% 6% 8%
8	h	132	22% 97%

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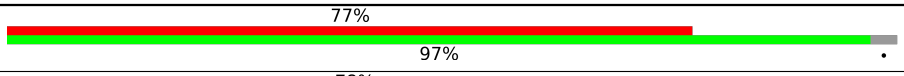
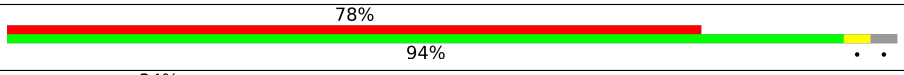
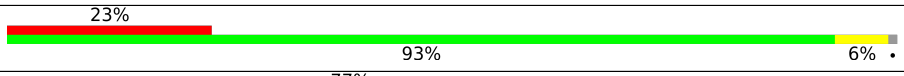
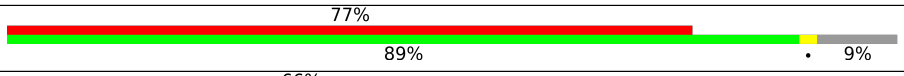
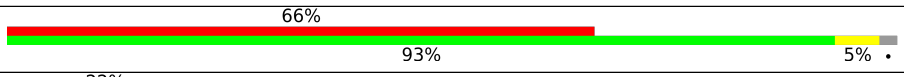
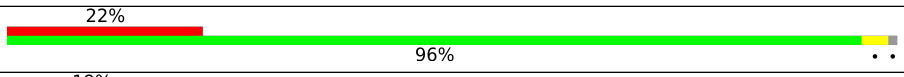
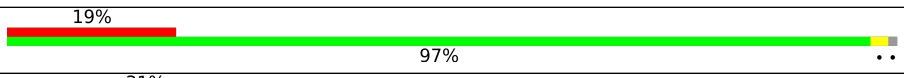
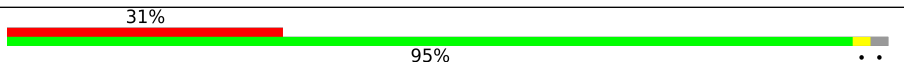
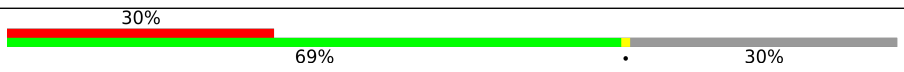
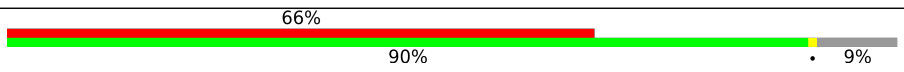
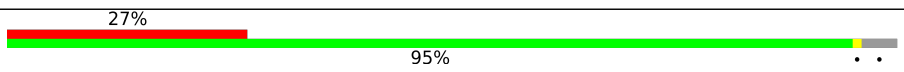
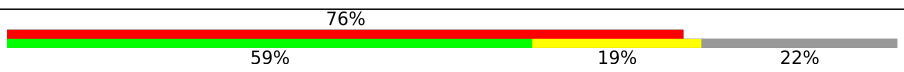
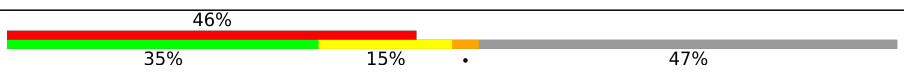
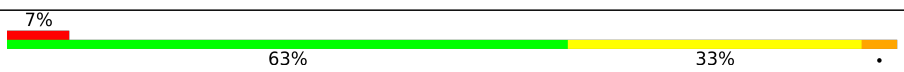
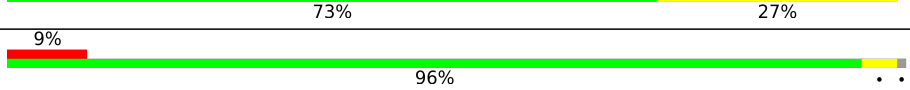
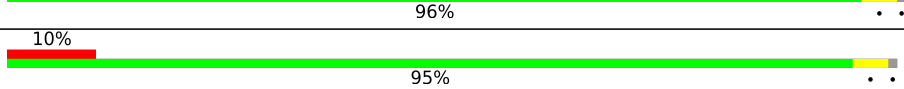
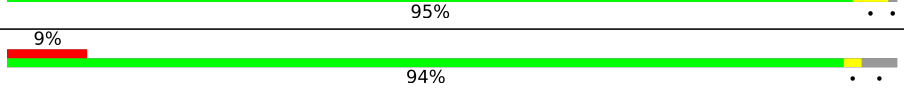
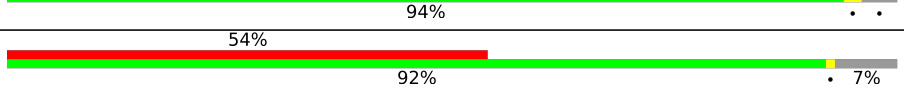
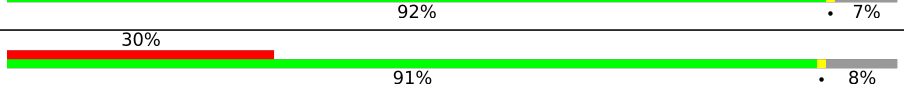
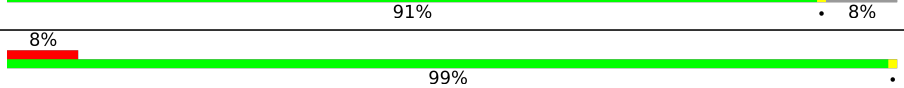
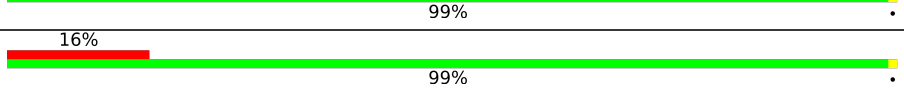
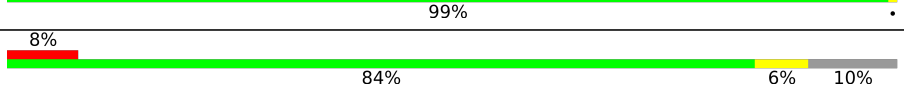
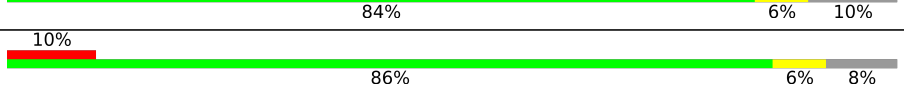
Mol	Chain	Length	Quality of chain
9	i	132	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	91	
17	q	87	
18	r	80	
19	s	92	
20	t	83	
21	u	58	
22	v	190	
23	A	2923	
24	B	114	
25	D	277	
26	E	220	
27	F	207	
28	G	179	
29	H	178	
30	M	145	
31	N	122	
32	O	146	
33	P	144	

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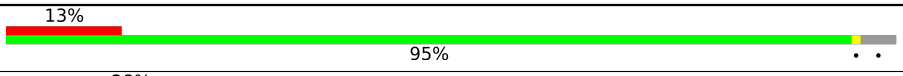
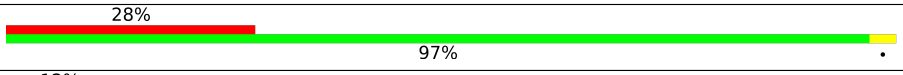
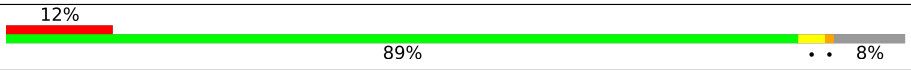
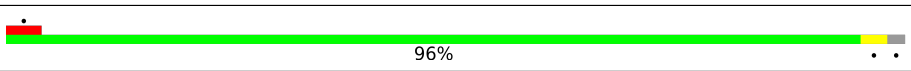
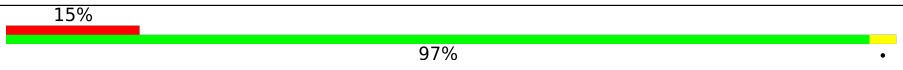
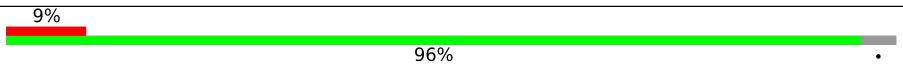
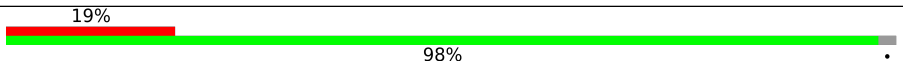
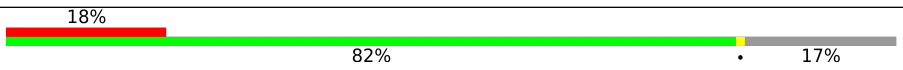
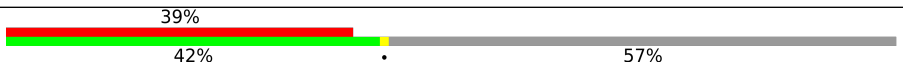
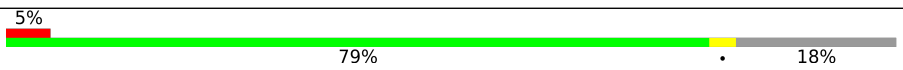
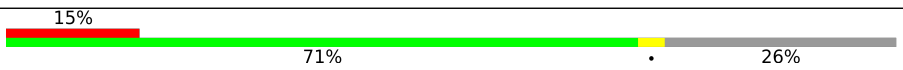
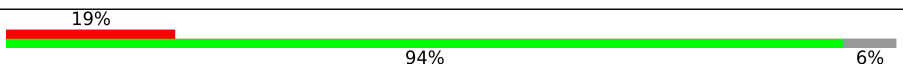
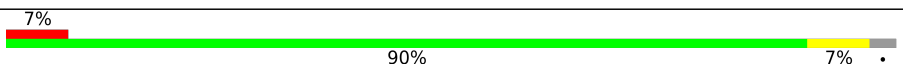
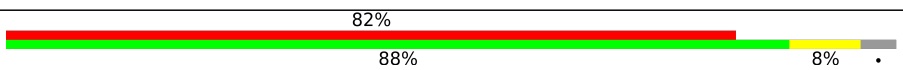
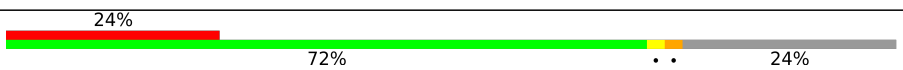
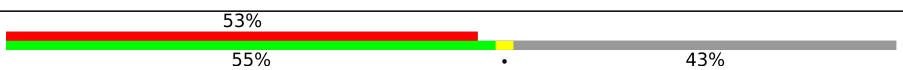
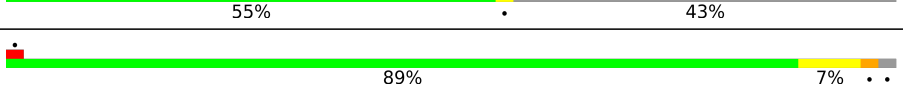
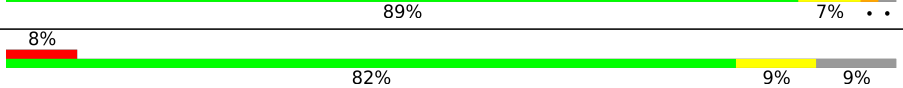
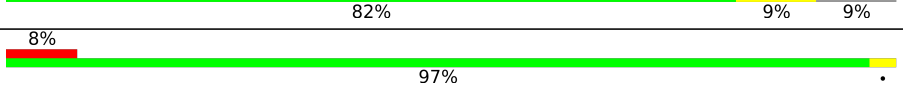
Mol	Chain	Length	Quality of chain
34	Q	122	
35	R	119	
36	S	116	
37	T	118	
38	U	102	
39	V	117	
40	W	91	
41	X	105	
42	Y	217	
43	Z	94	
44	0	62	
45	1	69	
46	2	59	
47	3	84	
48	4	58	
49	5	49	
50	6	45	
51	7	66	
52	8	37	

2 Entry composition (i)

There are 52 unique types of molecules in this entry. The entry contains 141051 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	a	1541	33006	14736	6021	10708	1541	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	b	222	1788	1139	313	330	6	0	0

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	c	203	1600	1007	301	290	2	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	d	197	1600	1009	300	289	2	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	e	160	1194	750	218	224	2	0	0

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	f	94	781	494	137	147	3	0	0

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	143	Total	C	N	O	S	0	0
			1142	712	216	210	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			791	498	144	147	2		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	115	Total	C	N	O	S	0	0
			851	526	160	162	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	110	Total	C	N	O	S	0	0
			877	537	175	164	1		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			502	317	100	80	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	85	Total	C	N	O	S	0	0
			698	441	125	131	1		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	56	Total	C	N	O	S	0	0
			466	295	88	81	2		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	84	Total	C	N	O	S	0	0
			677	434	120	121	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	u	45	Total	C	N	O	0	0
			377	233	76	68		

- Molecule 22 is a protein called Ribosome hibernation promotion factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	v	101	Total	C	N	O	0	0
			831	518	156	157		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	2914	Total	C	N	O	P	0	0
			62480	27894	11427	20245	2914		

- Molecule 24 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	275	Total	C	N	O	S	0	0
			2103	1309	417	372	5		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	218	Total	C	N	O	S	0	0
			1649	1030	304	310	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	199	Total	C	N	O	S	0	0
			1524	955	281	286	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	166	Total	C	N	O	S	0	0
			1311	832	223	250	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	164	Total	C	N	O	S	0	0
			1284	799	232	250	3		

- Molecule 30 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	145	Total	C	N	O	S	0	0
			1151	717	211	220	3		

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	122	Total	C	N	O	S	0	0
			920	572	174	170	4		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O	131	Total	C	N	O	S	0	0
			997	618	197	181	1		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P	133	Total	C	N	O	S	0	0
			1065	681	203	178	3		

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	117	Total	C	N	O	S	0	0
			924	564	179	180	1		

- Molecule 35 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R	119	Total	C	N	O	S	0	0
			922	574	174	173	1		

- Molecule 36 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	S	107	Total	C	N	O	0	0
			862	544	173	145		

- Molecule 37 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	T	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 38 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	U	102	Total	C	N	O	S	0	0
			799	506	142	150	1		

- Molecule 39 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	112	Total	C	N	O	S	0	0
			862	537	164	158	3		

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	W	89	Total	C	N	O	S	0	0
			725	457	130	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	X	87	Total	C	N	O	S	0	0
			668	423	122	122	1		

- Molecule 42 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Y	94	Total	C	N	O	S	0	0
			738	471	131	134	2		

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	Z	77	Total	C	N	O	0	0
			591	364	115	112		

- Molecule 44 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	0	46	Total	C	N	O	0	0
			373	231	83	59		

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	1	65	Total	C	N	O	0	0
			536	330	101	105		

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	2	57	Total	C	N	O	0	0
			441	274	83	84		

- Molecule 47 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	81	Total	C	N	O	S	0	0
			663	423	113	124	3		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	4	44	Total	C	N	O	S	0	0
			360	220	78	58	4		

- Molecule 49 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5	28	Total	C	N	O	S	0	0
			229	137	45	43	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	6	44	Total	C	N	O	S	0	0
			373	228	90	54	1		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	7	60	Total	C	N	O	S	0	0
			487	300	108	77	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

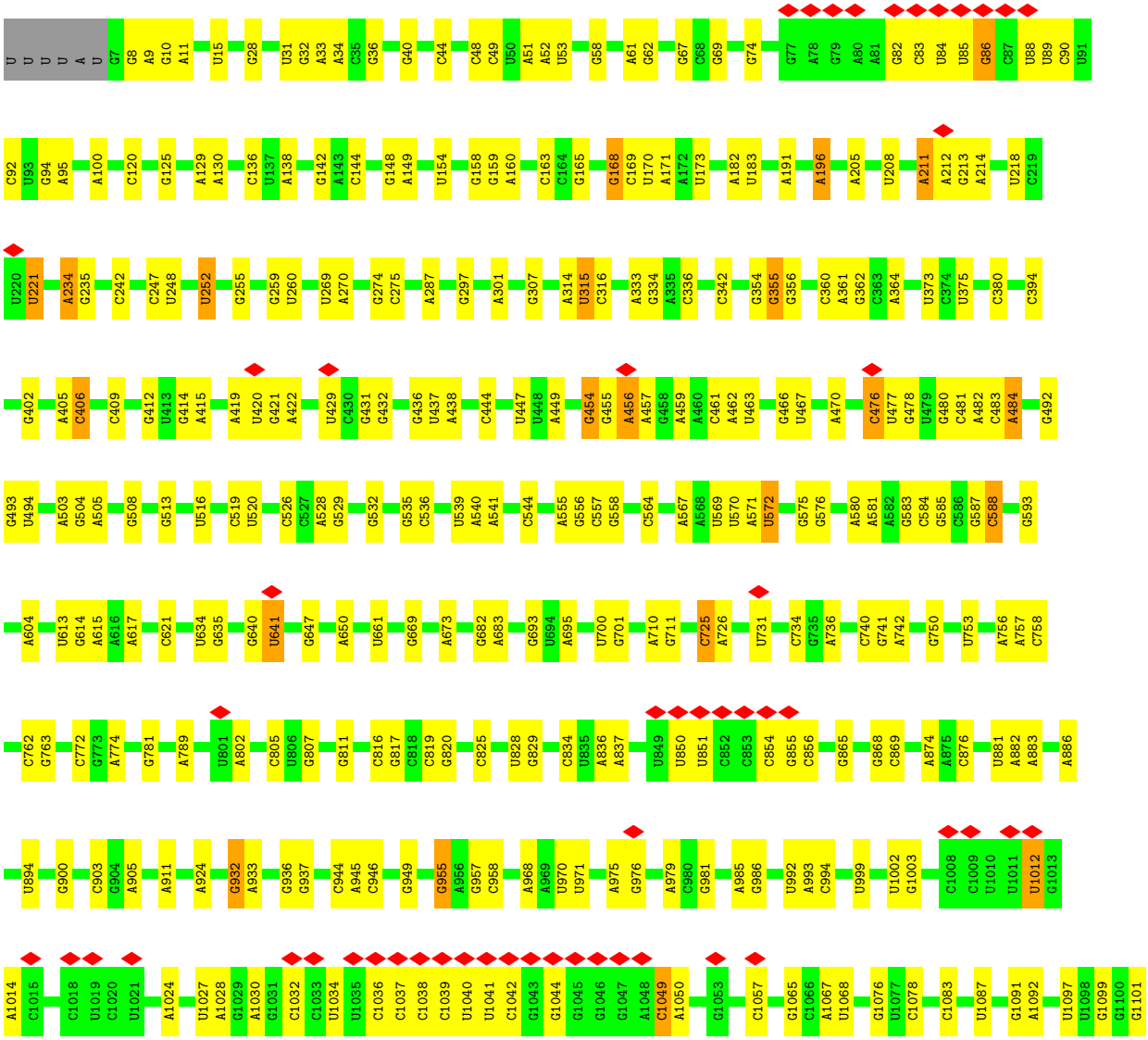
Mol	Chain	Residues	Atoms					AltConf	Trace
52	8	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

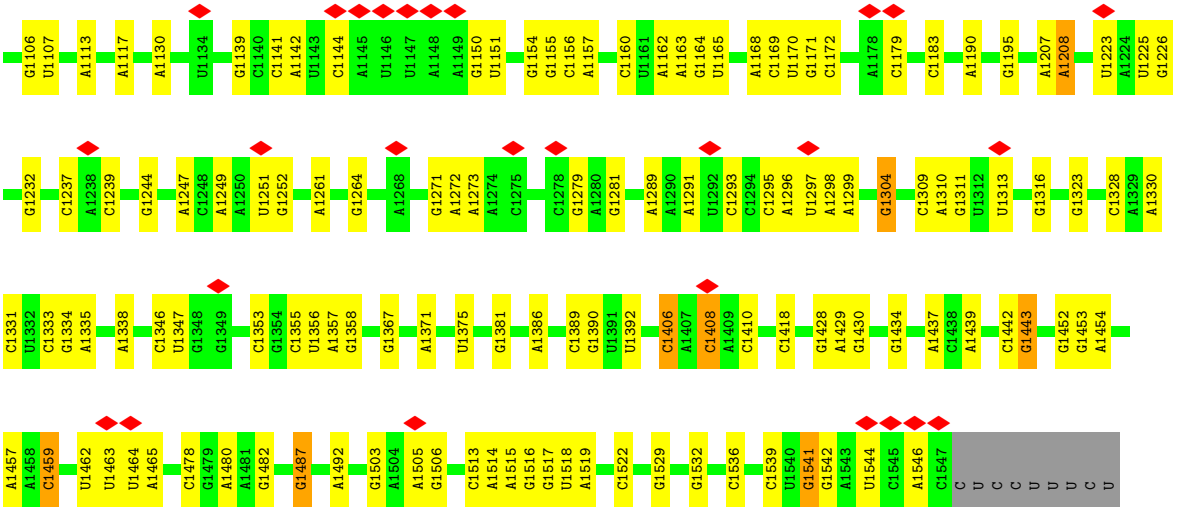
3 Residue-property plots (i)

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: 16S ribosomal RNA

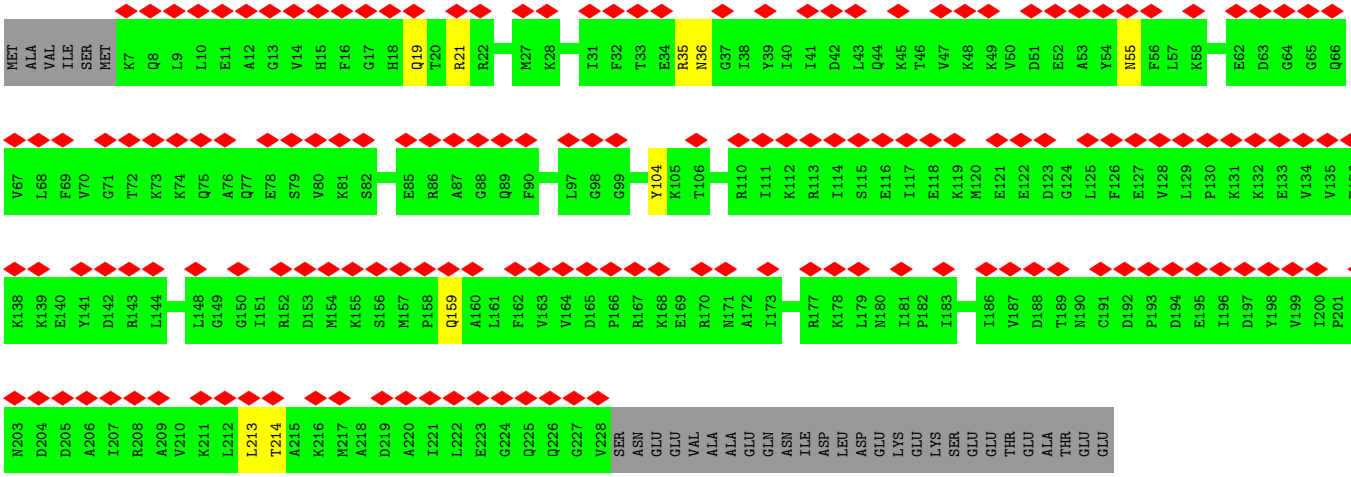
Chain a:





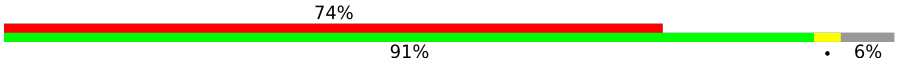
• Molecule 2: 30S ribosomal protein S2

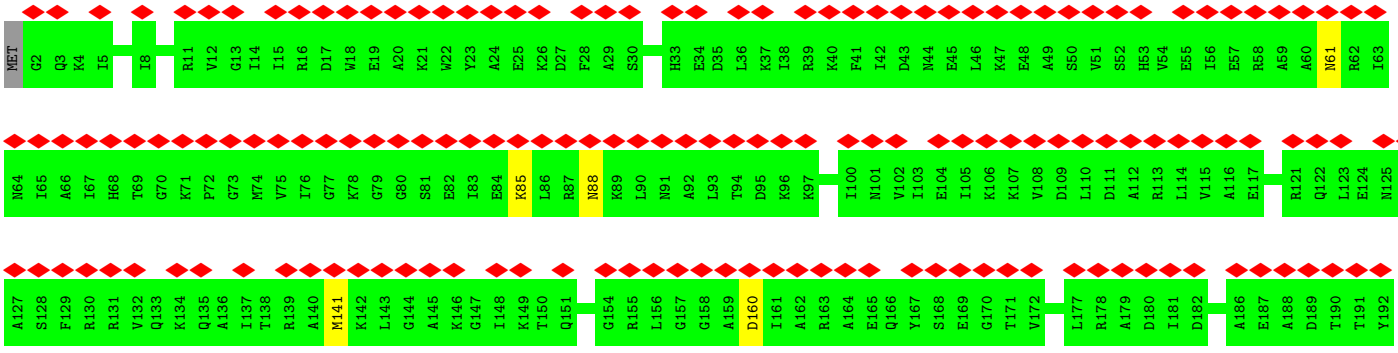
Chain b:

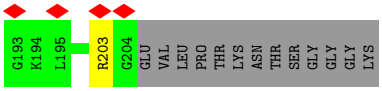


• Molecule 3: 30S ribosomal protein S3

Chain c:

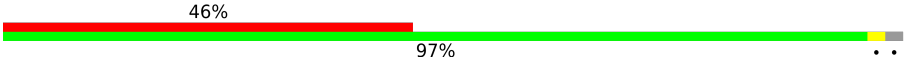


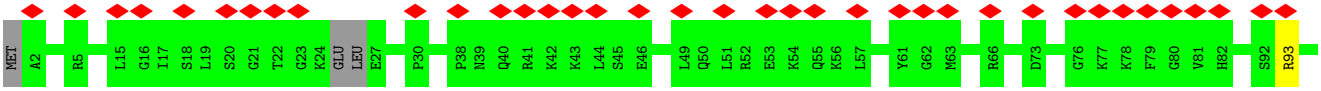


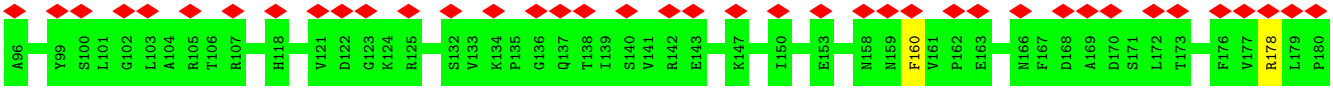


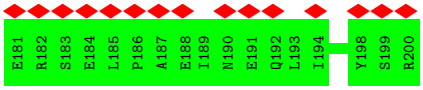
• Molecule 4: 30S ribosomal protein S4

Chain d:



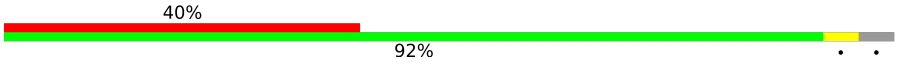


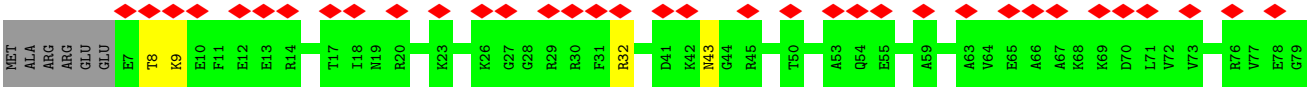


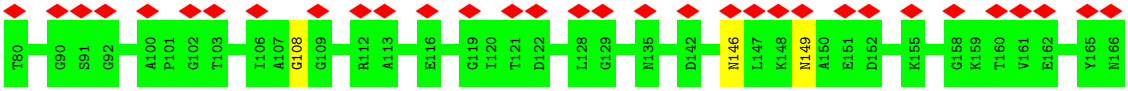


• Molecule 5: 30S ribosomal protein S5

Chain e:

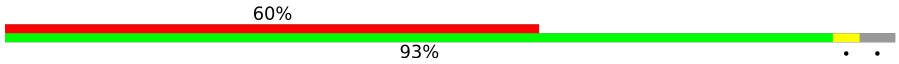


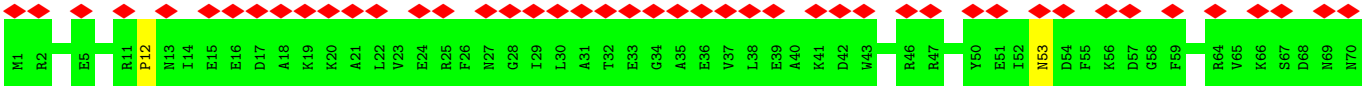


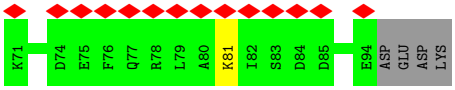


• Molecule 6: 30S ribosomal protein S6

Chain f:

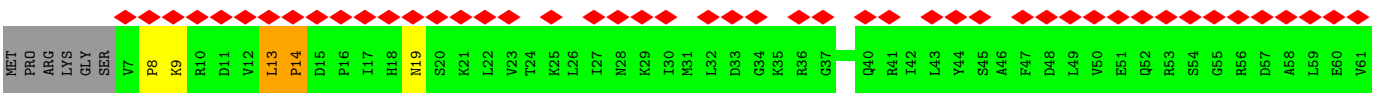


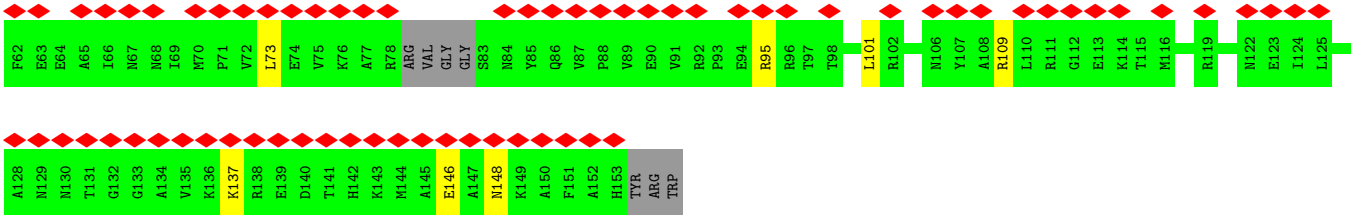




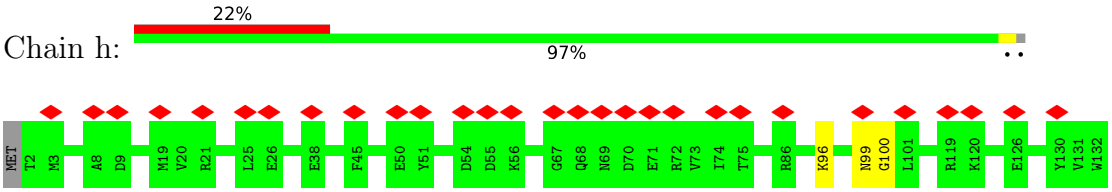
• Molecule 7: 30S ribosomal protein S7

Chain g:

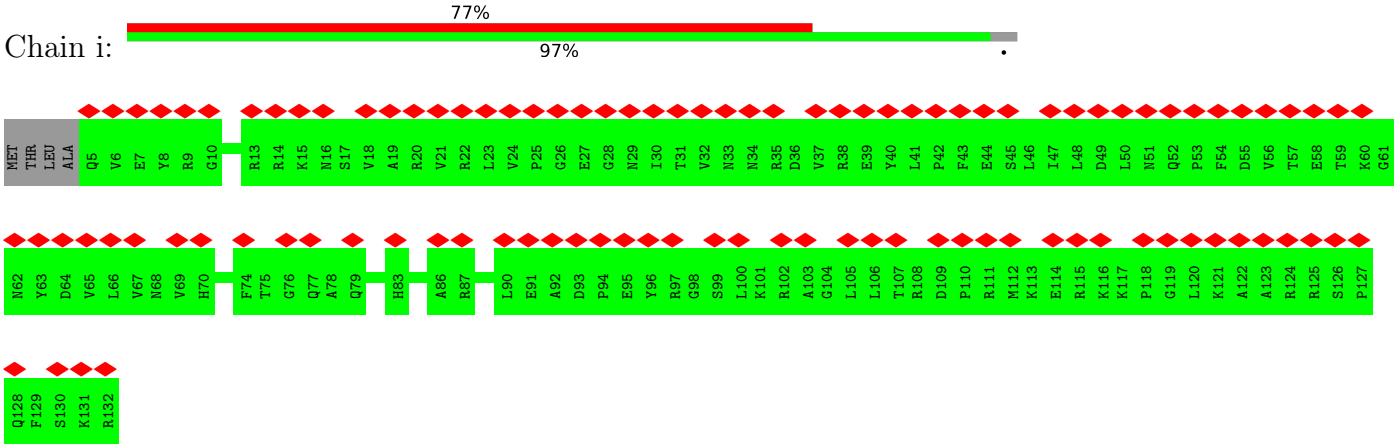




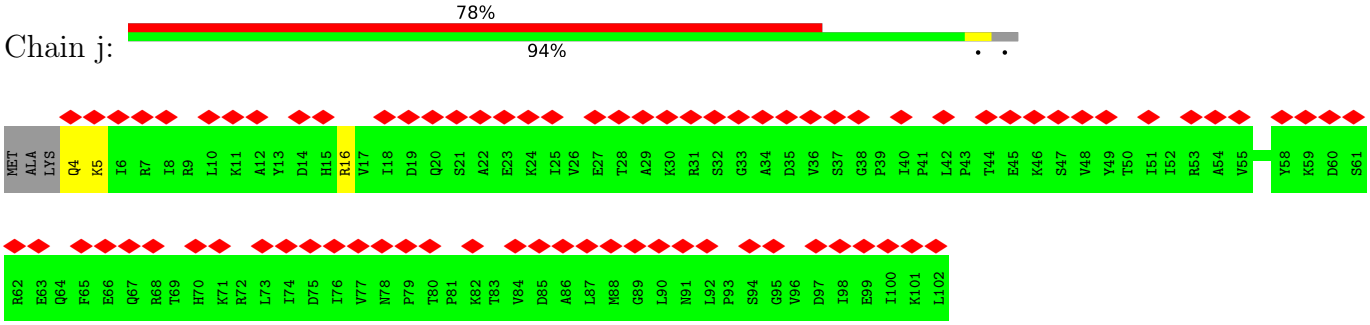
• Molecule 8: 30S ribosomal protein S8



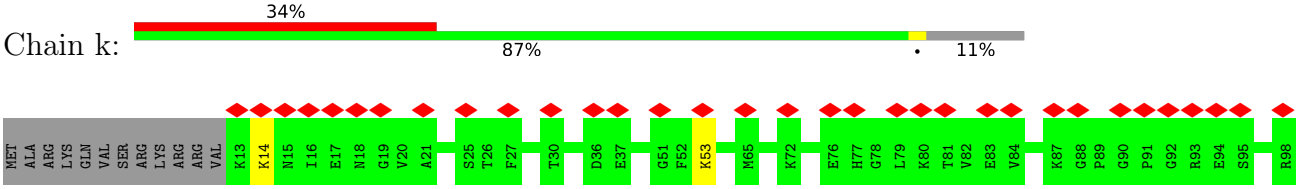
• Molecule 9: 30S ribosomal protein S9

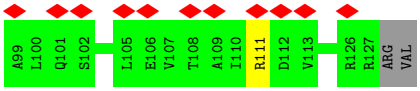


• Molecule 10: 30S ribosomal protein S10



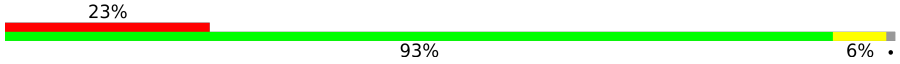
• Molecule 11: 30S ribosomal protein S11

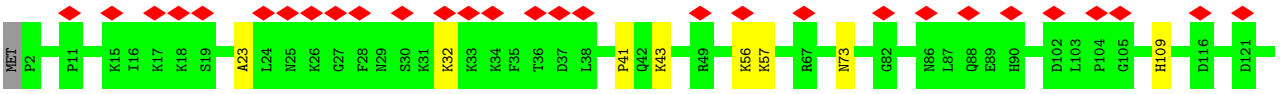


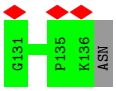


• Molecule 12: 30S ribosomal protein S12

Chain l:

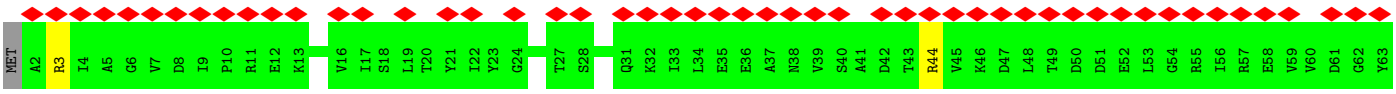


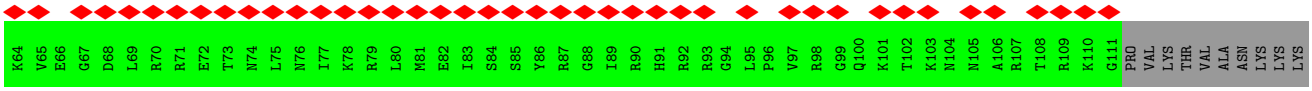




• Molecule 13: 30S ribosomal protein S13

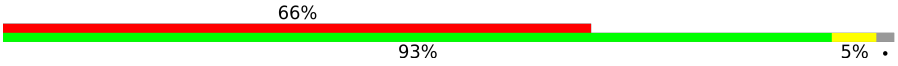
Chain m:

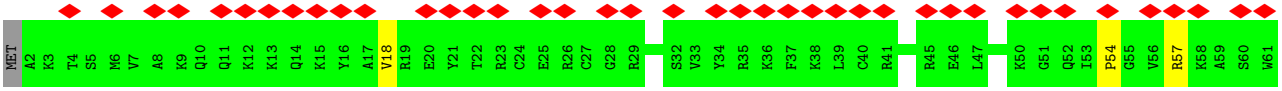




• Molecule 14: 30S ribosomal protein S14 type Z

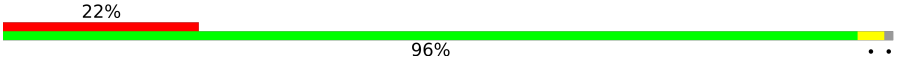
Chain n:

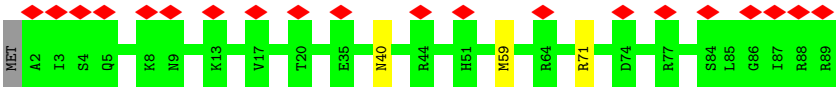




• Molecule 15: 30S ribosomal protein S15

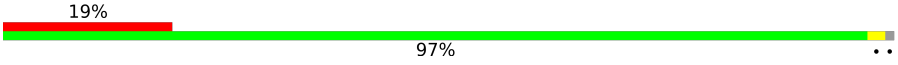
Chain o:

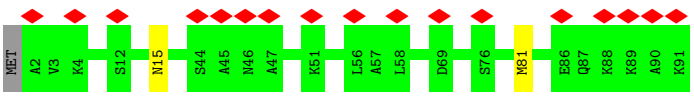




• Molecule 16: 30S ribosomal protein S16

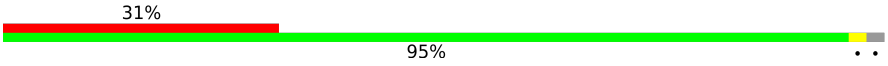
Chain p:

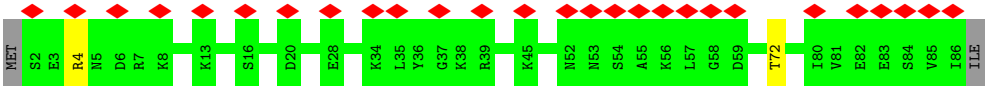




• Molecule 17: 30S ribosomal protein S17

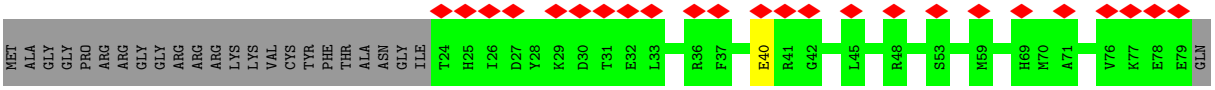
Chain q:





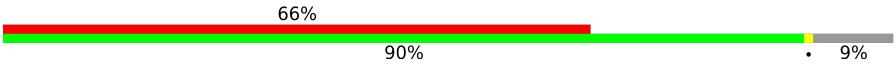
• Molecule 18: 30S ribosomal protein S18

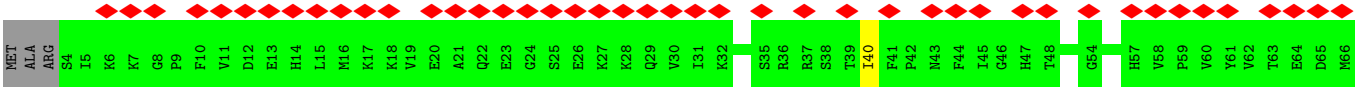
Chain r:

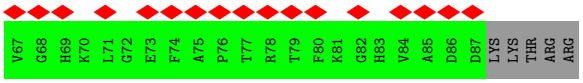


• Molecule 19: 30S ribosomal protein S19

Chain s:

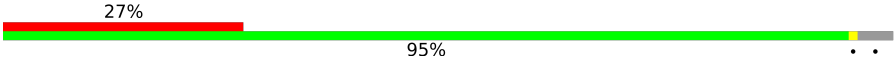


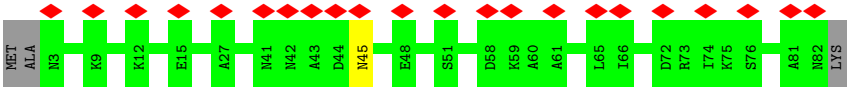




• Molecule 20: 30S ribosomal protein S20

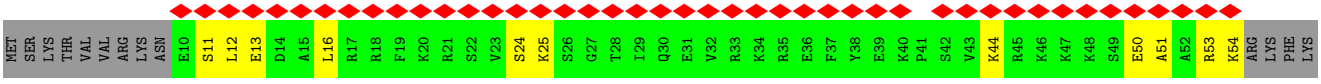
Chain t:





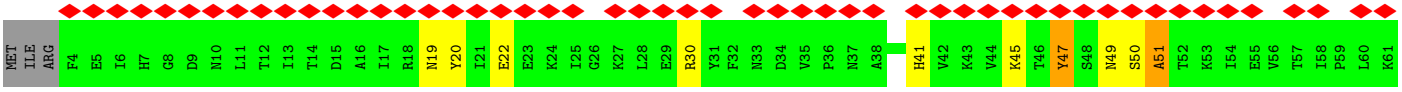
• Molecule 21: 30S ribosomal protein S21

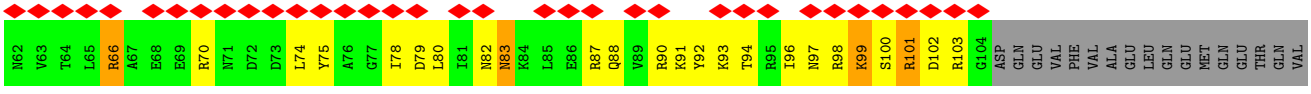
Chain u:

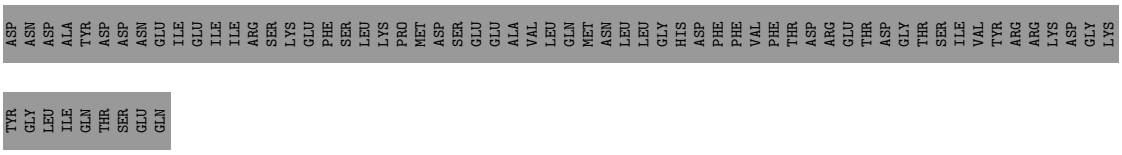


• Molecule 22: Ribosome hibernation promotion factor

Chain v:

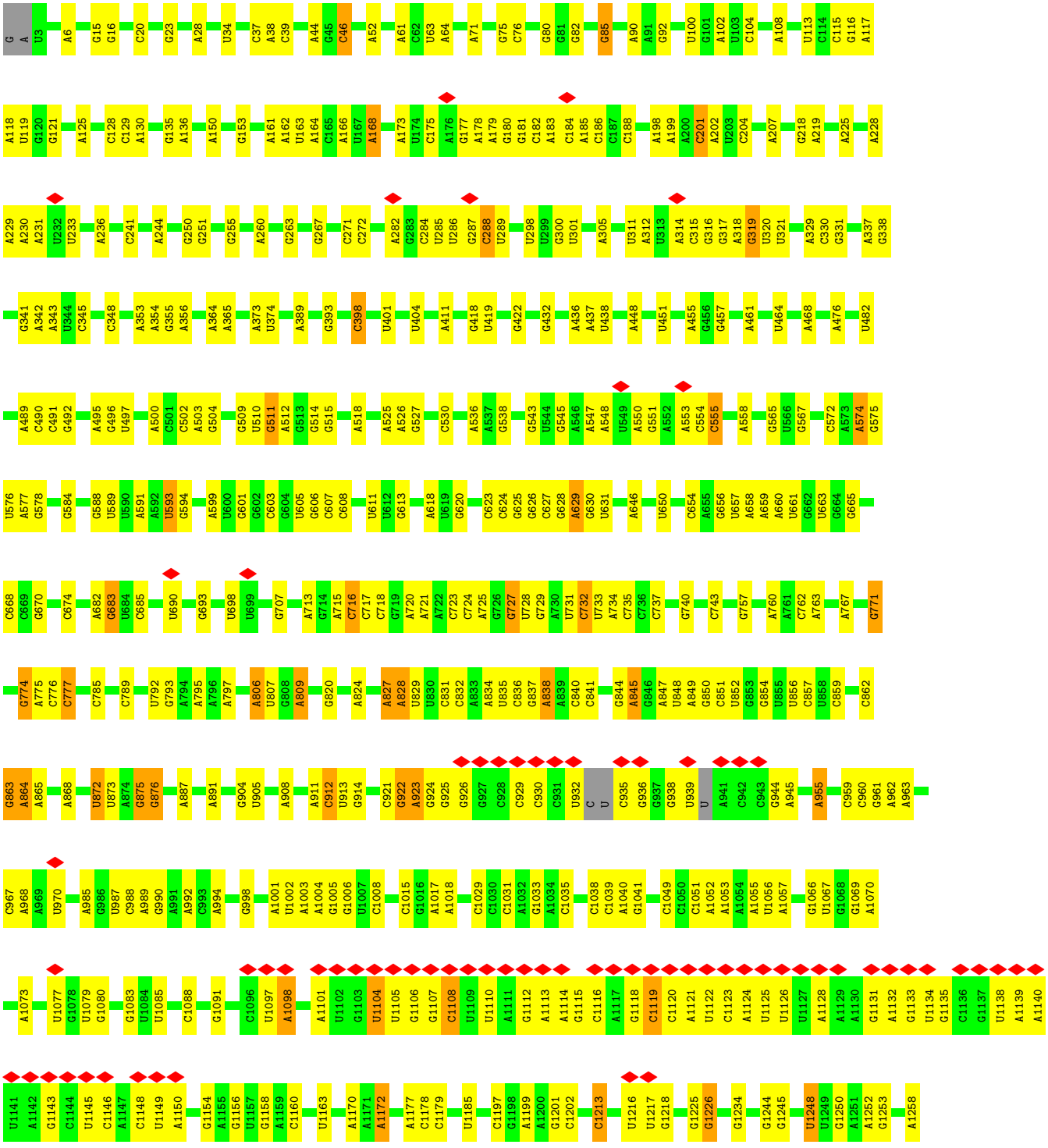


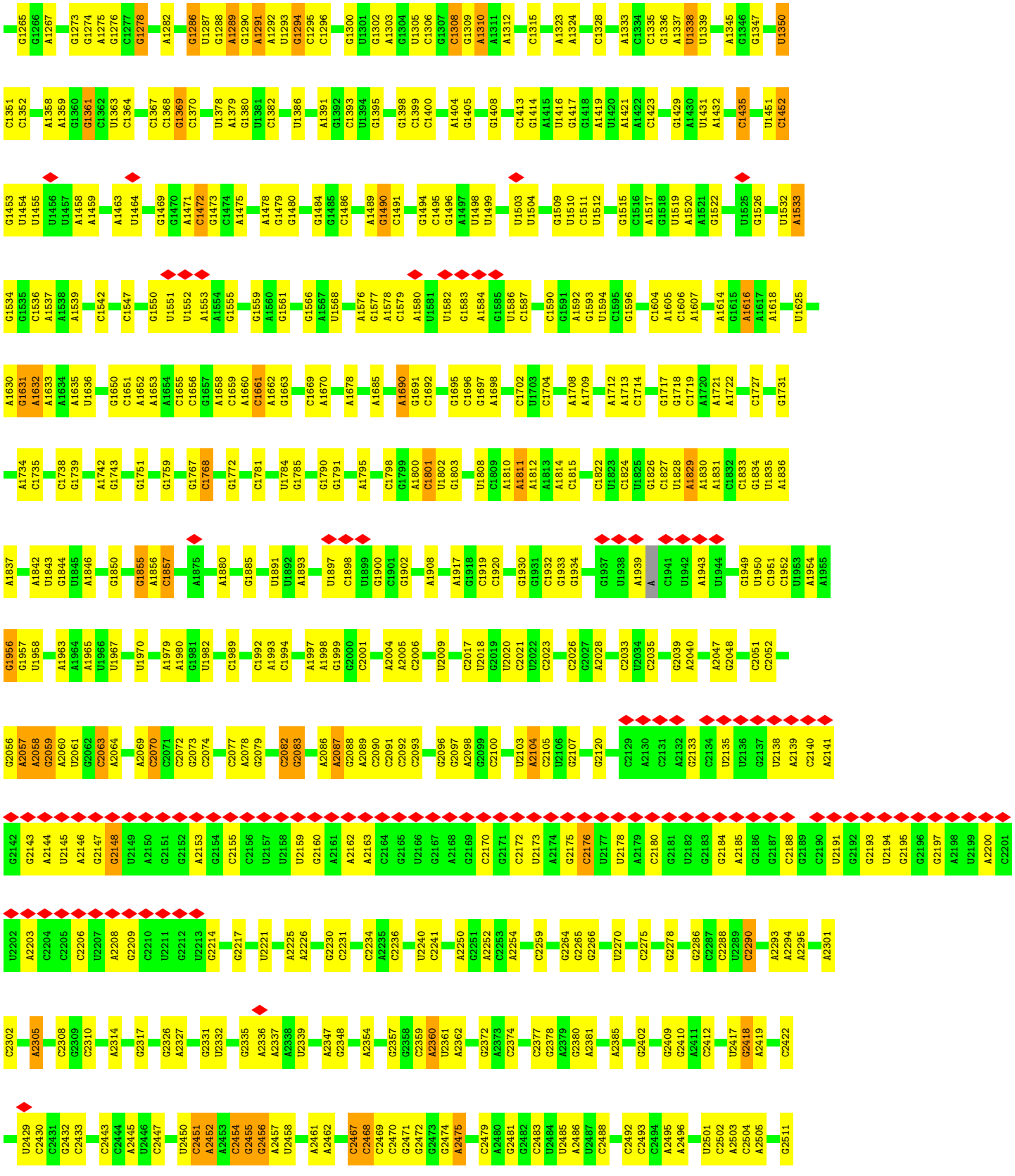


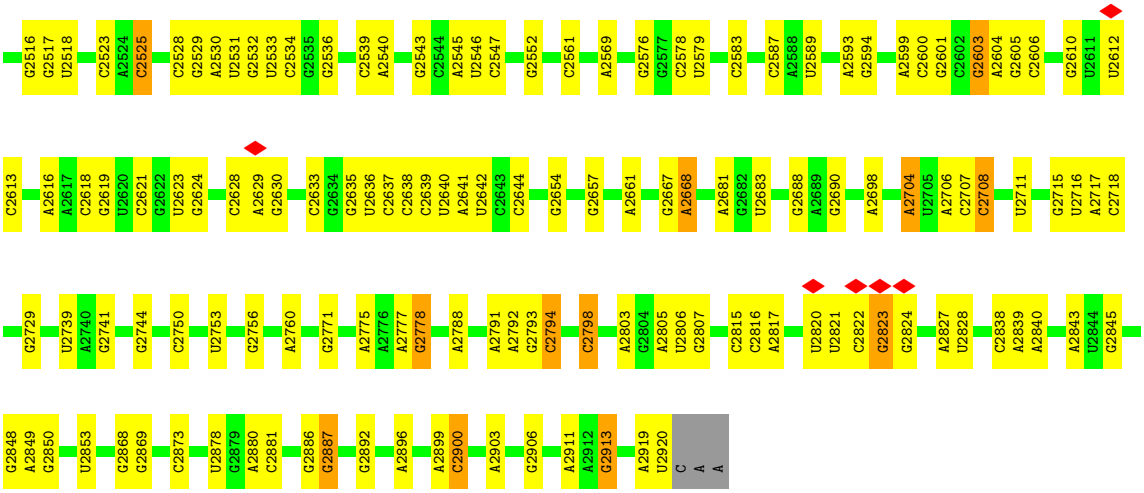


• Molecule 23: 23S ribosomal RNA

Chain A:

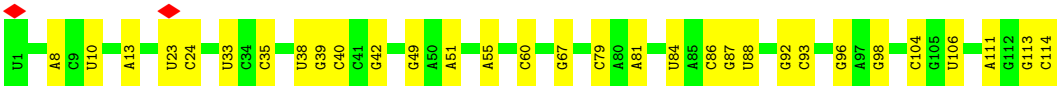



G1265 G1266 A1267 G1273 G1274 A1275 G1276 C1277 G1278 A1282 G1286 U1287 G1288 A1289 G1290 A1291 A1292 U1293 G1294 C1295 C1296 G1300 U1301 G1302 A1303 G1304 U1305 C1306 G1307 C1308 G1309 A1310 A1311 A1312 C1315 A1323 A1324 C1328 A1333 C1334 C1335 G1336 A1337 U1338 U1339 A1345 G1346 G1347 U1350
C1351 C1352 A1358 A1359 G1360 G1361 C1362 U1363 C1364 C1367 C1368 G1369 C1370 U1378 A1379 G1380 U1381 C1382 U1386 A1391 G1392 C1393 U1394 G1395 G1398 C1399 C1400 A1404 G1405 G1408 C1413 G1414 A1415 U1416 G1417 G1418 A1419 U1420 A1421 A1422 C1423 G1429 A1430 U1431 A1432 C1435 U1451 C1452
G1453 U1454 U1455 U1456 U1457 A1458 A1459 A1463 U1464 G1469 G1470 A1471 C1472 G1473 C1474 A1475 A1478 G1479 G1480 G1484 G1485 C1486 A1489 G1490 C1491 G1494 C1495 G1496 A1497 U1498 U1499 U1503 U1504 G1509 U1510 C1511 U1512 G1515 C1516 A1517 G1518 U1519 A1520 A1521 G1522 U1525 G1526 U1532 A1533
G1534 G1535 C1536 A1537 A1538 A1539 C1542 C1547 G1550 U1551 U1552 A1553 A1554 G1555 G1559 A1560 G1561 G1566 A1567 U1568 A1576 G1577 A1578 C1579 A1580 U1581 U1582 G1583 A1584 G1585 U1586 C1587 C1590 G1591 A1592 G1593 U1594 G1595 G1596 C1604 A1605 C1606 A1607 A1614 G1615 A1616 A1617 A1618 U1625
A1630 G1631 A1632 A1633 A1634 A1635 U1636 G1650 C1651 A1652 A1653 A1654 C1655 C1656 G1657 A1658 C1659 A1660 C1661 A1662 G1663 C1669 A1670 A1678 A1685 A1690 G1691 C1692 G1695 C1696 G1697 A1698 C1702 U1703 C1704 A1708 A1709 A1712 A1713 C1714 G1717 G1718 C1719 A1720 A1721 A1722 C1727 G1731
A1734 C1735 C1738 G1739 A1742 G1743 G1751 G1759 G1767 C1768 G1772 C1781 U1784 G1785 G1790 G1791 A1795 C1798 G1799 A1800 C1801 U1802 G1803 U1808 C1809 A1810 A1811 A1812 A1813 A1814 C1815 C1822 U1823 C1824 U1825 G1826 C1827 U1828 A1829 A1830 A1831 C1832 C1833 G1834 U1835 A1836
A1837 A1842 U1843 G1844 U1845 A1846 G1850 G1855 A1856 C1857 A1875 A1880 G1885 U1891 U1892 A1893 U1897 C1898 U1899 G1900 C1901 G1902 A1908 A1917 G1918 C1919 C1920 G1930 G1931 C1932 G1933 G1934 G1937 U1938 A1939 A C1941 U1942 A1943 U1944 G1949 U1950 C1951 C1952 U1953 A1954 A1955
G1956 G1957 U1958 A1963 A1964 A1965 U1966 U1967 U1970 A1979 A1980 G1981 U1982 C1989 C1992 A1993 C1994 A1997 A1998 G1999 G2000 C2001 A2004 A2005 C2006 U2009 C2017 U2018 G2019 U2020 C2021 U2022 C2023 C2026 G2027 A2028 C2033 U2034 C2035 G2039 A2040 A2047 G2048 C2051 C2052
G2056 A2057 A2058 G2059 A2060 U2061 G2062 C2063 A2064 A2069 C2070 C2071 C2072 G2073 C2074 C2077 A2078 G2079 C2082 G2083 A2086 A2087 G2088 A2089 C2090 C2091 C2092 C2093 G2096 G2097 A2098 G2099 C2100 U2103 A2104 C2105 U2106 G2107 G2120 C2129 A2130 C2131 A2132 G2133 C2134 U2135 U2136 G2137 U2138 A2139 C2140 A2141
G2142 G2143 A2144 U2145 A2146 G2147 G2148 U2149 A2150 G2151 G2152 A2153 G2154 C2155 C2156 U2157 U2158 U2159 G2160 A2161 A2162 A2163 C2164 G2165 U2166 G2167 A2168 G2169 C2170 G2171 C2172 U2173 A2174 G2175 C2176 U2177 U2178 A2179 C2180 G2181 U2182 G2183 G2184 A2185 G2186 G2187 C2188 G2189 C2190 U2191 G2192 G2193 U2194 G2195 G2196 G2197 A2198 U2199 A2200 C2201
U2202 A2203 C2204 C2205 C2206 U2207 A2208 G2209 C2210 U2211 G2212 U2213 G2214 G2217 U2221 A2225 A2226 G2230 C2231 C2234 A2235 C2236 U2240 C2241 A2250 G2251 A2252 C2253 A2254 C2259 G2264 C2265 G2266 U2270 C2275 G2278 G2286 C2287 C2288 U2289 C2290 A2293 A2294 A2295 A2301
C2302 A2305 C2308 G2309 C2310 A2314 G2317 G2326 A2327 G2331 U2332 G2335 A2336 A2337 A2338 U2339 A2347 G2348 A2354 G2357 G2358 C2359 A2360 U2361 A2362 G2372 A2373 C2374 C2377 G2378 A2379 G2380 A2381 A2385 G2402 G2409 G2410 A2411 C2412 U2417 G2418 A2419 C2422
U2429 C2430 C2431 G2432 C2433 C2443 C2444 A2445 U2446 C2447 U2450 C2451 A2452 A2453 C2454 G2455 G2456 A2457 U2458 A2461 A2462 C2467 C2468 C2469 C2470 G2471 G2472 G2473 G2474 A2475 C2479 A2480 G2481 G2482 C2483 U2484 U2485 A2486 U2487 C2488 C2492 C2493 C2494 A2495 A2496 U2501 C2502 A2503 C2504 A2505 G2511



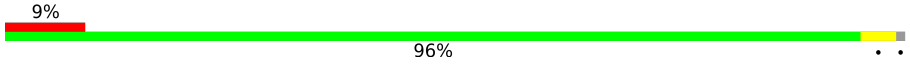
• Molecule 24: 5S ribosomal RNA

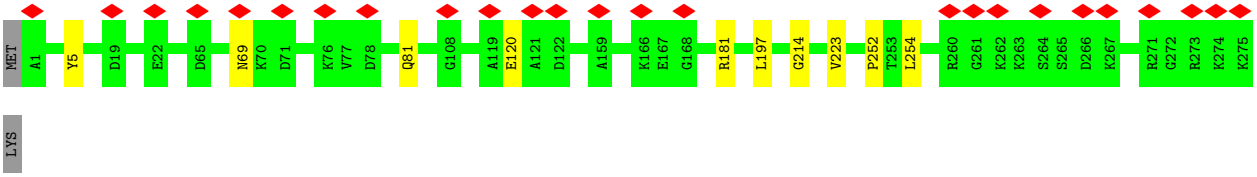
Chain B:



• Molecule 25: 50S ribosomal protein L2

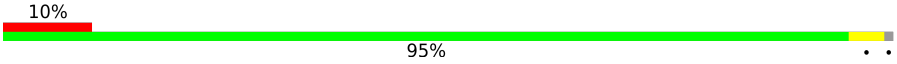
Chain D:

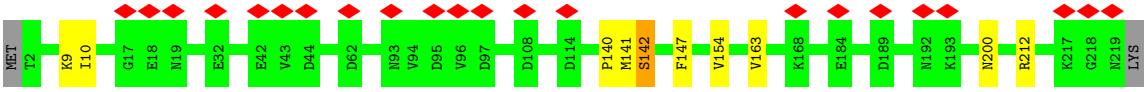




• Molecule 26: 50S ribosomal protein L3

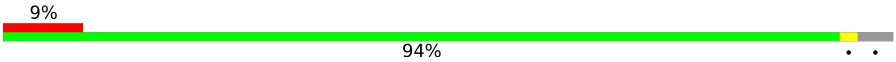
Chain E:

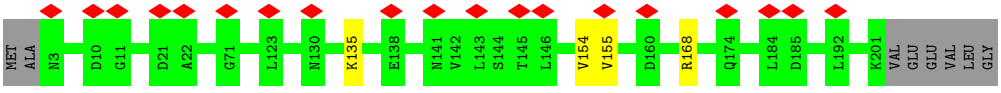




• Molecule 27: 50S ribosomal protein L4

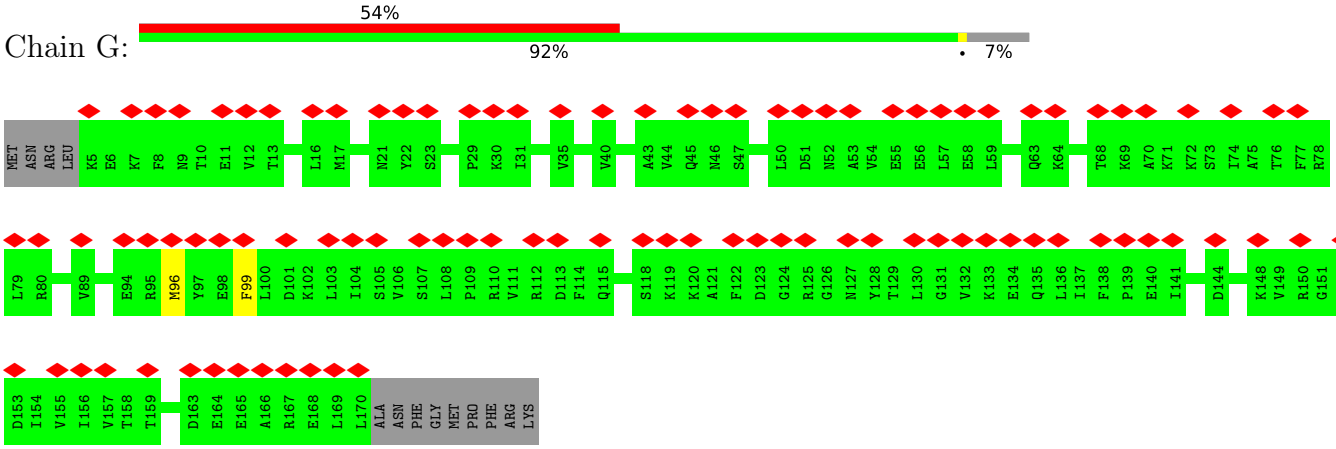
Chain F:





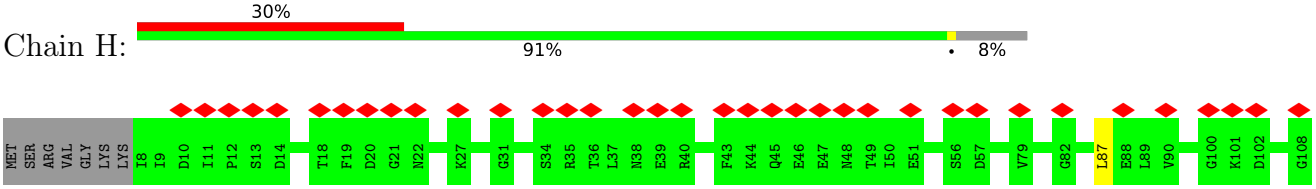
• Molecule 28: 50S ribosomal protein L5

Chain G:



• Molecule 29: 50S ribosomal protein L6

Chain H:



• Molecule 30: 50S ribosomal protein L13

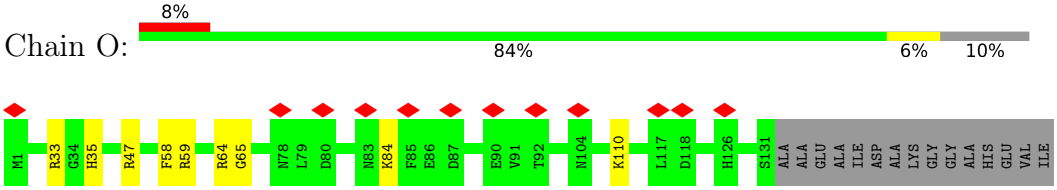
Chain M:

• Molecule 31: 50S ribosomal protein L14

Chain N:

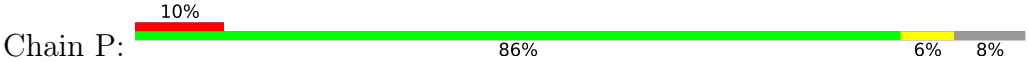
• Molecule 32: 50S ribosomal protein L15

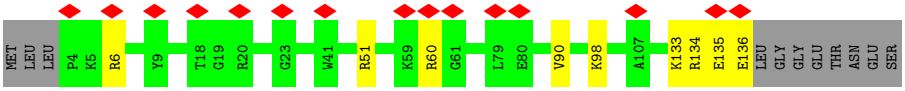
Chain O:



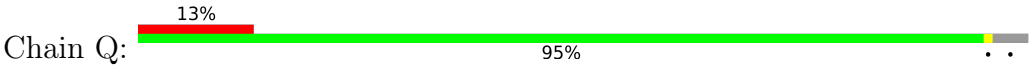
• Molecule 33: 50S ribosomal protein L16

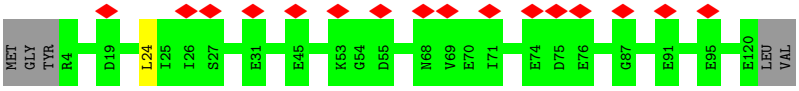
Chain P:



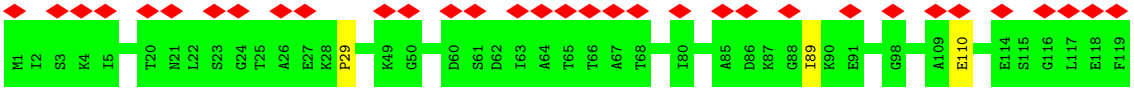


• Molecule 34: 50S ribosomal protein L17

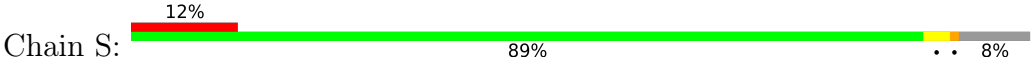


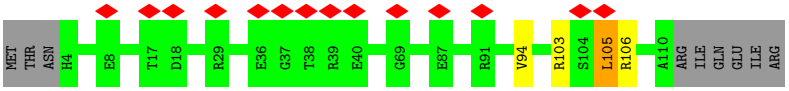


• Molecule 35: 50S ribosomal protein L18

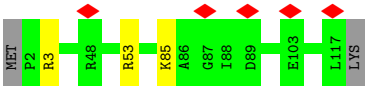


• Molecule 36: 50S ribosomal protein L19

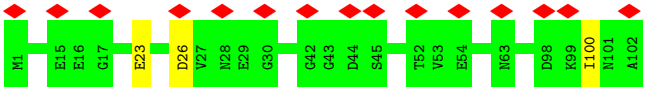




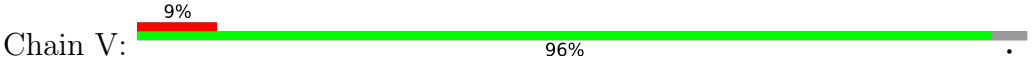
• Molecule 37: 50S ribosomal protein L20

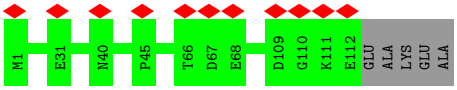


• Molecule 38: 50S ribosomal protein L21



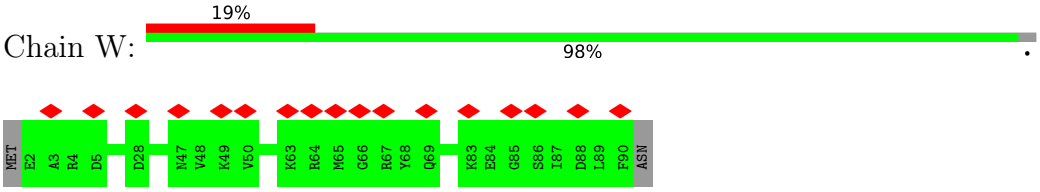
• Molecule 39: 50S ribosomal protein L22





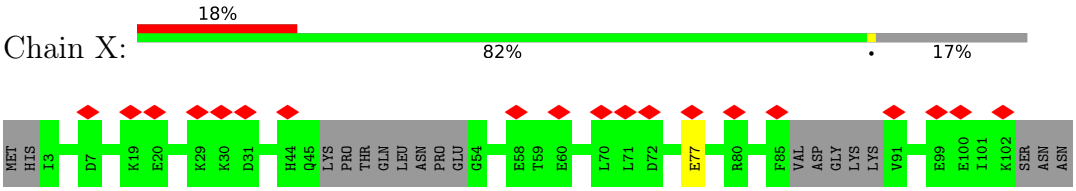
• Molecule 40: 50S ribosomal protein L23

Chain W:



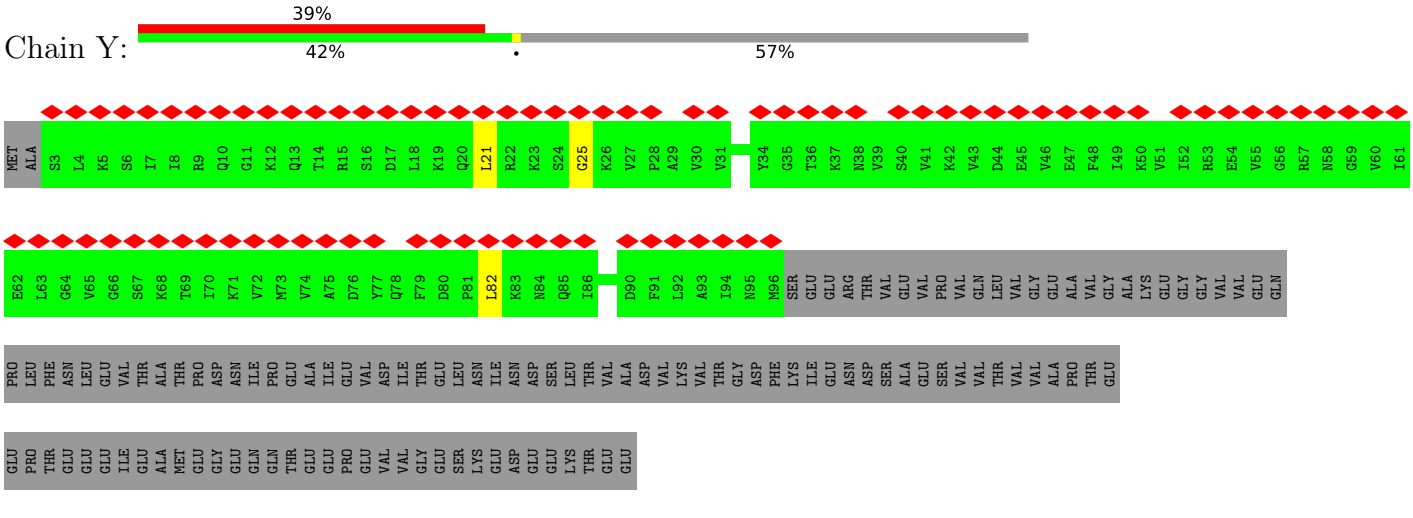
• Molecule 41: 50S ribosomal protein L24

Chain X:



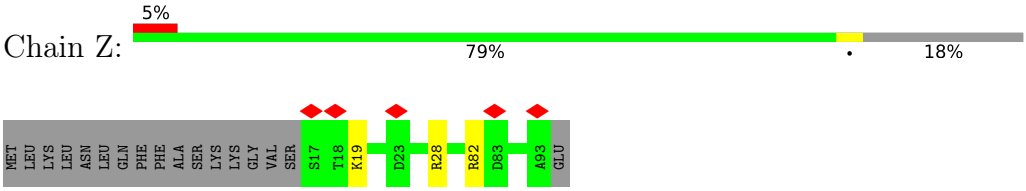
• Molecule 42: 50S ribosomal protein L25

Chain Y:



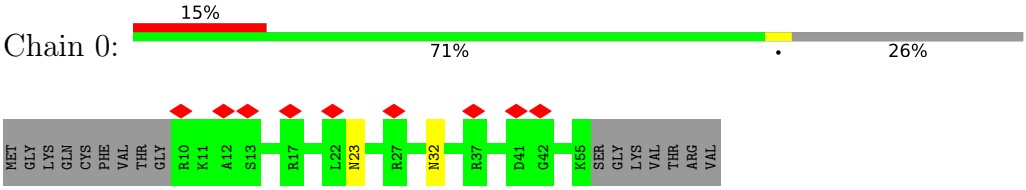
• Molecule 43: 50S ribosomal protein L27

Chain Z:



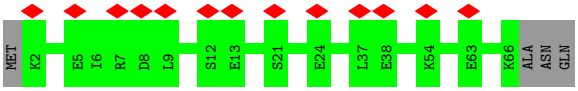
• Molecule 44: 50S ribosomal protein L28

Chain 0:

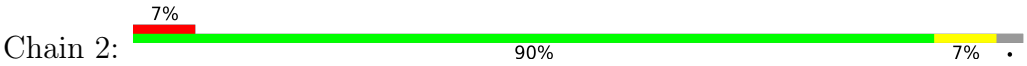


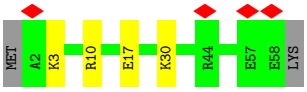
• Molecule 45: 50S ribosomal protein L29

Chain 1:

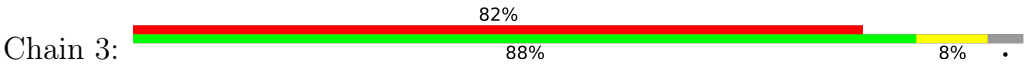


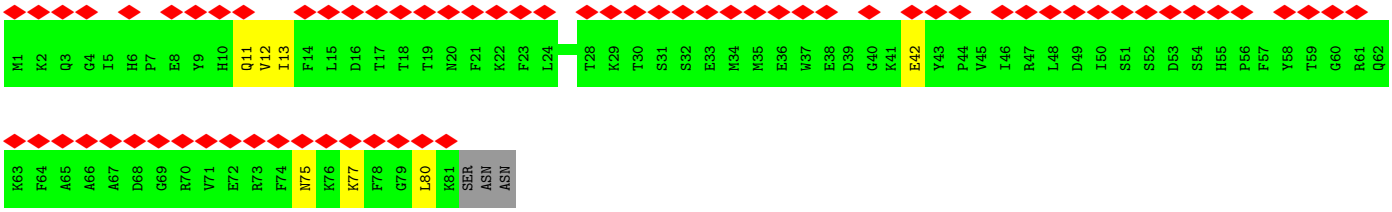
• Molecule 46: 50S ribosomal protein L30



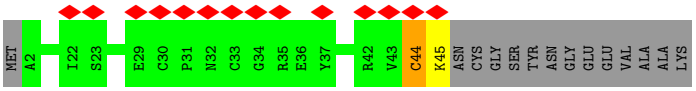


• Molecule 47: 50S ribosomal protein L31 type B



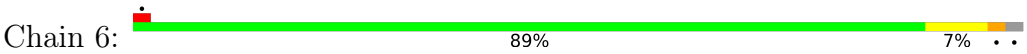


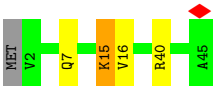
• Molecule 48: 50S ribosomal protein L32



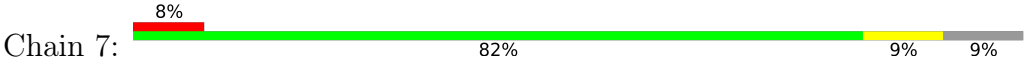
• Molecule 49: 50S ribosomal protein L33 2

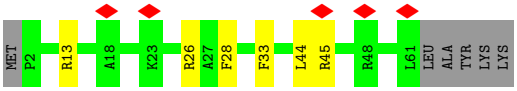
• Molecule 50: 50S ribosomal protein L34





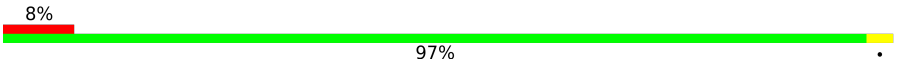
• Molecule 51: 50S ribosomal protein L35

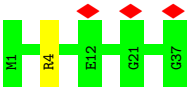




• Molecule 52: 50S ribosomal protein L36

Chain 8:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	83000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.299	Depositor
Minimum map value	-0.132	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	374.0, 374.0, 374.0	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	a	0.97	3/36954 (0.0%)	1.25	166/57629 (0.3%)
2	b	0.47	0/1815	0.72	3/2436 (0.1%)
3	c	0.39	0/1622	0.68	0/2178
4	d	0.46	0/1629	0.69	0/2185
5	e	0.53	0/1208	0.73	0/1628
6	f	0.54	0/792	0.68	0/1062
7	g	0.45	0/1157	0.73	2/1557 (0.1%)
8	h	0.58	0/1044	0.75	0/1401
9	i	0.41	0/1033	0.71	0/1386
10	j	0.42	0/803	0.69	0/1082
11	k	0.48	0/866	0.67	1/1169 (0.1%)
12	l	0.62	0/1075	0.80	0/1439
13	m	0.42	0/883	0.79	0/1182
14	n	0.46	0/512	0.81	0/678
15	o	0.53	0/747	0.80	0/996
16	p	0.56	0/723	0.69	0/971
17	q	0.57	0/706	0.73	0/944
18	r	0.51	0/473	0.76	0/632
19	s	0.40	0/695	0.68	0/934
20	t	0.43	0/606	0.69	0/810
21	u	0.35	0/380	0.53	0/498
22	v	0.37	0/841	0.72	0/1131
23	A	1.33	155/69971 (0.2%)	1.40	719/109124 (0.7%)
24	B	0.94	1/2717 (0.0%)	1.26	19/4232 (0.4%)
25	D	0.86	2/2138 (0.1%)	0.82	2/2869 (0.1%)
26	E	0.78	2/1673 (0.1%)	0.73	0/2243
27	F	0.72	0/1547	0.76	1/2088 (0.0%)
28	G	0.42	0/1326	0.73	0/1780
29	H	0.51	1/1302 (0.1%)	0.70	0/1757
30	M	0.68	0/1173	0.71	0/1578
31	N	0.77	0/927	0.83	0/1243
32	O	0.70	0/1010	0.89	4/1344 (0.3%)
33	P	0.75	0/1089	0.84	0/1460
34	Q	0.63	0/927	0.77	1/1238 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	R	0.48	0/931	0.74	0/1244
36	S	0.70	0/874	0.86	2/1168 (0.2%)
37	T	0.81	0/955	0.82	3/1265 (0.2%)
38	U	0.72	0/809	0.75	1/1080 (0.1%)
39	V	0.69	0/870	0.78	0/1171
40	W	0.69	0/733	0.76	0/978
41	X	0.50	0/672	0.66	0/893
42	Y	0.76	1/746 (0.1%)	1.56	4/1000 (0.4%)
43	Z	0.72	0/597	0.69	0/793
44	0	0.59	0/378	0.90	0/504
45	1	0.53	0/537	0.71	0/714
46	2	0.64	0/443	0.76	1/597 (0.2%)
47	3	0.47	0/680	0.83	1/911 (0.1%)
48	4	0.73	0/366	0.76	0/485
49	5	0.40	0/230	0.85	0/303
50	6	0.91	0/377	0.89	1/491 (0.2%)
51	7	0.73	0/491	0.96	2/643 (0.3%)
52	8	0.70	0/300	0.88	2/393 (0.5%)
All	All	1.08	165/153353 (0.1%)	1.23	935/229517 (0.4%)

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
2	b	0	2
3	c	0	1
4	d	0	2
5	e	0	1
6	f	0	1
7	g	0	6
11	k	0	1
12	l	0	3
13	m	0	1
14	n	0	2
17	q	0	2
19	s	0	1
22	v	0	7
25	D	0	2
26	E	0	5
27	F	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
30	M	0	1
31	N	0	1
32	O	0	4
33	P	0	3
35	R	0	3
36	S	0	2
37	T	0	1
38	U	0	1
41	X	0	1
43	Z	0	1
46	2	0	1
47	3	0	3
50	6	0	2
51	7	0	2
All	All	0	65

The worst 5 of 165 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
42	Y	25	GLY	C-N	17.38	1.74	1.34
26	E	147	PHE	CA-CB	-8.04	1.36	1.53
23	A	806	A	C5-C6	-7.55	1.34	1.41
23	A	2606	C	N1-C6	-7.36	1.32	1.37
23	A	2503	A	N9-C4	-7.23	1.33	1.37

The worst 5 of 935 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
42	Y	25	GLY	CA-C-N	-26.58	58.73	117.20
42	Y	25	GLY	O-C-N	25.46	163.44	122.70
42	Y	25	GLY	C-N-CA	-23.37	63.28	121.70
23	A	806	A	N1-C6-N6	18.77	129.86	118.60
23	A	2451	C	C6-N1-C2	-17.47	113.31	120.30

There are no chirality outliers.

5 of 65 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	b	19	GLN	Peptide
2	b	21	ARG	Peptide
3	c	160	ASP	Peptide

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Mol	Chain	Res	Type	Group
4	d	160	PHE	Peptide
4	d	93	ARG	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	b	220/255 (86%)	192 (87%)	27 (12%)	1 (0%)	29	66
3	c	201/217 (93%)	166 (83%)	34 (17%)	1 (0%)	29	66
4	d	193/200 (96%)	163 (84%)	30 (16%)	0	100	100
5	e	158/166 (95%)	124 (78%)	34 (22%)	0	100	100
6	f	92/98 (94%)	73 (79%)	18 (20%)	1 (1%)	14	50
7	g	139/156 (89%)	117 (84%)	20 (14%)	2 (1%)	11	45
8	h	129/132 (98%)	107 (83%)	21 (16%)	1 (1%)	19	56
9	i	126/132 (96%)	107 (85%)	19 (15%)	0	100	100
10	j	97/102 (95%)	87 (90%)	10 (10%)	0	100	100
11	k	113/129 (88%)	89 (79%)	24 (21%)	0	100	100
12	l	133/137 (97%)	98 (74%)	33 (25%)	2 (2%)	10	44
13	m	108/121 (89%)	87 (81%)	21 (19%)	0	100	100
14	n	58/61 (95%)	40 (69%)	18 (31%)	0	100	100
15	o	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
16	p	88/91 (97%)	69 (78%)	19 (22%)	0	100	100
17	q	83/87 (95%)	64 (77%)	19 (23%)	0	100	100
18	r	54/80 (68%)	41 (76%)	13 (24%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
19	s	82/92 (89%)	63 (77%)	19 (23%)	0	100 100
20	t	78/83 (94%)	73 (94%)	5 (6%)	0	100 100
21	u	43/58 (74%)	31 (72%)	9 (21%)	3 (7%)	1 15
22	v	99/190 (52%)	70 (71%)	21 (21%)	8 (8%)	1 11
25	D	273/277 (99%)	228 (84%)	44 (16%)	1 (0%)	34 69
26	E	216/220 (98%)	172 (80%)	41 (19%)	3 (1%)	11 45
27	F	197/207 (95%)	157 (80%)	40 (20%)	0	100 100
28	G	164/179 (92%)	123 (75%)	40 (24%)	1 (1%)	25 62
29	H	162/178 (91%)	140 (86%)	22 (14%)	0	100 100
30	M	143/145 (99%)	117 (82%)	25 (18%)	1 (1%)	22 59
31	N	120/122 (98%)	83 (69%)	37 (31%)	0	100 100
32	O	129/146 (88%)	90 (70%)	39 (30%)	0	100 100
33	P	131/144 (91%)	101 (77%)	30 (23%)	0	100 100
34	Q	115/122 (94%)	89 (77%)	26 (23%)	0	100 100
35	R	117/119 (98%)	95 (81%)	22 (19%)	0	100 100
36	S	105/116 (90%)	86 (82%)	17 (16%)	2 (2%)	8 40
37	T	114/118 (97%)	102 (90%)	12 (10%)	0	100 100
38	U	100/102 (98%)	79 (79%)	20 (20%)	1 (1%)	15 51
39	V	110/117 (94%)	98 (89%)	12 (11%)	0	100 100
40	W	87/91 (96%)	68 (78%)	19 (22%)	0	100 100
41	X	81/105 (77%)	50 (62%)	31 (38%)	0	100 100
42	Y	92/217 (42%)	68 (74%)	24 (26%)	0	100 100
43	Z	75/94 (80%)	65 (87%)	9 (12%)	1 (1%)	12 47
44	0	44/62 (71%)	33 (75%)	11 (25%)	0	100 100
45	1	63/69 (91%)	56 (89%)	7 (11%)	0	100 100
46	2	55/59 (93%)	48 (87%)	6 (11%)	1 (2%)	8 41
47	3	79/84 (94%)	47 (60%)	31 (39%)	1 (1%)	12 47
48	4	42/58 (72%)	36 (86%)	5 (12%)	1 (2%)	6 35
49	5	24/49 (49%)	19 (79%)	5 (21%)	0	100 100
50	6	42/45 (93%)	34 (81%)	6 (14%)	2 (5%)	2 22
51	7	58/66 (88%)	38 (66%)	20 (34%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
52	8	35/37 (95%)	27 (77%)	8 (23%)	0	100 100
All	All	5353/6024 (89%)	4288 (80%)	1031 (19%)	34 (1%)	29 62

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	u	13	GLU
21	u	50	GLU
22	v	97	ASN
22	v	99	LYS
22	v	100	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	b	192/221 (87%)	188 (98%)	4 (2%)	53 74
3	c	164/175 (94%)	160 (98%)	4 (2%)	49 71
4	d	172/175 (98%)	171 (99%)	1 (1%)	86 93
5	e	126/131 (96%)	120 (95%)	6 (5%)	25 56
6	f	82/86 (95%)	81 (99%)	1 (1%)	71 84
7	g	122/132 (92%)	118 (97%)	4 (3%)	38 64
8	h	112/113 (99%)	110 (98%)	2 (2%)	59 77
9	i	106/109 (97%)	106 (100%)	0	100 100
10	j	89/91 (98%)	86 (97%)	3 (3%)	37 64
11	k	91/104 (88%)	90 (99%)	1 (1%)	73 85
12	l	117/119 (98%)	114 (97%)	3 (3%)	46 69
13	m	94/104 (90%)	93 (99%)	1 (1%)	73 85
14	n	52/53 (98%)	51 (98%)	1 (2%)	57 76
15	o	80/81 (99%)	77 (96%)	3 (4%)	33 61
16	p	76/77 (99%)	74 (97%)	2 (3%)	46 69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	q	80/82 (98%)	80 (100%)	0	100 100
18	r	51/68 (75%)	50 (98%)	1 (2%)	55 74
19	s	73/80 (91%)	73 (100%)	0	100 100
20	t	67/69 (97%)	66 (98%)	1 (2%)	65 81
21	u	41/54 (76%)	33 (80%)	8 (20%)	1 9
22	v	91/173 (53%)	66 (72%)	25 (28%)	0 3
25	D	222/224 (99%)	219 (99%)	3 (1%)	67 82
26	E	175/177 (99%)	174 (99%)	1 (1%)	86 93
27	F	163/169 (96%)	162 (99%)	1 (1%)	86 93
28	G	147/158 (93%)	146 (99%)	1 (1%)	84 91
29	H	144/155 (93%)	143 (99%)	1 (1%)	84 91
30	M	123/123 (100%)	123 (100%)	0	100 100
31	N	100/100 (100%)	100 (100%)	0	100 100
32	O	104/112 (93%)	102 (98%)	2 (2%)	57 76
33	P	110/119 (92%)	104 (94%)	6 (6%)	21 53
34	Q	98/102 (96%)	98 (100%)	0	100 100
35	R	95/95 (100%)	95 (100%)	0	100 100
36	S	93/102 (91%)	93 (100%)	0	100 100
37	T	96/98 (98%)	96 (100%)	0	100 100
38	U	86/86 (100%)	86 (100%)	0	100 100
39	V	91/94 (97%)	91 (100%)	0	100 100
40	W	80/82 (98%)	80 (100%)	0	100 100
41	X	73/90 (81%)	73 (100%)	0	100 100
42	Y	83/190 (44%)	82 (99%)	1 (1%)	71 84
43	Z	60/75 (80%)	59 (98%)	1 (2%)	60 79
44	0	39/52 (75%)	37 (95%)	2 (5%)	24 55
45	1	59/62 (95%)	59 (100%)	0	100 100
46	2	51/53 (96%)	50 (98%)	1 (2%)	55 74
47	3	72/75 (96%)	70 (97%)	2 (3%)	43 67
48	4	41/51 (80%)	39 (95%)	2 (5%)	25 56
49	5	26/47 (55%)	25 (96%)	1 (4%)	33 61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
50	6	39/40 (98%)	39 (100%)	0	100 100
51	7	52/57 (91%)	50 (96%)	2 (4%)	33 61
52	8	35/35 (100%)	35 (100%)	0	100 100
All	All	4635/5120 (90%)	4537 (98%)	98 (2%)	56 74

5 of 98 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	v	78	ILE
25	D	69	ASN
22	v	82	ASN
22	v	93	LYS
27	F	135	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
22	v	88	GLN
27	F	148	GLN
44	0	32	ASN
22	v	97	ASN
26	E	50	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1540/1556 (98%)	373 (24%)	0
23	A	2909/2923 (99%)	727 (24%)	18 (0%)
24	B	113/114 (99%)	23 (20%)	0
All	All	4562/4593 (99%)	1123 (24%)	18 (0%)

5 of 1123 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	G
1	a	9	A
1	a	10	G
1	a	11	A
1	a	15	U

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	2418	G
23	A	2501	U
23	A	2467	C
23	A	1104	U
23	A	2360	A

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	A	1
42	Y	1
25	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1569:G	O3'	1570:G	P	3.00
1	Y	25:GLY	C	26:LYS	N	1.74
1	D	5:TYR	C	6:LYS	N	1.17

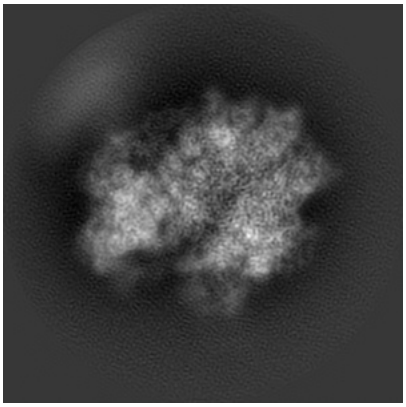
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-3625. These allow visual inspection of the internal detail of the map and identification of artifacts.

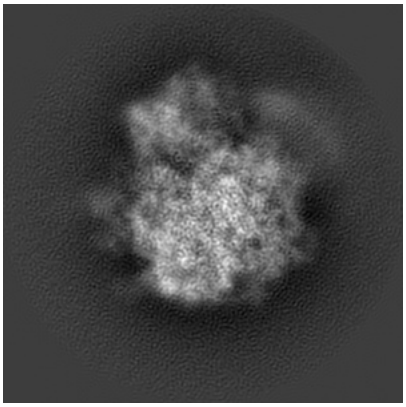
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

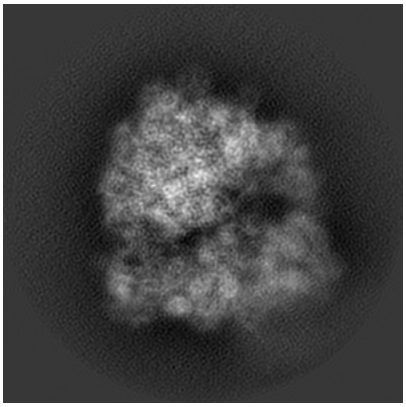
6.1.1 Primary map



X



Y

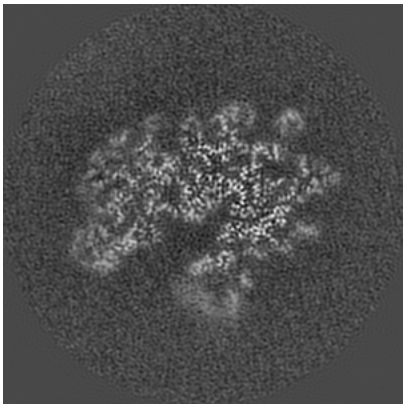


Z

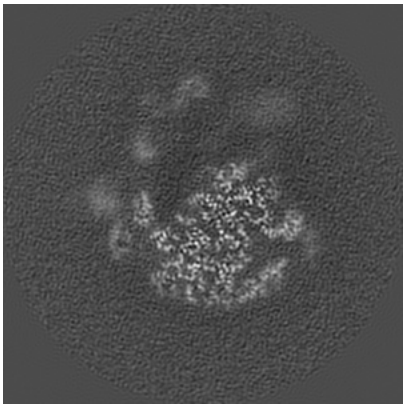
The images above show the map projected in three orthogonal directions.

6.2 Central slices

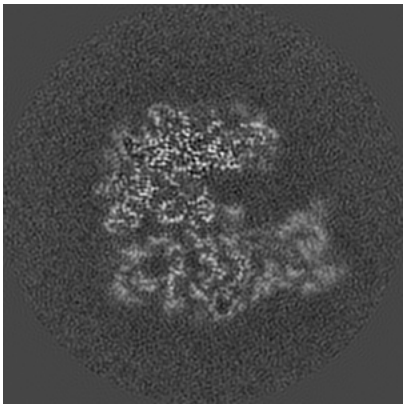
6.2.1 Primary map



X Index: 170



Y Index: 170

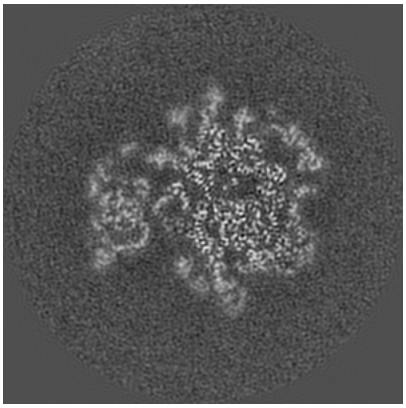


Z Index: 170

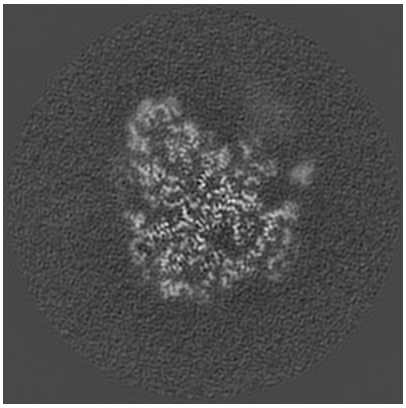
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

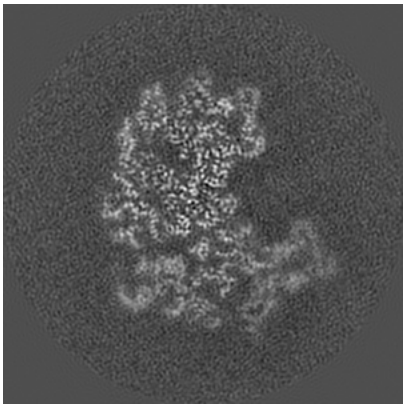
6.3.1 Primary map



X Index: 144



Y Index: 212



Z Index: 187

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

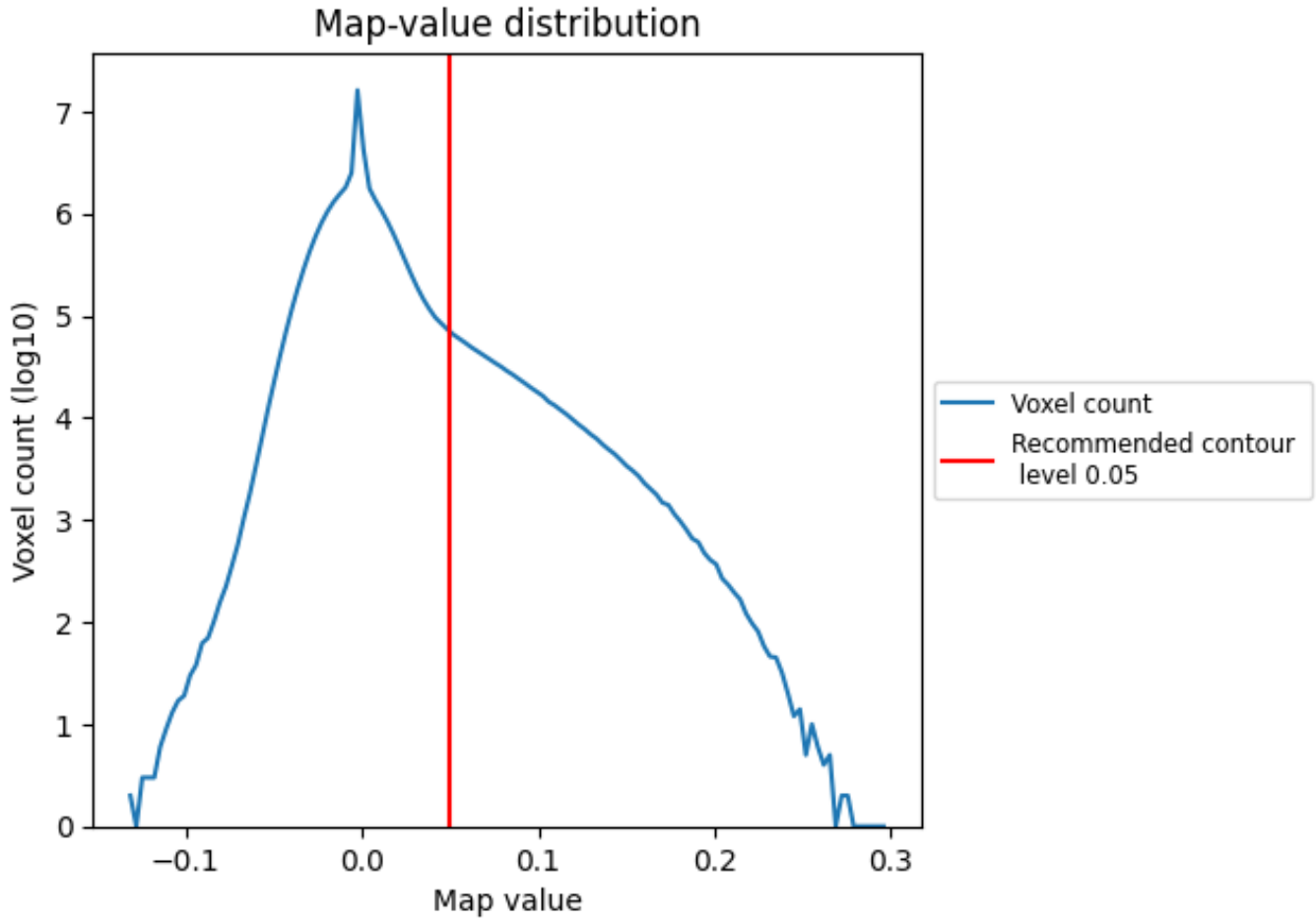
6.5 Mask visualisation (i)

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

7 Map analysis

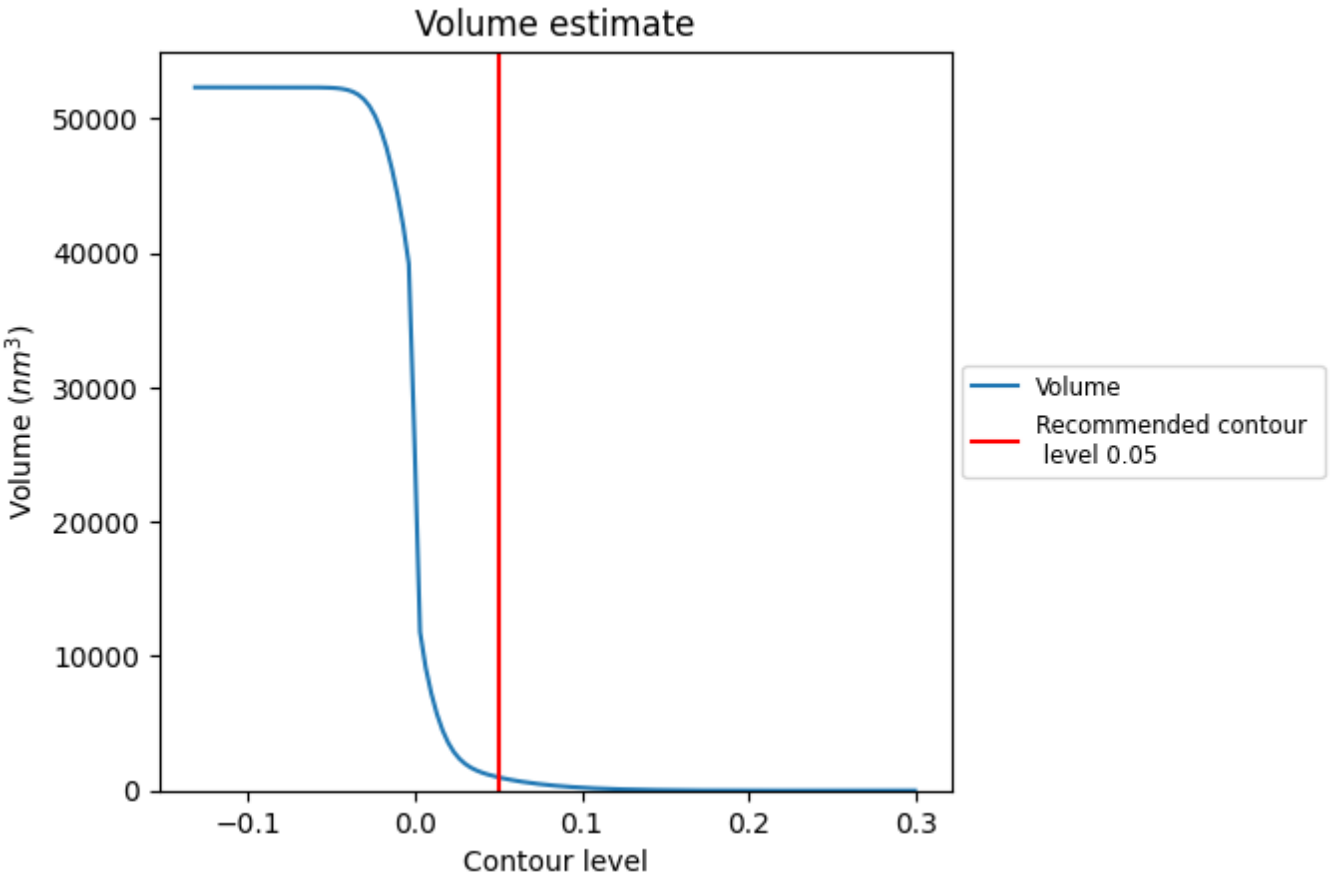
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

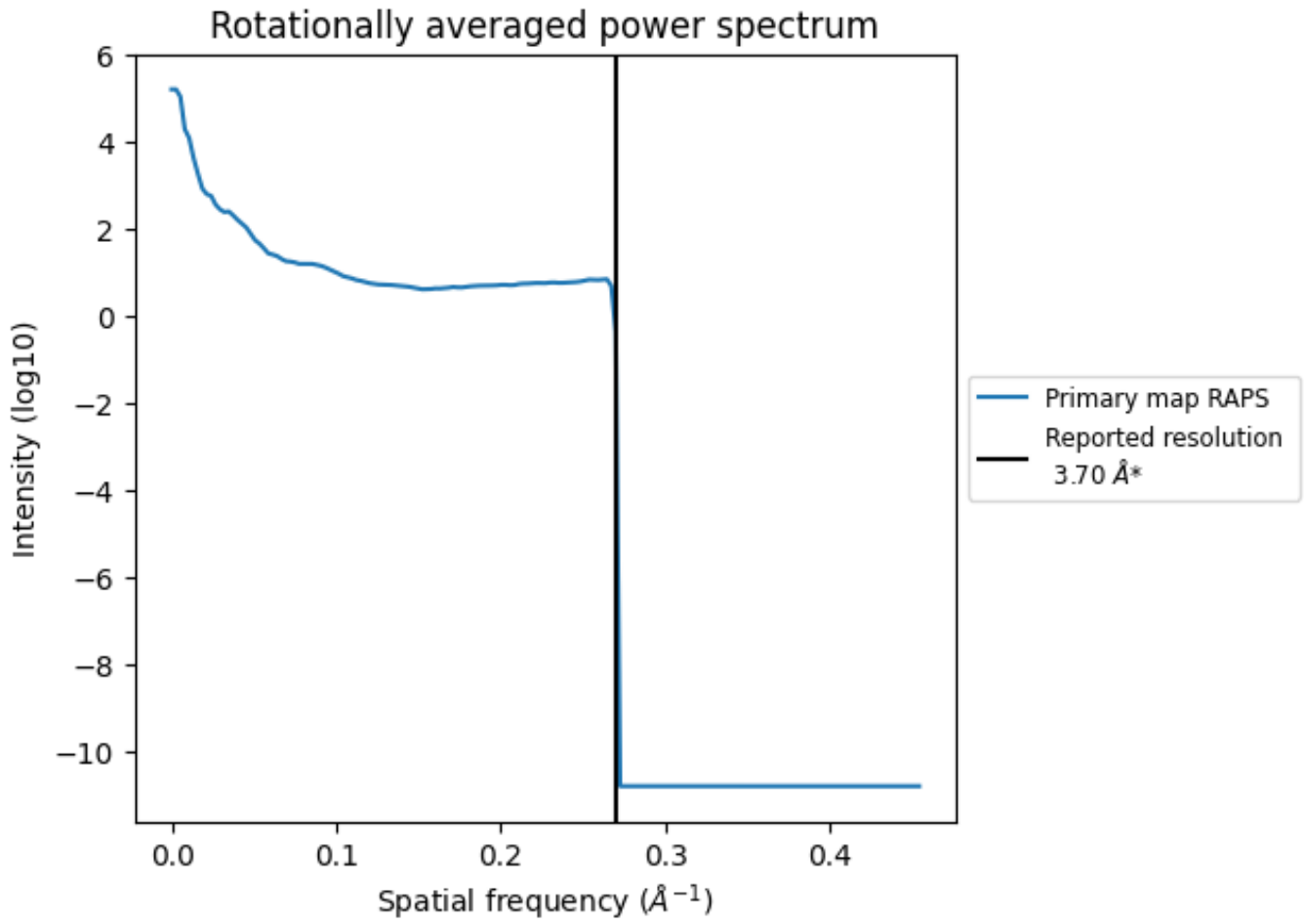
7.2 Volume estimate (i)



The volume at the recommended contour level is 989 nm^3; this corresponds to an approximate mass of 894 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.270 Å^{-1}

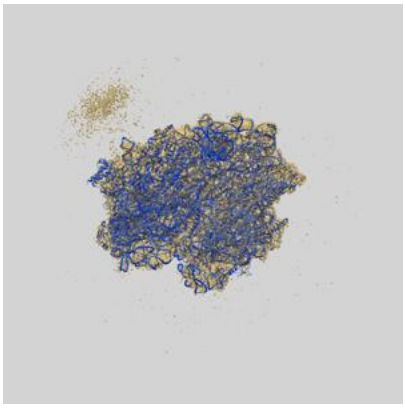
8 Fourier-Shell correlation (i)

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

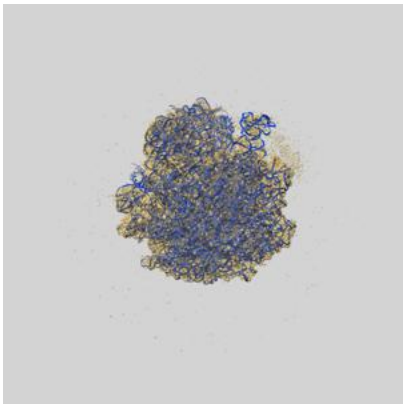
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-3625 and PDB model 5ND9. Per-residue inclusion information can be found in section 3 on page 13.

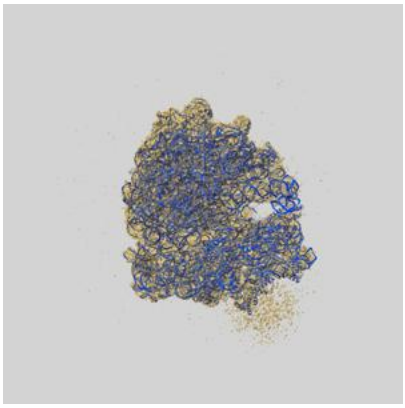
9.1 Map-model overlay



X



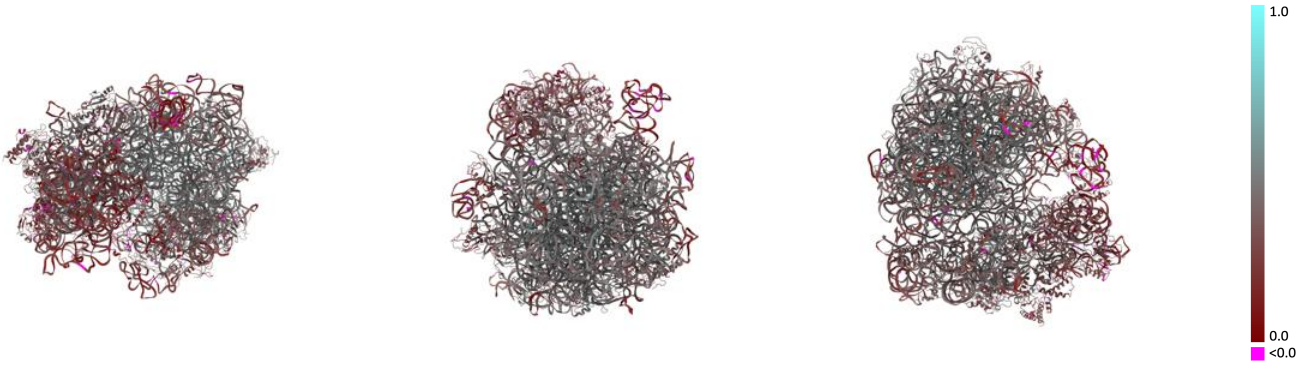
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

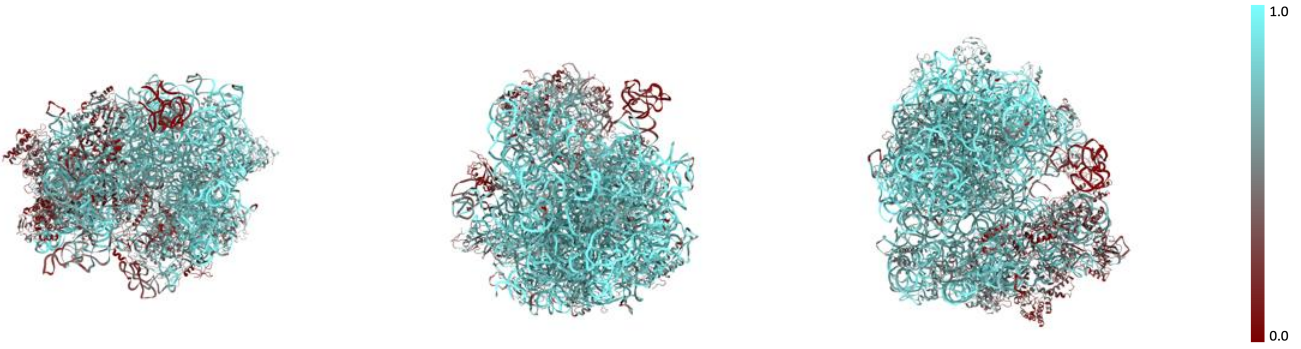
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

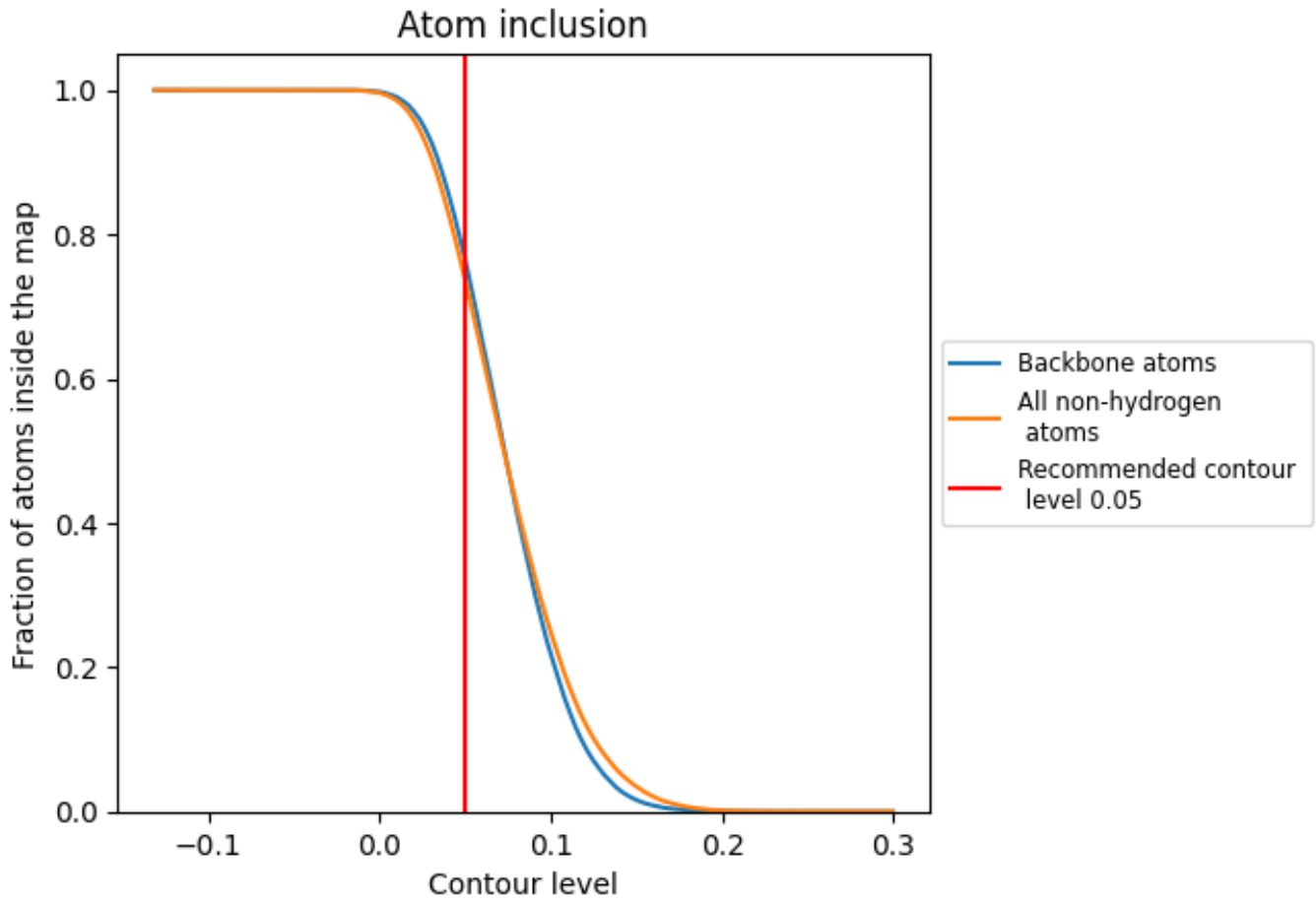
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.05).

9.4 Atom inclusion (i)



At the recommended contour level, 76% of all backbone atoms, 73% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7350	0.3860
0	0.5854	0.4000
1	0.5923	0.3850
2	0.6744	0.4350
3	0.1659	0.2440
4	0.5710	0.4250
5	0.1622	0.3020
6	0.7330	0.4740
7	0.6951	0.4180
8	0.6323	0.4370
A	0.8542	0.4220
B	0.8737	0.3600
D	0.7000	0.4740
E	0.6911	0.4530
F	0.6752	0.4230
G	0.3561	0.2770
H	0.5151	0.3260
M	0.7044	0.4470
N	0.5964	0.4550
O	0.6869	0.4070
P	0.6641	0.4230
Q	0.6614	0.4210
R	0.5611	0.3230
S	0.6389	0.4310
T	0.7330	0.4450
U	0.6518	0.4290
V	0.6833	0.4580
W	0.6153	0.4130
X	0.5825	0.3730
Y	0.1214	0.3050
Z	0.7203	0.4400
a	0.8055	0.3510
b	0.2801	0.3130
c	0.2192	0.2750
d	0.4103	0.2760

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Chain	Atom inclusion	Q-score
e	0.4342	0.3600
f	0.3646	0.3660
g	0.2342	0.2470
h	0.5302	0.3770
i	0.2431	0.2360
j	0.2085	0.2290
k	0.4844	0.3560
l	0.5712	0.3890
m	0.1998	0.2280
n	0.3222	0.2550
o	0.5416	0.3410
p	0.6014	0.3850
q	0.5242	0.3650
r	0.4321	0.3540
s	0.2568	0.1900
t	0.5401	0.3160
u	0.0801	0.2820
v	0.1948	0.2990