



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 02:53 PM UTC

PDB ID : 7QH4 / pdb_00007qh4
EMDB ID : EMD-13961
Title : Structure of the B. subtilis disome - collided 70S ribosome
Authors : Kratzat, H.; Buschauer, R.; Berninghausen, O.; Beckmann, R.
Deposited on : 2021-12-10
Resolution : 5.45 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:

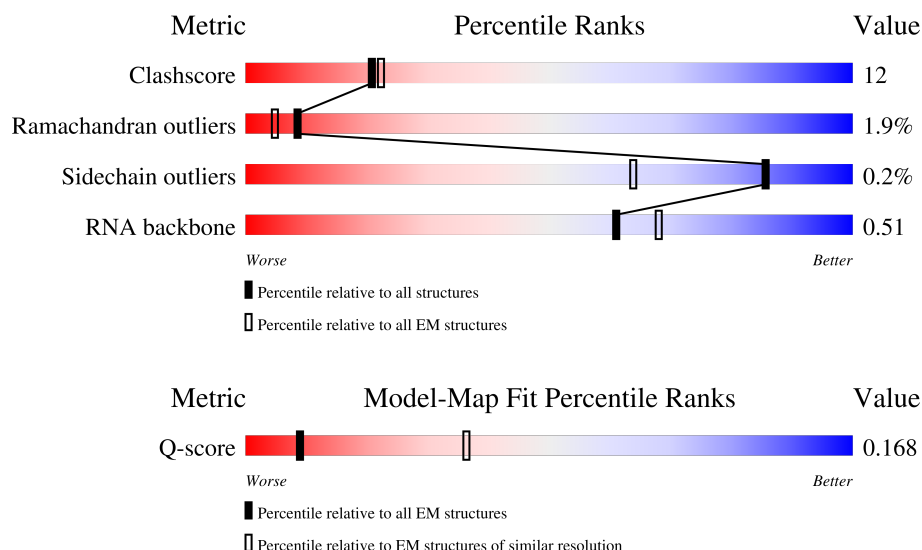
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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 5.45 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	469 (4.95 - 5.95)

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	A	2928	
2	B	119	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	208	
5	E	207	
6	F	179	
7	G	179	
8	H	166	
9	I	141	
10	J	145	
11	K	122	
12	L	146	
13	M	144	
14	N	120	
15	O	120	
16	P	115	
17	Q	119	
18	R	102	
19	S	113	
20	T	95	
21	U	103	
22	V	94	
23	Y	62	
24	Z	66	
25	a	59	
26	b	59	
27	c	49	
28	d	44	

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Mol	Chain	Length	Quality of chain
29	e	66	
30	f	37	
31	W	1555	
32	X	246	
33	g	218	
34	h	200	
35	i	166	
36	j	95	
37	k	156	
38	l	132	
39	m	130	
40	n	102	
41	o	131	
42	p	138	
43	q	121	
44	r	61	
45	s	89	
46	t	90	
47	u	87	
48	v	79	
49	w	92	
50	x	88	
51	l	77	
51	y	77	

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 136043 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	A	2923	Total	C	N	O	P	0	0
			62767	28002	11589	20253	2923		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1558	C	G	conflict	GB 1864548803

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	178	Total	C	N	O	S	0	0
			1404	893	245	259	7		

- Molecule 7 is a protein called Ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			955	602	163	189	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	154	THR	ALA	conflict	UNP A0A063X7V1

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	133	Total	C	N	O	S	0	0
			981	617	173	185	6		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	138	Total	C	N	O	S	0	0
			1097	703	208	181	5		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	101	Total	C	N	O	0	0
			786	501	139	146		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

- Molecule 31 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	1544	Total	C	N	O	P	0	0
			33115	14768	6067	10736	1544		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	X	224	Total	C	N	O	0	0
			896	448	224	224		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	g	210	Total	C	N	O	0	0
			840	420	210	210		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	h	199	Total	C	N	O	0	0
			797	398	199	200		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	i	165	Total	C	N	O	0	0
			661	330	165	166		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	j	95	Total	C	N	O	0	0
			381	190	95	96		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	k	153	Total	C	N	O	0	0
			613	306	153	154		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	l	131	Total	C	N	O	0	0
			525	262	131	132		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	m	130	Total	C	N	O	0	0
			521	260	130	131		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	n	102	Total	C	N	O	0	0
			409	204	102	103		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	o	118	Total	C	N	O	0	0
			472	236	118	118		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	p	137	Total	C	N	O	0	0
			549	274	137	138		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	q	119	Total	C	N	O	0	0
			476	238	119	119		

- Molecule 44 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r	60	Total	C	N	O	0	0
			241	120	60	61		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	s	88	Total	C	N	O	0	0
			353	176	88	89		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	t	89	Total	C	N	O	0	0
			357	178	89	90		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	u	86	Total	C	N	O	0	0
			345	172	86	87		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	v	71	Total	C	N	O	0	0
			285	142	71	72		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	w	84	Total	C	N	O	0	0
			336	168	84	84		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	x	86	Total	C	N	O	0	0
			345	172	86	87		

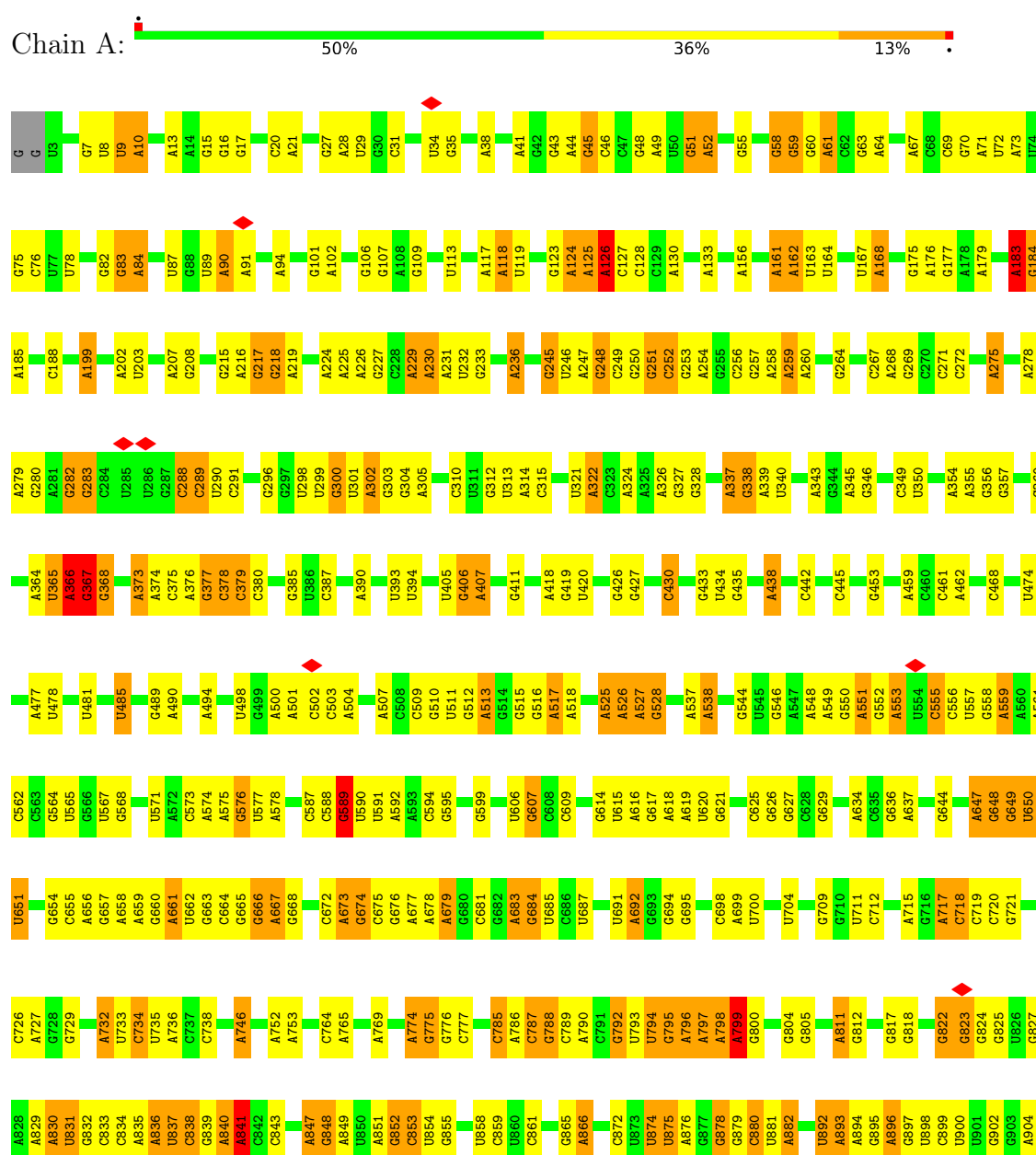
- Molecule 51 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		
51	1	77	Total	C	N	O	P	0	0
			1643	731	290	545	77		

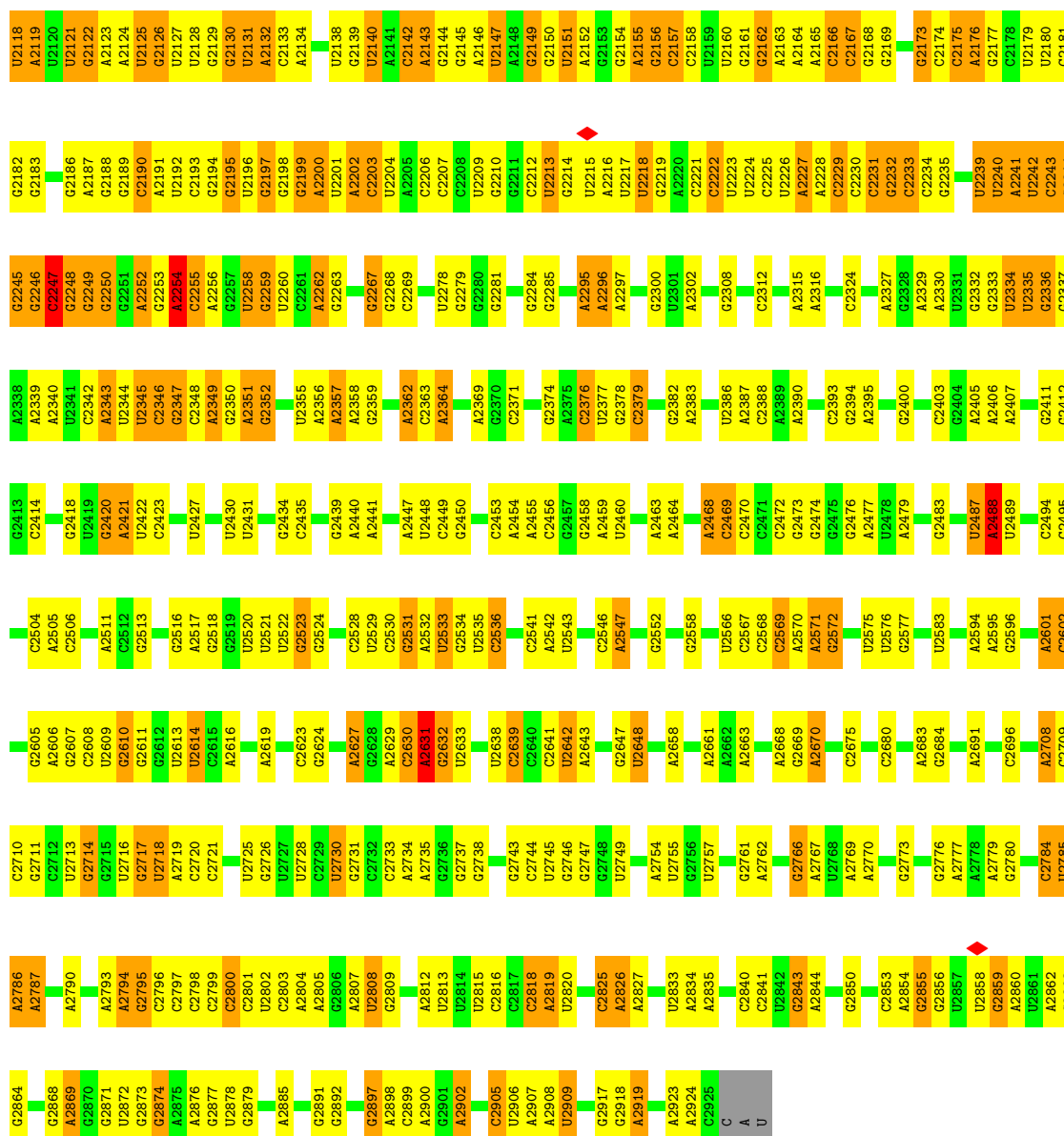
3 Residue-property plots

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.

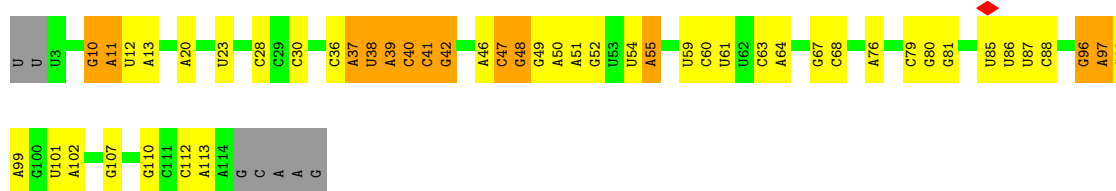
• Molecule 1: 23S rRNA



A2030	A2031	A2032	G2033	G2038	G2039	U2040	A2041	A2042	A2043	A2044	U2045	U2046	A2047	U2048	A2052	A2059	A2060	A2061	A2062	A2066	G2067	U2070	A2071	C2072	A2078	G2082	A2083	G2084	G2085	G2086	A2087	A2088	A2089	G2090	A2091	G2092	G2098	G2099	A2100	G2101	U2105	G2109	C2110	A2111	C2114	U2115	G2116	A2117							
A1948	U1952	C1953	C1954	A1957	G1958	G1959	U1960	A1965	A1966	A1967	U1968	U1969	U1972	G1979	U1980	A1981	A1982	G1983	U1984	U1985	G1988	A1989	C1990	C1991	C1992	A1995	C1996	G1997	A1998	A1999	A2000	G2001	A2006	A2007	G2008	G2009	A2010	U2011	C2012	U2020	G2021	U2022	G2023	U2024	C2025	A2026	A2027	C2028	G2029						
C1867	G1868	G1871	C1872	U1873	A1876	A1877	A1882	A1883	G1886	G1887	A1888	U1893	U1894	C1897	A1900	A1901	G1902	C1903	G1904	A1905	A1906	G1910	C1911	G1912	A1913	A1914	U1915	U1916	G1917	A1918	A1919	A1925	A1928	A1929	A1930	C1931	G1932	G1933	C1934	G1935	C1938	G1939	U1940	A1941	A1942	C1943	U1944	A1945							
A1784	G1785	U1786	G1787	A1788	A1789	U1790	A1791	G1792	G1793	C1796	G1797	G1799	A1802	U1808	A1809	G1810	A1812	A1813	A1814	A1815	A1816	C1817	A1818	U1823	C1824	U1825	C1826	U1827	C1828	C1829	G1830	A1831	A1832	G1833	C1834	C1835	A1839	G1840	G1841	G1846	A1848	U1849	A1850	G1851	C1855	A1858	A1942	U1943	C1862	G2029					
G1688	U1691	U1692	C1693	A1694	A1695	U1696	A1697	U1704	C1705	G1706	U1707	U1708	A1709	A1710	G1711	G1712	A1713	C1715	G1719	A1724	A1727	C1728	G1739	G1744	A1745	G1752	G1753	U1754	C1755	U1756	G1757	U1758	U1759	A1767	A1768	G1769	C1770	C1771	A1774	G1775	A1776	G1777	A1778	G1779	C1780	G1781	C1782	G1783							
U1595	U1596	U1599	A1601	A1602	U1607	A1608	G1613	A1614	A1615	G1616	U1708	A1710	G1711	A1618	A1620	U1626	A1627	G1628	C1629	G1630	A1631	G1632	A1638	G1639	G1640	C1644	U1647	A1648	G1651	C1652	A1653	A1654	A1655	C1656	C1657	G1658	A1659	C1660	A1661	G1664	A1667	G1674	A1679	A1680	A1686	G1687									
A1499	U1500	U1501	U1504	U1505	A1506	U1507	U1513	A1516	A1517	G1518	C1519	A1520	G1521	U1522	A1524	G1525	A1526	C1527	U1528	G1529	G1530	U1535	A1536	G1537	G1538	C1539	U1543	A1553	U1554	A1555	C1558	G1561	A1562	G1563	G1568	G1572	C1573	G1578	A1581	U1582	U1583	U1584	A1585	G1496	U1587										
C1395	C1396	A1397	A1398	C1402	G1403	A1404	G1407	G1408	U1411	A1412	U1417	U1418	A1423	A1424	C1425	A1426	G1431	A1432	U1433	A1434	U1435	U1436	C1437	C1438	G1439	C1440	A1442	C1450	U1451	C1452	A1453	C1454	C1455	A1456	U1459	G1460	A1464	A1473	C1474	A1477	G1478	G1479	C1495	G1497	U1498										
G1309	A1312	A1313	A1314	G1315	A1316	G1317	G1318	G1319	G1322	A1325	A1326	U1327	A1335	A1339	A1340	U1341	C1344	U1345	A1346	A1347	G1348	U1351	U1352	C1353	C1354	U1355	A1360	A1361	G1362	G1363	C1364	U1365	G1371	C1374	A1375	G1376	G1377	G1378	U1379	U1380	A1381	G1382	U1383	A1388	A1393	G1394									
G1225	U1226	G1227	G1228	U1229	A1230	G1231	G1236	U1242	A1243	A1244	G1245	G1246	G1247	U1248	U1249	G1250	U1251	A1252	A1253	A1254	C1255	C1256	C1257	A1258	A1260	C1261	G1262	G1263	G1264	G1268	A1269	G1278	G1285	A1286	U1289	G1290	A1291	G1292	A1293	A1294	U1295	G1296	C1297	C1298	G1299	A1302	U1303	G1304	G1306						
G1135	U1136	G1137	C1138	G1139	U1140	A1141	G1145	C1148	A1149	C1150	U1151	G1152	U1154	C1155	G1156	A1157	G1158	G1171	A1172	A1173	A1174	G1177	U1178	A1179	G1180	G1181	G1182	G1183	G1184	U1187	A1188	A1189	A1194	A1197	G1198	C1199	G1200	A1201	A1202	G1207	G1208	G1209	U1218	C1219	G1220	A1221	A1222	C1223	A1224						
U1064	U1065	A1066	U1067	G1068	U1069	G1070	G1071	A1072	A1073	A1074	A1075	G1076	G1077	A1078	U1079	G1080	A1082	G1083	C1085	A1086	A1097	A1100	G1101	G1102	A1103	U1104	G1105	U1106	U1107	G1108	G1109	C1110	U1111	U1112	A1113	G1114	A1115	A1116	G1117	C1118	A1119	G1120	C1121	C1122	A1123	C1124	C1125	A1126	U1127	U1128	U1129	A1130	A1131	A1132	A1133
U979	C980	C981	U982	U983	G984	G985	A987	G988	G992	C997	G998	A1003	U1004	A1005	A1006	G1007	G928	G929	C930	C931	C932	C933	U934	A935	C936	C937	G938	G939	U942	A943	C944	C945	G946	A947	A948	A952	G953	A956	A957	A958	C959	A964	A965	U966	A970	A971	U972	G973	A974	U1060	A1061	C1063			

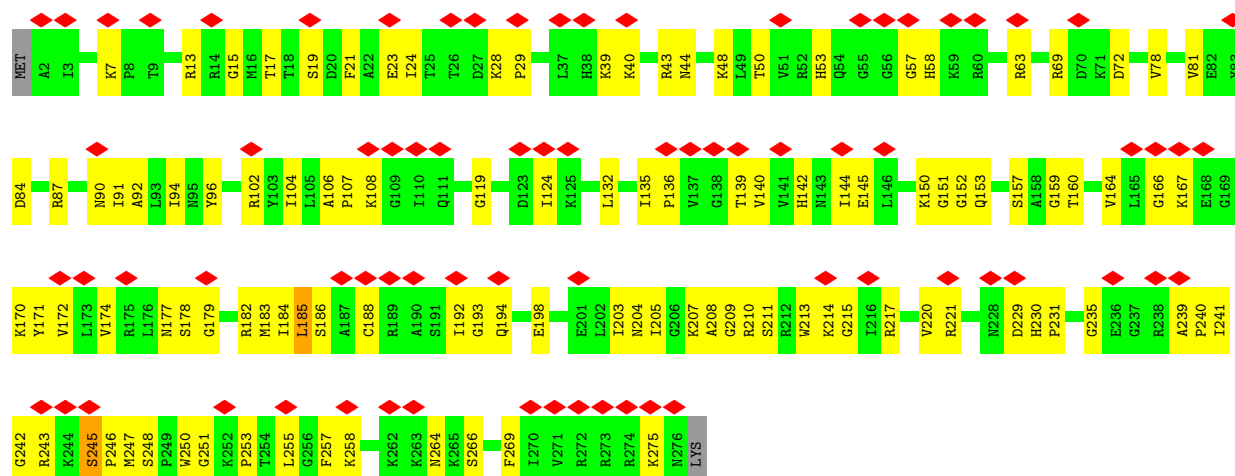


• Molecule 2: 5S rRNA

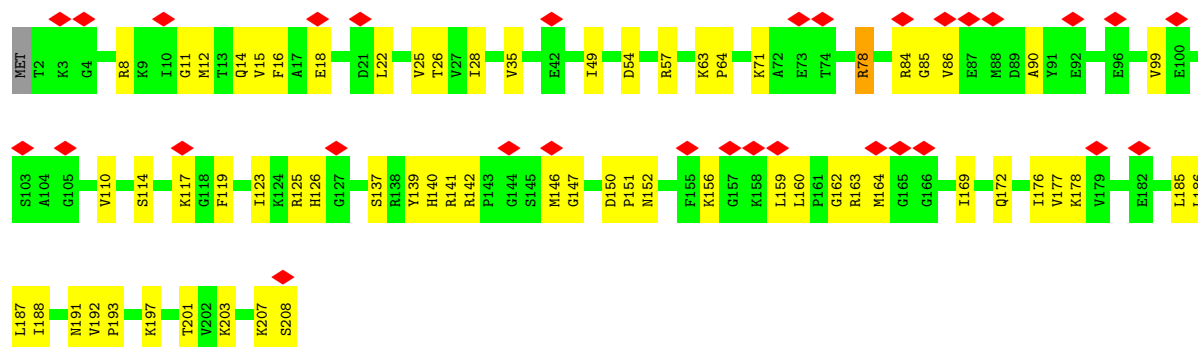


• Molecule 3: 50S ribosomal protein L2

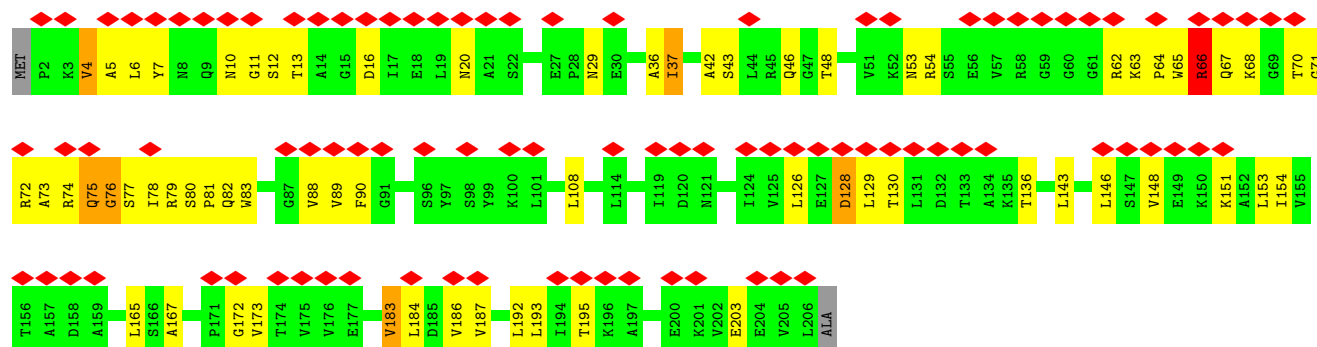




• Molecule 4: 50S ribosomal protein L3

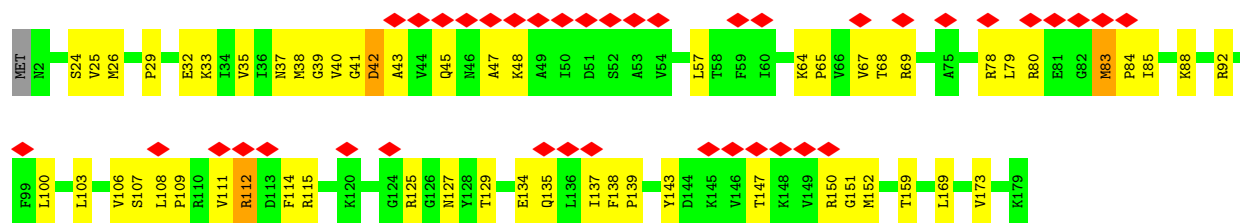


• Molecule 5: 50S ribosomal protein L4

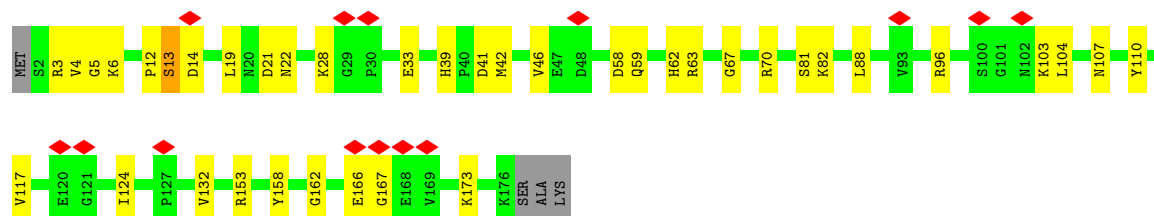
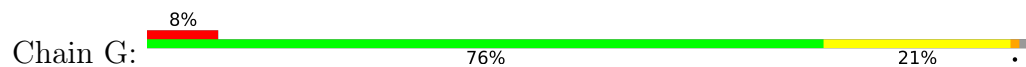


• Molecule 6: 50S ribosomal protein L5

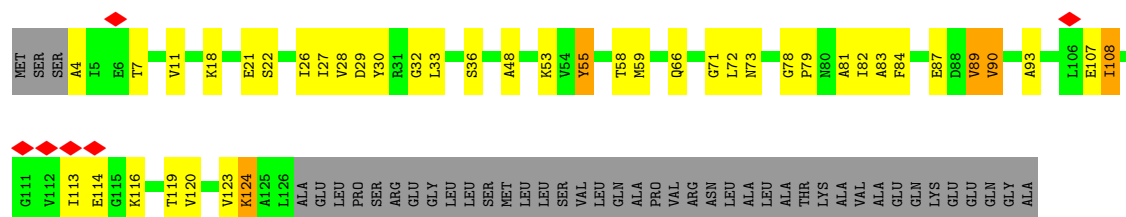




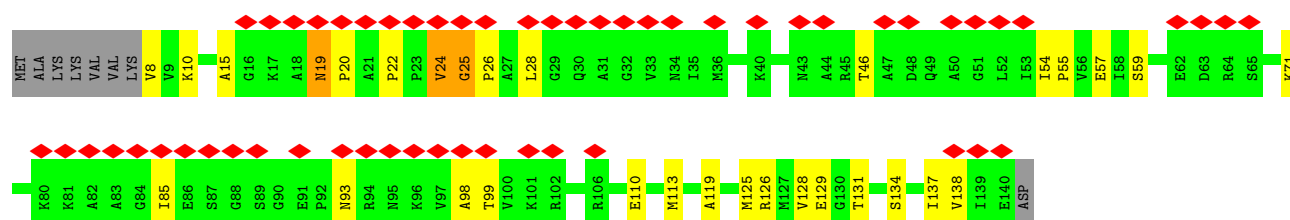
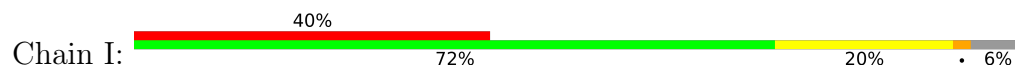
• Molecule 7: Ribosomal protein L6



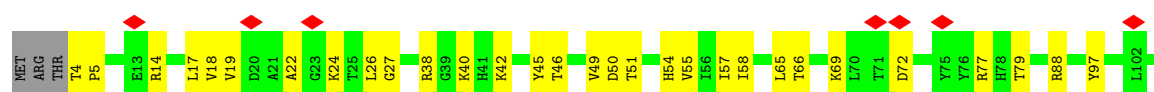
• Molecule 8: 50S ribosomal protein L10

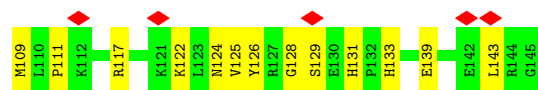


• Molecule 9: 50S ribosomal protein L11

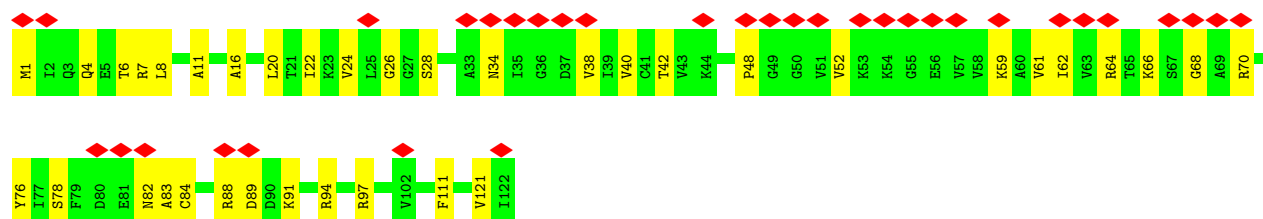


• Molecule 10: 50S ribosomal protein L13

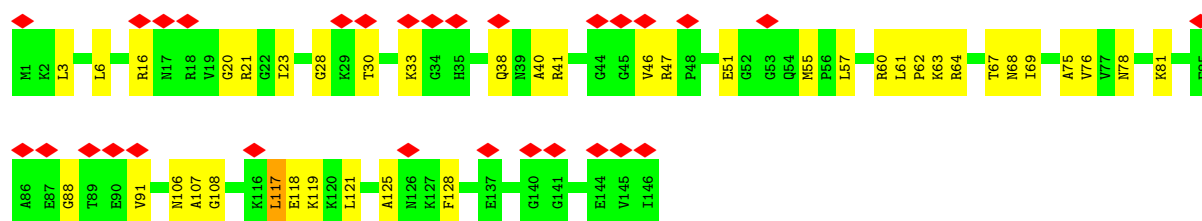
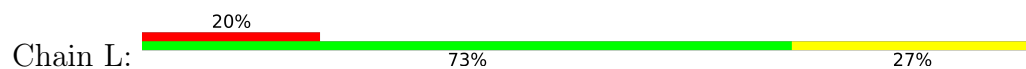




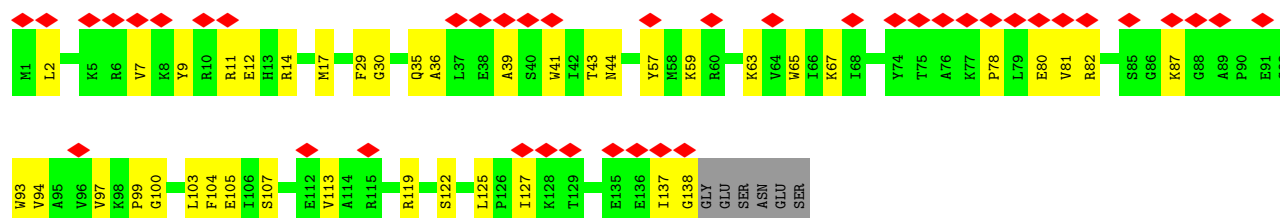
- Molecule 11: 50S ribosomal protein L14



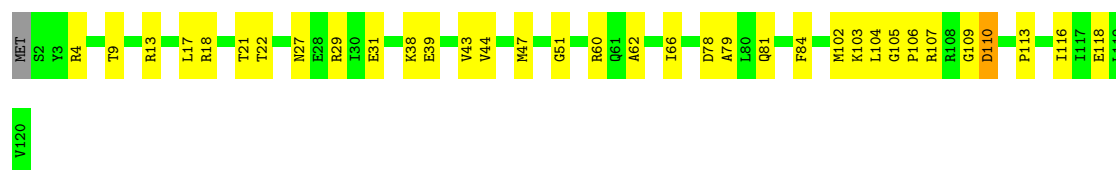
- Molecule 12: 50S ribosomal protein L15



- Molecule 13: 50S ribosomal protein L16

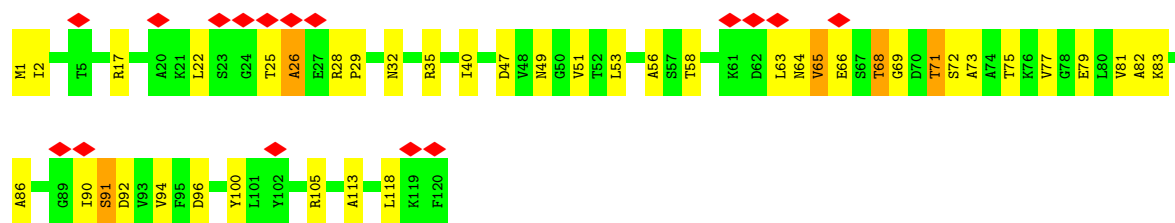


- Molecule 14: 50S ribosomal protein L17

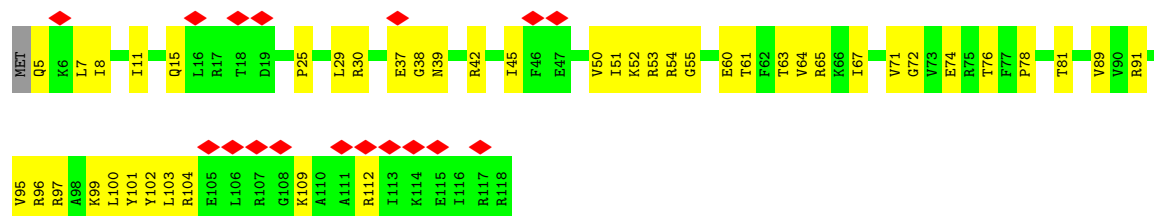


- Molecule 15: 50S ribosomal protein L18

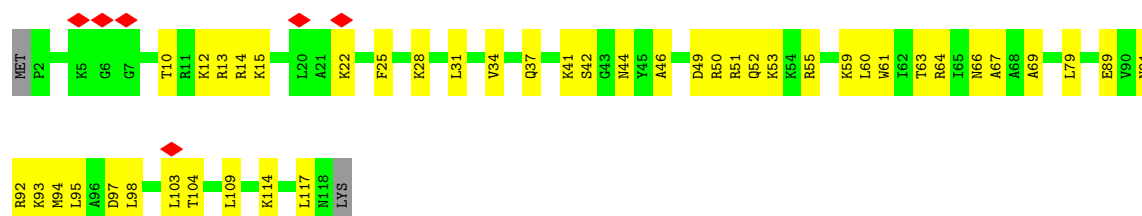




- Molecule 16: 50S ribosomal protein L19



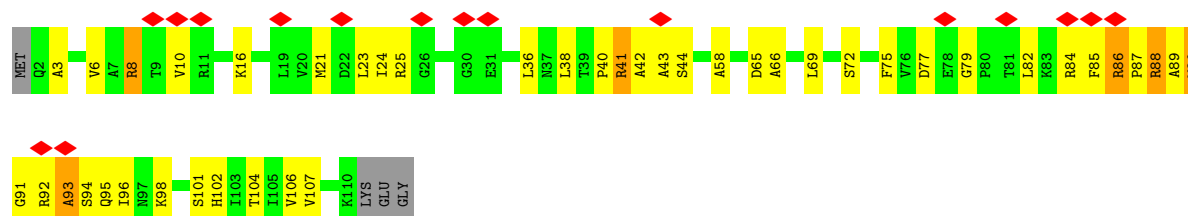
- Molecule 17: 50S ribosomal protein L20



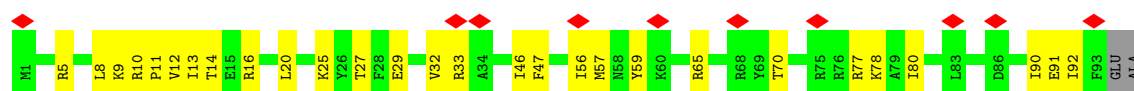
- Molecule 18: 50S ribosomal protein L21



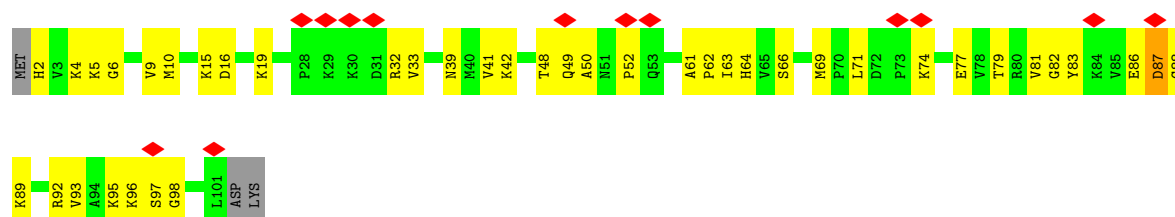
- Molecule 19: 50S ribosomal protein L22



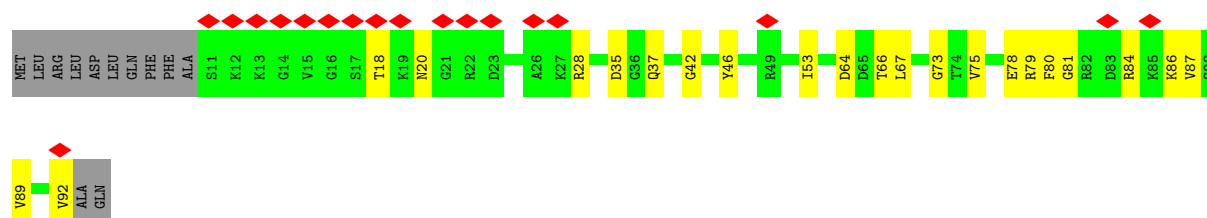
- Molecule 20: 50S ribosomal protein L23



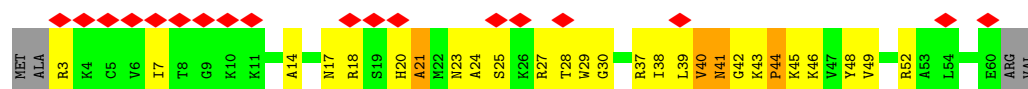
• Molecule 21: 50S ribosomal protein L24



• Molecule 22: 50S ribosomal protein L27



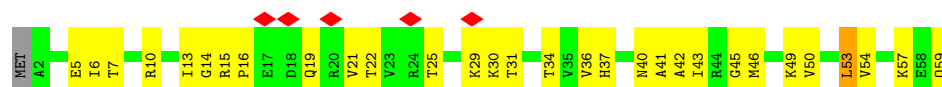
• Molecule 23: 50S ribosomal protein L28



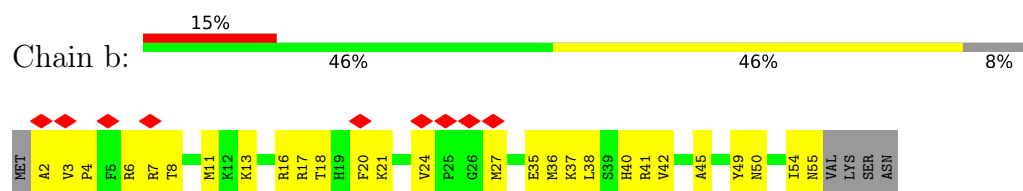
• Molecule 24: 50S ribosomal protein L29



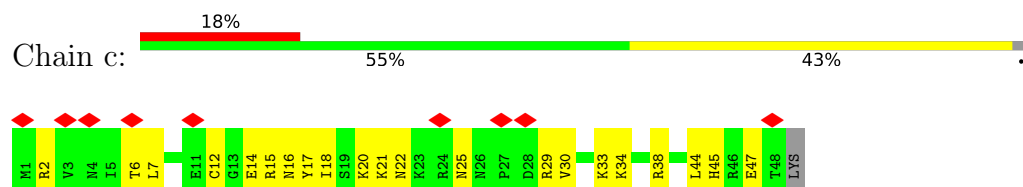
• Molecule 25: 50S ribosomal protein L30



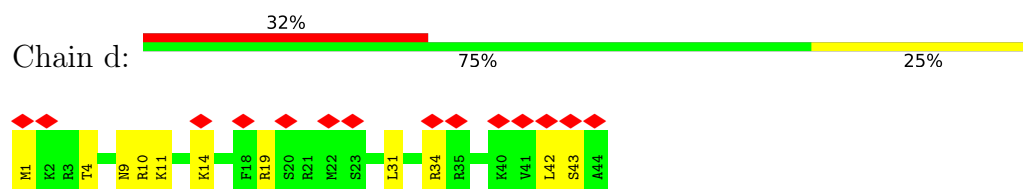
- Molecule 26: 50S ribosomal protein L32



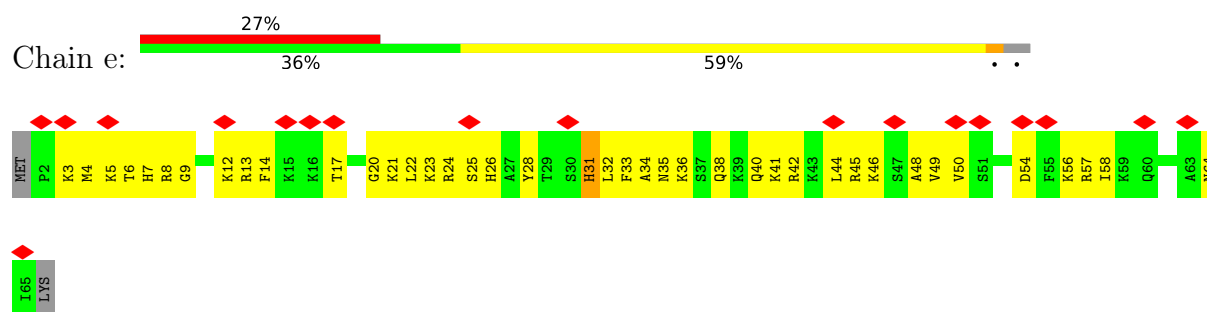
- Molecule 27: 50S ribosomal protein L33



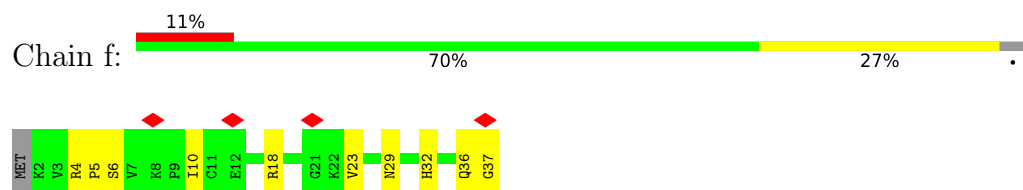
- Molecule 28: 50S ribosomal protein L34



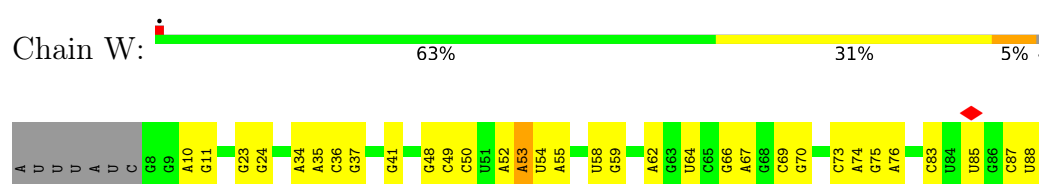
- Molecule 29: 50S ribosomal protein L35

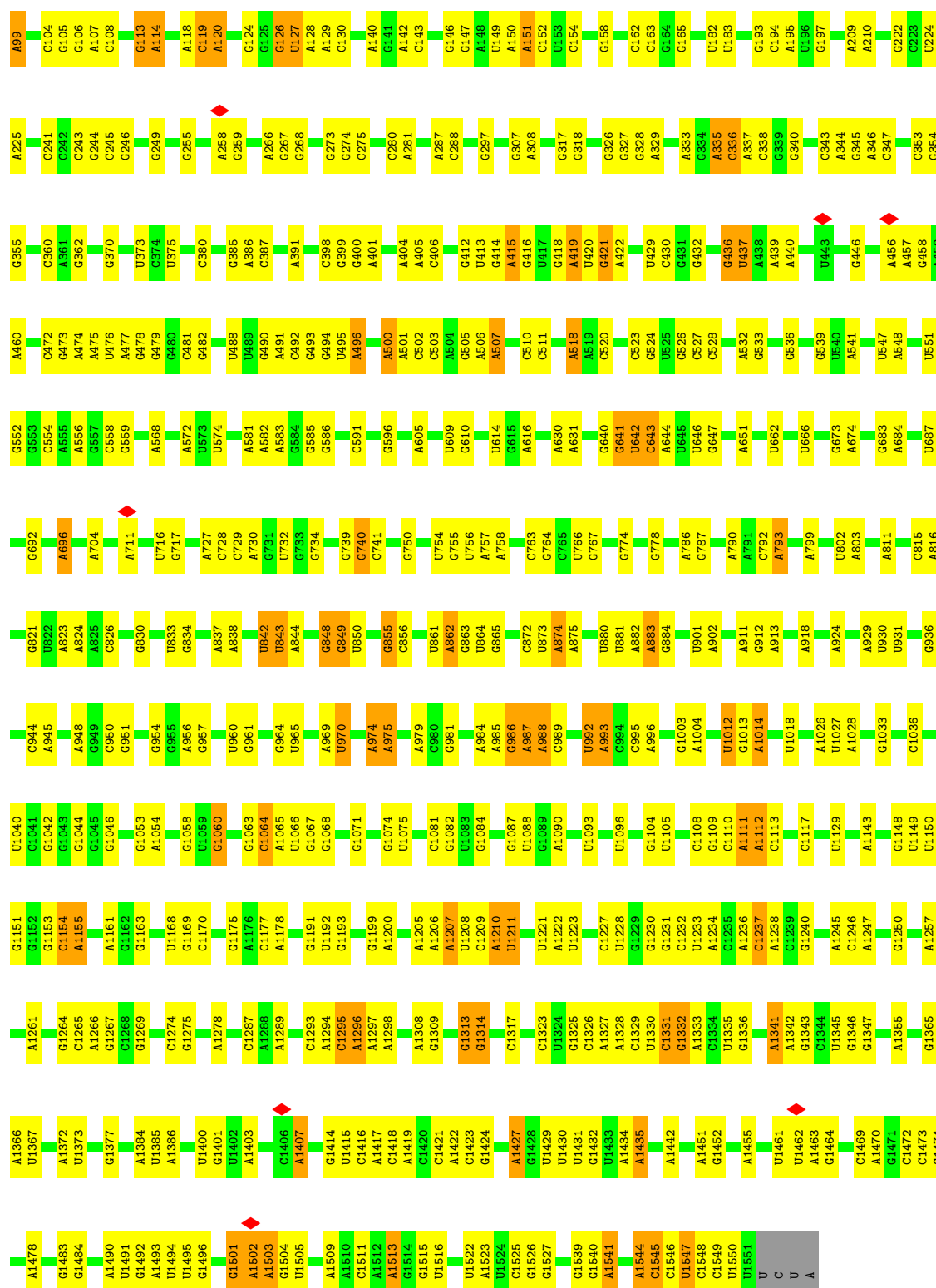


- Molecule 30: 50S ribosomal protein L36



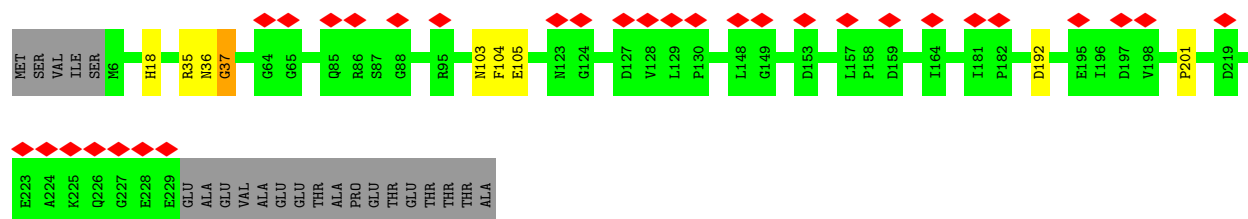
- Molecule 31: 16S rRNA



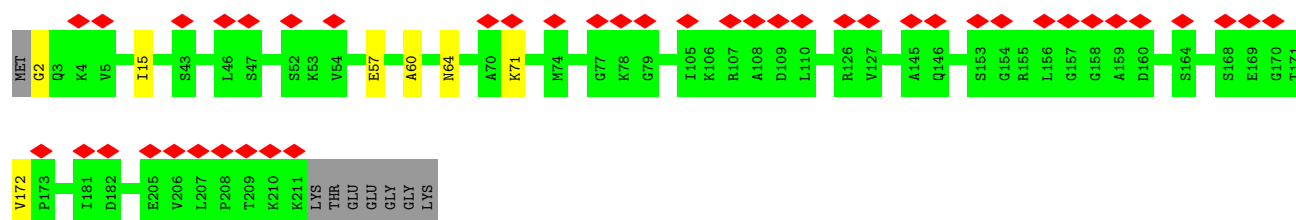
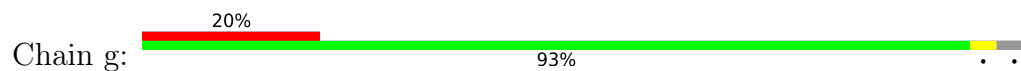


• Molecule 32: 30S ribosomal protein S2

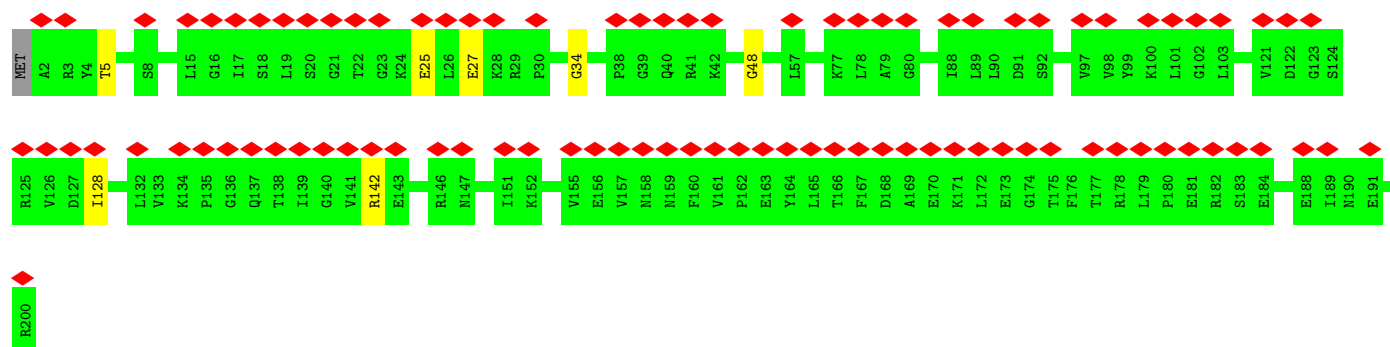
Chain X: 13% 87% 9%



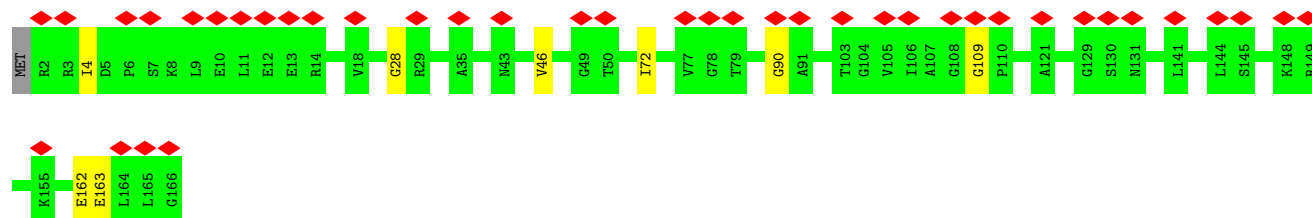
- Molecule 33: 30S ribosomal protein S3



- Molecule 34: 30S ribosomal protein S4

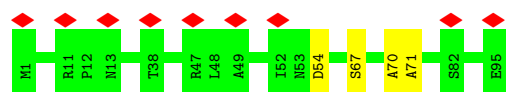


- Molecule 35: 30S ribosomal protein S5

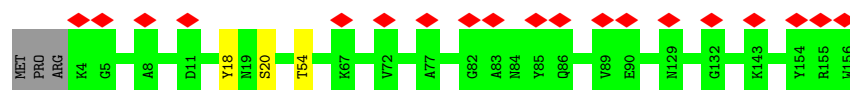


- Molecule 36: 30S ribosomal protein S6

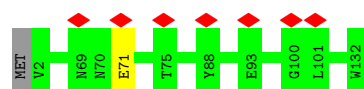




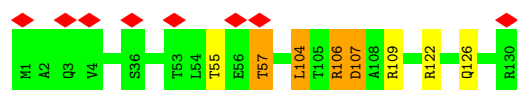
- Molecule 37: 30S ribosomal protein S7



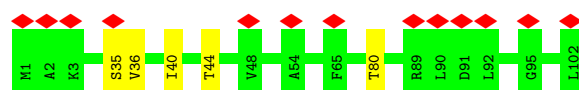
- Molecule 38: 30S ribosomal protein S8



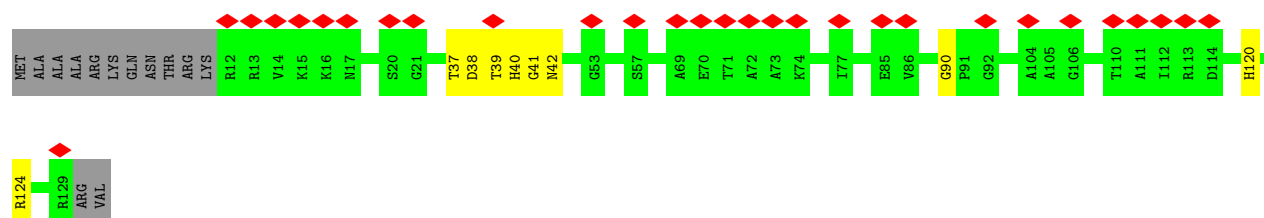
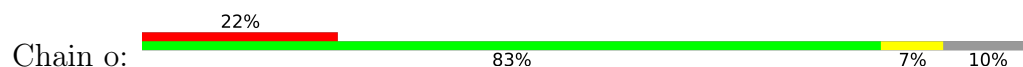
- Molecule 39: 30S ribosomal protein S9



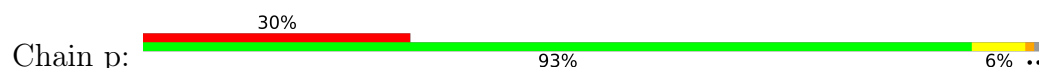
- Molecule 40: 30S ribosomal protein S10

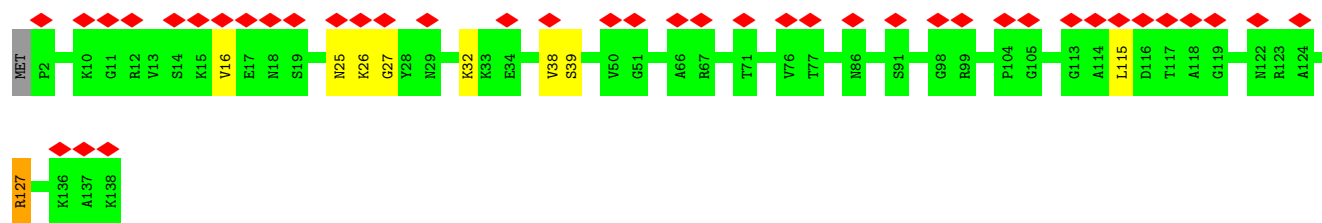


- Molecule 41: 30S ribosomal protein S11

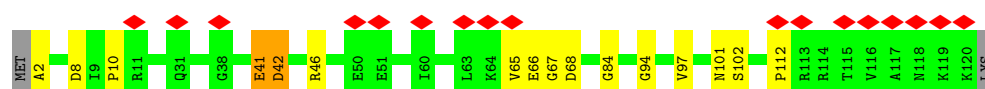
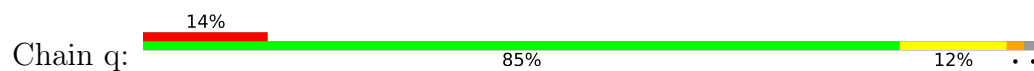


- Molecule 42: 30S ribosomal protein S12

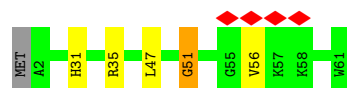
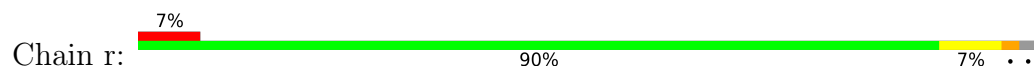




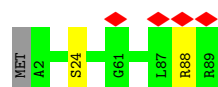
- Molecule 43: 30S ribosomal protein S13



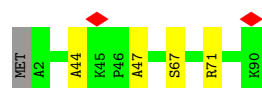
- Molecule 44: 30S ribosomal protein S14 type Z



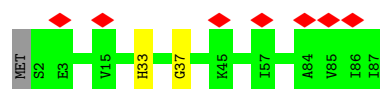
- Molecule 45: 30S ribosomal protein S15



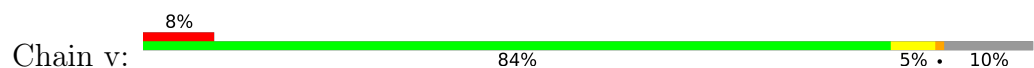
- Molecule 46: 30S ribosomal protein S16

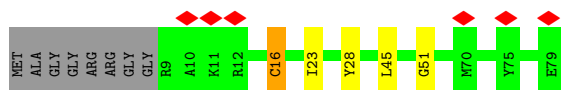


- Molecule 47: 30S ribosomal protein S17

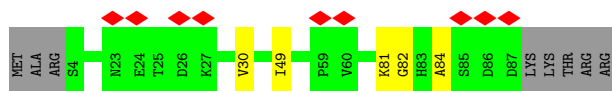
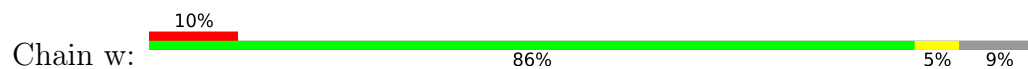


- Molecule 48: 30S ribosomal protein S18

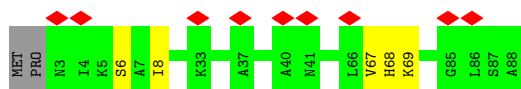
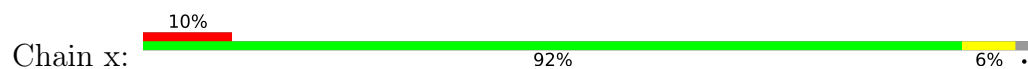




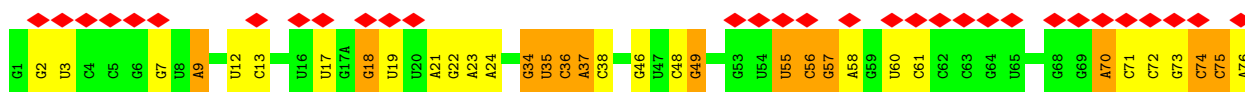
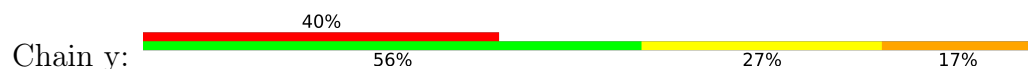
- Molecule 49: 30S ribosomal protein S19



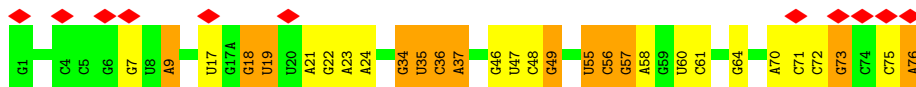
- Molecule 50: 30S ribosomal protein S20



- Molecule 51: tRNA



- Molecule 51: tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	12739	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.496	Depositor
Minimum map value	-0.769	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.082	Depositor
Recommended contour level	0.22	Depositor
Map size (Å)	650.4, 650.4, 650.4	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	A	0.53	0/70307	0.59	24/109687 (0.0%)
2	B	0.50	0/2678	0.52	0/4174
3	C	0.38	0/2148	0.85	2/2881 (0.1%)
4	D	0.39	0/1597	0.76	2/2140 (0.1%)
5	E	0.37	0/1580	0.80	3/2132 (0.1%)
6	F	0.40	0/1423	0.82	5/1910 (0.3%)
7	G	0.33	0/1360	0.76	0/1832
8	H	0.38	0/963	0.73	0/1298
9	I	0.42	0/995	0.90	5/1346 (0.4%)
10	J	0.36	0/1146	0.77	2/1542 (0.1%)
11	K	0.40	0/927	0.80	1/1245 (0.1%)
12	L	0.30	0/1093	0.78	2/1457 (0.1%)
13	M	0.29	0/1120	0.72	1/1496 (0.1%)
14	N	0.36	0/960	0.69	0/1284
15	O	0.44	0/921	0.83	1/1236 (0.1%)
16	P	0.33	0/949	0.73	0/1269
17	Q	0.35	0/952	0.66	0/1266
18	R	0.39	0/797	0.81	2/1070 (0.2%)
19	S	0.53	1/851 (0.1%)	0.88	2/1146 (0.2%)
20	T	0.41	0/759	0.74	0/1011
21	U	0.37	0/764	0.88	0/1022
22	V	0.40	0/638	0.77	0/847
23	Y	0.38	0/448	0.89	2/596 (0.3%)
24	Z	0.30	0/531	0.65	0/707
25	a	0.33	0/457	0.68	0/613
26	b	0.30	0/433	0.76	0/574
27	c	0.35	0/406	0.69	0/540
28	d	0.26	0/370	0.76	1/483 (0.2%)
29	e	0.29	0/519	0.64	0/680
30	f	0.26	0/291	0.76	0/383
31	W	0.52	0/37074	0.53	0/57834
32	X	0.52	0/895	0.94	2/1117 (0.2%)
33	g	0.47	0/839	0.92	3/1047 (0.3%)
34	h	0.44	0/796	1.03	4/992 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.45	0/660	1.05	1/822 (0.1%)
36	j	0.51	0/380	1.00	2/472 (0.4%)
37	k	0.43	0/612	0.82	0/762
38	l	0.42	0/524	0.95	0/652
39	m	0.44	0/520	0.96	1/647 (0.2%)
40	n	0.49	0/408	1.00	2/507 (0.4%)
41	o	0.44	0/471	1.14	4/587 (0.7%)
42	p	0.42	0/548	1.12	0/682
43	q	0.49	0/475	1.00	1/592 (0.2%)
44	r	0.39	0/240	1.03	0/297
45	s	0.43	0/352	0.83	0/437
46	t	0.46	0/356	0.95	0/442
47	u	0.44	0/344	0.90	0/427
48	v	0.48	0/284	0.96	2/352 (0.6%)
49	w	0.52	0/335	0.98	1/417 (0.2%)
50	x	0.44	0/344	0.75	0/427
51	1	0.41	0/1834	0.47	0/2858
51	y	0.41	0/1834	0.50	0/2858
All	All	0.50	1/148508 (0.0%)	0.63	78/223095 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	81
2	B	0	2
5	E	0	1
19	S	0	2
31	W	0	35
51	1	0	2
51	y	0	2
All	All	0	125

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	S	95	GLN	CA-C	-6.16	1.45	1.52

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	589	G	C4'-C3'-O3'	20.91	140.77	109.40
1	A	83	G	C4'-C3'-O3'	-17.73	82.80	109.40
1	A	82	G	C4'-C3'-O3'	-15.34	90.00	113.00
1	A	2487	U	C4'-C3'-O3'	14.73	131.50	109.40
1	A	366	A	C4'-C3'-O3'	12.39	127.98	109.40

There are no chirality outliers.

5 of 125 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	126	A	Sidechain
1	A	168	A	Sidechain
1	A	52	A	Sidechain
1	A	64	A	Sidechain
1	A	67	A	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	62767	0	31575	1348	0
2	B	2395	0	1212	19	0
3	C	2111	0	2200	92	0
4	D	1575	0	1642	47	0
5	E	1561	0	1647	93	0
6	F	1404	0	1466	61	0
7	G	1342	0	1388	27	0
8	H	955	0	990	28	0
9	I	981	0	1020	31	0
10	J	1123	0	1162	31	0
11	K	920	0	975	31	0
12	L	1081	0	1132	78	0
13	M	1097	0	1162	26	0
14	N	953	0	983	38	0
15	O	912	0	947	38	0
16	P	936	0	1006	56	0
17	Q	940	0	1005	44	0
18	R	786	0	826	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	S	842	0	899	50	0
20	T	752	0	802	65	0
21	U	754	0	809	33	0
22	V	630	0	644	17	0
23	Y	444	0	486	88	0
24	Z	530	0	568	65	0
25	a	455	0	491	70	0
26	b	426	0	445	60	0
27	c	401	0	413	20	0
28	d	367	0	409	36	0
29	e	512	0	563	152	0
30	f	288	0	330	24	0
31	W	33115	0	16675	378	0
32	X	896	0	244	2	0
33	g	840	0	241	3	0
34	h	797	0	224	2	0
35	i	661	0	197	2	0
36	j	381	0	104	0	0
37	k	613	0	164	1	0
38	l	525	0	146	0	0
39	m	521	0	155	3	0
40	n	409	0	104	0	0
41	o	472	0	135	8	0
42	p	549	0	157	2	0
43	q	476	0	137	12	0
44	r	241	0	62	2	0
45	s	353	0	94	0	0
46	t	357	0	95	1	0
47	u	345	0	90	1	0
48	v	285	0	76	1	0
49	w	336	0	93	2	0
50	x	345	0	89	3	0
51	l	1643	0	828	73	0
51	y	1643	0	830	66	0
All	All	136043	0	80137	2562	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 2562 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2121:U:C1'	1:A:2122:G:H5''	1.28	1.59
1:A:2246:G:C2'	1:A:2247:C:H5''	1.33	1.52
1:A:1942:A:H2'	31:W:1502:A:C2	1.50	1.47
1:A:2122:G:C8	1:A:2254:A:C2'	1.99	1.46
1:A:2246:G:H2'	1:A:2247:C:C5'	1.48	1.44

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/277 (99%)	264 (97%)	8 (3%)	1 (0%)	30	67
4	D	205/208 (99%)	189 (92%)	11 (5%)	5 (2%)	4	26
5	E	203/207 (98%)	184 (91%)	16 (8%)	3 (2%)	8	38
6	F	176/179 (98%)	154 (88%)	18 (10%)	4 (2%)	5	27
7	G	173/179 (97%)	164 (95%)	8 (5%)	1 (1%)	21	59
8	H	121/166 (73%)	97 (80%)	14 (12%)	10 (8%)	0	9
9	I	131/141 (93%)	122 (93%)	7 (5%)	2 (2%)	8	38
10	J	140/145 (97%)	130 (93%)	9 (6%)	1 (1%)	18	55
11	K	120/122 (98%)	112 (93%)	6 (5%)	2 (2%)	7	34
12	L	144/146 (99%)	132 (92%)	10 (7%)	2 (1%)	9	38
13	M	136/144 (94%)	129 (95%)	7 (5%)	0	100	100
14	N	117/120 (98%)	109 (93%)	7 (6%)	1 (1%)	14	50
15	O	118/120 (98%)	106 (90%)	7 (6%)	5 (4%)	2	17
16	P	112/115 (97%)	100 (89%)	12 (11%)	0	100	100
17	Q	115/119 (97%)	112 (97%)	3 (3%)	0	100	100
18	R	99/102 (97%)	82 (83%)	15 (15%)	2 (2%)	6	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	S	107/113 (95%)	96 (90%)	8 (8%)	3 (3%)	4	23
20	T	91/95 (96%)	86 (94%)	5 (6%)	0	100	100
21	U	98/103 (95%)	87 (89%)	8 (8%)	3 (3%)	3	21
22	V	80/94 (85%)	77 (96%)	3 (4%)	0	100	100
23	Y	56/62 (90%)	53 (95%)	1 (2%)	2 (4%)	2	19
24	Z	63/66 (96%)	60 (95%)	3 (5%)	0	100	100
25	a	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	6	33
26	b	52/59 (88%)	47 (90%)	4 (8%)	1 (2%)	6	31
27	c	46/49 (94%)	44 (96%)	2 (4%)	0	100	100
28	d	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
29	e	62/66 (94%)	56 (90%)	5 (8%)	1 (2%)	7	36
30	f	34/37 (92%)	33 (97%)	1 (3%)	0	100	100
32	X	222/246 (90%)	204 (92%)	13 (6%)	5 (2%)	5	27
33	g	208/218 (95%)	193 (93%)	14 (7%)	1 (0%)	24	63
34	h	197/200 (98%)	191 (97%)	4 (2%)	2 (1%)	12	47
35	i	163/166 (98%)	150 (92%)	9 (6%)	4 (2%)	4	25
36	j	93/95 (98%)	88 (95%)	3 (3%)	2 (2%)	5	28
37	k	151/156 (97%)	144 (95%)	6 (4%)	1 (1%)	18	55
38	l	129/132 (98%)	123 (95%)	5 (4%)	1 (1%)	16	53
39	m	128/130 (98%)	113 (88%)	10 (8%)	5 (4%)	2	18
40	n	100/102 (98%)	88 (88%)	8 (8%)	4 (4%)	2	17
41	o	116/131 (88%)	106 (91%)	9 (8%)	1 (1%)	14	50
42	p	135/138 (98%)	118 (87%)	10 (7%)	7 (5%)	1	14
43	q	117/121 (97%)	94 (80%)	13 (11%)	10 (8%)	0	8
44	r	58/61 (95%)	51 (88%)	4 (7%)	3 (5%)	1	14
45	s	86/89 (97%)	82 (95%)	2 (2%)	2 (2%)	5	27
46	t	87/90 (97%)	82 (94%)	3 (3%)	2 (2%)	5	27
47	u	84/87 (97%)	78 (93%)	6 (7%)	0	100	100
48	v	69/79 (87%)	64 (93%)	2 (3%)	3 (4%)	2	16
49	w	82/92 (89%)	75 (92%)	5 (6%)	2 (2%)	4	26
50	x	84/88 (96%)	77 (92%)	6 (7%)	1 (1%)	10	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	5479/5758 (95%)	5041 (92%)	332 (6%)	106 (2%)	8	31

5 of 106 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	H	93	ALA
9	I	19	ASN
15	O	26	ALA
21	U	87	ASP
35	i	4	ILE

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	
3	C	223/225 (99%)	222 (100%)	1 (0%)	84	83
4	D	168/169 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	167 (99%)	2 (1%)	63	74
6	F	153/154 (99%)	153 (100%)	0	100	100
7	G	148/151 (98%)	148 (100%)	0	100	100
8	H	105/139 (76%)	105 (100%)	0	100	100
9	I	103/110 (94%)	103 (100%)	0	100	100
10	J	120/123 (98%)	120 (100%)	0	100	100
11	K	101/101 (100%)	101 (100%)	0	100	100
12	L	110/110 (100%)	110 (100%)	0	100	100
13	M	111/116 (96%)	111 (100%)	0	100	100
14	N	99/100 (99%)	99 (100%)	0	100	100
15	O	93/93 (100%)	93 (100%)	0	100	100
16	P	99/100 (99%)	99 (100%)	0	100	100
17	Q	96/98 (98%)	96 (100%)	0	100	100
18	R	83/84 (99%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	S	90/93 (97%)	89 (99%)	1 (1%)	65	74
20	T	84/85 (99%)	84 (100%)	0	100	100
21	U	84/87 (97%)	84 (100%)	0	100	100
22	V	64/74 (86%)	64 (100%)	0	100	100
23	Y	47/50 (94%)	47 (100%)	0	100	100
24	Z	56/57 (98%)	56 (100%)	0	100	100
25	a	52/53 (98%)	51 (98%)	1 (2%)	50	66
26	b	48/53 (91%)	48 (100%)	0	100	100
27	c	46/47 (98%)	46 (100%)	0	100	100
28	d	39/39 (100%)	39 (100%)	0	100	100
29	e	54/56 (96%)	54 (100%)	0	100	100
30	f	34/35 (97%)	34 (100%)	0	100	100
All	All	2679/2772 (97%)	2674 (100%)	5 (0%)	85	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	185	LEU
5	E	37	ILE
5	E	66	ARG
19	S	90	MET
25	a	53	LEU

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

Mol	Chain	Res	Type
18	R	45	ASN
23	Y	23	ASN
19	S	60	HIS
21	U	39	ASN
25	a	40	ASN

5.3.3 RNA [i](#)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2922/2928 (99%)	818 (27%)	83 (2%)
2	B	111/119 (93%)	32 (28%)	4 (3%)
31	W	1543/1555 (99%)	235 (15%)	17 (1%)
51	1	76/77 (98%)	15 (19%)	1 (1%)
51	y	76/77 (98%)	18 (23%)	0
All	All	4728/4756 (99%)	1118 (23%)	105 (2%)

5 of 1118 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	9	U
1	A	10	A
1	A	13	A
1	A	27	G

5 of 105 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1965	A
1	A	2468	A
31	W	1154	C
1	A	2155	A
1	A	2278	U

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.

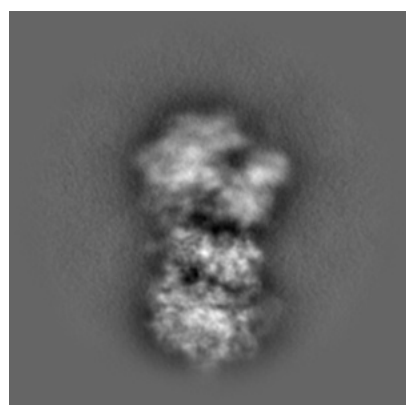
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13961. These allow visual inspection of the internal detail of the map and identification of artifacts.

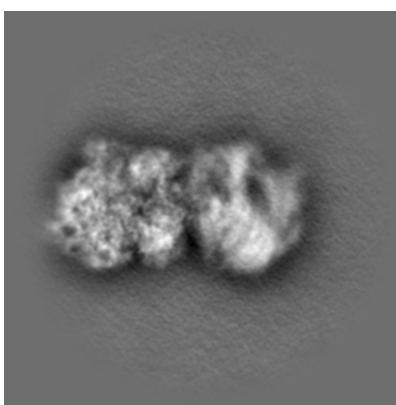
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

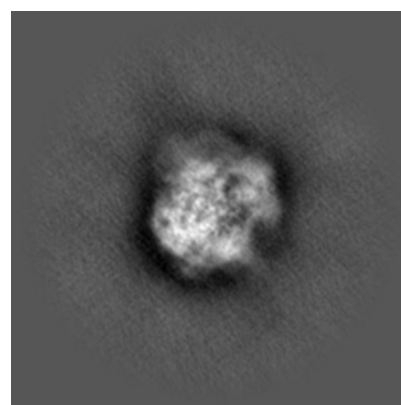
6.1.1 Primary map



X



Y

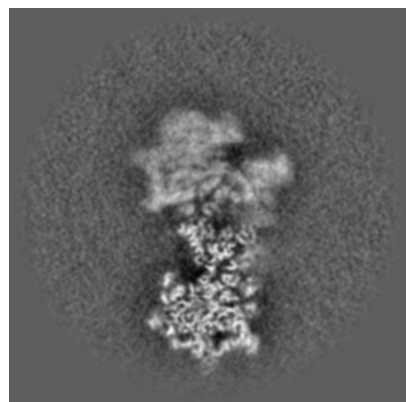


Z

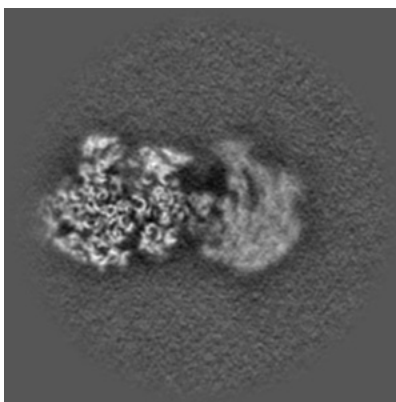
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

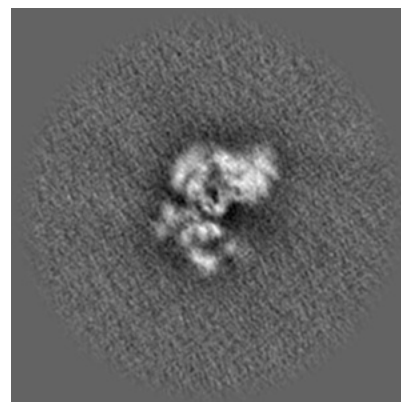
6.2.1 Primary map



X Index: 300



Y Index: 300

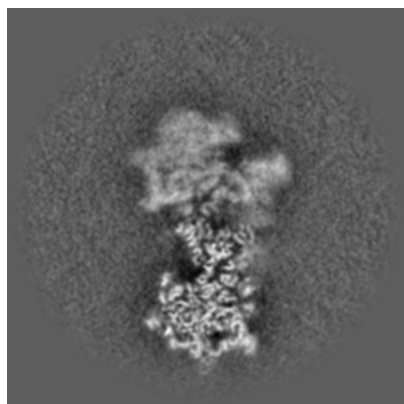


Z Index: 300

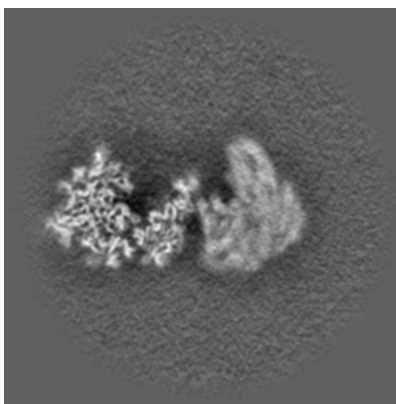
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

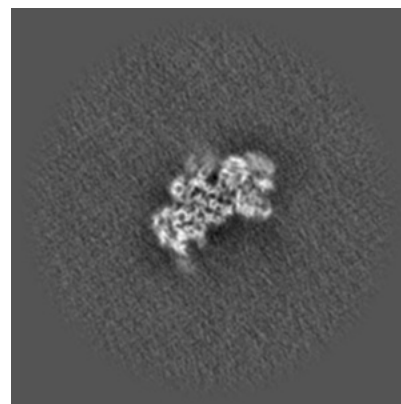
6.3.1 Primary map



X Index: 299



Y Index: 273

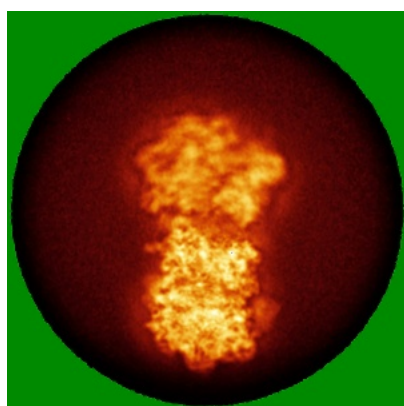


Z Index: 236

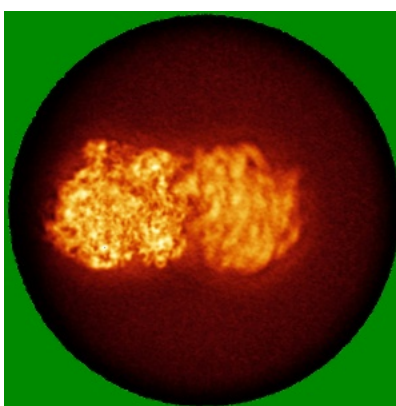
The images above show the largest variance slices of the map in three orthogonal directions.

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

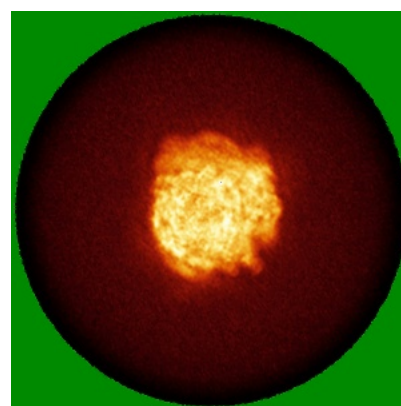
6.4.1 Primary map



X



Y

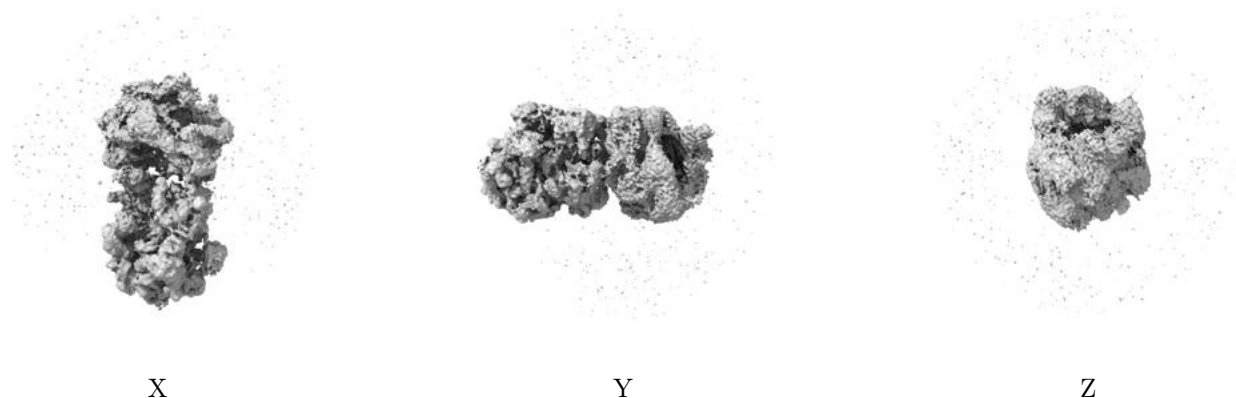


Z

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



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

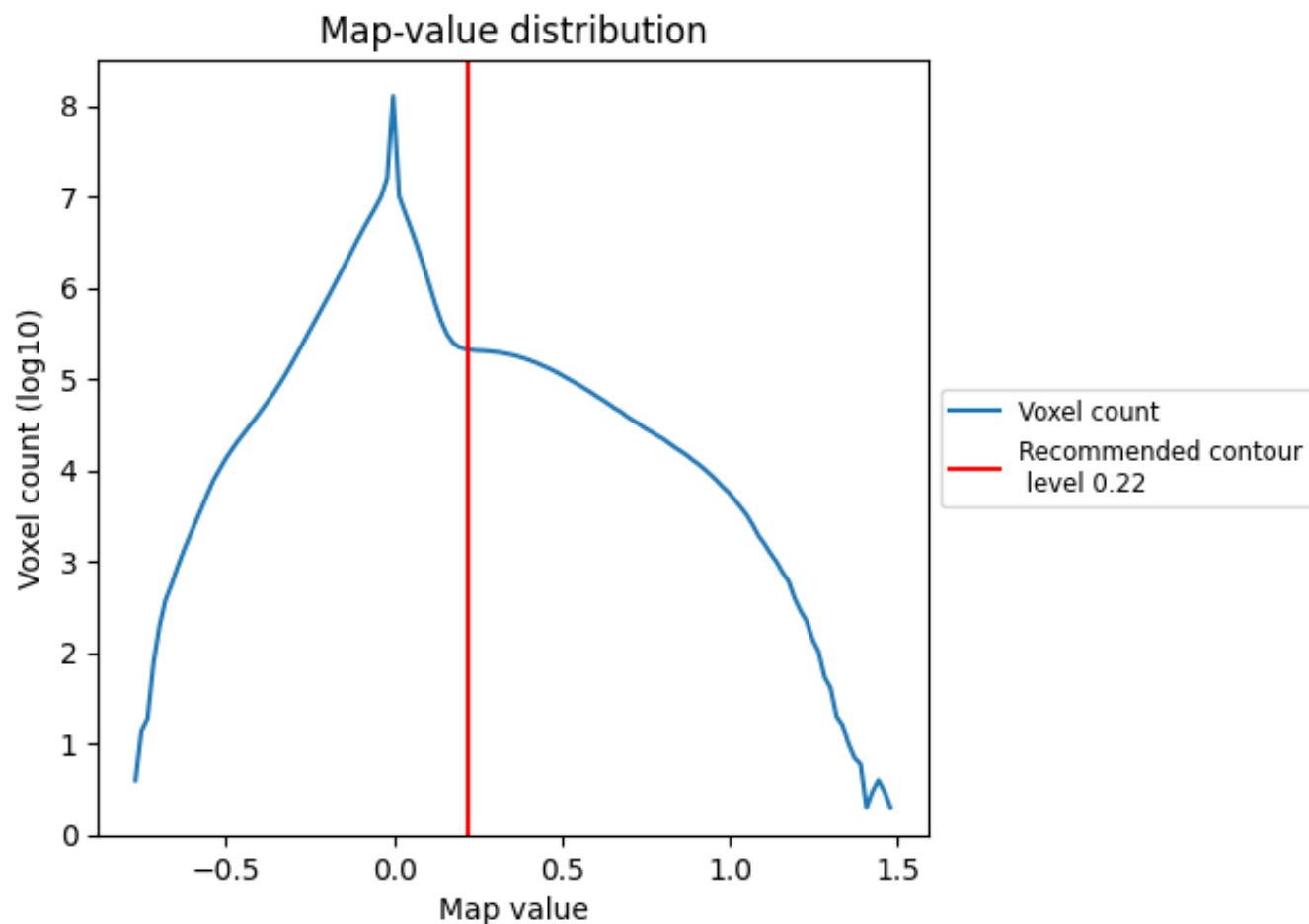
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

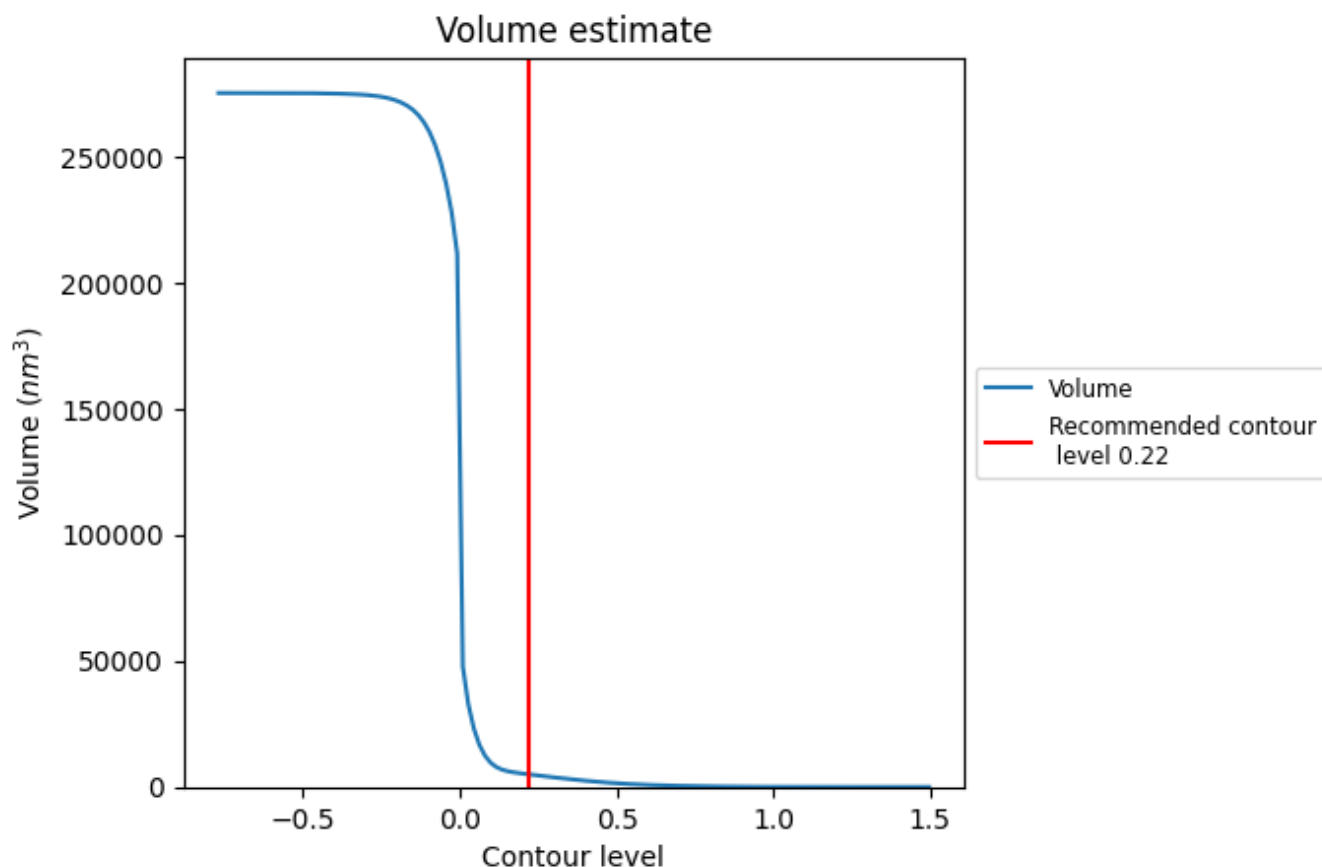
This section contains the results of statistical analysis of the map.

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.

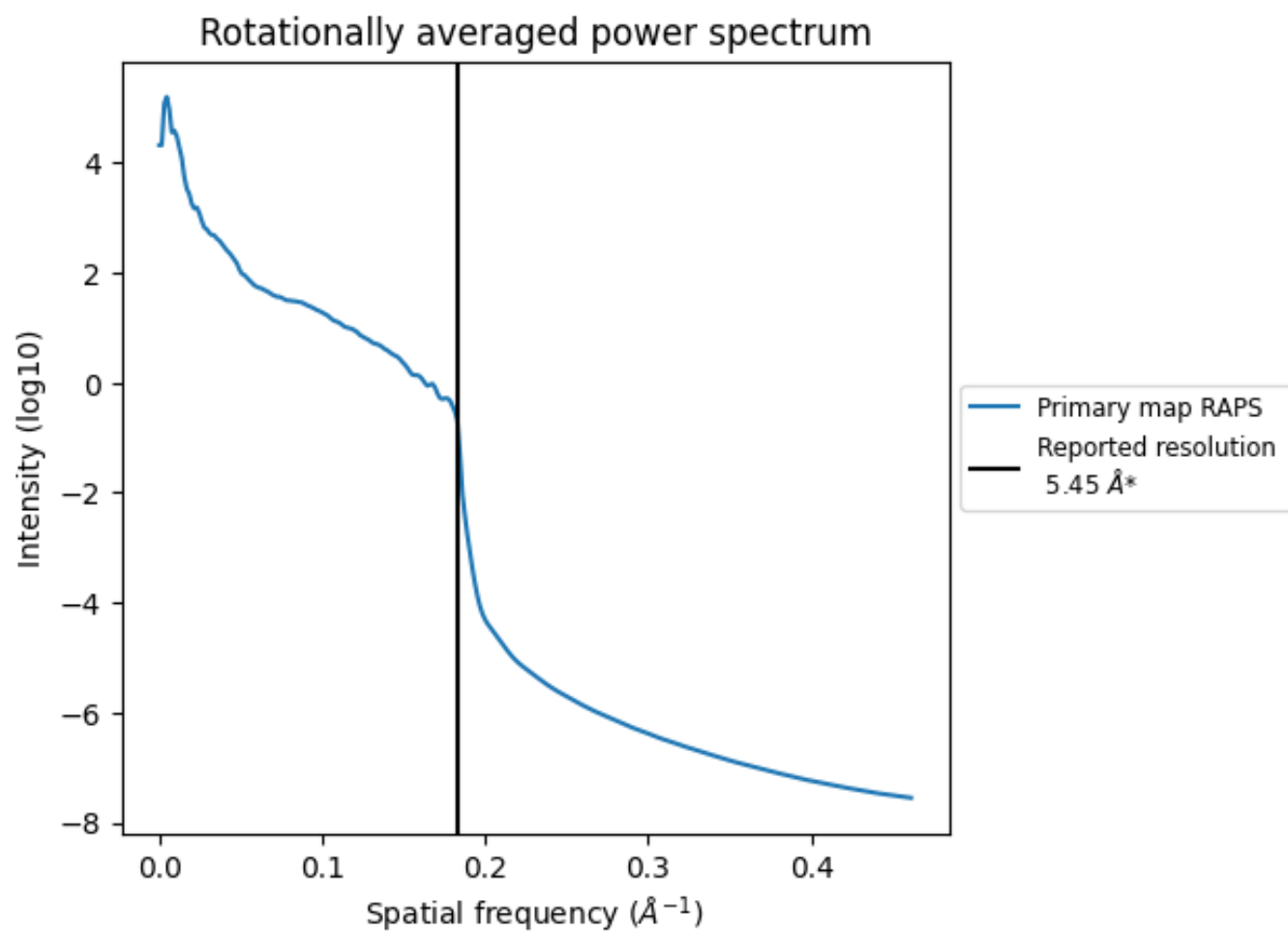
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4985 nm^3 ; this corresponds to an approximate mass of 4503 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 0.183 Å⁻¹

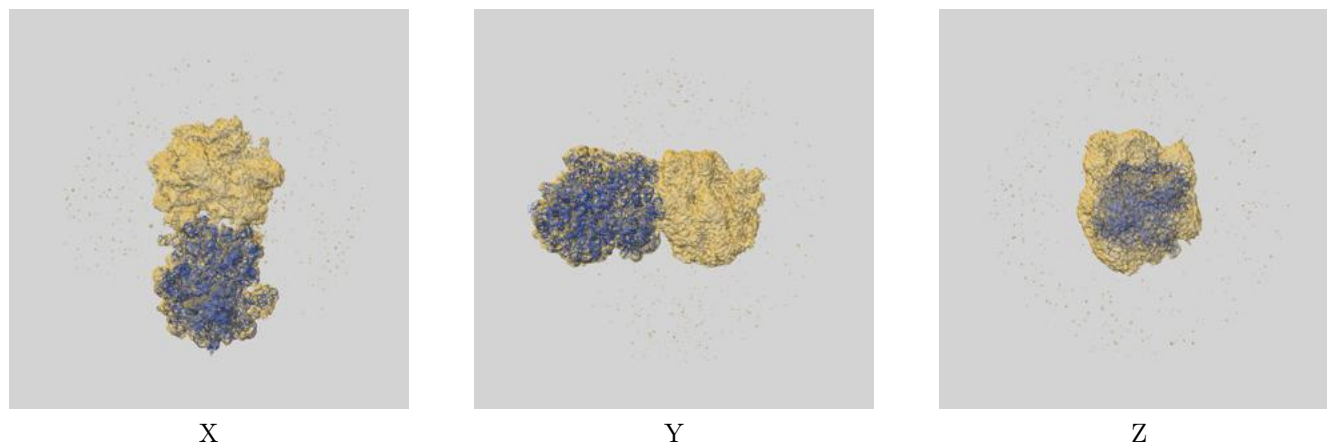
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

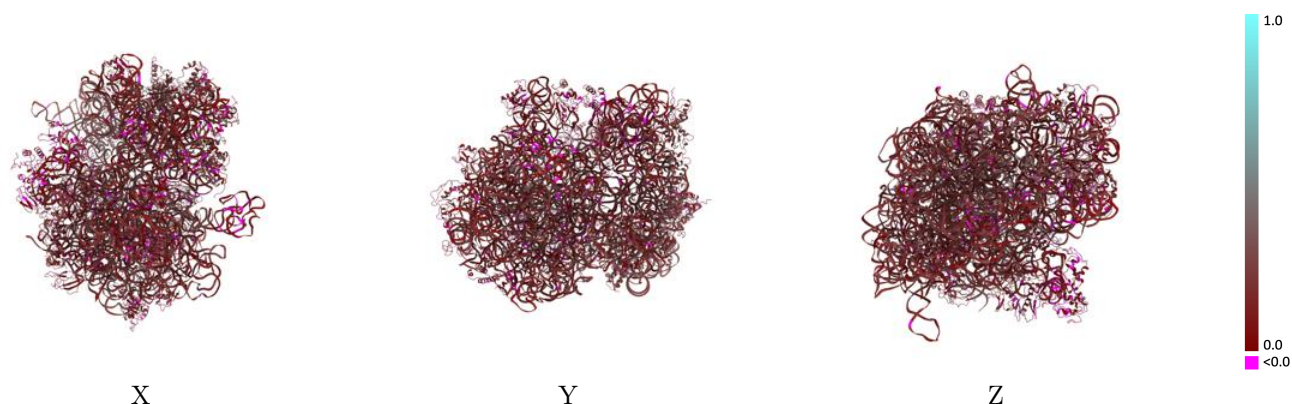
This section contains information regarding the fit between EMDB map EMD-13961 and PDB model 7QH4. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

9.1 Map-model overlay [i](#)



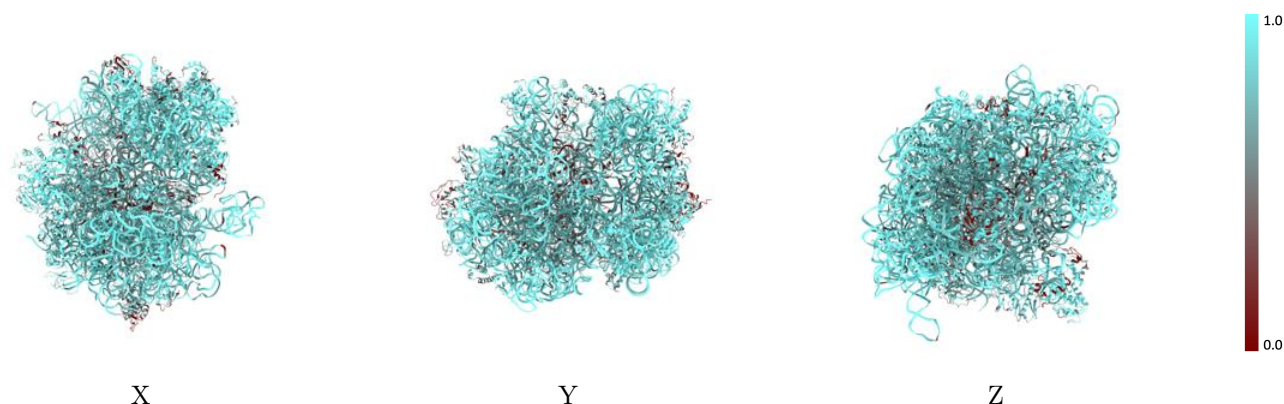
The images above show the 3D surface view of the map at the recommended contour level 0.22 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



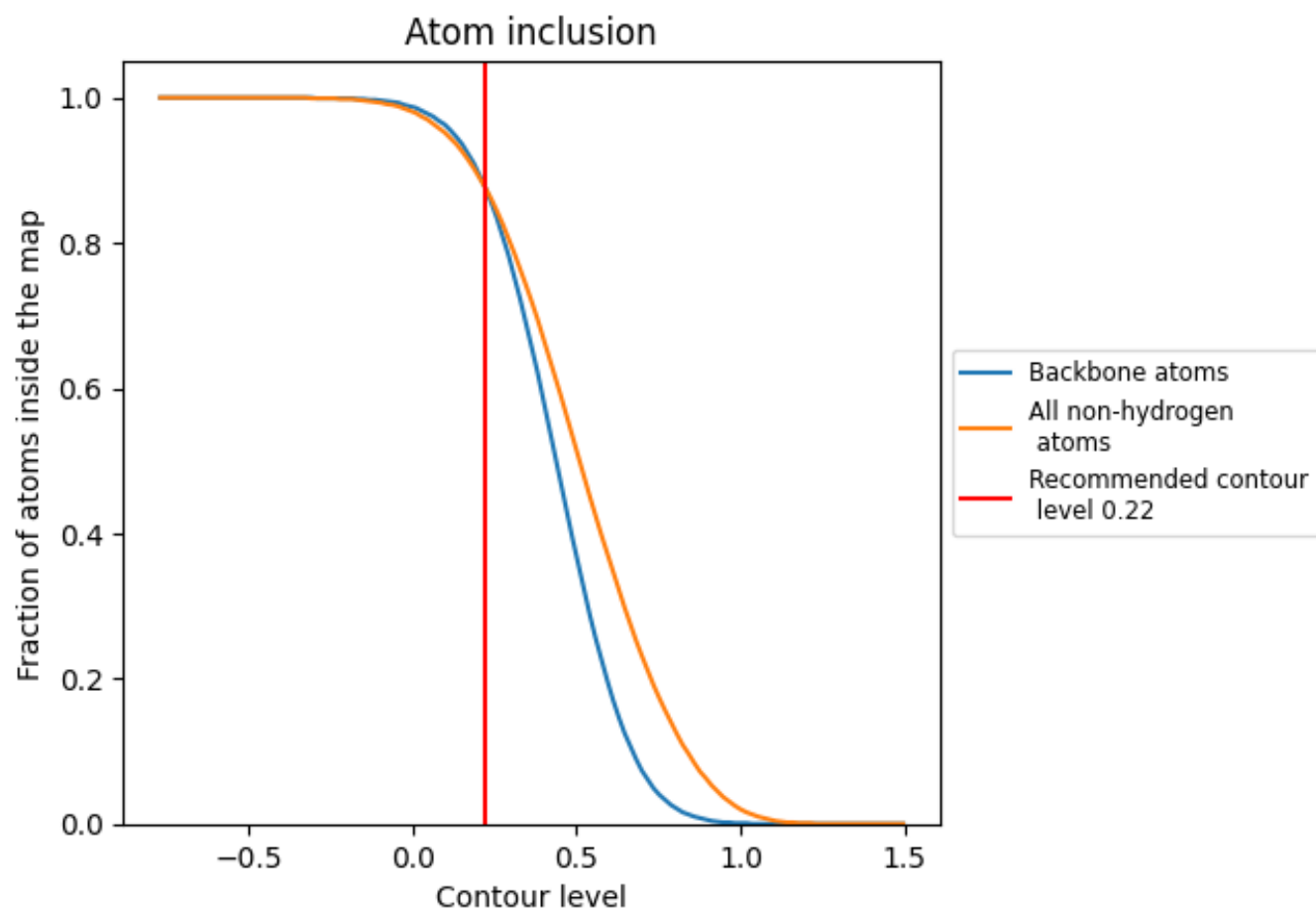
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.22).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.22) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8780	 0.1680
1	 0.6760	 0.1600
A	 0.9390	 0.1840
B	 0.9520	 0.1650
C	 0.5980	 0.1140
D	 0.7070	 0.1130
E	 0.4760	 0.1250
F	 0.6730	 0.0990
G	 0.8240	 0.1160
H	 0.8940	 0.0720
I	 0.5550	 0.0520
J	 0.7630	 0.1250
K	 0.5610	 0.1310
L	 0.6660	 0.0960
M	 0.5690	 0.1140
N	 0.8380	 0.1160
O	 0.8340	 0.0880
P	 0.7070	 0.1370
Q	 0.8000	 0.1090
R	 0.8330	 0.1260
S	 0.6950	 0.1250
T	 0.7780	 0.1180
U	 0.7400	 0.1070
V	 0.6720	 0.0670
W	 0.9460	 0.1760
X	 0.8000	 0.2430
Y	 0.5720	 0.0820
Z	 0.7940	 0.1240
a	 0.7980	 0.1210
b	 0.6930	 0.1170
c	 0.6820	 0.1240
d	 0.5250	 0.0910
e	 0.6070	 0.0990
f	 0.7770	 0.0850
g	 0.7330	 0.2560



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Chain	Atom inclusion	Q-score
h	 0.4820	 0.1830
i	 0.6810	 0.2470
j	 0.8710	 0.1880
k	 0.8400	 0.1880
l	 0.9240	 0.2310
m	 0.9190	 0.1480
n	 0.8440	 0.1840
o	 0.7030	 0.1710
p	 0.6320	 0.1890
q	 0.8300	 0.1190
r	 0.9210	 0.1960
s	 0.9460	 0.2380
t	 0.9440	 0.2470
u	 0.8870	 0.1770
v	 0.8700	 0.1880
w	 0.8720	 0.1060
x	 0.8640	 0.2110
y	 0.5150	 0.1260