



wwPDB EM Validation Summary Report ⓘ

Jun 26, 2026 – 05:31 AM EDT

PDB ID : 6OUO / pdb_00006ouo
EMDB ID : EMD-20204
Title : RF2 accommodated state bound 70S complex at long incubation time
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-05-05
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:

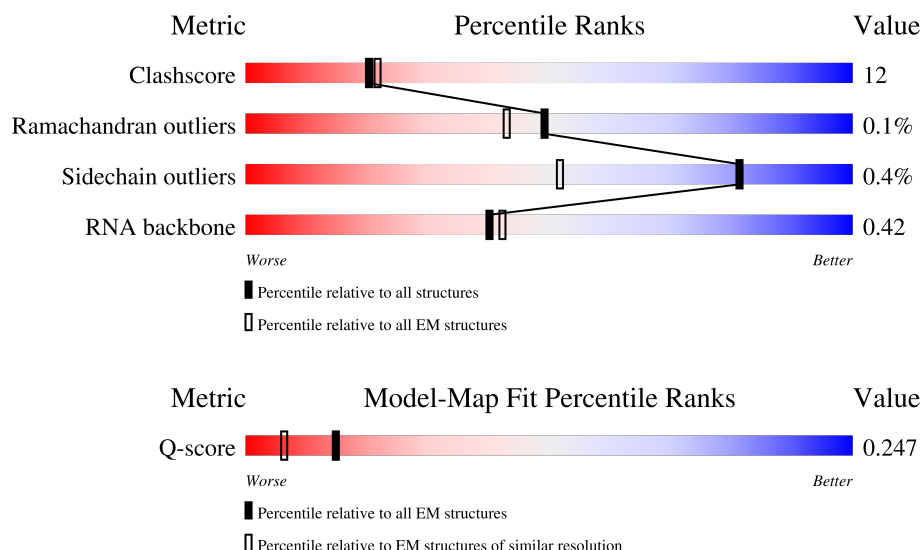
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 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.



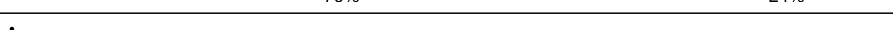
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	1	2903	
2	2	1534	
3	3	120	

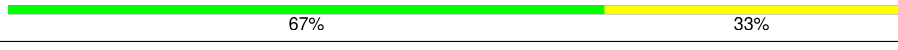
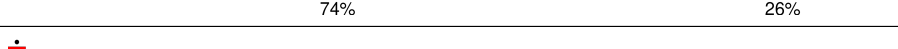
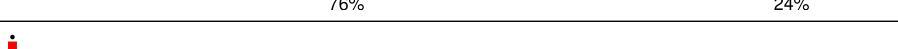
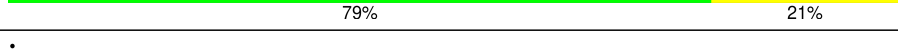
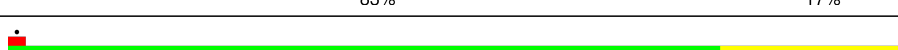
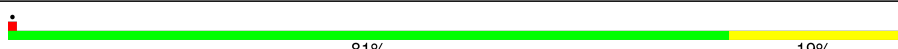
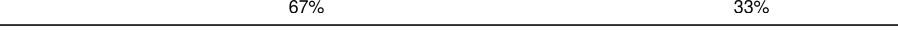
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Mol	Chain	Length	Quality of chain
4	4	9	
5	B	271	
6	C	209	
7	D	201	
8	E	177	
9	F	175	
10	G	149	
11	J	142	
12	K	123	
13	L	144	
14	M	136	
15	N	119	
16	O	116	
17	P	114	
18	Q	117	
19	R	103	
20	S	110	
21	T	94	
22	U	103	
23	V	94	
24	W	76	
25	X	77	
26	Y	62	
27	Z	58	
28	a	66	

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Mol	Chain	Length	Quality of chain
29	b	56	
30	c	52	
31	d	46	
32	e	64	
33	f	38	
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	87	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	

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Mol	Chain	Length	Quality of chain
54	5	76	46% 36% 14%
55	A	357	9% 69% 31%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146867 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	9	Total	C	N	O	P	0	0
			184	83	26	66	9		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	87	Total	C	N	O	S	0	0
			673	417	137	116	3		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A	357	Total	C	N	O	S	0	0
			2833	1742	498	583	10		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	2	Total 2	Mg 2	0
56	2	1	Total 1	Mg 1	0
56	3	8	Total 8	Mg 8	0
56	i	1	Total 1	Mg 1	0

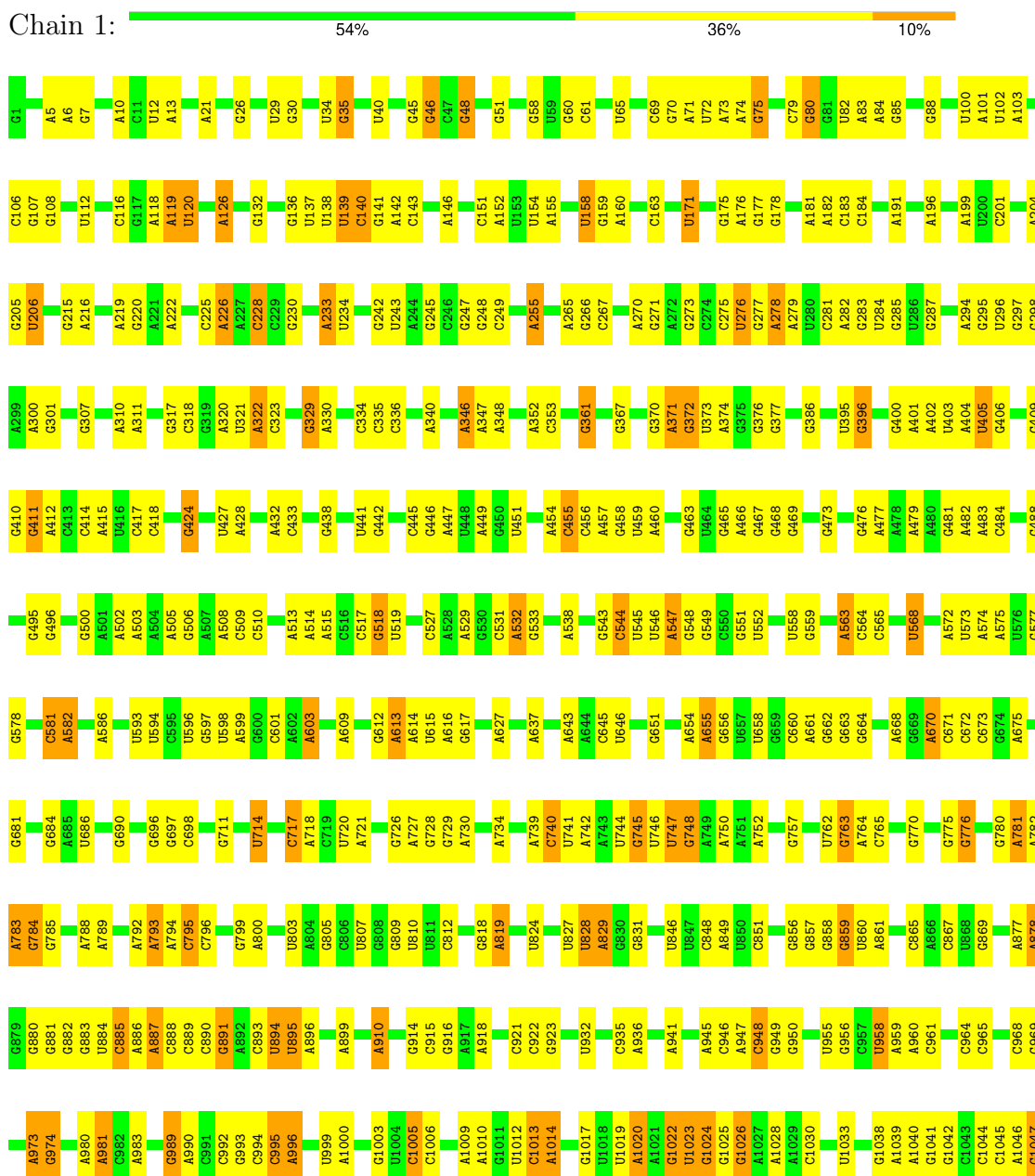
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	a	1	Total 1	Zn 1	0
57	f	1	Total 1	Zn 1	0

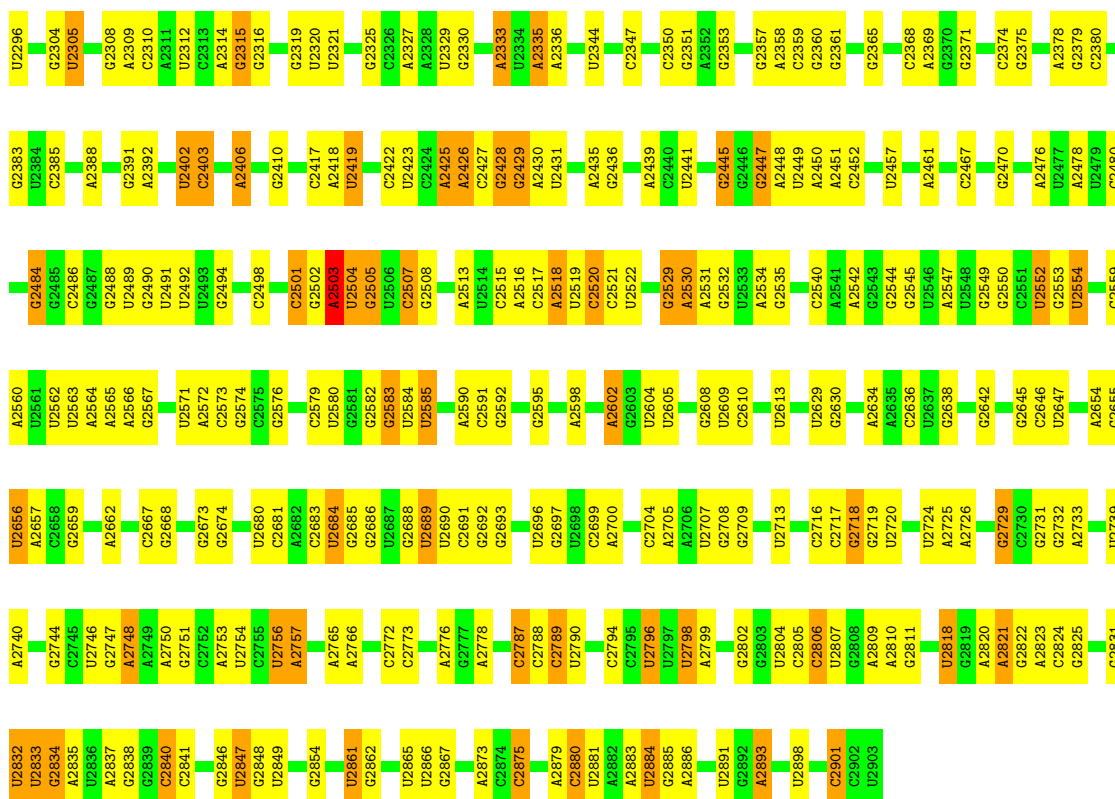
3 Residue-property plots

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 ribosomal RNA

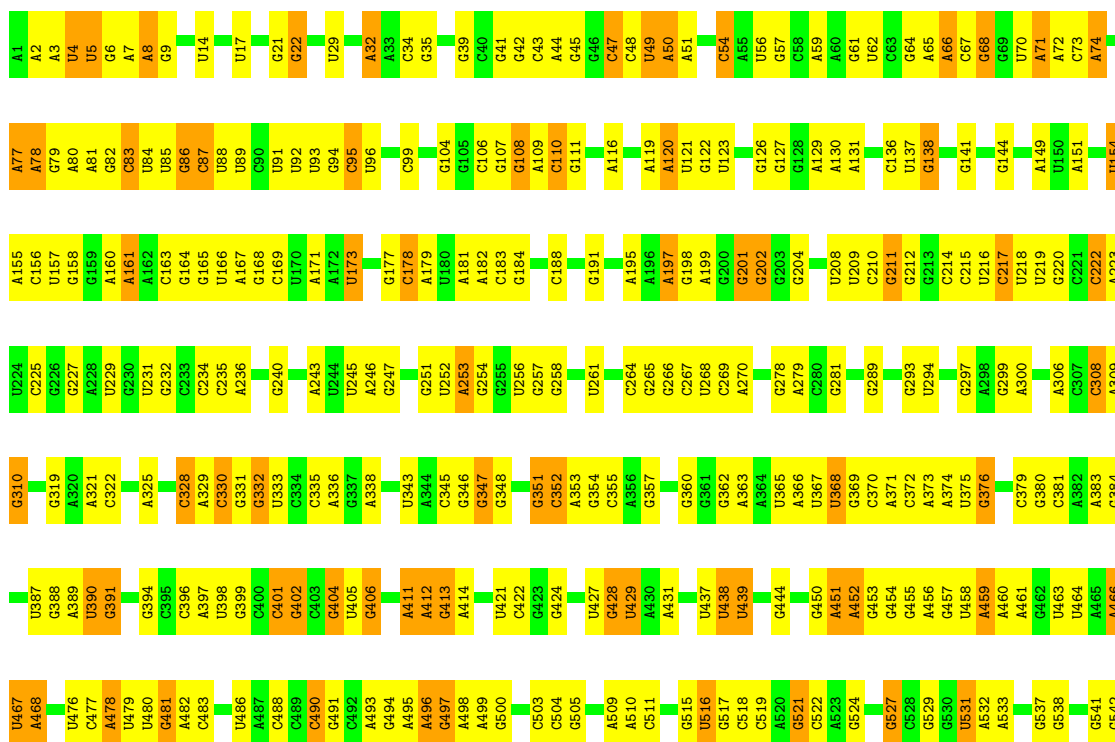


U2210	U2137	A2054	G1879	G1797	A1701	A1593	G1501	U1411	U1312	G1218	A1126	G1056
A2211	G2138	C2055	U1880	U1798	U1712	U1602	A1502	A1412	G1324	U1222	A1127	U1057
A2212	G2056	G2057	C1881	G1799	A1713	C1602	C1503	A1413	U1325	G1223	G1128	U1058
U2213	G2140			C1800	A1714	C1607	A1504	C1414	U1326	U1224	A1129	U1059
C2214	G2141	A2060	G1884	A1801	G1715	A1608	U1508	G1415	U1329	A1226	G1131	U1060
C2215	A2142	G2061	G1888	A1802	U1716	A1609	A1509	C1417		G1227	U1132	U1061
G2216	C2143	A2062	A1889	G1807		A1610		G1418			A1133	G1062
G2217	G2144		A1890	A1808	G1721	C1611		A1419	G1332	U1231	A1134	G1063
	C2145	A1987	A1899	A1809	A1722	C1612	A1515	A1420	G1338	G1232	A1135	C1064
G2223	C2146	G1988	A1900	A1810	G1723	G1613	G1516	G1421	G1339	G1236	G1137	U1066
A2225	G2148	U1991	C1902	C1846	U1725	C1614	A1522	G1425	U1340	A1237	G1138	A1067
C2226	U2149	A2082	G1903	G1817	C1726	A1615	U1523	G1426	G1341	G1238	G1139	G1068
A2227					C1727	C1617	G1524	A1427	A1342		G1140	A1069
G2228	C2153	G2087	G1906	U1820	U1728	C1617	A1525	C1428	G1343	A1246	U1141	U1070
U2229		A2088	U1995	A1821	U1729	G1619		A1437	G1338	A1247	A1142	G1071
U2233	G2156	G2093	U1911	G1822	C1730	A1626	A1528	G1437	G1345	G1248	A1143	C1072
G2234	C2157	A2094	A1912	G1823	G1731	G1631	G1529	U1438		U1249	A1144	A1073
	A2158		A1913	G1824	C1732		G1530	A1439	C1351	G1250		G1074
G2237	G2160	A2095	A1914	U1825	G1733	G1634	C1531	U1443	G1355	G1251	A1151	C1075
G2238	C2161	A2097	3TD1915	U1826		A1634	A1532	G1444	G1358	A1252	G1152	C1076
G2239	G2162	U2098	A1916	G1827	G1738		A1533	G1444	G1360	U1254	G1153	A1077
U2240	A2163	U2099	U1917	U1828			U1534	G1449	A1359	A1255	G1154	U1078
G2241	C2164		A1918	A1829	A1744	C1639	A1535	G1449	G1362	G1256	A1155	C1079
G2242	C2165	U2101	A1919	C1830			C1536	G1455	G1363		C1158	U1082
U2243	U2166	G2102	U1923	C1833	U1751	C1646	G1537	G1458	G1364	U1263		U1083
	U2167	A2103	C1924	G1834	C1752	U1647		U1458	G1365	G1266	G1161	A1084
G2250	G2168	U2105	G1925	U1835	G1753	U1648			G1366	A1267	G1162	A1085
G2251	A2169	U2106	C1926	G1836	A1754	G1649	G1543	C1461	A1365	U1267	A1086	A1086
G2252	C2170	G2023	U1927	C1837	G1755	A1650	C1550	C1462	A1366	A1268	G1168	G1087
G2253	A2171	C2024	A1928	G1844	G1756	G1651	G1559	G1463	A1367	A1269	A1169	A1088
	U2172	C2025	U1929	G1845	A1757	G1652	G1560	G1464	G1368	C1270	C1170	A1089
U2262	A2173	U2026	G1930	C1846	C1760	U1657		U1466	U1372	A1272	G1172	A1090
C2263	C2174	U2111	G1934	U1847		C1658	C1564	U1467		U1273	U1173	U1094
C2264	C2175	G2027	G1935	A1848	C1764	G1659	C1565	U1468	A1378	A1274	U1174	A1095
A2265	A2176	G2028	A1936	G1849	U1765	G1660	U1567	A1469	U1379	A1275	A1175	A1096
A2266	C2177	A2031	A1937	G1850			G1567		G1380		U1176	U1097
A2267	C2178	G2032	G1940	G1854	A1773	G1667	G1568	G1475		G1278	G1177	
G2269	U2181	A2033	U1939	A1854	C1774	A1668	A1569	A1476	A1383	G1279	C1178	U1101
A2270	U2182	U2034	U1940	G1857	U1775	A1669	A1570	G1477	A1384	A1287	C1102	C1102
G2271	A2183	G2035	C1941	A1858	G1776	C1670	A1571	G1478	A1385		A1103	A1103
U2272	A2184	C2036	C1942	U1859	U1777	U1671	A1572	G1479	C1386		G1182	G1104
A2273		A2037	U1943	U1860	U1778				C1387	U1294	U1105	U1105
	U2188	G2038	G1954	G1861	U1779	G1674	U1576	G1482	G1388	C1295	G1186	
G2277	U2189	U2039	U1955	G1862	A1780	G1682	A1579	U1484		G1296	G1187	G1110
A2278	G2190	G2040	U1956	G1863	U1781		A1580			G1297	U1188	A1111
G2279		C2043	U1960	U1864	A1784	U1688	G1581	G1489	U1394	G1300	G1189	G1112
	G2193	C2044	A1960	U1865	A1785	C1691	G1582	C1491	A1395	A1301	G1190	U1113
A2283	U2194	C2045	C1961	U1869	A1786	U1691	A1583	G1491	U1396	A1302	G1195	G1114
G2285	A2198	G2046	C1962		A1787	U1692	C1585	G1492	C1398		G1195	G1115
G2286	C2199	C2047	U1963	G1870	C1788	U1693	C1586	C1493	C1399	G1306	G1206	G1116
A2287	G2200	G2048	U1963	A1871	A1789	C1694	A1586	A1494	A1403	C1307	U1119	
		C2050	A1966	A1872	C1790	G1695	G1587	A1495		A1307	C1211	C1123
U2291	G2204	A2051	C1967	G1873	A1791		U1588	U1496	G1408	G1310	G1212	U1409
U2292		A2052	G1968			G1699	U1590	U1497	G1410	G1311	G1215	G1125
G2293	C2208	G2053	A1969	G1878	U1796	A1700	A1590					



• Molecule 2: 16S ribosomal RNA

Chain 2: 50% 41% 9%



Chain 4:  78% 11% 11%



• Molecule 5: 50S ribosomal protein L2

Chain B:  75% 25%



• Molecule 6: 50S ribosomal protein L3

Chain C:  76% 23%



• Molecule 7: 50S ribosomal protein L4

Chain D:  79% 21%



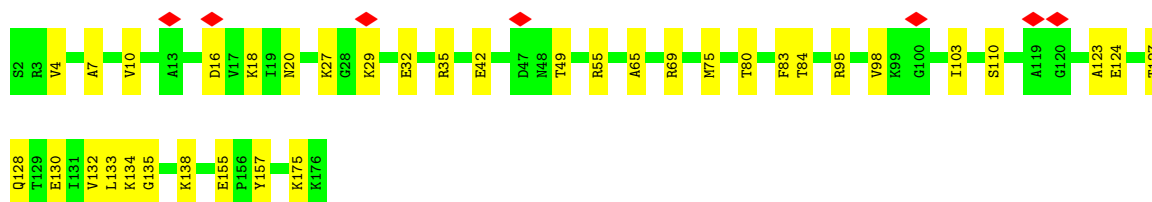
• Molecule 8: 50S ribosomal protein L5

Chain E:  75% 25%



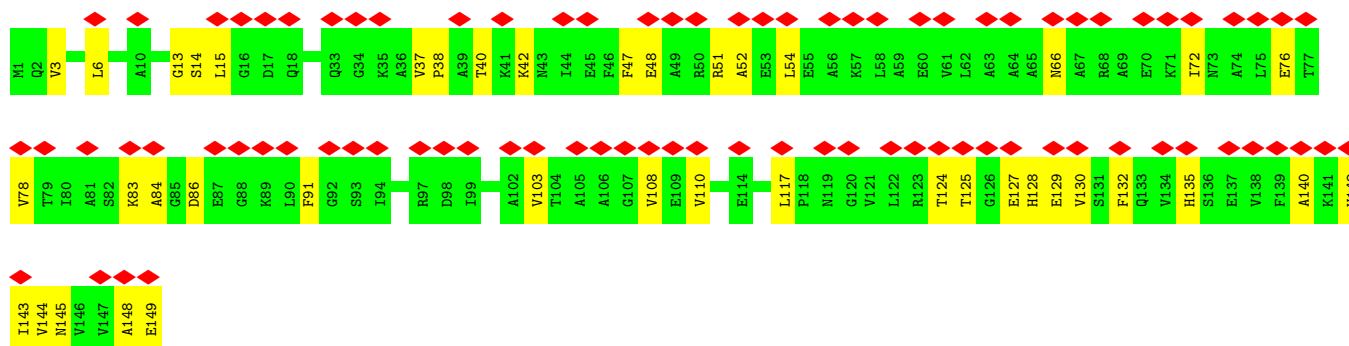
• Molecule 9: 50S ribosomal protein L6

Chain F:  79% 21%



- Molecule 10: 50S ribosomal protein L9

Chain G:  56% 72% 28%



- Molecule 11: 50S ribosomal protein L13

Chain J:  88% 12%



- Molecule 12: 50S ribosomal protein L14

Chain K:  77% 23%



- Molecule 13: 50S ribosomal protein L15

Chain L:  83% 17%

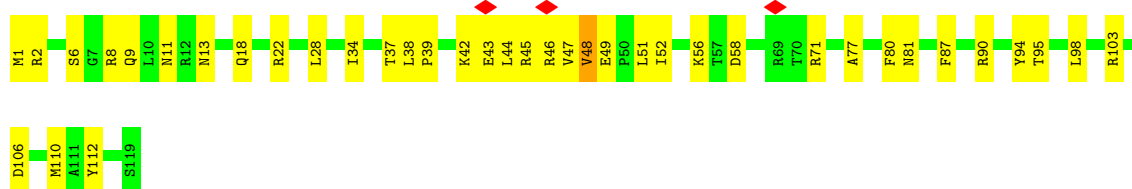


- Molecule 14: 50S ribosomal protein L16

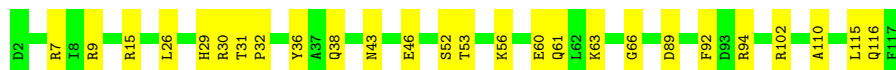
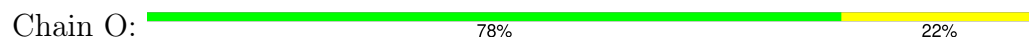
Chain M:  82% 18%



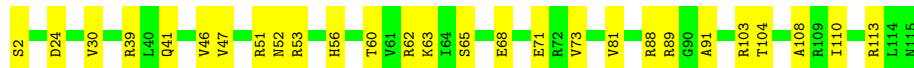
- Molecule 15: 50S ribosomal protein L17



- Molecule 16: 50S ribosomal protein L18



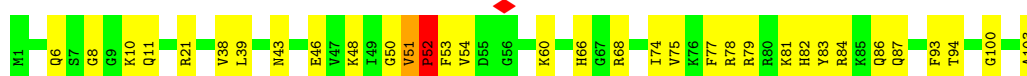
- Molecule 17: 50S ribosomal protein L19



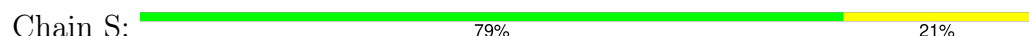
- Molecule 18: 50S ribosomal protein L20



- Molecule 19: 50S ribosomal protein L21

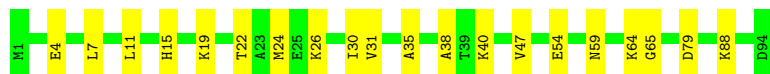


- Molecule 20: 50S ribosomal protein L22



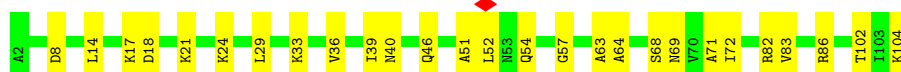
- Molecule 21: 50S ribosomal protein L23

Chain T:  79% 21%



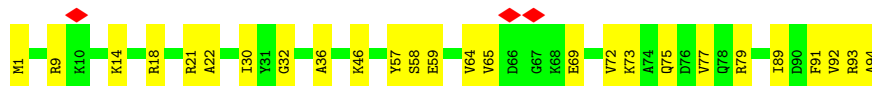
- Molecule 22: 50S ribosomal protein L24

Chain U:  74% 26%



- Molecule 23: 50S ribosomal protein L25

Chain V:  72% 28%



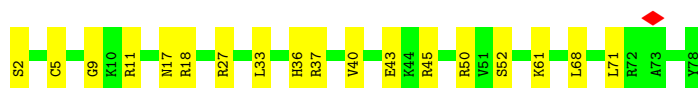
- Molecule 24: 50S ribosomal protein L27

Chain W:  72% 28%



- Molecule 25: 50S ribosomal protein L28

Chain X:  77% 23%



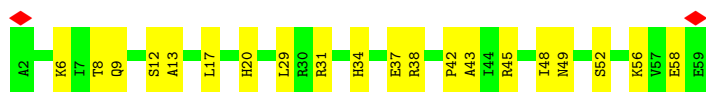
- Molecule 26: 50S ribosomal protein L29

Chain Y:  74% 26%

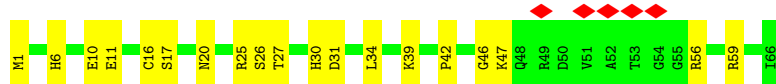


- Molecule 27: 50S ribosomal protein L30

Chain Z:  66% 34%



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



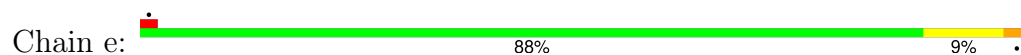
- Molecule 30: 50S ribosomal protein L33



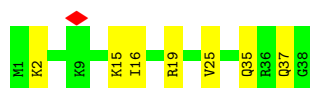
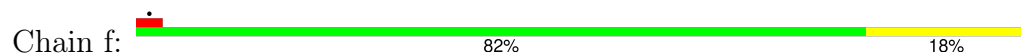
- Molecule 31: 50S ribosomal protein L34



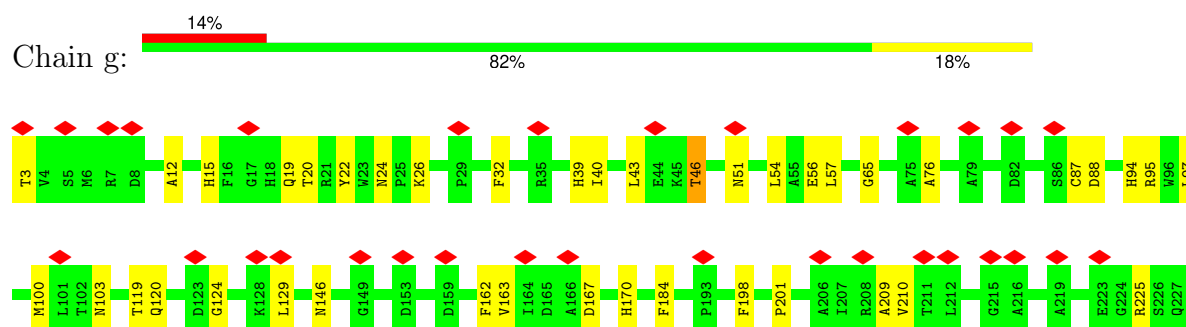
- Molecule 32: 50S ribosomal protein L35



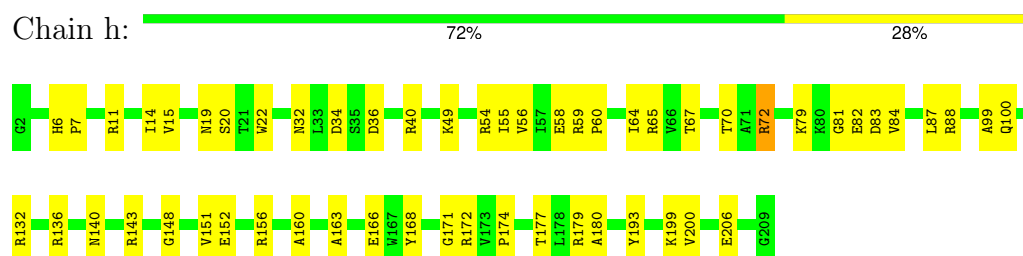
- Molecule 33: 50S ribosomal protein L36



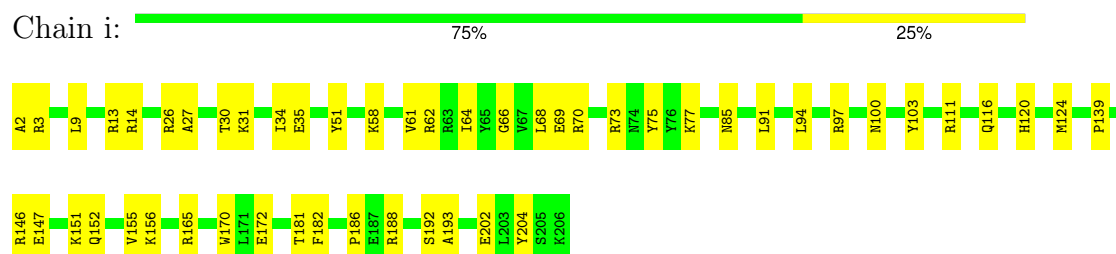
- Molecule 34: 30S ribosomal protein S2



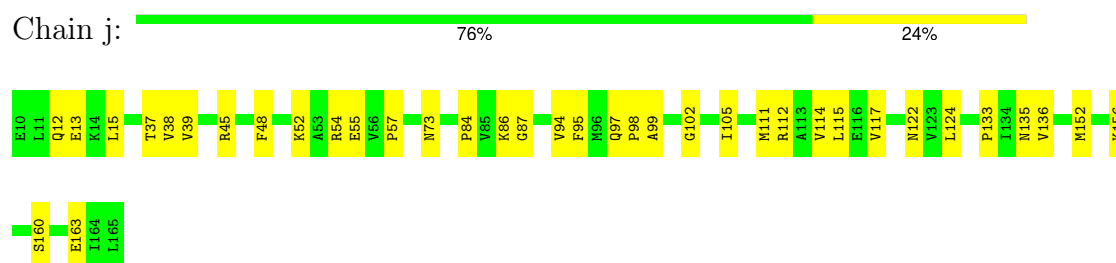
• Molecule 35: 30S ribosomal protein S3



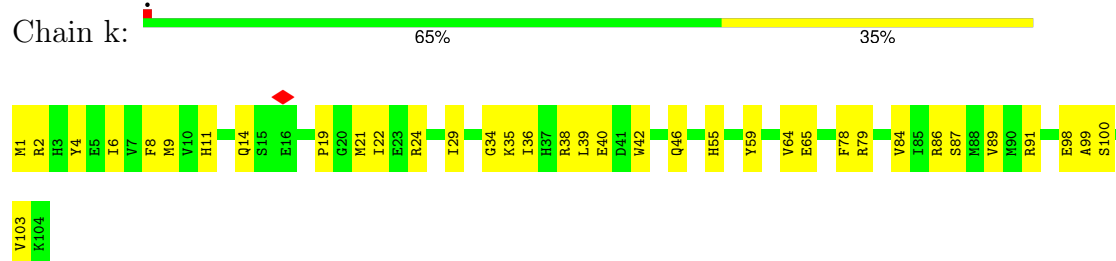
• Molecule 36: 30S ribosomal protein S4



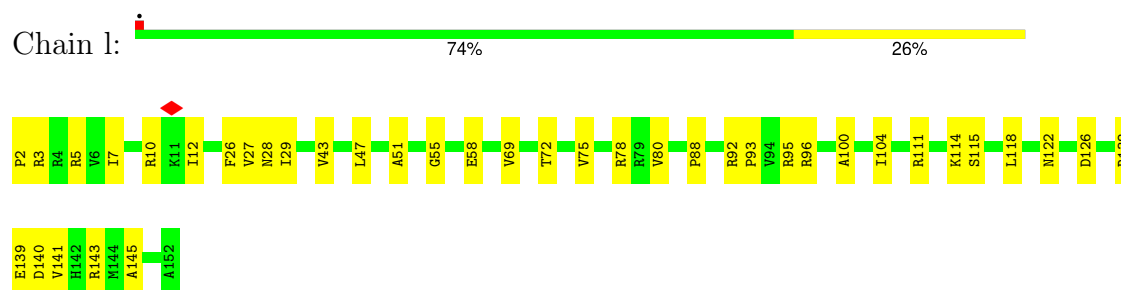
• Molecule 37: 30S ribosomal protein S5



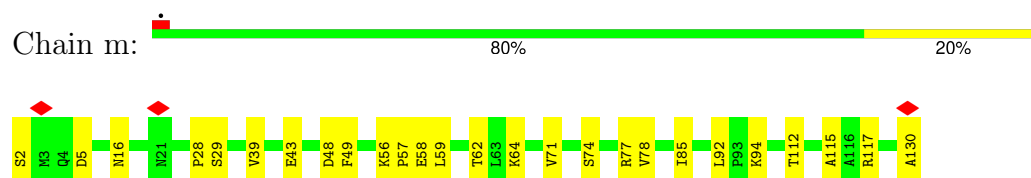
• Molecule 38: 30S ribosomal protein S6



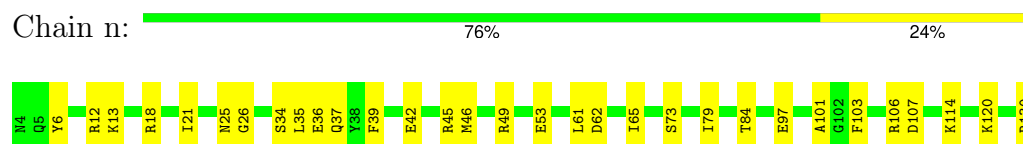
- Molecule 39: 30S ribosomal protein S7



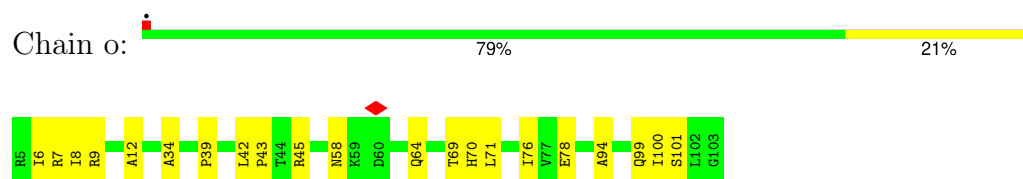
- Molecule 40: 30S ribosomal protein S8



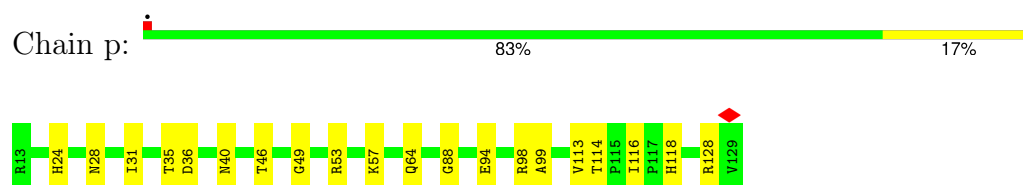
- Molecule 41: 30S ribosomal protein S9



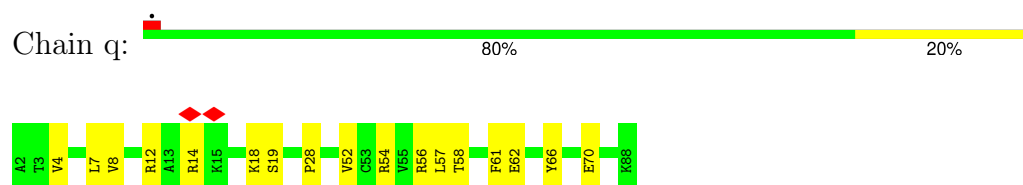
- Molecule 42: 30S ribosomal protein S10



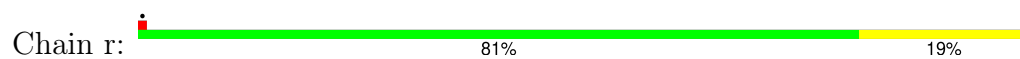
- Molecule 43: 30S ribosomal protein S11



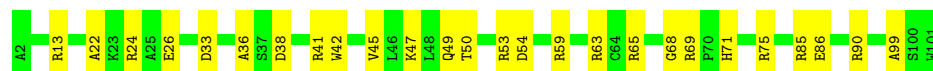
- Molecule 44: 30S ribosomal protein S12



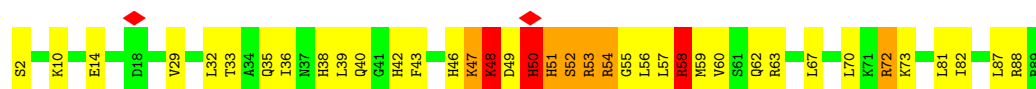
- Molecule 45: 30S ribosomal protein S13



- Molecule 46: 30S ribosomal protein S14



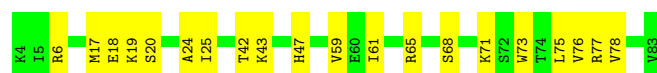
- Molecule 47: 30S ribosomal protein S15



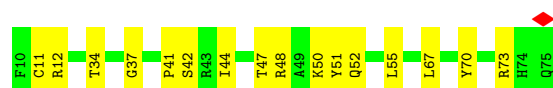
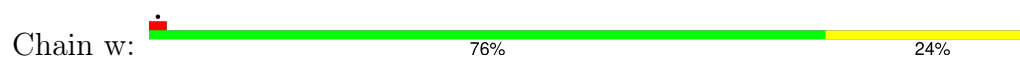
- Molecule 48: 30S ribosomal protein S16



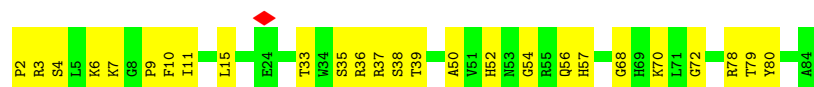
- Molecule 49: 30S ribosomal protein S17



- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20

Chain y:  86% 14%

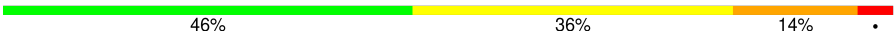


- Molecule 53: 30S ribosomal protein S21

Chain z:  9% 89% 11%



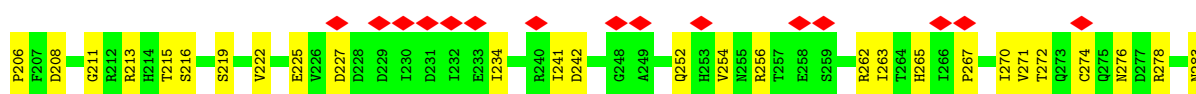
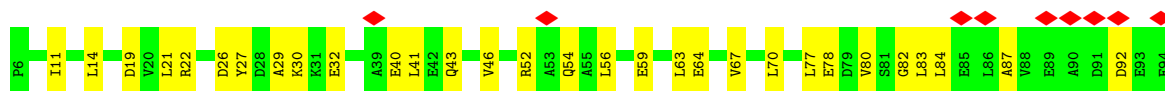
- Molecule 54: P-tRNA

Chain 5:  46% 36% 14%



- Molecule 55: Peptide chain release factor 2

Chain A:  9% 69% 31%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94709	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.089	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	526.4, 526.4, 526.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.6450001, 1.6450001, 1.6450001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	1	0.37	0/69286	0.37	2/108087 (0.0%)
2	2	0.35	0/36590	0.37	0/57074
3	3	0.33	0/2872	0.34	0/4478
4	4	0.29	0/203	0.36	0/312
5	B	0.36	0/2121	0.60	0/2852
6	C	0.38	0/1586	0.65	1/2134 (0.0%)
7	D	0.34	0/1571	0.56	0/2113
8	E	0.33	0/1434	0.57	0/1926
9	F	0.31	0/1333	0.52	0/1805
10	G	0.28	0/1122	0.62	1/1515 (0.1%)
11	J	0.35	0/1152	0.57	0/1551
12	K	0.34	0/955	0.61	0/1279
13	L	0.33	0/1062	0.59	0/1413
14	M	0.34	0/1093	0.57	0/1460
15	N	0.38	0/964	0.79	0/1289
16	O	0.30	0/902	0.56	0/1209
17	P	0.38	0/929	0.66	0/1242
18	Q	0.35	0/960	0.57	0/1278
19	R	0.43	1/829 (0.1%)	0.65	1/1107 (0.1%)
20	S	0.35	0/864	0.58	0/1156
21	T	0.33	0/752	0.57	0/1005
22	U	0.36	0/796	0.63	0/1062
23	V	0.32	0/766	0.51	0/1025
24	W	0.33	0/589	0.51	0/779
25	X	0.39	0/635	0.56	0/848
26	Y	0.32	0/502	0.57	0/667
27	Z	0.30	0/452	0.55	0/605
28	a	0.31	0/531	0.57	0/709
29	b	0.34	0/450	0.57	0/599
30	c	0.30	0/433	0.56	0/576
31	d	0.38	0/380	0.62	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.41	0/513	0.67	1/676 (0.1%)
33	f	0.30	0/303	0.60	0/397
34	g	0.32	0/1791	0.66	2/2413 (0.1%)
35	h	0.33	0/1663	0.59	0/2241
36	i	0.30	0/1665	0.55	0/2227
37	j	0.35	0/1165	0.61	0/1568
38	k	0.33	0/867	0.63	0/1171
39	l	0.29	0/1195	0.56	0/1602
40	m	0.32	0/989	0.55	0/1326
41	n	0.30	0/1034	0.61	0/1375
42	o	0.29	0/800	0.59	0/1082
43	p	0.31	0/893	0.52	0/1205
44	q	0.33	0/682	0.57	0/918
45	r	0.31	0/909	0.63	0/1215
46	s	0.30	0/817	0.53	0/1088
47	t	0.48	0/722	0.84	1/964 (0.1%)
48	u	0.33	0/659	0.66	0/884
49	v	0.32	0/657	0.64	0/881
50	w	0.30	0/553	0.54	0/743
51	x	0.30	0/680	0.55	0/915
52	y	0.34	0/675	0.54	0/895
53	z	0.29	0/597	0.56	0/792
54	5	0.33	0/1704	0.37	0/2654
55	A	0.32	0/2873	0.64	4/3870 (0.1%)
All	All	0.35	1/158520 (0.0%)	0.45	13/236755 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	52	PRO	N-CA	-6.14	1.39	1.47

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	784	G	C4'-C3'-O3'	6.65	122.97	113.00
32	e	31	HIS	O-C-N	6.46	130.62	123.25
34	g	46	THR	CA-C-N	5.84	126.04	120.43
34	g	46	THR	C-N-CA	5.84	126.04	120.43
55	A	338	THR	CA-C-N	5.50	131.60	121.70

There are no chirality outliers.

There are no planarity outliers.

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	1	62336	0	31370	662	0
2	2	32929	0	16587	410	0
3	3	2569	0	1301	34	0
4	4	184	0	95	1	0
5	B	2082	0	2154	50	0
6	C	1565	0	1616	48	0
7	D	1552	0	1619	31	0
8	E	1410	0	1444	32	0
9	F	1313	0	1358	22	0
10	G	1111	0	1148	28	0
11	J	1129	0	1162	13	0
12	K	946	0	1023	20	0
13	L	1053	0	1129	20	0
14	M	1074	0	1157	16	0
15	N	951	0	994	34	0
16	O	892	0	923	20	0
17	P	917	0	962	24	0
18	Q	947	0	1019	22	0
19	R	816	0	839	36	0
20	S	857	0	922	19	0
21	T	746	0	811	13	0
22	U	788	0	844	20	0
23	V	753	0	780	17	0
24	W	582	0	599	13	0
25	X	625	0	652	17	0
26	Y	501	0	531	10	0
27	Z	448	0	488	11	0
28	a	522	0	520	14	0
29	b	444	0	458	14	0
30	c	426	0	464	13	0
31	d	377	0	418	8	0
32	e	504	0	572	11	0
33	f	302	0	340	6	0
34	g	1760	0	1787	24	0
35	h	1636	0	1710	35	0
36	i	1643	0	1707	38	0
37	j	1152	0	1196	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	k	848	0	846	25	0
39	l	1181	0	1238	27	0
40	m	979	0	1031	17	0
41	n	1022	0	1070	22	0
42	o	790	0	831	16	0
43	p	877	0	887	13	0
44	q	673	0	720	14	0
45	r	900	0	965	17	0
46	s	805	0	844	21	0
47	t	714	0	734	90	0
48	u	649	0	666	22	0
49	v	648	0	691	14	0
50	w	544	0	560	10	0
51	x	663	0	688	23	0
52	y	669	0	719	8	0
53	z	589	0	629	5	0
54	5	1627	0	832	25	0
55	A	2833	0	2729	79	0
56	1	2	0	0	0	0
56	2	1	0	0	0	0
56	3	8	0	0	0	0
56	i	1	0	0	0	0
57	a	1	0	0	0	0
57	f	1	0	0	0	0
All	All	146867	0	99379	1926	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 1926 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)
19:R:51:VAL:HG13	19:R:52:PRO:CD	1.51	1.38
19:R:51:VAL:CG1	19:R:52:PRO:HD3	1.55	1.35
2:2:764:C:C5'	47:t:53:ARG:HH11	1.40	1.35
2:2:764:C:H5'	47:t:53:ARG:NH1	1.51	1.23
6:C:151:THR:OG1	6:C:152:PRO:HD3	1.34	1.22

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
5	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	198 (96%)	7 (3%)	2 (1%)	12	43
7	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	52
9	F	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
10	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
11	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
12	K	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
13	L	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	N	117/119 (98%)	106 (91%)	11 (9%)	0	100	100
16	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	R	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	43
20	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
21	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
23	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
25	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
28	a	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
29	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	d	44/46 (96%)	44 (100%)	0	0	100	100
32	e	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	35
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
35	h	206/208 (99%)	189 (92%)	17 (8%)	0	100	100
36	i	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
37	j	154/156 (99%)	142 (92%)	12 (8%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
40	m	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
41	n	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
44	q	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
45	r	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
46	s	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	t	86/88 (98%)	73 (85%)	11 (13%)	2 (2%)	5	30
48	u	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
49	v	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
50	w	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	x	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
52	y	84/86 (98%)	84 (100%)	0	0	100	100
53	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	A	355/357 (99%)	331 (93%)	24 (7%)	0	100	100
All	All	5928/6028 (98%)	5619 (95%)	302 (5%)	7 (0%)	49	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	151	THR
47	t	48	LYS
19	R	52	PRO

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Mol	Chain	Res	Type
47	t	50	HIS
32	e	32	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	
5	B	216/216 (100%)	216 (100%)	0	100	100
6	C	164/164 (100%)	163 (99%)	1 (1%)	78	79
7	D	165/165 (100%)	165 (100%)	0	100	100
8	E	148/148 (100%)	147 (99%)	1 (1%)	76	77
9	F	136/136 (100%)	136 (100%)	0	100	100
10	G	114/114 (100%)	114 (100%)	0	100	100
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	104/104 (100%)	104 (100%)	0	100	100
13	L	103/103 (100%)	103 (100%)	0	100	100
14	M	109/109 (100%)	109 (100%)	0	100	100
15	N	99/99 (100%)	97 (98%)	2 (2%)	48	64
16	O	86/86 (100%)	86 (100%)	0	100	100
17	P	99/99 (100%)	99 (100%)	0	100	100
18	Q	89/89 (100%)	89 (100%)	0	100	100
19	R	84/84 (100%)	83 (99%)	1 (1%)	63	72
20	S	93/93 (100%)	93 (100%)	0	100	100
21	T	81/81 (100%)	81 (100%)	0	100	100
22	U	84/84 (100%)	84 (100%)	0	100	100
23	V	78/78 (100%)	77 (99%)	1 (1%)	61	71
24	W	58/58 (100%)	58 (100%)	0	100	100
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	54/54 (100%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Z	48/48 (100%)	48 (100%)	0	100	100
28	a	59/59 (100%)	59 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/51 (100%)	51 (100%)	0	100	100
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	186 (100%)	1 (0%)	81	80
35	h	171/171 (100%)	169 (99%)	2 (1%)	63	72
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	119 (100%)	0	100	100
38	k	91/91 (100%)	91 (100%)	0	100	100
39	l	124/124 (100%)	124 (100%)	0	100	100
40	m	104/104 (100%)	104 (100%)	0	100	100
41	n	105/105 (100%)	105 (100%)	0	100	100
42	o	86/86 (100%)	86 (100%)	0	100	100
43	p	90/90 (100%)	90 (100%)	0	100	100
44	q	74/74 (100%)	74 (100%)	0	100	100
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	67 (88%)	9 (12%)	5	23
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	72 (100%)	0	100	100
52	y	65/65 (100%)	65 (100%)	0	100	100
53	z	60/60 (100%)	60 (100%)	0	100	100
55	A	304/305 (100%)	304 (100%)	0	100	100
All	All	4944/4945 (100%)	4926 (100%)	18 (0%)	81	81

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
47	t	53	ARG
47	t	72	ARG
47	t	58	ARG
35	h	179	ARG
47	t	52	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
38	k	46	GLN
50	w	52	GLN
38	k	68	GLN
44	q	5	ASN
55	A	255	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	758 (26%)	15 (0%)
2	2	1531/1534 (99%)	415 (27%)	4 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	2 (25%)	0
54	5	75/76 (98%)	22 (29%)	1 (1%)
All	All	4635/4642 (99%)	1220 (26%)	20 (0%)

5 of 1220 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	34	U
1	1	35	G
1	1	40	U
1	1	46	G

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2756	U
2	2	496	A
54	5	15	C
2	2	516	PSU

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Mol	Chain	Res	Type
1	1	1252	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	1	2498	1	19,22,23	2.90	7 (36%)	25,31,34	0.91	1 (4%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.08	6 (28%)
54	4SU	5	8	54	18,21,22	3.70	7 (38%)	25,30,33	2.22	5 (20%)
1	6MZ	1	1618	1	22,25,26	2.85	6 (27%)	29,36,39	4.44	14 (48%)
1	5MU	1	747	1	19,22,23	4.81	7 (36%)	27,32,35	3.93	9 (33%)
1	PSU	1	2605	1	18,21,22	1.13	2 (11%)	21,30,33	2.08	5 (23%)
1	2MG	1	1835	1	23,26,27	2.89	7 (30%)	33,38,41	2.20	10 (30%)
1	5MU	1	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.83	10 (37%)
54	4OC	5	32	54	20,23,24	3.00	8 (40%)	25,32,35	1.02	2 (8%)
1	OMG	1	2251	1,54	23,26,27	2.40	8 (34%)	32,38,41	1.96	8 (25%)
2	UR3	2	1498	2	19,22,23	2.53	7 (36%)	26,32,35	1.56	3 (11%)
1	PSU	1	1911	1	18,21,22	1.13	2 (11%)	21,30,33	2.16	5 (23%)
54	H2U	5	20	54	18,21,22	3.37	5 (27%)	19,30,33	1.54	4 (21%)
1	G7M	1	2069	1	23,26,27	2.58	8 (34%)	34,39,42	2.51	11 (32%)
1	2MA	1	2503	1	22,25,26	3.71	8 (36%)	32,37,40	2.44	7 (21%)
2	5MC	2	967	2	19,22,23	3.84	8 (42%)	26,32,35	0.99	1 (3%)
1	1MG	1	745	1	23,26,27	2.83	7 (30%)	33,39,42	2.07	9 (27%)
1	PSU	1	746	1	18,21,22	1.09	2 (11%)	21,30,33	1.80	3 (14%)
1	3TD	1	1915	1	19,22,23	4.26	5 (26%)	23,32,35	2.01	4 (17%)
2	MA6	2	1518	2	23,26,27	1.56	5 (21%)	33,38,41	2.71	12 (36%)
54	5MU	5	54	54	19,22,23	4.81	7 (36%)	27,32,35	3.53	8 (29%)
1	PSU	1	955	1	18,21,22	1.04	1 (5%)	21,30,33	1.80	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	2MG	1	2445	1	23,26,27	2.94	6 (26%)	33,38,41	2.27	7 (21%)
2	2MG	2	1207	2	23,26,27	2.89	7 (30%)	33,38,41	2.33	9 (27%)
1	PSU	1	2504	1	18,21,22	1.21	2 (11%)	21,30,33	1.93	4 (19%)
2	2MG	2	966	2	23,26,27	3.00	7 (30%)	33,38,41	2.30	7 (21%)
1	6MZ	1	2030	1	22,25,26	2.90	6 (27%)	29,36,39	4.48	13 (44%)
2	4OC	2	1402	2	20,23,24	3.00	8 (40%)	25,32,35	1.26	4 (16%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.12	2 (7%)
1	PSU	1	1917	1	18,21,22	1.11	1 (5%)	21,30,33	1.88	4 (19%)
1	5MC	1	1962	1	19,22,23	3.79	8 (42%)	26,32,35	1.02	2 (7%)
1	OMU	1	2552	1	19,22,23	2.88	8 (42%)	25,31,34	1.92	5 (20%)
2	G7M	2	527	2	23,26,27	3.59	12 (52%)	34,39,42	1.58	7 (20%)
2	PSU	2	516	2	18,21,22	1.02	1 (5%)	21,30,33	1.94	5 (23%)
54	PSU	5	55	54	18,21,22	1.11	1 (5%)	21,30,33	1.88	4 (19%)
2	2MG	2	1516	2	23,26,27	2.95	8 (34%)	33,38,41	2.14	10 (30%)
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.03	6 (28%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	2.76	13 (39%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	1	2498	1	–	0/9/27/28	0/2/2/2
1	PSU	1	2580	1	–	0/7/25/26	0/2/2/2
54	4SU	5	8	54	–	3/7/25/26	0/2/2/2
1	6MZ	1	1618	1	–	4/9/27/28	0/3/3/3
1	5MU	1	747	1	–	1/7/25/26	0/2/2/2
1	PSU	1	2605	1	–	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	–	2/9/27/28	0/3/3/3
1	5MU	1	1939	1	–	0/7/25/26	0/2/2/2
54	4OC	5	32	54	–	0/9/29/30	0/2/2/2
1	OMG	1	2251	1,54	–	0/9/27/28	0/3/3/3
2	UR3	2	1498	2	–	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	–	0/7/25/26	0/2/2/2
54	H2U	5	20	54	–	4/7/38/39	0/2/2/2
1	G7M	1	2069	1	–	1/7/25/26	0/3/3/3
1	2MA	1	2503	1	–	5/7/25/26	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	746	1	-	2/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3

The worst 5 of 216 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.15	1.49	1.35
1	1	2503	2MA	C4-N3	11.40	1.49	1.34
1	1	2030	6MZ	C6-N6	11.37	1.47	1.34
1	1	747	5MU	C2-N1	11.29	1.56	1.38
54	5	20	H2U	C2-N1	11.12	1.51	1.35

The worst 5 of 242 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C4-N9-C8	14.18	120.63	105.74
1	1	2030	6MZ	C4-N9-C8	13.95	120.39	105.74
1	1	747	5MU	C5-C4-N3	12.91	126.55	115.32
1	1	1939	5MU	C5-C4-N3	12.57	126.25	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
54	5	54	5MU	C5-C4-N3	12.04	125.79	115.32

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2504	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

15 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	5	8	4SU	1	0
54	5	32	4OC	1	0
54	5	20	H2U	1	0
1	1	2503	2MA	4	0
1	1	745	1MG	1	0
1	1	1915	3TD	4	0
54	5	54	5MU	1	0
1	1	2030	6MZ	1	0
2	2	1402	4OC	1	0
2	2	1407	5MC	2	0
1	1	1962	5MC	1	0
1	1	2552	OMU	2	0
54	5	55	PSU	1	0
2	2	1516	2MG	1	0
2	2	1519	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

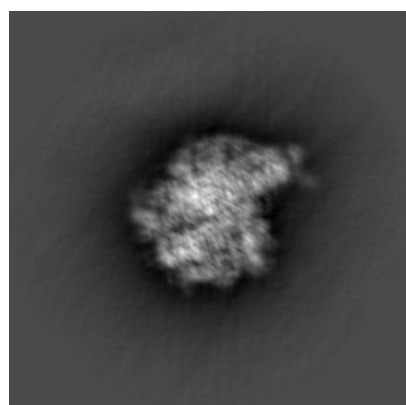
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20204. These allow visual inspection of the internal detail of the map and identification of artifacts.

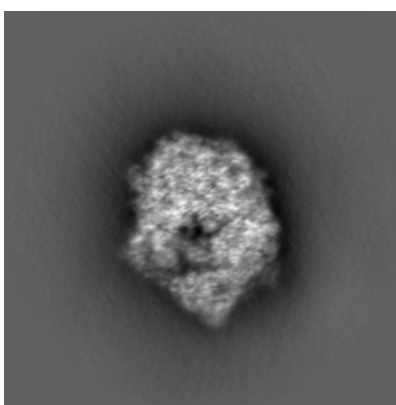
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

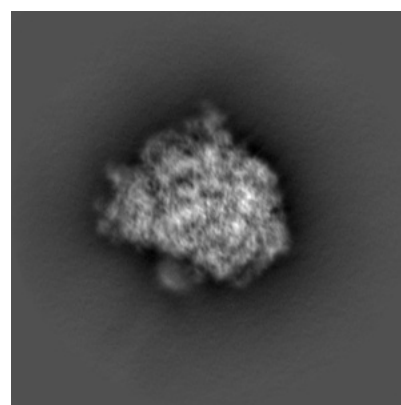
6.1.1 Primary map



X



Y

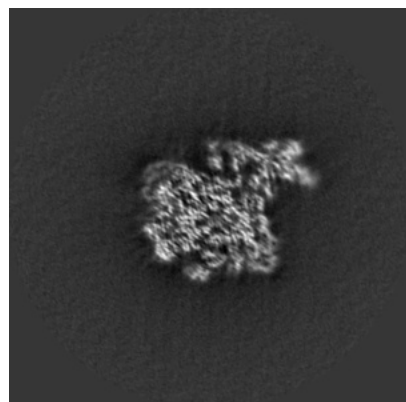


Z

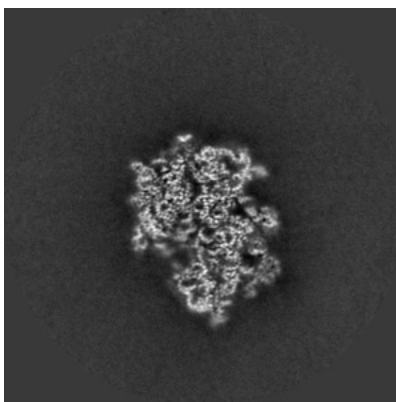
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

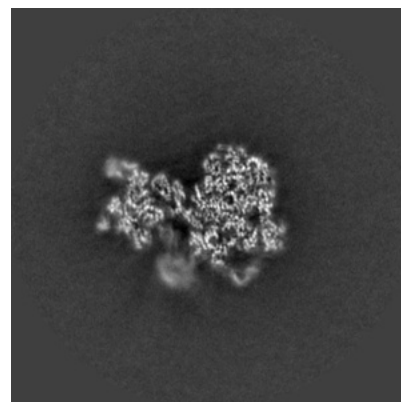
6.2.1 Primary map



X Index: 160



Y Index: 160

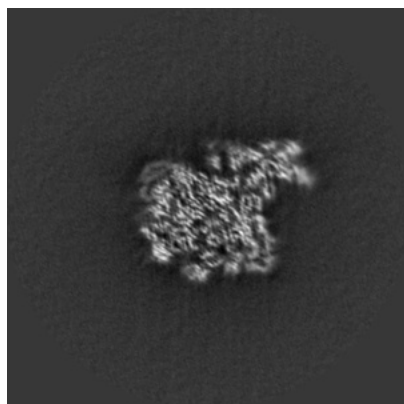


Z Index: 160

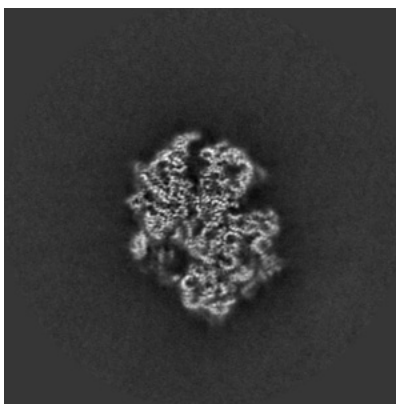
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

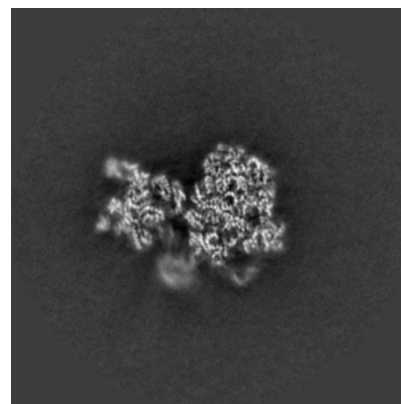
6.3.1 Primary map



X Index: 161



Y Index: 156

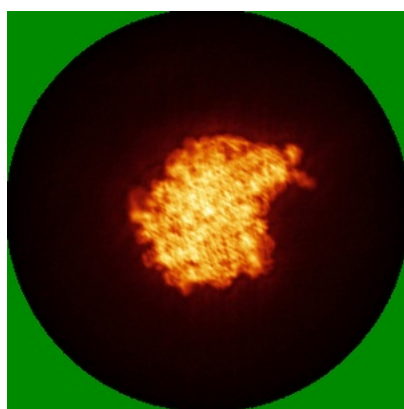


Z Index: 161

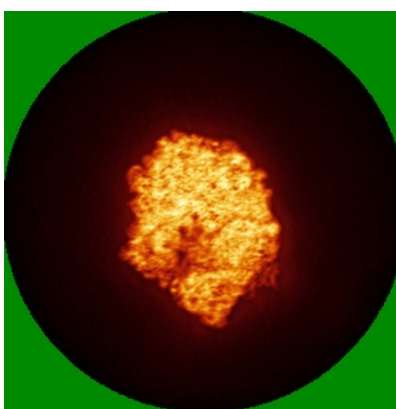
The images above show the largest variance slices of the map in three orthogonal directions.

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

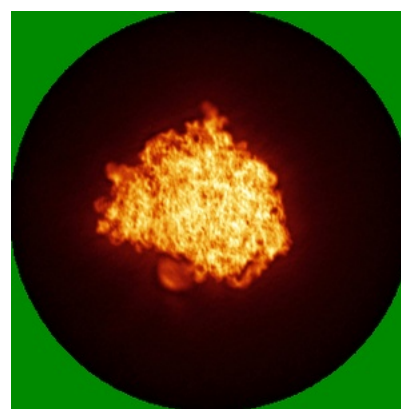
6.4.1 Primary map



X



Y

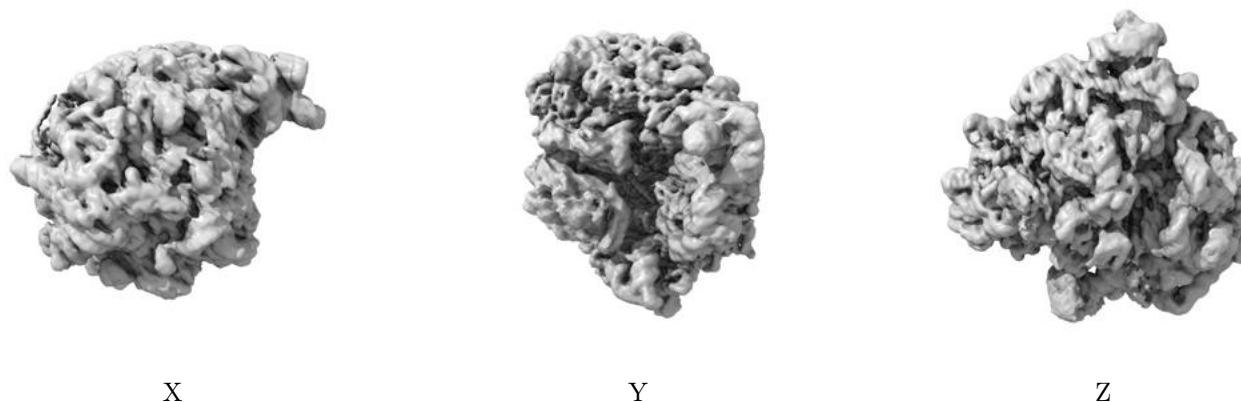


Z

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 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

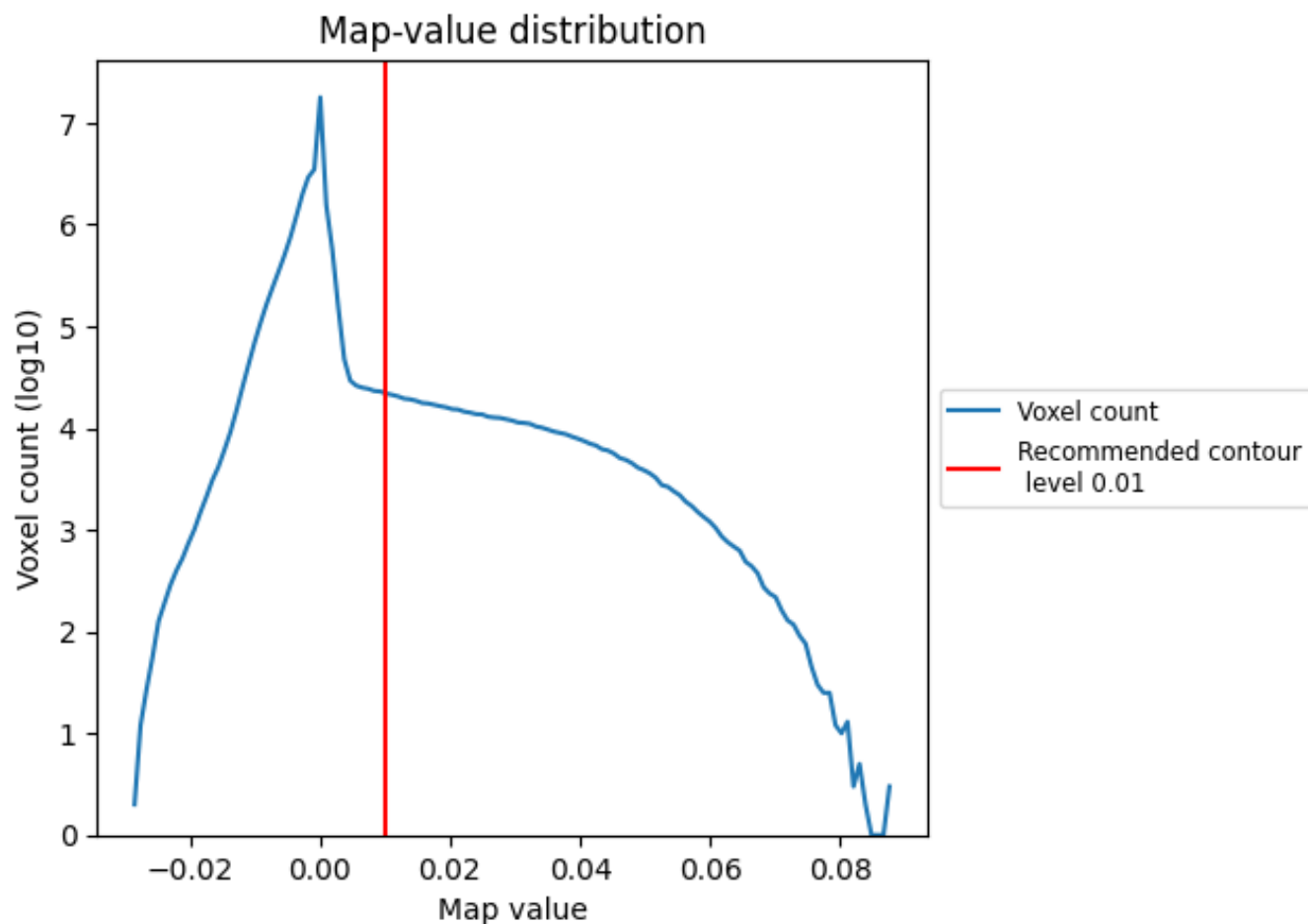
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

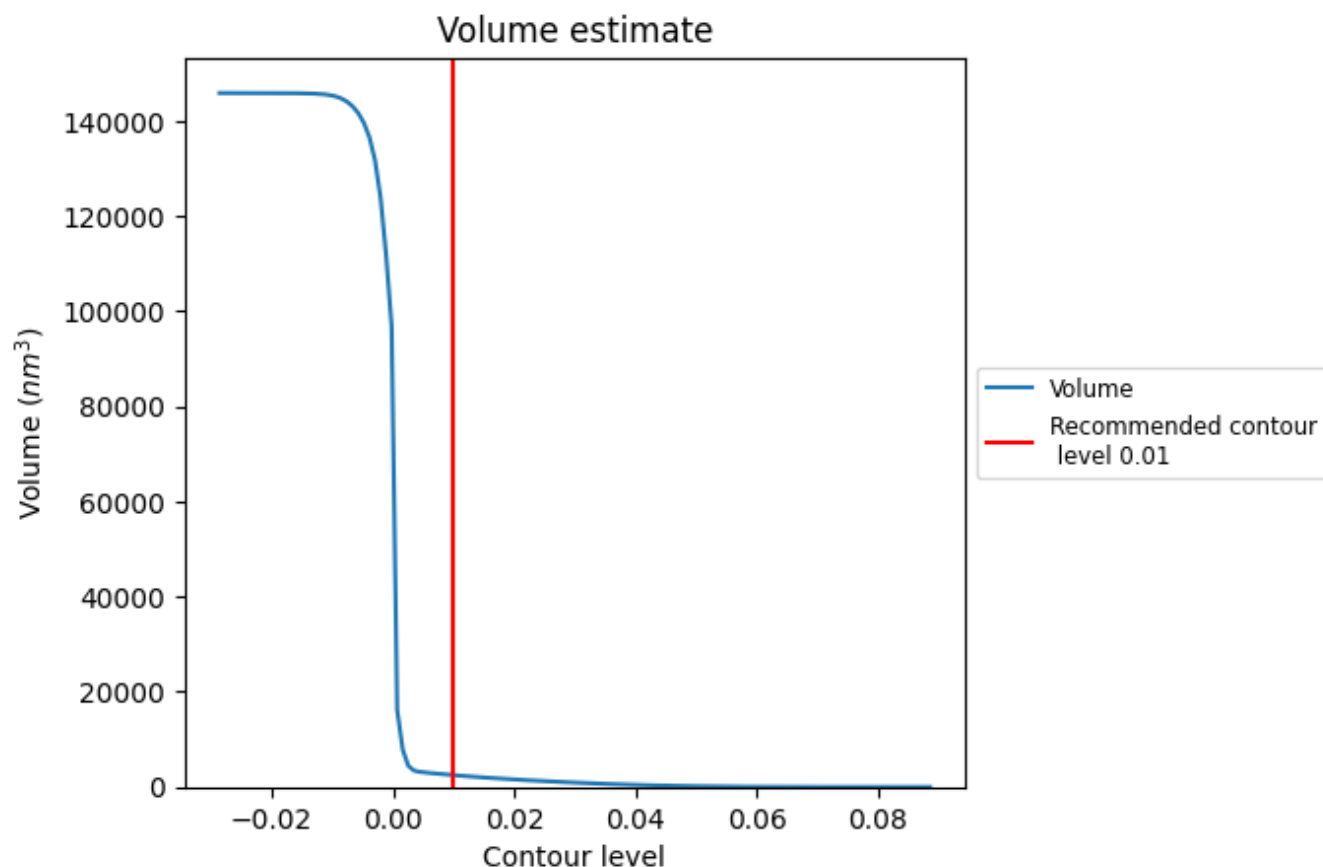
This section contains the results of statistical analysis of the map.

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.

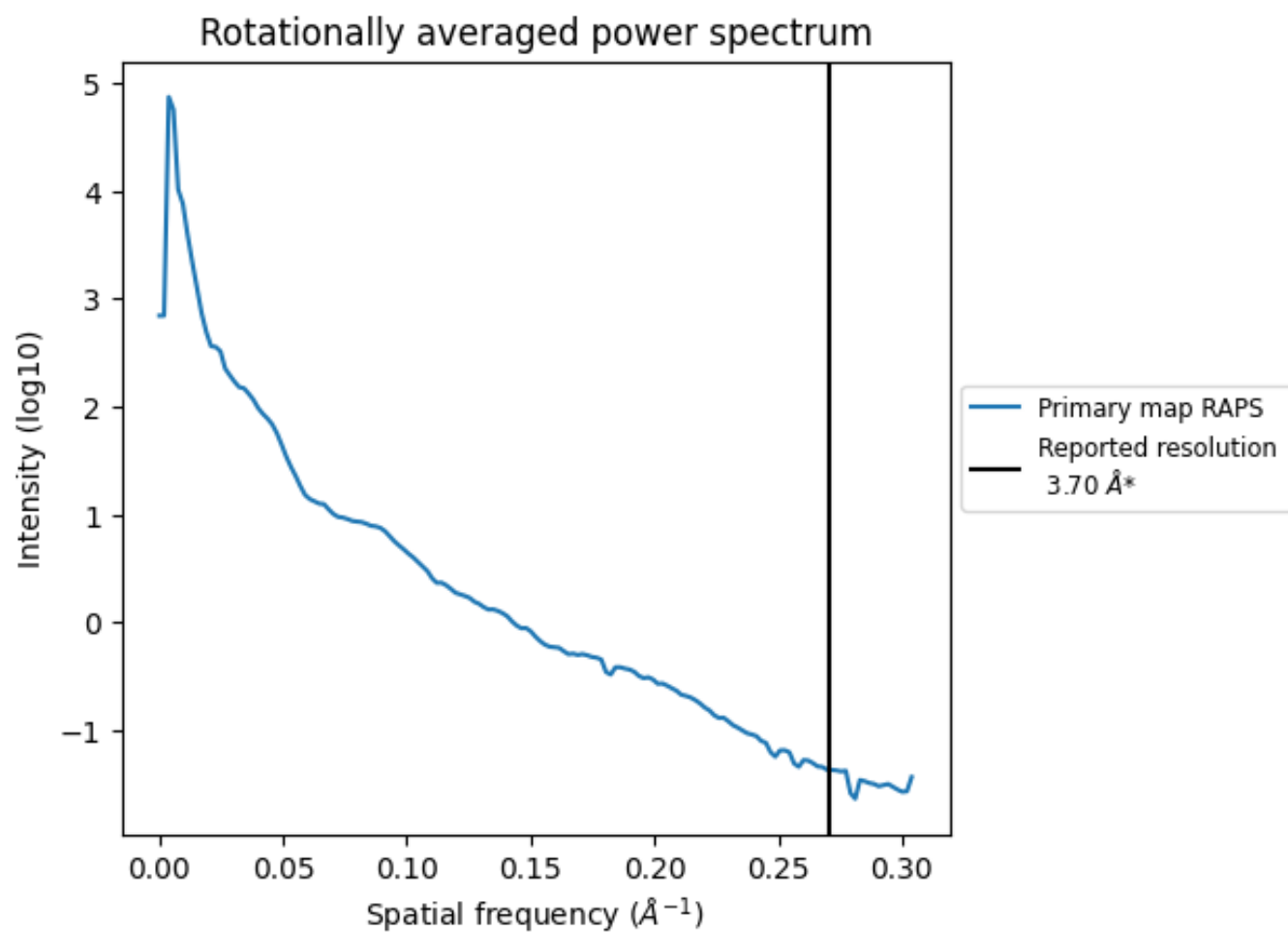
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2485 nm^3 ; this corresponds to an approximate mass of 2245 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 0.270 Å⁻¹

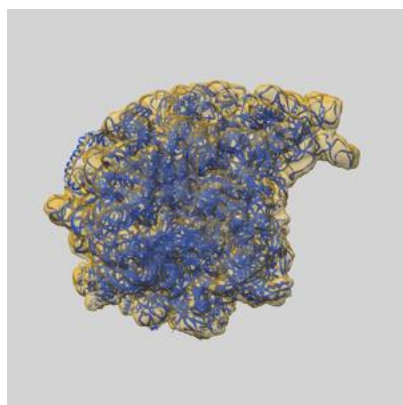
8 Fourier-Shell correlation ⓘ

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

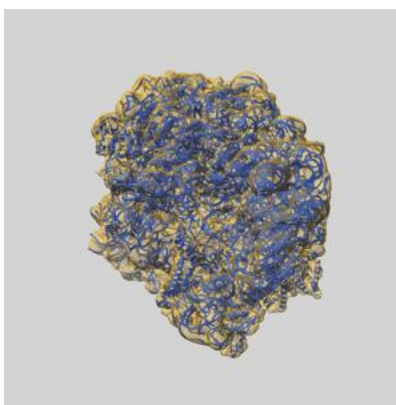
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20204 and PDB model 6OUO. Per-residue inclusion information can be found in section [3](#) on page [15](#).

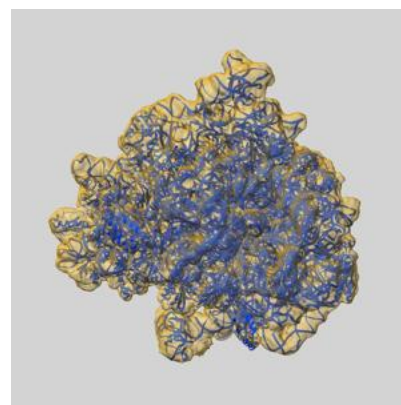
9.1 Map-model overlay [i](#)



X



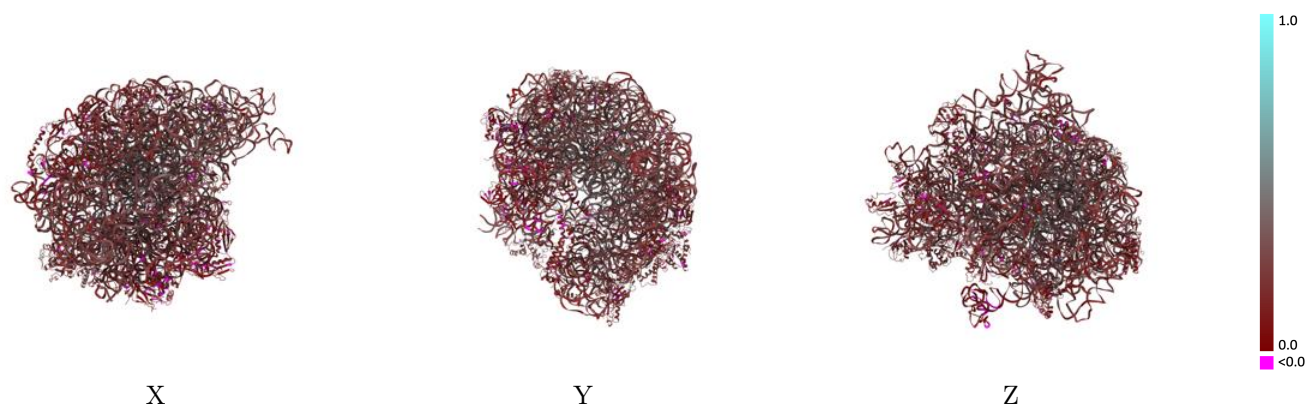
Y



Z

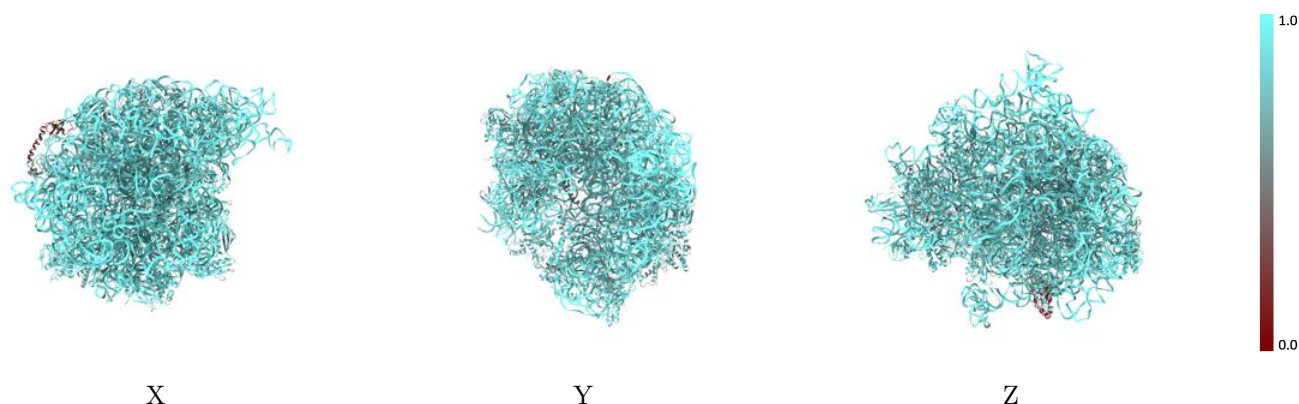
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



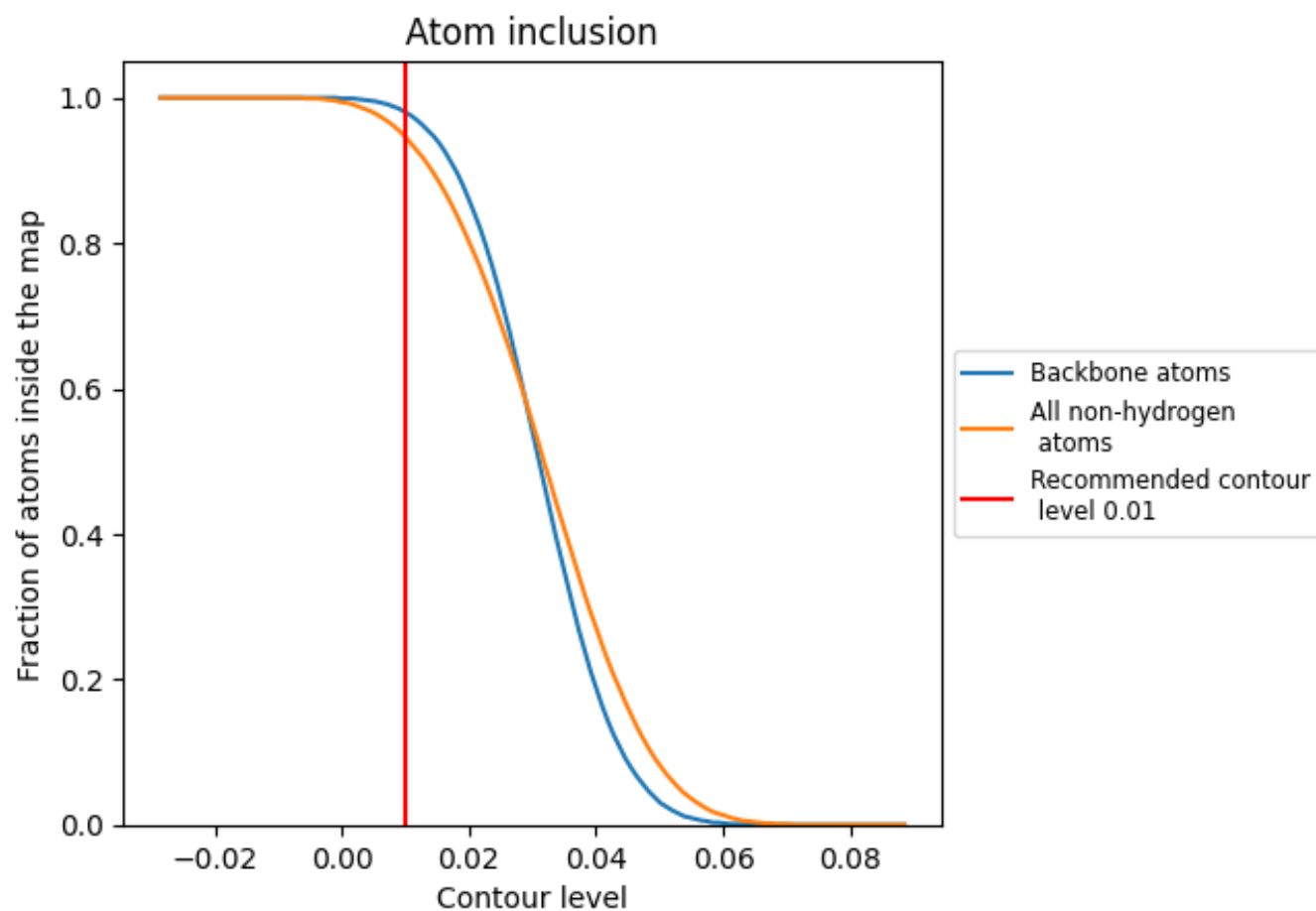
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.2470
1	 0.9870	 0.2690
2	 0.9910	 0.2690
3	 0.9860	 0.1870
4	 0.9840	 0.3390
5	 0.9670	 0.2880
A	 0.7720	 0.1830
B	 0.8420	 0.2390
C	 0.8790	 0.2320
D	 0.8940	 0.2430
E	 0.9020	 0.1880
F	 0.8590	 0.1350
G	 0.3830	 0.1430
J	 0.8440	 0.1710
K	 0.8400	 0.2770
L	 0.9050	 0.2800
M	 0.8610	 0.1910
N	 0.9100	 0.2220
O	 0.9370	 0.1770
P	 0.8720	 0.2470
Q	 0.8700	 0.1650
R	 0.8880	 0.1620
S	 0.8760	 0.2750
T	 0.8810	 0.1940
U	 0.9140	 0.1960
V	 0.8580	 0.1450
W	 0.8710	 0.2180
X	 0.8340	 0.2310
Y	 0.8670	 0.1680
Z	 0.8370	 0.1800
a	 0.8610	 0.2030
b	 0.8850	 0.2450
c	 0.9380	 0.2860
d	 0.9130	 0.2800
e	 0.8820	 0.2890



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Chain	Atom inclusion	Q-score
f	 0.8500	 0.1160
g	 0.7430	 0.1740
h	 0.8810	 0.2050
i	 0.8940	 0.2100
j	 0.8750	 0.2260
k	 0.8590	 0.1670
l	 0.9160	 0.2370
m	 0.8720	 0.1770
n	 0.9240	 0.1990
o	 0.8780	 0.1870
p	 0.8890	 0.2240
q	 0.8650	 0.2650
r	 0.9050	 0.1950
s	 0.9070	 0.1920
t	 0.8570	 0.1270
u	 0.8840	 0.2020
v	 0.8830	 0.2110
w	 0.8390	 0.1670
x	 0.8900	 0.1540
y	 0.9170	 0.2160
z	 0.7530	 0.1820