



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 08:46 AM EDT

PDB ID : 6OSQ / pdb_00006osq
EMDB ID : EMD-20187
Title : RF1 accommodated state bound Release complex 70S at long incubation time point
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-05-02
Resolution : 3.50 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:

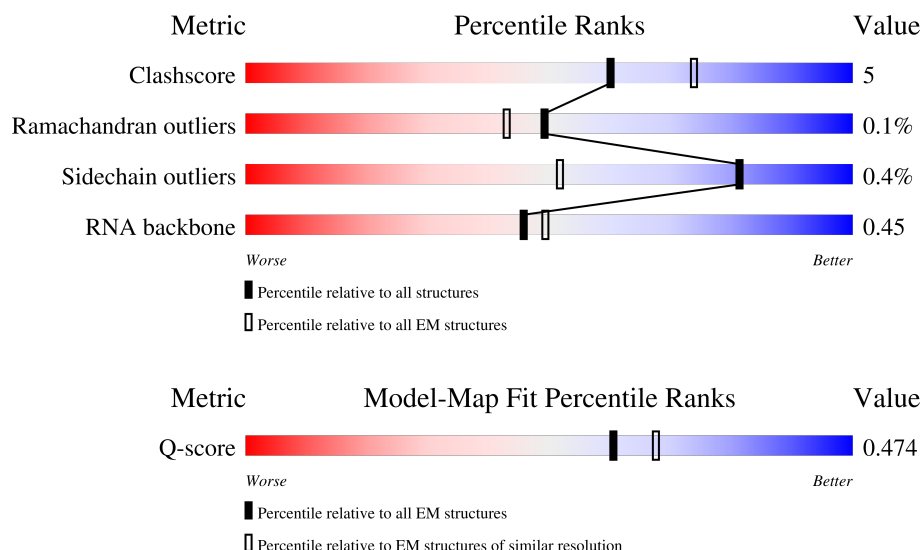
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.50 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	13950 (3.00 - 4.00)

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

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Mol	Chain	Length	Quality of chain
29	a	66	
30	b	56	
31	c	52	
32	d	46	
33	e	64	
34	f	38	
35	g	225	
36	h	208	
37	i	205	
38	j	156	
39	k	104	
40	l	151	
41	m	129	
42	n	127	
43	o	99	
44	p	117	
45	q	123	
46	r	116	
47	s	100	
48	t	88	
49	u	82	
50	v	80	
51	w	66	
52	x	83	
53	y	86	

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Mol	Chain	Length	Quality of chain
54	z	70	70% 84% 16%
55	A	259	39% 75% 24%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146756 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 RNA chain called P-tRNA.

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

- Molecule 6 is a protein called 50S ribosomal protein L2.

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

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

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

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

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

- Molecule 14 is a protein called 50S ribosomal protein L15.

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

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

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

- Molecule 17 is a protein called 50S ribosomal protein L18.

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

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

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

- Molecule 23 is a protein called 50S ribosomal protein L24.

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

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

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

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

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

- Molecule 28 is a protein called 50S ribosomal protein L30.

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

- Molecule 29 is a protein called 50S ribosomal protein L31.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

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

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

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

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

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

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

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

- Molecule 52 is a protein called 30S ribosomal protein S19.

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

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

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

- Molecule 55 is a protein called Peptide chain release factor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A	259	Total	C	N	O	S	0	0
			2014	1235	382	389	8		

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

Mol	Chain	Residues	Atoms		AltConf
56	1	289	Total 289	Mg 289	0
56	2	126	Total 126	Mg 126	0
56	3	8	Total 8	Mg 8	0
56	5	4	Total 4	Mg 4	0
56	C	2	Total 2	Mg 2	0
56	D	1	Total 1	Mg 1	0
56	N	1	Total 1	Mg 1	0
56	Q	1	Total 1	Mg 1	0
56	b	1	Total 1	Mg 1	0
56	f	1	Total 1	Mg 1	0
56	h	1	Total 1	Mg 1	0
56	i	1	Total 1	Mg 1	0

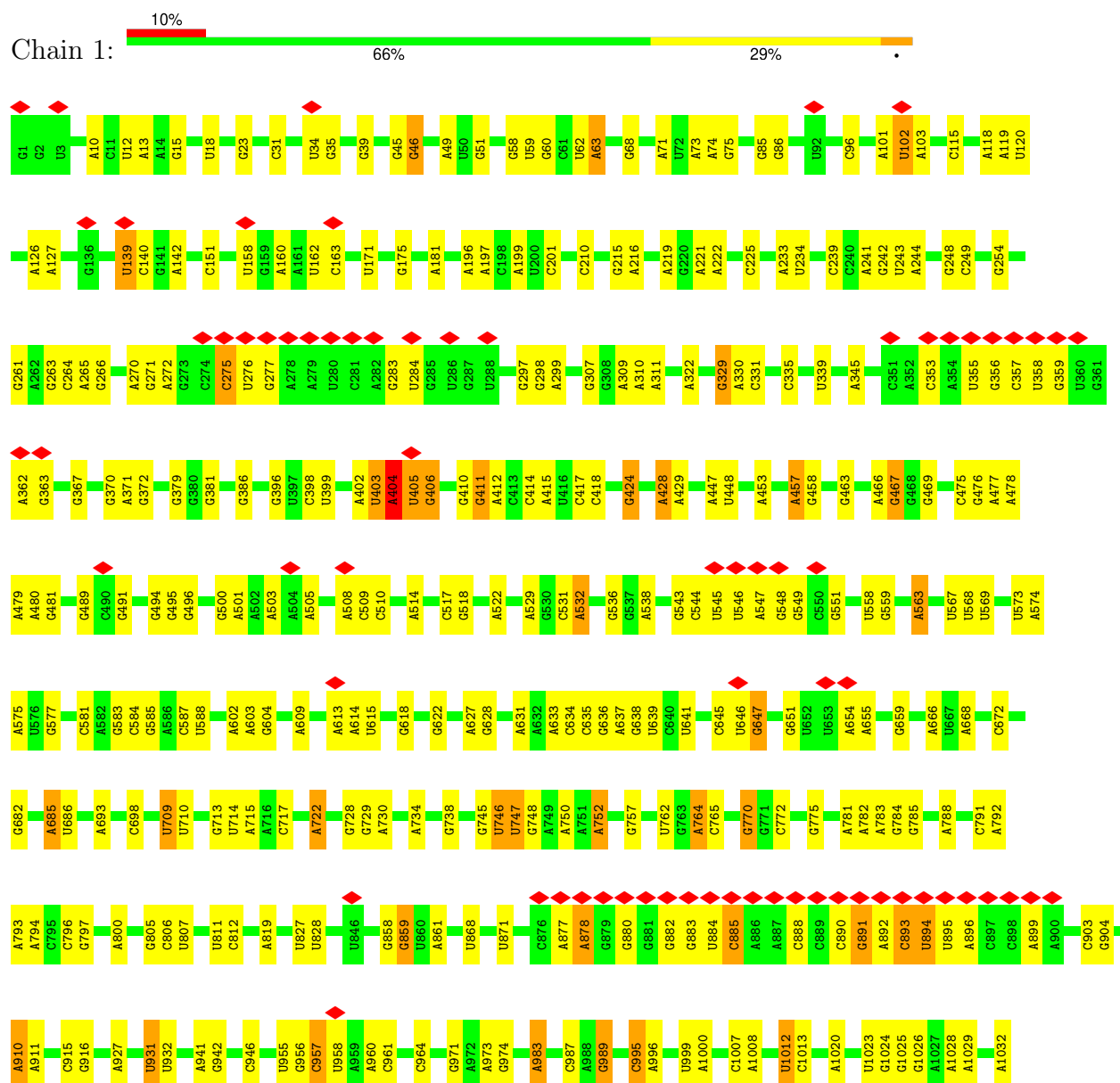
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

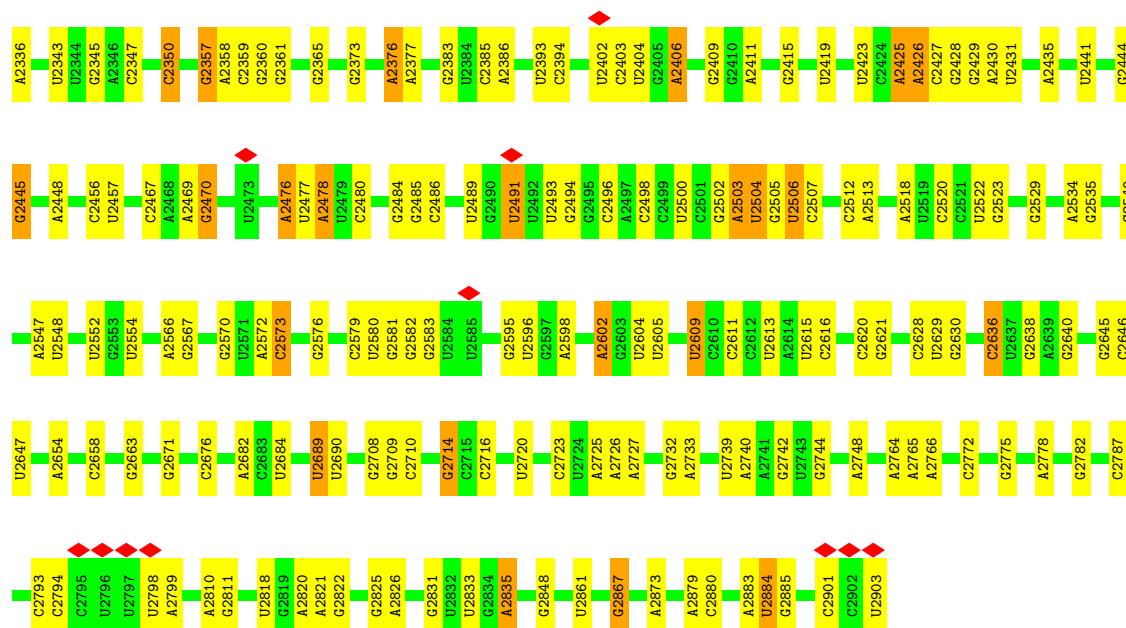
3 Residue-property plots

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.

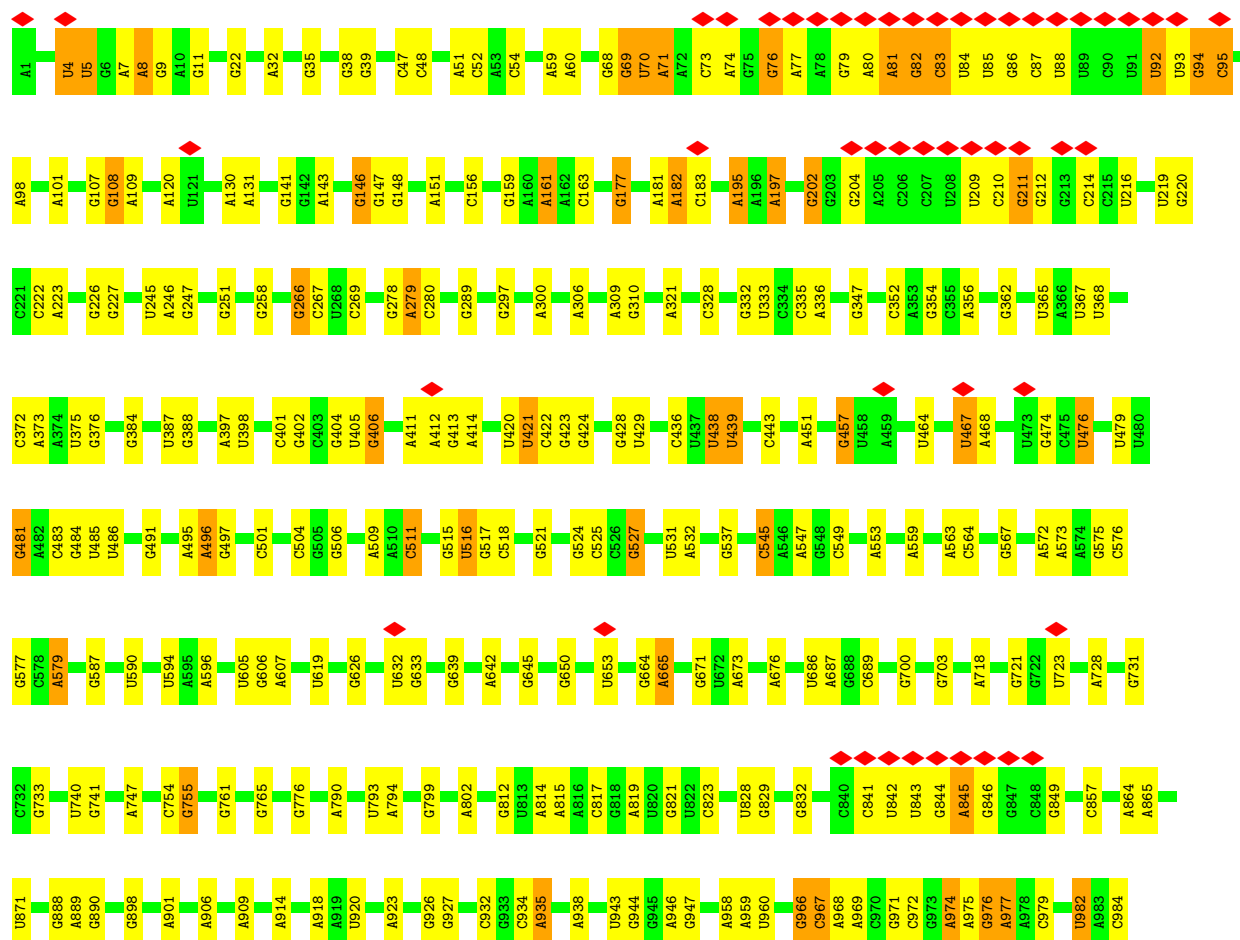
• Molecule 1: 23S ribosomal RNA

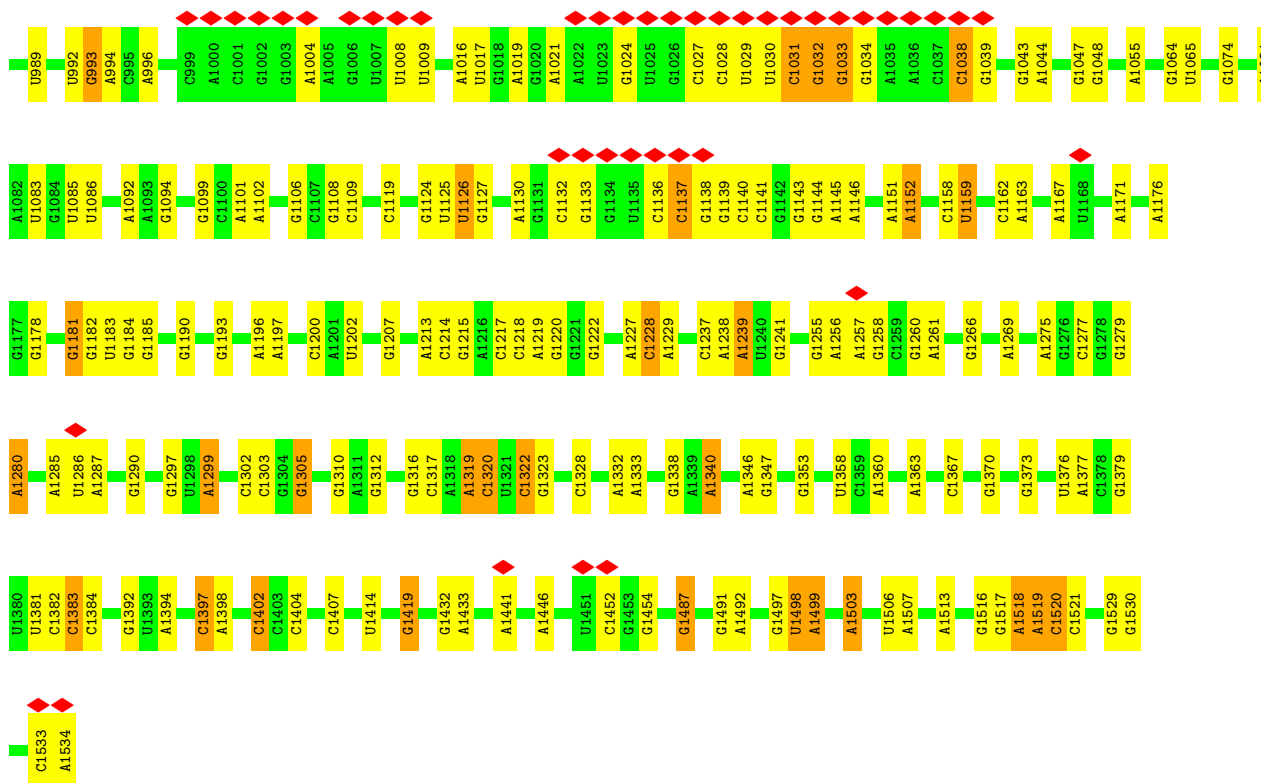


C2226	C2232	C2233	C2234	G2235	G2238	C2239	U2243	G2250	G2251	C2258	C2264	U2265	A2266	G2271	U2272	A2273	G2277	A2278	G2279	C2283	A2284	C2285	G2286	A2287	G2293	A2297	A2298	G2303	G2304	U2305	C2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	G2319	G2325	G2326	A2327	U2334	A2335														
A2154	U2155	G2156	G2157	A2158	G2159	C2160	C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174	C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	U2186	U2187	U2188	U2189	G2190	A2191	U2192	C2193	U2194	U2195	A2198	U2202	U2203	G2204	C2208	A2211	A2212	U2213	G2221	G2222	G2223	G2224	A2225				
G2093	A2097	U2098	U2099	U2098	U2099	G2100	A2101	G2102	C2103	C2104	U2105	U2106	A2107	A2108	U2109	G2110	U2111	G2112	U2113	A2114	G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	C2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152
G1980	A1981	U1982	G1989	C1990	U1991	G1992	U1993	C1996	C1997	C2001	G2002	A2005	G2010	U2011	U2012	A2013	A2020	C2021	U2022	C2023	A2030	A2031	C2032	A2033	U2034	G2035	C2036	A2037	C2043	G2048	C2049	A2052	C2055	G2056	A2060	G2061	A2062	G2069	A2070	C2071	C2072	U2075	U2076	U2077	A2090													
G1869	C1870	A1871	A1872	G1873	U1882	U1883	G1884	G1891	G1896	G1904	C1905	G1906	G1907	U1911	G1912	A1913	C1914	3TD1915	U1916	U1917	C1924	C1925	U1926	A1927	A1928	G1929	G1930	C1934	U1935	A1936	A1937	A1938	U1939	U1943	U1944	G1949	U1955	C1962	U1963	G1964	C1967	A1970	U1971	U1976	G1972	A1977												
A1773	C1774	U1775	U1779	A1780	U1781	U1782	A1783	A1784	C1788	A1789	C1790	G1792	U1796	G1797	U1798	G1799	C1800	A1801	A1802	C1806	G1807	A1808	A1809	A1810	G1811	G1814	A1815	C1816	G1817	U1818	A1819	G1828	A1829	C1830	C1833	U1834	G1835	A1847	A1848	G1857	A1858	G1862	G1863	U1864	U1865	A1866												
A1640	C1646	U1647	U1648	G1651	A1652	A1655	G1666	G1667	A1672	C1673	G1674	G1682	U1693	C1694	A1698	G1699	A1713	U1714	G1715	G1721	G1724	A1725	C1726	C1727	C1728	U1729	C1730	G1731	C1732	G1733	G1738	A1739	A1744	A1745	A1746	U1747	U1748	A1749	G1756	A1757	U1758	A1759	C1764															
C1536	G1537	G1538	U1539	G1540	C1541	U1542	G1543	A1544	U1554	C1565	A1566	G1567	G1568	A1569	C1577	U1578	A1579	A1580	A1583	U1584	C1585	A1586	G1587	U1588	U1589	A1590	C1591	C1592	A1593	A1597	A1598	G1601	U1602	A1603	C1604	C1607	A1608	A1609	A1610	G1613	A1614	C1615	A1618	G1619	G1622	A1626	A1634											
C1437	G1441	C1447	G1450	C1451	G1452	A1453	C1454	G1455	U1458	G1459	U1460	U1468	G1471	G1475	G1478	G1479	C1480	U1481	G1482	U1485	A1490	C1493	A1496	U1497	A1502	A1503	A1508	A1509	G1510	U1513	G1514	A1515	U1523	G1524	A1528	G1529	G1530	C1531	A1532	C1533	U1534	A1535																
G1338	U1352	A1353	A1359	G1360	G1361	C1362	C1363	G1364	A1365	G1368	A1378	U1379	G1380	A1383	A1384	A1385	C1386	A1387	A1392	A1393	A1394	A1395	U1396	C1399	U1400	A1403	G1407	G1408	U1409	G1410	U1411	U1412	A1413	C1414	U1415	G1416	C1417	G1418	A1419	A1420	G1421	A1427	C1428	A1431	A1434													
A1189	G1190	A1204	G1210	C1211	G1212	G1223	G1235	G1236	A1237	G1238	G1248	U1249	G1250	C1251	G1252	A1253	A1254	U1255	G1256	U1263	A1264	A1265	G1266	C1270	G1271	A1272	U1273	A1274	A1275	G1288	G1296	C1297	G1298	G1299	G1300	A1301	A1302	C1306	C1314	C1315	A1321	U1325	U1326	A1327	G1332													
C1100	U1101	C1102	A1103	C1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	G1115	G1122	G1125	U1126	G1128	A1129	U1130	G1131	U1132	A1133	A1134	C1135	G1136	U1141	A1142	A1143	A1144	A1155	A1156	G1162	G1166	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	U1175	U1176	G1177	C1178	G1179	U1180	U1181	G1182	G1186								
U1033	A1040	G1041	G1042	C1043	C1044	C1045	A1046	G1047	G1051	C1052	C1053	A1054	G1055	G1056	A1057	U1058	G1059	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1072	A1073	G1074	C1075	C1076	A1077	U1078	C1079	A1080	U1081	U1082	U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1091	C1092	G1093	U1094	A1095	A1096	U1097	A1098	G1099	



• Molecule 2: 16S ribosomal RNA

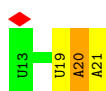




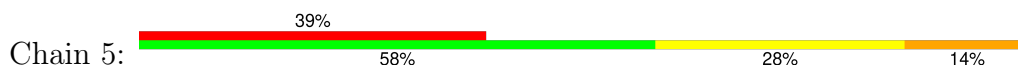
• Molecule 3: 5S ribosomal RNA



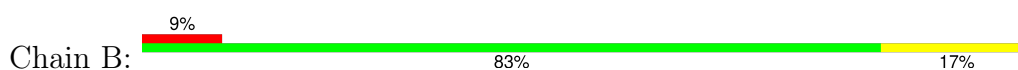
• Molecule 4: mRNA

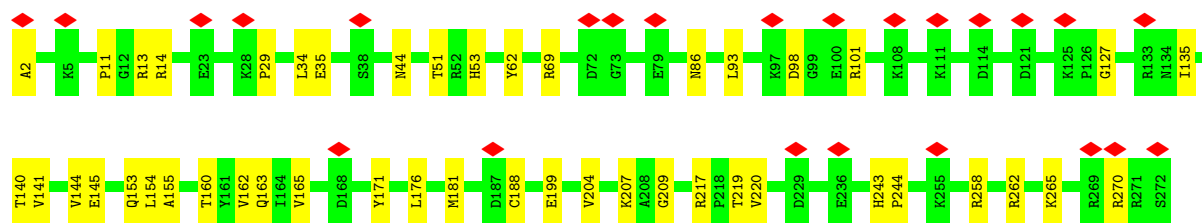


• Molecule 5: P-tRNA

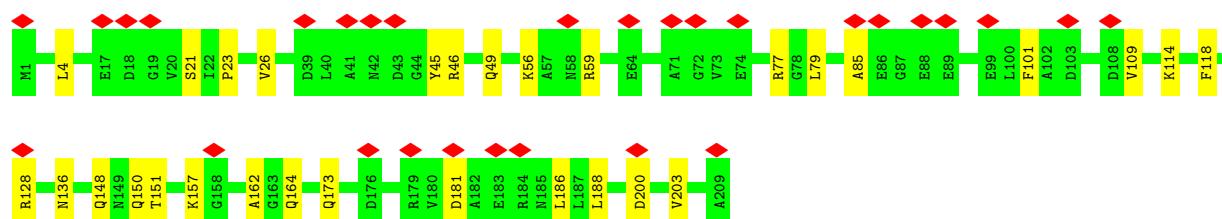
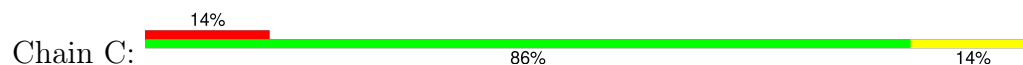


• Molecule 6: 50S ribosomal protein L2

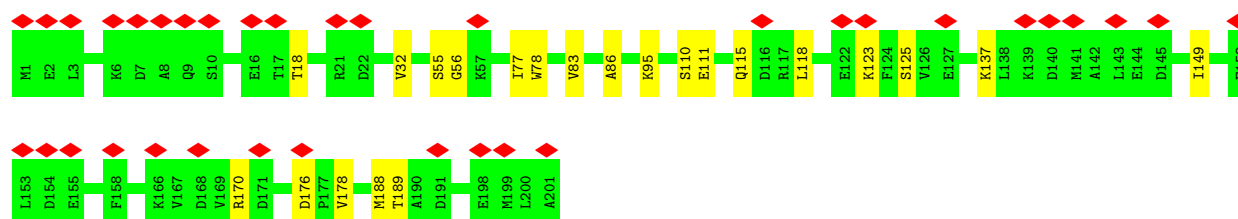
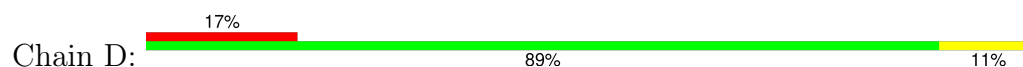




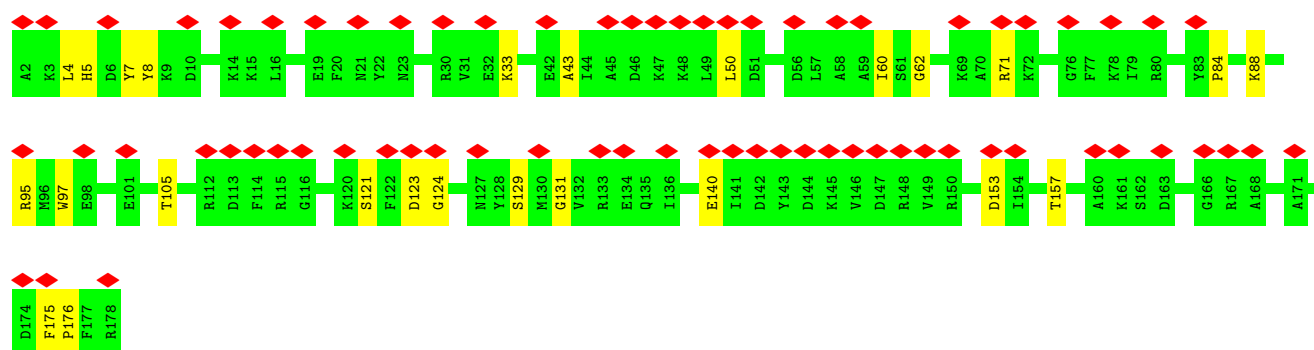
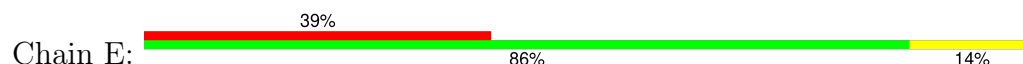
• Molecule 7: 50S ribosomal protein L3



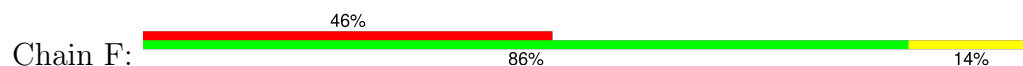
• Molecule 8: 50S ribosomal protein L4

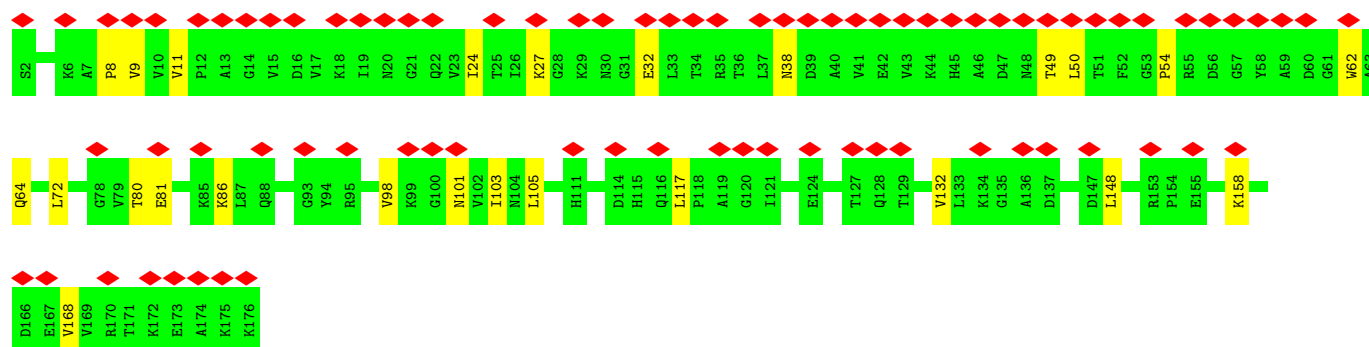


• Molecule 9: 50S ribosomal protein L5

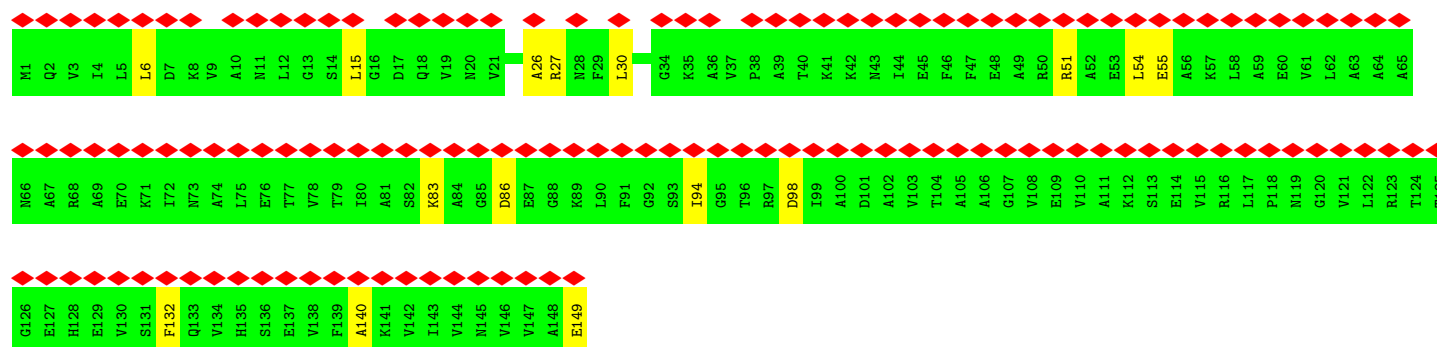
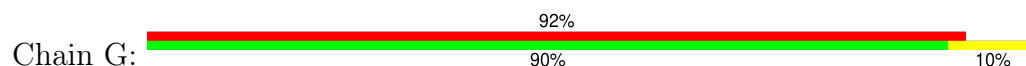


• Molecule 10: 50S ribosomal protein L6

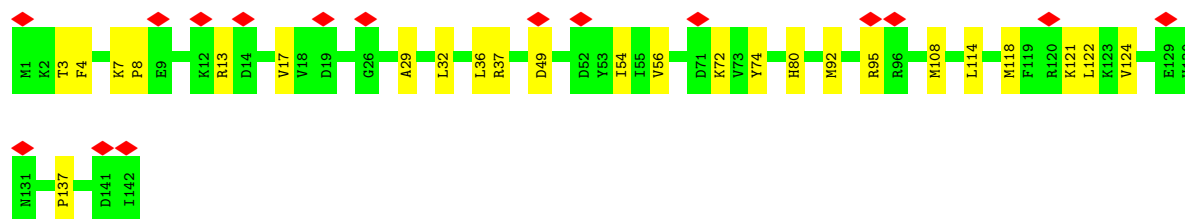
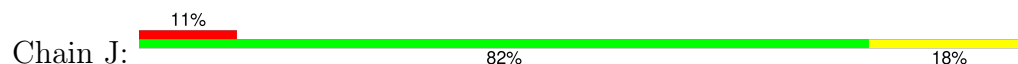




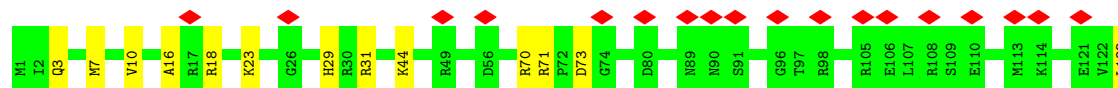
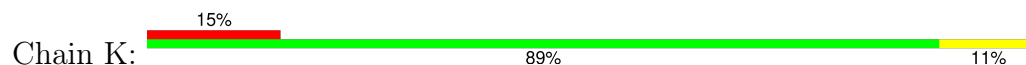
• Molecule 11: 50S ribosomal protein L9



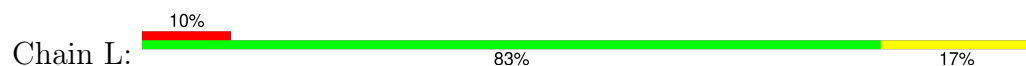
• Molecule 12: 50S ribosomal protein L13

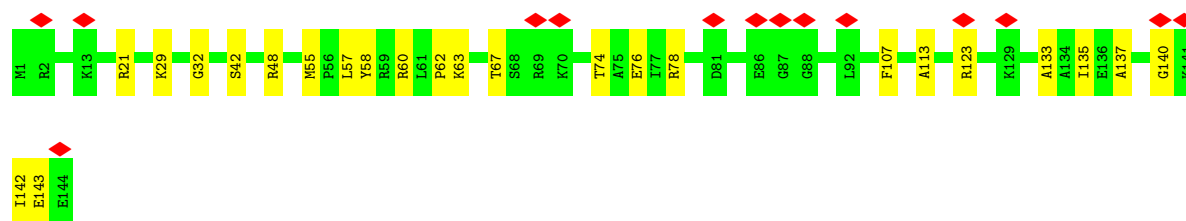


• Molecule 13: 50S ribosomal protein L14

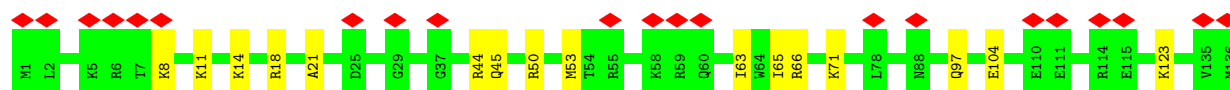
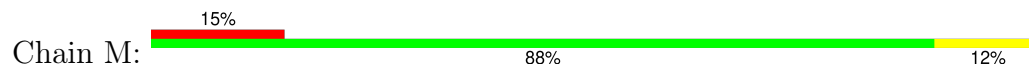


• Molecule 14: 50S ribosomal protein L15

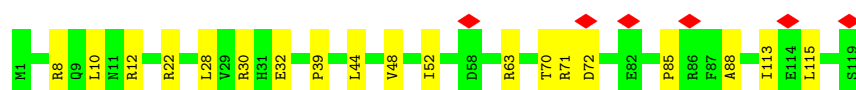
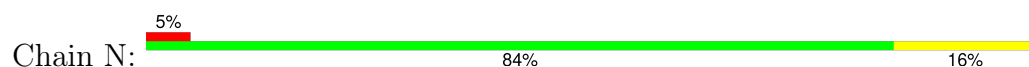




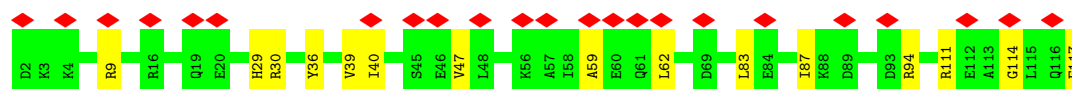
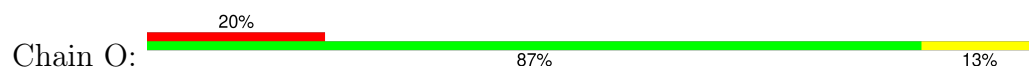
- Molecule 15: 50S ribosomal protein L16



- Molecule 16: 50S ribosomal protein L17



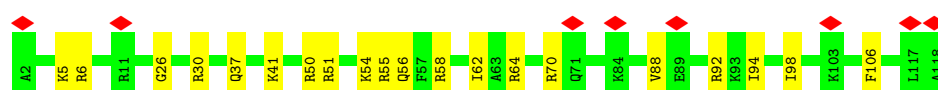
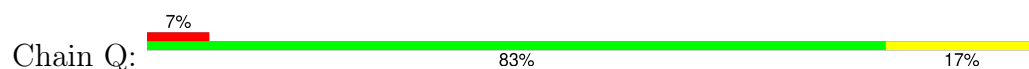
- Molecule 17: 50S ribosomal protein L18



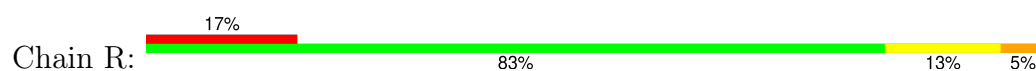
- Molecule 18: 50S ribosomal protein L19

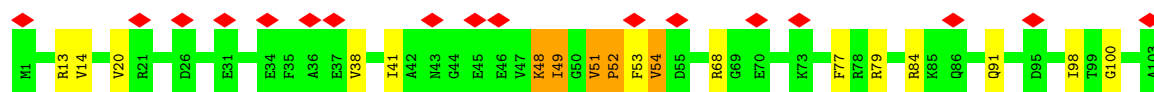


- Molecule 19: 50S ribosomal protein L20

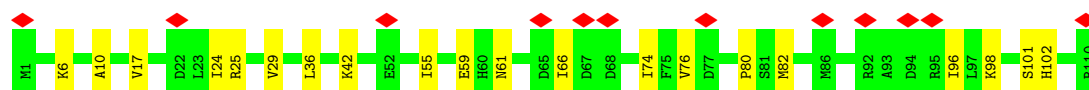
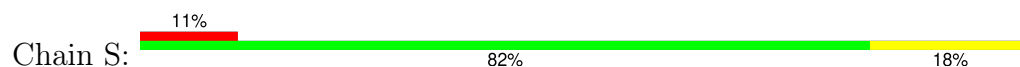


- Molecule 20: 50S ribosomal protein L21

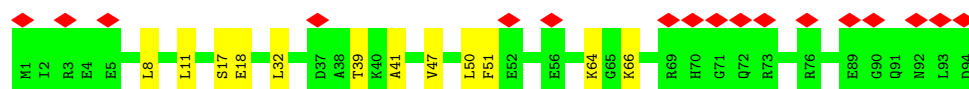
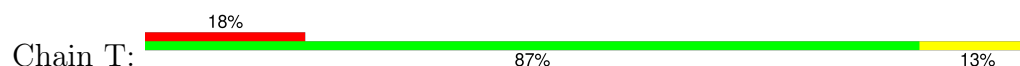




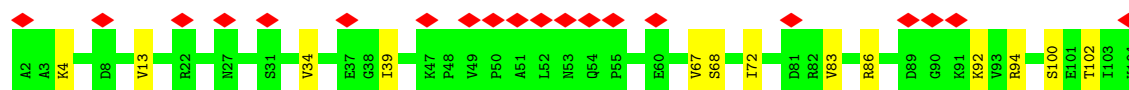
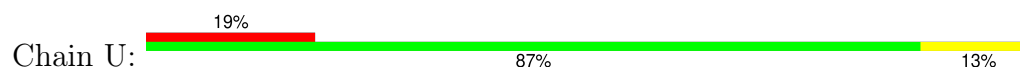
- Molecule 21: 50S ribosomal protein L22



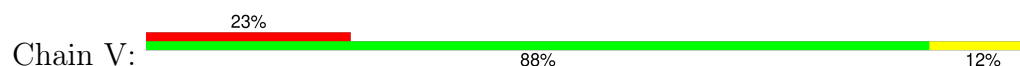
- Molecule 22: 50S ribosomal protein L23



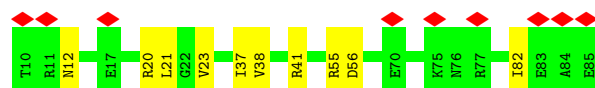
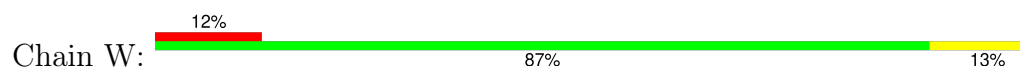
- Molecule 23: 50S ribosomal protein L24



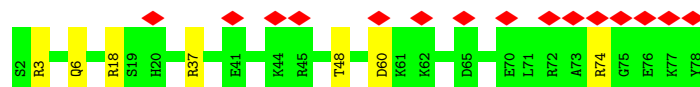
- Molecule 24: 50S ribosomal protein L25



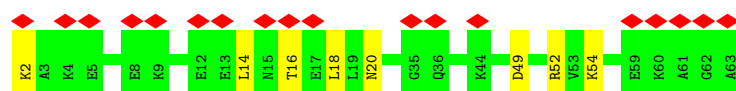
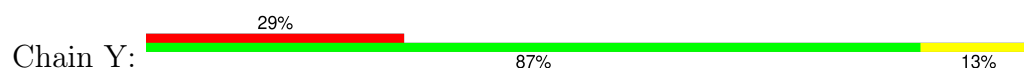
- Molecule 25: 50S ribosomal protein L27



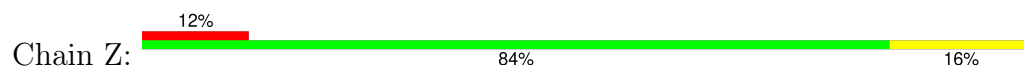
- Molecule 26: 50S ribosomal protein L28



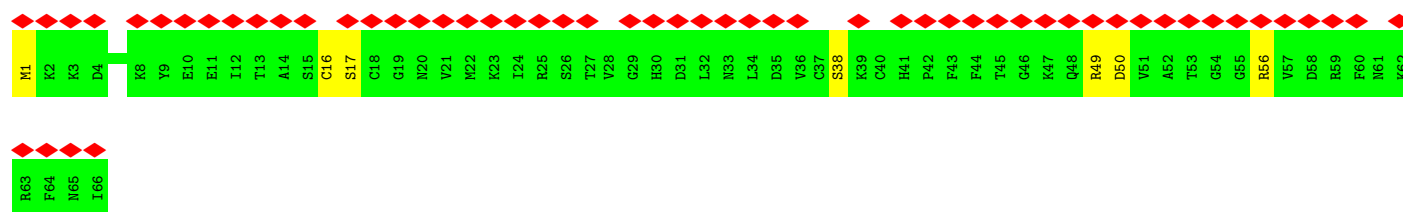
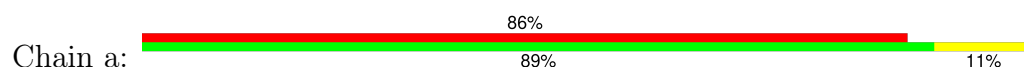
- Molecule 27: 50S ribosomal protein L29



- Molecule 28: 50S ribosomal protein L30



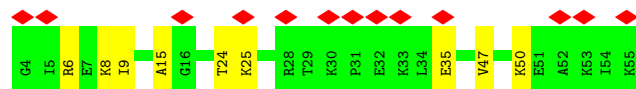
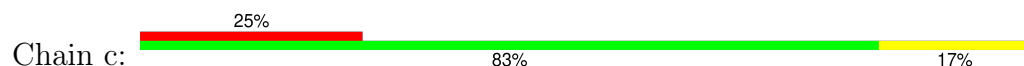
- Molecule 29: 50S ribosomal protein L31



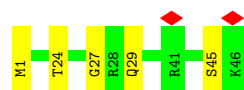
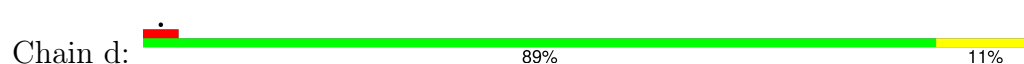
- Molecule 30: 50S ribosomal protein L32



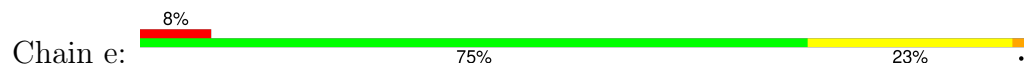
- Molecule 31: 50S ribosomal protein L33



- Molecule 32: 50S ribosomal protein L34

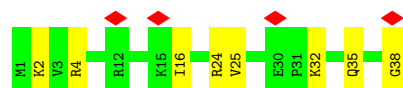
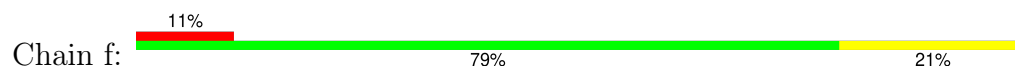


- Molecule 33: 50S ribosomal protein L35

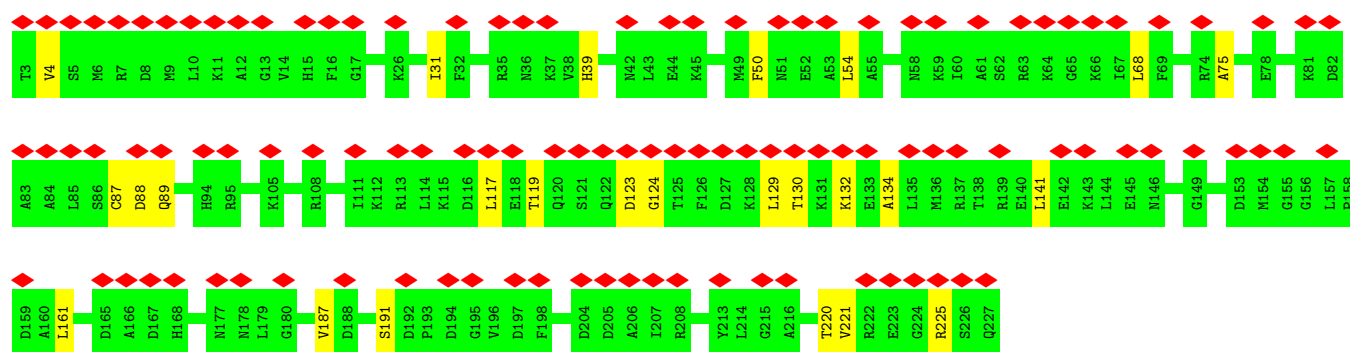
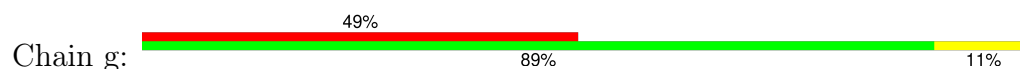




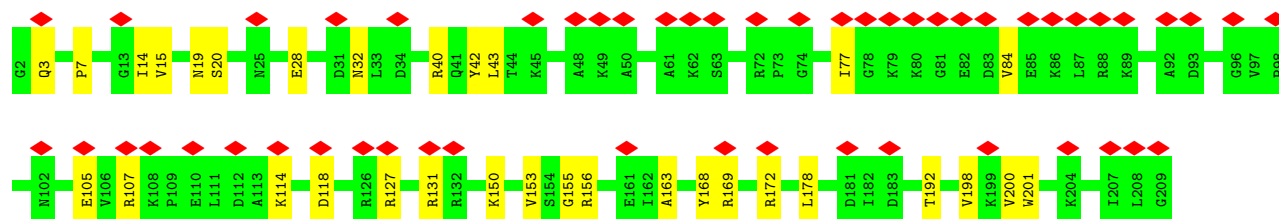
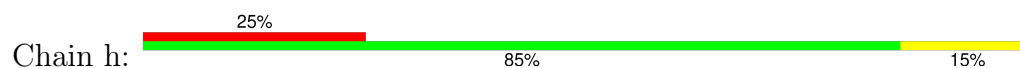
- Molecule 34: 50S ribosomal protein L36



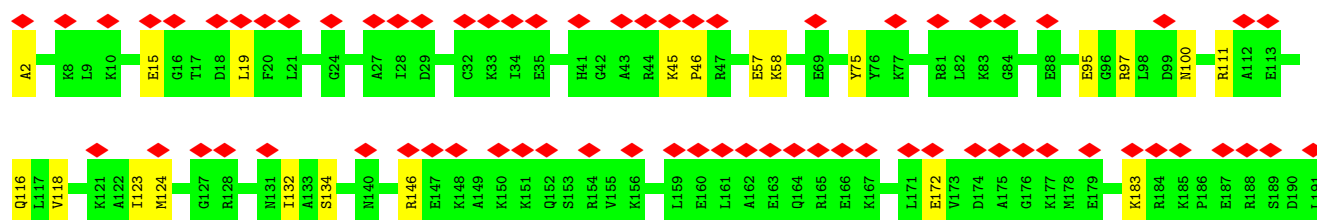
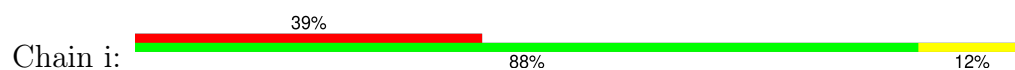
- Molecule 35: 30S ribosomal protein S2

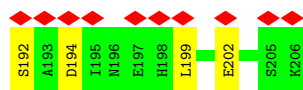


- Molecule 36: 30S ribosomal protein S3

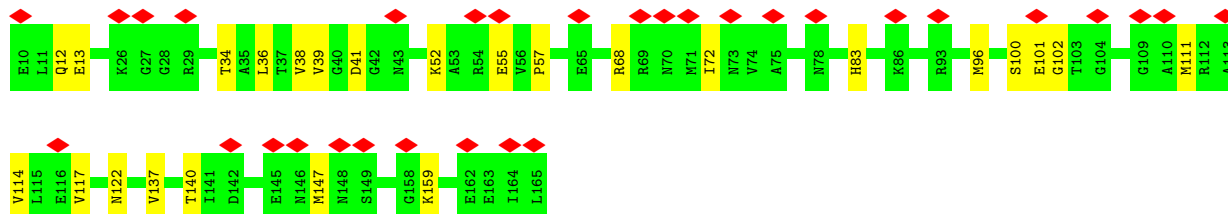
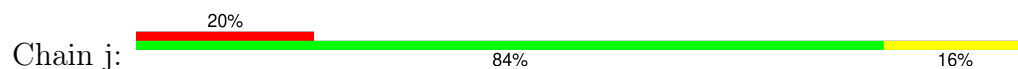


- Molecule 37: 30S ribosomal protein S4

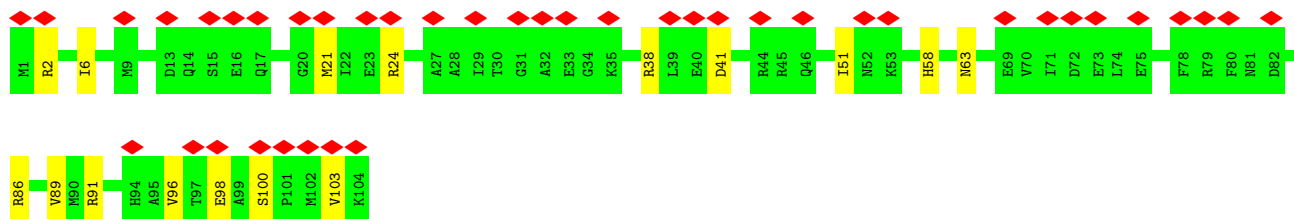
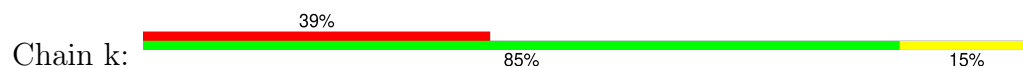




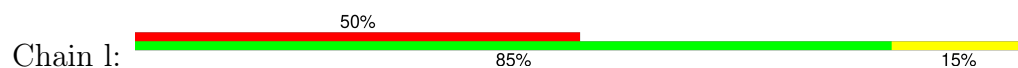
- Molecule 38: 30S ribosomal protein S5



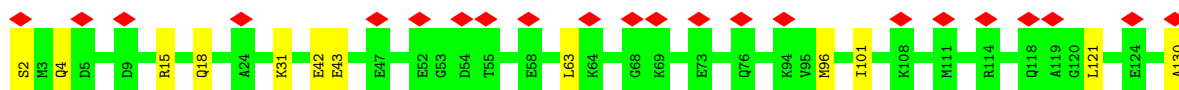
- Molecule 39: 30S ribosomal protein S6



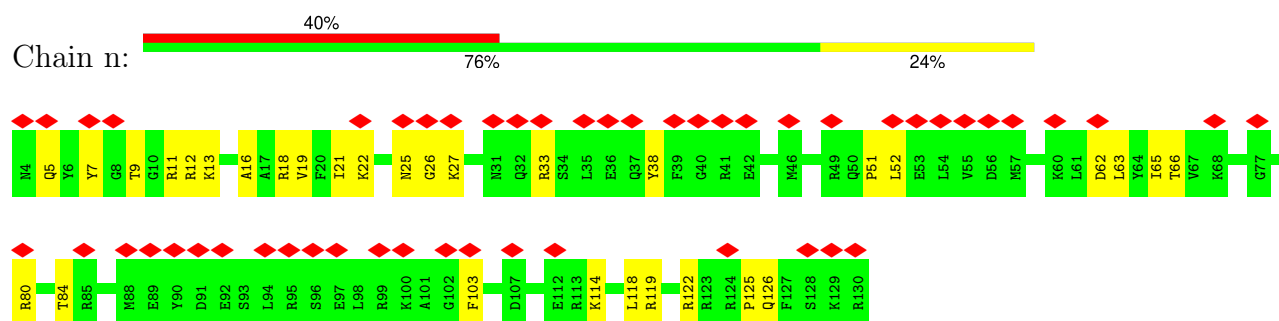
- Molecule 40: 30S ribosomal protein S7



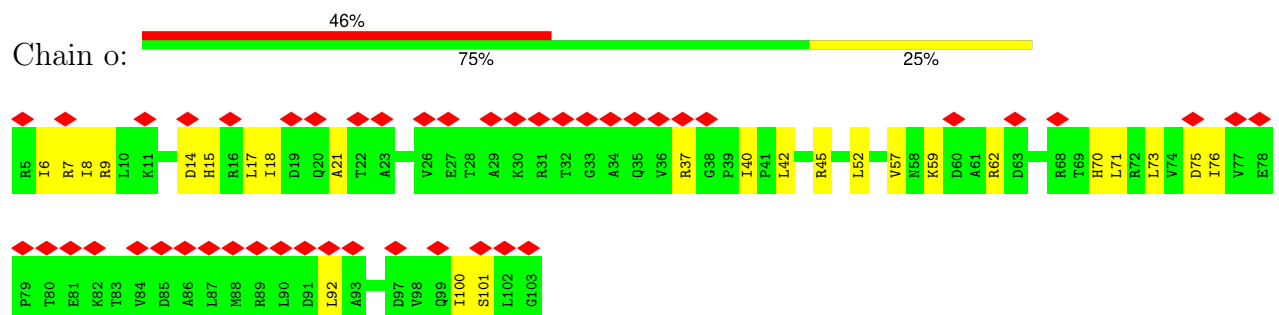
- Molecule 41: 30S ribosomal protein S8



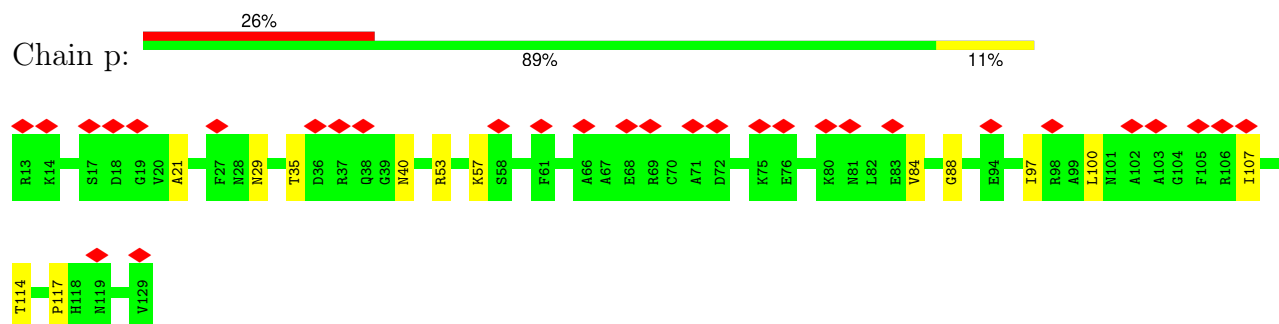
- Molecule 42: 30S ribosomal protein S9



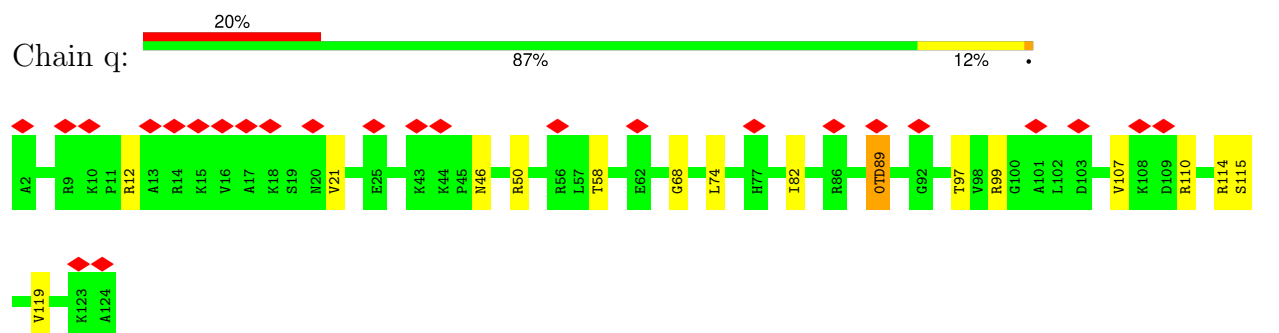
- Molecule 43: 30S ribosomal protein S10



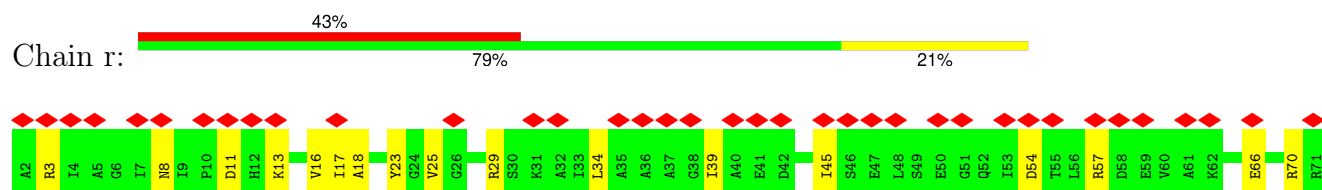
- Molecule 44: 30S ribosomal protein S11



- Molecule 45: 30S ribosomal protein S12

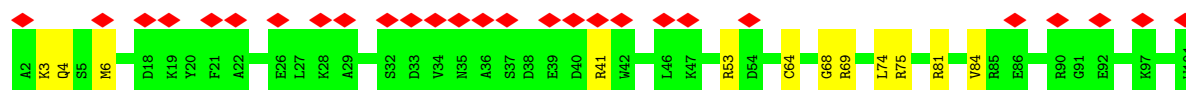
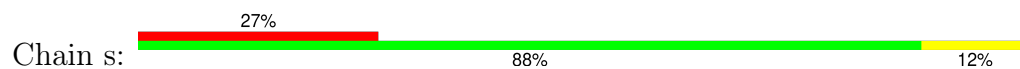


- Molecule 46: 30S ribosomal protein S13

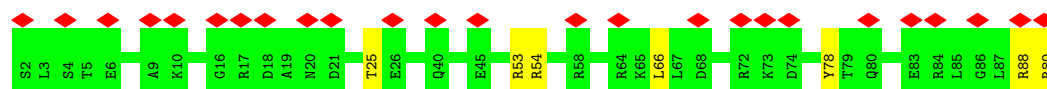




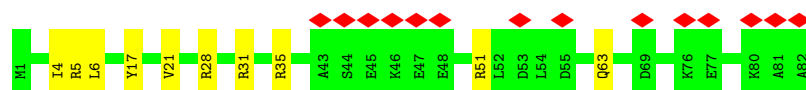
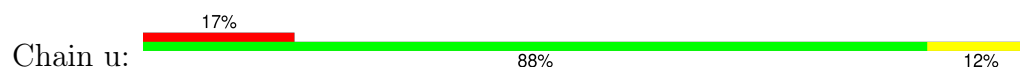
- Molecule 47: 30S ribosomal protein S14



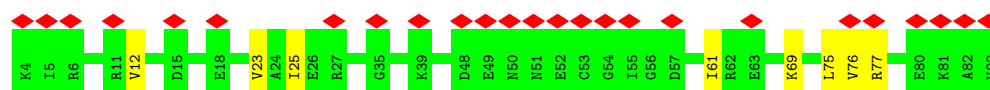
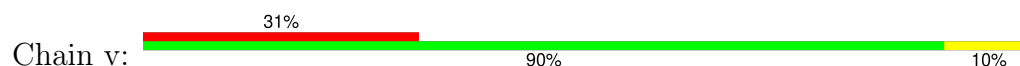
- Molecule 48: 30S ribosomal protein S15



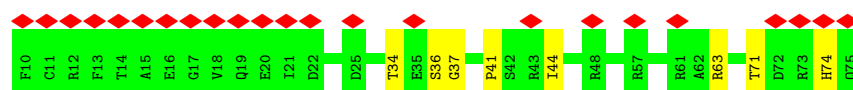
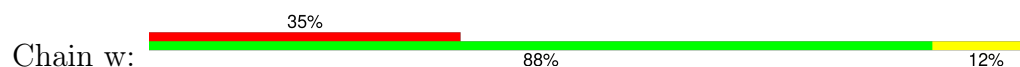
- Molecule 49: 30S ribosomal protein S16



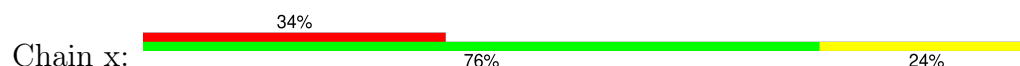
- Molecule 50: 30S ribosomal protein S17

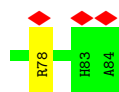


- Molecule 51: 30S ribosomal protein S18

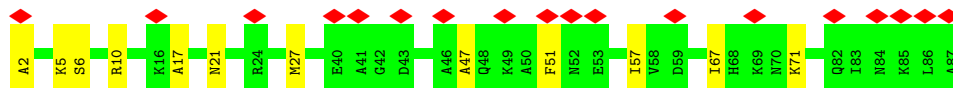
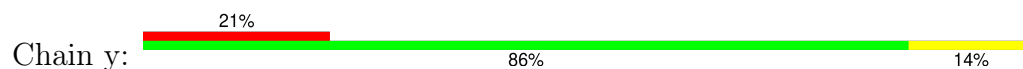


- Molecule 52: 30S ribosomal protein S19

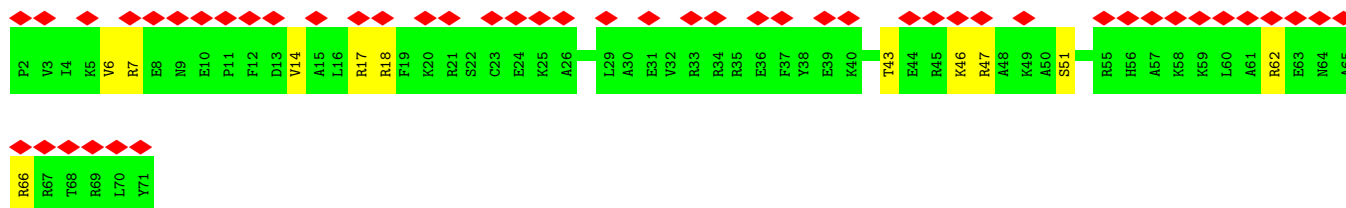
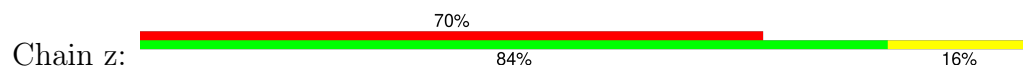




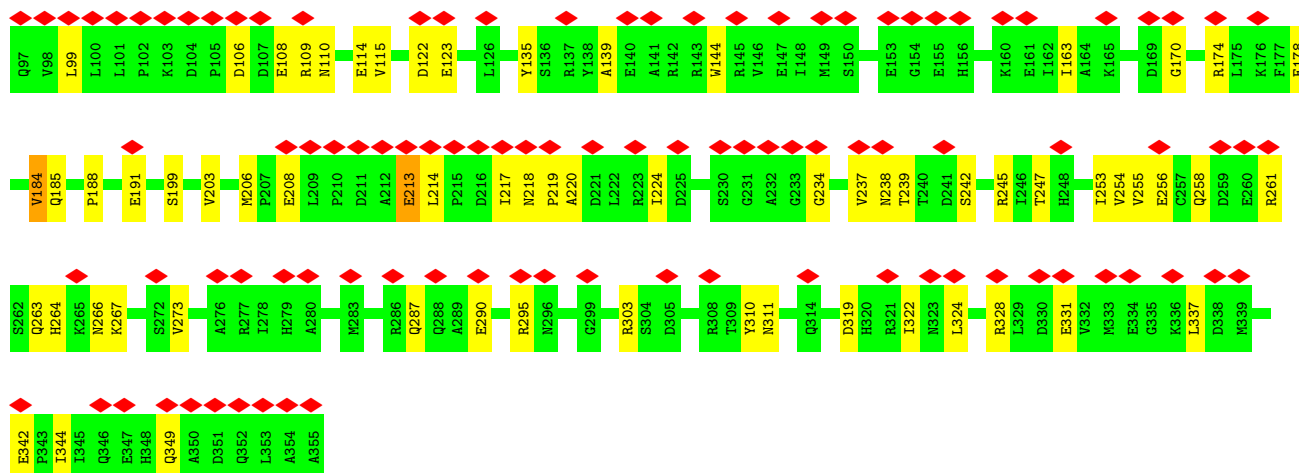
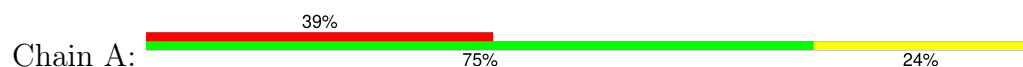
- Molecule 53: 30S ribosomal protein S20



- Molecule 54: 30S ribosomal protein S21



- Molecule 55: Peptide chain release factor 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72251	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	0.502	Depositor
Minimum map value	-0.385	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 6MZ, 4OC, OMU, ZN, 5MU, MA6, OMG, 2MG, MG, 3TD, UR3, 0TD, 5MC, G7M, OMC, PSU, H2U, 1MG, 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	0.43	0/69286	0.42	5/108087 (0.0%)
2	2	0.37	0/36590	0.39	0/57074
3	3	0.34	0/2872	0.36	0/4478
4	4	0.43	0/203	0.46	0/312
5	5	0.33	0/1704	0.42	1/2654 (0.0%)
6	B	0.49	0/2121	0.60	0/2852
7	C	0.47	0/1586	0.61	0/2134
8	D	0.43	0/1571	0.57	0/2113
9	E	0.35	0/1434	0.61	0/1926
10	F	0.28	0/1333	0.49	0/1805
11	G	0.25	0/1122	0.57	0/1515
12	J	0.43	0/1152	0.52	0/1551
13	K	0.46	0/955	0.59	0/1279
14	L	0.43	0/1062	0.58	0/1413
15	M	0.43	0/1093	0.55	0/1460
16	N	0.46	0/964	0.65	1/1289 (0.1%)
17	O	0.35	0/902	0.57	0/1209
18	P	0.42	0/929	0.53	0/1242
19	Q	0.50	0/960	0.60	0/1278
20	R	0.47	0/829	0.69	0/1107
21	S	0.43	0/864	0.58	0/1156
22	T	0.37	0/752	0.53	0/1005
23	U	0.37	0/796	0.59	0/1062
24	V	0.35	0/766	0.53	0/1025
25	W	0.45	0/589	0.58	0/779
26	X	0.44	0/635	0.54	0/848
27	Y	0.33	0/502	0.47	0/667
28	Z	0.42	0/452	0.57	0/605
29	a	0.25	0/531	0.55	0/709
30	b	0.43	0/450	0.65	0/599
31	c	0.36	0/433	0.60	0/576

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	0.50	0/380	0.65	0/498
33	e	0.52	0/513	0.72	0/676
34	f	0.42	0/303	0.53	0/397
35	g	0.30	0/1791	0.55	1/2413 (0.0%)
36	h	0.34	0/1663	0.54	0/2241
37	i	0.32	0/1665	0.50	0/2227
38	j	0.41	0/1165	0.60	0/1568
39	k	0.33	0/867	0.60	0/1171
40	l	0.30	0/1195	0.55	0/1602
41	m	0.38	0/989	0.55	0/1326
42	n	0.35	0/1034	0.63	0/1375
43	o	0.33	0/800	0.56	0/1082
44	p	0.36	0/893	0.54	0/1205
45	q	0.43	0/960	0.64	0/1286
46	r	0.32	0/909	0.62	0/1215
47	s	0.36	0/817	0.54	0/1088
48	t	0.35	0/722	0.56	0/964
49	u	0.35	0/659	0.58	0/884
50	v	0.35	0/657	0.56	0/881
51	w	0.35	0/553	0.51	0/743
52	x	0.29	0/680	0.52	0/915
53	y	0.33	0/675	0.49	0/895
54	z	0.28	0/597	0.55	0/792
55	A	0.41	0/2046	0.69	1/2759 (0.0%)
All	All	0.40	0/157971	0.46	9/236012 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	g	75	ALA	N-CA-C	-6.27	106.85	114.75
1	1	894	U	C2'-C3'-O3'	6.05	118.58	109.50
16	N	52	ILE	N-CA-C	-6.01	106.95	112.96
1	1	404	A	C2'-C3'-O3'	5.58	117.87	109.50
55	A	273	VAL	N-CA-C	-5.42	107.08	113.42

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	31368	360	0
2	2	32929	0	16585	177	0
3	3	2569	0	1301	11	0
4	4	184	0	95	2	0
5	5	1627	0	832	10	0
6	B	2082	0	2154	33	0
7	C	1565	0	1616	24	0
8	D	1552	0	1619	14	0
9	E	1410	0	1444	17	0
10	F	1313	0	1358	13	0
11	G	1111	0	1148	9	0
12	J	1129	0	1162	19	0
13	K	946	0	1023	9	0
14	L	1053	0	1129	19	0
15	M	1074	0	1157	12	0
16	N	951	0	994	11	0
17	O	892	0	923	10	0
18	P	917	0	962	6	0
19	Q	947	0	1019	15	0
20	R	816	0	839	15	0
21	S	857	0	922	12	0
22	T	746	0	811	7	0
23	U	788	0	844	10	0
24	V	753	0	780	6	0
25	W	582	0	599	9	0
26	X	625	0	652	5	0
27	Y	501	0	531	5	0
28	Z	448	0	488	5	0
29	a	522	0	520	5	0
30	b	444	0	458	5	0
31	c	426	0	464	5	0
32	d	377	0	418	4	0
33	e	504	0	572	17	0
34	f	302	0	340	7	0
35	g	1760	0	1787	14	0
36	h	1636	0	1710	20	0
37	i	1643	0	1707	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	j	1152	0	1196	17	0
39	k	848	0	846	10	0
40	l	1181	0	1238	16	0
41	m	979	0	1031	9	0
42	n	1022	0	1070	19	0
43	o	790	0	831	19	0
44	p	877	0	887	8	0
45	q	957	0	1017	12	0
46	r	900	0	965	16	0
47	s	805	0	844	11	0
48	t	714	0	734	6	0
49	u	649	0	666	8	0
50	v	648	0	691	5	0
51	w	544	0	560	4	0
52	x	663	0	688	14	0
53	y	669	0	719	8	0
54	z	589	0	629	6	0
55	A	2014	0	1981	38	0
56	1	289	0	0	0	0
56	2	126	0	0	0	0
56	3	8	0	0	0	0
56	5	4	0	0	0	0
56	C	2	0	0	0	0
56	D	1	0	0	0	0
56	N	1	0	0	0	0
56	Q	1	0	0	0	0
56	b	1	0	0	0	0
56	f	1	0	0	0	0
56	h	1	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	146756	0	98924	956	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 5.

The worst 5 of 956 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)
2:2:765:G:H1	2:2:812:G:HO2'	1.10	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:g:87:CYS:O	35:g:88:ASP:OD1	2.03	0.75
1:1:2512:C:H5"	1:1:2512:C:H6	1.49	0.75
12:J:29:ALA:O	12:J:108:MET:SD	2.49	0.71
1:1:885:C:H5"	1:1:885:C:H6	1.57	0.68

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	
6	B	269/271 (99%)	250 (93%)	19 (7%)	0	100	100
7	C	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
8	D	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
9	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	54
10	F	173/175 (99%)	160 (92%)	13 (8%)	0	100	100
11	G	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
12	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
13	K	121/123 (98%)	112 (93%)	9 (7%)	0	100	100
14	L	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
15	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
16	N	117/119 (98%)	111 (95%)	6 (5%)	0	100	100
17	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
18	P	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
19	Q	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
20	R	101/103 (98%)	88 (87%)	11 (11%)	2 (2%)	6	32
21	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
23	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
24	V	92/94 (98%)	84 (91%)	8 (9%)	0	100	100
25	W	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
26	X	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
27	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
28	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
29	a	64/66 (97%)	59 (92%)	5 (8%)	0	100	100
30	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
31	c	50/52 (96%)	50 (100%)	0	0	100	100
32	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
33	e	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
34	f	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
35	g	223/225 (99%)	204 (92%)	19 (8%)	0	100	100
36	h	206/208 (99%)	194 (94%)	12 (6%)	0	100	100
37	i	203/205 (99%)	196 (97%)	7 (3%)	0	100	100
38	j	154/156 (99%)	145 (94%)	9 (6%)	0	100	100
39	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
40	l	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
41	m	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
42	n	125/127 (98%)	115 (92%)	10 (8%)	0	100	100
43	o	97/99 (98%)	85 (88%)	12 (12%)	0	100	100
44	p	115/117 (98%)	105 (91%)	10 (9%)	0	100	100
45	q	120/123 (98%)	109 (91%)	11 (9%)	0	100	100
46	r	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
47	s	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
48	t	86/88 (98%)	82 (95%)	4 (5%)	0	100	100
49	u	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
50	v	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
51	w	64/66 (97%)	62 (97%)	2 (3%)	0	100	100
52	x	81/83 (98%)	77 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	y	84/86 (98%)	84 (100%)	0	0	100	100
54	z	68/70 (97%)	67 (98%)	1 (2%)	0	100	100
55	A	257/259 (99%)	235 (91%)	22 (9%)	0	100	100
All	All	5865/5966 (98%)	5512 (94%)	350 (6%)	3 (0%)	49	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	R	52	PRO
9	E	124	GLY
20	R	49	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	
6	B	216/216 (100%)	216 (100%)	0	100	100
7	C	164/164 (100%)	164 (100%)	0	100	100
8	D	165/165 (100%)	165 (100%)	0	100	100
9	E	148/148 (100%)	148 (100%)	0	100	100
10	F	136/136 (100%)	134 (98%)	2 (2%)	57	71
11	G	114/114 (100%)	114 (100%)	0	100	100
12	J	116/116 (100%)	116 (100%)	0	100	100
13	K	104/104 (100%)	104 (100%)	0	100	100
14	L	103/103 (100%)	103 (100%)	0	100	100
15	M	109/109 (100%)	109 (100%)	0	100	100
16	N	99/99 (100%)	99 (100%)	0	100	100
17	O	86/86 (100%)	86 (100%)	0	100	100
18	P	99/99 (100%)	98 (99%)	1 (1%)	68	75
19	Q	89/89 (100%)	88 (99%)	1 (1%)	65	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	R	84/84 (100%)	81 (96%)	3 (4%)	31	57
21	S	93/93 (100%)	93 (100%)	0	100	100
22	T	81/81 (100%)	81 (100%)	0	100	100
23	U	84/84 (100%)	84 (100%)	0	100	100
24	V	78/78 (100%)	77 (99%)	1 (1%)	61	72
25	W	58/58 (100%)	58 (100%)	0	100	100
26	X	67/67 (100%)	67 (100%)	0	100	100
27	Y	54/54 (100%)	54 (100%)	0	100	100
28	Z	48/48 (100%)	48 (100%)	0	100	100
29	a	59/59 (100%)	59 (100%)	0	100	100
30	b	47/47 (100%)	46 (98%)	1 (2%)	47	66
31	c	47/47 (100%)	47 (100%)	0	100	100
32	d	38/38 (100%)	38 (100%)	0	100	100
33	e	51/51 (100%)	50 (98%)	1 (2%)	48	67
34	f	34/34 (100%)	34 (100%)	0	100	100
35	g	187/187 (100%)	187 (100%)	0	100	100
36	h	171/171 (100%)	170 (99%)	1 (1%)	78	79
37	i	172/172 (100%)	172 (100%)	0	100	100
38	j	119/119 (100%)	119 (100%)	0	100	100
39	k	91/91 (100%)	91 (100%)	0	100	100
40	l	124/124 (100%)	124 (100%)	0	100	100
41	m	104/104 (100%)	103 (99%)	1 (1%)	68	75
42	n	105/105 (100%)	105 (100%)	0	100	100
43	o	86/86 (100%)	86 (100%)	0	100	100
44	p	90/90 (100%)	90 (100%)	0	100	100
45	q	102/102 (100%)	102 (100%)	0	100	100
46	r	94/94 (100%)	94 (100%)	0	100	100
47	s	83/83 (100%)	83 (100%)	0	100	100
48	t	76/76 (100%)	76 (100%)	0	100	100
49	u	65/65 (100%)	65 (100%)	0	100	100
50	v	74/74 (100%)	74 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	w	57/57 (100%)	57 (100%)	0	100	100
52	x	72/72 (100%)	72 (100%)	0	100	100
53	y	65/65 (100%)	65 (100%)	0	100	100
54	z	60/60 (100%)	60 (100%)	0	100	100
55	A	210/210 (100%)	204 (97%)	6 (3%)	37	60
All	All	4878/4878 (100%)	4860 (100%)	18 (0%)	81	81

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

Mol	Chain	Res	Type
55	A	217	ILE
55	A	337	LEU
55	A	255	VAL
30	b	9	THR
55	A	213	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 63 such sidechains are listed below:

Mol	Chain	Res	Type
37	i	116	GLN
54	z	56	HIS
39	k	3	HIS
53	y	78	ASN
55	A	266	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	572 (19%)	10 (0%)
2	2	1532/1534 (99%)	297 (19%)	4 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	8/9 (88%)	2 (25%)	0
5	5	75/76 (98%)	24 (32%)	1 (1%)
All	All	4636/4642 (99%)	915 (19%)	15 (0%)

5 of 915 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	12	U
1	1	23	G
1	1	34	U
1	1	35	G

5 of 15 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2193	G
2	2	1322	C
1	1	2286	G
5	5	17	U
2	2	516	PSU

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

39 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
45	0TD	q	89	45	8,9,10	2.66	1 (12%)	6,11,13	1.28	0
1	6MZ	1	1618	1	22,25,26	2.94	5 (22%)	29,36,39	4.38	11 (37%)
2	G7M	2	527	2	23,26,27	3.53	10 (43%)	34,39,42	1.72	8 (23%)
1	PSU	1	2504	1	18,21,22	1.22	2 (11%)	21,30,33	2.02	4 (19%)
1	1MG	1	745	1	23,26,27	2.75	7 (30%)	33,39,42	2.20	12 (36%)
1	3TD	1	1915	1	19,22,23	4.31	5 (26%)	23,32,35	1.91	3 (13%)
1	5MU	1	1939	56,1	19,22,23	4.65	7 (36%)	27,32,35	3.88	9 (33%)
1	OMU	1	2552	1	19,22,23	2.81	7 (36%)	25,31,34	1.90	5 (20%)
2	UR3	2	1498	2	19,22,23	2.50	6 (31%)	26,32,35	1.58	4 (15%)
1	2MA	1	2503	56,1	22,25,26	3.69	8 (36%)	32,37,40	2.30	7 (21%)
2	2MG	2	966	2	23,26,27	2.83	7 (30%)	33,38,41	2.62	10 (30%)
1	5MU	1	747	1	19,22,23	4.68	7 (36%)	27,32,35	3.87	10 (37%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	1	2605	1	18,21,22	1.20	2 (11%)	21,30,33	1.91	6 (28%)
2	2MG	2	1516	2	23,26,27	2.92	9 (39%)	33,38,41	2.44	13 (39%)
1	6MZ	1	2030	1	22,25,26	2.98	6 (27%)	29,36,39	4.72	14 (48%)
5	H2U	5	20	5	18,21,22	3.38	5 (27%)	19,30,33	1.55	4 (21%)
1	2MG	1	1835	1	23,26,27	2.83	8 (34%)	33,38,41	2.68	13 (39%)
1	PSU	1	1917	1	18,21,22	1.08	1 (5%)	21,30,33	1.92	4 (19%)
1	OMC	1	2498	56,1	19,22,23	2.69	7 (36%)	25,31,34	1.04	2 (8%)
1	PSU	1	1911	1	18,21,22	1.14	2 (11%)	21,30,33	1.91	4 (19%)
1	5MC	1	1962	1	19,22,23	3.70	8 (42%)	26,32,35	1.30	5 (19%)
2	PSU	2	516	2	18,21,22	1.49	4 (22%)	21,30,33	2.24	8 (38%)
2	MA6	2	1519	2	23,26,27	1.57	5 (21%)	33,38,41	2.73	12 (36%)
2	4OC	2	1402	2	20,23,24	2.89	8 (40%)	25,32,35	1.06	2 (8%)
1	2MG	1	2445	1	23,26,27	2.83	9 (39%)	33,38,41	2.63	13 (39%)
1	PSU	1	955	56,1	18,21,22	1.10	2 (11%)	21,30,33	1.84	4 (19%)
2	2MG	2	1207	2	23,26,27	2.99	8 (34%)	33,38,41	2.21	11 (33%)
5	4OC	5	32	5	20,23,24	2.99	8 (40%)	25,32,35	0.90	0
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.15	6 (28%)
2	5MC	2	967	2	19,22,23	3.86	8 (42%)	26,32,35	1.01	2 (7%)
2	MA6	2	1518	2	23,26,27	1.60	4 (17%)	33,38,41	2.73	13 (39%)
1	PSU	1	746	56,1	18,21,22	1.10	2 (11%)	21,30,33	1.80	5 (23%)
5	5MU	5	54	5	19,22,23	4.83	7 (36%)	27,32,35	3.89	9 (33%)
1	PSU	1	2580	1	18,21,22	1.12	3 (16%)	21,30,33	1.96	4 (19%)
5	4SU	5	8	5	18,21,22	3.82	8 (44%)	25,30,33	2.37	8 (32%)
1	OMG	1	2251	5,1	23,26,27	2.41	9 (39%)	32,38,41	1.86	8 (25%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.17	3 (11%)
1	G7M	1	2069	1	23,26,27	2.57	8 (34%)	34,39,42	2.42	12 (35%)
5	PSU	5	55	5	18,21,22	1.02	1 (5%)	21,30,33	1.75	3 (14%)

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
45	0TD	q	89	45	-	3/7/12/14	-
1	6MZ	1	1618	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2
1	5MU	1	1939	56,1	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
1	2MA	1	2503	56,1	-	2/7/25/26	0/3/3/3
2	2MG	2	966	2	-	2/9/27/28	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
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	6MZ	1	2030	1	-	2/9/27/28	0/3/3/3
5	H2U	5	20	5	-	4/7/38/39	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	56,1	-	0/9/27/28	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	3/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
1	PSU	1	955	56,1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
5	4OC	5	32	5	-	0/9/29/30	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	3/11/29/30	0/3/3/3
1	PSU	1	746	56,1	-	2/7/25/26	0/2/2/2
5	5MU	5	54	5	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
5	4SU	5	8	5	-	4/7/25/26	0/2/2/2
1	OMG	1	2251	5,1	-	1/9/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
5	PSU	5	55	5	-	2/7/25/26	0/2/2/2

The worst 5 of 225 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.49	1.50	1.35
1	1	1618	6MZ	C6-N6	11.80	1.47	1.34
1	1	2503	2MA	C4-N3	11.31	1.48	1.34
1	1	2030	6MZ	C6-N6	11.30	1.47	1.34
5	5	54	5MU	C2-N1	11.24	1.56	1.38

The worst 5 of 271 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2030	6MZ	C4-N9-C8	15.46	121.97	105.74
1	1	1618	6MZ	C4-N9-C8	13.31	119.71	105.74
5	5	54	5MU	C5-C4-N3	13.09	126.70	115.32
1	1	747	5MU	C5-C4-N3	12.37	126.07	115.32
1	1	1939	5MU	C5-C4-N3	12.35	126.06	115.32

There are no chirality outliers.

5 of 52 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
2	2	516	PSU	O4'-C1'-C5-C4

There are no ring outliers.

8 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	q	89	0TD	2	0
1	1	2504	PSU	1	0
1	1	1939	5MU	1	0
2	2	1498	UR3	1	0
1	1	2030	6MZ	1	0
2	2	1518	MA6	1	0
1	1	746	PSU	1	0
1	1	2251	OMG	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 438 ligands modelled in this entry, 438 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.

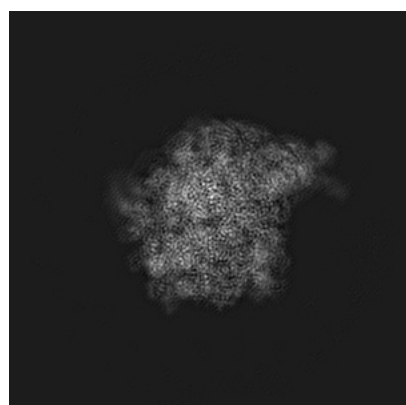
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20187. These allow visual inspection of the internal detail of the map and identification of artifacts.

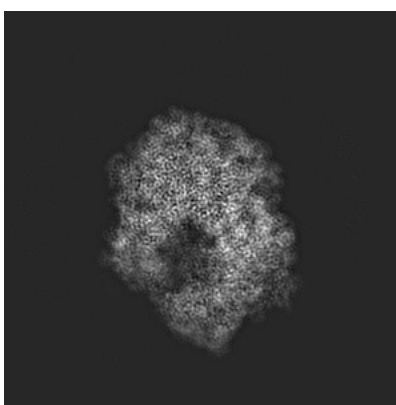
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

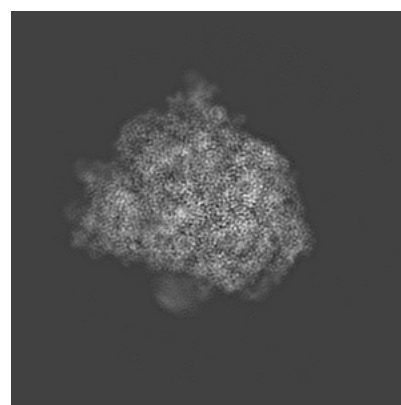
6.1.1 Primary map



X



Y



Z

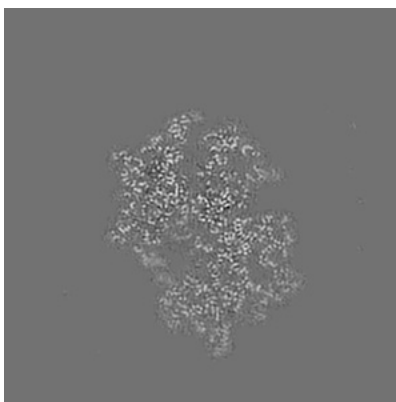
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

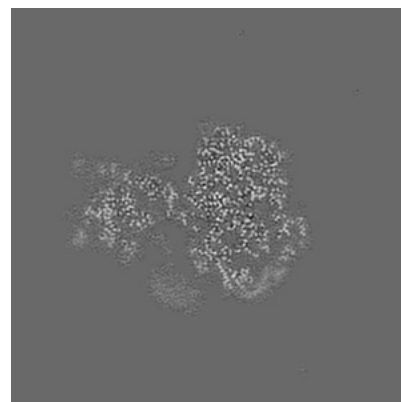
6.2.1 Primary map



X Index: 128



Y Index: 128

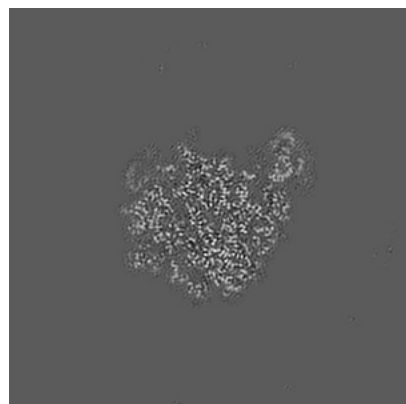


Z Index: 128

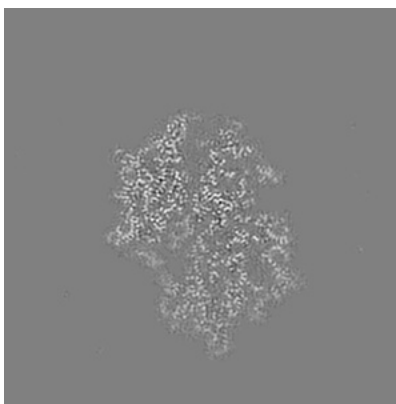
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

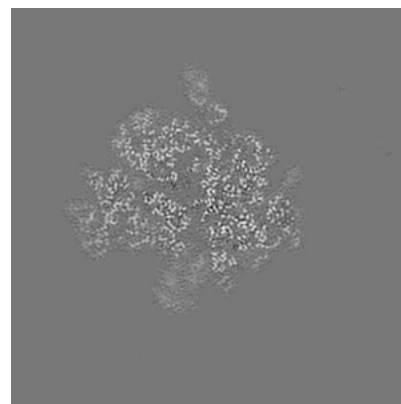
6.3.1 Primary map



X Index: 138



Y Index: 126

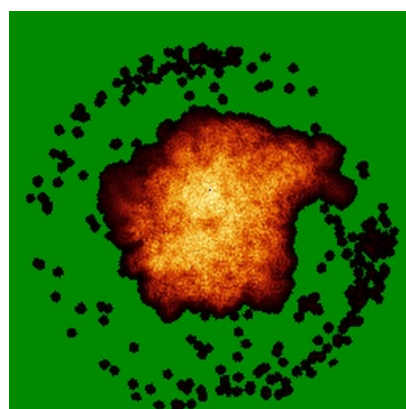


Z Index: 143

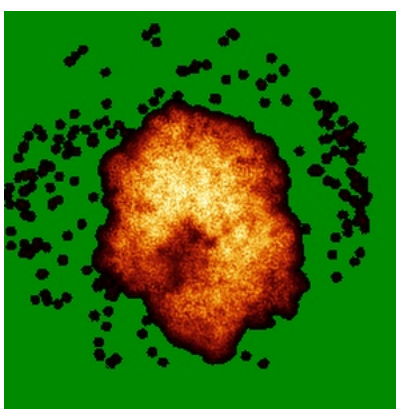
The images above show the largest variance slices of the map in three orthogonal directions.

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

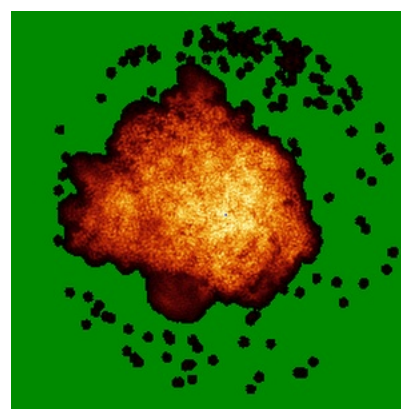
6.4.1 Primary map



X



Y

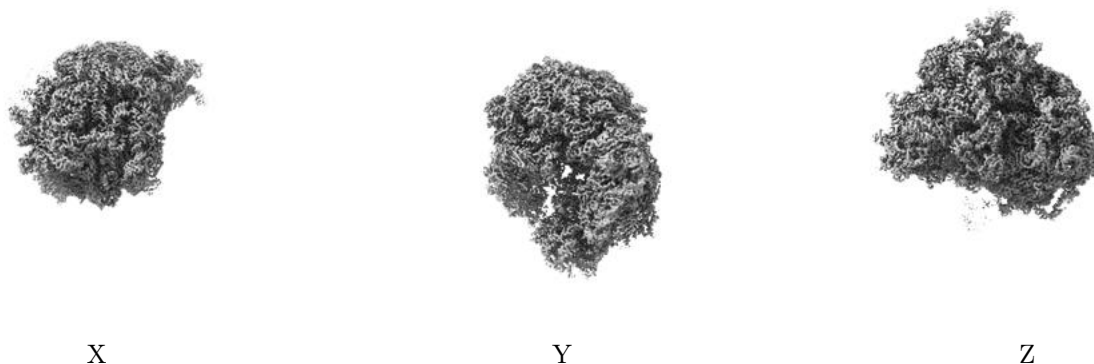


Z

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

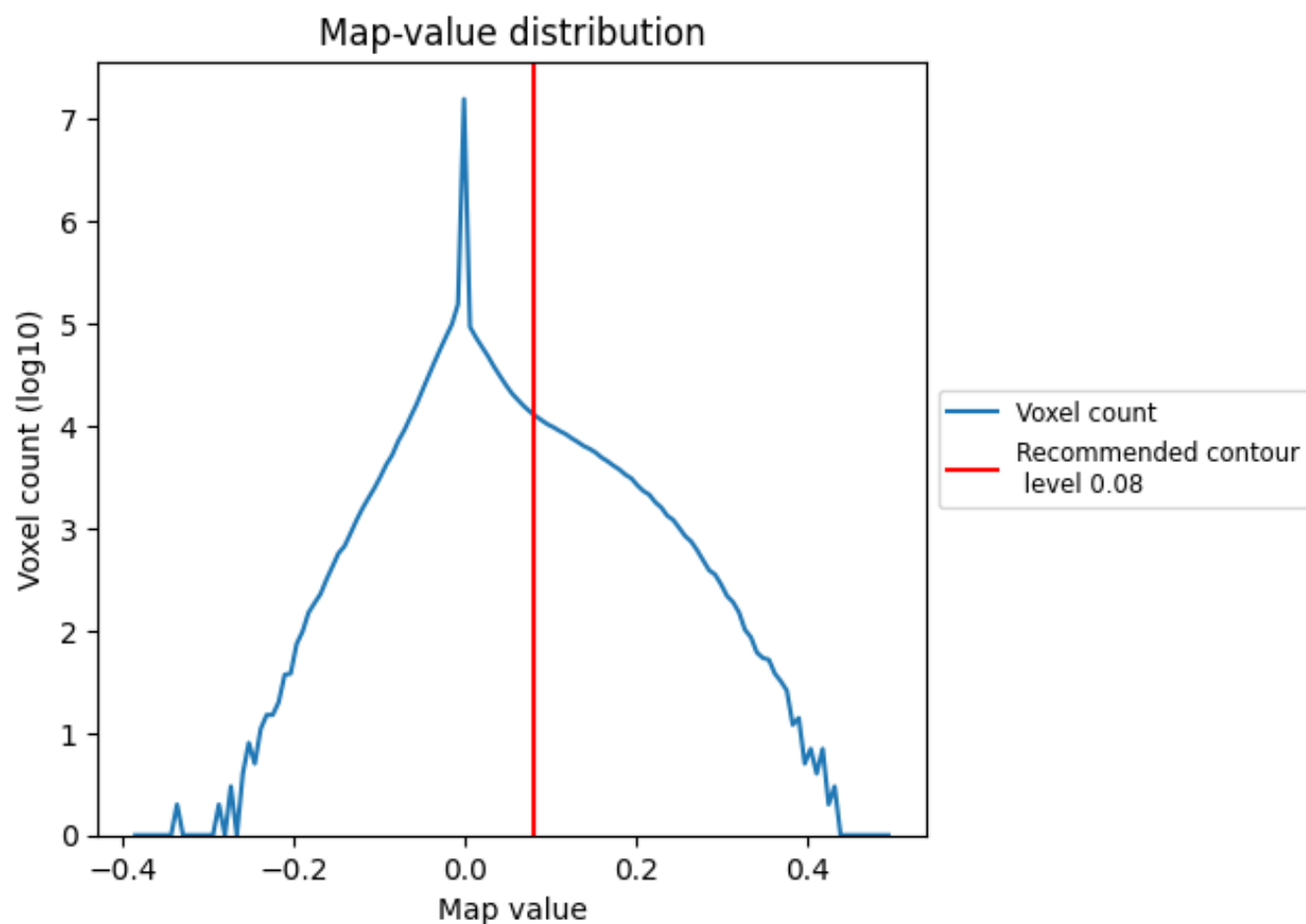
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

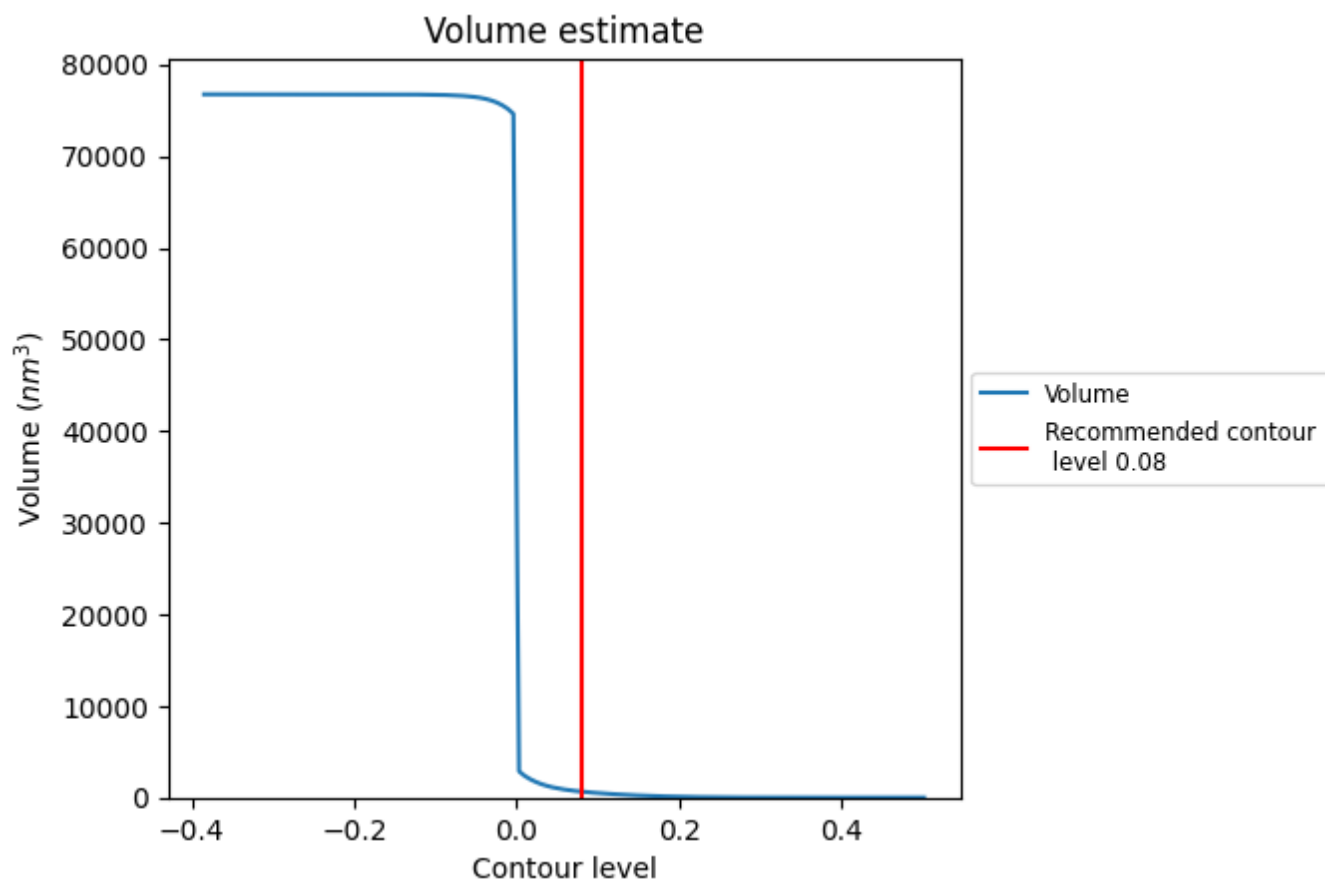
This section contains the results of statistical analysis of the map.

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.

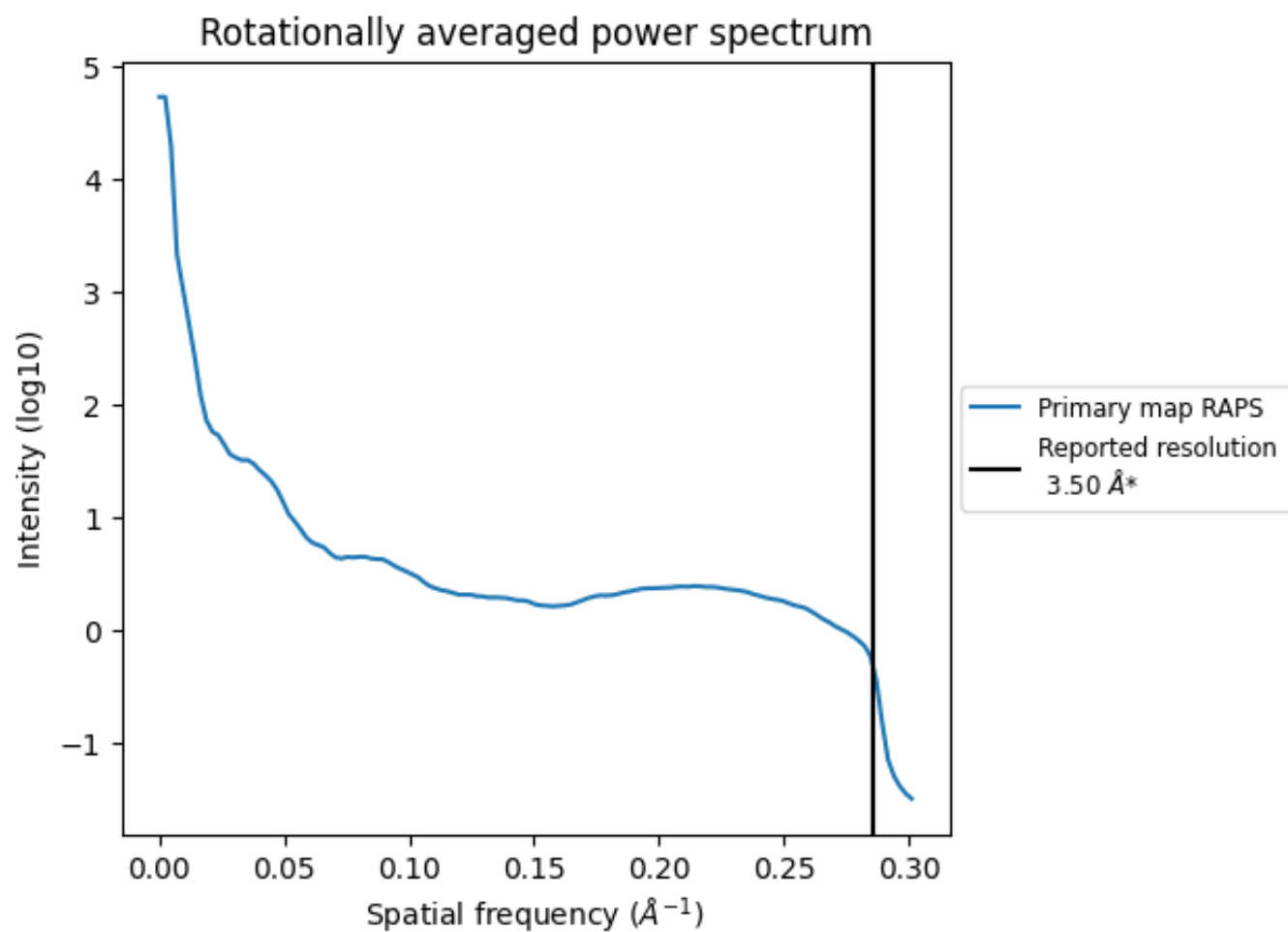
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 648 nm³; this corresponds to an approximate mass of 585 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 0.286 Å⁻¹

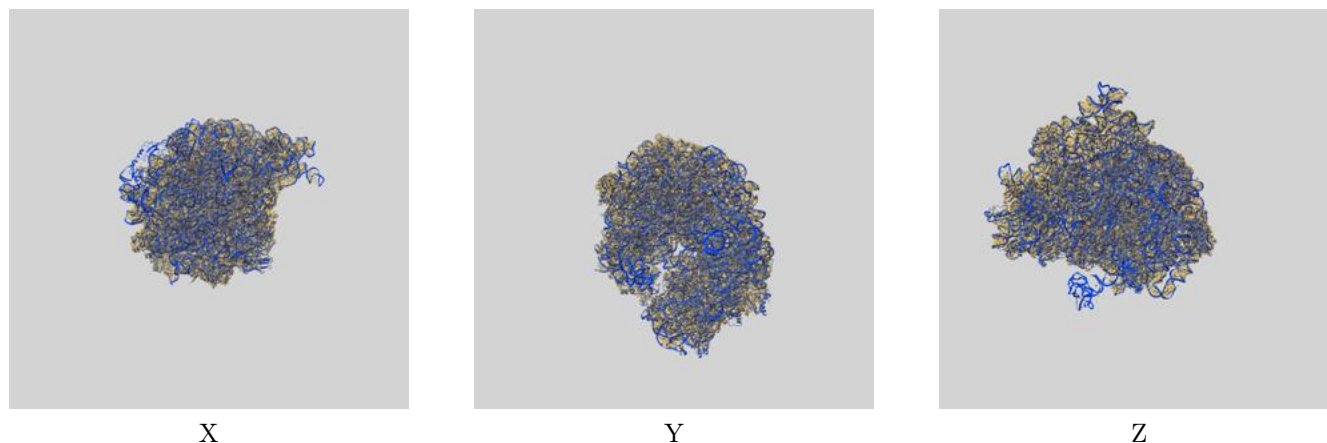
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

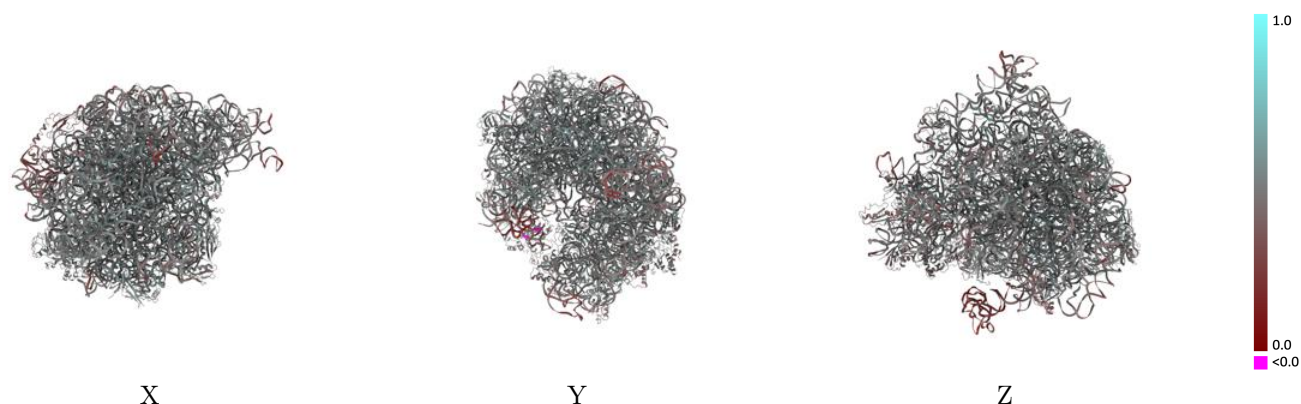
This section contains information regarding the fit between EMDB map EMD-20187 and PDB model 6OSQ. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



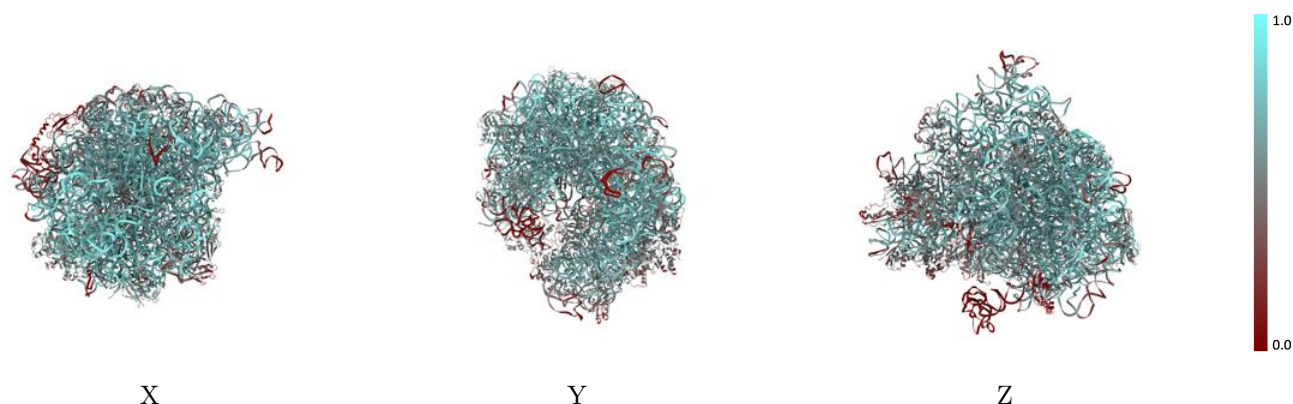
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



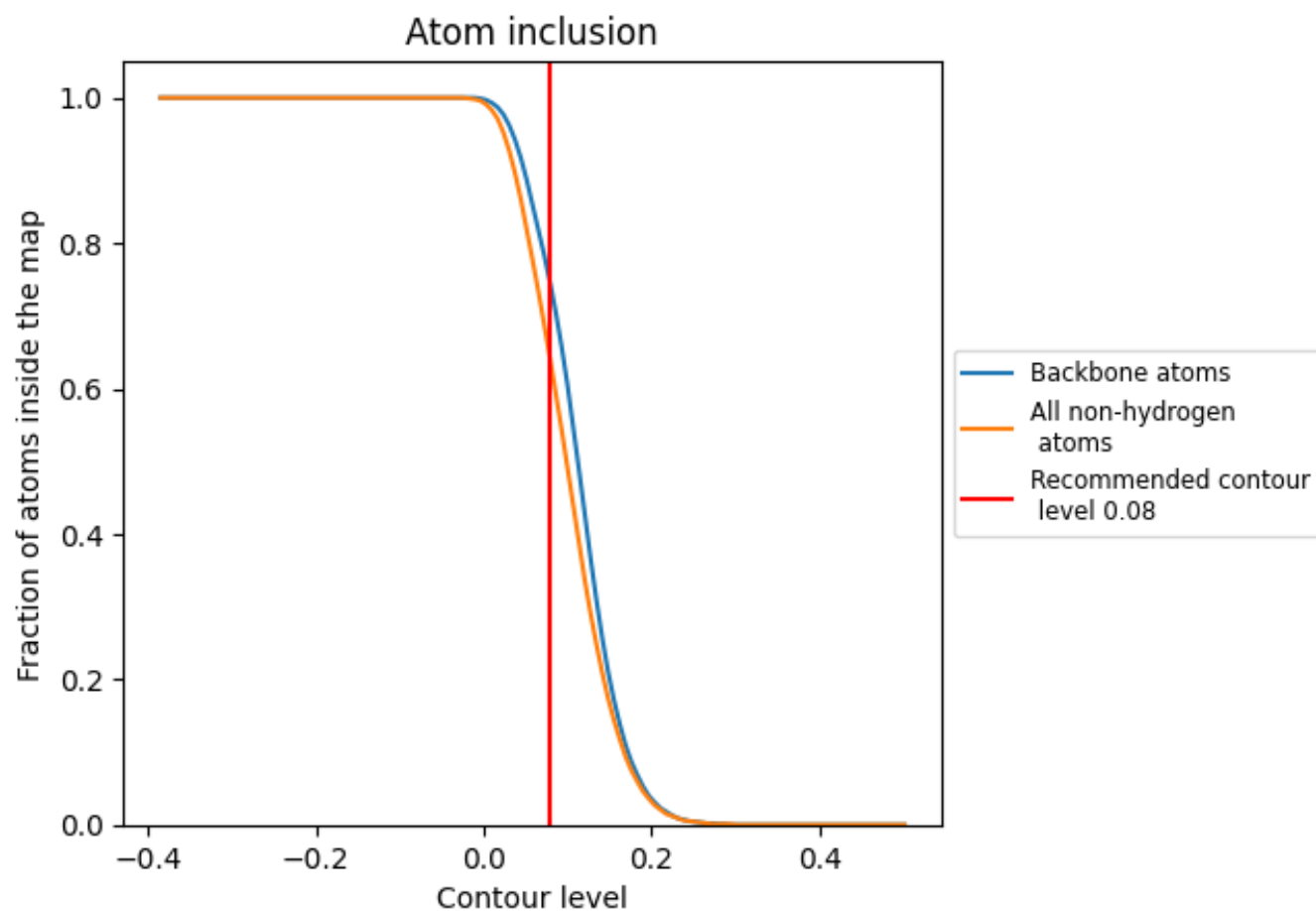
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 64% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6370	 0.4740
1	 0.7000	 0.4710
2	 0.6960	 0.4700
3	 0.6830	 0.4630
4	 0.6470	 0.4760
5	 0.4570	 0.4500
A	 0.4540	 0.4710
B	 0.6250	 0.5240
C	 0.6010	 0.5100
D	 0.5660	 0.4940
E	 0.4350	 0.4510
F	 0.3970	 0.4630
G	 0.0780	 0.3710
J	 0.5980	 0.5090
K	 0.5770	 0.5080
L	 0.5970	 0.4960
M	 0.5780	 0.5040
N	 0.6610	 0.5110
O	 0.5420	 0.4760
P	 0.5830	 0.5070
Q	 0.6570	 0.5140
R	 0.5850	 0.5080
S	 0.6080	 0.5070
T	 0.5470	 0.5020
U	 0.5190	 0.4820
V	 0.5150	 0.4890
W	 0.6030	 0.5150
X	 0.5740	 0.5030
Y	 0.4990	 0.4780
Z	 0.5920	 0.4970
a	 0.1680	 0.3940
b	 0.6250	 0.5060
c	 0.5240	 0.5000
d	 0.6510	 0.5150
e	 0.6700	 0.5320



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Chain	Atom inclusion	Q-score
f	 0.5990	 0.5110
g	 0.3920	 0.4390
h	 0.5180	 0.4870
i	 0.4760	 0.4660
j	 0.5400	 0.4820
k	 0.4530	 0.4670
l	 0.3970	 0.4370
m	 0.5460	 0.4820
n	 0.4670	 0.4550
o	 0.4010	 0.4420
p	 0.5240	 0.4760
q	 0.5590	 0.5060
r	 0.4470	 0.4560
s	 0.5220	 0.4810
t	 0.5200	 0.4810
u	 0.5630	 0.4900
v	 0.4680	 0.4760
w	 0.4780	 0.4800
x	 0.4530	 0.4650
y	 0.5340	 0.4870
z	 0.3260	 0.4350