



wwPDB EM Validation Summary Report ⓘ

Jun 19, 2026 – 04:19 am BST

PDB ID : 8RCM / pdb_00008rcm
EMDB ID : EMD-19055
Title : Escherichia coli paused disome complex (Non-rotated disome interface class 2)
Authors : Fluegel, T.; Schacherl, M.
Deposited on : 2023-12-06
Resolution : 3.59 Å(reported)
Based on initial model : 7N1P

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:

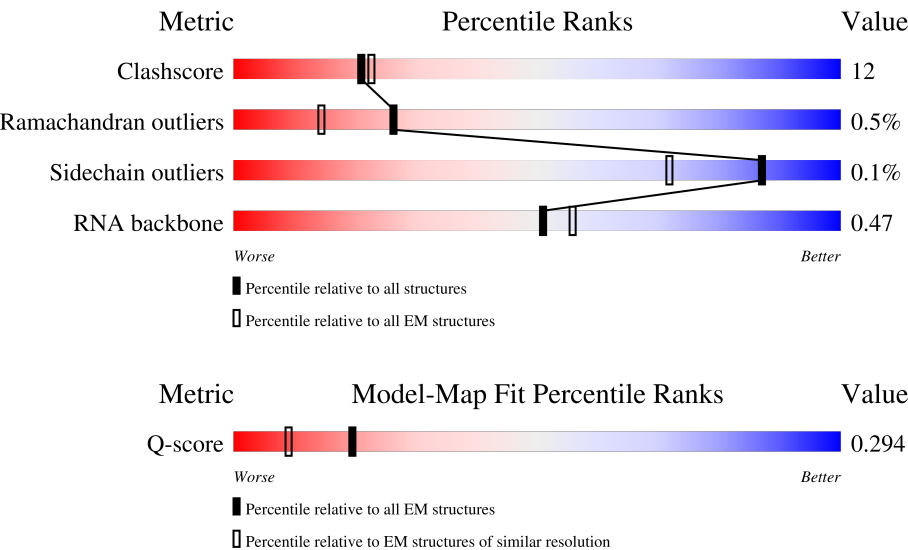
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 i

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

The reported resolution of this entry is 3.59 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	12565 (3.09 - 4.09)

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	12	78	
2	32	59	
3	4	70	

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Mol	Chain	Length	Quality of chain
4	62	65	
5	71	2904	
5	72	2904	
6	82	120	
7	A1	1542	
7	A2	1542	
8	B	241	
8	B2	241	
9	C1	233	
9	C2	233	
10	D1	206	
10	D2	206	
11	E1	167	
11	E2	167	
12	F1	135	
12	F2	135	
13	G1	179	
13	G2	179	
14	H1	130	
14	H2	130	
15	I1	130	
15	I2	130	
16	J1	103	
16	J2	103	
17	K1	129	

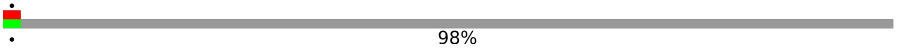
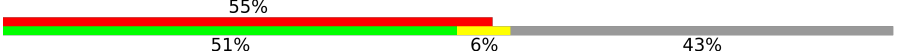
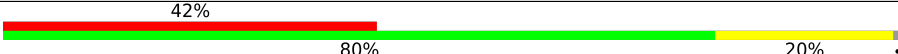
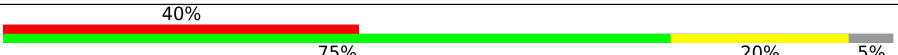
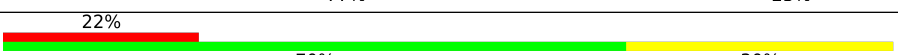
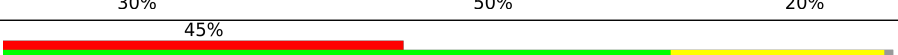
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Mol	Chain	Length	Quality of chain
17	K2	129	
18	L1	124	
18	L2	124	
19	M1	118	
19	M2	118	
20	N1	101	
20	N2	101	
21	O1	89	
21	O2	89	
22	P1	82	
23	Q1	84	
23	Q2	84	
24	R1	75	
24	R2	75	
25	S1	92	
25	S2	92	
26	T1	87	
27	U1	71	
27	U2	71	
28	V2	64	
29	W	76	
30	W1	76	
31	X2	77	
32	Y1	76	
33	Y2	76	

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Mol	Chain	Length	Quality of chain
34	Z1	557	
35	a2	234	
36	b2	273	
37	e2	179	
38	g2	55	
39	h2	136	
40	i2	149	
41	l2	46	
42	o2	144	
43	p	10	
44	r2	117	
45	z2	85	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
49	ALA	Y2	102	-	-	X	-

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 188215 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 protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	12	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 2 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	32	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	67	Total	C	N	O	S	0	0
			529	328	100	95	6		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	62	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	71	19	Total	C	N	O	P	0	0
			406	182	73	132	19		
5	72	2904	Total	C	N	O	P	0	0
			62355	27824	11468	20159	2904		

- Molecule 6 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	82	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 7 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A1	1542	Total	C	N	O	P	0	0
			33092	14767	6064	10719	1542		
7	A2	1537	Total	C	N	O	P	0	0
			32990	14721	6049	10683	1537		

- Molecule 8 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	233	Total	C	N	O	S	0	0
			1815	1145	325	337	8		
8	B2	227	Total	C	N	O	S	0	0
			1776	1123	318	327	8		

- Molecule 9 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C1	213	Total	C	N	O	S	0	0
			1665	1054	312	295	4		
9	C2	212	Total	C	N	O	S	0	0
			1658	1049	311	294	4		

- Molecule 10 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D1	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		
10	D2	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E1	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		
11	E2	158	Total	C	N	O	S	0	0
			1166	725	220	215	6		

- Molecule 12 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F1	106	Total	C	N	O	S	0	0
			862	545	156	154	7		
12	F2	106	Total	C	N	O	S	0	0
			862	545	156	154	7		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G1	155	Total	C	N	O	S	0	0
			1228	767	237	220	4		
13	G2	154	Total	C	N	O	S	0	0
			1214	756	235	219	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H1	129	Total	C	N	O	S	0	0
			979	616	173	184	6		
14	H2	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 15 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I1	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		
15	I2	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 16 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J1	102	Total	C	N	O	S	0	0
			817	509	157	150	1		
16	J2	100	Total	C	N	O	S	0	0
			803	502	154	146	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K1	115	Total	C	N	O	S	0	0
			857	528	168	158	3		
17	K2	118	Total	C	N	O	S	0	0
			884	545	175	161	3		

- Molecule 18 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L1	123	Total	C	N	O	S	0	0
			955	590	196	165	4		
18	L2	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M1	115	Total	C	N	O	S	0	0
			891	552	179	157	3		
19	M2	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N1	100	Total	C	N	O	S	0	0
			805	499	164	139	3		
20	N2	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 21 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O1	88	Total	C	N	O	S	0	0
			714	439	144	130	1		
21	O2	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 22 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P1	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q1	80	Total	C	N	O	S	0	0
			648	411	121	113	3		
23	Q2	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 24 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R1	68	Total	C	N	O	S	0	0
			566	357	110	98	1		
24	R2	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S1	83	Total	C	N	O	S	0	0
			663	424	126	111	2		
25	S2	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T1	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 27 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U1	70	Total	C	N	O	S	0	0
			590	366	125	98	1		
27	U2	70	Total	C	N	O	S	0	0
			584	363	122	98	1		

- Molecule 28 is a RNA chain called messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V2	58	Total	C	N	O	P	0	0
			1250	559	237	396	58		

- Molecule 29 is a RNA chain called tRNA-Trp (P-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
29	W	76	Total	C	N	O	P	S	0	0
			1630	730	286	536	76	2		

- Molecule 30 is a RNA chain called tRNA-Phe (P-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
30	W1	36	Total	C	N	O	P	S	0	0
			781	352	143	248	36	2		

- Molecule 31 is a RNA chain called tRNA-Arg (E-site).

Mol	Chain	Residues	Atoms						AltConf	Trace
31	X2	77	Total	C	N	O	P	S	0	0
			1654	740	297	538	77	2		

- Molecule 32 is a RNA chain called tRNA-Val (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Y1	36	Total	C	N	O	P	0	0
			778	348	142	252	36		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y1	34	CM0	U	variant	GB 1847302804

- Molecule 33 is a RNA chain called tRNA-Ala (A-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y2	76	Total	C	N	O	P	0	0
			1628	726	293	533	76		

- Molecule 34 is a protein called 30S ribosomal protein S1.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	Z1	9	Total	C	N	O	0	0
			75	49	10	16		

- Molecule 35 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a2	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 36 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b2	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 37 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e2	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 38 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	g2	52	Total	C	N	O	0	0
			427	275	78	74		

- Molecule 39 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h2	136	Total	C	N	O	S	1	0
			1085	692	209	178	6		

- Molecule 40 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i2	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 41 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 42 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o2	51	Total	C	N	O	S	0	0
			377	231	83	62	1		

- Molecule 43 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	p	10	Total	C	N	O	0	0
			76	47	18	11		

- Molecule 44 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
44	r2	116	Total	C	N	O	0	0
			891	552	178	161		

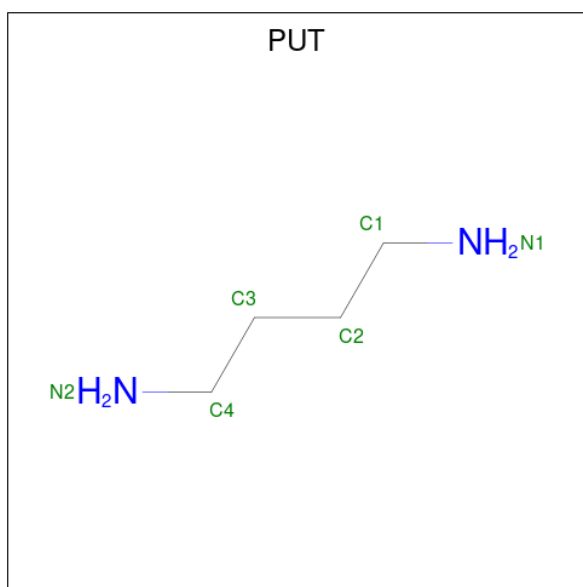
- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	z2	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 46 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
46	4	1	Total	Zn	0
			1	1	
46	B	1	Total	Zn	0
			1	1	

- Molecule 47 is 1,4-DIAMINO BUTANE (CCD ID: PUT) (formula: C₄H₁₂N₂).

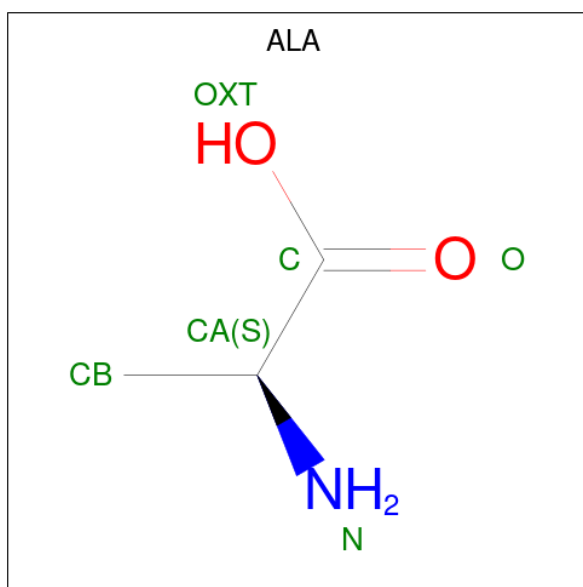


Mol	Chain	Residues	Atoms			AltConf
47	72	1	Total	C	N	0
			6	4	2	
47	72	1	Total	C	N	0
			6	4	2	

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	72	191	Total	Mg	0
			191	191	
48	82	1	Total	Mg	0
			1	1	
48	A1	59	Total	Mg	0
			59	59	
48	A2	42	Total	Mg	0
			42	42	
48	V2	1	Total	Mg	0
			1	1	
48	W	1	Total	Mg	0
			1	1	
48	Y2	1	Total	Mg	0
			1	1	

- Molecule 49 is ALANINE (CCD ID: ALA) (formula: C₃H₇NO₂).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
49	Y2	1	5	3	1	1	0

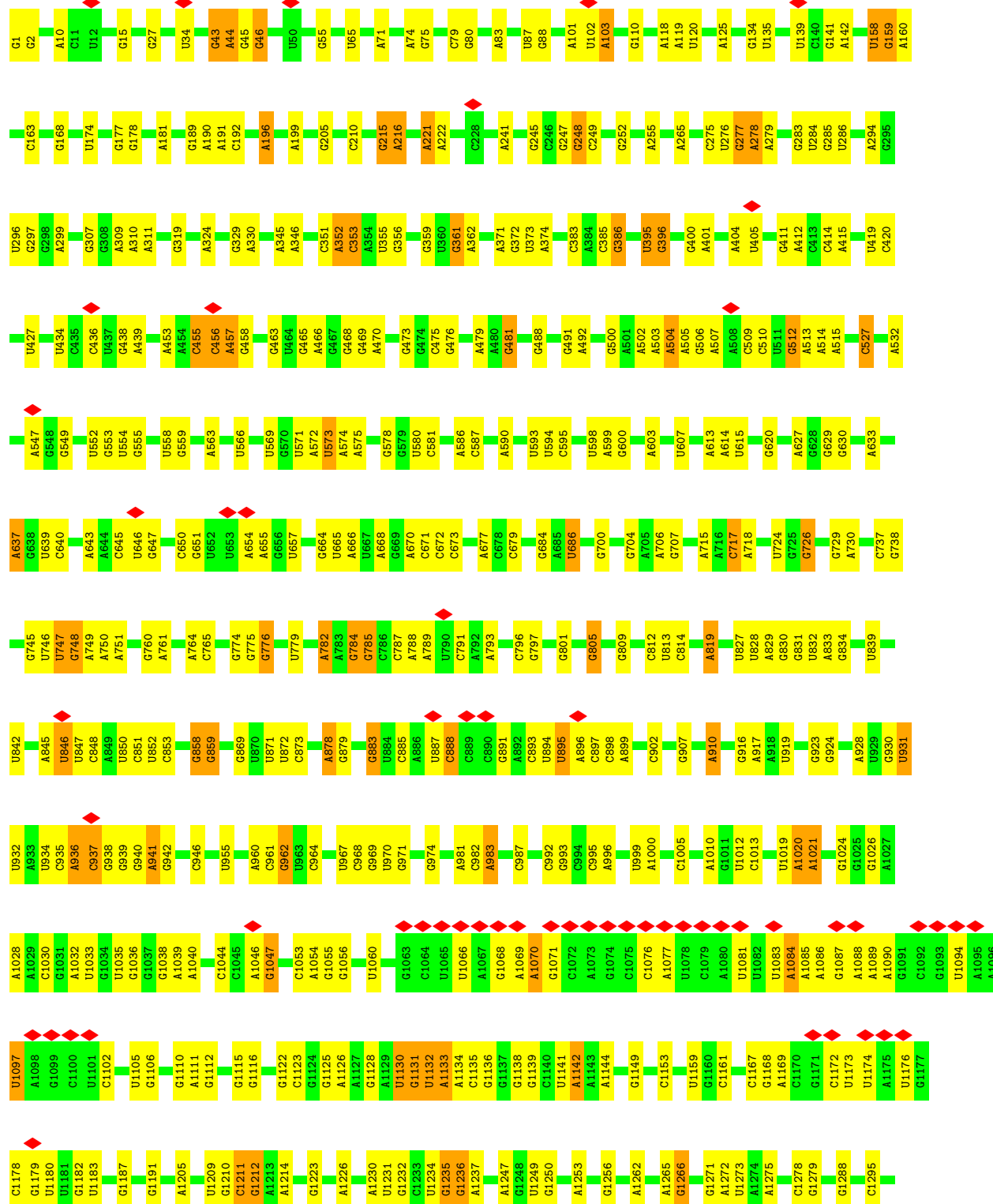




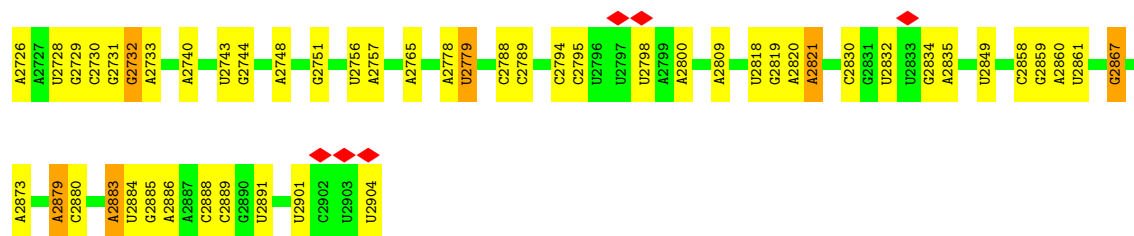
A
C
C
G
U
U
G
A
G
G
C
C
U
U
U
A
A
U
U
C
C
U
U

● Molecule 5: 23S ribosomal RNA

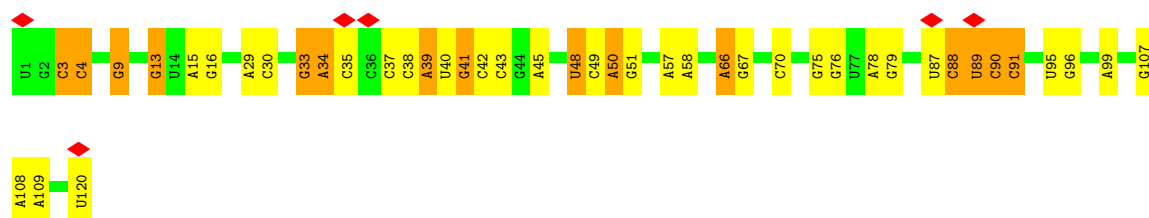
Chain 72:  65% 30% 5%



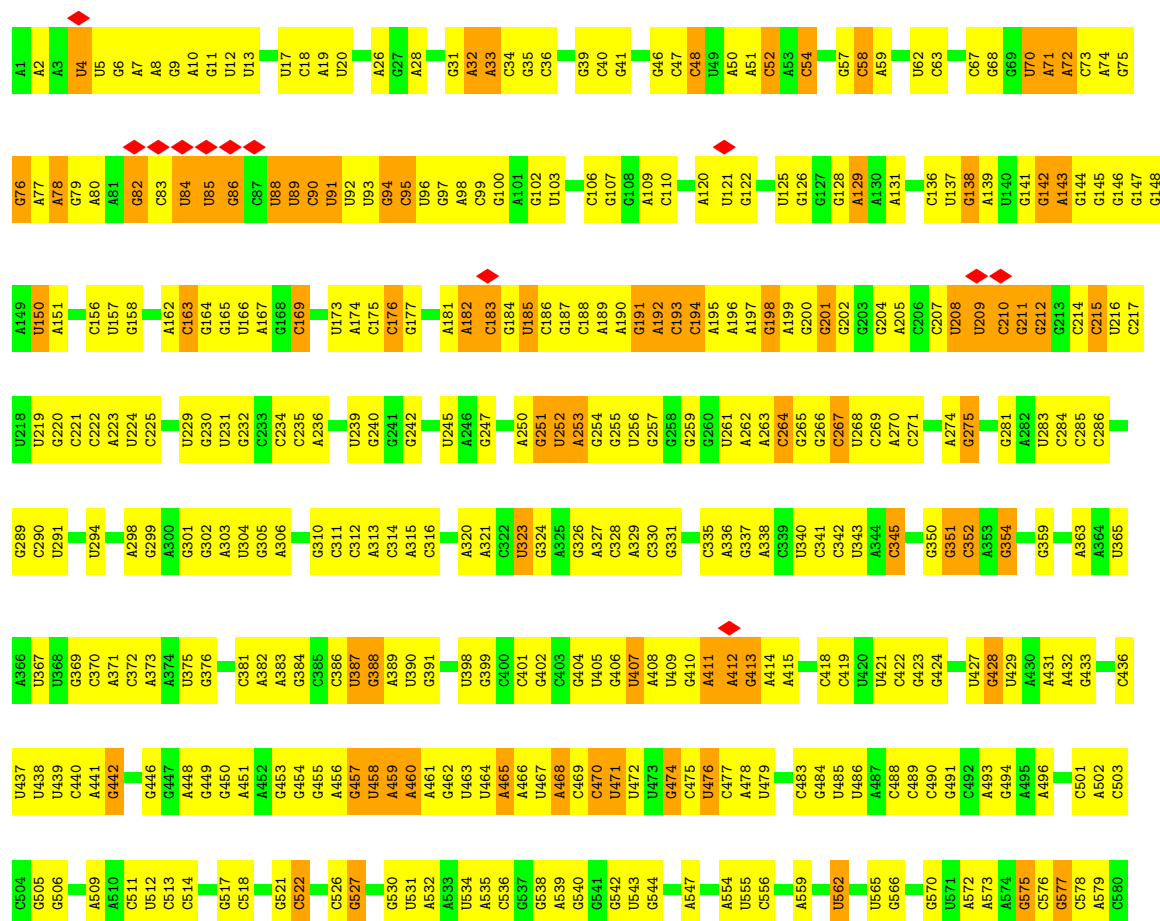
G1299	G1432	U1539	G1682	A1801	A1928	G2032	G2127	A2199	G2391	C2498	G2585
G1300	A1433	G1540	U1688	G1807	G1929	A2033	G2128	G2200	U2402	G2499	U2586
A1301	A1434	C1541	U1700	A1808	G1930	U2034	C2129	G2201	C2403	U2501	C2586
G1309	C1447	G1542	A1700	A1809	G1935	G2039	U2130	G2204	U2404	G2502	A2590
C1315	G1448	G1543	A1544	C1816	A1936	G2040	U2132	C2208	G2405	A2503	C2591
U1318	G1452	U1566	U1709	G1817	A1937	C2043	G2133	C2208	A2311	U2504	G2592
C1319	A1453	A1569	G1710	A1818	A1938	C2043	A2134	A2211	U2312	U2506	U2593
G1320	U1460	A1570	U1714	A1819	U1939	G2056	G2135	U2212	G2410	U2506	C2594
A1321	C1461	A1571	G1715	A1820	U1940	C2056	G2136	U2213	A2411	C2507	G2595
U1326	U1469	U1578	U1720	U1825	U1943	A2059	U2139	A2225	U2423	C2512	A2598
A1327	A1470	A1579	G1721	G1826	A1952	A2060	G2140	A2225	C2424	A2513	G2599
A1328	U1476	A1580	A1722	U1827	G1953	G2061	G2141	G2230	A2425	U2514	A2600
U1329	G1476	G1581	A1723	A2062	G1954	A2062	A2142	U2231	A2426	C2515	C2601
C1330	U1477	C1582	G1724	G1835	U1955	C2063	G2143	G2232	C2427	G2518	U2603
G1343	U1478	A1583	G1724	U1836	U1956	G2069	G2144	U2233	G2428	U2519	U2604
U1344	G1478	U1584	C1727	C1837	A1960	A2070	C2145	U2234	G2429	U2605	U2605
C1345	G1482	C1585	U1729	A1847	C1961	A2071	G2146	G2238	A2430	U2522	C2606
U1352	U1486	G1586	C1730	A1848	U1962	C2072	G2147	U2239	U2441	G2526	G2608
C1357	U1487	A1594	G1731	U1852	G1963	U2079	U2149	U2240	G2445	G2529	C2610
G1358	C1488	C1595	G1738	U1859	U1966	G2087	G2150	U2242	G2446	G2535	U2613
C1363	C1489	C1596	U1744	G1860	C1967	A2088	U2151	U2243	C2447	G2536	A2614
G1364	A1490	A1597	A1745	U1864	U1967	U2092	G2152	G2246	A2448	U2537	U2615
A1365	G1492	A1598	G1753	U1870	G1964	G2093	C2153	A2247	A2450	C2540	U2629
G1368	G1494	A1603	A1754	A1871	U1970	G2093	A2154	C2248	A2451	A2541	G2630
U1378	U1497	C1604	A1755	G1872	G1972	U2098	A2158	G2251	U2457	A2542	G2645
U1379	C1496	A1608	G1756	G1873	G1975	U2099	C2159	C2258	A2461	U2547	C2646
G1380	A1503	A1609	A1759	U1880	U1982	A2101	G2160	C2258	G2464	U2548	U2647
A1383	A1504	A1610	C1764	C1881	U1991	G2102	C2161	U2262	U2469	U2552	G2655
C1386	A1505	A1611	A1773	A1889	U1993	C2103	A2162	C2263	C2470	G2553	A2660
A1392	A1508	G1631	U1779	A1890	G1992	C2104	G2163	C2264	U2474	U2555	C2661
A1393	A1509	A1632	U1782	A1901	U1997	U2106	C2164	C2264	G2475	C2556	G2662
U1394	G1513	G1633	A1783	G1906	C1998	G2107	C2165	A2267	A2476	G2557	G2663
A1395	G1514	A1634	A1784	G1907	C2000	A2109	U2166	G2271	U2477	C2558	G2664
U1396	A1515	A1640	A1785	C1908	G2010	G2110	U2167	U2272	A2478	C2559	A2675
U1405	U1523	G1645	A1786	C1909	A2014	U2111	A2170	U2273	G2481	A2560	U2687
U1406	G1524	U1647	A1786	G1910	A2015	G2112	C2174	G2277	A2482	A2566	G2688
G1416	A1528	U1648	A1789	A1913	A2016	A2114	C2175	G2278	C2483	G2567	U2689
G1417	C1531	G1649	C1790	C1914	U2017	G2116	A2176	G2279	G2484	C2571	U2690
G1418	A1532	A1664	A1791	3TD1915	U2017	A2117	C2179	C2283	G2485	G2375	U2698
A1419	C1533	A1674	A1795	C1920	C2022	U2118	U2180	A2284	C2486	G2379	C2699
A1420	U1534	A1677	U1796	C1923	C2023	U2119	U2181	A2285	U2489	C2380	G2714
A1427	A1535	A1678	G1797	U1923	C2024	G2120	U2182	G2286	G2490	A2381	C2575
C1428	C1536	U1799	C1800	C1924	C2025	U2122	A2183	A2287	U2491	G2382	G2576
G1537	G1538			A1927	A2031	G2125	U2185	U2291	U2492	G2383	U2580
						A2031	U2187	G2292	U2493	U2384	C2581
							A2188	G2293	U2494	U2385	G2582
							A2189				
							A2198				



• Molecule 6: 5S ribosomal RNA



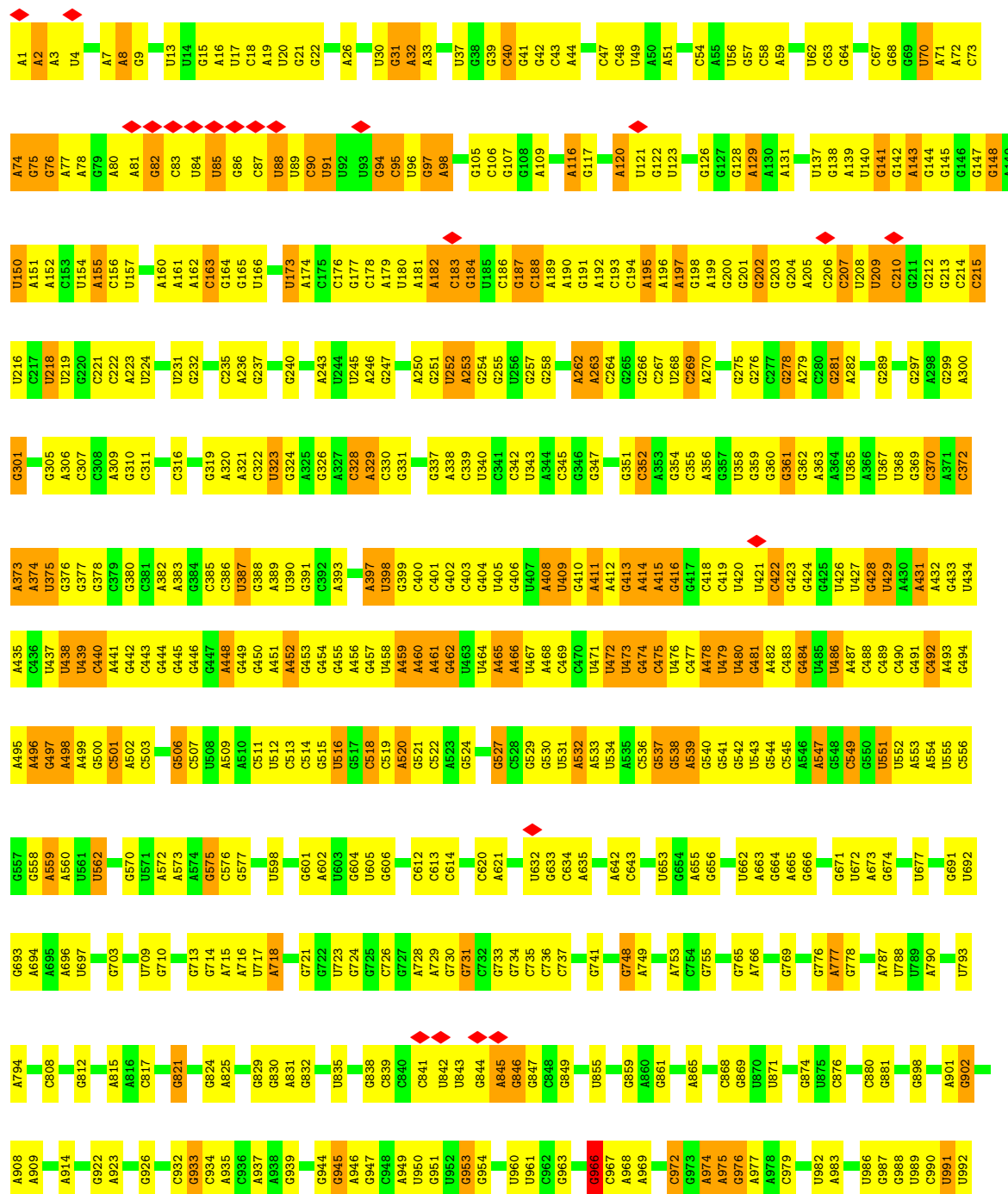
• Molecule 7: 16S ribosomal RNA

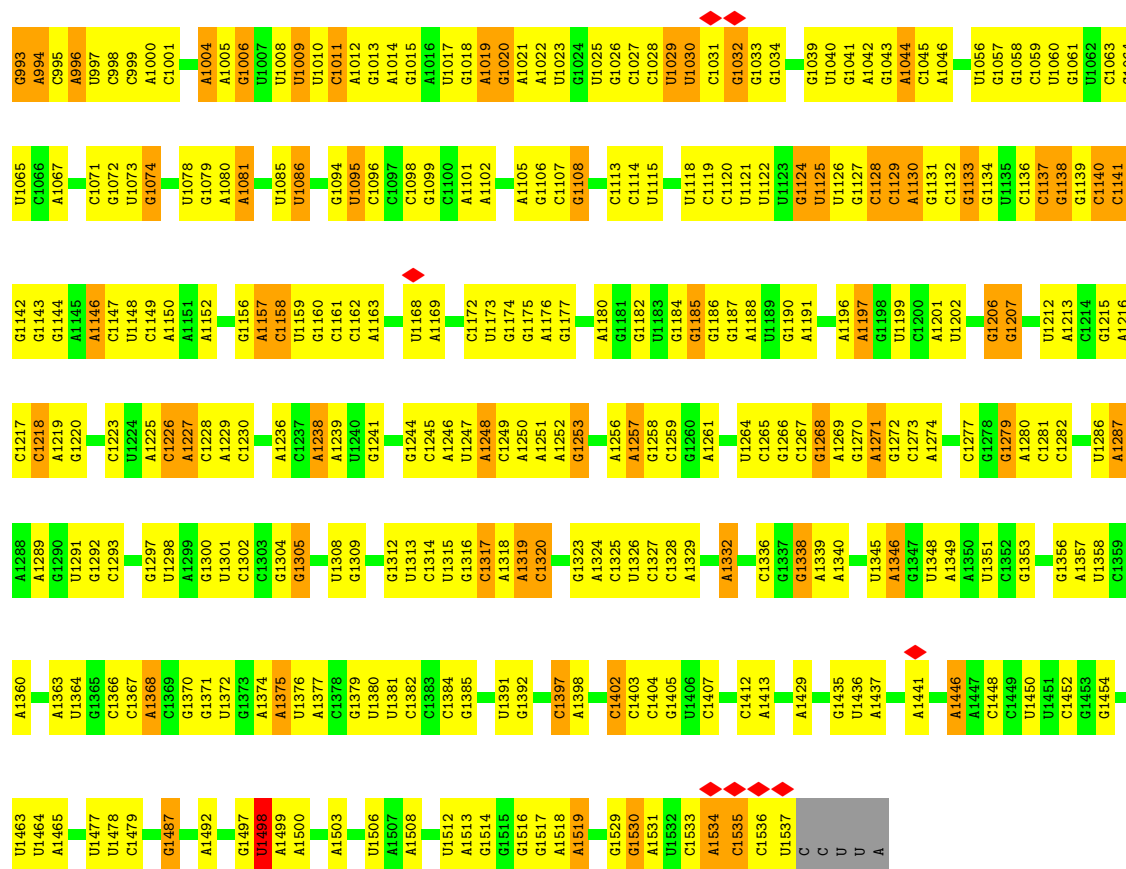




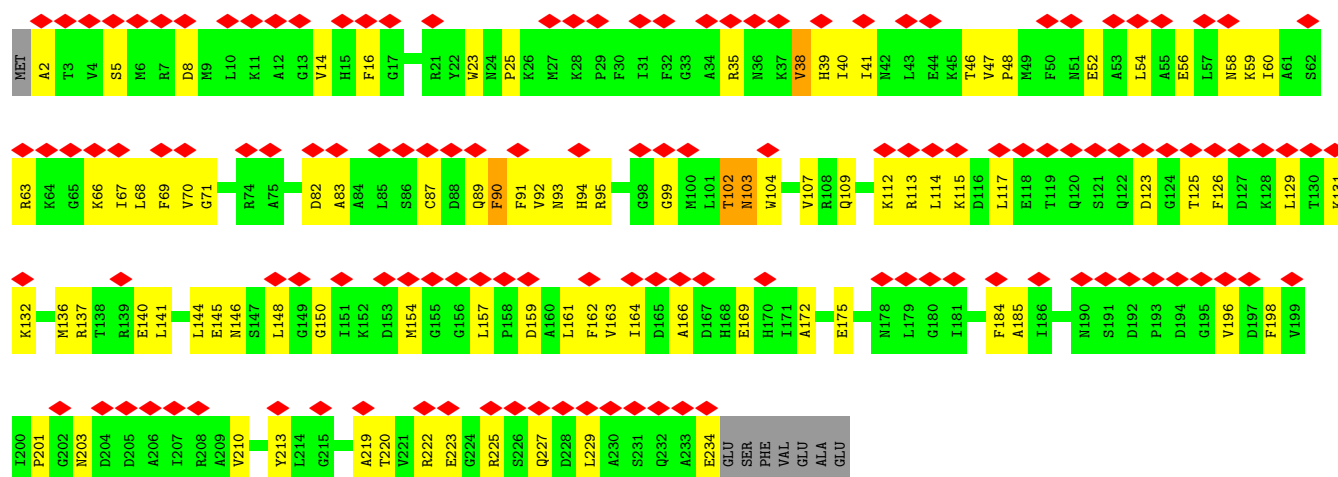


• Molecule 7: 16S ribosomal RNA



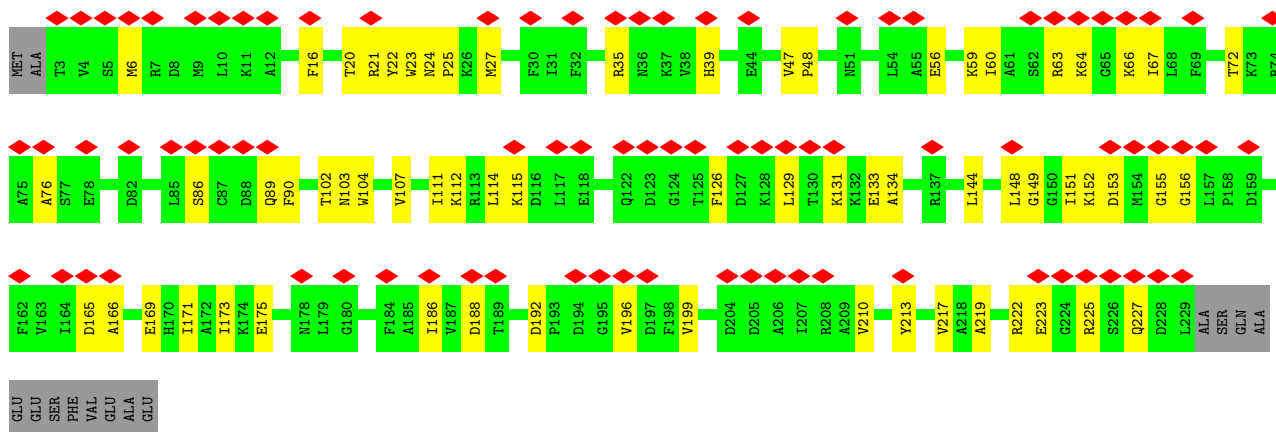


• Molecule 8: Small ribosomal subunit protein uS2

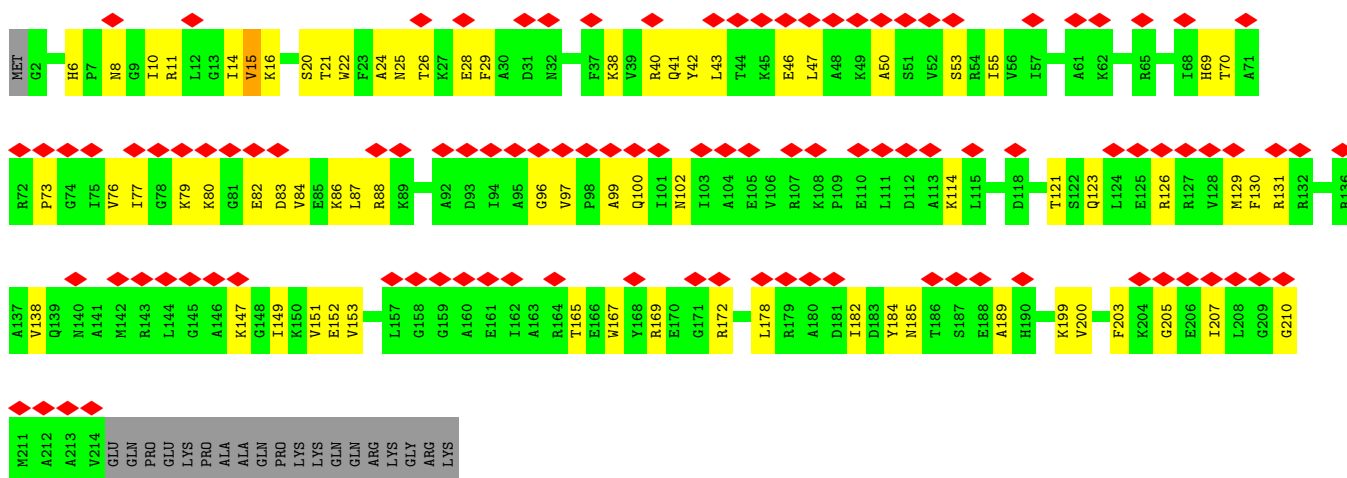


• Molecule 8: Small ribosomal subunit protein uS2

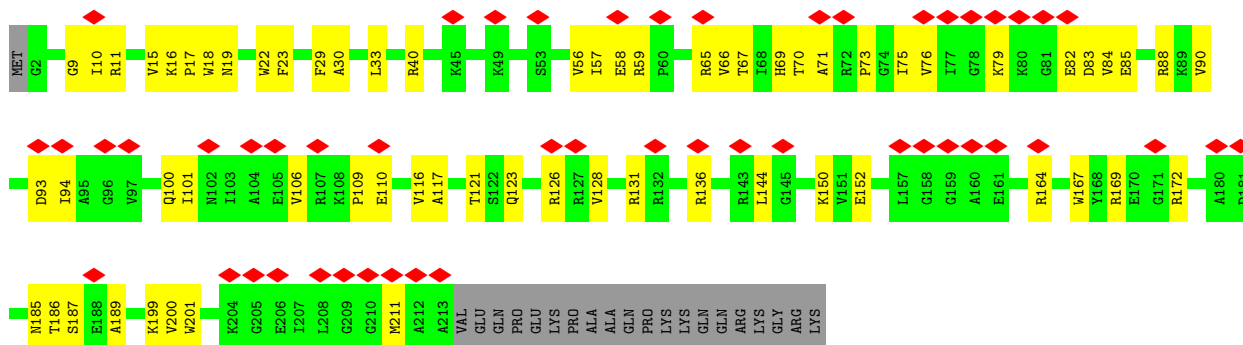




• Molecule 9: Small ribosomal subunit protein uS3

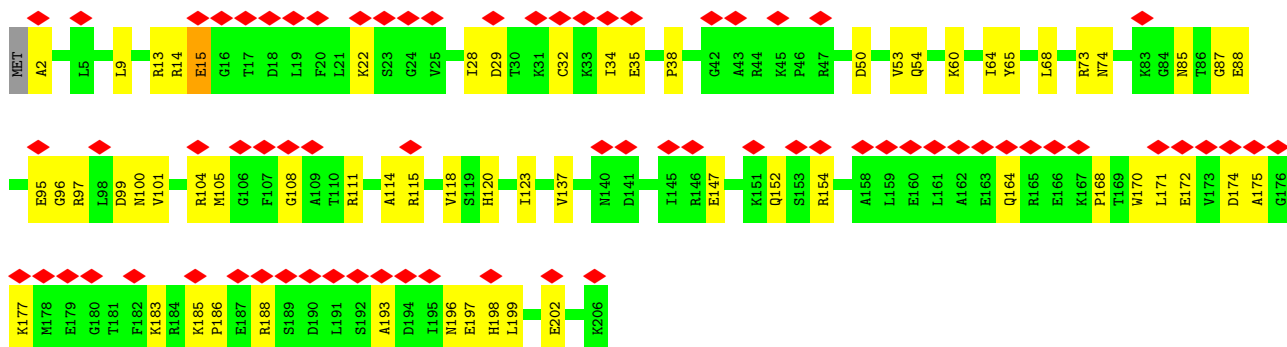


• Molecule 9: Small ribosomal subunit protein uS3

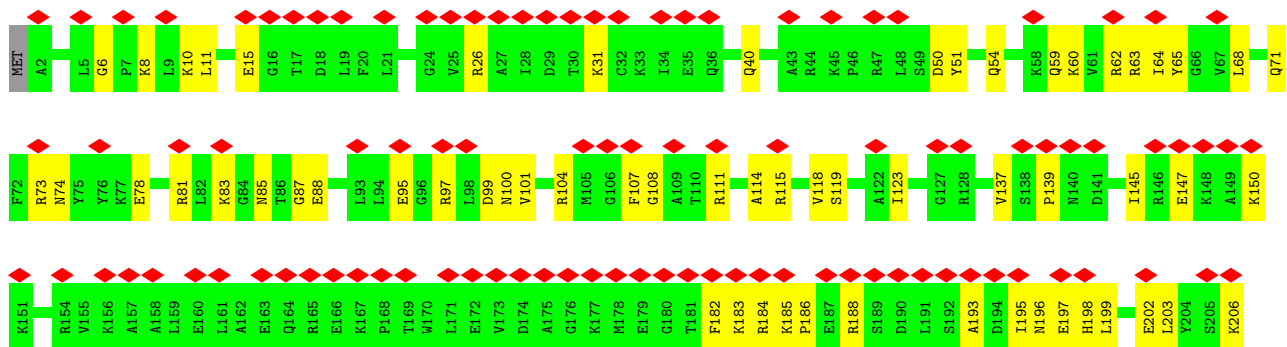


• Molecule 10: Small ribosomal subunit protein uS4

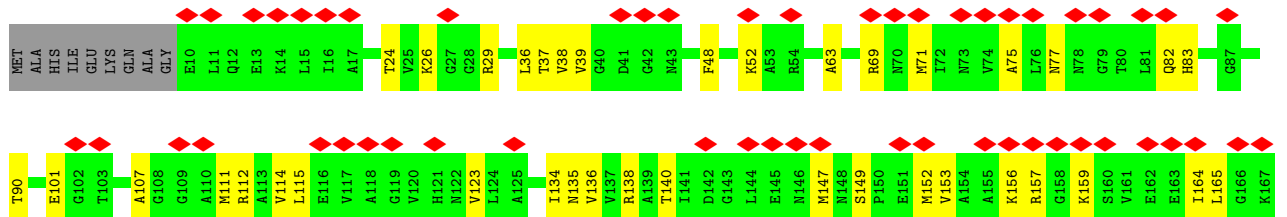
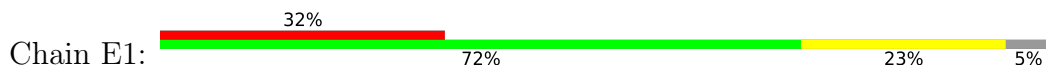




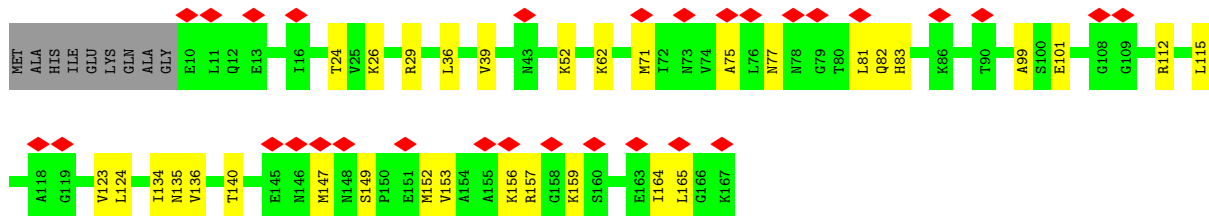
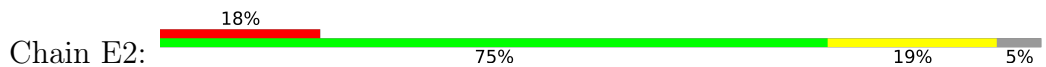
- Molecule 10: Small ribosomal subunit protein uS4



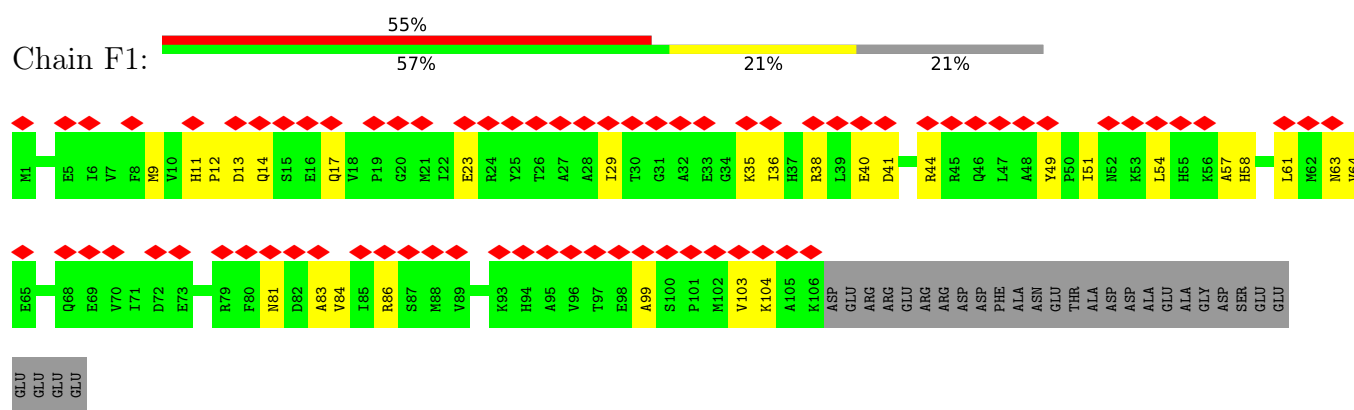
- Molecule 11: Small ribosomal subunit protein uS5



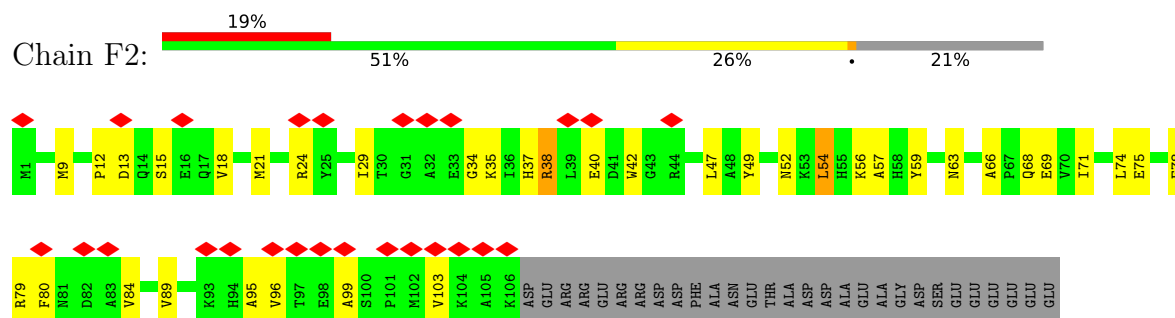
- Molecule 11: Small ribosomal subunit protein uS5



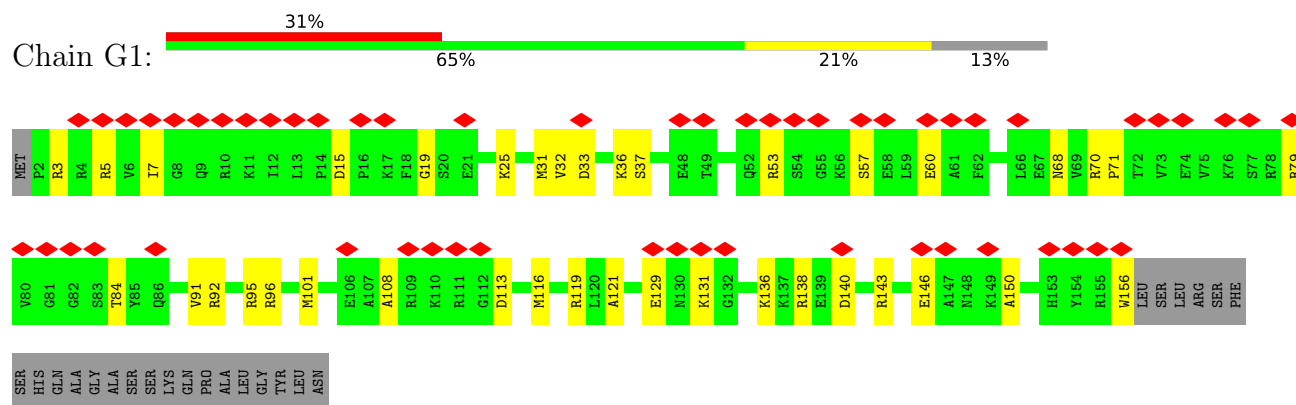
- Molecule 12: 30S ribosomal protein S6



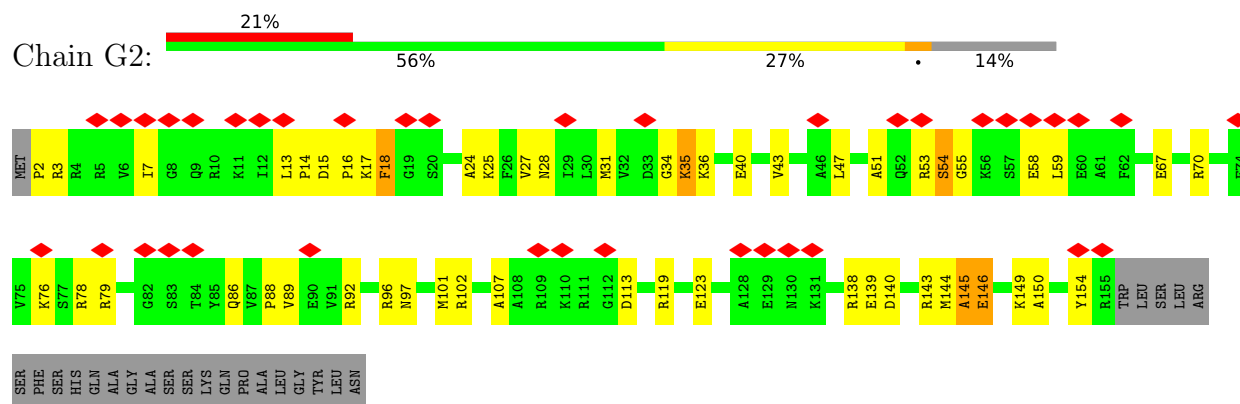
• Molecule 12: 30S ribosomal protein S6



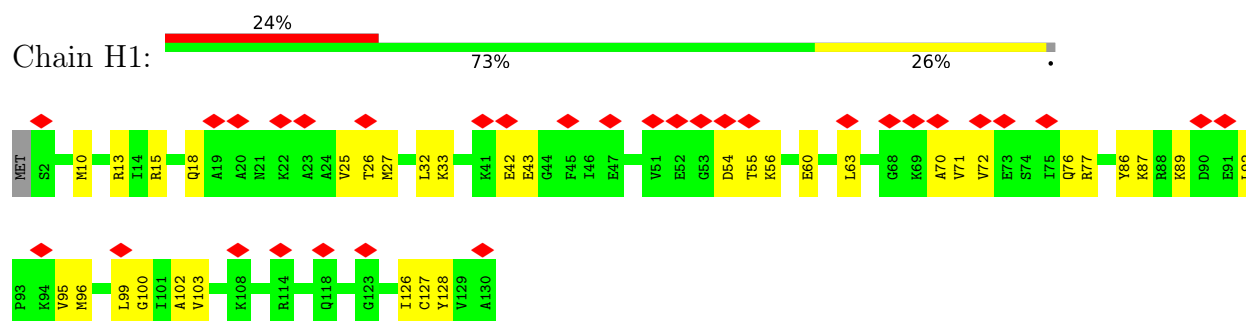
• Molecule 13: 30S ribosomal protein S7



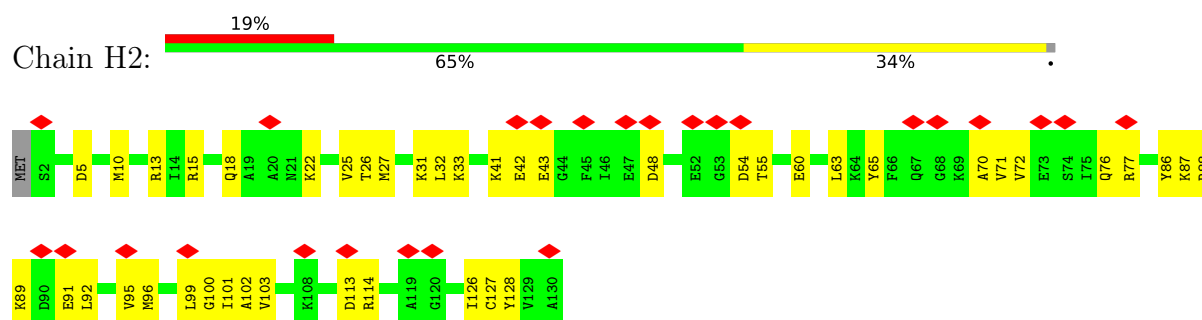
• Molecule 13: 30S ribosomal protein S7



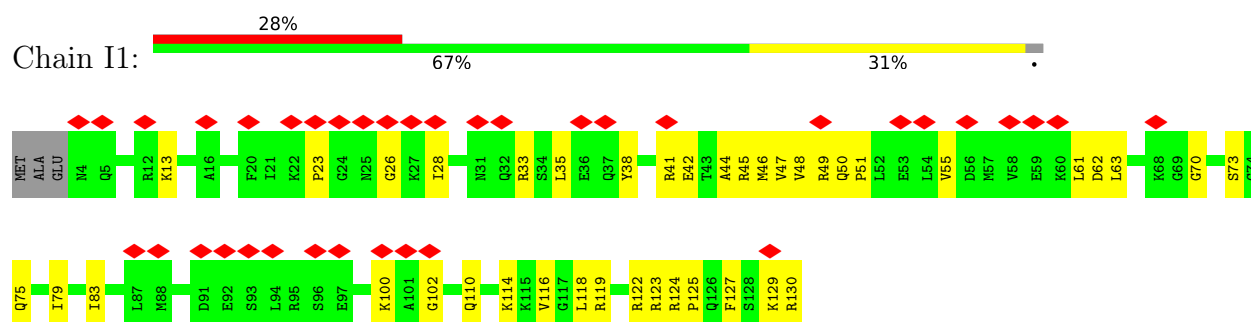
- Molecule 14: Small ribosomal subunit protein uS8



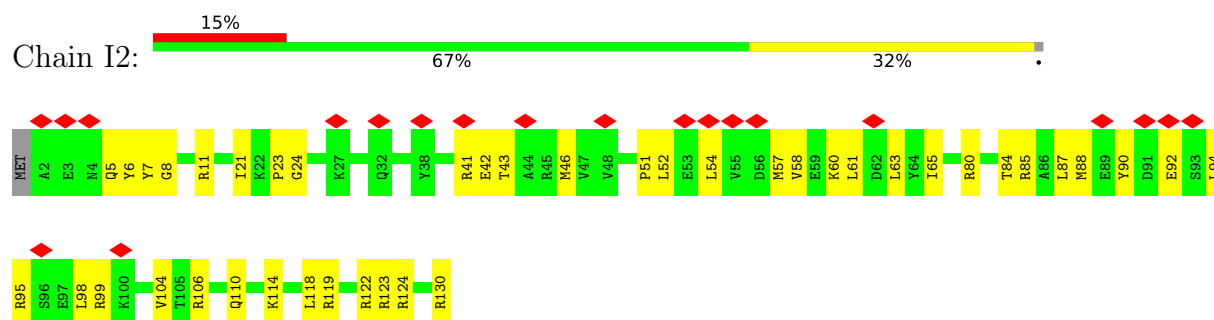
- Molecule 14: Small ribosomal subunit protein uS8



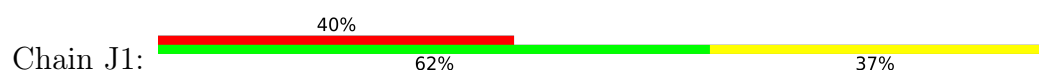
- Molecule 15: Small ribosomal subunit protein uS9

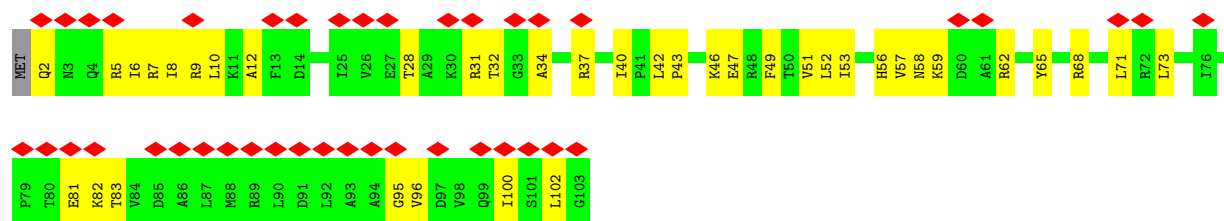


- Molecule 15: Small ribosomal subunit protein uS9

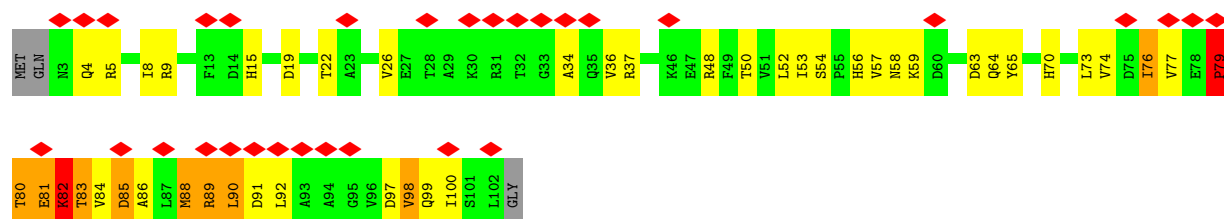


- Molecule 16: 30S ribosomal protein S10

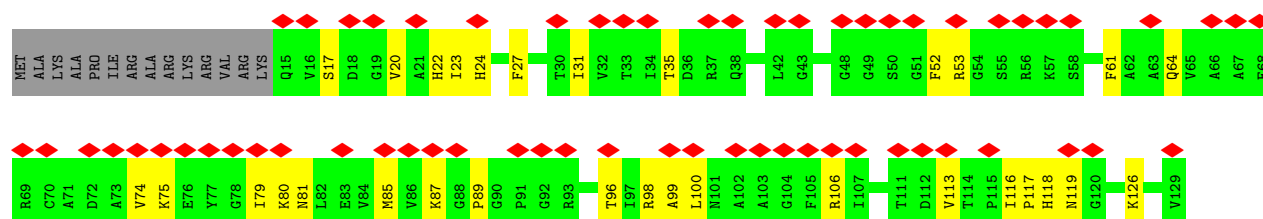




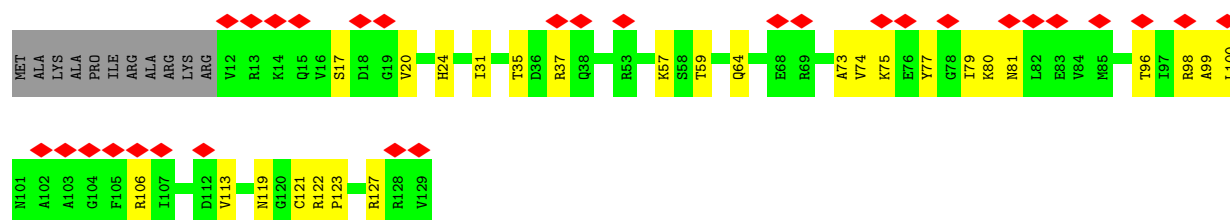
• Molecule 16: 30S ribosomal protein S10



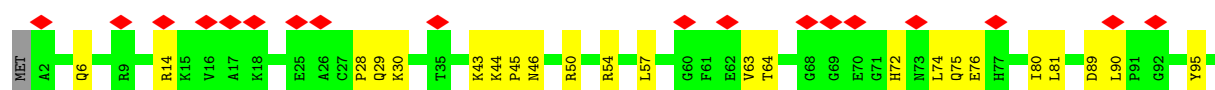
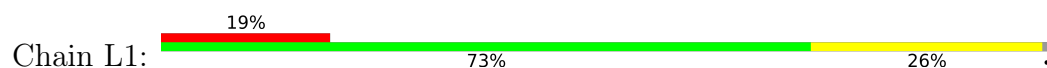
• Molecule 17: Small ribosomal subunit protein uS11



• Molecule 17: Small ribosomal subunit protein uS11



• Molecule 18: Small ribosomal subunit protein uS12

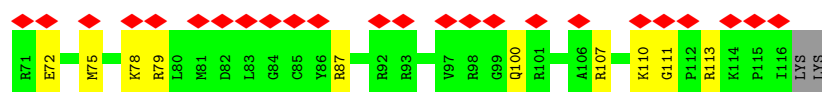
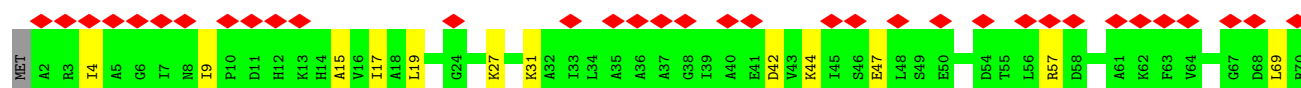
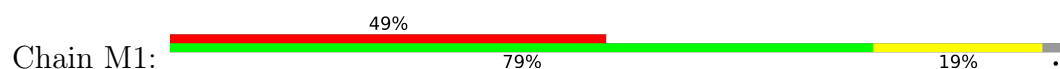




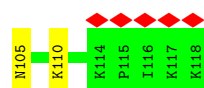
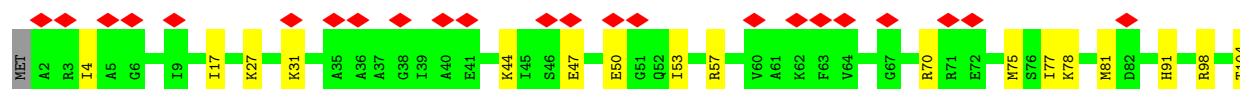
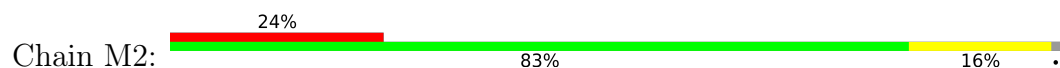
- Molecule 18: Small ribosomal subunit protein uS12



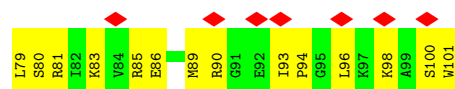
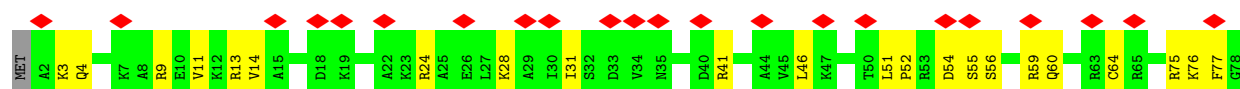
- Molecule 19: Small ribosomal subunit protein uS13



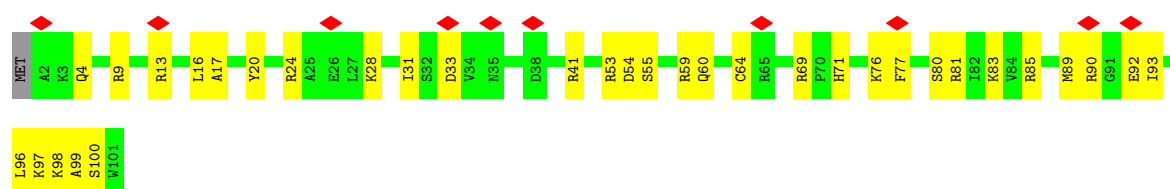
- Molecule 19: Small ribosomal subunit protein uS13



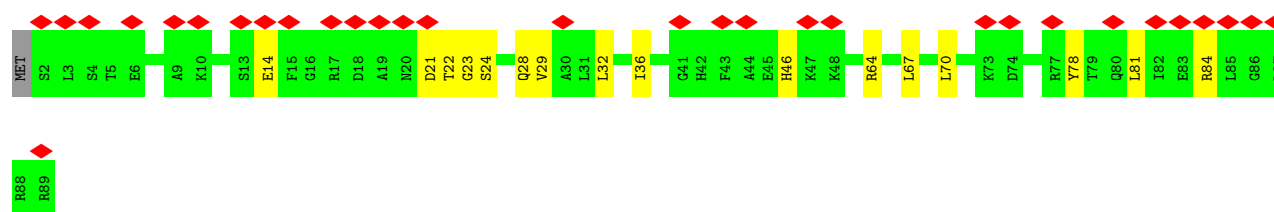
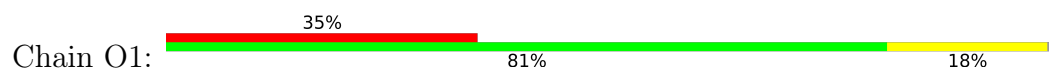
- Molecule 20: Small ribosomal subunit protein uS14



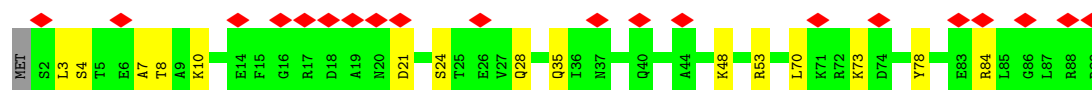
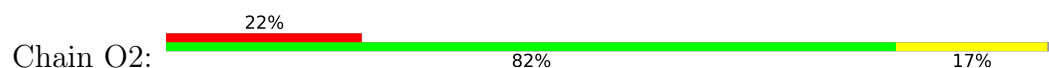
- Molecule 20: Small ribosomal subunit protein uS14



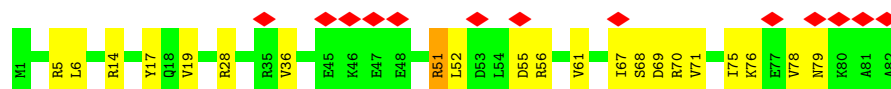
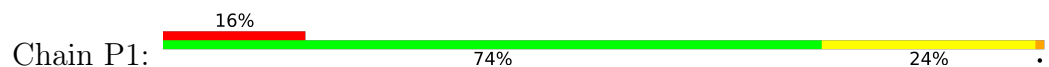
- Molecule 21: 30S ribosomal protein S15



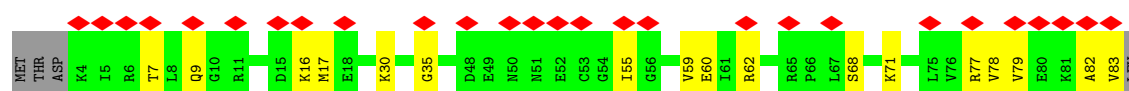
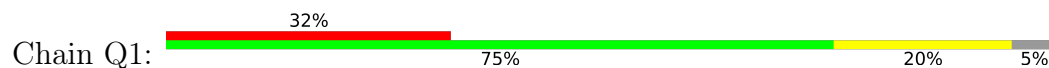
- Molecule 21: 30S ribosomal protein S15



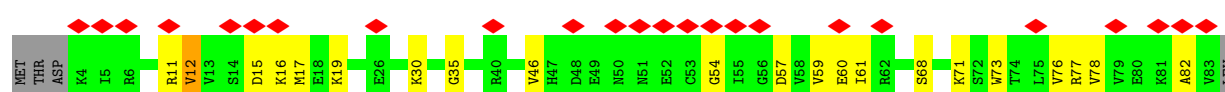
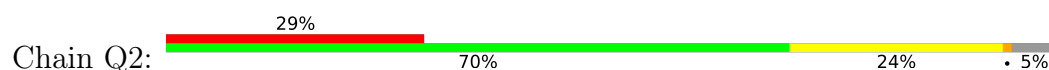
- Molecule 22: 30S ribosomal protein S16



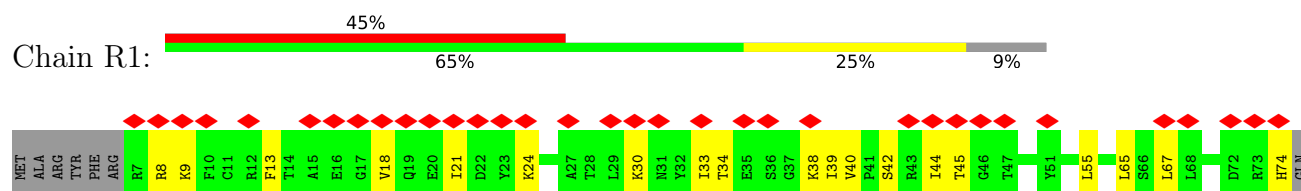
- Molecule 23: Small ribosomal subunit protein uS17



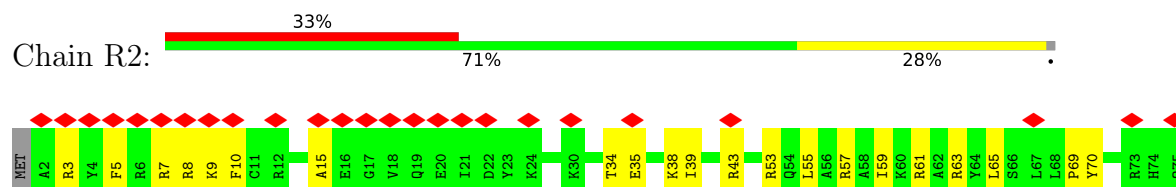
- Molecule 23: Small ribosomal subunit protein uS17



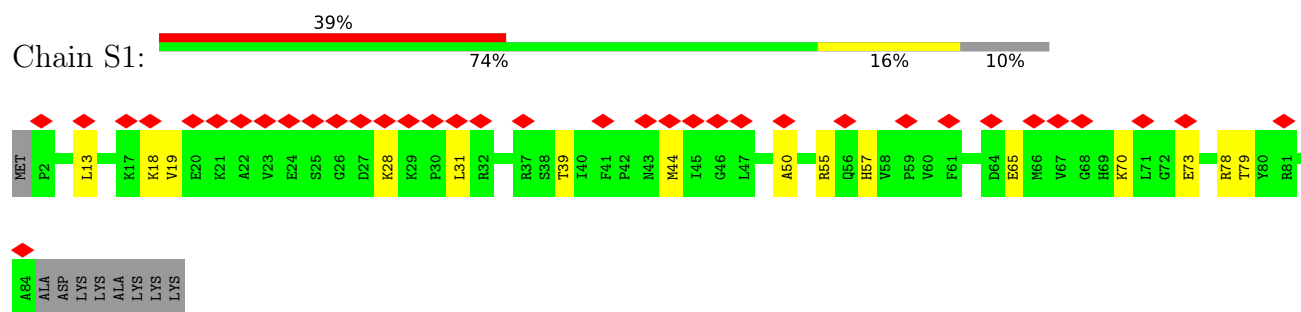
- Molecule 24: Small ribosomal subunit protein bS18



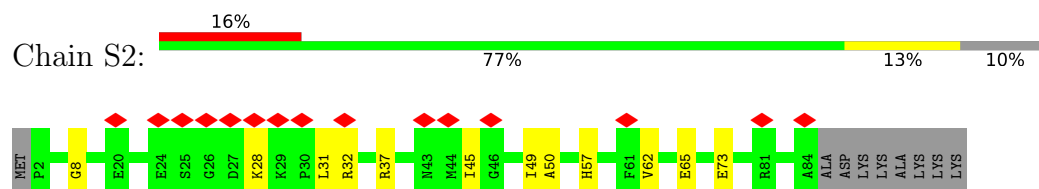
- Molecule 24: Small ribosomal subunit protein bS18



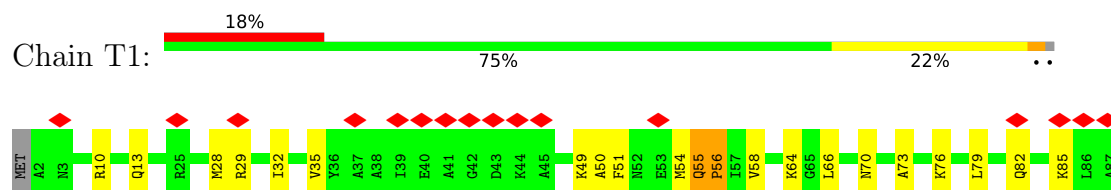
- Molecule 25: Small ribosomal subunit protein uS19



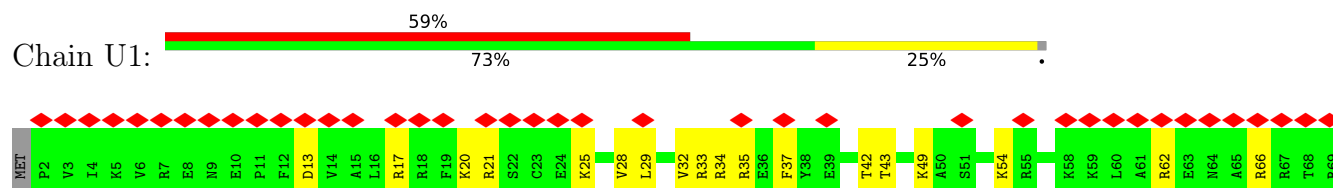
- Molecule 25: Small ribosomal subunit protein uS19



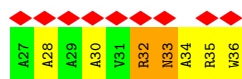
- Molecule 26: Small ribosomal subunit protein bS20



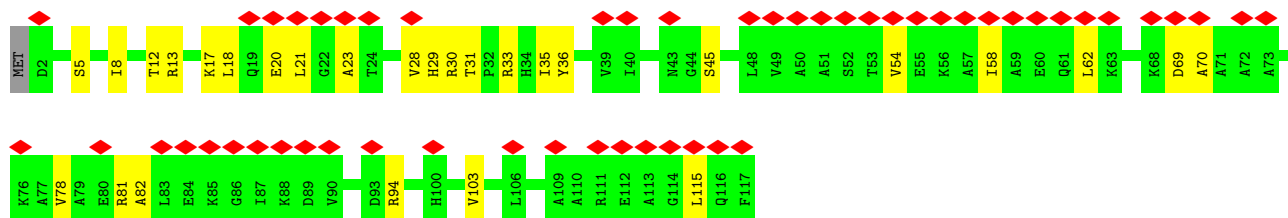
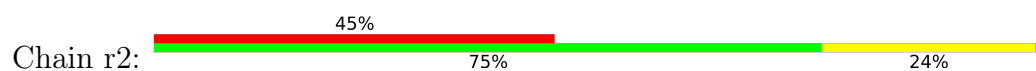
- Molecule 27: 30S ribosomal protein S21



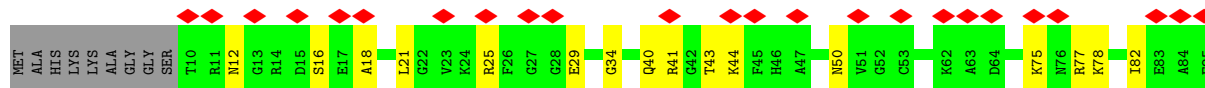




• Molecule 44: 50S ribosomal protein L18



• Molecule 45: 50S ribosomal protein L27



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	29998	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	19.921	Depositor
Minimum map value	-4.946	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.874	Depositor
Recommended contour level	5.5	Depositor
Map size (Å)	744.12, 744.12, 744.12	wwPDB
Map dimensions	468, 468, 468	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.59, 1.59, 1.59	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, G7M, 2MG, 3AU, 5MU, RSP, H2U, UR3, 7MG, 2MA, 5MC, MG, 1MG, 3TD, 4OC, OMG, 4SU, 6MZ, ZN, CM0, MIA, MA6, PSU, PUT, OMC

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	12	0.11	0/635	0.33	0/848
2	32	0.09	0/453	0.32	0/605
3	4	0.16	0/539	0.54	0/721
4	62	2.47	1/513 (0.2%)	0.75	2/676 (0.3%)
5	71	0.10	0/429	0.23	0/664
5	72	0.12	0/69306	0.24	5/108116 (0.0%)
6	82	0.16	1/2872 (0.0%)	0.27	0/4478
7	A1	0.17	0/36794	0.33	0/57392
7	A2	0.16	0/36681	0.30	0/57217
8	B	0.13	0/1846	0.44	0/2488
8	B2	0.13	0/1807	0.38	0/2435
9	C1	0.13	0/1692	0.39	0/2280
9	C2	0.14	0/1685	0.37	0/2270
10	D1	0.12	0/1665	0.37	0/2227
10	D2	0.10	0/1665	0.31	0/2227
11	E1	0.13	0/1179	0.33	0/1584
11	E2	0.13	0/1179	0.33	0/1584
12	F1	0.09	0/881	0.28	0/1189
12	F2	0.13	0/881	0.39	0/1189
13	G1	0.10	0/1246	0.32	0/1672
13	G2	0.13	0/1230	0.45	0/1649
14	H1	0.11	0/989	0.32	0/1326
14	H2	0.12	0/989	0.33	0/1326
15	I1	0.11	0/1034	0.36	0/1375
15	I2	0.12	0/1048	0.35	0/1394
16	J1	0.13	0/827	0.39	0/1117
16	J2	0.40	0/813	0.93	5/1100 (0.5%)
17	K1	0.11	0/873	0.34	0/1180
17	K2	0.12	0/900	0.33	0/1215
18	L1	0.12	0/969	0.35	0/1300
18	L2	0.12	0/969	0.34	0/1300

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
19	M1	0.10	0/900	0.32	0/1204
19	M2	0.11	0/919	0.33	0/1226
20	N1	0.13	0/817	0.36	0/1088
20	N2	0.11	0/817	0.38	0/1088
21	O1	0.10	0/722	0.31	0/964
21	O2	0.11	0/722	0.37	0/964
22	P1	0.12	0/659	0.33	0/884
23	Q1	0.13	0/657	0.38	0/881
23	Q2	0.13	0/657	0.39	0/881
24	R1	0.13	0/575	0.35	0/770
24	R2	0.14	0/637	0.45	0/851
25	S1	0.11	0/680	0.33	0/915
25	S2	0.13	0/680	0.33	0/915
26	T1	0.14	0/676	0.40	0/895
27	U1	0.13	0/598	0.43	0/792
27	U2	0.13	0/592	0.38	0/785
28	V2	0.21	0/1402	0.47	0/2185
29	W	0.29	0/1604	0.50	2/2496 (0.1%)
30	W1	0.28	0/747	0.28	0/1161
31	X2	0.44	2/1628 (0.1%)	0.47	1/2526 (0.0%)
32	Y1	0.14	0/786	0.42	0/1216
33	Y2	0.24	0/1725	0.38	1/2687 (0.0%)
34	Z1	0.09	0/76	0.21	0/101
35	a2	0.08	0/1033	0.25	0/1387
36	b2	0.12	0/2121	0.34	0/2852
37	e2	0.10	0/1444	0.29	0/1937
38	g2	0.12	0/434	0.33	0/576
39	h2	0.09	0/1104	0.28	0/1474
40	i2	0.13	0/1122	0.38	0/1515
41	l2	0.08	0/380	0.25	0/498
42	o2	2.24	6/383 (1.6%)	1.26	2/501 (0.4%)
43	p	0.92	0/77	1.39	1/104 (1.0%)
44	r2	0.10	0/901	0.35	0/1209
45	z2	0.09	0/589	0.29	0/779
All	All	0.22	10/203453 (0.0%)	0.32	19/306451 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
10	D1	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	D2	0	1
16	J2	0	4
17	K1	0	1
17	K2	0	1
21	O2	0	1
22	P1	0	1
43	p	0	1
All	All	0	12

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	62	52	LYS	CB-CG	55.55	3.19	1.52
42	o2	50	PHE	CD1-CE1	21.22	2.02	1.38
42	o2	50	PHE	CE2-CZ	20.15	1.99	1.38
42	o2	50	PHE	CD2-CE2	18.70	1.94	1.38
42	o2	50	PHE	CE1-CZ	18.31	1.93	1.38

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	62	52	LYS	CB-CG-CD	11.51	137.78	111.30
4	62	52	LYS	CA-CB-CG	10.06	134.22	114.10
29	W	73	G	P-O3'-C3'	-9.41	106.08	120.20
16	J2	82	LYS	N-CA-C	-7.92	102.65	111.28
42	o2	47	ARG	CB-CG-CD	-7.46	94.13	111.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
10	D1	104	ARG	Sidechain
10	D1	15	GLU	Peptide
10	D2	104	ARG	Sidechain
16	J2	37	ARG	Sidechain
16	J2	48	ARG	Sidechain

5.2 Too-close contacts [i](#)

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	12	625	0	652	16	0
2	32	449	0	491	16	0
3	4	529	0	527	19	0
4	62	504	0	572	39	0
5	71	406	0	208	4	0
5	72	62355	0	31379	529	0
6	82	2569	0	1301	28	0
7	A1	33092	0	16675	767	0
7	A2	32990	0	16622	549	0
8	B	1815	0	1836	71	0
8	B2	1776	0	1802	50	0
9	C1	1665	0	1741	51	0
9	C2	1658	0	1732	55	0
10	D1	1643	0	1707	42	0
10	D2	1643	0	1707	40	0
11	E1	1166	0	1212	28	0
11	E2	1166	0	1212	32	0
12	F1	862	0	864	21	0
12	F2	862	0	864	31	0
13	G1	1228	0	1277	26	0
13	G2	1214	0	1267	46	0
14	H1	979	0	1031	31	0
14	H2	979	0	1031	41	0
15	I1	1022	0	1070	34	0
15	I2	1036	0	1081	36	0
16	J1	817	0	853	31	0
16	J2	803	0	842	47	0
17	K1	857	0	861	21	0
17	K2	884	0	896	19	0
18	L1	955	0	1016	24	0
18	L2	955	0	1016	29	0
19	M1	891	0	952	20	0
19	M2	910	0	978	17	0
20	N1	805	0	844	34	0
20	N2	805	0	844	34	0
21	O1	714	0	734	11	0
21	O2	714	0	734	9	0
22	P1	649	0	666	16	0
23	Q1	648	0	691	12	0
23	Q2	648	0	691	15	0
24	R1	566	0	591	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	R2	626	0	648	17	0
25	S1	663	0	688	10	0
25	S2	663	0	688	9	0
26	T1	670	0	719	16	0
27	U1	590	0	629	19	0
27	U2	584	0	618	10	0
28	V2	1250	0	628	36	0
29	W	1630	0	840	32	0
30	W1	781	0	405	12	0
31	X2	1654	0	848	27	0
32	Y1	778	0	399	6	0
33	Y2	1628	0	828	13	0
34	Z1	75	0	65	0	0
35	a2	1026	0	1092	9	0
36	b2	2082	0	2154	52	0
37	e2	1420	0	1457	22	0
38	g2	427	0	464	8	0
39	h2	1085	0	1169	17	0
40	i2	1111	0	1148	20	0
41	l2	377	0	418	11	0
42	o2	377	0	389	80	0
43	p	76	0	75	14	0
44	r2	891	0	923	18	0
45	z2	582	0	599	14	0
46	4	1	0	0	0	0
46	B	1	0	0	0	0
47	72	12	0	24	0	0
48	72	191	0	0	0	0
48	82	1	0	0	0	0
48	A1	59	0	0	0	0
48	A2	42	0	0	0	0
48	V2	1	0	0	0	0
48	W	1	0	0	0	0
48	Y2	1	0	0	0	0
49	Y2	5	0	4	8	0
All	All	188215	0	120989	3027	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 3027 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)
42:o2:50:PHE:CE1	42:o2:50:PHE:CZ	1.93	1.57
42:o2:50:PHE:CD2	42:o2:50:PHE:CE2	1.94	1.52
42:o2:50:PHE:CZ	42:o2:50:PHE:CE2	1.99	1.50
42:o2:50:PHE:CE1	42:o2:50:PHE:CD1	2.02	1.45
4:62:52:LYS:CG	42:o2:50:PHE:CE2	2.32	1.12

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	
1	12	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
2	32	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	34
3	4	65/70 (93%)	52 (80%)	13 (20%)	0	100	100
4	62	62/65 (95%)	58 (94%)	4 (6%)	0	100	100
8	B	231/241 (96%)	193 (84%)	34 (15%)	4 (2%)	7	35
8	B2	225/241 (93%)	189 (84%)	36 (16%)	0	100	100
9	C1	211/233 (91%)	186 (88%)	23 (11%)	2 (1%)	14	46
9	C2	210/233 (90%)	184 (88%)	26 (12%)	0	100	100
10	D1	203/206 (98%)	181 (89%)	21 (10%)	1 (0%)	24	57
10	D2	203/206 (98%)	200 (98%)	3 (2%)	0	100	100
11	E1	156/167 (93%)	152 (97%)	4 (3%)	0	100	100
11	E2	156/167 (93%)	152 (97%)	4 (3%)	0	100	100
12	F1	104/135 (77%)	104 (100%)	0	0	100	100
12	F2	104/135 (77%)	79 (76%)	23 (22%)	2 (2%)	6	33
13	G1	153/179 (86%)	151 (99%)	2 (1%)	0	100	100
13	G2	152/179 (85%)	122 (80%)	24 (16%)	6 (4%)	2	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	H1	127/130 (98%)	127 (100%)	0	0	100	100
14	H2	127/130 (98%)	127 (100%)	0	0	100	100
15	I1	125/130 (96%)	103 (82%)	22 (18%)	0	100	100
15	I2	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
16	J1	100/103 (97%)	92 (92%)	8 (8%)	0	100	100
16	J2	98/103 (95%)	86 (88%)	9 (9%)	3 (3%)	3	25
17	K1	113/129 (88%)	97 (86%)	15 (13%)	1 (1%)	14	46
17	K2	116/129 (90%)	100 (86%)	15 (13%)	1 (1%)	14	46
18	L1	121/124 (98%)	114 (94%)	6 (5%)	1 (1%)	16	49
18	L2	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
19	M1	113/118 (96%)	109 (96%)	4 (4%)	0	100	100
19	M2	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
20	N1	98/101 (97%)	87 (89%)	11 (11%)	0	100	100
20	N2	98/101 (97%)	95 (97%)	3 (3%)	0	100	100
21	O1	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
21	O2	86/89 (97%)	84 (98%)	2 (2%)	0	100	100
22	P1	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
23	Q1	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
23	Q2	78/84 (93%)	75 (96%)	2 (3%)	1 (1%)	9	39
24	R1	66/75 (88%)	60 (91%)	5 (8%)	1 (2%)	8	37
24	R2	72/75 (96%)	52 (72%)	19 (26%)	1 (1%)	9	38
25	S1	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
25	S2	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
26	T1	84/87 (97%)	79 (94%)	3 (4%)	2 (2%)	4	29
27	U1	68/71 (96%)	57 (84%)	11 (16%)	0	100	100
27	U2	68/71 (96%)	59 (87%)	7 (10%)	2 (3%)	3	26
34	Z1	7/557 (1%)	7 (100%)	0	0	100	100
35	a2	130/234 (56%)	124 (95%)	6 (5%)	0	100	100
36	b2	269/273 (98%)	264 (98%)	5 (2%)	0	100	100
37	e2	176/179 (98%)	172 (98%)	4 (2%)	0	100	100
38	g2	50/55 (91%)	50 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
39	h2	135/136 (99%)	135 (100%)	0	0	100	100
40	i2	147/149 (99%)	116 (79%)	29 (20%)	2 (1%)	9	38
41	l2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
42	o2	49/144 (34%)	45 (92%)	4 (8%)	0	100	100
43	p	8/10 (80%)	4 (50%)	2 (25%)	2 (25%)	0	0
44	r2	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
45	z2	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
All	All	6096/7240 (84%)	5606 (92%)	457 (8%)	33 (0%)	26	57

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C1	15	VAL
13	G2	18	PHE
13	G2	35	LYS
13	G2	54	SER
13	G2	146	GLU

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	
1	12	67/68 (98%)	67 (100%)	0	100	100
2	32	48/49 (98%)	48 (100%)	0	100	100
3	4	60/62 (97%)	60 (100%)	0	100	100
4	62	51/52 (98%)	51 (100%)	0	100	100
8	B	192/199 (96%)	192 (100%)	0	100	100
8	B2	189/199 (95%)	189 (100%)	0	100	100
9	C1	173/190 (91%)	173 (100%)	0	100	100
9	C2	172/190 (90%)	172 (100%)	0	100	100
10	D1	172/173 (99%)	172 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	D2	172/173 (99%)	172 (100%)	0	100	100
11	E1	120/126 (95%)	120 (100%)	0	100	100
11	E2	120/126 (95%)	120 (100%)	0	100	100
12	F1	92/116 (79%)	92 (100%)	0	100	100
12	F2	92/116 (79%)	92 (100%)	0	100	100
13	G1	128/147 (87%)	128 (100%)	0	100	100
13	G2	127/147 (86%)	127 (100%)	0	100	100
14	H1	104/105 (99%)	104 (100%)	0	100	100
14	H2	104/105 (99%)	104 (100%)	0	100	100
15	I1	105/107 (98%)	105 (100%)	0	100	100
15	I2	106/107 (99%)	106 (100%)	0	100	100
16	J1	89/90 (99%)	89 (100%)	0	100	100
16	J2	88/90 (98%)	84 (96%)	4 (4%)	24	51
17	K1	88/99 (89%)	88 (100%)	0	100	100
17	K2	91/99 (92%)	91 (100%)	0	100	100
18	L1	103/104 (99%)	103 (100%)	0	100	100
18	L2	103/104 (99%)	103 (100%)	0	100	100
19	M1	93/96 (97%)	93 (100%)	0	100	100
19	M2	95/96 (99%)	95 (100%)	0	100	100
20	N1	83/84 (99%)	83 (100%)	0	100	100
20	N2	83/84 (99%)	83 (100%)	0	100	100
21	O1	76/77 (99%)	76 (100%)	0	100	100
21	O2	76/77 (99%)	76 (100%)	0	100	100
22	P1	65/65 (100%)	65 (100%)	0	100	100
23	Q1	74/78 (95%)	74 (100%)	0	100	100
23	Q2	74/78 (95%)	74 (100%)	0	100	100
24	R1	59/65 (91%)	59 (100%)	0	100	100
24	R2	64/65 (98%)	64 (100%)	0	100	100
25	S1	72/79 (91%)	72 (100%)	0	100	100
25	S2	72/79 (91%)	72 (100%)	0	100	100
26	T1	65/66 (98%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	U1	60/61 (98%)	60 (100%)	0	100	100
27	U2	59/61 (97%)	59 (100%)	0	100	100
34	Z1	8/461 (2%)	8 (100%)	0	100	100
35	a2	110/181 (61%)	110 (100%)	0	100	100
36	b2	216/218 (99%)	216 (100%)	0	100	100
37	e2	149/150 (99%)	149 (100%)	0	100	100
38	g2	47/49 (96%)	47 (100%)	0	100	100
39	h2	110/109 (101%)	110 (100%)	0	100	100
40	i2	114/114 (100%)	114 (100%)	0	100	100
41	l2	38/38 (100%)	38 (100%)	0	100	100
42	o2	35/103 (34%)	35 (100%)	0	100	100
43	p	5/5 (100%)	5 (100%)	0	100	100
44	r2	86/87 (99%)	86 (100%)	0	100	100
45	z2	58/63 (92%)	58 (100%)	0	100	100
All	All	5102/5932 (86%)	5098 (100%)	4 (0%)	87	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	J2	82	LYS
16	J2	83	THR
16	J2	85	ASP
16	J2	98	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
20	N2	43	ASN
39	h2	13	HIS
21	O1	28	GLN
36	b2	143	ASN
40	i2	133	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	V2	58/64 (90%)	38 (65%)	8 (13%)
29	W	75/76 (98%)	23 (30%)	4 (5%)
30	W1	34/76 (44%)	9 (26%)	2 (5%)
31	X2	74/77 (96%)	29 (39%)	5 (6%)
32	Y1	34/76 (44%)	6 (17%)	2 (5%)
33	Y2	75/76 (98%)	23 (30%)	2 (2%)
5	71	18/2904 (0%)	1 (5%)	0
5	72	2903/2904 (99%)	460 (15%)	32 (1%)
6	82	119/120 (99%)	21 (17%)	4 (3%)
7	A1	1541/1542 (99%)	450 (29%)	37 (2%)
7	A2	1536/1542 (99%)	404 (26%)	33 (2%)
All	All	6467/9457 (68%)	1464 (22%)	129 (1%)

5 of 1464 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	71	1907	G
5	72	10	A
5	72	15	G
5	72	34	U
5	72	44	A

5 of 129 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	W	18	G
30	W1	43	C
7	A1	421	U
7	A1	412	A
31	X2	22	A

5.4 Non-standard residues in protein, DNA, RNA chains

73 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
32	CM0	Y1	34	32	23,26,27	3.72	6 (26%)	27,37,40	1.54	2 (7%)
29	H2U	W	16	29	18,21,22	3.05	5 (27%)	21,30,33	2.00	5 (23%)
7	4OC	A1	1402	7	20,23,24	3.23	8 (40%)	26,32,35	0.93	1 (3%)
5	PSU	72	955	5	18,21,22	4.65	8 (44%)	22,30,33	1.89	5 (22%)
29	PSU	W	55	29	18,21,22	0.88	1 (5%)	22,30,33	0.73	0
29	4SU	W	8	29	18,21,22	3.78	7 (38%)	26,30,33	2.26	5 (19%)
30	PSU	W1	39	30	18,21,22	4.66	8 (44%)	22,30,33	1.82	5 (22%)
32	6MZ	Y1	37	32	22,25,26	2.81	5 (22%)	30,36,39	2.48	12 (40%)
29	MIA	W	37	29	28,31,32	2.39	5 (17%)	40,44,47	2.66	17 (42%)
7	G7M	A1	527	7	23,26,27	2.84	9 (39%)	35,39,42	1.73	8 (22%)
5	H2U	72	2449	5,48	18,21,22	3.05	5 (27%)	21,30,33	2.04	5 (23%)
5	PSU	72	2504	5,48	18,21,22	4.67	8 (44%)	22,30,33	1.85	5 (22%)
30	4SU	W1	8	30	18,21,22	3.77	7 (38%)	26,30,33	2.20	4 (15%)
7	MA6	A2	1519	7	23,26,27	1.35	3 (13%)	34,38,41	3.35	14 (41%)
7	2MG	A1	966	7	23,26,27	3.10	8 (34%)	32,38,41	2.56	11 (34%)
5	PSU	72	746	5,48	18,21,22	0.84	1 (5%)	22,30,33	0.92	1 (4%)
7	2MG	A2	1516	7	23,26,27	3.09	8 (34%)	32,38,41	2.49	11 (34%)
33	5MU	Y2	54	33	19,22,23	0.23	0	28,32,35	0.25	0
5	2MG	72	1835	5	23,26,27	3.07	8 (34%)	32,38,41	2.52	11 (34%)
31	RSP	X2	33	31	17,21,22	4.14	7 (41%)	22,30,33	0.77	0
5	6MZ	72	1618	5	22,25,26	2.77	4 (18%)	30,36,39	2.51	11 (36%)
30	G7M	W1	46	30	23,26,27	2.85	8 (34%)	35,39,42	1.93	8 (22%)
7	5MC	A1	967	7	18,22,23	4.03	7 (38%)	26,32,35	1.01	2 (7%)
31	4SU	X2	8	31	18,21,22	3.79	7 (38%)	26,30,33	2.29	4 (15%)
5	2MG	72	2445	5	23,26,27	3.09	8 (34%)	32,38,41	2.49	10 (31%)
30	PSU	W1	32	30	18,21,22	4.66	8 (44%)	22,30,33	1.82	5 (22%)
5	5MU	72	1939	5	19,22,23	0.28	0	28,32,35	0.24	0
5	PSU	72	2605	5	18,21,22	4.64	8 (44%)	22,30,33	1.82	5 (22%)
29	PSU	W	32	29	18,21,22	4.61	8 (44%)	22,30,33	1.91	5 (22%)
31	5MU	X2	55	31	19,22,23	0.25	0	28,32,35	0.38	0
31	PSU	X2	56	31	18,21,22	0.88	1 (5%)	22,30,33	0.73	0
7	5MC	A1	1407	7	18,22,23	4.01	7 (38%)	26,32,35	1.01	2 (7%)
7	UR3	A2	1498	7	19,22,23	2.73	8 (42%)	26,32,35	1.28	1 (3%)
7	UR3	A1	1498	7	19,22,23	2.74	8 (42%)	26,32,35	1.28	2 (7%)
5	OMC	72	2498	5,48	19,22,23	3.31	8 (42%)	26,31,34	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	3TD	71	1915	5	19,22,23	4.07	7 (36%)	21,32,35	1.66	2 (9%)
5	OMU	72	2552	5	19,22,23	3.21	8 (42%)	26,31,34	1.69	5 (19%)
7	2MG	A1	1516	7	23,26,27	3.10	8 (34%)	32,38,41	2.53	11 (34%)
31	H2U	X2	17	31	18,21,22	3.09	5 (27%)	21,30,33	1.98	5 (23%)
7	2MG	A2	966	7	23,26,27	3.10	8 (34%)	32,38,41	2.51	11 (34%)
33	G7M	Y2	46	33	23,26,27	2.84	9 (39%)	35,39,42	1.74	8 (22%)
29	5MU	W	54	29	19,22,23	0.27	0	28,32,35	0.49	0
7	5MC	A2	967	7	18,22,23	4.03	7 (38%)	26,32,35	1.01	2 (7%)
5	1MG	72	745	5	22,26,27	2.73	5 (22%)	33,39,42	2.29	8 (24%)
29	G7M	W	46	29	23,26,27	2.84	8 (34%)	35,39,42	1.94	8 (22%)
5	G7M	72	2069	5	23,26,27	2.82	9 (39%)	35,39,42	1.76	8 (22%)
5	PSU	72	2457	5	18,21,22	4.65	8 (44%)	22,30,33	1.89	5 (22%)
5	PSU	72	2604	5	18,21,22	4.64	8 (44%)	22,30,33	1.85	5 (22%)
7	MA6	A1	1518	7	23,26,27	1.35	3 (13%)	34,38,41	3.33	14 (41%)
5	3TD	72	1915	5	19,22,23	4.05	7 (36%)	21,32,35	1.76	3 (14%)
5	5MC	72	1962	5	18,22,23	4.01	7 (38%)	26,32,35	1.07	2 (7%)
29	H2U	W	20	29	18,21,22	3.05	5 (27%)	21,30,33	2.02	5 (23%)
31	G7M	X2	47	31	23,26,27	2.84	8 (34%)	35,39,42	1.94	9 (25%)
5	6MZ	72	2030	5	22,25,26	2.83	5 (22%)	30,36,39	2.41	11 (36%)
31	H2U	X2	21	31	18,21,22	3.08	5 (27%)	21,30,33	2.02	5 (23%)
32	7MG	Y1	46	32	22,26,27	3.88	10 (45%)	29,39,42	2.07	9 (31%)
7	2MG	A2	1207	7	23,26,27	3.09	8 (34%)	32,38,41	2.50	10 (31%)
7	G7M	A2	527	7	23,26,27	2.84	9 (39%)	35,39,42	1.71	8 (22%)
7	MA6	A1	1519	7	23,26,27	1.34	3 (13%)	34,38,41	3.31	13 (38%)
7	4OC	A2	1402	7	20,23,24	3.24	8 (40%)	26,32,35	0.91	1 (3%)
5	5MU	72	747	5	19,22,23	0.25	0	28,32,35	0.67	0
5	PSU	72	2580	5	18,21,22	4.63	8 (44%)	22,30,33	1.86	6 (27%)
31	2MA	X2	38	31	22,25,26	4.13	8 (36%)	33,37,40	3.46	10 (30%)
33	H2U	Y2	17	33	18,21,22	3.07	5 (27%)	21,30,33	2.03	5 (23%)
33	PSU	Y2	55	33	18,21,22	0.88	1 (5%)	22,30,33	0.65	0
5	OMG	72	2251	5,29	23,26,27	2.58	6 (26%)	33,38,41	2.41	10 (30%)
30	MIA	W1	37	30	28,31,32	2.42	5 (17%)	40,44,47	2.79	13 (32%)
31	3AU	X2	48	31	24,28,29	2.82	8 (33%)	33,40,43	1.29	3 (9%)
7	5MC	A2	1407	7	18,22,23	4.01	7 (38%)	26,32,35	0.96	2 (7%)
29	H2U	W	17	29	18,21,22	3.06	5 (27%)	21,30,33	2.00	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	2MA	72	2503	5,48	22,25,26	4.05	8 (36%)	33,37,40	3.50	11 (33%)
7	MA6	A2	1518	7	23,26,27	1.37	3 (13%)	34,38,41	3.28	14 (41%)
7	2MG	A1	1207	7	23,26,27	3.10	8 (34%)	32,38,41	2.52	10 (31%)

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
32	CM0	Y1	34	32	-	2/12/30/31	0/2/2/2
29	H2U	W	16	29	-	1/7/38/39	0/2/2/2
7	4OC	A1	1402	7	-	0/9/29/30	0/2/2/2
5	PSU	72	955	5	-	0/7/25/26	0/2/2/2
29	PSU	W	55	29	-	0/7/25/26	0/2/2/2
29	4SU	W	8	29	-	2/7/25/26	0/2/2/2
30	PSU	W1	39	30	-	0/7/25/26	0/2/2/2
32	6MZ	Y1	37	32	-	2/9/27/28	0/3/3/3
29	MIA	W	37	29	-	1/15/33/34	0/3/3/3
7	G7M	A1	527	7	-	1/7/25/26	0/3/3/3
5	H2U	72	2449	5,48	-	0/7/38/39	0/2/2/2
5	PSU	72	2504	5,48	-	0/7/25/26	0/2/2/2
30	4SU	W1	8	30	-	2/7/25/26	0/2/2/2
7	MA6	A2	1519	7	-	2/11/29/30	0/3/3/3
7	2MG	A1	966	7	-	0/9/27/28	0/3/3/3
5	PSU	72	746	5,48	-	3/7/25/26	0/2/2/2
7	2MG	A2	1516	7	-	0/9/27/28	0/3/3/3
33	5MU	Y2	54	33	-	0/7/25/26	0/2/2/2
5	2MG	72	1835	5	-	0/9/27/28	0/3/3/3
31	RSP	X2	33	31	-	1/7/25/26	0/2/2/2
5	6MZ	72	1618	5	-	4/9/27/28	0/3/3/3
30	G7M	W1	46	30	-	4/7/25/26	0/3/3/3
7	5MC	A1	967	7	-	0/7/25/26	0/2/2/2
31	4SU	X2	8	31	-	2/7/25/26	0/2/2/2
5	2MG	72	2445	5	-	0/9/27/28	0/3/3/3
30	PSU	W1	32	30	-	0/7/25/26	0/2/2/2
5	5MU	72	1939	5	-	0/7/25/26	0/2/2/2
5	PSU	72	2605	5	-	0/7/25/26	0/2/2/2
29	PSU	W	32	29	-	0/7/25/26	0/2/2/2
31	5MU	X2	55	31	-	3/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	PSU	X2	56	31	-	1/7/25/26	0/2/2/2
7	5MC	A1	1407	7	-	0/7/25/26	0/2/2/2
7	UR3	A2	1498	7	-	2/7/25/26	0/2/2/2
7	UR3	A1	1498	7	-	2/7/25/26	0/2/2/2
5	OMC	72	2498	5,48	-	2/9/27/28	0/2/2/2
5	3TD	71	1915	5	-	1/7/25/26	0/2/2/2
5	OMU	72	2552	5	-	0/9/27/28	0/2/2/2
7	2MG	A1	1516	7	-	0/9/27/28	0/3/3/3
31	H2U	X2	17	31	-	6/7/38/39	0/2/2/2
7	2MG	A2	966	7	-	0/9/27/28	0/3/3/3
33	G7M	Y2	46	33	-	2/7/25/26	0/3/3/3
29	5MU	W	54	29	-	2/7/25/26	0/2/2/2
7	5MC	A2	967	7	-	1/7/25/26	0/2/2/2
5	1MG	72	745	5	-	0/7/25/26	0/3/3/3
29	G7M	W	46	29	-	3/7/25/26	0/3/3/3
5	G7M	72	2069	5	-	2/7/25/26	0/3/3/3
5	PSU	72	2457	5	-	0/7/25/26	0/2/2/2
5	PSU	72	2604	5	-	0/7/25/26	0/2/2/2
7	MA6	A1	1518	7	-	3/11/29/30	0/3/3/3
5	3TD	72	1915	5	-	2/7/25/26	0/2/2/2
5	5MC	72	1962	5	-	0/7/25/26	0/2/2/2
29	H2U	W	20	29	-	2/7/38/39	0/2/2/2
31	G7M	X2	47	31	-	3/7/25/26	0/3/3/3
5	6MZ	72	2030	5	-	3/9/27/28	0/3/3/3
31	H2U	X2	21	31	-	1/7/38/39	0/2/2/2
32	7MG	Y1	46	32	-	1/7/37/38	0/3/3/3
7	2MG	A2	1207	7	-	0/9/27/28	0/3/3/3
7	G7M	A2	527	7	-	3/7/25/26	0/3/3/3
7	MA6	A1	1519	7	-	3/11/29/30	0/3/3/3
7	4OC	A2	1402	7	-	1/9/29/30	0/2/2/2
5	5MU	72	747	5	-	0/7/25/26	0/2/2/2
5	PSU	72	2580	5	-	0/7/25/26	0/2/2/2
31	2MA	X2	38	31	-	5/7/25/26	0/3/3/3
33	H2U	Y2	17	33	-	7/7/38/39	0/2/2/2
33	PSU	Y2	55	33	-	0/7/25/26	0/2/2/2
5	OMG	72	2251	5,29	-	3/9/27/28	0/3/3/3
30	MIA	W1	37	30	-	6/15/33/34	0/3/3/3
31	3AU	X2	48	31	-	4/16/34/35	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	5MC	A2	1407	7	-	0/7/25/26	0/2/2/2
29	H2U	W	17	29	-	1/7/38/39	0/2/2/2
5	2MA	72	2503	5,48	-	0/7/25/26	0/3/3/3
7	MA6	A2	1518	7	-	0/11/29/30	0/3/3/3
7	2MG	A1	1207	7	-	0/9/27/28	0/3/3/3

The worst 5 of 447 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	Y1	34	CM0	C6-C5	12.68	1.48	1.34
31	X2	38	2MA	C4-N3	12.66	1.50	1.34
5	72	1915	3TD	C6-C5	12.65	1.50	1.35
5	71	1915	3TD	C6-C5	12.64	1.50	1.35
5	72	2503	2MA	C4-N3	12.27	1.49	1.34

The worst 5 of 434 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	72	2503	2MA	C1'-N9-C8	-12.68	98.51	127.14
31	X2	38	2MA	C1'-N9-C8	-12.32	99.31	127.14
7	A2	1519	MA6	N1-C6-N6	-12.17	103.78	117.08
7	A1	1519	MA6	N1-C6-N6	-11.92	104.05	117.08
7	A2	1518	MA6	N1-C6-N6	-11.87	104.11	117.08

There are no chirality outliers.

5 of 102 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A1	1518	MA6	C5-C6-N6-C9
7	A1	1518	MA6	C5-C6-N6-C10
7	A1	1519	MA6	C3'-C4'-C5'-O5'
7	A2	1402	4OC	C1'-C2'-O2'-CM2
7	A2	1498	UR3	O4'-C4'-C5'-O5'

There are no ring outliers.

32 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	W	16	H2U	5	0
29	W	37	MIA	3	0
5	72	2449	H2U	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	72	2504	PSU	1	0
7	A1	966	2MG	1	0
33	Y2	54	5MU	1	0
31	X2	33	RSP	1	0
30	W1	46	G7M	1	0
7	A1	967	5MC	1	0
5	72	2605	PSU	2	0
31	X2	55	5MU	3	0
31	X2	56	PSU	1	0
7	A2	1498	UR3	1	0
7	A2	966	2MG	1	0
33	Y2	46	G7M	1	0
29	W	54	5MU	1	0
29	W	46	G7M	1	0
5	72	2604	PSU	3	0
5	72	1915	3TD	1	0
5	72	1962	5MC	1	0
31	X2	47	G7M	1	0
5	72	2030	6MZ	1	0
7	A2	1207	2MG	1	0
7	A2	1402	4OC	3	0
5	72	747	5MU	1	0
31	X2	38	2MA	3	0
33	Y2	55	PSU	1	0
5	72	2251	OMG	1	0
30	W1	37	MIA	2	0
31	X2	48	3AU	2	0
5	72	2503	2MA	2	0
7	A1	1207	2MG	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 301 ligands modelled in this entry, 298 are monoatomic - leaving 3 for Mogul analysis.

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	$\# Z > 2$
49	ALA	Y2	102	33	3,4,5	0.53	0	2,4,6	1.62	1 (50%)
47	PUT	72	3002	-	5,5,5	0.25	0	4,4,4	0.55	0
47	PUT	72	3001	-	5,5,5	0.25	0	4,4,4	0.51	0

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
49	ALA	Y2	102	33	-	0/0/2/4	-
47	PUT	72	3002	-	-	0/3/3/3	-
47	PUT	72	3001	-	-	1/3/3/3	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	Y2	102	ALA	O-C-CA	-2.29	117.03	124.28

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	72	3001	PUT	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	Y2	102	ALA	8	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

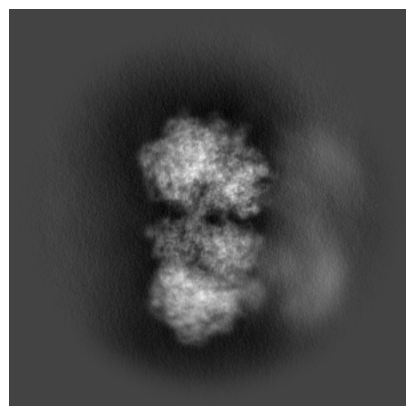
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19055. These allow visual inspection of the internal detail of the map and identification of artifacts.

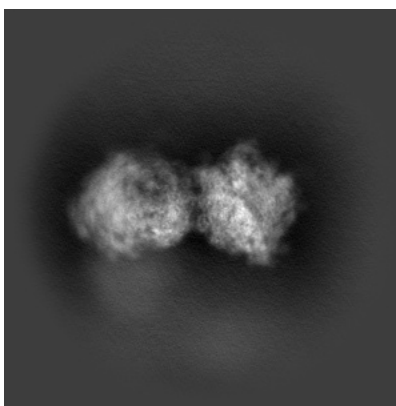
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

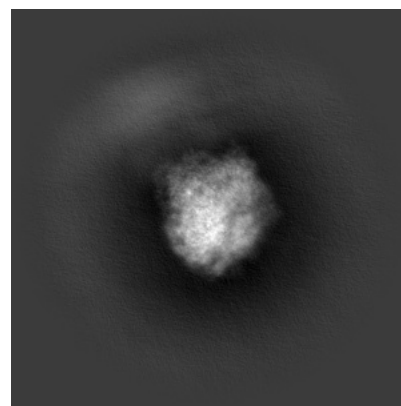
6.1.1 Primary map



X

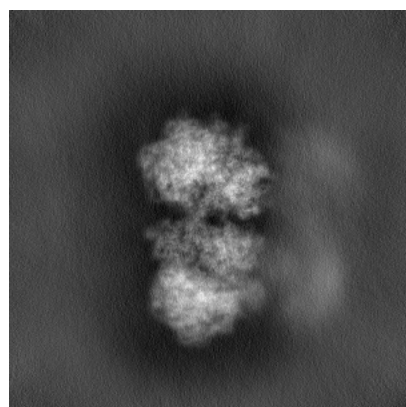


Y

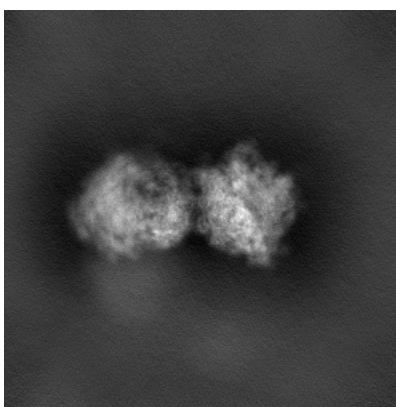


Z

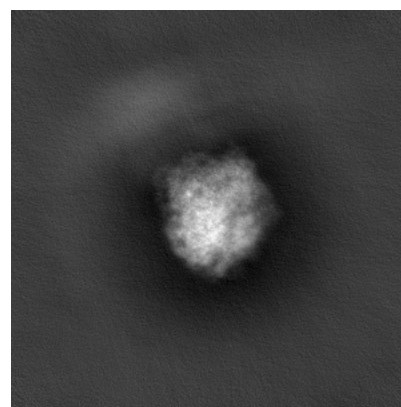
6.1.2 Raw map



X



Y

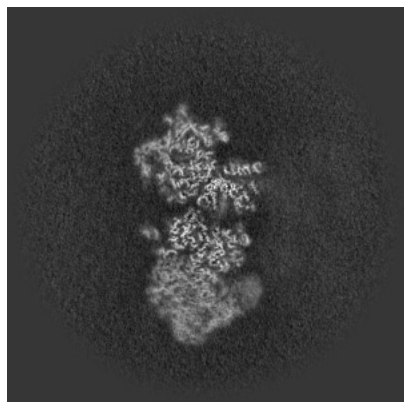


Z

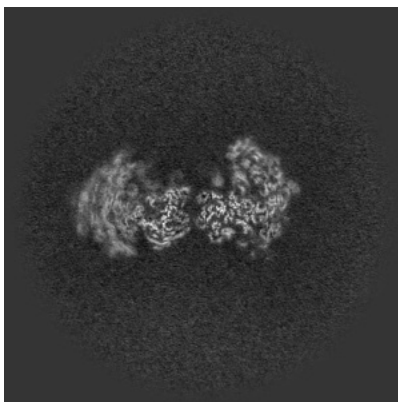
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

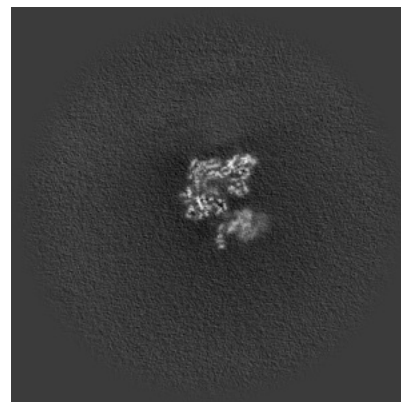
6.2.1 Primary map



X Index: 234

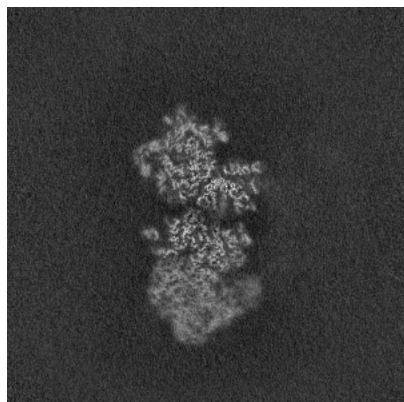


Y Index: 234

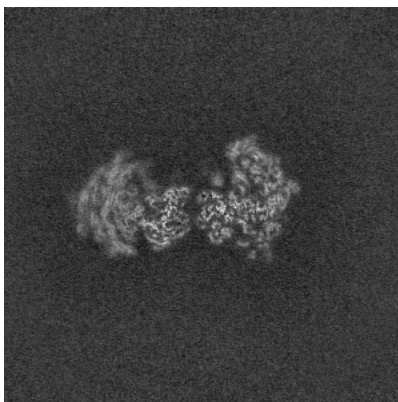


Z Index: 234

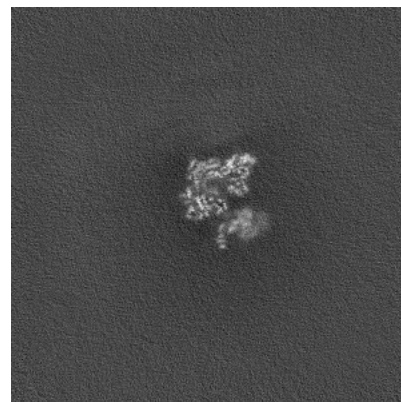
6.2.2 Raw map



X Index: 234



Y Index: 234

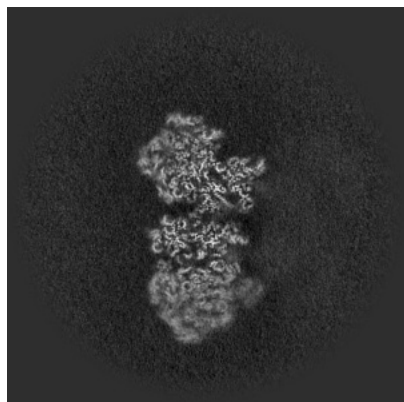


Z Index: 234

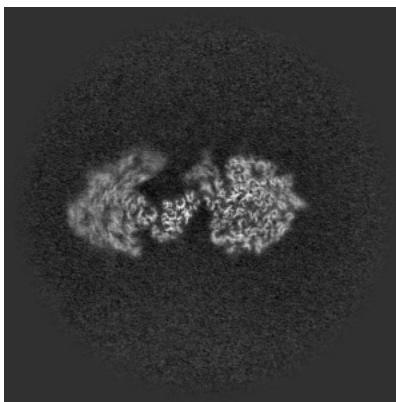
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

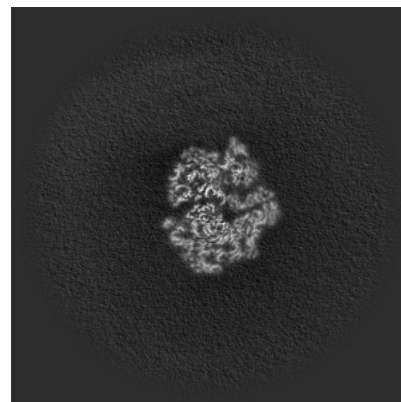
6.3.1 Primary map



X Index: 226

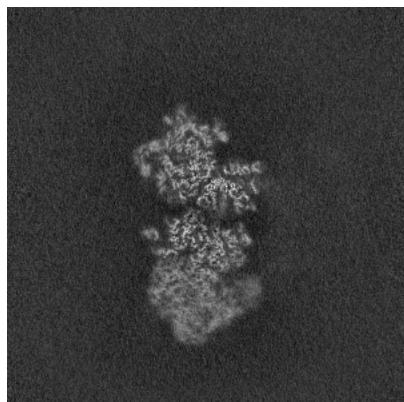


Y Index: 208

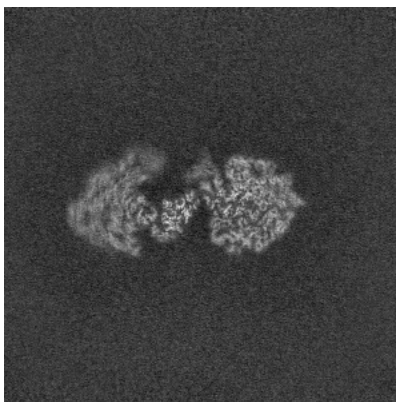


Z Index: 274

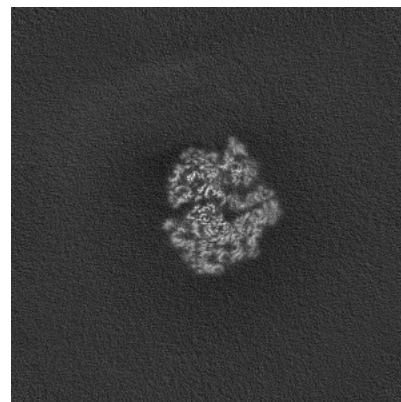
6.3.2 Raw map



X Index: 234



Y Index: 208

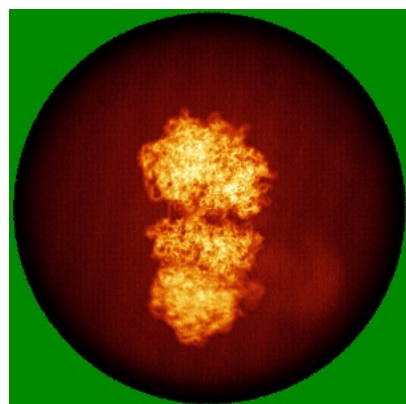


Z Index: 274

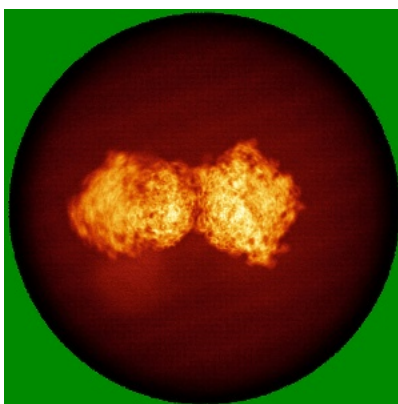
The images above show the largest variance slices of the map in three orthogonal directions.

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

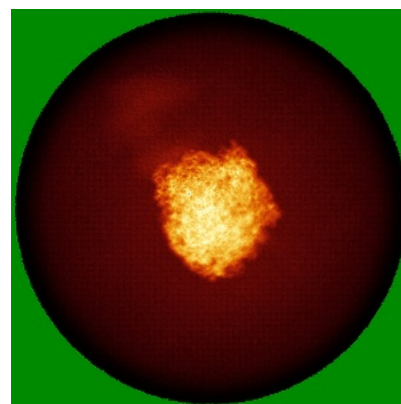
6.4.1 Primary map



X

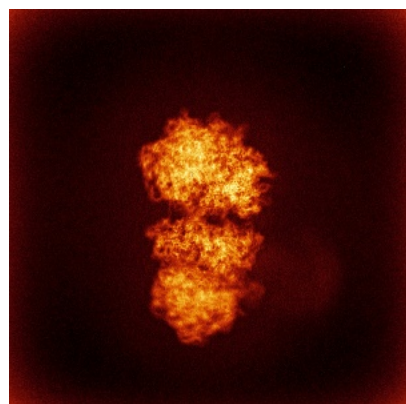


Y

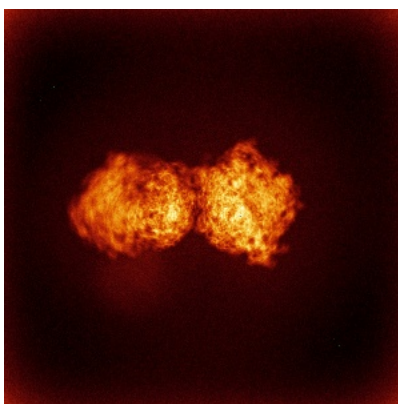


Z

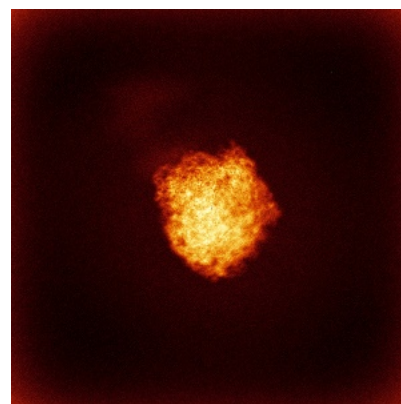
6.4.2 Raw map



X



Y

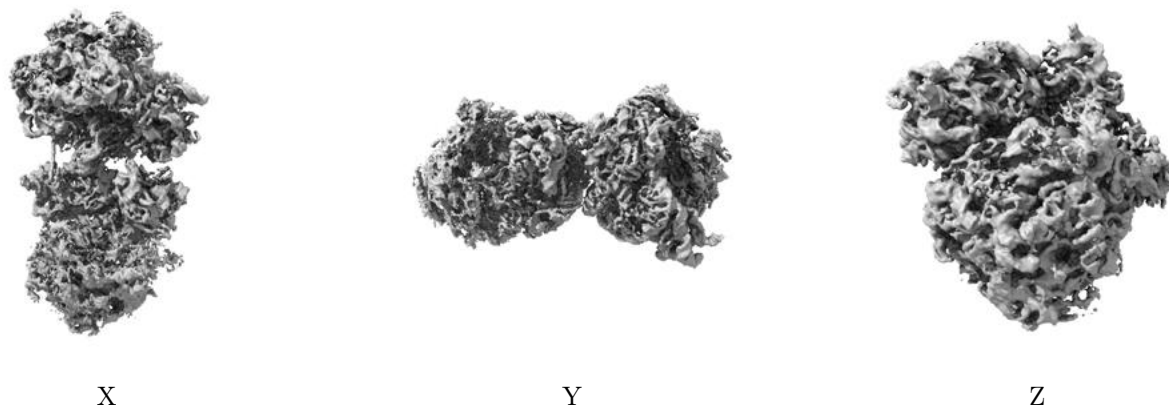


Z

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.

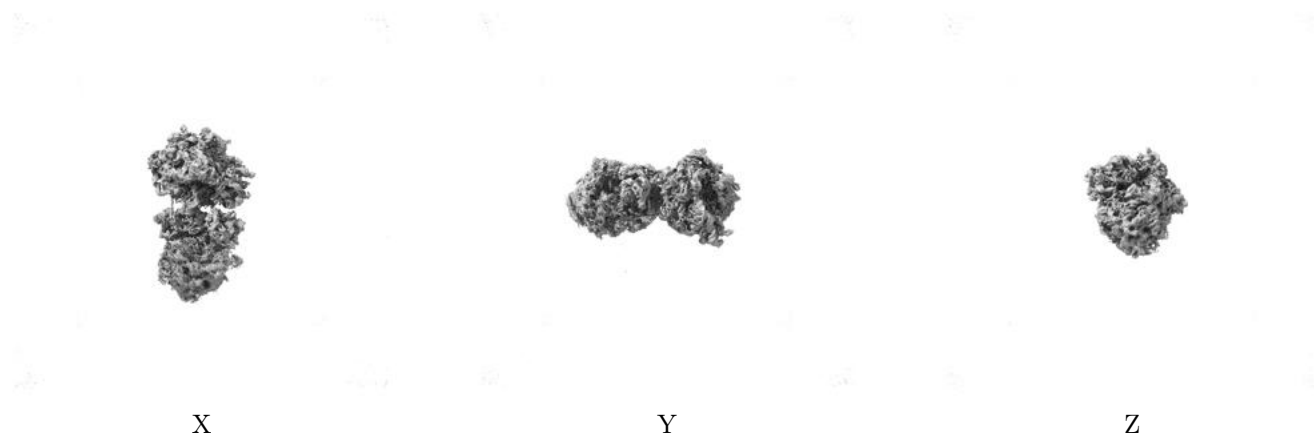
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

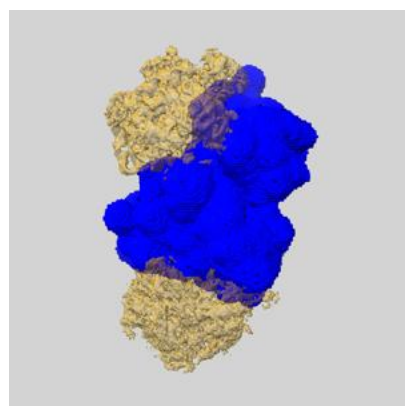
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

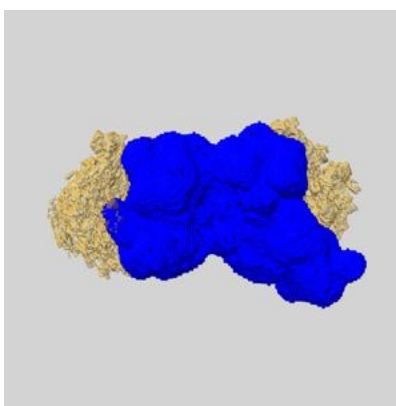
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

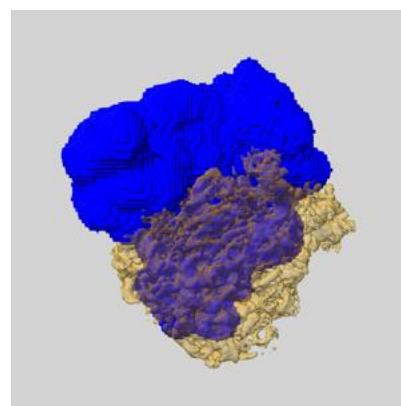
6.6.1 emd_19055_msk_1.map [i](#)



X



Y

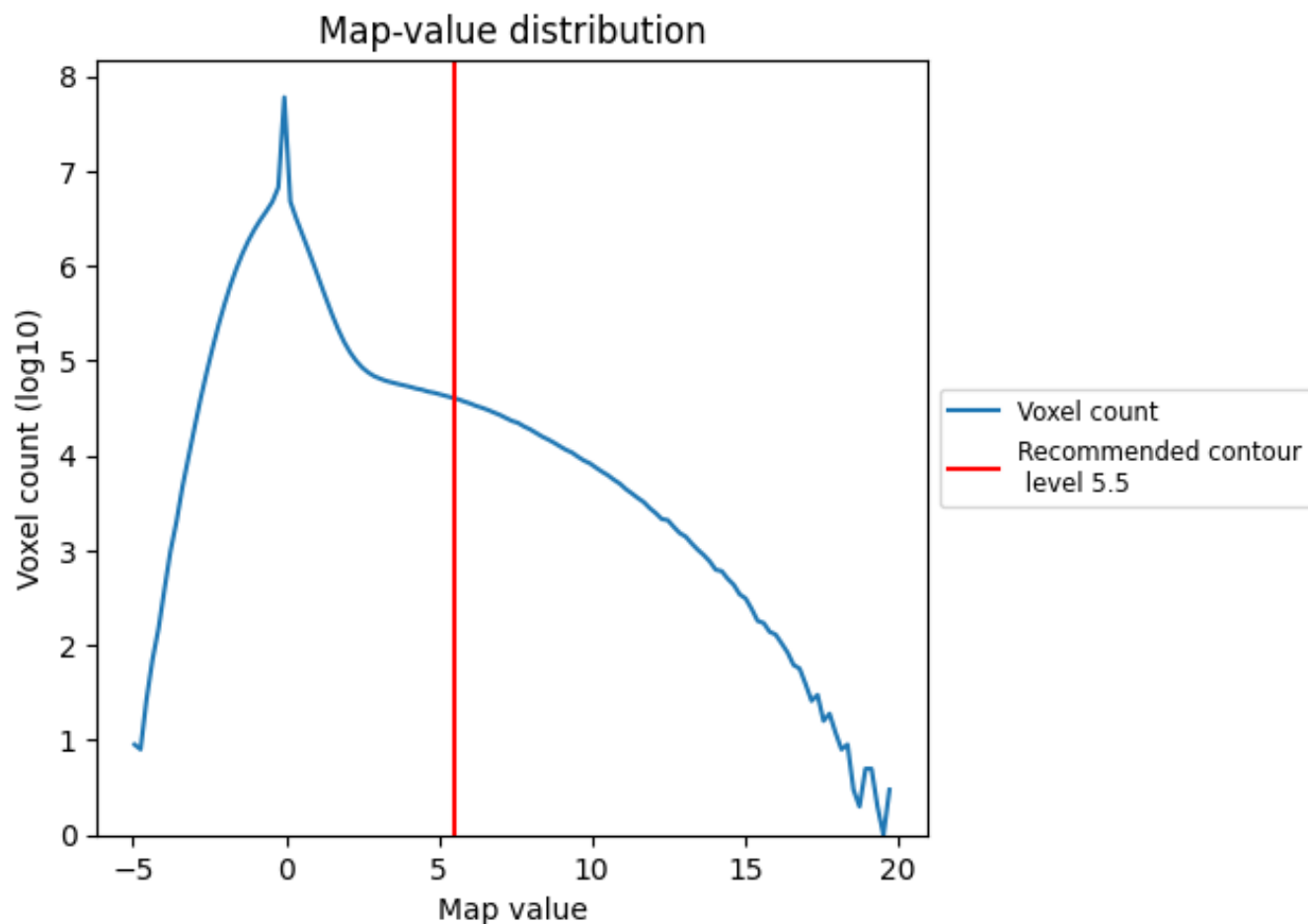


Z

7 Map analysis [i](#)

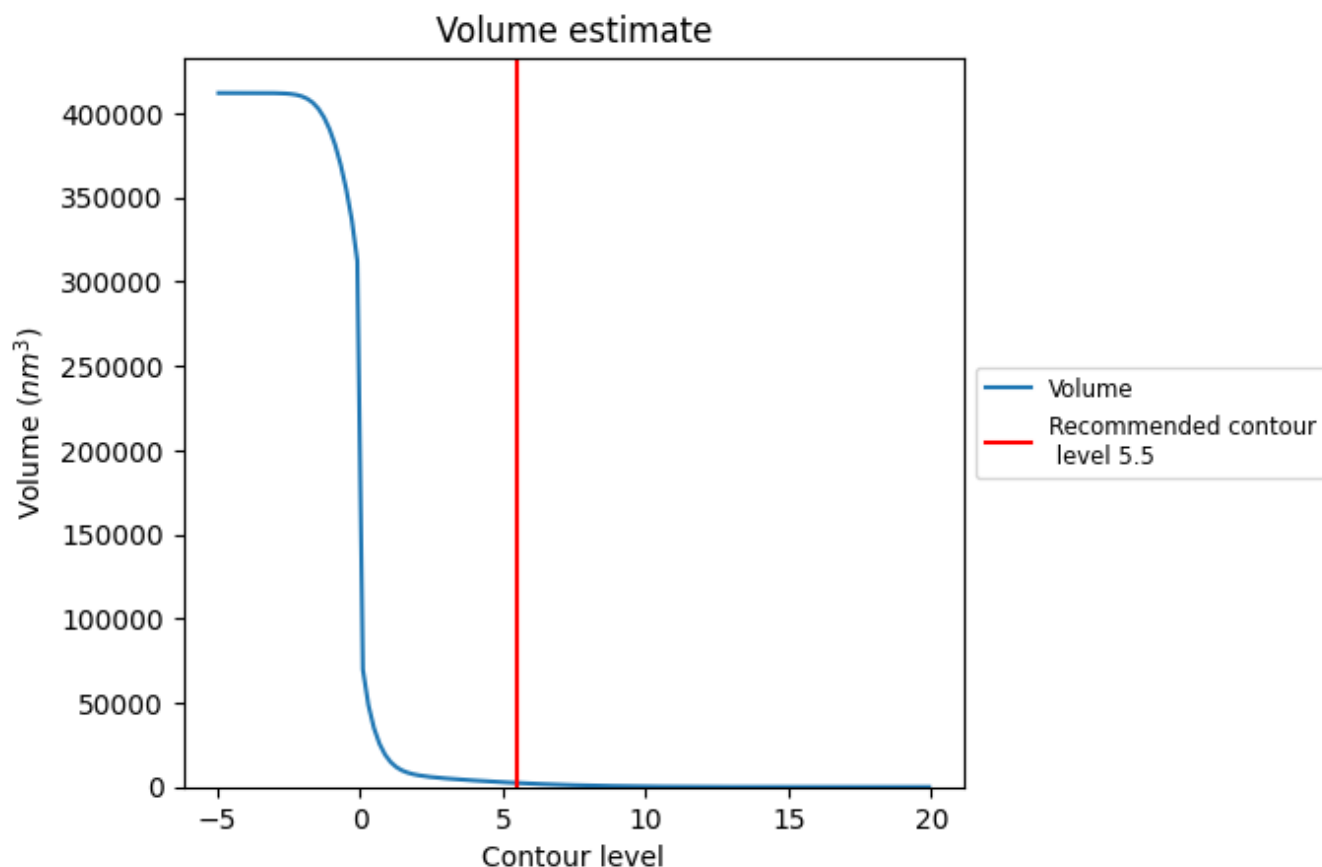
This section contains the results of statistical analysis of the map.

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.

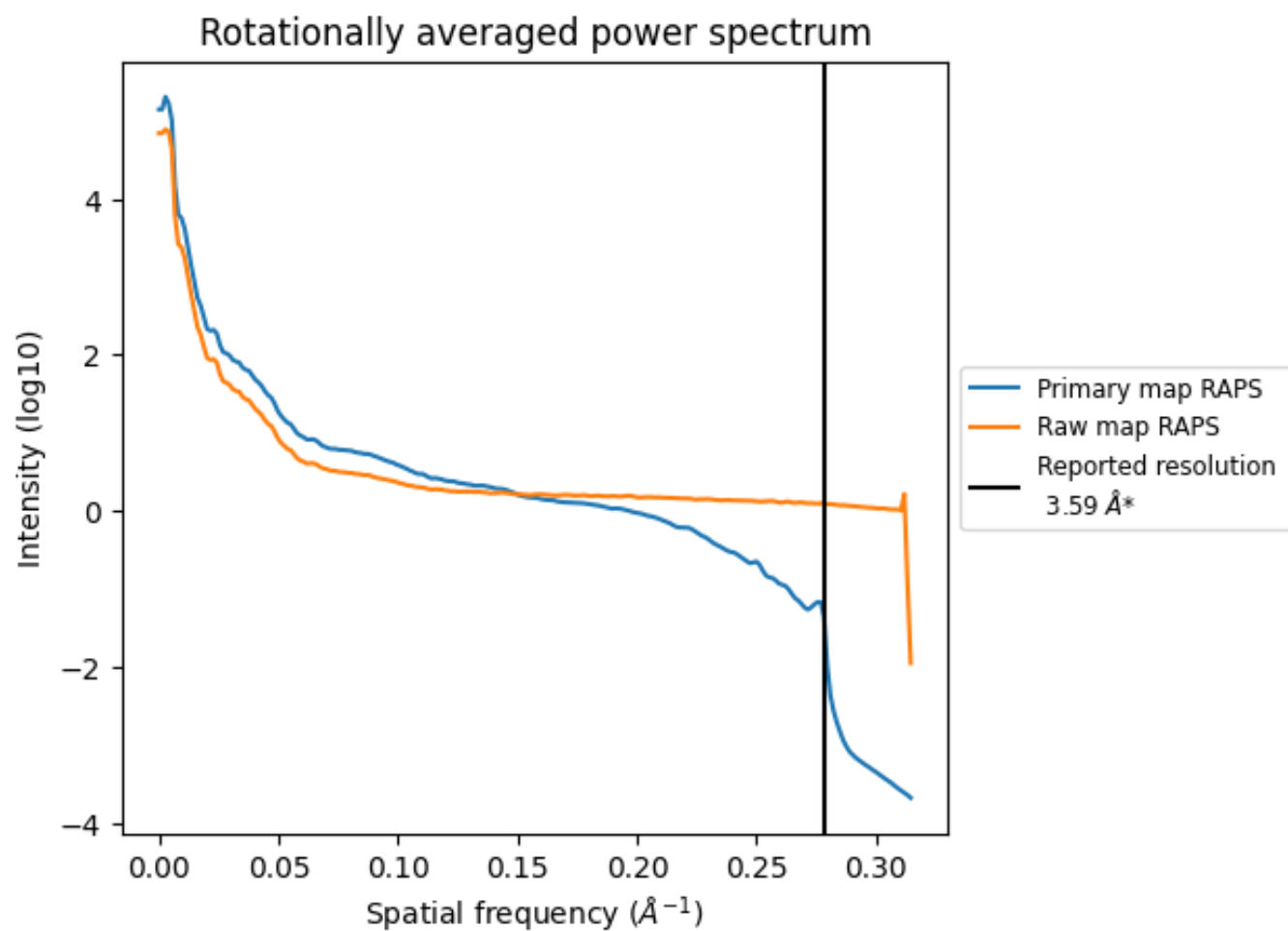
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2378 nm³; this corresponds to an approximate mass of 2148 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 ⓘ

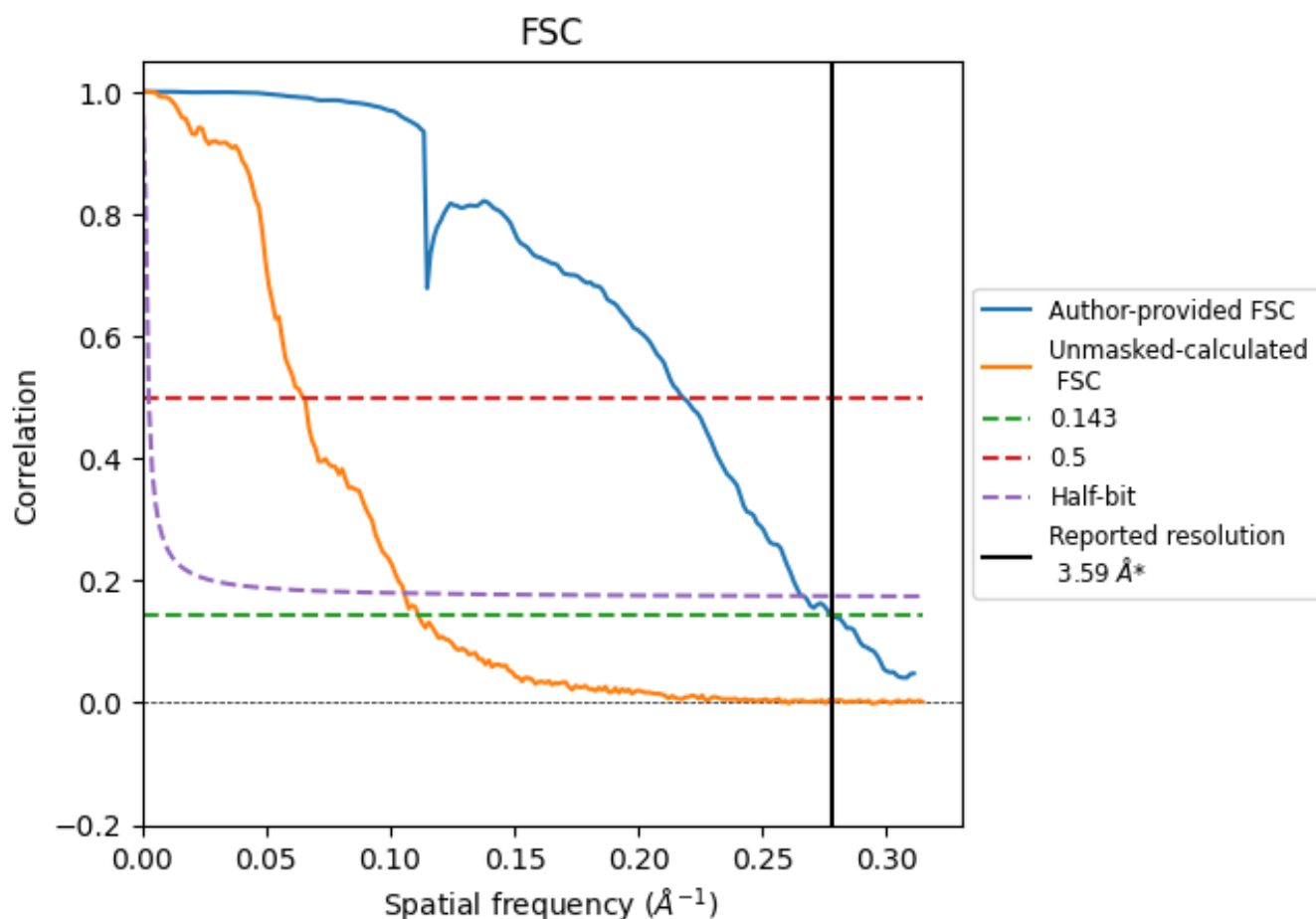


*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

8.2 Resolution estimates [i](#)

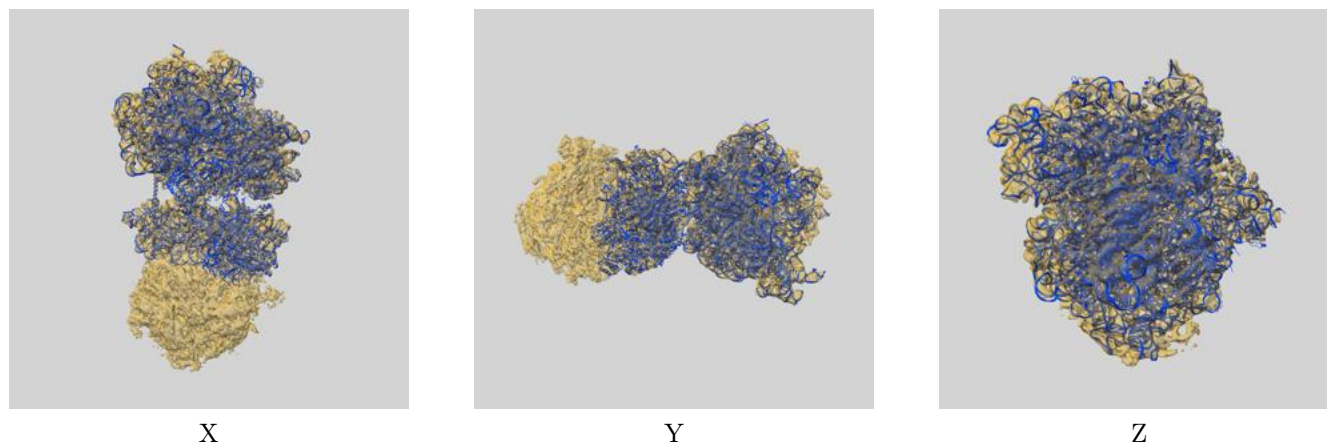
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.59	-	-
Author-provided FSC curve	3.59	4.59	3.75
Unmasked-calculated*	8.98	15.43	9.46

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.98 differs from the reported value 3.59 by more than 10 %

9 Map-model fit [i](#)

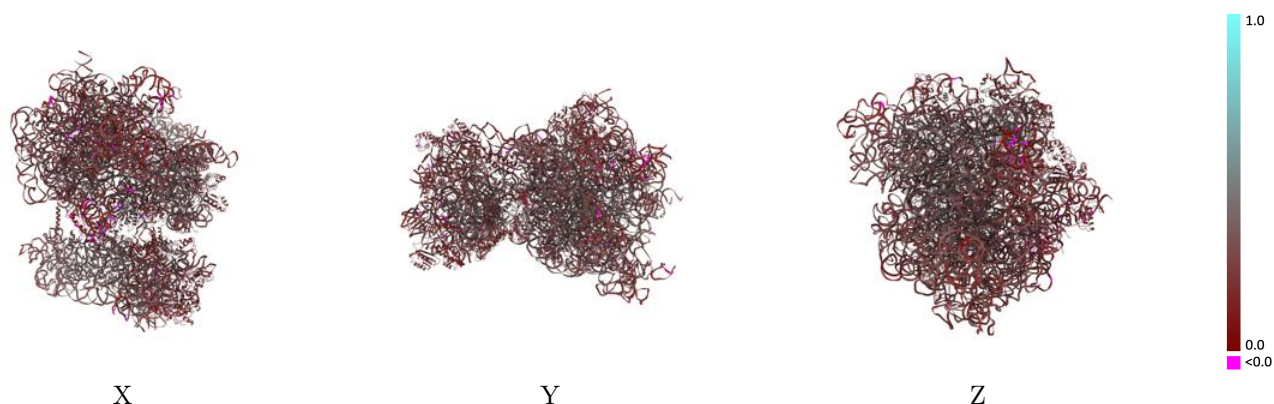
This section contains information regarding the fit between EMDB map EMD-19055 and PDB model 8RCM. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

9.1 Map-model overlay [i](#)



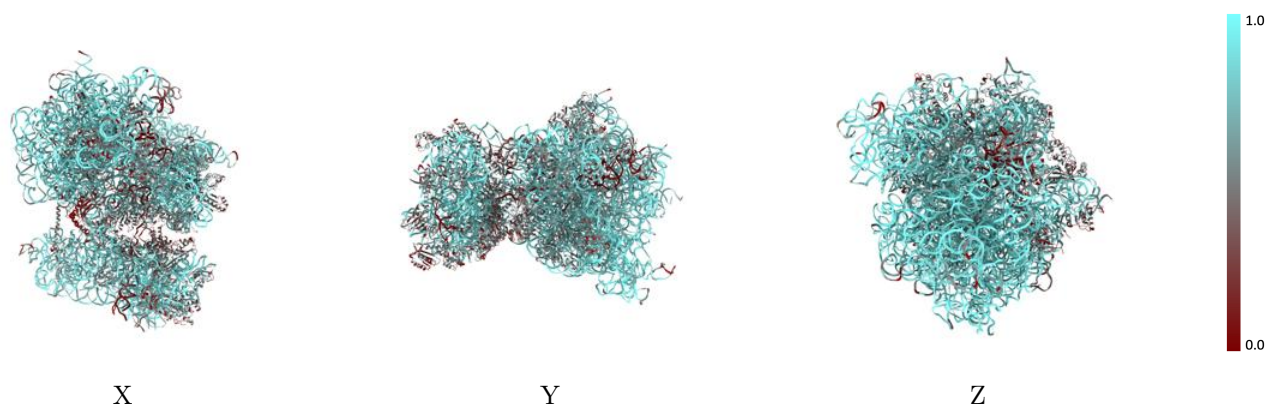
The images above show the 3D surface view of the map at the recommended contour level 5.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



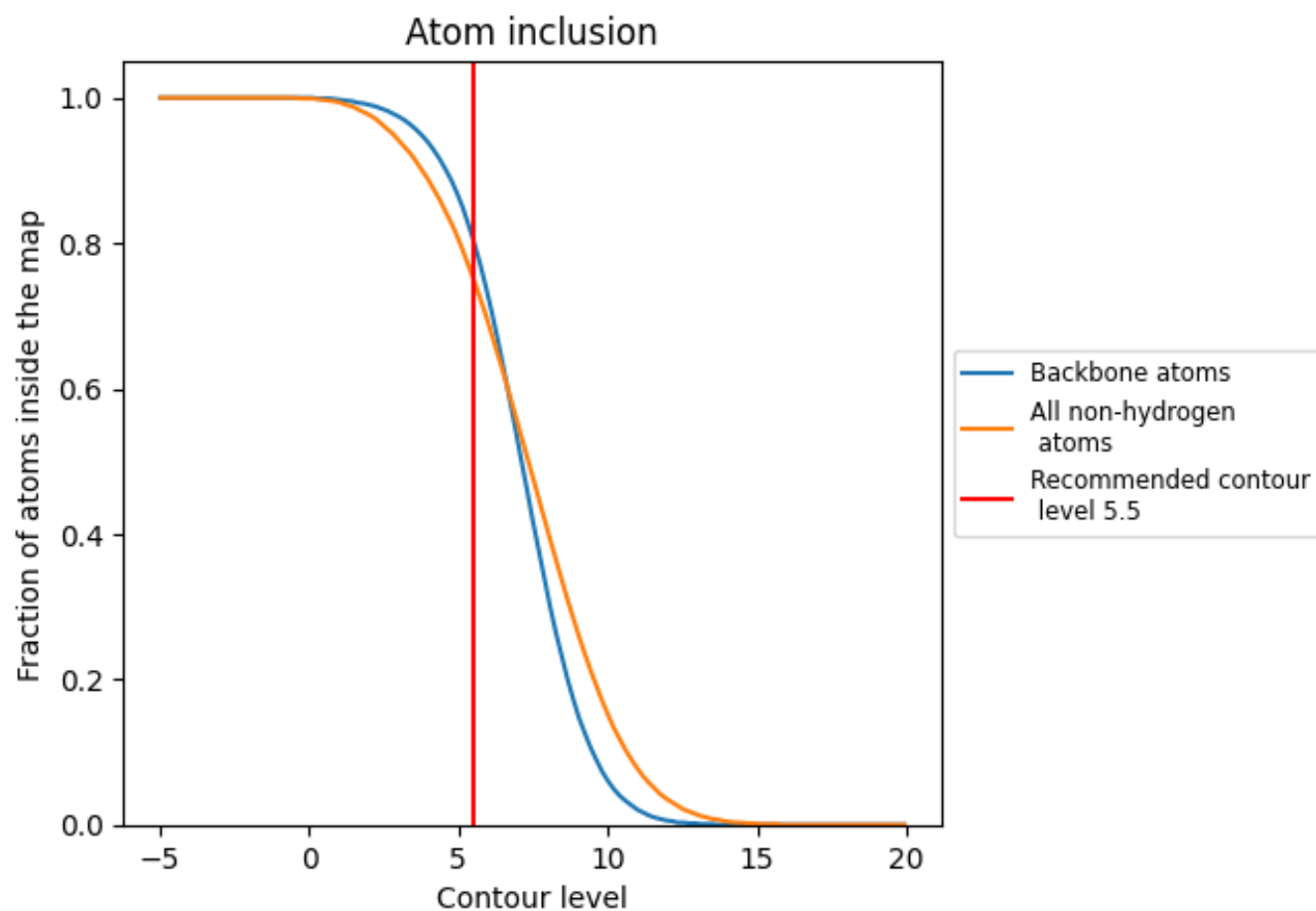
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 75% 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 (5.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7520	 0.2940
12	 0.5270	 0.2910
32	 0.4620	 0.2190
4	 0.3430	 0.2070
62	 0.4910	 0.2360
71	 0.8470	 0.2920
72	 0.8650	 0.2920
82	 0.8060	 0.2330
A1	 0.8830	 0.3190
A2	 0.8970	 0.3360
B	 0.3540	 0.2340
B2	 0.4440	 0.2820
C1	 0.4210	 0.2750
C2	 0.5570	 0.3060
D1	 0.4800	 0.3110
D2	 0.3930	 0.2480
E1	 0.4830	 0.2960
E2	 0.5480	 0.3340
F1	 0.2740	 0.2360
F2	 0.5110	 0.3180
G1	 0.4380	 0.2290
G2	 0.5260	 0.2900
H1	 0.5020	 0.2720
H2	 0.5360	 0.3120
I1	 0.5150	 0.2550
I2	 0.5860	 0.3060
J1	 0.4190	 0.2760
J2	 0.4860	 0.3120
K1	 0.4080	 0.2440
K2	 0.5220	 0.3430
L1	 0.5570	 0.3230
L2	 0.5650	 0.3120
M1	 0.4270	 0.2010
M2	 0.5560	 0.2720
N1	 0.5150	 0.2500



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Chain	Atom inclusion	Q-score
N2	 0.6150	 0.2860
O1	 0.4930	 0.2440
O2	 0.5670	 0.2910
P1	 0.5770	 0.3270
Q1	 0.4760	 0.2590
Q2	 0.5140	 0.2970
R1	 0.3700	 0.2170
R2	 0.4700	 0.2970
S1	 0.4480	 0.2090
S2	 0.6000	 0.2810
T1	 0.5700	 0.2290
U1	 0.3340	 0.2020
U2	 0.4390	 0.2850
V2	 0.2970	 0.2080
W	 0.7610	 0.2860
W1	 0.7040	 0.2790
X2	 0.3830	 0.1750
Y1	 0.0680	 0.1700
Y2	 0.0530	 0.1930
Z1	 0.0130	 0.2250
a2	 0.0620	 0.1240
b2	 0.5690	 0.3390
e2	 0.4320	 0.2030
g2	 0.4180	 0.2360
h2	 0.4110	 0.2530
i2	 0.4300	 0.2880
l2	 0.5550	 0.2580
o2	 0.1220	 -0.0450
p	 0.0850	 0.3140
r2	 0.4130	 0.1690
z2	 0.4770	 0.1930