



wwPDB EM Validation Summary Report ⓘ

Jun 18, 2026 – 01:55 am BST

PDB ID : 7NWW / pdb_00007nww
EMDB ID : EMD-12636
Title : CspA-27 cotranslational folding intermediate 1
Authors : Agirrezabala, X.; Samatova, E.; Macher, M.; Liutkute, M.; Gil-Carton, D.;
Novacek, J.; Valle, M.; Rodnina, M.V.
Deposited on : 2021-03-17
Resolution : 3.05 Å(reported)
Based on initial model : 6ORE

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

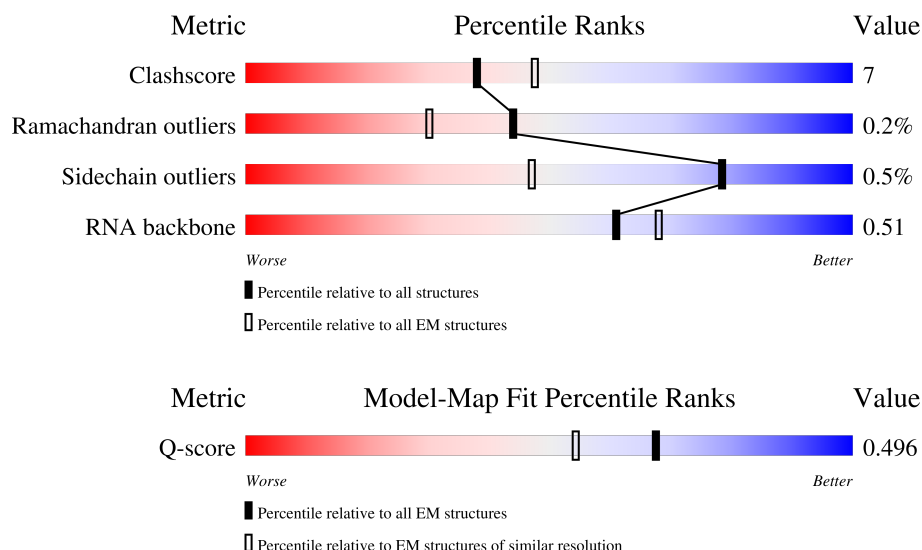
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 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	13971 (2.55 - 3.55)

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	

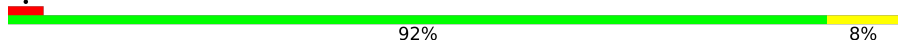
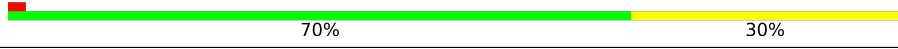
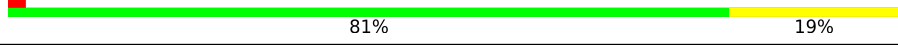
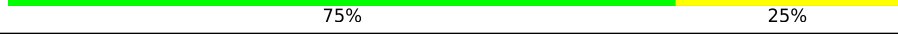
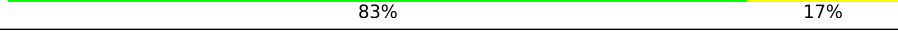
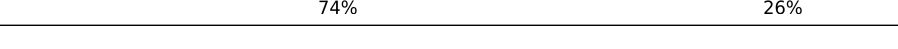
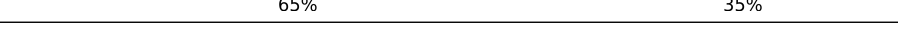
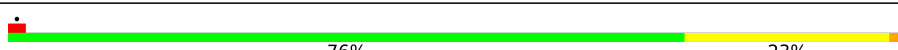
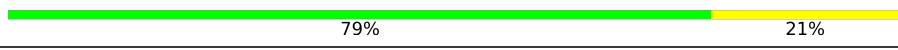
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Mol	Chain	Length	Quality of chain
4	4	6	
5	C	271	
6	D	209	
7	E	201	
8	F	177	
9	G	175	
10	H	149	
11	I	142	
12	J	123	
13	K	144	
14	L	136	
15	M	119	
16	N	116	
17	O	114	
18	P	117	
19	Q	103	
20	R	110	
21	S	94	
22	T	103	
23	U	94	
24	V	80	
25	W	77	
26	X	62	
27	Y	58	
28	Z	66	

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Mol	Chain	Length	Quality of chain
29	a	56	
30	b	52	
31	c	46	
32	d	64	
33	e	38	
34	f	225	
35	g	208	
36	h	205	
37	i	156	
38	j	104	
39	k	151	
40	l	129	
41	m	127	
42	n	99	
43	o	117	
44	p	123	
45	q	116	
46	r	100	
47	s	88	
48	t	82	
49	u	80	
50	v	66	
51	w	83	
52	x	86	
53	y	70	

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Mol	Chain	Length	Quality of chain
54	z	88	38% 40% 20%
55	B	27	19% 19% 52% 19% 11%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145149 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 23S rRNA.

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

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

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 rRNA.

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	6	Total	C	N	O	P	0	0
			126	56	20	44	6		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	80	Total	C	N	O	S	0	0
			601	370	121	109	1		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	88	Total	C	N	O	P	0	0
			1891	841	341	621	88		

- Molecule 55 is a protein called 7.4 kDa cold shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	27	Total	C	N	O	S	0	0
			205	132	32	39	2		

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

Mol	Chain	Residues	Atoms		AltConf
56	1	278	Total 278	Mg 278	0
56	2	119	Total 119	Mg 119	0
56	3	8	Total 8	Mg 8	0
56	C	1	Total 1	Mg 1	0
56	D	1	Total 1	Mg 1	0
56	P	1	Total 1	Mg 1	0
56	a	1	Total 1	Mg 1	0
56	h	1	Total 1	Mg 1	0
56	q	1	Total 1	Mg 1	0
56	z	2	Total 2	Mg 2	0

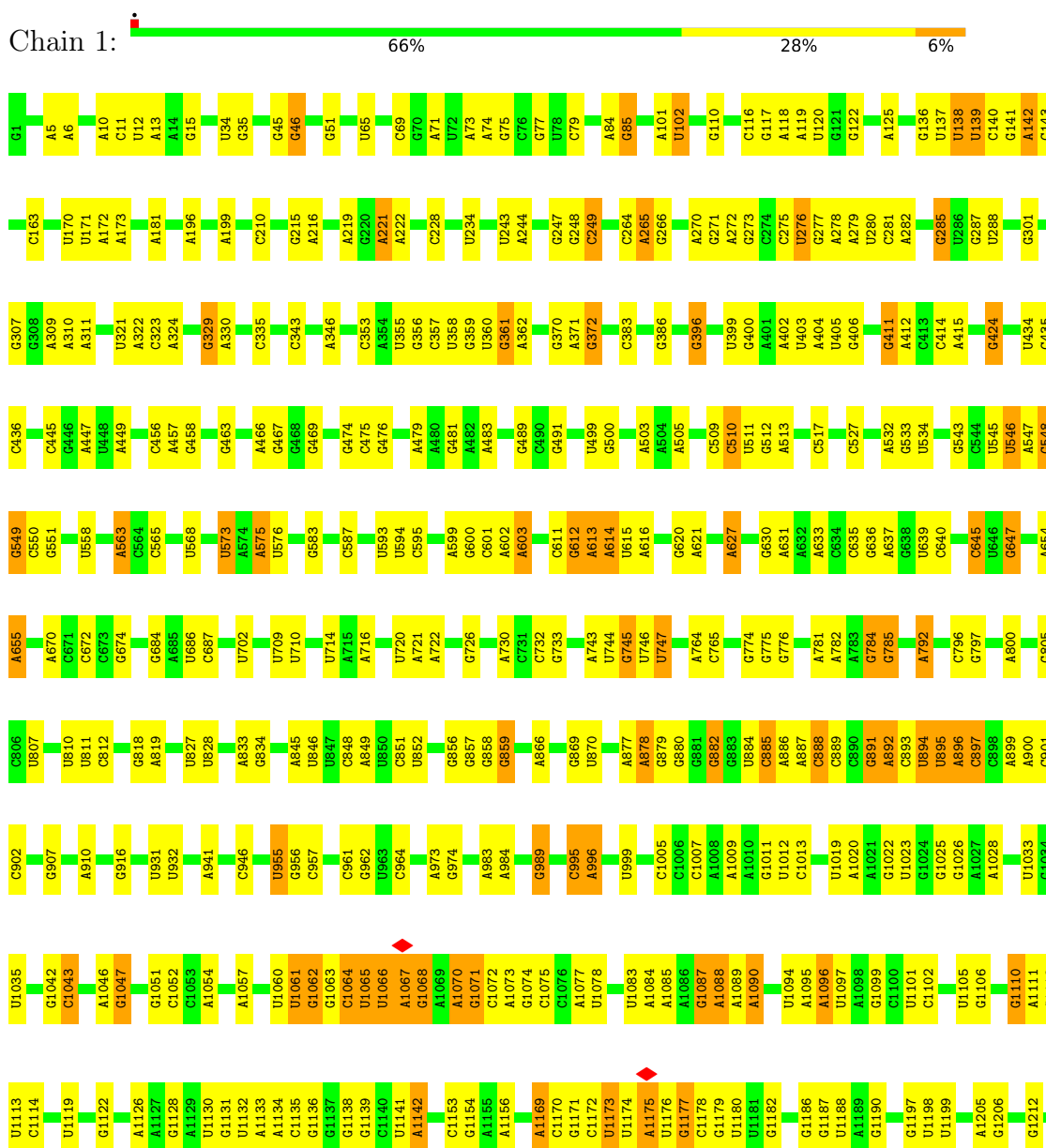
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Z	1	Total 1	Zn 1	0
57	e	1	Total 1	Zn 1	0

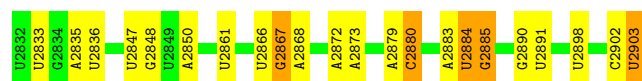
3 Residue-property plots

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 rRNA

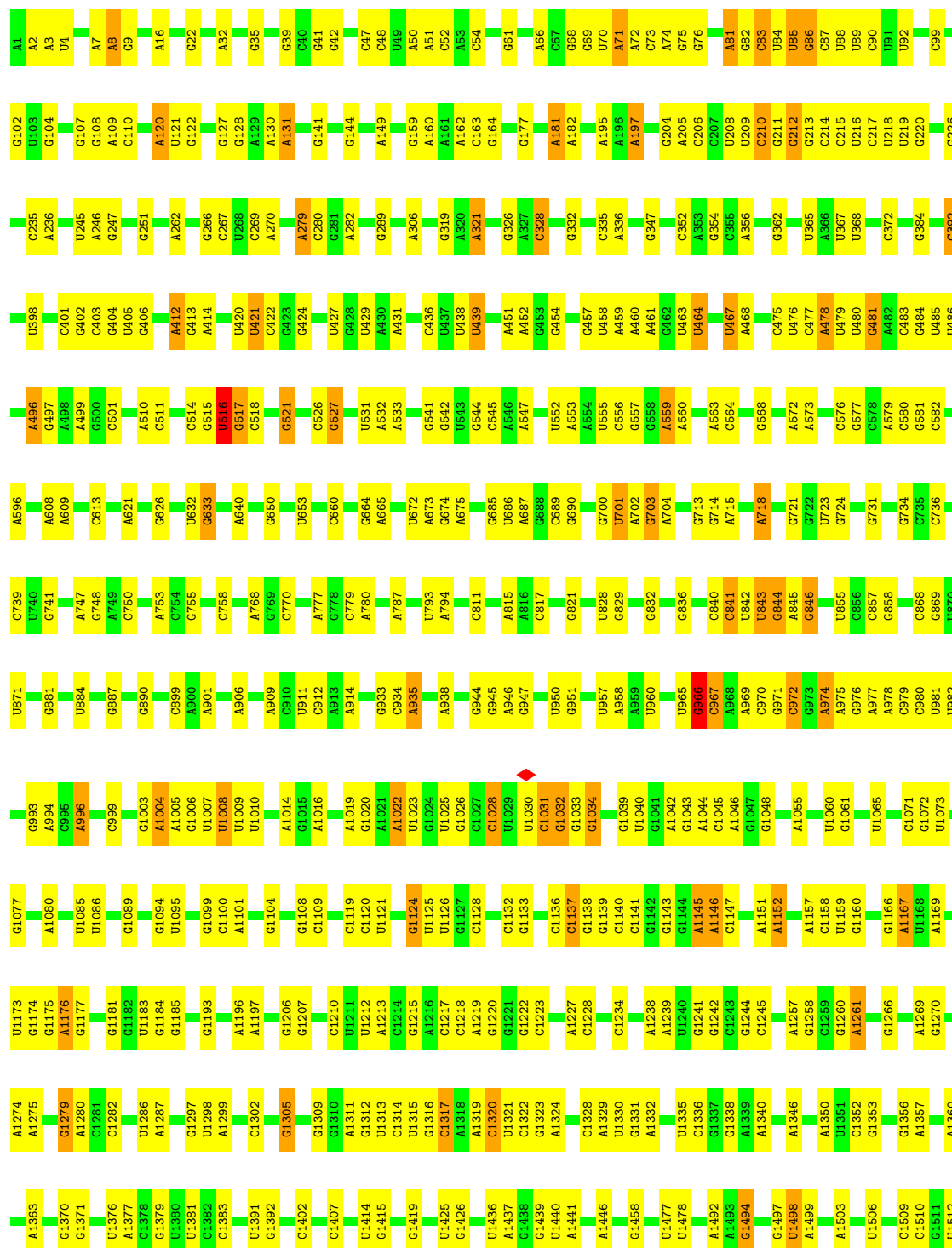


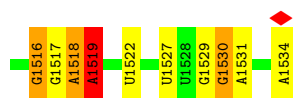
A2725	G2567	A2476	C2347	C2258	U2167	A2101	U1993	A1858	G1738	A1569	U1468	C1349	U1217
A2726	G2570	U2477	C2350	A2266	G2168	G2102	C1997	G1862	G1743	C1577	A1469	C1350	G1218
U2728	U2571	A2478	A2267	A2267	A2169	C2103	G2002	G1863	U1705	U1578	A1470	U1351	U1231
G2729	A2572	U2479	G2357	A2273	A2170	U2106	A2009	U1865	A1746	A1579	G1475	G1357	G1232
G2732	C2573	A2480	A2358	A2276	A2172	G2107	G2012	C1868	U1747	A1580	U1476	G1358	G1236
A2733	G2574	G2481	C2359	G2279	A2173	A2108	G2012	G1869	A1754	G1581	G1482	A1237	A1237
A2733	C2575	A2482	G2360	G2279	C2174	U2109	U2022	U1870	A1755	A1583	G1363	G1238	G1238
G2744	U2580	G2483	G2361	C2283	A2176	G2110	G2023	A1871	G1756	U1584	U1485	A1365	A1244
G2744	G2581	G2484	C2364	C2283	U2177	U2111	C2024	A1872	A1872	C1585	U1486	A1365	A1244
A2748	U2585	C2486	G2365	G2286	C2178	G2112	G2024	G1873	C1764	A1586	G1368	G1368	A1247
G2751	U2586	U2491	G2375	A2287	C2179	U2113	C2025	U1883	G1770	G1587	A1490	G1369	G1248
A2752	C2591	G2494	A2377	A2288	U2180	A2114	U2026	G1884	U1770	U1588	C1370	U1249	U1249
A2753	G2592	G2495	A2378	U2291	U2181	G2115	A2030	A1912	A1773	U1590	C1493	G1371	G1250
U2756	G2593	G2496	A2378	G2292	U2182	G2116	G2032	A1913	U1779	A1494	C1251	G1251	C1251
A2757	A2602	A2497	G2383	G2293	A2184	U2118	G2033	G1896	U1779	A1591	A1496	U1379	A1253
A2757	C2498	C2498	U2384	G2294	U2185	A2119	A2033	G1906	U1782	A1608	A1503	G1380	A1253
A2764	U2605	C2499	C2385	A2297	U2186	G2120	C2043	G1907	U1782	A1618	A1503	G1256	G1256
A2766	U2609	G2502	A2386	U2300	U2187	G2121	C2043	U1911	A1784	A1622	A1504	A1383	G1266
A2766	U2609	A2503	U2387	C2301	U2188	U2122	C2050	A1912	A1789	A1634	A1509	A1386	G1271
C2767	U2613	U2504	U2402	U2302	U2189	G2123	A2051	A1913	C1790	U1634	G1510	A1387	A1272
G2777	A2614	G2505	C2403	U2302	A2190	G2124	A2052	G1914	A1791	U1647	G1514	A1393	A1275
A2778	U2616	U2506	A2406	U2305	U2192	G2125	G2053	3TD1915	A1791	U1648	A1515	U1394	C1278
U2779	C2619	C2507	A2407	U2306	G2193	A2126	A2054	A1916	U1796	G1649	A1515	U1394	C1278
G2780	U2629	G2508	A2407	U2308	U2194	G2127	G2055	U1917	U1798	A1650	A1522	U1397	G1279
C2788	U2636	U2511	G2415	G2308	U2195	G2128	A2060	U1923	U1799	G1651	U1523	U1407	G1283
G2791	U2637	A2512	U2423	A2309	G2196	C2129	G2061	C1924	C1800	A1652	U1524	G1407	G1283
A2792	U2637	U2513	U2423	C2310	U2197	U2130	A2062	A1801	A1801	G1659	A1525	U1408	A1286
C2793	C2646	G2515	A2424	C2312	U2198	U2131	C2063	G1930	A1802	U1659	C1526	G1410	A1286
C2794	U2655	A2516	A2426	A2314	G2204	U2132	C2064	C2064	A1808	A1664	A1527	U1411	C1286
U2797	U2656	A2517	C2427	G2315	A2211	A2134	C2065	A1936	A1809	U1664	A1528	U1411	C1286
U2798	A2657	U2518	G2428	G2316	A2211	U2139	A2065	A1937	A1809	A1668	G1529	G1300	G1300
U2798	C2658	U2519	G2429	A2317	A2225	G2140	G2069	A1938	A1810	A1671	G1530	A1301	A1301
A2800	U2663	G2520	A2430	G2318	A2225	G2141	C2072	U1939	A1811	U1671	A1532	G1416	G1416
U2804	G2664	G2523	U2431	G2319	U2229	A2142	C2072	G1964	C1816	U1672	A1532	G1417	G1417
C2805	U2676	G2529	A2435	U2321	U2233	C2143	U2076	U1955	G1817	G1673	A1534	A1419	C1315
G2808	U2687	G2532	U2441	G2323	G2234	C2145	U2079	C1962	G1824	G1686	C1536	A1420	A1321
A2809	G2687	G2535	G2445	U2324	G2235	C2146	A2080	U1962	G1824	G1687	G1537	A1427	A1322
A2810	U2689	G2535	G2448	U2325	U2236	A2147	U2081	C1967	U1827	U1688	G1538	C1428	C1323
G2811	U2690	A2542	U2449	A2326	G2238	U2149	A2082	U1971	G1828	U1688	U1539	G1429	U1326
U2818	U2698	A2547	U2450	A2328	G2239	U2150	U2086	A1970	A1829	A1700	U1541	G1430	A1327
A2820	C2699	U2547	U2457	U2329	U2243	C2151	G2087	U1971	C1833	G1715	U1542	A1432	A1328
A2821	U2552	G2458	G2458	A2333	G2246	G2152	G2093	U1972	U1834	A1544	U1543	A1433	U1330
G2822	G2714	G2553	A2459	U2334	A2247	G2157	A2094	G1980	G1835	A1722	A1544	C1437	G1341
A2823	C2715	U2554	A2459	A2335	A2248	A2168	A2095	A1981	U1835	G1723	U1554	G1450	A1342
G2824	C2716	C2467	G2467	A2336	U2249	G2159	C2096	U1982	A1847	U1729	U1554	G1451	G1343
G2825	G2717	A2468	A2468	A2336	U2250	C2160	A2097	G1983	A1848	G1730	U1559	G1452	U1344
G2831	G2718	A2469	A2469	G2345	G2251	G2161	U2098	U1991	U1856	G1732	U1566	G1452	C1345
		G2470	G2470	A2346	G2253	C2164	G2100	G1992	G1857			U1460	C1348
						C2165							
						U2166							



• Molecule 2: 16S rRNA

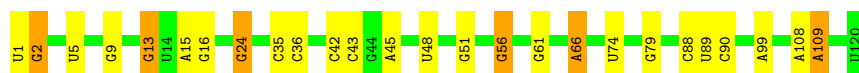
Chain 2: 66% 30%





• Molecule 3: 5S rRNA

Chain 3: 78% 17% 5%



• Molecule 4: mRNA

Chain 4: 67% 33%



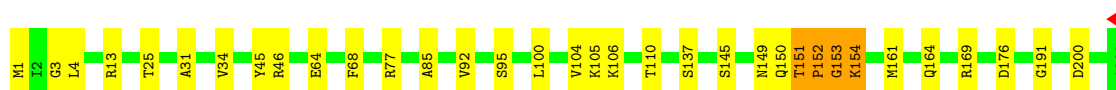
• Molecule 5: 50S ribosomal protein L2

Chain C: 78% 22%



• Molecule 6: 50S ribosomal protein L3

Chain D: 84% 14% .



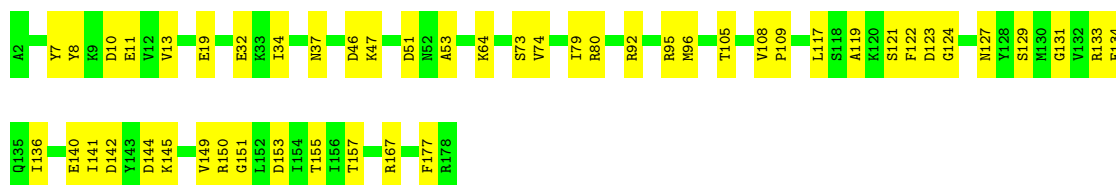
• Molecule 7: 50S ribosomal protein L4

Chain E: 79% 21%



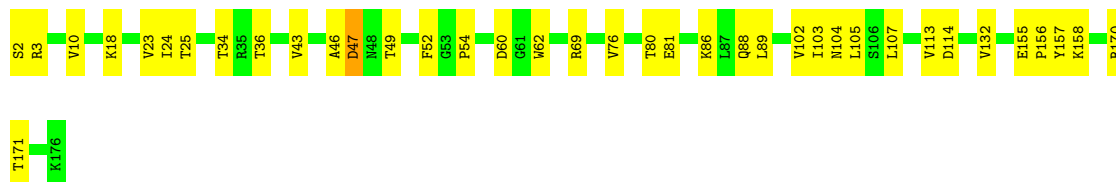
• Molecule 8: 50S ribosomal protein L5

Chain F: 72% 28%



• Molecule 9: 50S ribosomal protein L6

Chain G: 78% 21% .



• Molecule 10: 50S ribosomal protein L9

Chain H: 56% 50% 47% .



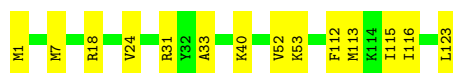
• Molecule 11: 50S ribosomal protein L13

Chain I: 85% 14% .



• Molecule 12: 50S ribosomal protein L14

Chain J: 89% 11%

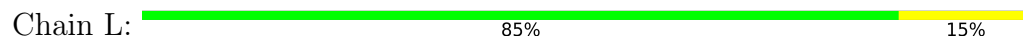


• Molecule 13: 50S ribosomal protein L15

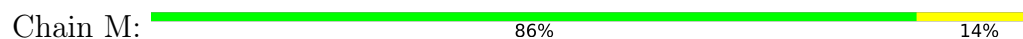
Chain K: 81% 19%



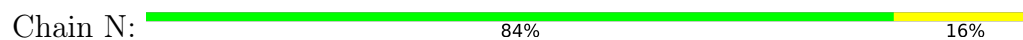
- Molecule 14: 50S ribosomal protein L16



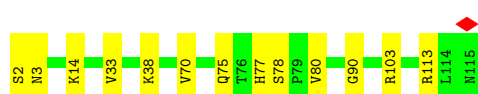
- Molecule 15: 50S ribosomal protein L17



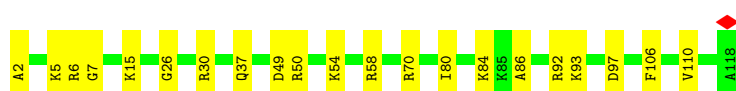
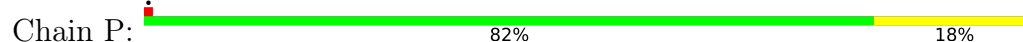
- Molecule 16: 50S ribosomal protein L18



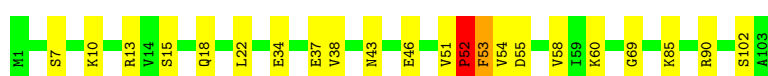
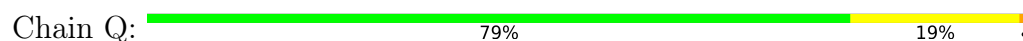
- Molecule 17: 50S ribosomal protein L19



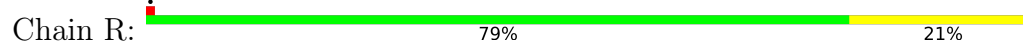
- Molecule 18: 50S ribosomal protein L20



- Molecule 19: 50S ribosomal protein L21

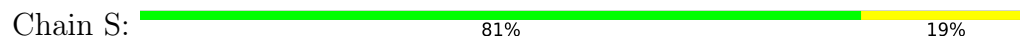


- Molecule 20: 50S ribosomal protein L22

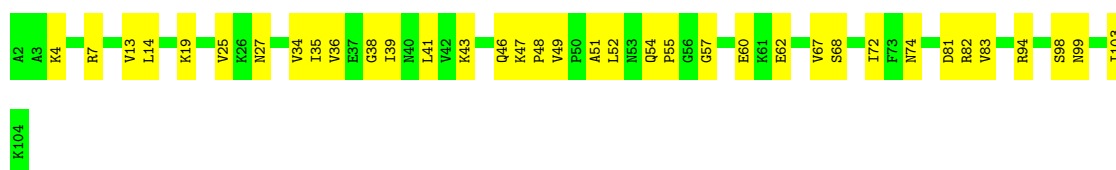




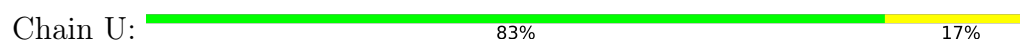
- Molecule 21: 50S ribosomal protein L23



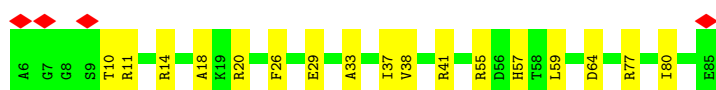
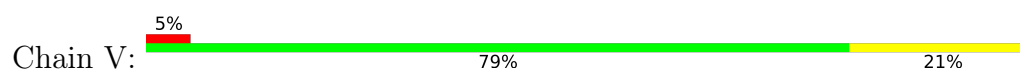
- Molecule 22: 50S ribosomal protein L24



- Molecule 23: 50S ribosomal protein L25



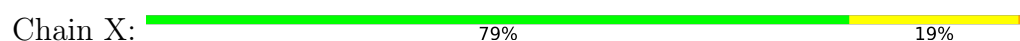
- Molecule 24: 50S ribosomal protein L27



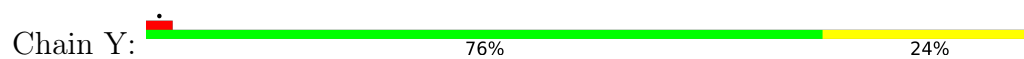
- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



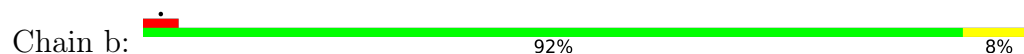
- Molecule 28: 50S ribosomal protein L31



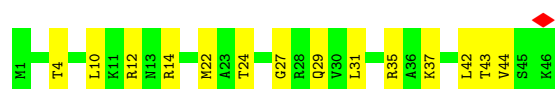
- Molecule 29: 50S ribosomal protein L32



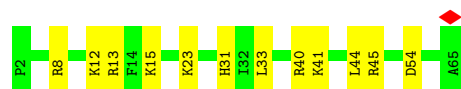
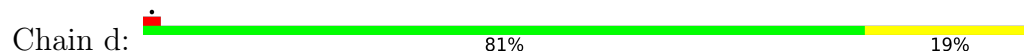
- Molecule 30: 50S ribosomal protein L33



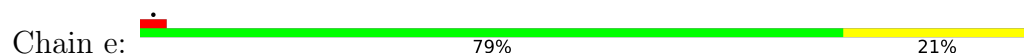
- Molecule 31: 50S ribosomal protein L34



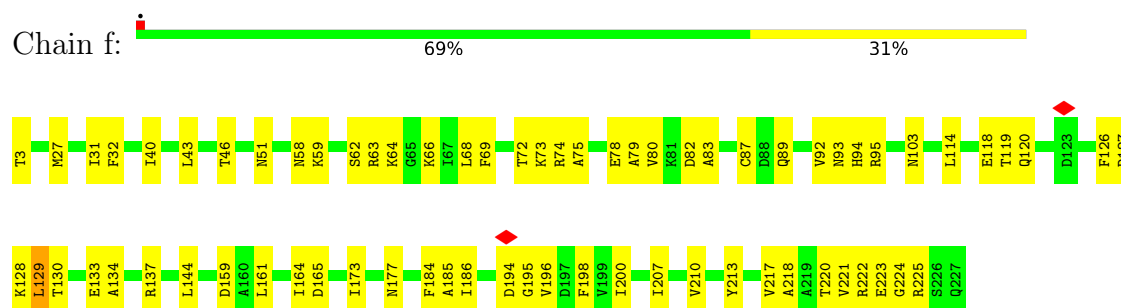
- Molecule 32: 50S ribosomal protein L35



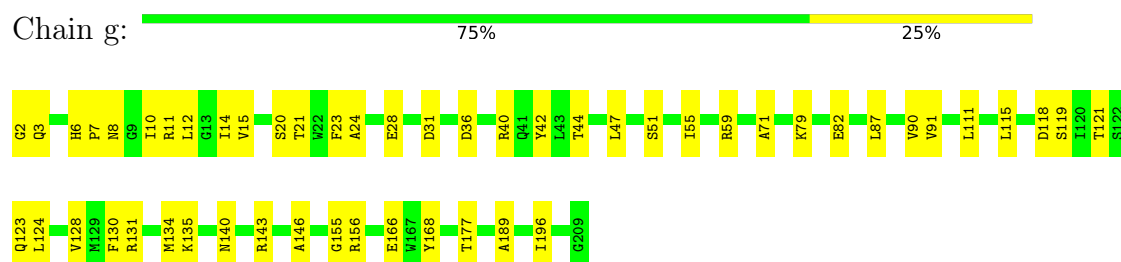
- Molecule 33: 50S ribosomal protein L36



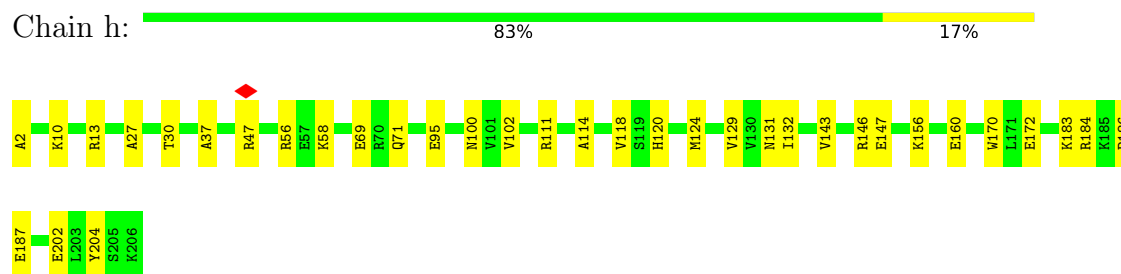
- Molecule 34: 30S ribosomal protein S2



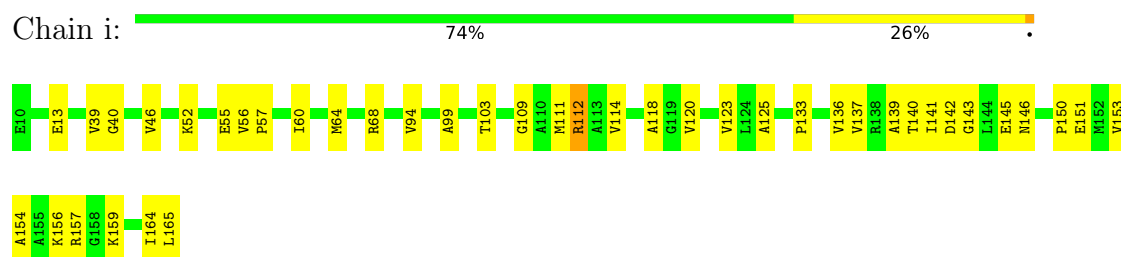
- Molecule 35: 30S ribosomal protein S3



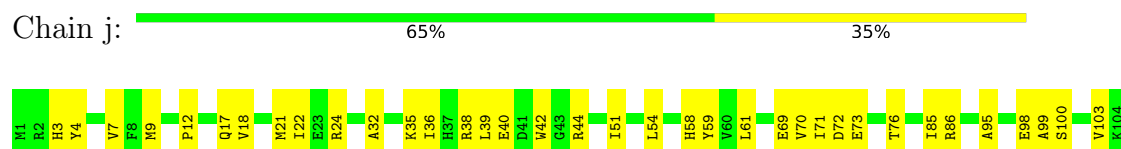
- Molecule 36: 30S ribosomal protein S4



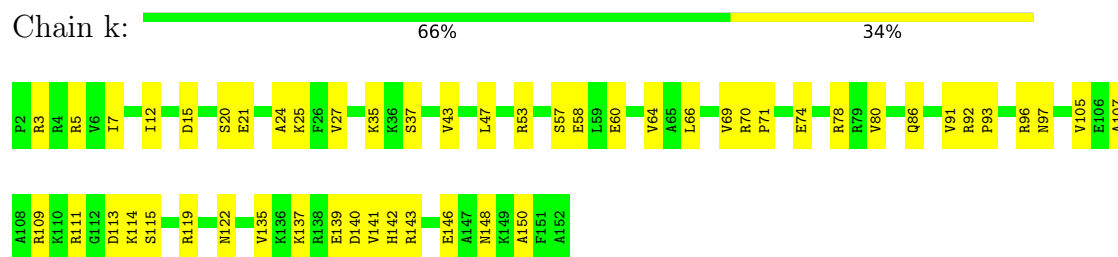
- Molecule 37: 30S ribosomal protein S5



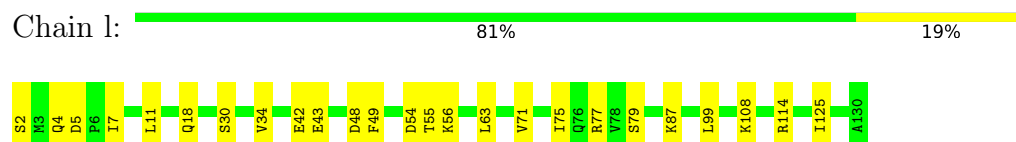
- Molecule 38: 30S ribosomal protein S6



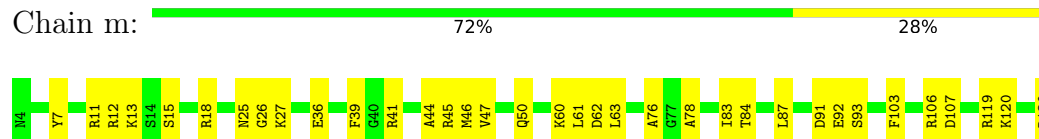
- Molecule 39: 30S ribosomal protein S7



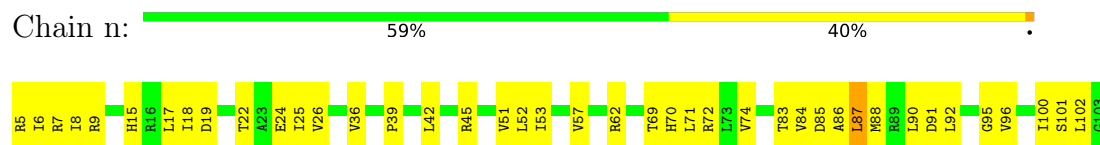
- Molecule 40: 30S ribosomal protein S8



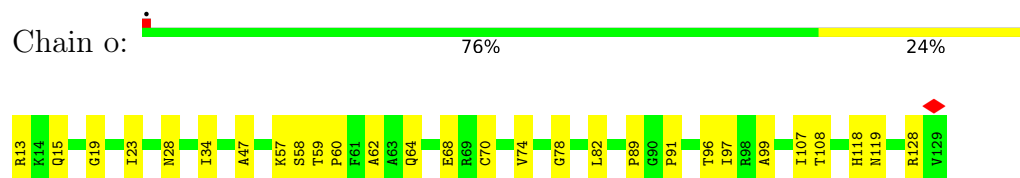
- Molecule 41: 30S ribosomal protein S9



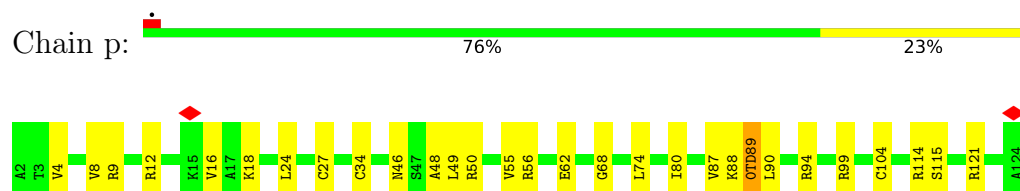
- Molecule 42: 30S ribosomal protein S10



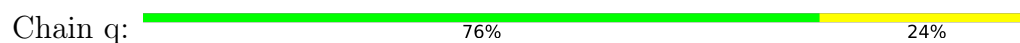
- Molecule 43: 30S ribosomal protein S11



- Molecule 44: 30S ribosomal protein S12

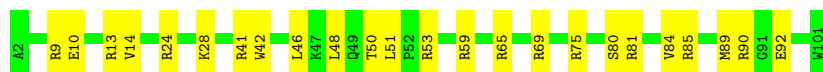


- Molecule 45: 30S ribosomal protein S13

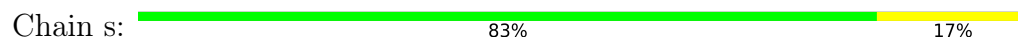




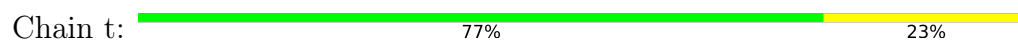
- Molecule 46: 30S ribosomal protein S14



- Molecule 47: 30S ribosomal protein S15



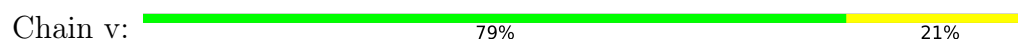
- Molecule 48: 30S ribosomal protein S16



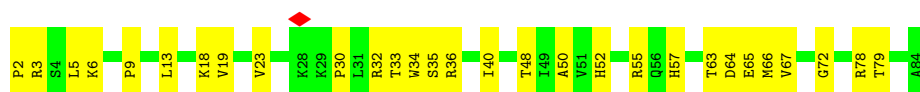
- Molecule 49: 30S ribosomal protein S17



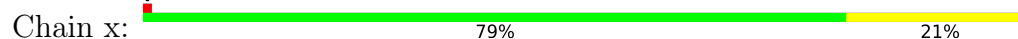
- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19

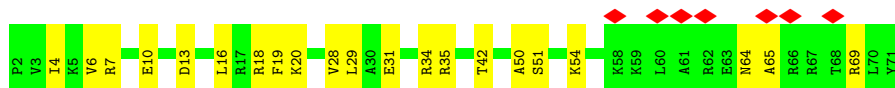


- Molecule 52: 30S ribosomal protein S20

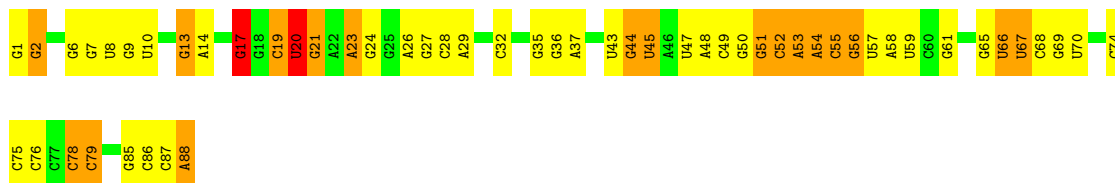




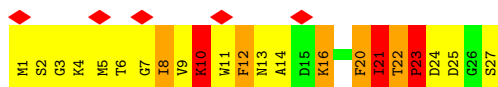
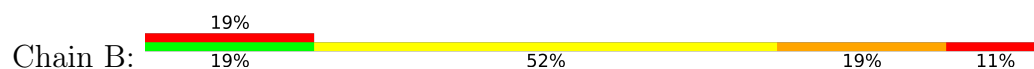
- Molecule 53: 30S ribosomal protein S21



- Molecule 54: tRNA-Ser



- Molecule 55: 7.4 kDa cold shock protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35573	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.2	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	2.2	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.136	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 1MG, PSU, 2MA, OMG, ZN, 3TD, G7M, MA6, 0TD, 5MC, UR3, 2MG, 5MU, 4OC, OMC, 6MZ, OMU, FME

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	0.49	0/69286	0.47	2/108087 (0.0%)
2	2	0.44	0/36590	0.44	0/57074
3	3	0.42	0/2872	0.42	0/4478
4	4	0.35	0/139	0.31	0/214
5	C	0.65	0/2121	0.56	0/2852
6	D	0.65	0/1586	0.55	0/2134
7	E	0.59	0/1571	0.60	0/2113
8	F	0.48	0/1434	0.60	0/1926
9	G	0.44	0/1333	0.60	0/1805
10	H	0.40	0/1122	0.90	0/1515
11	I	0.64	0/1152	0.55	0/1551
12	J	0.62	0/955	0.56	0/1279
13	K	0.62	0/1062	0.59	0/1413
14	L	0.61	0/1093	0.57	0/1460
15	M	0.66	0/964	0.63	0/1289
16	N	0.53	0/902	0.61	0/1209
17	O	0.61	0/929	0.50	0/1242
18	P	0.71	0/960	0.66	0/1278
19	Q	0.57	0/829	0.57	2/1107 (0.2%)
20	R	0.67	0/864	0.64	0/1156
21	S	0.57	0/752	0.54	0/1005
22	T	0.48	0/796	0.52	0/1062
23	U	0.54	0/766	0.54	0/1025
24	V	0.64	0/608	0.53	0/804
25	W	0.61	0/635	0.58	0/848
26	X	0.52	0/502	0.70	1/667 (0.1%)
27	Y	0.61	0/452	0.53	0/605
28	Z	0.35	0/531	0.62	0/709
29	a	0.60	0/450	0.56	0/599
30	b	0.51	0/433	0.53	0/576
31	c	0.69	0/380	0.61	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	0.68	0/513	0.64	0/676
33	e	0.64	0/303	0.55	0/397
34	f	0.44	0/1791	0.71	0/2413
35	g	0.50	0/1663	0.59	0/2241
36	h	0.51	0/1665	0.58	0/2227
37	i	0.61	0/1165	0.68	0/1568
38	j	0.49	0/867	0.58	0/1171
39	k	0.46	0/1195	0.63	0/1602
40	l	0.57	0/989	0.55	0/1326
41	m	0.50	0/1034	0.61	0/1375
42	n	0.47	0/800	0.67	0/1082
43	o	0.48	0/893	0.55	0/1205
44	p	0.55	0/960	0.59	0/1286
45	q	0.50	0/909	0.67	0/1215
46	r	0.53	0/817	0.62	0/1088
47	s	0.54	0/722	0.60	0/964
48	t	0.55	0/659	0.58	0/884
49	u	0.47	0/657	0.51	0/881
50	v	0.52	0/553	0.62	0/743
51	w	0.45	0/680	0.58	0/915
52	x	0.55	0/675	0.67	0/895
53	y	0.42	0/597	0.68	0/792
54	z	0.46	2/2062 (0.1%)	0.55	4/3208 (0.1%)
55	B	0.74	0/200	1.52	4/267 (1.5%)
All	All	0.50	2/156438 (0.0%)	0.50	13/234001 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	z	20	U	C5-C6	6.83	1.47	1.34
54	z	20	U	C2-N3	5.56	1.48	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	B	22	THR	CA-C-N	8.44	130.39	119.84
55	B	22	THR	C-N-CA	8.44	130.39	119.84
55	B	23	PRO	CA-N-CD	-8.38	100.26	112.00
54	z	8	U	O5'-P-OP1	-7.61	85.19	108.00
54	z	67	U	O5'-P-OP1	-7.23	86.32	108.00

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	535	0
2	2	32929	0	16585	274	0
3	3	2569	0	1301	13	0
4	4	126	0	65	2	0
5	C	2082	0	2154	39	0
6	D	1565	0	1616	24	0
7	E	1552	0	1619	32	0
8	F	1410	0	1444	38	0
9	G	1313	0	1358	26	0
10	H	1111	0	1148	84	0
11	I	1129	0	1162	17	0
12	J	946	0	1023	11	0
13	K	1053	0	1129	22	0
14	L	1074	0	1157	16	0
15	M	951	0	994	13	0
16	N	892	0	923	17	0
17	O	917	0	962	9	0
18	P	947	0	1019	21	0
19	Q	816	0	839	18	0
20	R	857	0	922	16	0
21	S	746	0	811	13	0
22	T	788	0	843	26	0
23	U	753	0	780	10	0
24	V	601	0	615	12	0
25	W	625	0	652	8	0
26	X	501	0	531	9	0
27	Y	448	0	488	8	0
28	Z	522	0	520	23	0
29	a	444	0	458	13	0
30	b	426	0	464	2	0
31	c	377	0	418	12	0
32	d	504	0	572	10	0
33	e	302	0	340	6	0
34	f	1760	0	1787	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	g	1636	0	1710	40	0
36	h	1643	0	1706	37	0
37	i	1152	0	1196	36	0
38	j	848	0	846	31	0
39	k	1181	0	1238	36	0
40	l	979	0	1031	18	0
41	m	1022	0	1070	29	0
42	n	790	0	831	31	0
43	o	877	0	887	22	0
44	p	957	0	1017	24	0
45	q	900	0	965	25	0
46	r	805	0	844	23	0
47	s	714	0	734	12	0
48	t	649	0	666	13	0
49	u	648	0	691	15	0
50	v	544	0	560	8	0
51	w	663	0	688	26	0
52	x	669	0	719	17	0
53	y	589	0	629	19	0
54	z	1891	0	956	58	0
55	B	205	0	195	40	0
56	1	278	0	0	0	0
56	2	119	0	0	0	0
56	3	8	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	P	1	0	0	0	0
56	a	1	0	0	0	0
56	h	1	0	0	0	0
56	q	1	0	0	0	0
56	z	2	0	0	0	0
57	Z	1	0	0	0	0
57	e	1	0	0	0	0
All	All	145149	0	97246	1718	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 7.

The worst 5 of 1718 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)
6:D:151:THR:HG23	6:D:152:PRO:HD3	1.31	1.05
1:1:2147:A:H62	1:1:2148:G:H21	1.06	1.01
7:E:67:ARG:HD2	55:B:10:LYS:HE3	1.45	0.97
54:z:55:C:O2'	54:z:56:G:O4'	1.85	0.95
55:B:9:VAL:CG2	55:B:11:TRP:CD1	2.56	0.89

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	
5	C	269/271 (99%)	256 (95%)	13 (5%)	0	100	100
6	D	207/209 (99%)	201 (97%)	3 (1%)	3 (1%)	9	29
7	E	199/201 (99%)	198 (100%)	1 (0%)	0	100	100
8	F	175/177 (99%)	166 (95%)	8 (5%)	1 (1%)	21	48
9	G	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
10	H	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
11	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
12	J	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
13	K	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	L	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	M	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	O	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
18	P	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	Q	101/103 (98%)	94 (93%)	5 (5%)	2 (2%)	6	21
20	R	108/110 (98%)	106 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	S	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
22	T	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
23	U	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
24	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
25	W	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	X	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
28	Z	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
29	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	b	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	c	44/46 (96%)	44 (100%)	0	0	100	100
32	d	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
33	e	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
34	f	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
35	g	206/208 (99%)	197 (96%)	9 (4%)	0	100	100
36	h	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	i	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
38	j	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
39	k	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
40	l	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
41	m	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
42	n	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
43	o	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
44	p	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
45	q	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
46	r	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	s	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
48	t	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
49	u	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
50	v	64/66 (97%)	64 (100%)	0	0	100	100
51	w	81/83 (98%)	79 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	x	84/86 (98%)	84 (100%)	0	0	100	100
53	y	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	B	25/27 (93%)	17 (68%)	5 (20%)	3 (12%)	0	1
All	All	5637/5738 (98%)	5426 (96%)	202 (4%)	9 (0%)	44	70

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	152	PRO
55	B	21	ILE
55	B	23	PRO
6	D	153	GLY
6	D	154	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	C	216/216 (100%)	216 (100%)	0	100	100
6	D	164/164 (100%)	163 (99%)	1 (1%)	78	81
7	E	165/165 (100%)	165 (100%)	0	100	100
8	F	148/148 (100%)	147 (99%)	1 (1%)	76	80
9	G	136/136 (100%)	135 (99%)	1 (1%)	76	80
10	H	114/114 (100%)	110 (96%)	4 (4%)	32	59
11	I	116/116 (100%)	115 (99%)	1 (1%)	70	78
12	J	104/104 (100%)	104 (100%)	0	100	100
13	K	103/103 (100%)	103 (100%)	0	100	100
14	L	109/109 (100%)	109 (100%)	0	100	100
15	M	99/99 (100%)	99 (100%)	0	100	100
16	N	86/86 (100%)	86 (100%)	0	100	100
17	O	99/99 (100%)	99 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	P	89/89 (100%)	89 (100%)	0	100	100
19	Q	84/84 (100%)	84 (100%)	0	100	100
20	R	93/93 (100%)	93 (100%)	0	100	100
21	S	81/81 (100%)	81 (100%)	0	100	100
22	T	84/84 (100%)	84 (100%)	0	100	100
23	U	78/78 (100%)	78 (100%)	0	100	100
24	V	59/59 (100%)	58 (98%)	1 (2%)	53	71
25	W	67/67 (100%)	67 (100%)	0	100	100
26	X	54/54 (100%)	53 (98%)	1 (2%)	50	69
27	Y	48/48 (100%)	48 (100%)	0	100	100
28	Z	59/59 (100%)	59 (100%)	0	100	100
29	a	47/47 (100%)	47 (100%)	0	100	100
30	b	47/47 (100%)	47 (100%)	0	100	100
31	c	38/38 (100%)	38 (100%)	0	100	100
32	d	51/51 (100%)	50 (98%)	1 (2%)	48	69
33	e	34/34 (100%)	34 (100%)	0	100	100
34	f	187/187 (100%)	185 (99%)	2 (1%)	65	76
35	g	171/171 (100%)	171 (100%)	0	100	100
36	h	172/172 (100%)	172 (100%)	0	100	100
37	i	119/119 (100%)	118 (99%)	1 (1%)	73	79
38	j	91/91 (100%)	91 (100%)	0	100	100
39	k	124/124 (100%)	124 (100%)	0	100	100
40	l	104/104 (100%)	104 (100%)	0	100	100
41	m	105/105 (100%)	105 (100%)	0	100	100
42	n	86/86 (100%)	85 (99%)	1 (1%)	63	75
43	o	90/90 (100%)	90 (100%)	0	100	100
44	p	102/102 (100%)	102 (100%)	0	100	100
45	q	94/94 (100%)	94 (100%)	0	100	100
46	r	83/83 (100%)	83 (100%)	0	100	100
47	s	76/76 (100%)	76 (100%)	0	100	100
48	t	65/65 (100%)	65 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	u	74/74 (100%)	74 (100%)	0	100	100
50	v	57/57 (100%)	57 (100%)	0	100	100
51	w	72/72 (100%)	72 (100%)	0	100	100
52	x	65/65 (100%)	64 (98%)	1 (2%)	57	73
53	y	60/60 (100%)	60 (100%)	0	100	100
55	B	20/20 (100%)	13 (65%)	7 (35%)	0	0
All	All	4689/4689 (100%)	4666 (100%)	23 (0%)	78	82

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	n	87	LEU
55	B	10	LYS
55	B	8	ILE
55	B	12	PHE
10	H	122	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
45	q	14	HIS
46	r	66	GLN
17	O	56	HIS
16	N	98	GLN
47	s	50	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	492 (16%)	9 (0%)
2	2	1532/1534 (99%)	255 (16%)	5 (0%)
3	3	119/120 (99%)	15 (12%)	0
4	4	5/6 (83%)	0	0
54	z	87/88 (98%)	26 (29%)	0
All	All	4645/4651 (99%)	788 (16%)	14 (0%)

5 of 788 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	46	G

5 of 14 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2189	U
1	1	2756	U
2	2	1145	A
2	2	966	2MG
2	2	1109	C

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	1	955	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.97	4 (18%)
1	OMU	1	2552	1	19,22,23	2.86	8 (42%)	26,31,34	1.63	4 (15%)
1	6MZ	1	2030	1	22,25,26	2.40	6 (27%)	30,36,39	3.35	11 (36%)
2	MA6	2	1518	2	23,26,27	1.46	4 (17%)	34,38,41	3.28	11 (32%)
2	UR3	2	1498	2	19,22,23	2.58	6 (31%)	26,32,35	1.08	1 (3%)
1	OMG	1	2251	1,54	23,26,27	2.20	7 (30%)	33,38,41	1.67	7 (21%)
1	5MU	1	1939	1,56	19,22,23	4.58	7 (36%)	28,32,35	3.66	9 (32%)
2	2MG	2	1516	2	23,26,27	2.66	8 (34%)	32,38,41	2.07	10 (31%)
2	G7M	2	527	2	23,26,27	2.67	8 (34%)	35,39,42	2.25	11 (31%)
1	2MA	1	2503	1,56	22,25,26	3.62	9 (40%)	33,37,40	2.27	9 (27%)
1	PSU	1	746	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.70	3 (13%)
2	PSU	2	516	56,2	18,21,22	0.94	2 (11%)	22,30,33	1.86	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5MC	2	1407	2	18,22,23	3.25	7 (38%)	26,32,35	1.07	1 (3%)
44	0TD	p	89	44	7,9,10	1.43	1 (14%)	6,11,13	1.86	2 (33%)
54	5MU	z	66	54	19,22,23	4.72	7 (36%)	28,32,35	3.94	9 (32%)
2	5MC	2	967	2	18,22,23	3.41	7 (38%)	26,32,35	0.98	2 (7%)
1	OMC	1	2498	1,56	19,22,23	2.68	7 (36%)	26,31,34	0.83	0
1	PSU	1	2457	1	18,21,22	1.00	2 (11%)	22,30,33	2.02	5 (22%)
1	PSU	1	2580	1	18,21,22	1.02	1 (5%)	22,30,33	2.02	6 (27%)
1	PSU	1	2605	1	18,21,22	0.98	2 (11%)	22,30,33	1.92	4 (18%)
2	2MG	2	1207	2	23,26,27	2.74	8 (34%)	32,38,41	1.99	8 (25%)
2	2MG	2	966	2	23,26,27	2.76	9 (39%)	32,38,41	2.08	9 (28%)
1	2MG	1	1835	1	23,26,27	2.69	8 (34%)	32,38,41	2.02	7 (21%)
2	MA6	2	1519	2	23,26,27	1.48	4 (17%)	34,38,41	3.38	11 (32%)
1	PSU	1	1911	1	18,21,22	0.99	1 (5%)	22,30,33	1.89	4 (18%)
2	4OC	2	1402	2	20,23,24	2.91	8 (40%)	26,32,35	0.91	0
1	2MG	1	2445	1	23,26,27	2.60	8 (34%)	32,38,41	1.95	9 (28%)
1	1MG	1	745	1	22,26,27	2.81	7 (31%)	33,39,42	2.08	7 (21%)
1	5MC	1	1962	1	18,22,23	3.31	7 (38%)	26,32,35	1.07	2 (7%)
1	5MU	1	747	1	19,22,23	4.60	7 (36%)	28,32,35	3.68	9 (32%)
1	6MZ	1	1618	1	22,25,26	2.37	6 (27%)	30,36,39	3.40	11 (36%)
55	FME	B	1	55	8,9,10	0.96	0	7,9,11	0.69	0
1	G7M	1	2069	1	23,26,27	2.63	9 (39%)	35,39,42	2.18	12 (34%)
54	OMG	z	17	54	27,27,27	3.47	9 (33%)	40,41,41	6.56	15 (37%)
1	PSU	1	2504	1	18,21,22	1.03	2 (11%)	22,30,33	1.81	4 (18%)
1	PSU	1	1917	1	18,21,22	1.02	2 (11%)	22,30,33	1.99	5 (22%)
1	3TD	1	1915	1	18,22,23	4.06	7 (38%)	22,32,35	1.56	2 (9%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	955	1,56	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	6MZ	1	2030	1	-	4/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	2MA	1	2503	1,56	-	2/7/25/26	0/3/3/3
1	PSU	1	746	1,56	-	1/7/25/26	0/2/2/2
2	PSU	2	516	56,2	-	2/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
44	0TD	p	89	44	-	2/7/12/14	-
54	5MU	z	66	54	-	4/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1,56	-	0/9/27/28	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	2MG	2	966	2	-	2/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
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	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
55	FME	B	1	55	-	5/7/9/11	-
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
54	OMG	z	17	54	-	6/12/28/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2

The worst 5 of 203 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	11.81	1.49	1.35
1	1	2503	2MA	C4-N3	11.06	1.48	1.34
54	z	66	5MU	C6-N1	10.76	1.56	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	747	5MU	C2-N1	10.70	1.55	1.38
1	1	1939	5MU	C2-N1	10.26	1.54	1.38

The worst 5 of 229 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	17	OMG	O6-C6-N1	-29.89	62.83	120.12
54	z	17	OMG	O6-C6-C5	-23.73	63.64	126.60
2	2	1519	MA6	N1-C6-N6	-14.09	101.67	117.08
2	2	1518	MA6	N1-C6-N6	-13.31	102.53	117.08
1	1	747	5MU	C5-C4-N3	12.34	125.85	115.31

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
55	B	1	FME	O1-CN-N-CA

There are no ring outliers.

19 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	955	PSU	1	0
1	1	2030	6MZ	2	0
2	2	1518	MA6	2	0
2	2	1498	UR3	1	0
2	2	1516	2MG	1	0
1	1	2503	2MA	1	0
2	2	516	PSU	2	0
44	p	89	0TD	1	0
54	z	66	5MU	2	0
1	1	2457	PSU	1	0
1	1	2580	PSU	2	0
2	2	966	2MG	1	0
2	2	1519	MA6	2	0
1	1	2445	2MG	1	0
1	1	745	1MG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	1962	5MC	1	0
55	B	1	FME	1	0
54	z	17	OMG	2	0
1	1	1915	3TD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 415 ligands modelled in this entry, 415 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

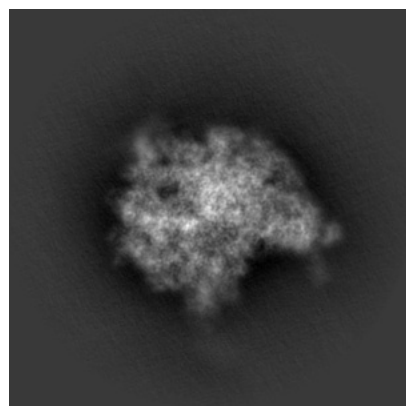
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12636. These allow visual inspection of the internal detail of the map and identification of artifacts.

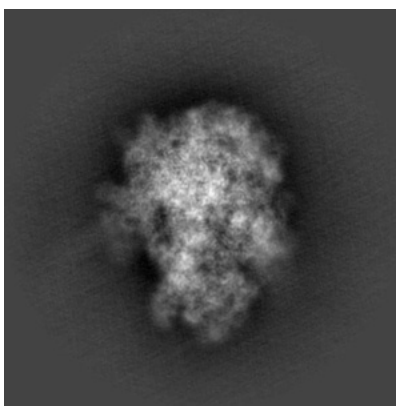
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

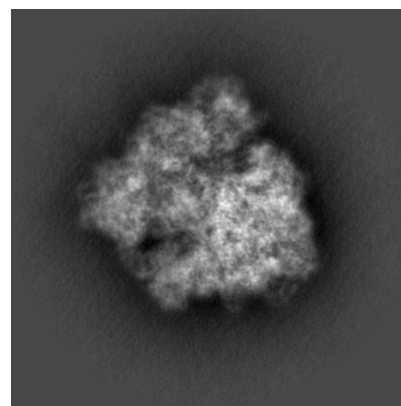
6.1.1 Primary map



X

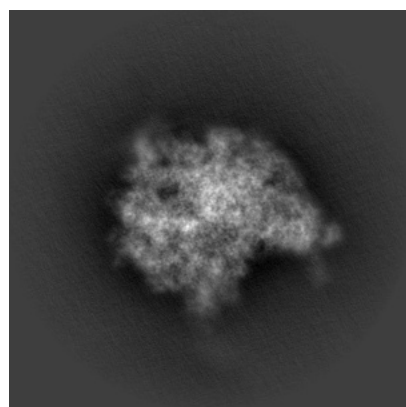


Y

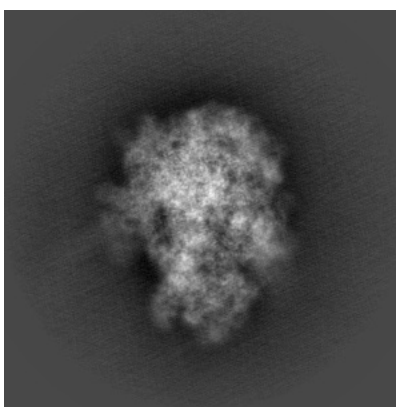


Z

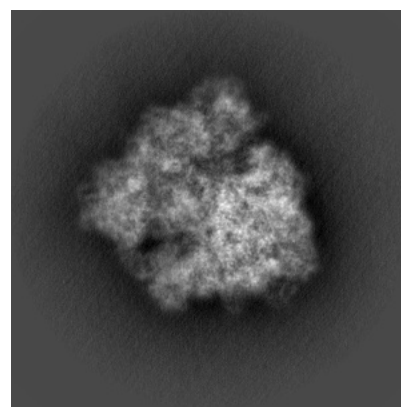
6.1.2 Raw map



X



Y

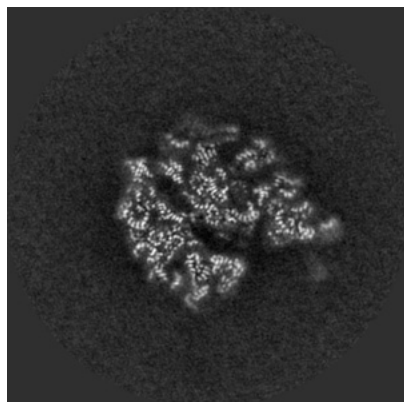


Z

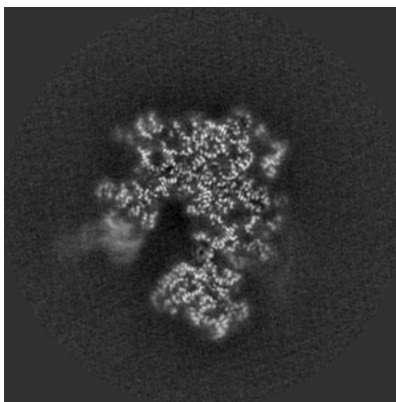
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

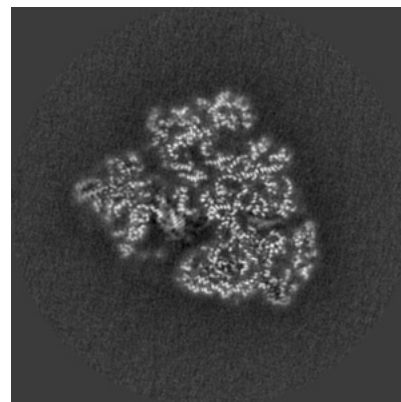
6.2.1 Primary map



X Index: 200

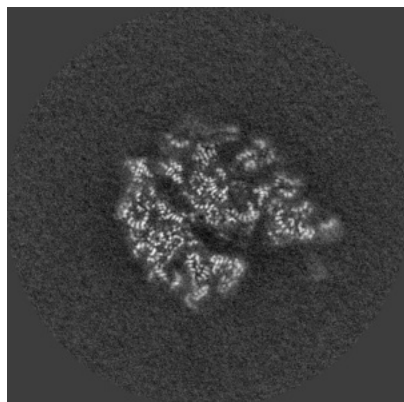


Y Index: 200

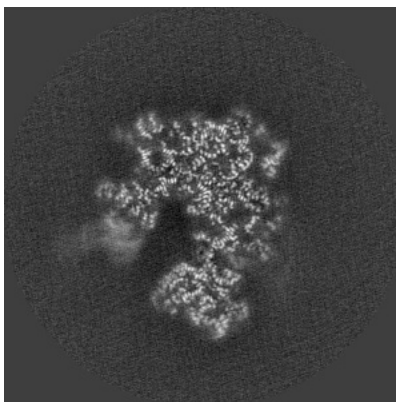


Z Index: 200

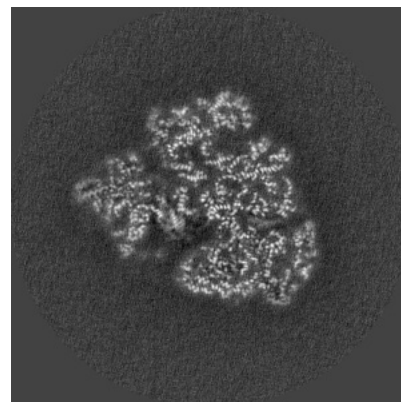
6.2.2 Raw map



X Index: 200



Y Index: 200

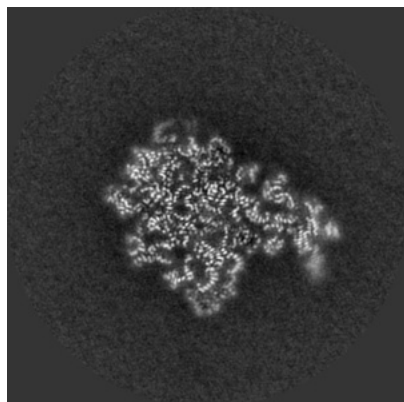


Z Index: 200

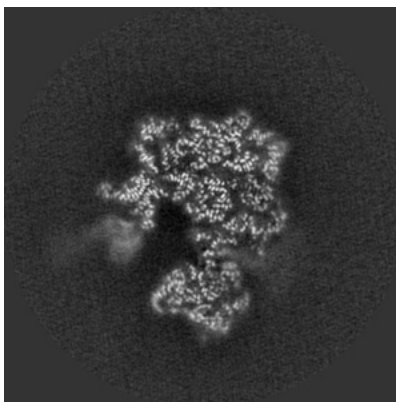
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

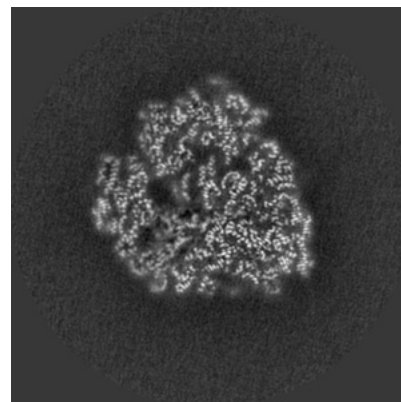
6.3.1 Primary map



X Index: 216

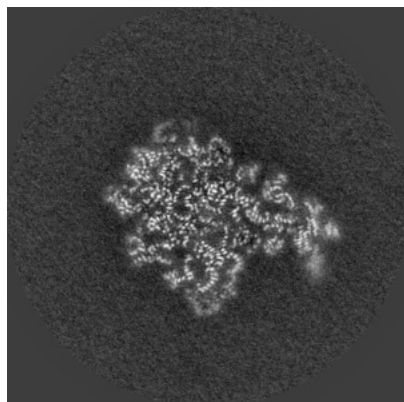


Y Index: 205

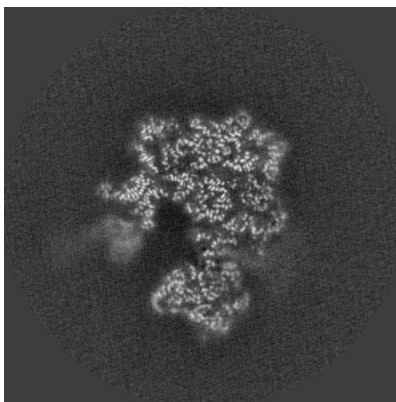


Z Index: 188

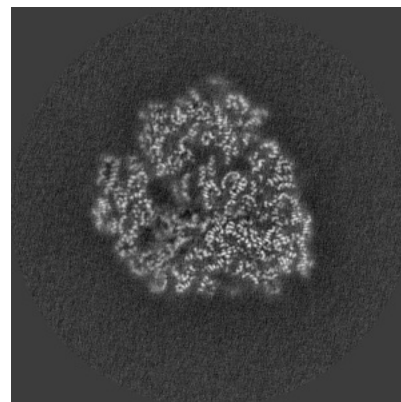
6.3.2 Raw map



X Index: 216



Y Index: 205

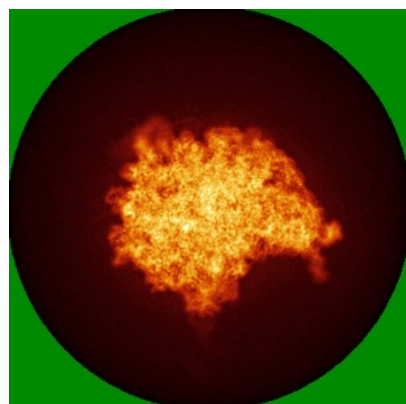


Z Index: 188

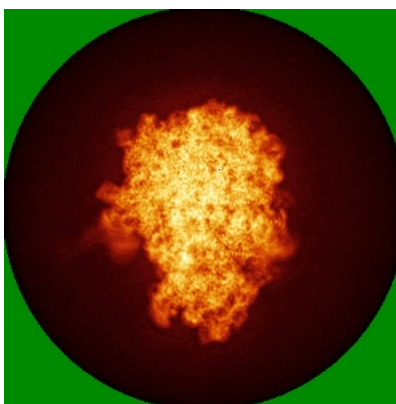
The images above show the largest variance slices of the map in three orthogonal directions.

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

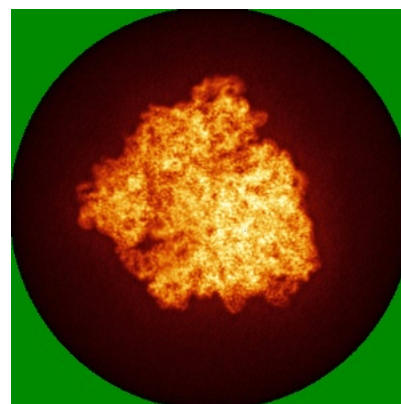
6.4.1 Primary map



X

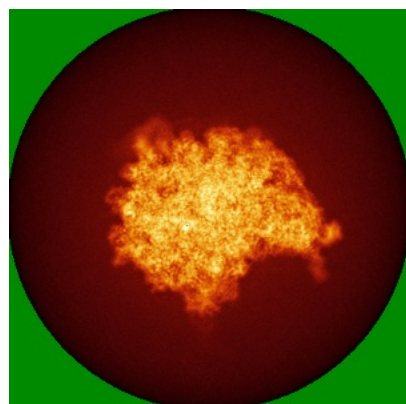


Y

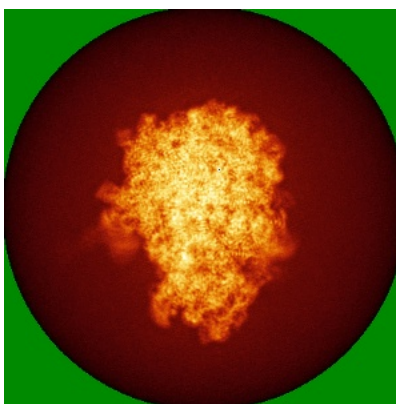


Z

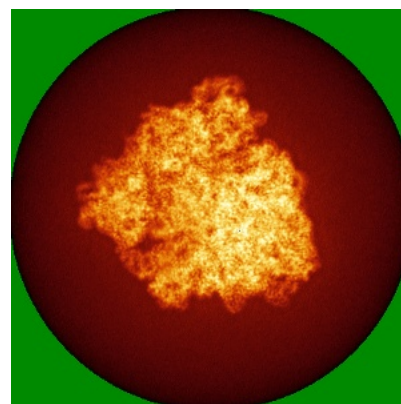
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. 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



X



Y



Z

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.

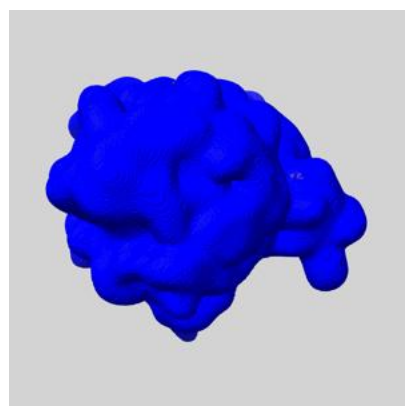
6.6 Mask visualisation [i](#)

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

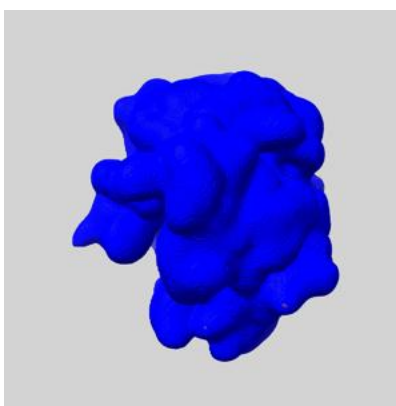
A mask typically either:

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

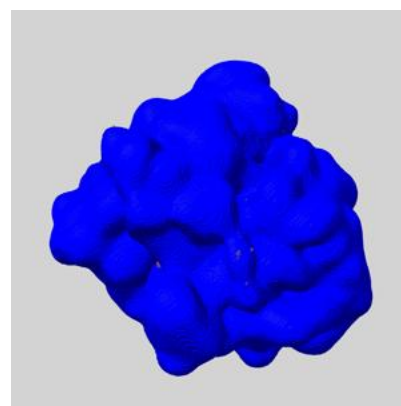
6.6.1 emd_12636_msk_1.map [i](#)



X



Y

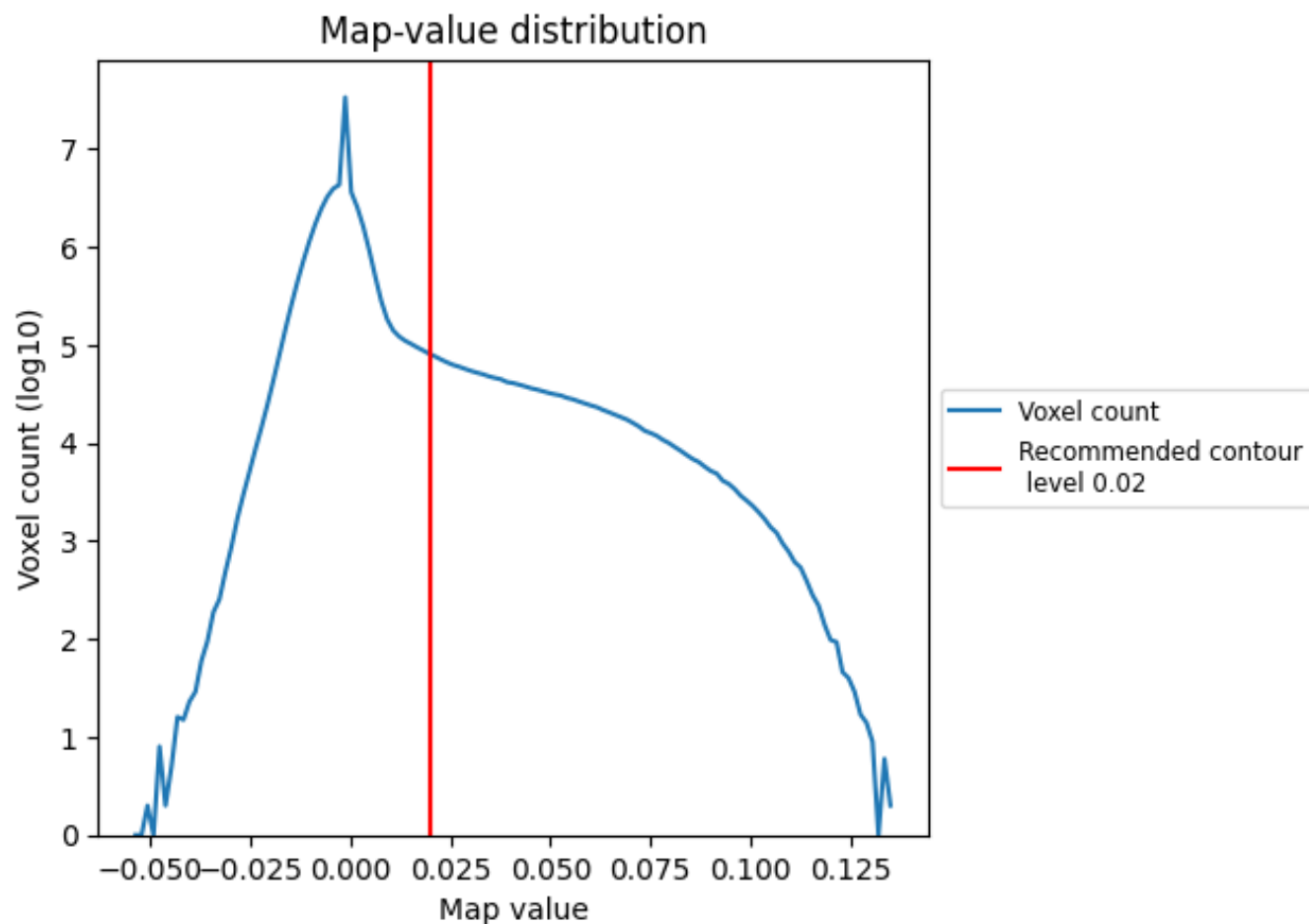


Z

7 Map analysis [i](#)

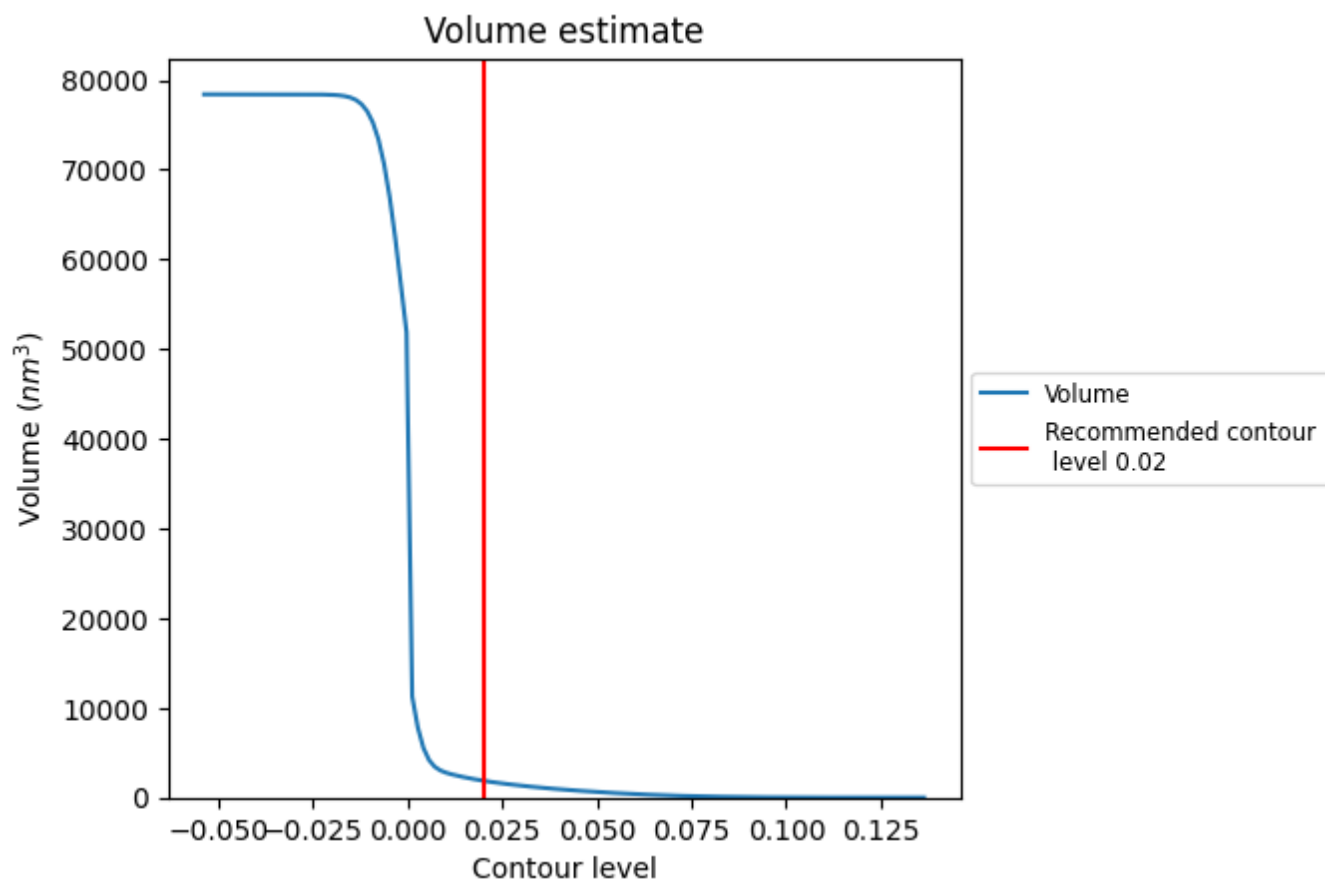
This section contains the results of statistical analysis of the map.

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.

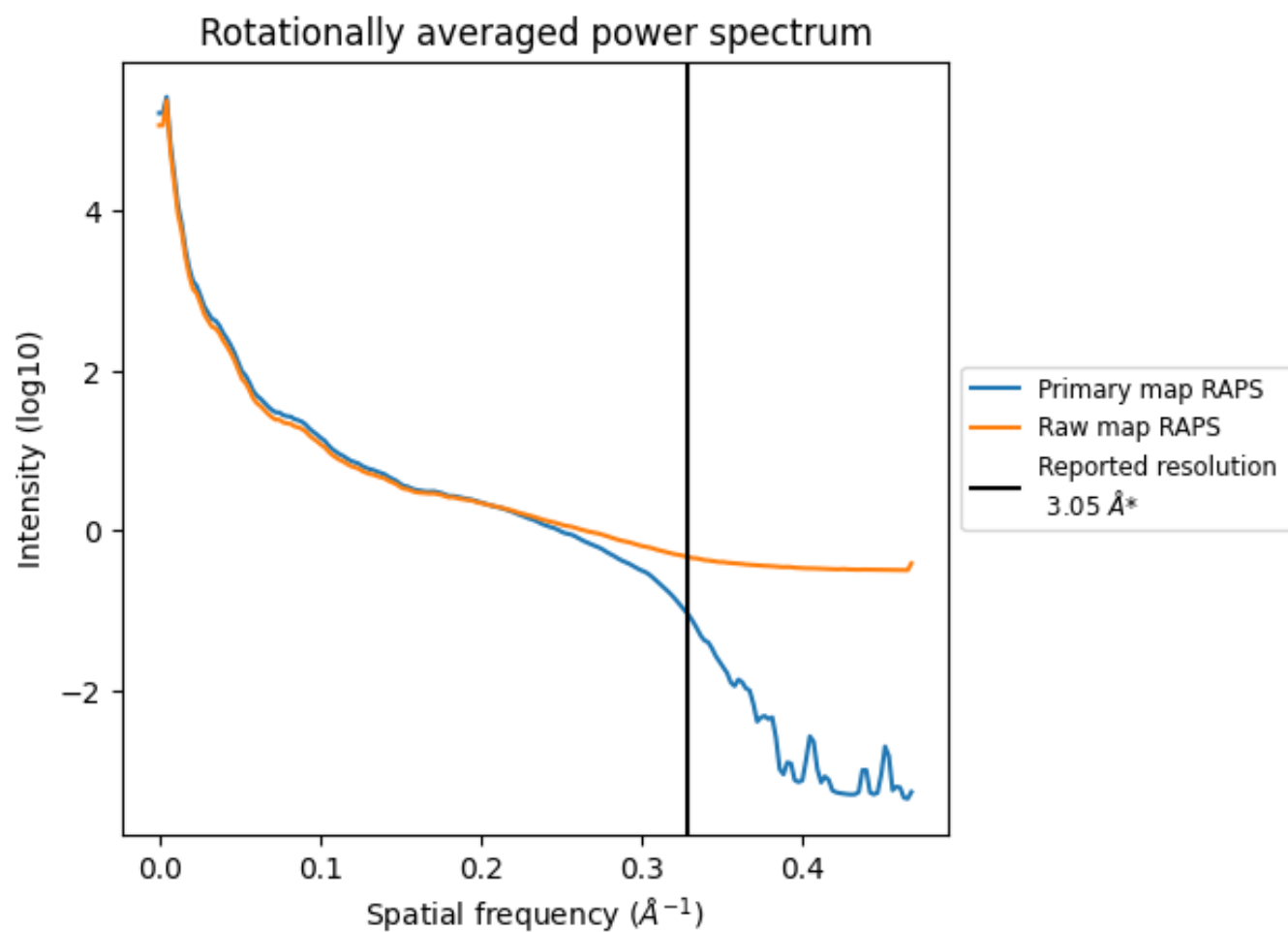
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1881 nm^3 ; this corresponds to an approximate mass of 1699 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 ⓘ

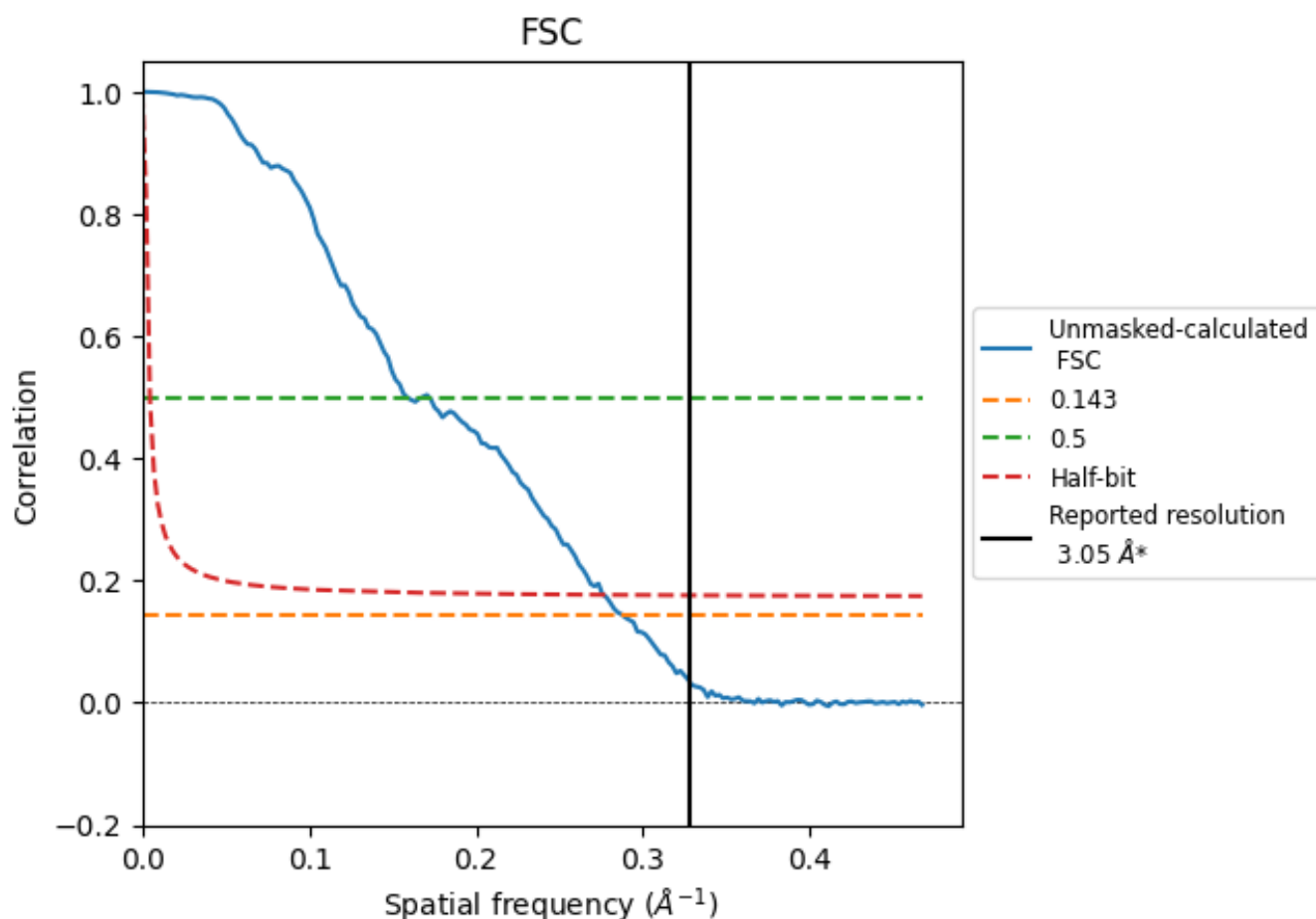


*Reported resolution corresponds to spatial frequency of 0.328 $\text{\AA}^{-1}$

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 0.328 Å⁻¹

8.2 Resolution estimates [i](#)

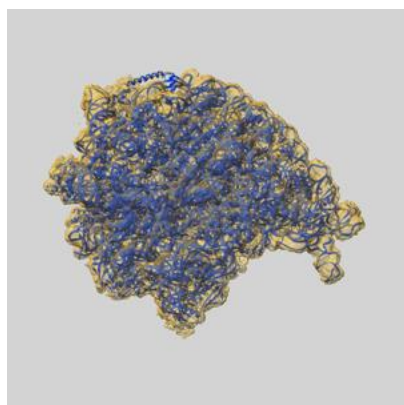
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.47	6.31	3.62

*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 3.47 differs from the reported value 3.05 by more than 10 %

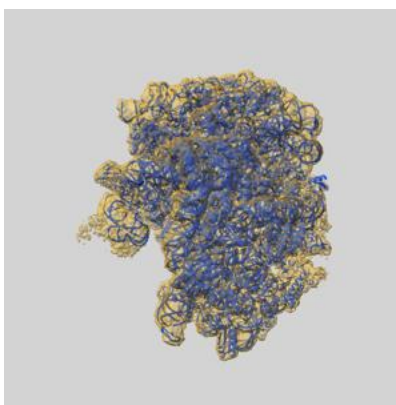
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12636 and PDB model 7NWW. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

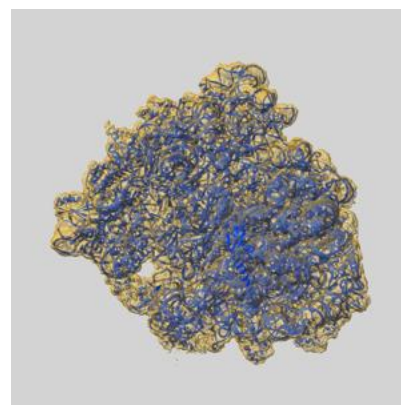
9.1 Map-model overlay [i](#)



X



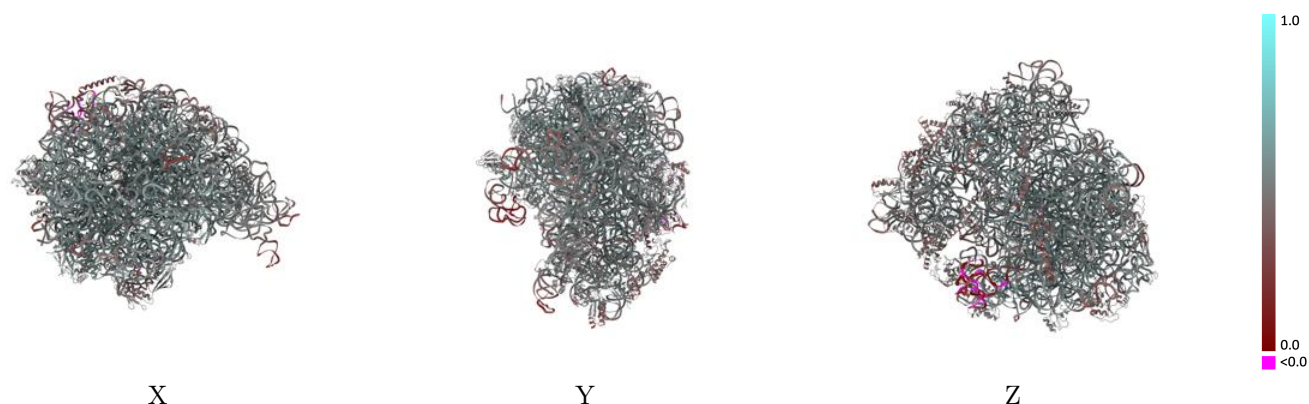
Y



Z

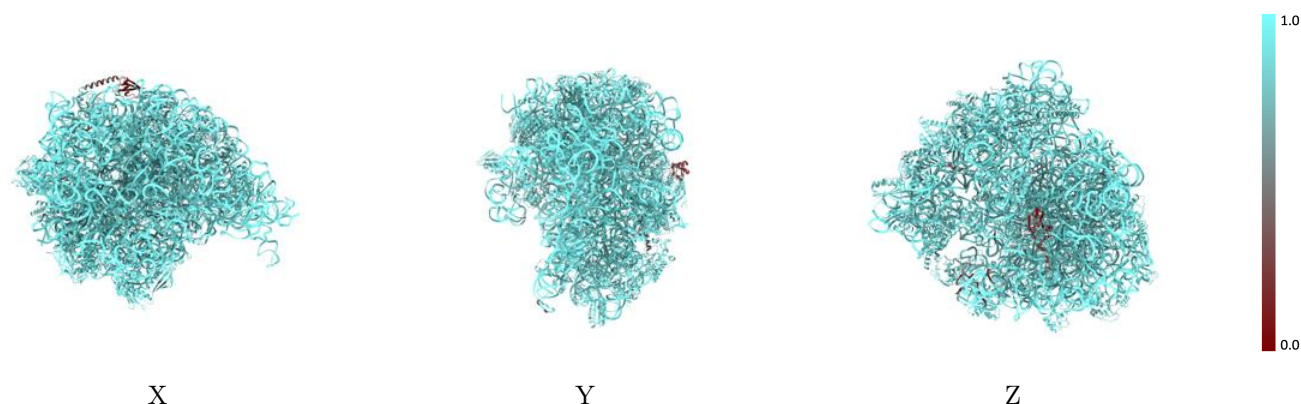
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



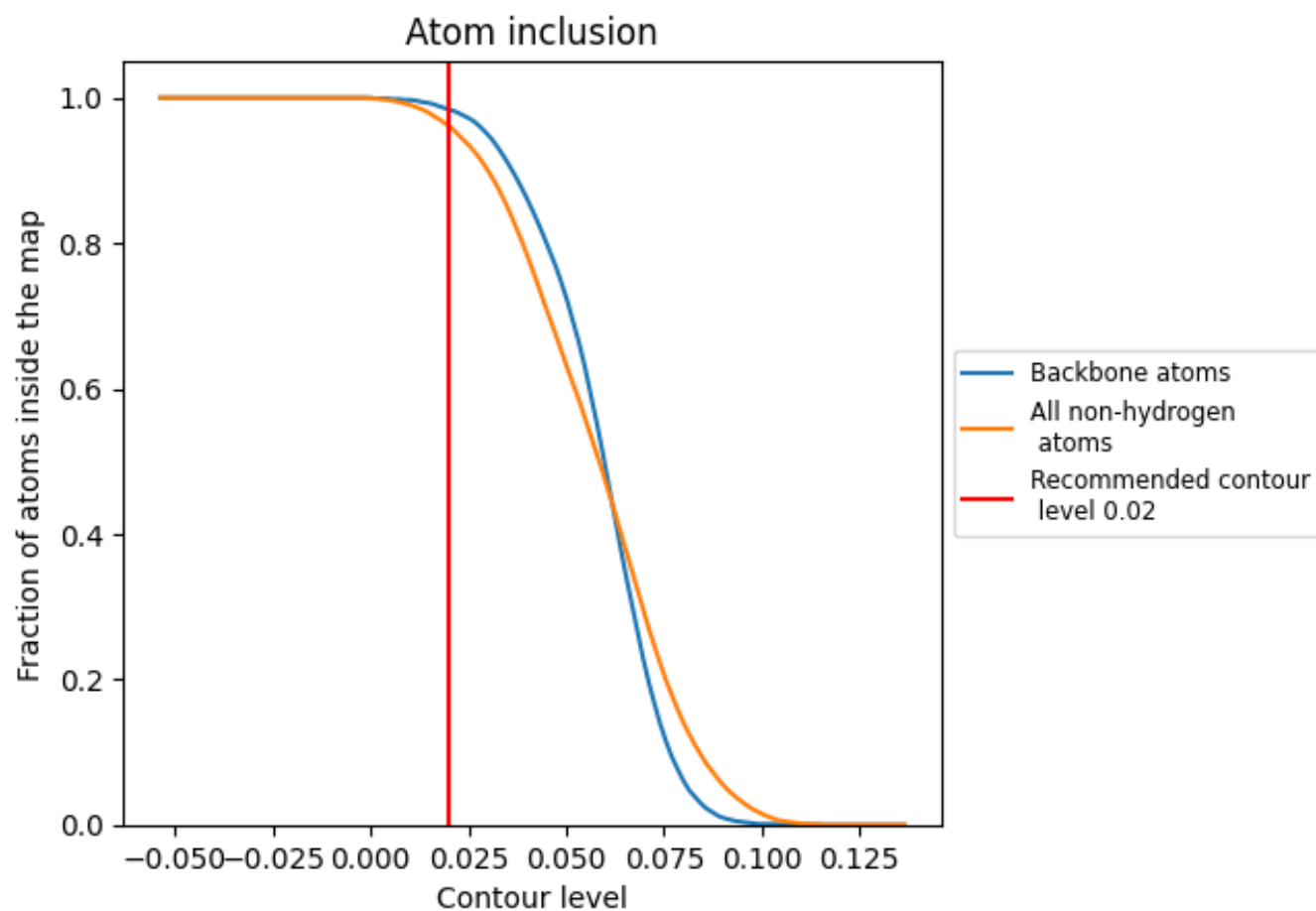
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.4960
1	 0.9870	 0.5060
2	 0.9950	 0.5000
3	 0.9970	 0.5020
4	 0.9760	 0.4690
B	 0.5780	 0.2920
C	 0.9170	 0.5390
D	 0.9280	 0.5320
E	 0.9100	 0.4950
F	 0.9060	 0.4440
G	 0.9250	 0.4540
H	 0.4140	 0.3480
I	 0.9240	 0.5180
J	 0.8690	 0.5220
K	 0.9320	 0.5170
L	 0.9080	 0.5180
M	 0.9540	 0.5300
N	 0.9440	 0.4750
O	 0.9080	 0.5250
P	 0.9480	 0.5200
Q	 0.9370	 0.5140
R	 0.8890	 0.5150
S	 0.9080	 0.4890
T	 0.9120	 0.4820
U	 0.9040	 0.4910
V	 0.9060	 0.5380
W	 0.9180	 0.5130
X	 0.9000	 0.4340
Y	 0.9110	 0.5020
Z	 0.8810	 0.3970
a	 0.9230	 0.5150
b	 0.8540	 0.5010
c	 0.9270	 0.5390
d	 0.9230	 0.5500
e	 0.9280	 0.5300



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Chain	Atom inclusion	Q-score
f	 0.8690	 0.4140
g	 0.9050	 0.4620
h	 0.9040	 0.4580
i	 0.9180	 0.4910
j	 0.9060	 0.4500
k	 0.8810	 0.4250
l	 0.9170	 0.4930
m	 0.9200	 0.4560
n	 0.8810	 0.4370
o	 0.9110	 0.4710
p	 0.8810	 0.5070
q	 0.9080	 0.4460
r	 0.9350	 0.4710
s	 0.9260	 0.4570
t	 0.9470	 0.4950
u	 0.8910	 0.4700
v	 0.9230	 0.4760
w	 0.9400	 0.4700
x	 0.9270	 0.4650
y	 0.7640	 0.4020
z	 0.9710	 0.4330