



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:00 PM UTC

PDB ID : 9HYM / pdb_00009hym
EMDB ID : EMD-52512
Title : Structure of WT E.coli ribosome with complexed filament nascent chain at length 34, with mRNA, P-site and A-site tRNAs, and mRNA
Authors : Mitropoulou, A.; Wlodarski, T.; Plessa, E.; Cabrita, L.D.; Christodoulou, J.
Deposited on : 2025-01-10
Resolution : 2.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at
<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

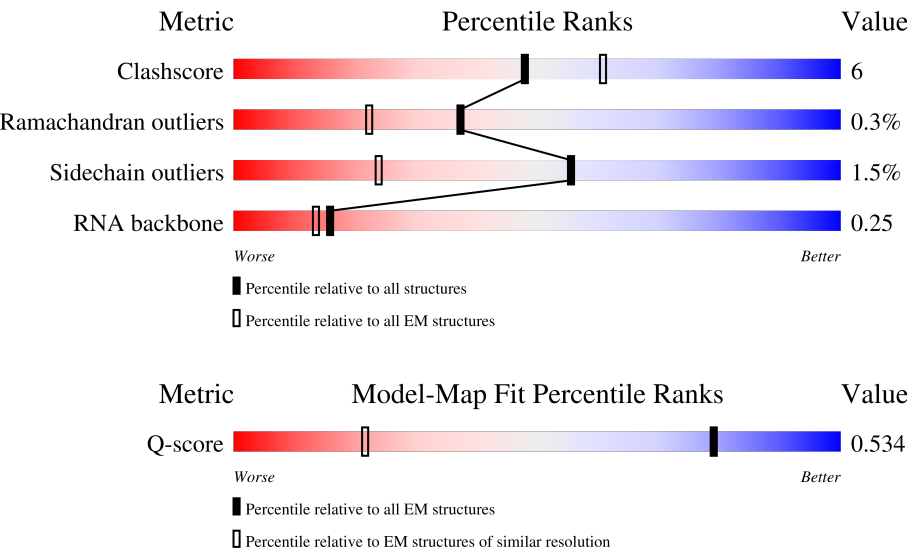
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.20 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.





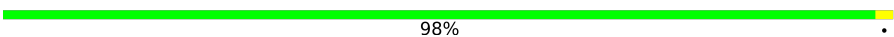
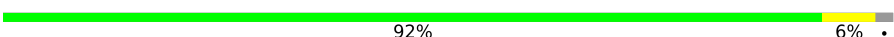






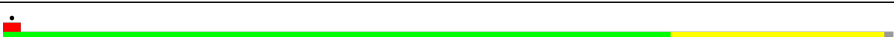


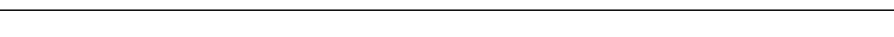
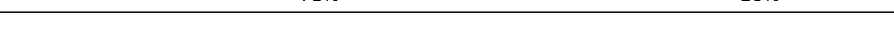
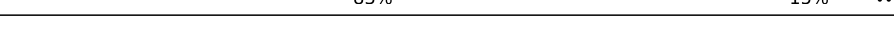



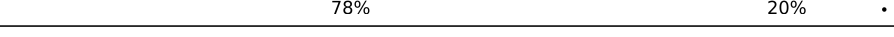





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3184 (1.71 - 2.70)

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.



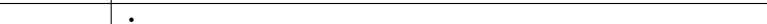

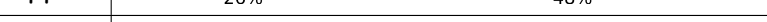

Mol	Chain	Length	Quality of chain
1	0	78	<div><div>85%</div><div>14%</div><div>.</div></div>
2	1	63	<div><div>67%</div><div>30%</div><div>.</div></div>
3	2	59	<div><div>80%</div><div>17%</div><div>.</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	57	
5	4	55	
6	6	46	
7	7	65	
8	8	50	
9	a	120	
10	c	273	
11	d	209	
12	e	201	
13	f	179	
14	g	177	
15	h	149	
16	j	142	
17	k	123	
18	l	144	
19	m	136	
20	n	127	
21	o	117	
22	p	115	
23	q	118	
24	r	103	
25	s	110	
26	t	100	
27	u	104	
28	w	94	

Continued on next page...

Mol	Chain	Length	Quality of chain
29	y	85	
30	v	77	
31	A	77	
32	X	9	
33	z	148	
34	b	2904	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 92691 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 Large ribosomal subunit protein bL28.

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

- Molecule 2 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	61	Total	C	N	O	S	0	0
			495	305	97	92	1		

- Molecule 3 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	57	Total	C	N	O	S	0	0
			439	276	86	75	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	55	Total	C	N	O	S	0	0
			434	263	92	78	1		

- Molecule 5 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 6 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 7 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 8 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 9 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 10 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 15 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	h	39	Total	C	N	O	S	0	0
			287	184	51	51	1		

- Molecule 16 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 17 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 18 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	l	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 19 is a protein called 50S ribosomal protein L16.

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

- Molecule 20 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 22 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	p	113	Total	C	N	O	S	0
			908	570	177	160	1	0

- Molecule 23 is a protein called Large ribosomal subunit protein bL20.

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

- Molecule 24 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	r	102	Total	C	N	O	S	0
			810	513	152	143	2	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	s	109	Total	C	N	O	S	0
			845	526	162	154	3	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	t	93	Total	C	N	O	S	0
			738	466	139	131	2	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	u	102	Total	C	N	O		0
			779	492	146	141		0

- Molecule 28 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 29 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	y	82	Total	C	N	O	S	0	0
			619	383	127	108	1		

- Molecule 30 is a RNA chain called Peptidyl Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	v	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 31 is a RNA chain called Acetyl Pro-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	76	Total	C	N	O	P	0	0
			1626	724	291	535	76		

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	9	Total	C	N	O	P	0	0
			190	84	32	65	9		

- Molecule 33 is a protein called Gelation factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	z	20	Total	C	N	O	0	0
			181	126	30	25		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	1	MET	-	initiating methionine	UNP P13466
z	2	HIS	-	expression tag	UNP P13466
z	3	HIS	-	expression tag	UNP P13466
z	4	HIS	-	expression tag	UNP P13466
z	5	HIS	-	expression tag	UNP P13466
z	6	HIS	-	expression tag	UNP P13466

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
z	7	HIS	-	expression tag	UNP P13466
z	8	ALA	-	expression tag	UNP P13466
z	9	SER	-	expression tag	UNP P13466
z	130	GLU	-	expression tag	UNP P13466
z	131	LEU	-	expression tag	UNP P13466
z	132	PHE	-	expression tag	UNP P13466
z	133	SER	-	expression tag	UNP P13466
z	134	THR	-	expression tag	UNP P13466
z	135	PRO	-	expression tag	UNP P13466
z	136	VAL	-	expression tag	UNP P13466
z	137	TRP	-	expression tag	UNP P13466
z	138	ILE	-	expression tag	UNP P13466
z	139	TRP	-	expression tag	UNP P13466
z	140	TRP	-	expression tag	UNP P13466
z	141	TRP	-	expression tag	UNP P13466
z	142	PRO	-	expression tag	UNP P13466
z	143	ARG	-	expression tag	UNP P13466
z	144	ILE	-	expression tag	UNP P13466
z	145	ARG	-	expression tag	UNP P13466
z	146	GLY	-	expression tag	UNP P13466
z	147	PRO	-	expression tag	UNP P13466
z	148	PRO	-	expression tag	UNP P13466


- Molecule 34 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	2901	Total	C	N	O	P	0	0
			62281	27784	11464	20132	2901		

3 Residue-property plots [i](#)

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: Large ribosomal subunit protein bL28

Chain 0: 




- Molecule 2: Large ribosomal subunit protein uL29

Chain 1: 



- Molecule 3: Large ribosomal subunit protein uL30

Chain 2: 



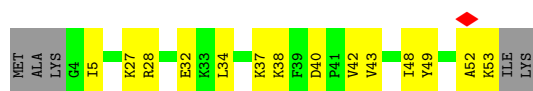
- Molecule 4: Large ribosomal subunit protein bL32

Chain 3: 



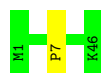
- Molecule 5: Large ribosomal subunit protein bL33

Chain 4: 



- Molecule 6: Large ribosomal subunit protein bL34

Chain 6:  98% .



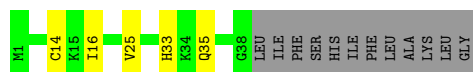
- Molecule 7: Large ribosomal subunit protein bL35

Chain 7:  92% 6% .



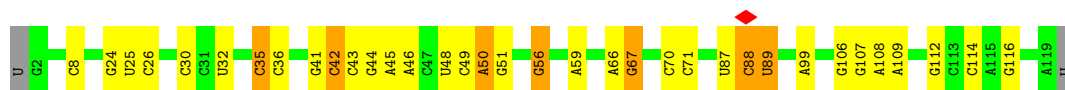
- Molecule 8: 50S ribosomal protein L36

Chain 8:  66% 10% 24%




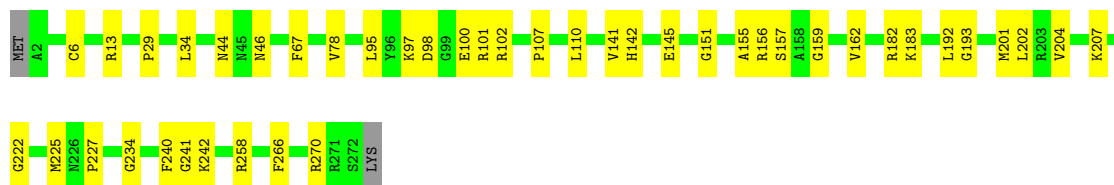
- Molecule 9: 5S rRNA

Chain a:  69% 23% 6% .



- Molecule 10: Large ribosomal subunit protein uL2

Chain c:  84% 16% .




- Molecule 11: 50S ribosomal protein L3

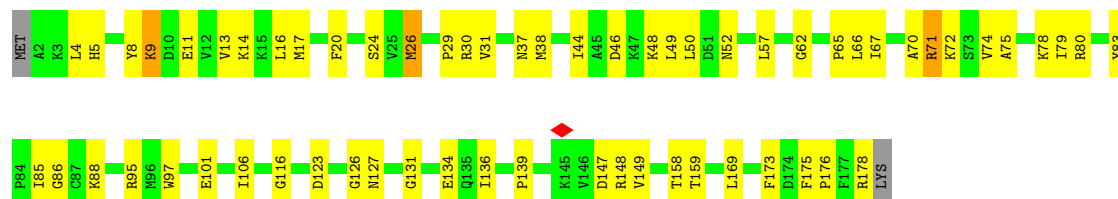
Chain d:  89% 11%



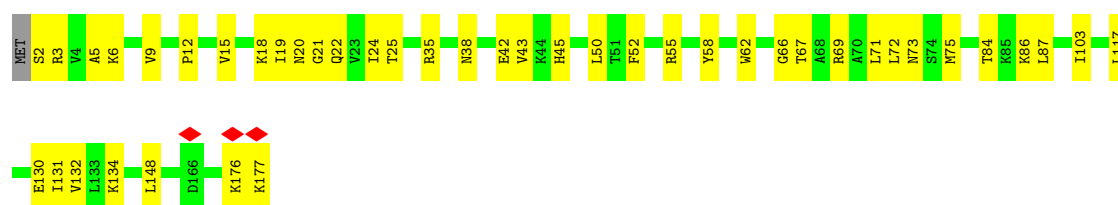
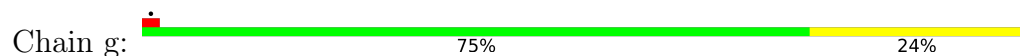
- Molecule 12: Large ribosomal subunit protein uL4

Chain e:  81% 18%

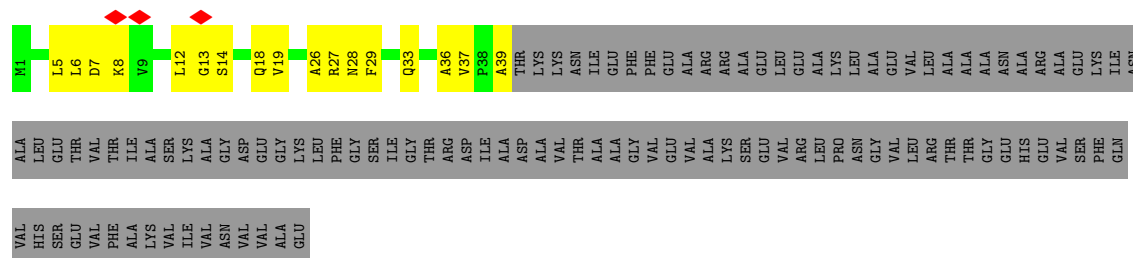
- Molecule 13: Large ribosomal subunit protein uL5



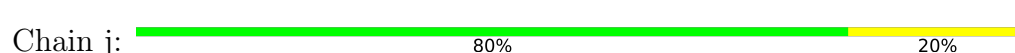
- Molecule 14: Large ribosomal subunit protein uL6



- Molecule 15: Large ribosomal subunit protein bL9

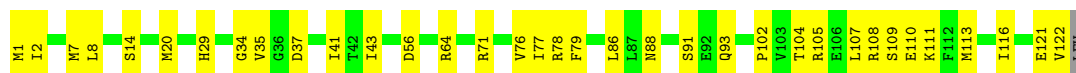


- Molecule 16: Large ribosomal subunit protein uL13




- Molecule 17: Large ribosomal subunit protein uL14

Chain k:  71% 28% .



- Molecule 18: Large ribosomal subunit protein uL15

Chain l:  83% 15% ..



- Molecule 19: 50S ribosomal protein L16

Chain m:  91% 9%



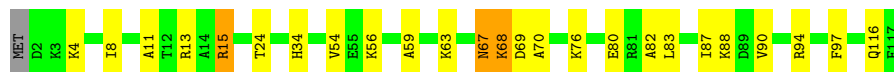
- Molecule 20: Large ribosomal subunit protein bL17

Chain n:  73% 21% 6%




- Molecule 21: Large ribosomal subunit protein uL18

Chain o:  78% 19% ..




- Molecule 22: Large ribosomal subunit protein bL19

Chain p:  78% 20% .




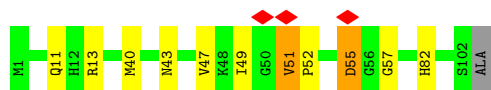
- Molecule 23: Large ribosomal subunit protein bL20

Chain q:  86% 14% .




- Molecule 24: Large ribosomal subunit protein bL21

Chain r:  88% 9% ..




- Molecule 25: Large ribosomal subunit protein uL22

Chain s:  82% 17% .



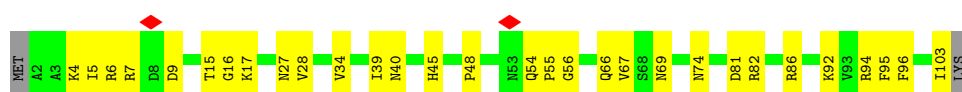
- Molecule 26: Large ribosomal subunit protein uL23

Chain t:  80% 11% • 7%



- Molecule 27: Large ribosomal subunit protein uL24

Chain u:  69% 29% .



- Molecule 28: Large ribosomal subunit protein bL25

Chain w:  88% 12%



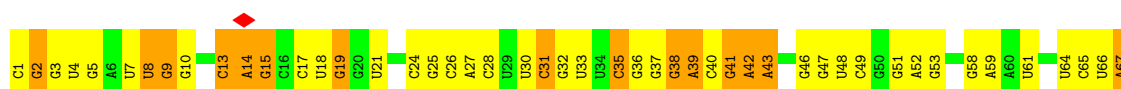
- Molecule 29: Large ribosomal subunit protein bL27

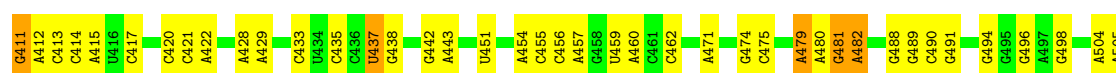
Chain y:  71% 25% ..

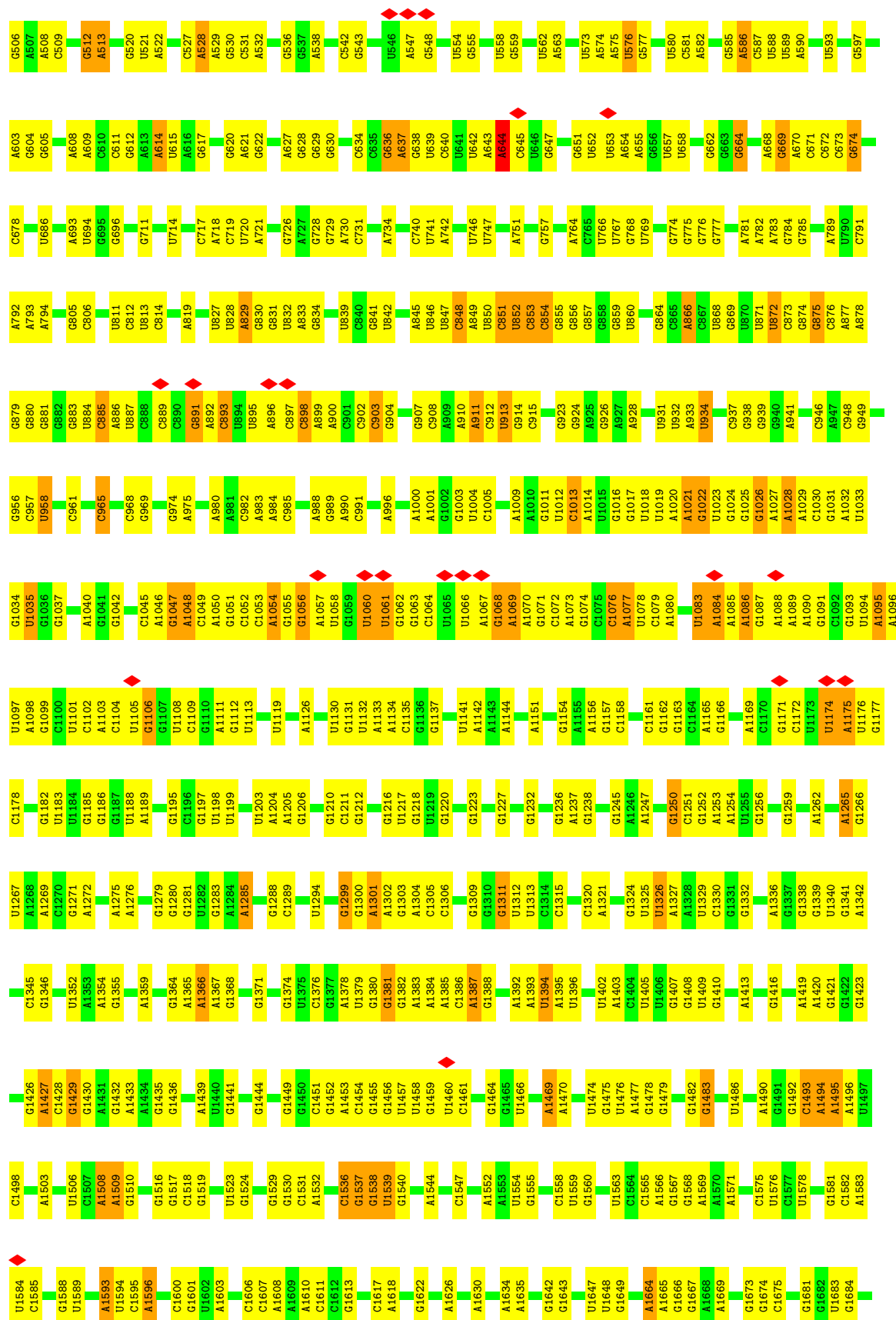


- Molecule 30: Peptidyl Pro-tRNA

Chain v:  26% 48% 26%







C2772	C2691	G2608	A2516	A2435	G2351	G2286	U2181	G2121	U2041	C1957	A1871	G1776	A1689
C2773	G2692	U2609	C2517	U2441	A2352	A2288	U2182	U2122	A2042	C1958	A1872	G1777	A1690
G2777	U2696	C2610	U2519	C2611	G2353	A2289	A2183	G2123	C2043	C1961	C1873	U1779	U1693
A2778	G2697	U2612	C2520	G2445	G2355	U2291	G2186	G2125	A2051	G1964	A1875	U1782	C1694
G2780	A2700	U2613	G2526	G2446	G2361	U2292	G2190	A2126	C2055	C1965	U1882	A1783	G1699
A2781	U2701	A2614	C2527	G2447	U2292	U2292	A2191	G2127	G2056	C1966	U1883	A1784	A1700
G2782	G2702	U2615	U2528	A2448	G2294	G2294	U2192	G2128	G2057	C1967	U1884	A1785	A1701
U2783	U2703	G2616	G2529	G2454	C2364	G2295	G2193	C2129	A2058	A1970	A1887	A1786	G1702
U2784	A2705	G2618	G2533	U2455	G2367	U2296	G2197	C2130	A2059	A1971	C1887	A1787	G1703
C2788	U2713	G2623	A2534	U2457	C2368	A2297	U2198	U2130	G2060	U1972	G1888	C1704	C1704
C2789	U2716	G2624	G2535	A2458	A2377	A2298	A2198	U2131	A2061	G1972	G1889	C1705	A1705
U2790	G2717	C2625	G2536	A2459	A2378	U2299	A2199	A2132	A2062	C1973	C1793	C1706	C1706
U2796	G2718	C2626	U2537	G2464	G2379	C2300	U2203	A2133	C2063	G1975	A1890	A1794	G1707
U2797	U2720	U2629	G2543	A2468	G2383	U2302	G2204	A2134	U2068	C1895	C1800	U1713	U1713
U2798	U2724	G2630	U2546	A2469	U2384	G2303	C2208	A2135	G2069	G1980	A1801	U1714	U1714
A2799	A2725	U2634	G2547	G2470	C2385	U2304	G2209	G2136	U2074	A1891	A1802	G1715	G1715
G2800	A2726	A2635	G2548	A2471	U2306	C2305	A2211	U2137	U2075	C1985	C1803	U1716	U1716
G2801	U2727	G2635	U2550	G2472	G2307	C2307	A2212	G2138	U2076	C1986	A1804	A1717	A1717
G2802	U2728	C2636	G2554	U2473	G2308	U2308	U2213	U2139	C2078	A1987	G1907	A1805	A1805
G2803	U2731	A2639	U2555	G2475	G2309	C2309	C2214	G2140	U2079	U1991	C1908	A1808	G1721
U2804	G2732	G2643	C2556	A2476	A2311	A2311	A2225	G2141	A2080	G1992	C1909	C1725	C1725
U2807	A2733	G2644	U2561	U2477	U2397	U2312	A2226	A2142	U2081	U1993	A1913	G1726	G1726
G2808	U2736	C2646	G2562	A2478	U2398	C2313	G2228	C2143	U2085	C1996	C1914	U1729	U1729
A2809	G2737	U2661	U2563	U2479	G2399	A2314	G2230	G2144	U2086	C1997	U1915	U1730	U1730
A2810	U2738	G2655	U2564	G2480	G2405	G2315	U2233	G2145	U2087	A1998	U1917	G1731	G1731
U2818	U2739	A2656	U2565	A2481	U2402	G2316	G2234	C2146	G2087	C1999	U1918	C1732	C1732
G2820	G2744	C2657	A2566	C2482	U2403	G2317	G2235	A2147	G2093	G2002	G1921	C1733	U1733
A2821	C2745	G2658	G2567	C2483	U2404	G2318	G2236	G2148	A2094	G2003	G1922	C1734	C1734
G2822	U2746	A2660	G2568	G2484	G2405	U2320	G2237	U2149	A2095	C2008	U1923	G1735	U1735
A2823	U2747	G2661	G2569	G2485	A2406	U2321	U2240	C2150	C2096	A2009	C1924	G1736	U1736
G2824	G2747	G2662	U2572	G2486	U2407	A2322	A2241	C2151	A2097	G2010	C1925	G1737	G1737
G2825	A2748	C2663	G2573	U2488	G2408	G2323	G2242	U2151	U2098	G2011	U1926	G1738	U1738
U2829	A2749	G2664	G2574	U2489	G2409	U2324	U2243	G2152	U2099	G2012	A1927	G1739	G1739
G2830	G2751	G2665	C2575	U2491	G2410	G2325	U2244	C2153	G2100	A2013	A1928	G1740	G1740
U2831	C2752	G2666	G2576	U2492	G2411	C2326	C2249	A2154	A2101	G1930	G1929	A1744	A1744
U2832	U2753	G2667	U2579	U2493	G2412	A2327	U2249	U2155	G2103	A2020	U1931	A1745	A1745
U2833	U2754	G2668	U2580	G2494	C2416	A2328	G2250	G2156	C2104	C2021	C1836	A1749	A1749
G2834	C2755	G2669	G2581	A2497	U2419	G2331	C2258	G2157	U2105	U2022	G1935	G1750	G1750
A2835	U2756	A2670	G2582	C2498	G2420	C2332	U2259	A2158	U2106	C2023	A1848	U1751	U1751
U2836	A2757	G2671	G2583	C2499	G2421	A2333	C2260	G2159	G2107	G2024	A1937	G1752	G1752
G2837	U2758	C2672	A2590	G2500	U2422	A2335	C2261	C2160	U2109	G2029	A1938	G1753	G1753
C2840	G2759	A2673	U2593	G2502	U2423	A2336	A2266	C2161	G2110	A2030	U1939	A1754	A1754
G2841	U2761	G2674	U2594	A2503	C2424	G2337	A2267	G2162	G2111	A2031	U1940	A1755	A1755
G2842	C2762	U2680	G2597	U2504	A2425	C2338	A2268	A2163	G2112	G2032	U1944	G1756	G1756
G2843	G2763	G2681	G2598	U2505	A2426	C2339	A2269	C2164	U2113	A2033	U1945	A1857	A1857
G2844	A2764	A2682	C2601	U2506	G2427	G2340	A2273	C2165	U2114	U2034	U1946	A1758	A1758
U2845	U2765	U2683	G2602	G2507	G2428	A2340	A2274	G2166	G2115	G2035	A1952	G1862	G1862
G2846	G2766	U2684	A2603	G2508	G2429	A2341	A2275	U2167	G2116	A2037	A1953	U1864	U1864
U2847	U2767	G2685	U2604	A2513	A2430	G2342	A2276	G2168	G2117	G2038	U1955	G1869	G1869
G2848	U2768	U2686	G2605	U2514	A2432	C2347	G2282	U2169	U2118	U2039	G1956	C1764	C1764
U2849	G2771	U2690	G2607	C2515	A2434	C2350	C2283	A2170	A2119	G2040	U1956	A1773	A1773

G2859	A2860	U2861	C2862	C2863	U2864	U2865	U2866	G2867	U2871	A2879	A2883	U2884	G2885	A2886	A2887	G2892	A2893	G2894	G2895	U2898	A2899	A2900	C2901	C	U	U
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	---	---	---

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	281242	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	14.45	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.103	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.011	Depositor
Map size (Å)	411.648, 411.648, 411.648	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.072, 1.072, 1.072	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.39	0/635	0.52	0/848
2	1	0.31	0/496	0.46	0/660
3	2	0.35	0/443	0.40	0/593
4	3	0.47	0/440	0.72	0/588
5	4	0.47	0/416	0.66	0/554
6	6	0.39	0/380	0.48	0/498
7	7	0.46	0/513	0.57	0/676
8	8	0.39	0/302	0.48	0/397
9	a	0.38	0/2828	0.36	0/4410
10	c	0.37	0/2121	0.48	0/2852
11	d	0.40	0/1586	0.48	0/2134
12	e	0.33	0/1571	0.43	1/2113 (0.0%)
13	f	0.40	0/1434	0.62	0/1926
14	g	0.35	0/1343	0.52	0/1816
15	h	0.28	0/290	0.63	0/392
16	j	0.42	0/1152	0.47	1/1551 (0.1%)
17	k	0.40	0/947	0.47	0/1268
18	l	0.63	0/1052	0.82	1/1401 (0.1%)
19	m	0.36	0/1093	0.50	0/1460
20	n	0.40	0/973	0.52	0/1301
21	o	0.42	0/902	0.60	0/1209
22	p	0.38	0/920	0.43	0/1231
23	q	0.41	0/960	0.47	0/1278
24	r	0.53	0/823	0.65	0/1100
25	s	0.37	0/852	0.41	0/1142
26	t	0.39	0/744	0.53	0/994
27	u	0.39	0/787	0.57	0/1051
28	w	0.33	0/766	0.43	0/1025
29	y	0.50	0/627	0.60	0/829
30	v	0.46	0/1839	0.52	0/2866
31	A	0.42	0/1817	0.41	0/2832
32	X	0.59	0/210	0.81	0/323
33	z	1.96	3/192 (1.6%)	2.13	5/267 (1.9%)
34	b	0.51	0/69757	0.72	14/108827 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.49	3/101211 (0.0%)	0.67	22/152412 (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
33	z	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	z	131	LEU	C-N	-16.48	1.11	1.33
33	z	130	GLU	C-N	14.87	1.59	1.33
33	z	130	GLU	N-CA	7.40	1.55	1.46

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	z	130	GLU	O-C-N	-26.05	87.95	122.59
34	b	2832	U	C4'-C3'-O3'	7.78	121.06	109.40
34	b	228	C	C4'-C3'-O3'	6.95	119.82	109.40
33	z	130	GLU	CA-C-N	6.81	133.22	123.14
33	z	130	GLU	C-N-CA	6.81	133.22	123.14

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	z	130	GLU	Mainchain
33	z	131	LEU	Mainchain
33	z	143	ARG	Sidechain
33	z	145	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	625	0	652	7	0
2	1	495	0	526	15	0
3	2	439	0	482	6	0
4	3	434	0	445	12	0
5	4	409	0	440	8	0
6	6	377	0	418	1	0
7	7	504	0	572	3	0
8	8	301	0	341	3	0
9	a	2529	0	1281	15	0
10	c	2082	0	2154	27	0
11	d	1565	0	1616	21	0
12	e	1552	0	1619	23	0
13	f	1410	0	1444	51	0
14	g	1323	0	1371	26	0
15	h	287	0	307	12	0
16	j	1129	0	1162	21	0
17	k	938	0	1012	25	0
18	l	1043	0	1123	10	0
19	m	1074	0	1157	9	0
20	n	960	0	1000	19	0
21	o	892	0	923	18	0
22	p	908	0	956	21	0
23	q	947	0	1019	15	0
24	r	810	0	834	6	0
25	s	845	0	909	29	0
26	t	738	0	807	9	0
27	u	779	0	831	23	0
28	w	753	0	780	7	0
29	y	619	0	642	16	0
30	v	1646	0	832	61	0
31	A	1626	0	819	51	0
32	X	190	0	99	6	0
33	z	181	0	173	19	0
34	b	62281	0	31323	428	0
All	All	92691	0	60069	904	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 6.

The worst 5 of 904 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)
34:b:892:A:C8	34:b:893:C:C6	1.96	1.54
34:b:892:A:H8	34:b:893:C:C6	1.26	1.52
34:b:892:A:C8	34:b:893:C:C5	2.13	1.34
34:b:370:G:OP2	34:b:370:G:C8	1.81	1.30
25:s:85:ILE:CD1	33:z:131:LEU:HD23	1.60	1.29

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	0	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
2	1	59/63 (94%)	56 (95%)	3 (5%)	0	100	100
3	2	55/59 (93%)	52 (94%)	3 (6%)	0	100	100
4	3	53/57 (93%)	49 (92%)	4 (8%)	0	100	100
5	4	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
6	6	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
7	7	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
8	8	36/50 (72%)	35 (97%)	1 (3%)	0	100	100
10	c	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
11	d	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
12	e	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
13	f	175/179 (98%)	164 (94%)	10 (6%)	1 (1%)	21	23
14	g	174/177 (98%)	159 (91%)	15 (9%)	0	100	100
15	h	37/149 (25%)	32 (86%)	5 (14%)	0	100	100
16	j	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
17	k	120/123 (98%)	116 (97%)	4 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	l	141/144 (98%)	132 (94%)	9 (6%)	0	100	100
19	m	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
20	n	118/127 (93%)	111 (94%)	7 (6%)	0	100	100
21	o	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
22	p	111/115 (96%)	110 (99%)	1 (1%)	0	100	100
23	q	115/118 (98%)	115 (100%)	0	0	100	100
24	r	100/103 (97%)	93 (93%)	5 (5%)	2 (2%)	6	4
25	s	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
26	t	91/100 (91%)	87 (96%)	4 (4%)	0	100	100
27	u	100/104 (96%)	83 (83%)	17 (17%)	0	100	100
28	w	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
29	y	80/85 (94%)	71 (89%)	6 (8%)	3 (4%)	2	1
33	z	18/148 (12%)	15 (83%)	1 (6%)	2 (11%)	0	0
All	All	3074/3427 (90%)	2923 (95%)	143 (5%)	8 (0%)	37	42

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	r	52	PRO
29	y	9	SER
29	y	6	ALA
33	z	130	GLU
24	r	51	VAL

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	0	67/68 (98%)	67 (100%)	0	100	100
2	1	54/55 (98%)	54 (100%)	0	100	100
3	2	47/49 (96%)	47 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	46/48 (96%)	44 (96%)	2 (4%)	26	35
5	4	45/49 (92%)	44 (98%)	1 (2%)	45	61
6	6	38/38 (100%)	38 (100%)	0	100	100
7	7	51/52 (98%)	51 (100%)	0	100	100
8	8	34/44 (77%)	34 (100%)	0	100	100
10	c	216/218 (99%)	216 (100%)	0	100	100
11	d	164/164 (100%)	164 (100%)	0	100	100
12	e	165/165 (100%)	165 (100%)	0	100	100
13	f	148/150 (99%)	144 (97%)	4 (3%)	39	53
14	g	137/138 (99%)	136 (99%)	1 (1%)	76	87
15	h	30/114 (26%)	30 (100%)	0	100	100
16	j	116/116 (100%)	116 (100%)	0	100	100
17	k	103/104 (99%)	103 (100%)	0	100	100
18	l	102/103 (99%)	94 (92%)	8 (8%)	11	13
19	m	109/109 (100%)	109 (100%)	0	100	100
20	n	100/103 (97%)	100 (100%)	0	100	100
21	o	86/87 (99%)	82 (95%)	4 (5%)	23	31
22	p	98/100 (98%)	98 (100%)	0	100	100
23	q	89/90 (99%)	89 (100%)	0	100	100
24	r	84/84 (100%)	79 (94%)	5 (6%)	17	21
25	s	92/93 (99%)	92 (100%)	0	100	100
26	t	80/84 (95%)	78 (98%)	2 (2%)	42	56
27	u	83/85 (98%)	82 (99%)	1 (1%)	63	78
28	w	78/78 (100%)	78 (100%)	0	100	100
29	y	61/63 (97%)	58 (95%)	3 (5%)	22	29
33	z	19/121 (16%)	13 (68%)	6 (32%)	0	0
All	All	2542/2772 (92%)	2505 (98%)	37 (2%)	55	73

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	y	4	LYS
33	z	144	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
29	y	5	LYS
33	z	129	VAL
18	l	85	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
21	o	98	GLN
23	q	81	ASN
21	o	116	GLN
22	p	66	ASN
25	s	7	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	v	76/77 (98%)	28 (36%)	0
31	A	75/77 (97%)	16 (21%)	3 (4%)
32	X	9/9 (100%)	5 (55%)	3 (33%)
34	b	2900/2904 (99%)	1196 (41%)	0
9	a	117/120 (97%)	21 (17%)	0
All	All	3177/3187 (99%)	1266 (39%)	6 (0%)

5 of 1266 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	a	25	U
9	a	26	C
9	a	30	C
9	a	32	U
9	a	35	C

5 of 6 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
32	X	12	G
32	X	14	U
32	X	17	G
31	A	14	A
31	A	9	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	z	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	z	131:LEU	C	132:PHE	N	1.11

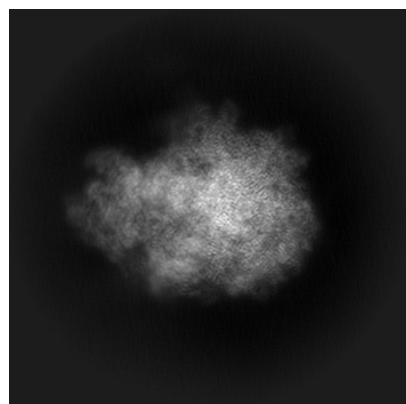
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52512. These allow visual inspection of the internal detail of the map and identification of artifacts.

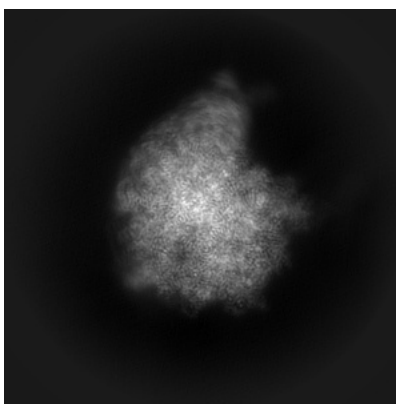
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

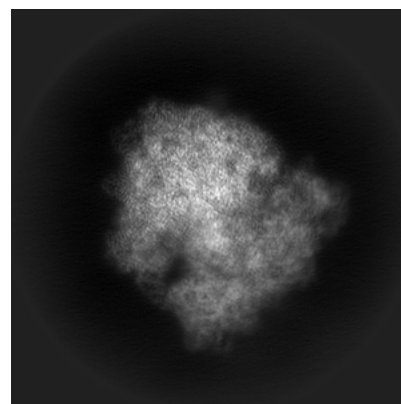
6.1.1 Primary map



X

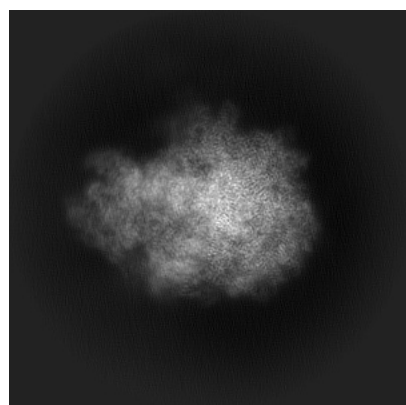


Y

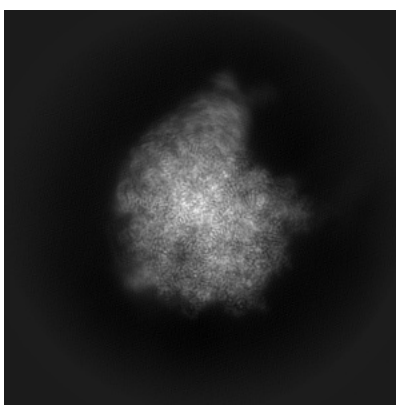


Z

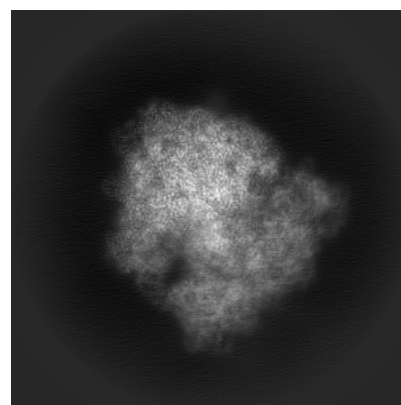
6.1.2 Raw map



X



Y

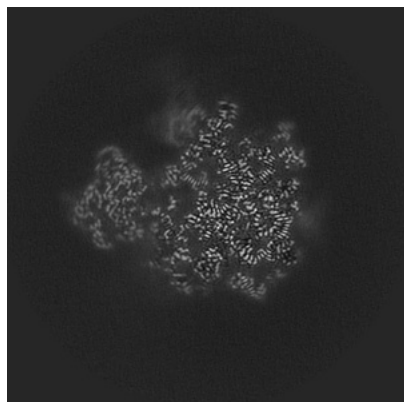


Z

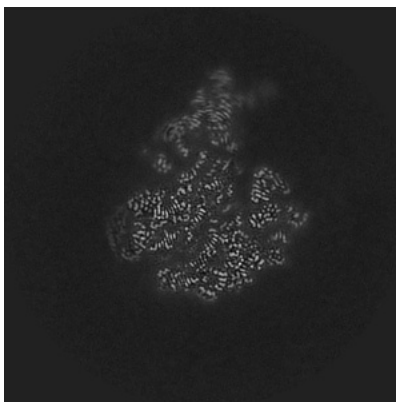
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

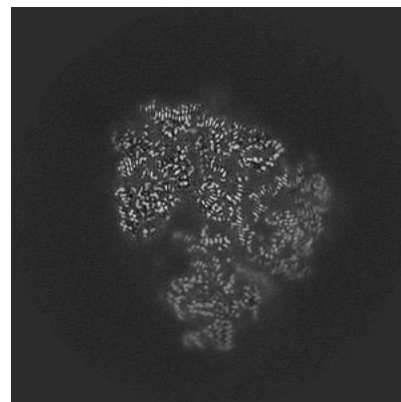
6.2.1 Primary map



X Index: 192

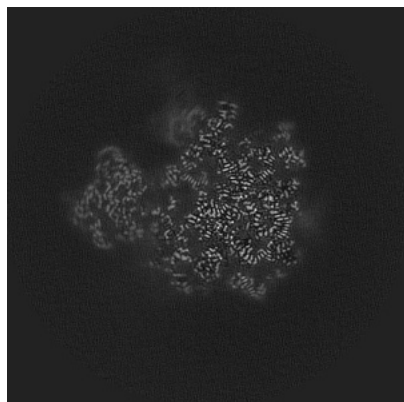


Y Index: 192

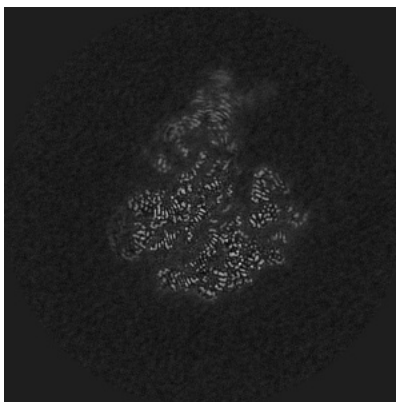


Z Index: 192

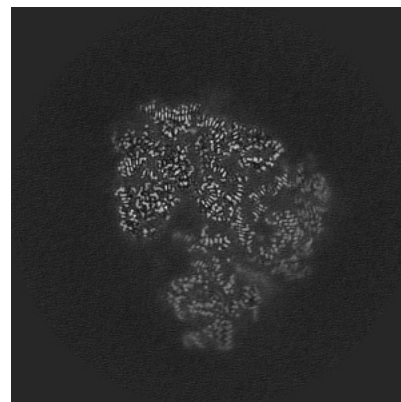
6.2.2 Raw map



X Index: 192



Y Index: 192

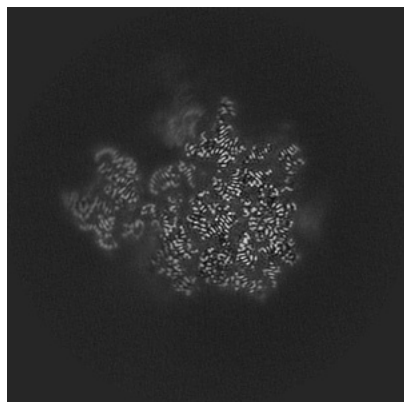


Z Index: 192

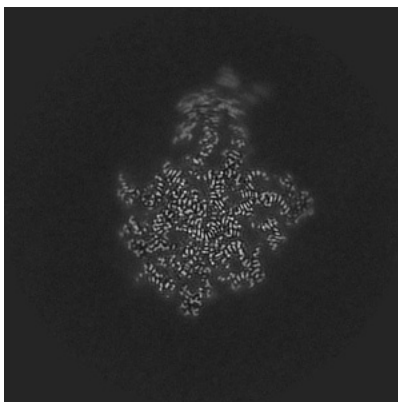
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

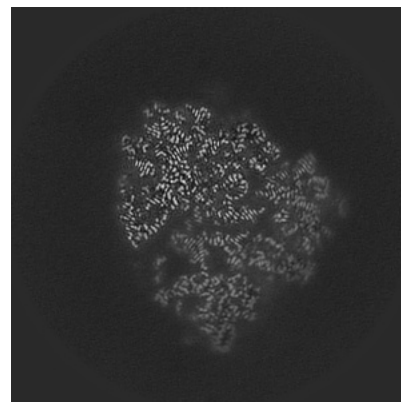
6.3.1 Primary map



X Index: 197

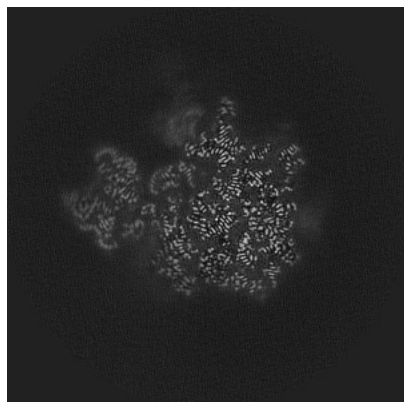


Y Index: 211

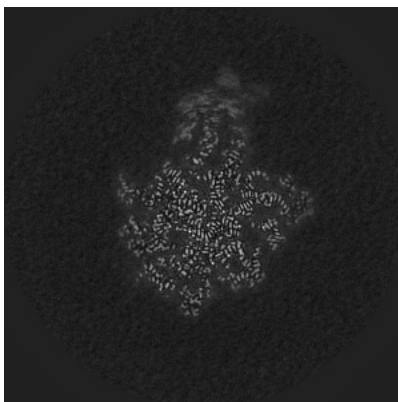


Z Index: 198

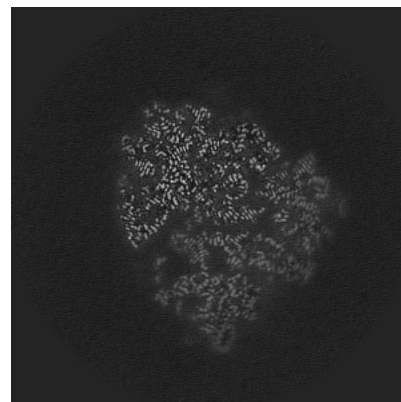
6.3.2 Raw map



X Index: 197



Y Index: 211



Z Index: 198

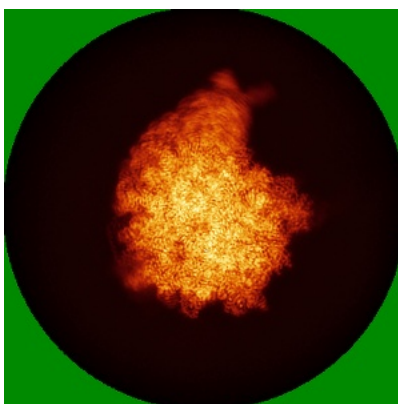
The images above show the largest variance slices of the map in three orthogonal directions.

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

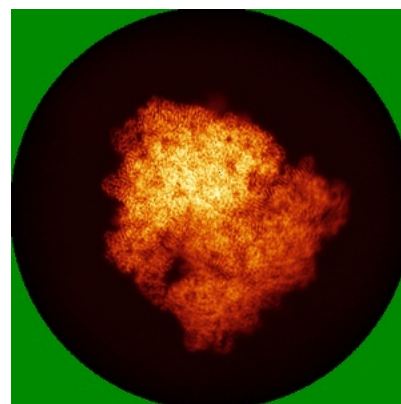
6.4.1 Primary map



X

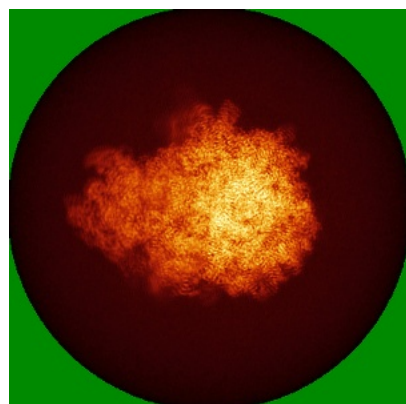


Y

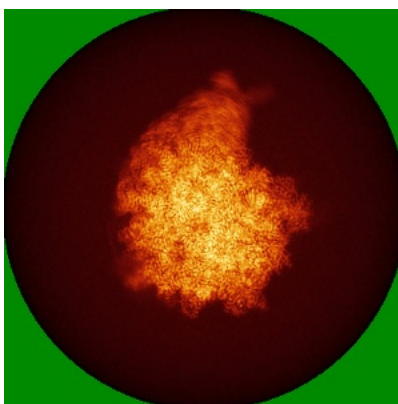


Z

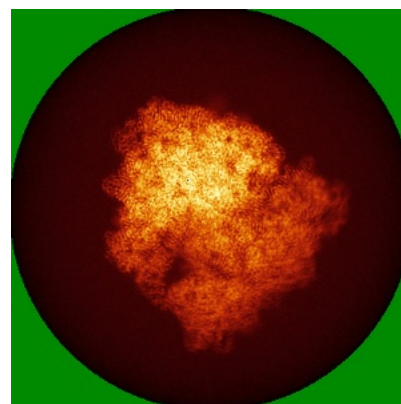
6.4.2 Raw map



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](#)

This section was not generated.

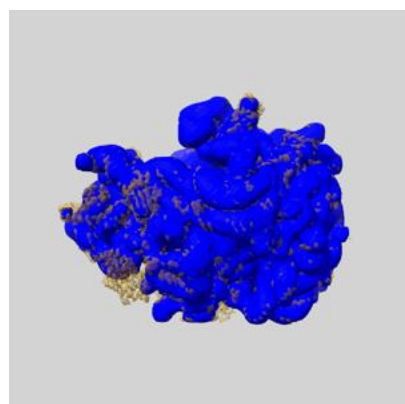
6.6 Mask visualisation [i](#)

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

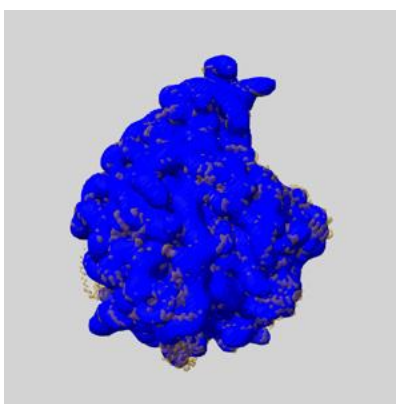
A mask typically either:

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

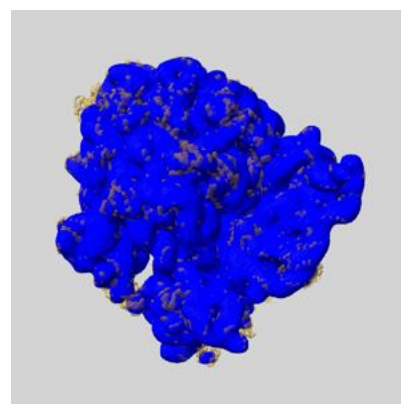
6.6.1 emd_52512_msk_1.map [i](#)



X



Y

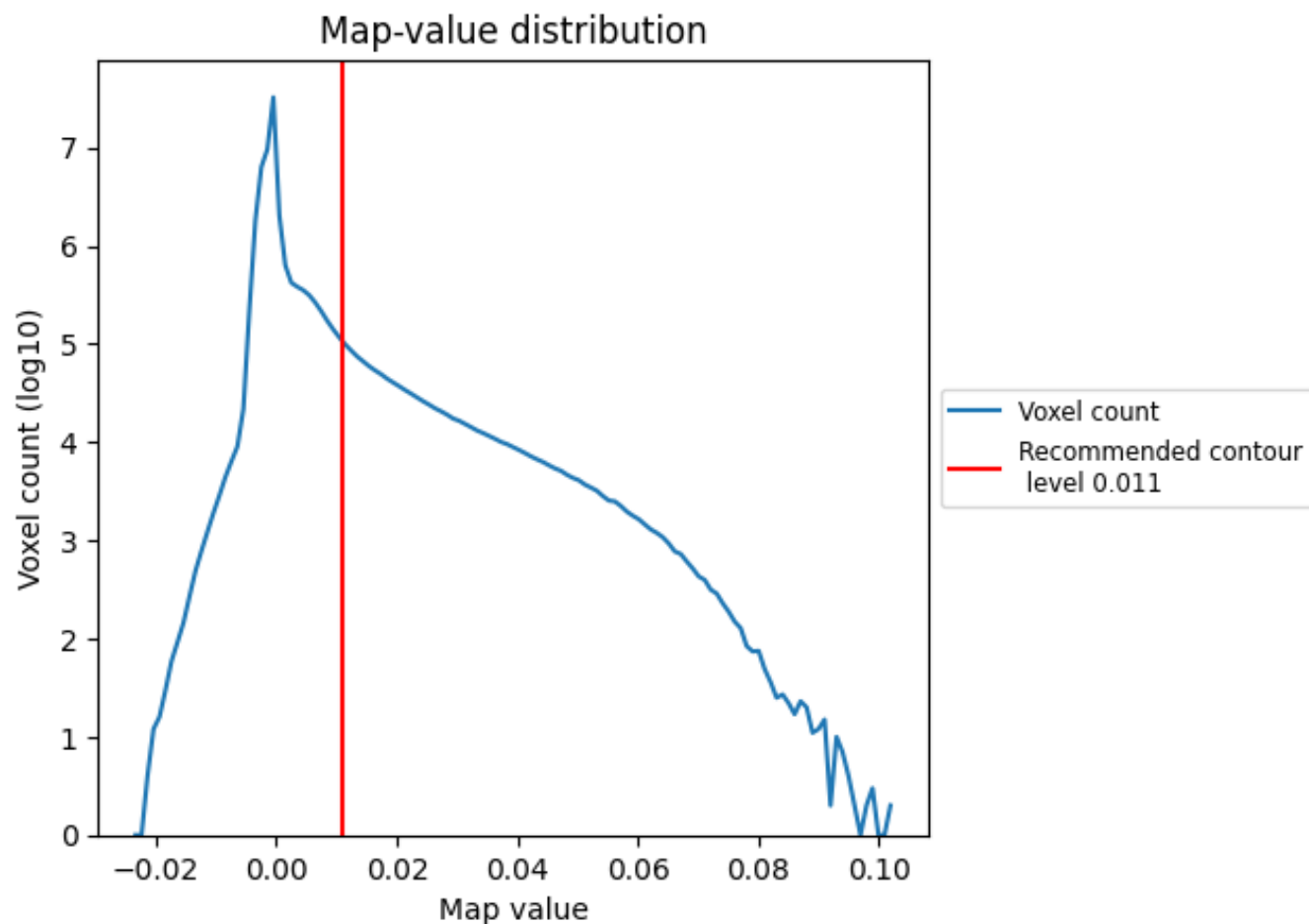


Z

7 Map analysis [i](#)

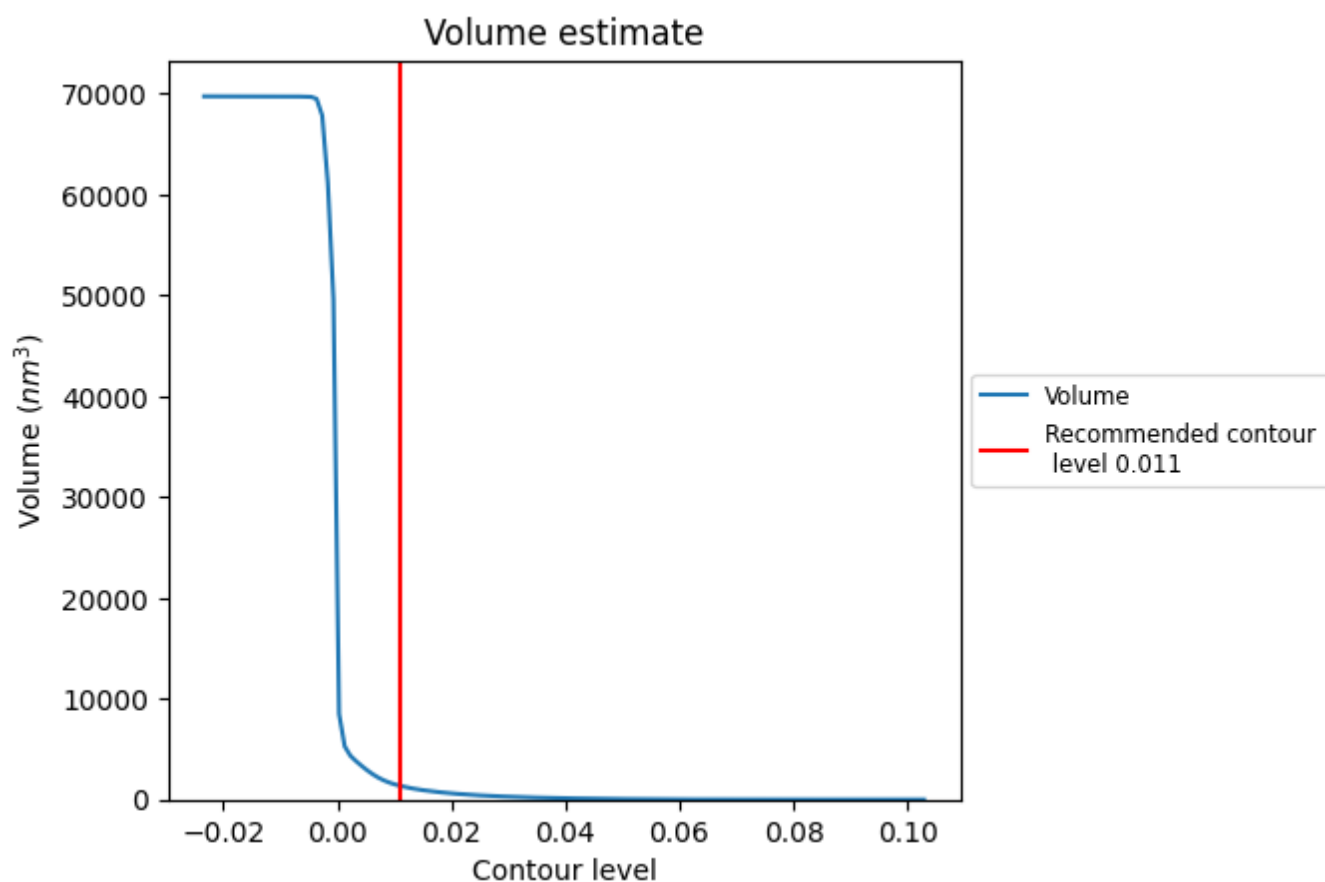
This section contains the results of statistical analysis of the map.

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.

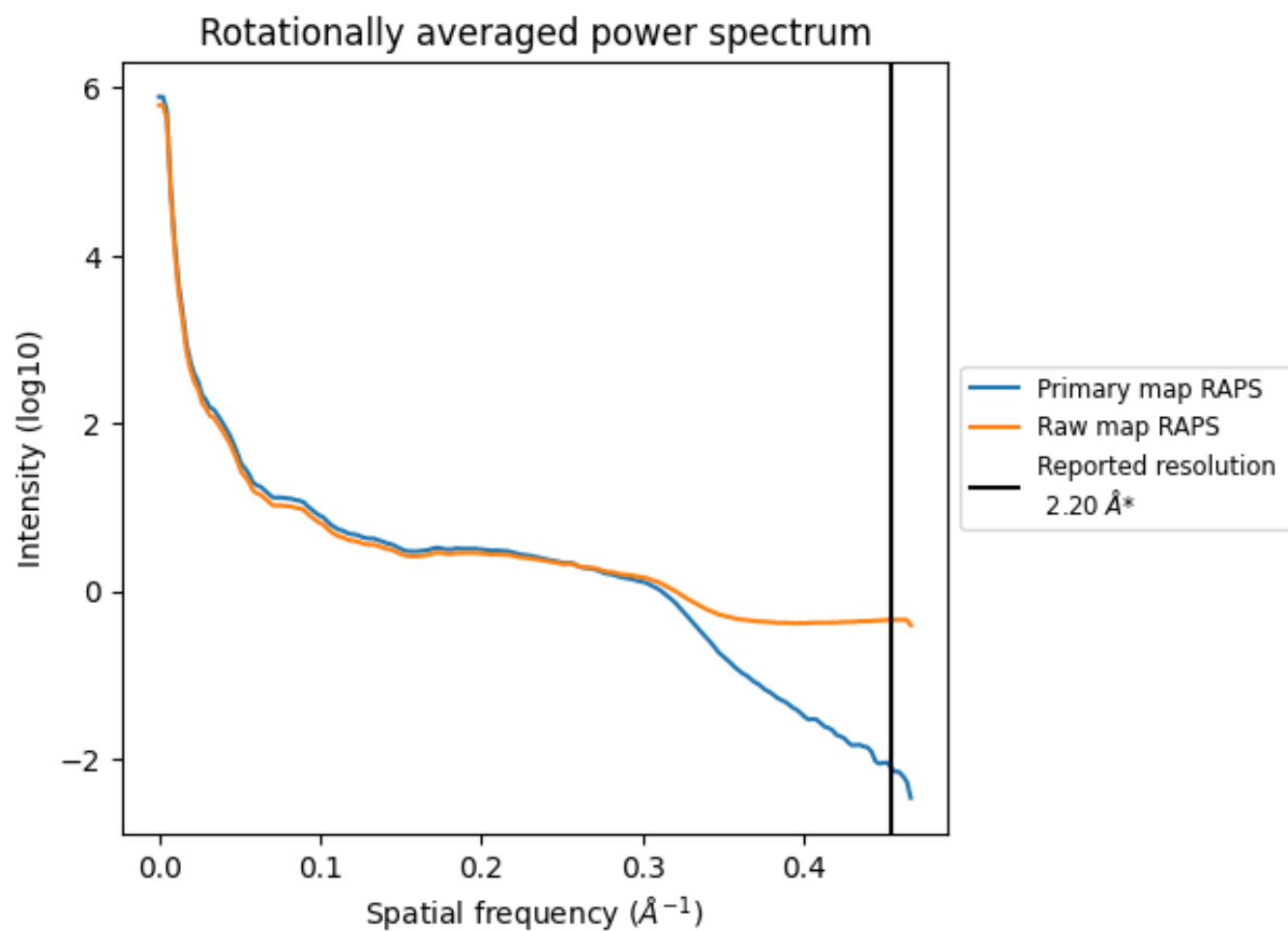
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1365 nm^3 ; this corresponds to an approximate mass of 1233 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 ⓘ

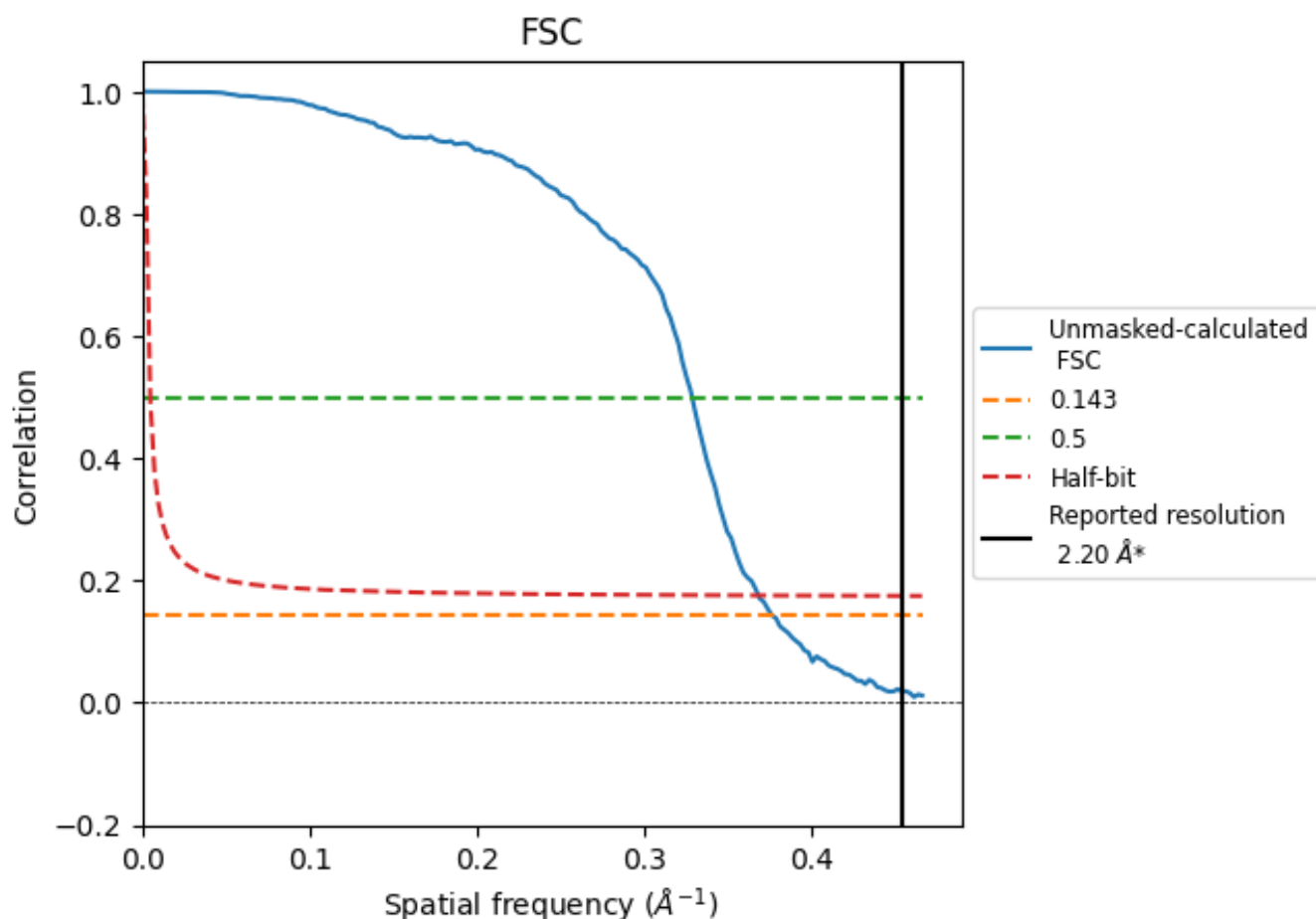


*Reported resolution corresponds to spatial frequency of 0.455 Å⁻¹

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 0.455 Å⁻¹

8.2 Resolution estimates [i](#)

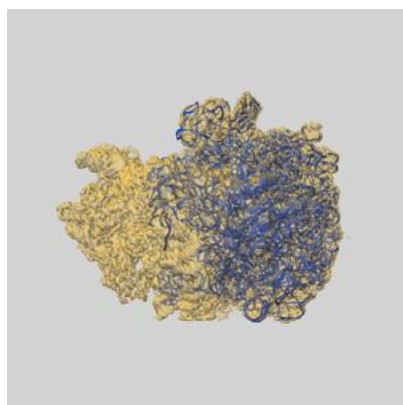
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	2.66	3.04	2.71

*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 2.66 differs from the reported value 2.2 by more than 10 %

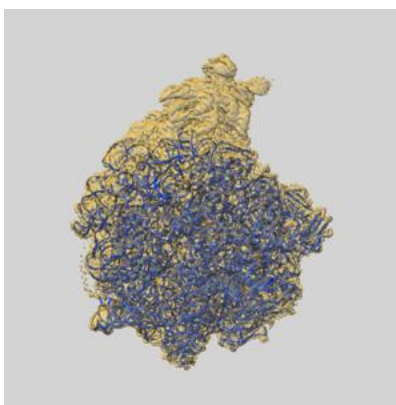
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52512 and PDB model 9HYM. Per-residue inclusion information can be found in section [3](#) on page [11](#).

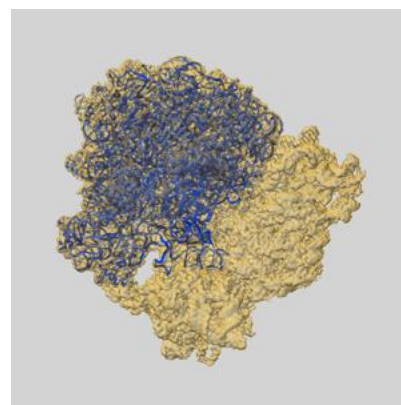
9.1 Map-model overlay [i](#)



X



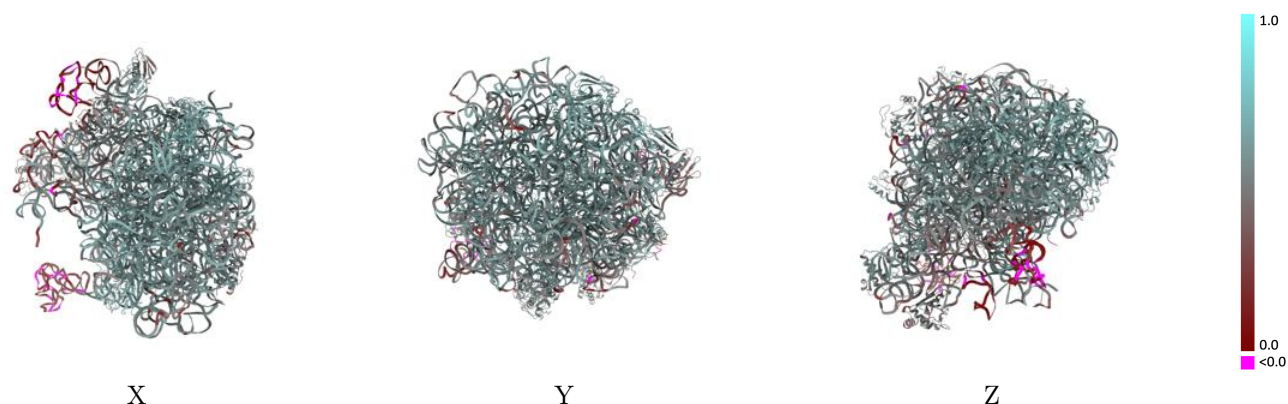
Y



Z

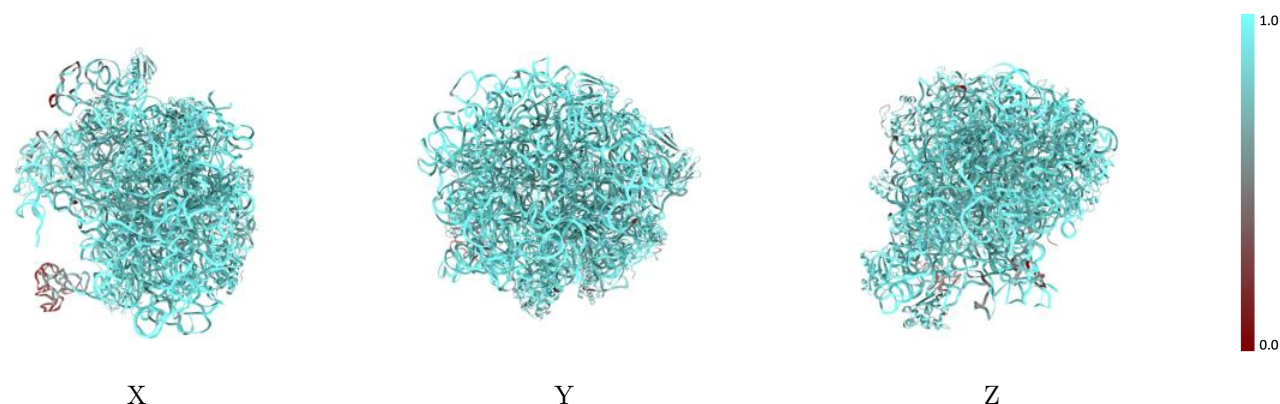
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



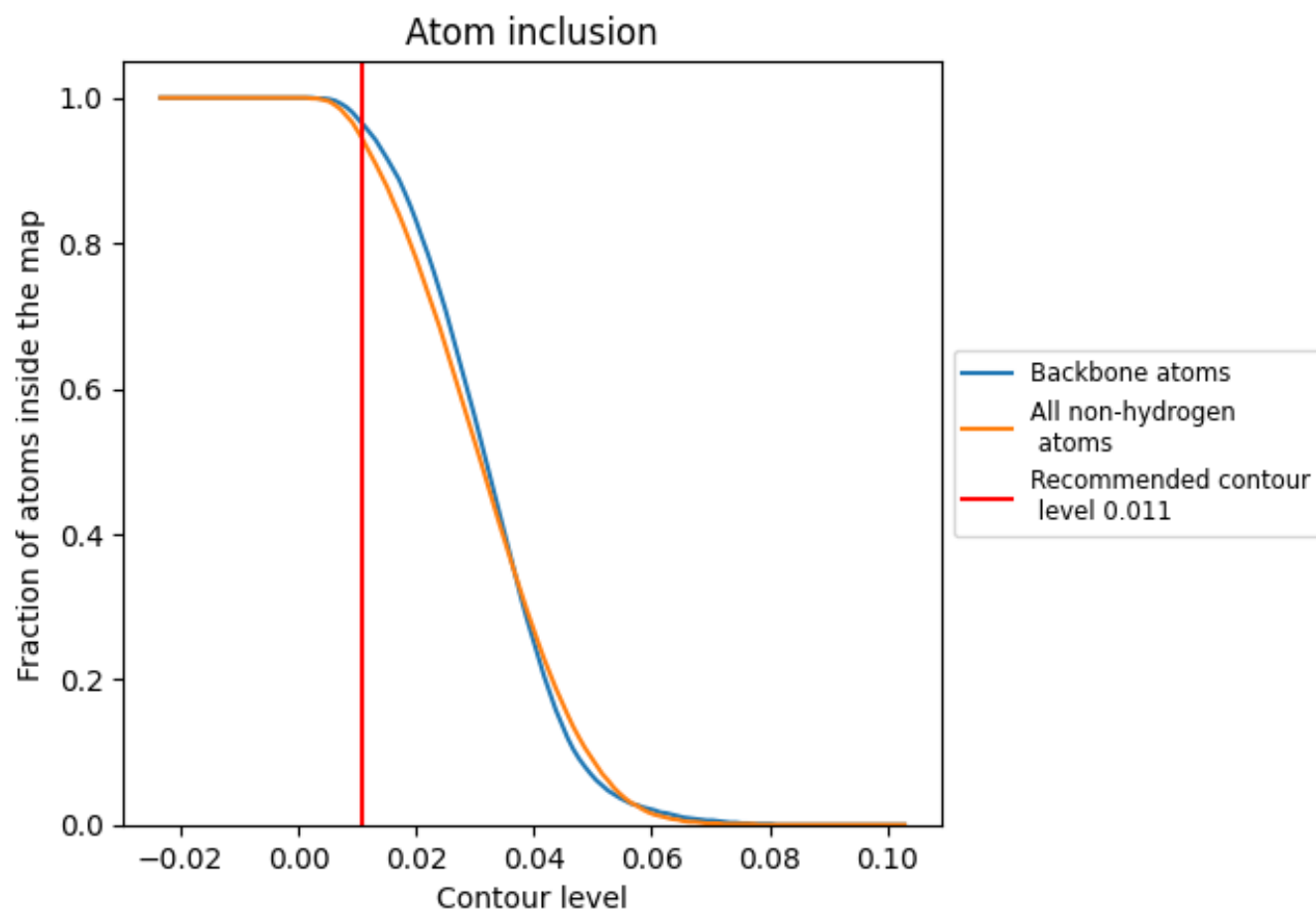
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 94% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9420	 0.5340
0	 0.9720	 0.6330
1	 0.8760	 0.5140
2	 0.9180	 0.5320
3	 0.9620	 0.5960
4	 0.9100	 0.5540
6	 0.9890	 0.6540
7	 0.9880	 0.6340
8	 0.9520	 0.5510
A	 0.9660	 0.5060
X	 0.9580	 0.4690
a	 0.9700	 0.5010
b	 0.9470	 0.5260
c	 0.9830	 0.6400
d	 0.9650	 0.6350
e	 0.8720	 0.5490
f	 0.8410	 0.4520
g	 0.8390	 0.4970
h	 0.7820	 0.5150
j	 0.9560	 0.5950
k	 0.9560	 0.5900
l	 0.9430	 0.5900
m	 0.9120	 0.4960
n	 0.9810	 0.6210
o	 0.8790	 0.5110
p	 0.9360	 0.5860
q	 0.9710	 0.5950
r	 0.8760	 0.5290
s	 0.9590	 0.6100
t	 0.9220	 0.5520
u	 0.8640	 0.4990
v	 0.9530	 0.4850
w	 0.8430	 0.4430
y	 0.9100	 0.5290
z	 0.9420	 0.5670

