



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:22 AM UTC

PDB ID : 9K10 / pdb_00009k10
EMDB ID : EMD-61960
Title : EF-G2 bound 50S ribosome subunit complex of M. smegmatis
Authors : Sengupta, J.; Baid, P.
Deposited on : 2024-10-16
Resolution : 3.60 Å(reported)
Based on initial model : 7XAM

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

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

A user guide is available at

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

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

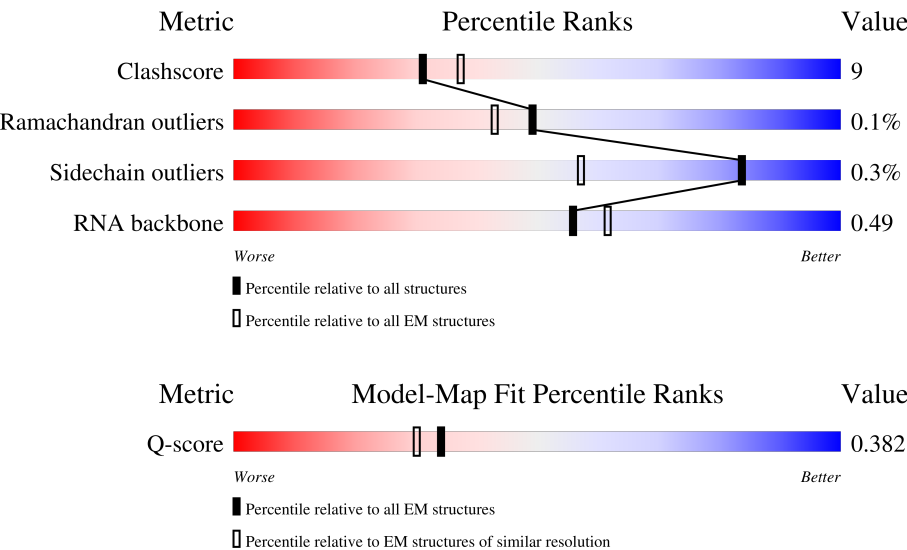
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.60 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.



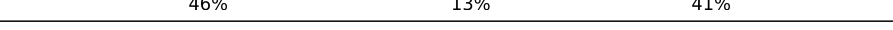
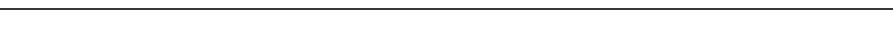
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12797 (3.10 - 4.10)

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	3	24	79% 17% .
2	5	709	11% 68% 31% .
2	6	709	31% 70% 29% .

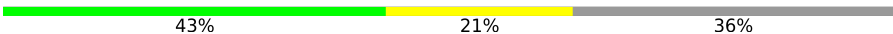
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Mol	Chain	Length	Quality of chain
3	B	118	
4	C	278	
5	D	217	
6	E	215	
7	F	187	
8	G	179	
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	

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Mol	Chain	Length	Quality of chain
28	a	61	 89% 8% .
29	b	57	 75% 19% 5% .
30	c	55	 67% 22% 11% .
31	d	47	 85% 13% .
32	e	64	 77% 22% .
33	f	37	 78% 22%
34	g	75	 43% 21% 36%
35	A	3127	 58% 33% 7% .

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 107523 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a protein called Translation elongation factor EF-G.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		
2	6	709	Total	C	N	O	S	0	0
			5299	3311	931	1039	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	P	126	Total	C	N	O	0	0
			956	586	199	171		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
19	R	124	Total	C	N	O	0	0
			988	613	203	172		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
20	S	100	Total	C	N	O	0	0
			754	478	137	139		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	114	Total	C	N	O	0	0
			873	543	171	159		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

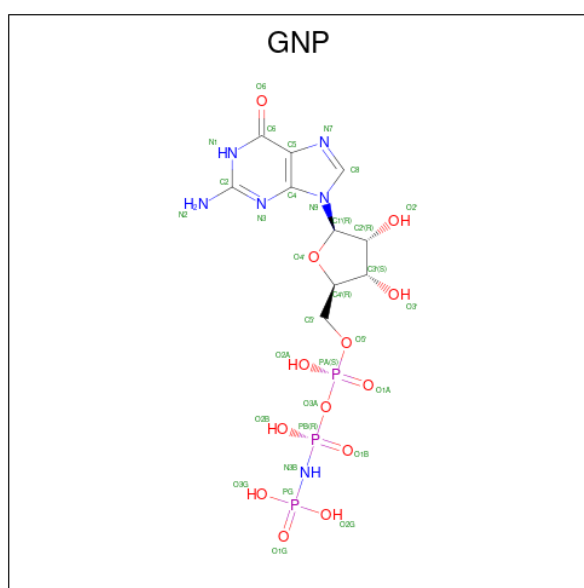
- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 35 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	3062	Total	C	N	O	P	0	0
			65763	29311	12094	21296	3062		

- Molecule 36 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
36	5	1	Total	C	N	O	P	0
			32	10	6	13	3	
36	6	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	B	9	Total	Mg	0
			9	9	
37	C	5	Total	Mg	0
			5	5	
37	D	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
37	F	1	Total 1	Mg 1	0
37	N	1	Total 1	Mg 1	0
37	T	1	Total 1	Mg 1	0
37	X	1	Total 1	Mg 1	0
37	A	388	Total 388	Mg 388	0

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	Y	1	Total 1	Zn 1	0
38	c	1	Total 1	Zn 1	0
38	f	1	Total 1	Zn 1	0
38	g	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.

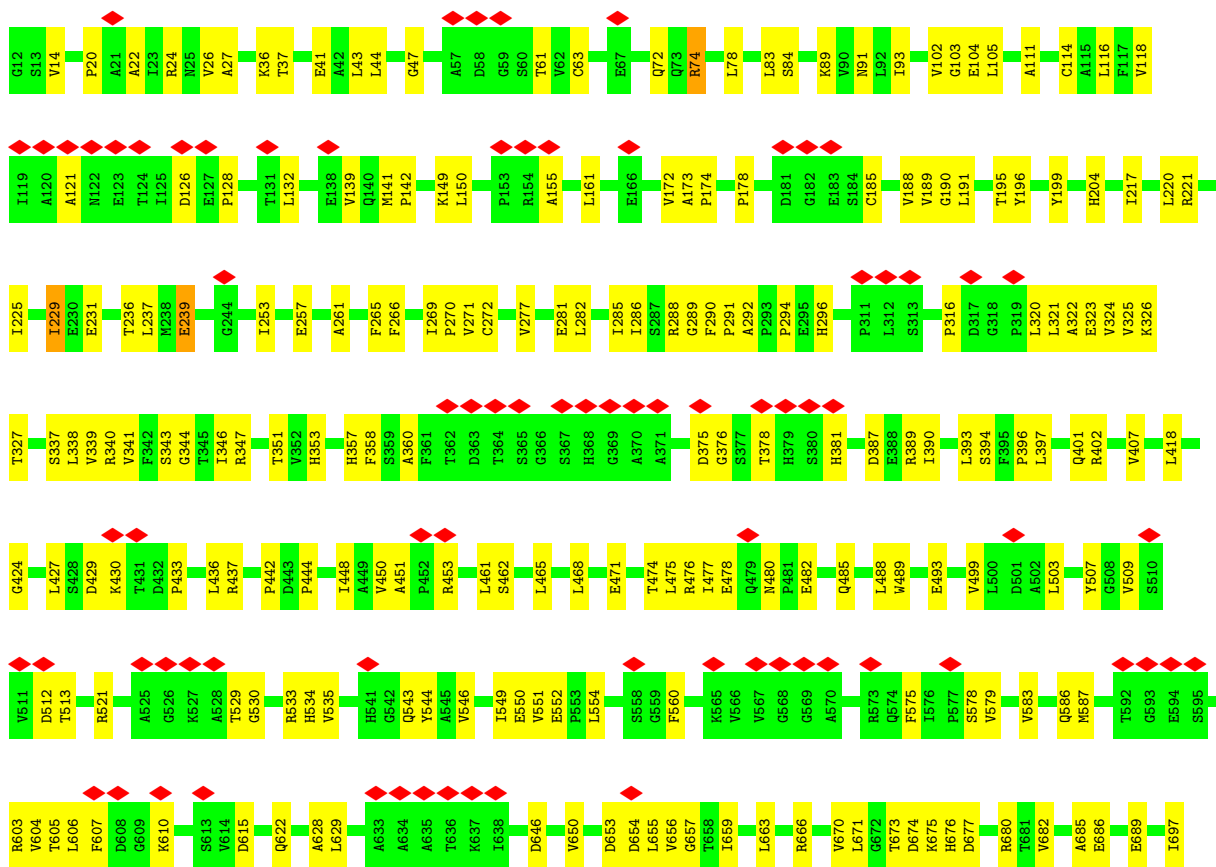
- Molecule 1: 50S ribosomal protein bL37

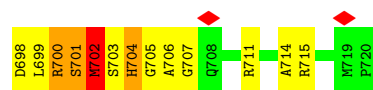
Chain 3: 



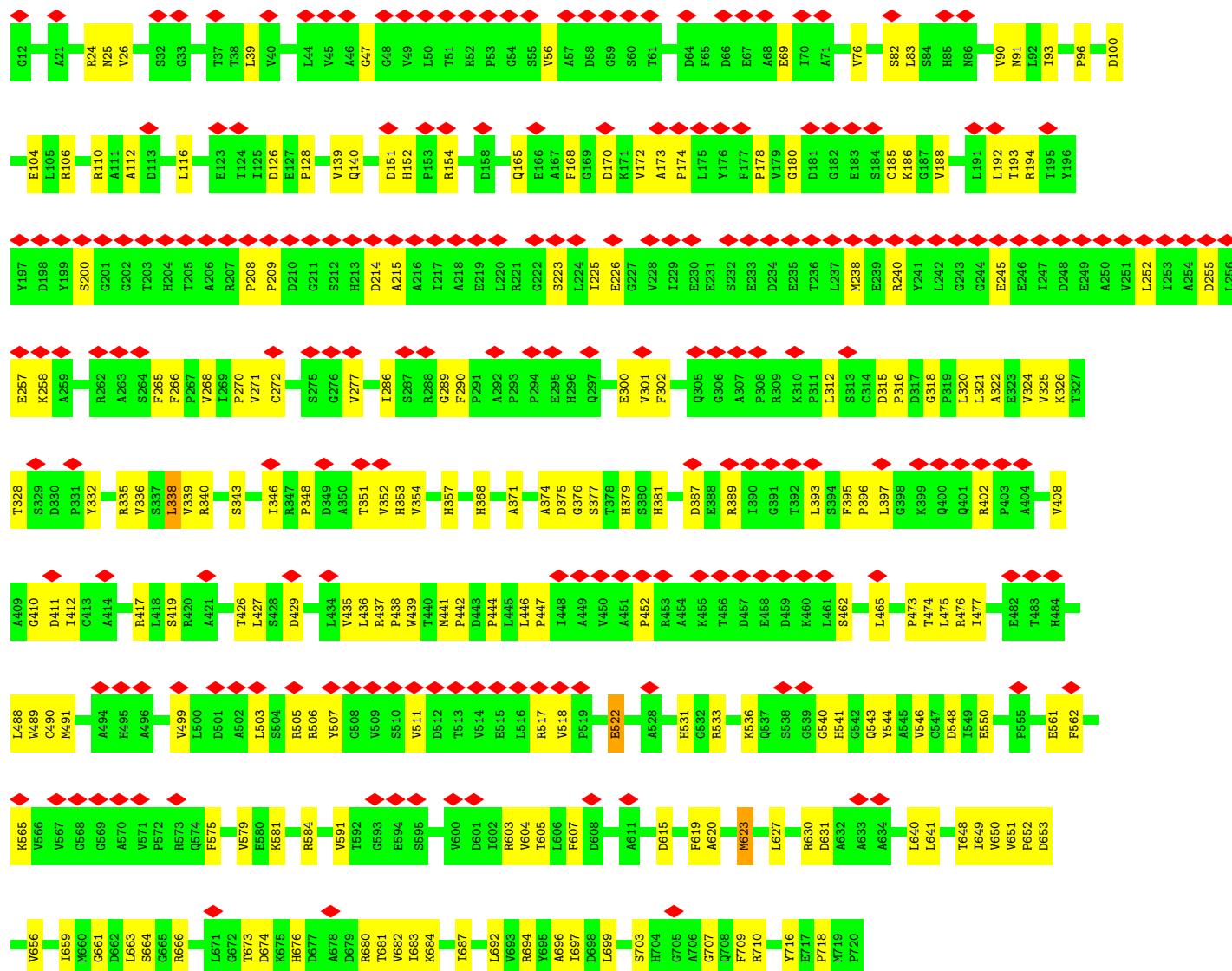
- Molecule 2: Translation elongation factor EF-G

Chain 5: 

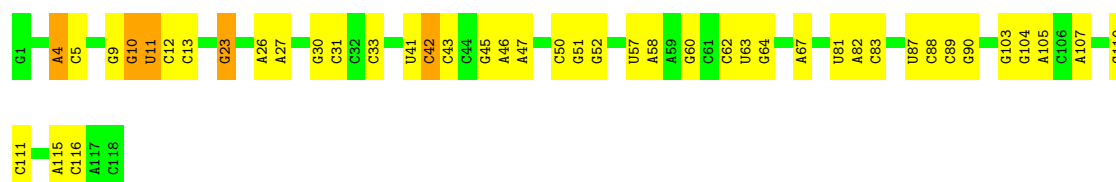




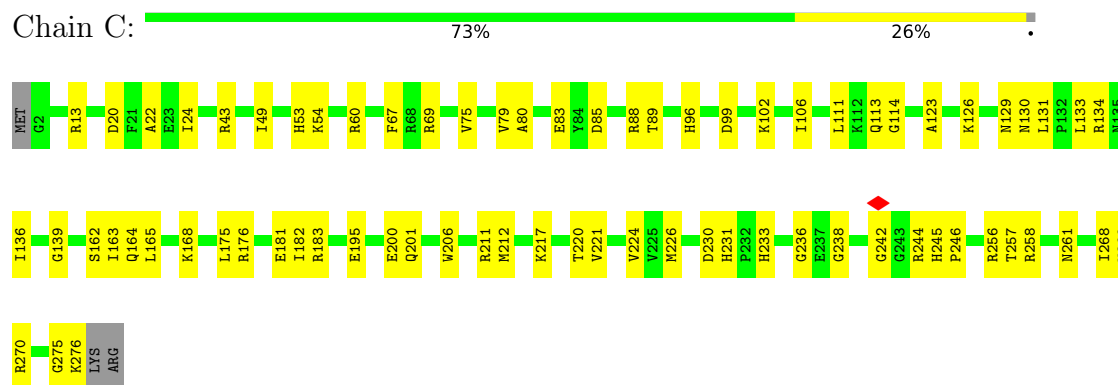
• Molecule 2: Translation elongation factor EF-G



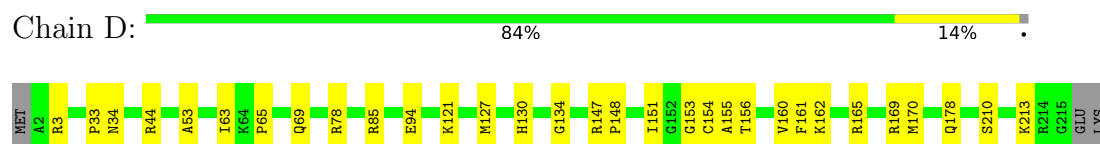
• Molecule 3: 5S ribosomal RNA



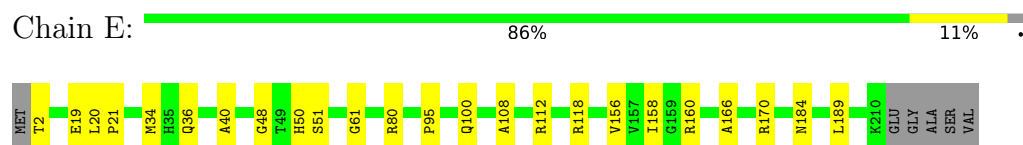
- Molecule 4: 50S ribosomal protein L2



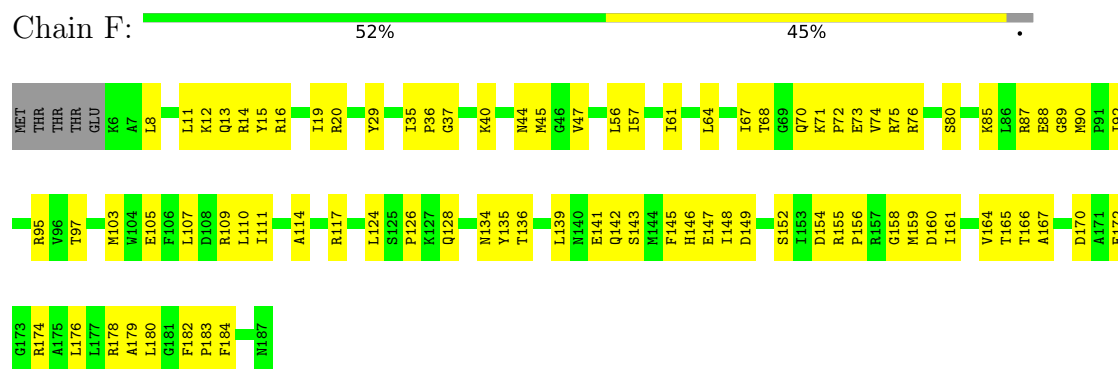
- Molecule 5: 50S ribosomal protein L3



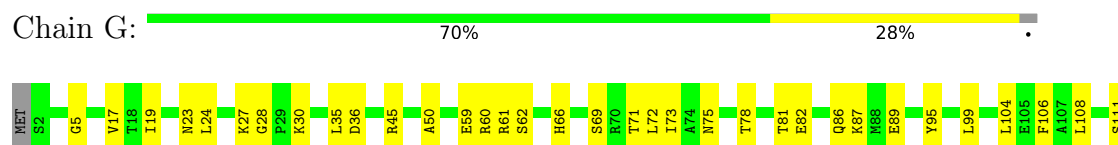
- Molecule 6: 50S ribosomal protein L4



- Molecule 7: 50S ribosomal protein L5

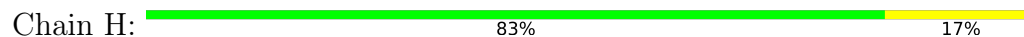


- Molecule 8: 50S ribosomal protein L6

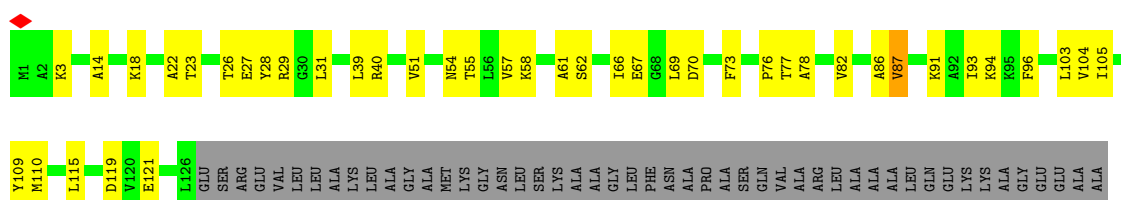




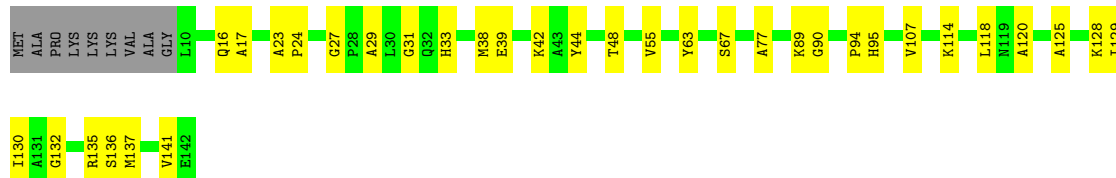
- Molecule 9: 50S ribosomal protein L9



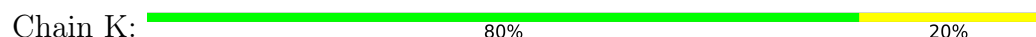
- Molecule 10: 50S ribosomal protein L10



- Molecule 11: 50S ribosomal protein L11



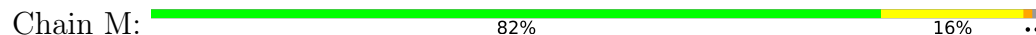
- Molecule 12: 50S ribosomal protein L13

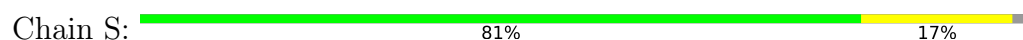


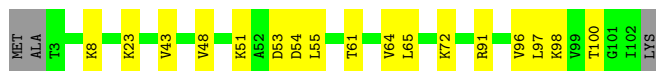
- Molecule 13: 50S ribosomal protein L14



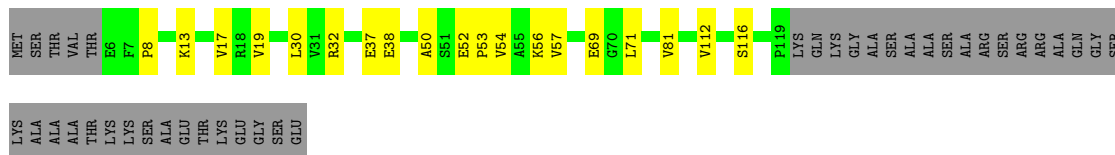
- Molecule 14: 50S ribosomal protein L15



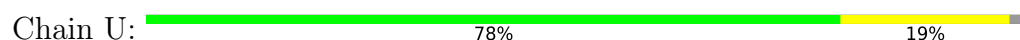




- Molecule 21: 50S ribosomal protein L22



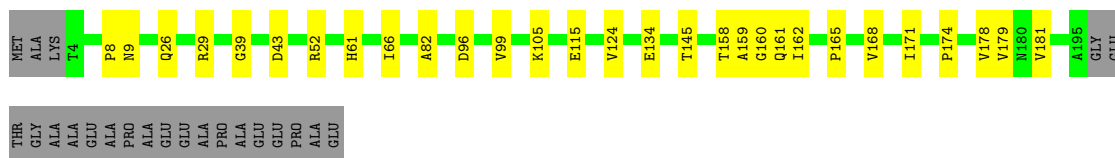
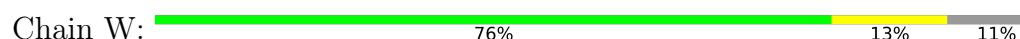
- Molecule 22: 50S ribosomal protein L23



- Molecule 23: Large ribosomal subunit protein uL24



- Molecule 24: 50S ribosomal protein L25



- Molecule 25: 50S ribosomal protein L27



- Molecule 26: 50S ribosomal protein L28



- Molecule 27: 50S ribosomal protein L29

Chain Z:  64% 19% 17%



- Molecule 28: 50S ribosomal protein L30

Chain a:  89% 8% .



- Molecule 29: 50S ribosomal protein L32

Chain b:  75% 19% 5%



- Molecule 30: 50S ribosomal protein L33 1

Chain c:  67% 22% 11%



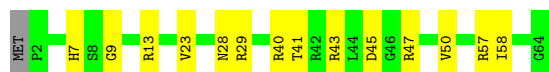
- Molecule 31: 50S ribosomal protein L34

Chain d:  85% 13% .



- Molecule 32: 50S ribosomal protein L35

Chain e:  77% 22% .

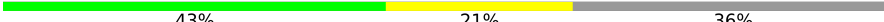


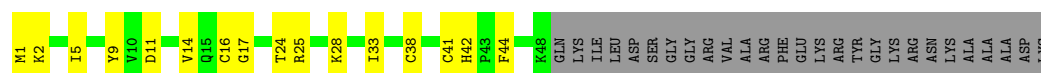
- Molecule 33: 50S ribosomal protein L36

Chain f:  78% 22%



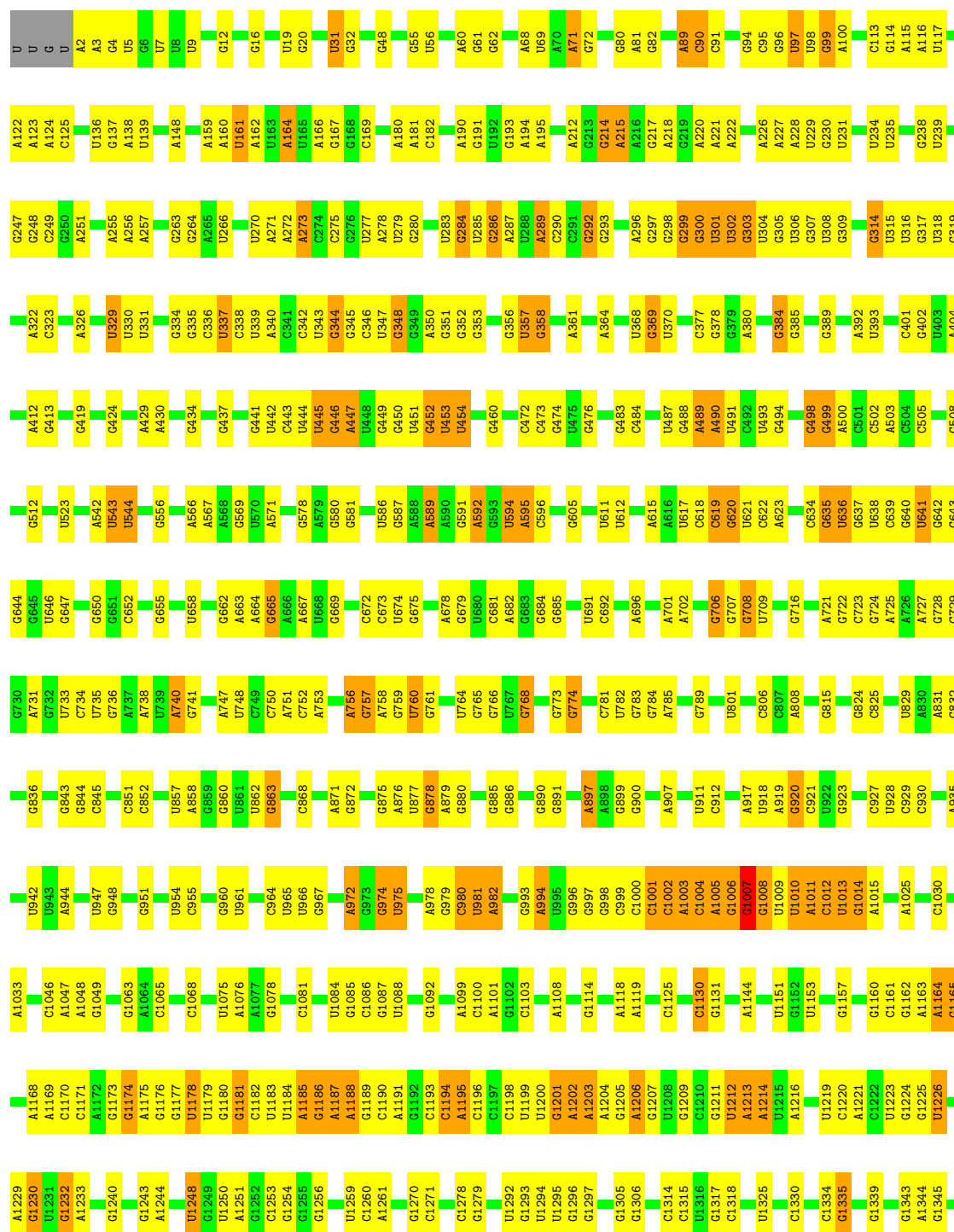
- Molecule 34: 50S ribosomal protein L31

Chain g:  43% 21% 36%



• Molecule 35: 23S ribosomal RNA

Chain A:  58% 33% 7% .



A2609	A2522	U2411	A2342	G2251	G2158	U2098	C2025	A1865	U1732	G1629	C	G1479	G1353
C2610	A2523	U2412	G2343	A2254	G2159	G2099	A2026	C1866	C1733	U1630	C	A1480	G1359
U2611	C2524	G2413	U2344	A2255	A2160	A2100	A2026	C1867	C1734	G1631	A	C1485	G1359
A2616	C2525	U2345	U2345	A2256	A2161	A2101	G2033	G1870	U1735	G1632	C	G1486	A1362
C2622	U2526	U2420	G2346	A2257	A2162	G2102	G2034	G1871	G1736	C1633	C	A1493	G1365
A2623	G2527	A2421	G2347	U2261	U2163	C2103	G2040	A1872	A1737	U1634	U	U1494	G1365
C2627	G2528	C2424	G2348	C2261	U2164	G2104	G2040		A1750	G1639	A	A1499	G1371
C2627	C2529	U2425	A2349	C2262	C2166	G2105	C2043	U1877	C1753	U1641	C	A1500	A1377
A2630	G2530	C2426	A2351	G2263	U2167	A2106	C2043	G1885	G1754	U1641	C	G1501	G1384
G2631	C2531	G2427	C2352	U2264	U2168	G2107	A2046	A1886	A1755	G1645	C	G1507	G1385
G2640	C2532	A2434	U2353	U2265	C2169	A2108	C2047	A1648	U1757		A	U1508	G1396
G2645	G2533	U2435	G2354	A2266	U2170	A2109	G2048	A1649	G1758		C	U1509	A1387
U2647	A2534	U2436	U2355	C2267	C2171	U2110	G2049	A1650	U1760	C1651	U	A1510	U1388
C2648	U2437	A2436	U2356	G2276	G2172	U2111	C2050	C1927	G1761		U	U1389	
A2649	C2537	A2357	A2357	G2277	C2173	U2112	C2050	C1928	U1766		U	G1513	
A2650	A2538	A2358	A2358	G2278	G2174	A2113	C2053	A1929	G1767		U	C1514	
G2653	G2539	C2362	A2363	A2278	U2175	G2114	C2054		C1762		C	G1522	
A2654	G2540	A2364	C2364	C2279	A2176	G2115	C2055	U1937	G1763	A1656	G	G1523	
U2655	G2541	C2365	C2365	G2280	A2177	C2116	C2059	G1938	A1764	G1657	U	G1524	
A2659	U2542	G2366	G2366	A2284	U2178	C2117	G2061	U1939	U1765		G		
C2665	G2543	G2367	G2367	G2285	C2118	C2118	U2062	A1940	U1766	U1665	G		
G2669	U2544	C2368	C2368	A2286	C2119	G2119	G2062		U1767	A1666	U		
A2672	G2545	C2369	C2369	C2287	A2182	A2120	G2063	U1946	C1768	G1670	G		
G2677	A2546	G2370	G2370	C2288	A2184	G2121	A2064	U1947	G1769		U		
G2678	U2547	U2371	U2371	C2289	C2185	U2122	A2065	A1948	C1781	U1675	U		
G2679	C2548	A2465	A2465	C2290	C2186	A2123	G2066	G1950	U1782	G1676	U		
U2686	U2549	G2467	G2467	A2294	U2187	A2124	G2067		G1766	G1677	C		
A2687	G2550	U2468	U2468	C2295	C2188	A2125	U2068	G1953	A1787	U1678	G		
A2688	C2551	U2469	U2469	C2296	A2190	C2126	U2069	C1954	G1788	A1679	U		
C2689	U2552	U2470	U2470	U2297	C2191	G2127	A2070	A1680	U1789	U1681	U		
C2690	G2553	A2471	G2380	U2298	G2192	C2128	A2071	G1963	A1790	G1687	U		
C2691	U2554	C2472	A2381	U2315	A2194	G2130	G2072	U1964	A1791		G		
A2692	G2555	A2480	U2383	G2316	U2195	U2132	A2073		A1792		U		
A2693	C2556	A2491	G2384	C2320	G2196	G2133	G2074	G1973	U1798	A1690	G		
A2694	U2557	A2492	G2385	U2321	G2197	U2135	G2075	A1974		A1691	G		
C2698	G2558	G2495	U2386	C2322	U2215	A	A2076	U1981	G1802	G1703	U		
C2699	C2559	U2496	G2387	C2323	G2216	C	C2077	U1996	A1803	C1705	U		
C2700	U2560	A2497	U2388	A2324	G2217	U	C2078	C1998	G1804	A1715	U		
A2701	G2561	A2498	U2389	U2325	C2220	A	C2079	A2001	G1805	A1716	U		
A2702	C2562	A2502	G2391	A2326	A2221	U	G2080	U1825	C1825	U1713	U		
G2705	U2563	C2507	A2392	C2327	A2227	C	U2081	A1826	U1714	G1613	U		
U2715	G2564	C2508	A2393	G2328	C2227	C2145	U2082	G1840	A1715	G1614	U		
U2716	C2565	C2509	A2394	U2331	A2238	C2085	A2084		A1716	G1615	U		
U2717	G2566	A2510	U2395	U2332	A2239	C2086	U2086	G1719	G1716	C1617	U		
	C2567	A2511	C2400	U2333	A2244	U2087	C2087	G1720	U1620	C1561	C		
	G2568	U2512	U2401	G2335	A2245	C2148	G2014	G1724	G1622	C1465	A		
	U2569	U2515	C2402	A2337	U2246	C2149	G2015	U1728	G1625	U1467	A		
	C2570	U2516	U2406	G2338	A2247	U2150	G2017	A1730	U1626	A1468	A		
	U2571	G2517	G2408	G2339	C2248	A2151	C2017	U1731	U1627	A1469	A		
	C2572	U2518	U2409	U2341	A2250	G2152	G2019	A1731	A1628		A		

A3081	G2718	U2833	C2950
U3082	G2719	U2837	G2953
C3088	C2720	A2838	U2953
A3089	G2726	U2839	A2957
A3093	A2727	C2853	G2961
U3096	U2728	A2854	A2962
C3101	G2729	G2857	G2968
A3104	U2730	A2858	C2969
C3105	G2731	G2861	U2970
C3106	C2732	G2862	G2971
G3107	U2735	G2865	A2972
A3112	G2738	A2866	A2982
A3113	C2739	A2867	G2985
A3114	A2742	A2868	G2986
A3115	U2743	G2869	A3002
C3116	C2744	C2870	U3009
U3117	C2745	U2871	C3013
U3118	G2749	G2872	A3014
A3119	G2750	U2873	C3015
C3120	G2760	C2874	C3019
A	U2761	G2879	U3020
A	C2762	A2884	A3021
C	G2774	G2885	G3022
A	C2775	G2886	G3023
	U2778	G2887	A3024
	U2779	G2888	A3030
	C2780	C2891	A3031
	G2781	A2902	G3032
	C2782	A2903	G3033
	G2783	U2908	G3034
	C2784	A2912	C3038
	A2785	U2913	C3039
	U2786	A2914	G3040
	U2787	C2915	C3041
	A2788	U2922	A3042
	U2789	C2923	C3046
	A2790	G2924	A3056
	G2791	C2925	C3067
	C2796	A2926	U3068
	C2797	G2933	G3069
	G2800	G2805	G3070
	G2806	C2936	A3071
	U2810	G2937	G3078
	U2810	G2938	U3079
	A2826	G2941	A3080
	G2827	G2942	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	39621	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.118	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.00715	Depositor
Map size (Å)	483.0, 483.0, 483.0	wwPDB
Map dimensions	350, 350, 350	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GNP, MG

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	3	0.27	0/191	0.41	0/247
2	5	0.17	0/5405	0.38	1/7360 (0.0%)
2	6	0.20	1/5405 (0.0%)	0.39	0/7360
3	B	0.27	0/2821	0.27	0/4396
4	C	0.36	0/2153	0.45	0/2895
5	D	0.35	0/1609	0.45	0/2165
6	E	0.32	0/1592	0.39	0/2153
7	F	0.21	0/1467	0.42	0/1973
8	G	0.24	0/1369	0.36	0/1848
9	H	0.18	0/1027	0.36	0/1398
10	I	0.16	0/925	0.39	2/1246 (0.2%)
11	J	0.16	0/1006	0.36	0/1364
12	K	0.36	0/1157	0.37	0/1567
13	L	0.33	0/946	0.39	0/1268
14	M	0.31	0/1091	0.49	2/1457 (0.1%)
15	N	0.32	0/1118	0.46	0/1506
16	O	0.36	0/945	0.43	0/1267
17	P	0.27	0/966	0.48	0/1298
18	Q	0.30	0/921	0.41	0/1236
19	R	0.35	0/1000	0.37	0/1341
20	S	0.34	0/764	0.42	0/1030
21	T	0.34	0/887	0.40	0/1204
22	U	0.30	0/766	0.34	0/1030
23	V	0.28	0/738	0.35	0/987
24	W	0.24	0/1443	0.35	0/1970
25	X	0.33	0/595	0.33	0/798
26	Y	0.35	0/478	0.44	0/641
27	Z	0.34	0/534	0.47	0/713
28	a	0.33	0/477	0.30	0/640
29	b	0.34	0/427	0.45	0/572
30	c	0.20	0/413	0.36	0/553
31	d	0.35	0/380	0.45	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.20	0/507	0.33	0/672
33	f	0.31	0/303	0.37	0/401
34	g	0.14	0/372	0.32	0/503
35	A	0.34	0/73637	0.33	5/114895 (0.0%)
All	All	0.32	1/115835 (0.0%)	0.35	10/172454 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	6	517	ARG	C-N	6.23	1.40	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	A	1761	G	P-O3'-C3'	20.49	150.93	120.20
35	A	1538	G	P-O3'-C3'	7.56	131.54	120.20
35	A	1007	G	C2'-C3'-O3'	-6.78	103.52	113.70
35	A	1761	G	OP1-P-O3'	6.57	127.71	108.00
14	M	43	ARG	CA-C-N	-6.24	114.04	121.90

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	3	189	0	205	3	0
2	5	5299	0	5230	167	0
2	6	5299	0	5229	163	0
3	B	2522	0	1285	23	0
4	C	2110	0	2165	65	0
5	D	1587	0	1629	24	0
6	E	1569	0	1607	19	0
7	F	1445	0	1476	69	0
8	G	1348	0	1399	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	H	1018	0	988	19	0
10	I	918	0	959	32	0
11	J	990	0	1021	43	0
12	K	1130	0	1167	24	0
13	L	938	0	999	28	0
14	M	1078	0	1151	20	0
15	N	1092	0	1128	22	0
16	O	928	0	972	21	0
17	P	956	0	991	20	0
18	Q	907	0	938	13	0
19	R	988	0	1038	15	0
20	S	754	0	802	10	0
21	T	873	0	909	12	0
22	U	756	0	802	12	0
23	V	732	0	782	18	0
24	W	1428	0	1443	18	0
25	X	586	0	601	12	0
26	Y	470	0	480	12	0
27	Z	531	0	541	16	0
28	a	474	0	500	5	0
29	b	423	0	463	11	0
30	c	405	0	407	13	0
31	d	377	0	411	5	0
32	e	502	0	541	13	0
33	f	299	0	321	6	0
34	g	364	0	348	15	0
35	A	65763	0	33080	774	0
36	5	32	0	13	1	0
36	6	32	0	13	2	0
37	A	388	0	0	0	0
37	B	9	0	0	0	0
37	C	5	0	0	0	0
37	D	1	0	0	0	0
37	F	1	0	0	0	0
37	N	1	0	0	0	0
37	T	1	0	0	0	0
37	X	1	0	0	0	0
38	Y	1	0	0	0	0
38	c	1	0	0	0	0
38	f	1	0	0	0	0
38	g	1	0	0	0	0
All	All	107523	0	74034	1581	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 9.

The worst 5 of 1581 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:6:332:TYR:OH	13:L:47:ILE:HD12	1.68	0.92
35:A:2086:U:H3	35:A:2096:G:H1	1.25	0.84
11:J:89:LYS:HB3	35:A:1182:C:H5''	1.60	0.82
35:A:860:G:HO2'	35:A:863:G:HO2'	1.26	0.81
4:C:261:ASN:HD21	35:A:2451:A:H5''	1.45	0.81

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	3	21/24 (88%)	19 (90%)	2 (10%)	0	100	100
2	5	707/709 (100%)	673 (95%)	31 (4%)	3 (0%)	30	61
2	6	707/709 (100%)	679 (96%)	27 (4%)	1 (0%)	48	79
4	C	273/278 (98%)	258 (94%)	15 (6%)	0	100	100
5	D	212/217 (98%)	200 (94%)	12 (6%)	0	100	100
6	E	207/215 (96%)	203 (98%)	4 (2%)	0	100	100
7	F	180/187 (96%)	175 (97%)	5 (3%)	0	100	100
8	G	174/179 (97%)	169 (97%)	5 (3%)	0	100	100
9	H	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
10	I	124/175 (71%)	120 (97%)	4 (3%)	0	100	100
11	J	131/142 (92%)	126 (96%)	5 (4%)	0	100	100
12	K	144/147 (98%)	139 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	L	120/122 (98%)	115 (96%)	5 (4%)	0	100	100
14	M	143/147 (97%)	129 (90%)	14 (10%)	0	100	100
15	N	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
16	O	116/199 (58%)	111 (96%)	5 (4%)	0	100	100
17	P	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
18	Q	111/113 (98%)	103 (93%)	8 (7%)	0	100	100
19	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
20	S	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
21	T	112/153 (73%)	106 (95%)	6 (5%)	0	100	100
22	U	95/100 (95%)	93 (98%)	2 (2%)	0	100	100
23	V	93/105 (89%)	90 (97%)	3 (3%)	0	100	100
24	W	190/215 (88%)	182 (96%)	8 (4%)	0	100	100
25	X	77/88 (88%)	73 (95%)	4 (5%)	0	100	100
26	Y	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
27	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	52 (100%)	0	0	100	100
30	c	47/55 (86%)	43 (92%)	3 (6%)	1 (2%)	5	31
31	d	44/47 (94%)	43 (98%)	1 (2%)	0	100	100
32	e	61/64 (95%)	59 (97%)	2 (3%)	0	100	100
33	f	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
34	g	46/75 (61%)	45 (98%)	1 (2%)	0	100	100
All	All	5029/5409 (93%)	4820 (96%)	204 (4%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	5	375	ASP
2	6	381	HIS
30	c	7	VAL
2	5	702	MET
2	5	381	HIS

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	3	18/19 (95%)	18 (100%)	0	100	100
2	5	564/564 (100%)	557 (99%)	7 (1%)	63	73
2	6	564/564 (100%)	558 (99%)	6 (1%)	65	74
4	C	215/218 (99%)	215 (100%)	0	100	100
5	D	160/163 (98%)	160 (100%)	0	100	100
6	E	169/173 (98%)	169 (100%)	0	100	100
7	F	151/156 (97%)	150 (99%)	1 (1%)	76	78
8	G	148/150 (99%)	148 (100%)	0	100	100
9	H	90/116 (78%)	90 (100%)	0	100	100
10	I	89/120 (74%)	89 (100%)	0	100	100
11	J	102/108 (94%)	102 (100%)	0	100	100
12	K	119/120 (99%)	119 (100%)	0	100	100
13	L	100/100 (100%)	100 (100%)	0	100	100
14	M	112/114 (98%)	112 (100%)	0	100	100
15	N	114/116 (98%)	114 (100%)	0	100	100
16	O	97/158 (61%)	97 (100%)	0	100	100
17	P	93/94 (99%)	93 (100%)	0	100	100
18	Q	100/100 (100%)	100 (100%)	0	100	100
19	R	97/99 (98%)	97 (100%)	0	100	100
20	S	81/83 (98%)	81 (100%)	0	100	100
21	T	90/117 (77%)	90 (100%)	0	100	100
22	U	83/85 (98%)	83 (100%)	0	100	100
23	V	81/86 (94%)	81 (100%)	0	100	100
24	W	155/168 (92%)	155 (100%)	0	100	100
25	X	58/63 (92%)	58 (100%)	0	100	100
26	Y	50/51 (98%)	50 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Z	58/66 (88%)	58 (100%)	0	100	100
28	a	52/54 (96%)	52 (100%)	0	100	100
29	b	43/46 (94%)	43 (100%)	0	100	100
30	c	47/52 (90%)	47 (100%)	0	100	100
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	53/54 (98%)	53 (100%)	0	100	100
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/63 (68%)	43 (100%)	0	100	100
All	All	4066/4311 (94%)	4052 (100%)	14 (0%)	84	83

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	6	338	LEU
2	6	346	ILE
7	F	161	ILE
2	6	522	GLU
2	6	623	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
24	W	6	ASN
26	Y	47	GLN
24	W	9	ASN
24	W	91	ASN
31	d	9	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	B	117/118 (99%)	18 (15%)	1 (0%)
35	A	3059/3127 (97%)	640 (20%)	34 (1%)
All	All	3176/3245 (97%)	658 (20%)	35 (1%)

5 of 658 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	B	4	A
3	B	9	G
3	B	11	U
3	B	12	C
3	B	13	C

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	A	2163	U
35	A	2168	U
35	A	2350	G
35	A	980	C
35	A	974	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](#)

Of 413 ligands modelled in this entry, 411 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
36	GNP	6	801	-	34,34,34	1.29	5 (14%)	47,54,54	0.67	0
36	GNP	5	801	-	34,34,34	1.29	5 (14%)	47,54,54	0.69	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GNP	6	801	-	-	3/18/38/38	0/3/3/3
36	GNP	5	801	-	-	4/18/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	6	801	GNP	PB-O3A	4.45	1.64	1.59
36	5	801	GNP	PB-O3A	4.31	1.64	1.59
36	6	801	GNP	PB-O1B	3.23	1.51	1.46
36	5	801	GNP	PB-O1B	3.17	1.51	1.46
36	5	801	GNP	PG-N3B	3.01	1.71	1.63

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	5	801	GNP	C5'-O5'-PA-O3A
36	5	801	GNP	C5'-O5'-PA-O1A
36	5	801	GNP	O4'-C4'-C5'-O5'
36	6	801	GNP	O4'-C4'-C5'-O5'
36	6	801	GNP	C3'-C4'-C5'-O5'

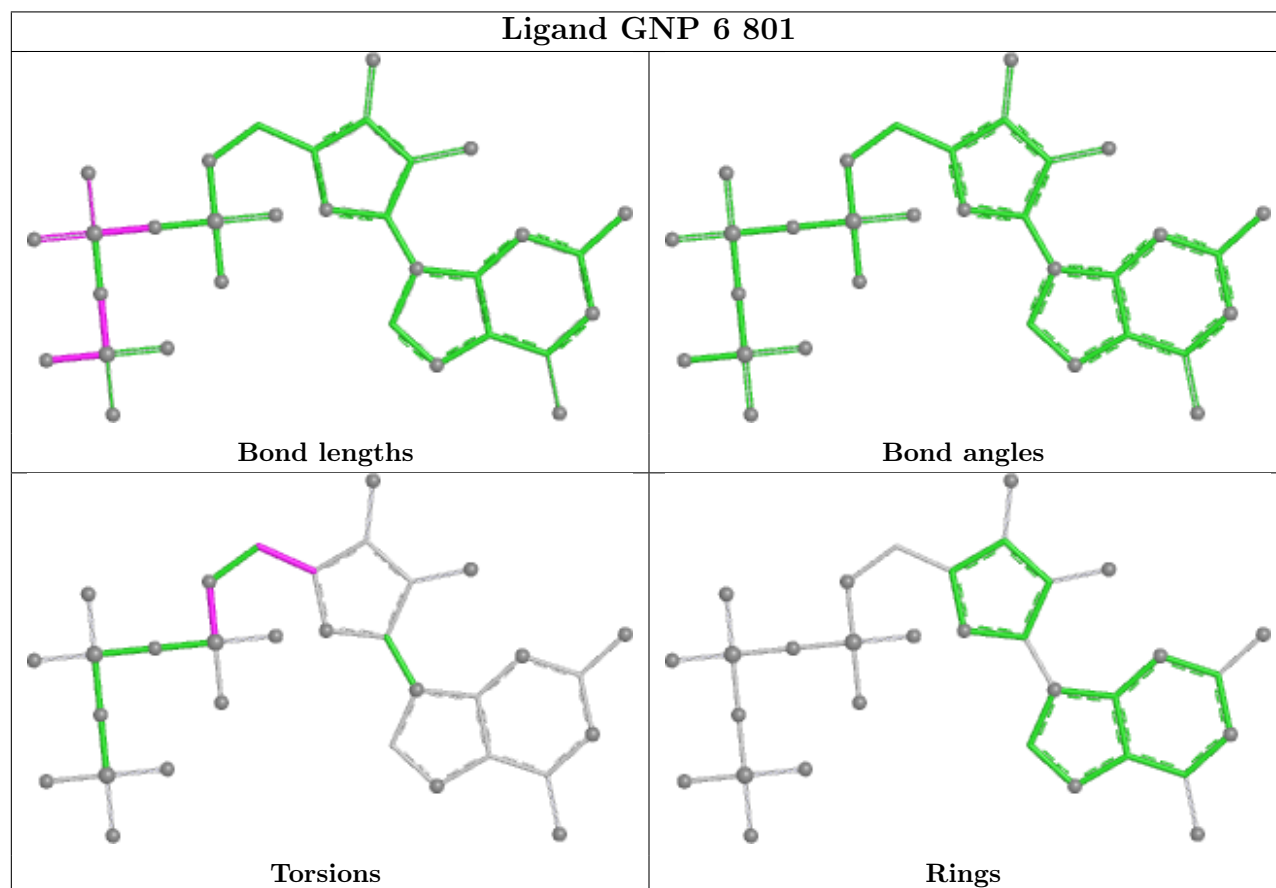
There are no ring outliers.

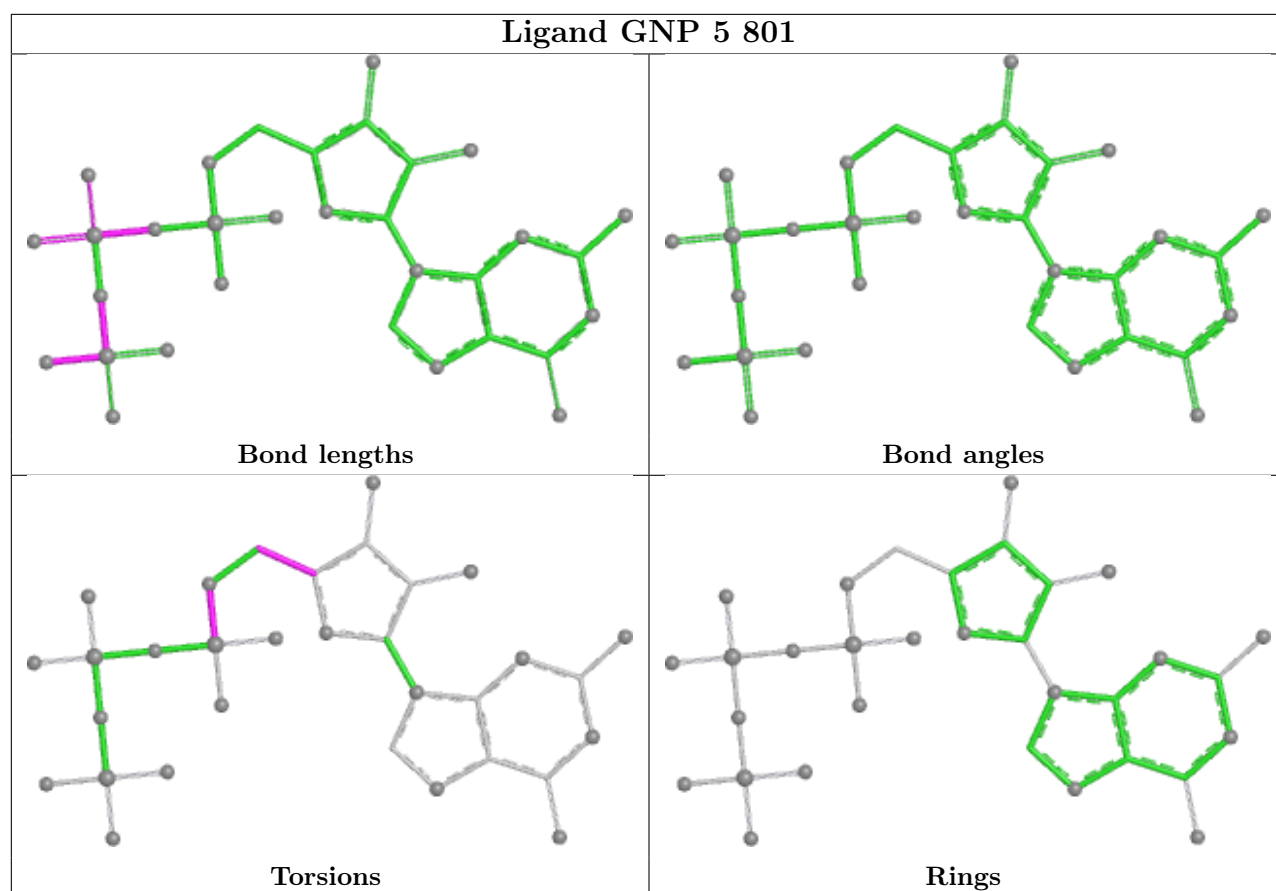
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	6	801	GNP	2	0
36	5	801	GNP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.

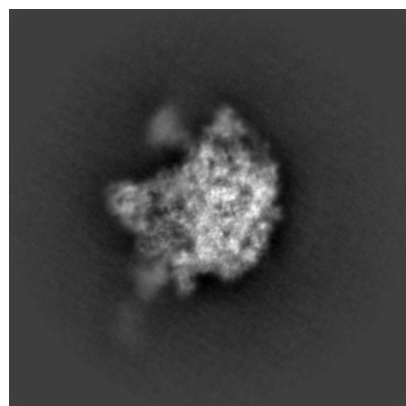
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-61960. These allow visual inspection of the internal detail of the map and identification of artifacts.

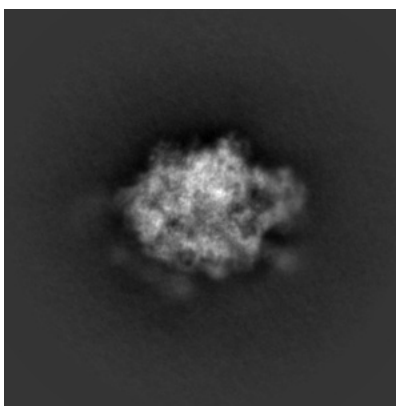
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

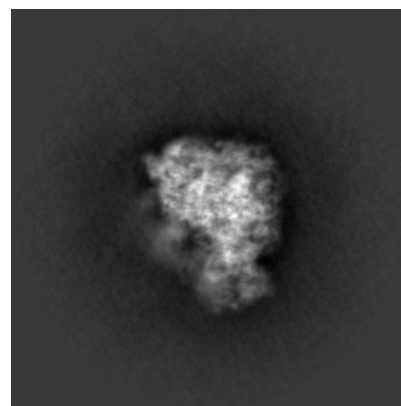
6.1.1 Primary map



X

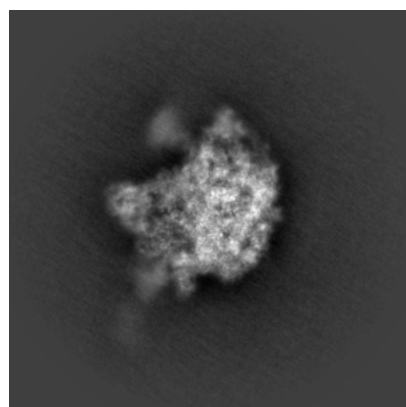


Y

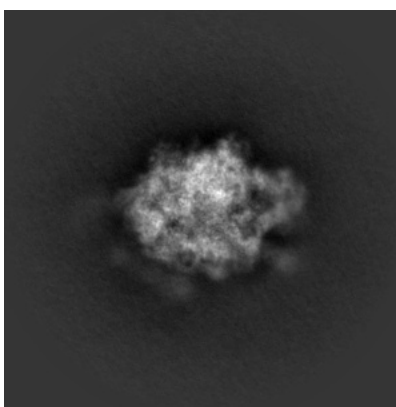


Z

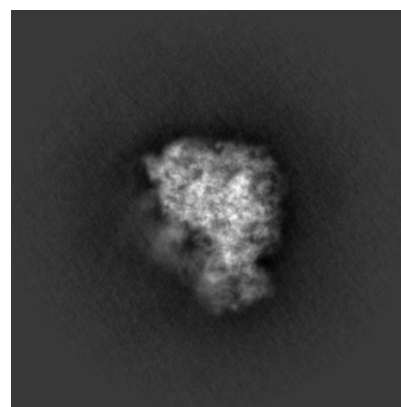
6.1.2 Raw map



X



Y

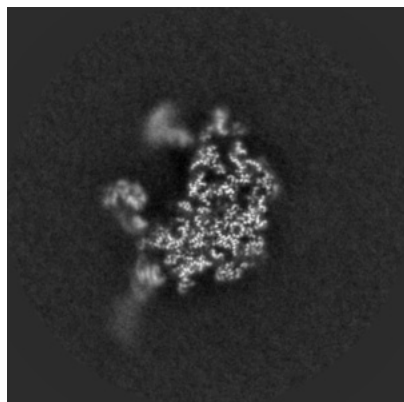


Z

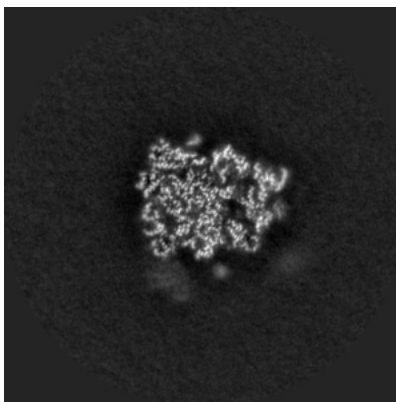
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

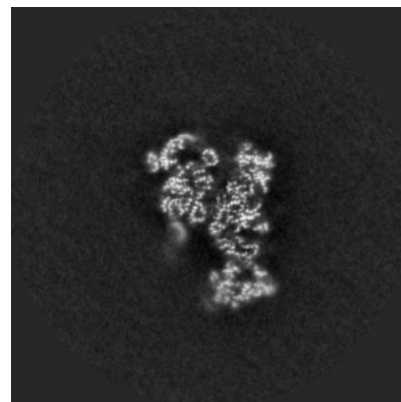
6.2.1 Primary map



X Index: 175

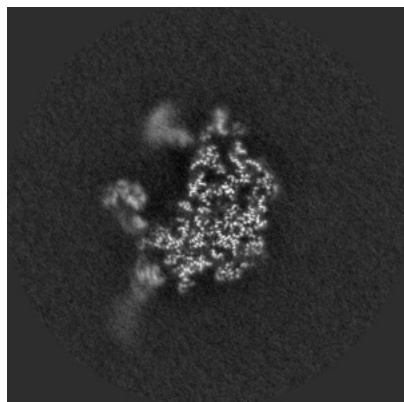


Y Index: 175

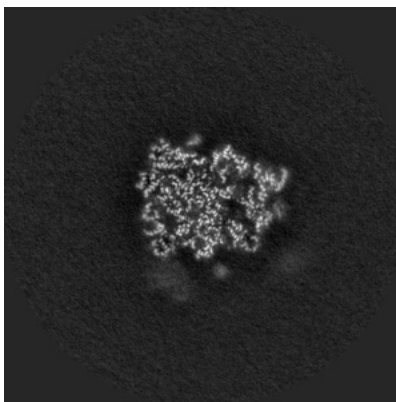


Z Index: 175

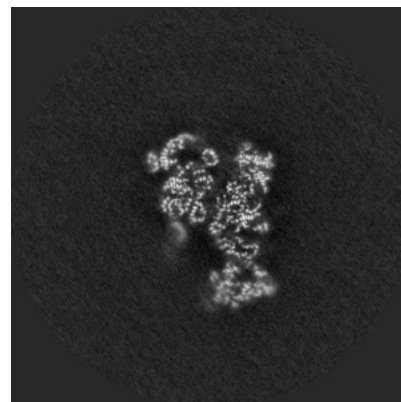
6.2.2 Raw map



X Index: 175



Y Index: 175

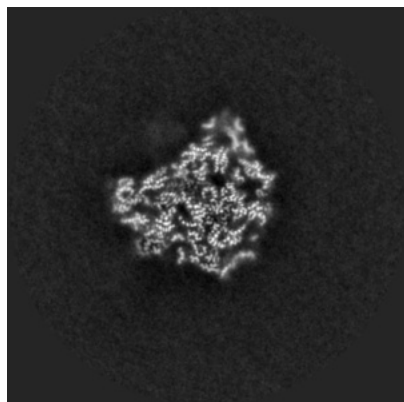


Z Index: 175

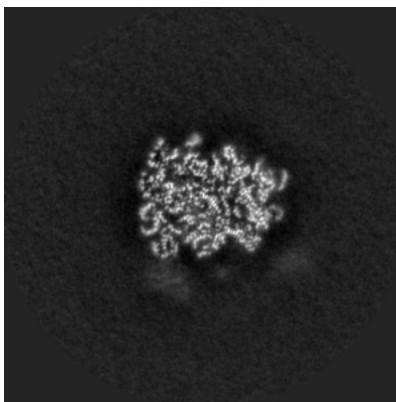
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

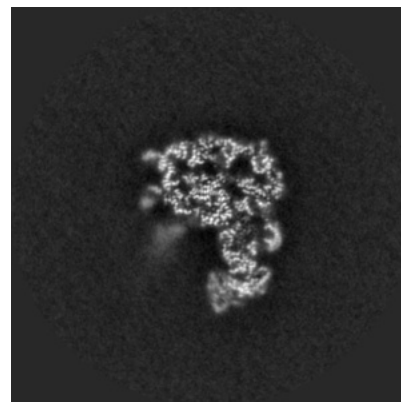
6.3.1 Primary map



X Index: 203

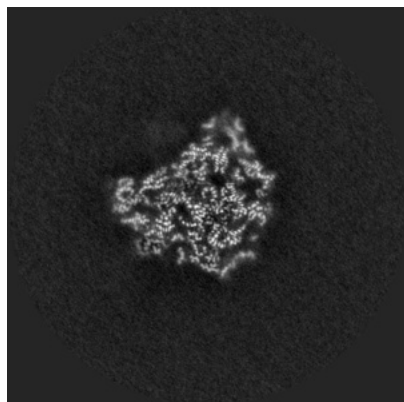


Y Index: 172

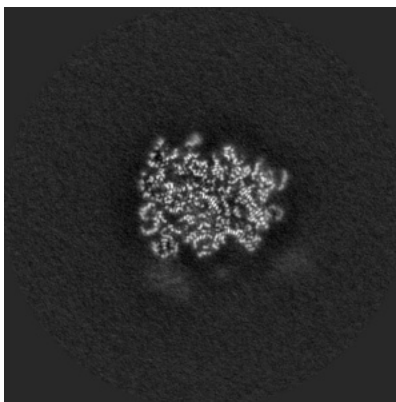


Z Index: 191

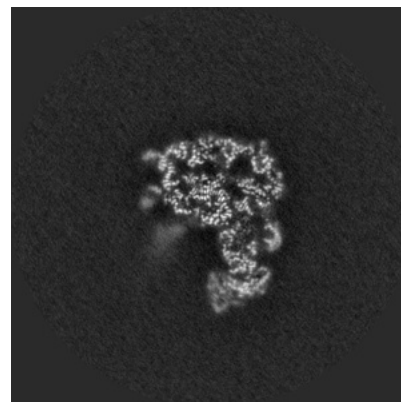
6.3.2 Raw map



X Index: 203



Y Index: 172

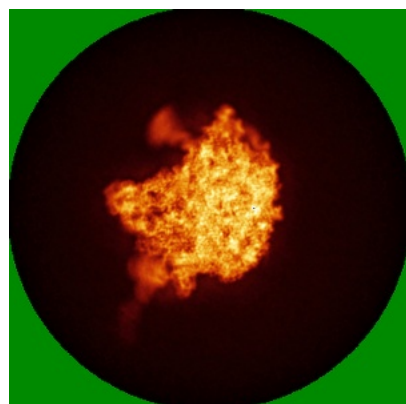


Z Index: 191

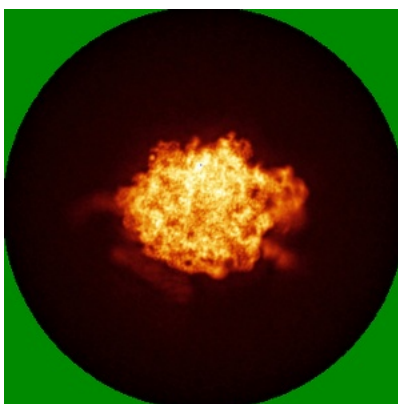
The images above show the largest variance slices of the map in three orthogonal directions.

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

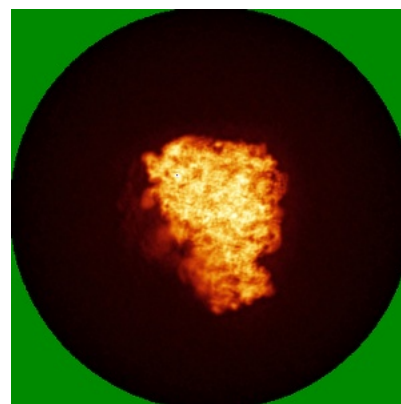
6.4.1 Primary map



X

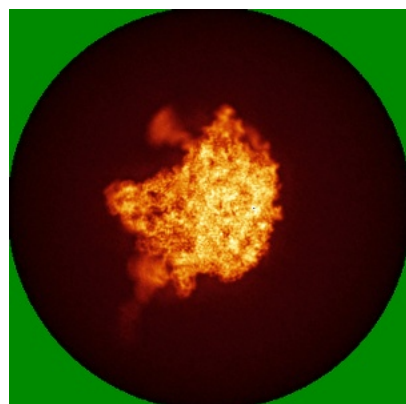


Y

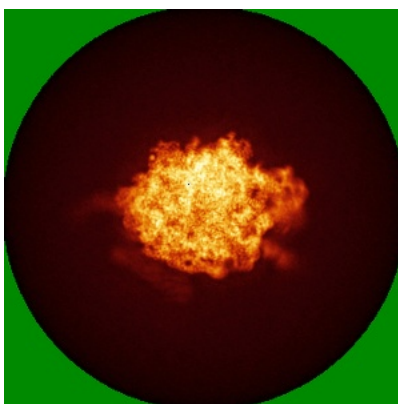


Z

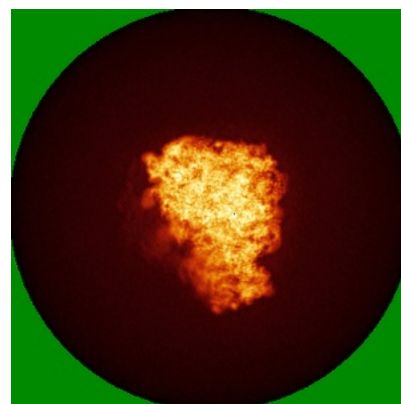
6.4.2 Raw map



X



Y

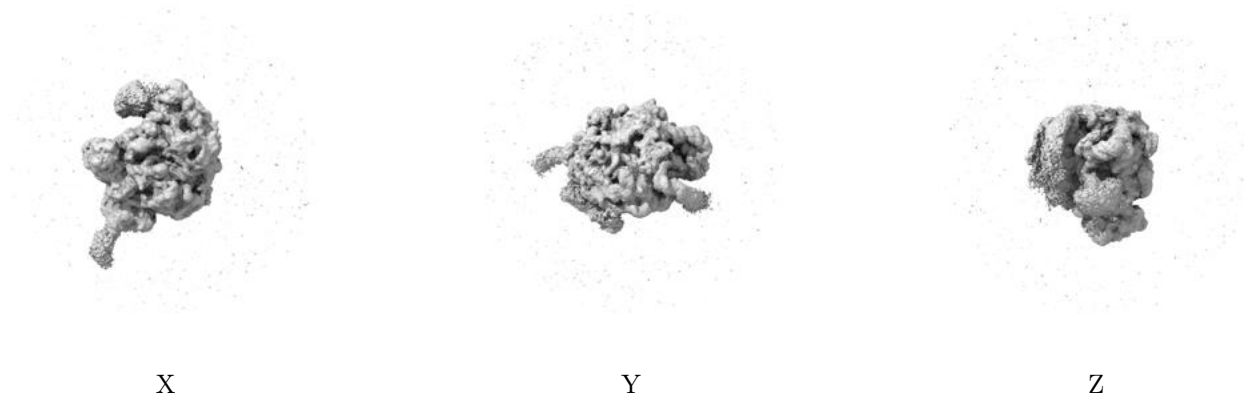


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

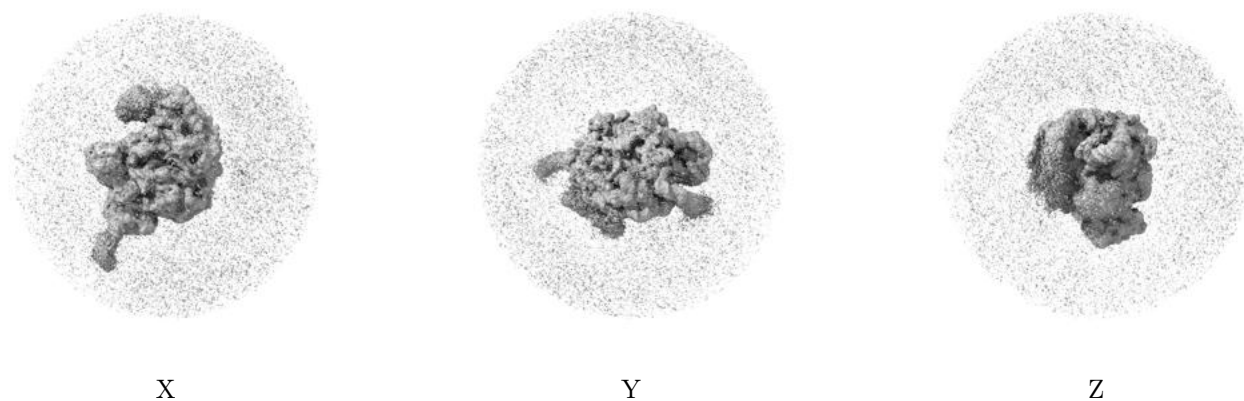
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00715. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

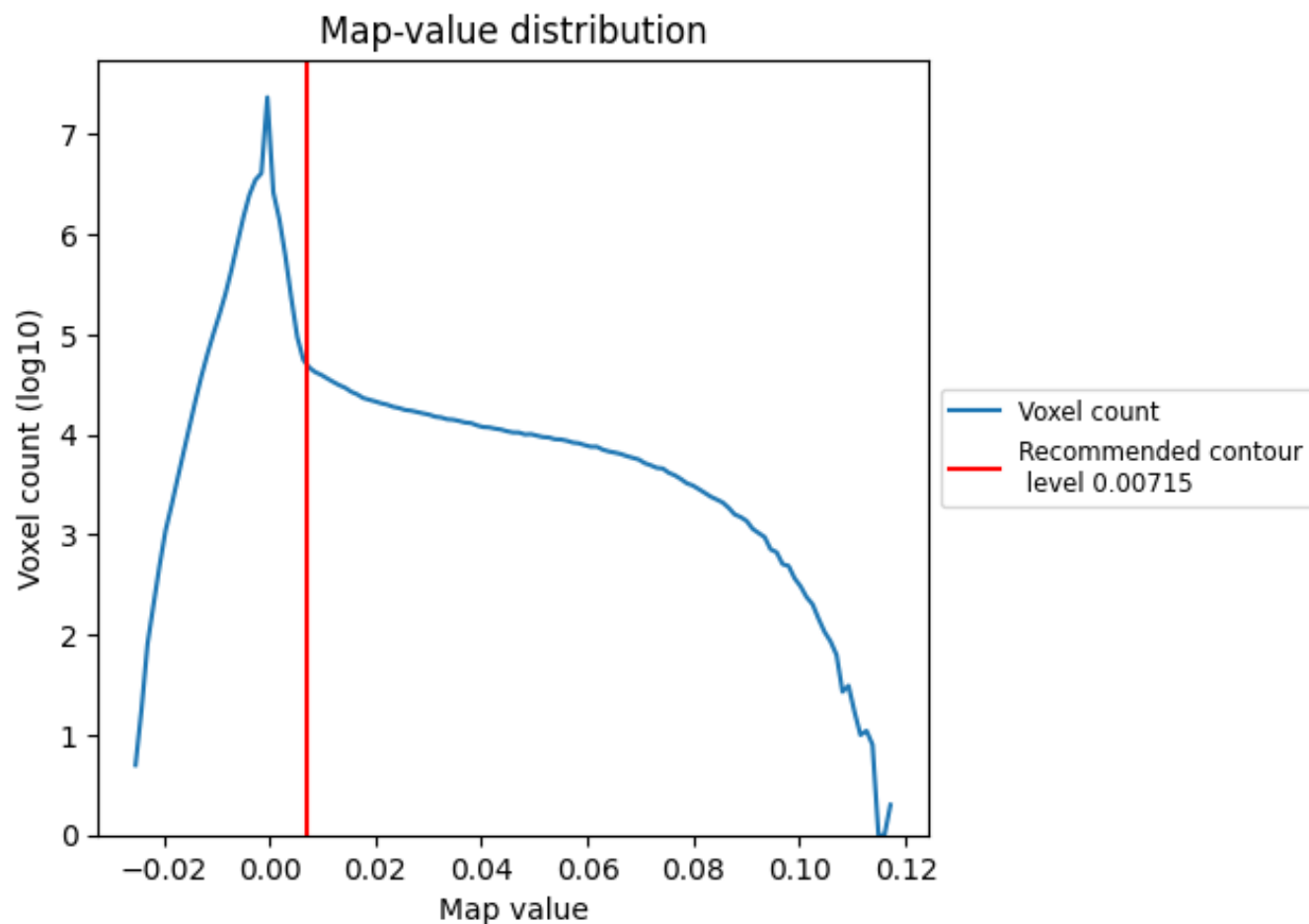
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

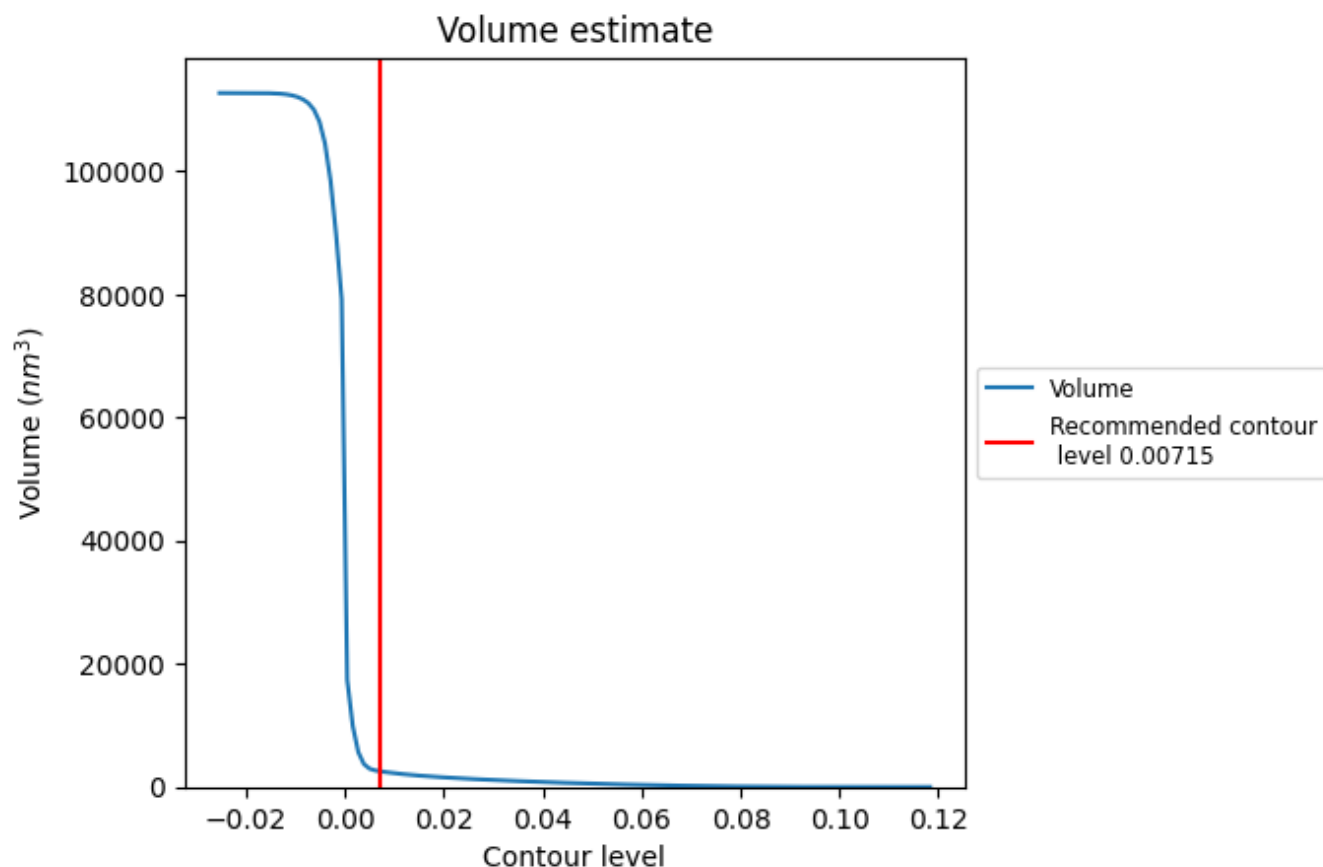
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

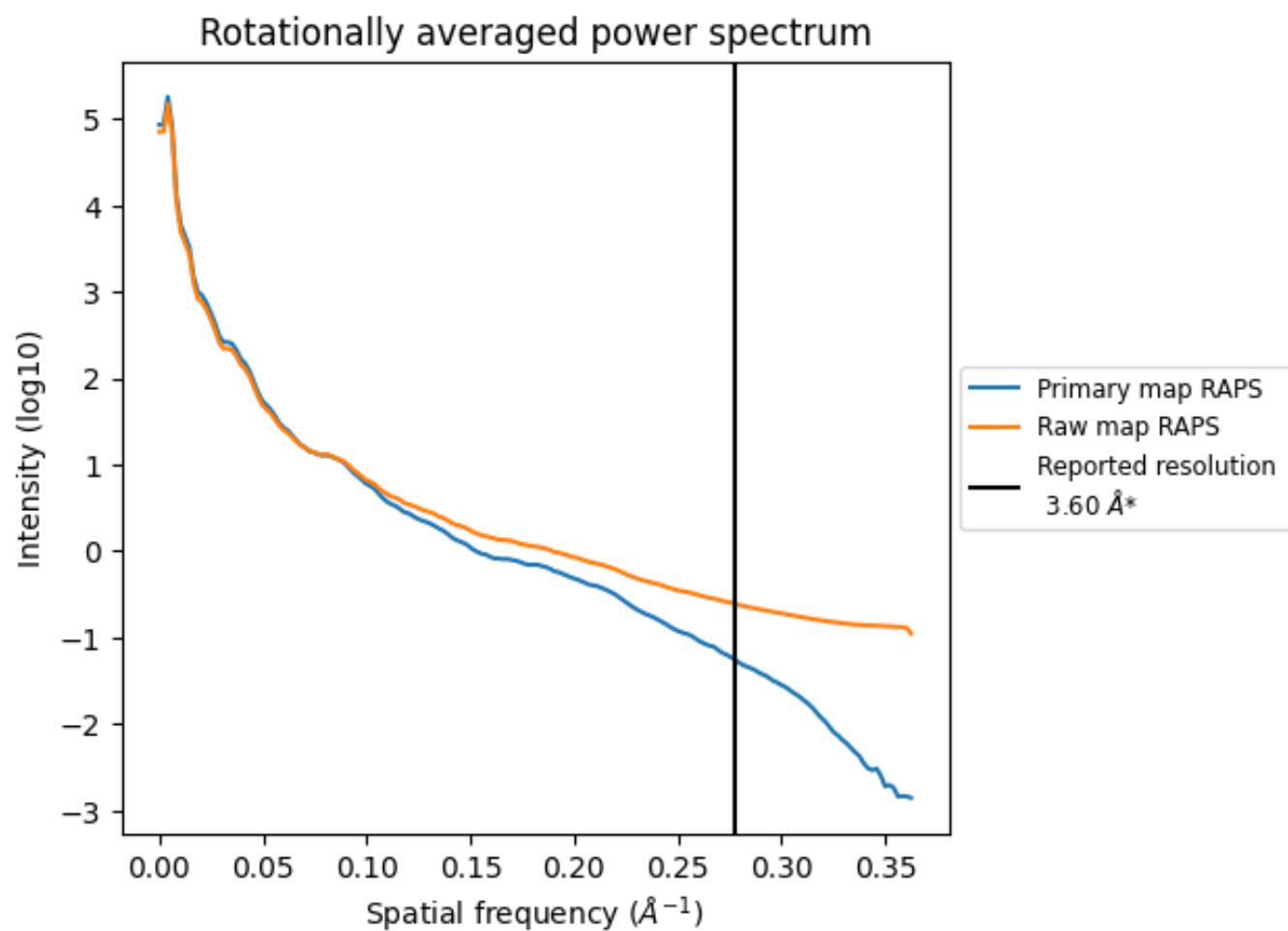
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2544 nm^3 ; this corresponds to an approximate mass of 2298 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 ⓘ

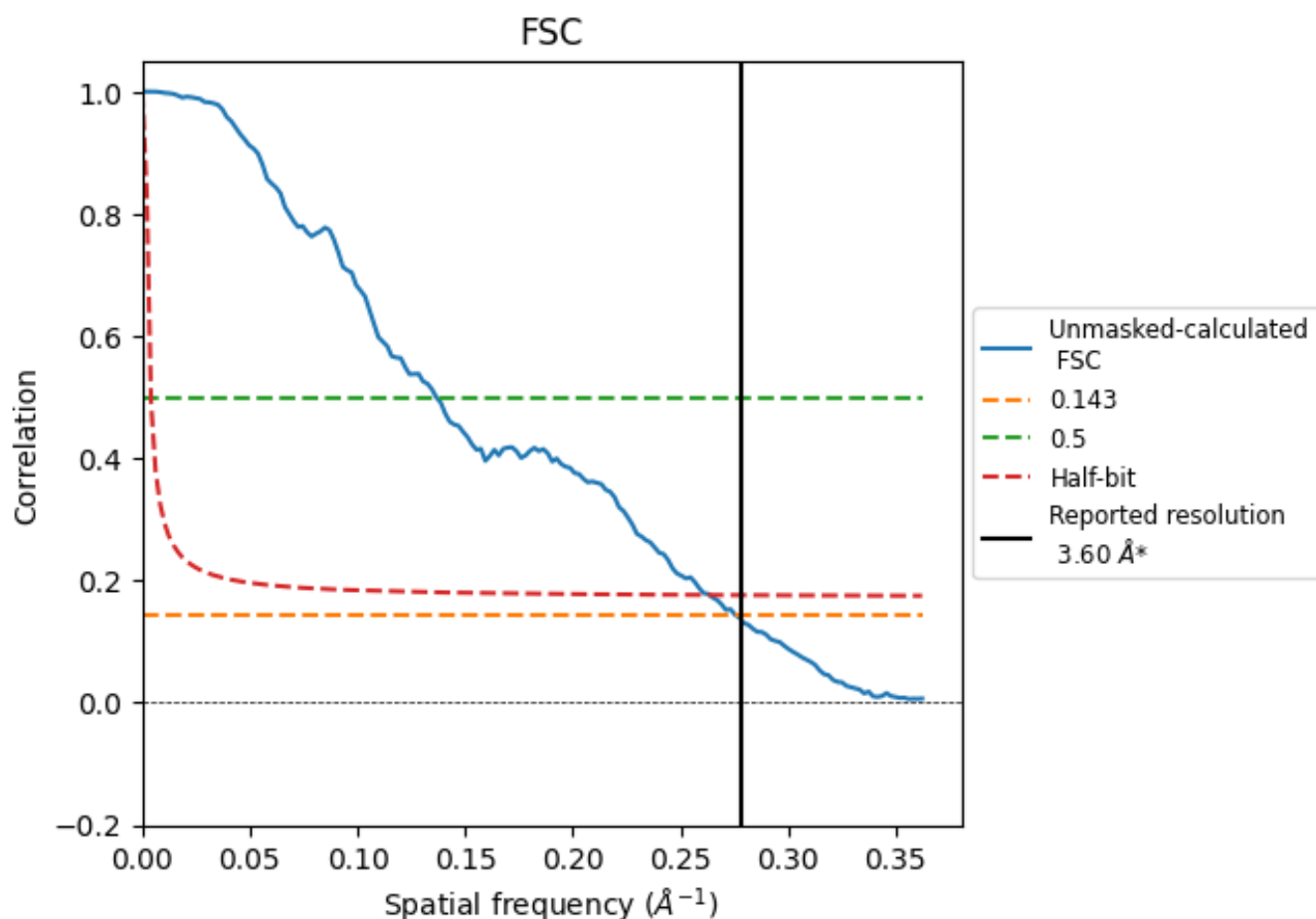


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.63	7.32	3.79

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

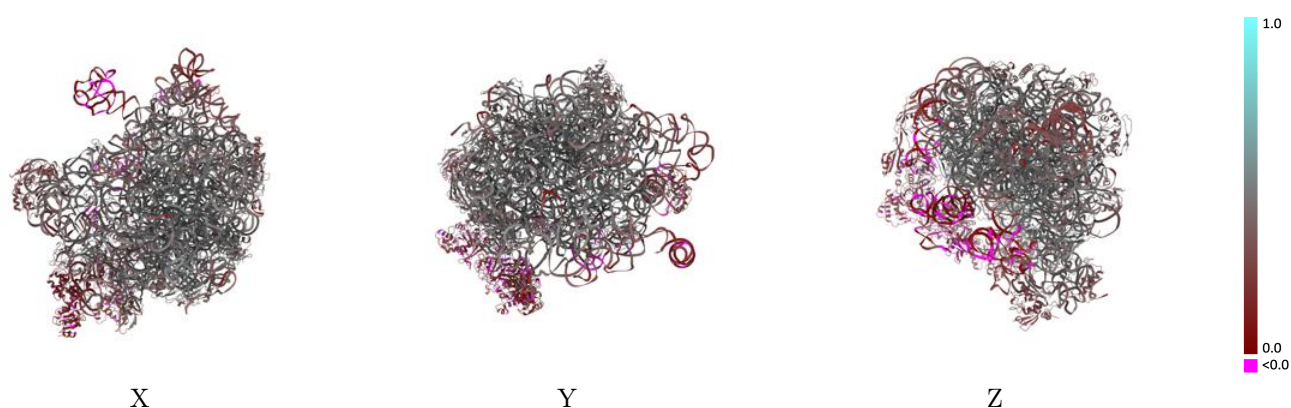
9 Map-model fit [i](#)

This section contains information regarding the fit between EMD map EMD-61960 and PDB model 9K10. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

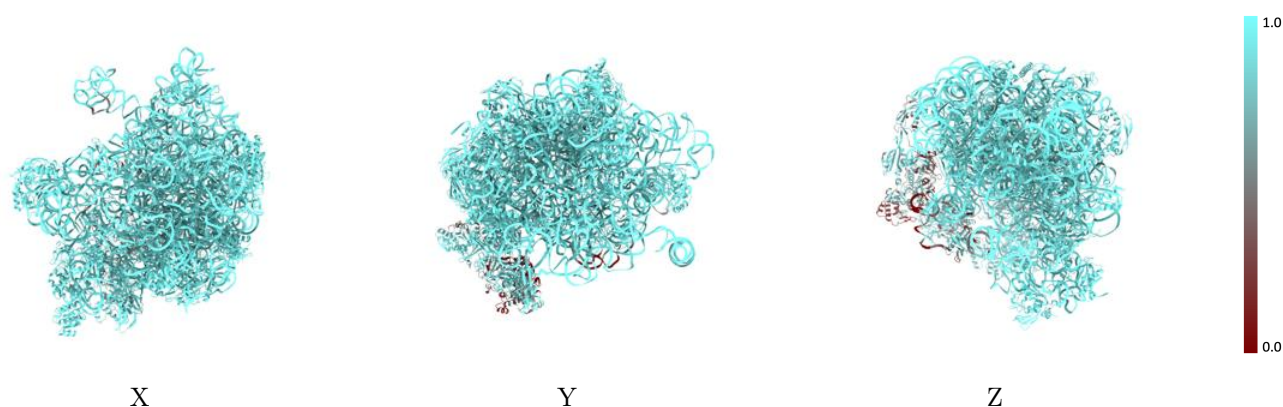
This section was not generated.

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



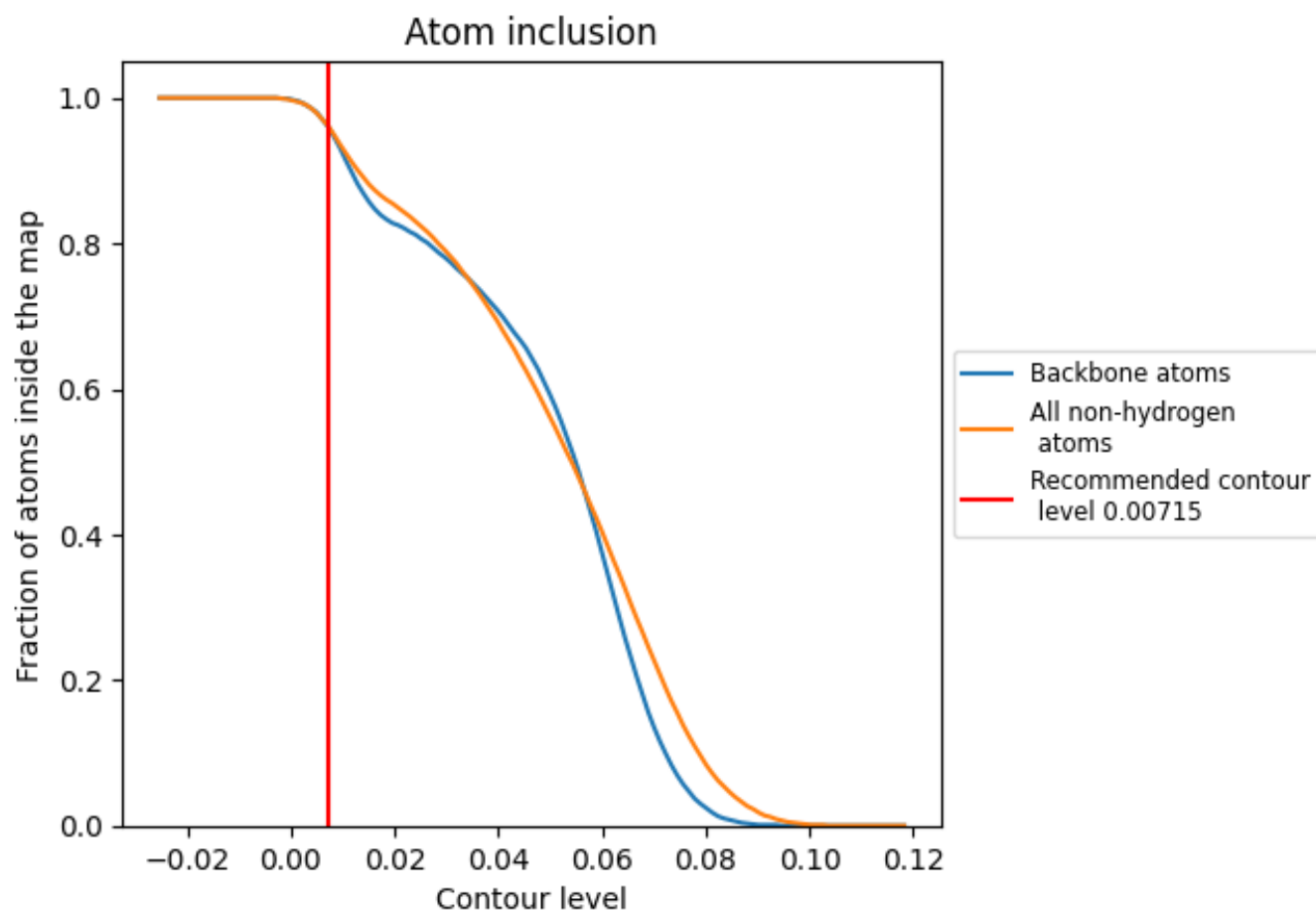
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00715).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.00715) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9620	 0.3820
3	 0.9890	 0.4380
5	 0.8110	 0.1370
6	 0.6100	 0.1690
A	 0.9880	 0.4100
B	 0.9980	 0.4130
C	 0.9910	 0.4470
D	 1.0000	 0.4660
E	 0.9940	 0.4420
F	 0.9960	 0.3000
G	 0.9920	 0.3840
H	 0.9680	 0.3500
I	 0.9760	 0.1390
J	 0.9830	 0.1250
K	 0.9940	 0.4520
L	 0.9950	 0.4460
M	 0.9970	 0.4300
N	 0.9960	 0.4480
O	 0.9960	 0.4470
P	 0.9980	 0.3820
Q	 0.9810	 0.4250
R	 0.9970	 0.4460
S	 0.9990	 0.4760
T	 0.9950	 0.4590
U	 0.9910	 0.4310
V	 0.9930	 0.3930
W	 0.9890	 0.3860
X	 1.0000	 0.4690
Y	 0.9960	 0.4550
Z	 0.9980	 0.3900
a	 0.9940	 0.4370
b	 0.9930	 0.4610
c	 0.9870	 0.4290
d	 0.9940	 0.4630
e	 0.9580	 0.4030



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Chain	Atom inclusion	Q-score
f	 0.9970	 0.4590
g	 0.9890	 0.2600