



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 10:18 PM UTC

PDB ID : 8Y38 / pdb_00008y38
EMDB ID : EMD-38875
Title : Cryo-EM structure of Staphylococcus aureus 70S ribosome (strain 15B196) in complex with MCX-190.
Authors : Li, Y.; Lu, G.; Li, J.; Pei, X.; Lin, J.
Deposited on : 2024-01-28
Resolution : 2.58 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

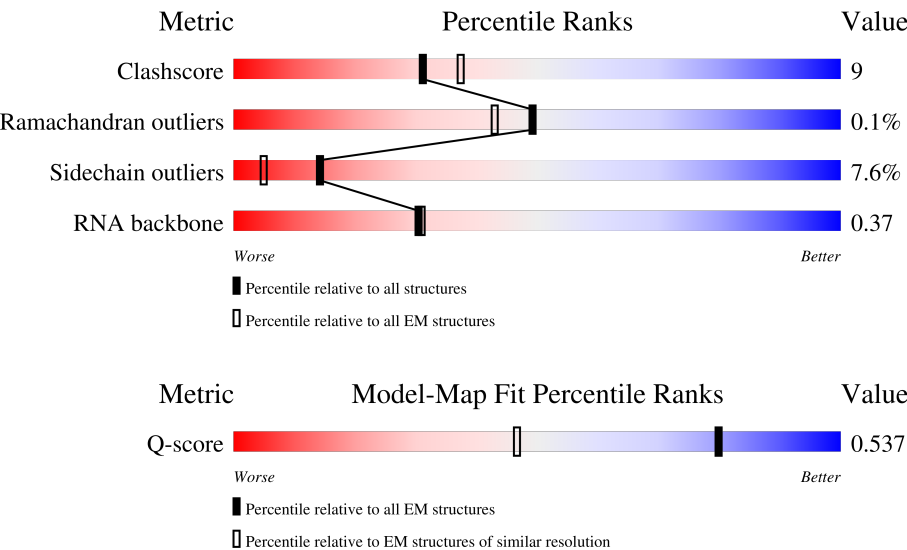
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.58 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	7675 (2.08 - 3.08)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	47	70% 26% .
2	2	43	84% 16%
3	3	64	70% 30%

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Mol	Chain	Length	Quality of chain
4	4	37	
5	A	2921	
6	B	115	
7	C	274	
8	D	215	
9	E	206	
10	F	175	
11	G	175	
12	H	145	
13	I	122	
14	J	146	
15	K	137	
16	L	120	
17	M	119	
18	N	114	
19	O	116	
20	P	102	
21	Q	117	
22	R	89	
23	S	103	
24	T	94	
25	U	82	
26	V	58	
27	W	67	
28	X	58	

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Mol	Chain	Length	Quality of chain
29	Y	59	
30	Z	48	
31	a	1548	
32	b	232	
33	c	217	
34	d	200	
35	e	166	
36	f	98	
37	g	156	
38	h	132	
39	i	130	
40	j	102	
41	k	129	
42	l	149	
43	m	121	
44	n	61	
45	o	89	
46	p	91	
47	q	87	
48	r	80	
49	s	108	
50	t	83	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 138224 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 bL33B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	47	Total	C	N	O	S	0	0
			390	238	78	70	4		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	2885	Total	C	N	O	P	0	0
			61861	27621	11312	20043	2885		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	115	Total	C	N	O	P	0	0
			2445	1094	436	801	114		

- Molecule 7 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	274	Total	C	N	O	S	0	0
			2090	1301	415	369	5		

- Molecule 8 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 9 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 10 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	175	Total	C	N	O	S	0	0
			1317	835	223	253	6		

- Molecule 11 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	175	Total	C	N	O	S	0	0
			1259	788	239	229	3		

- Molecule 12 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	145	Total	C	N	O	S	0	0
			1143	714	208	218	3		

- Molecule 13 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 14 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 15 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 16 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	120	Total	C	N	O	S	0	0
			932	576	182	173	1		

- Molecule 17 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	119	Total	C	N	O	S	0	0
			891	557	174	159	1		

- Molecule 18 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	114	Total	C	N	O		0	0
			889	563	175	151			

- Molecule 19 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 20 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 21 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	112	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 22 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 24 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	94	Total	C	N	O		0	0
			711	456	127	128			

- Molecule 25 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	U	82	Total	C	N	O		0	0
			615	380	121	114			

- Molecule 26 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	58	Total	C	N	O		0	0
			445	277	96	72			

- Molecule 27 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	W	67	Total	C	N	O		0	0
			541	333	102	106			

- Molecule 28 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	X	58	Total	C	N	O	0	0
			449	280	85	84		

- Molecule 29 is a protein called Large ribosomal subunit protein bL31B.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	Y	57	Total	C	N	O	0	0
			353	214	65	74		

- Molecule 30 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Z	48	Total	C	N	O	S	0	0
			361	222	77	59	3		

- Molecule 31 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	a	1479	Total	C	N	O	P	0	0
			31706	14154	5809	10264	1479		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	1032	N	C	conflict	GB 1747281577

- Molecule 32 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	b	224	Total	C	N	O	S	0	0
			1802	1149	314	332	7		

- Molecule 33 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	c	202	Total	C	N	O	S	0	0
			1596	1005	300	289	2		

- Molecule 34 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	199	Total	C	N	O	S	0	0
			1616	1020	302	292	2		

- Molecule 35 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	156	Total	C	N	O	S	0	0
			1160	731	212	215	2		

- Molecule 36 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	f	95	Total	C	N	O	S	0	0
			789	498	138	150	3		

- Molecule 37 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	155	Total	C	N	O	S	0	0
			1242	775	239	224	4		

- Molecule 38 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	131	Total	C	N	O	S	0	0
			1031	652	183	192	4		

- Molecule 39 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			1007	624	201	181	1		

- Molecule 40 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	j	97	Total	C	N	O	S	0	0
			773	488	141	143	1		

- Molecule 41 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	114	Total	C	N	O	S	0	0
			844	520	160	161	3		

- Molecule 42 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

- Molecule 43 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	m	116	Total	C	N	O	S	0	0
			922	566	183	172	1		

- Molecule 44 is a protein called Small ribosomal subunit protein uS14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	60	Total	C	N	O	S	0	0
			501	317	100	79	5		

- Molecule 45 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	87	Total	C	N	O	S	0	0
			726	448	149	128	1		

- Molecule 46 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	87	Total	C	N	O	S	0	0
			688	433	127	127	1		

- Molecule 47 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	q	80	Total	C	N	O	S	0	0
			657	416	117	123	1		

- Molecule 48 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	r	64	Total	C	N	O	S	0	0
			525	336	98	88	3		

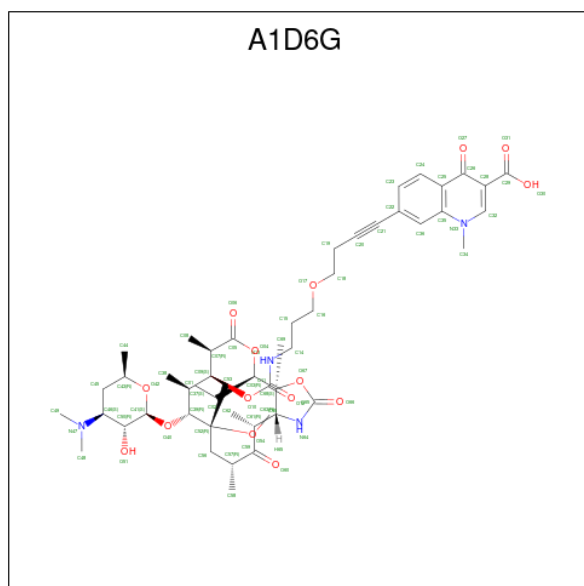
- Molecule 49 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	82	Total	C	N	O	S	0	0
			665	427	121	115	2		

- Molecule 50 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	81	Total	C	N	O	S	0	0
			611	370	120	119	2		

- Molecule 51 is 7-[4-[3-[(1 {S},2 {R},5 {R},6 {S},7 {S},8 {R},9 {R},11 {R},13 {R},14 {R})-8-[(2 {S},3 {R},4 {S},6 {R})-4-(dimethylamino)-6-methyl-3-oxidanyl-oxan-2-yl]oxy-2-ethyl-9-methoxy-1,5,7,9,11,13-hexamethyl-4,12,16-tris(oxidanylidene)-3,17-dioxo-15-azabicyclo[1 2.3.0]heptadecan-6-yl]oxycarbonylamino]propoxy]but-1-ynyl]-1-methyl-4-oxidanylidene-quinoline-3-carboxylic acid (CCD ID: A1D6G) (formula: C₅₀H₇₂N₄O₁₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
51	A	1	Total	C	N	O	0
			69	50	4	15	

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
52	A	12	Total	Mg	0
			12	12	

- Molecule 53 is water.

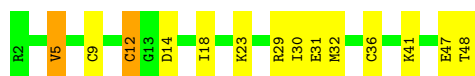
Mol	Chain	Residues	Atoms		AltConf
53	A	4	Total	O	0
			4	4	

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 bL33B

Chain 1: 



- Molecule 2: Large ribosomal subunit protein bL34

Chain 2: 



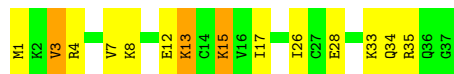
- Molecule 3: Large ribosomal subunit protein bL35

Chain 3: 



- Molecule 4: Large ribosomal subunit protein bL36

Chain 4: 



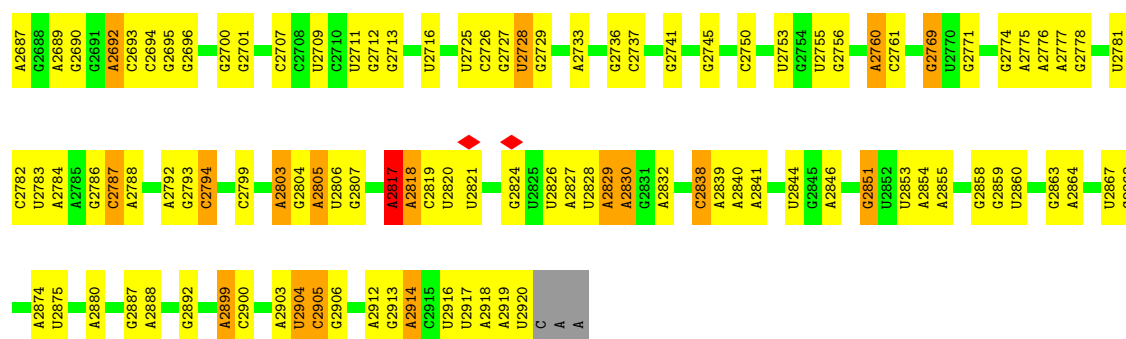
- Molecule 5: 23S ribosomal RNA

Chain A: 

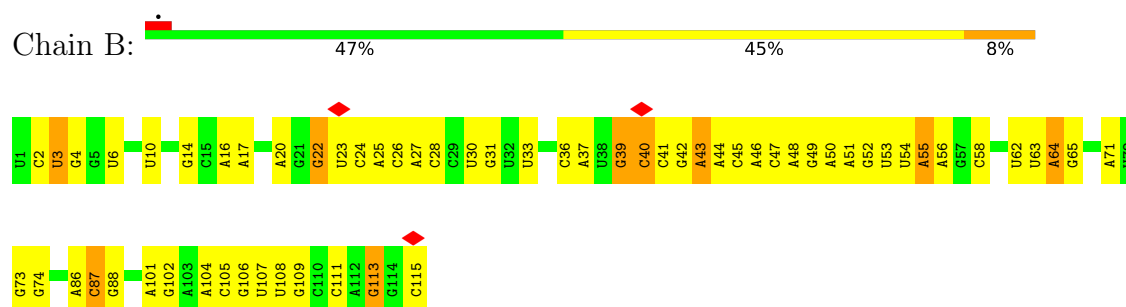




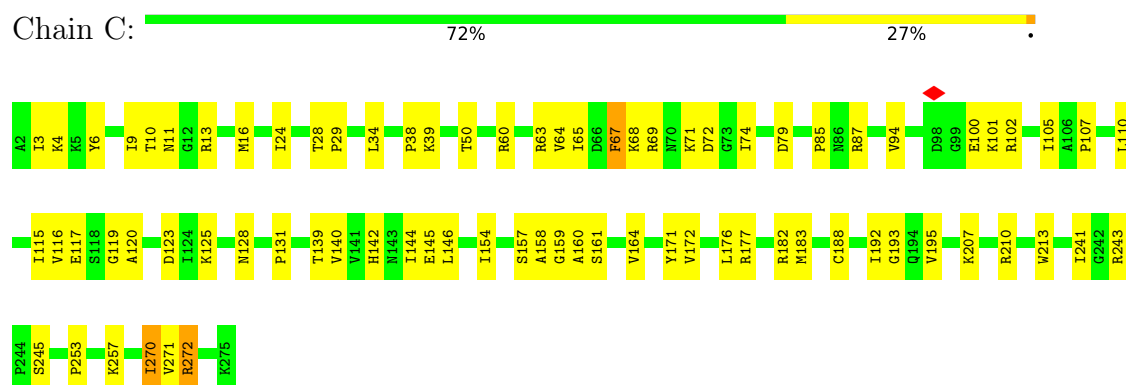
G2609	G2610	G2611	G2612	G2613	A2617	G2618	G2619	G2622	G2623	G2624	G2625	G2626	A2627	G2628	A2629	G2632	G2633	G2636	G2640	G2641	G2642	G2645	G2648	G2649	G2650	G2651	G2652	G2653	A2656	A2661	G2668	G2669	G2670	G2671	G2672	G2673	G2677	G2678	G2679	G2680	G2681	G2682	G2683	A2684	G2685	G2686													
G2521	G2525	G2528	G2529	A2530	G2531	G2532	G2533	G2534	A2540	G2541	G2542	G2543	G2544	A2545	G2546	G2547	G2552	G2553	G2554	G2555	G2556	G2557	G2558	G2559	G2562	G2563	G2564	G2565	G2566	G2567	G2568	A2569	G2570	U2574	G2575	G2579	G2580	U2581	U2582	U2589	U2590	A2591	A2592	A2593	G2594	U2598	A2599	G2600	G2601	G2605									
C2408	G2409	G2410	A2411	C2412	G2416	G2417	G2418	A2419	C2430	C2431	G2432	G2433	A2434	G2435	G2436	G2437	A2441	A2438	G2441	U2450	C2451	A2452	A2453	C2454	G2455	G2456	A2457	G2458	A2459	A2460	A2461	A2462	G2463	C2464	U2465	C2468	G2472	G2473	G2474	A2475	C2493	C2494	A2495	A2496	G2497	A2498	G2499	A2505	U2506	G2507	G2508								
U2319	C2320	G2326	A2327	A2328	U2329	G2330	G2331	U2332	U2333	G2334	G2335	A2336	A2337	A2338	U2339	A2340	U2341	U2342	A2345	U2346	A2347	G2348	A2349	G2350	U2351	G2352	U2353	A2354	A2355	A2356	G2357	G2358	G2359	A2360	U2361	A2362	A2363	G2364	G2369	U2370	U2371	G2372	A2373	C2374	C2377	A2388	A2396	G2397	G2398	G2399	A2404								
C2223	U2224	A2225	A2226	C2227	C2228	C2229	G2230	G2231	A2232	A2235	U2238	A2239	U2240	C2241	G2244	G2245	G2251	A2252	G2253	A2254	G2257	G2260	G2261	G2265	G2266	U2272	G2273	A2274	G2278	G2279	C2287	A2294	A2295	A2296	G2304	A2305	G2306	C2310	U2311	G2312	A2313	A2314	A2315	G2316	G2317	U2318													
G2097	A2098	G2099	C2100	U2101	U2106	G2107	U2108	A2109	G2110	G2114	A2115	U2116	A2117	U2118	U2119	G2120	A2121	A2122	A2123	U2124	U2125	C2126	G2127	G2128	C2129	A2130	C2131	A2132	G2133	C2134	U2135	U2136	G2137	U2138	G2139	A2140	C2141	A2141	G2142	G2143	A2144	U2145	A2146	A2147	G2147	G2148	U2149	A2150	G2151	G2152	U2153	G2154	C2155	U2156	U2157	U2158	U2159	G2160	A2161
A2162	A2163	C2164	G2165	U2166	G2167	A2168	G2169	C2170	G2171	C2172	U2173	A2174	G2175	C2176	U2177	U2178	A2179	C2180	G2181	U2182	G2183	G2184	A2185	G2186	G2187	C2188	G2189	C2190	U2191	U2191	G2192	G2193	U2194	G2195	G2196	G2197	A2198	U2199	A2200	C2201	U2202	A2203	C2204	C2205	C2206	U2207	A2208	G2209	C2210	U2211	G2212	U2213	G2214	U2215	U2216	G2217	G2218	U2221	U2222
C2223	U2224	A2225	A2226	C2227	C2228	C2229	G2230	G2231	A2232	A2235	U2238	A2239	U2240	C2241	G2244	G2245	G2251	A2252	G2253	A2254	G2257	G2260	G2261	G2265	G2266	U2272	G2273	A2274	G2278	G2279	C2287	A2294	A2295	A2296	G2304	A2305	G2306	C2310	U2311	G2312	A2313	A2314	A2315	G2316	G2317	U2318													
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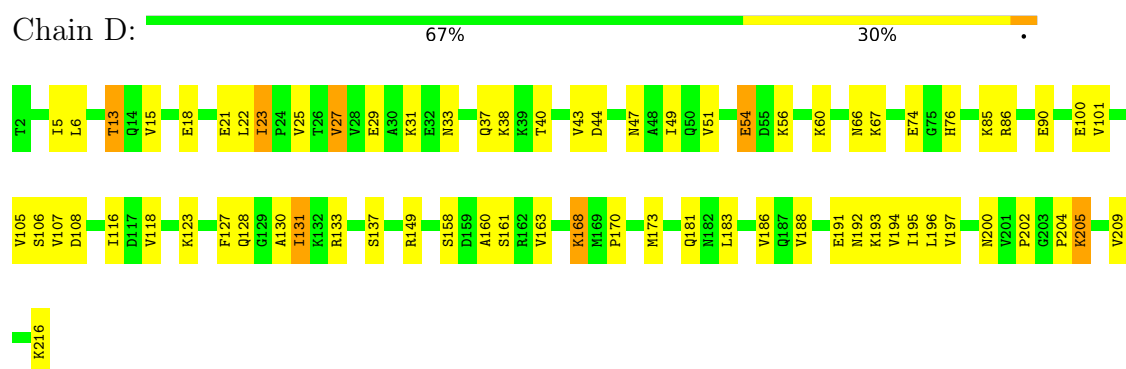
- Molecule 6: 5S ribosomal RNA



- Molecule 7: Large ribosomal subunit protein uL2

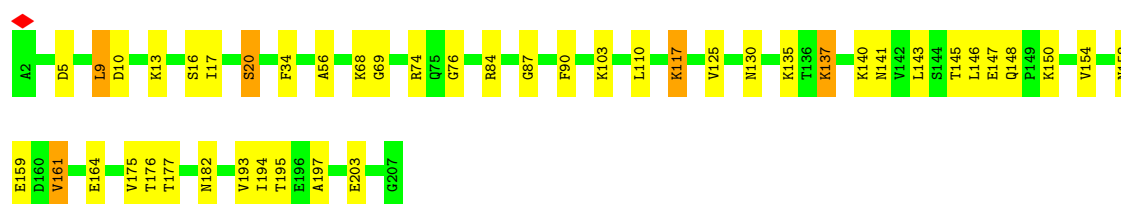


- Molecule 8: Large ribosomal subunit protein uL3



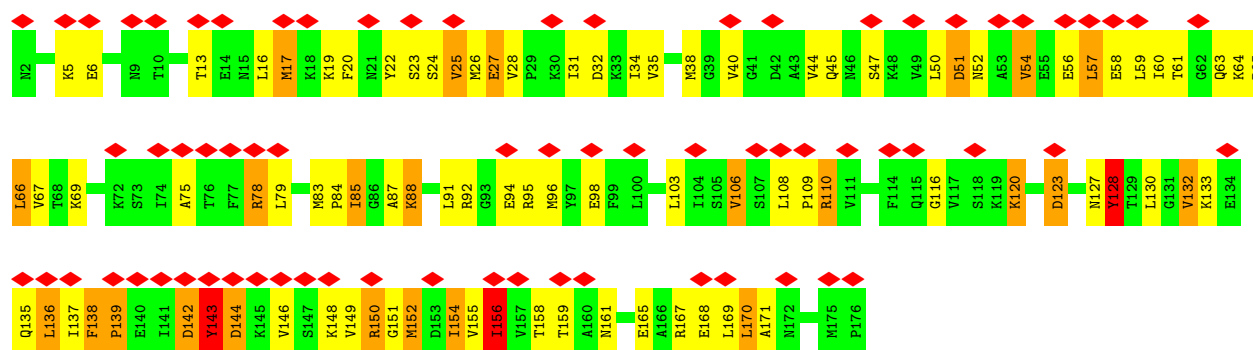
- Molecule 9: Large ribosomal subunit protein uL4

Chain E:  78% 19%



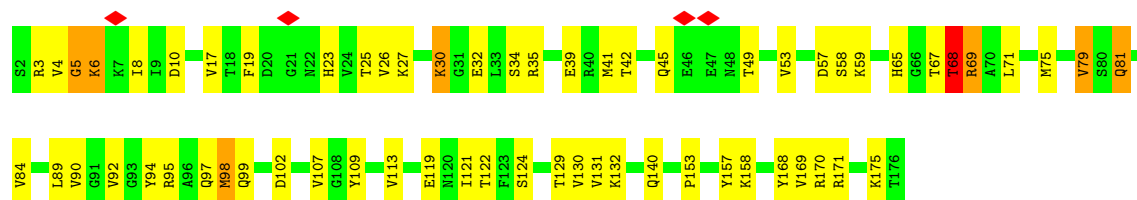
- Molecule 10: Large ribosomal subunit protein uL5

Chain F:  41% 47% 37% 14%



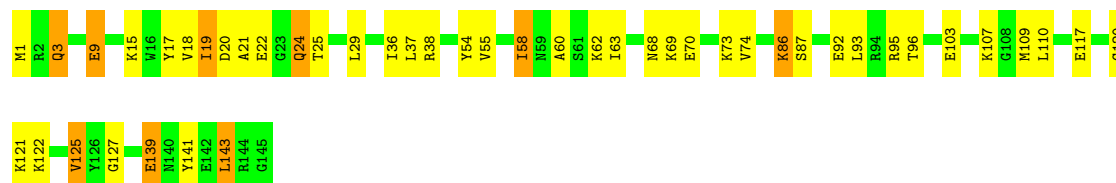
- Molecule 11: Large ribosomal subunit protein uL6

Chain G:  64% 31%



- Molecule 12: Large ribosomal subunit protein uL13

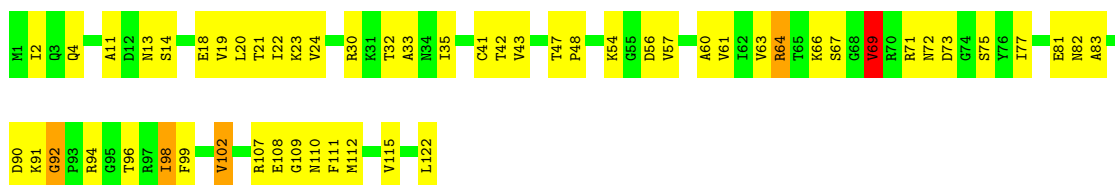
Chain H:  68% 26% 6%



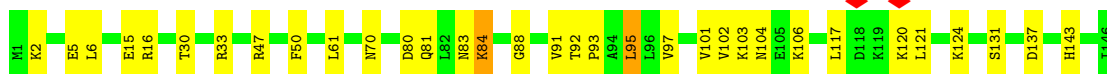
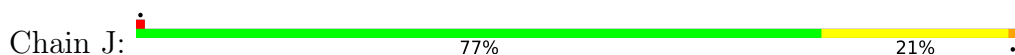
- Molecule 13: Large ribosomal subunit protein uL14

Chain I:  55% 41%

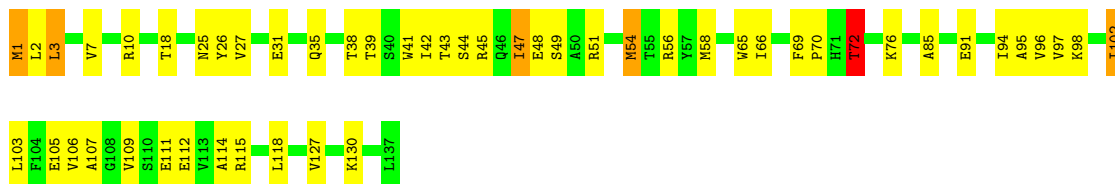




- Molecule 14: Large ribosomal subunit protein uL15



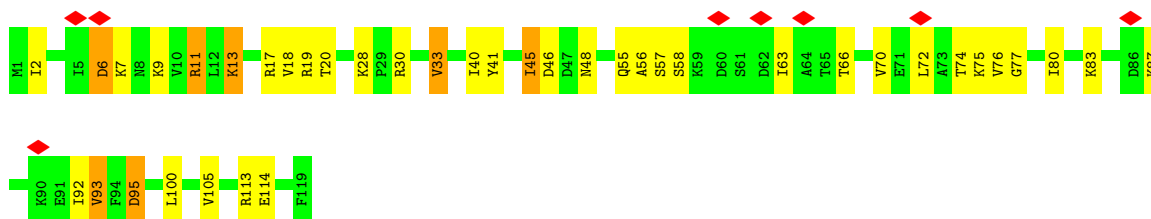
- Molecule 15: Large ribosomal subunit protein uL16



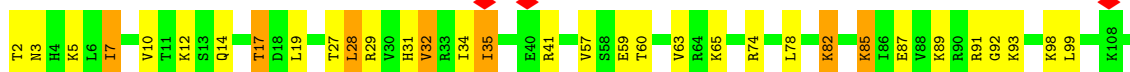
- Molecule 16: Large ribosomal subunit protein bL17



- Molecule 17: Large ribosomal subunit protein uL18



- Molecule 18: Large ribosomal subunit protein bL19





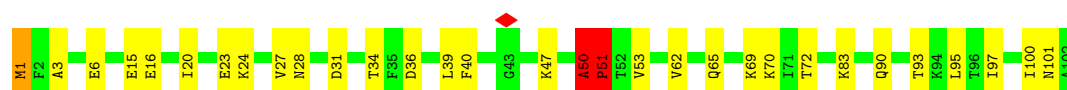
- Molecule 19: Large ribosomal subunit protein bL20

Chain O: 75% 24%



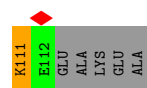
- Molecule 20: Large ribosomal subunit protein bL21

Chain P: 70% 27%



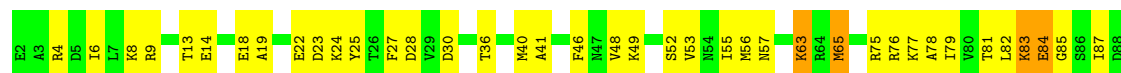
- Molecule 21: Large ribosomal subunit protein uL22

Chain Q: 65% 29%



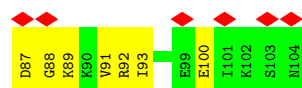
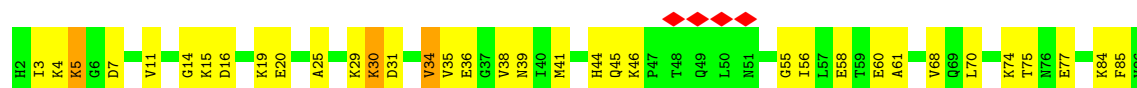
- Molecule 22: Large ribosomal subunit protein uL23

Chain R: 54% 39% 7%

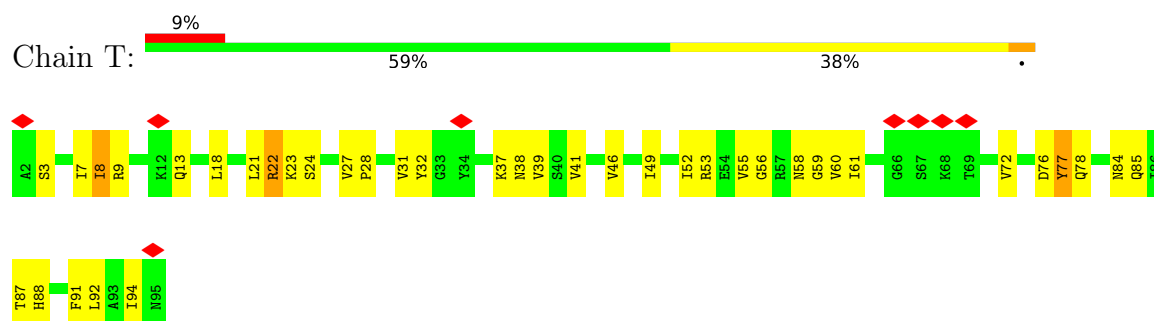


- Molecule 23: Large ribosomal subunit protein uL24

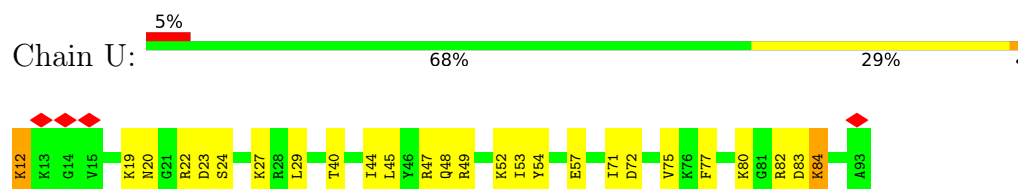
Chain S: 10% 59% 38%



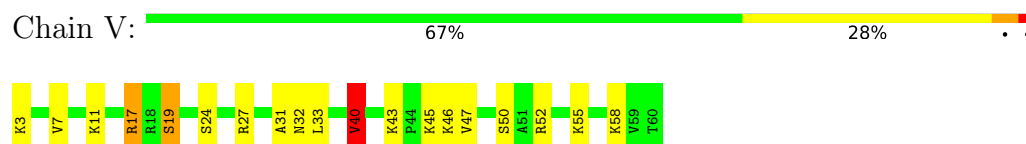
- Molecule 24: Large ribosomal subunit protein bL25



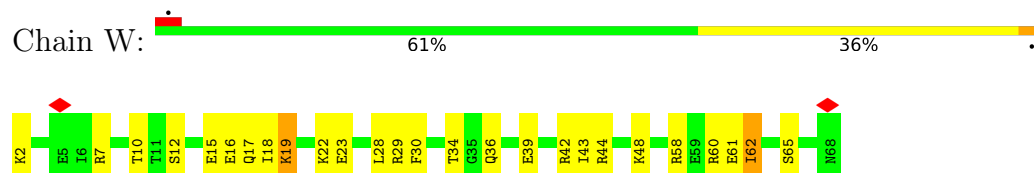
- Molecule 25: Large ribosomal subunit protein bL27



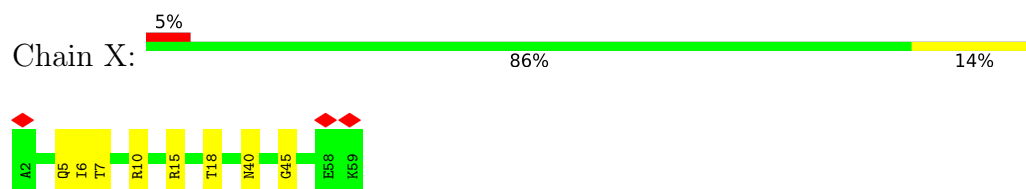
- Molecule 26: Large ribosomal subunit protein bL28



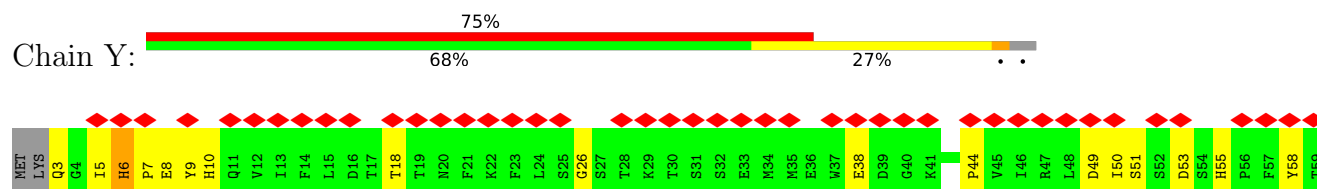
- Molecule 27: Large ribosomal subunit protein uL29



- Molecule 28: Large ribosomal subunit protein uL30



- Molecule 29: Large ribosomal subunit protein bL31B

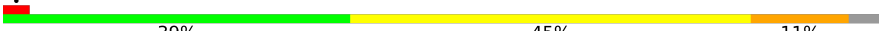


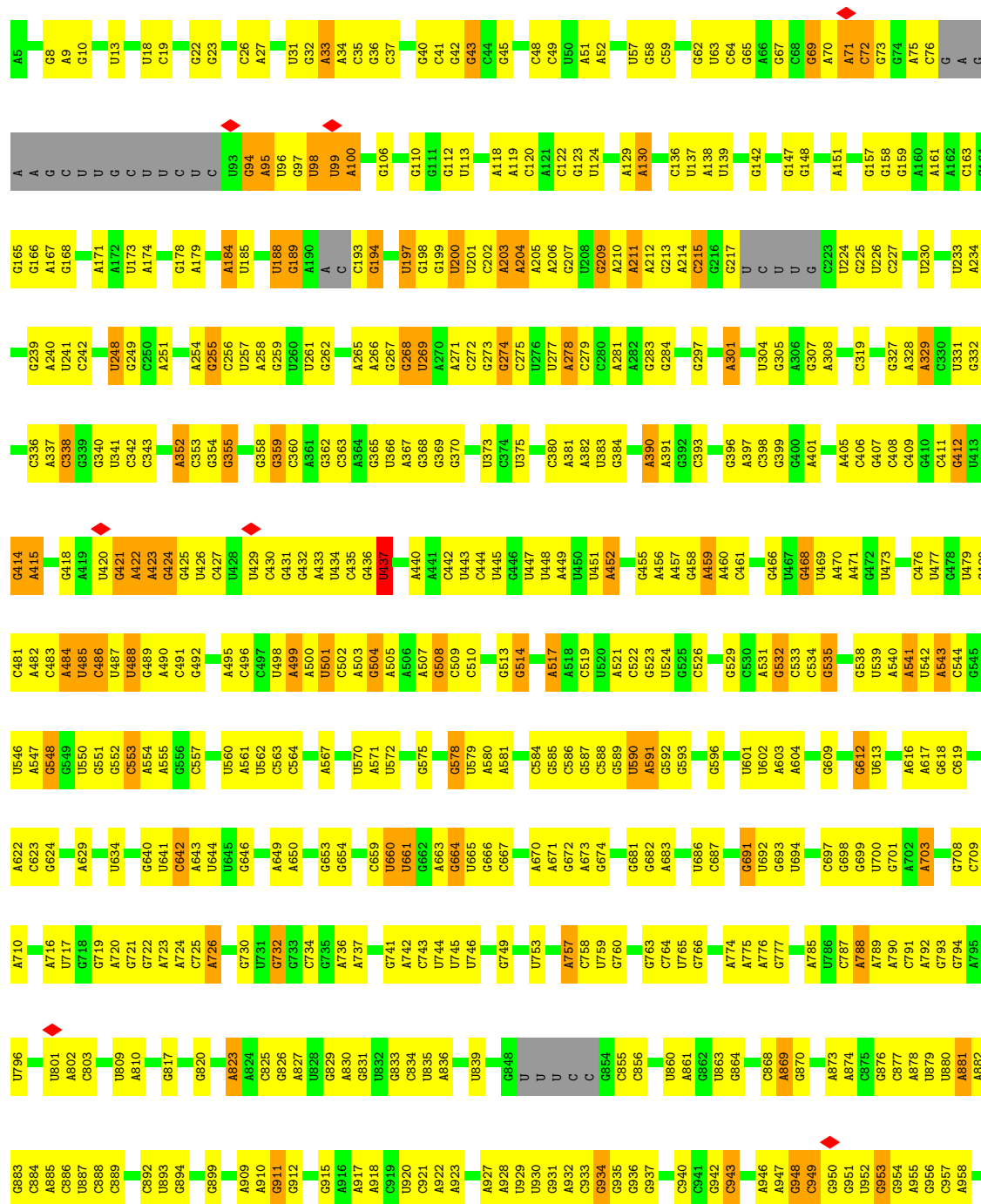
- Molecule 30: Large ribosomal subunit protein bL32

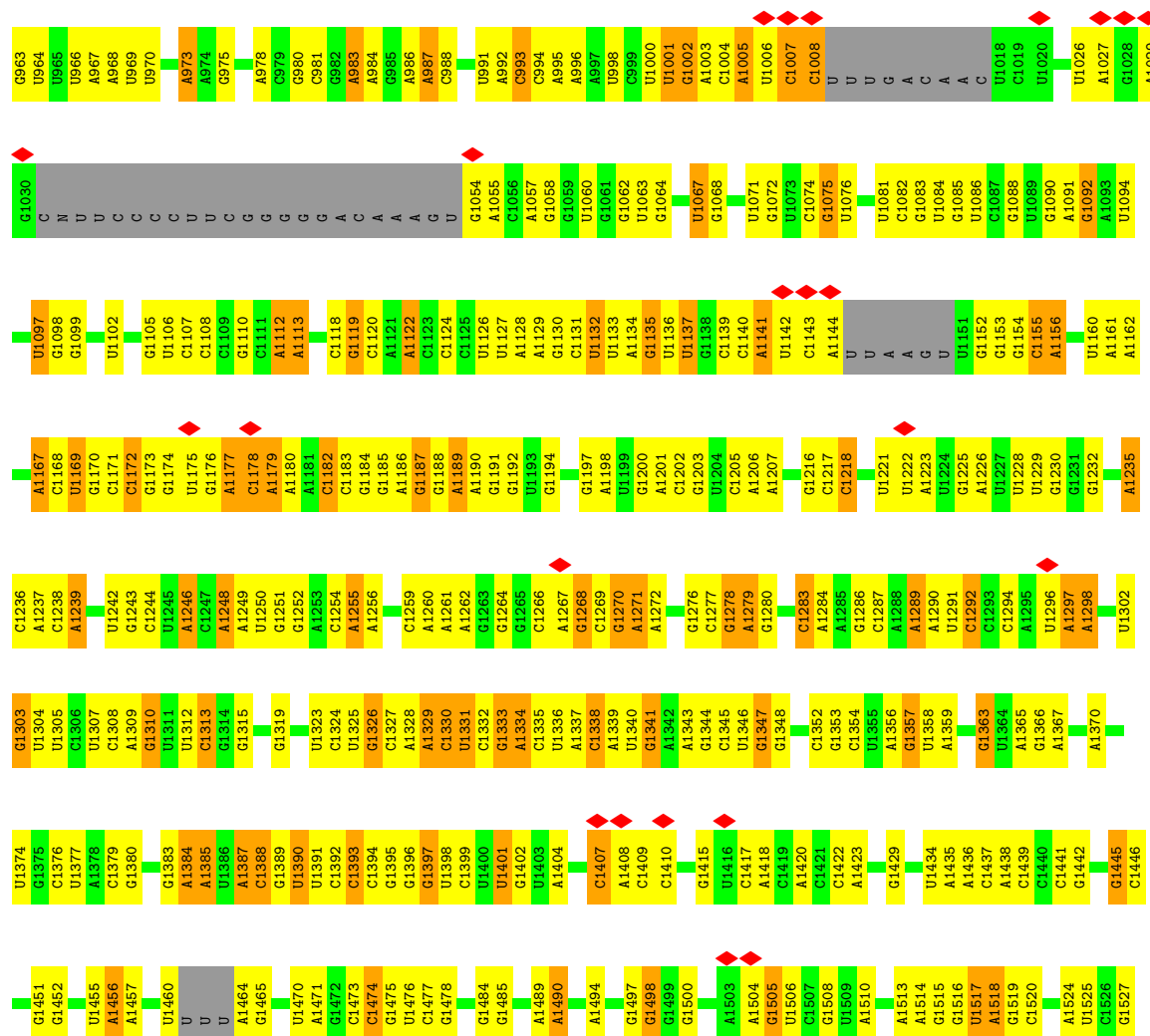
Chain Z:  75% 25%



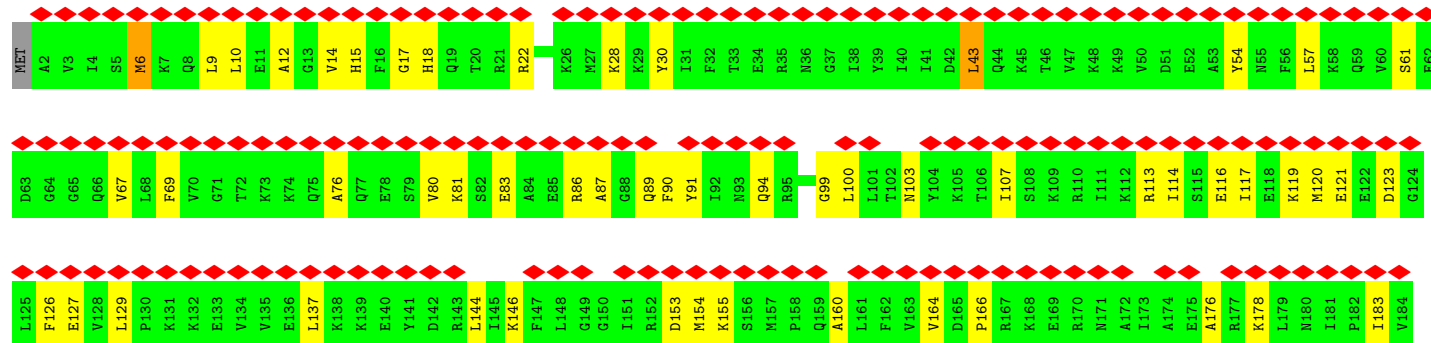
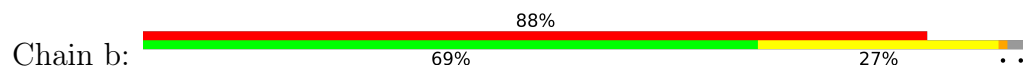
• Molecule 31: 16S ribosomal RNA

Chain a:  39% 45% 11%



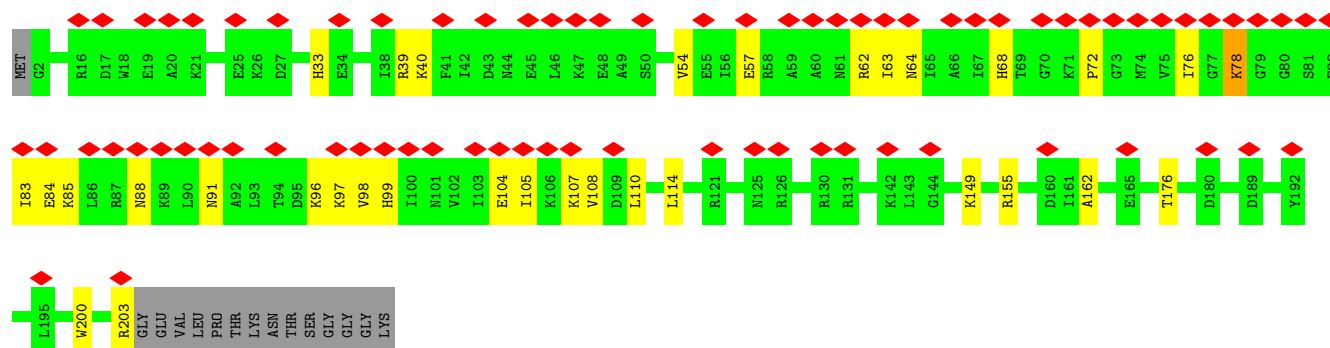
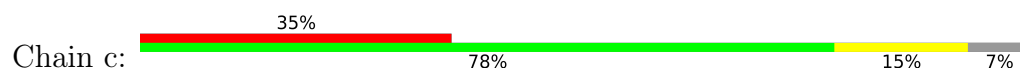


• Molecule 32: Small ribosomal subunit protein uS2

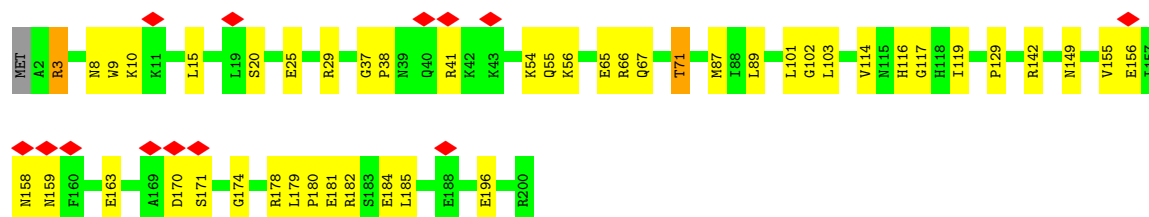
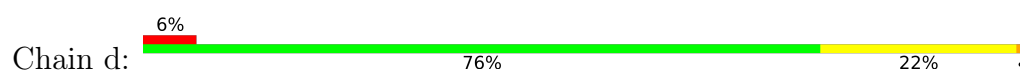




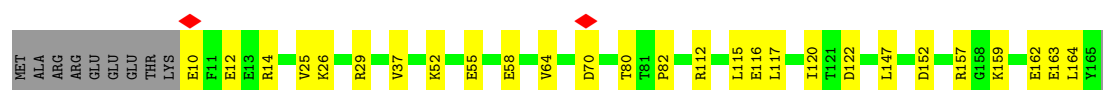
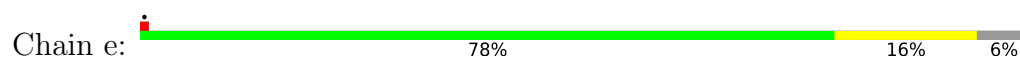
- Molecule 33: Small ribosomal subunit protein uS3



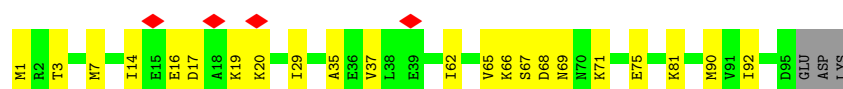
- Molecule 34: Small ribosomal subunit protein uS4



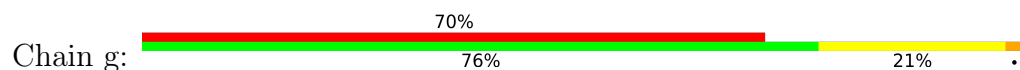
- Molecule 35: Small ribosomal subunit protein uS5

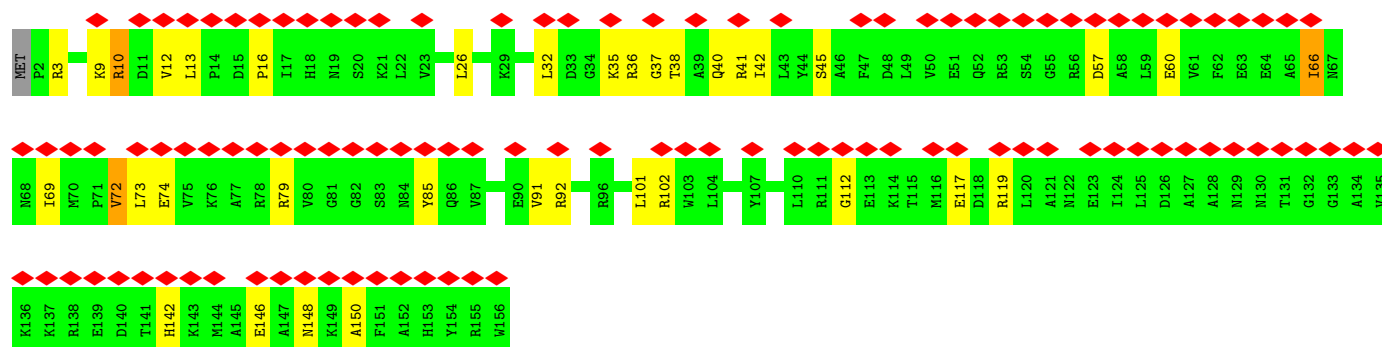


- Molecule 36: Small ribosomal subunit protein bS6

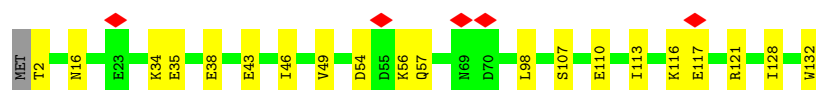
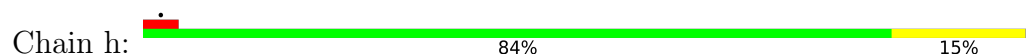


- Molecule 37: Small ribosomal subunit protein uS7

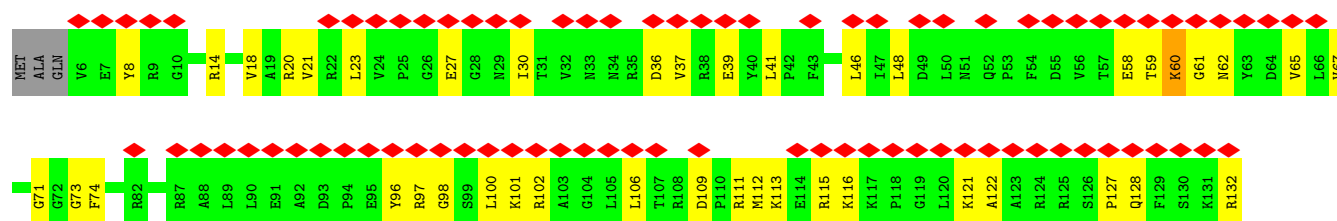




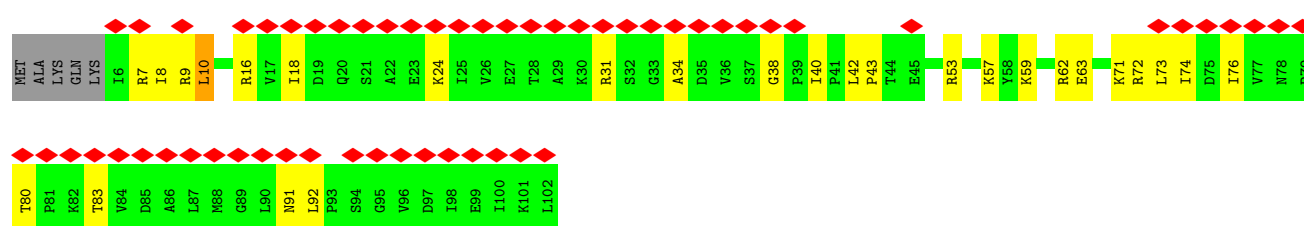
- Molecule 38: Small ribosomal subunit protein uS8



- Molecule 39: Small ribosomal subunit protein uS9

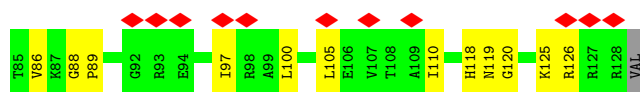


- Molecule 40: Small ribosomal subunit protein uS10

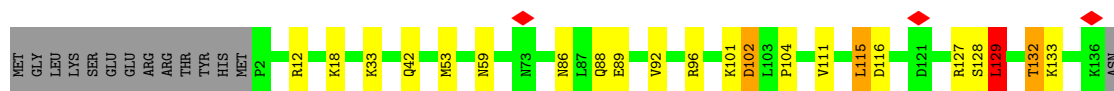
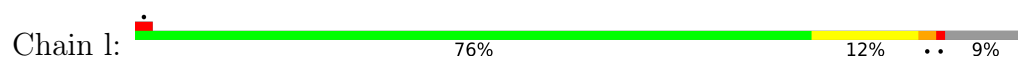


- Molecule 41: Small ribosomal subunit protein uS11

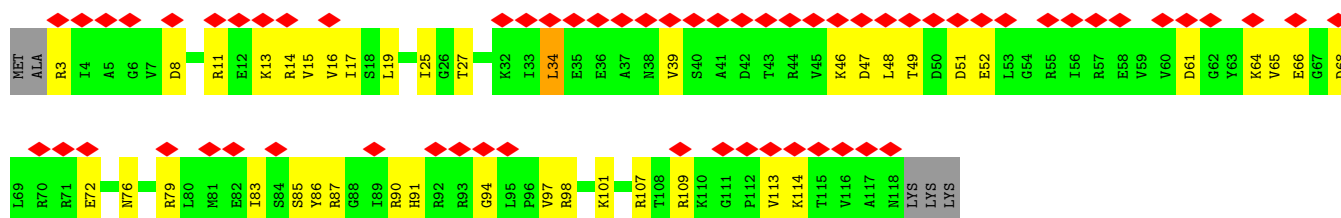




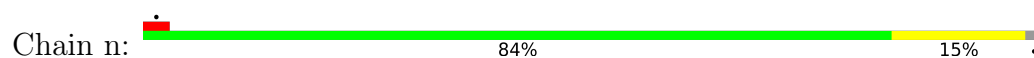
- Molecule 42: Small ribosomal subunit protein uS12



- Molecule 43: Small ribosomal subunit protein uS13



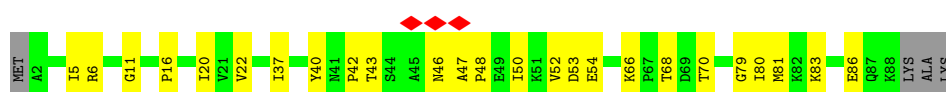
- Molecule 44: Small ribosomal subunit protein uS14B



- Molecule 45: Small ribosomal subunit protein uS15

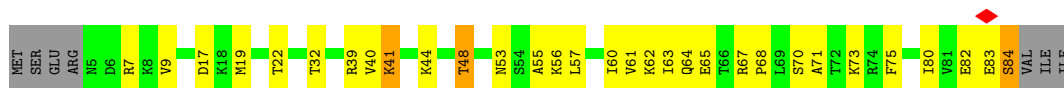


- Molecule 46: Small ribosomal subunit protein bS16

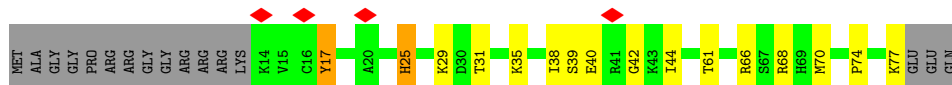


- Molecule 47: Small ribosomal subunit protein uS17

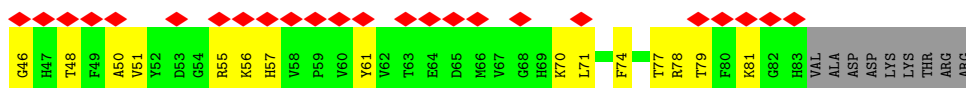
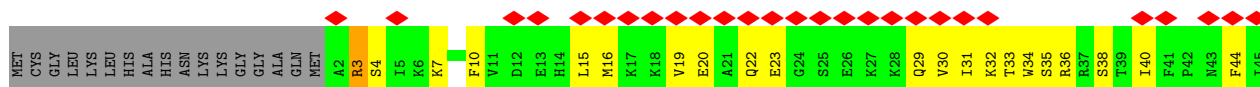
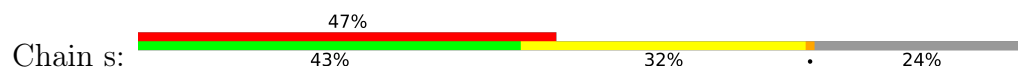




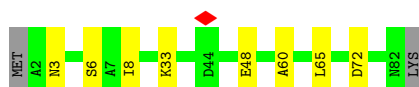
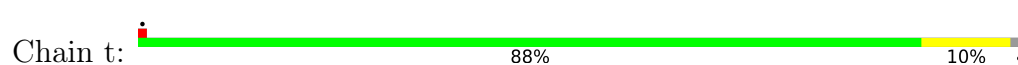
- Molecule 48: Small ribosomal subunit protein bS18



- Molecule 49: Small ribosomal subunit protein uS19



- Molecule 50: Small ribosomal subunit protein bS20



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47560	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.041	Depositor
Minimum map value	-0.010	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ($\text{\AA}$)	395.52, 395.52, 395.52	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.824, 0.824, 0.824	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: A1D6G, MA6, 5MU, OMG, 2MA, 2MG, 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	1	0.90	0/395	1.23	3/530 (0.6%)
2	2	0.51	0/371	0.75	0/484
3	3	0.89	0/526	1.13	5/690 (0.7%)
4	4	1.12	0/299	1.42	6/393 (1.5%)
5	A	0.44	0/69122	0.68	35/107793 (0.0%)
6	B	0.40	0/2733	0.73	1/4257 (0.0%)
7	C	0.96	0/2125	1.23	10/2853 (0.4%)
8	D	1.08	3/1651 (0.2%)	1.18	10/2215 (0.5%)
9	E	0.98	1/1595 (0.1%)	1.21	11/2154 (0.5%)
10	F	0.67	0/1332	1.29	24/1798 (1.3%)
11	G	0.92	1/1277 (0.1%)	1.31	9/1731 (0.5%)
12	H	0.74	0/1165	0.98	5/1570 (0.3%)
13	I	0.93	0/925	1.10	6/1242 (0.5%)
14	J	0.61	0/1100	0.80	3/1467 (0.2%)
15	K	0.96	1/1095 (0.1%)	1.10	10/1472 (0.7%)
16	L	0.63	0/936	0.64	0/1253
17	M	0.90	0/900	1.23	5/1205 (0.4%)
18	N	0.91	1/901 (0.1%)	0.92	3/1209 (0.2%)
19	O	0.54	0/954	0.61	1/1264 (0.1%)
20	P	0.71	1/800 (0.1%)	0.96	3/1070 (0.3%)
21	Q	0.97	1/861 (0.1%)	1.01	3/1161 (0.3%)
22	R	0.75	0/723	0.96	2/966 (0.2%)
23	S	0.68	0/779	1.02	5/1043 (0.5%)
24	T	0.68	2/719 (0.3%)	0.89	3/969 (0.3%)
25	U	0.72	0/621	0.89	1/825 (0.1%)
26	V	1.05	1/451 (0.2%)	1.25	4/603 (0.7%)
27	W	0.82	0/542	0.86	1/722 (0.1%)
28	X	0.77	0/451	0.73	2/606 (0.3%)
29	Y	0.48	0/361	0.89	2/500 (0.4%)
30	Z	0.84	0/367	0.99	0/490
31	a	0.15	0/35498	0.34	1/55345 (0.0%)
32	b	0.19	0/1829	0.46	0/2455

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	c	0.12	0/1618	0.33	0/2173
34	d	0.15	0/1646	0.38	0/2211
35	e	0.25	0/1174	0.47	0/1584
36	f	0.17	0/800	0.45	0/1073
37	g	0.18	0/1262	0.47	1/1698 (0.1%)
38	h	0.22	0/1043	0.41	0/1401
39	i	0.15	0/1023	0.45	0/1374
40	j	0.16	0/785	0.43	0/1060
41	k	0.24	0/859	0.59	0/1161
42	l	0.26	0/1075	0.49	1/1439 (0.1%)
43	m	0.15	0/929	0.40	0/1246
44	n	0.10	0/511	0.33	0/678
45	o	0.12	0/735	0.33	0/982
46	p	0.16	0/699	0.45	0/942
47	q	0.26	0/665	0.48	0/889
48	r	0.25	0/534	0.56	0/715
49	s	0.17	0/683	0.53	1/916 (0.1%)
50	t	0.11	0/611	0.37	0/817
All	All	0.46	12/150056 (0.0%)	0.67	177/224694 (0.1%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	T	76	ASP	CA-C	6.56	1.60	1.52
8	D	160	ALA	CA-C	-6.51	1.44	1.52
15	K	97	VAL	C-O	-5.86	1.17	1.24
18	N	59	GLU	CA-C	-5.81	1.45	1.52
8	D	127	PHE	C-O	-5.75	1.17	1.24

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	G	140	GLN	N-CA-C	-10.45	100.27	113.43
10	F	170	LEU	N-CA-C	-10.32	100.68	113.38
10	F	128	TYR	N-CA-C	10.06	122.01	111.14
12	H	58	ILE	N-CA-C	9.41	122.37	112.96
11	G	69	ARG	N-CA-C	-9.06	102.74	113.88

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	390	0	394	3	0
2	2	367	0	415	5	0
3	3	521	0	586	7	0
4	4	296	0	340	7	0
5	A	61861	0	31103	436	0
6	B	2445	0	1240	20	0
7	C	2090	0	2201	47	0
8	D	1627	0	1667	36	0
9	E	1572	0	1619	33	0
10	F	1317	0	1323	62	0
11	G	1259	0	1221	38	0
12	H	1143	0	1134	34	0
13	I	918	0	981	50	0
14	J	1086	0	1125	21	0
15	K	1071	0	1123	26	0
16	L	932	0	983	33	0
17	M	891	0	925	28	0
18	N	889	0	937	22	0
19	O	942	0	1014	37	0
20	P	790	0	830	23	0
21	Q	853	0	905	19	0
22	R	715	0	748	28	0
23	S	770	0	809	34	0
24	T	711	0	740	34	0
25	U	615	0	622	18	0
26	V	445	0	466	10	0
27	W	541	0	563	8	0
28	X	449	0	491	2	0
29	Y	353	0	218	13	0
30	Z	361	0	361	11	0
31	a	31706	0	15964	655	0
32	b	1802	0	1866	49	0
33	c	1596	0	1659	24	0
34	d	1616	0	1646	37	0
35	e	1160	0	1223	13	0
36	f	789	0	788	15	0
37	g	1242	0	1276	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	h	1031	0	1082	14	0
39	i	1007	0	1031	30	0
40	j	773	0	812	19	0
41	k	844	0	851	32	0
42	l	1058	0	1130	16	0
43	m	922	0	970	28	0
44	n	501	0	527	9	0
45	o	726	0	756	15	0
46	p	688	0	713	16	0
47	q	657	0	694	25	0
48	r	525	0	561	11	0
49	s	665	0	668	34	0
50	t	611	0	655	7	0
51	A	69	0	0	0	0
52	A	12	0	0	0	0
53	A	4	0	0	0	0
All	All	138224	0	91956	1998	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 1998 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)
24:T:32:TYR:CE1	24:T:92:LEU:HD21	1.62	1.35
24:T:32:TYR:CD1	24:T:92:LEU:HD23	1.74	1.23
24:T:32:TYR:CD1	24:T:92:LEU:CD2	2.21	1.22
24:T:32:TYR:CE1	24:T:92:LEU:CD2	2.22	1.21
5:A:104:C:H5"	5:A:104:C:H6	1.30	0.96

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	1	45/47 (96%)	41 (91%)	4 (9%)	0	100	100
2	2	41/43 (95%)	38 (93%)	3 (7%)	0	100	100
3	3	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
4	4	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
7	C	272/274 (99%)	245 (90%)	26 (10%)	1 (0%)	30	49
8	D	213/215 (99%)	200 (94%)	13 (6%)	0	100	100
9	E	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
10	F	173/175 (99%)	144 (83%)	28 (16%)	1 (1%)	21	39
11	G	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
12	H	143/145 (99%)	131 (92%)	12 (8%)	0	100	100
13	I	120/122 (98%)	113 (94%)	6 (5%)	1 (1%)	16	32
14	J	144/146 (99%)	135 (94%)	9 (6%)	0	100	100
15	K	135/137 (98%)	128 (95%)	7 (5%)	0	100	100
16	L	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
17	M	117/119 (98%)	107 (92%)	10 (8%)	0	100	100
18	N	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
19	O	114/116 (98%)	112 (98%)	2 (2%)	0	100	100
20	P	100/102 (98%)	93 (93%)	5 (5%)	2 (2%)	6	11
21	Q	110/117 (94%)	105 (96%)	5 (4%)	0	100	100
22	R	87/89 (98%)	84 (97%)	3 (3%)	0	100	100
23	S	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
24	T	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
25	U	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
26	V	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
27	W	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
28	X	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
29	Y	55/59 (93%)	51 (93%)	4 (7%)	0	100	100
30	Z	46/48 (96%)	44 (96%)	2 (4%)	0	100	100
32	b	222/232 (96%)	212 (96%)	10 (4%)	0	100	100
33	c	200/217 (92%)	190 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	d	197/200 (98%)	187 (95%)	10 (5%)	0	100	100
35	e	154/166 (93%)	149 (97%)	5 (3%)	0	100	100
36	f	93/98 (95%)	87 (94%)	6 (6%)	0	100	100
37	g	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
38	h	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
39	i	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
40	j	95/102 (93%)	89 (94%)	6 (6%)	0	100	100
41	k	112/129 (87%)	102 (91%)	10 (9%)	0	100	100
42	l	133/149 (89%)	122 (92%)	10 (8%)	1 (1%)	16	32
43	m	114/121 (94%)	105 (92%)	9 (8%)	0	100	100
44	n	58/61 (95%)	57 (98%)	1 (2%)	0	100	100
45	o	85/89 (96%)	82 (96%)	3 (4%)	0	100	100
46	p	85/91 (93%)	84 (99%)	1 (1%)	0	100	100
47	q	78/87 (90%)	74 (95%)	4 (5%)	0	100	100
48	r	62/80 (78%)	60 (97%)	2 (3%)	0	100	100
49	s	80/108 (74%)	73 (91%)	7 (9%)	0	100	100
50	t	79/83 (95%)	78 (99%)	1 (1%)	0	100	100
All	All	5323/5563 (96%)	4979 (94%)	338 (6%)	6 (0%)	49	69

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	P	51	PRO
13	I	98	ILE
10	F	139	PRO
20	P	50	ALA
42	l	132	THR

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	1	44/45 (98%)	35 (80%)	9 (20%)	1	2
2	2	39/39 (100%)	38 (97%)	1 (3%)	40	66
3	3	55/55 (100%)	51 (93%)	4 (7%)	13	27
4	4	35/35 (100%)	31 (89%)	4 (11%)	5	11
7	C	220/221 (100%)	203 (92%)	17 (8%)	12	25
8	D	173/173 (100%)	155 (90%)	18 (10%)	7	13
9	E	168/168 (100%)	155 (92%)	13 (8%)	12	25
10	F	139/154 (90%)	100 (72%)	39 (28%)	0	1
11	G	123/153 (80%)	101 (82%)	22 (18%)	2	3
12	H	122/123 (99%)	110 (90%)	12 (10%)	7	16
13	I	100/100 (100%)	91 (91%)	9 (9%)	9	19
14	J	109/112 (97%)	99 (91%)	10 (9%)	8	18
15	K	108/114 (95%)	95 (88%)	13 (12%)	5	9
16	L	96/101 (95%)	96 (100%)	0	100	100
17	M	86/95 (90%)	75 (87%)	11 (13%)	4	8
18	N	93/100 (93%)	74 (80%)	19 (20%)	1	2
19	O	96/96 (100%)	91 (95%)	5 (5%)	21	42
20	P	84/86 (98%)	80 (95%)	4 (5%)	23	45
21	Q	89/94 (95%)	78 (88%)	11 (12%)	4	8
22	R	78/80 (98%)	66 (85%)	12 (15%)	2	4
23	S	81/88 (92%)	73 (90%)	8 (10%)	7	15
24	T	75/82 (92%)	64 (85%)	11 (15%)	3	5
25	U	60/64 (94%)	53 (88%)	7 (12%)	5	10
26	V	44/49 (90%)	38 (86%)	6 (14%)	3	7
27	W	58/60 (97%)	43 (74%)	15 (26%)	0	1
28	X	52/52 (100%)	47 (90%)	5 (10%)	8	16
29	Y	21/56 (38%)	17 (81%)	4 (19%)	1	2
30	Z	36/44 (82%)	36 (100%)	0	100	100
32	b	194/201 (96%)	192 (99%)	2 (1%)	68	84
33	c	164/175 (94%)	163 (99%)	1 (1%)	78	89
34	d	174/175 (99%)	172 (99%)	2 (1%)	65	83
35	e	122/131 (93%)	117 (96%)	5 (4%)	27	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	f	83/86 (96%)	81 (98%)	2 (2%)	43	68
37	g	131/132 (99%)	122 (93%)	9 (7%)	14	30
38	h	112/113 (99%)	111 (99%)	1 (1%)	70	85
39	i	105/107 (98%)	102 (97%)	3 (3%)	37	63
40	j	87/91 (96%)	84 (97%)	3 (3%)	32	58
41	k	90/104 (86%)	88 (98%)	2 (2%)	45	70
42	l	117/130 (90%)	111 (95%)	6 (5%)	21	43
43	m	100/104 (96%)	98 (98%)	2 (2%)	48	72
44	n	52/53 (98%)	52 (100%)	0	100	100
45	o	79/81 (98%)	78 (99%)	1 (1%)	61	81
46	p	74/77 (96%)	72 (97%)	2 (3%)	39	65
47	q	75/82 (92%)	70 (93%)	5 (7%)	15	31
48	r	57/68 (84%)	55 (96%)	2 (4%)	32	57
49	s	71/91 (78%)	70 (99%)	1 (1%)	59	79
50	t	67/69 (97%)	67 (100%)	0	100	100
All	All	4438/4709 (94%)	4100 (92%)	338 (8%)	14	26

5 of 338 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	R	89	LEU
29	Y	5	ILE
23	S	38	VAL
26	V	11	LYS
36	f	81	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
21	Q	40	ASN
32	b	15	HIS
22	R	37	GLN
24	T	20	GLN
33	c	88	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
31	a	1470/1548 (94%)	382 (25%)	0
5	A	2879/2921 (98%)	951 (33%)	78 (2%)
6	B	114/115 (99%)	47 (41%)	4 (3%)
All	All	4463/4584 (97%)	1380 (30%)	82 (1%)

5 of 1380 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	A	5	A
5	A	13	A
5	A	18	C
5	A	19	G
5	A	23	G

5 of 82 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	A	1826	G
5	A	2533	U
5	A	2094	G
5	A	2347	A
5	A	2829	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	5MU	A	1966	5	19,22,23	1.66	5 (26%)	27,32,35	2.35	8 (29%)
5	MA6	A	2085	5	23,26,27	1.53	5 (21%)	33,38,41	2.36	13 (39%)
5	2MA	A	2530	5,52	22,25,26	1.46	5 (22%)	32,37,40	2.45	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	2MG	A	2472	5	23,26,27	1.37	3 (13%)	33,38,41	2.75	12 (36%)
5	OMG	A	2278	5	23,26,27	1.27	4 (17%)	32,38,41	2.07	7 (21%)
5	5MU	A	792	5	19,22,23	1.48	5 (26%)	27,32,35	2.29	8 (29%)

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
5	5MU	A	1966	5	-	0/7/25/26	0/2/2/2
5	MA6	A	2085	5	-	2/11/29/30	0/3/3/3
5	2MA	A	2530	5,52	-	0/7/25/26	0/3/3/3
5	2MG	A	2472	5	-	0/9/27/28	0/3/3/3
5	OMG	A	2278	5	-	1/9/27/28	0/3/3/3
5	5MU	A	792	5	-	0/7/25/26	0/2/2/2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2085	MA6	C5-C4	4.25	1.46	1.39
5	A	2530	2MA	C5-C4	4.00	1.46	1.39
5	A	2472	2MG	C6-N1	-3.42	1.32	1.38
5	A	1966	5MU	C4-N3	-3.25	1.32	1.38
5	A	792	5MU	C4-N3	-3.24	1.32	1.38

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2472	2MG	C2-N3-C4	8.92	123.16	112.00
5	A	2530	2MA	C5-C4-N3	-8.23	118.51	127.18
5	A	2472	2MG	N1-C2-N2	7.06	123.76	116.56
5	A	2530	2MA	N3-C4-N9	6.92	135.77	126.99
5	A	2278	OMG	C5-C4-N3	-6.16	118.58	128.39

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2085	MA6	C5-C6-N6-C10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
5	A	2278	OMG	C1'-C2'-O2'-CM2
5	A	2085	MA6	N1-C6-N6-C10

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2085	MA6	1	0
5	A	2278	OMG	1	0
5	A	792	5MU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 12 are monoatomic - leaving 1 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	$\# Z > 2$
51	A1D6G	A	3000	52	72,73,73	2.44	26 (36%)	97,107,107	1.84	30 (30%)

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
51	A1D6G	A	3000	52	-	11/82/113/113	0/5/5/5

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	A	3000	A1D6G	C65-N64	8.77	1.45	1.33
51	A	3000	A1D6G	C11-N13	7.43	1.50	1.34
51	A	3000	A1D6G	O67-C65	4.92	1.43	1.36
51	A	3000	A1D6G	O10-C11	4.88	1.43	1.35
51	A	3000	A1D6G	C22-C21	4.59	1.55	1.44

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	A	3000	A1D6G	C63-N64-C65	-4.32	106.75	112.39
51	A	3000	A1D6G	O10-C11-N13	4.31	118.03	111.01
51	A	3000	A1D6G	O42-C43-C45	4.27	115.45	109.34
51	A	3000	A1D6G	C52-C39-C37	-4.12	107.24	113.54
51	A	3000	A1D6G	C02-C03-C68	-3.95	109.79	115.23

There are no chirality outliers.

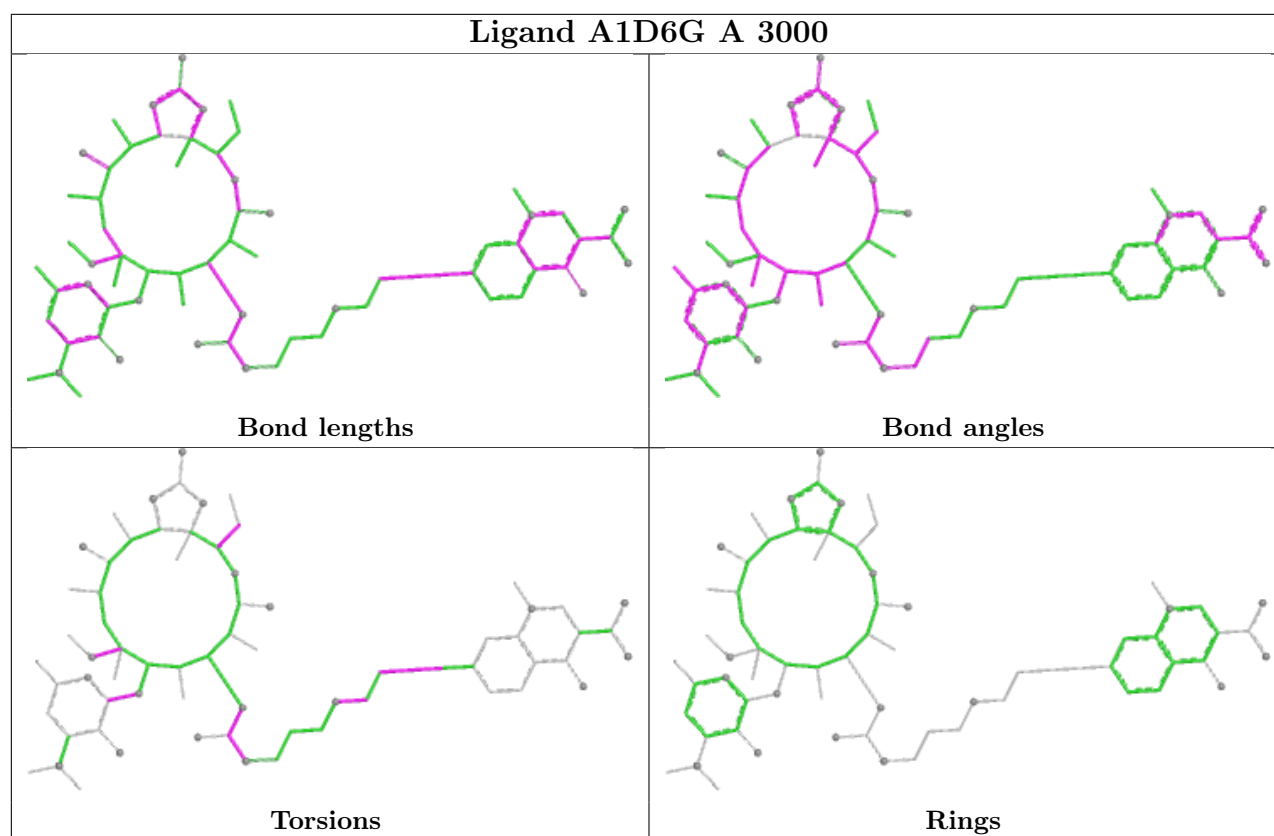
5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
51	A	3000	A1D6G	C18-C19-C20-C21
51	A	3000	A1D6G	O10-C11-N13-C14
51	A	3000	A1D6G	O12-C11-N13-C14
51	A	3000	A1D6G	C19-C20-C21-C22
51	A	3000	A1D6G	N13-C11-O10-C09

There are no ring outliers.

No monomer is involved in short contacts.

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.

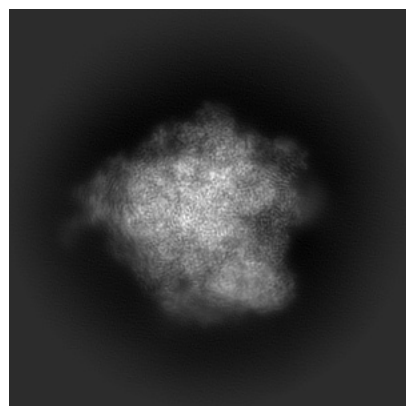
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38875. These allow visual inspection of the internal detail of the map and identification of artifacts.

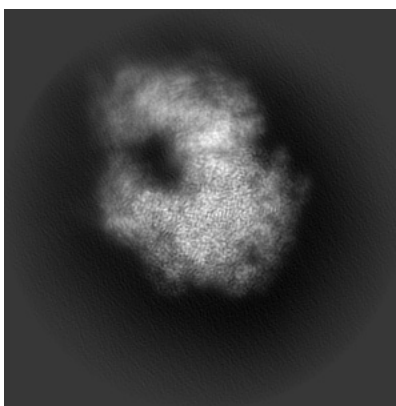
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

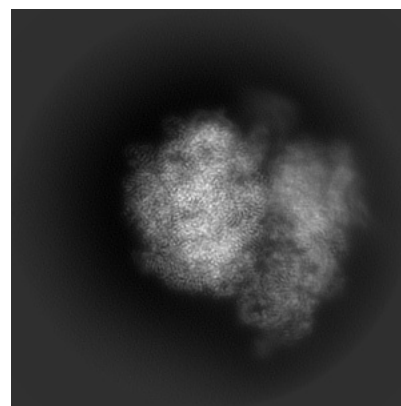
6.1.1 Primary map



X

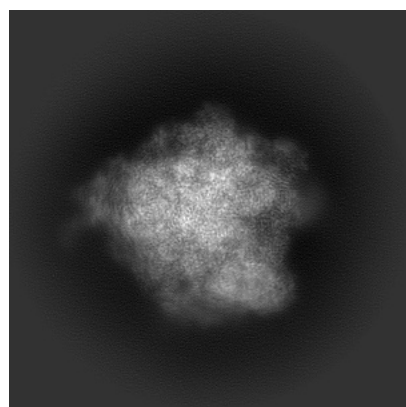


Y

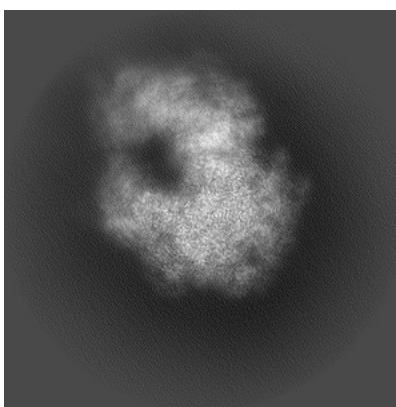


Z

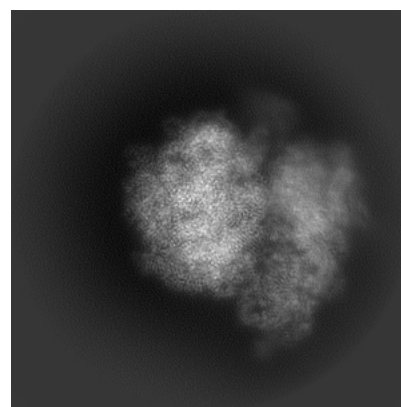
6.1.2 Raw map



X



Y

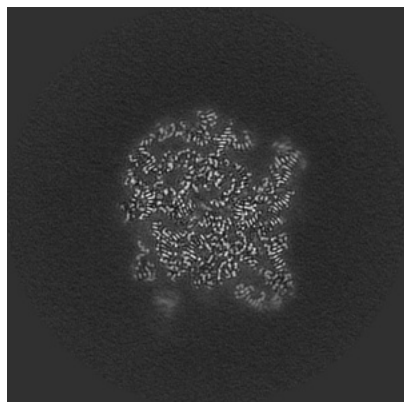


Z

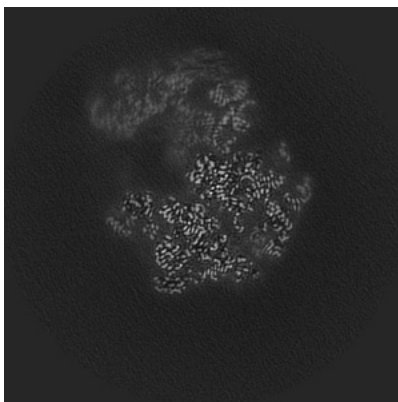
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

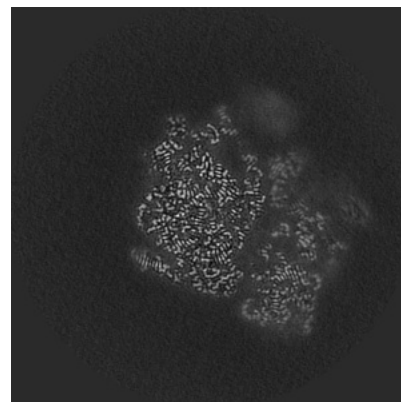
6.2.1 Primary map



X Index: 240

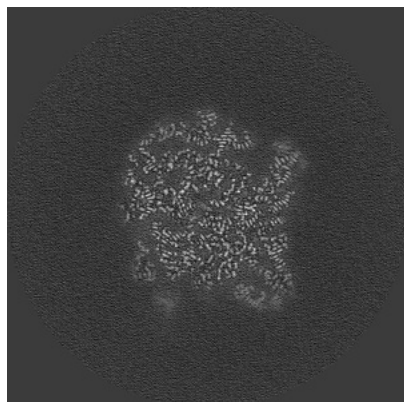


Y Index: 240

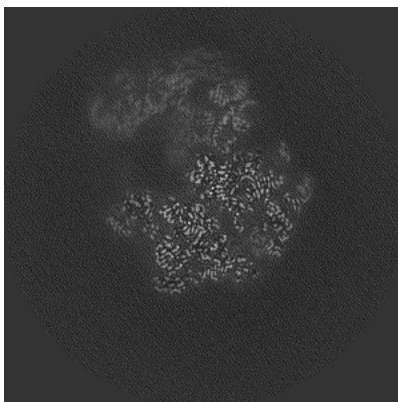


Z Index: 240

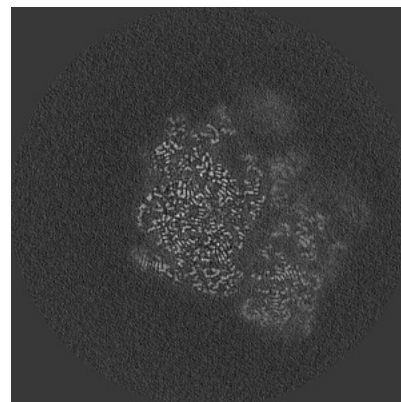
6.2.2 Raw map



X Index: 240



Y Index: 240

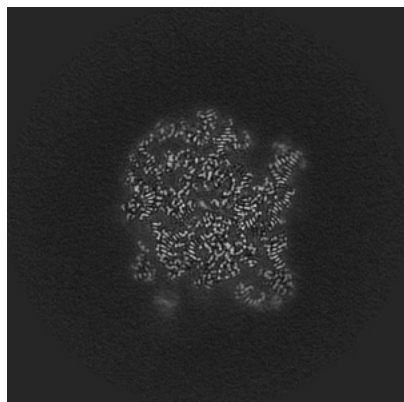


Z Index: 240

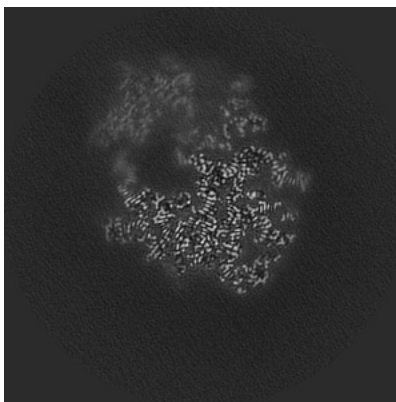
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

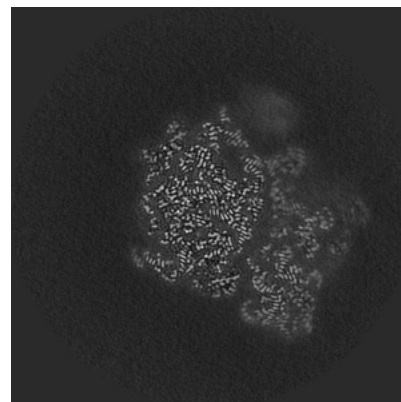
6.3.1 Primary map



X Index: 239

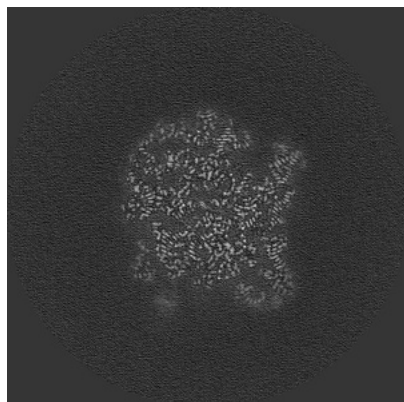


Y Index: 257

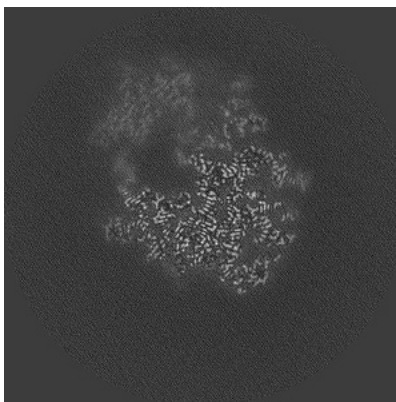


Z Index: 244

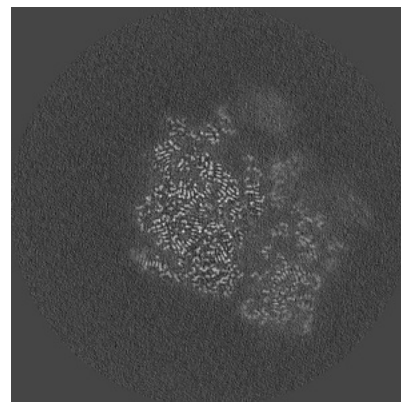
6.3.2 Raw map



X Index: 239



Y Index: 257

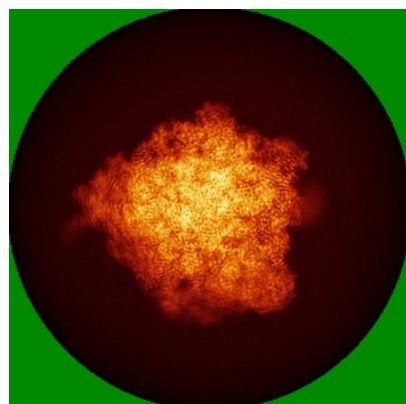


Z Index: 239

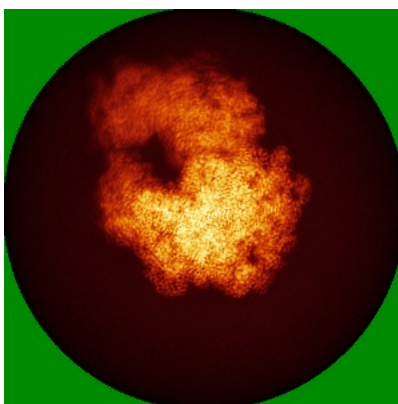
The images above show the largest variance slices of the map in three orthogonal directions.

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

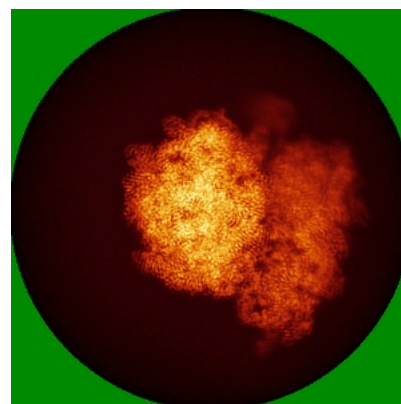
6.4.1 Primary map



X

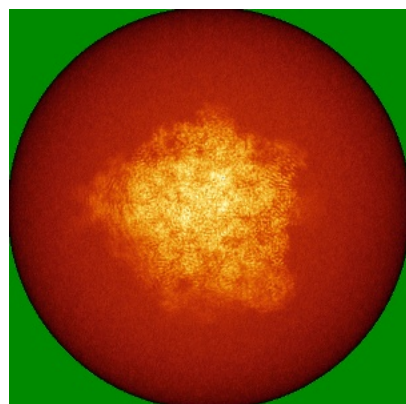


Y

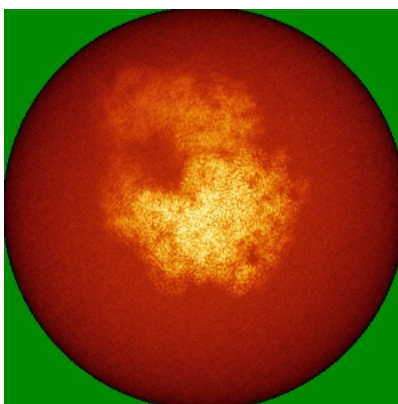


Z

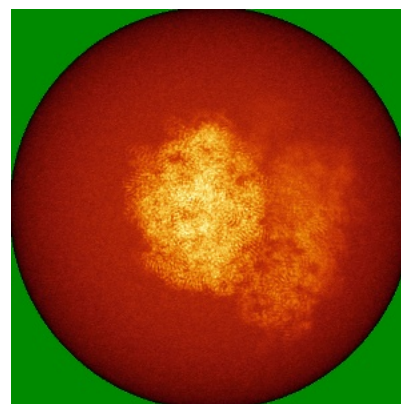
6.4.2 Raw map



X



Y

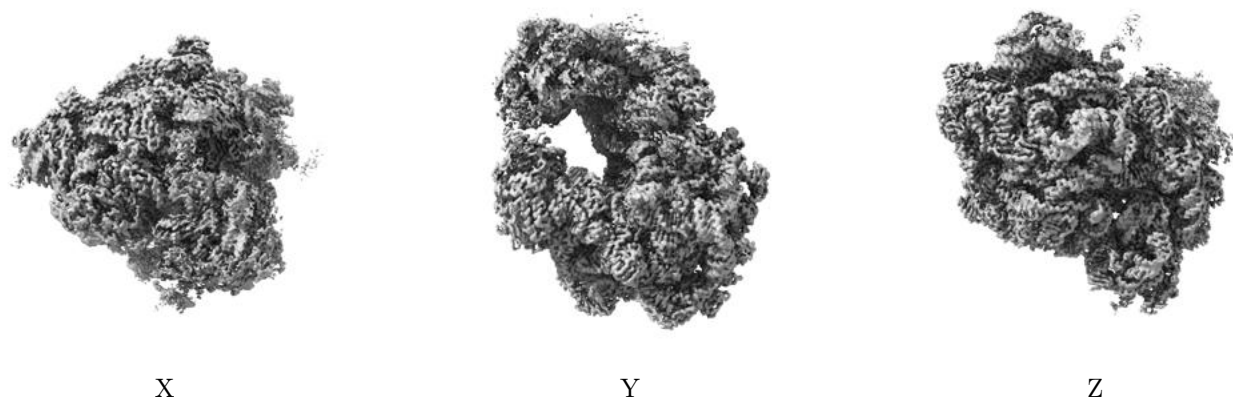


Z

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.

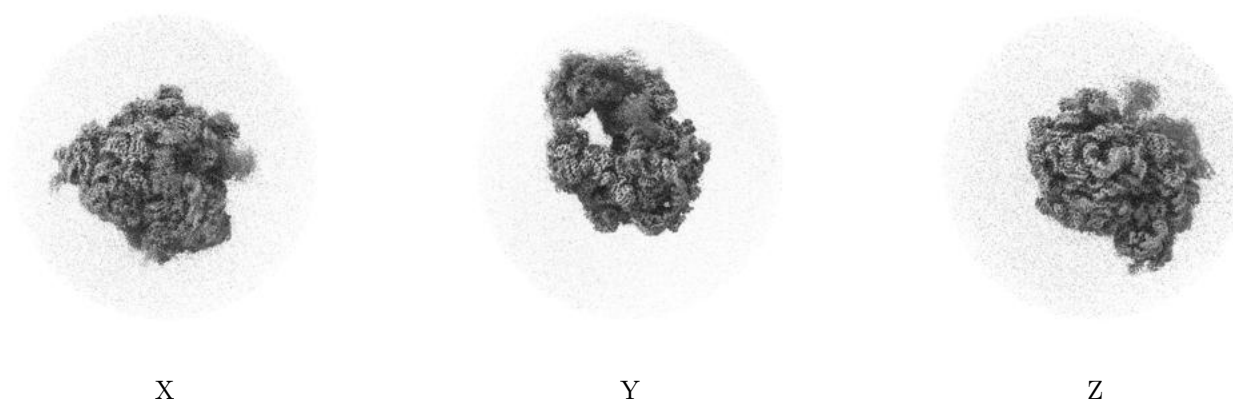
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

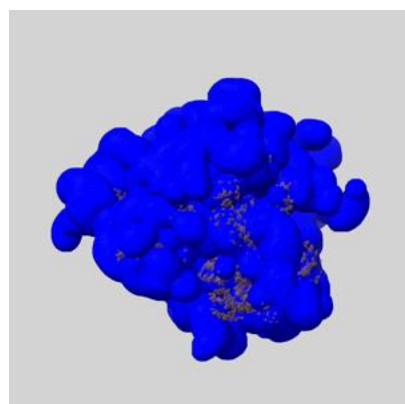
6.6 Mask visualisation [i](#)

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

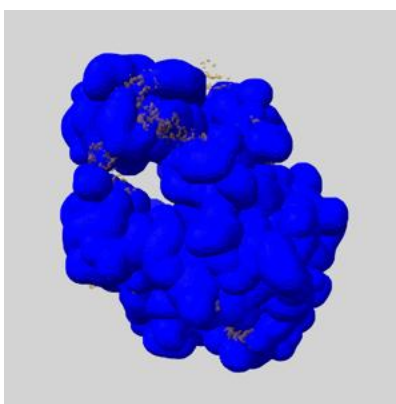
A mask typically either:

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

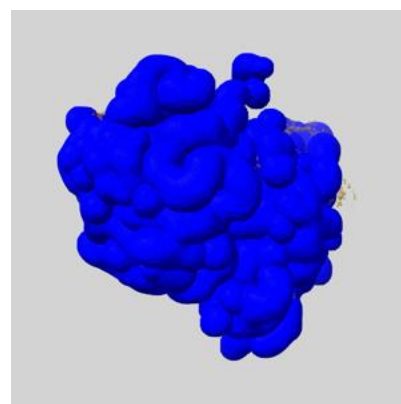
6.6.1 emd_38875_msk_1.map [i](#)



X



Y

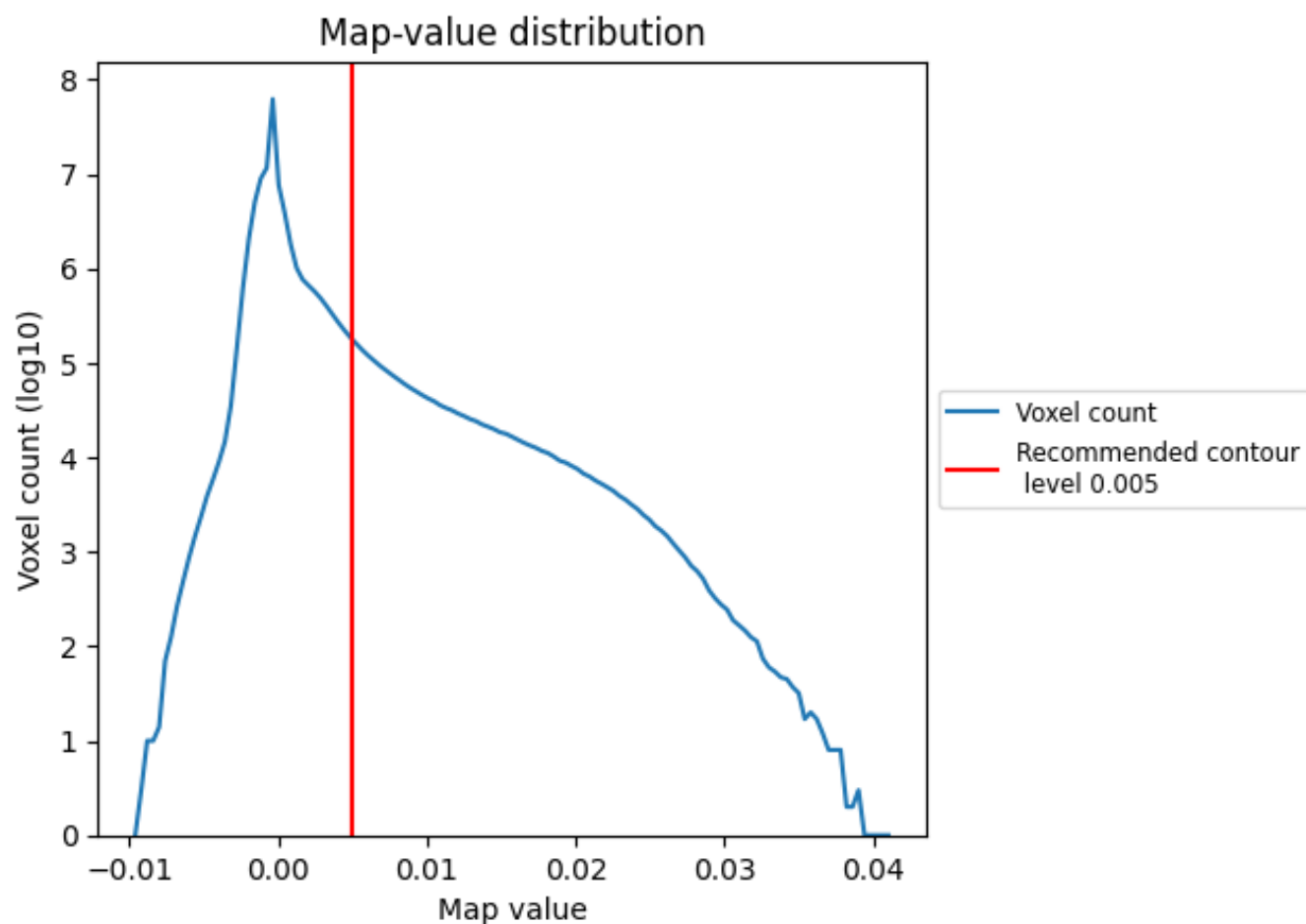


Z

7 Map analysis [i](#)

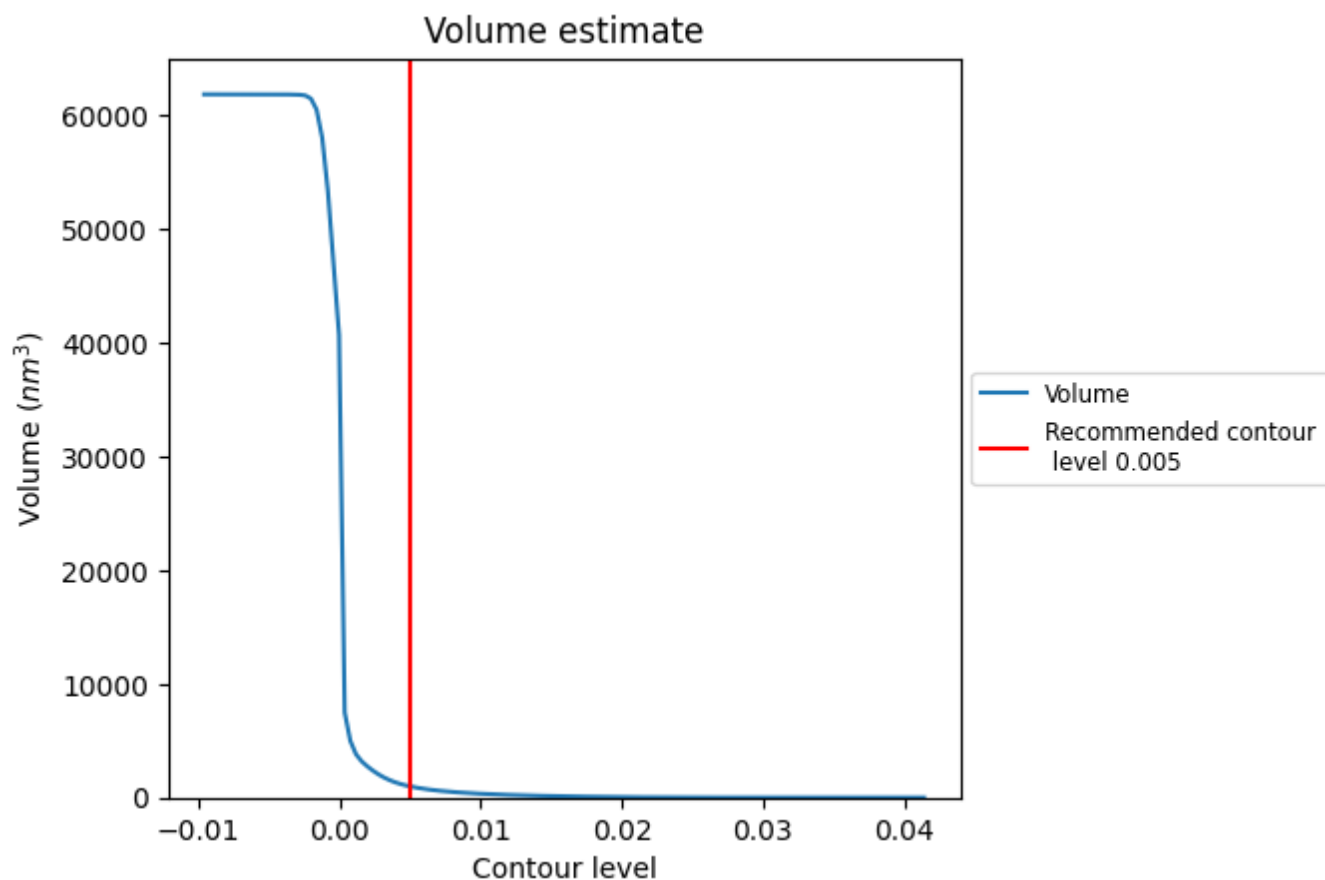
This section contains the results of statistical analysis of the map.

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.

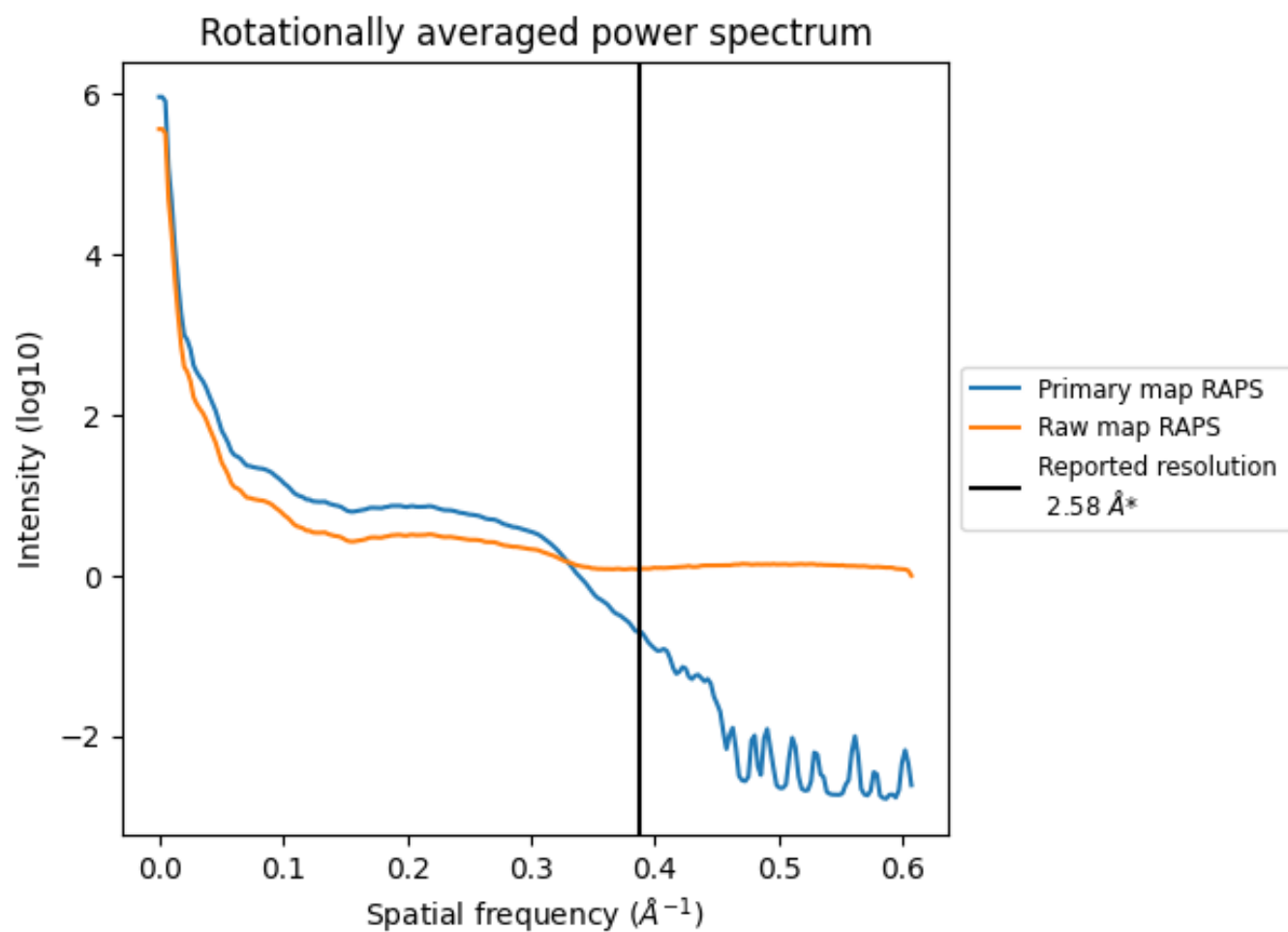
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 985 nm³; this corresponds to an approximate mass of 889 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 ⓘ

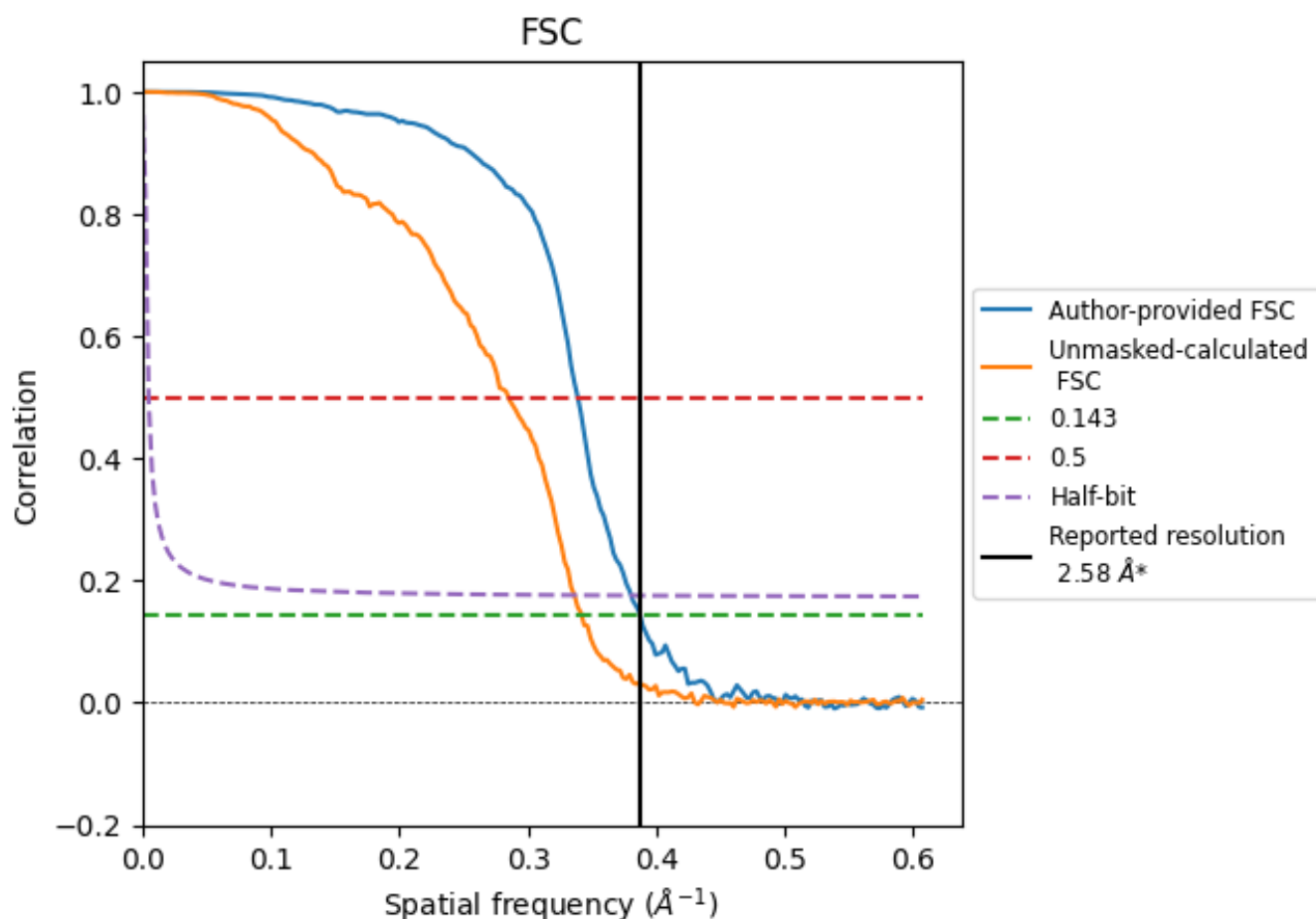


*Reported resolution corresponds to spatial frequency of 0.388 Å⁻¹

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 0.388 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

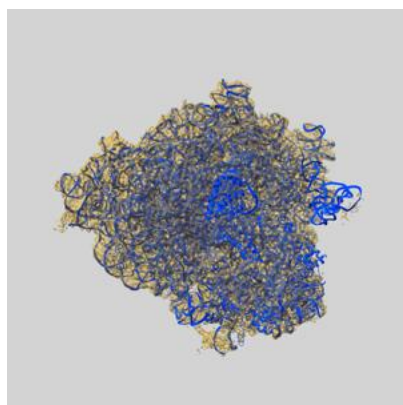
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.58	-	-
Author-provided FSC curve	2.58	2.95	2.63
Unmasked-calculated*	2.92	3.51	2.97

*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 2.92 differs from the reported value 2.58 by more than 10 %

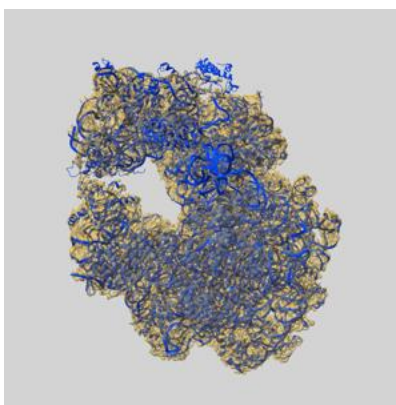
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-38875 and PDB model 8Y38. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

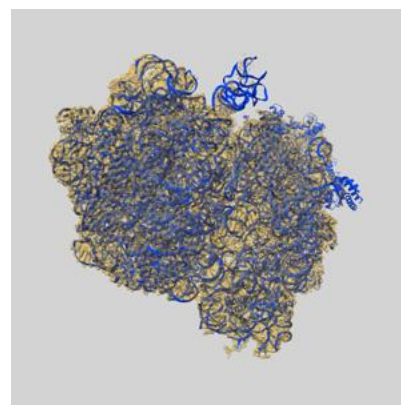
9.1 Map-model overlay [i](#)



X



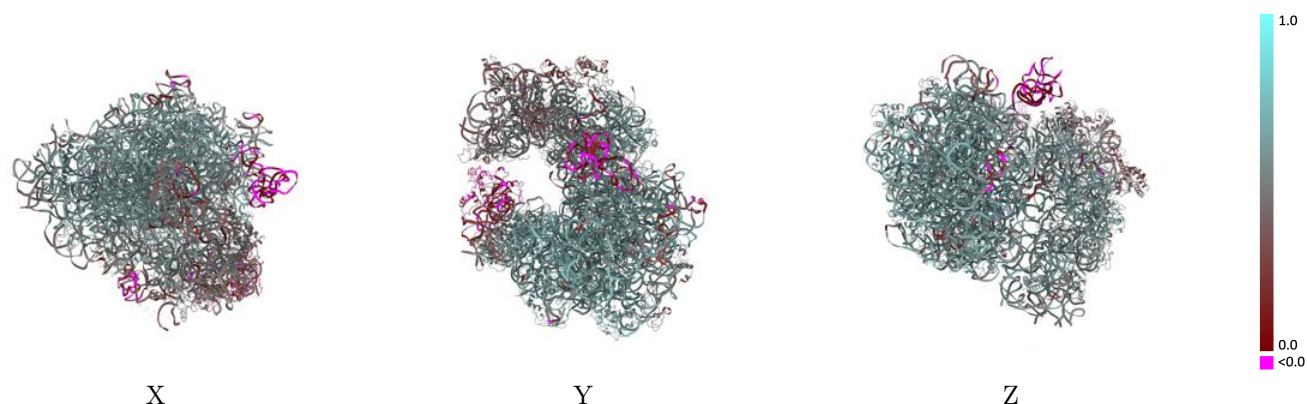
Y



Z

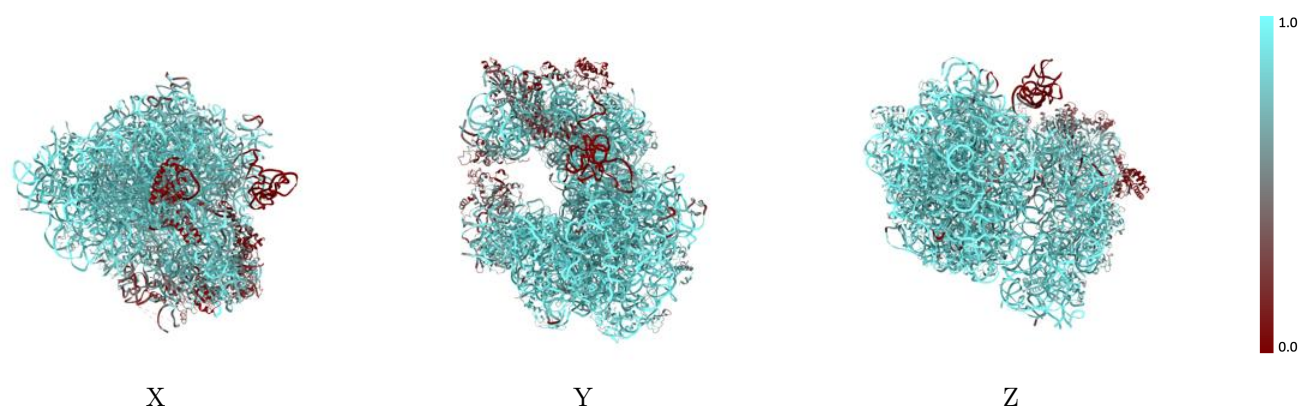
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



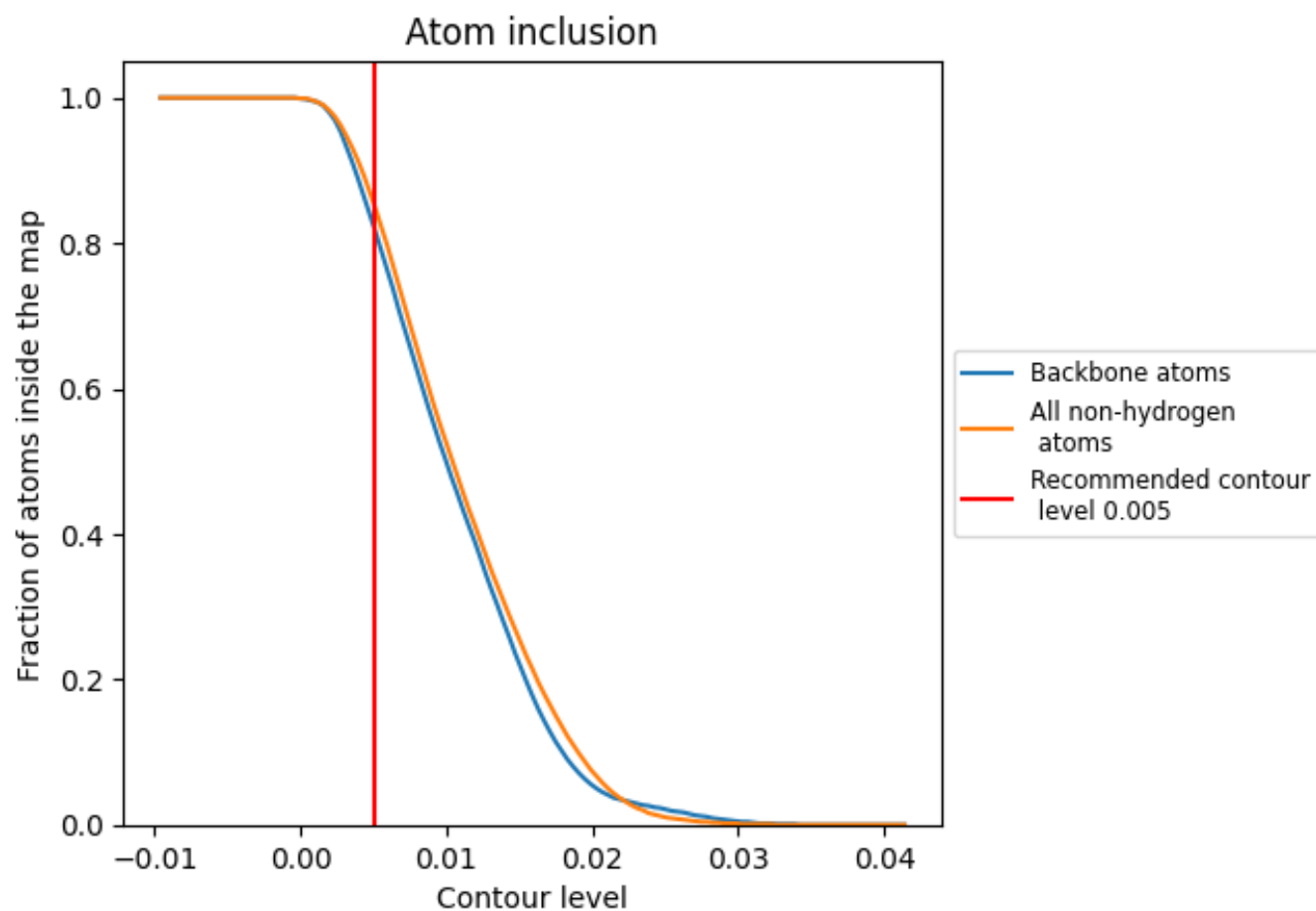
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 86% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8560	 0.5370
1	 0.9150	 0.6010
2	 0.9650	 0.6280
3	 0.9780	 0.6410
4	 0.9520	 0.6130
A	 0.9110	 0.5610
B	 0.8620	 0.4350
C	 0.9310	 0.6040
D	 0.9300	 0.6140
E	 0.8810	 0.6110
F	 0.4590	 0.1610
G	 0.8080	 0.5210
H	 0.9380	 0.6060
I	 0.9210	 0.5850
J	 0.8810	 0.5700
K	 0.9490	 0.6130
L	 0.9080	 0.5820
M	 0.7370	 0.4210
N	 0.8660	 0.5210
O	 0.9490	 0.6200
P	 0.8820	 0.5940
Q	 0.9290	 0.6110
R	 0.8680	 0.5560
S	 0.7570	 0.5060
T	 0.7550	 0.5000
U	 0.9130	 0.5670
V	 0.9390	 0.5930
W	 0.7960	 0.5230
X	 0.9140	 0.5950
Y	 0.2280	 0.0600
Z	 0.9680	 0.6280
a	 0.9050	 0.5210
b	 0.1260	 0.3690
c	 0.4970	 0.4630
d	 0.7720	 0.5150



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Chain	Atom inclusion	Q-score
e	 0.8350	 0.5620
f	 0.7560	 0.5730
g	 0.2920	 0.4130
h	 0.8120	 0.5700
i	 0.2990	 0.3510
j	 0.3950	 0.3980
k	 0.5990	 0.4590
l	 0.8060	 0.5570
m	 0.3840	 0.4140
n	 0.6980	 0.4990
o	 0.8370	 0.5790
p	 0.8500	 0.5570
q	 0.8410	 0.5580
r	 0.7750	 0.5620
s	 0.3530	 0.4190
t	 0.8670	 0.5790