



wwPDB EM Validation Summary Report ⓘ

Dec 28, 2024 – 02:00 PM EST

PDB ID : 7BL6
EMDB ID : EMD-12219
Title : 50S-ObgE-GMPPNP particle
Authors : Hilal, T.; Nikolay, R.; Schmidt, S.; Spahn, C.M.T.
Deposited on : 2021-01-18
Resolution : 4.00 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.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

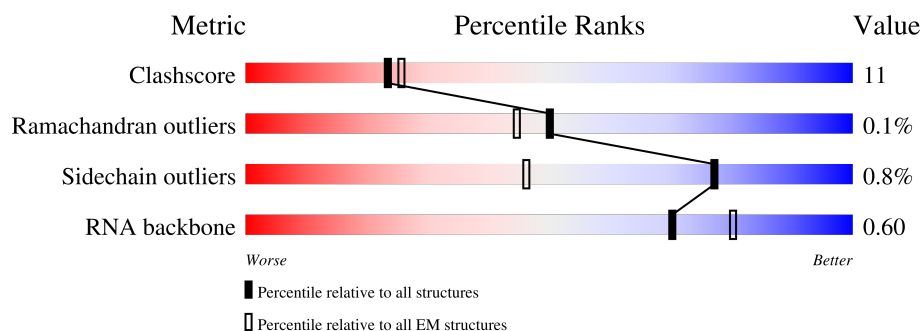
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 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.





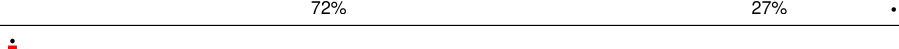
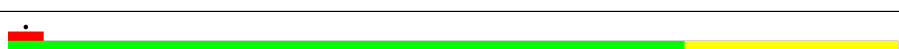



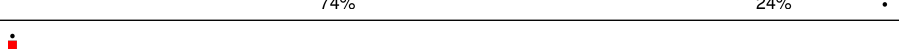



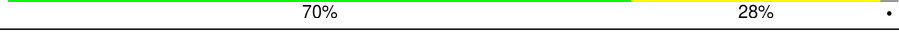

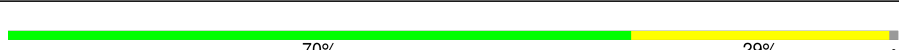


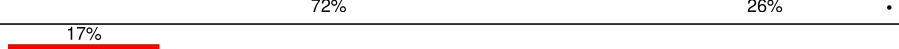







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	g	38	100%
2	C	273	73% 26% ..
3	D	209	74% 26%
4	E	201	76% 20% .
5	F	179	68% 31% .
6	G	177	5% 74% 24% ..
7	J	142	82% 18% .

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Mol	Chain	Length	Quality of chain
8	L	144	
9	N	120	
10	O	117	
11	Q	118	
12	R	103	
13	S	110	
14	T	100	
15	U	104	
16	V	94	
17	W	85	
18	X	78	
19	Y	63	
20	Z	59	
21	0	57	
22	1	55	
23	2	46	
24	K	123	
25	P	115	
26	M	136	
27	H	149	
28	d	70	
29	A	2904	
30	B	119	
31	9	390	
32	3	65	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 92769 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 L36.

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

- Molecule 2 is a protein called 50S ribosomal protein L2.

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

- Molecule 3 is a protein called 50S ribosomal protein L3.

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

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	193	Total	C	N	O	S	0	0
			1483	932	266	280	5		

- Molecule 5 is a protein called 50S ribosomal protein L5.

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

- Molecule 6 is a protein called 50S ribosomal protein L6.

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

- Molecule 7 is a protein called 50S ribosomal protein L13.

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

- Molecule 8 is a protein called 50S ribosomal protein L15.

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

- Molecule 9 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	N	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 10 is a protein called 50S ribosomal protein L18.

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

- Molecule 11 is a protein called 50S ribosomal protein L20.

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

- Molecule 12 is a protein called 50S ribosomal protein L21.

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

- Molecule 13 is a protein called 50S ribosomal protein L22.

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

- Molecule 14 is a protein called 50S ribosomal protein L23.

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

- Molecule 15 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	U	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 16 is a protein called 50S ribosomal protein L25.

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

- Molecule 17 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	W	76	Total	C	N	O	S	0	0
			577	357	117	102	1		

- Molecule 18 is a protein called 50S ribosomal protein L28.

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

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

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

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	1	50	Total	C	N	O	S	0	0
			409	263	75	71			

- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 24 is a protein called 50S ribosomal protein L14.

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

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			911	571	178	161	1		

- Molecule 26 is a protein called 50S ribosomal protein L16.

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

- Molecule 27 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	47	Total	C	N	O	S	0	0
			364	227	64	67	6		

- Molecule 29 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 30 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B	119	Total	C	N	O	P	0	0
			2548	1135	466	829	118		

- Molecule 31 is a protein called GTPase ObgE/CgtA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	9	338	Total	C	N	O	S	0	0
			2582	1626	453	490	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

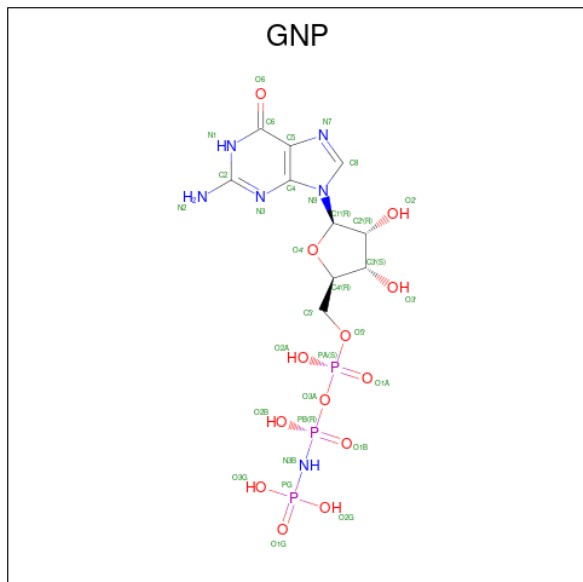
- Molecule 33 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
33	g	1	Total	Zn	0
			1	1	
33	d	1	Total	Zn	0
			1	1	

- Molecule 34 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
34	A	1	Total	Mg	0
			1	1	
34	9	1	Total	Mg	0
			1	1	

- Molecule 35 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
35	9	1	Total	C	N	O	P	0
			32	10	6	13	3	

- Molecule 36 is water.

Mol	Chain	Residues	Atoms		AltConf
36	C	1	Total	O	0
			1	1	
36	F	1	Total	O	0
			1	1	
36	N	3	Total	O	0
			3	3	
36	S	1	Total	O	0
			1	1	
36	A	20	Total	O	0
			20	20	
36	B	1	Total	O	0
			1	1	

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.

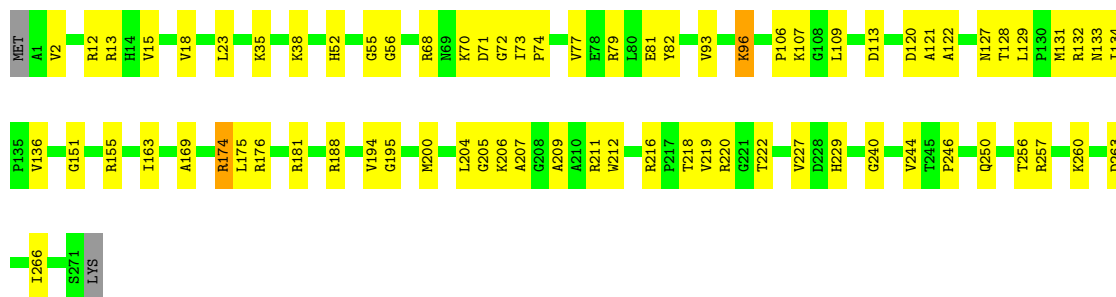
• Molecule 1: 50S ribosomal protein L36

Chain g:  100%

There are no outlier residues recorded for this chain.

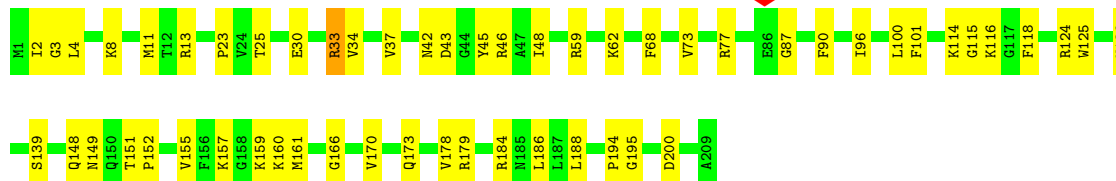
• Molecule 2: 50S ribosomal protein L2

Chain C:  73% 26% ..




• Molecule 3: 50S ribosomal protein L3

Chain D:  74% 26%



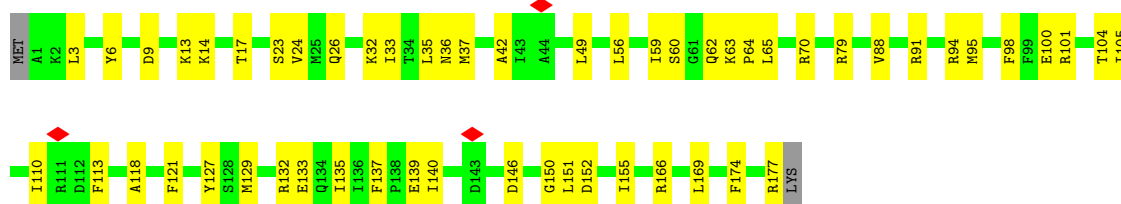
• Molecule 4: 50S ribosomal protein L4

Chain E:  76% 20% .

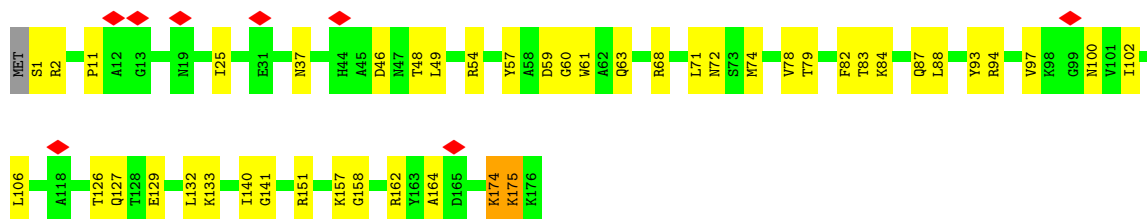
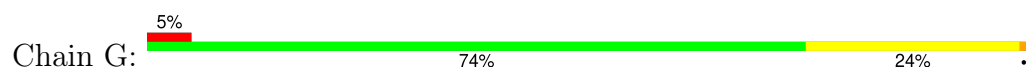




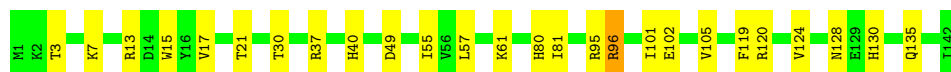
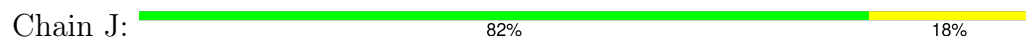
- Molecule 5: 50S ribosomal protein L5



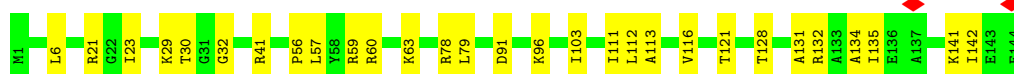
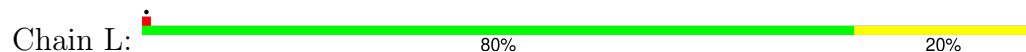
- Molecule 6: 50S ribosomal protein L6



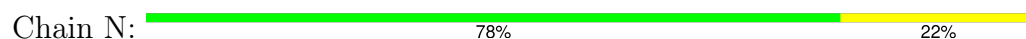
- Molecule 7: 50S ribosomal protein L13



- Molecule 8: 50S ribosomal protein L15



- Molecule 9: 50S ribosomal protein L17

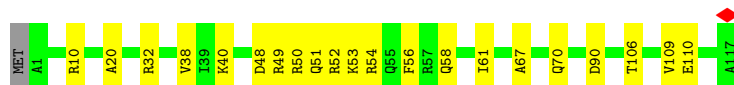
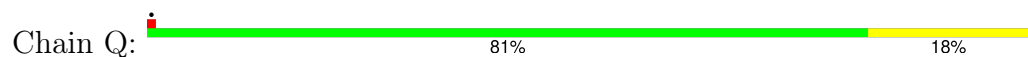


- Molecule 10: 50S ribosomal protein L18

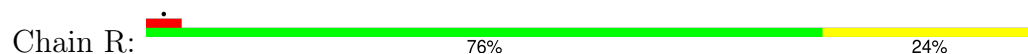




- Molecule 11: 50S ribosomal protein L20



- Molecule 12: 50S ribosomal protein L21



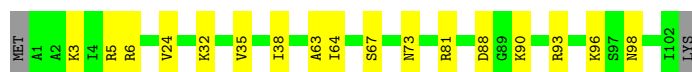
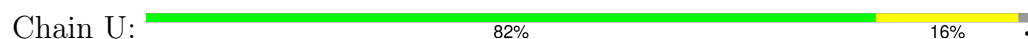
- Molecule 13: 50S ribosomal protein L22



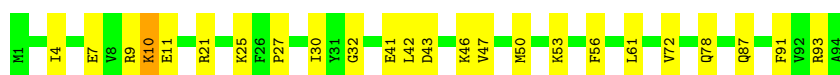
- Molecule 14: 50S ribosomal protein L23



- Molecule 15: 50S ribosomal protein L24



- Molecule 16: 50S ribosomal protein L25



- Molecule 17: 50S ribosomal protein L27

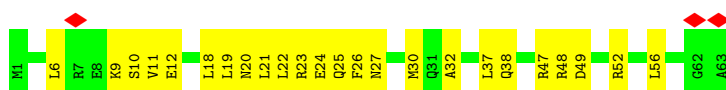




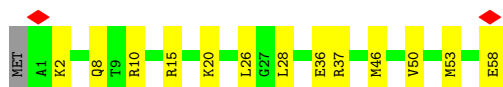
- Molecule 18: 50S ribosomal protein L28



- Molecule 19: 50S ribosomal protein L29



- Molecule 20: 50S ribosomal protein L30



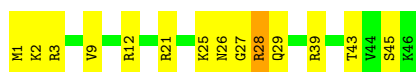
- Molecule 21: 50S ribosomal protein L32



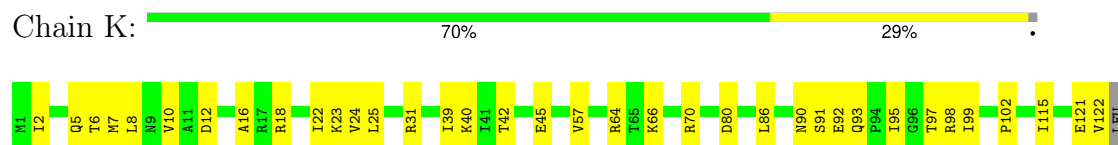
- Molecule 22: 50S ribosomal protein L33



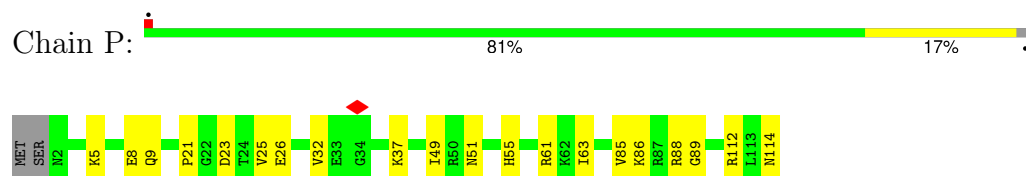
- Molecule 23: 50S ribosomal protein L34



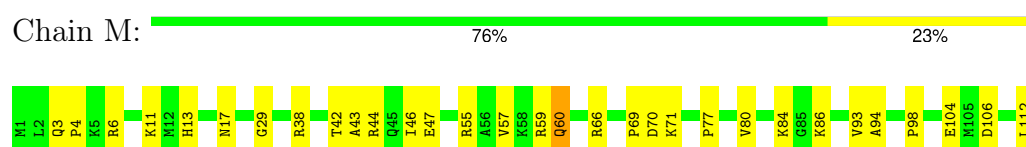
- Molecule 24: 50S ribosomal protein L14



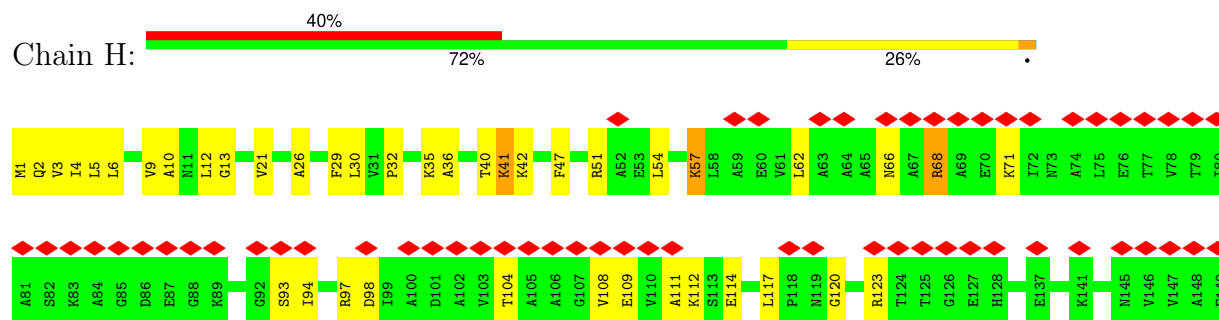
- Molecule 25: 50S ribosomal protein L19



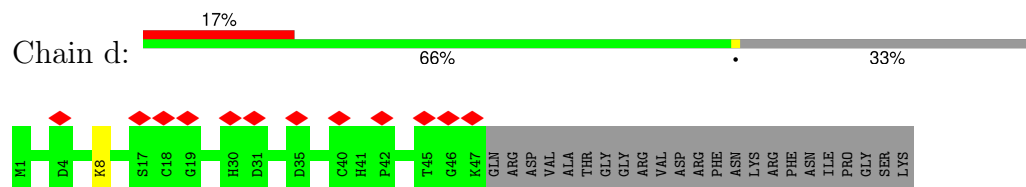
- Molecule 26: 50S ribosomal protein L16



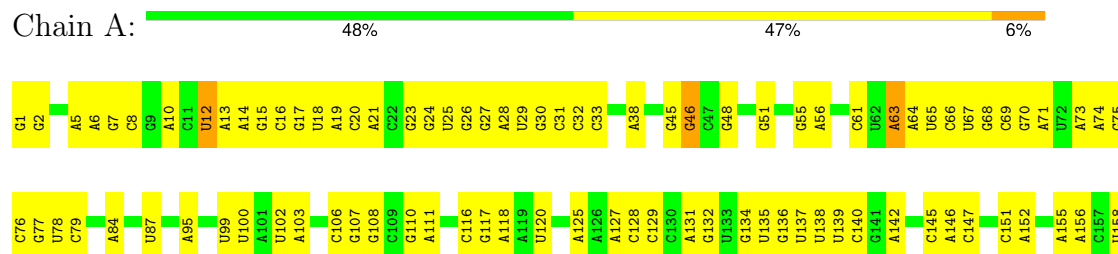
- Molecule 27: 50S ribosomal protein L9



- Molecule 28: 50S ribosomal protein L31

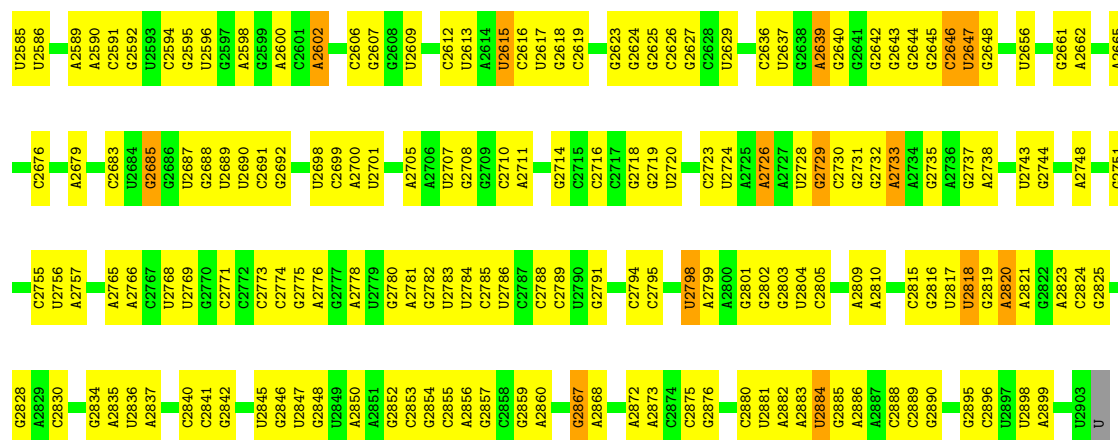


- Molecule 29: 23S ribosomal RNA



G1288	G1291	G1292	G1293	U1294	G1295	G1298	G1299	A1300	A1301	A1302	A1308	G1309	G1310	U1313	C1314	C1315	C1319	C1320	A1321	U1325	U1326	A1327	A1328	U1329	A1336	G1337	G1341	C1345	G1346	A1347	C1351	A1352	A1353	A1354	G1355	G1356	G1357	G1358	G1361	C1362	C1363	G1364	A1365	G1368	U1372										
U1219	G1220	C1221	U1222	U1223	U1224	G1225	A1226	C1229	G1230	U1231	G1232	C1233	U1234	G1235	G1236	A1237	U1238	U1242	C1243	A1244	G1250	G1251	G1252	A1253	A1254	U1255	G1256	C1257	U1258	G1259	C1261	A1262	U1263	A1264	A1265	G1266	U1267	A1268	A1269	C1270	G1271	A1272	A1275	A1276	G1277	C1278	G1279	G1280	G1281	U1282	G1283	A1286	A1287		
C1135	G1136	G1137	G1138	G1139	C1140	U1141	U1142	A1147	C1153	G1154	A1155	A1156	G1157	C1161	G1162	G1163	C1164	A1165	G1166	C1167	G1168	A1169	C1170	G1171	C1172	U1173	U1174	A1175	U1176	C1177	G1178	G1179	U1180	U1188	A1189	G1190	C1196	G1197	U1198	U1199	G1202	U1203	A1204	A1205	G1206	C1207	G1208	G1212	A1213	U1217	G1218				
A1048	A1049	G1056	A1057	U1058	G1059	U1060	U1061	U1066	A1067	G1068	A1069	A1070	G1071	C1072	U1073	G1074	C1079	A1080	U1081	A1084	A1085	A1086	G1087	A1088	A1089	A1098	A1099	U1100	U1101	C1102	A1103	G1104	U1105	G1106	G1107	U1108	C1109	G1110	A1111	G1112	U1113	C1114	G1115	G1116	C1123	G1124	G1125	A1126	U1130	G1131	U1132	A1133	A1134		
U970	G971	A972	A973	G974	A975	G976	G977	G978	A979	C982	A983	C987	A988	G989	G993	C994	C995	A996	G997	A1000	C1005	C1006	C1007	A1008	A1009	U1012	C1013	U1014	U1015	G1016	U1019	G1022	G1026	A1027	A1028	U1033	G1034	U1035	G1038	A1039	A1040	G1041	U1042	G1043	C1044	C1045	A1046	G1047							
G809	U810	U811	C812	U813	C814	C817	G818	A819	A825	U826	U827	U828	A829	G830	C831	U832	A833	C834	C837	C838	U839	A845	U846	U847	C848	A849	U850	C851	U852	G857	G858	G859	U860	G864	U870	C873	G874	A877	A878	G881	G882	G883	U884	C885	A	U	C	C							
A739	C740	U741	A742	U743	A744	U745	U746	U747	G748	A749	A750	A751	A752	C753	U754	C758	G759	A764	U765	U766	U767	G768	U769	G770	G775	G776	G777	G778	U779	G780	A781	A782	U783	G784	G785	C786	C787	A788	A789	A792	A793	C796	G797	G798	G799	A800	U801	A802	G805	C806	U807	G808			
G649	C650	G651	A654	A655	A656	C660	A661	G662	G663	A668	G669	A670	C671	C672	C678	C679	C680	G681	G682	U683	U684	A685	U686	C687	A689	C692	G693	A694	U695	G696	G697	C698	G711	G712	U713	U714	A715	A718	C719	U720	U724	G725	G726	A727	G728	U729	A730	C731	C732	U733	A734				
A574	A575	U576	C577	C578	C579	U580	C581	A582	C583	C584	G585	A586	U589	A590	C591	U592	U593	U594	C595	U596	U597	U598	A599	G600	C601	A603	C611	G612	A613	U614	U615	A621	G625	A626	A627	G628	G629	G630	A631	A632	A633	C634	C635	G636	A637	C638	U639	U640	U641	C645	U646	A647	G648		
U419	C420	A424	A430	U431	A432	A433	U434	C435	C436	U437	C438	A439	G442	U451	A452	A453	A457	U459	A460	G463	U464	C465	A466	G467	G468	A472	C475	U476	A477	A478	A479	A480	G481	A482	C487	G488	A491	A492	G493	A497	G498	C499	C500	A503	U504	A505	U506	A507	A508	U509	U510				
G506	A507	A508	C509	C510	A513	A514	A515	C516	C517	U518	U519	G520	U521	A522	C523	A526	G527	C528	C529	A532	G536	G537	A538	G539	C540	A541	C542	G543	U545	U546	A547	G548	G549	C550	G551	U552	G553	U554	G555	U558	G559	A563	C564	A565	C566	A567	C568	U566	U567	U568	U569	G570	U571	A572	U573
U243	A244	G245	U249	G248	C249	C253	G254	A255	G259	A265	G266	C267	G271	A272	G273	A278	A282	G283	U284	G285	U286	C287	A288	G289	U290	U296	G297	U298	A299	A300	G301	C302	G303	U304	G305	U306	G307	G308	A309	A310	A311	G319	A320	U321	A322	G323	C324	A325	G327	U328	G329				
A330	C331	U339	A340	C341	A342	A345	C346	A347	C351	A352	C353	A354	U355	G356	G359	U360	C364	U365	C366	C367	A368	U369	A371	G372	U373	A374	G377	G386	C389	C394	U395	G396	U397	A401	A402	U403	A404	U405	G408	A411	A412	U413	C414	A415	U416	U417	C418								

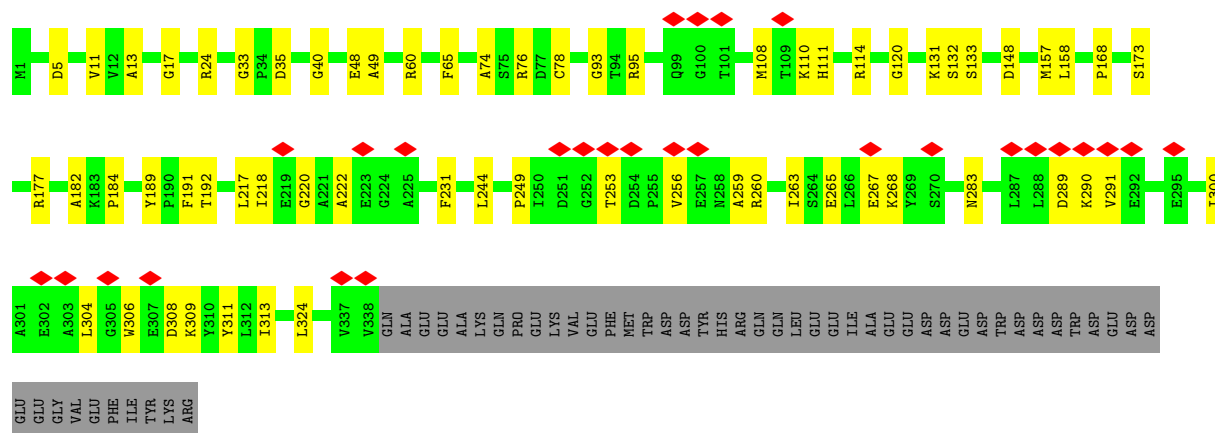
U2506	C2507	G2508	C2512	A2513	U2514	C2515	U2516	U2517	C2518	U2519	C2520	G2521	U2522	G2525	U2526	U2529	A2530	A2531	G2532	U2533	A2534	U2537	G2543	G2544	A2547	U2548	G2549	G2550	U2554	U2555	A2560	U2561	U2562	U2563	A2564	A2565	G2487	G2488	G2567	U2568	G2569	G2570	U2571	A2572	G2576	A2577	G2581	G2582	G2583	U2584					
A2430	A2435	G2436	U2437	U2438	A2439	U2440	U2441	C2442	C2443	G2444	G2445	G2446	G2447	U2448	U2449	A2450	A2451	G2455	U2456	G2457	G2458	U2459	U2460	A2461	G2462	G2463	G2464	C2465	A2468	A2469	G2470	A2471	G2472	U2473	U2474	G2475	A2476	U2477	A2478	G2487	G2488	G2567	U2568	U2491	U2492	U2493	G2494	G2495	G2496	A2497	G2498	G2502	A2503	U2504	G2505
U2343	U2344	G2345	A2346	C2347	C2350	G2357	G2360	G2361	G2362	G2363	G2364	G2365	G2366	G2367	G2368	A2369	G2370	G2371	U2372	G2373	C2374	A2377	U2384	G2385	A2386	G2389	U2390	G2391	C2394	U2402	U2403	U2404	G2405	A2406	A2411	A2412	G2413	G2414	G2415	G2416	C2417	A2418	U2419	C2424	A2425	A2426	G2427	G2428	G2429						
U2257	C2258	U2262	C2263	C2264	U2265	A2266	A2267	G2271	C2283	A2284	C2285	G2286	A2287	A2288	G2289	G2290	U2291	U2292	G2293	A2297	A2298	G2304	U2305	G2308	A2311	U2312	U2313	A2314	G2315	G2316	A2317	U2320	U2321	A2322	G2325	C2326	A2327	G2413	G2414	G2415	G2416	C2417	A2418	U2419	C2424	A2425	A2426	G2427	G2428	G2429					
U2086	G2087	A2088	C2089	A2090	G2093	C2096	U2099	G2100	A2101	G2102	U2109	U2110	U2111	G2112	G2116	A2117	U2118	A2119	G2120	G2121	U2122	A2126	G2127	G2128	C2129	U2130	U2131	A2132	G2133	U2134	C2135	G2136	U2139	G2140	C2145	C2146	A2147	G2148	G2157	A2163	C2164	G2165	U2166	A2170	U2171	U2172	A2173								
U2011	G2012	A2013	U2017	G2018	A2019	C2021	U2022	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032	A2033	U2034	C2035	A2037	G2038	U2039	G2040	C2043	C2047	G2048	A2052	C2055	G2056	G2057	A2058	A2059	A2060	G2061	A2062	C2063	C2064	C2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	U2076	U2081	A2082							
G1910	A1913	C1914	U1915	A1918	A1919	U1923	U1926	A1927	G1930	U1931	U1936	A1937	C1941	U1943	U1944	C1947	G1948	G1954	U1955	U1956	C1962	C1965	C1967	G1968	A1969	U1970	U1971	U1972	A1977	A1987	G1988	U1991	G1992	U1993	C1996	C1997	A1998	C1999	C2000	C2008	A2009														
A1808	A1809	A1810	G1811	U1812	G1813	C1816	U1817	U1818	A1821	G1822	G1823	U1824	U1825	U1826	U1827	G1828	A1829	C1830	G1831	U1834	G1835	C1836	C1837	U1841	G1842	A1847	A1848	G1849	G1850	U1851	U1852	A1858	U1859	G1862	G1869	C1870	A1871	C1874	G1875	U1880	C1881	A1890	C1893	G1907	C1908	C1909									
G1723	G1724	U1725	C1726	G1727	G1728	U1729	G1730	G1731	G1732	G1733	G1734	U1735	U1736	G1737	G1738	A1739	U1742	G1743	A1744	A1745	G1748	A1749	G1750	U1751	G1752	G1753	A1754	G1757	A1762	G1763	C1764	C1771	A1772	A1773	U1779	A1780	G1784	C1788	A1789	G1790	A1791	U1796	G1797	U1798	G1799	C1800	A1801	A1802	G1807						
A1630	G1631	A1634	A1637	G1638	C1639	G1645	G1646	U1647	U1648	G1649	A1650	G1651	G1652	G1653	A1654	A1655	A1664	A1665	G1666	G1667	A1668	A1669	A1674	A1675	G1676	A1677	G1678	G1679	A1680	G1681	G1682	U1688	U1693	G1696	G1699	A1700	C1704	A1705	U1709	G1710	A1711	G1715	U1720	G1721	A1722										
G1543	A1544	A1545	A1548	U1549	C1550	A1551	G1555	G1556	C1557	G1558	U1559	G1560	A1561	U1562	U1563	C1564	A1566	A1569	A1570	A1571	A1572	U1578	C1582	A1583	U1584	C1585	U1589	A1590	C1591	A1592	A1593	U1594	A1597	A1598	G1601	U1602	A1603	A1607	A1608	C1611	A1614	C1615	G1620	U1629											
U1443	G1444	G1445	C1446	C1447	G1452	A1453	U1458	C1461	U1462	C1463	G1464	G1465	A1466	U1467	U1468	A1469	G1475	U1476	A1477	G1482	A1490	C1493	A1494	A1495	A1496	U1497	A1498	G1501	A1502	A1503	A1504	A1515	G1516	G1517	C1518	G1519	U1520	G1521	A1522	U1523	G1524	A1528	U1533	U1534	A1535	U1539	U1540								
G1377	A1378	U1379	G1380	G1381	G1382	A1383	C1386	A1387	G1388	G1389	U1390	U1391	A1392	U1394	A1395	U1396	U1397	C1398	C1399	U1400	G1401	C1404	U1405	U1406	G1407	G1408	U1409	G1410	U1411	U1412	A1413	G1416	C1417	G1418	A1419	A1420	G1424	G1425	C1428	G1429	G1430	A1431	G1432	A1433	A1434	G1435	G1436	G1437	U1438	A1439	U1440	U1441	U1442		



• Molecule 30: 5S ribosomal RNA



• Molecule 31: GTPase ObgE/CgtA



• Molecule 32: 50S ribosomal protein L35



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45746	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.195	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.034	Depositor
Map value standard deviation	0.170	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	417.6, 417.6, 417.6	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.74, 1.74, 1.74	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	g	0.23	0/303	0.44	0/397
2	C	0.23	0/2121	0.43	0/2852
3	D	0.24	0/1586	0.45	0/2134
4	E	0.23	0/1499	0.41	0/2016
5	F	0.24	0/1434	0.44	0/1926
6	G	0.24	0/1343	0.45	0/1816
7	J	0.23	0/1152	0.40	0/1551
8	L	0.25	0/1062	0.48	0/1413
9	N	0.24	0/974	0.42	0/1301
10	O	0.25	0/902	0.47	0/1209
11	Q	0.28	0/960	0.40	0/1278
12	R	0.25	0/829	0.46	0/1107
13	S	0.23	0/864	0.41	0/1156
14	T	0.23	0/744	0.44	0/994
15	U	0.24	0/787	0.46	0/1051
16	V	0.25	0/766	0.48	0/1025
17	W	0.25	0/584	0.42	0/772
18	X	0.22	0/635	0.41	0/848
19	Y	0.26	0/510	0.63	0/677
20	Z	0.23	0/453	0.44	0/605
21	0	0.21	0/450	0.48	0/599
22	1	0.24	0/416	0.44	0/554
23	2	0.22	0/380	0.39	0/498
24	K	0.24	0/947	0.47	0/1268
25	P	0.24	0/923	0.42	0/1234
26	M	0.24	0/1093	0.44	0/1460
27	H	0.24	0/1121	0.47	0/1515
28	d	0.24	0/371	0.48	0/496
29	A	0.16	0/69659	0.73	7/108672 (0.0%)
30	B	0.14	0/2847	0.70	0/4440
31	9	0.24	0/2626	0.45	0/3542
32	3	0.23	0/513	0.47	0/676

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.18	0/100854	0.67	7/151082 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	A	1313	U	C2-N1-C1'	6.94	126.03	117.70
29	A	1893	C	N3-C2-O2	-6.47	117.37	121.90
29	A	1313	U	N1-C2-O2	5.97	126.98	122.80
29	A	1313	U	N3-C2-O2	-5.66	118.24	122.20
29	A	1893	C	N1-C2-O2	5.39	122.13	118.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	g	302	0	340	0	0
2	C	2082	0	2157	58	0
3	D	1565	0	1616	40	0
4	E	1483	0	1548	25	0
5	F	1410	0	1447	39	0
6	G	1323	0	1374	28	0
7	J	1129	0	1162	19	0
8	L	1053	0	1129	24	0
9	N	961	0	1000	20	0
10	O	892	0	923	22	0
11	Q	947	0	1022	17	0
12	R	816	0	839	18	0
13	S	857	0	922	22	0
14	T	738	0	807	23	0
15	U	779	0	834	14	0
16	V	753	0	780	19	0
17	W	577	0	594	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	X	625	0	655	15	0
19	Y	509	0	543	20	0
20	Z	449	0	491	9	0
21	0	444	0	461	12	0
22	1	409	0	440	12	0
23	2	377	0	418	11	0
24	K	938	0	1012	24	0
25	P	911	0	957	13	0
26	M	1074	0	1157	20	0
27	H	1110	0	1148	30	0
28	d	364	0	364	0	0
29	A	62195	0	31280	1102	0
30	B	2548	0	1292	55	0
31	9	2582	0	2606	40	0
32	3	504	0	574	14	0
33	d	1	0	0	0	0
33	g	1	0	0	0	0
34	9	1	0	0	0	0
34	A	1	0	0	0	0
35	9	32	0	13	2	0
36	A	20	0	0	0	0
36	B	1	0	0	0	0
36	C	1	0	0	0	0
36	F	1	0	0	0	0
36	N	3	0	0	0	0
36	S	1	0	0	0	0
All	All	92769	0	61905	1601	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 11.

The worst 5 of 1601 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)
29:A:1433:A:N6	29:A:1560:G:H1	1.63	0.96
29:A:408:G:H1	29:A:419:U:H3	1.08	0.95
29:A:2102:G:H1	29:A:2187:U:H3	1.17	0.92
29:A:2475:C:H42	29:A:2529:G:H22	1.13	0.91
29:A:377:G:H1	29:A:397:U:H3	0.93	0.90

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	g	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
2	C	269/273 (98%)	258 (96%)	11 (4%)	0	100	100
3	D	207/209 (99%)	195 (94%)	12 (6%)	0	100	100
4	E	189/201 (94%)	180 (95%)	9 (5%)	0	100	100
5	F	175/179 (98%)	163 (93%)	12 (7%)	0	100	100
6	G	174/177 (98%)	165 (95%)	9 (5%)	0	100	100
7	J	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
8	L	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
9	N	118/120 (98%)	112 (95%)	6 (5%)	0	100	100
10	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
11	Q	115/118 (98%)	111 (96%)	4 (4%)	0	100	100
12	R	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
13	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
14	T	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
15	U	100/104 (96%)	91 (91%)	9 (9%)	0	100	100
16	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
17	W	74/85 (87%)	71 (96%)	3 (4%)	0	100	100
18	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
19	Y	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
20	Z	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
21	0	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
22	1	48/55 (87%)	48 (100%)	0	0	100	100
23	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
24	K	120/123 (98%)	114 (95%)	6 (5%)	0	100	100
25	P	111/115 (96%)	108 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	M	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
27	H	147/149 (99%)	131 (89%)	16 (11%)	0	100	100
28	d	45/70 (64%)	44 (98%)	1 (2%)	0	100	100
31	9	336/390 (86%)	321 (96%)	15 (4%)	0	100	100
32	3	62/65 (95%)	59 (95%)	1 (2%)	2 (3%)	3	26
All	All	3538/3720 (95%)	3370 (95%)	166 (5%)	2 (0%)	50	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
32	3	31	ILE
32	3	32	LEU

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	g	34/34 (100%)	34 (100%)	0	100	100
2	C	216/218 (99%)	214 (99%)	2 (1%)	75	83
3	D	164/164 (100%)	163 (99%)	1 (1%)	84	88
4	E	159/165 (96%)	159 (100%)	0	100	100
5	F	148/150 (99%)	147 (99%)	1 (1%)	81	86
6	G	137/138 (99%)	133 (97%)	4 (3%)	37	58
7	J	116/116 (100%)	114 (98%)	2 (2%)	56	72
8	L	103/103 (100%)	103 (100%)	0	100	100
9	N	100/100 (100%)	100 (100%)	0	100	100
10	O	86/87 (99%)	86 (100%)	0	100	100
11	Q	89/90 (99%)	89 (100%)	0	100	100
12	R	84/84 (100%)	84 (100%)	0	100	100
13	S	93/93 (100%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	T	80/84 (95%)	80 (100%)	0	100	100
15	U	83/85 (98%)	83 (100%)	0	100	100
16	V	78/78 (100%)	77 (99%)	1 (1%)	65	77
17	W	57/63 (90%)	57 (100%)	0	100	100
18	X	67/68 (98%)	67 (100%)	0	100	100
19	Y	55/55 (100%)	54 (98%)	1 (2%)	54	71
20	Z	48/49 (98%)	48 (100%)	0	100	100
21	0	47/48 (98%)	47 (100%)	0	100	100
22	1	45/49 (92%)	44 (98%)	1 (2%)	47	65
23	2	38/38 (100%)	37 (97%)	1 (3%)	41	61
24	K	103/104 (99%)	103 (100%)	0	100	100
25	P	98/100 (98%)	98 (100%)	0	100	100
26	M	109/109 (100%)	108 (99%)	1 (1%)	75	83
27	H	114/114 (100%)	110 (96%)	4 (4%)	31	53
28	d	43/62 (69%)	42 (98%)	1 (2%)	45	64
31	9	273/321 (85%)	271 (99%)	2 (1%)	81	86
32	3	51/52 (98%)	51 (100%)	0	100	100
All	All	2918/3021 (97%)	2896 (99%)	22 (1%)	77	84

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	M	60	GLN
27	H	57	LYS
27	H	42	LYS
27	H	68	ARG
6	G	174	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	g	37	GLN
5	F	126	ASN
15	U	73	ASN
16	V	87	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	A	2895/2904 (99%)	390 (13%)	9 (0%)
30	B	118/119 (99%)	9 (7%)	0
All	All	3013/3023 (99%)	399 (13%)	9 (0%)

5 of 399 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
29	A	10	A
29	A	12	U
29	A	14	A
29	A	27	G
29	A	46	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
29	A	2505	G
29	A	2756	U
29	A	1328	A
29	A	1378	A
29	A	2127	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 5 ligands modelled in this entry, 4 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	$\# Z > 2$
35	GNP	9	402	34	29,34,34	1.66	7 (24%)	33,54,54	2.18	4 (12%)

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
35	GNP	9	402	34	-	2/14/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	9	402	GNP	PB-O3A	4.59	1.64	1.59
35	9	402	GNP	PB-O1B	3.25	1.51	1.46
35	9	402	GNP	C6-N1	3.21	1.38	1.33
35	9	402	GNP	PG-N3B	3.04	1.71	1.63
35	9	402	GNP	PG-O1G	2.84	1.50	1.46

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	9	402	GNP	C5-C6-N1	-8.61	111.91	123.42
35	9	402	GNP	C2-N1-C6	6.63	125.18	115.96
35	9	402	GNP	N3-C2-N1	-2.84	123.60	127.21
35	9	402	GNP	C2-N3-C4	-2.47	112.82	115.48

There are no chirality outliers.

All (2) torsion outliers are listed below:

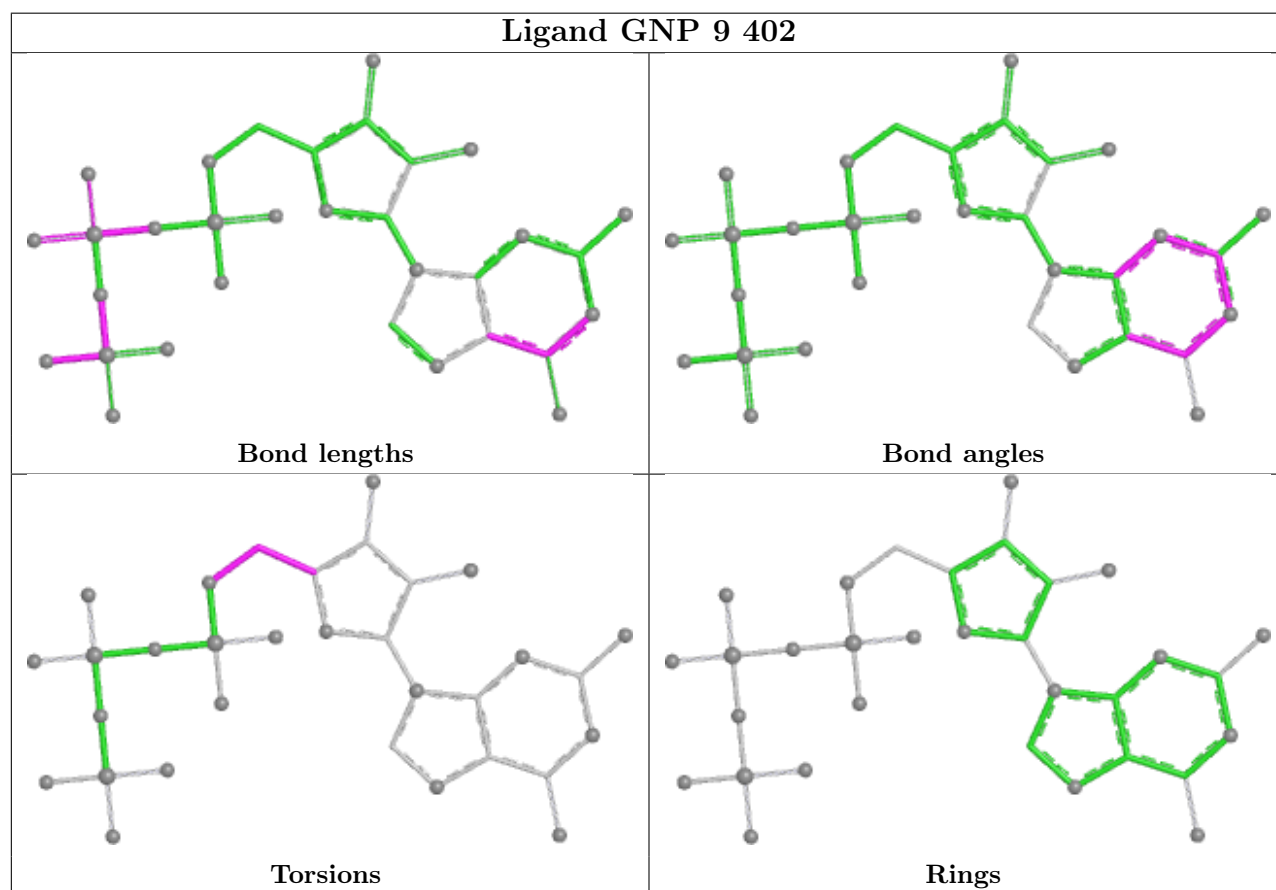
Mol	Chain	Res	Type	Atoms
35	9	402	GNP	C4'-C5'-O5'-PA
35	9	402	GNP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
35	9	402	GNP	2	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 ⓘ

There are no chain breaks in this entry.

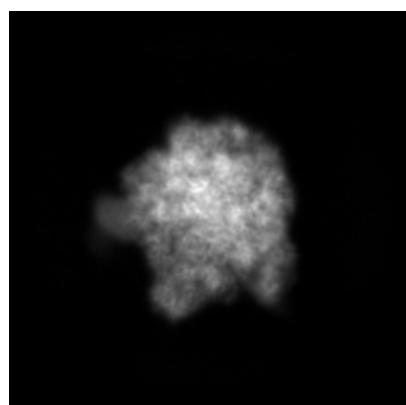
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12219. These allow visual inspection of the internal detail of the map and identification of artifacts.

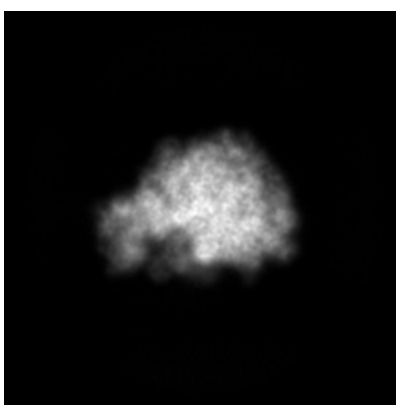
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

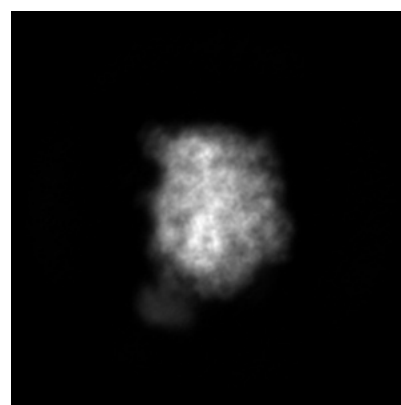
6.1.1 Primary map



X



Y

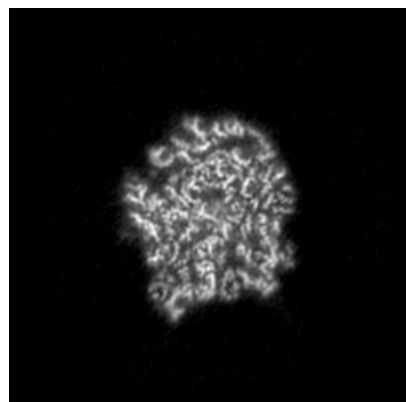


Z

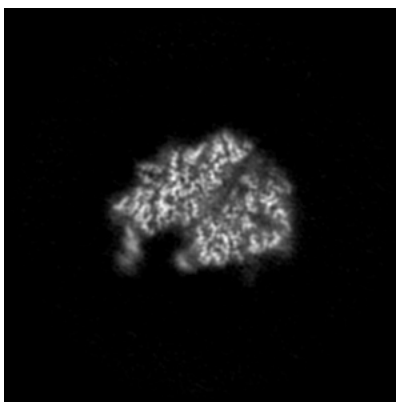
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

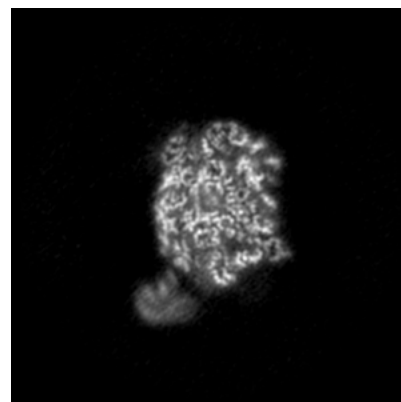
6.2.1 Primary map



X Index: 120



Y Index: 120

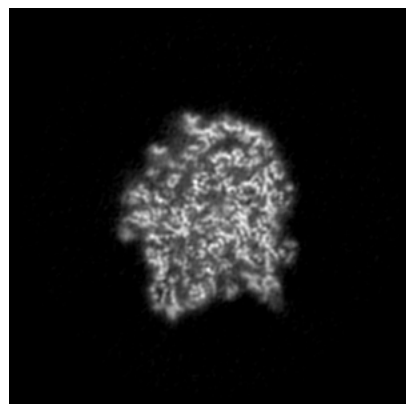


Z Index: 120

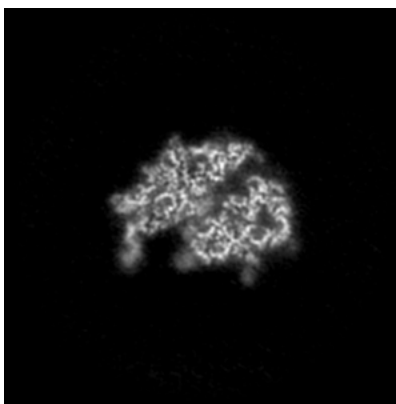
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

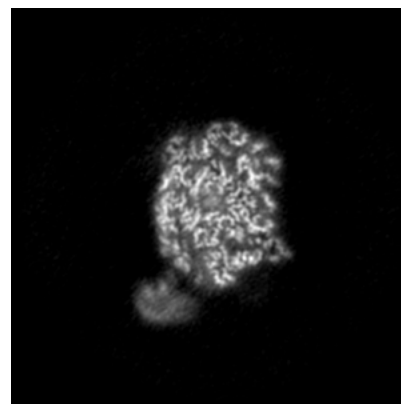
6.3.1 Primary map



X Index: 117



Y Index: 123

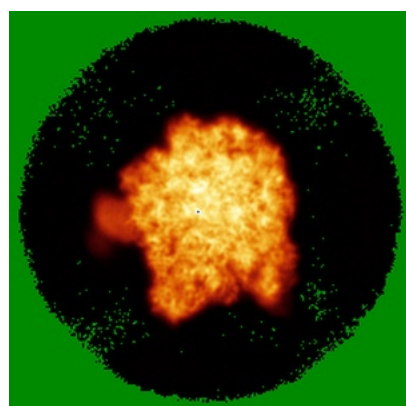


Z Index: 119

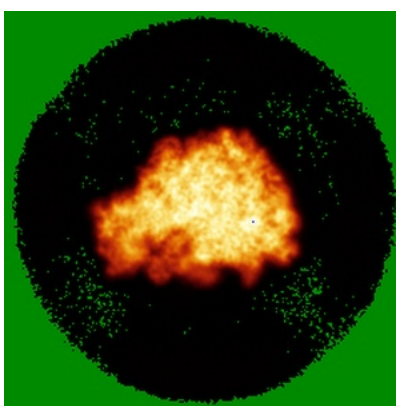
The images above show the largest variance slices of the map in three orthogonal directions.

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

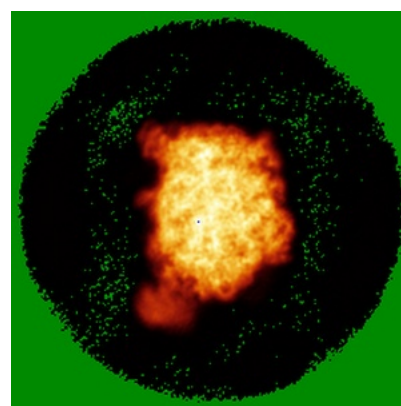
6.4.1 Primary map



X



Y

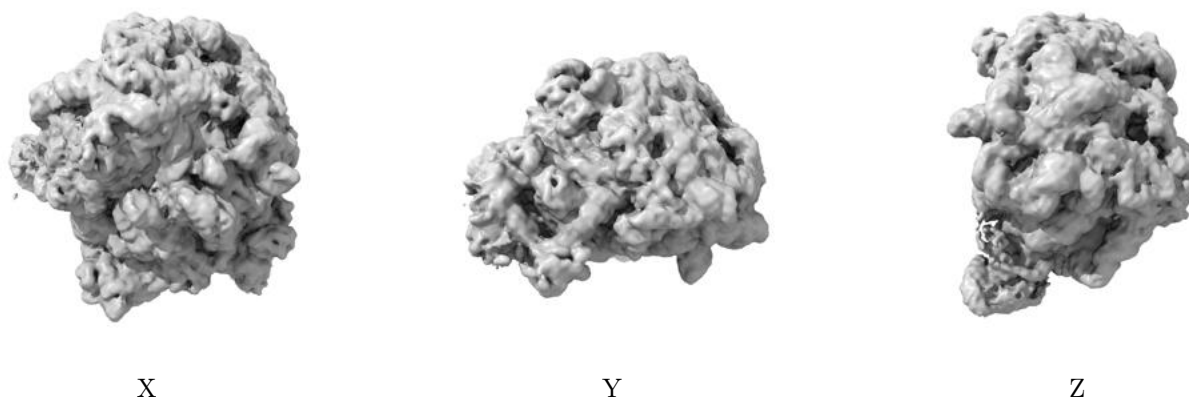


Z

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

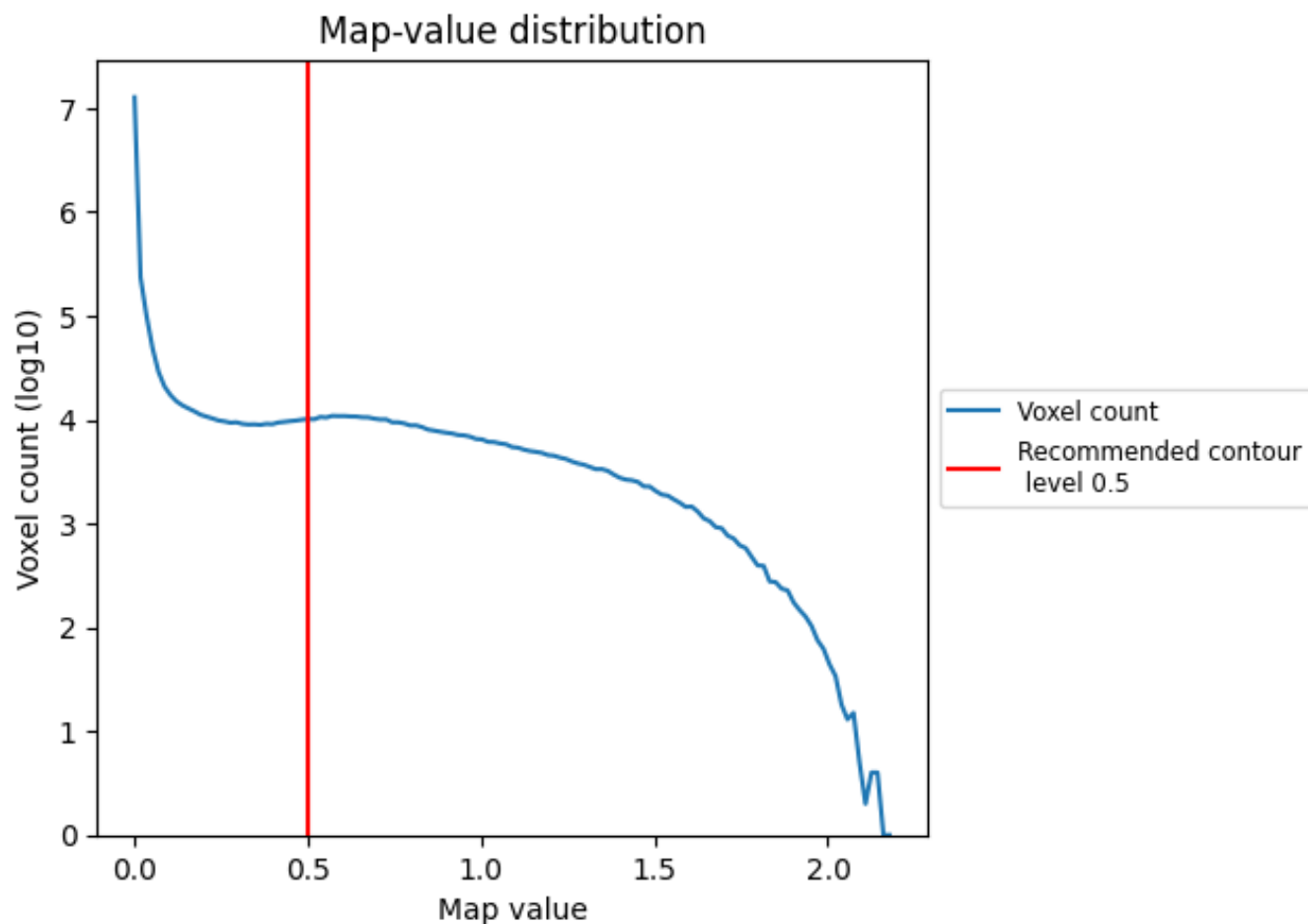
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

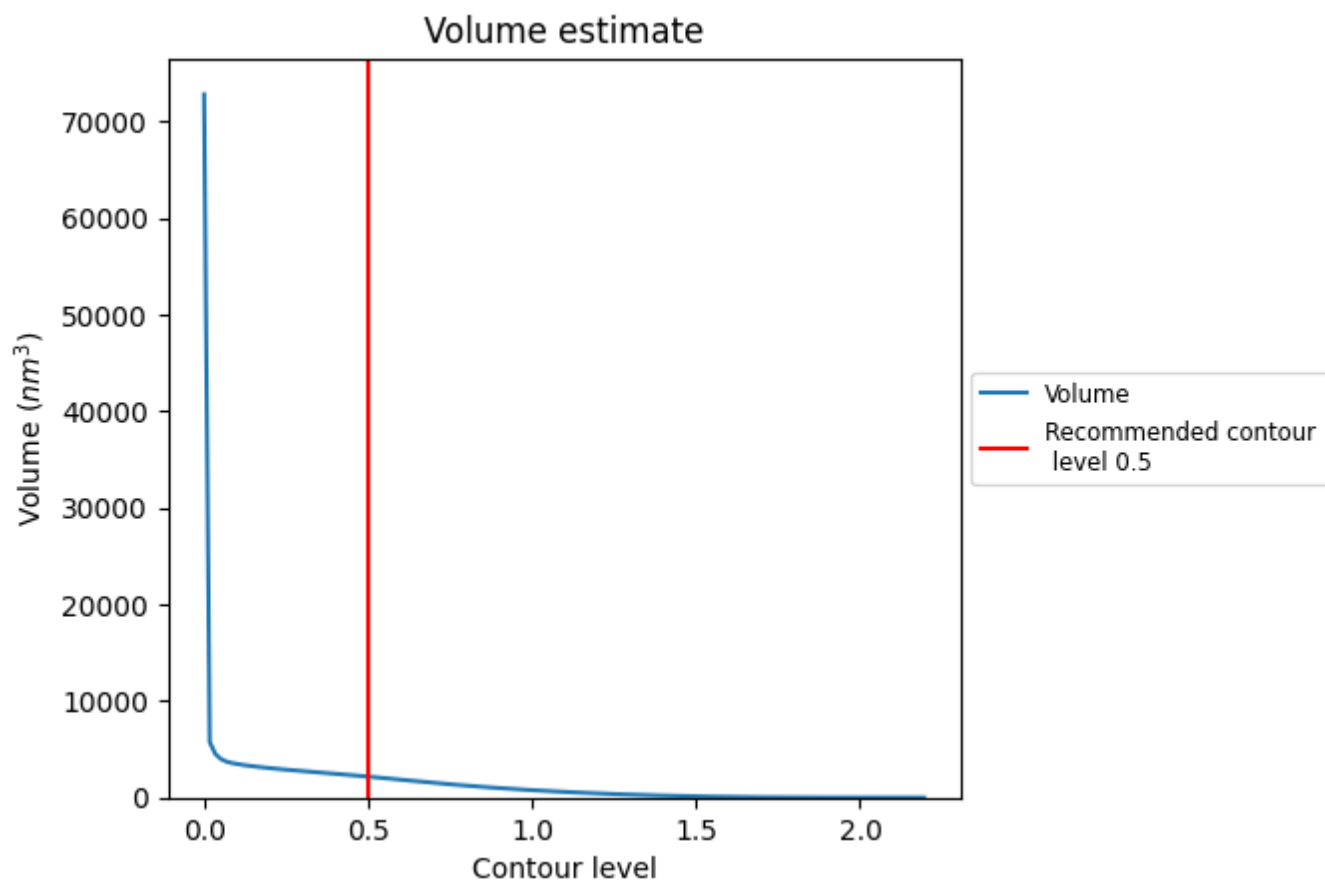
This section contains the results of statistical analysis of the map.

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.

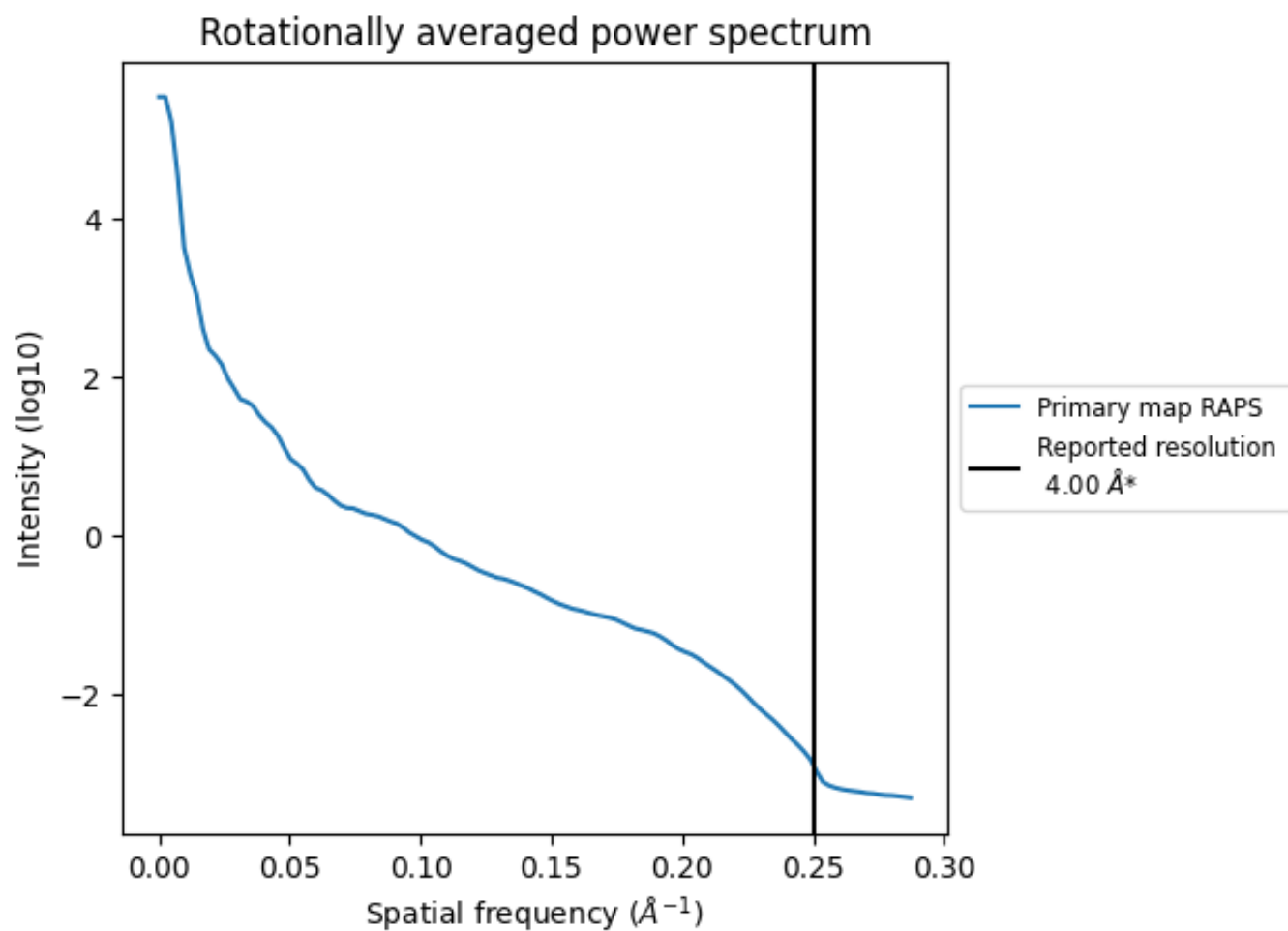
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2171 nm³; this corresponds to an approximate mass of 1962 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 ⓘ

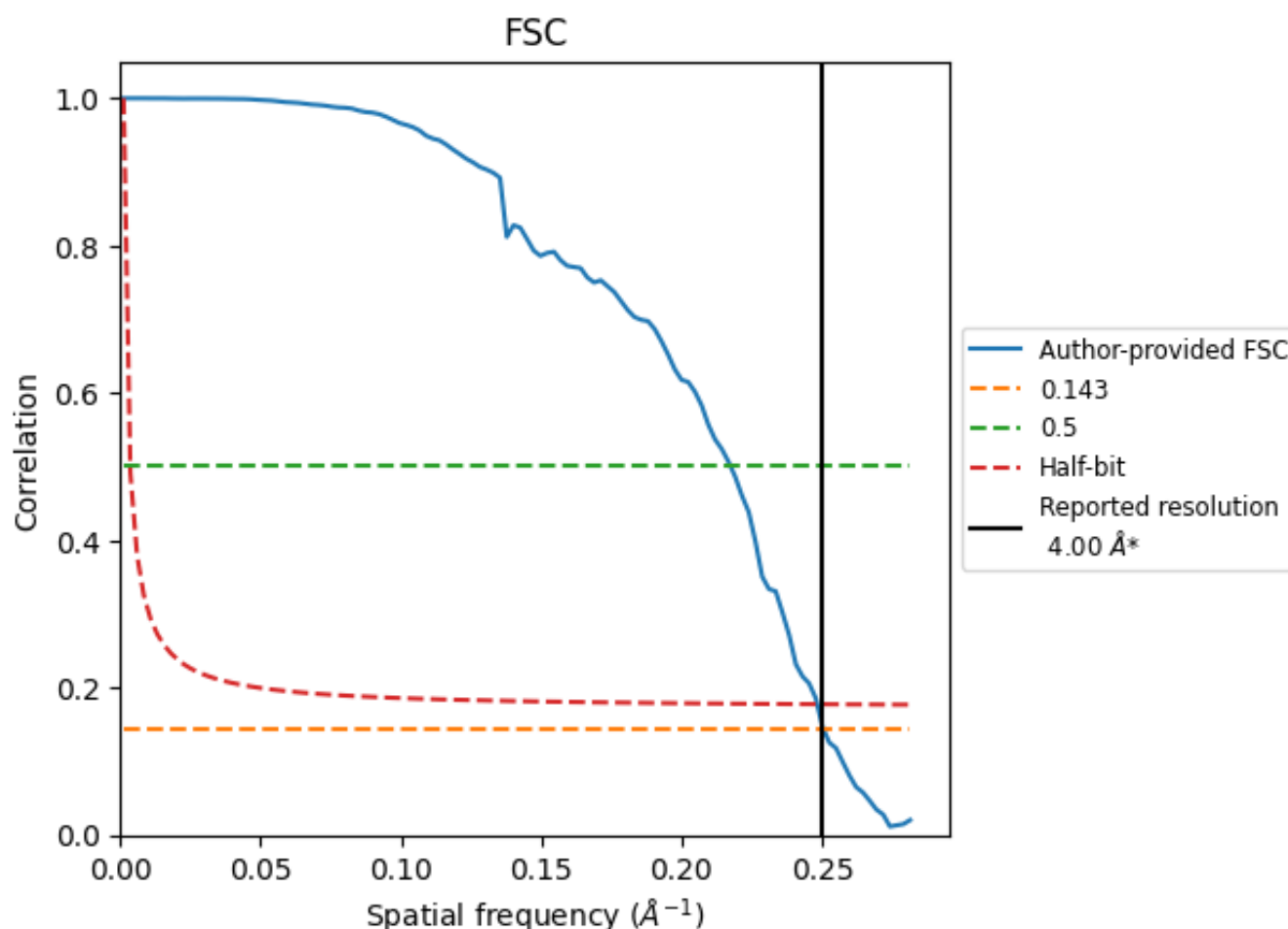


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

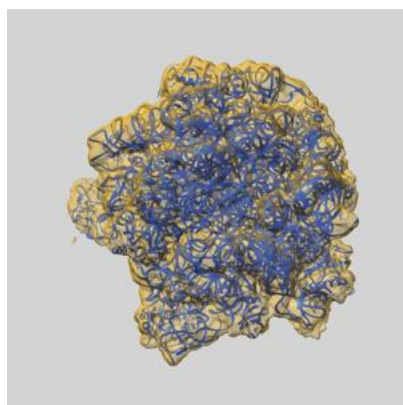
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	3.99	4.60	4.03
Unmasked-calculated*	-	-	-

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

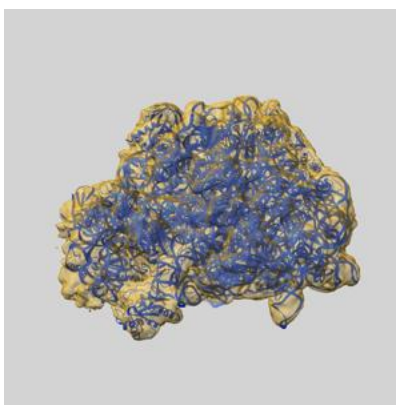
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12219 and PDB model 7BL6. Per-residue inclusion information can be found in section [3](#) on page [10](#).

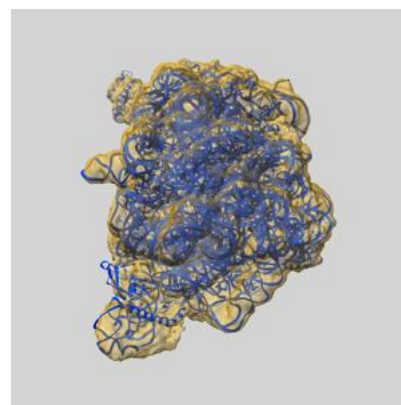
9.1 Map-model overlay [i](#)



X



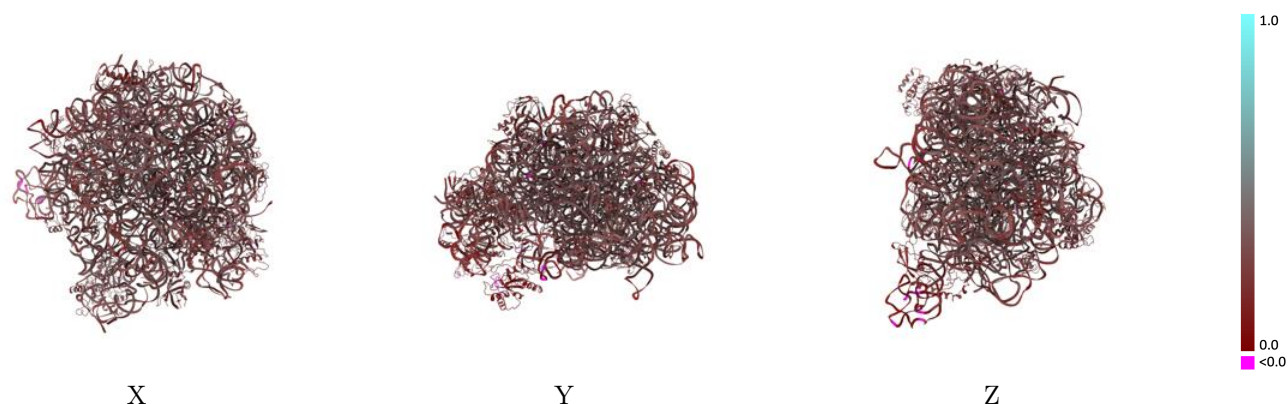
Y



Z

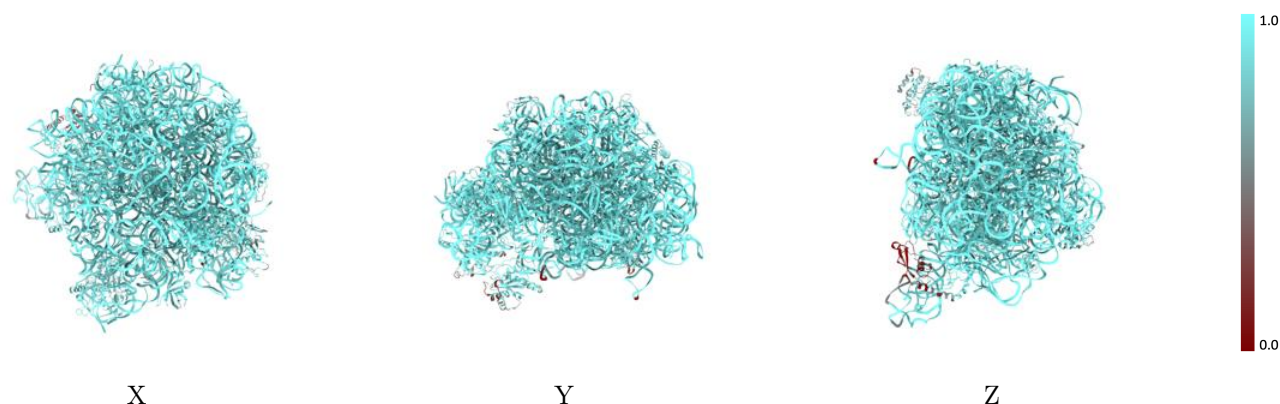
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



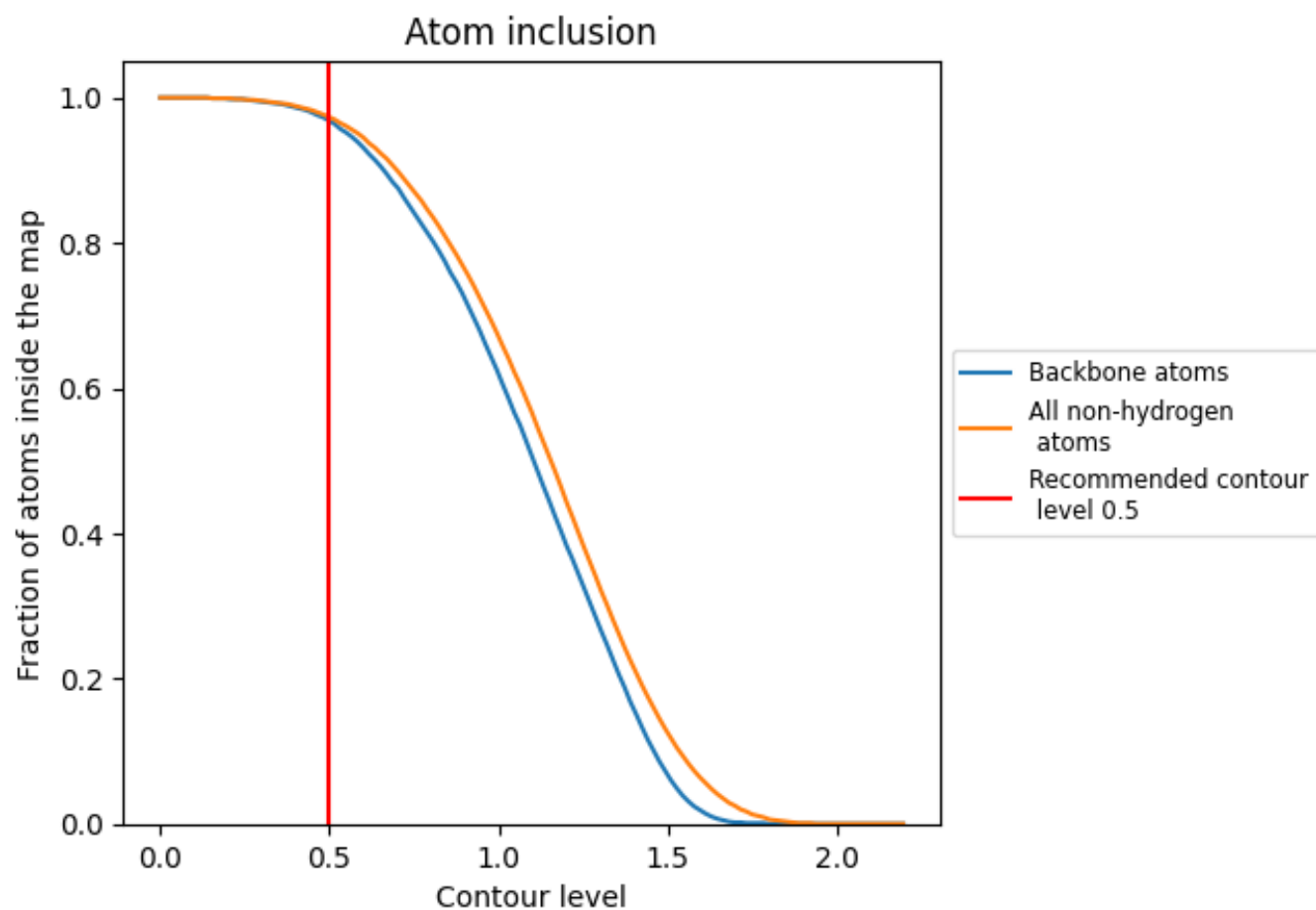
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).



































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 97% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9730	 0.2890
0	 0.9810	 0.2670
1	 0.9950	 0.2680
2	 0.9970	 0.2870
3	 1.0000	 0.2860
9	 0.8530	 0.1990
A	 0.9900	 0.3010
B	 0.9970	 0.2850
C	 0.9910	 0.3020
D	 0.9700	 0.3000
E	 0.9160	 0.2710
F	 0.8990	 0.2090
G	 0.9000	 0.2490
H	 0.5700	 0.2020
J	 0.9850	 0.2910
K	 0.9770	 0.2810
L	 0.9560	 0.2820
M	 0.9810	 0.2930
N	 0.9920	 0.2700
O	 0.9710	 0.2530
P	 0.9600	 0.2810
Q	 0.9850	 0.2690
R	 0.9270	 0.2820
S	 0.9820	 0.2780
T	 0.9830	 0.2920
U	 0.9620	 0.2600
V	 0.9510	 0.2710
W	 0.9930	 0.2860
X	 0.9900	 0.2870
Y	 0.9500	 0.2140
Z	 0.9410	 0.2580
d	 0.6740	 0.1790
g	 0.9930	 0.2860

