



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:31 AM UTC

PDB ID : 8PVL / pdb_00008pvl
EMDB ID : EMD-17970
Title : Chaetomium thermophilum pre-60S State 7 - pre-5S rotation lacking
Utp30/ITS2 - composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.19 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:

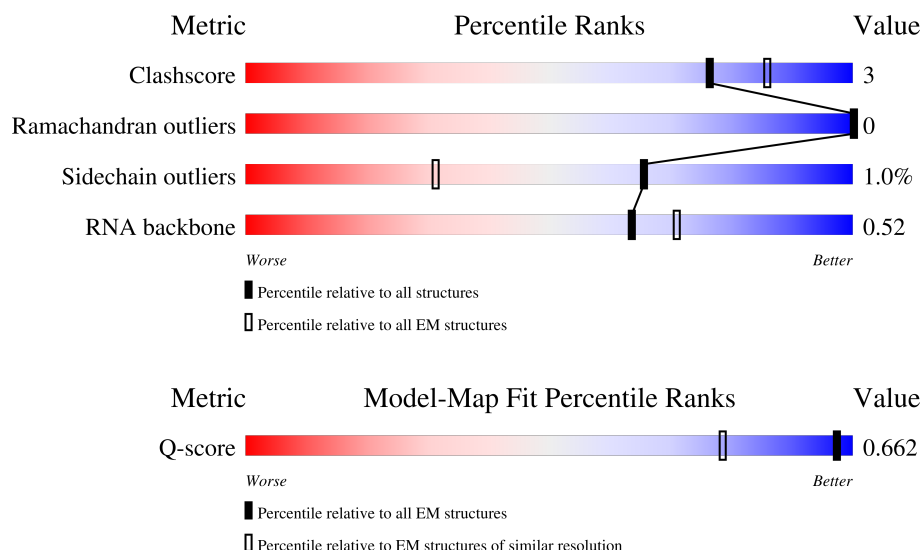
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 2.19 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.











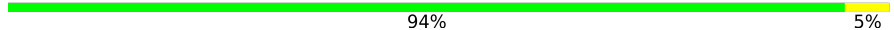


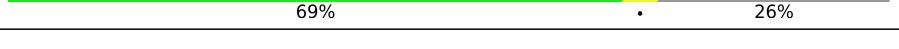


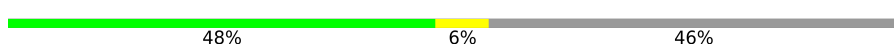





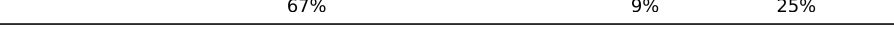
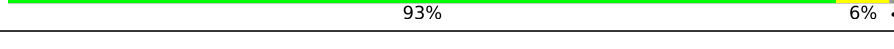
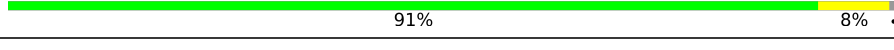
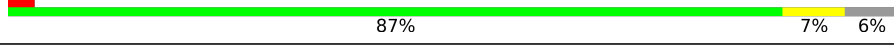
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2745 (1.70 - 2.69)

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	C1	3342	
2	C2	156	
3	C3	162	

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Mol	Chain	Length	Quality of chain
4	C4	119	
5	CF	270	
6	CH	661	
7	CI	414	
8	CJ	679	
9	CK	261	
10	CL	558	
11	CM	249	
11	LF	249	
12	CN	246	
13	CO	120	
14	CQ	225	
15	Cb	117	
16	Cd	627	
17	Ce	443	
18	Cf	350	
19	Cg	202	
20	Ch	517	
21	Cz	123	
22	LA	254	
23	LB	392	
24	LC	365	
25	LD	304	
26	LE	200	
27	LG	262	






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Mol	Chain	Length	Quality of chain
28	LH	229	
29	LJ	173	
30	LK	165	
31	LL	213	
32	LM	142	
33	LN	203	
34	LO	204	
35	LP	187	
36	LQ	213	
37	LR	2898	
38	LS	174	
39	LT	160	
40	LU	127	
41	LV	139	
42	LX	156	
43	LY	138	
44	LZ	135	
45	La	149	
46	Lc	108	
47	Ld	120	
48	Le	131	
49	Lf	109	
50	Lg	119	
51	Lh	935	
52	Li	110	

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Mol	Chain	Length	Quality of chain
53	Lj	95	
54	Lk	94	
55	Ll	51	
56	Lp	92	
57	Lq	147	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	OMC	C1	1420	X	-	-	-
1	OMG	C1	1433	X	-	-	-
1	OMC	C1	1491	X	-	-	-
1	OMC	C1	1812	X	-	-	-
1	OMC	C1	1836	X	-	-	-
1	OMC	C1	2300	X	-	-	-
1	OMG	C1	2358	X	-	-	-
1	OMG	C1	2578	X	-	-	-
1	OMG	C1	2774	X	-	-	-
1	OMC	C1	2838	X	-	-	-
1	OMG	C1	2876	X	-	-	-
1	OMG	C1	2881	X	-	-	-
1	OMC	C1	2918	X	-	-	-
1	OMG	C1	385	X	-	-	-
1	OMG	C1	627	X	-	-	-
1	OMG	C1	646	X	-	-	-
1	OMC	C1	778	X	-	-	-
1	OMG	C1	787	X	-	-	-

2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 152760 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 26S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3078	Total	C	N	O	P	0	0
			65888	29429	11926	21455	3078		

- Molecule 2 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	156	Total	C	N	O	P	0	0
			3319	1484	589	1090	156		

- Molecule 3 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	3	Total	C	N	O	P	0	0
			60	27	7	23	3		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C4	119	Total	C	N	O	P	0	0
			2536	1131	453	833	119		

- Molecule 5 is a protein called Large ribosomal subunit protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CF	245	Total	C	N	O	S	0	0
			1934	1215	350	360	9		

- Molecule 6 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CH	627	Total	C	N	O	S	0	0
			5063	3181	924	939	19		

- Molecule 7 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	91	Total	C	N	O	S	0	0
			720	467	130	120	3		

- Molecule 8 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CJ	382	Total	C	N	O	S	0	0
			3116	2008	548	550	10		

- Molecule 9 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CK	237	Total	C	N	O	S	0	0
			1903	1198	368	333	4		

- Molecule 10 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CL	79	Total	C	N	O	S	0	0
			622	389	125	108			

- Molecule 11 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CM	216	Total	C	N	O	S	0	0
			1769	1142	328	296	3		
11	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 12 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CN	246	Total	C	N	O	S	0	0
			1853	1156	322	368	7		

- Molecule 13 is a protein called DUF2423 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	CO	62	Total	C	N	O	S	0	0
			468	290	94	82	2		

- Molecule 14 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CQ	183	Total	C	N	O	S	0	0
			1480	925	304	241	10		

- Molecule 15 is a protein called Zinc finger domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Cb	101	Total	C	N	O	S	0	0
			830	517	161	148	4		

- Molecule 16 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Cd	462	Total	C	N	O	S	0	0
			3691	2350	671	659	11		

- Molecule 17 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Ce	239	Total	C	N	O	S	0	0
			1977	1231	378	364	4		

- Molecule 18 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Cf	285	Total	C	N	O	S	0	0
			2282	1443	417	401	21		

- Molecule 19 is a protein called Ribosome biogenesis regulatory protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cg	188	Total	C	N	O	S	0	0
			1478	924	283	270	1		

- Molecule 20 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Ch	485	Total	C	N	O	S	1	0
			3812	2396	696	710	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ch	117	ASP	GLU	engineered mutation	UNP G0SC29

- Molecule 21 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Cz	101	Total	C	N	O	S	0	0
			869	541	180	144	4		

- Molecule 22 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LA	191	Total	C	N	O	S	0	0
			1454	917	278	256	3		

- Molecule 23 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LB	389	Total	C	N	O	S	0	0
			3104	1973	579	539	13		

- Molecule 24 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LC	363	Total	C	N	O	S	0	0
			2751	1737	527	478	9		

- Molecule 25 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LD	286	Total	C	N	O	S	0	0
			2266	1434	407	422	3		

- Molecule 26 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LE	191	Total	C	N	O	S	0	0
			1477	944	267	263	3		

- Molecule 27 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LG	235	Total	C	N	O	S	0	0
			1889	1210	350	324	5		

- Molecule 28 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LH	190	Total	C	N	O	S	0	0
			1495	949	268	272	6		

- Molecule 29 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LJ	169	Total	C	N	O	S	0	0
			1357	850	266	235	6		

- Molecule 30 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LK	158	Total	C	N	O	S	0	0
			1184	743	215	224	2		

- Molecule 31 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LL	203	Total	C	N	O	S	0	0
			1587	989	325	271	2		

- Molecule 32 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LM	141	Total	C	N	O	S	0	0
			1126	714	216	195	1		

- Molecule 33 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LN	202	Total	C	N	O	S	0	0
			1704	1062	360	278	4		

- Molecule 34 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LO	203	Total	C	N	O	S	0	0
			1611	1034	305	267	5		

- Molecule 35 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LP	171	Total	C	N	O	S	0	0
			1343	834	274	232	3		

- Molecule 36 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LQ	150	Total	C	N	O	S	0	0
			1200	759	239	200	2		

- Molecule 37 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LR	155	Total	C	N	O	S	0	0
			1241	772	262	203	4		

- Molecule 38 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LS	174	Total	C	N	O	S	0	0
			1426	917	266	238	5		

- Molecule 39 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LT	129	Total	C	N	O	S	0	0
			1027	651	195	179	2		

- Molecule 40 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LU	105	Total	C	N	O	S	0	0
			846	548	146	151	1		

- Molecule 41 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LV	135	Total	C	N	O	S	0	0
			991	630	184	170	7		

- Molecule 42 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LX	145	Total	C	N	O	S	0	0
			1133	723	211	199			

- Molecule 43 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	LY	133	Total	C	N	O	S	0	0
			1056	658	213	183	2		

- Molecule 44 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LZ	135	Total	C	N	O	S	0	0
			1112	713	207	188	4		

- Molecule 45 is a protein called 60S ribosomal protein L28-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	La	108	Total	C	N	O	S	0	0
			872	556	168	147	1		

- Molecule 46 is a protein called 60S ribosomal protein l30-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lc	95	Total	C	N	O	S	0	0
			705	449	122	129	5		

- Molecule 47 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Ld	110	Total	C	N	O	S	0	0
			875	555	171	148	1		

- Molecule 48 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Le	126	Total	C	N	O	S	0	0
			1017	640	208	163	6		

- Molecule 49 is a protein called 60S ribosomal protein l33-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lf	108	Total	C	N	O	S	0	0
			862	546	171	144	1		

- Molecule 50 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lg	118	Total	C	N	O	S	0	0
			914	567	186	157	4		

- Molecule 51 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lh	122	Total	C	N	O		0	0
			1003	637	198	168			

- Molecule 52 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Li	101	Total	C	N	O	S	0	0
			827	509	181	136	1		

- Molecule 53 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Lj	88	Total	C	N	O	S	0	0
			698	427	154	112	5		

- Molecule 54 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Lk	76	Total	C	N	O	S	0	0
			632	400	121	109	2		

- Molecule 55 is a protein called Ribosomal protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	Ll	50	Total	C	N	O	0	0
			436	275	97	64		

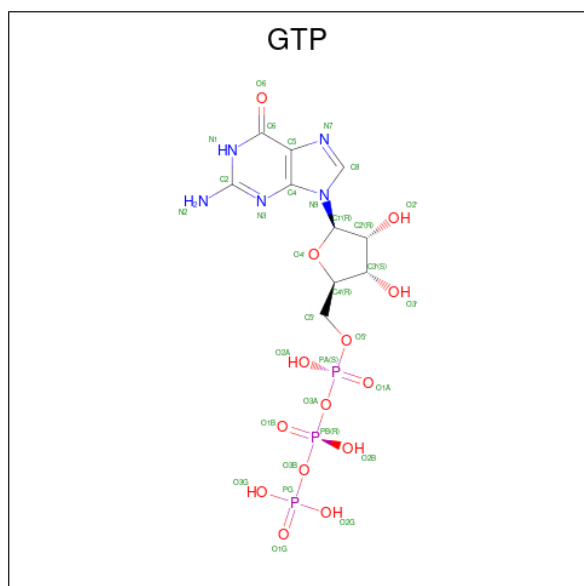
- Molecule 56 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Lp	91	Total	C	N	O	S	0	0
			698	430	138	124	6		

- Molecule 57 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Lq	139	Total	C	N	O	0	0
			1073	672	213	188		

- Molecule 58 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
58	CH	1	Total	C	N	O	P	0
			32	10	5	14	3	
58	Cd	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	CH	1	Total 1	Mg 1	0
59	Cd	2	Total 2	Mg 2	0

- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	CQ	1	Total 1	Zn 1	0
60	Cb	1	Total 1	Zn 1	0
60	Lg	1	Total 1	Zn 1	0
60	Lj	1	Total 1	Zn 1	0
60	Lp	1	Total 1	Zn 1	0

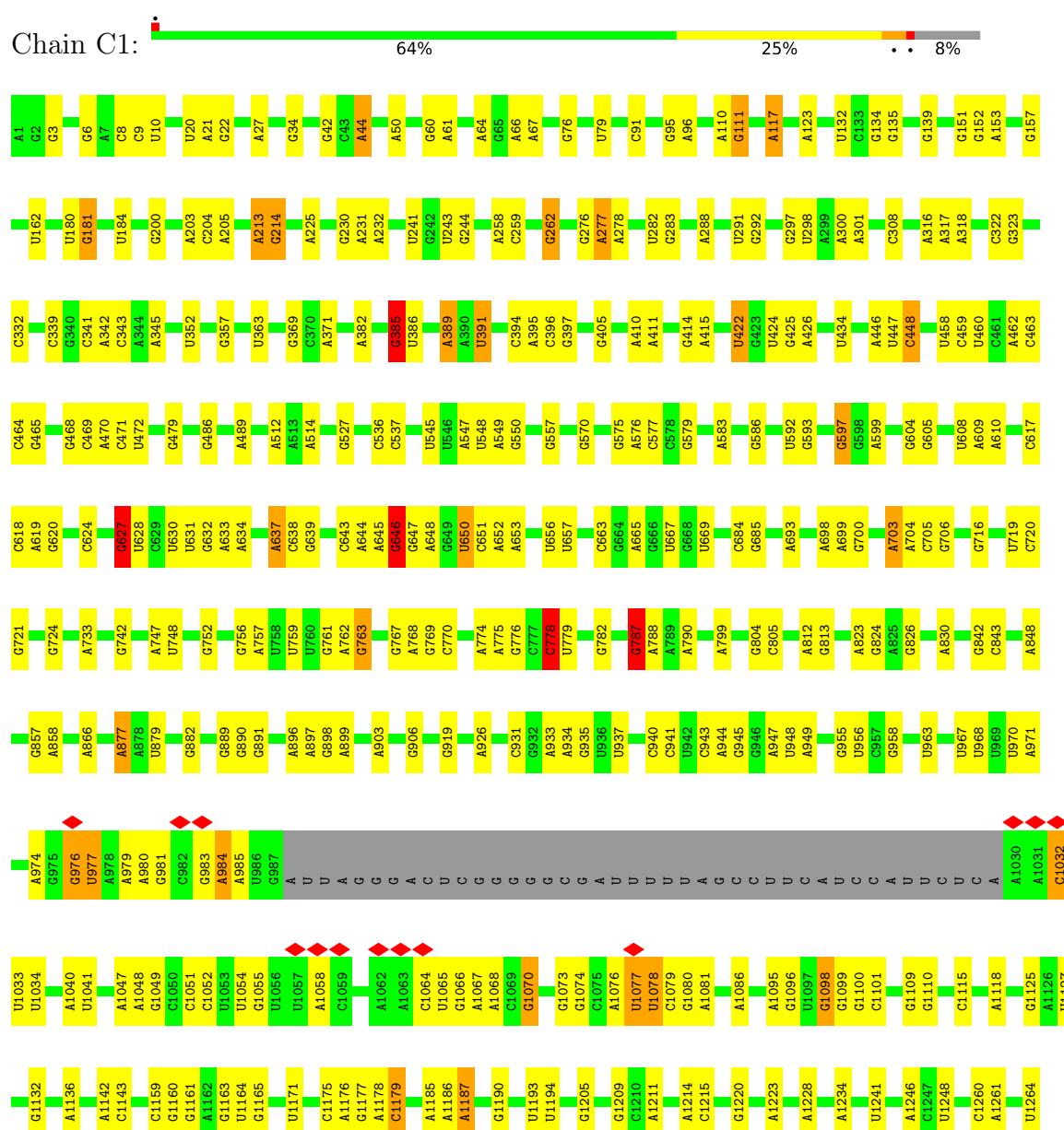
- Molecule 61 is water.

Mol	Chain	Residues	Atoms		AltConf
61	CH	1	Total 1	O 1	0
61	Cd	2	Total 2	O 2	0

3 Residue-property plots

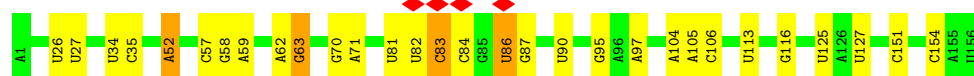
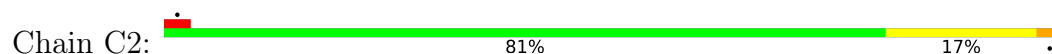
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 26S rRNA

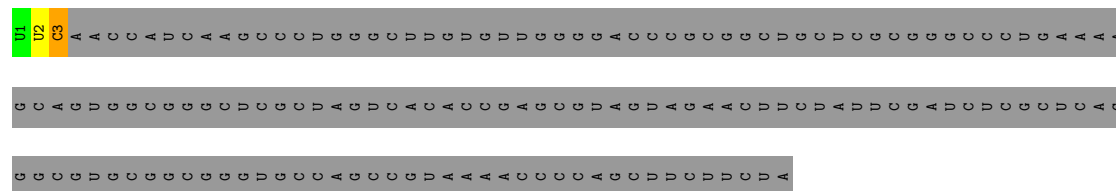


C2771	A2663	U2571	C2394	A2289	C2220	A2121	G2045	A1866	G1758	C1577	U1431	G1285
A2772	A2664	U2572	G2400	U2297	U2221	U2122	C2046	A1867	C1759	G1578	A1432	C1286
G2773	G2665	G2573	A	G2298	A2222	G2123	G2047	U1868	G1760	U1584	G1433	C1287
G2774	G2666	G2574	G2405	G2299	U2223	U2124	C2048	G	C1761	U1585	C1434	G1288
A2775	C2667	U2575	A2406	C2300	U2224	G2125	G2049	A1871	U1762	A1586	A1269	A1289
U	U	G2576	C	C2301	A2225	C2126	G2050	U1872	C1763	U1587	A1270	A1290
A2671	U2671	G2577	U2467	C2302	C2226	U2127	U2051	A1873	G1766	G1588	G1448	G1283
A2672	U2672	G2578	U2468	U2307	U2227	A2130	U2052	G1879	A1767	C1589	A1449	A1287
A2673	U2673	G2579	A	A2308	U2229	G2132	G2053	A1880	U1770	A1599	U1450	A1288
A2674	U2674	G2580	U2473	A2314	C2230	U2133	G2054	G	U1771	U1609	U1455	G1289
U2675	U2675	G2581	G	U2315	U2231	U2134	U2055	G1886	G1776	G1609	G1455	G1290
A2680	U2680	G2582	G	G2316	A	U2135	U2056	C1887	A1777	C1611	G1458	A1291
U2681	U2681	G2583	G	C2317	G	U2136	U2057	A1883	A1778	G1612	G1463	U1292
A2682	U2682	G2584	U2478	C2318	A2236	A2137	U2058	G	A1779	C1613	A1464	U1293
A2683	U2683	G2585	G	U2319	U2237	U2138	U2059	U1900	A1780	C1614	G1465	G1294
U2684	U2684	G2586	A	A2320	U2238	U2139	U2060	A1901	U1781	A1622	U1466	G1295
U2685	U2685	G2587	G	A2321	A2239	U2140	U2061	A1902	G1782	C1623	G1467	G1304
U2686	U2686	G2588	U2479	A2322	U2240	U2141	U2062	A1912	G1783	A1624	U1468	U1305
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U2796	U2796	G2594	U2481	U2328	U2246	U2147	U2068	G1920	A1796	G1642	G1483	A1335
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C2803	U2803	G2596	G	U2330	U2248	U2149	U2070	U1922	U1798	A1676	A1517	G1345
A2804	U2804	G2597	U2482	A2331	U2249	U2150	U2071	G	C1800	A1677	A1518	A1346
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A2806	U2806	G2599	U2483	U2333	U2251	U2152	U2073	G	A1816	G1679	U1537	G1362
U2810	U2810	G2600	A	U2334	U2252	U2153	U2074	U	A1817	U1683	U1538	G1370
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U2812	U2812	G2602	U2484	U2336	U2254	U2155	U2076	U	C1822	U1685	A1540	G1371
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C2819	U2819	G2607	A	A2341	U2259	U2160	U2081	G	G1843	C1705	U1550	A1401
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U2832	U2832	G2620	G	U2353	U2272	U2173	U2094	G	U1859	U1750	U1575	U1575
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U2840	U2840	G2628	G	U2361	U2280	U2181	U2102	G	U1867	U1758	U1583	U1583
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U2849	U2849	G2637	A	A2370	U2289	U2190	U2111	G	U1876	U1767	U1592	U1592
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U2851	U2851	G2639	G	U2372	U2291	U2192	U2113	G	U1878	U1769	U1594	U1594
U2852	U2852	G2640	U2499	U2373	U2292	U2193	U2114	G	U1879	U1770	U1595	U1595
U2853	U2853	G2641	A	A2374	U2293	U2194	U2115	G	U1880	U1771	U1596	U1596
U2854	U2854	G2642	G	U2375	U2294	U2195	U2116	G	U1881	U1772	U1597	U1597
U2855	U2855	G2643	U2500	U2376	U2295	U2196	U2117	G	U1882	U1773	U1598	U1598
U2856	U2856	G2644	G	A2377	U2296	U2197	U2118	G	U1883	U1774	U1599	U1599
U2857	U2857	G2645	A	U2378	U2297	U2198	U2119	G	U1884	U1775	U1600	U1600
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U2860	U2860	G2648	G	U2381	U2300	U2201	U2122	G	U1887	U1778	U1603	U1603
U2861	U2861	G2649	U2503	A2382	U2301	U2202	U2123	G	U1888	U1779	U1604	U1604
U2862	U2862	G2650	A	U2383	U2302	U2203	U2124	G	U1889	U1780	U1605	U1605
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U2864	U2864	G2652	U2504	U2385	U2304	U2205	U2126	G	U1891	U1782	U1607	U1607
U2865	U2865	G2653	G	A2386	U2305	U2206	U2127	G	U1892	U1783	U1608	U1608
U2866	U2866	G2654	U2505	U2387	U2306	U2207	U2128	G	U1893	U1784	U1609	U1609
U2867	U2867	G2655	A	U2388	U2307	U2208	U2129	G	U1894	U1785	U1610	U1610
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U2869	U2869	G2657	U2506	U2390	U2309	U2210	U2131	G	U1896	U1787	U1612	U1612
U2870	U2870	G2658	U2507	U2391	U2310	U2211	U2132	G	U1897	U1788	U1613	U1613
U2871	U2871	G2659	A	A2392	U2311	U2212	U2133	G	U1898	U1789	U1614	U1614
U2872	U2872	G2660	G	U2393	U2312	U2213	U2134	G	U1899	U1790	U1615	U1615
U2873	U2873	G2661	U2508	U2394	U2313	U2214	U2135	G	U1900	U1791	U1616	U1616
U2874	U2874	G2662	G	U2395	U2314	U2215	U2136	G	U1901	U1792	U1617	U1617
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U2876	U2876	G2664	U2509	U2397	U2316	U2217	U2138	G	A1912	U1794	U1619	U1619
U2877	U2877	G2665	G	U2398	U2317	U2218	U2139	G	U1913	U1795	U1620	U1620
U2878	U2878	G2666	U2510	U2399	U2318	U2219	U2140	G	U1914	U1796	U1621	U1621
U2879	U2879	G2667	A	A2399	U2319	U2220	U2141	G	U1915	U1797	U1622	U1622
U2880	U2880	G2668	G	U2400	U2320	U2221	U2142	G	U1916	U1798	U1623	U1623
U2881	U2881	G2669	U2511	U2401	U2321	U2222	U2143	G	U1917	U1799	U1624	U1624

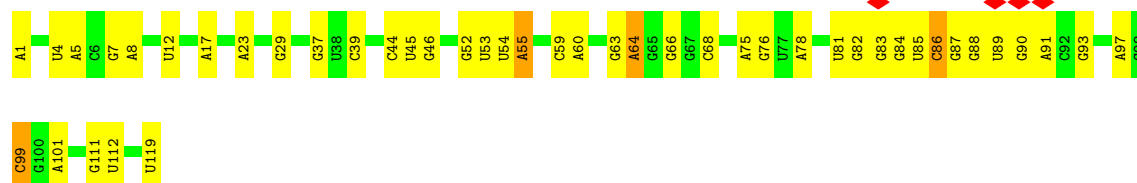
- Molecule 2: 5.8S rRNA



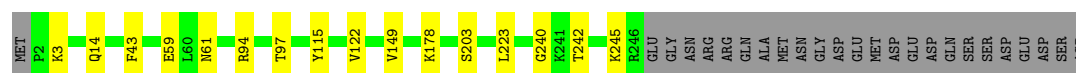
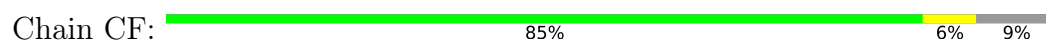
- Molecule 3: ITS2




- Molecule 4: 5S rRNA

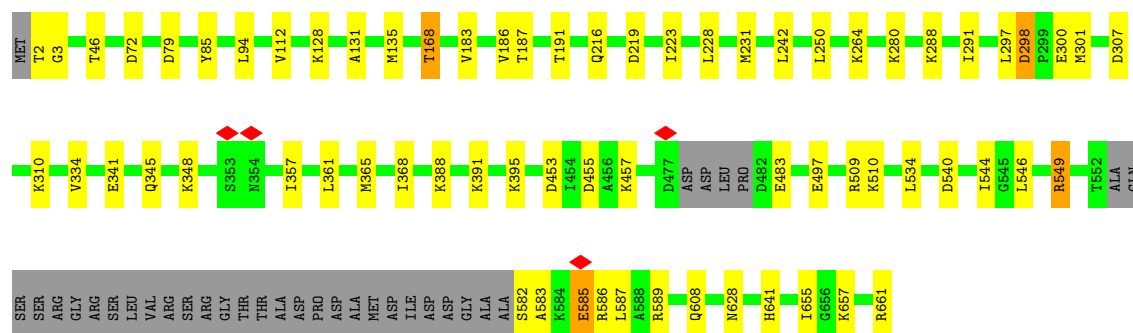


- Molecule 5: Large ribosomal subunit protein uL10



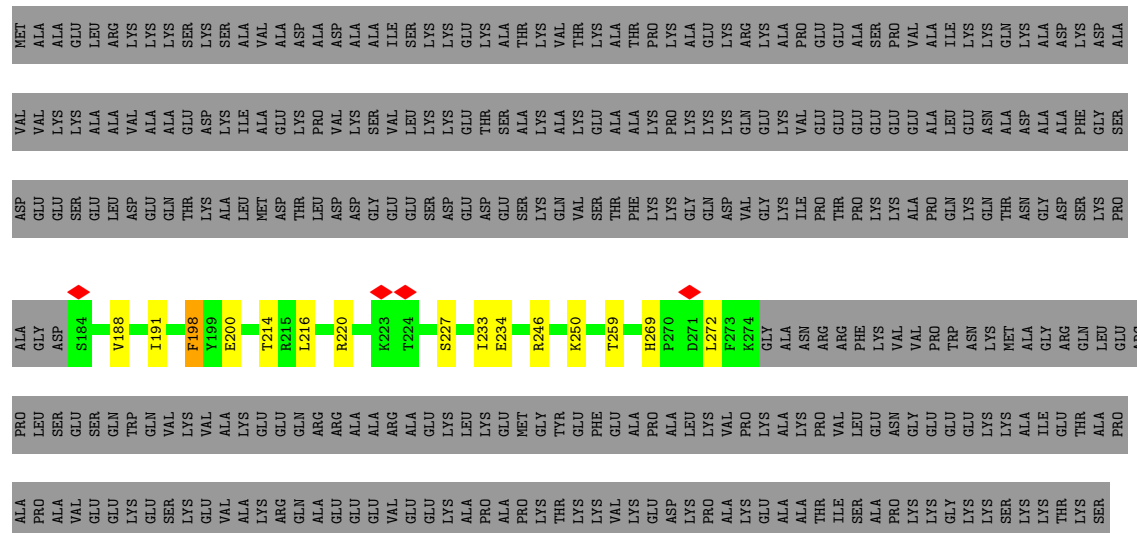
- Molecule 6: Nucleolar GTP-binding protein 1

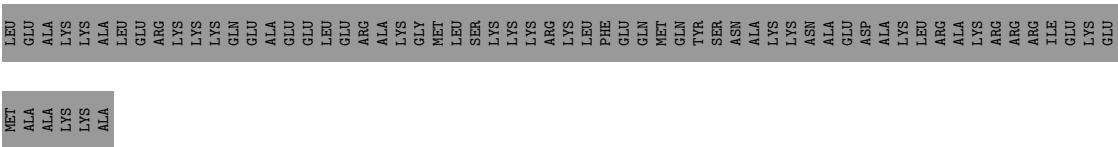
Chain CH:  85% 10% 5%



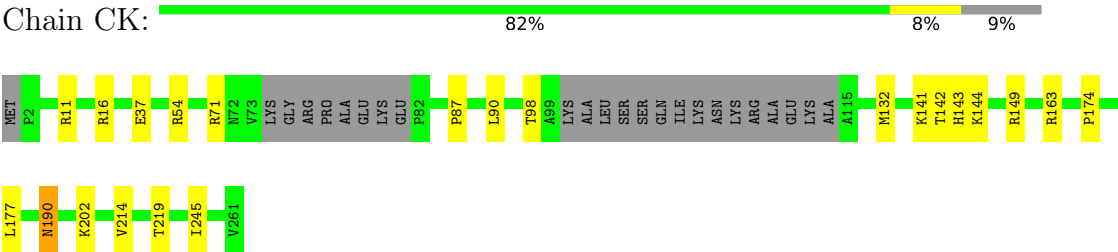
• Molecule 7: Putative RNA-binding protein

Chain CI:  18% 78%

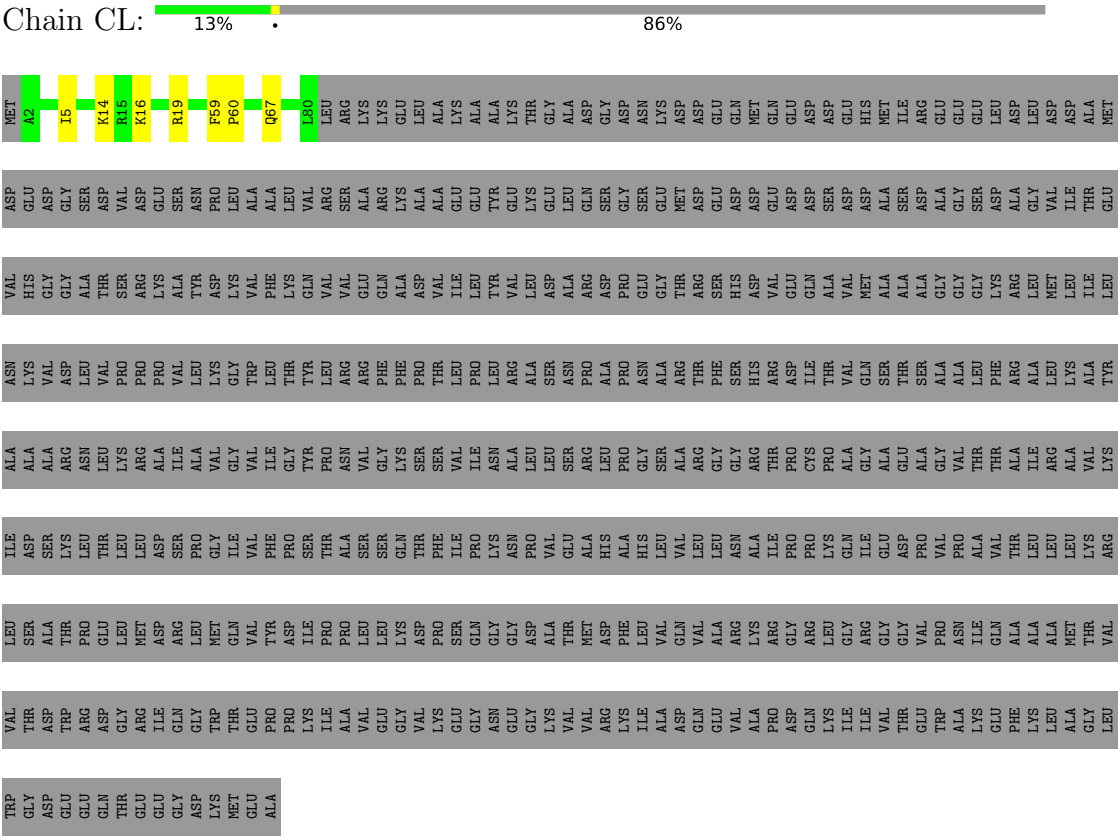




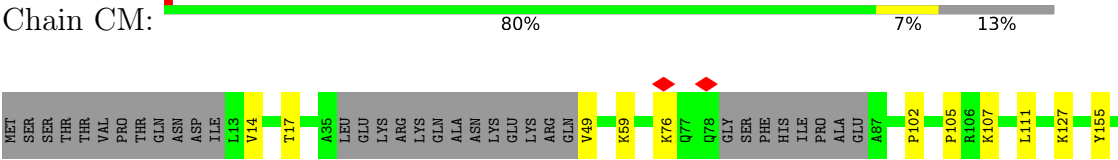
• Molecule 9: Ribosome biogenesis protein NSA2 homolog



• Molecule 10: Putative GTP binding protein



• Molecule 11: 60S ribosomal protein l7-like protein





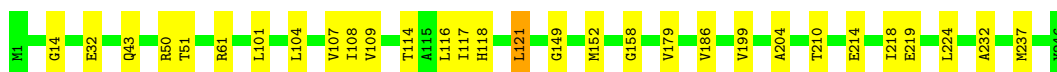
- Molecule 11: 60S ribosomal protein l7-like protein

Chain LF: 94% 5%



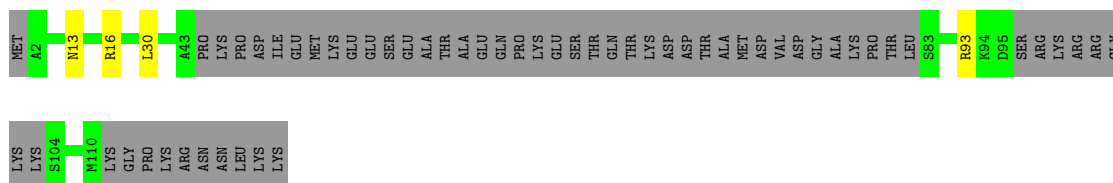
- Molecule 12: Eukaryotic translation initiation factor 6

Chain CN: 88% 12%



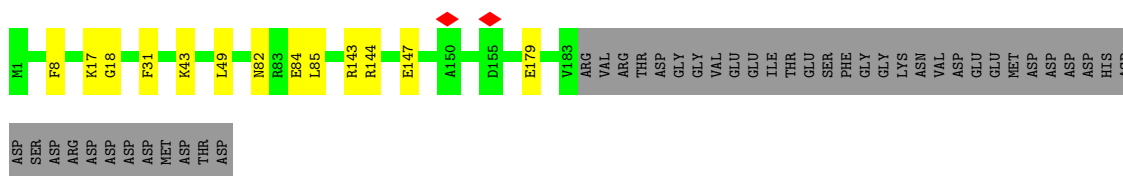
- Molecule 13: DUF2423 domain-containing protein

Chain CO: 48% . 48%



- Molecule 14: Ribosome biogenesis protein RLP24

Chain CQ: 76% 6% 19%



- Molecule 15: Zinc finger domain-containing protein

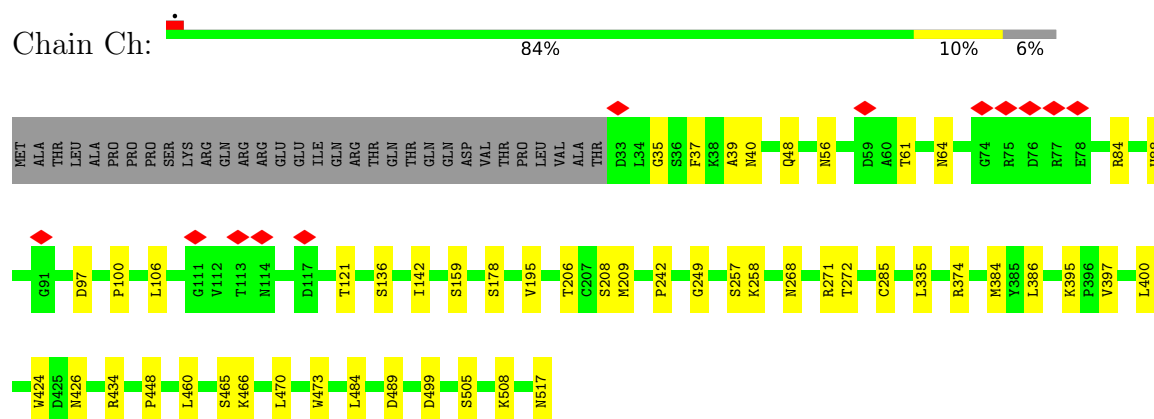
Chain Cb: 77% 9% . 14%



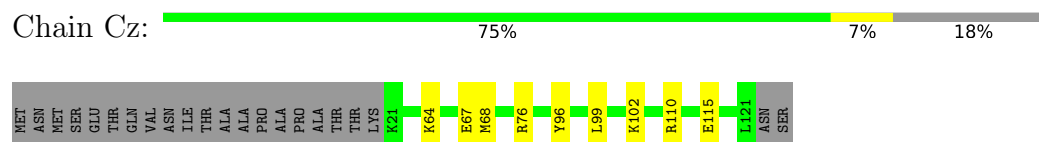
- Molecule 16: Nucleolar GTP-binding protein 2

Chain Cd: 69% . 26%

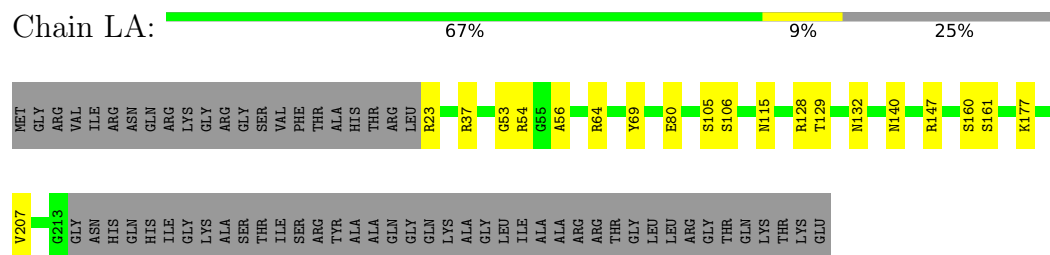
- Molecule 20: Ribosome assembly protein 4



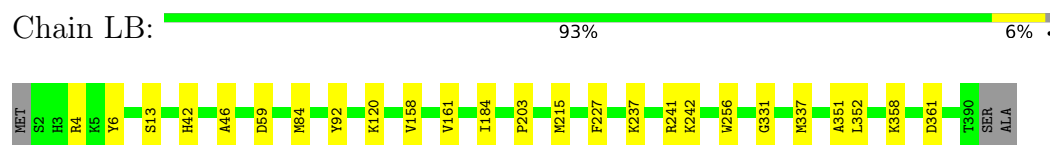
- Molecule 21: rRNA-processing protein



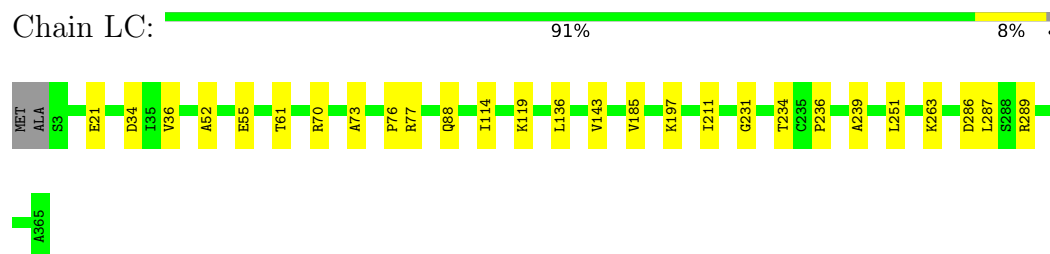
- Molecule 22: 60S ribosomal protein L2-like protein



- Molecule 23: 60S ribosomal protein L3-like protein

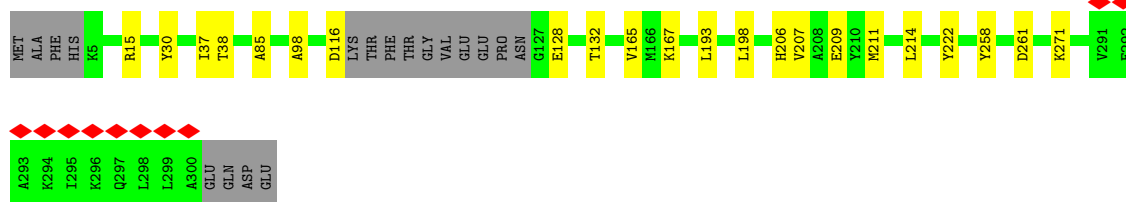


- Molecule 24: 60S ribosomal protein L4-like protein




- Molecule 25: 60S ribosomal protein l5-like protein

Chain LD:  87% 7% 6%




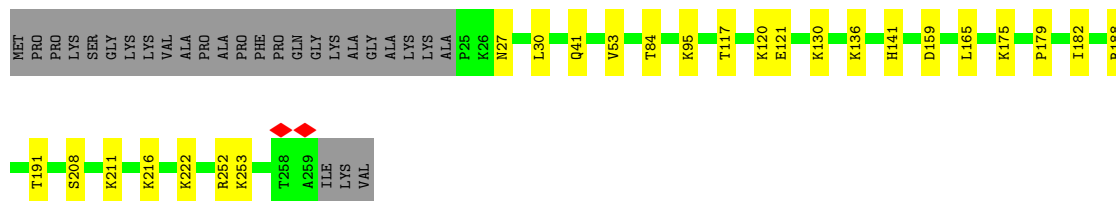
- Molecule 26: 60S ribosomal protein L6

Chain LE:  88% 8% .




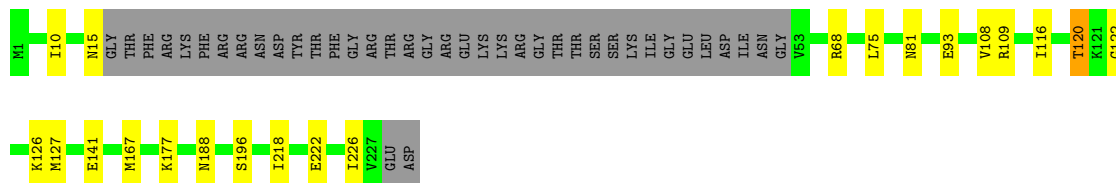
- Molecule 27: 60S ribosomal protein L8

Chain LG:  80% 10% 10%




- Molecule 28: 60S ribosomal protein 19-like protein

Chain LH:  74% 9% 17%



- Molecule 29: Putative ribosomal protein

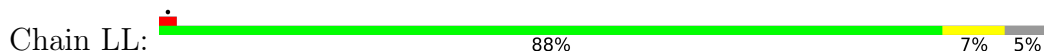
Chain LJ:  84% 13% ..



- Molecule 30: 60S ribosomal protein L12-like protein

Chain LK:  88% 6% ..

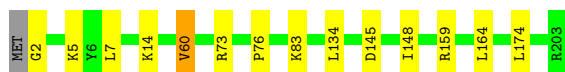
- Molecule 31: 60S ribosomal protein L13



- Molecule 32: 60S ribosomal protein L14-like protein



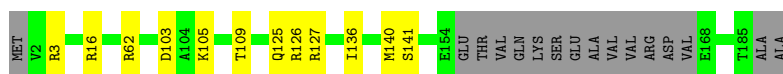
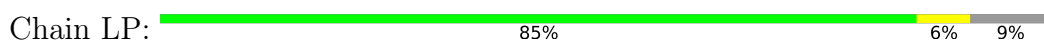
- Molecule 33: Ribosomal protein L15



- Molecule 34: 60S ribosomal protein L16-like protein



- Molecule 35: 60S ribosomal protein l17-like protein



- Molecule 36: Ribosomal protein L18-like protein



- Molecule 37: Ribosomal protein L19

95%






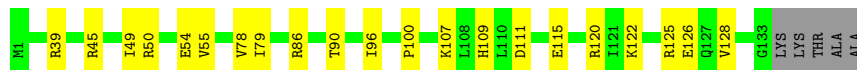
- Molecule 42: 60S ribosomal protein L25-like protein

Chain LX:  87% 6% 7%



- Molecule 43: 60S ribosomal protein L26-like protein

Chain LY:  81% 15% .



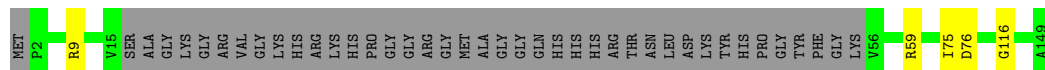
- Molecule 44: 60S ribosomal protein L27

Chain LZ:  85% 15%




- Molecule 45: 60S ribosomal protein L28-like protein

Chain La:  69% 28%




- Molecule 46: 60S ribosomal protein l30-like protein

Chain Lc:  78% 9% 12%




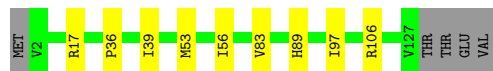
- Molecule 47: Putative 60S ribosomal protein

Chain Ld:  84% 8% 8%

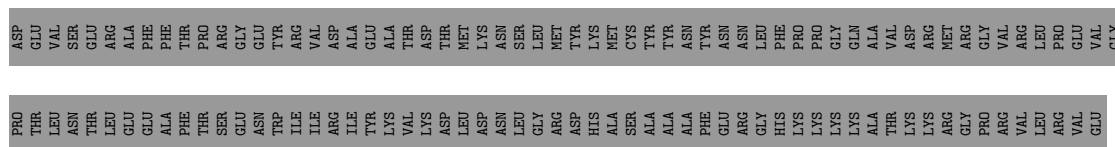


- Molecule 48: 60S ribosomal protein L32-like protein

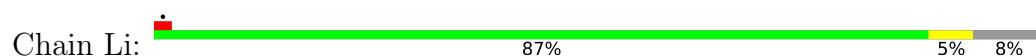
Chain Le:  89% 7%



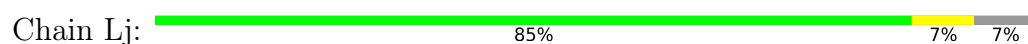
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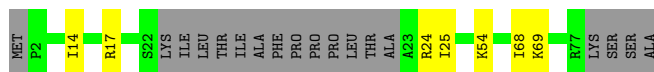
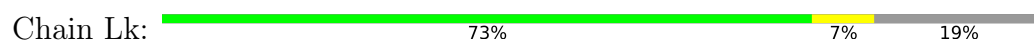
- Molecule 52: 60S ribosomal protein L36



- Molecule 53: Ribosomal protein L37



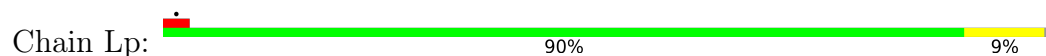
- Molecule 54: 60S ribosomal protein L38-like protein



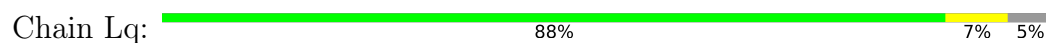
- Molecule 55: Ribosomal protein eL39



- Molecule 56: 60S ribosomal protein L43-like protein



- Molecule 57: Putative 60S ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	276213	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.906	Depositor
Minimum map value	0.000	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.160	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, ZN, OMC, GTP, A2M, OMU, 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	C1	0.18	1/72882 (0.0%)	0.35	1/113631 (0.0%)
2	C2	0.17	0/3710	0.32	0/5778
3	C3	0.07	0/65	0.17	0/98
4	C4	0.17	0/2833	0.33	0/4414
5	CF	0.14	0/1972	0.32	0/2660
6	CH	0.18	0/5147	0.42	1/6926 (0.0%)
7	CI	0.17	0/740	0.49	0/1001
8	CJ	0.17	0/3196	0.34	0/4319
9	CK	0.16	0/1939	0.38	0/2608
10	CL	0.17	0/631	0.35	0/843
11	CM	0.20	0/1801	0.48	0/2412
11	LF	0.18	0/2061	0.39	0/2765
12	CN	0.17	0/1878	0.42	0/2555
13	CO	0.16	0/470	0.35	0/619
14	CQ	0.20	0/1504	0.42	0/2000
15	Cb	0.18	0/845	0.42	0/1128
16	Cd	0.15	0/3770	0.34	0/5082
17	Ce	0.17	0/2002	0.36	1/2662 (0.0%)
18	Cf	0.14	0/2326	0.33	0/3113
19	Cg	0.18	0/1508	0.44	1/2051 (0.0%)
20	Ch	0.17	0/3914	0.46	0/5319
21	Cz	0.23	0/877	0.47	0/1148
22	LA	0.15	0/1488	0.39	0/2009
23	LB	0.16	0/3172	0.41	0/4260
24	LC	0.15	0/2808	0.36	0/3785
25	LD	0.14	0/2308	0.33	0/3105
26	LE	0.16	0/1504	0.36	1/2027 (0.0%)
27	LG	0.16	0/1918	0.38	0/2565
28	LH	0.15	0/1515	0.38	0/2037
29	LJ	0.21	0/1379	0.54	4/1844 (0.2%)
30	LK	0.20	0/1198	0.47	0/1611
31	LL	0.16	0/1614	0.35	0/2168

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LM	0.16	0/1145	0.35	0/1539
33	LN	0.16	0/1741	0.36	0/2332
34	LO	0.20	0/1645	0.44	1/2205 (0.0%)
35	LP	0.16	0/1364	0.39	0/1835
36	LQ	0.16	0/1218	0.39	0/1639
37	LR	0.15	0/1260	0.33	0/1683
38	LS	0.16	0/1461	0.37	0/1966
39	LT	0.21	0/1046	0.50	1/1409 (0.1%)
40	LU	0.18	0/859	0.42	0/1151
41	LV	0.14	0/1009	0.38	0/1357
42	LX	0.17	0/1151	0.43	0/1547
43	LY	0.16	0/1070	0.42	0/1432
44	LZ	0.17	0/1135	0.39	0/1519
45	La	0.14	0/892	0.32	0/1200
46	Lc	0.15	0/714	0.33	0/960
47	Ld	0.16	0/889	0.34	0/1192
48	Le	0.15	0/1035	0.37	0/1379
49	Lf	0.14	0/883	0.33	0/1187
50	Lg	0.17	0/927	0.38	0/1244
51	Lh	0.21	0/1014	0.44	0/1349
52	Li	0.15	0/834	0.36	0/1099
53	Lj	0.16	0/712	0.39	0/944
54	Lk	0.17	0/640	0.37	0/850
55	Ll	0.14	0/446	0.28	0/593
56	Lp	0.17	0/706	0.45	0/940
57	Lq	0.16	0/1091	0.39	0/1468
All	All	0.17	1/161862 (0.0%)	0.37	11/234562 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C1	36	0
6	CH	0	1
All	All	36	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	848	A2M	O3'-P	5.05	1.61	1.56

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	LO	197	GLU	CA-CB-CG	8.82	131.74	114.10
39	LT	125	PRO	CA-N-CD	-7.81	101.07	112.00
19	Cg	49	GLN	CA-CB-CG	7.78	129.65	114.10
29	LJ	40	GLN	CA-CB-CG	6.16	126.43	114.10
29	LJ	39	GLU	CA-C-N	-5.94	111.62	122.38

5 of 36 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	C1	385	OMG	C3',C4'
1	C1	627	OMG	C3',C4'
1	C1	646	OMG	C3',C4'
1	C1	778	OMC	C3',C4'
1	C1	787	OMG	C3',C4'

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	CH	298	ASP	Peptide

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	C1	65888	0	33223	347	0
2	C2	3319	0	1678	12	0
3	C3	60	0	32	1	0
4	C4	2536	0	1286	20	0
5	CF	1934	0	1945	8	0
6	CH	5063	0	5157	47	0
7	CI	720	0	699	9	0
8	CJ	3116	0	3122	19	0
9	CK	1903	0	1990	16	0
10	CL	622	0	641	6	0
11	CM	1769	0	1876	10	0
11	LF	2023	0	2132	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	CN	1853	0	1852	17	0
13	CO	468	0	503	4	0
14	CQ	1480	0	1523	8	0
15	Cb	830	0	838	5	0
16	Cd	3691	0	3818	23	0
17	Ce	1977	0	2061	18	0
18	Cf	2282	0	2347	21	0
19	Cg	1478	0	1517	8	0
20	Ch	3812	0	3715	26	0
21	Cz	869	0	956	7	0
22	LA	1454	0	1490	14	0
23	LB	3104	0	3221	17	0
24	LC	2751	0	2875	19	0
25	LD	2266	0	2219	17	0
26	LE	1477	0	1567	8	0
27	LG	1889	0	2043	18	0
28	LH	1495	0	1573	12	0
29	LJ	1357	0	1385	15	0
30	LK	1184	0	1249	9	0
31	LL	1587	0	1655	11	0
32	LM	1126	0	1198	8	0
33	LN	1704	0	1767	11	0
34	LO	1611	0	1702	15	0
35	LP	1343	0	1369	11	0
36	LQ	1200	0	1296	7	0
37	LR	1241	0	1298	8	0
38	LS	1426	0	1481	14	0
39	LT	1027	0	1076	9	0
40	LU	846	0	883	8	0
41	LV	991	0	1044	7	0
42	LX	1133	0	1234	8	0
43	LY	1056	0	1143	14	0
44	LZ	1112	0	1181	13	0
45	La	872	0	903	4	0
46	Lc	705	0	751	6	0
47	Ld	875	0	918	6	0
48	Le	1017	0	1092	6	0
49	Lf	862	0	891	6	0
50	Lg	914	0	960	5	0
51	Lh	1003	0	1116	9	0
52	Li	827	0	906	4	0
53	Lj	698	0	726	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	Lk	632	0	693	4	0
55	Ll	436	0	473	3	0
56	Lp	698	0	737	4	0
57	Lq	1073	0	1130	6	0
58	CH	32	0	12	1	0
58	Cd	32	0	12	0	0
59	CH	1	0	0	0	0
59	Cd	2	0	0	0	0
60	CQ	1	0	0	0	0
60	Cb	1	0	0	0	0
60	Lg	1	0	0	0	0
60	Lj	1	0	0	0	0
60	Lp	1	0	0	0	0
61	CH	1	0	0	0	0
61	Cd	2	0	0	0	0
All	All	152760	0	120180	803	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 3.

The worst 5 of 803 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)
1:C1:2400:G:H1	1:C1:2473:U:H3	0.97	0.93
1:C1:3289:G:H1	1:C1:3298:U:H3	1.19	0.90
30:LK:8:ASN:HD22	30:LK:8:ASN:N	1.73	0.86
1:C1:1054:U:H3	1:C1:1070:G:H1	0.89	0.83
44:LZ:81:PRO:HB2	46:Lc:65:MET:HE1	1.68	0.74

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CF	243/270 (90%)	240 (99%)	3 (1%)	0	100	100
6	CH	621/661 (94%)	616 (99%)	5 (1%)	0	100	100
7	CI	89/414 (22%)	87 (98%)	2 (2%)	0	100	100
8	CJ	376/679 (55%)	371 (99%)	5 (1%)	0	100	100
9	CK	231/261 (88%)	225 (97%)	6 (3%)	0	100	100
10	CL	77/558 (14%)	77 (100%)	0	0	100	100
11	CM	210/249 (84%)	206 (98%)	4 (2%)	0	100	100
11	LF	246/249 (99%)	239 (97%)	7 (3%)	0	100	100
12	CN	244/246 (99%)	239 (98%)	5 (2%)	0	100	100
13	CO	56/120 (47%)	56 (100%)	0	0	100	100
14	CQ	181/225 (80%)	179 (99%)	2 (1%)	0	100	100
15	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
16	Cd	458/627 (73%)	449 (98%)	9 (2%)	0	100	100
17	Ce	231/443 (52%)	229 (99%)	2 (1%)	0	100	100
18	Cf	281/350 (80%)	280 (100%)	1 (0%)	0	100	100
19	Cg	186/202 (92%)	186 (100%)	0	0	100	100
20	Ch	484/517 (94%)	468 (97%)	16 (3%)	0	100	100
21	Cz	99/123 (80%)	98 (99%)	1 (1%)	0	100	100
22	LA	189/254 (74%)	186 (98%)	3 (2%)	0	100	100
23	LB	387/392 (99%)	380 (98%)	7 (2%)	0	100	100
24	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
25	LD	282/304 (93%)	280 (99%)	2 (1%)	0	100	100
26	LE	187/200 (94%)	183 (98%)	4 (2%)	0	100	100
27	LG	233/262 (89%)	229 (98%)	4 (2%)	0	100	100
28	LH	188/229 (82%)	185 (98%)	3 (2%)	0	100	100
29	LJ	167/173 (96%)	165 (99%)	2 (1%)	0	100	100
30	LK	156/165 (94%)	156 (100%)	0	0	100	100
31	LL	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
32	LM	139/142 (98%)	135 (97%)	4 (3%)	0	100	100
33	LN	200/203 (98%)	195 (98%)	5 (2%)	0	100	100
34	LO	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
35	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	LQ	148/213 (70%)	146 (99%)	2 (1%)	0	100	100
37	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
38	LS	172/174 (99%)	170 (99%)	2 (1%)	0	100	100
39	LT	127/160 (79%)	125 (98%)	2 (2%)	0	100	100
40	LU	103/127 (81%)	100 (97%)	3 (3%)	0	100	100
41	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
42	LX	143/156 (92%)	141 (99%)	2 (1%)	0	100	100
43	LY	131/138 (95%)	126 (96%)	5 (4%)	0	100	100
44	LZ	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
45	La	104/149 (70%)	104 (100%)	0	0	100	100
46	Lc	93/108 (86%)	93 (100%)	0	0	100	100
47	Ld	108/120 (90%)	107 (99%)	1 (1%)	0	100	100
48	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
49	Lf	106/109 (97%)	106 (100%)	0	0	100	100
50	Lg	116/119 (98%)	115 (99%)	1 (1%)	0	100	100
51	Lh	120/935 (13%)	118 (98%)	2 (2%)	0	100	100
52	Li	99/110 (90%)	98 (99%)	1 (1%)	0	100	100
53	Lj	86/95 (90%)	85 (99%)	1 (1%)	0	100	100
54	Lk	74/94 (79%)	74 (100%)	0	0	100	100
55	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
56	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
57	Lq	137/147 (93%)	133 (97%)	4 (3%)	0	100	100
All	All	10017/16004 (63%)	9867 (98%)	150 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CF	212/236 (90%)	207 (98%)	5 (2%)	43	58
6	CH	549/575 (96%)	541 (98%)	8 (2%)	57	73
7	CI	70/336 (21%)	68 (97%)	2 (3%)	37	51
8	CJ	331/579 (57%)	324 (98%)	7 (2%)	47	63
9	CK	206/225 (92%)	203 (98%)	3 (2%)	57	73
10	CL	61/458 (13%)	61 (100%)	0	100	100
11	CM	185/215 (86%)	183 (99%)	2 (1%)	65	79
11	LF	213/215 (99%)	211 (99%)	2 (1%)	70	84
12	CN	205/206 (100%)	202 (98%)	3 (2%)	57	73
13	CO	48/99 (48%)	48 (100%)	0	100	100
14	CQ	144/192 (75%)	143 (99%)	1 (1%)	76	87
15	Cb	85/101 (84%)	82 (96%)	3 (4%)	32	43
16	Cd	403/541 (74%)	401 (100%)	2 (0%)	81	90
17	Ce	206/383 (54%)	206 (100%)	0	100	100
18	Cf	250/310 (81%)	247 (99%)	3 (1%)	63	78
19	Cg	158/176 (90%)	152 (96%)	6 (4%)	29	40
20	Ch	408/436 (94%)	405 (99%)	3 (1%)	76	87
21	Cz	89/107 (83%)	88 (99%)	1 (1%)	65	79
22	LA	150/198 (76%)	146 (97%)	4 (3%)	39	53
23	LB	329/331 (99%)	328 (100%)	1 (0%)	86	93
24	LC	282/285 (99%)	280 (99%)	2 (1%)	76	87
25	LD	221/253 (87%)	221 (100%)	0	100	100
26	LE	157/166 (95%)	155 (99%)	2 (1%)	61	76
27	LG	200/222 (90%)	200 (100%)	0	100	100
28	LH	167/200 (84%)	166 (99%)	1 (1%)	78	89
29	LJ	140/150 (93%)	139 (99%)	1 (1%)	76	87
30	LK	127/136 (93%)	123 (97%)	4 (3%)	35	48
31	LL	158/176 (90%)	157 (99%)	1 (1%)	78	89
32	LM	116/117 (99%)	115 (99%)	1 (1%)	70	84
33	LN	179/180 (99%)	178 (99%)	1 (1%)	78	89
34	LO	162/163 (99%)	161 (99%)	1 (1%)	78	89
35	LP	133/152 (88%)	133 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	LQ	128/178 (72%)	127 (99%)	1 (1%)	73	85
37	LR	125/2396 (5%)	125 (100%)	0	100	100
38	LS	152/154 (99%)	151 (99%)	1 (1%)	76	87
39	LT	110/135 (82%)	109 (99%)	1 (1%)	70	84
40	LU	92/108 (85%)	91 (99%)	1 (1%)	65	79
41	LV	98/102 (96%)	97 (99%)	1 (1%)	68	81
42	LX	122/129 (95%)	121 (99%)	1 (1%)	73	85
43	LY	116/119 (98%)	115 (99%)	1 (1%)	70	84
44	LZ	121/121 (100%)	119 (98%)	2 (2%)	53	69
45	La	93/122 (76%)	92 (99%)	1 (1%)	65	79
46	Lc	76/88 (86%)	74 (97%)	2 (3%)	40	55
47	Ld	90/105 (86%)	90 (100%)	0	100	100
48	Le	109/114 (96%)	108 (99%)	1 (1%)	70	84
49	Lf	89/90 (99%)	86 (97%)	3 (3%)	32	44
50	Lg	95/102 (93%)	95 (100%)	0	100	100
51	Lh	109/781 (14%)	109 (100%)	0	100	100
52	Li	85/93 (91%)	85 (100%)	0	100	100
53	Lj	72/78 (92%)	71 (99%)	1 (1%)	59	75
54	Lk	73/88 (83%)	73 (100%)	0	100	100
55	Ll	45/46 (98%)	45 (100%)	0	100	100
56	Lp	73/74 (99%)	71 (97%)	2 (3%)	39	53
57	Lq	109/112 (97%)	109 (100%)	0	100	100
All	All	8526/13454 (63%)	8437 (99%)	89 (1%)	65	81

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	LE	155	SER
38	LS	79	LEU
11	LF	90	VAL
30	LK	164	ASP
42	LX	37	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
20	Ch	432	ASN
47	Ld	64	ASN
28	LH	133	HIS
47	Ld	62	GLN
51	Lh	37	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3069/3342 (91%)	550 (17%)	43 (1%)
2	C2	155/156 (99%)	23 (14%)	0
3	C3	2/162 (1%)	2 (100%)	0
4	C4	118/119 (99%)	24 (20%)	0
All	All	3344/3779 (88%)	599 (17%)	43 (1%)

5 of 599 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	G
1	C1	27	A
1	C1	44	A
1	C1	50	A
1	C1	60	G

5 of 43 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	2838	OMC
1	C1	3205	G
1	C1	2876	OMG
1	C1	2918	OMC
1	C1	3230	G

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMC	C1	2300	1	19,22,23	3.02	8 (42%)	25,31,34	2.76	9 (36%)
1	OMG	C1	627	1	23,26,27	2.51	8 (34%)	32,38,41	2.80	18 (56%)
1	OMC	C1	1420	1	19,22,23	3.00	8 (42%)	25,31,34	2.55	9 (36%)
1	OMC	C1	1836	1	19,22,23	3.04	8 (42%)	25,31,34	2.74	11 (44%)
1	OMG	C1	2358	1	23,26,27	2.53	9 (39%)	32,38,41	2.79	18 (56%)
1	OMG	C1	385	1	23,26,27	2.51	9 (39%)	32,38,41	2.91	19 (59%)
1	A2M	C1	1432	1	22,25,26	4.00	12 (54%)	30,36,39	3.34	12 (40%)
1	A2M	C1	389	1	22,25,26	3.95	11 (50%)	30,36,39	3.34	11 (36%)
1	OMG	C1	2881	1	23,26,27	2.47	8 (34%)	32,38,41	2.86	17 (53%)
1	A2M	C1	637	1	22,25,26	3.96	12 (54%)	30,36,39	3.42	14 (46%)
1	OMU	C1	2380	1	19,22,23	3.08	6 (31%)	25,31,34	1.80	5 (20%)
1	OMU	C1	2384	1	19,22,23	3.12	6 (31%)	25,31,34	1.77	4 (16%)
1	OMG	C1	646	1	23,26,27	2.50	8 (34%)	32,38,41	2.86	17 (53%)
1	OMU	C1	1917	1	19,22,23	3.15	6 (31%)	25,31,34	1.83	5 (20%)
1	OMG	C1	2578	1	23,26,27	2.51	9 (39%)	32,38,41	2.84	18 (56%)
1	A2M	C1	858	1	22,25,26	4.01	12 (54%)	30,36,39	3.38	12 (40%)
1	A2M	C1	1223	1	22,25,26	3.97	10 (45%)	30,36,39	3.30	12 (40%)
1	OMC	C1	2838	1	19,22,23	3.08	8 (42%)	25,31,34	2.63	9 (36%)
1	OMU	C1	2277	1	19,22,23	3.12	6 (31%)	25,31,34	1.76	5 (20%)
1	A2M	C1	2289	1	22,25,26	4.00	11 (50%)	30,36,39	3.29	14 (46%)
1	OMU	C1	2690	1	19,22,23	3.10	6 (31%)	25,31,34	1.80	5 (20%)
1	A2M	C1	848	1	22,25,26	3.99	11 (50%)	30,36,39	3.39	14 (46%)
1	OMG	C1	787	1	23,26,27	2.46	9 (39%)	32,38,41	2.90	16 (50%)
1	OMC	C1	778	1	19,22,23	3.10	8 (42%)	25,31,34	2.62	9 (36%)
1	OMC	C1	1812	1	19,22,23	3.05	8 (42%)	25,31,34	2.60	11 (44%)
1	OMC	C1	2918	1	19,22,23	3.11	8 (42%)	25,31,34	2.71	9 (36%)
1	OMC	C1	1491	1	19,22,23	2.92	8 (42%)	25,31,34	2.75	11 (44%)
1	OMU	C1	2683	1	19,22,23	3.07	6 (31%)	25,31,34	1.68	5 (20%)
1	OMG	C1	2876	1	23,26,27	2.53	8 (34%)	32,38,41	3.17	16 (50%)
1	A2M	C1	1847	1	22,25,26	3.98	12 (54%)	30,36,39	3.46	13 (43%)
1	OMU	C1	2688	1	19,22,23	3.13	6 (31%)	25,31,34	1.79	5 (20%)
1	OMG	C1	1433	1	23,26,27	2.48	9 (39%)	32,38,41	2.83	18 (56%)
1	OMU	C1	1868	1	19,22,23	3.12	6 (31%)	25,31,34	1.89	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	C1	2774	1	23,26,27	2.50	9 (39%)	32,38,41	2.82	17 (53%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	C1	2300	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMG	C1	627	1	2/2/5/5	2/9/27/28	0/3/3/3
1	OMC	C1	1420	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMC	C1	1836	1	2/2/5/5	4/9/27/28	0/2/2/2
1	OMG	C1	2358	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMG	C1	385	1	2/2/5/5	5/9/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	389	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	2881	1	2/2/5/5	4/9/27/28	0/3/3/3
1	A2M	C1	637	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2380	1	-	1/9/27/28	0/2/2/2
1	OMU	C1	2384	1	-	1/9/27/28	0/2/2/2
1	OMG	C1	646	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMU	C1	1917	1	-	2/9/27/28	0/2/2/2
1	OMG	C1	2578	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMC	C1	2838	1	2/2/5/5	5/9/27/28	0/2/2/2
1	A2M	C1	858	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	1223	1	-	1/9/27/28	0/3/3/3
1	OMU	C1	2277	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2690	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	848	1	-	1/9/27/28	0/3/3/3
1	OMG	C1	787	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMC	C1	778	1	2/2/5/5	4/9/27/28	0/2/2/2
1	OMC	C1	1812	1	2/2/5/5	4/9/27/28	0/2/2/2
1	OMC	C1	2918	1	2/2/5/5	4/9/27/28	0/2/2/2
1	OMG	C1	2876	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMC	C1	1491	1	2/2/5/5	6/9/27/28	0/2/2/2
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	1433	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2774	1	2/2/5/5	4/9/27/28	0/3/3/3

The worst 5 of 289 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	858	A2M	C3'-C2'	-13.16	1.24	1.53
1	C1	2289	A2M	C3'-C2'	-13.03	1.24	1.53
1	C1	1432	A2M	C3'-C2'	-13.00	1.24	1.53
1	C1	848	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	1847	A2M	C3'-C2'	-12.96	1.24	1.53

The worst 5 of 393 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1847	A2M	C1'-N9-C8	-9.48	106.06	127.09
1	C1	637	A2M	C1'-N9-C8	-9.32	106.41	127.09
1	C1	858	A2M	C1'-N9-C8	-9.05	107.00	127.09
1	C1	1432	A2M	C1'-N9-C8	-8.90	107.33	127.09
1	C1	389	A2M	C1'-N9-C8	-8.88	107.39	127.09

5 of 36 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	C1	385	OMG	C3'
1	C1	385	OMG	C4'
1	C1	627	OMG	C3'
1	C1	627	OMG	C4'
1	C1	646	OMG	C3'

5 of 87 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	385	OMG	O4'-C4'-C5'-O5'
1	C1	385	OMG	C3'-C4'-C5'-O5'
1	C1	385	OMG	C3'-C2'-O2'-CM2
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	627	OMG	C3'-C2'-O2'-CM2

There are no ring outliers.

11 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	1420	OMC	1	0
1	C1	1432	A2M	1	0
1	C1	637	A2M	1	0
1	C1	2384	OMU	1	0
1	C1	2578	OMG	1	0
1	C1	2838	OMC	2	0
1	C1	787	OMG	1	0
1	C1	1812	OMC	1	0
1	C1	1491	OMC	3	0
1	C1	2683	OMU	1	0
1	C1	2876	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
58	GTP	CH	701	59	33,34,34	0.88	1 (3%)	50,54,54	1.58	9 (18%)
58	GTP	Cd	703	59	33,34,34	0.91	0	50,54,54	1.60	8 (16%)

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
58	GTP	CH	701	59	-	6/22/38/38	0/3/3/3
58	GTP	Cd	703	59	-	3/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
58	CH	701	GTP	C2-N3	2.11	1.38	1.33

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	CH	701	GTP	C5-C4-N3	-4.96	120.50	128.39
58	Cd	703	GTP	C5-C4-N3	-4.81	120.73	128.39
58	Cd	703	GTP	C2-N3-C4	4.58	120.19	112.30
58	CH	701	GTP	C2-N3-C4	4.55	120.13	112.30
58	CH	701	GTP	N9-C4-N3	3.14	132.24	125.95

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	CH	701	GTP	C5'-O5'-PA-O3A
58	CH	701	GTP	C5'-O5'-PA-O1A
58	CH	701	GTP	C5'-O5'-PA-O2A
58	Cd	703	GTP	C5'-O5'-PA-O1A
58	CH	701	GTP	O4'-C4'-C5'-O5'

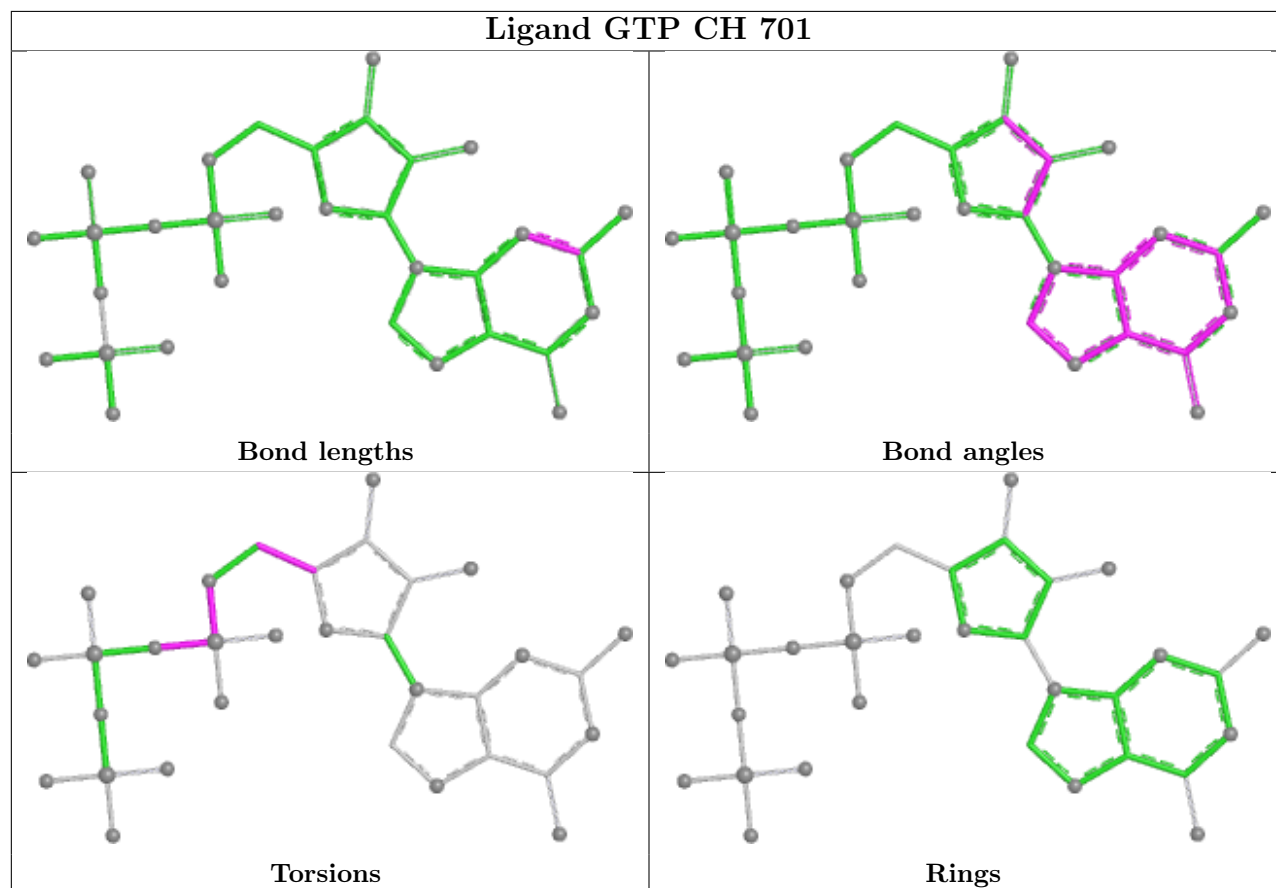
There are no ring outliers.

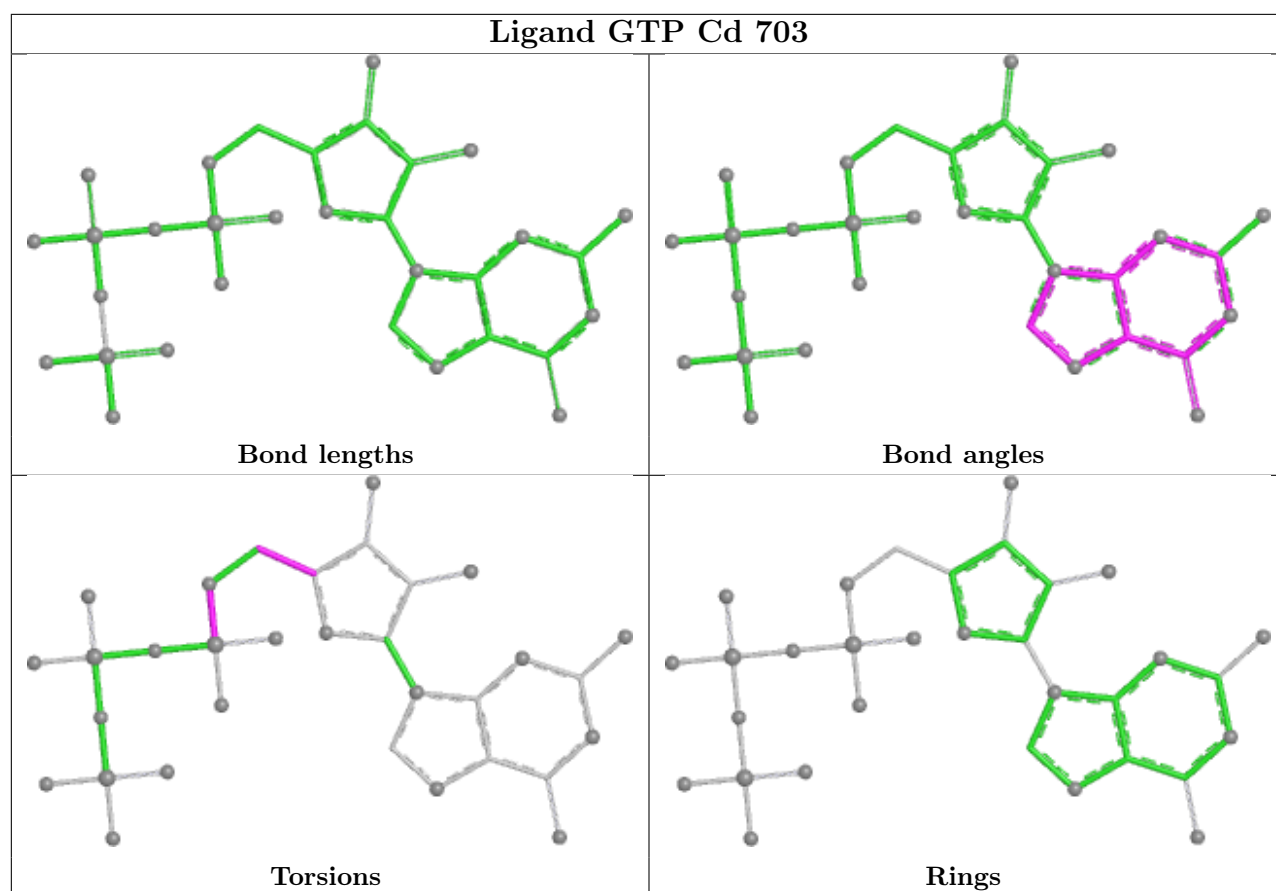
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
58	CH	701	GTP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

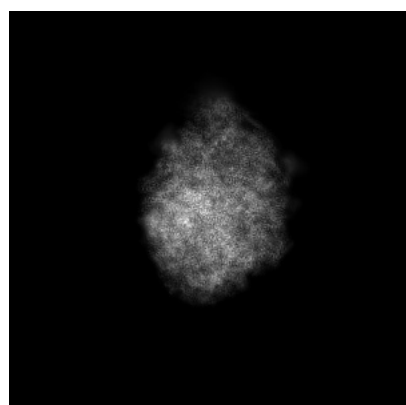
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17970. These allow visual inspection of the internal detail of the map and identification of artifacts.

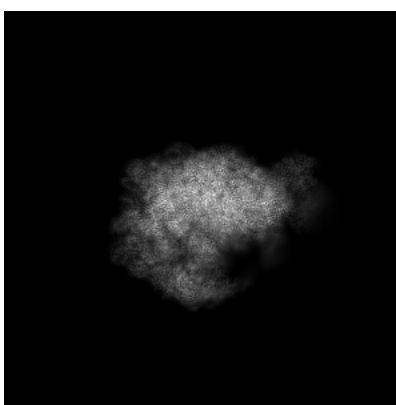
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

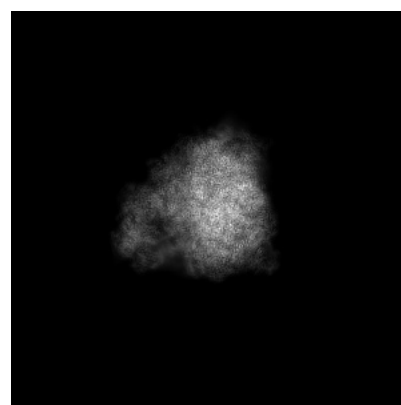
6.1.1 Primary map



X



Y

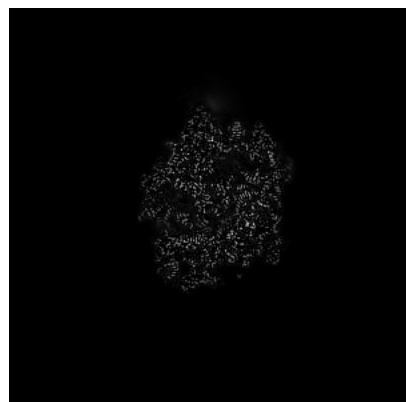


Z

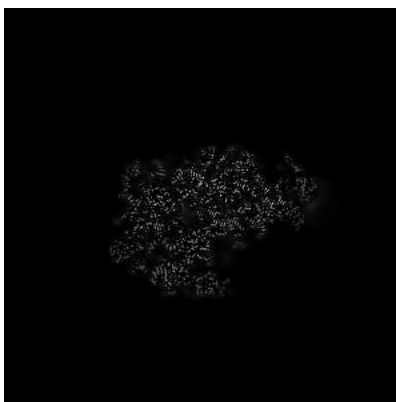
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

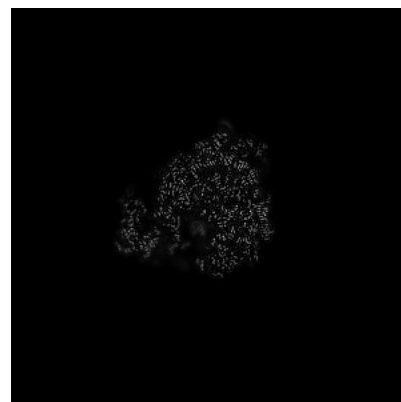
6.2.1 Primary map



X Index: 250



Y Index: 250

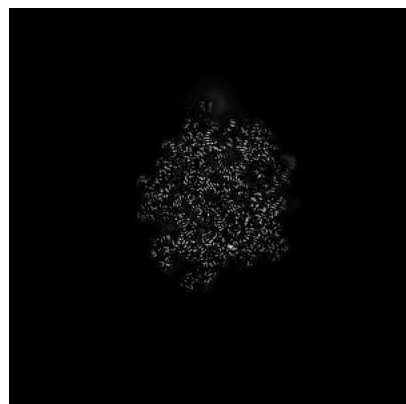


Z Index: 250

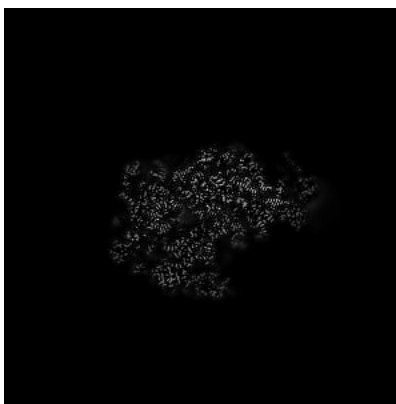
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

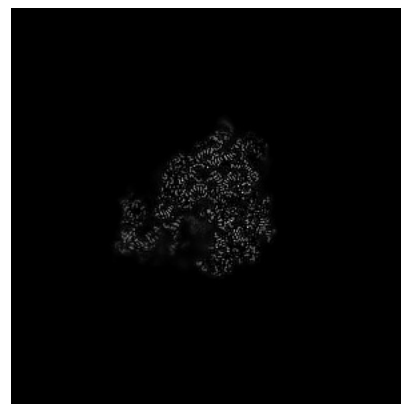
6.3.1 Primary map



X Index: 259



Y Index: 248

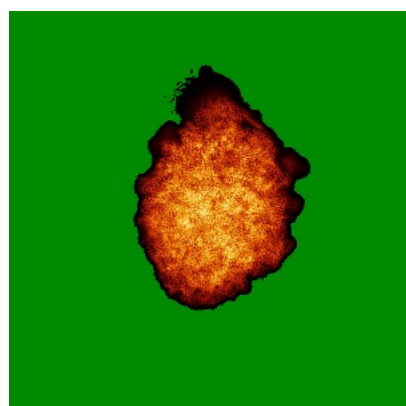


Z Index: 252

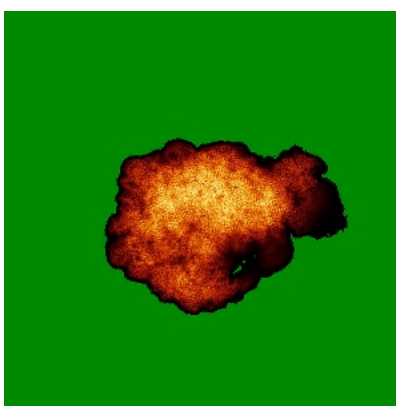
The images above show the largest variance slices of the map in three orthogonal directions.

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

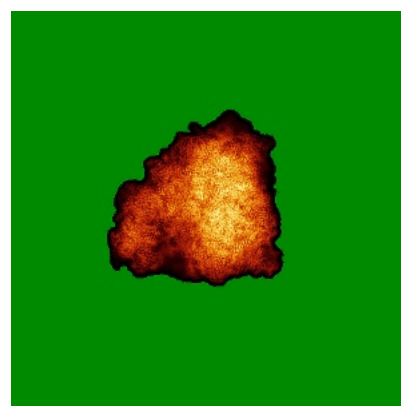
6.4.1 Primary map



X



Y

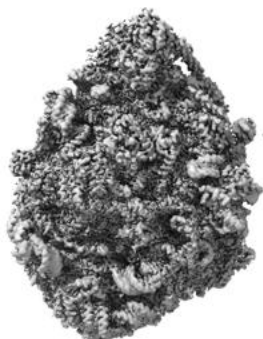


Z

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](#)

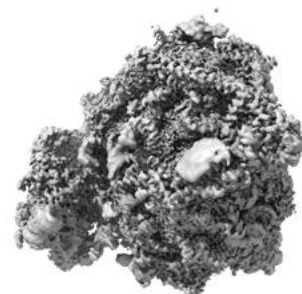
6.5.1 Primary map



X



Y



Z

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.

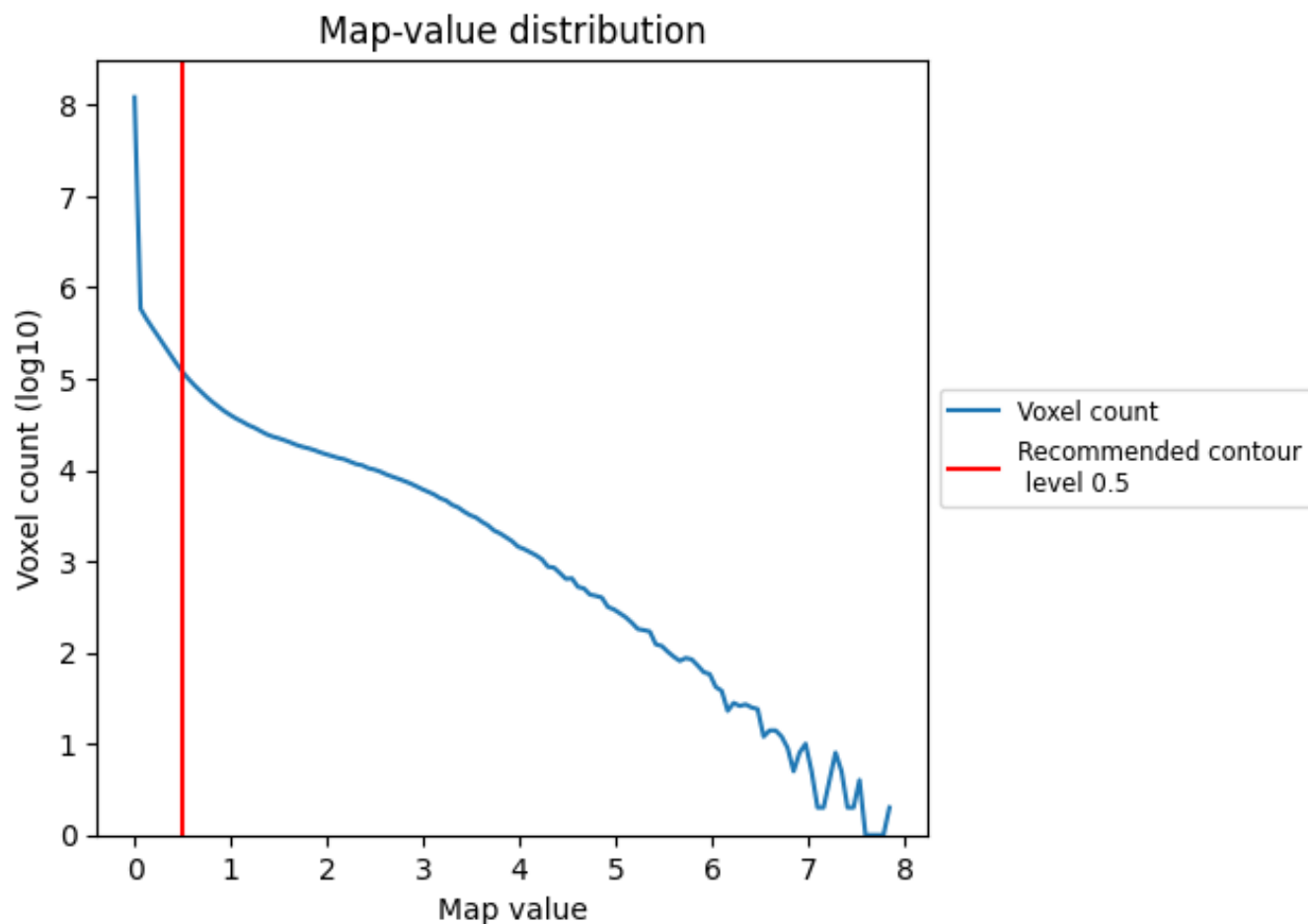
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

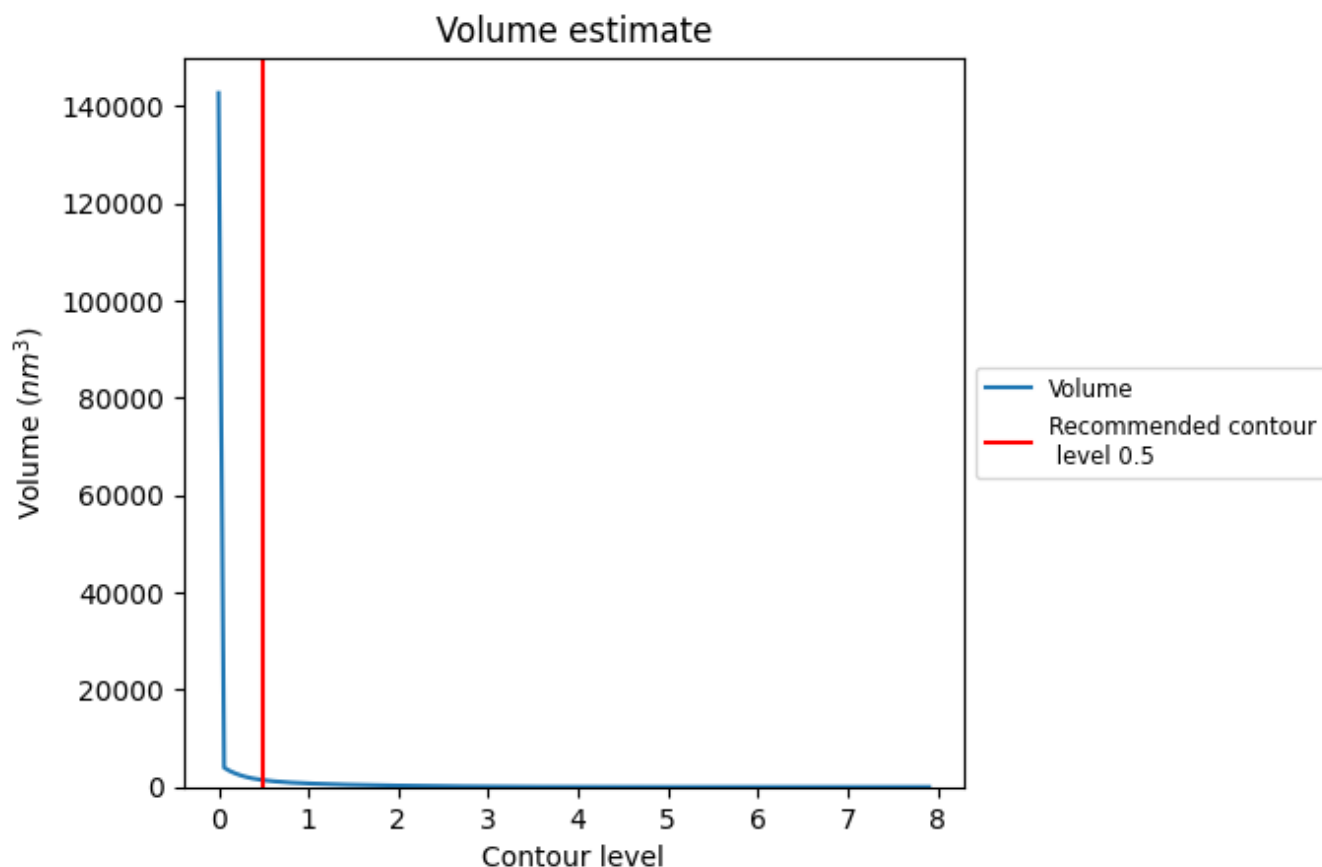
This section contains the results of statistical analysis of the map.

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.

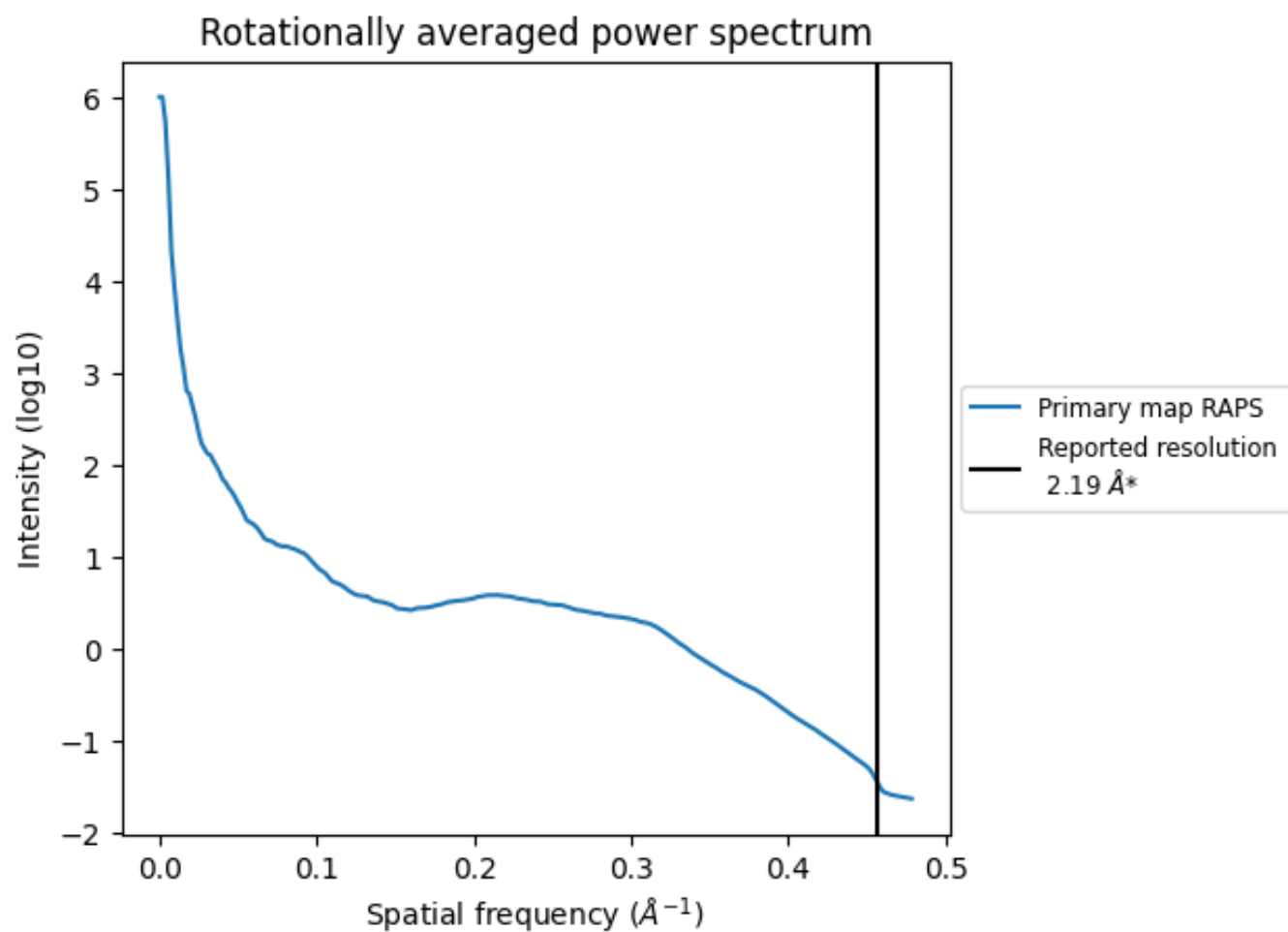
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1395 nm^3 ; this corresponds to an approximate mass of 1260 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 0.457 Å⁻¹

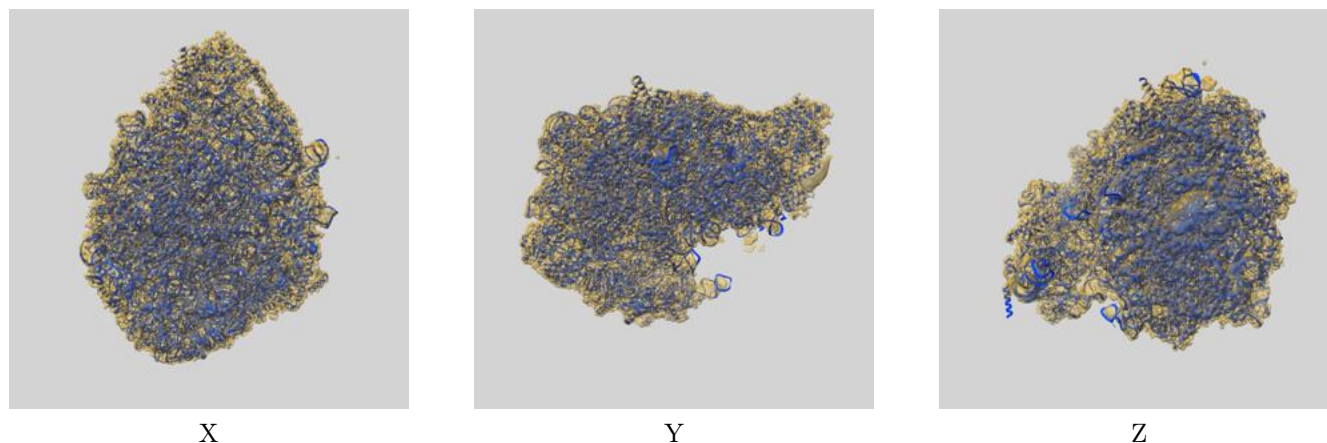
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

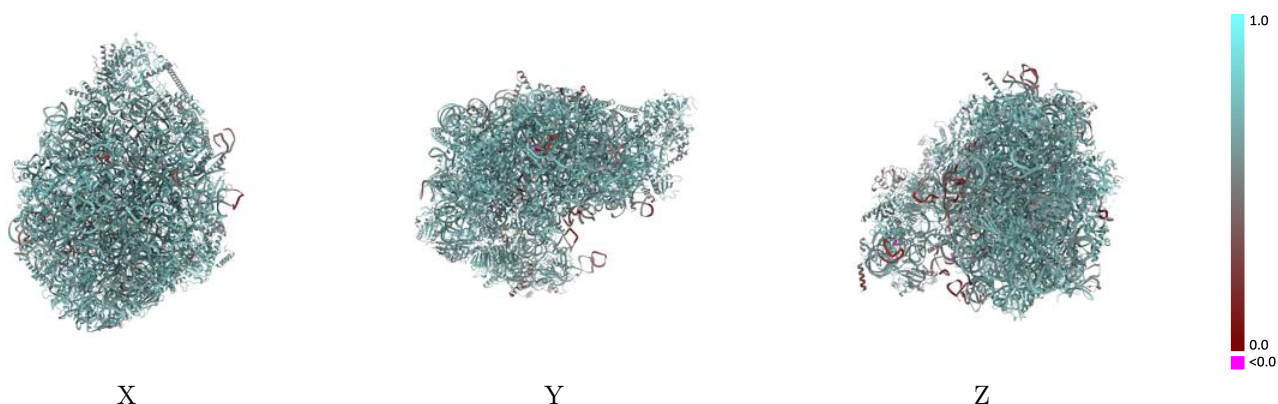
This section contains information regarding the fit between EMDB map EMD-17970 and PDB model 8PVL. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



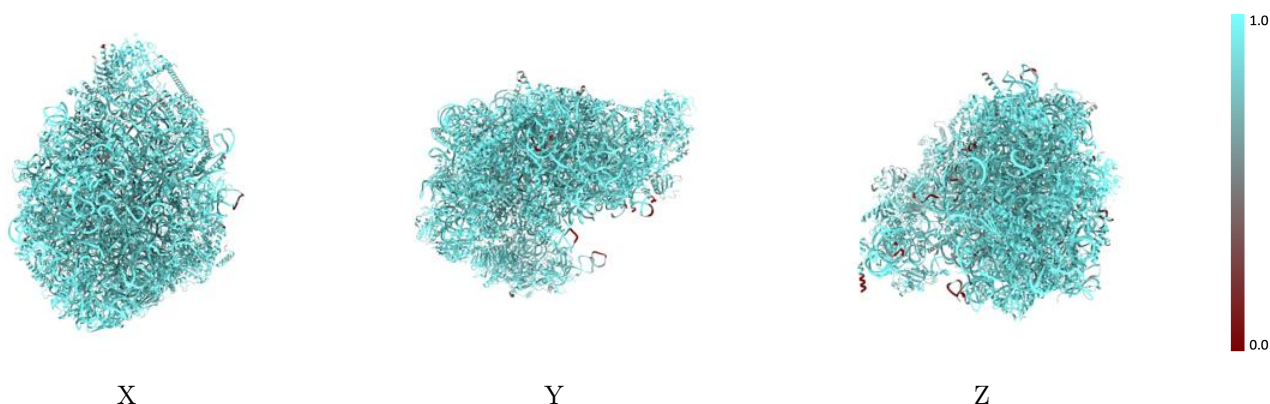
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



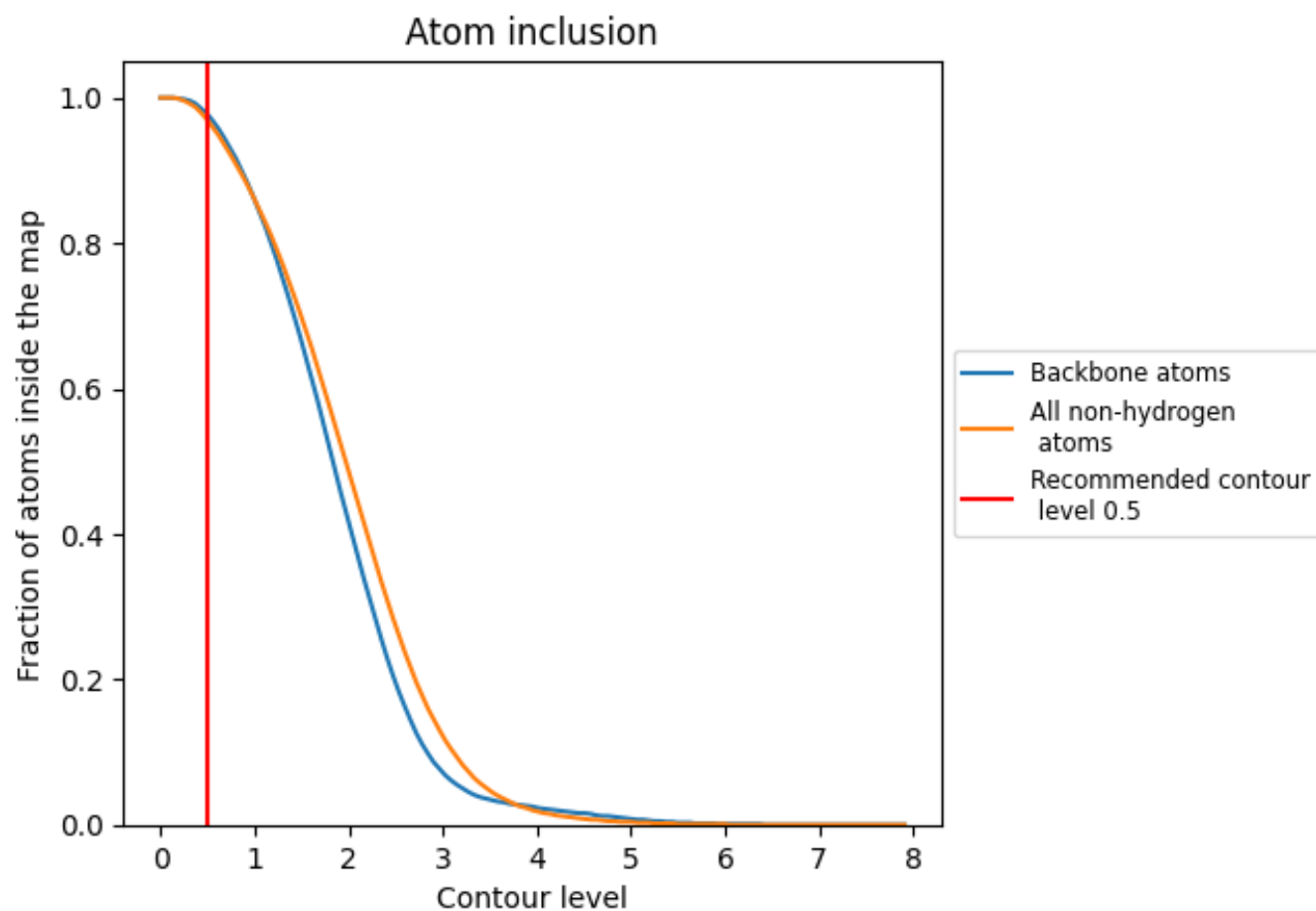
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 98% 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	 0.9690	 0.6620
C1	 0.9800	 0.6510
C2	 0.9780	 0.6760
C3	 0.8670	 0.5710
C4	 0.9330	 0.5790
CF	 0.9470	 0.6370
CH	 0.9490	 0.6660
CI	 0.8830	 0.6030
CJ	 0.9790	 0.6670
CK	 0.9850	 0.7000
CL	 0.9520	 0.6360
CM	 0.9040	 0.6030
CN	 0.9740	 0.6950
CO	 0.9560	 0.6790
CQ	 0.9370	 0.6650
Cb	 0.9850	 0.6930
Cd	 0.9740	 0.6850
Ce	 0.8950	 0.6110
Cf	 0.9650	 0.6480
Cg	 0.9620	 0.6320
Ch	 0.9340	 0.6380
Cz	 0.8850	 0.5770
LA	 0.9890	 0.7000
LB	 0.9890	 0.7190
LC	 0.9860	 0.7170
LD	 0.9390	 0.6360
LE	 0.9590	 0.6730
LF	 0.9740	 0.7010
LG	 0.9700	 0.6730
LH	 0.9690	 0.6870
LJ	 0.9360	 0.5660
LK	 0.9290	 0.6040
LL	 0.9620	 0.6900
LM	 0.9730	 0.6900
LN	 0.9970	 0.7180



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Chain	Atom inclusion	Q-score
LO	 0.9890	 0.7170
LP	 0.9940	 0.7130
LQ	 0.9780	 0.6950
LR	 0.9750	 0.7060
LS	 0.9830	 0.6900
LT	 0.9310	 0.5880
LU	 0.9580	 0.6480
LV	 0.9960	 0.7150
LX	 0.9690	 0.6770
LY	 0.9800	 0.6990
LZ	 0.9740	 0.6880
La	 0.9700	 0.6960
Lc	 0.9610	 0.6770
Ld	 0.9740	 0.7070
Le	 0.9920	 0.7240
Lf	 0.9960	 0.7330
Lg	 0.9430	 0.6850
Lh	 0.9560	 0.6460
Li	 0.9540	 0.6590
Lj	 0.9930	 0.7280
Lk	 0.9370	 0.6590
Ll	 1.0000	 0.7330
Lp	 0.9500	 0.6840
Lq	 0.9720	 0.6880