



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 12:58 AM UTC

PDB ID : 8PVK / pdb_00008pvk
EMDB ID : EMD-17969
Title : Chaetomium thermophilum pre-60S State 5 - pre-5S rotation - L1 inward - composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.55 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:

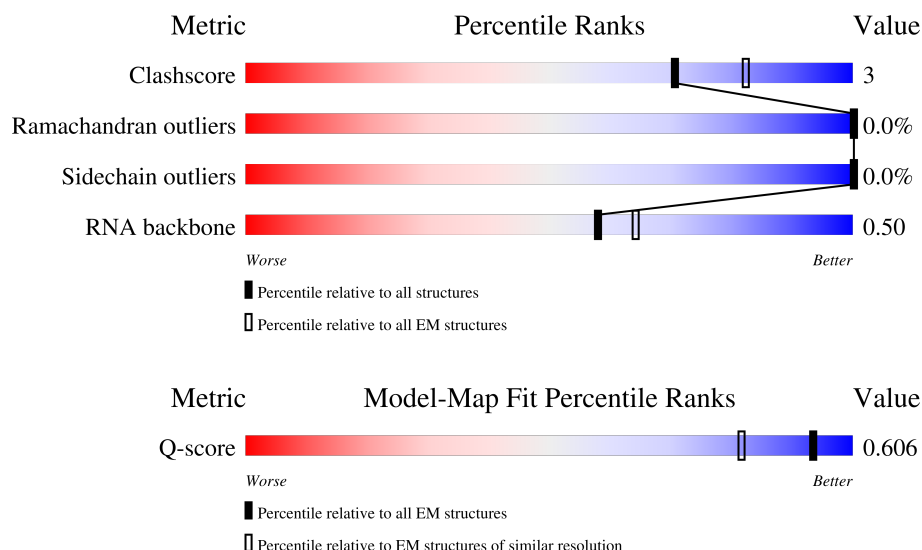
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.55 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.



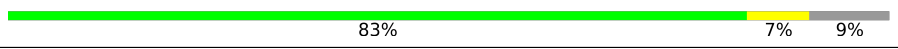
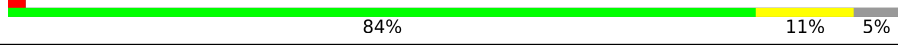
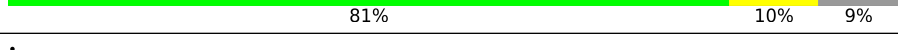
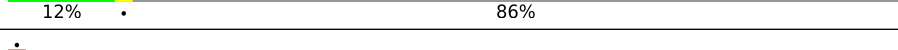
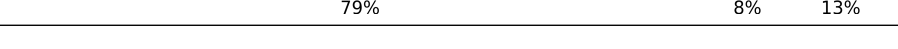
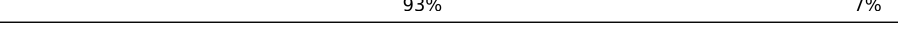
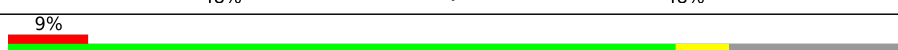
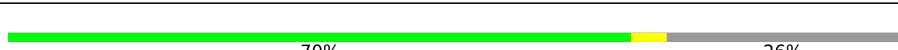
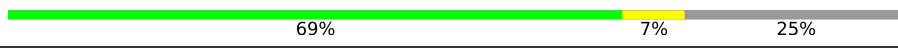
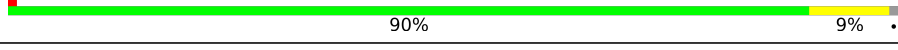
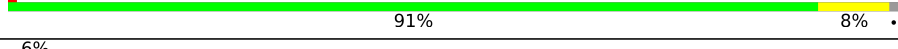
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7475 (2.05 - 3.05)

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	

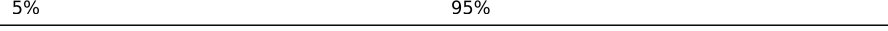
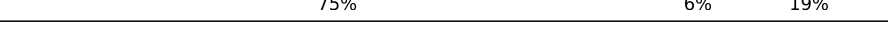
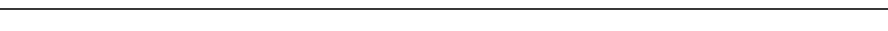
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	C4	119	
5	CB	391	
6	CF	270	
7	CH	661	
8	CI	414	
9	CJ	679	
10	CK	261	
11	CL	558	
12	CM	249	
12	LF	249	
13	CN	246	
14	CO	120	
15	CQ	225	
16	Lq	147	
17	Cb	117	
18	Cd	627	
19	Ce	443	
20	Cf	350	
21	Cg	202	
22	Ch	517	
23	Cz	123	
24	LA	254	
25	LB	392	
26	LC	365	
27	LD	304	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	LE	200	
29	LG	262	
30	LH	229	
31	LJ	173	
32	LK	165	
33	LL	213	
34	LM	142	
35	LN	203	
36	LO	204	
37	LP	187	
38	LQ	213	
39	LR	2898	
40	LS	174	
41	LT	160	
42	LU	127	
43	LV	139	
44	LX	156	
45	LY	138	
46	LZ	135	
47	La	149	
48	Lc	108	
49	Ld	120	
50	Le	131	
51	Lf	109	
52	Lg	119	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
53	Lh	935	
54	Li	110	
55	Lj	95	
56	Lk	94	
57	Ll	51	
58	Lp	92	
59	Lr	217	

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

There are 63 unique types of molecules in this entry. The entry contains 160598 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	3138	Total	C	N	O	P	0	0
			67174	30003	12160	21873	3138		

- 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	82	Total	C	N	O	P	0	0
			1754	780	316	576	82		

- 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 Utp30.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CB	265	Total	C	N	O	S	0	0
			2107	1351	371	382	3		

- Molecule 6 is a protein called Large ribosomal subunit protein uL10.

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

- Molecule 7 is a protein called Nucleolar GTP-binding protein 1.

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

- Molecule 8 is a protein called Putative RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CI	152	Total	C	N	O	S	0	0
			1234	791	230	208	5		

- Molecule 9 is a protein called Pescadillo homolog.

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

- Molecule 10 is a protein called Ribosome biogenesis protein NSA2 homolog.

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

- Molecule 11 is a protein called Putative GTP binding protein.

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

- Molecule 12 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CM	217	Total	C	N	O	S	0	0
			1773	1144	329	297	3		
12	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 13 is a protein called Eukaryotic translation initiation factor 6.

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

- Molecule 14 is a protein called DUF2423 domain-containing protein.

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

- Molecule 15 is a protein called Ribosome biogenesis protein RLP24.

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

- Molecule 16 is a protein called Putative 60S ribosomal protein.

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

- Molecule 17 is a protein called Zinc finger domain-containing protein.

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

- Molecule 18 is a protein called Nucleolar GTP-binding protein 2.

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

- Molecule 19 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Ce	313	Total	C	N	O	S	0	0
			2549	1585	487	473	4		

- Molecule 20 is a protein called Ribosome production factor 2 homolog.

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

- Molecule 21 is a protein called Ribosome biogenesis regulatory protein.

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

- Molecule 22 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ch	485	Total	C	N	O	S	1	0
			3813	2396	697	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 23 is a protein called rRNA-processing protein.

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

- Molecule 24 is a protein called 60S ribosomal protein L2-like protein.

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

- Molecule 25 is a protein called 60S ribosomal protein L3-like protein.

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

- Molecule 26 is a protein called 60S ribosomal protein L4-like protein.

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

- Molecule 27 is a protein called 60S ribosomal protein l5-like protein.

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

- Molecule 28 is a protein called 60S ribosomal protein L6.

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

- Molecule 29 is a protein called 60S ribosomal protein L8.

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

- Molecule 30 is a protein called 60S ribosomal protein l9-like protein.

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

- Molecule 31 is a protein called Putative ribosomal protein.

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

- Molecule 32 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 33 is a protein called 60S ribosomal protein L13.

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

- Molecule 34 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 35 is a protein called Ribosomal protein L15.

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

- Molecule 36 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 37 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 38 is a protein called Ribosomal protein L18-like protein.

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

- Molecule 39 is a protein called Ribosomal protein L19.

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

- Molecule 40 is a protein called 60S ribosomal protein L20.

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

- Molecule 41 is a protein called 60S ribosomal protein l21-like protein.

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

- Molecule 42 is a protein called 60S ribosomal protein L22-like protein.

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

- Molecule 43 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 44 is a protein called 60S ribosomal protein L25-like protein.

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

- Molecule 45 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 46 is a protein called 60S ribosomal protein L27.

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

- Molecule 47 is a protein called 60S ribosomal protein L28-like protein.

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

- Molecule 48 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 49 is a protein called Putative 60S ribosomal protein.

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

- Molecule 50 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 51 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 52 is a protein called Ribosomal protein l34-like protein.

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

- Molecule 53 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

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

- Molecule 55 is a protein called Ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38-like protein.

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

- Molecule 57 is a protein called Ribosomal protein eL39.

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

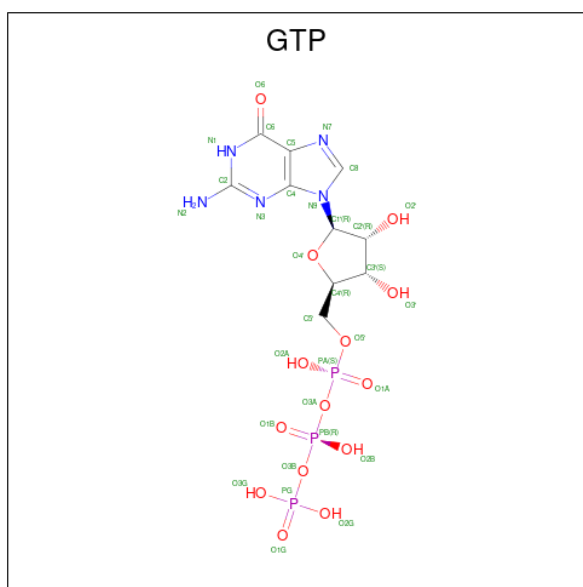
- Molecule 58 is a protein called 60S ribosomal protein L43-like protein.

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

- Molecule 59 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Lr	214	Total	C	N	O	S	0	0
			1660	1056	296	300	8		

- Molecule 60 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

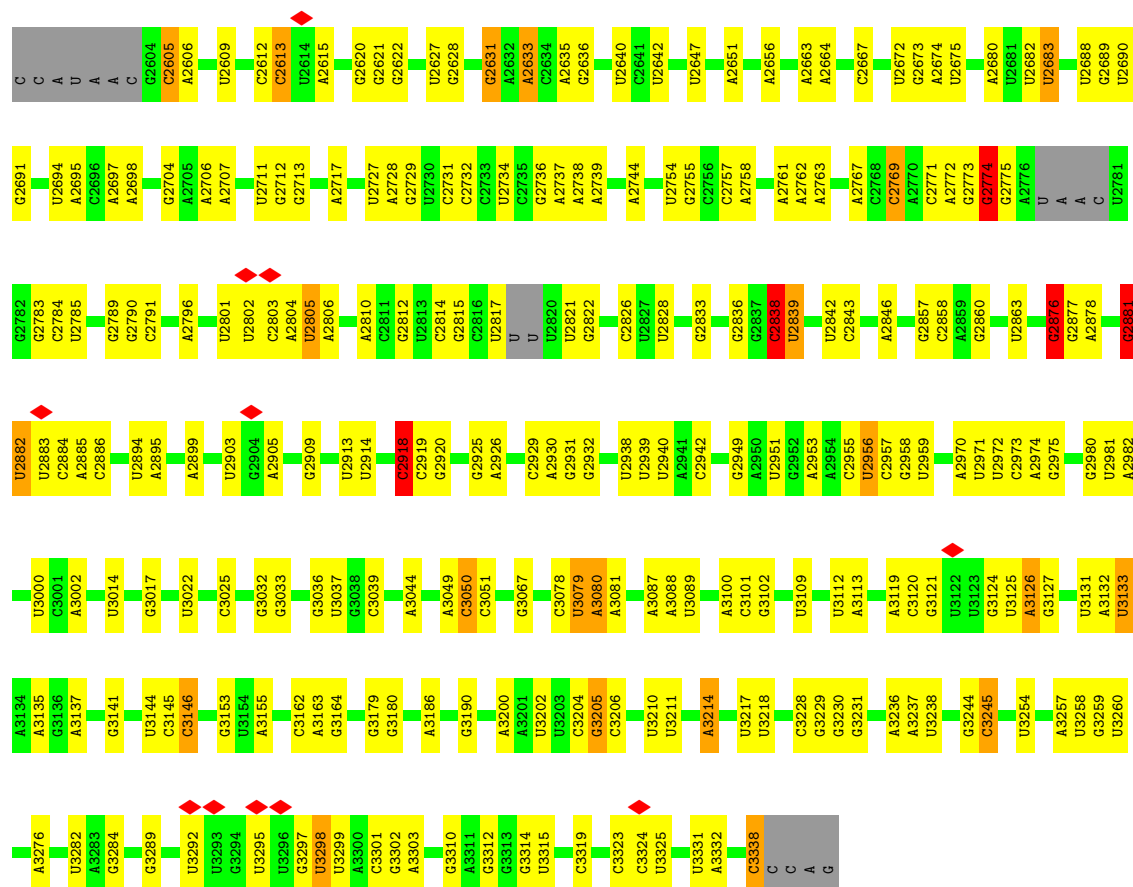
- Molecule 62 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

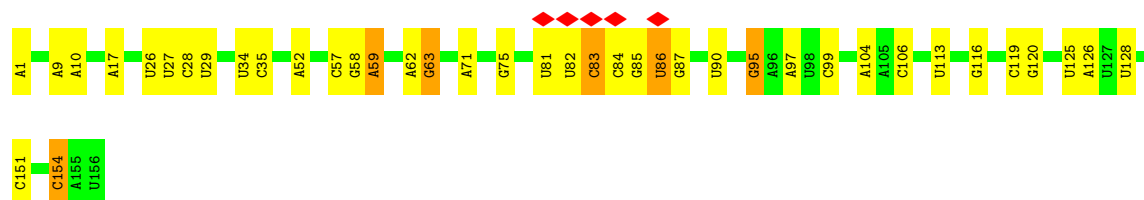
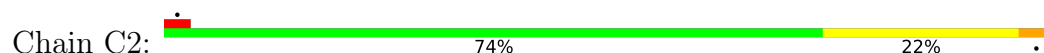
- Molecule 63 is water.

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

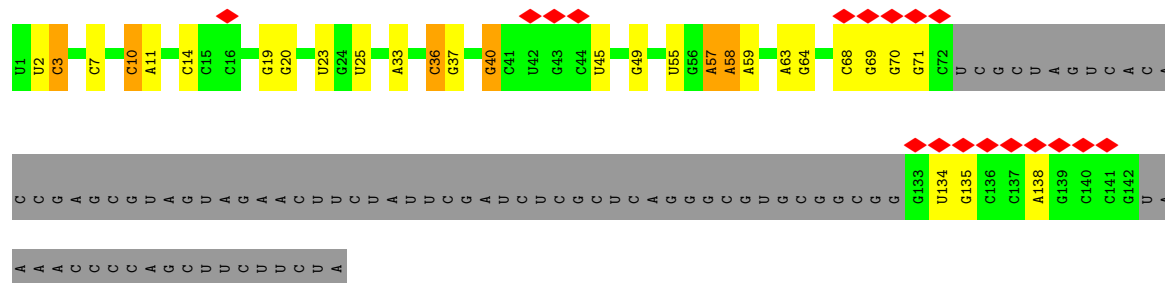
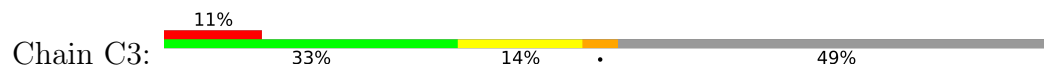
C2499	U2409	U2307	C2230	C2125	G1776	A1623	U1506	G1375	U1241	A1126
U2500	A2410	A2308	U2231	C2126	A1777	C1624	A1517	A1382	U1241	U1127
U2501	G2411	U2314	A	A2130	A1778	U1625	A1518	G1383	A1246	G1128
G2502	G2415	A2315	A	A2131	A1779	G1638	G1519	G1387	U1248	G1132
G2503	U2416	C2317	G	G2132	A1780	A1639	G1526	A1390	A1136	A1137
G2504	U2417	G2318	U2237	U2147	G1783	C1640	U1536	A1395	U1252	C1143
G2505	U2418	A2319	A2243	G2150	G1784	G1642	U1537	G1396	C1255	G1148
G2506	A2419	A2320	U	A2151	G1792	G1646	U1538	A1401	U1264	G1159
G2508	G2420	A2321	G	G2045	A1793	G1647	U1539	A1404	G1265	G1160
G2515	G2327	G2328	C	U2156	A1794	U1661	A1540	G1404	C1266	G1161
G2516	C2329	C2329	U	G2046	A1795	A1676	A1541	G1405	C1267	A1162
A2517	U2423	A2330	C	G2047	U1797	A1677	G1543	G1417	A1269	U1164
G2518	U2424	A2331	G	G2048	U1798	U1681	G1549	A1418	A1270	G1165
A2521	G2425	G2334	C	G2050	U1799	U1682	U1550	U1419	G1278	
A2522	G2426	U2427	U	G2051	C1800	U1685	G1551	G1420	G1283	
G2523	U2427	G2340	A	U2052	U1801	U1685	U1552	U1421	A1287	
G2524	G2428	A2348	U	G2053	U1802	U1697	G1553	U1422	U1174	
C2527	A2431	G2355	C	A2054	U1803	C1697	G1554	U1425	A1175	
G2533	G2432	U2434	U	A2055	A1809	A1698	G1559	U1429	U1288	
G2544	G2433	G2356	C	A2056	G1812	G1699	U1560	A1430	G1289	
G2545	U2434	G2357	A	U2057	G1813	U1704	G1563	U1431	G1290	
A2552	U2435	G2358	U	G2058	A1814	G1707	A1567	A1432	U1291	
G2556	G2436	G2359	G	G2059	A1815	U1710	A1568	G1434	U1292	
G2557	G2437	G2362	U	U2060	A1816	G1722	A1572	U1438	U1305	
G2562	G2438	A2364	A	A2061	A1822	U1726	G1576	U1449	A1313	
G2565	G2439	G2365	C	G2062	C1826	A1730	G1577	U1454	G1316	
G2566	G2440	A2366	C	A2063	U1827	G1731	G1578	G1458	A1331	
G2567	G2441	G2368	U	G2064	C1828	G1737	A1585	G1459	G1332	
G2568	U2442	U2373	C	G2065	A1830	U1842	U1586	A1460	A1333	
G2569	G2443	G2375	G	G2066	C1833	G1843	U1587	G1463	A1334	
G2570	G2444	A2376	C	A2067	A1834	G1844	C1588	A1464	A1335	
G2571	G2445	G2377	A	G2068	A1845	G1845	U1595	G1465	G1337	
G2575	A2454	U2380	A	A2069	C1846	U1744	U1596	G1466	A1211	
U2576	G2455	G2381	U2276	U2092	A1847	U1745	G1604	G1476	A1214	
U2577	U2456	A2382	U2277	G2093	U1851	G1746	U1609	G1480	C1215	
U2578	A2457	G2383	G2278	A2100	U1856	G1751	G1610	A1481	G1220	
G2579	C2458	U2384	G2279	A2101	G1857	G1758	C1611	G1485	A1223	
G2582	U2459	G2389	U2281	U2102	U1859	C1759	G1614	G1486	A1228	
G2583	G2465	A2392	A2282	U2103	U1860	C1761	G1615	C1481	A1234	
G2584	G2466	A2393	A2283	U2104	A1866	U1762	A1618	G1492	C1238	
G2585	U2472	G2398	A2284	A2105	A1867	G1763	C1619	G1493	G1372	
G2586	U2473	A2404	A2285	A2112	U1868	G1766		U1505		
G2587	A2474	G2405	U2287	U2117	A1871					
G2588	U2475	A2406	U2288	G2118						
G2589	U2476	G2407	U2289	G2119						
G2590	U2477	A2408	C2301	A2121						
G2591	U2478		U2290	U2122						
G2592	U2479		C2302	G2123						
G2593	U2480		U2291	G2124						
G2594	U2481		U2292							
G2595	U2482		U2293							
G2596	U2483		U2294							
G2597	U2484		U2295							
G2598	U2485		U2296							
G2599	U2486		U2297							
G2600	U2487		U2298							
G2601	U2488		U2299							
G2602	U2489		U2300							
G2603	U2490		U2301							
G2604	U2491		U2302							
G2605	U2492		U2303							
G2606	U2493		U2304							
G2607	U2494		U2305							
G2608	U2495		U2306							
G2609	U2496		U2307							
G2610	U2497		U2308							
G2611	U2498		U2309							
G2612	U2499		U2310							
G2613	U2500		U2311							
G2614	U2501		U2312							
G2615	U2502		U2313							
G2616	U2503		U2314							
G2617	U2504		U2315							
G2618	U2505		U2316							
G2619	U2506		U2317							
G2620	U2507		U2318							
G2621	U2508		U2319							
G2622	U2509		U2320							
G2623	U2510		U2321							
G2624	U2511		U2322							
G2625	U2512		U2323							
G2626	U2513		U2324							
G2627	U2514		U2325							
G2628	U2515		U2326							
G2629	U2516		U2327							
G2630	U2517		U2328							
G2631	U2518		U2329							
G2632	U2519		U2330							
G2633	U2520		U2331							
G2634	U2521		U2332							
G2635	U2522		U2333							
G2636	U2523		U2334							
G2637	U2524		U2335							
G2638	U2525		U2336							
G2639	U2526		U2337							
G2640	U2527		U2338							
G2641	U2528		U2339							
G2642	U2529		U2340							
G2643	U2530		U2341							
G2644	U2531		U2342							
G2645	U2532		U2343							
G2646	U2533		U2344							
G2647	U2534		U2345							
G2648	U2535		U2346							
G2649	U2536		U2347							
G2650	U2537		U2348							
G2651	U2538		U2349							
G2652	U2539		U2350							
G2653	U2540		U2351							
G2654	U2541		U2352							
G2655	U2542		U2353							
G2656	U2543		U2354							
G2657	U2544		U2355							
G2658	U2545		U2356							
G2659	U2546		U2357							
G2660	U2547		U2358							
G2661	U2548		U2359							
G2662	U2549		U2360							
G2663	U2550		U2361							
G2664	U2551		U2362							
G2665	U2552		U2363							
G2666	U2553		U2364							
G2667	U2554		U2365							
G2668	U2555		U2366							
G2669	U2556		U2367							
G2670	U2557		U2368							
G2671	U2558		U2369							
G2672	U2559		U2370							
G2673	U2560		U2371							
G2674	U2561		U2372							
G2675	U2562		U2373							
G2676	U2563		U2374							
G2677	U2564		U2375							
G2678	U2565		U2376							
G2679	U2566		U2377							
G2680	U2567		U2378							
G2681	U2568		U2379							
G2682	U2569		U2380							
G2683	U2570		U2381							
G2684	U2571		U2382							
G2685	U2572		U2383							
G2686	U2573		U2384							
G2687	U2574		U2385							
G2688	U2575		U2386							
G2689	U2576		U2387							
G2690	U2577		U2388							
G2691	U2578		U2389							
G2692	U2579		U2390							
G2693	U2580		U2391							
G2694	U2581		U2392							
G2695	U2582		U2393							
G2696	U2583		U2394							
G2697	U2584		U2395							
G2698	U2585		U2396							
G2699	U2586		U2397							
G2700	U2587		U2398							
G2701	U2588		U2399							
G2702	U2589		U2400							
G2703	U2590		U2401							
G2704	U2591		U2402							
G2705	U2592		U2							



- Molecule 2: 5.8S rRNA



- Molecule 3: ITS2



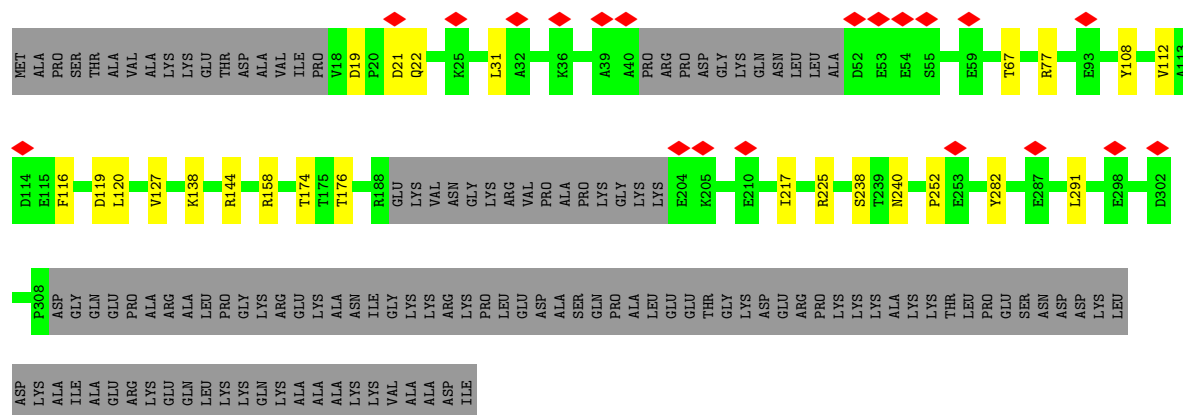
- Molecule 4: 5S rRNA

Chain C4: 



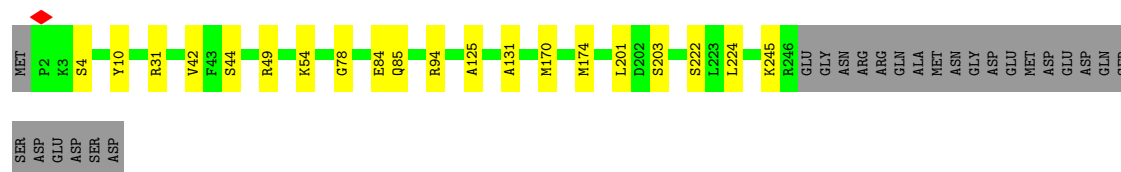
• Molecule 5: Utp30

Chain CB: 



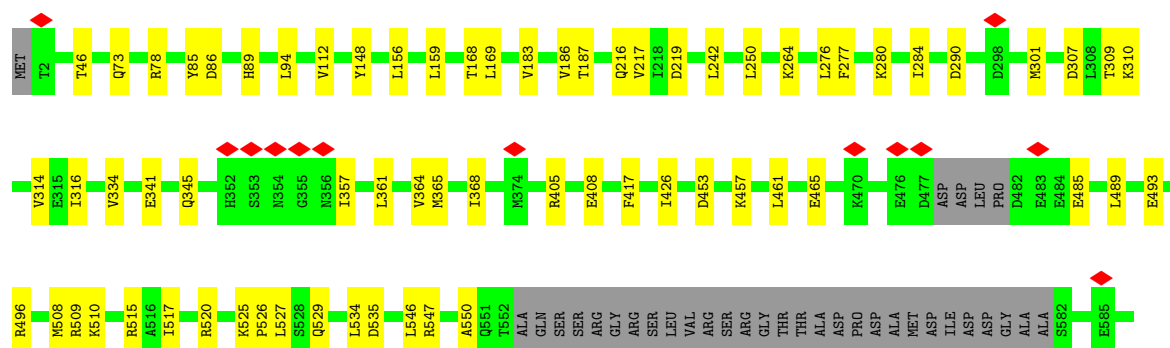
• Molecule 6: Large ribosomal subunit protein uL10

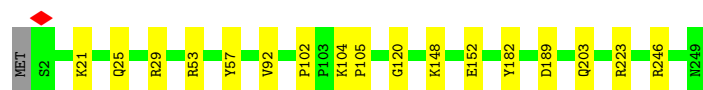
Chain CF: 



• Molecule 7: Nucleolar GTP-binding protein 1

Chain CH: 





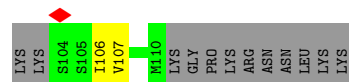
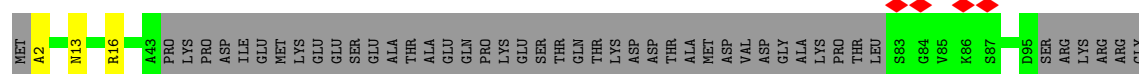
- Molecule 13: Eukaryotic translation initiation factor 6

Chain CN: 88% 12%



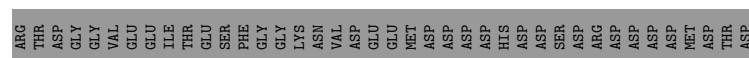
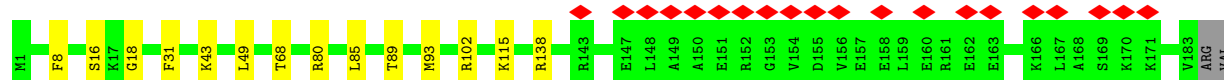
- Molecule 14: DUF2423 domain-containing protein

Chain CO: 48% 48%



- Molecule 15: Ribosome biogenesis protein RLP24

Chain CQ: 9% 75% 6% 19%



- Molecule 16: Putative 60S ribosomal protein

Chain Lq: 85% 10% 5%



- Molecule 17: Zinc finger domain-containing protein

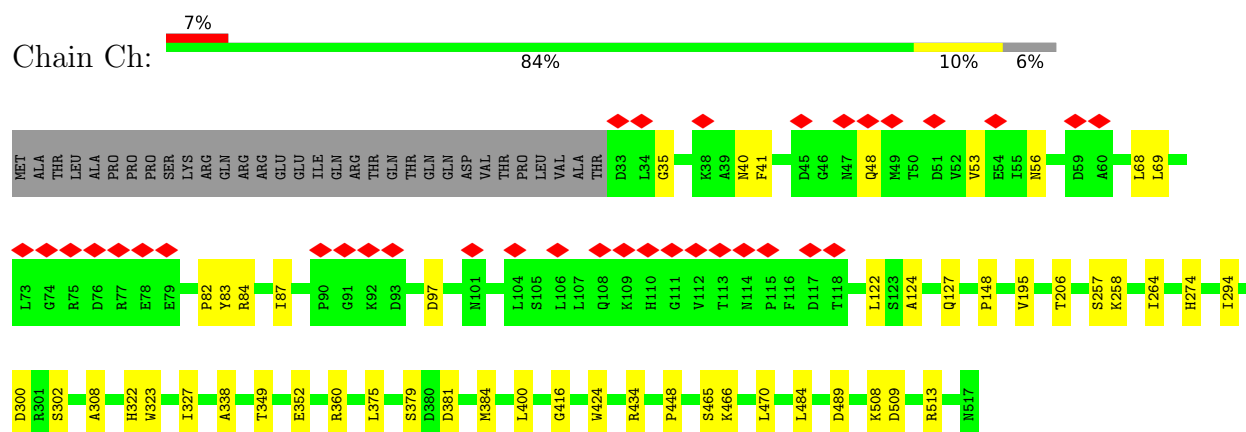
Chain Cb: 79% 8% 14%



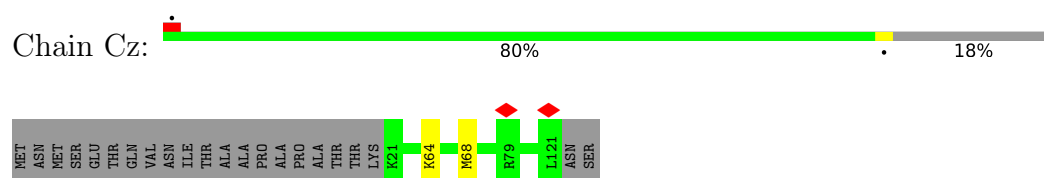
- Molecule 18: Nucleolar GTP-binding protein 2

Chain Cd: 70% 26%

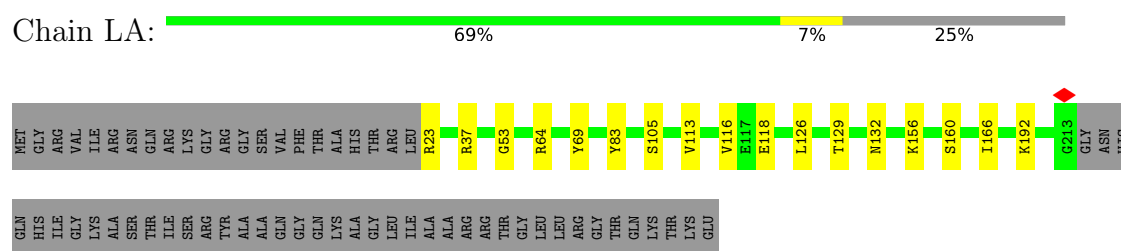
- Molecule 22: Ribosome assembly protein 4



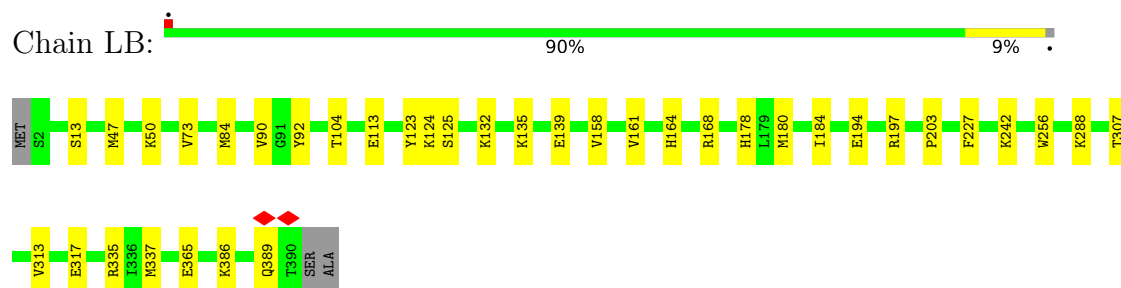
- Molecule 23: rRNA-processing protein



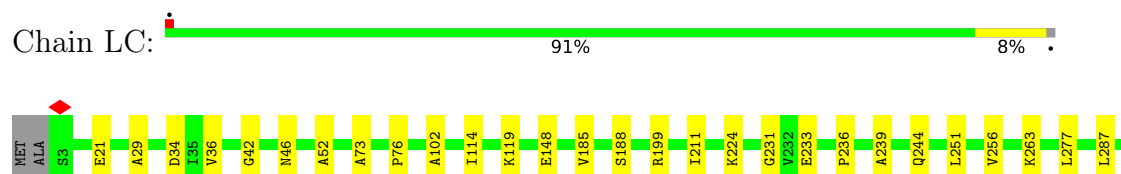
- Molecule 24: 60S ribosomal protein L2-like protein



- Molecule 25: 60S ribosomal protein L3-like protein

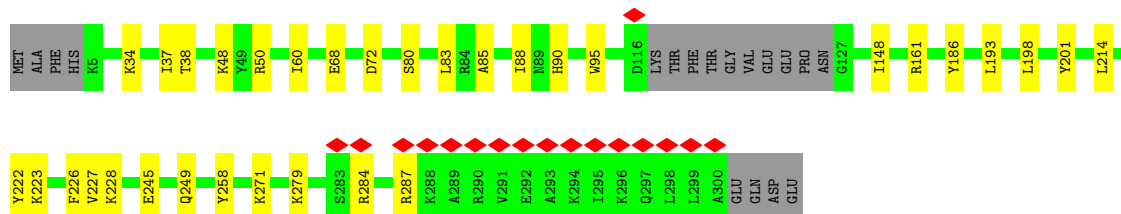
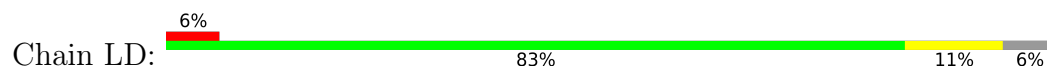


- Molecule 26: 60S ribosomal protein L4-like protein

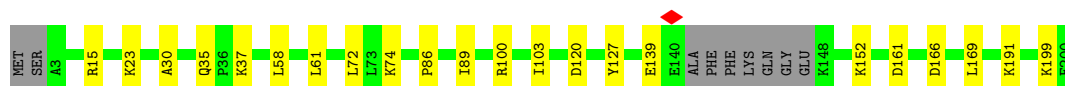
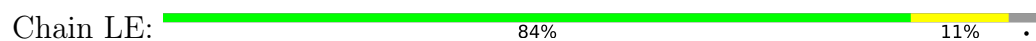




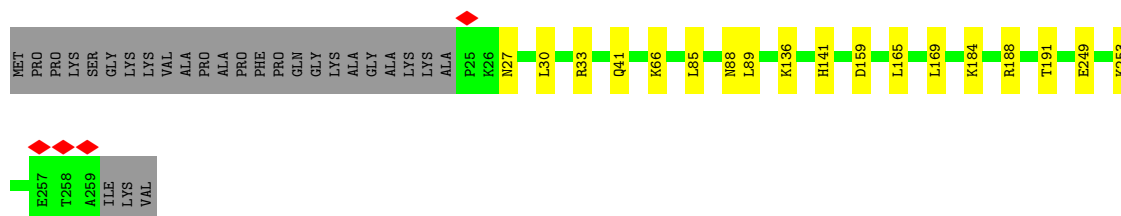
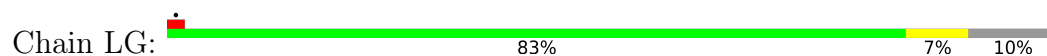
- Molecule 27: 60S ribosomal protein l5-like protein



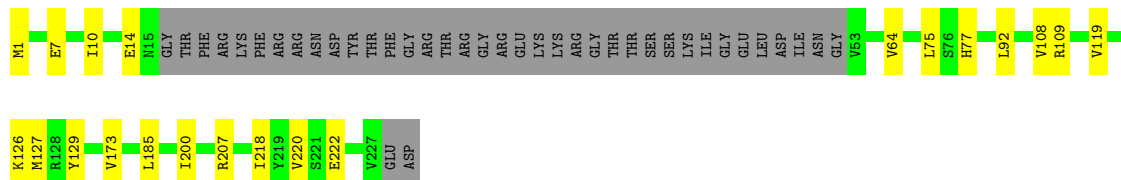
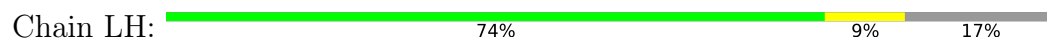
- Molecule 28: 60S ribosomal protein L6



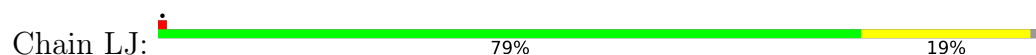
- Molecule 29: 60S ribosomal protein L8

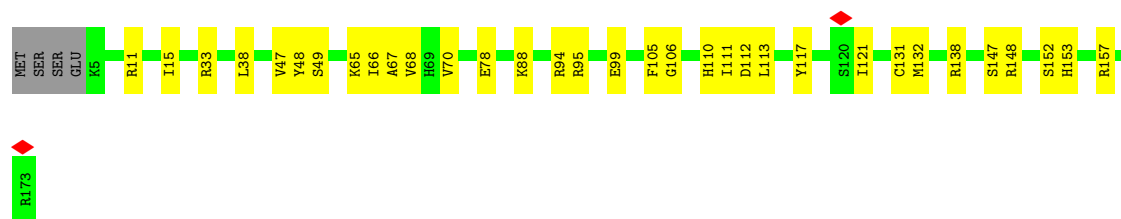


- Molecule 30: 60S ribosomal protein l9-like protein



- Molecule 31: Putative ribosomal protein

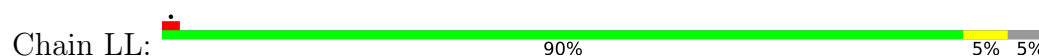




- Molecule 32: 60S ribosomal protein L12-like protein



- Molecule 33: 60S ribosomal protein L13



- Molecule 34: 60S ribosomal protein L14-like protein



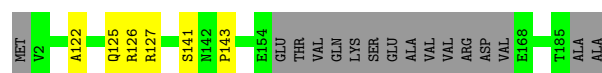
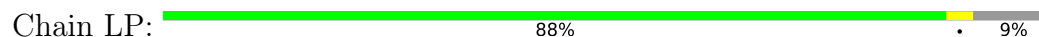
- Molecule 35: Ribosomal protein L15

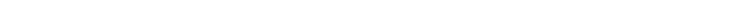


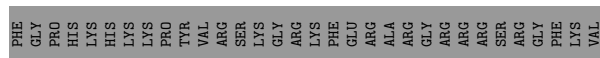
- Molecule 36: 60S ribosomal protein L16-like protein

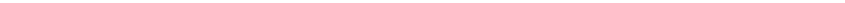


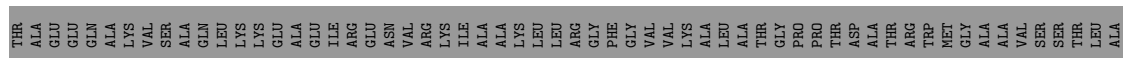
- Molecule 37: 60S ribosomal protein l17-like protein



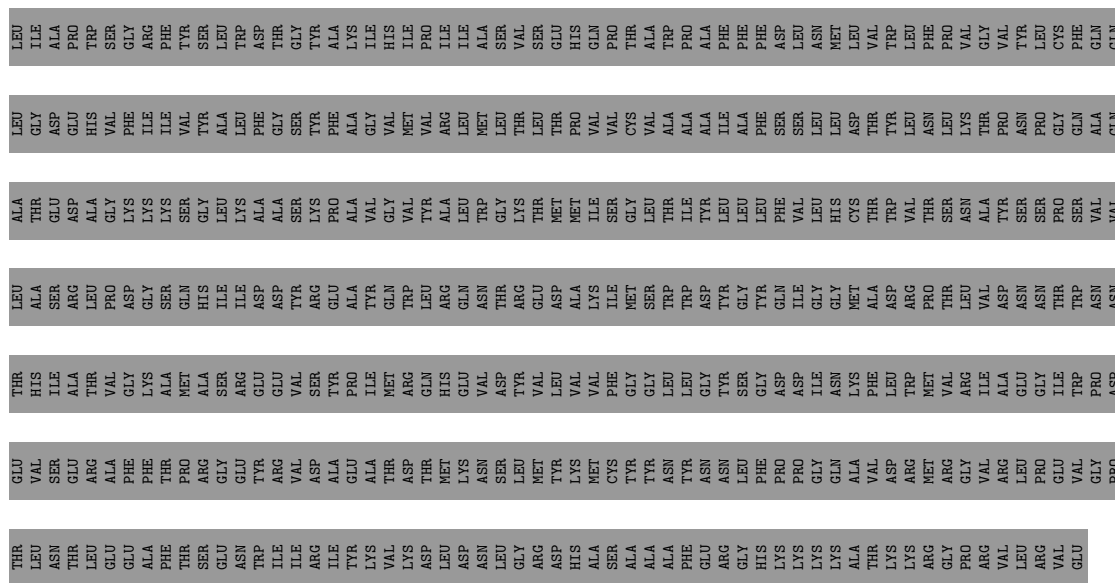
- Chain LQ: 



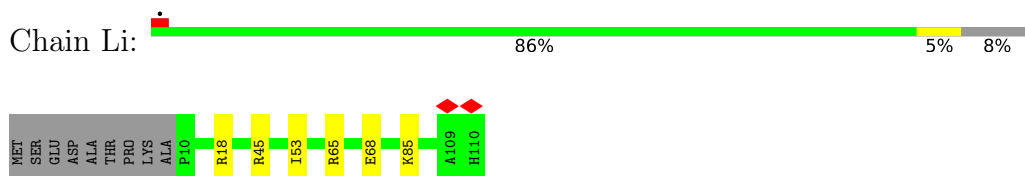
- Chain LR:  5% 95%



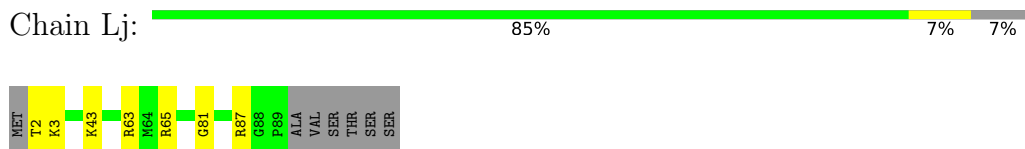




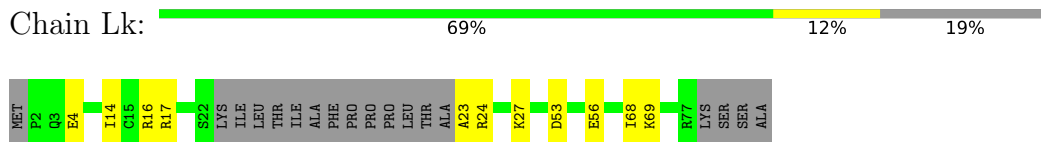
- Molecule 54: 60S ribosomal protein L36



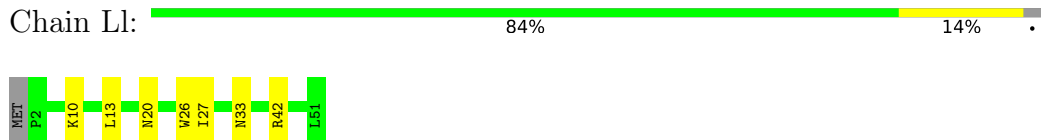
- Molecule 55: Ribosomal protein L37



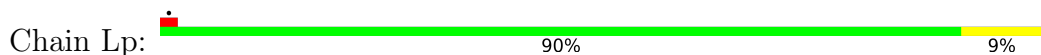
- Molecule 56: 60S ribosomal protein L38-like protein



- Molecule 57: Ribosomal protein eL39

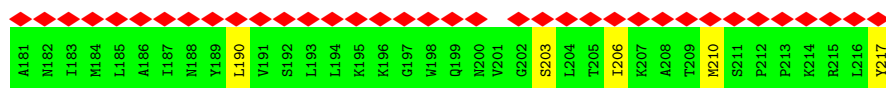
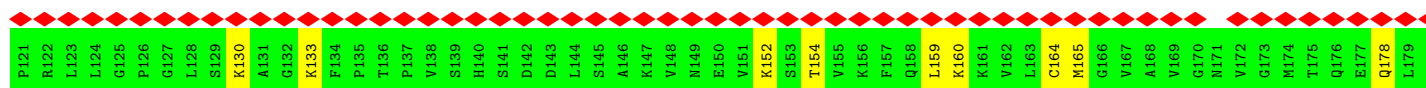
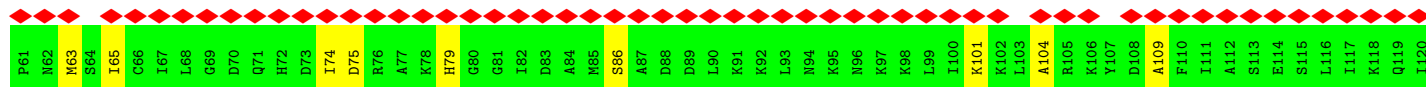
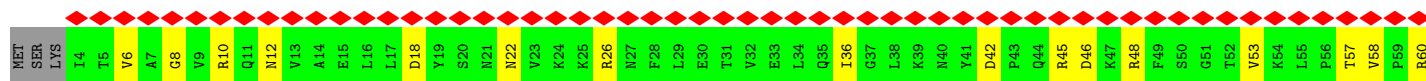
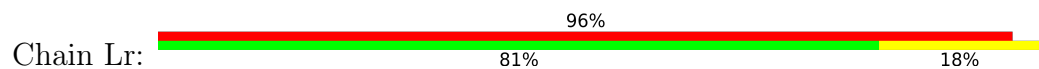


- Molecule 58: 60S ribosomal protein L43-like protein





• Molecule 59: Ribosomal protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74129	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	8.766	Depositor
Minimum map value	0.000	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.167	Depositor
Recommended contour level	0.6	Depositor
Map size ($\text{\AA}$)	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 ($\text{\AA}$)	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: GTP, OMC, ZN, OMG, MG, OMU, A2M

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	0.16	1/74323 (0.0%)	0.33	0/115881
2	C2	0.14	0/3710	0.30	0/5778
3	C3	0.13	0/1958	0.30	0/3050
4	C4	0.16	0/2833	0.35	0/4414
5	CB	0.15	0/2153	0.37	0/2926
6	CF	0.14	0/1972	0.34	0/2660
7	CH	0.16	0/5147	0.38	0/6926
8	CI	0.20	0/1265	0.60	4/1702 (0.2%)
9	CJ	0.15	0/3196	0.33	0/4319
10	CK	0.14	0/1939	0.34	0/2608
11	CL	0.14	0/631	0.30	0/843
12	CM	0.15	0/1805	0.38	1/2417 (0.0%)
12	LF	0.17	0/2061	0.38	0/2765
13	CN	0.14	0/1878	0.38	0/2555
14	CO	0.14	0/470	0.32	0/619
15	CQ	0.18	0/1504	0.38	0/2000
16	Lq	0.15	0/1091	0.36	0/1468
17	Cb	0.18	0/845	0.46	0/1128
18	Cd	0.15	0/3770	0.36	0/5082
19	Ce	0.16	0/2579	0.37	0/3434
20	Cf	0.14	0/2326	0.35	0/3113
21	Cg	0.16	0/1508	0.37	0/2051
22	Ch	0.14	0/3914	0.40	0/5319
23	Cz	0.17	0/877	0.33	0/1148
24	LA	0.15	0/1488	0.39	0/2009
25	LB	0.14	0/3172	0.37	0/4260
26	LC	0.14	0/2808	0.34	0/3785
27	LD	0.14	0/2308	0.33	0/3105
28	LE	0.13	0/1504	0.30	0/2027
29	LG	0.15	0/1918	0.35	0/2565
30	LH	0.14	0/1515	0.38	0/2037
31	LJ	0.15	0/1379	0.43	0/1844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LK	0.17	0/1198	0.41	0/1611
33	LL	0.16	0/1614	0.37	0/2168
34	LM	0.16	0/1145	0.34	0/1539
35	LN	0.15	0/1741	0.37	0/2332
36	LO	0.17	0/1645	0.41	1/2205 (0.0%)
37	LP	0.15	0/1364	0.38	0/1835
38	LQ	0.15	0/1218	0.37	0/1639
39	LR	0.13	0/1260	0.31	0/1683
40	LS	0.14	0/1461	0.37	0/1966
41	LT	0.16	0/1046	0.41	0/1409
42	LU	0.13	0/859	0.36	0/1151
43	LV	0.13	0/1009	0.36	0/1357
44	LX	0.16	0/1151	0.39	0/1547
45	LY	0.17	0/1070	0.45	0/1432
46	LZ	0.13	0/1135	0.33	0/1519
47	La	0.14	0/892	0.33	0/1200
48	Lc	0.14	0/714	0.34	0/960
49	Ld	0.15	0/889	0.32	0/1192
50	Le	0.15	0/1035	0.36	0/1379
51	Lf	0.12	0/883	0.30	0/1187
52	Lg	0.15	0/927	0.36	0/1244
53	Lh	0.17	0/1014	0.39	0/1349
54	Li	0.15	0/834	0.35	0/1099
55	Lj	0.16	0/712	0.39	0/944
56	Lk	0.15	0/640	0.36	0/850
57	Ll	0.13	0/446	0.27	0/593
58	Lp	0.13	0/706	0.40	0/940
59	Lr	0.14	0/1684	0.37	0/2266
All	All	0.16	1/170139 (0.0%)	0.35	6/246434 (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
53	Lh	0	1
56	Lk	0	1
All	All	36	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	848	A2M	O3'-P	5.15	1.61	1.56

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	CI	310	GLU	CA-C-N	-6.13	110.40	121.14
8	CI	310	GLU	C-N-CA	-6.13	110.40	121.14
8	CI	310	GLU	N-CA-CB	6.05	119.65	110.28
8	CI	311	GLN	N-CA-CB	5.32	119.08	110.40
12	CM	78	GLN	CB-CA-C	-5.15	110.22	117.23

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 (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	Lh	16	ASN	Peptide
56	Lk	16	ARG	Sidechain

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	67174	0	33866	417	0
2	C2	3319	0	1678	23	0
3	C3	1754	0	890	17	0
4	C4	2536	0	1286	28	0
5	CB	2107	0	2161	17	0
6	CF	1934	0	1945	13	0
7	CH	5063	0	5157	44	0
8	CI	1234	0	1245	13	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	CJ	3116	0	3122	27	0
10	CK	1903	0	1990	17	0
11	CL	622	0	641	8	0
12	CM	1773	0	1879	10	0
12	LF	2023	0	2132	11	0
13	CN	1853	0	1852	18	0
14	CO	468	0	503	3	0
15	CQ	1480	0	1523	11	0
16	Lq	1073	0	1130	11	0
17	Cb	830	0	838	6	0
18	Cd	3691	0	3817	19	0
19	Ce	2549	0	2660	22	0
20	Cf	2282	0	2347	26	0
21	Cg	1478	0	1517	12	0
22	Ch	3813	0	3715	27	0
23	Cz	869	0	956	2	0
24	LA	1454	0	1490	11	0
25	LB	3104	0	3221	24	0
26	LC	2751	0	2875	25	0
27	LD	2266	0	2219	22	0
28	LE	1477	0	1567	16	0
29	LG	1889	0	2043	13	0
30	LH	1495	0	1573	13	0
31	LJ	1357	0	1385	23	0
32	LK	1184	0	1249	6	0
33	LL	1587	0	1655	9	0
34	LM	1126	0	1198	12	0
35	LN	1704	0	1767	15	0
36	LO	1611	0	1702	12	0
37	LP	1343	0	1369	5	0
38	LQ	1200	0	1296	11	0
39	LR	1241	0	1298	9	0
40	LS	1426	0	1481	17	0
41	LT	1027	0	1076	7	0
42	LU	846	0	883	3	0
43	LV	991	0	1044	11	0
44	LX	1133	0	1234	8	0
45	LY	1056	0	1143	13	0
46	LZ	1112	0	1181	11	0
47	La	872	0	903	8	0
48	Lc	705	0	751	3	0
49	Ld	875	0	918	5	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	Le	1017	0	1092	9	0
51	Lf	862	0	891	9	0
52	Lg	914	0	960	4	0
53	Lh	1003	0	1116	7	0
54	Li	827	0	906	5	0
55	Lj	698	0	726	8	0
56	Lk	632	0	693	6	0
57	Ll	436	0	473	5	0
58	Lp	698	0	737	5	0
59	Lr	1660	0	1768	26	0
60	CH	32	0	12	0	0
60	Cd	32	0	12	1	0
61	CH	1	0	0	0	0
61	Cd	2	0	0	0	0
62	CQ	1	0	0	0	0
62	Cb	1	0	0	0	0
62	Lg	1	0	0	0	0
62	Lj	1	0	0	0	0
62	Lp	1	0	0	0	0
63	CH	1	0	0	0	0
63	Cd	2	0	0	0	0
All	All	160598	0	126757	973	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 973 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:C1:3289:G:H1	1:C1:3298:U:H3	1.05	1.00
1:C1:1054:U:H3	1:C1:1070:G:H1	0.90	0.84
1:C1:1809:G:HO2'	9:CJ:2:GLY:N	1.76	0.82
33:LL:199:GLU:HG2	33:LL:203:LYS:HZ3	1.43	0.81
20:Cf:87:MET:HB2	20:Cf:103:VAL:HB	1.72	0.71

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	
5	CB	259/391 (66%)	255 (98%)	4 (2%)	0	100	100
6	CF	243/270 (90%)	241 (99%)	2 (1%)	0	100	100
7	CH	621/661 (94%)	617 (99%)	4 (1%)	0	100	100
8	CI	150/414 (36%)	147 (98%)	3 (2%)	0	100	100
9	CJ	376/679 (55%)	373 (99%)	3 (1%)	0	100	100
10	CK	231/261 (88%)	225 (97%)	6 (3%)	0	100	100
11	CL	77/558 (14%)	76 (99%)	1 (1%)	0	100	100
12	CM	211/249 (85%)	207 (98%)	3 (1%)	1 (0%)	24	34
12	LF	246/249 (99%)	240 (98%)	6 (2%)	0	100	100
13	CN	244/246 (99%)	238 (98%)	6 (2%)	0	100	100
14	CO	56/120 (47%)	56 (100%)	0	0	100	100
15	CQ	181/225 (80%)	180 (99%)	1 (1%)	0	100	100
16	Lq	137/147 (93%)	134 (98%)	3 (2%)	0	100	100
17	Cb	99/117 (85%)	98 (99%)	1 (1%)	0	100	100
18	Cd	458/627 (73%)	450 (98%)	8 (2%)	0	100	100
19	Ce	301/443 (68%)	299 (99%)	2 (1%)	0	100	100
20	Cf	281/350 (80%)	276 (98%)	5 (2%)	0	100	100
21	Cg	186/202 (92%)	185 (100%)	1 (0%)	0	100	100
22	Ch	484/517 (94%)	468 (97%)	16 (3%)	0	100	100
23	Cz	99/123 (80%)	98 (99%)	1 (1%)	0	100	100
24	LA	189/254 (74%)	185 (98%)	4 (2%)	0	100	100
25	LB	387/392 (99%)	380 (98%)	7 (2%)	0	100	100
26	LC	361/365 (99%)	355 (98%)	6 (2%)	0	100	100
27	LD	282/304 (93%)	280 (99%)	2 (1%)	0	100	100
28	LE	187/200 (94%)	182 (97%)	5 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	LG	233/262 (89%)	230 (99%)	3 (1%)	0	100	100
30	LH	188/229 (82%)	184 (98%)	4 (2%)	0	100	100
31	LJ	167/173 (96%)	166 (99%)	1 (1%)	0	100	100
32	LK	156/165 (94%)	155 (99%)	1 (1%)	0	100	100
33	LL	201/213 (94%)	199 (99%)	2 (1%)	0	100	100
34	LM	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
35	LN	200/203 (98%)	193 (96%)	7 (4%)	0	100	100
36	LO	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
37	LP	167/187 (89%)	166 (99%)	1 (1%)	0	100	100
38	LQ	148/213 (70%)	145 (98%)	3 (2%)	0	100	100
39	LR	153/2898 (5%)	152 (99%)	1 (1%)	0	100	100
40	LS	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
41	LT	127/160 (79%)	125 (98%)	2 (2%)	0	100	100
42	LU	103/127 (81%)	100 (97%)	3 (3%)	0	100	100
43	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
44	LX	143/156 (92%)	140 (98%)	3 (2%)	0	100	100
45	LY	131/138 (95%)	125 (95%)	6 (5%)	0	100	100
46	LZ	133/135 (98%)	132 (99%)	1 (1%)	0	100	100
47	La	104/149 (70%)	102 (98%)	2 (2%)	0	100	100
48	Lc	93/108 (86%)	92 (99%)	1 (1%)	0	100	100
49	Ld	108/120 (90%)	107 (99%)	1 (1%)	0	100	100
50	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
51	Lf	106/109 (97%)	105 (99%)	1 (1%)	0	100	100
52	Lg	116/119 (98%)	114 (98%)	2 (2%)	0	100	100
53	Lh	120/935 (13%)	116 (97%)	4 (3%)	0	100	100
54	Li	99/110 (90%)	99 (100%)	0	0	100	100
55	Lj	86/95 (90%)	84 (98%)	2 (2%)	0	100	100
56	Lk	74/94 (79%)	73 (99%)	1 (1%)	0	100	100
57	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
58	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
59	Lr	212/217 (98%)	201 (95%)	11 (5%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	10620/16612 (64%)	10440 (98%)	179 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	CM	197	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	CB	227/329 (69%)	227 (100%)	0	100	100
6	CF	212/236 (90%)	212 (100%)	0	100	100
7	CH	549/575 (96%)	549 (100%)	0	100	100
8	CI	124/336 (37%)	124 (100%)	0	100	100
9	CJ	331/579 (57%)	331 (100%)	0	100	100
10	CK	206/225 (92%)	205 (100%)	1 (0%)	81	88
11	CL	61/458 (13%)	61 (100%)	0	100	100
12	CM	185/215 (86%)	185 (100%)	0	100	100
12	LF	213/215 (99%)	213 (100%)	0	100	100
13	CN	205/206 (100%)	205 (100%)	0	100	100
14	CO	48/99 (48%)	48 (100%)	0	100	100
15	CQ	144/192 (75%)	144 (100%)	0	100	100
16	Lq	109/112 (97%)	109 (100%)	0	100	100
17	Cb	85/101 (84%)	85 (100%)	0	100	100
18	Cd	403/541 (74%)	403 (100%)	0	100	100
19	Ce	267/383 (70%)	267 (100%)	0	100	100
20	Cf	250/310 (81%)	250 (100%)	0	100	100
21	Cg	158/176 (90%)	158 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	Ch	408/436 (94%)	408 (100%)	0	100	100
23	Cz	89/107 (83%)	89 (100%)	0	100	100
24	LA	150/198 (76%)	150 (100%)	0	100	100
25	LB	329/331 (99%)	329 (100%)	0	100	100
26	LC	282/285 (99%)	282 (100%)	0	100	100
27	LD	221/253 (87%)	221 (100%)	0	100	100
28	LE	157/166 (95%)	157 (100%)	0	100	100
29	LG	200/222 (90%)	200 (100%)	0	100	100
30	LH	167/200 (84%)	167 (100%)	0	100	100
31	LJ	140/150 (93%)	140 (100%)	0	100	100
32	LK	127/136 (93%)	127 (100%)	0	100	100
33	LL	158/176 (90%)	158 (100%)	0	100	100
34	LM	116/117 (99%)	116 (100%)	0	100	100
35	LN	179/180 (99%)	179 (100%)	0	100	100
36	LO	162/163 (99%)	162 (100%)	0	100	100
37	LP	133/152 (88%)	133 (100%)	0	100	100
38	LQ	128/178 (72%)	128 (100%)	0	100	100
39	LR	125/2396 (5%)	125 (100%)	0	100	100
40	LS	152/154 (99%)	152 (100%)	0	100	100
41	LT	110/135 (82%)	110 (100%)	0	100	100
42	LU	92/108 (85%)	92 (100%)	0	100	100
43	LV	98/102 (96%)	98 (100%)	0	100	100
44	LX	122/129 (95%)	122 (100%)	0	100	100
45	LY	116/119 (98%)	116 (100%)	0	100	100
46	LZ	121/121 (100%)	121 (100%)	0	100	100
47	La	93/122 (76%)	93 (100%)	0	100	100
48	Lc	76/88 (86%)	76 (100%)	0	100	100
49	Ld	90/105 (86%)	90 (100%)	0	100	100
50	Le	109/114 (96%)	109 (100%)	0	100	100
51	Lf	89/90 (99%)	89 (100%)	0	100	100
52	Lg	95/102 (93%)	95 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	Lh	109/781 (14%)	109 (100%)	0	100	100
54	Li	85/93 (91%)	85 (100%)	0	100	100
55	Lj	72/78 (92%)	72 (100%)	0	100	100
56	Lk	73/88 (83%)	73 (100%)	0	100	100
57	Ll	45/46 (98%)	45 (100%)	0	100	100
58	Lp	73/74 (99%)	73 (100%)	0	100	100
59	Lr	186/189 (98%)	186 (100%)	0	100	100
All	All	9054/13972 (65%)	9053 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
10	CK	190	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
35	LN	95	GLN
58	Lp	45	ASN
37	LP	75	GLN
41	LT	131	GLN
21	Cg	185	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3130/3342 (93%)	590 (18%)	41 (1%)
2	C2	155/156 (99%)	21 (13%)	0
3	C3	80/162 (49%)	19 (23%)	0
4	C4	118/119 (99%)	25 (21%)	2 (1%)
All	All	3483/3779 (92%)	655 (18%)	43 (1%)

5 of 655 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	G
1	C1	27	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
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	2918	1	19,22,23	3.13	8 (42%)	25,31,34	2.67	9 (36%)
1	A2M	C1	1223	1	22,25,26	3.96	10 (45%)	30,36,39	3.33	13 (43%)
1	OMC	C1	2300	1	19,22,23	3.04	8 (42%)	25,31,34	2.79	11 (44%)
1	OMC	C1	1812	1	19,22,23	3.14	8 (42%)	25,31,34	2.60	10 (40%)
1	OMG	C1	787	1	23,26,27	2.48	9 (39%)	32,38,41	2.98	16 (50%)
1	OMC	C1	778	1	19,22,23	3.12	8 (42%)	25,31,34	2.63	9 (36%)
1	OMU	C1	2683	1	19,22,23	3.10	6 (31%)	25,31,34	1.76	5 (20%)
1	OMC	C1	1420	1	19,22,23	3.03	8 (42%)	25,31,34	2.61	9 (36%)
1	A2M	C1	389	1	22,25,26	4.00	12 (54%)	30,36,39	3.41	12 (40%)
1	OMC	C1	1491	1	19,22,23	3.08	8 (42%)	25,31,34	2.71	10 (40%)
1	A2M	C1	848	1	22,25,26	3.99	12 (54%)	30,36,39	3.44	14 (46%)
1	A2M	C1	1432	1	22,25,26	3.98	12 (54%)	30,36,39	3.43	13 (43%)
1	A2M	C1	2289	1	22,25,26	4.00	11 (50%)	30,36,39	3.32	13 (43%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	C1	2838	1	19,22,23	3.16	8 (42%)	25,31,34	2.63	8 (32%)
1	OMC	C1	1836	1	19,22,23	3.11	8 (42%)	25,31,34	2.75	10 (40%)
1	OMU	C1	1868	1	19,22,23	3.14	6 (31%)	25,31,34	1.86	5 (20%)
1	A2M	C1	1847	1	22,25,26	3.97	12 (54%)	30,36,39	3.47	14 (46%)
1	OMG	C1	2358	1	23,26,27	2.50	9 (39%)	32,38,41	2.82	18 (56%)
1	OMG	C1	385	1	23,26,27	2.49	9 (39%)	32,38,41	2.92	19 (59%)
1	OMG	C1	2881	1	23,26,27	2.48	9 (39%)	32,38,41	2.86	17 (53%)
1	OMG	C1	2774	1	23,26,27	2.51	9 (39%)	32,38,41	2.87	18 (56%)
1	A2M	C1	858	1	22,25,26	4.00	12 (54%)	30,36,39	3.37	12 (40%)
1	OMG	C1	1433	1	23,26,27	2.51	9 (39%)	32,38,41	2.86	18 (56%)
1	OMU	C1	2277	1	19,22,23	3.13	6 (31%)	25,31,34	1.76	5 (20%)
1	OMG	C1	2578	1	23,26,27	2.53	9 (39%)	32,38,41	2.90	18 (56%)
1	OMG	C1	2876	1	23,26,27	2.55	8 (34%)	32,38,41	3.15	16 (50%)
1	OMG	C1	627	1	23,26,27	2.52	9 (39%)	32,38,41	2.85	17 (53%)
1	OMU	C1	1917	1	19,22,23	3.17	6 (31%)	25,31,34	1.80	5 (20%)
1	OMU	C1	2380	1	19,22,23	3.10	6 (31%)	25,31,34	1.78	5 (20%)
1	OMU	C1	2690	1	19,22,23	3.11	6 (31%)	25,31,34	1.78	4 (16%)
1	OMU	C1	2688	1	19,22,23	3.13	6 (31%)	25,31,34	1.78	5 (20%)
1	OMG	C1	646	1	23,26,27	2.54	9 (39%)	32,38,41	2.85	17 (53%)
1	A2M	C1	637	1	22,25,26	3.98	11 (50%)	30,36,39	3.36	13 (43%)
1	OMU	C1	2384	1	19,22,23	3.16	6 (31%)	25,31,34	1.75	5 (20%)

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	2918	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMC	C1	2300	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMG	C1	646	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMC	C1	1812	1	2/2/5/5	3/9/27/28	0/2/2/2
1	OMG	C1	787	1	2/2/5/5	1/9/27/28	0/3/3/3
1	A2M	C1	1223	1	-	2/9/27/28	0/3/3/3
1	OMC	C1	778	1	2/2/5/5	4/9/27/28	0/2/2/2
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	C1	1420	1	2/2/5/5	5/9/27/28	0/2/2/2
1	A2M	C1	389	1	-	3/9/27/28	0/3/3/3
1	OMC	C1	1491	1	2/2/5/5	6/9/27/28	0/2/2/2
1	A2M	C1	848	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	2838	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMC	C1	1836	1	2/2/5/5	5/9/27/28	0/2/2/2
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3
1	OMG	C1	385	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMG	C1	2881	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMG	C1	2774	1	2/2/5/5	4/9/27/28	0/3/3/3
1	A2M	C1	858	1	-	1/9/27/28	0/3/3/3
1	OMG	C1	1433	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMU	C1	2277	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2578	1	2/2/5/5	4/9/27/28	0/3/3/3
1	OMG	C1	2876	1	2/2/5/5	3/9/27/28	0/3/3/3
1	OMG	C1	627	1	2/2/5/5	2/9/27/28	0/3/3/3
1	OMU	C1	1917	1	-	3/9/27/28	0/2/2/2
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2690	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2688	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	2358	1	2/2/5/5	4/9/27/28	0/3/3/3
1	A2M	C1	637	1	-	1/9/27/28	0/3/3/3
1	OMU	C1	2384	1	-	1/9/27/28	0/2/2/2

The worst 5 of 293 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2289	A2M	C3'-C2'	-13.08	1.24	1.53
1	C1	858	A2M	C3'-C2'	-13.04	1.24	1.53
1	C1	637	A2M	C3'-C2'	-12.99	1.24	1.53
1	C1	848	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	389	A2M	C3'-C2'	-12.89	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	-9.56	105.88	127.09
1	C1	389	A2M	C1'-N9-C8	-9.33	106.40	127.09
1	C1	1432	A2M	C1'-N9-C8	-9.29	106.47	127.09
1	C1	637	A2M	C1'-N9-C8	-9.20	106.67	127.09
1	C1	858	A2M	C1'-N9-C8	-9.16	106.76	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 85 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	385	OMG	O4'-C4'-C5'-O5'
1	C1	389	A2M	O4'-C4'-C5'-O5'
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	627	OMG	C3'-C2'-O2'-CM2
1	C1	637	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

16 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	2300	OMC	1	0
1	C1	1812	OMC	1	0
1	C1	787	OMG	3	0
1	C1	2683	OMU	1	0
1	C1	1420	OMC	1	0
1	C1	389	A2M	1	0
1	C1	1491	OMC	4	0
1	C1	1432	A2M	1	0
1	C1	2838	OMC	2	0
1	C1	2881	OMG	1	0
1	C1	2578	OMG	1	0
1	C1	2876	OMG	1	0
1	C1	627	OMG	1	0
1	C1	1917	OMU	1	0
1	C1	646	OMG	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	637	A2M	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
60	GTP	CH	701	61	33,34,34	0.92	1 (3%)	50,54,54	1.57	9 (18%)
60	GTP	Cd	1000	61	33,34,34	0.92	1 (3%)	50,54,54	1.65	9 (18%)

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
60	GTP	CH	701	61	-	7/22/38/38	0/3/3/3
60	GTP	Cd	1000	61	-	1/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	CH	701	GTP	C2-N3	2.18	1.38	1.33
60	Cd	1000	GTP	C2-N3	2.04	1.38	1.33

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	CH	701	GTP	C5-C4-N3	-4.99	120.44	128.39
60	Cd	1000	GTP	C5-C4-N3	-4.97	120.48	128.39
60	Cd	1000	GTP	C2-N3-C4	4.65	120.31	112.30
60	CH	701	GTP	C2-N3-C4	4.57	120.17	112.30
60	CH	701	GTP	N9-C4-N3	3.21	132.37	125.95

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	CH	701	GTP	C5'-O5'-PA-O3A
60	CH	701	GTP	C5'-O5'-PA-O1A
60	CH	701	GTP	C5'-O5'-PA-O2A
60	CH	701	GTP	C3'-C4'-C5'-O5'
60	CH	701	GTP	O4'-C4'-C5'-O5'

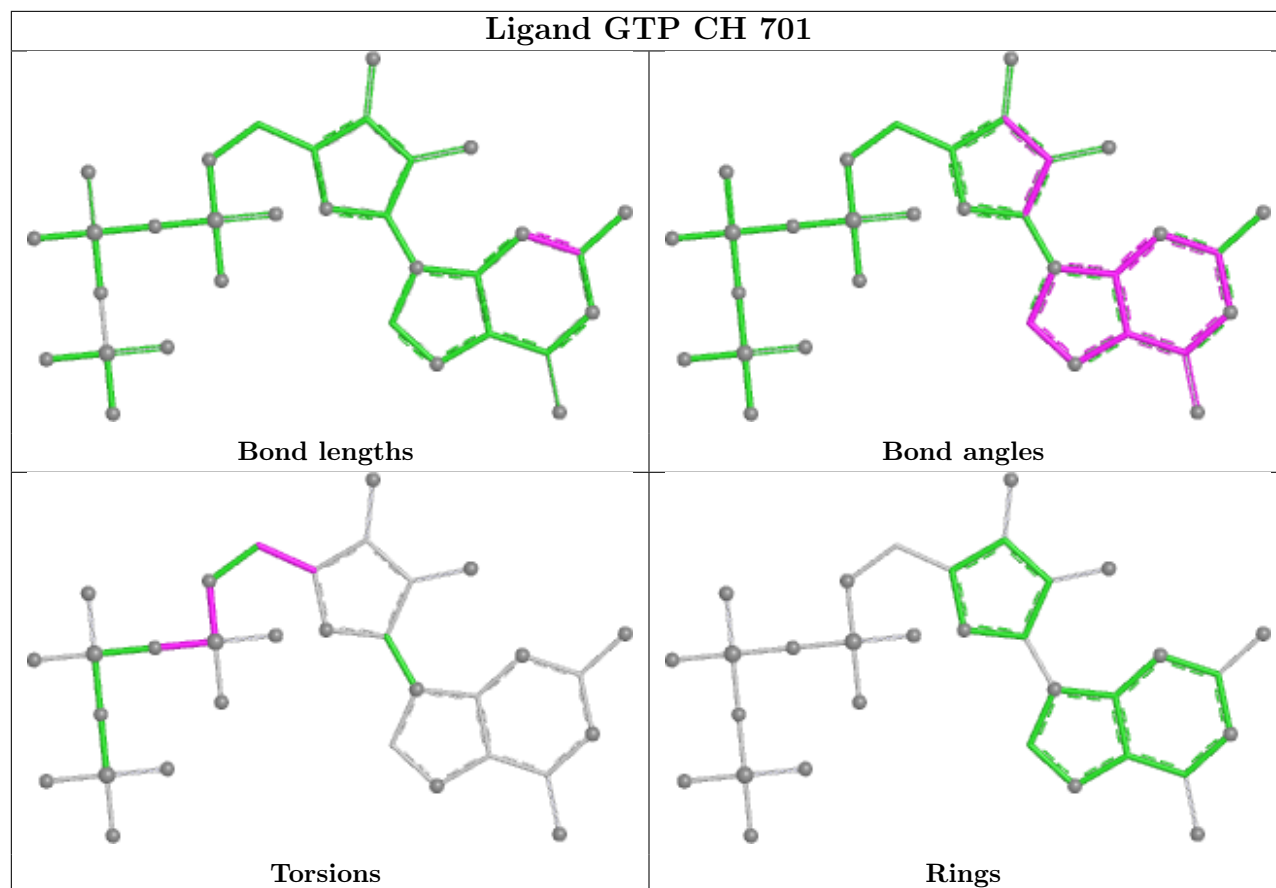
There are no ring outliers.

1 monomer is involved in 1 short contact:

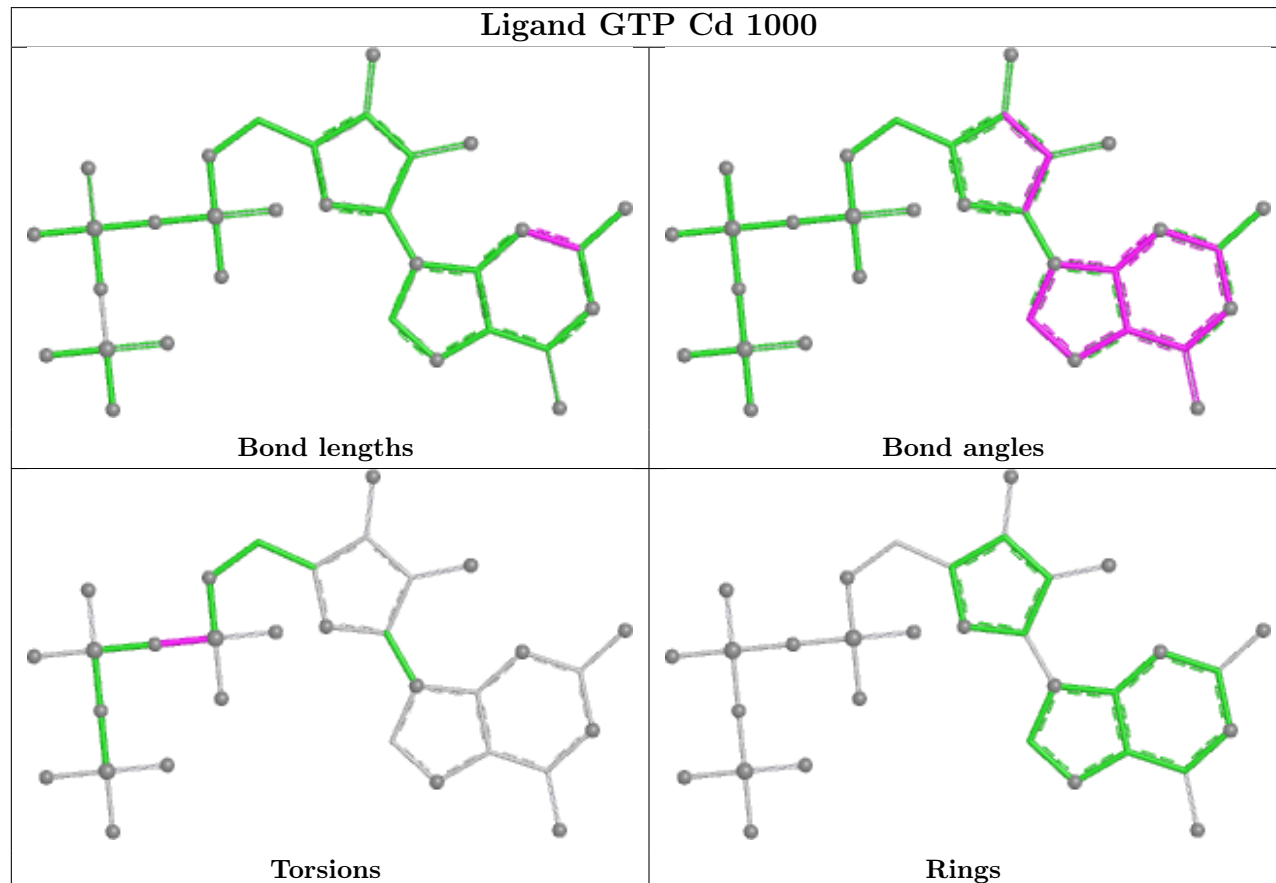
Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	Cd	1000	GTP	1	0

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.

Ligand GTP CH 701



Ligand GTP Cd 1000



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.

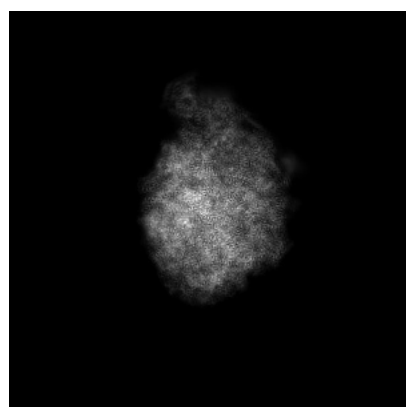
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17969. These allow visual inspection of the internal detail of the map and identification of artifacts.

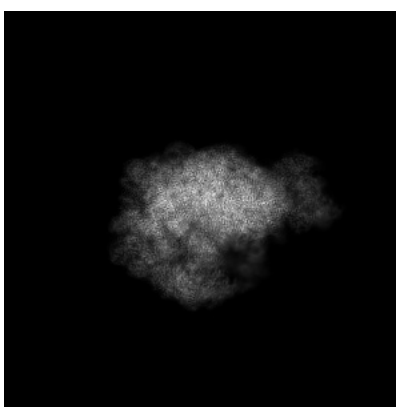
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

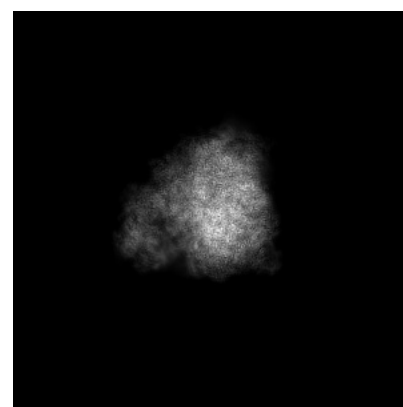
6.1.1 Primary map



X



Y

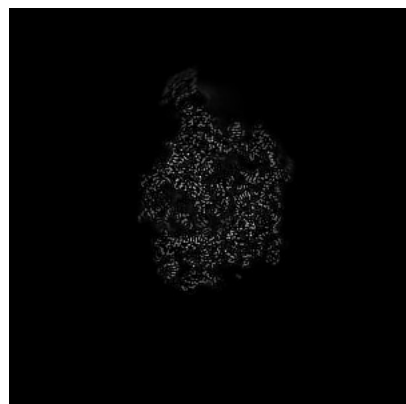


Z

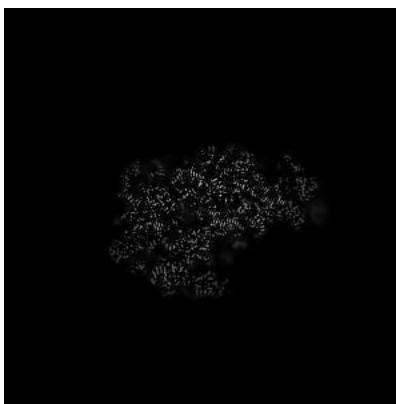
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

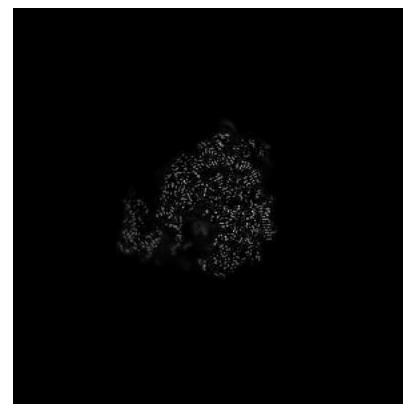
6.2.1 Primary map



X Index: 250



Y Index: 250

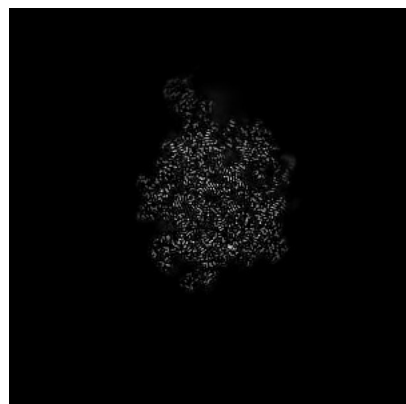


Z Index: 250

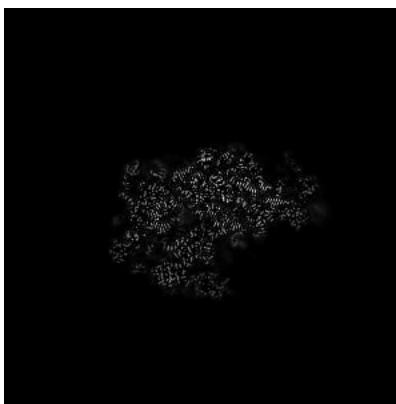
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

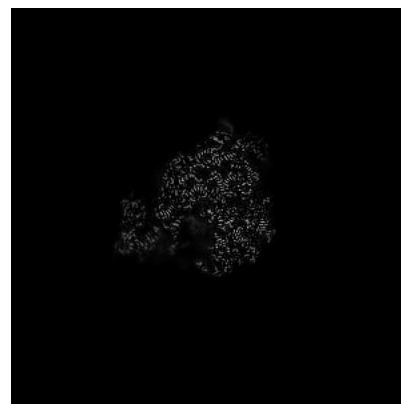
6.3.1 Primary map



X Index: 259



Y Index: 248

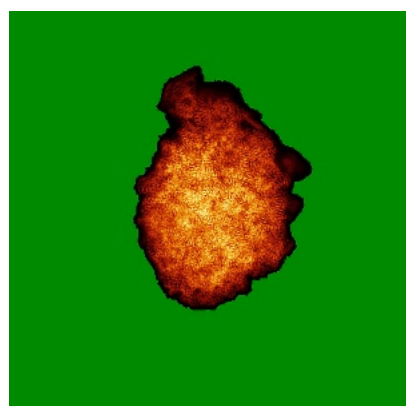


Z Index: 252

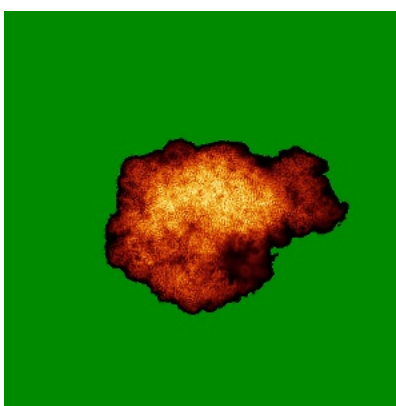
The images above show the largest variance slices of the map in three orthogonal directions.

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

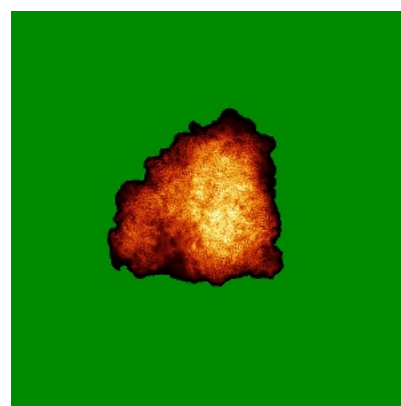
6.4.1 Primary map



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

This section was not generated.

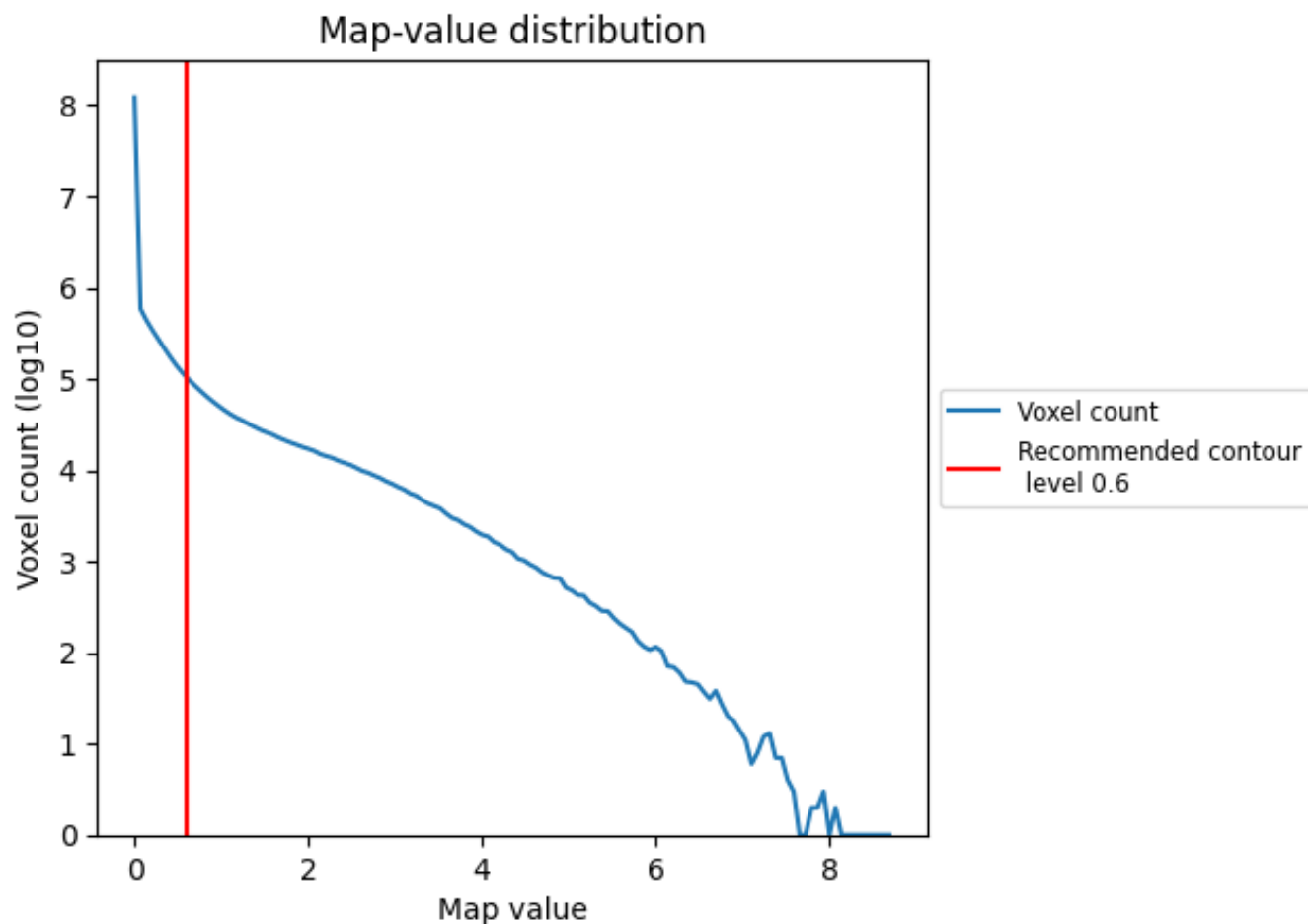
6.6 Mask visualisation

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

7 Map analysis [i](#)

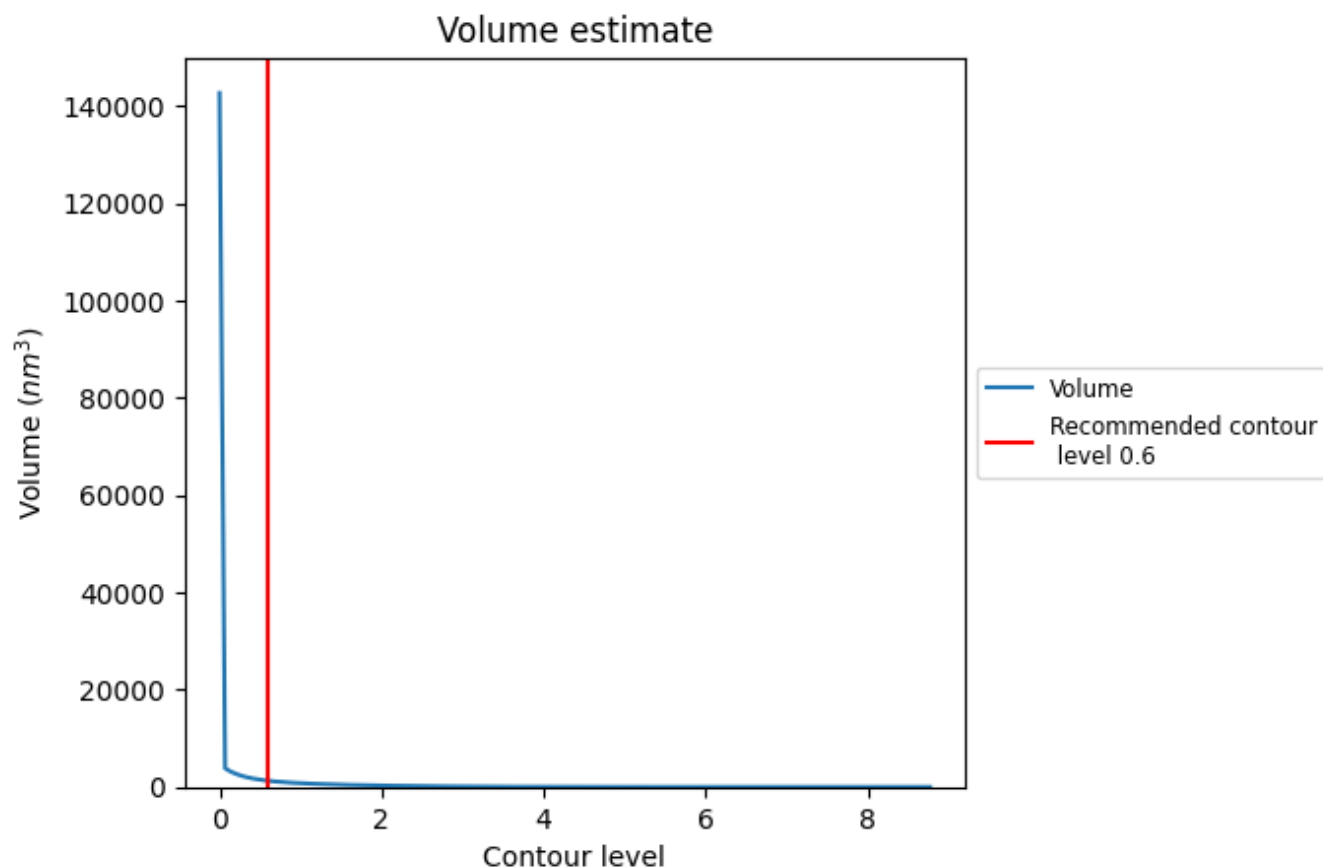
This section contains the results of statistical analysis of the map.

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.

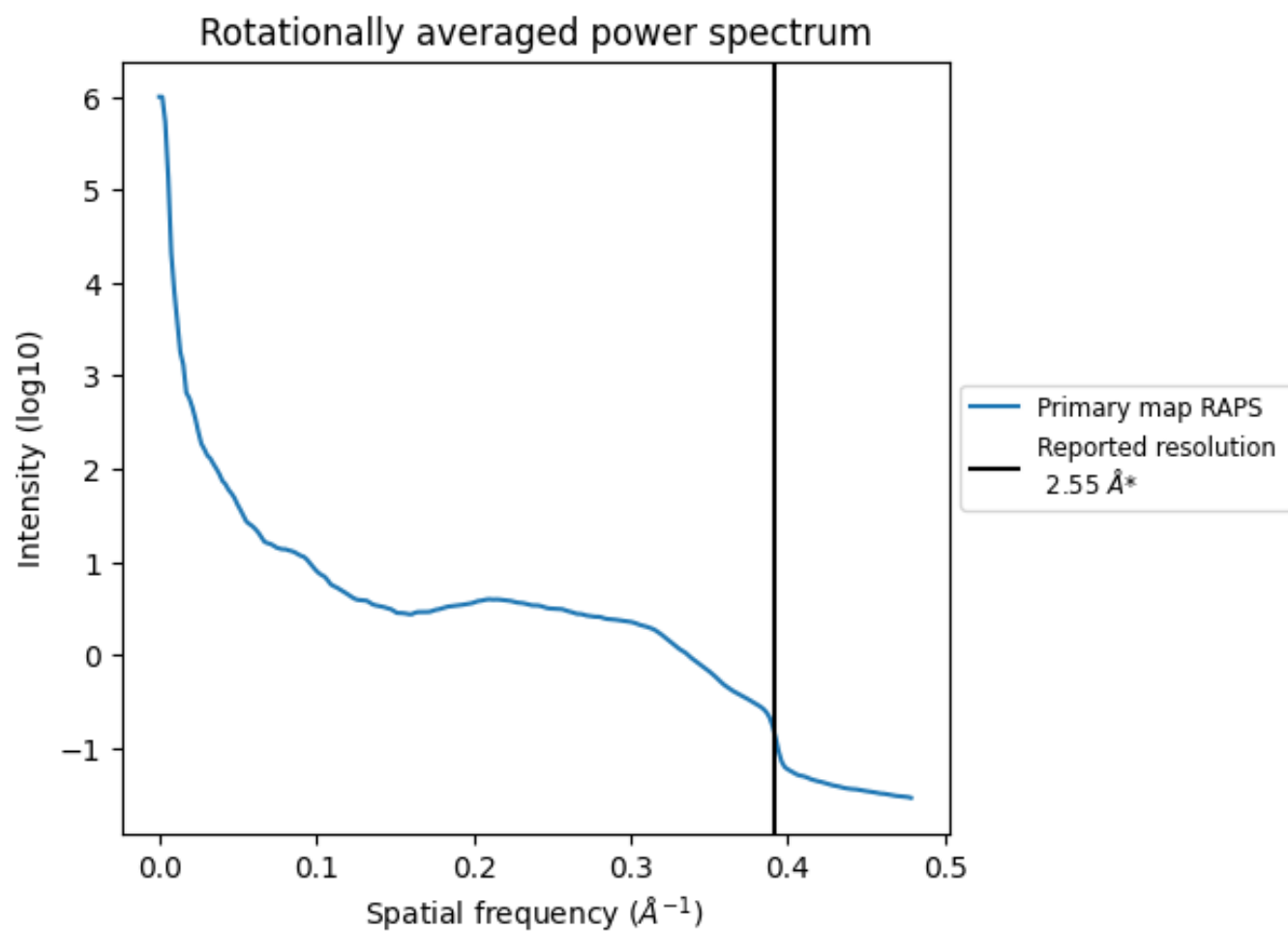
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1273 nm³; this corresponds to an approximate mass of 1150 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 0.392 Å⁻¹

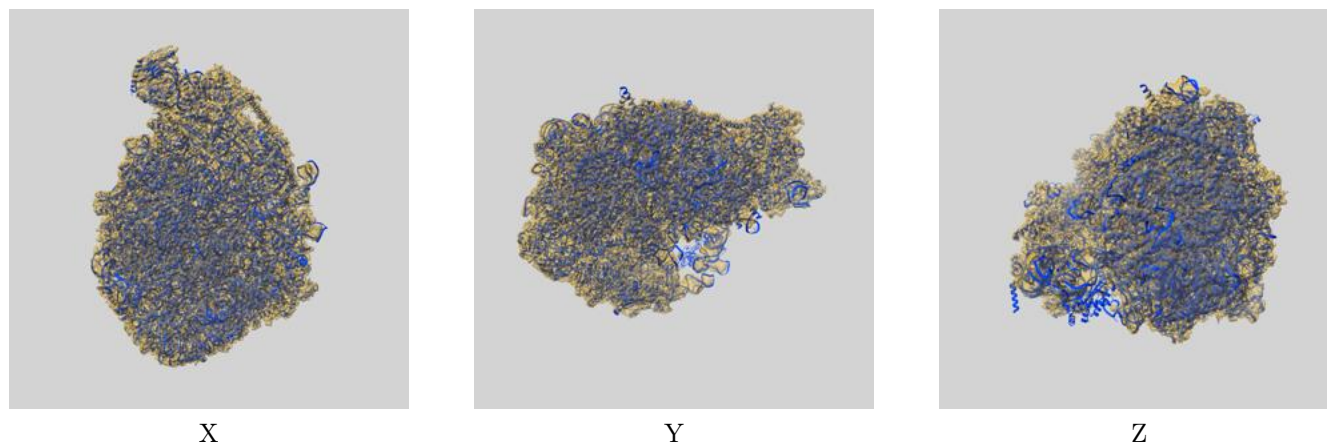
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

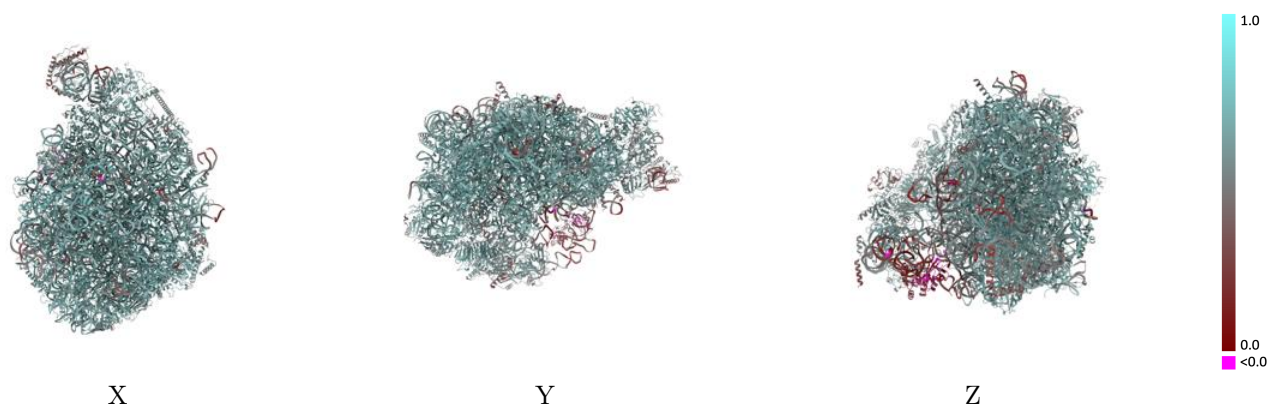
This section contains information regarding the fit between EMDB map EMD-17969 and PDB model 8PVK. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



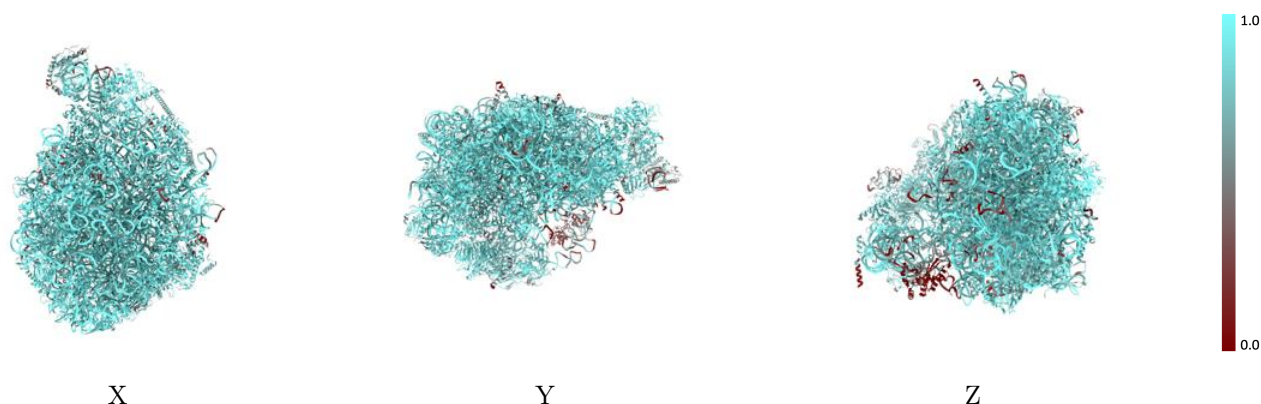
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



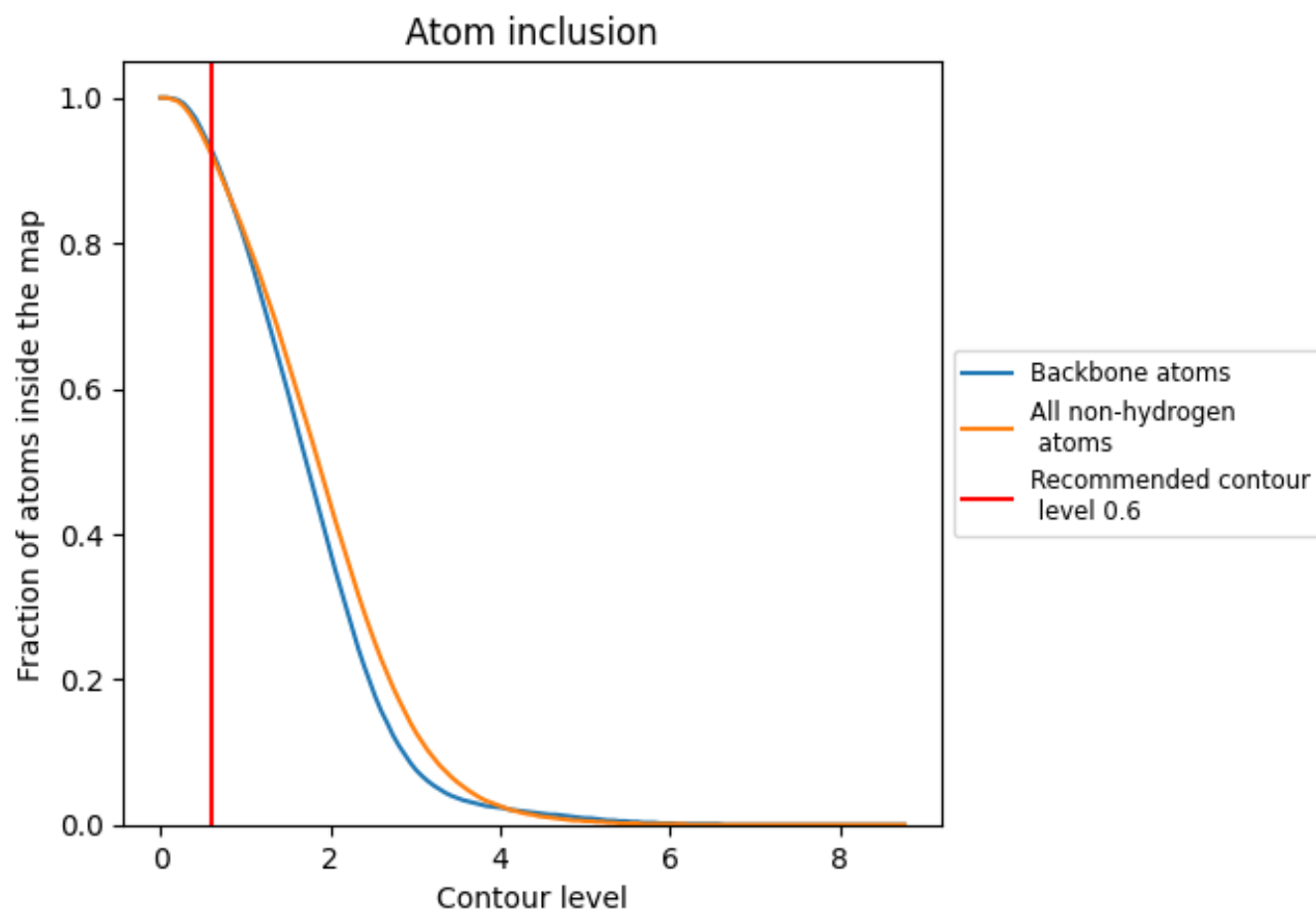
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 92% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9220	 0.6060
C1	 0.9550	 0.6080
C2	 0.9690	 0.6450
C3	 0.7300	 0.4480
C4	 0.9180	 0.5110
CB	 0.7580	 0.5000
CF	 0.8970	 0.5920
CH	 0.8990	 0.6180
CI	 0.8100	 0.5130
CJ	 0.9510	 0.6240
CK	 0.9640	 0.6650
CL	 0.8570	 0.5710
CM	 0.8750	 0.5730
CN	 0.9440	 0.6480
CO	 0.8860	 0.6390
CQ	 0.8610	 0.6100
Cb	 0.9430	 0.6410
Cd	 0.9490	 0.6360
Ce	 0.8150	 0.5550
Cf	 0.9210	 0.5690
Cg	 0.9030	 0.5700
Ch	 0.8730	 0.5910
Cz	 0.7990	 0.5320
LA	 0.9700	 0.6550
LB	 0.9680	 0.6780
LC	 0.9690	 0.6690
LD	 0.8850	 0.5800
LE	 0.9110	 0.6200
LF	 0.9510	 0.6470
LG	 0.9420	 0.6310
LH	 0.9420	 0.6490
LJ	 0.8340	 0.5000
LK	 0.8410	 0.5490
LL	 0.9350	 0.6400
LM	 0.9520	 0.6370



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
LN	 0.9910	 0.6760
LO	 0.9760	 0.6770
LP	 0.9750	 0.6720
LQ	 0.9310	 0.6420
LR	 0.9450	 0.6560
LS	 0.9610	 0.6490
LT	 0.8200	 0.5330
LU	 0.8900	 0.5980
LV	 0.9750	 0.6750
LX	 0.9340	 0.6300
LY	 0.9390	 0.6390
LZ	 0.9450	 0.6390
La	 0.9500	 0.6430
Lc	 0.9020	 0.6170
Ld	 0.9300	 0.6560
Le	 0.9810	 0.6760
Lf	 0.9830	 0.6880
Lg	 0.9160	 0.6430
Lh	 0.9070	 0.5950
Li	 0.9500	 0.6030
Lj	 0.9900	 0.6940
Lk	 0.8830	 0.6050
Ll	 1.0000	 0.7020
Lp	 0.9150	 0.6290
Lq	 0.9490	 0.6390
Lr	 0.0380	 0.1190