



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:34 PM UTC

PDB ID : 8PV8 / pdb_00008pv8
EMDB ID : EMD-17957
Title : Chaetomium thermophilum pre-60S State 4 - post-5S rotation with Rix1 complex without Foot - composite structure
Authors : Thoms, M.; Cheng, J.; Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2023-07-17
Resolution : 2.91 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

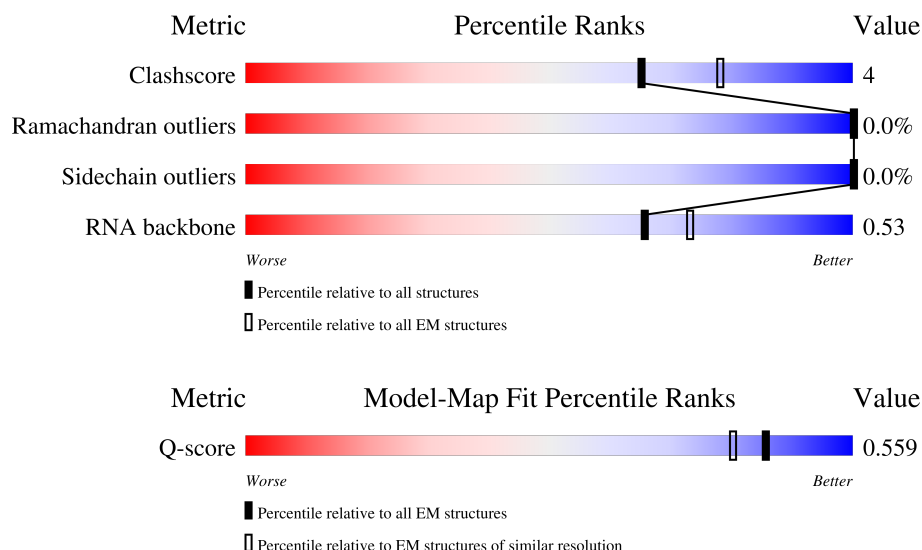
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.91 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.



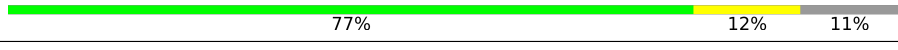
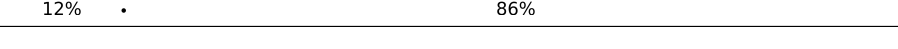
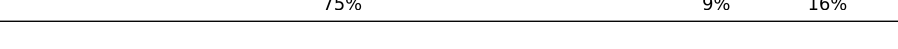
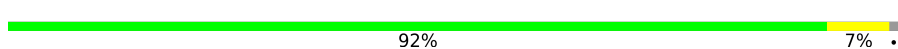
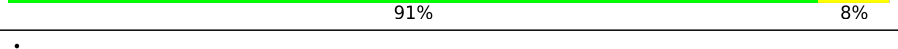
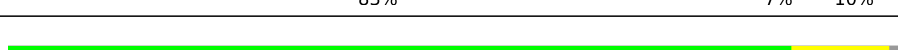
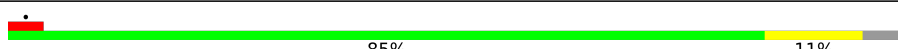
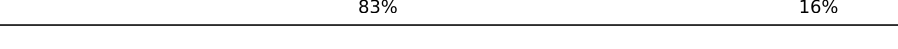
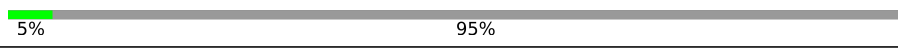
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12972 (2.41 - 3.41)

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	CF	270	

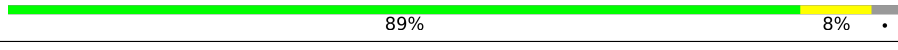
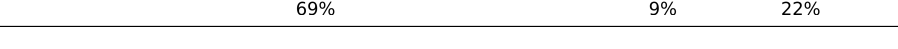
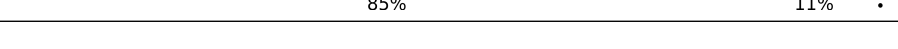
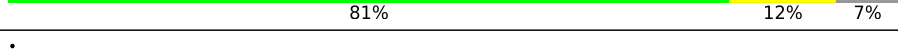
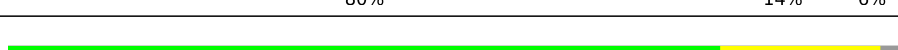
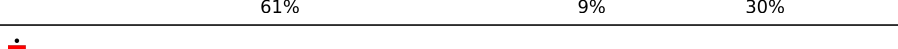
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Mol	Chain	Length	Quality of chain
4	CH	661	
5	CK	261	
6	CL	558	
7	CN	246	
8	CO	120	
9	CQ	225	
10	Cb	117	
11	Cd	627	
12	Cz	123	
13	LA	254	
14	LB	392	
15	LC	365	
16	LE	200	
17	LF	249	
18	LG	262	
19	LH	192	
20	LK	165	
21	LL	213	
22	LM	142	
23	LN	203	
24	LO	204	
25	LP	187	
26	LQ	213	
27	LR	2898	
28	LS	174	

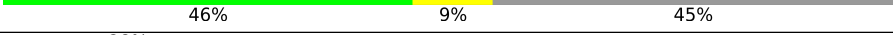
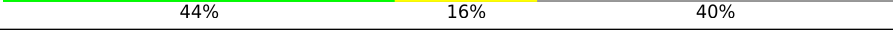
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Mol	Chain	Length	Quality of chain
29	LU	127	
30	LV	139	
31	LX	156	
32	LY	138	
33	LZ	135	
34	La	149	
35	Lc	108	
36	Ld	120	
37	Le	131	
38	Lf	109	
39	Lg	119	
40	Lh	935	
41	Li	110	
42	Lj	95	
43	Lk	81	
44	Ll	51	
45	Lp	92	
46	CT	437	
46	CU	437	
47	CV	781	
47	CW	781	
48	CS	338	
49	CR	767	
50	Lt	217	
51	Ch	517	

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Mol	Chain	Length	Quality of chain
52	LJ	173	
53	LD	304	
54	C4	119	
55	Lq	147	
56	LT	160	
57	Lb	65	
58	Lr	25	

2 Entry composition

There are 62 unique types of molecules in this entry. The entry contains 163368 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	3085	Total	C	N	O	P	0	0
			66031	29491	11948	21507	3085		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C2	150	Total	C	N	O	P	0	0
			3196	1429	572	1045	150		

- Molecule 3 is a protein called Large ribosomal subunit protein uL10.

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

- Molecule 4 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CH	627	Total	C	N	O	S	0	0
			5061	3180	924	938	19		

- Molecule 5 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CK	233	Total	C	N	O	S	0	0
			1878	1183	363	328	4		

- Molecule 6 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	CL	79	Total	C	N	O	0	0
			618	386	124	108		

- Molecule 7 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CN	246	Total	C	N	O	S	0	0
			1850	1154	322	368	6		

- Molecule 8 is a protein called DUF2423 domain-containing protein.

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

- Molecule 9 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CQ	183	Total	C	N	O	S	0	0
			1476	923	304	239	10		

- Molecule 10 is a protein called Zinc finger domain-containing protein.

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

- Molecule 11 is a protein called Nucleolar GTP-binding protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Cd	451	Total	C	N	O	S	0	0
			3614	2301	660	642	11		

- Molecule 12 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Cz	103	Total	C	N	O	S	0	0
			884	548	183	149	4		

- Molecule 13 is a protein called 60S ribosomal protein L2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LA	247	Total	C	N	O	S	0	0
			1878	1175	374	326	3		

- Molecule 14 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LB	388	Total	C	N	O	S	0	0
			3097	1969	578	537	13		

- Molecule 15 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LC	363	Total	C	N	O	S	0	0
			2745	1734	524	478	9		

- Molecule 16 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LE	191	Total	C	N	O	S	0	0
			1470	941	267	259	3		

- Molecule 17 is a protein called 60S ribosomal protein L7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LF	248	Total	C	N	O	S	0	0
			2023	1297	377	346	3		

- Molecule 18 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LG	235	Total	C	N	O	S	0	0
			1880	1204	348	323	5		

- Molecule 19 is a protein called 60S ribosomal protein L9-like protein.

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

- Molecule 20 is a protein called 60S ribosomal protein L12-like protein.

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

- Molecule 21 is a protein called 60S ribosomal protein L13.

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

- Molecule 22 is a protein called 60S ribosomal protein L14-like protein.

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

- Molecule 23 is a protein called Ribosomal protein L15.

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

- Molecule 24 is a protein called 60S ribosomal protein L16-like protein.

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

- Molecule 25 is a protein called 60S ribosomal protein l17-like protein.

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

- Molecule 26 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LQ	146	Total	C	N	O	S	0	0
			1156	730	228	196	2		

- Molecule 27 is a protein called Ribosomal protein L19.

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

- Molecule 28 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LS	174	Total	C	N	O	S	0	0
			1430	920	267	238	5		

- Molecule 29 is a protein called 60S ribosomal protein L22-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LU	105	Total	C	N	O	S	0	0
			838	542	144	151	1		

- Molecule 30 is a protein called 60S ribosomal protein l23-like protein.

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

- Molecule 31 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LX	121	Total	C	N	O		0	0
			962	617	174	171			

- Molecule 32 is a protein called 60S ribosomal protein L26-like protein.

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

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LZ	135	Total	C	N	O	S	0	0
			1102	707	203	188	4		

- Molecule 34 is a protein called 60S ribosomal protein L28-like protein.

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

- Molecule 35 is a protein called 60S ribosomal protein l30-like protein.

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

- Molecule 36 is a protein called Putative 60S ribosomal protein.

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

- Molecule 37 is a protein called 60S ribosomal protein L32-like protein.

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

- Molecule 38 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 39 is a protein called Ribosomal protein l34-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lg	115	Total	C	N	O	S	0	0
			885	552	181	148	4		

- Molecule 40 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

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

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	101	Total	C	N	O	S	0	0
			821	506	178	136	1		

- Molecule 42 is a protein called Ribosomal protein L37.

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

- Molecule 43 is a protein called 60S ribosomal protein L38-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lk	76	Total	C	N	O	S	0	0
			624	394	119	109	2		

- Molecule 44 is a protein called Ribosomal protein eL39.

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

- Molecule 45 is a protein called 60S ribosomal protein L43-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lp	91	Total	C	N	O	S	0	0
			694	428	138	122	6		

- Molecule 46 is a protein called Pre-rRNA-processing protein IPI3.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CT	393	Total	C	N	O	S	0	0
			2938	1863	492	566	17		
46	CU	393	Total	C	N	O	S	0	0
			2950	1871	494	568	17		

- Molecule 47 is a protein called Pre-rRNA-processing protein RIX1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CW	550	Total	C	N	O	S	0	0
			4204	2685	729	776	14		
47	CV	550	Total	C	N	O	S	0	0
			4217	2691	735	777	14		

- Molecule 48 is a protein called Pre-rRNA-processing protein IPI1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CS	307	Total	C	N	O	S	0	0
			2391	1520	418	446	7		

- Molecule 49 is a protein called Protein SDA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CR	516	Total	C	N	O	S	0	0
			3844	2445	683	703	13		

- Molecule 50 is a protein called Ribosomal protein.

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

- Molecule 51 is a protein called Ribosome assembly protein 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ch	389	Total	C	N	O	S	1	0
			3050	1916	568	557	9		

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 52 is a protein called Putative ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LJ	168	Total	C	N	O	S	0	0
			1367	854	266	241	6		

- Molecule 53 is a protein called 60S ribosomal protein l5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LD	298	Total	C	N	O	S	0	0
			2366	1496	424	443	3		

- Molecule 54 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	C4	115	Total	C	N	O	P	0	0
			2451	1093	438	805	115		

- Molecule 55 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	Lq	139	Total	C	N	O	0	0
			1061	666	207	188		

- Molecule 56 is a protein called 60S ribosomal protein l21-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	LT	141	Total	C	N	O	S	0
			1124	712	215	195	2	0

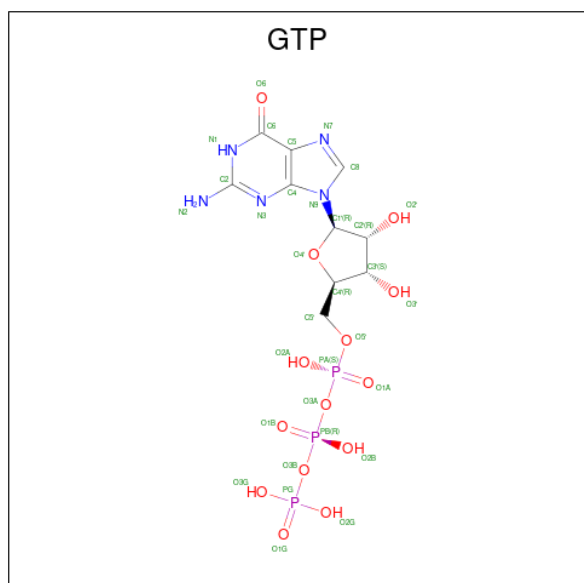
- Molecule 57 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	Lb	36	Total	C	N	O		0
			280	175	60	45		0

- Molecule 58 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	Lr	15	Total	C	N	O	S	0
			138	86	35	16	1	0

- Molecule 59 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

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

- Molecule 60 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

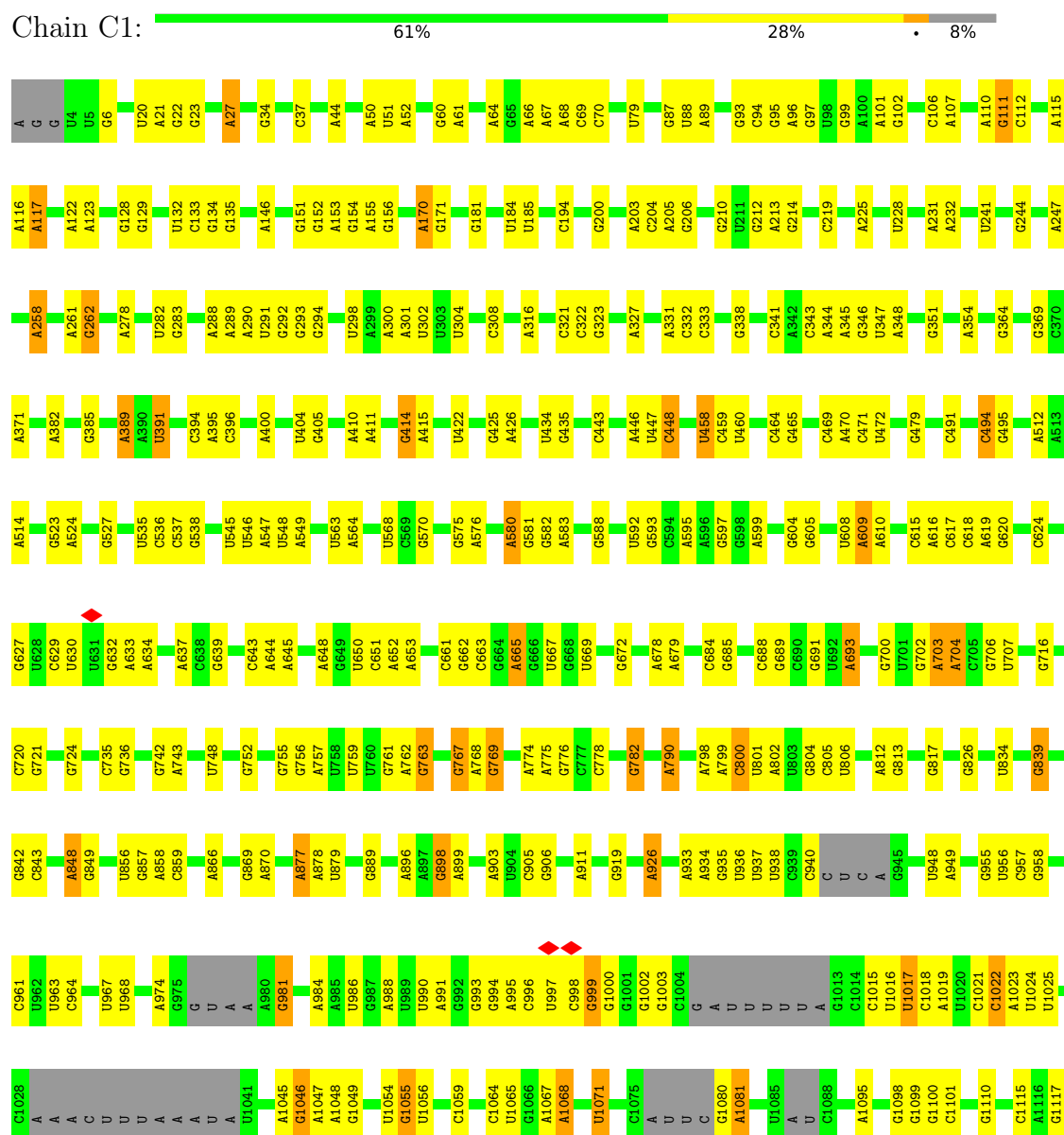
- Molecule 62 is water.

Mol	Chain	Residues	Atoms		AltConf
62	C1	1	Total	O	0
			1	1	
62	CH	1	Total	O	0
			1	1	
62	Cd	2	Total	O	0
			2	2	

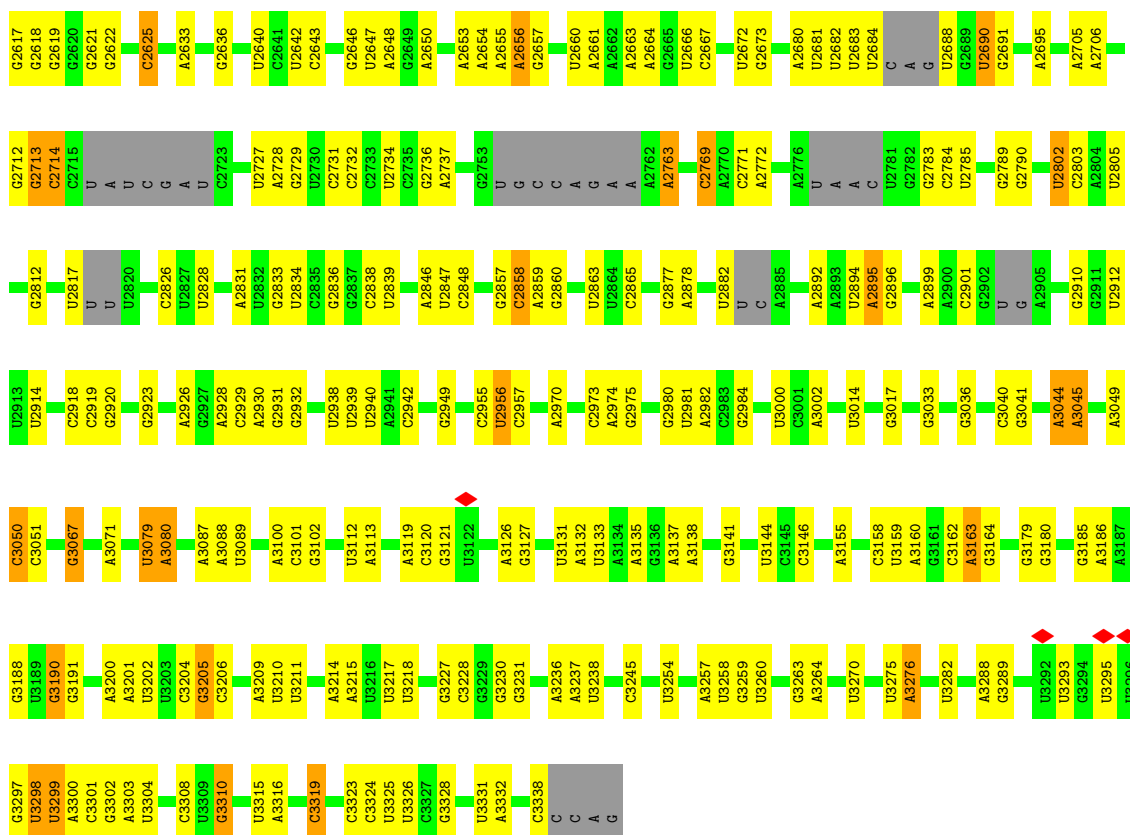
3 Residue-property plots

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

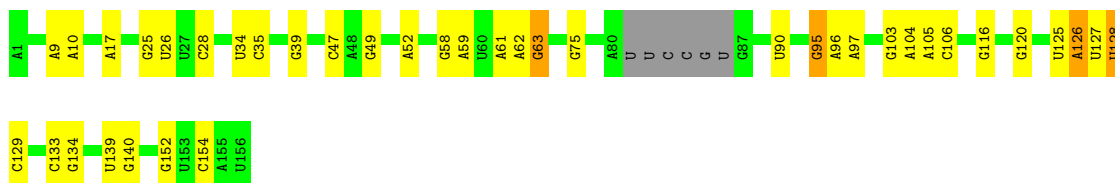






• Molecule 2: 5.8S rRNA

Chain C2: 71% 22%



• Molecule 3: Large ribosomal subunit protein uL10

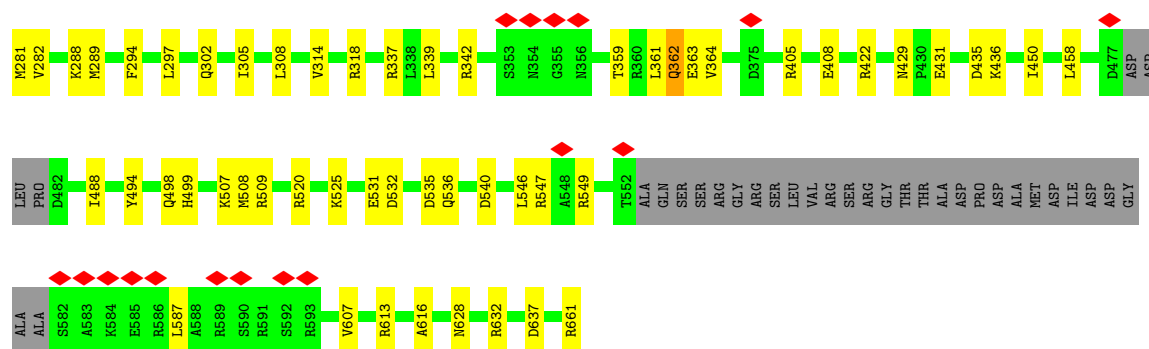
Chain CF: 85% 6% 9%



• Molecule 4: Nucleolar GTP-binding protein 1

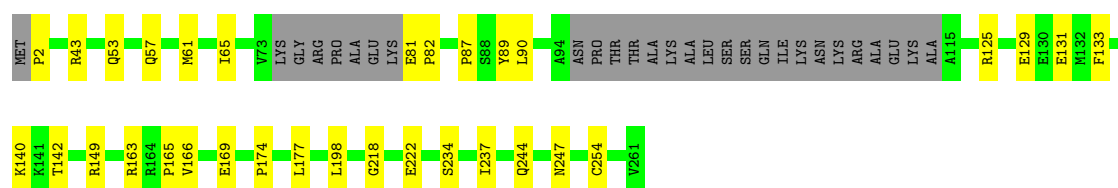
Chain CH: 82% 13% 5%





- Molecule 5: Ribosome biogenesis protein NSA2 homolog

Chain CK: 77% 12% 11%



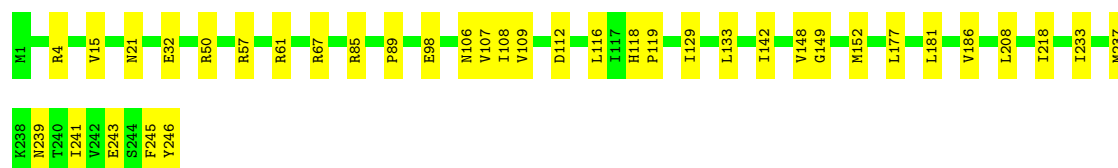
- Molecule 6: Putative GTP binding protein

Chain CL: 12% 86%



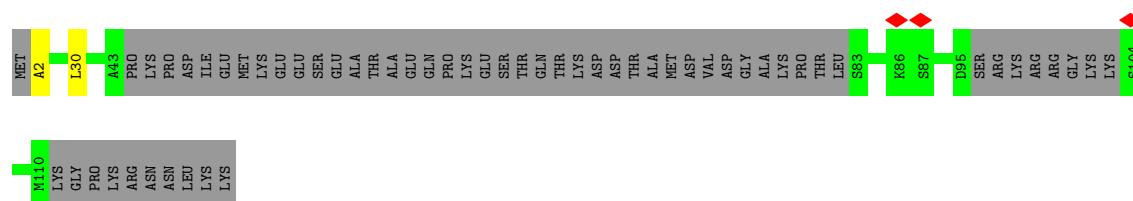
- Molecule 7: Eukaryotic translation initiation factor 6

Chain CN:  85% 15%



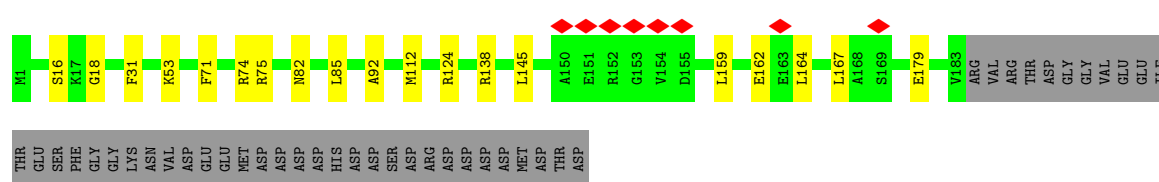
- Molecule 8: DUF2423 domain-containing protein

Chain CO:  50% 48%



- Molecule 9: Ribosome biogenesis protein RLP24

Chain CQ:  73% 8% 19%



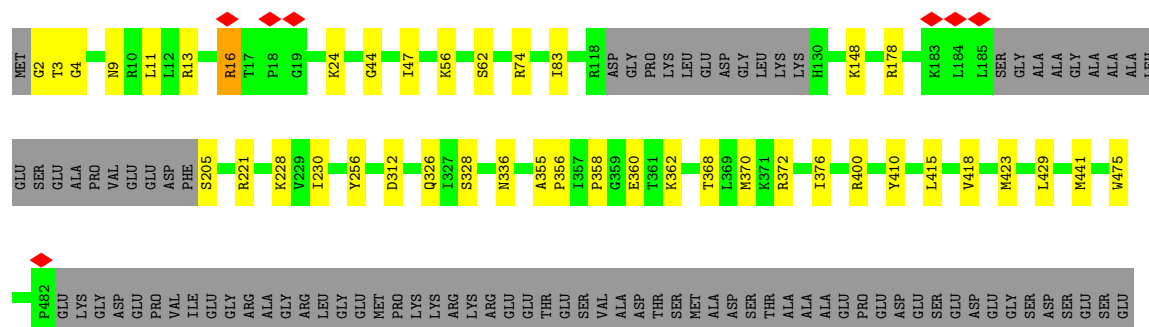
- Molecule 10: Zinc finger domain-containing protein

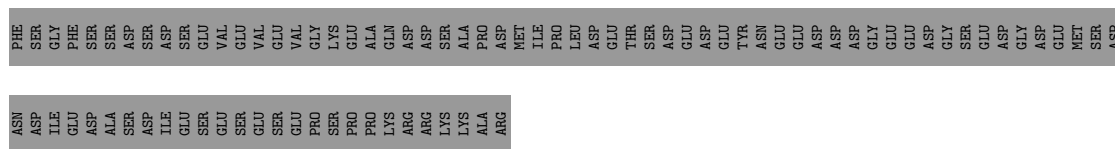
Chain Cb:  74% 12% 14%



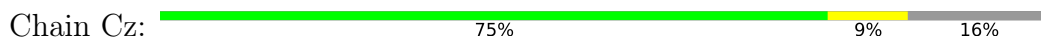
- Molecule 11: Nucleolar GTP-binding protein 2

Chain Cd:  65% 7% 28%

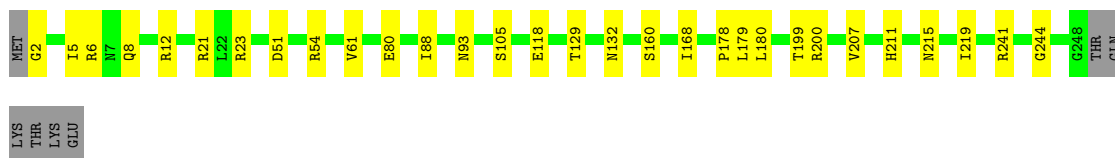
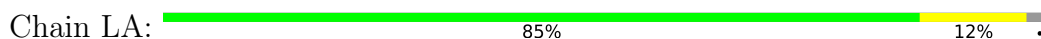




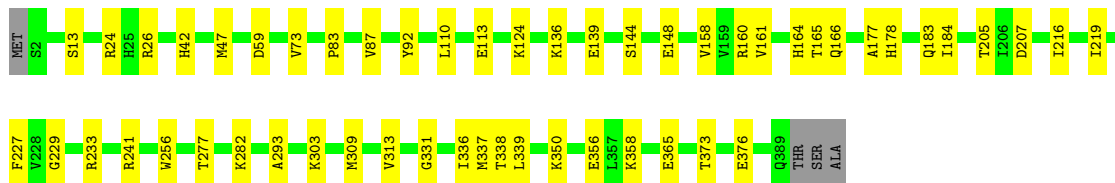
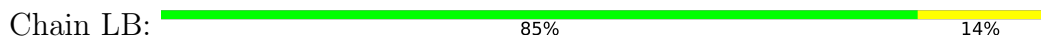
- Molecule 12: rRNA-processing protein



- Molecule 13: 60S ribosomal protein L2-like protein



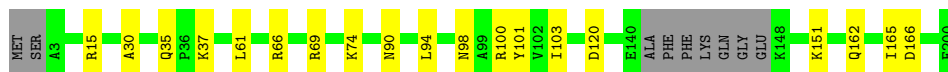
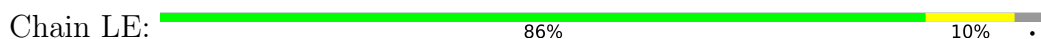
- Molecule 14: 60S ribosomal protein L3-like protein



- Molecule 15: 60S ribosomal protein L4-like protein

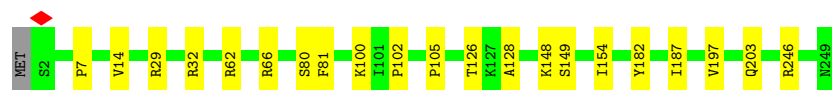


- Molecule 16: 60S ribosomal protein L6

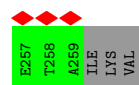
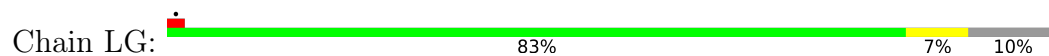


- Molecule 17: 60S ribosomal protein 17-like protein





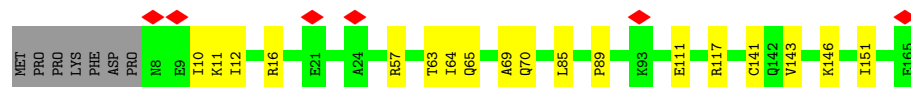
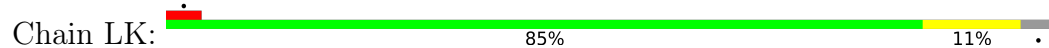
- Molecule 18: 60S ribosomal protein L8



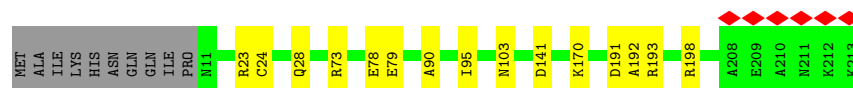
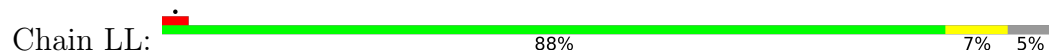
- Molecule 19: 60S ribosomal protein l9-like protein



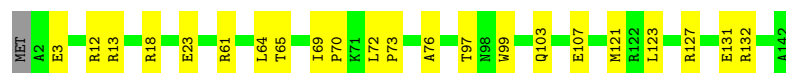
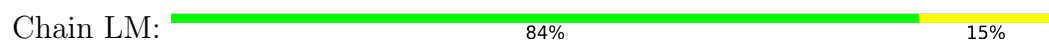
- Molecule 20: 60S ribosomal protein L12-like protein



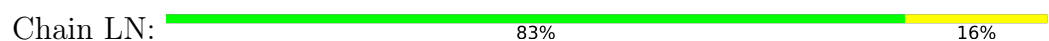
- Molecule 21: 60S ribosomal protein L13



- Molecule 22: 60S ribosomal protein L14-like protein



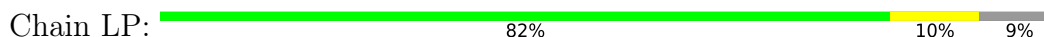
- Molecule 23: Ribosomal protein L15



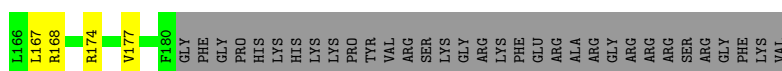
- Molecule 24: 60S ribosomal protein L16-like protein



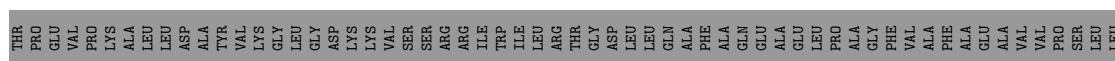
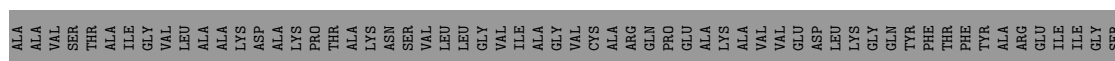
- Molecule 25: 60S ribosomal protein l17-like protein



- Molecule 26: Ribosomal protein L18-like protein

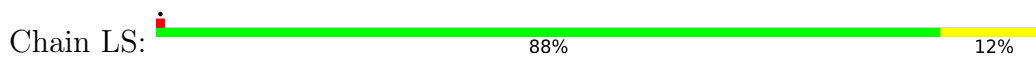


- Molecule 27: Ribosomal protein L19

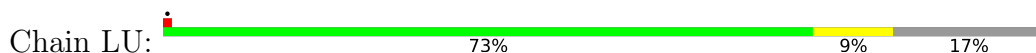




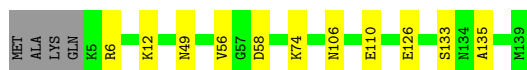
- Molecule 28: 60S ribosomal protein L20



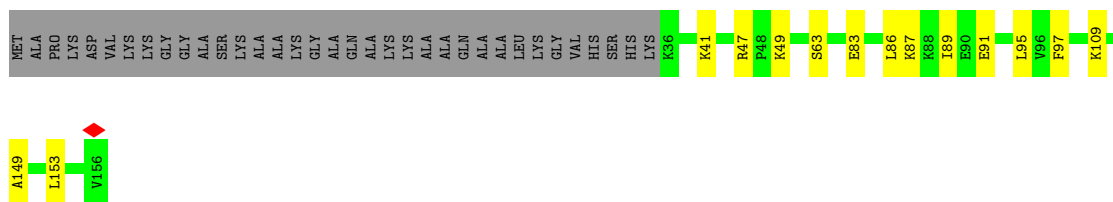
- Molecule 29: 60S ribosomal protein L22-like protein



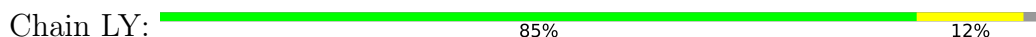
- Molecule 30: 60S ribosomal protein l23-like protein



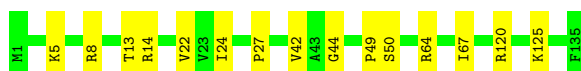
- Molecule 31: 60S ribosomal protein L25-like protein



- Molecule 32: 60S ribosomal protein L26-like protein

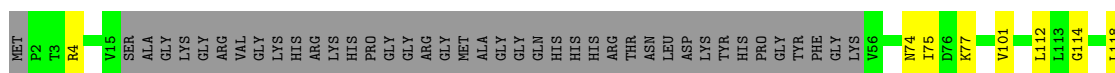


- Molecule 33: 60S ribosomal protein L27

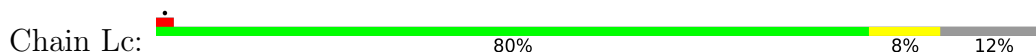


- Molecule 34: 60S ribosomal protein L28-like protein





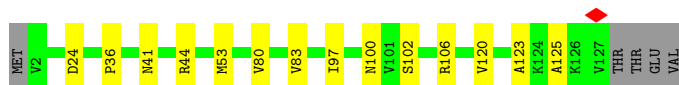
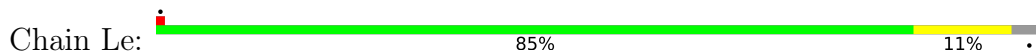
- Molecule 35: 60S ribosomal protein l30-like protein



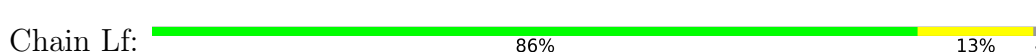
- Molecule 36: Putative 60S ribosomal protein



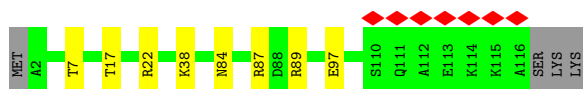
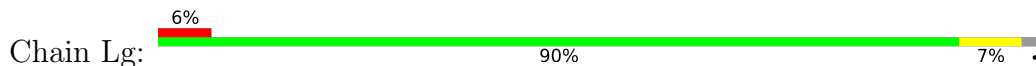
- Molecule 37: 60S ribosomal protein L32-like protein



- Molecule 38: 60S ribosomal protein l33-like protein



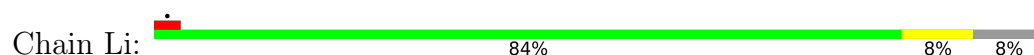
- Molecule 39: Ribosomal protein l34-like protein



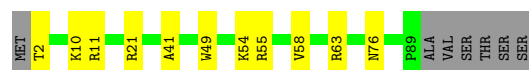
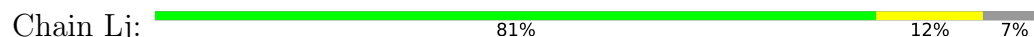
- Molecule 40: dolichyl-diphosphooligosaccharide--protein glycotransferase

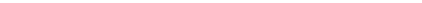


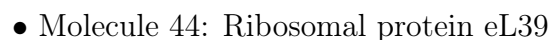
- Molecule 41: 60S ribosomal protein L36

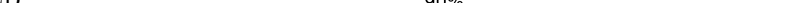


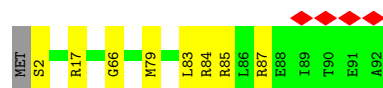
- Molecule 42: Ribosomal protein L37

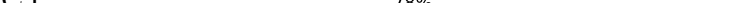


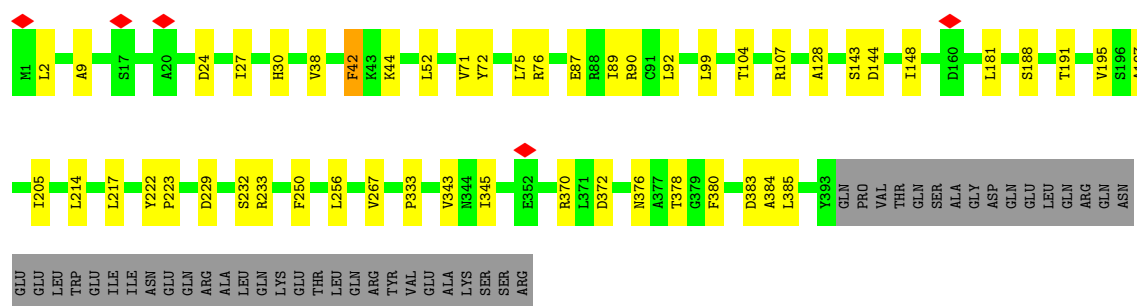
- Chain Lk: 

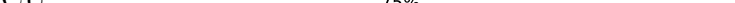


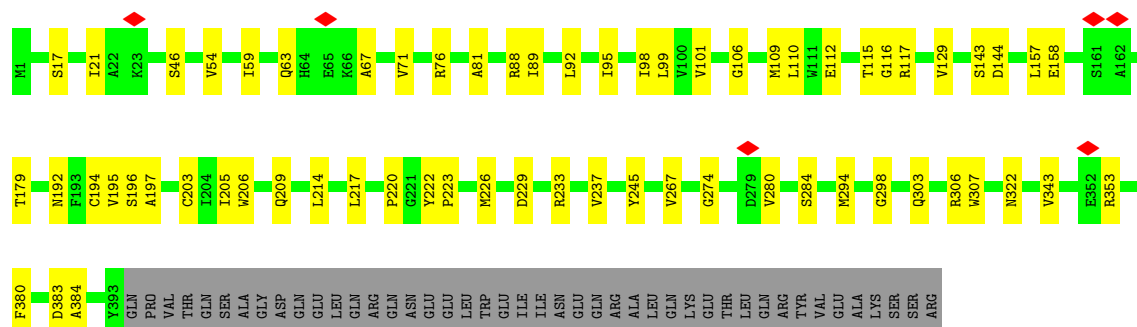
- Chain Lp:  90% 9%



- Chain CT:  78% 11% 10%



- Chain CU: 

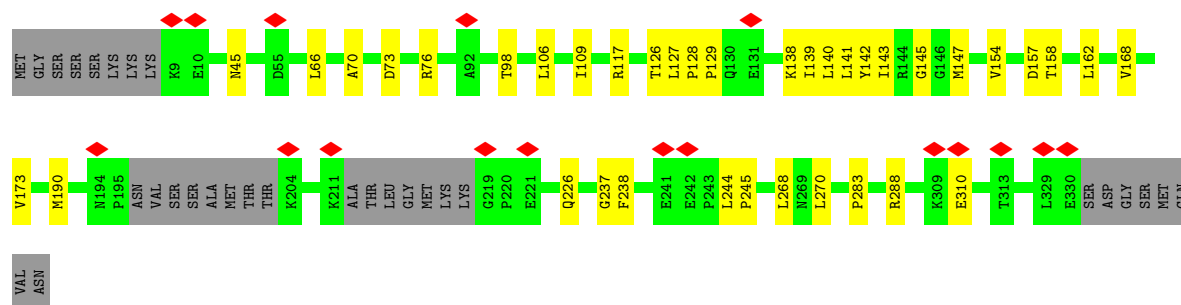
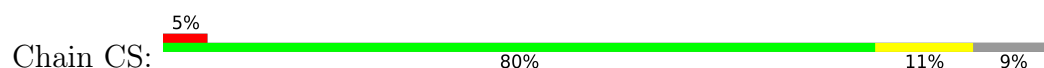


[illegible]

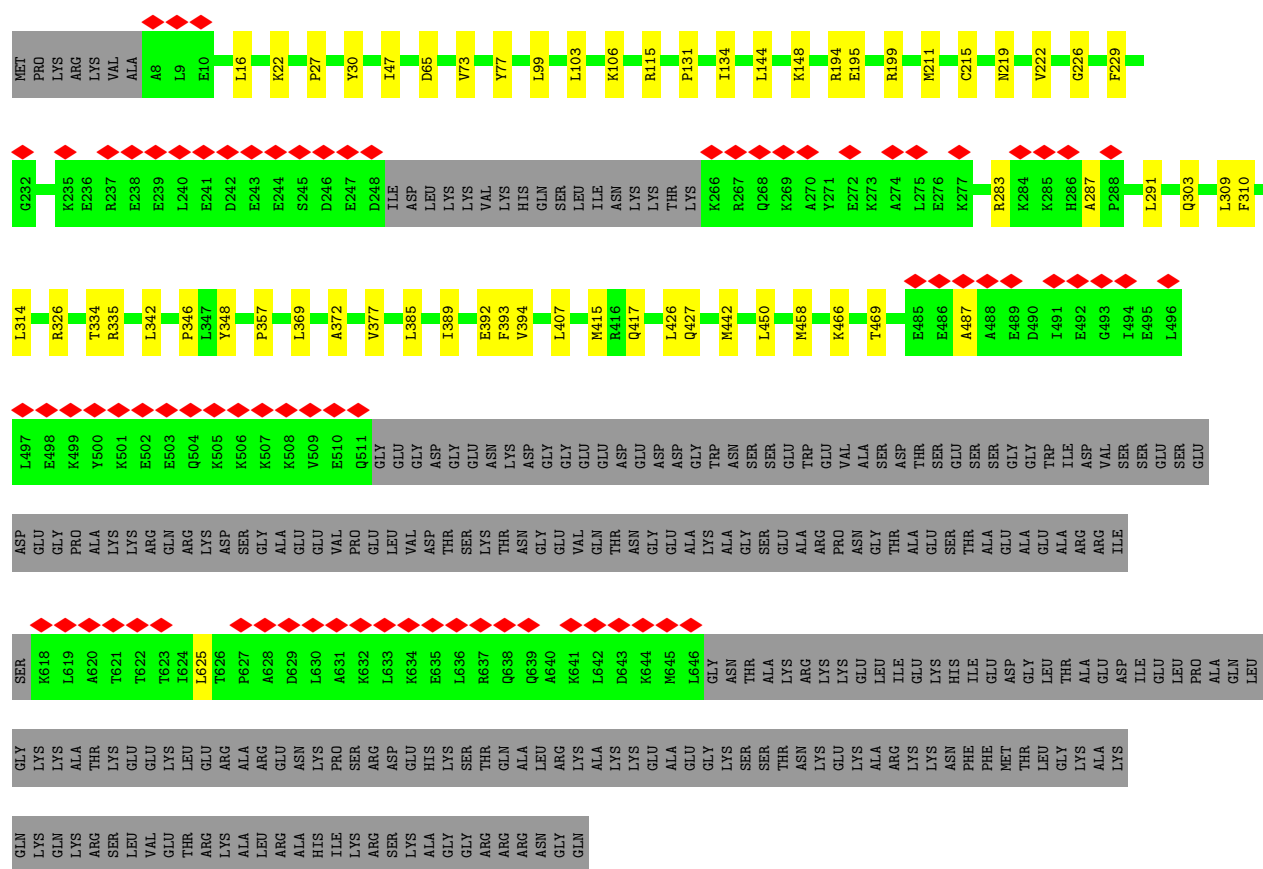
Chain CV:

Protein structure visualization showing a chain (CV) with a high degree of conservation (61% green, 9% yellow, 30% grey). The structure is a complex fold, likely a dimer or oligomer, with multiple alpha-helices and beta-sheets. The residues are labeled with their three-letter codes and positions, such as MET, T2, A3, L7, R8, I30, L34, R35, C36, Q44, ASP, ALA, LYS, LYS, ASP, ARG, T52, S53, E54, T55, I56, R78, L84, A87, V91, E95, S96, L97, R98, E101, V110, L117, K120, E121, L133, L134, Q138, T139, L140, M144, A153, L157, K161, P162, A164, S165, G166, R167, P168, L169, D177, T178, W181, M194, A210, V219, L223, N226, A262, D263, Q264, V265, A268, Y279, P301, R312, L313, L320, Y323, F324, N325, L340, R345, I350, L354, G355, A356, E357, and D358. The structure is shown in a 3D perspective view, with the ribbon color transitioning from green to yellow to grey.

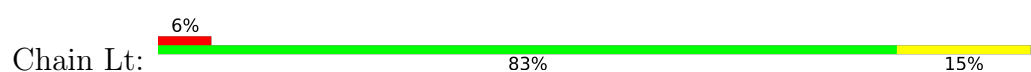
- Molecule 48: Pre-rRNA-processing protein IPI1

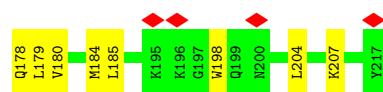


- Molecule 49: Protein SDA1



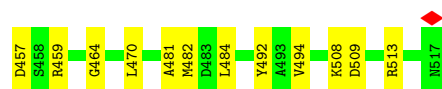
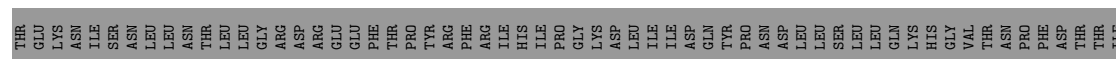
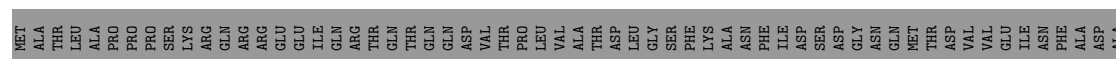
- Molecule 50: Ribosomal protein





- Molecule 51: Ribosome assembly protein 4

Chain Ch: 68% 7% 25%



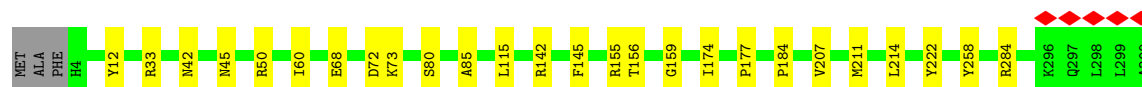
- Molecule 52: Putative ribosomal protein

Chain LJ: 82% 15% .



- Molecule 53: 60S ribosomal protein 15-like protein

Chain LD: 89% 9% .

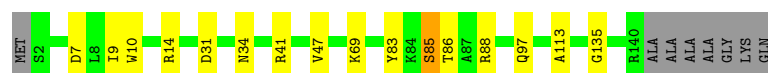


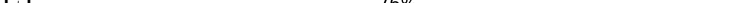
- Molecule 54: 5S rRNA

Chain C4: 66% 29% . .



- Molecule 55: Putative 60S ribosomal protein

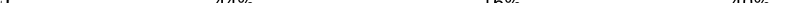


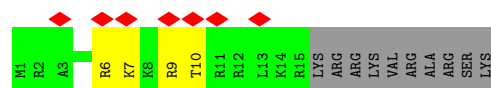
- Chain LT:  76% 12% 12%



- Chain Lb:



- Chain Lr: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	21061	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 ($e^-/\text{\AA}^2$)	46	Depositor
Minimum defocus (nm)	400	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.451	Depositor
Minimum map value	-0.169	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	522.5, 522.5, 522.5	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	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: OMC, ZN, MG, OMG, A2M, OMU, GTP

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	0.15	1/73080 (0.0%)	0.31	0/113915
2	C2	0.13	0/3573	0.31	0/5563
3	CF	0.17	0/1972	0.45	0/2660
4	CH	0.18	0/5145	0.41	1/6923 (0.0%)
5	CK	0.16	0/1913	0.37	0/2571
6	CL	0.17	0/627	0.34	0/839
7	CN	0.17	0/1875	0.45	0/2552
8	CO	0.15	0/470	0.34	0/619
9	CQ	0.20	0/1500	0.48	1/1995 (0.1%)
10	Cb	0.16	0/845	0.40	0/1128
11	Cd	0.16	0/3691	0.45	4/4975 (0.1%)
12	Cz	0.20	0/892	0.44	0/1167
13	LA	0.16	0/1917	0.44	0/2580
14	LB	0.16	0/3165	0.41	0/4250
15	LC	0.15	0/2802	0.36	0/3778
16	LE	0.18	0/1497	0.46	0/2018
17	LF	0.19	0/2061	0.43	0/2765
18	LG	0.17	0/1909	0.41	0/2556
19	LH	0.16	0/1515	0.39	0/2037
20	LK	0.23	0/1198	0.59	2/1611 (0.1%)
21	LL	0.16	0/1614	0.37	0/2168
22	LM	0.16	0/1145	0.36	0/1539
23	LN	0.16	0/1741	0.40	0/2332
24	LO	0.17	0/1645	0.41	0/2205
25	LP	0.16	0/1364	0.40	0/1835
26	LQ	0.16	0/1170	0.37	0/1573
27	LR	0.17	0/1260	0.38	0/1683
28	LS	0.17	0/1465	0.39	0/1970
29	LU	0.21	0/851	0.53	0/1143
30	LV	0.16	0/1009	0.37	0/1357
31	LX	0.18	0/978	0.48	0/1320
32	LY	0.16	0/1070	0.41	0/1432

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LZ	0.17	0/1125	0.44	0/1508
34	La	0.19	0/892	0.47	0/1200
35	Lc	0.17	0/714	0.41	0/960
36	Ld	0.14	0/889	0.36	0/1192
37	Le	0.18	0/1035	0.43	0/1379
38	Lf	0.16	0/883	0.38	0/1187
39	Lg	0.17	0/898	0.39	0/1207
40	Lh	0.19	0/1014	0.43	0/1349
41	Li	0.17	0/828	0.44	0/1092
42	Lj	0.15	0/712	0.40	0/944
43	Lk	0.21	0/632	0.47	0/842
44	Ll	0.15	0/446	0.38	0/593
45	Lp	0.19	0/702	0.48	0/935
46	CT	0.19	0/3006	0.47	0/4110
46	CU	0.18	0/3018	0.49	0/4125
47	CV	0.21	0/4312	0.47	2/5897 (0.0%)
47	CW	0.22	0/4299	0.50	3/5882 (0.1%)
48	CS	0.19	0/2442	0.49	2/3315 (0.1%)
49	CR	0.18	0/3912	0.44	2/5320 (0.0%)
50	Lt	0.21	0/1684	0.52	0/2266
51	Ch	0.17	0/3137	0.49	0/4262
52	LJ	0.17	0/1389	0.47	0/1856
53	LD	0.15	0/2412	0.41	0/3247
54	C4	0.15	0/2737	0.32	0/4262
55	Lq	0.16	0/1079	0.40	0/1454
56	LT	0.19	0/1146	0.51	0/1546
57	Lb	0.17	0/287	0.54	0/384
58	Lr	0.15	0/139	0.41	0/179
All	All	0.17	1/172728 (0.0%)	0.38	17/249552 (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
46	CT	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	1847	A2M	O3'-P	5.03	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	Cd	16	ARG	CA-C-N	9.65	134.20	120.49
11	Cd	16	ARG	C-N-CA	9.65	134.20	120.49
48	CS	126	THR	CA-C-N	7.77	131.19	120.39
48	CS	126	THR	C-N-CA	7.77	131.19	120.39
47	CV	400	ALA	CA-C-N	6.08	124.07	120.24

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
46	CT	42	PHE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C1	66031	0	33324	449	0
2	C2	3196	0	1616	18	0
3	CF	1934	0	1945	11	0
4	CH	5061	0	5152	59	0
5	CK	1878	0	1963	23	0
6	CL	618	0	630	10	0
7	CN	1850	0	1845	23	0
8	CO	468	0	503	2	0
9	CQ	1476	0	1519	14	0
10	Cb	830	0	838	9	0
11	Cd	3614	0	3741	28	0
12	Cz	884	0	967	9	0
13	LA	1878	0	1940	23	0
14	LB	3097	0	3214	32	0
15	LC	2745	0	2864	20	0
16	LE	1470	0	1561	13	0
17	LF	2023	0	2132	15	0
18	LG	1880	0	2018	14	0
19	LH	1495	0	1573	12	0
20	LK	1184	0	1249	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	LL	1587	0	1655	11	0
22	LM	1126	0	1198	15	0
23	LN	1704	0	1767	27	0
24	LO	1611	0	1702	15	0
25	LP	1343	0	1369	12	0
26	LQ	1156	0	1252	12	0
27	LR	1241	0	1298	10	0
28	LS	1430	0	1492	16	0
29	LU	838	0	861	7	0
30	LV	991	0	1044	10	0
31	LX	962	0	1039	11	0
32	LY	1056	0	1143	11	0
33	LZ	1102	0	1159	9	0
34	La	872	0	903	12	0
35	Lc	705	0	751	5	0
36	Ld	875	0	918	6	0
37	Le	1017	0	1092	10	0
38	Lf	862	0	891	9	0
39	Lg	885	0	935	7	0
40	Lh	1003	0	1116	5	0
41	Li	821	0	895	10	0
42	Lj	698	0	726	9	0
43	Lk	624	0	671	7	0
44	Ll	436	0	473	9	0
45	Lp	694	0	733	10	0
46	CT	2938	0	2870	33	0
46	CU	2950	0	2899	36	0
47	CV	4217	0	4334	43	0
47	CW	4204	0	4309	57	0
48	CS	2391	0	2411	24	0
49	CR	3844	0	3684	37	0
50	Lt	1660	0	1768	23	0
51	Ch	3050	0	2974	22	0
52	LJ	1367	0	1399	18	0
53	LD	2366	0	2315	19	0
54	C4	2451	0	1244	12	0
55	Lq	1061	0	1108	11	0
56	LT	1124	0	1170	16	0
57	Lb	280	0	275	5	0
58	Lr	138	0	163	3	0
59	CH	32	0	12	1	0
59	Cd	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
60	CH	1	0	0	0	0
60	Cd	2	0	0	0	0
61	CQ	1	0	0	0	0
61	Cb	1	0	0	0	0
61	Lg	1	0	0	0	0
61	Lj	1	0	0	0	0
61	Lp	1	0	0	0	0
62	C1	1	0	0	0	0
62	CH	1	0	0	0	0
62	Cd	2	0	0	0	0
All	All	163368	0	130624	1141	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 4.

The worst 5 of 1141 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	1.27	0.82
49:CR:283:ARG:O	49:CR:287:ALA:HB2	1.89	0.72
16:LE:162:GLN:NE2	16:LE:166:ASP:OD2	2.24	0.71
17:LF:149:SER:OG	17:LF:246:ARG:NH1	2.24	0.70
53:LD:284:ARG:NH2	54:C4:109:G:OP2	2.24	0.70

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	
3	CF	243/270 (90%)	238 (98%)	5 (2%)	0	100	100
4	CH	621/661 (94%)	619 (100%)	2 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CK	227/261 (87%)	223 (98%)	4 (2%)	0	100	100
6	CL	77/558 (14%)	76 (99%)	1 (1%)	0	100	100
7	CN	244/246 (99%)	237 (97%)	7 (3%)	0	100	100
8	CO	56/120 (47%)	55 (98%)	1 (2%)	0	100	100
9	CQ	181/225 (80%)	180 (99%)	1 (1%)	0	100	100
10	Cb	99/117 (85%)	97 (98%)	2 (2%)	0	100	100
11	Cd	445/627 (71%)	437 (98%)	8 (2%)	0	100	100
12	Cz	101/123 (82%)	100 (99%)	1 (1%)	0	100	100
13	LA	245/254 (96%)	237 (97%)	8 (3%)	0	100	100
14	LB	386/392 (98%)	383 (99%)	3 (1%)	0	100	100
15	LC	361/365 (99%)	356 (99%)	5 (1%)	0	100	100
16	LE	187/200 (94%)	180 (96%)	7 (4%)	0	100	100
17	LF	246/249 (99%)	242 (98%)	3 (1%)	1 (0%)	30	58
18	LG	233/262 (89%)	230 (99%)	3 (1%)	0	100	100
19	LH	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
20	LK	156/165 (94%)	155 (99%)	1 (1%)	0	100	100
21	LL	201/213 (94%)	200 (100%)	1 (0%)	0	100	100
22	LM	139/142 (98%)	136 (98%)	3 (2%)	0	100	100
23	LN	200/203 (98%)	195 (98%)	5 (2%)	0	100	100
24	LO	201/204 (98%)	198 (98%)	3 (2%)	0	100	100
25	LP	167/187 (89%)	164 (98%)	3 (2%)	0	100	100
26	LQ	142/213 (67%)	139 (98%)	3 (2%)	0	100	100
27	LR	153/2898 (5%)	151 (99%)	2 (1%)	0	100	100
28	LS	172/174 (99%)	169 (98%)	3 (2%)	0	100	100
29	LU	103/127 (81%)	99 (96%)	4 (4%)	0	100	100
30	LV	133/139 (96%)	132 (99%)	1 (1%)	0	100	100
31	LX	119/156 (76%)	118 (99%)	1 (1%)	0	100	100
32	LY	131/138 (95%)	127 (97%)	4 (3%)	0	100	100
33	LZ	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
34	La	104/149 (70%)	101 (97%)	3 (3%)	0	100	100
35	Lc	93/108 (86%)	92 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Ld	108/120 (90%)	107 (99%)	1 (1%)	0	100	100
37	Le	124/131 (95%)	123 (99%)	1 (1%)	0	100	100
38	Lf	106/109 (97%)	105 (99%)	1 (1%)	0	100	100
39	Lg	113/119 (95%)	112 (99%)	1 (1%)	0	100	100
40	Lh	120/935 (13%)	117 (98%)	3 (2%)	0	100	100
41	Li	99/110 (90%)	99 (100%)	0	0	100	100
42	Lj	86/95 (90%)	85 (99%)	1 (1%)	0	100	100
43	Lk	74/81 (91%)	72 (97%)	2 (3%)	0	100	100
44	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
45	Lp	89/92 (97%)	88 (99%)	1 (1%)	0	100	100
46	CT	391/437 (90%)	382 (98%)	9 (2%)	0	100	100
46	CU	391/437 (90%)	377 (96%)	14 (4%)	0	100	100
47	CV	544/781 (70%)	537 (99%)	7 (1%)	0	100	100
47	CW	544/781 (70%)	539 (99%)	5 (1%)	0	100	100
48	CS	301/338 (89%)	297 (99%)	4 (1%)	0	100	100
49	CR	510/767 (66%)	506 (99%)	4 (1%)	0	100	100
50	Lt	212/217 (98%)	207 (98%)	5 (2%)	0	100	100
51	Ch	388/517 (75%)	372 (96%)	16 (4%)	0	100	100
52	LJ	166/173 (96%)	166 (100%)	0	0	100	100
53	LD	296/304 (97%)	290 (98%)	6 (2%)	0	100	100
55	Lq	137/147 (93%)	134 (98%)	2 (2%)	1 (1%)	18	46
56	LT	139/160 (87%)	136 (98%)	3 (2%)	0	100	100
57	Lb	34/65 (52%)	34 (100%)	0	0	100	100
58	Lr	13/25 (52%)	13 (100%)	0	0	100	100
All	All	11520/17465 (66%)	11326 (98%)	192 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
55	Lq	85	SER
17	LF	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	
3	CF	212/236 (90%)	212 (100%)	0	100	100
4	CH	548/575 (95%)	548 (100%)	0	100	100
5	CK	203/225 (90%)	203 (100%)	0	100	100
6	CL	60/458 (13%)	60 (100%)	0	100	100
7	CN	204/206 (99%)	204 (100%)	0	100	100
8	CO	48/99 (48%)	48 (100%)	0	100	100
9	CQ	143/192 (74%)	143 (100%)	0	100	100
10	Cb	85/101 (84%)	85 (100%)	0	100	100
11	Cd	395/541 (73%)	395 (100%)	0	100	100
12	Cz	91/107 (85%)	91 (100%)	0	100	100
13	LA	190/198 (96%)	190 (100%)	0	100	100
14	LB	328/331 (99%)	328 (100%)	0	100	100
15	LC	281/285 (99%)	281 (100%)	0	100	100
16	LE	155/166 (93%)	155 (100%)	0	100	100
17	LF	213/215 (99%)	213 (100%)	0	100	100
18	LG	197/222 (89%)	197 (100%)	0	100	100
19	LH	167/169 (99%)	167 (100%)	0	100	100
20	LK	127/136 (93%)	126 (99%)	1 (1%)	73	89
21	LL	158/176 (90%)	158 (100%)	0	100	100
22	LM	116/117 (99%)	116 (100%)	0	100	100
23	LN	179/180 (99%)	179 (100%)	0	100	100
24	LO	162/163 (99%)	162 (100%)	0	100	100
25	LP	133/152 (88%)	133 (100%)	0	100	100
26	LQ	124/178 (70%)	124 (100%)	0	100	100
27	LR	125/2396 (5%)	125 (100%)	0	100	100
28	LS	153/154 (99%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	LU	90/108 (83%)	90 (100%)	0	100	100
30	LV	98/102 (96%)	98 (100%)	0	100	100
31	LX	107/129 (83%)	107 (100%)	0	100	100
32	LY	116/119 (98%)	116 (100%)	0	100	100
33	LZ	119/121 (98%)	119 (100%)	0	100	100
34	La	93/122 (76%)	93 (100%)	0	100	100
35	Lc	76/88 (86%)	76 (100%)	0	100	100
36	Ld	90/105 (86%)	90 (100%)	0	100	100
37	Le	109/114 (96%)	109 (100%)	0	100	100
38	Lf	89/90 (99%)	89 (100%)	0	100	100
39	Lg	91/102 (89%)	91 (100%)	0	100	100
40	Lh	109/781 (14%)	109 (100%)	0	100	100
41	Li	84/93 (90%)	84 (100%)	0	100	100
42	Lj	72/78 (92%)	72 (100%)	0	100	100
43	Lk	71/77 (92%)	71 (100%)	0	100	100
44	Ll	45/46 (98%)	45 (100%)	0	100	100
45	Lp	72/74 (97%)	72 (100%)	0	100	100
46	CT	322/376 (86%)	322 (100%)	0	100	100
46	CU	326/376 (87%)	326 (100%)	0	100	100
47	CV	472/675 (70%)	471 (100%)	1 (0%)	87	96
47	CW	469/675 (70%)	469 (100%)	0	100	100
48	CS	260/291 (89%)	260 (100%)	0	100	100
49	CR	374/663 (56%)	374 (100%)	0	100	100
50	Lt	186/189 (98%)	186 (100%)	0	100	100
51	Ch	322/436 (74%)	321 (100%)	1 (0%)	86	95
52	LJ	144/150 (96%)	144 (100%)	0	100	100
53	LD	233/253 (92%)	233 (100%)	0	100	100
55	Lq	107/112 (96%)	107 (100%)	0	100	100
56	LT	120/135 (89%)	120 (100%)	0	100	100
57	Lb	26/55 (47%)	26 (100%)	0	100	100
58	Lr	13/23 (56%)	13 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9702/14736 (66%)	9699 (100%)	3 (0%)	100 100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	LK	70	GLN
51	Ch	441	ASN
47	CV	138	GLN

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

Mol	Chain	Res	Type
23	LN	86	ASN
55	Lq	43	HIS
33	LZ	105	GLN
53	LD	39	GLN
56	LT	127	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3065/3342 (91%)	562 (18%)	17 (0%)
2	C2	148/156 (94%)	18 (12%)	1 (0%)
54	C4	113/119 (94%)	21 (18%)	0
All	All	3326/3617 (91%)	601 (18%)	18 (0%)

5 of 601 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	G
1	C1	23	G
1	C1	27	A
1	C1	50	A
1	C1	60	G

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3258	U

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Mol	Chain	Res	Type
2	C2	127	U
1	C1	3301	C
1	C1	2712	G
1	C1	3230	G

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

32 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	OMG	C1	627	1	23,26,27	0.51	0	32,38,41	0.47	0
1	OMG	C1	646	1	23,26,27	0.47	0	32,38,41	0.49	0
1	OMC	C1	2918	1	19,22,23	0.54	0	25,31,34	0.80	1 (4%)
1	OMC	C1	778	1	19,22,23	0.56	0	25,31,34	0.93	1 (4%)
1	OMU	C1	2683	1	19,22,23	3.13	6 (31%)	25,31,34	1.83	5 (20%)
1	OMC	C1	2838	1	19,22,23	0.57	0	25,31,34	0.98	2 (8%)
1	OMC	C1	1491	1	19,22,23	0.52	0	25,31,34	0.77	0
1	OMU	C1	1868	1	19,22,23	3.13	6 (31%)	25,31,34	1.88	5 (20%)
1	A2M	C1	389	1	22,25,26	3.98	12 (54%)	30,36,39	3.41	14 (46%)
1	OMG	C1	2881	1	23,26,27	0.46	0	32,38,41	0.47	0
1	OMG	C1	2774	1	23,26,27	0.46	0	32,38,41	0.45	0
1	A2M	C1	1847	1	22,25,26	4.00	12 (54%)	30,36,39	3.49	15 (50%)
1	OMU	C1	1917	1	19,22,23	3.18	6 (31%)	25,31,34	1.84	5 (20%)
1	OMG	C1	385	1	23,26,27	0.47	0	32,38,41	0.51	0
1	OMG	C1	2876	1	23,26,27	0.45	0	32,38,41	0.48	0
1	OMG	C1	787	1	23,26,27	0.47	0	32,38,41	0.57	0
1	A2M	C1	1432	1	22,25,26	4.00	11 (50%)	30,36,39	3.39	12 (40%)
1	OMU	C1	2380	1	19,22,23	3.11	6 (31%)	25,31,34	1.78	5 (20%)
1	OMU	C1	2688	1	19,22,23	3.17	6 (31%)	25,31,34	1.76	4 (16%)
1	OMU	C1	2384	1	19,22,23	3.11	6 (31%)	25,31,34	1.79	4 (16%)
1	OMG	C1	1433	1	23,26,27	0.47	0	32,38,41	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	C1	848	1	22,25,26	4.00	12 (54%)	30,36,39	3.41	15 (50%)
1	A2M	C1	858	1	22,25,26	4.00	12 (54%)	30,36,39	3.38	13 (43%)
1	OMG	C1	2358	1	23,26,27	0.47	0	32,38,41	0.55	0
1	A2M	C1	1223	1	22,25,26	3.98	12 (54%)	30,36,39	3.35	13 (43%)
1	OMC	C1	1836	1	19,22,23	0.58	0	25,31,34	0.91	1 (4%)
1	OMC	C1	1812	1	19,22,23	0.52	0	25,31,34	0.73	0
1	OMC	C1	2300	1	19,22,23	0.50	0	25,31,34	0.65	0
1	A2M	C1	637	1	22,25,26	3.96	11 (50%)	30,36,39	3.36	13 (43%)
1	A2M	C1	2289	1	22,25,26	4.00	10 (45%)	30,36,39	3.32	13 (43%)
1	OMC	C1	1420	1	19,22,23	0.56	0	25,31,34	1.05	1 (4%)
1	OMU	C1	2690	1	19,22,23	3.25	6 (31%)	25,31,34	1.86	6 (24%)

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	OMG	C1	627	1	-	2/9/27/28	0/3/3/3
1	OMG	C1	646	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	2918	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	778	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2683	1	-	1/9/27/28	0/2/2/2
1	OMC	C1	2838	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1491	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	1868	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	389	1	-	2/9/27/28	0/3/3/3
1	OMG	C1	2881	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	2774	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	1847	1	-	3/9/27/28	0/3/3/3
1	OMU	C1	1917	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	385	1	-	2/9/27/28	0/3/3/3
1	OMG	C1	2876	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	787	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	1432	1	-	0/9/27/28	0/3/3/3
1	OMU	C1	2380	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2688	1	-	3/9/27/28	0/2/2/2
1	OMU	C1	2384	1	-	0/9/27/28	0/2/2/2
1	OMG	C1	1433	1	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	A2M	C1	848	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	858	1	-	0/9/27/28	0/3/3/3
1	OMG	C1	2358	1	-	0/9/27/28	0/3/3/3
1	A2M	C1	1223	1	-	2/9/27/28	0/3/3/3
1	OMC	C1	1836	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	1812	1	-	0/9/27/28	0/2/2/2
1	OMC	C1	2300	1	-	0/9/27/28	0/2/2/2
1	A2M	C1	637	1	-	1/9/27/28	0/3/3/3
1	A2M	C1	2289	1	-	0/9/27/28	0/3/3/3
1	OMC	C1	1420	1	-	0/9/27/28	0/2/2/2
1	OMU	C1	2690	1	-	3/9/27/28	0/2/2/2

The worst 5 of 134 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C1	2289	A2M	C3'-C2'	-13.06	1.24	1.53
1	C1	858	A2M	C3'-C2'	-13.04	1.24	1.53
1	C1	848	A2M	C3'-C2'	-12.98	1.24	1.53
1	C1	1432	A2M	C3'-C2'	-12.95	1.24	1.53
1	C1	1847	A2M	C3'-C2'	-12.93	1.24	1.53

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1847	A2M	C1'-N9-C8	-9.54	105.92	127.09
1	C1	1432	A2M	C1'-N9-C8	-9.34	106.36	127.09
1	C1	389	A2M	C1'-N9-C8	-9.27	106.51	127.09
1	C1	858	A2M	C1'-N9-C8	-9.15	106.80	127.09
1	C1	637	A2M	C1'-N9-C8	-9.13	106.84	127.09

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C1	389	A2M	C1'-C2'-O2'-CM'
1	C1	637	A2M	C1'-C2'-O2'-CM'
1	C1	1223	A2M	C1'-C2'-O2'-CM'
1	C1	1433	OMG	O4'-C4'-C5'-O5'
1	C1	2683	OMU	C1'-C2'-O2'-CM2

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C1	389	A2M	1	0
1	C1	1432	A2M	1	0
1	C1	2384	OMU	1	0
1	C1	848	A2M	1	0
1	C1	1420	OMC	2	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	$\# Z > 2$
59	GTP	Cd	1000	60	33,34,34	0.99	2 (6%)	50,54,54	1.60	9 (18%)
59	GTP	CH	701	60	33,34,34	0.91	1 (3%)	50,54,54	1.58	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
59	GTP	Cd	1000	60	-	4/22/38/38	0/3/3/3
59	GTP	CH	701	60	-	5/22/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	CH	701	GTP	C2-N3	2.14	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Cd	1000	GTP	C2-N3	2.12	1.38	1.33
59	Cd	1000	GTP	PA-O3A	2.10	1.61	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	CH	701	GTP	C5-C4-N3	-5.02	120.41	128.39
59	Cd	1000	GTP	C5-C4-N3	-4.90	120.59	128.39
59	CH	701	GTP	C2-N3-C4	4.58	120.18	112.30
59	Cd	1000	GTP	C2-N3-C4	4.54	120.12	112.30
59	CH	701	GTP	N9-C4-N3	3.23	132.41	125.95

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	Cd	1000	GTP	C5'-O5'-PA-O1A
59	Cd	1000	GTP	C3'-C4'-C5'-O5'
59	Cd	1000	GTP	O4'-C4'-C5'-O5'
59	CH	701	GTP	O4'-C4'-C5'-O5'
59	Cd	1000	GTP	PB-O3B-PG-O1G

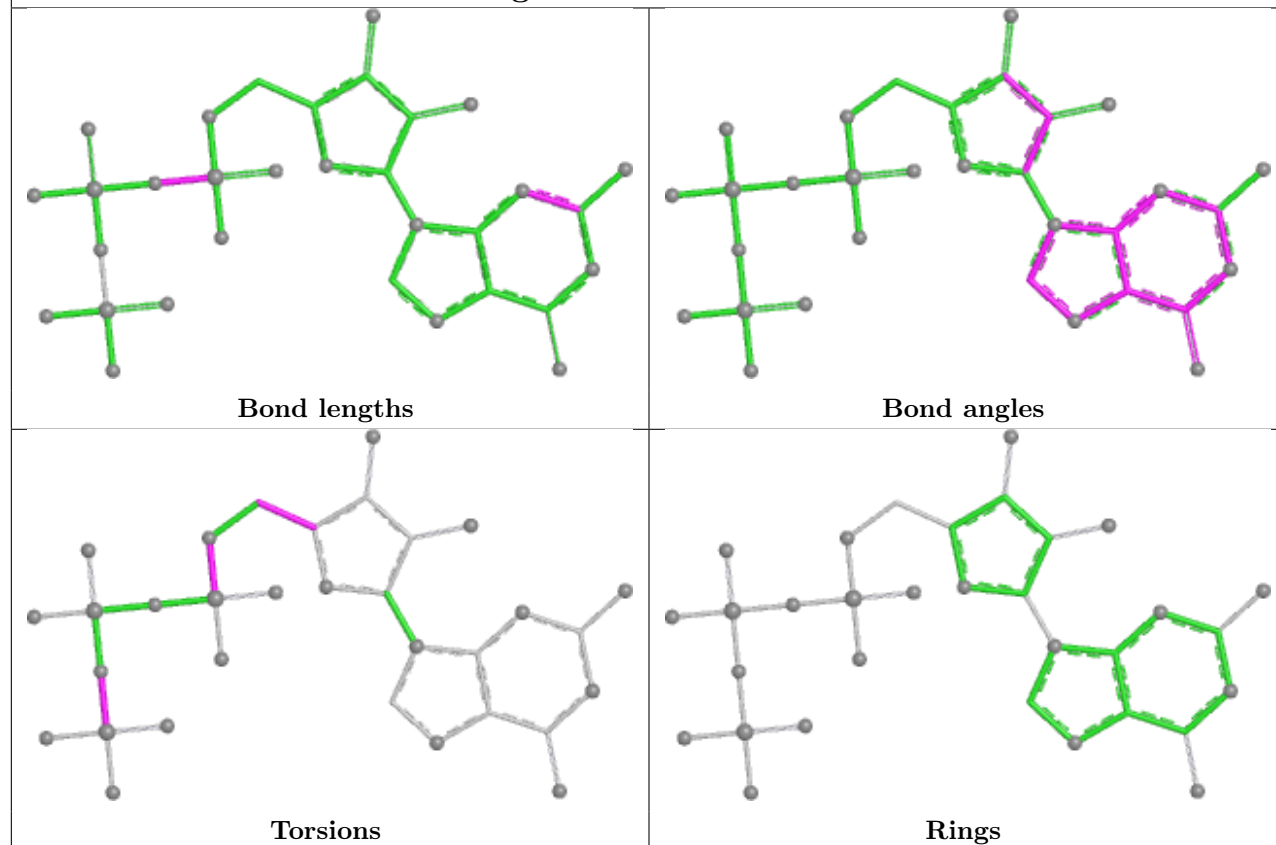
There are no ring outliers.

1 monomer is involved in 1 short contact:

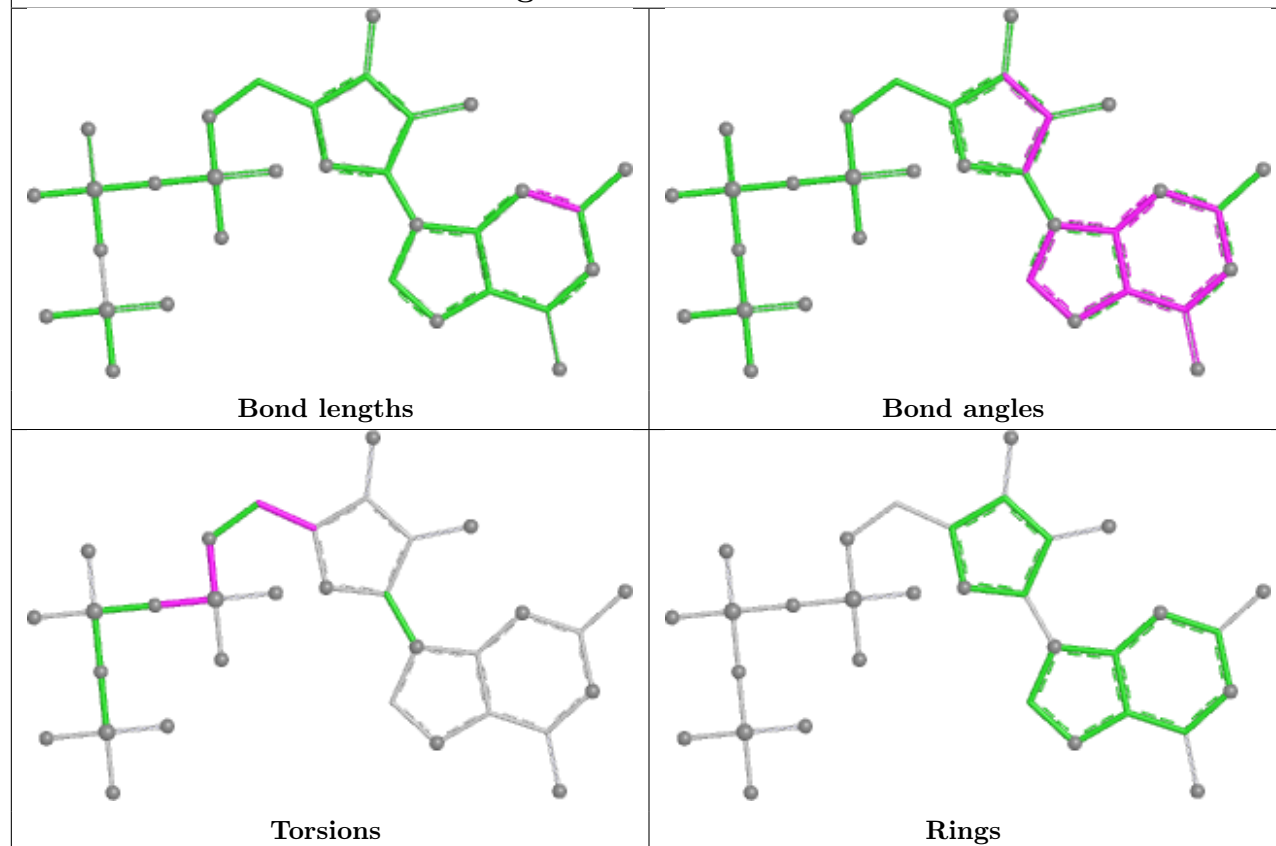
Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	CH	701	GTP	1	0

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.

Ligand GTP Cd 1000



Ligand GTP CH 701



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.

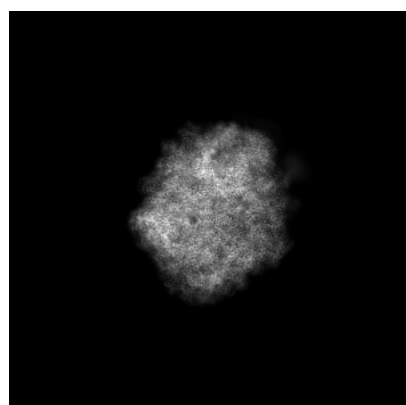
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-17957. These allow visual inspection of the internal detail of the map and identification of artifacts.

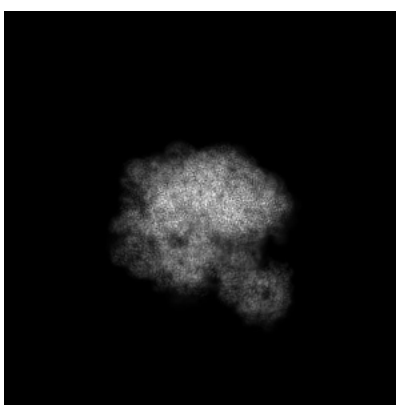
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

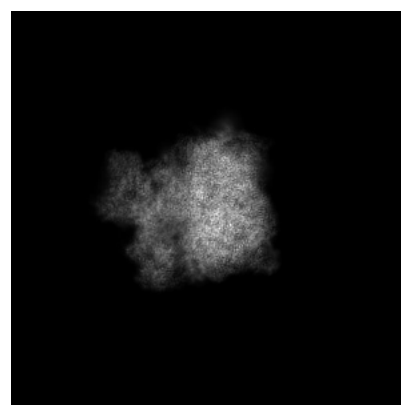
6.1.1 Primary map



X



Y

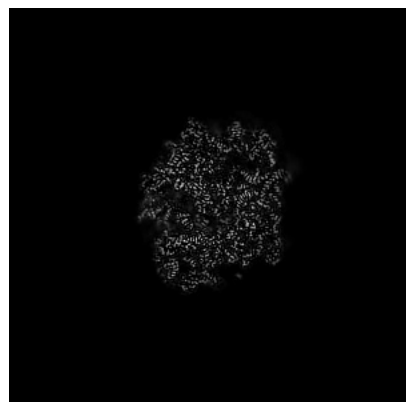


Z

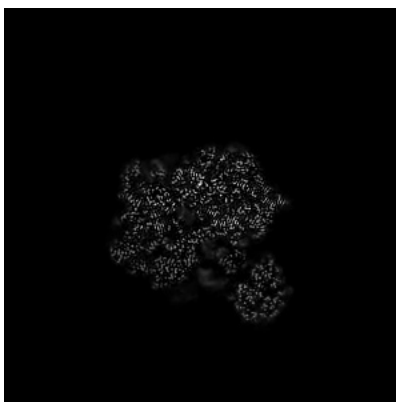
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

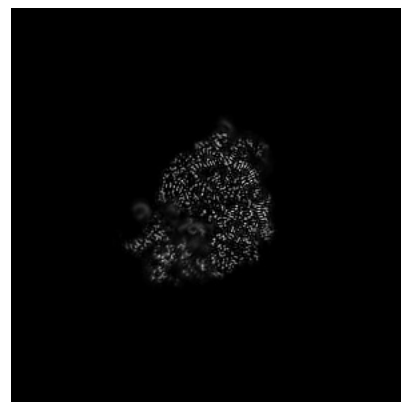
6.2.1 Primary map



X Index: 250



Y Index: 250

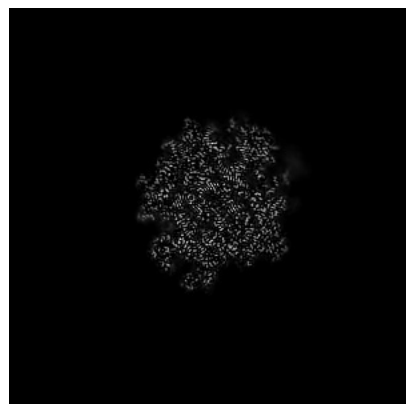


Z Index: 250

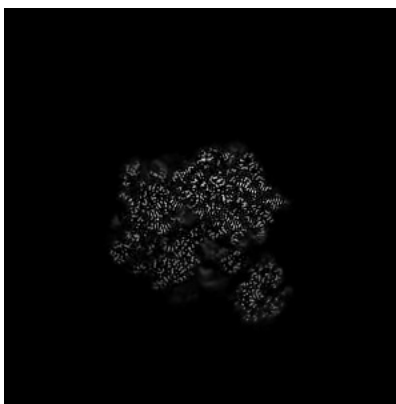
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

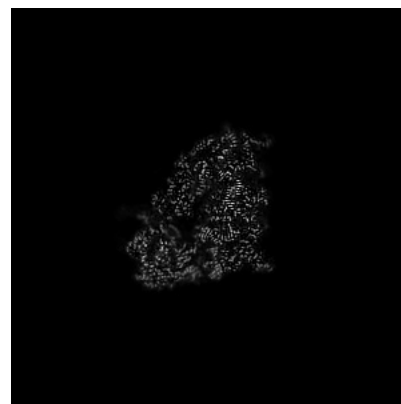
6.3.1 Primary map



X Index: 259



Y Index: 248

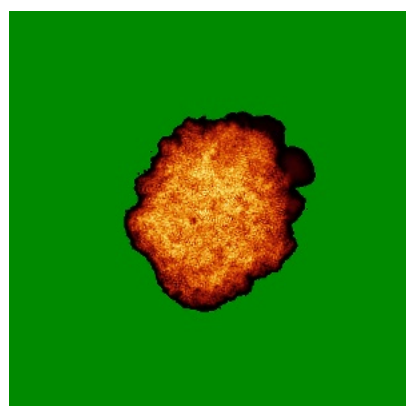


Z Index: 239

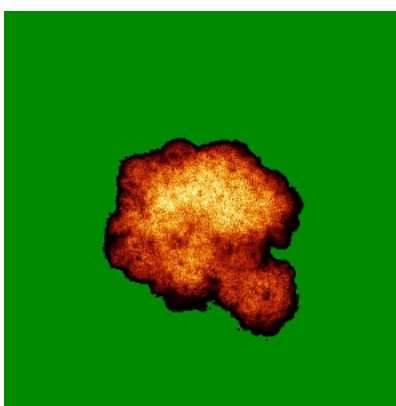
The images above show the largest variance slices of the map in three orthogonal directions.

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

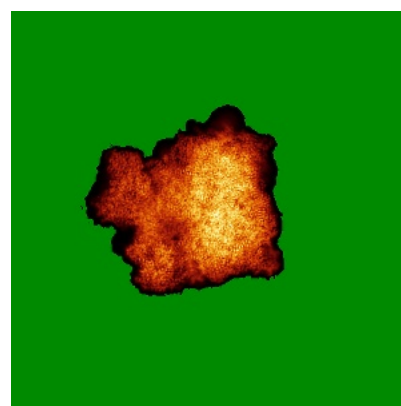
6.4.1 Primary map



X



Y

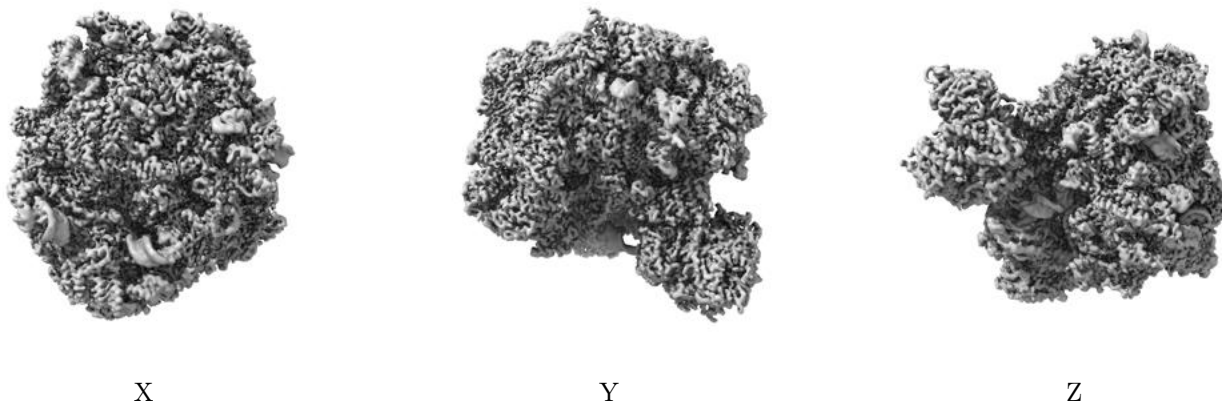


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

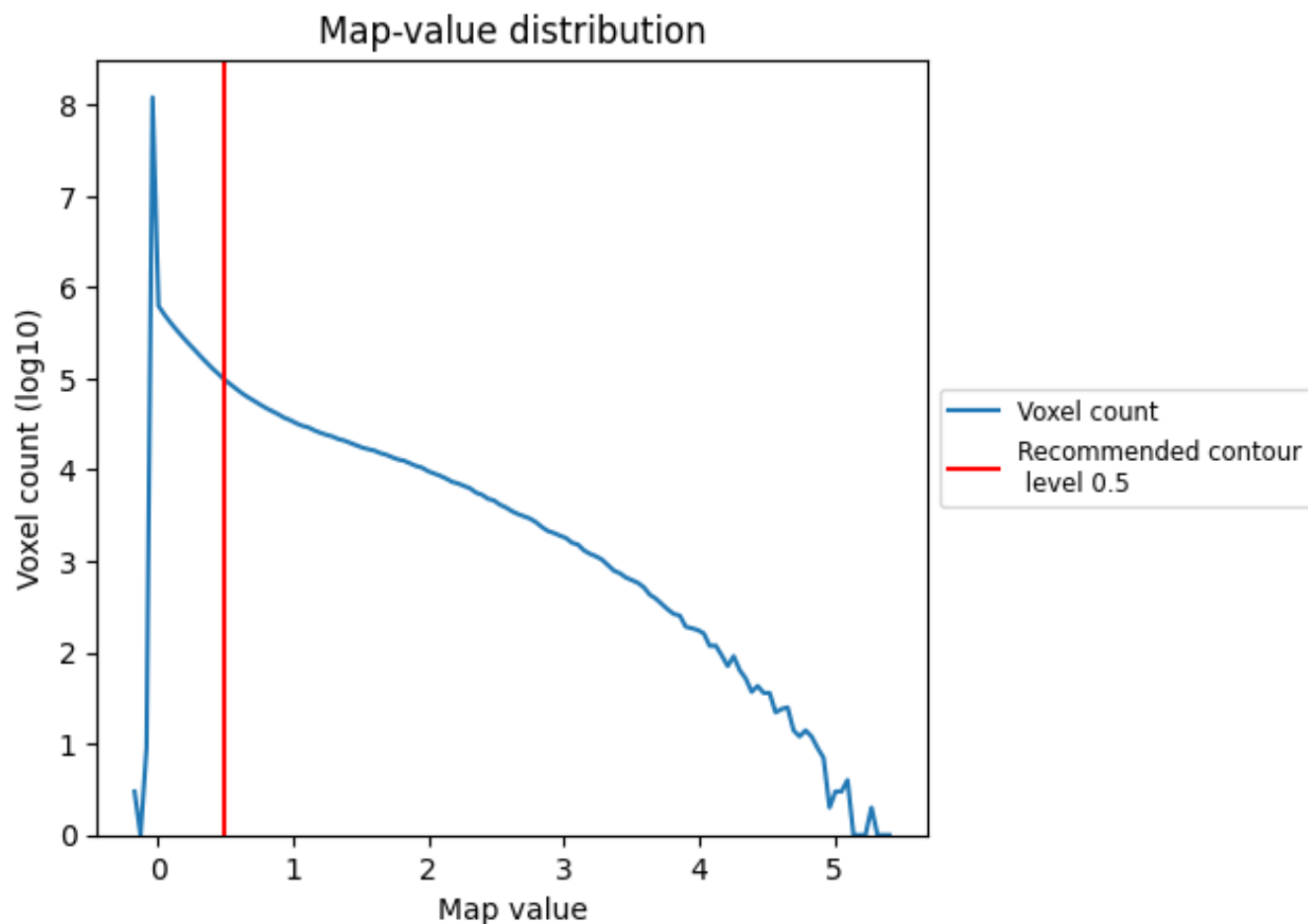
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

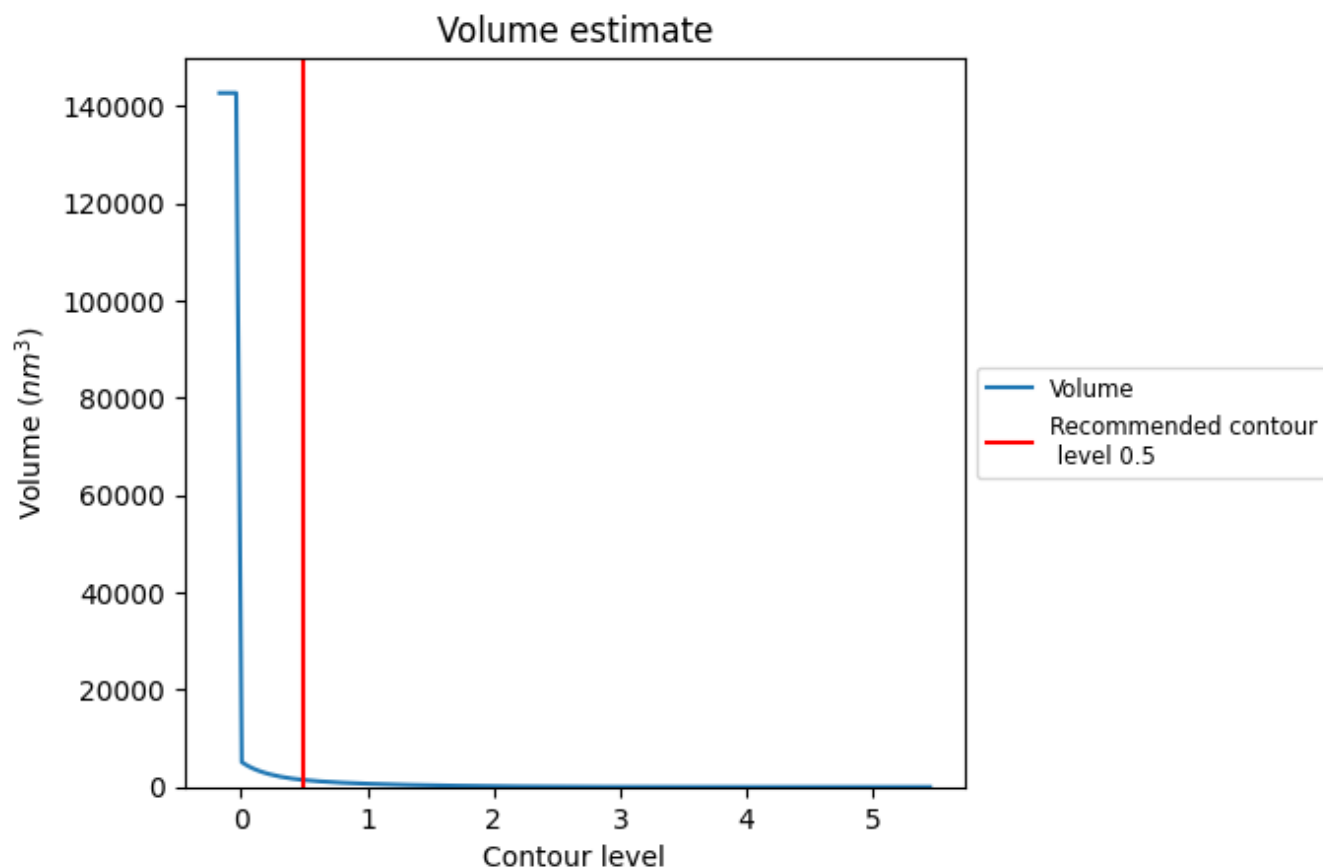
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

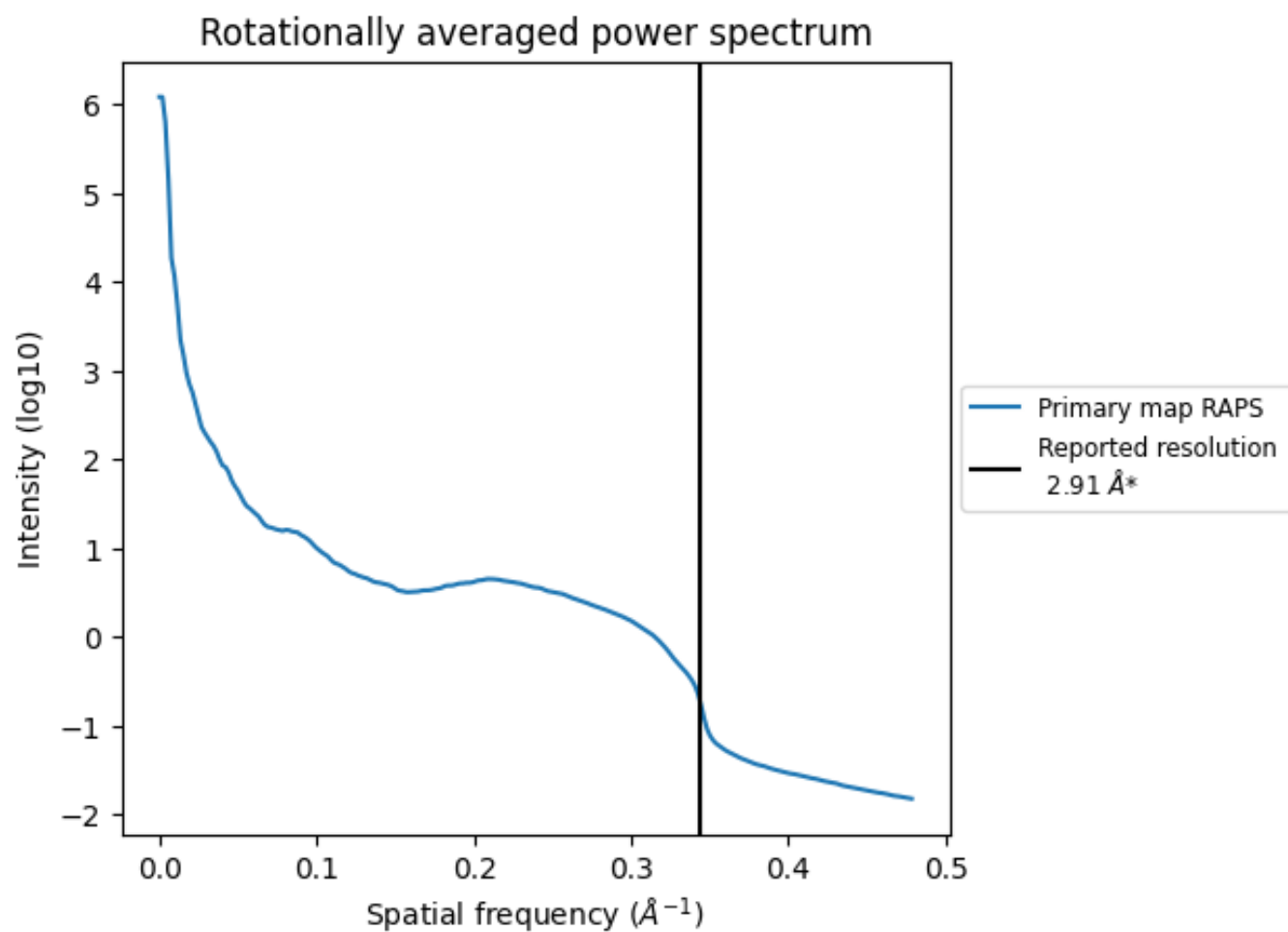
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1429 nm^3 ; this corresponds to an approximate mass of 1291 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 0.344 Å⁻¹

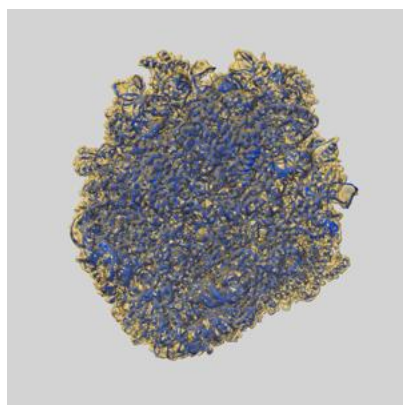
8 Fourier-Shell correlation

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

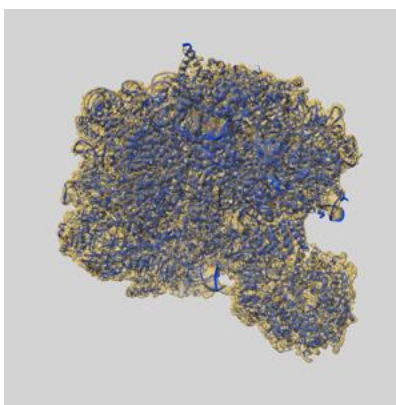
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-17957 and PDB model 8PV8. Per-residue inclusion information can be found in section [3](#) on page [16](#).

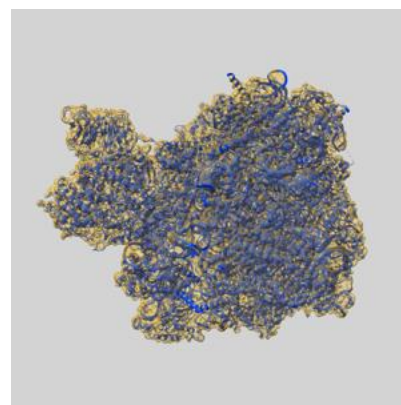
9.1 Map-model overlay [i](#)



X



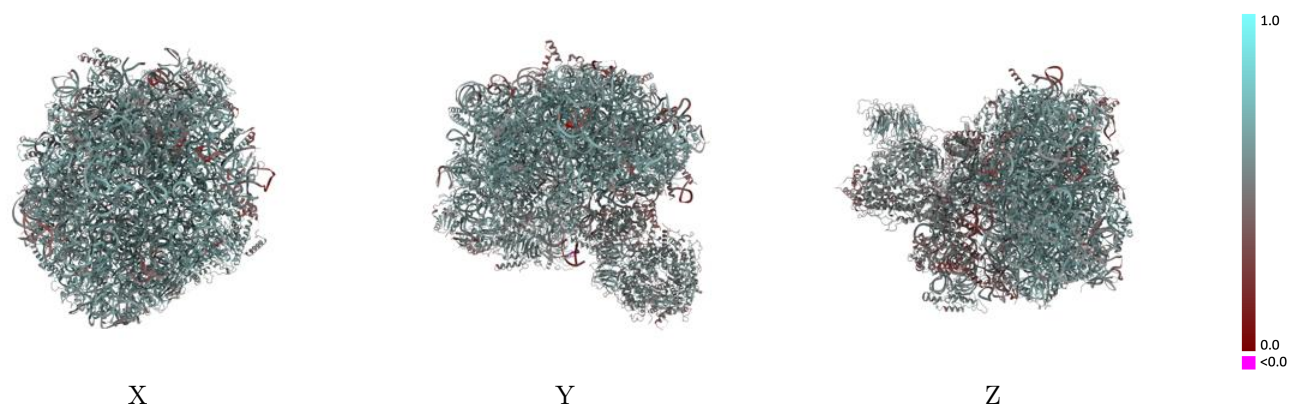
Y



Z

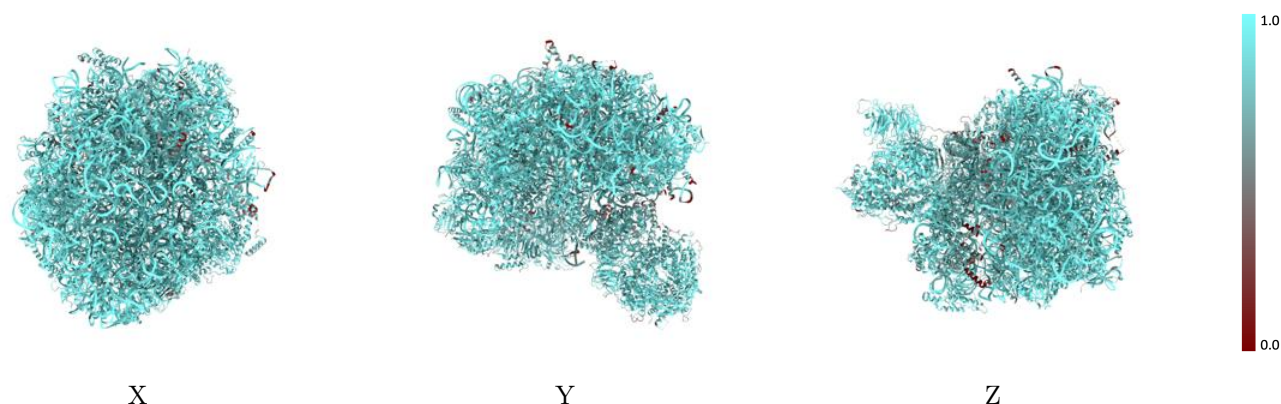
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



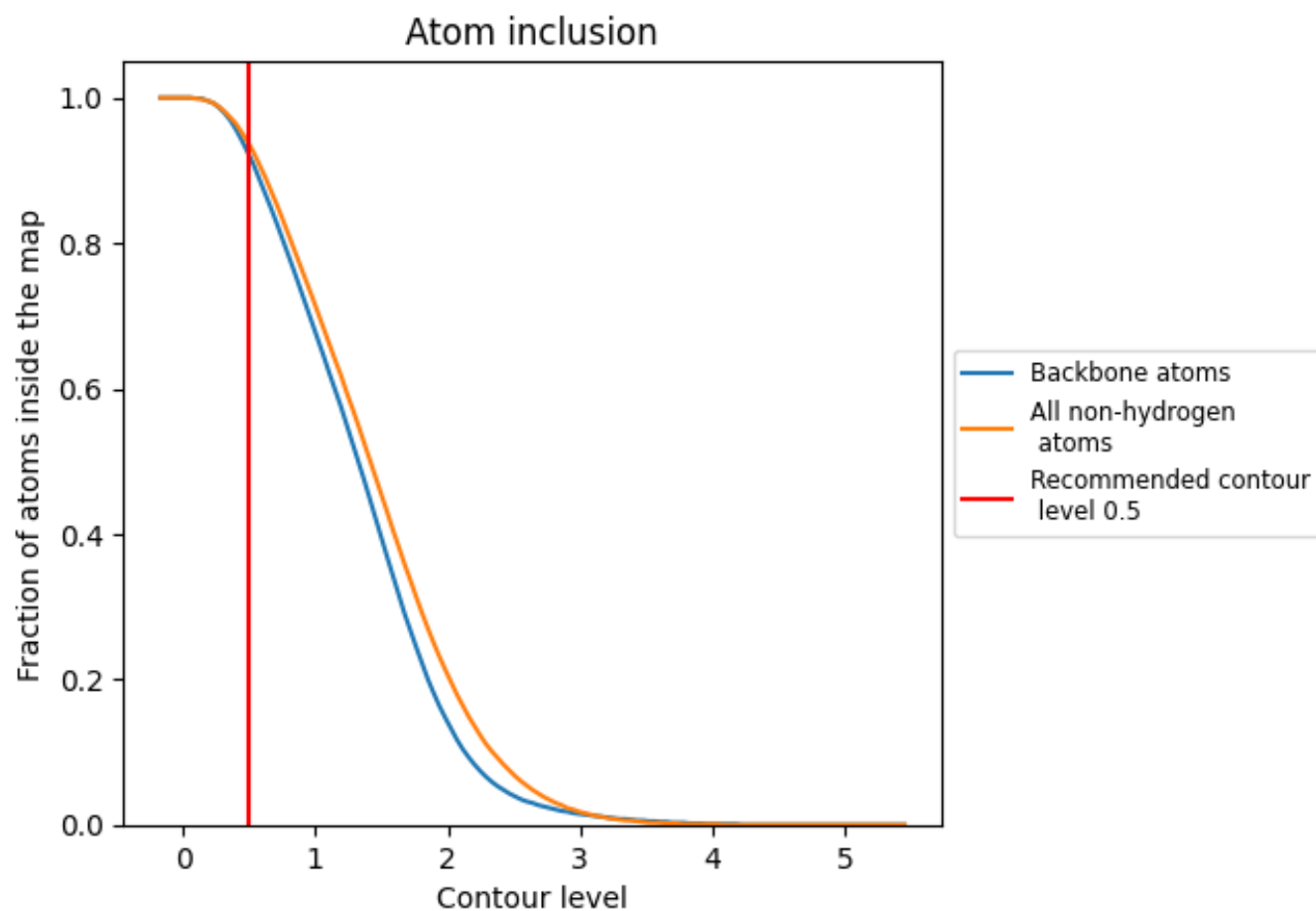
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 94% 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	 0.9360	 0.5590
C1	 0.9780	 0.5720
C2	 0.9940	 0.6040
C4	 0.9880	 0.5390
CF	 0.8830	 0.5240
CH	 0.8790	 0.5440
CK	 0.9460	 0.5920
CL	 0.8760	 0.5150
CN	 0.9410	 0.5810
CO	 0.8950	 0.5610
CQ	 0.8830	 0.5440
CR	 0.8040	 0.4930
CS	 0.7560	 0.4720
CT	 0.8830	 0.5080
CU	 0.8820	 0.5190
CV	 0.8780	 0.4930
CW	 0.8810	 0.5020
Cb	 0.9300	 0.5660
Cd	 0.8940	 0.5620
Ch	 0.9090	 0.5320
Cz	 0.8690	 0.5170
LA	 0.9730	 0.6160
LB	 0.9710	 0.6150
LC	 0.9580	 0.6020
LD	 0.9230	 0.5160
LE	 0.9160	 0.5510
LF	 0.9500	 0.5860
LG	 0.8940	 0.5530
LH	 0.9240	 0.5770
LJ	 0.9420	 0.5300
LK	 0.8170	 0.4590
LL	 0.9260	 0.5770
LM	 0.9410	 0.5820
LN	 0.9910	 0.6300
LO	 0.9680	 0.6100



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Chain	Atom inclusion	Q-score
LP	 0.9700	 0.6070
LQ	 0.9610	 0.5980
LR	 0.9390	 0.5820
LS	 0.9620	 0.5980
LT	 0.9160	 0.5000
LU	 0.8970	 0.5210
LV	 0.9630	 0.5920
LX	 0.9160	 0.5680
LY	 0.9350	 0.5790
LZ	 0.9360	 0.5690
La	 0.9470	 0.5910
Lb	 0.7050	 0.3870
Lc	 0.9130	 0.5560
Ld	 0.9330	 0.5980
Le	 0.9630	 0.6130
Lf	 0.9750	 0.6220
Lg	 0.9310	 0.5920
Lh	 0.8940	 0.5410
Li	 0.9350	 0.5610
Lj	 0.9780	 0.6210
Lk	 0.8620	 0.5140
Ll	 0.9760	 0.6230
Lp	 0.9180	 0.5690
Lq	 0.9560	 0.5890
Lr	 0.4250	 0.3730
Lt	 0.7160	 0.3850