



wwPDB EM Validation Summary Report ⓘ

Sep 20, 2026 – 11:00 pm BST

PDB ID : 9QER / pdb_00009qer
EMDB ID : EMD-53090
Title : Human pre-60S - State 1A
Authors : Thoms, M.; Denk, T.; Beckmann, R.
Deposited on : 2025-03-11
Resolution : 2.90 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:

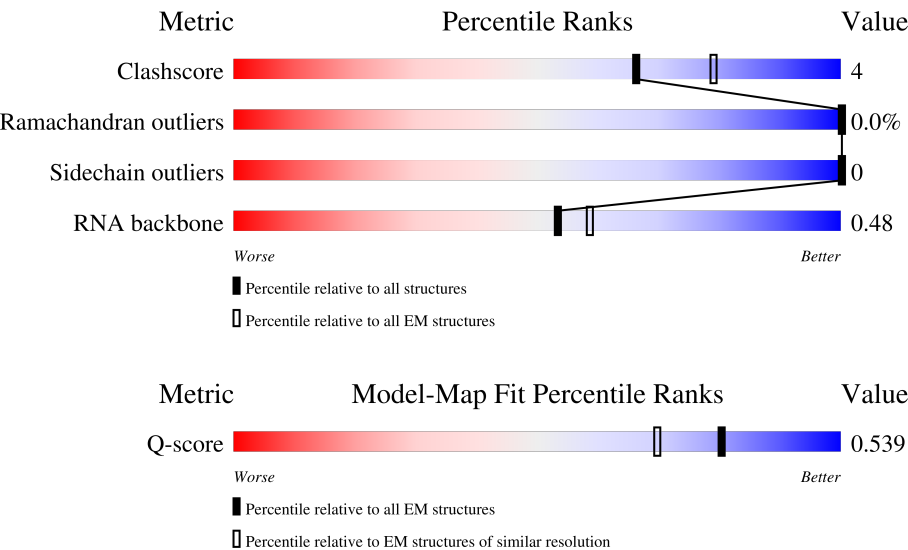
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.90 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.



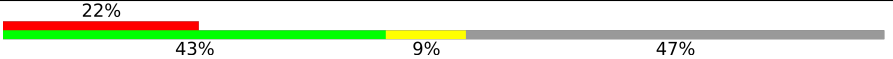
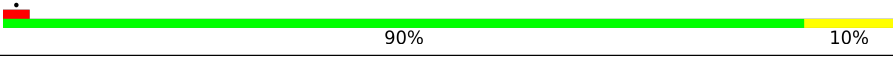
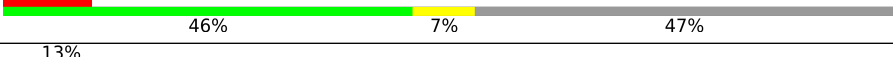
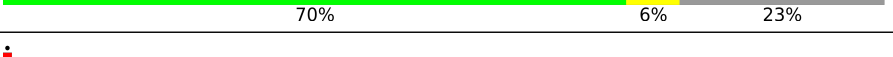
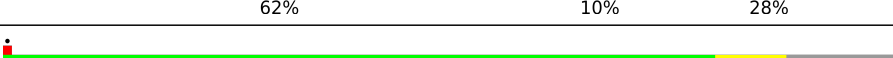
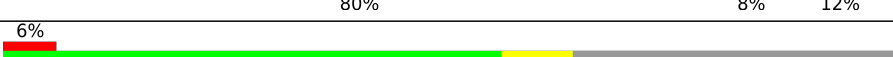
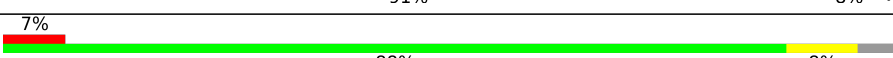
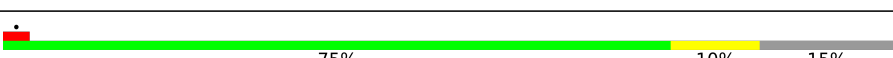
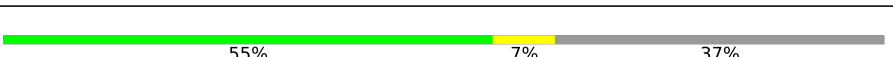
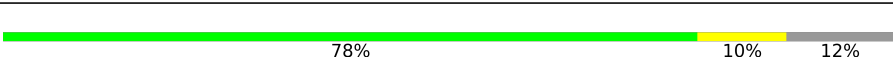
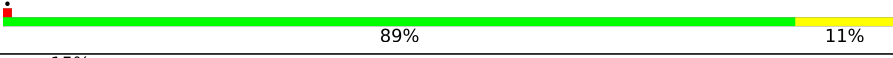
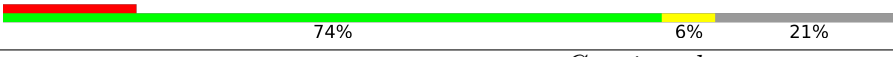
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	CA	245	
2	CB	731	
3	CC	549	

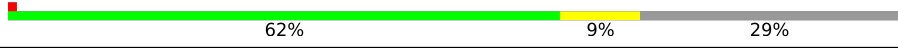
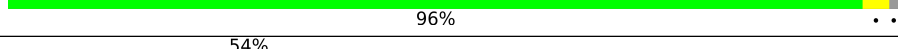
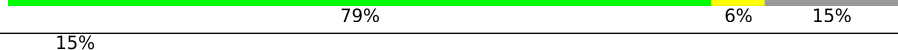
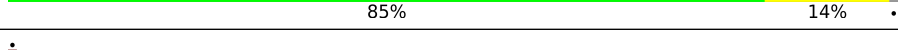
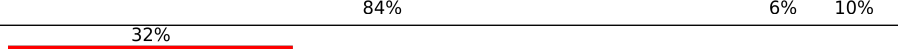
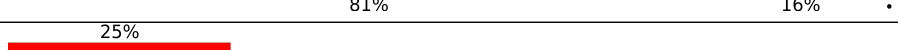
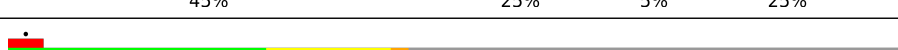
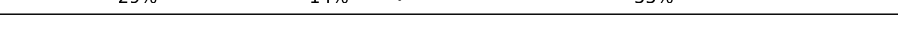
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Mol	Chain	Length	Quality of chain
4	CD	464	
5	CE	129	
6	CF	239	
7	CG	485	
8	CH	260	
9	CI	163	
10	CJ	306	
11	CK	365	
12	L7	121	
13	LB	403	
14	LC	427	
15	LD	297	
16	LE	288	
17	LF	248	
18	LG	266	
19	LH	192	
20	LJ	178	
21	LL	211	
22	LM	215	
23	LN	204	
24	LO	203	
25	LP	184	
26	LQ	188	
27	LS	176	
28	LT	160	

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Mol	Chain	Length	Quality of chain
29	LV	140	
30	LY	145	
31	La	148	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lh	123	
36	Li	105	
37	Lr	137	
38	Lt	165	
39	L8	157	
40	L5	5070	

2 Entry composition

There are 44 unique types of molecules in this entry. The entry contains 110676 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	245	Total	C	N	O	S	0	0
			1860	1153	319	375	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	448	Total	C	N	O	S	0	0
			3506	2220	631	644	11		

- Molecule 3 is a protein called Guanine nucleotide-binding protein-like 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CC	80	Total	C	N	O	S	0	0
			594	369	126	96	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CD	460	Total	C	N	O	S	0	0
			3735	2374	660	684	17		

- Molecule 5 is a protein called Protein LLP homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CE	68	Total	C	N	O	S	0	0
			537	333	115	87	2		

- Molecule 6 is a protein called mRNA turnover protein 4 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CF	218	Total	C	N	O	S	0	0
			1775	1131	312	321	11		

- Molecule 7 is a protein called Notchless protein homolog 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CG	471	Total	C	N	O	S	0	0
			3449	2149	641	648	11		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CG	85	ALA	GLU	engineered mutation	UNP Q9NVX2

- Molecule 8 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CH	259	Total	C	N	O	S	0	0
			2066	1315	389	353	9		

- Molecule 9 is a protein called Probable ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CI	115	Total	C	N	O	S	0	0
			987	628	192	157	10		

- Molecule 10 is a protein called Ribosome production factor 2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CJ	275	Total	C	N	O	S	0	0
			2176	1393	381	391	11		

- Molecule 11 is a protein called Ribosome biogenesis regulatory protein homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	CK	195	Total	C	N	O	0	0
			1545	968	304	273		

- Molecule 12 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 13 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LB	381	Total	C	N	O	S	0	0
			3054	1942	568	531	13		

- Molecule 14 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LC	328	Total	C	N	O	S	0	0
			2628	1664	518	433	13		

- Molecule 15 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LD	230	Total	C	N	O	S	0	0
			1879	1192	338	336	13		

- Molecule 16 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LE	208	Total	C	N	O	S	0	0
			1673	1081	315	273	4		

- Molecule 17 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LF	219	Total	C	N	O	S	0	0
			1790	1148	341	292	9		

- Molecule 18 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LG	170	Total	C	N	O	S	0	0
			1376	872	268	232	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 20 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LJ	170	Total	C	N	O	S	0	0
			1335	845	245	239	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LL	180	Total	C	N	O	S	0	0
			1440	902	299	236	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LM	135	Total	C	N	O	S	0	0
			1105	707	213	178	7		

- Molecule 23 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LN	179	Total	C	N	O	S	0	0
			1516	955	319	238	4		

- Molecule 24 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LO	201	Total	C	N	O	S	0	0
			1642	1058	320	259	5		

- Molecule 25 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LP	136	Total	C	N	O	S	0	0
			1089	683	206	193	7		

- Molecule 26 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LQ	151	Total	C	N	O	S	0	0
			1223	768	247	203	5		

- Molecule 27 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LS	176	Total	C	N	O	S	0	0
			1457	927	283	236	11		

- Molecule 28 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LT	127	Total	C	N	O	S	0	0
			994	630	190	172	2		

- Molecule 29 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LV	137	Total	C	N	O	S	0	0
			1019	639	196	179	5		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LY	132	Total	C	N	O	S	0	0
			1092	686	219	184	3		

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	La	105	Total	C	N	O	S	0	0
			823	524	160	136	3		

- Molecule 32 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	93	Total	C	N	O		0	0
			613	390	121	102			

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lh	104	Total	C	N	O	S	0	0
			666	407	139	119	1		

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Li	104	Total	C	N	O	S	0	0
			839	524	178	132	5		

- Molecule 37 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lr	123	Total	C	N	O	S	0	0
			984	611	205	164	4		

- Molecule 38 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lt	159	Total	C	N	O	S	0	0
			1186	736	223	223	4		

- Molecule 39 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	L8	117	Total	C	N	O	P	0	0
			2490	1113	445	816	116		

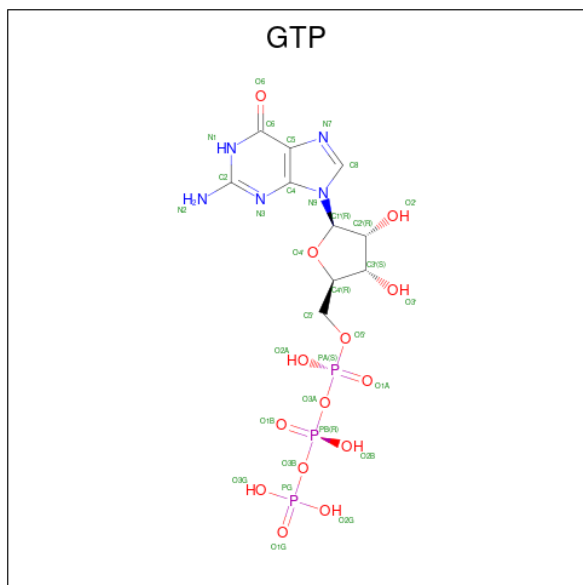
- Molecule 40 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	L5	2261	Total	C	N	O	P	0	0
			48474	21581	8881	15752	2260		

- Molecule 41 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
41	CB	1	Total	Mg	0
			1	1	
41	CD	1	Total	Mg	0
			1	1	

- Molecule 42 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
43	CD	1	Total	C	N	O	P	0
			28	10	5	11	2	

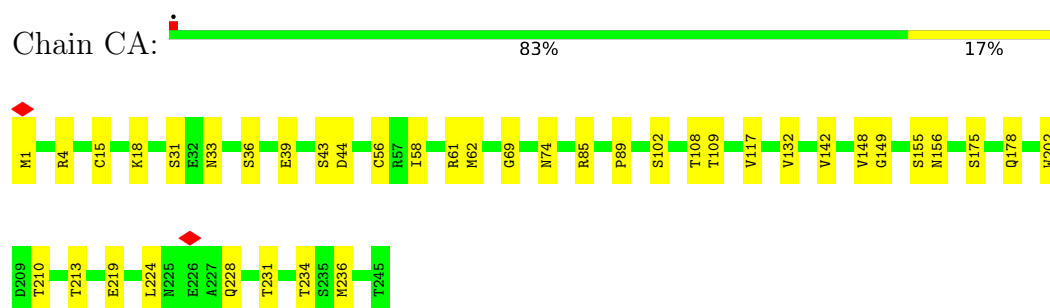
- Molecule 44 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
44	CI	1	Total	Zn	0
			1	1	

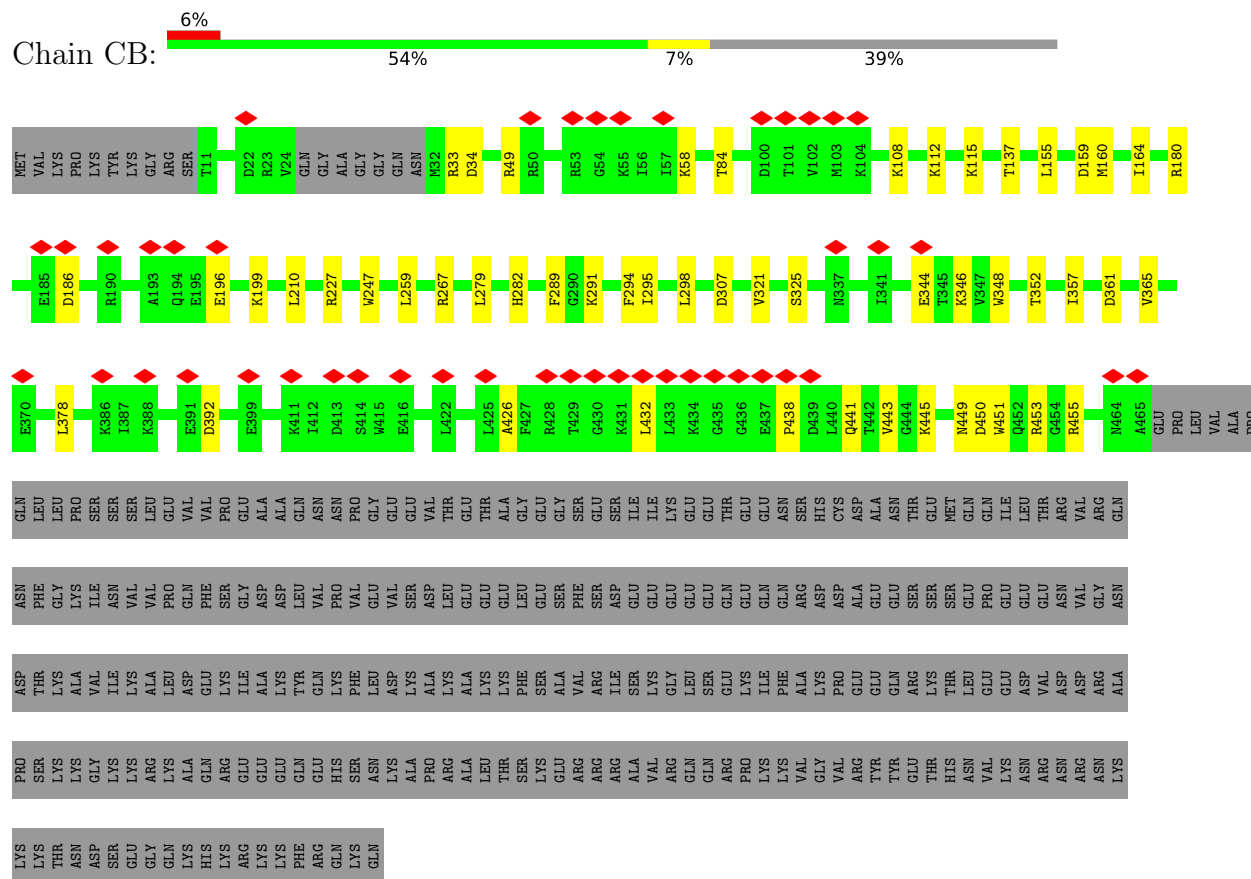
3 Residue-property plots

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

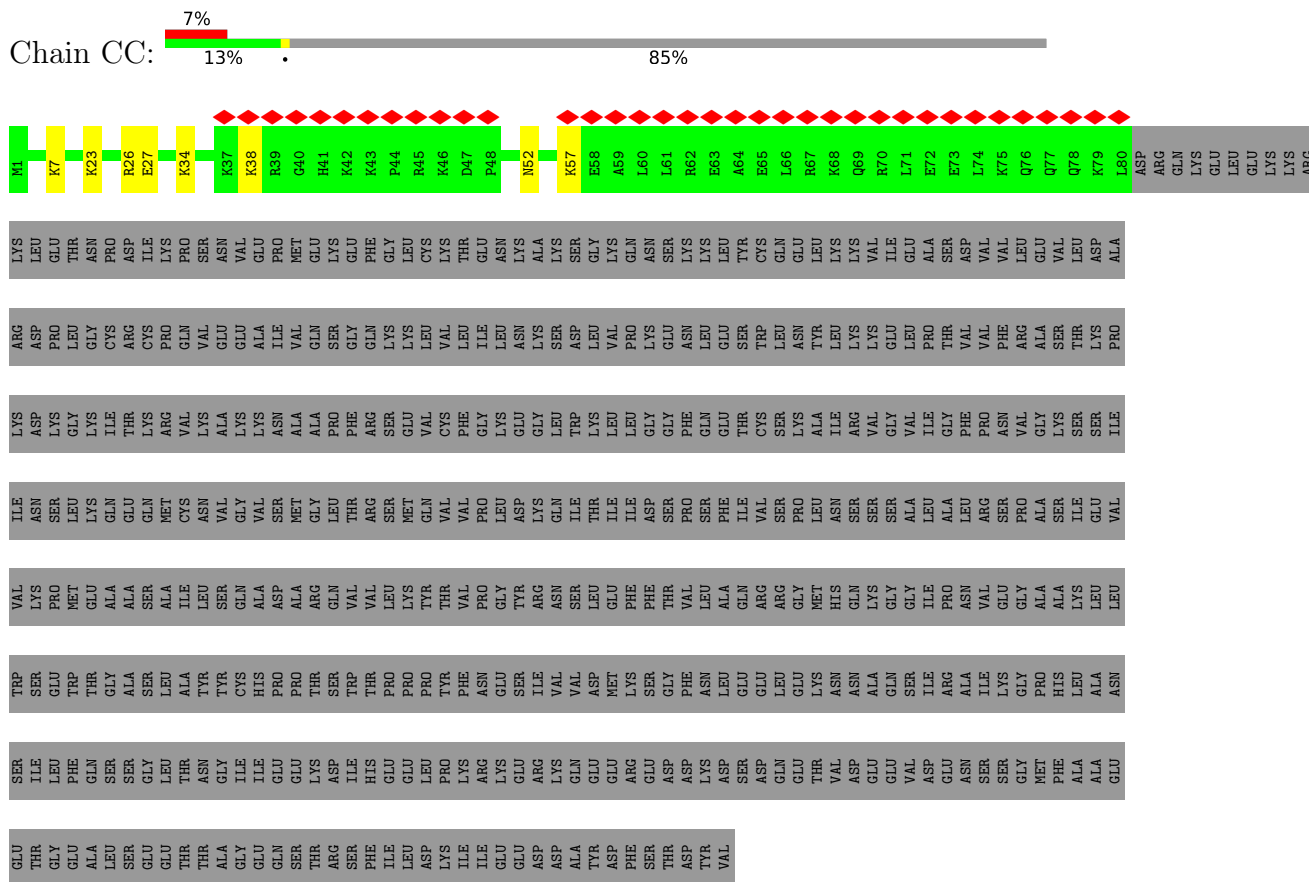
- Molecule 1: Eukaryotic translation initiation factor 6



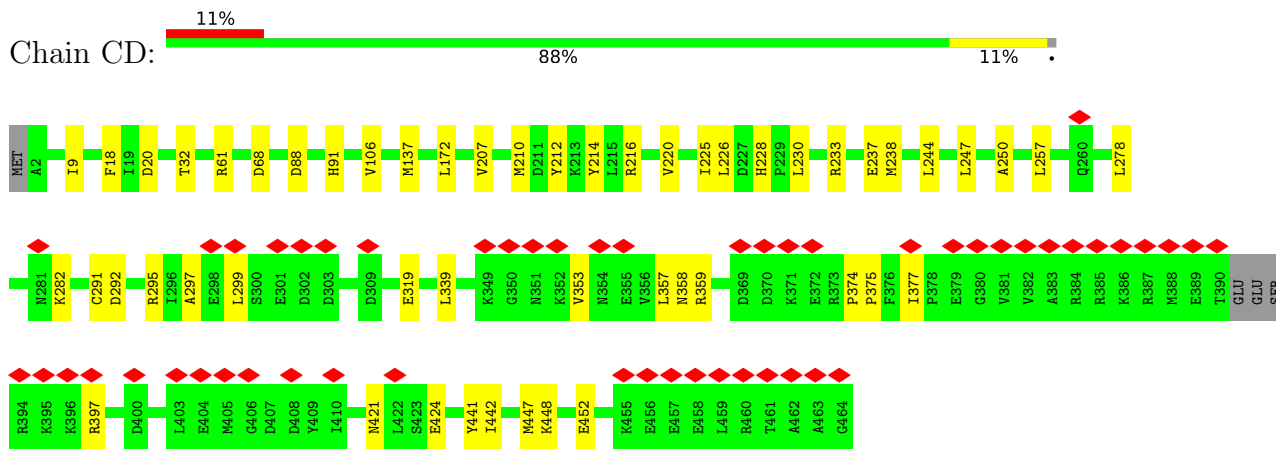
- Molecule 2: Nucleolar GTP-binding protein 2



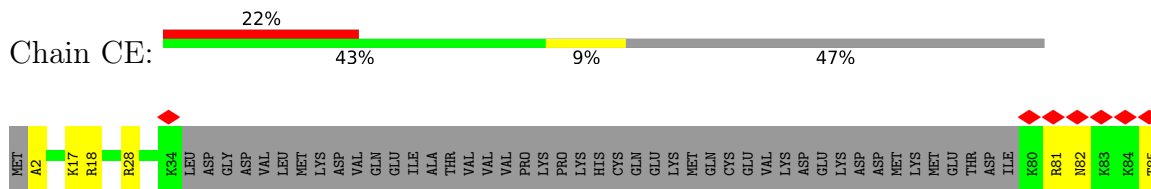
- Molecule 3: Guanine nucleotide-binding protein-like 3

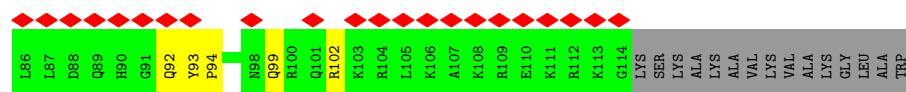


- Molecule 4: GTP-binding protein 4

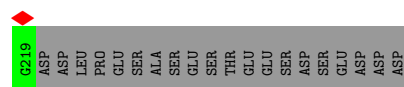
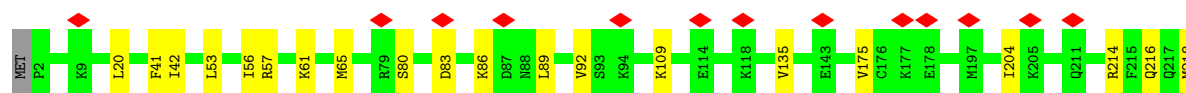
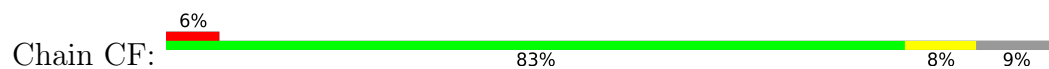


- Molecule 5: Protein LLP homolog

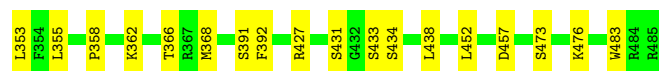
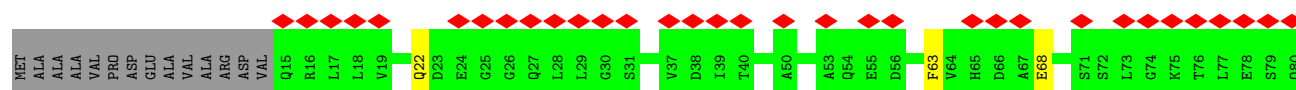
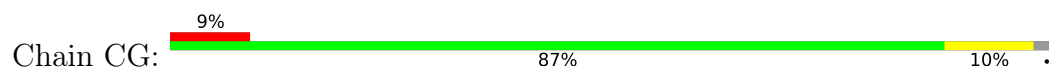




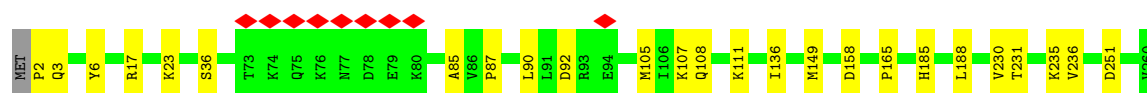
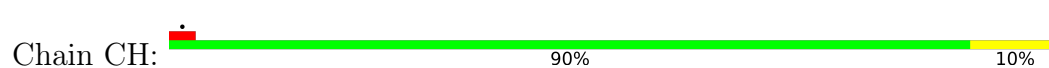
- Molecule 6: mRNA turnover protein 4 homolog



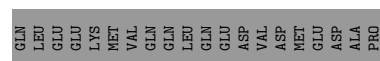
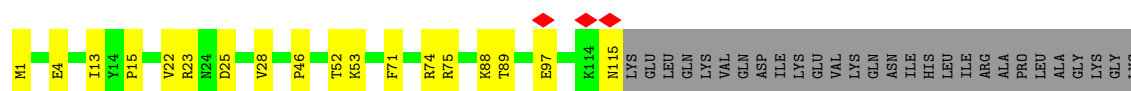
- Molecule 7: Notchless protein homolog 1



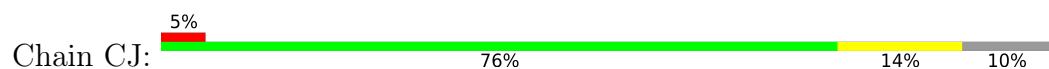
- Molecule 8: Ribosome biogenesis protein NSA2 homolog

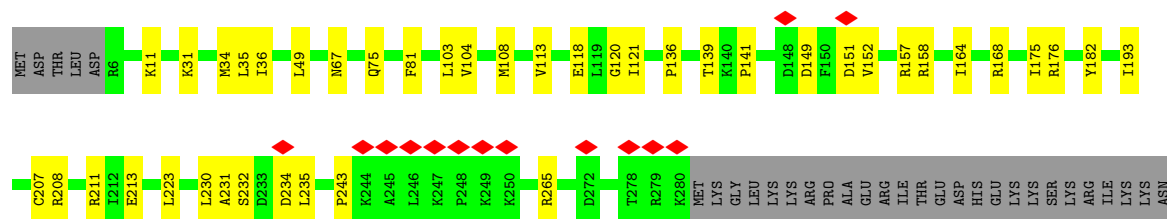


- Molecule 9: Probable ribosome biogenesis protein RLP24

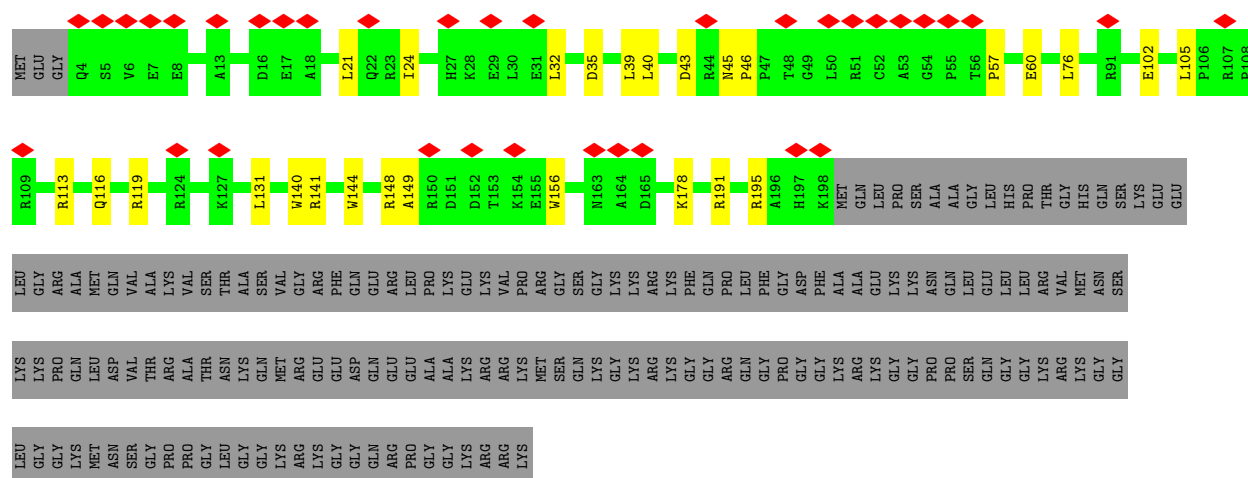


- Molecule 10: Ribosome production factor 2 homolog

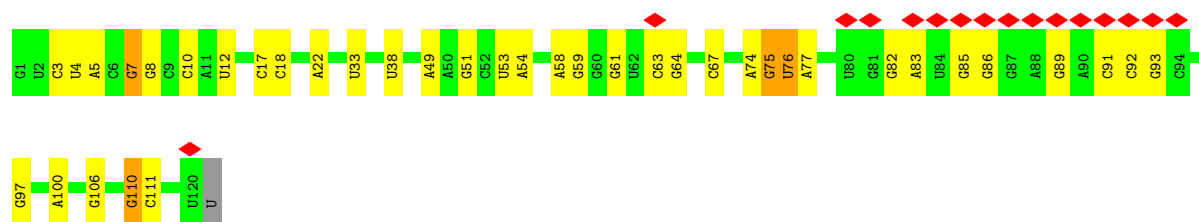




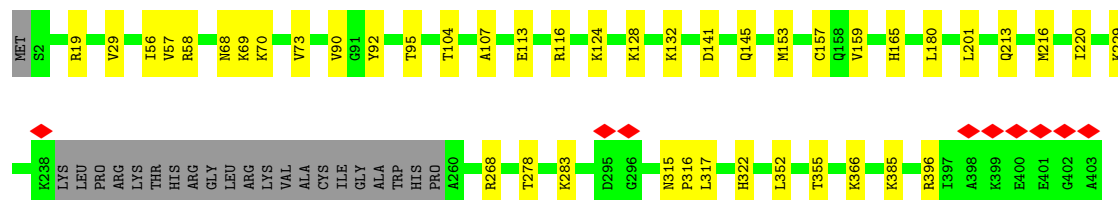
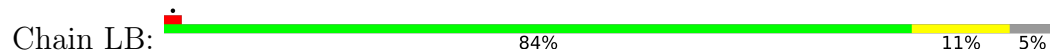
- Molecule 11: Ribosome biogenesis regulatory protein homolog



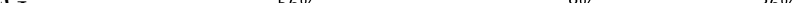
- Molecule 12: 5S rRNA

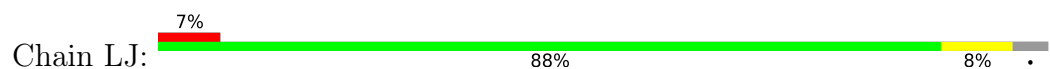


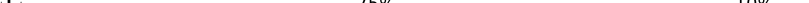
- Molecule 13: 60S ribosomal protein L3

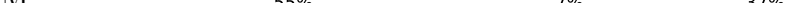


- Molecule 14: 60S ribosomal protein L4

- Chain LG: 



Chain LL: 

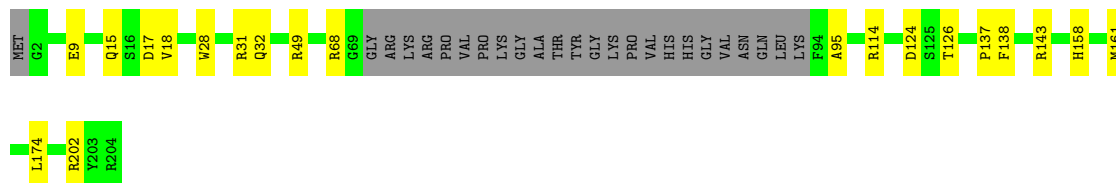
Chain LM:  55% 7% 37%



WORLDWIDE
PDB
PROTEIN DATA BANK

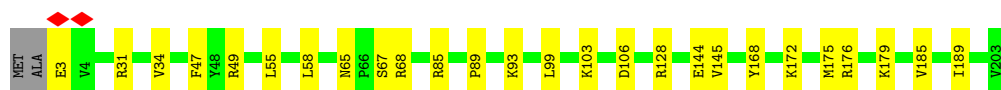
- Molecule 23: 60S ribosomal protein L15

Chain LN:  78% 10% 12%



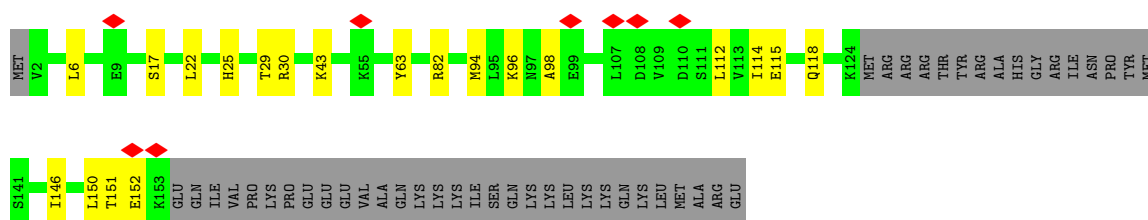
- Molecule 24: 60S ribosomal protein L13a

Chain LO:  86% 13% .



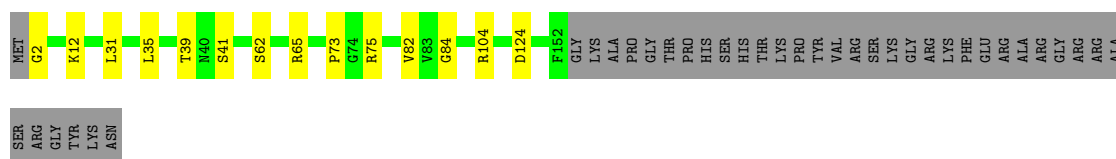
- Molecule 25: 60S ribosomal protein L17

Chain LP:  63% 11% 26%



- Molecule 26: 60S ribosomal protein L18

Chain LQ:  73% 7% 20%



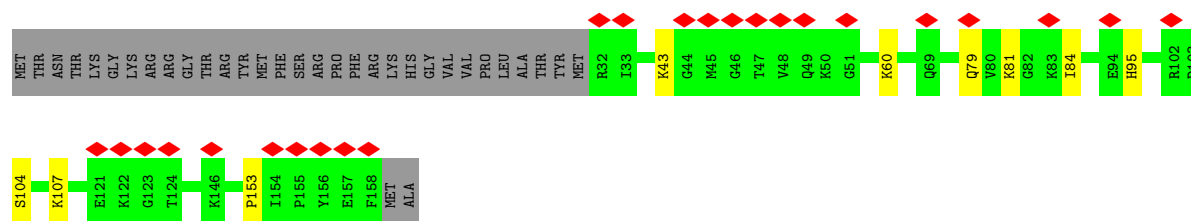
- Molecule 27: 60S ribosomal protein L18a

Chain LS:  89% 11%

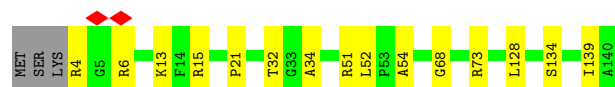


- Molecule 28: 60S ribosomal protein L21

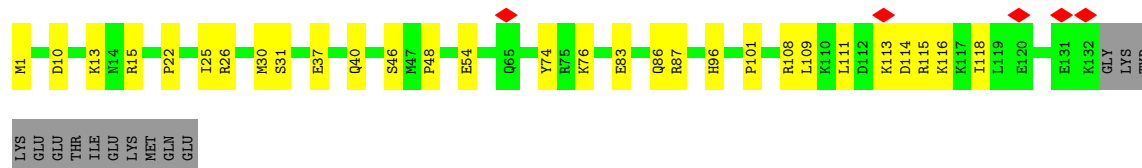
Chain LT:  15% 74% 6% 21%



- Molecule 29: 60S ribosomal protein L23



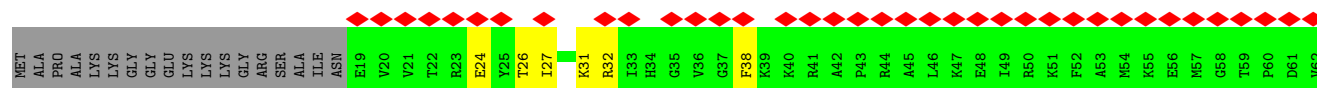
- Molecule 30: 60S ribosomal protein L26



- Molecule 31: 60S ribosomal protein L27a



- Molecule 32: 60S ribosomal protein L31

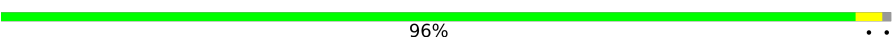


- Molecule 33: 60S ribosomal protein L32

Chain Le:  84% 11% 5%



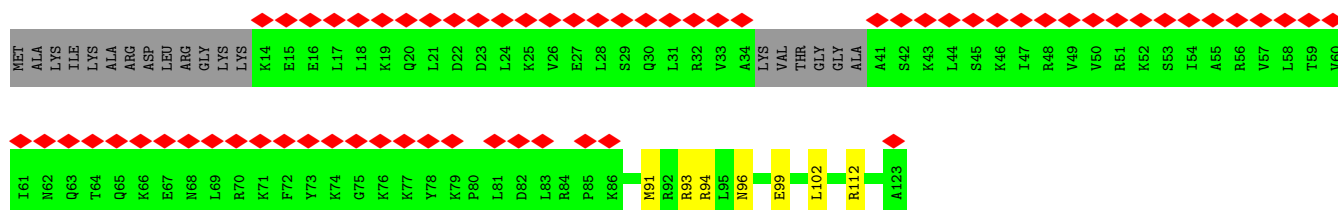
- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  96% ..



- Molecule 35: 60S ribosomal protein L35

Chain Lh:  54% 79% 6% 15%



- Molecule 36: 60S ribosomal protein L36

Chain Li:  15% 85% 14%



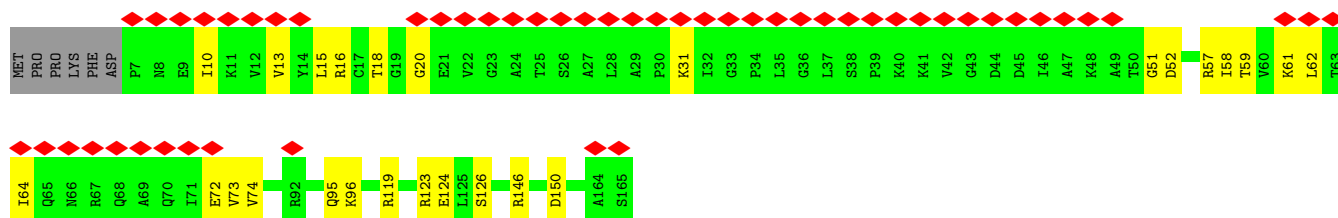
- Molecule 37: 60S ribosomal protein L28

Chain Lr:  84% 6% 10%



- Molecule 38: Large ribosomal subunit protein uL11

Chain Lt:  32% 81% 16%



Chain L8:

25% 45% 25% 5% 25%

C1 C2 A3 U8 A9 C19 A20 G25 U30 C31 G39 C47 A48 C49 C50 U A G C54 U55 C56 A59 G60 A61 A62 U63 U64 A65 A66 U67 G68 U69 G70 A71 A72 U73 U74 G75 C76 A77 G78 A79 G79 A80 C81 A C A C U U U G87 U88 U89 C90

[illegible]









4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	102619	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43.6	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	5.208	Depositor
Minimum map value	0.000	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.087	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: ZN, GTP, MG, GDP

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	CA	0.24	0/1885	0.52	0/2564
2	CB	0.22	0/3579	0.45	0/4846
3	CC	0.20	0/602	0.39	0/800
4	CD	0.26	0/3808	0.54	0/5145
5	CE	0.21	0/543	0.42	0/718
6	CF	0.21	0/1810	0.49	0/2425
7	CG	0.27	0/3526	0.54	0/4799
8	CH	0.26	0/2106	0.45	0/2820
9	CI	0.26	0/1008	0.57	0/1333
10	CJ	0.22	0/2218	0.44	0/2983
11	CK	0.19	0/1577	0.41	0/2141
12	L7	0.23	0/2861	0.31	0/4459
13	LB	0.25	0/3115	0.48	0/4167
14	LC	0.25	0/2676	0.45	0/3593
15	LD	0.27	0/1916	0.48	0/2566
16	LE	0.24	0/1705	0.50	0/2290
17	LF	0.27	0/1824	0.47	0/2437
18	LG	0.23	0/1398	0.55	0/1885
19	LH	0.22	0/1529	0.45	0/2058
20	LJ	0.25	0/1358	0.53	0/1820
21	LL	0.24	0/1464	0.46	0/1960
22	LM	0.25	0/1127	0.45	0/1508
23	LN	0.24	0/1554	0.44	0/2078
24	LO	0.26	0/1674	0.47	0/2241
25	LP	0.21	0/1110	0.48	0/1489
26	LQ	0.25	0/1239	0.50	0/1658
27	LS	0.25	0/1497	0.49	0/2009
28	LT	0.23	0/1015	0.56	0/1365
29	LV	0.22	0/1033	0.47	0/1383
30	LY	0.23	0/1109	0.62	2/1477 (0.1%)
31	La	0.23	0/837	0.47	0/1118
32	Ld	0.18	0/624	0.51	0/856

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.29	0/1071	0.51	0/1429
34	Lf	0.29	0/891	0.44	0/1194
35	Lh	0.16	0/670	0.43	0/907
36	Li	0.25	0/850	0.55	0/1125
37	Lr	0.23	0/999	0.46	0/1340
38	Lt	0.19	0/1202	0.49	0/1622
39	L8	0.21	0/2780	0.35	0/4324
40	L5	0.24	0/54186	0.34	0/84448
All	All	0.24	0/117976	0.42	2/171380 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	LY	83	GLU	CA-C-N	5.13	131.34	121.54
30	LY	83	GLU	C-N-CA	5.13	131.34	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CA	1860	0	1835	30	0
2	CB	3506	0	3476	37	0
3	CC	594	0	584	6	0
4	CD	3735	0	3746	35	0
5	CE	537	0	549	9	0
6	CF	1775	0	1813	11	0
7	CG	3449	0	3178	29	0
8	CH	2066	0	2168	20	0
9	CI	987	0	1029	12	0
10	CJ	2176	0	2200	28	0
11	CK	1545	0	1525	17	0
12	L7	2561	0	1295	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	LB	3054	0	3161	29	0
14	LC	2628	0	2801	19	0
15	LD	1879	0	1887	19	0
16	LE	1673	0	1803	22	0
17	LF	1790	0	1873	14	0
18	LG	1376	0	1468	12	0
19	LH	1510	0	1579	12	0
20	LJ	1335	0	1345	9	0
21	LL	1440	0	1549	20	0
22	LM	1105	0	1156	13	0
23	LN	1516	0	1550	14	0
24	LO	1642	0	1779	19	0
25	LP	1089	0	1115	13	0
26	LQ	1223	0	1330	13	0
27	LS	1457	0	1491	14	0
28	LT	994	0	996	7	0
29	LV	1019	0	1079	10	0
30	LY	1092	0	1167	18	0
31	La	823	0	879	9	0
32	Ld	613	0	493	7	0
33	Le	1053	0	1147	12	0
34	Lf	872	0	901	3	0
35	Lh	666	0	516	5	0
36	Li	839	0	910	9	0
37	Lr	984	0	1048	5	0
38	Lt	1186	0	1226	17	0
39	L8	2490	0	1266	19	0
40	L5	48474	0	24548	322	0
41	CB	1	0	0	0	0
41	CD	1	0	0	0	0
42	CB	32	0	12	2	0
43	CD	28	0	12	0	0
44	CI	1	0	0	0	0
All	All	110676	0	85485	754	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 754 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)
40:L5:4295:U:H3	40:L5:4316:G:H1	0.98	0.94
40:L5:3930:U:H3	40:L5:4180:G:H1	1.14	0.94
40:L5:3929:G:H1	40:L5:4181:U:H3	1.08	0.92
40:L5:4745:G:H1	40:L5:4955:A:H61	1.14	0.91
40:L5:4534:G:H1	40:L5:4552:U:H3	1.22	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CA	243/245 (99%)	234 (96%)	9 (4%)	0	100	100
2	CB	444/731 (61%)	439 (99%)	5 (1%)	0	100	100
3	CC	78/549 (14%)	76 (97%)	2 (3%)	0	100	100
4	CD	456/464 (98%)	454 (100%)	2 (0%)	0	100	100
5	CE	64/129 (50%)	63 (98%)	1 (2%)	0	100	100
6	CF	216/239 (90%)	214 (99%)	2 (1%)	0	100	100
7	CG	469/485 (97%)	453 (97%)	16 (3%)	0	100	100
8	CH	257/260 (99%)	250 (97%)	7 (3%)	0	100	100
9	CI	113/163 (69%)	112 (99%)	1 (1%)	0	100	100
10	CJ	273/306 (89%)	267 (98%)	6 (2%)	0	100	100
11	CK	193/365 (53%)	190 (98%)	3 (2%)	0	100	100
13	LB	377/403 (94%)	372 (99%)	4 (1%)	1 (0%)	36	65
14	LC	324/427 (76%)	318 (98%)	6 (2%)	0	100	100
15	LD	226/297 (76%)	218 (96%)	8 (4%)	0	100	100
16	LE	200/288 (69%)	197 (98%)	3 (2%)	0	100	100
17	LF	217/248 (88%)	211 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	LG	166/266 (62%)	164 (99%)	2 (1%)	0	100	100
19	LH	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
20	LJ	168/178 (94%)	164 (98%)	4 (2%)	0	100	100
21	LL	178/211 (84%)	176 (99%)	2 (1%)	0	100	100
22	LM	133/215 (62%)	130 (98%)	3 (2%)	0	100	100
23	LN	175/204 (86%)	174 (99%)	1 (1%)	0	100	100
24	LO	199/203 (98%)	195 (98%)	4 (2%)	0	100	100
25	LP	132/184 (72%)	129 (98%)	3 (2%)	0	100	100
26	LQ	149/188 (79%)	147 (99%)	2 (1%)	0	100	100
27	LS	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
28	LT	125/160 (78%)	123 (98%)	2 (2%)	0	100	100
29	LV	135/140 (96%)	133 (98%)	2 (2%)	0	100	100
30	LY	130/145 (90%)	128 (98%)	2 (2%)	0	100	100
31	La	101/148 (68%)	101 (100%)	0	0	100	100
32	Ld	89/125 (71%)	88 (99%)	1 (1%)	0	100	100
33	Le	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
34	Lf	107/110 (97%)	107 (100%)	0	0	100	100
35	Lh	100/123 (81%)	100 (100%)	0	0	100	100
36	Li	102/105 (97%)	101 (99%)	1 (1%)	0	100	100
37	Lr	121/137 (88%)	118 (98%)	3 (2%)	0	100	100
38	Lt	157/165 (95%)	152 (97%)	5 (3%)	0	100	100
All	All	7105/9109 (78%)	6979 (98%)	125 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	LB	29	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	
1	CA	213/213 (100%)	213 (100%)	0	100	100
2	CB	374/654 (57%)	374 (100%)	0	100	100
3	CC	51/485 (10%)	51 (100%)	0	100	100
4	CD	406/423 (96%)	406 (100%)	0	100	100
5	CE	50/115 (44%)	50 (100%)	0	100	100
6	CF	194/214 (91%)	194 (100%)	0	100	100
7	CG	327/403 (81%)	327 (100%)	0	100	100
8	CH	217/228 (95%)	217 (100%)	0	100	100
9	CI	106/149 (71%)	106 (100%)	0	100	100
10	CJ	234/279 (84%)	234 (100%)	0	100	100
11	CK	151/300 (50%)	151 (100%)	0	100	100
13	LB	327/349 (94%)	327 (100%)	0	100	100
14	LC	276/348 (79%)	276 (100%)	0	100	100
15	LD	193/250 (77%)	193 (100%)	0	100	100
16	LE	183/252 (73%)	183 (100%)	0	100	100
17	LF	182/215 (85%)	182 (100%)	0	100	100
18	LG	147/223 (66%)	147 (100%)	0	100	100
19	LH	167/171 (98%)	167 (100%)	0	100	100
20	LJ	137/149 (92%)	137 (100%)	0	100	100
21	LL	148/177 (84%)	148 (100%)	0	100	100
22	LM	113/161 (70%)	113 (100%)	0	100	100
23	LN	152/172 (88%)	152 (100%)	0	100	100
24	LO	171/174 (98%)	171 (100%)	0	100	100
25	LP	119/163 (73%)	119 (100%)	0	100	100
26	LQ	136/165 (82%)	136 (100%)	0	100	100
27	LS	156/157 (99%)	156 (100%)	0	100	100
28	LT	101/140 (72%)	101 (100%)	0	100	100
29	LV	104/107 (97%)	104 (100%)	0	100	100
30	LY	121/135 (90%)	121 (100%)	0	100	100
31	La	87/121 (72%)	87 (100%)	0	100	100
32	Ld	39/110 (36%)	39 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	87/89 (98%)	87 (100%)	0	100	100
35	Lh	36/110 (33%)	36 (100%)	0	100	100
36	Li	85/89 (96%)	85 (100%)	0	100	100
37	Lr	106/121 (88%)	106 (100%)	0	100	100
38	Lt	127/137 (93%)	127 (100%)	0	100	100
All	All	5937/7869 (75%)	5937 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
24	LO	42	ASN
30	LY	20	ASN
25	LP	34	GLN
26	LQ	45	GLN
30	LY	127	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	L7	119/121 (98%)	20 (16%)	1 (0%)
39	L8	113/157 (71%)	27 (23%)	2 (1%)
40	L5	2219/5070 (43%)	501 (22%)	13 (0%)
All	All	2451/5348 (45%)	548 (22%)	16 (0%)

5 of 548 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	L7	7	G
12	L7	10	C
12	L7	22	A
12	L7	33	U
12	L7	38	U

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
40	L5	4774	C
40	L5	4699	U
40	L5	2854	G
40	L5	4597	U
40	L5	1082	C

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 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$
43	GDP	CD	502	41	28,30,30	1.15	3 (10%)	44,47,47	1.84	8 (18%)
42	GTP	CB	802	41	30,34,34	0.87	1 (3%)	46,54,54	1.76	10 (21%)

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
43	GDP	CD	502	41	-	5/16/32/32	0/3/3/3
42	GTP	CB	802	41	-	6/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
43	CD	502	GDP	C5-C4	3.00	1.47	1.38
43	CD	502	GDP	C6-N1	-2.56	1.34	1.38
43	CD	502	GDP	C5-N7	-2.15	1.34	1.39
42	CB	802	GTP	C2-N3	2.11	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	CD	502	GDP	C5-C4-N3	-6.12	118.53	128.46
42	CB	802	GTP	C5-C4-N3	-4.92	120.48	128.46
43	CD	502	GDP	C2-N3-C4	4.86	120.96	112.30
43	CD	502	GDP	N9-C4-N3	4.56	135.10	125.94
42	CB	802	GTP	C2-N3-C4	4.44	120.21	112.30

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

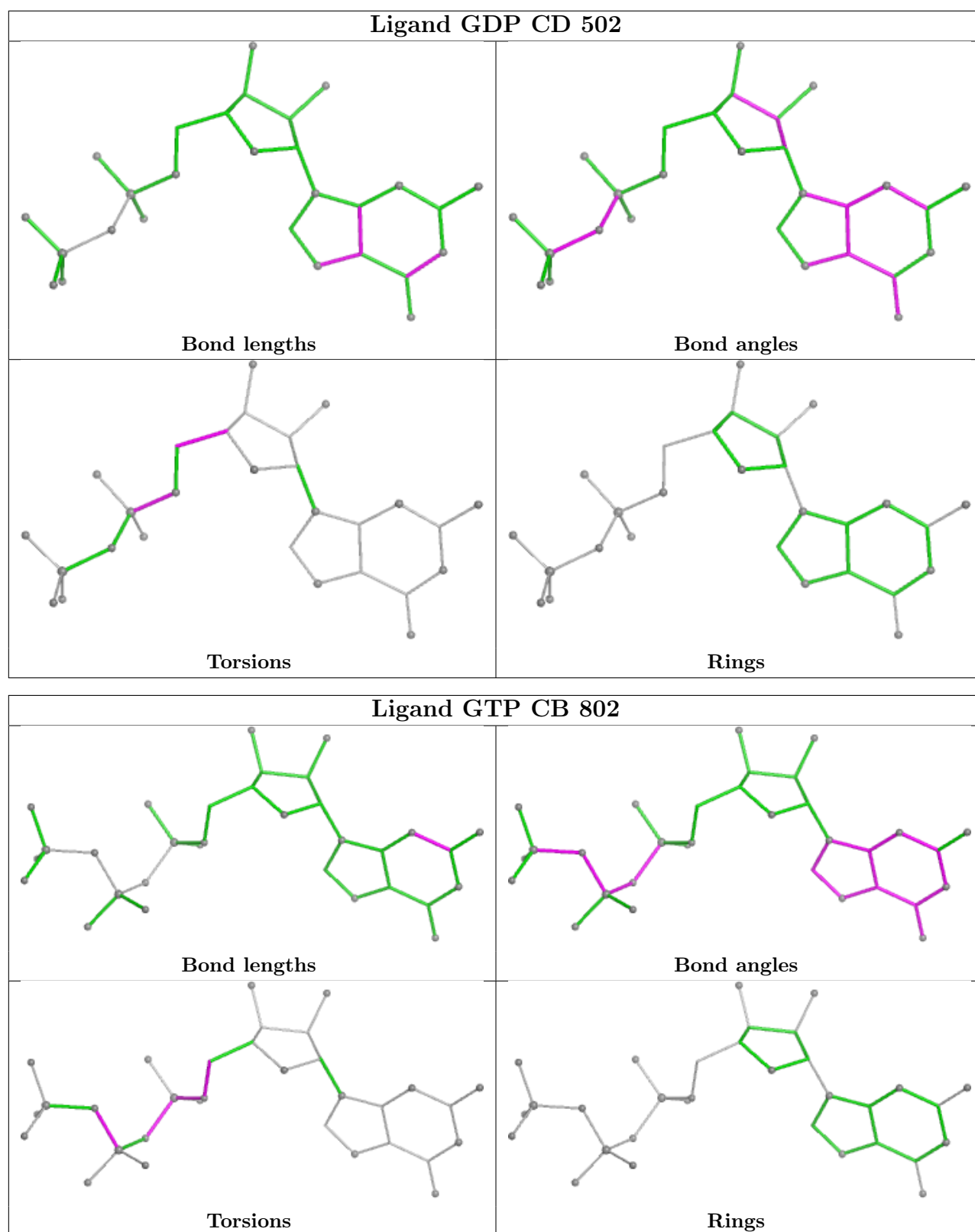
Mol	Chain	Res	Type	Atoms
42	CB	802	GTP	PB-O3A-PA-O5'
42	CB	802	GTP	C5'-O5'-PA-O1A
42	CB	802	GTP	C5'-O5'-PA-O2A
43	CD	502	GDP	C5'-O5'-PA-O1A
43	CD	502	GDP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
42	CB	802	GTP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

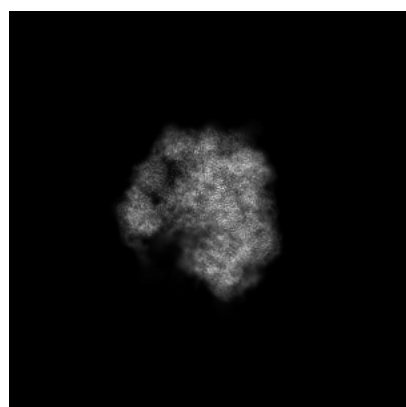
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53090. These allow visual inspection of the internal detail of the map and identification of artifacts.

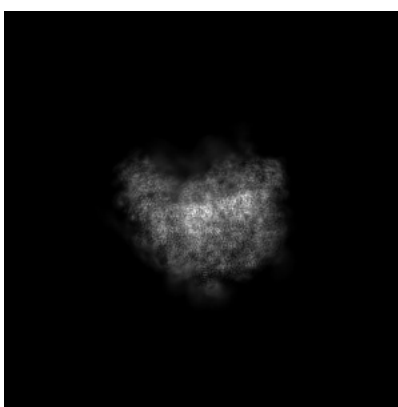
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

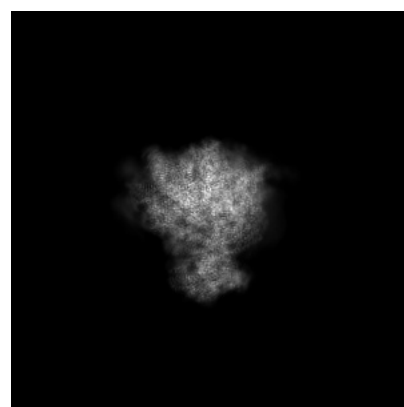
6.1.1 Primary map



X



Y

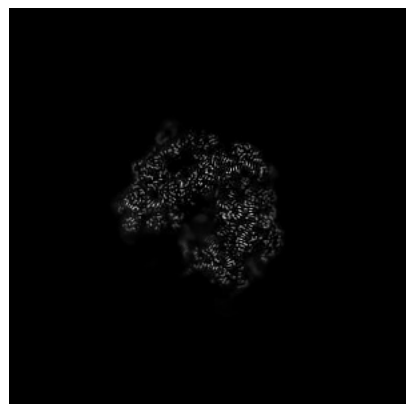


Z

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

6.2 Central slices [i](#)

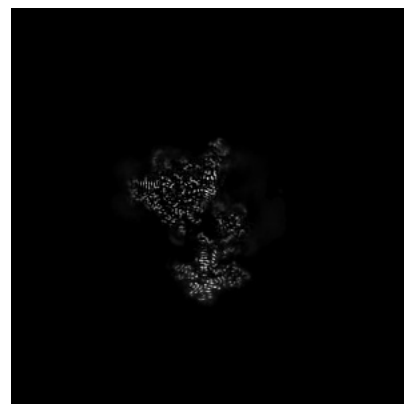
6.2.1 Primary map



X Index: 250



Y Index: 250

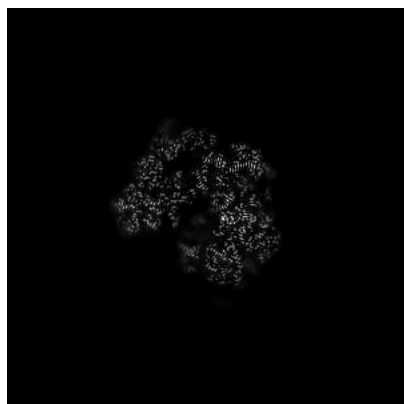


Z Index: 250

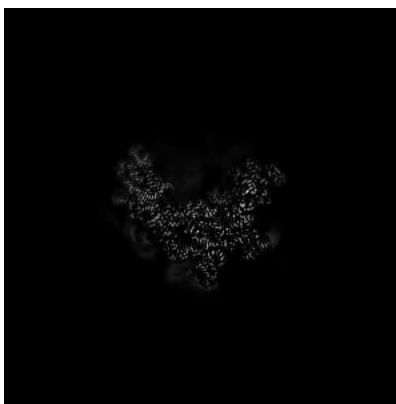
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 246



Y Index: 274

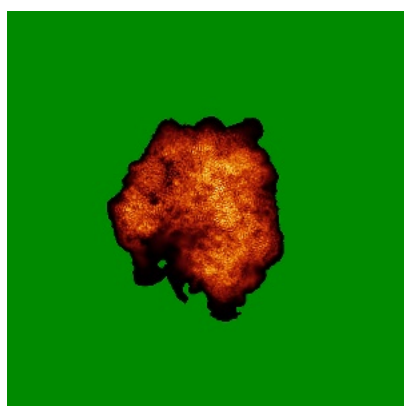


Z Index: 257

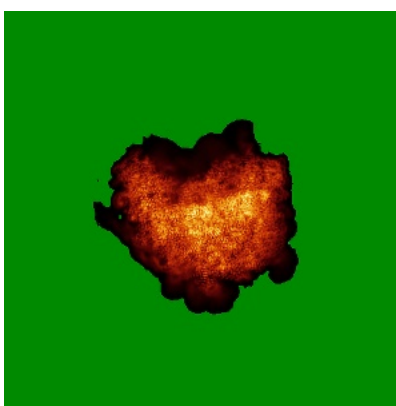
The images above show the largest variance slices of the map in three orthogonal directions.

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

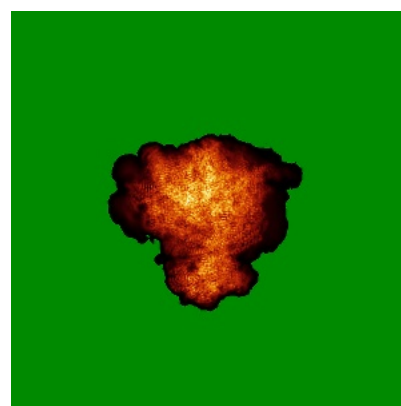
6.4.1 Primary map



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.

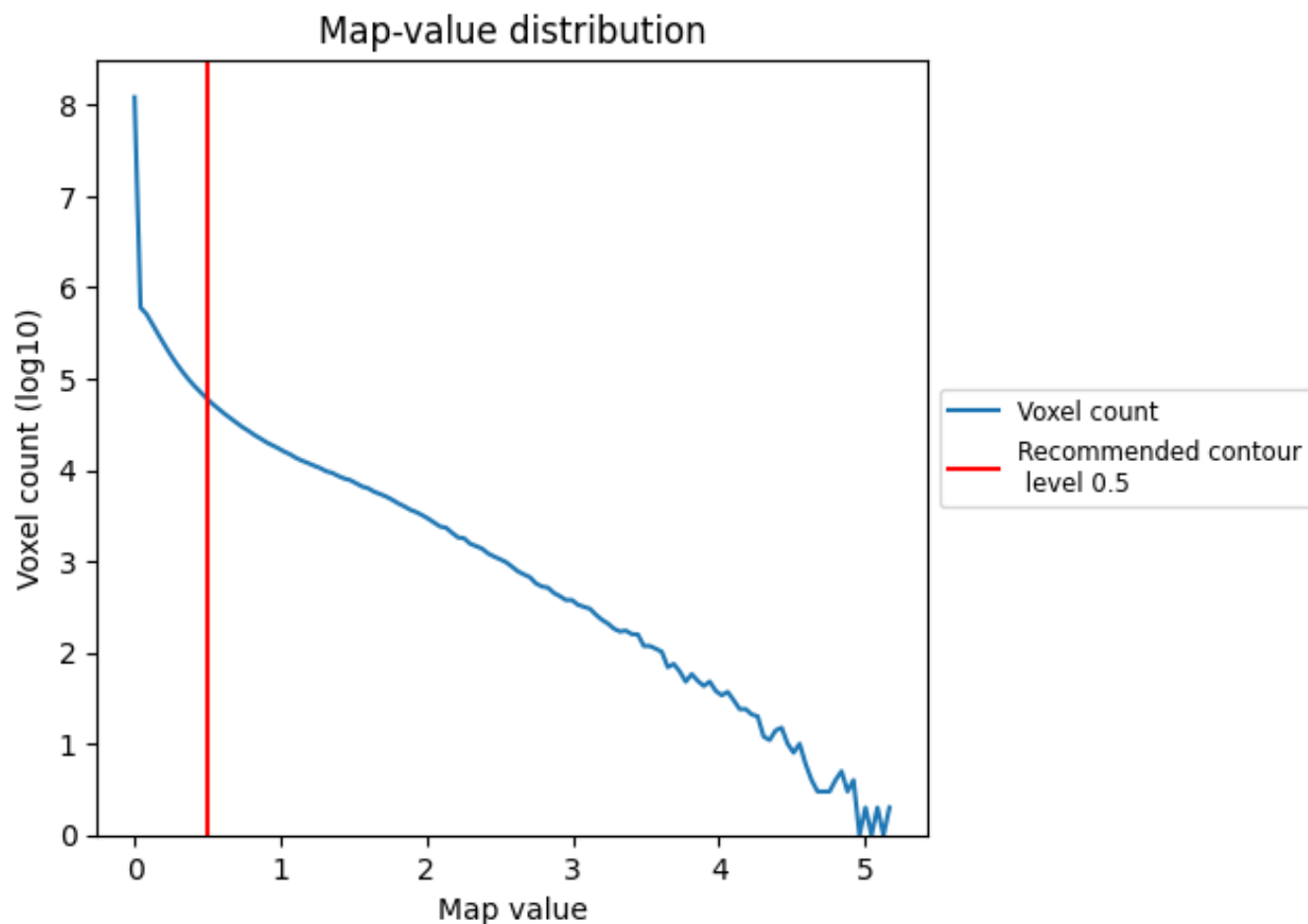
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

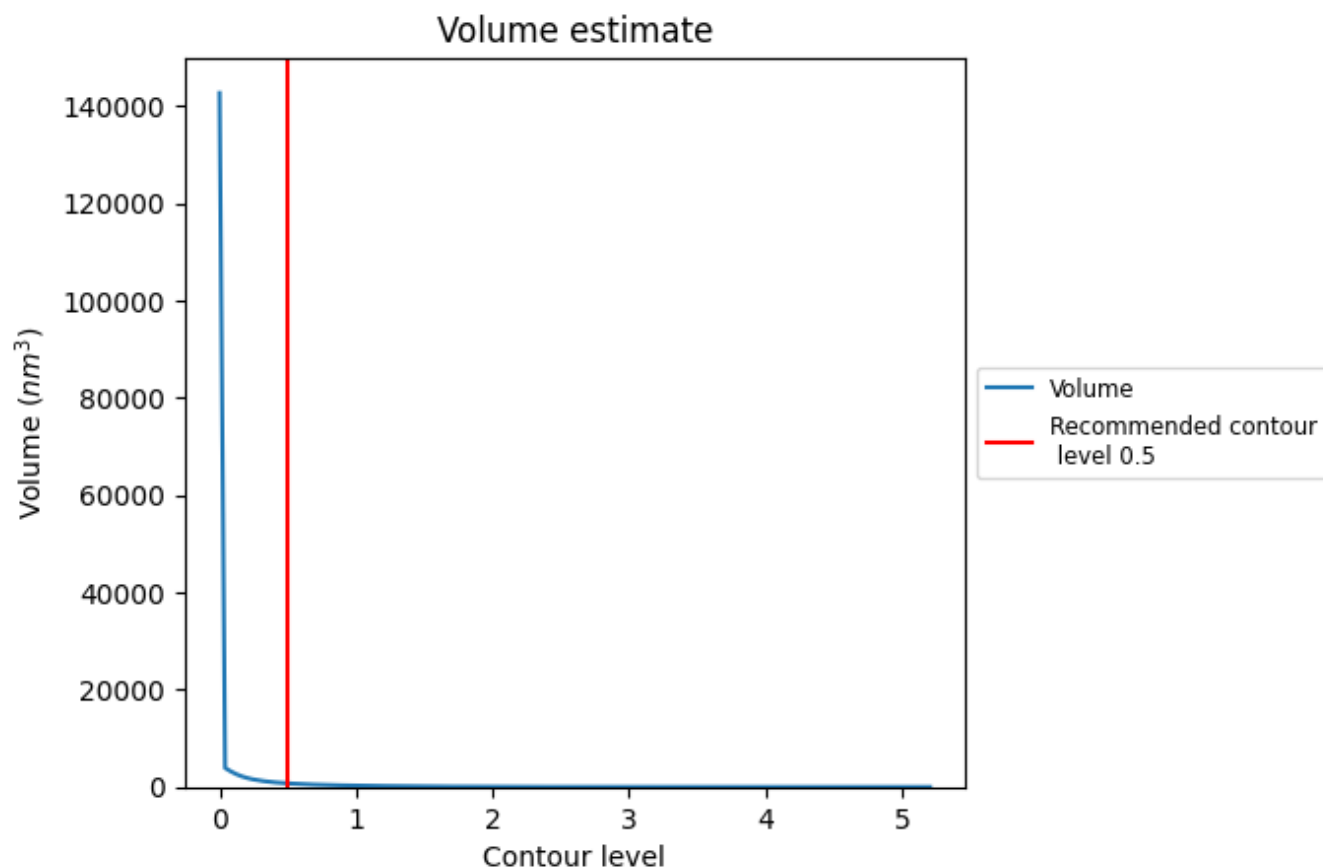
This section contains the results of statistical analysis of the map.

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.

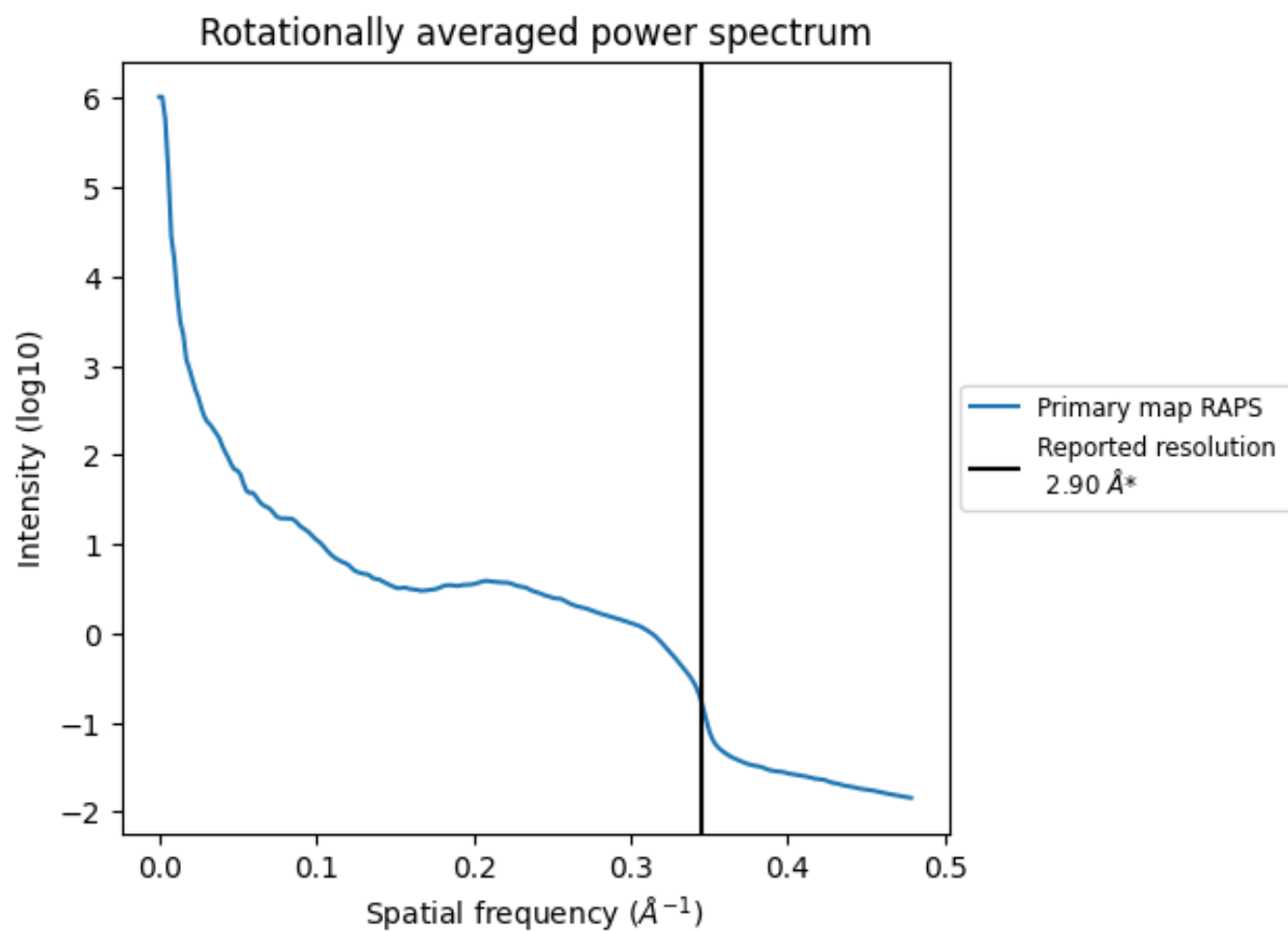
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 740 nm^3 ; this corresponds to an approximate mass of 669 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 0.345 Å⁻¹

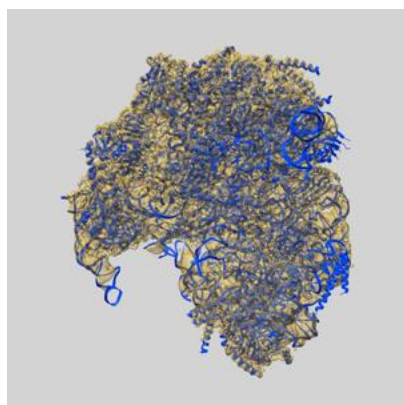
8 Fourier-Shell correlation

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

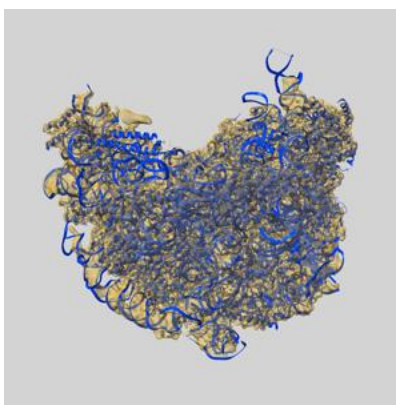
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53090 and PDB model 9QER. Per-residue inclusion information can be found in section [3](#) on page [13](#).

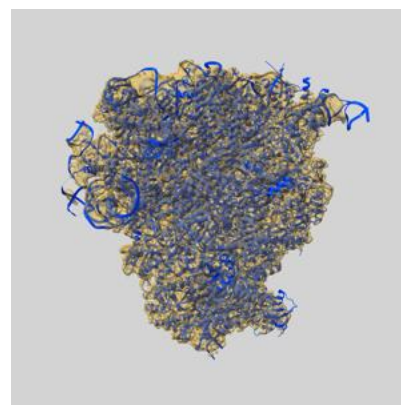
9.1 Map-model overlay [i](#)



X



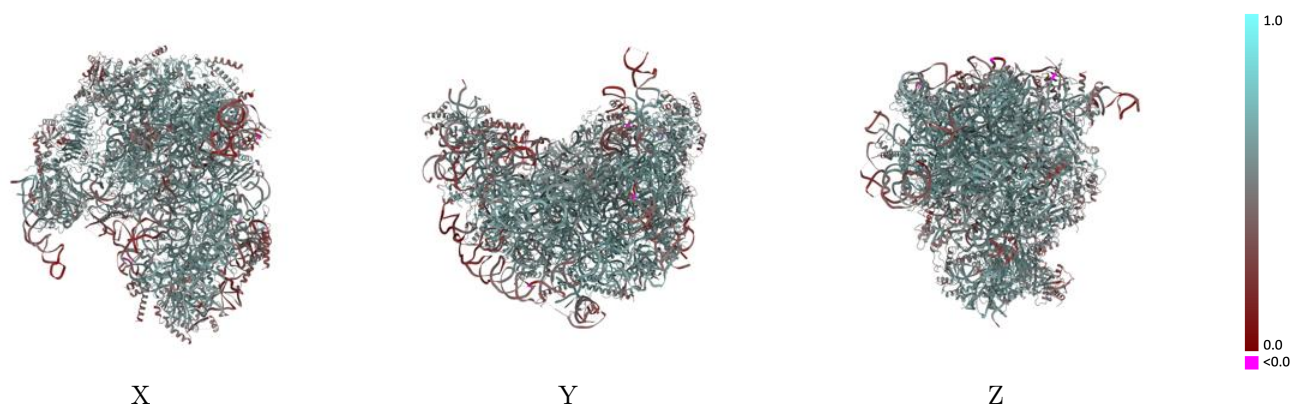
Y



Z

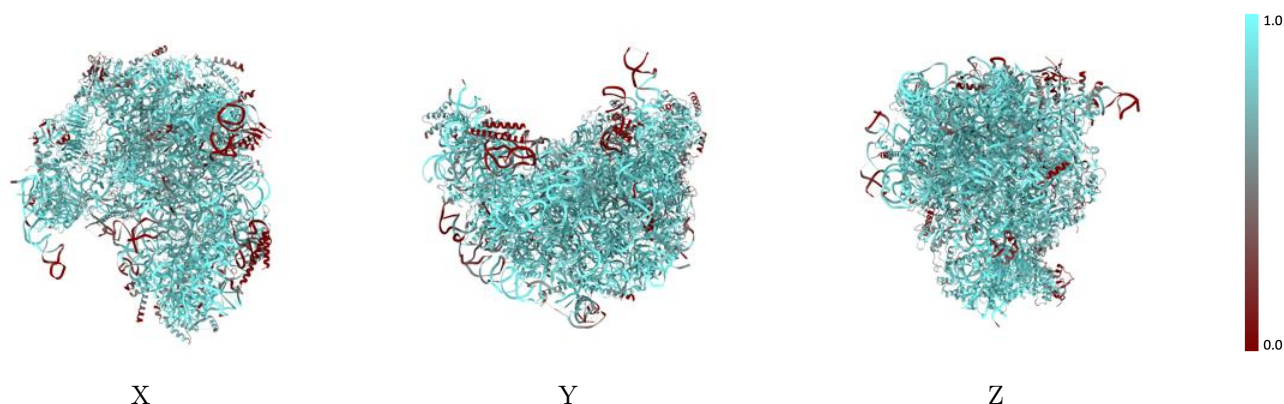
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



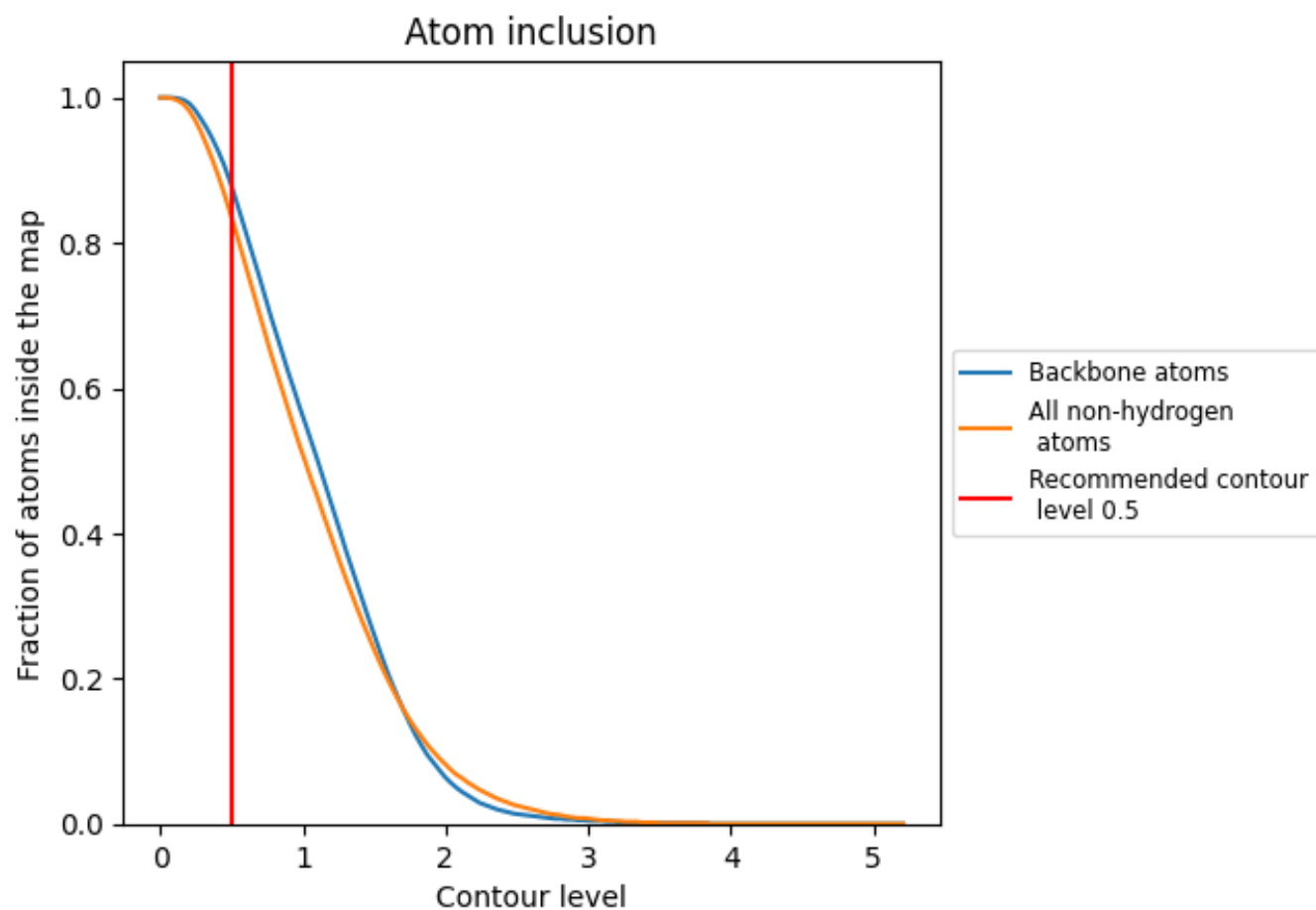
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 88% of all backbone atoms, 84% 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	 0.8350	 0.5390
CA	 0.8680	 0.5640
CB	 0.7770	 0.5230
CC	 0.5580	 0.5040
CD	 0.7970	 0.5470
CE	 0.5100	 0.4690
CF	 0.7210	 0.5030
CG	 0.8870	 0.5690
CH	 0.8980	 0.6060
CI	 0.8190	 0.5440
CJ	 0.8340	 0.5310
CK	 0.6890	 0.4680
L5	 0.8560	 0.5240
L7	 0.8330	 0.4910
L8	 0.6380	 0.4720
LB	 0.9000	 0.6100
LC	 0.9100	 0.6080
LD	 0.9100	 0.5740
LE	 0.8440	 0.5740
LF	 0.9080	 0.6170
LG	 0.7440	 0.4720
LH	 0.8860	 0.5990
LJ	 0.8030	 0.5060
LL	 0.8510	 0.5560
LM	 0.9250	 0.6100
LN	 0.9470	 0.6020
LO	 0.9350	 0.6320
LP	 0.8000	 0.5470
LQ	 0.8910	 0.5960
LS	 0.8980	 0.6120
LT	 0.6510	 0.4710
LV	 0.8780	 0.5820
LY	 0.8350	 0.5370
La	 0.9050	 0.5850
Ld	 0.1490	 0.3880



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Chain	Atom inclusion	Q-score
Le	 0.9260	 0.6260
Lf	 0.9580	 0.6550
Lh	 0.4250	 0.4230
Li	 0.7420	 0.4810
Lr	 0.9100	 0.5920
Lt	 0.5580	 0.4010