



wwPDB EM Validation Summary Report ⓘ

Jul 12, 2023 – 02:49 PM JST

PDB ID : 8I9V
EMDB ID : EMD-35285
Title : Cryo-EM structure of a Chaetomium thermophilum pre-60S ribosomal subunit
- State Dbp10-2
Authors : Lau, B.; Huang, Z.; Beckmann, R.; Hurt, E.; Cheng, J.
Deposited on : 2023-02-07
Resolution : 3.10 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:

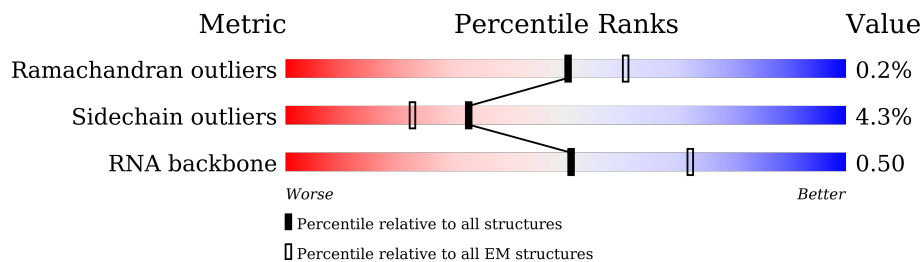
EMDB validation analysis : 0.0.1.dev50
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

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 3.10 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	3341	
2	C2	256	
3	C3	161	
4	CA	316	
5	CB	391	
6	CC	801	
7	CE	598	
8	CF	270	



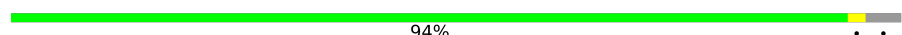

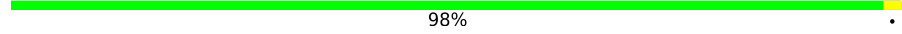

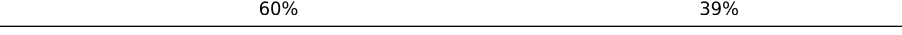
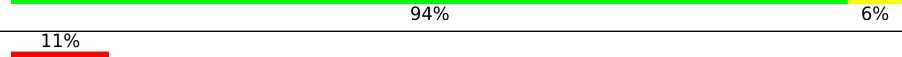
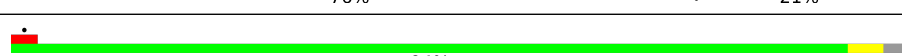

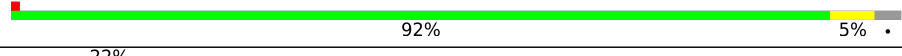

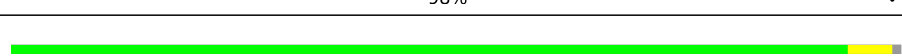

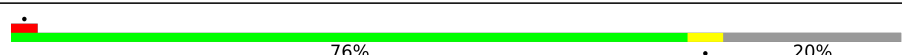

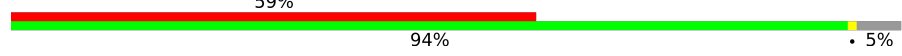
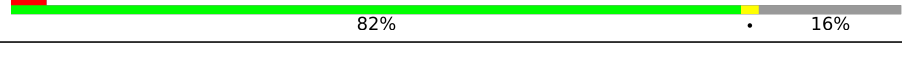





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Mol	Chain	Length	Quality of chain
9	CG	184	91% 5%
10	CH	661	68% 28%
11	CI	414	34% 65%
12	CJ	679	28% 55% 44%
13	CK	261	84% 5% 11%
14	CL	558	51% 68% 30%
15	CM	249	17% 71% 25%
15	LF	249	94%
16	CN	246	97%
17	CO	120	51% 48%
18	CP	751	40% 57%
19	CQ	225	46% 50%
20	CR	237	67% 30%
21	CS	834	33% 35% 64%
22	CT	688	49% 66% 33%
23	CU	451	39% 61%
24	CX	203	21% 42% 57%
25	CY	788	22% 41% 59%
26	Cz	123	16% 56% 43%
27	Cb	924	67% 31%
28	LB	392	84% 13%
29	LC	365	97%
30	LE	200	83% 15%
31	LG	262	7% 73% 25%
32	LH	192	92% 7%

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Mol	Chain	Length	Quality of chain
33	LK	165	 84% 12%
34	LL	213	 54% 45%
35	LM	142	 94%
36	LN	203	 87% 10%
37	LO	204	 98%
38	LP	187	 78% 5% 18%
39	LQ	213	 60% 39%
40	LS	174	 94% 6%
41	LT	160	 11% 76% 21%
42	LV	139	 94%
43	LX	156	 9% 14% 86%
44	LY	138	 92% 5%
45	Ld	120	 22% 88% 9%
46	Le	131	 98%
47	Lf	109	 94% 5%
48	Lh	935	 13% 87%
49	Li	110	 76% 20%
50	Lj	95	 74% 22%
51	Lq	217	 59% 94% 5%
52	Cc	282	 82% 16%
53	Cd	436	 76% 22%
54	Ce	336	 55% 42%
55	Cf	570	 10% 90%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 138001 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 RNA (3341-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	C1	2152	46025	20547	8331	14995	2152	0	0

- Molecule 2 is a RNA chain called RNA (256-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	C2	158	3359	1502	593	1106	158	0	0

- Molecule 3 is a RNA chain called RNA (161-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C3	98	2097	933	381	685	98	0	0

- Molecule 4 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	CA	260	2144	1371	393	373	7	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	CB	260	2063	1322	367	371	3	0	0

- Molecule 6 is a protein called Ribosome biogenesis protein ERB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	CC	289	2388	1520	399	462	7	0	0

- Molecule 7 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	CE	463	3673	2352	643	667	11	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CE	543	LYS	-	insertion	UNP G0RYU9
CE	544	SER	-	insertion	UNP G0RYU9
CE	545	PHE	-	insertion	UNP G0RYU9
CE	546	GLY	-	insertion	UNP G0RYU9
CE	547	PHE	-	insertion	UNP G0RYU9
CE	548	SER	-	insertion	UNP G0RYU9
CE	549	THR	-	insertion	UNP G0RYU9
CE	550	PRO	-	insertion	UNP G0RYU9
CE	551	PRO	-	insertion	UNP G0RYU9
CE	552	ARG	-	insertion	UNP G0RYU9
CE	553	VAL	-	insertion	UNP G0RYU9
CE	554	ASP	-	insertion	UNP G0RYU9
CE	555	ILE	-	insertion	UNP G0RYU9
CE	556	THR	-	insertion	UNP G0RYU9
CE	557	LEU	-	insertion	UNP G0RYU9
CE	558	SER	-	insertion	UNP G0RYU9
CE	559	ALA	-	insertion	UNP G0RYU9
CE	560	SER	-	insertion	UNP G0RYU9
CE	561	LEU	-	insertion	UNP G0RYU9
CE	562	SER	-	insertion	UNP G0RYU9
CE	563	ARG	-	insertion	UNP G0RYU9
CE	564	ASP	-	insertion	UNP G0RYU9
CE	565	LYS	-	insertion	UNP G0RYU9
CE	566	LYS	-	insertion	UNP G0RYU9
CE	567	PRO	-	insertion	UNP G0RYU9
CE	568	GLN	-	insertion	UNP G0RYU9
CE	569	GLY	-	insertion	UNP G0RYU9
CE	570	ARG	-	insertion	UNP G0RYU9
CE	571	ARG	-	insertion	UNP G0RYU9
CE	572	ALA	-	insertion	UNP G0RYU9
CE	573	TYR	-	insertion	UNP G0RYU9
CE	574	GLY	-	insertion	UNP G0RYU9
CE	575	SER	-	insertion	UNP G0RYU9
CE	576	GLN	-	insertion	UNP G0RYU9
CE	577	PRO	-	insertion	UNP G0RYU9
CE	578	ARG	-	insertion	UNP G0RYU9

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Chain	Residue	Modelled	Actual	Comment	Reference
CE	579	GLN	-	insertion	UNP G0RYU9
CE	580	GLY	-	insertion	UNP G0RYU9
CE	581	GLY	-	insertion	UNP G0RYU9
CE	582	ARG	-	insertion	UNP G0RYU9
CE	583	TYR	-	insertion	UNP G0RYU9
CE	584	LYS	-	insertion	UNP G0RYU9

- Molecule 8 is a protein called Ribosome assembly factor mrt4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CF	245	Total	C	N	O	S	0	0
			1945	1222	352	362	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CF	13	ILE	THR	conflict	UNP G0S616
CF	139	THR	PRO	conflict	UNP G0S616
CF	228	ASN	SER	conflict	UNP G0S616
CF	259	ILE	MET	conflict	UNP G0S616

- Molecule 9 is a protein called 60S ribosome subunit biogenesis protein NIP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CG	177	Total	C	N	O	S	0	0
			1396	884	247	253	12		

- Molecule 10 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CH	476	Total	C	N	O	S	0	0
			3851	2451	669	716	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CI	146	Total	C	N	O	S	0	0
			1196	763	224	204	5		

- Molecule 12 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	CJ	380	3109	2003	547	549	10	0	0

- Molecule 13 is a protein called Ribosome biogenesis protein NSA2 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	CK	232	1855	1165	363	323	4	0	0

- Molecule 14 is a protein called Putative GTP binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	CL	390	2173	1307	446	420	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CL	69	ARG	ILE	conflict	UNP G0SEW3

- Molecule 15 is a protein called 60S ribosomal protein l7-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	CM	187	1525	987	278	257	3	0	0
15	LF	240	1967	1264	368	332	3	0	0

- Molecule 16 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	CN	246	1856	1158	322	369	7	0	0

- Molecule 17 is a protein called DUF2423 domain-containing protein.

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

- Molecule 18 is a protein called RNA methyltransferase nop2-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	CP	324	Total	C	N	O	S	0	0
			2535	1618	445	457	15		

- Molecule 19 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	CQ	112	Total	C	N	O	S	0	0
			960	607	195	148	10		

- Molecule 20 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	CR	167	Total	C	N	O	S	0	0
			1354	827	278	247	2		

- Molecule 21 is a protein called AdoMet-dependent rRNA methyltransferase SPB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	CS	298	Total	C	N	O	S	0	0
			1750	1072	330	347	1		

- Molecule 22 is a protein called Nucleolar complex-associated protein 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	CT	458	Total	C	N	O	0	0
			2269	1353	458	458		

- Molecule 23 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	CU	178	Total	C	N	O	S	0	0
			1415	876	265	271	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	CX	88	Total	C	N	O	S	0	0
			701	435	128	135	3		

- Molecule 25 is a protein called Putative NOC2 family protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	CY	324	1608	960	324	324	0	0

- Molecule 26 is a protein called rRNA-processing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Cz	70	592	368	120	101	3	0	0

- Molecule 27 is a protein called ATP-dependent RNA helicase DBP10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Cb	642	5058	3216	918	911	13	0	0

- Molecule 28 is a protein called 60S ribosomal protein L3-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	LB	341	2708	1721	493	482	12	0	0

- Molecule 29 is a protein called 60S ribosomal protein L4-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	LC	362	2752	1738	526	479	9	0	0

- Molecule 30 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	LE	170	1338	861	241	233	3	0	0

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	LG	196	1583	1021	287	270	5	0	0

- Molecule 32 is a protein called 60S ribosomal protein l9-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	LH	190	1496	950	268	272	6	0	0

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	TYR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	PHE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ARG	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	THR	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	SER	deletion	UNP G0S0E5
LH	?	-	LYS	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5
LH	?	-	GLU	deletion	UNP G0S0E5
LH	?	-	LEU	deletion	UNP G0S0E5
LH	?	-	ASP	deletion	UNP G0S0E5
LH	?	-	ILE	deletion	UNP G0S0E5
LH	?	-	ASN	deletion	UNP G0S0E5
LH	?	-	GLY	deletion	UNP G0S0E5

- Molecule 33 is a protein called 60S ribosomal protein L12-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	LK	146	1112	701	203	206	2	0	0

- Molecule 34 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	LL	117	964	608	206	148	2	0	0

- Molecule 35 is a protein called 60S ribosomal protein L14-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	LM	137	1101	699	211	190	1	0	0

- Molecule 36 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	LN	183	1563	974	332	253	4	0	0

- Molecule 37 is a protein called 60S ribosomal protein L16-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	LO	204	1618	1039	306	267	6	0	0

- Molecule 38 is a protein called 60S ribosomal protein l17-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	LP	154	1212	758	233	218	3	0	0

- Molecule 39 is a protein called Ribosomal protein L18-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	LQ	129	1021	646	200	173	2	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	LS	174	1433	922	267	239	5	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	LT	126	1014	643	196	173	2	0	0

- Molecule 42 is a protein called 60S ribosomal protein l23-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	LV	135	995	633	185	170	7	0	0

- Molecule 43 is a protein called 60S ribosomal protein L25-like protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	LX	22	148	91	31	26	0	0

- Molecule 44 is a protein called 60S ribosomal protein L26-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	LY	134	1065	664	215	184	2	0	0

- Molecule 45 is a protein called Putative 60S ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	Ld	109	890	563	171	155	1	0	0

- Molecule 46 is a protein called 60S ribosomal protein L32-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	Le	131	1055	663	213	172	7	0	0

- Molecule 47 is a protein called 60S ribosomal protein l33-like protein.

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

- Molecule 48 is a protein called dolichyl-diphosphooligosaccharide--protein glycotransferase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	Lh	121	995	633	196	166		0	0

- Molecule 49 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	Li	88	731	449	162	119	1	0	0

- Molecule 50 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	Lj	74	595	365	132	93	5	0	0

- Molecule 51 is a protein called Ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Lq	207	1600	1016	285	291	8	0	0

- Molecule 52 is a protein called Ribosomal RNA-processing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Cc	236	1898	1208	337	343	10	0	0

- Molecule 53 is a protein called Brix domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	Cd	342	2763	1743	533	483	4	0	0

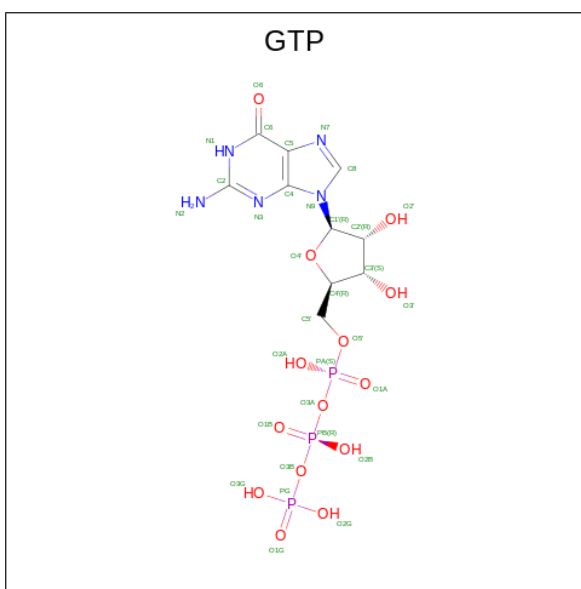
- Molecule 54 is a protein called Protein MAK16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Ce	194	1609	1020	304	276	9	0	0

- Molecule 55 is a protein called 60S ribosome biogenesis protein Rrp14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	Cf	59	513	310	111	92	0	0

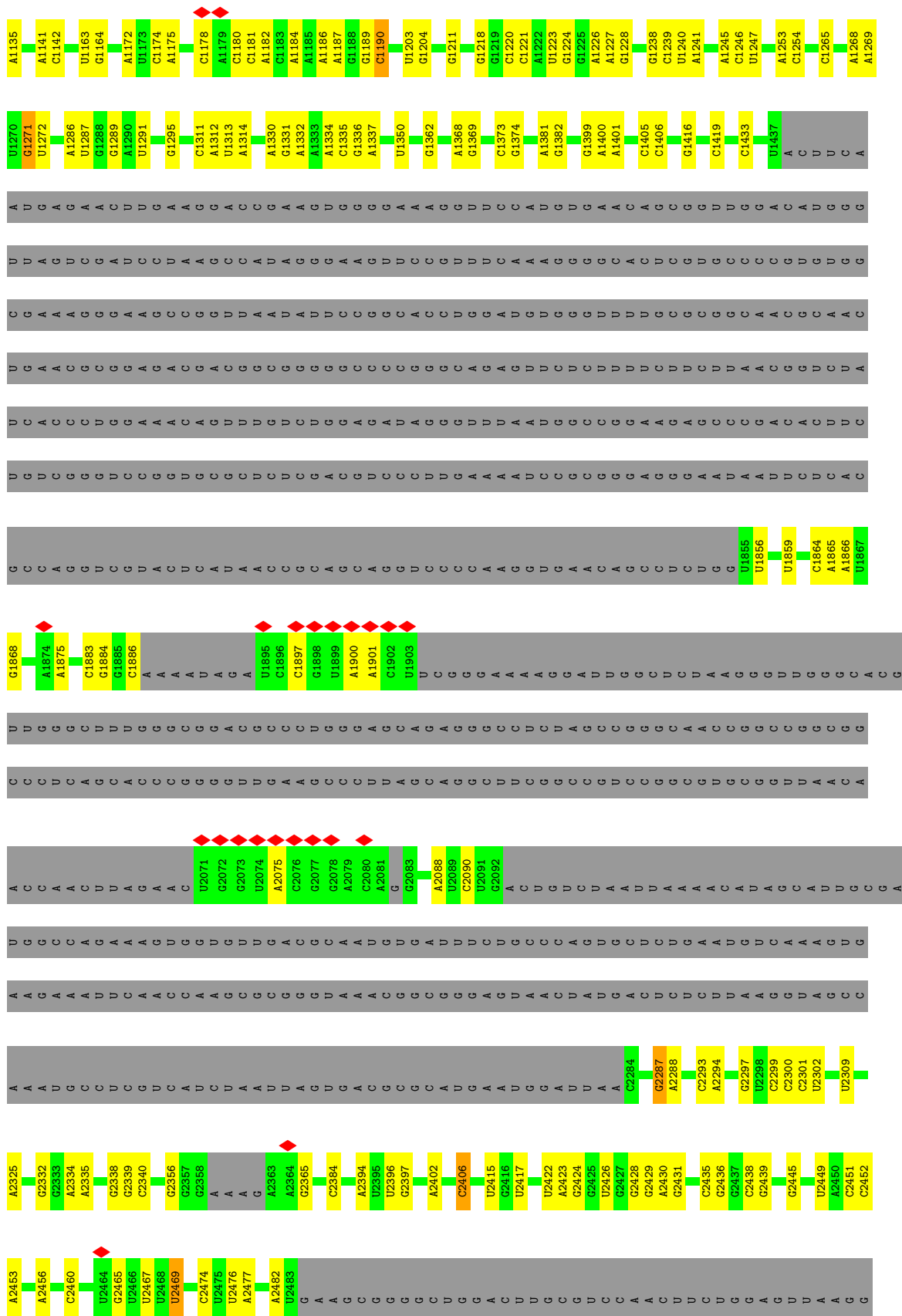
- Molecule 56 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

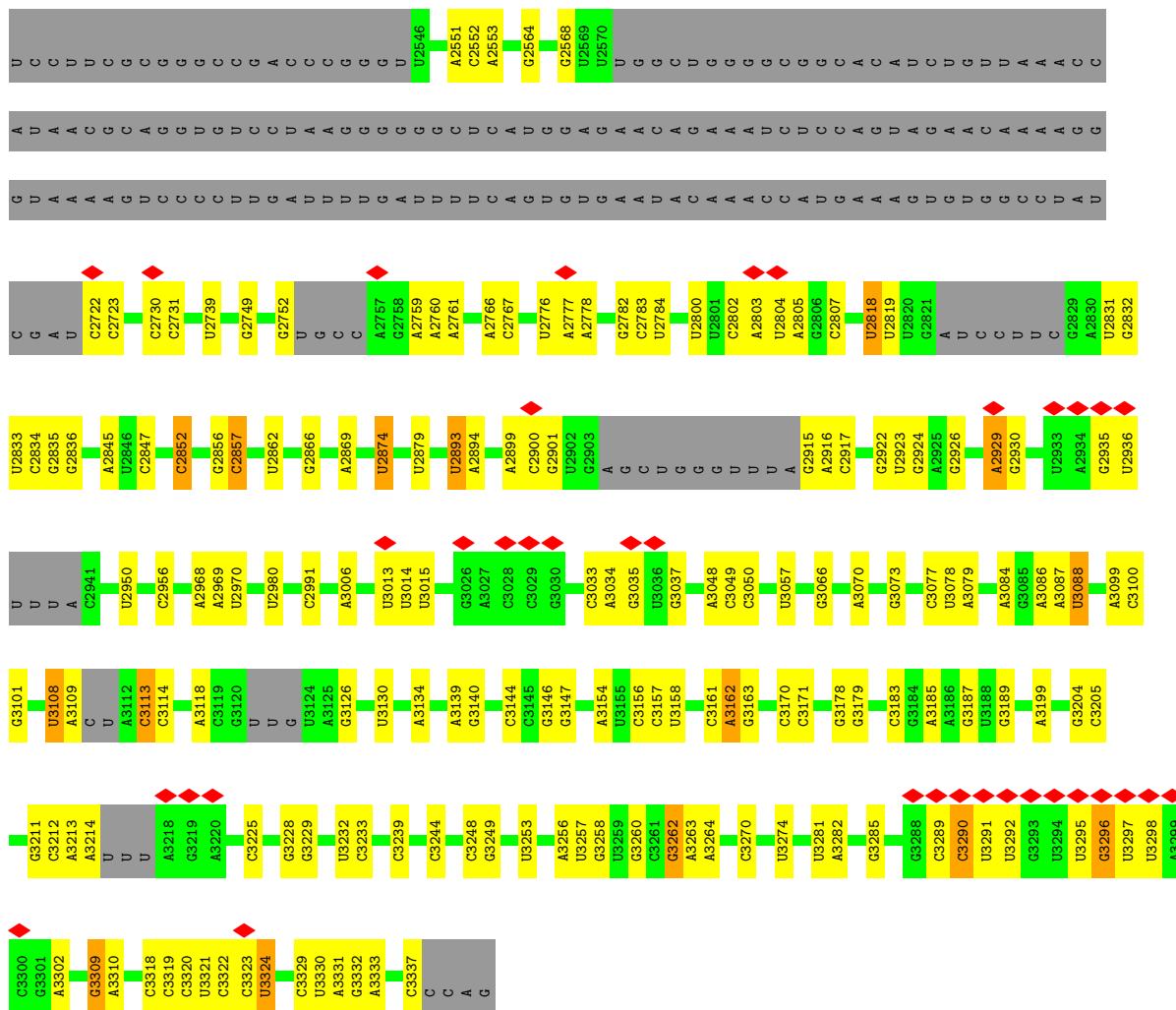


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
56	CH	1	32	10	5	14	3	0

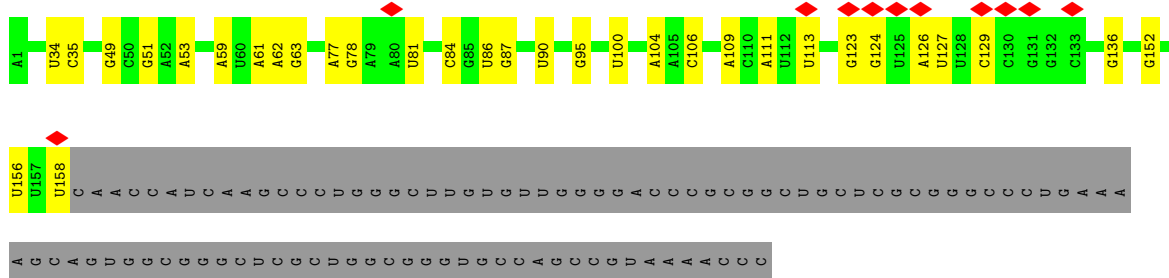
- Molecule 57 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
57	CQ	1	1	1	0
57	Lj	1	1	1	0
57	Ce	1	1	1	0



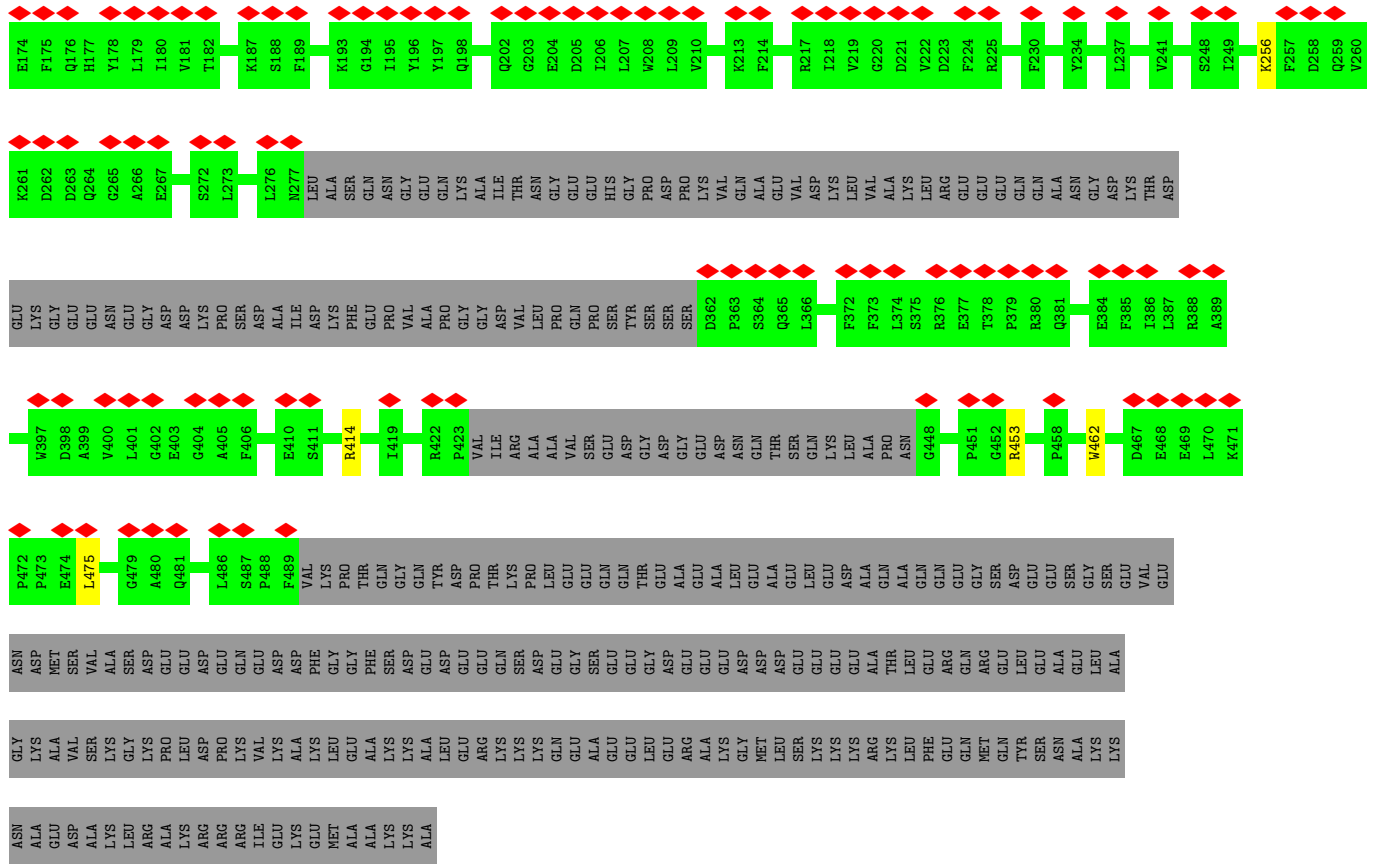


• Molecule 2: RNA (256-MER)

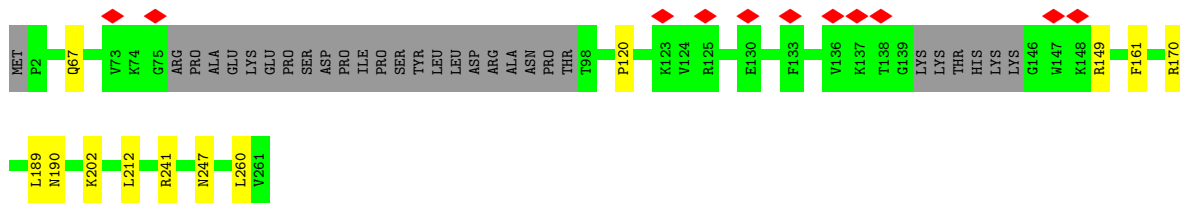
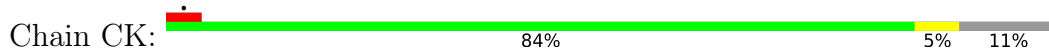


• Molecule 3: RNA (161-MER)

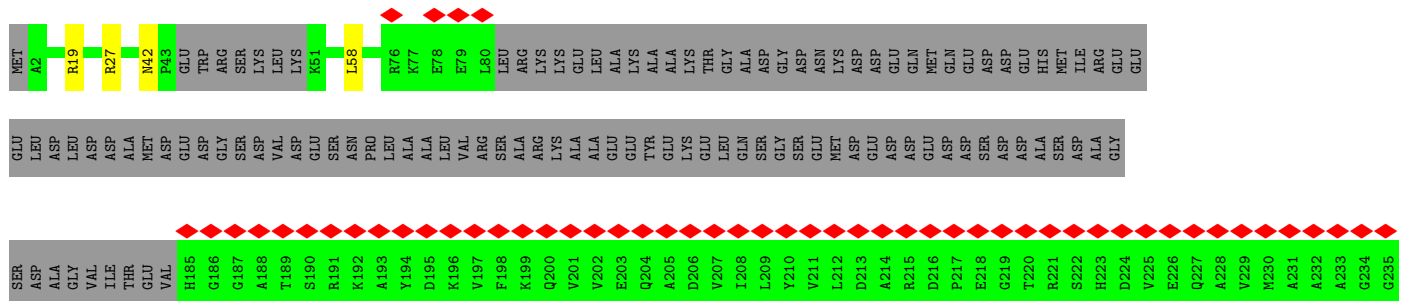


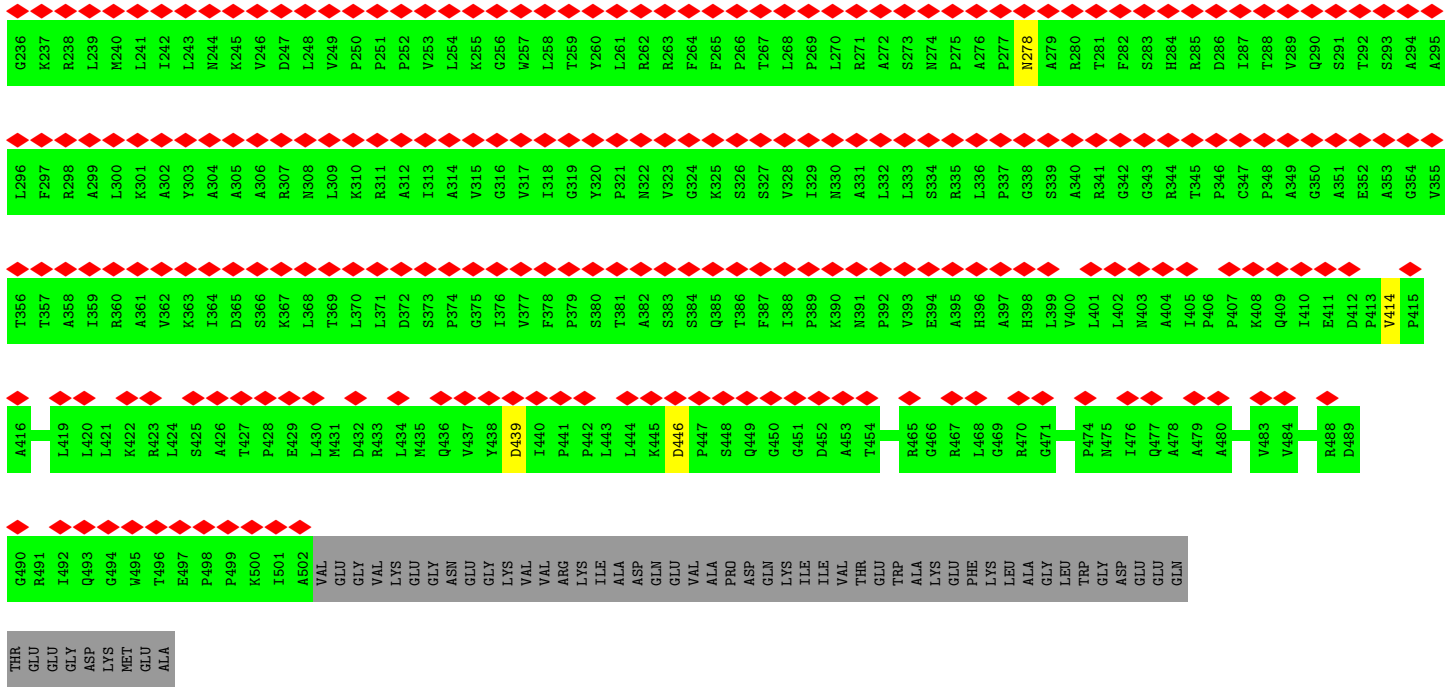


• Molecule 13: Ribosome biogenesis protein NSA2 homolog

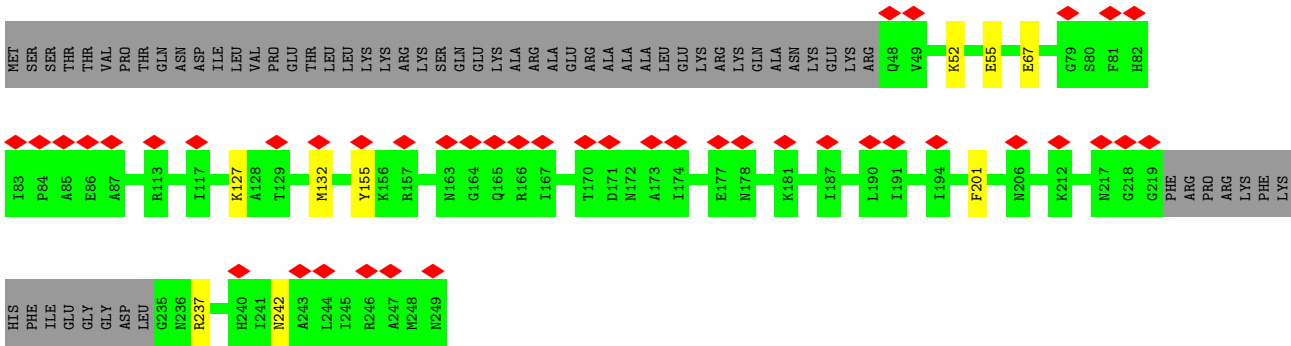
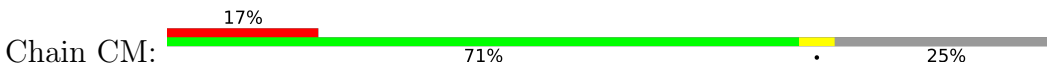


• Molecule 14: Putative GTP binding protein





- Molecule 15: 60S ribosomal protein l7-like protein



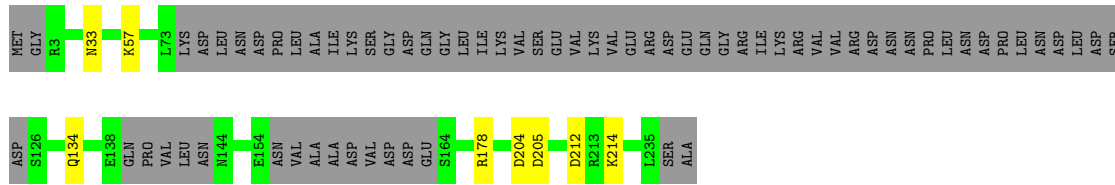
- Molecule 15: 60S ribosomal protein l7-like protein



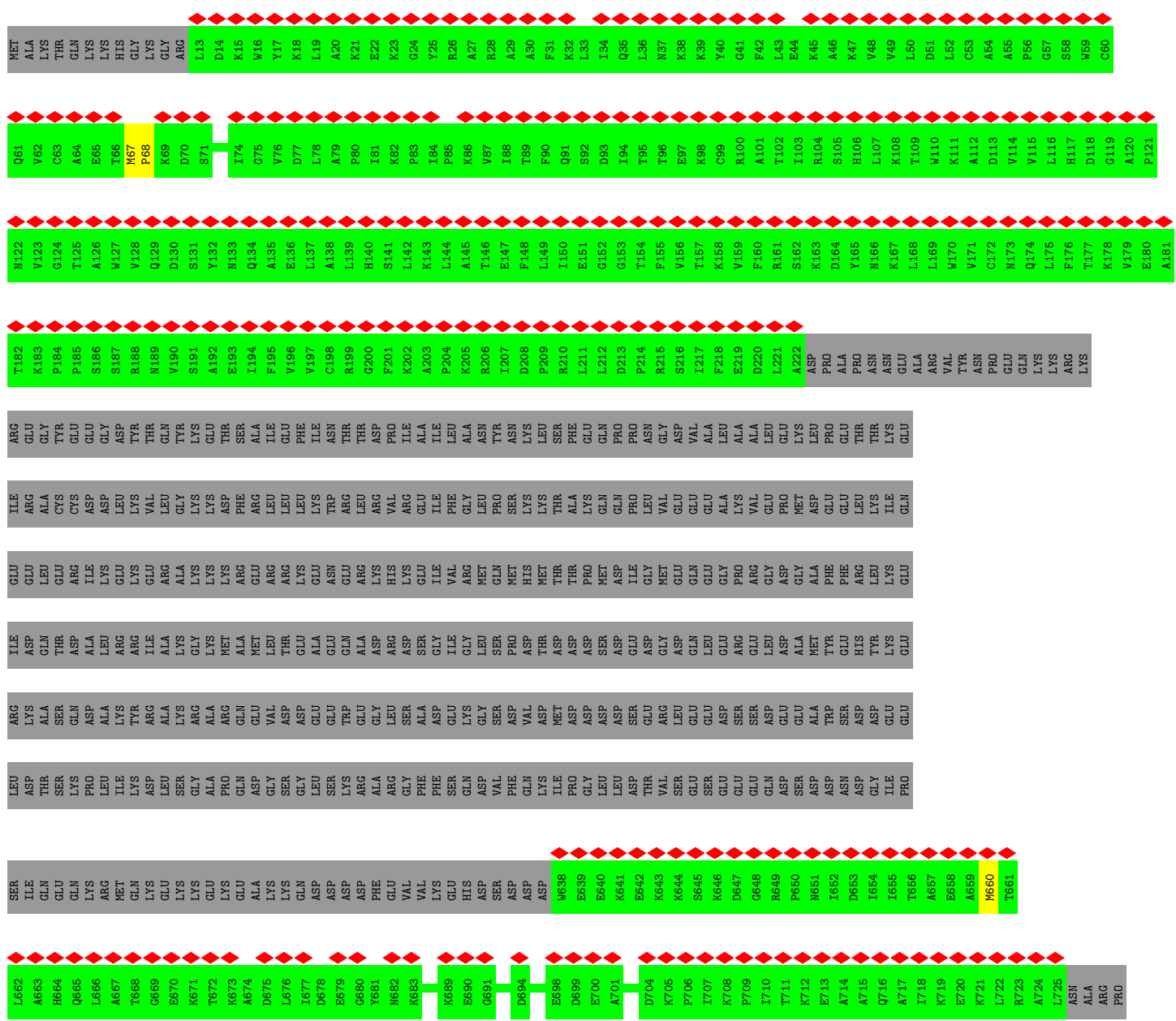
- Molecule 16: Eukaryotic translation initiation factor 6

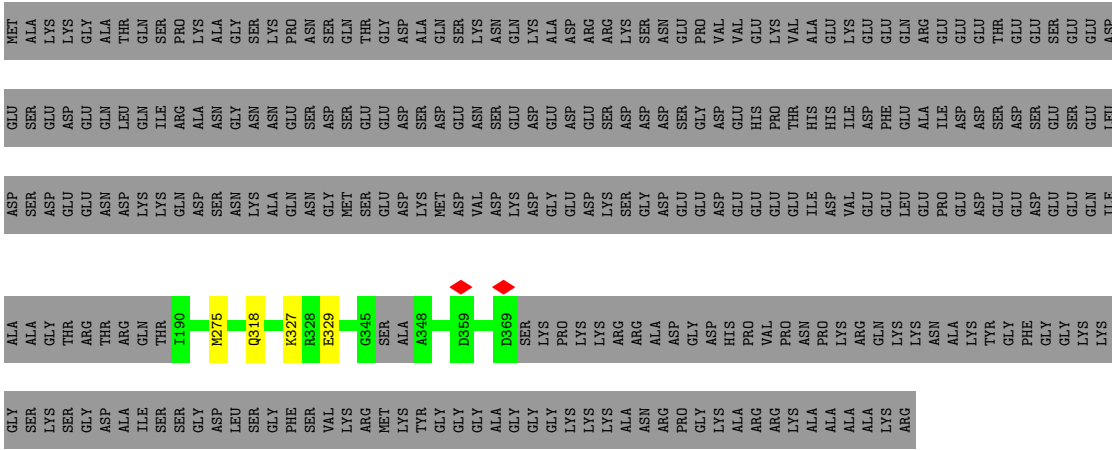


Molecule 20: Nucleolar protein 16

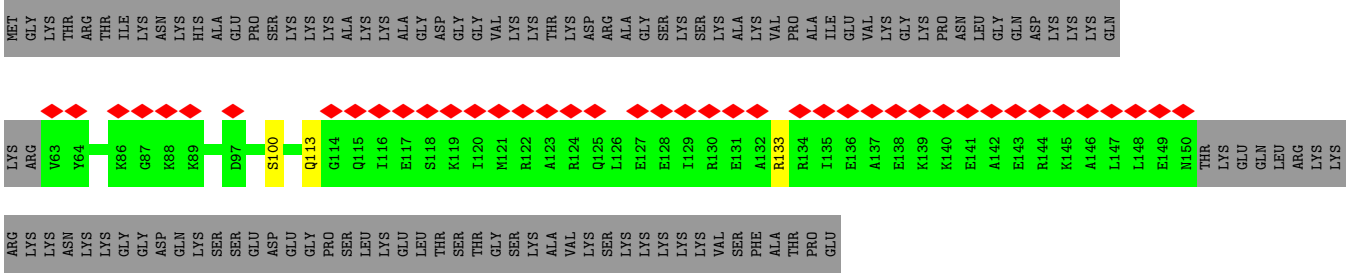


Molecule 21: AdoMet-dependent rRNA methyltransferase SPB1

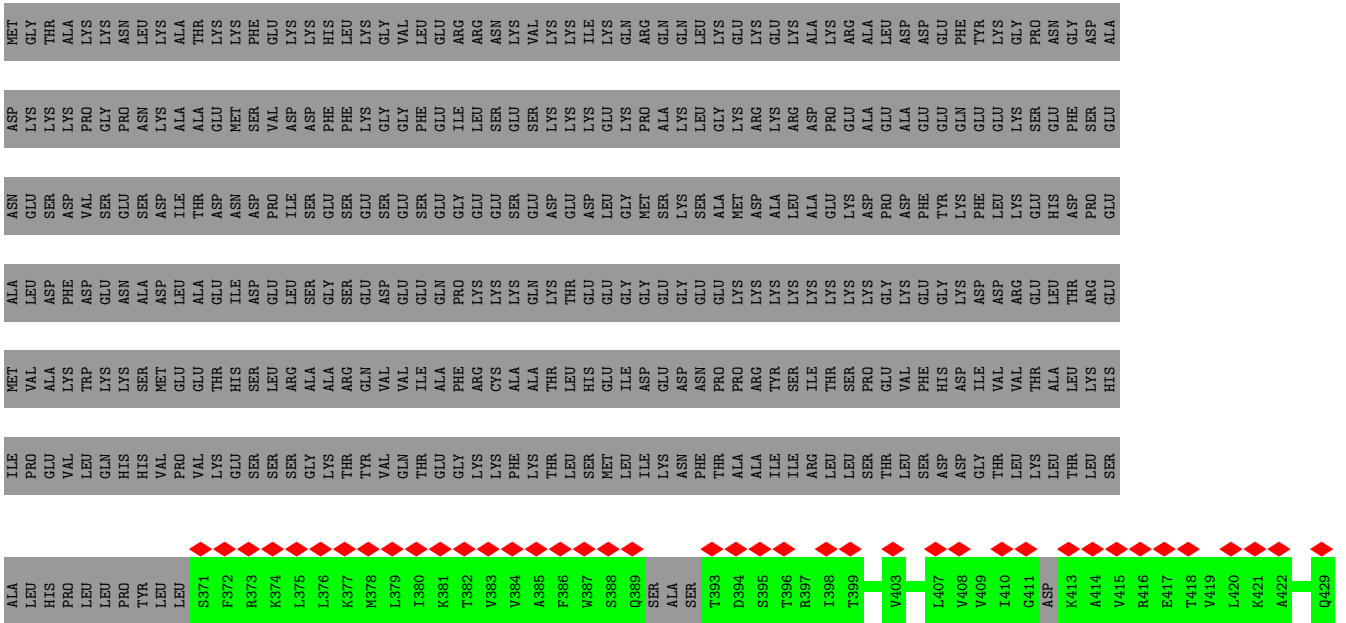




• Molecule 24: 60S ribosomal subunit-like protein

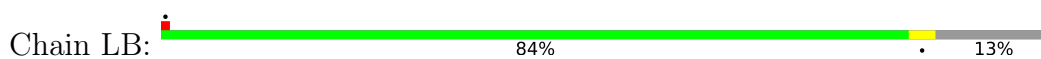


• Molecule 25: Putative NOC2 family protein



LYS
ALA
LYS
GLU
LEU
LYS
GLU
ARG
ARG
GLU
LYS
LYS
ASN
ALA
ARG
PRO
SER
SER
LYS
LYS
PRO
LYS
LYS
LYS

- Molecule 28: 60S ribosomal protein L3-like protein



MET
SER
HIS
VAL
TRP
GLY
THR
LYS
LEU
ARG
VAL
THR
LYS
LEU
PRO
ARG
LYS
THR
HIS
LYS
GLY
LEU
ARG
VAL
LYS
VAL
ALA
CYS
ILE
GLY
ALA
TRP
HIS
PRO

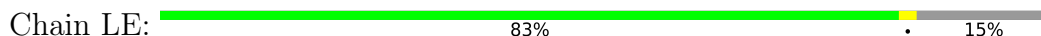
SER
HIS
VAL
GLN
TRP
THR
VAL
ALA
ARG
A268
E298
K354
K378
T390
S391
ALA

- Molecule 29: 60S ribosomal protein L4-like protein



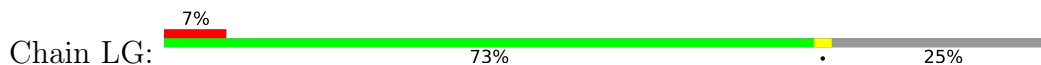
MET
ALA
SER
R4
S62
A63
E64
R70
F121
S271
R321
K359
E360
A365

- Molecule 30: 60S ribosomal protein L6



MET
SER
ALA
PRO
THR
THR
LYS
PHE
GLY
LYS
THR
ARG
VAL
PRO
ALA
PRO
SER
GLU
LYS
LYS
ALA
Q25
A150
LYS
ALA
LYS
GLU
LYS
A137
K167
K191
K199
F200

- Molecule 31: 60S ribosomal protein L8



MET
PRO
PRO
LYS
SER
GLY
LYS
VAL
ALA
PRO
ALA
PHE
PRO
GLN
GLY
LYS
ALA
GLY
ALA
LYS
LYS
ALA
PRO
LYS
ASN
PRO
LEU
LEU
GLU
LYS
ARG
PRO
ARG
ASN
PHE
GLY
ILE
GLN
ASP
GLN
ILE
PRO
LYS
ARG
ASN
SER
LEU
SER
ARG
M52
V53
K54
E107
E121
GLY
LYS

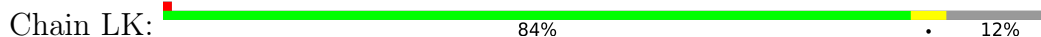
LYS
LYS
GLU
ASP
V128
M140
K216
K228
G239
I240
M241
G242
F243
K244
A245
K247
R248
E249
E250
K251
K252
K253
LYS
SER
LEU
GLU
THR
PHE
ALA
ILE
LYS
VAL

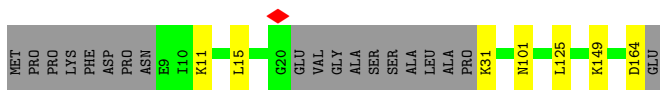
- Molecule 32: 60S ribosomal protein I9-like protein



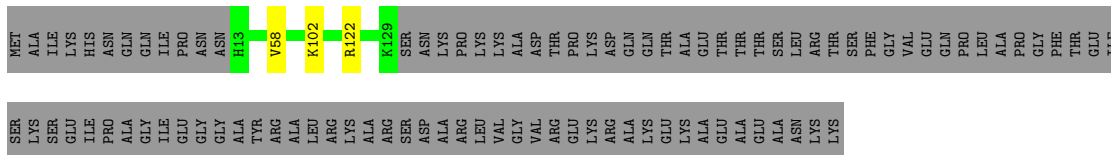
M1
K17
V18
S19
R23
K33
K36
D37
L65
K63
P88
E108
S149
G150
M151
S157
V190
GLU
ASP

- Molecule 33: 60S ribosomal protein L12-like protein

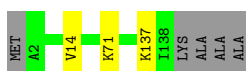




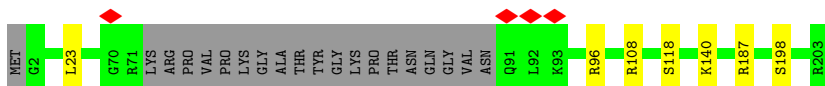
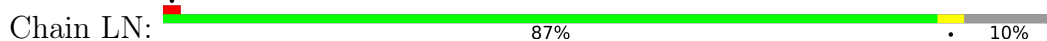
• Molecule 34: 60S ribosomal protein L13



• Molecule 35: 60S ribosomal protein L14-like protein



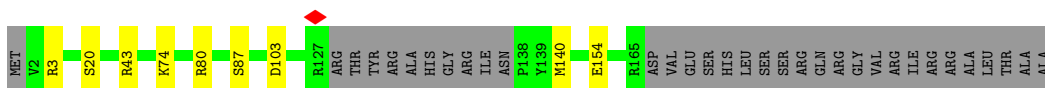
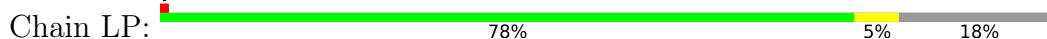
• Molecule 36: Ribosomal protein L15



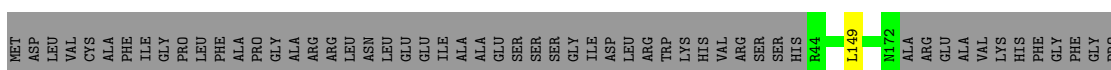
• Molecule 37: 60S ribosomal protein L16-like protein

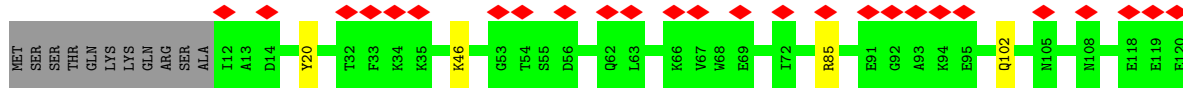
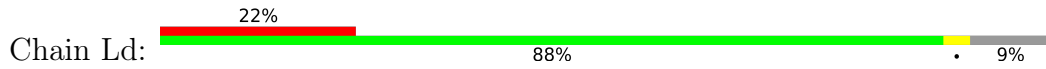


• Molecule 38: 60S ribosomal protein l17-like protein



• Molecule 39: Ribosomal protein L18-like protein





- Molecule 46: 60S ribosomal protein L32-like protein



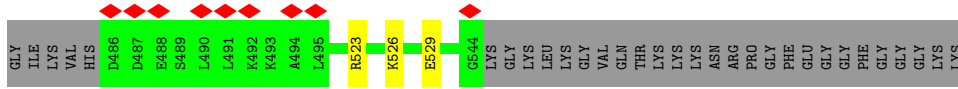
- Molecule 47: 60S ribosomal protein L33-like protein



- Molecule 48: dolichyl-diphosphooligosaccharide--protein glycotransferase



MET	SER	THR	GLN	LYS	GLN	ARG	SER	ALA	I12	A13	D14	Y20	T32	F33	K34	K35	K46	G53	T54	S55	D66	Q62	L63	R66	V67	W68	E69	I72	R85	E91	G92	A93	K94	E95	Q102	M105	H108	E118	E119	E120												
VAL	ALA	ALA	LEU	LEU	LEU	GLY	PRO	ARG	ASN	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR							
ALA	SER	ARG	LEU	PHE	LEU	VAL	ILE	LEU	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR					
LEU	MET	THR	THR	GLY	VAL	VAL	ILE	LEU	THR	PHE	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR				
MET	GLY	ILE	ALA	PRO	GLY	TYR	ILE	LEU	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR			
GLY	TYR	ALA	PHE	ASP	THR	CYS	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU		
LEU	GLY	ILE	PHE	GLY	PHE	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	
TYR	SER	LEU	TRP	ASP	THR	TYR	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
VAL	TYR	ALA	PHE	GLY	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
SER	GLY	LEU	LYS	ALA	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER	SER



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16465	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.458	Depositor
Minimum map value	-0.239	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	438.9, 438.9, 438.9	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.43	0/51490	1.00	169/80245 (0.2%)
2	C2	0.39	0/3754	0.90	1/5846 (0.0%)
3	C3	0.39	0/2342	1.07	11/3649 (0.3%)
4	CA	0.30	0/2190	0.61	1/2940 (0.0%)
5	CB	0.36	0/2109	0.72	3/2866 (0.1%)
6	CC	0.29	0/2459	0.56	0/3350
7	CE	0.31	0/3743	0.64	5/5045 (0.1%)
8	CF	0.30	0/1982	0.65	0/2671
9	CG	0.32	0/1422	0.70	2/1920 (0.1%)
10	CH	0.35	0/3927	0.70	7/5307 (0.1%)
11	CI	0.33	0/1225	0.68	1/1645 (0.1%)
12	CJ	0.27	0/3189	0.53	0/4309
13	CK	0.30	0/1885	0.64	2/2529 (0.1%)
14	CL	0.26	0/2178	0.48	0/2983
15	CM	0.32	0/1555	0.67	2/2091 (0.1%)
15	LF	0.29	0/2004	0.56	0/2686
16	CN	0.29	0/1881	0.64	1/2560 (0.0%)
17	CO	0.29	0/470	0.55	0/619
18	CP	0.33	0/2594	0.68	4/3514 (0.1%)
19	CQ	0.32	0/981	0.70	1/1301 (0.1%)
20	CR	0.29	0/1369	0.64	1/1828 (0.1%)
21	CS	0.26	0/1762	0.45	0/2417
22	CT	0.28	0/2264	0.47	0/3149
23	CU	0.33	0/1428	0.66	1/1910 (0.1%)
24	CX	0.27	0/705	0.57	0/938
25	CY	0.31	0/1600	0.47	0/2220
26	Cz	0.29	0/598	0.56	0/785
27	Cb	0.32	0/5150	0.68	4/6936 (0.1%)
28	LB	0.33	0/2760	0.65	2/3701 (0.1%)
29	LC	0.32	0/2809	0.57	0/3787
30	LE	0.30	0/1363	0.55	0/1833
31	LG	0.32	0/1606	0.57	0/2149

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	LH	0.29	0/1516	0.58	1/2038 (0.0%)
33	LK	0.30	0/1124	0.70	2/1507 (0.1%)
34	LL	0.34	0/983	0.65	0/1318
35	LM	0.29	0/1120	0.57	0/1507
36	LN	0.30	0/1595	0.62	0/2132
37	LO	0.31	0/1652	0.56	0/2215
38	LP	0.31	0/1231	0.61	0/1658
39	LQ	0.30	0/1033	0.63	0/1391
40	LS	0.31	0/1468	0.61	0/1975
41	LT	0.28	0/1033	0.68	1/1389 (0.1%)
42	LV	0.32	0/1013	0.57	0/1361
43	LX	0.24	0/148	0.35	0/194
44	LY	0.29	0/1079	0.61	0/1443
45	Ld	0.26	0/904	0.61	0/1209
46	Le	0.29	0/1073	0.56	0/1431
47	Lf	0.33	0/883	0.63	0/1187
48	Lh	0.28	0/1006	0.59	0/1338
49	Li	0.30	0/738	0.64	0/971
50	Lj	0.32	0/606	0.65	0/803
51	Lq	0.25	0/1621	0.55	0/2180
52	Cc	0.31	0/1934	0.57	0/2614
53	Cd	0.31	0/2818	0.61	0/3786
54	Ce	0.30	0/1638	0.56	0/2196
55	Cf	0.27	0/514	0.57	0/669
All	All	0.36	0/145524	0.80	222/208241 (0.1%)

There are no bond length outliers.

The worst 5 of 222 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1050	C	N3-C2-O2	-11.53	113.83	121.90
1	C1	136	C	N3-C2-O2	-10.12	114.82	121.90
1	C1	2852	C	N3-C2-O2	-10.01	114.89	121.90
1	C1	939	C	N3-C2-O2	-9.73	115.09	121.90
28	LB	171	PRO	CA-N-CD	-9.15	98.69	111.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
4	CA	254/316 (80%)	234 (92%)	19 (8%)	1 (0%)	34	69
5	CB	256/391 (66%)	244 (95%)	10 (4%)	2 (1%)	19	54
6	CC	283/801 (35%)	272 (96%)	11 (4%)	0	100	100
7	CE	459/598 (77%)	445 (97%)	13 (3%)	1 (0%)	47	79
8	CF	243/270 (90%)	234 (96%)	9 (4%)	0	100	100
9	CG	175/184 (95%)	167 (95%)	8 (5%)	0	100	100
10	CH	474/661 (72%)	456 (96%)	18 (4%)	0	100	100
11	CI	144/414 (35%)	136 (94%)	8 (6%)	0	100	100
12	CJ	374/679 (55%)	365 (98%)	9 (2%)	0	100	100
13	CK	226/261 (87%)	216 (96%)	10 (4%)	0	100	100
14	CL	384/558 (69%)	357 (93%)	22 (6%)	5 (1%)	12	42
15	CM	183/249 (74%)	175 (96%)	8 (4%)	0	100	100
15	LF	238/249 (96%)	228 (96%)	9 (4%)	1 (0%)	34	69
16	CN	244/246 (99%)	236 (97%)	8 (3%)	0	100	100
17	CO	56/120 (47%)	56 (100%)	0	0	100	100
18	CP	322/751 (43%)	307 (95%)	15 (5%)	0	100	100
19	CQ	110/225 (49%)	106 (96%)	4 (4%)	0	100	100
20	CR	159/237 (67%)	155 (98%)	4 (2%)	0	100	100
21	CS	294/834 (35%)	286 (97%)	6 (2%)	2 (1%)	22	57
22	CT	448/688 (65%)	425 (95%)	21 (5%)	2 (0%)	34	69
23	CU	174/451 (39%)	166 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	CX	86/203 (42%)	82 (95%)	4 (5%)	0	100	100
25	CY	308/788 (39%)	292 (95%)	15 (5%)	1 (0%)	41	73
26	Cz	68/123 (55%)	67 (98%)	1 (2%)	0	100	100
27	Cb	630/924 (68%)	597 (95%)	33 (5%)	0	100	100
28	LB	337/392 (86%)	320 (95%)	17 (5%)	0	100	100
29	LC	360/365 (99%)	348 (97%)	12 (3%)	0	100	100
30	LE	166/200 (83%)	160 (96%)	6 (4%)	0	100	100
31	LG	192/262 (73%)	188 (98%)	4 (2%)	0	100	100
32	LH	188/192 (98%)	178 (95%)	10 (5%)	0	100	100
33	LK	142/165 (86%)	132 (93%)	10 (7%)	0	100	100
34	LL	115/213 (54%)	109 (95%)	6 (5%)	0	100	100
35	LM	135/142 (95%)	131 (97%)	4 (3%)	0	100	100
36	LN	179/203 (88%)	174 (97%)	5 (3%)	0	100	100
37	LO	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
38	LP	150/187 (80%)	149 (99%)	1 (1%)	0	100	100
39	LQ	127/213 (60%)	123 (97%)	4 (3%)	0	100	100
40	LS	172/174 (99%)	166 (96%)	6 (4%)	0	100	100
41	LT	124/160 (78%)	117 (94%)	6 (5%)	1 (1%)	19	54
42	LV	133/139 (96%)	131 (98%)	2 (2%)	0	100	100
43	LX	20/156 (13%)	20 (100%)	0	0	100	100
44	LY	132/138 (96%)	130 (98%)	2 (2%)	0	100	100
45	Ld	107/120 (89%)	102 (95%)	5 (5%)	0	100	100
46	Le	129/131 (98%)	126 (98%)	3 (2%)	0	100	100
47	Lf	106/109 (97%)	102 (96%)	3 (3%)	1 (1%)	17	52
48	Lh	119/935 (13%)	117 (98%)	2 (2%)	0	100	100
49	Li	86/110 (78%)	84 (98%)	2 (2%)	0	100	100
50	Lj	72/95 (76%)	70 (97%)	2 (3%)	0	100	100
51	Lq	205/217 (94%)	186 (91%)	19 (9%)	0	100	100
52	Cc	232/282 (82%)	226 (97%)	6 (3%)	0	100	100
53	Cd	334/436 (77%)	323 (97%)	11 (3%)	0	100	100
54	Ce	192/336 (57%)	185 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	Cf	57/570 (10%)	57 (100%)	0	0	100	100
All	All	11105/18067 (62%)	10656 (96%)	432 (4%)	17 (0%)	50	79

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	CA	236	PRO
5	CB	103	ASP
14	CL	414	VAL
21	CS	67	MET
22	CT	254	PRO

5.3.2 Protein sidechains [i](#)

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	
4	CA	231/276 (84%)	218 (94%)	13 (6%)	21	52
5	CB	222/329 (68%)	202 (91%)	20 (9%)	9	34
6	CC	266/710 (38%)	252 (95%)	14 (5%)	22	54
7	CE	398/517 (77%)	376 (94%)	22 (6%)	21	53
8	CF	214/236 (91%)	202 (94%)	12 (6%)	21	52
9	CG	150/155 (97%)	143 (95%)	7 (5%)	26	59
10	CH	424/575 (74%)	405 (96%)	19 (4%)	27	60
11	CI	121/336 (36%)	116 (96%)	5 (4%)	30	64
12	CJ	332/579 (57%)	324 (98%)	8 (2%)	49	76
13	CK	198/225 (88%)	188 (95%)	10 (5%)	24	56
14	CL	65/458 (14%)	62 (95%)	3 (5%)	27	59
15	CM	161/215 (75%)	153 (95%)	8 (5%)	24	57
15	LF	206/215 (96%)	200 (97%)	6 (3%)	42	72
16	CN	206/206 (100%)	199 (97%)	7 (3%)	37	69
17	CO	48/99 (48%)	47 (98%)	1 (2%)	53	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	CP	273/632 (43%)	251 (92%)	22 (8%)	11	39
19	CQ	100/192 (52%)	93 (93%)	7 (7%)	15	45
20	CR	144/206 (70%)	137 (95%)	7 (5%)	25	57
21	CS	73/716 (10%)	72 (99%)	1 (1%)	67	86
23	CU	149/376 (40%)	146 (98%)	3 (2%)	55	80
24	CX	76/172 (44%)	73 (96%)	3 (4%)	32	65
26	Cz	60/107 (56%)	59 (98%)	1 (2%)	60	83
27	Cb	540/779 (69%)	517 (96%)	23 (4%)	29	62
28	LB	290/331 (88%)	282 (97%)	8 (3%)	43	73
29	LC	283/285 (99%)	275 (97%)	8 (3%)	43	73
30	LE	143/166 (86%)	139 (97%)	4 (3%)	43	73
31	LG	168/222 (76%)	163 (97%)	5 (3%)	41	71
32	LH	167/169 (99%)	155 (93%)	12 (7%)	14	44
33	LK	121/136 (89%)	116 (96%)	5 (4%)	30	64
34	LL	99/176 (56%)	96 (97%)	3 (3%)	41	71
35	LM	115/117 (98%)	112 (97%)	3 (3%)	46	74
36	LN	164/180 (91%)	157 (96%)	7 (4%)	29	62
37	LO	163/163 (100%)	159 (98%)	4 (2%)	47	75
38	LP	125/152 (82%)	116 (93%)	9 (7%)	14	44
39	LQ	110/178 (62%)	109 (99%)	1 (1%)	78	91
40	LS	154/154 (100%)	144 (94%)	10 (6%)	17	47
41	LT	109/135 (81%)	107 (98%)	2 (2%)	59	82
42	LV	99/102 (97%)	94 (95%)	5 (5%)	24	56
43	LX	12/129 (9%)	12 (100%)	0	100	100
44	LY	117/119 (98%)	110 (94%)	7 (6%)	19	49
45	Ld	95/105 (90%)	91 (96%)	4 (4%)	30	62
46	Le	114/114 (100%)	112 (98%)	2 (2%)	59	82
47	Lf	89/90 (99%)	85 (96%)	4 (4%)	27	60
48	Lh	108/781 (14%)	105 (97%)	3 (3%)	43	73
49	Li	75/93 (81%)	71 (95%)	4 (5%)	22	54
50	Lj	61/78 (78%)	57 (93%)	4 (7%)	16	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	Lq	179/189 (95%)	176 (98%)	3 (2%)	60	83
52	Cc	204/244 (84%)	199 (98%)	5 (2%)	47	75
53	Cd	291/367 (79%)	282 (97%)	9 (3%)	40	70
54	Ce	173/297 (58%)	165 (95%)	8 (5%)	27	59
55	Cf	53/482 (11%)	50 (94%)	3 (6%)	20	52
All	All	8538/14065 (61%)	8174 (96%)	364 (4%)	33	62

5 of 364 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	LC	360	GLU
38	LP	87	SER
15	LF	100	LYS
33	LK	31	LYS
40	LS	160	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
48	Lh	37	GLN
54	Ce	185	ASN
19	CQ	58	ASN
20	CR	133	GLN
20	CR	148	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	2134/3341 (63%)	479 (22%)	15 (0%)
2	C2	157/256 (61%)	30 (19%)	1 (0%)
3	C3	96/161 (59%)	34 (35%)	0
All	All	2387/3758 (63%)	543 (22%)	16 (0%)

5 of 543 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	6	A
1	C1	26	A

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Mol	Chain	Res	Type
1	C1	40	A
1	C1	43	A
1	C1	49	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	C1	3297	U
1	C1	3296	G
1	C1	3078	U
1	C1	3263	A
1	C1	2929	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	GTP	CH	701	-	26,34,34	1.16	2 (7%)	32,54,54	1.60	7 (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
56	GTP	CH	701	-	-	6/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	CH	701	GTP	C5-C6	-4.17	1.38	1.47
56	CH	701	GTP	C2-N3	2.11	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	CH	701	GTP	PB-O3B-PG	-3.73	120.02	132.83
56	CH	701	GTP	PA-O3A-PB	-3.20	121.86	132.83
56	CH	701	GTP	C5-C6-N1	3.15	119.51	113.95
56	CH	701	GTP	C3'-C2'-C1'	2.97	105.46	100.98
56	CH	701	GTP	C8-N7-C5	2.92	108.55	102.99

There are no chirality outliers.

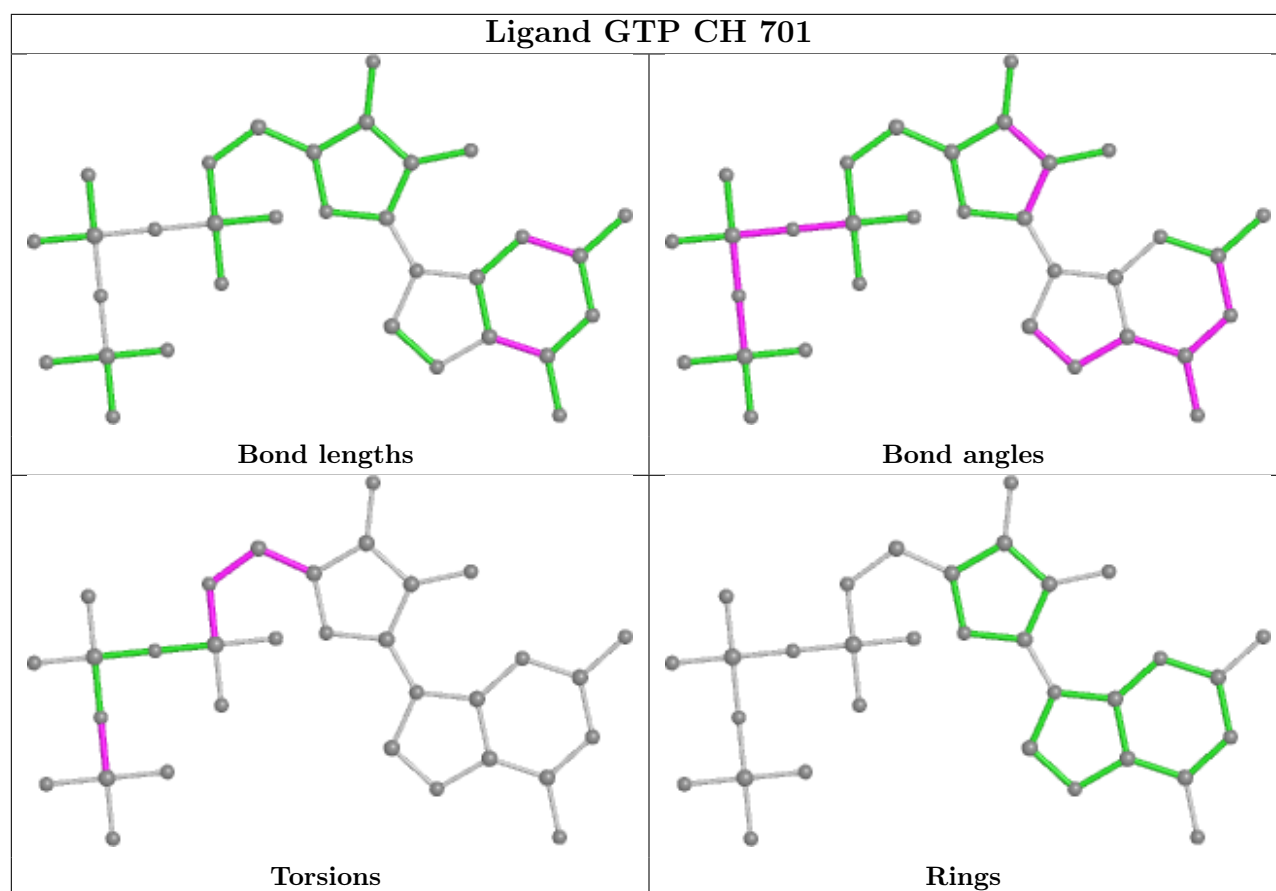
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
56	CH	701	GTP	PB-O3B-PG-O2G
56	CH	701	GTP	PB-O3B-PG-O3G
56	CH	701	GTP	C5'-O5'-PA-O3A
56	CH	701	GTP	C4'-C5'-O5'-PA
56	CH	701	GTP	C5'-O5'-PA-O2A

There are no ring outliers.

No monomer is involved in short contacts.

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



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

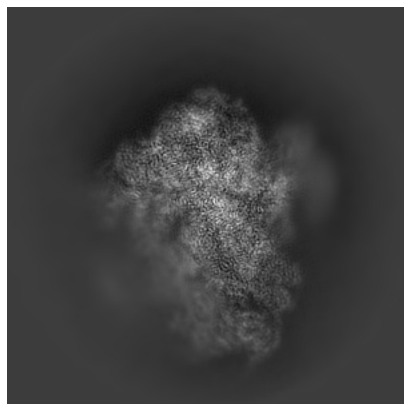
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35285. These allow visual inspection of the internal detail of the map and identification of artifacts.

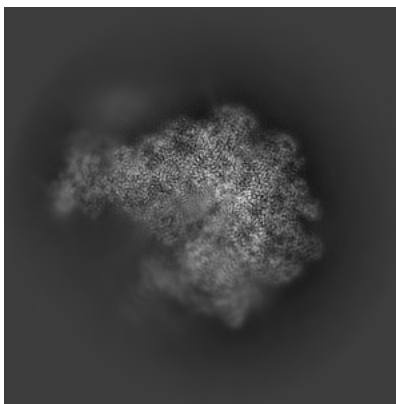
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

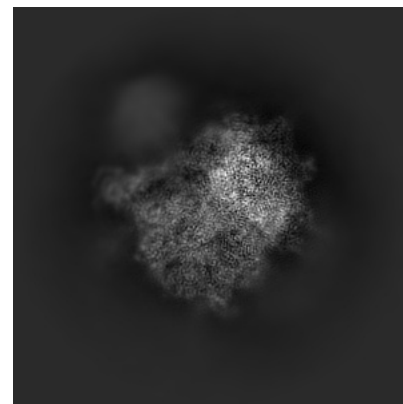
6.1.1 Primary map



X

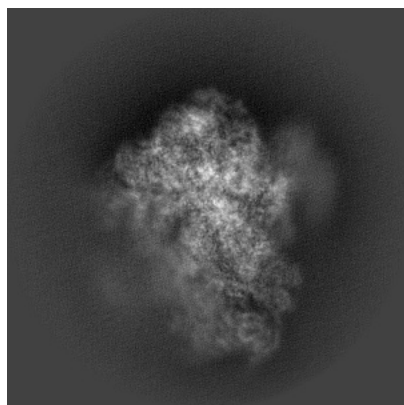


Y

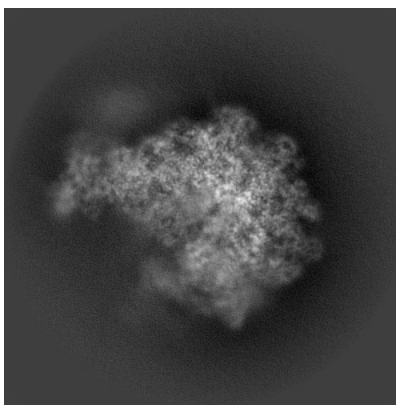


Z

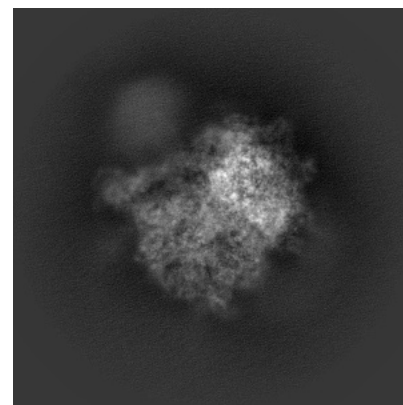
6.1.2 Raw map



X



Y

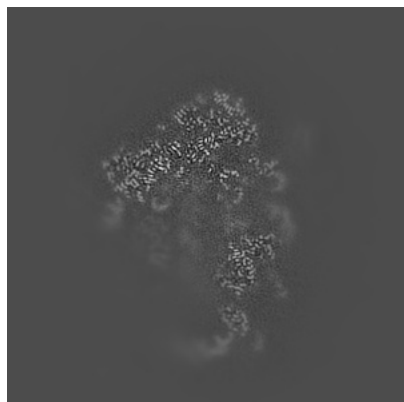


Z

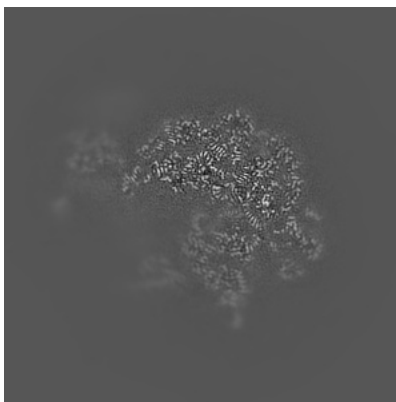
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

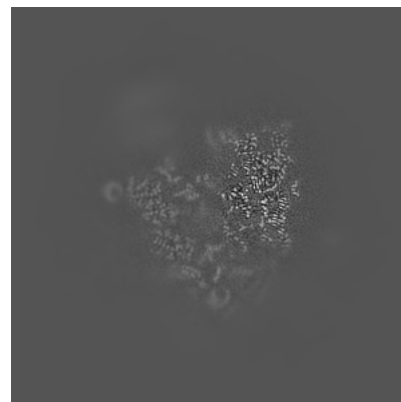
6.2.1 Primary map



X Index: 210

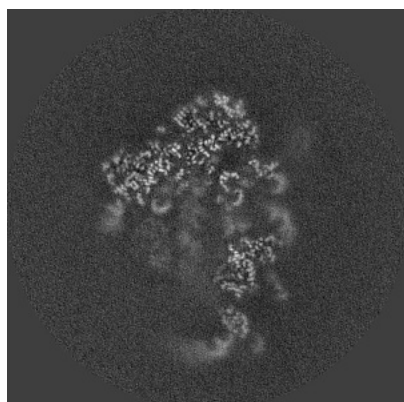


Y Index: 210

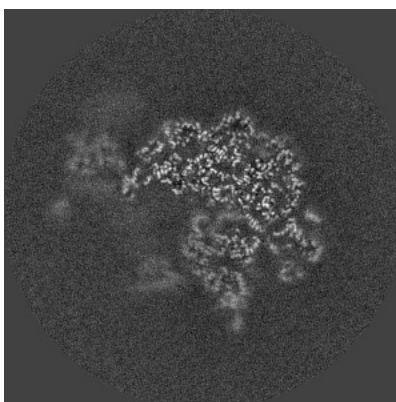


Z Index: 210

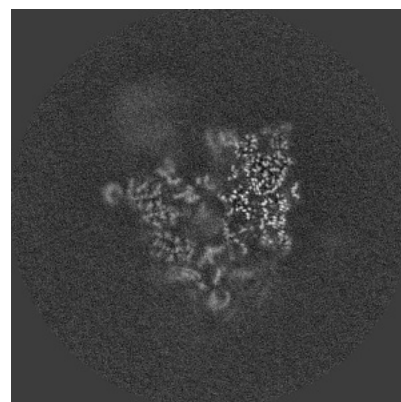
6.2.2 Raw map



X Index: 210



Y Index: 210

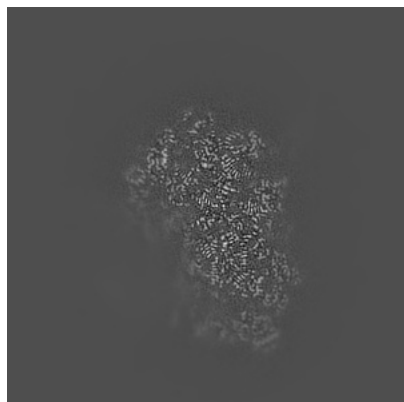


Z Index: 210

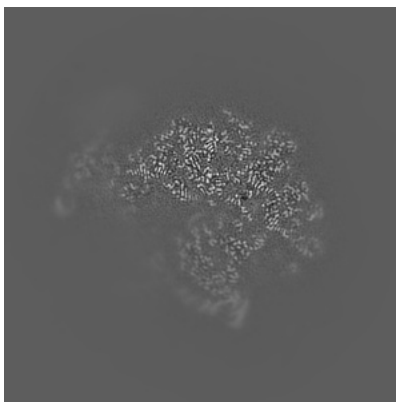
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

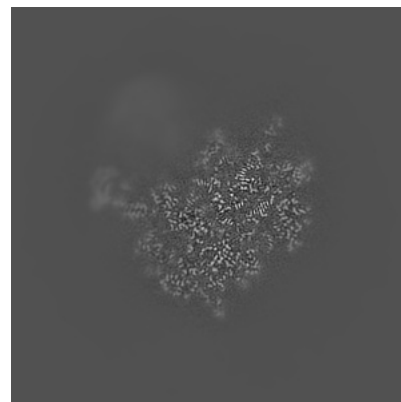
6.3.1 Primary map



X Index: 247

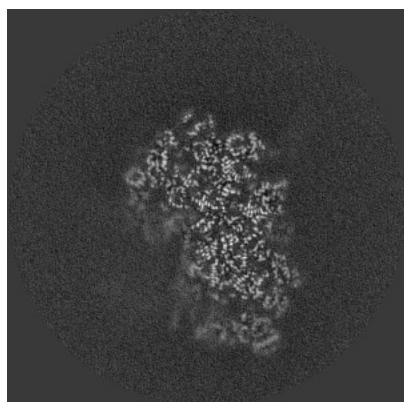


Y Index: 217

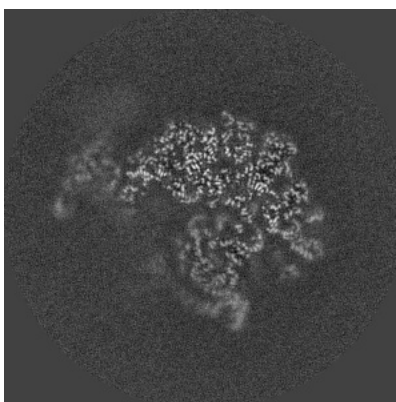


Z Index: 247

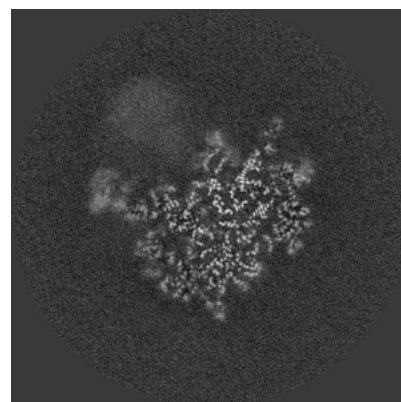
6.3.2 Raw map



X Index: 247



Y Index: 216

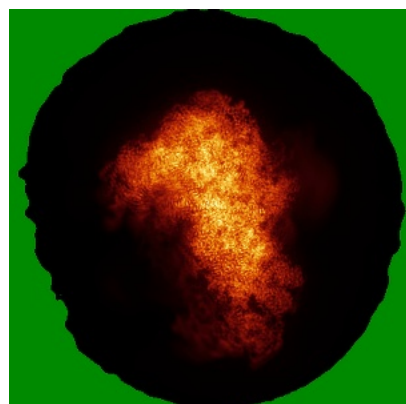


Z Index: 246

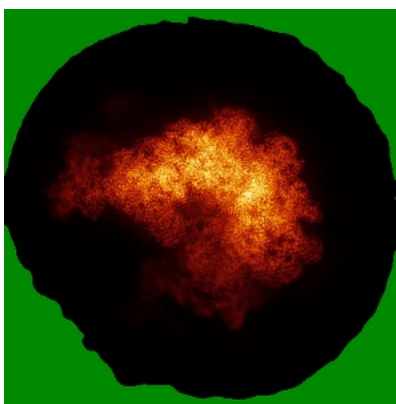
The images above show the largest variance slices of the map in three orthogonal directions.

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

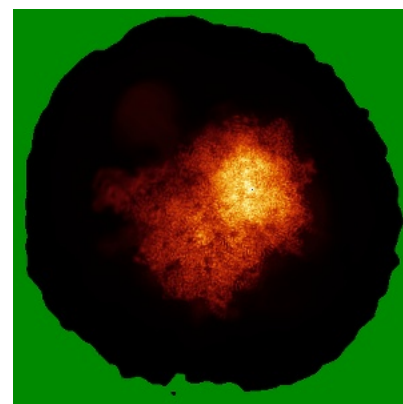
6.4.1 Primary map



X

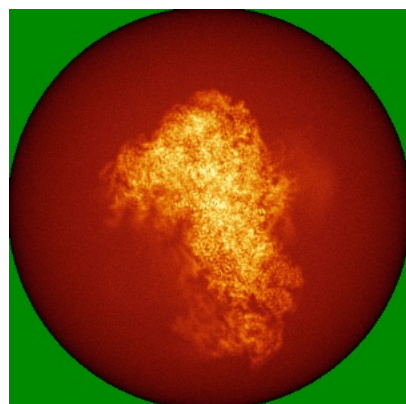


Y

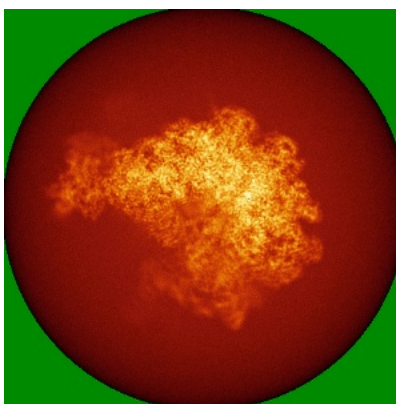


Z

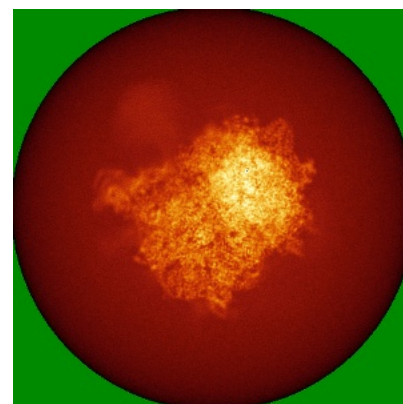
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



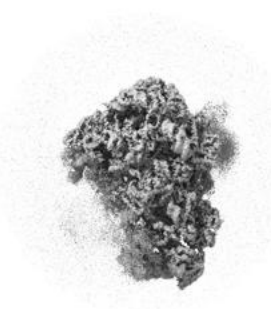
Y



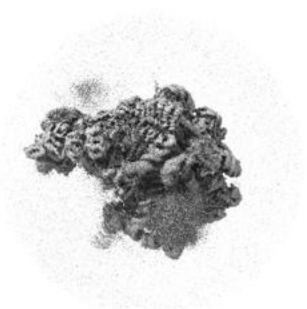
Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

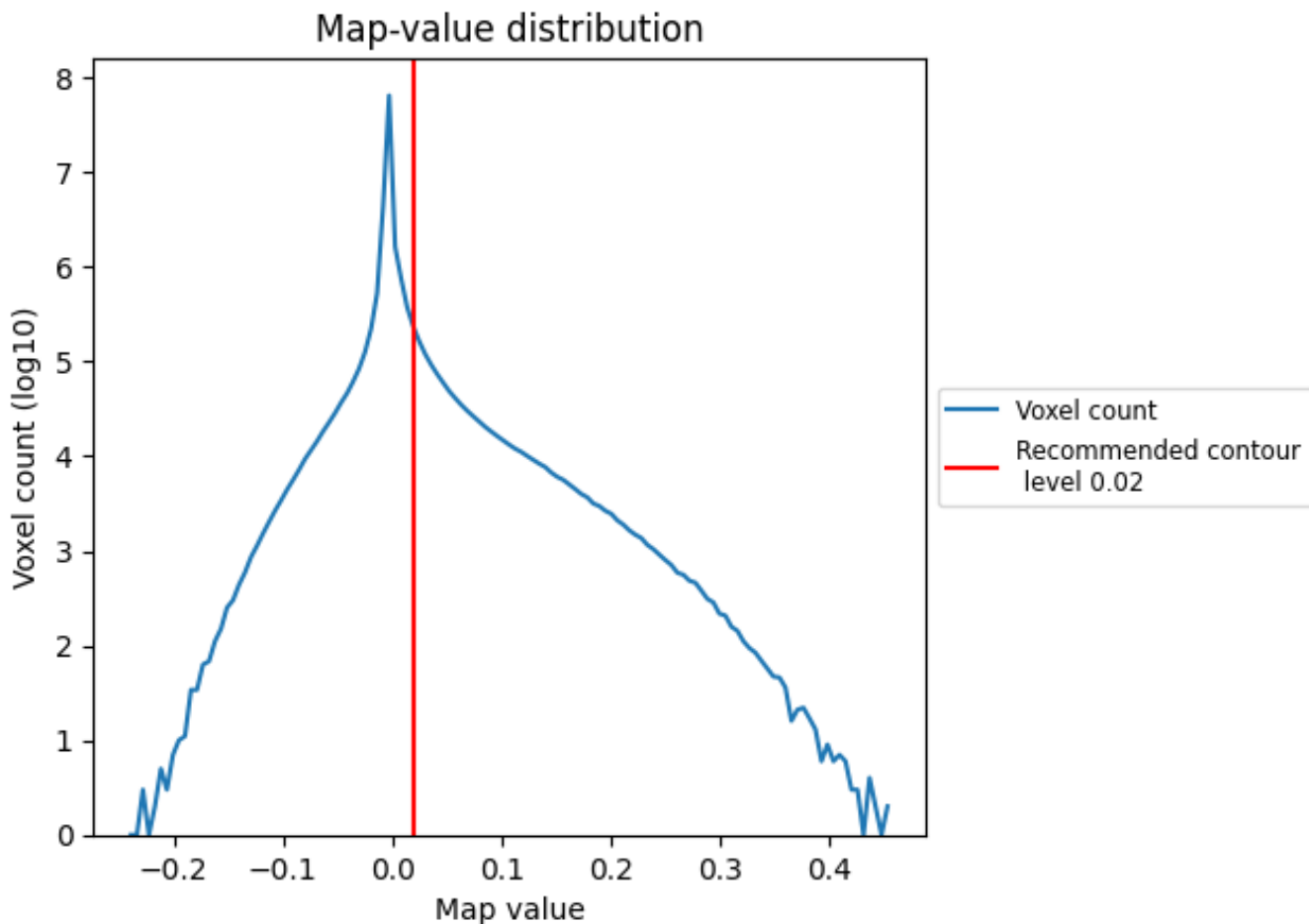
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

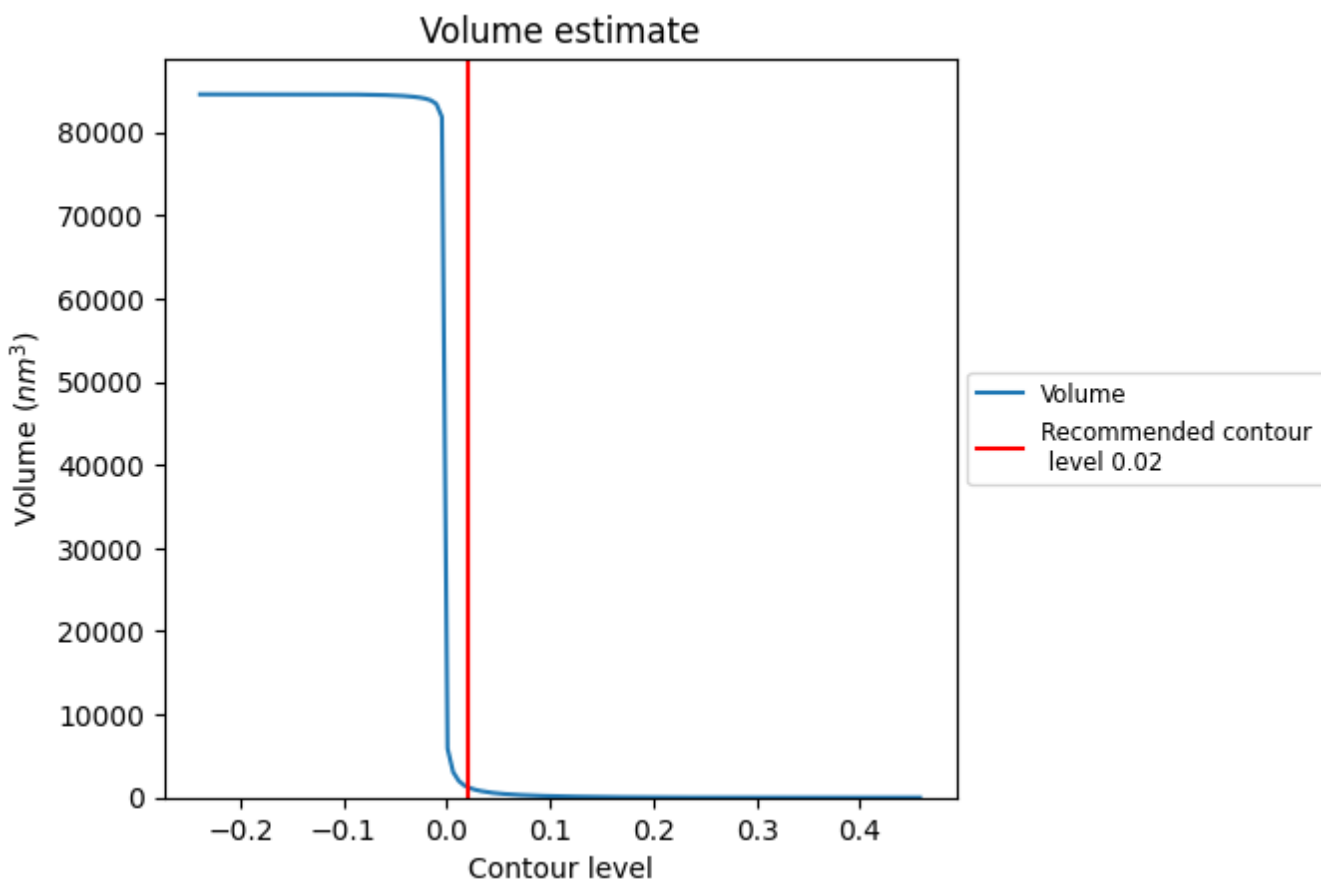
This section contains the results of statistical analysis of the map.

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.

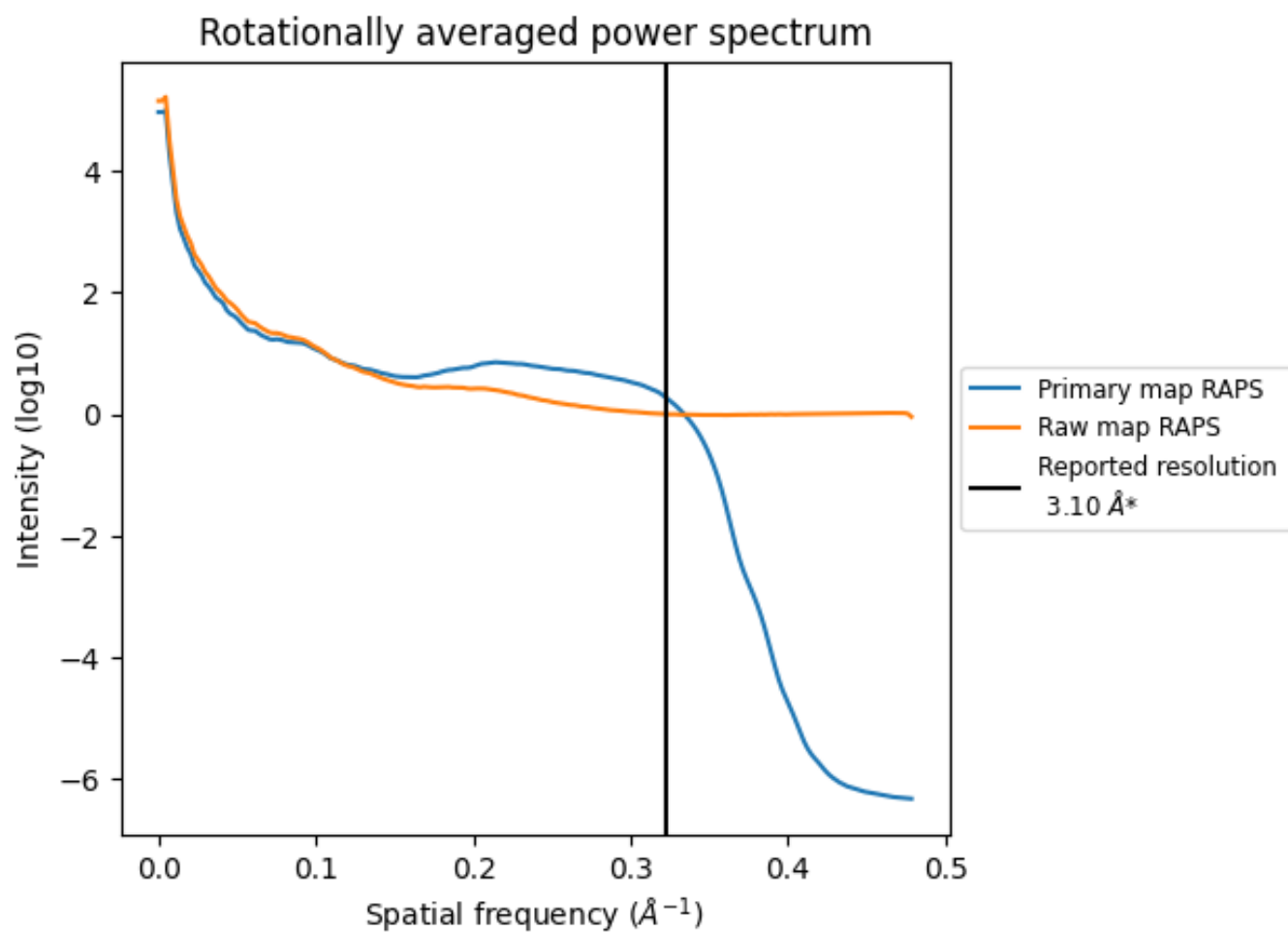
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1277 nm^3 ; this corresponds to an approximate mass of 1154 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 [i](#)

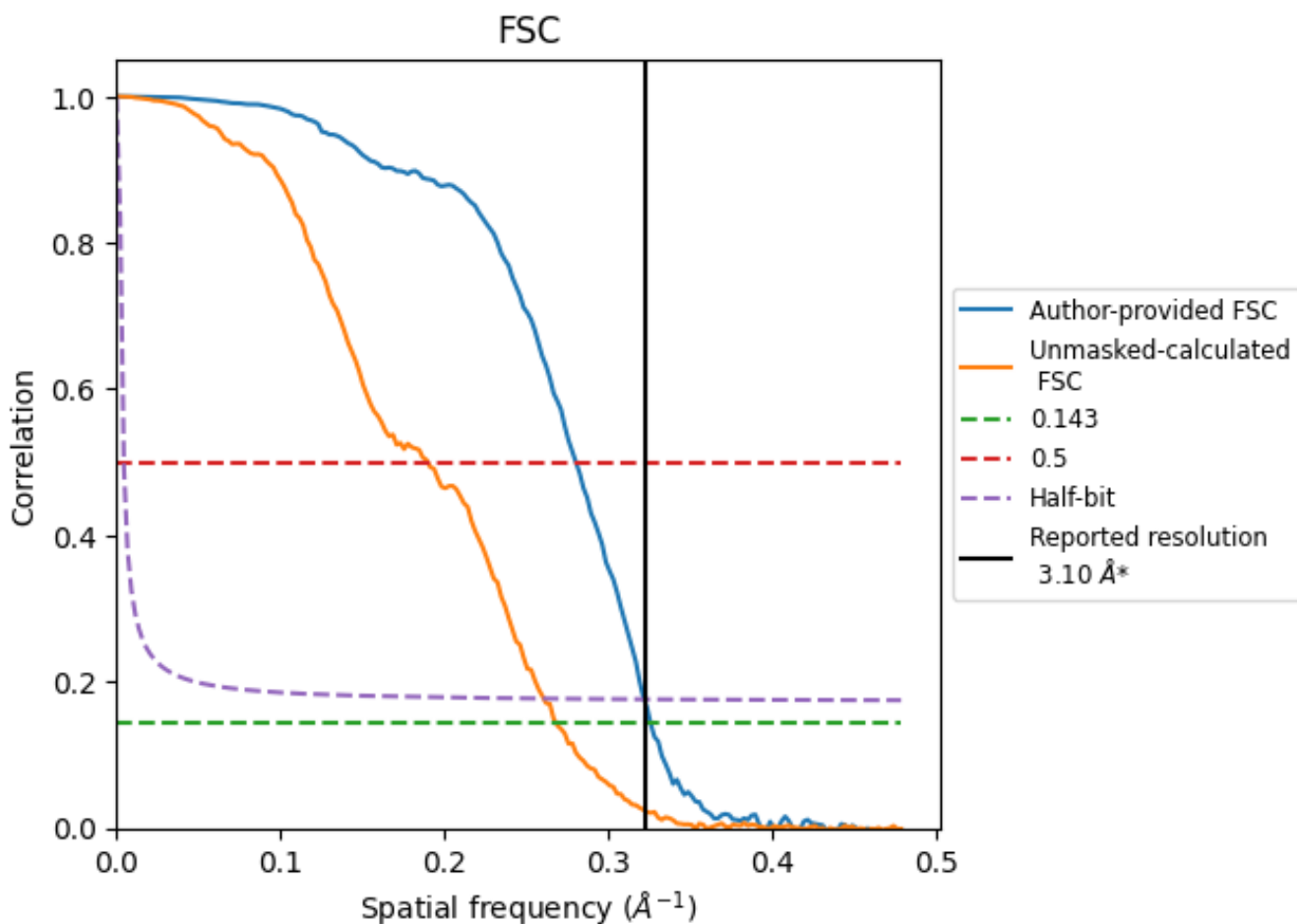


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

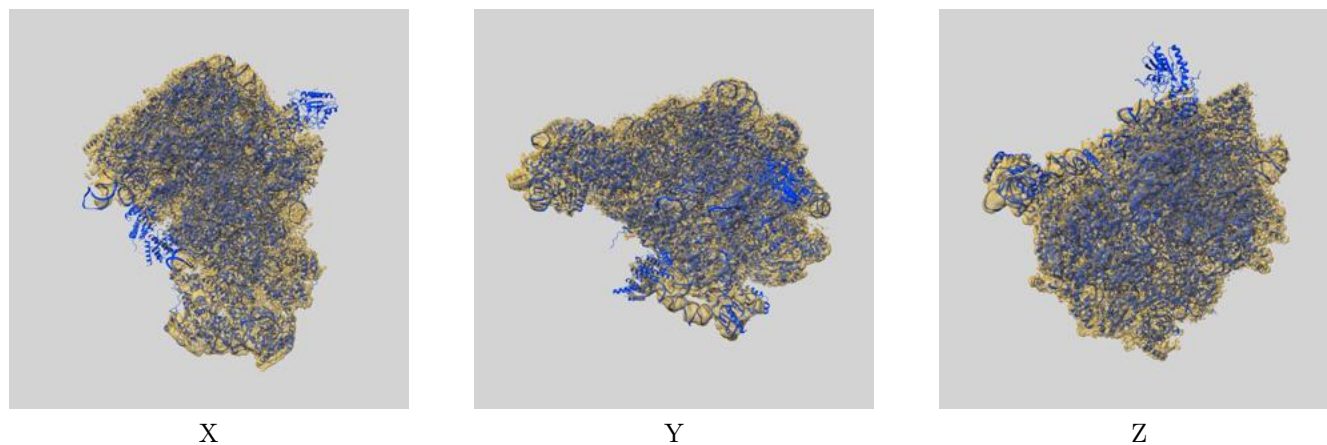
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.07	3.57	3.11
Unmasked-calculated*	3.73	5.27	3.84

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.73 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

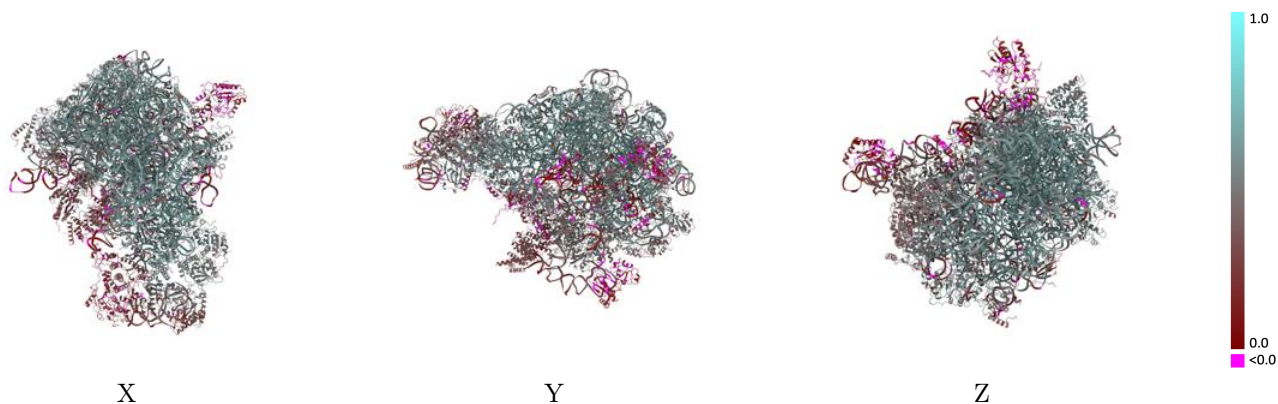
This section contains information regarding the fit between EMDB map EMD-35285 and PDB model 8I9V. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



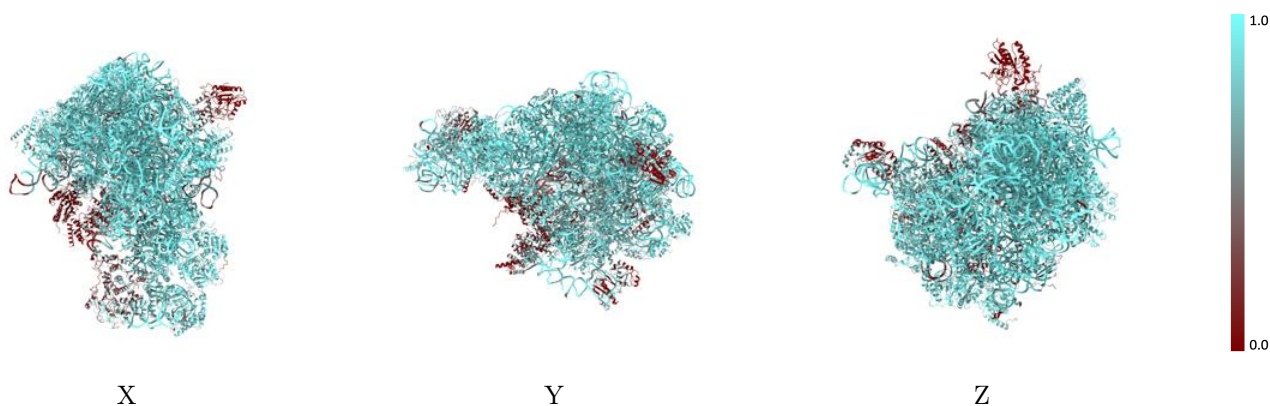
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



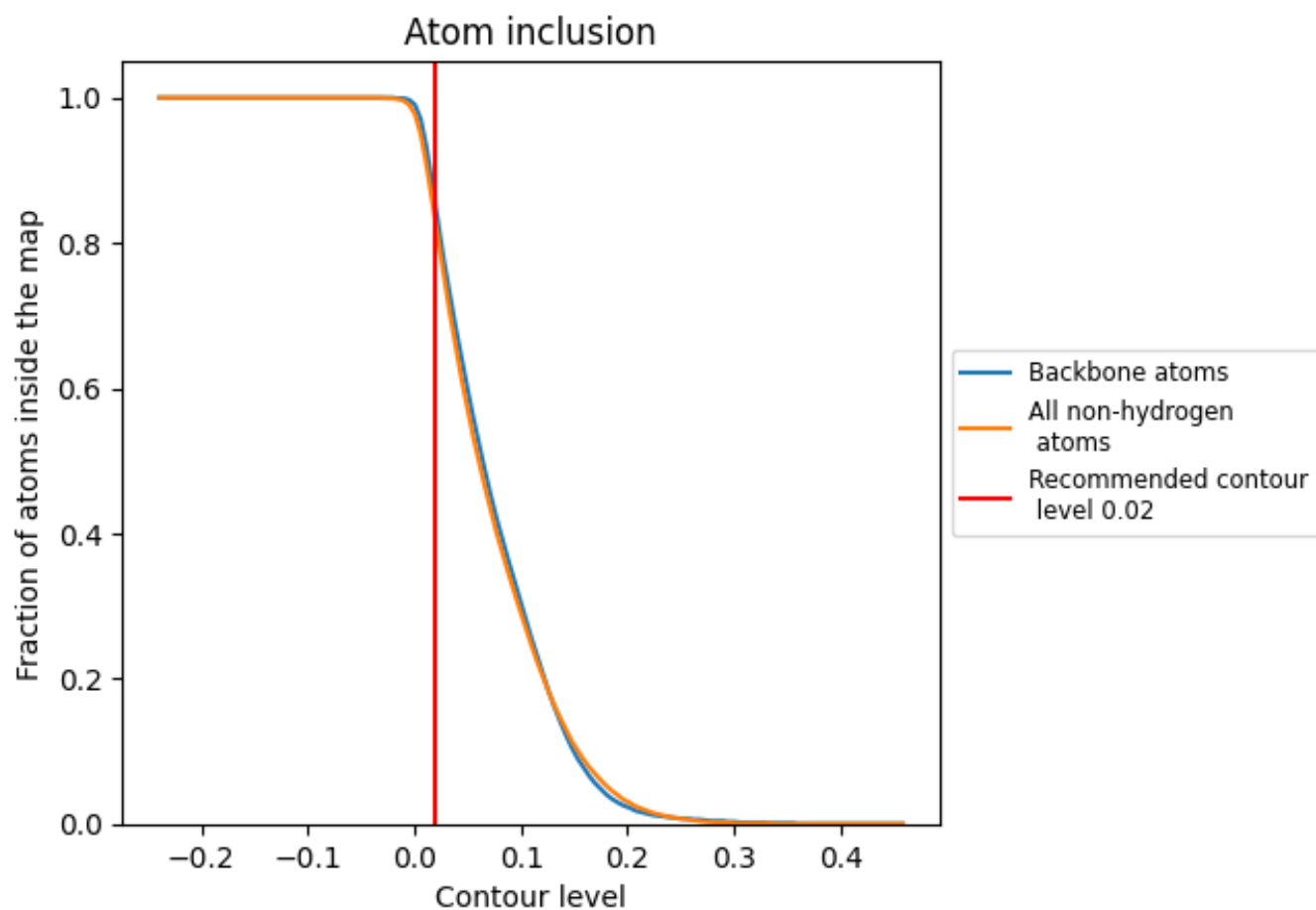
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8270	0.4600
C1	0.9160	0.4920
C2	0.8890	0.4890
C3	0.8700	0.3460
CA	0.9100	0.5190
CB	0.7890	0.3810
CC	0.5130	0.2890
CE	0.8820	0.4970
CF	0.8700	0.4630
CG	0.7850	0.4060
CH	0.8810	0.4950
CI	0.8400	0.4180
CJ	0.4520	0.1900
CK	0.8500	0.4840
CL	0.3040	0.1920
CM	0.6100	0.2570
CN	0.8960	0.5130
CO	0.9340	0.5560
CP	0.8240	0.4390
CQ	0.9170	0.5070
CR	0.9130	0.5330
CS	0.0980	0.2140
CT	0.2590	0.2500
CU	0.8290	0.4480
CX	0.3990	0.1990
CY	0.4070	0.2780
Cb	0.7750	0.4150
Cc	0.8570	0.5040
Cd	0.9220	0.5390
Ce	0.9420	0.5730
Cf	0.6860	0.3770
Cz	0.6190	0.3280
LB	0.9320	0.5570
LC	0.9480	0.5860
LE	0.9180	0.5360



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Chain	Atom inclusion	Q-score
LF	 0.9230	 0.5600
LG	 0.8410	 0.5040
LH	 0.9300	 0.5580
LK	 0.8110	 0.3740
LL	 0.9530	 0.5840
LM	 0.9440	 0.5590
LN	 0.9430	 0.5890
LO	 0.9520	 0.5830
LP	 0.9240	 0.5510
LQ	 0.9390	 0.5720
LS	 0.9310	 0.5570
LT	 0.7100	 0.3300
LV	 0.8870	 0.5150
LX	 0.3240	 0.2180
LY	 0.9190	 0.5550
Ld	 0.6000	 0.2850
Le	 0.9510	 0.5970
Lf	 0.9530	 0.5990
Lh	 0.8630	 0.4980
Li	 0.8880	 0.5080
Lj	 0.9590	 0.5960
Lq	 0.3400	 0.0810