



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:41 PM UTC

PDB ID : 9OU7 / pdb_00009ou7
EMDB ID : EMD-70864
Title : Methanosarcina acetivorans large (50S) subunit dimer
Authors : Ghosh, A.; Fordjour, G.N.R.; Armache, J.-P.; Ferry, J.G.; Murakami, K.S.; Bevilacqua, P.C.
Deposited on : 2025-05-28
Resolution : 3.51 Å(reported)
Based on initial model : 6SKF

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

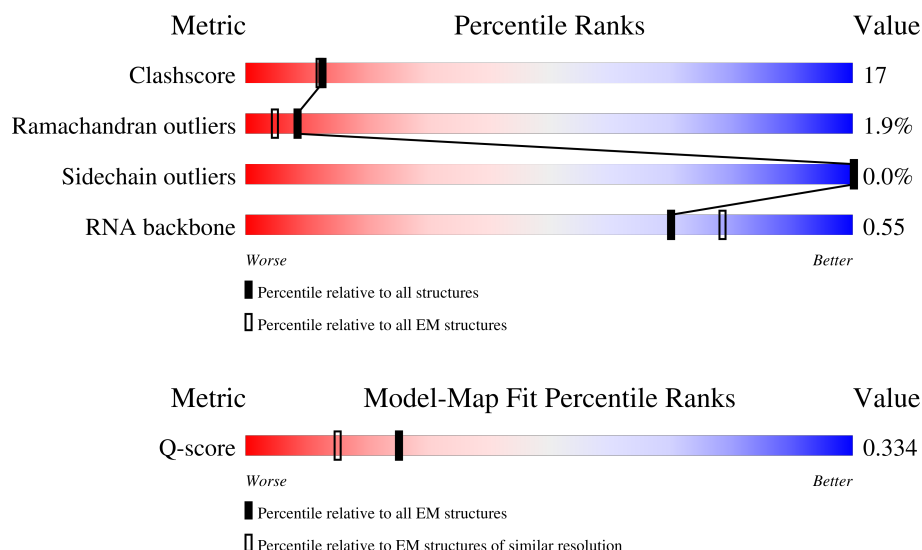
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.51 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.



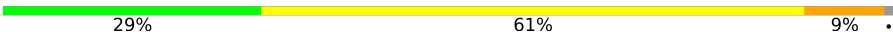
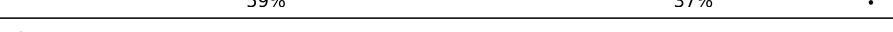
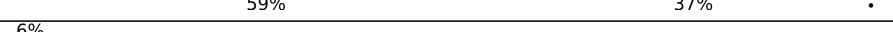
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13085 (3.01 - 4.01)

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	BA	2899	
1	CA	2899	
2	BB	129	

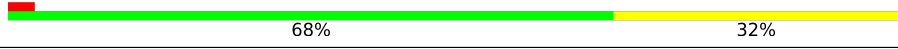
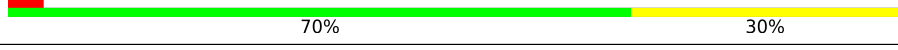
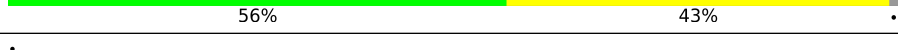
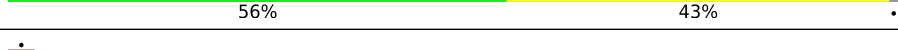
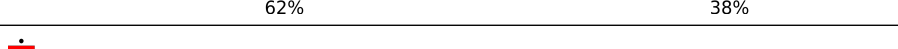
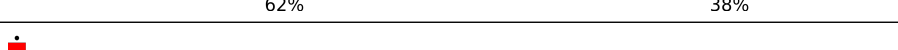
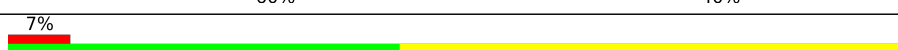
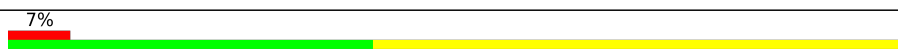
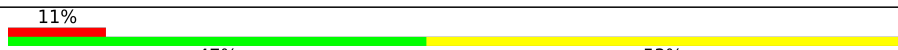
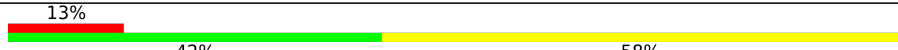
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Mol	Chain	Length	Quality of chain
2	CB	129	
3	BC	238	
3	CC	238	
4	BD	337	
4	CD	337	
5	BE	253	
5	CE	253	
6	BF	165	
6	CF	165	
7	BG	176	
7	CG	176	
8	BH	120	
8	CH	120	
9	BI	173	
9	CI	173	
10	BJ	143	
10	CJ	143	
11	BK	132	
11	CK	132	
12	BL	140	
12	CL	140	
13	BM	196	
13	CM	196	
14	BN	174	
14	CN	174	

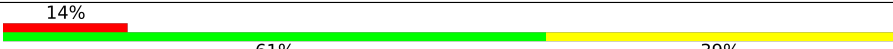
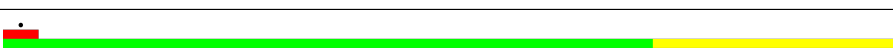
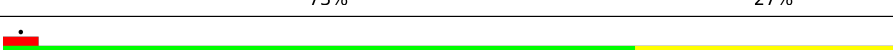
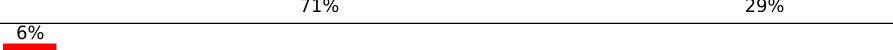
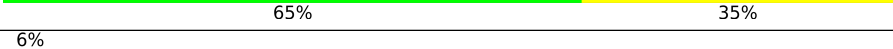
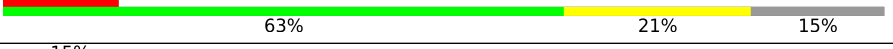
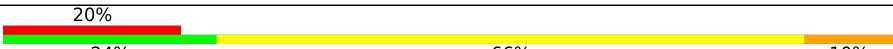
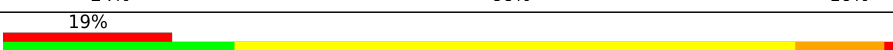
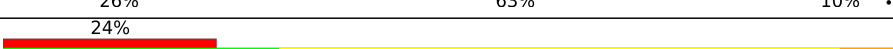
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Mol	Chain	Length	Quality of chain
15	BO	126	
15	CO	126	
16	BP	151	
16	CP	151	
17	BQ	61	
17	CQ	61	
18	BR	97	
18	CR	97	
19	BS	151	
19	CS	151	
20	BT	82	
20	CT	82	
21	BU	119	
21	CU	119	
22	BV	62	
22	CV	62	
23	BW	67	
23	CW	67	
24	BX	153	
24	CX	153	
25	BY	99	
25	CY	99	
26	BZ	89	
26	CZ	89	
27	Ba	161	

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Mol	Chain	Length	Quality of chain
27	Ca	161	
28	Bb	94	
28	Cb	94	
29	Bc	56	
29	Cc	56	
30	Bd	51	
30	Cd	51	
31	Be	52	
31	Ce	52	
32	Bf	92	
32	Cf	92	
33	DA	538	
33	DB	538	
34	DC	730	
34	DD	730	

2 Entry composition [i](#)

There are 34 unique types of molecules in this entry. The entry contains 272158 atoms, of which 62224 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 23S rRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	BA	2884	Total	C	H	N	O	P	0	0
			92834	27549	31112	11225	20065	2883		
1	CA	2884	Total	C	H	N	O	P	0	0
			92834	27549	31112	11225	20065	2883		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BB	128	Total	C	N	O	P	0	0
			2720	1214	481	897	128		
2	CB	128	Total	C	N	O	P	0	0
			2720	1214	481	897	128		

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	BC	238	Total	C	N	O	S	0	0
			1808	1129	350	321	8		
3	CC	238	Total	C	N	O	S	0	0
			1808	1129	350	321	8		

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	BD	337	Total	C	N	O	S	0	0
			2597	1639	474	476	8		
4	CD	337	Total	C	N	O	S	0	0
			2597	1639	474	476	8		

- Molecule 5 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	BE	252	Total	C	N	O	S	0	0
			1930	1208	368	353	1		
5	CE	252	Total	C	N	O	S	0	0
			1930	1208	368	353	1		

- Molecule 6 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	BF	165	Total	C	N	O	S	0	0
			1289	812	234	235	8		
6	CF	165	Total	C	N	O	S	0	0
			1289	812	234	235	8		

- Molecule 7 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	BG	176	Total	C	N	O	S	0	0
			1371	876	235	254	6		
7	CG	176	Total	C	N	O	S	0	0
			1371	876	235	254	6		

- Molecule 8 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	BH	115	Total	C	N	O	S	0	0
			857	541	144	170	2		
8	CH	115	Total	C	N	O	S	0	0
			857	541	144	170	2		

- Molecule 9 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	BI	159	Total	C	N	O	S	0	0
			1261	794	240	218	9		
9	CI	159	Total	C	N	O	S	0	0
			1261	794	240	218	9		

- Molecule 10 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BJ	138	Total	C	N	O	S	0	0
			1086	683	200	199	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	CJ	138	Total	C	N	O	S	0	0
			1086	683	200	199	4		

- Molecule 11 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BK	132	Total	C	N	O	S	0	0
			999	623	185	182	9		
11	CK	132	Total	C	N	O	S	0	0
			999	623	185	182	9		

- Molecule 12 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	BL	140	Total	C	N	O	S	0	0
			1058	643	204	205	6		
12	CL	140	Total	C	N	O	S	0	0
			1058	643	204	205	6		

- Molecule 13 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BM	196	Total	C	N	O	S	0	0
			1593	986	329	273	5		
13	CM	196	Total	C	N	O	S	0	0
			1593	986	329	273	5		

- Molecule 14 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	BN	174	Total	C	N	O	S	0	0
			1356	853	242	259	2		
14	CN	174	Total	C	N	O	S	0	0
			1356	853	242	259	2		

- Molecule 15 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	BO	126	Total	C	N	O	S	0	0
			962	608	173	178	3		
15	CO	126	Total	C	N	O	S	0	0
			962	608	173	178	3		

- Molecule 16 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BP	151	Total	C	N	O	S	0	0
			1195	739	242	210	4		
16	CP	151	Total	C	N	O	S	0	0
			1195	739	242	210	4		

- Molecule 17 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	BQ	57	Total	C	N	O	0	0
			457	289	79	89		
17	CQ	57	Total	C	N	O	0	0
			457	289	79	89		

- Molecule 18 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	BR	96	Total	C	N	O	S	0	0
			766	475	146	141	4		
18	CR	96	Total	C	N	O	S	0	0
			766	475	146	141	4		

- Molecule 19 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BS	151	Total	C	N	O	S	0	0
			1169	729	218	212	10		
19	CS	151	Total	C	N	O	S	0	0
			1169	729	218	212	10		

- Molecule 20 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	BT	82	Total	C	N	O	S	0	0
			656	418	108	122	8		
20	CT	82	Total	C	N	O	S	0	0
			656	418	108	122	8		

- Molecule 21 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BU	119	Total	C	N	O	S	0	0
			910	564	170	169	7		
21	CU	119	Total	C	N	O	S	0	0
			910	564	170	169	7		

- Molecule 22 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BV	62	Total	C	N	O	S	0	0
			499	316	88	87	8		
22	CV	62	Total	C	N	O	S	0	0
			499	316	88	87	8		

- Molecule 23 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BW	67	Total	C	N	O	S	0	0
			532	321	103	106	2		
23	CW	67	Total	C	N	O	S	0	0
			532	321	103	106	2		

- Molecule 24 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BX	153	Total	C	N	O	S	0	0
			1237	779	230	222	6		
24	CX	153	Total	C	N	O	S	0	0
			1237	779	230	222	6		

- Molecule 25 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BY	92	Total	C	N	O	S	0	0
			658	415	108	131	4		
25	CY	92	Total	C	N	O	S	0	0
			658	415	108	131	4		

- Molecule 26 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BZ	86	Total	C	N	O	S	0	0
			703	446	131	123	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
26	CZ	86	Total	C	N	O	S	0	0
			703	446	131	123	3		

- Molecule 27 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Ba	132	Total	C	N	O	S	0	0
			1028	645	197	184	2		
27	Ca	132	Total	C	N	O	S	0	0
			1028	645	197	184	2		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ba	-2	MET	-	initiating methionine	UNP A0A832W8Z7
Ba	-1	ILE	-	conflict	UNP A0A832W8Z7
Ba	0	MET	-	conflict	UNP A0A832W8Z7
Ca	-2	MET	-	initiating methionine	UNP A0A832W8Z7
Ca	-1	ILE	-	conflict	UNP A0A832W8Z7
Ca	0	MET	-	conflict	UNP A0A832W8Z7

- Molecule 28 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Bb	94	Total	C	N	O	S	0	0
			736	459	145	125	7		
28	Cb	94	Total	C	N	O	S	0	0
			736	459	145	125	7		

- Molecule 29 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bc	56	Total	C	N	O	S	0	0
			445	269	92	76	8		
29	Cc	56	Total	C	N	O	S	0	0
			445	269	92	76	8		

- Molecule 30 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bd	51	Total	C	N	O	S	0	0
			439	272	101	64	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
30	Cd	51	Total	C	N	O	S	0	0
			439	272	101	64	2		

- Molecule 31 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Be	44	Total	C	N	O	S	0	0
			353	215	74	59	5		
31	Ce	44	Total	C	N	O	S	0	0
			353	215	74	59	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Be	-2	MET	-	initiating methionine	UNP Q8TJ19
Be	-1	THR	-	conflict	UNP Q8TJ19
Be	0	LYS	-	conflict	UNP Q8TJ19
Ce	-2	MET	-	initiating methionine	UNP Q8TJ19
Ce	-1	THR	-	conflict	UNP Q8TJ19
Ce	0	LYS	-	conflict	UNP Q8TJ19

- Molecule 32 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	92	Total	C	N	O	S	0	0
			760	480	151	122	7		
32	Cf	92	Total	C	N	O	S	0	0
			760	480	151	122	7		

- Molecule 33 is a protein called Bifunctional phosphoribosylaminoimidazolecarboxamide for myltransferase/IMP cyclohydrolase.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	DA	538	Total	C	N	O	S	0	0
			4172	2644	706	804	18		
33	DB	538	Total	C	N	O	S	0	0
			4172	2644	706	804	18		

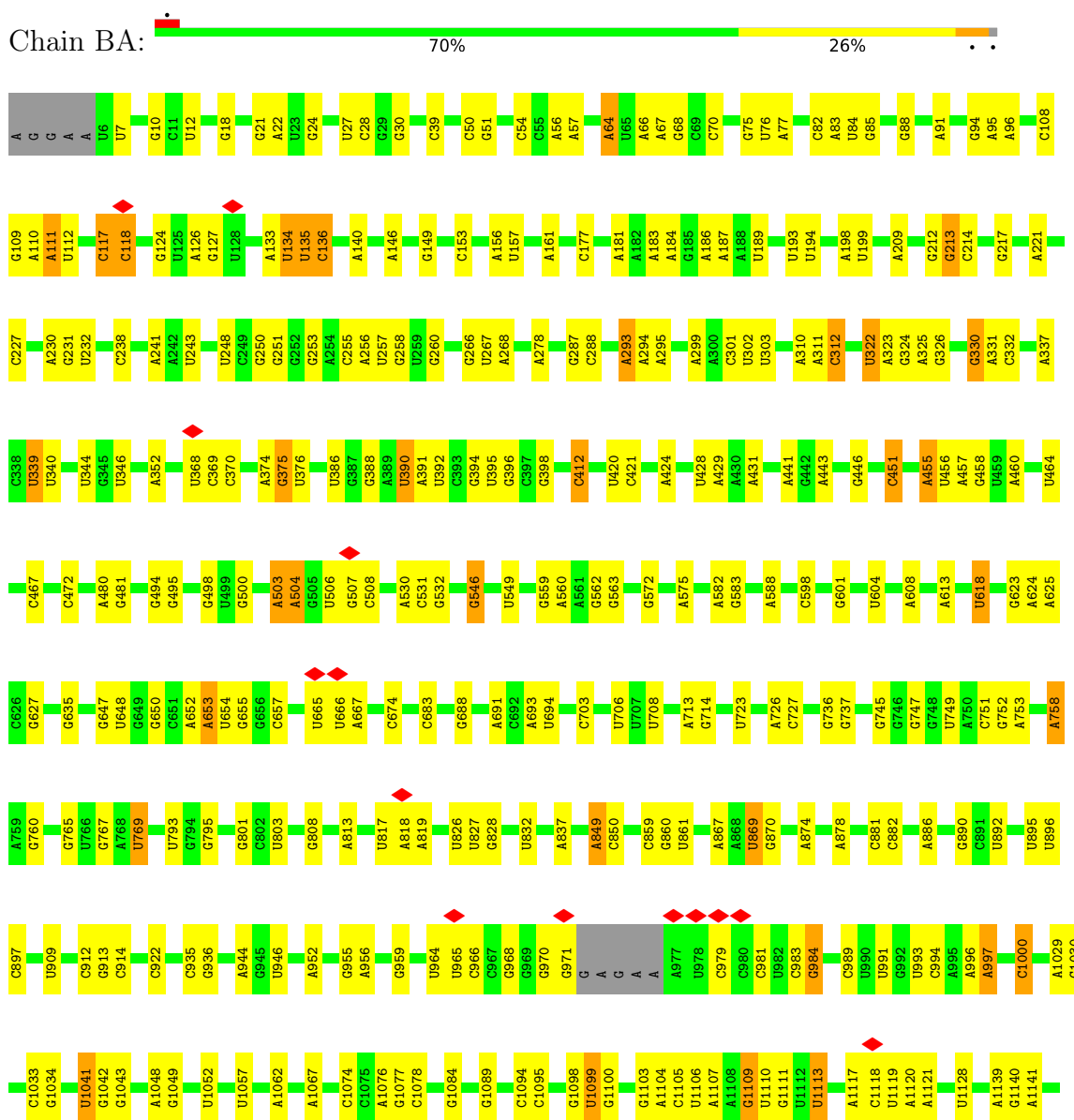
- Molecule 34 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	DC	730	Total 5643	C 3547	N 985	O 1075	S 36	0	0
34	DD	730	Total 5643	C 3547	N 985	O 1075	S 36	0	0

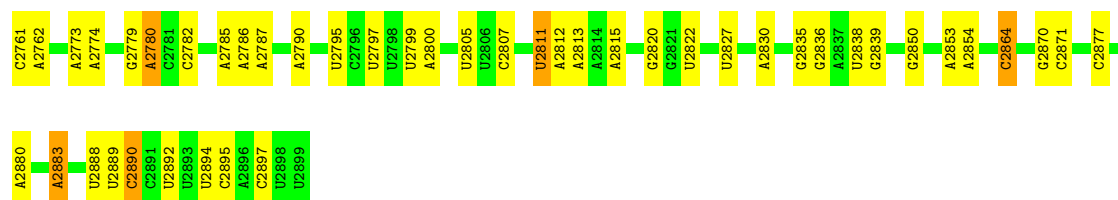
3 Residue-property plots

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

• Molecule 1: 23S rRNA

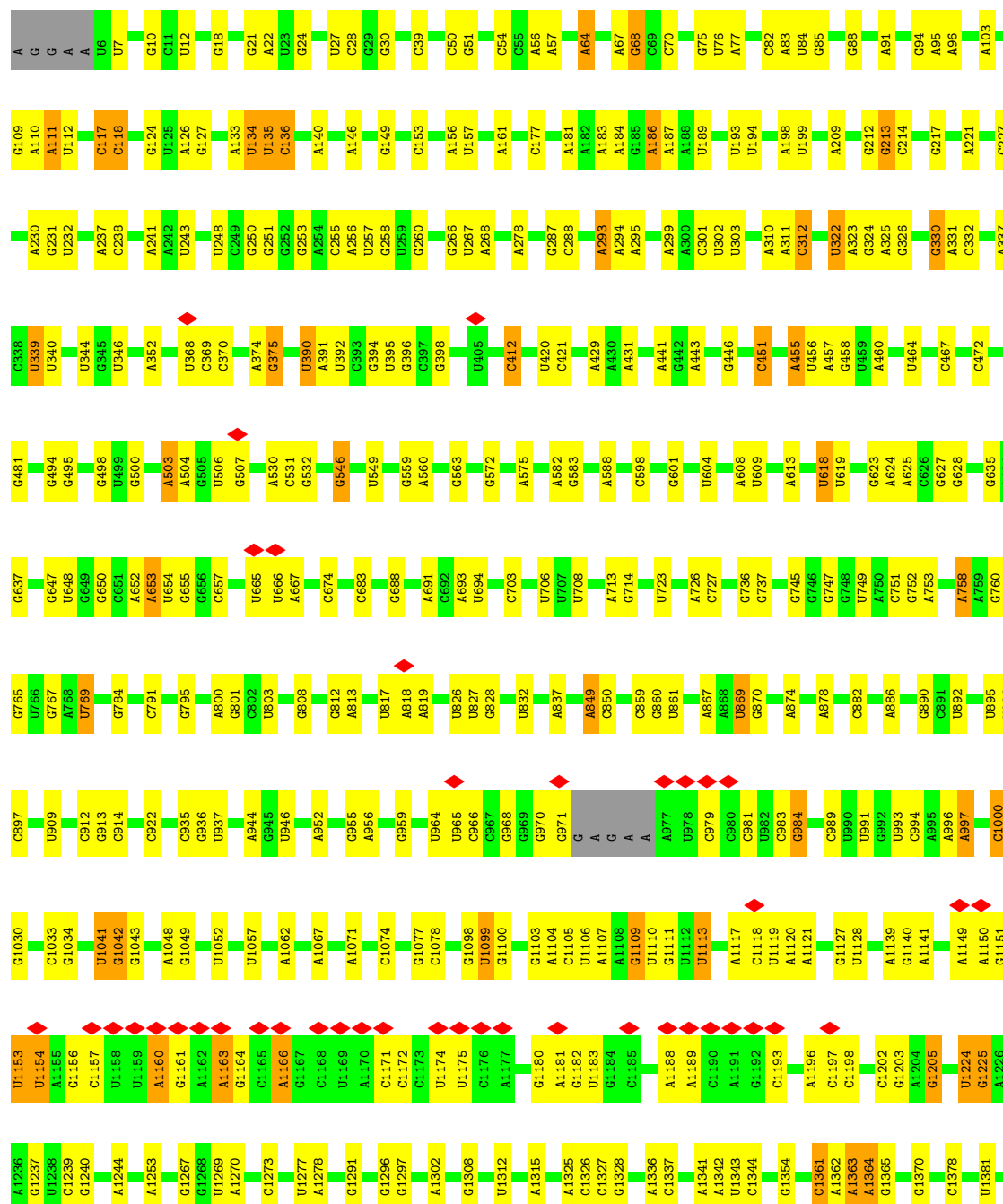


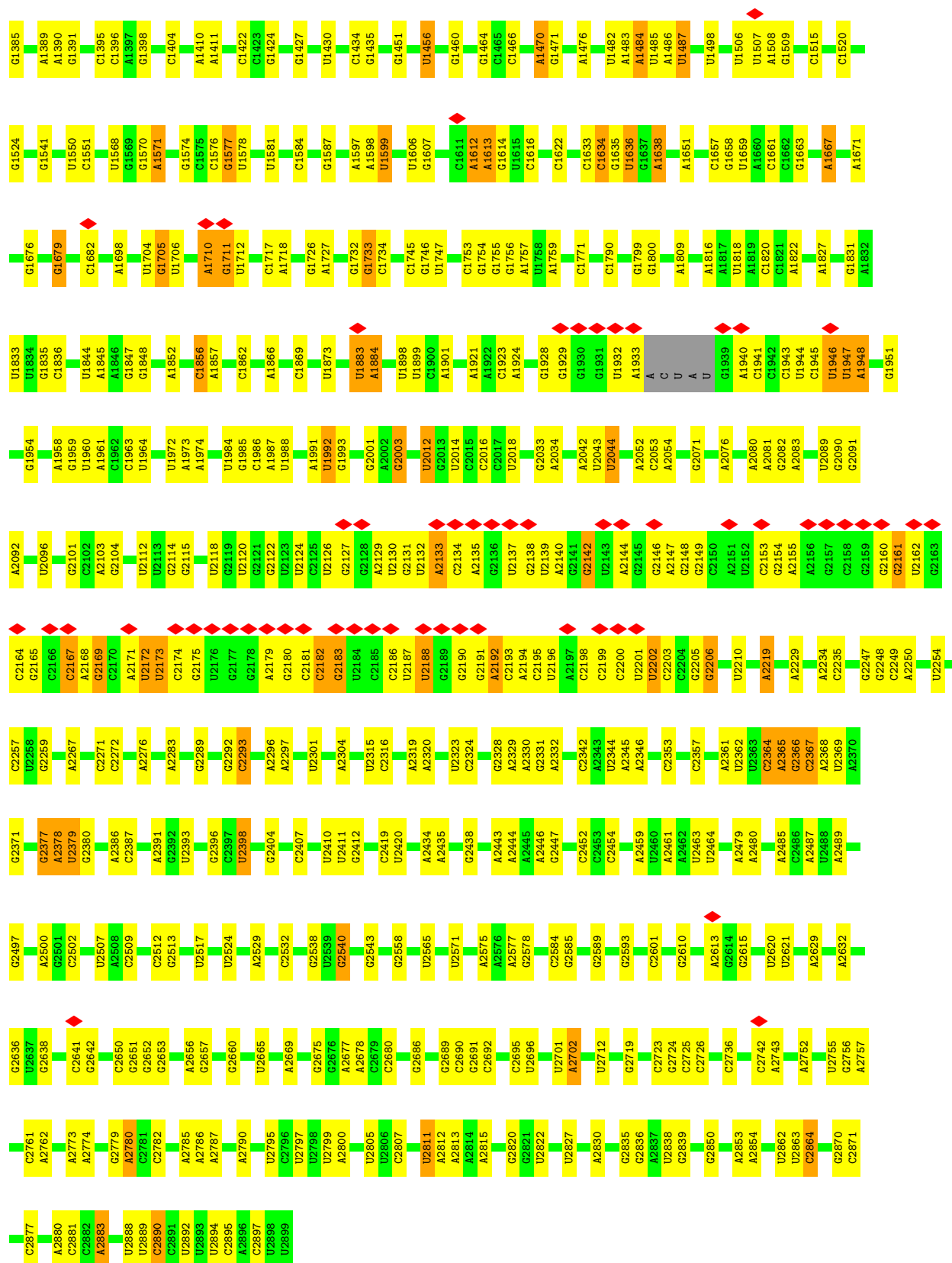




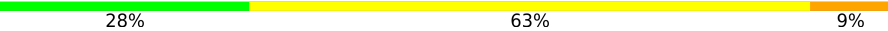
• Molecule 1: 23S rRNA

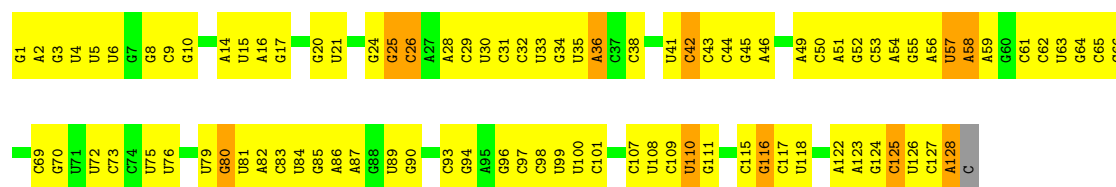
Chain CA: 70% 26%





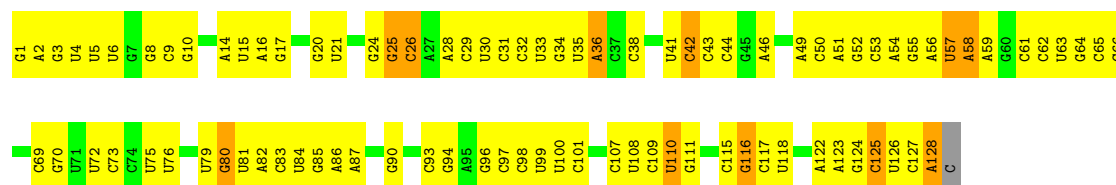
• Molecule 2: 5S rRNA

Chain BB:  28% 63% 9%



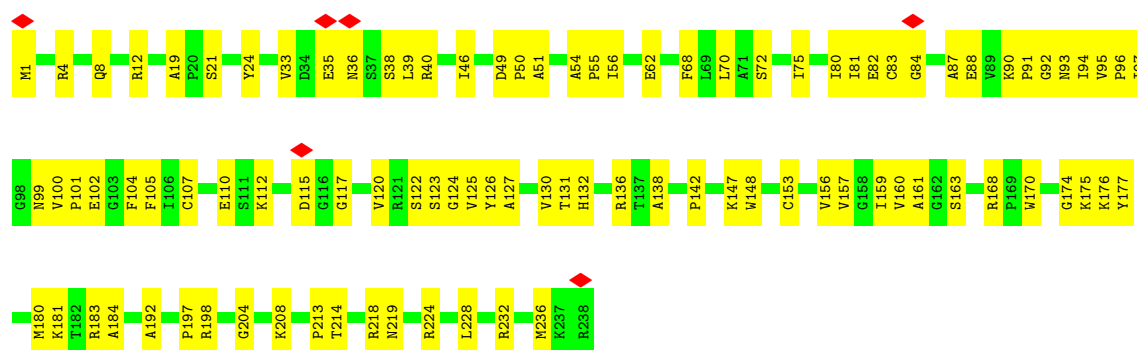
• Molecule 2: 5S rRNA

Chain CB:  29% 61% 9%



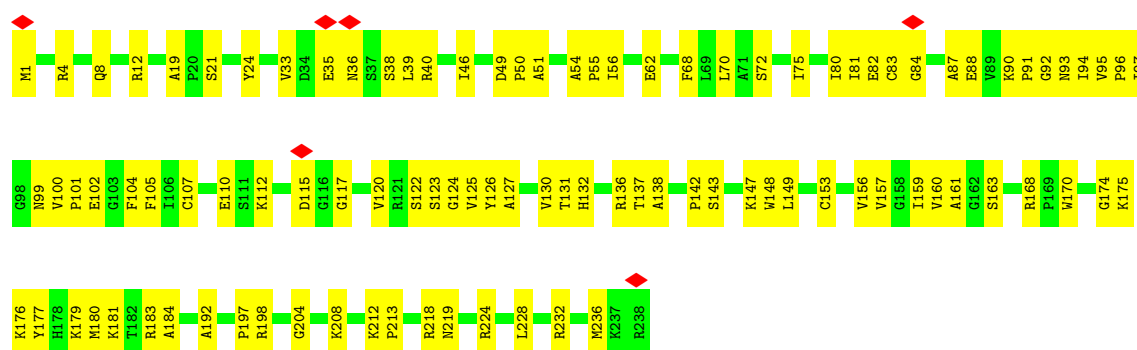
• Molecule 3: Large ribosomal subunit protein uL2

Chain BC:  60% 40%

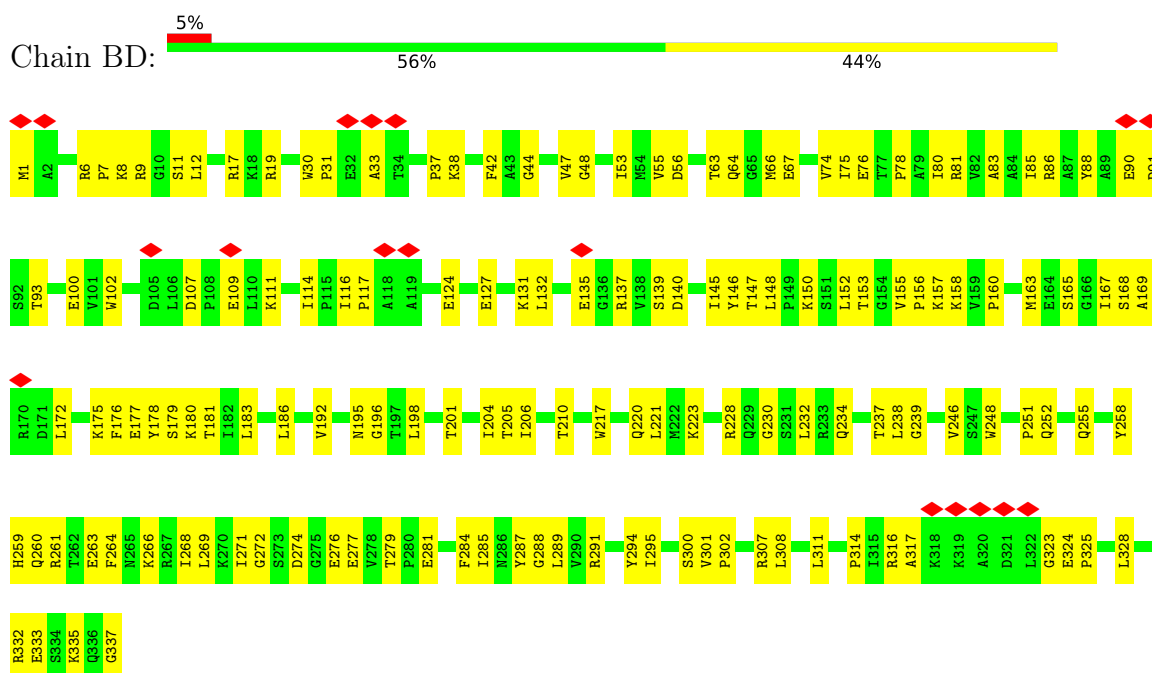


• Molecule 3: Large ribosomal subunit protein uL2

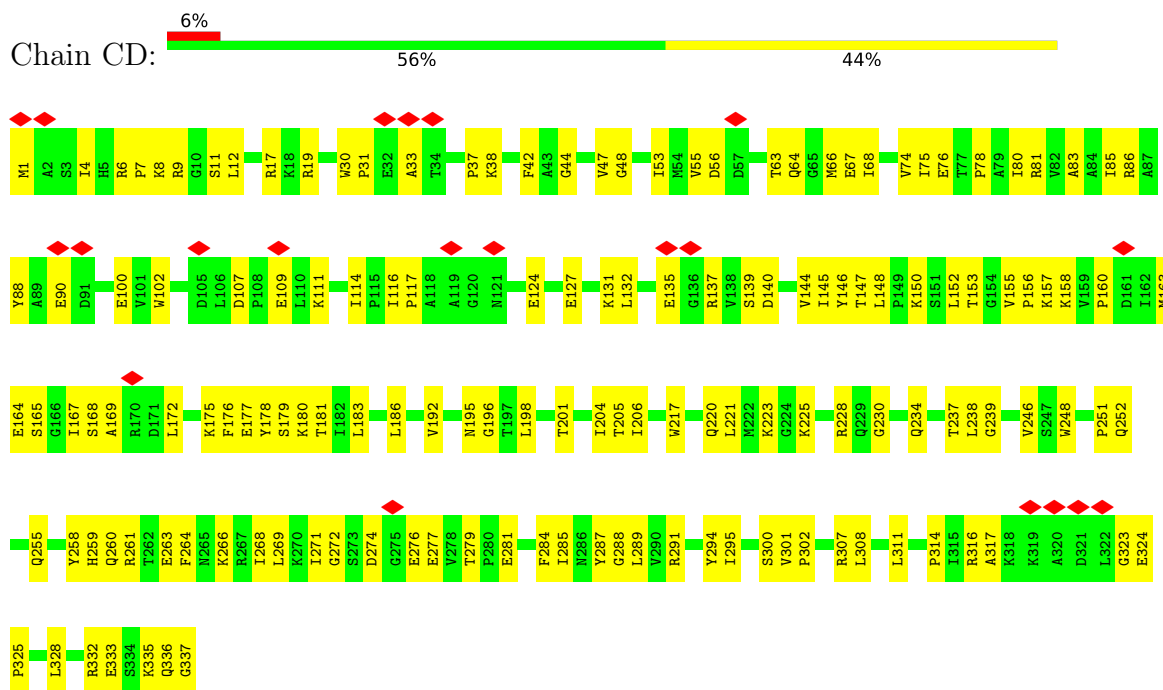
Chain CC:  58% 42%



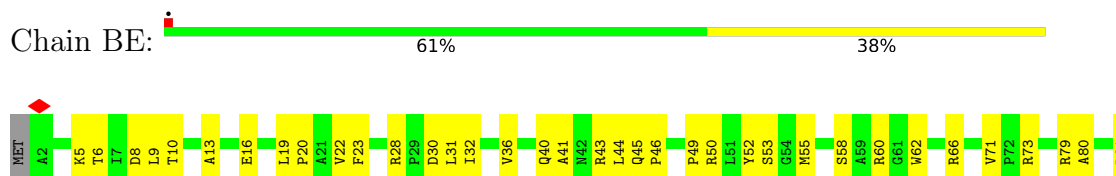
• Molecule 4: Large ribosomal subunit protein uL3

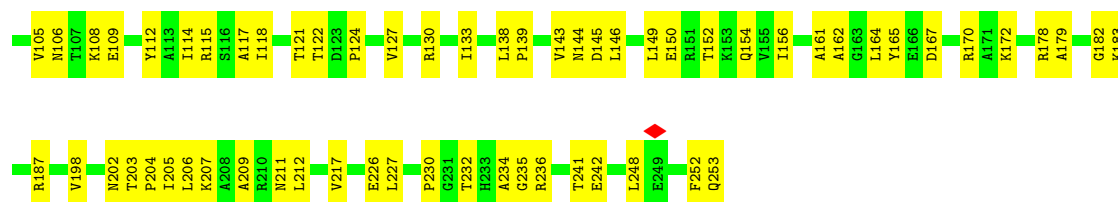


• Molecule 4: Large ribosomal subunit protein uL3

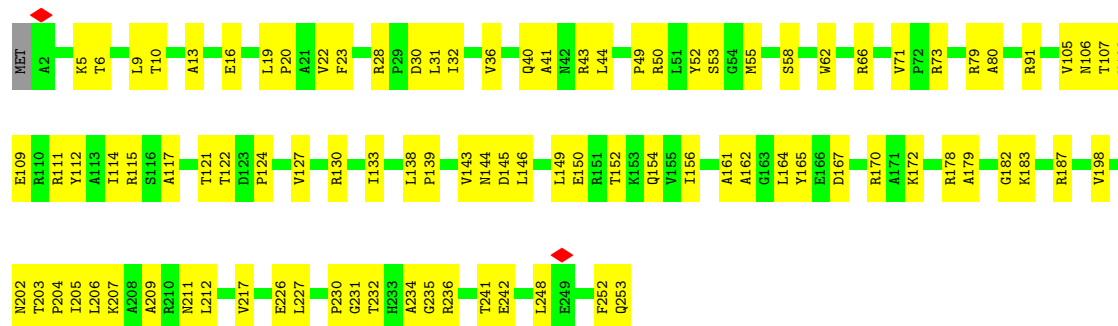


• Molecule 5: Large ribosomal subunit protein uL4

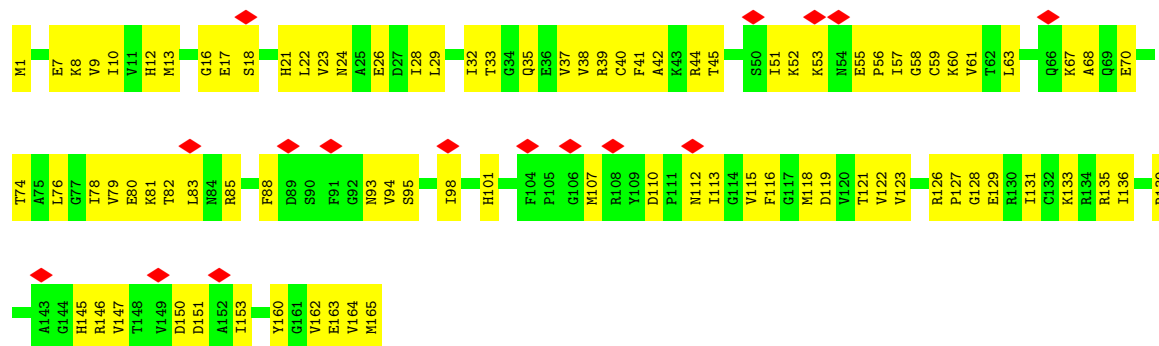




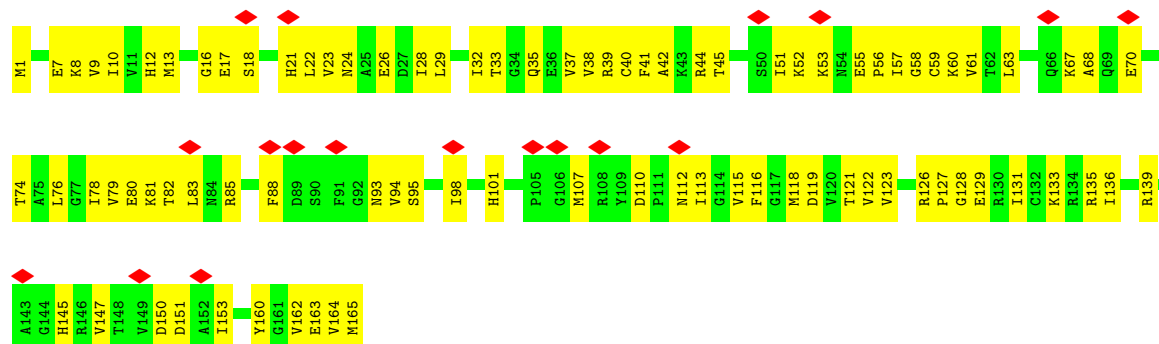
• Molecule 5: Large ribosomal subunit protein uL4



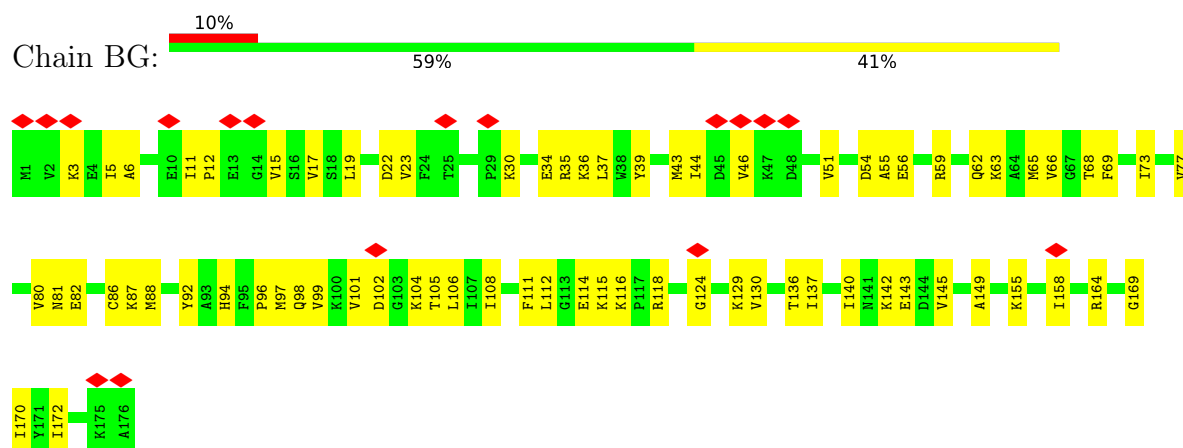
• Molecule 6: Large ribosomal subunit protein uL5



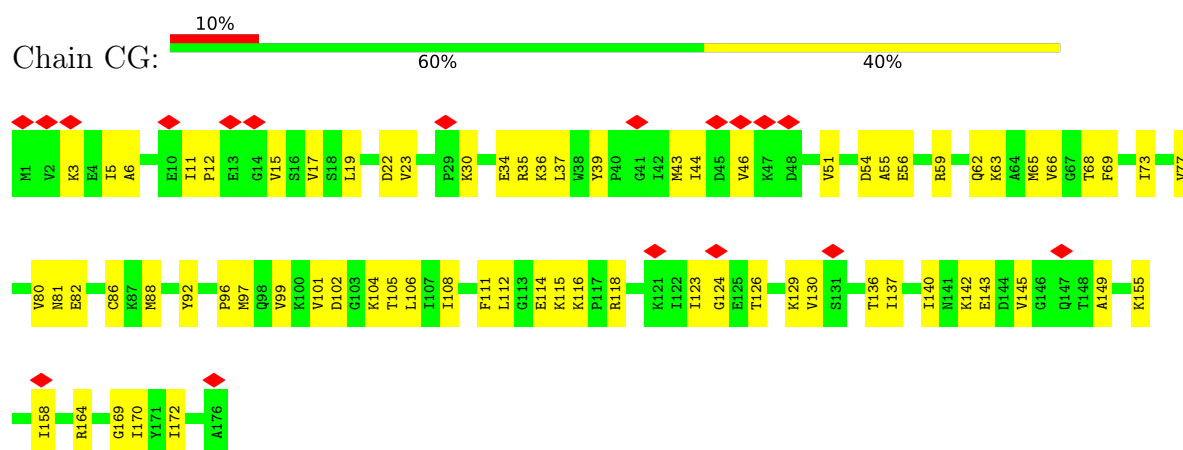
• Molecule 6: Large ribosomal subunit protein uL5



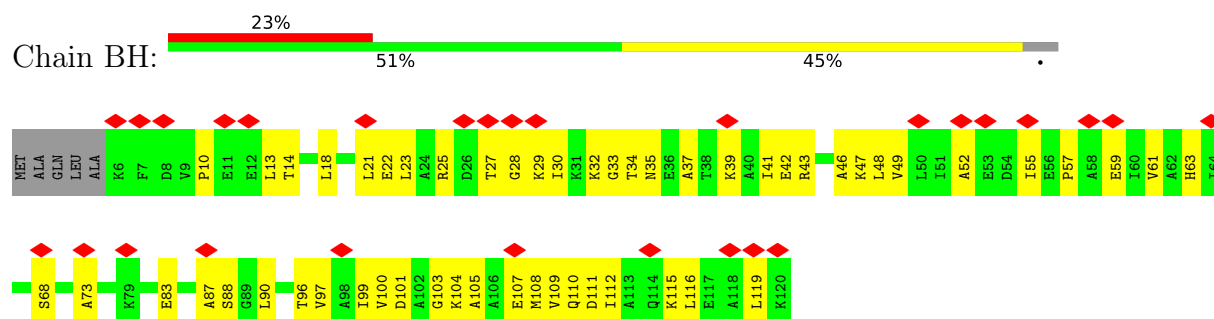
- Molecule 7: Large ribosomal subunit protein uL6



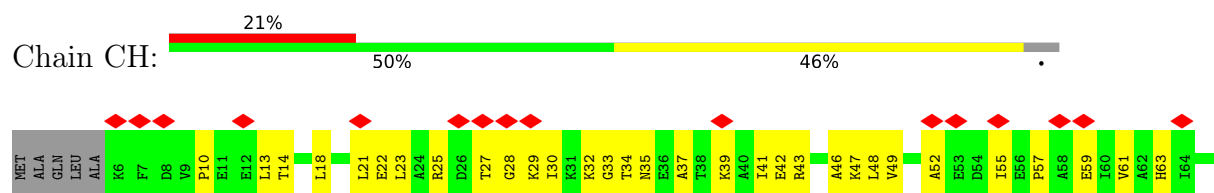
- Molecule 7: Large ribosomal subunit protein uL6



- Molecule 8: Large ribosomal subunit protein eL8



- Molecule 8: Large ribosomal subunit protein eL8





- Molecule 9: Large ribosomal subunit protein uL16



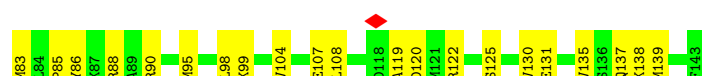
- Molecule 9: Large ribosomal subunit protein uL16



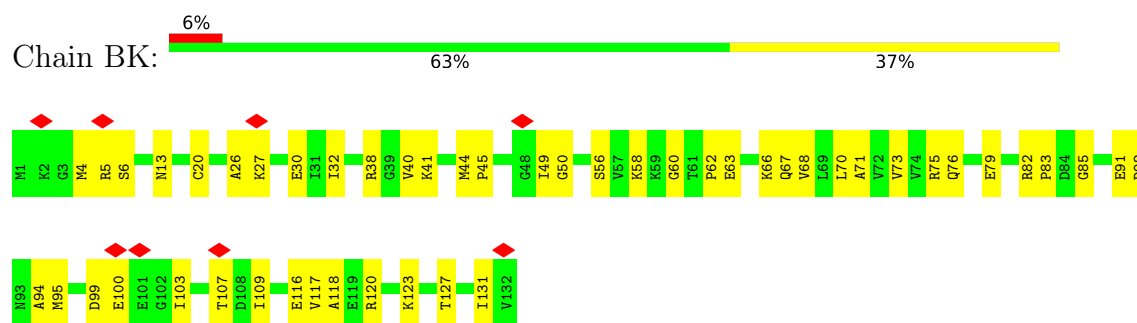
- Molecule 10: Large ribosomal subunit protein uL13



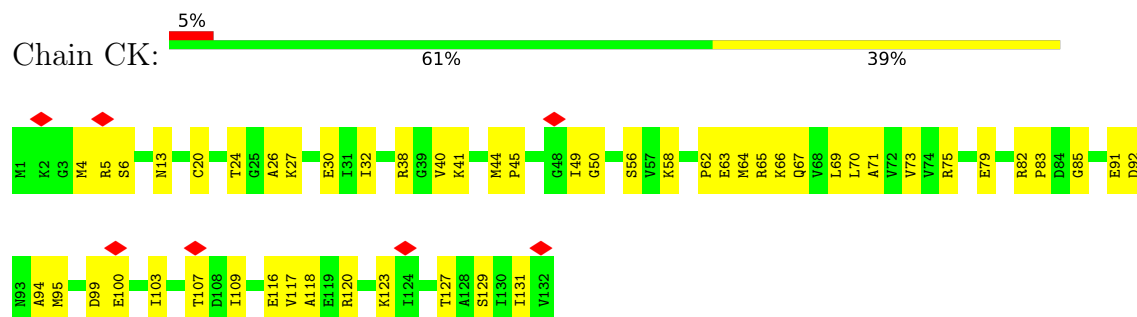
- Molecule 10: Large ribosomal subunit protein uL13



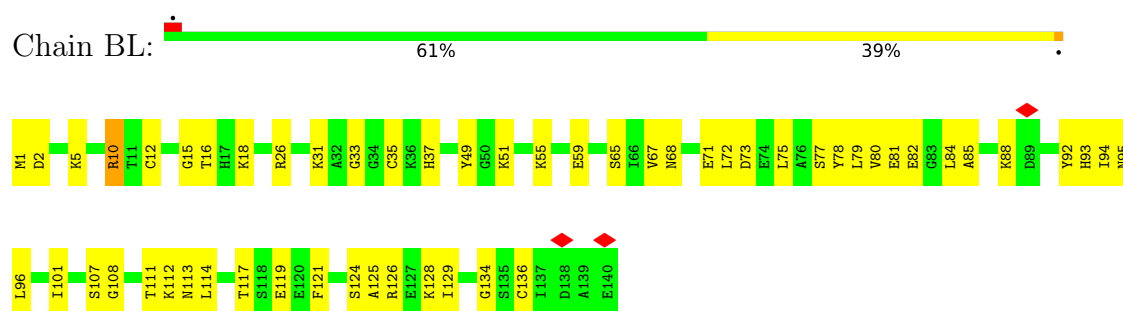
- Molecule 11: Large ribosomal subunit protein uL14



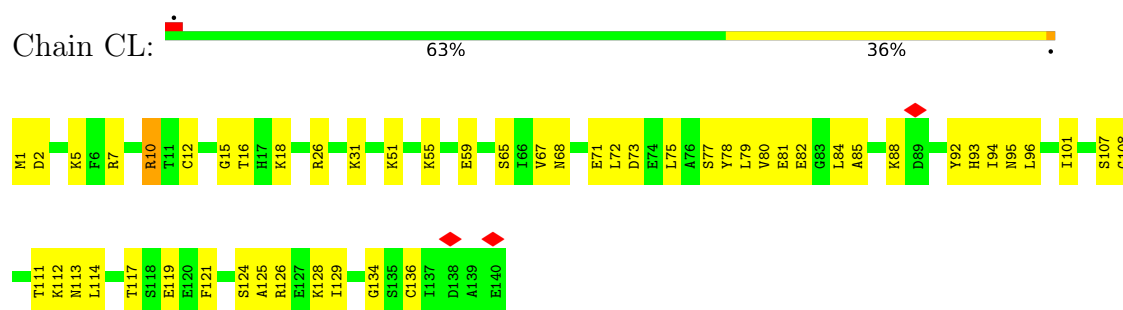
- Molecule 11: Large ribosomal subunit protein uL14



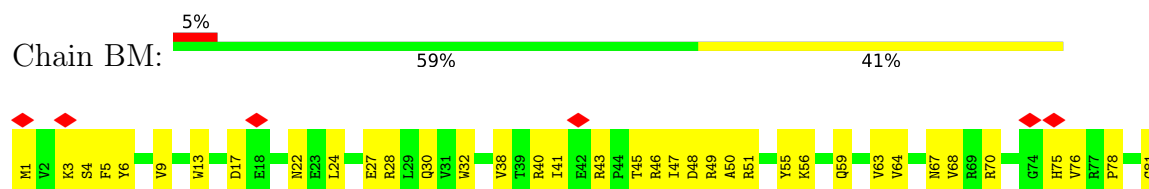
- Molecule 12: Large ribosomal subunit protein uL15

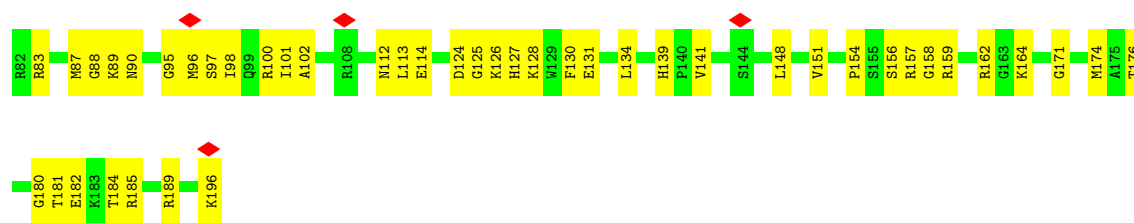


- Molecule 12: Large ribosomal subunit protein uL15



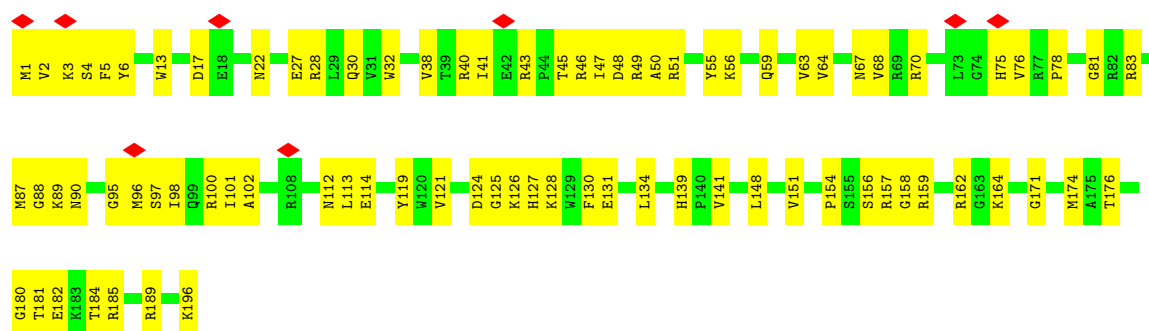
- Molecule 13: Large ribosomal subunit protein eL15





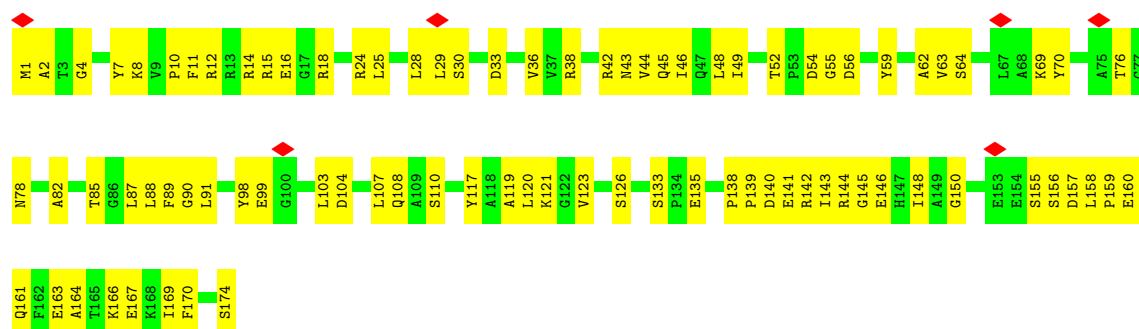
- Molecule 13: Large ribosomal subunit protein eL15

Chain CM: 58% 42%



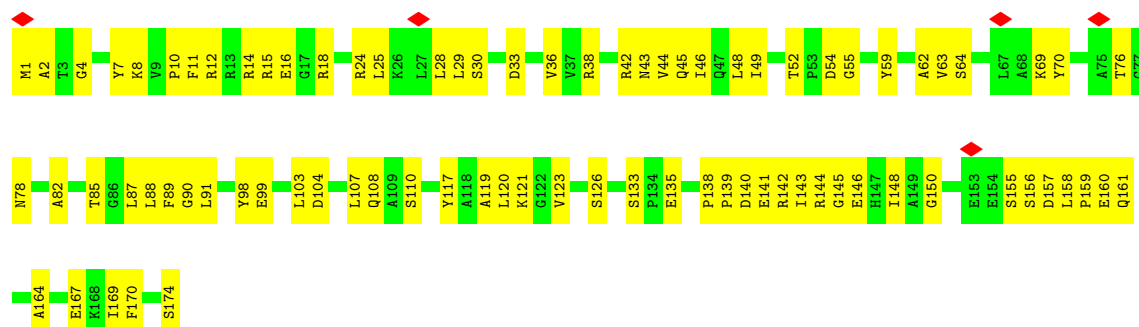
- Molecule 14: Large ribosomal subunit protein uL18

Chain BN: 51% 49%

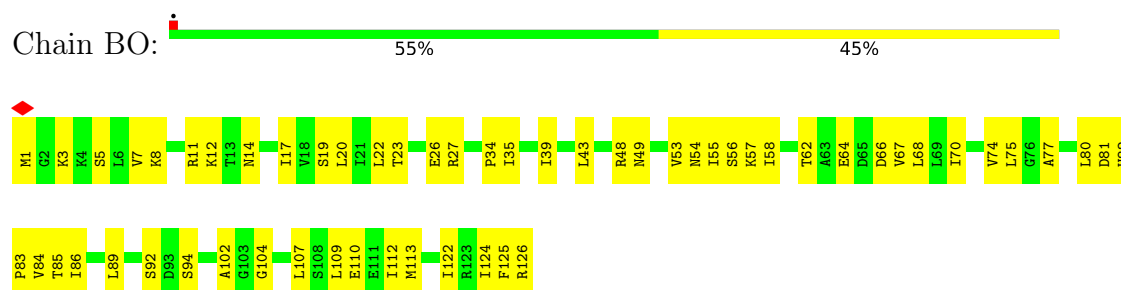


- Molecule 14: Large ribosomal subunit protein uL18

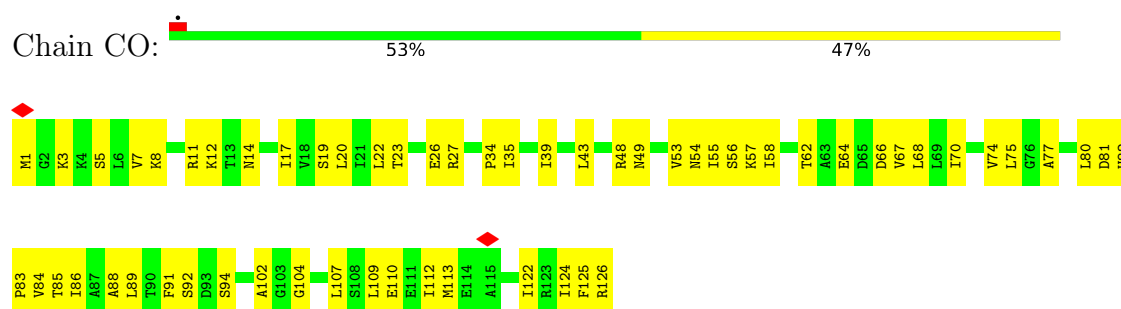
Chain CN: 52% 48%



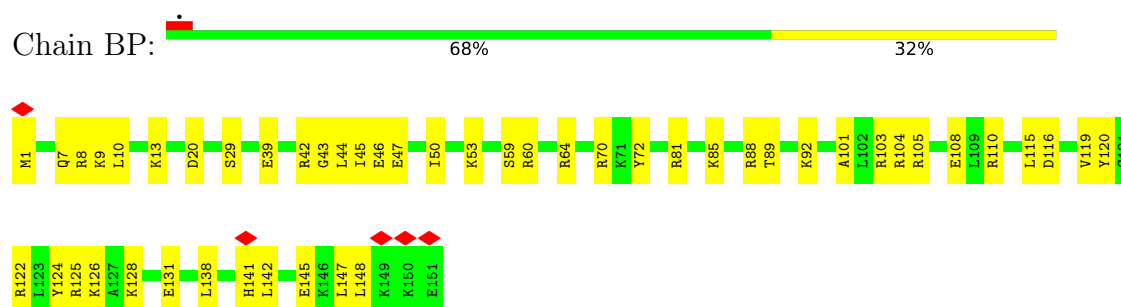
- Molecule 15: Large ribosomal subunit protein eL18



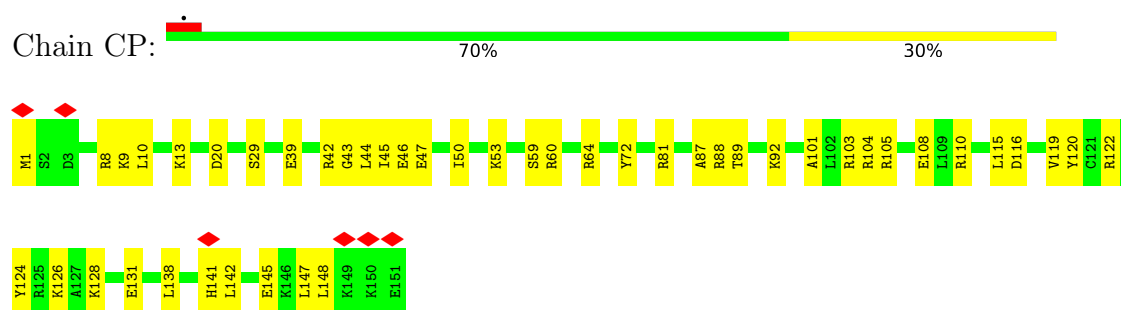
- Molecule 15: Large ribosomal subunit protein eL18



- Molecule 16: Large ribosomal subunit protein eL19



- Molecule 16: Large ribosomal subunit protein eL19

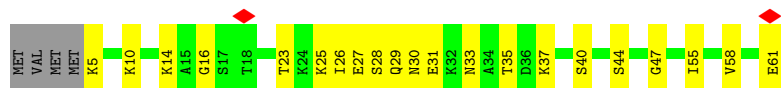


- Molecule 17: Large ribosomal subunit protein eL20

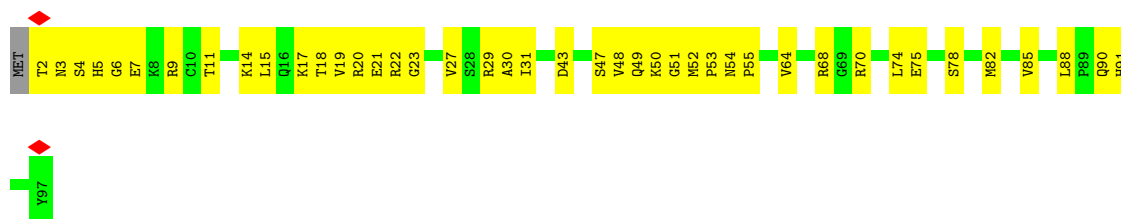




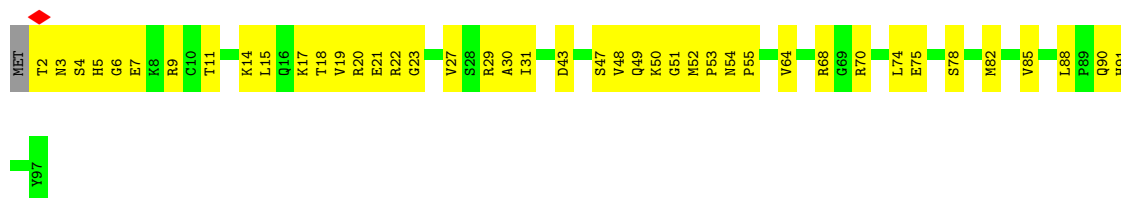
- Molecule 17: Large ribosomal subunit protein eL20



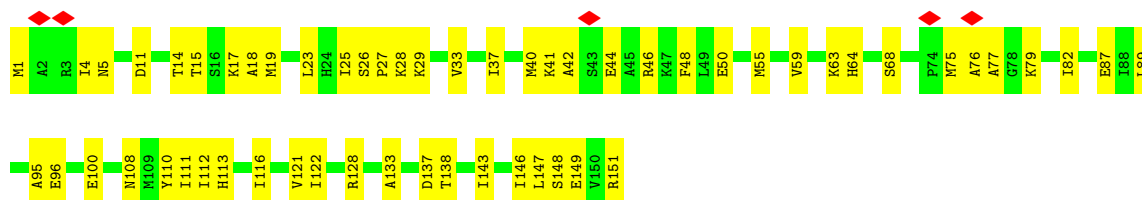
- Molecule 18: Large ribosomal subunit protein eL21



- Molecule 18: Large ribosomal subunit protein eL21

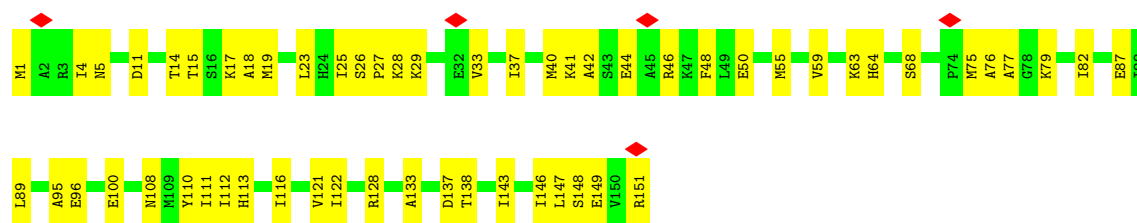


- Molecule 19: Large ribosomal subunit protein uL22



- Molecule 19: Large ribosomal subunit protein uL22





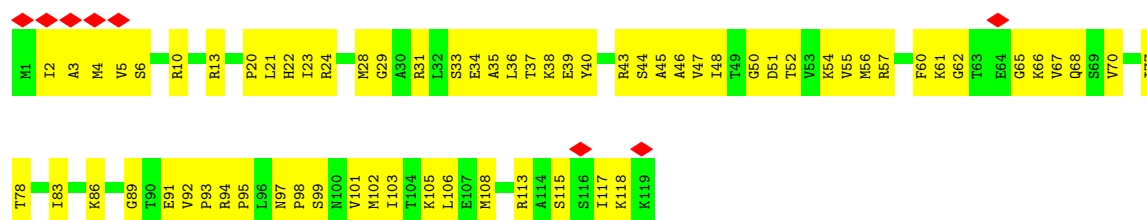
- Molecule 20: Large ribosomal subunit protein uL23



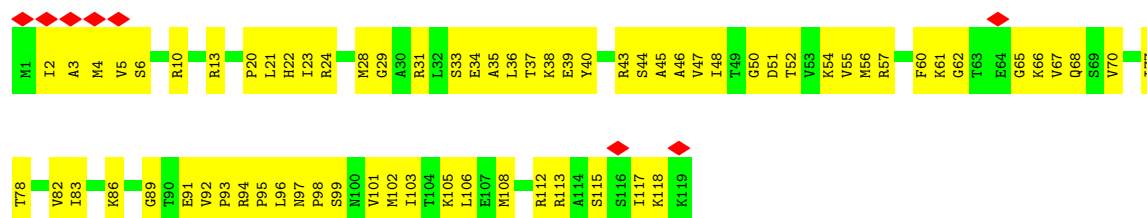
- Molecule 20: Large ribosomal subunit protein uL23



- Molecule 21: Large ribosomal subunit protein uL24

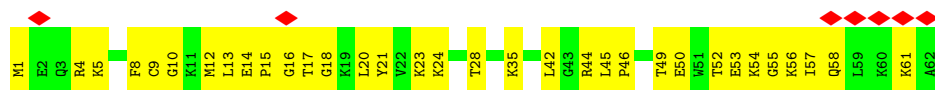


- Molecule 21: Large ribosomal subunit protein uL24

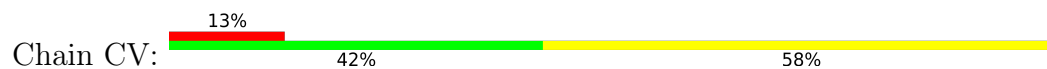


- Molecule 22: Large ribosomal subunit protein eL24

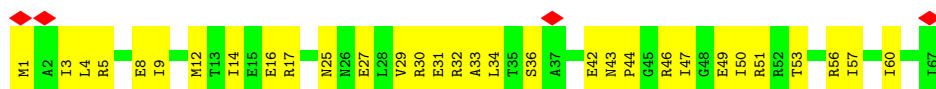




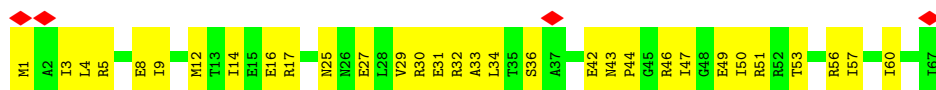
- Molecule 22: Large ribosomal subunit protein eL24



- Molecule 23: Large ribosomal subunit protein uL29



- Molecule 23: Large ribosomal subunit protein uL29



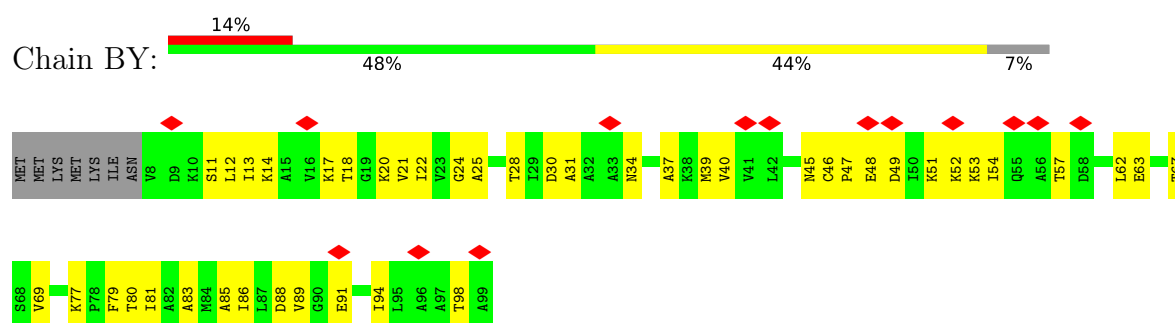
- Molecule 24: Large ribosomal subunit protein uL30



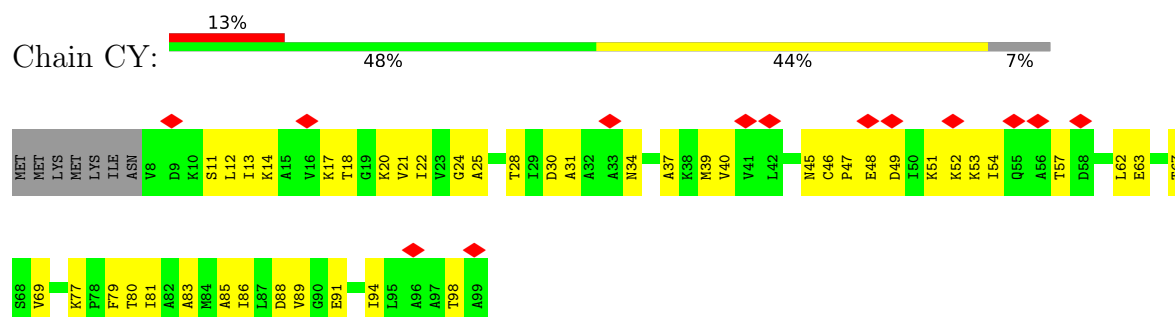
- Molecule 24: Large ribosomal subunit protein uL30



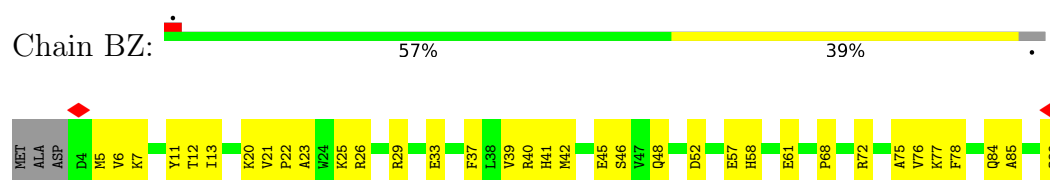
- Molecule 25: Large ribosomal subunit protein eL30



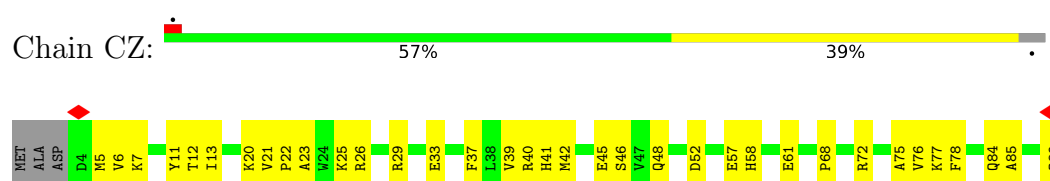
- Molecule 25: Large ribosomal subunit protein eL30



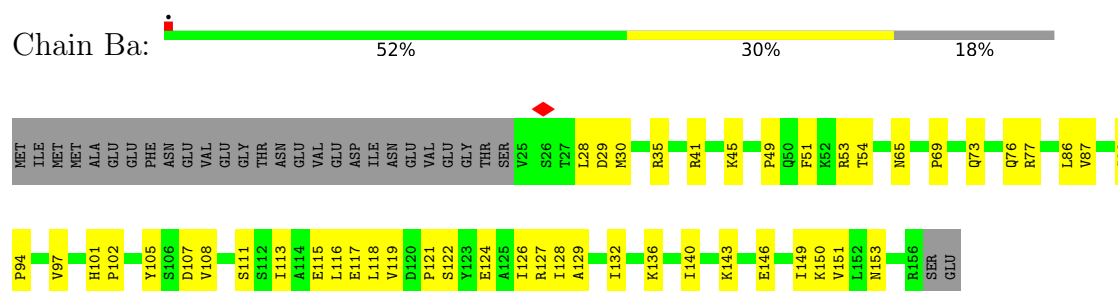
- Molecule 26: Large ribosomal subunit protein eL31



- Molecule 26: Large ribosomal subunit protein eL31

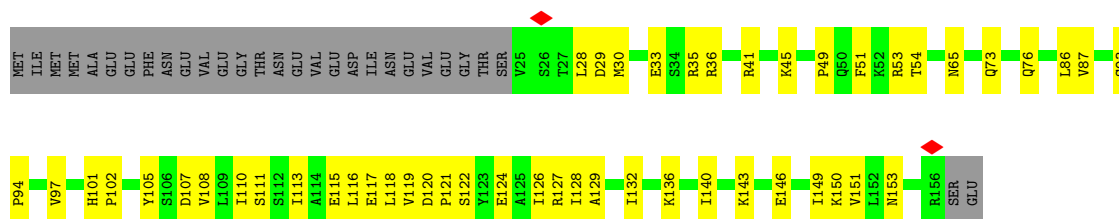


- Molecule 27: Large ribosomal subunit protein eL32

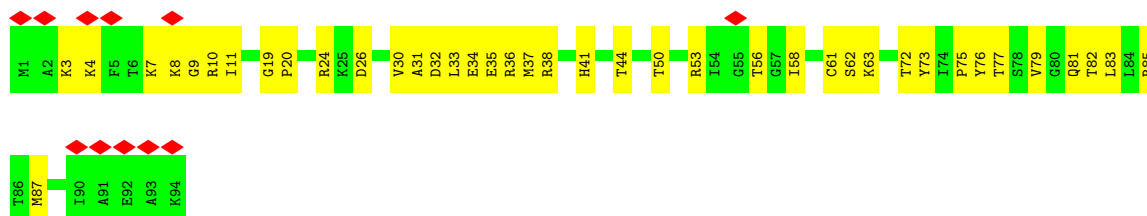


- Molecule 27: Large ribosomal subunit protein eL32

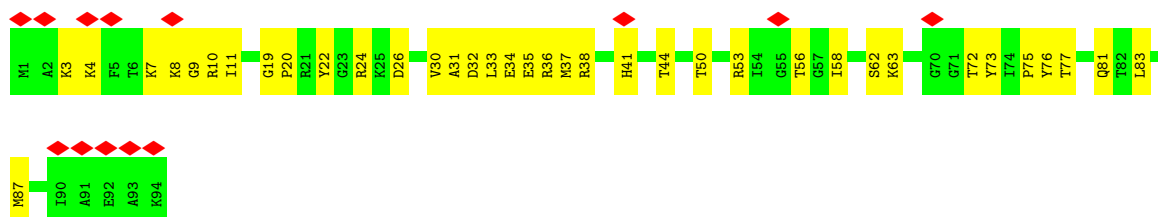




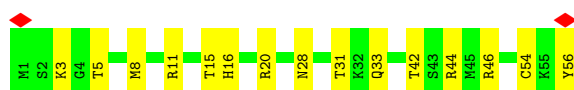
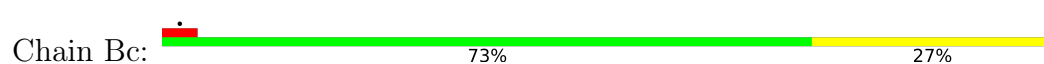
- Molecule 28: Large ribosomal subunit protein eL43



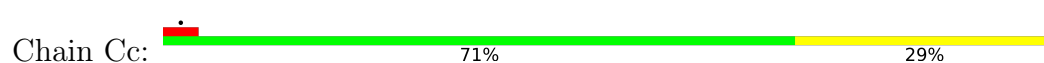
- Molecule 28: Large ribosomal subunit protein eL43



- Molecule 29: Large ribosomal subunit protein eL37

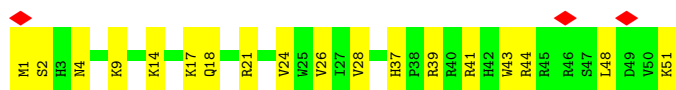


- Molecule 29: Large ribosomal subunit protein eL37

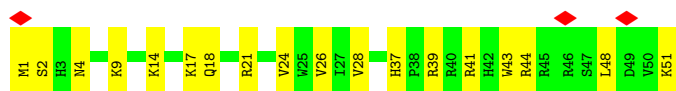


- Molecule 30: Large ribosomal subunit protein eL39





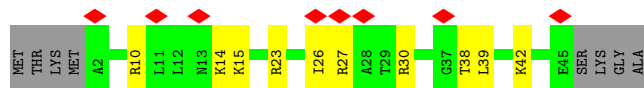
- Molecule 30: Large ribosomal subunit protein eL39



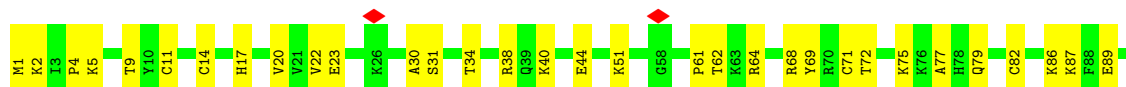
- Molecule 31: Large ribosomal subunit protein eL40



- Molecule 31: Large ribosomal subunit protein eL40



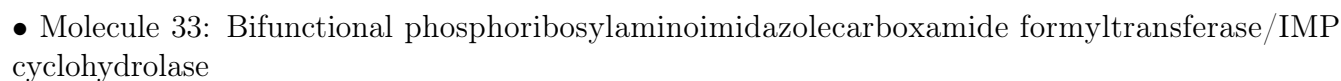
- Molecule 32: Large ribosomal subunit protein eL42

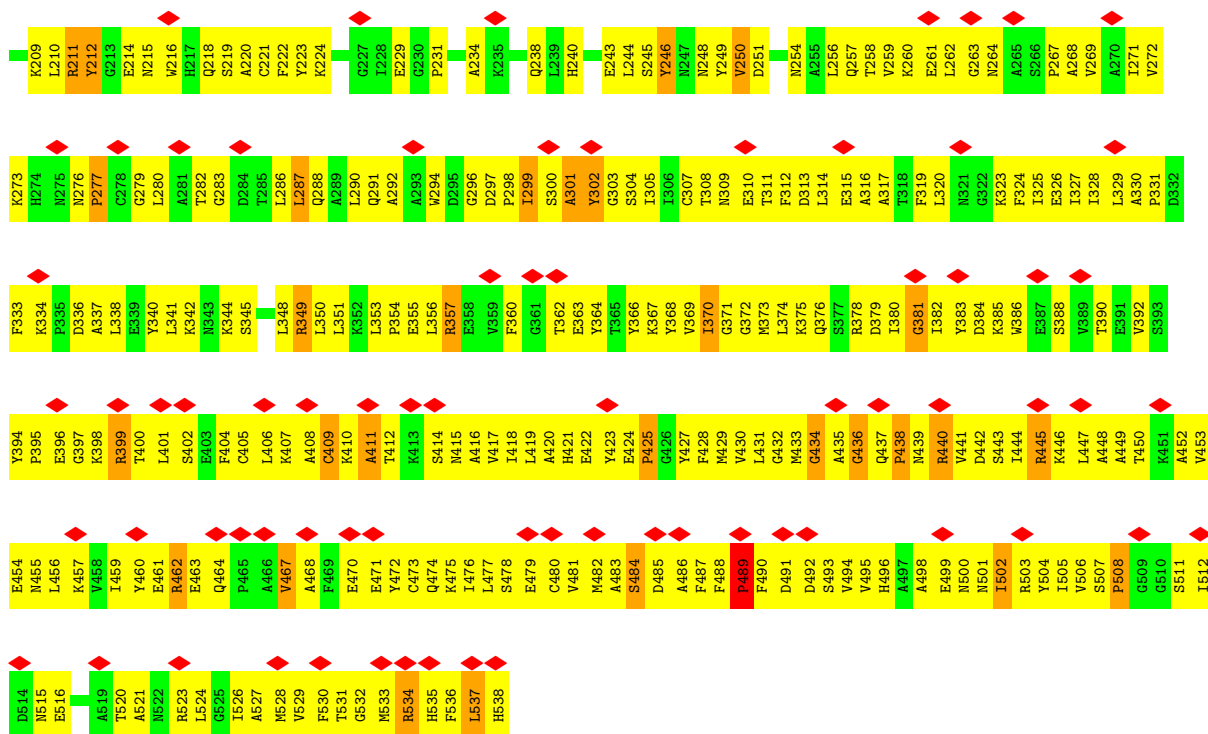


- Molecule 32: Large ribosomal subunit protein eL42

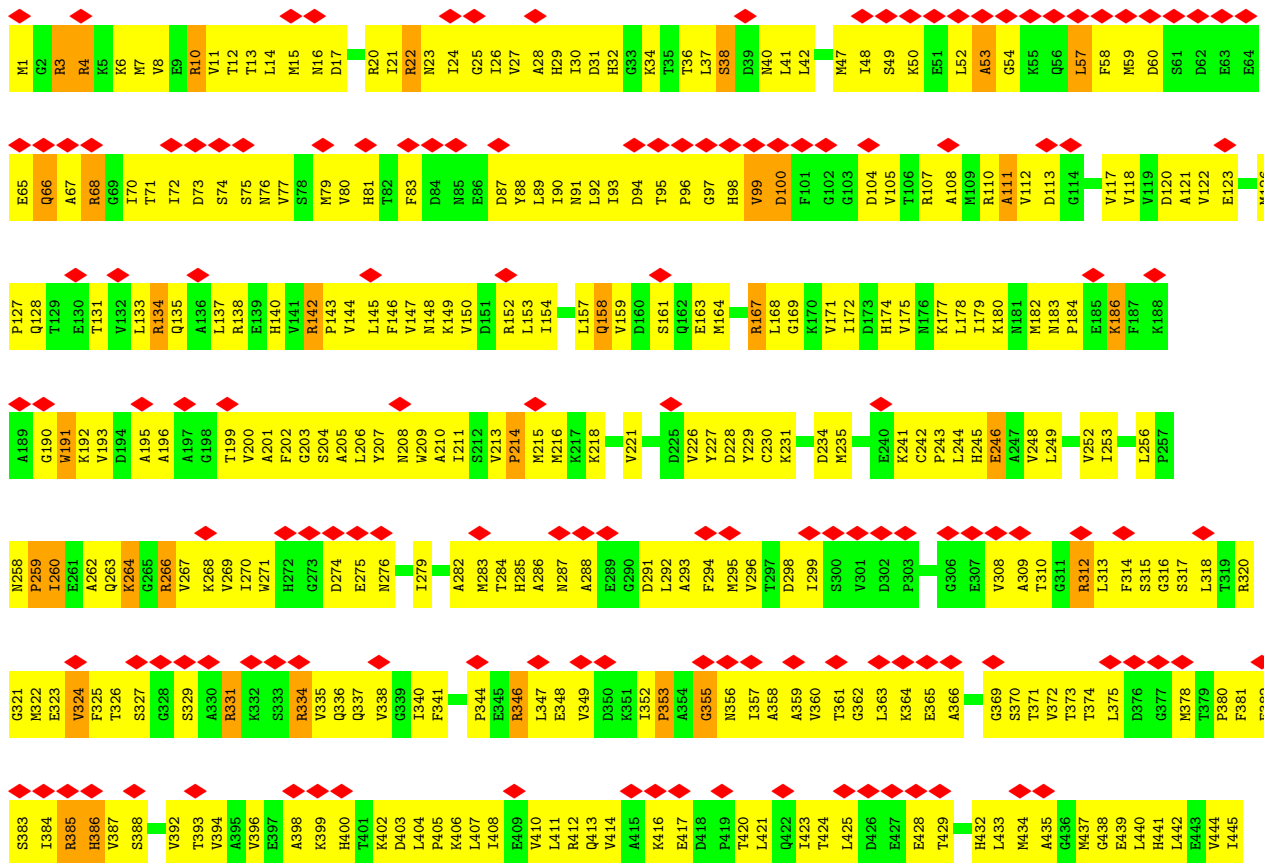


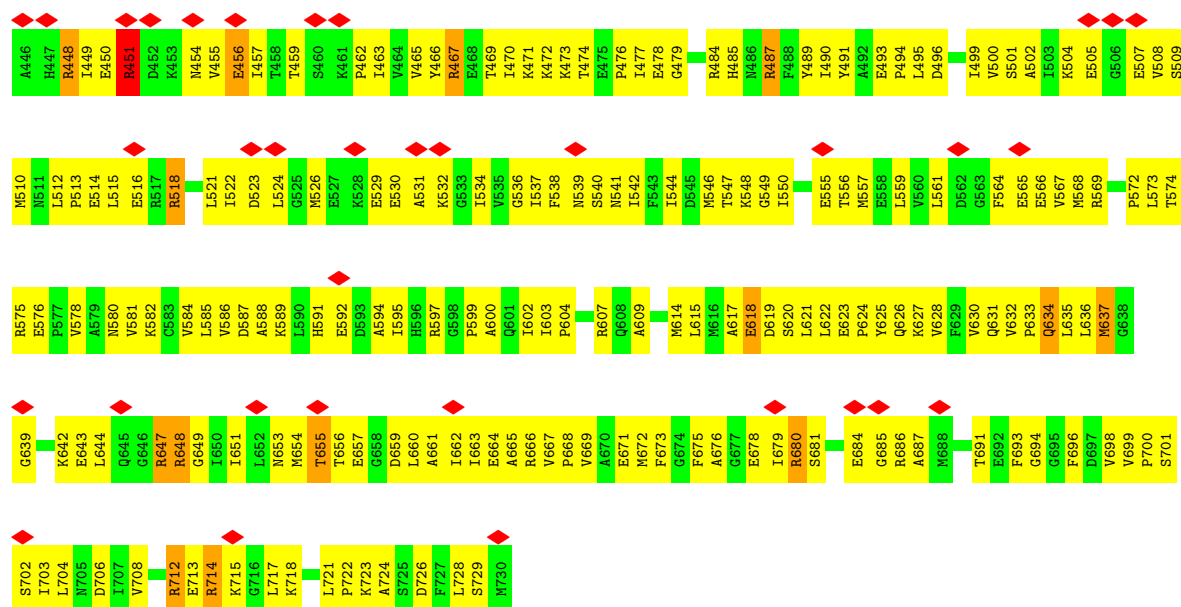
- Molecule 33: Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase



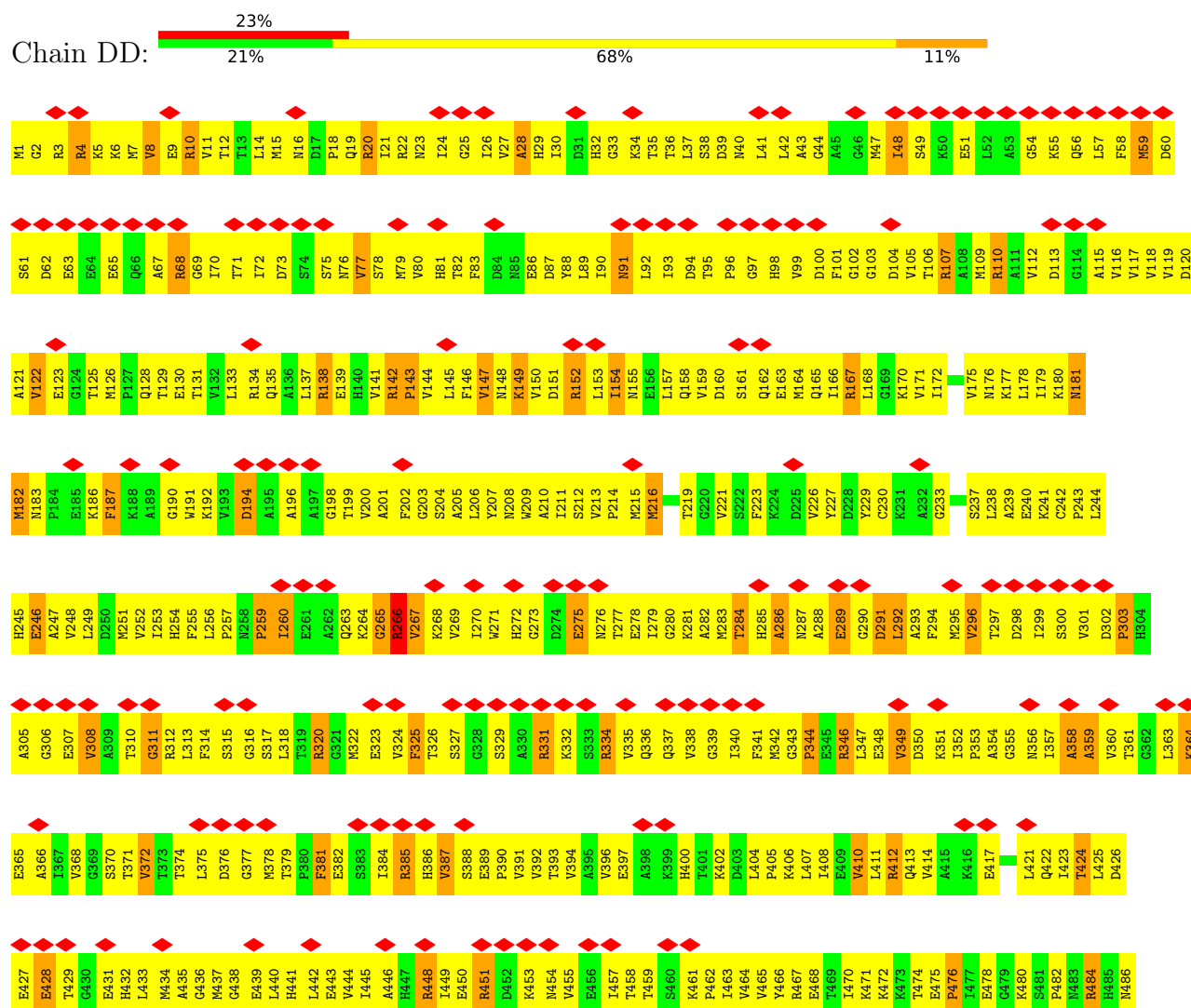


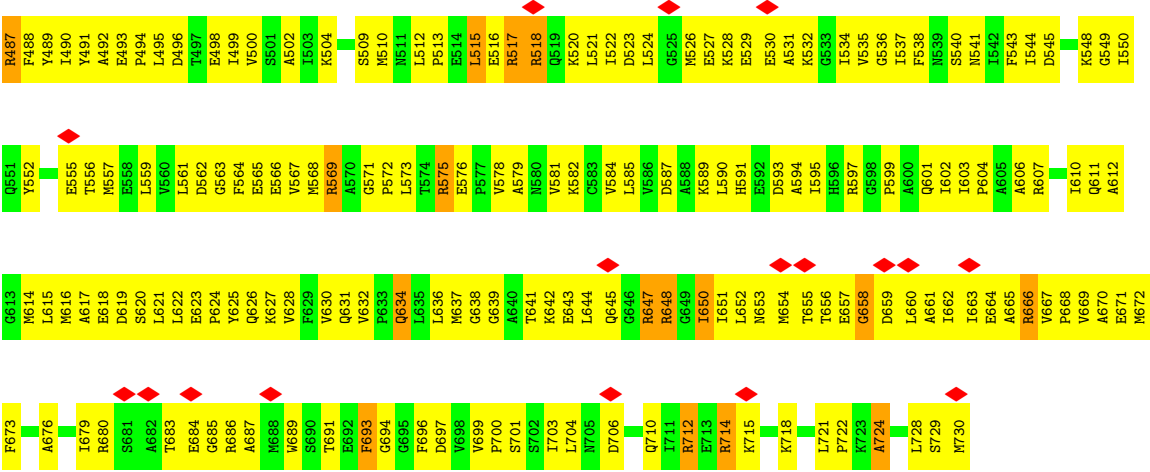
• Molecule 34: Elongation factor 2





Chain DD:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	15110	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	2.041	Depositor
Minimum map value	-0.964	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.311	Depositor
Map size ($\text{\AA}$)	586.2, 586.2, 586.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.977, 0.977, 0.977	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	BA	0.16	0/69080	0.37	0/107723
1	CA	0.16	0/69080	0.37	0/107723
2	BB	0.12	0/3037	0.28	0/4728
2	CB	0.12	0/3037	0.28	0/4728
3	BC	0.12	0/1850	0.33	0/2497
3	CC	0.12	0/1850	0.33	0/2497
4	BD	0.12	0/2646	0.32	0/3569
4	CD	0.12	0/2646	0.32	0/3569
5	BE	0.12	0/1964	0.33	0/2654
5	CE	0.12	0/1964	0.33	0/2654
6	BF	0.11	0/1310	0.30	0/1762
6	CF	0.11	0/1310	0.30	0/1762
7	BG	0.10	0/1392	0.28	0/1870
7	CG	0.10	0/1392	0.28	0/1870
8	BH	0.11	0/864	0.30	0/1161
8	CH	0.11	0/864	0.30	0/1161
9	BI	0.12	0/1284	0.30	0/1719
9	CI	0.12	0/1284	0.32	0/1719
10	BJ	0.11	0/1101	0.31	0/1474
10	CJ	0.11	0/1101	0.31	0/1474
11	BK	0.12	0/1010	0.33	0/1355
11	CK	0.13	0/1010	0.34	0/1355
12	BL	0.12	0/1071	0.36	0/1425
12	CL	0.12	0/1071	0.36	0/1425
13	BM	0.12	0/1625	0.34	0/2176
13	CM	0.12	0/1625	0.34	0/2176
14	BN	0.09	0/1382	0.28	0/1863
14	CN	0.09	0/1382	0.28	0/1863
15	BO	0.12	0/975	0.32	0/1312
15	CO	0.12	0/975	0.32	0/1312
16	BP	0.12	0/1209	0.32	0/1602
16	CP	0.12	0/1209	0.32	0/1602
17	BQ	0.12	0/464	0.30	0/614
17	CQ	0.11	0/464	0.30	0/614

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
18	BR	0.12	0/780	0.32	0/1042
18	CR	0.12	0/780	0.32	0/1042
19	BS	0.12	0/1189	0.32	0/1588
19	CS	0.12	0/1189	0.32	0/1588
20	BT	0.12	0/664	0.32	0/884
20	CT	0.12	0/664	0.32	0/884
21	BU	0.11	0/919	0.33	0/1227
21	CU	0.11	0/919	0.34	0/1227
22	BV	0.09	0/508	0.26	0/670
22	CV	0.09	0/508	0.26	0/670
23	BW	0.11	0/534	0.29	0/716
23	CW	0.10	0/534	0.29	0/716
24	BX	0.11	0/1259	0.28	0/1692
24	CX	0.12	0/1259	0.28	0/1692
25	BY	0.10	0/663	0.28	0/897
25	CY	0.10	0/663	0.28	0/897
26	BZ	0.13	0/715	0.31	0/960
26	CZ	0.12	0/715	0.31	0/960
27	Ba	0.11	0/1044	0.28	0/1397
27	Ca	0.11	0/1044	0.28	0/1397
28	Bb	0.12	0/749	0.34	0/997
28	Cb	0.12	0/749	0.34	0/997
29	Bc	0.16	0/452	0.34	0/593
29	Cc	0.15	0/452	0.34	0/593
30	Bd	0.14	0/448	0.34	0/595
30	Cd	0.14	0/448	0.34	0/595
31	Be	0.09	0/355	0.29	0/468
31	Ce	0.09	0/355	0.29	0/468
32	Bf	0.10	0/777	0.30	0/1029
32	Cf	0.11	0/777	0.30	0/1029
33	DA	0.34	0/4247	0.97	5/5744 (0.1%)
33	DB	0.34	0/4247	0.97	7/5744 (0.1%)
34	DC	1.29	7/5731 (0.1%)	0.81	2/7735 (0.0%)
34	DD	0.32	0/5731	0.88	3/7735 (0.0%)
All	All	0.26	7/226596 (0.0%)	0.42	17/335476 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
33	DA	0	20

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Mol	Chain	#Chirality outliers	#Planarity outliers
33	DB	0	21
34	DC	0	31
34	DD	0	30
All	All	0	102

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	DC	186	LYS	CE-NZ	85.26	4.05	1.49
34	DC	191	TRP	CE3-CZ3	23.80	2.10	1.38
34	DC	191	TRP	CE2-CZ2	18.51	1.78	1.39
34	DC	191	TRP	CZ3-CH2	18.05	1.85	1.40
34	DC	191	TRP	CZ2-CH2	14.57	1.65	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	DA	70	ILE	N-CA-C	-11.87	102.15	112.12
33	DB	68	PRO	CA-N-CD	-9.90	98.14	112.00
33	DA	409	CYS	CA-CB-SG	6.72	129.86	114.40
34	DD	48	ILE	N-CA-C	-6.46	100.64	108.53
34	DC	186	LYS	CD-CE-NZ	6.44	132.52	111.90

There are no chirality outliers.

5 of 102 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
33	DA	132	ARG	Sidechain
33	DA	20	ARG	Sidechain
33	DA	40	ARG	Sidechain
33	DA	69	ARG	Sidechain
33	DA	78	ARG	Sidechain

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	BA	61722	31112	31115	453	0
1	CA	61722	31112	31115	464	0
2	BB	2720	0	1382	88	0
2	CB	2720	0	1382	82	0
3	BC	1808	0	1842	91	0
3	CC	1808	0	1842	93	0
4	BD	2597	0	2692	124	0
4	CD	2597	0	2692	127	0
5	BE	1930	0	1989	89	0
5	CE	1930	0	1989	87	0
6	BF	1289	0	1317	108	0
6	CF	1289	0	1317	101	0
7	BG	1371	0	1426	56	0
7	CG	1371	0	1426	60	0
8	BH	857	0	898	52	0
8	CH	857	0	898	54	0
9	BI	1261	0	1300	36	0
9	CI	1261	0	1300	37	0
10	BJ	1086	0	1135	46	0
10	CJ	1086	0	1135	47	0
11	BK	999	0	1059	56	0
11	CK	999	0	1059	61	0
12	BL	1058	0	1044	51	0
12	CL	1058	0	1044	50	0
13	BM	1593	0	1637	70	0
13	CM	1593	0	1637	71	0
14	BN	1356	0	1358	85	0
14	CN	1356	0	1358	82	0
15	BO	962	0	1021	53	0
15	CO	962	0	1021	52	0
16	BP	1195	0	1277	44	0
16	CP	1195	0	1277	40	0
17	BQ	457	0	463	18	0
17	CQ	457	0	463	18	0
18	BR	766	0	777	47	0
18	CR	766	0	777	46	0
19	BS	1169	0	1211	52	0
19	CS	1169	0	1211	52	0
20	BT	656	0	688	33	0
20	CT	656	0	688	32	0
21	BU	910	0	972	57	0
21	CU	910	0	972	59	0
22	BV	499	0	519	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	CV	499	0	519	30	0
23	BW	532	0	547	38	0
23	CW	532	0	547	36	0
24	BX	1237	0	1269	41	0
24	CX	1237	0	1269	42	0
25	BY	658	0	696	44	0
25	CY	658	0	696	46	0
26	BZ	703	0	735	30	0
26	CZ	703	0	735	32	0
27	Ba	1028	0	1079	38	0
27	Ca	1028	0	1079	40	0
28	Bb	736	0	775	39	0
28	Cb	736	0	775	37	0
29	Bc	445	0	459	19	0
29	Cc	445	0	459	19	0
30	Bd	439	0	479	19	0
30	Cd	439	0	479	20	0
31	Be	353	0	378	9	0
31	Ce	353	0	378	9	0
32	Bf	760	0	801	23	0
32	Cf	760	0	801	24	0
33	DA	4172	0	4180	602	0
33	DB	4172	0	4180	645	0
34	DC	5643	0	5735	636	0
34	DD	5643	0	5735	838	0
All	All	209934	62224	148510	5940	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 17.

The worst 5 of 5940 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)
34:DC:191:TRP:CZ2	34:DC:191:TRP:CE2	1.78	1.70
34:DC:191:TRP:CH2	34:DC:191:TRP:CZ3	1.85	1.63
34:DC:191:TRP:CZ3	34:DC:191:TRP:CE3	2.10	1.38
33:DA:434:GLY:HA2	33:DA:447:LEU:HG	1.26	1.12
33:DA:215:ASN:HB2	33:DA:218:GLN:HG3	1.35	1.08

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	
3	BC	236/238 (99%)	228 (97%)	8 (3%)	0	100	100
3	CC	236/238 (99%)	228 (97%)	8 (3%)	0	100	100
4	BD	335/337 (99%)	328 (98%)	7 (2%)	0	100	100
4	CD	335/337 (99%)	328 (98%)	7 (2%)	0	100	100
5	BE	250/253 (99%)	244 (98%)	6 (2%)	0	100	100
5	CE	250/253 (99%)	244 (98%)	6 (2%)	0	100	100
6	BF	163/165 (99%)	155 (95%)	8 (5%)	0	100	100
6	CF	163/165 (99%)	156 (96%)	7 (4%)	0	100	100
7	BG	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
7	CG	174/176 (99%)	167 (96%)	7 (4%)	0	100	100
8	BH	113/120 (94%)	111 (98%)	2 (2%)	0	100	100
8	CH	113/120 (94%)	111 (98%)	2 (2%)	0	100	100
9	BI	155/173 (90%)	148 (96%)	7 (4%)	0	100	100
9	CI	155/173 (90%)	148 (96%)	7 (4%)	0	100	100
10	BJ	136/143 (95%)	134 (98%)	2 (2%)	0	100	100
10	CJ	136/143 (95%)	134 (98%)	2 (2%)	0	100	100
11	BK	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
11	CK	130/132 (98%)	126 (97%)	4 (3%)	0	100	100
12	BL	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	18	52
12	CL	138/140 (99%)	132 (96%)	5 (4%)	1 (1%)	18	52
13	BM	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
13	CM	194/196 (99%)	189 (97%)	5 (3%)	0	100	100
14	BN	172/174 (99%)	167 (97%)	5 (3%)	0	100	100
14	CN	172/174 (99%)	167 (97%)	5 (3%)	0	100	100
15	BO	124/126 (98%)	123 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	CO	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
16	BP	149/151 (99%)	146 (98%)	3 (2%)	0	100	100
16	CP	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
17	BQ	55/61 (90%)	55 (100%)	0	0	100	100
17	CQ	55/61 (90%)	55 (100%)	0	0	100	100
18	BR	94/97 (97%)	89 (95%)	5 (5%)	0	100	100
18	CR	94/97 (97%)	89 (95%)	5 (5%)	0	100	100
19	BS	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
19	CS	149/151 (99%)	142 (95%)	7 (5%)	0	100	100
20	BT	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
20	CT	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
21	BU	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
21	CU	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
22	BV	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
22	CV	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
23	BW	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
23	CW	65/67 (97%)	64 (98%)	1 (2%)	0	100	100
24	BX	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
24	CX	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
25	BY	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
25	CY	90/99 (91%)	87 (97%)	3 (3%)	0	100	100
26	BZ	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
26	CZ	84/89 (94%)	82 (98%)	2 (2%)	0	100	100
27	Ba	130/161 (81%)	129 (99%)	1 (1%)	0	100	100
27	Ca	130/161 (81%)	129 (99%)	1 (1%)	0	100	100
28	Bb	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
28	Cb	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
29	Bc	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
29	Cc	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
30	Bd	49/51 (96%)	41 (84%)	8 (16%)	0	100	100
30	Cd	49/51 (96%)	41 (84%)	8 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	Be	42/52 (81%)	41 (98%)	1 (2%)	0	100	100
31	Ce	42/52 (81%)	41 (98%)	1 (2%)	0	100	100
32	Bf	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
32	Cf	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
33	DA	536/538 (100%)	336 (63%)	151 (28%)	49 (9%)	0	6
33	DB	536/538 (100%)	345 (64%)	146 (27%)	45 (8%)	0	7
34	DC	728/730 (100%)	535 (74%)	157 (22%)	36 (5%)	1	16
34	DD	728/730 (100%)	449 (62%)	217 (30%)	62 (8%)	0	7
All	All	10270/10556 (97%)	9161 (89%)	915 (9%)	194 (2%)	8	33

5 of 194 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	DA	56	PRO
33	DA	59	MET
33	DA	63	VAL
33	DA	66	LEU
33	DA	75	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BC	188/188 (100%)	188 (100%)	0	100	100
3	CC	188/188 (100%)	188 (100%)	0	100	100
4	BD	277/277 (100%)	277 (100%)	0	100	100
4	CD	277/277 (100%)	277 (100%)	0	100	100
5	BE	197/198 (100%)	197 (100%)	0	100	100
5	CE	197/198 (100%)	197 (100%)	0	100	100
6	BF	140/140 (100%)	140 (100%)	0	100	100
6	CF	140/140 (100%)	140 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	BG	148/148 (100%)	148 (100%)	0	100	100
7	CG	148/148 (100%)	148 (100%)	0	100	100
8	BH	88/91 (97%)	88 (100%)	0	100	100
8	CH	88/91 (97%)	88 (100%)	0	100	100
9	BI	132/141 (94%)	132 (100%)	0	100	100
9	CI	132/141 (94%)	132 (100%)	0	100	100
10	BJ	114/119 (96%)	114 (100%)	0	100	100
10	CJ	114/119 (96%)	114 (100%)	0	100	100
11	BK	109/109 (100%)	109 (100%)	0	100	100
11	CK	109/109 (100%)	109 (100%)	0	100	100
12	BL	108/108 (100%)	108 (100%)	0	100	100
12	CL	108/108 (100%)	108 (100%)	0	100	100
13	BM	166/166 (100%)	166 (100%)	0	100	100
13	CM	166/166 (100%)	166 (100%)	0	100	100
14	BN	143/143 (100%)	143 (100%)	0	100	100
14	CN	143/143 (100%)	143 (100%)	0	100	100
15	BO	104/104 (100%)	104 (100%)	0	100	100
15	CO	104/104 (100%)	104 (100%)	0	100	100
16	BP	123/123 (100%)	123 (100%)	0	100	100
16	CP	123/123 (100%)	123 (100%)	0	100	100
17	BQ	50/54 (93%)	50 (100%)	0	100	100
17	CQ	50/54 (93%)	50 (100%)	0	100	100
18	BR	85/86 (99%)	85 (100%)	0	100	100
18	CR	85/86 (99%)	85 (100%)	0	100	100
19	BS	124/124 (100%)	124 (100%)	0	100	100
19	CS	124/124 (100%)	124 (100%)	0	100	100
20	BT	73/73 (100%)	73 (100%)	0	100	100
20	CT	73/73 (100%)	73 (100%)	0	100	100
21	BU	100/100 (100%)	100 (100%)	0	100	100
21	CU	100/100 (100%)	100 (100%)	0	100	100
22	BV	54/54 (100%)	54 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	CV	54/54 (100%)	54 (100%)	0	100	100
23	BW	57/57 (100%)	57 (100%)	0	100	100
23	CW	57/57 (100%)	57 (100%)	0	100	100
24	BX	134/134 (100%)	134 (100%)	0	100	100
24	CX	134/134 (100%)	134 (100%)	0	100	100
25	BY	71/78 (91%)	71 (100%)	0	100	100
25	CY	71/78 (91%)	71 (100%)	0	100	100
26	BZ	76/78 (97%)	76 (100%)	0	100	100
26	CZ	76/78 (97%)	76 (100%)	0	100	100
27	Ba	109/135 (81%)	109 (100%)	0	100	100
27	Ca	109/135 (81%)	109 (100%)	0	100	100
28	Bb	76/76 (100%)	76 (100%)	0	100	100
28	Cb	76/76 (100%)	76 (100%)	0	100	100
29	Bc	49/49 (100%)	49 (100%)	0	100	100
29	Cc	49/49 (100%)	49 (100%)	0	100	100
30	Bd	48/48 (100%)	48 (100%)	0	100	100
30	Cd	48/48 (100%)	48 (100%)	0	100	100
31	Be	37/43 (86%)	37 (100%)	0	100	100
31	Ce	37/43 (86%)	37 (100%)	0	100	100
32	Bf	82/82 (100%)	82 (100%)	0	100	100
32	Cf	82/82 (100%)	82 (100%)	0	100	100
33	DA	447/447 (100%)	447 (100%)	0	100	100
33	DB	447/447 (100%)	446 (100%)	1 (0%)	87	85
34	DC	614/614 (100%)	614 (100%)	0	100	100
34	DD	614/614 (100%)	614 (100%)	0	100	100
All	All	8646/8774 (98%)	8645 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
33	DB	425	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72

such sidechains are listed below:

Mol	Chain	Res	Type
33	DB	496	HIS
34	DD	591	HIS
34	DC	174	HIS
34	DC	653	ASN
6	CF	24	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	BA	2881/2899 (99%)	466 (16%)	13 (0%)
1	CA	2881/2899 (99%)	466 (16%)	13 (0%)
2	BB	127/129 (98%)	15 (11%)	0
2	CB	127/129 (98%)	15 (11%)	0
All	All	6016/6056 (99%)	962 (15%)	26 (0%)

5 of 962 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	BA	7	U
1	BA	39	C
1	BA	56	A
1	BA	64	A
1	BA	67	A

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	455	A
1	CA	869	U
1	CA	2365	A
1	CA	826	U
1	CA	1160	A

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

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](#)

There are no ligands in this entry.

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.

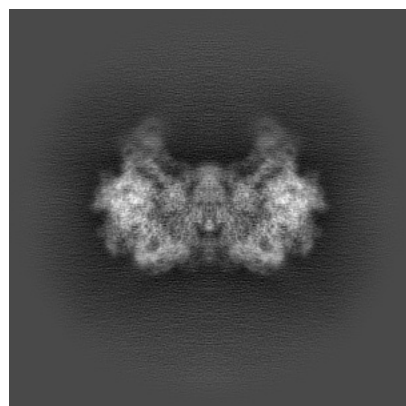
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70864. These allow visual inspection of the internal detail of the map and identification of artifacts.

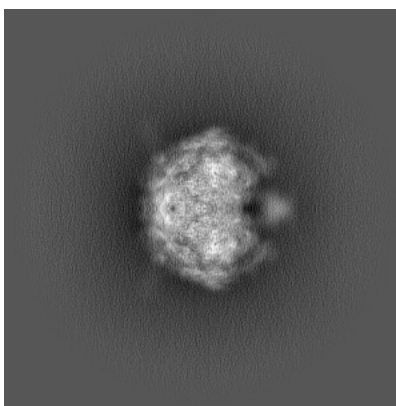
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

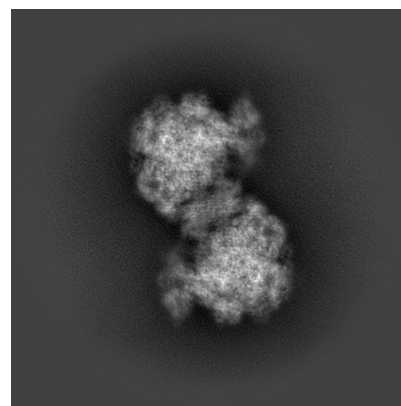
6.1.1 Primary map



X

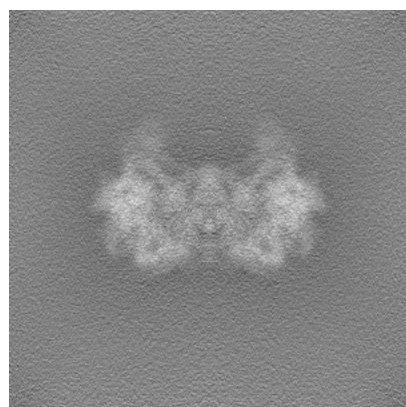


Y

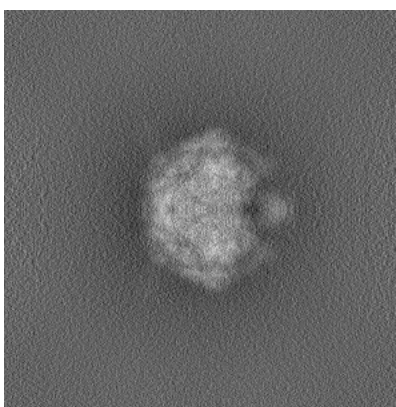


Z

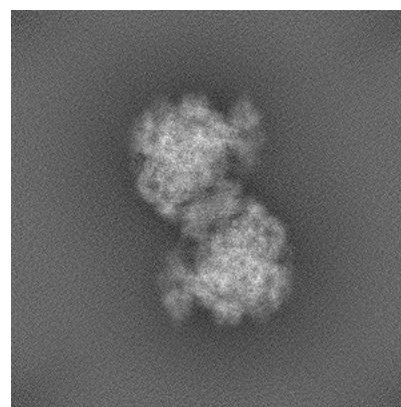
6.1.2 Raw map



X



Y

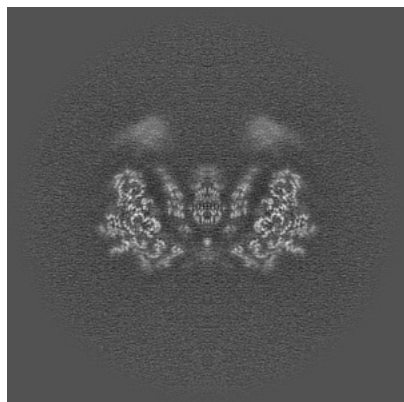


Z

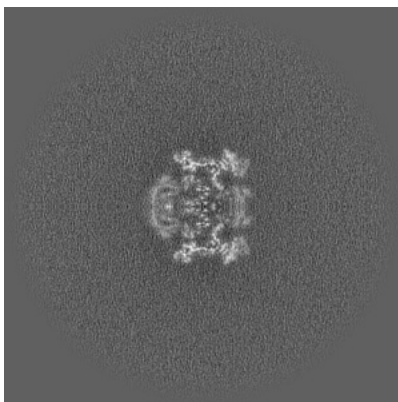
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

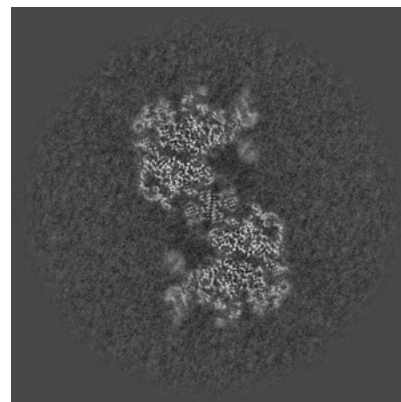
6.2.1 Primary map



X Index: 300

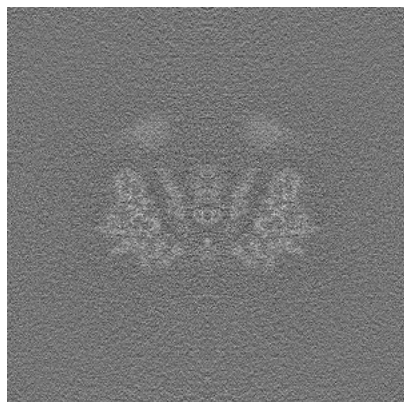


Y Index: 300

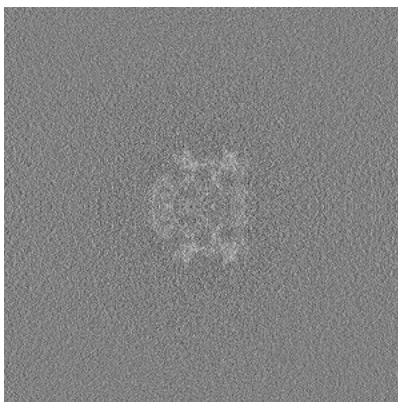


Z Index: 300

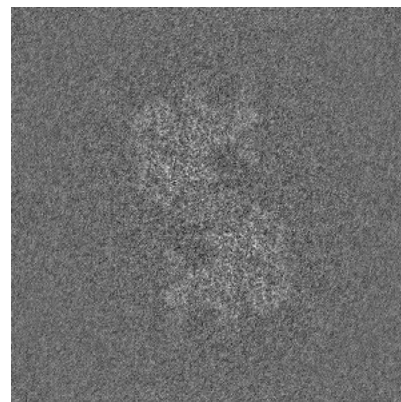
6.2.2 Raw map



X Index: 300



Y Index: 300

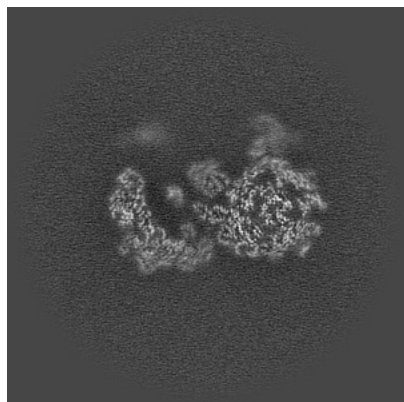


Z Index: 300

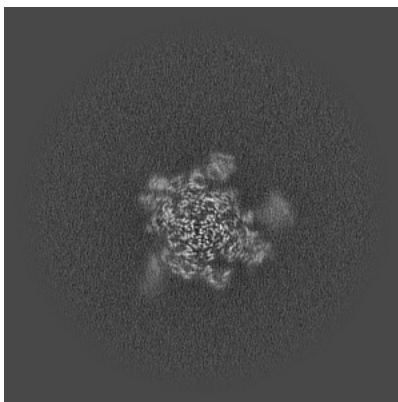
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

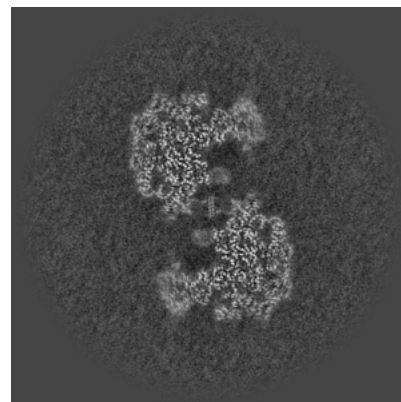
6.3.1 Primary map



X Index: 285

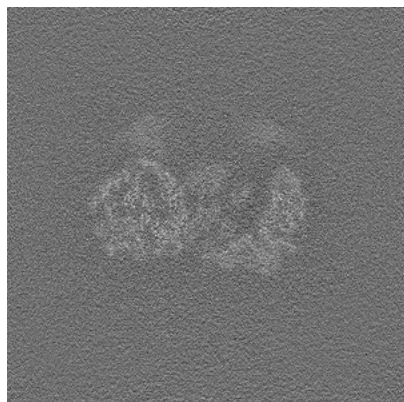


Y Index: 400

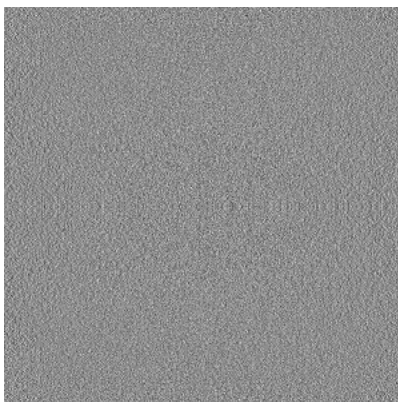


Z Index: 313

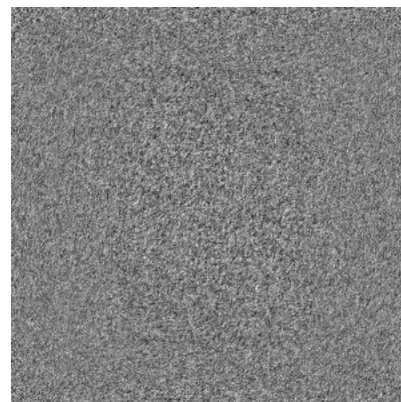
6.3.2 Raw map



X Index: 310



Y Index: 0

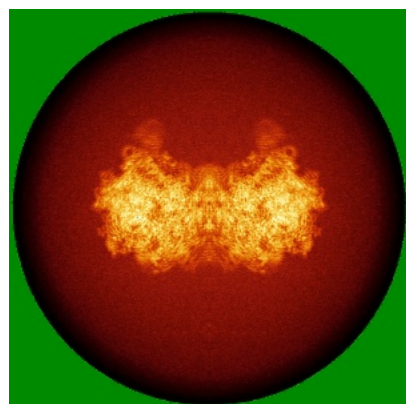


Z Index: 0

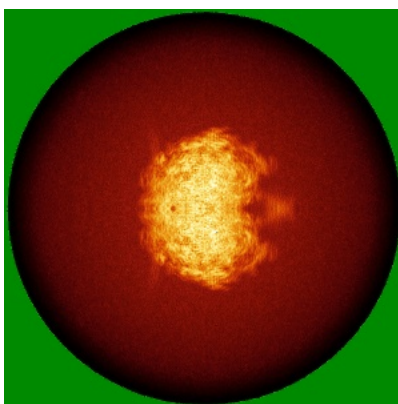
The images above show the largest variance slices of the map in three orthogonal directions.

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

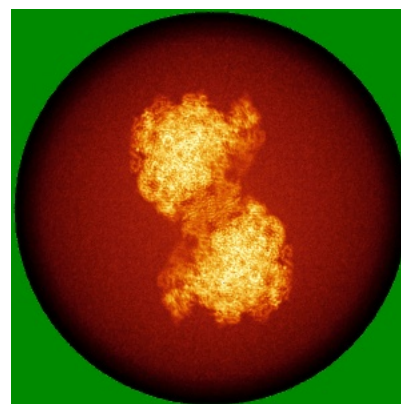
6.4.1 Primary map



X

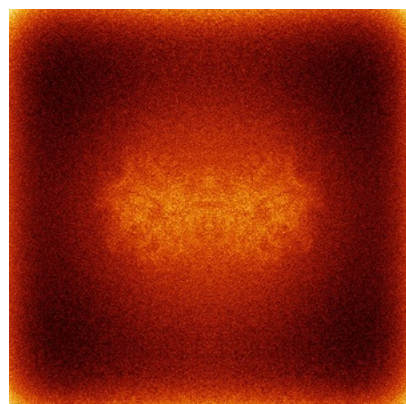


Y

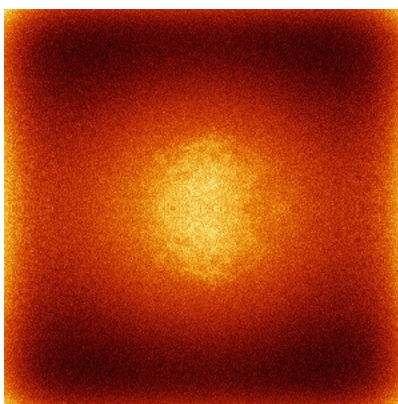


Z

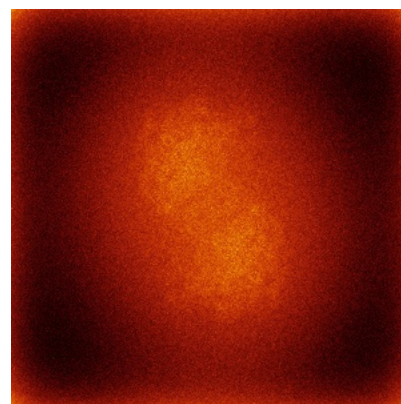
6.4.2 Raw map



X



Y

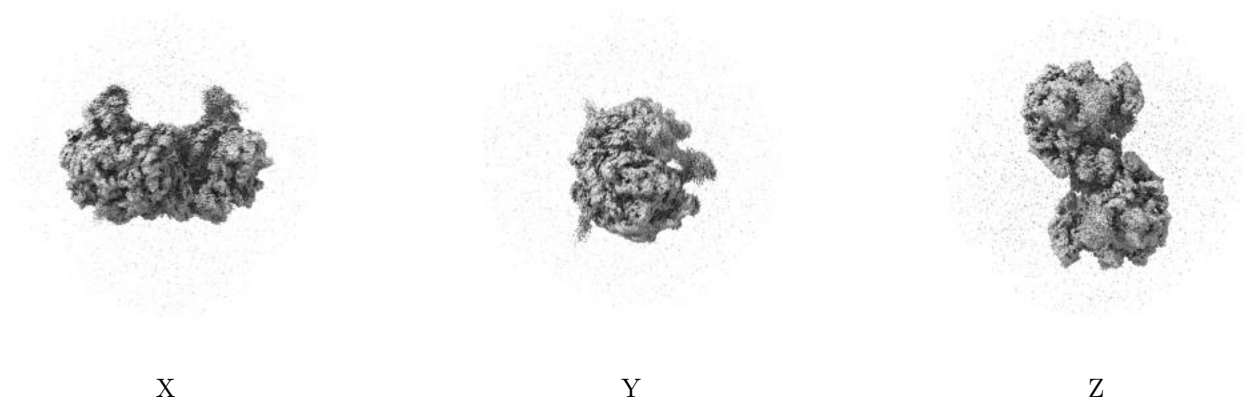


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.311. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

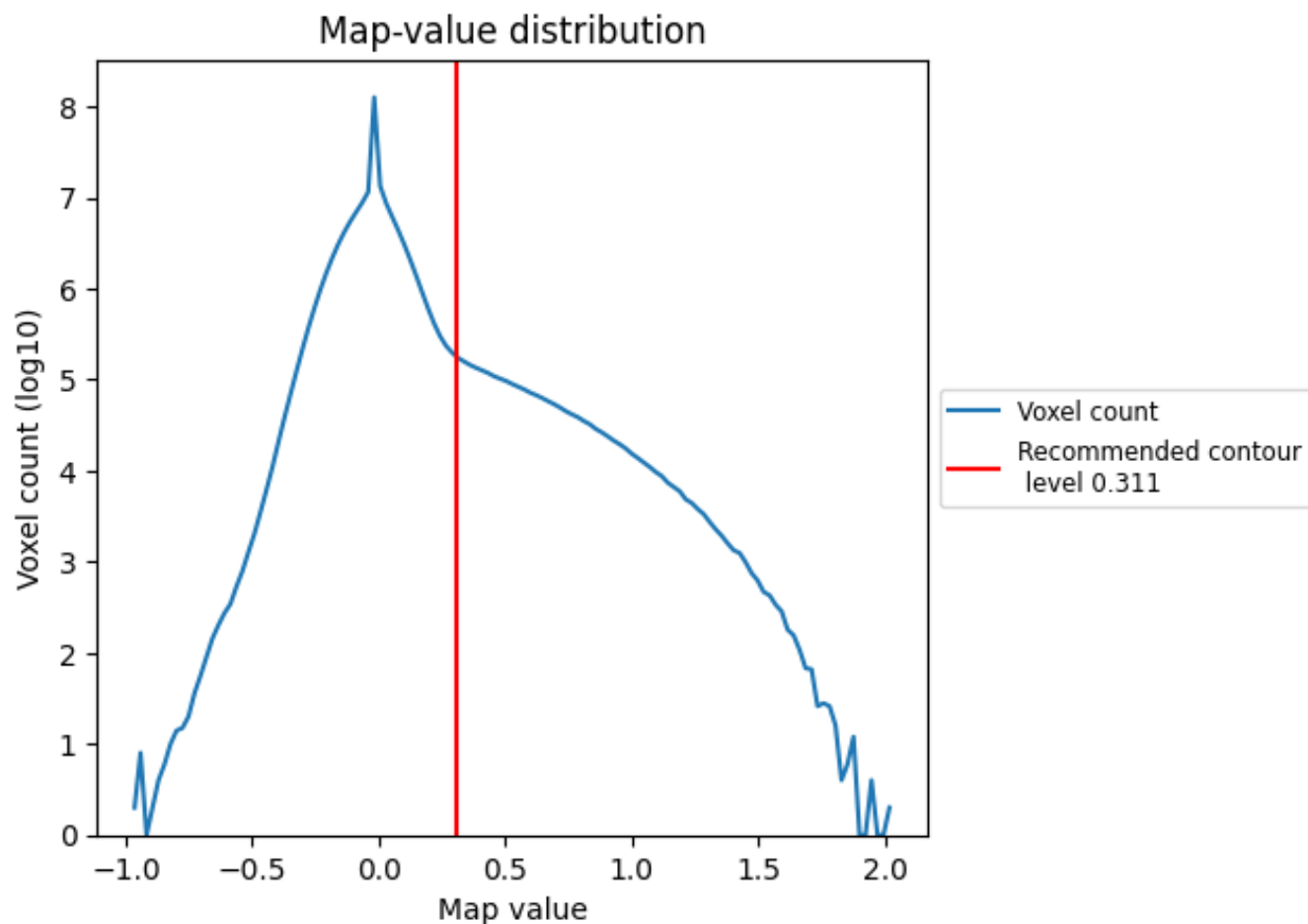
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

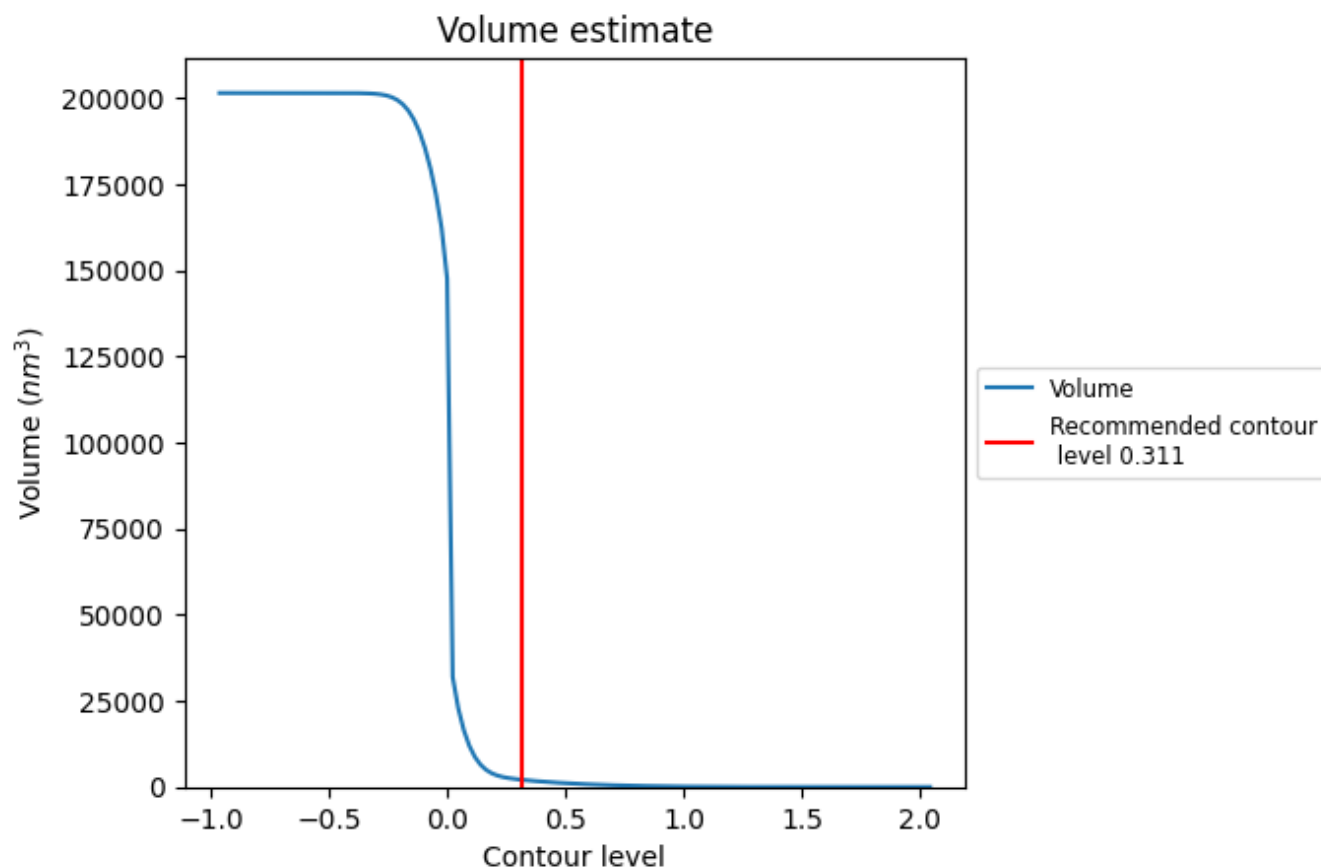
This section contains the results of statistical analysis of the map.

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.

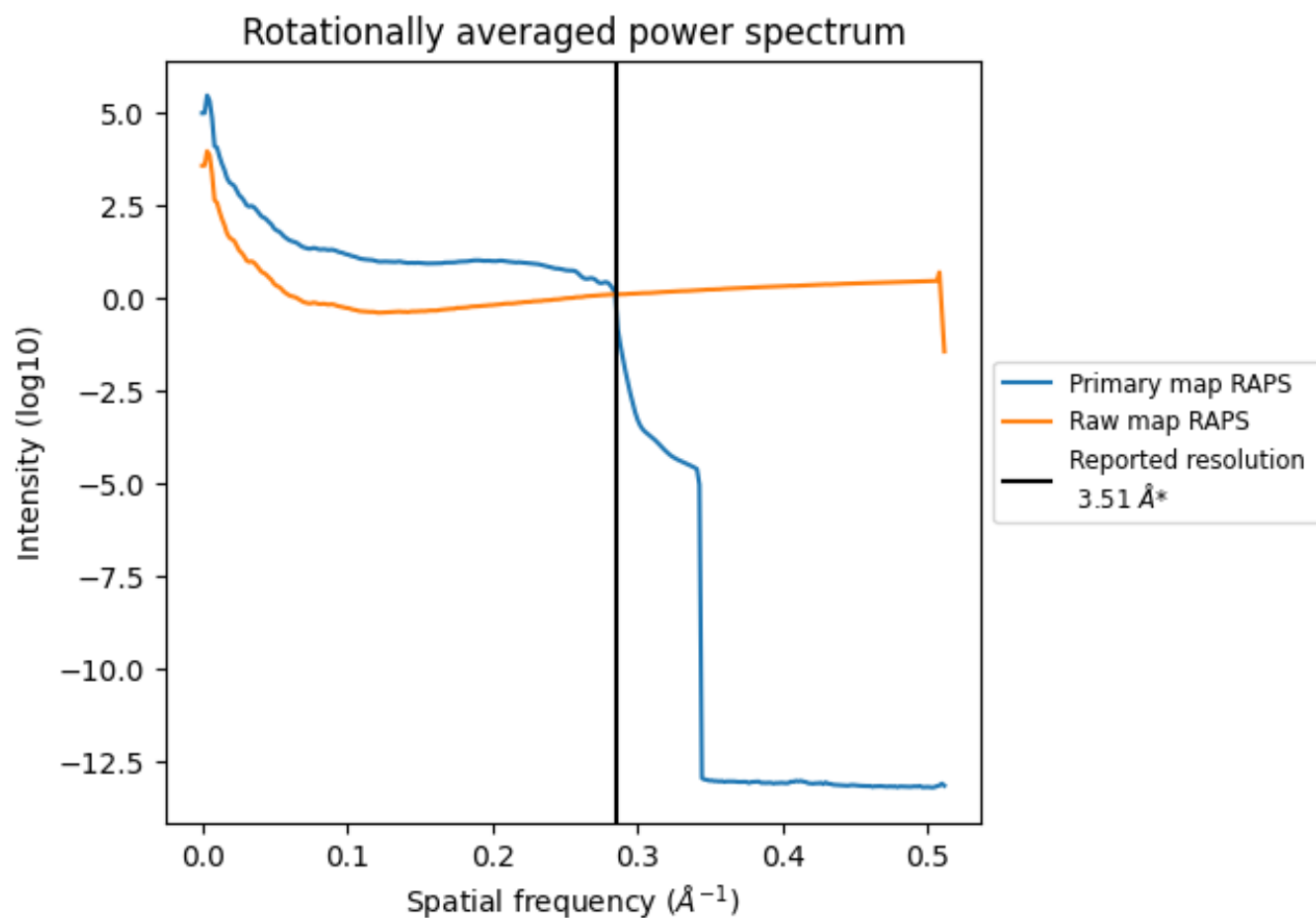
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2105 nm³; this corresponds to an approximate mass of 1902 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 ⓘ

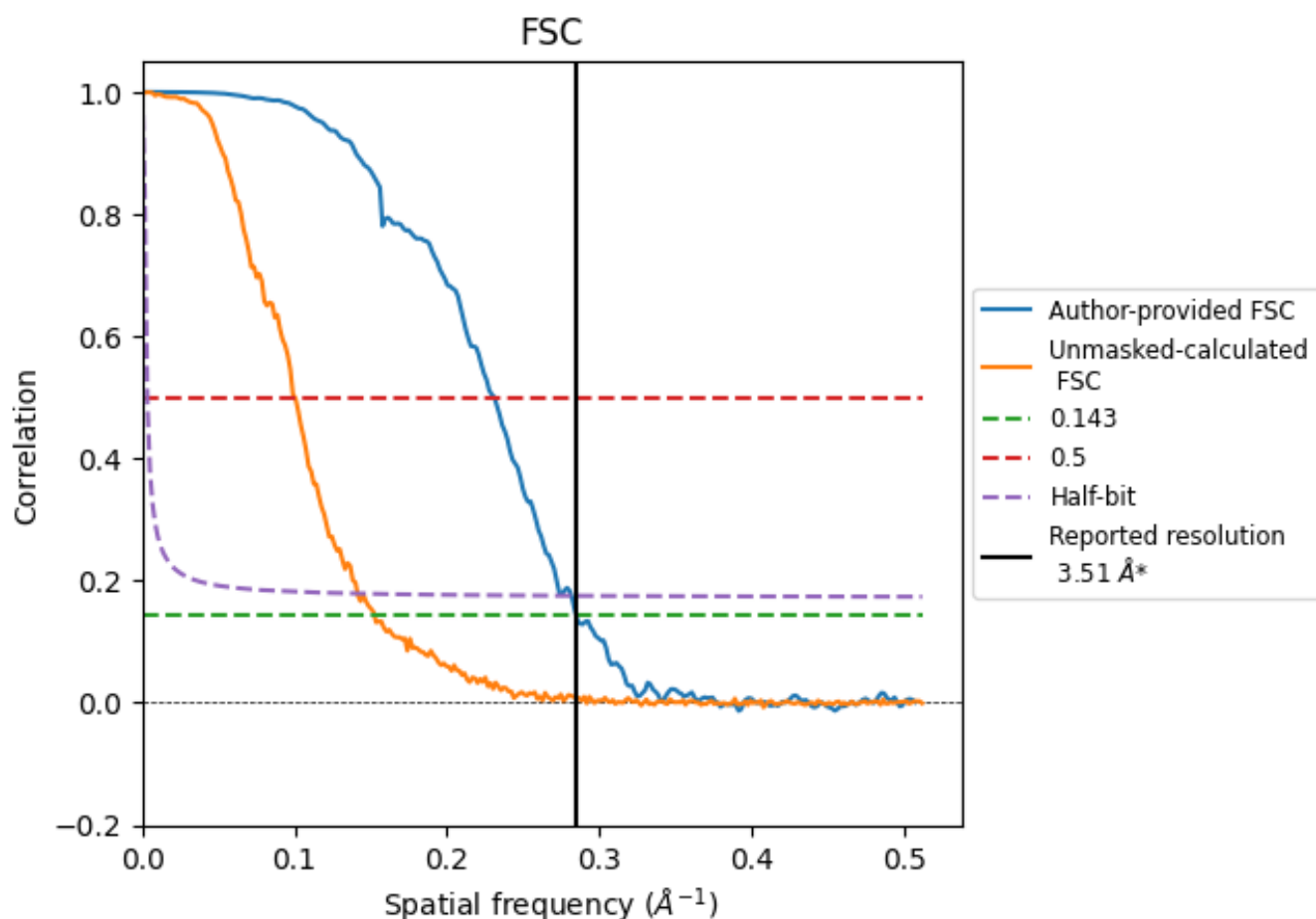


*Reported resolution corresponds to spatial frequency of 0.285 $\text{\AA}^{-1}$

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 0.285 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

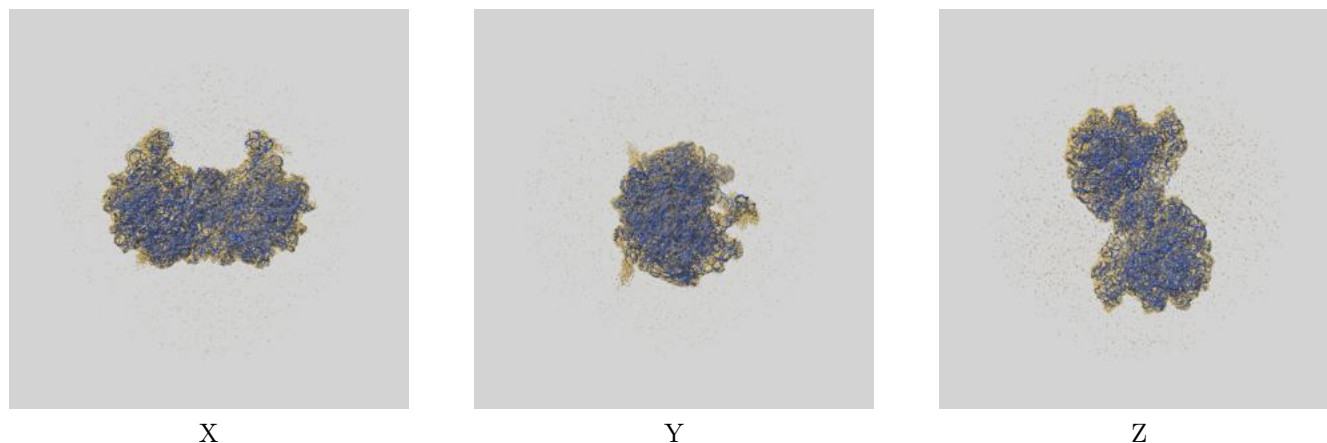
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.51	-	-
Author-provided FSC curve	3.51	4.33	3.55
Unmasked-calculated*	6.56	9.98	7.08

*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 6.56 differs from the reported value 3.51 by more than 10 %

9 Map-model fit [i](#)

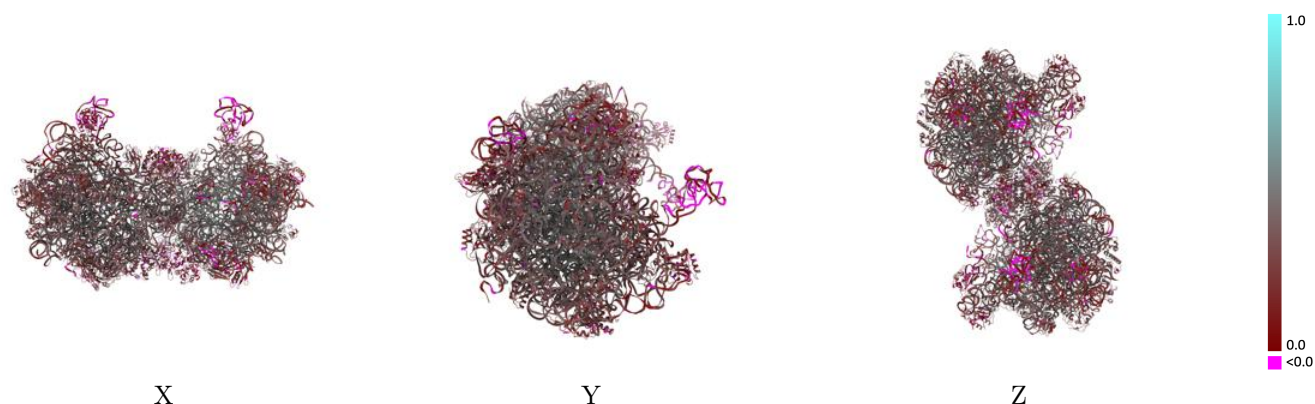
This section contains information regarding the fit between EMDB map EMD-70864 and PDB model 9OU7. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.311 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](#)

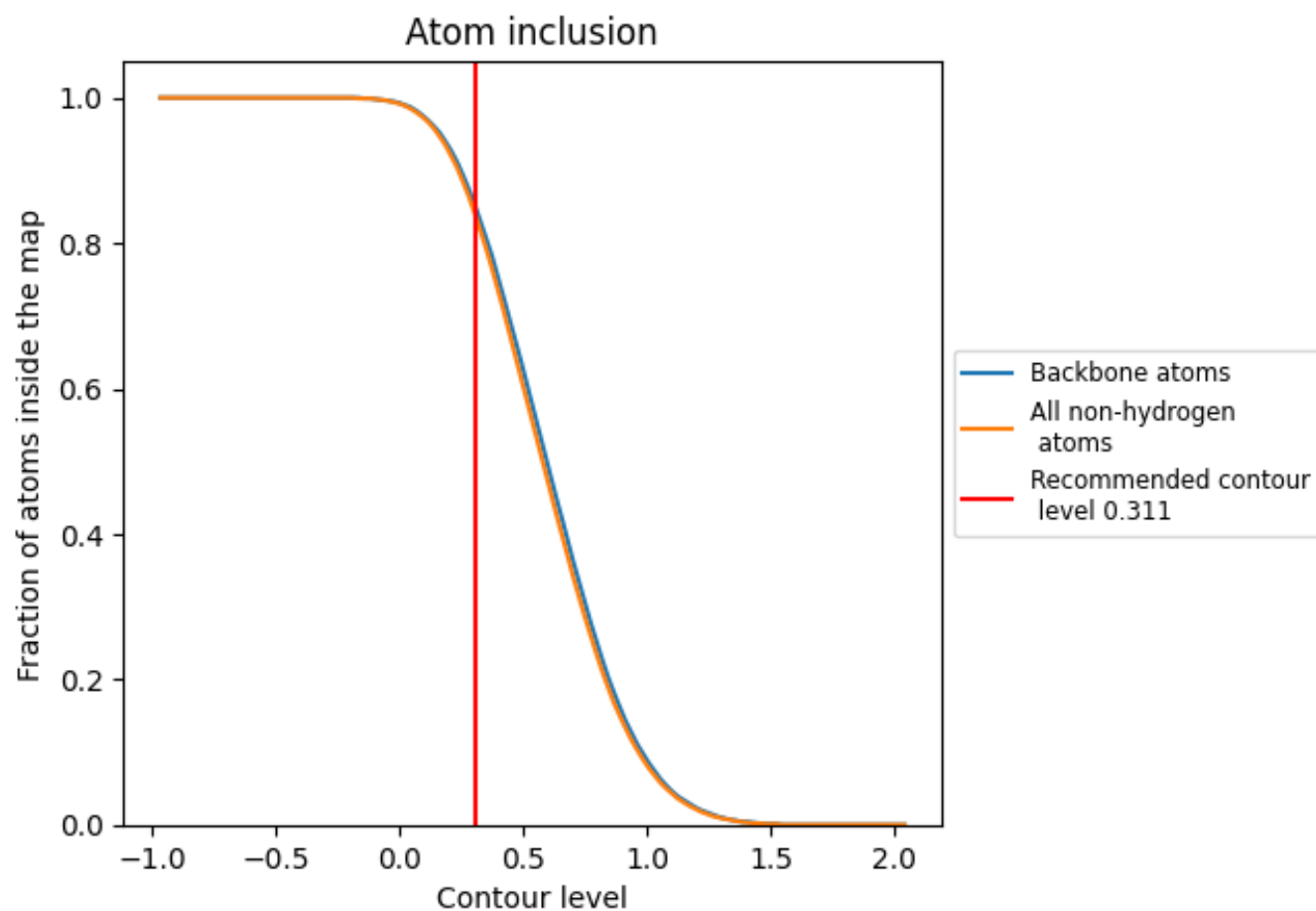


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% 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 (0.311) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8350	 0.3340
BA	 0.9080	 0.3570
BB	 0.9530	 0.3130
BC	 0.7780	 0.3710
BD	 0.7370	 0.3260
BE	 0.8060	 0.3590
BF	 0.6710	 0.1710
BG	 0.6570	 0.2440
BH	 0.5940	 0.1630
BI	 0.7770	 0.3720
BJ	 0.7410	 0.3250
BK	 0.6940	 0.3840
BL	 0.8090	 0.3460
BM	 0.7500	 0.3340
BN	 0.7960	 0.2580
BO	 0.8150	 0.3520
BP	 0.7980	 0.3740
BQ	 0.7260	 0.3040
BR	 0.7830	 0.3960
BS	 0.7610	 0.3610
BT	 0.7470	 0.3060
BU	 0.7750	 0.2700
BV	 0.6920	 0.3300
BW	 0.7550	 0.2690
BX	 0.8120	 0.3640
BY	 0.6560	 0.1930
BZ	 0.7860	 0.3640
Ba	 0.8080	 0.3770
Bb	 0.7280	 0.3130
Bc	 0.8210	 0.4500
Bd	 0.8160	 0.3980
Be	 0.6600	 0.2650
Bf	 0.7540	 0.3160
CA	 0.9060	 0.3560
CB	 0.9520	 0.3090



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Chain	Atom inclusion	Q-score
CC	 0.7860	 0.3730
CD	 0.7330	 0.3260
CE	 0.8120	 0.3580
CF	 0.6760	 0.1750
CG	 0.6520	 0.2370
CH	 0.6000	 0.1620
CI	 0.7730	 0.3650
CJ	 0.7390	 0.3240
CK	 0.7040	 0.3780
CL	 0.8020	 0.3470
CM	 0.7500	 0.3330
CN	 0.7800	 0.2580
CO	 0.8150	 0.3460
CP	 0.7920	 0.3740
CQ	 0.7000	 0.3000
CR	 0.7950	 0.3900
CS	 0.7550	 0.3630
CT	 0.7500	 0.3030
CU	 0.7750	 0.2660
CV	 0.6900	 0.3270
CW	 0.7490	 0.2680
CX	 0.8110	 0.3640
CY	 0.6560	 0.1960
CZ	 0.7720	 0.3670
Ca	 0.8040	 0.3780
Cb	 0.7110	 0.3160
Cc	 0.8260	 0.4500
Cd	 0.8070	 0.3980
Ce	 0.6570	 0.2570
Cf	 0.7560	 0.3190
DA	 0.5900	 0.2490
DB	 0.5920	 0.2570
DC	 0.5700	 0.2200
DD	 0.5680	 0.2210