



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:29 PM UTC

PDB ID : 9FNZ / pdb_00009fnz
EMDB ID : EMD-50612
Title : PF30S-PF30S dimer mediated by aRDF from P. furiosus (Structure II)
Authors : Hassan, A.H.; Demo, G.
Deposited on : 2024-06-11
Resolution : 3.20 Å (reported)
Based on initial models : ., 4V6U, 7ZHG

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:

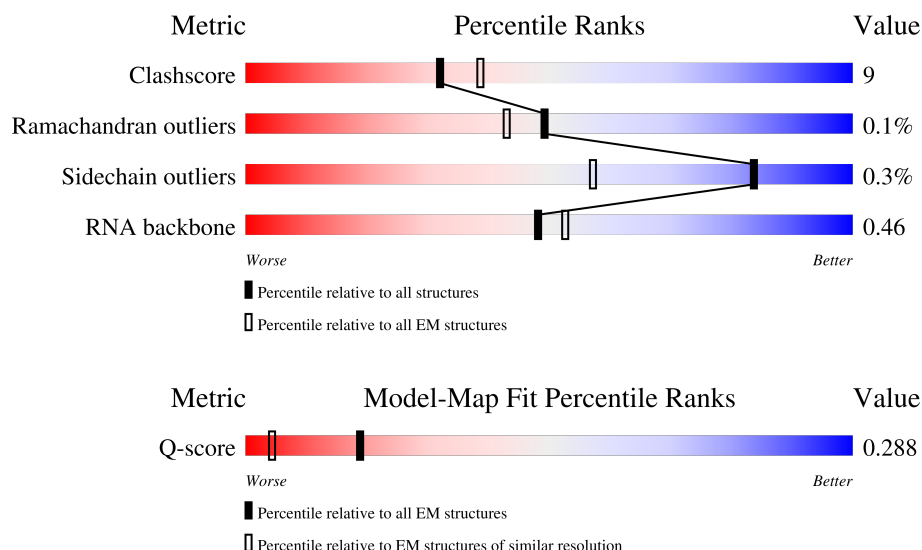
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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.



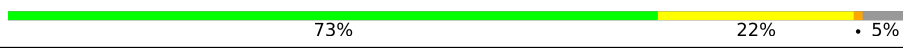
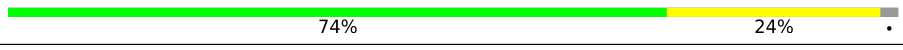
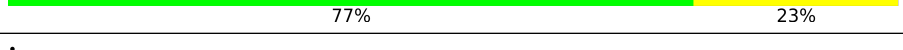
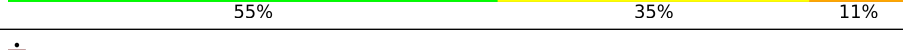
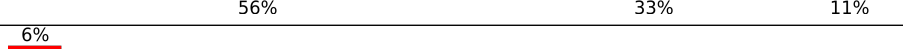
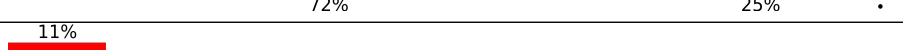
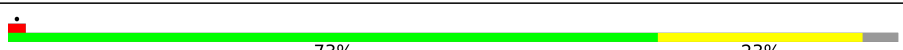
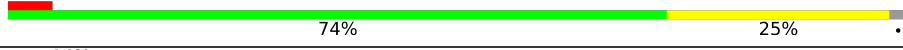
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	A1	60	
1	B1	60	
2	A2	37	

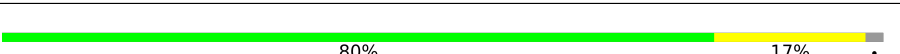
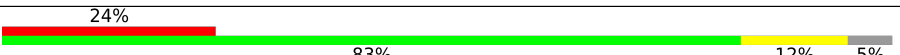
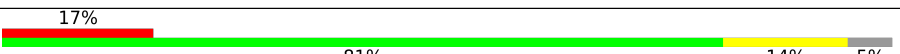
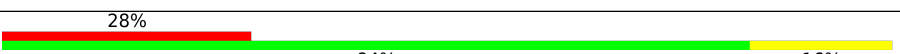
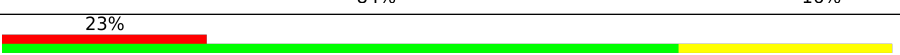
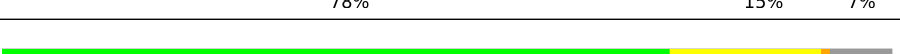
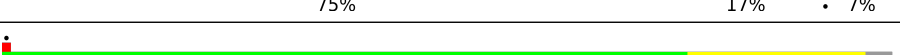
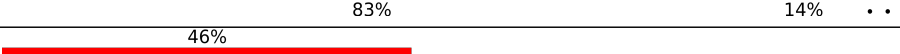
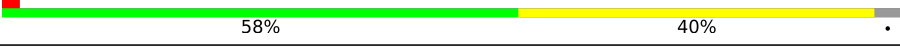
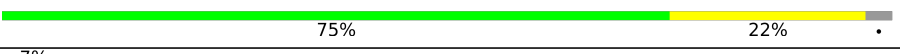
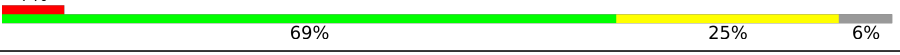
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Mol	Chain	Length	Quality of chain
2	B2	37	
3	A3	306	
3	A4	306	
3	B3	306	
3	B4	306	
4	A5	123	
4	B5	123	
5	AA	1495	
5	BA	1495	
6	AB	202	
6	BB	202	
7	AC	210	
7	BC	210	
8	AD	198	
8	BD	198	
9	AE	180	
9	BE	180	
10	AF	243	
10	BF	243	
11	AG	236	
11	BG	236	
12	AH	125	
12	BH	125	
13	AI	215	
13	BI	215	

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Mol	Chain	Length	Quality of chain
14	AJ	130	
14	BJ	130	
15	AK	127	
15	BK	127	
16	AL	135	
16	BL	135	
17	AM	102	
17	BM	102	
18	AN	137	
18	BN	137	
19	AO	147	
19	BO	147	
20	AP	148	
20	BP	148	
21	AQ	56	
21	BQ	56	
22	AR	158	
22	BR	158	
23	AS	113	
23	BS	113	
24	AT	67	
24	BT	67	
25	AU	132	
25	BU	132	
26	AV	150	

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Mol	Chain	Length	Quality of chain
26	BV	150	
27	AW	99	
27	BW	99	
28	AX	50	
28	BX	50	
29	AY	63	
29	BY	63	
30	AZ	71	
30	BZ	71	

2 Entry composition

There are 30 unique types of molecules in this entry. The entry contains 130980 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	60	Total	C	N	O	S	0	0
			471	295	83	83	10		
1	B1	60	Total	C	N	O	S	0	0
			471	295	83	83	10		

- Molecule 2 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A2	35	Total	C	N	O	S	0	0
			335	212	83	38	2		
2	B2	35	Total	C	N	O	S	0	0
			335	212	83	38	2		

- Molecule 3 is a protein called Archaeal Ribosome Dimerizing Factor (aRDF).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A3	298	Total	C	N	O	S	0	0
			2375	1537	395	439	4		
3	A4	291	Total	C	N	O	S	0	0
			2321	1503	387	427	4		
3	B3	299	Total	C	N	O	S	0	0
			2381	1540	396	441	4		
3	B4	289	Total	C	N	O	S	0	0
			2301	1491	381	425	4		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A3	301	HIS	-	expression tag	UNP Q8U3B0
A3	302	HIS	-	expression tag	UNP Q8U3B0
A3	303	HIS	-	expression tag	UNP Q8U3B0
A3	304	HIS	-	expression tag	UNP Q8U3B0
A3	305	HIS	-	expression tag	UNP Q8U3B0

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Chain	Residue	Modelled	Actual	Comment	Reference
A3	306	HIS	-	expression tag	UNP Q8U3B0
A4	301	HIS	-	expression tag	UNP Q8U3B0
A4	302	HIS	-	expression tag	UNP Q8U3B0
A4	303	HIS	-	expression tag	UNP Q8U3B0
A4	304	HIS	-	expression tag	UNP Q8U3B0
A4	305	HIS	-	expression tag	UNP Q8U3B0
A4	306	HIS	-	expression tag	UNP Q8U3B0
B3	301	HIS	-	expression tag	UNP Q8U3B0
B3	302	HIS	-	expression tag	UNP Q8U3B0
B3	303	HIS	-	expression tag	UNP Q8U3B0
B3	304	HIS	-	expression tag	UNP Q8U3B0
B3	305	HIS	-	expression tag	UNP Q8U3B0
B3	306	HIS	-	expression tag	UNP Q8U3B0
B4	301	HIS	-	expression tag	UNP Q8U3B0
B4	302	HIS	-	expression tag	UNP Q8U3B0
B4	303	HIS	-	expression tag	UNP Q8U3B0
B4	304	HIS	-	expression tag	UNP Q8U3B0
B4	305	HIS	-	expression tag	UNP Q8U3B0
B4	306	HIS	-	expression tag	UNP Q8U3B0

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A5	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
4	B5	123	Total	C	N	O	S	0	0
			939	599	155	181	4		

- Molecule 5 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AA	1495	Total	C	N	O	P	0	0
			32135	14297	5954	10389	1495		
5	BA	1495	Total	C	N	O	P	0	0
			32135	14297	5954	10389	1495		

- Molecule 6 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AB	197	Total	C	N	O	S	0	0
			1579	1022	271	282	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	BB	197	Total	C	N	O	S	0	0
			1579	1022	271	282	4		

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AC	195	Total	C	N	O	S	0	0
			1532	980	283	266	3		
7	BC	195	Total	C	N	O	S	0	0
			1532	980	283	266	3		

- Molecule 8 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AD	184	Total	C	N	O	S	0	0
			1511	978	263	265	5		
8	BD	184	Total	C	N	O	S	0	0
			1511	978	263	265	5		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AE	173	Total	C	N	O	S	0	0
			1455	915	282	254	4		
9	BE	173	Total	C	N	O	S	0	0
			1455	915	282	254	4		

- Molecule 10 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AF	242	Total	C	N	O	S	0	0
			1981	1280	356	340	5		
10	BF	242	Total	C	N	O	S	0	0
			1981	1280	356	340	5		

- Molecule 11 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AG	227	Total	C	N	O	S	0	0
			1794	1134	335	318	7		
11	BG	227	Total	C	N	O	S	0	0
			1794	1134	335	318	7		

- Molecule 12 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AH	123	Total	C	N	O	S	0	0
			971	615	178	177	1		
12	BH	123	Total	C	N	O	S	0	0
			971	615	178	177	1		

- Molecule 13 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AI	214	Total	C	N	O	S	0	0
			1728	1095	325	301	7		
13	BI	214	Total	C	N	O	S	0	0
			1728	1095	325	301	7		

- Molecule 14 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AJ	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		
14	BJ	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 15 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	AK	124	Total	C	N	O	0	0
			977	607	204	166		
15	BK	124	Total	C	N	O	0	0
			977	607	204	166		

- Molecule 16 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AL	128	Total	C	N	O	S	0	0
			1006	630	191	180	5		
16	BL	128	Total	C	N	O	S	0	0
			1006	630	191	180	5		

- Molecule 17 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AM	102	Total	C	N	O	S	0	0
			822	507	159	152	4		
17	BM	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 18 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AN	127	Total	C	N	O	S	0	0
			954	591	190	171	2		
18	BN	127	Total	C	N	O	S	0	0
			954	591	190	171	2		

- Molecule 19 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AO	143	Total	C	N	O	S	0	0
			1118	710	215	190	3		
19	BO	143	Total	C	N	O	S	0	0
			1118	710	215	190	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AP	131	Total	C	N	O	S	0	0
			1052	663	206	178	5		
20	BP	131	Total	C	N	O	S	0	0
			1052	663	206	178	5		

- Molecule 21 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AQ	50	Total	C	N	O	S	0	0
			417	266	88	58	5		
21	BQ	50	Total	C	N	O	S	0	0
			417	266	88	58	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AR	155	Total	C	N	O	S	0	0
			1283	818	244	217	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
22	BR	155	Total	C	N	O	S	0	0
			1283	818	244	217	4		

- Molecule 23 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AS	110	Total	C	N	O	S	0	0
			903	575	168	156	4		
23	BS	110	Total	C	N	O	S	0	0
			903	575	168	156	4		

- Molecule 24 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AT	63	Total	C	N	O	S	0	0
			522	330	100	90	2		
24	BT	63	Total	C	N	O	S	0	0
			522	330	100	90	2		

- Molecule 25 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AU	115	Total	C	N	O	S	0	0
			948	609	177	156	6		
25	BU	115	Total	C	N	O	S	0	0
			948	609	177	156	6		

- Molecule 26 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AV	148	Total	C	N	O		0	0
			1209	781	218	210			
26	BV	148	Total	C	N	O		0	0
			1209	781	218	210			

- Molecule 27 is a protein called Small ribosomal subunit protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AW	93	Total	C	N	O	S	0	0
			774	503	126	143	2		
27	BW	93	Total	C	N	O	S	0	0
			774	503	126	143	2		

- Molecule 28 is a protein called Small ribosomal subunit protein eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AX	45	Total	C	N	O	S	0	0
			369	238	67	59	5		
28	BX	45	Total	C	N	O	S	0	0
			369	238	67	59	5		

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AY	61	Total	C	N	O	S	0	0
			465	298	83	79	5		
29	BY	61	Total	C	N	O	S	0	0
			465	298	83	79	5		

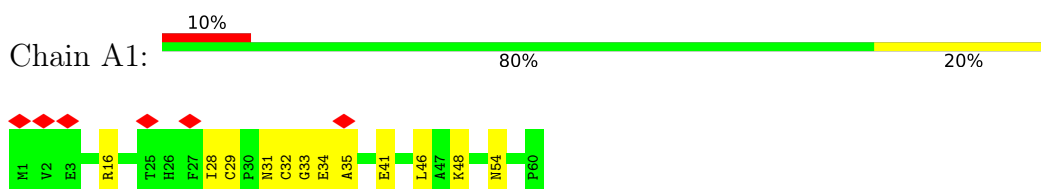
- Molecule 30 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	AZ	66	Total	C	N	O	0	0
			523	320	104	99		
30	BZ	66	Total	C	N	O	0	0
			523	320	104	99		

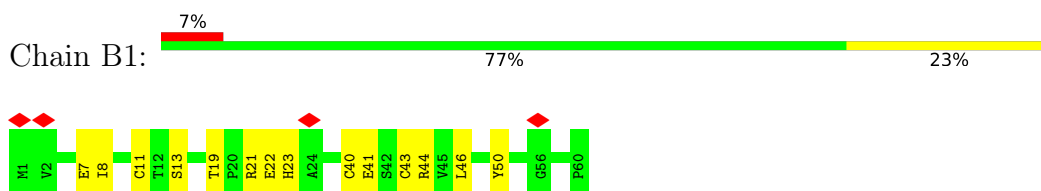
3 Residue-property plots [i](#)

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.

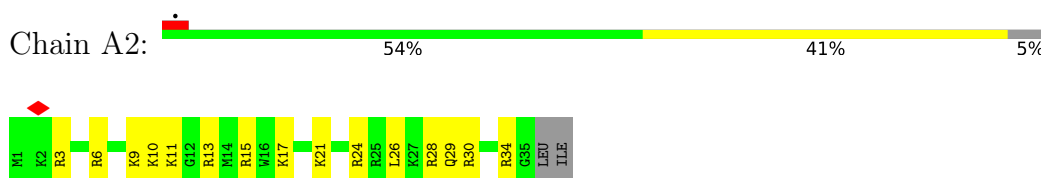
- Molecule 1: RNA-binding protein



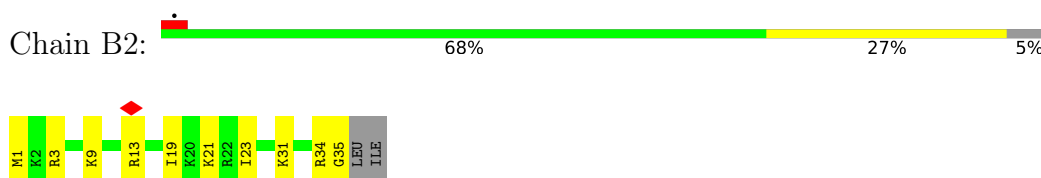
- Molecule 1: RNA-binding protein



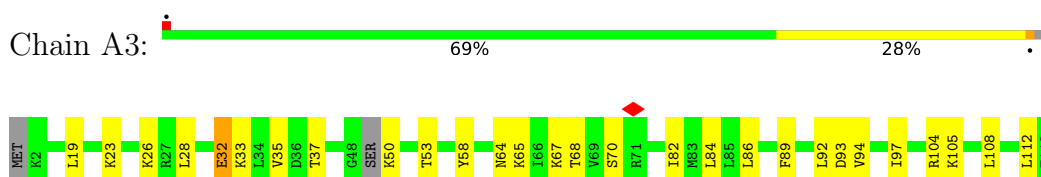
- Molecule 2: Small ribosomal subunit protein eS32

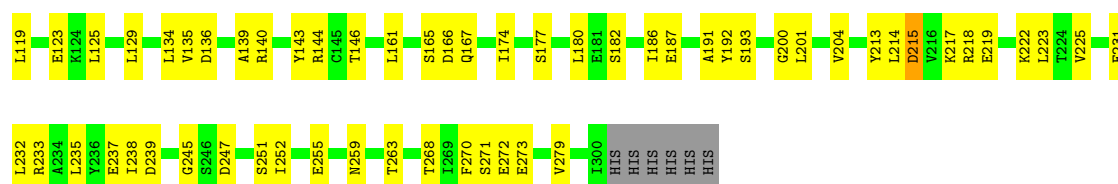


- Molecule 2: Small ribosomal subunit protein eS32



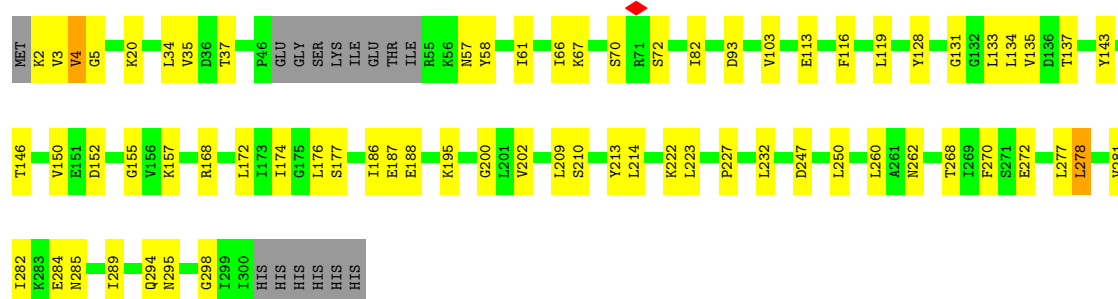
- Molecule 3: Archaeal Ribosome Dimerizing Factor (aRDF)





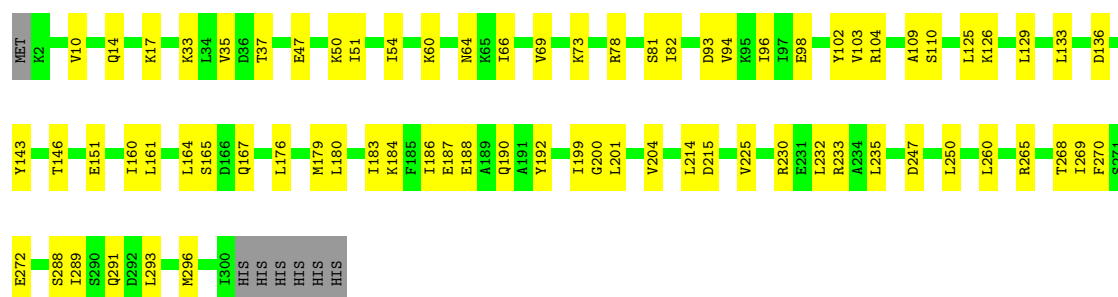
• Molecule 3: Archaeal Ribosome Dimerizing Factor (aRDF)

Chain A4: 73% 22% 5%



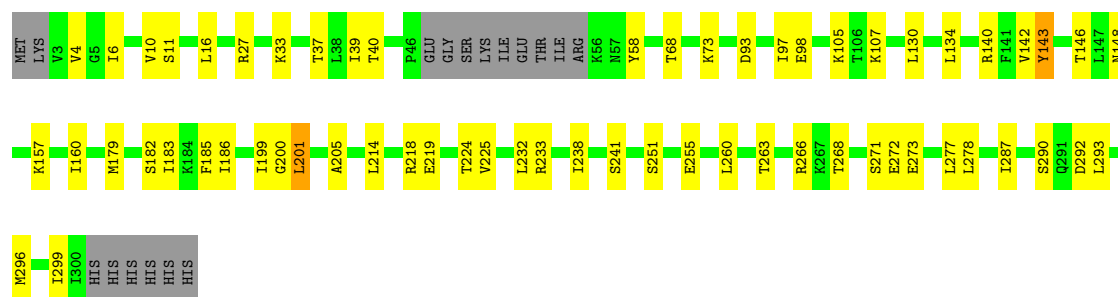
• Molecule 3: Archaeal Ribosome Dimerizing Factor (aRDF)

Chain B3: 74% 24%



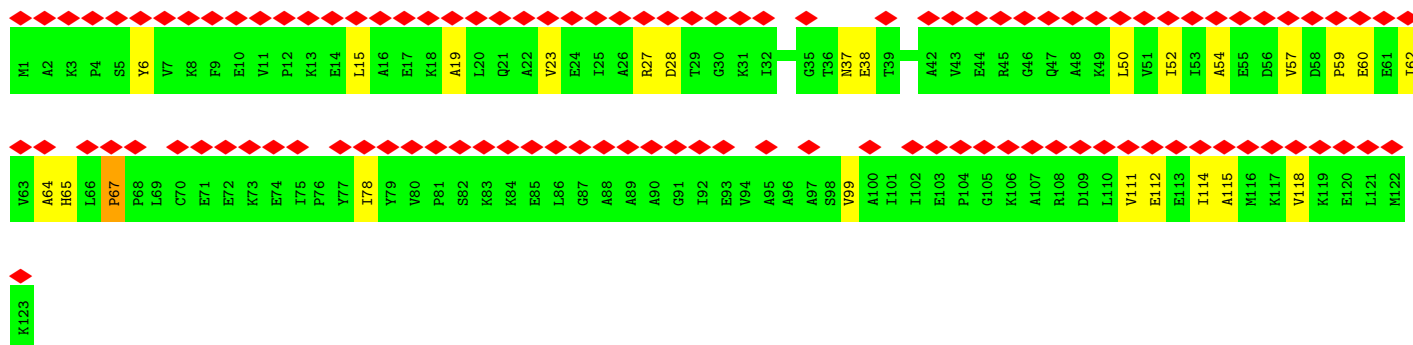
• Molecule 3: Archaeal Ribosome Dimerizing Factor (aRDF)

Chain B4: 74% 20% 6%

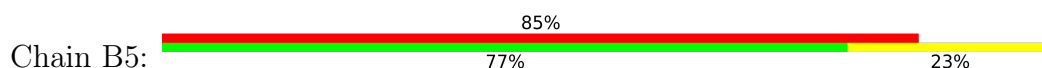


• Molecule 4: Large ribosomal subunit protein eL8

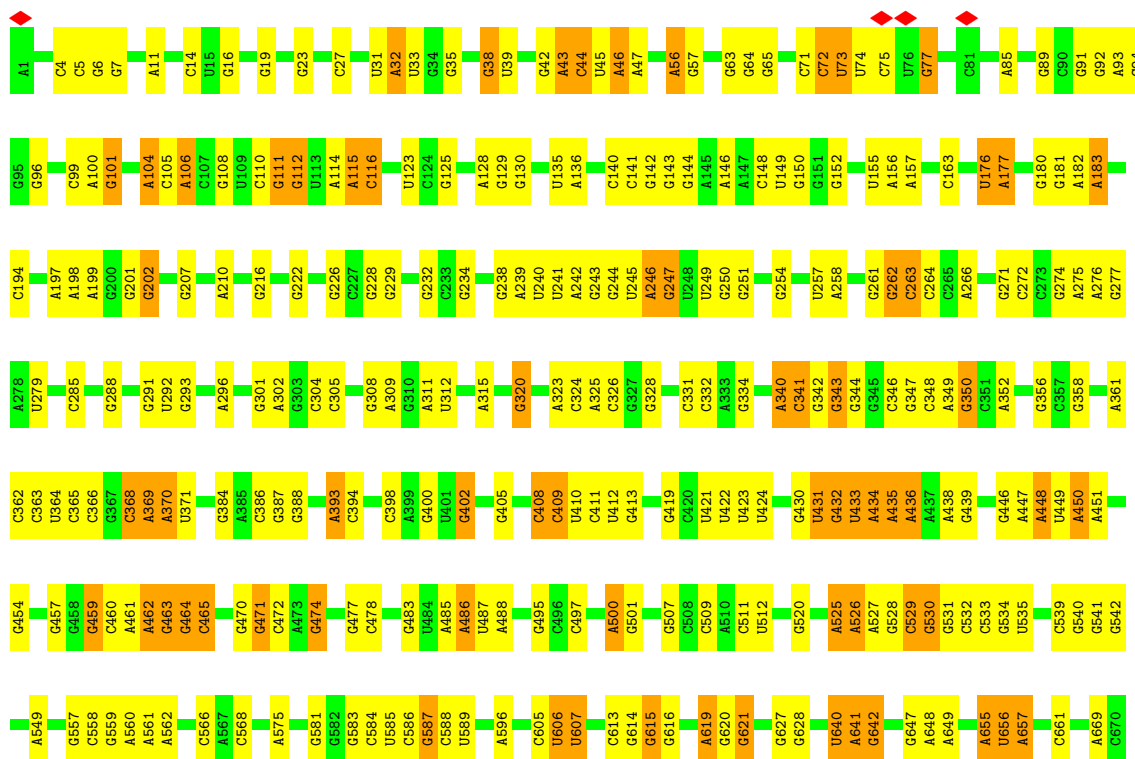
Chain A5: 88% 80% 20%

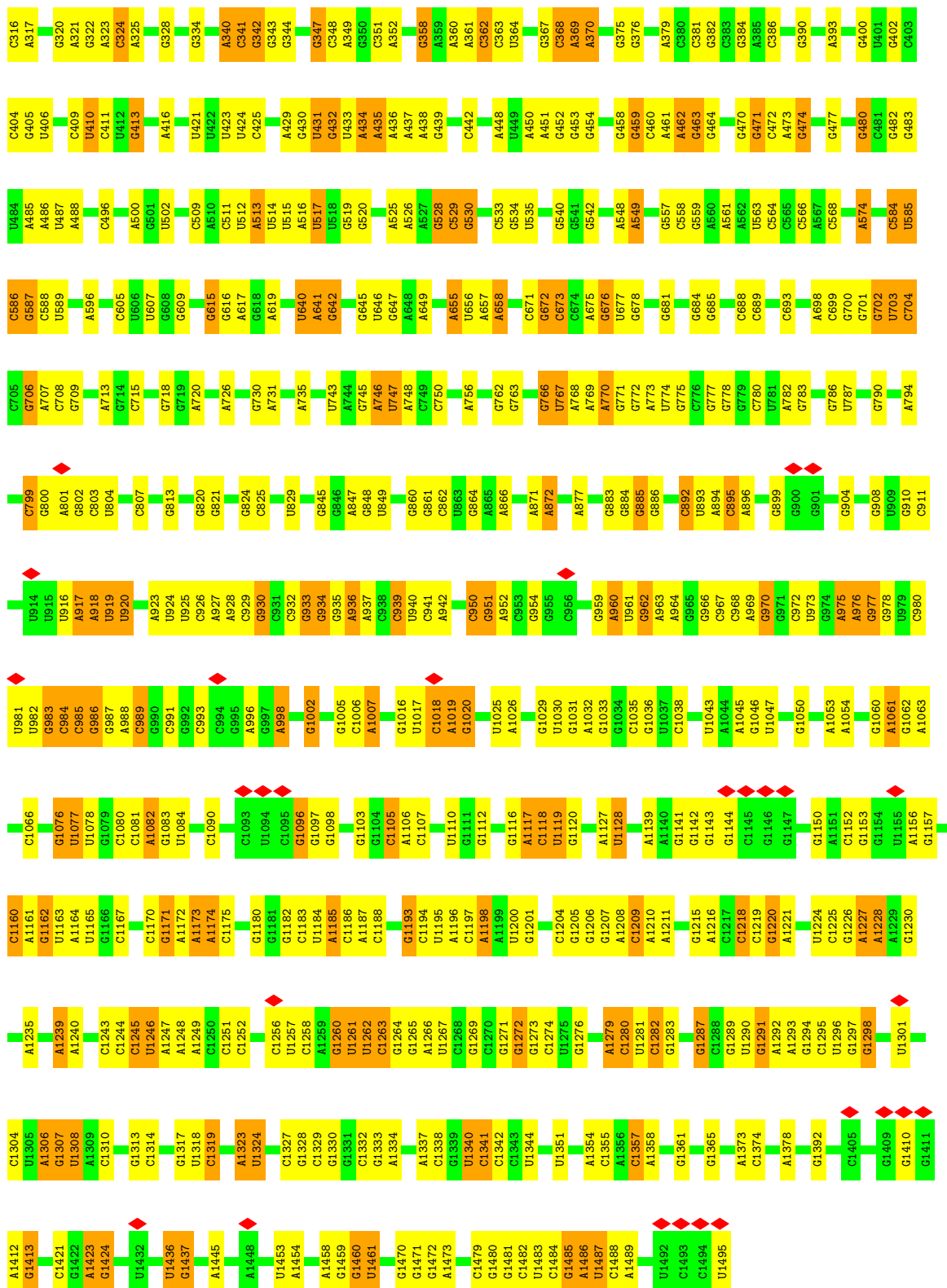


- Molecule 4: Large ribosomal subunit protein eL8

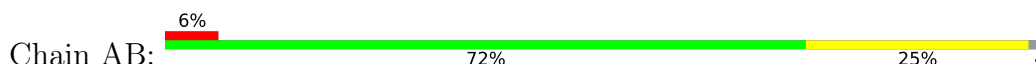


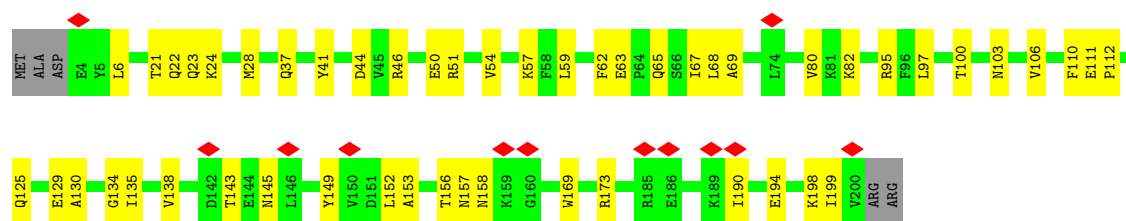
- Molecule 5: 16S rRNA





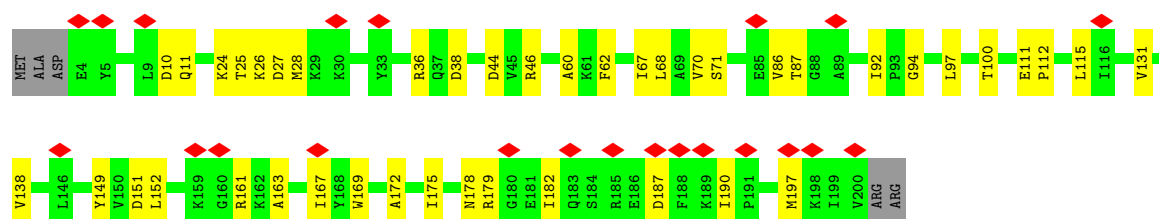
• Molecule 6: Small ribosomal subunit protein uS2





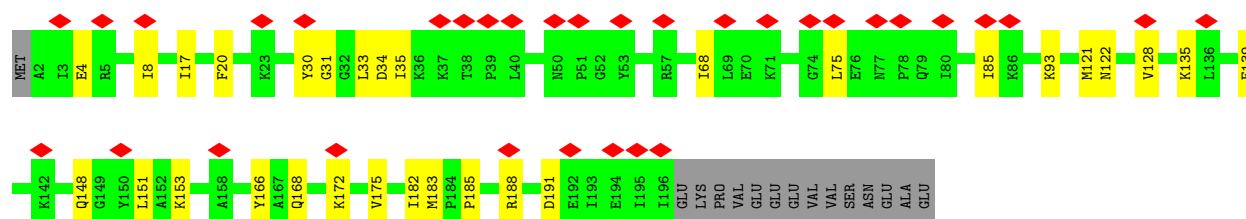
• Molecule 6: Small ribosomal subunit protein uS2

Chain BB: 11% 76% 21%



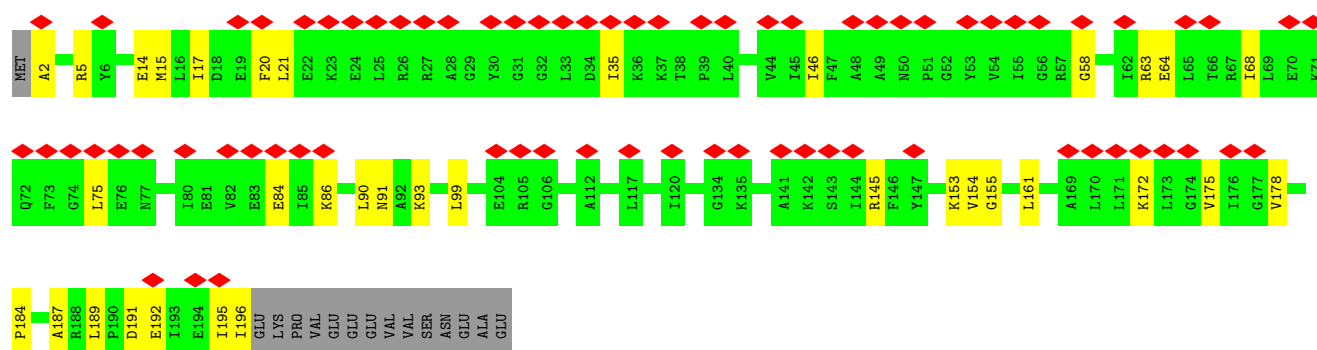
• Molecule 7: Small ribosomal subunit protein uS3

Chain AC: 16% 79% 14% 7%



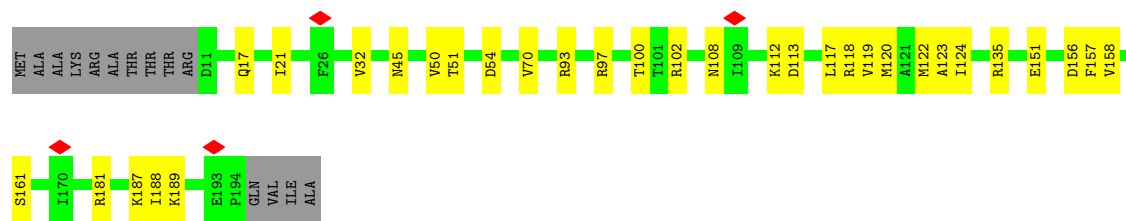
• Molecule 7: Small ribosomal subunit protein uS3

Chain BC: 35% 76% 17% 7%



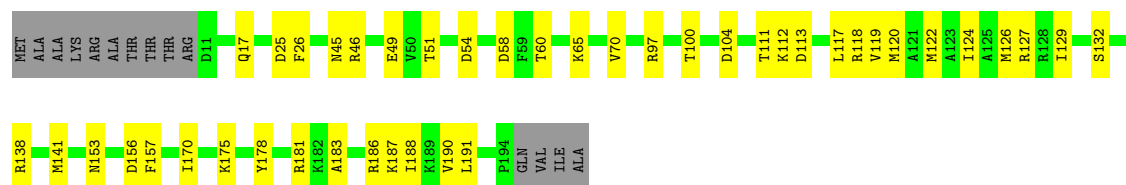
• Molecule 8: Small ribosomal subunit protein eS1

Chain AD: 77% 16% 7%



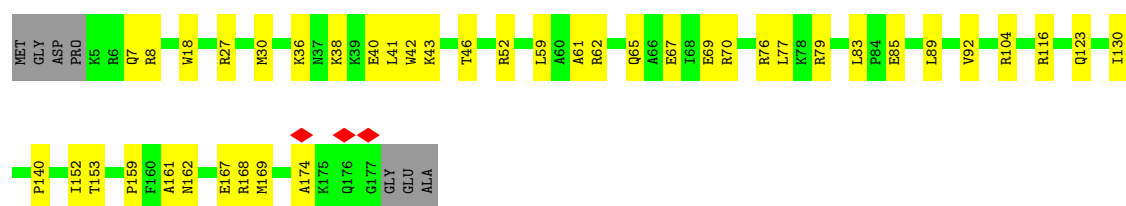
- Molecule 8: Small ribosomal subunit protein eS1

Chain BD: 71% 22% 7%



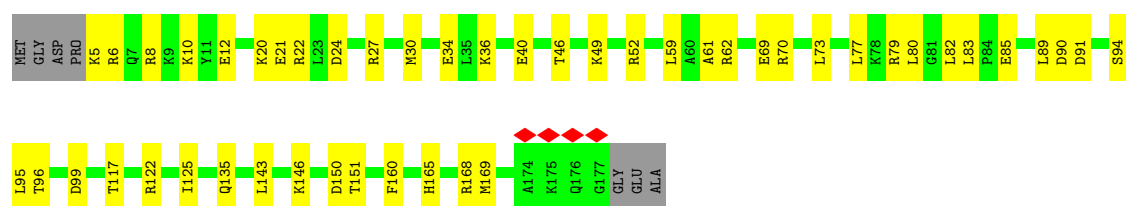
- Molecule 9: Small ribosomal subunit protein uS4

Chain AE: 73% 23% .



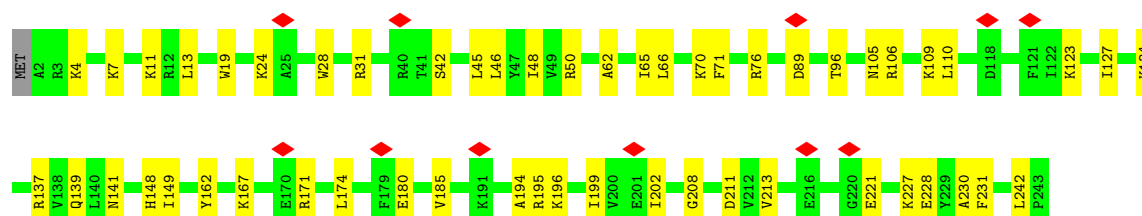
- Molecule 9: Small ribosomal subunit protein uS4

Chain BE: 69% 27% .



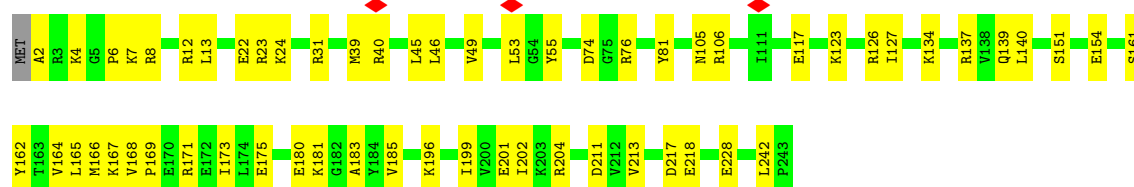
- Molecule 10: Small ribosomal subunit protein eS4

Chain AF: 5% 78% 22%



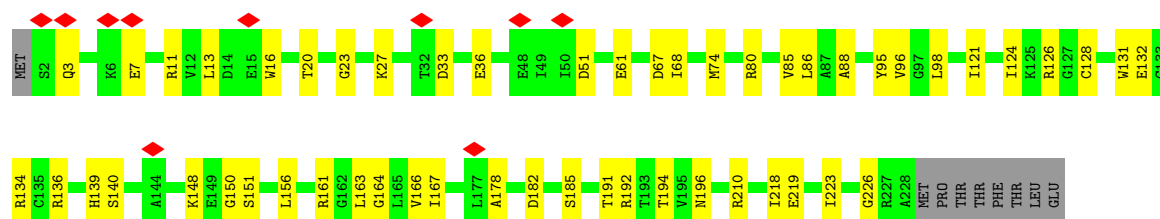
- Molecule 10: Small ribosomal subunit protein eS4

Chain BF:  75% 24%



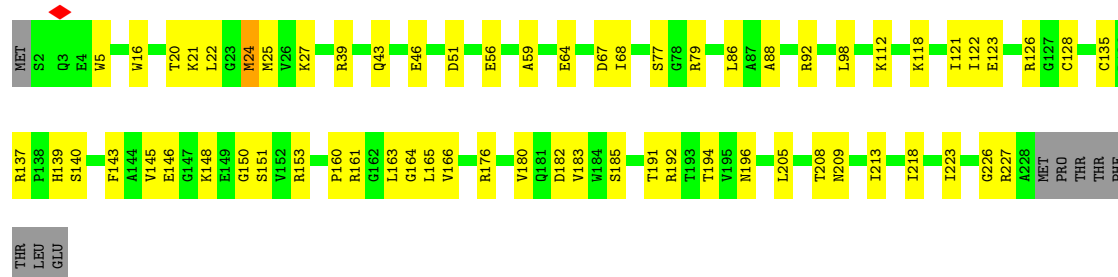
- Molecule 11: Small ribosomal subunit protein uS5

Chain AG:  74% 22%



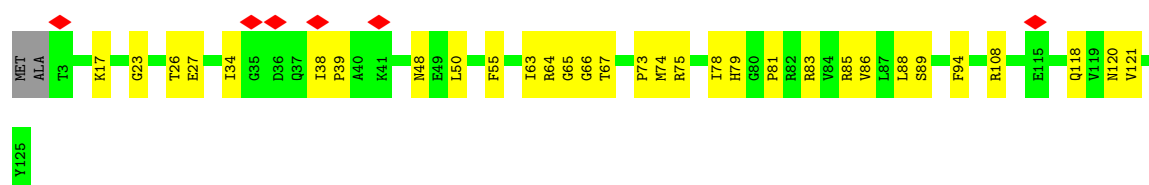
- Molecule 11: Small ribosomal subunit protein uS5

Chain BG:  69% 27%



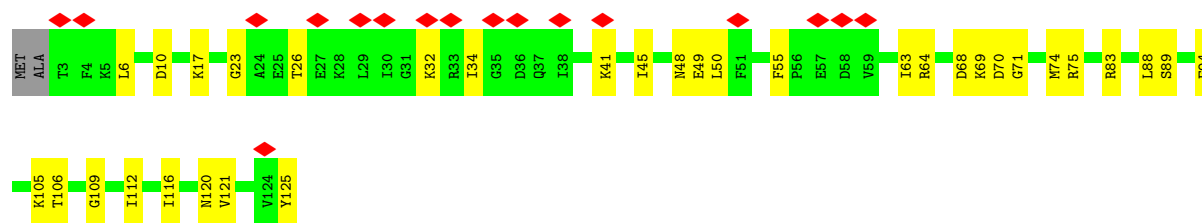
- Molecule 12: Small ribosomal subunit protein eS6

Chain AH:  5% 74% 21%

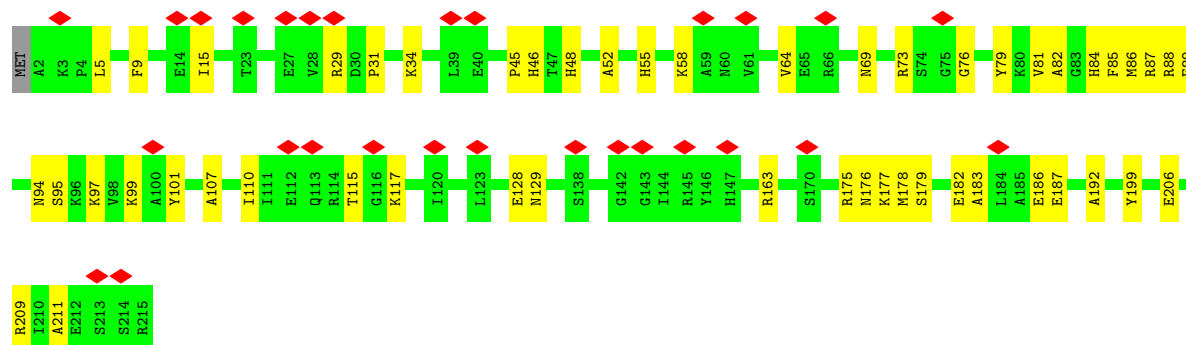
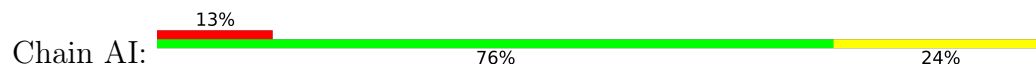


- Molecule 12: Small ribosomal subunit protein eS6

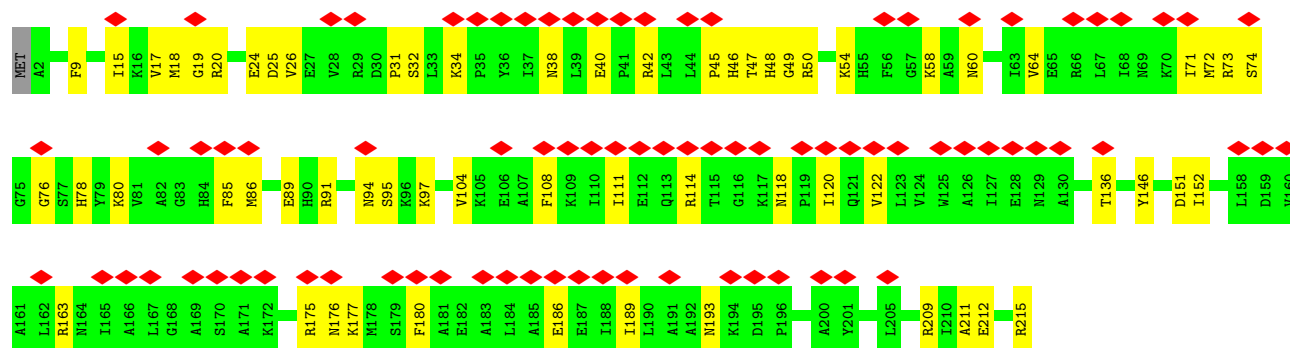
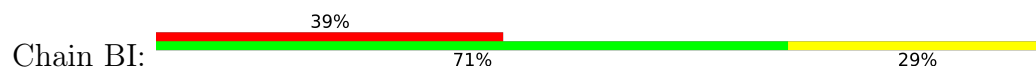
Chain BH:  14% 72% 14%



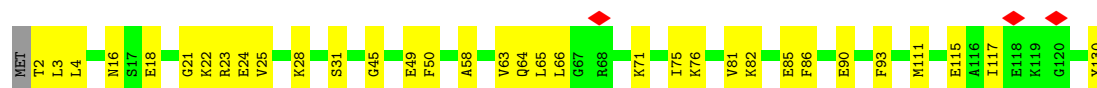
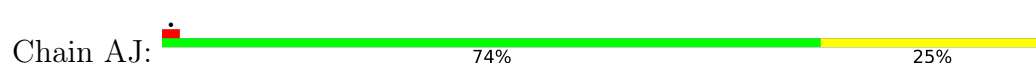
- Molecule 13: Small ribosomal subunit protein uS7



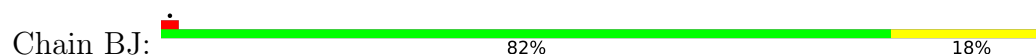
- Molecule 13: Small ribosomal subunit protein uS7

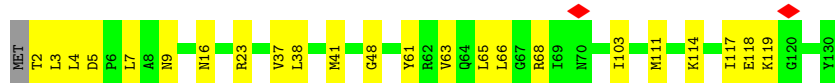


- Molecule 14: Small ribosomal subunit protein uS8

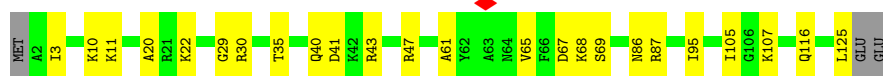
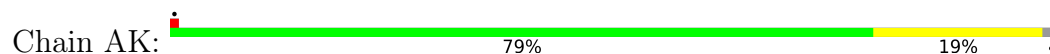


- Molecule 14: Small ribosomal subunit protein uS8

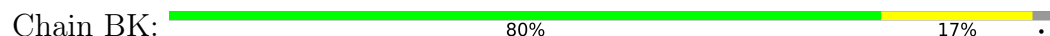




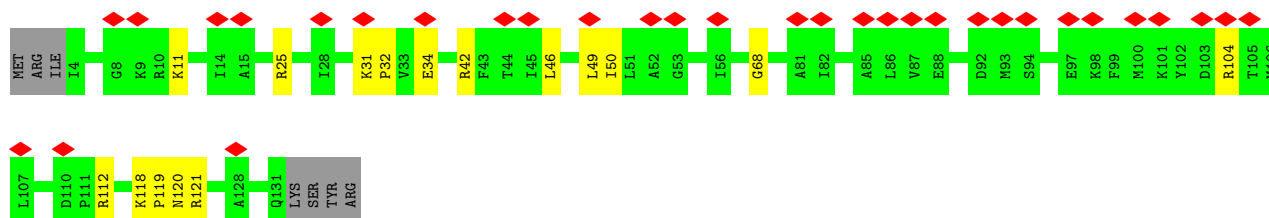
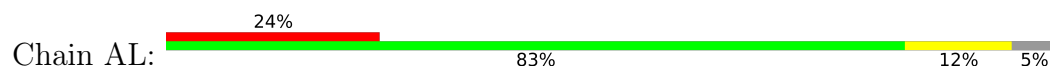
- Molecule 15: Small ribosomal subunit protein eS8



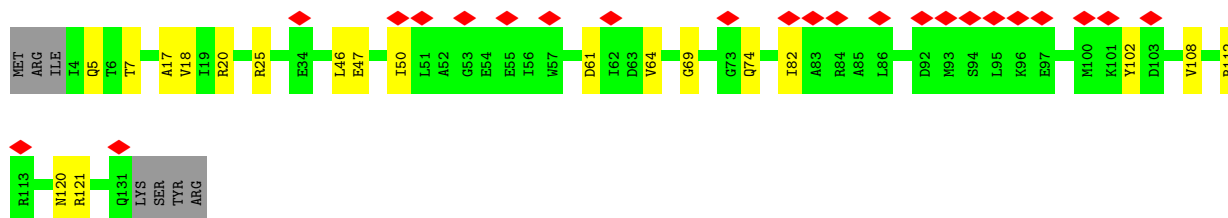
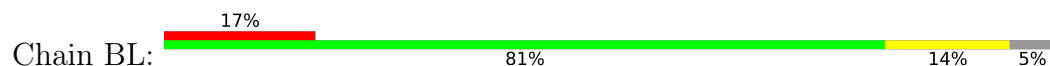
- Molecule 15: Small ribosomal subunit protein eS8



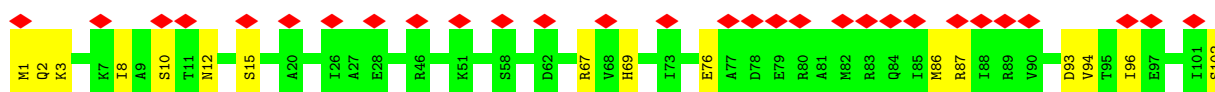
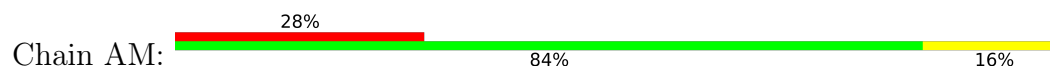
- Molecule 16: Small ribosomal subunit protein uS9



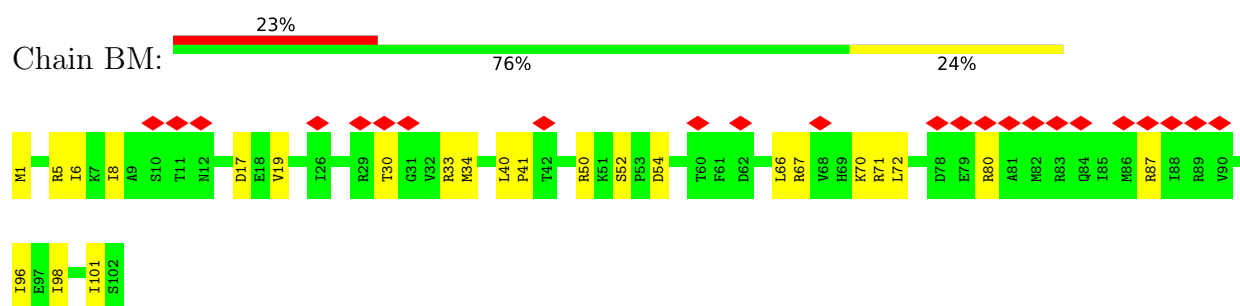
- Molecule 16: Small ribosomal subunit protein uS9



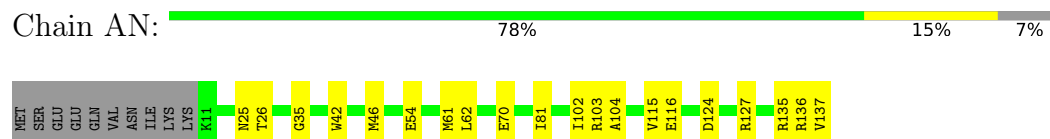
- Molecule 17: Small ribosomal subunit protein uS10



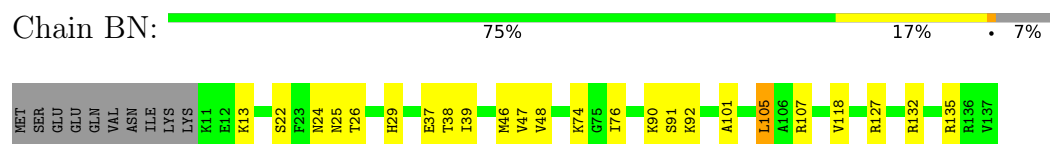
- Molecule 17: Small ribosomal subunit protein uS10



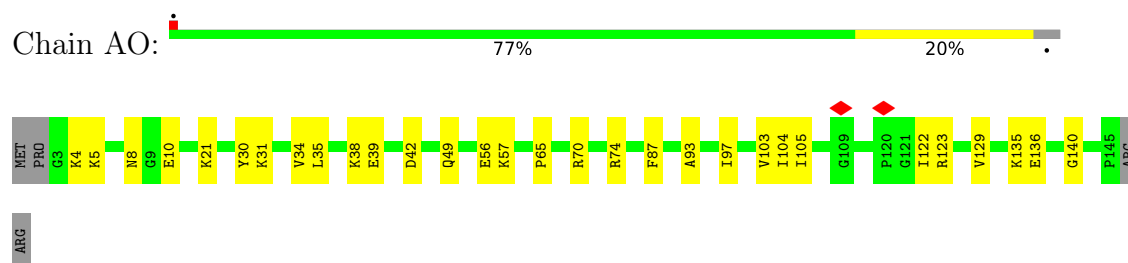
- Molecule 18: Small ribosomal subunit protein uS11



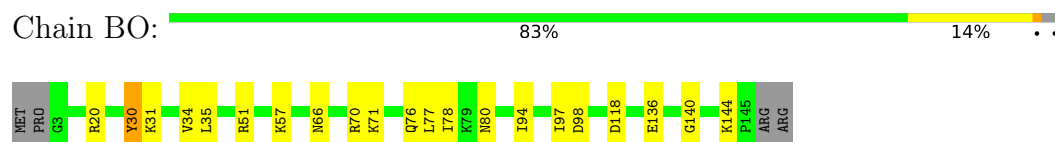
- Molecule 18: Small ribosomal subunit protein uS11



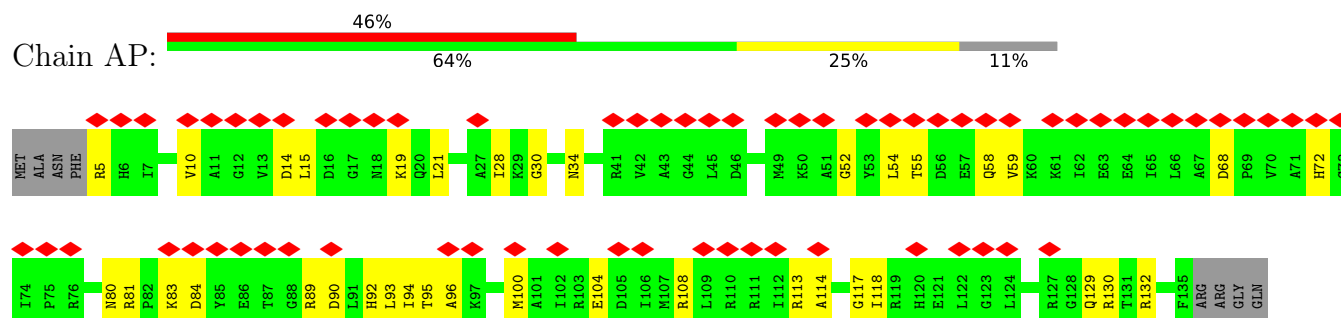
- Molecule 19: Small ribosomal subunit protein uS12



- Molecule 19: Small ribosomal subunit protein uS12

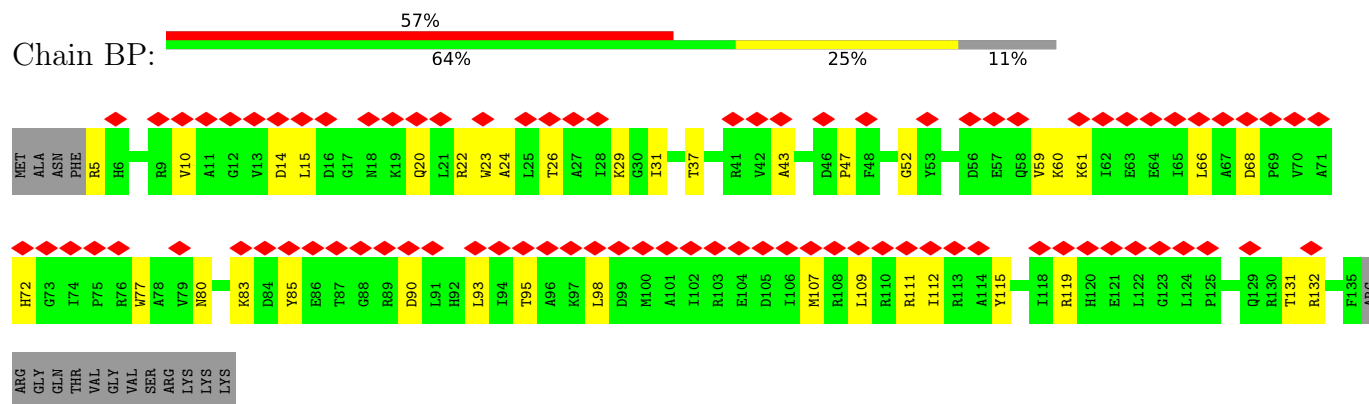


- Molecule 20: Small ribosomal subunit protein uS13

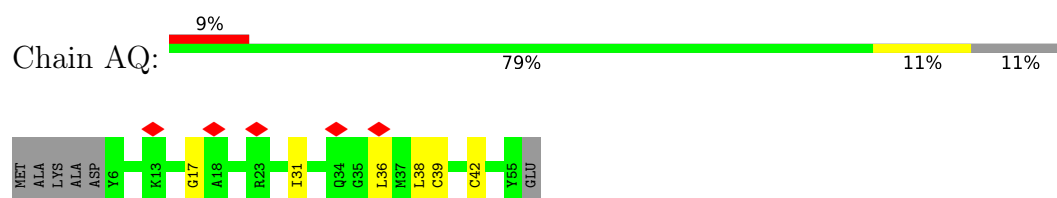


THR
VAL
GLY
VAL
SER
ARG
LYS
LYS

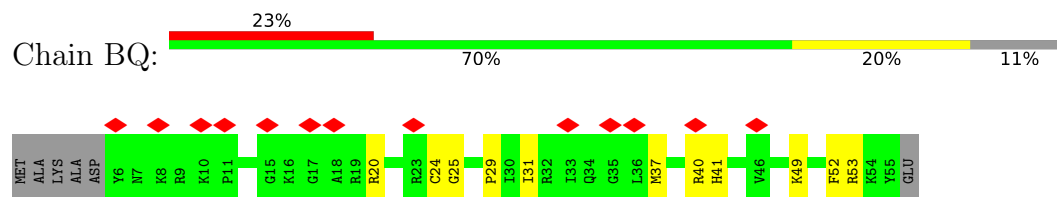
- Molecule 20: Small ribosomal subunit protein uS13



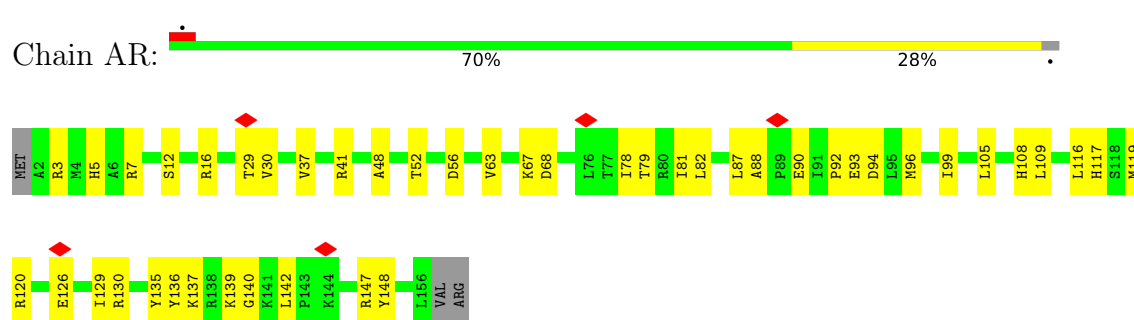
- Molecule 21: Small ribosomal subunit protein uS14



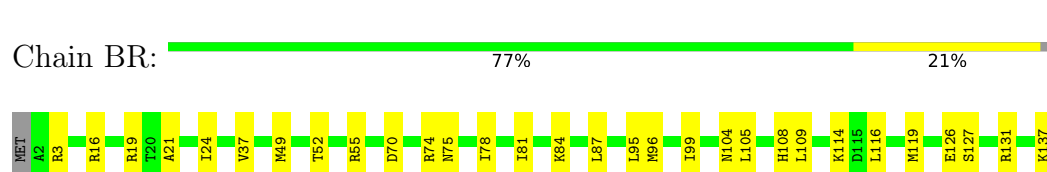
- Molecule 21: Small ribosomal subunit protein uS14

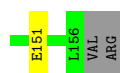


- Molecule 22: Small ribosomal subunit protein uS15



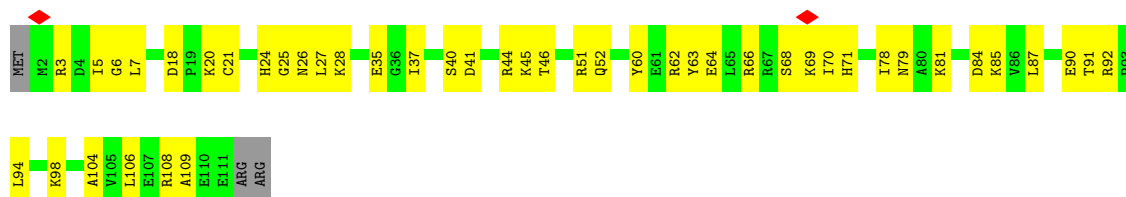
- Molecule 22: Small ribosomal subunit protein uS15





- Molecule 23: Small ribosomal subunit protein uS17

Chain AS: 58% 40%



- Molecule 23: Small ribosomal subunit protein uS17

Chain BS: 75% 22%



- Molecule 24: Small ribosomal subunit protein eS17

Chain AT: 7% 69% 25% 6%



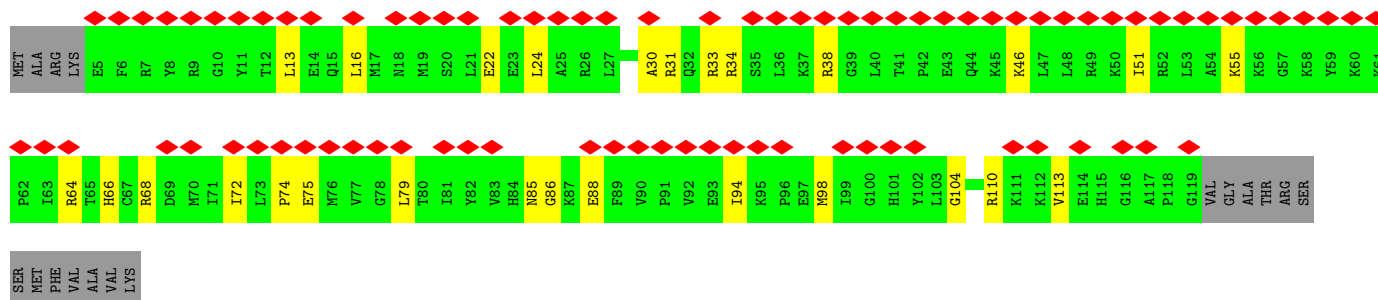
- Molecule 24: Small ribosomal subunit protein eS17

Chain BT: 67% 27% 6%

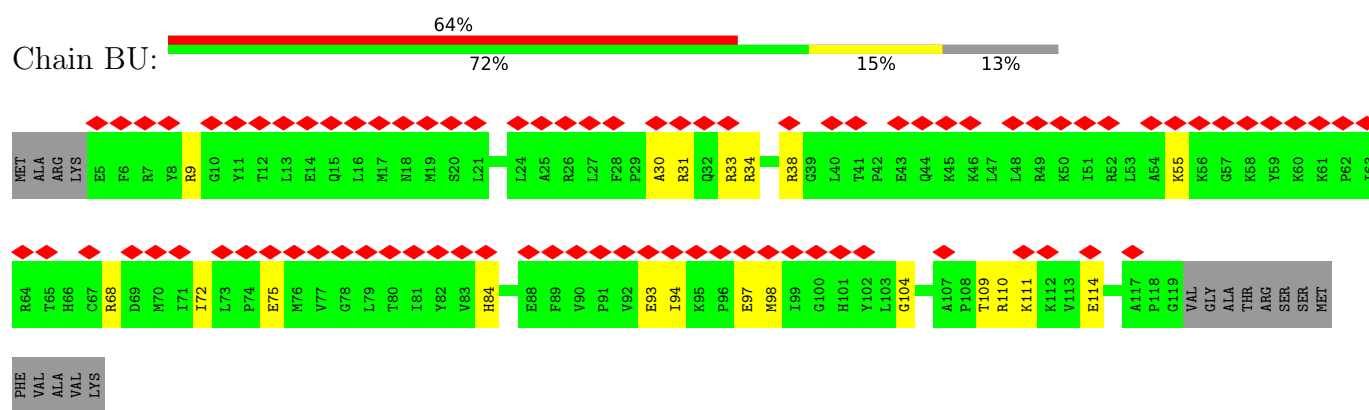


- Molecule 25: Small ribosomal subunit protein uS19

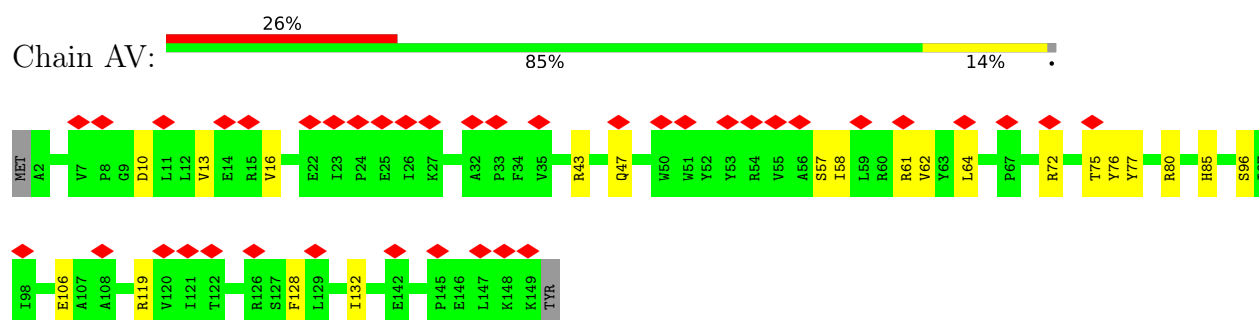
Chain AU: 64% 67% 20% 13%



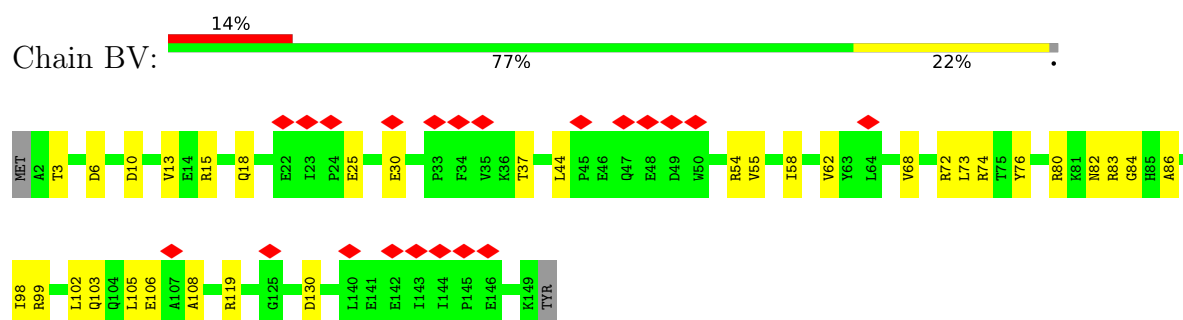
- Molecule 25: Small ribosomal subunit protein uS19



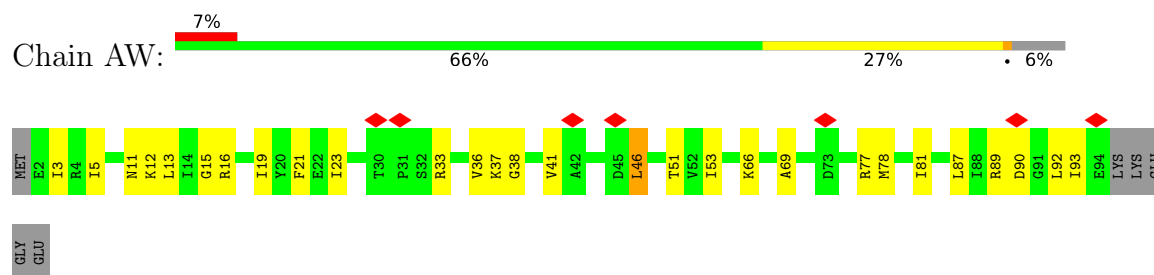
- Molecule 26: Small ribosomal subunit protein eS19



- Molecule 26: Small ribosomal subunit protein eS19

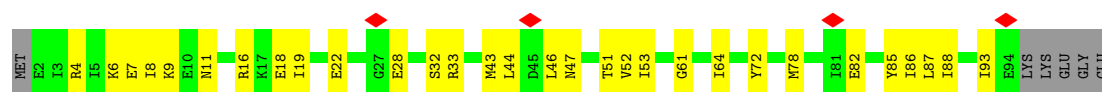


- Molecule 27: Small ribosomal subunit protein eS24

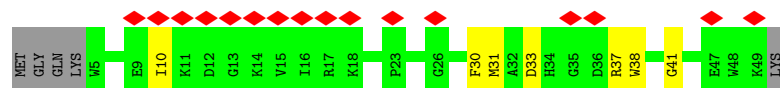
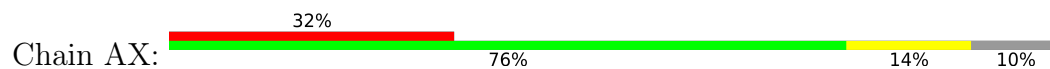


- Molecule 27: Small ribosomal subunit protein eS24

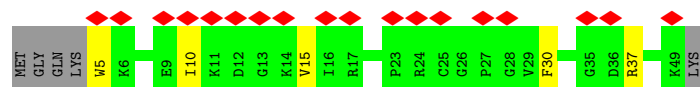
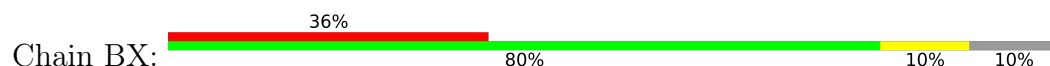




- Molecule 28: Small ribosomal subunit protein eS31



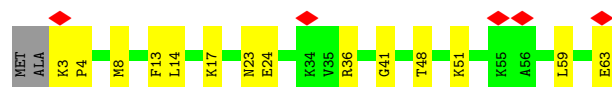
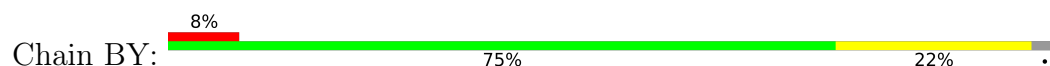
- Molecule 28: Small ribosomal subunit protein eS31



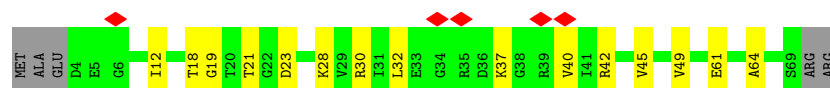
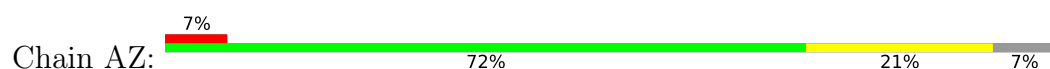
- Molecule 29: Small ribosomal subunit protein eS27



- Molecule 29: Small ribosomal subunit protein eS27



- Molecule 30: Small ribosomal subunit protein eS28



- Molecule 30: Small ribosomal subunit protein eS28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	63890	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.620	Depositor
Minimum map value	-7.838	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.848	Depositor
Recommended contour level	3	Depositor
Map size (Å)	480.384, 480.384, 480.384	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	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	A1	0.27	0/485	0.51	0/656
1	B1	0.26	0/485	0.44	0/656
2	A2	0.42	0/341	0.65	0/440
2	B2	0.34	0/341	0.61	0/440
3	A3	0.30	0/2407	0.48	0/3233
3	A4	0.33	0/2353	0.51	1/3161 (0.0%)
3	B3	0.28	0/2414	0.49	0/3244
3	B4	0.31	0/2333	0.51	0/3136
4	A5	0.21	0/951	0.48	1/1281 (0.1%)
4	B5	0.19	0/951	0.38	0/1281
5	AA	0.30	0/35966	0.40	0/56138
5	BA	0.30	0/35966	0.39	0/56138
6	AB	0.24	0/1610	0.45	0/2177
6	BB	0.24	0/1610	0.45	0/2177
7	AC	0.19	0/1554	0.43	0/2087
7	BC	0.20	0/1554	0.39	0/2087
8	AD	0.27	0/1537	0.50	0/2060
8	BD	0.27	0/1537	0.44	0/2060
9	AE	0.25	0/1478	0.47	0/1980
9	BE	0.25	0/1478	0.41	0/1980
10	AF	0.26	0/2030	0.46	0/2739
10	BF	0.23	0/2030	0.42	0/2739
11	AG	0.27	0/1824	0.46	0/2457
11	BG	0.27	0/1824	0.46	0/2457
12	AH	0.21	0/986	0.41	0/1320
12	BH	0.23	0/986	0.41	0/1320
13	AI	0.21	0/1765	0.46	0/2371
13	BI	0.22	0/1765	0.51	0/2371
14	AJ	0.25	0/1049	0.50	0/1408
14	BJ	0.30	0/1049	0.55	0/1408
15	AK	0.23	0/986	0.41	0/1315
15	BK	0.23	0/986	0.36	0/1315
16	AL	0.28	0/1021	0.54	0/1369
16	BL	0.19	0/1021	0.42	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
17	AM	0.20	0/830	0.42	0/1113
17	BM	0.22	0/830	0.44	0/1113
18	AN	0.28	0/972	0.47	0/1309
18	BN	0.30	0/972	0.44	0/1309
19	AO	0.33	0/1134	0.51	0/1508
19	BO	0.28	0/1134	0.47	0/1508
20	AP	0.20	0/1070	0.43	0/1440
20	BP	0.32	1/1070 (0.1%)	0.51	0/1440
21	AQ	0.20	0/426	0.48	0/562
21	BQ	0.32	0/426	0.67	1/562 (0.2%)
22	AR	0.27	0/1311	0.49	0/1763
22	BR	0.28	0/1311	0.52	0/1763
23	AS	0.26	0/925	0.49	0/1249
23	BS	0.28	0/925	0.44	0/1249
24	AT	0.23	0/528	0.51	0/701
24	BT	0.22	0/528	0.47	0/701
25	AU	0.20	0/968	0.45	0/1293
25	BU	0.21	0/968	0.46	0/1293
26	AV	0.19	0/1238	0.43	0/1668
26	BV	0.19	0/1238	0.39	0/1668
27	AW	0.23	0/790	0.54	0/1061
27	BW	0.22	0/790	0.50	0/1061
28	AX	0.18	0/381	0.43	0/509
28	BX	0.19	0/381	0.46	0/509
29	AY	0.23	0/472	0.40	0/634
29	BY	0.24	0/472	0.51	0/634
30	AZ	0.20	0/525	0.38	0/703
30	BZ	0.19	0/525	0.39	0/703
All	All	0.28	1/139813 (0.0%)	0.43	3/203396 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
20	BP	47	PRO	C-O	-7.08	1.14	1.24

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	BQ	29	PRO	N-CA-CB	-7.11	95.78	103.25
3	A4	67	LYS	N-CA-C	-6.29	106.58	114.56
4	A5	67	PRO	CB-CG-CD	-5.62	88.12	106.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A1	471	0	455	14	0
1	B1	471	0	457	13	0
2	A2	335	0	396	16	0
2	B2	335	0	396	11	0
3	A3	2375	0	2527	60	0
3	A4	2321	0	2470	45	0
3	B3	2381	0	2533	46	0
3	B4	2301	0	2444	44	0
4	A5	939	0	994	16	0
4	B5	939	0	994	20	0
5	AA	32135	0	16231	449	0
5	BA	32135	0	16231	433	0
6	AB	1579	0	1638	35	0
6	BB	1579	0	1638	29	0
7	AC	1532	0	1622	22	0
7	BC	1532	0	1622	28	0
8	AD	1511	0	1595	21	0
8	BD	1511	0	1595	29	0
9	AE	1455	0	1531	30	0
9	BE	1455	0	1531	39	0
10	AF	1981	0	2051	41	0
10	BF	1981	0	2051	42	0
11	AG	1794	0	1850	39	0
11	BG	1794	0	1850	50	0
12	AH	971	0	1027	26	0
12	BH	971	0	1027	25	0
13	AI	1728	0	1775	36	0
13	BI	1728	0	1775	48	0
14	AJ	1028	0	1065	23	0
14	BJ	1028	0	1065	21	0
15	AK	977	0	1064	20	0
15	BK	977	0	1064	15	0
16	AL	1006	0	1052	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	BL	1006	0	1052	18	0
17	AM	822	0	870	10	0
17	BM	822	0	870	16	0
18	AN	954	0	981	16	0
18	BN	954	0	981	19	0
19	AO	1118	0	1214	29	0
19	BO	1118	0	1214	15	0
20	AP	1052	0	1094	26	0
20	BP	1052	0	1094	30	0
21	AQ	417	0	445	6	0
21	BQ	417	0	445	10	0
22	AR	1283	0	1358	37	0
22	BR	1283	0	1358	33	0
23	AS	903	0	922	37	0
23	BS	903	0	922	24	0
24	AT	522	0	557	14	0
24	BT	522	0	557	15	0
25	AU	948	0	1007	28	0
25	BU	948	0	1007	20	0
26	AV	1209	0	1254	19	0
26	BV	1209	0	1254	30	0
27	AW	774	0	794	18	0
27	BW	774	0	794	21	0
28	AX	369	0	361	8	0
28	BX	369	0	361	7	0
29	AY	465	0	507	19	0
29	BY	465	0	507	10	0
30	AZ	523	0	551	9	0
30	BZ	523	0	551	13	0
All	All	130980	0	102498	1915	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 9.

The worst 5 of 1915 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)
5:BA:473:A:N6	5:BA:482:G:C2	2.19	1.11
5:BA:777:G:HO2'	14:BJ:2:THR:N	1.51	1.09
5:BA:16:G:H21	5:BA:872:A:H62	1.12	0.97
5:AA:998:A:H61	5:AA:1173:A:H61	1.17	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BA:106:A:H62	5:BA:235:G:N2	1.67	0.91

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A1	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
1	B1	58/60 (97%)	52 (90%)	6 (10%)	0	100	100
2	A2	33/37 (89%)	32 (97%)	1 (3%)	0	100	100
2	B2	33/37 (89%)	32 (97%)	1 (3%)	0	100	100
3	A3	294/306 (96%)	272 (92%)	22 (8%)	0	100	100
3	A4	287/306 (94%)	263 (92%)	22 (8%)	2 (1%)	18	52
3	B3	297/306 (97%)	273 (92%)	23 (8%)	1 (0%)	36	68
3	B4	285/306 (93%)	262 (92%)	23 (8%)	0	100	100
4	A5	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
4	B5	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
6	AB	195/202 (96%)	179 (92%)	16 (8%)	0	100	100
6	BB	195/202 (96%)	188 (96%)	7 (4%)	0	100	100
7	AC	193/210 (92%)	189 (98%)	4 (2%)	0	100	100
7	BC	193/210 (92%)	191 (99%)	2 (1%)	0	100	100
8	AD	182/198 (92%)	179 (98%)	3 (2%)	0	100	100
8	BD	182/198 (92%)	177 (97%)	5 (3%)	0	100	100
9	AE	171/180 (95%)	169 (99%)	2 (1%)	0	100	100
9	BE	171/180 (95%)	167 (98%)	4 (2%)	0	100	100
10	AF	240/243 (99%)	228 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	BF	240/243 (99%)	230 (96%)	10 (4%)	0	100	100
11	AG	225/236 (95%)	210 (93%)	15 (7%)	0	100	100
11	BG	225/236 (95%)	215 (96%)	10 (4%)	0	100	100
12	AH	121/125 (97%)	116 (96%)	5 (4%)	0	100	100
12	BH	121/125 (97%)	119 (98%)	2 (2%)	0	100	100
13	AI	212/215 (99%)	195 (92%)	16 (8%)	1 (0%)	24	59
13	BI	212/215 (99%)	198 (93%)	13 (6%)	1 (0%)	24	59
14	AJ	127/130 (98%)	111 (87%)	16 (13%)	0	100	100
14	BJ	127/130 (98%)	116 (91%)	11 (9%)	0	100	100
15	AK	122/127 (96%)	117 (96%)	5 (4%)	0	100	100
15	BK	122/127 (96%)	117 (96%)	5 (4%)	0	100	100
16	AL	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
16	BL	126/135 (93%)	119 (94%)	7 (6%)	0	100	100
17	AM	100/102 (98%)	98 (98%)	2 (2%)	0	100	100
17	BM	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
18	AN	125/137 (91%)	119 (95%)	6 (5%)	0	100	100
18	BN	125/137 (91%)	117 (94%)	8 (6%)	0	100	100
19	AO	141/147 (96%)	134 (95%)	7 (5%)	0	100	100
19	BO	141/147 (96%)	138 (98%)	3 (2%)	0	100	100
20	AP	129/148 (87%)	124 (96%)	5 (4%)	0	100	100
20	BP	129/148 (87%)	124 (96%)	5 (4%)	0	100	100
21	AQ	48/56 (86%)	42 (88%)	6 (12%)	0	100	100
21	BQ	48/56 (86%)	43 (90%)	5 (10%)	0	100	100
22	AR	153/158 (97%)	147 (96%)	6 (4%)	0	100	100
22	BR	153/158 (97%)	148 (97%)	5 (3%)	0	100	100
23	AS	108/113 (96%)	103 (95%)	5 (5%)	0	100	100
23	BS	108/113 (96%)	104 (96%)	4 (4%)	0	100	100
24	AT	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
24	BT	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
25	AU	113/132 (86%)	111 (98%)	2 (2%)	0	100	100
25	BU	113/132 (86%)	109 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	AV	146/150 (97%)	144 (99%)	2 (1%)	0	100	100
26	BV	146/150 (97%)	143 (98%)	3 (2%)	0	100	100
27	AW	91/99 (92%)	90 (99%)	1 (1%)	0	100	100
27	BW	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
28	AX	43/50 (86%)	41 (95%)	2 (5%)	0	100	100
28	BX	43/50 (86%)	40 (93%)	3 (7%)	0	100	100
29	AY	59/63 (94%)	57 (97%)	2 (3%)	0	100	100
29	BY	59/63 (94%)	55 (93%)	4 (7%)	0	100	100
30	AZ	64/71 (90%)	64 (100%)	0	0	100	100
30	BZ	64/71 (90%)	63 (98%)	1 (2%)	0	100	100
All	All	8177/8652 (94%)	7782 (95%)	390 (5%)	5 (0%)	49	79

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A4	4	VAL
13	BI	15	ILE
13	AI	15	ILE
3	B3	269	ILE
3	A4	66	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A1	53/53 (100%)	53 (100%)	0	100	100
1	B1	53/53 (100%)	52 (98%)	1 (2%)	50	73
2	A2	33/35 (94%)	33 (100%)	0	100	100
2	B2	33/35 (94%)	33 (100%)	0	100	100
3	A3	265/273 (97%)	262 (99%)	3 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A4	259/273 (95%)	258 (100%)	1 (0%)	84	86
3	B3	266/273 (97%)	266 (100%)	0	100	100
3	B4	257/273 (94%)	255 (99%)	2 (1%)	73	82
4	A5	99/99 (100%)	99 (100%)	0	100	100
4	B5	99/99 (100%)	99 (100%)	0	100	100
6	AB	169/173 (98%)	169 (100%)	0	100	100
6	BB	169/173 (98%)	169 (100%)	0	100	100
7	AC	153/167 (92%)	153 (100%)	0	100	100
7	BC	153/167 (92%)	153 (100%)	0	100	100
8	AD	161/171 (94%)	160 (99%)	1 (1%)	78	84
8	BD	161/171 (94%)	160 (99%)	1 (1%)	78	84
9	AE	156/160 (98%)	155 (99%)	1 (1%)	78	84
9	BE	156/160 (98%)	156 (100%)	0	100	100
10	AF	212/213 (100%)	212 (100%)	0	100	100
10	BF	212/213 (100%)	212 (100%)	0	100	100
11	AG	188/197 (95%)	188 (100%)	0	100	100
11	BG	188/197 (95%)	187 (100%)	1 (0%)	81	85
12	AH	107/108 (99%)	107 (100%)	0	100	100
12	BH	107/108 (99%)	107 (100%)	0	100	100
13	AI	183/184 (100%)	181 (99%)	2 (1%)	65	79
13	BI	183/184 (100%)	183 (100%)	0	100	100
14	AJ	107/108 (99%)	107 (100%)	0	100	100
14	BJ	107/108 (99%)	107 (100%)	0	100	100
15	AK	100/103 (97%)	100 (100%)	0	100	100
15	BK	100/103 (97%)	100 (100%)	0	100	100
16	AL	104/111 (94%)	103 (99%)	1 (1%)	68	80
16	BL	104/111 (94%)	104 (100%)	0	100	100
17	AM	91/91 (100%)	91 (100%)	0	100	100
17	BM	91/91 (100%)	91 (100%)	0	100	100
18	AN	94/104 (90%)	94 (100%)	0	100	100
18	BN	94/104 (90%)	93 (99%)	1 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AO	117/121 (97%)	117 (100%)	0	100	100
19	BO	117/121 (97%)	116 (99%)	1 (1%)	70	81
20	AP	108/122 (88%)	108 (100%)	0	100	100
20	BP	108/122 (88%)	108 (100%)	0	100	100
21	AQ	42/46 (91%)	42 (100%)	0	100	100
21	BQ	42/46 (91%)	42 (100%)	0	100	100
22	AR	140/143 (98%)	140 (100%)	0	100	100
22	BR	140/143 (98%)	140 (100%)	0	100	100
23	AS	99/102 (97%)	97 (98%)	2 (2%)	48	72
23	BS	99/102 (97%)	99 (100%)	0	100	100
24	AT	57/61 (93%)	57 (100%)	0	100	100
24	BT	57/61 (93%)	57 (100%)	0	100	100
25	AU	101/114 (89%)	101 (100%)	0	100	100
25	BU	101/114 (89%)	101 (100%)	0	100	100
26	AV	125/127 (98%)	124 (99%)	1 (1%)	73	82
26	BV	125/127 (98%)	125 (100%)	0	100	100
27	AW	84/89 (94%)	82 (98%)	2 (2%)	43	70
27	BW	84/89 (94%)	84 (100%)	0	100	100
28	AX	37/41 (90%)	37 (100%)	0	100	100
28	BX	37/41 (90%)	36 (97%)	1 (3%)	39	68
29	AY	53/54 (98%)	53 (100%)	0	100	100
29	BY	53/54 (98%)	53 (100%)	0	100	100
30	AZ	56/60 (93%)	56 (100%)	0	100	100
30	BZ	56/60 (93%)	56 (100%)	0	100	100
All	All	7105/7406 (96%)	7083 (100%)	22 (0%)	84	88

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B1	7	GLU
8	BD	153	ASN
3	B4	201	LEU
11	BG	24	MET
13	AI	94	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
6	BB	125	GLN
9	BE	164	GLN
27	BW	11	ASN
8	BD	63	HIS
9	BE	165	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	AA	1494/1495 (99%)	325 (21%)	46 (3%)
5	BA	1494/1495 (99%)	317 (21%)	46 (3%)
All	All	2988/2990 (99%)	642 (21%)	92 (3%)

5 of 642 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	AA	4	C
5	AA	32	A
5	AA	35	G
5	AA	38	G
5	AA	39	U

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	BA	368	C
5	BA	960	A
5	BA	431	U
5	BA	672	G
5	BA	1053	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 ⓘ

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.

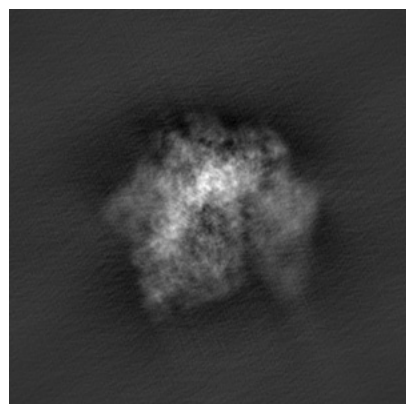
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-50612. These allow visual inspection of the internal detail of the map and identification of artifacts.

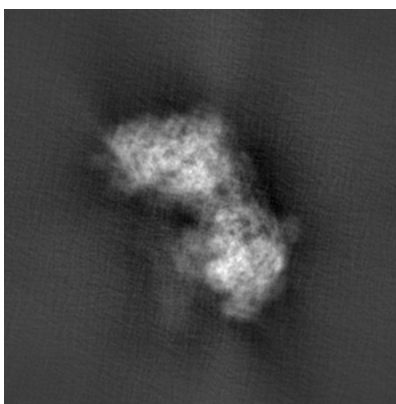
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

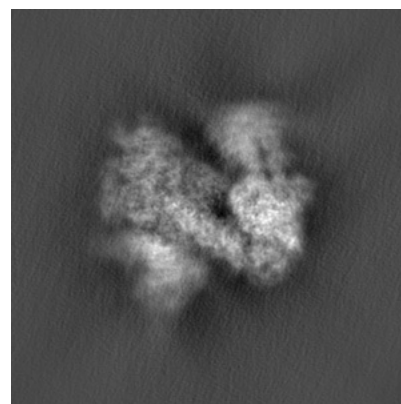
6.1.1 Primary map



X

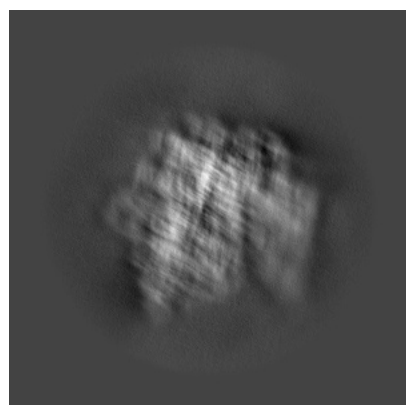


Y

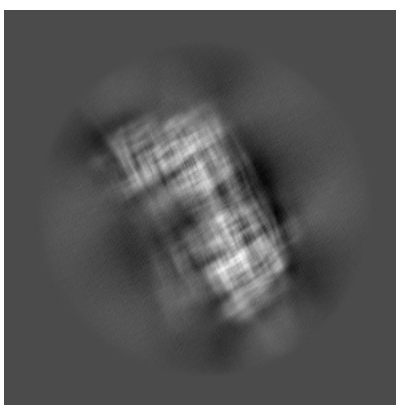


Z

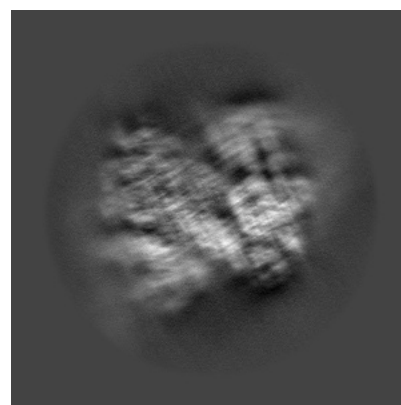
6.1.2 Raw map



X



Y

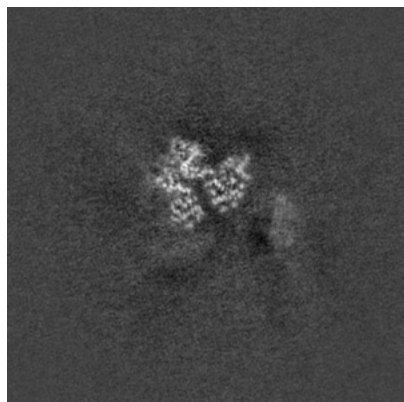


Z

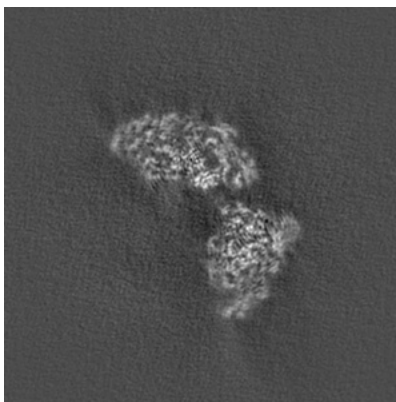
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

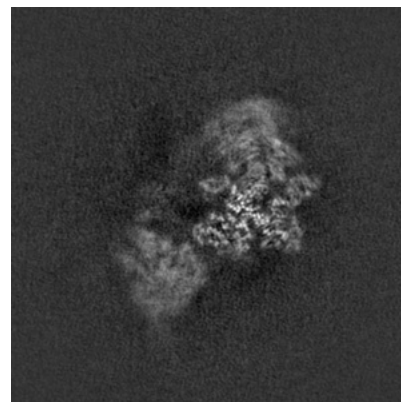
6.2.1 Primary map



X Index: 288

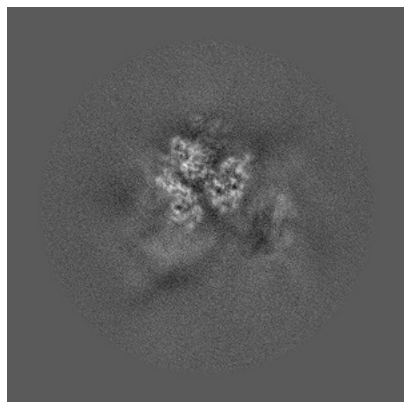


Y Index: 288

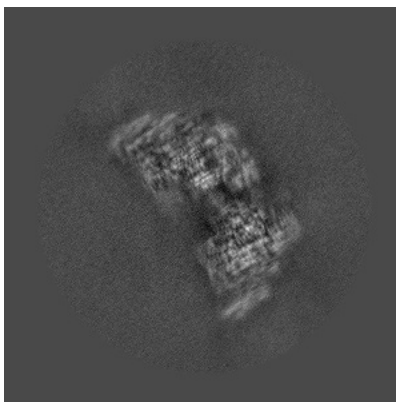


Z Index: 288

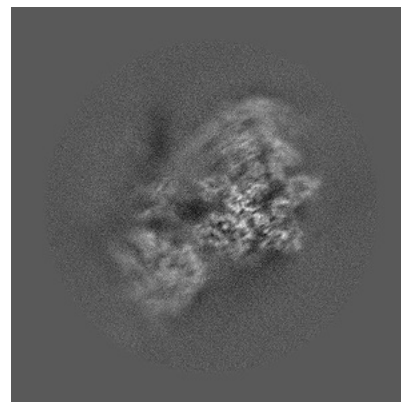
6.2.2 Raw map



X Index: 288



Y Index: 288

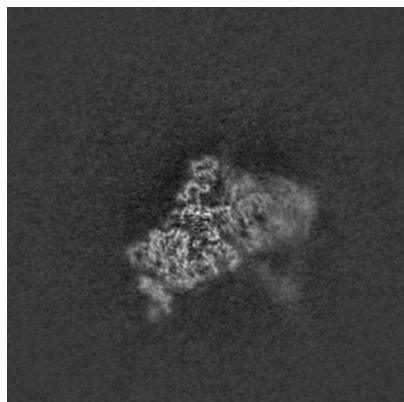


Z Index: 288

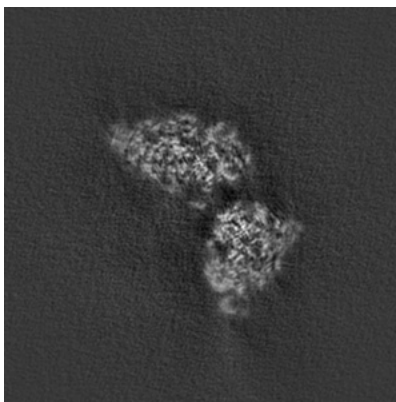
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

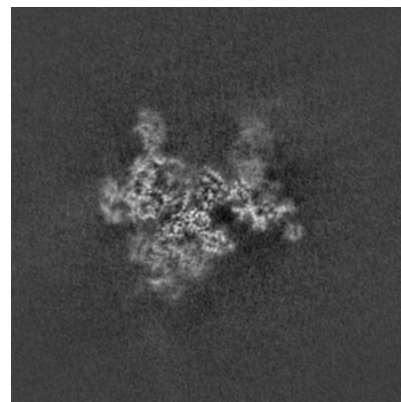
6.3.1 Primary map



X Index: 354

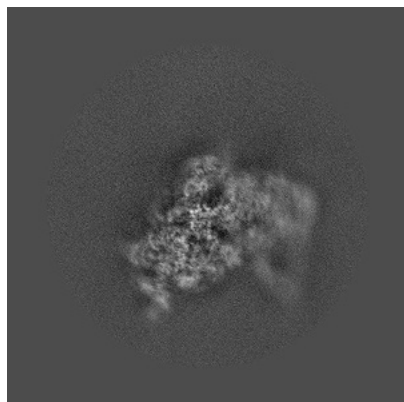


Y Index: 278

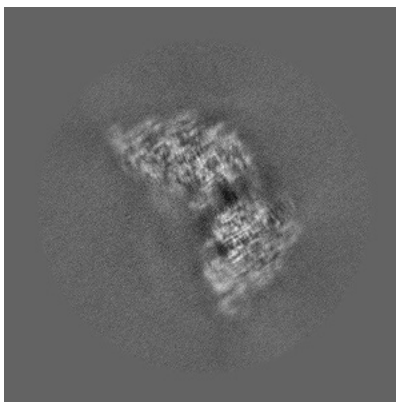


Z Index: 320

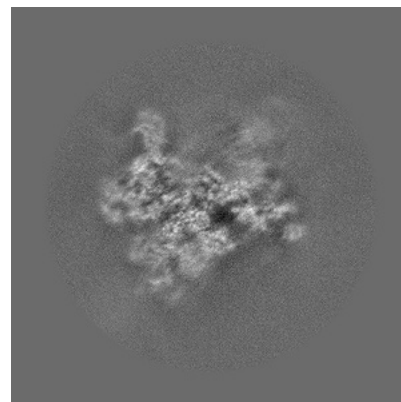
6.3.2 Raw map



X Index: 349



Y Index: 277



Z Index: 320

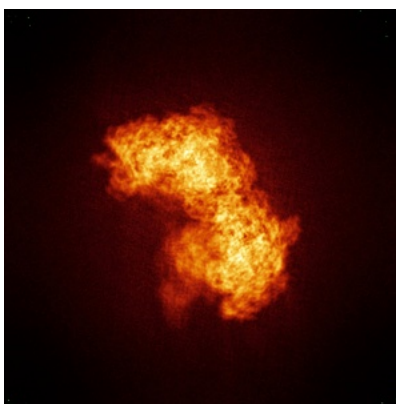
The images above show the largest variance slices of the map in three orthogonal directions.

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

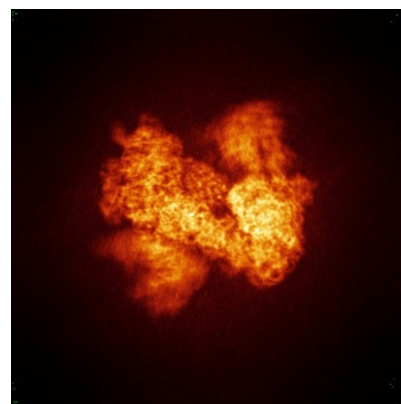
6.4.1 Primary map



X

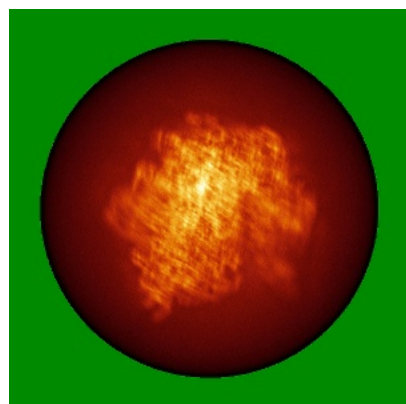


Y

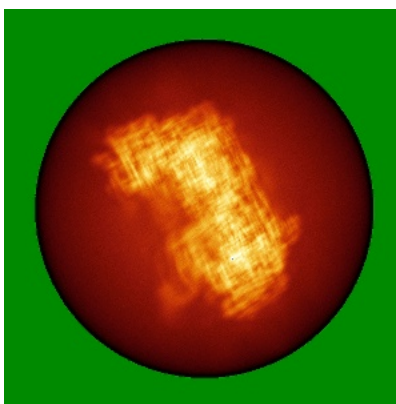


Z

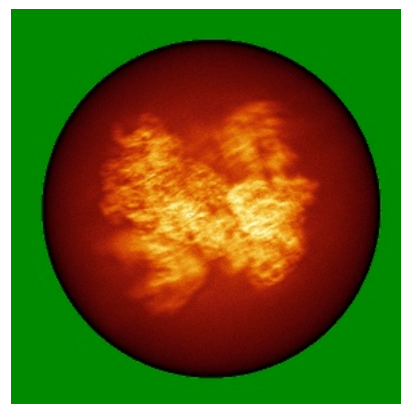
6.4.2 Raw map



X



Y

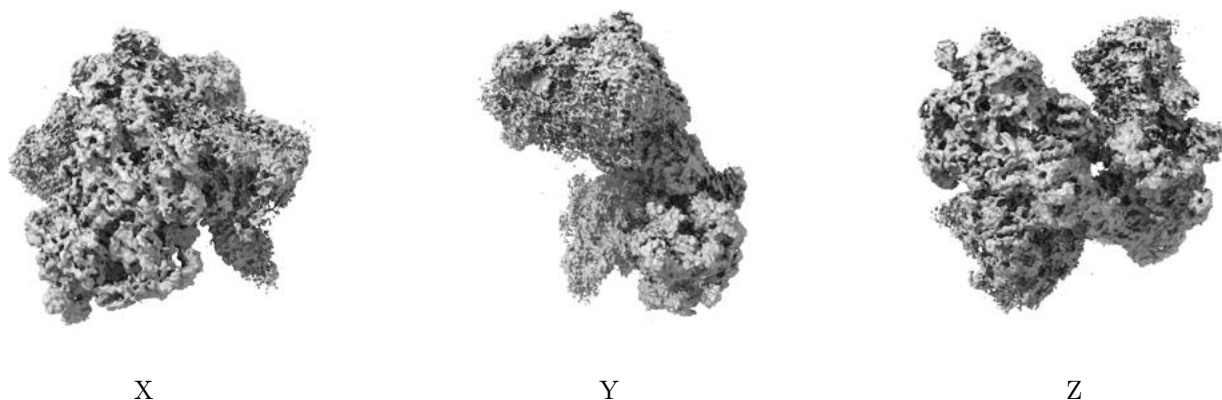


Z

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 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

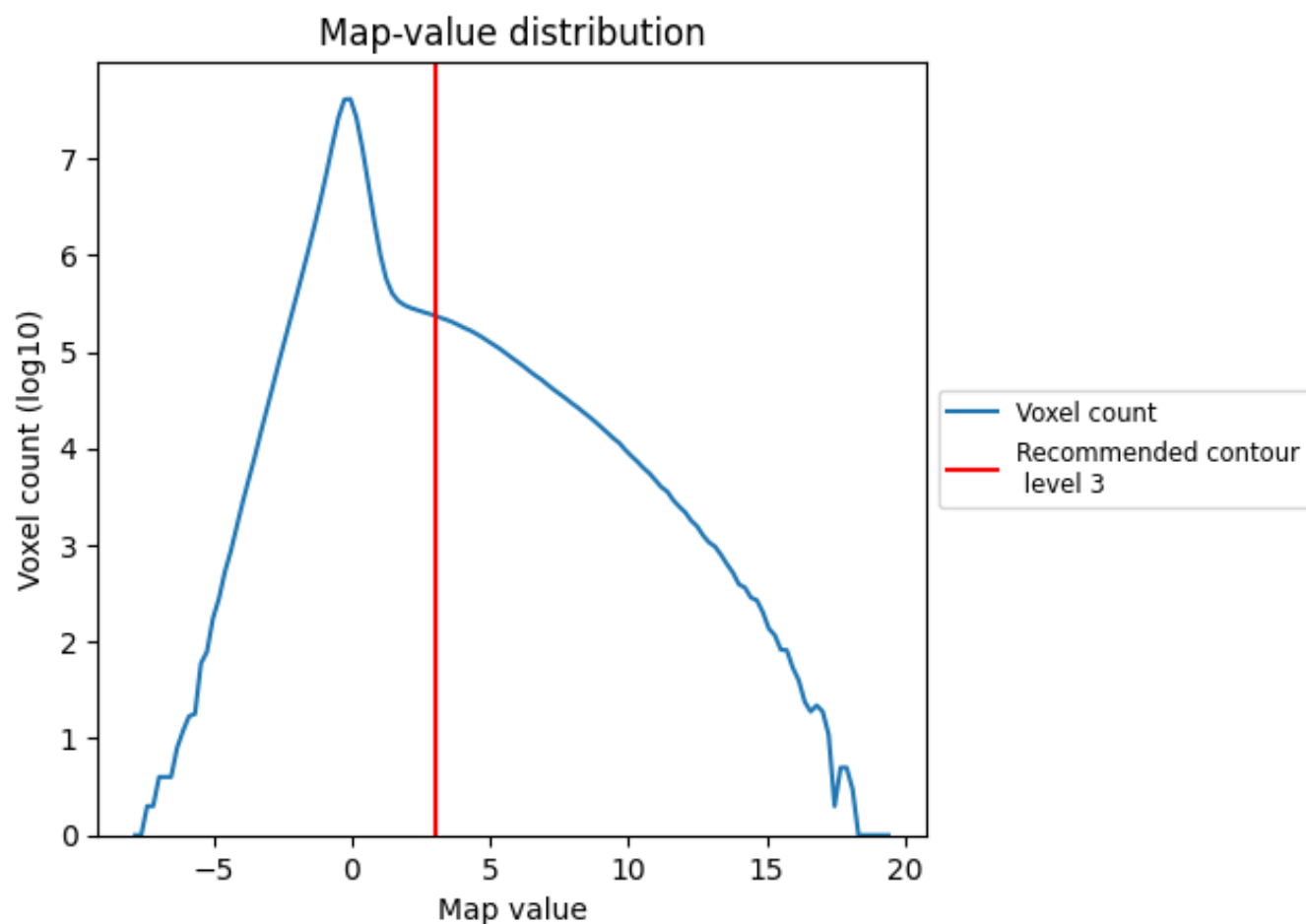
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

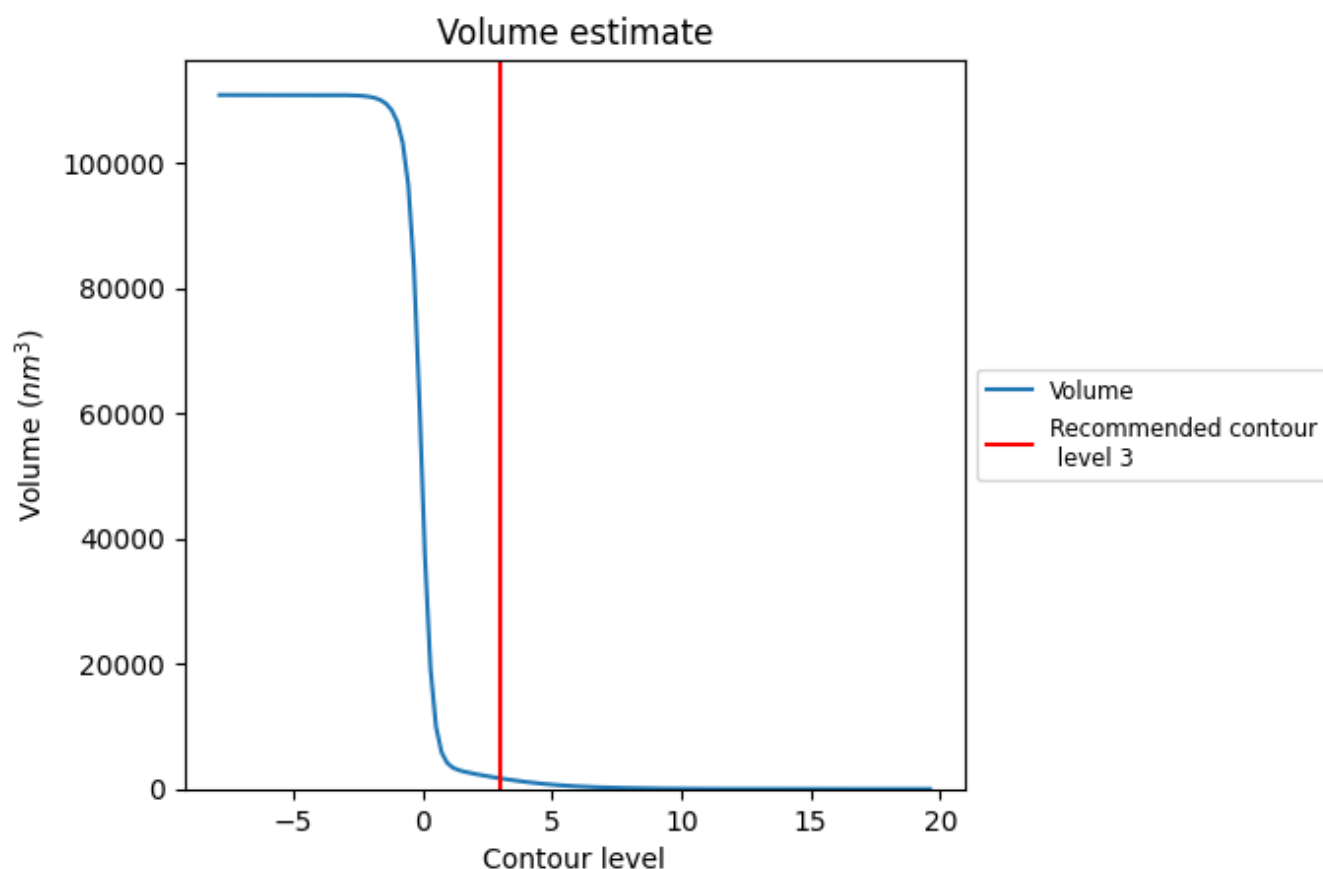
This section contains the results of statistical analysis of the map.

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.

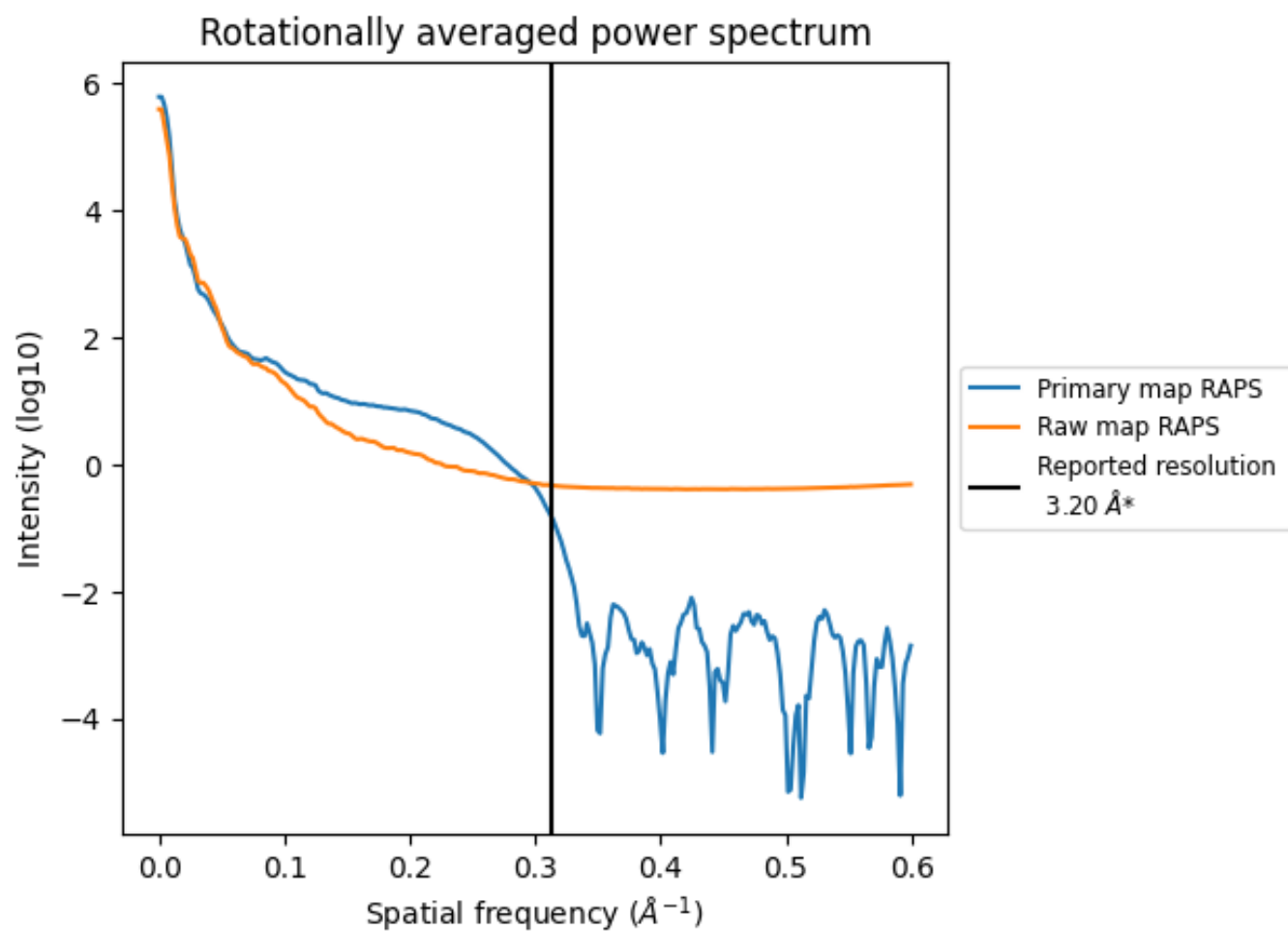
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1704 nm^3 ; this corresponds to an approximate mass of 1539 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 ⓘ

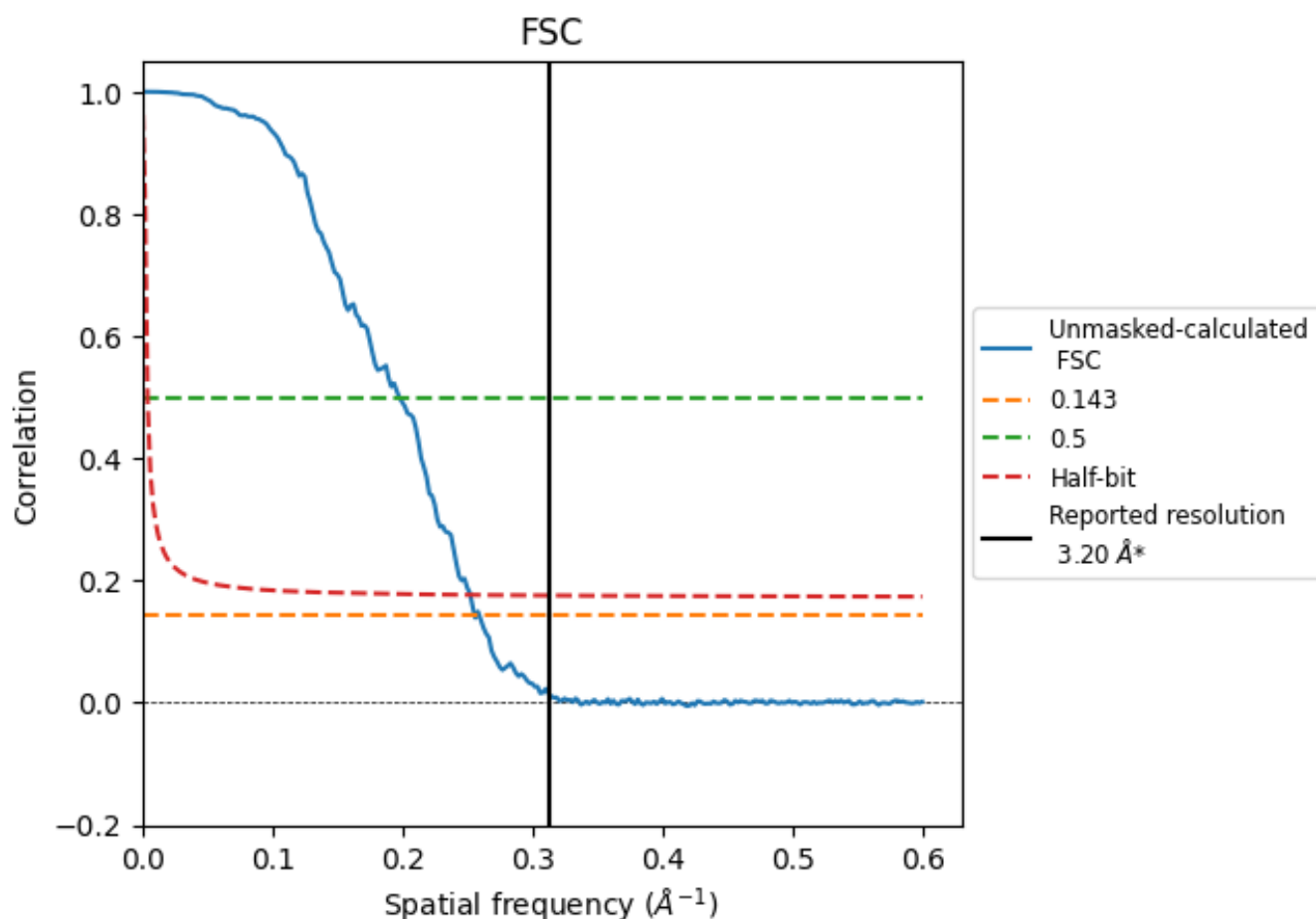


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

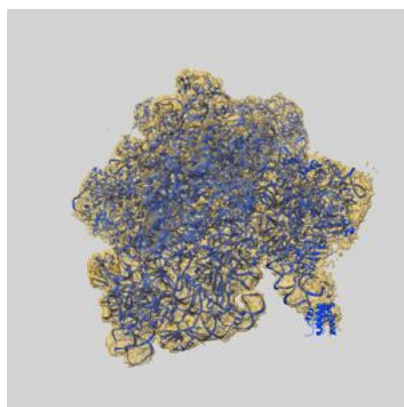
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.91	5.06	3.97

*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 3.91 differs from the reported value 3.2 by more than 10 %

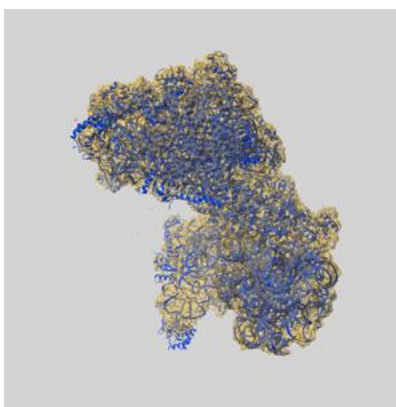
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-50612 and PDB model 9FNZ. Per-residue inclusion information can be found in section [3](#) on page [13](#).

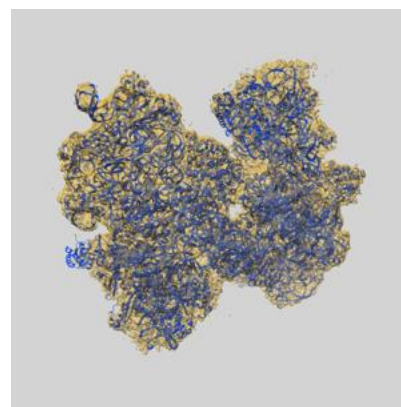
9.1 Map-model overlay [i](#)



X



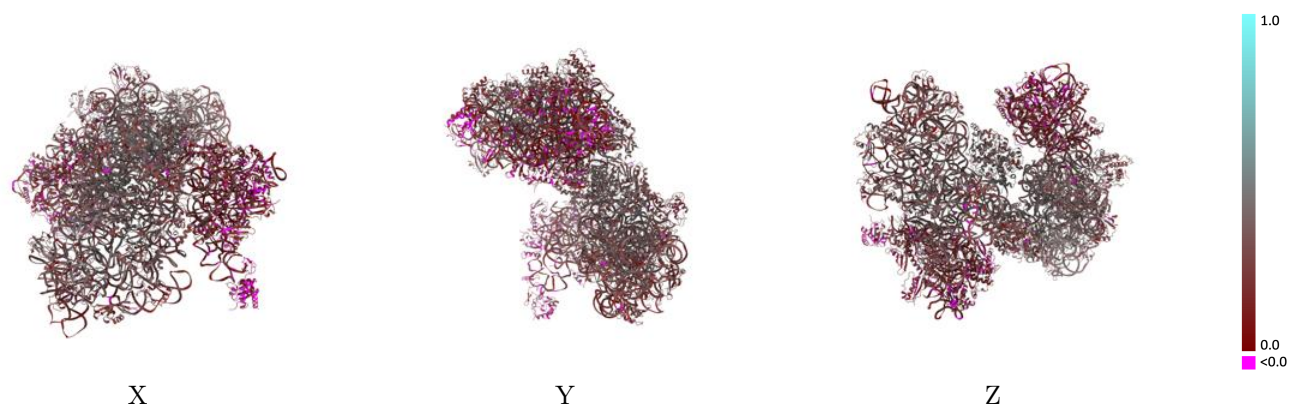
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0 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](#)

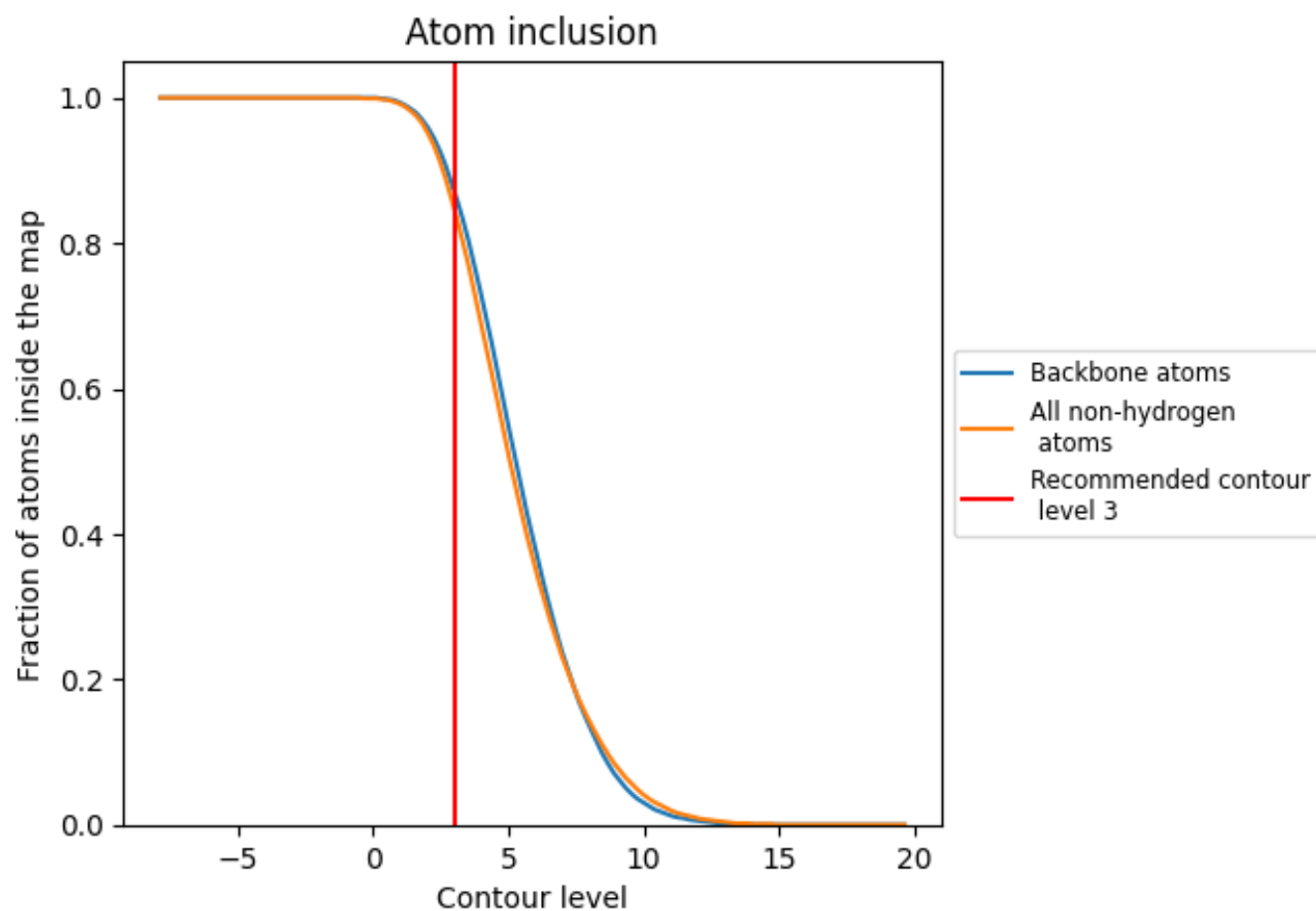


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 87% of all backbone atoms, 85% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8480	 0.2880
A1	 0.7700	 0.3230
A2	 0.9160	 0.4060
A3	 0.8850	 0.3810
A4	 0.8940	 0.3920
A5	 0.1290	 0.1080
AA	 0.9460	 0.2950
AB	 0.7650	 0.3130
AC	 0.6690	 0.1930
AD	 0.8940	 0.2980
AE	 0.8730	 0.3250
AF	 0.7950	 0.3170
AG	 0.8080	 0.3530
AH	 0.8180	 0.3060
AI	 0.7490	 0.1520
AJ	 0.8590	 0.3590
AK	 0.9140	 0.3250
AL	 0.6320	 0.1520
AM	 0.6030	 0.1880
AN	 0.9630	 0.3570
AO	 0.8930	 0.3520
AP	 0.4330	 0.1120
AQ	 0.7750	 0.1940
AR	 0.8260	 0.3050
AS	 0.8430	 0.3310
AT	 0.7560	 0.2600
AU	 0.2680	 0.1180
AV	 0.6120	 0.1150
AW	 0.7780	 0.2880
AX	 0.5560	 0.0980
AY	 0.8880	 0.2640
AZ	 0.8440	 0.2140
B1	 0.8240	 0.3170
B2	 0.8580	 0.3730
B3	 0.8640	 0.3800



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Chain	Atom inclusion	Q-score
B4	 0.8940	 0.3920
B5	 0.1660	 0.0680
BA	 0.9300	 0.2990
BB	 0.7470	 0.2880
BC	 0.5240	 0.1930
BD	 0.8970	 0.3500
BE	 0.8640	 0.3160
BF	 0.8350	 0.3470
BG	 0.8600	 0.3490
BH	 0.7320	 0.2860
BI	 0.5460	 0.1610
BJ	 0.8720	 0.3660
BK	 0.9150	 0.3580
BL	 0.7160	 0.1490
BM	 0.7100	 0.1520
BN	 0.9730	 0.3870
BO	 0.9230	 0.3680
BP	 0.3030	 0.1340
BQ	 0.6720	 0.1430
BR	 0.8810	 0.3530
BS	 0.9110	 0.4010
BT	 0.8230	 0.2370
BU	 0.2780	 0.1380
BV	 0.7570	 0.1120
BW	 0.7760	 0.2710
BX	 0.6450	 0.0820
BY	 0.8470	 0.2820
BZ	 0.7120	 0.1860