



wwPDB EM Validation Summary Report ⓘ

Oct 8, 2024 – 02:26 AM EDT

PDB ID : 4V7A
EMDB ID : EMD-1724
Title : E. coli 70S-fMetVal-tRNAVal post-translocation complex (post4)
Authors : Blau, C.; Bock, L.V.; Schroder, G.F.; Davydov, I.; Fischer, N.; Stark, H.;
Rodnina, M.V.; Vaiana, A.C.; Grubmuller, H.
Deposited on : 2013-10-14
Resolution : 9.00 Å(reported)
Based on initial models : 2K4C, 2WRI, 3I1O, 2HGP

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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

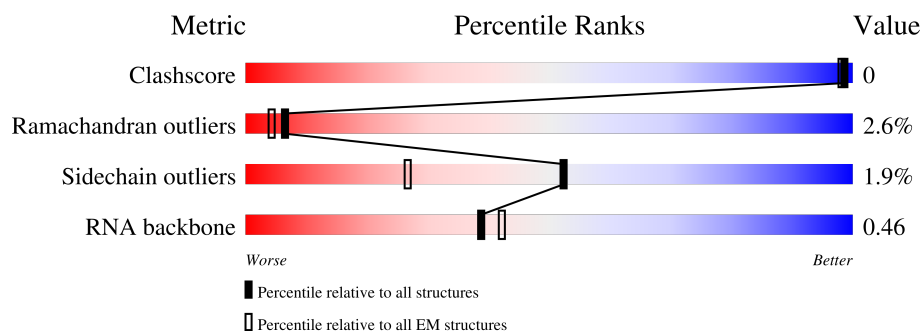
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	AB	220	<div> <div>71%</div> <div>94%6%</div> </div>
2	AC	208	<div> <div>62%</div> <div>87%12%</div> </div>
3	AD	206	<div> <div>60%</div> <div>91%8%</div> </div>
4	AE	152	<div> <div>57%</div> <div>91%8%</div> </div>
5	AF	101	<div> <div>70%</div> <div>90%10%</div> </div>
6	AG	152	<div> <div>53%</div> <div>89%11%</div> </div>
7	AH	130	<div> <div>47%</div> <div>95%</div> </div>

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Mol	Chain	Length	Quality of chain
8	AI	128	
9	AJ	100	
10	AK	118	
11	AL	124	
12	AM	115	
13	AN	101	
14	AO	89	
15	AP	81	
16	AQ	82	
17	AR	57	
18	AS	81	
19	AT	86	
20	AU	53	
21	AA	1533	
22	A1	76	
23	A2	15	
24	BC	273	
25	BD	209	
26	BE	201	
27	BF	179	
28	BG	177	
29	BH	149	
30	BI	142	
31	BJ	142	
32	BK	123	

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Mol	Chain	Length	Quality of chain
33	BL	144	
34	BM	136	
35	BN	121	
36	BO	117	
37	BP	115	
38	BQ	118	
39	BR	103	
40	BS	110	
41	BT	94	
42	BU	104	
43	BV	94	
44	BW	80	
45	BX	79	
46	BY	63	
47	BZ	59	
48	B0	57	
49	B1	52	
50	B2	46	
51	B3	65	
52	B4	38	
53	BA	2903	
54	BB	118	
55	B5	234	

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146011 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 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB	220	Total	C	N	O	S	0	1
			1708	1083	306	312	7		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AB	7	ACE	-	acetylation	UNP P0A7V0
AB	226	NH2	-	amidation	UNP P0A7V0

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AC	207	Total	C	N	O	S	0	1
			1625	1028	306	288	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	207	NH2	-	amidation	UNP P0A7V3

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AD	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AE	152	Total	C	N	O	S	0	1
			1109	689	212	202	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	8	ACE	-	acetylation	UNP P0A7W1
AE	159	NH2	-	amidation	UNP P0A7W1

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AF	101	Total	C	N	O	S	0	1
			818	515	149	148	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AF	101	NH2	-	amidation	UNP P02358

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	152	Total	C	N	O	S	0	1
			1178	732	227	215	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AG	1	ACE	-	acetylation	UNP P02359
AG	152	NH2	-	amidation	UNP P02359

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	128	Total	C	N	O	S	0	0
			1025	636	206	180	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	2	ACE	-	acetylation	UNP P0A7X3

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	100	Total	C	N	O	S	0	1
			790	495	151	143	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AJ	4	ACE	-	acetylation	UNP P0A7R5
AJ	103	NH2	-	amidation	UNP P0A7R5

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	118	Total	C	N	O	S	0	0
			880	542	174	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	11	ACE	-	acetylation	UNP P0A7R9

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	114	Total	C	N	O	S	0	1
			877	541	178	155	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AM	114	NH2	-	amidation	UNP P0A7S9

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AP	81	Total	C	N	O	S	0	1
			639	400	127	111	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	81	NH2	-	amidation	UNP P0A7T3

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	82	Total	C	N	O	S	0	1
			652	413	122	114	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AQ	2	ACE	-	acetylation	UNP P0AG63
AQ	83	NH2	-	amidation	UNP P0AG63

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	AR	57	Total	C	N	O	0	1
			459	290	87	82		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	18	ACE	-	acetylation	UNP P0A7T7

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Chain	Residue	Modelled	Actual	Comment	Reference
AR	74	NH2	-	amidation	UNP P0A7T7

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	81	Total	C	N	O	S	0	1
			641	410	121	108	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AS	1	ACE	-	acetylation	UNP P0A7U3
AS	81	NH2	-	amidation	UNP P0A7U3

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	86	Total	C	N	O	S	0	0
			668	413	137	115	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AT	1	ACE	-	acetylation	UNP P0A7U7

- Molecule 20 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	53	Total	C	N	O	S	0	1
			429	267	87	74	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AU	2	ACE	-	acetylation	UNP P68679
AU	54	NH2	-	amidation	UNP P68679

- Molecule 21 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AA	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 22 is a RNA chain called fMet-Val-tRNA-Val.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	A1	76	Total	C	N	O	P	S	0	0
			1627	728	292	531	75	1		

- Molecule 23 is a RNA chain called 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*P*AP*UP*U)-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A2	15	Total	C	N	O	P	0	0
			309	140	46	109	14		

- Molecule 24 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BC	272	Total	C	N	O	S	0	1
			2083	1288	424	364	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BC	272	NH2	-	amidation	UNP P60422

- Molecule 25 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BD	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 26 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BE	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BF	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 28 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BG	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 29 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BH	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 30 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BI	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 31 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BJ	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 32 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BK	123	Total	C	N	O	S	0	1
			939	587	181	165	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	123	NH2	-	amidation	UNP P0ADY3

- Molecule 33 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BL	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 34 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BM	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 35 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BN	121	Total	C	N	O	S	0	1
			961	593	197	166	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BN	121	NH2	-	amidation	UNP P0AG44

- Molecule 36 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	BO	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 37 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BP	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 38 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BQ	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 39 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BR	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 40 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BS	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 41 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BT	94	Total	C	N	O	S	0	1
			739	466	140	131	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	94	NH2	-	amidation	UNP P0ADZ0

- Molecule 42 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BU	103	Total	C	N	O	0	1
			780	492	147	141		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	103	NH2	-	amidation	UNP P60624

- Molecule 43 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BV	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 44 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BW	80	Total	C	N	O	S	0	0
			599	369	120	109	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BW	5	ACE	-	acetylation	UNP P0A7L8

- Molecule 45 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BX	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BX	-1	ACE	-	acetylation	UNP P0A7M2

- Molecule 46 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BY	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 47 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BZ	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	B1	52	Total	C	N	O	0	1
			413	265	76	72		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B1	2	ACE	-	acetylation	UNP P0A7N9
B1	53	NH2	-	amidation	UNP P0A7N9

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BA	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

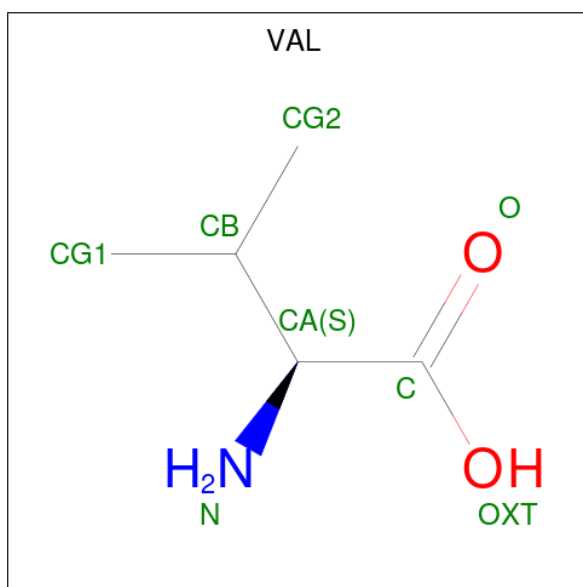
- Molecule 54 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BB	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 55 is a protein called 50S ribosomal protein L1.

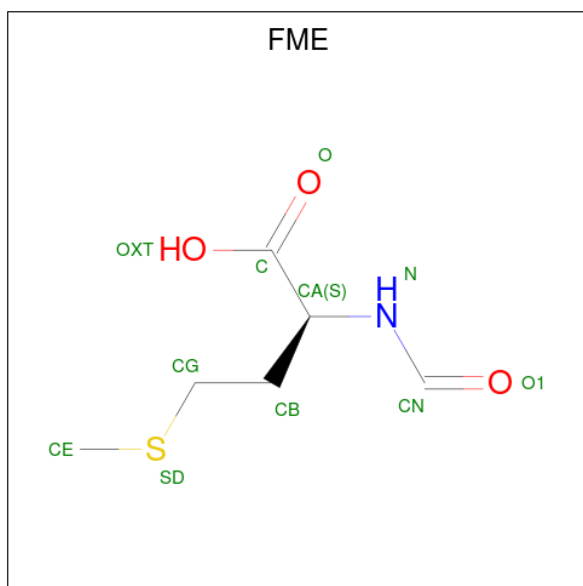
Mol	Chain	Residues	Atoms					AltConf	Trace
55	B5	223	Total	C	N	O	S	0	0
			1658	1038	302	312	6		

- Molecule 56 is VALINE (three-letter code: VAL) (formula: C₅H₁₁NO₂).



Mol	Chain	Residues	Atoms				AltConf
56	A1	1	Total	C	N	O	0
			7	5	1	1	

- Molecule 57 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: C₆H₁₁NO₃S).

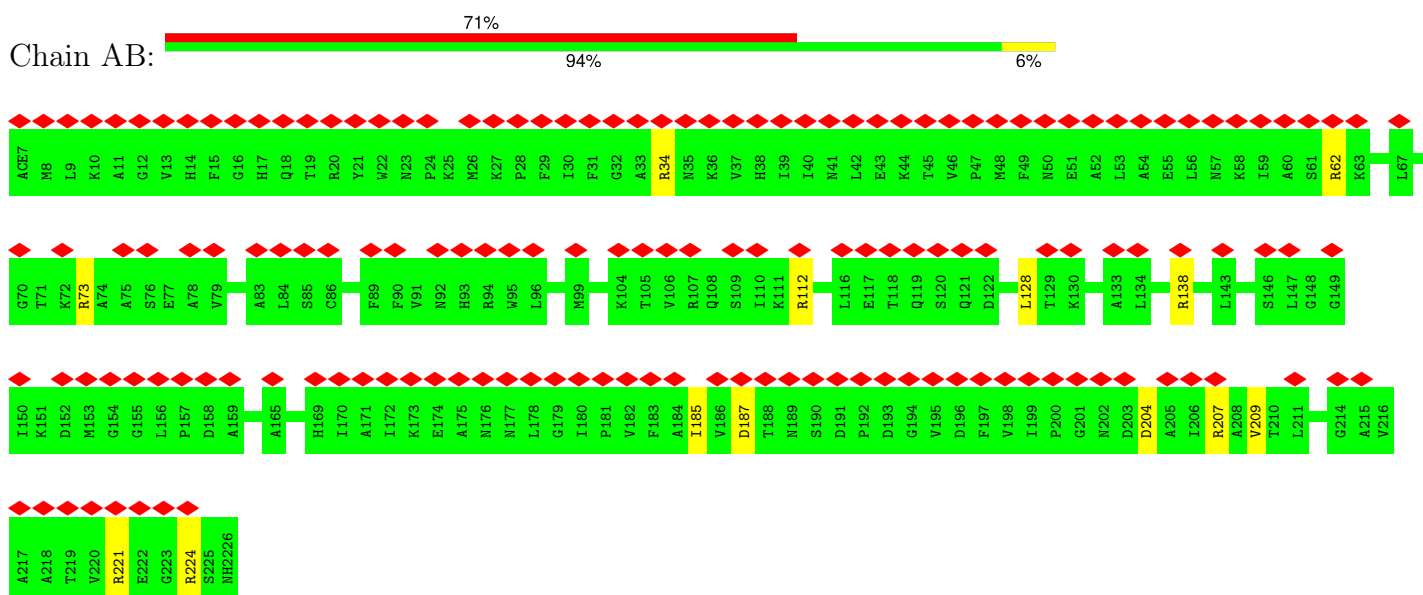


Mol	Chain	Residues	Atoms					AltConf
57	BA	1	Total	C	N	O	S	0
			10	6	1	2	1	

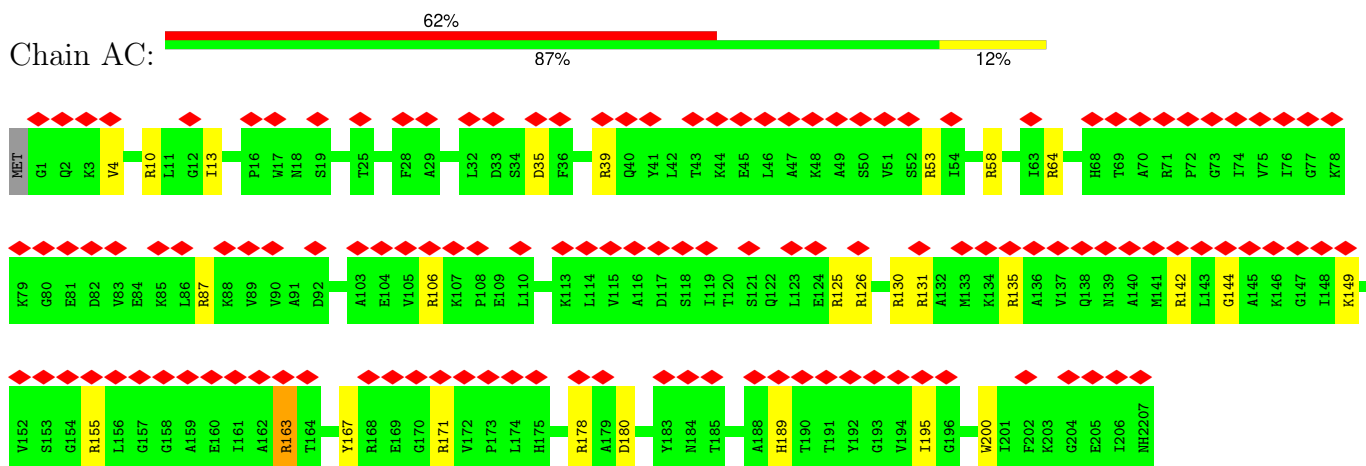
3 Residue-property plots

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

• Molecule 1: 30S ribosomal protein S2

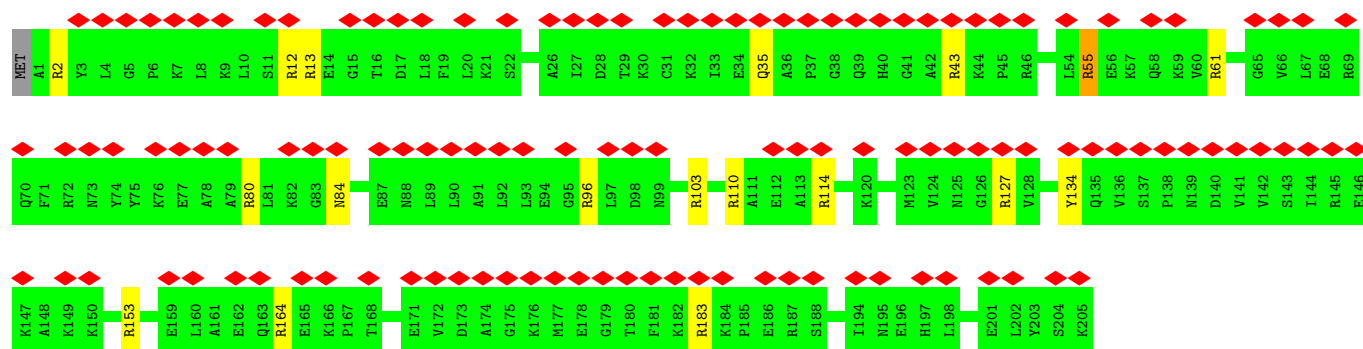


• Molecule 2: 30S ribosomal protein S3

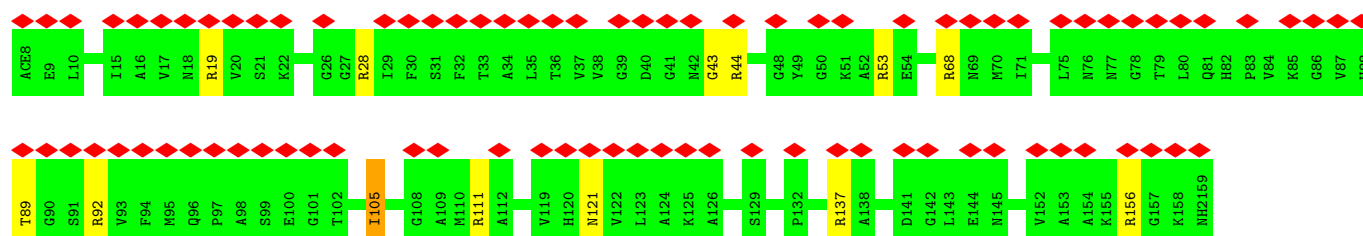


• Molecule 3: 30S ribosomal protein S4

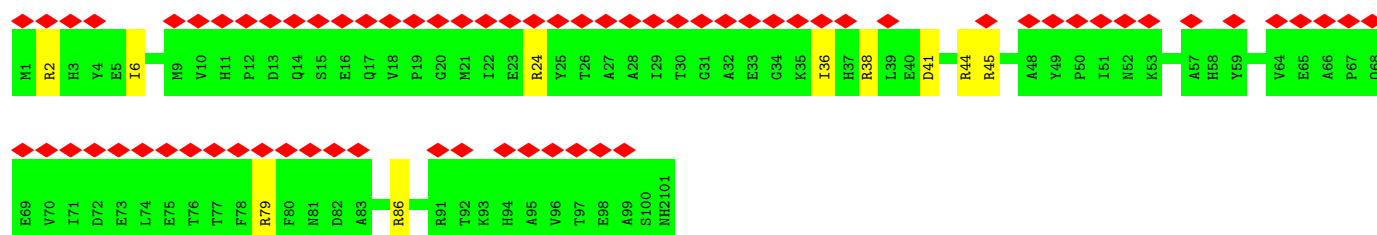
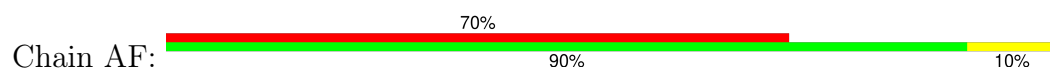




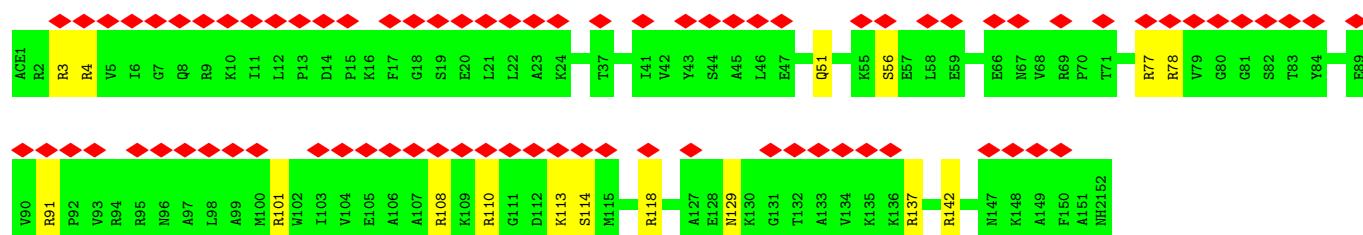
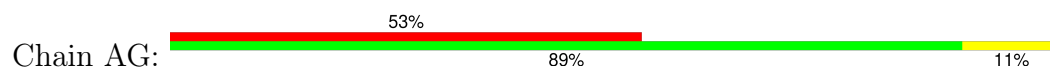
• Molecule 4: 30S ribosomal protein S5



• Molecule 5: 30S ribosomal protein S6

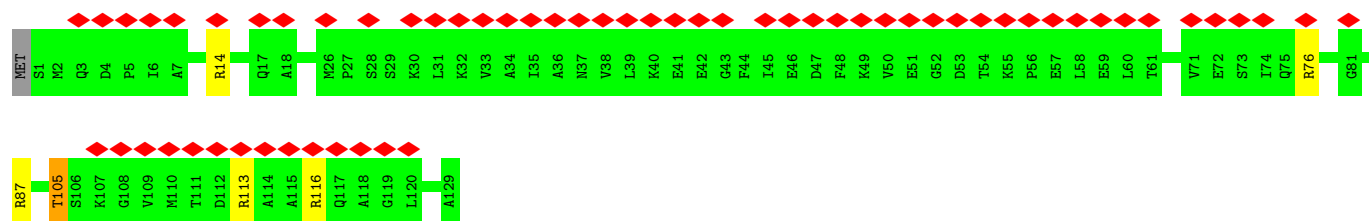


• Molecule 6: 30S ribosomal protein S7

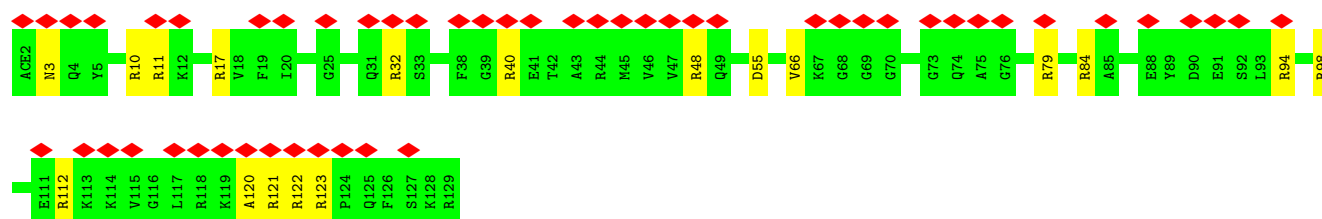
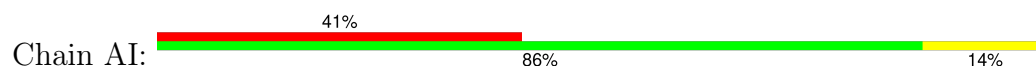


• Molecule 7: 30S ribosomal protein S8

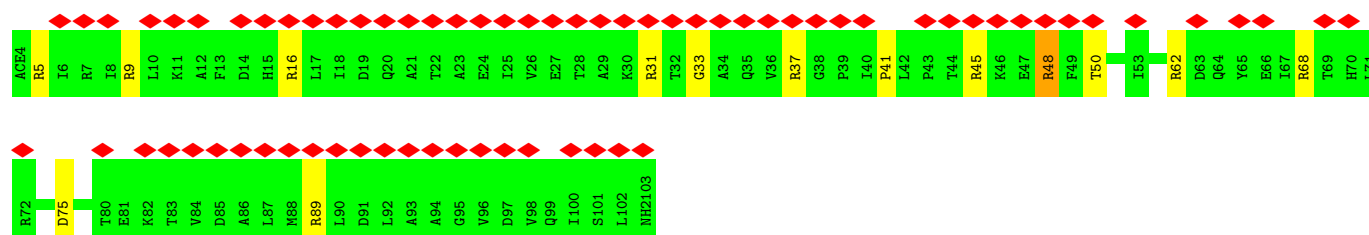
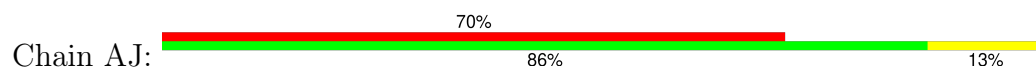




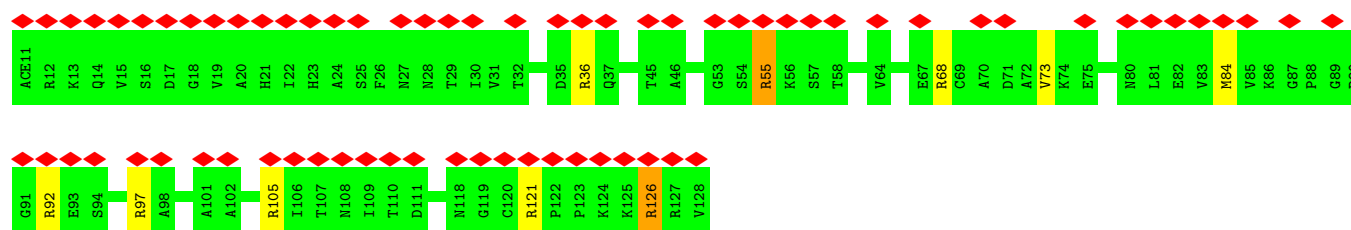
• Molecule 8: 30S ribosomal protein S9



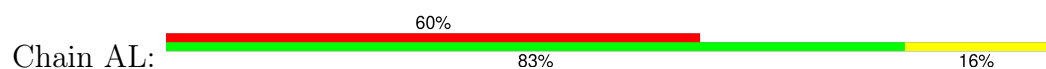
• Molecule 9: 30S ribosomal protein S10

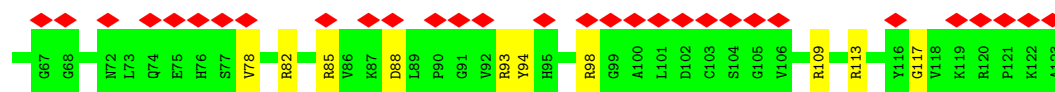


• Molecule 10: 30S ribosomal protein S11

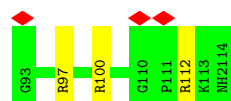
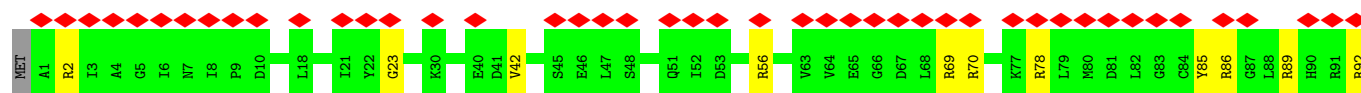
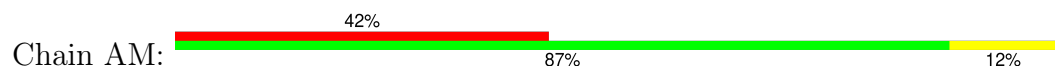


• Molecule 11: 30S ribosomal protein S12

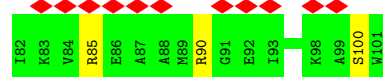
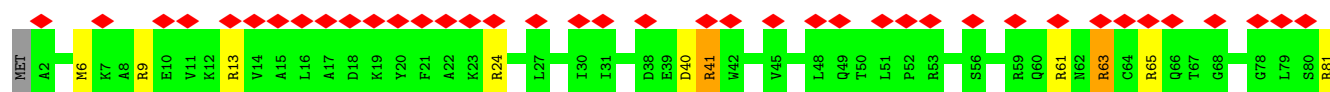
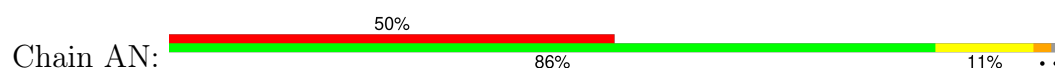




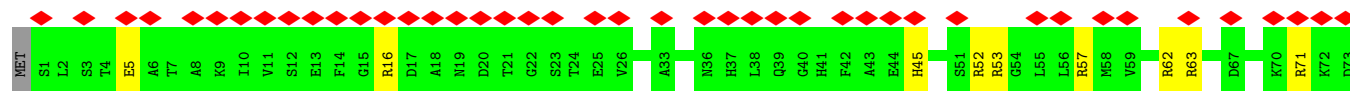
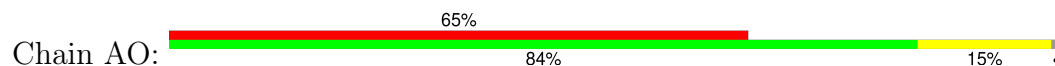
- Molecule 12: 30S ribosomal protein S13



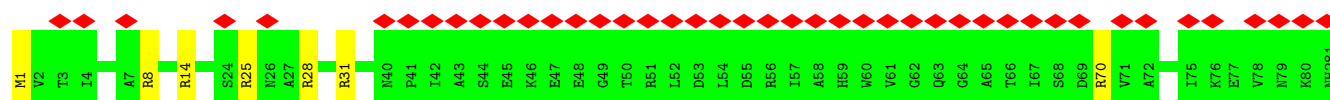
- Molecule 13: 30S ribosomal protein S14



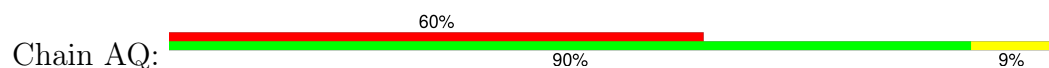
- Molecule 14: 30S ribosomal protein S15

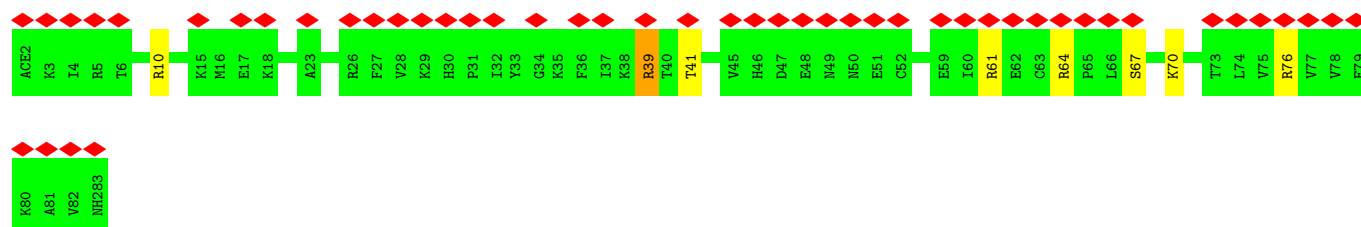


- Molecule 15: 30S ribosomal protein S16

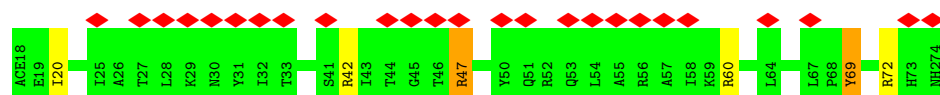


- Molecule 16: 30S ribosomal protein S17

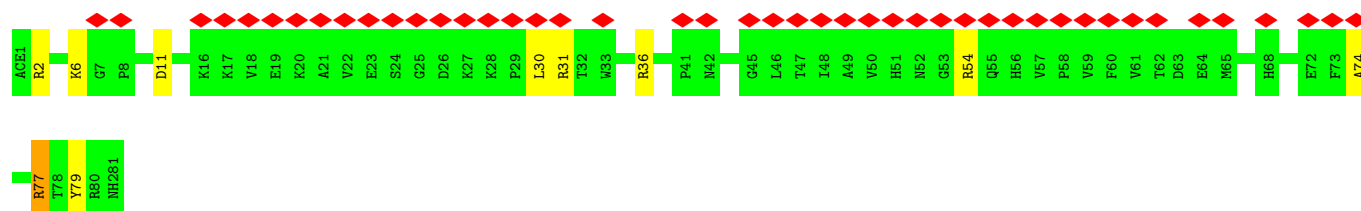




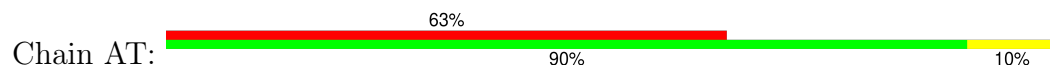
- Molecule 17: 30S ribosomal protein S18



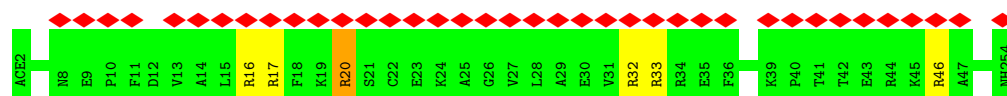
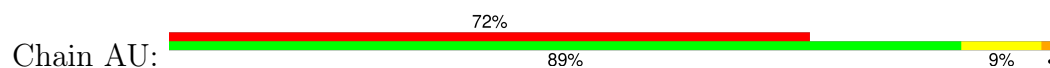
- Molecule 18: 30S ribosomal protein S19



- Molecule 19: 30S ribosomal protein S20

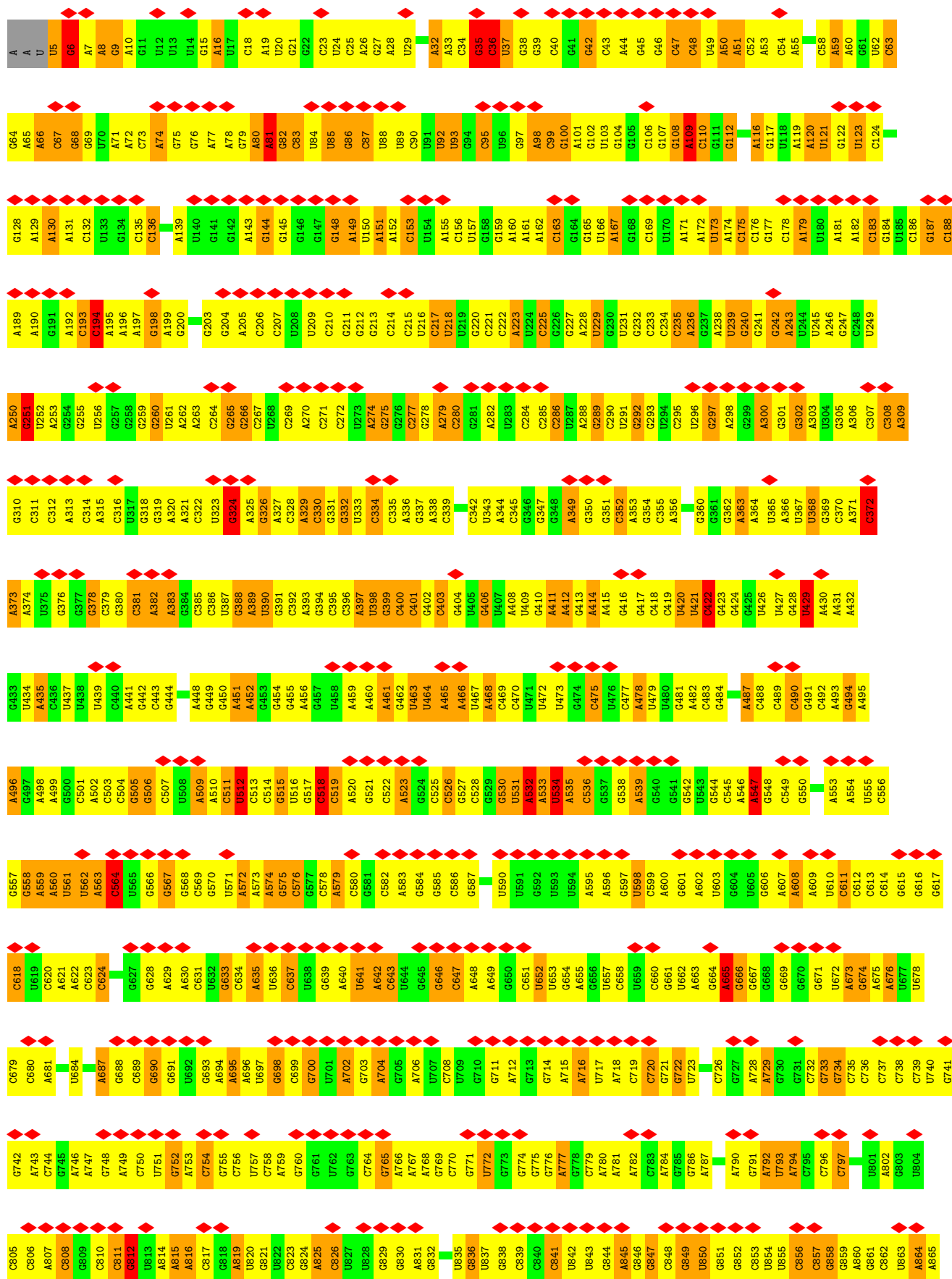


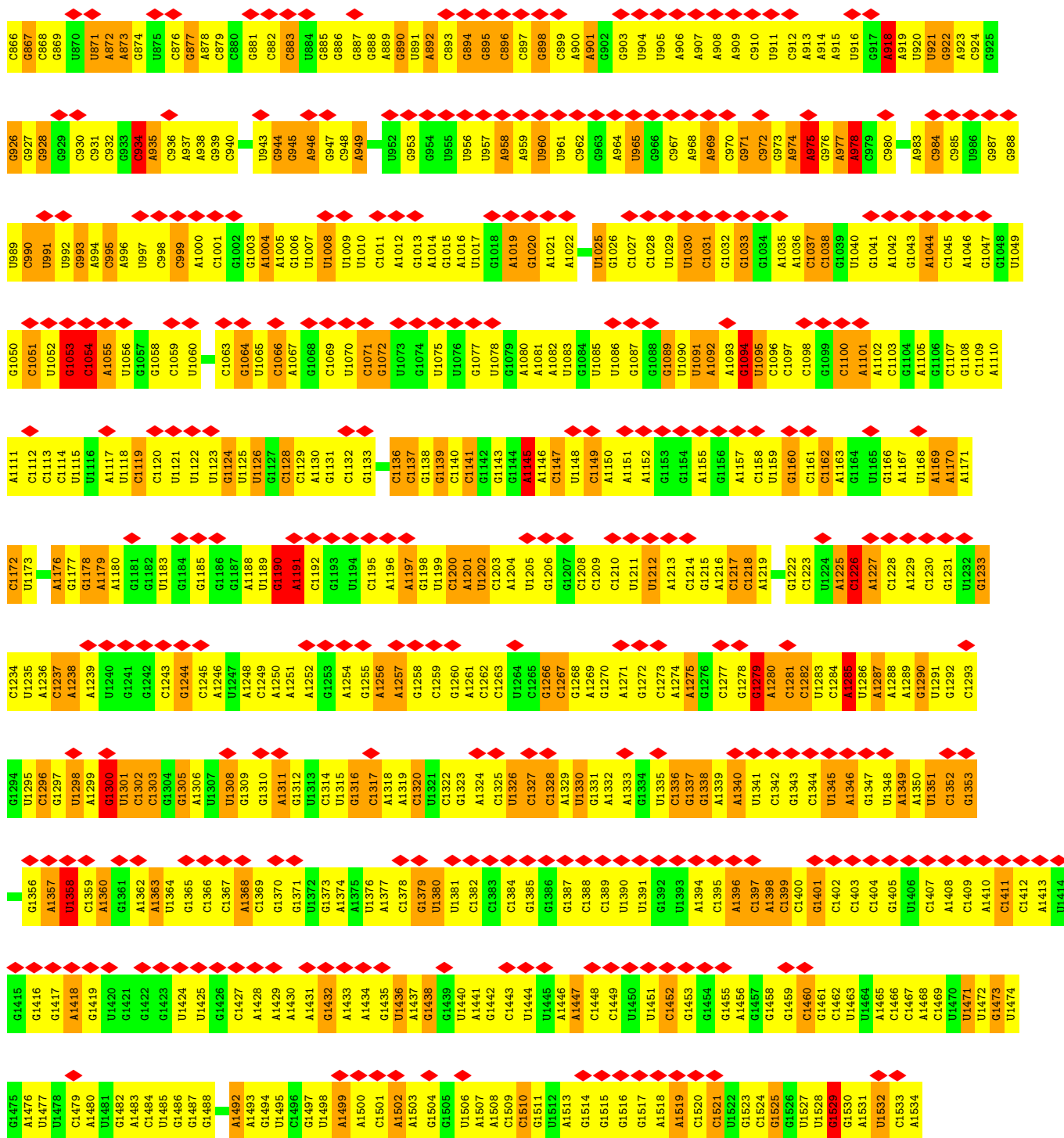
- Molecule 20: 30S ribosomal protein S21



- Molecule 21: 16S ribosomal RNA

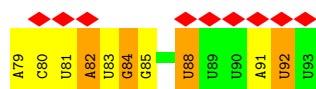




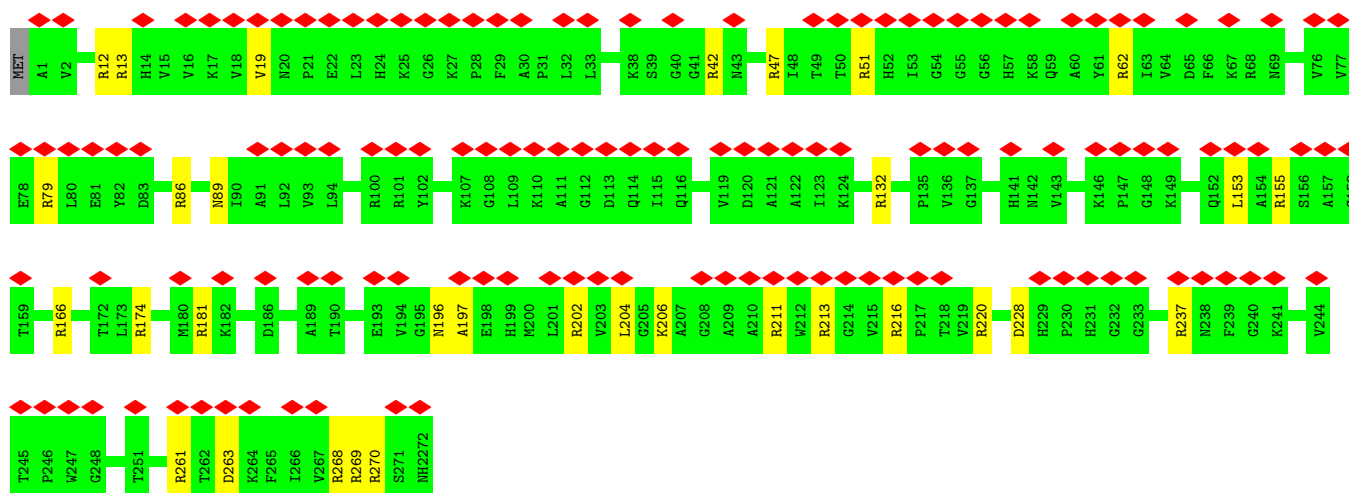




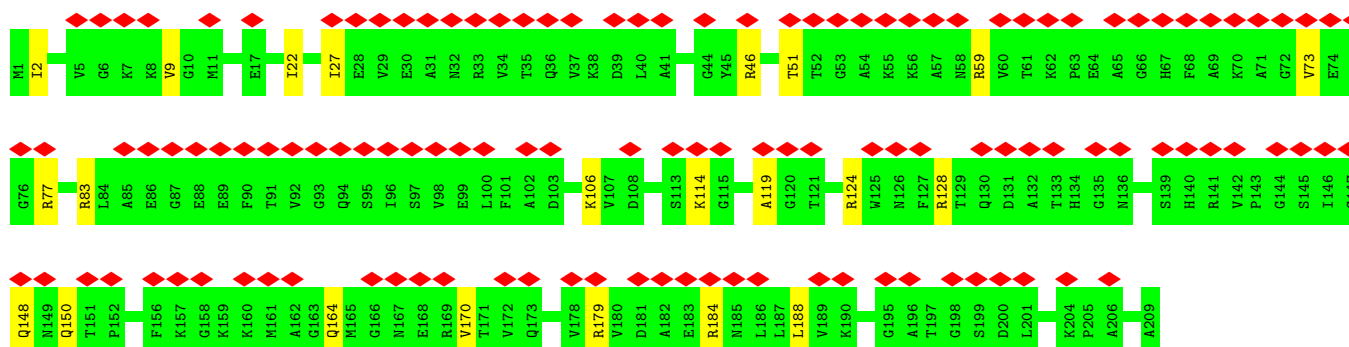
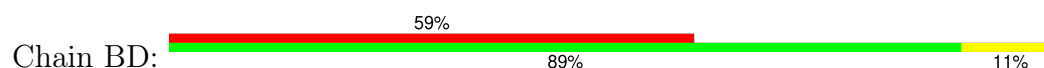
- Molecule 23: 5'-R(*AP*CP*UP*AP*UP*GP*GP*UP*UP*UP*UP*UP*AP*UP*U)-3'



- Molecule 24: 50S ribosomal protein L2

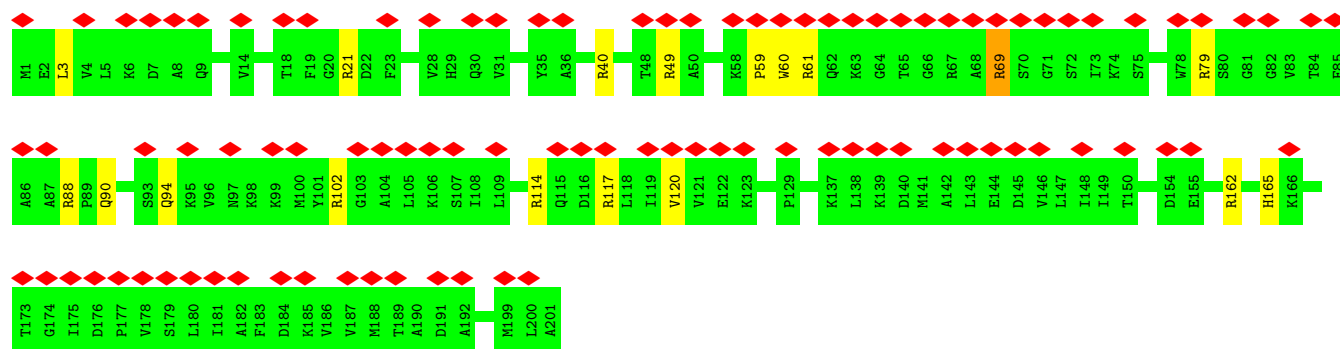


- Molecule 25: 50S ribosomal protein L3



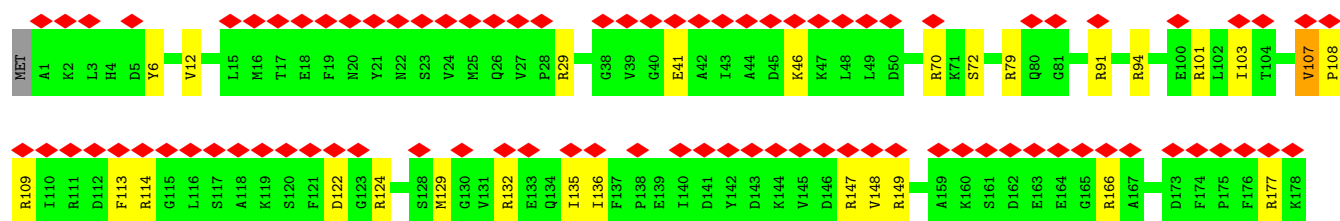
- Molecule 26: 50S ribosomal protein L4





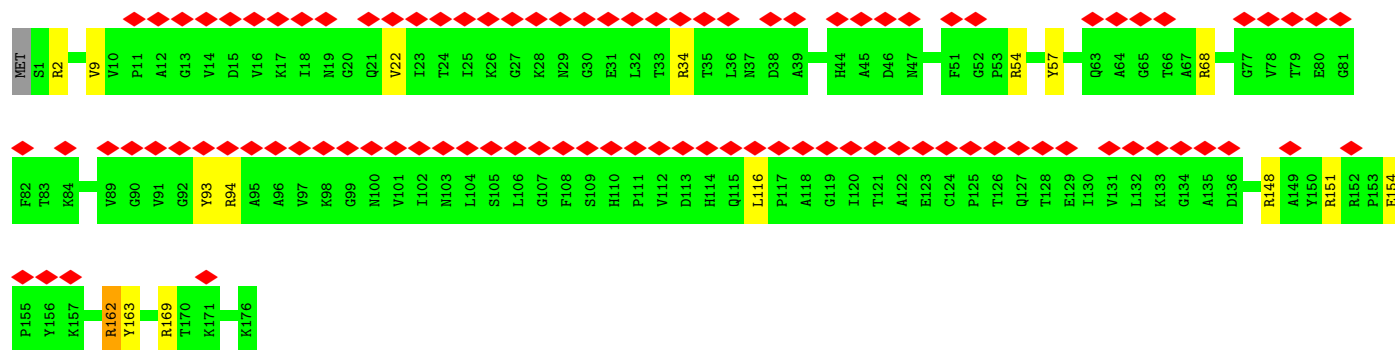
• Molecule 27: 50S ribosomal protein L5

Chain BF: 49% 84% 15% ..



• Molecule 28: 50S ribosomal protein L6

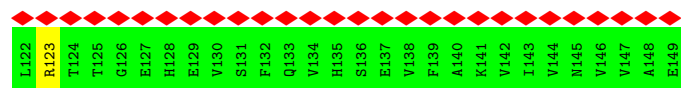
Chain BG: 55% 90% 8% ..



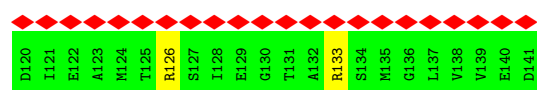
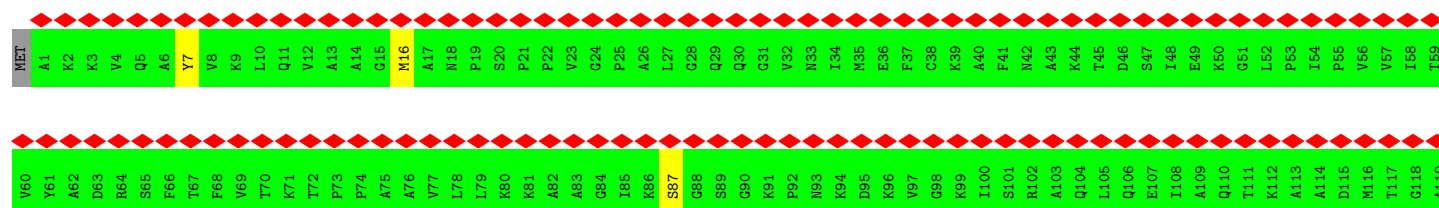
• Molecule 29: 50S ribosomal protein L9

Chain BH: 97% 94% 6%

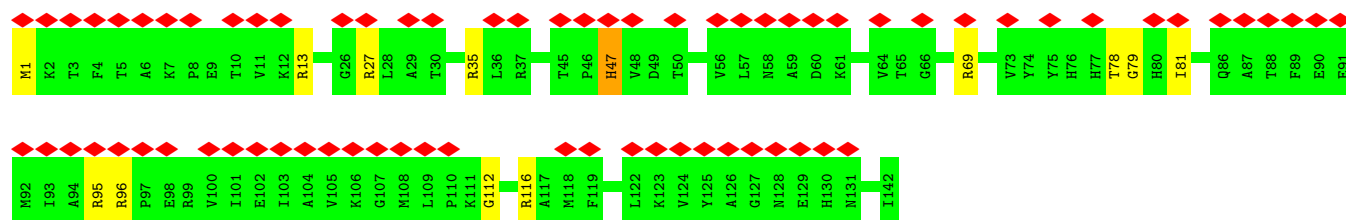
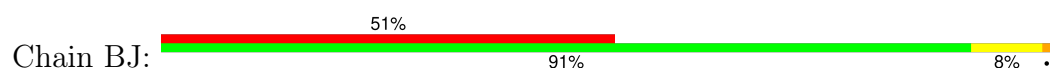




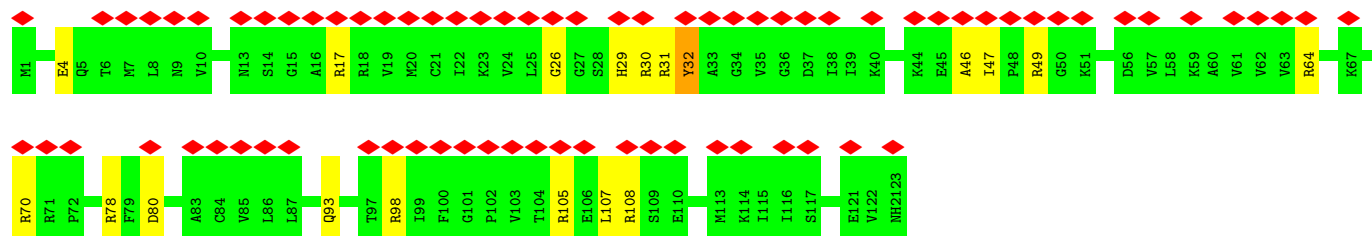
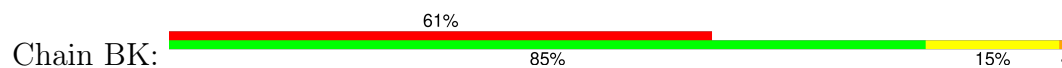
• Molecule 30: 50S ribosomal protein L11



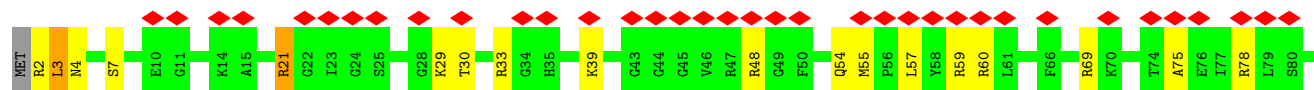
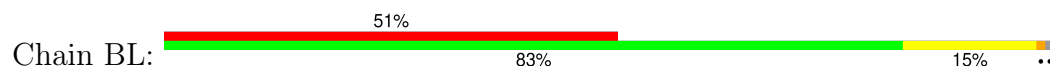
• Molecule 31: 50S ribosomal protein L13

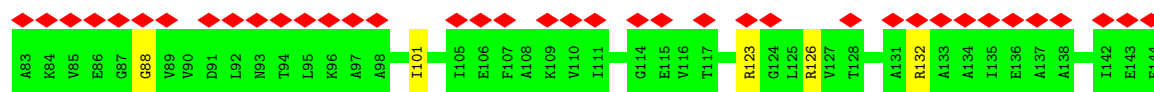


• Molecule 32: 50S ribosomal protein L14

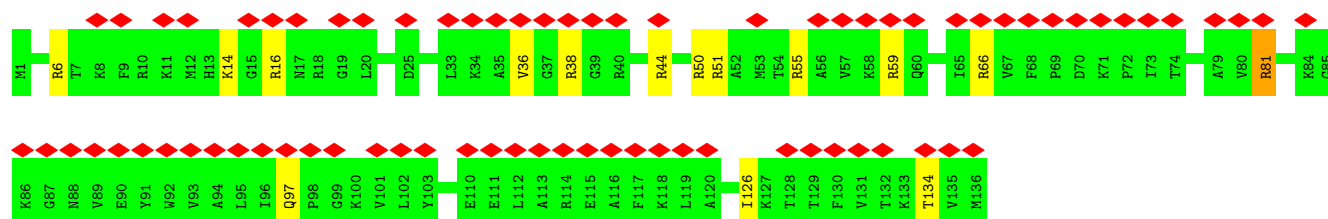


• Molecule 33: 50S ribosomal protein L15

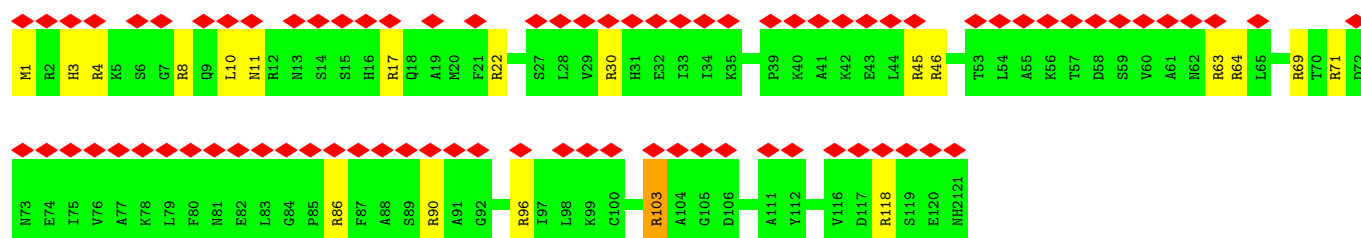
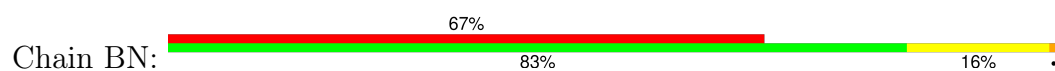




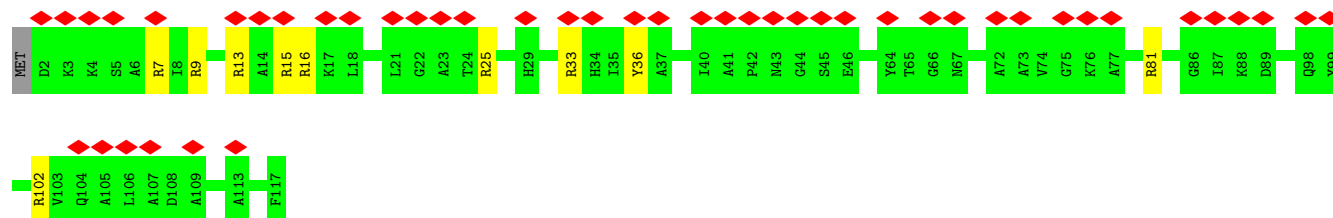
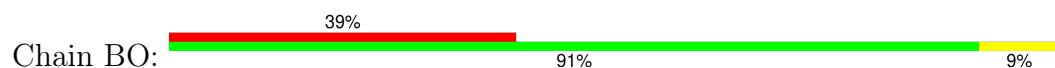
• Molecule 34: 50S ribosomal protein L16



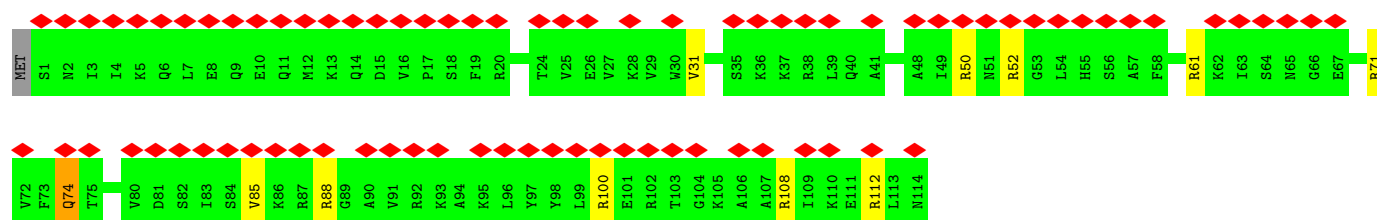
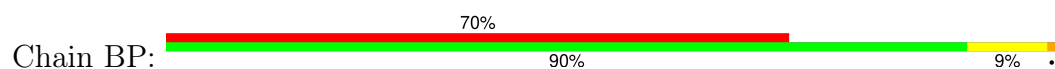
• Molecule 35: 50S ribosomal protein L17



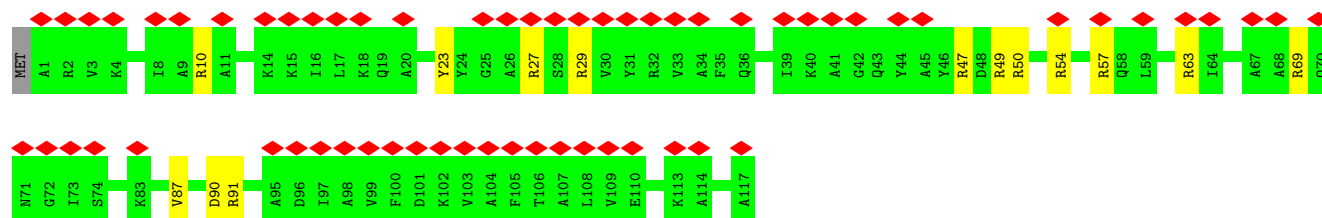
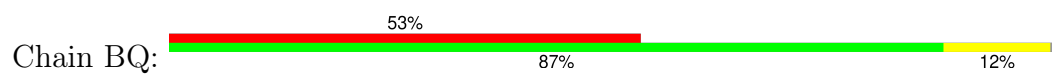
• Molecule 36: 50S ribosomal protein L18



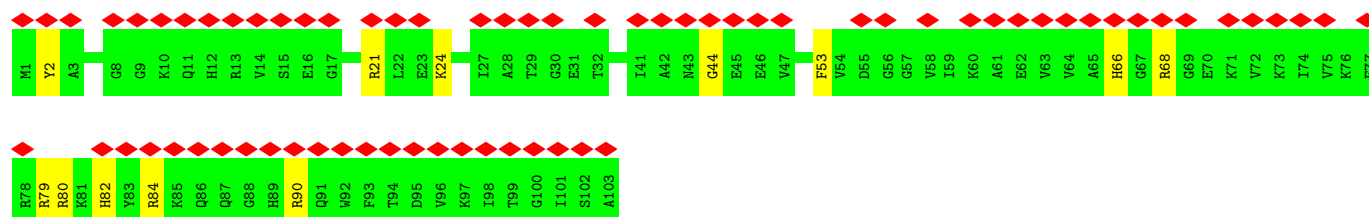
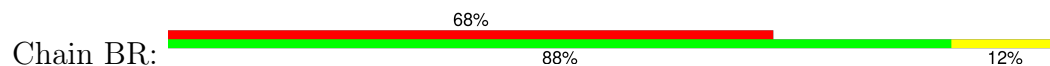
• Molecule 37: 50S ribosomal protein L19



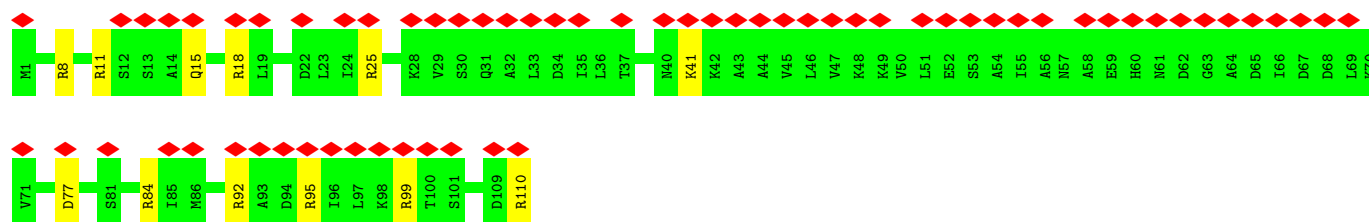
• Molecule 38: 50S ribosomal protein L20



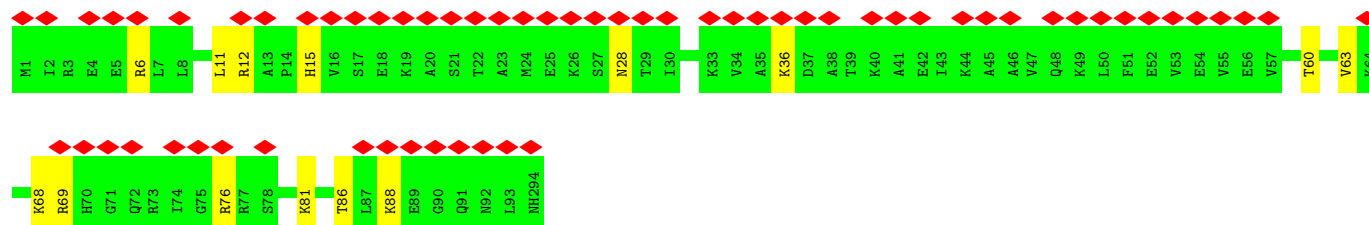
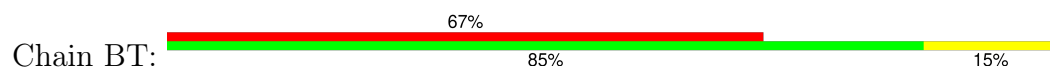
• Molecule 39: 50S ribosomal protein L21



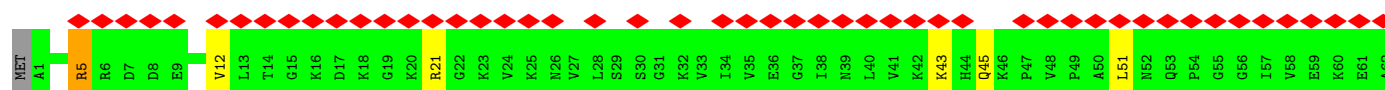
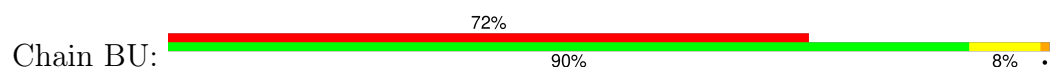
• Molecule 40: 50S ribosomal protein L22

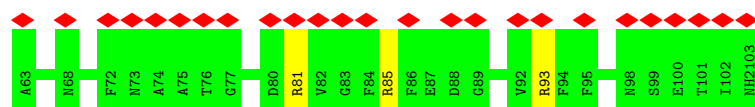


• Molecule 41: 50S ribosomal protein L23

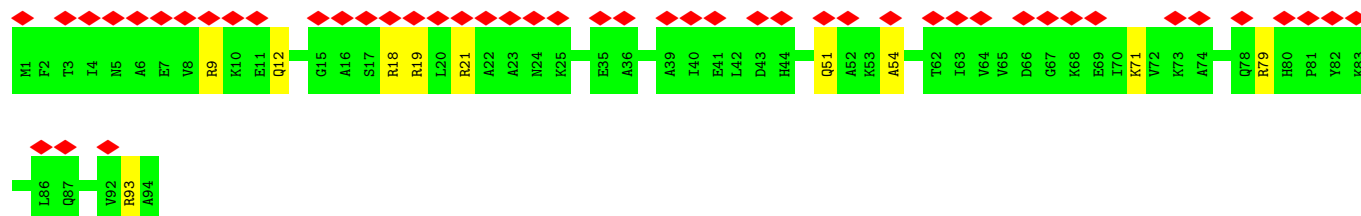
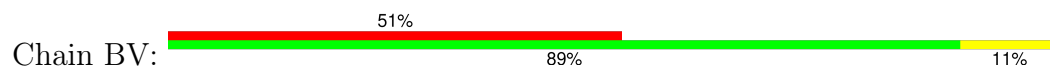


• Molecule 42: 50S ribosomal protein L24

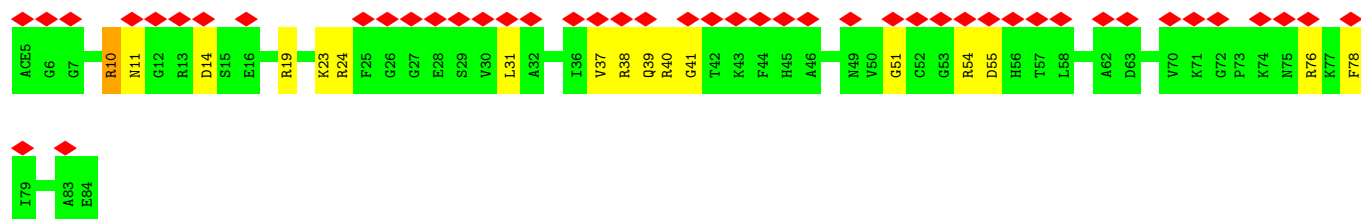
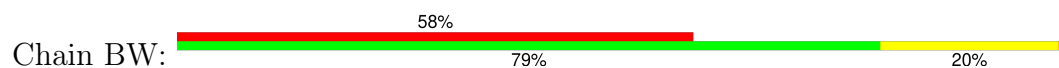




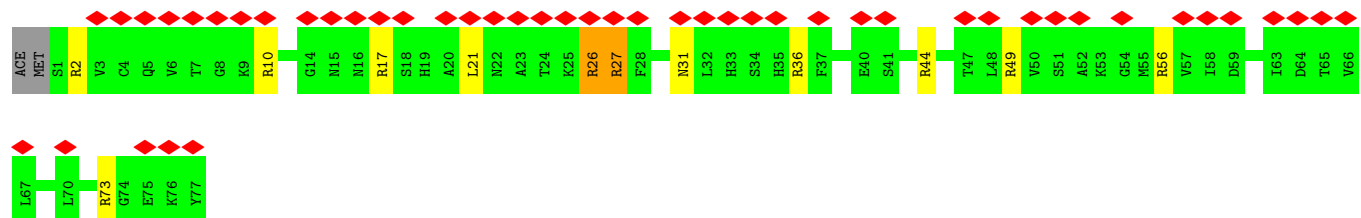
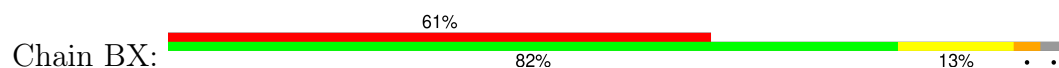
- Molecule 43: 50S ribosomal protein L25



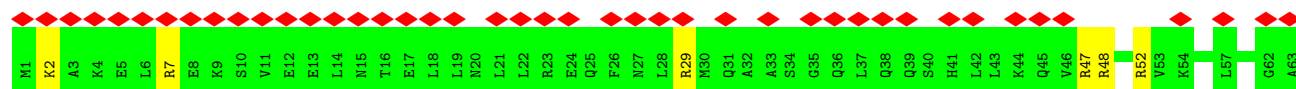
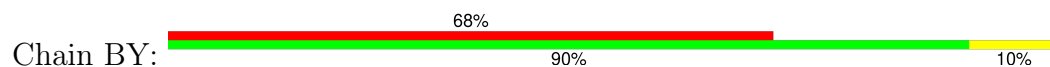
- Molecule 44: 50S ribosomal protein L27



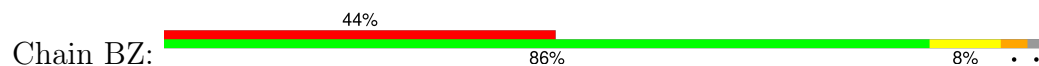
- Molecule 45: 50S ribosomal protein L28



- Molecule 46: 50S ribosomal protein L29

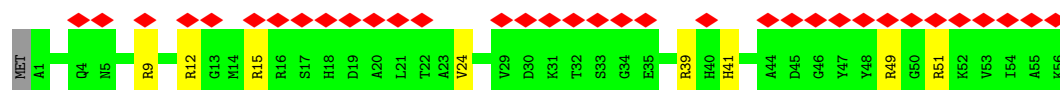
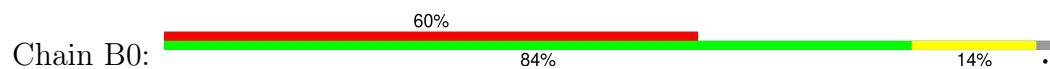


- Molecule 47: 50S ribosomal protein L30

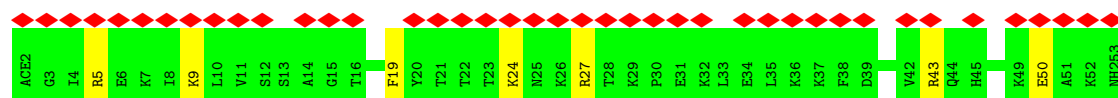
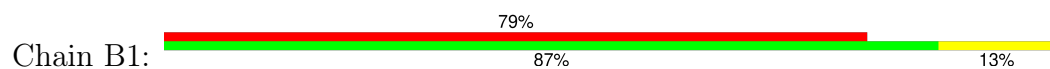




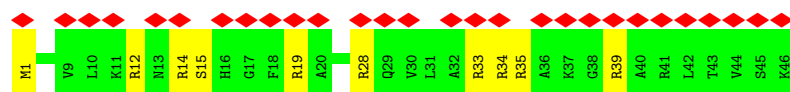
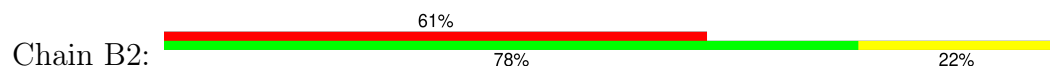
- Molecule 48: 50S ribosomal protein L32



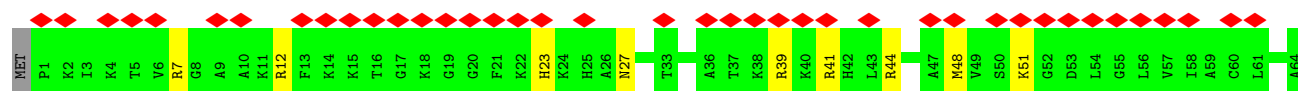
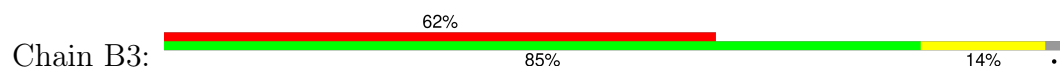
- Molecule 49: 50S ribosomal protein L33



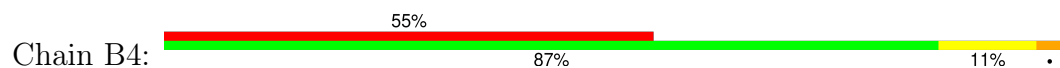
- Molecule 50: 50S ribosomal protein L34



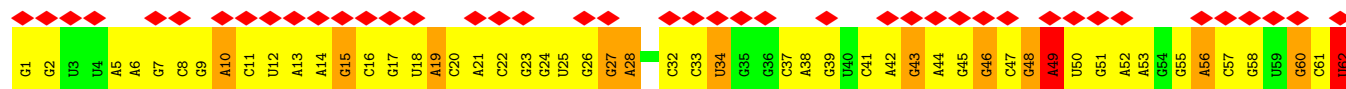
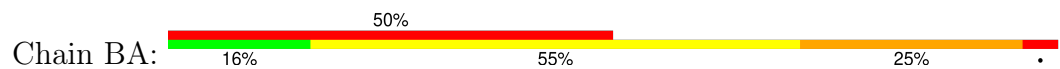
- Molecule 51: 50S ribosomal protein L35



- Molecule 52: 50S ribosomal protein L36



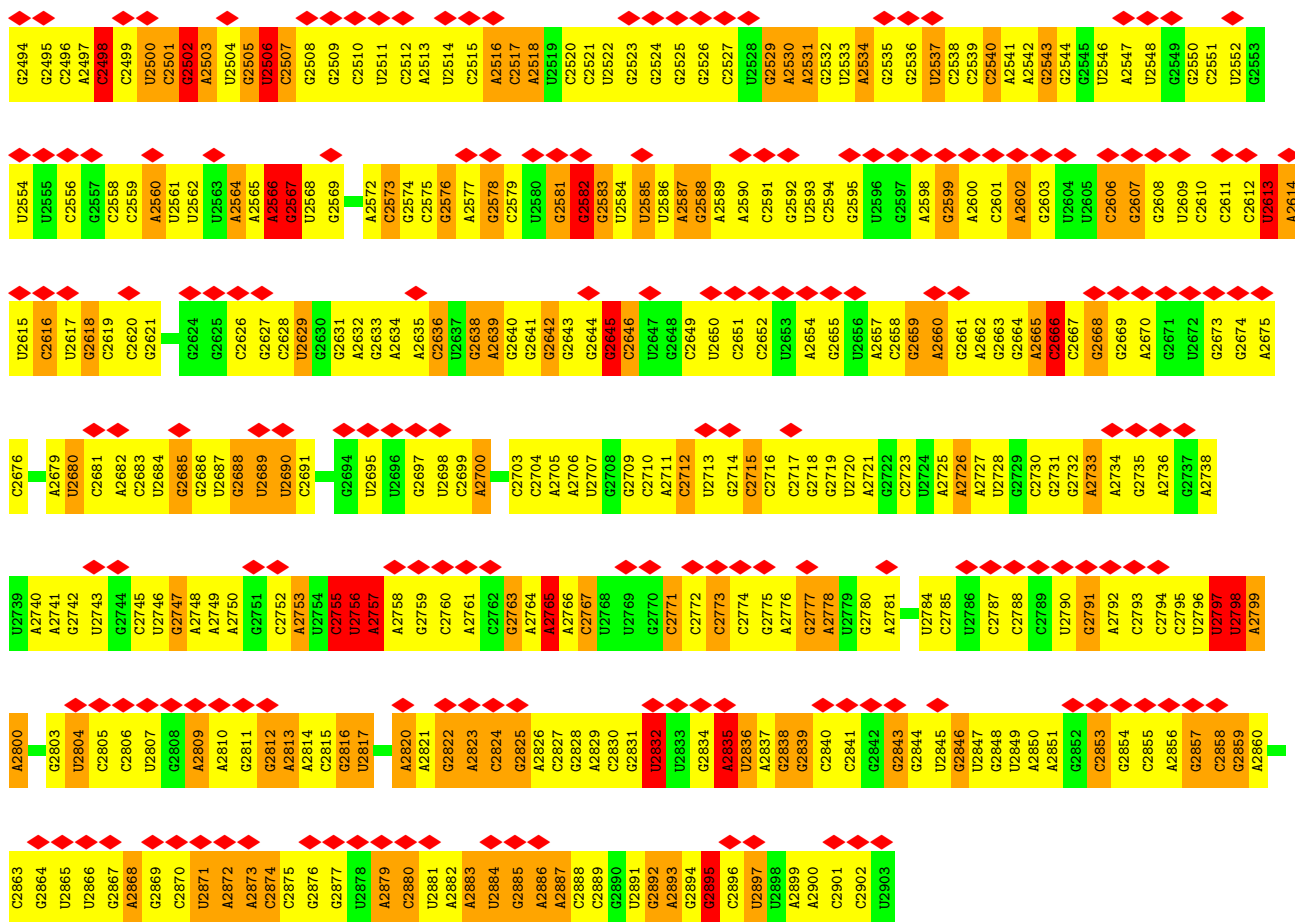
- Molecule 53: 23S ribosomal RNA



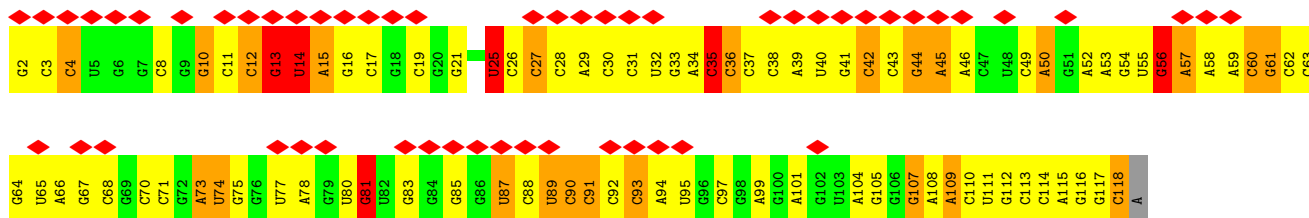
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U852	U85	G187	G247	A309	U369	A429	G489	G549	C610	C672	G732	A792	U852
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G855	G88	A190	G250	G312	G372	A432	C492	U852	A613	A675	C735	C795	G855
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G862	G76	C198	C257	A320	G378	A439	U499	U859	A621	G682	A743	G801	G862
A863	C77	A199	C258	U321	G379	A440	G500	C560	A622	U683	U744	A802	A863
G864	G77	U200	U201	G322	G380	C441	A501	G561	G623	G684	G745	U803	G864
C865	U78	U202	U202	C323	G381	U442	A502	U861	C624	A685	U746	A804	C865
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C867	G80	A204	G205	G325	C383	A444	A504	C564	A626	C687	U748	U807	C867
U868	A83	U206	A265	G327	C385	C445	A505	C565	A627	U688	U749	G808	U868
G869	A84	G207	G266	U328	G386	G446	A506	U867	G628	U689	A751	A809	G869
U870	G85	C208	C267	G329	U387	A447	C509	U868	G629	C691	A752	U810	U870
U871	G86	C209	C268	A330	U388	U448	C510	U869	A631	A692	A753	U811	U871
U872	U87	C210	C269	G331	G389	A449	G511	G570	A632	C693	U754	U812	U872
C873	A88	C211	A270	G332	U390	U451	G512	U871	A633	A694	U755	U813	C873
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C875	U90	G213	G272	C334	U392	A453	A514	U872	C635	G696	A757	C815	C875
U876	A91	G214	A272	C335	U393	A454	A515	A573	G636	C697	A758	C816	U876
C877	U92	G215	G273	C336	G394	C455	C516	A574	U637	U698	U759	C817	C877
A878	G93	C216	C274	G337	U395	C456	C517	U875	A638	A699	G760	A818	A878
C879	A94	A217	U275	G338	U397	A457	G518	U876	C639	G700	A761	A819	C879
G880	A95	A218	U276	U339	G398	G458	G519	U877	U640	U701	U762	A820	G880
U881	C96	A219	G277	A340	C399	U459	G520	U878	U641	G702	G763	A821	U881
G882	C97	G220	A278	C341	U399	A460	A521	C581	U642	U703	A764	A822	G882
C883	U98	G221	G281	C342	G400	C461	A522	A582	U643	G704	C765	A823	C883
U884	U100	A222	U280	C343	A402	C462	C523	C583	U644	A705	U766	U824	U884
C885	A101	A223	A342	C344	U403	G463	G524	U885	U645	A706	U767	U825	C885
A886	U102	A224	G282	A345	U404	U464	U525	C587	G646	G707	G768	U826	A886
U887	A103	C225	G283	U346	A405	G465	A526	U888	U647	G708	U769	U827	U887
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C890	G106	G228	C287	C351	G408	U467	A529	U891	C650	G711	G772	G830	C890
A891	C107	C229	U288	C352	G409	G468	A530	U892	U651	U712	A773	A831	A891
C892	U107	G230	G289	C353	U410	U469	A531	U893	U652	G713	G774	U832	C892
U893	G108	A231	U290	A354	G411	A470	A532	U894	U653	G714	G775	A833	U893
C894	C109	G232	G291	U355	A412	A471	G533	U895	A654	U715	G776	C834	C894
U895	G110	U233	U292	G356	C413	A472	U534	U896	A655	A716	G777	U835	U895
A896	A111	U234	G293	C357	U414	G473	C535	U897	G656	G717	G778	C836	A896
C897	U112	U235	U294	U358	U415	U474	G536	U898	U657	C718	U779	U837	C897
G898	U113	G236	U295	U359	U416	C475	G537	U899	U658	A719	G780	U838	G898
A899	U114	C237	G296	G359	U417	G476	G538	A599	U659	C720	A781	U839	A899
C900	C115	U238	U297	U360	C418	A477	G539	G600	C660	U721	A782	A840	C900
G901	G116	C239	G298	G361	U419	A478	G540	C601	A661	A722	A783	A841	G901
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U903	G117	G241	G301	G363	C421	A480	A541	A603	U663	A724	G785	U843	U903
A905	A118	U242	C302	U365	U422	A481	C542	U606	G664	C725	C786	U844	A905
G906	A119	G243	G303	U366	A423	A482	G543	U607	U665	U726	C787	U845	G906
C907	U120	U244	U304	C366	A424	A483	C544	U608	U666	G727	A788	A846	C907
U908	G121	A181	C305	U306	C425	C484	U545	U609	U667	G728	A789	A847	U908
A909	G122	C182	U306	U306	C426	C485	U546	U610	A668	A729	G789	A848	A909
	G123	C183				C486			G669	G729		A849	

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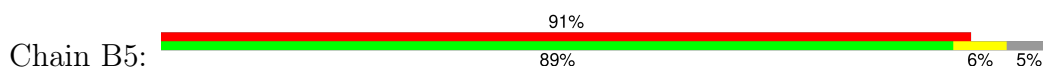
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C2374	C2375	A2376	A2377	A2378	C2379	C2380	A2381	C2382	G2383	U2384	C2385	A2386	U2387	A2388	G2389	U2390	C2391	A2392	U2393	C2394	C2395	G2396	U2397	U2398	G2399	G2400	U2401	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	A2410	A2411	A2412	G2413	G2414	C2415	C2416	C2417	A2418	U2419	C2420	G2421	C2422	U2423	C2424	A2425	A2426	C2427	G2428	G2429	A2430	U2431	A2432	A2433	
U2312	C2313	A2314	G2315	C2316	A2317	G2318	G2319	U2320	U2321	A2322	G2323	U2324	G2325	A2326	C2327	A2328	G2331	C2332	A2333	U2334	A2335	A2336	G2337	C2338	C2339	A2340	G2341	U2342	C2343	U2344	G2345	A2346	C2347	U2348	G2349	C2350	C2351	A2352	C2353	C2354	G2355	U2356	C2357	A2358	C2359	G2360	G2361	C2362	G2363	U2364	G2365	A2366	G2367	C2368	A2369	U2372	G2373			
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- Molecule 54: 5S ribosomal RNA



- Molecule 55: 50S ribosomal protein L1



V124	G125	Q126	L127	G128	Q129	V130	L131	G132	P133	R134	G135	L136	M137	P138	N139	P140	K141	V142	G143	T144	V145	T146	P147	N148	V149	A150	E151	A152	V153	K154	N155	A156	K157	A158	G159	Q160	V161	R162	Y163	R164	N165	D166	K167	N168	G169	I170	I171	H172	T173	T174	I175	G176	K177	V178	D179	F180	D181	A182	D183
K184	L185	K186	E187	N188	L189	E190	A191	L192	L193	V194	A195	L196	K197	K198	A199	K200	P201	A204	K205	G206	V207	Y208	I209	K210	K211	V212	S213	I214	S215	T216	T217	M218	G219	A220	G221	V222	A223	V224	ASP	GLN	ALA	GLY	LEU	SER	ALA	SER	VAL	ASN											

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	26429	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	local	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	160	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	162740	Depositor
Image detector	GENERIC TVIPS (4k x 4k)	Depositor
Maximum map value	223.953	Depositor
Minimum map value	-122.023	Depositor
Average map value	-0.756	Depositor
Map value standard deviation	22.478	Depositor
Recommended contour level	40	Depositor
Map size (\AA)	359.04, 359.04, 359.04	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.87, 1.87, 1.87	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CM0, 6MZ, ACE, PSU, NH2, 7MG, 4SU, 5MU, FME

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	AB	0.69	0/1736	1.15	8/2340 (0.3%)
2	AC	0.77	0/1651	1.28	18/2225 (0.8%)
3	AD	0.80	0/1665	1.26	20/2227 (0.9%)
4	AE	0.72	0/1119	1.20	11/1506 (0.7%)
5	AF	0.76	0/835	1.23	7/1128 (0.6%)
6	AG	0.76	0/1188	1.28	12/1593 (0.8%)
7	AH	0.71	0/989	1.11	5/1326 (0.4%)
8	AI	0.83	0/1035	1.37	14/1377 (1.0%)
9	AJ	0.78	0/797	1.33	11/1079 (1.0%)
10	AK	0.76	0/894	1.26	9/1207 (0.7%)
11	AL	0.77	0/969	1.37	17/1300 (1.3%)
12	AM	0.79	0/884	1.35	11/1181 (0.9%)
13	AN	0.82	0/817	1.41	11/1088 (1.0%)
14	AO	0.72	0/722	1.29	13/964 (1.3%)
15	AP	0.84	0/648	1.28	7/870 (0.8%)
16	AQ	0.73	0/658	1.19	5/883 (0.6%)
17	AR	0.80	0/463	1.21	5/623 (0.8%)
18	AS	0.76	0/653	1.27	4/879 (0.5%)
19	AT	0.71	0/672	1.12	5/890 (0.6%)
20	AU	0.85	0/431	1.31	6/572 (1.0%)
21	AA	1.75	365/36759 (1.0%)	2.28	2447/57346 (4.3%)
22	A1	1.75	20/1668 (1.2%)	2.26	110/2595 (4.2%)
23	A2	1.66	1/343 (0.3%)	2.18	17/531 (3.2%)
24	BC	0.81	0/2121	1.35	26/2852 (0.9%)
25	BD	0.71	0/1586	1.18	9/2134 (0.4%)
26	BE	0.72	0/1571	1.19	11/2113 (0.5%)
27	BF	0.77	0/1444	1.26	16/1937 (0.8%)
28	BG	0.71	0/1343	1.18	10/1816 (0.6%)
29	BH	0.68	0/1122	1.16	7/1515 (0.5%)
30	BI	0.68	0/1046	1.07	5/1410 (0.4%)
31	BJ	0.75	0/1152	1.23	9/1551 (0.6%)
32	BK	0.76	0/947	1.23	10/1268 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BL	0.79	0/1054	1.29	12/1403 (0.9%)
34	BM	0.80	0/1093	1.22	10/1460 (0.7%)
35	BN	0.83	0/973	1.44	18/1301 (1.4%)
36	BO	0.77	0/902	1.29	9/1209 (0.7%)
37	BP	0.78	0/929	1.25	9/1242 (0.7%)
38	BQ	0.81	0/960	1.36	14/1278 (1.1%)
39	BR	0.72	0/829	1.13	6/1107 (0.5%)
40	BS	0.70	0/864	1.28	10/1156 (0.9%)
41	BT	0.72	0/744	1.22	4/994 (0.4%)
42	BU	0.72	0/787	1.15	5/1051 (0.5%)
43	BV	0.74	0/766	1.27	8/1025 (0.8%)
44	BW	0.78	0/604	1.24	6/799 (0.8%)
45	BX	0.84	0/635	1.35	10/848 (1.2%)
46	BY	0.71	0/510	1.24	4/677 (0.6%)
47	BZ	0.73	0/453	1.31	6/605 (1.0%)
48	B0	0.80	0/450	1.26	8/599 (1.3%)
49	B1	0.73	0/417	1.14	3/556 (0.5%)
50	B2	0.89	0/380	1.58	10/498 (2.0%)
51	B3	0.79	0/513	1.23	6/676 (0.9%)
52	B4	0.80	0/303	1.35	6/397 (1.5%)
53	BA	1.77	819/69796 (1.2%)	2.30	4869/108888 (4.5%)
54	BB	1.74	17/2800 (0.6%)	2.24	176/4367 (4.0%)
55	B5	0.69	0/1673	1.11	8/2255 (0.4%)
All	All	1.54	1222/158363 (0.8%)	2.07	8093/236717 (3.4%)

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
18	AS	0	1
21	AA	0	328
22	A1	0	18
23	A2	0	2
53	BA	0	652
54	BB	0	27
All	All	0	1028

The worst 5 of 1222 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	BA	2078	C	C4-N4	-7.15	1.27	1.33
21	AA	1521	C	C4-N4	-7.01	1.27	1.33
53	BA	897	C	C4-N4	-6.68	1.27	1.33
21	AA	1214	C	C4-N4	-6.67	1.27	1.33
21	AA	637	C	C4-N4	-6.64	1.27	1.33

The worst 5 of 8093 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	BA	323	C	O4'-C1'-N1	14.98	120.18	108.20
53	BA	1932	A	N1-C6-N6	-13.12	110.73	118.60
53	BA	800	A	N1-C6-N6	-12.78	110.93	118.60
21	AA	1502	A	N1-C6-N6	-12.44	111.14	118.60
53	BA	219	A	N1-C6-N6	-12.42	111.15	118.60

There are no chirality outliers.

5 of 1028 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	AA	21	G	Sidechain
21	AA	35	G	Sidechain
21	AA	36	C	Sidechain
21	AA	6	G	Sidechain
18	AS	74	ALA	Peptide

5.2 Too-close contacts [i](#)

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	AB	1708	0	1736	1	0
2	AC	1625	0	1699	2	0
3	AD	1643	0	1710	0	0
4	AE	1109	0	1152	0	0
5	AF	818	0	808	0	0
6	AG	1178	0	1234	0	0
7	AH	979	0	1034	0	0
8	AI	1025	0	1074	0	0
9	AJ	790	0	832	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	AK	880	0	891	0	0
11	AL	955	0	1019	0	0
12	AM	877	0	937	0	0
13	AN	805	0	844	0	0
14	AO	714	0	737	0	0
15	AP	639	0	656	0	0
16	AQ	652	0	695	1	0
17	AR	459	0	482	0	0
18	AS	641	0	669	0	0
19	AT	668	0	718	0	0
20	AU	429	0	453	0	0
21	AA	32828	0	16108	7	0
22	A1	1627	0	808	0	0
23	A2	309	0	158	0	0
24	BC	2083	0	2157	0	0
25	BD	1565	0	1616	0	0
26	BE	1552	0	1619	0	0
27	BF	1420	0	1460	1	0
28	BG	1323	0	1374	0	0
29	BH	1111	0	1148	0	0
30	BI	1032	0	1088	0	0
31	BJ	1129	0	1162	1	0
32	BK	939	0	1012	1	0
33	BL	1045	0	1117	2	0
34	BM	1074	0	1157	1	0
35	BN	961	0	1000	0	0
36	BO	892	0	923	0	0
37	BP	917	0	965	0	0
38	BQ	947	0	1022	0	0
39	BR	816	0	839	1	0
40	BS	857	0	922	0	0
41	BT	739	0	807	0	0
42	BU	780	0	834	0	0
43	BV	753	0	780	0	0
44	BW	599	0	614	0	0
45	BX	625	0	655	0	0
46	BY	509	0	543	0	0
47	BZ	449	0	491	1	0
48	B0	444	0	461	0	0
49	B1	413	0	444	1	0
50	B2	377	0	418	0	0
51	B3	504	0	574	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	B4	302	0	343	0	0
53	BA	62317	0	30428	10	0
54	BB	2504	0	1247	0	0
55	B5	1658	0	1751	0	0
56	A1	7	0	8	0	0
57	BA	10	0	10	1	0
All	All	146011	0	97443	27	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 0.

The worst 5 of 27 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)
53:BA:2644:G:H2'	53:BA:2645:G:C8	2.46	0.51
53:BA:1287:A:H2'	53:BA:1288:G:C2	2.47	0.50
49:B1:9:LYS:HE3	49:B1:19:PHE:CD2	2.49	0.48
21:AA:292:G:C5	21:AA:293:G:H1'	2.48	0.47
33:BL:54:GLN:HE21	53:BA:2428:G:N2	2.11	0.47

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	AB	218/220 (99%)	193 (88%)	24 (11%)	1 (0%)	25 64
2	AC	205/208 (99%)	186 (91%)	11 (5%)	8 (4%)	2 19
3	AD	203/206 (98%)	192 (95%)	9 (4%)	2 (1%)	13 49
4	AE	150/152 (99%)	141 (94%)	5 (3%)	4 (3%)	4 25
5	AF	99/101 (98%)	87 (88%)	11 (11%)	1 (1%)	13 49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AG	150/152 (99%)	138 (92%)	8 (5%)	4 (3%)	4	25
7	AH	127/130 (98%)	121 (95%)	5 (4%)	1 (1%)	16	55
8	AI	126/128 (98%)	115 (91%)	9 (7%)	2 (2%)	8	38
9	AJ	98/100 (98%)	87 (89%)	8 (8%)	3 (3%)	3	22
10	AK	116/118 (98%)	108 (93%)	6 (5%)	2 (2%)	7	37
11	AL	121/124 (98%)	111 (92%)	6 (5%)	4 (3%)	3	21
12	AM	112/115 (97%)	94 (84%)	15 (13%)	3 (3%)	4	25
13	AN	98/101 (97%)	89 (91%)	7 (7%)	2 (2%)	6	32
14	AO	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
15	AP	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
16	AQ	80/82 (98%)	73 (91%)	6 (8%)	1 (1%)	10	43
17	AR	55/57 (96%)	51 (93%)	2 (4%)	2 (4%)	3	20
18	AS	79/81 (98%)	73 (92%)	3 (4%)	3 (4%)	2	19
19	AT	84/86 (98%)	74 (88%)	7 (8%)	3 (4%)	3	20
20	AU	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
24	BC	270/273 (99%)	245 (91%)	17 (6%)	8 (3%)	3	23
25	BD	207/209 (99%)	174 (84%)	21 (10%)	12 (6%)	1	14
26	BE	199/201 (99%)	182 (92%)	13 (6%)	4 (2%)	6	32
27	BF	176/179 (98%)	143 (81%)	26 (15%)	7 (4%)	2	18
28	BG	174/177 (98%)	152 (87%)	18 (10%)	4 (2%)	5	28
29	BH	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	19	57
30	BI	139/142 (98%)	128 (92%)	11 (8%)	0	100	100
31	BJ	140/142 (99%)	129 (92%)	6 (4%)	5 (4%)	3	20
32	BK	121/123 (98%)	105 (87%)	11 (9%)	5 (4%)	2	18
33	BL	141/144 (98%)	117 (83%)	14 (10%)	10 (7%)	1	11
34	BM	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	8	40
35	BN	119/121 (98%)	103 (87%)	13 (11%)	3 (2%)	4	26
36	BO	114/117 (97%)	108 (95%)	6 (5%)	0	100	100
37	BP	112/115 (97%)	99 (88%)	10 (9%)	3 (3%)	4	25
38	BQ	115/118 (98%)	108 (94%)	5 (4%)	2 (2%)	7	37
39	BR	101/103 (98%)	91 (90%)	8 (8%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	BS	108/110 (98%)	97 (90%)	10 (9%)	1 (1%)	14	52
41	BT	92/94 (98%)	73 (79%)	11 (12%)	8 (9%)	0	9
42	BU	101/104 (97%)	86 (85%)	10 (10%)	5 (5%)	1	16
43	BV	92/94 (98%)	82 (89%)	8 (9%)	2 (2%)	5	29
44	BW	78/80 (98%)	62 (80%)	8 (10%)	8 (10%)	0	6
45	BX	75/79 (95%)	64 (85%)	8 (11%)	3 (4%)	2	18
46	BY	61/63 (97%)	55 (90%)	4 (7%)	2 (3%)	3	21
47	BZ	56/59 (95%)	50 (89%)	5 (9%)	1 (2%)	7	35
48	B0	54/57 (95%)	50 (93%)	3 (6%)	1 (2%)	6	32
49	B1	50/52 (96%)	45 (90%)	4 (8%)	1 (2%)	6	32
50	B2	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	5	28
51	B3	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
52	B4	36/38 (95%)	32 (89%)	2 (6%)	2 (6%)	1	14
55	B5	221/234 (94%)	211 (96%)	8 (4%)	2 (1%)	14	52
All	All	5876/6008 (98%)	5278 (90%)	447 (8%)	151 (3%)	6	26

5 of 151 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AE	105	ILE
24	BC	206	LYS
25	BD	9	VAL
25	BD	150	GLN
25	BD	188	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	
1	AB	180/180 (100%)	177 (98%)	3 (2%)	56	72
2	AC	170/171 (99%)	169 (99%)	1 (1%)	84	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AD	172/173 (99%)	171 (99%)	1 (1%)	84	88
4	AE	113/113 (100%)	112 (99%)	1 (1%)	75	83
5	AF	87/87 (100%)	85 (98%)	2 (2%)	45	64
6	AG	123/123 (100%)	122 (99%)	1 (1%)	79	85
7	AH	104/105 (99%)	103 (99%)	1 (1%)	73	82
8	AI	105/105 (100%)	102 (97%)	3 (3%)	37	56
9	AJ	86/86 (100%)	84 (98%)	2 (2%)	45	64
10	AK	90/90 (100%)	88 (98%)	2 (2%)	47	65
11	AL	103/104 (99%)	101 (98%)	2 (2%)	52	69
12	AM	91/92 (99%)	91 (100%)	0	100	100
13	AN	83/84 (99%)	80 (96%)	3 (4%)	30	50
14	AO	76/77 (99%)	74 (97%)	2 (3%)	41	59
15	AP	65/65 (100%)	64 (98%)	1 (2%)	60	75
16	AQ	74/74 (100%)	73 (99%)	1 (1%)	62	75
17	AR	48/48 (100%)	47 (98%)	1 (2%)	48	66
18	AS	70/70 (100%)	67 (96%)	3 (4%)	25	46
19	AT	65/65 (100%)	64 (98%)	1 (2%)	60	75
20	AU	44/44 (100%)	43 (98%)	1 (2%)	45	64
24	BC	216/217 (100%)	214 (99%)	2 (1%)	75	83
25	BD	164/164 (100%)	162 (99%)	2 (1%)	67	78
26	BE	165/165 (100%)	161 (98%)	4 (2%)	44	62
27	BF	149/150 (99%)	144 (97%)	5 (3%)	32	51
28	BG	137/138 (99%)	134 (98%)	3 (2%)	47	65
29	BH	114/114 (100%)	113 (99%)	1 (1%)	75	83
30	BI	109/110 (99%)	108 (99%)	1 (1%)	75	83
31	BJ	116/116 (100%)	115 (99%)	1 (1%)	75	83
32	BK	103/103 (100%)	98 (95%)	5 (5%)	21	42
33	BL	102/103 (99%)	100 (98%)	2 (2%)	50	68
34	BM	109/109 (100%)	106 (97%)	3 (3%)	38	57
35	BN	100/100 (100%)	98 (98%)	2 (2%)	50	68
36	BO	86/87 (99%)	85 (99%)	1 (1%)	67	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BP	99/100 (99%)	98 (99%)	1 (1%)	73	82
38	BQ	89/90 (99%)	89 (100%)	0	100	100
39	BR	84/84 (100%)	82 (98%)	2 (2%)	44	62
40	BS	93/93 (100%)	91 (98%)	2 (2%)	47	65
41	BT	80/80 (100%)	78 (98%)	2 (2%)	42	61
42	BU	83/84 (99%)	83 (100%)	0	100	100
43	BV	78/78 (100%)	76 (97%)	2 (3%)	41	59
44	BW	59/59 (100%)	55 (93%)	4 (7%)	13	34
45	BX	67/68 (98%)	65 (97%)	2 (3%)	36	55
46	BY	55/55 (100%)	55 (100%)	0	100	100
47	BZ	48/49 (98%)	45 (94%)	3 (6%)	15	36
48	B0	47/48 (98%)	46 (98%)	1 (2%)	48	66
49	B1	45/45 (100%)	44 (98%)	1 (2%)	47	65
50	B2	38/38 (100%)	37 (97%)	1 (3%)	41	59
51	B3	51/52 (98%)	48 (94%)	3 (6%)	16	37
52	B4	34/34 (100%)	34 (100%)	0	100	100
55	B5	173/181 (96%)	167 (96%)	6 (4%)	31	51
All	All	4842/4870 (99%)	4748 (98%)	94 (2%)	52	69

5 of 94 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	BL	39	LYS
43	BV	12	GLN
34	BM	97	GLN
39	BR	2	TYR
44	BW	39	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
52	B4	37	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
21	AA	1530/1533 (99%)	195 (12%)	46 (3%)
22	A1	73/76 (96%)	7 (9%)	2 (2%)
23	A2	14/15 (93%)	4 (28%)	2 (14%)
53	BA	2902/2903 (99%)	455 (15%)	123 (4%)
54	BB	116/118 (98%)	19 (16%)	2 (1%)
All	All	4635/4645 (99%)	680 (14%)	175 (3%)

5 of 680 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
21	AA	6	G
21	AA	8	A
21	AA	9	G
21	AA	16	A
21	AA	32	A

5 of 175 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	BA	1266	G
53	BA	2062	A
53	BA	1289	C
53	BA	1625	C
53	BA	2288	A

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
22	7MG	A1	46	22	23,26,27	4.69	2 (8%)	27,39,42	1.49	1 (3%)
22	4SU	A1	7	22	18,21,22	1.51	2 (11%)	25,30,33	0.88	1 (4%)
22	5MU	A1	54	22	19,22,23	0.75	0	27,32,35	1.43	3 (11%)
22	CM0	A1	34	22,23	21,26,27	1.31	2 (9%)	26,37,40	1.11	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
22	PSU	A1	55	22	18,21,22	0.83	0	21,30,33	1.09	1 (4%)
22	6MZ	A1	37	22	17,25,26	1.07	1 (5%)	15,36,39	1.55	3 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	7MG	A1	46	22	-	0/7/37/38	0/3/3/3
22	4SU	A1	7	22	-	0/7/25/26	0/2/2/2
22	5MU	A1	54	22	-	0/7/25/26	0/2/2/2
22	CM0	A1	34	22,23	-	4/12/30/31	0/2/2/2
22	PSU	A1	55	22	-	1/7/25/26	0/2/2/2
22	6MZ	A1	37	22	-	0/5/27/28	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	A1	46	7MG	C8-N9	-22.10	1.31	1.45
22	A1	7	4SU	C5-C4	-5.34	1.36	1.42
22	A1	34	CM0	O5-C5	-4.69	1.25	1.36
22	A1	37	6MZ	C8-N7	-2.44	1.30	1.34
22	A1	46	7MG	C8-N7	-2.38	1.30	1.42

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	A1	46	7MG	N9-C8-N7	5.72	111.47	103.37
22	A1	54	5MU	C5M-C5-C6	-3.70	117.84	122.85
22	A1	37	6MZ	C2-N1-C6	3.20	119.08	116.60
22	A1	54	5MU	C6-C5-C4	3.07	120.55	118.02
22	A1	55	PSU	C6-C5-C4	2.95	120.17	118.17

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	A1	34	CM0	O5-C7-C8-O8
22	A1	34	CM0	O5-C7-C8-O9
22	A1	55	PSU	O4'-C1'-C5-C6

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Mol	Chain	Res	Type	Atoms
22	A1	34	CM0	C6-C5-O5-C7
22	A1	34	CM0	C4-C5-O5-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
57	FME	BA	3001	56	8,9,10	0.54	0	8,9,11	1.29	1 (12%)
56	VAL	A1	101	22,57	4,6,7	0.51	0	6,7,9	1.48	1 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
57	FME	BA	3001	56	-	2/7/9/11	-
56	VAL	A1	101	22,57	-	0/5/6/8	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	A1	101	VAL	O-C-CA	-3.58	115.55	124.77
57	BA	3001	FME	C-CA-N	2.46	114.25	109.50

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	BA	3001	FME	O1-CN-N-CA
57	BA	3001	FME	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
57	BA	3001	FME	1	0

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.

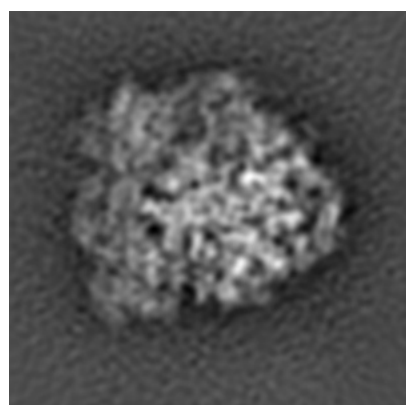
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1724. These allow visual inspection of the internal detail of the map and identification of artifacts.

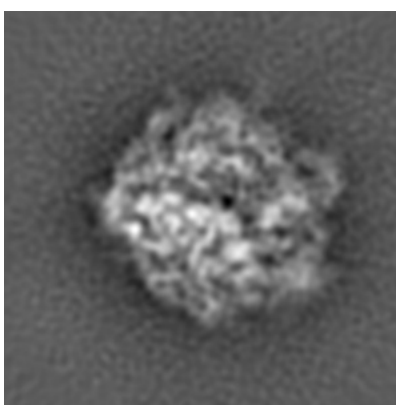
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

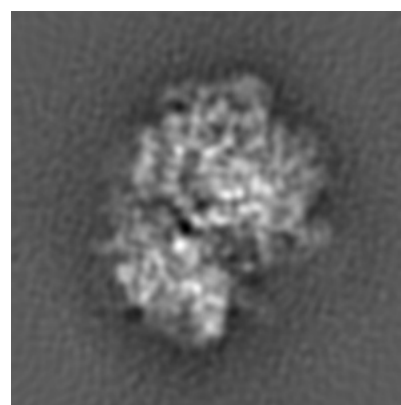
6.1.1 Primary map



X



Y

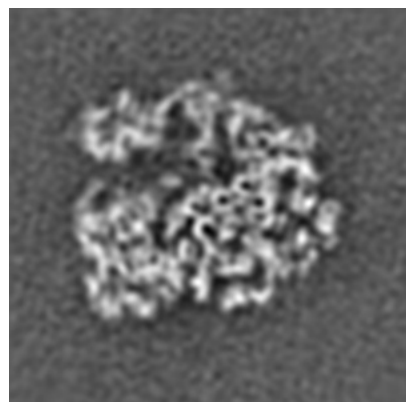


Z

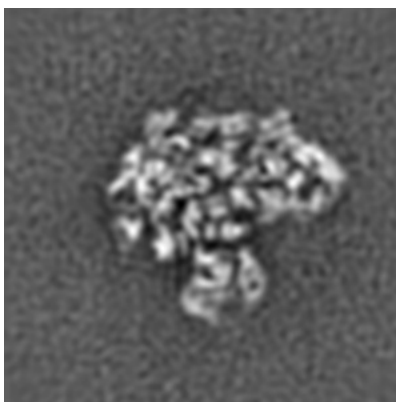
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

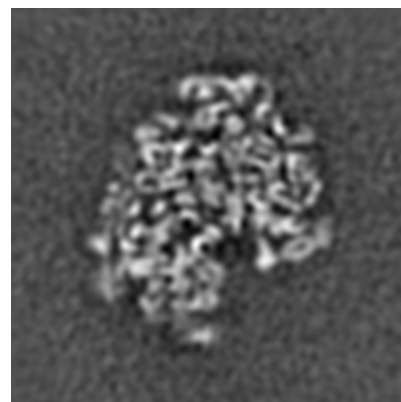
6.2.1 Primary map



X Index: 96



Y Index: 96

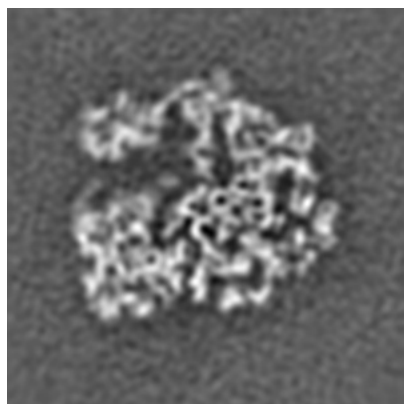


Z Index: 96

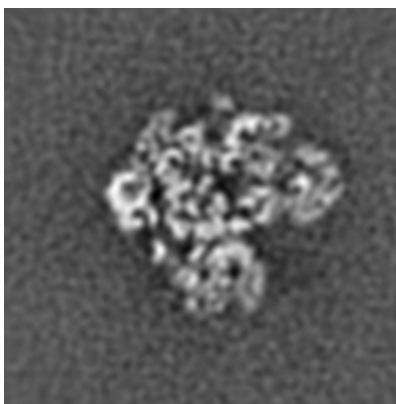
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

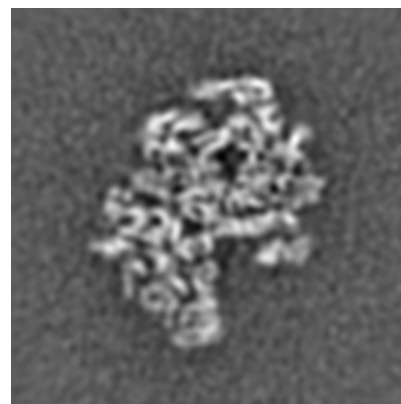
6.3.1 Primary map



X Index: 97



Y Index: 92

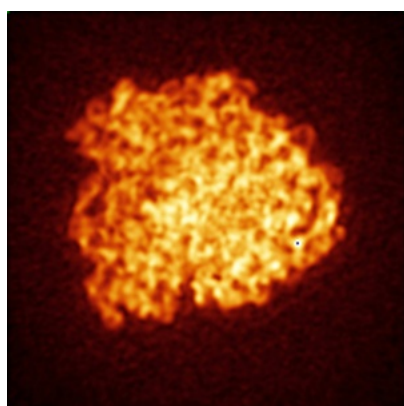


Z Index: 91

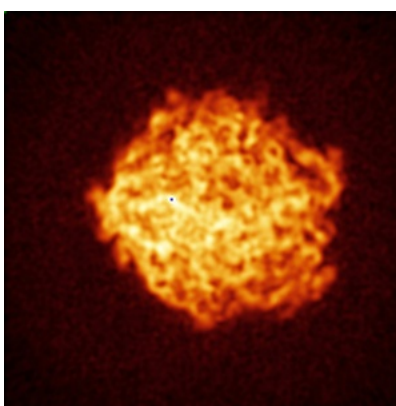
The images above show the largest variance slices of the map in three orthogonal directions.

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

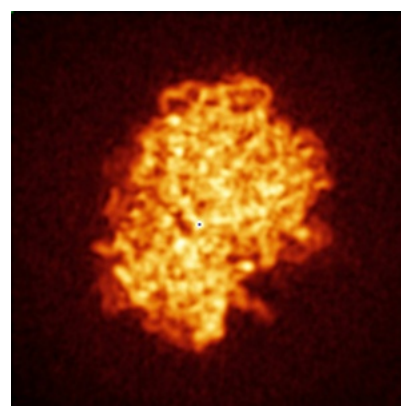
6.4.1 Primary map



X



Y

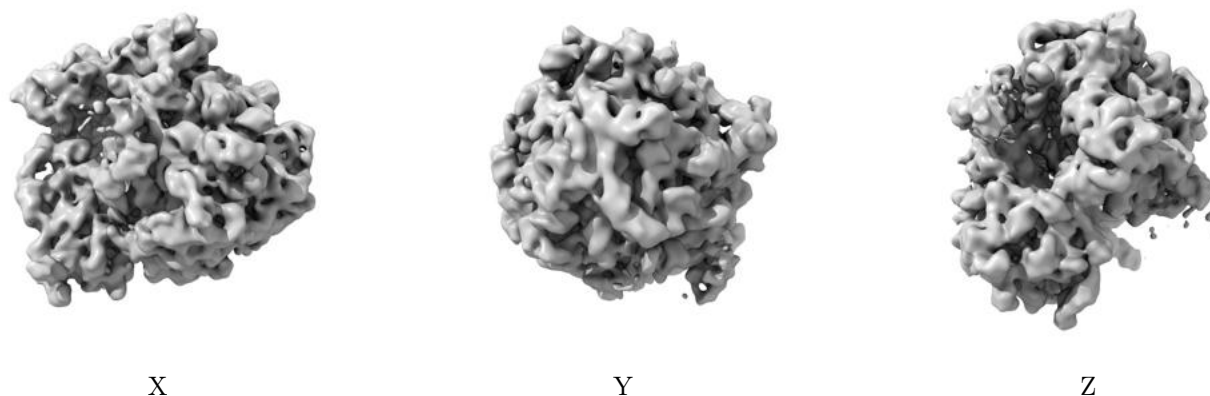


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 40.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

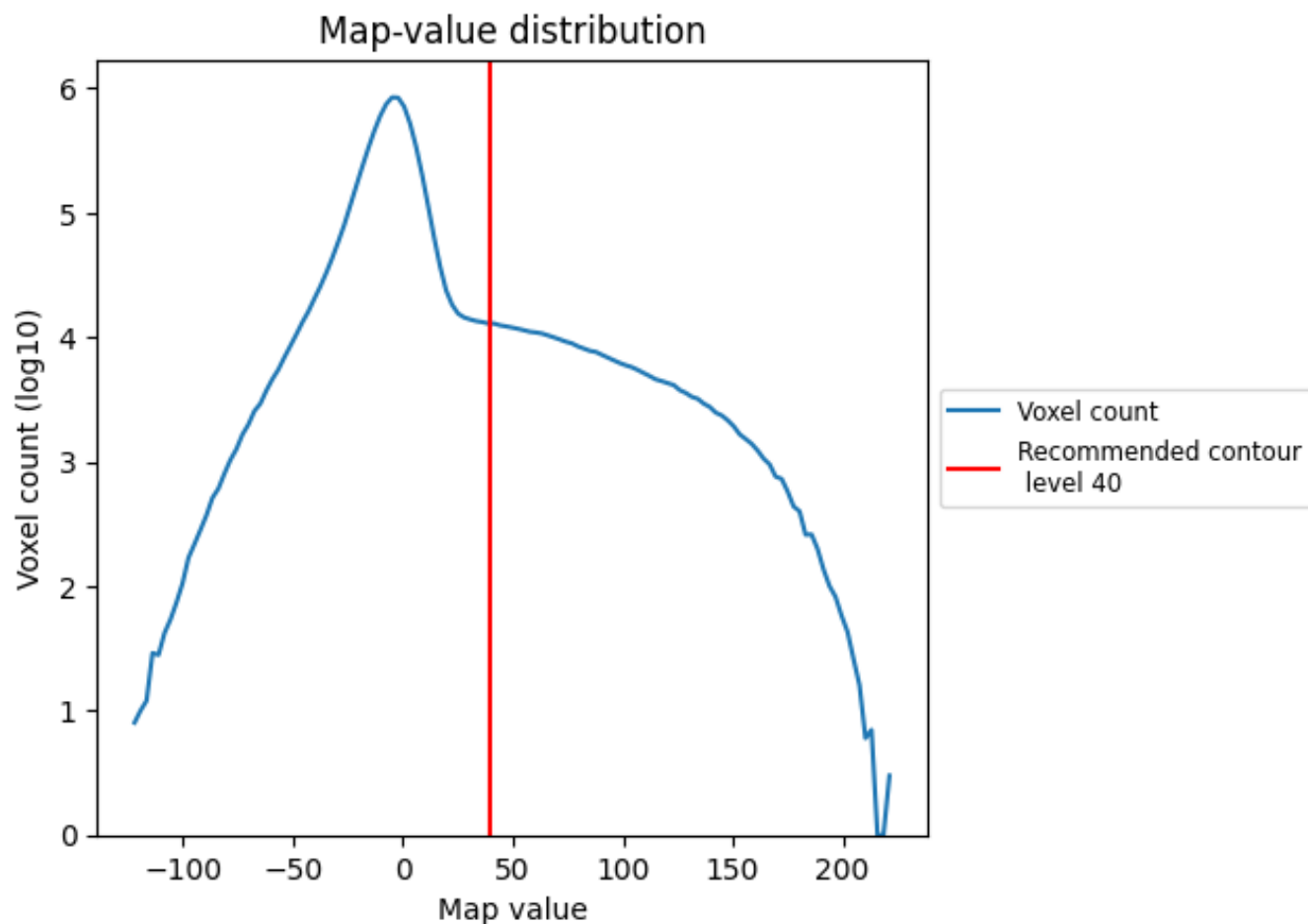
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

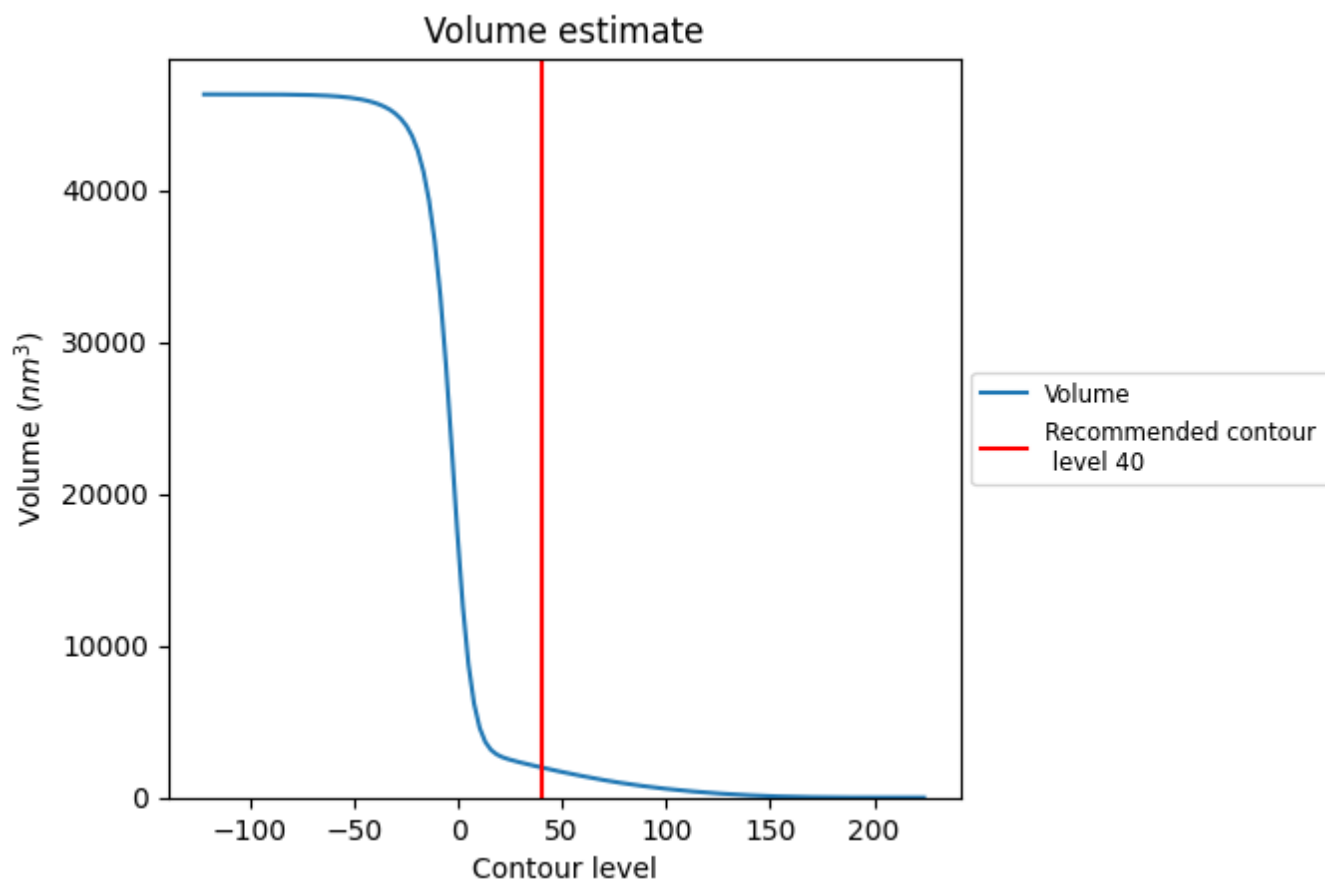
This section contains the results of statistical analysis of the map.

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.

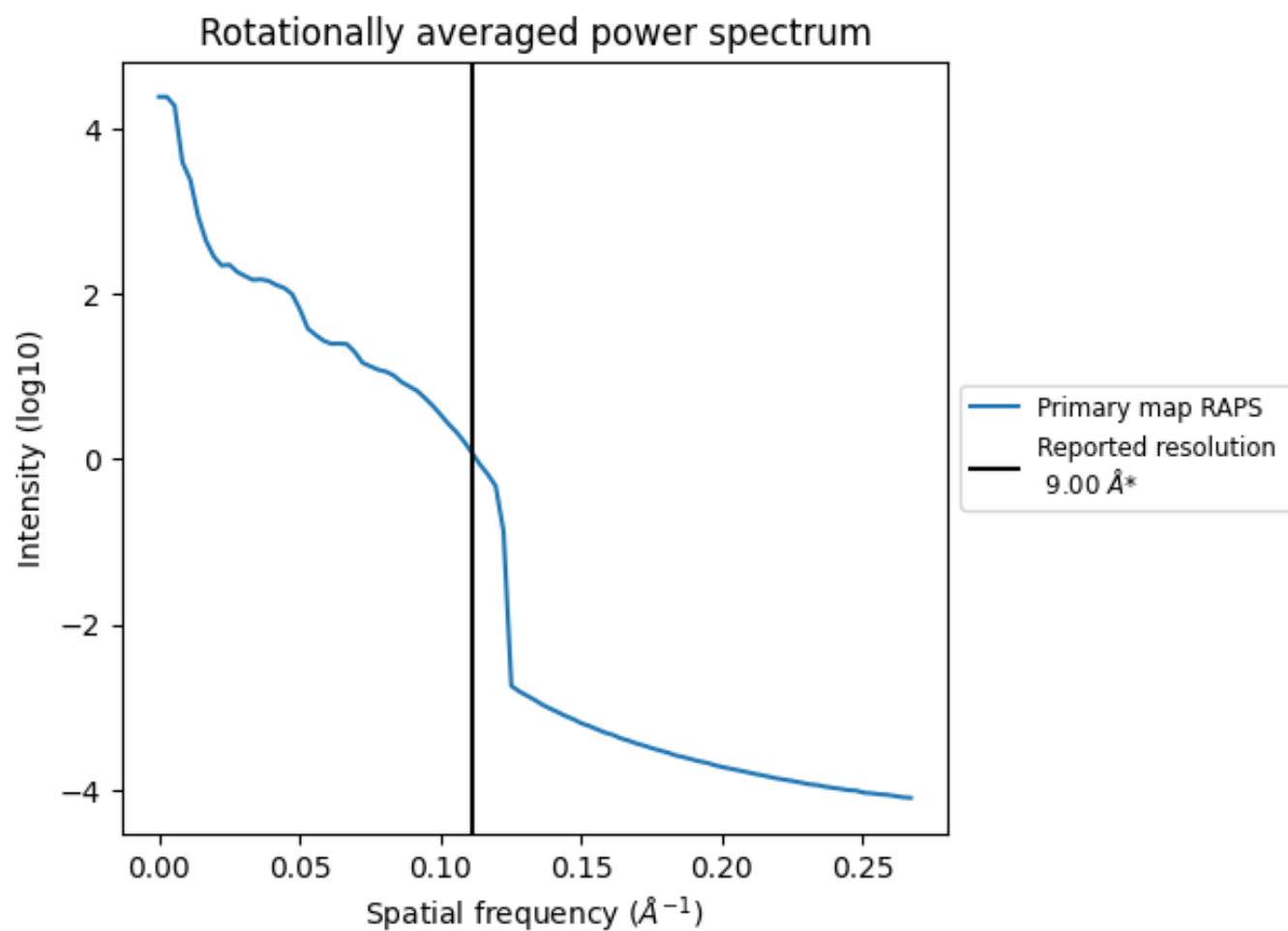
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1986 nm³; this corresponds to an approximate mass of 1794 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 0.111 Å⁻¹

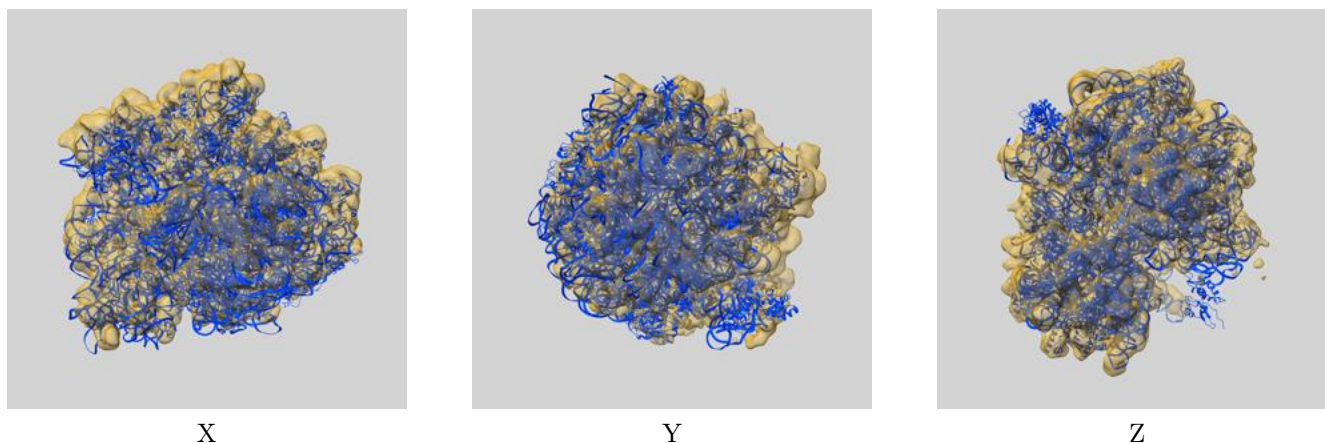
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

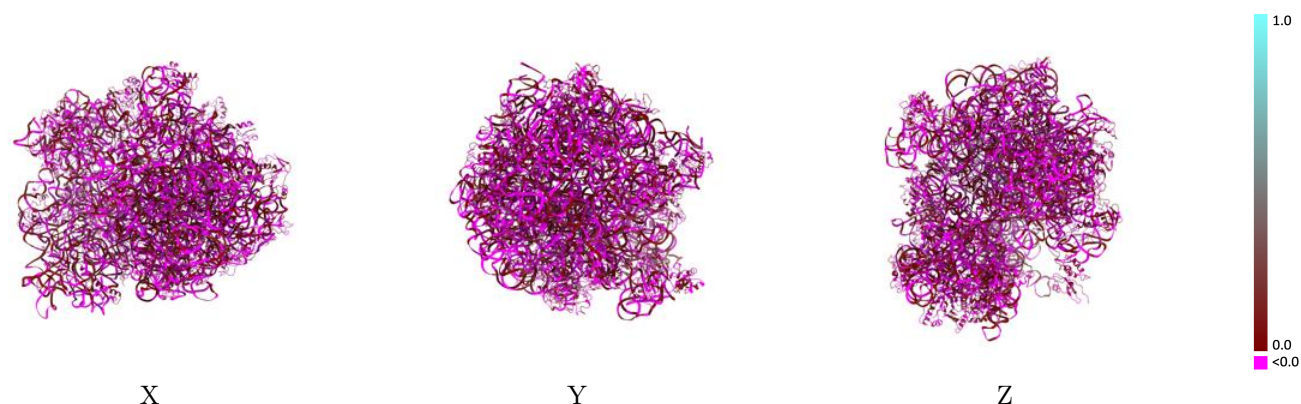
This section contains information regarding the fit between EMDB map EMD-1724 and PDB model 4V7A. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



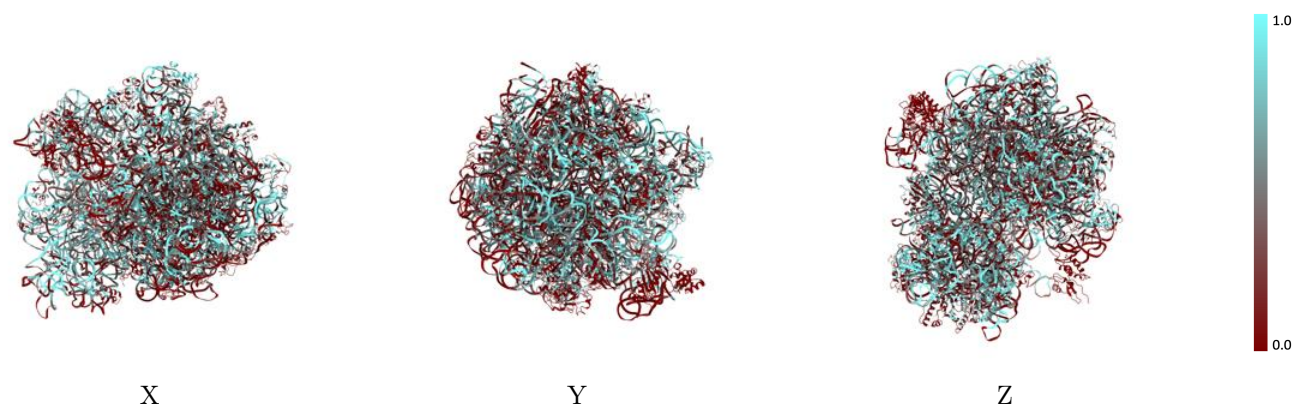
The images above show the 3D surface view of the map at the recommended contour level 40.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



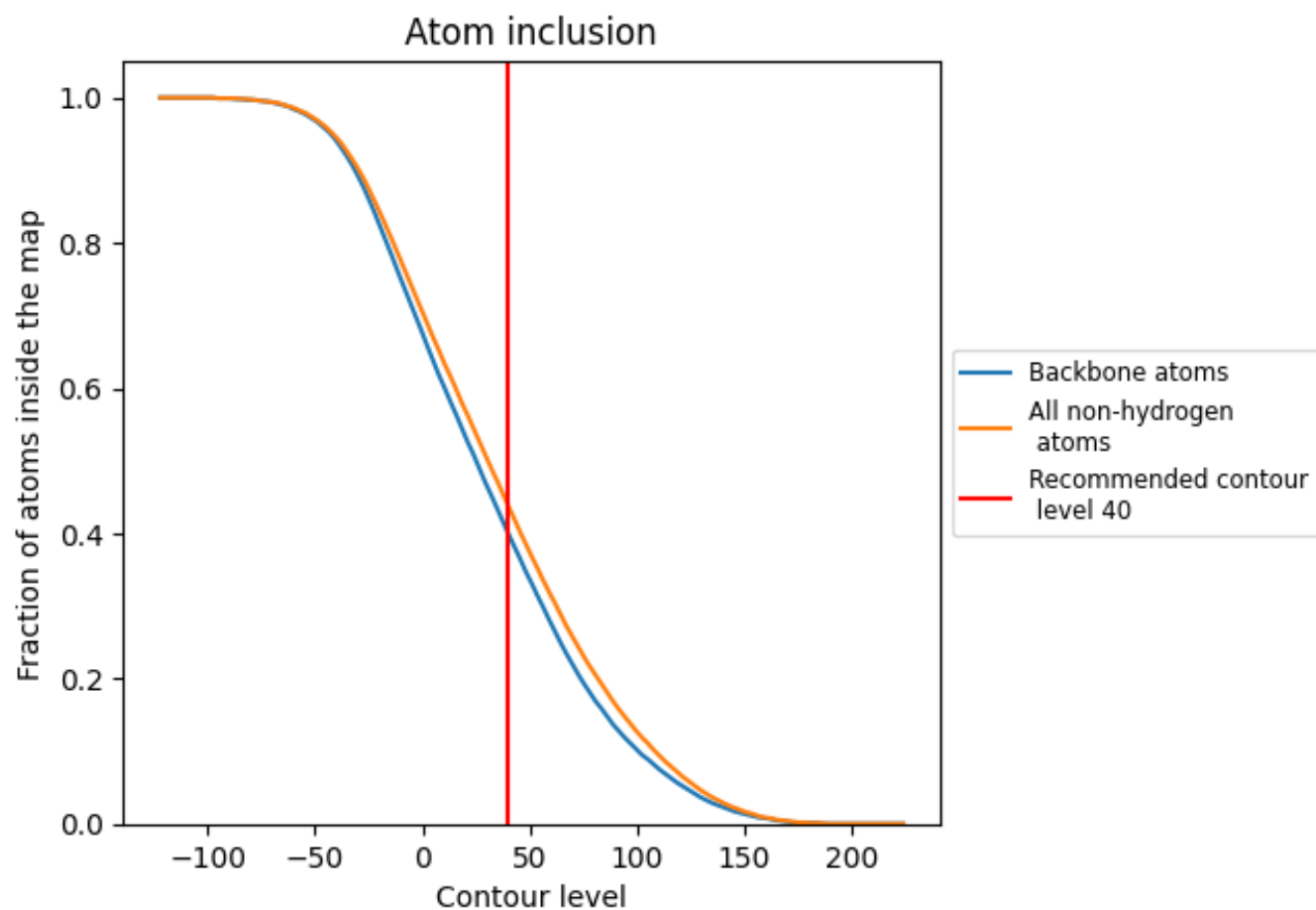
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (40).

9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 44% 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 (40) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4380	-0.0050
A1	0.4500	0.0020
A2	0.3240	-0.0520
AA	0.5080	-0.0040
AB	0.2660	-0.0000
AC	0.3560	-0.0030
AD	0.3420	-0.0160
AE	0.4300	0.0150
AF	0.2810	-0.0160
AG	0.4370	0.0260
AH	0.4790	-0.0000
AI	0.5390	0.0110
AJ	0.3010	0.0130
AK	0.3970	-0.0220
AL	0.3900	-0.0020
AM	0.5240	0.0280
AN	0.4630	0.0020
AO	0.3170	-0.0060
AP	0.4340	0.0060
AQ	0.3620	-0.0190
AR	0.4870	0.0390
AS	0.4380	0.0020
AT	0.3700	-0.0400
AU	0.2520	-0.0130
B0	0.3810	0.0110
B1	0.2010	-0.0140
B2	0.3630	-0.0360
B3	0.3400	-0.0240
B4	0.4420	-0.0230
B5	0.0340	0.0060
BA	0.4550	-0.0070
BB	0.4770	-0.0150
BC	0.4550	0.0110
BD	0.3840	-0.0090
BE	0.4580	-0.0020



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Chain	Atom inclusion	Q-score
BF	 0.4680	 0.0020
BG	 0.4030	 0.0180
BH	 0.0280	 -0.0480
BI	 0.0000	 0.0060
BJ	 0.4180	 0.0070
BK	 0.3750	 -0.0060
BL	 0.4410	 -0.0070
BM	 0.4380	 -0.0040
BN	 0.3220	 -0.0170
BO	 0.5420	 -0.0110
BP	 0.2450	 -0.0350
BQ	 0.4450	 0.0000
BR	 0.3090	 -0.0060
BS	 0.3840	 0.0010
BT	 0.3380	 -0.0040
BU	 0.2710	 -0.0030
BV	 0.4630	 -0.0050
BW	 0.3920	 -0.0280
BX	 0.3580	 -0.0250
BY	 0.2450	 -0.0170
BZ	 0.4780	 0.0010