



# wwPDB EM Validation Summary Report ⓘ

Feb 22, 2024 – 04:03 PM EST

PDB ID : 4V61  
EMDB ID : EMD-1417  
Title : Homology model for the Spinach chloroplast 30S subunit fitted to 9.4Å cryo-EM map of the 70S chlororibosome.  
Authors : Sharma, M.R.; Wilson, D.N.; Datta, P.P.; Barat, C.; Schluenzen, F.; Fucini, P.; Agrawal, R.K.  
Deposited on : 2007-11-09  
Resolution : 9.40 Å(reported)  
Based on initial models : 2XYZ, 2ZXY

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

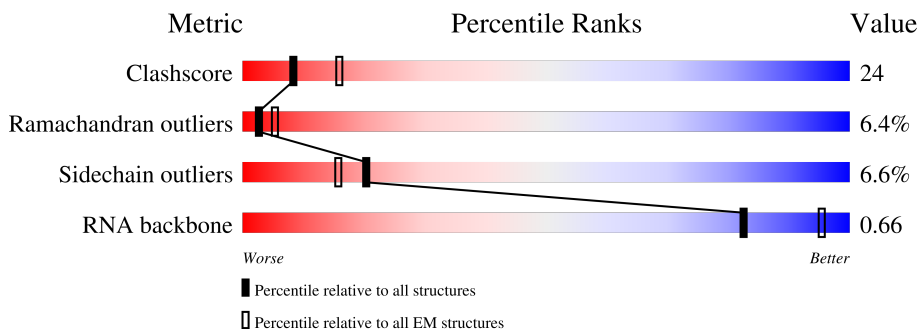
EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 9.40 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	AA	1491	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>16%</p> </div> <div style="text-align: center;"> <p>39%</p> </div> </div>
2	AB	231	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>88%</p> </div> <div style="text-align: center;"> <p>84%</p> </div> </div>
3	AC	218	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>39%</p> </div> <div style="text-align: center;"> <p>85%</p> </div> </div>
4	AD	201	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>45%</p> </div> <div style="text-align: center;"> <p>84%</p> </div> </div>
5	AE	308	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>24%</p> </div> <div style="text-align: center;"> <p>43%</p> </div> </div>
6	AF	168	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>29%</p> </div> <div style="text-align: center;"> <p>48%</p> </div> </div>
7	AG	155	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>72%</p> </div> <div style="text-align: center;"> <p>87%</p> </div> </div>

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Mol	Chain	Length	Quality of chain
8	AH	134	
9	AI	197	
10	AJ	197	
11	AK	140	
12	AL	123	
13	AM	145	
14	AN	100	
15	AO	90	
16	AP	88	
17	AQ	142	
18	AR	103	
19	AS	92	
20	AT	202	
21	AU	190	
22	BA	2810	
23	BB	117	
24	BC	103	
25	BD	352	
26	BE	269	
27	BF	259	
28	BG	293	
29	BH	220	
30	BI	223	
31	BJ	197	
32	BK	224	

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Mol	Chain	Length	Quality of chain
33	BL	250	
34	BM	121	
35	BN	257	
36	BO	135	
37	BP	205	
38	BQ	161	
39	BR	233	
40	BS	119	
41	BT	257	
42	BU	199	
43	BV	198	
44	BW	191	
45	BX	198	
46	BY	151	
47	BZ	173	
48	B1	144	
49	B2	57	
50	B3	66	
51	B4	152	
52	B5	159	
53	B6	104	

## 2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142250 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1478	31745	14154	5865	10249	1477	0	0

- Molecule 2 is a protein called Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AB	231	1827	1152	334	328	13	0	0

- Molecule 3 is a protein called Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AC	217	1744	1113	314	310	7	0	0

- Molecule 4 is a protein called Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AD	199	1632	1032	318	277	5	0	0

- Molecule 5 is a protein called Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AE	158	1190	742	230	212	6	0	0

- Molecule 6 is a protein called Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AF	107	872	558	145	166	3	0	0

- Molecule 7 is a protein called Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AG	154	1211	753	244	211	3	0	0

- Molecule 8 is a protein called Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AH	134	1088	684	211	187	6	0	0

- Molecule 9 is a protein called Ribosomal Protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AI	127	988	627	188	172	1	0	0

- Molecule 10 is a protein called Ribosomal Protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AJ	99	803	515	144	139	5	0	0

- Molecule 11 is a protein called Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AK	118	888	549	182	152	5	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	21	SER	-	insertion	UNP P06506
AK	22	ALA	-	insertion	UNP P06506

- Molecule 12 is a protein called Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AL	123	968	604	198	163	3	0	0

- Molecule 13 is a protein called Ribosomal Protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AM	99	824	513	168	141	2	0	0

- Molecule 14 is a protein called Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AN	99	820	507	174	136	3	0	0

- Molecule 15 is a protein called Ribosomal Protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AO	85	713	454	134	124	1	0	0

- Molecule 16 is a protein called Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AP	80	664	425	123	114	2	0	0

- Molecule 17 is a protein called Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AQ	83	662	416	130	112	4	0	0

- Molecule 18 is a protein called Ribosomal Protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AR	58	478	300	94	83	1	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	81	GLU	-	insertion	UNP Q9M3K7
AR	82	LYS	-	insertion	UNP Q9M3K7

- Molecule 19 is a protein called Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	92	Total	C	N	O	S	0	0
			747	472	146	126	3		

- Molecule 20 is a protein called Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	102	Total	C	N	O	S	0	0
			799	493	163	142	1		

- Molecule 21 is a protein called Ribosomal Protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	53	Total	C	N	O	S	0	0
			455	276	96	81	2		

- Molecule 22 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BA	2732	Total	C	N	O	P	0	0
			58665	26173	10857	18904	2731		

- Molecule 23 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	BB	117	Total	C	N	O	P	0	0
			2497	1116	452	813	116		

- Molecule 24 is a RNA chain called 4.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BC	103	Total	C	N	O	P	0	0
			2207	987	408	710	102		

- Molecule 25 is a protein called Ribosomal Protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BD	227	Total	C	N	O	S	0	0
			1760	1117	307	329	7		

- Molecule 26 is a protein called Ribosomal Protein L2.



Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	BE	266	2049	1268	418	357	6	0	0

- Molecule 27 is a protein called Ribosomal Protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	BF	154	1196	756	230	205	5	0	0

- Molecule 28 is a protein called Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	BG	211	1664	1057	309	295	3	0	0

- Molecule 29 is a protein called Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	BH	175	1351	862	233	248	8	0	0

- Molecule 30 is a protein called Ribosomal Protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	BI	182	1429	907	257	262	3	0	0

- Molecule 31 is a protein called Ribosomal Protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	BJ	148	1177	753	206	215	3	0	0

- Molecule 32 is a protein called Ribosomal Protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	BK	145	1060	679	177	198	6	0	0

- Molecule 33 is a protein called Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BL	125	Total	C	N	O	S	0	0
			998	634	192	169	3		

- Molecule 34 is a protein called Ribosomal Protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BM	121	Total	C	N	O	S	0	0
			943	588	179	171	5		

- Molecule 35 is a protein called Ribosomal Protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BN	176	Total	C	N	O	S	0	0
			1333	835	257	235	6		

- Molecule 36 is a protein called Ribosomal Protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BO	135	Total	C	N	O	S	0	0
			1076	677	218	175	6		

- Molecule 37 is a protein called Ribosomal Protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BP	116	Total	C	N	O	S	0	0
			948	594	195	155	4		

- Molecule 38 is a protein called Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BQ	122	Total	C	N	O	S	0	0
			962	597	183	178	4		

- Molecule 39 is a protein called Ribosomal Protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BR	113	Total	C	N	O	S	0	0
			915	586	177	151	1		

- Molecule 40 is a protein called Ribosomal Protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BS	119	1030	653	213	161	3	0	0

- Molecule 41 is a protein called Ribosomal Protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	BT	104	826	537	150	139		0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BT	122	ILE	-	insertion	UNP P24613

- Molecule 42 is a protein called Ribosomal Protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BU	122	986	627	178	175	6	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BU	126	LEU	LYS	conflict	UNP P09594

- Molecule 43 is a protein called Ribosomal Protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	BV	85	677	436	115	124	2	0	0

- Molecule 44 is a protein called Ribosomal Protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BW	110	869	548	160	160	1	0	0

- Molecule 45 is a protein called Ribosomal Protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
45	BX	86	660	419	127	114	0	0

- Molecule 46 is a protein called Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	BY	76	619	395	120	103	1	0	0

- Molecule 47 is a protein called Ribosomal Protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	BZ	65	551	341	106	101	3	0	0

- Molecule 48 is a protein called Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	B1	72	581	369	99	109	4	0	0

- Molecule 49 is a protein called Ribosomal Protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	B2	57	469	305	87	76	1	0	0

- Molecule 50 is a protein called Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	B3	65	524	326	105	88	5	0	0

- Molecule 51 is a protein called Ribosomal Protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	B4	37	297	180	70	45	2	0	0

- Molecule 52 is a protein called Ribosomal Protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	B5	62	504	315	107	81	1	0	0

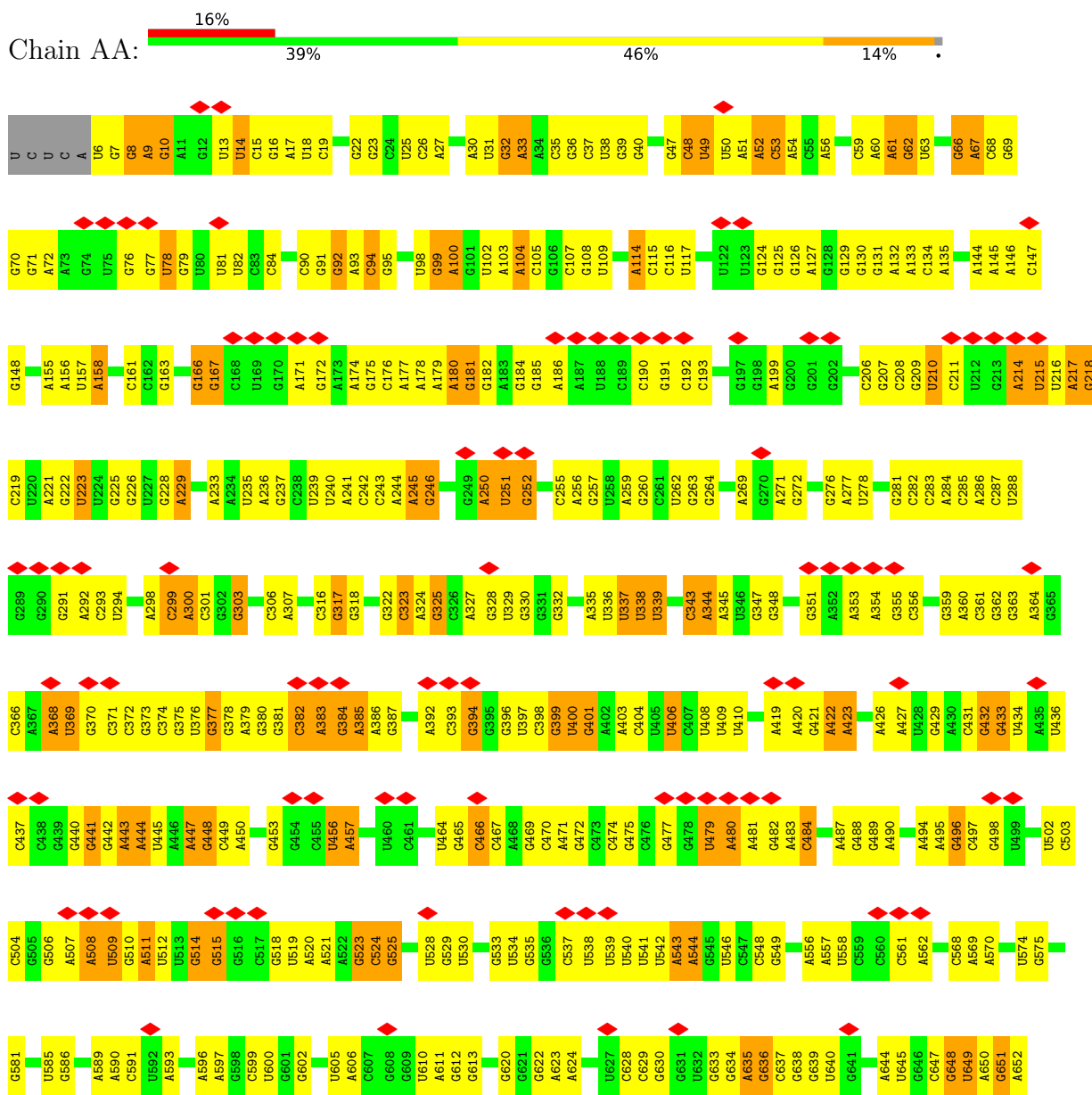
- Molecule 53 is a protein called Ribosomal Protein L36.

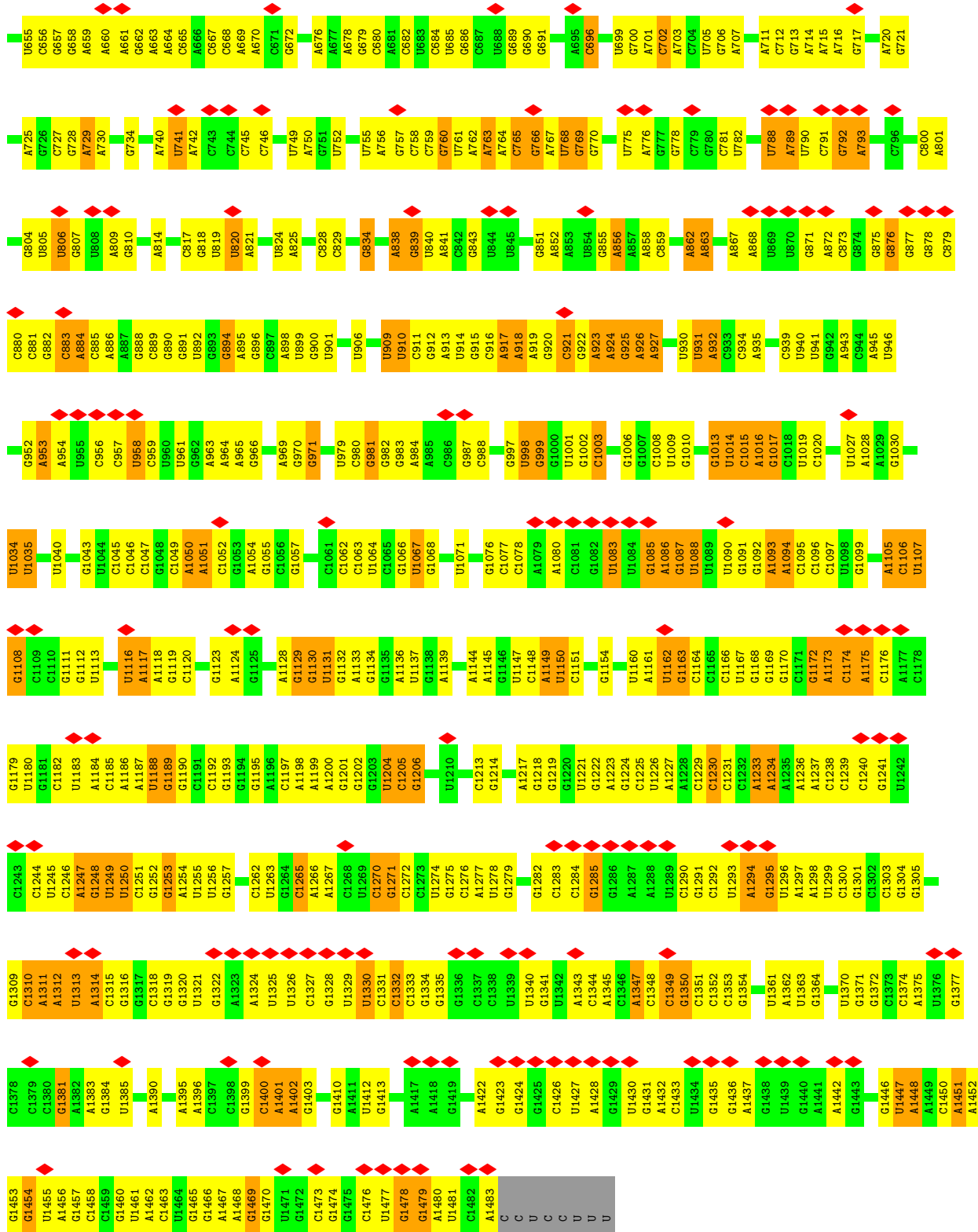
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	B6	38	309	190	65	49	5	0	0

### 3 Residue-property plots

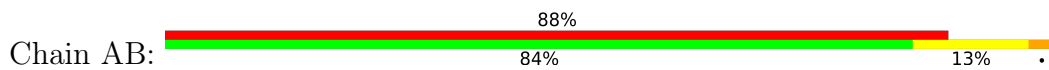
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

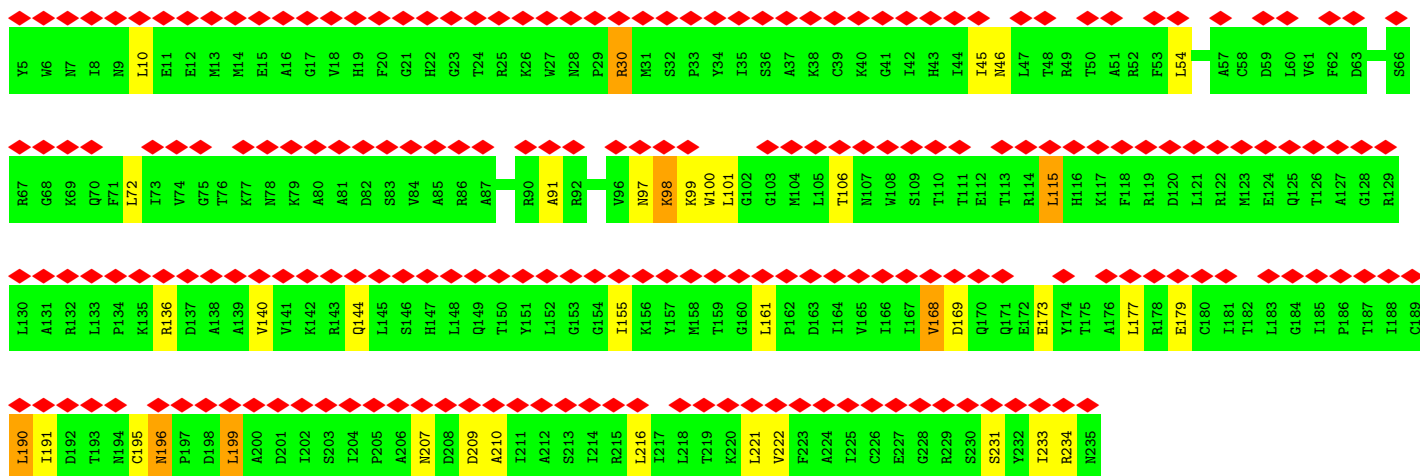
#### • Molecule 1: 16S rRNA



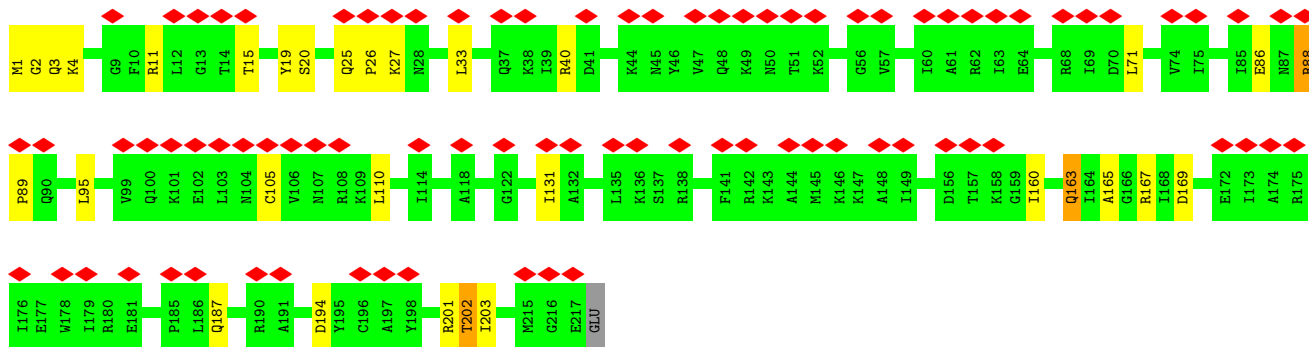
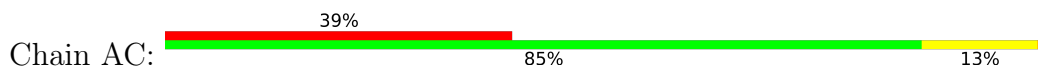


• Molecule 2: Ribosomal Protein S2

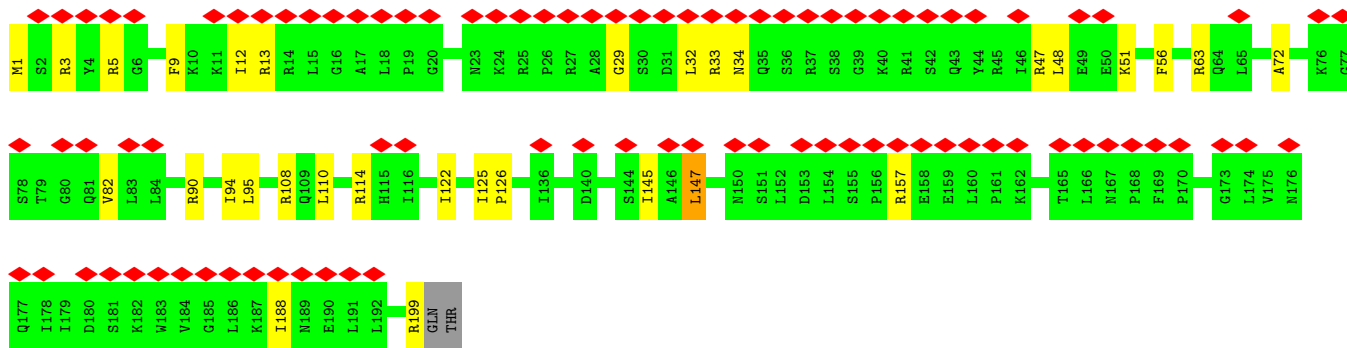
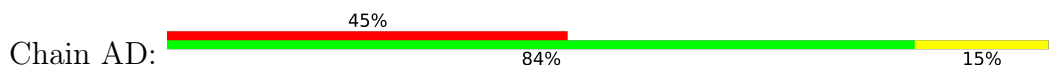




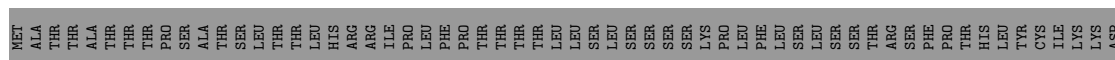
• Molecule 3: Ribosomal Protein S3



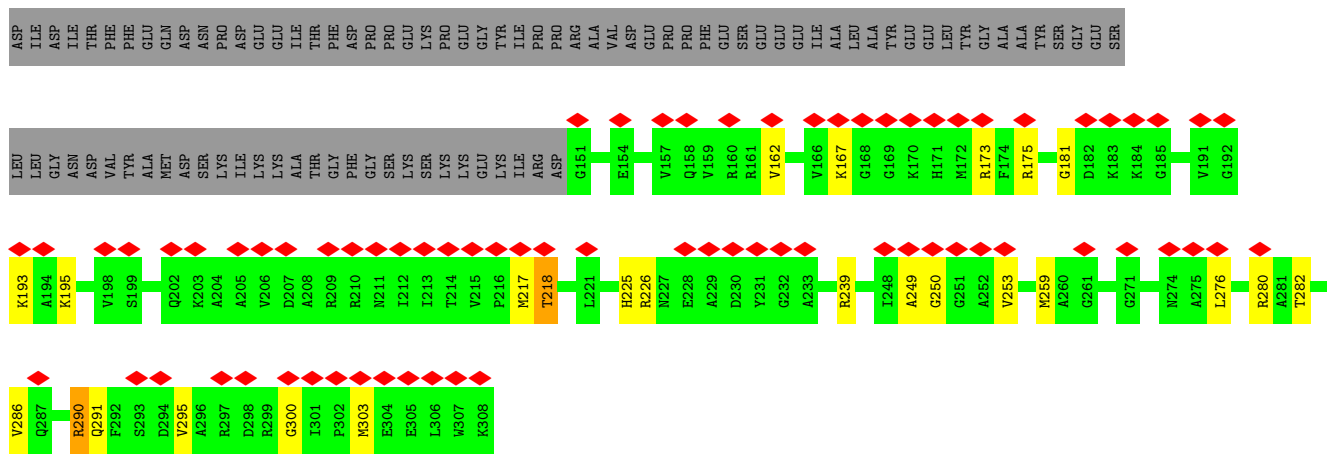
• Molecule 4: Ribosomal Protein S4



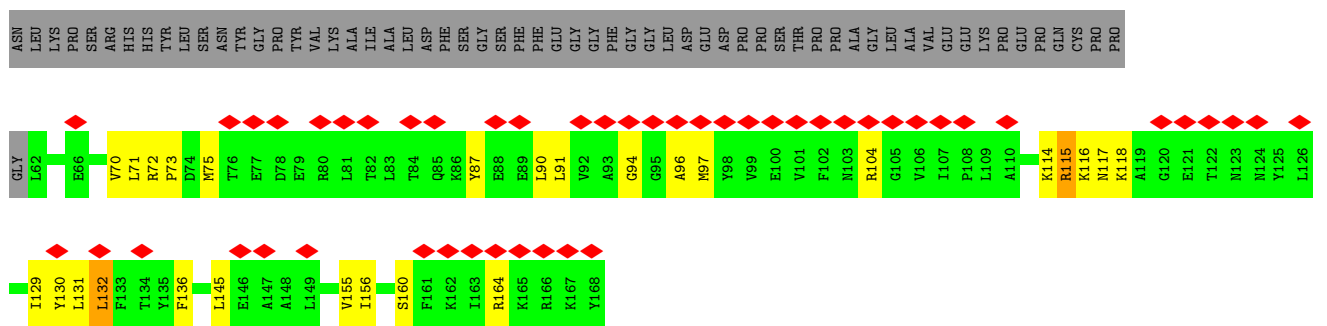
• Molecule 5: Ribosomal Protein S5



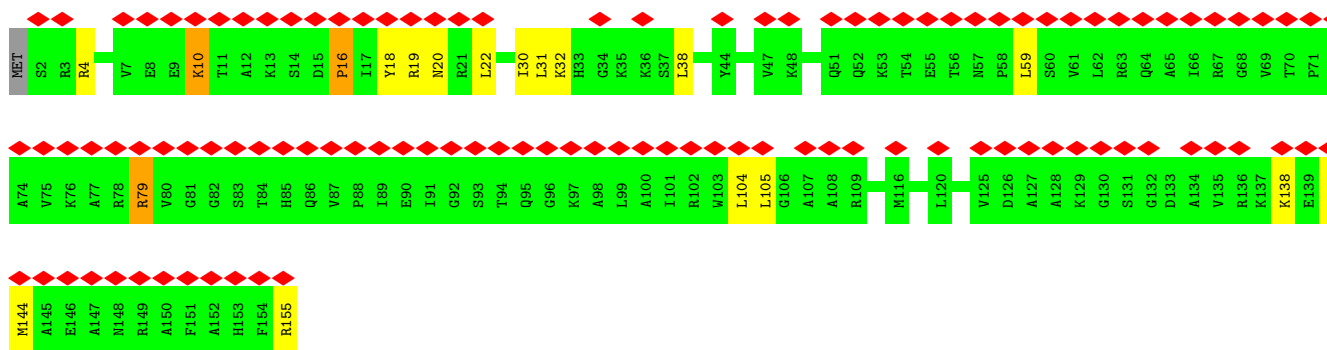
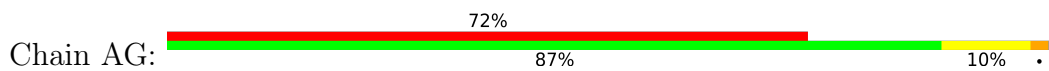




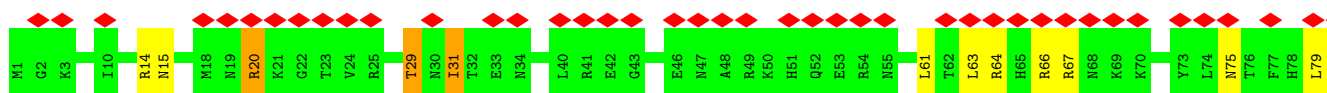
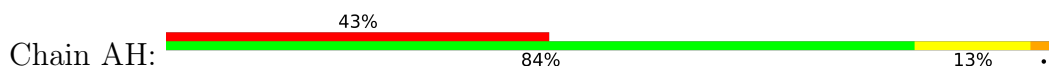
• Molecule 6: Ribosomal Protein S6



• Molecule 7: Ribosomal Protein S7

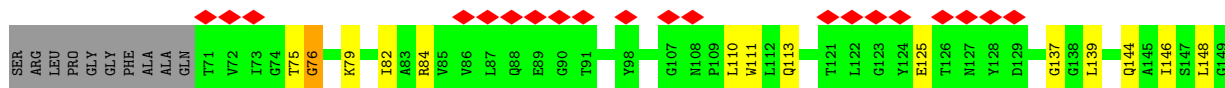
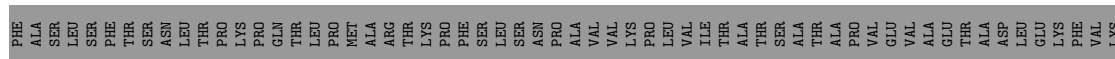


• Molecule 8: Ribosomal Protein S8

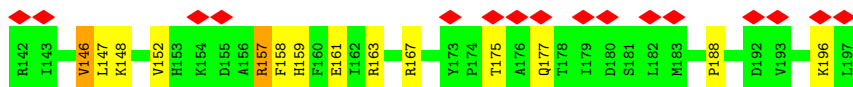
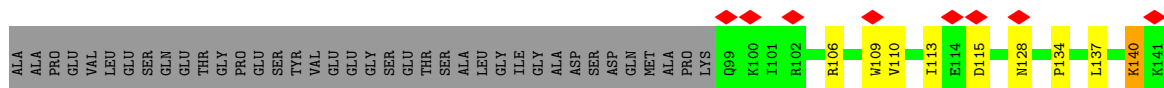
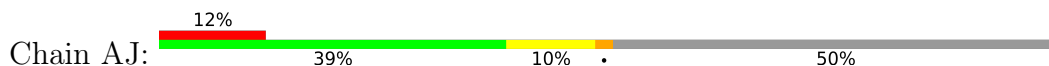




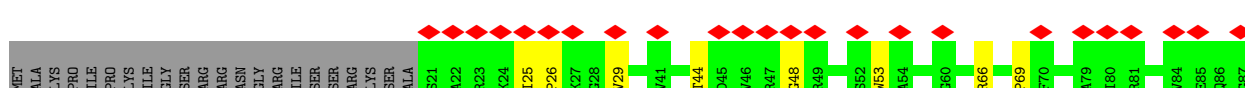
• Molecule 9: Ribosomal Protein S9



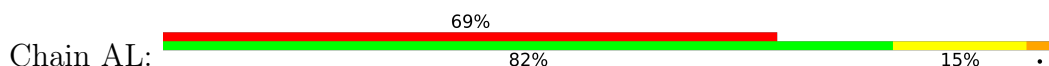
• Molecule 10: Ribosomal Protein S10

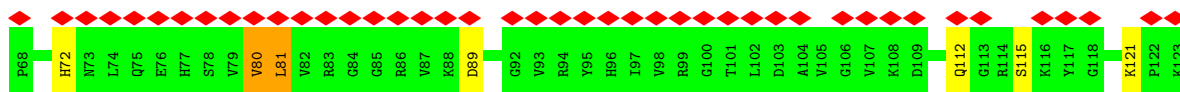


• Molecule 11: Ribosomal Protein S11

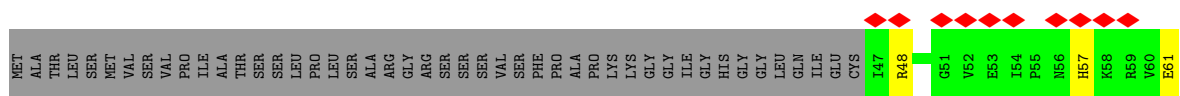


• Molecule 12: Ribosomal Protein S12

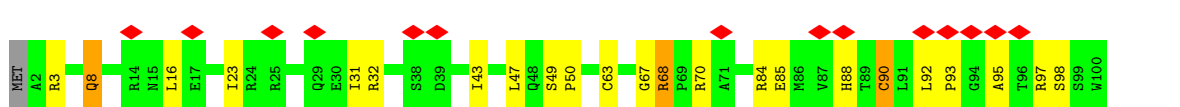
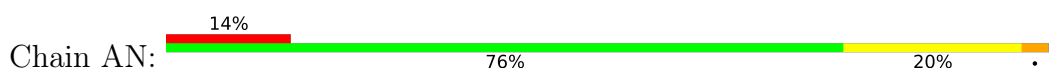




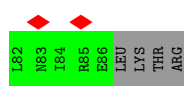
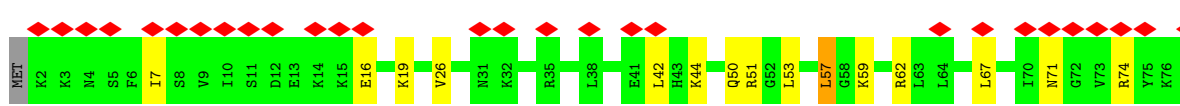
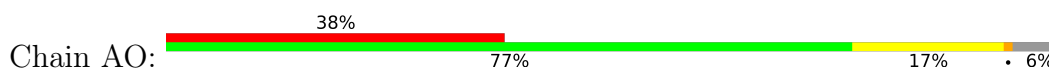
• Molecule 13: Ribosomal Protein S13



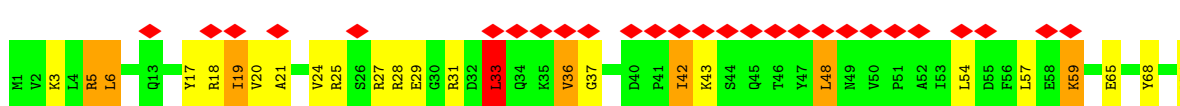
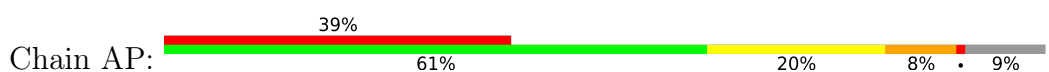
• Molecule 14: Ribosomal Protein S14



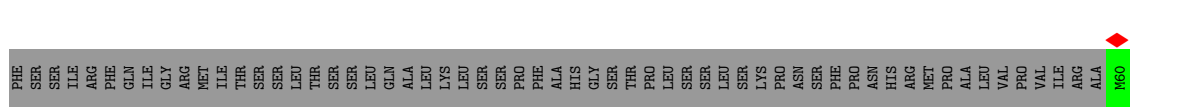
• Molecule 15: Ribosomal Protein S15

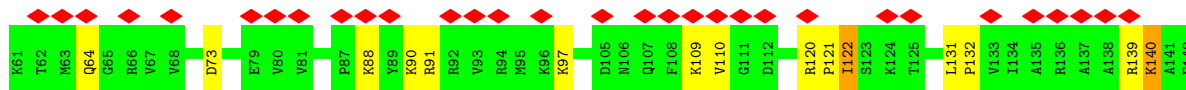


• Molecule 16: Ribosomal Protein S16

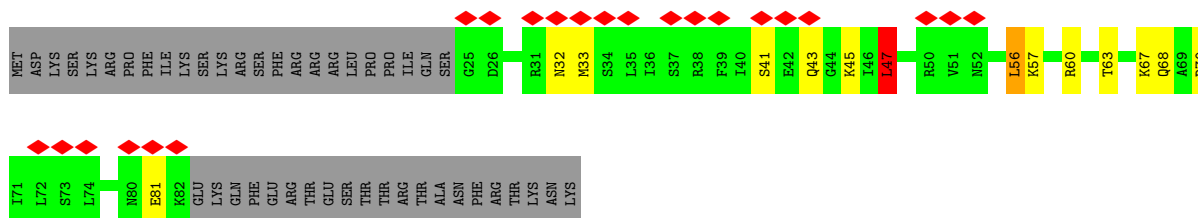
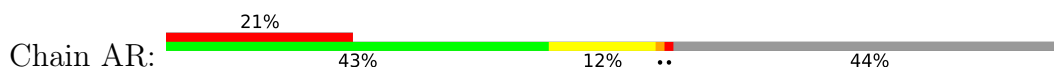


• Molecule 17: Ribosomal Protein S17

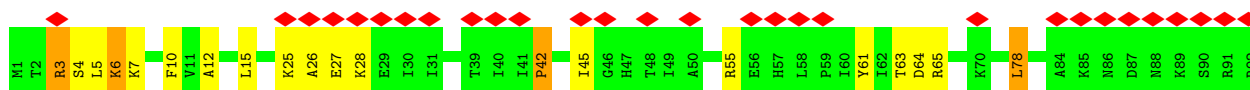
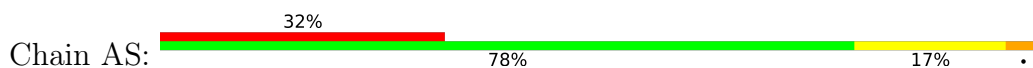




• Molecule 18: Ribosomal Protein S18



• Molecule 19: Ribosomal Protein S19



• Molecule 20: Ribosomal Protein S20

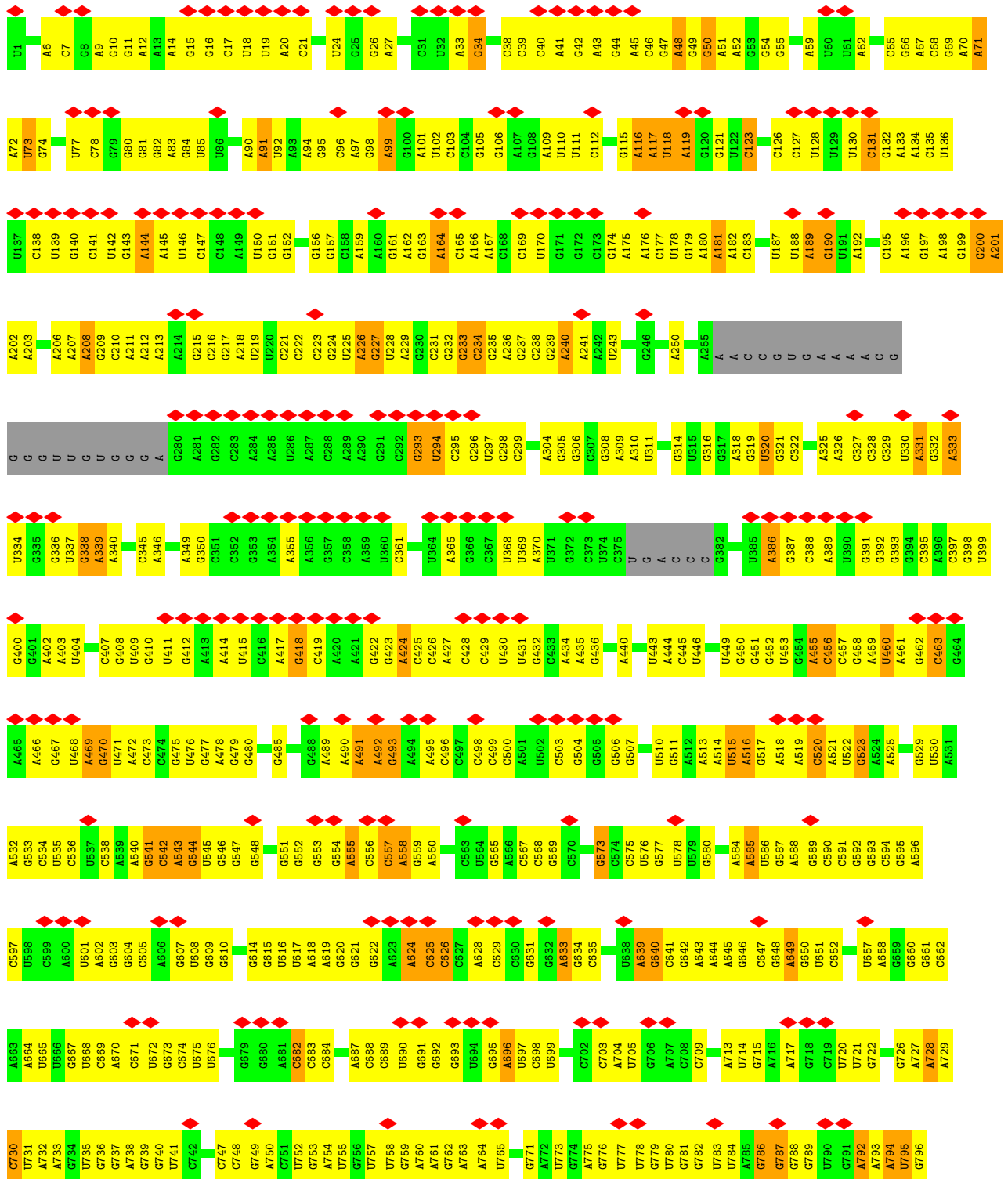


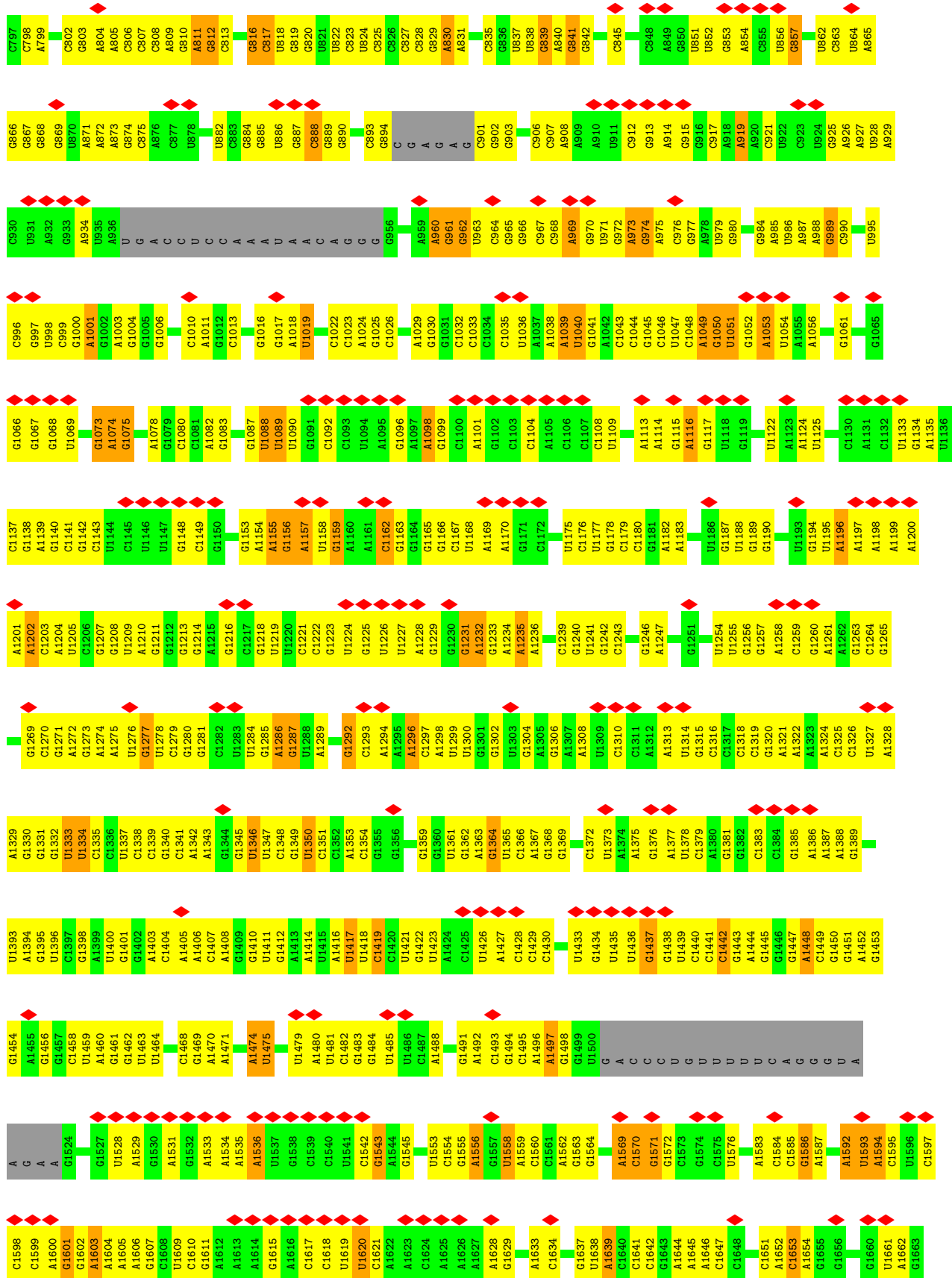
• Molecule 21: Ribosomal Protein S21

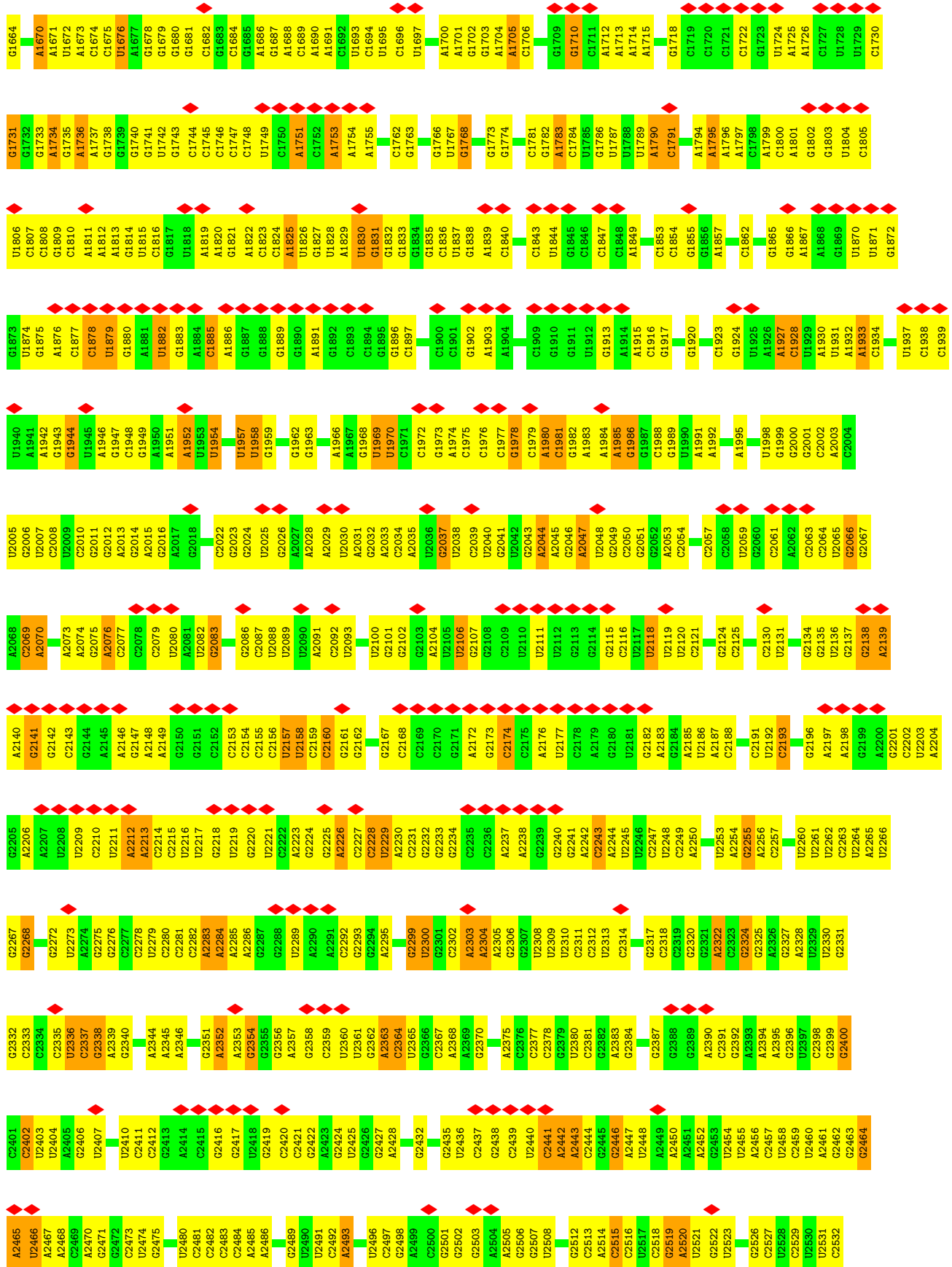


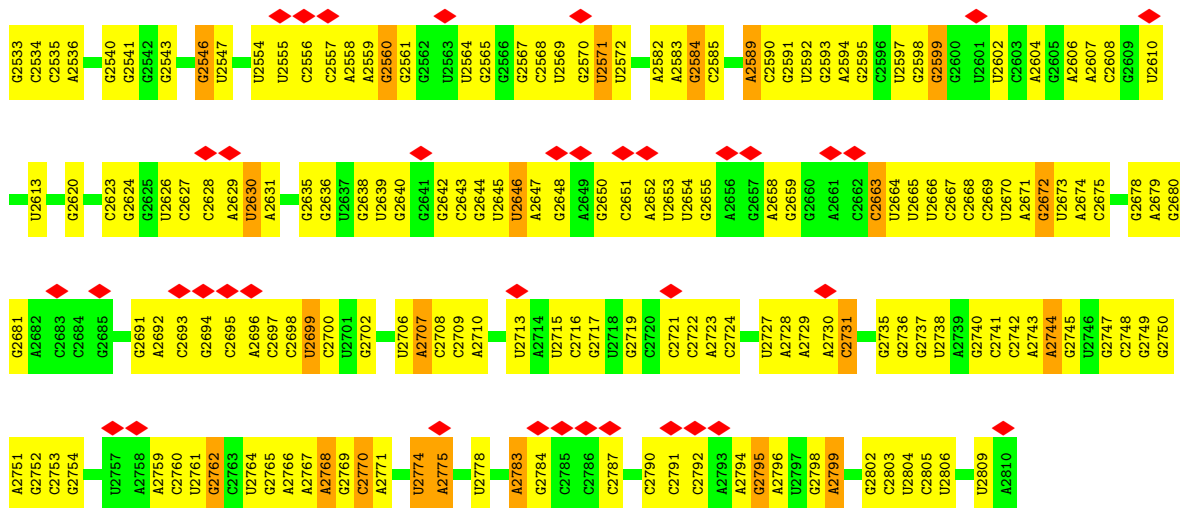
PRO  
SER

• Molecule 22: 23S rRNA

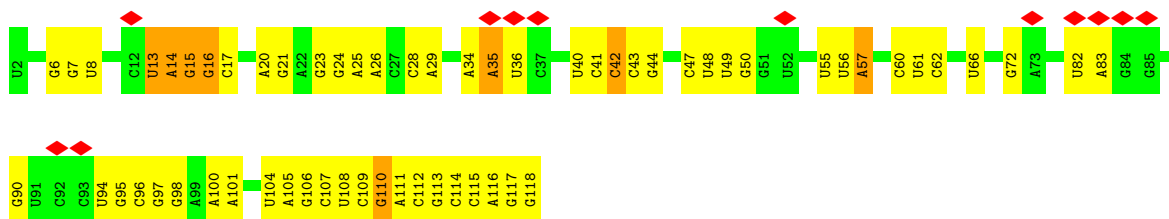




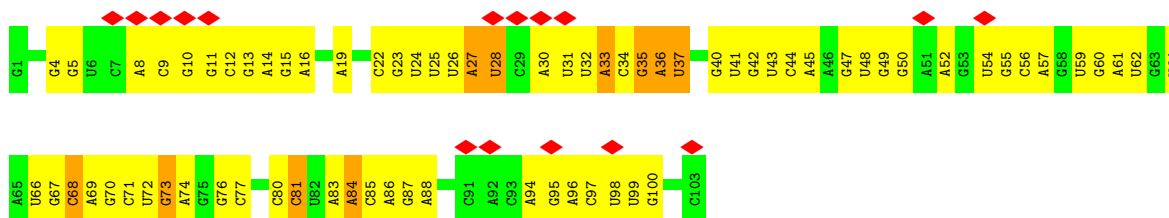




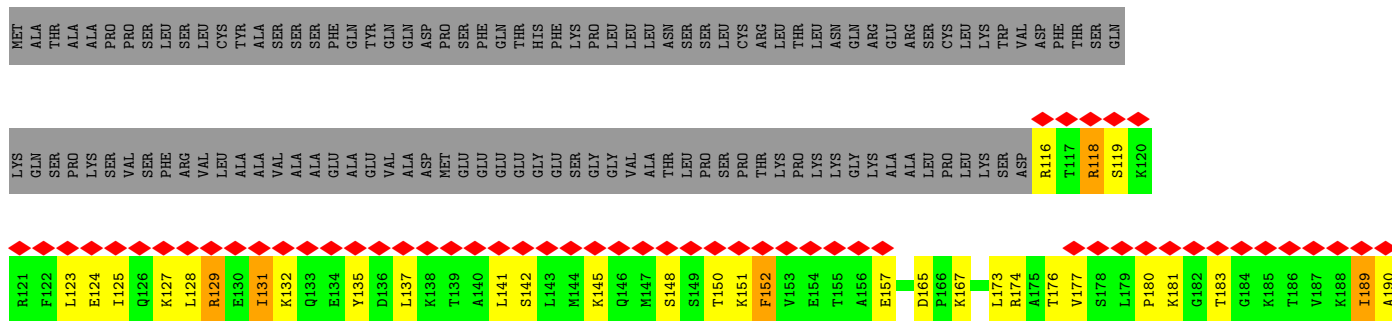
• Molecule 23: 5S rRNA



• Molecule 24: 4.8S rRNA



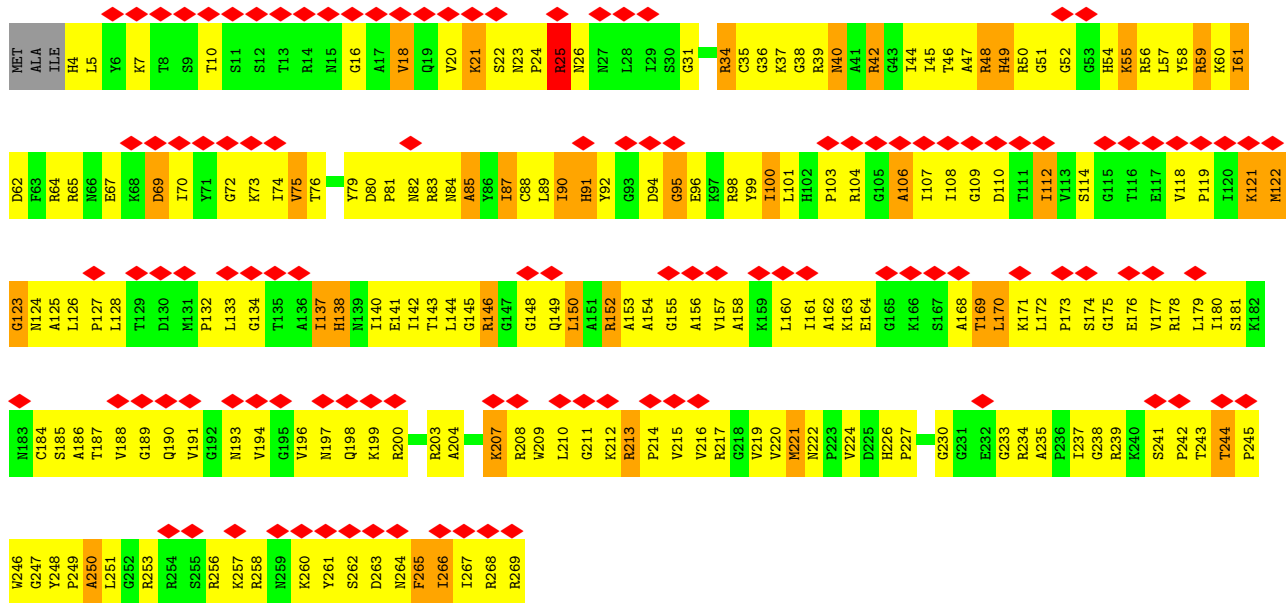
• Molecule 25: Ribosomal Protein L1



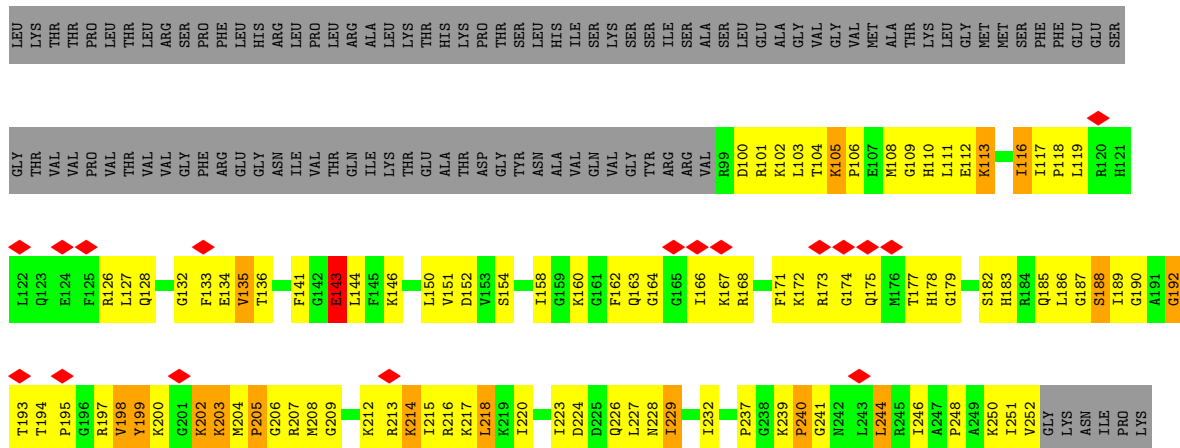
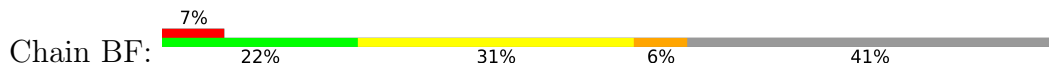




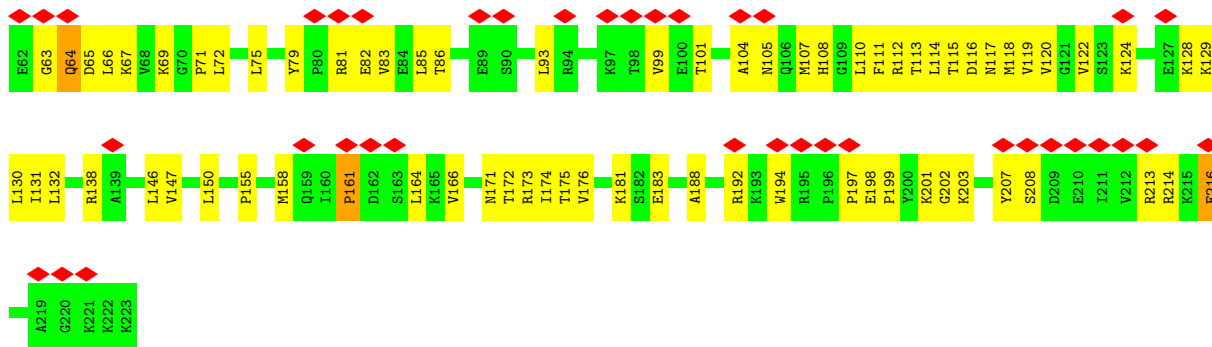
• Molecule 26: Ribosomal Protein L2



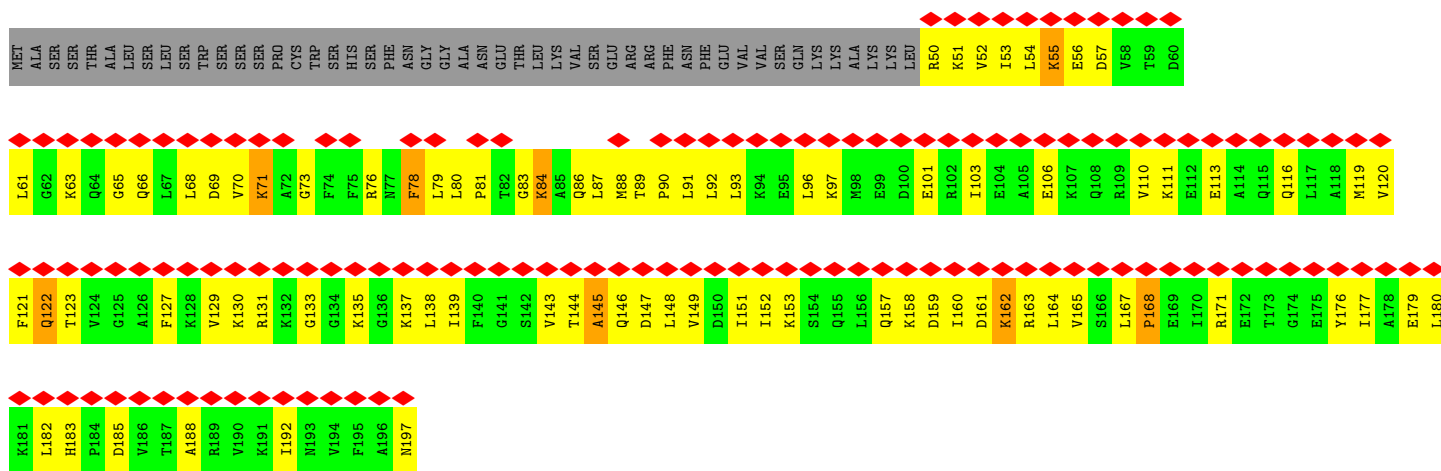
• Molecule 27: Ribosomal Protein L3



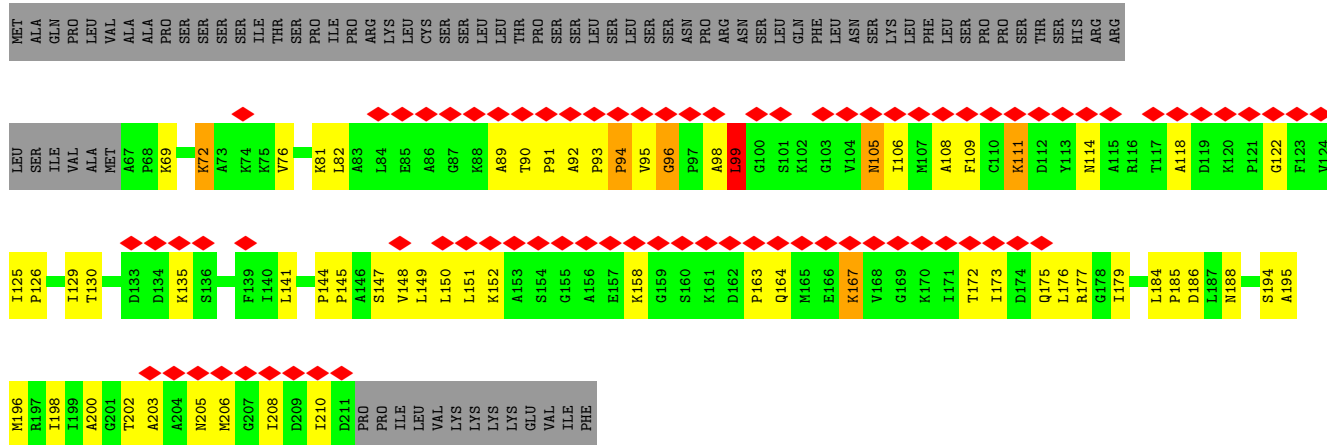




• Molecule 31: Ribosomal Protein L9

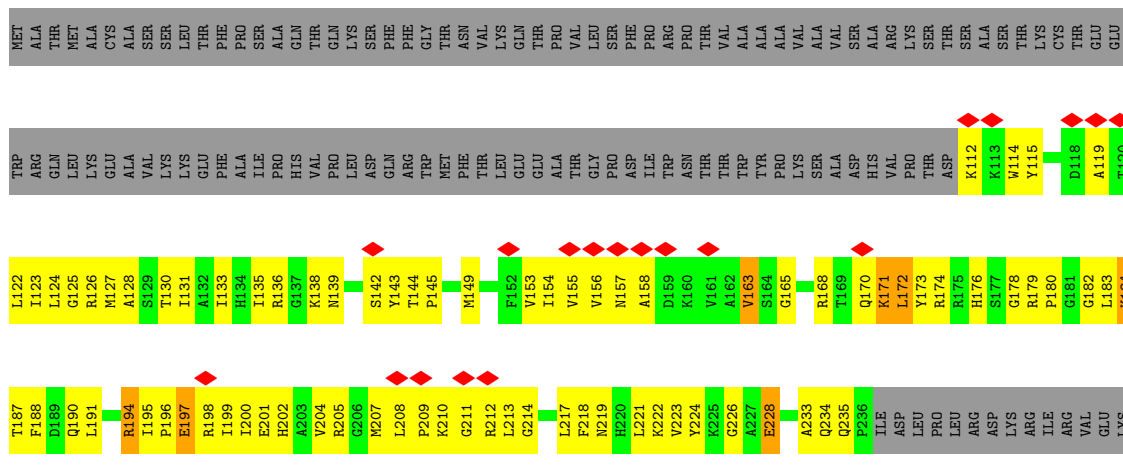


• Molecule 32: Ribosomal Protein L11

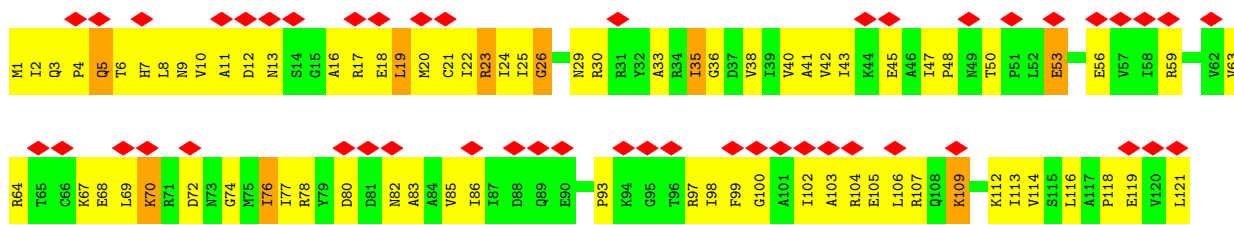
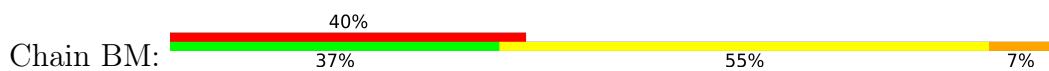


• Molecule 33: Ribosomal Protein L13

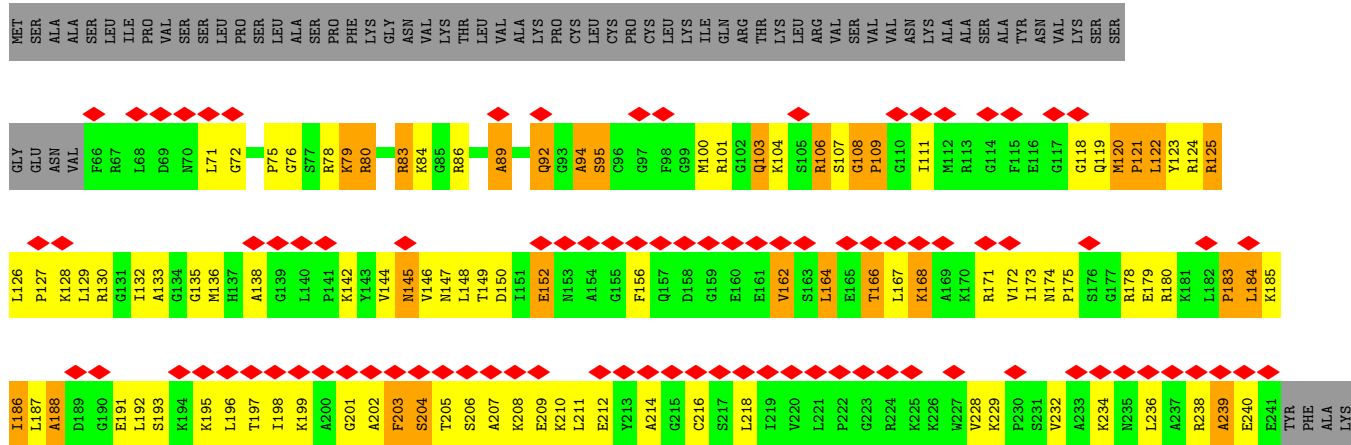
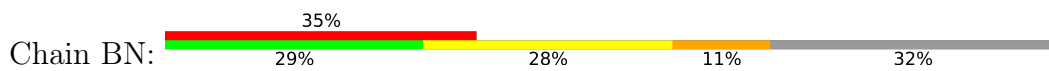




• Molecule 34: Ribosomal Protein L14



• Molecule 35: Ribosomal Protein L15

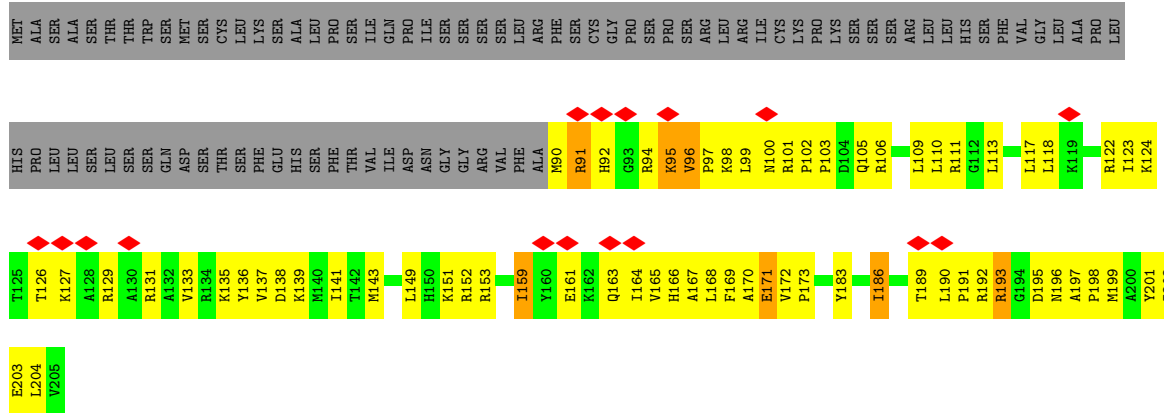
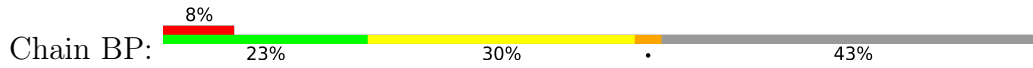


• Molecule 36: Ribosomal Protein L16

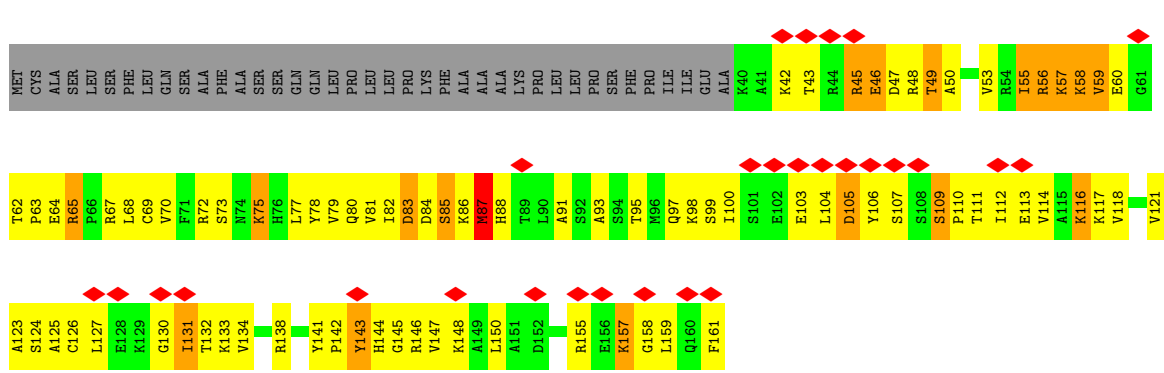
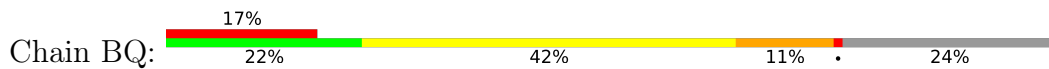




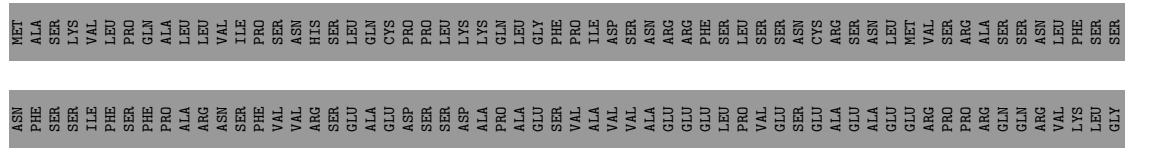
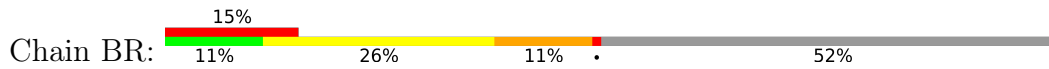
• Molecule 37: Ribosomal Protein L17

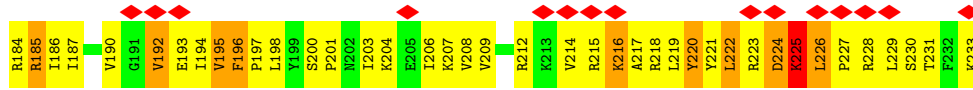
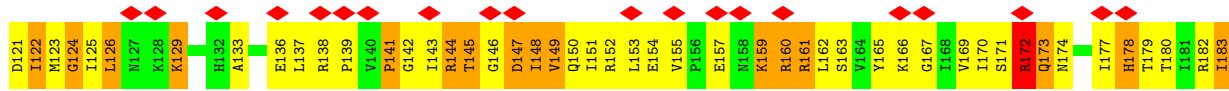


• Molecule 38: Ribosomal Protein L18

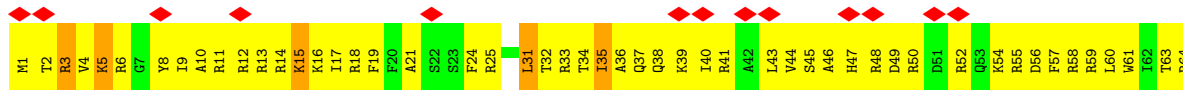


• Molecule 39: Ribosomal Protein L19

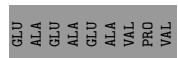
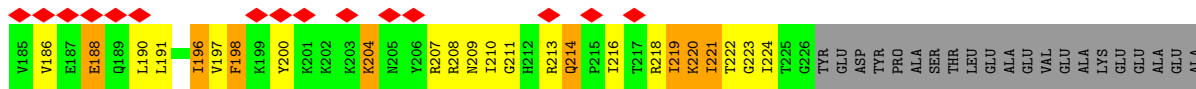
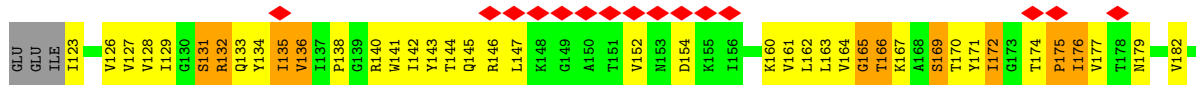
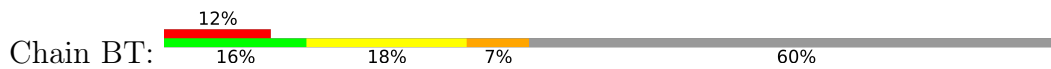




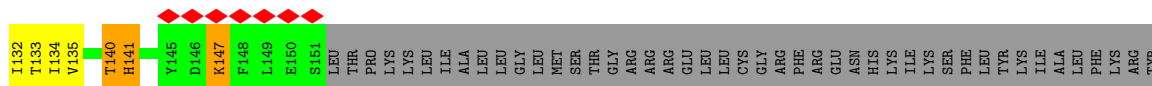
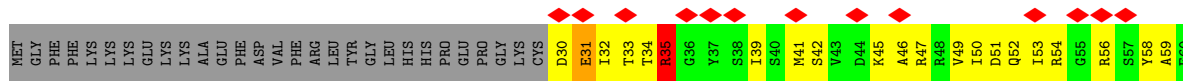
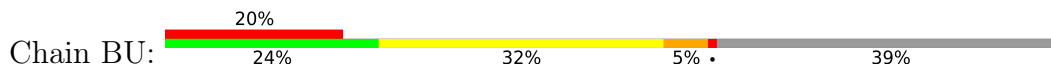
• Molecule 40: Ribosomal Protein L20



• Molecule 41: Ribosomal Protein L21

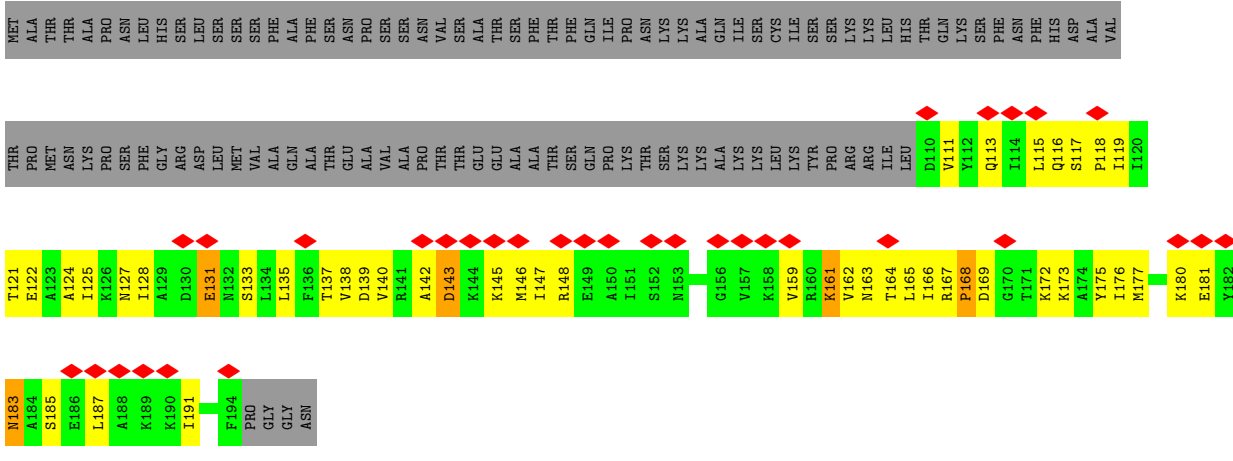
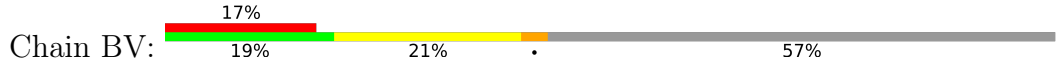


• Molecule 42: Ribosomal Protein L22

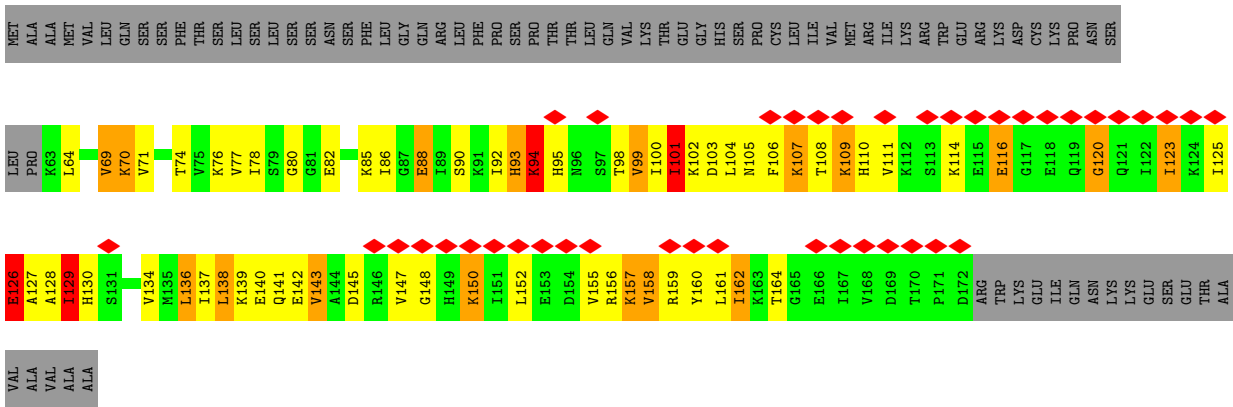
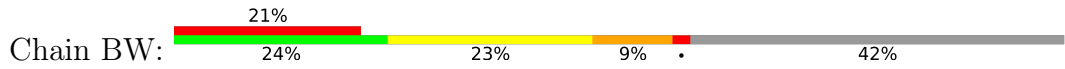


GLU  
VAL  
MET

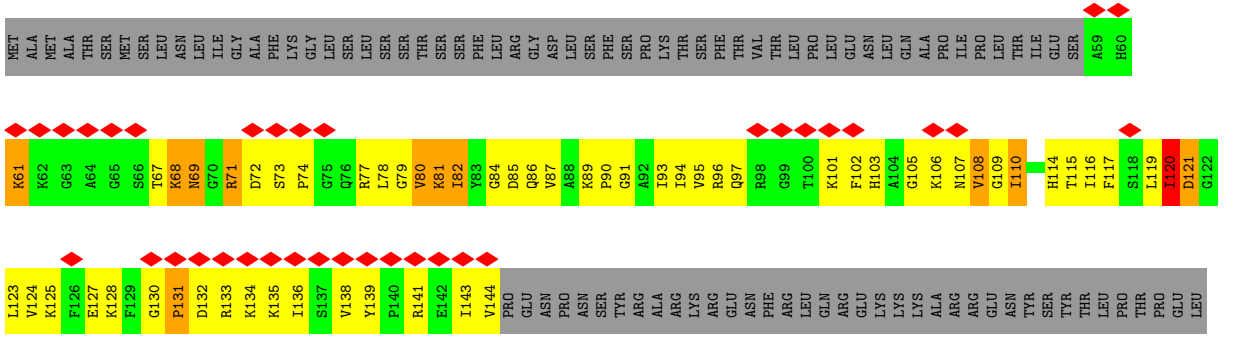
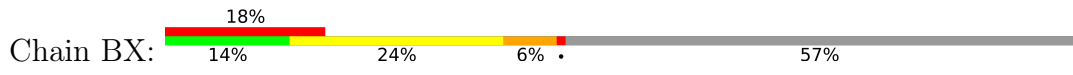
● Molecule 43: Ribosomal Protein L23



● Molecule 44: Ribosomal Protein L24



● Molecule 45: Ribosomal Protein L27









## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	86370	Depositor
Resolution determination method	Not provided	
CTF correction method	CTF correction for each Micrograph	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	50760	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	262.374	Depositor
Minimum map value	-126.152	Depositor
Average map value	3.285	Depositor
Map value standard deviation	26.943	Depositor
Recommended contour level	49.0	Depositor
Map size ( $\text{\AA}$ )	358.8, 358.8, 358.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ( $^\circ$ )	90, 90, 90	wwPDB
Pixel spacing ( $\text{\AA}$ )	2.76, 2.76, 2.76	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	AA	0.22	0/35552	0.66	1/55472 (0.0%)
2	AB	0.62	0/1860	0.69	3/2512 (0.1%)
3	AC	0.63	0/1771	0.75	3/2380 (0.1%)
4	AD	0.61	0/1660	0.74	1/2228 (0.0%)
5	AE	0.56	0/1204	0.64	0/1620
6	AF	0.71	0/887	0.76	2/1195 (0.2%)
7	AG	0.56	0/1227	0.70	2/1641 (0.1%)
8	AH	0.59	0/1103	0.70	0/1477
9	AI	0.63	0/1004	0.75	1/1347 (0.1%)
10	AJ	0.59	0/820	0.69	0/1108
11	AK	0.57	0/902	0.68	0/1214
12	AL	0.56	0/984	0.71	1/1323 (0.1%)
13	AM	0.60	0/833	0.78	1/1108 (0.1%)
14	AN	0.53	0/836	0.77	0/1116
15	AO	0.63	0/721	0.69	0/956
16	AP	0.72	0/674	0.86	2/902 (0.2%)
17	AQ	0.57	0/672	0.69	1/898 (0.1%)
18	AR	0.57	0/481	0.79	1/641 (0.2%)
19	AS	0.59	0/762	0.67	0/1021
20	AT	0.47	0/803	0.64	0/1063
21	AU	0.59	0/458	0.76	0/608
22	BA	0.13	0/65708	0.63	0/102501
23	BB	0.13	0/2793	0.63	0/4353
24	BC	0.13	0/2472	0.63	0/3854
25	BD	0.24	0/1786	0.40	0/2397
26	BE	0.21	0/2085	0.42	0/2800
27	BF	0.24	0/1214	0.42	0/1613
28	BG	0.25	0/1696	0.43	0/2283
29	BH	0.24	0/1372	0.41	0/1848
30	BI	0.23	0/1451	0.42	0/1944
31	BJ	0.24	0/1189	0.40	0/1589
32	BK	0.23	0/1077	0.43	0/1456
33	BL	0.23	0/1019	0.40	0/1369
34	BM	0.22	0/952	0.42	0/1282

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	BN	0.23	0/1354	0.40	0/1806
36	BO	0.24	0/1098	0.41	0/1471
37	BP	0.23	0/964	0.41	0/1288
38	BQ	0.23	0/976	0.41	0/1305
39	BR	0.22	0/929	0.46	0/1248
40	BS	0.24	0/1047	0.40	0/1394
41	BT	0.23	0/839	0.43	0/1135
42	BU	0.23	0/1003	0.40	0/1348
43	BV	0.24	0/685	0.40	0/920
44	BW	0.21	0/878	0.42	0/1171
45	BX	0.25	0/672	0.41	0/896
46	BY	0.25	0/629	0.44	0/835
47	BZ	0.25	0/553	0.40	0/728
48	B1	0.26	0/594	0.37	0/797
49	B2	0.28	0/478	0.39	0/633
50	B3	0.23	0/532	0.40	0/708
51	B4	0.25	0/298	0.39	0/390
52	B5	0.23	0/509	0.38	0/672
53	B6	0.25	0/312	0.37	0/409
All	All	0.27	0/154378	0.62	19/230273 (0.0%)

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
6	AF	132	LEU	CA-CB-CG	7.67	132.94	115.30
13	AM	82	LEU	CA-CB-CG	7.39	132.30	115.30
16	AP	6	LEU	CA-CB-CG	7.02	131.45	115.30
7	AG	31	LEU	CA-CB-CG	6.96	131.32	115.30
16	AP	33	LEU	CA-CB-CG	6.96	131.30	115.30

There are no chirality outliers.

There are no planarity outliers.

## 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	AA	31745	0	15984	1134	0
2	AB	1827	0	1867	17	0
3	AC	1744	0	1831	18	0
4	AD	1632	0	1734	17	0
5	AE	1190	0	1245	18	0
6	AF	872	0	884	41	0
7	AG	1211	0	1284	11	0
8	AH	1088	0	1149	14	0
9	AI	988	0	1047	12	0
10	AJ	803	0	845	14	0
11	AK	888	0	933	10	0
12	AL	968	0	1046	12	0
13	AM	824	0	872	26	0
14	AN	820	0	858	13	0
15	AO	713	0	765	48	0
16	AP	664	0	703	13	0
17	AQ	662	0	715	11	0
18	AR	478	0	519	14	0
19	AS	747	0	787	22	0
20	AT	799	0	879	11	0
21	AU	455	0	466	10	0
22	BA	58665	0	29550	2028	0
23	BB	2497	0	1264	51	0
24	BC	2207	0	1114	89	0
25	BD	1760	0	1834	107	0
26	BE	2049	0	2128	412	0
27	BF	1196	0	1282	135	0
28	BG	1664	0	1731	187	0
29	BH	1351	0	1405	129	0
30	BI	1429	0	1510	94	0
31	BJ	1177	0	1259	86	0
32	BK	1060	0	1129	59	0
33	BL	998	0	1038	94	0
34	BM	943	0	996	101	0
35	BN	1333	0	1406	155	0
36	BO	1076	0	1134	127	0
37	BP	948	0	1009	96	0
38	BQ	962	0	992	120	0
39	BR	915	0	1001	153	0
40	BS	1030	0	1100	150	0
41	BT	826	0	900	83	0
42	BU	986	0	1025	106	0
43	BV	677	0	716	55	0

*Continued on next page...*

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BW	869	0	929	107	0
45	BX	660	0	693	92	0
46	BY	619	0	672	97	0
47	BZ	551	0	587	38	0
48	B1	581	0	562	46	0
49	B2	469	0	516	77	0
50	B3	524	0	557	64	0
51	B4	297	0	336	40	0
52	B5	504	0	559	77	0
53	B6	309	0	340	25	0
All	All	142250	0	97687	5825	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 24.

The worst 5 of 5825 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)
1:AA:755:U:H3	26:BE:5:LEU:CD1	1.02	1.62
1:AA:1423:G:C4'	22:BA:1737:A:C2	1.80	1.61
15:AO:44:LYS:HE3	26:BE:7:LYS:CE	1.25	1.61
1:AA:660:A:C5'	26:BE:161:ILE:HA	1.32	1.54
1:AA:1423:G:H4'	22:BA:1737:A:C2	1.37	1.49

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	
2	AB	229/231 (99%)	201 (88%)	25 (11%)	3 (1%)	12	48
3	AC	215/218 (99%)	179 (83%)	29 (14%)	7 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AD	197/201 (98%)	179 (91%)	17 (9%)	1 (0%)	29	69
5	AE	156/308 (51%)	138 (88%)	16 (10%)	2 (1%)	12	48
6	AF	105/168 (62%)	92 (88%)	10 (10%)	3 (3%)	4	29
7	AG	152/155 (98%)	136 (90%)	14 (9%)	2 (1%)	12	48
8	AH	132/134 (98%)	118 (89%)	13 (10%)	1 (1%)	19	60
9	AI	125/197 (64%)	110 (88%)	13 (10%)	2 (2%)	9	44
10	AJ	97/197 (49%)	85 (88%)	10 (10%)	2 (2%)	7	36
11	AK	116/140 (83%)	95 (82%)	16 (14%)	5 (4%)	2	22
12	AL	121/123 (98%)	99 (82%)	17 (14%)	5 (4%)	3	23
13	AM	97/145 (67%)	75 (77%)	15 (16%)	7 (7%)	1	14
14	AN	97/100 (97%)	83 (86%)	13 (13%)	1 (1%)	15	55
15	AO	83/90 (92%)	77 (93%)	6 (7%)	0	100	100
16	AP	78/88 (89%)	59 (76%)	12 (15%)	7 (9%)	1	11
17	AQ	81/142 (57%)	69 (85%)	11 (14%)	1 (1%)	13	50
18	AR	56/103 (54%)	51 (91%)	4 (7%)	1 (2%)	8	40
19	AS	90/92 (98%)	75 (83%)	12 (13%)	3 (3%)	4	26
20	AT	100/202 (50%)	93 (93%)	7 (7%)	0	100	100
21	AU	51/190 (27%)	37 (72%)	10 (20%)	4 (8%)	1	13
25	BD	225/352 (64%)	189 (84%)	33 (15%)	3 (1%)	12	48
26	BE	264/269 (98%)	126 (48%)	94 (36%)	44 (17%)	0	3
27	BF	152/259 (59%)	91 (60%)	32 (21%)	29 (19%)	0	2
28	BG	209/293 (71%)	159 (76%)	39 (19%)	11 (5%)	2	19
29	BH	173/220 (79%)	130 (75%)	32 (18%)	11 (6%)	1	16
30	BI	180/223 (81%)	143 (79%)	30 (17%)	7 (4%)	3	23
31	BJ	146/197 (74%)	105 (72%)	33 (23%)	8 (6%)	2	19
32	BK	143/224 (64%)	115 (80%)	22 (15%)	6 (4%)	3	22
33	BL	123/250 (49%)	92 (75%)	24 (20%)	7 (6%)	1	18
34	BM	119/121 (98%)	96 (81%)	20 (17%)	3 (2%)	5	32
35	BN	174/257 (68%)	98 (56%)	48 (28%)	28 (16%)	0	3
36	BO	133/135 (98%)	93 (70%)	30 (23%)	10 (8%)	1	13
37	BP	114/205 (56%)	94 (82%)	16 (14%)	4 (4%)	3	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	BQ	120/161 (74%)	81 (68%)	23 (19%)	16 (13%)	0	5
39	BR	111/233 (48%)	66 (60%)	25 (22%)	20 (18%)	0	3
40	BS	117/119 (98%)	96 (82%)	12 (10%)	9 (8%)	1	13
41	BT	102/257 (40%)	62 (61%)	23 (22%)	17 (17%)	0	3
42	BU	120/199 (60%)	92 (77%)	20 (17%)	8 (7%)	1	15
43	BV	83/198 (42%)	63 (76%)	15 (18%)	5 (6%)	1	17
44	BW	108/191 (56%)	59 (55%)	34 (32%)	15 (14%)	0	4
45	BX	84/198 (42%)	52 (62%)	21 (25%)	11 (13%)	0	5
46	BY	74/151 (49%)	43 (58%)	20 (27%)	11 (15%)	0	3
47	BZ	63/173 (36%)	58 (92%)	5 (8%)	0	100	100
48	B1	70/144 (49%)	52 (74%)	14 (20%)	4 (6%)	1	18
49	B2	55/57 (96%)	32 (58%)	11 (20%)	12 (22%)	0	2
50	B3	63/66 (96%)	33 (52%)	23 (36%)	7 (11%)	0	7
51	B4	35/152 (23%)	28 (80%)	7 (20%)	0	100	100
52	B5	60/159 (38%)	39 (65%)	15 (25%)	6 (10%)	0	9
53	B6	36/104 (35%)	26 (72%)	6 (17%)	4 (11%)	0	7
All	All	5834/8791 (66%)	4464 (76%)	997 (17%)	373 (6%)	3	16

5 of 373 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	88	ARG
3	AC	89	PRO
3	AC	202	THR
5	AE	218	THR
6	AF	155	VAL

### 5.3.2 Protein sidechains [i](#)

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

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



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AB	196/196 (100%)	177 (90%)	19 (10%)	8	27
3	AC	187/188 (100%)	177 (95%)	10 (5%)	22	47
4	AD	178/180 (99%)	167 (94%)	11 (6%)	18	43
5	AE	121/255 (48%)	118 (98%)	3 (2%)	47	68
6	AF	95/144 (66%)	84 (88%)	11 (12%)	5	21
7	AG	125/126 (99%)	113 (90%)	12 (10%)	8	27
8	AH	117/117 (100%)	105 (90%)	12 (10%)	7	25
9	AI	101/159 (64%)	93 (92%)	8 (8%)	12	35
10	AJ	91/178 (51%)	79 (87%)	12 (13%)	4	18
11	AK	92/110 (84%)	86 (94%)	6 (6%)	17	42
12	AL	106/106 (100%)	98 (92%)	8 (8%)	13	38
13	AM	90/126 (71%)	80 (89%)	10 (11%)	6	22
14	AN	89/90 (99%)	77 (86%)	12 (14%)	4	17
15	AO	80/85 (94%)	75 (94%)	5 (6%)	18	43
16	AP	71/79 (90%)	58 (82%)	13 (18%)	1	10
17	AQ	72/125 (58%)	67 (93%)	5 (7%)	15	40
18	AR	54/98 (55%)	49 (91%)	5 (9%)	9	28
19	AS	81/81 (100%)	74 (91%)	7 (9%)	10	32
20	AT	80/163 (49%)	72 (90%)	8 (10%)	7	26
21	AU	49/170 (29%)	46 (94%)	3 (6%)	18	44
25	BD	190/297 (64%)	181 (95%)	9 (5%)	26	51
26	BE	212/214 (99%)	205 (97%)	7 (3%)	38	61
27	BF	127/217 (58%)	123 (97%)	4 (3%)	40	62
28	BG	177/254 (70%)	172 (97%)	5 (3%)	43	65
29	BH	148/183 (81%)	139 (94%)	9 (6%)	18	44
30	BI	156/192 (81%)	152 (97%)	4 (3%)	46	66
31	BJ	128/171 (75%)	125 (98%)	3 (2%)	50	70
32	BK	114/189 (60%)	109 (96%)	5 (4%)	28	53
33	BL	104/213 (49%)	101 (97%)	3 (3%)	42	64
34	BM	101/101 (100%)	94 (93%)	7 (7%)	15	40
35	BN	136/203 (67%)	126 (93%)	10 (7%)	13	38
36	BO	108/108 (100%)	100 (93%)	8 (7%)	13	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	BP	97/177 (55%)	92 (95%)	5 (5%)	23	48
38	BQ	103/135 (76%)	94 (91%)	9 (9%)	10	31
39	BR	100/207 (48%)	89 (89%)	11 (11%)	6	22
40	BS	106/106 (100%)	101 (95%)	5 (5%)	26	51
41	BT	90/224 (40%)	86 (96%)	4 (4%)	28	53
42	BU	108/176 (61%)	104 (96%)	4 (4%)	34	58
43	BV	74/171 (43%)	72 (97%)	2 (3%)	44	65
44	BW	98/171 (57%)	88 (90%)	10 (10%)	7	25
45	BX	68/167 (41%)	62 (91%)	6 (9%)	10	31
46	BY	66/133 (50%)	63 (96%)	3 (4%)	27	52
47	BZ	61/149 (41%)	55 (90%)	6 (10%)	8	26
48	B1	62/126 (49%)	61 (98%)	1 (2%)	62	79
49	B2	50/50 (100%)	46 (92%)	4 (8%)	12	35
50	B3	59/60 (98%)	55 (93%)	4 (7%)	16	41
51	B4	31/125 (25%)	29 (94%)	2 (6%)	17	42
52	B5	53/140 (38%)	50 (94%)	3 (6%)	20	45
53	B6	36/87 (41%)	36 (100%)	0	100	100
All	All	5038/7522 (67%)	4705 (93%)	333 (7%)	20	41

5 of 333 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	BM	35	ILE
41	BT	198	PHE
35	BN	83	ARG
38	BQ	46	GLU
44	BW	129	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
30	BI	117	ASN
51	B4	112	HIS
34	BM	29	ASN
50	B3	40	HIS

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Mol	Chain	Res	Type
45	BX	107	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1477/1491 (99%)	245 (16%)	51 (3%)
22	BA	2726/2810 (97%)	387 (14%)	12 (0%)
23	BB	116/117 (99%)	12 (10%)	0
24	BC	102/103 (99%)	14 (13%)	0
All	All	4421/4521 (97%)	658 (14%)	63 (1%)

5 of 658 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	A
1	AA	10	G
1	AA	14	U
1	AA	15	C
1	AA	32	G

5 of 63 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	862	A
22	BA	639	A
1	AA	1014	U
22	BA	625	C
22	BA	1927	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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.

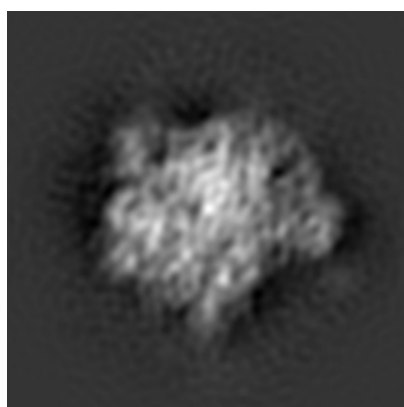
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1417. These allow visual inspection of the internal detail of the map and identification of artifacts.

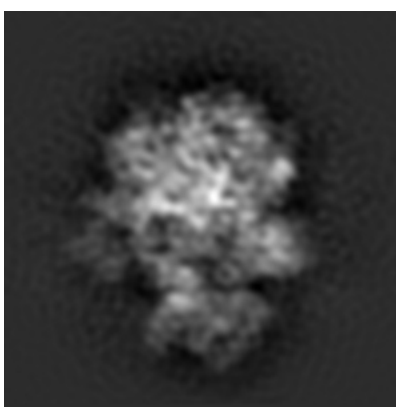
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

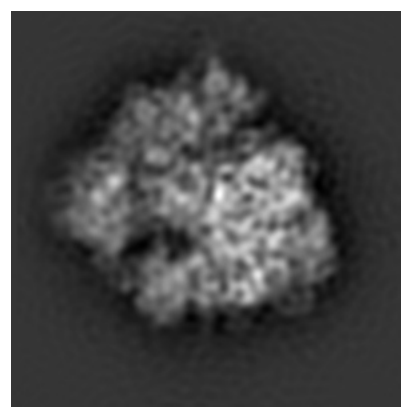
#### 6.1.1 Primary map



X



Y

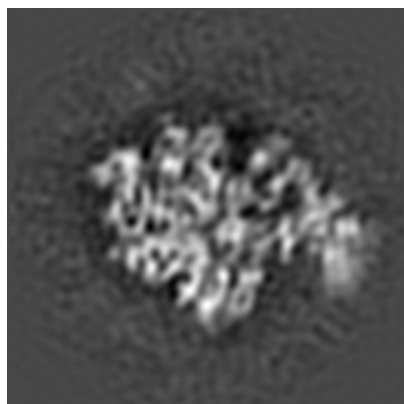


Z

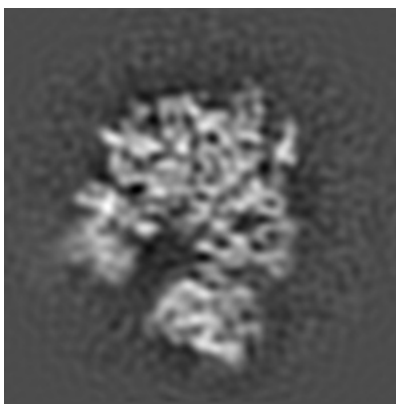
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

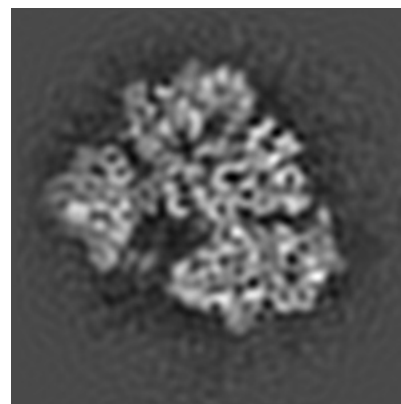
#### 6.2.1 Primary map



X Index: 65



Y Index: 65

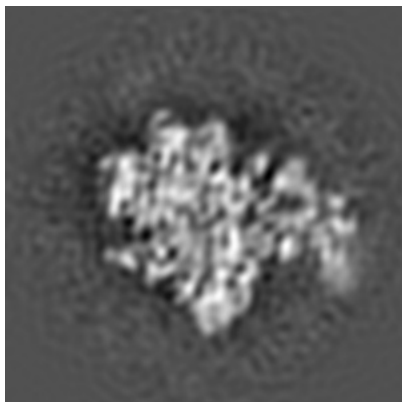


Z Index: 65

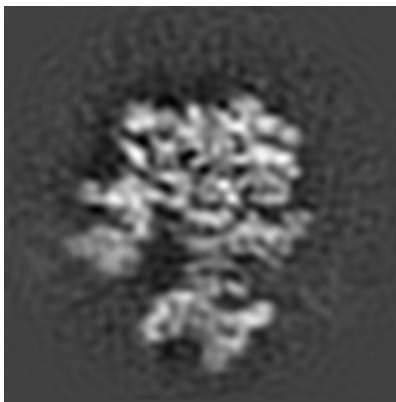
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

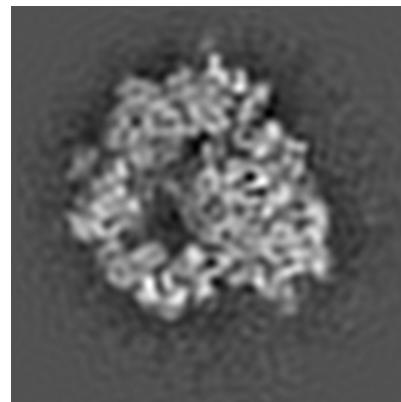
### 6.3.1 Primary map



X Index: 67



Y Index: 69

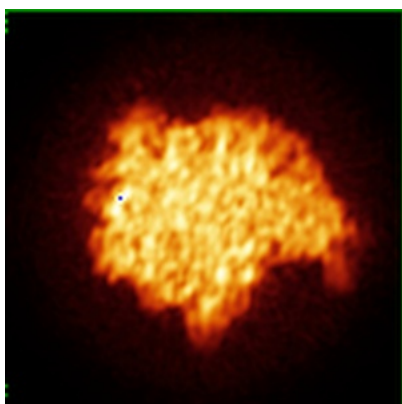


Z Index: 59

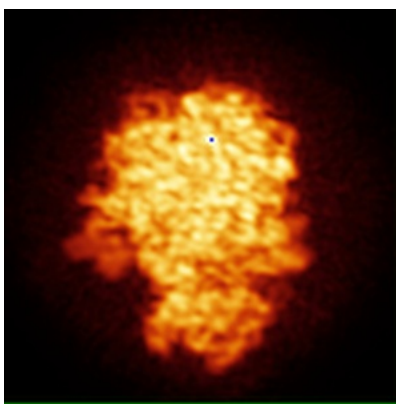
The images above show the largest variance slices of the map in three orthogonal directions.

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

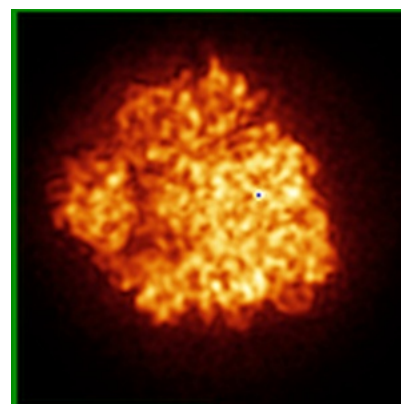
### 6.4.1 Primary map



X



Y

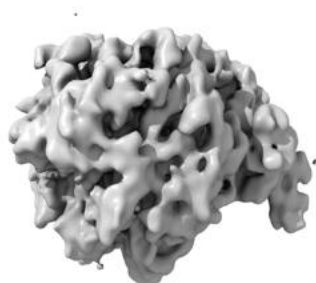


Z

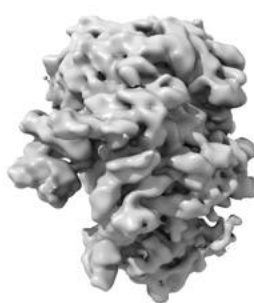
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

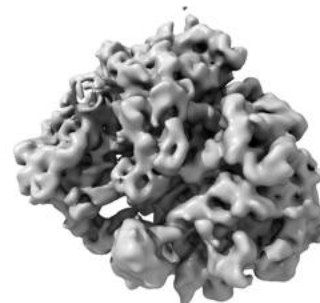
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 49.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

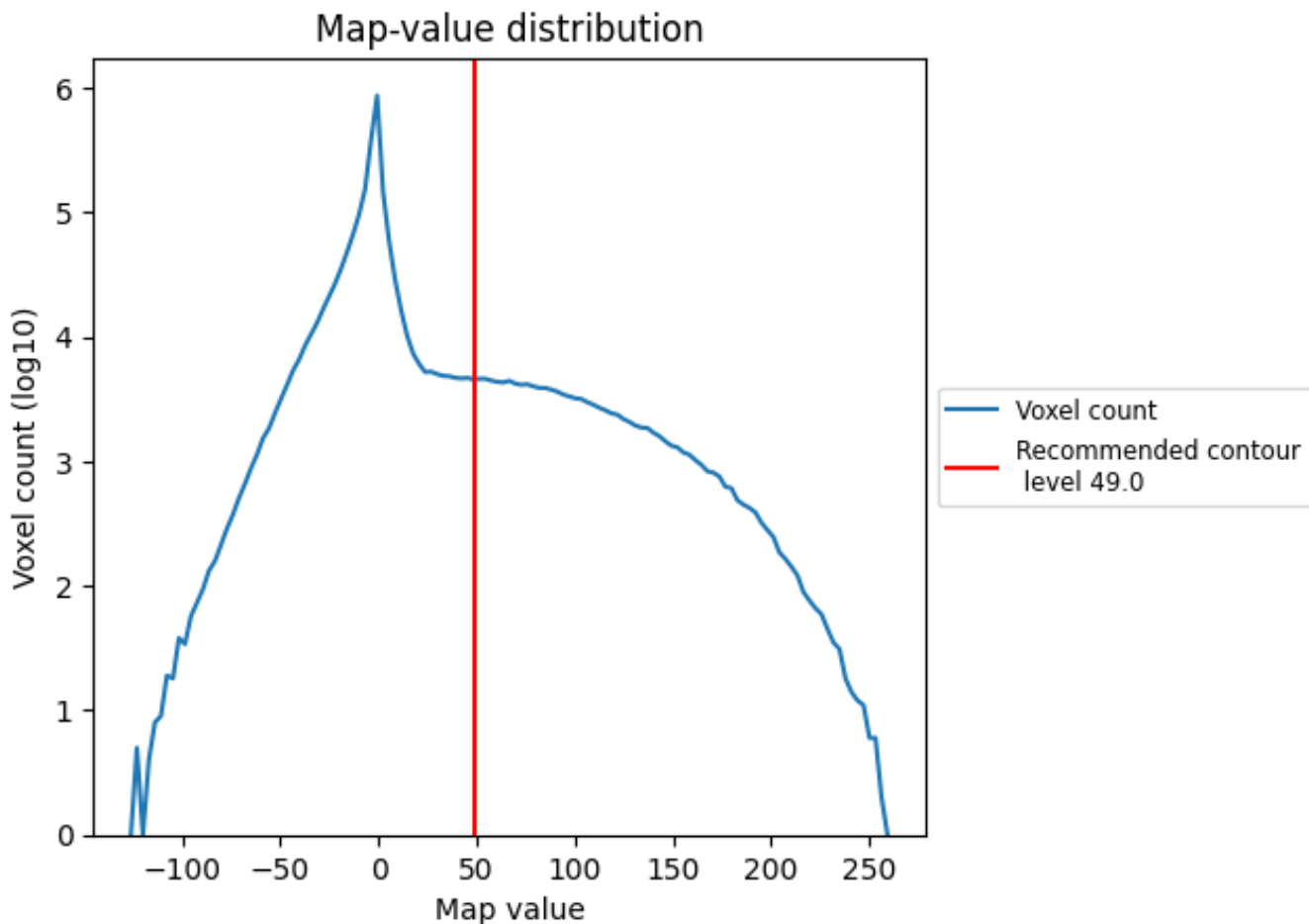
## 6.6 Mask visualisation [i](#)

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.

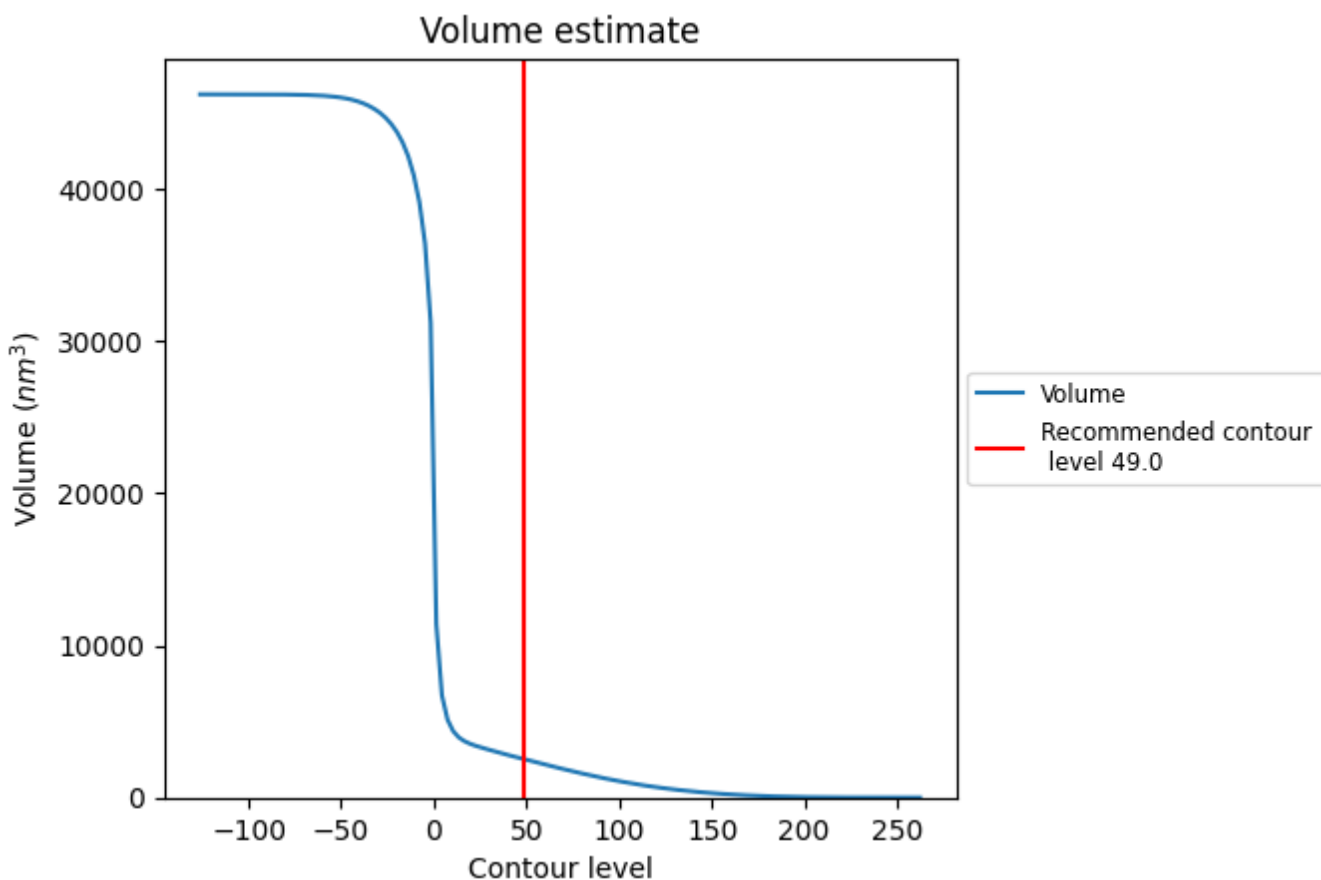
### 7.1 Map-value distribution [i](#)



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.



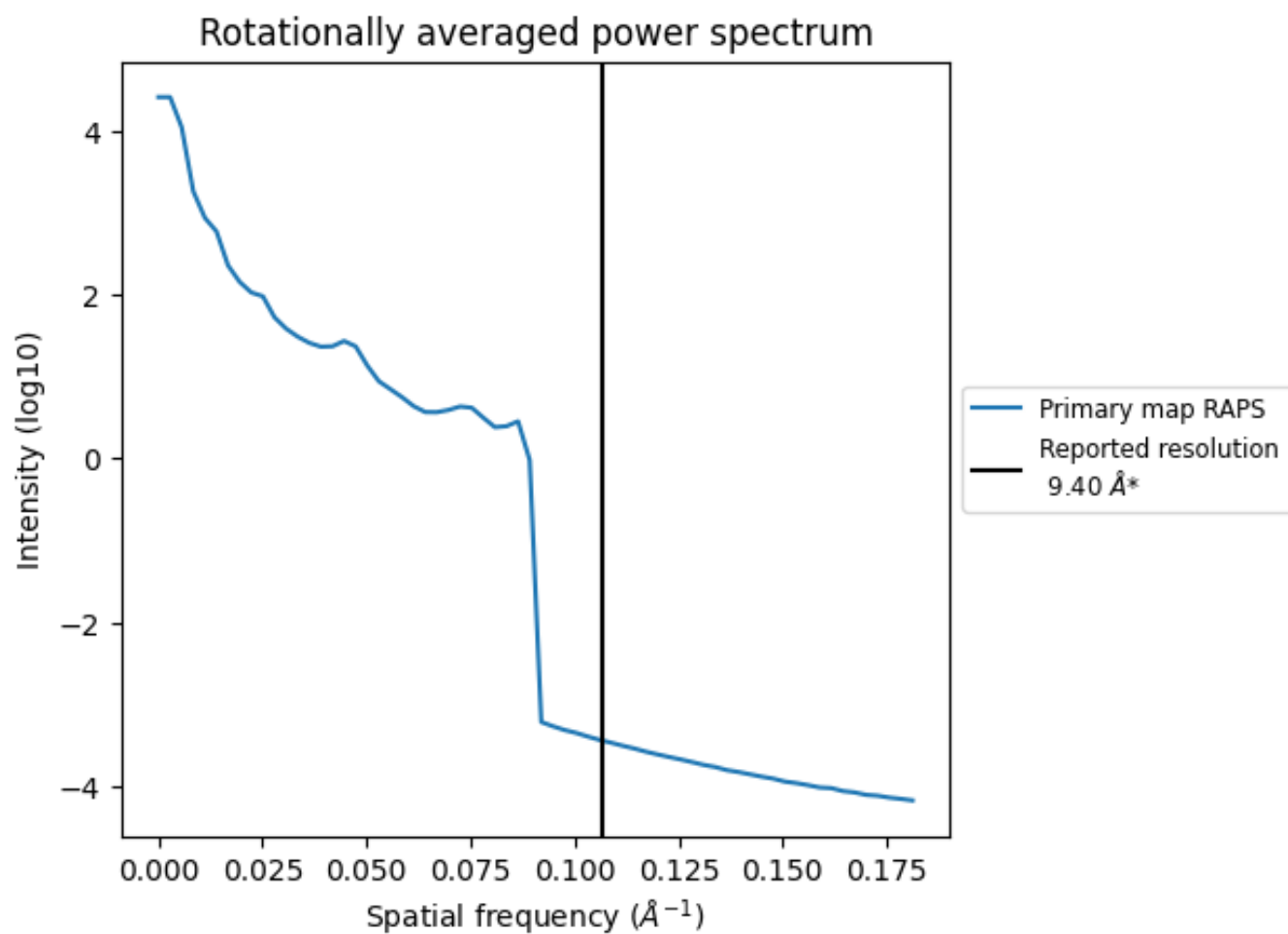
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2510 nm<sup>3</sup>; this corresponds to an approximate mass of 2268 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.106 \text{\AA}^{-1}$

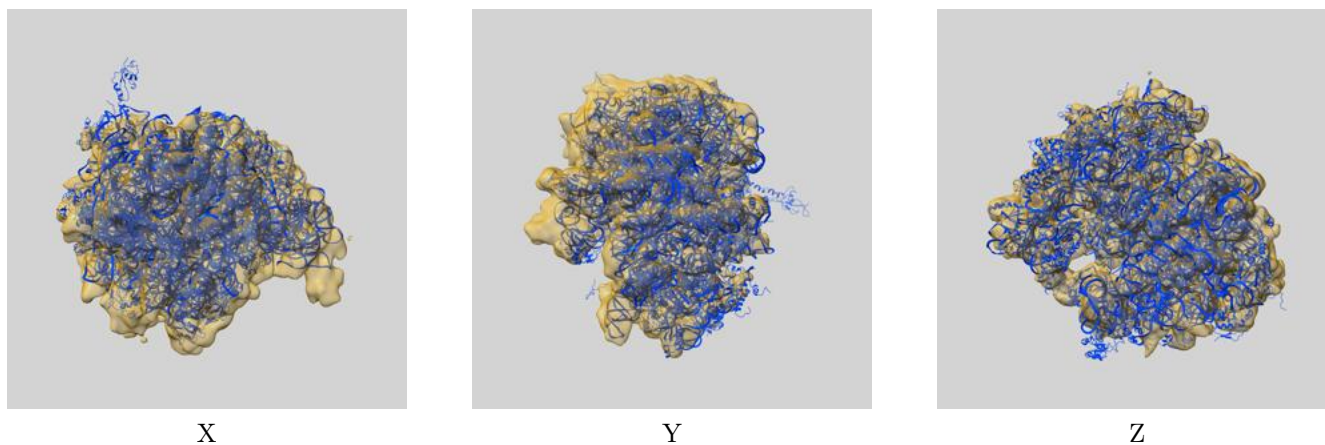
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

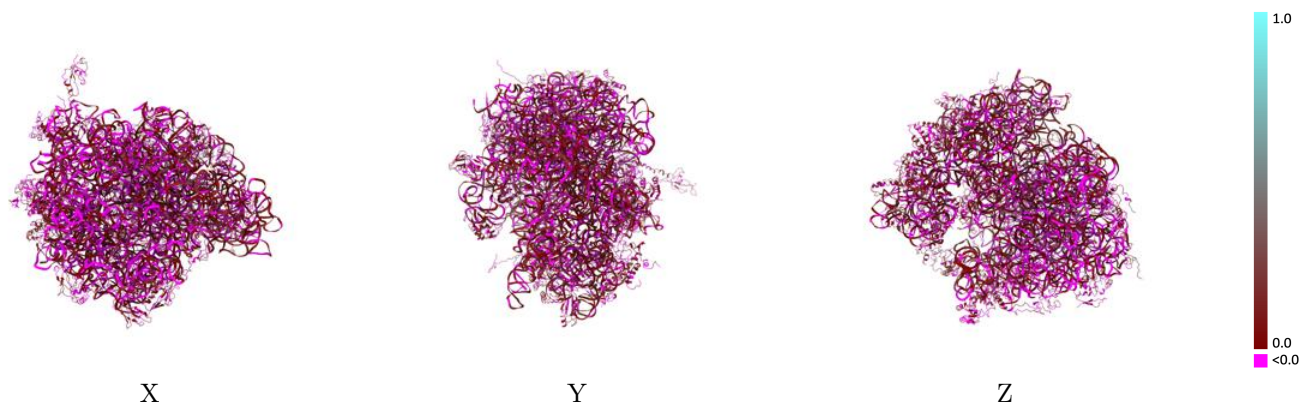
This section contains information regarding the fit between EMDB map EMD-1417 and PDB model 4V61. Per-residue inclusion information can be found in section 3 on page 14.

### 9.1 Map-model overlay [i](#)



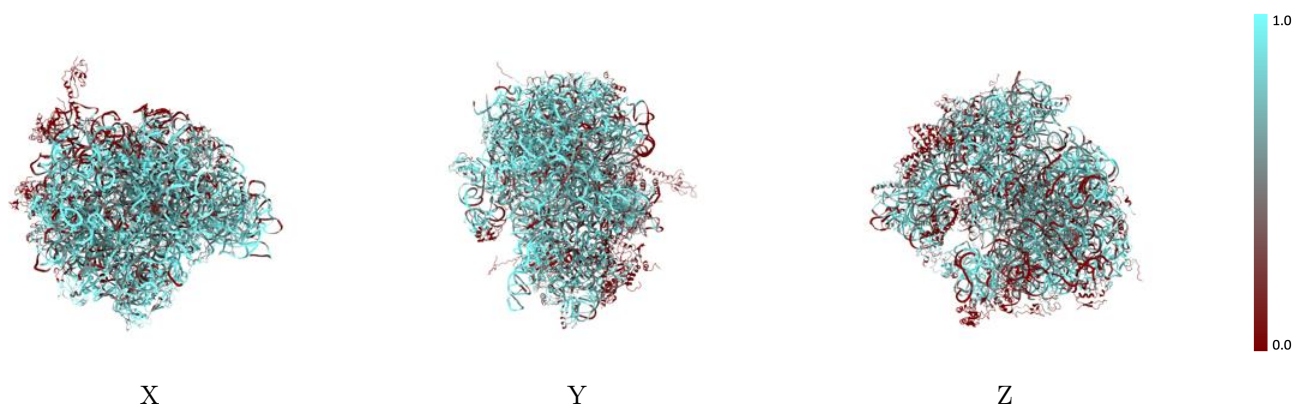
The images above show the 3D surface view of the map at the recommended contour level 49.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



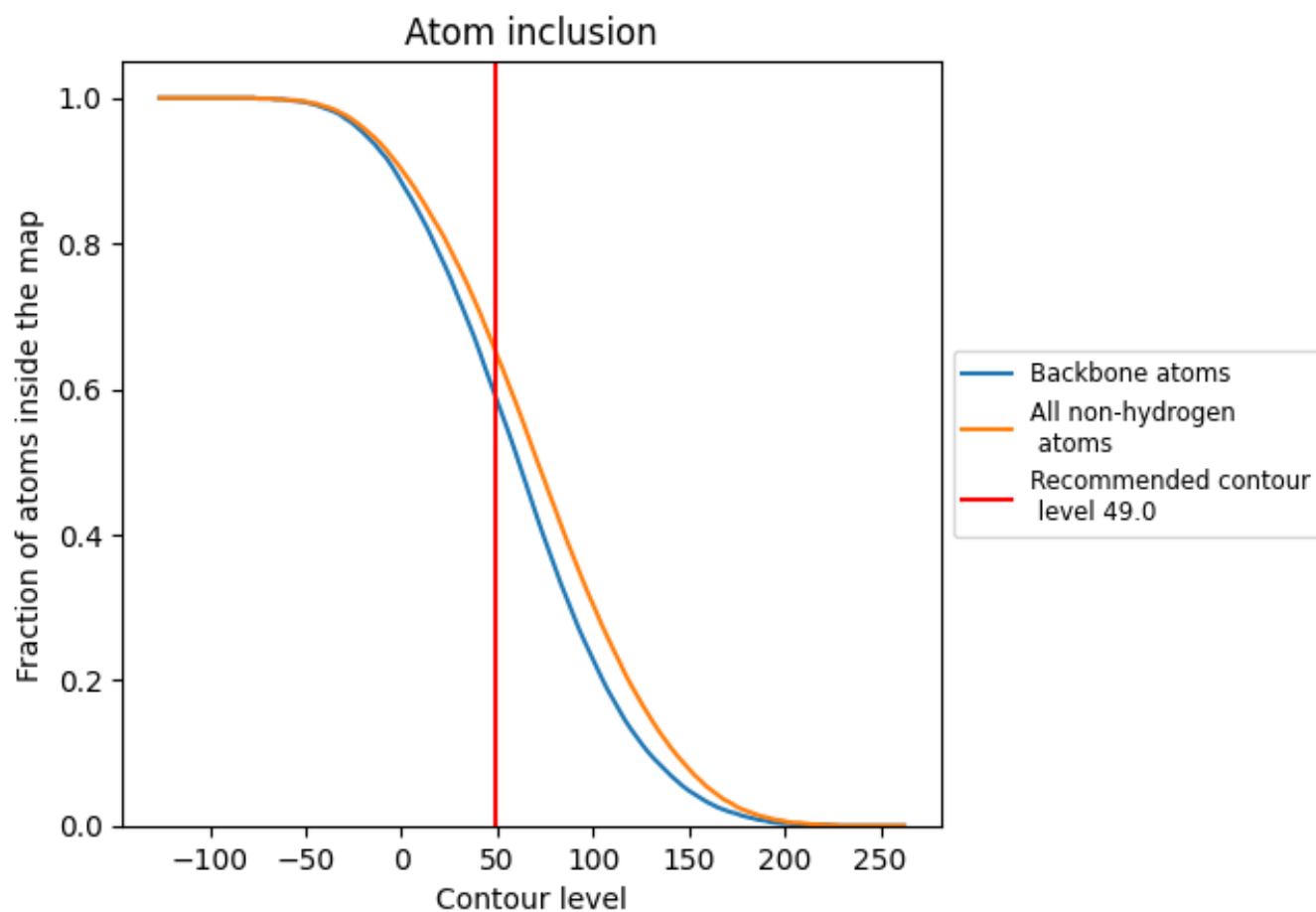
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (49.0).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 65% 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 (49.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6530	 0.0350
AA	 0.7460	 0.0630
AB	 0.1170	 0.0450
AC	 0.5420	 0.0510
AD	 0.5020	 0.0540
AE	 0.4820	 0.0260
AF	 0.4760	 0.0370
AG	 0.2700	 0.0190
AH	 0.4940	 0.0320
AI	 0.6570	 0.0510
AJ	 0.6830	 0.0540
AK	 0.5540	 0.0570
AL	 0.2680	 0.0020
AM	 0.5630	 0.0270
AN	 0.8320	 0.0120
AO	 0.5550	 0.0390
AP	 0.5110	 -0.0080
AQ	 0.5610	 0.0200
AR	 0.5340	 0.0340
AS	 0.6530	 0.0090
AT	 0.6180	 0.0120
AU	 0.3350	 0.0590
B1	 0.2240	 0.0370
B2	 0.4750	 -0.0230
B3	 0.3570	 0.0340
B4	 0.5840	 -0.0360
B5	 0.7240	 -0.0040
B6	 0.7890	 -0.0010
BA	 0.6890	 0.0290
BB	 0.8210	 0.0610
BC	 0.7840	 0.0570
BD	 0.2430	 0.0060
BE	 0.5130	 0.0080
BF	 0.8060	 -0.0090
BG	 0.4020	 -0.0250



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Chain	Atom inclusion	Q-score
BH	 0.7930	 0.0580
BI	 0.7140	 0.0320
BJ	 0.0570	 0.0110
BK	 0.4330	 0.0400
BL	 0.7780	 0.0080
BM	 0.5550	 0.0170
BN	 0.4500	 -0.0160
BO	 0.4370	 0.0060
BP	 0.8040	 0.0160
BQ	 0.7100	 0.0330
BR	 0.6310	 0.0140
BS	 0.7650	 -0.0110
BT	 0.6650	 0.0260
BU	 0.6310	 0.0280
BV	 0.5620	 0.0170
BW	 0.6060	 -0.0010
BX	 0.5460	 0.0070
BY	 0.6510	 0.0000
BZ	 0.5870	 0.0340