wwPDB EM Validation Summary Report (i)

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 9.4A 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

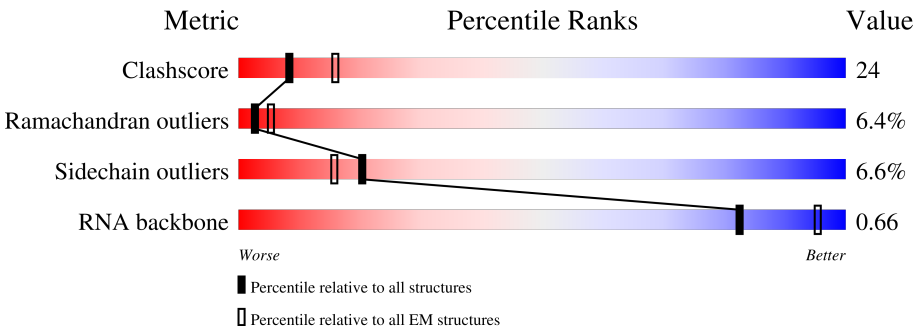
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 >=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 <=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	16% 39% 46% 14% •
2	AB	231	88% 84% 13% •
3	AC	218	39% 85% 13% •
4	AD	201	45% 84% 15% •
5	AE	308	24% 43% 7% • 49%
6	AF	168	29% 48% 15% • 36%
7	AG	155	72% 87% 10% • •

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Mol	Chain	Length	Quality of chain
8	AH	134	43% 84% 13%
9	AI	197	18% 52% 12% 36%
10	AJ	197	12% 39% 10% 50%
11	AK	140	32% 67% 16% 16%
12	AL	123	69% 82% 15%
13	AM	145	26% 53% 12% 32%
14	AN	100	14% 76% 20%
15	AO	90	38% 77% 17% 6%
16	AP	88	39% 61% 20% 8% 9%
17	AQ	142	23% 48% 9% 42%
18	AR	103	21% 43% 12% 44%
19	AS	92	32% 78% 17%
20	AT	202	18% 43% 7% 50%
21	AU	190	16% 19% 6% 72%
22	BA	2810	23% 34% 54% 9%
23	BB	117	10% 48% 45% 7%
24	BC	103	16% 29% 61% 10%
25	BD	352	49% 36% 25% 36%
26	BE	269	43% 26% 59% 14%
27	BF	259	7% 22% 31% 6% 41%
28	BG	293	41% 26% 43% 28%
29	BH	220	12% 35% 39% 5% 20%
30	BI	223	18% 43% 36% 18%
31	BJ	197	70% 31% 40% 25%
32	BK	224	36% 37% 25% 35%

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Mol	Chain	Length	Quality of chain
33	BL	250	8% 18% 29% 50%
34	BM	121	40% 37% 55% 7%
35	BN	257	35% 29% 28% 11% 32%
36	BO	135	53% 34% 56% 10%
37	BP	205	8% 23% 30% 43%
38	BQ	161	17% 22% 42% 11% 24%
39	BR	233	15% 11% 26% 11% 52%
40	BS	119	18% 27% 66% 6%
41	BT	257	12% 16% 18% 7% 60%
42	BU	199	20% 24% 32% 5% 39%
43	BV	198	17% 19% 21% 57%
44	BW	191	21% 24% 23% 9% 42%
45	BX	198	18% 14% 24% 6% 57%
46	BY	151	15% 15% 28% 6% 50%
47	BZ	173	13% 20% 14% 62%
48	B1	144	38% 28% 19% 50%
49	B2	57	49% 25% 54% 21%
50	B3	66	64% 30% 55% 14%
51	B4	152	9% 8% 15% 76%
52	B5	159	8% 14% 20% 5% 61%
53	B6	104	5% 14% 18% 63%

2 Entry composition (i)

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
			Total	C	N	O	S		
19	AS	92	747	472	146	126	3	0	0

- Molecule 20 is a protein called Ribosomal Protein S20.

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

- Molecule 21 is a protein called Ribosomal Protein S21.

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

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

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

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

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

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

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

- Molecule 25 is a protein called Ribosomal Protein L1.

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

- 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
			Total	C	N	O	S		
33	BL	125	998	634	192	169	3	0	0

- Molecule 34 is a protein called Ribosomal Protein L14.

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

- Molecule 35 is a protein called Ribosomal Protein L15.

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

- Molecule 36 is a protein called Ribosomal Protein L16.

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

- Molecule 37 is a protein called Ribosomal Protein L17.

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

- Molecule 38 is a protein called Ribosomal Protein L18.

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

- Molecule 39 is a protein called Ribosomal Protein L19.

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

- 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		
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.

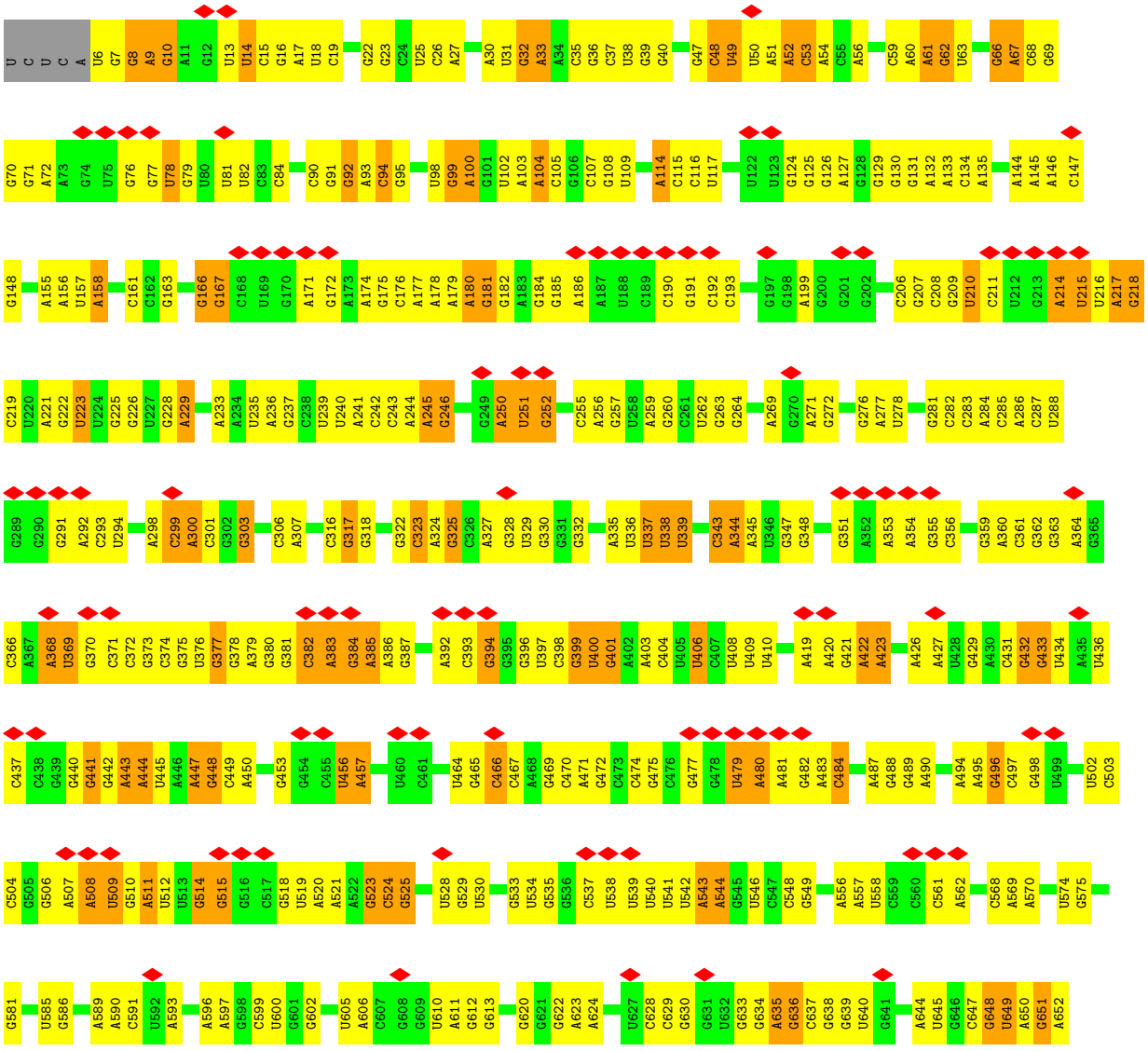
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	B6	38	309	190	65	49	5	0	0

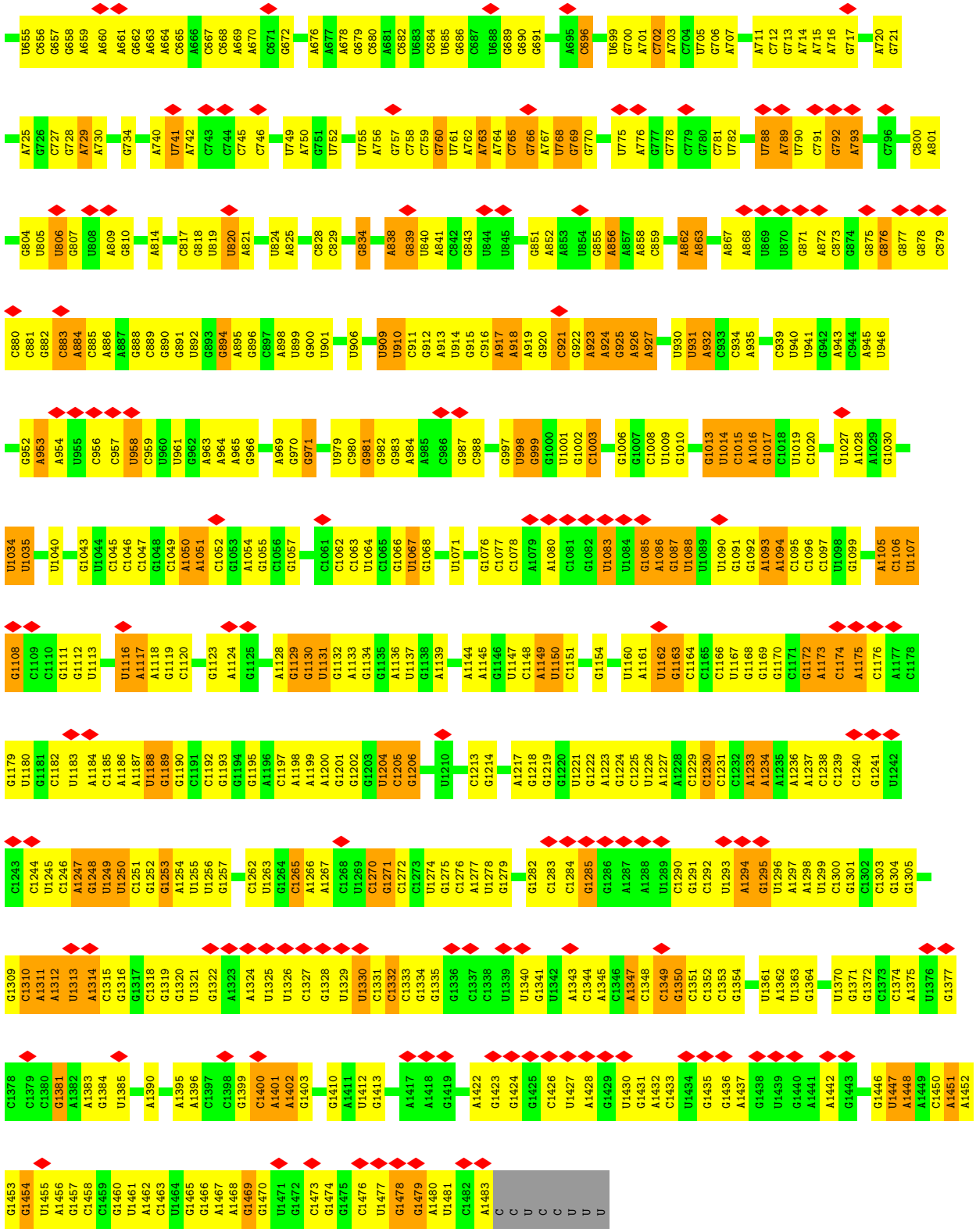
3 Residue-property plots (i)

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

- Molecule 1: 16S rRNA

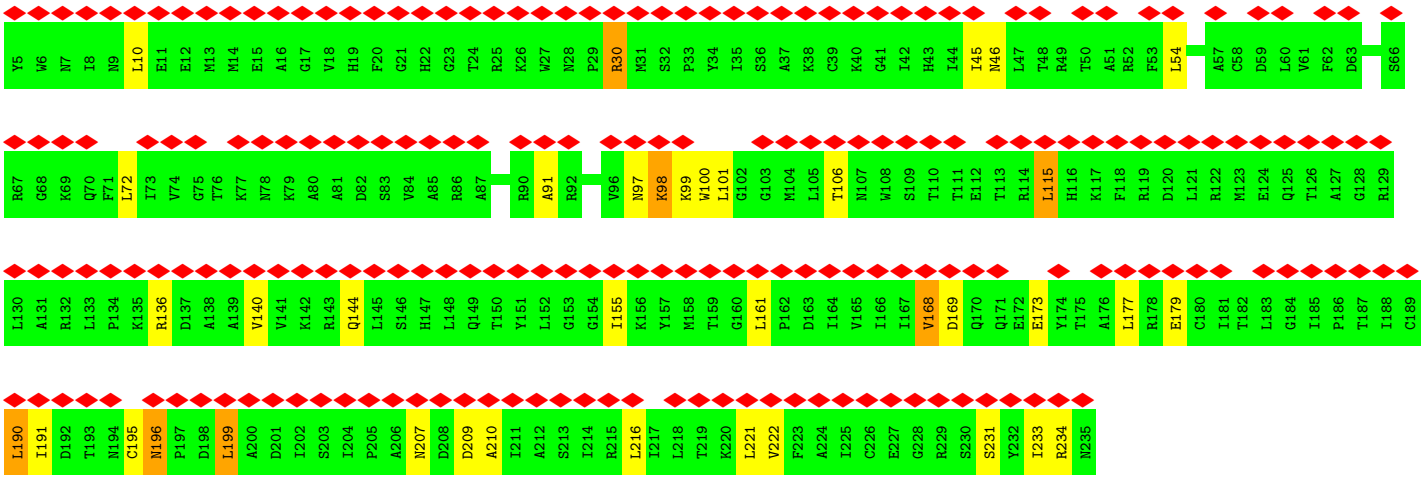
Chain AA: 16% 39% 46% 14%





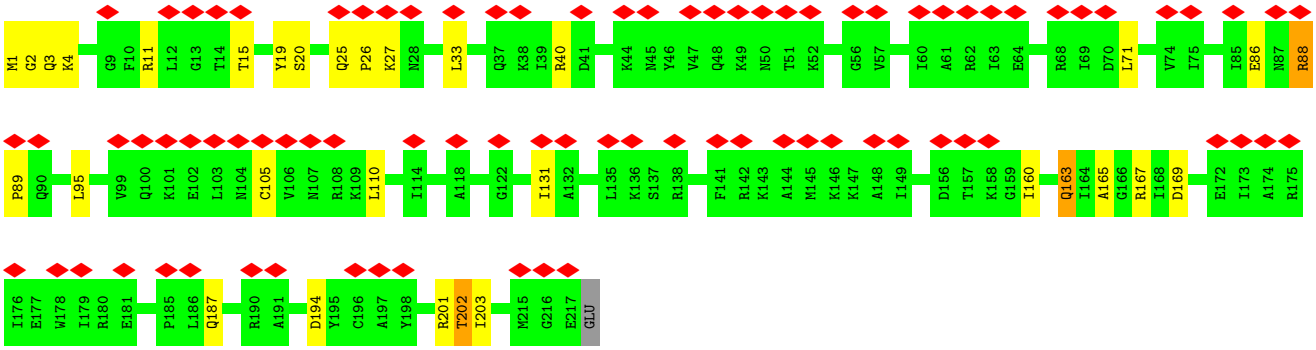
- Molecule 2: Ribosomal Protein S2

Chain AB:



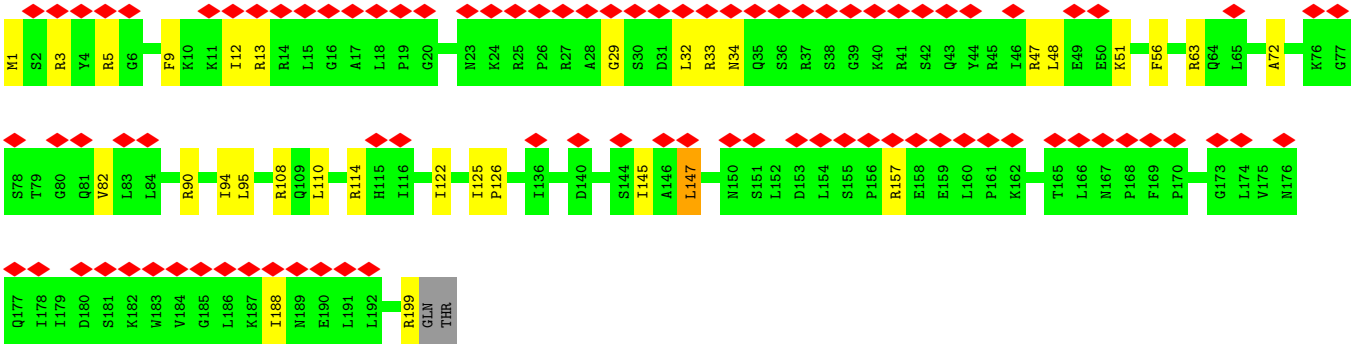
- Molecule 3: Ribosomal Protein S3

Chain AC:



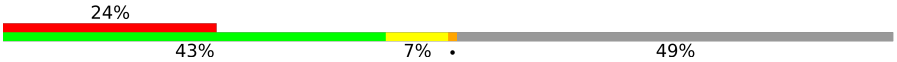
- Molecule 4: Ribosomal Protein S4

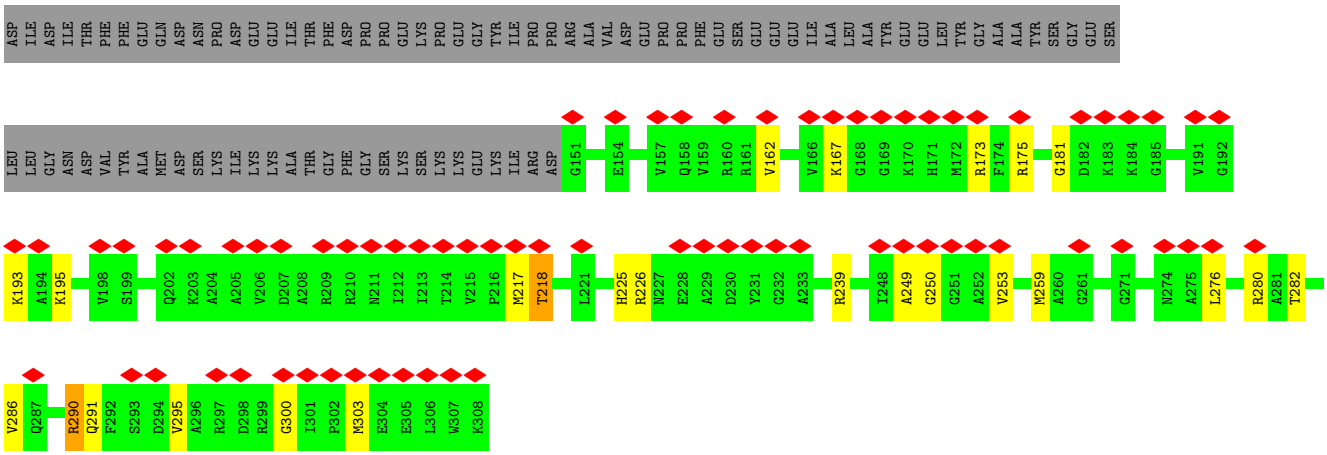
Chain AD:



- Molecule 5: Ribosomal Protein S5

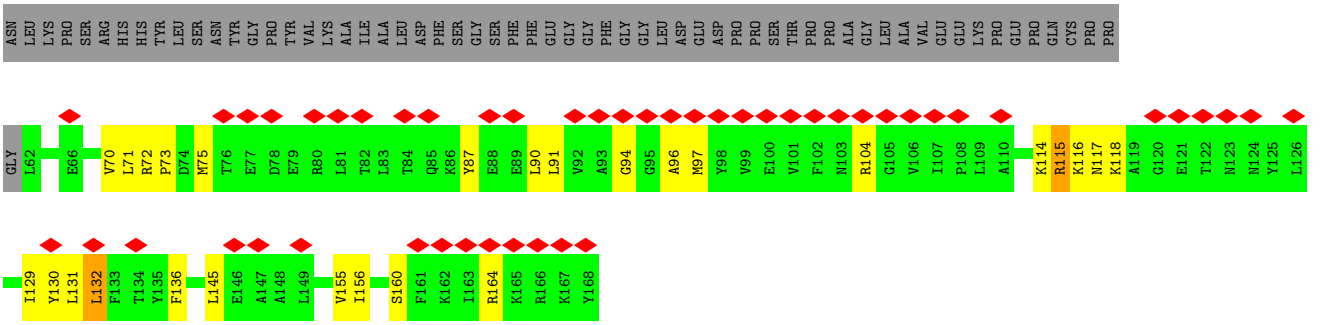
Chain AE:





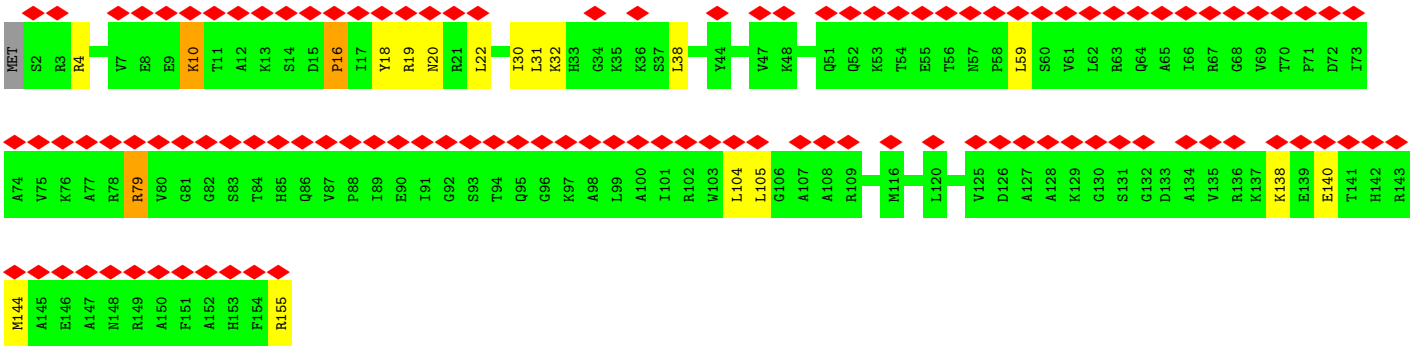
- Molecule 6: Ribosomal Protein S6

Chain AF:



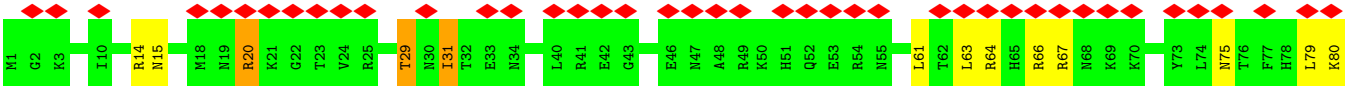
- Molecule 7: Ribosomal Protein S7

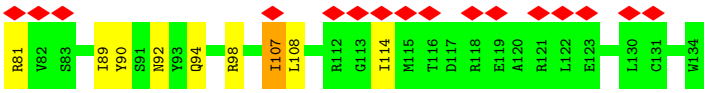
Chain AG:



- Molecule 8: Ribosomal Protein S8

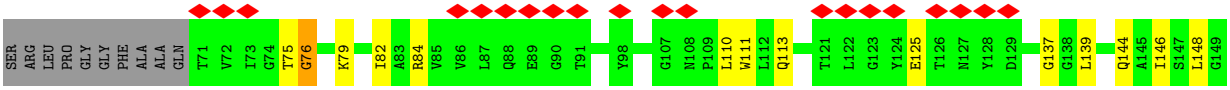
Chain AH:

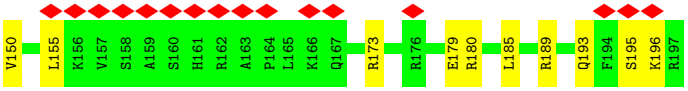




• Molecule 9: Ribosomal Protein S9

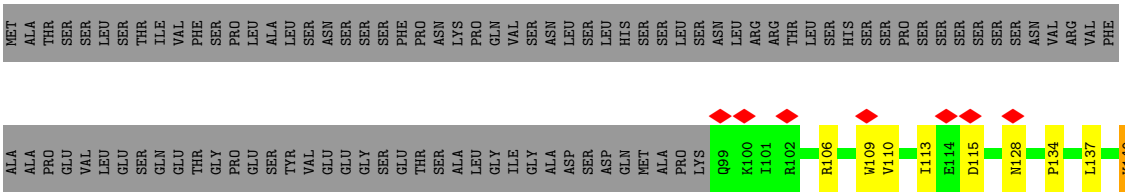
Chain AI:

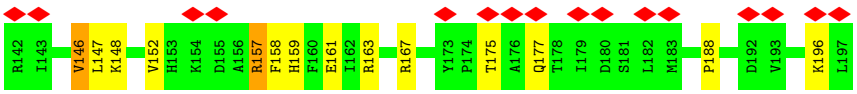




• Molecule 10: Ribosomal Protein S10

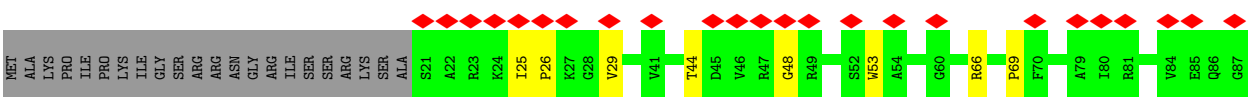
Chain AJ:

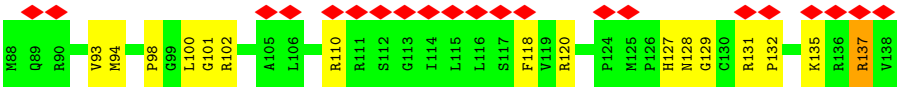




• Molecule 11: Ribosomal Protein S11

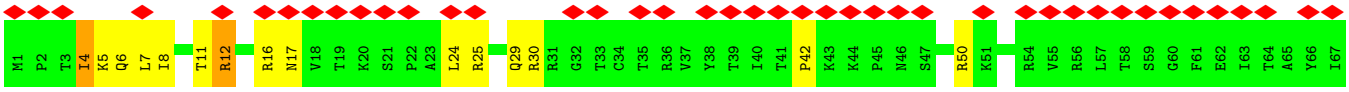
Chain AK:

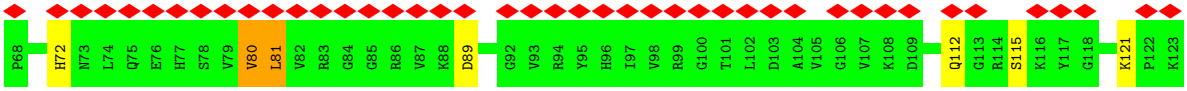




• Molecule 12: Ribosomal Protein S12

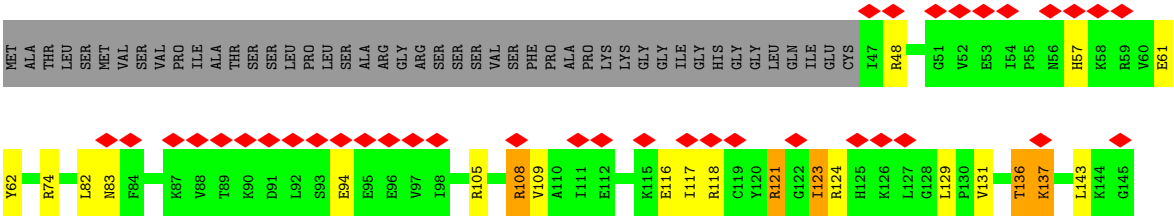
Chain AL:





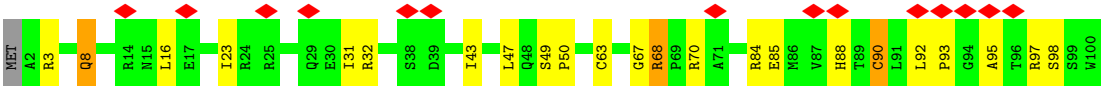
- Molecule 13: Ribosomal Protein S13

Chain AM:



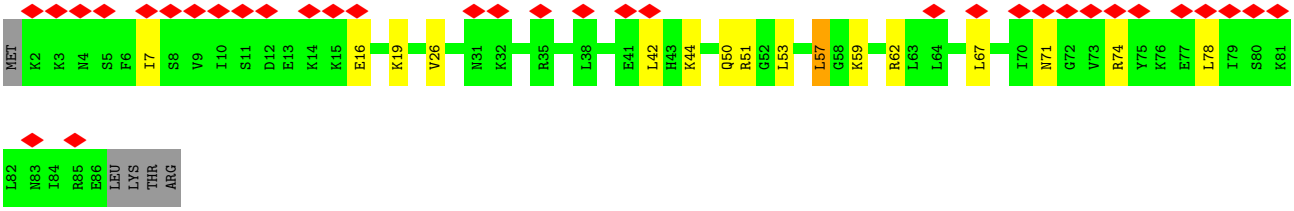
- Molecule 14: Ribosomal Protein S14

Chain AN:



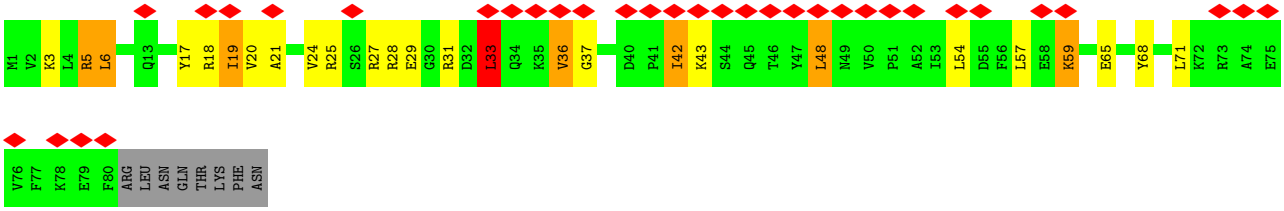
- Molecule 15: Ribosomal Protein S15

Chain AO:



- Molecule 16: Ribosomal Protein S16

Chain AP:



- Molecule 17: Ribosomal Protein S17

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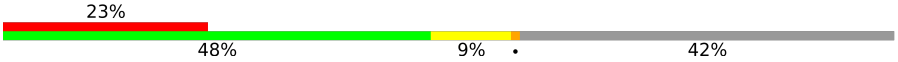
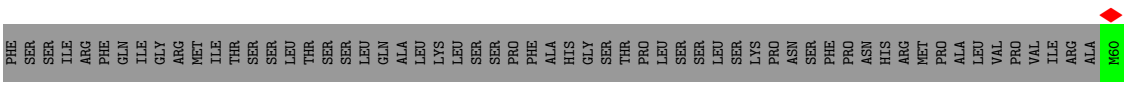
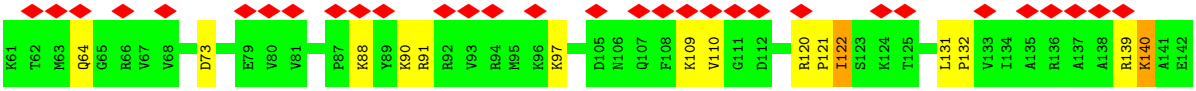
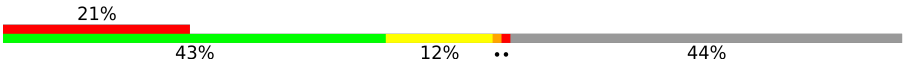


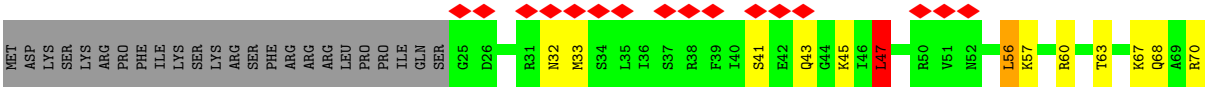


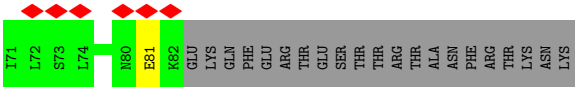


- Molecule 18: Ribosomal Protein S18

Chain AR:

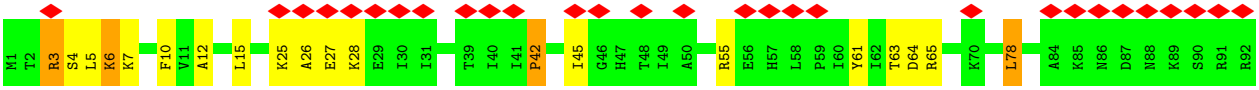






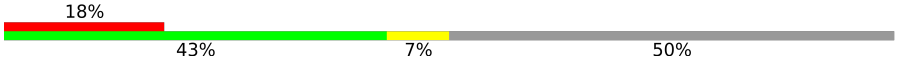
- Molecule 19: Ribosomal Protein S19

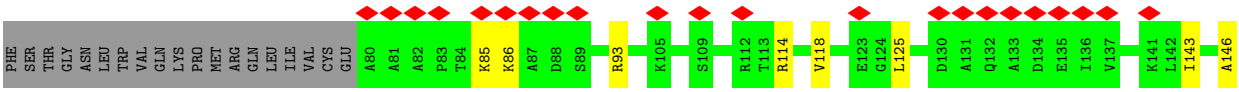
Chain AS:

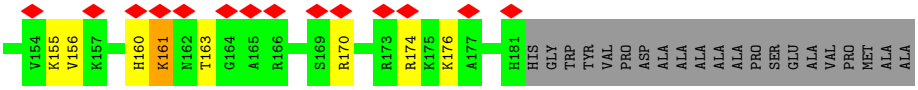


- Molecule 20: Ribosomal Protein S20

Chain AT:

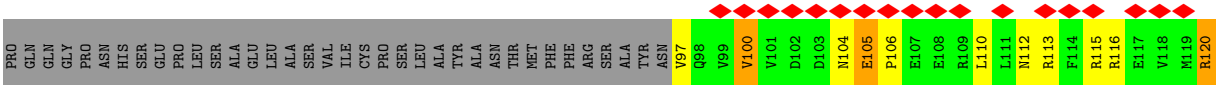


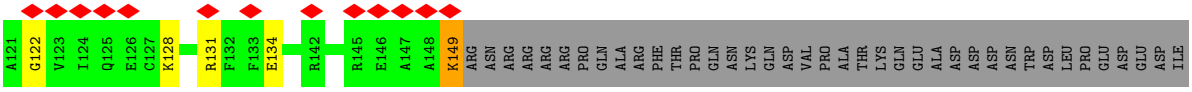




- Molecule 21: Ribosomal Protein S21

Chain AU:

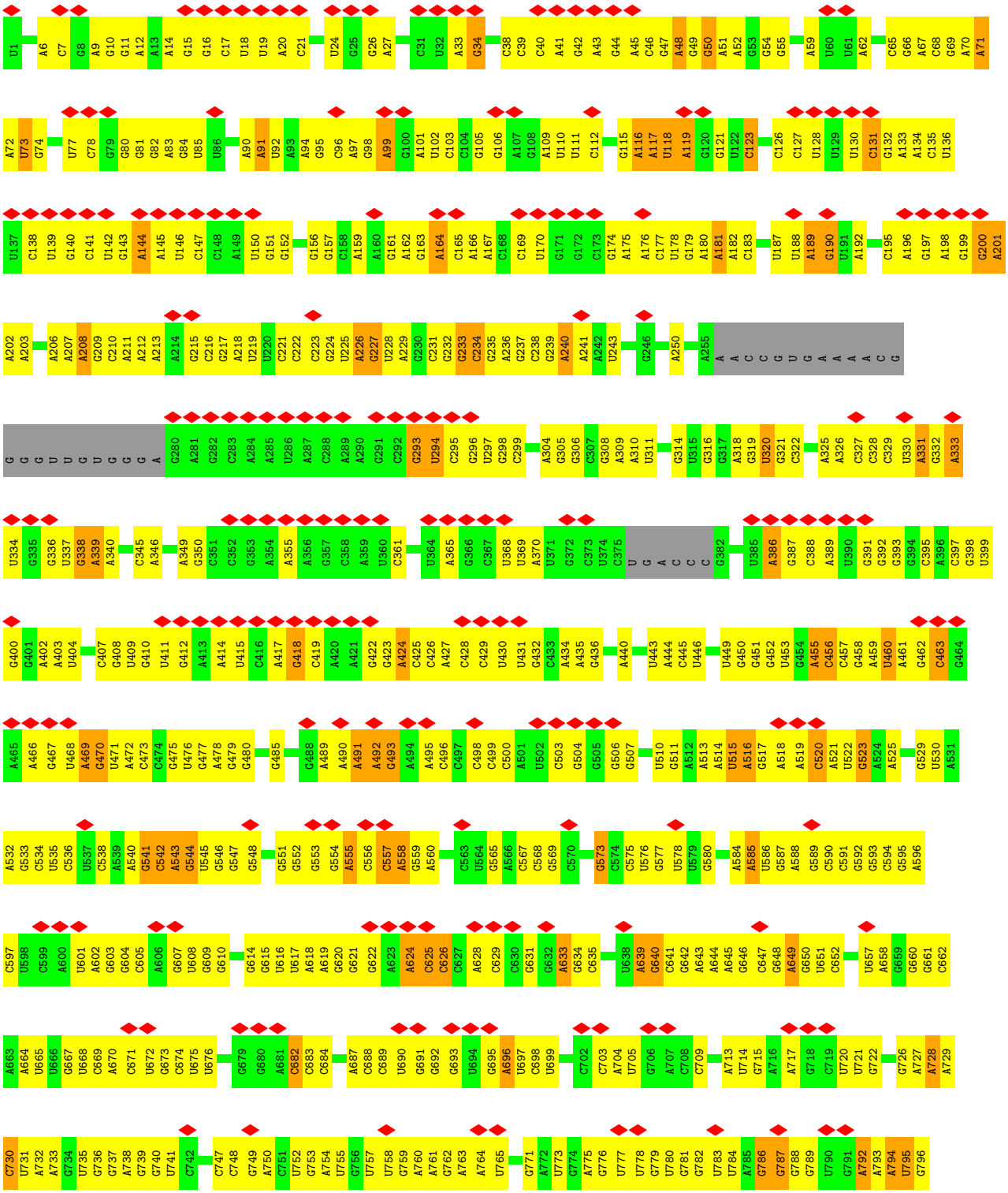


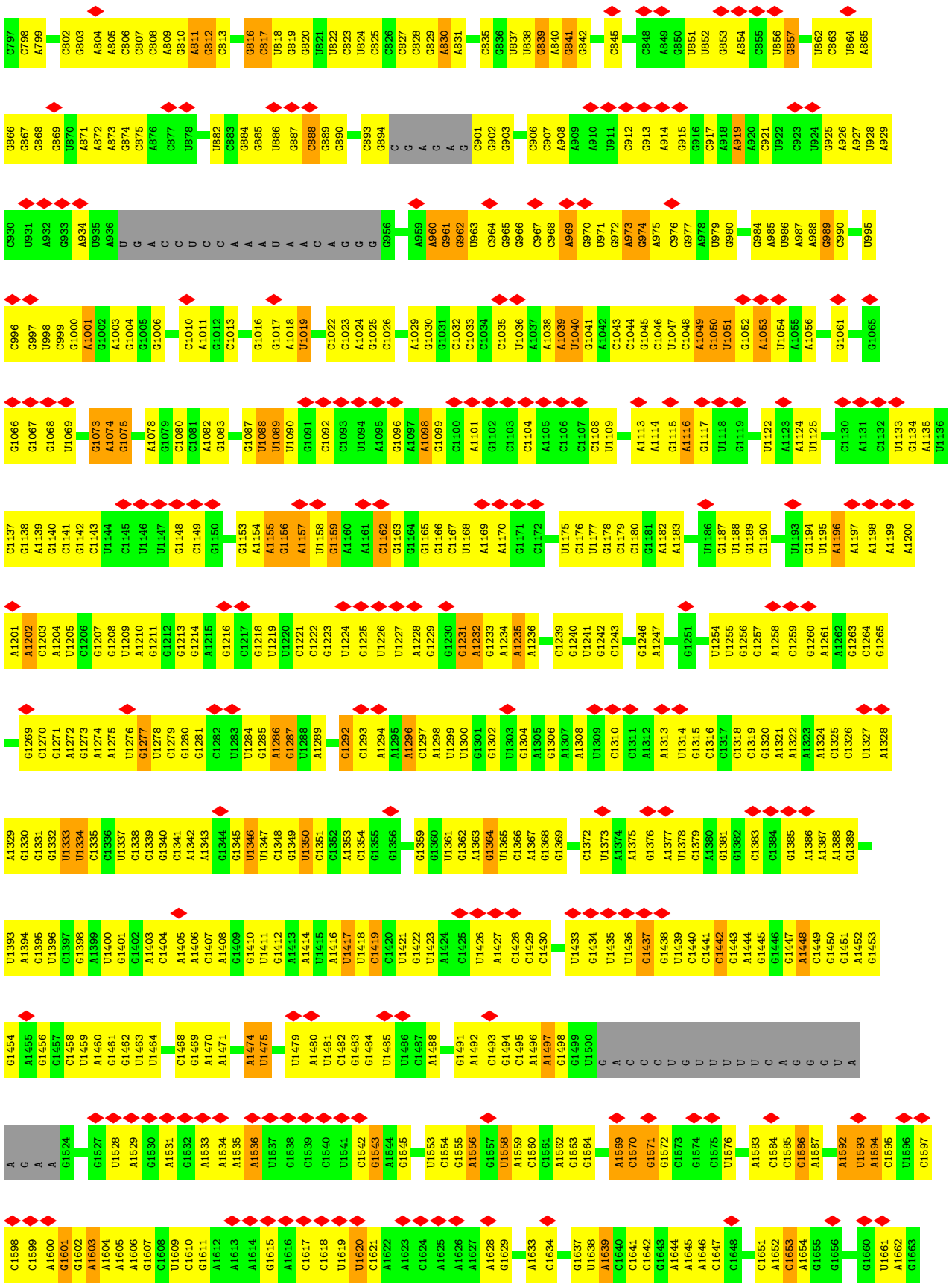


PRO
SER

- Molecule 22: 23S rRNA

Chain BA: 23% 34% 54% 9%

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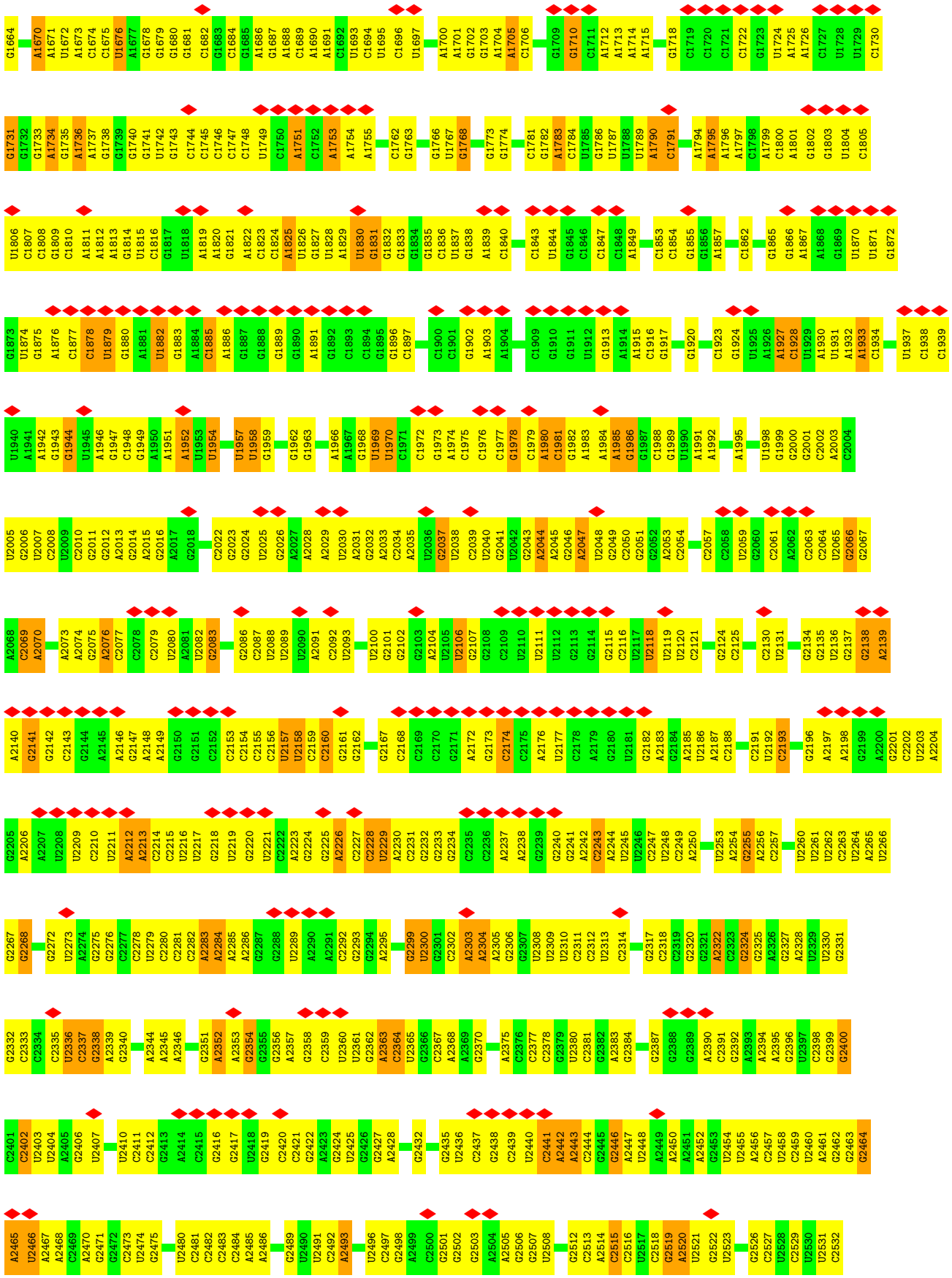
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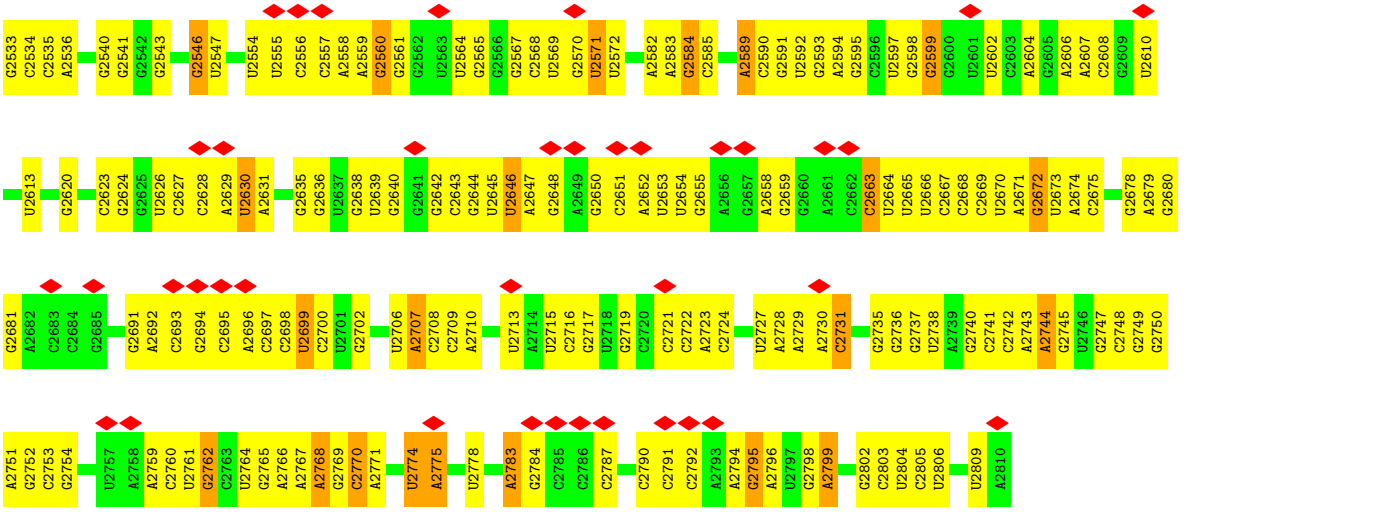
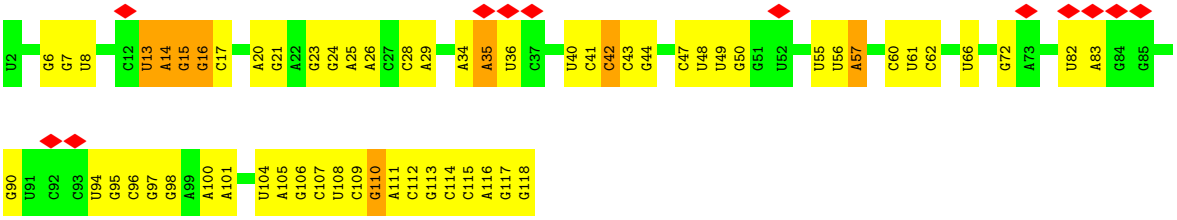


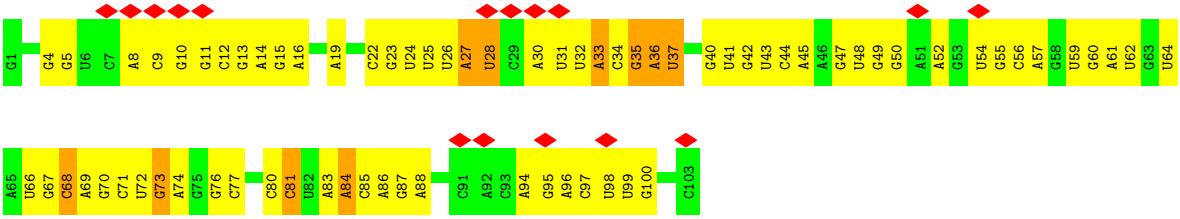
- Molecule 23: 5S rRNA

Chain BB:



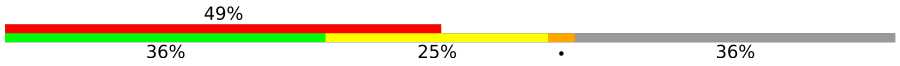
- Molecule 24: 4.8S rRNA

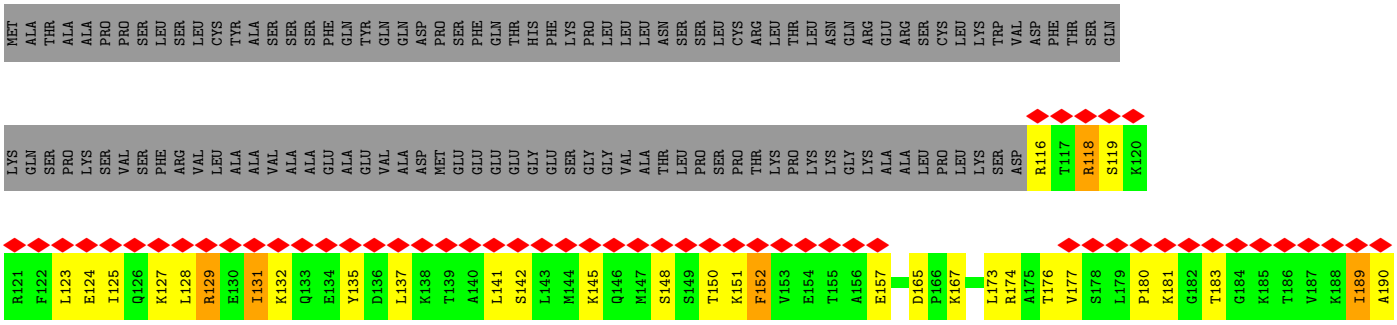
Chain BC:

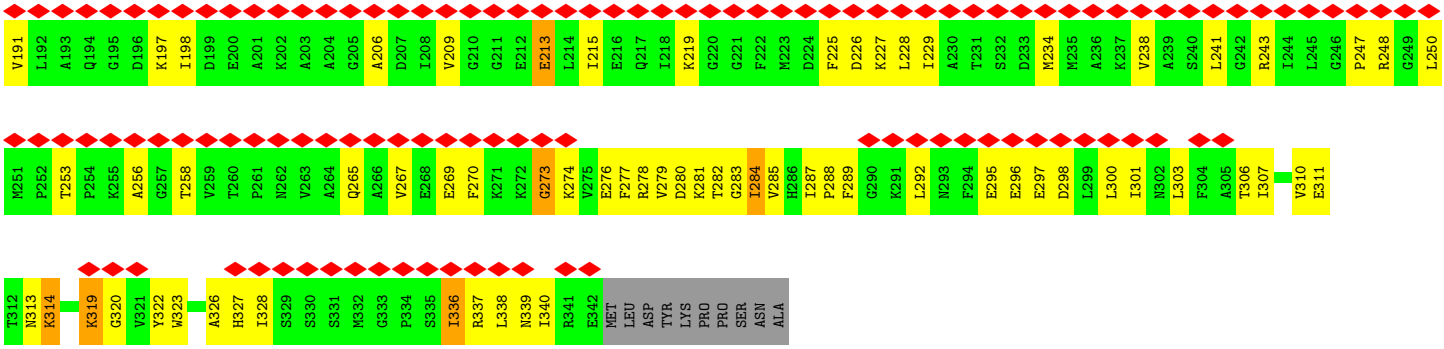


- Molecule 25: Ribosomal Protein L1

Chain BD:

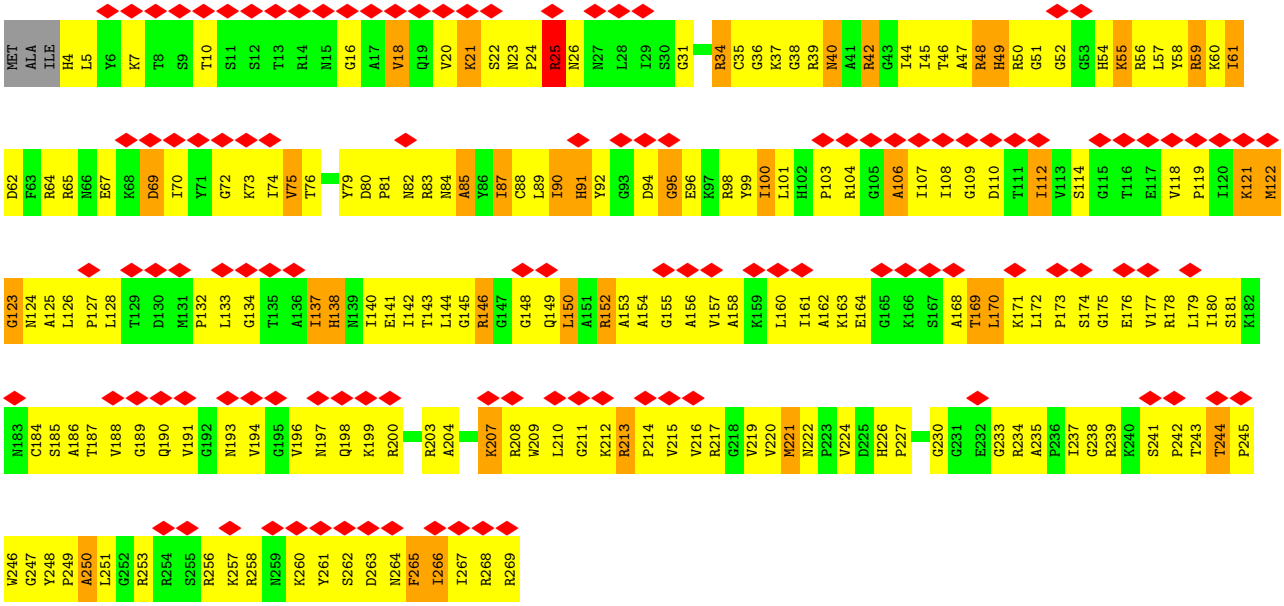






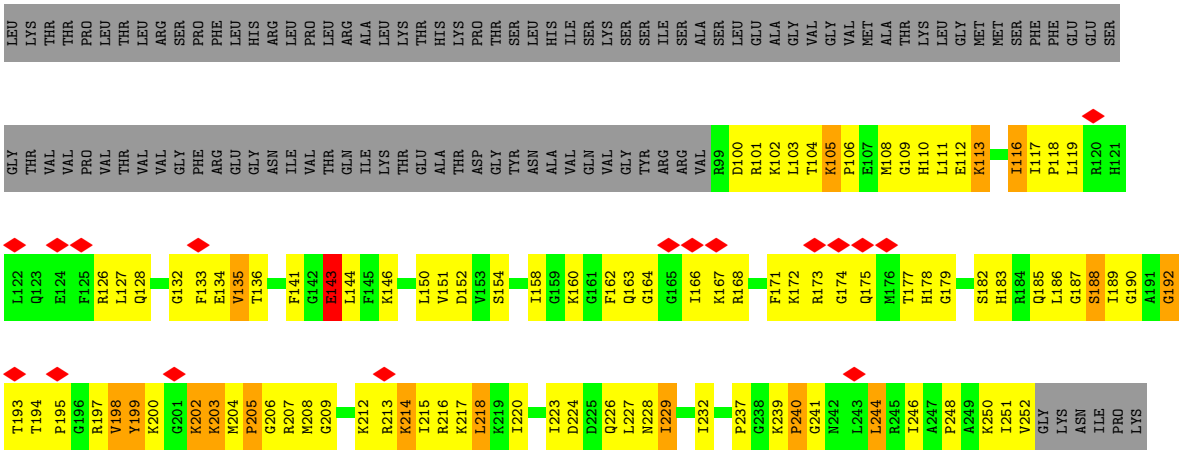
• Molecule 26: Ribosomal Protein L2

Chain BE:



• Molecule 27: Ribosomal Protein L3

Chain BF:



SER

• Molecule 28: Ribosomal Protein L4

Chain BG: 41% 26% 43% • 28%

MET ALA THR SER THR SER SER SER SER LEU SER LEU SER PHE PHE SER SER SER SER LEU PHE SER SER LYS SER SER ARG ASN PHE SER SER LYS PRO ILE LEU LYS LEU PRO SER SER SER HIS SER GLN THR SER LEU SER LEU SER ILE LYS SER E51 L52 I53 P54 L55 P56 I57 L58 N59 F60

S61 G62 E63 K64 V65 G66 E67 T68 F69 L70 N71 L72 K73 T74 A75 P76 P77 E78 K79 A80 R81 A82 V83 V84 H85 R86 G87 L88 I89 T90 H91 L92 Q93 N94 K95 R96 R97 G98 T99 A100 S101 T102 L103 T104 R105 A106 E107 V108 R109 G110 G111 G112 R113 K114 P115 Y116 P117 Q118 K119 K120

T121 R125 R126 G127 S128 Q129 G130 S131 P132 L133 R134 P135 G136 G137 G138 V139 I140 F141 G142 P143 K144 P145 R146 D147 W148 T149 I150 K151 M152 N153 K154 K155 E156 R157 R158 L159 A160 L161 S162 T163 A164 S167 A168 N171 S172 F173 V174 V175 E176 E177 F178 A179 E180 N181 F182 E183 K184

P185 K186 T187 K188 I191 M194 Q195 R196 W197 G198 L199 D200 P201 A202 E203 K204 S205 L206 F207 F208 L209 M210 D211 L212 V213 E214 N215 V216 E217 K218 S219 G220 R221 N222 I223 R224 T225 L226 K227 L228 L229 T230 P231 R232 S233 L234 N235 L236 F237 D238 V239 L240 N241 A242 E243 K244 L245 V246

F247 T248 E249 G250 T251 I252 Q253 Y254 L255 N256 Q257 R258 Y259 G260 V261 ASP THR LEU GLU ASP GLU ASP GLU GLU GLU GLU GLU GLU GLU GLU GLU GLU GLY GLU GLU VAL ASP ASP GLY VAL GLU ASP GLY THR PRO GLU PRO ALA GLU

• Molecule 29: Ribosomal Protein L5

Chain BH: 12% 35% 39% 5% 20%

ALA ALA GLY THR ALA VAL PHE VAL ASP LYS ALA GLU ALA GLU THR ILE ASN R18 L19 K20 Y23 I24 E25 K26 M27 V28 P29 L30 L31 K32 E33 E34 Y37 S38 N39 I40 L41 E42 V43 P44 K45 V46 V47 K48 I49 V50 V51 N52 C53 A58 S59 Q60 N61 A62 K63 G64 L65

D66 A67 A68 I69 N70 E71 L72 A73 L74 I75 T76 P80 V81 K82 T83 K84 A85 R95 E96 G97 L100 G101 I102 A103 V104 T105 L106 R107 G108 N109 L110 M111 Y112 S113 F114 L115 D116 R117 L121 A122 L123 P124 R125 T126 R127 Q130 P134 N135 S136 F137 D138 G141 N142

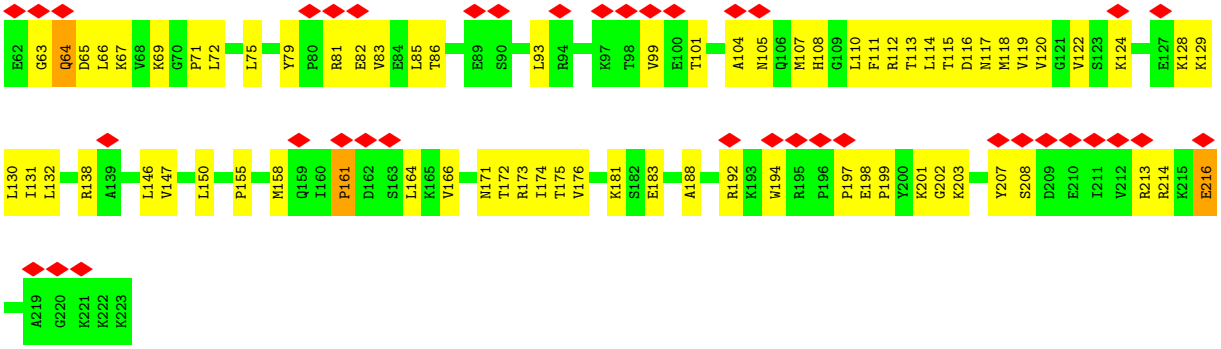
Y143 S144 V145 G146 F147 R148 E149 Q150 F153 P154 E155 I156 K157 P158 E159 I160 V161 G162 V169 C170 I171 T172 T173 T174 A175 K176 K179 Y182 K183 L184 L185 M188 G189 M190 P191 F192 ARG GLU GLY SER GLY PRO SER THR LEU VAL ARG LYS LYS LYS LEU LYS SER HIS HIS

PHE ASP ALA LYS LYS GLY ARG ARG TYR

• Molecule 30: Ribosomal Protein L6

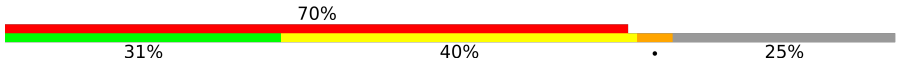
Chain BI: 18% 43% 36% • 18%

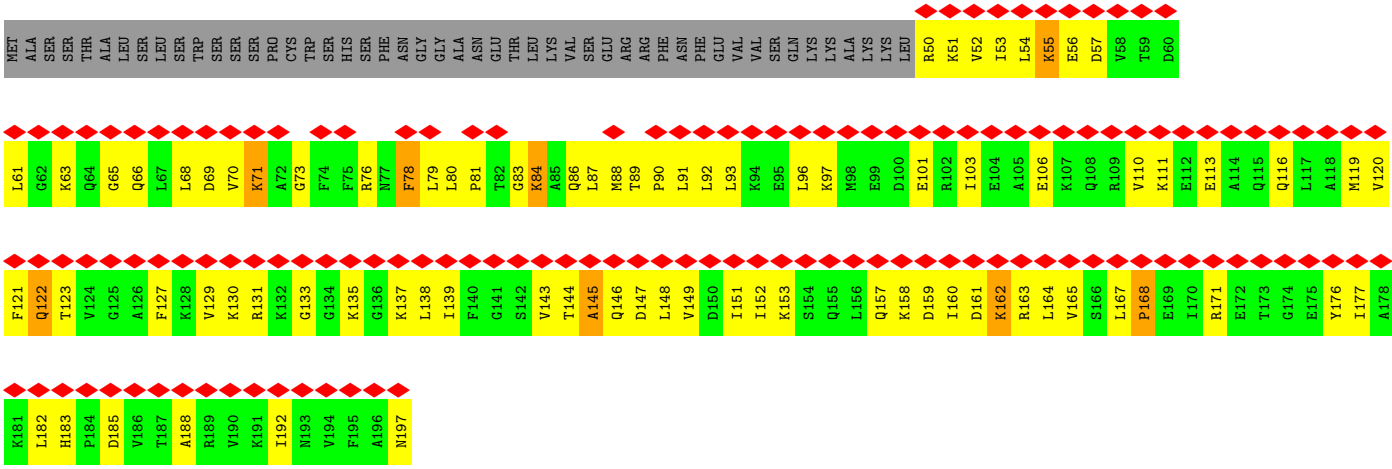
MET ALA SER SER LEU VAL SER SER PHE GLN PRO ARG SER ALA PHE LEU GLY ASP ARG ASN VAL PHE LYS VAL SER SER THR PRO PHE ALA GLN VAL GLY TYR SER SER LYS THR ILE GLU CYS K42 E43 S44 R45 I46 G47 K48 Q49 P50 I51 A52 V53 P54 S55 N56 V57 T58 L61



• Molecule 31: Ribosomal Protein L9

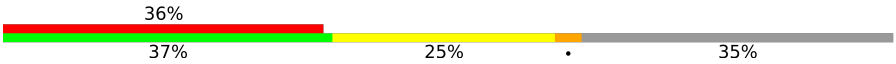
Chain BJ:

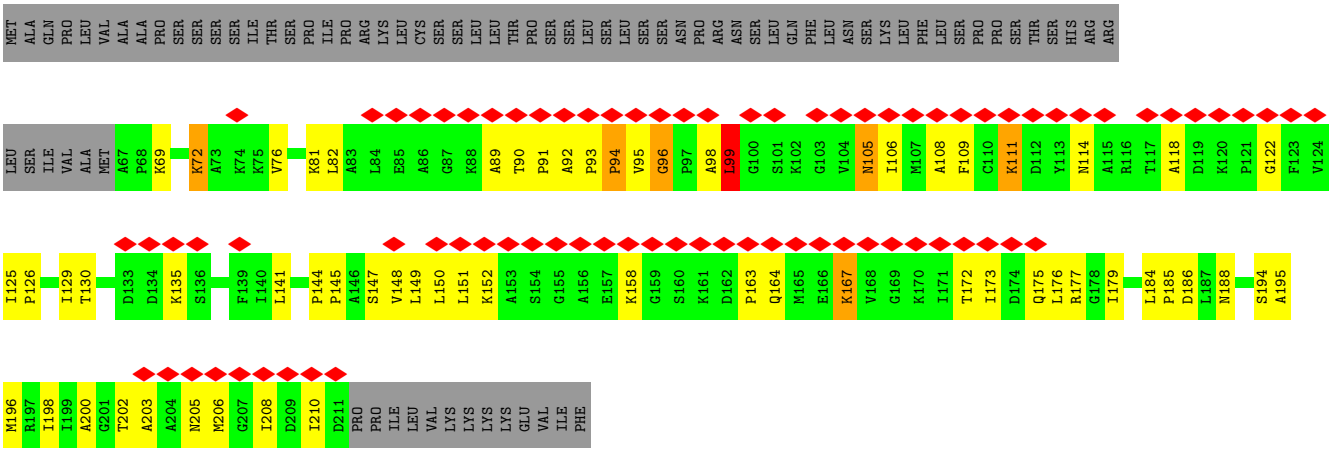




• Molecule 32: Ribosomal Protein L11

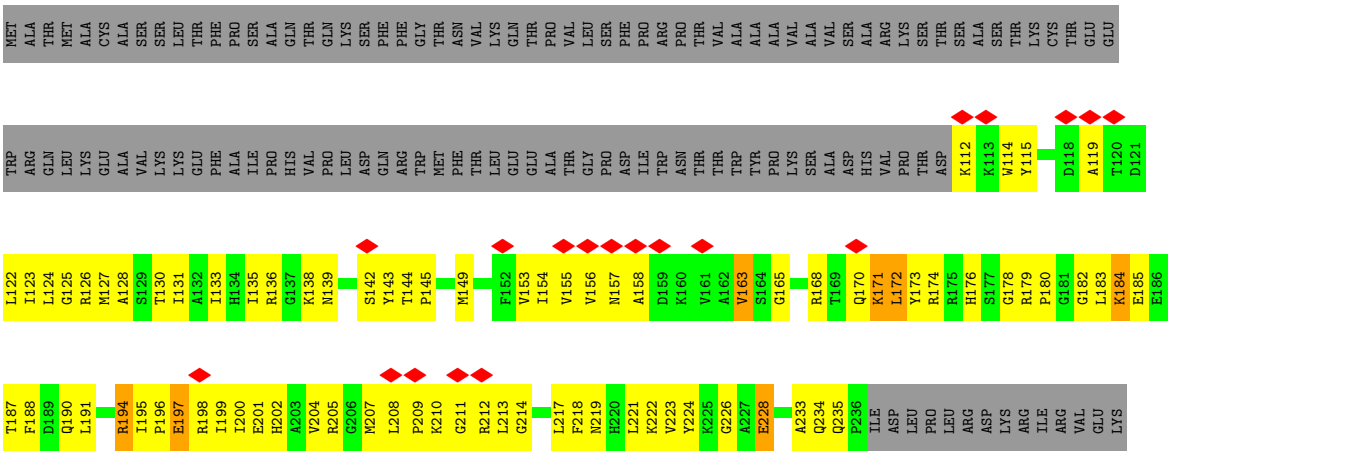
Chain BK:





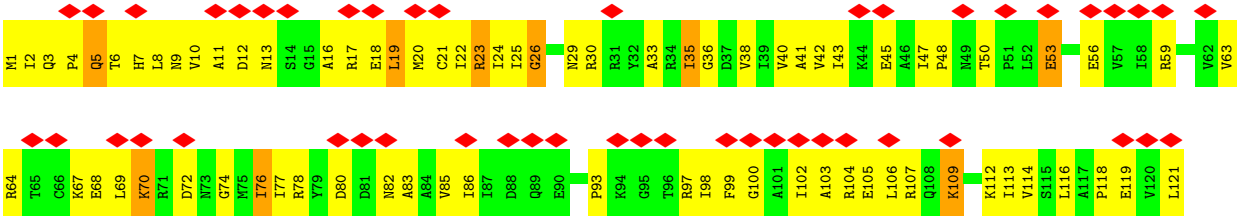
• Molecule 33: Ribosomal Protein L13

Chain BL:



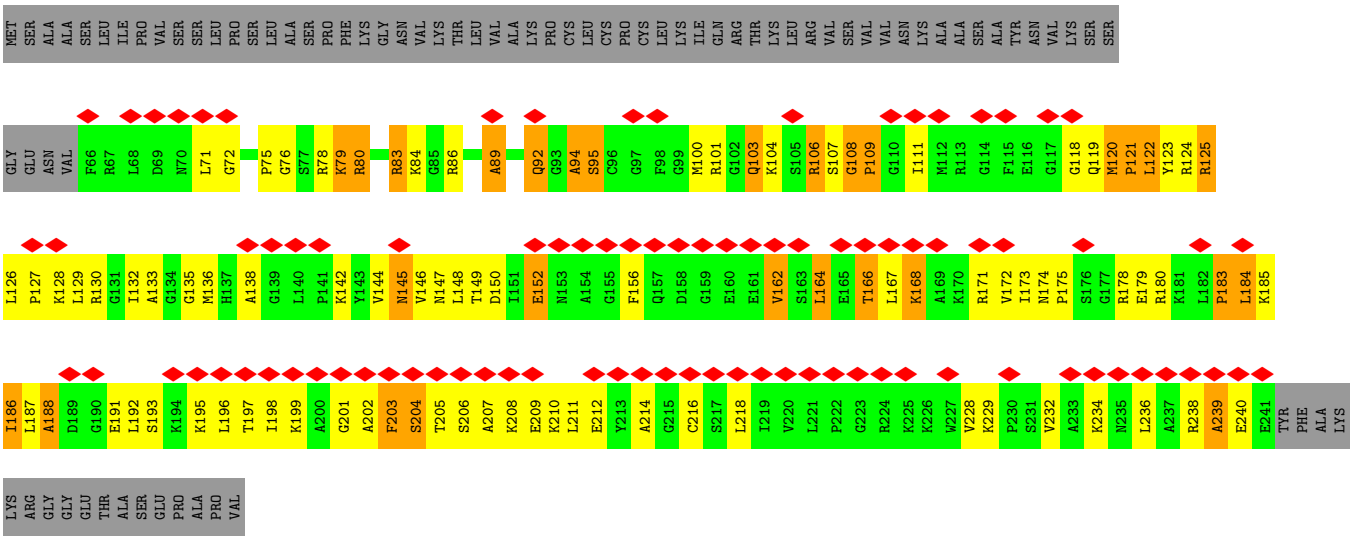
• Molecule 34: Ribosomal Protein L14

Chain BM:



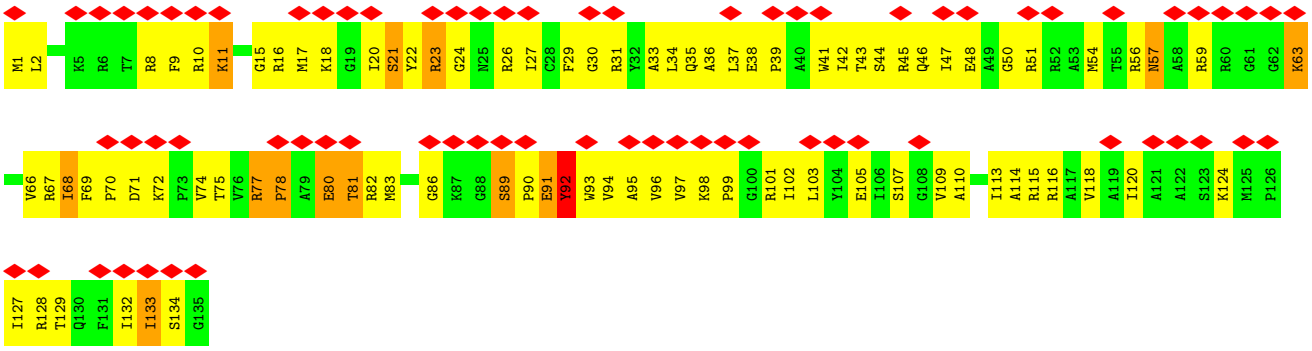
• Molecule 35: Ribosomal Protein L15

Chain BN:



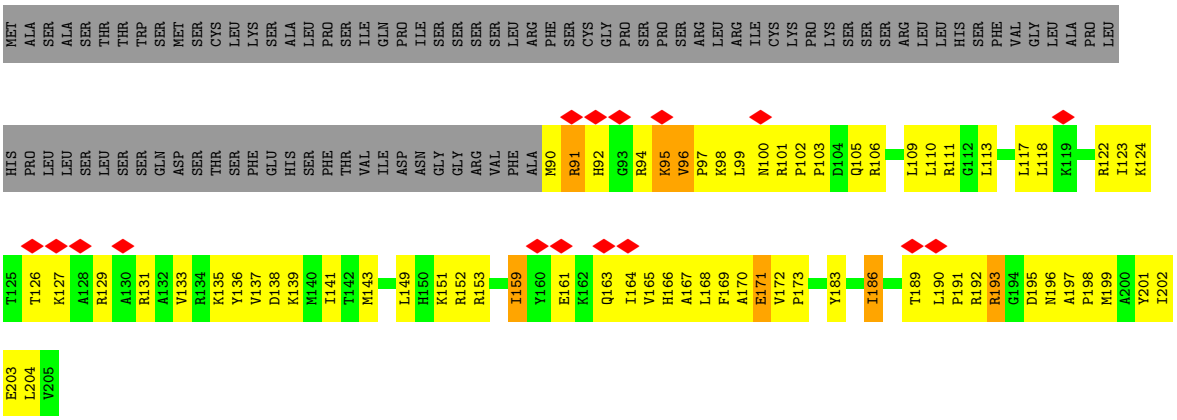
• Molecule 36: Ribosomal Protein L16

Chain BO:



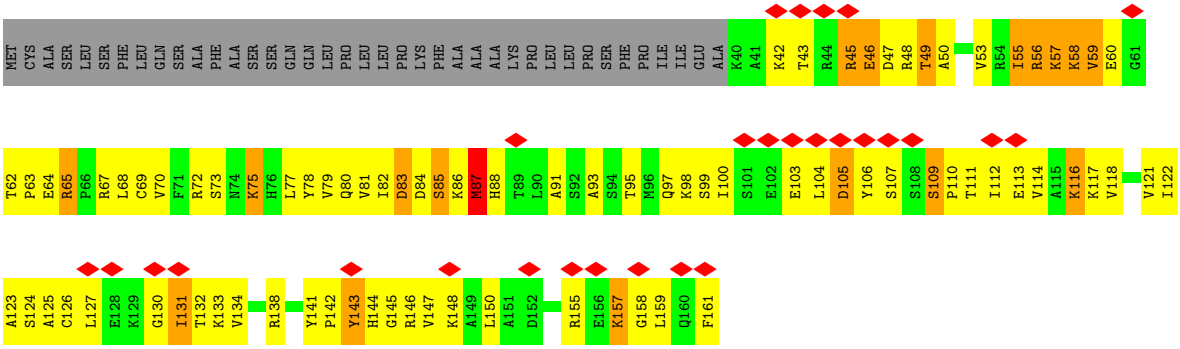
• Molecule 37: Ribosomal Protein L17

Chain BP:



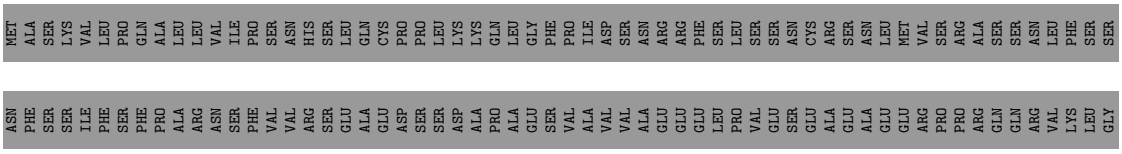
• Molecule 38: Ribosomal Protein L18

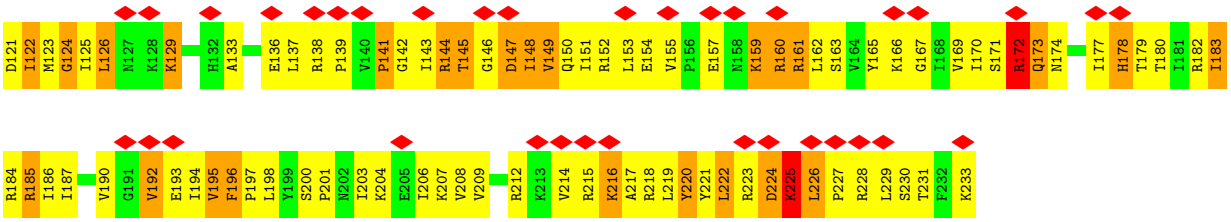
Chain BQ:



• Molecule 39: Ribosomal Protein L19

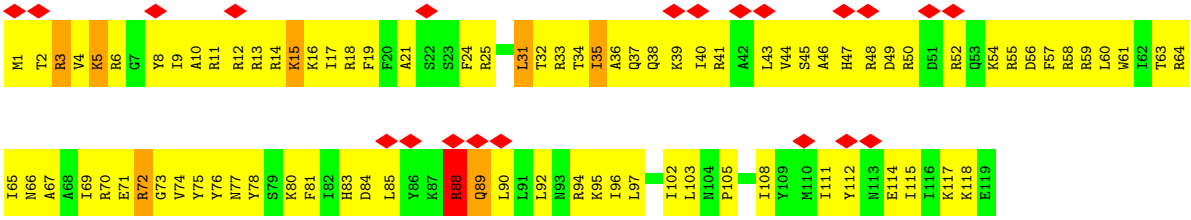
Chain BR:





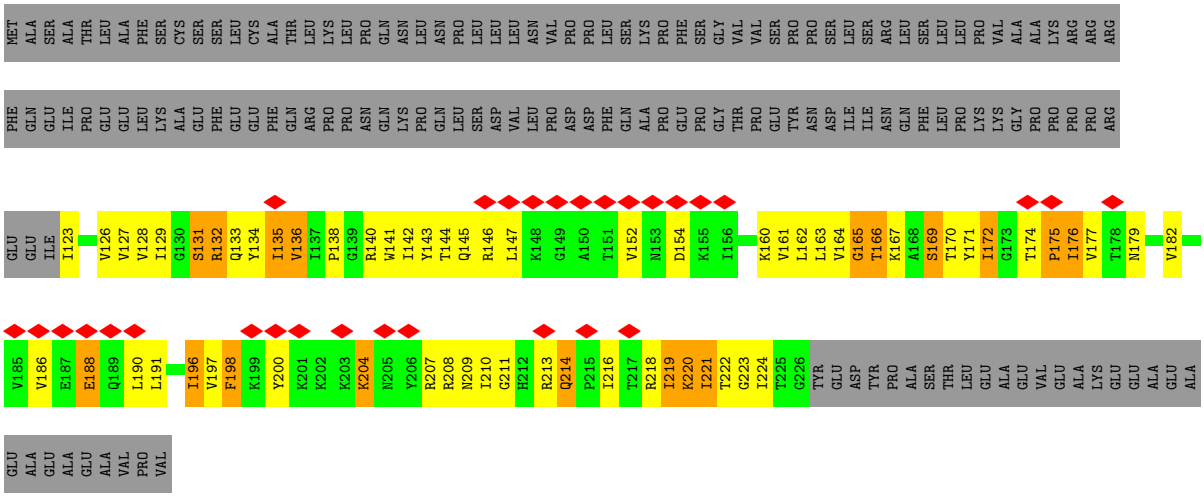
• Molecule 40: Ribosomal Protein L20

Chain BS:



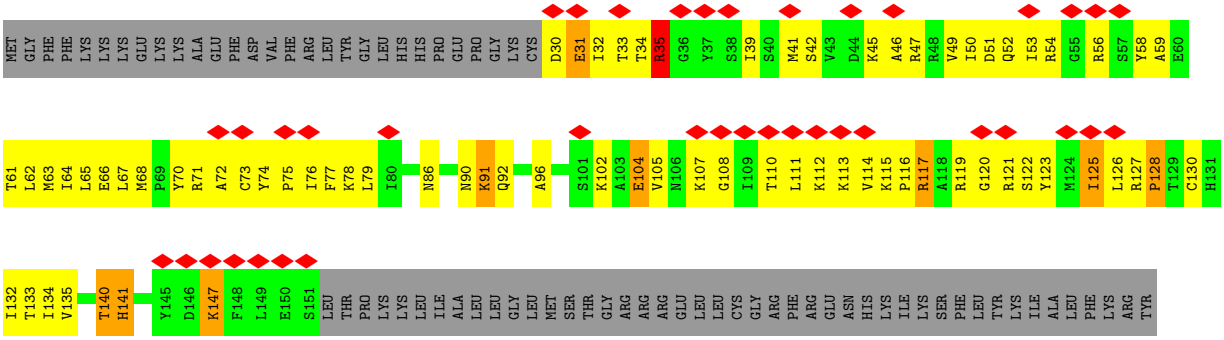
• Molecule 41: Ribosomal Protein L21

Chain BT:



• Molecule 42: Ribosomal Protein L22

Chain BU:



GLU VAL MET

- Molecule 43: Ribosomal Protein L23

Chain BV: 17% 19% 21% • 57%

MET ALA THR THR ALA PRO ASN LEU HIS SER LEU SER SER SER PHE ALA PHE SER ASN PRO SER SER ASN VAL SER ALA THR SER PHE THR PHE GLN ILE PRO ASN LYS LYS ALA GLN ILE SER CYS ILE SER SER LYS LYS LEU HIS THR GLN LYS SER PHE ASN PHE HIS ASP ALA VAL

THR PRO MET ASN LYS PRO SER PHE GLY ARG ASP LEU MET VAL ALA GLN ALA THR GLU ALA VAL ALA PRO THR THR GLU GLU ALA ALA THR SER GLN PRO LYS THR SER LYS LYS ALA LYS LYS LEU LYS TYR PRO ARG ARG ILE LEU D110 V111 Y112 Q113 I114 L115 Q116 S117 P118 I119 I120

T121 E122 A123 A124 I125 K126 N127 I128 A129 D130 E131 N132 S133 L134 L135 F136 T137 V138 D139 V140 R141 A142 D143 K144 K145 M146 I147 R148 E149 A150 I151 S152 N153 G156 V157 K158 V159 R160 K161 V162 N163 T164 L165 I166 R167 P168 D169 G170 T171 K172 K173 A174 Y175 I176 M177 K180 E181 Y182

N183 A184 S185 E186 L187 A188 K189 K190 I191 F194 PRO GLY GLY ASN

- Molecule 44: Ribosomal Protein L24

Chain BW: 21% 24% 23% 9% • 42%

MET ALA ALA MET VAL LEU GLN SER SER PHE THR SER LEU SER LEU SER SER ASN SER PHE LEU GLY GLN ARG LEU PHE PRO SER PRO THR THR LEU GLN VAL LYS THR GLU GLY HIS SER PRO CYS LEU ILE VAL MET ARG ILE LYS ARG TRP GLU ARG LYS ASP CYS LYS PRO ASN SER

LEU PRO K63 L64 V69 K70 V71 T74 V75 K76 V77 T78 S79 G80 G81 E82 K85 I86 G87 E88 I89 S90 K91 I92 H93 K94 H95 N96 S97 T98 V99 I100 I101 K102 D103 L104 N105 F106 K107 T108 K109 H110 V111 K112 S113 K114 E115 E116 G117 E118 Q119 G120 Q121 I122 I123 K124 I125

E126 A127 A128 I129 H130 S131 V134 M135 L136 I137 L138 K139 E140 Q141 E142 V143 A144 D145 R146 V147 G148 H149 K150 I151 L152 E153 D154 V155 R156 K157 V158 R159 Y160 L161 I162 K163 T164 G165 E166 I167 V168 D169 T170 P171 D172 ARG TRP LYS GLU ILE GLN ASN LYS LYS GLU SER GLU THR ALA

VAL ALA VAL ALA ALA

- Molecule 45: Ribosomal Protein L27

Chain BX: 18% 14% 24% 6% • 57%

MET ALA MET ALA THR SER MET SER LEU ASN LEU ILE GLY ALA PHE LYS GLY LEU SER LEU SER SER THR SER SER PHE LEU ARG GLY ASP LEU SER PHE SER PRO LYS THR SER PHE THR VAL THR LEU PRO LEU GLU ASN LEU GLN ALA PRO ILE PRO LEU THR ILE GLU SER A59 H60

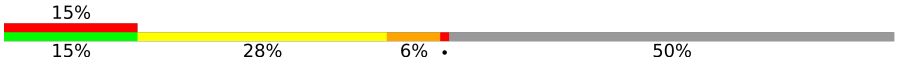
K61 K62 G63 A64 G65 S66 T67 K68 N69 G70 R71 D72 S73 P74 G75 Q76 R77 L78 G79 V80 K81 I82 Y83 G84 D85 Q86 V87 A88 K89 P90 G91 A92 I93 I94 V95 R96 Q97 R98 G99 T100 K101 F102 H103 A104 G105 K106 N107 V108 G109 I110 H114 T115 I116 F117 S118 L119 I120 D121 G122

L123 V124 K125 F126 E127 K128 F129 G130 P131 D132 R133 K134 K135 I136 S137 V138 Y139 P140 R141 E142 I143 V144 PRO GLU ASN PRO ASN SER TYR ARG ALA ARG LYS ARG GLU ASN PHE ARG LEU GLN ARG GLU LYS LYS LYS ALA ARG ARG GLU ASN TYR SER TYR THR LEU PRO THR PRO GLU LEU

VAL LEU ALA SER ALA SER VAL ASP ASP ALA GLU ALA ASN PRO GLU CYS

- Molecule 46: Ribosomal Protein L28

Chain BY:



MET ALA THR MET VAL ALA GLY ILE SER LEU ARG GLY PRO VAL MET SER SER HIS ARG THR PHE SER VAL THR LYS ARG ALA SER LEU PRO GLN SER LYS LEU SER SER GLU LEU SER PHE VAL THR SER GLN LEU SER GLY LEU LYS ILE SER SER THR HIS PHE ILE SER SER SER ALA

PRO LEU SER VAL PRO PHE LYS PRO SER LEU GLN PRO VAL ALA ALA ARG R76 I77 C78 P79 F80 T81 G82 K83 K84 S85 N86 R87 A88 N89 K90 V91 S92 H93 S94 N95 H96 K97 T98 L101 Q102 F103 V104 N105 L106 Q107 Y108 K109 R110 I111 W112 W113 E114 A115 G116 K117 R118 Y119 V120 K121

L122 R123 L124 S125 T126 K127 A128 I129 K130 T131 I132 E133 K134 N135 G136 L137 D138 A139 V140 A141 K142 K143 I146 D147 L148 S149 K150 K151

- Molecule 47: Ribosomal Protein L29

Chain BZ:

MET LEU SER LEU SER ILE ALA THR PRO GLY THR ALA ALA ILE PHE ARG ARG GLY THR ALA SER ALA THR SER THR SER SER SER PHE HIS GLY VAL ARG ILE GLN HIS GLN VAL SER ALA ARG VAL PRO ALA ALA ALA THR ILE SER SER SER SER PRO LYS PRO SER VAL VAL MET MET

SER K62 R63 L67 K68 E69 I70 R71 S72 K73 T74 T75 E76 Q77 L78 Q79 E80 E81 V82 V83 D84 L85 K86 L89 S97 A98 R99 F102 K103 S104 S105 R109 K112 Q113 V114 A115 R116 M117 L118 T119 V120 K121 R122 E123 R124 E125 I126 LYS GLU GLY ILE LYS LYS ARG

LEU SER ARG LYS LEU ASP ARG GLN TRP LYS LYS SER ILE VAL PRO ARG PRO PRO PRO SER LEU LYS LYS LEU GLN GLU GLU GLU ALA ALA GLU GLU GLU ALA ALA GLU ALA ALA LYS SER ALA

- Molecule 48: Ribosomal Protein L31

Chain B1:

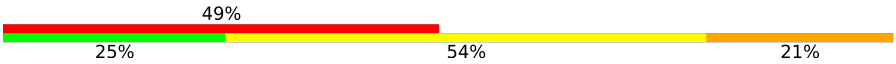
MET ALA VAL SER LEU PRO ASN SER PHE LEU GLN ILE SER PRO CYS VAL PRO SER LEU GLN LEU ARG LYS PRO VAL MET ALA ALA VAL LYS GLY GLY LYS GLN SER VAL ARG ARG SER SER ASN THR VAL VAL GLN ILE THR CYS ARG K50 K51 E52 L53 H54 P55 E56 F57 H58 E59 D60

A61 K62 V63 Y64 C65 N66 L69 V70 M71 T72 T73 T76 K77 K78 V81 V82 D83 V84 W85 S86 G87 N88 H89 P90 F91 Y92 L93 G94 N95 R96 S97 A98 L99 M100 V101 D102 A103 D104 Q105 V106 E107 K108 F109 R110 K111 R112 F113 A114 G115 L116 S117 E118 I119 M120 E121 ILE PRO

VAL LEU LYS GLY GLU ILE ILE MET PRO THR LYS LYS SER LYS GLY PRO LYS GLY LYS LYS LYS

- Molecule 49: Ribosomal Protein L32

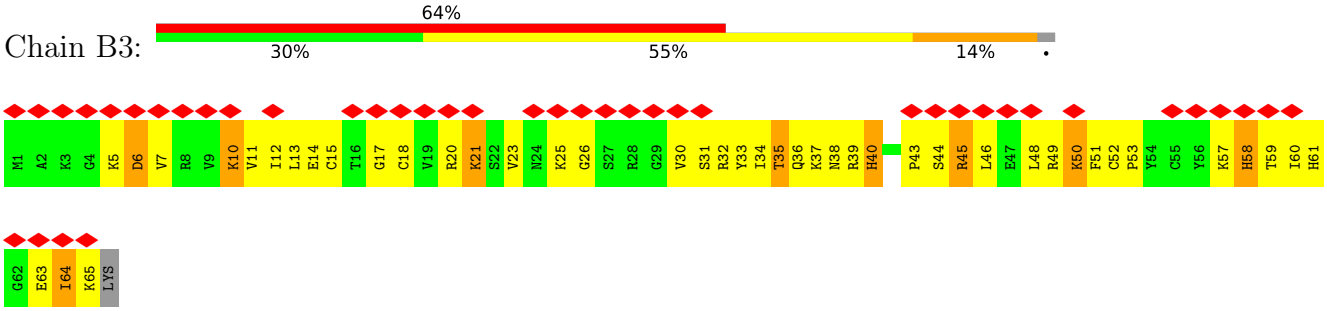
Chain B2:



M1 A2 K5 K6 R7 T8 S9 I10 Y11 K12 K13 R14 I15 R16 K17 N18 I19 W20 K21 K22 K23 G24 Y25 W26 A27 A28 L29 K30 A31 F32 S33 L34 A35 K36 S37 L38 S39 T40 G41 N42 S43 K44 S45 F46 F47 V48 R49 K50 I51 S52 N53 Q54 T55 L56 E57

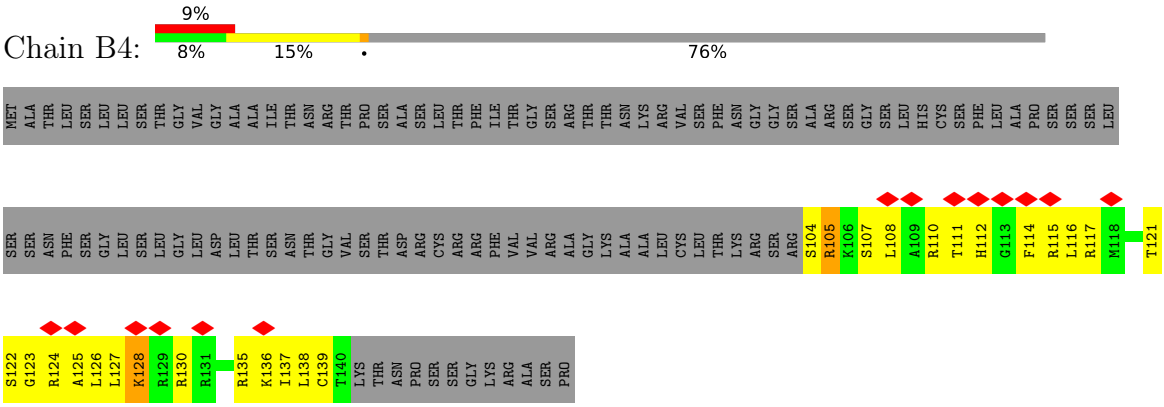
- Molecule 50: Ribosomal Protein L33

Chain B3:



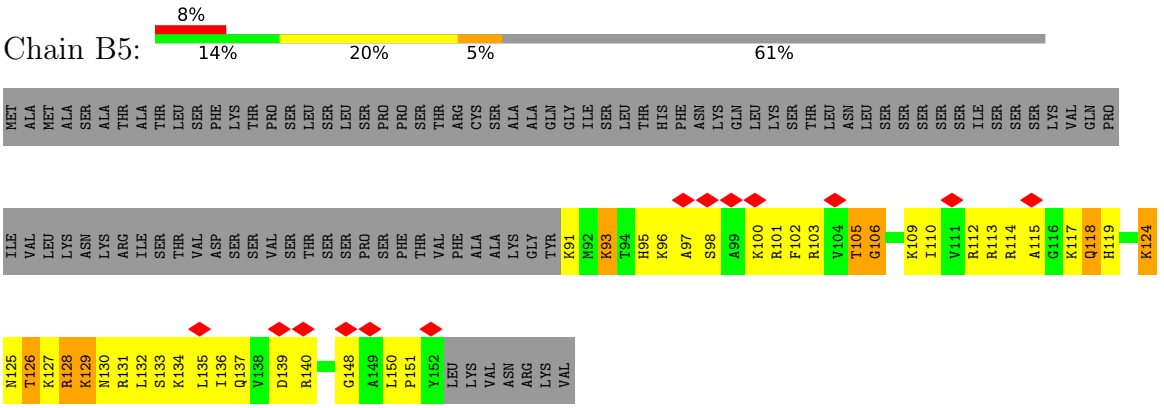
- Molecule 51: Ribosomal Protein L34

Chain B4:



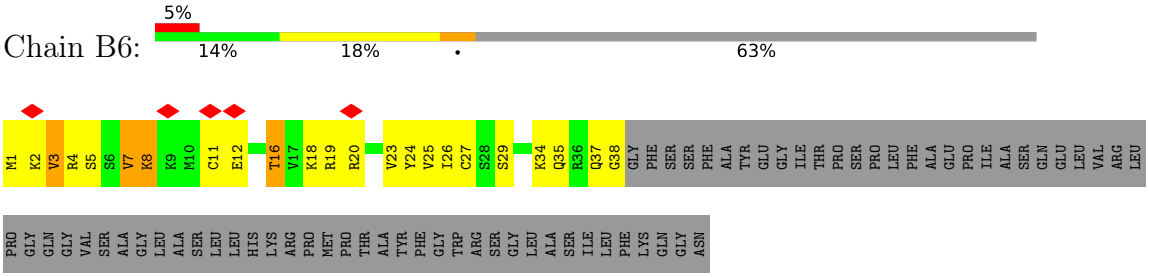
- Molecule 52: Ribosomal Protein L35

Chain B5:



- Molecule 53: Ribosomal Protein L36

Chain B6:



4 Experimental information (i)

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 ($e^-/Å^2$)	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 (Å)	358.8, 358.8, 358.8	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	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(^{o})	Ideal(^{o})
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

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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.

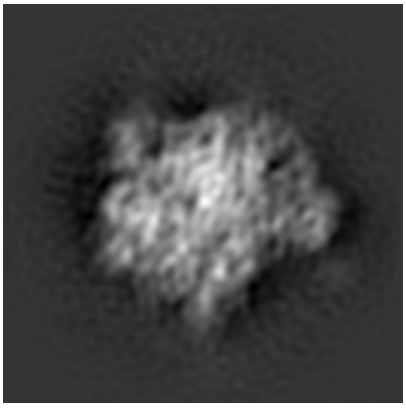
6 Map visualisation (i)

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.

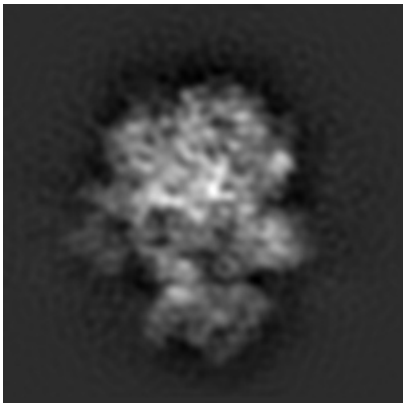
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

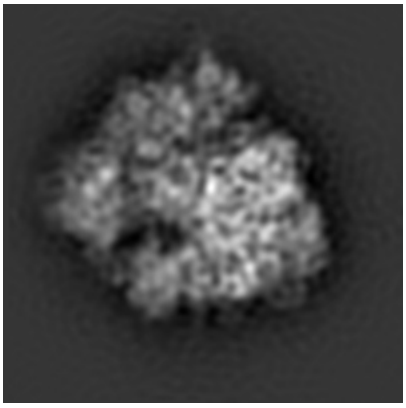
6.1.1 Primary map



X



Y

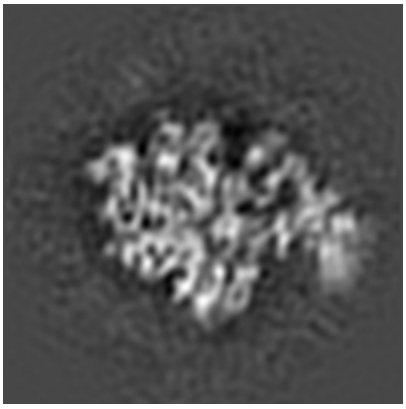


Z

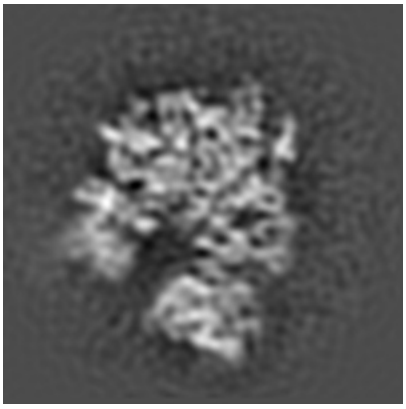
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

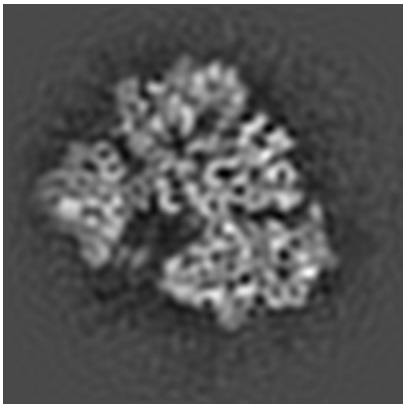
6.2.1 Primary map



X Index: 65



Y Index: 65

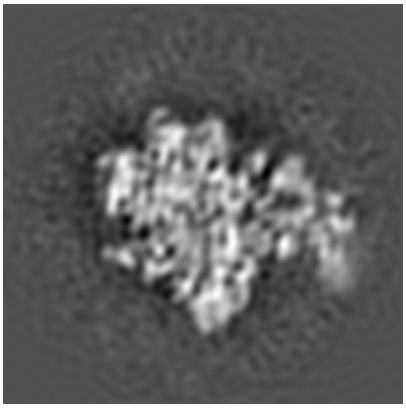


Z Index: 65

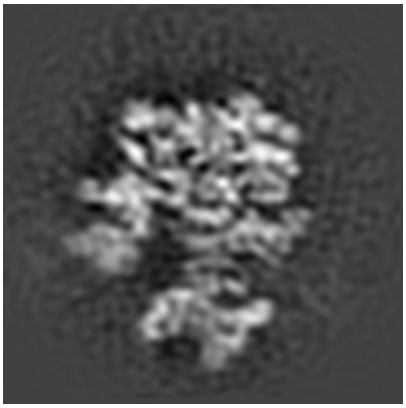
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

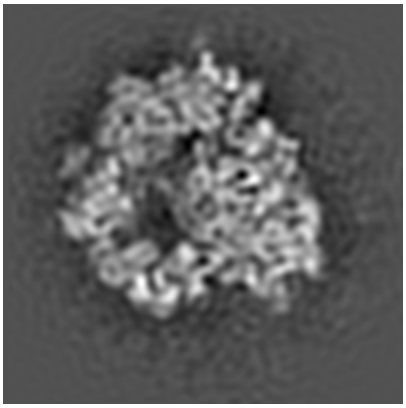
6.3.1 Primary map



X Index: 67



Y Index: 69

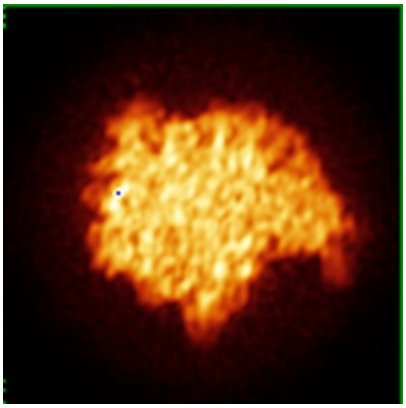


Z Index: 59

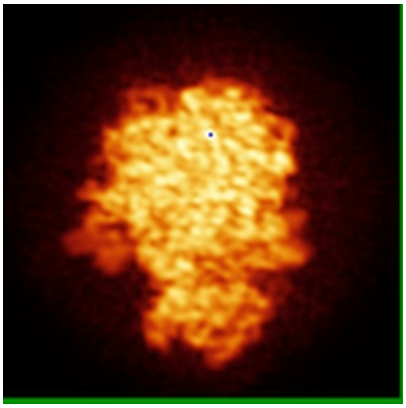
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

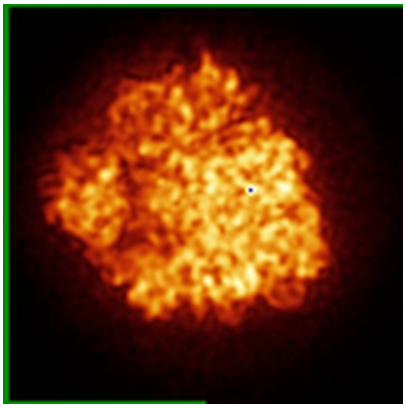
6.4.1 Primary map



X



Y

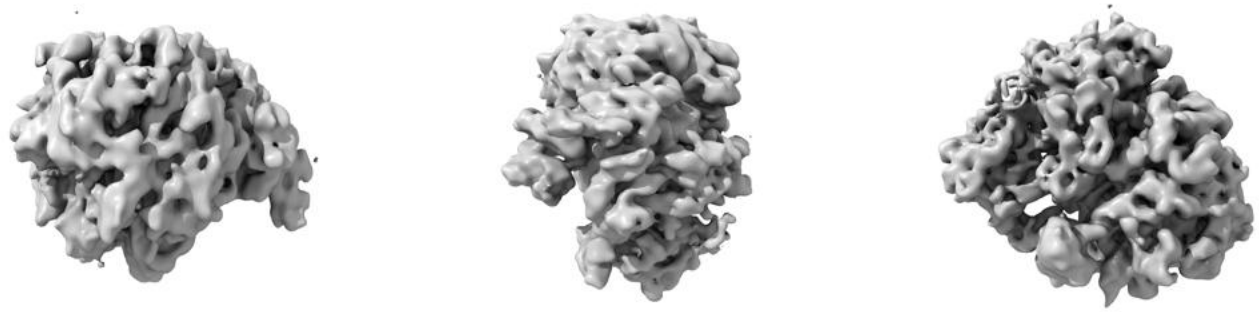


Z

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.

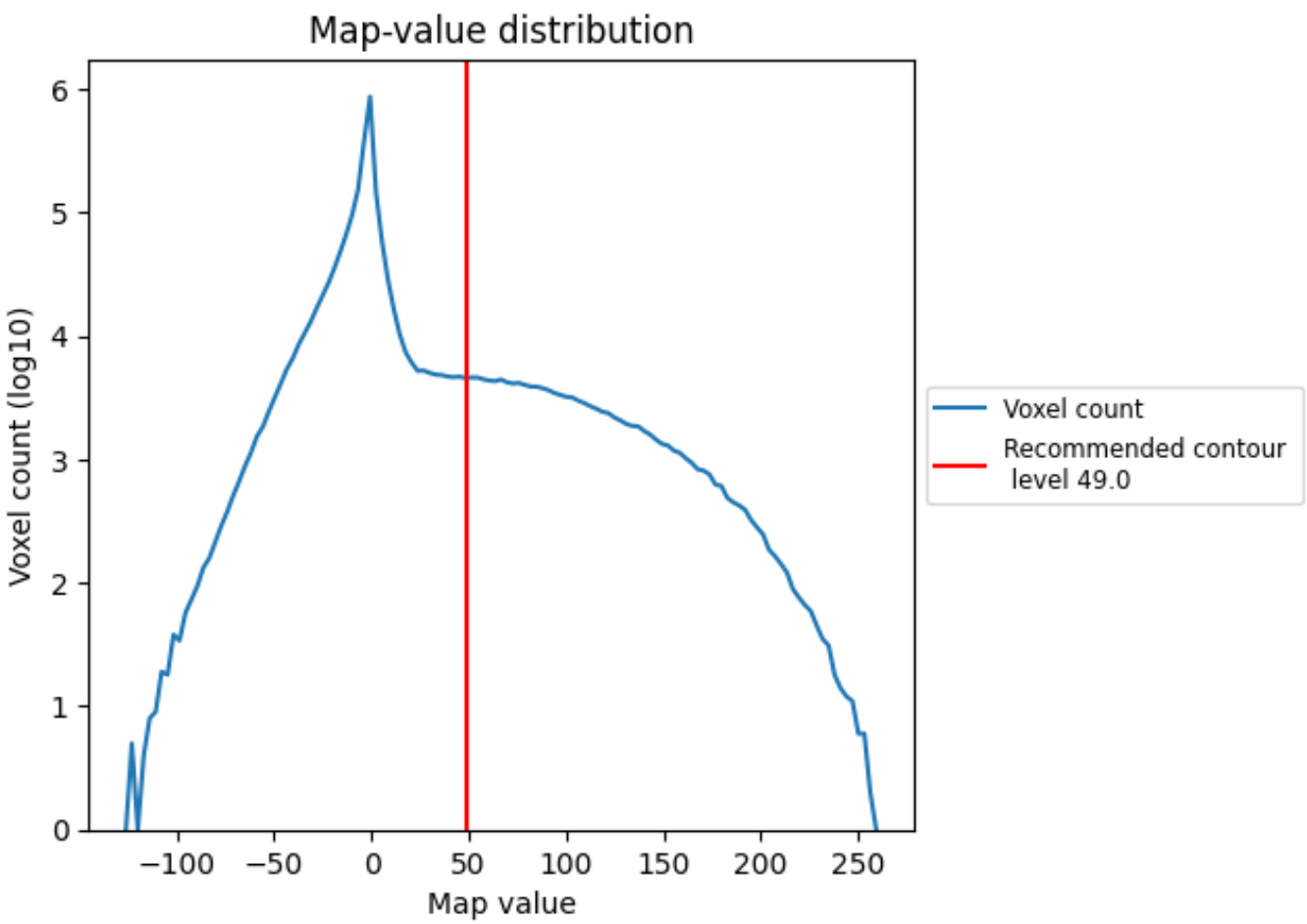
6.6 Mask visualisation (i)

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

7 Map analysis (i)

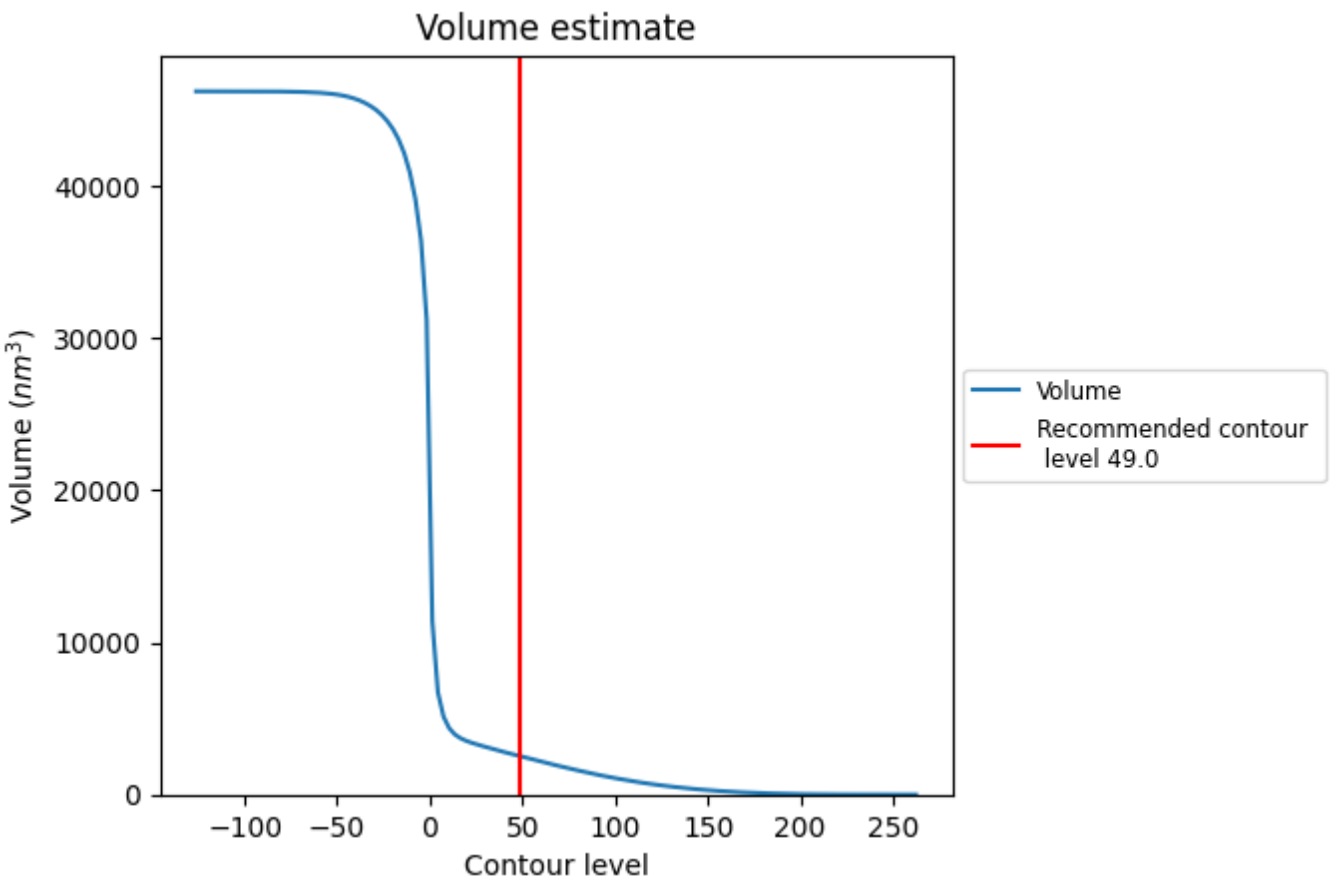
This section contains the results of statistical analysis of the map.

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.

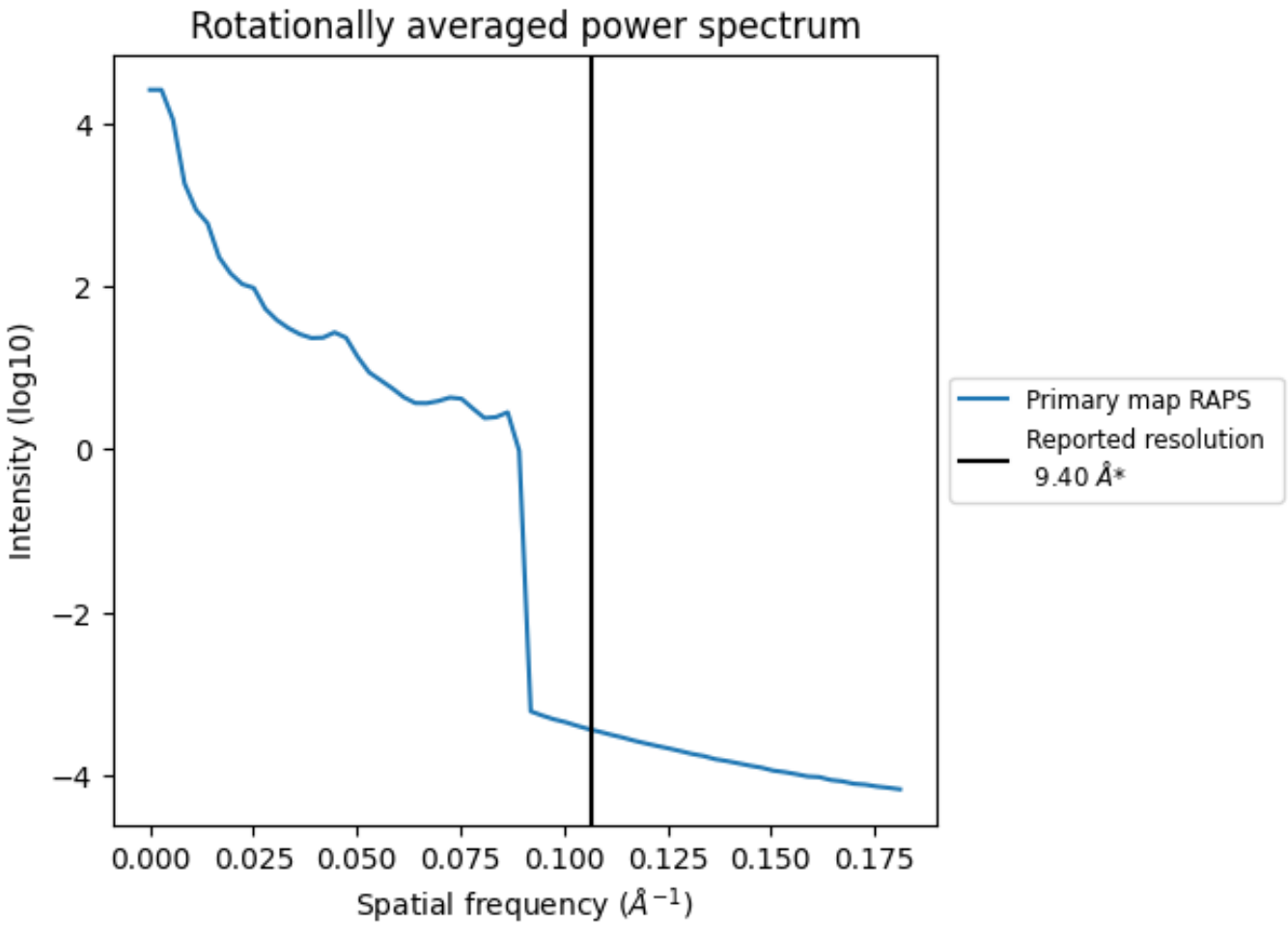
7.2 Volume estimate (i)



The volume at the recommended contour level is 2510 nm^3; 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 Å^{-1}

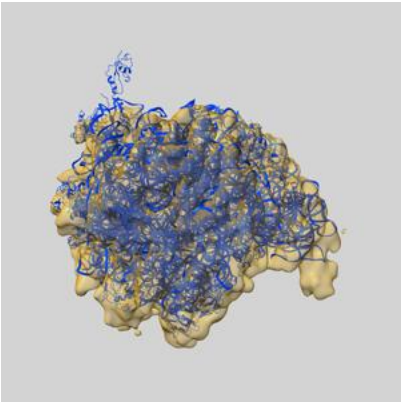
8 Fourier-Shell correlation (i)

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

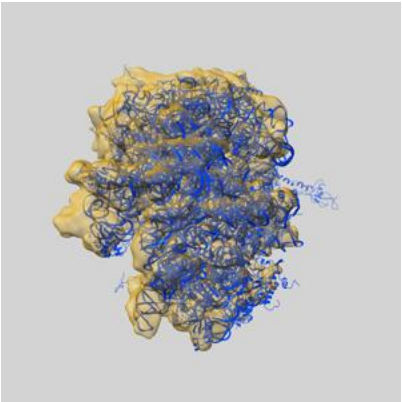
9 Map-model fit (i)

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.

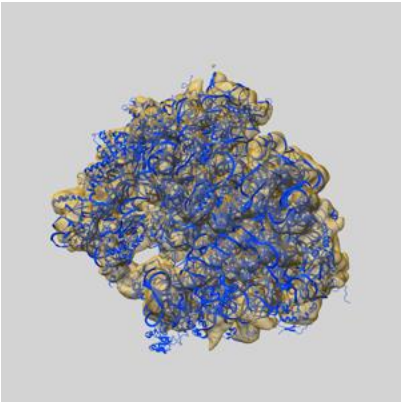
9.1 Map-model overlay (i)



X



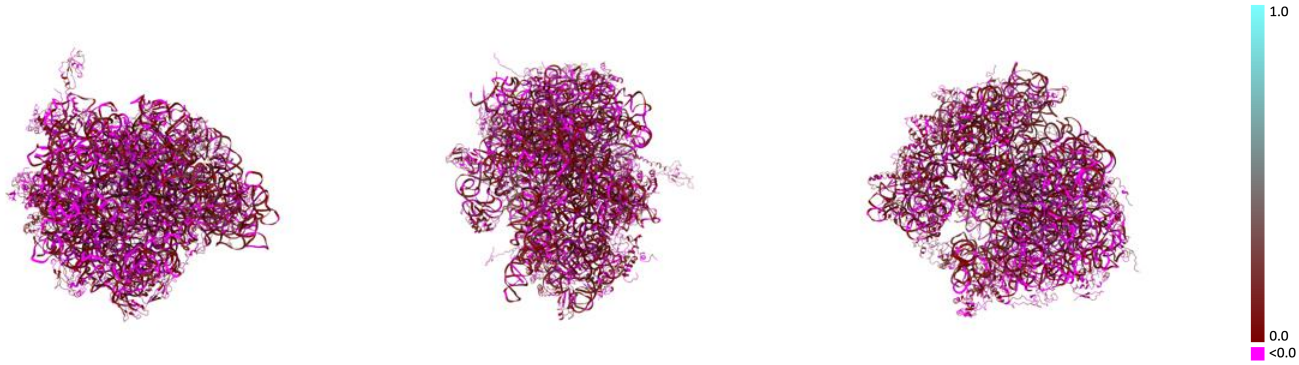
Y



Z

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.

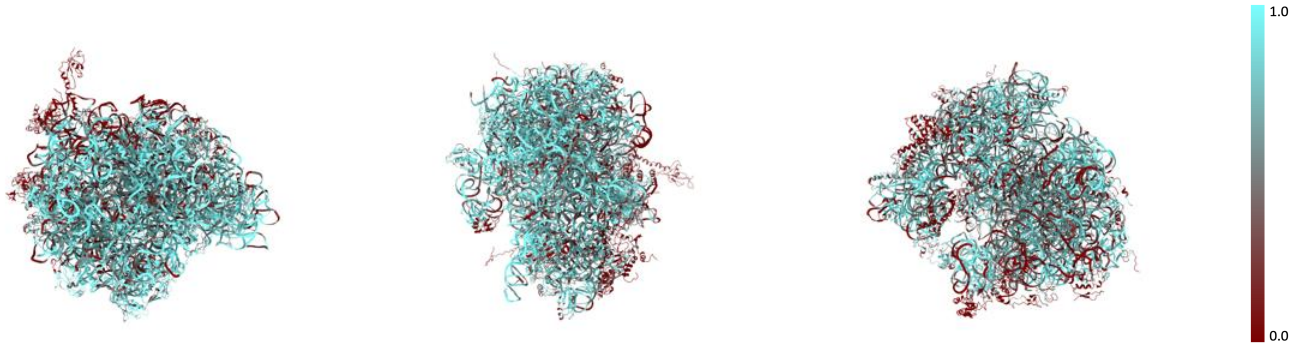
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

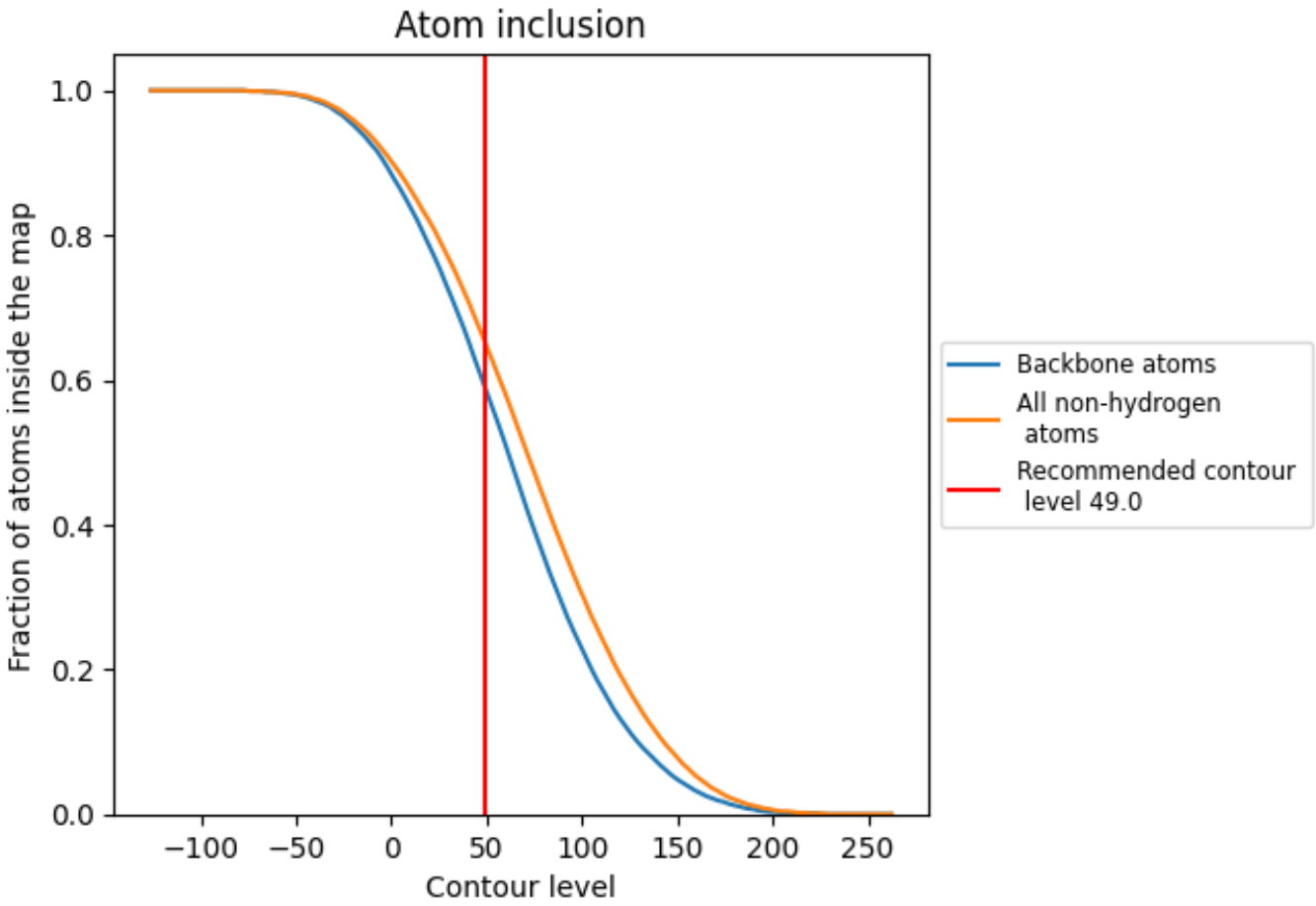
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (i)

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