



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 06:47 PM EST

PDB ID : 4V6U  
EMDB ID : EMD-2009  
Title : Promiscuous behavior of proteins in archaeal ribosomes revealed by cryo-EM: implications for evolution of eukaryotic ribosomes  
Authors : Armache, J.-P.; Anger, A.M.; Marquez, V.; Frankenberg, S.; Froehlich, T.; Villa, E.; Berninghausen, O.; Thomm, M.; Arnold, G.J.; Beckmann, R.; Wilson, D.N.  
Deposited on : 2012-08-09  
Resolution : 6.60 Å(reported)

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:

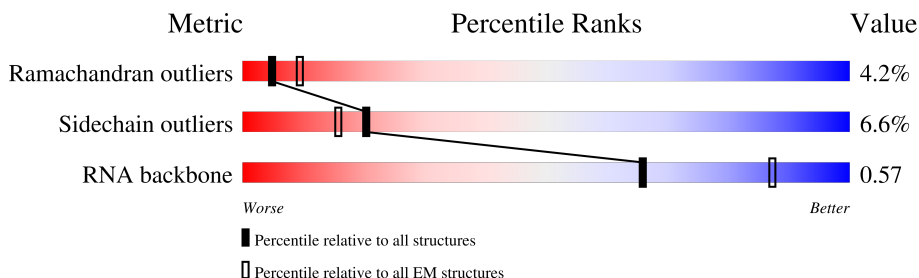
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

# 1 Overall quality at a glance

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

The reported resolution of this entry is 6.60 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)
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	AQ	158	
2	AK	135	
3	AI	130	
4	AG	125	
5	AW	63	
6	AC	210	
7	AB	202	
8	AR	113	

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Mol	Chain	Length	Quality of chain
9	A9	57	
10	AD	180	
11	A1	77	
12	AN	147	
13	AX	71	
14	AM	137	
15	AE	243	
16	AJ	127	
17	AO	148	
18	AF	236	
19	AS	67	
20	A3	123	
20	B4	123	
20	BG	123	
21	A2	1495	
22	AY	50	
23	AT	132	
24	AA	198	
25	AH	215	
26	AP	56	
27	A0	76	
28	AV	99	
28	B6	99	
29	AL	102	
30	AU	150	

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Mol	Chain	Length	Quality of chain
31	BY	155	
32	BO	203	
33	BC	365	
34	B5	83	
34	BK	83	
35	BL	147	
36	Bf	51	
37	BU	121	
38	Bb	130	
39	Be	62	
40	BE	186	
41	Ba	95	
42	BT	86	
43	Bk	339	
44	BW	72	
45	Bi	83	
46	BA	216	
47	BI	142	
48	BR	97	
49	BQ	150	
50	BV	66	
51	Bj	94	
52	BB	239	
53	BD	255	
54	BF	184	

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Mol	Chain	Length	Quality of chain
55	Bh	24	
56	BH	164	
57	BZ	99	
58	BP	120	
59	BM	194	
60	BS	155	
61	Bd	89	
62	BN	181	
63	Bg	51	
64	Bc	87	
65	BJ	141	
66	Bl	77	
67	B1	3049	
68	B3	126	

## 2 Entry composition

There are 68 unique types of molecules in this entry. The entry contains 173979 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 30S ribosomal protein S15P/S13e.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AQ	158	Total	C	N	O	S	0	0
			1310	834	250	221	5		

- Molecule 2 is a protein called 30S ribosomal protein S9P.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AK	135	Total	C	N	O	S	0	0
			1072	671	205	190	6		

- Molecule 3 is a protein called 30S ribosomal protein S8P.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AI	129	Total	C	N	O	S	0	0
			1028	668	178	180	2		

- Molecule 4 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AG	125	Total	C	N	O	S	0	0
			984	623	180	179	2		

- Molecule 5 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AW	63	Total	C	N	O	S	0	0
			478	306	85	81	6		

- Molecule 6 is a protein called 30S ribosomal protein S3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	186	Total	C	N	O	S	0	0
			1459	933	271	251	4		

- Molecule 7 is a protein called 30S ribosomal protein S2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	202	Total	C	N	O	S	0	0
			1623	1046	282	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S17P.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AR	113	Total	C	N	O	S	0	0
			934	592	177	160	5		

- Molecule 9 is a protein called unknown 30S ribosomal protein SX.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	A9	57	Total	C	N	O	0	0
			286	171	57	58		

- Molecule 10 is a protein called 30S ribosomal protein S4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AD	172	Total	C	N	O	S	0	0
			1434	902	273	255	4		

- Molecule 11 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A1	77	Total	C	N	O	P	0	0
			1649	734	303	535	77		

- Molecule 12 is a protein called 30S ribosomal protein S12P.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AN	145	Total	C	N	O	S	0	0
			1140	722	222	193	3		

- Molecule 13 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AX	71	Total	C	N	O	S	0	0
			568	345	115	107	1		

- Molecule 14 is a protein called 30S ribosomal protein S11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AM	133	Total	C	N	O	S	0	0
			1004	623	200	179	2		

- Molecule 15 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AE	241	Total	C	N	O	S	0	0
			1976	1277	355	339	5		

- Molecule 16 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AJ	127	Total	C	N	O	S	0	0
			1004	622	207	174	1		

- Molecule 17 is a protein called 30S ribosomal protein S13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	148	Total	C	N	O	S	0	0
			1189	746	237	200	6		

- Molecule 18 is a protein called 30S ribosomal protein S5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AF	217	Total	C	N	O	S	0	0
			1716	1084	319	305	8		

- Molecule 19 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	67	Total	C	N	O	S	0	0
			556	353	105	95	3		

- Molecule 20 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	A3	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
20	BG	123	Total	C	N	O	S	0	0
			939	599	155	181	4		
20	B4	123	Total	C	N	O	S	0	0
			939	599	155	181	4		



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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A2	1495	Total	C	N	O	P	0	0
			32135	14297	5954	10389	1495		

- Molecule 22 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AY	50	Total	C	N	O	S	0	0
			409	262	75	66	6		

- Molecule 23 is a protein called 30S ribosomal protein S19P.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AT	111	Total	C	N	O	S	0	0
			923	594	173	150	6		

- Molecule 24 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AA	190	Total	C	N	O	S	0	0
			1559	1007	273	274	5		

- Molecule 25 is a protein called 30S ribosomal protein S7P.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AH	215	Total	C	N	O	S	0	0
			1736	1100	326	302	8		

- Molecule 26 is a protein called 30S ribosomal protein S14P type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AP	56	Total	C	N	O	S	0	0
			462	292	95	69	6		

- Molecule 27 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A0	76	Total	C	N	O	P	0	0
			1625	722	291	536	76		

- Molecule 28 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AV	99	Total	C	N	O	S	0	0
			823	532	134	154	3		
28	B6	94	Total	C	N	O	S	0	0
			782	508	127	144	3		

- Molecule 29 is a protein called 30S ribosomal protein S10P.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AL	102	Total	C	N	O	S	0	0
			822	507	159	152	4		

- Molecule 30 is a protein called SSU ribosomal protein S19E.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AU	144	Total	C	N	O	S	0	0
			1175	758	212	204	1		

- Molecule 31 is a protein called 50S ribosomal protein L30P.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BY	155	Total	C	N	O	S	0	0
			1243	788	235	213	7		

- Molecule 32 is a protein called 50S ribosomal protein L18P.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BO	197	Total	C	N	O	S	0	0
			1597	1021	299	274	3		

- Molecule 33 is a protein called 50S ribosomal protein L3P.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BC	365	Total	C	N	O	S	0	0
			2912	1870	527	500	15		

- Molecule 34 is a protein called 50S ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	81	Total	C	N	O	S	0	0
			614	386	119	108	1		
34	BK	81	Total	C	N	O	S	0	0
			614	386	119	108	1		

- Molecule 35 is a protein called 50S ribosomal protein L15P.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	147	Total	C	N	O	S	0	0
			1154	727	227	195	5		

- Molecule 36 is a protein called 50S ribosomal protein L39e.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bf	51	Total	C	N	O	S	0	0
			445	284	98	62	1		

- Molecule 37 is a protein called 50S ribosomal protein L24P.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BU	121	Total	C	N	O	S	0	0
			1008	637	195	172	4		

- Molecule 38 is a protein called 50S ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bb	127	Total	C	N	O	S	0	0
			1074	689	217	167	1		

- Molecule 39 is a protein called 50S ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Be	62	Total	C	N	O	S	0	0
			506	312	111	78	5		

- Molecule 40 is a protein called 50S ribosomal protein L5P.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BE	186	Total	C	N	O	S	0	0
			1489	937	278	265	9		

- Molecule 41 is a protein called 50S ribosomal protein L31e.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	Ba	90	Total	C	N	O	0	0
			746	483	138	125		

- Molecule 42 is a protein called 50S ribosomal protein L23P.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BT	84	Total	C	N	O		
			680	440	118	122	0	0

- Molecule 43 is a protein called Acidic ribosomal protein P0 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Bk	212	Total	C	N	O	S		
			1632	1051	272	303	6	0	0

- Molecule 44 is a protein called 50S ribosomal protein L29P.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BW	72	Total	C	N	O	S		
			594	369	115	106	4	0	0

- Molecule 45 is a protein called 50S ribosomal protein L37Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Bi	78	Total	C	N	O	S		
			590	368	122	95	5	0	0

- Molecule 46 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BA	216	Total	C	N	O	S		
			1677	1068	300	304	5	0	0

- Molecule 47 is a protein called 50S ribosomal protein L13P.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BI	142	Total	C	N	O	S		
			1150	737	215	195	3	0	0

- Molecule 48 is a protein called 50S ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BR	95	Total	C	N	O	S		
			787	501	160	125	1	0	0

- Molecule 49 is a protein called 50S ribosomal protein L19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BQ	150	Total	C	N	O	S	0	0
			1256	794	255	202	5		

- Molecule 50 is a protein called 50S ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BV	66	Total	C	N	O	S	0	0
			555	351	106	91	7		

- Molecule 51 is a protein called 50S ribosomal protein L44E.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Bj	94	Total	C	N	O	S	0	0
			787	499	161	122	5		

- Molecule 52 is a protein called 50S ribosomal protein L2P.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	239	Total	C	N	O	S	0	0
			1838	1169	347	317	5		

- Molecule 53 is a protein called 50S ribosomal protein L4P.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BD	255	Total	C	N	O	S	0	0
			2026	1288	391	342	5		

- Molecule 54 is a protein called 50S ribosomal protein L6P.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BF	184	Total	C	N	O	S	0	0
			1476	956	252	266	2		

- Molecule 55 is a protein called 50S ribosomal protein L41e.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Bh	24	Total	C	N	O	S	0	0
			230	147	54	28	1		

- Molecule 56 is a protein called 50S ribosomal protein L11P.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BH	134	Total	C	N	O	S	0	0
			988	635	164	183	6		

- Molecule 57 is a protein called 50S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BZ	99	Total	C	N	O	S	0	0
			754	489	121	142	2		

- Molecule 58 is a protein called 50S ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BP	120	Total	C	N	O	S	0	0
			966	606	186	171	3		

- Molecule 59 is a protein called 50S ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BM	194	Total	C	N	O	S	0	0
			1595	1020	316	253	6		

- Molecule 60 is a protein called 50S ribosomal protein L22P.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BS	150	Total	C	N	O	S	0	0
			1200	764	230	202	4		

- Molecule 61 is a protein called 50S ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Bd	89	Total	C	N	O	S	0	0
			740	463	158	108	11		

- Molecule 62 is a protein called 50S ribosomal protein L10e.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BN	168	Total	C	N	O	S	0	0
			1378	872	268	232	6		

- Molecule 63 is a protein called 50S ribosomal protein L40e.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bg	45	Total	C	N	O	S	0	0
			371	236	76	55	4		

- Molecule 64 is a protein called 50S ribosomal protein L35Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Bc	87	Total	C	N	O	S	0	0
			685	434	132	117	2		

- Molecule 65 is a protein called 50S ribosomal protein L14P.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BJ	132	Total	C	N	O	S	0	0
			1014	631	204	176	3		

- Molecule 66 is a protein called 50S ribosomal protein LX.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bl	77	Total	C	N	O	S	0	0
			659	425	118	115	1		

- Molecule 67 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	B1	3049	Total	C	N	O	P	0	0
			65577	29172	12191	21165	3049		


- Molecule 68 is a RNA chain called 5S rRNA.

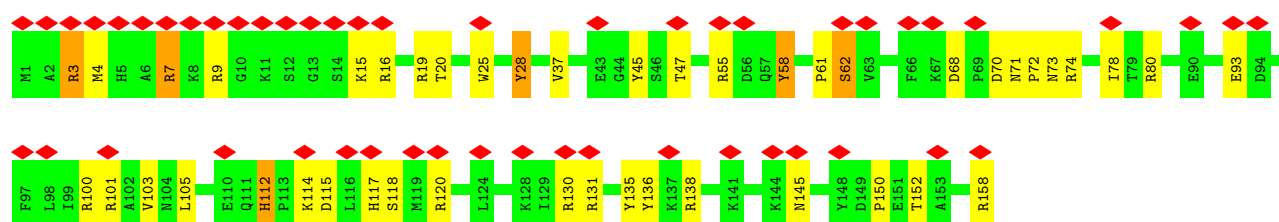
Mol	Chain	Residues	Atoms					AltConf	Trace
68	B3	126	Total	C	N	O	P	0	0
			2694	1199	492	877	126		

### 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.

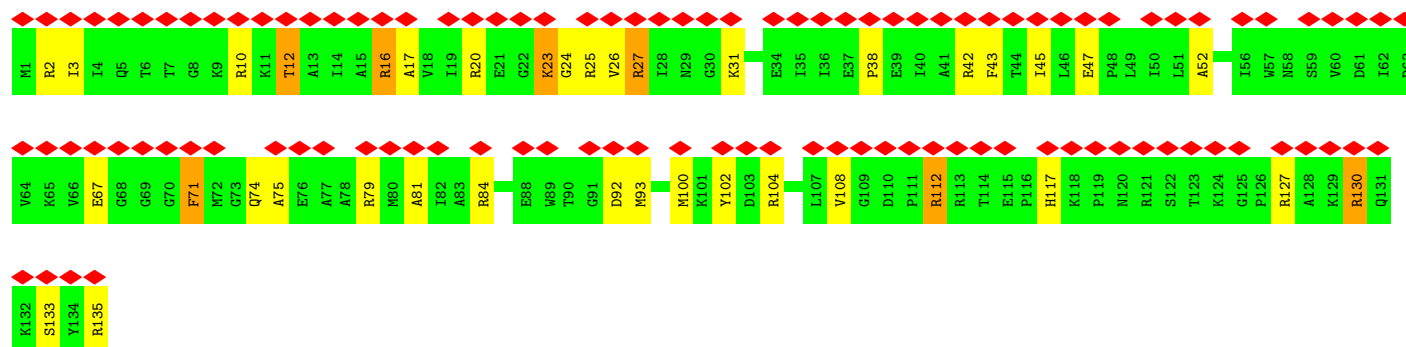
- Molecule 1: 30S ribosomal protein S15P/S13e

Chain AQ: 




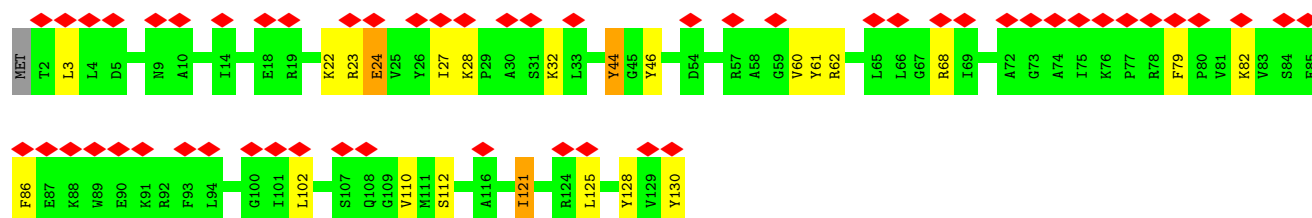
- Molecule 2: 30S ribosomal protein S9P

Chain AK: 



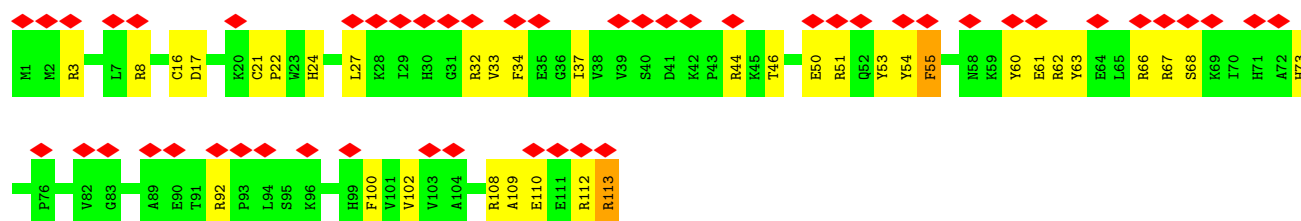
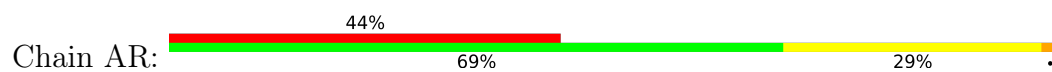
- Molecule 3: 30S ribosomal protein S8P

Chain AI: 

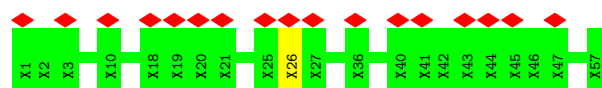




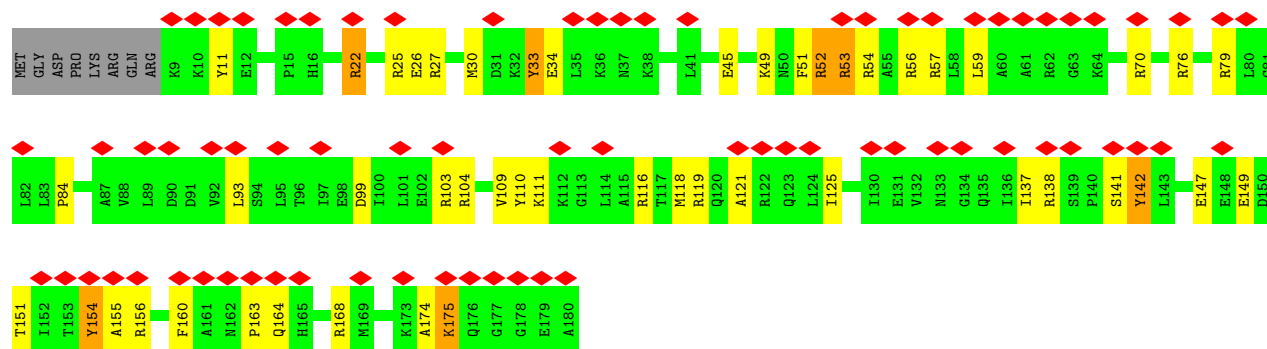




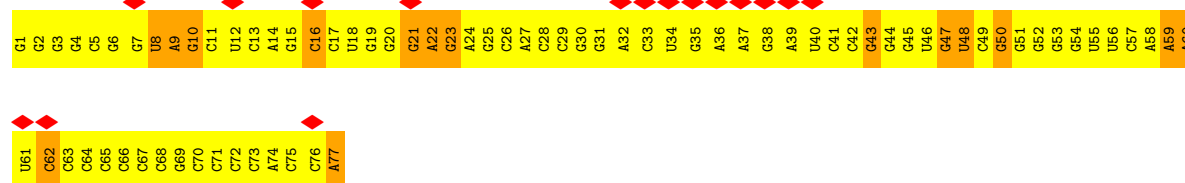
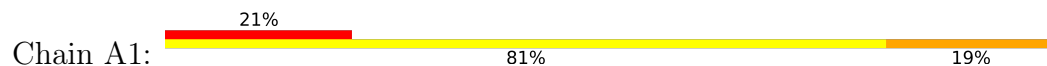
- Molecule 9: unknown 30S ribosomal protein SX



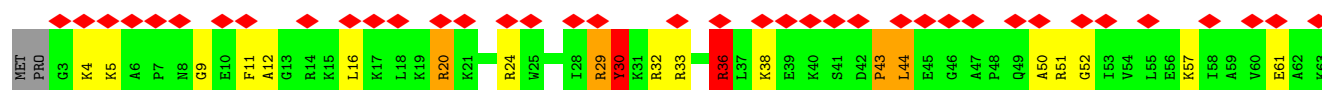
- Molecule 10: 30S ribosomal protein S4P

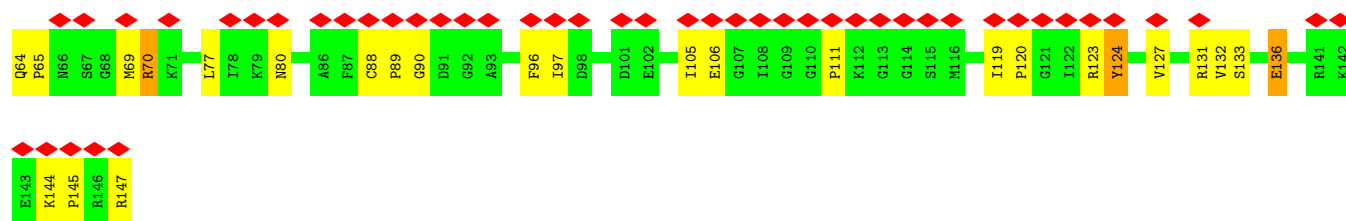


- Molecule 11: E-tRNA

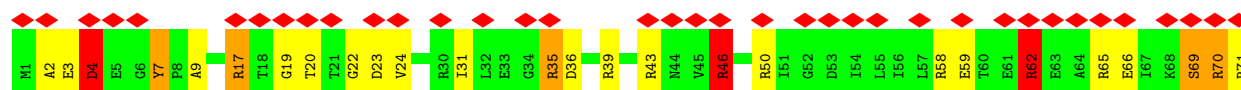


- Molecule 12: 30S ribosomal protein S12P

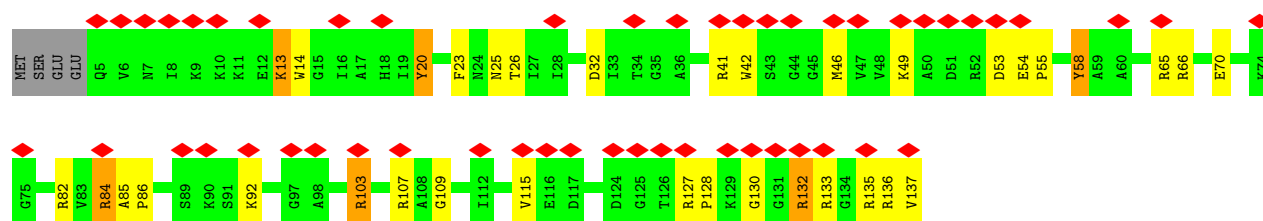
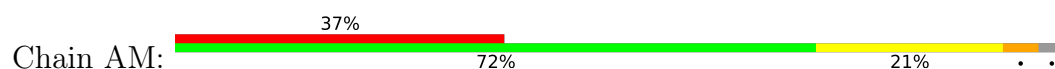




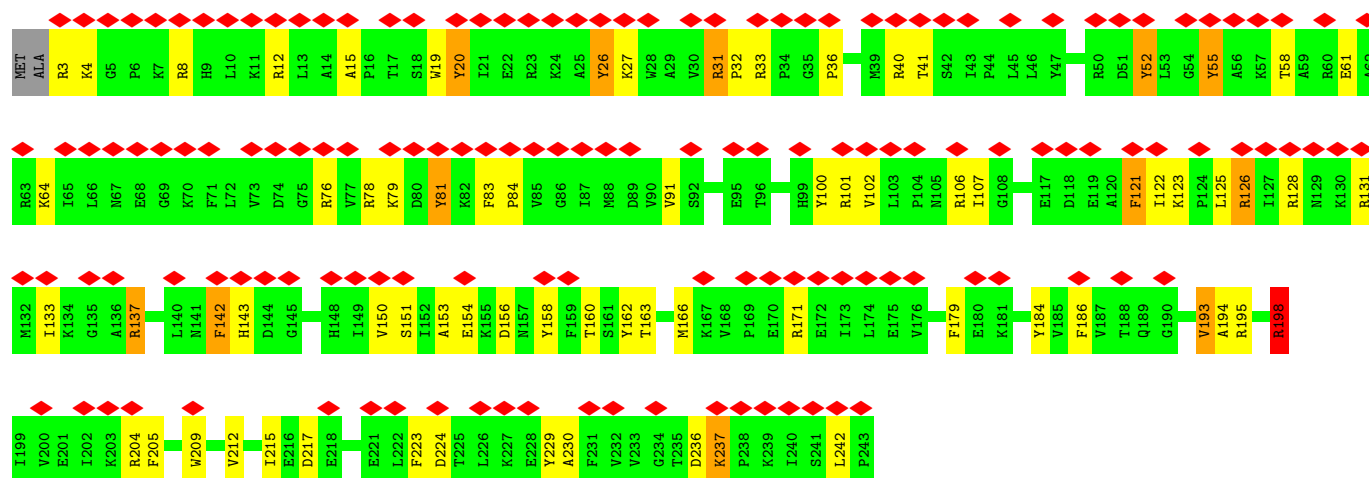
- Molecule 13: 30S ribosomal protein S28e



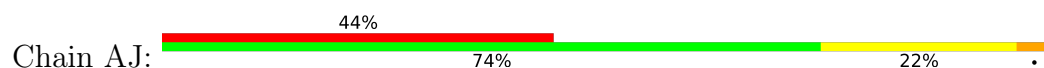
- Molecule 14: 30S ribosomal protein S11P

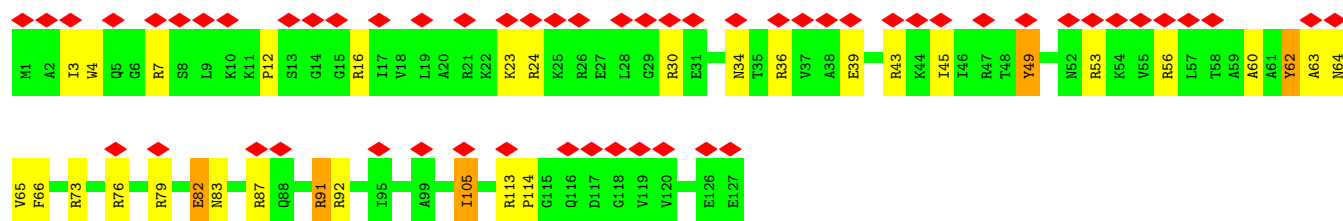


- Molecule 15: 30S ribosomal protein S4e



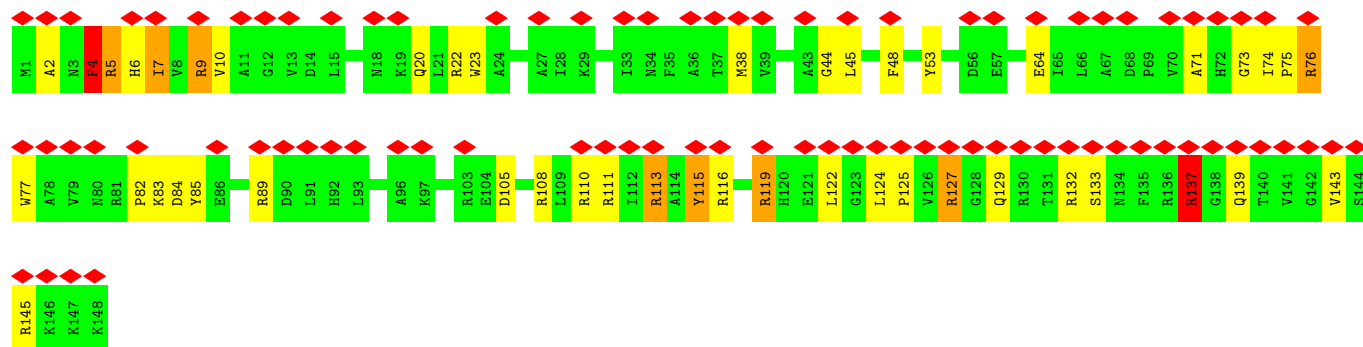
- Molecule 16: 30S ribosomal protein S8e





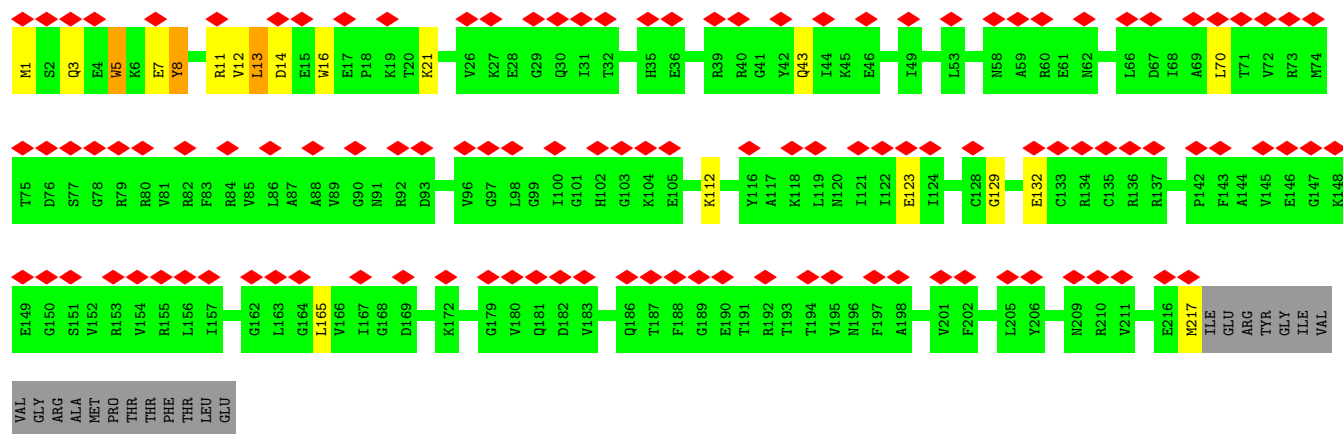
• Molecule 17: 30S ribosomal protein S13P

Chain AO: 57% 69% 24% 5% •



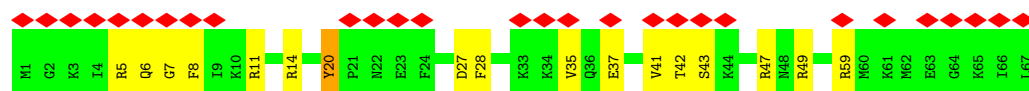
• Molecule 18: 30S ribosomal protein S5P

Chain AF: 49% 84% 7% • 8%



• Molecule 19: 30S ribosomal protein S17e

Chain AS: 42% 75% 24% •

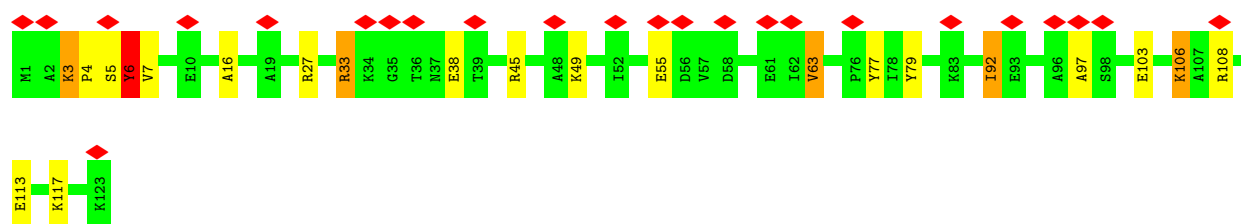
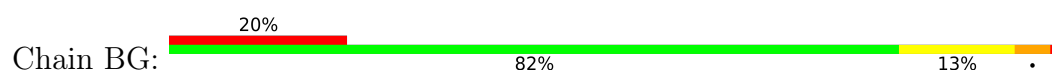


• Molecule 20: 50S ribosomal protein L7Ae

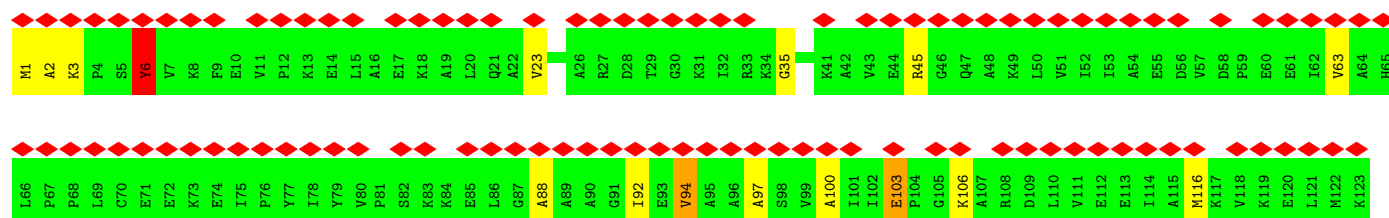
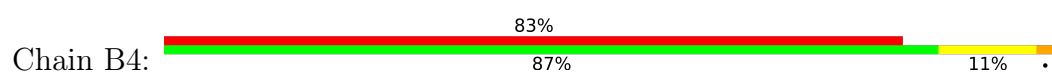
Chain A3: 97% 75% 24% •



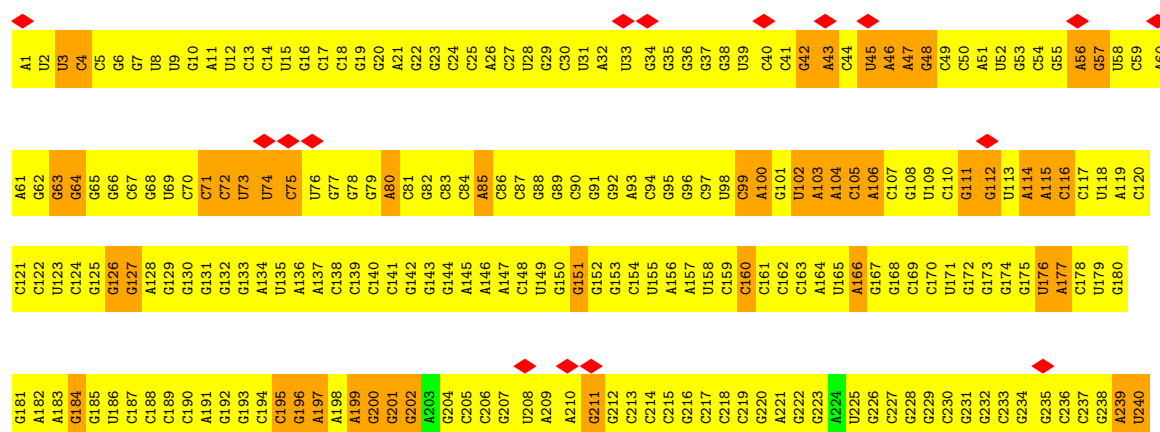
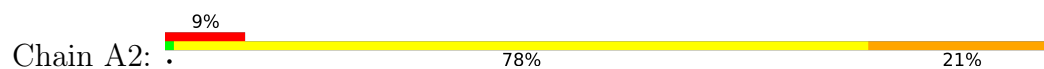
• Molecule 20: 50S ribosomal protein L7Ae



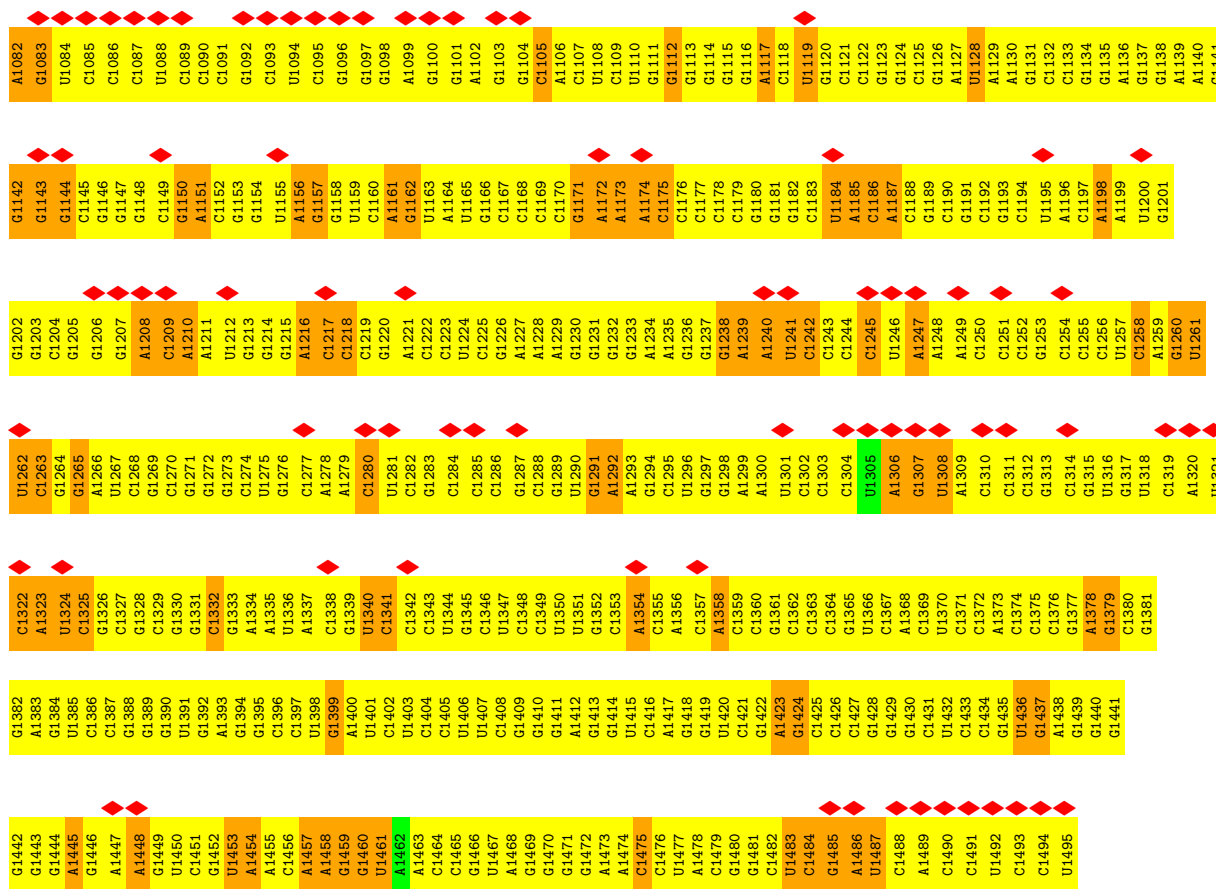
• Molecule 20: 50S ribosomal protein L7Ae



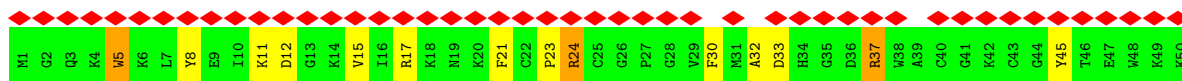
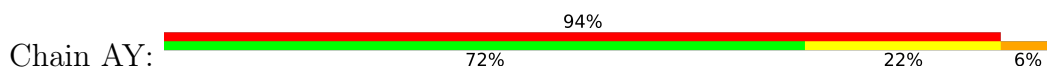
• Molecule 21: 16S rRNA



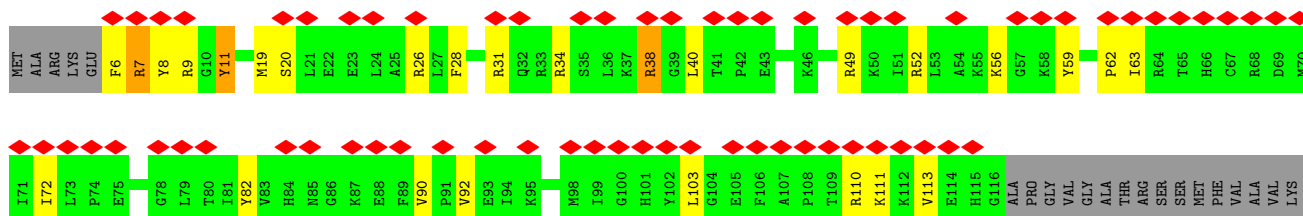
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G962	A963	A964	G965	G966	C967	C968	G969	G970	G971	C972	U973	G974	A975	A976	G977	G978	U979	C980	U981	U982	G983	C984	C985	G986	G987	A988	C989	G990	C991	G992	C993	C994	G995	A996	G997	A998	G999	G1000	A1001	G1002	G1003	U1004	C1005	C1006	A1007	U1008	G1009	G1010	C1011	C1012	G1013	C1014	C1015	G1016	U1017	U1018	A1019	G1020	C1021		
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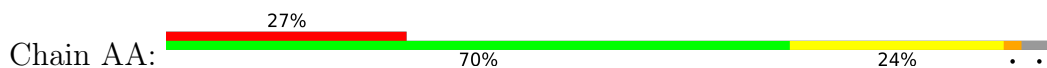
• Molecule 22: 30S ribosomal protein S27ae

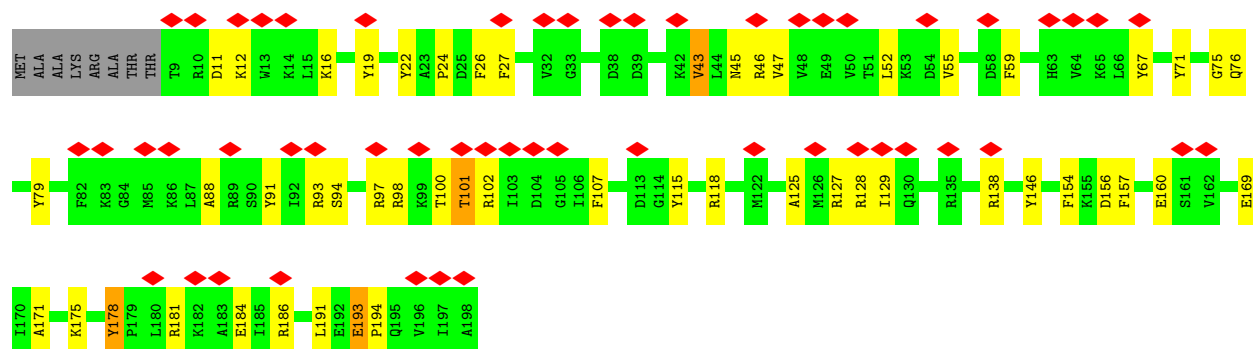


• Molecule 23: 30S ribosomal protein S19P

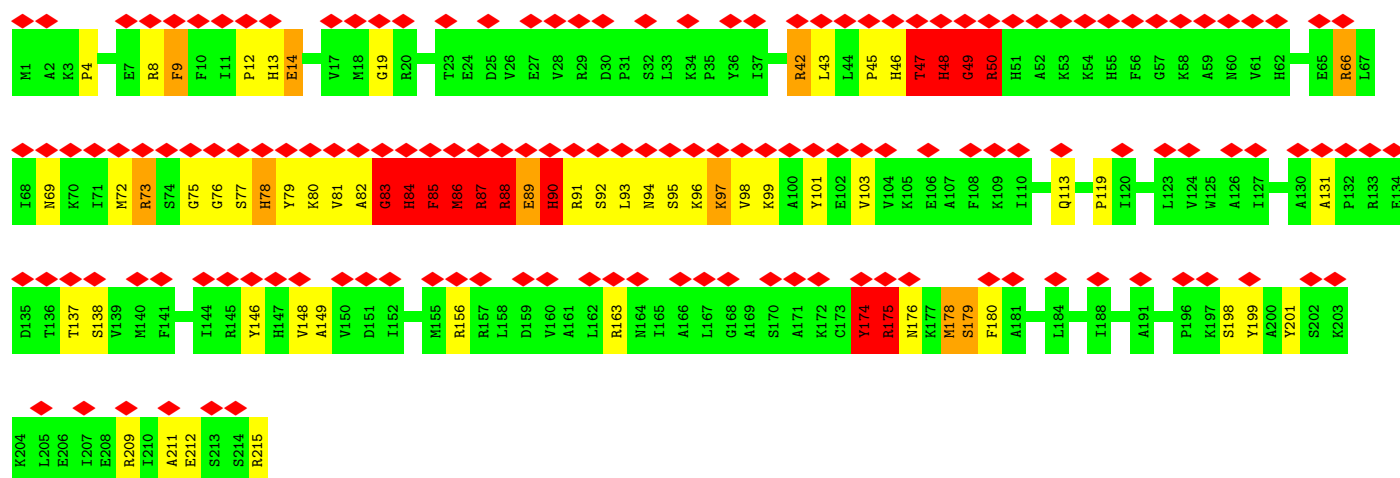


• Molecule 24: 30S ribosomal protein S3Ae

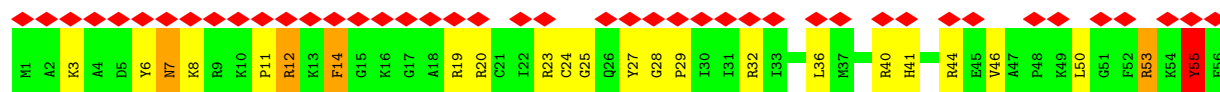
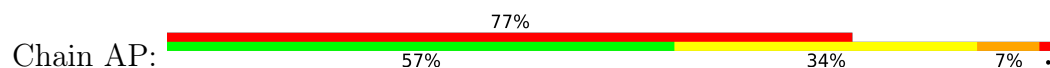




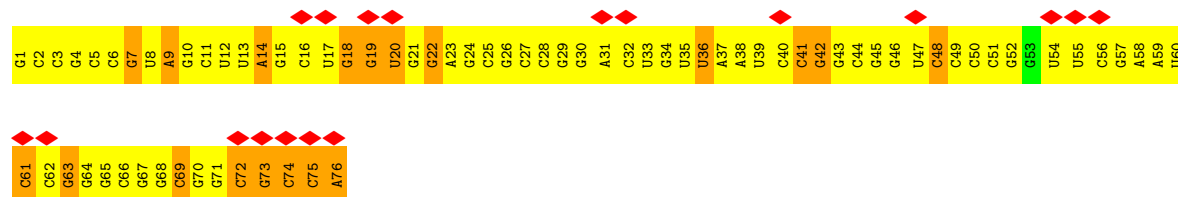
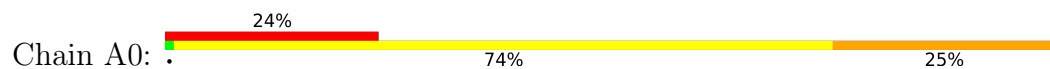
• Molecule 25: 30S ribosomal protein S7P



• Molecule 26: 30S ribosomal protein S14P type Z



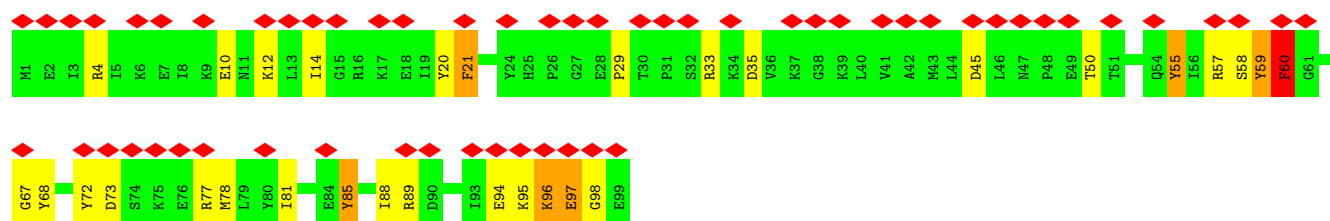
• Molecule 27: P-tRNA



• Molecule 28: 30S ribosomal protein S24e

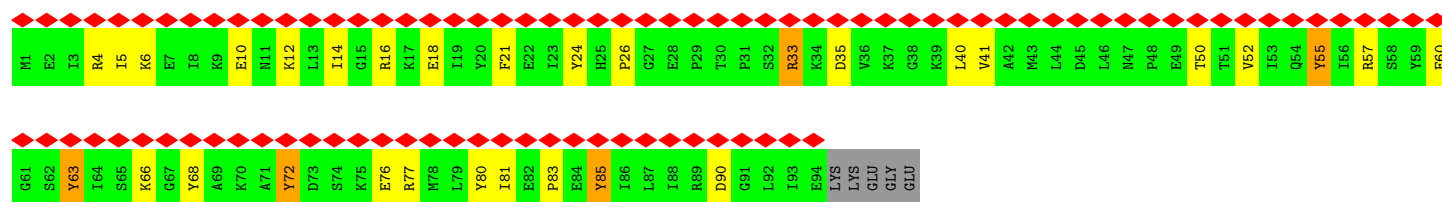


Chain AV: 




- Molecule 28: 30S ribosomal protein S24e

Chain B6: 




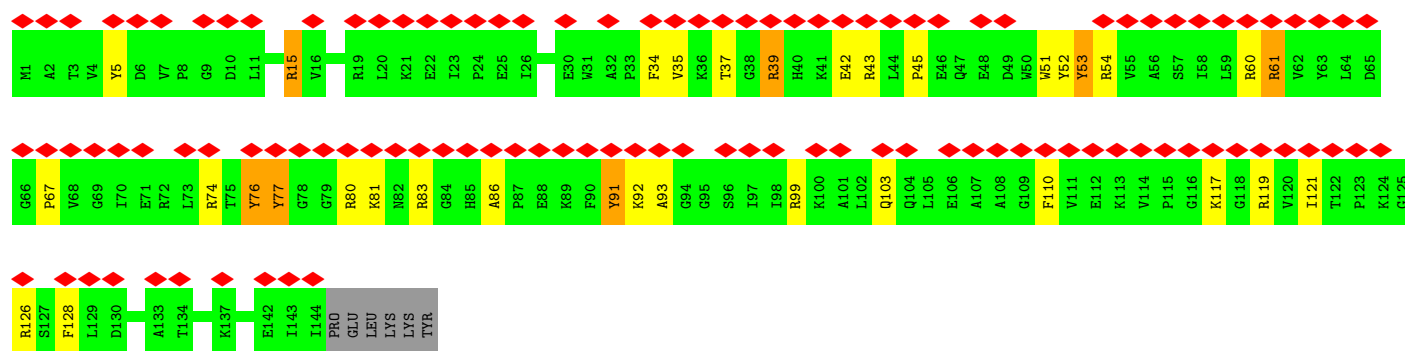
- Molecule 29: 30S ribosomal protein S10P

Chain AL: 



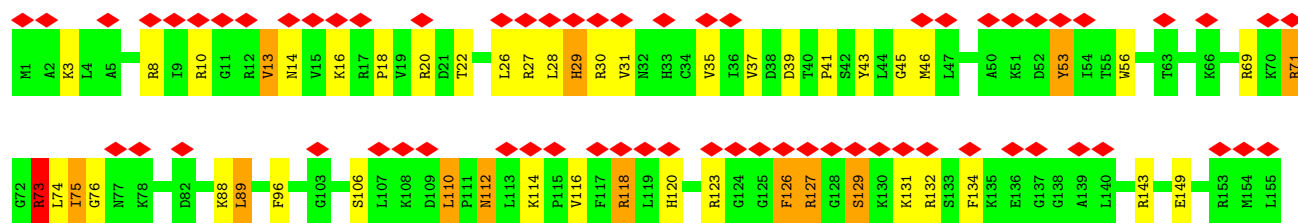
- Molecule 30: SSU ribosomal protein S19E

Chain AU: 

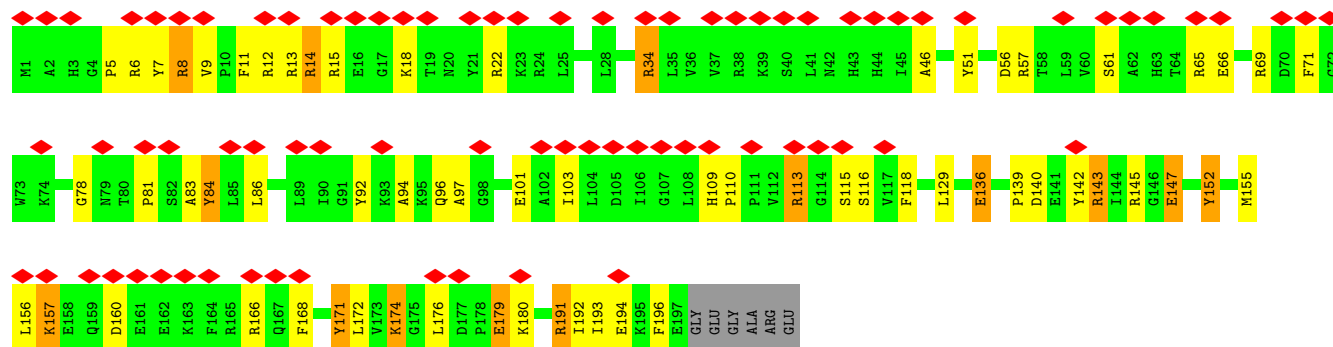
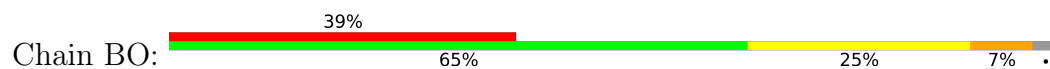


- Molecule 31: 50S ribosomal protein L30P

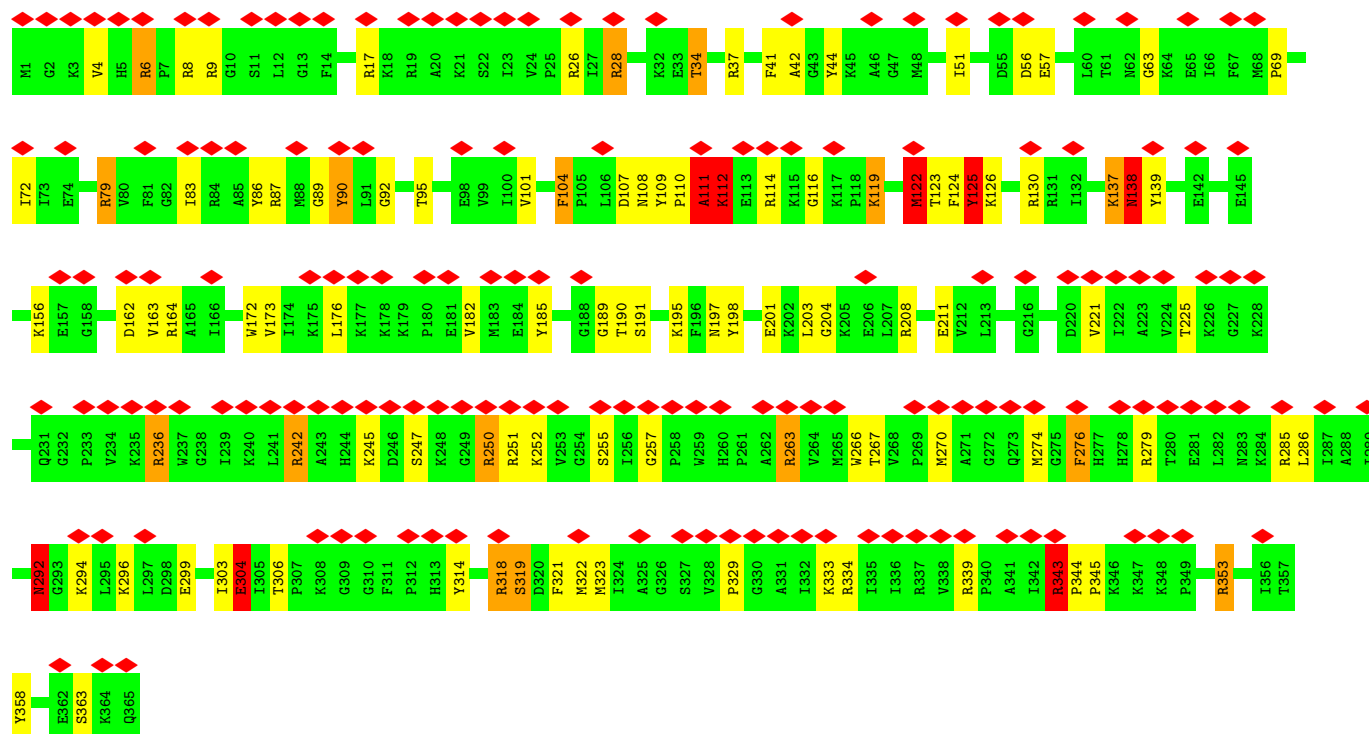
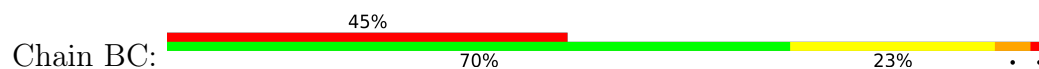
Chain BY: 



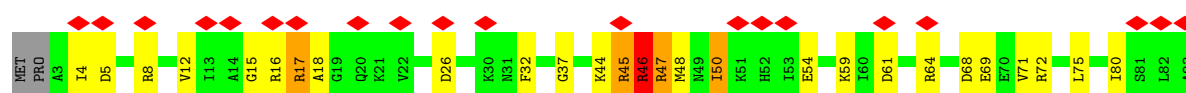
• Molecule 32: 50S ribosomal protein L18P



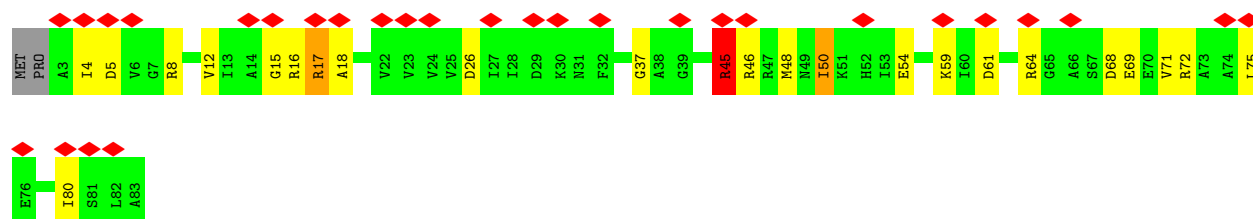
• Molecule 33: 50S ribosomal protein L3P



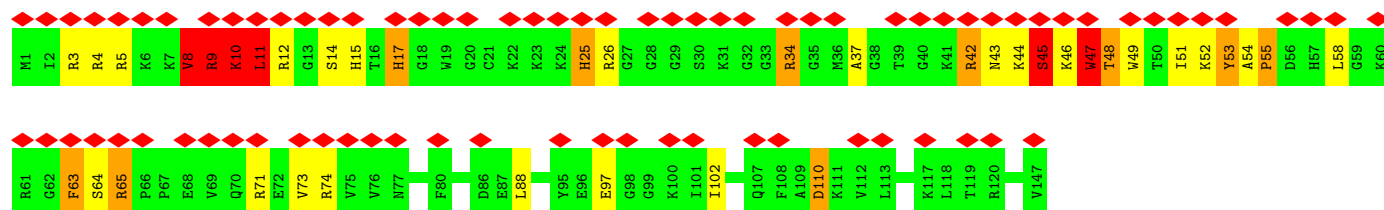
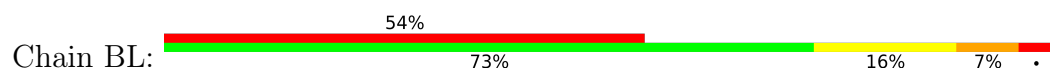
• Molecule 34: 50S ribosomal protein L14e



- Molecule 34: 50S ribosomal protein L14e



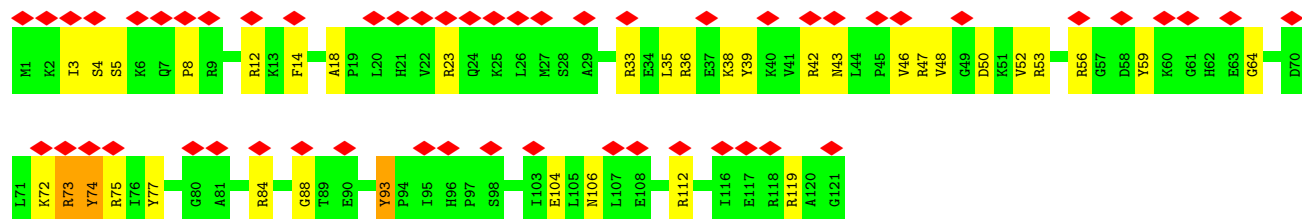
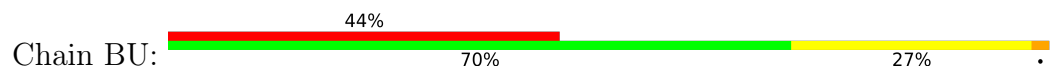
- Molecule 35: 50S ribosomal protein L15P



- Molecule 36: 50S ribosomal protein L39e

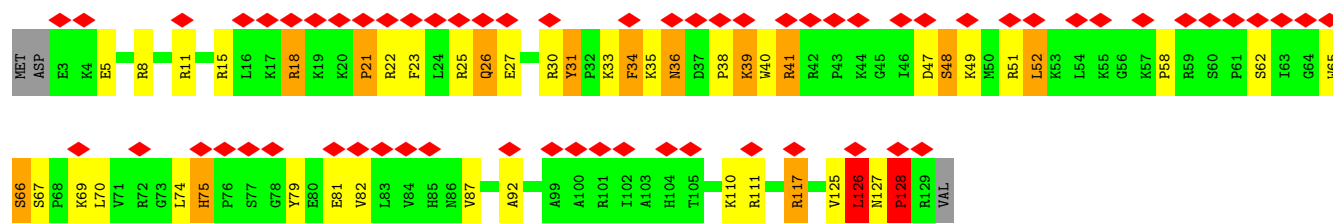


- Molecule 37: 50S ribosomal protein L24P

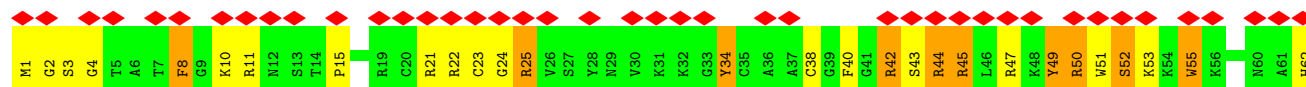


- Molecule 38: 50S ribosomal protein L32e

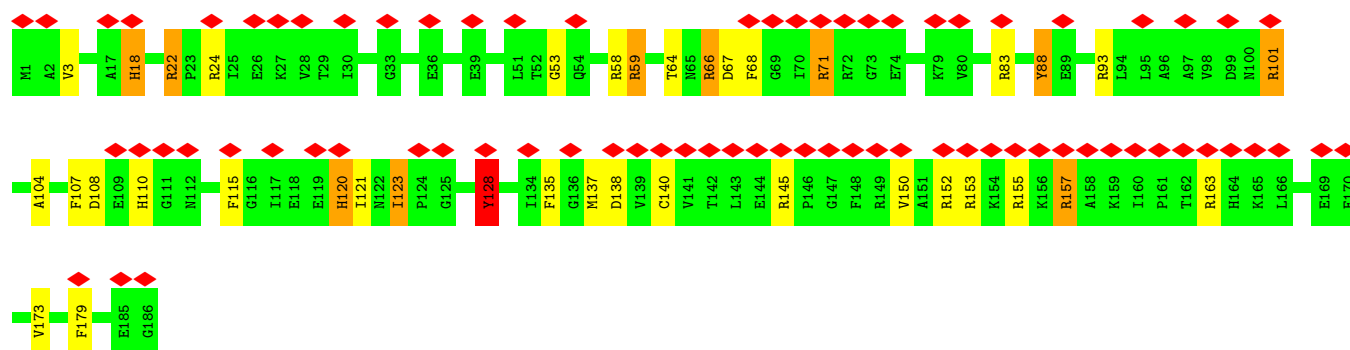
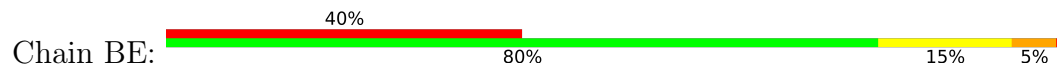




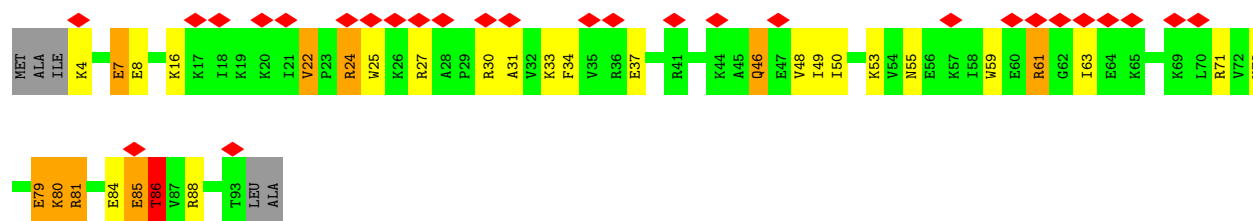
• Molecule 39: 50S ribosomal protein L37e



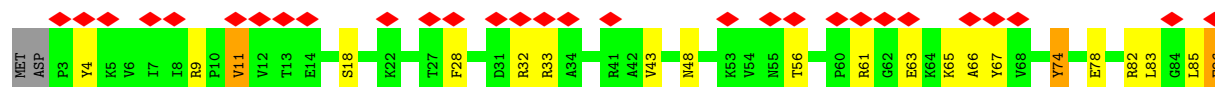
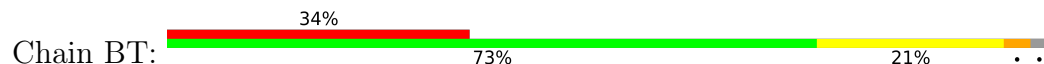
• Molecule 40: 50S ribosomal protein L5P



• Molecule 41: 50S ribosomal protein L31e



• Molecule 42: 50S ribosomal protein L23P

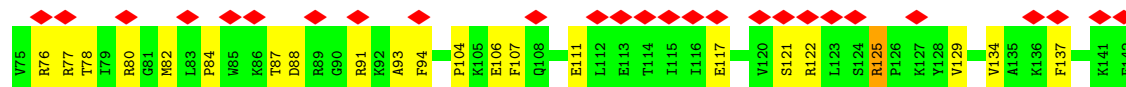
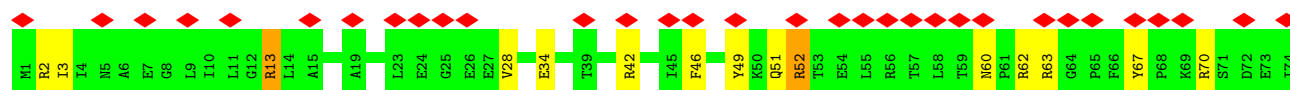
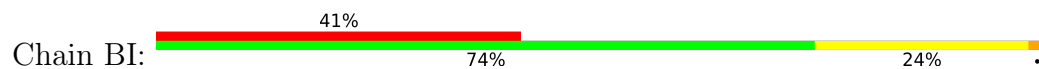


• Molecule 43: Acidic ribosomal protein P0 homolog

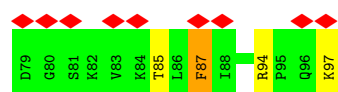
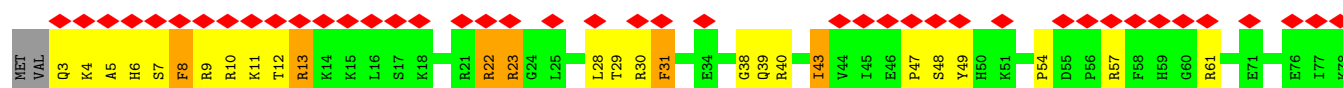




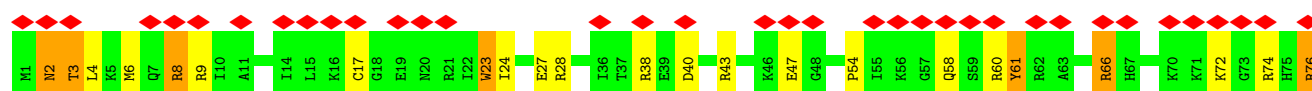
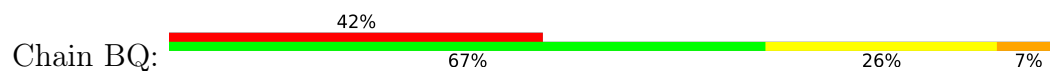
• Molecule 47: 50S ribosomal protein L13P



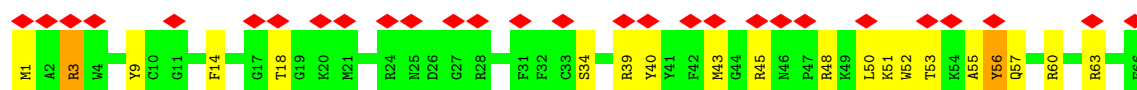
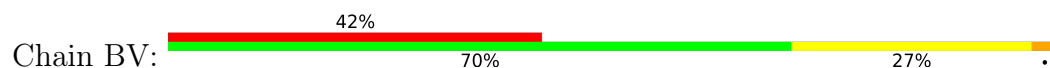
• Molecule 48: 50S ribosomal protein L21e



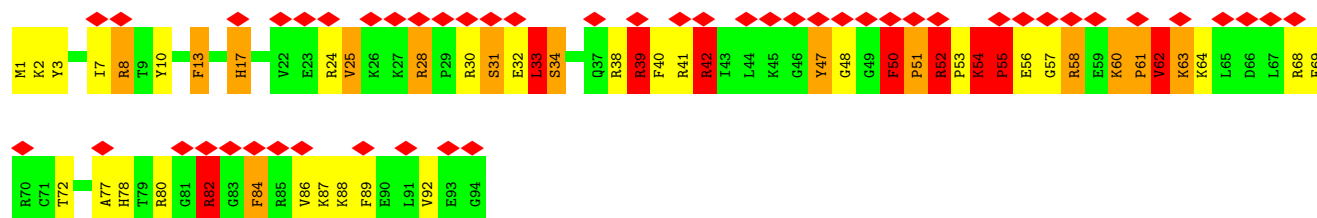
• Molecule 49: 50S ribosomal protein L19e



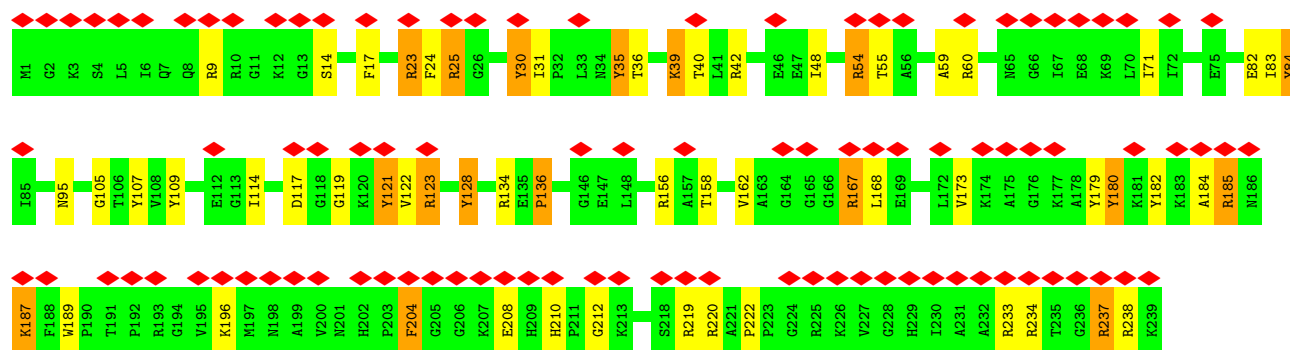
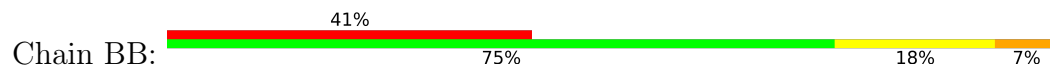
• Molecule 50: 50S ribosomal protein L24e



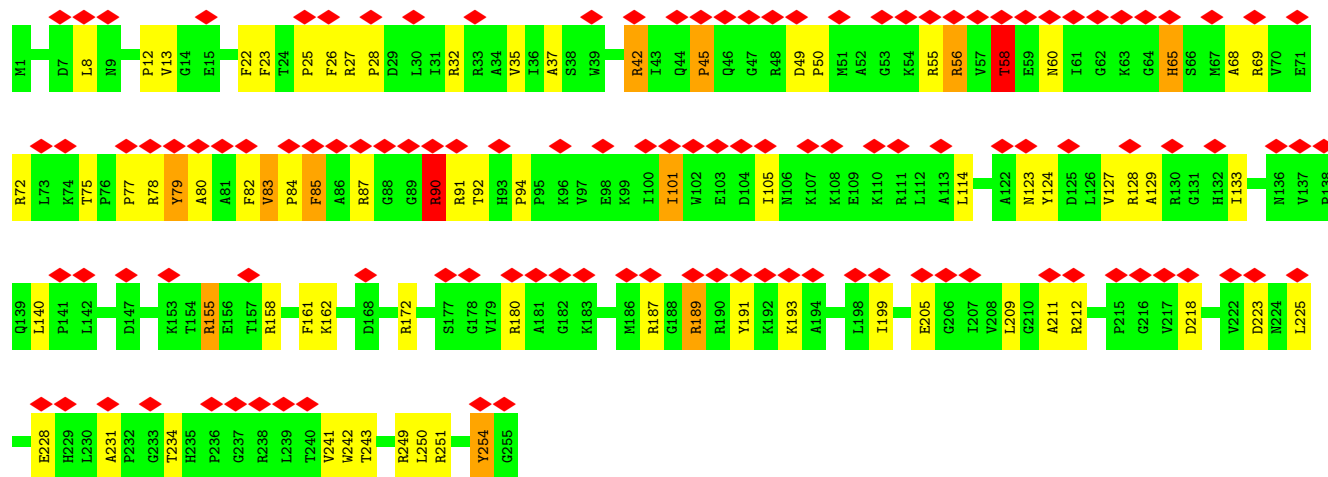
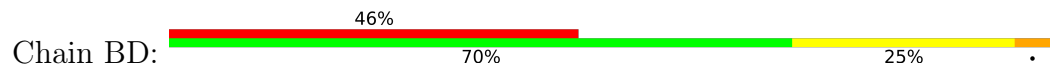
• Molecule 51: 50S ribosomal protein L44E



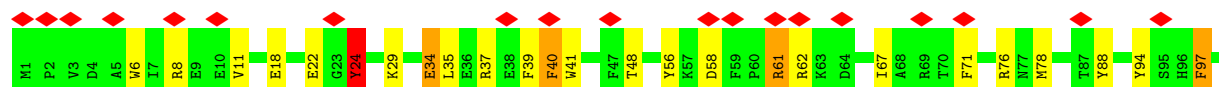
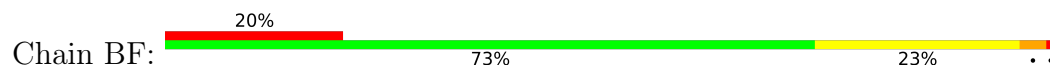
• Molecule 52: 50S ribosomal protein L2P

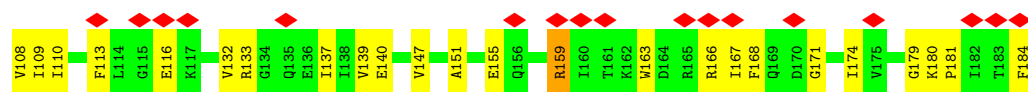


• Molecule 53: 50S ribosomal protein L4P

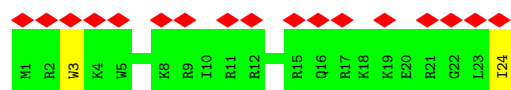
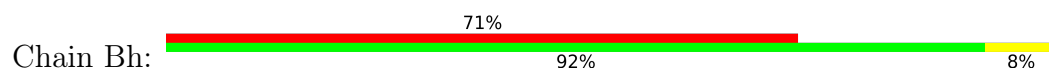


• Molecule 54: 50S ribosomal protein L6P

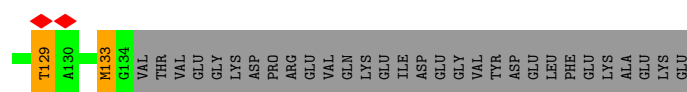
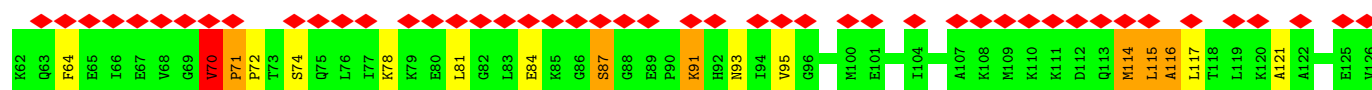
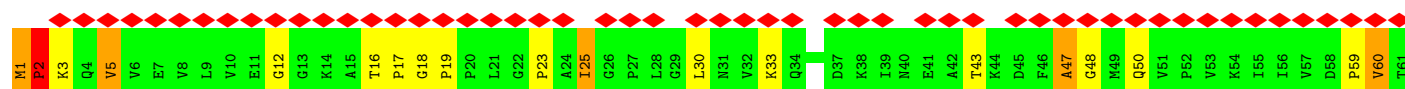




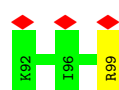
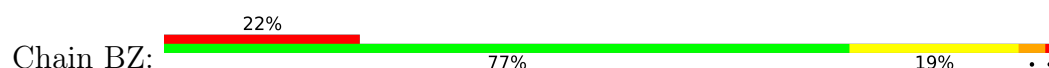
- Molecule 55: 50S ribosomal protein L41e



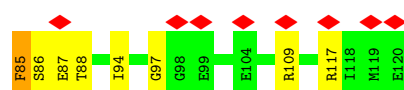
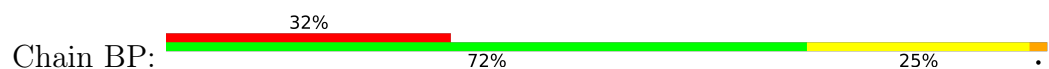
- Molecule 56: 50S ribosomal protein L11P



- Molecule 57: 50S ribosomal protein L30e

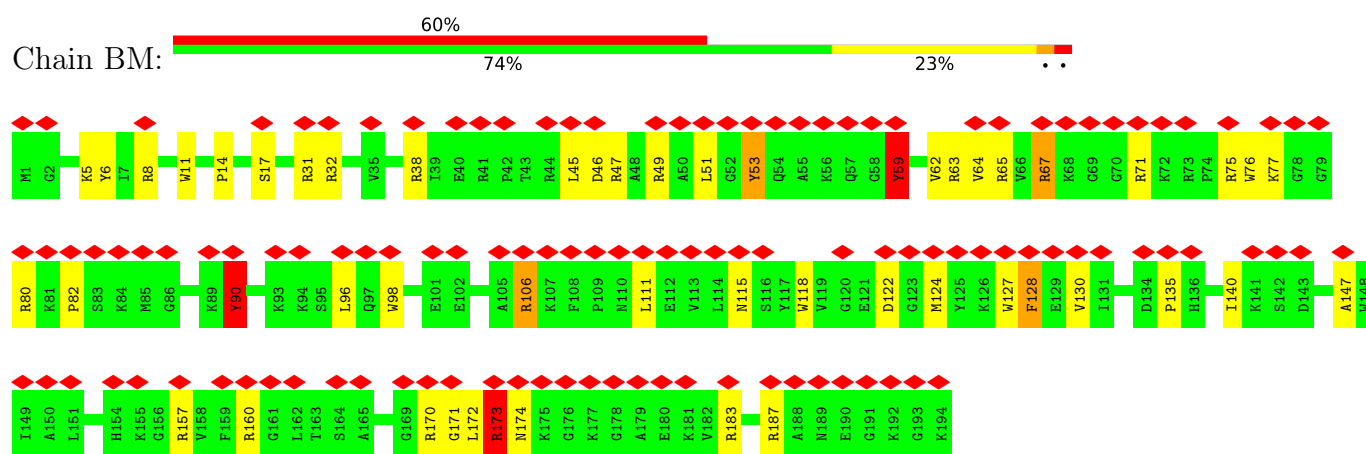


- Molecule 58: 50S ribosomal protein L18e

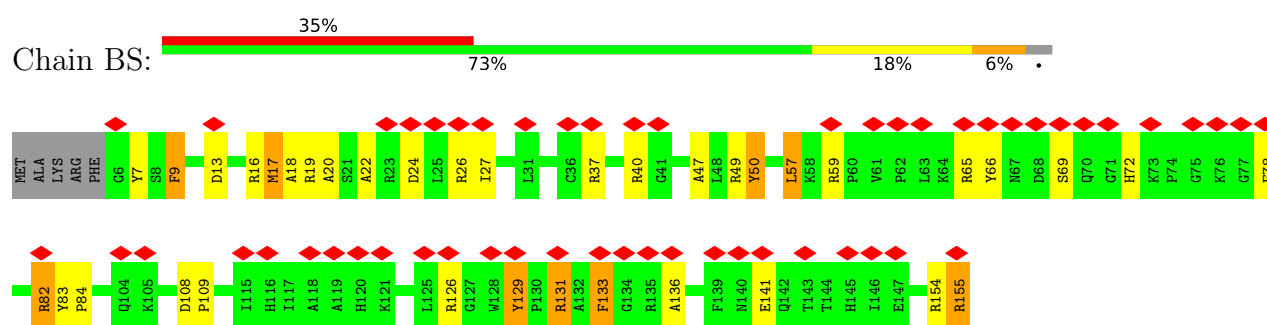


- Molecule 59: 50S ribosomal protein L15e

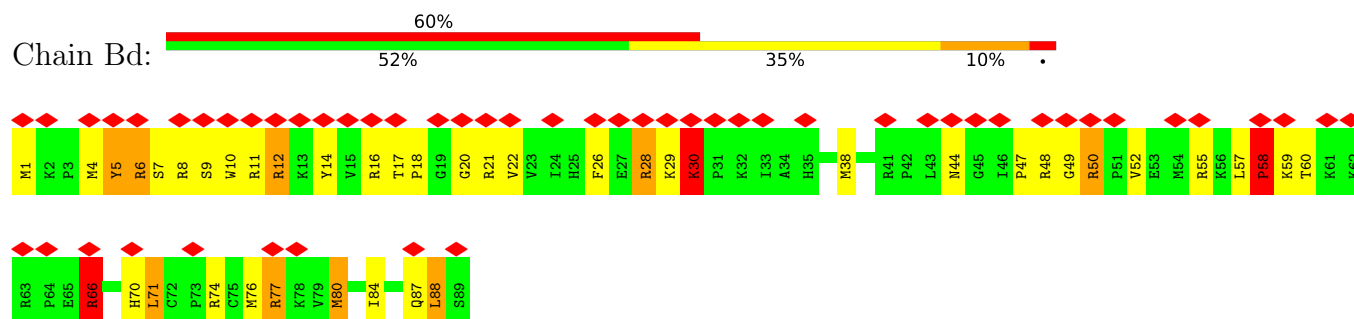




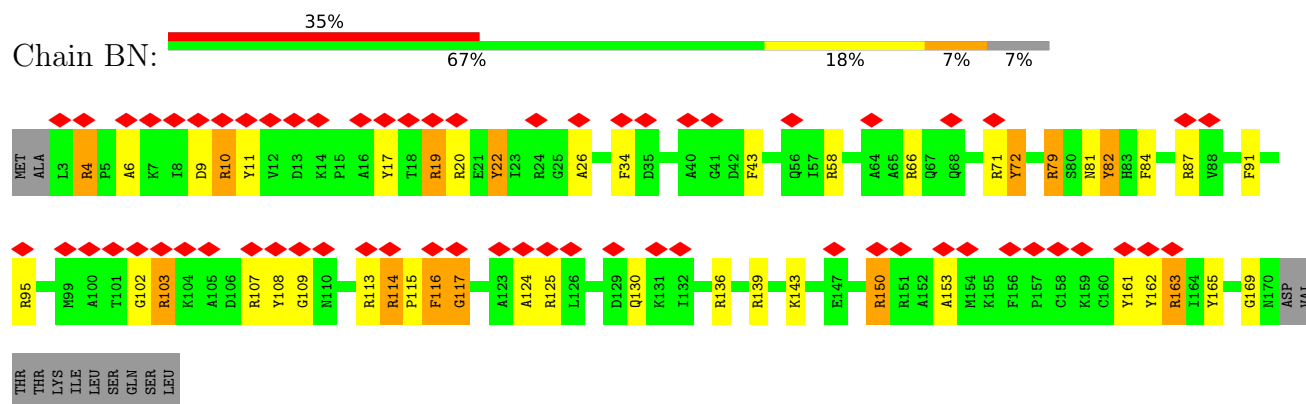
- Molecule 60: 50S ribosomal protein L22P

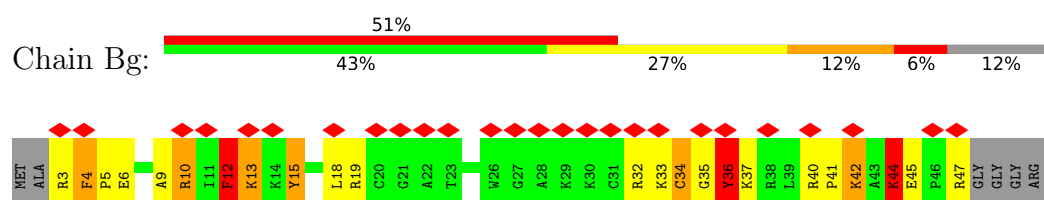


- Molecule 61: 50S ribosomal protein L34e

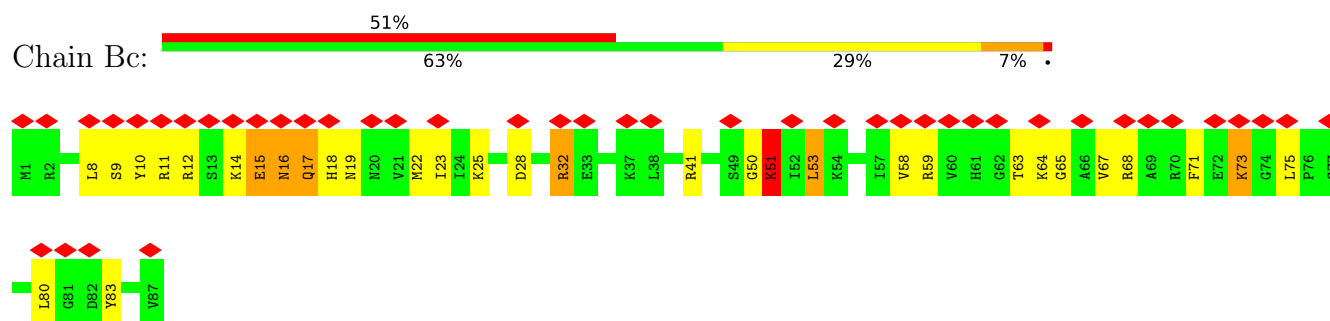


- Molecule 62: 50S ribosomal protein L10e

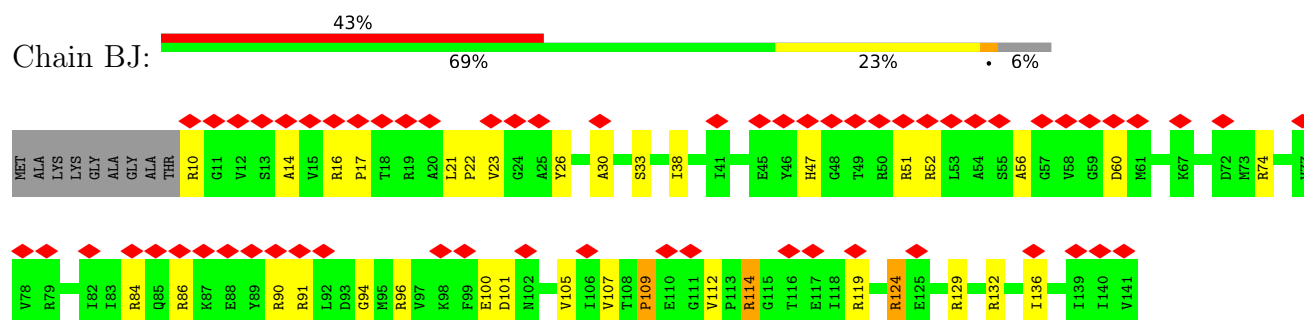




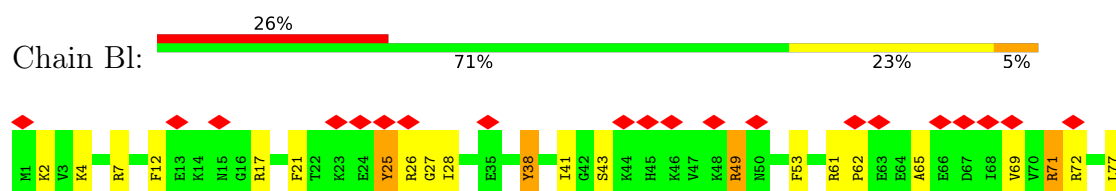
• Molecule 64: 50S ribosomal protein L35Ae



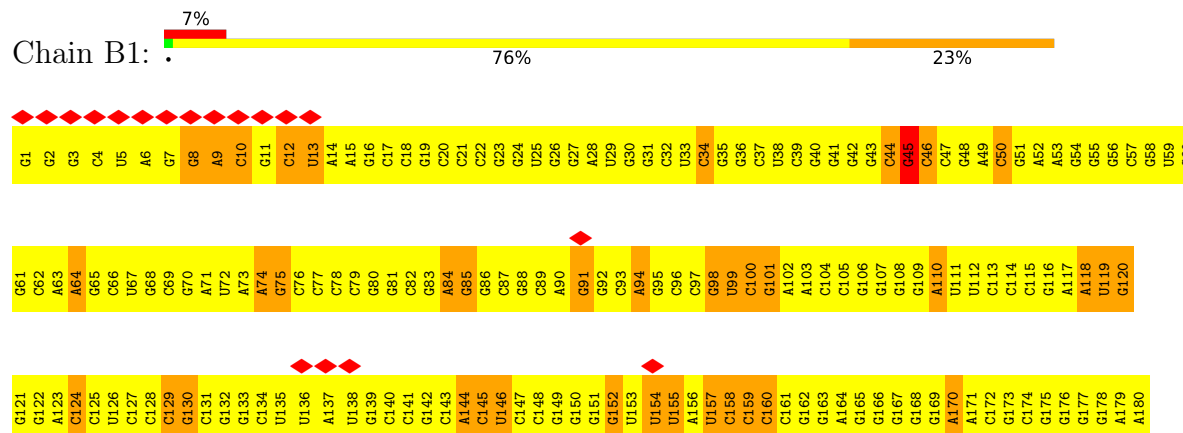
• Molecule 65: 50S ribosomal protein L14P



• Molecule 66: 50S ribosomal protein LX



• Molecule 67: 23S rRNA



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C1321	G1322	U1323	C1324	U1325	A1326	C1327	G1328	G1329	U1330	U1331	A1332	G1333	G1334	C1335	G1336	C1337	G1338	C1339	G1340	U1341	C1342	C1343	C1344	G1345	G1346	U1347	G1348	C1349	C1350	C1351	U1352	A1353	G1354	C1355	G1356	A1357	C1358	C1359	G1360	G1361	C1362	C1363	C1364	G1365	U1366	A1367	G1368	A1369	G1370	U1371	C1372	C1373	G1374	G1375	U1376	G1377	A1378	G1379	C1380
C1261	C1262	C1263	G1264	A1265	C1266	A1267	A1268	U1269	G1270	G1271	A1272	C1273	G1274	G1275	G1276	G1277	G1278	C1279	U1280	A1281	C1282	G1283	C1284	G1285	G1286	G1287	C1288	C1289	G1290	C1291	C1292	G1293	A1294	G1295	A1296	C1297	C1298	C1299	G1300	G1301	C1302	C1303	G1304	C1305	A1306	C1307	G1308	C1309	A1310	C1311	G1312	C1313	A1314	C1315	U1316	G1317	C1318	U1319	C1320
G1201	G1202	C1203	U1204	U1205	A1206	G1207	A1208	U1209	C1210	C1211	A1212	C1213	C1214	C1215	A1216	U1217	C1218	C1219	U1220	U1221	U1222	A1223	A1224	G1225	A1226	A1227	C1228	U1229	G1230	C1231	G1232	U1233	A1234	G1235	C1236	A1237	G1238	C1239	U1240	C1241	A1242	C1243	C1244	G1245	G1246	U1247	C1248	G1249	A1250	G1251	G1252	U1253	C1254	C1255	G1256	G1257	U1258	G1259	C1260
C1141	A1142	A1143	A1144	U1145	U1146	G1147	C1148	C1149	G1150	G1151	C1152	U1153	A1154	A1155	G1156	U1157	G1158	U1159	U1160	A1161	C1162	U1163	C1164	A1165	A1166	A1167	A1168	G1169	G1170	G1171	U1172	G1173	G1174	C1175	C1176	C1177	G1178	G1179	G1180	C1181	C1182	U1183	U1184	A1185	G1186	A1187	A1188	A1189	G1190	C1191	G1192	U1193	G1194	G1195	A1196	G1197	U1198	U1199	A1200
U1081	A1082	G1083	G1084	U1085	U1086	G1087	G1088	C1089	G1090	C1091	U1092	G1093	U1094	A1095	C1096	C1097	C1098	C1099	U1100	U1101	C1102	U1103	A1104	C1105	C1106	G1107	A1108	G1109	A1110	U1111	G1112	G1113	C1114	A1115	C1116	C1117	A1118	A1119	C1120	C1121	C1122	A1123	G1124	A1125	C1126	C1127	G1128	G1129	U1130	G1131	U1132	U1133	A1134	A1135	G1136	G1137	C1138	C1139	C1140
G1021	G1022	C1023	G1024	A1025	A1026	A1027	G1028	C1029	C1030	C1031	C1032	G1033	G1034	G1035	C1036	C1037	U1038	C1039	U1040	U1041	G1042	U1043	C1044	A1045	A1046	A1047	C1048	U1049	C1050	G1051	C1052	A1053	A1054	C1055	C1056	C1057	A1058	C1059	C1060	G1061	C1062	C1063	G1064	C1065	C1066	G1067	U1068	A1069	G1070	U1071	U1072	G1073	G1074	G1075	G1076	G1077	A1078	G1079	G1080

C2522	C2523	C2524	C2525	C2526	C2527	C2528	C2529	C2530	C2531	C2532	C2533	C2534	C2535	A2476	A2477	C2478	C2479	C2480	C2481	C2482	C2483	C2484	C2485	A2486	A2487	C2488	C2489	A2490	C2491	C2492	C2493	C2494	A2495	A2496	C2497	C2498	C2499	C2500	C2501	C2502	C2503	U2504	A2505	A2506	C2507	C2508	A2509	C2510	C2511	C2512	C2513	C2514	U2515	C2516	C2517	C2518	C2519	C2520	C2521	
G1801	G1802	U1803	G1804	U1805	C1806	G1807	G1808	G1809	G1810	G1811	G1812	A1813	A1814	C1815	C1816	C1817	G1818	G1819	C1820	C1821	G1822	A1823	G1824	G1825	G1826	A1827	A1828	C1829	U1830	C1831	G1832	G1833	C1834	A1835	A1836	A1837	C1838	U1839	G1840	G1841	C1842	C1843	C1844	C1845	G1846	U1847	A1848	A1849	C1850	U1851	U1852	C1853	G1854	G1855	G1856	A1857	G1858	A1859	A1860	
G1861	G1862	G1863	G1864	U1865	G1866	C1867	C1868	U1869	G1870	C1871	G1872	G1873	G1874	U1875	C1876	C1877	G1878	G1879	A1880	C1881	C1882	C1883	C1884	G1885	G1886	A1887	G1888	U1889	U1890	C1891	G1892	C1893	A1894	G1895	U1896	G1897	A1898	C1899	U1900	U1901	G1902	G1903	G1904	G1905	G1906	G1907	U1908	C1909	G1910	G1911	A1912	C1913	U1914	G1915	U1916	U1917	A1918	A1919	A1920	
U1921	A1922	A1923	G1924	A1925	A1926	C1927	C1928	A1929	U1930	G1931	G1932	U1933	C1934	C1935	C1936	A1937	G1938	C1939	U1940	A1941	G1942	C1943	C1944	G1945	G1946	A1947	A1948	A1949	G1950	G1951	G1952	U1953	U1954	U1955	G1956	U1957	A1958	C1959	U1960	G1961	G1962	G1963	G1964	C1965	C1966	G1967	U1968	C1969	G1970	C1971	U1972	U1973	G1974	C1975	C1976	C1977	A1978	G1979	U1980	
G1981	C1982	C1983	G1984	G1985	U1986	A1987	U1988	C1989	U1990	G1991	A1992	A1993	G1994	C1995	C1996	C1997	G1998	C1999	G2000	U2001	A2002	C2003	A2004	A2005	C2006	C2007	G2008	G2009	G2010	U2011	G2012	A2013	A2014	G2015	C2016	A2017	C2018	C2019	G2020	G2021	U2022	A2023	A2024	A2025	C2026	G2027	G2028	C2029	G2030	G2031	G2032	C2033	G2034	U2035	A2036	C1976	C2037	C2038	U2039	A2040
U2041	A2042	A2043	A2044	C2045	C2046	U2047	C2048	U2049	U2050	A2051	A2052	G2053	G2054	U2055	A2056	G2057	C2058	G2059	A2060	A2061	A2062	U2063	U2064	C2065	C2066	C2067	U2068	U2069	G2070	C2071	G2072	G2073	U2074	U2075	A2076	A2077	A2078	U2079	C2080	C2081	C2082	C2083	A2084	C2085	C2086	U2087	G2088	C2089	A2090	U2091	G2092	C2093	A2094	U2095	G2096	G2097	C2098	G2099	U2100	
A2101	A2102	C2103	G2104	A2105	C2106	G2107	U2108	C2109	C2110	C2111	C2112	C2113	G2114	U2115	C2116	U2117	C2118	C2119	C2120	C2121	G2122	G2123	C2124	C2125	C2126	G2127	G2128	G2129	C2130	C2131	C2132	C2133	G2134	C2135	C2136	A2137	A2138	A2139	C2140	C2141	U2142	C2143	U2144	C2145	C2146	U2147	U2148	C2149	G2150	C2151	G2152	C2153	G2154	C2155	A2156	U2157	C2158	C2159	C2160	
A2161	G2162	G2163	C2164	A2165	C2166	C2167	C2168	C2169	C2170	G2171	G2172	U2173	G2174	G2175	A2176	A2177	A2178	G2179	C2180	G2181	A2182	A2183	G2184	A2185	C2186	C2187	C2188	C2189	A2190	U2191	G2192	G2193	A2194	G2195	C2196	U2197	U2198	U2199	A2200	C2201	U2202	A2205	G2206	C2207	C2208	U2209	C2210	C2211	C2212	G2213	U2214	U2215	G2216	C2217	C2218	A2219	C2220	A2221		
C2222	G2223	C2224	C2225	G2226	G2227	G2228	G2229	G2230	G2231	U2232	G2233	C2234	G2235	G2236	A2237	G2238	C2239	G2240	U2241	A2242	G2243	G2244	C2245	G2246	G2247	G2248	A2249	G2250	G2251	C2252	G2253	U2254	C2255	G2256	G2257	A2258	C2259	G2260	C2261	C2262	G2263	G2264	C2265	C2266	U2267	C2268	C2269	G2270	G2271	G2272	U2273	C2274	G2275	G2276	G2277	U2278	G2279	G2280	A2281	
G2282	C2283	C2284	C2285	U2286	C2287	C2288	A2289	U2290	C2291	A2292	C2293	A2294	C2295	A2296	C2297	C2298	G2299	C2300	C2301	G2302	A2303	C2304	U2305	C2306	C2307	C2308	C2309	G2310	C2311	U2312	C2313	U2314	G2315	U2316	C2317	C2318	C2319	U2320	A2321	A2322	C2323	C2324	C2325	C2326	C2327	G2328	A2329	A2330	A2331	G2332	G2333	G2334	C2335	G2336	C2337	A2338	C2339	A2340	G2341	
C2342	G2343	G2344	U2345	A2346	G2347	G2348	U2349	C2350	G2351	C2352	C2353	A2354	G2355	U2356	U2357	U2358	G2359	G2360	C2361	U2362	G2363	G2364	G2365	G2366	C2367	G2368	G2369	C2370	A2371	C2372	G2373	C2374	C2375	U2376	C2377	C2378	G2379	A2380	U2381	A2382	A2383	G2384	G2385	U2386	A2387	U2388	C2389	G2390	C2391	A2392	G2393	C2394	G2395	C2396	C2397	C2398	C2399	U2400	A2401	
A2402	G2403	G2404	C2405	U2406	G2407	G2408	C2409	U2410	C2411	A2412	G2413	G2414	C2415	G2416	G2417	U2418	U2419	C2420	A2421	G2422	G2423	A2424	A2425	U2426	C2427	G2428	C2429	A2430	C2431	G2432	U2433	A2434	G2435	A2436	G2437	U2438	G2439	C2440	A2441	A2442	G2443	G2444	G2445	G2446	A2447	A2448	A2449	A2450	G2451	C2452	C2453	G2454	G2455	C2456	G2457	U2458	A2459	A2460	C2461	
U2462	G2463	G2464	A2465	C2466	G2467	C2468	C2469	U2470	A2471	A2472	C2473	A2474	C2475	A2476	C2477	C2478	C2479	G2480	C2481	C2482	C2483	C2484	C2485	A2486	A2487	C2488	C2489	C2490	C2491	C2492	A2493	A2494	A2495	G2496	G2497	C2498	C2499	C2500	C2501	C2502	C2503	U2504	A2505	A2506	C2507	C2508	A2509	C2510	C2511	C2512	C2513	C2514	U2515	C2516	C2517	U2518	C2519	C2520	C2521	



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	10000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Wiener Filter	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3600	Depositor
Magnification	75000	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	0.745	Depositor
Minimum map value	-0.497	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.040	Depositor
Recommended contour level	0.13	Depositor
Map size ( $\text{\AA}$ )	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.2375, 1.2375, 1.2375	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	AQ	1.71	11/1338 (0.8%)	1.93	30/1797 (1.7%)
2	AK	1.74	12/1088 (1.1%)	2.01	32/1455 (2.2%)
3	AI	1.54	5/1049 (0.5%)	1.70	9/1408 (0.6%)
4	AG	1.48	3/999 (0.3%)	1.97	31/1337 (2.3%)
5	AW	1.76	3/485 (0.6%)	1.86	11/651 (1.7%)
6	AC	1.81	19/1480 (1.3%)	1.99	34/1985 (1.7%)
7	AB	1.79	18/1654 (1.1%)	2.06	51/2233 (2.3%)
8	AR	1.83	14/956 (1.5%)	2.07	35/1287 (2.7%)
10	AD	1.73	15/1457 (1.0%)	1.93	36/1953 (1.8%)
11	A1	3.43	155/1843 (8.4%)	2.59	167/2873 (5.8%)
12	AN	1.58	12/1156 (1.0%)	1.95	31/1535 (2.0%)
13	AX	1.92	9/570 (1.6%)	2.14	19/760 (2.5%)
14	AM	1.71	11/1022 (1.1%)	1.98	27/1375 (2.0%)
15	AE	1.80	28/2025 (1.4%)	2.16	66/2732 (2.4%)
16	AJ	1.85	16/1013 (1.6%)	2.04	20/1349 (1.5%)
17	AO	1.88	16/1208 (1.3%)	2.11	39/1619 (2.4%)
18	AF	1.23	5/1745 (0.3%)	1.38	18/2350 (0.8%)
19	AS	1.71	8/562 (1.4%)	1.86	14/744 (1.9%)
20	A3	1.67	7/951 (0.7%)	1.95	24/1281 (1.9%)
20	B4	1.41	2/951 (0.2%)	1.64	11/1281 (0.9%)
20	BG	1.34	0/951	1.79	21/1281 (1.6%)
21	A2	3.29	2781/35966 (7.7%)	2.59	3540/56138 (6.3%)
22	AY	1.72	4/421 (1.0%)	1.85	8/558 (1.4%)
23	AT	1.81	7/942 (0.7%)	1.95	24/1257 (1.9%)
24	AA	1.71	13/1585 (0.8%)	2.12	53/2124 (2.5%)
25	AH	1.62	20/1773 (1.1%)	2.11	75/2381 (3.1%)
26	AP	1.87	6/471 (1.3%)	2.06	15/620 (2.4%)
27	A0	3.33	158/1814 (8.7%)	2.51	182/2828 (6.4%)
28	AV	1.57	7/839 (0.8%)	1.75	17/1122 (1.5%)
28	B6	1.73	9/798 (1.1%)	2.09	32/1071 (3.0%)
29	AL	1.52	3/830 (0.4%)	2.03	28/1113 (2.5%)
30	AU	1.79	14/1203 (1.2%)	2.05	29/1621 (1.8%)
31	BY	1.73	13/1262 (1.0%)	2.04	31/1687 (1.8%)
32	BO	1.85	29/1635 (1.8%)	1.96	37/2196 (1.7%)



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	BC	1.72	27/2978 (0.9%)	2.06	96/4003 (2.4%)
34	B5	1.76	7/618 (1.1%)	2.12	24/829 (2.9%)
34	BK	1.80	8/618 (1.3%)	1.98	19/829 (2.3%)
35	BL	1.71	13/1175 (1.1%)	2.07	46/1563 (2.9%)
36	Bf	1.94	13/453 (2.9%)	2.75	38/603 (6.3%)
37	BU	1.77	16/1024 (1.6%)	2.05	29/1365 (2.1%)
38	Bb	1.77	12/1099 (1.1%)	2.14	36/1466 (2.5%)
39	Be	1.82	10/517 (1.9%)	2.11	19/681 (2.8%)
40	BE	1.72	12/1513 (0.8%)	1.99	39/2026 (1.9%)
41	Ba	1.61	1/760 (0.1%)	2.04	30/1019 (2.9%)
42	BT	1.66	5/689 (0.7%)	1.97	19/924 (2.1%)
43	Bk	1.48	8/1659 (0.5%)	1.82	44/2253 (2.0%)
44	BW	1.85	13/595 (2.2%)	2.02	19/784 (2.4%)
45	Bi	1.57	0/599	1.85	16/798 (2.0%)
46	BA	1.73	23/1702 (1.4%)	1.98	46/2293 (2.0%)
47	BI	1.80	18/1168 (1.5%)	1.96	30/1561 (1.9%)
48	BR	1.65	4/808 (0.5%)	1.92	22/1080 (2.0%)
49	BQ	1.69	15/1272 (1.2%)	2.17	43/1676 (2.6%)
50	BV	1.67	3/570 (0.5%)	2.07	23/758 (3.0%)
51	Bj	1.75	6/805 (0.7%)	2.36	51/1064 (4.8%)
52	BB	1.77	19/1883 (1.0%)	2.08	56/2540 (2.2%)
53	BD	1.81	25/2068 (1.2%)	1.99	57/2787 (2.0%)
54	BF	1.74	13/1507 (0.9%)	2.01	44/2033 (2.2%)
55	Bh	1.34	2/233 (0.9%)	1.11	3/301 (1.0%)
56	BH	1.46	5/1001 (0.5%)	1.88	31/1351 (2.3%)
57	BZ	1.69	6/764 (0.8%)	1.99	20/1028 (1.9%)
58	BP	1.89	12/980 (1.2%)	1.97	24/1313 (1.8%)
59	BM	1.84	23/1634 (1.4%)	1.97	35/2179 (1.6%)
60	BS	1.76	7/1226 (0.6%)	2.16	38/1649 (2.3%)
61	Bd	1.60	5/758 (0.7%)	2.22	41/1007 (4.1%)
62	BN	1.86	16/1409 (1.1%)	2.09	51/1890 (2.7%)
63	Bg	1.58	2/380 (0.5%)	2.02	17/504 (3.4%)
64	Bc	1.67	6/694 (0.9%)	2.12	30/926 (3.2%)
65	BJ	1.88	14/1027 (1.4%)	1.95	24/1385 (1.7%)
66	Bl	1.81	7/669 (1.0%)	1.92	15/884 (1.7%)
67	B1	3.31	5858/73410 (8.0%)	2.59	7158/114595 (6.2%)
68	B3	3.47	234/3010 (7.8%)	2.74	322/4693 (6.9%)
All	All	2.81	9901/187317 (5.3%)	2.41	13452/276642 (4.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AQ	0	7
2	AK	0	4
3	AI	0	5
4	AG	1	9
5	AW	0	2
6	AC	0	11
7	AB	0	6
8	AR	0	3
9	A9	0	1
10	AD	0	6
12	AN	0	10
13	AX	0	7
14	AM	0	2
15	AE	0	11
16	AJ	0	4
17	AO	0	11
18	AF	0	1
19	AS	0	1
20	B4	0	1
20	BG	0	3
21	A2	1	7
22	AY	0	4
23	AT	0	5
24	AA	0	2
25	AH	4	21
26	AP	0	6
28	AV	0	10
28	B6	0	2
29	AL	1	5
30	AU	0	6
31	BY	0	7
32	BO	0	11
33	BC	0	18
34	B5	1	3
34	BK	1	1
35	BL	3	12
36	Bf	0	13
37	BU	0	3
38	Bb	0	10
39	Be	1	12
40	BE	0	6
41	Ba	0	7
42	BT	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	Bk	0	10
44	BW	0	2
45	Bi	0	4
46	BA	0	4
47	BI	0	3
48	BR	0	6
49	BQ	3	10
50	BV	1	4
51	Bj	1	18
52	BB	0	16
53	BD	0	8
54	BF	0	8
56	BH	1	9
57	BZ	0	1
58	BP	0	2
59	BM	0	7
60	BS	0	7
61	Bd	1	7
62	BN	0	8
63	Bg	1	4
64	Bc	1	7
65	BJ	0	3
66	Bl	0	3
67	B1	0	12
All	All	22	442

The worst 5 of 9901 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	B1	1565	G	O4'-C1'	51.72	2.08	1.41
67	B1	2507	C	O4'-C1'	37.95	1.91	1.41
67	B1	1570	C	O4'-C1'	37.84	1.90	1.41
67	B1	1642	G	C2'-C1'	35.02	1.91	1.53
21	A2	85	A	C2'-C1'	34.42	1.91	1.53

The worst 5 of 13452 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	2363	G	O4'-C1'-N9	44.16	143.53	108.20
67	B1	1754	A	O4'-C1'-N9	36.92	137.74	108.20
21	A2	1207	G	O4'-C1'-N9	31.50	133.40	108.20
11	A1	49	C	O4'-C1'-N1	30.68	132.75	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	2174	G	O4'-C1'-N9	30.40	132.52	108.20

5 of 22 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	AG	53	LYS	CA
21	A2	1317	G	C1'
25	AH	85	PHE	CA
25	AH	86	MET	CA
25	AH	87	ARG	CA

5 of 442 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AQ	28	TYR	Sidechain
1	AQ	3	ARG	Sidechain
1	AQ	58	TYR	Sidechain
1	AQ	68	ASP	Peptide
1	AQ	74	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AQ	156/158 (99%)	139 (89%)	8 (5%)	9 (6%)	1	18
2	AK	133/135 (98%)	119 (90%)	12 (9%)	2 (2%)	10	46
3	AI	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	9	44
4	AG	123/125 (98%)	103 (84%)	11 (9%)	9 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AW	61/63 (97%)	55 (90%)	4 (7%)	2 (3%)	4	26
6	AC	184/210 (88%)	175 (95%)	6 (3%)	3 (2%)	9	44
7	AB	200/202 (99%)	177 (88%)	19 (10%)	4 (2%)	7	38
8	AR	111/113 (98%)	100 (90%)	9 (8%)	2 (2%)	8	40
10	AD	170/180 (94%)	151 (89%)	14 (8%)	5 (3%)	4	29
12	AN	143/147 (97%)	129 (90%)	8 (6%)	6 (4%)	3	22
13	AX	69/71 (97%)	59 (86%)	4 (6%)	6 (9%)	1	11
14	AM	131/137 (96%)	118 (90%)	8 (6%)	5 (4%)	3	24
15	AE	239/243 (98%)	210 (88%)	23 (10%)	6 (2%)	5	32
16	AJ	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	2	21
17	AO	146/148 (99%)	122 (84%)	15 (10%)	9 (6%)	1	17
18	AF	215/236 (91%)	191 (89%)	22 (10%)	2 (1%)	17	57
19	AS	65/67 (97%)	64 (98%)	0	1 (2%)	10	46
20	A3	121/123 (98%)	105 (87%)	8 (7%)	8 (7%)	1	15
20	B4	121/123 (98%)	113 (93%)	6 (5%)	2 (2%)	9	42
20	BG	121/123 (98%)	109 (90%)	8 (7%)	4 (3%)	4	26
22	AY	48/50 (96%)	43 (90%)	3 (6%)	2 (4%)	3	22
23	AT	109/132 (83%)	98 (90%)	9 (8%)	2 (2%)	8	40
24	AA	188/198 (95%)	170 (90%)	12 (6%)	6 (3%)	4	26
25	AH	213/215 (99%)	181 (85%)	14 (7%)	18 (8%)	1	11
26	AP	54/56 (96%)	43 (80%)	8 (15%)	3 (6%)	2	18
28	AV	97/99 (98%)	86 (89%)	6 (6%)	5 (5%)	2	19
28	B6	92/99 (93%)	84 (91%)	4 (4%)	4 (4%)	2	22
29	AL	100/102 (98%)	92 (92%)	1 (1%)	7 (7%)	1	14
30	AU	142/150 (95%)	134 (94%)	5 (4%)	3 (2%)	7	36
31	BY	153/155 (99%)	143 (94%)	5 (3%)	5 (3%)	4	26
32	BO	195/203 (96%)	164 (84%)	17 (9%)	14 (7%)	1	14
33	BC	363/365 (100%)	303 (84%)	34 (9%)	26 (7%)	1	14
34	B5	79/83 (95%)	69 (87%)	5 (6%)	5 (6%)	1	16
34	BK	79/83 (95%)	68 (86%)	6 (8%)	5 (6%)	1	16
35	BL	145/147 (99%)	128 (88%)	8 (6%)	9 (6%)	1	17

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Bf	49/51 (96%)	37 (76%)	8 (16%)	4 (8%)	1	12
37	BU	119/121 (98%)	113 (95%)	3 (2%)	3 (2%)	5	32
38	Bb	125/130 (96%)	102 (82%)	13 (10%)	10 (8%)	1	12
39	Be	60/62 (97%)	45 (75%)	11 (18%)	4 (7%)	1	15
40	BE	184/186 (99%)	170 (92%)	8 (4%)	6 (3%)	4	26
41	Ba	88/95 (93%)	74 (84%)	7 (8%)	7 (8%)	1	12
42	BT	82/86 (95%)	78 (95%)	3 (4%)	1 (1%)	13	50
43	Bk	210/339 (62%)	187 (89%)	12 (6%)	11 (5%)	2	19
44	BW	70/72 (97%)	70 (100%)	0	0	100	100
45	Bi	76/83 (92%)	70 (92%)	6 (8%)	0	100	100
46	BA	214/216 (99%)	190 (89%)	12 (6%)	12 (6%)	2	18
47	BI	140/142 (99%)	129 (92%)	7 (5%)	4 (3%)	4	29
48	BR	93/97 (96%)	85 (91%)	6 (6%)	2 (2%)	6	35
49	BQ	148/150 (99%)	141 (95%)	4 (3%)	3 (2%)	7	38
50	BV	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	Bj	92/94 (98%)	71 (77%)	8 (9%)	13 (14%)	0	4
52	BB	237/239 (99%)	213 (90%)	17 (7%)	7 (3%)	4	28
53	BD	253/255 (99%)	218 (86%)	21 (8%)	14 (6%)	2	19
54	BF	182/184 (99%)	169 (93%)	13 (7%)	0	100	100
55	Bh	22/24 (92%)	21 (96%)	1 (4%)	0	100	100
56	BH	132/164 (80%)	108 (82%)	14 (11%)	10 (8%)	1	13
57	BZ	97/99 (98%)	84 (87%)	7 (7%)	6 (6%)	1	17
58	BP	118/120 (98%)	102 (86%)	13 (11%)	3 (2%)	5	32
59	BM	192/194 (99%)	173 (90%)	17 (9%)	2 (1%)	15	54
60	BS	148/155 (96%)	137 (93%)	8 (5%)	3 (2%)	7	38
61	Bd	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	26
62	BN	166/181 (92%)	137 (82%)	20 (12%)	9 (5%)	2	19
63	Bg	43/51 (84%)	31 (72%)	3 (7%)	9 (21%)	0	2
64	Bc	85/87 (98%)	74 (87%)	7 (8%)	4 (5%)	2	21
65	BJ	130/141 (92%)	124 (95%)	4 (3%)	2 (2%)	10	46
66	Bl	75/77 (97%)	69 (92%)	4 (5%)	2 (3%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	8599/9048 (95%)	7630 (89%)	608 (7%)	361 (4%)	5	22

5 of 361 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AQ	78	ILE
2	AK	133	SER
3	AI	121	ILE
4	AG	48	ASN
4	AG	50	LEU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AQ	143/143 (100%)	138 (96%)	5 (4%)	36	59
2	AK	111/111 (100%)	105 (95%)	6 (5%)	22	47
3	AI	107/108 (99%)	100 (94%)	7 (6%)	17	42
4	AG	108/108 (100%)	88 (82%)	20 (18%)	1	10
5	AW	54/54 (100%)	52 (96%)	2 (4%)	34	58
6	AC	145/167 (87%)	143 (99%)	2 (1%)	67	80
7	AB	173/173 (100%)	164 (95%)	9 (5%)	23	48
8	AR	102/102 (100%)	101 (99%)	1 (1%)	76	86
10	AD	153/160 (96%)	147 (96%)	6 (4%)	32	56
12	AN	118/121 (98%)	104 (88%)	14 (12%)	5	20
13	AX	60/60 (100%)	55 (92%)	5 (8%)	11	34
14	AM	100/104 (96%)	94 (94%)	6 (6%)	19	44
15	AE	212/213 (100%)	198 (93%)	14 (7%)	16	41
16	AJ	103/103 (100%)	98 (95%)	5 (5%)	25	50
17	AO	122/122 (100%)	119 (98%)	3 (2%)	47	68
18	AF	181/197 (92%)	176 (97%)	5 (3%)	43	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	AS	61/61 (100%)	61 (100%)	0	100	100
20	A3	99/99 (100%)	95 (96%)	4 (4%)	31	55
20	B4	99/99 (100%)	95 (96%)	4 (4%)	31	55
20	BG	99/99 (100%)	92 (93%)	7 (7%)	14	39
22	AY	41/41 (100%)	39 (95%)	2 (5%)	25	50
23	AT	99/114 (87%)	99 (100%)	0	100	100
24	AA	166/171 (97%)	163 (98%)	3 (2%)	59	77
25	AH	184/184 (100%)	166 (90%)	18 (10%)	8	27
26	AP	46/46 (100%)	39 (85%)	7 (15%)	3	15
28	AV	89/89 (100%)	81 (91%)	8 (9%)	9	30
28	B6	85/89 (96%)	78 (92%)	7 (8%)	11	34
29	AL	91/91 (100%)	82 (90%)	9 (10%)	8	26
30	AU	121/127 (95%)	114 (94%)	7 (6%)	20	45
31	BY	133/133 (100%)	112 (84%)	21 (16%)	2	14
32	BO	166/169 (98%)	157 (95%)	9 (5%)	22	47
33	BC	312/312 (100%)	293 (94%)	19 (6%)	18	44
34	B5	64/66 (97%)	60 (94%)	4 (6%)	18	43
34	BK	64/66 (97%)	62 (97%)	2 (3%)	40	62
35	BL	117/117 (100%)	102 (87%)	15 (13%)	4	19
36	Bf	47/47 (100%)	40 (85%)	7 (15%)	3	15
37	BU	110/110 (100%)	106 (96%)	4 (4%)	35	59
38	Bb	114/117 (97%)	105 (92%)	9 (8%)	12	36
39	Be	51/51 (100%)	46 (90%)	5 (10%)	8	27
40	BE	158/158 (100%)	152 (96%)	6 (4%)	33	57
41	Ba	80/83 (96%)	71 (89%)	9 (11%)	6	21
42	BT	75/77 (97%)	72 (96%)	3 (4%)	31	55
43	Bk	179/280 (64%)	159 (89%)	20 (11%)	6	22
44	BW	66/66 (100%)	63 (96%)	3 (4%)	27	52
45	Bi	57/61 (93%)	55 (96%)	2 (4%)	36	59
46	BA	182/182 (100%)	174 (96%)	8 (4%)	28	53
47	BI	122/122 (100%)	119 (98%)	3 (2%)	47	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	BR	85/87 (98%)	75 (88%)	10 (12%)	5	20
49	BQ	130/130 (100%)	121 (93%)	9 (7%)	15	40
50	BV	56/56 (100%)	54 (96%)	2 (4%)	35	59
51	Bj	82/83 (99%)	65 (79%)	17 (21%)	1	7
52	BB	189/189 (100%)	180 (95%)	9 (5%)	25	51
53	BD	213/213 (100%)	197 (92%)	16 (8%)	13	38
54	BF	156/156 (100%)	150 (96%)	6 (4%)	33	57
55	Bh	23/23 (100%)	23 (100%)	0	100	100
56	BH	110/137 (80%)	96 (87%)	14 (13%)	4	19
57	BZ	80/80 (100%)	73 (91%)	7 (9%)	10	31
58	BP	101/101 (100%)	98 (97%)	3 (3%)	41	63
59	BM	162/162 (100%)	152 (94%)	10 (6%)	18	43
60	BS	126/130 (97%)	121 (96%)	5 (4%)	31	55
61	Bd	81/81 (100%)	66 (82%)	15 (18%)	1	10
62	BN	140/152 (92%)	138 (99%)	2 (1%)	67	80
63	Bg	37/39 (95%)	29 (78%)	8 (22%)	1	6
64	Bc	74/74 (100%)	65 (88%)	9 (12%)	5	20
65	BJ	104/108 (96%)	99 (95%)	5 (5%)	25	51
66	Bl	72/72 (100%)	68 (94%)	4 (6%)	21	46
All	All	7390/7646 (97%)	6904 (93%)	486 (7%)	20	41

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BL	47	TRP
61	Bd	30	LYS
43	Bk	56	ARG
60	BS	155	ARG
64	Bc	51	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
28	B6	11	ASN

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Mol	Chain	Res	Type
59	BM	25	GLN
25	AH	69	ASN
25	AH	48	HIS
61	Bd	25	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A1	76/77 (98%)	15 (19%)	3 (3%)
21	A2	1494/1495 (99%)	260 (17%)	118 (7%)
27	A0	75/76 (98%)	18 (24%)	3 (4%)
67	B1	3047/3049 (99%)	603 (19%)	194 (6%)
68	B3	126/126 (100%)	35 (27%)	13 (10%)
All	All	4818/4823 (99%)	931 (19%)	331 (6%)

5 of 931 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A1	8	U
11	A1	9	A
11	A1	10	G
11	A1	16	C
11	A1	21	G

5 of 331 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
67	B1	1665	G
67	B1	2507	C
67	B1	1734	G
67	B1	2043	A
67	B1	2805	U

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

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

## 5.5 Carbohydrates ⓘ

There are no 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
67	B1	1
56	BH	1
53	BD	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B1	2506:G	O3'	2507:C	P	1.83
1	BH	18:GLY	C	19:PRO	N	1.19
1	BD	91:ARG	C	92:THR	N	0.93

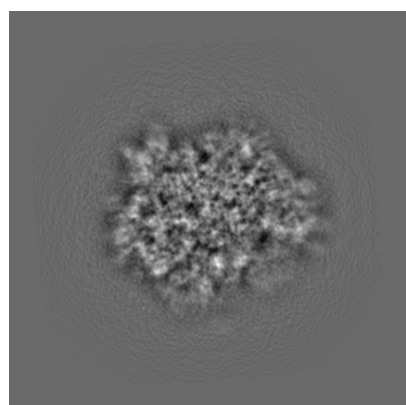
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2009. These allow visual inspection of the internal detail of the map and identification of artifacts.

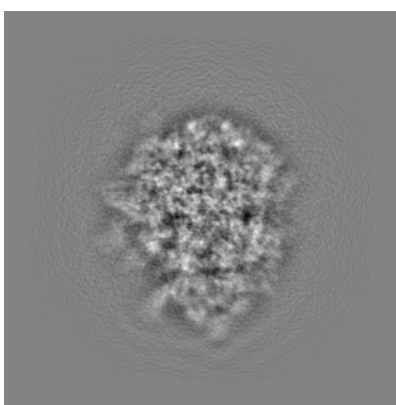
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

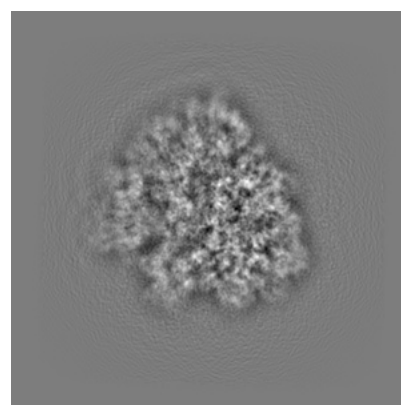
#### 6.1.1 Primary map



X



Y

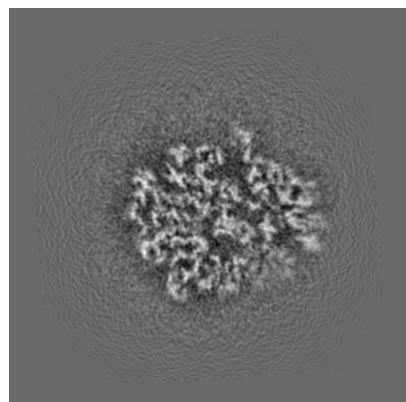


Z

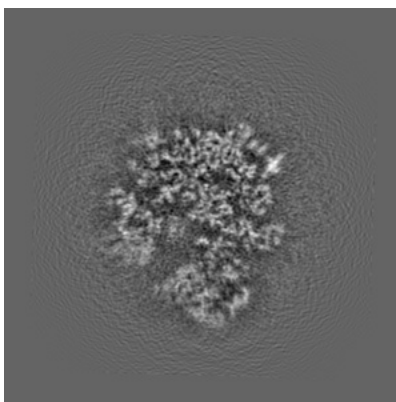
The images above show the map projected in three orthogonal directions.

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

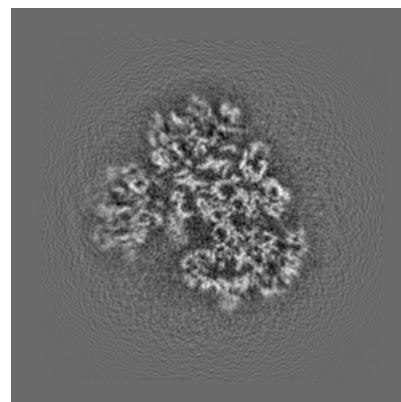
#### 6.2.1 Primary map



X Index: 184



Y Index: 184

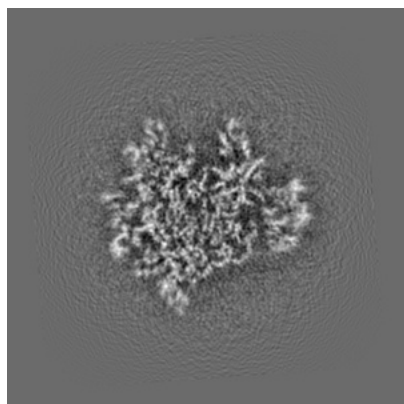


Z Index: 184

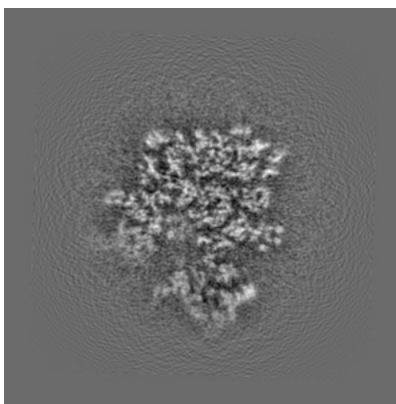
The images above show central slices of the map in three orthogonal directions.

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

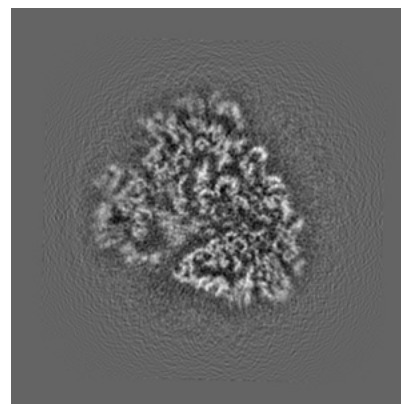
### 6.3.1 Primary map



X Index: 207



Y Index: 187



Z Index: 178

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

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

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

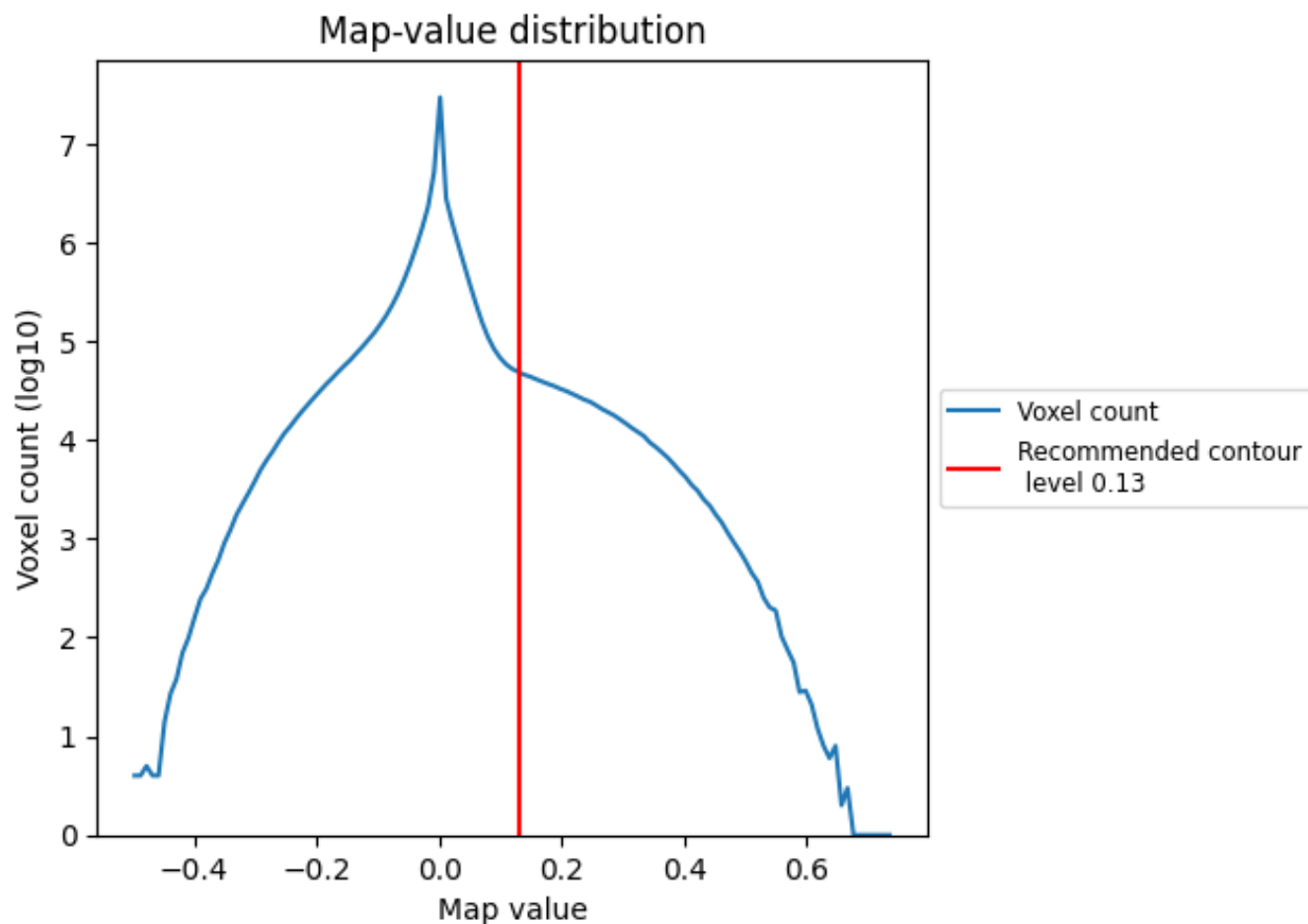
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

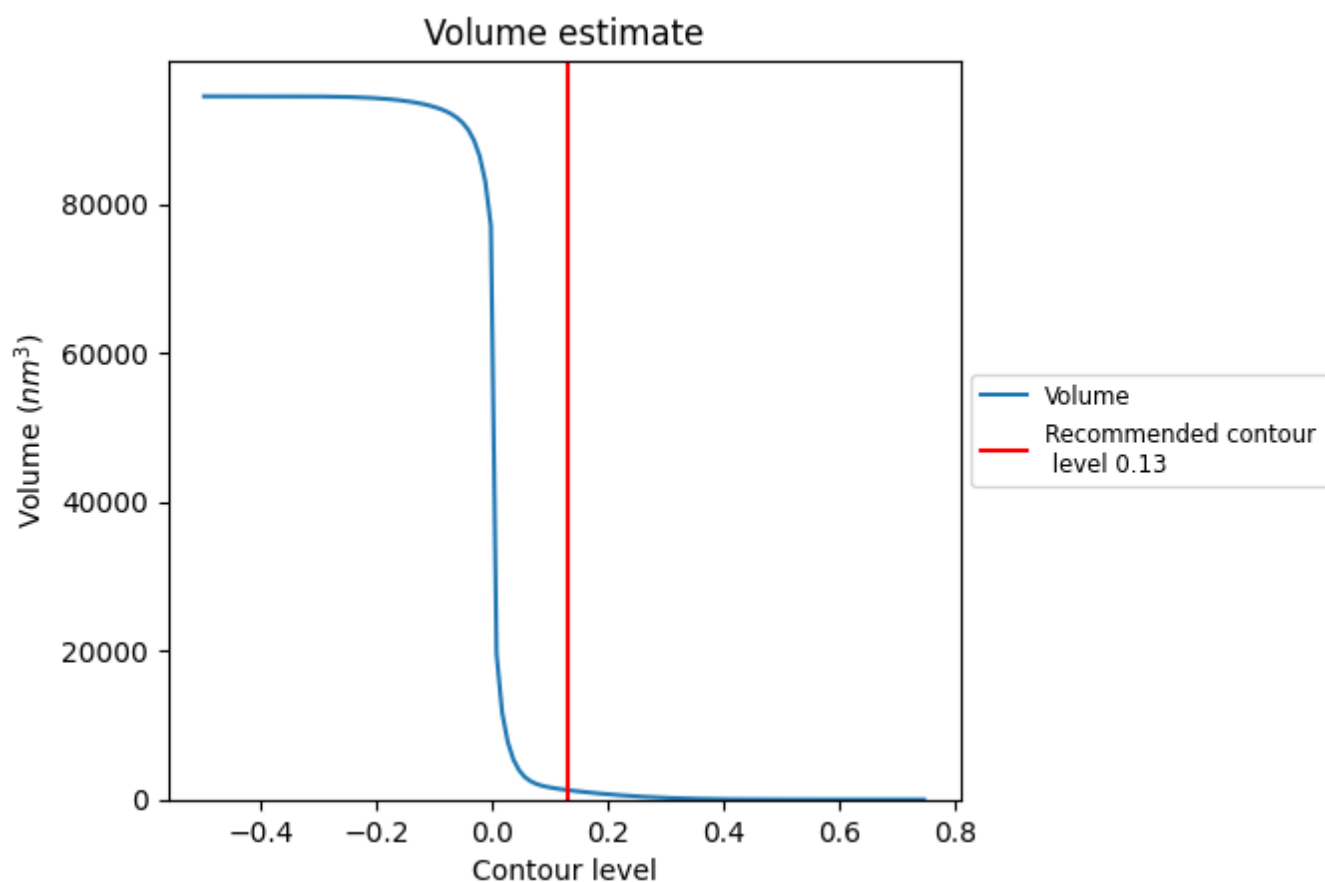
This section contains the results of statistical analysis of the map.

### 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](#)

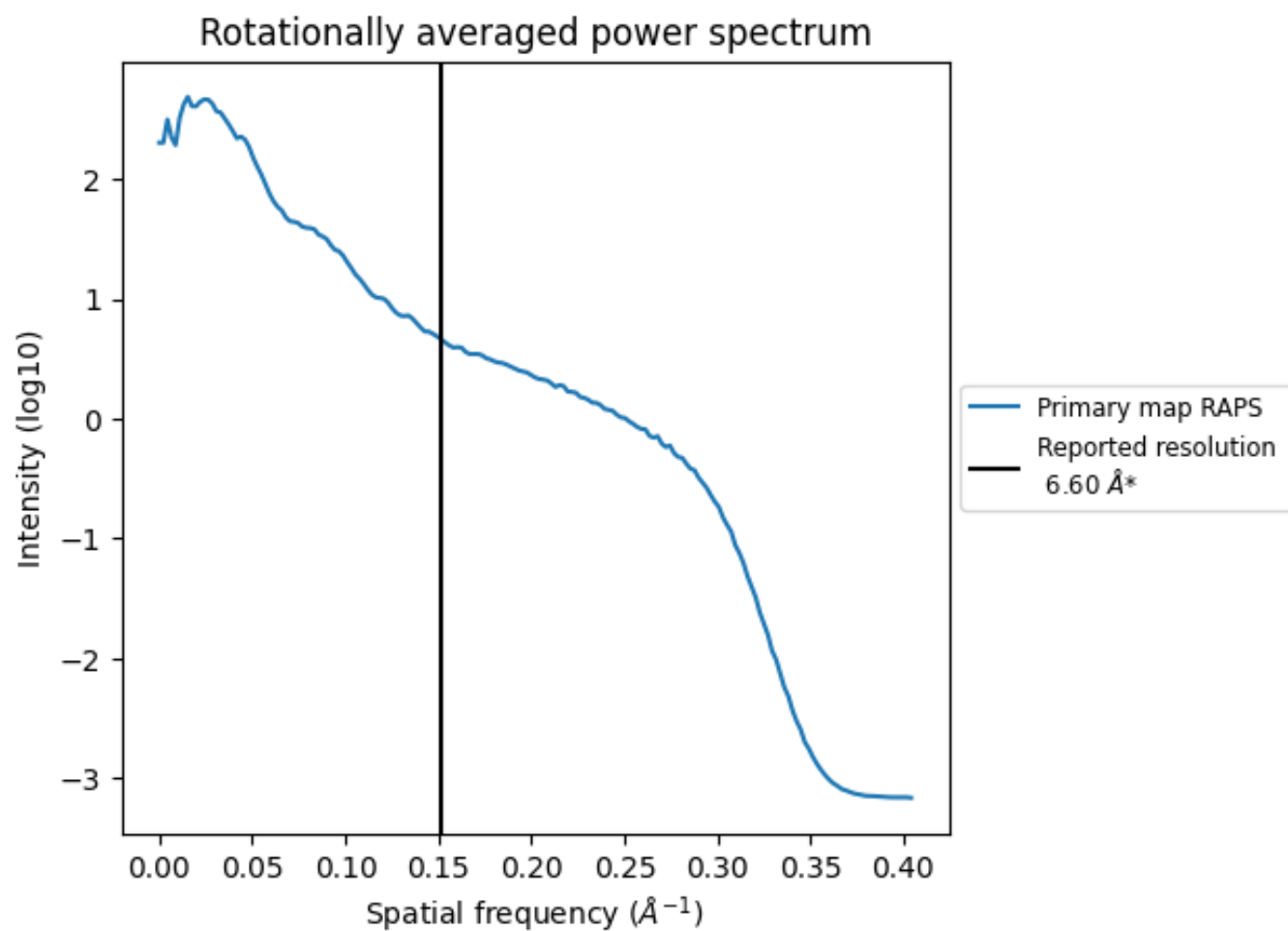


The volume at the recommended contour level is 1275 nm<sup>3</sup>; this corresponds to an approximate mass of 1152 kDa.

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



### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.152 Å<sup>-1</sup>

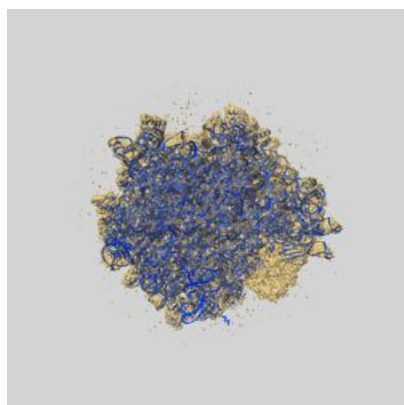
## 8 Fourier-Shell correlation

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

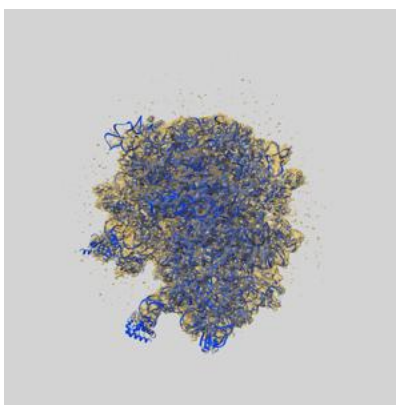
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2009 and PDB model 4V6U. Per-residue inclusion information can be found in [section 3](#) on [page 16](#).

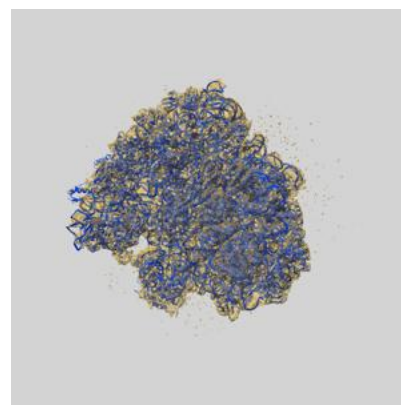
### 9.1 Map-model overlay [i](#)



X



Y



Z

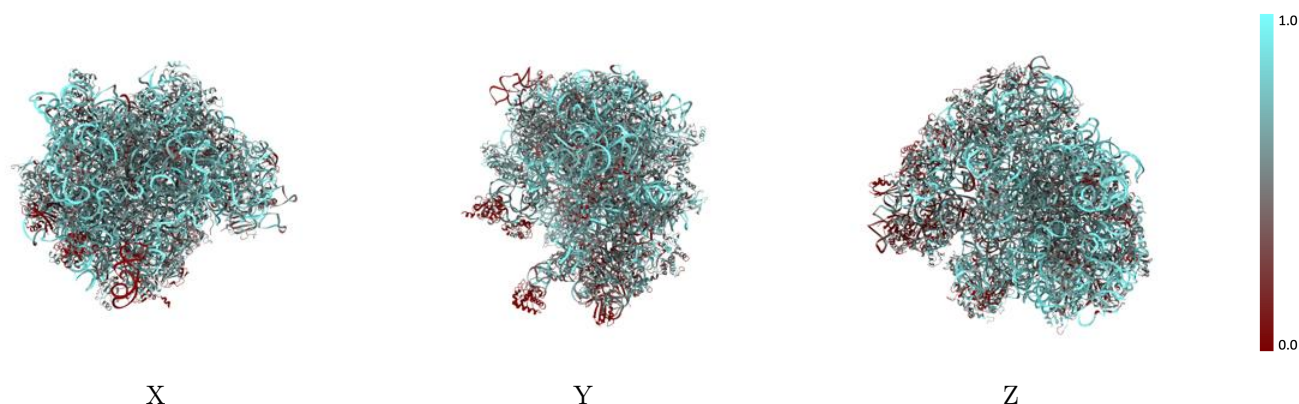
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



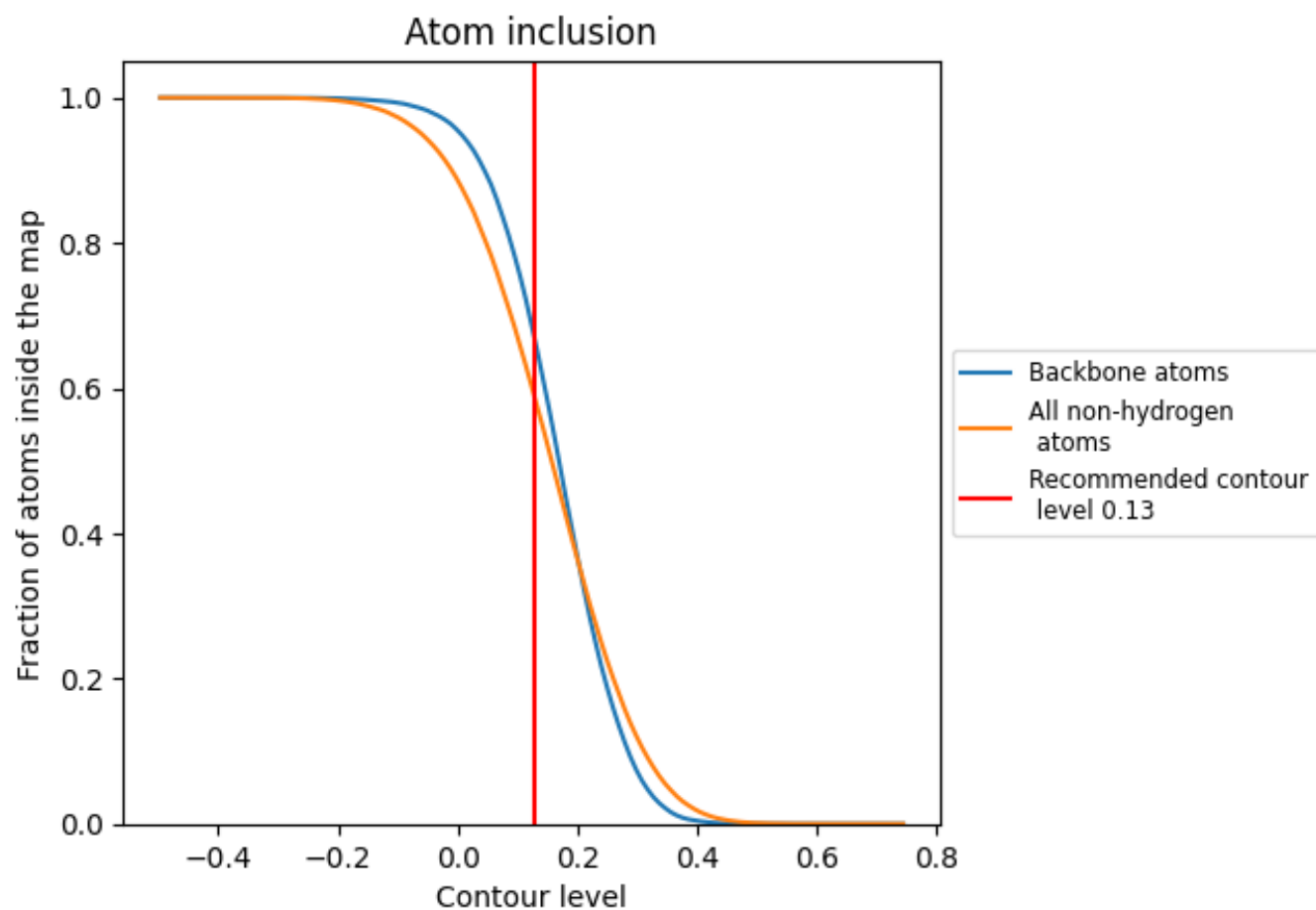
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 66% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary













































































The table lists the average atom inclusion at the recommended contour level (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5849	 0.1970
A0	 0.5348	 0.1690
A1	 0.5731	 0.1410
A2	 0.6951	 0.2250
A3	 0.0388	 0.0200
A9	 0.6783	 0.2060
AA	 0.5368	 0.1380
AB	 0.4356	 0.1460
AC	 0.4006	 0.1390
AD	 0.4182	 0.1260
AE	 0.3493	 0.1190
AF	 0.3928	 0.1500
AG	 0.3915	 0.0820
AH	 0.2889	 0.0810
AI	 0.4307	 0.1390
AJ	 0.4062	 0.1520
AK	 0.1950	 0.1020
AL	 0.1400	 0.0710
AM	 0.4444	 0.1560
AN	 0.3731	 0.1420
AO	 0.3785	 0.1050
AP	 0.2358	 0.0950
AQ	 0.4921	 0.1430
AR	 0.4237	 0.1750
AS	 0.4262	 0.1170
AT	 0.3557	 0.0990
AU	 0.2278	 0.0850
AV	 0.3491	 0.1020
AW	 0.5255	 0.1240
AX	 0.3956	 0.1410
AY	 0.0980	 0.0320
B1	 0.7262	 0.2500
B3	 0.7984	 0.2180
B4	 0.1961	 0.1010
B5	 0.5635	 0.1560



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Chain	Atom inclusion	Q-score
B6	 0.0171	 0.0390
BA	 0.2176	 0.0480
BB	 0.4494	 0.2180
BC	 0.4304	 0.1680
BD	 0.4160	 0.1590
BE	 0.4775	 0.1130
BF	 0.5643	 0.1920
BG	 0.5603	 0.1520
BH	 0.2308	 0.0610
BI	 0.4295	 0.1670
BJ	 0.4342	 0.2070
BK	 0.5251	 0.1440
BL	 0.3961	 0.1390
BM	 0.3396	 0.1790
BN	 0.4502	 0.1800
BO	 0.4606	 0.1510
BP	 0.4882	 0.1710
BQ	 0.4513	 0.1440
BR	 0.3653	 0.1810
BS	 0.4527	 0.1730
BT	 0.4692	 0.1790
BU	 0.4496	 0.1560
BV	 0.4302	 0.1440
BW	 0.5401	 0.1570
BY	 0.4660	 0.1800
BZ	 0.5685	 0.1650
Ba	 0.4979	 0.1790
Bb	 0.3983	 0.1540
Bc	 0.3919	 0.1610
Bd	 0.3206	 0.1200
Be	 0.2931	 0.1250
Bf	 0.3294	 0.1430
Bg	 0.3672	 0.1280
Bh	 0.3318	 0.0850
Bi	 0.5062	 0.2030
Bj	 0.3952	 0.1330
Bk	 0.1443	 0.0340
Bl	 0.5093	 0.1590