



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 09:58 AM UTC

PDB ID : 4V6U / pdb_00004v6u
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

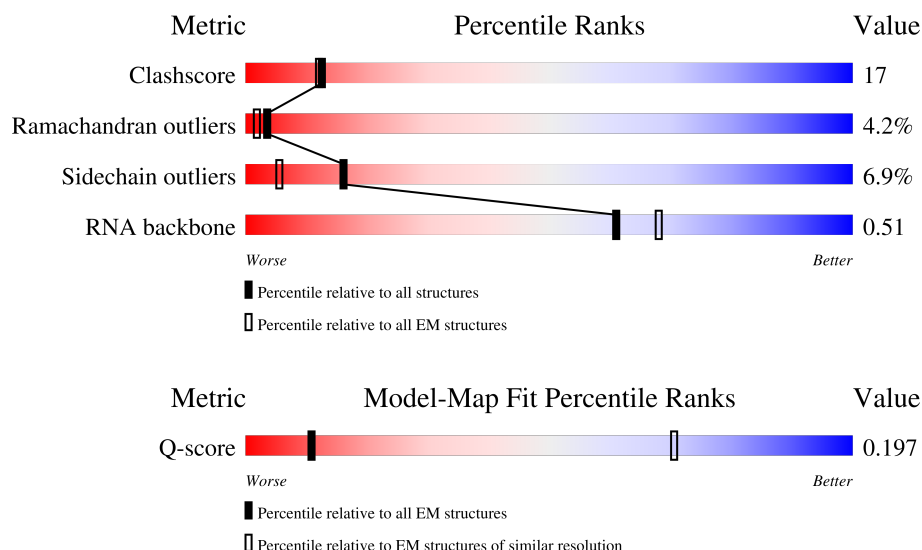
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	531 (6.10 - 7.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AQ	158	
2	AK	135	
3	AI	130	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	AG	125	
5	AW	63	
6	AC	210	
7	AB	202	
8	AR	113	
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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
27	A0	76	
28	AV	99	
28	B6	99	
29	AL	102	
30	AU	150	
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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
50	BV	66	
51	Bj	94	
52	BB	239	
53	BD	255	
54	BF	184	
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		

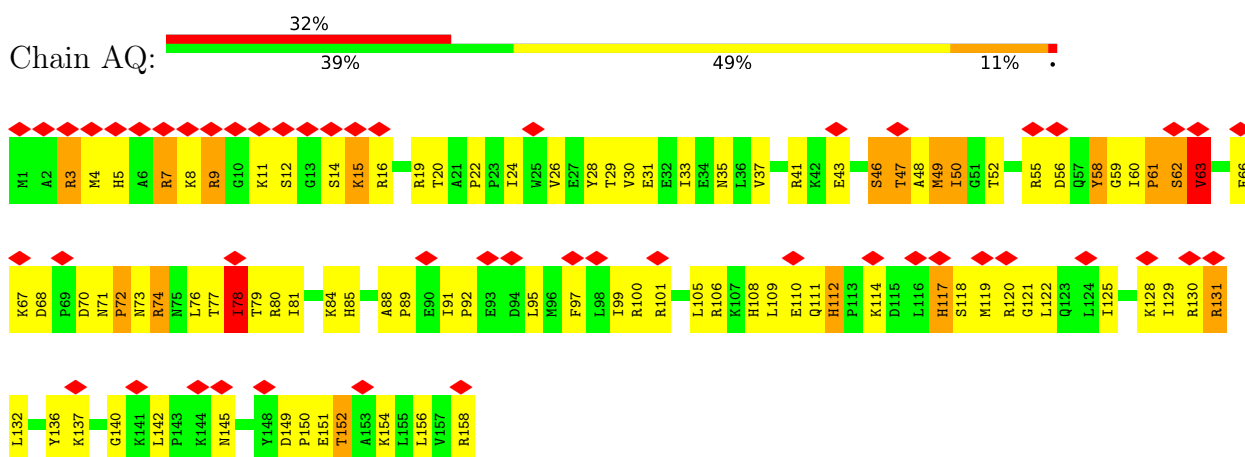
- Molecule 68 is a RNA chain called 5S rRNA.

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

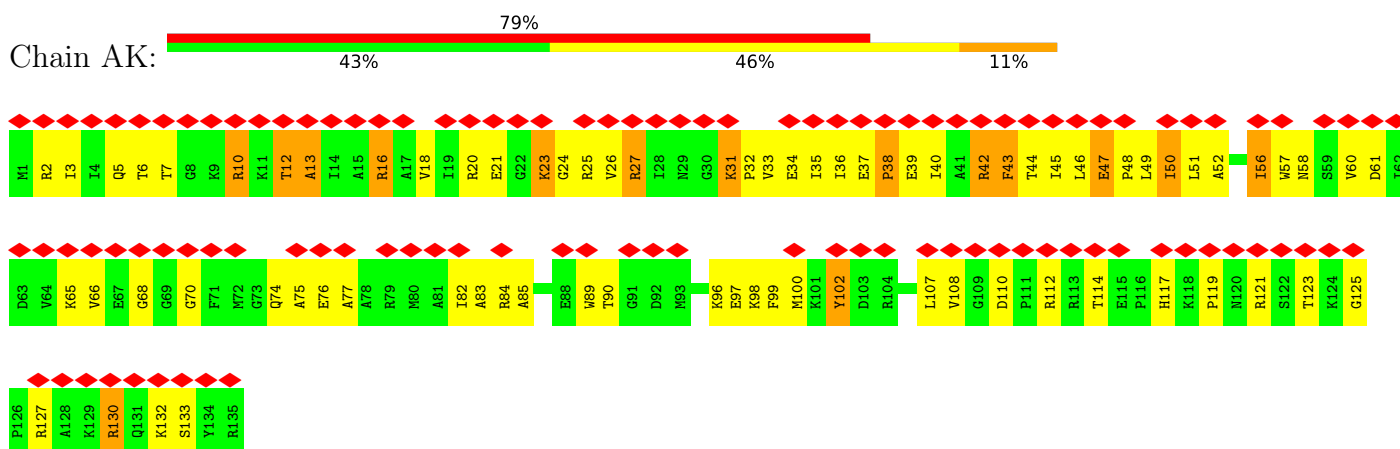
3 Residue-property plots

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.

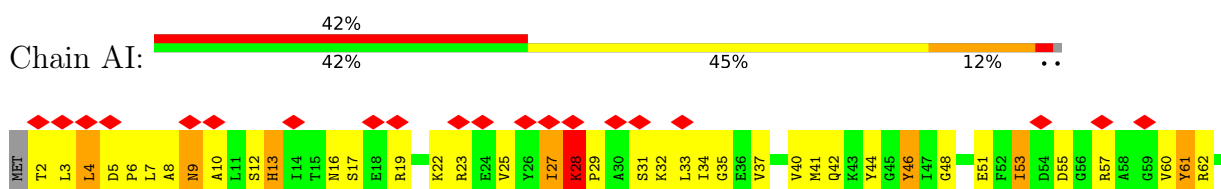
- Molecule 1: 30S ribosomal protein S15P/S13e

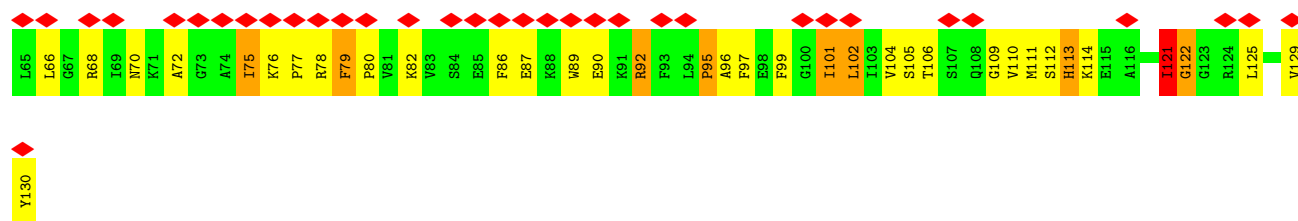


- Molecule 2: 30S ribosomal protein S9P

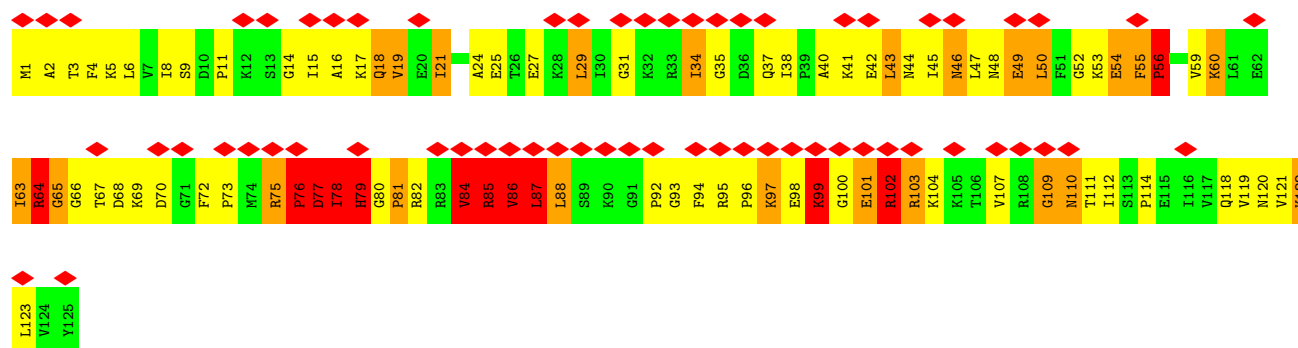


- Molecule 3: 30S ribosomal protein S8P





• Molecule 4: 30S ribosomal protein S6e



• Molecule 5: 30S ribosomal protein S27e

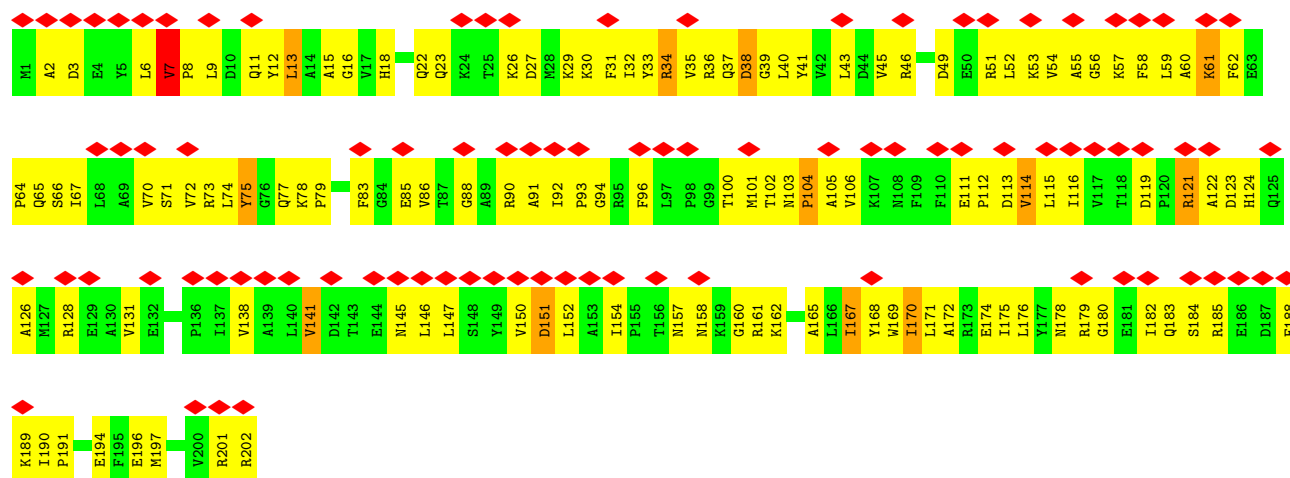


• Molecule 6: 30S ribosomal protein S3P

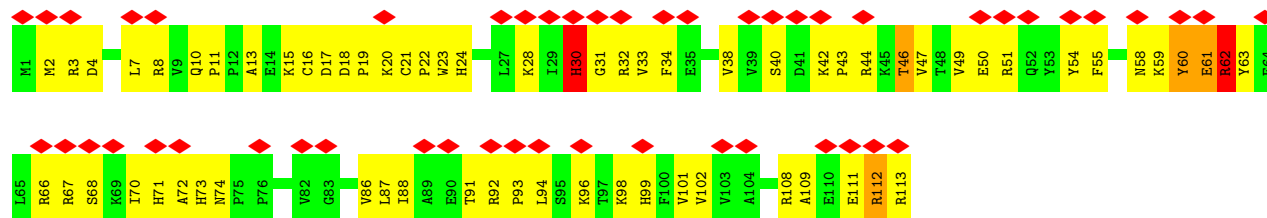


• Molecule 7: 30S ribosomal protein S2P





• Molecule 8: 30S ribosomal protein S17P



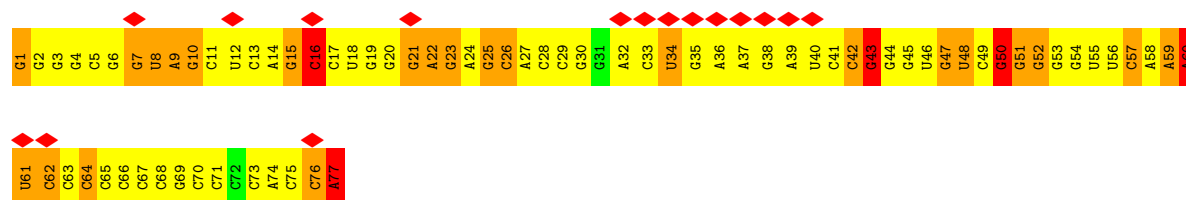
• Molecule 9: unknown 30S ribosomal protein SX



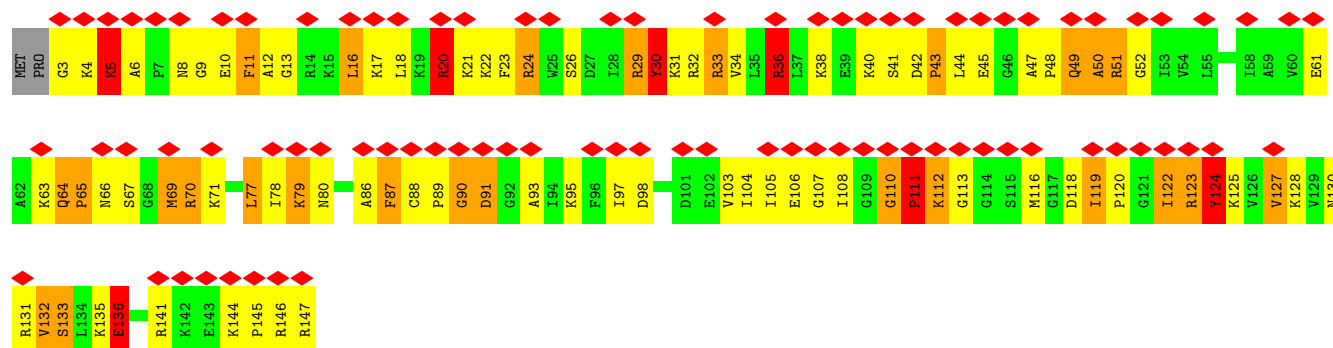
• Molecule 10: 30S ribosomal protein S4P



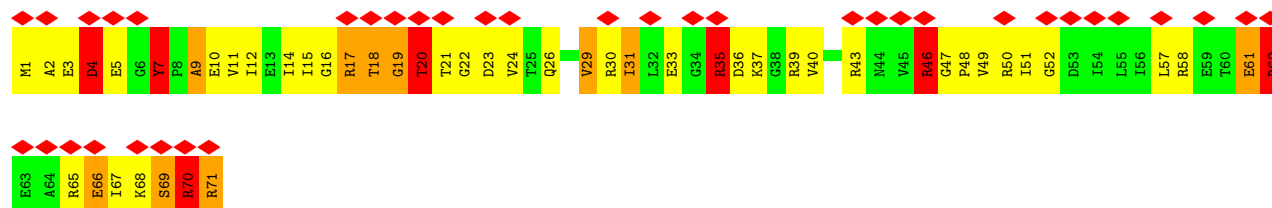
• Molecule 11: E-tRNA



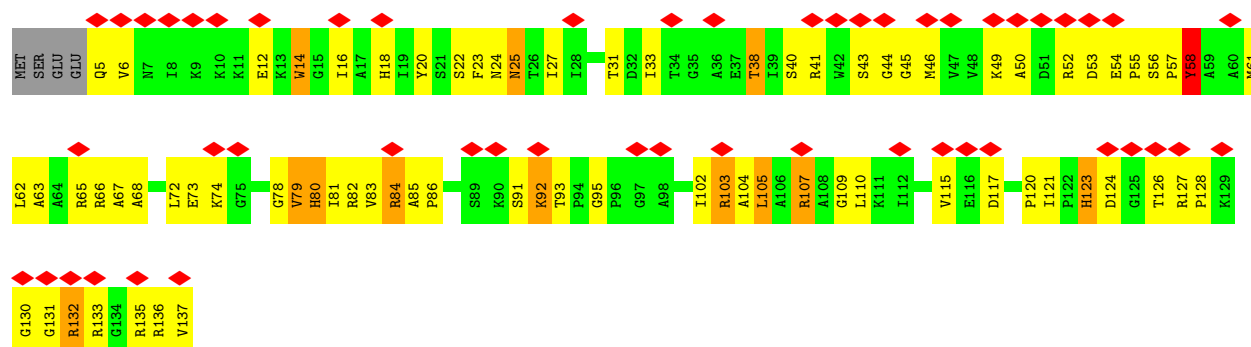
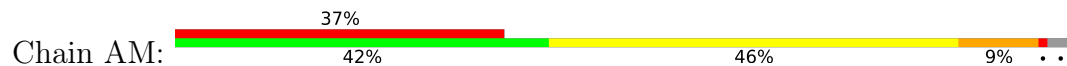
• Molecule 12: 30S ribosomal protein S12P



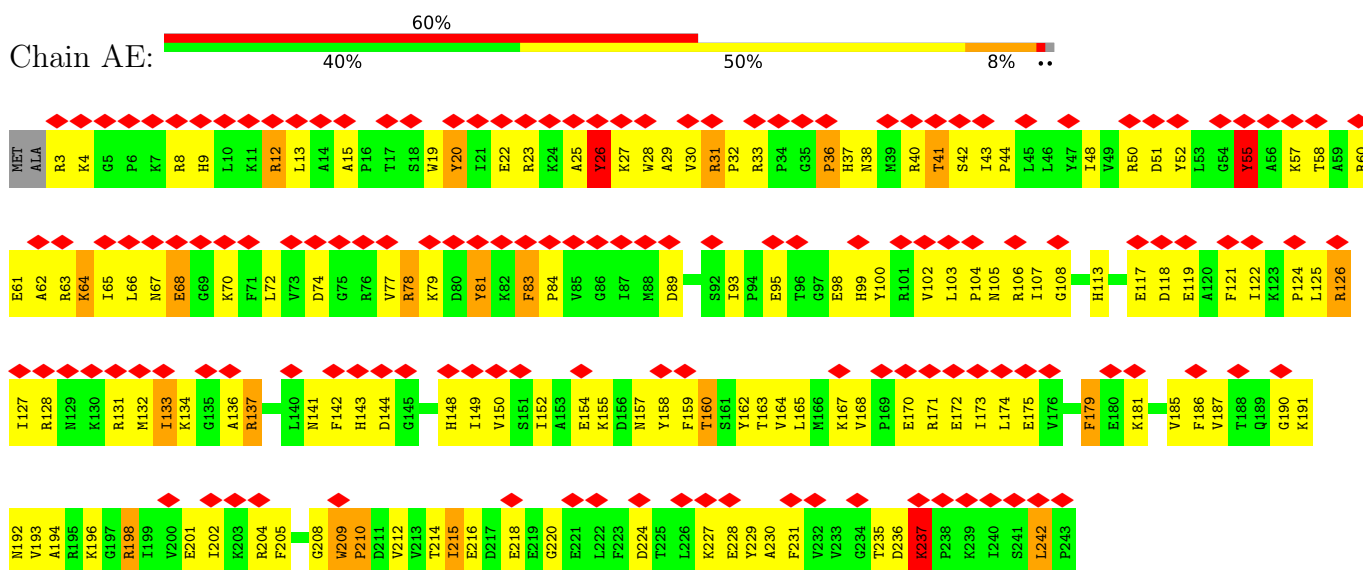
• Molecule 13: 30S ribosomal protein S28e



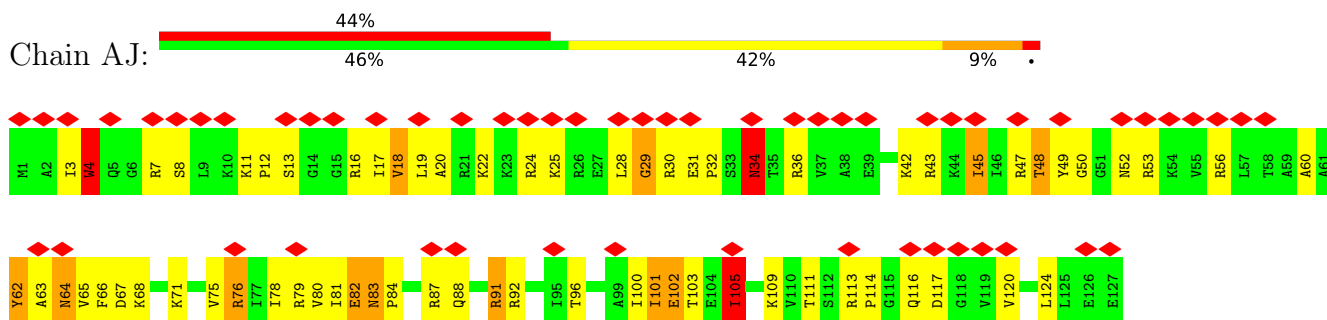
• Molecule 14: 30S ribosomal protein S11P



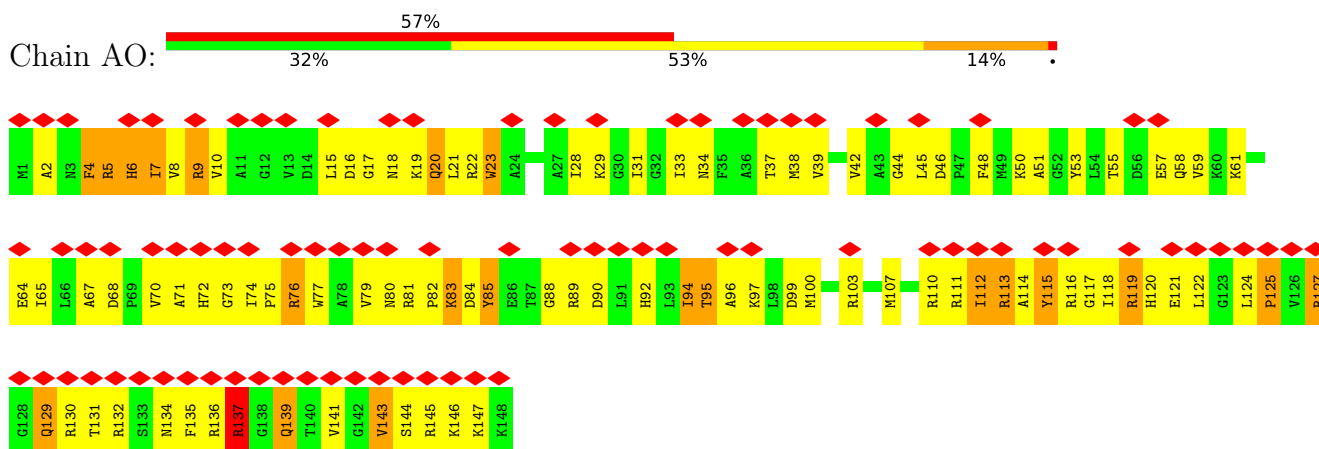
• Molecule 15: 30S ribosomal protein S4e



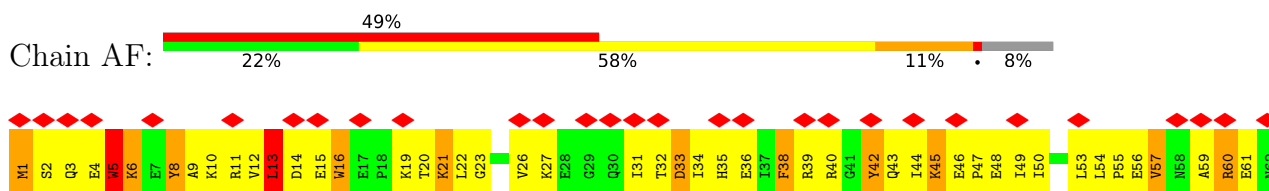
• Molecule 16: 30S ribosomal protein S8e

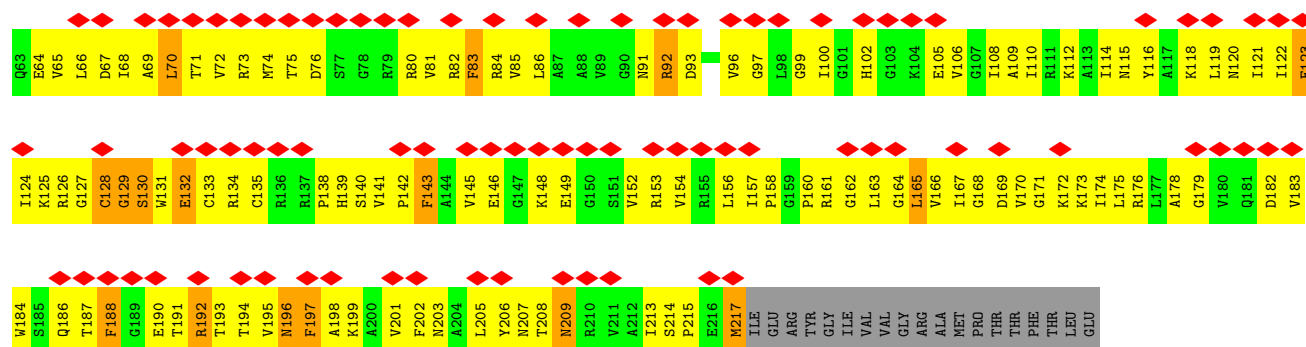


• Molecule 17: 30S ribosomal protein S13P

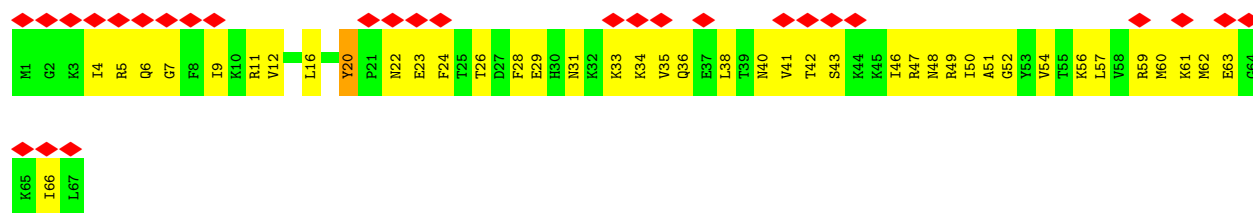
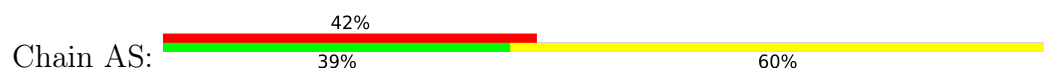


• Molecule 18: 30S ribosomal protein S5P

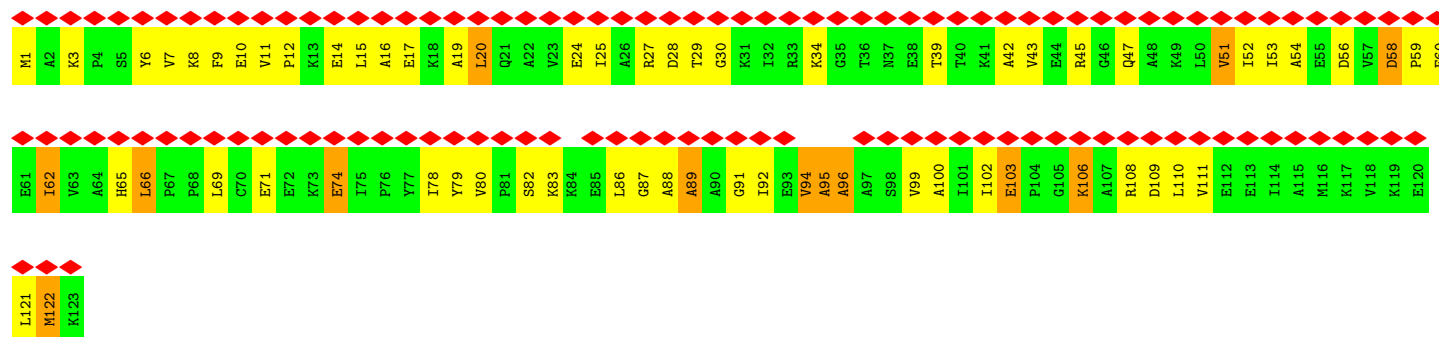




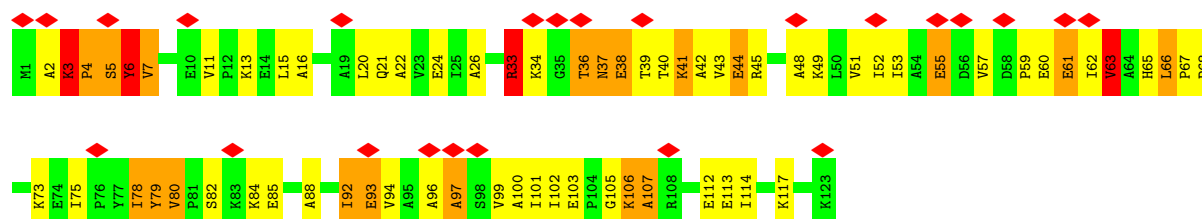
• Molecule 19: 30S ribosomal protein S17e



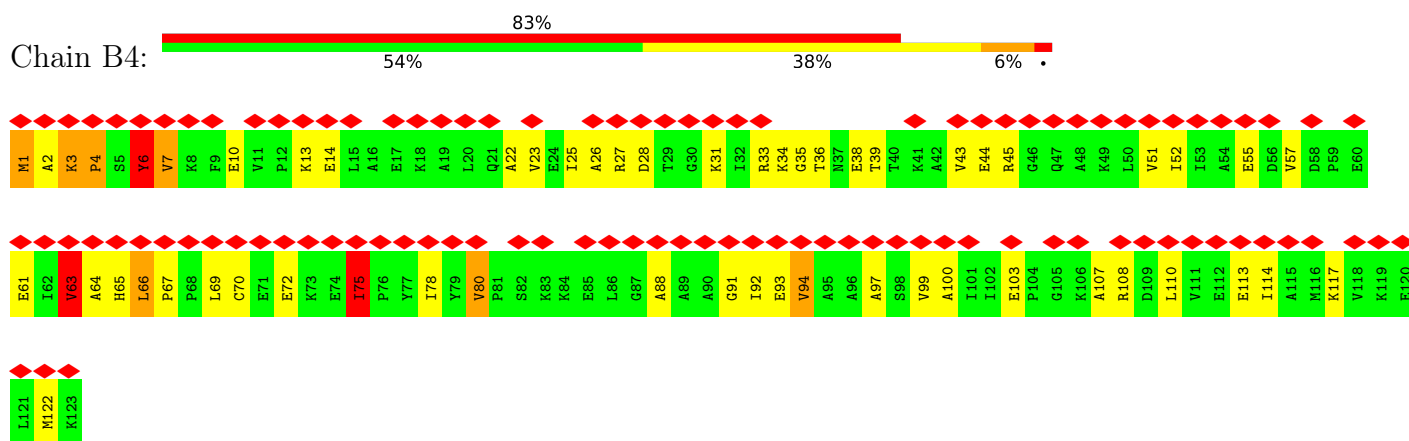
• Molecule 20: 50S ribosomal protein L7Ae



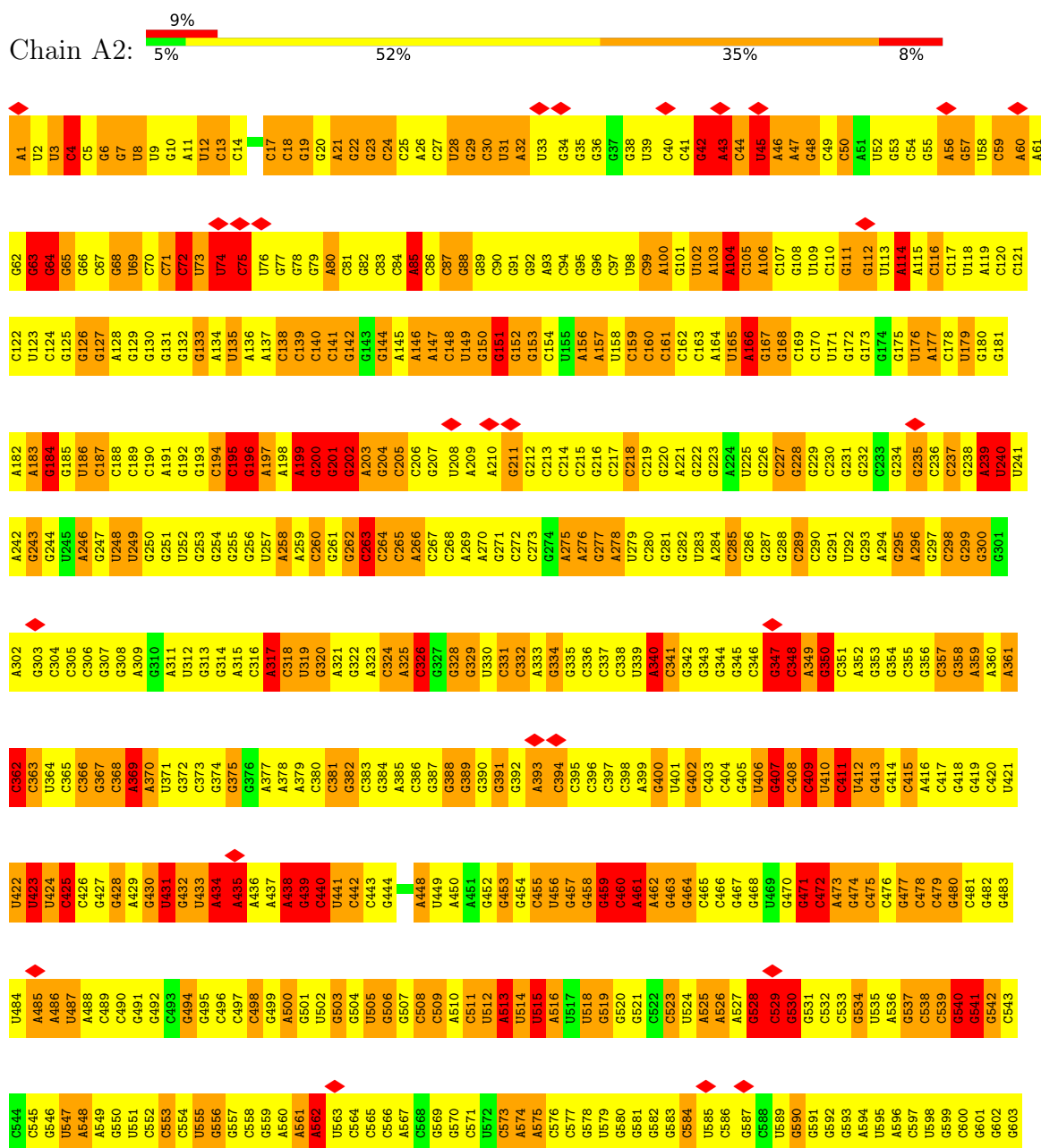
• Molecule 20: 50S ribosomal protein L7Ae



• Molecule 20: 50S ribosomal protein L7Ae



• Molecule 21: 16S rRNA



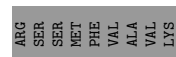
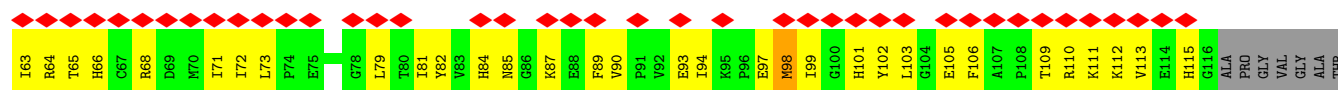
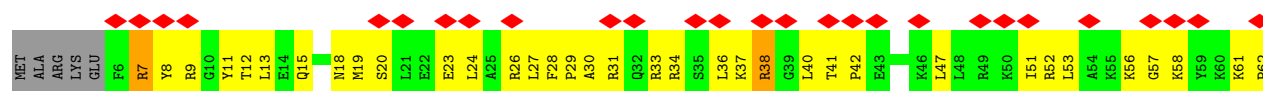
G1387	G1388	G1389	G1390	G1391	G1392	G1393	G1394	G1395	G1396	G1397	G1398	G1399	A1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	G1410	G1411	A1412	G1413	U1414	U1415	U1416	U1417	G1418	G1419	U1420	G1421	G1422	A1423	G1424	G1425	G1426	G1427	G1428	G1429	G1430	G1431	U1432	U1433	G1434	G1435	U1436	G1437	A1438	G1439	G1440	G1441	G1442	G1443	G1444	A1445	G1446			
C1327	G1328	G1329	G1330	G1331	G1332	G1333	G1334	A1335	G1336	G1337	G1338	G1339	U1340	C1341	C1342	C1343	U1344	G1345	G1346	U1347	U1348	U1349	U1350	U1351	G1352	C1353	A1354	G1355	G1356	A1357	U1358	G1359	U1360	G1361	G1362	C1363	G1364	G1365	U1366	G1367	G1368	G1369	G1370	U1371	C1372	A1373	G1374	G1375	G1376	G1377	A1378	G1379	G1380	G1381	G1382	A1383	G1384	U1385	C1386			
A1266	G1267	G1268	G1269	G1270	A1208	G1271	G1272	G1273	C1274	G1275	G1276	G1277	A1278	A1279	C1280	U1281	G1282	G1283	C1284	G1285	G1286	G1287	G1288	G1289	U1290	A1291	A1292	G1293	G1294	G1295	U1296	G1297	G1298	U1299	A1300	U1301	A1240	U1241	C1242	C1243	G1244	C1245	U1246	A1247	A1248	A1249	C1250	C1251	C1252	G1253	C1254	C1255	C1256	U1257	U1258	A1259	G1260	U1261	U1262	A1263	G1264	G1265
G1146	G1147	G1148	G1149	G1150	A1151	G1152	G1153	G1154	U1155	A1156	G1157	G1158	U1159	C1160	A1161	G1162	U1163	A1164	U1165	G1166	G1167	G1168	G1169	C1170	G1171	A1172	A1173	A1174	G1175	C1176	C1177	C1178	C1179	G1180	G1181	G1182	C1183	U1184	A1185	G1186	A1187	C1188	G1189	G1190	G1191	C1192	G1193	C1194	U1195	A1196	C1197	A1198	A1199	U1200	G1201	G1202	G1203	G1204	G1205			
C1086	C1087	U1088	C1089	C1090	C1091	G1092	U1093	U1094	C1095	G1096	G1097	G1098	A1099	G1100	G1101	A1102	G1103	G1104	C1105	A1106	C1107	U1108	C1109	U1110	G1111	G1112	G1113	G1114	G1115	G1116	A1117	C1118	U1119	G1120	C1121	C1122	G1123	G1124	C1125	G1126	A1127	U1128	A1129	G1130	C1131	C1132	C1133	G1134	G1135	A1136	G1137	C1138	A1139	A1140	G1141	G1142	G1143	G1144	C1145			
A1026	C1027	G1028	G1029	U1030	G1031	A1032	G1033	G1034	C1035	U1036	C1037	A1038	C1039	A1040	U1041	U1042	U1043	A1044	A1045	U1046	U1047	U1048	U1049	G1050	G1051	U1052	A1053	A1054	C1055	G1056	A1057	G1058	C1059	G1060	A1061	G1062	A1063	C1064	C1065	C1066	G1067	C1068	G1069	C1070	C1071	C1072	C1073	C1074	A1075	G1076	U1077	U1078	G1079	C1080	C1081	A1082	G1083	U1084	C1085			
G904	A905	G906	C907	G908	U909	G910	C911	G912	G913	U914	G915	U916	A917	A918	U919	U920	G921	G922	A923	U924	U925	C926	A927	A928	C929	G930	A931	C932	G933	G934	G935	A936	A937	C938	C939	U940	C941	A942	C943	C944	G945	G946	G947	G948	G949	C950	A951	A952	C953	G954	G955	G956	C957	G958	G959	A960	U961	A963				
A964	G965	G966	C967	G968	A969	G970	G971	G972	U973	G974	A975	A976	G977	G978	U979	U980	G981	U982	G983	G984	C985	G986	G987	A988	C989	G990	G991	G992	C993	G994	G995	A996	G997	G998	G999	G1000	A1001	G1002	G1003	U1004	G1005	C1006	A1007	U1008	G1009	G1010	C1011	C1012	G1013	G1016	U1017	C1018	A1019	G1020	C1021	U1022	G1023	G1024	U1025			
G844	G845	G846	A847	G848	U849	A850	C851	G852	G853	C854	G855	G856	C857	A858	U859	G860	G861	C862	U863	G864	A865	A866	A867	C868	U869	U870	A871	A872	C873	G874	G875	A876	A877	U878	U879	G880	G881	C882	G883	G884	G885	G886	G887	A888	G889	C890	A891	C892	U893	A894	C895	A896	A897	G898	G899	G900	G901	U902	G903			
G784	U785	G786	U787	G788	G789	G790	G791	C792	G793	A794	G795	A796	U797	U798	G799	G800	A801	G802	C803	U804	C805	G806	C807	C808	C809	G810	G811	U812	G813	C814	C815	G816	U817	A818	G819	G820	A821	A822	G823	G824	C825	C826	G827	U828	U829	A830	A831	G832	C833	C834	C835	G836	C837	G838	G839	C840	U841	U842	G843			
C724	C725	G726	G727	G728	G729	G730	A731	G732	C733	G734	A735	A736	C737	G738	G739	G740	A741	U742	U743	A744	G745	A746	G747	U748	C749	G750	C751	G752	G753	G754	U755	A756	G757	U758	C759	C760	U761	G762	G763	C764	U765	G766	G767	A768	A769	U770	A771	G772	C773	A774	G775	C776	G777	G778	G779	C780	U781	A782	G783			
G664	G665	G666	G667	G668	A669	G670	C671	G672	C673	G674	A675	G676	U677	U678	G679	G680	G681	A682	G683	G684	G685	G686	G687	C688	C689	C690	G691	G692	C693	G694	C695	G696	A697	A698	C699	U640	G701	G702	U703	G704	C705	G706	A707	C708	U709	G710	U711	C712	A713	G714	C715	A657	U658	G659	C660	C661	A721	G722				
G604	C605	U606	U607	G608	G609	G610	A611	C612	G613	G614	G615	G616	A617	U618	A619	G620	G621	C622	C623	G624	G625	G626	G627	U628	U629	A630	C631	C632	C633	C634	C635	G636	G637	G638	G639	U640	A641	G642	G643	G644	G645	U646	G647	A648	A649	U651	C652	C653	U654	A655	U656	A657	U658	C659	C660	C661	G662	G663				



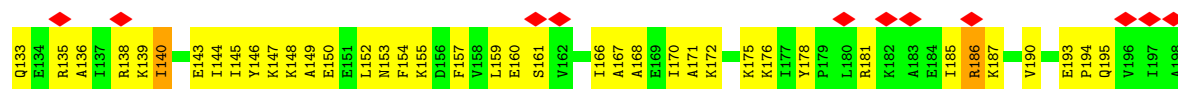
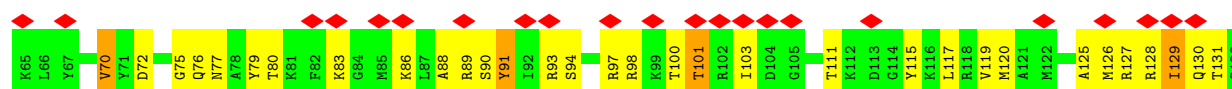
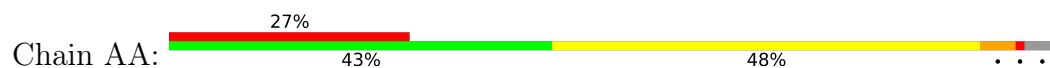
• Molecule 22: 30S ribosomal protein S27ae



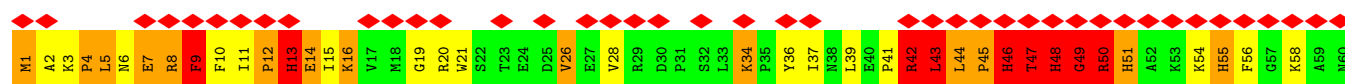
• Molecule 23: 30S ribosomal protein S19P

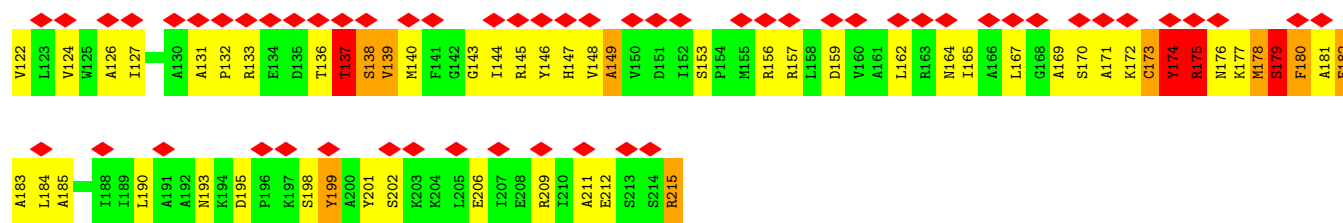


• Molecule 24: 30S ribosomal protein S3Ae

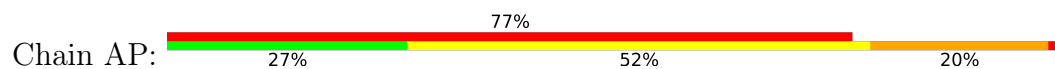


• Molecule 25: 30S ribosomal protein S7P

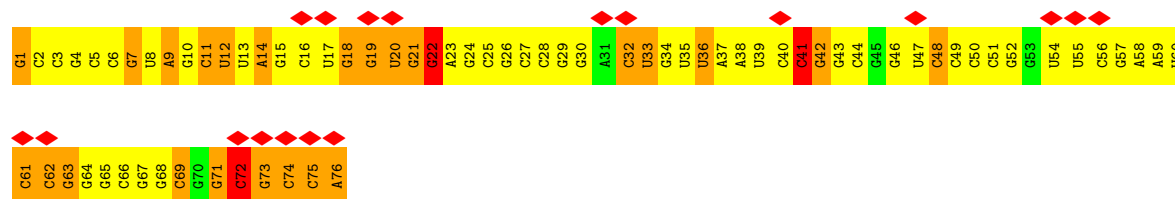




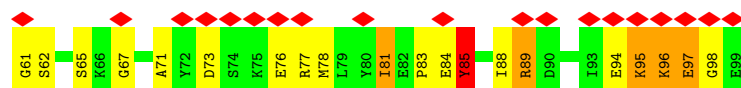
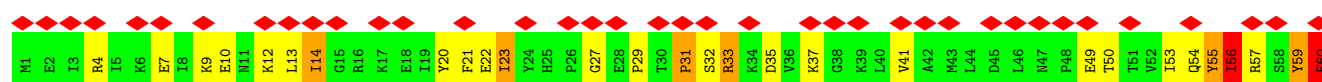
- Molecule 26: 30S ribosomal protein S14P type Z



- Molecule 27: P-tRNA



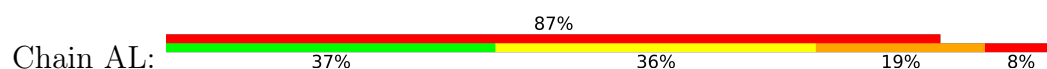
- Molecule 28: 30S ribosomal protein S24e

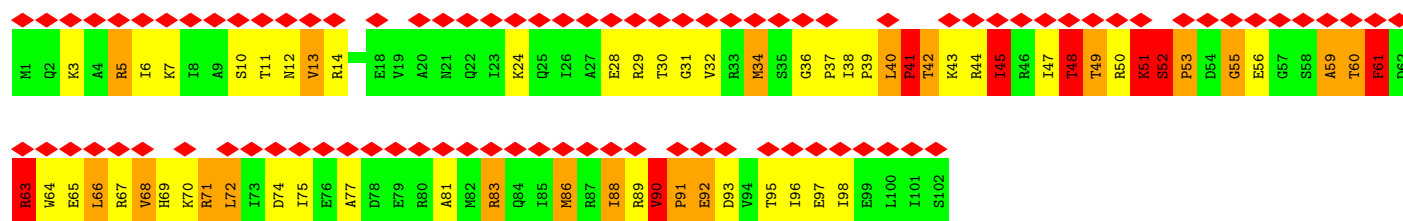


- Molecule 28: 30S ribosomal protein S24e

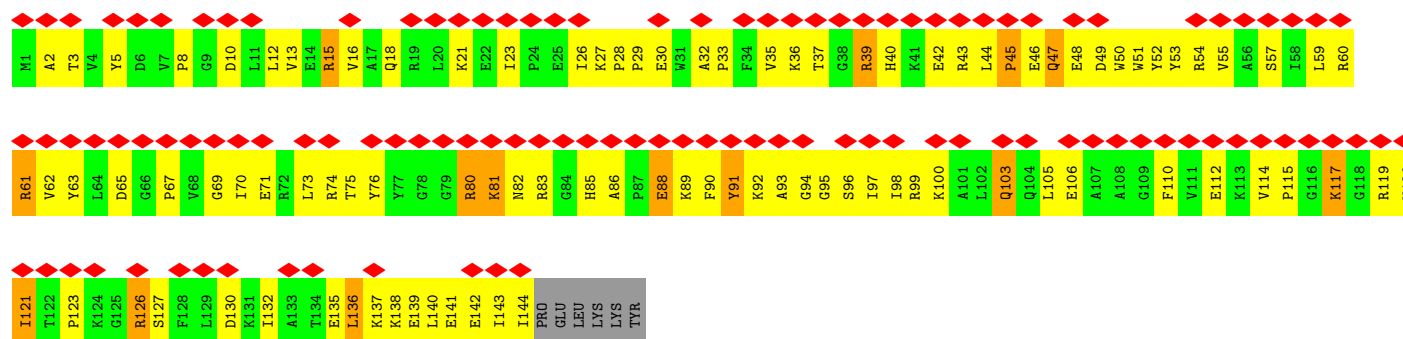
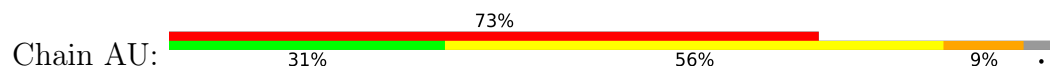


- Molecule 29: 30S ribosomal protein S10P

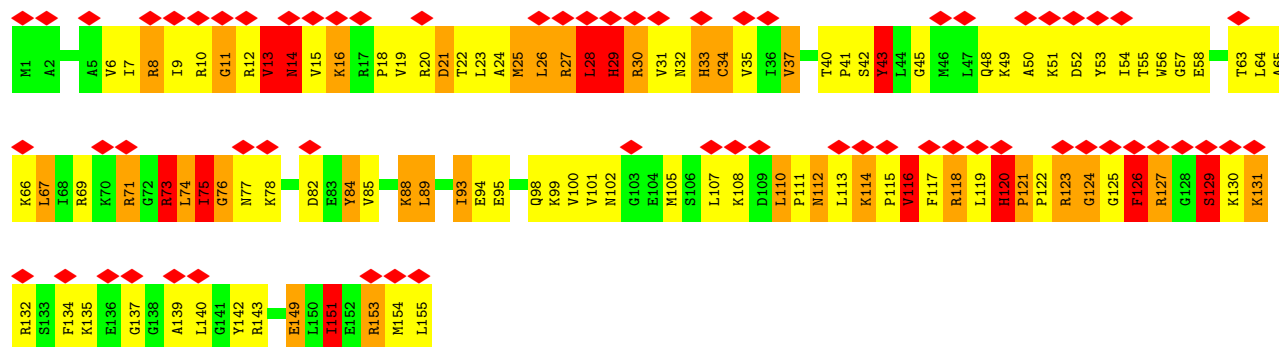




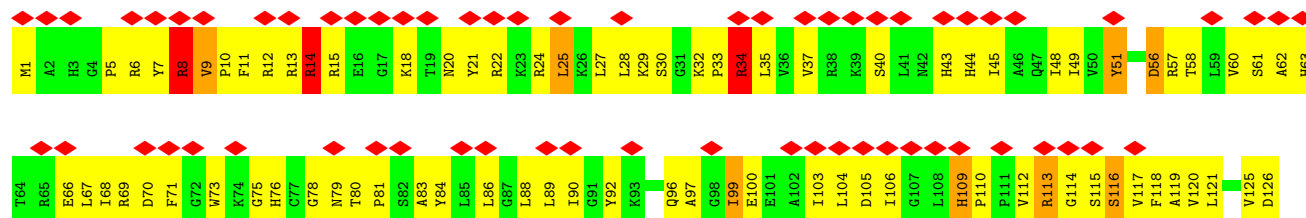
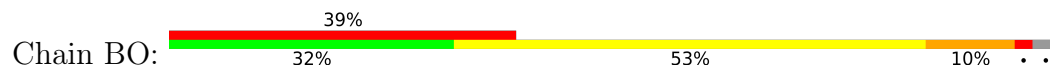
• Molecule 30: SSU ribosomal protein S19E

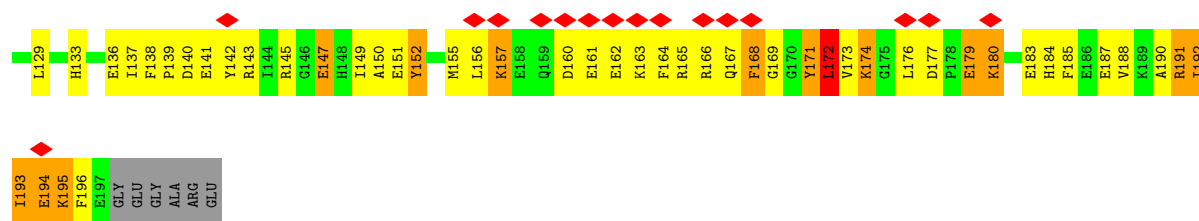


• Molecule 31: 50S ribosomal protein L30P

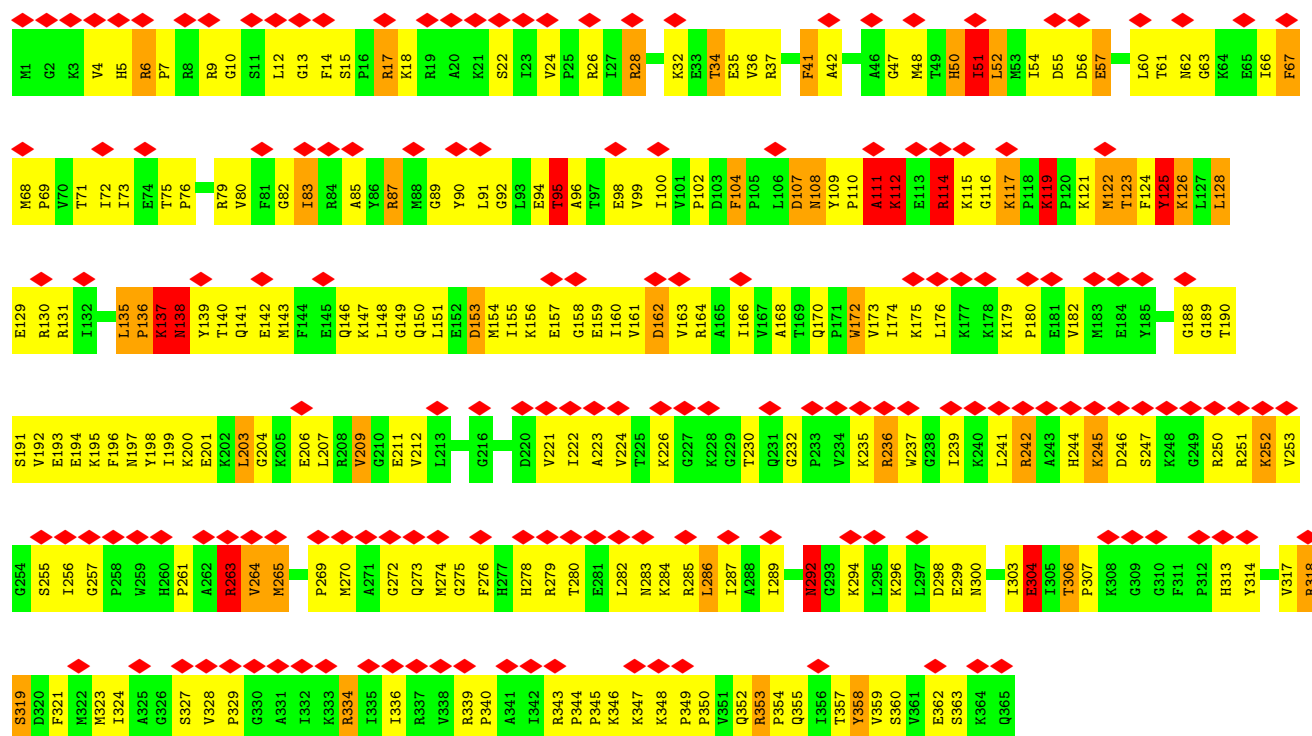
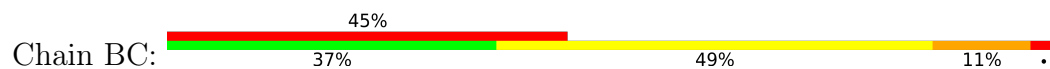


• Molecule 32: 50S ribosomal protein L18P

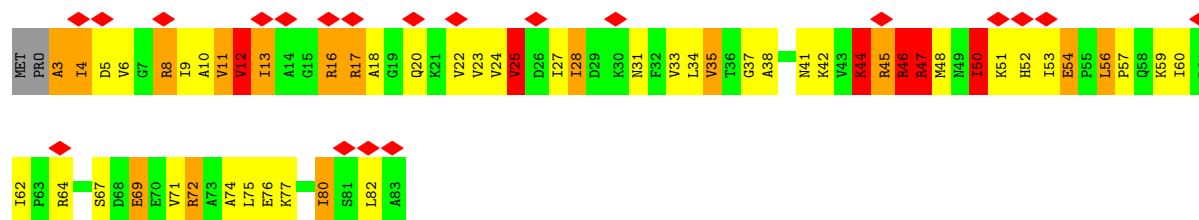




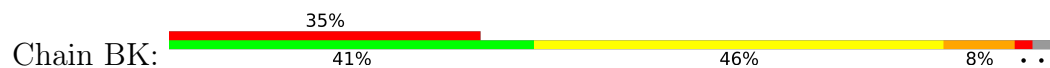
• Molecule 33: 50S ribosomal protein L3P

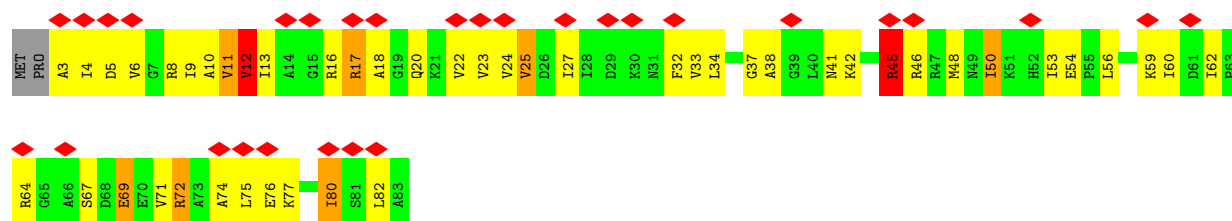


• Molecule 34: 50S ribosomal protein L14e

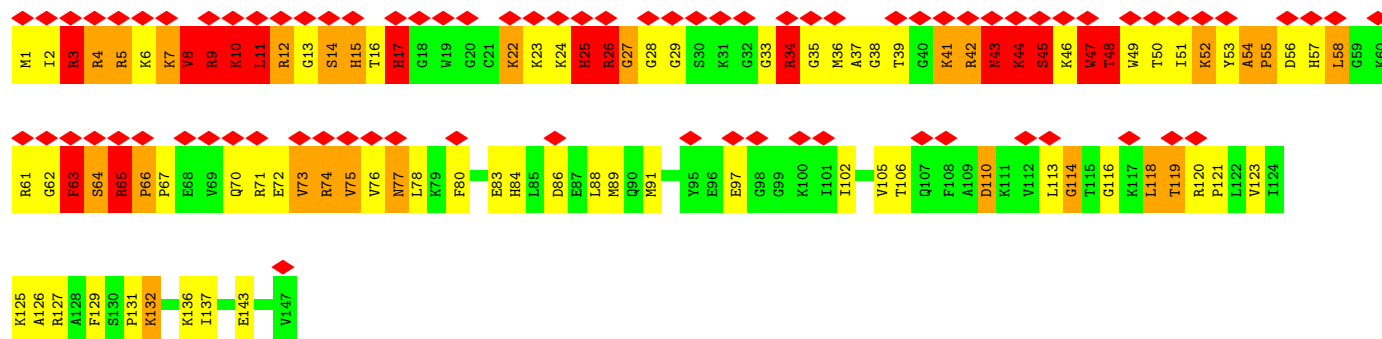


• Molecule 34: 50S ribosomal protein L14e





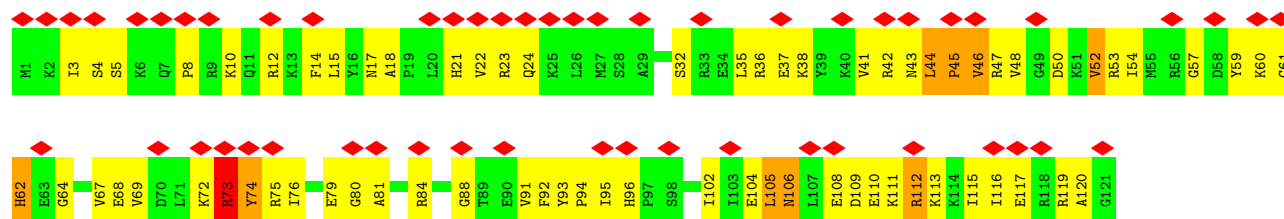
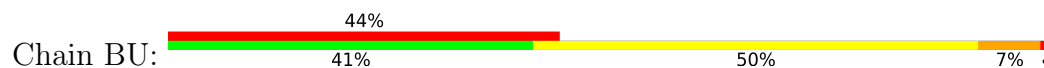
• Molecule 35: 50S ribosomal protein L15P



• Molecule 36: 50S ribosomal protein L39e

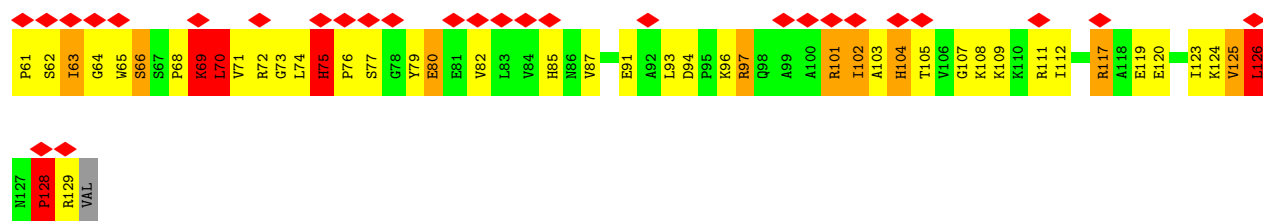


• Molecule 37: 50S ribosomal protein L24P

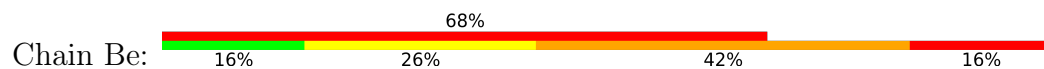


• Molecule 38: 50S ribosomal protein L32e

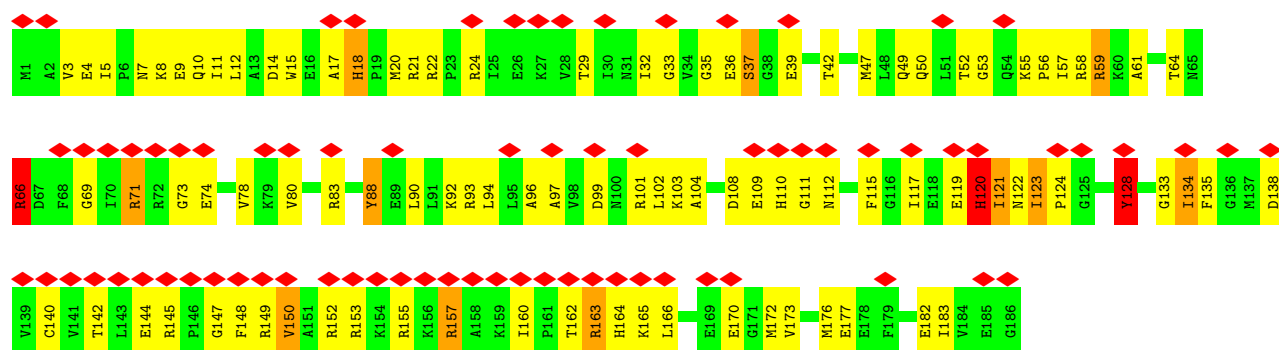
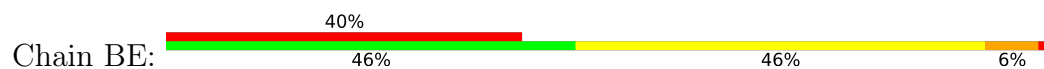




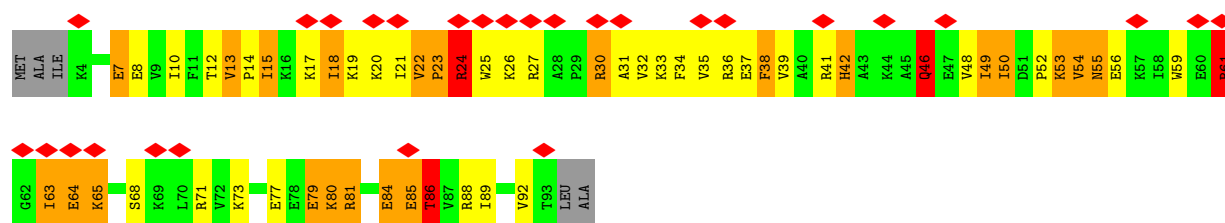
• Molecule 39: 50S ribosomal protein L37e



• Molecule 40: 50S ribosomal protein L5P



• Molecule 41: 50S ribosomal protein L31e

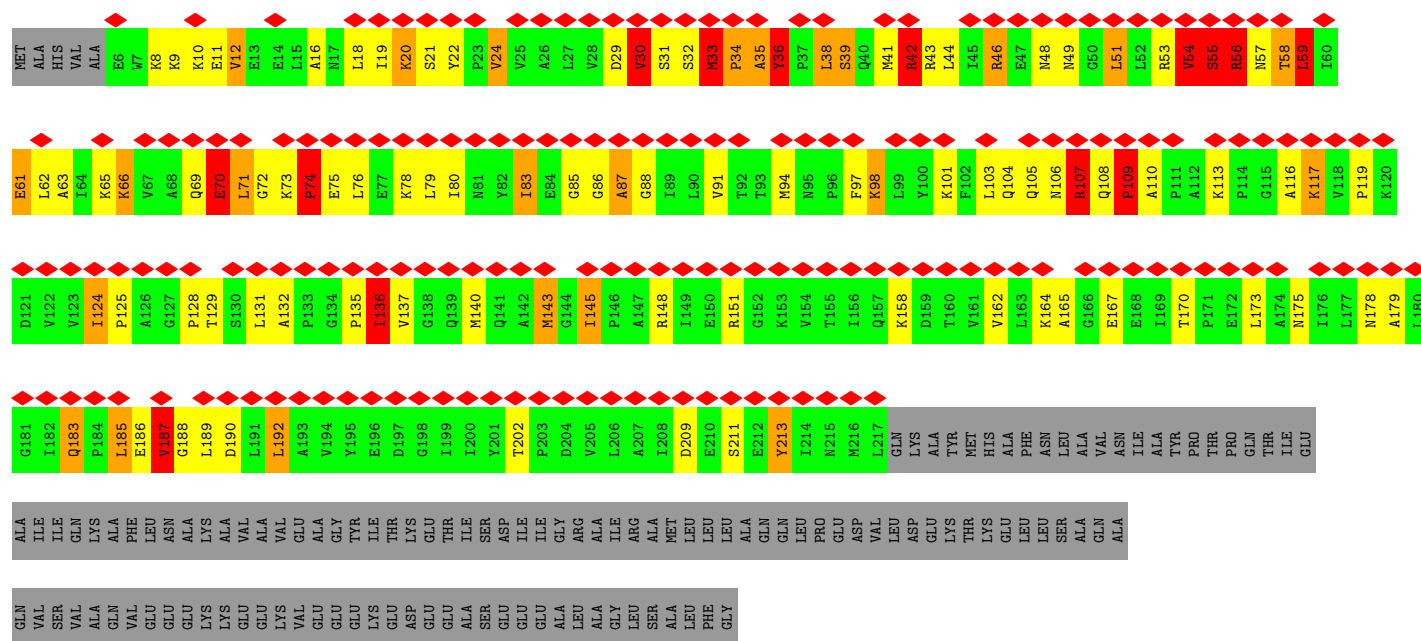
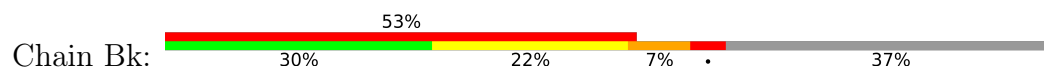


• Molecule 42: 50S ribosomal protein L23P

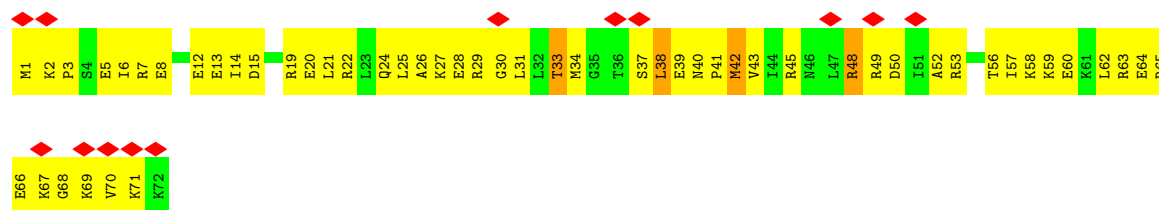




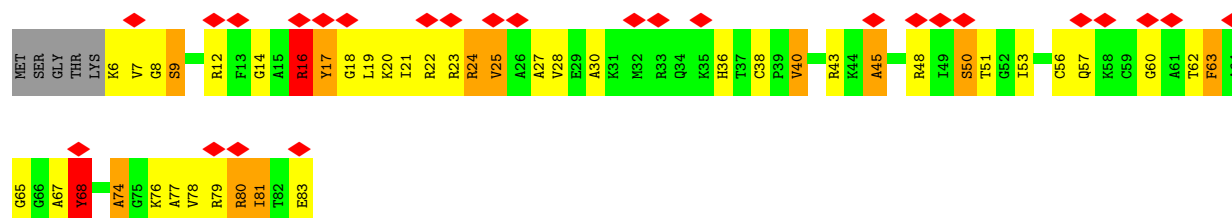
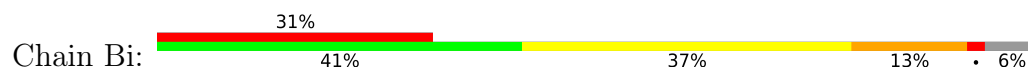
• Molecule 43: Acidic ribosomal protein P0 homolog



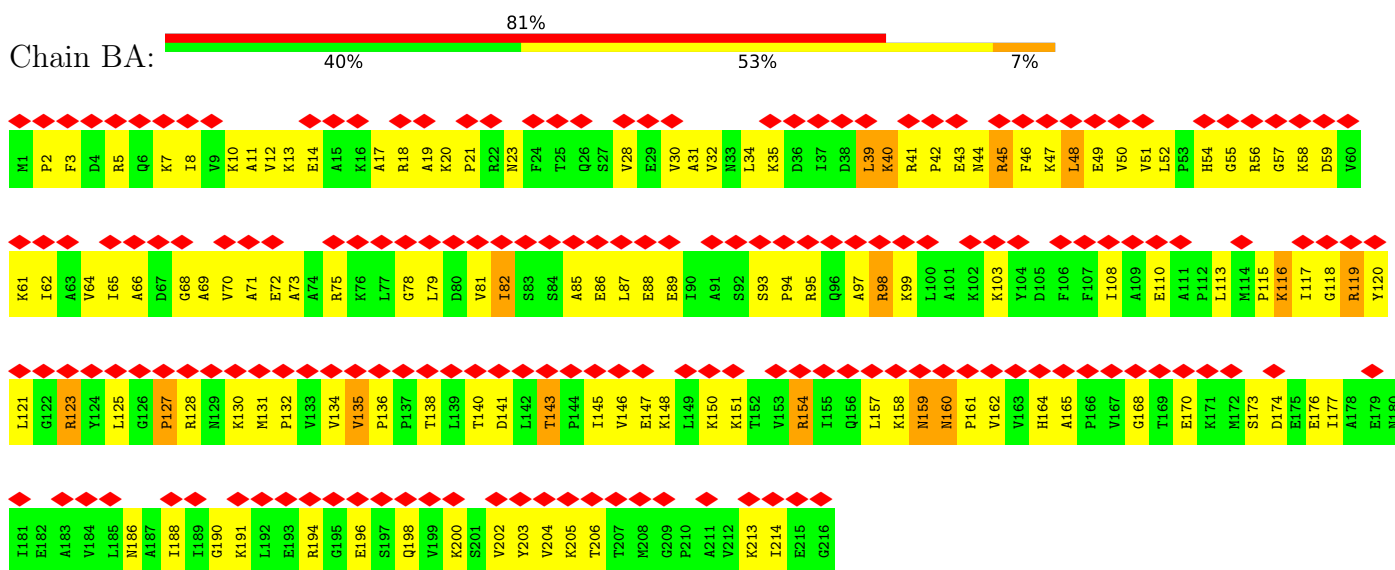
• Molecule 44: 50S ribosomal protein L29P



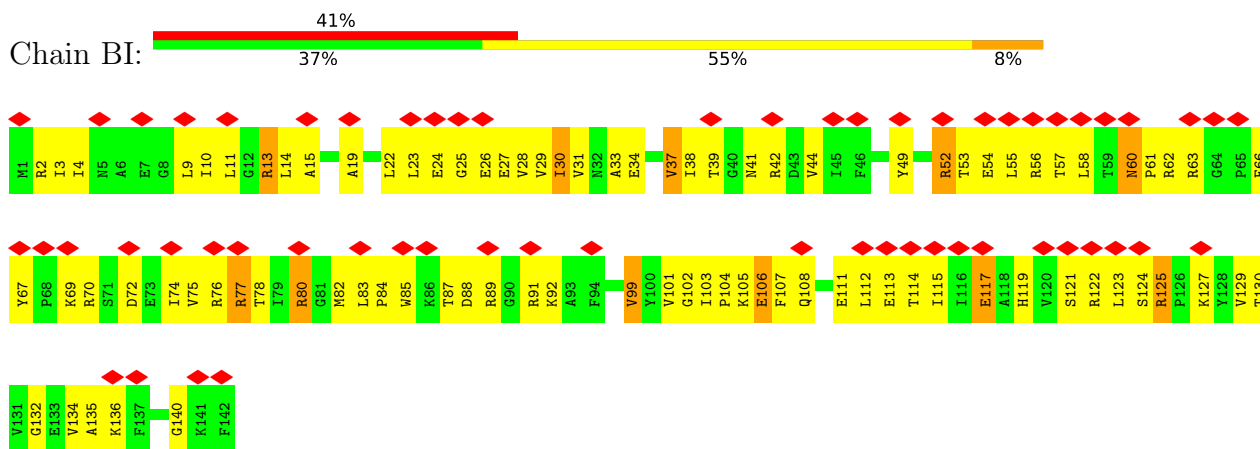
• Molecule 45: 50S ribosomal protein L37Ae



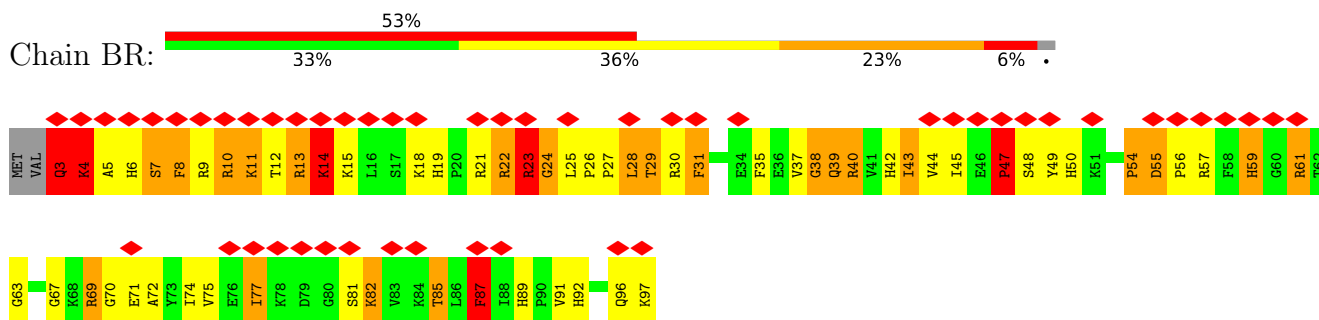
• Molecule 46: 50S ribosomal protein L1P



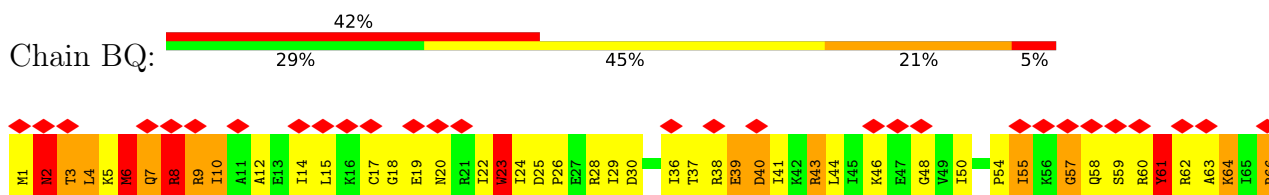
• Molecule 47: 50S ribosomal protein L13P

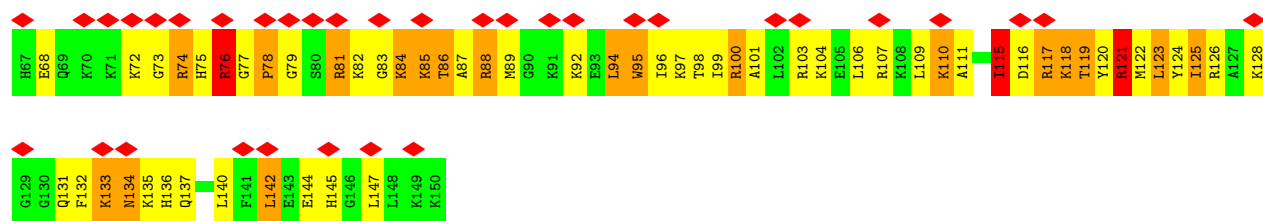


• Molecule 48: 50S ribosomal protein L21e

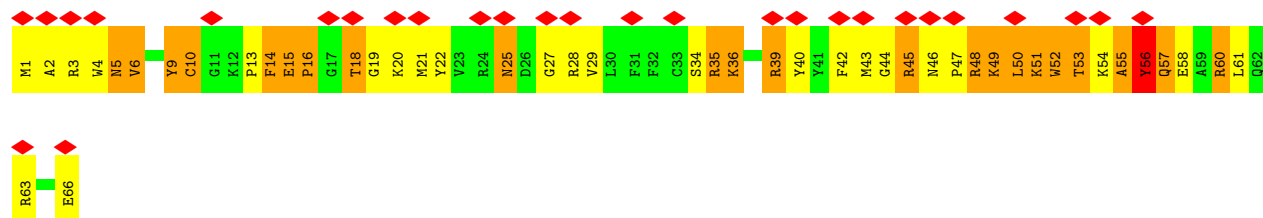


• Molecule 49: 50S ribosomal protein L19e

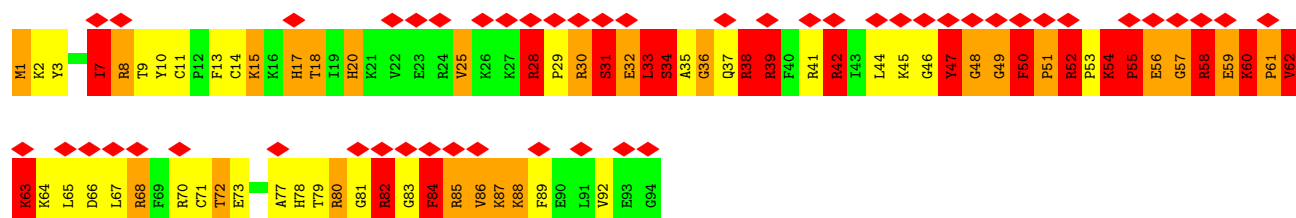
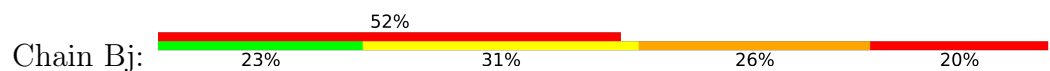




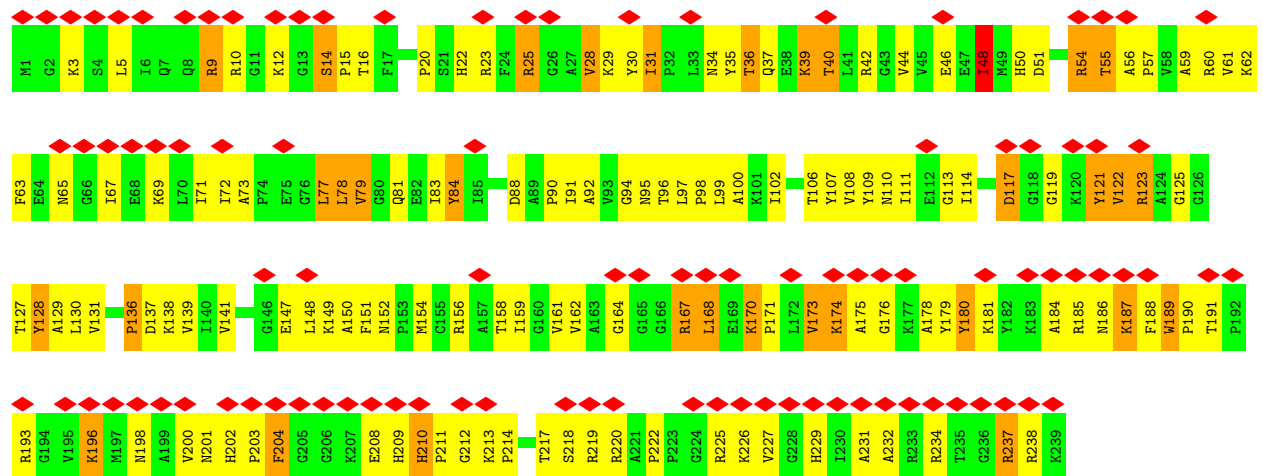
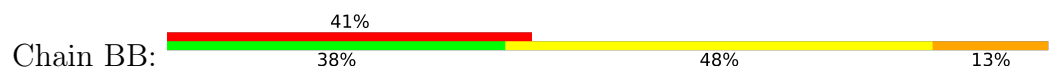
- Molecule 50: 50S ribosomal protein L24e



- Molecule 51: 50S ribosomal protein L44E

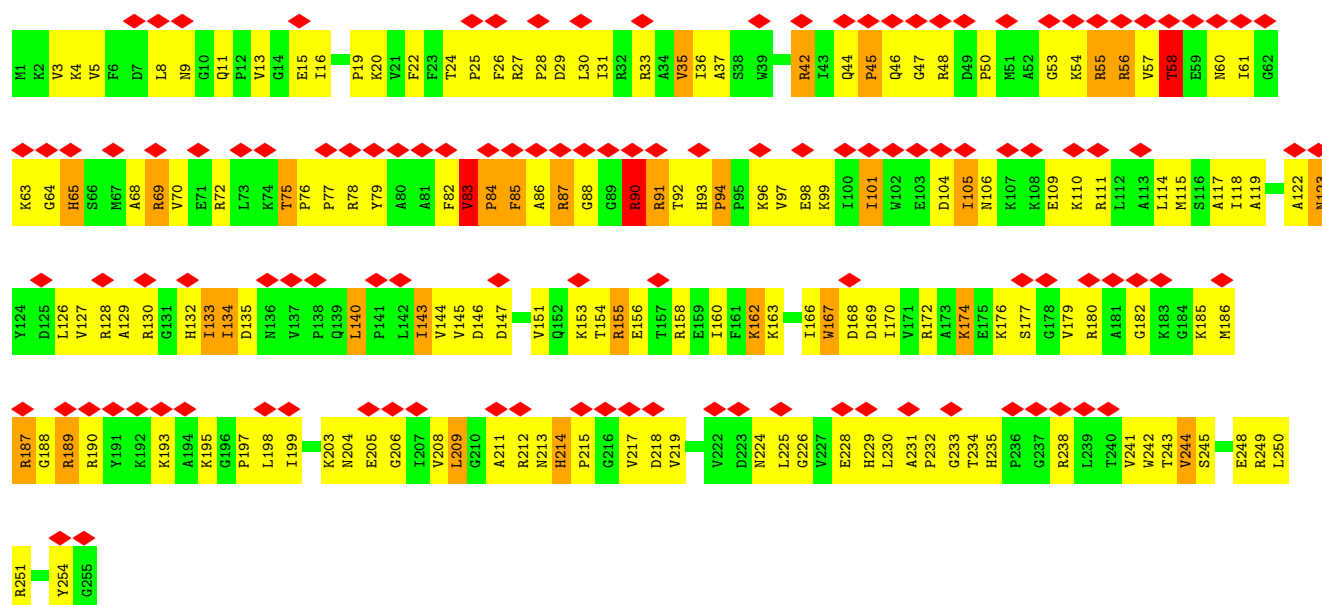


- Molecule 52: 50S ribosomal protein L2P



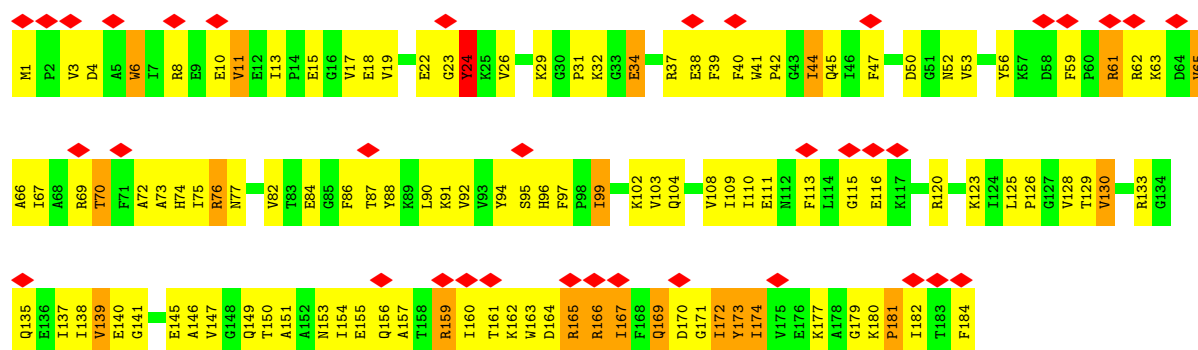
- Molecule 53: 50S ribosomal protein L4P

Chain BD: 

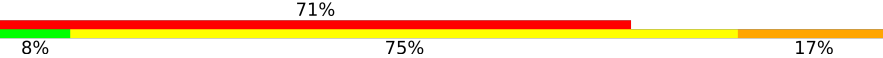


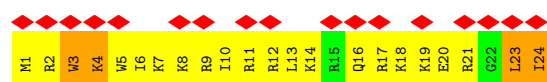
• Molecule 54: 50S ribosomal protein L6P

Chain BF: 



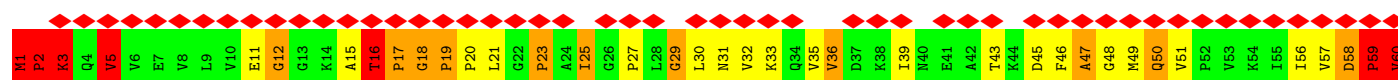
• Molecule 55: 50S ribosomal protein L41e

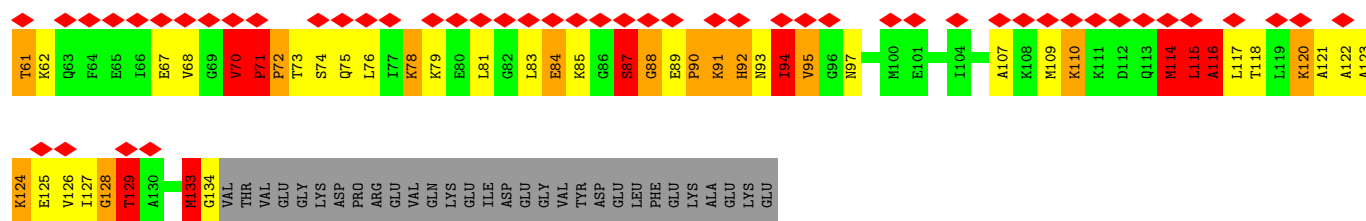
Chain Bh: 



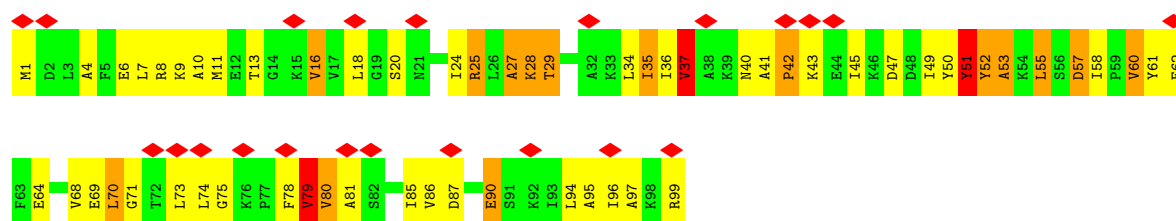
• Molecule 56: 50S ribosomal protein L11P

Chain BH: 

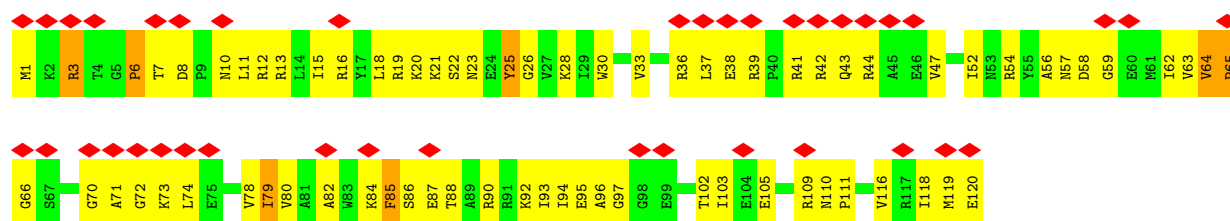




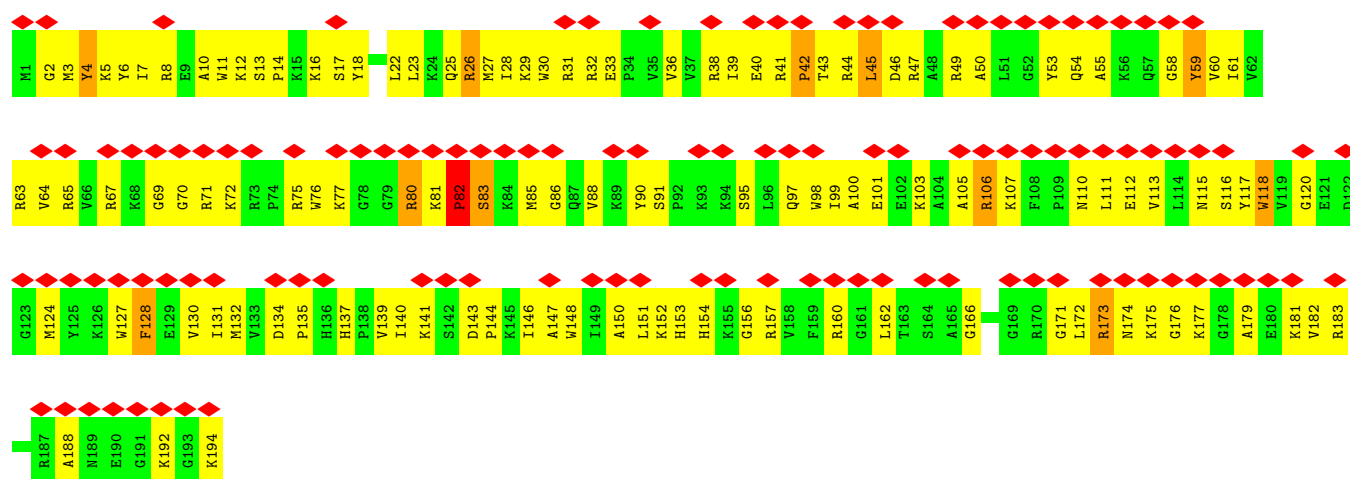
• Molecule 57: 50S ribosomal protein L30e



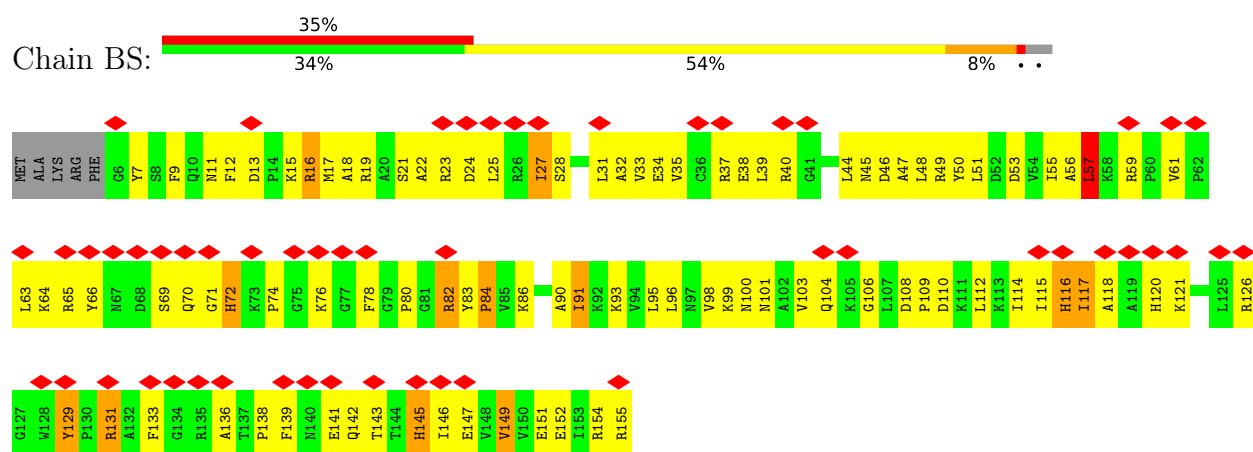
• Molecule 58: 50S ribosomal protein L18e



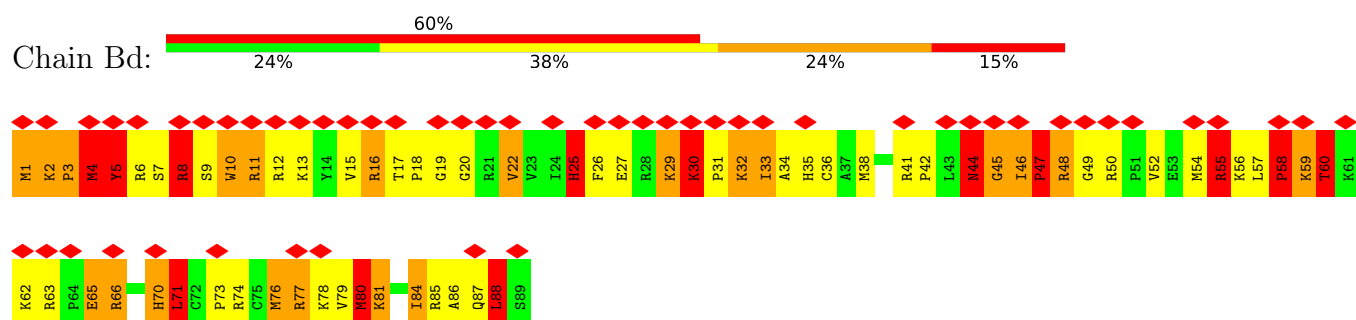
• Molecule 59: 50S ribosomal protein L15e



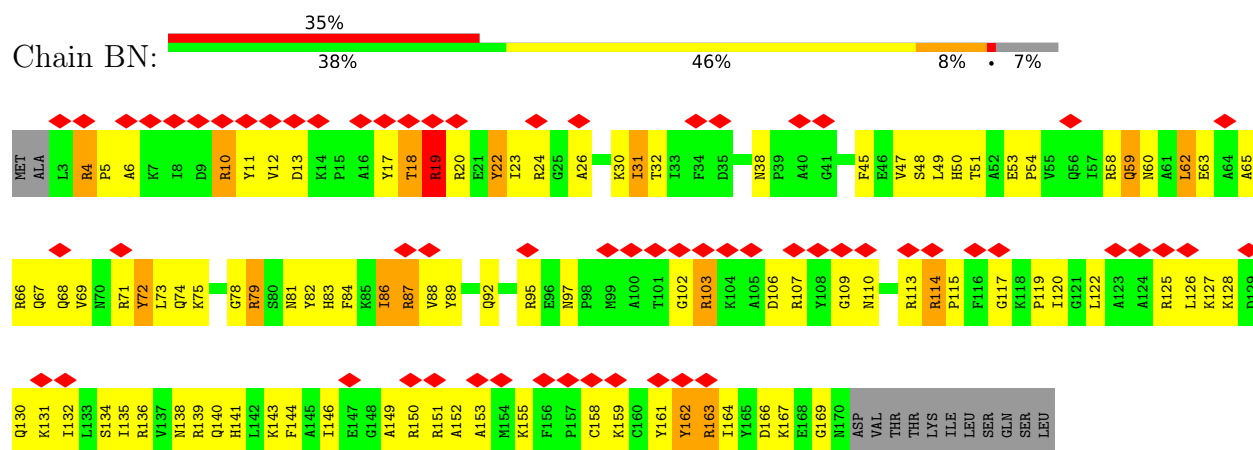
• Molecule 60: 50S ribosomal protein L22P



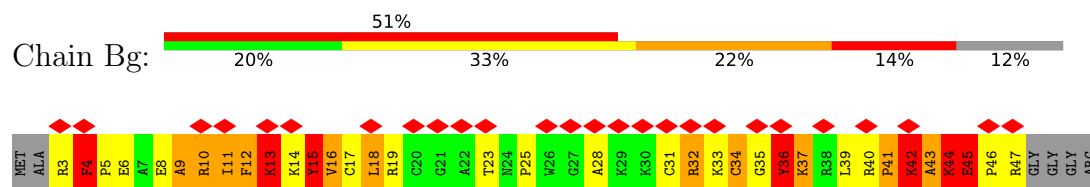
• Molecule 61: 50S ribosomal protein L34e



• Molecule 62: 50S ribosomal protein L10e

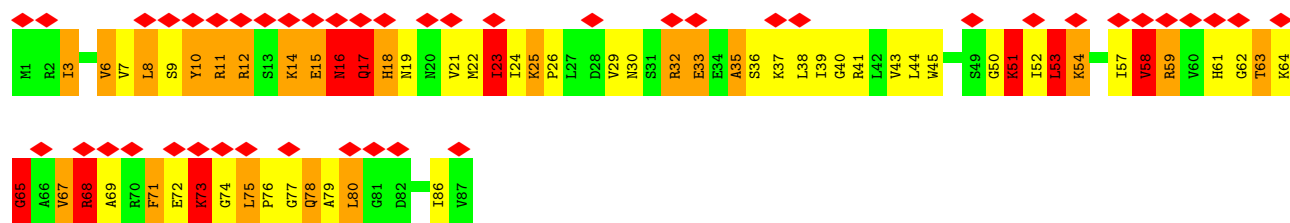


• Molecule 63: 50S ribosomal protein L40e

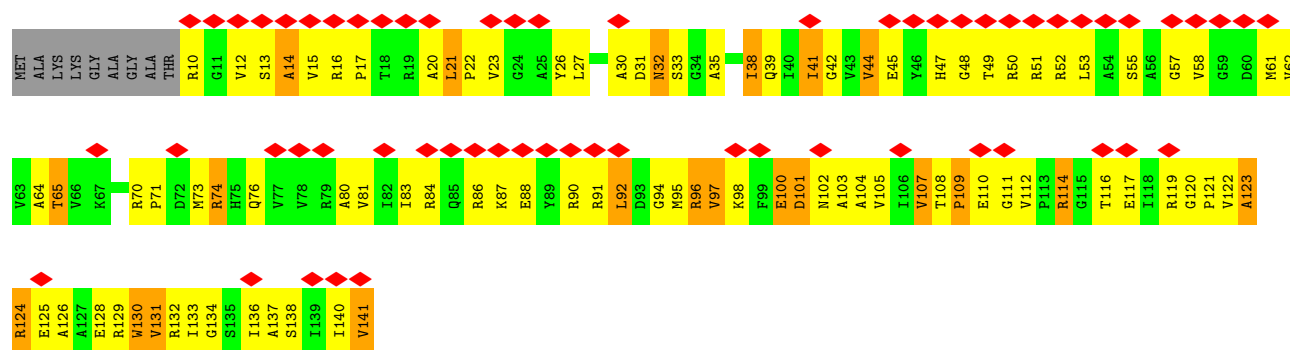
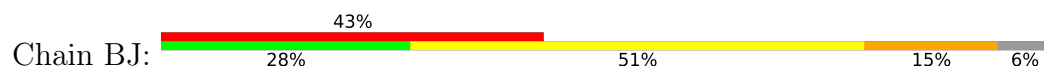


• Molecule 64: 50S ribosomal protein L35Ae

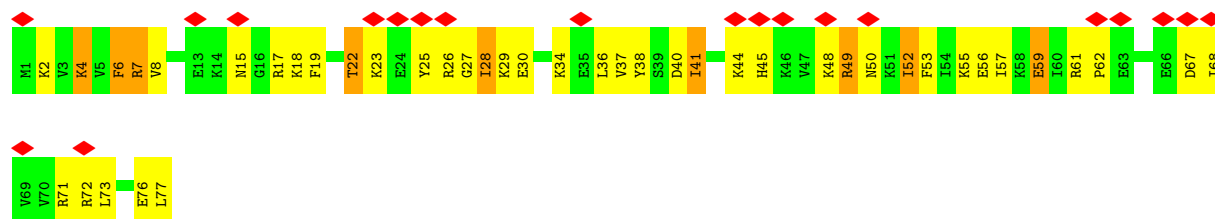
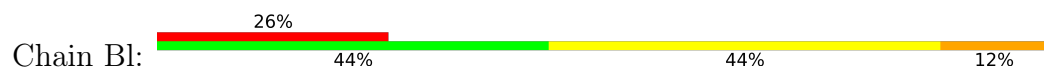




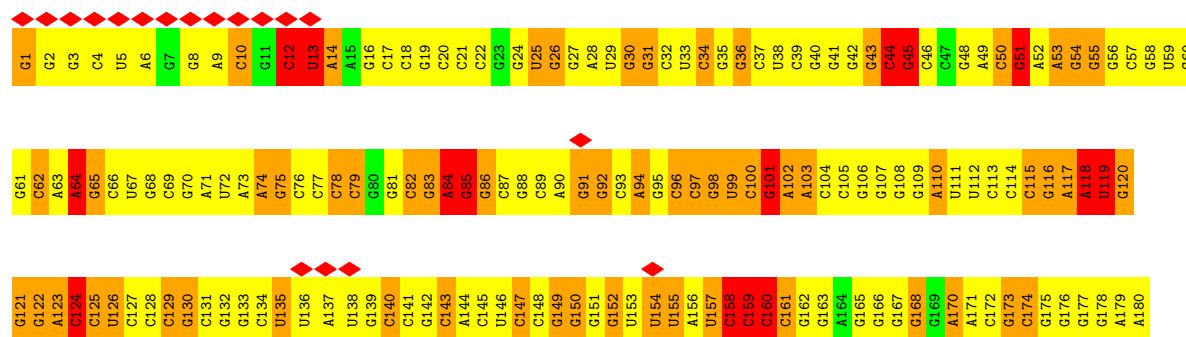
• Molecule 65: 50S ribosomal protein L14P



• Molecule 66: 50S ribosomal protein LX



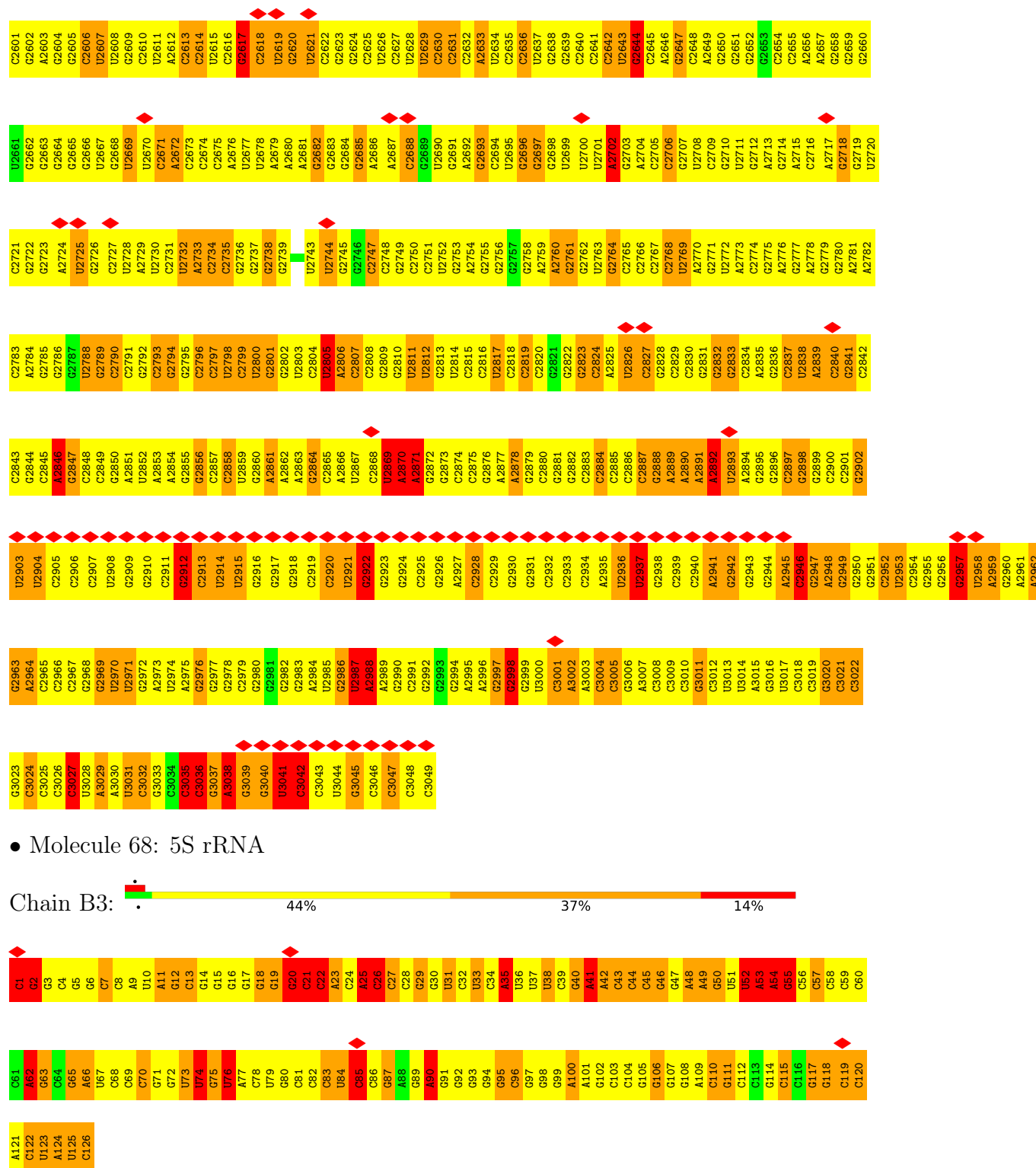
• Molecule 67: 23S rRNA



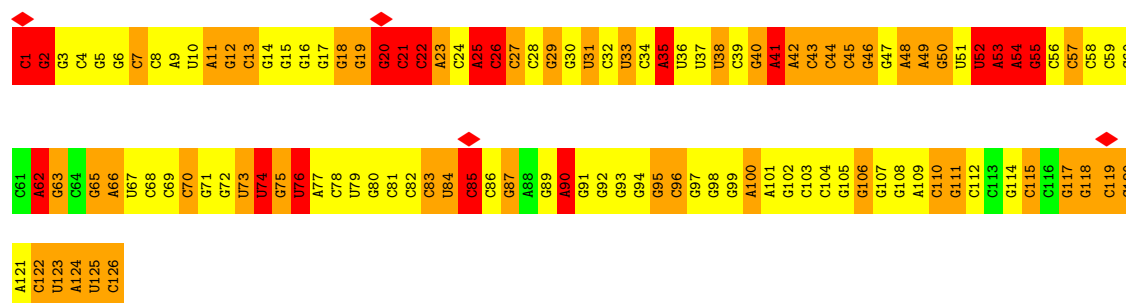
A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	G1000	C1001	A1002	A1003	A1004	A1005	A1006	A1007	A1008	A1009	A1010	A1011	A1012	A1013	A1014	A1015	A1016	A1017	A1018	A1019	A1020	A1021	A1022	A1023	A1024	A1025	A1026	A1027	A1028	C1029	C1030																																																																																																																																																																																																																																																																																																																																											
U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000																																																																																																																																																																																																																																																																																																													
U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930																																																																																																																																																																																																																																																																																																																							
U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900																																																																																																																																																																																																																																																																																									
A728	A729	A730	A731	A732	A733	A734	A735	A736	A737	A738	A739	A740	A741	A742	A743	A744	A745	A746	A747	A748	A749	A750	A751	A752	A753	A754	A755	A756	A757	A758	A759	A760	A761	A762	A763	A764	A765	A766	A767	A768	A769	A770	A771	A772	A773	A774	A775	A776	A777	A778	A779	A780	A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836	A837	A838	A839	A840	A841	A842	A843	A844	A845	A846	A847	A848	A849	A850	A851	A852	A853	A854	A855	A856	A857	A858	A859	A860	A861	A862	A863	A864	A865	A866	A867	A868	A869	A870	A871	A872	A873	A874	A875	A876	A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960	A961	A962	A963	A964	A965	A966	A967	A968	A969	A970	A971	A972	A973	A974	A975	A976	A977	A978	A979	A980	A981	A982	A983	A984	A985	A986	A987	A988	A989	A990	A991	A992	A993	A994	A995	A996	A997	A998	A999	U900																																																																																																																									
C607	C608	C609	C610	C611	C612	C613	C614	C615	C616	C617	C618	C619	C620	C621	C622	C623	C624	C625	C626	C627	C628	C629	C630	C631	C632	C633	C634	C635	C636	C637	C638	C639	C640	C641	C642	C643	C644	C645	C646	C647	C648	C649	C650	C651	C652	C653	C654	C655	C656	C657	C658	C659	C660	C661	C662	C663	C664	C665	C666	C667	C668	C669	C670	C671	C672	C673	C674	C675	C676	C677	C678	C679	C680	C681	C682	C683	C684	C685	C686	C687	C688	C689	C690	C691	C692	C693	C694	C695	C696	C697	C698	C699	C700	C701	C702	C703	C704	C705	C706	C707	C708	C709	C710	C711	C712	C713	C714	C715	C716	C717	C718	C719	C720	C721	C722	C723	C724	C725	C726	C727	C728	C729	C730	C731	C732	C733	C734	C735	C736	C737	C738	C739	C740	C741	C742	C743	C744	C745	C746	C747	C748	C749	C750	C751	C752	C753	C754	C755	C756	C757	C758	C759	C760	C761	C762	C763	C764	C765	C766	C767	C768	C769	C770	C771	C772	C773	C774	C775	C776	C777	C778	C779	C780	C781	C782	C783	C784	C785	C786	C787	C788	C789	C790	C791	C792	C793	C794	C795	C796	C797	C798	C799	C800	C801	C802	C803	C804	C805	C806	C807	C808	C809	C810	C811	C812	C813	C814	C815	C816	C817	C818	C819	C820	C821	C822	C823	C824	C825	C826	C827	C828	C829	C830	C831	C832	C833	C834	C835	C836	C837	C838	C839	C840	C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	U900
C547	U548	U549	U550	U551	U552	U553	U554	U555	U556	U557	U558	U559	U560	U561	U562	U563	U564	U565	U566	U567	U568	U569	U570	U571	U572	U573	U574	U575	U576	U577	U578	U579	U580	U581	U582	U583	U584	U585	U586	U587	U588	U589	U590	U591	U592	U593	U594	U595	U596	U597	U598	U599	U600	U601	U602	U603	U604	U605	U606	U607	U608	U609	U610	U611	U612	U613	U614	U615	U616	U617	U618	U619	U620	U621	U622	U623	U624	U625	U626	U627	U628	U629	U630	U631	U632	U633	U634	U635	U636	U637	U638	U639	U640	U641	U642	U643	U644	U645	U646	U647	U648	U649	U650	U651	U652	U653	U654	U655	U656	U657	U658	U659	U660	U661	U662	U663	U664	U665	U666	U667	U668	U669	U670	U671	U672	U673	U674	U675	U676	U677	U678	U679	U680	U681	U682	U683	U684	U685	U686	U687	U688	U689	U690	U691	U692	U693	U694	U695	U696	U697	U698	U699	U700	U701	U702	U703	U704	U705	U706	U707	U708	U709	U710	U711	U712	U713	U714	U715	U716	U717	U718	U719	U720	U721	U722	U723	U724	U725	U726	U727	U728	U729	U730	U731	U732	U733	U734	U735	U736	U737	U738	U739	U740	U741	U742	U743	U744	U745	U746	U747	U748	U749	U750	U751	U752	U753	U754	U755	U756	U757	U758	U759	U760	U761	U762	U763	U764	U765	U766	U767	U768	U769	U770	U771	U772	U773	U774	U775	U776	U777	U778	U779	U780	U781	U782	U783	U784	U785	U786	U787	U788	U789	U790	U791	U792	U793	U794	U795	U796	U797	U798	U799	U800	U801	U802	U803	U804	U805	U806	U807	U808	U809	U810	U811	U812	U813	U814	U815	U816	U817	U818	U819	U820	U821	U822	U823	U824	U825	U826	U827	U828	U829	U830	U831	U832	U833	U834	U835	U836	U837	U838	U839	U840	U841	U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900																																								
U487	A488	C489	C490	C491	C492	C493	C494	C495	C496	C497	C498	C499	C500	C501	C502	C503	C504	C505	C506	C507	C508	C509	C510	C511	C512	C513	C514	C515	C516	C517	C518	C519	C520	C521	C522	C523	C524	C525	C526	C527	C528	C529	C530	C531	C532	C533	C534	C535	C536	C537	C538	C539	C540	C541	C542	C543	C544	C545	C546	C547	C548	C549	C550	C551	C552	C553	C554	C555	C556																																																																																																																																																																																																																																																																																																																																				

G1757	G1697	G1635	G1575	G1513	G1453	G1393	G1333	G1273	G1213	U1153	G1091	G1031
U1758	G1698	C1636	C1576	C1514	G1454	G1394	G1334	G1274	C1214	A1154	U1092	C1032
A1759	G1699	C1637	C1577	U1455	G1455	G1395	C1335	G1275	C1215	A1155	G1093	C1033
G1760	U1700	C1638	C1578	U1456	U1456	A1396	G1336	G1276	A1216	G1156	U1094	G1034
C1761	G1701	G1639	G1579	G1517	C1457	U1397	G1337	G1277	G1217	U1157	A1095	G1035
G1762	G1702	G1640	G1580	G1518	C1458	C1398	G1338	G1278	C1218	G1158	A1096	G1036
A1763	G1703	G1641	A1581	G1519	A1459	C1399	C1339	U1279	U1219	U1159	G1097	C1037
G1764	C1704	G1642	G1582	G1520	G1460	U1400	G1340	C1280	U1220	U1160	C1098	U1038
A1765	G1705	A1643	G1583	G1461	G1461	A1401	U1341	A1281	U1221	A1161	C1099	C1039
G1766	G1706	G1644	U1584	C1462	G1462	C1402	C1342	A1282	U1222	C1162	G1100	C1040
C1767	A1707	U1645	U1585	A1522	C1463	C1403	C1343	G1283	A1223	U1163	U1101	U1041
G1768	U1708	G1646	G1586	A1524	A1464	G1404	C1344	C1284	A1224	U1164	C1103	G1042
G1769	G1709	C1647	A1587	A1465	G1405	G1405	G1345	C1285	A1225	C1165	U1043	U1043
A1770	C1710	G1648	C1588	U1466	U1466	G1406	G1346	G1286	G1226	C1166	C1044	C1044
C1771	G1711	G1649	G1589	G1467	A1407	U1347	U1347	G1287	A1227	A1166	A1045	A1045
G1772	U1712	U1650	C1590	G1468	G1408	G1348	G1348	C1288	G1228	A1167	A1046	A1046
A1773	G1713	A1651	C1591	U1469	U1409	G1349	G1349	C1289	U1229	C1106	A1047	A1047
C1774	G1714	A1652	U1592	A1470	A1410	C1350	G1350	G1290	G1230	A1107	G1048	G1048
G1775	G1715	U1653	C1593	G1471	A1411	G1351	G1351	C1291	C1231	G1109	U1049	U1049
G1776	G1716	G1654	G1594	U1472	C1412	U1352	U1352	C1292	G1232	G1170	G1050	C1050
U1777	C1717	G1655	G1595	A1473	A1413	A1353	G1353	G1293	U1233	G1171	A1110	C1051
G1778	C1718	C1656	G1596	A1474	G1414	G1354	G1354	A1294	U1234	G1172	G1052	G1052
C1779	G1719	G1657	G1597	A1475	C1415	A1355	A1355	G1295	A1235	G1173	A1053	A1053
C1780	G1720	A1658	U1598	C1476	G1416	A1356	A1356	A1296	A1236	U1174	A1054	A1054
G1781	U1721	G1659	A1599	C1477	U1417	G1357	G1357	C1297	C1237	C1175	C1055	C1055
C1782	G1722	G1660	G1600	G1478	A1418	A1358	C1358	C1298	G1238	C1177	C1056	C1056
U1783	A1723	G1661	G1601	U1479	G1419	C1359	C1359	C1299	C1239	G1178	A1118	A1057
G1784	A1724	G1664	U1602	G1480	U1420	G1360	G1360	C1300	U1240	G1179	A1058	A1058
G1785	A1725	G1665	G1603	G1481	C1421	G1361	G1361	G1301	G1180	C1120	U1068	U1068
A1786	G1726	G1666	G1604	U1482	G1422	G1362	G1362	G1302	C1181	C1121	A1069	A1069
G1787	G1727	A1605	C1605	U1483	G1423	C1363	C1363	C1303	C1182	C1122	G1070	G1070
G1788	C1728	G1606	G1606	U1484	G1424	C1364	C1364	C1304	U1183	A1123	C1062	C1062
G1789	G1729	C1607	C1607	U1485	G1425	G1365	G1365	C1305	U1184	G1124	C1063	C1063
A1790	C1730	A1670	G1608	A1486	G1426	U1367	A1367	C1307	C1245	A1125	G1064	G1064
A1791	U1731	A1671	G1609	G1487	A1427	A1368	A1368	C1308	G1246	C1126	C1065	C1065
A1792	C1732	G1672	C1610	U1488	G1428	G1369	G1369	G1309	U1247	C1127	G1066	G1066
G1793	G1733	C1673	C1611	G1489	A1429	G1370	G1370	A1310	G1248	G1128	G1067	G1067
C1794	G1734	G1674	G1612	U1490	A1430	U1371	U1371	C1311	A1189	G1129	U1068	U1068
C1795	G1735	C1675	A1613	U1491	U1431	C1372	C1372	C1312	G1190	G1131	A1069	A1069
U1796	G1736	G1676	U1614	G1492	C1432	G1373	G1373	G1313	C1191	U1132	G1070	G1070
A1797	A1737	A1677	G1615	C1493	C1433	G1374	G1374	A1314	G1192	U1133	U1072	U1072
G1798	A1738	A1678	A1616	U1494	C1434	G1375	G1375	U1315	G1193	A1134	G1073	G1073
G1799	U1739	U1679	G1617	A1495	G1435	U1376	U1376	U1316	G1194	A1135	G1074	G1074
G1800	U1740	G1680	U1558	A1496	A1436	G1377	G1377	G1317	G1195	G1136	G1075	G1075
C1801	C1741	G1681	C1619	A1497	C1437	G1378	G1378	G1318	A1196	G1137	G1076	G1076
G1802	G1742	C1682	G1620	U1498	G1438	G1379	G1379	G1319	G1197	C1138	G1077	G1077
C1803	G1743	C1683	G1622	C1499	G1439	A1380	U1380	U1319	G1198	C1139	G1078	G1078
U1804	A1744	C1684	C1623	U1500	C1440	C1381	C1381	C1320	U1199	G1141	A1079	A1079
U1805	U1745	C1685	G1624	G1501	C1441	C1382	G1382	C1321	A1200	A1142	G1080	G1080
C1806	G1746	C1686	A1625	C1502	G1442	G1383	G1383	U1322	C1261	A1143	U1081	U1081
G1807	C1747	C1687	A1626	G1503	G1443	C1384	C1384	U1323	C1262	A1144	A1082	A1082
G1808	C1748	G1688	G1627	G1504	A1444	G1385	G1385	G1324	G1263	G1145	G1083	G1083
G1809	C1749	C1689	C1628	G1505	G1445	G1386	G1386	A1325	G1264	U1146	G1084	G1084
G1810	U1750	U1690	A1568	U1506	G1446	G1387	G1387	U1326	A1265	U1205	G1085	G1085
G1811	G1751	U1691	G1629	A1507	G1447	U1388	U1388	G1327	A1266	G1206	U1086	U1086
C1762	C1752	A1692	U1630	A1508	G1448	A1389	A1389	G1328	A1267	A1207	G1087	G1087
A1812	G1753	U1692	U1631	C1509	G1449	U1390	U1390	G1329	U1269	A1208	G1088	G1088
A1813	A1754	G1693	U1632	U1510	C1450	C1391	C1391	U1330	G1270	A1209	G1089	G1089
A1814	C1755	G1694	A1633	G1511	A1451	U1331	U1331	U1331	G1271	G1210	C1089	C1089
G1815	G1756	G1695	A1634	G1512	G1452	G1392	G1392	A1332	A1272	C1212	C1152	C1152
C1816	C1756	G1696	A1574	G1512	G1452	G1392	G1392	A1332	A1272	C1212	C1152	C1152

A2540	G2480	C2300	G2240	G2180	C2118	G2057	C1997	A1937	G1877	C1817
U2541	G2481	C2301	U2441	G2181	C2119	C2058	G1998	G1938	G1878	G1818
G2542	A2421	G2302	A2241	A2182	C2120	G2059	G1999	G1939	U1879	G1819
A2543	G2422	A2303	G2242	A2183	C2121	A2060	G2000	U1940	A1880	C1820
G2544	G2423	G2304	G2243	G2184	G2122	A2061	U2001	A1941	A1881	C1821
A2545	A2424	U2305	G2244	G2185	G2123	A2062	A2002	G1942	C1882	G1822
G2546	A2425	G2306	G2245	A2186	C2124	C2063	C2003	C1943	A1883	A1823
A2547	G2427	C2307	G2246	C2187	C2125	U2064	A2004	C1944	C1884	G1824
G2548	C2428	G2308	G2247	C2188	C2126	C2065	A2005	G1945	G1885	G1825
A2549	G2429	C2309	G2248	C2189	G2127	C2066	C2006	G1946	C1886	G1826
C2552	G2430	G2310	A2249	G2190	G2128	U2067	C2007	A1947	A1887	A1827
U2553	A2371	C2311	G2250	A2191	G2129	U2068	G2008	A1948	A1828	
G2554	C2372	U2312	G2251	U2191	G2130	G2069	G2009	A1949	A1829	
A2555	G2373	G2313	G2252	G2192	C2131	U2070	G2010	G1950	U1890	
C2556	C2374	U2314	G2253	G2193	C2132	G2071	U2011	G1951	C1891	
G2557	C2375	G2315	U2254	A2194	C2133	G2072	G2012	G1952	G1892	
U2558	U2376	U2316	C2255	G2195	G2134	G2073	A2013	G1953	C1893	
G2559	C2377	G2317	G2256	C2196	G2135	U2074	G2015	U1954	C1894	
G2560	C2378	G2318	A2257	U2197	G2136	U2075	C2016	U1955	A1895	
G2561	G2379	C2319	G2258	U2198	A2137	A2076	A2017	G1956	U1896	
A2562	A2380	U2320	G2259	U2199	A2138	A2077	C2018	U1957	A1897	
G2563	A2381	A2321	C2260	A2200	U2142	U2078	C2019	A1958	C1898	
A2564	A2382	C2322	C2261	C2201	U2143	G2080	C2020	C1959	G1840	
A2565	A2383	G2323	C2262	U2202	U2144	C2081	G2021	G1960	A1841	
A2566	G2384	C2324	G2263	G2203	U2145	C2082	U2022	G1961	G1842	
C2567	G2385	C2325	G2264	A2204	G2145		A2023	G1962	C1843	
A2568	U2386	G2326	C2265	G2205	C2146		A2024	G1963	C1844	
G2569	A2387	C2327	G2266	C2206	C2147		A2025	C1965	C1845	
U2570	U2388	G2328	U2267	C2207	C2148		C2026	C1966	G1846	
A2571	G2389	A2329	U2268	C2208	U2149		G2027	G1967	U1847	
G2572	C2390	A2330	C2269	U2209	G2149		G2028	A1968	C1908	
C2573	G2391	G2331	G2270	G2210	C2150		C2029	C1969	A1848	
G2574	A2392	G2332	G2271	C2211	G2151		G2030	G1970	C1909	
C2575	G2393	G2333	G2272	G2212	C2152		G2031	G1971	C1910	
U2576	G2394	G2334	U2273	G2213	C2153			C1972	G1911	
C2577	C2395	G2335	G2274	U2214	G2154			C1973	U1852	
U2577	G2396	G2336	G2275	U2215	C2155			C1974	C1853	
C2578	C2397	A2337	U2276	G2216	A2156			U1975	G1854	
G2579	C2398	G2338	G2277	C2217	U2157			C1976	G1856	
U2580	C2399	G2339	U2278	C2218	C2158			U1916	G1857	
G2581	A2400	A2340	G2279	A2219	C2159			U1917	A1858	
C2582	U2401	C2341	G2280	C2220	C2160			U1918	A1859	
G2583	A2402	G2342	A2281	A2221	A2161			A1919	A1860	
A2584	G2403	G2343	G2282	C2222	G2162			A1920	G1861	
G2585	U2404	G2344	C2283	G2223	G2163			U1921	G1862	
A2586	G2405	U2345	C2284	G2224	G2164			A1922	G1863	
C2587	U2406	A2346	G2285	G2225	A2165			A1923	G1864	
G2588	G2407	G2347	U2286	G2226	C2166			A1924	U1865	
U2589	U2408	G2348	C2287	G2227	C2167			A1925	G1866	
C2590	G2409	U2349	C2288	G2228	G2168			U1926	C1867	
G2591	U2410	G2350	A2289	G2229	C2169			C1927	G1868	
U2592	C2411	G2351	U2290	G2230	C2170			U1928	U1869	
A2593	A2412	C2352	G2291	G2231	G2171			C1929	G1870	
U2594	G2413	G2353	A2292	G2232	U2172			A1930	C1871	
C2595	C2414	A2354	G2293	G2233	G2173			G1931	G1872	
G2596	G2415	U2355	G2294	C2234	G2174			A1992	G1873	
A2597	C2416	G2356	A2295	G2235	G2175			G1993	G1874	
U2598	U2417	U2357	C2296	G2236	A2177			C1994	U1875	
G2599	G2418	G2358	A2296	A2237	G2178			C1995	C1876	
C2600	U2419	C2359	C2297	G2238	G2179					
			G2298	G2239						



• Molecule 68: 5S rRNA



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	2.28	52/1338 (3.9%)	2.57	113/1797 (6.3%)
2	AK	2.30	39/1088 (3.6%)	2.48	74/1455 (5.1%)
3	AI	2.04	28/1049 (2.7%)	2.29	58/1408 (4.1%)
4	AG	2.03	25/999 (2.5%)	2.58	90/1337 (6.7%)
5	AW	2.37	20/485 (4.1%)	2.31	22/651 (3.4%)
6	AC	2.37	68/1480 (4.6%)	2.51	107/1985 (5.4%)
7	AB	2.31	65/1654 (3.9%)	2.52	135/2233 (6.0%)
8	AR	2.40	44/956 (4.6%)	2.40	64/1287 (5.0%)
10	AD	2.29	62/1457 (4.3%)	2.50	106/1953 (5.4%)
11	A1	2.75	106/1843 (5.8%)	2.24	152/2873 (5.3%)
12	AN	2.08	31/1156 (2.7%)	2.50	78/1535 (5.1%)
13	AX	2.47	28/570 (4.9%)	2.58	37/760 (4.9%)
14	AM	2.35	40/1022 (3.9%)	2.52	57/1375 (4.1%)
15	AE	2.30	75/2025 (3.7%)	2.47	144/2732 (5.3%)
16	AJ	2.40	42/1013 (4.1%)	2.41	57/1349 (4.2%)
17	AO	2.50	64/1208 (5.3%)	2.64	105/1619 (6.5%)
18	AF	1.63	10/1745 (0.6%)	1.91	45/2350 (1.9%)
19	AS	2.21	22/562 (3.9%)	2.48	37/744 (5.0%)
20	A3	2.25	34/951 (3.6%)	2.58	86/1281 (6.7%)
20	B4	1.91	14/951 (1.5%)	2.41	64/1281 (5.0%)
20	BG	1.77	6/951 (0.6%)	2.34	58/1281 (4.5%)
21	A2	2.61	1909/35966 (5.3%)	2.27	2956/56138 (5.3%)
22	AY	2.19	16/421 (3.8%)	2.28	21/558 (3.8%)
23	AT	2.40	48/942 (5.1%)	2.46	66/1257 (5.3%)
24	AA	2.28	58/1585 (3.7%)	2.49	117/2124 (5.5%)
25	AH	2.24	60/1773 (3.4%)	2.93	216/2381 (9.1%)
26	AP	2.38	27/471 (5.7%)	2.51	29/620 (4.7%)
27	A0	2.68	105/1814 (5.8%)	2.28	148/2828 (5.2%)
28	AV	1.98	15/839 (1.8%)	2.18	32/1122 (2.9%)
28	B6	2.20	23/798 (2.9%)	2.28	45/1071 (4.2%)
29	AL	2.10	17/830 (2.0%)	2.73	76/1113 (6.8%)
30	AU	2.28	44/1203 (3.7%)	2.63	109/1621 (6.7%)
31	BY	2.31	53/1262 (4.2%)	2.66	119/1687 (7.1%)
32	BO	2.36	70/1635 (4.3%)	2.50	136/2196 (6.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BC	2.28	120/2978 (4.0%)	2.51	227/4003 (5.7%)
34	B5	2.35	24/618 (3.9%)	2.66	49/829 (5.9%)
34	BK	2.40	27/618 (4.4%)	2.50	44/829 (5.3%)
35	BL	2.35	47/1175 (4.0%)	2.76	117/1563 (7.5%)
36	Bf	2.62	33/453 (7.3%)	3.24	59/603 (9.8%)
37	BU	2.31	41/1024 (4.0%)	2.39	70/1365 (5.1%)
38	Bb	2.26	43/1099 (3.9%)	2.55	89/1466 (6.1%)
39	Be	2.36	22/517 (4.3%)	2.55	40/681 (5.9%)
40	BE	2.31	61/1513 (4.0%)	2.49	114/2026 (5.6%)
41	Ba	2.18	25/760 (3.3%)	2.66	68/1019 (6.7%)
42	BT	2.22	29/689 (4.2%)	2.38	41/924 (4.4%)
43	Bk	2.00	35/1659 (2.1%)	2.37	105/2253 (4.7%)
44	BW	2.43	31/595 (5.2%)	2.71	60/784 (7.7%)
45	Bi	2.03	10/599 (1.7%)	2.41	40/798 (5.0%)
46	BA	2.26	66/1702 (3.9%)	2.58	129/2293 (5.6%)
47	BI	2.39	53/1168 (4.5%)	2.44	77/1561 (4.9%)
48	BR	2.14	23/808 (2.8%)	2.46	58/1080 (5.4%)
49	BQ	2.25	50/1272 (3.9%)	2.81	141/1676 (8.4%)
50	BV	2.04	11/570 (1.9%)	2.55	44/758 (5.8%)
51	Bj	2.19	24/805 (3.0%)	2.75	74/1064 (7.0%)
52	BB	2.29	74/1883 (3.9%)	2.50	133/2540 (5.2%)
53	BD	2.44	82/2068 (4.0%)	2.53	158/2787 (5.7%)
54	BF	2.25	60/1507 (4.0%)	2.43	112/2033 (5.5%)
55	Bh	1.65	3/233 (1.3%)	1.84	7/301 (2.3%)
56	BH	2.09	28/1001 (2.8%)	2.63	80/1351 (5.9%)
57	BZ	2.20	22/764 (2.9%)	2.62	60/1028 (5.8%)
58	BP	2.33	43/980 (4.4%)	2.42	62/1313 (4.7%)
59	BM	2.34	68/1634 (4.2%)	2.48	122/2179 (5.6%)
60	BS	2.38	51/1226 (4.2%)	2.56	110/1649 (6.7%)
61	Bd	2.18	29/758 (3.8%)	2.88	84/1007 (8.3%)
62	BN	2.49	72/1409 (5.1%)	2.36	81/1890 (4.3%)
63	Bg	2.06	10/380 (2.6%)	2.45	34/504 (6.7%)
64	Bc	2.24	23/694 (3.3%)	2.71	62/926 (6.7%)
65	BJ	2.50	53/1027 (5.2%)	2.39	66/1385 (4.8%)
66	Bl	2.37	23/669 (3.4%)	2.43	34/884 (3.8%)
67	B1	2.63	4063/73410 (5.5%)	2.27	5986/114595 (5.2%)
68	B3	2.76	168/3010 (5.6%)	2.41	287/4693 (6.1%)
All	All	2.50	8967/187317 (4.8%)	2.36	14883/276642 (5.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
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

Continued on next page...

Continued from previous page...

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 8967 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
67	B1	1565	G	O4'-C1'	33.62	2.08	1.41
67	B1	2507	C	O4'-C1'	32.89	1.91	1.41
67	B1	1570	C	O4'-C1'	32.79	1.90	1.41
53	BD	91	ARG	C-N	-29.03	0.93	1.33
67	B1	1567	C	O4'-C1'	28.85	1.84	1.41

The worst 5 of 14883 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	2507	C	O4'-C1'-C2'	-30.58	77.02	107.60
67	B1	1642	G	O4'-C1'-C2'	-25.94	79.86	105.80
67	B1	2363	G	O4'-C1'-N9	23.35	143.53	108.50
67	B1	1037	C	P-O3'-C3'	22.64	154.16	120.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	B1	1612	G	P-O3'-C3'	21.78	152.87	120.20

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

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	AQ	1310	0	1392	9	0
2	AK	1072	0	1128	101	0
3	AI	1028	0	1065	121	0
4	AG	984	0	1043	184	0
5	AW	478	0	524	18	0
6	AC	1459	0	1549	18	0
7	AB	1623	0	1685	18	0
8	AR	934	0	959	25	0
9	A9	286	0	62	4	0
10	AD	1434	0	1498	44	0
11	A1	1649	0	838	23	0
12	AN	1140	0	1235	118	0
13	AX	568	0	600	40	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	AM	1004	0	1041	16	0
15	AE	1976	0	2046	29	0
16	AJ	1004	0	1088	6	0
17	AO	1189	0	1248	3	0
18	AF	1716	0	1768	368	0
19	AS	556	0	604	0	0
20	A3	939	0	994	3	0
20	B4	939	0	994	13	0
20	BG	939	0	994	71	0
21	A2	32135	0	16230	1056	0
22	AY	409	0	410	2	0
23	AT	923	0	986	1	0
24	AA	1559	0	1648	3	0
25	AH	1736	0	1787	363	0
26	AP	462	0	492	43	0
27	A0	1625	0	824	12	0
28	AV	823	0	847	78	0
28	B6	782	0	806	8	0
29	AL	822	0	870	74	0
30	AU	1175	0	1216	37	0
31	BY	1243	0	1326	111	0
32	BO	1597	0	1639	11	0
33	BC	2912	0	3073	37	0
34	B5	614	0	670	128	0
34	BK	614	0	670	2	0
35	BL	1154	0	1218	272	0
36	Bf	445	0	510	155	0
37	BU	1008	0	1077	8	0
38	Bb	1074	0	1167	157	0
39	Be	506	0	528	205	0
40	BE	1489	0	1550	9	0
41	Ba	746	0	808	86	0
42	BT	680	0	739	0	0
43	Bk	1632	0	1725	59	0
44	BW	594	0	665	1	0
45	Bi	590	0	631	107	0
46	BA	1677	0	1796	7	0
47	BI	1150	0	1240	19	0
48	BR	787	0	827	90	0
49	BQ	1256	0	1389	84	0
50	BV	555	0	548	66	0
51	Bj	787	0	837	194	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	BB	1838	0	1914	67	0
53	BD	2026	0	2134	48	0
54	BF	1476	0	1518	32	0
55	Bh	230	0	269	73	0
56	BH	988	0	1077	84	0
57	BZ	754	0	804	60	0
58	BP	966	0	1019	10	0
59	BM	1595	0	1695	72	0
60	BS	1200	0	1255	4	0
61	Bd	740	0	806	166	0
62	BN	1378	0	1405	4	0
63	Bg	371	0	395	76	0
64	Bc	685	0	743	84	0
65	BJ	1014	0	1073	36	0
66	Bl	659	0	699	5	0
67	B1	65577	0	33094	2123	0
68	B3	2694	0	1371	60	0
All	All	173979	0	126375	4935	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 17.

The worst 5 of 4935 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)
36:Bf:30:LYS:HE2	67:B1:92:G:C6	1.28	1.68
64:Bc:14:LYS:HD3	67:B1:1142:A:C2	1.17	1.64
21:A2:340:A:C2'	21:A2:340:A:C1'	1.74	1.63
67:B1:404:G:C1'	67:B1:404:G:C2'	1.76	1.62
36:Bf:30:LYS:HG2	67:B1:92:G:C8	1.17	1.61

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	13
2	AK	133/135 (98%)	119 (90%)	12 (9%)	2 (2%)	8	40
3	AI	127/130 (98%)	121 (95%)	4 (3%)	2 (2%)	7	38
4	AG	123/125 (98%)	103 (84%)	11 (9%)	9 (7%)	1	10
5	AW	61/63 (97%)	55 (90%)	4 (7%)	2 (3%)	3	21
6	AC	184/210 (88%)	175 (95%)	6 (3%)	3 (2%)	7	38
7	AB	200/202 (99%)	177 (88%)	19 (10%)	4 (2%)	6	31
8	AR	111/113 (98%)	100 (90%)	9 (8%)	2 (2%)	6	34
10	AD	170/180 (94%)	151 (89%)	14 (8%)	5 (3%)	3	23
12	AN	143/147 (97%)	129 (90%)	8 (6%)	6 (4%)	2	17
13	AX	69/71 (97%)	59 (86%)	4 (6%)	6 (9%)	0	9
14	AM	131/137 (96%)	118 (90%)	8 (6%)	5 (4%)	2	19
15	AE	239/243 (98%)	210 (88%)	23 (10%)	6 (2%)	4	26
16	AJ	125/127 (98%)	101 (81%)	18 (14%)	6 (5%)	2	16
17	AO	146/148 (99%)	122 (84%)	15 (10%)	9 (6%)	1	12
18	AF	215/236 (91%)	191 (89%)	22 (10%)	2 (1%)	14	51
19	AS	65/67 (97%)	64 (98%)	0	1 (2%)	8	40
20	A3	121/123 (98%)	105 (87%)	8 (7%)	8 (7%)	1	12
20	B4	121/123 (98%)	113 (93%)	6 (5%)	2 (2%)	7	36
20	BG	121/123 (98%)	109 (90%)	8 (7%)	4 (3%)	3	21
22	AY	48/50 (96%)	43 (90%)	3 (6%)	2 (4%)	2	17
23	AT	109/132 (83%)	98 (90%)	9 (8%)	2 (2%)	6	34
24	AA	188/198 (95%)	170 (90%)	12 (6%)	6 (3%)	3	21
25	AH	213/215 (99%)	181 (85%)	14 (7%)	18 (8%)	0	9
26	AP	54/56 (96%)	43 (80%)	8 (15%)	3 (6%)	1	14
28	AV	97/99 (98%)	86 (89%)	6 (6%)	5 (5%)	1	15
28	B6	92/99 (93%)	84 (91%)	4 (4%)	4 (4%)	2	17
29	AL	100/102 (98%)	92 (92%)	1 (1%)	7 (7%)	1	11
30	AU	142/150 (95%)	134 (94%)	5 (4%)	3 (2%)	5	30
31	BY	153/155 (99%)	143 (94%)	5 (3%)	5 (3%)	3	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	BO	195/203 (96%)	164 (84%)	17 (9%)	14 (7%)	1	11
33	BC	363/365 (100%)	303 (84%)	34 (9%)	26 (7%)	1	11
34	B5	79/83 (95%)	69 (87%)	5 (6%)	5 (6%)	1	12
34	BK	79/83 (95%)	68 (86%)	6 (8%)	5 (6%)	1	12
35	BL	145/147 (99%)	128 (88%)	8 (6%)	9 (6%)	1	12
36	Bf	49/51 (96%)	37 (76%)	8 (16%)	4 (8%)	0	9
37	BU	119/121 (98%)	113 (95%)	3 (2%)	3 (2%)	4	26
38	Bb	125/130 (96%)	102 (82%)	13 (10%)	10 (8%)	1	9
39	Be	60/62 (97%)	45 (75%)	11 (18%)	4 (7%)	1	12
40	BE	184/186 (99%)	170 (92%)	8 (4%)	6 (3%)	3	21
41	Ba	88/95 (93%)	74 (84%)	7 (8%)	7 (8%)	1	9
42	BT	82/86 (95%)	78 (95%)	3 (4%)	1 (1%)	10	44
43	Bk	210/339 (62%)	187 (89%)	12 (6%)	11 (5%)	1	15
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%)	1	14
47	BI	140/142 (99%)	129 (92%)	7 (5%)	4 (3%)	3	23
48	BR	93/97 (96%)	85 (91%)	6 (6%)	2 (2%)	5	29
49	BQ	148/150 (99%)	141 (95%)	4 (3%)	3 (2%)	6	31
50	BV	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	Bj	92/94 (98%)	71 (77%)	8 (9%)	13 (14%)	0	3
52	BB	237/239 (99%)	213 (90%)	17 (7%)	7 (3%)	3	22
53	BD	253/255 (99%)	218 (86%)	21 (8%)	14 (6%)	1	14
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	10
57	BZ	97/99 (98%)	84 (87%)	7 (7%)	6 (6%)	1	12
58	BP	118/120 (98%)	102 (86%)	13 (11%)	3 (2%)	4	26
59	BM	192/194 (99%)	173 (90%)	17 (9%)	2 (1%)	12	48
60	BS	148/155 (96%)	137 (93%)	8 (5%)	3 (2%)	6	31
61	Bd	87/89 (98%)	78 (90%)	6 (7%)	3 (3%)	3	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	BN	166/181 (92%)	137 (82%)	20 (12%)	9 (5%)	1	14
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	16
65	BJ	130/141 (92%)	124 (95%)	4 (3%)	2 (2%)	8	40
66	Bl	75/77 (97%)	69 (92%)	4 (5%)	2 (3%)	4	25
All	All	8599/9048 (95%)	7630 (89%)	608 (7%)	361 (4%)	3	17

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%)	137 (96%)	6 (4%)	26	48
2	AK	111/111 (100%)	106 (96%)	5 (4%)	24	46
3	AI	107/108 (99%)	100 (94%)	7 (6%)	15	37
4	AG	108/108 (100%)	91 (84%)	17 (16%)	2	12
5	AW	54/54 (100%)	52 (96%)	2 (4%)	30	51
6	AC	145/167 (87%)	142 (98%)	3 (2%)	47	65
7	AB	173/173 (100%)	164 (95%)	9 (5%)	21	42
8	AR	102/102 (100%)	100 (98%)	2 (2%)	48	66
10	AD	153/160 (96%)	146 (95%)	7 (5%)	24	45
12	AN	118/121 (98%)	105 (89%)	13 (11%)	6	20
13	AX	60/60 (100%)	53 (88%)	7 (12%)	5	18

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	AM	100/104 (96%)	94 (94%)	6 (6%)	17	39
15	AE	212/213 (100%)	199 (94%)	13 (6%)	17	38
16	AJ	103/103 (100%)	97 (94%)	6 (6%)	18	40
17	AO	122/122 (100%)	119 (98%)	3 (2%)	42	63
18	AF	181/197 (92%)	174 (96%)	7 (4%)	28	49
19	AS	61/61 (100%)	60 (98%)	1 (2%)	55	70
20	A3	99/99 (100%)	95 (96%)	4 (4%)	28	49
20	B4	99/99 (100%)	94 (95%)	5 (5%)	21	42
20	BG	99/99 (100%)	90 (91%)	9 (9%)	9	27
22	AY	41/41 (100%)	38 (93%)	3 (7%)	13	34
23	AT	99/114 (87%)	99 (100%)	0	100	100
24	AA	166/171 (97%)	161 (97%)	5 (3%)	36	57
25	AH	184/184 (100%)	164 (89%)	20 (11%)	6	21
26	AP	46/46 (100%)	41 (89%)	5 (11%)	6	21
28	AV	89/89 (100%)	82 (92%)	7 (8%)	11	32
28	B6	85/89 (96%)	78 (92%)	7 (8%)	10	31
29	AL	91/91 (100%)	80 (88%)	11 (12%)	5	17
30	AU	121/127 (95%)	116 (96%)	5 (4%)	27	49
31	BY	133/133 (100%)	112 (84%)	21 (16%)	2	12
32	BO	166/169 (98%)	157 (95%)	9 (5%)	20	41
33	BC	312/312 (100%)	295 (95%)	17 (5%)	20	41
34	B5	64/66 (97%)	58 (91%)	6 (9%)	8	26
34	BK	64/66 (97%)	60 (94%)	4 (6%)	16	37
35	BL	117/117 (100%)	102 (87%)	15 (13%)	4	15
36	Bf	47/47 (100%)	37 (79%)	10 (21%)	1	6
37	BU	110/110 (100%)	106 (96%)	4 (4%)	31	52
38	Bb	114/117 (97%)	103 (90%)	11 (10%)	8	25
39	Be	51/51 (100%)	44 (86%)	7 (14%)	3	14
40	BE	158/158 (100%)	154 (98%)	4 (2%)	42	63
41	Ba	80/83 (96%)	70 (88%)	10 (12%)	4	16
42	BT	75/77 (97%)	71 (95%)	4 (5%)	20	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	Bk	179/280 (64%)	157 (88%)	22 (12%)	4	17
44	BW	66/66 (100%)	64 (97%)	2 (3%)	36	57
45	Bi	57/61 (93%)	56 (98%)	1 (2%)	51	68
46	BA	182/182 (100%)	175 (96%)	7 (4%)	29	50
47	BI	122/122 (100%)	118 (97%)	4 (3%)	33	55
48	BR	85/87 (98%)	73 (86%)	12 (14%)	3	13
49	BQ	130/130 (100%)	120 (92%)	10 (8%)	12	32
50	BV	56/56 (100%)	52 (93%)	4 (7%)	13	35
51	Bj	82/83 (99%)	67 (82%)	15 (18%)	2	9
52	BB	189/189 (100%)	178 (94%)	11 (6%)	18	40
53	BD	213/213 (100%)	198 (93%)	15 (7%)	14	35
54	BF	156/156 (100%)	149 (96%)	7 (4%)	24	46
55	Bh	23/23 (100%)	23 (100%)	0	100	100
56	BH	110/137 (80%)	91 (83%)	19 (17%)	2	9
57	BZ	80/80 (100%)	72 (90%)	8 (10%)	7	24
58	BP	101/101 (100%)	98 (97%)	3 (3%)	36	57
59	BM	162/162 (100%)	156 (96%)	6 (4%)	30	51
60	BS	126/130 (97%)	121 (96%)	5 (4%)	28	49
61	Bd	81/81 (100%)	69 (85%)	12 (15%)	3	13
62	BN	140/152 (92%)	138 (99%)	2 (1%)	59	72
63	Bg	37/39 (95%)	33 (89%)	4 (11%)	6	21
64	Bc	74/74 (100%)	60 (81%)	14 (19%)	1	8
65	BJ	104/108 (96%)	96 (92%)	8 (8%)	12	32
66	Bl	72/72 (100%)	69 (96%)	3 (4%)	26	48
All	All	7390/7646 (97%)	6879 (93%)	511 (7%)	16	36

5 of 511 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BL	22	LYS
28	B6	14	ILE
41	Ba	77	GLU
57	BZ	55	LEU
61	Bd	80	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 134 such sidechains are listed below:

Mol	Chain	Res	Type
54	BF	112	ASN
58	BP	110	ASN
62	BN	56	GLN
24	AA	133	GLN
24	AA	69	GLN

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%)	261 (17%)	118 (7%)
27	A0	75/76 (98%)	18 (24%)	3 (4%)
67	B1	3047/3049 (99%)	614 (20%)	194 (6%)
68	B3	126/126 (100%)	35 (27%)	13 (10%)
All	All	4818/4823 (99%)	943 (19%)	331 (6%)

5 of 943 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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

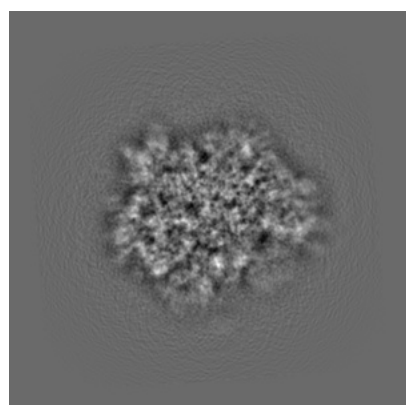
6 Map visualisation [i](#)

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.

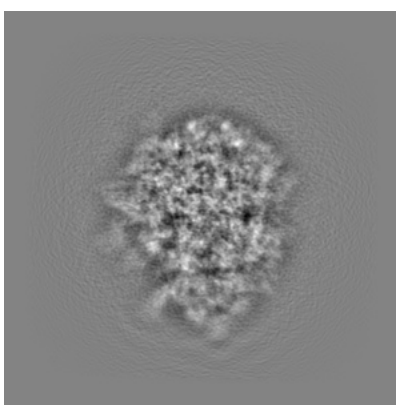
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

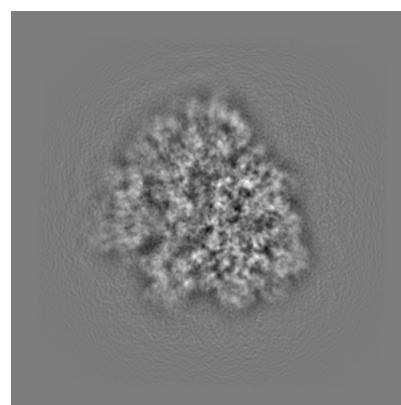
6.1.1 Primary map



X



Y

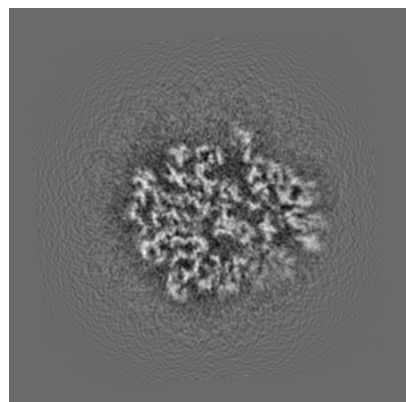


Z

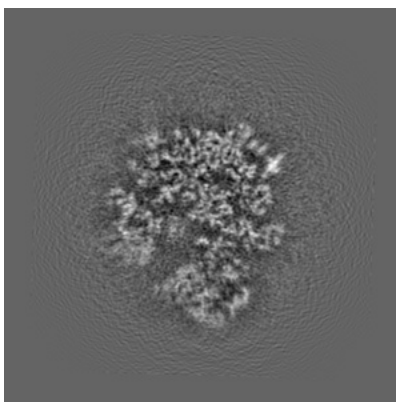
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

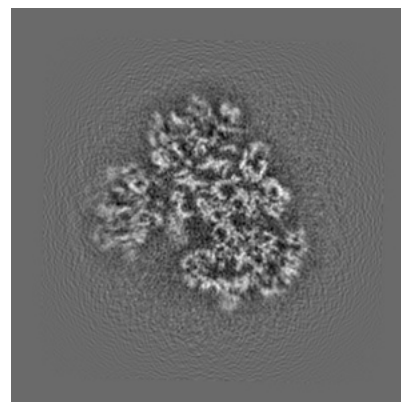
6.2.1 Primary map



X Index: 184



Y Index: 184

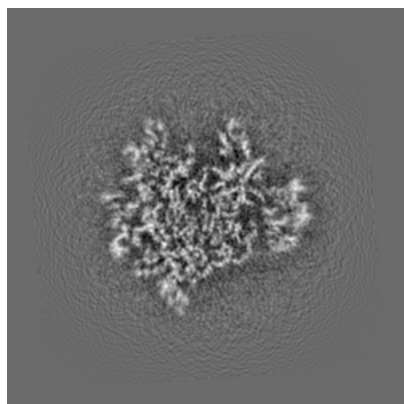


Z Index: 184

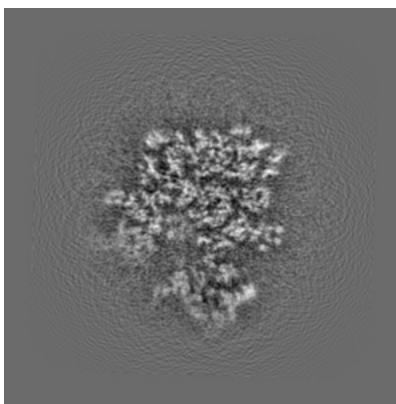
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

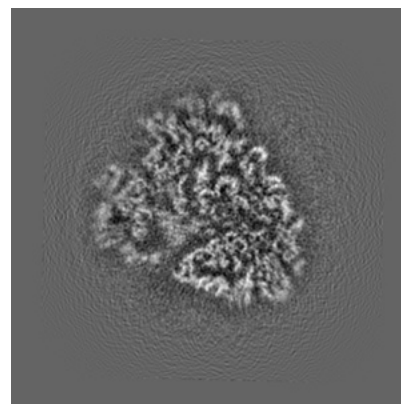
6.3.1 Primary map



X Index: 207



Y Index: 187

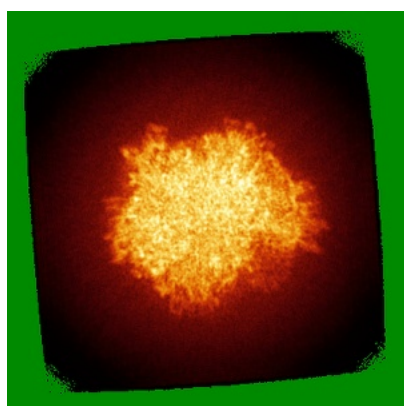


Z Index: 178

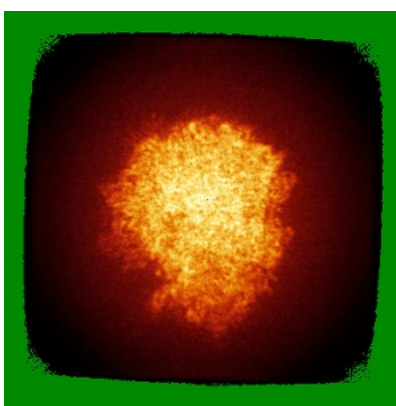
The images above show the largest variance slices of the map in three orthogonal directions.

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

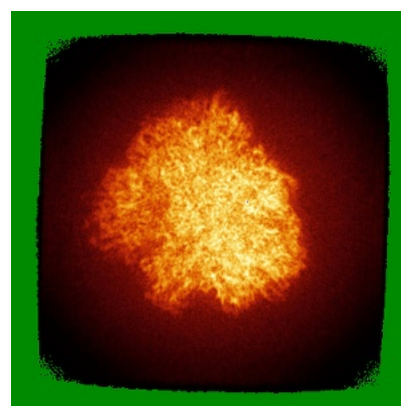
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

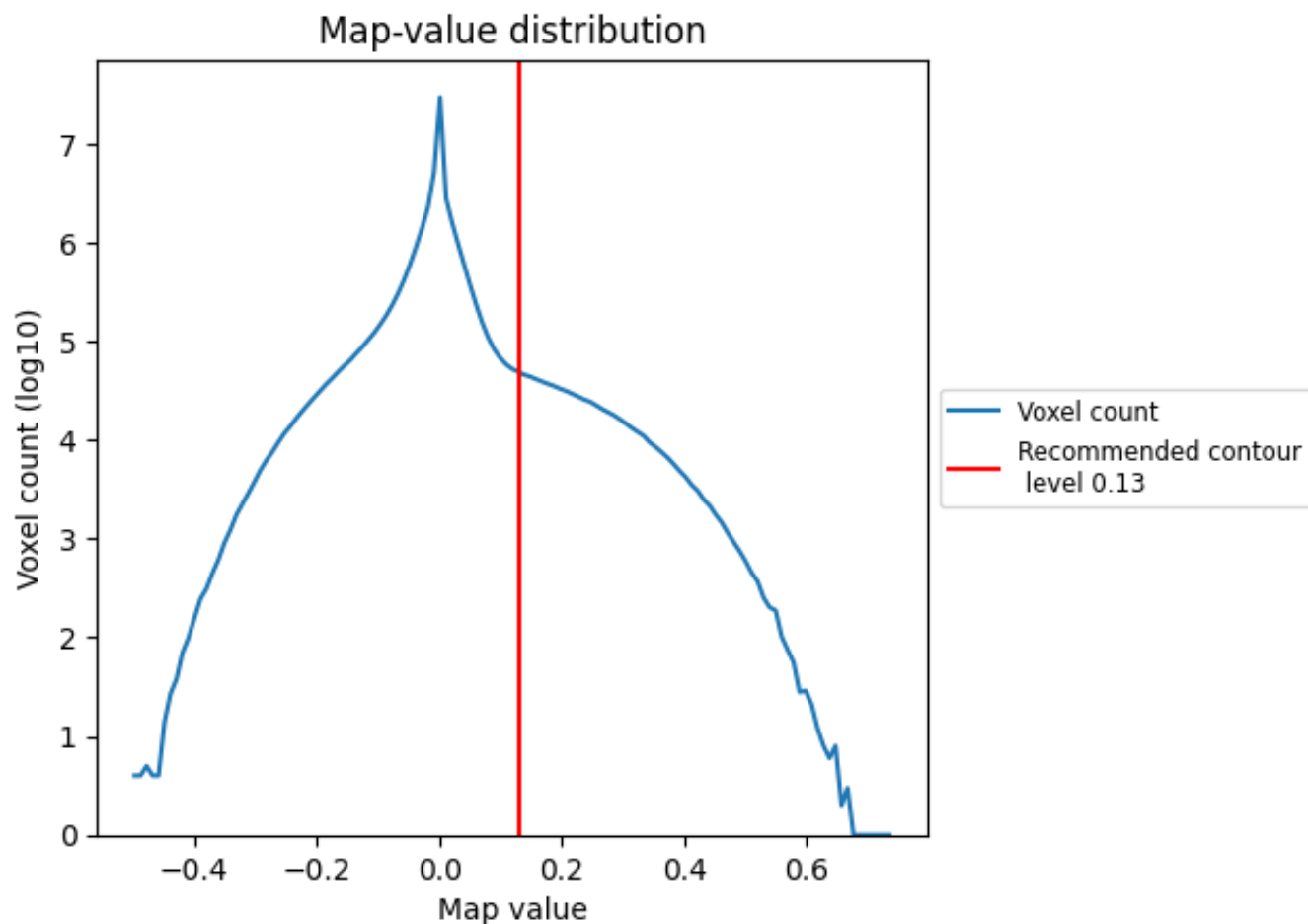
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

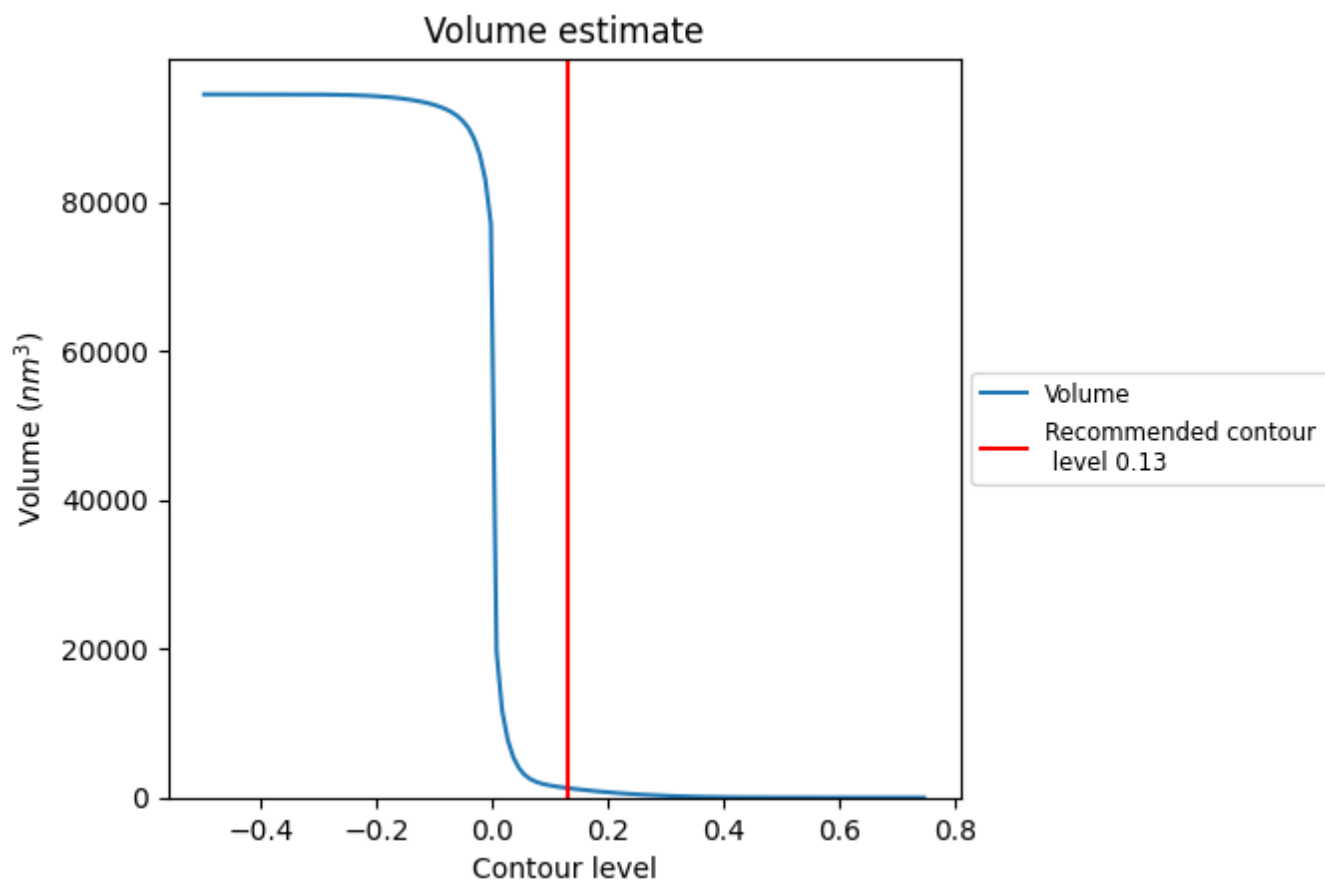
This section contains the results of statistical analysis of the map.

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.

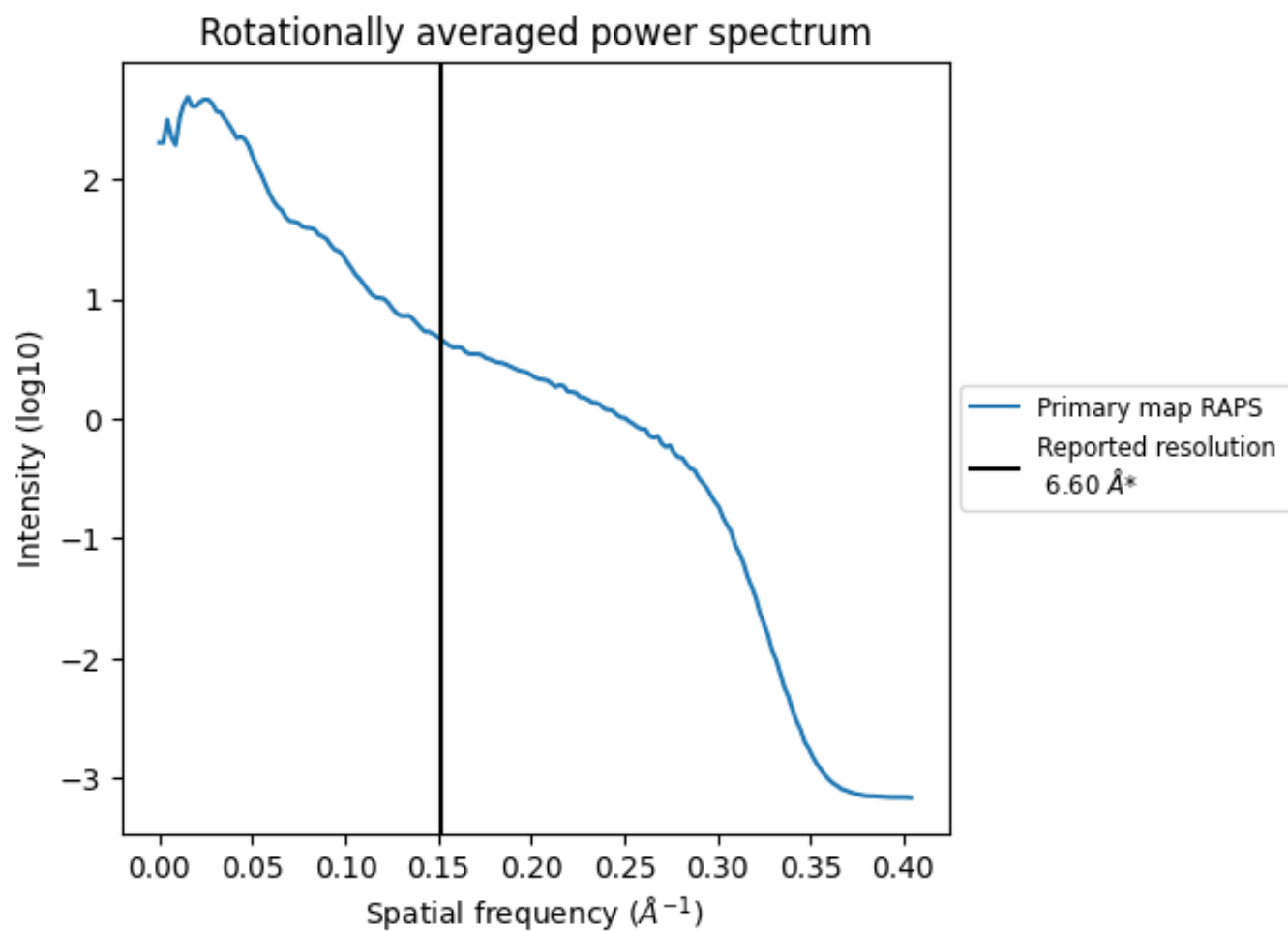
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1275 nm³; 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⁻¹

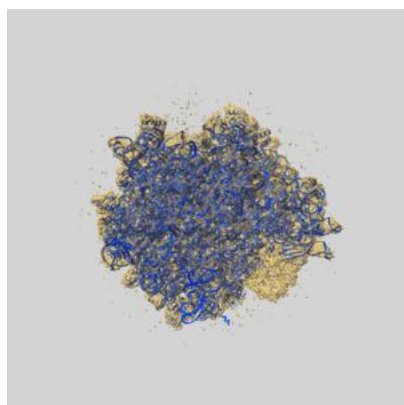
8 Fourier-Shell correlation

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

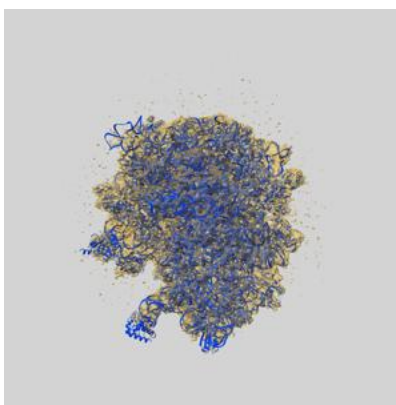
9 Map-model fit [i](#)

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

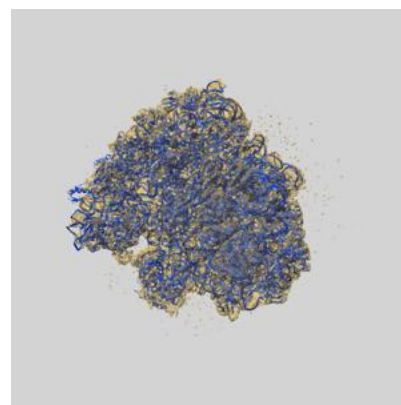
9.1 Map-model overlay [i](#)



X



Y



Z

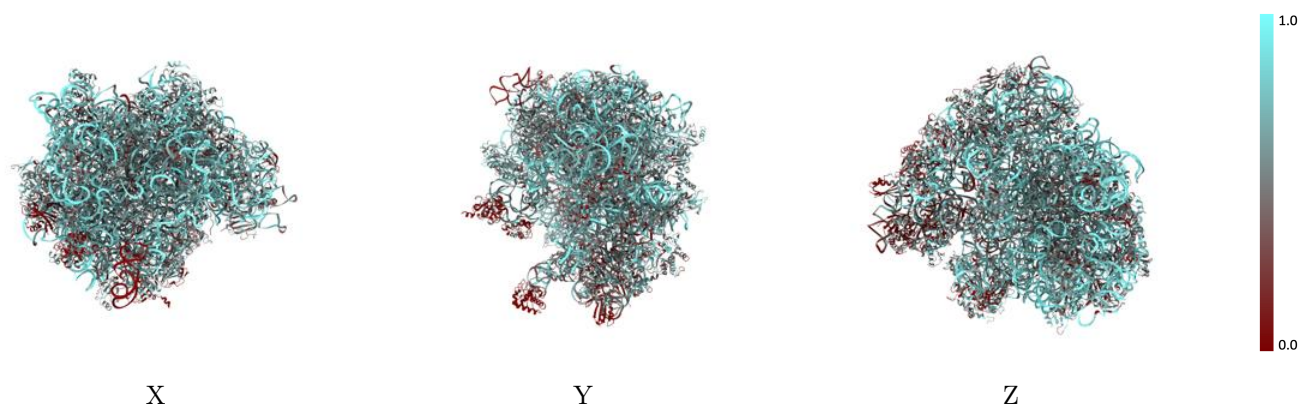
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



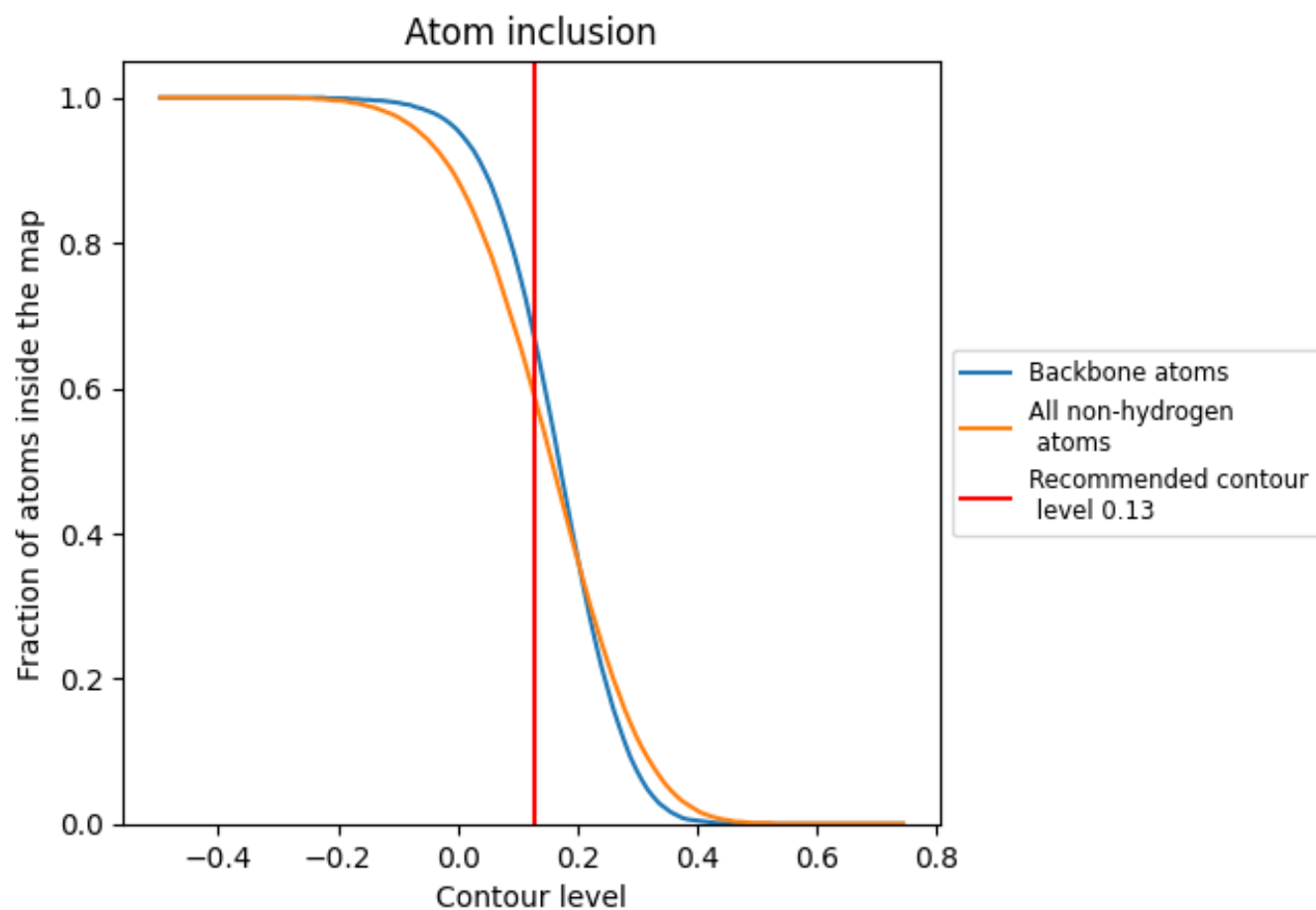
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.5850	 0.1970
A0	 0.5350	 0.1690
A1	 0.5730	 0.1410
A2	 0.6950	 0.2250
A3	 0.0390	 0.0200
A9	 0.6780	 0.2060
AA	 0.5370	 0.1380
AB	 0.4360	 0.1460
AC	 0.4010	 0.1390
AD	 0.4180	 0.1260
AE	 0.3490	 0.1190
AF	 0.3930	 0.1500
AG	 0.3920	 0.0820
AH	 0.2890	 0.0810
AI	 0.4310	 0.1390
AJ	 0.4060	 0.1520
AK	 0.1950	 0.1020
AL	 0.1400	 0.0710
AM	 0.4440	 0.1560
AN	 0.3730	 0.1420
AO	 0.3790	 0.1050
AP	 0.2360	 0.0950
AQ	 0.4920	 0.1430
AR	 0.4240	 0.1750
AS	 0.4260	 0.1170
AT	 0.3560	 0.0990
AU	 0.2280	 0.0850
AV	 0.3490	 0.1020
AW	 0.5250	 0.1240
AX	 0.3960	 0.1410
AY	 0.0980	 0.0320
B1	 0.7260	 0.2500
B3	 0.7980	 0.2180
B4	 0.1960	 0.1010
B5	 0.5640	 0.1560



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
B6	 0.0170	 0.0390
BA	 0.2180	 0.0480
BB	 0.4490	 0.2180
BC	 0.4300	 0.1680
BD	 0.4160	 0.1590
BE	 0.4770	 0.1130
BF	 0.5640	 0.1920
BG	 0.5600	 0.1520
BH	 0.2310	 0.0610
BI	 0.4290	 0.1670
BJ	 0.4340	 0.2070
BK	 0.5250	 0.1440
BL	 0.3960	 0.1390
BM	 0.3400	 0.1790
BN	 0.4500	 0.1800
BO	 0.4610	 0.1510
BP	 0.4880	 0.1710
BQ	 0.4510	 0.1440
BR	 0.3650	 0.1810
BS	 0.4530	 0.1740
BT	 0.4690	 0.1790
BU	 0.4500	 0.1560
BV	 0.4300	 0.1440
BW	 0.5400	 0.1570
BY	 0.4660	 0.1800
BZ	 0.5690	 0.1650
Ba	 0.4980	 0.1790
Bb	 0.3980	 0.1540
Bc	 0.3920	 0.1610
Bd	 0.3210	 0.1200
Be	 0.2930	 0.1250
Bf	 0.3290	 0.1430
Bg	 0.3670	 0.1280
Bh	 0.3320	 0.0850
Bi	 0.5060	 0.2030
Bj	 0.3950	 0.1330
Bk	 0.1440	 0.0340
Bl	 0.5090	 0.1590