



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 06:20 PM UTC

PDB ID : 4V7H / pdb_00004v7h
EMDB ID : EMD-1345
Title : Structure of the 80S rRNA and proteins and P/E tRNA for eukaryotic ribosome based on cryo-EM map of *Thermomyces lanuginosus* ribosome at 8.9Å resolution
Authors : Taylor, D.J.; Devkota, B.; Huang, A.D.; Topf, M.; Narayanan, E.; Sali, A.; Harvey, S.C.; Frank, J.
Deposited on : 2009-09-22
Resolution : 8.90 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:

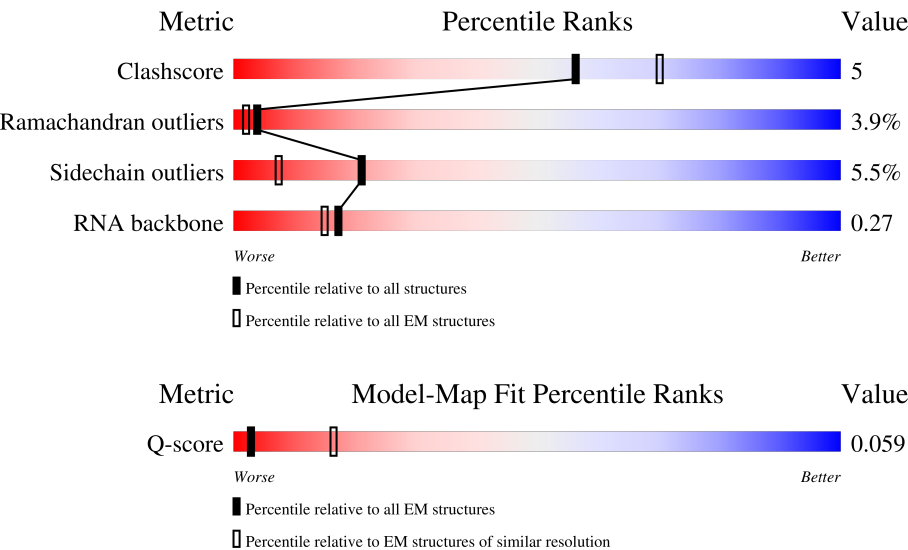
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 i

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

The reported resolution of this entry is 8.90 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	258 (8.40 - 9.40)

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	AA	1761	15% 72% 21% 5% .
2	AB	193	35% 96% . .
3	AC	188	52% 91% 9% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	AD	158	
5	AE	162	
6	AG	186	
7	AH	125	
8	AI	138	
9	AJ	96	
10	AK	125	
11	AL	118	
12	AM	130	
13	AN	50	
14	AO	84	
15	AQ	80	
16	AS	71	
17	AR	313	
18	AT	141	
19	A7	76	
20	B0	109	
21	B1	48	
22	B2	98	
23	B8	118	
24	B9	72	
25	BA	213	
26	BB	243	
27	BC	362	
28	BD	257	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	BE	237	
30	BF	213	
31	BG	113	
32	BH	179	
33	BI	165	
34	BJ	151	
35	BK	138	
36	BL	192	
37	BM	178	
38	BN	150	
39	BO	121	
40	BP	176	
41	BQ	116	
42	BR	131	
43	BS	45	
44	BT	80	
45	BU	116	
46	BV	142	
47	BW	79	
48	BX	86	
49	BY	52	
50	BZ	92	
51	B3	113	
52	B4	157	
53	B5	3170	

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 165754 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1761	Total	C	N	O	P	0	3
			37458	16745	6626	12327	1760		

- Molecule 2 is a protein called 40S ribosomal protein S0(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	193	Total	C	N	O	S	0	0
			1500	958	269	271	2		

- Molecule 3 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	188	Total	C	N	O	S	0	0
			1469	929	271	263	6		

- Molecule 4 is a protein called 40S ribosomal protein S9(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	124	Total	C	N	O	S	0	0
			1018	647	189	181	1		

- Molecule 5 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	162	Total	C	N	O	S	0	0
			1207	765	222	218	2		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AG	186	Total	C	N	O	S	0	0
			1456	908	277	268	3		

- Molecule 7 is a protein called 40S ribosomal protein S22(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AH	125	Total	C	N	O	S	0	0
			992	634	181	174	3		

- Molecule 8 is a protein called 40S ribosomal protein S16(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AI	138	Total	C	N	O	S	0	0
			1087	695	200	192			

- Molecule 9 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AJ	96	Total	C	N	O	S	0	0
			771	487	140	143	1		

- Molecule 10 is a protein called 40S ribosomal protein S14(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AK	125	Total	C	N	O	S	0	0
			924	566	179	176	3		

- Molecule 11 is a protein called 40S ribosomal protein S23(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	118	Total	C	N	O	S	0	0
			906	579	166	159	2		

- Molecule 12 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AM	130	Total	C	N	O	S	0	0
			1077	669	217	189	2		

- Molecule 13 is a protein called 40S ribosomal protein S29(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AN	50	Total	C	N	O	S	0	0
			417	258	87	68	4		

- Molecule 14 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AO	84	Total	C	N	O	S	0	0
			694	446	129	118	1		

- Molecule 15 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AQ	80	Total	C	N	O	S	0	0
			643	410	127	104	2		

- Molecule 16 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AS	71	Total	C	N	O	S	0	0
			548	348	101	93	6		

- Molecule 17 is a protein called RACK1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	313	Total	C	N	O	S	0	0
			2410	1526	413	463	8		

- Molecule 18 is a protein called s19e protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AT	141	Total	C	N	O	S	0	0
			1102	687	206	207	2		

- Molecule 19 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	A7	76	Total	C	N	O	P	0	0
			1648	746	294	533	75		

- Molecule 20 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	B0	109	Total	C	N	O	S	0	0
			881	555	176	149	1		

- Molecule 21 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B1	48	Total	C	N	O	S	0	0
			424	263	95	64	2		

- Molecule 22 is a protein called 60S ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B2	98	Total	C	N	O	S	0	0
			752	484	125	142	1		

- Molecule 23 is a protein called 60S ribosomal protein LP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	B8	118	Total	C	N	O	S	0	0
			947	609	167	168	3		

- Molecule 24 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B9	72	Total	C	N	O	S	0	0
			539	332	104	98	5		

- Molecule 25 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BA	213	Total	C	N	O	S	0	0
			1683	1074	294	306	9		

- Molecule 26 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BB	243	Total	C	N	O	S	0	0
			1848	1150	374	323	1		

- Molecule 27 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BC	362	Total	C	N	O	S	0	0
			2887	1833	545	502	7		

- Molecule 28 is a protein called 60S ribosomal protein L4(B).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BD	257	Total	C	N	O	S	0	0
			1950	1226	375	346	3		

- Molecule 29 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BE	237	Total	C	N	O	S	0	0
			1913	1210	329	372	2		

- Molecule 30 is a protein called 60S ribosomal protein L7(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BF	213	Total	C	N	O	S	0	0
			1561	1010	281	269	1		

- Molecule 31 is a protein called 60S ribosomal protein L8(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BG	113	Total	C	N	O	S	0	0
			844	540	144	158	2		

- Molecule 32 is a protein called 60S ribosomal protein L9(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BH	179	Total	C	N	O	S	0	0
			1418	896	260	259	3		

- Molecule 33 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BI	165	Total	C	N	O	S	0	0
			1326	834	257	228	7		

- Molecule 34 is a protein called 60S ribosomal protein L11(B).

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BJ	151	Total	C	N	O	S	0	0
			1195	744	229	218	4		

- Molecule 35 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	138	Total	C	N	O	S	0	0
			1038	651	190	195	2		

- Molecule 36 is a protein called 60S ribosomal protein L15(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BL	192	Total	C	N	O	S	0	0
			1618	1011	340	266	1		

- Molecule 37 is a protein called 60S ribosomal protein L16(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BM	178	Total	C	N	O	S	0	0
			1317	845	254	217	1		

- Molecule 38 is a protein called 60S ribosomal protein L17(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BN	150	Total	C	N	O		0	0
			1189	742	230	217			

- Molecule 39 is a protein called 60S ribosomal protein L18(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BO	121	Total	C	N	O	S	0	0
			931	598	170	162	1		

- Molecule 40 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BP	176	Total	C	N	O		0	0
			1317	816	277	224			

- Molecule 41 is a protein called 60S ribosomal protein L21(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BQ	116	Total	C	N	O	S	0	0
			893	564	173	153	3		

- Molecule 42 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BR	131	Total	C	N	O	S	0	0
			977	614	183	173	7		

- Molecule 43 is a protein called 60S ribosomal protein L24(A).

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BS	45	Total	C	N	O	0	0
			371	238	73	60		

- Molecule 44 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BT	80	Total	C	N	O	S	0	0
			642	411	108	121	2		

- Molecule 45 is a protein called 60S ribosomal protein L26(A).

Mol	Chain	Residues	Atoms				AltConf	Trace
45	BU	116	Total	C	N	O	0	0
			916	576	179	161		

- Molecule 46 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BV	142	Total	C	N	O	S	0	0
			1123	717	218	185	3		

- Molecule 47 is a protein called 60S ribosomal protein L31(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	79	Total	C	N	O	S	0	0
			663	415	135	112	1		

- Molecule 48 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BX	86	Total	C	N	O	S	0	0
			605	379	111	114	1		

- Molecule 49 is a protein called 60S ribosomal protein L37(A).

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BY	52	Total	C	N	O	S	0	0
			403	245	85	69	4		

- Molecule 50 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	92	Total	C	N	O	S	0	0
			749	472	151	121	5		

- Molecule 51 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B3	113	Total	C	N	O	P	0	0
			2403	1075	429	787	112		

- Molecule 52 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B4	157	Total	C	N	O	P	0	0
			3329	1490	581	1102	156		

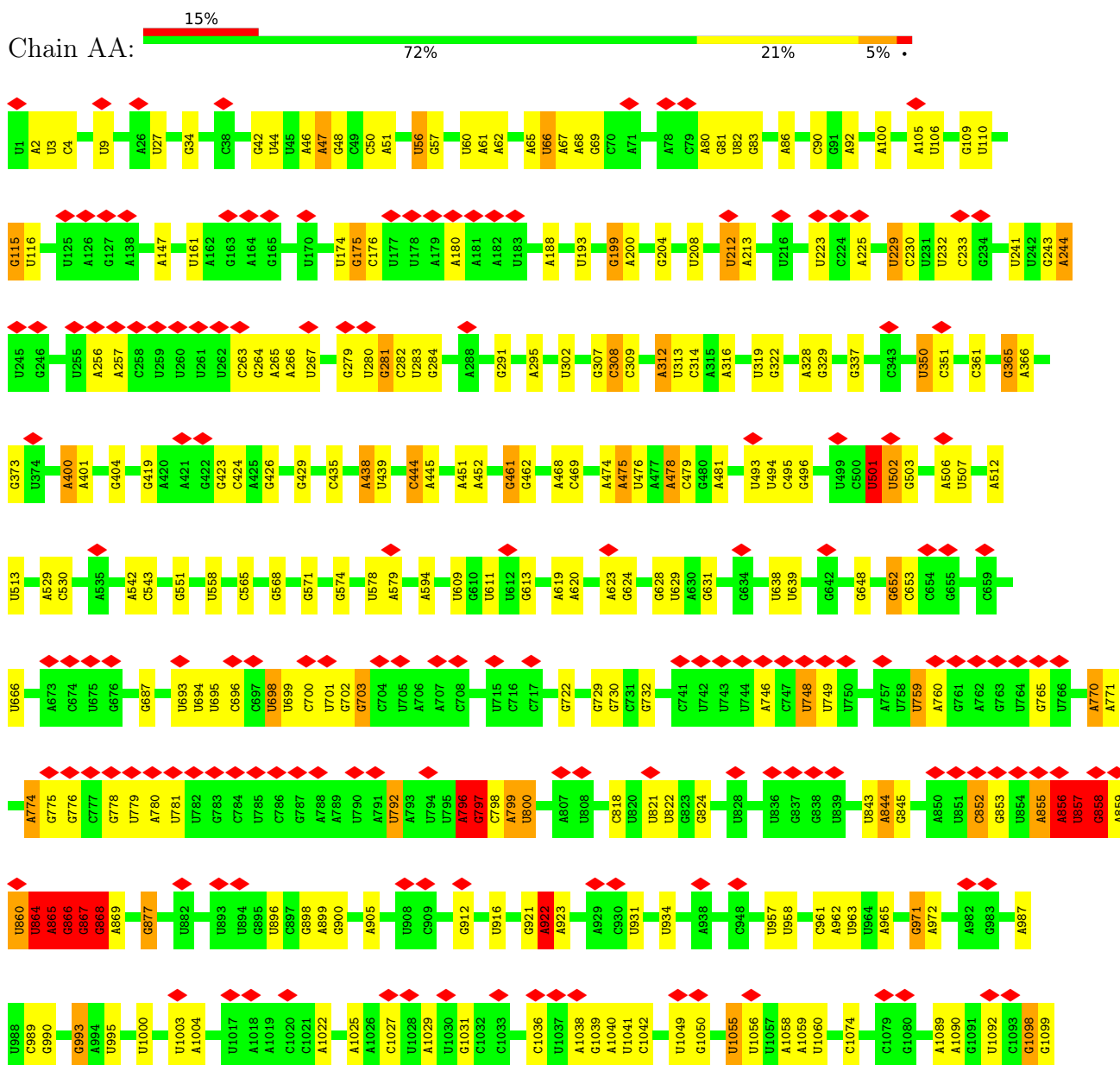
- Molecule 53 is a RNA chain called 26S ribosomal RNA.

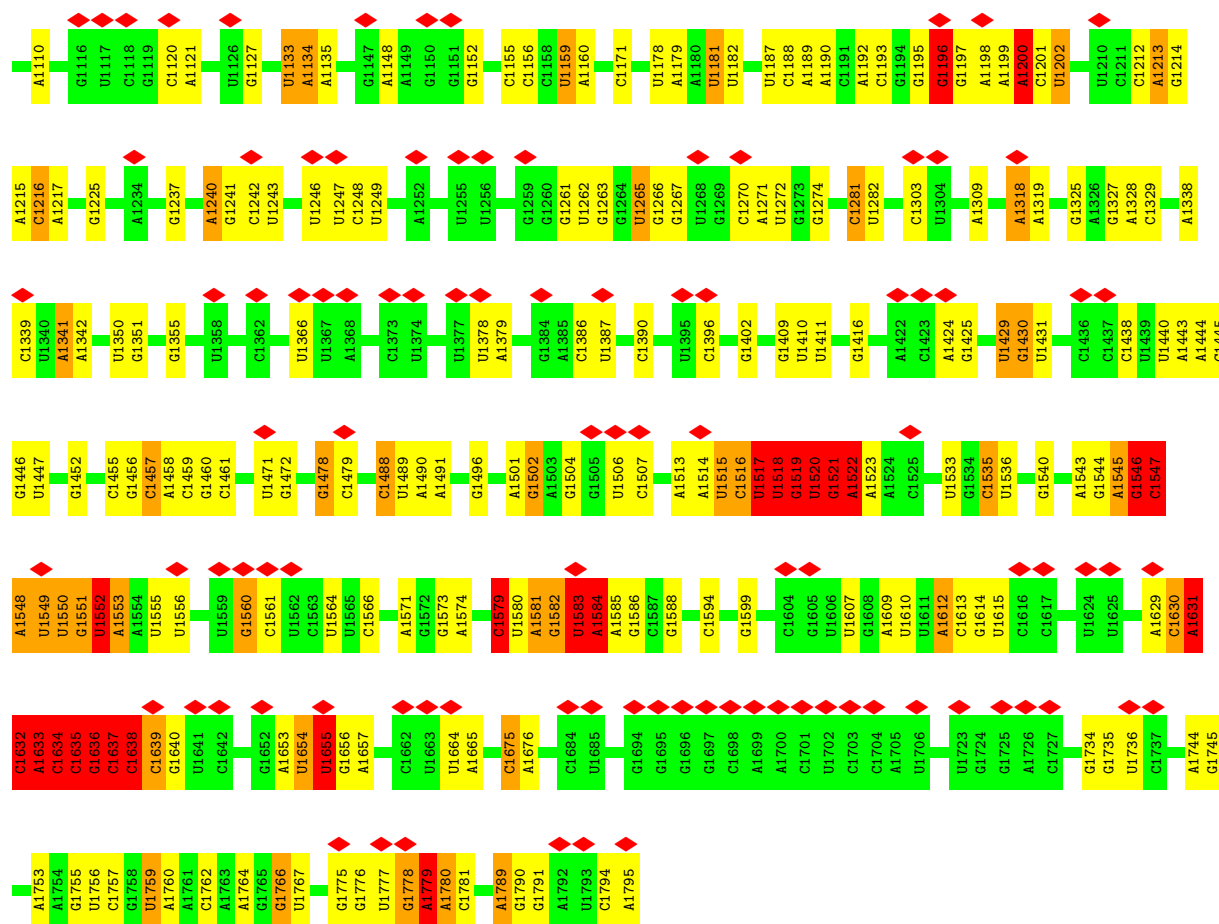
Mol	Chain	Residues	Atoms					AltConf	Trace
53	B5	3170	Total	C	N	O	P	0	0
			67775	30273	12178	22155	3169		

3 Residue-property plots

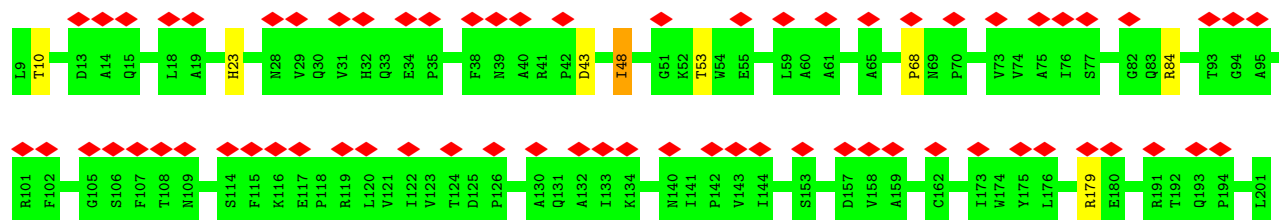
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA

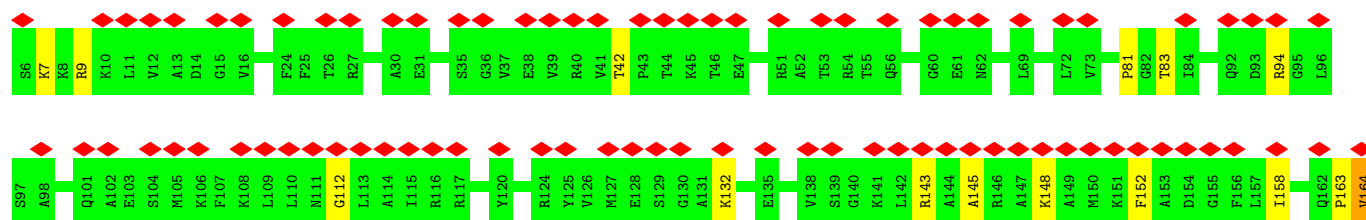
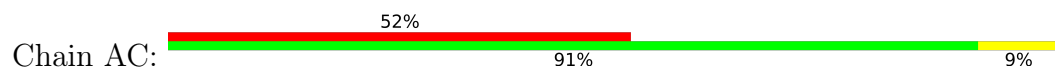


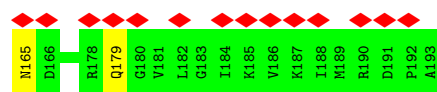


• Molecule 2: 40S ribosomal protein S0(A)

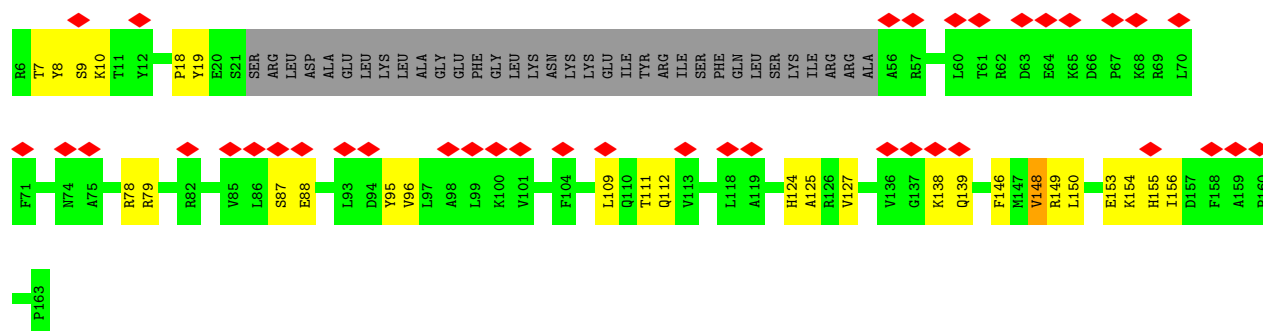


• Molecule 3: 40S ribosomal protein S3

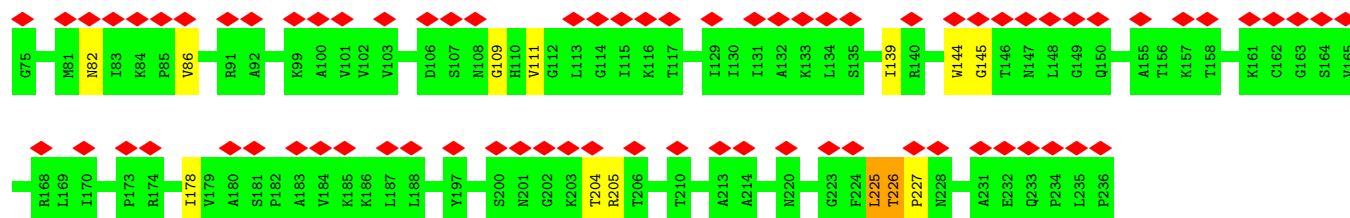




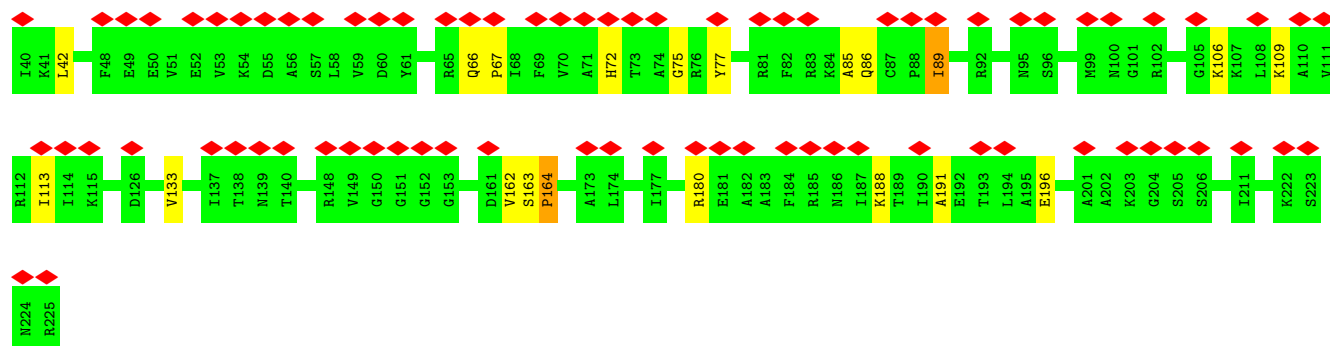
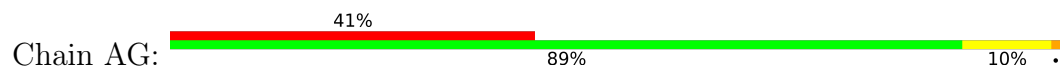
• Molecule 4: 40S ribosomal protein S9(A)



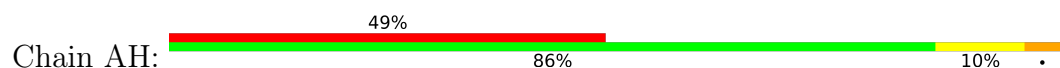
• Molecule 5: 40S ribosomal protein S2

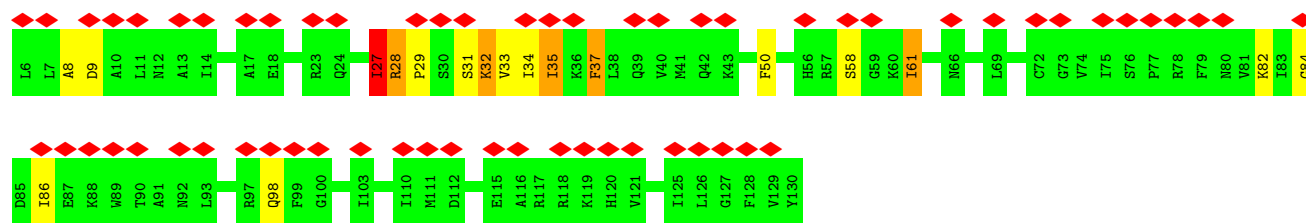


• Molecule 6: 40S ribosomal protein S5

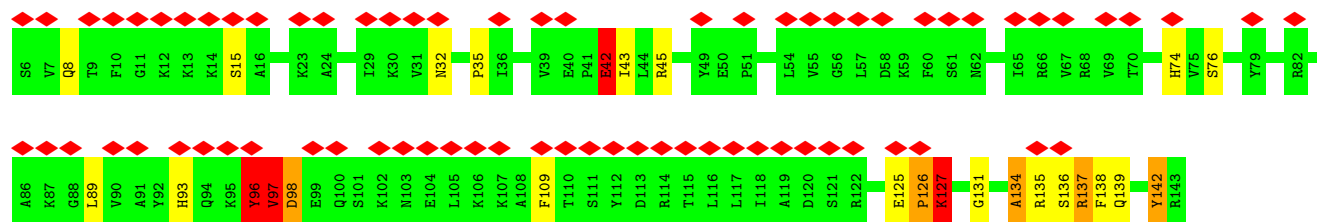
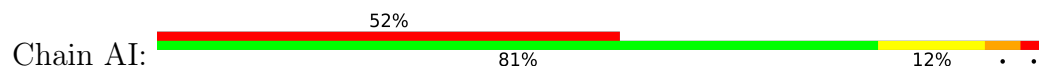


• Molecule 7: 40S ribosomal protein S22(A)

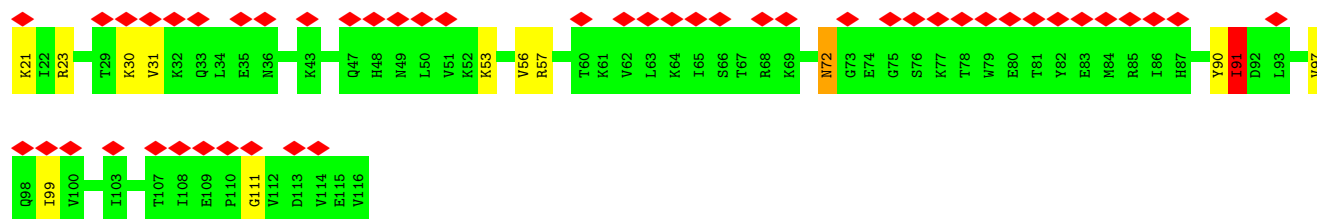
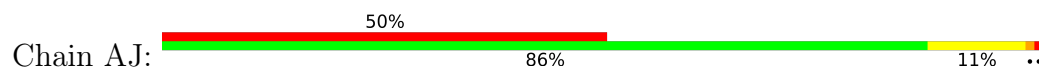




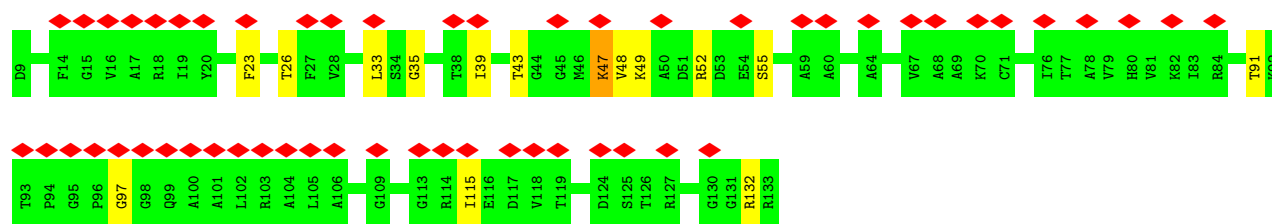
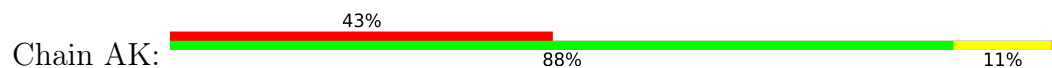
• Molecule 8: 40S ribosomal protein S16(A)



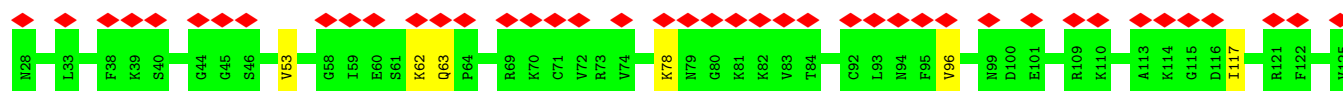
• Molecule 9: 40S ribosomal protein S20

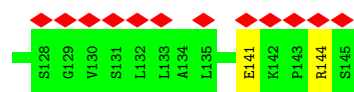


• Molecule 10: 40S ribosomal protein S14(A)

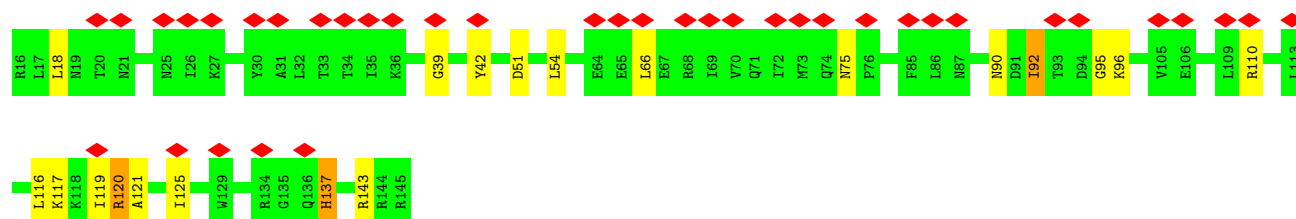
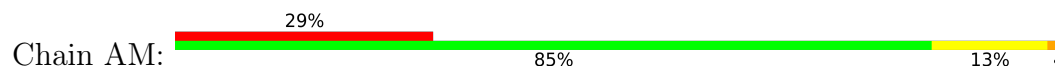


• Molecule 11: 40S ribosomal protein S23(A)

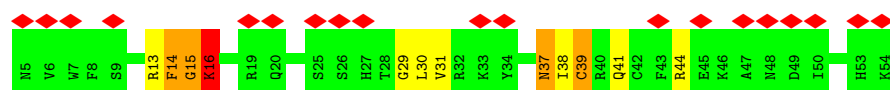
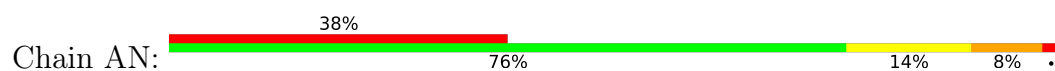




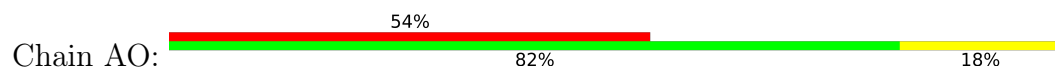
- Molecule 12: 40S ribosomal protein S18



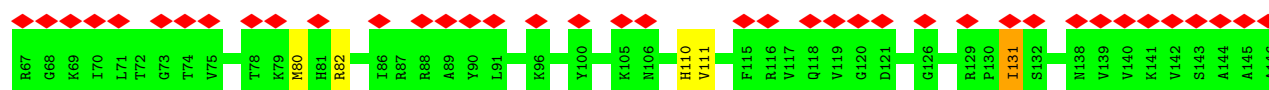
- Molecule 13: 40S ribosomal protein S29(A)



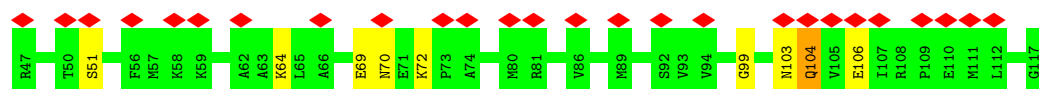
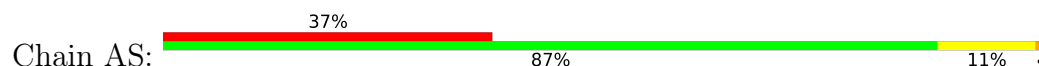
- Molecule 14: 40S ribosomal protein S13



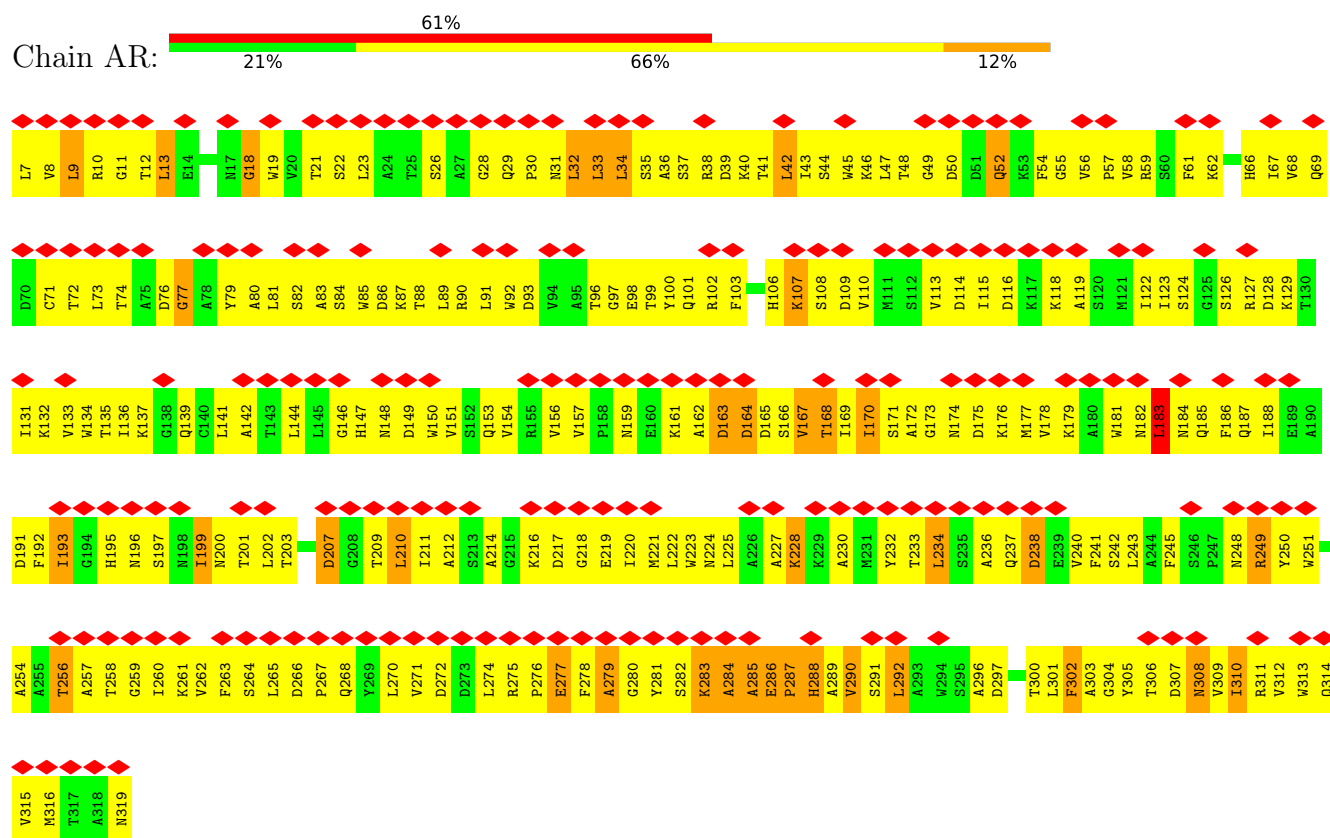
- Molecule 15: 40S ribosomal protein S11



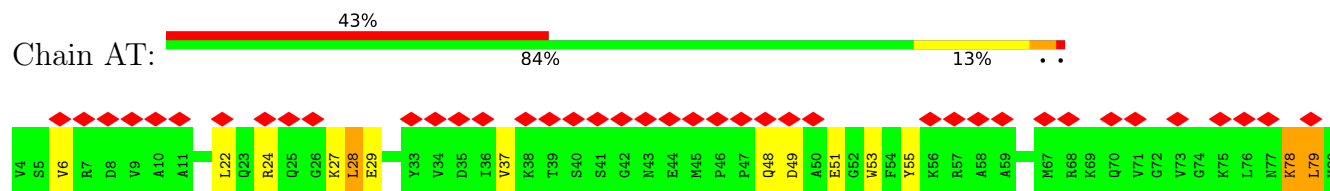
- Molecule 16: 40S ribosomal protein S15



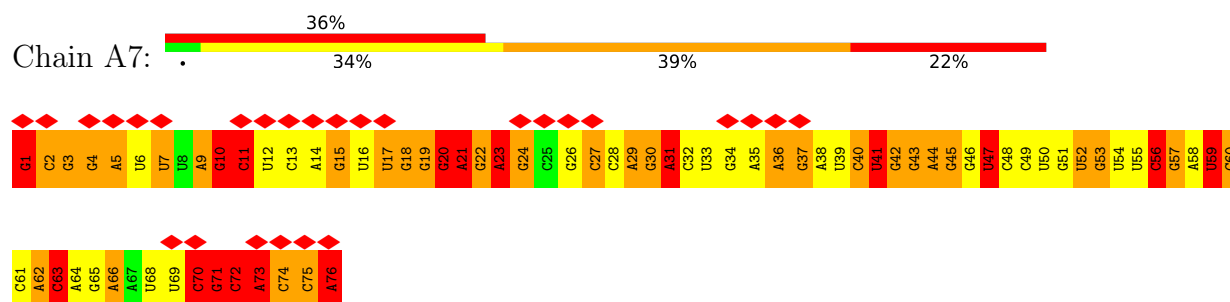
- Molecule 17: RACK1 protein



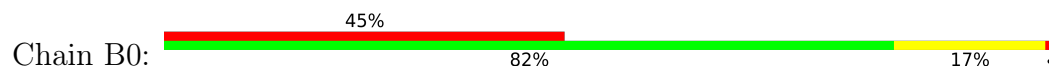
• Molecule 18: s19e protein

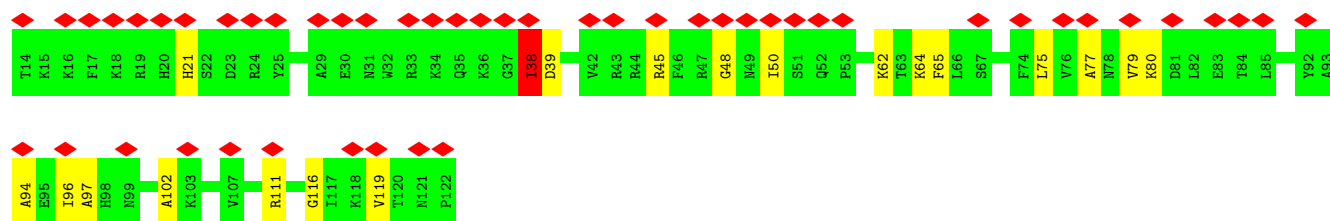


• Molecule 19: P/E tRNA

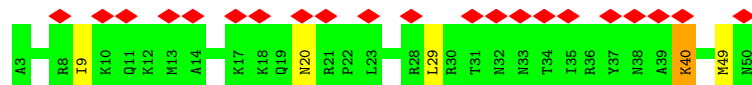


• Molecule 20: 60S ribosomal protein L32

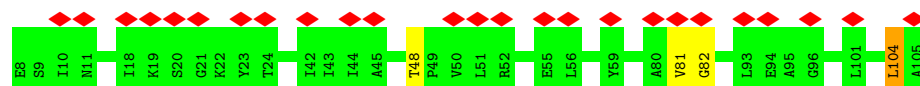




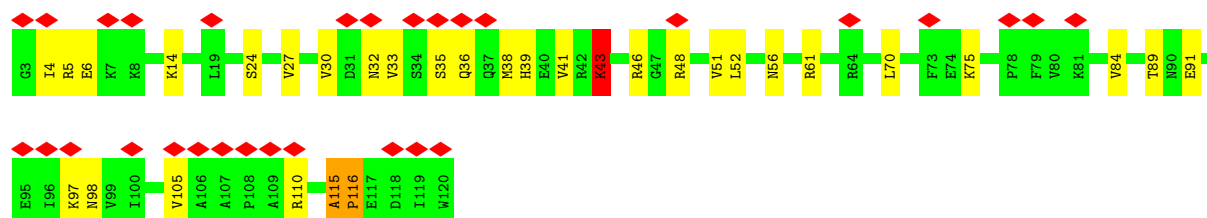
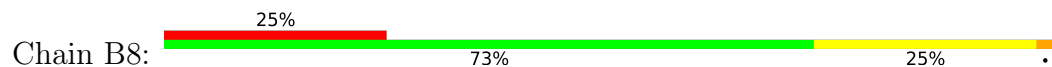
• Molecule 21: 60S ribosomal protein L39



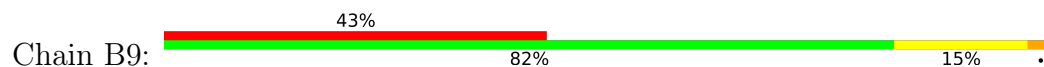
• Molecule 22: 60S ribosomal protein L30e



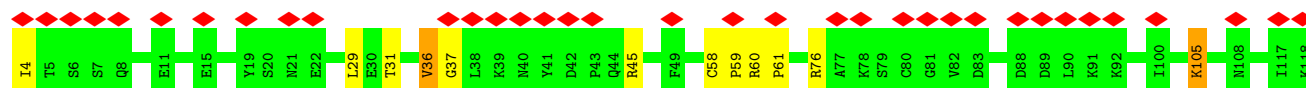
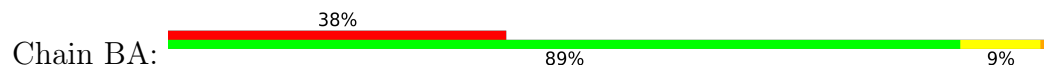
• Molecule 23: 60S ribosomal protein LP0

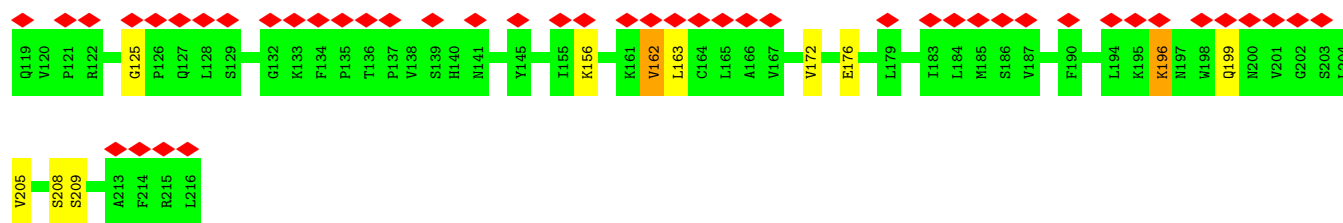


• Molecule 24: 60S ribosomal protein L43

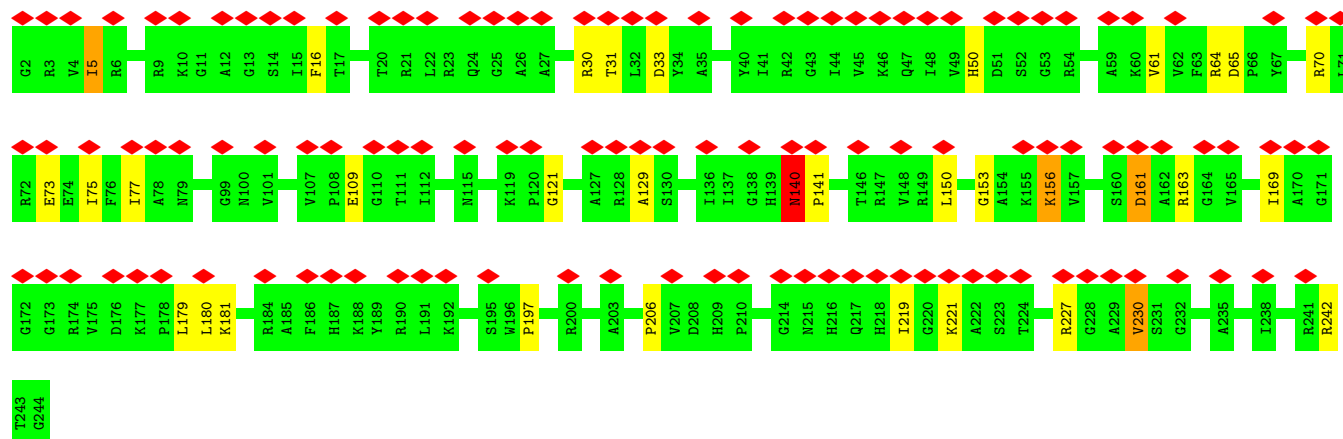
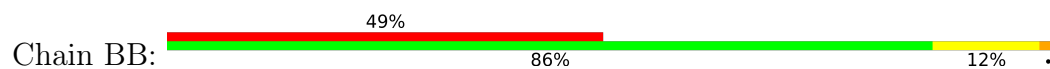


• Molecule 25: 60S ribosomal protein L1

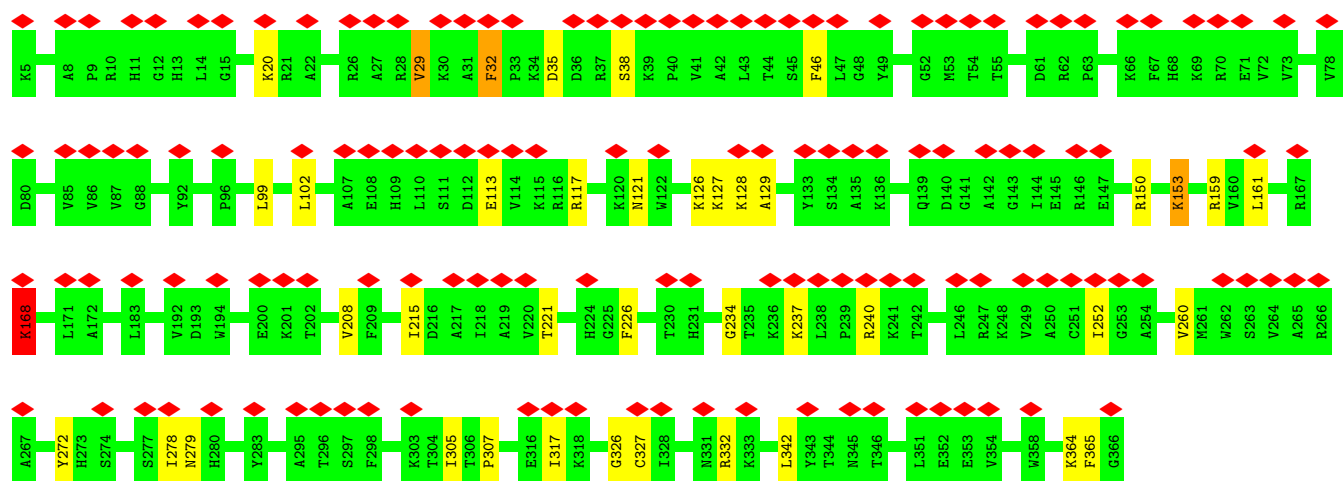
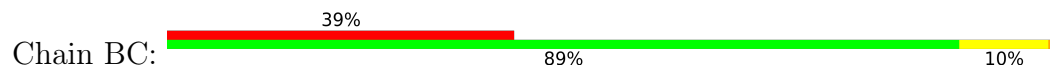




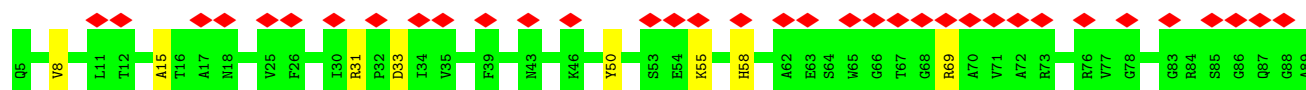
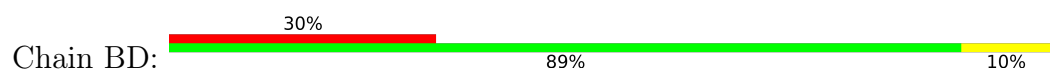
• Molecule 26: 60S ribosomal protein L2

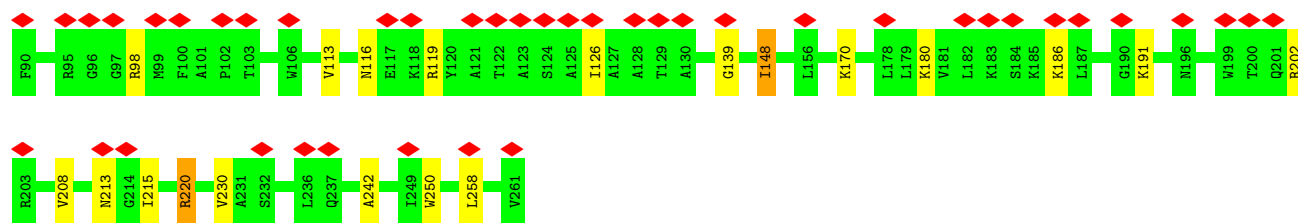


• Molecule 27: 60S ribosomal protein L3

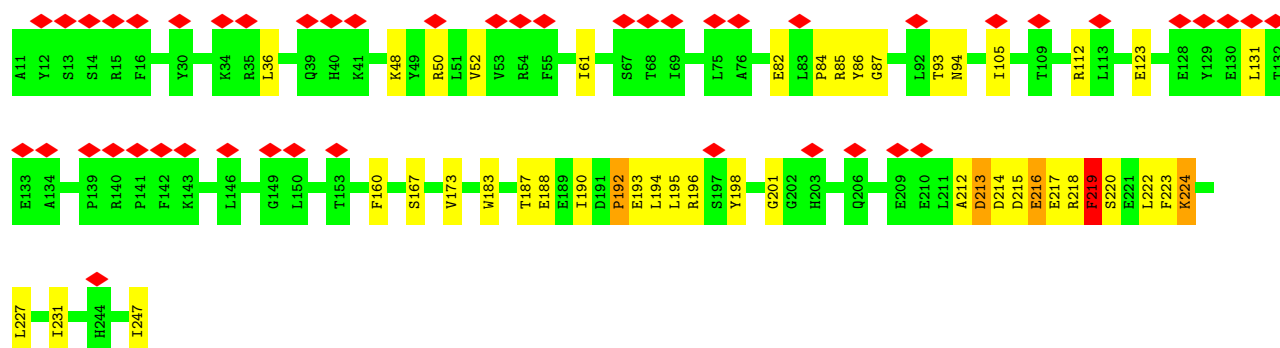
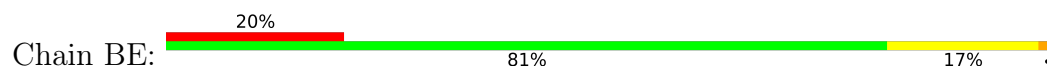


• Molecule 28: 60S ribosomal protein L4(B)

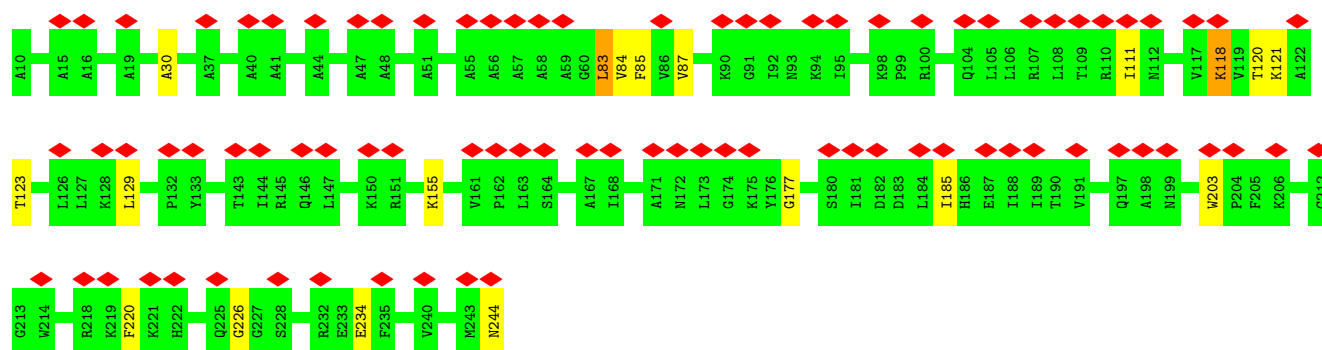
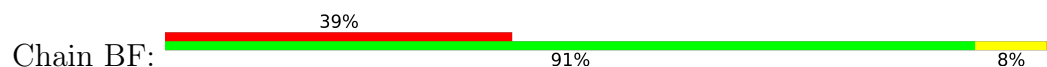




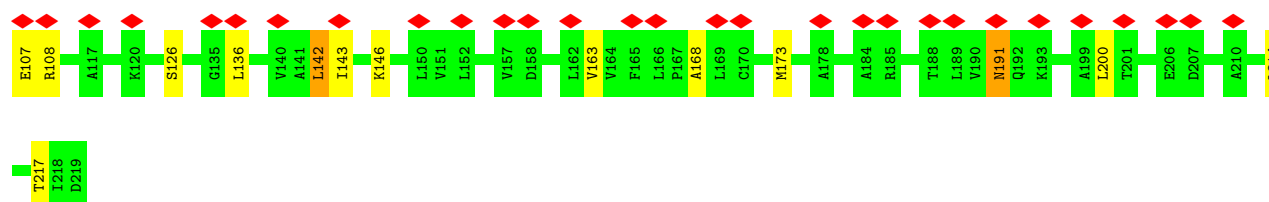
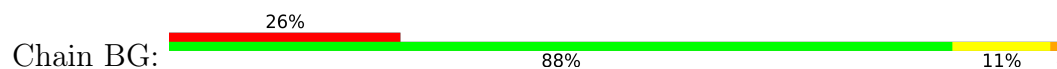
- Molecule 29: 60S ribosomal protein L5



- Molecule 30: 60S ribosomal protein L7(A)

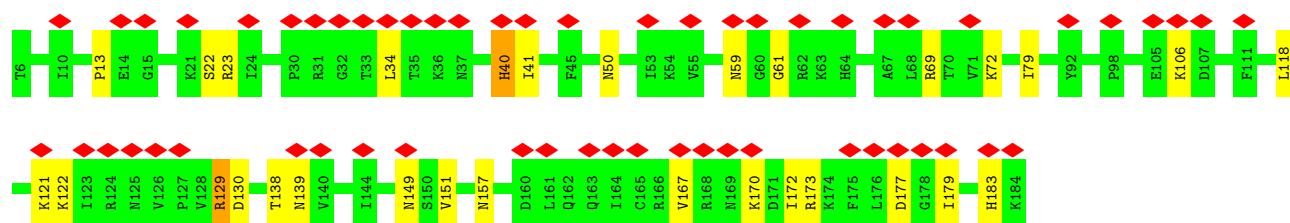


- Molecule 31: 60S ribosomal protein L8(A)



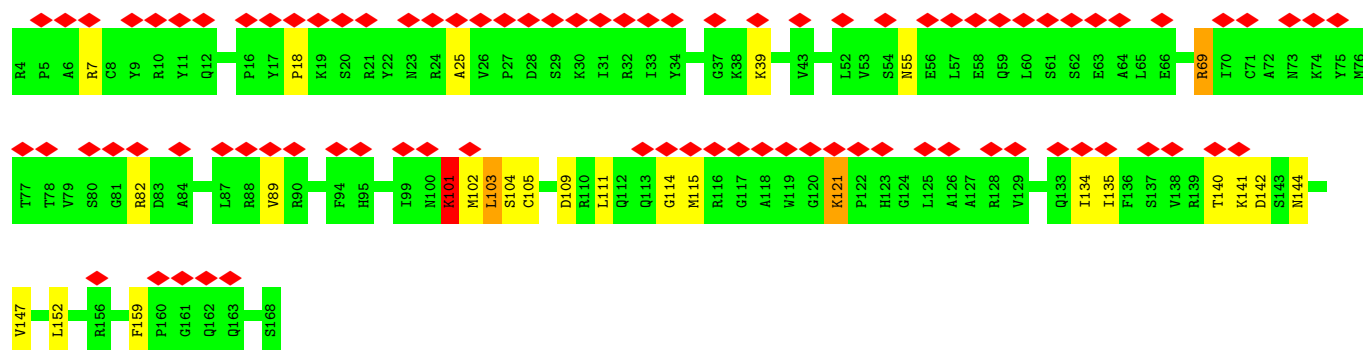
- Molecule 32: 60S ribosomal protein L9(A)

Chain BH: 

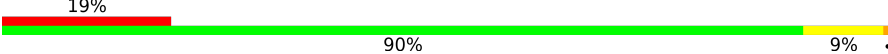


• Molecule 33: 60S ribosomal protein L10

Chain BI: 



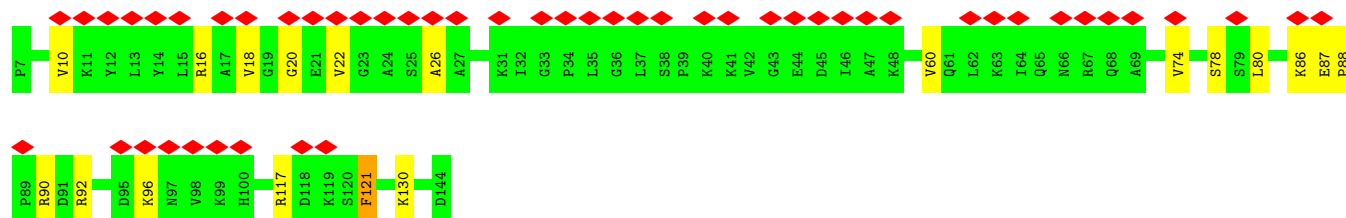
• Molecule 34: 60S ribosomal protein L11(B)

Chain BJ: 



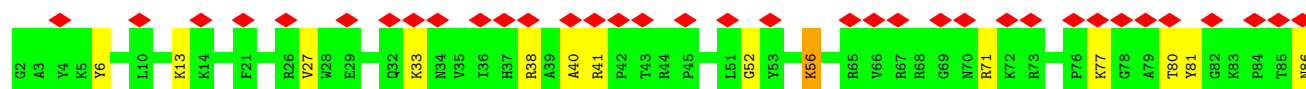
• Molecule 35: 60S ribosomal protein L12

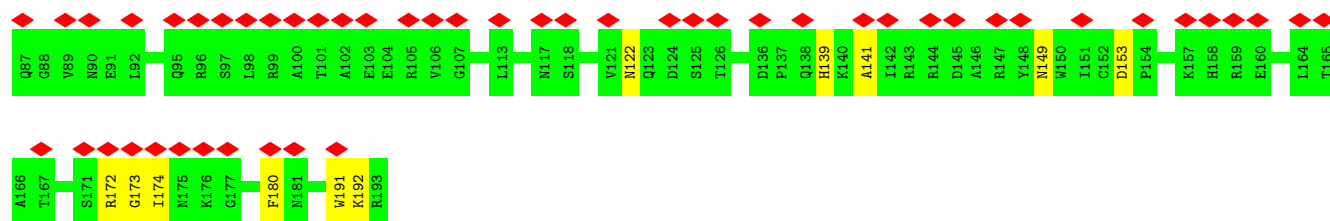
Chain BK: 



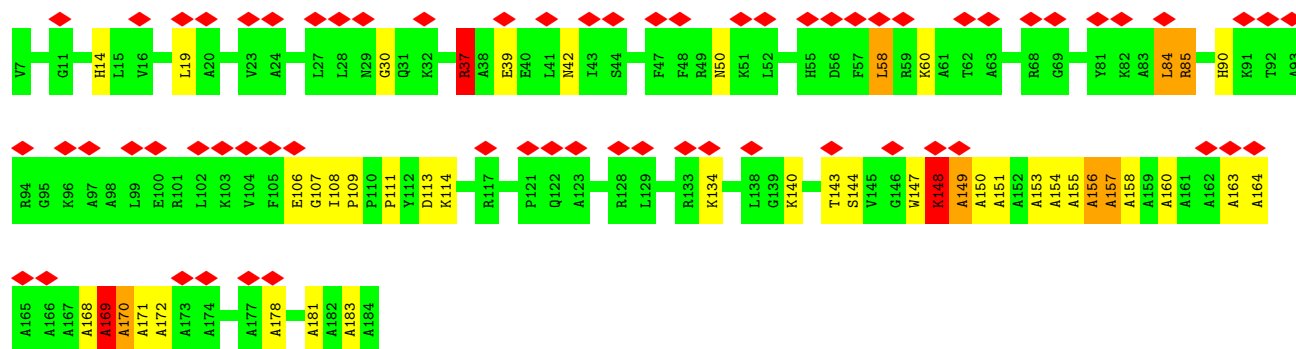
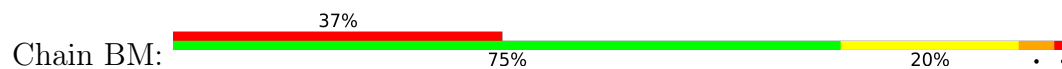
• Molecule 36: 60S ribosomal protein L15(A)

Chain BL: 

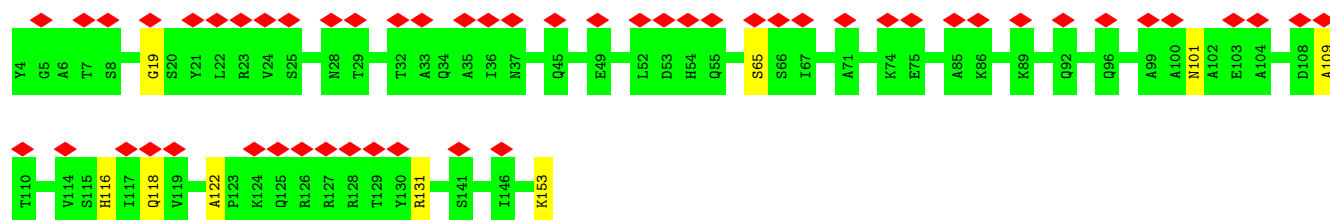




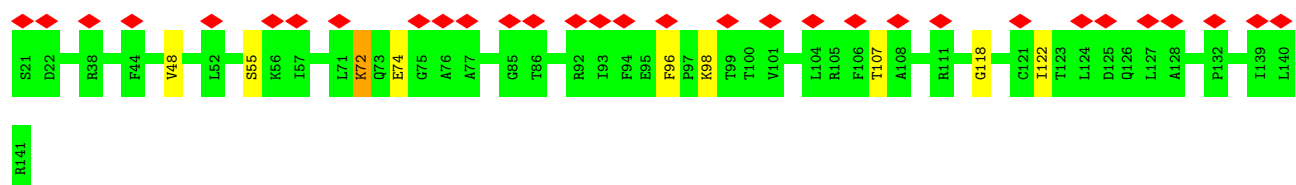
• Molecule 37: 60S ribosomal protein L16(A)



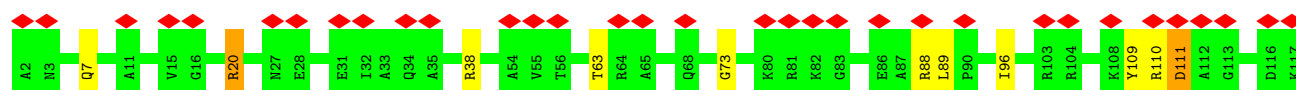
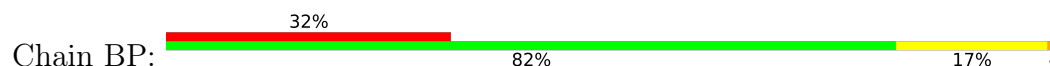
• Molecule 38: 60S ribosomal protein L17(A)

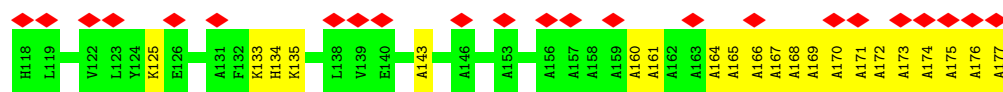


• Molecule 39: 60S ribosomal protein L18(A)

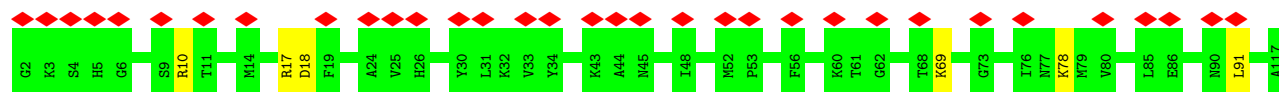


• Molecule 40: 60S ribosomal protein L19

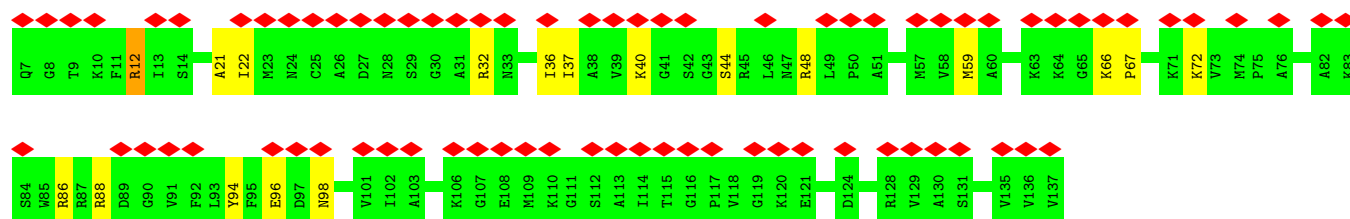
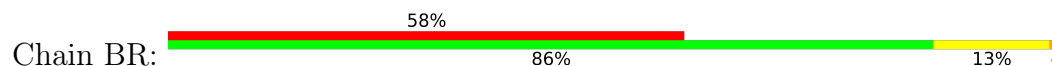




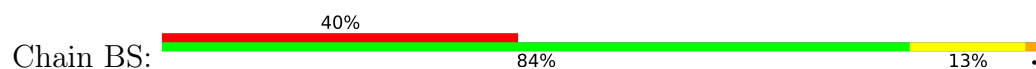
- Molecule 41: 60S ribosomal protein L21(A)



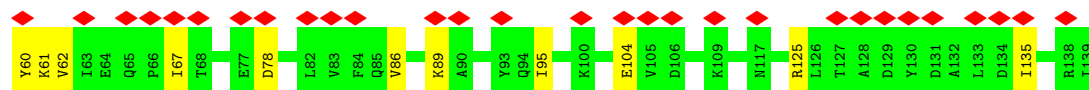
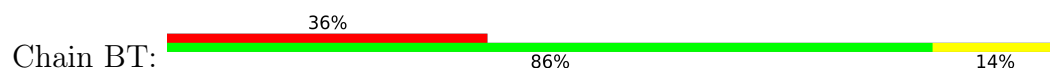
- Molecule 42: 60S ribosomal protein L23



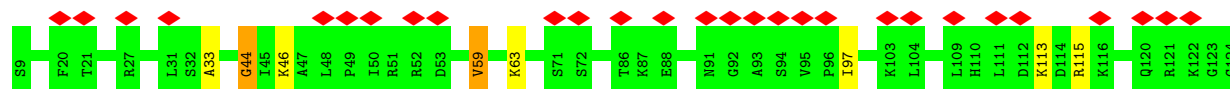
- Molecule 43: 60S ribosomal protein L24(A)



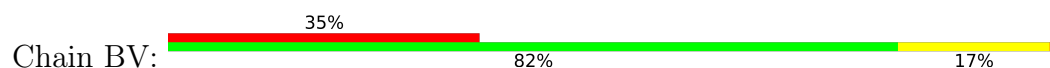
- Molecule 44: 60S ribosomal protein L25

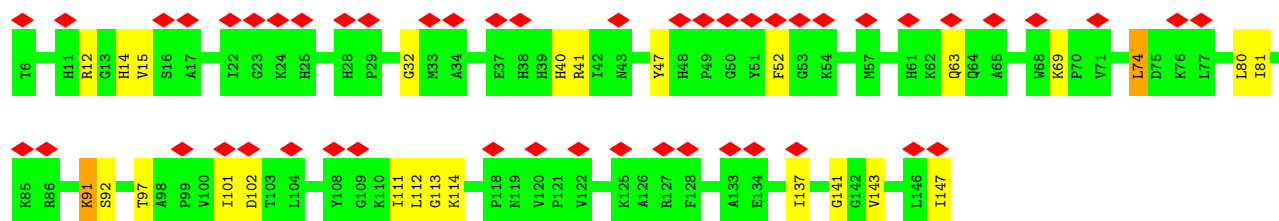


- Molecule 45: 60S ribosomal protein L26(A)

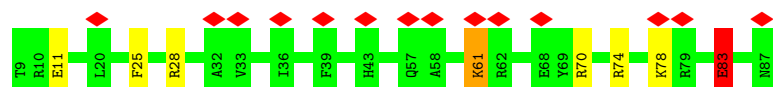
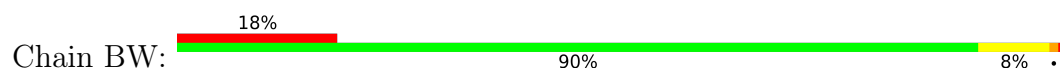


- Molecule 46: 60S ribosomal protein L28

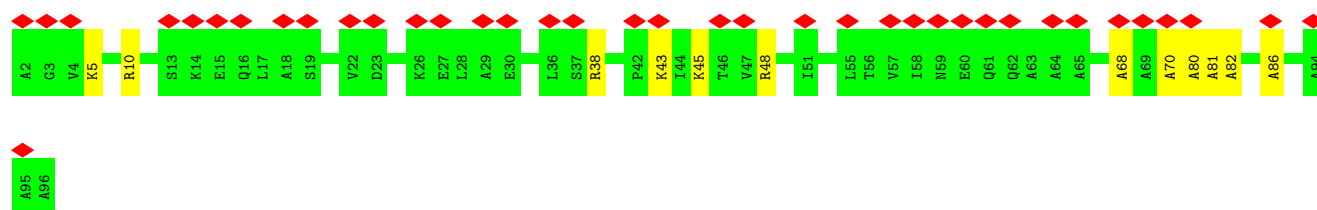
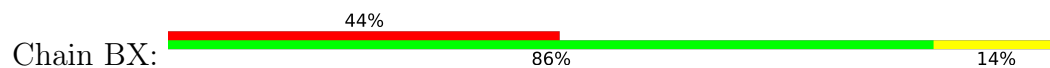




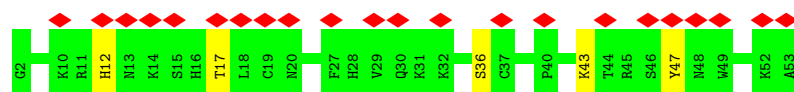
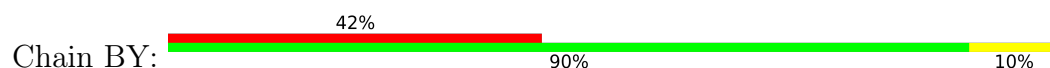
• Molecule 47: 60S ribosomal protein L31(A)



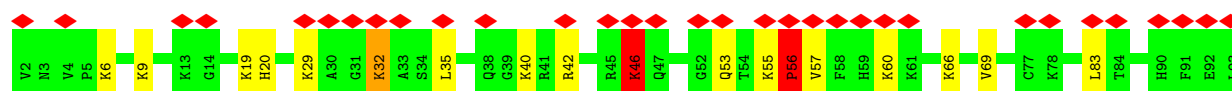
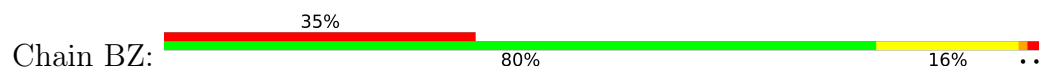
• Molecule 48: 60S ribosomal protein L35



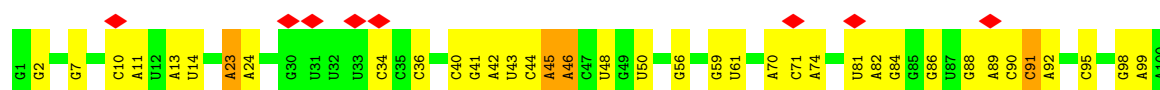
• Molecule 49: 60S ribosomal protein L37(A)

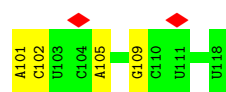


• Molecule 50: 60S ribosomal protein L42

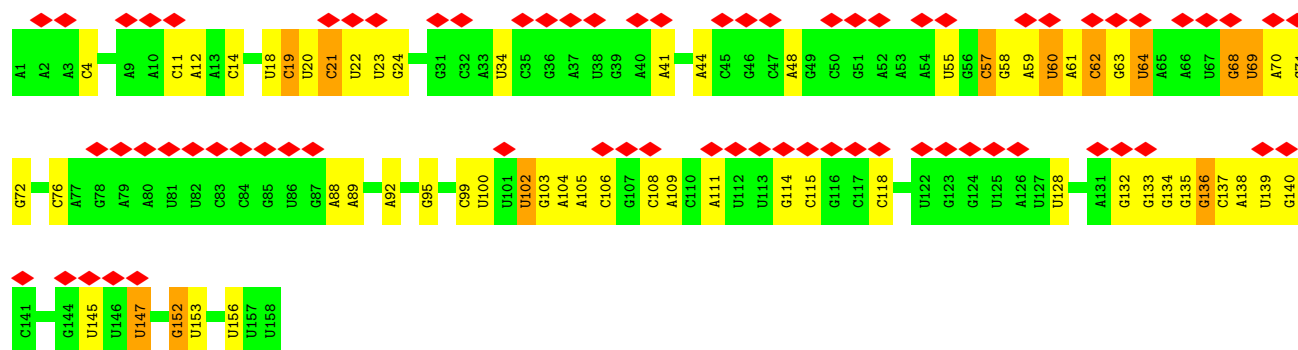


• Molecule 51: 5S ribosomal RNA

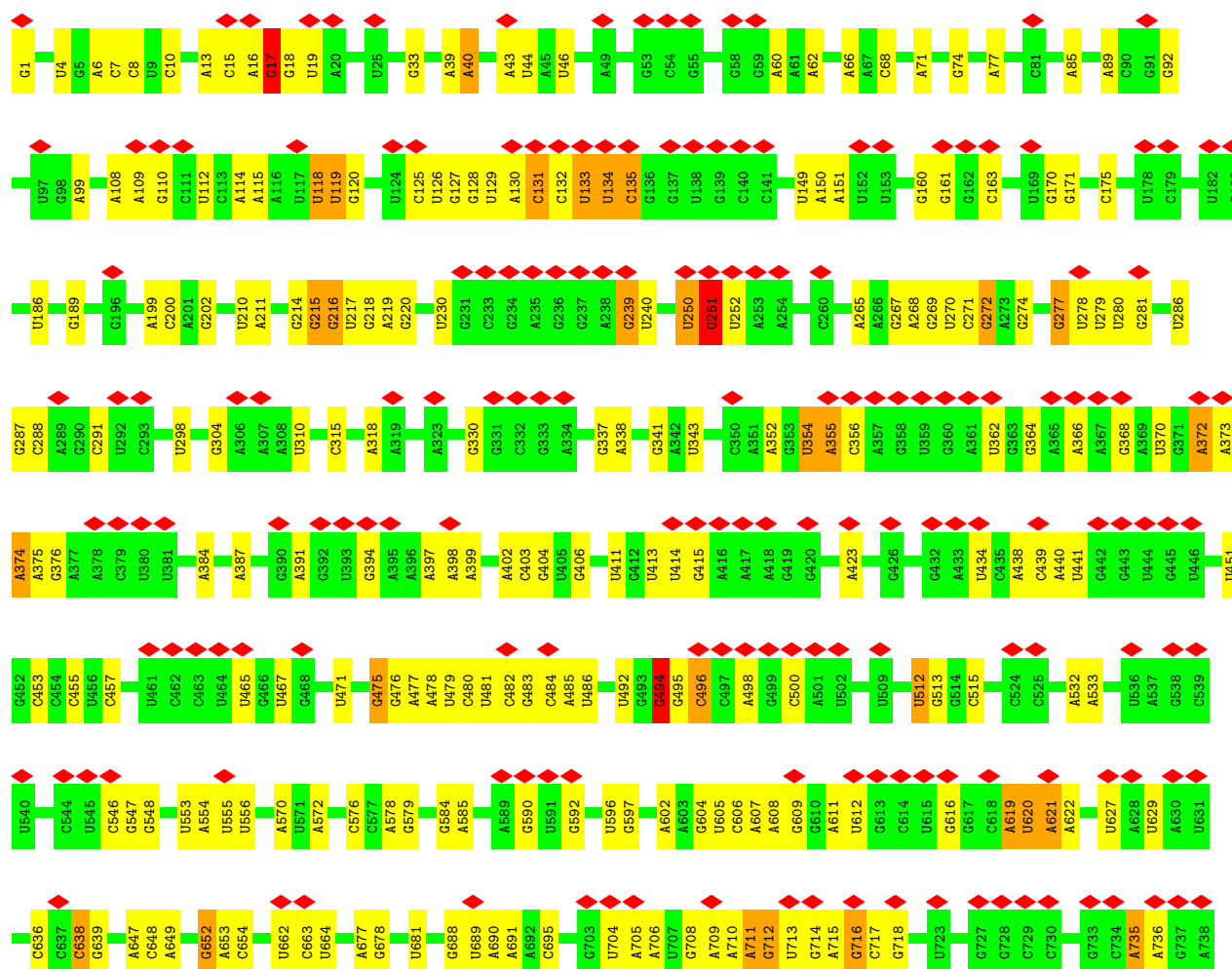


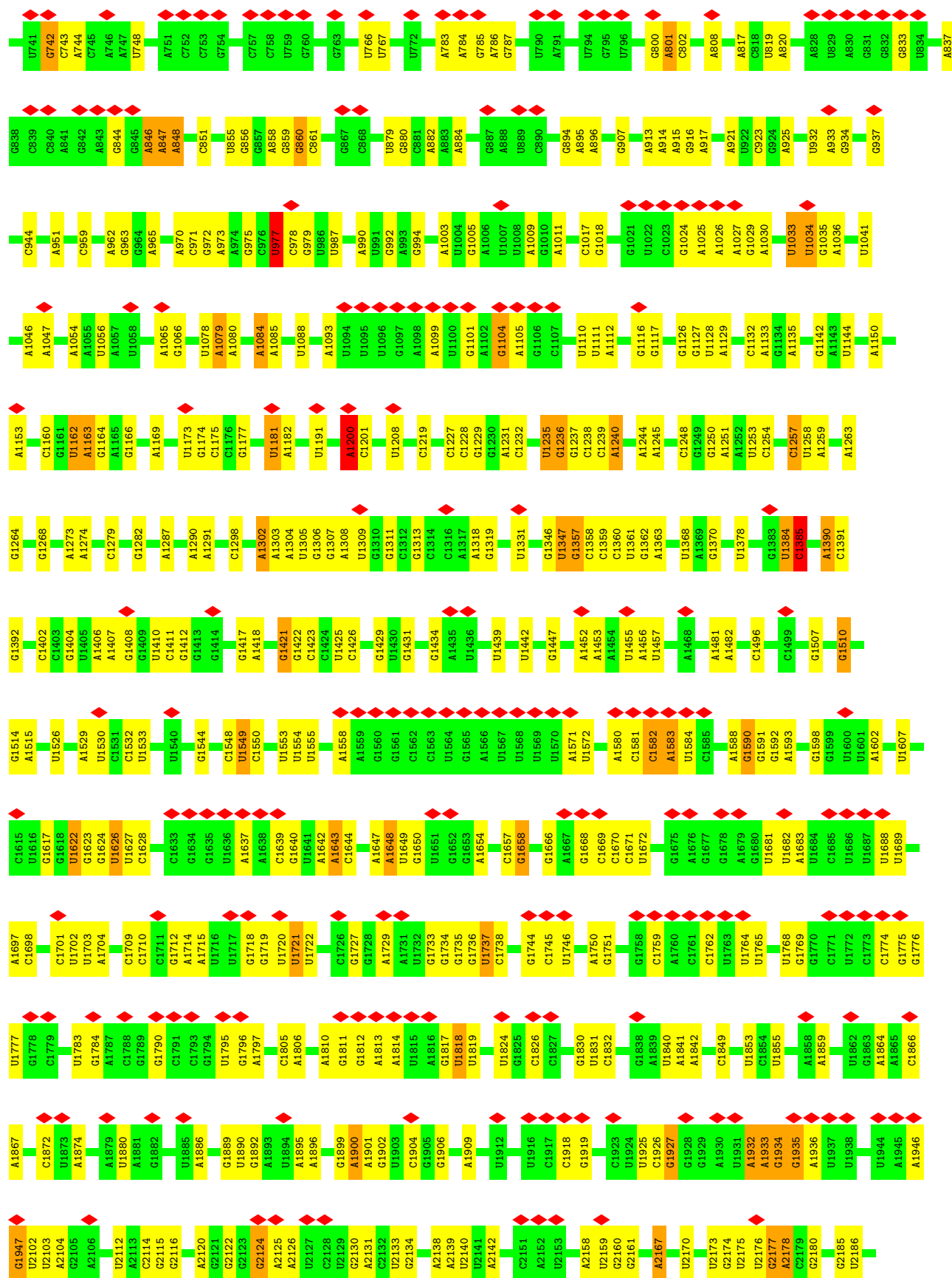


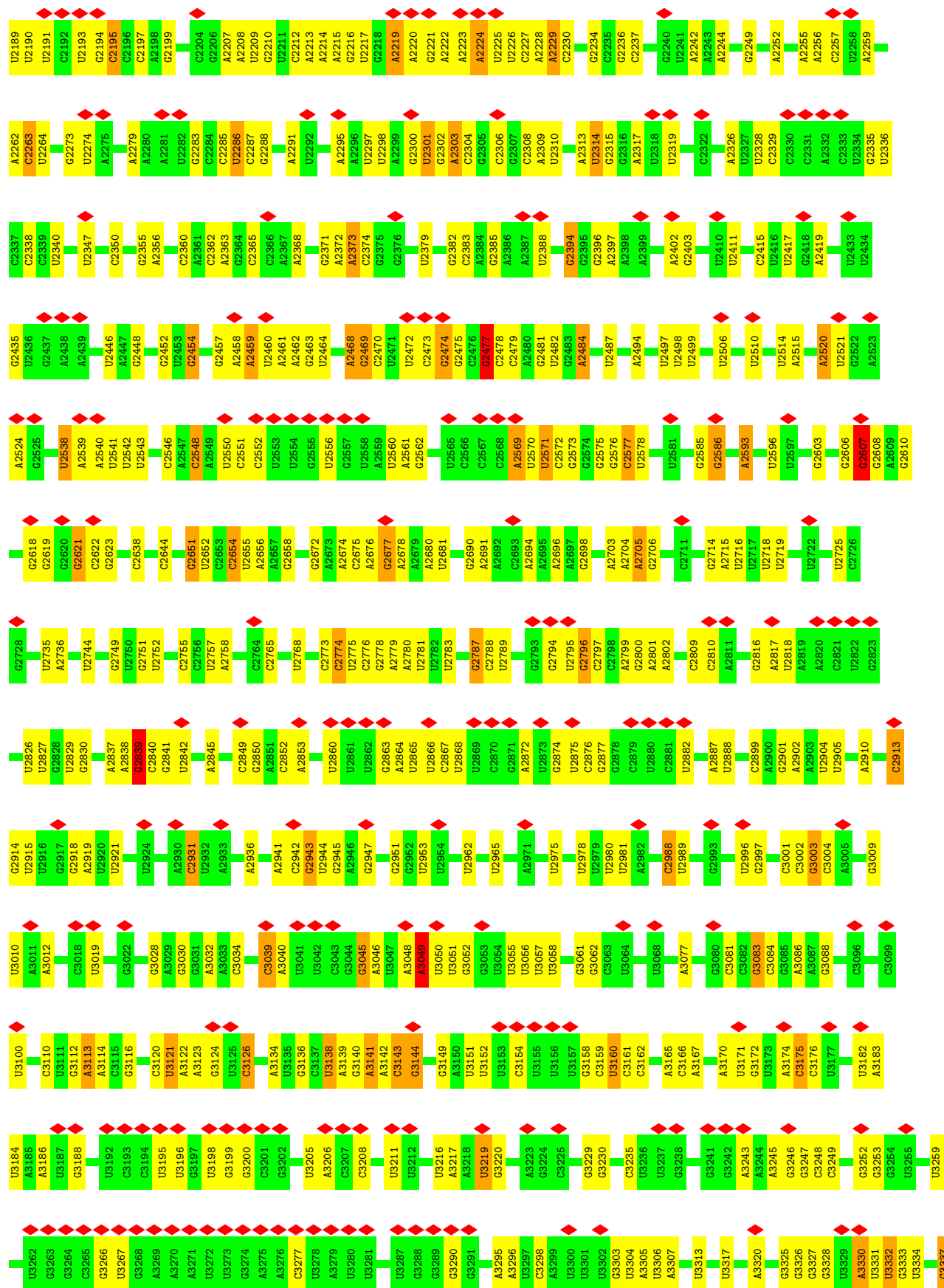
- Molecule 52: 5.8S ribosomal RNA



- Molecule 53: 26S ribosomal RNA







C3338	A3339	G3340	I3341	A3342	G3343	A3344	G3345	I3351	I3352	G3353	I3354	I3355	G3356	I3357	I3358	C3364	I3368	G3369	I3374	I3384	I3385	G3386	I3387	G3388	I3389	G3390	A3391	I3392	I3393	I3394	G3395	I3396
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	102689	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1400	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	280.857	Depositor
Minimum map value	-103.711	Depositor
Average map value	7.703	Depositor
Map value standard deviation	27.906	Depositor
Recommended contour level	70.4	Depositor
Map size ($\text{\AA}$)	381.3, 381.3, 381.3	wwPDB
Map dimensions	205, 205, 205	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	1.86, 1.86, 1.86	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 1MA, M2G, 2MG, PSU, 7MG, OMG, 5MC, H2U, YYG, OMC, 5MU

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	AA	1.02	39/41893 (0.1%)	1.16	265/65278 (0.4%)
2	AB	1.11	0/1535	1.33	3/2097 (0.1%)
3	AC	1.16	0/1488	1.32	2/1996 (0.1%)
4	AD	1.16	0/1035	1.52	13/1390 (0.9%)
5	AE	1.11	0/1227	1.32	2/1663 (0.1%)
6	AG	1.14	0/1472	1.40	9/1982 (0.5%)
7	AH	1.27	3/1008 (0.3%)	1.65	11/1351 (0.8%)
8	AI	1.96	7/1106 (0.6%)	1.54	14/1481 (0.9%)
9	AJ	1.12	0/781	1.36	3/1053 (0.3%)
10	AK	1.19	0/935	1.39	2/1257 (0.2%)
11	AL	1.11	0/920	1.25	1/1226 (0.1%)
12	AM	1.19	0/1094	1.45	1/1468 (0.1%)
13	AN	3.93	4/427 (0.9%)	1.93	8/567 (1.4%)
14	AO	1.13	0/707	1.46	5/950 (0.5%)
15	AQ	1.23	0/656	1.30	0/885
16	AS	1.14	0/559	1.30	1/748 (0.1%)
17	AR	1.34	5/2463 (0.2%)	1.77	38/3350 (1.1%)
18	AT	1.20	2/1118 (0.2%)	1.59	9/1498 (0.6%)
19	A7	1.88	16/1483 (1.1%)	2.07	82/2311 (3.5%)
20	B0	1.18	0/898	1.46	4/1201 (0.3%)
21	B1	1.25	0/431	1.42	1/570 (0.2%)
22	B2	1.07	0/760	1.29	1/1020 (0.1%)
23	B8	1.14	0/965	1.48	7/1298 (0.5%)
24	B9	1.16	0/546	1.40	3/729 (0.4%)
25	BA	1.06	0/1709	1.36	3/2295 (0.1%)
26	BB	1.20	0/1882	1.40	5/2528 (0.2%)
27	BC	1.18	0/2953	1.37	8/3974 (0.2%)
28	BD	1.13	0/1987	1.33	1/2690 (0.0%)
29	BE	1.18	0/1956	1.49	25/2646 (0.9%)
30	BF	1.10	1/1593 (0.1%)	1.40	4/2160 (0.2%)
31	BG	1.06	0/853	1.43	9/1153 (0.8%)
32	BH	1.17	0/1437	1.42	11/1935 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BI	1.22	0/1352	1.49	10/1815 (0.6%)
34	BJ	1.19	0/1212	1.35	2/1622 (0.1%)
35	BK	1.64	6/1049 (0.6%)	1.40	5/1408 (0.4%)
36	BL	1.23	0/1652	1.38	10/2211 (0.5%)
37	BM	1.29	2/1341 (0.1%)	1.63	15/1808 (0.8%)
38	BN	1.17	0/1212	1.35	2/1631 (0.1%)
39	BO	1.14	0/943	1.35	4/1274 (0.3%)
40	BP	1.19	0/1334	1.51	4/1791 (0.2%)
41	BQ	1.16	0/909	1.36	0/1216
42	BR	1.15	0/992	1.42	2/1333 (0.2%)
43	BS	1.23	0/380	1.42	6/504 (1.2%)
44	BT	1.08	0/649	1.26	1/873 (0.1%)
45	BU	1.16	0/927	1.33	5/1237 (0.4%)
46	BV	1.16	0/1152	1.49	7/1542 (0.5%)
47	BW	1.24	0/673	1.42	2/894 (0.2%)
48	BX	1.04	0/607	1.39	2/818 (0.2%)
49	BY	1.21	0/413	1.29	0/548
50	BZ	1.19	0/761	1.45	5/1006 (0.5%)
51	B3	0.87	0/2686	1.08	4/4184 (0.1%)
52	B4	0.88	0/3719	1.11	12/5791 (0.2%)
53	B5	0.87	0/75857	1.05	112/118271 (0.1%)
All	All	1.04	85/179697 (0.0%)	1.21	761/268527 (0.3%)

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	AA	2	28
2	AB	0	1
4	AD	0	3
5	AE	0	1
7	AH	1	0
8	AI	0	3
9	AJ	0	3
10	AK	0	4
12	AM	0	3
13	AN	0	2
14	AO	0	4
19	A7	0	44
20	B0	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
23	B8	0	3
24	B9	0	3
26	BB	1	4
27	BC	0	1
28	BD	0	3
29	BE	1	7
30	BF	1	0
31	BG	2	2
32	BH	0	3
33	BI	0	2
34	BJ	0	3
35	BK	0	2
36	BL	1	7
37	BM	0	5
38	BN	0	2
39	BO	0	1
40	BP	0	4
42	BR	0	3
43	BS	0	1
44	BT	0	1
45	BU	0	1
46	BV	0	3
47	BW	0	2
48	BX	2	1
49	BY	0	1
50	BZ	0	5
51	B3	1	0
52	B4	0	6
53	B5	33	112
All	All	45	285

The worst 5 of 85 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	AN	16	LYS	N-CA	75.73	2.90	1.46
1	AA	501	U	C4-C5	30.64	2.04	1.43
1	AA	856	A	C5-C6	29.28	1.99	1.41
1	AA	856	A	C5-C4	29.21	1.97	1.38
1	AA	856	A	N3-C4	28.45	1.91	1.34

The worst 5 of 761 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	864	U	P-O3'-C3'	-35.57	66.85	120.20
1	AA	1519	G	O3'-P-O5'	30.05	149.08	104.00
1	AA	1520	U	O3'-P-O5'	29.37	148.06	104.00
1	AA	1545	A	O5'-P-OP1	-25.95	30.14	108.00
1	AA	1520	U	C4'-C3'-O3'	-25.52	74.72	113.00

5 of 45 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	109	G	C3'
1	AA	933	C	C2'
7	AH	34	ILE	CB
26	BB	161	ASP	CA
29	BE	216	GLU	CA

5 of 285 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	225	A	Sidechain
1	AA	244	A	Sidechain
1	AA	474	A	Sidechain
1	AA	475	A	Sidechain
1	AA	80	A	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	AA	37458	0	18828	603	0
2	AB	1500	0	1524	1	0
3	AC	1469	0	1534	1	0
4	AD	1018	0	1067	1	0
5	AE	1207	0	1274	0	0
6	AG	1456	0	1523	2	0
7	AH	992	0	1027	39	0
8	AI	1087	0	1145	19	0
9	AJ	771	0	829	2	0
10	AK	924	0	949	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AL	906	0	970	1	0
12	AM	1077	0	1107	19	0
13	AN	417	0	408	23	0
14	AO	694	0	740	13	0
15	AQ	643	0	688	2	0
16	AS	548	0	574	3	0
17	AR	2410	0	2367	555	0
18	AT	1102	0	1112	38	0
19	A7	1648	0	830	55	0
20	B0	881	0	926	1	0
21	B1	424	0	459	1	0
22	B2	752	0	803	1	0
23	B8	947	0	972	19	0
24	B9	539	0	555	1	0
25	BA	1683	0	1772	3	0
26	BB	1848	0	1908	16	0
27	BC	2887	0	2964	3	0
28	BD	1950	0	2019	3	0
29	BE	1913	0	1842	1	0
30	BF	1561	0	1633	1	0
31	BG	844	0	909	0	0
32	BH	1418	0	1483	4	0
33	BI	1326	0	1368	3	0
34	BJ	1195	0	1230	15	0
35	BK	1038	0	1110	23	0
36	BL	1618	0	1673	1	0
37	BM	1317	0	1407	63	0
38	BN	1189	0	1201	0	0
39	BO	931	0	1010	0	0
40	BP	1317	0	1389	115	0
41	BQ	893	0	924	0	0
42	BR	977	0	1026	14	0
43	BS	371	0	382	1	0
44	BT	642	0	679	0	0
45	BU	916	0	996	0	0
46	BV	1123	0	1160	2	0
47	BW	663	0	700	0	0
48	BX	605	0	661	1	0
49	BY	403	0	398	0	0
50	BZ	749	0	815	0	0
51	B3	2403	0	1219	0	0
52	B4	3329	0	1685	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	B5	67775	0	34047	225	0
All	All	165754	0	111821	1353	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 5.

The worst 5 of 1353 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)
35:BK:121:PHE:CZ	35:BK:121:PHE:CE1	1.78	1.71
35:BK:121:PHE:CZ	35:BK:121:PHE:CE2	1.79	1.69
35:BK:121:PHE:CE2	35:BK:121:PHE:CD2	1.76	1.69
35:BK:121:PHE:CE1	35:BK:121:PHE:CD1	1.80	1.69
35:BK:121:PHE:CD2	35:BK:121:PHE:CG	1.82	1.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AB	191/193 (99%)	173 (91%)	16 (8%)	2 (1%)	12	49
3	AC	186/188 (99%)	148 (80%)	28 (15%)	10 (5%)	1	15
4	AD	120/158 (76%)	97 (81%)	16 (13%)	7 (6%)	1	14
5	AE	160/162 (99%)	141 (88%)	13 (8%)	6 (4%)	2	19
6	AG	184/186 (99%)	156 (85%)	20 (11%)	8 (4%)	2	17
7	AH	121/125 (97%)	105 (87%)	11 (9%)	5 (4%)	2	18
8	AI	136/138 (99%)	106 (78%)	21 (15%)	9 (7%)	1	12
9	AJ	94/96 (98%)	77 (82%)	14 (15%)	3 (3%)	3	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	AK	123/125 (98%)	99 (80%)	20 (16%)	4 (3%)	3	21
11	AL	116/118 (98%)	89 (77%)	25 (22%)	2 (2%)	7	36
12	AM	128/130 (98%)	103 (80%)	20 (16%)	5 (4%)	2	19
13	AN	48/50 (96%)	36 (75%)	8 (17%)	4 (8%)	0	9
14	AO	82/84 (98%)	68 (83%)	11 (13%)	3 (4%)	2	20
15	AQ	78/80 (98%)	66 (85%)	11 (14%)	1 (1%)	9	42
16	AS	69/71 (97%)	54 (78%)	12 (17%)	3 (4%)	2	17
17	AR	311/313 (99%)	282 (91%)	28 (9%)	1 (0%)	36	72
18	AT	137/141 (97%)	110 (80%)	21 (15%)	6 (4%)	2	17
20	B0	107/109 (98%)	75 (70%)	20 (19%)	12 (11%)	0	5
21	B1	46/48 (96%)	36 (78%)	9 (20%)	1 (2%)	5	29
22	B2	96/98 (98%)	87 (91%)	7 (7%)	2 (2%)	5	30
23	B8	116/118 (98%)	85 (73%)	25 (22%)	6 (5%)	1	15
24	B9	70/72 (97%)	48 (69%)	16 (23%)	6 (9%)	0	9
25	BA	211/213 (99%)	172 (82%)	30 (14%)	9 (4%)	2	17
26	BB	241/243 (99%)	174 (72%)	53 (22%)	14 (6%)	1	14
27	BC	360/362 (99%)	279 (78%)	68 (19%)	13 (4%)	2	20
28	BD	255/257 (99%)	208 (82%)	41 (16%)	6 (2%)	4	27
29	BE	235/237 (99%)	175 (74%)	47 (20%)	13 (6%)	1	15
30	BF	211/213 (99%)	150 (71%)	55 (26%)	6 (3%)	4	24
31	BG	111/113 (98%)	88 (79%)	20 (18%)	3 (3%)	4	25
32	BH	177/179 (99%)	146 (82%)	25 (14%)	6 (3%)	3	21
33	BI	163/165 (99%)	123 (76%)	31 (19%)	9 (6%)	1	15
34	BJ	149/151 (99%)	112 (75%)	33 (22%)	4 (3%)	4	25
35	BK	136/138 (99%)	107 (79%)	22 (16%)	7 (5%)	1	15
36	BL	190/192 (99%)	156 (82%)	29 (15%)	5 (3%)	4	25
37	BM	176/178 (99%)	134 (76%)	34 (19%)	8 (4%)	2	17
38	BN	148/150 (99%)	122 (82%)	23 (16%)	3 (2%)	6	31
39	BO	119/121 (98%)	92 (77%)	23 (19%)	4 (3%)	3	21
40	BP	174/176 (99%)	155 (89%)	15 (9%)	4 (2%)	5	28
41	BQ	114/116 (98%)	94 (82%)	16 (14%)	4 (4%)	3	20

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BR	129/131 (98%)	96 (74%)	28 (22%)	5 (4%)	2	19
43	BS	43/45 (96%)	33 (77%)	10 (23%)	0	100	100
44	BT	78/80 (98%)	59 (76%)	16 (20%)	3 (4%)	2	19
45	BU	114/116 (98%)	95 (83%)	15 (13%)	4 (4%)	3	20
46	BV	140/142 (99%)	98 (70%)	31 (22%)	11 (8%)	1	10
47	BW	77/79 (98%)	58 (75%)	16 (21%)	3 (4%)	2	19
48	BX	84/86 (98%)	63 (75%)	14 (17%)	7 (8%)	0	9
49	BY	50/52 (96%)	39 (78%)	10 (20%)	1 (2%)	6	31
50	BZ	90/92 (98%)	68 (76%)	18 (20%)	4 (4%)	2	17
All	All	6694/6830 (98%)	5337 (80%)	1095 (16%)	262 (4%)	4	19

5 of 262 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	81	PRO
3	AC	179	GLN
4	AD	96	VAL
5	AE	86	VAL
5	AE	226	THR

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	
2	AB	161/161 (100%)	159 (99%)	2 (1%)	63	75
3	AC	152/152 (100%)	148 (97%)	4 (3%)	40	62
4	AD	113/142 (80%)	103 (91%)	10 (9%)	9	28
5	AE	127/127 (100%)	121 (95%)	6 (5%)	23	45
6	AG	155/155 (100%)	150 (97%)	5 (3%)	34	56
7	AH	106/106 (100%)	100 (94%)	6 (6%)	18	40
8	AI	115/115 (100%)	108 (94%)	7 (6%)	17	38

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	AJ	90/90 (100%)	87 (97%)	3 (3%)	33	55
10	AK	95/95 (100%)	88 (93%)	7 (7%)	13	33
11	AL	98/98 (100%)	95 (97%)	3 (3%)	35	56
12	AM	115/115 (100%)	107 (93%)	8 (7%)	14	35
13	AN	45/45 (100%)	42 (93%)	3 (7%)	15	36
14	AO	74/74 (100%)	71 (96%)	3 (4%)	27	49
15	AQ	71/71 (100%)	69 (97%)	2 (3%)	38	60
16	AS	57/57 (100%)	55 (96%)	2 (4%)	32	53
17	AR	257/257 (100%)	241 (94%)	16 (6%)	16	38
18	AT	114/114 (100%)	105 (92%)	9 (8%)	11	32
20	B0	94/94 (100%)	89 (95%)	5 (5%)	20	41
21	B1	44/44 (100%)	41 (93%)	3 (7%)	14	36
22	B2	82/82 (100%)	81 (99%)	1 (1%)	63	75
23	B8	100/100 (100%)	84 (84%)	16 (16%)	2	11
24	B9	55/55 (100%)	53 (96%)	2 (4%)	31	52
25	BA	194/194 (100%)	181 (93%)	13 (7%)	15	36
26	BB	186/186 (100%)	177 (95%)	9 (5%)	23	44
27	BC	302/302 (100%)	281 (93%)	21 (7%)	14	35
28	BD	199/199 (100%)	184 (92%)	15 (8%)	12	33
29	BE	199/199 (100%)	186 (94%)	13 (6%)	15	37
30	BF	143/143 (100%)	134 (94%)	9 (6%)	16	37
31	BG	89/89 (100%)	84 (94%)	5 (6%)	19	40
32	BH	160/160 (100%)	150 (94%)	10 (6%)	16	37
33	BI	141/141 (100%)	134 (95%)	7 (5%)	22	43
34	BJ	129/129 (100%)	123 (95%)	6 (5%)	23	45
35	BK	112/112 (100%)	107 (96%)	5 (4%)	24	46
36	BL	164/164 (100%)	158 (96%)	6 (4%)	30	51
37	BM	119/119 (100%)	110 (92%)	9 (8%)	12	33
38	BN	122/122 (100%)	120 (98%)	2 (2%)	55	70
39	BO	99/99 (100%)	96 (97%)	3 (3%)	36	57
40	BP	118/118 (100%)	113 (96%)	5 (4%)	26	48

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	BQ	87/87 (100%)	85 (98%)	2 (2%)	44	64
42	BR	102/102 (100%)	96 (94%)	6 (6%)	18	39
43	BS	38/38 (100%)	36 (95%)	2 (5%)	20	41
44	BT	71/71 (100%)	65 (92%)	6 (8%)	10	29
45	BU	100/100 (100%)	98 (98%)	2 (2%)	48	66
46	BV	113/113 (100%)	106 (94%)	7 (6%)	16	38
47	BW	69/69 (100%)	65 (94%)	4 (6%)	18	40
48	BX	55/55 (100%)	53 (96%)	2 (4%)	31	52
49	BY	42/42 (100%)	39 (93%)	3 (7%)	13	35
50	BZ	81/81 (100%)	71 (88%)	10 (12%)	4	17
All	All	5554/5583 (100%)	5249 (94%)	305 (6%)	21	41

5 of 305 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	BK	18	VAL
47	BW	11	GLU
36	BL	77	LYS
40	BP	125	LYS
50	BZ	46	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 131 such sidechains are listed below:

Mol	Chain	Res	Type
41	BQ	26	HIS
41	BQ	98	HIS
50	BZ	23	HIS
23	B8	103	ASN
21	B1	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1757/1761 (99%)	382 (21%)	79 (4%)
19	A7	75/76 (98%)	9 (12%)	3 (4%)
51	B3	112/113 (99%)	40 (35%)	4 (3%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
52	B4	156/157 (99%)	55 (35%)	10 (6%)
53	B5	3169/3170 (99%)	949 (29%)	139 (4%)
All	All	5269/5277 (99%)	1435 (27%)	235 (4%)

5 of 1435 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	A
1	AA	3	U
1	AA	4	C
1	AA	9	U
1	AA	27	U

5 of 235 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	B5	554	A
53	B5	3121	U
53	B5	1240	A
53	B5	3110	C
53	B5	2651	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
19	5MC	A7	40	19	19,22,23	1.87	5 (26%)	26,32,35	2.38	12 (46%)
19	H2U	A7	16	19	18,21,22	1.94	3 (16%)	19,30,33	1.96	6 (31%)
19	PSU	A7	55	19	18,21,22	1.74	4 (22%)	21,30,33	1.43	2 (9%)
19	M2G	A7	26	19	24,27,28	1.34	4 (16%)	33,40,43	1.49	6 (18%)
19	H2U	A7	17	19	18,21,22	2.59	7 (38%)	19,30,33	2.70	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
19	YYG	A7	37	19	38,42,43	1.69	6 (15%)	45,62,65	2.92	15 (33%)
19	PSU	A7	39	19	18,21,22	1.64	6 (33%)	21,30,33	1.89	6 (28%)
19	5MC	A7	49	19	19,22,23	1.59	2 (10%)	26,32,35	2.17	11 (42%)
19	2MG	A7	10	19	23,26,27	1.35	4 (17%)	33,38,41	1.62	5 (15%)
19	OMG	A7	34	19	23,26,27	1.27	2 (8%)	32,38,41	1.23	2 (6%)
19	OMC	A7	32	19	19,22,23	1.37	2 (10%)	25,31,34	2.01	8 (32%)
19	5MU	A7	54	19	19,22,23	1.37	2 (10%)	27,32,35	2.53	11 (40%)
19	1MA	A7	58	19	21,25,26	1.31	3 (14%)	30,37,40	1.73	9 (30%)
19	7MG	A7	46	19	23,26,27	1.79	2 (8%)	27,39,42	2.52	9 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
19	5MC	A7	40	19	-	2/7/25/26	0/2/2/2
19	H2U	A7	16	19	-	0/7/38/39	0/2/2/2
19	PSU	A7	55	19	-	1/7/25/26	0/2/2/2
19	M2G	A7	26	19	-	0/11/29/30	0/3/3/3
19	H2U	A7	17	19	-	0/7/38/39	0/2/2/2
19	YYG	A7	37	19	-	7/24/42/43	0/4/4/4
19	PSU	A7	39	19	-	3/7/25/26	0/2/2/2
19	5MC	A7	49	19	-	0/7/25/26	0/2/2/2
19	2MG	A7	10	19	-	0/9/27/28	0/3/3/3
19	OMG	A7	34	19	-	0/9/27/28	0/3/3/3
19	OMC	A7	32	19	-	0/9/27/28	0/2/2/2
19	5MU	A7	54	19	-	0/7/25/26	0/2/2/2
19	1MA	A7	58	19	-	0/7/25/26	0/3/3/3
19	7MG	A7	46	19	-	2/7/37/38	0/3/3/3

The worst 5 of 52 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	A7	46	7MG	C8-N9	-6.58	1.41	1.45
19	A7	17	H2U	C2-N3	-6.33	1.26	1.38
19	A7	37	YYG	C2-N1	-6.00	1.29	1.38
19	A7	17	H2U	C4-N3	-5.75	1.28	1.37
19	A7	49	5MC	C5-C4	5.30	1.48	1.44

The worst 5 of 106 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	A7	17	H2U	N3-C2-N1	9.33	126.03	116.65
19	A7	37	YYG	C11-C12-N1	-9.29	98.76	105.31
19	A7	54	5MU	C6-C5-C4	6.82	123.64	118.02
19	A7	37	YYG	C24-O23-C21	6.81	123.52	115.63
19	A7	37	YYG	C5-C4-N3	-6.59	118.64	123.99

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	A7	39	PSU	O4'-C1'-C5-C4
19	A7	39	PSU	O4'-C1'-C5-C6
19	A7	40	5MC	O4'-C4'-C5'-O5'
19	A7	37	YYG	N20-C15-C16-O18
19	A7	37	YYG	N20-C15-C16-O17

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
19	A7	40	5MC	2	0
19	A7	37	YYG	1	0
19	A7	10	2MG	1	0

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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	AH	1
18	AT	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AH	32:LYS	C	33:VAL	N	2.59
1	AT	78:LYS	C	79:LEU	N	2.49

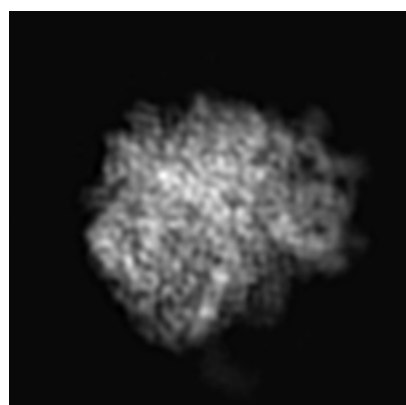
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1345. These allow visual inspection of the internal detail of the map and identification of artifacts.

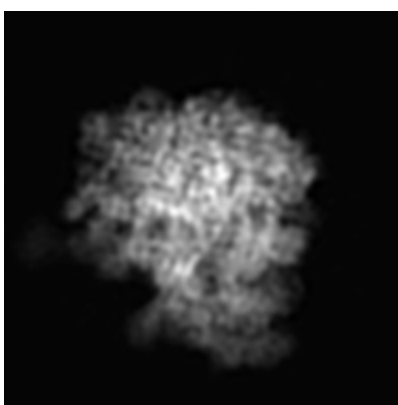
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

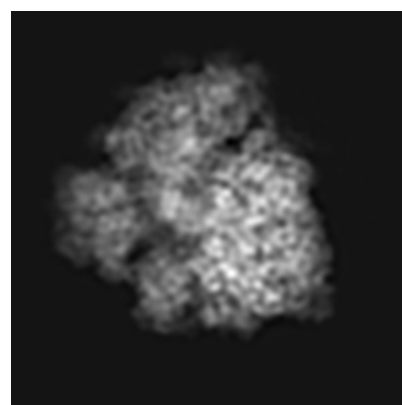
6.1.1 Primary map



X



Y

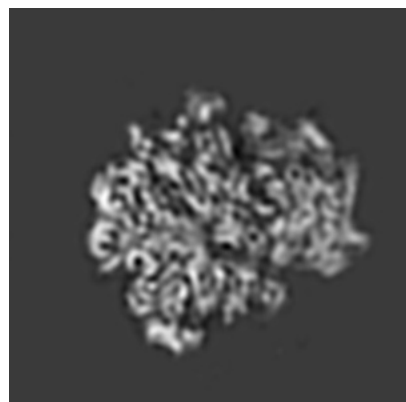


Z

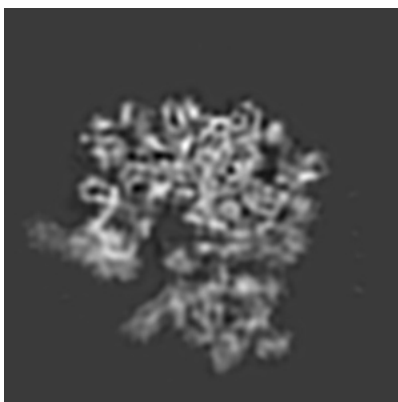
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

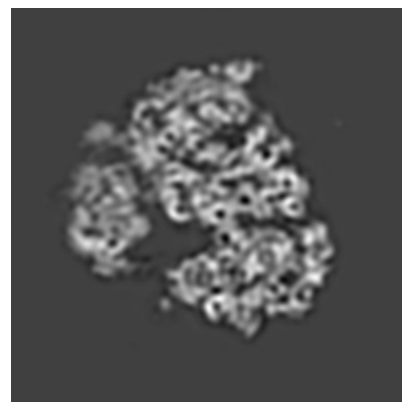
6.2.1 Primary map



X Index: 102



Y Index: 102

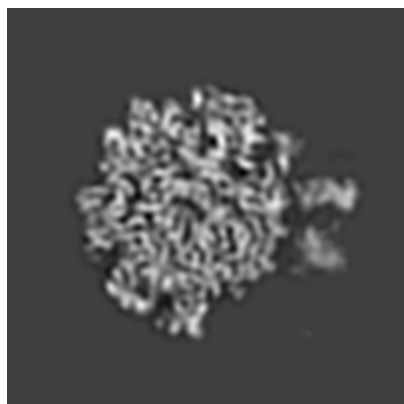


Z Index: 102

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

6.3 Largest variance slices [i](#)

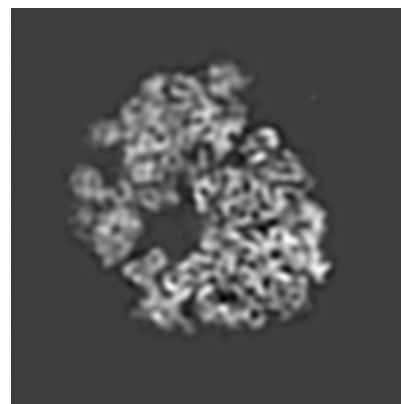
6.3.1 Primary map



X Index: 123



Y Index: 72

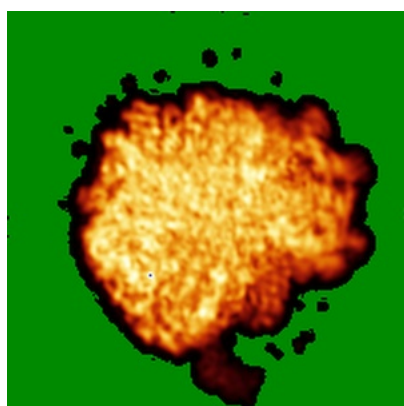


Z Index: 95

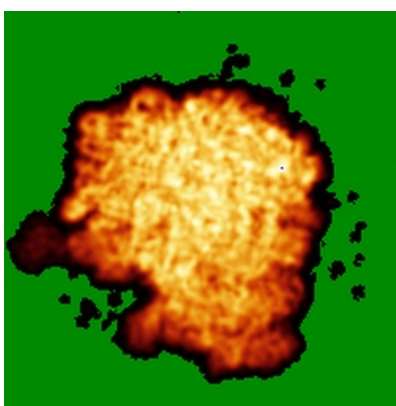
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X



Y

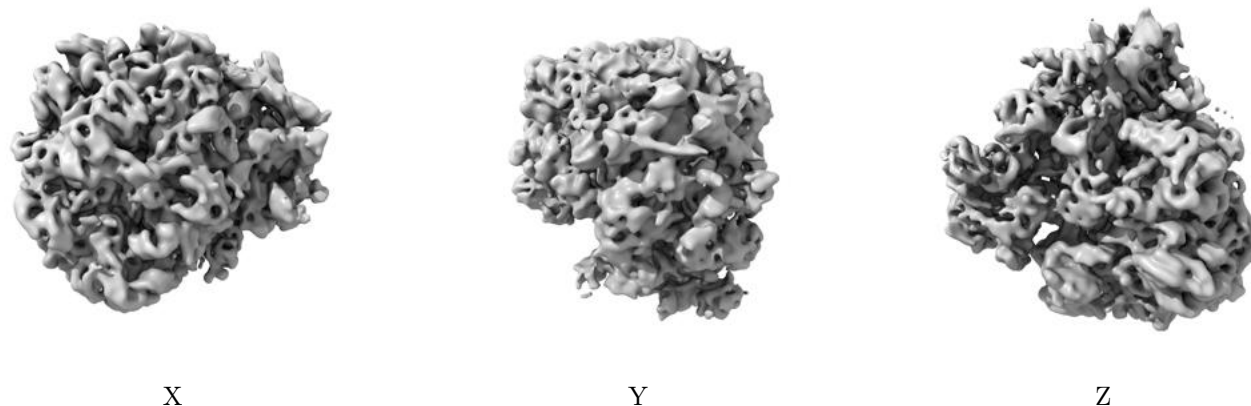


Z

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 70.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

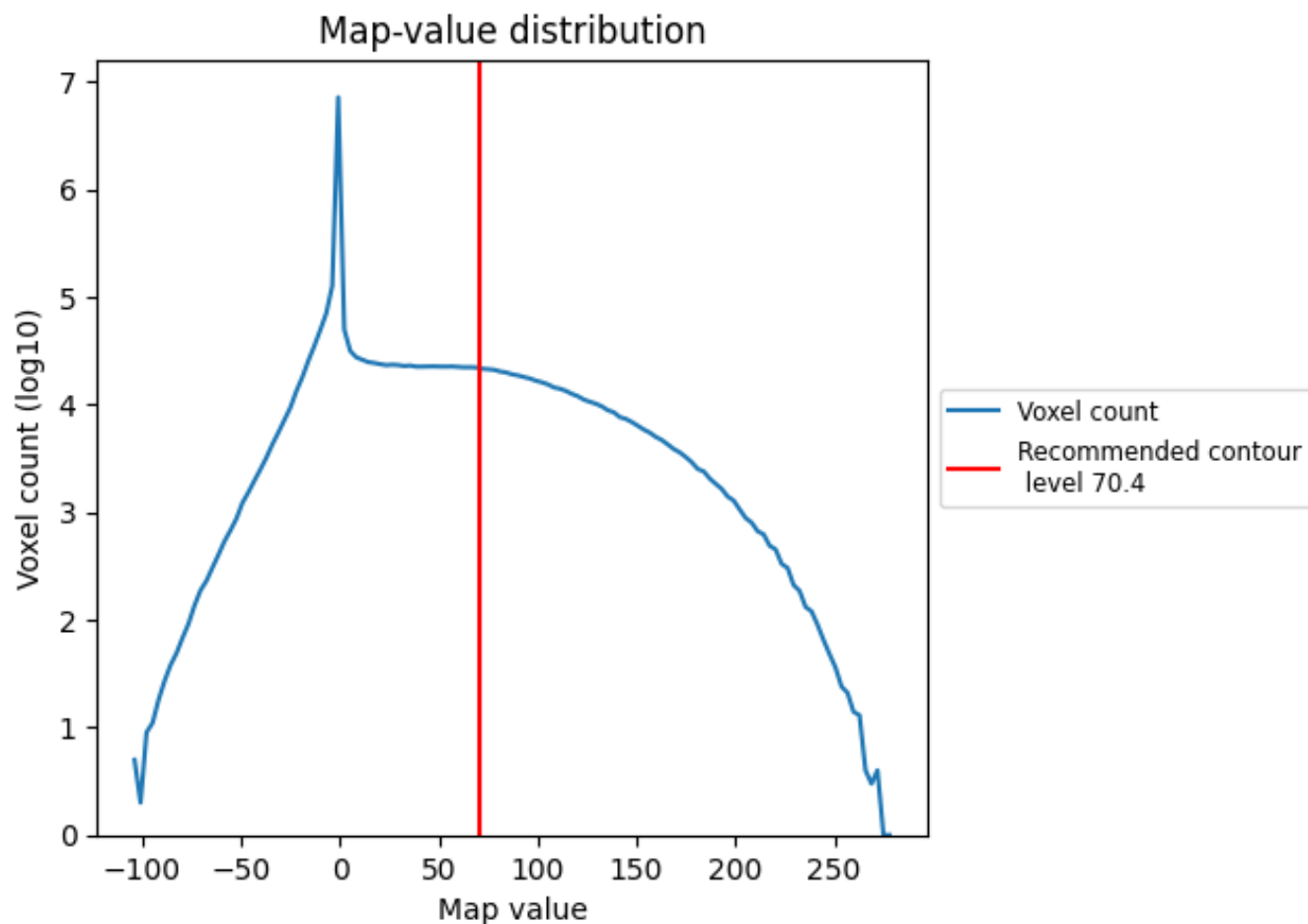
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

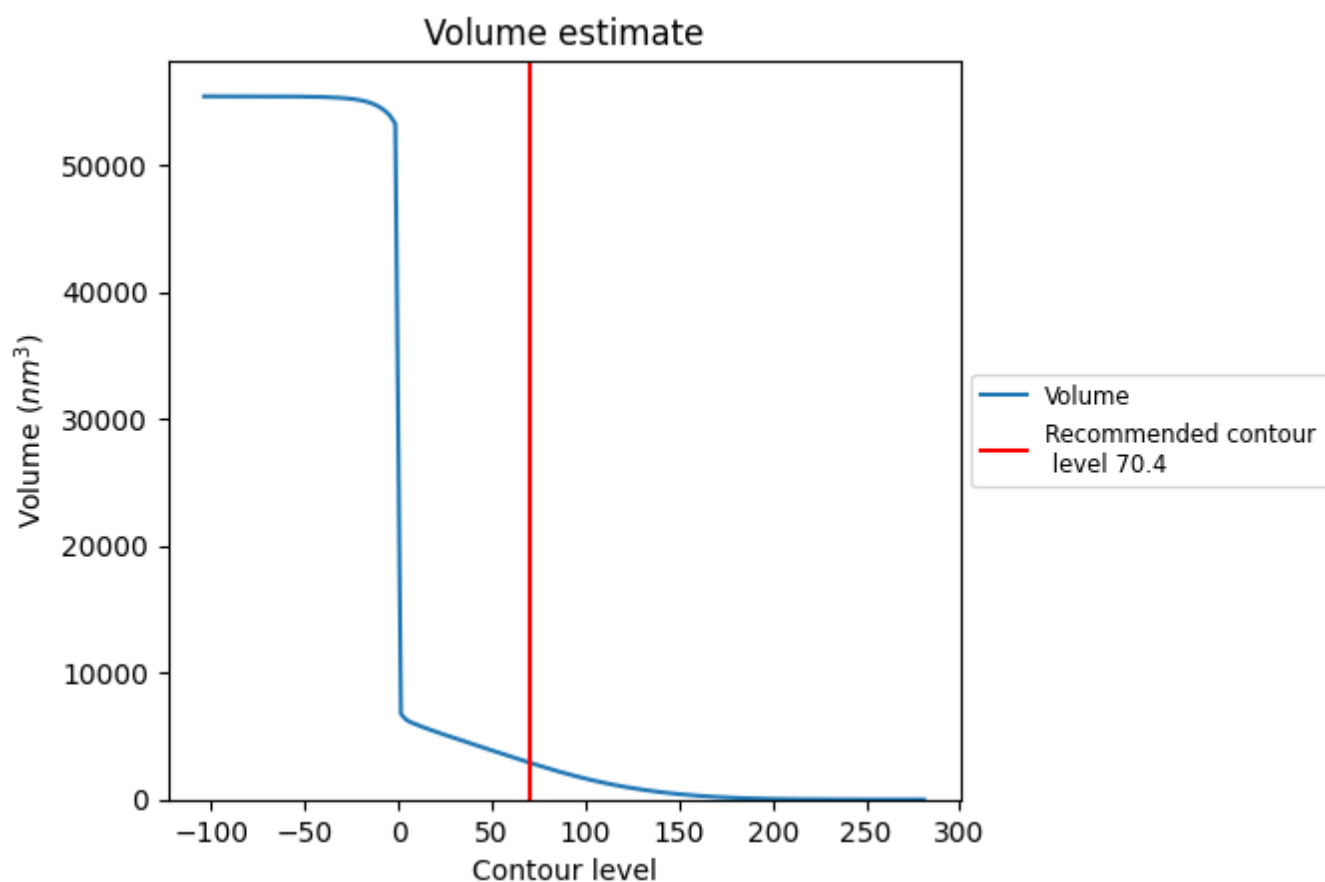
This section contains the results of statistical analysis of the map.

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.

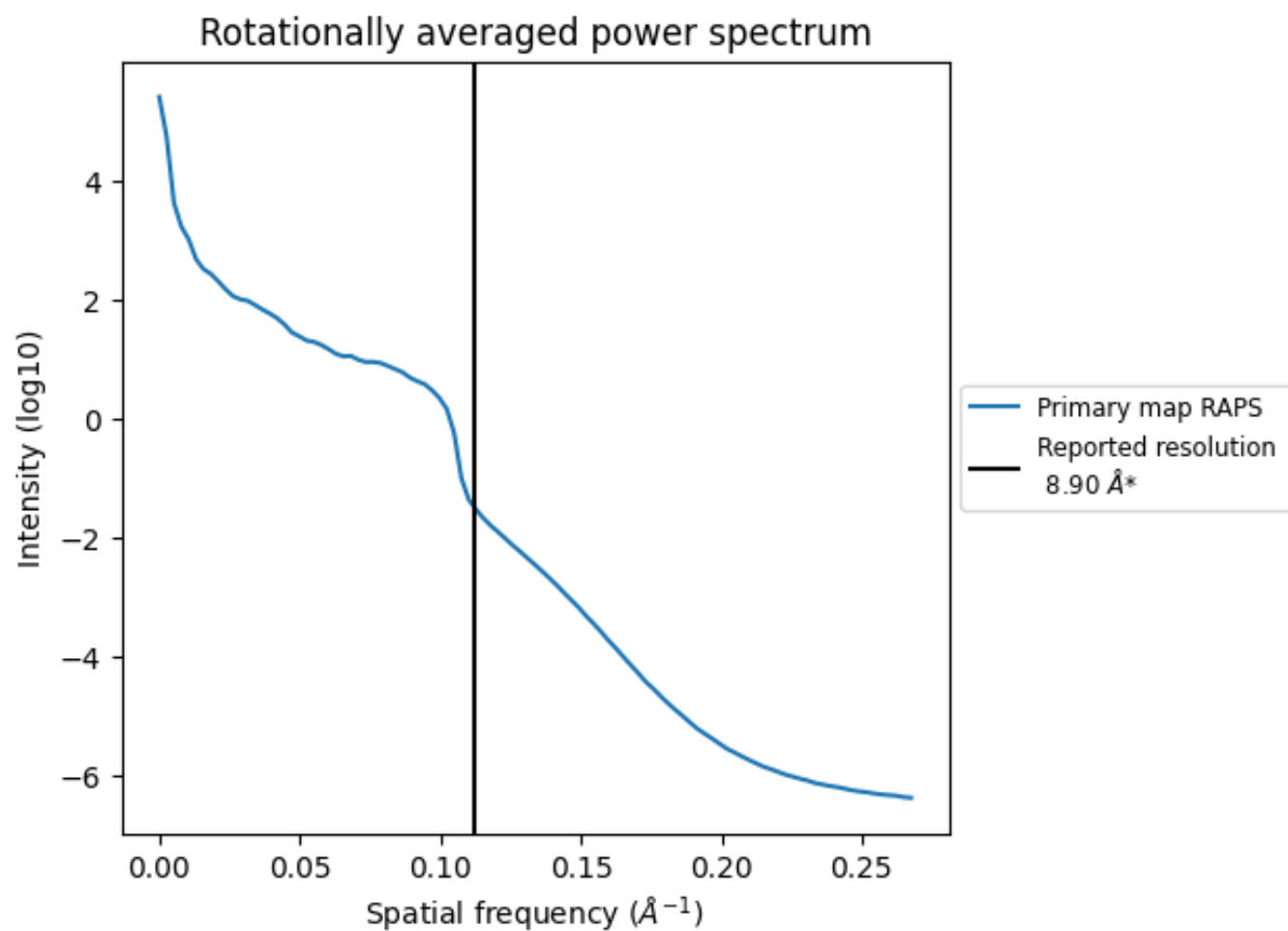
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2899 nm³; this corresponds to an approximate mass of 2619 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 0.112 Å⁻¹

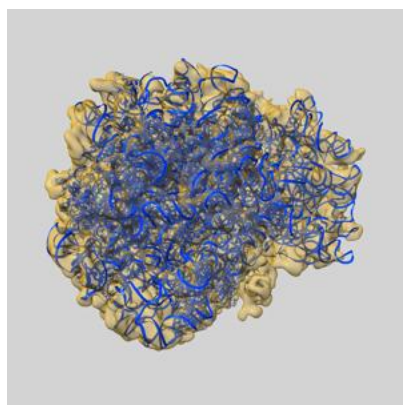
8 Fourier-Shell correlation

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

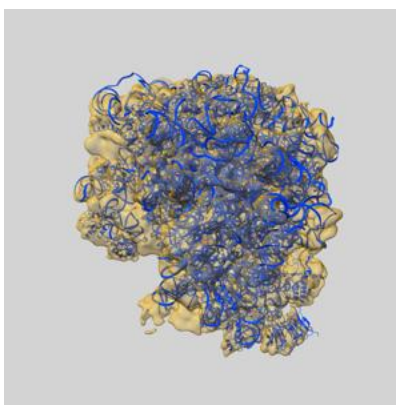
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1345 and PDB model 4V7H. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

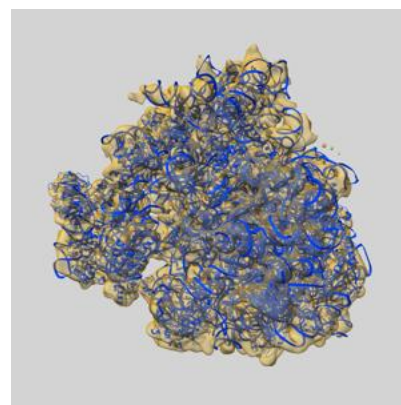
9.1 Map-model overlay [i](#)



X



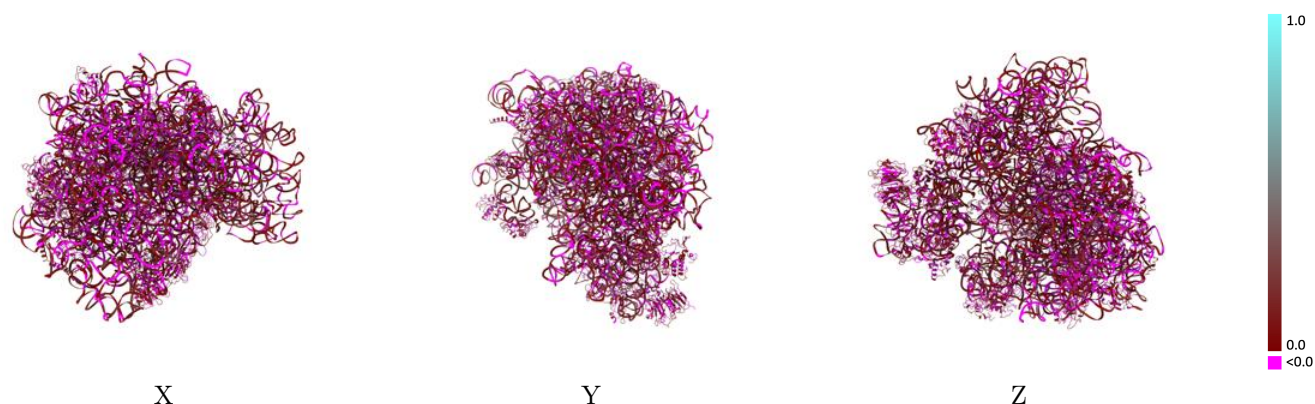
Y



Z

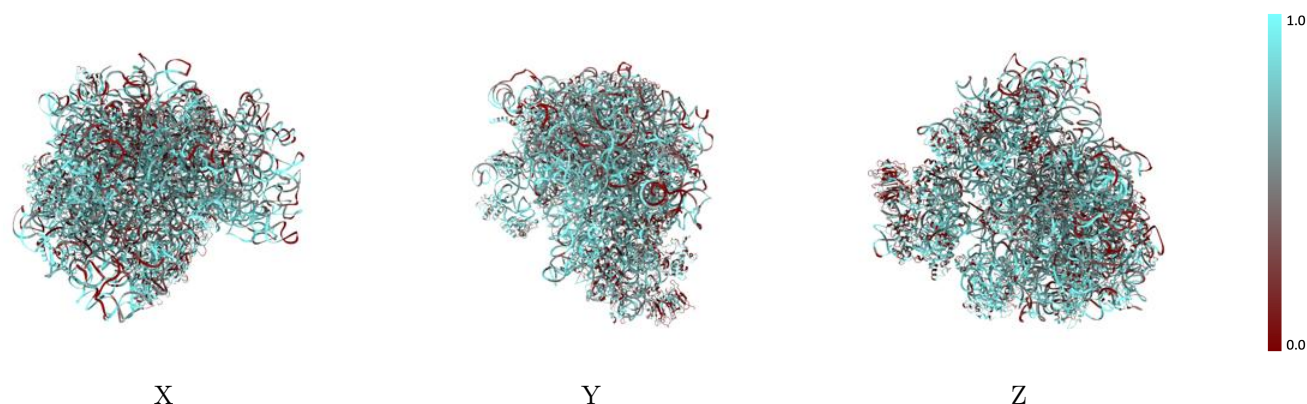
The images above show the 3D surface view of the map at the recommended contour level 70.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



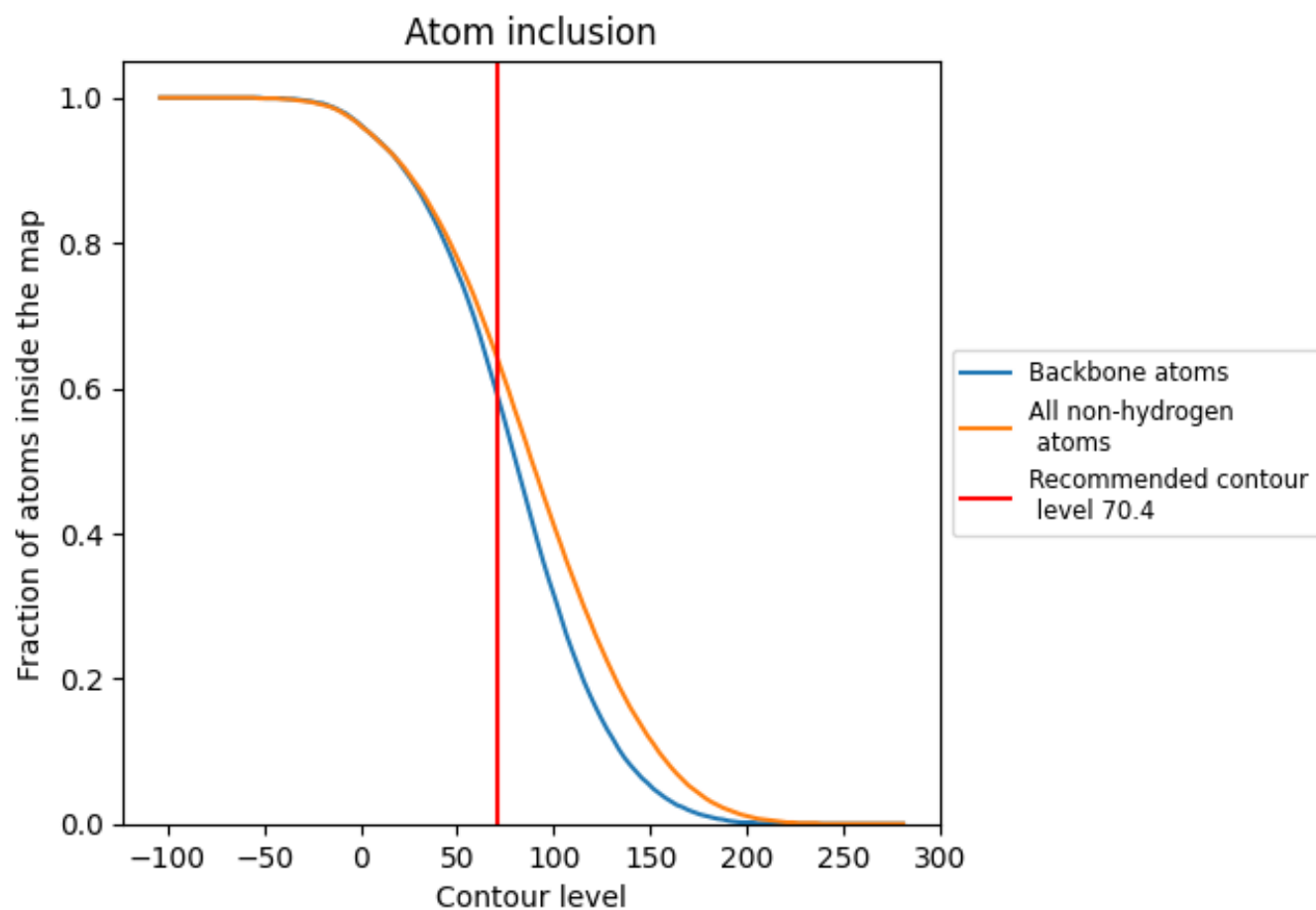
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (70.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 64% 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 (70.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6440	 0.0590
A7	 0.6250	 0.0690
AA	 0.7150	 0.0810
AB	 0.5860	 0.0440
AC	 0.4370	 0.0790
AD	 0.6270	 0.0740
AE	 0.4930	 0.0380
AG	 0.5130	 0.0470
AH	 0.4520	 0.0510
AI	 0.4310	 0.0380
AJ	 0.4360	 0.0600
AK	 0.5070	 0.0250
AL	 0.4450	 0.0330
AM	 0.6320	 0.0330
AN	 0.5590	 0.0070
AO	 0.3760	 0.0450
AQ	 0.4540	 0.0400
AR	 0.3520	 0.0550
AS	 0.5710	 0.0410
AT	 0.4880	 0.0450
B0	 0.4680	 0.0460
B1	 0.5210	 0.0470
B2	 0.6660	 0.0540
B3	 0.7910	 0.0860
B4	 0.5150	 0.0090
B5	 0.6860	 0.0610
B8	 0.6470	 0.0680
B9	 0.4460	 0.0210
BA	 0.5860	 0.0200
BB	 0.4580	 0.0210
BC	 0.5450	 0.0230
BD	 0.6210	 0.0550
BE	 0.7260	 0.0290
BF	 0.5320	 0.0470
BG	 0.6530	 0.0250



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
BH	 0.5830	 0.0570
BI	 0.4170	 0.0070
BJ	 0.7080	 0.0700
BK	 0.5710	 0.0460
BL	 0.5070	 0.0290
BM	 0.5470	 0.0580
BN	 0.5850	 0.0310
BO	 0.6280	 0.0600
BP	 0.6030	 0.0800
BQ	 0.5990	 0.0300
BR	 0.3650	 0.0500
BS	 0.5490	 0.0290
BT	 0.5170	 0.0780
BU	 0.6370	 0.0850
BV	 0.5750	 0.0340
BW	 0.7120	 0.0670
BX	 0.5120	 0.0720
BY	 0.5080	 -0.0070
BZ	 0.5470	 0.0380