



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:28 PM UTC

PDB ID : 4V66 / pdb_00004v66
EMDB ID : EMD-1056
Title : Structure of the E. coli ribosome and the tRNAs in Post-accommodation state
Authors : Devkota, B.; Caulfield, T.R.; Tan, R.-Z.; Harvey, S.C.
Deposited on : 2008-08-03
Resolution : 9.00 Å(reported)
Based on initial models : 1EHZ, 2I2P

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:

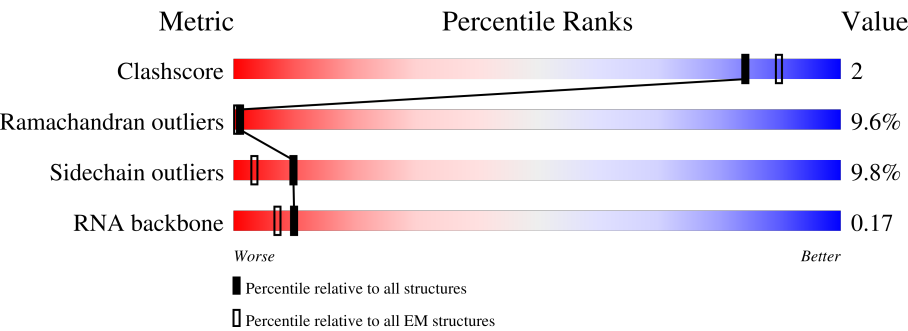
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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	76	64% 5% 21% 41% 32% .
1	AE	76	54% . 25% 59% 13%
1	AP	76	57% . 26% 47% 22% .
2	AM	20	10% 10% 5% 35% 50%
3	A1	1530	66% . 18% 45% 34%
4	AB	241	70% 38% 43% 8% 10%
5	AC	129	46% 33% 46% 9% 9%

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Mol	Chain	Length	Quality of chain
6	AD	124	
7	AF	118	
8	AG	101	
9	AH	89	
10	AI	82	
11	AJ	84	
12	AK	75	
13	AL	92	
14	AN	87	
15	AO	233	
16	AQ	71	
17	AR	206	
18	AS	159	
19	AT	135	
20	AU	179	
21	AV	130	
22	AW	130	
23	AX	103	
24	BA	117	
25	BB	2903	
26	BC	94	
27	BD	123	
28	BE	144	
29	BF	136	
30	BG	127	

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Mol	Chain	Length	Quality of chain
31	BH	117	
32	BI	115	
33	BJ	118	
34	BK	103	
35	BL	110	
36	BM	99	
37	BN	270	
38	BO	103	
39	BP	85	
40	BQ	63	
41	BR	59	
42	BS	70	
43	BT	57	
44	BU	54	
45	BV	46	
46	BW	64	
47	BX	38	
48	BY	209	
49	BZ	213	
50	B1	201	
51	B2	178	
52	B3	177	
53	B4	149	
54	B5	142	
55	B6	140	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 149248 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 A/T, P and E-site tRNAs.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AP	75	Total	C	N	O	P	0	0
			1600	715	288	523	74		
1	AE	76	Total	C	N	O	P	0	0
			1622	725	293	529	75		

- Molecule 2 is a RNA chain called mRNA model.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AM	20	Total	C	N	O	P	0	0
			397	180	40	158	19		

- Molecule 3 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A1	1530	Total	C	N	O	P	0	0
			32828	14642	6024	10633	1529		

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AB	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 5 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AC	117	Total	C	N	O	S	0	0
			876	540	174	159	3		

- Molecule 6 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AD	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 7 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 8 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	96	Total	C	N	O	S	0	0
			773	483	160	127	3		

- Molecule 9 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	88	Total	C	N	O	S	0	0
			715	440	146	128	1		

- Molecule 10 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AI	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AJ	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 12 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 15 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 16 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AQ	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

- Molecule 17 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AR	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 18 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AS	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 19 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AT	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 20 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AU	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 21 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AV	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 22 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AW	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

- Molecule 23 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AX	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 24 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BA	117	Total	C	N	O	P	0	0
			2504	1116	459	813	116		

- Molecule 25 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BB	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BC	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 27 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BD	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- Molecule 28 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BE	144	Total	C	N	O	S	0	0
			1052	654	207	189	2		

- Molecule 29 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BF	136	Total	C	N	O	S	0	0
			1073	686	205	176	6		

- Molecule 30 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BG	127	Total	C	N	O	S	0	0
			1007	621	204	177	5		

- Molecule 31 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BH	117	Total	C	N	O	S	0	0
			899	557	179	162	1		

- Molecule 32 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BI	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 33 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	BJ	117	Total	C	N	O	0	0
			946	604	192	150		

- Molecule 34 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BK	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 35 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BL	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 36 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BM	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

- Molecule 37 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BN	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 38 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	BO	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 39 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BP	84	Total	C	N	O	S	0	0
			633	391	129	112	1		

- Molecule 40 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BQ	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 41 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BR	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 42 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BS	70	Total	C	N	O	S	0	0
			548	339	104	99	6		

- Molecule 43 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BT	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 44 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BU	54	Total	C	N	O	S	0	0
			440	284	81	75			

- Molecule 45 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BV	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 46 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BW	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 47 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BX	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

- Molecule 48 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BY	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 49 is a protein called 50S ribosomal protein L1P.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BZ	213	Total	C	N	O	S	0	0
			1687	1078	300	308	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BZ	1	MET	-	insertion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	70	SER	PHE	conflict	UNP P35024
BZ	82	LYS	ASN	conflict	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024
BZ	?	-	MET	deletion	UNP P35024

- Molecule 50 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B1	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 51 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B2	178	Total	C	N	O	S	0	0
			1419	905	251	257	6		

- Molecule 52 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B3	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 53 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B4	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 54 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B5	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

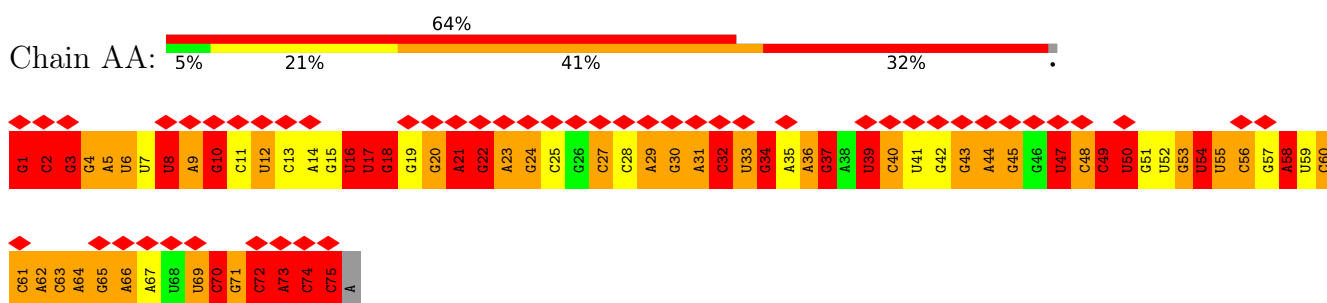
- Molecule 55 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B6	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

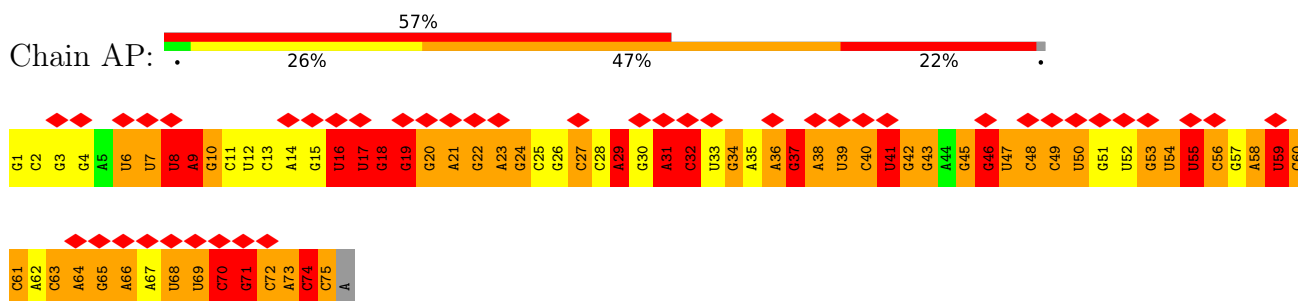
3 Residue-property plots

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.

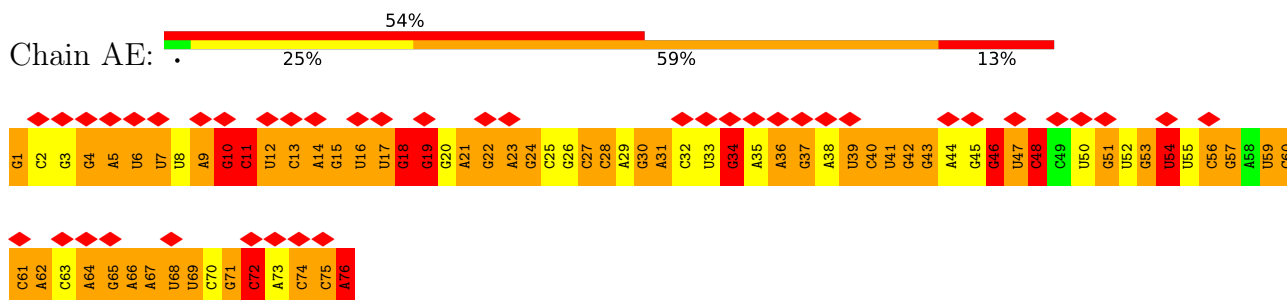
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 1: A/T, P and E-site tRNAs



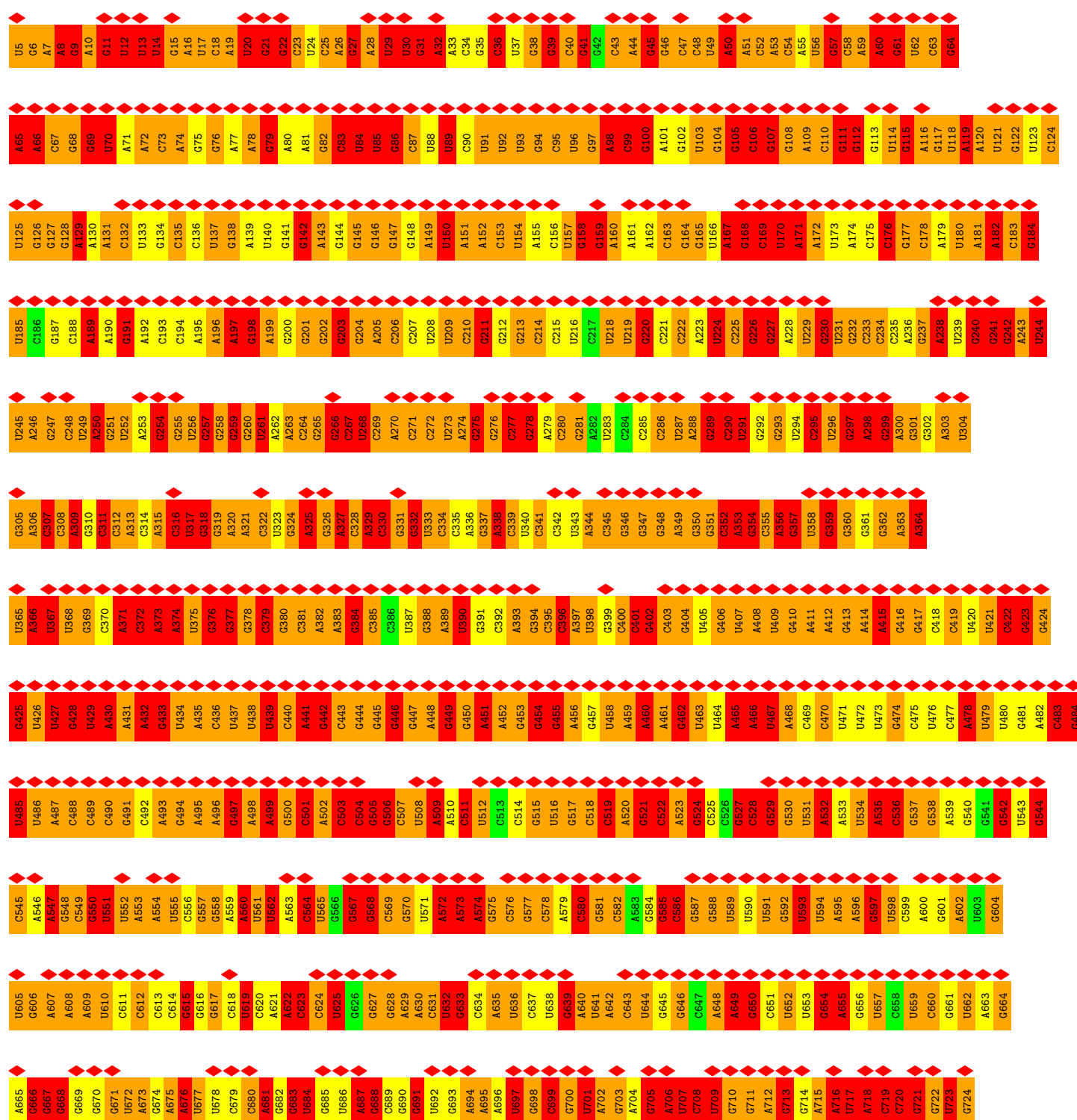
- Molecule 1: A/T, P and E-site tRNAs



- Molecule 2: mRNA model



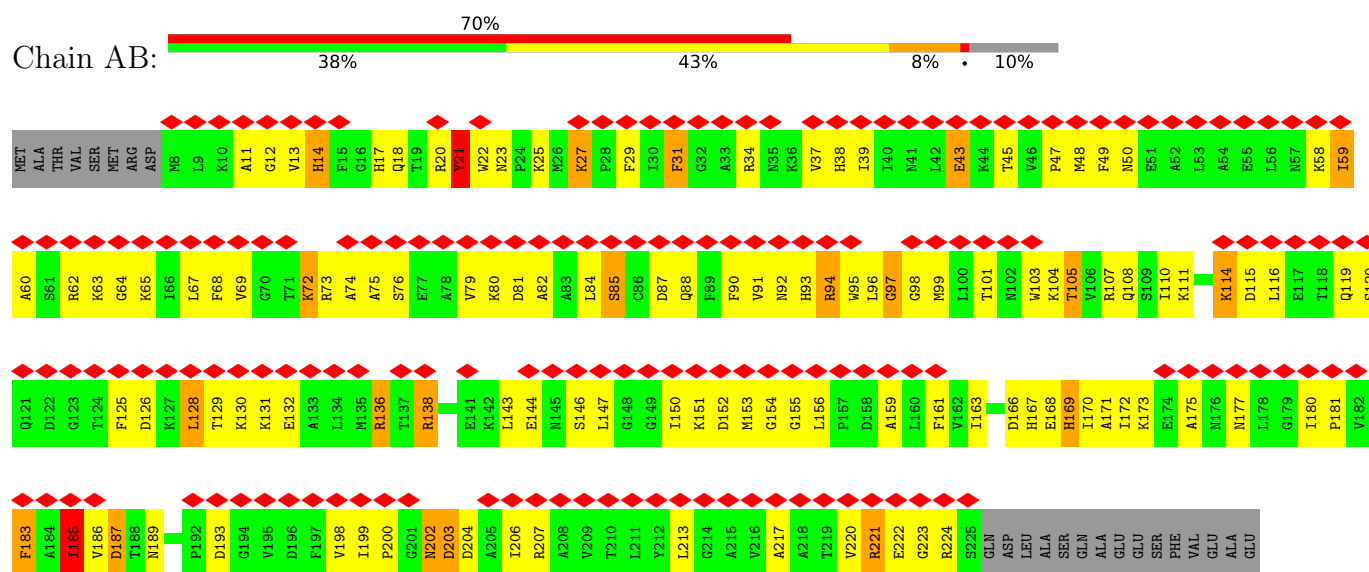
Chain A1: 18% 66% 34%



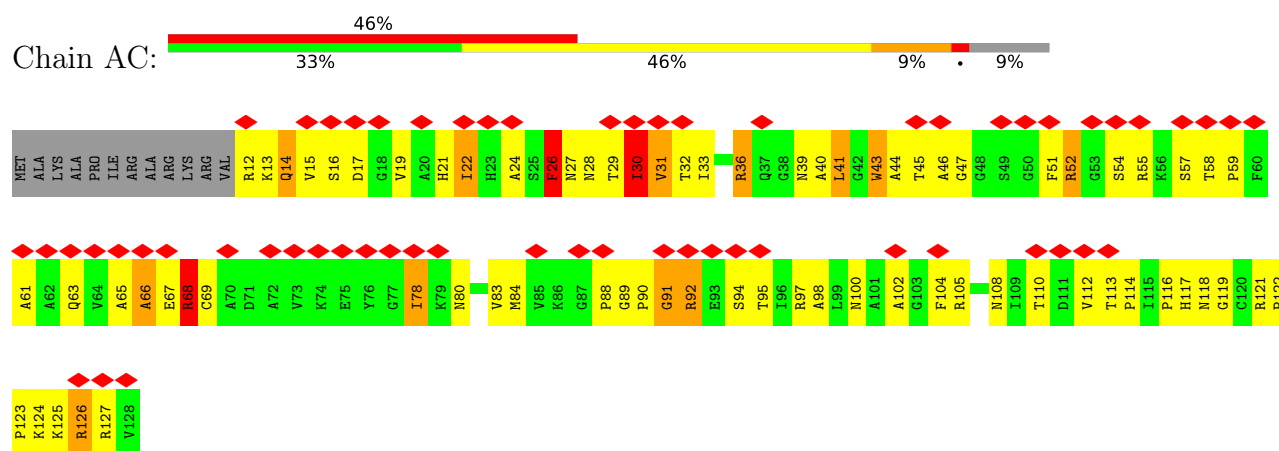
U1445	C1385	G1325	U1205	A1145	U1085	U1025	G785	G725
A1446	G1266	U1326	G1206	A1146	U1086	G1026	G786	C726
C1447	G1267	C1327	G1207	C1147	G1087	C1027	A787	G727
C1328	G1268	C1328	C1208	U1148	G1088	C1028	U788	A728
U1330	A1269	U1329	C1209	C1149	A969	A909	G789	A729
C1331	G1270	U1331	C1210	U1090	C970	U1029	A790	G730
A1332	A1271	U1332	U1211	A1151	U1091	U1030	G791	A731
G1333	G1272	A1333	U1212	A1152	A1092	C1031	G792	G732
G1334	C1273	G1334	A1213	G1153	A1093	G1032	G793	G733
U1335	A1274	U1335	C1214	U1094	A975	A914	A794	G734
C1336	A1275	C1336	G1215	U1095	G976	G1033	U795	G735
G1337	G1276	G1337	A1216	C1096	G977	A1034	C796	C735
G1338	C1277	G1338	C1217	G1097	A778	A1035	C797	C736
A1339	G1278	A1339	A1157	C1098	A788	A1036	U798	C737
C1340	G1279	C1340	C1158	U1099	A789	C1037	G799	C738
U1341	A1280	U1341	U1159	C1100	C980	U920	G800	C739
C1342	C1281	C1342	G1160	A1101	U981	U921	U801	U740
G1343	C1282	G1343	C1161	A1102	U982	G922	A802	G741
C1344	U1283	C1344	C1162	G1103	A983	A923	G803	G742
U1345	C1284	U1345	A1163	G1104	C984	C924	U804	A743
A1346	A1285	A1346	A1164	G1106	C985	G925	C805	A744
G1347	U1286	G1347	U1165	C1107	U986	G926	C806	G745
U1348	A1287	U1348	G1166	G1108	U987	G927	A807	A746
A1408	C1288	A1408	A1167	C1109	G988	G928	C808	G747
C1409	U1289	C1409	U1168	A1110	U989	G929	G809	G748
A1410	C1290	A1410	A1169	A1111	C990	C931	C810	A749
U1351	U1291	U1351	A1170	C1112	U991	C932	C811	G750
C1352	G1292	C1352	A1171	C1113	U992	G933	G812	U751
G1353	C1293	G1353	C1172	C1114	G993	C934	U813	G752
U1354	U1294	U1354	U1173	C1115	U994	A935	A814	A753
G1355	U1295	G1355	G1174	U1116	A94	C936	A815	C754
C1356	C1296	C1356	G1175	A1117	C995	A937	A816	G755
U1297	U1295	U1297	U1235	C1054	A996	A938	C817	G756
A1236	A1236	A1236	A1176	A1055	U997	A939	G818	C756
C1237	C1237	C1237	G1177	U1056	U997	G939	A819	U757
U1298	G1300	U1298	G1178	C1057	C998	C940	U820	C758
A1360	U1301	A1360	A1179	G1058	C999	G941	A759	G760
G1361	C1302	G1361	A1239	U1059	A1000	G942	G821	G761
A1362	C1303	A1362	U1240	G1061	C1001	U943	C822	U762
C1363	G1304	C1363	G1241	U1062	G1002	G944	G823	G763
U1364	C1305	U1364	C1242	G1063	G1003	G945	A824	A764
G1365	A1306	G1365	C1243	U1064	A1004	A946	C826	C765
C1366	U1307	C1366	G1244	G1065	G947	C948	U827	G766
C1367	G1308	C1367	G1184	U1066	A889	A949	G829	A767
A1368	C1309	A1368	G1185	C1067	G890	U950	G830	G768
C1369	U1310	C1369	G1186	A1067	A891	G951	A831	A769
G1370	A1311	G1370	G1187	U1070	U1007	U952	G832	G770
C1371	C1312	C1371	A1188	C1071	U1008	G954	U834	G771
U1372	U1313	U1372	U1189	G1072	U955	U955	U835	U772
G1373	C1314	G1373	C1249	U1073	U956	U956	G836	G773
A1374	C1315	A1374	A1191	G1074	U957	U957	U837	G774
C1375	U1315	C1375	A1196	U1075	A958	C959	G838	G775
U1376	G1316	U1376	A1197	U1076	U959	U960	C839	G776
A1377	C1317	A1377	G1193	C1077	U961	G902	C841	A777
C1378	A1254	C1378	U1194	G1078	U962	U904	U842	G778
G1379	G1255	G1379	C1195	U1079	C962	U843	U843	A780
U1380	A1256	U1380	A1196	G1080	G963	A964	G844	A782
C1381	C1257	C1381	A1197	A1081	U1023			C783
U1382	G1258	U1382	U1198	U1082	G1024			A784
A1383	C1322	A1383	U1199	A1082				
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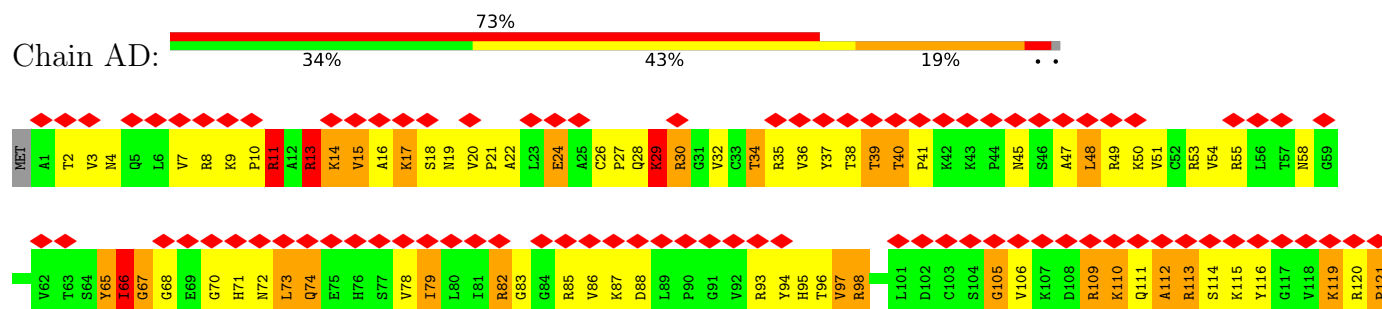
• Molecule 4: 30S ribosomal protein S2



• Molecule 5: 30S ribosomal protein S11

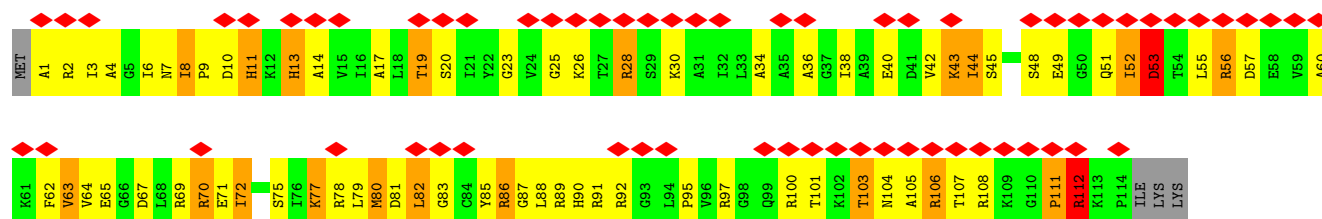


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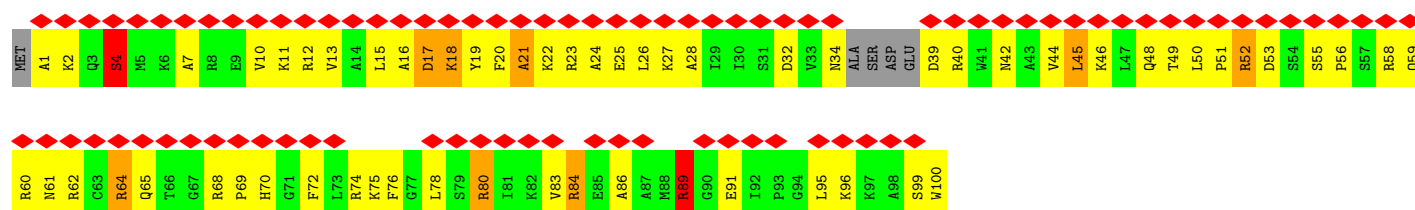
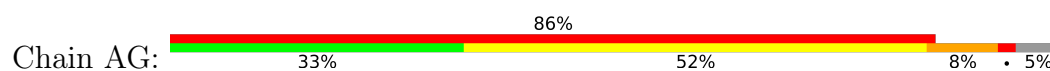




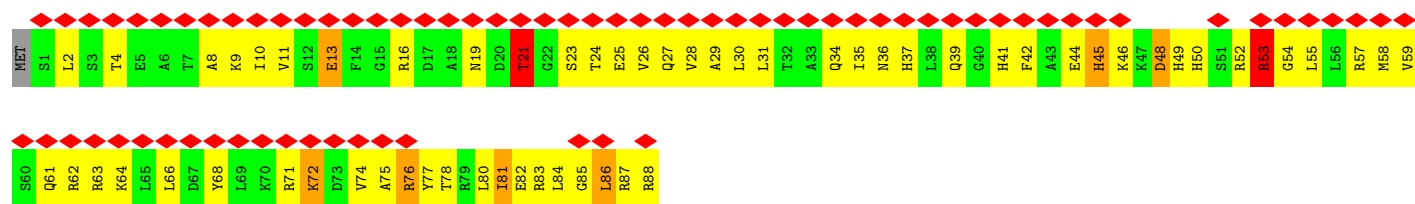
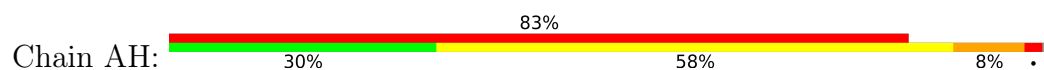
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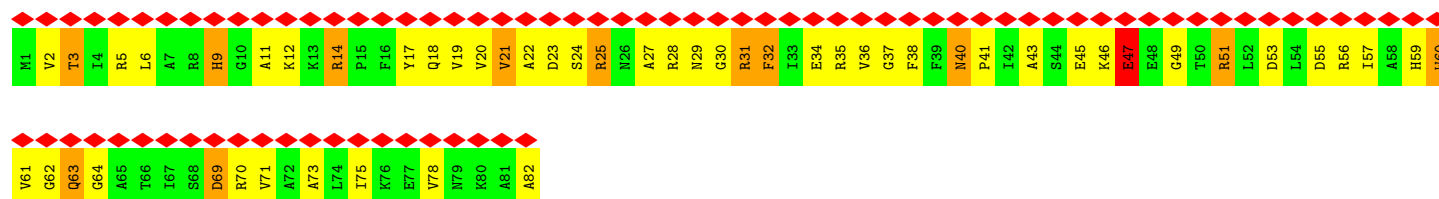
• Molecule 8: 30S ribosomal protein S14



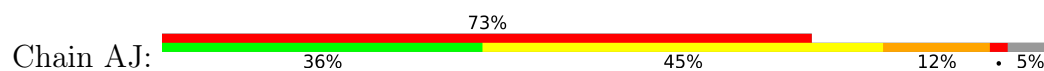
• Molecule 9: 30S ribosomal protein S15

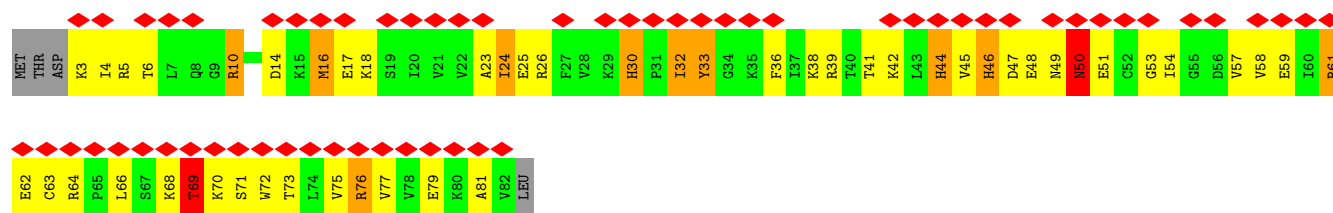


• Molecule 10: 30S ribosomal protein S16

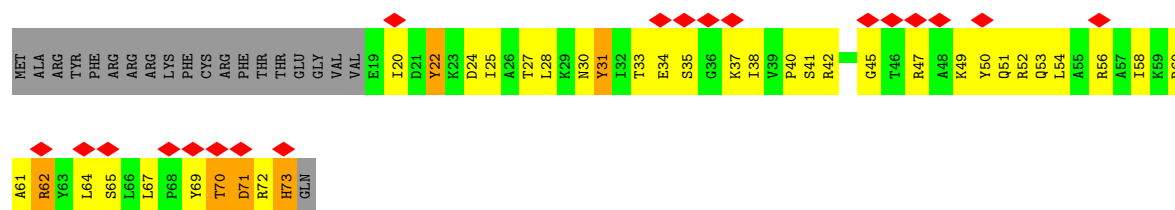
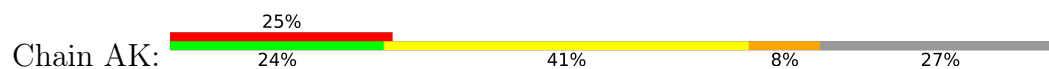


• Molecule 11: 30S ribosomal protein S17

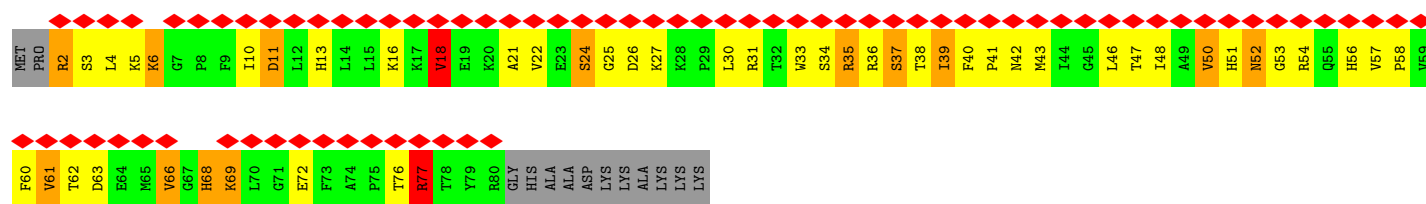
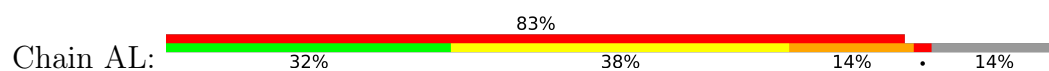




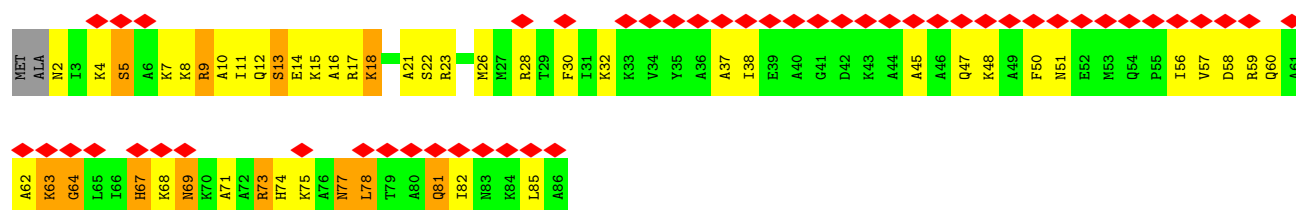
• Molecule 12: 30S ribosomal protein S18



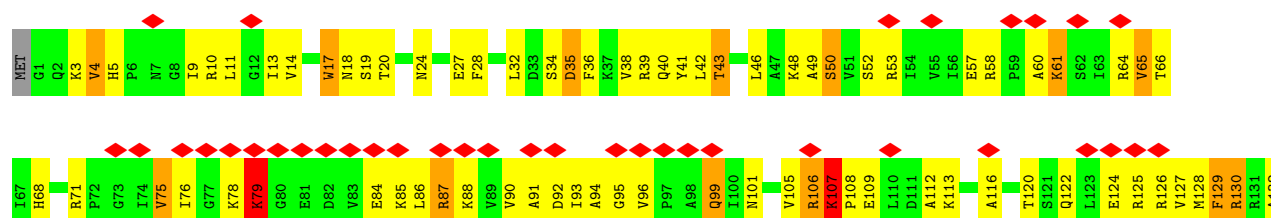
• Molecule 13: 30S ribosomal protein S19

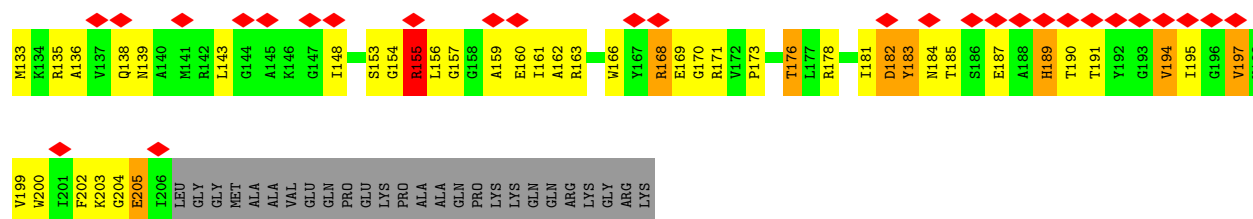


• Molecule 14: 30S ribosomal protein S20

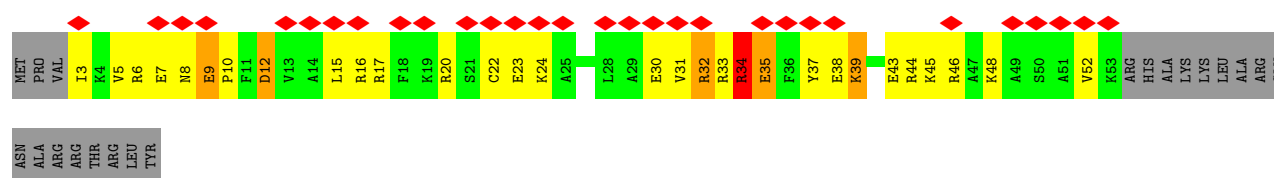
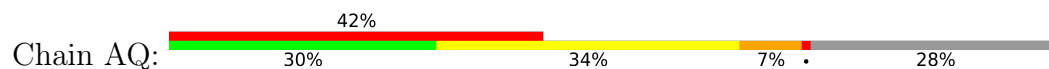


• Molecule 15: 30S ribosomal protein S3

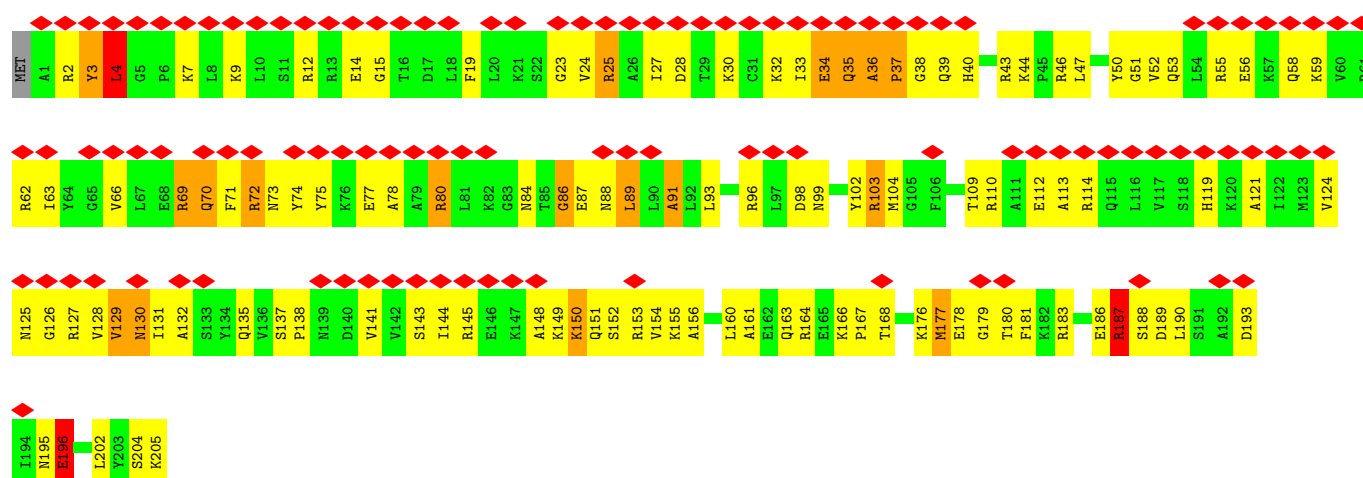




• Molecule 16: 30S ribosomal protein S21



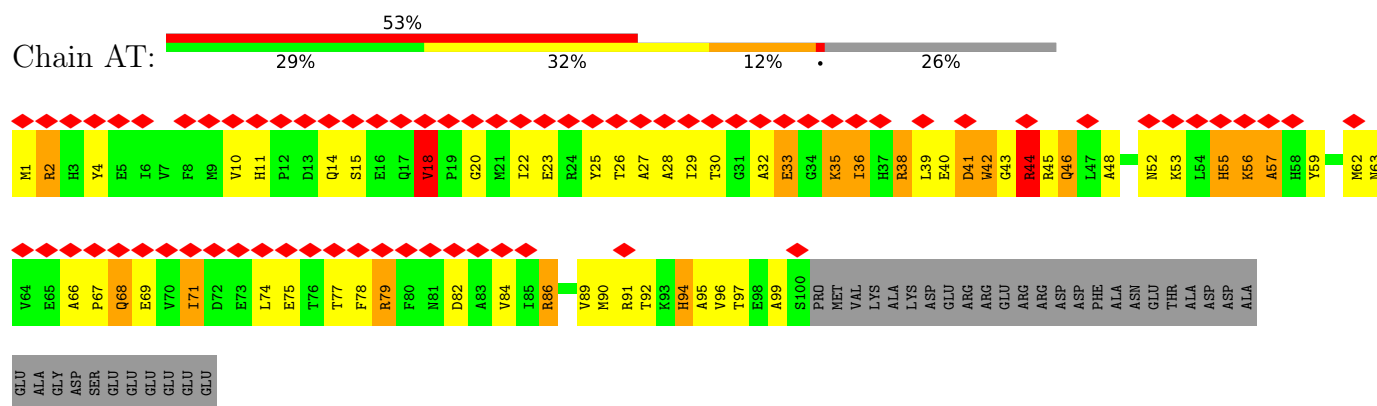
• Molecule 17: 30S ribosomal protein S4



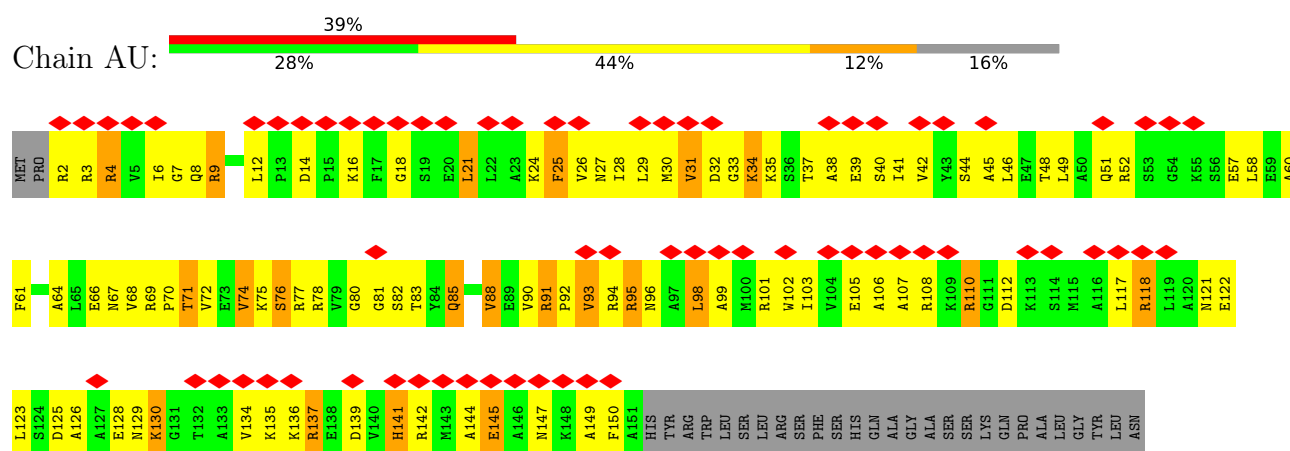
• Molecule 18: 30S ribosomal protein S5



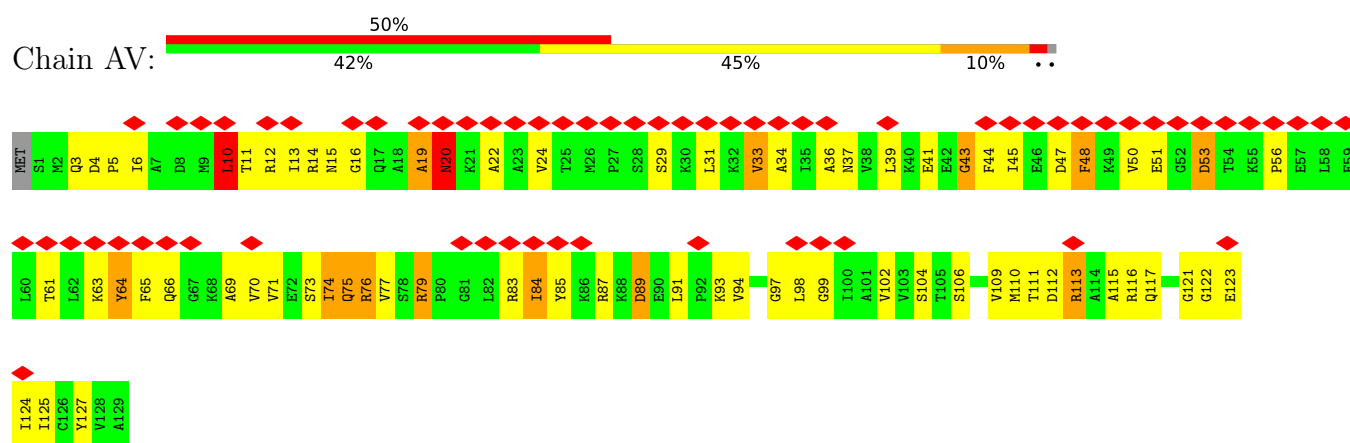
- Molecule 19: 30S ribosomal protein S6



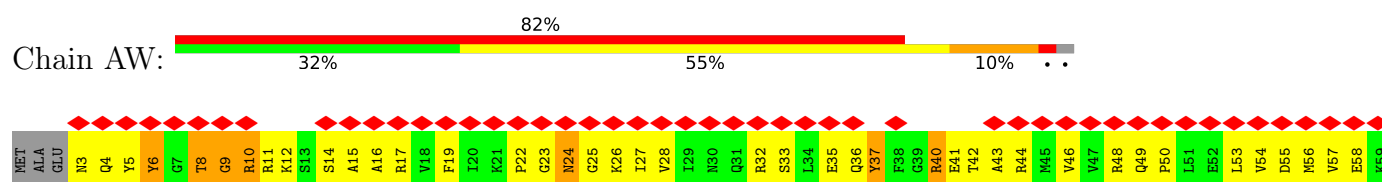
- Molecule 20: 30S ribosomal protein S7

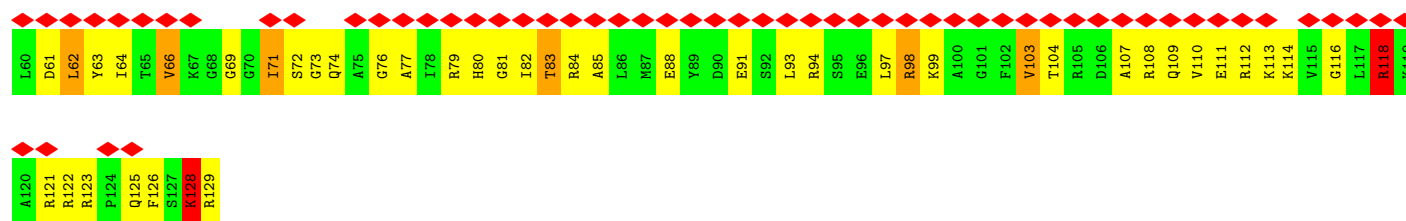


- Molecule 21: 30S ribosomal protein S8

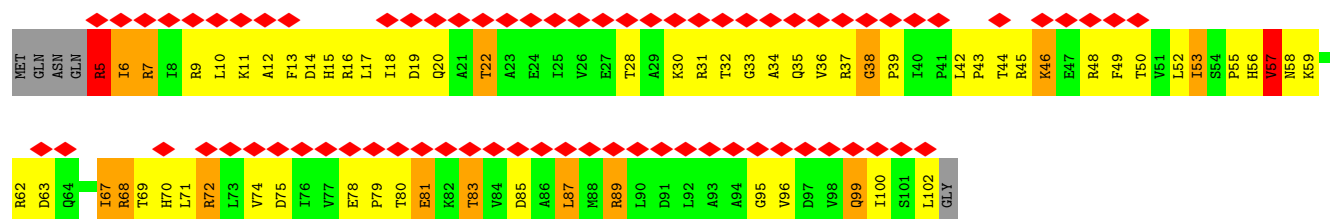
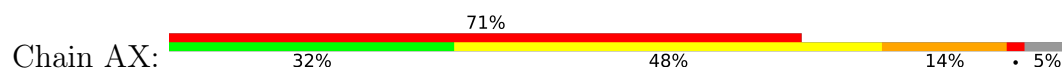


- Molecule 22: 30S ribosomal protein S9

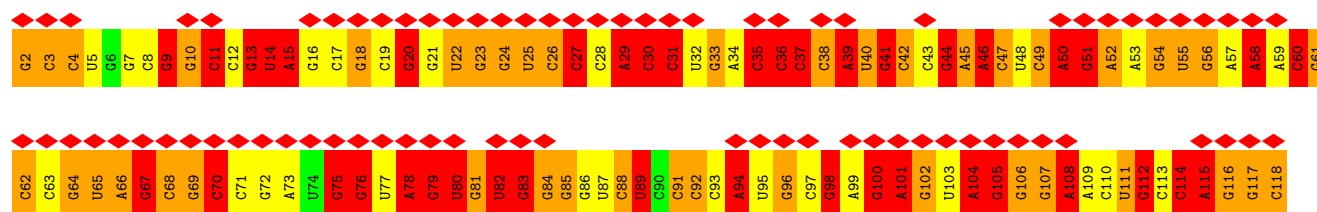




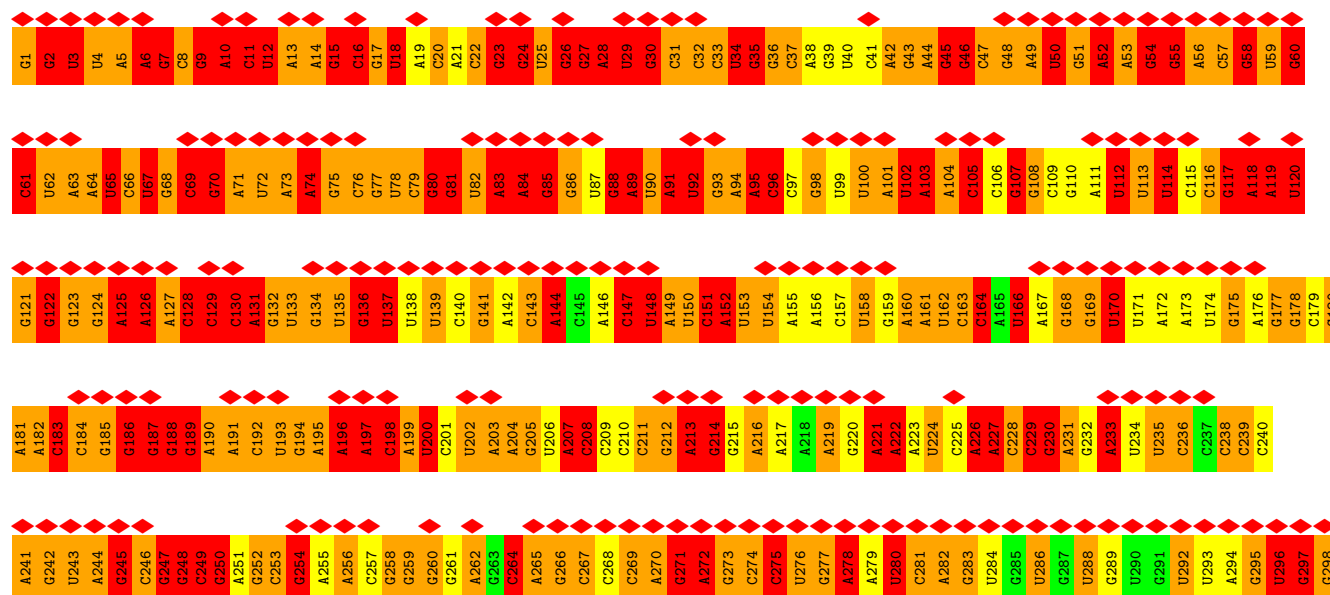
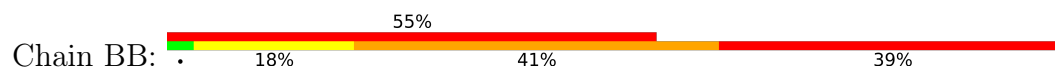
• Molecule 23: 30S ribosomal protein S10



• Molecule 24: 5S rRNA



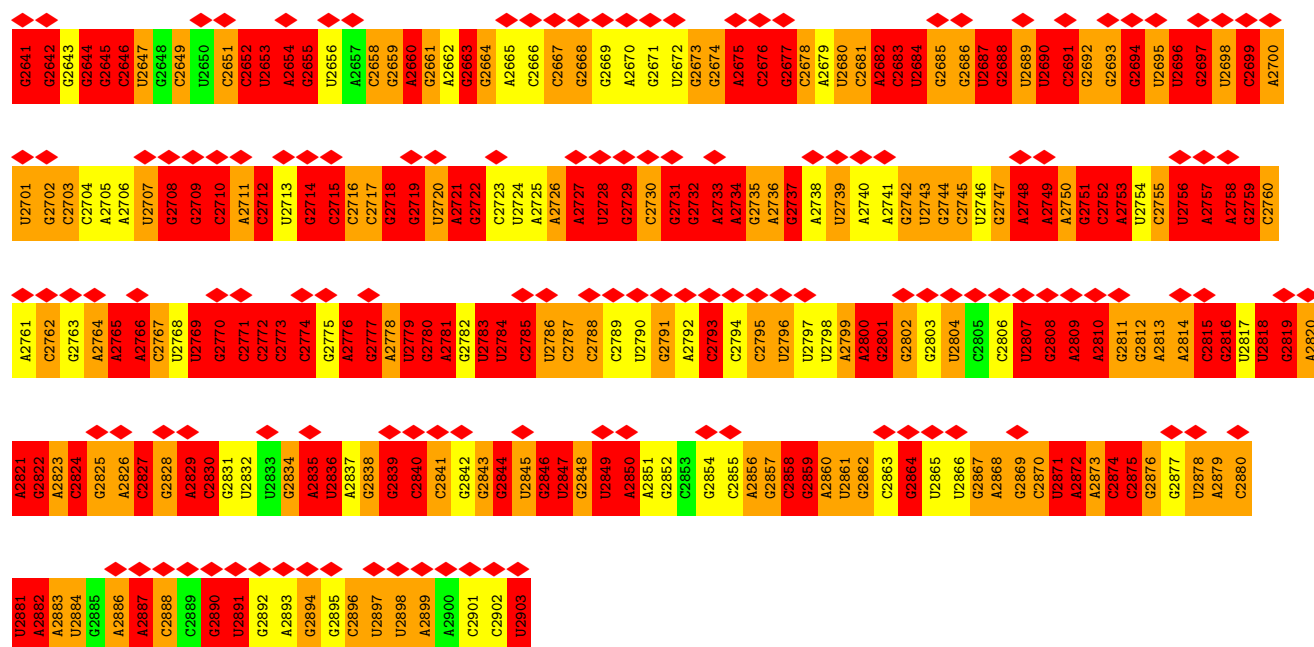
• Molecule 25: 23S rRNA



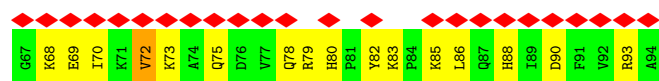
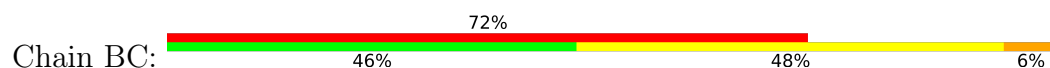
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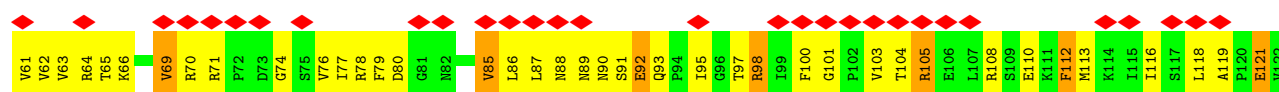
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U2401	U2402	C2403	U2404	G2405	A2406	A2407	U2408	G2409	G2410	A2411	G2412	G2413	G2414	G2415	G2416	G2417	A2418	U2419	G2420	G2421	A2422	U2423	C2424	A2425	A2426	G2427	G2428	G2429	A2430	U2431	U2432	A2433	A2434	A2435	G2436	G2437	U2438	A2439	C2501	G2502	A2503	U2504	G2505	U2506	G2507	G2508	G2509	C2510	U2511	C2512	A2513	U2514	C2515	A2516	G2517	U2518	U2519	G2520	
A2461	C2462	G2463	G2464	G2465	G2466	G2467	A2468	A2469	G2470	A2471	G2472	U2473	G2474	G2475	A2476	U2477	A2478	U2479	G2480	G2481	A2482	G2483	G2484	G2485	G2486	G2487	G2488	U2489	G2490	U2491	U2492	G2493	G2494	G2495	G2496	A2497	G2498	G2499	U2500	C2501	G2502	A2503	U2504	G2505	U2506	G2507	G2508	G2509	C2510	U2511	C2512	A2513	U2514	C2515	A2516	G2517	U2518	U2519	G2520
G2521	U2522	G2523	G2524	G2525	G2526	G2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	G2538	G2539	G2540	A2541	A2542	G2543	G2544	G2545	G2546	G2547	U2548	G2549	G2550	G2551	U2552	G2553	U2554	G2555	G2556	G2557	G2558	G2559	U2560	U2561	U2562	U2563	A2564	A2565	A2566	G2567	U2568	G2569	G2570	U2571	A2572	G2573	G2574	A2575	G2576	U2577	G2578	G2579	U2580
G2581	G2582	G2583	U2584	U2585	U2586	G2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	G2538	G2539	G2540	A2541	A2542	G2543	G2544	G2545	G2546	G2547	U2548	G2549	G2550	G2551	U2552	G2553	U2554	G2555	G2556	G2557	G2558	G2559	U2560	U2561	U2562	U2563	A2564	A2565	A2566	G2567	U2568	G2569	G2570	U2571	A2572	G2573	G2574	A2575	G2576	U2577	G2578	G2579	U2580
G2581	G2582	G2583	U2584	U2585	U2586	G2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	G2538	G2539	G2540	A2541	A2542	G2543	G2544	G2545	G2546	G2547	U2548	G2549	G2550	G2551	U2552	G2553	U2554	G2555	G2556	G2557	G2558	G2559	U2560	U2561	U2562	U2563	A2564	A2565	A2566	G2567	U2568	G2569	G2570	U2571	A2572	G2573	G2574	A2575	G2576	U2577	G2578	G2579	U2580
G2581	G2582	G2583	U2584	U2585	U2586	G2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	G2538	G2539	G2540	A2541	A2542	G2543	G2544	G2545	G2546	G2547	U2548	G2549	G2550	G2551	U2552	G2553	U2554	G2555	G2556	G2557	G2558	G2559	U2560	U2561	U2562	U2563	A2564	A2565	A2566	G2567	U2568	G2569	G2570	U2571	A2572	G2573	G2574	A2575	G2576	U2577	G2578	G2579	U2580
G2581	G2582	G2583	U2584	U2585	U2586	G2527	U2528	G2529	A2530	A2531	G2532	U2533	A2534	G2535	G2536	U2537	G2538	G2539	G2540	A2541	A2542	G2543	G2544	G2545	G2546	G2547	U2548	G2549	G2550	G2551	U2552	G2553	U2554	G2555	G2556	G2557	G2558	G2559	U2560	U2561	U2562	U2563	A2564	A2565	A2566	G2567	U2568	G2569	G2570	U2571	A2572	G2573	G2574	A2575	G2576	U2577	G2578	G2579	U2580



• Molecule 26: 50S ribosomal protein L25



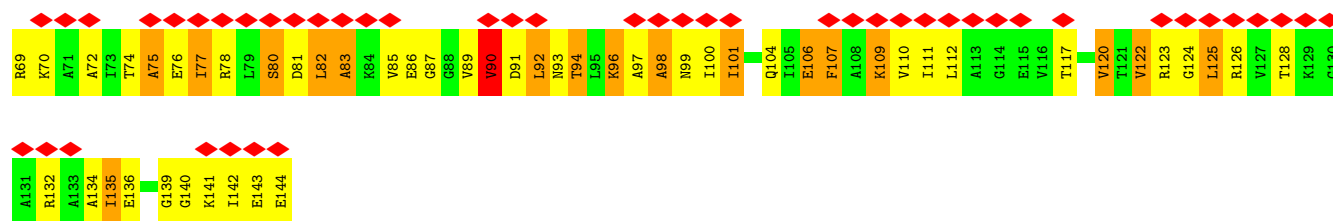
• Molecule 27: 50S ribosomal protein L14



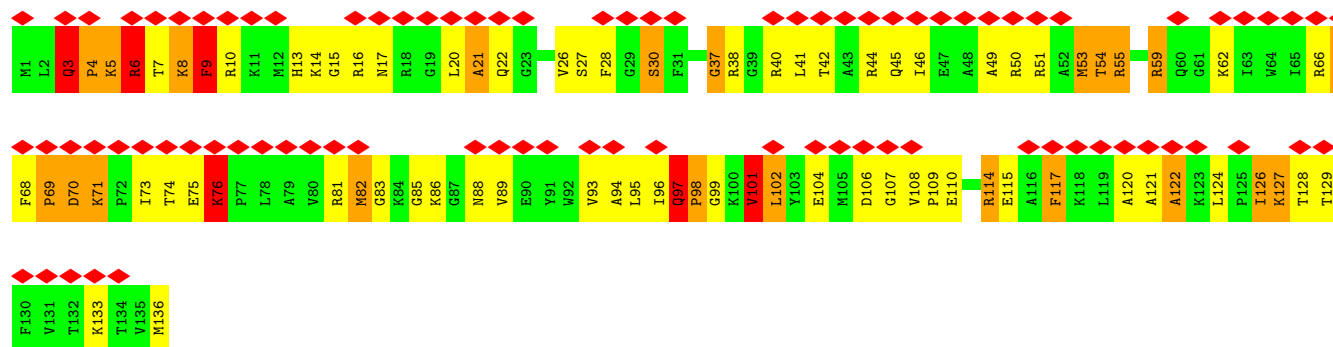
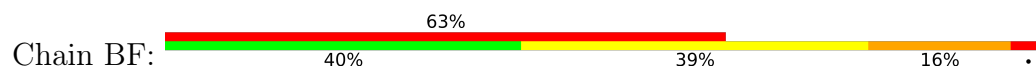
LEU

• Molecule 28: 50S ribosomal protein L15

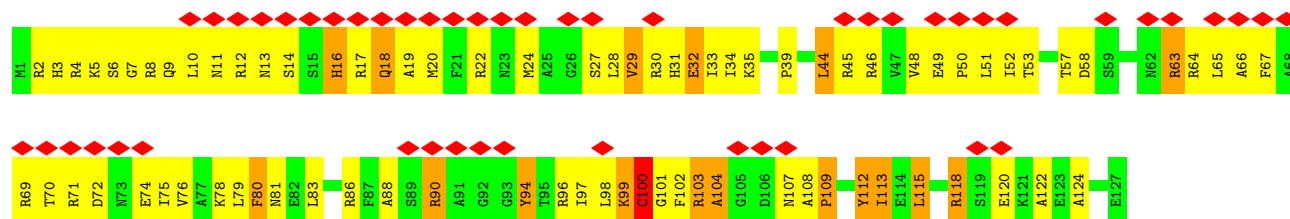




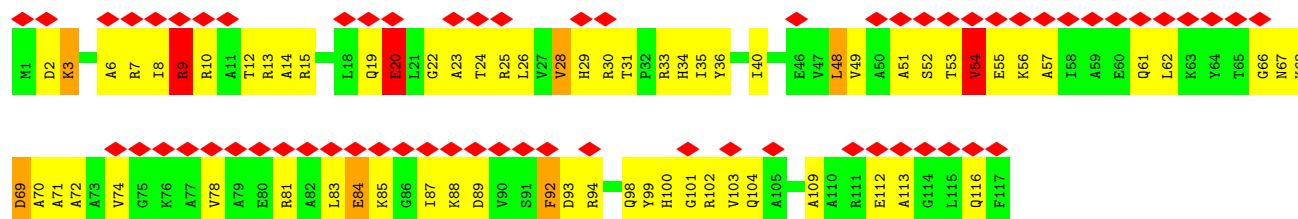
• Molecule 29: 50S ribosomal protein L16



• Molecule 30: 50S ribosomal protein L17

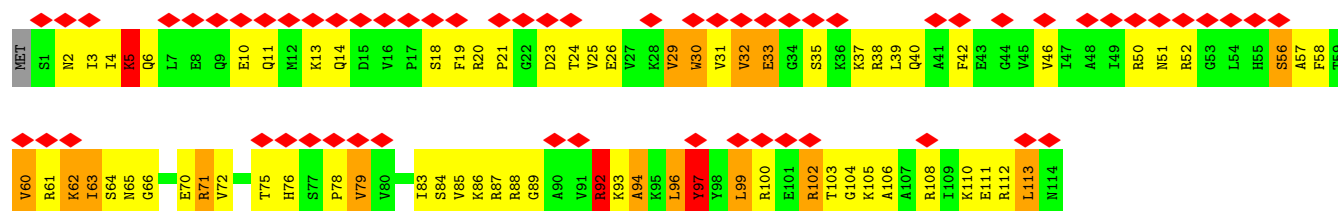


• Molecule 31: 50S ribosomal protein L18

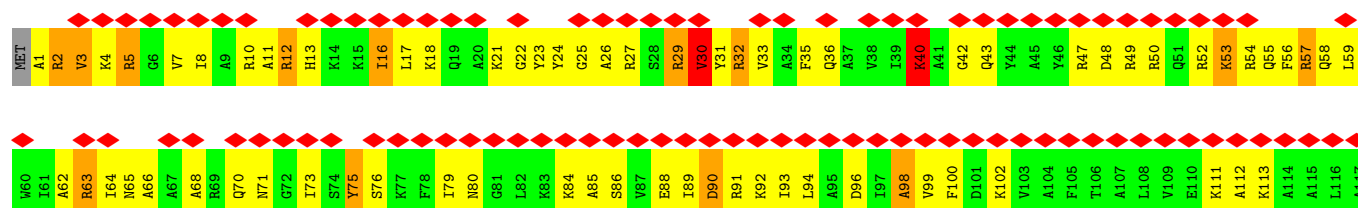
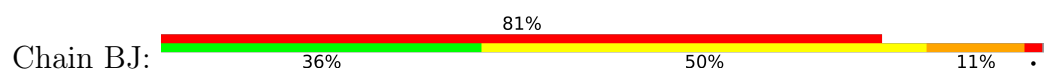


• Molecule 32: 50S ribosomal protein L19

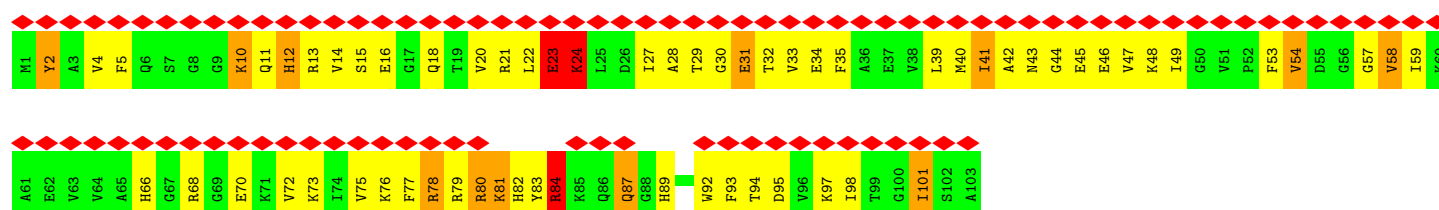




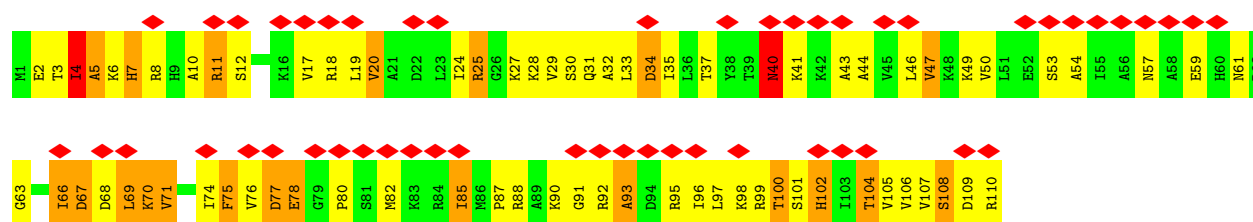
• Molecule 33: 50S ribosomal protein L20



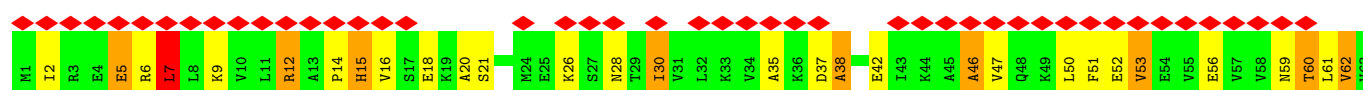
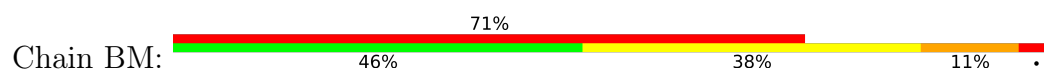
• Molecule 34: 50S ribosomal protein L21

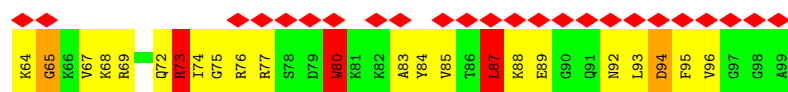


• Molecule 35: 50S ribosomal protein L22

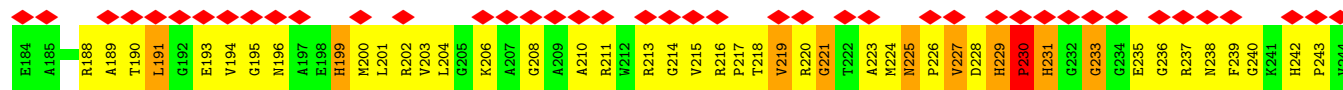
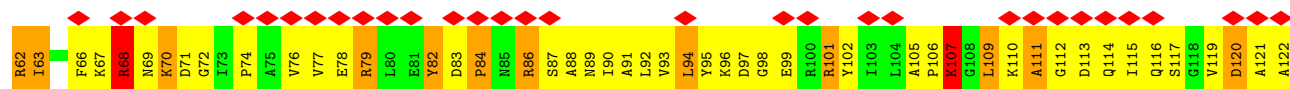
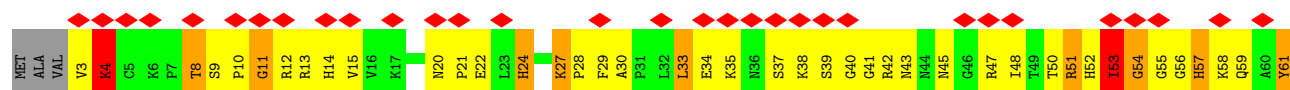


• Molecule 36: 50S ribosomal protein L23





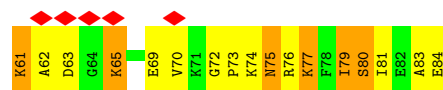
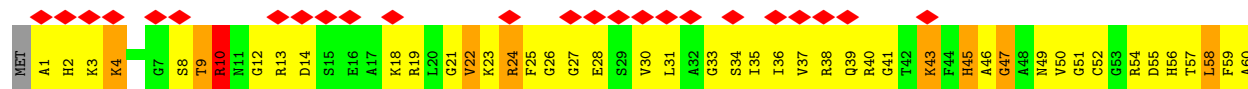
• Molecule 37: 50S ribosomal protein L2



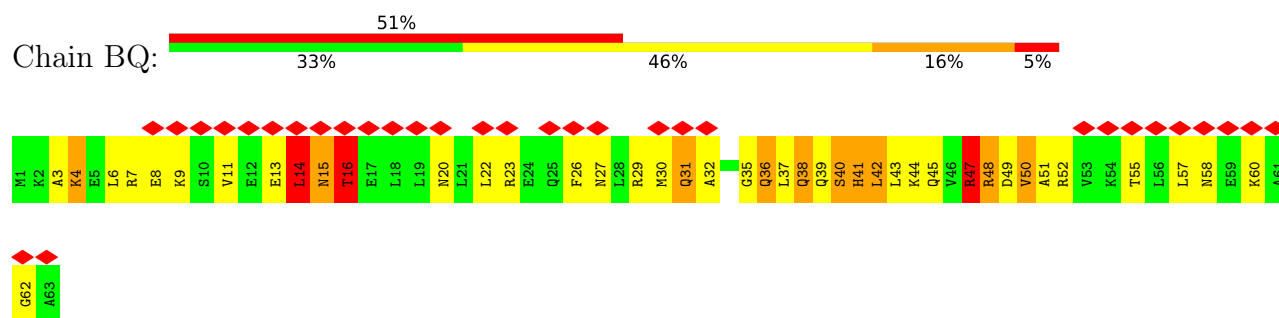
• Molecule 38: 50S ribosomal protein L24



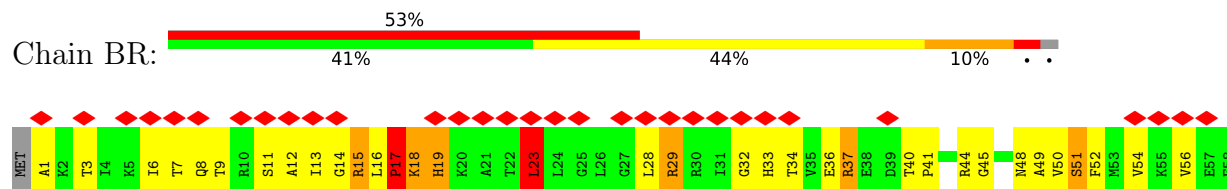
• Molecule 39: 50S ribosomal protein L27



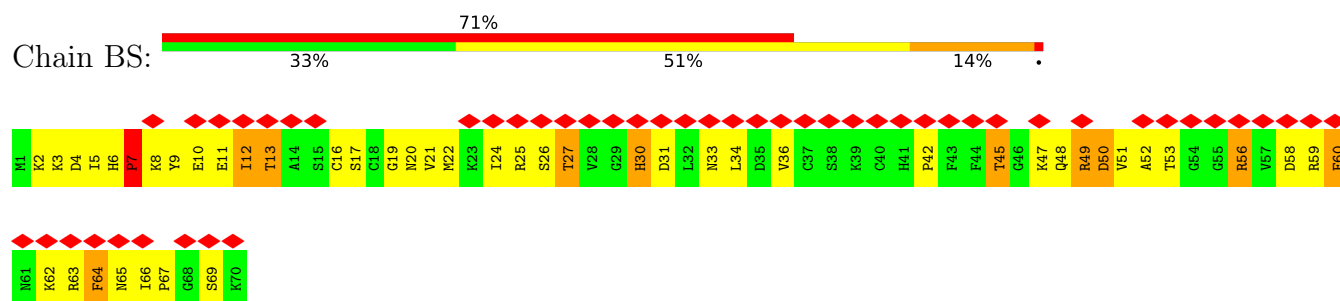
• Molecule 40: 50S ribosomal protein L29



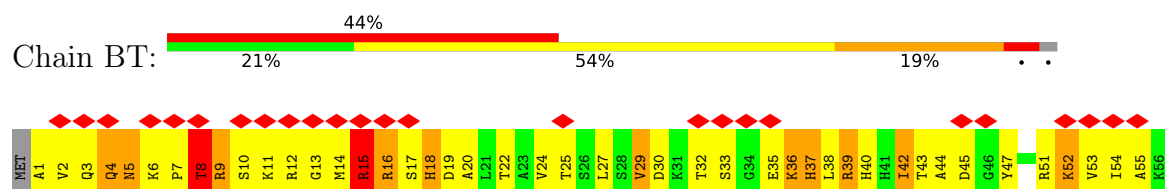
- Molecule 41: 50S ribosomal protein L30



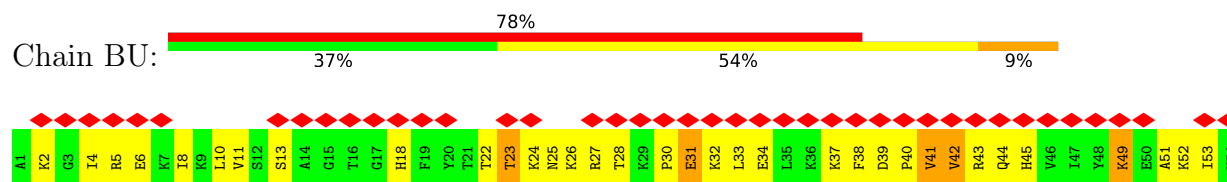
- Molecule 42: 50S ribosomal protein L31



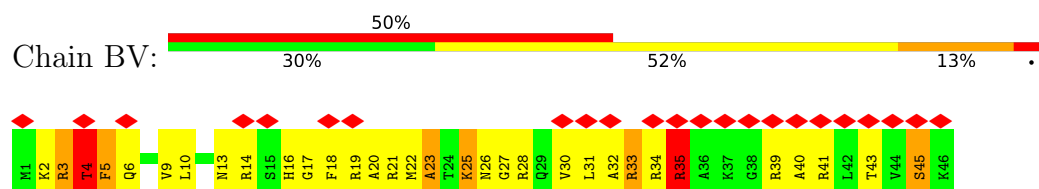
- Molecule 43: 50S ribosomal protein L32



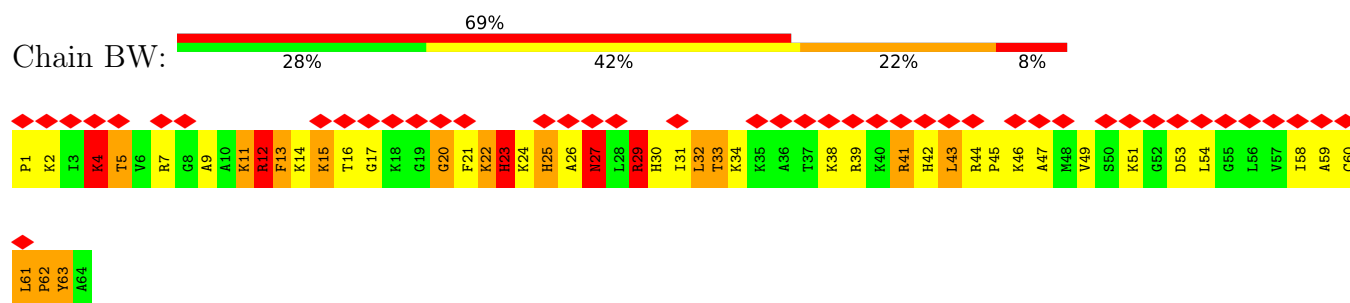
- Molecule 44: 50S ribosomal protein L33



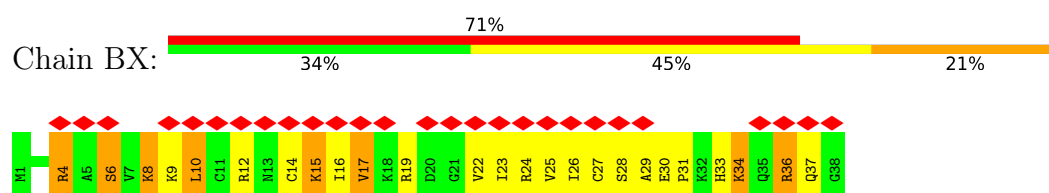
- Molecule 45: 50S ribosomal protein L34



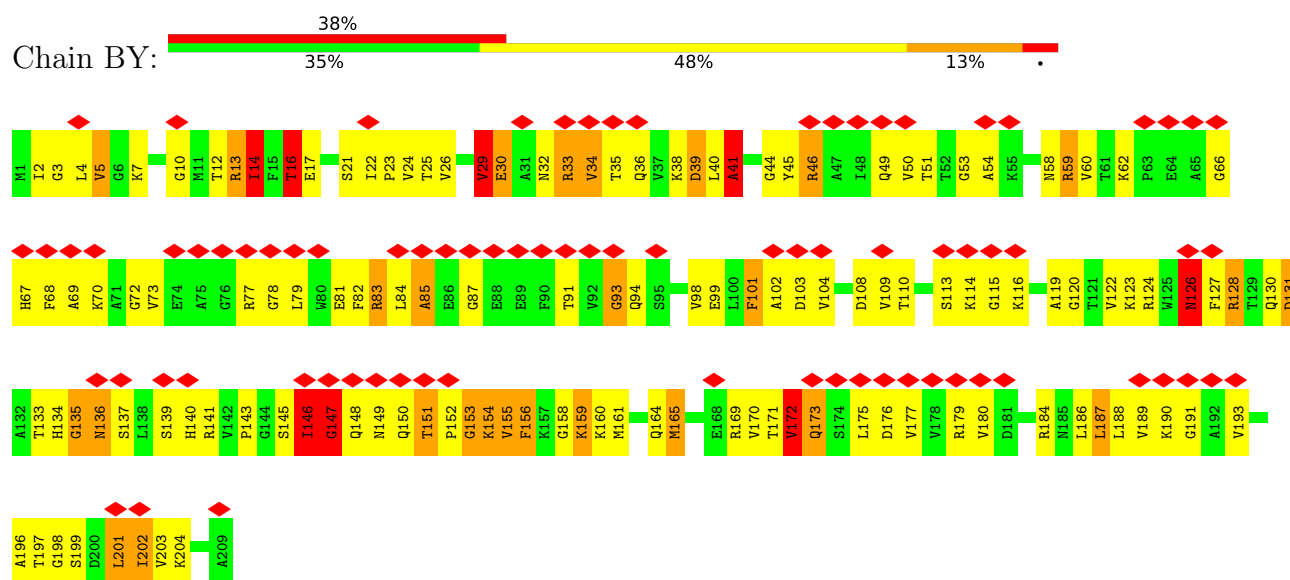
- Molecule 46: 50S ribosomal protein L35



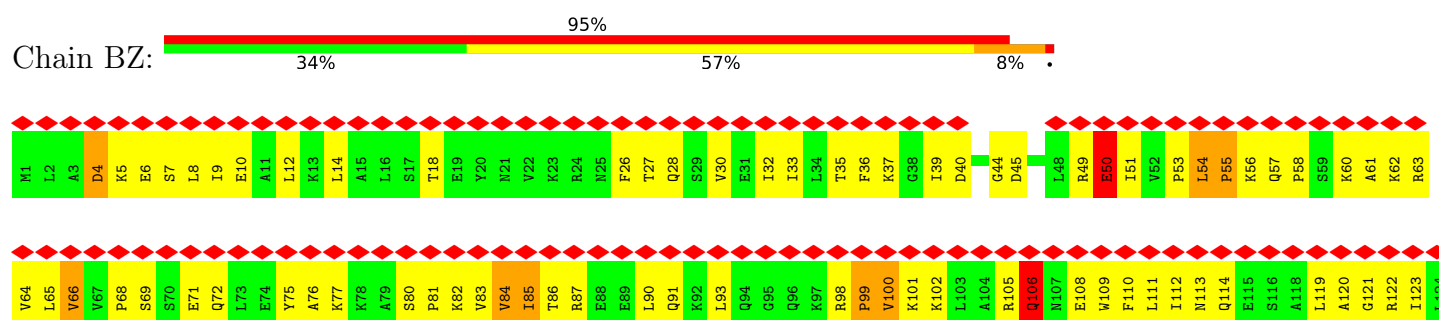
- Molecule 47: 50S ribosomal protein L36

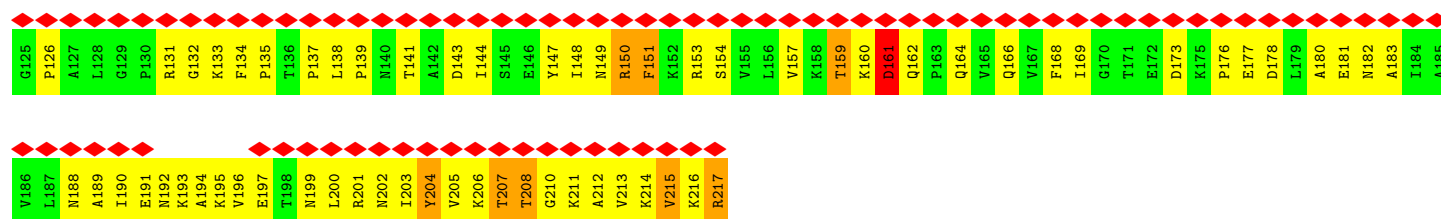


- Molecule 48: 50S ribosomal protein L3

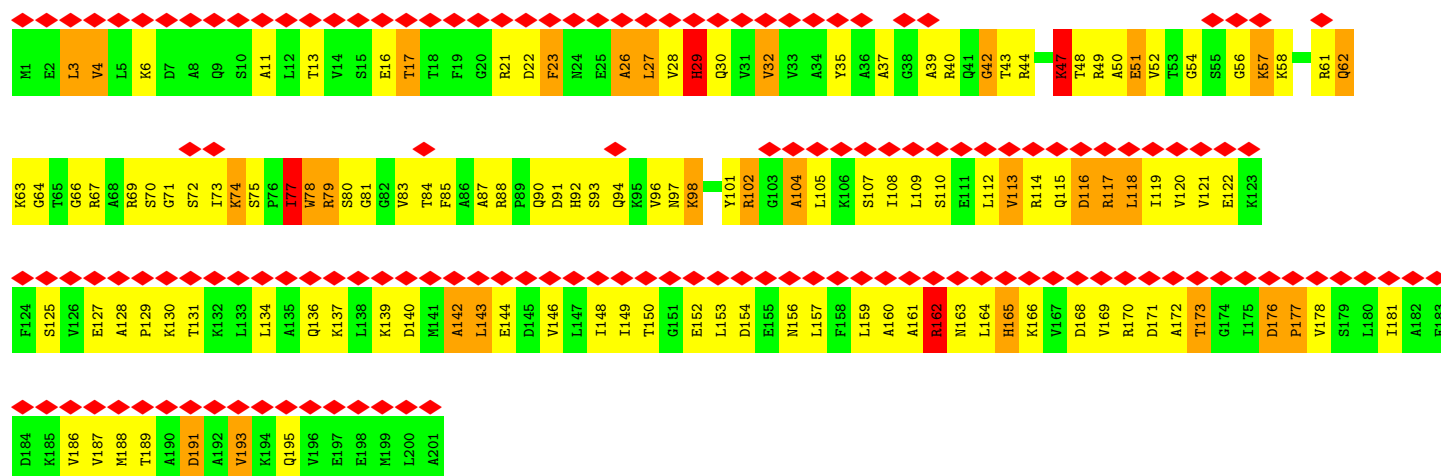
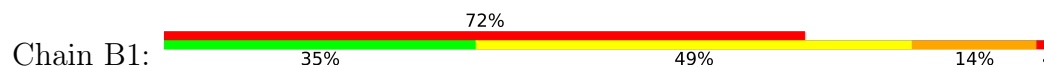


- Molecule 49: 50S ribosomal protein L1P

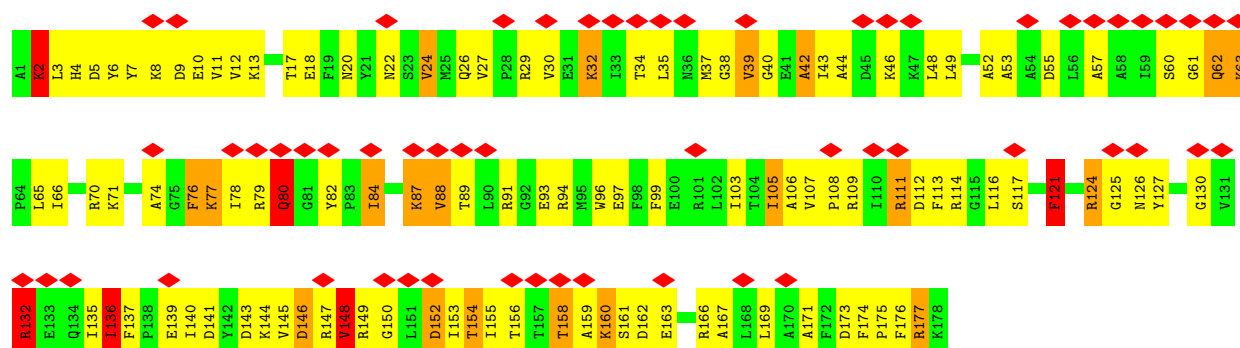




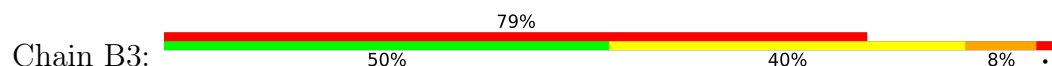
• Molecule 50: 50S ribosomal protein L4

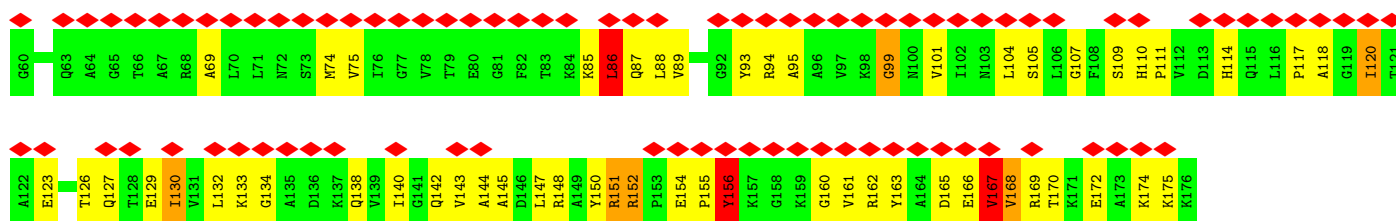


• Molecule 51: 50S ribosomal protein L5

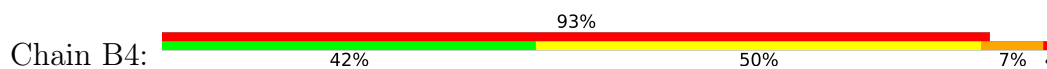


• Molecule 52: 50S ribosomal protein L6

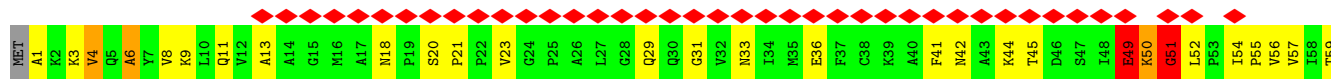




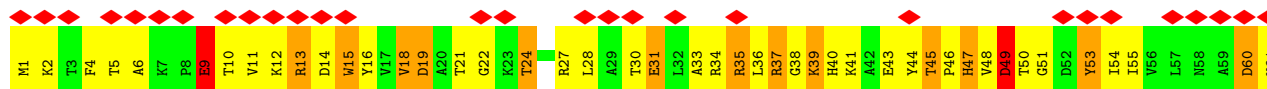
• Molecule 53: 50S ribosomal protein L9



• Molecule 54: 50S ribosomal protein L11



• Molecule 55: 50S ribosomal protein L13



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52181	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	250.773	Depositor
Minimum map value	-142.587	Depositor
Average map value	1.513	Depositor
Map value standard deviation	24.331	Depositor
Recommended contour level	43.4	Depositor
Map size ($\text{\AA}$)	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	2.82, 2.82, 2.82	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	AA	2.02	34/1789 (1.9%)	2.42	140/2788 (5.0%)
1	AE	2.00	37/1814 (2.0%)	2.15	124/2827 (4.4%)
1	AP	2.41	34/1789 (1.9%)	2.70	129/2788 (4.6%)
2	AM	1.89	6/436 (1.4%)	2.44	40/672 (6.0%)
3	A1	2.07	614/36759 (1.7%)	2.18	2490/57346 (4.3%)
4	AB	2.19	52/1735 (3.0%)	2.63	145/2338 (6.2%)
5	AC	2.22	37/892 (4.1%)	2.89	107/1205 (8.9%)
6	AD	2.26	43/968 (4.4%)	2.63	82/1300 (6.3%)
7	AF	2.13	22/892 (2.5%)	2.81	91/1193 (7.6%)
8	AG	2.15	27/785 (3.4%)	2.81	95/1046 (9.1%)
9	AH	2.40	36/723 (5.0%)	2.71	77/966 (8.0%)
10	AI	2.17	16/658 (2.4%)	2.77	59/884 (6.7%)
11	AJ	2.14	19/657 (2.9%)	2.64	62/881 (7.0%)
12	AK	2.24	16/462 (3.5%)	2.63	41/621 (6.6%)
13	AL	2.17	16/652 (2.5%)	2.64	61/877 (7.0%)
14	AN	2.11	14/670 (2.1%)	2.74	61/888 (6.9%)
15	AO	2.18	56/1651 (3.4%)	2.61	142/2225 (6.4%)
16	AQ	2.13	11/430 (2.6%)	2.76	35/570 (6.1%)
17	AR	2.13	53/1664 (3.2%)	2.68	144/2227 (6.5%)
18	AS	2.26	50/1118 (4.5%)	2.70	93/1504 (6.2%)
19	AT	2.13	20/835 (2.4%)	2.72	78/1128 (6.9%)
20	AU	2.20	36/1187 (3.0%)	2.68	114/1591 (7.2%)
21	AV	2.17	35/988 (3.5%)	2.63	88/1326 (6.6%)
22	AW	2.27	45/1033 (4.4%)	2.77	93/1375 (6.8%)
23	AX	2.17	28/796 (3.5%)	2.67	71/1077 (6.6%)
24	BA	1.97	41/2800 (1.5%)	2.22	191/4367 (4.4%)
25	BB	6.77	1207/69795 (1.7%)	2.22	4965/108884 (4.6%)
26	BC	2.12	26/765 (3.4%)	2.60	64/1025 (6.2%)
27	BD	2.29	39/939 (4.2%)	2.87	111/1258 (8.8%)
28	BE	2.22	38/1061 (3.6%)	2.68	96/1413 (6.8%)
29	BF	2.12	24/1092 (2.2%)	2.65	85/1460 (5.8%)
30	BG	2.18	33/1020 (3.2%)	2.77	111/1364 (8.1%)
31	BH	2.19	24/909 (2.6%)	2.71	81/1219 (6.6%)
32	BI	2.24	34/928 (3.7%)	2.61	69/1242 (5.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BJ	2.15	29/959 (3.0%)	2.78	87/1278 (6.8%)
34	BK	2.12	21/828 (2.5%)	2.60	57/1107 (5.1%)
35	BL	2.15	28/863 (3.2%)	2.74	90/1156 (7.8%)
36	BM	2.07	23/784 (2.9%)	2.51	56/1048 (5.3%)
37	BN	2.30	80/2092 (3.8%)	2.72	216/2813 (7.7%)
38	BO	2.15	24/787 (3.0%)	2.71	70/1051 (6.7%)
39	BP	2.22	23/641 (3.6%)	2.78	69/848 (8.1%)
40	BQ	2.21	22/509 (4.3%)	2.69	42/677 (6.2%)
41	BR	2.17	16/452 (3.5%)	2.59	35/605 (5.8%)
42	BS	2.20	20/558 (3.6%)	2.74	51/745 (6.8%)
43	BT	2.35	25/449 (5.6%)	2.83	47/599 (7.8%)
44	BU	2.21	12/447 (2.7%)	2.74	36/594 (6.1%)
45	BV	2.25	8/379 (2.1%)	2.94	47/498 (9.4%)
46	BW	2.09	15/512 (2.9%)	2.61	45/676 (6.7%)
47	BX	2.17	10/302 (3.3%)	3.14	35/397 (8.8%)
48	BY	2.27	55/1585 (3.5%)	2.74	135/2134 (6.3%)
49	BZ	2.15	55/1711 (3.2%)	2.68	145/2305 (6.3%)
50	B1	2.19	52/1570 (3.3%)	2.72	146/2113 (6.9%)
51	B2	2.17	45/1443 (3.1%)	2.71	131/1937 (6.8%)
52	B3	2.14	44/1342 (3.3%)	2.56	85/1816 (4.7%)
53	B4	2.11	36/1121 (3.2%)	2.58	81/1515 (5.3%)
54	B5	2.06	28/1045 (2.7%)	2.66	84/1410 (6.0%)
55	B6	2.27	47/1135 (4.1%)	2.74	111/1529 (7.3%)
All	All	4.72	3541/162206 (2.2%)	2.35	12336/242726 (5.1%)

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	0	52
1	AE	0	46
1	AP	2	51
2	AM	0	12
3	A1	4	995
4	AB	0	8
5	AC	0	4
6	AD	0	9
7	AF	0	8
8	AG	0	3
9	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	AI	0	9
11	AJ	0	4
12	AK	0	3
13	AL	0	8
14	AN	1	0
15	AO	0	9
16	AQ	0	5
17	AR	0	5
18	AS	0	2
19	AT	0	9
20	AU	0	8
21	AV	0	4
22	AW	0	9
23	AX	0	2
24	BA	0	81
25	BB	3	1853
26	BC	0	2
27	BD	0	4
28	BE	0	5
29	BF	0	9
30	BG	0	5
31	BH	0	7
32	BI	0	6
33	BJ	0	3
34	BK	0	11
35	BL	0	4
36	BM	0	3
37	BN	0	12
38	BO	0	4
39	BP	0	7
41	BR	0	4
42	BS	0	7
43	BT	0	3
44	BU	0	3
45	BV	0	4
46	BW	0	7
47	BX	0	1
48	BY	0	8
49	BZ	0	9
50	B1	0	9
51	B2	0	7
52	B3	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	B4	0	3
54	B5	0	3
55	B6	0	12
All	All	10	3370

The worst 5 of 3541 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	BB	995	C	C4-N4	1059.90	22.53	1.33
25	BB	995	C	C4-C5	954.00	20.50	1.43
25	BB	995	C	C2-N3	945.45	20.26	1.35
3	A1	1429	A	P-O5'	89.03	3.37	1.59
3	A1	1340	A	C3'-O3'	72.25	2.86	1.42

The worst 5 of 12336 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AP	74	C	P-O3'-C3'	-73.08	10.58	120.20
1	AP	74	C	O3'-P-O5'	-41.61	41.58	104.00
25	BB	995	C	C5-C4-N4	-39.06	3.01	120.20
25	BB	995	C	C4-C5-C6	-27.65	34.44	117.40
25	BB	995	C	N1-C2-N3	-25.87	41.59	119.20

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AP	31	A	C2',C1'
3	A1	13	U	C2',C1'
3	A1	1198	G	C4'
3	A1	1483	A	C2'
14	AN	13	SER	CA

5 of 3370 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	G	Sidechain
1	AA	3	G	Sidechain
1	AA	4	G	Sidechain
1	AA	5	A	Sidechain
1	AA	6	U	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	1600	0	754	13	0
1	AE	1622	0	773	5	0
1	AP	1600	0	756	42	0
2	AM	397	0	202	4	0
3	A1	32828	0	15398	146	0
4	AB	1704	0	1732	8	0
5	AC	876	0	887	5	0
6	AD	954	0	1019	5	0
7	AF	883	0	944	5	0
8	AG	773	0	825	4	0
9	AH	715	0	742	3	0
10	AI	648	0	666	0	0
11	AJ	648	0	691	2	0
12	AK	455	0	478	1	0
13	AL	637	0	665	5	0
14	AN	664	0	714	5	0
15	AO	1624	0	1699	3	0
16	AQ	425	0	449	1	0
17	AR	1642	0	1710	7	0
18	AS	1105	0	1148	5	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	1	0
21	AV	978	0	1034	3	0
22	AW	1021	0	1070	0	0
23	AX	786	0	828	8	0
24	BA	2504	0	1160	13	0
25	BB	62317	0	29301	263	0
26	BC	752	0	780	2	0
27	BD	930	0	1000	1	0
28	BE	1052	0	1129	7	0
29	BF	1073	0	1157	10	0
30	BG	1007	0	1045	6	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	3	0
34	BK	815	0	839	5	0
35	BL	856	0	922	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	5	0
37	BN	2053	0	2122	11	0
38	BO	779	0	834	8	0
39	BP	633	0	656	0	0
40	BQ	508	0	543	5	0
41	BR	448	0	491	0	0
42	BS	548	0	552	0	0
43	BT	443	0	461	1	0
44	BU	440	0	485	1	0
45	BV	376	0	418	5	0
46	BW	503	0	574	4	0
47	BX	301	0	343	0	0
48	BY	1564	0	1616	8	0
49	BZ	1687	0	1814	4	0
50	B1	1551	0	1619	5	0
51	B2	1419	0	1460	6	0
52	B3	1322	0	1374	5	0
53	B4	1110	0	1148	2	0
54	B5	1031	0	1088	2	0
55	B6	1112	0	1147	2	0
All	All	149248	0	97062	558	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 2.

The worst 5 of 558 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)
25:BB:1687:G:C2'	25:BB:1687:G:C3'	1.94	1.42
25:BB:1687:G:C2'	25:BB:1687:G:C1'	1.98	1.40
1:AP:31:A:C2'	3:A1:1340:A:H3'	1.50	1.40
25:BB:1687:G:C3'	25:BB:1687:G:C4'	1.99	1.37
1:AP:31:A:C2'	1:AP:31:A:C1'	2.04	1.35

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	
4	AB	216/241 (90%)	173 (80%)	35 (16%)	8 (4%)	2	20
5	AC	115/129 (89%)	85 (74%)	26 (23%)	4 (4%)	3	20
6	AD	121/124 (98%)	71 (59%)	35 (29%)	15 (12%)	0	4
7	AF	112/118 (95%)	76 (68%)	27 (24%)	9 (8%)	1	9
8	AG	94/101 (93%)	71 (76%)	18 (19%)	5 (5%)	1	15
9	AH	86/89 (97%)	67 (78%)	14 (16%)	5 (6%)	1	14
10	AI	80/82 (98%)	56 (70%)	15 (19%)	9 (11%)	0	5
11	AJ	78/84 (93%)	51 (65%)	22 (28%)	5 (6%)	1	12
12	AK	53/75 (71%)	40 (76%)	9 (17%)	4 (8%)	1	10
13	AL	77/92 (84%)	57 (74%)	13 (17%)	7 (9%)	0	8
14	AN	83/87 (95%)	68 (82%)	12 (14%)	3 (4%)	2	20
15	AO	204/233 (88%)	157 (77%)	33 (16%)	14 (7%)	1	11
16	AQ	49/71 (69%)	38 (78%)	7 (14%)	4 (8%)	0	9
17	AR	203/206 (98%)	165 (81%)	29 (14%)	9 (4%)	2	17
18	AS	148/159 (93%)	111 (75%)	26 (18%)	11 (7%)	1	10
19	AT	98/135 (73%)	76 (78%)	15 (15%)	7 (7%)	1	11
20	AU	148/179 (83%)	118 (80%)	20 (14%)	10 (7%)	1	11
21	AV	127/130 (98%)	102 (80%)	17 (13%)	8 (6%)	1	13
22	AW	125/130 (96%)	96 (77%)	22 (18%)	7 (6%)	1	14
23	AX	96/103 (93%)	73 (76%)	15 (16%)	8 (8%)	0	9
26	BC	92/94 (98%)	70 (76%)	16 (17%)	6 (6%)	1	12
27	BD	119/123 (97%)	84 (71%)	25 (21%)	10 (8%)	0	9
28	BE	142/144 (99%)	90 (63%)	27 (19%)	25 (18%)	0	2
29	BF	134/136 (98%)	74 (55%)	37 (28%)	23 (17%)	0	2
30	BG	125/127 (98%)	82 (66%)	32 (26%)	11 (9%)	0	8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	78 (68%)	27 (24%)	10 (9%)	0	9
32	BI	112/115 (97%)	67 (60%)	32 (29%)	13 (12%)	0	5
33	BJ	115/118 (98%)	84 (73%)	19 (16%)	12 (10%)	0	6
34	BK	101/103 (98%)	57 (56%)	32 (32%)	12 (12%)	0	4
35	BL	108/110 (98%)	71 (66%)	18 (17%)	19 (18%)	0	2
36	BM	97/99 (98%)	70 (72%)	19 (20%)	8 (8%)	0	9
37	BN	265/270 (98%)	167 (63%)	49 (18%)	49 (18%)	0	2
38	BO	100/103 (97%)	51 (51%)	31 (31%)	18 (18%)	0	2
39	BP	82/85 (96%)	42 (51%)	26 (32%)	14 (17%)	0	2
40	BQ	61/63 (97%)	44 (72%)	13 (21%)	4 (7%)	1	12
41	BR	56/59 (95%)	39 (70%)	10 (18%)	7 (12%)	0	4
42	BS	68/70 (97%)	47 (69%)	14 (21%)	7 (10%)	0	6
43	BT	54/57 (95%)	37 (68%)	11 (20%)	6 (11%)	0	5
44	BU	52/54 (96%)	35 (67%)	14 (27%)	3 (6%)	1	14
45	BV	44/46 (96%)	33 (75%)	9 (20%)	2 (4%)	2	17
46	BW	62/64 (97%)	31 (50%)	16 (26%)	15 (24%)	0	1
47	BX	36/38 (95%)	23 (64%)	6 (17%)	7 (19%)	0	2
48	BY	207/209 (99%)	120 (58%)	54 (26%)	33 (16%)	0	2
49	BZ	211/213 (99%)	169 (80%)	33 (16%)	9 (4%)	2	17
50	B1	199/201 (99%)	117 (59%)	53 (27%)	29 (15%)	0	3
51	B2	176/178 (99%)	125 (71%)	35 (20%)	16 (9%)	0	8
52	B3	174/177 (98%)	145 (83%)	19 (11%)	10 (6%)	1	14
53	B4	147/149 (99%)	109 (74%)	31 (21%)	7 (5%)	2	16
54	B5	139/142 (98%)	116 (84%)	17 (12%)	6 (4%)	2	17
55	B6	138/140 (99%)	78 (56%)	40 (29%)	20 (14%)	0	3
All	All	5844/6172 (95%)	4106 (70%)	1175 (20%)	563 (10%)	1	7

5 of 563 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	21	TYR
4	AB	97	GLY
4	AB	169	HIS

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Mol	Chain	Res	Type
5	AC	118	ASN
6	AD	15	VAL

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	
4	AB	180/199 (90%)	169 (94%)	11 (6%)	17	38
5	AC	90/99 (91%)	82 (91%)	8 (9%)	9	28
6	AD	103/104 (99%)	88 (85%)	15 (15%)	3	13
7	AF	92/96 (96%)	83 (90%)	9 (10%)	7	24
8	AG	79/84 (94%)	77 (98%)	2 (2%)	42	63
9	AH	76/77 (99%)	71 (93%)	5 (7%)	15	37
10	AI	65/65 (100%)	59 (91%)	6 (9%)	8	27
11	AJ	74/78 (95%)	67 (90%)	7 (10%)	8	25
12	AK	48/66 (73%)	43 (90%)	5 (10%)	7	22
13	AL	70/79 (89%)	61 (87%)	9 (13%)	4	15
14	AN	65/66 (98%)	58 (89%)	7 (11%)	6	21
15	AO	170/190 (90%)	158 (93%)	12 (7%)	13	35
16	AQ	44/61 (72%)	40 (91%)	4 (9%)	9	27
17	AR	172/173 (99%)	159 (92%)	13 (8%)	12	33
18	AS	113/119 (95%)	96 (85%)	17 (15%)	3	12
19	AT	87/116 (75%)	78 (90%)	9 (10%)	7	23
20	AU	123/147 (84%)	110 (89%)	13 (11%)	6	21
21	AV	104/105 (99%)	97 (93%)	7 (7%)	15	36
22	AW	105/107 (98%)	93 (89%)	12 (11%)	5	18
23	AX	86/90 (96%)	77 (90%)	9 (10%)	6	21
26	BC	78/78 (100%)	77 (99%)	1 (1%)	61	74
27	BD	102/104 (98%)	93 (91%)	9 (9%)	9	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	1	8
29	BF	109/109 (100%)	97 (89%)	12 (11%)	6	20
30	BG	103/103 (100%)	95 (92%)	8 (8%)	11	32
31	BH	87/87 (100%)	82 (94%)	5 (6%)	18	40
32	BI	99/100 (99%)	96 (97%)	3 (3%)	36	57
33	BJ	89/90 (99%)	80 (90%)	9 (10%)	7	23
34	BK	84/84 (100%)	75 (89%)	9 (11%)	6	21
35	BL	93/93 (100%)	81 (87%)	12 (13%)	4	15
36	BM	83/83 (100%)	72 (87%)	11 (13%)	4	14
37	BN	213/215 (99%)	189 (89%)	24 (11%)	5	19
38	BO	83/84 (99%)	75 (90%)	8 (10%)	8	25
39	BP	62/63 (98%)	52 (84%)	10 (16%)	2	11
40	BQ	55/55 (100%)	45 (82%)	10 (18%)	2	9
41	BR	48/49 (98%)	45 (94%)	3 (6%)	16	37
42	BS	62/62 (100%)	57 (92%)	5 (8%)	11	31
43	BT	47/48 (98%)	37 (79%)	10 (21%)	1	6
44	BU	48/48 (100%)	45 (94%)	3 (6%)	16	37
45	BV	38/38 (100%)	34 (90%)	4 (10%)	6	21
46	BW	51/51 (100%)	45 (88%)	6 (12%)	5	18
47	BX	34/34 (100%)	33 (97%)	1 (3%)	37	58
48	BY	164/164 (100%)	151 (92%)	13 (8%)	11	32
49	BZ	187/187 (100%)	171 (91%)	16 (9%)	10	29
50	B1	165/165 (100%)	142 (86%)	23 (14%)	3	14
51	B2	149/149 (100%)	131 (88%)	18 (12%)	5	17
52	B3	137/138 (99%)	125 (91%)	12 (9%)	9	28
53	B4	114/114 (100%)	103 (90%)	11 (10%)	8	25
54	B5	109/110 (99%)	101 (93%)	8 (7%)	13	34
55	B6	114/114 (100%)	101 (89%)	13 (11%)	5	18
All	All	4856/5043 (96%)	4380 (90%)	476 (10%)	10	24

5 of 476 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	BH	54	VAL
52	B3	167	VAL
37	BN	82	TYR
52	B3	88	LEU
55	B6	102	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
40	BQ	41	HIS
50	B1	29	HIS
43	BT	3	GLN
48	BY	148	GLN
52	B3	63	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	23 (30%)	10 (13%)
1	AE	75/76 (98%)	13 (17%)	5 (6%)
1	AP	74/76 (97%)	14 (18%)	9 (12%)
2	AM	20/20 (100%)	10 (50%)	8 (40%)
24	BA	116/117 (99%)	39 (33%)	18 (15%)
25	BB	2902/2903 (99%)	1547 (53%)	494 (17%)
3	A1	1529/1530 (99%)	756 (49%)	270 (17%)
All	All	4791/4798 (99%)	2402 (50%)	814 (16%)

5 of 2402 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	16	U
1	AA	17	U

5 of 814 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BB	814	C
25	BB	1497	U

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Mol	Chain	Res	Type
25	BB	2799	A
25	BB	958	U
25	BB	811	U

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

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

5.5 Carbohydrates [i](#)

There are no 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
25	BB	1
1	AP	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1959:G	O3'	1960:A	P	3.49
1	AP	74:C	O3'	75:C	P	1.29

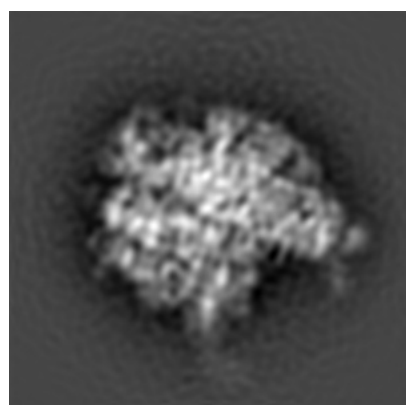
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1056. These allow visual inspection of the internal detail of the map and identification of artifacts.

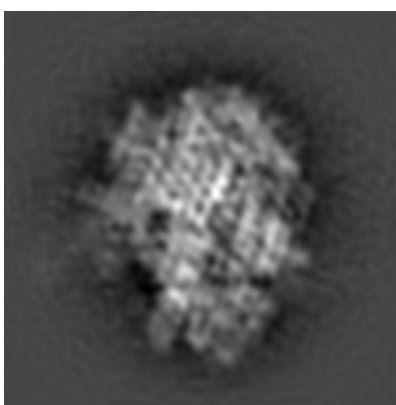
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

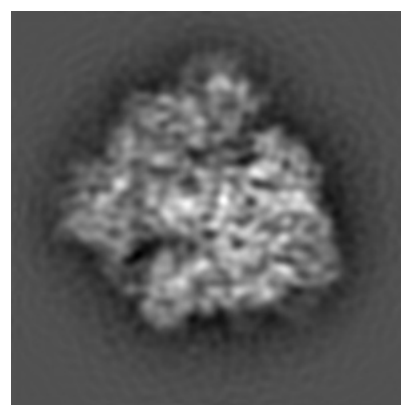
6.1.1 Primary map



X



Y

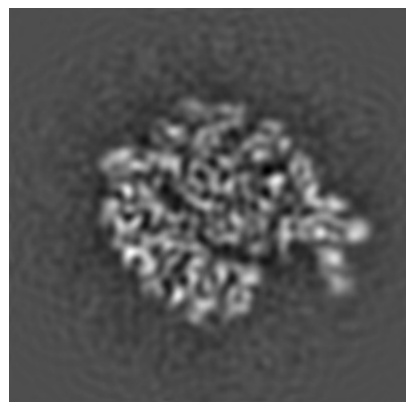


Z

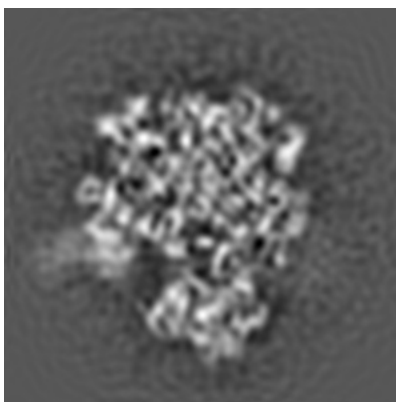
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

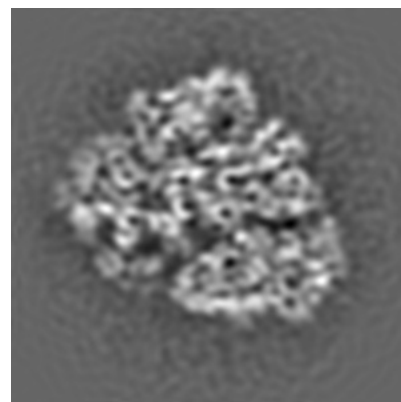
6.2.1 Primary map



X Index: 65



Y Index: 65

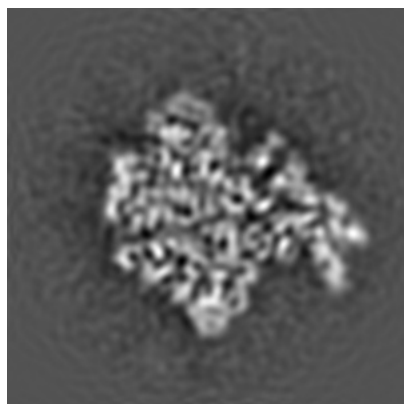


Z Index: 65

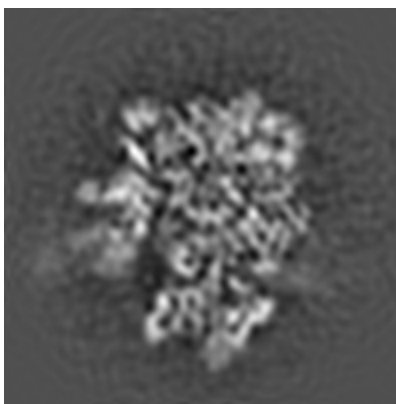
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

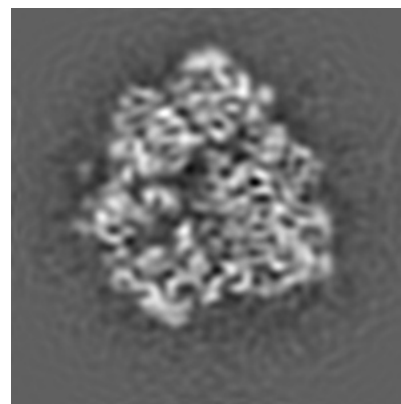
6.3.1 Primary map



X Index: 68



Y Index: 68

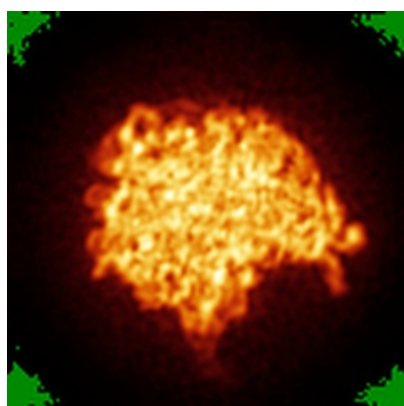


Z Index: 58

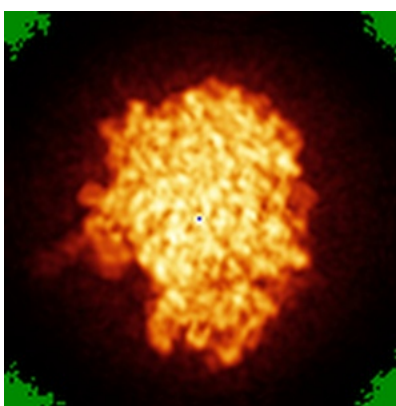
The images above show the largest variance slices of the map in three orthogonal directions.

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

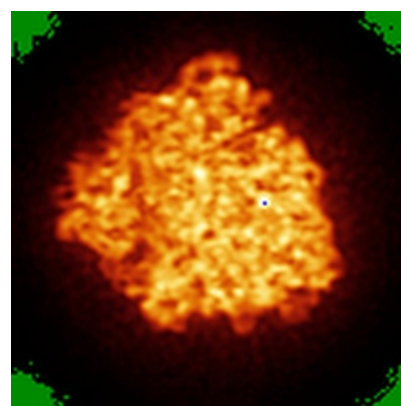
6.4.1 Primary map



X



Y

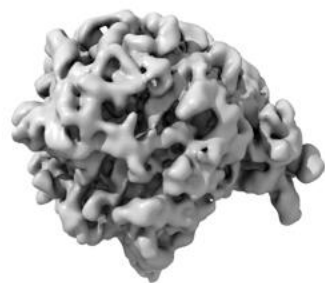


Z

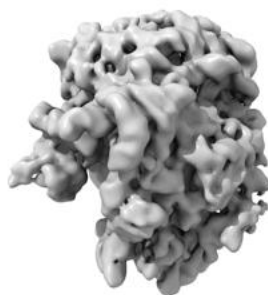
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

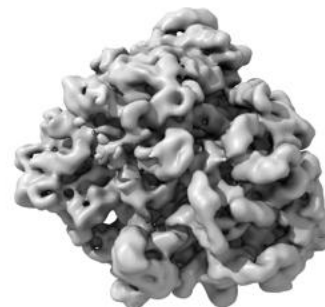
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 43.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

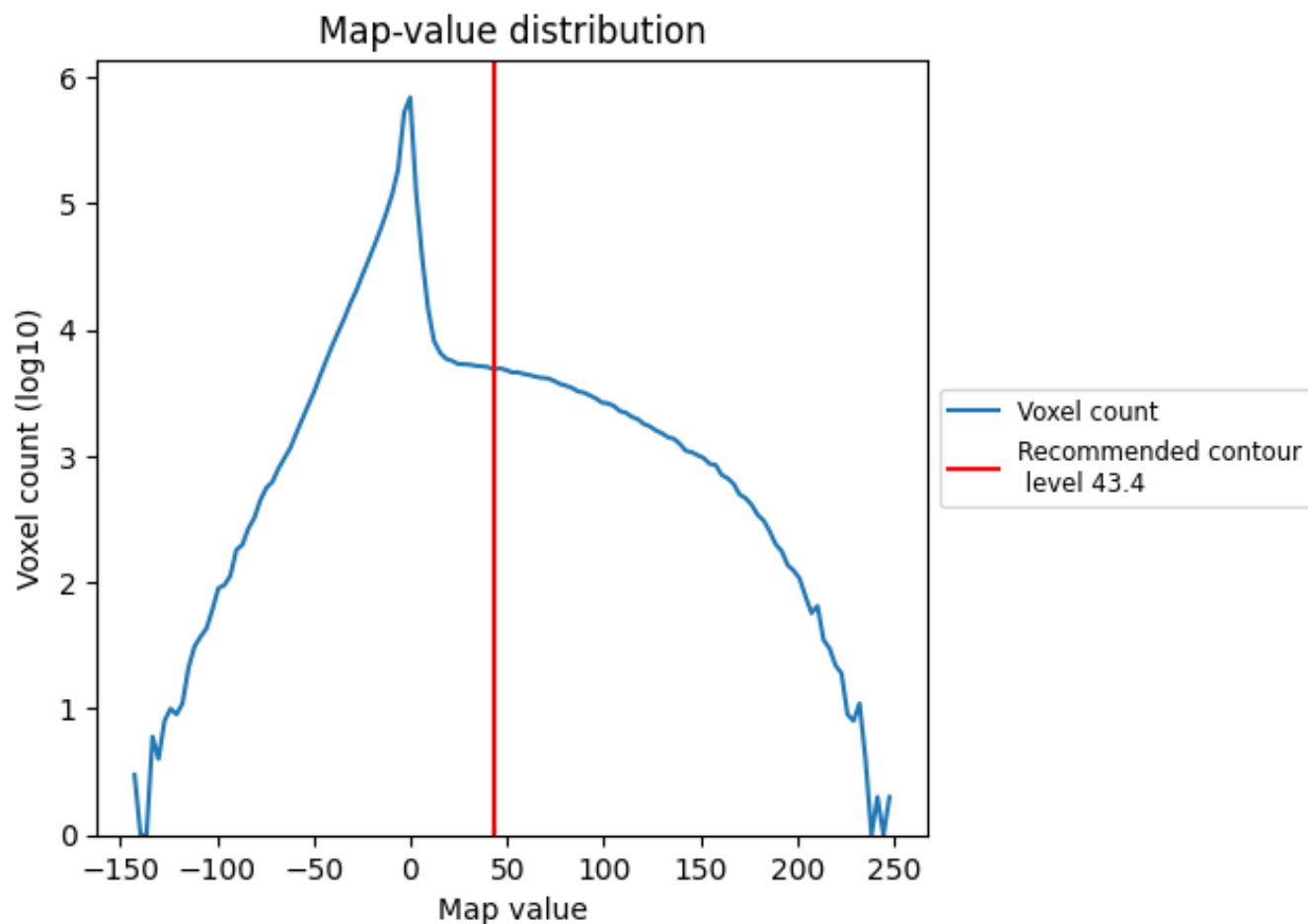
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

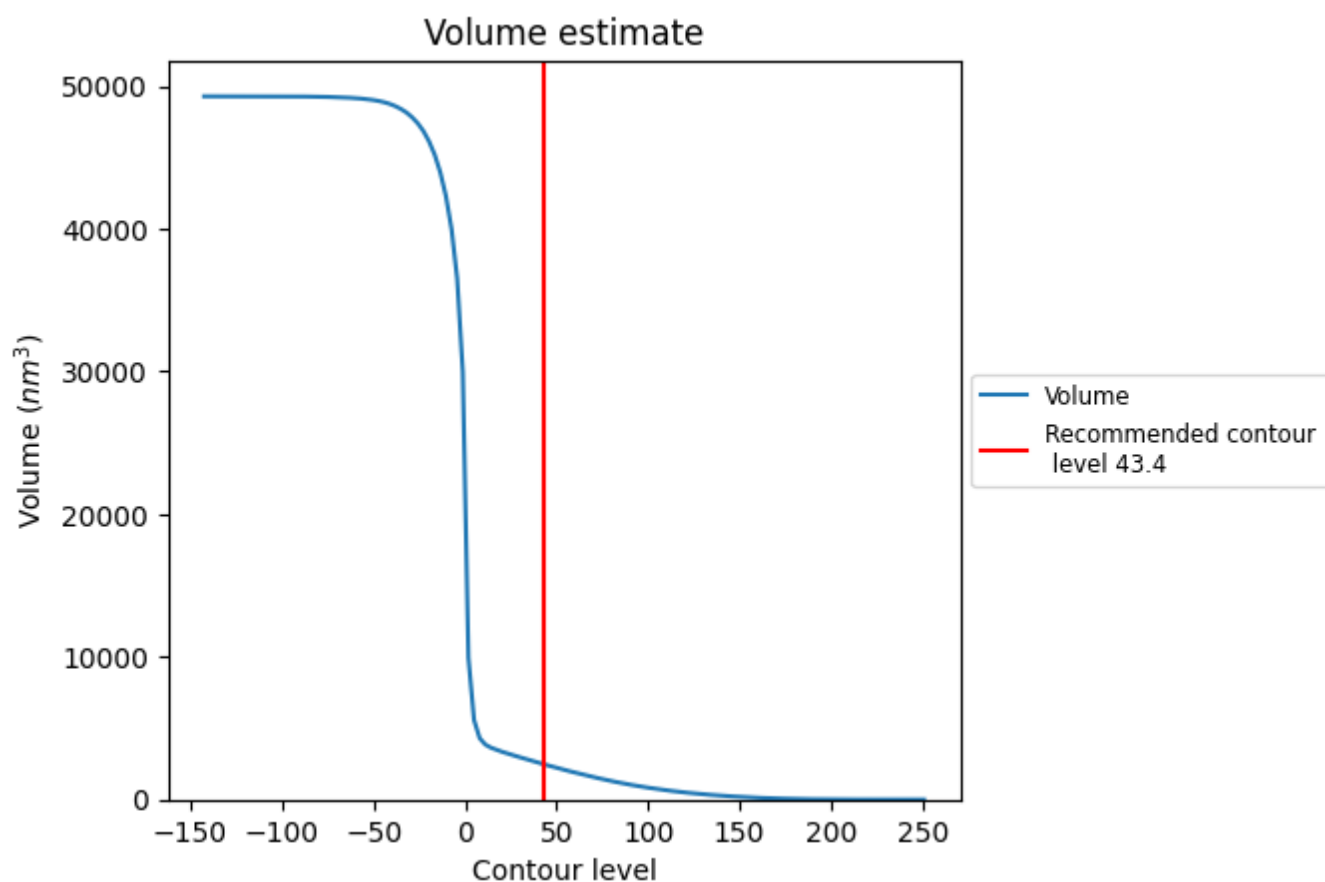
This section contains the results of statistical analysis of the map.

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.

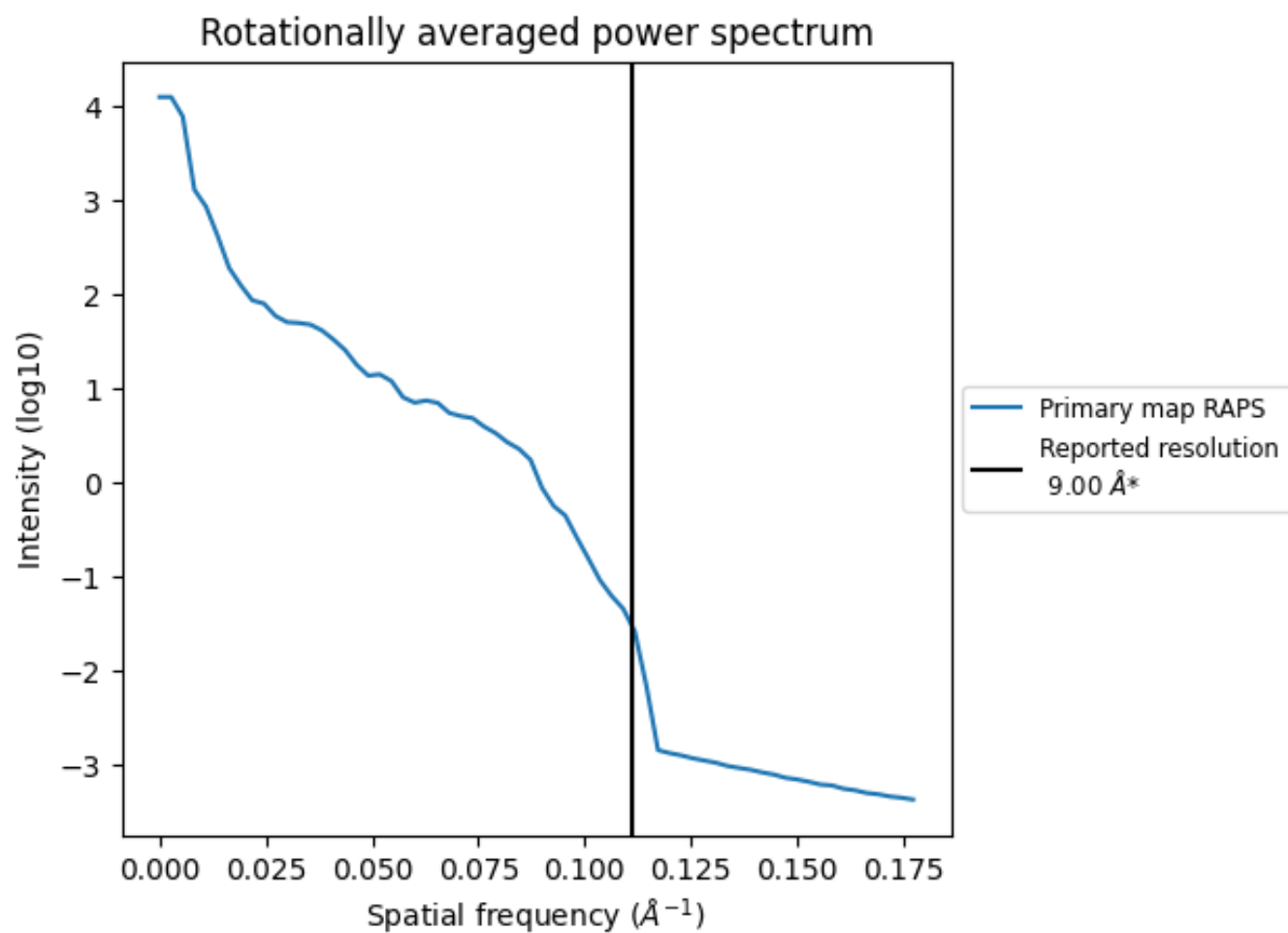
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2462 nm³; this corresponds to an approximate mass of 2224 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 0.111 Å⁻¹

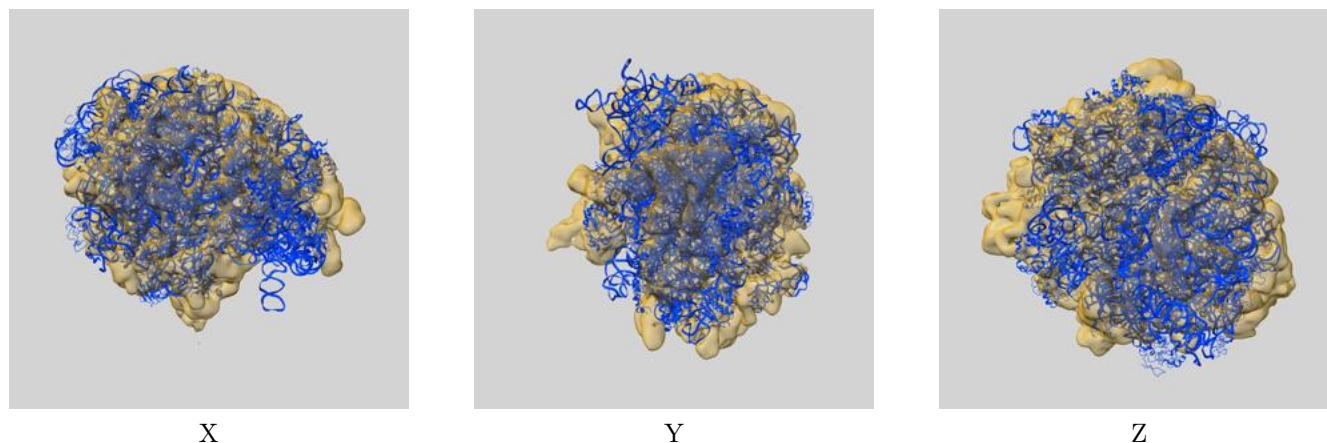
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

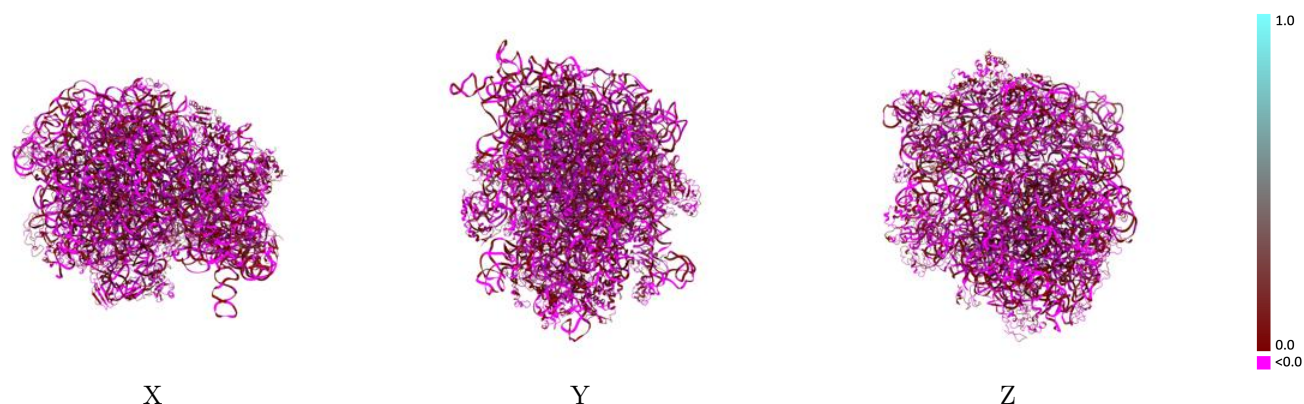
This section contains information regarding the fit between EMDB map EMD-1056 and PDB model 4V66. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



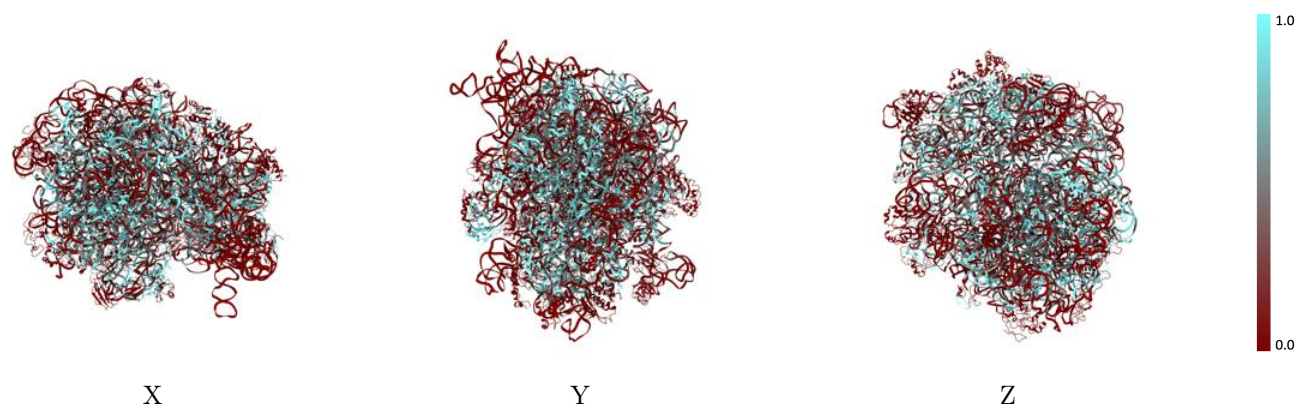
The images above show the 3D surface view of the map at the recommended contour level 43.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



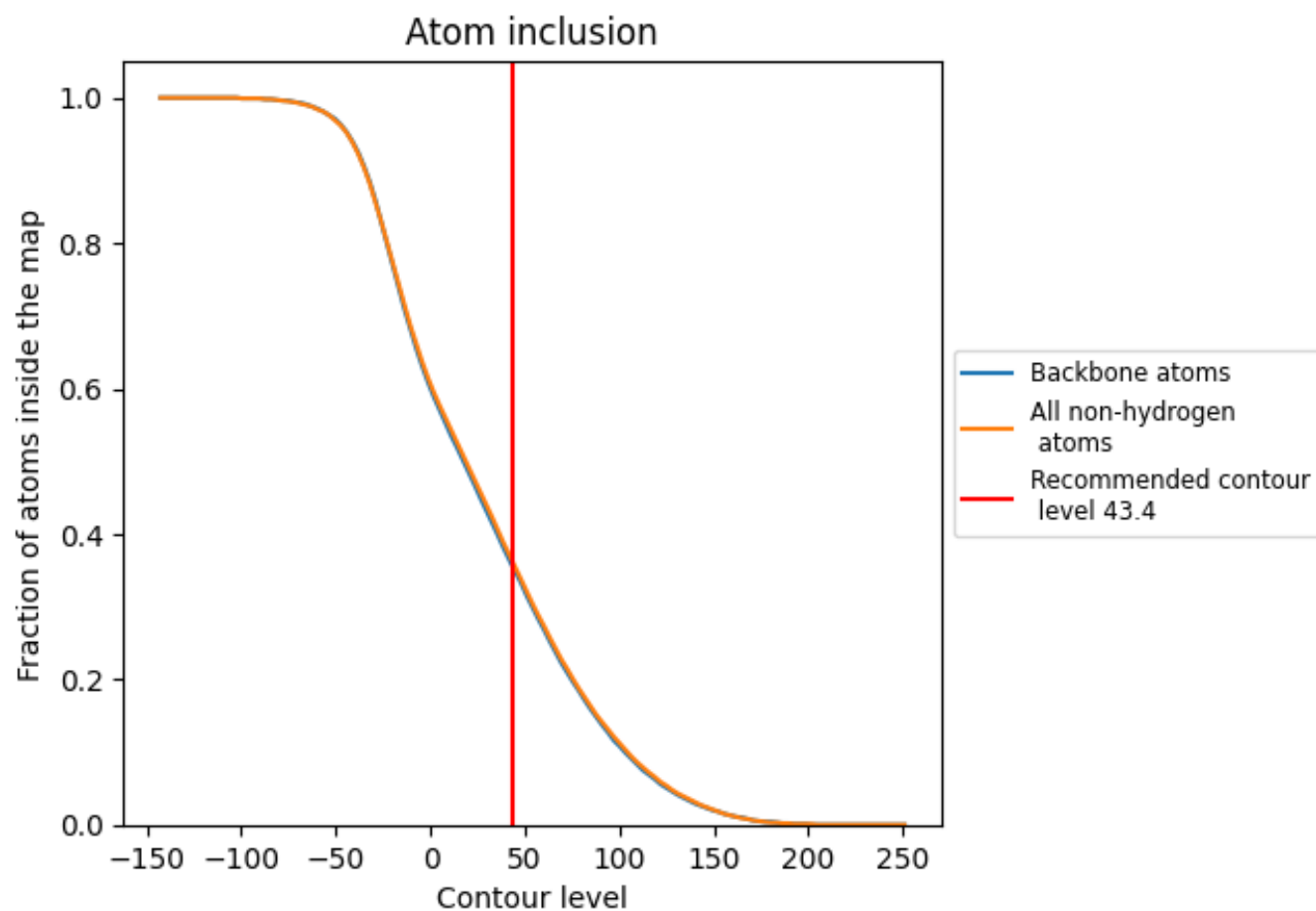
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (43.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 36% of all backbone atoms, 36% 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 (43.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3630	-0.0040
A1	0.3040	-0.0060
AA	0.3110	0.0030
AB	0.2260	-0.0120
AC	0.4430	0.0120
AD	0.2320	-0.0130
AE	0.4020	-0.0090
AF	0.4050	-0.0120
AG	0.1040	-0.0300
AH	0.1730	0.0060
AI	0.0000	-0.0250
AJ	0.2610	-0.0340
AK	0.6440	0.0240
AL	0.0370	-0.0070
AM	0.7100	0.0400
AN	0.4180	0.0020
AO	0.6430	0.0220
AP	0.3780	-0.0140
AQ	0.3890	-0.0540
AR	0.4320	-0.0070
AS	0.5970	-0.0040
AT	0.2310	0.0030
AU	0.5160	-0.0040
AV	0.4660	0.0180
AW	0.1320	0.0180
AX	0.2560	-0.0200
B1	0.2470	-0.0070
B2	0.6610	0.0260
B3	0.1920	-0.0360
B4	0.0750	-0.0060
B5	0.5770	-0.0120
B6	0.5010	0.0050
BA	0.3050	-0.0250
BB	0.4050	-0.0030
BC	0.2330	-0.0090



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Chain	Atom inclusion	Q-score
BD	 0.3820	 -0.0020
BE	 0.3730	 -0.0020
BF	 0.3480	 -0.0040
BG	 0.5840	 -0.0030
BH	 0.4220	 0.0030
BI	 0.4100	 -0.0180
BJ	 0.1770	 -0.0330
BK	 0.0770	 0.0020
BL	 0.4600	 0.0040
BM	 0.2620	 -0.0100
BN	 0.3830	 0.0020
BO	 0.0010	 -0.0340
BP	 0.5960	 0.0340
BQ	 0.4780	 0.0290
BR	 0.4430	 -0.0030
BS	 0.2920	 0.0010
BT	 0.4890	 -0.0090
BU	 0.1710	 -0.0080
BV	 0.4440	 0.0120
BW	 0.2550	 -0.0220
BX	 0.2890	 -0.0030
BY	 0.5370	 0.0070
BZ	 0.0450	 -0.0170