wwPDB EM Validation Summary Report

Nov 19, 2022 – 09:35 pm GMT

PDB ID	:	5JTE
EMDB ID	:	EMD-8175
Title	:	Cryo-EM structure of an ErmBL-stalled ribosome in complex with A-, P-, and E-tRNA
Authors	:	Arenz, S.; Bock, L.V.; Graf, M.; Innis, C.A.; Beckmann, R.; Grubmueller, H.; Vaiana, A.C.; Wilson, D.N.
Deposited on	:	2016-05-09
Resolution	:	3.60 Å(reported)
Based on initial model	:	5AFI

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

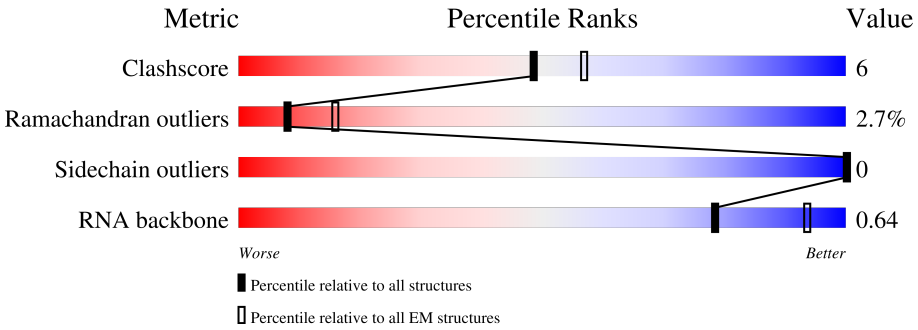
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	AA	1539	67% 53% 35% 11% ·
2	AB	240	91% 65% 25% · 9%
3	AC	233	88% 64% 24% 12%
4	AD	206	100% 55% 43% ·
5	AE	167	87% 66% 22% · 10%
6	AF	135	73% 56% 18% · 26%
7	AG	179	84% 66% 18% 16%

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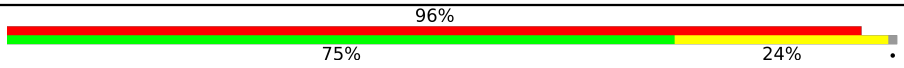
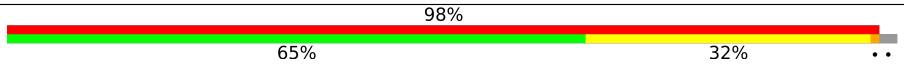
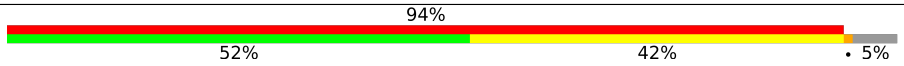
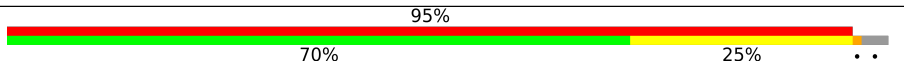
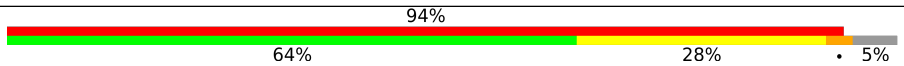
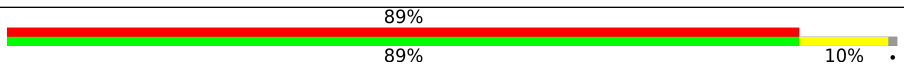
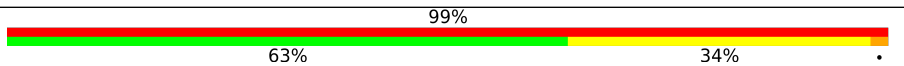
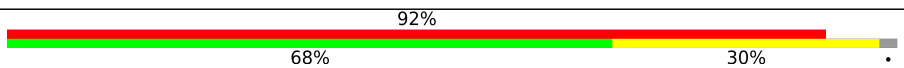
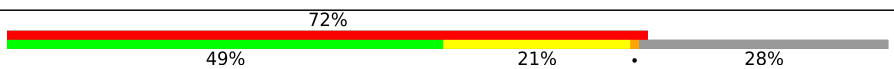
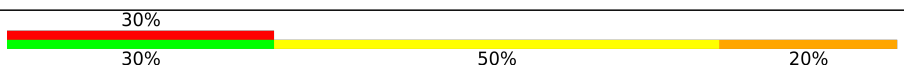
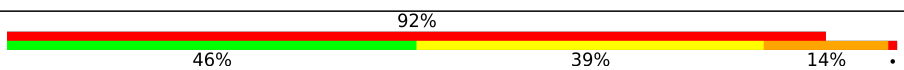
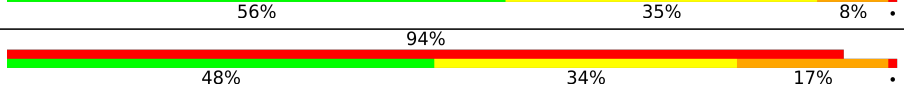
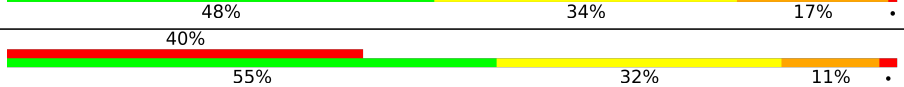
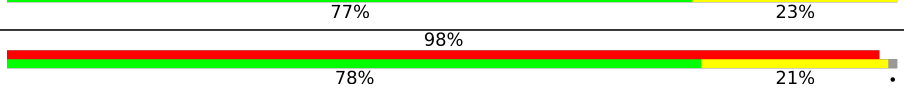
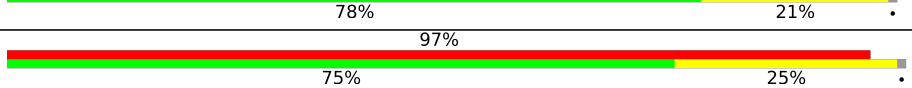
Mol	Chain	Length	Quality of chain
8	AH	130	
9	AI	130	
10	AJ	103	
11	AK	129	
12	AL	124	
13	AM	118	
14	AN	101	
15	AO	89	
16	AP	82	
17	AQ	84	
18	AR	75	
19	AS	92	
20	AT	87	
21	AU	71	
22	AV	10	
23	AW	74	
24	AX	77	
25	AY	71	
26	BA	2897	
27	BB	120	
28	BC	273	
29	BD	209	
30	BE	201	
31	BF	179	
32	BG	177	

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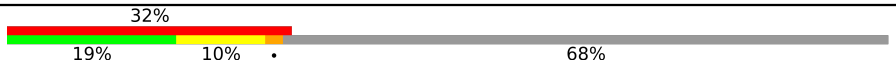
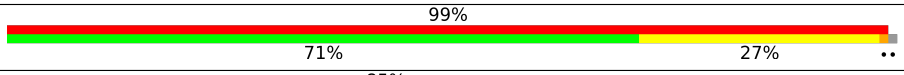
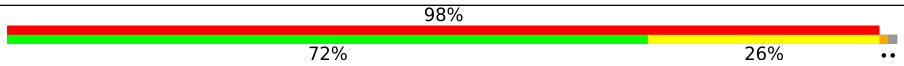
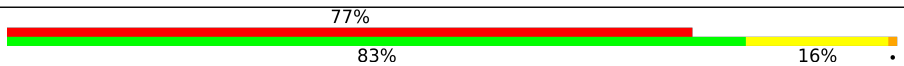
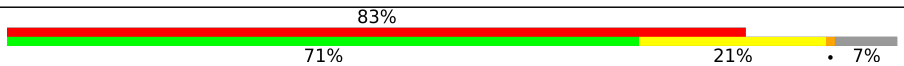
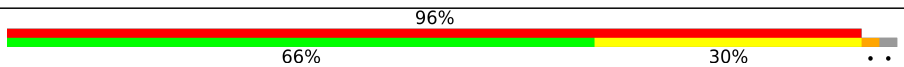
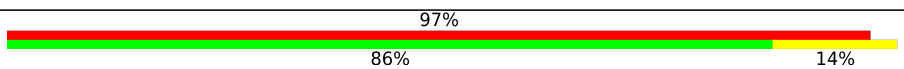
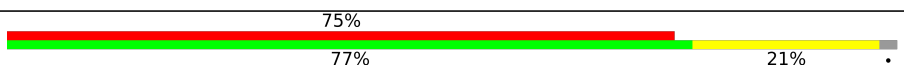
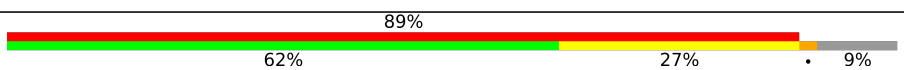
Mol	Chain	Length	Quality of chain
33	BH	149	
34	BI	142	
35	BJ	142	
36	BK	123	
37	BL	144	
38	BM	136	
39	BN	127	
40	BO	117	
41	BP	115	
42	BQ	118	
43	BR	103	
44	BS	110	
45	BT	100	
46	BU	104	
47	BV	94	
48	BW	85	
49	BX	78	
50	BY	63	
51	BZ	59	
52	B0	57	
53	B1	55	
54	B2	46	
55	B3	65	
56	B4	38	
57	B5	9	

2 Entry composition (i)

There are 59 unique types of molecules in this entry. The entry contains 146760 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1539	33015	14725	6052	10699	1539	0	0

- Molecule 2 is a protein called 30S ribosomal protein S2.

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

- Molecule 3 is a protein called 30S ribosomal protein S3.

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

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AD	205	1643	1026	315	298	4	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

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

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 10 is a protein called 30S ribosomal protein S10.

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

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	88	Total	C	N	O	S	0	0
			710	437	143	129	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

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

- Molecule 19 is a protein called 30S ribosomal protein S19.

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

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 21 is a protein called 30S ribosomal protein S21.

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

- Molecule 22 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	10	Total	C	N	O	P	0	0
			218	98	44	66	10		

- Molecule 23 is a RNA chain called A-site Lysine tRNA Lysine.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AW	74	Total	C	N	O	P	S	0	0
			1593	716	280	522	73	2		

- Molecule 24 is a RNA chain called P-site tRNA Aspartate.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AX	77	Total	C	N	O	P	S	0	0
			1656	741	290	547	77	1		

- Molecule 25 is a RNA chain called E-site tRNA Valine.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	AY	71	Total	C	N	O	P	S	0	0
			1525	682	276	496	70	1		

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BA	2897	Total	C	N	O	P	0	0
			62195	27745	11446	20107	2897		

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BB	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 28 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BC	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 29 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BD	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 30 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BE	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 31 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BF	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 32 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BG	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 33 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BH	47	Total	C	N	O	S	0	0
			359	233	62	63	1		

- Molecule 34 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BI	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 35 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BJ	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 36 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BK	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 37 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 38 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BM	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 39 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BN	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 40 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BO	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 41 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 42 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	BQ	117	Total 947	C 604	N 192	O 151	0	0

- Molecule 43 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	103	Total 816	C 516	N 153	O 145	S 2	0	0

- Molecule 44 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	110	Total 857	C 532	N 166	O 156	S 3	0	0

- Molecule 45 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	93	Total 738	C 466	N 139	O 131	S 2	0	0

- Molecule 46 is a protein called 50S ribosomal protein L24.

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

- Molecule 47 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BV	94	Total 753	C 479	N 137	O 134	S 3	0	0

- Molecule 48 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BW	75	Total 569	C 353	N 113	O 102	S 1	0	0

- Molecule 49 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BX	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BY	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 51 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BZ	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 52 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 53 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	B1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 54 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 55 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

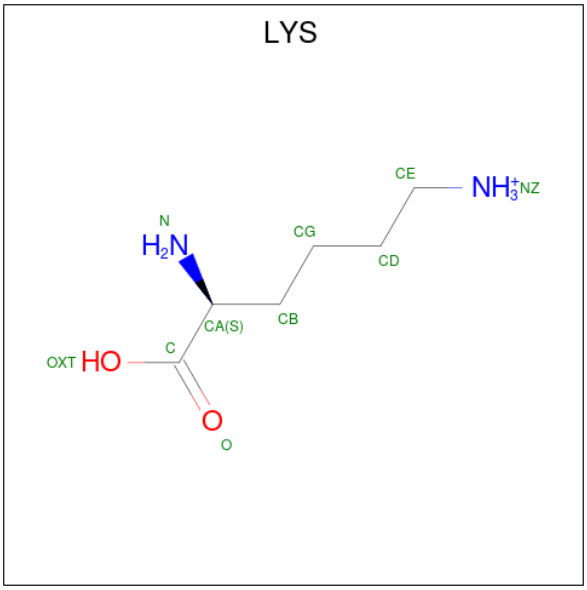
- Molecule 56 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 57 is a protein called ErmBL.

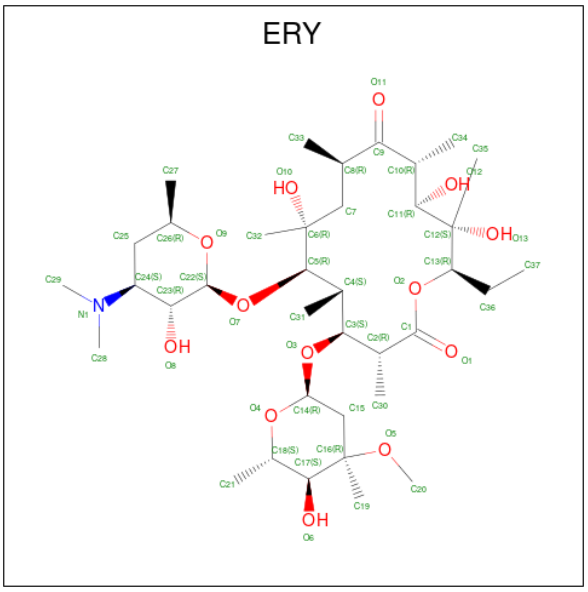
Mol	Chain	Residues	Atoms					AltConf	Trace
57	B5	9	Total	C	N	O	S	0	0
			74	46	14	13	1		

- Molecule 58 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
58	AW	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 59 is ERYTHROMYCIN A (three-letter code: ERY) (formula: $C_{37}H_{67}NO_{13}$).



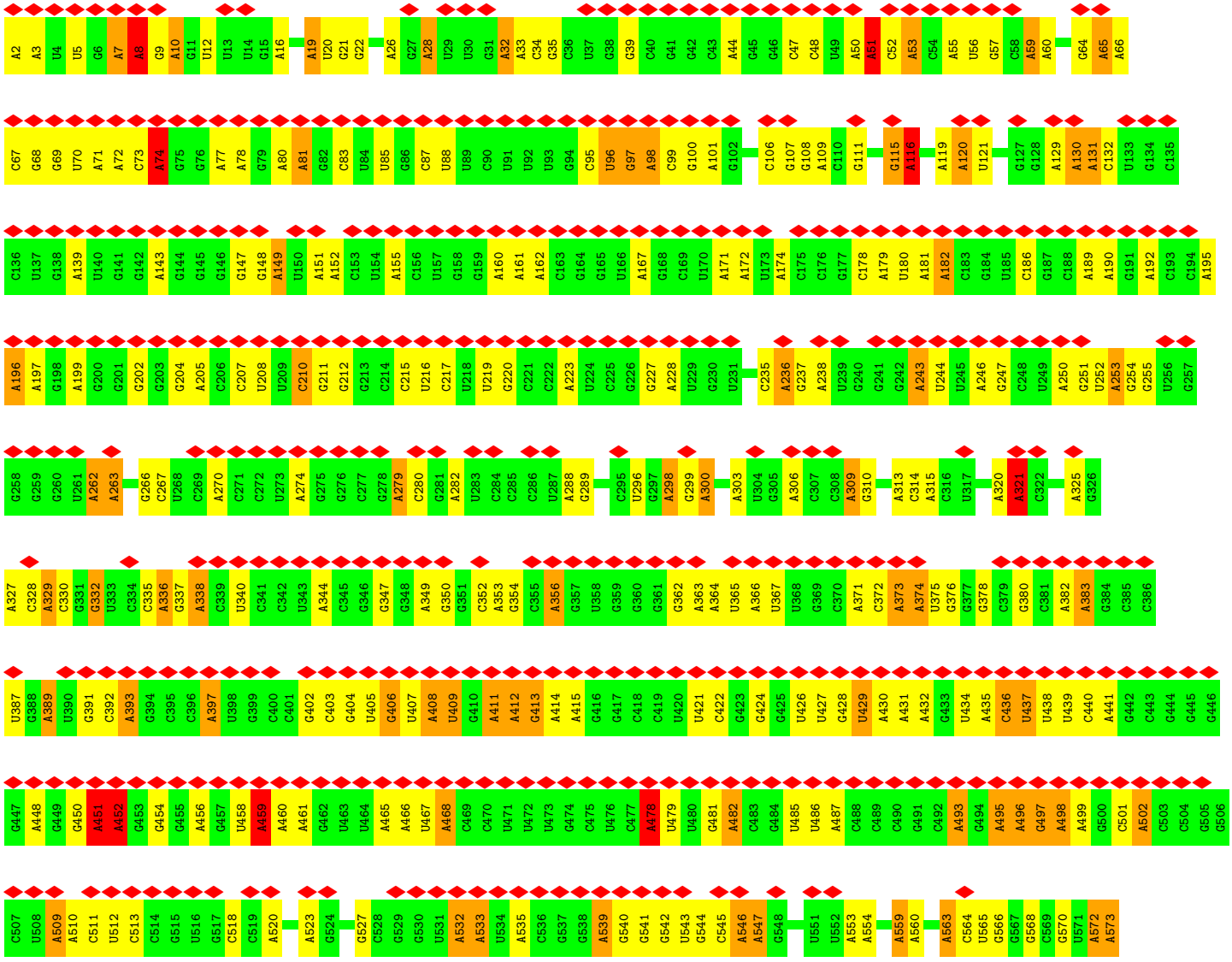
Mol	Chain	Residues	Atoms				AltConf
59	BA	1	Total	C	N	O	0
			51	37	1	13	

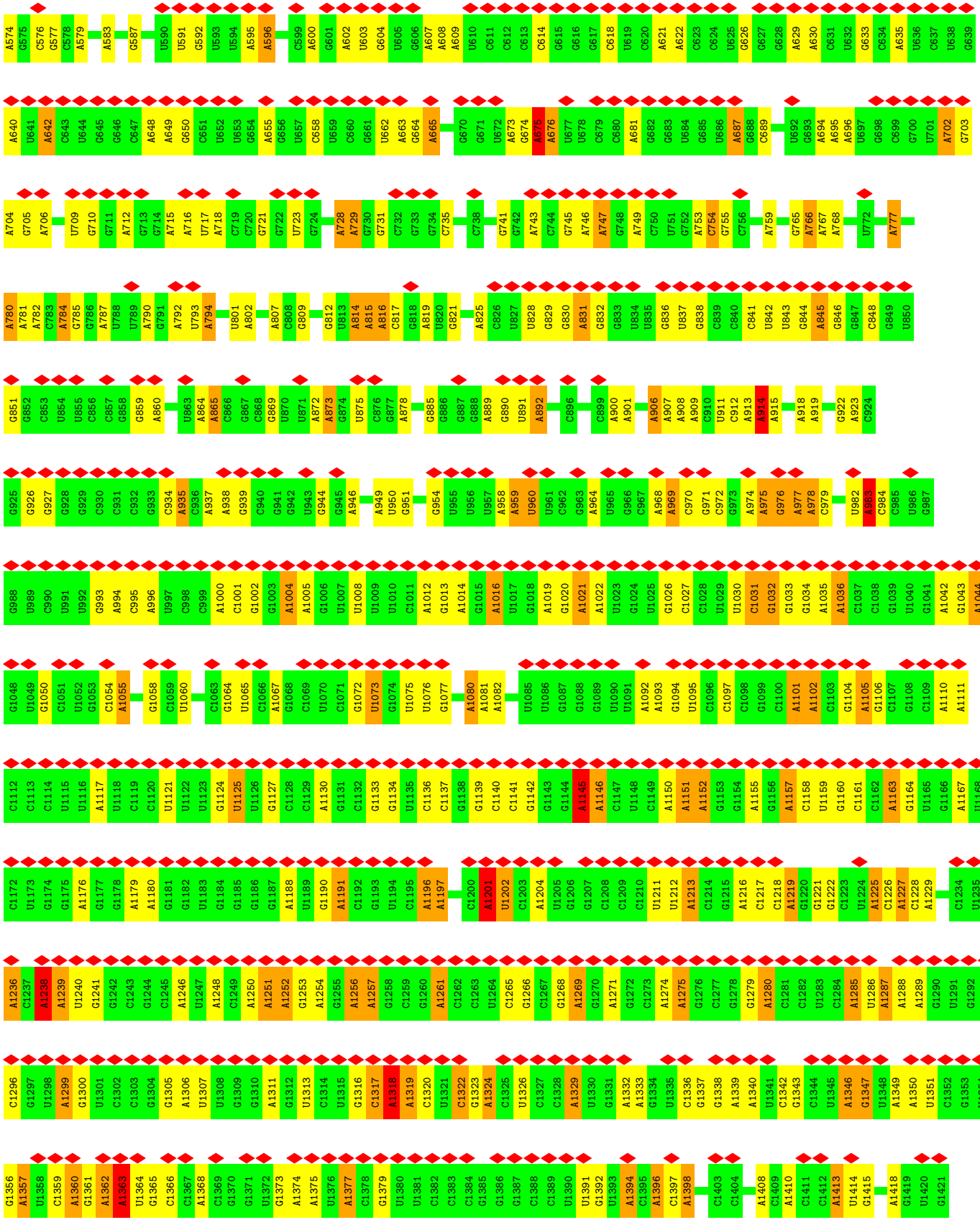
3 Residue-property plots (i)

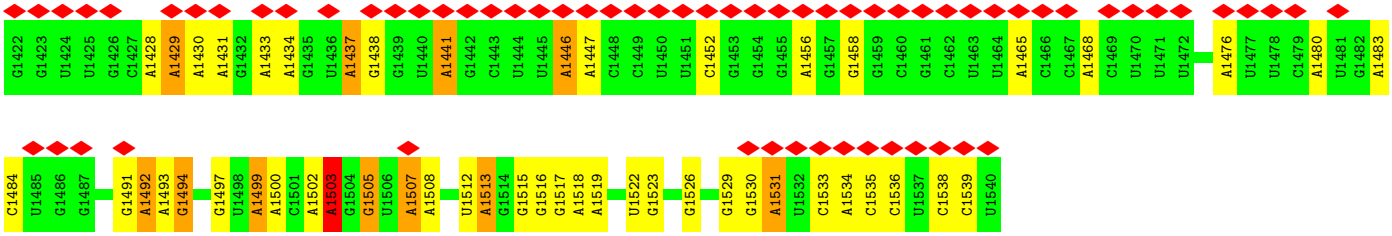
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 16S ribosomal RNA

Chain AA:

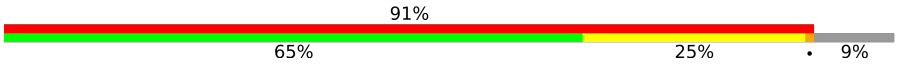


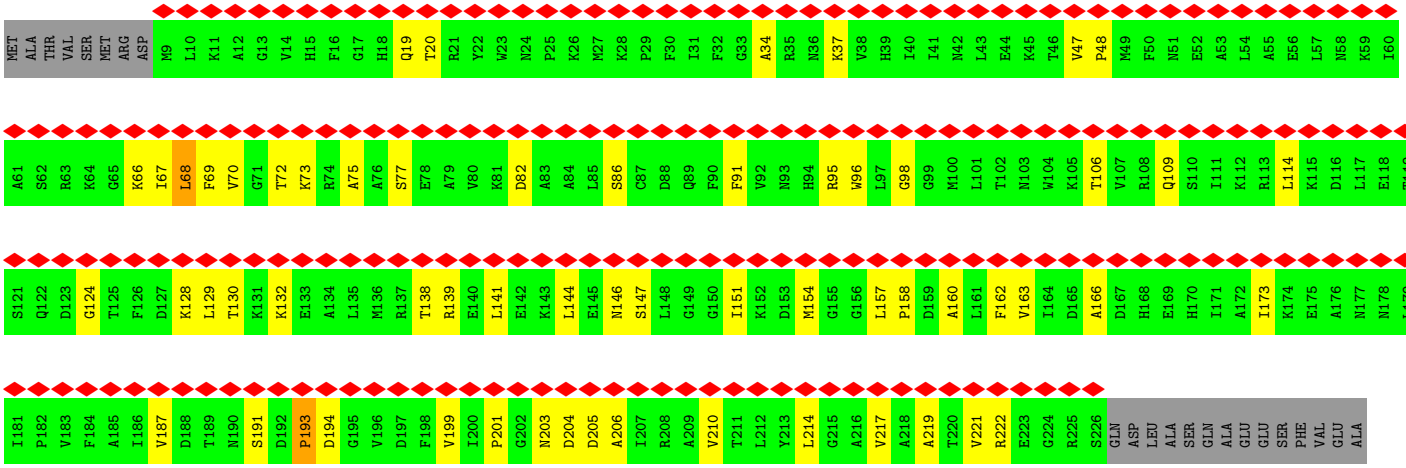

A574 G575 C576 G577 C578 A579 A583 G587 U590 U591 G592 U593 U594 A595 A596 C599 A600 G601 A602 U603 G604 U605 G606 A607 A608 A609 U610 C611 C612 C613 C614 G615 G616 G617 C618 U619 C620 A621 A622 C623 C624 U625 G626 G627 G628 A629 A630 C631 U632 G633 C634 A635 U636 C637 U638 G639
A640 U641 A642 C643 U644 G645 G646 C647 A648 A649 G650 C651 U652 U653 G654 A655 G656 U657 C658 U659 C660 G661 U662 A663 G664 A665 G670 G671 U672 A673 G674 A675 A676 U677 U678 C679 C680 A681 G682 G683 U684 G685 U686 A687 G688 C689 U692 G693 A694 A695 A696 U697 G698 C699 G700 U701 A702 G703
A704 G705 A706 U709 G710 G711 A712 G713 G714 A715 A716 U717 A718 C719 G720 G721 G722 U723 G724 A728 A729 G730 G731 C732 G733 G734 C735 C738 G741 G742 A743 C744 G745 A746 A747 G748 A749 C750 U751 G752 A753 C754 G755 C756 A759 G765 A766 A767 A768 U772 A777
A780 A781 A782 C783 A784 G785 G786 A787 U788 U789 A790 G791 A792 U793 A794 U801 A802 A807 C808 G809 G812 U813 A814 A815 A816 C817 G818 A819 U820 G821 A825 C826 U827 U828 G829 G830 A831 G832 G833 U834 U835 G836 U837 G838 C839 C840 C841 U842 U843 G844 A845 G846 G847 C848 G849 U850
G851 G852 C853 U854 U855 C856 C857 C858 G859 A860 U863 A864 A865 C866 G867 C868 G869 U870 U871 A872 A873 G874 U875 C876 G877 A878 G885 G886 G887 G888 A889 G890 U891 A892 C896 C899 A900 A901 A906 A907 A908 A909 C910 U911 C912 A913 A914 A915 A918 A919 G922 A923 C924
G925 G926 G927 G928 G929 C930 C931 C932 G933 C934 A935 C936 A937 A938 G939 C940 G941 G942 U943 G944 G945 A946 A949 U950 G951 G954 U955 U956 U957 A958 A959 U960 U961 C962 G963 A964 U965 G966 C967 A968 A969 C970 G971 C972 G973 A974 A975 G976 A977 A978 C979 U982 A983 C984 C985 U986 G987
G988 U989 C990 U991 U992 G993 A994 C995 A996 U997 C998 C999 A1000 C1001 G1002 G1003 A1004 A1005 G1006 U1007 U1008 U1009 U1010 C1011 A1012 G1013 A1014 G1015 A1016 U1017 G1018 A1019 G1020 A1021 A1022 U1023 G1024 U1025 G1026 C1027 C1028 U1029 U1030 C1031 G1032 G1033 G1034 A1035 A1036 C1037 C1038 G1039 U1040 G1041 A1042 G1043 A1044 C1045 A1046 G1047
G1048 U1049 G1050 C1051 U1052 G1053 C1054 A1055 G1058 C1059 U1060 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 G1074 U1075 U1076 G1077 A1080 A1081 A1082 U1085 U1086 G1087 G1088 G1089 U1090 U1091 A1092 A1093 G1094 U1095 C1096 C1097 C1098 G1099 C1100 A1101 A1102 C1103 G1104 A1105 G1106 C1107 G1108 C1109 A1110 A1111
C1112 C1113 C1114 U1115 U1116 A1117 U1118 C1119 C1120 U1121 U1122 U1123 G1124 U1125 U1126 G1127 C1128 C1129 A1130 G1131 C1132 G1133 G1134 U1135 C1136 C1137 G1138 G1139 C1140 C1141 G1142 G1143 G1144 A1145 A1146 C1147 U1148 C1149 A1150 A1151 A1152 G1153 G1154 A1155 G1156 A1157 C1158 U1159 G1160 C1161 C1162 A1163 G1164 U1165 G1166 A1167 U1168 A1169 A1170 A1171
C1172 U1173 G1174 U1175 A1176 G1177 C1178 A1179 A1180 G1181 C1182 U1183 G1184 C1185 G1186 G1187 A1188 U1189 G1190 A1191 C1192 G1193 U1194 C1195 A1196 A1197 C1200 A1201 A1202 C1203 A1204 U1205 G1206 C1207 C1208 C1209 C1210 U1211 U1212 A1213 C1214 G1215 A1216 C1217 C1218 A1219 G1220 G1221 G1222 C1223 U1224 A1225 C1226 A1227 C1228 A1229 C1234 U1235
A1236 C1237 A1238 A1239 U1240 G1241 G1242 C1243 G1244 C1245 A1246 U1247 A1248 C1249 A1250 A1251 A1252 G1253 A1254 G1255 A1256 A1257 G1258 C1259 G1260 A1261 C1262 C1263 U1264 C1265 G1266 C1267 G1268 A1269 G1270 A1271 G1272 C1273 A1274 A1275 G1276 C1277 G1278 C1279 A1280 C1281 C1282 U1283 C1284 A1285 U1286 A1287 A1288 A1289 G1290 U1291 C1292 C1293 G1294 U1295
C1296 G1297 U1298 A1299 G1300 U1301 C1302 C1303 G1304 G1305 A1306 U1307 U1308 G1309 G1310 A1311 G1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 U1321 C1322 G1323 A1324 C1325 U1326 C1327 C1328 A1329 U1330 G1331 A1332 A1333 G1334 U1335 C1336 G1337 G1338 A1339 A1340 U1341 C1342 G1343 C1344 U1345 A1346 G1347 U1348 A1349 A1350 U1351 C1352 G1353 U1354 G1355
G1356 A1357 U1358 C1359 A1360 G1361 A1362 A1363 U1364 G1365 C1366 C1367 A1368 C1369 G1370 G1371 U1372 G1373 A1374 A1375 U1376 A1377 C1378 G1379 U1380 U1381 C1382 C1383 C1384 G1385 G1386 G1387 C1388 C1389 U1390 U1391 G1392 U1393 A1394 C1395 A1396 C1397 A1398 C1403 C1404 A1408 C1409 A1410 C1411 C1412 A1413 U1414 G1415 A1418 G1419 U1420 G1421



• Molecule 2: 30S ribosomal protein S2

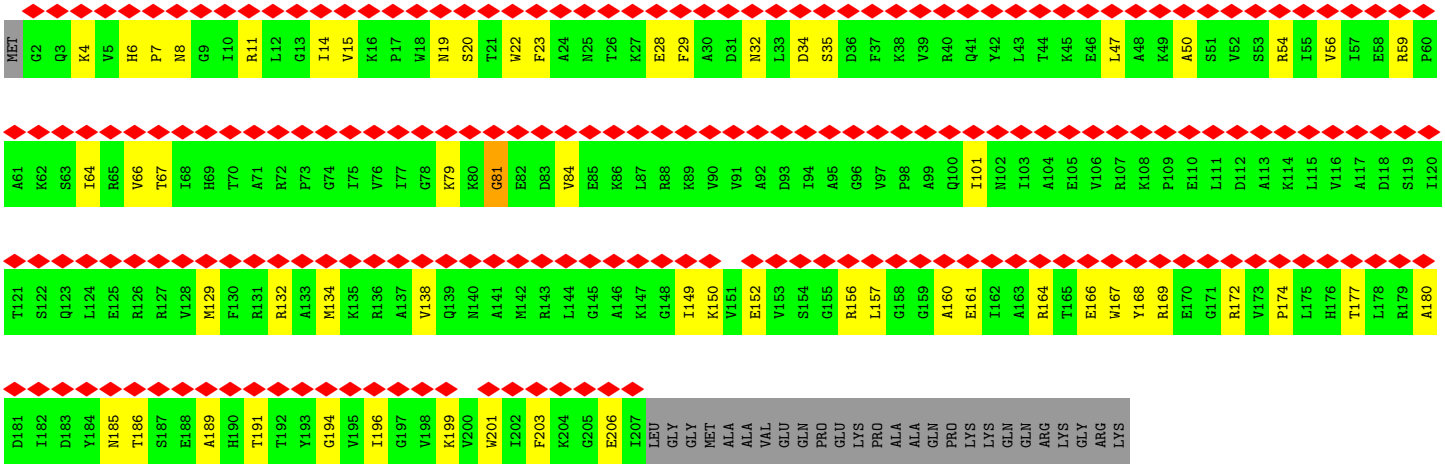
Chain AB:





• Molecule 3: 30S ribosomal protein S3

Chain AC:

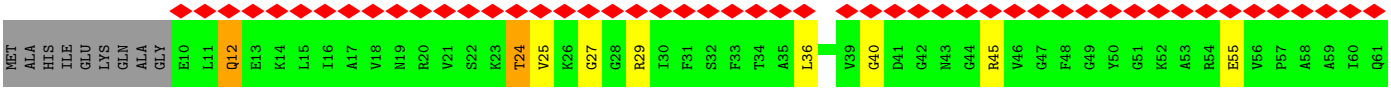


• Molecule 4: 30S ribosomal protein S4

Chain AD:

• Molecule 5: 30S ribosomal protein S5

Chain AE:

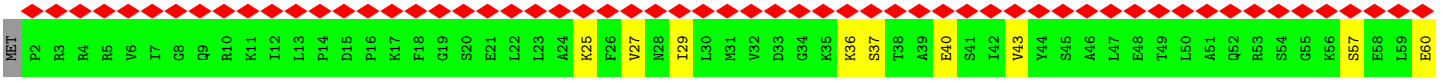


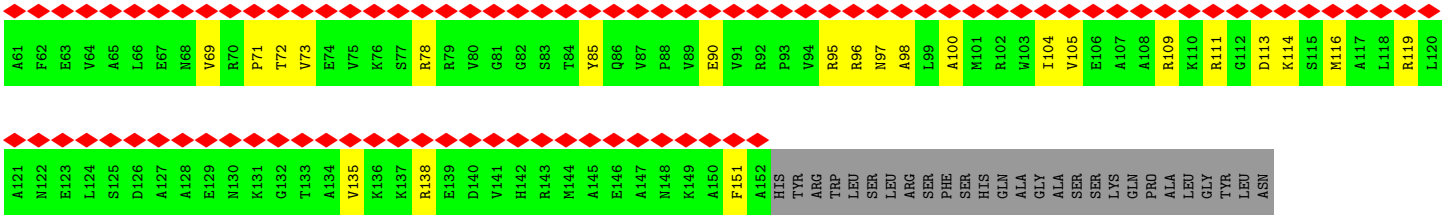
• Molecule 6: 30S ribosomal protein S6

Chain AF:

• Molecule 7: 30S ribosomal protein S7

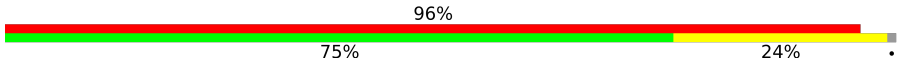
Chain AG:

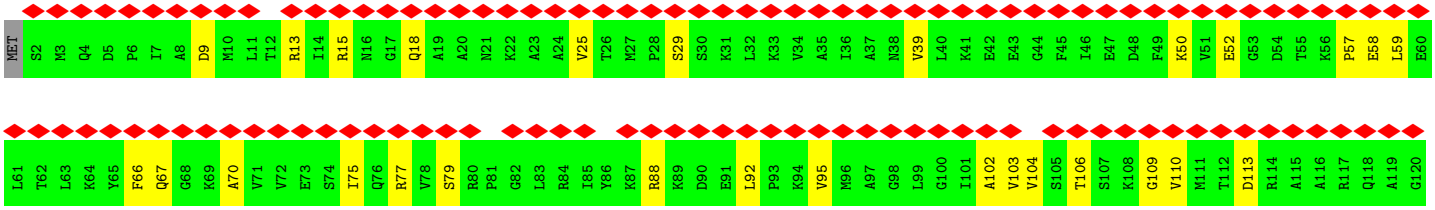




• Molecule 8: 30S ribosomal protein S8

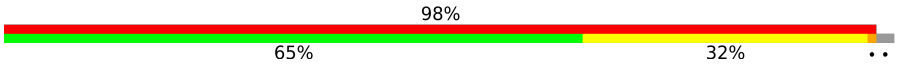
Chain AH:

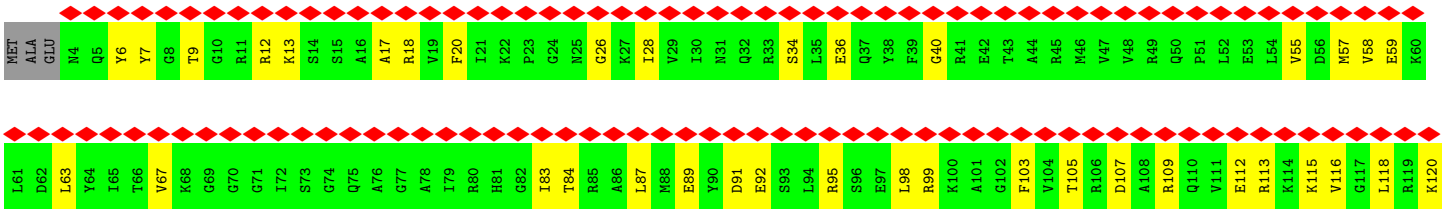




• Molecule 9: 30S ribosomal protein S9

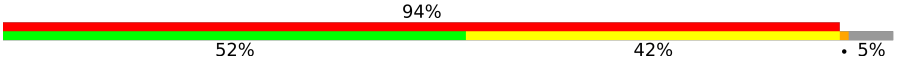
Chain AI:

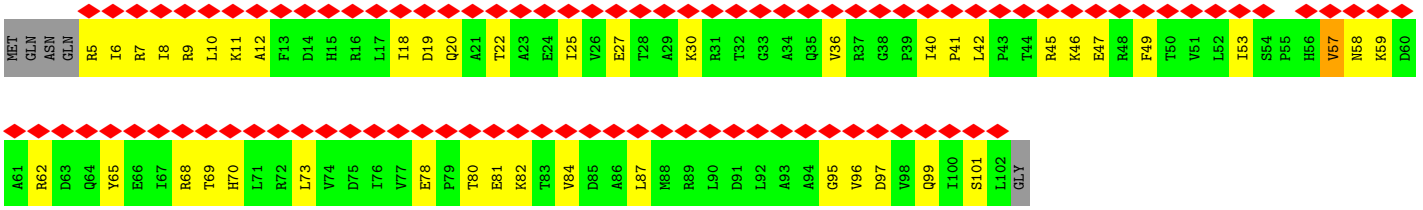




• Molecule 10: 30S ribosomal protein S10

Chain AJ:

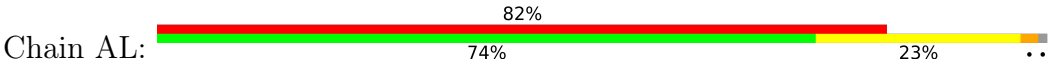


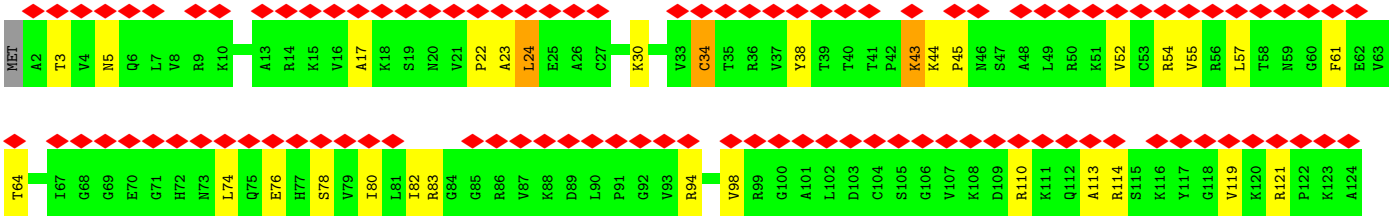


• Molecule 11: 30S ribosomal protein S11

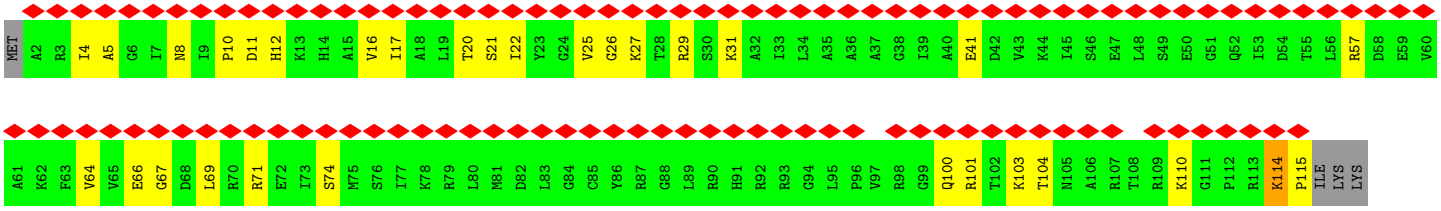
Chain AK:

• Molecule 12: 30S ribosomal protein S12

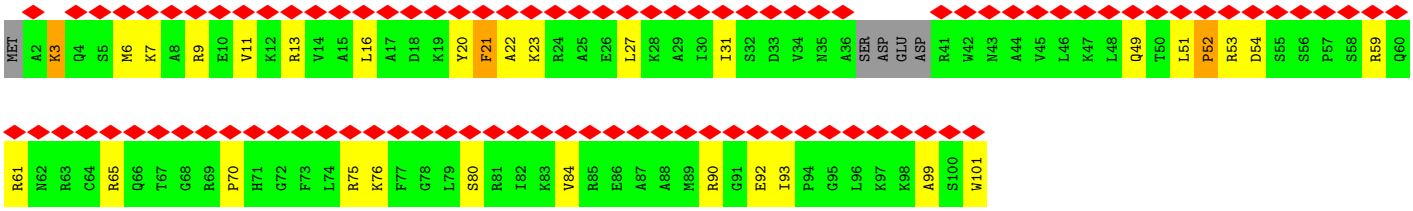




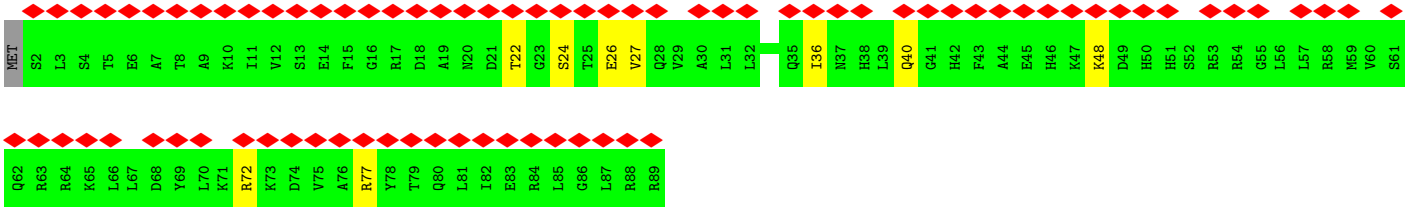
• Molecule 13: 30S ribosomal protein S13



• Molecule 14: 30S ribosomal protein S14

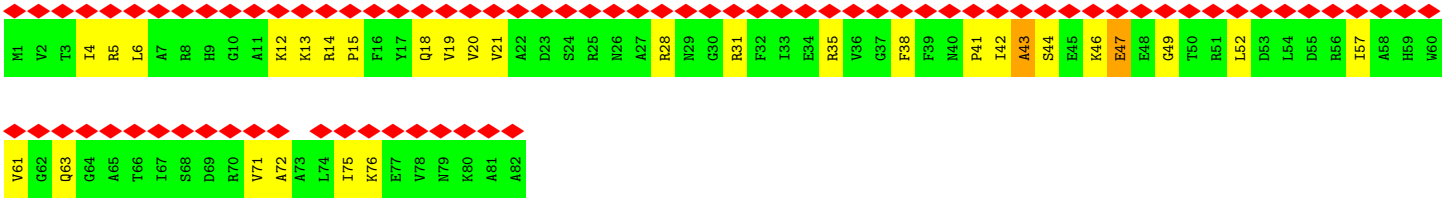


• Molecule 15: 30S ribosomal protein S15



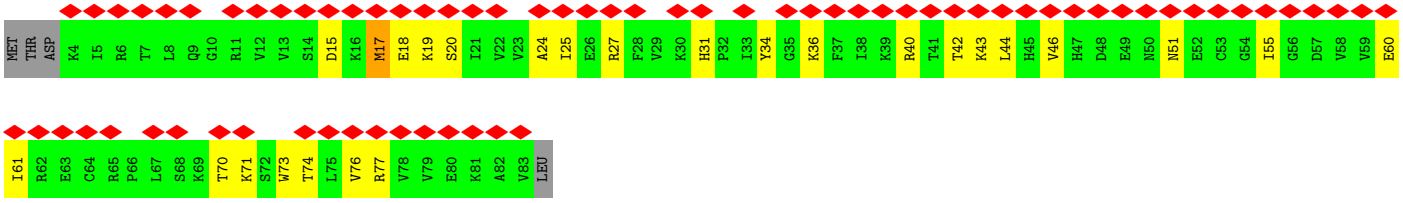
• Molecule 16: 30S ribosomal protein S16

Chain AP:



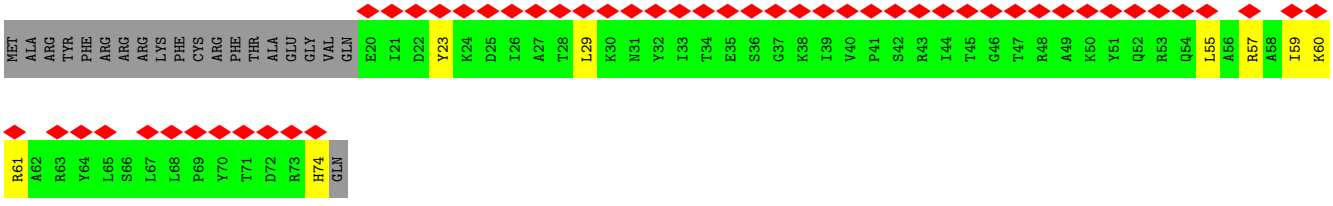
• Molecule 17: 30S ribosomal protein S17

Chain AQ:



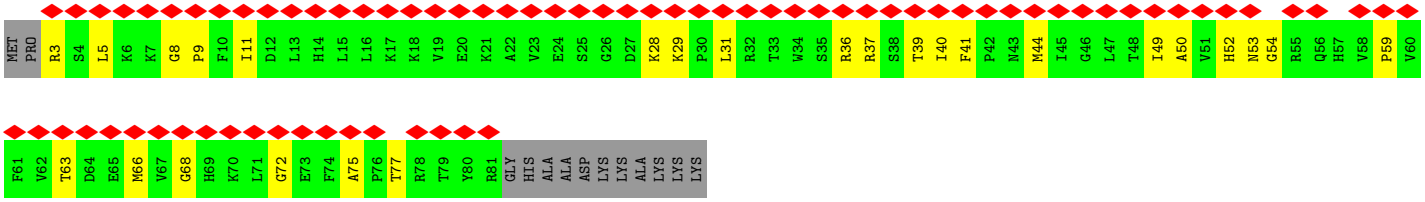
• Molecule 18: 30S ribosomal protein S18

Chain AR:



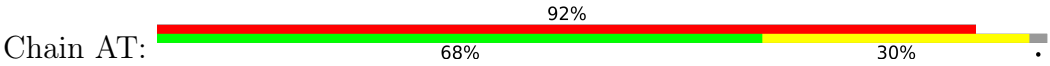
• Molecule 19: 30S ribosomal protein S19

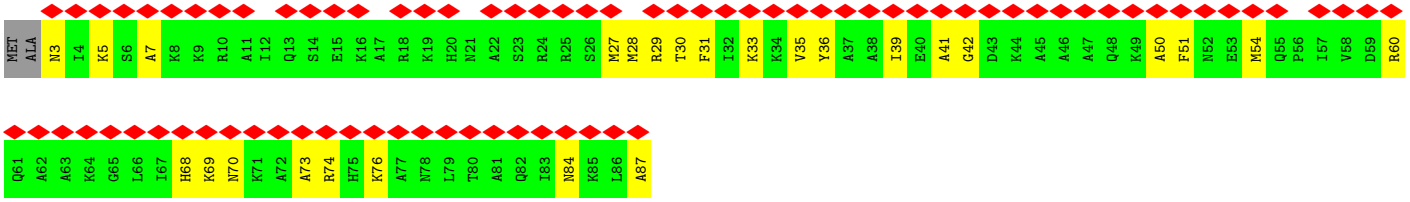
Chain AS:



• Molecule 20: 30S ribosomal protein S20

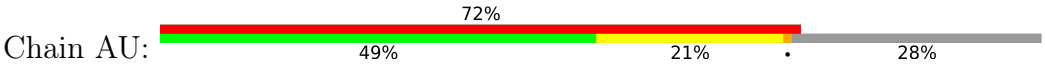
Chain AT:

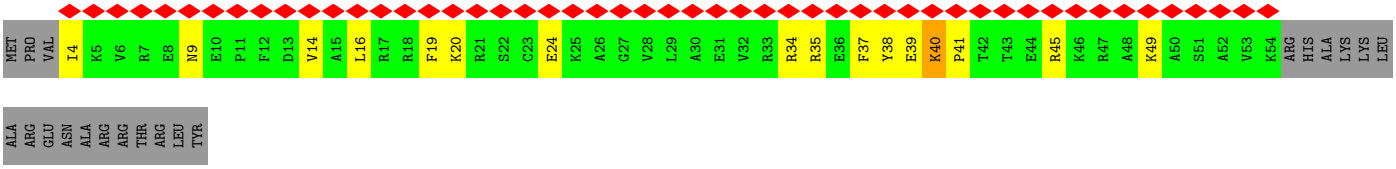




• Molecule 21: 30S ribosomal protein S21

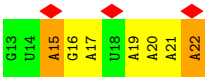
Chain AU:





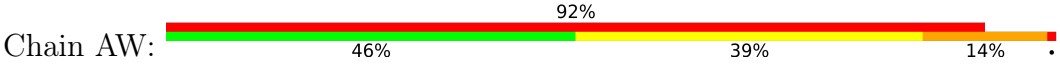
• Molecule 22: mRNA

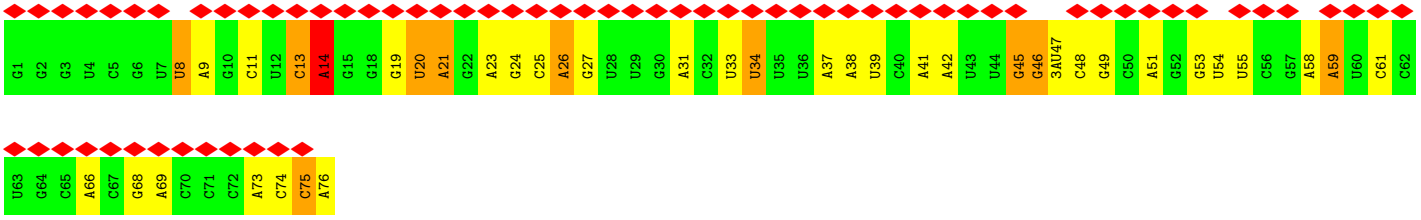
Chain AV:



• Molecule 23: A-site Lysine tRNA Lysine

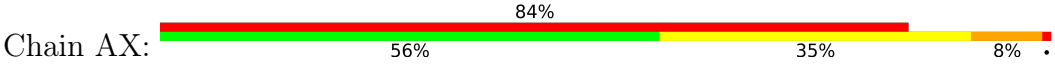
Chain AW:

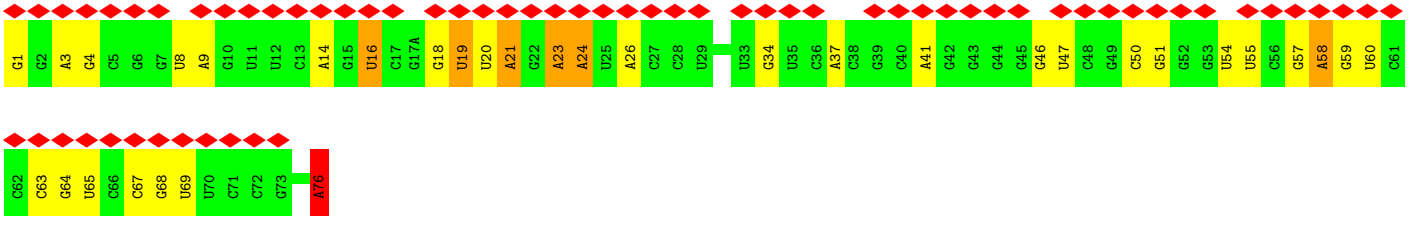




• Molecule 24: P-site tRNA Aspartate

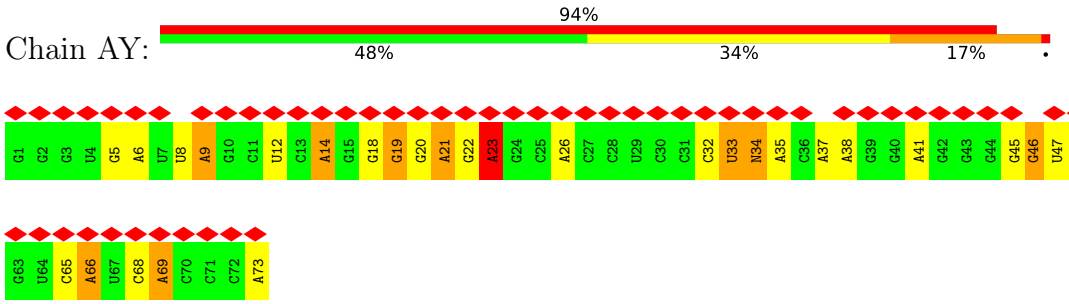
Chain AX:





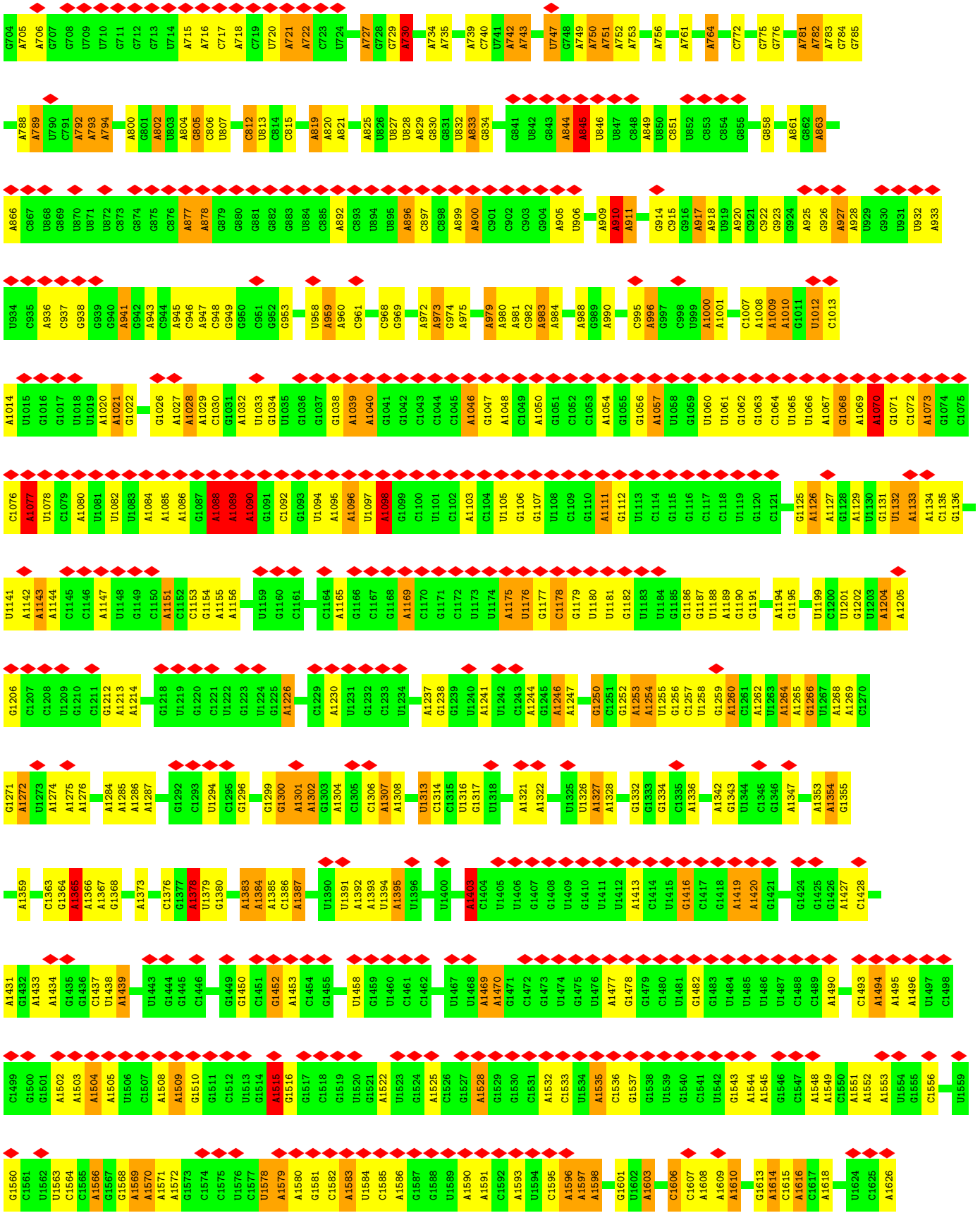
• Molecule 25: E-site tRNA Valine

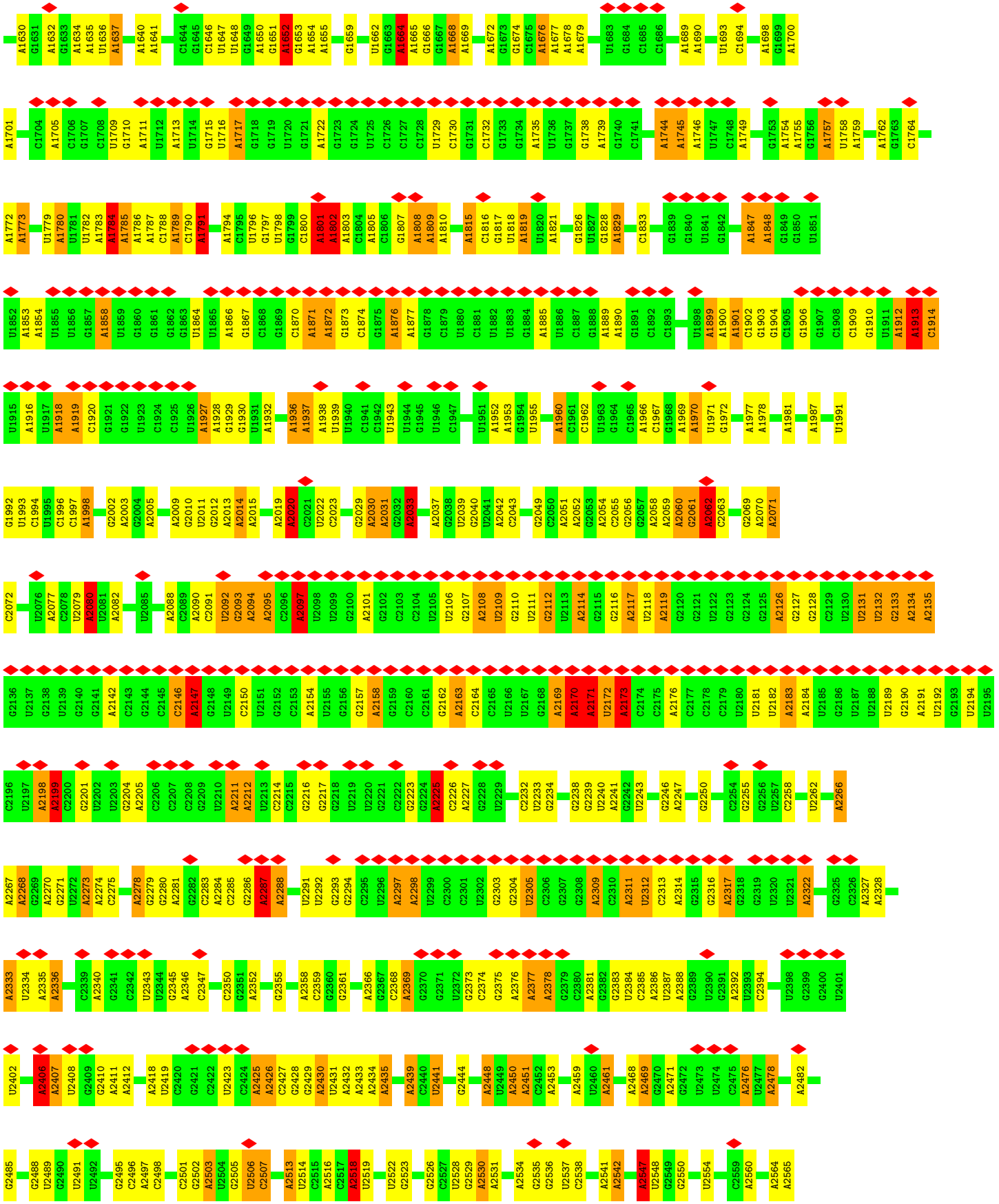
Chain AY:

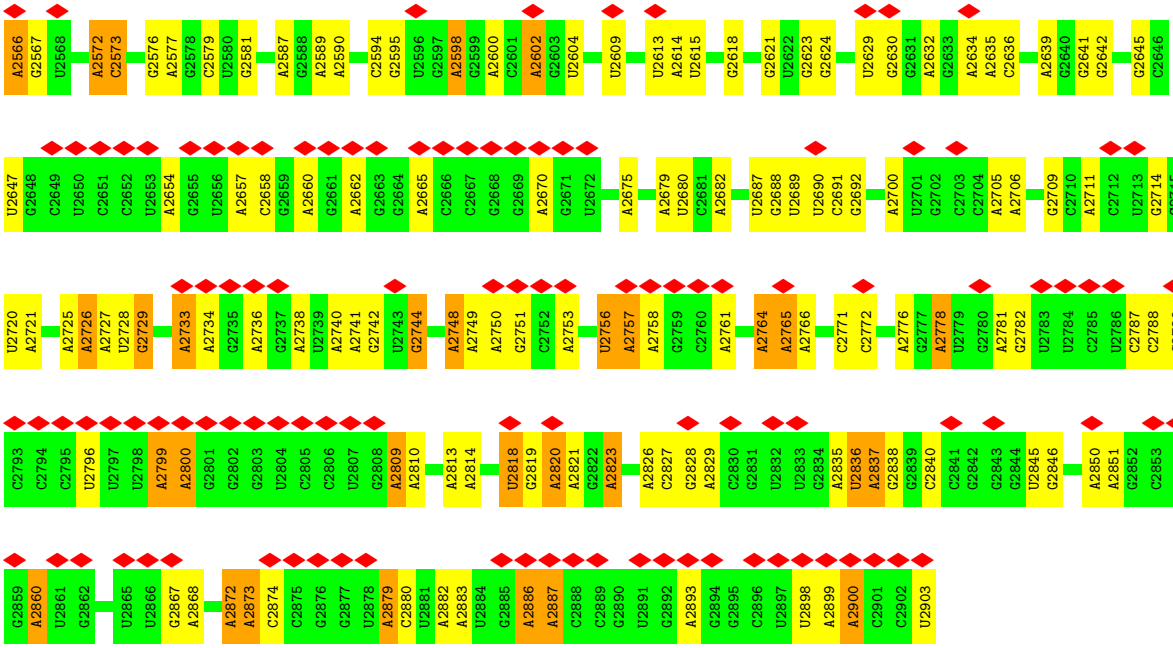


• Molecule 26: 23S ribosomal RNA

Chain BA:

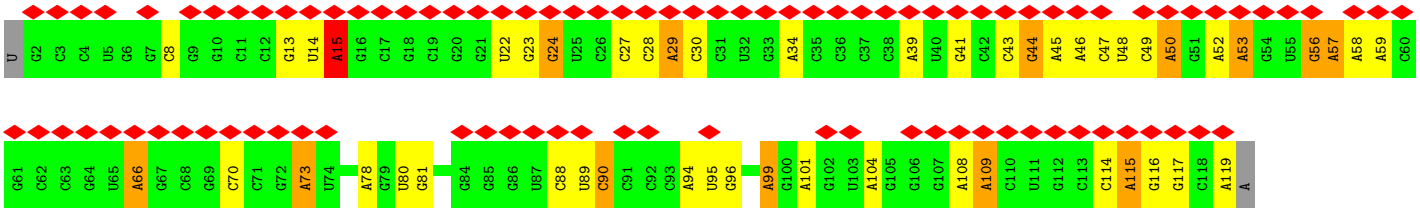

G704 A705 A706 G707 G708 U709 U710 G711 G712 G713 U714 A715 A716 C717 A718 C719 U720 A721 A722 C723 U724 A727 G728 G729 A730 A734 A735 A739 C740 U741 A742 A743 U747 G748 A749 A750 A751 A752 A753 A756 A761 A764 C772 G775 G776 A781 A782 A783 G784 G785
A788 A789 U790 C791 A792 A793 A794 A800 G801 A802 U803 A804 G805 C806 U807 C812 U813 C814 C815 A819 A820 A821 A825 U826 U827 U828 A829 G830 G831 U832 A833 G834 G841 U842 G843 A844 A845 U846 U847 C848 A849 U850 C851 U852 C853 C854 G855 G858 A861 G862 A863
A866 C867 U868 G869 U870 U871 U872 C873 G874 G875 C876 A877 A878 G879 G880 G881 G882 G883 U884 C885 A892 C893 U894 U895 A896 C897 C898 A899 A900 C901 C902 C903 G904 A905 U906 A909 A910 A911 G914 C915 G916 A917 A918 U919 A920 C921 C922 G923 G924 A925 G926 A927 A928 U929 G930 U931 U932 A933
U934 C935 A936 C937 G938 G939 G940 A941 G942 A943 C944 A945 C946 A947 C948 G949 G950 C951 G952 G953 U958 A959 A960 C961 C968 G969 A972 A973 G974 A975 A979 A980 A981 C982 A983 A984 A988 G989 A990 C995 A996 G997 C998 U999 A1000 A1001 C1007 A1008 A1009 A1010 G1011 U1012 C1013
A1014 U1015 G1016 G1017 U1018 U1019 A1020 A1021 G1022 G1026 A1027 A1028 A1029 C1030 G1031 A1032 U1033 G1034 U1035 G1036 G1037 G1038 A1039 A1040 G1041 G1042 C1043 C1044 C1045 A1046 G1047 A1048 C1049 A1050 G1051 C1052 C1053 A1054 G1055 G1056 A1057 U1058 G1059 U1060 U1061 G1062 G1063 C1064 U1065 U1066 A1067 G1068 A1069 A1070 G1071 C1072 A1073 G1074 C1075
C1076 A1077 U1078 C1079 A1080 U1081 U1082 U1083 A1084 A1085 A1086 G1087 A1088 A1089 A1090 G1091 C1092 G1093 U1094 A1095 A1096 U1097 A1098 G1099 C1100 U1101 C1102 A1103 C1104 U1105 G1106 G1107 U1108 C1109 G1110 A1111 G1112 U1113 C1114 G1115 G1116 C1117 C1118 U1119 G1120 C1121 G1125 A1126 A1127 G1128 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136
U1141 A1142 A1143 A1144 C1145 C1146 A1147 U1148 G1149 C1150 A1151 C1152 C1153 G1154 A1155 A1156 U1159 G1160 C1161 C1164 A1165 G1166 C1167 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 U1180 U1181 G1182 U1183 U1184 G1185 G1186 G1187 U1188 A1189 G1190 G1191 A1194 G1195 U1199 C1200 U1201 G1202 U1203 A1204 A1205
G1206 C1207 C1208 U1209 G1210 C1211 G1212 A1213 A1214 G1218 U1219 G1220 C1221 U1222 G1223 U1224 G1225 A1226 C1229 A1230 U1231 G1232 C1233 U1234 A1237 G1238 G1239 U1240 A1241 U1242 C1243 A1244 G1245 A1246 A1247 G1250 C1251 G1252 A1253 A1254 U1255 G1256 C1257 U1258 G1259 A1260 C1261 A1262 U1263 A1264 A1265 G1266 U1267 A1268 A1269 C1270
G1271 A1272 U1273 A1274 A1275 A1276 A1284 A1285 A1286 A1287 G1292 C1293 U1294 C1295 G1296 G1299 G1300 A1301 A1302 G1303 A1304 C1305 C1306 A1307 A1308 U1313 C1314 C1315 U1316 G1317 U1318 A1321 A1322 U1325 U1326 A1327 A1328 G1332 G1333 G1334 C1335 A1336 A1342 G1343 U1344 C1345 G1346 A1347 A1353 A1354 G1355
A1359 C1363 G1364 A1365 A1366 A1367 G1368 A1373 C1376 G1377 A1378 U1379 G1380 A1383 A1384 A1385 C1386 A1387 U1390 U1391 A1392 A1393 U1394 A1395 U1396 U1400 A1403 C1404 U1405 U1406 G1407 G1408 U1409 G1410 U1411 U1412 A1413 C1414 U1415 G1416 C1417 G1418 A1419 A1420 G1421 G1424 G1425 G1426 A1427 C1428
A1431 G1432 A1433 A1434 G1435 G1436 C1437 U1438 A1439 U1443 G1444 G1445 C1446 G1449 G1450 C1451 G1452 A1453 C1454 G1455 U1458 G1459 U1460 C1461 C1462 U1467 U1468 A1469 A1470 G1471 C1472 G1473 U1474 G1475 U1476 A1477 G1478 G1479 C1480 U1481 G1482 U1483 U1484 U1485 U1486 U1487 C1488 C1489 A1490 C1493 A1494 A1495 A1496 U1497 C1498
C1499 G1500 G1501 A1502 A1503 A1504 A1505 U1506 C1507 A1508 A1509 G1510 G1511 C1512 U1513 G1514 A1515 G1516 G1517 C1518 G1519 U1520 G1521 A1522 U1523 G1524 A1525 C1526 G1527 A1528 G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1538 U1539 G1540 C1541 U1542 G1543 A1544 A1545 G1546 C1547 A1548 A1549 C1550 A1551 A1552 A1553 U1554 G1555 C1556 U1559
G1560 C1561 U1562 A1563 C1564 C1565 A1566 G1567 G1568 A1569 A1570 A1571 A1572 G1573 C1574 C1575 U1576 C1577 U1578 A1579 A1580 G1581 C1582 A1583 U1584 C1585 A1586 G1587 G1588 U1589 A1590 A1591 C1592 A1593 U1594 C1595 A1596 A1597 A1598 G1601 U1602 A1603 C1606 C1607 A1608 A1609 A1610 G1613 A1614 C1615 A1616 C1617 A1618 U1624 C1625 A1626





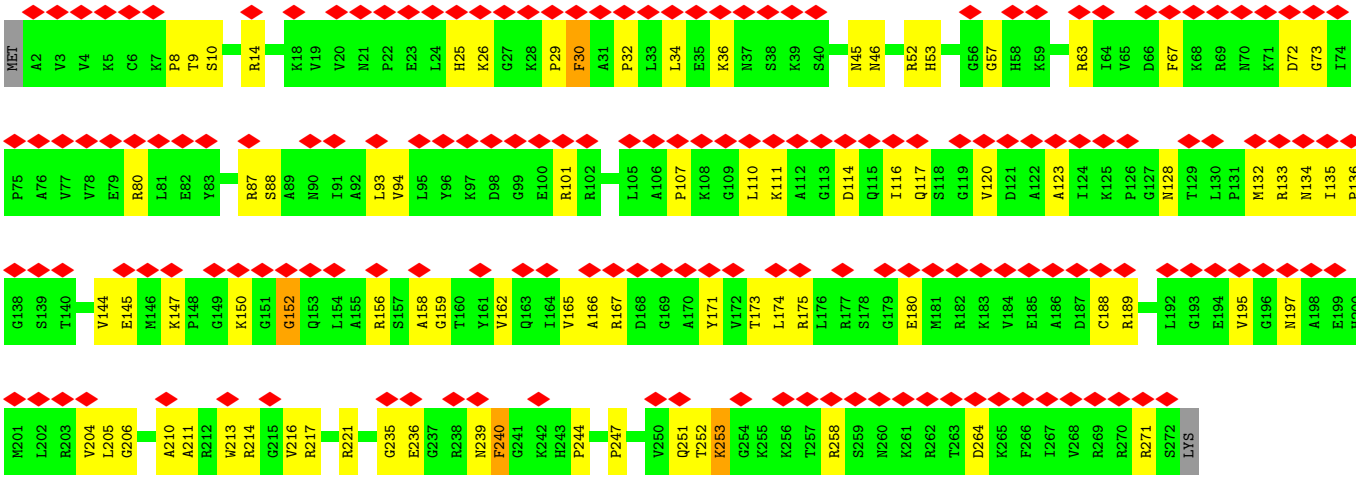
• Molecule 27: 5S ribosomal RNA

Chain BB:



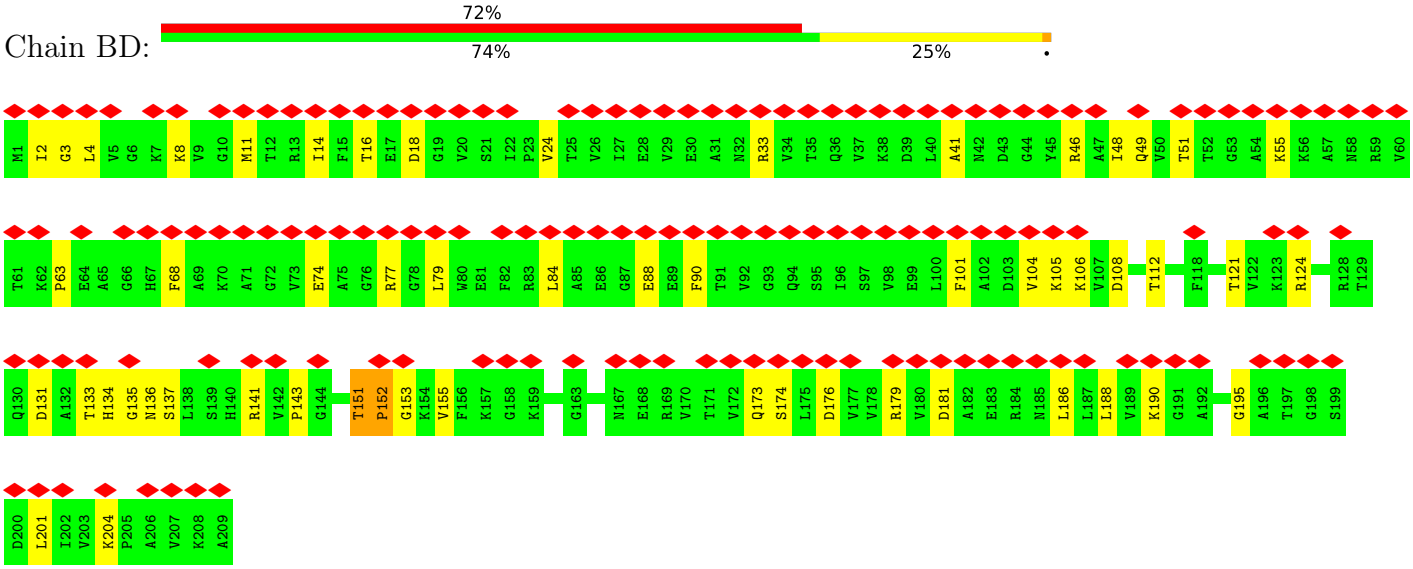
• Molecule 28: 50S ribosomal protein L2

Chain BC:



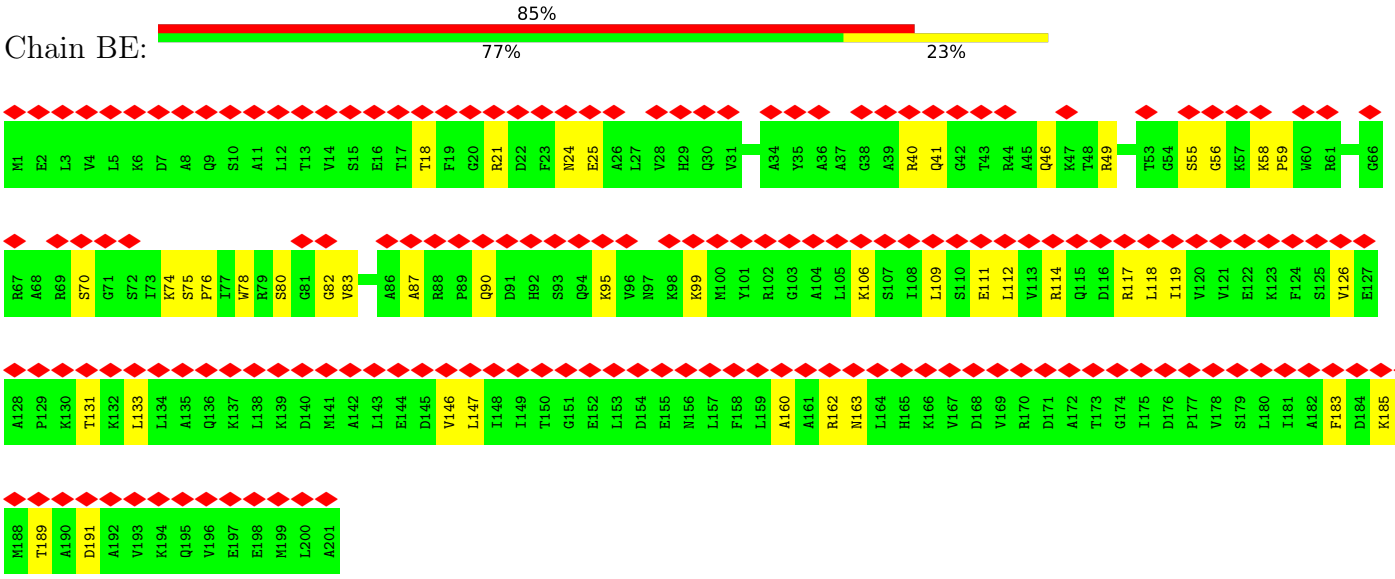
• Molecule 29: 50S ribosomal protein L3

Chain BD:



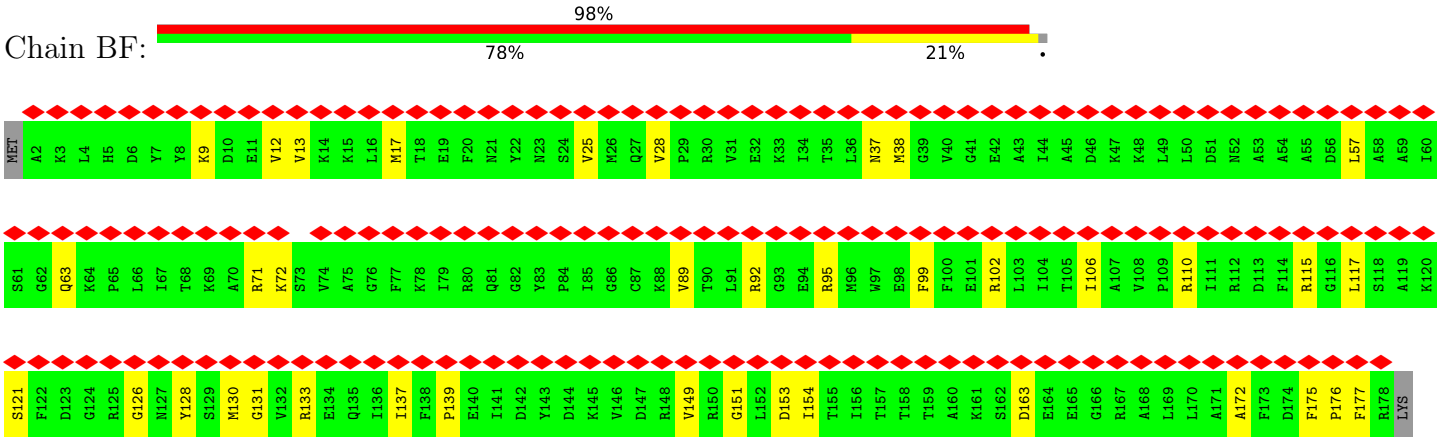
• Molecule 30: 50S ribosomal protein L4

Chain BE:



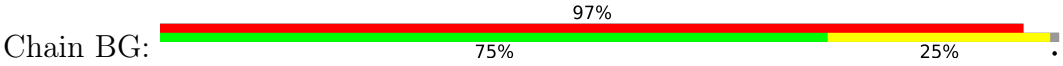
• Molecule 31: 50S ribosomal protein L5

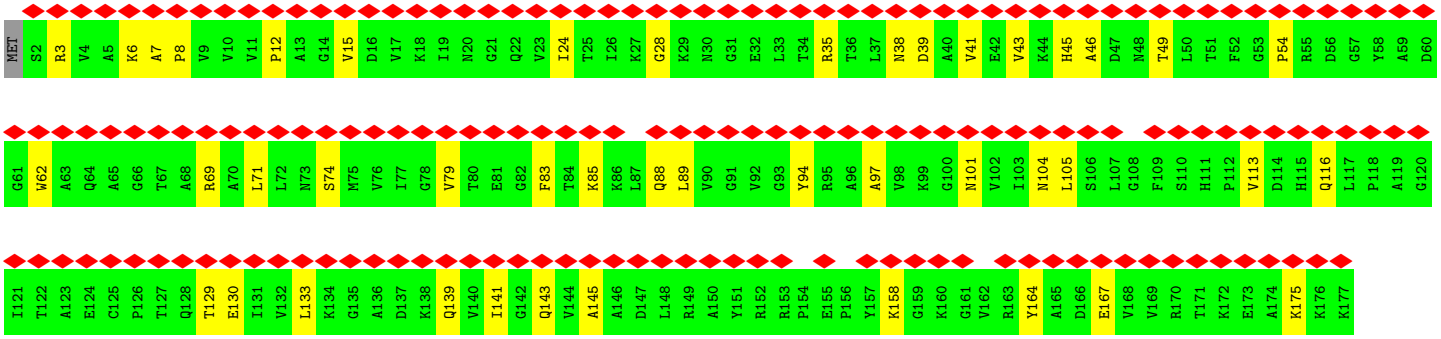
Chain BF:



• Molecule 32: 50S ribosomal protein L6

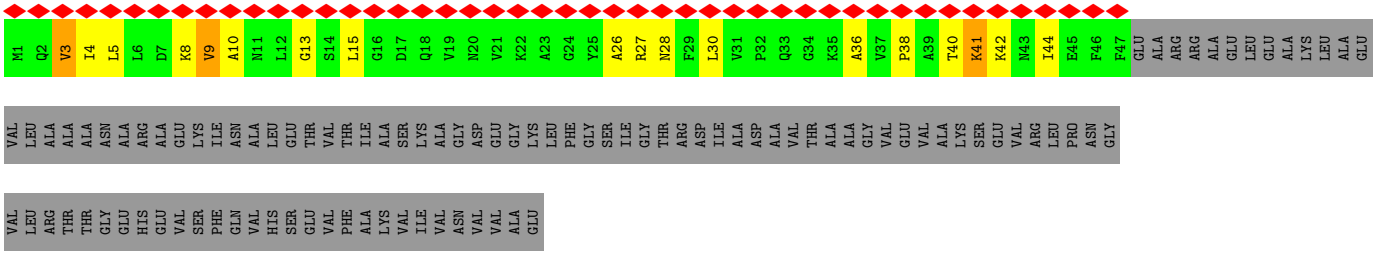
Chain BG:





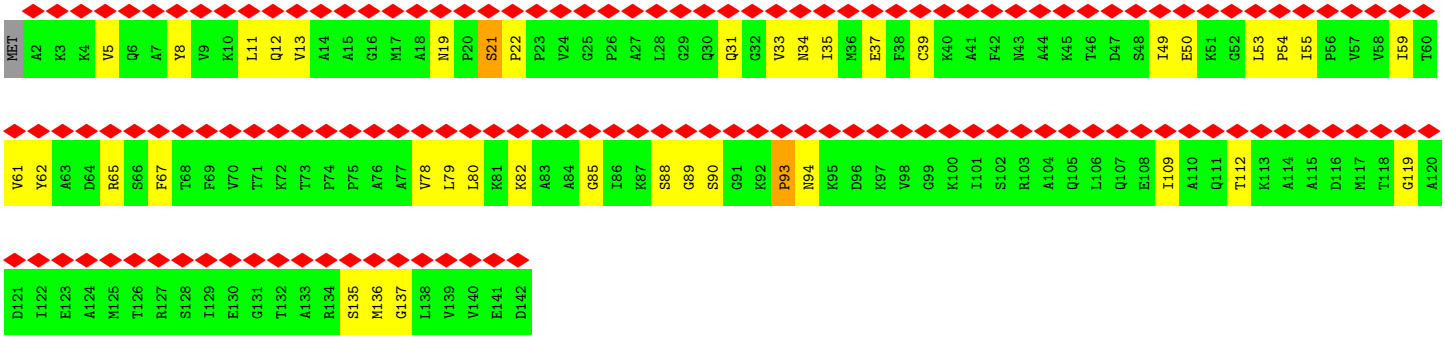
• Molecule 33: 50S ribosomal protein L9

Chain BH:



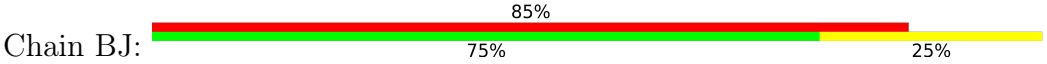
• Molecule 34: 50S ribosomal protein L11

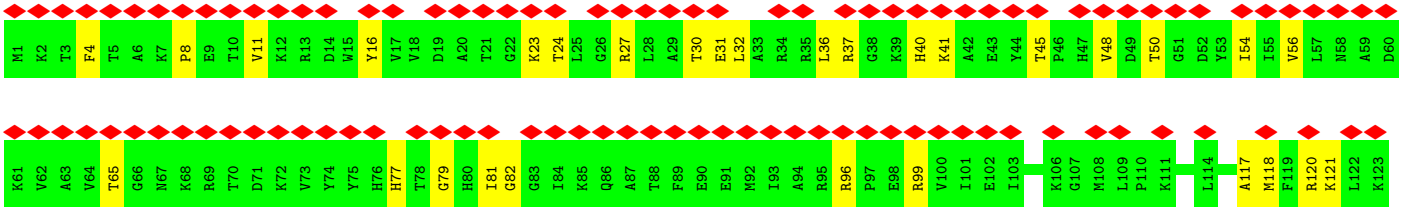
Chain BI:

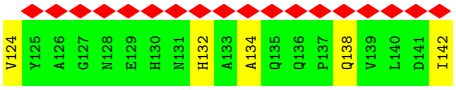


• Molecule 35: 50S ribosomal protein L13

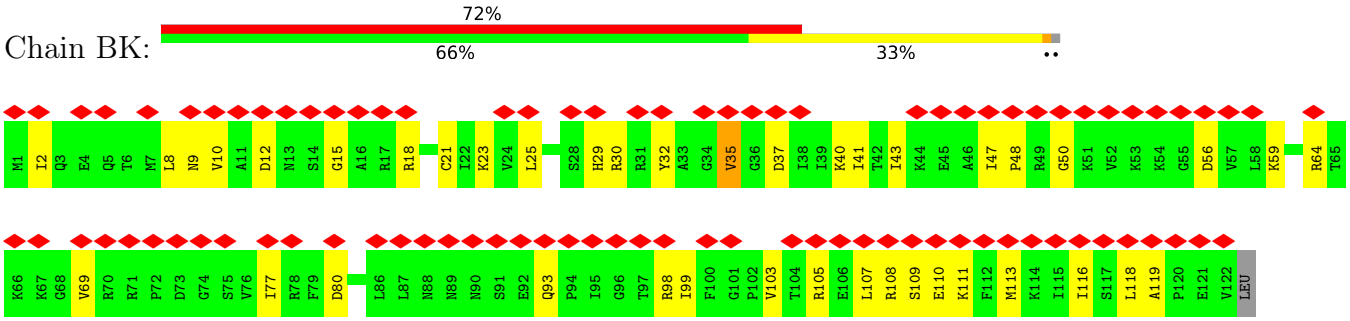
Chain BJ:



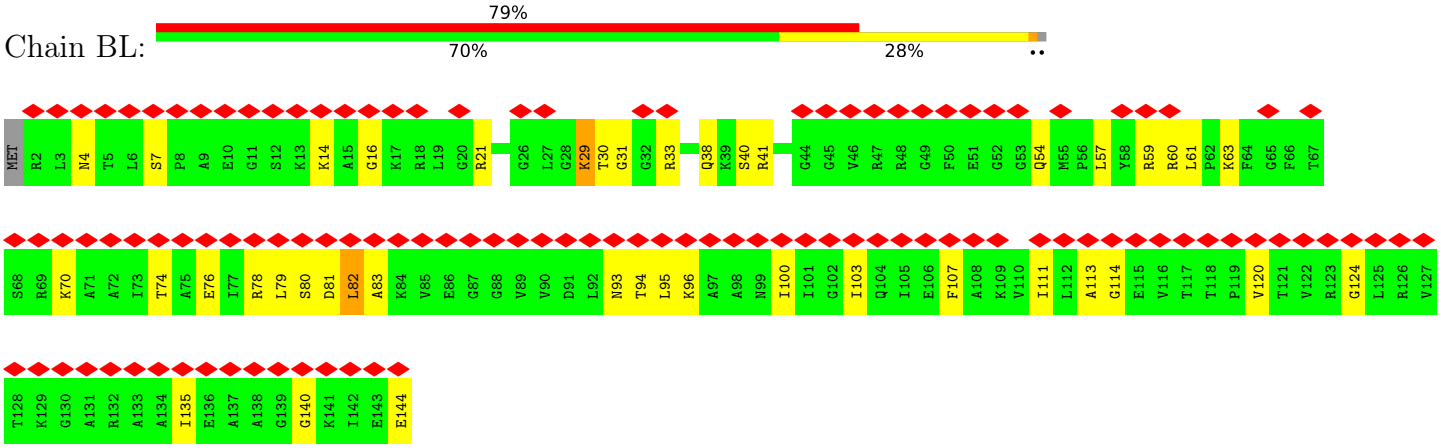




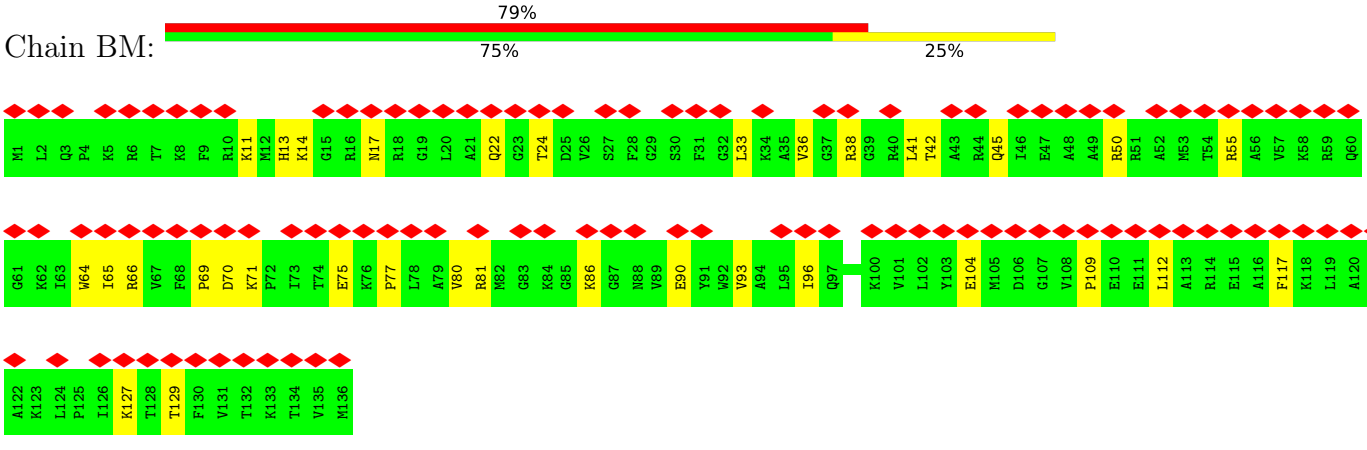
• Molecule 36: 50S ribosomal protein L14



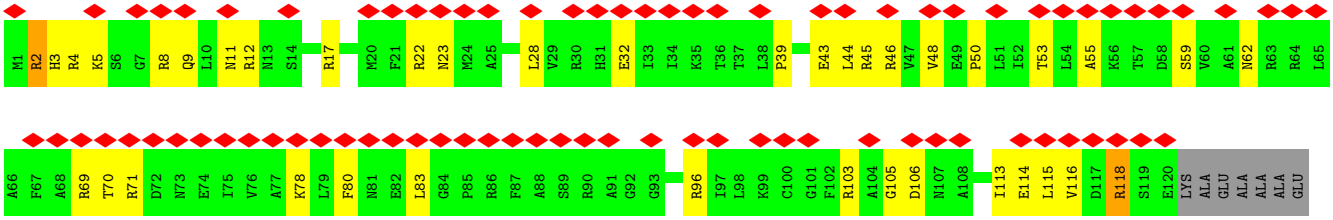
• Molecule 37: 50S ribosomal protein L15



• Molecule 38: 50S ribosomal protein L16

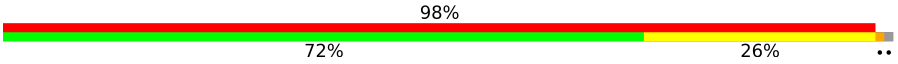


• Molecule 39: 50S ribosomal protein L17



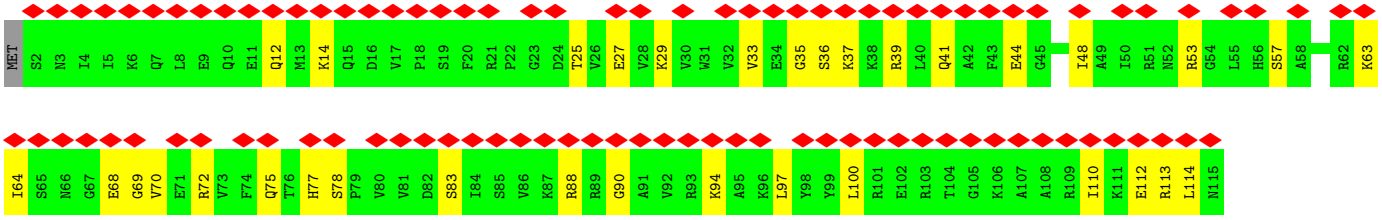
• Molecule 40: 50S ribosomal protein L18

Chain BO:



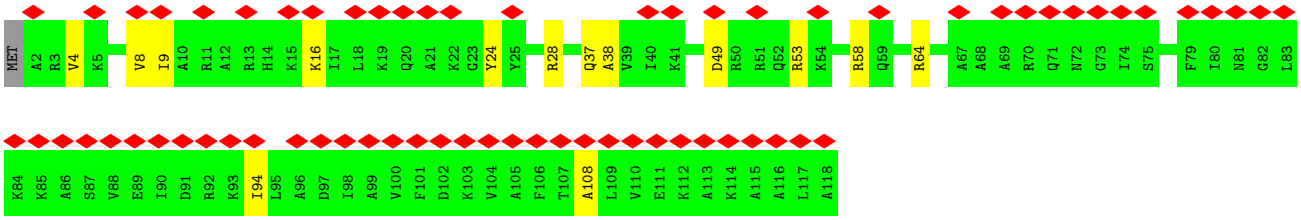
• Molecule 41: 50S ribosomal protein L19

Chain BP:



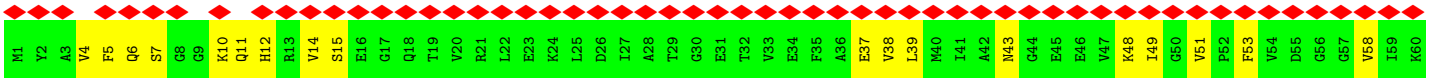
• Molecule 42: 50S ribosomal protein L20

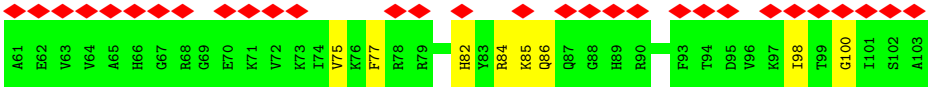
Chain BQ:



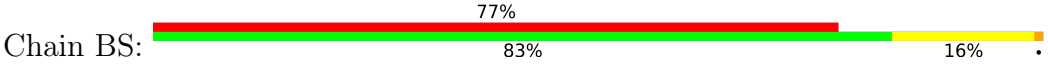
• Molecule 43: 50S ribosomal protein L21

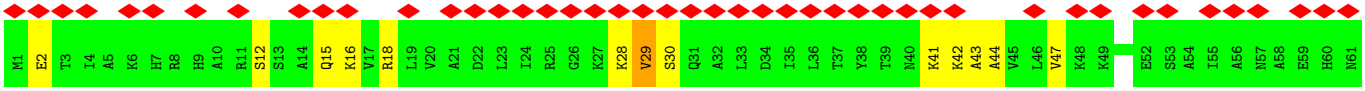
Chain BR:

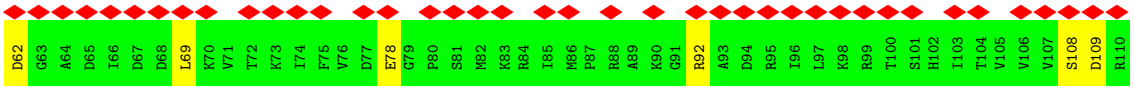




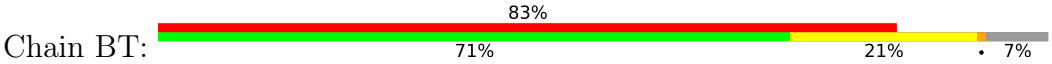
• Molecule 44: 50S ribosomal protein L22

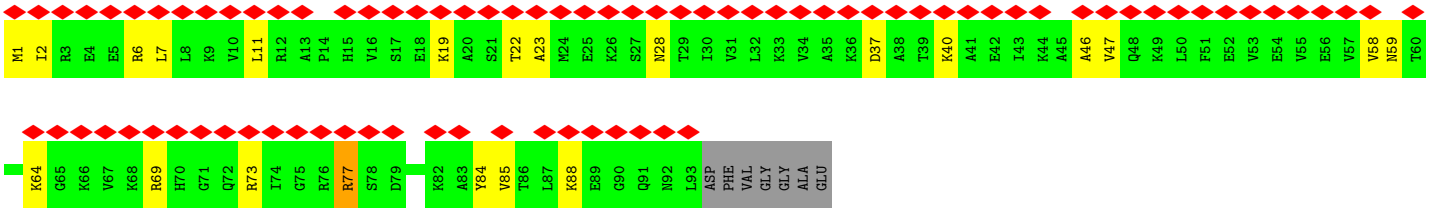




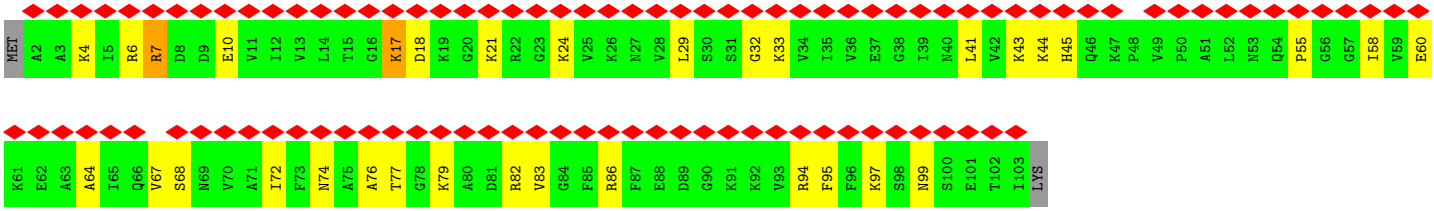


• Molecule 45: 50S ribosomal protein L23

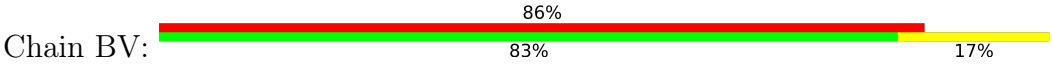


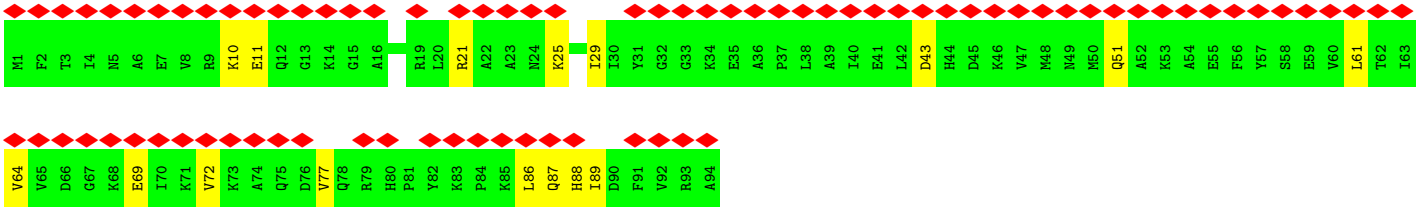


• Molecule 46: 50S ribosomal protein L24



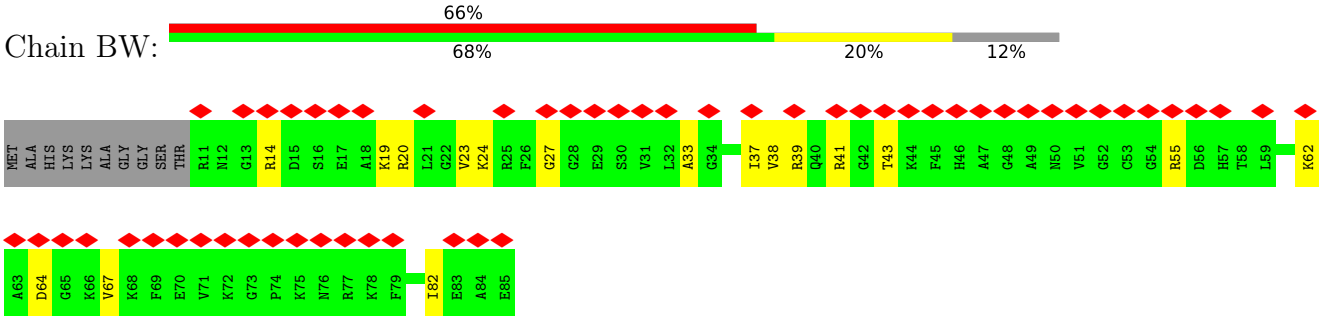
• Molecule 47: 50S ribosomal protein L25





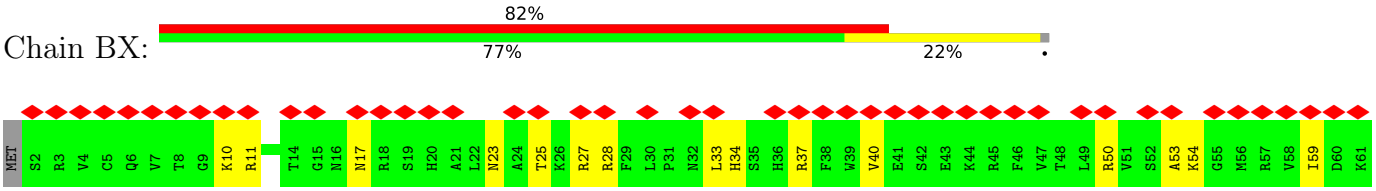
• Molecule 48: 50S ribosomal protein L27

Chain BW:



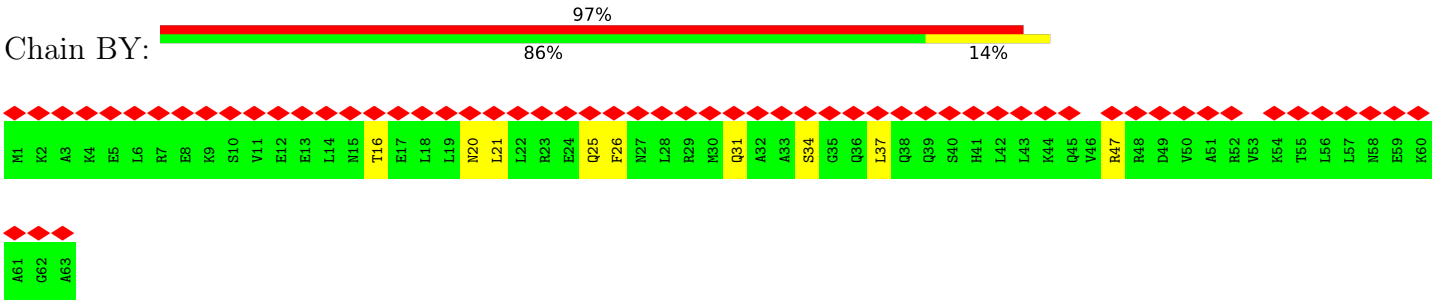
• Molecule 49: 50S ribosomal protein L28

Chain BX:



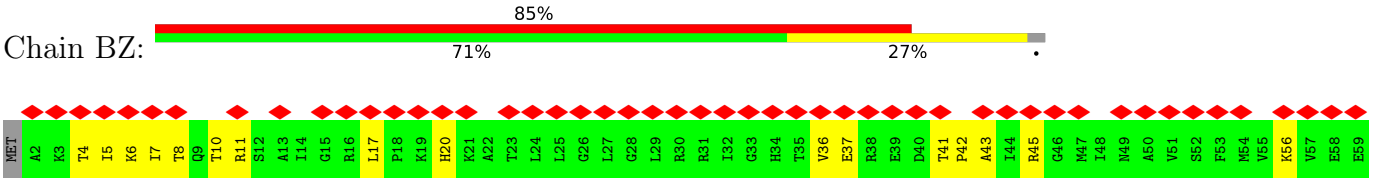
• Molecule 50: 50S ribosomal protein L29

Chain BY:



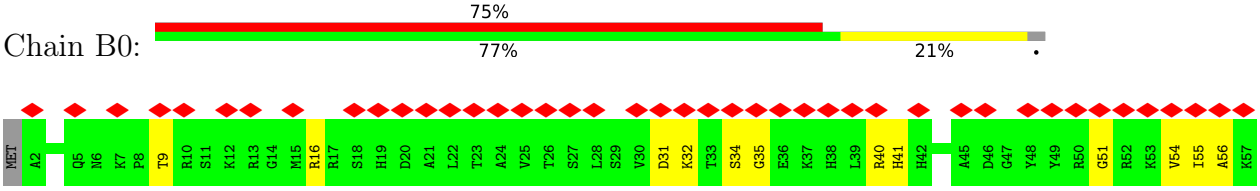
• Molecule 51: 50S ribosomal protein L30

Chain BZ:



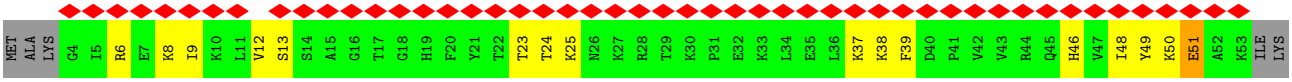
• Molecule 52: 50S ribosomal protein L32

Chain B0:



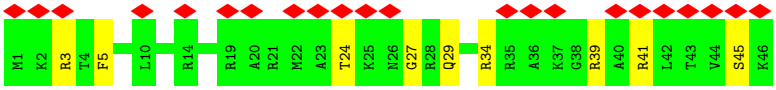
• Molecule 53: 50S ribosomal protein L33

Chain B1:



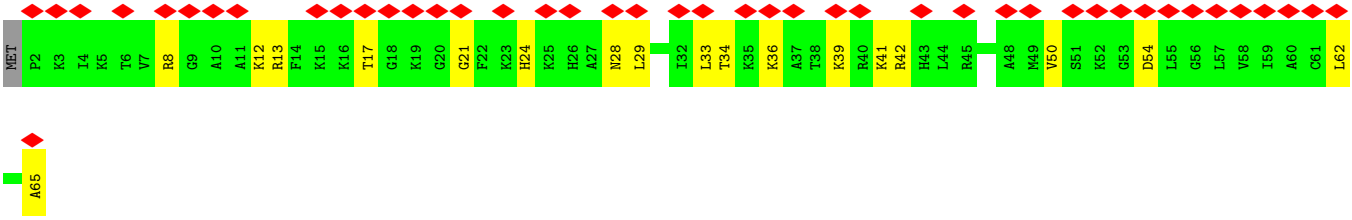
• Molecule 54: 50S ribosomal protein L34

Chain B2:



• Molecule 55: 50S ribosomal protein L35

Chain B3:

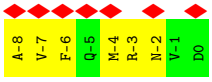


• Molecule 56: 50S ribosomal protein L36

Chain B4:

• Molecule 57: ErmBL

Chain B5:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85393	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	4	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.010	Depositor
Minimum map value	-0.006	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00194	Depositor
Map size (Å)	407.74402, 407.74402, 407.74402	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.108, 1.108, 1.108	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, 7MG, T6A, 6MZ, 3AU, ERY, 4SU, QUO, PSU, 2MA, U8U, CM0

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	2.20	1353/36965 (3.7%)	3.39	4664/57662 (8.1%)
2	AB	0.30	0/1735	0.49	0/2338
3	AC	0.25	0/1651	0.44	0/2225
4	AD	0.27	0/1665	0.47	0/2227
5	AE	0.24	0/1118	0.46	0/1504
6	AF	0.25	0/835	0.46	0/1128
7	AG	0.25	0/1195	0.42	0/1602
8	AH	0.27	0/989	0.45	0/1326
9	AI	0.28	0/1034	0.48	0/1375
10	AJ	0.31	0/796	0.53	0/1077
11	AK	0.25	0/893	0.44	0/1205
12	AL	0.25	0/969	0.45	0/1300
13	AM	0.27	0/892	0.49	0/1193
14	AN	0.24	0/785	0.42	0/1043
15	AO	0.28	0/718	0.45	0/959
16	AP	0.26	0/659	0.44	0/884
17	AQ	0.26	0/657	0.49	0/881
18	AR	0.27	0/462	0.44	0/621
19	AS	0.26	0/652	0.43	0/877
20	AT	0.25	0/671	0.43	0/888
21	AU	0.25	0/430	0.50	0/570
22	AV	3.36	21/245 (8.6%)	5.13	72/380 (18.9%)
23	AW	2.30	58/1569 (3.7%)	3.39	201/2437 (8.2%)
24	AX	2.07	48/1668 (2.9%)	2.69	139/2593 (5.4%)
25	AY	1.97	44/1554 (2.8%)	3.05	157/2416 (6.5%)
26	BA	2.25	2626/69659 (3.8%)	3.46	9154/108672 (8.4%)
27	BB	1.94	79/2828 (2.8%)	3.00	278/4410 (6.3%)
28	BC	0.25	0/2121	0.45	0/2852
29	BD	0.27	0/1586	0.45	0/2134
30	BE	0.27	0/1571	0.45	0/2113
31	BF	0.30	0/1434	0.47	0/1926
32	BG	0.27	0/1343	0.44	0/1816

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
33	BH	0.29	0/364	0.52	0/490
34	BI	0.28	0/1046	0.49	0/1410
35	BJ	0.27	0/1152	0.44	0/1551
36	BK	0.26	0/947	0.46	0/1268
37	BL	0.24	0/1054	0.44	0/1403
38	BM	0.26	0/1093	0.43	0/1460
39	BN	0.25	0/973	0.43	0/1301
40	BO	0.25	0/902	0.40	0/1209
41	BP	0.24	0/929	0.43	0/1242
42	BQ	0.24	0/960	0.38	0/1278
43	BR	0.25	0/829	0.43	0/1107
44	BS	0.29	0/864	0.48	0/1156
45	BT	0.23	0/744	0.43	0/994
46	BU	0.28	0/787	0.45	0/1051
47	BV	0.27	0/766	0.44	0/1025
48	BW	0.25	0/576	0.39	0/762
49	BX	0.23	0/635	0.39	0/848
50	BY	0.22	0/510	0.38	0/677
51	BZ	0.23	0/453	0.44	0/605
52	B0	0.27	0/450	0.44	0/599
53	B1	0.24	0/416	0.43	0/554
54	B2	0.20	0/380	0.37	0/498
55	B3	0.22	0/513	0.41	0/676
56	B4	0.23	0/303	0.39	0/397
57	B5	0.36	0/74	0.59	0/98
All	All	1.89	4229/159069 (2.7%)	2.97	14665/238293 (6.2%)

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
29	BD	0	1

The worst 5 of 4229 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	20	U	C5-C6	23.31	1.55	1.34
23	AW	20	U	C5-C6	23.29	1.55	1.34
24	AX	16	U	C5-C6	23.26	1.55	1.34
24	AX	19	U	C5-C6	23.18	1.55	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BA	454	A	C6-N6	17.20	1.47	1.33

The worst 5 of 14665 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	BA	278	A	C2-N3-C4	20.42	120.81	110.60
1	AA	983	A	C2-N3-C4	20.30	120.75	110.60
26	BA	2114	A	C2-N3-C4	20.19	120.70	110.60
26	BA	514	A	C2-N3-C4	19.99	120.60	110.60
26	BA	2451	A	N1-C6-N6	-19.89	106.67	118.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	BD	151	THR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	33015	0	16618	253	0
2	AB	1704	0	1732	31	0
3	AC	1624	0	1696	37	0
4	AD	1643	0	1707	74	0
5	AE	1105	0	1148	24	0
6	AF	817	0	808	12	0
7	AG	1181	0	1238	21	0
8	AH	979	0	1031	18	0
9	AI	1022	0	1070	25	0
10	AJ	786	0	828	32	0
11	AK	877	0	887	25	0
12	AL	955	0	1016	20	0
13	AM	883	0	941	22	0
14	AN	774	0	824	26	0
15	AO	710	0	728	7	0
16	AP	649	0	666	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	AQ	648	0	691	17	0
18	AR	455	0	478	7	0
19	AS	637	0	665	15	0
20	AT	665	0	714	18	0
21	AU	425	0	449	7	0
22	AV	218	0	109	3	0
23	AW	1593	0	820	8	0
24	AX	1656	0	849	10	0
25	AY	1525	0	780	11	0
26	BA	62195	0	31280	430	0
27	BB	2529	0	1281	22	0
28	BC	2082	0	2154	53	0
29	BD	1565	0	1616	40	0
30	BE	1552	0	1619	32	0
31	BF	1410	0	1444	23	0
32	BG	1323	0	1371	27	0
33	BH	359	0	381	13	0
34	BI	1032	0	1085	26	0
35	BJ	1129	0	1162	22	0
36	BK	938	0	1012	26	0
37	BL	1045	0	1117	26	0
38	BM	1074	0	1157	25	0
39	BN	960	0	1000	29	0
40	BO	892	0	923	21	0
41	BP	917	0	962	22	0
42	BQ	947	0	1019	11	0
43	BR	816	0	839	15	0
44	BS	857	0	922	13	0
45	BT	738	0	807	14	0
46	BU	779	0	831	23	0
47	BV	753	0	780	9	0
48	BW	569	0	581	15	0
49	BX	625	0	652	13	0
50	BY	509	0	543	8	0
51	BZ	449	0	488	10	0
52	B0	444	0	458	8	0
53	B1	409	0	440	12	0
54	B2	377	0	418	7	0
55	B3	504	0	572	15	0
56	B4	302	0	343	8	0
57	B5	74	0	74	23	0
58	AW	9	0	12	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	BA	51	0	67	12	0
All	All	146760	0	97903	1470	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 6.

The worst 5 of 1470 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)
59:BA:9000:ERY:C27	57:B5:-2:ASN:ND2	2.18	1.07
59:BA:9000:ERY:H271	57:B5:-2:ASN:HD21	1.13	1.06
59:BA:9000:ERY:H271	57:B5:-2:ASN:ND2	1.74	1.01
59:BA:9000:ERY:C27	57:B5:-2:ASN:HD21	1.72	0.98
58:AW:101:LYS:N	24:AX:76:A:HO2'	1.69	0.91

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	216/240 (90%)	190 (88%)	19 (9%)	7 (3%)	4 31
3	AC	204/233 (88%)	180 (88%)	20 (10%)	4 (2%)	7 41
4	AD	203/206 (98%)	188 (93%)	8 (4%)	7 (3%)	3 31
5	AE	148/167 (89%)	124 (84%)	17 (12%)	7 (5%)	2 22
6	AF	98/135 (73%)	85 (87%)	8 (8%)	5 (5%)	2 20
7	AG	149/179 (83%)	140 (94%)	8 (5%)	1 (1%)	22 61
8	AH	127/130 (98%)	116 (91%)	10 (8%)	1 (1%)	19 59
9	AI	125/130 (96%)	113 (90%)	6 (5%)	6 (5%)	2 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
10	AJ	96/103 (93%)	82 (85%)	8 (8%)	6 (6%)	1 17
11	AK	115/129 (89%)	99 (86%)	13 (11%)	3 (3%)	5 35
12	AL	121/124 (98%)	108 (89%)	6 (5%)	7 (6%)	1 18
13	AM	112/118 (95%)	104 (93%)	7 (6%)	1 (1%)	17 57
14	AN	92/101 (91%)	79 (86%)	8 (9%)	5 (5%)	2 19
15	AO	86/89 (97%)	79 (92%)	7 (8%)	0	100 100
16	AP	80/82 (98%)	67 (84%)	11 (14%)	2 (2%)	5 36
17	AQ	78/84 (93%)	64 (82%)	11 (14%)	3 (4%)	3 27
18	AR	53/75 (71%)	51 (96%)	2 (4%)	0	100 100
19	AS	77/92 (84%)	71 (92%)	5 (6%)	1 (1%)	12 50
20	AT	83/87 (95%)	76 (92%)	4 (5%)	3 (4%)	3 29
21	AU	49/71 (69%)	36 (74%)	8 (16%)	5 (10%)	0 7
28	BC	269/273 (98%)	247 (92%)	16 (6%)	6 (2%)	6 39
29	BD	207/209 (99%)	190 (92%)	15 (7%)	2 (1%)	15 55
30	BE	199/201 (99%)	188 (94%)	9 (4%)	2 (1%)	15 55
31	BF	175/179 (98%)	154 (88%)	16 (9%)	5 (3%)	4 33
32	BG	174/177 (98%)	161 (92%)	10 (6%)	3 (2%)	9 45
33	BH	45/149 (30%)	37 (82%)	4 (9%)	4 (9%)	1 9
34	BI	139/142 (98%)	116 (84%)	15 (11%)	8 (6%)	1 18
35	BJ	140/142 (99%)	131 (94%)	8 (6%)	1 (1%)	22 61
36	BK	120/123 (98%)	106 (88%)	9 (8%)	5 (4%)	3 25
37	BL	141/144 (98%)	117 (83%)	16 (11%)	8 (6%)	1 18
38	BM	134/136 (98%)	124 (92%)	7 (5%)	3 (2%)	6 39
39	BN	118/127 (93%)	104 (88%)	9 (8%)	5 (4%)	3 25
40	BO	114/117 (97%)	104 (91%)	7 (6%)	3 (3%)	5 35
41	BP	112/115 (97%)	105 (94%)	5 (4%)	2 (2%)	8 43
42	BQ	115/118 (98%)	113 (98%)	2 (2%)	0	100 100
43	BR	101/103 (98%)	91 (90%)	6 (6%)	4 (4%)	3 26
44	BS	108/110 (98%)	97 (90%)	9 (8%)	2 (2%)	8 42
45	BT	91/100 (91%)	80 (88%)	9 (10%)	2 (2%)	6 39
46	BU	100/104 (96%)	82 (82%)	13 (13%)	5 (5%)	2 21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
47	BV	92/94 (98%)	87 (95%)	5 (5%)	0	100 100
48	BW	73/85 (86%)	69 (94%)	4 (6%)	0	100 100
49	BX	75/78 (96%)	73 (97%)	2 (3%)	0	100 100
50	BY	61/63 (97%)	56 (92%)	5 (8%)	0	100 100
51	BZ	56/59 (95%)	54 (96%)	1 (2%)	1 (2%)	8 43
52	B0	54/57 (95%)	52 (96%)	2 (4%)	0	100 100
53	B1	48/55 (87%)	45 (94%)	2 (4%)	1 (2%)	7 40
54	B2	44/46 (96%)	41 (93%)	2 (4%)	1 (2%)	6 38
55	B3	62/65 (95%)	57 (92%)	5 (8%)	0	100 100
56	B4	36/38 (95%)	32 (89%)	4 (11%)	0	100 100
57	B5	7/9 (78%)	3 (43%)	3 (43%)	1 (14%)	0 4
All	All	5522/5993 (92%)	4968 (90%)	406 (7%)	148 (3%)	8 35

5 of 148 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	AE	105	ILE
9	AI	55	VAL
11	AK	127	ARG
12	AL	23	ALA
17	AQ	17	MET

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	AB	180/198 (91%)	180 (100%)	0	100 100
3	AC	170/190 (90%)	170 (100%)	0	100 100
4	AD	172/173 (99%)	172 (100%)	0	100 100
5	AE	113/126 (90%)	113 (100%)	0	100 100
6	AF	87/116 (75%)	87 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	AG	124/147 (84%)	124 (100%)	0	100	100
8	AH	104/105 (99%)	104 (100%)	0	100	100
9	AI	105/107 (98%)	105 (100%)	0	100	100
10	AJ	86/90 (96%)	86 (100%)	0	100	100
11	AK	90/99 (91%)	90 (100%)	0	100	100
12	AL	103/104 (99%)	103 (100%)	0	100	100
13	AM	92/96 (96%)	92 (100%)	0	100	100
14	AN	79/84 (94%)	79 (100%)	0	100	100
15	AO	75/77 (97%)	75 (100%)	0	100	100
16	AP	65/65 (100%)	65 (100%)	0	100	100
17	AQ	74/78 (95%)	74 (100%)	0	100	100
18	AR	48/65 (74%)	48 (100%)	0	100	100
19	AS	70/79 (89%)	70 (100%)	0	100	100
20	AT	65/66 (98%)	65 (100%)	0	100	100
21	AU	44/61 (72%)	44 (100%)	0	100	100
28	BC	216/218 (99%)	216 (100%)	0	100	100
29	BD	164/164 (100%)	164 (100%)	0	100	100
30	BE	165/165 (100%)	165 (100%)	0	100	100
31	BF	148/150 (99%)	148 (100%)	0	100	100
32	BG	137/138 (99%)	137 (100%)	0	100	100
33	BH	38/114 (33%)	38 (100%)	0	100	100
34	BI	109/110 (99%)	109 (100%)	0	100	100
35	BJ	116/116 (100%)	116 (100%)	0	100	100
36	BK	103/104 (99%)	103 (100%)	0	100	100
37	BL	102/103 (99%)	102 (100%)	0	100	100
38	BM	109/109 (100%)	109 (100%)	0	100	100
39	BN	100/103 (97%)	100 (100%)	0	100	100
40	BO	86/87 (99%)	86 (100%)	0	100	100
41	BP	99/100 (99%)	99 (100%)	0	100	100
42	BQ	89/90 (99%)	89 (100%)	0	100	100
43	BR	84/84 (100%)	84 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	BS	93/93 (100%)	93 (100%)	0	100	100
45	BT	80/84 (95%)	80 (100%)	0	100	100
46	BU	83/85 (98%)	83 (100%)	0	100	100
47	BV	78/78 (100%)	78 (100%)	0	100	100
48	BW	56/63 (89%)	56 (100%)	0	100	100
49	BX	67/68 (98%)	67 (100%)	0	100	100
50	BY	55/55 (100%)	55 (100%)	0	100	100
51	BZ	48/49 (98%)	48 (100%)	0	100	100
52	B0	47/48 (98%)	47 (100%)	0	100	100
53	B1	45/49 (92%)	45 (100%)	0	100	100
54	B2	38/38 (100%)	38 (100%)	0	100	100
55	B3	51/52 (98%)	51 (100%)	0	100	100
56	B4	34/34 (100%)	34 (100%)	0	100	100
57	B5	8/8 (100%)	8 (100%)	0	100	100
All	All	4594/4885 (94%)	4594 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
31	BF	63	GLN
37	BL	54	GLN
51	BZ	20	HIS
32	BG	116	GLN
34	BI	12	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1537/1539 (99%)	218 (14%)	4 (0%)
22	AV	9/10 (90%)	0	0
23	AW	70/74 (94%)	13 (18%)	1 (1%)
24	AX	74/77 (96%)	6 (8%)	0
25	AY	67/71 (94%)	13 (19%)	1 (1%)
26	BA	2895/2897 (99%)	425 (14%)	10 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	BB	117/120 (97%)	13 (11%)	0
All	All	4769/4788 (99%)	688 (14%)	16 (0%)

5 of 688 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	5	U
1	AA	7	A
1	AA	8	A
1	AA	9	G
1	AA	32	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BA	2506	U
26	BA	2225	A
26	BA	479	A
26	BA	2146	C
26	BA	404	A

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

21 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	$\#\|Z\| > 2$
23	T6A	AW	37	23	27,34,35	1.25	4 (14%)	29,49,52	1.43	4 (13%)
23	PSU	AW	39	23	18,21,22	1.30	3 (16%)	22,30,33	1.62	4 (18%)
24	4SU	AX	8	24	18,21,22	1.09	2 (11%)	26,30,33	0.82	2 (7%)
23	PSU	AW	55	23	18,21,22	1.30	3 (16%)	22,30,33	1.63	4 (18%)
25	PSU	AY	55	25	18,21,22	1.29	3 (16%)	22,30,33	1.62	4 (18%)
23	5MU	AW	54	23	19,22,23	0.92	2 (10%)	28,32,35	1.13	2 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
23	3AU	AW	47	23	25,28,29	1.08	1 (4%)	32,40,43	0.93	2 (6%)
24	2MA	AX	37	24	17,25,26	0.95	1 (5%)	17,37,40	0.93	1 (5%)
23	4SU	AW	8	23	18,21,22	1.08	2 (11%)	26,30,33	0.82	2 (7%)
25	5MU	AY	54	25	19,22,23	0.94	2 (10%)	28,32,35	1.14	2 (7%)
24	PSU	AX	55	24	18,21,22	1.30	3 (16%)	22,30,33	1.61	4 (18%)
23	U8U	AW	34	22,23	19,24,25	0.88	1 (5%)	23,34,37	1.23	4 (17%)
23	7MG	AW	46	23	22,26,27	2.01	3 (13%)	29,39,42	1.22	4 (13%)
24	7MG	AX	46	24	22,26,27	2.05	3 (13%)	29,39,42	1.22	4 (13%)
25	6MZ	AY	37	25	18,25,26	1.25	3 (16%)	16,36,39	0.88	0
25	4SU	AY	8	25	18,21,22	1.08	2 (11%)	26,30,33	0.83	2 (7%)
24	5MU	AX	54	24	19,22,23	0.92	2 (10%)	28,32,35	1.13	2 (7%)
25	7MG	AY	46	25	22,26,27	2.05	3 (13%)	29,39,42	1.22	4 (13%)
24	QUO	AX	34	22,24	29,35,36	1.32	4 (13%)	31,52,55	1.47	7 (22%)
25	CM0	AY	34	25	22,26,27	0.96	1 (4%)	28,37,40	1.27	3 (10%)
24	PSU	AX	65	24	18,21,22	1.26	3 (16%)	22,30,33	1.55	5 (22%)

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
23	T6A	AW	37	23	-	0/19/41/42	0/3/3/3
23	PSU	AW	39	23	-	0/7/25/26	0/2/2/2
24	4SU	AX	8	24	-	0/7/25/26	0/2/2/2
23	PSU	AW	55	23	-	0/7/25/26	0/2/2/2
25	PSU	AY	55	25	-	0/7/25/26	0/2/2/2
23	5MU	AW	54	23	-	0/7/25/26	0/2/2/2
23	3AU	AW	47	23	-	6/16/34/35	0/2/2/2
24	2MA	AX	37	24	-	0/3/25/26	0/3/3/3
23	4SU	AW	8	23	-	0/7/25/26	0/2/2/2
25	5MU	AY	54	25	-	2/7/25/26	0/2/2/2
24	PSU	AX	55	24	-	0/7/25/26	0/2/2/2
23	U8U	AW	34	22,23	-	2/9/28/29	0/2/2/2
23	7MG	AW	46	23	-	3/7/37/38	0/3/3/3
24	7MG	AX	46	24	-	0/7/37/38	0/3/3/3
25	6MZ	AY	37	25	-	1/5/27/28	0/3/3/3
25	4SU	AY	8	25	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
24	5MU	AX	54	24	-	0/7/25/26	0/2/2/2
25	7MG	AY	46	25	-	2/7/37/38	0/3/3/3
24	QUO	AX	34	22,24	-	2/6/43/44	0/4/4/4
25	CM0	AY	34	25	-	3/12/30/31	0/2/2/2
24	PSU	AX	65	24	-	4/7/25/26	0/2/2/2

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	AX	46	7MG	C8-N9	6.25	1.49	1.46
25	AY	46	7MG	C8-N9	6.23	1.49	1.46
23	AW	46	7MG	C8-N9	6.03	1.49	1.46
25	AY	46	7MG	C5-N7	5.84	1.42	1.35
24	AX	46	7MG	C5-N7	5.74	1.42	1.35

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
23	AW	55	PSU	C6-C5-C4	5.07	121.74	118.20
24	AX	55	PSU	C6-C5-C4	4.99	121.69	118.20
23	AW	39	PSU	C6-C5-C4	4.96	121.67	118.20
25	AY	55	PSU	C6-C5-C4	4.94	121.65	118.20
23	AW	37	T6A	C12-N11-C10	-4.44	114.53	121.94

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	AW	34	U8U	C3'-C4'-C5'-O5'
23	AW	34	U8U	O4'-C4'-C5'-O5'
23	AW	46	7MG	C3'-C4'-C5'-O5'
23	AW	47	3AU	C10-C11-C12-N40
24	AX	34	QUO	C13-C12-N11-C10

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	AY	55	PSU	1	0
23	AW	34	U8U	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	AY	34	CM0	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	$\#\|Z\| > 2$
59	ERY	BA	9000	-	53,53,53	1.16	5 (9%)	82,82,82	1.69	23 (28%)
58	LYS	AW	101	23	7,8,9	0.81	0	3,8,10	0.76	0

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
59	ERY	BA	9000	-	-	13/72/107/107	0/3/3/3
58	LYS	AW	101	23	-	1/6/7/9	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	BA	9000	ERY	O13-C12	-2.82	1.39	1.44
59	BA	9000	ERY	O9-C26	-2.77	1.39	1.44
59	BA	9000	ERY	O10-C6	-2.64	1.40	1.44
59	BA	9000	ERY	O2-C13	-2.53	1.42	1.46
59	BA	9000	ERY	C23-C24	2.09	1.58	1.53

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
59	BA	9000	ERY	C36-C13-C12	-3.91	107.79	115.20
59	BA	9000	ERY	C34-C10-C11	-3.82	109.62	114.38
59	BA	9000	ERY	C12-C11-C10	-3.39	112.18	116.43
59	BA	9000	ERY	O13-C12-C13	3.29	112.56	107.28
59	BA	9000	ERY	O2-C1-C2	3.26	118.70	111.56

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
58	AW	101	LYS	O-C-CA-CB
59	BA	9000	ERY	C34-C10-C11-C12
59	BA	9000	ERY	O13-C12-C13-O2
59	BA	9000	ERY	O13-C12-C13-C36
59	BA	9000	ERY	C35-C12-C13-O2

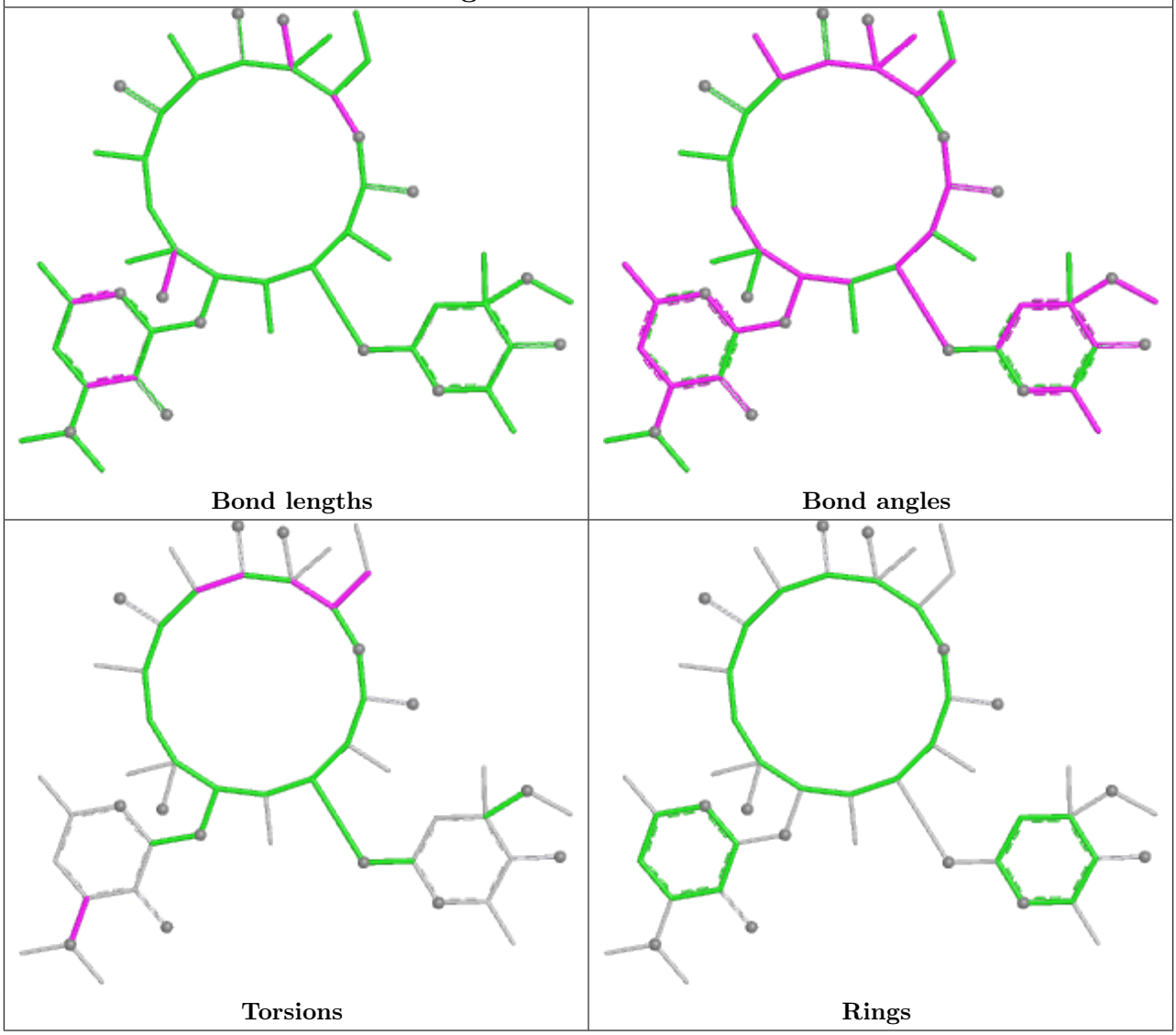
There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	BA	9000	ERY	12	0
58	AW	101	LYS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ERY BA 9000



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
26	BA	1
23	AW	1
25	AY	1
1	AA	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BA	885:C	O3'	892:A	P	13.72
1	AW	15:G	O3'	18:G	P	9.77
1	AY	15:G	O3'	18:G	P	6.82
1	AA	99:C	O3'	100:G	P	4.17

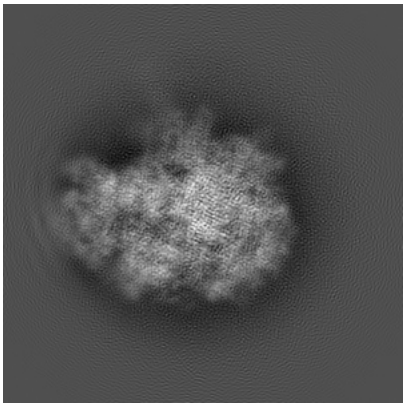
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-8175. These allow visual inspection of the internal detail of the map and identification of artifacts.

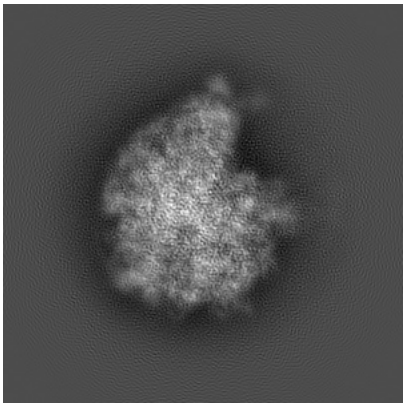
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

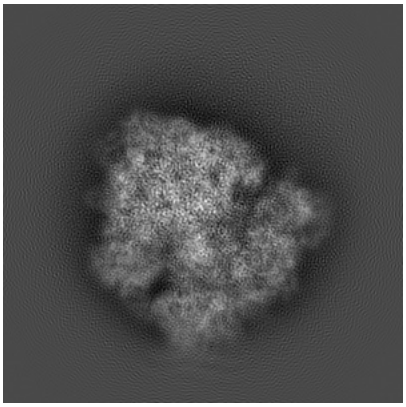
6.1.1 Primary map



X



Y

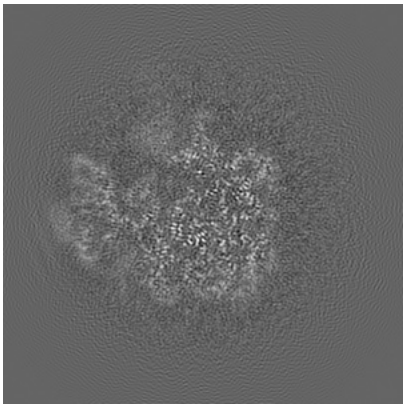


Z

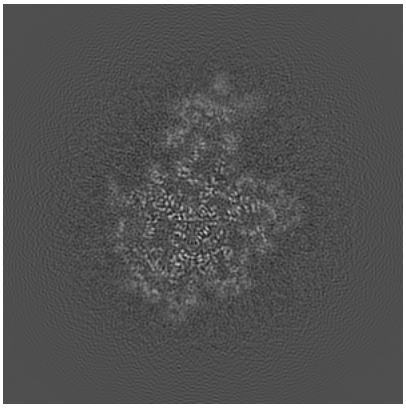
The images above show the map projected in three orthogonal directions.

6.2 Central slices

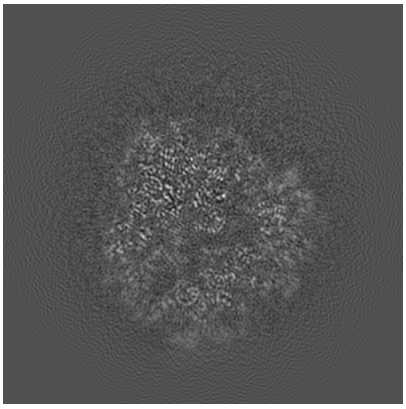
6.2.1 Primary map



X Index: 184



Y Index: 184

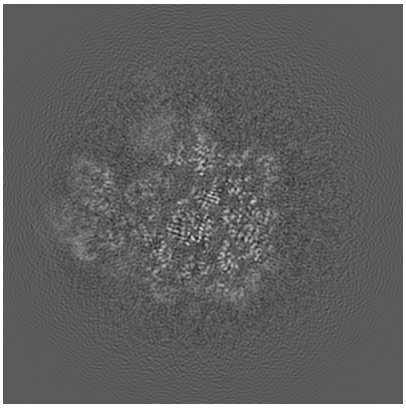


Z Index: 184

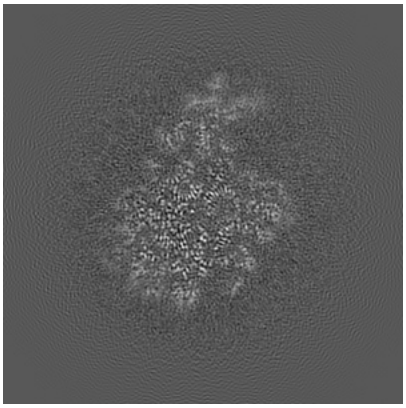
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

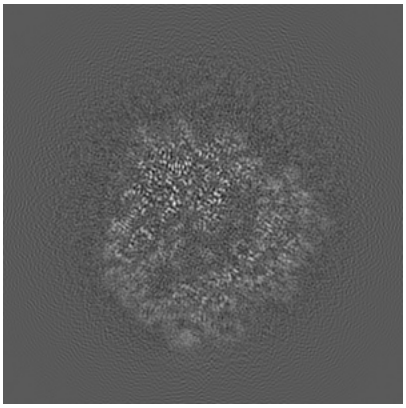
6.3.1 Primary map



X Index: 181



Y Index: 177



Z Index: 186

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.00194. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

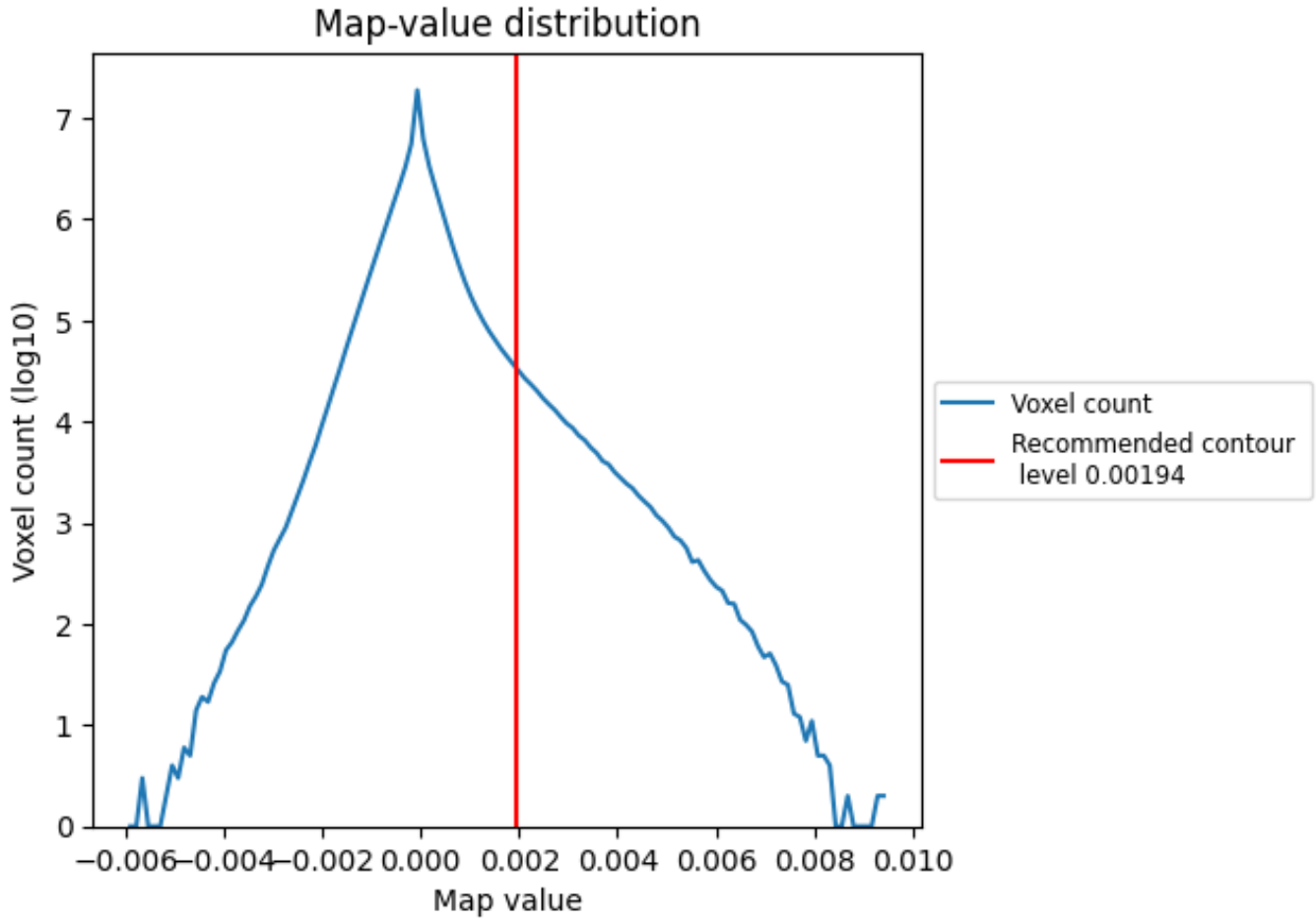
6.5 Mask visualisation (i)

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

7 Map analysis

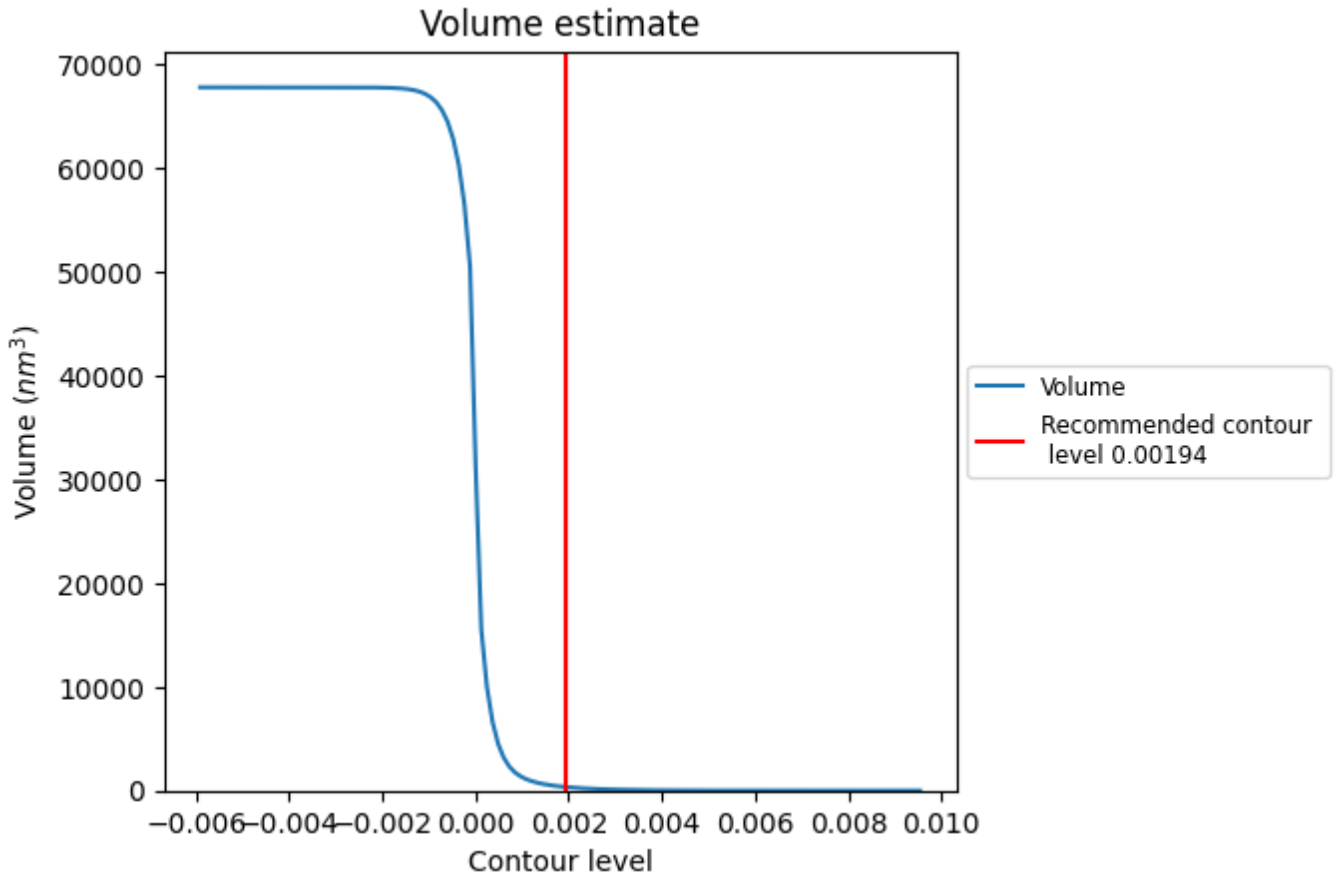
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

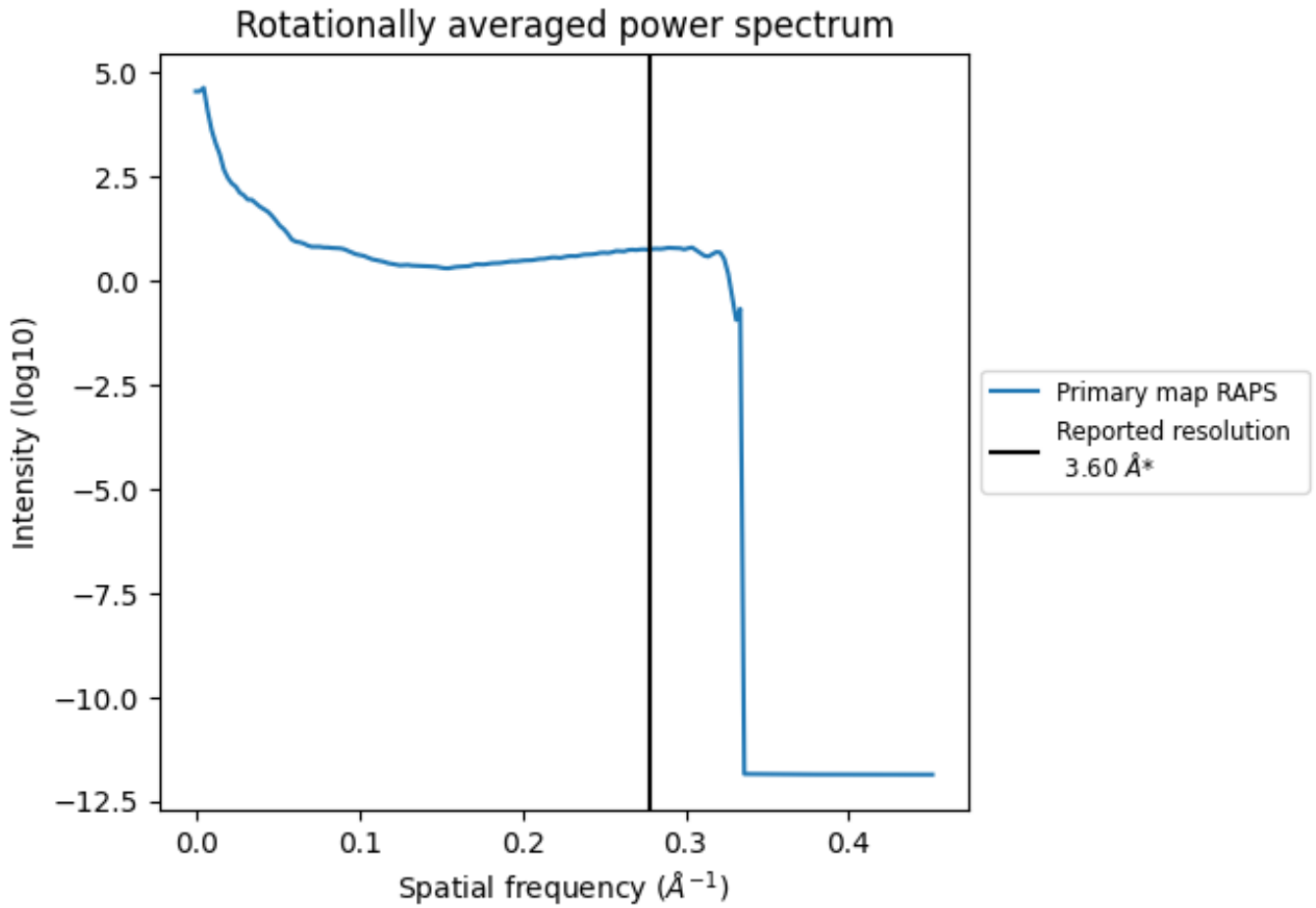
7.2 Volume estimate (i)



The volume at the recommended contour level is 337 nm^3; this corresponds to an approximate mass of 305 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

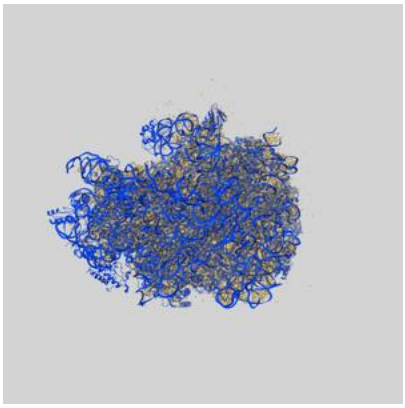
8 Fourier-Shell correlation

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

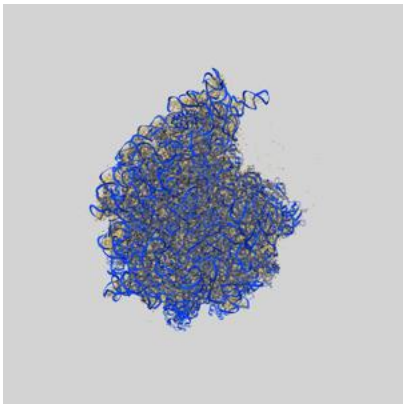
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-8175 and PDB model 5JTE. Per-residue inclusion information can be found in section 3 on page 15.

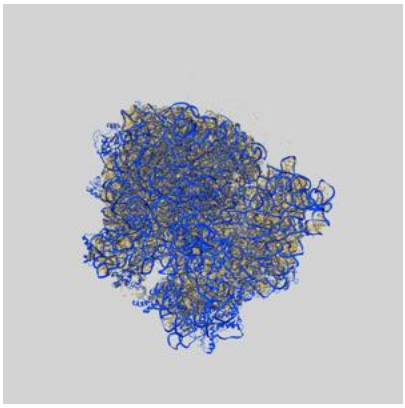
9.1 Map-model overlay



X



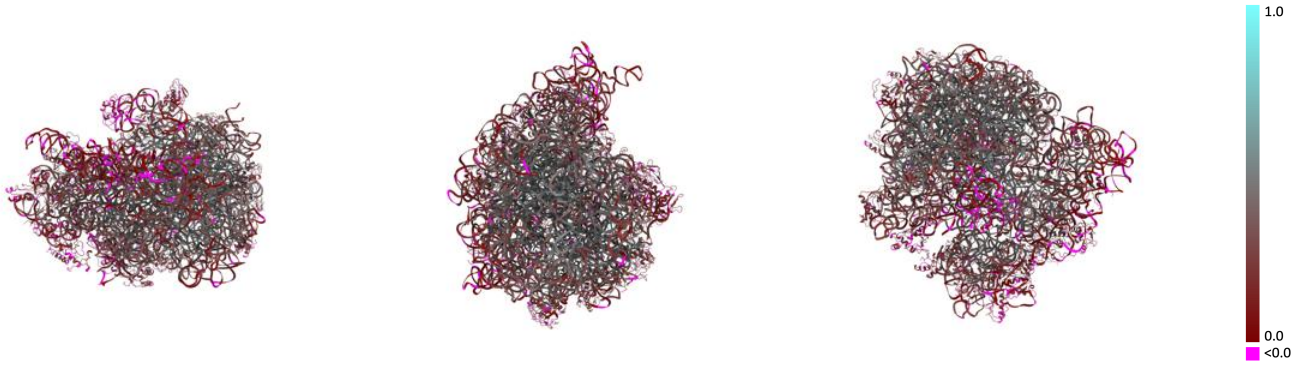
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00194 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.

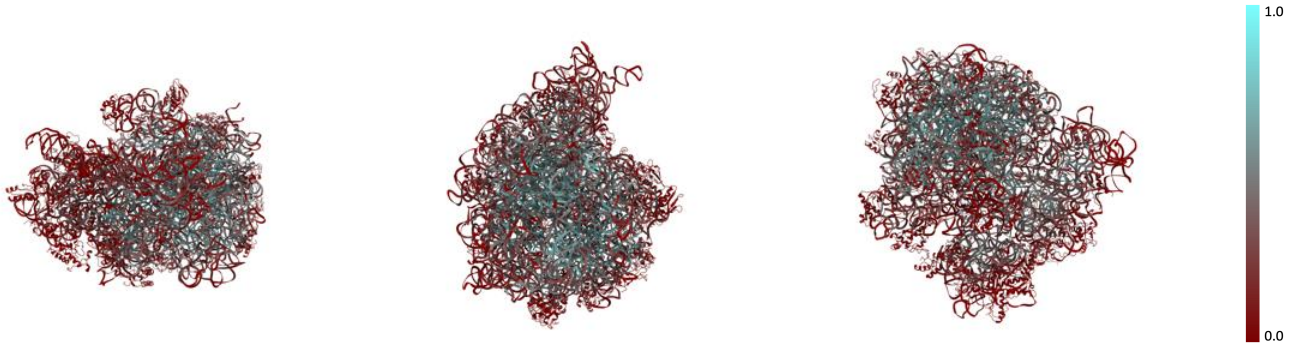
9.2 Q-score mapped to coordinate model



X Y Z

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

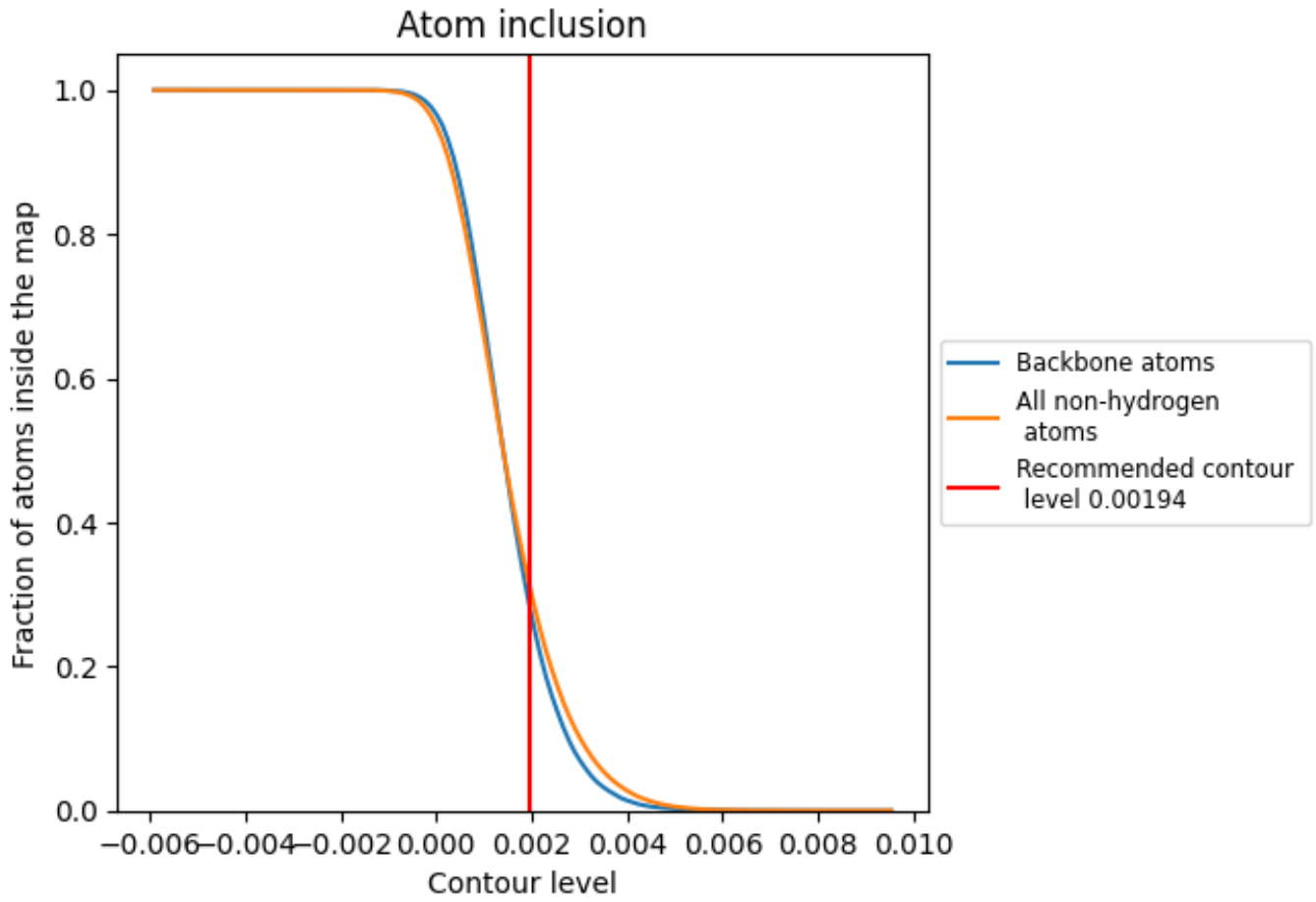
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00194).

9.4 Atom inclusion (i)



At the recommended contour level, 29% of all backbone atoms, 32% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00194) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3164	0.3150
AA	0.3038	0.2960
AB	0.0042	0.1140
AC	0.0526	0.2080
AD	0.0503	0.1960
AE	0.1163	0.2570
AF	0.0741	0.1890
AG	0.0358	0.2010
AH	0.1094	0.2610
AI	0.0225	0.1760
AJ	0.0250	0.1550
AK	0.1043	0.2310
AL	0.1976	0.2820
AM	0.0611	0.1920
AN	0.0834	0.2330
AO	0.1866	0.3100
AP	0.0813	0.1500
AQ	0.1551	0.2000
AR	0.1376	0.2600
AS	0.0725	0.2110
AT	0.1462	0.2250
AU	0.0222	0.1370
AV	0.4450	0.4210
AW	0.1273	0.1380
AX	0.2446	0.3190
AY	0.0807	0.1960
B0	0.2734	0.3400
B1	0.1022	0.3010
B2	0.3972	0.3760
B3	0.3279	0.3790
B4	0.2740	0.3260
B5	0.2361	0.3650
BA	0.4516	0.3820
BB	0.2720	0.2950
BC	0.3219	0.3360

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Chain	Atom inclusion	Q-score
BD	0.2711	0.3410
BE	0.1500	0.2550
BF	0.0503	0.1400
BG	0.0817	0.1870
BH	0.0112	0.0990
BI	0.0010	0.0320
BJ	0.2382	0.3250
BK	0.2662	0.3370
BL	0.2087	0.2950
BM	0.2697	0.3220
BN	0.3286	0.3430
BO	0.0579	0.2200
BP	0.2117	0.2850
BQ	0.3722	0.3620
BR	0.1819	0.2870
BS	0.2416	0.3220
BT	0.1537	0.2370
BU	0.0847	0.2060
BV	0.1558	0.2680
BW	0.2847	0.3480
BX	0.2263	0.3140
BY	0.1026	0.1930
BZ	0.2128	0.3060