wwPDB EM Validation Summary Report (i)

Apr 29, 2024 – 06:38 am BST

PDB ID	:	4V5H
EMDB ID	:	EMD-1657
Title	:	E.Coli 70s Ribosome Stalled During Translation Of Tnac Leader Peptide.
Authors	:	Seidelt, B.; Innis, C.A.; Wilson, D.N.; Gartmann, M.; Armache, J.; Villa, E.; Trabuco, L.G.; Becker, T.; Mielke, T.; Schulten, K.; Steitz, T.A.; Beckmann, R.
Deposited on	:	2009-10-26
Resolution	:	5.80 Å(reported)
Based on initial models	:	3FIH, 3FIK

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:

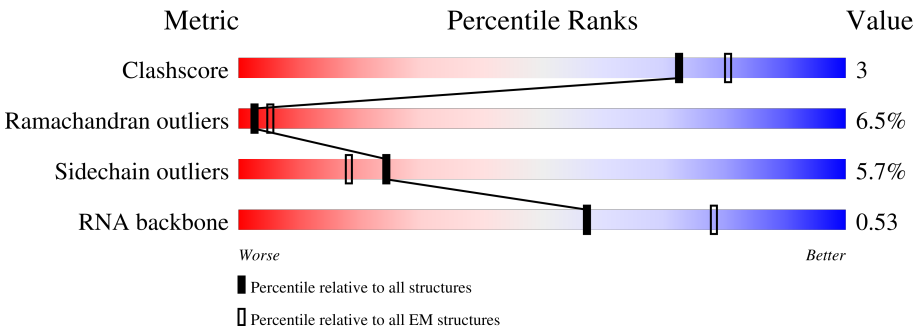
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 5.80 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	1530	35% 47% 18%
2	AB	218	54% 68% 28%
3	AC	206	37% 65% 25% 9%
4	AD	205	43% 67% 24% 8%
5	AE	150	29% 65% 28% 7%
6	AF	100	21% 65% 28% 6%
7	AG	150	39% 67% 25% 7%

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Mol	Chain	Length	Quality of chain
8	AH	129	29% 71% 26%
9	AI	127	38% 59% 33% 7%
10	AJ	98	65% 54% 42%
11	AK	117	30% 70% 26%
12	AL	123	37% 66% 25% 8%
13	AM	113	28% 60% 28% 9%
14	AN	96	27% 64% 27% 9%
15	AO	88	28% 67% 25% 7%
16	AP	80	39% 64% 32%
17	AQ	80	25% 65% 26% 8%
18	AR	55	20% 64% 27% 9%
19	AS	79	25% 59% 30% 10%
20	AT	85	31% 73% 22%
21	AU	51	57% 65% 27% 8%
22	AV	77	26% 58% 29% 13%
23	AX	11	64% 9% 18% 27% 45%
24	AZ	20	55% 80% 20%
25	B0	77	26% 70% 25% 5%
26	B1	63	25% 65% 32%
27	B2	58	22% 76% 24%
28	B3	56	32% 66% 25% 7%
29	B4	50	26% 66% 30%
30	B5	234	99% 77% 20%
31	B6	46	37% 59% 20% 20%
32	B7	64	23% 59% 39%

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Mol	Chain	Length	Quality of chain
33	B8	38	21% 76% 24%
34	BA	117	42% 43% 14%
35	BB	2903	38% 45% 17%
36	BC	271	27% 68% 25% 6%
37	BD	209	20% 67% 23% 8%
38	BE	201	39% 66% 27% 6%
39	BF	178	22% 63% 26% 10%
40	BG	176	14% 72% 22% 6%
41	BH	149	71% 74% 21% 5%
42	BI	141	75% 35% 59% 6%
43	BJ	142	18% 69% 21% 8%
44	BK	121	33% 64% 26% 8%
45	BL	143	30% 67% 29%
46	BM	136	24% 68% 29%
47	BN	120	26% 67% 27% 7%
48	BO	116	20% 74% 22%
49	BP	114	27% 68% 25% 7%
50	BQ	117	22% 60% 31% 7%
51	BR	103	17% 59% 32% 7%
52	BS	110	25% 61% 27% 12%
53	BT	93	37% 56% 39% 5%
54	BU	102	19% 62% 26% 6%
55	BW	94	16% 61% 31% 7%
56	BY	79	32% 63% 27% 6%

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 145960 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	1530	32831	14642	6024	10635	1530	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
			Total	C	N	O	S		
7	AG	150	1174	730	226	214	4	0	0

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AM	113	876	541	177	155	3	0	0

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AO	88	716	440	146	129	1	0	0

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AP	80	638	400	126	111	1	0	0

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S21.

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

- Molecule 22 is a RNA chain called P-SITE TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	AV	77	1649	733	297	542	77	0	0

- Molecule 23 is a RNA chain called MRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
23	AX	11	236	106	46	73	11	0	0

- Molecule 24 is a protein called POLY-ALA NASCENT CHAIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	AZ	20	100	60	20	20	0	0

- Molecule 25 is a protein called 50S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	B0	77	625	388	129	106	2	0	0

- Molecule 26 is a protein called 50S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	B1	63	509	313	99	95	2	0	0

- Molecule 27 is a protein called 50S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	B2	58	449	281	87	79	2	0	0

- Molecule 28 is a protein called 50S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	B3	56	444	269	94	80	1	0	0

- Molecule 29 is a protein called 50S RIBOSOMAL PROTEIN L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	B4	50	409	263	75	71	0	0

- Molecule 30 is a protein called 50S RIBOSOMAL PROTEIN L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	B5	234	1733	1081	315	330	7	0	0

- Molecule 31 is a protein called 50S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	B6	46	377	228	90	57	2	0	0

- Molecule 32 is a protein called 50S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	B7	64	504	323	105	74	2	0	0

- Molecule 33 is a protein called 50S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	B8	38	302	185	65	48	4	0	0

- Molecule 34 is a RNA chain called 5S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	BA	115	2464	1097	451	801	115	0	0

- Molecule 35 is a RNA chain called 23S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	BB	2903	62321	27801	11467	20150	2903	0	0

- Molecule 36 is a protein called 50S RIBOSOMAL PROTEIN L2.

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

- Molecule 37 is a protein called 50S RIBOSOMAL PROTEIN L3.

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

- Molecule 38 is a protein called 50S RIBOSOMAL PROTEIN L4.

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

- Molecule 39 is a protein called 50S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	BF	178	1420	905	251	258	6	0	0

- Molecule 40 is a protein called 50S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BG	175	1316	827	242	245	2	0	0

- Molecule 41 is a protein called 50S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	BH	149	1111	699	197	214	1	0	0

- Molecule 42 is a protein called 50S RIBOSOMAL PROTEIN L11.

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

- Molecule 43 is a protein called 50S RIBOSOMAL PROTEIN L13.

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

- Molecule 44 is a protein called 50S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BK	121	930	582	179	163	6	0	0

- Molecule 45 is a protein called 50S RIBOSOMAL PROTEIN L15.

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

- Molecule 46 is a protein called 50S RIBOSOMAL PROTEIN L16.

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

- Molecule 47 is a protein called 50S RIBOSOMAL PROTEIN L17.

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

- Molecule 48 is a protein called 50S RIBOSOMAL PROTEIN L18.

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

- Molecule 49 is a protein called 50S RIBOSOMAL PROTEIN L19.

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

- Molecule 50 is a protein called 50S RIBOSOMAL PROTEIN L20.

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

- Molecule 51 is a protein called 50S RIBOSOMAL PROTEIN L21.

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

- Molecule 52 is a protein called 50S RIBOSOMAL PROTEIN L22.

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

- Molecule 53 is a protein called 50S RIBOSOMAL PROTEIN L23.

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

- Molecule 54 is a protein called 50S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
54	BU	99	755	479	140	136	0	0

- Molecule 55 is a protein called 50S RIBOSOMAL PROTEIN L25.

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

- Molecule 56 is a protein called 50S RIBOSOMAL PROTEIN L27.

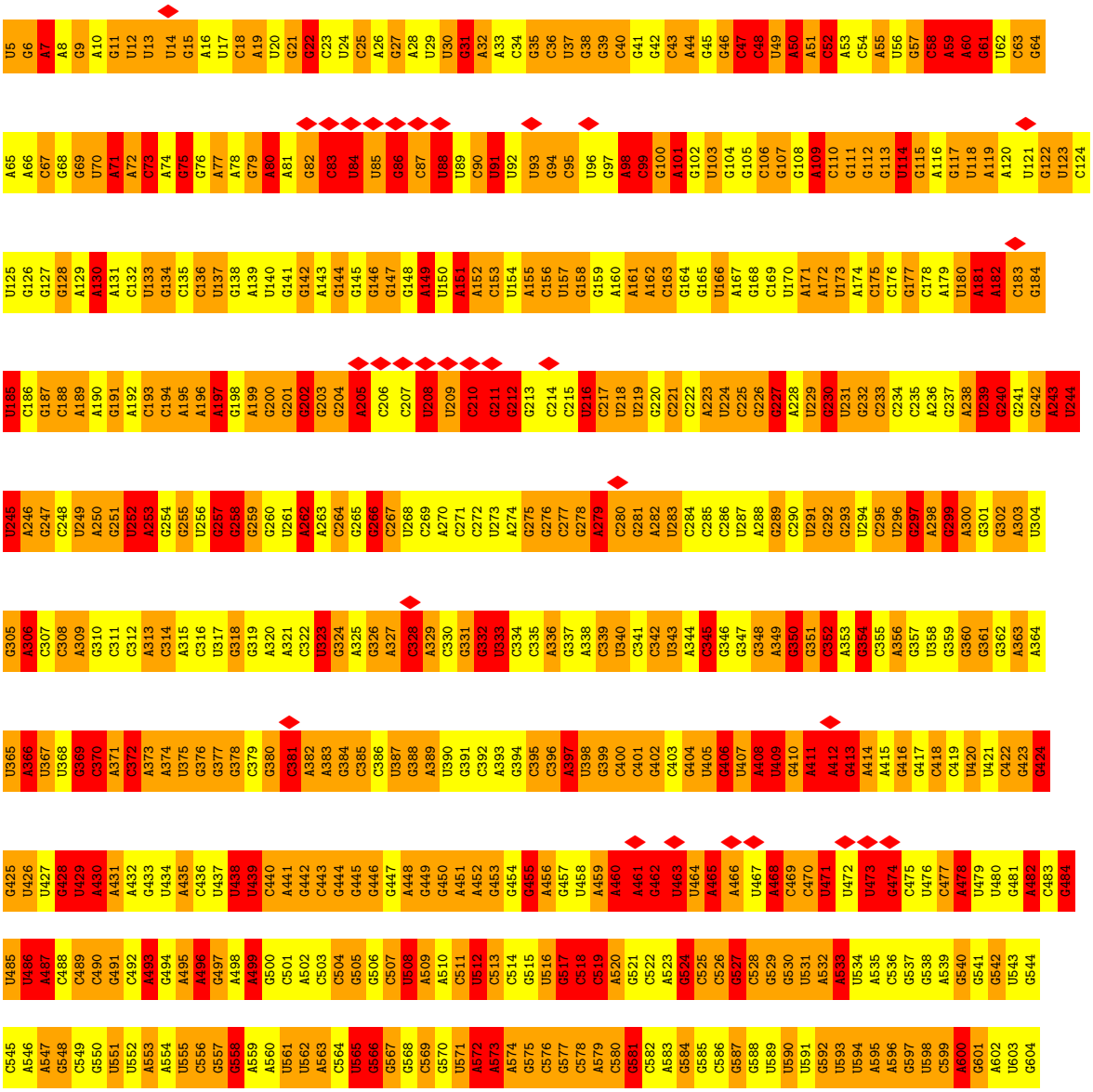
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	BY	79	596	367	120	108	1	0	0

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: 35% 47% 18%



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 G666 G667 G668 G669 G670 G671 U672 A673 G674 A675 A676 U677 U678 C679 C680 A681 G682 G683 U684 G685 U686 A687 G688 C689 G690 G691 U692 G693 A694 A695 A696 U697 G698 C699 G700 U701 A702 G703 A704 G705 A706 U707 C708 U709 G710 G711 A712 G713 G714 A715 A716 U717 A718 C719 C720 G721 G722 U723 G724

G725 C726 G727 A728 A729 G730 G731 U732 G733 G734 C735 C736 C737 C738 C739 U740 G741 G742 A743 C744 G745 A746 A747 G748 A749 C750 U751 G752 A753 C754 G755 C756 U757 C758 A759 G760 G761 U762 G763 C764 G765 A766 A767 A768 G769 C770 G771 U772 G773 G774 A775 G776 A777 G778 C779 A780 A781 A782 C783 A784

G785 G786 A787 U788 U789 A790 G791 A792 U793 A794 C795 C796 C797 U798 C799 G800 U801 A802 G803 U804 C805 C806 A807 C808 G809 C810 C811 G812 U813 A814 A815 A816 G817 G818 A819 U820 G821 U822 C823 G824 A825 C826 U827 U828 G829 G830 A831 G832 G833 U834 U835 G836 U837 G838 C839 C840 G841 U842 U843 G844

A845 G846 G847 C848 G849 U850 G851 G852 C853 U854 U855 C856 C857 G858 G859 A860 G861 C862 U863 A864 A865 C866 G867 C868 G869 U870 U871 A872 A873 G874 U875 C876 G877 A878 C879 C880 G881 C882 C883 U884 G885 G886 G887 G888 A889 G890 U891 A892 C893 G894 G895 C896 U897 G898 C899 A900 A901 G902 G903 U904

U905 A906 A907 A908 A909 C910 U911 C912 A913 A914 A915 U916 G917 A918 A919 U920 U921 G922 A923 C924 G925 G926 G927 G928 G929 C930 C931 G932 G933 C934 A935 C936 A937 A938 G939 C940 G941 G942 U943 G944 G945 A946 G947 C948 A949 U950 G951 U952 G953 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 C980 U981 U982 A983 C984 C985 U986 G987 G988 U989 C990 U991 U992 G993 A994 C995 A996 U997 C998 C999 A1000 C1001 G1002 G1003 A1004 A1005 C1006 U1007 U1008 U1009 U1010 C1011 A1012 G1013 A1014 G1015 A1016 U1017 G1018 A1019 G1020 A1021 A1022 U1023 G1024

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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 G1175 A1176 G1177 G1178 A1179 A1180 G1181 U1182 U1183 G1184 G1185 G1186 G1187 A1188 U1189 G1190 A1191 C1192 G1193 U1194 C1195 A1196 A1197 G1198 U1199 C1200 A1201 U1202 C1203 A1204

U1205 G1206 G1207 C1208 C1209 C1210 U1211 U1212 A1213 C1214 G1215 A1216 C1217 C1218 A1219 G1220 G1221 G1222 C1223 U1224 A1225 C1226 A1227 C1228 A1229 C1230 G1231 U1232 G1233 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 C1270 A1271 G1272 C1273 A1274 A1275 G1276 C1277 G1278 G1279 A1280 C1281 C1282 U1283 C1284 A1285 U1286 A1287 A1288 A1289 U1290 U1291 G1292 G1293 G1294 U1295 C1296 G1297 U1298 A1299 G1300 U1301 C1302 C1303 G1304 A1305 A1306 U1307 U1308 G1309 G1310 A1311 A1312 U1313 C1314 U1315 G1316 C1317 A1318 A1319 C1320 U1321 C1322 G1323 A1324

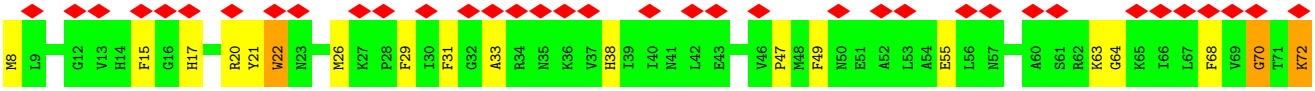
C1325 U1326 C1327 C1328 A1329 U1330 G1331 A1332 A1333 G1334 U1335 C1336 G1337 G1338 A1339 A1340 U1341 C1342 G1343 C1344 U1345 A1346 G1347 U1348 A1349 A1350 U1351 C1352 G1353 U1354 G1355 G1356 A1357 U1358 C1359 A1360 G1361 A1362 A1363 U1364 G1365 C1366 C1367 A1368 C1369 G1370 G1371 U1372 G1373 A1374 A1375 U1376 A1377 C1378 G1379 U1380 U1381 C1382 C1383 C1384

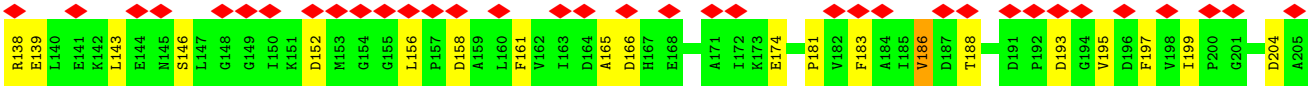
G1385 G1386 G1387 C1388 C1389 U1390 U1391 G1392 U1393 A1394 C1395 A1396 C1397 A1398 G1399 C1400 G1401 C1402 C1403 C1404 G1405 U1406 C1407 A1408 C1409 A1410 C1411 C1412 A1413 U1414 G1415 G1416 G1417 A1418 G1419 U1420 G1421 G1422 G1423 U1424 U1425 G1426 C1427 A1428 A1429 A1430 A1431 G1432 A1433 A1434 G1435 U1436 A1437 G1438 G1439 U1440 A1441 G1442 C1443 U1444

U1445 A1446 A1447 C1448 C1449 U1450 U1451 C1452 G1453 G1454 G1455 A1456 G1457 G1458 G1459 C1460 G1461 C1462 U1463 U1464 A1465 C1466 C1467 A1468 C1469 U1470 U1471 U1472 G1473 U1474 G1475 A1476 U1477 U1478 C1479 A1480 U1481 G1482 A1483 C1484 U1485 G1486 G1487 G1488 G1489 U1490 G1491 A1492 A1493 G1494 U1495 C1496 G1497 U1498 A1499 A1500 C1501 A1502 A1503 G1504

- Molecule 2: 30S RIBOSOMAL PROTEIN S2

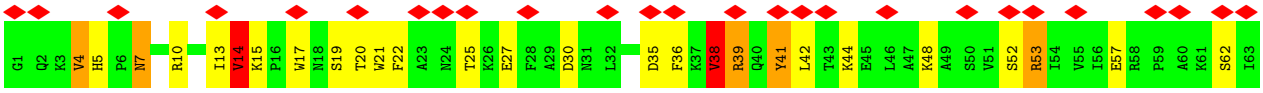
Chain AB:

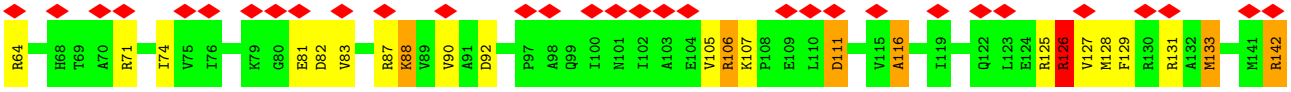


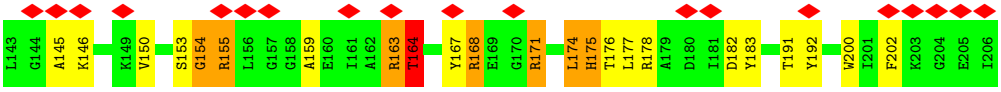


- Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain AC:

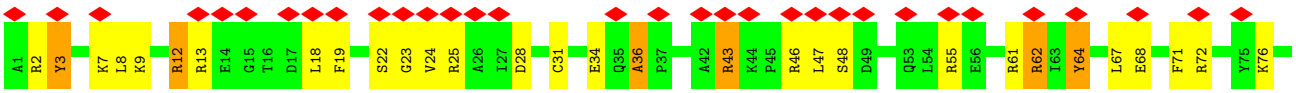


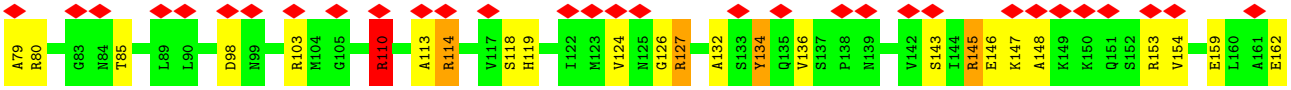


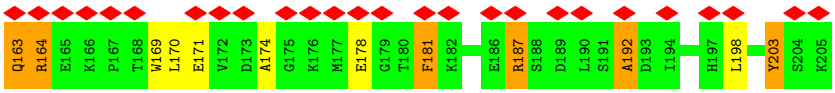


- Molecule 4: 30S RIBOSOMAL PROTEIN S4

Chain AD:

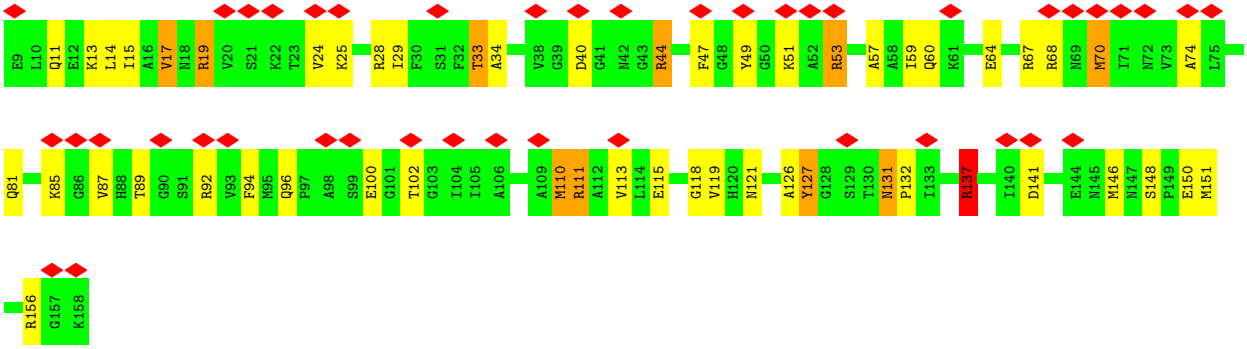






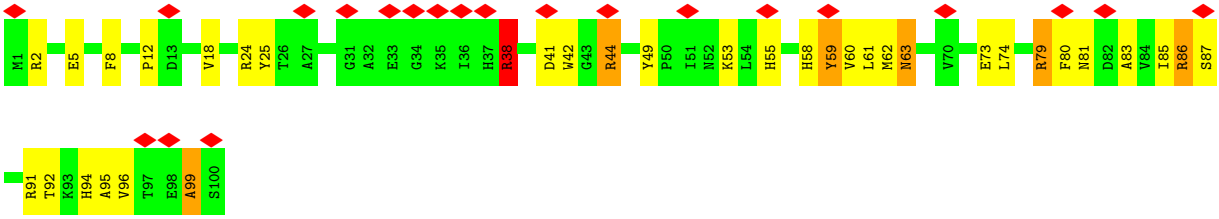
• Molecule 5: 30S RIBOSOMAL PROTEIN S5

Chain AE:



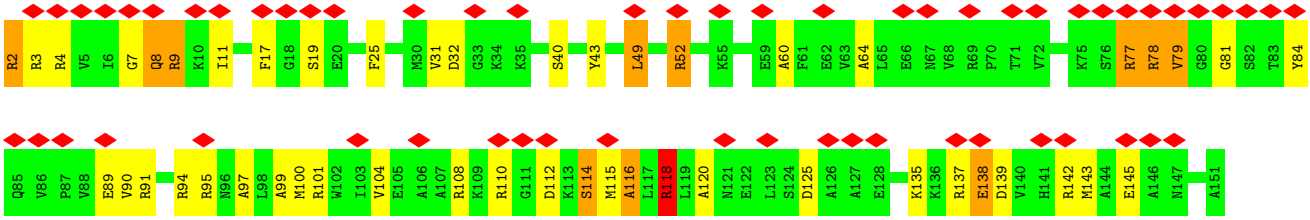
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain AF:



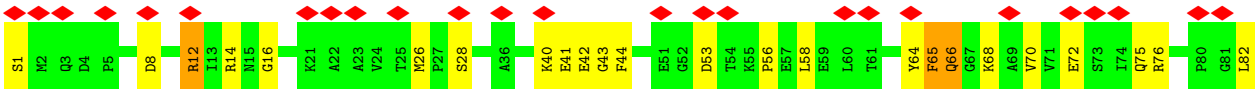
• Molecule 7: 30S RIBOSOMAL PROTEIN S7

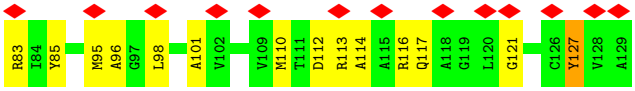
Chain AG:



• Molecule 8: 30S RIBOSOMAL PROTEIN S8

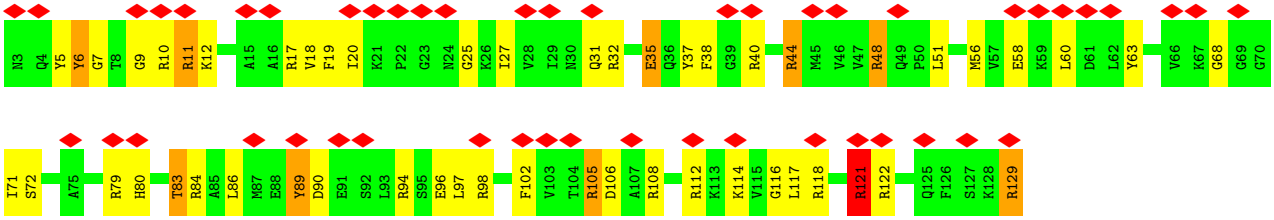
Chain AH:





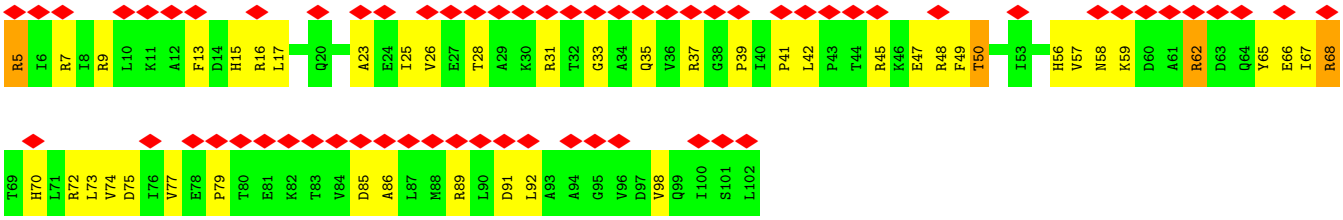
- Molecule 9: 30S RIBOSOMAL PROTEIN S9

Chain AI:



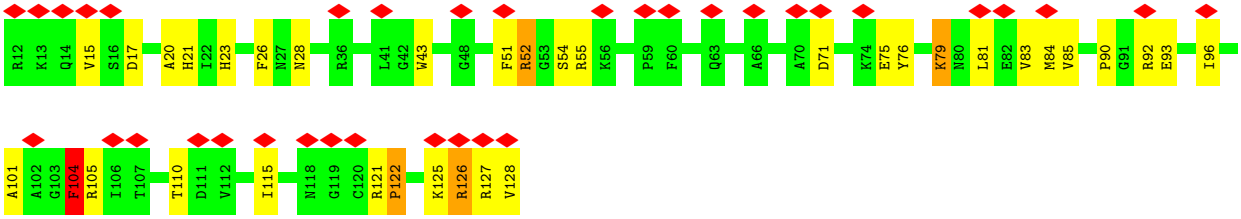
- Molecule 10: 30S RIBOSOMAL PROTEIN S10

Chain AJ:



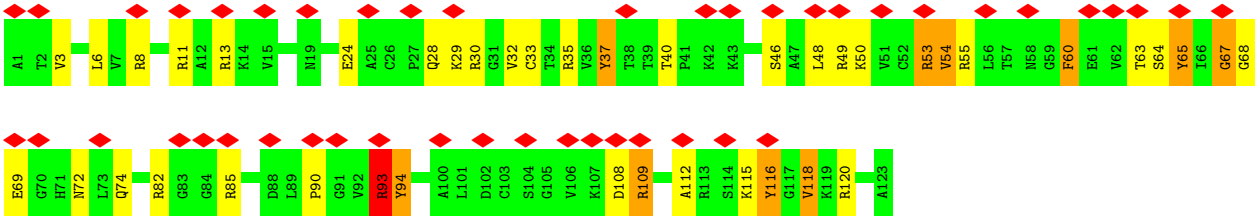
- Molecule 11: 30S RIBOSOMAL PROTEIN S11

Chain AK:



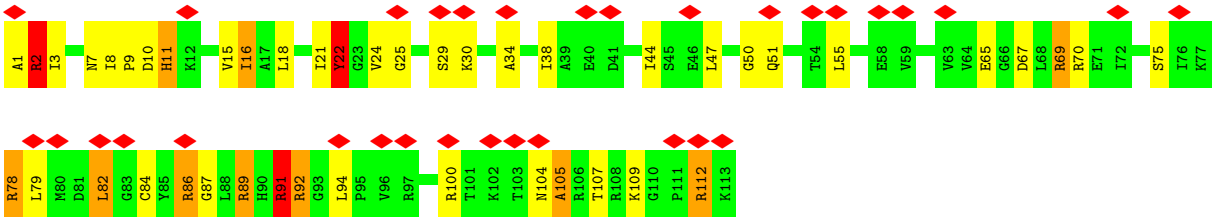
- Molecule 12: 30S RIBOSOMAL PROTEIN S12

Chain AL:



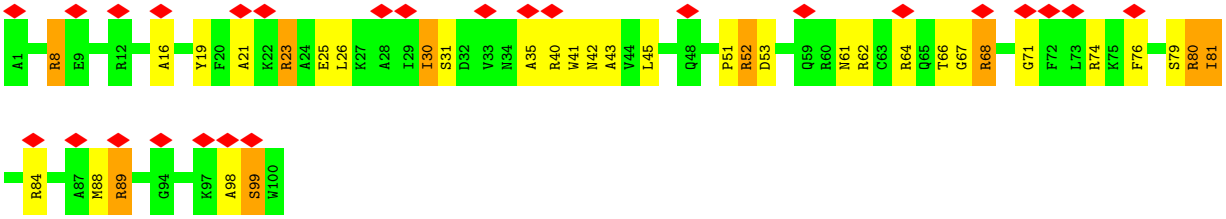
- Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain AM:



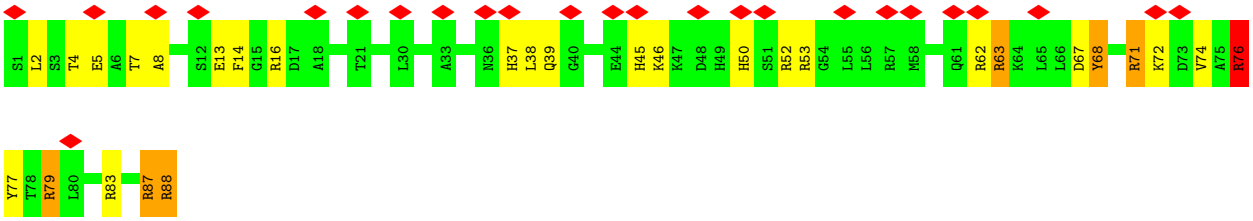
- Molecule 14: 30S RIBOSOMAL PROTEIN S14

Chain AN:



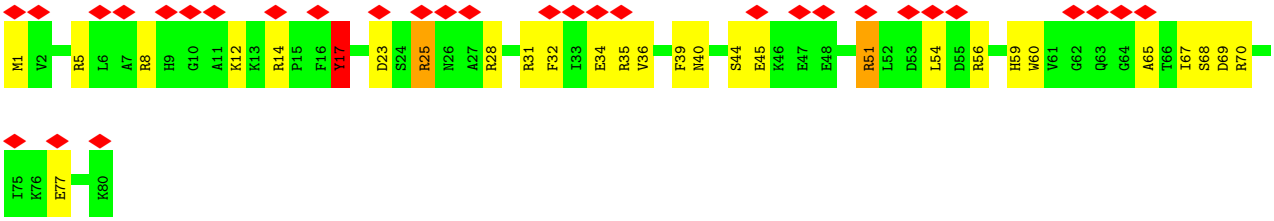
- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain AO:



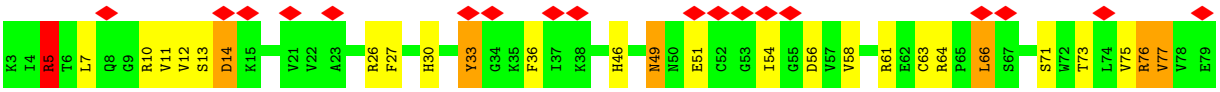
- Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain AP:



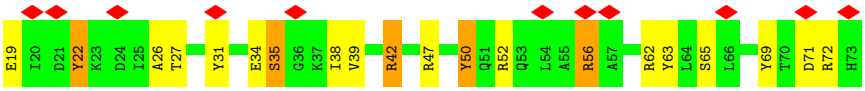
- Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain AQ:



• Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain AR:

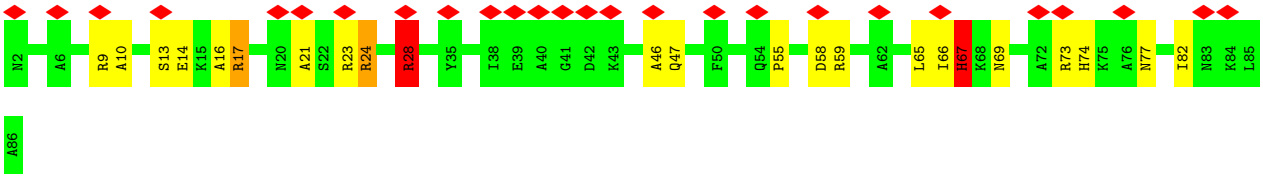


• Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain AS:

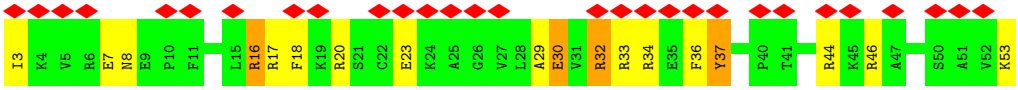
• Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain AT:



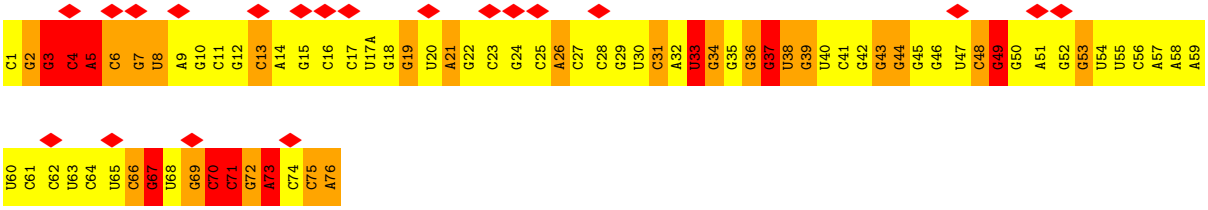
• Molecule 21: 30S RIBOSOMAL PROTEIN S21

Chain AU:



• Molecule 22: P-SITE TRNA

Chain AV:



• Molecule 23: MRNA

Chain AX: 64% (9% 18% 27% 45%)

A12 A13 A14 A15 C16 C17 C18 A19 G20 U21 A22

- Molecule 24: POLY-ALA NASCENT CHAIN

Chain AZ: 55% (80% 20%)

A5 A6 A7 A11 A12 A13 A14 A15 A16 A17 A18 A23 A24

- Molecule 25: 50S RIBOSOMAL PROTEIN L28

Chain B0: 26% (70% 25% 5%)

S1 R2 V3 C4 Q5 V6 R10 G14 N15 N16 R17 K25 R26 R27 F28 L32 H33 S34 H35 R36 E40 K43 R44 F45 V46 T47 L48 R49 V50 S51 A52 R56 D59 K60 K61 G62 I63 D64 L67 A68 R71 A72 R73 G74 Y77

- Molecule 26: 50S RIBOSOMAL PROTEIN L29

Chain B1: 25% (65% 32% •)

M1 K2 E5 L6 R7 E8 K9 S10 V11 E12 N15 L18 L21 L22 R23 E24 Q25 F26 R29 L37 Q38 Q39 V46 R47 R48 D49 V50 A51 R52 T55 L56 L57 A61 G62 A63

- Molecule 27: 50S RIBOSOMAL PROTEIN L30

Chain B2: 22% (76% 24%)

A1 K2 T3 T9 R10 K18 L24 G27 L28 R29 R30 H33 T34 R37 R44 G45 M46 A49 V50 S51 F52 M53 V54 K55 V56 E57 E58

- Molecule 28: 50S RIBOSOMAL PROTEIN L32

Chain B3: 32% (66% 25% 7% •)

A1 V2 Q3 Q4 N5 K6 R9 S10 K11 R12 R15 R16 A20 L21 T22 A23 V24 T25 S26 L27 S28 V29 D30 E35 K36 R39 H40 H41 I42 T43 A44 D45 G46 Y47 Y48 R49 G50 R51 A55 K56

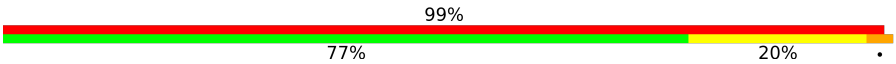
- Molecule 29: 50S RIBOSOMAL PROTEIN L33

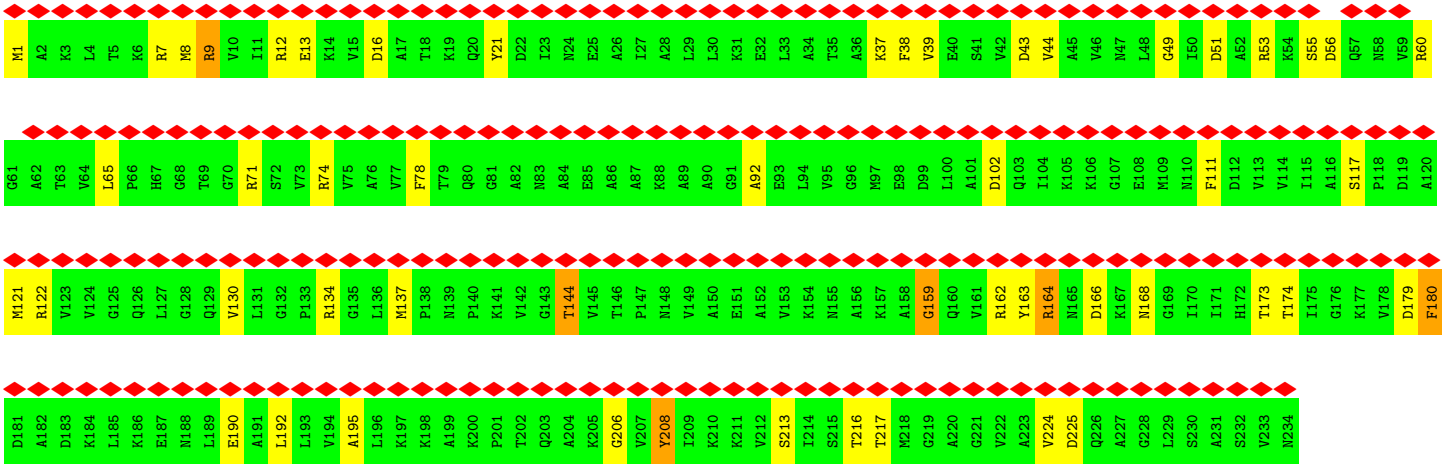
Chain B4: 26% (66% 30% •)

G3 I4 R5 E6 K7 I8 V11 S12 S13 A14 G15 T16 G17 H18 F19 Y20 R27 K32 L33 K37 F38 D39 V42 R43 Q44 H45 Y48 K49 E50 A51 K52

- Molecule 30: 50S RIBOSOMAL PROTEIN L1

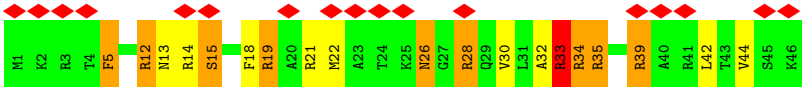
Chain B5:





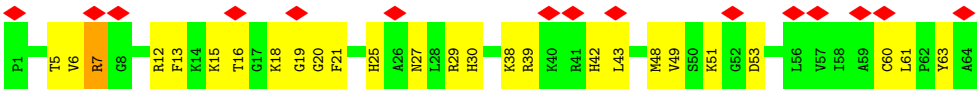
- Molecule 31: 50S RIBOSOMAL PROTEIN L34

Chain B6:



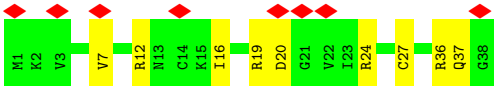
- Molecule 32: 50S RIBOSOMAL PROTEIN L35

Chain B7:



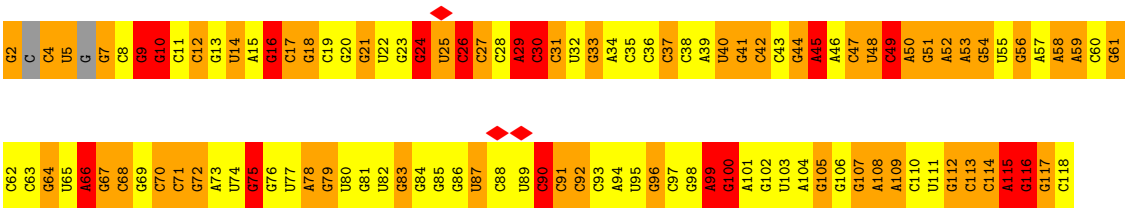
- Molecule 33: 50S RIBOSOMAL PROTEIN L36

Chain B8:



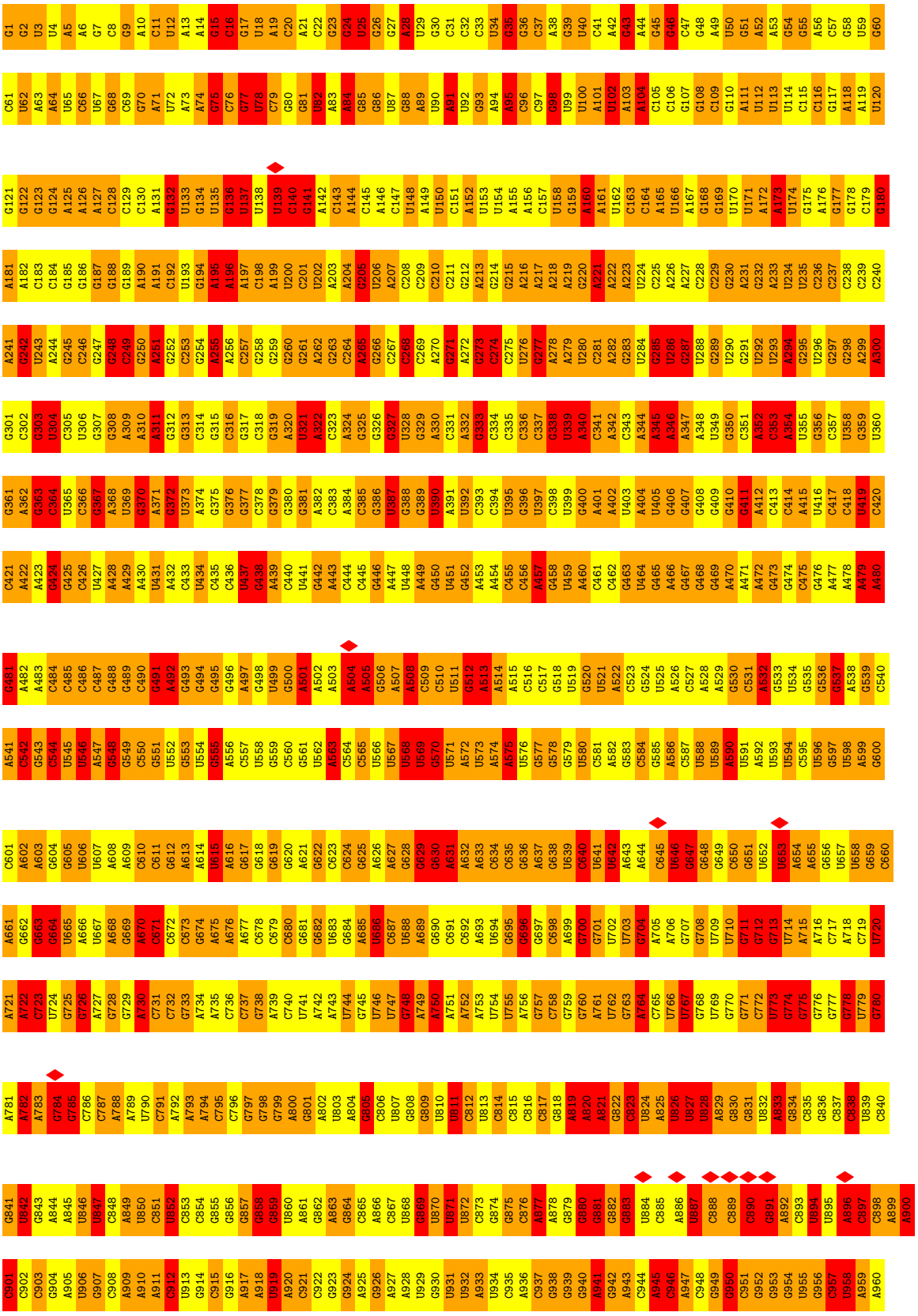
- Molecule 34: 5S RIBOSOMAL RNA

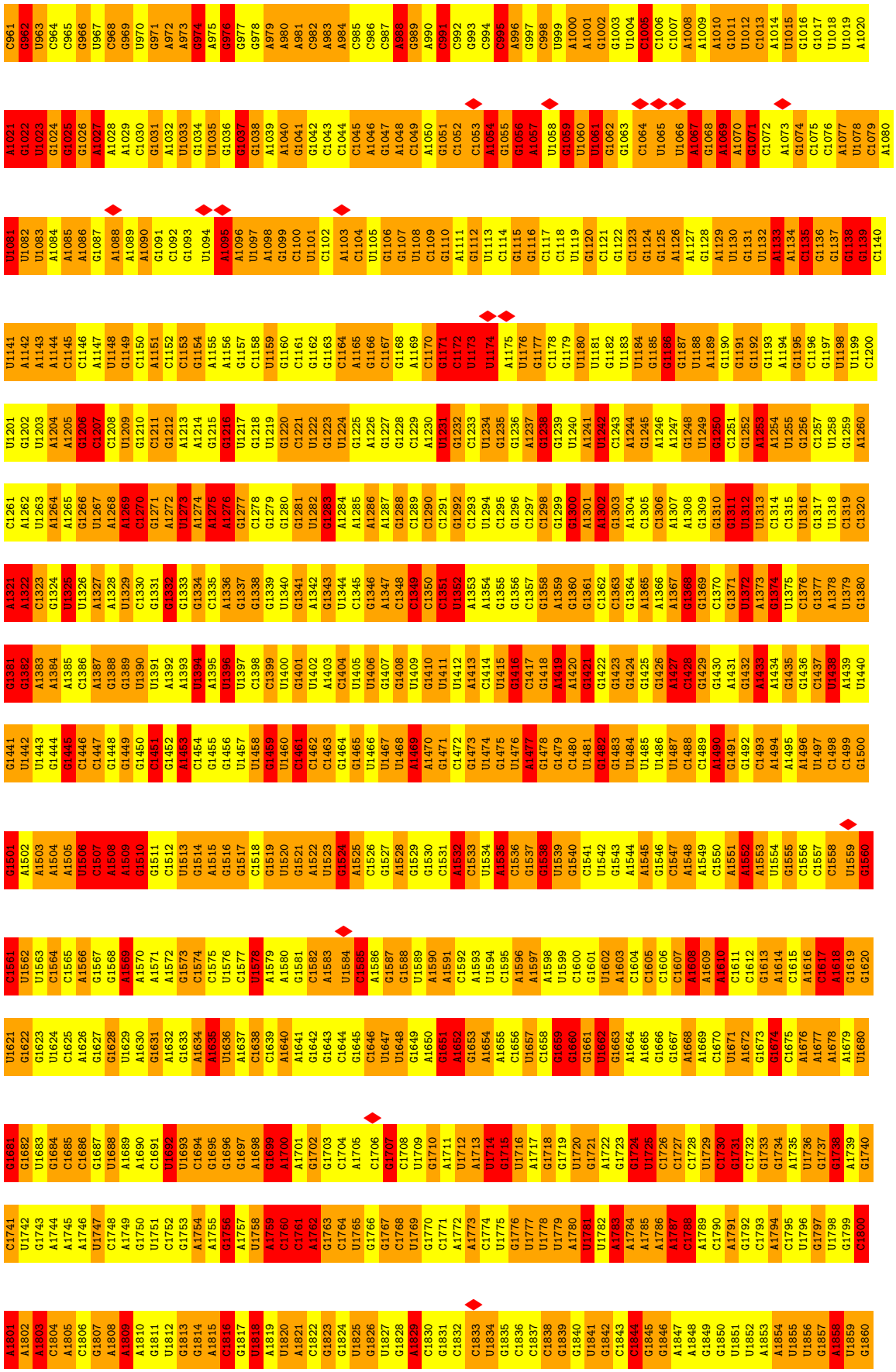
Chain BA:



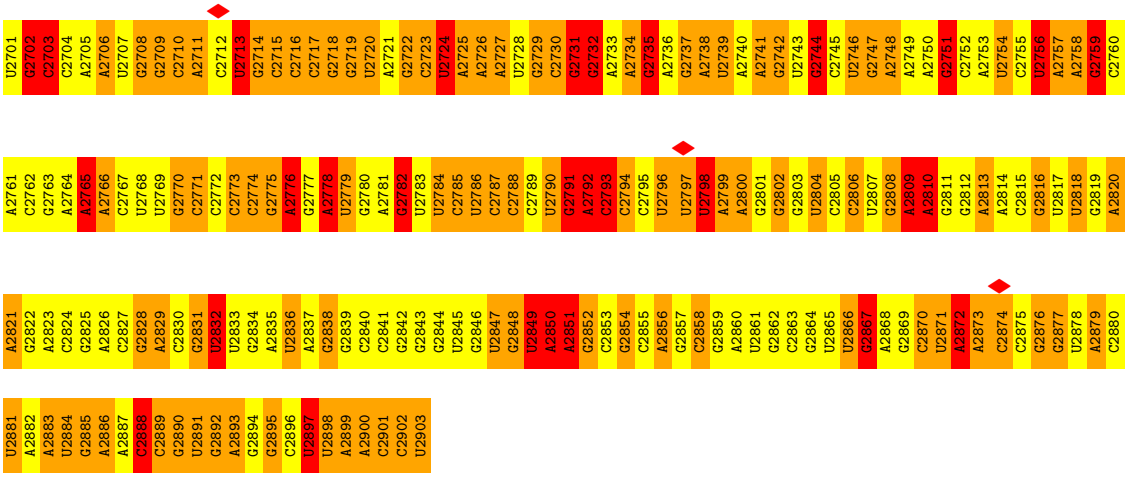
- Molecule 35: 23S RIBOSOMAL RNA

Chain BB: 38% 45% 17%



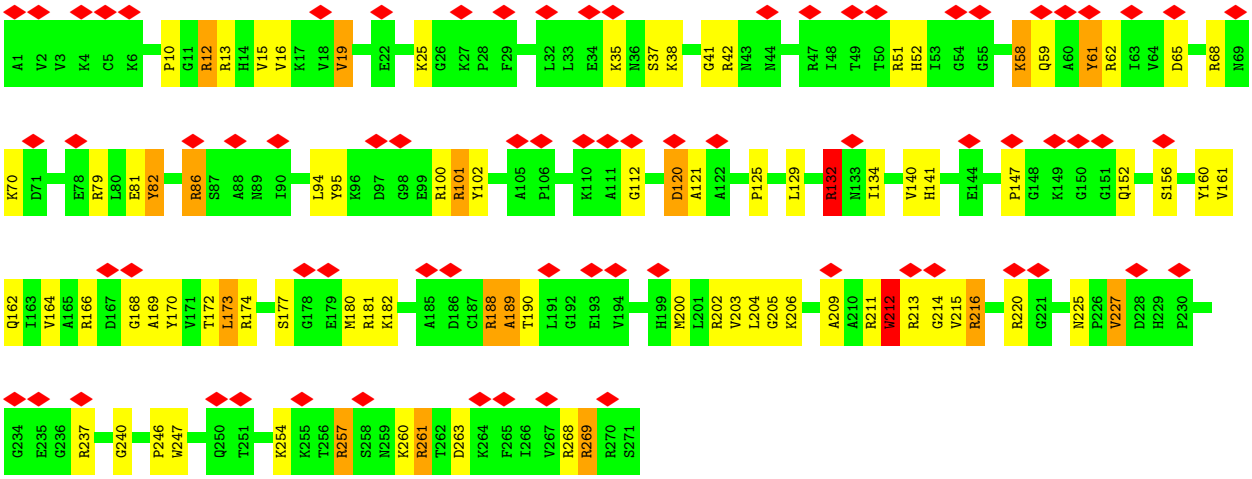


G1861 G1862 G1863 U1864 U1865 A1866 G1867 C1868 G1869 C1870 A1871 A1872 G1873 C1874 G1875 A1876 A1877 G1878 C1879 U1880 C1881 U1882 U1883 G1884 A1885 U1886 C1887 G1888 A1889 A1890 G1891 C1892 C1893 C1894 C1895 G1896 G1897 U1898 A1899 A1900 A1901 C1902 G1903 G1904 C1905 G1906 G1907 C1908 C1909 G1910 U1911 A1912 A1913 C1914 U1915 A1916 U1917 A1918 A1919 C1920
G1921 G1922 U1923 C1924 C1925 U1926 A1927 A1928 G1929 G1930 U1931 A1932 G1933 C1934 G1935 A1936 A1937 A1938 U1939 U1940 C1941 C1942 U1943 G1944 G1945 U1946 C1947 G1948 G1949 G1950 U1951 A1952 A1953 G1954 U1955 U1956 C1957 C1958 G1959 A1960 C1961 C1962 U1963 G1964 C1965 A1966 C1967 G1968 A1969 A1970 U1971 G1972 G1973 C1974 G1975 U1976 A1977 A1978 U1979 G1980
A1981 U1982 G1983 G1984 C1985 C1986 A1987 G1988 G1989 C1990 U1991 G1992 U1993 C1994 U1995 C1996 C1997 A1998 C1999 C2000 C2001 G2002 A2003 G2004 A2005 C2006 U2007 C2008 A2009 G2010 U2011 G2012 A2013 A2014 A2015 U2016 U2017 G2018 A2019 A2020 C2021 U2022 C2023 G2024 C2025 U2026 G2027 U2028 G2029 A2030 A2031 G2032 A2033 U2034 G2035 C2036 A2037 G2038 U2039 G2040
U2041 A2042 C2043 C2044 C2045 G2046 C2047 G2048 G2049 C2050 A2051 A2052 G2053 A2054 C2055 G2056 G2057 A2058 A2059 A2060 G2061 A2062 A2063 C2064 C2065 C2066 G2067 U2068 G2069 A2070 A2071 C2072 C2073 U2074 U2075 U2076 A2077 C2078 U2079 A2080 U2081 A2082 G2083 C2084 U2085 U2086 G2087 A2088 C2089 A2090 C2091 U2092 G2093 A2094 A2095 C2096 A2097 U2098 U2099 G2100
A2101 G2102 C2103 C2104 U2105 U2106 G2107 A2108 U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133 A2134 A2135 G2136 U2137 G2138 U2139 G2140 G2141 A2142 G2143 G2144 C2145 C2146 A2147 G2148 U2149 C2150 U2151 G2152 C2153 A2154 U2155 G2156 G2157 A2158 G2159 C2160
C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 U2180 U2181 U2182 A2183 A2184 U2185 G2186 U2187 U2188 U2189 G2190 A2191 U2192 G2193 U2194 U2195 C2196 U2197 A2198 A2199 C2200 G2201 U2202 U2203 G2204 A2205 C2206 C2207 C2208 G2209 U2210 A2211 A2212 U2213 C2214 C2215 G2216 G2217 G2218 U2219 U2220
G2221 C2222 G2223 G2224 A2225 C2226 A2227 G2228 U2229 G2230 U2231 C2232 U2233 G2234 G2235 U2236 G2237 G2238 G2239 U2240 A2241 G2242 U2243 U2244 U2245 G2246 A2247 C2248 U2249 G2250 G2251 G2252 G2253 C2254 G2255 G2256 U2257 C2258 U2259 C2260 C2261 U2262 C2263 C2264 U2265 A2266 A2267 A2268 G2269 A2270 G2271 U2272 A2273 A2274 C2275 G2276 G2277 A2278 G2279 G2280
A2281 G2282 C2283 A2284 C2285 G2286 A2287 A2288 G2289 G2290 U2291 U2292 G2293 G2294 C2295 U2296 A2297 A2298 U2299 C2300 C2301 U2302 G2303 G2304 U2305 C2306 G2307 G2308 A2309 C2310 A2311 U2312 C2313 A2314 G2315 G2316 A2317 G2318 G2319 U2320 U2321 A2322 G2323 U2324 G2325 C2326 A2327 A2328 U2329 G2330 G2331 C2332 A2333 U2334 A2335 A2336 G2337 C2338 G2339 A2340
G2341 C2342 U2343 U2344 G2345 A2346 C2347 U2348 G2349 C2350 G2351 A2352 G2353 C2354 G2355 U2356 G2357 A2358 C2359 G2360 G2361 C2362 G2363 C2364 G2365 A2366 G2367 C2368 A2369 G2370 G2371 U2372 G2373 C2374 G2375 A2376 A2377 A2378 G2379 C2380 A2381 G2382 G2383 U2384 C2385 A2386 U2387 A2388 G2389 U2390 G2391 A2392 U2393 C2394 C2395 G2396 G2397 U2398 C2399 G2400
U2401 U2402 C2403 U2404 G2405 A2406 A2407 U2408 G2409 G2410 A2411 A2412 G2413 G2414 G2415 C2416 C2417 A2418 U2419 C2420 G2421 C2422 U2423 C2424 A2425 A2426 C2427 G2428 G2429 A2430 U2431 A2432 A2433 A2434 A2435 G2436 G2437 A2438 A2439 C2440 U2441 C2442 C2443 A2444 G2445 G2446 A2447 A2448 U2449 A2450 A2451 C2452 A2453 G2454 G2455 C2456 U2457 G2458 A2459 U2460
A2461 C2462 C2463 G2464 C2465 C2466 C2467 A2468 A2469 G2470 A2471 G2472 U2473 U2474 C2475 A2476 U2477 A2478 U2479 C2480 G2481 A2482 C2483 G2484 C2485 U2486 A2487 U2488 G2489 G2490 U2491 U2492 U2493 G2494 G2495 C2496 A2497 C2498 C2499 U2500 C2501 G2502 A2503 U2504 G2505 U2506 C2507 G2508 G2509 C2510 U2511 C2512 A2513 U2514 C2515 A2516 C2517 A2518 U2519 C2520
C2521 U2522 G2523 G2524 G2525 G2526 C2527 U2528 G2529 A2530 A2531 G2532 U2533 A2534 G2535 G2536 U2537 C2538 C2539 C2540 A2541 A2542 G2543 G2544 G2545 U2546 A2547 U2548 G2549 G2550 C2551 U2552 G2553 U2554 A2555 C2556 G2557 C2558 C2559 A2560 U2561 U2562 U2563 A2564 A2565 A2566 G2567 U2568 G2569 G2570 U2571 A2572 C2573 G2574 C2575 G2576 A2577 G2578 C2579 U2580
G2581 C2582 G2583 U2584 U2585 U2586 A2587 G2588 A2589 A2590 C2591 G2592 U2593 C2594 G2595 U2596 A2597 G2598 G2599 A2600 C2601 A2602 G2603 U2604 U2605 C2606 G2607 G2608 U2609 C2610 C2611 C2612 U2613 A2614 U2615 C2616 U2617 G2618 C2619 C2620 G2621 U2622 G2623 G2624 G2625 C2626 G2627 C2628 U2629 G2630 G2631 A2632 G2633 A2634 A2635 C2636 U2637 G2638 A2639 G2640
G2641 G2642 G2643 G2644 G2645 C2646 U2647 G2648 C2649 U2650 C2651 C2652 U2653 A2654 G2655 U2656 A2657 C2658 G2659 A2660 G2661 A2662 G2663 G2664 A2665 C2666 C2667 G2668 G2669 A2670 G2671 U2672 G2673 G2674 A2675 C2676 G2677 C2678 A2679 U2680 C2681 A2682 C2683 U2684 G2685 G2686 U2687 G2688 U2689 U2690 C2691 G2692 G2693 G2694 U2695 U2696 G2697 U2698 C2699 A2700



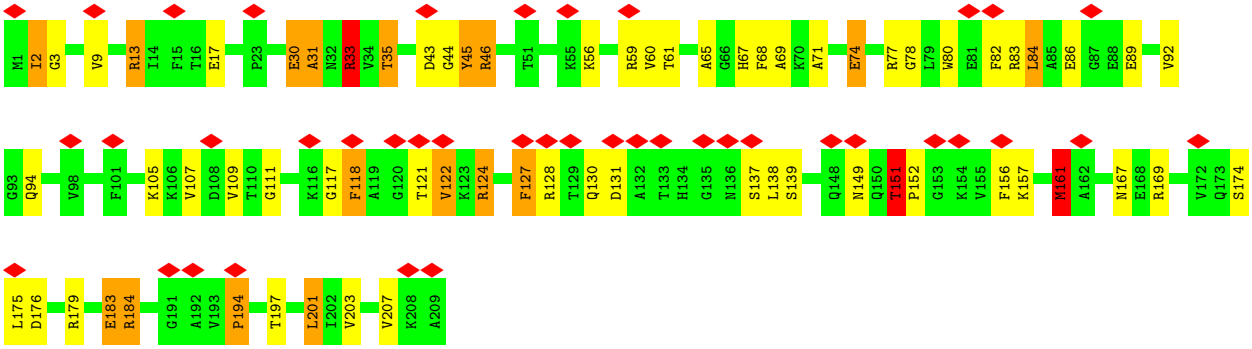
- Molecule 36: 50S RIBOSOMAL PROTEIN L2

Chain BC:



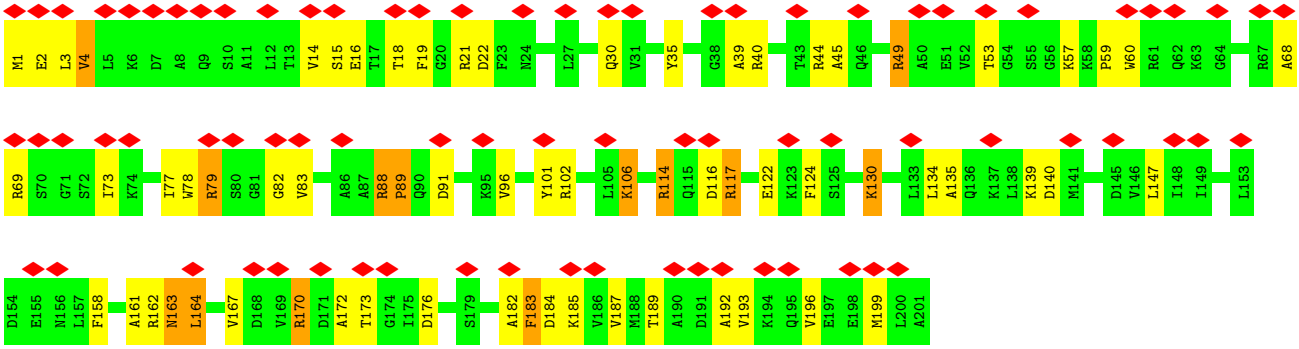
- Molecule 37: 50S RIBOSOMAL PROTEIN L3

Chain BD:



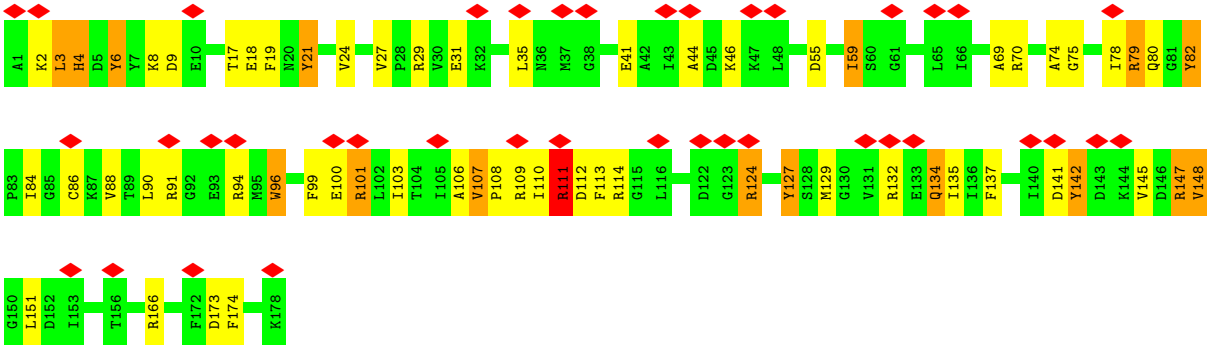
- Molecule 38: 50S RIBOSOMAL PROTEIN L4

Chain BE:



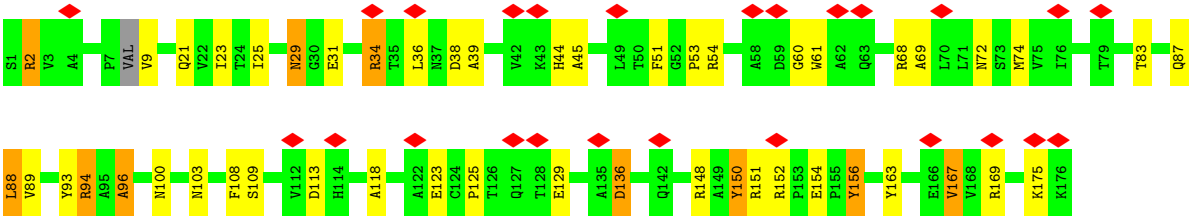
- Molecule 39: 50S RIBOSOMAL PROTEIN L5

Chain BF:



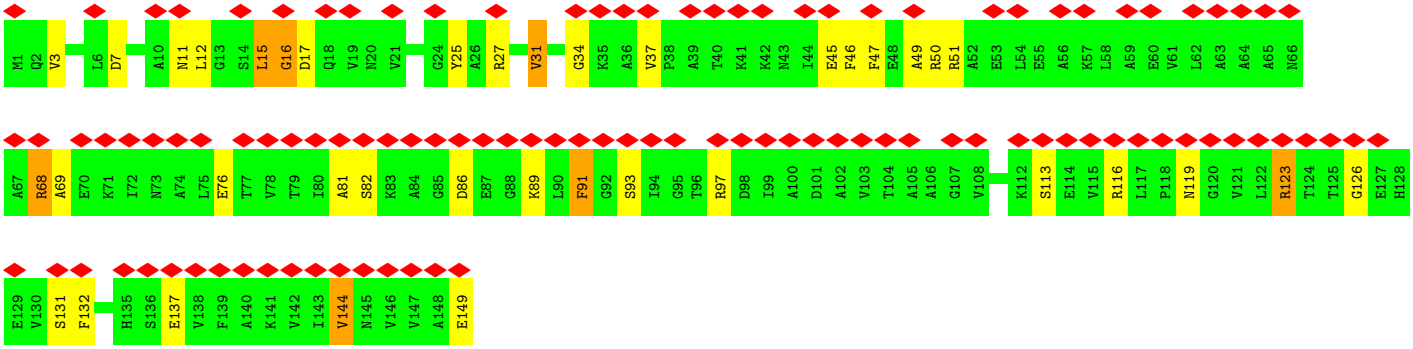
- Molecule 40: 50S RIBOSOMAL PROTEIN L6

Chain BG:



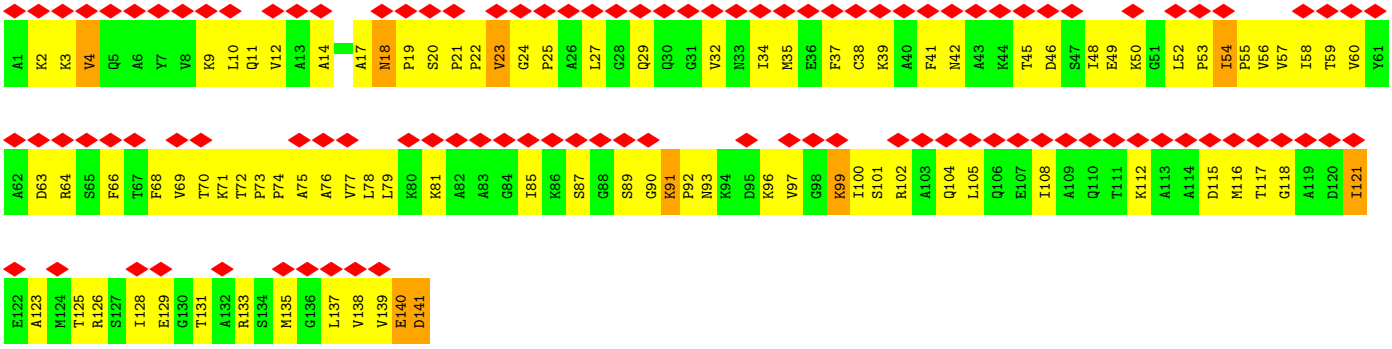
- Molecule 41: 50S RIBOSOMAL PROTEIN L9

Chain BH:



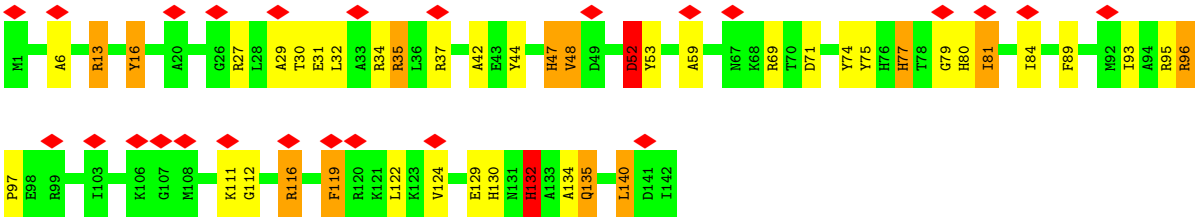
- Molecule 42: 50S RIBOSOMAL PROTEIN L11

Chain BI: 75% 35% 59% 6%



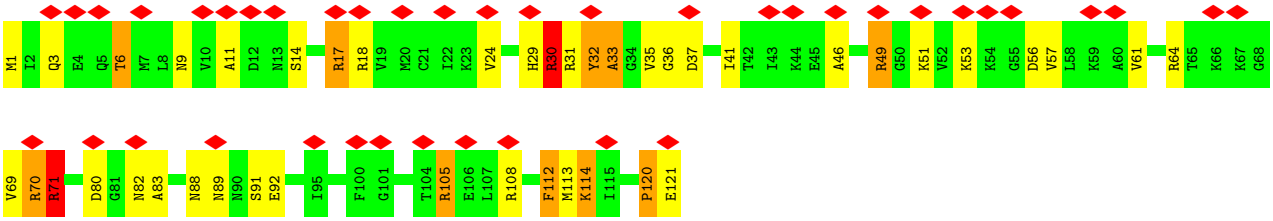
- Molecule 43: 50S RIBOSOMAL PROTEIN L13

Chain BJ: 18% 69% 21% 8%



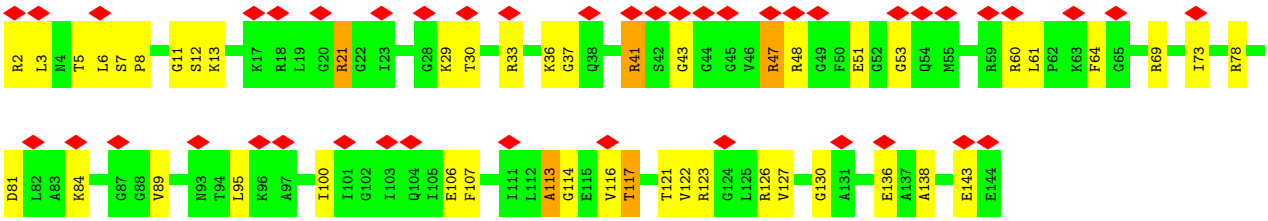
- Molecule 44: 50S RIBOSOMAL PROTEIN L14

Chain BK: 33% 64% 26% 8%



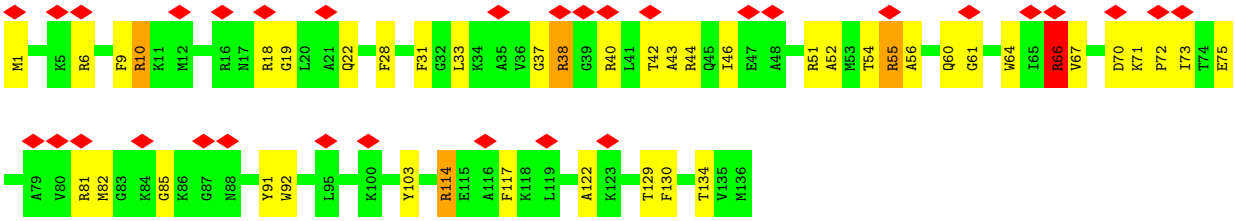
- Molecule 45: 50S RIBOSOMAL PROTEIN L15

Chain BL: 30% 67% 29%



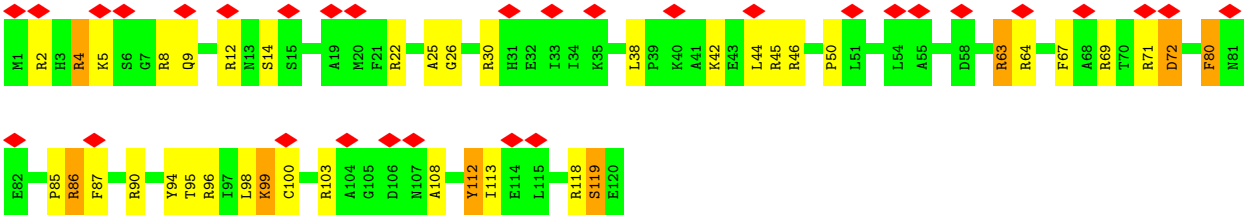
- Molecule 46: 50S RIBOSOMAL PROTEIN L16

Chain BM:



- Molecule 47: 50S RIBOSOMAL PROTEIN L17

Chain BN:

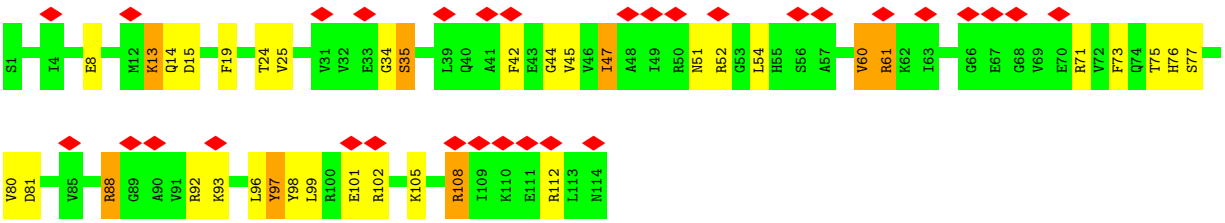


- Molecule 48: 50S RIBOSOMAL PROTEIN L18

Chain BO:

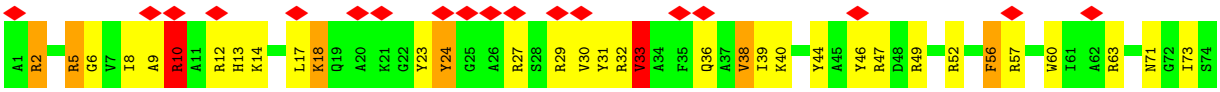
- Molecule 49: 50S RIBOSOMAL PROTEIN L19

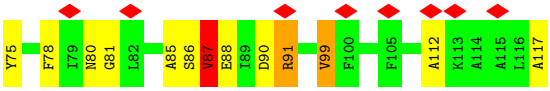
Chain BP:



- Molecule 50: 50S RIBOSOMAL PROTEIN L20

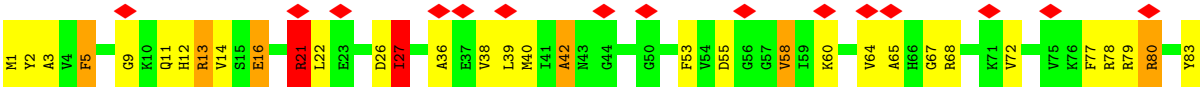
Chain BQ:

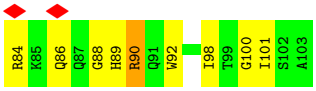




- Molecule 51: 50S RIBOSOMAL PROTEIN L21

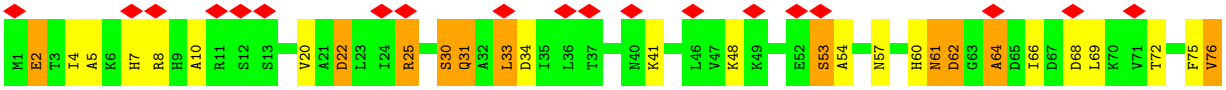
Chain BR:

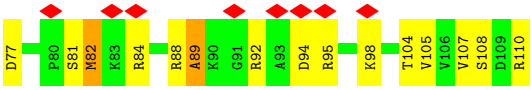




- Molecule 52: 50S RIBOSOMAL PROTEIN L22

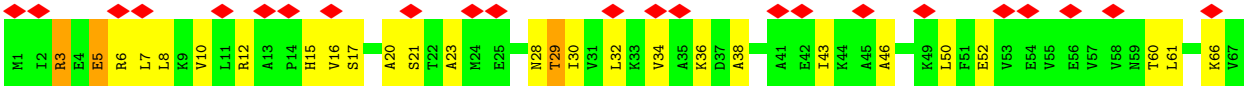
Chain BS:

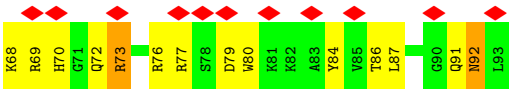




- Molecule 53: 50S RIBOSOMAL PROTEIN L23

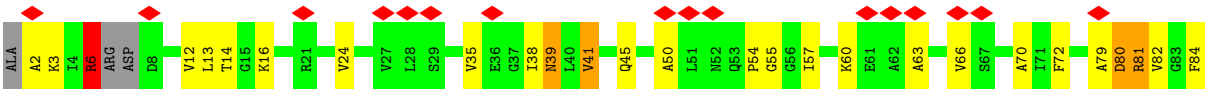
Chain BT:

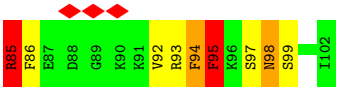




- Molecule 54: 50S RIBOSOMAL PROTEIN L24

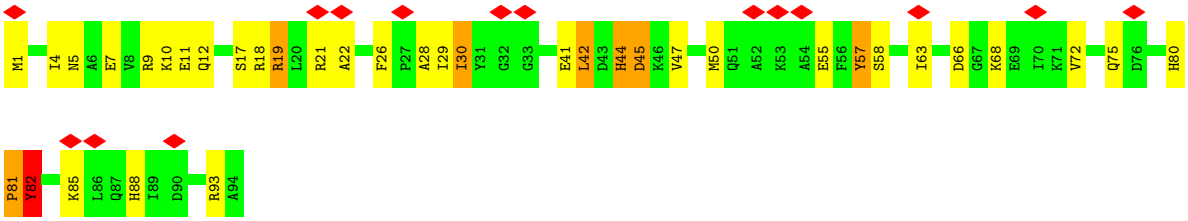
Chain BU:





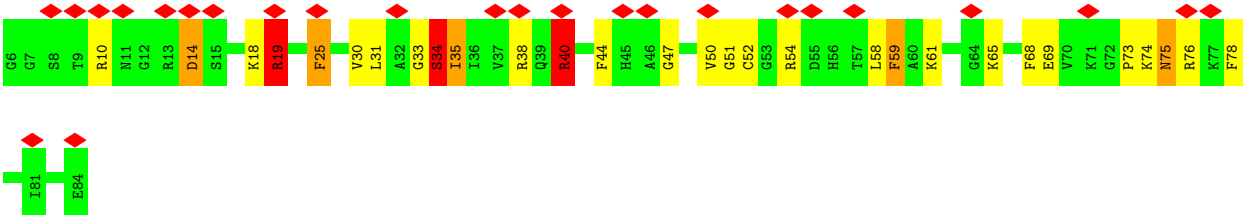
- Molecule 55: 50S RIBOSOMAL PROTEIN L25

Chain BW:



- Molecule 56: 50S RIBOSOMAL PROTEIN L27

Chain BY:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	263000	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUP VOLUMES	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	38900	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	0.760	Depositor
Minimum map value	-0.510	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.047	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	361.62, 363.82498, 361.62	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.23, 1.2375, 1.23	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

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	3.37	4837/36762 (13.2%)	3.72	8282/57350 (14.4%)
2	AB	1.71	14/1735 (0.8%)	2.05	53/2338 (2.3%)
3	AC	1.73	20/1651 (1.2%)	2.05	55/2225 (2.5%)
4	AD	1.80	24/1665 (1.4%)	2.05	48/2227 (2.2%)
5	AE	1.73	17/1118 (1.5%)	1.97	27/1504 (1.8%)
6	AF	1.77	7/835 (0.8%)	1.96	17/1128 (1.5%)
7	AG	1.82	18/1187 (1.5%)	2.01	40/1591 (2.5%)
8	AH	1.79	10/989 (1.0%)	2.07	29/1326 (2.2%)
9	AI	1.97	21/1034 (2.0%)	2.09	33/1375 (2.4%)
10	AJ	1.78	11/796 (1.4%)	1.89	15/1077 (1.4%)
11	AK	1.75	7/893 (0.8%)	1.96	18/1205 (1.5%)
12	AL	1.85	13/969 (1.3%)	1.98	28/1300 (2.2%)
13	AM	1.73	12/884 (1.4%)	2.02	28/1181 (2.4%)
14	AN	1.80	6/785 (0.8%)	1.92	19/1043 (1.8%)
15	AO	1.77	11/724 (1.5%)	1.90	24/966 (2.5%)
16	AP	1.84	9/648 (1.4%)	2.16	26/870 (3.0%)
17	AQ	1.73	4/657 (0.6%)	1.93	18/881 (2.0%)
18	AR	1.74	6/462 (1.3%)	2.28	16/621 (2.6%)
19	AS	1.78	8/652 (1.2%)	2.15	26/877 (3.0%)
20	AT	1.66	4/671 (0.6%)	1.93	17/888 (1.9%)
21	AU	1.82	6/430 (1.4%)	2.16	13/570 (2.3%)
22	AV	2.38	76/1820 (4.2%)	2.84	256/2836 (9.0%)
23	AX	1.81	4/264 (1.5%)	2.14	19/407 (4.7%)
24	AZ	1.97	1/99 (1.0%)	1.94	5/137 (3.6%)
25	B0	1.75	7/635 (1.1%)	2.27	19/848 (2.2%)
26	B1	1.72	5/510 (1.0%)	1.94	14/677 (2.1%)
27	B2	1.75	4/453 (0.9%)	1.86	10/605 (1.7%)
28	B3	1.82	6/450 (1.3%)	2.19	16/599 (2.7%)
29	B4	1.63	4/416 (1.0%)	2.02	13/554 (2.3%)
30	B5	1.56	11/1748 (0.6%)	1.95	40/2355 (1.7%)
31	B6	1.85	4/380 (1.1%)	2.31	17/498 (3.4%)
32	B7	1.68	4/513 (0.8%)	2.03	12/676 (1.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	B8	1.83	4/303 (1.3%)	2.01	7/397 (1.8%)
34	BA	3.34	356/2753 (12.9%)	3.78	615/4288 (14.3%)
35	BB	3.39	9308/69800 (13.3%)	3.73	15832/108892 (14.5%)
36	BC	1.81	24/2121 (1.1%)	2.05	60/2852 (2.1%)
37	BD	1.77	16/1586 (1.0%)	2.01	31/2134 (1.5%)
38	BE	1.69	8/1571 (0.5%)	1.97	41/2113 (1.9%)
39	BF	1.73	14/1444 (1.0%)	2.17	40/1937 (2.1%)
40	BG	1.76	13/1335 (1.0%)	2.04	28/1803 (1.6%)
41	BH	1.74	11/1122 (1.0%)	2.05	35/1515 (2.3%)
42	BI	0.62	2/1046 (0.2%)	0.56	1/1410 (0.1%)
43	BJ	1.77	12/1152 (1.0%)	2.04	30/1551 (1.9%)
44	BK	1.76	13/939 (1.4%)	1.99	23/1257 (1.8%)
45	BL	1.78	10/1054 (0.9%)	1.94	28/1403 (2.0%)
46	BM	1.83	9/1093 (0.8%)	2.07	30/1460 (2.1%)
47	BN	1.76	12/973 (1.2%)	2.22	32/1301 (2.5%)
48	BO	1.79	15/902 (1.7%)	2.02	24/1209 (2.0%)
49	BP	1.68	5/929 (0.5%)	2.03	20/1242 (1.6%)
50	BQ	1.89	15/960 (1.6%)	2.11	29/1278 (2.3%)
51	BR	1.80	11/829 (1.3%)	2.03	23/1107 (2.1%)
52	BS	1.71	7/864 (0.8%)	2.16	34/1156 (2.9%)
53	BT	1.69	5/744 (0.7%)	1.99	18/994 (1.8%)
54	BU	1.73	3/761 (0.4%)	2.02	25/1013 (2.5%)
55	BW	1.79	13/766 (1.7%)	2.05	18/1025 (1.8%)
56	BY	1.73	3/603 (0.5%)	2.11	23/797 (2.9%)
All	All	2.98	15080/158485 (9.5%)	3.34	26300/236869 (11.1%)

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	740
2	AB	0	5
3	AC	0	7
4	AD	0	11
5	AE	0	5
6	AF	0	3
7	AG	0	3
8	AH	0	3
9	AI	0	7
10	AJ	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	AK	0	3
12	AL	0	5
13	AM	0	9
14	AN	0	3
15	AO	0	6
16	AP	0	4
17	AQ	0	1
18	AR	0	5
19	AS	0	4
20	AT	0	3
22	AV	0	13
23	AX	0	4
25	B0	0	4
26	B1	0	1
28	B3	0	2
29	B4	0	3
30	B5	0	6
31	B6	0	3
32	B7	0	1
34	BA	0	50
35	BB	0	1343
36	BC	0	8
37	BD	0	6
38	BE	0	5
39	BF	0	10
40	BG	0	3
41	BH	0	1
43	BJ	0	4
44	BK	0	5
45	BL	0	1
46	BM	0	3
47	BN	0	5
48	BO	0	2
49	BP	0	5
50	BQ	0	5
51	BR	0	3
52	BS	0	1
53	BT	0	1
54	BU	0	2
55	BW	0	4
56	BY	0	5
All	All	0	2342

The worst 5 of 15080 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	BB	1403	A	N9-C4	21.34	1.50	1.37
35	BB	1301	A	N7-C5	-20.38	1.27	1.39
1	AA	930	C	N1-C6	19.80	1.49	1.37
1	AA	816	A	N7-C5	-19.29	1.27	1.39
35	BB	1821	A	N9-C4	19.18	1.49	1.37

The worst 5 of 26300 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AA	753	A	N1-C6-N6	30.52	136.91	118.60
35	BB	666	A	N1-C6-N6	26.10	134.26	118.60
35	BB	533	G	N1-C6-O6	25.90	135.44	119.90
1	AA	242	G	C5-C6-O6	-25.60	113.24	128.60
35	BB	1014	A	N1-C6-N6	25.57	133.94	118.60

There are no chirality outliers.

5 of 2342 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	12	U	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	Sidechain
1	AA	7	A	Sidechain

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	32831	0	16502	183	0
2	AB	1704	0	1732	3	0
3	AC	1624	0	1699	12	0
4	AD	1643	0	1710	5	0
5	AE	1105	0	1148	6	0
6	AF	817	0	808	7	0
7	AG	1174	0	1230	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	AH	979	0	1034	1	0
9	AI	1022	0	1070	9	0
10	AJ	786	0	828	3	0
11	AK	877	0	887	9	0
12	AL	955	0	1019	2	0
13	AM	876	0	937	7	0
14	AN	774	0	827	2	0
15	AO	716	0	742	3	0
16	AP	638	0	656	0	0
17	AQ	648	0	691	4	0
18	AR	455	0	478	1	0
19	AS	637	0	665	5	0
20	AT	665	0	714	4	0
21	AU	425	0	449	2	0
22	AV	1649	0	832	21	0
23	AX	236	0	121	10	0
24	AZ	100	0	99	0	0
25	B0	625	0	655	1	0
26	B1	509	0	543	1	0
27	B2	449	0	491	1	0
28	B3	444	0	461	3	0
29	B4	409	0	440	0	0
30	B5	1733	0	1824	4	0
31	B6	377	0	418	3	0
32	B7	504	0	574	5	0
33	B8	302	0	343	0	0
34	BA	2464	0	1246	8	0
35	BB	62321	0	31294	336	0
36	BC	2082	0	2157	14	0
37	BD	1565	0	1616	8	0
38	BE	1552	0	1619	9	0
39	BF	1420	0	1460	9	0
40	BG	1316	0	1364	4	0
41	BH	1111	0	1148	1	0
42	BI	1032	0	1088	118	0
43	BJ	1129	0	1162	8	0
44	BK	930	0	1003	6	0
45	BL	1045	0	1117	6	0
46	BM	1074	0	1157	4	0
47	BN	960	0	1000	2	0
48	BO	892	0	923	2	0
49	BP	917	0	965	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	BQ	947	0	1022	8	0
51	BR	816	0	839	8	0
52	BS	857	0	922	3	0
53	BT	738	0	807	5	0
54	BU	755	0	807	10	0
55	BW	753	0	780	5	0
56	BY	596	0	610	1	0
All	All	145960	0	98733	840	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 3.

The worst 5 of 840 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)
22:AV:35:G:N2	23:AX:18:C:C2	2.08	1.22
42:BI:11:GLN:HG2	42:BI:55:PRO:HB3	1.51	0.91
42:BI:140:GLU:O	42:BI:141:ASP:OXT	1.91	0.89
42:BI:27:LEU:HD23	42:BI:27:LEU:H	1.43	0.82
42:BI:121:ILE:HD13	42:BI:121:ILE:H	1.44	0.82

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	216/218 (99%)	159 (74%)	41 (19%)	16 (7%)	1 13
3	AC	204/206 (99%)	158 (78%)	31 (15%)	15 (7%)	1 13
4	AD	203/205 (99%)	160 (79%)	34 (17%)	9 (4%)	2 22
5	AE	148/150 (99%)	110 (74%)	27 (18%)	11 (7%)	1 13

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AF	98/100 (98%)	73 (74%)	18 (18%)	7 (7%)	1	14
7	AG	148/150 (99%)	109 (74%)	33 (22%)	6 (4%)	3	22
8	AH	127/129 (98%)	94 (74%)	27 (21%)	6 (5%)	2	21
9	AI	125/127 (98%)	99 (79%)	21 (17%)	5 (4%)	3	23
10	AJ	96/98 (98%)	71 (74%)	14 (15%)	11 (12%)	0	6
11	AK	115/117 (98%)	96 (84%)	14 (12%)	5 (4%)	2	22
12	AL	121/123 (98%)	100 (83%)	12 (10%)	9 (7%)	1	13
13	AM	111/113 (98%)	80 (72%)	19 (17%)	12 (11%)	0	7
14	AN	92/96 (96%)	57 (62%)	22 (24%)	13 (14%)	0	4
15	AO	86/88 (98%)	73 (85%)	11 (13%)	2 (2%)	6	33
16	AP	78/80 (98%)	62 (80%)	10 (13%)	6 (8%)	1	12
17	AQ	78/80 (98%)	65 (83%)	7 (9%)	6 (8%)	1	12
18	AR	53/55 (96%)	42 (79%)	8 (15%)	3 (6%)	1	17
19	AS	77/79 (98%)	61 (79%)	13 (17%)	3 (4%)	3	23
20	AT	83/85 (98%)	68 (82%)	13 (16%)	2 (2%)	6	33
21	AU	49/51 (96%)	41 (84%)	5 (10%)	3 (6%)	1	16
24	AZ	18/20 (90%)	16 (89%)	1 (6%)	1 (6%)	2	18
25	B0	75/77 (97%)	52 (69%)	20 (27%)	3 (4%)	3	23
26	B1	61/63 (97%)	45 (74%)	14 (23%)	2 (3%)	4	26
27	B2	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
28	B3	54/56 (96%)	42 (78%)	9 (17%)	3 (6%)	2	18
29	B4	48/50 (96%)	39 (81%)	7 (15%)	2 (4%)	3	22
30	B5	232/234 (99%)	190 (82%)	37 (16%)	5 (2%)	6	35
31	B6	44/46 (96%)	29 (66%)	11 (25%)	4 (9%)	1	10
32	B7	62/64 (97%)	52 (84%)	5 (8%)	5 (8%)	1	12
33	B8	36/38 (95%)	30 (83%)	4 (11%)	2 (6%)	2	18
36	BC	269/271 (99%)	209 (78%)	47 (18%)	13 (5%)	2	20
37	BD	207/209 (99%)	149 (72%)	37 (18%)	21 (10%)	0	9
38	BE	199/201 (99%)	161 (81%)	23 (12%)	15 (8%)	1	13
39	BF	176/178 (99%)	131 (74%)	26 (15%)	19 (11%)	0	7
40	BG	171/176 (97%)	134 (78%)	28 (16%)	9 (5%)	2	19

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BH	147/149 (99%)	111 (76%)	31 (21%)	5 (3%)	3	26
42	BI	139/141 (99%)	113 (81%)	21 (15%)	5 (4%)	3	25
43	BJ	140/142 (99%)	106 (76%)	24 (17%)	10 (7%)	1	14
44	BK	119/121 (98%)	95 (80%)	14 (12%)	10 (8%)	1	11
45	BL	141/143 (99%)	115 (82%)	16 (11%)	10 (7%)	1	14
46	BM	134/136 (98%)	105 (78%)	21 (16%)	8 (6%)	1	16
47	BN	118/120 (98%)	96 (81%)	16 (14%)	6 (5%)	2	19
48	BO	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	8	40
49	BP	112/114 (98%)	85 (76%)	19 (17%)	8 (7%)	1	14
50	BQ	115/117 (98%)	84 (73%)	21 (18%)	10 (9%)	1	11
51	BR	101/103 (98%)	80 (79%)	13 (13%)	8 (8%)	1	12
52	BS	108/110 (98%)	76 (70%)	21 (19%)	11 (10%)	0	8
53	BT	91/93 (98%)	60 (66%)	25 (28%)	6 (7%)	1	15
54	BU	94/102 (92%)	71 (76%)	16 (17%)	7 (7%)	1	13
55	BW	92/94 (98%)	76 (83%)	10 (11%)	6 (6%)	1	15
56	BY	77/79 (98%)	46 (60%)	18 (23%)	13 (17%)	0	3
All	All	5858/5971 (98%)	4523 (77%)	956 (16%)	379 (6%)	2	15

5 of 379 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AC	17	TRP
3	AC	116	ALA
5	AE	11	GLN
5	AE	17	VAL
9	AI	58	GLU

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	180/180 (100%)	171 (95%)	9 (5%)	24	49
3	AC	170/170 (100%)	158 (93%)	12 (7%)	14	39
4	AD	172/172 (100%)	165 (96%)	7 (4%)	30	55
5	AE	113/113 (100%)	103 (91%)	10 (9%)	10	31
6	AF	87/87 (100%)	85 (98%)	2 (2%)	50	70
7	AG	123/123 (100%)	120 (98%)	3 (2%)	49	69
8	AH	104/104 (100%)	99 (95%)	5 (5%)	25	51
9	AI	105/105 (100%)	100 (95%)	5 (5%)	25	51
10	AJ	86/86 (100%)	81 (94%)	5 (6%)	20	45
11	AK	90/90 (100%)	86 (96%)	4 (4%)	28	53
12	AL	103/103 (100%)	98 (95%)	5 (5%)	25	50
13	AM	91/91 (100%)	89 (98%)	2 (2%)	52	71
14	AN	79/79 (100%)	76 (96%)	3 (4%)	33	57
15	AO	76/76 (100%)	69 (91%)	7 (9%)	9	29
16	AP	65/65 (100%)	62 (95%)	3 (5%)	27	52
17	AQ	74/74 (100%)	68 (92%)	6 (8%)	11	35
18	AR	48/48 (100%)	44 (92%)	4 (8%)	11	34
19	AS	70/70 (100%)	64 (91%)	6 (9%)	10	32
20	AT	65/65 (100%)	64 (98%)	1 (2%)	65	80
21	AU	44/44 (100%)	38 (86%)	6 (14%)	3	17
25	B0	67/67 (100%)	65 (97%)	2 (3%)	41	63
26	B1	55/55 (100%)	50 (91%)	5 (9%)	9	30
27	B2	48/48 (100%)	47 (98%)	1 (2%)	53	72
28	B3	47/47 (100%)	46 (98%)	1 (2%)	53	72
29	B4	45/45 (100%)	42 (93%)	3 (7%)	16	40
30	B5	181/181 (100%)	175 (97%)	6 (3%)	38	61
31	B6	38/38 (100%)	33 (87%)	5 (13%)	4	18
32	B7	51/51 (100%)	48 (94%)	3 (6%)	19	45
33	B8	34/34 (100%)	34 (100%)	0	100	100
36	BC	216/216 (100%)	204 (94%)	12 (6%)	21	46
37	BD	164/164 (100%)	146 (89%)	18 (11%)	6	22
38	BE	165/165 (100%)	157 (95%)	8 (5%)	25	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BF	149/149 (100%)	143 (96%)	6 (4%)	31	55
40	BG	136/137 (99%)	125 (92%)	11 (8%)	11	35
41	BH	114/114 (100%)	110 (96%)	4 (4%)	36	59
42	BI	109/109 (100%)	104 (95%)	5 (5%)	27	52
43	BJ	116/116 (100%)	112 (97%)	4 (3%)	37	60
44	BK	102/102 (100%)	92 (90%)	10 (10%)	8	26
45	BL	102/102 (100%)	98 (96%)	4 (4%)	32	56
46	BM	109/109 (100%)	104 (95%)	5 (5%)	27	52
47	BN	100/100 (100%)	96 (96%)	4 (4%)	31	55
48	BO	86/86 (100%)	84 (98%)	2 (2%)	50	70
49	BP	99/99 (100%)	96 (97%)	3 (3%)	41	63
50	BQ	89/89 (100%)	83 (93%)	6 (7%)	16	40
51	BR	84/84 (100%)	76 (90%)	8 (10%)	8	28
52	BS	93/93 (100%)	87 (94%)	6 (6%)	17	42
53	BT	80/80 (100%)	68 (85%)	12 (15%)	3	15
54	BU	81/83 (98%)	76 (94%)	5 (6%)	18	43
55	BW	78/78 (100%)	73 (94%)	5 (6%)	17	42
56	BY	59/59 (100%)	54 (92%)	5 (8%)	10	33
All	All	4842/4845 (100%)	4568 (94%)	274 (6%)	24	45

5 of 274 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	BQ	40	LYS
51	BR	78	ARG
54	BU	14	THR
19	AS	60	PHE
19	AS	22	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
43	BJ	40	HIS
51	BR	91	GLN
43	BJ	80	HIS

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Mol	Chain	Res	Type
49	BP	76	HIS
54	BU	39	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1529/1530 (99%)	269 (17%)	34 (2%)
22	AV	76/77 (98%)	15 (19%)	0
23	AX	10/11 (90%)	8 (80%)	0
34	BA	112/117 (95%)	16 (14%)	2 (1%)
35	BB	2902/2903 (99%)	471 (16%)	56 (1%)
All	All	4629/4638 (99%)	779 (16%)	92 (1%)

5 of 779 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	7	A
1	AA	9	G
1	AA	15	G
1	AA	31	G
1	AA	32	A

5 of 92 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BB	1332	G
35	BB	2131	U
35	BB	1459	G
35	BB	1808	A
35	BB	2145	C

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

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
22	5MU	AV	54	22	18,21,23	0.64	0	26,30,35	0.71	1 (3%)

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
22	5MU	AV	54	22	-	0/7/25/26	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	AV	54	5MU	O4'-C1'-N1	2.42	113.90	108.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	BU	1
14	AN	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BU	4:ILE	C	6:ARG	N	4.65
1	AN	35:ALA	C	40:ARG	N	4.56

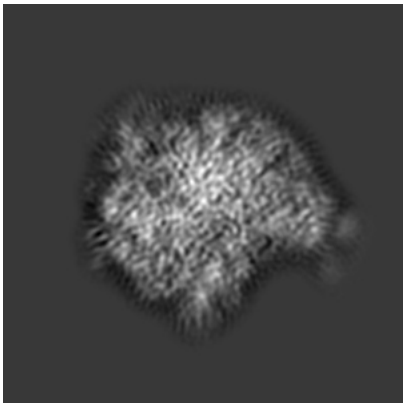
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-1657. These allow visual inspection of the internal detail of the map and identification of artifacts.

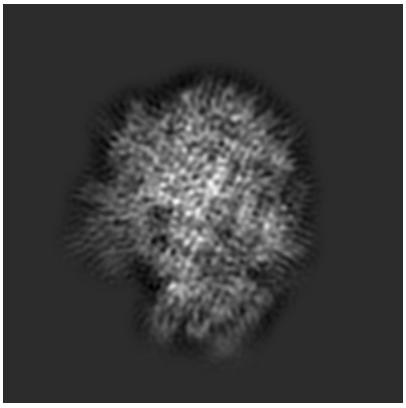
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

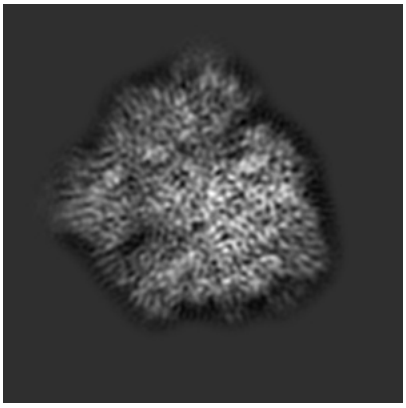
6.1.1 Primary map



X



Y

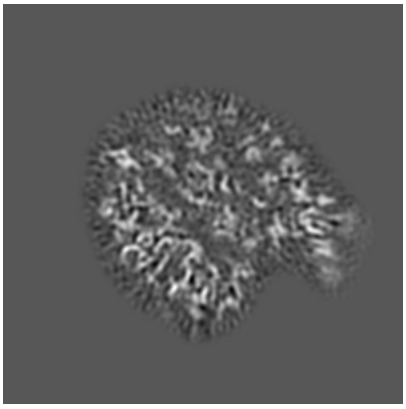


Z

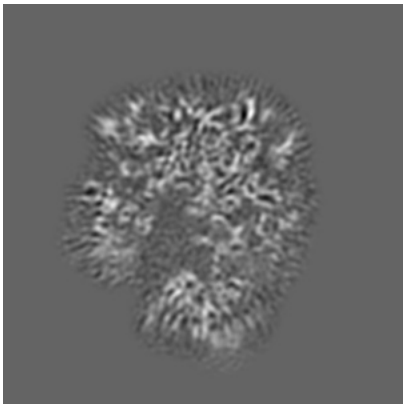
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

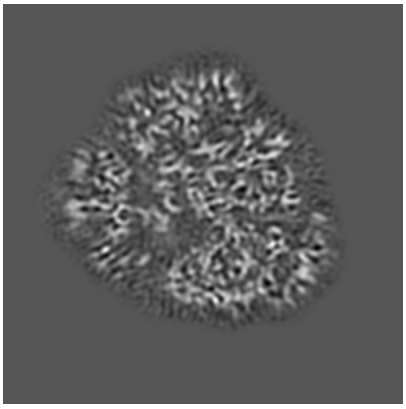
6.2.1 Primary map



X Index: 147



Y Index: 147

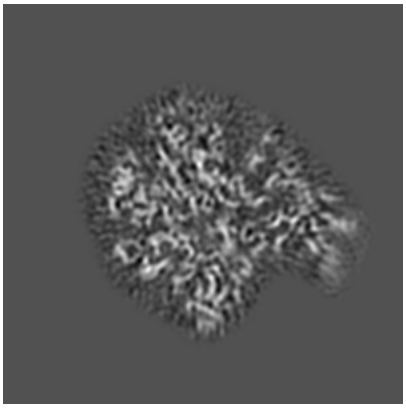


Z Index: 147

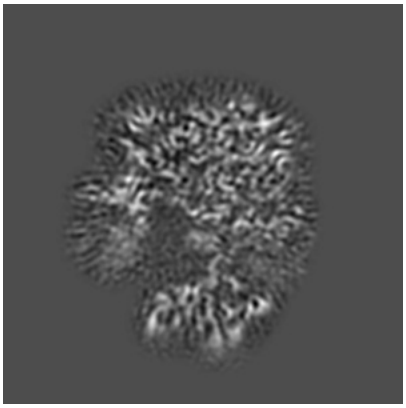
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

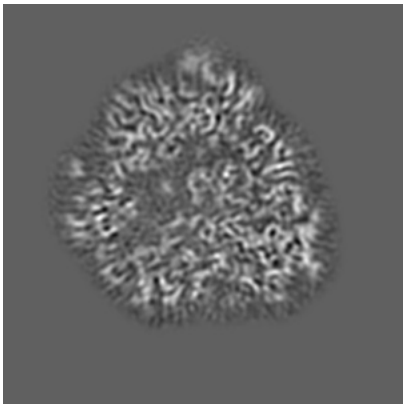
6.3.1 Primary map



X Index: 152



Y Index: 155



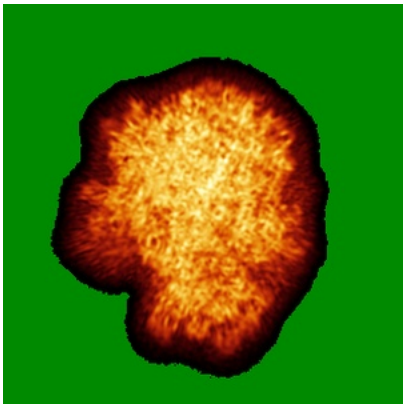
Z Index: 136

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

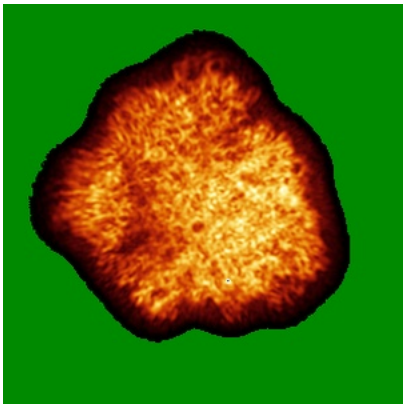
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map

X



Y

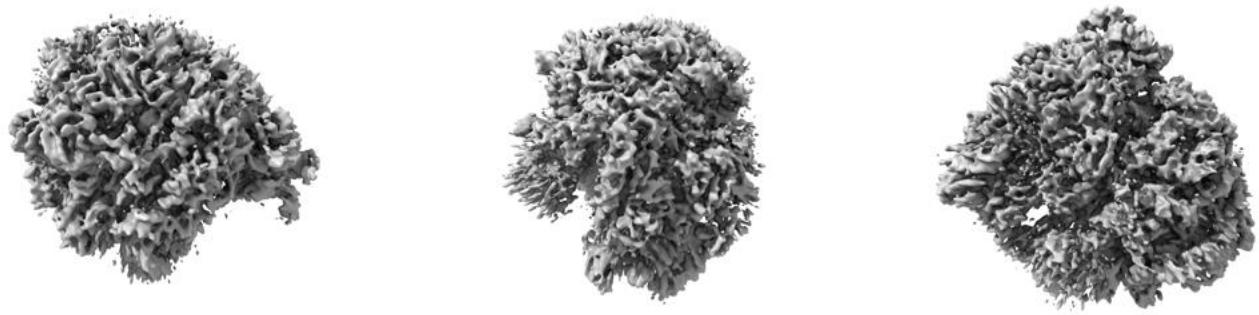


Z

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

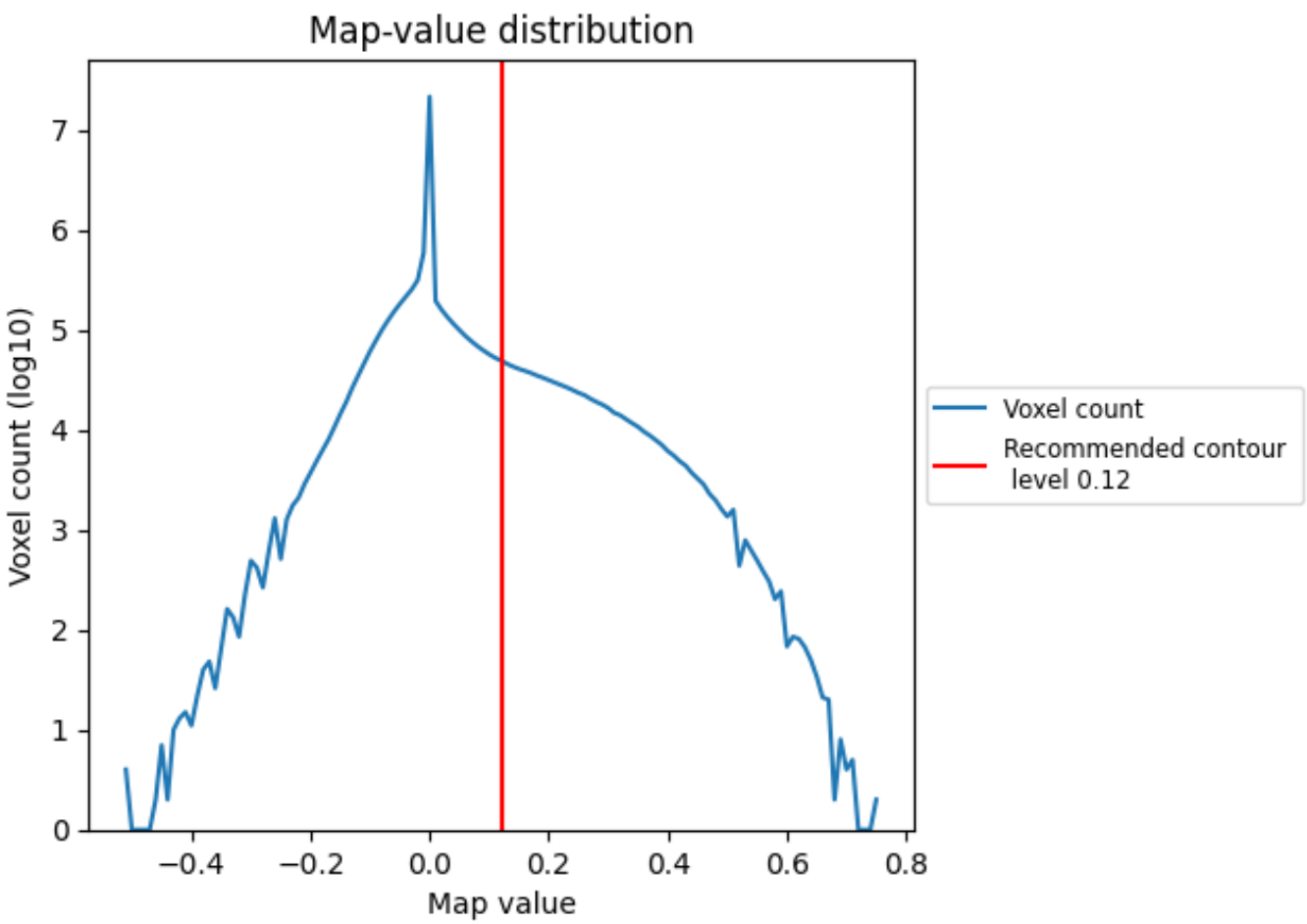
6.6 Mask visualisation (i)

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

7 Map analysis (i)

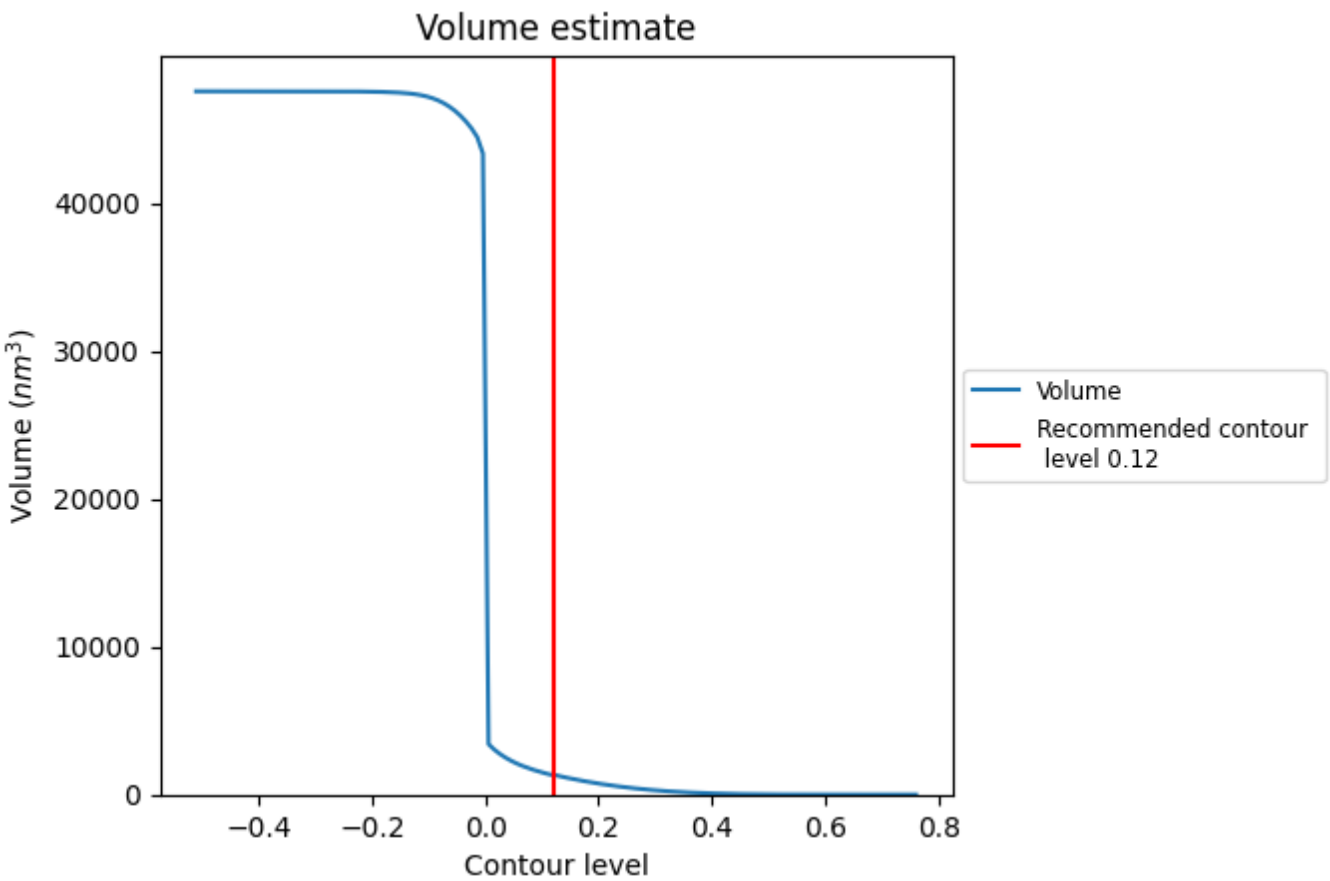
This section contains the results of statistical analysis of the map.

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.

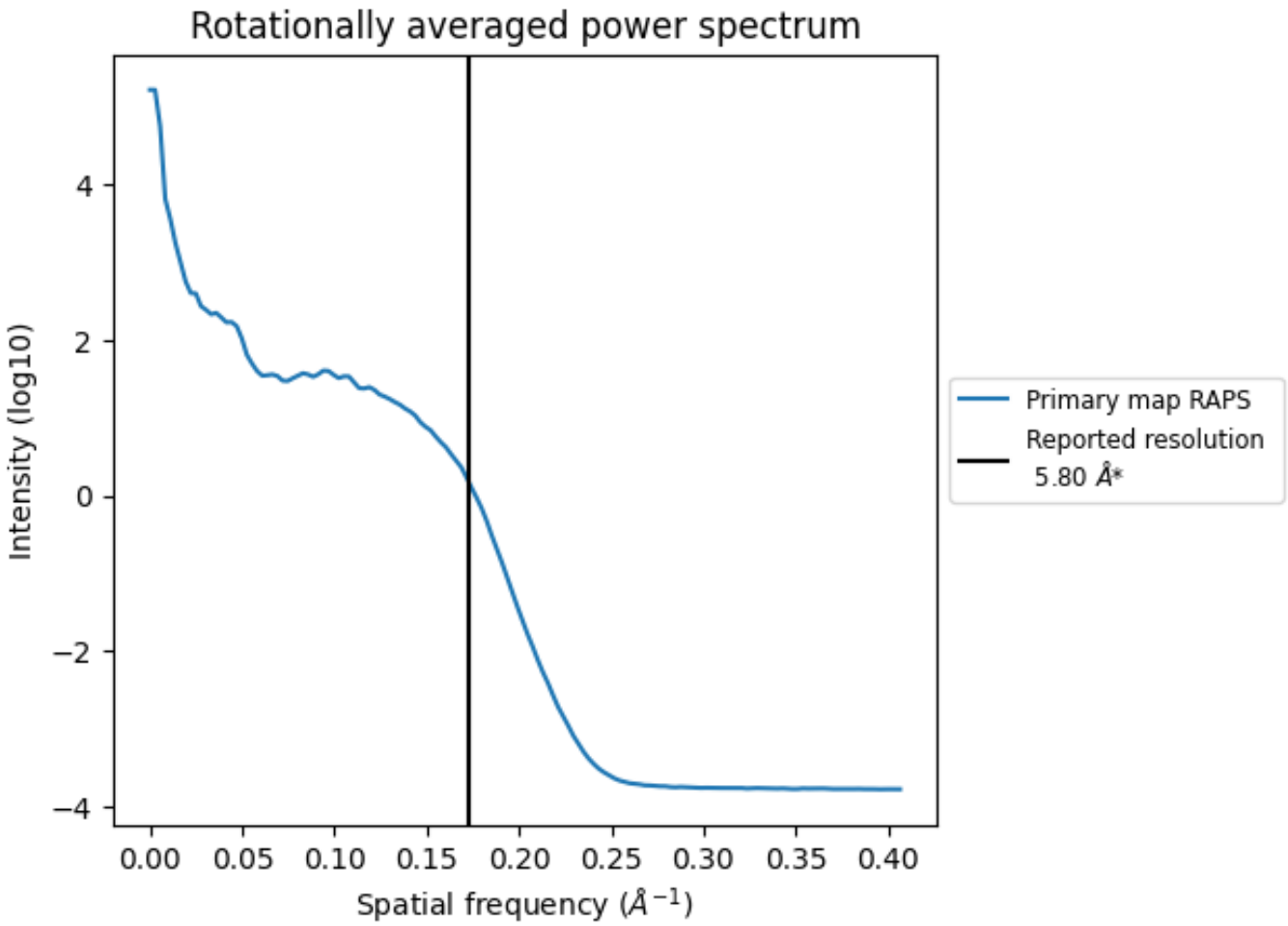
7.2 Volume estimate (i)



The volume at the recommended contour level is 1327 nm^3; this corresponds to an approximate mass of 1198 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 0.172 Å^{-1}

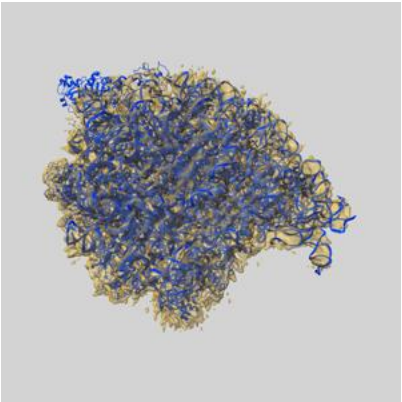
8 Fourier-Shell correlation (i)

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

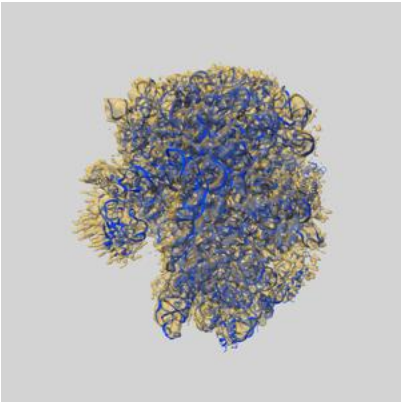
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-1657 and PDB model 4V5H. Per-residue inclusion information can be found in section 3 on page 14.

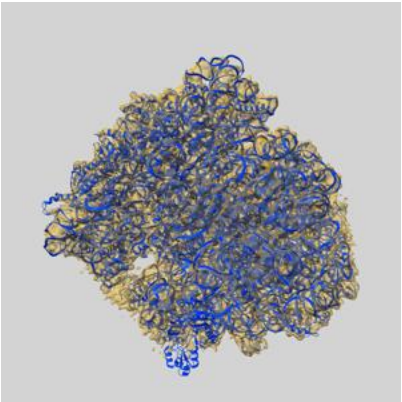
9.1 Map-model overlay (i)



X



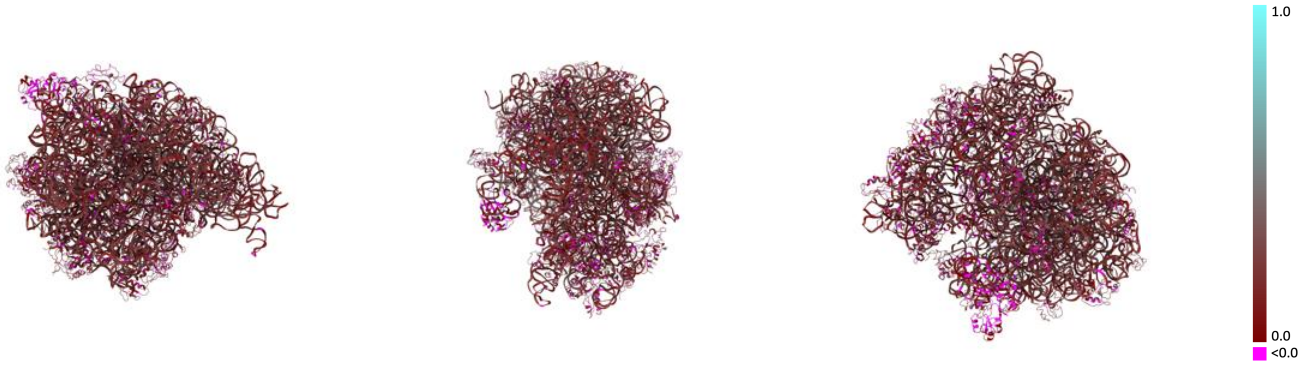
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12 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.

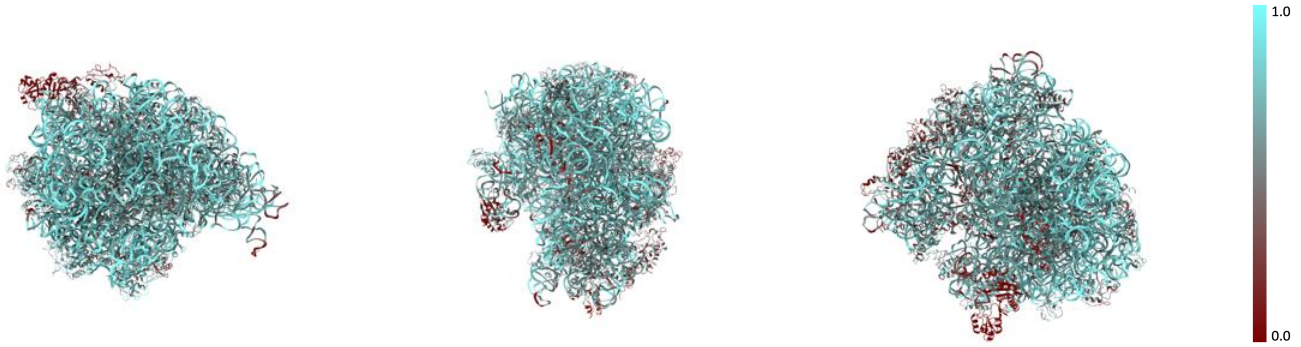
9.2 Q-score mapped to coordinate model (i)



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.

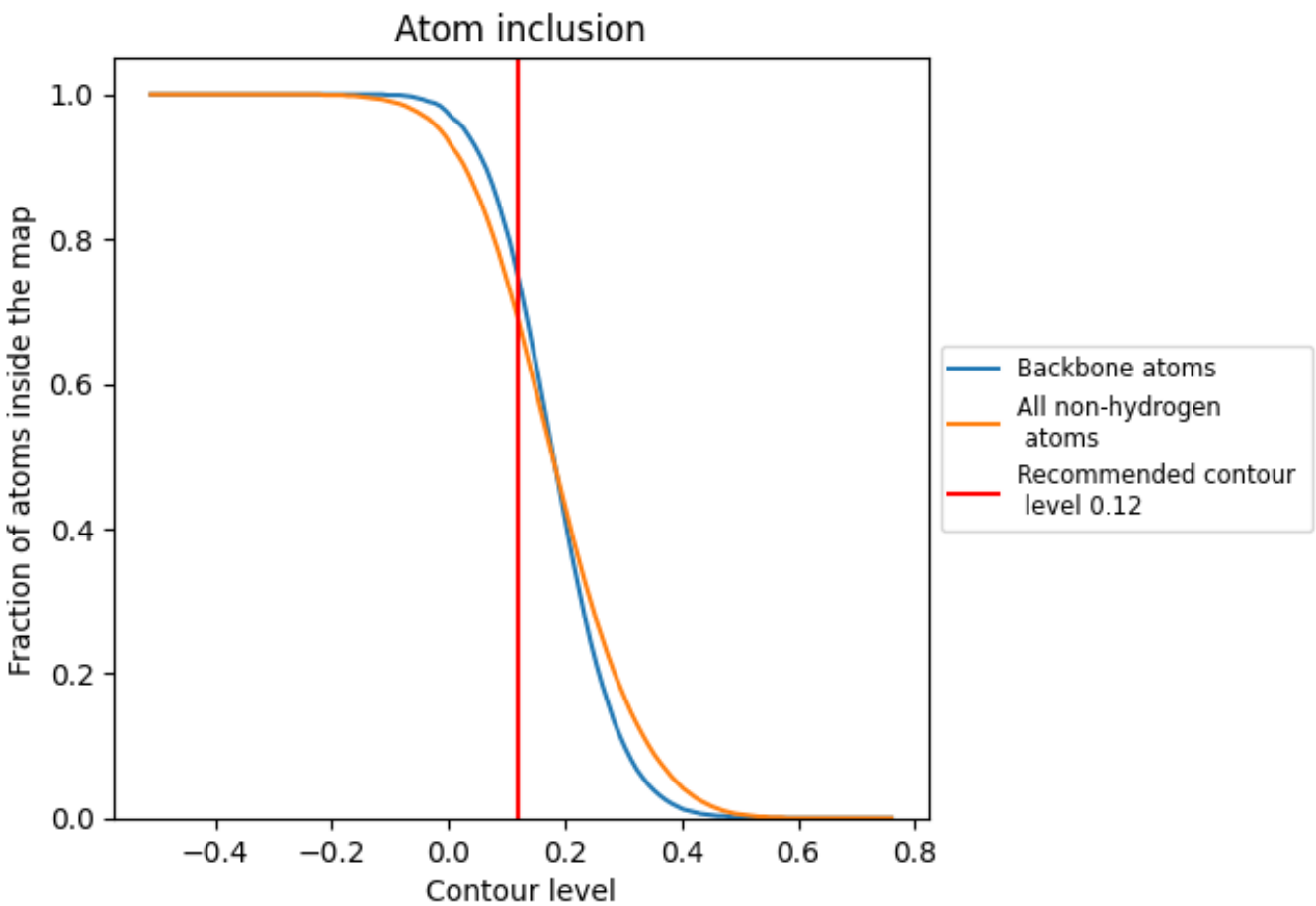
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.12).

9.4 Atom inclusion (i)



At the recommended contour level, 75% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6880	0.1890
AA	0.7560	0.2050
AB	0.3910	0.1500
AC	0.4960	0.1420
AD	0.4610	0.1350
AE	0.5320	0.1500
AF	0.6060	0.1760
AG	0.4700	0.1610
AH	0.5290	0.1450
AI	0.4710	0.1220
AJ	0.3250	0.1070
AK	0.5430	0.1610
AL	0.5160	0.1630
AM	0.5490	0.1550
AN	0.5610	0.1400
AO	0.5640	0.1650
AP	0.5310	0.1390
AQ	0.5680	0.1720
AR	0.5870	0.1720
AS	0.5860	0.1570
AT	0.5280	0.1460
AU	0.3500	0.1570
AV	0.5620	0.1430
AX	0.2630	0.1480
AZ	0.4900	0.3070
B0	0.5410	0.1620
B1	0.5510	0.1390
B2	0.5810	0.1740
B3	0.5650	0.1600
B4	0.5760	0.1680
B5	0.0180	-0.0010
B6	0.4650	0.1340
B7	0.5580	0.1530
B8	0.5620	0.1810
BA	0.8170	0.2140

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Chain	Atom inclusion	Q-score
BB	0.7850	0.2140
BC	0.5570	0.1700
BD	0.5980	0.1590
BE	0.4930	0.1400
BF	0.5940	0.1600
BG	0.6720	0.1850
BH	0.2460	0.1340
BI	0.2170	0.0320
BJ	0.6080	0.1750
BK	0.5070	0.1660
BL	0.5340	0.1610
BM	0.5540	0.1740
BN	0.5570	0.1360
BO	0.6230	0.1600
BP	0.5640	0.1720
BQ	0.5560	0.1160
BR	0.6200	0.1840
BS	0.5420	0.1360
BT	0.5230	0.1380
BU	0.5570	0.1560
BW	0.6440	0.1700
BY	0.5190	0.1080