wwPDB EM Validation Summary Report

May 5, 2024 – 07:37 PM EDT

PDB ID	:	4V6S
EMDB ID	:	EMD-5360
Title	:	Structural characterization of mRNA-tRNA translocation intermediates (class 3 of the six classes)
Authors	:	Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on	:	2011-12-09
Resolution	:	13.10 Å(reported)
Based on initial model	:	2I2V

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:

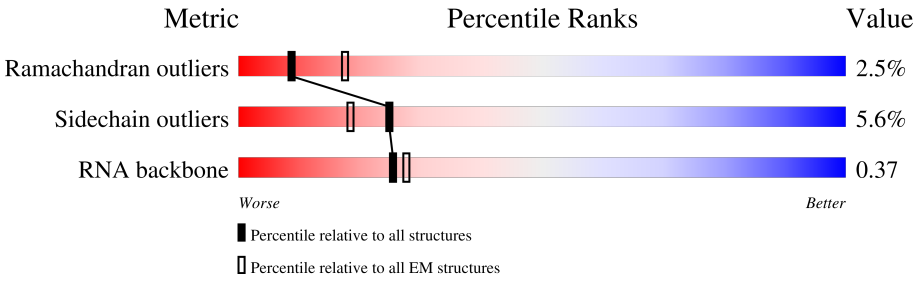
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 13.10 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)
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	120	37% 48% 15%
2	AB	2904	34% 54% 12%
3	AC	234	85% 14%
4	AD	272	73% 24%
5	AE	209	78% 18%
6	AF	201	77% 20%
7	AG	178	72% 25%
8	AH	176	75% 22%

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Mol	Chain	Length	Quality of chain
9	AI	149	19% 81% 16%
10	AJ	164	12% 78% 18%
11	AK	141	85% 13%
12	AL	142	75% 21%
13	AM	123	76% 20%
14	AN	144	86% 11%
15	AO	136	79% 17%
16	AP	127	78% 19%
17	AQ	117	75% 20% 5%
18	AR	114	76% 18% 5%
19	AS	117	70% 29%
20	AT	103	73% 23%
21	AU	110	75% 22%
22	AV	100	74% 25%
23	AW	103	81% 19%
24	AX	94	71% 27%
25	AY	84	73% 24%
26	AZ	77	60% 36%
27	A0	63	79% 14% 6%
28	A1	58	74% 19% 7%
29	A2	70	6% 81% 16%
30	A3	56	77% 18%
31	A4	54	80% 17%
32	A5	46	61% 39%
33	A6	64	83% 12% 5%

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Mol	Chain	Length	Quality of chain
34	A7	38	68% 29%
35	BA	1542	33% 54% 13%
36	BB	47	26% 23% 47% 30%
37	BC	77	38% 53% 9%
38	BD	240	7% 82% 15%
39	BE	232	76% 20%
40	BF	205	78% 20%
41	BG	166	80% 17%
42	BH	135	72% 25%
43	BI	178	76% 21%
44	BJ	129	77% 19%
45	BK	129	78% 17% 5%
46	BL	103	75% 19% 6%
47	BM	128	5% 80% 17%
48	BN	123	72% 24%
49	BO	117	78% 18%
50	BP	100	75% 22%
51	BQ	88	82% 15%
52	BR	82	65% 34%
53	BS	83	75% 20% 5%
54	BT	74	74% 20% 5%
55	BU	91	70% 27%
56	BV	86	86% 13%
57	BW	70	66% 27% 6%

2 Entry composition (i)

There are 57 unique types of molecules in this entry. The entry contains 150700 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 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	120	2566	1144	468	835	119	0	0

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AB	2904	62351	27824	11469	20155	2903	0	0

- Molecule 3 is a protein called 50S ribosomal protein L1.

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

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AD	272	2092	1294	425	366	7	0	0

- Molecule 5 is a protein called 50S ribosomal protein L3.

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

- Molecule 6 is a protein called 50S ribosomal protein L4.

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

- Molecule 7 is a protein called 50S ribosomal protein L5.

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

- Molecule 8 is a protein called 50S ribosomal protein L6.

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

- Molecule 9 is a protein called 50S ribosomal protein L9.

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

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 11 is a protein called 50S ribosomal protein L11.

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

- Molecule 12 is a protein called 50S ribosomal protein L13.

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

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 15 is a protein called 50S ribosomal protein L16.

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

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L19.

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

- Molecule 19 is a protein called 50S ribosomal protein L20.

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

- Molecule 20 is a protein called 50S ribosomal protein L21.

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

- Molecule 21 is a protein called 50S ribosomal protein L22.

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

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AW	103	Total	C	N	O	0	0
			789	498	148	143		

- Molecule 24 is a protein called 50S ribosomal protein L25.

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

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	84	Total	C	N	O	S	0	0
			634	391	129	113	1		

- Molecule 26 is a protein called 50S ribosomal protein L28.

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

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	A1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	A2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	A4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	A5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	A6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	A7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 35 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 36 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BB	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 37 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	BC	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

- Molecule 38 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BD	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 39 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BE	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 40 is a protein called 30S ribosomal protein S4.

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

- Molecule 41 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BG	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 42 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BH	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 43 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BI	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 44 is a protein called 30S ribosomal protein S8.

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

- Molecule 45 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BK	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 46 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BL	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 47 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BM	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 48 is a protein called 30S ribosomal protein S12.

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

- Molecule 49 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BO	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 50 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BP	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 51 is a protein called 30S ribosomal protein S15.

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

- Molecule 52 is a protein called 30S ribosomal protein S16.

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

- Molecule 53 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BS	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 54 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BT	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 55 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BU	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 56 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BV	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 57 is a protein called 30S ribosomal protein S21.

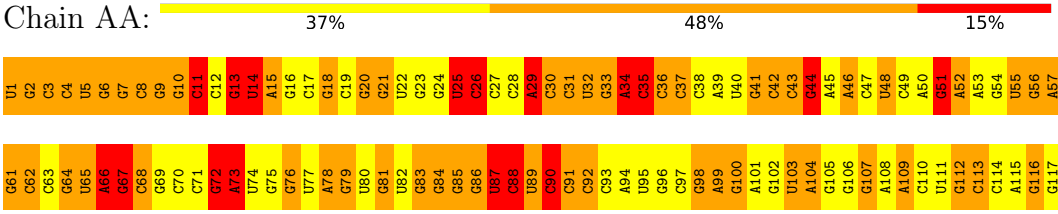
Mol	Chain	Residues	Atoms					AltConf	Trace
57	BW	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

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.

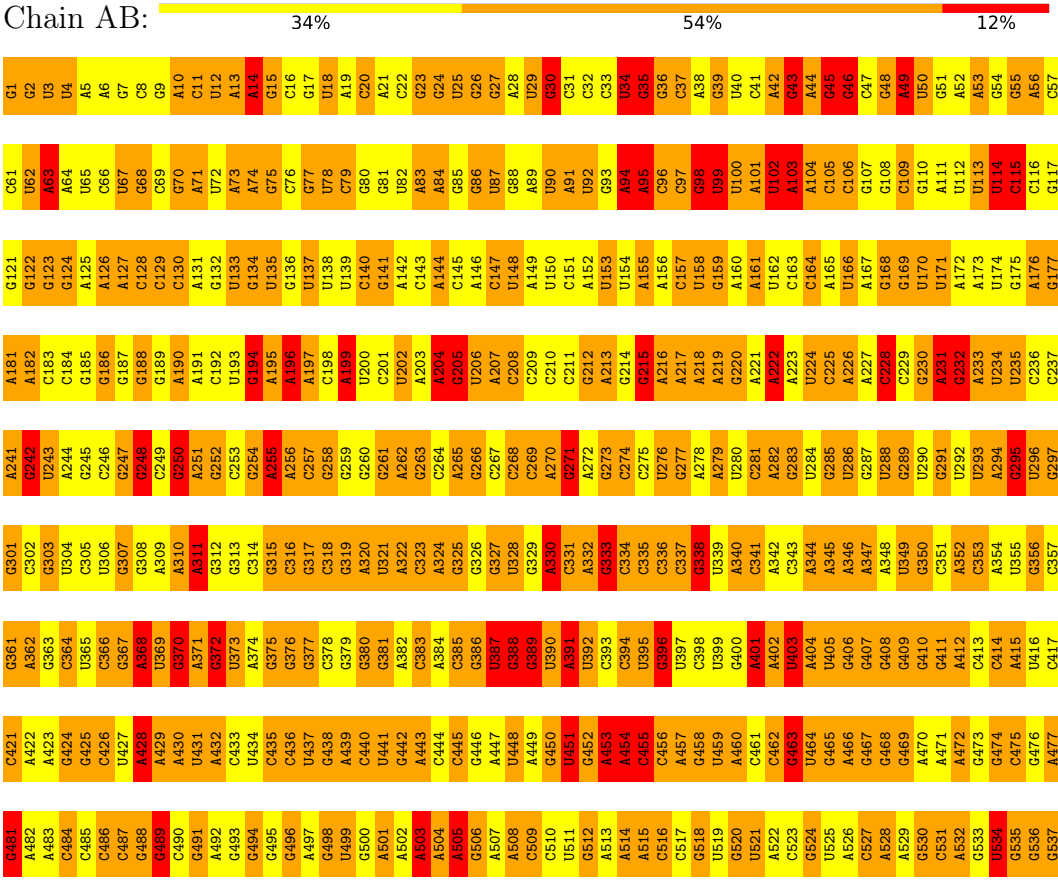
- Molecule 1: 5S ribosomal RNA

Chain AA:



- Molecule 2: 23S ribosomal RNA

Chain AB:



A541 C542 G543 C544 U545 U546 A547 G548 G549 C550 G551 U552 G553 U554 G555 A556 C557 U558 G559 C560 G561 U562 A563 C564 C565 U566 U567 U568 U569 G570 U571 A572 U573 A574 A575 U576 G577 G578 G579 U580 C581 A582 G583 C584 G585 A586 C587 U588 U589 A590 U591 A592 U593 U594 C595 U596 G597 U598 A599 G600

C601 A602 A603 G604 G605 U606 U607 A608 A609 C610 C611 G612 A613 A614 U615 A616 G617 G618 G619 G620 A621 G622 C623 C624 G625 A626 A627 G628 G629 G630 A631 A632 A633 C634 G635 G636 A637 G638 U639 C640 U641 U642 A643 A644 C645 U646 G647 G648 G649 C650 G651 U652 U653 A654 A655 G656 U657 U658 G659 C660

A661 G662 G663 G664 U665 A666 U667 A668 G669 A670 C671 C672 C673 G674 A675 A676 A677 C678 C679 C680 G681 G682 U683 G684 A685 U686 C687 U688 A689 G690 C691 C692 A693 U694 G695 G696 G697 C698 A699 G700 G701 U702 U703 G704 A705 A706 G707 G708 U709 U710 G711 G712 G713 U714 A715 A716 C717 A718 C719 U720

A721 A722 C723 U724 G725 G726 A727 G728 G729 A730 C731 C732 G733 A734 A735 C736 C737 G738 A739 C740 U741 A742 A743 U744 G745 U746 U747 G748 A749 A750 A751 A752 A753 U754 U755 A756 G757 C758 G759 G760 A761 U762 G763 A764 C765 U766 U767 G768 U769 G770 G771 C772 U773 G774 G775 G776 G777 G778 U779 G780

A781 A782 A783 G784 G785 C786 C787 A788 A789 U790 C791 A792 A793 A794 C795 C796 G797 G798 G799 A800 G801 A802 U803 A804 G805 C806 U807 G808 G809 U810 U811 C812 U813 C814 C815 C816 C817 G818 A819 A820 A821 G822 C823 U824 A825 U826 U827 U828 A829 G830 G831 U832 A833 G834 C835 G836 C837 C838 U839 C840

G841 U842 G843 A844 A845 U846 U847 C848 A849 U850 C851 U852 C853 C854 G855 G856 G857 G858 G859 U860 A861 G862 A863 G864 C865 A866 C867 U868 G869 U870 U871 U872 C873 G874 G875 C876 A877 A878 G879 G880 G881 G882 G883 U884 C885 A886 U887 C888 C889 C890 G891 A892 C893 U894 U895 A896 C897 C898 A899 A900

C901 C902 C903 G904 A905 U906 G907 C908 A909 A910 A911 C912 U913 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 G948 G949 G950 C951 G952 G953 G954 U955 G956 C957 U958 A959 A960

C961 G962 U963 C964 C965 G966 U967 C968 G969 U970 G971 A972 A973 G974 A975 G976 G977 G978 A979 A980 A981 C982 A983 A984 C985 C986 C987 A988 G989 A990 C991 C992 G993 C994 C995 A996 G997 C998 U999 A1000 A1001 G1002 G1003 U1004 C1005 C1006 C1007 A1008 A1009 A1010 G1011 U1012 C1013 A1014 U1015 G1016 G1017 U1018 U1019 A1020

A1021 G1022 U1023 G1024 G1025 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 G1122 C1123 G1124 G1125 A1126 A1127 G1128 A1129 U1130 G1131 U1132 A1133 A1134 C1135 G1136 G1137 G1138 G1139 C1140

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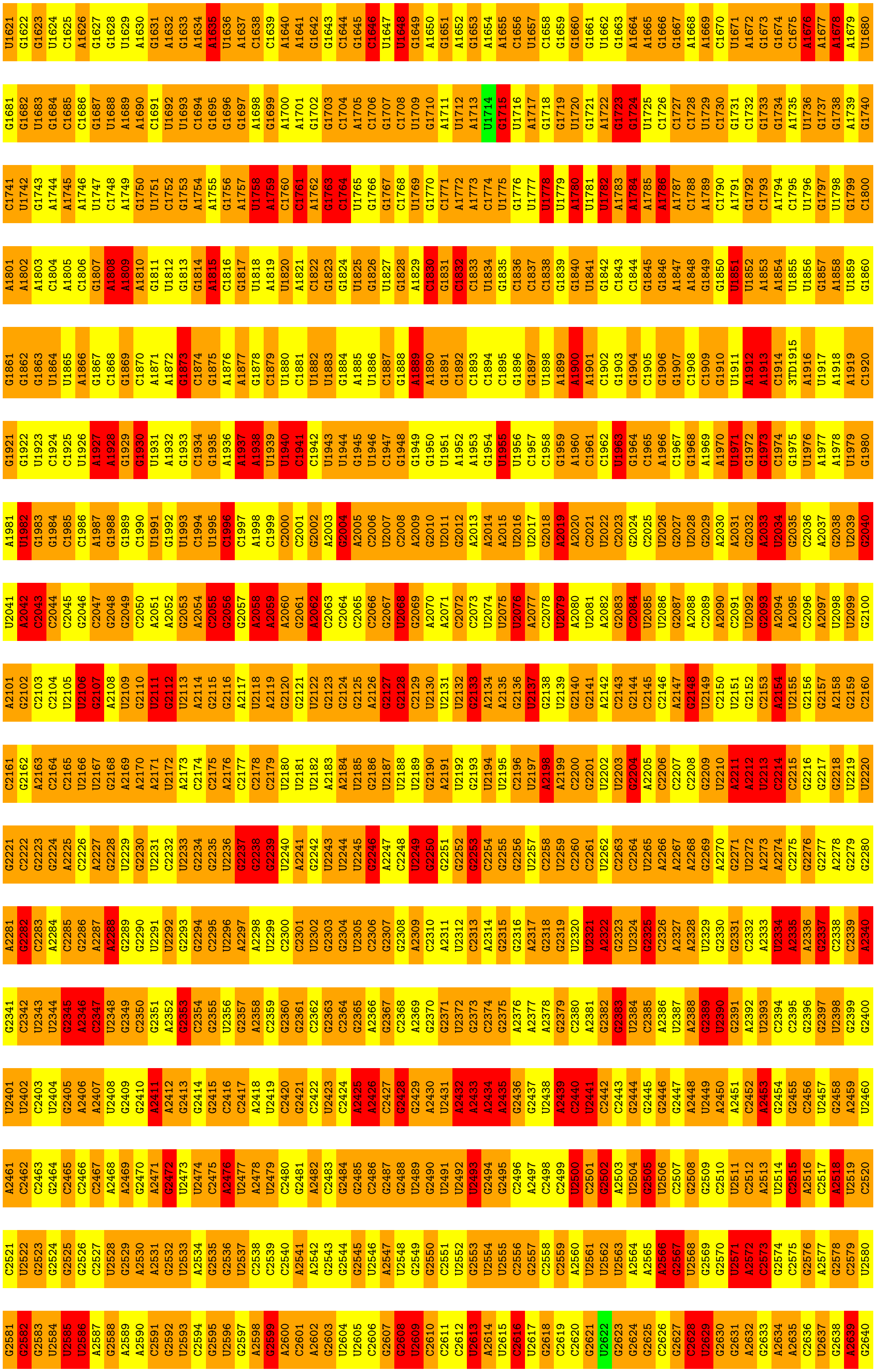
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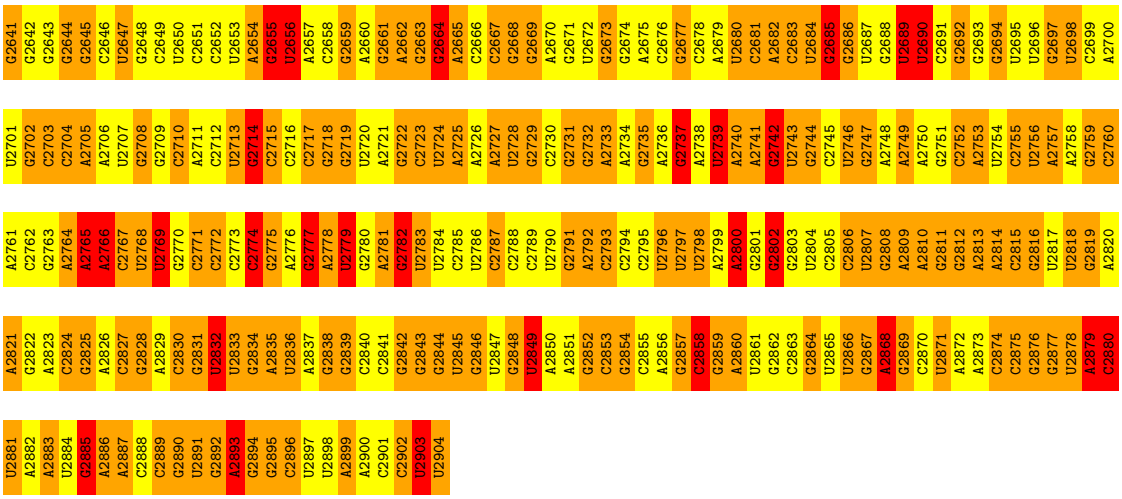
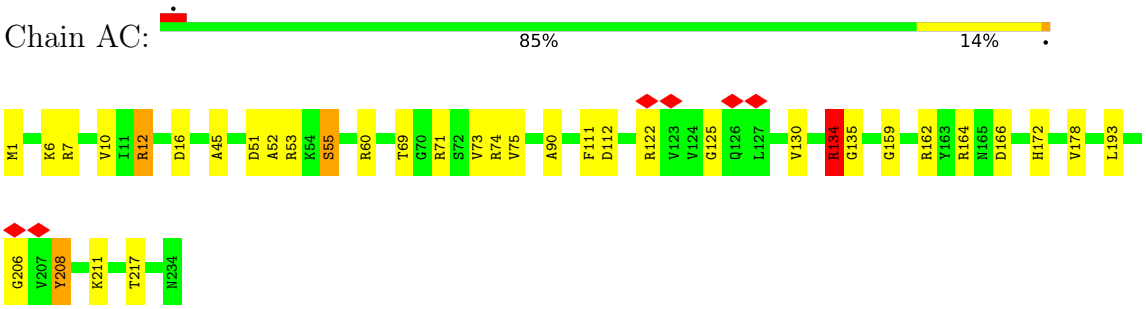


• Molecule 3: 50S ribosomal protein L1



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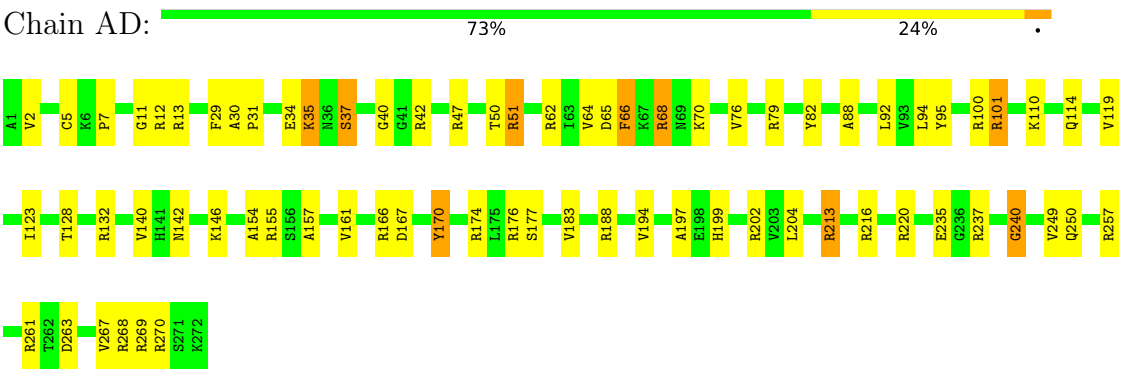
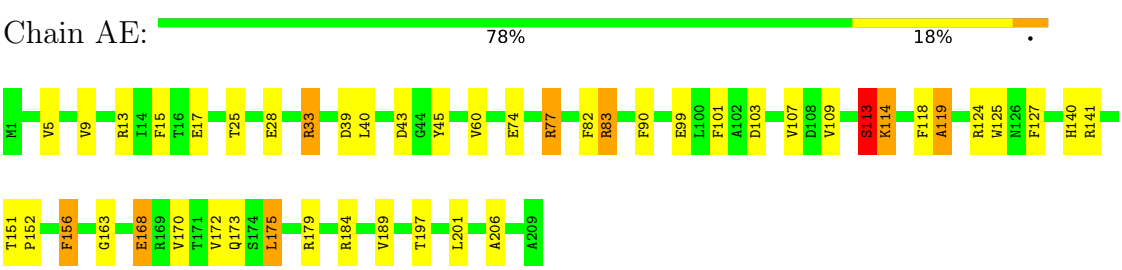


• Molecule 5: 50S ribosomal protein L3



• Molecule 6: 50S ribosomal protein L4

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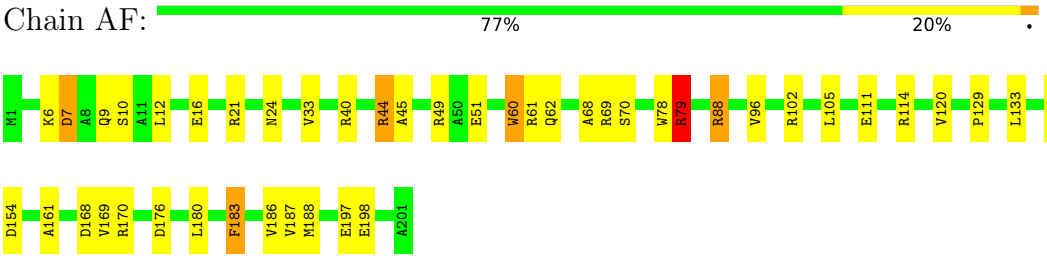

• Molecule 7: 50S ribosomal protein L5

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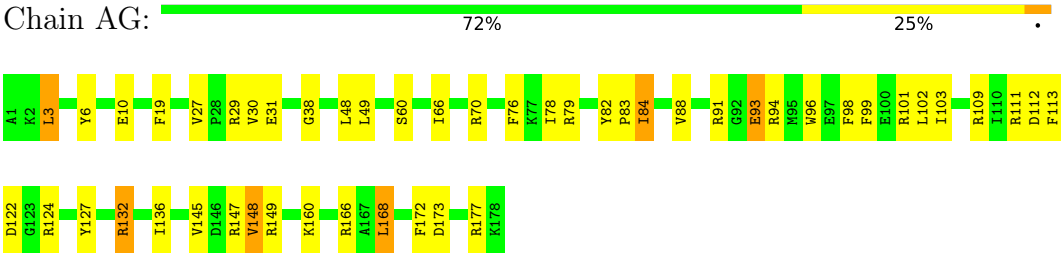

• Molecule 8: 50S ribosomal protein L6

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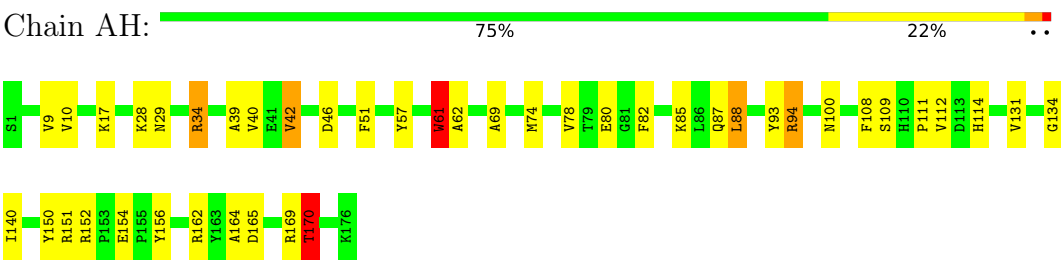

• Molecule 9: 50S ribosomal protein L9

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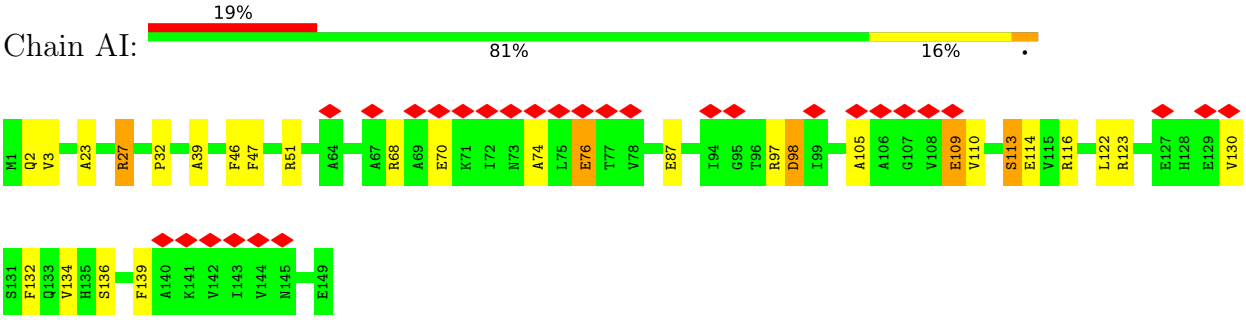

• Molecule 10: 50S ribosomal protein L10

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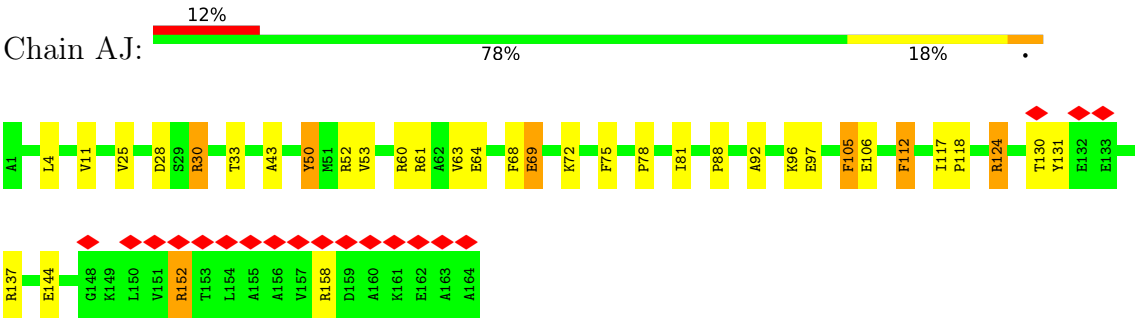

• Molecule 11: 50S ribosomal protein L11

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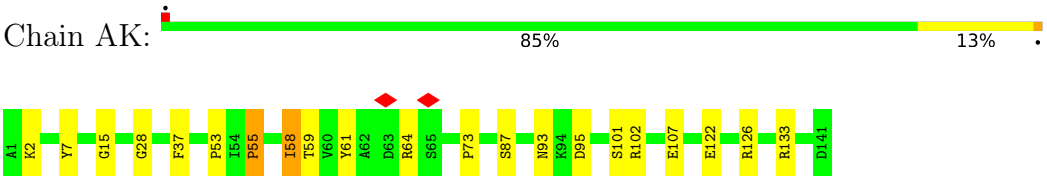

• Molecule 12: 50S ribosomal protein L13

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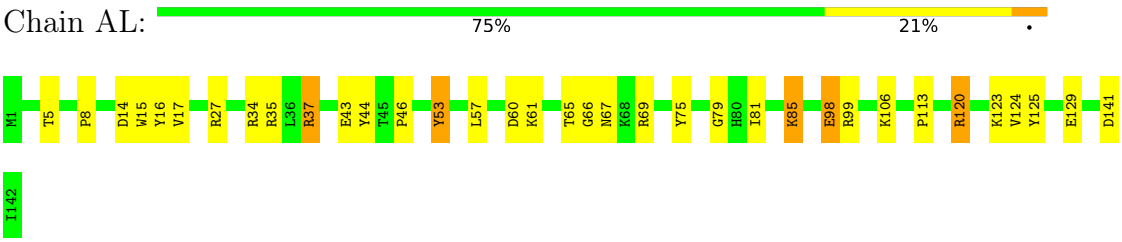

• Molecule 13: 50S ribosomal protein L14

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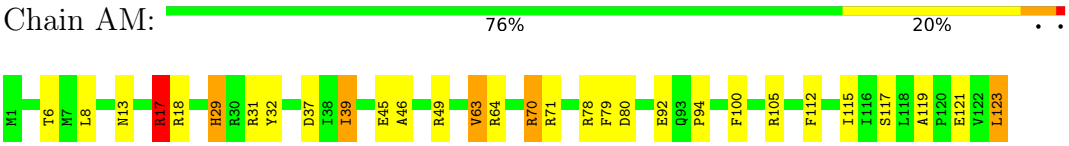
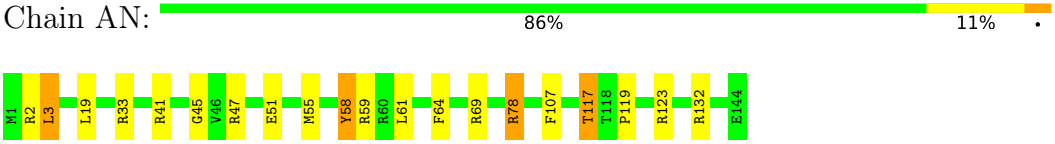


• Molecule 14: 50S ribosomal protein L15

Chain AN:



• Molecule 15: 50S ribosomal protein L16

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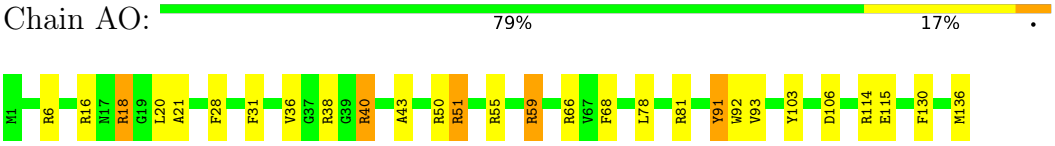

• Molecule 16: 50S ribosomal protein L17

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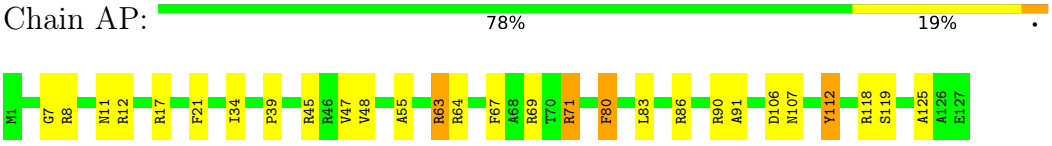
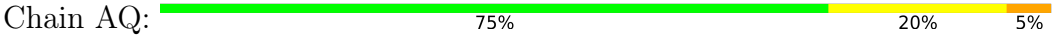
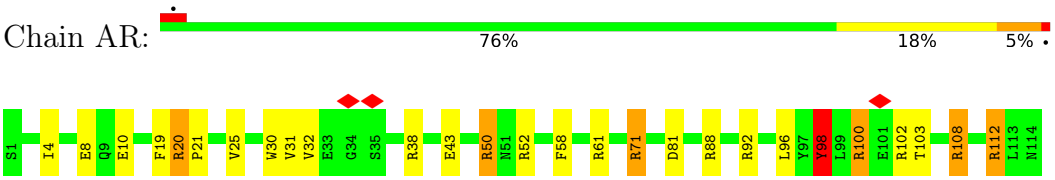


• Molecule 17: 50S ribosomal protein L18

Chain AQ:



• Molecule 18: 50S ribosomal protein L19



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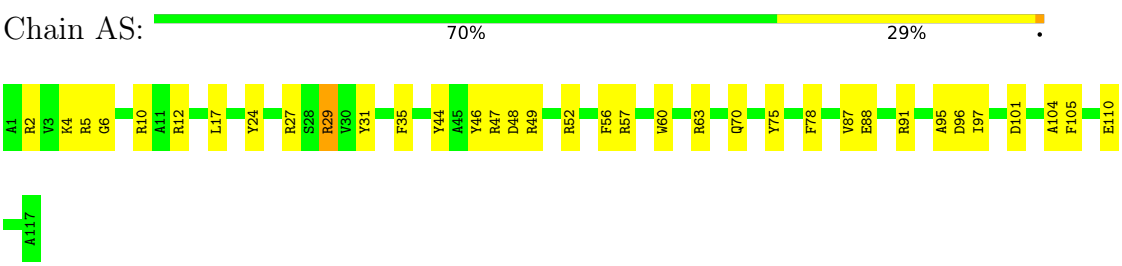

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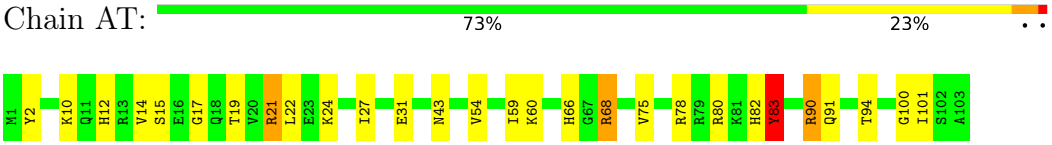

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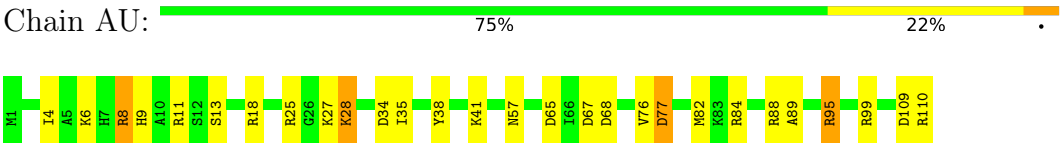

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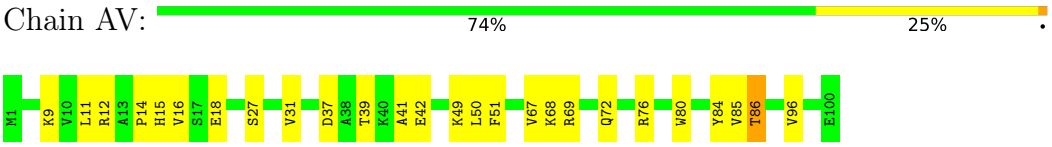

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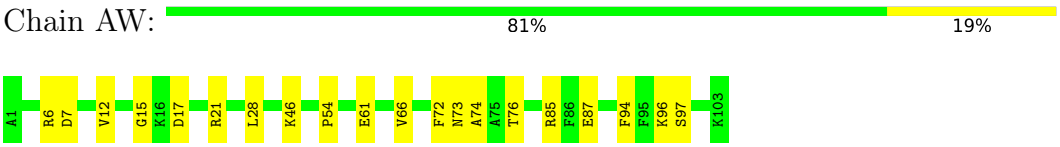

• Molecule 24: 50S ribosomal protein L25

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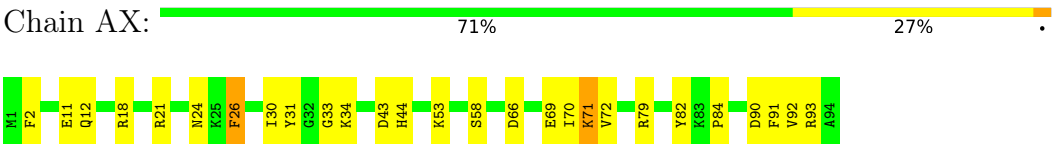

• Molecule 25: 50S ribosomal protein L27

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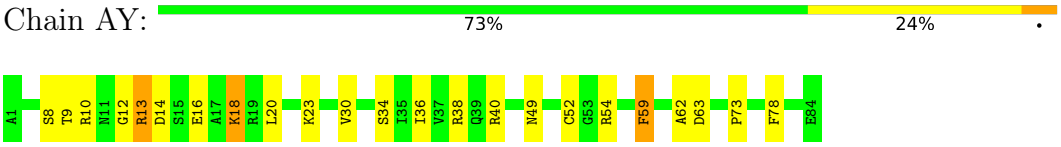

• Molecule 26: 50S ribosomal protein L28

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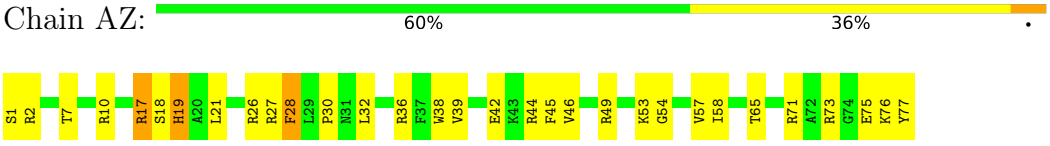
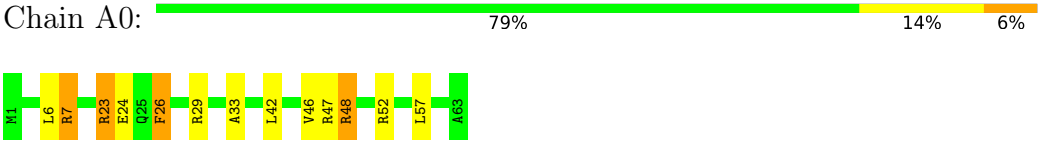


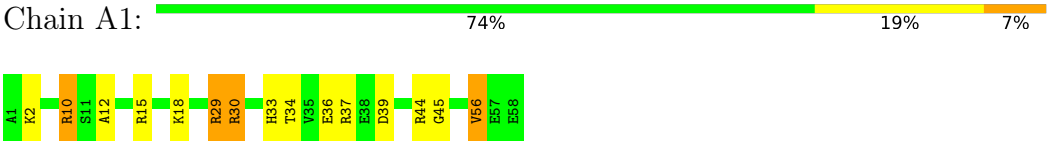
• Molecule 27: 50S ribosomal protein L29

Chain A0:



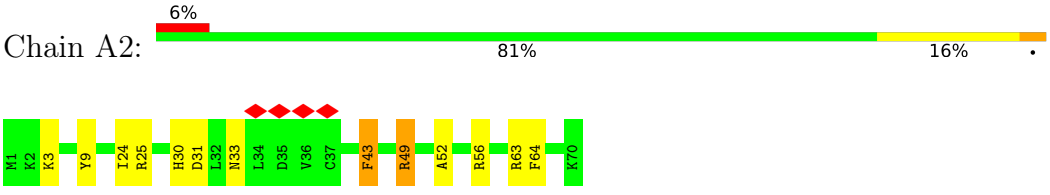
• Molecule 28: 50S ribosomal protein L30

Chain A1:



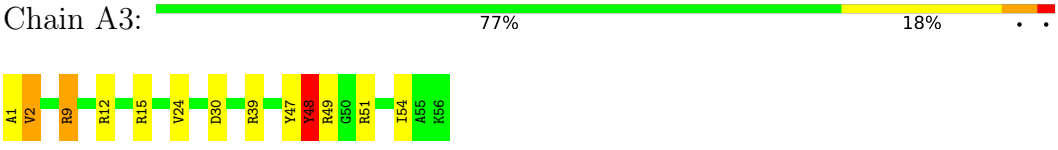
• Molecule 29: 50S ribosomal protein L31

Chain A2:



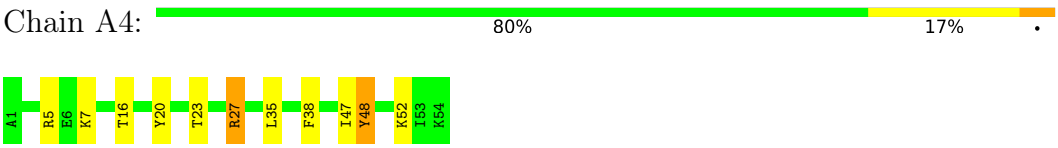
• Molecule 30: 50S ribosomal protein L32

Chain A3:



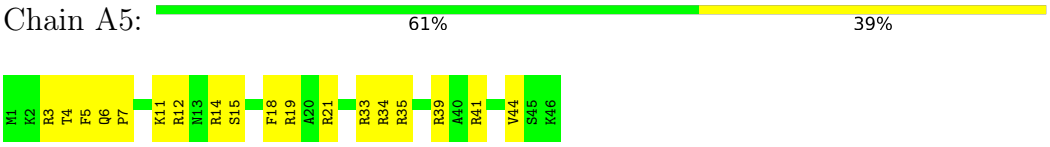
• Molecule 31: 50S ribosomal protein L33

Chain A4:



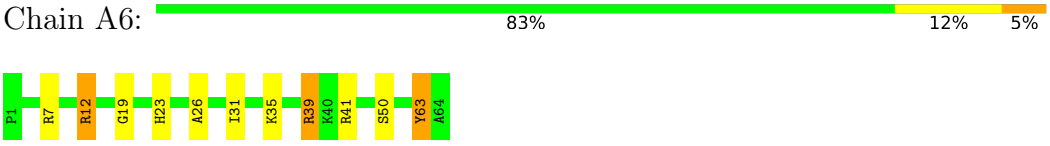
• Molecule 32: 50S ribosomal protein L34

Chain A5:



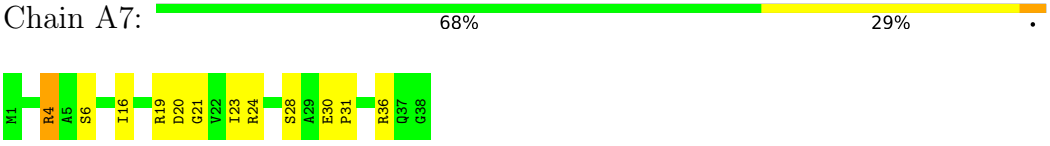
• Molecule 33: 50S ribosomal protein L35

Chain A6:



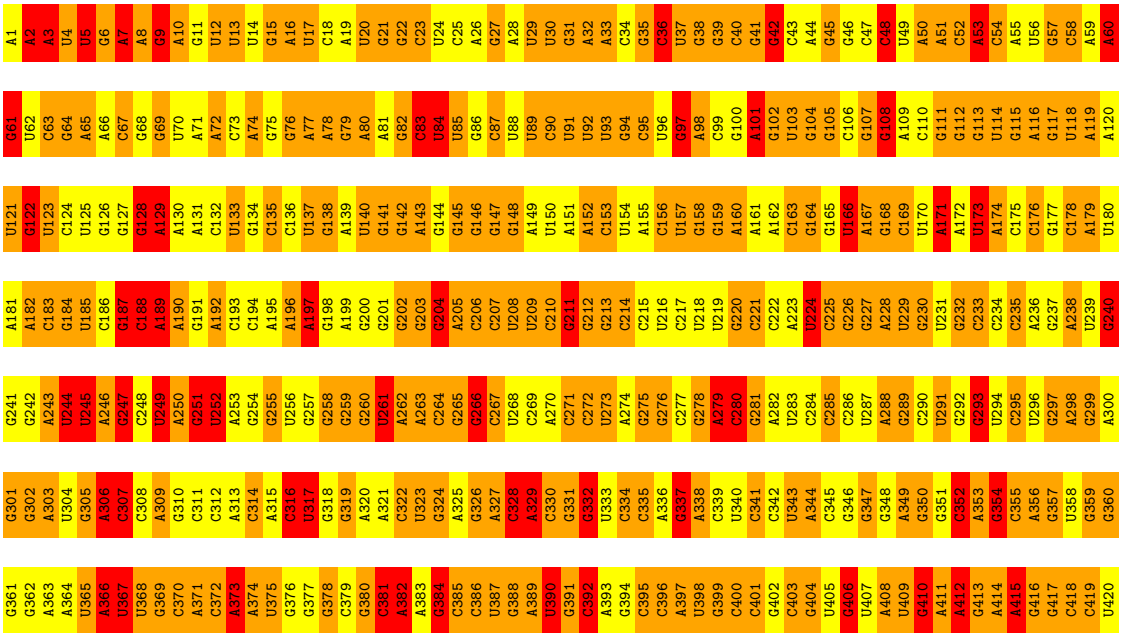
• Molecule 34: 50S ribosomal protein L36

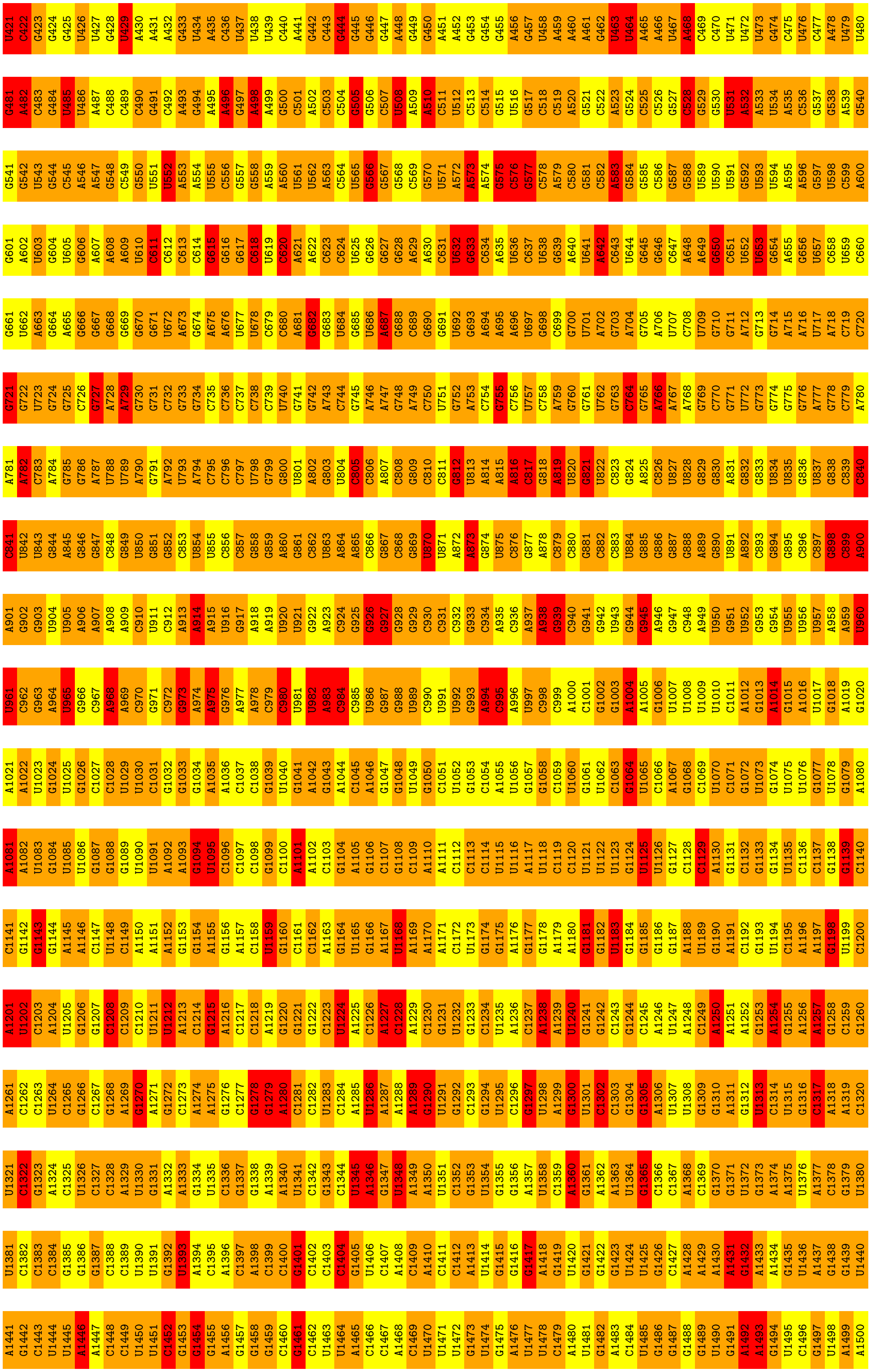
Chain A7:



• Molecule 35: 16S ribosomal RNA

Chain BA:

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G481 A482 C483 G484 U485 U486 A487 C488 C489 C490 G491 C492 A493 G494 A495 A496 G497 A498 A499 G500 C501 A502 C503 C504 G505 G506 C507 U508 A509 A510 C511 U512 C513 C514 G515 U516 G517 C518 C519 A520 G521 C522 A523 G524 C525 C526 G527 C528 G529 G530 U531 A532 A533 U534 A535 C536 G537 G538 A539 G540
G541 G542 U543 G544 C545 A546 A547 G548 C549 G550 U551 U552 A553 A554 U555 C556 G557 G558 A559 A560 U561 U562 A563 C564 U565 G566 C567 G568 C569 G570 U571 A572 A573 A574 C575 C576 G577 C578 A579 C580 G581 C582 A583 G584 G585 C586 G587 G588 U589 U590 U591 G592 U593 U594 A595 A596 G597 U598 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 C627 G628 A629 A630 C631 U632 G633 C634 A635 U636 C637 G638 G639 A640 U641 A642 C643 U644 G645 G646 C647 A648 A649 G650 C651 U652 U653 G654 A655 G656 U657 C658 U659 C660
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C841 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 C897 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 C932 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
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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 U1056 G1057 G1058 C1059 U1060 G1061 U1062 C1063 G1064 U1065 C1066 A1067 G1068 C1069 U1070 C1071 G1072 U1073 G1074 U1075 U1076 G1077 U1078 G1079 A1080
A1081 A1082 U1083 G1084 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 G1182 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
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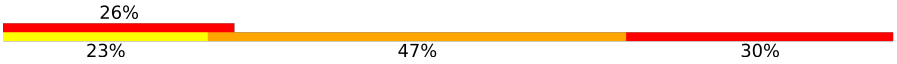
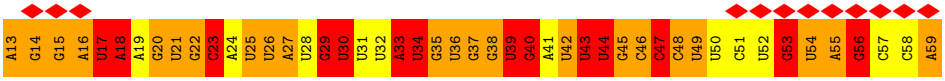
A1441 G1442 C1443 U1444 U1445 A1446 A1447 C1448 C1449 U1450 U1451 C1452 G1453 G1454 G1455 A1456 G1457 G1458 G1459 C1460 G1461 C1462 U1463 U1464 A1465 C1466 C1467 A1468 C1469 U1470 U1471 U1472 G1473 U1474 G1475 A1476 U1477 U1478 C1479 A1480 U1481 G1482 A1483 C1484 U1485 G1486 G1487 G1488 G1489 U1490 G1491 A1492 A1493 G1494 U1495 C1496 G1497 U1498 A1499 A1500

• Molecule 36: mRNA

Chain BB:



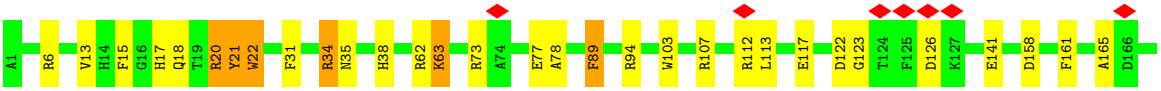


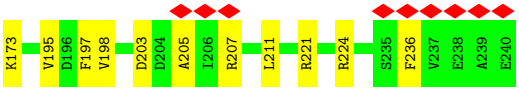
• Molecule 37: P site tRNA

Chain BC:

• Molecule 38: 30S ribosomal protein S2

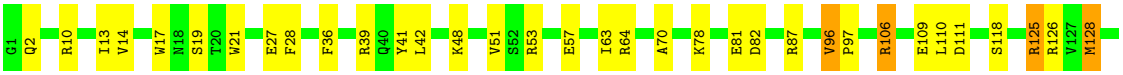
Chain BD:

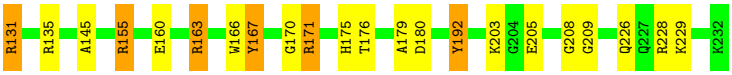




• Molecule 39: 30S ribosomal protein S3

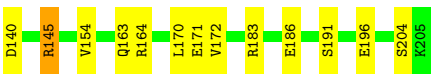
Chain BE:





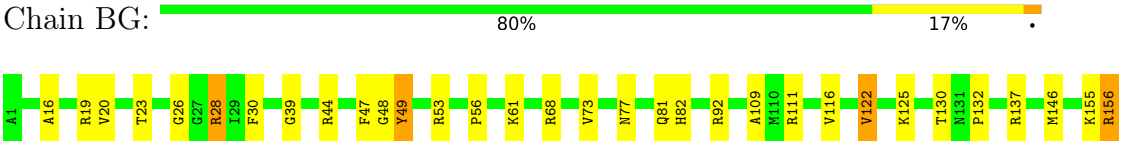
• Molecule 40: 30S ribosomal protein S4

Chain BF:



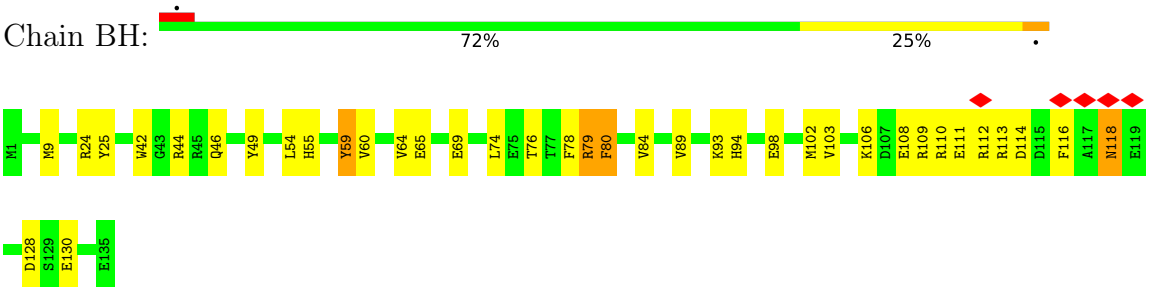
• Molecule 41: 30S ribosomal protein S5

Chain BG:



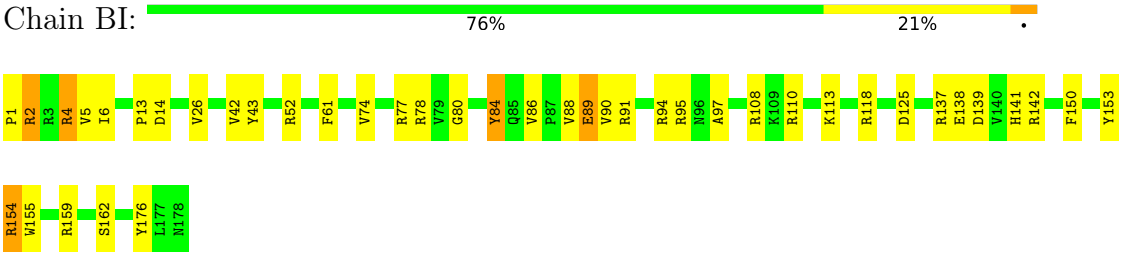
• Molecule 42: 30S ribosomal protein S6

Chain BH:



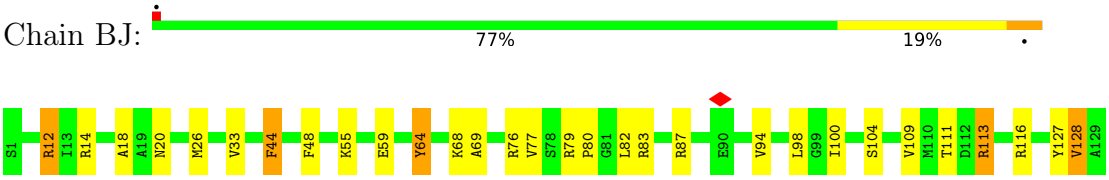
• Molecule 43: 30S ribosomal protein S7

Chain BI:



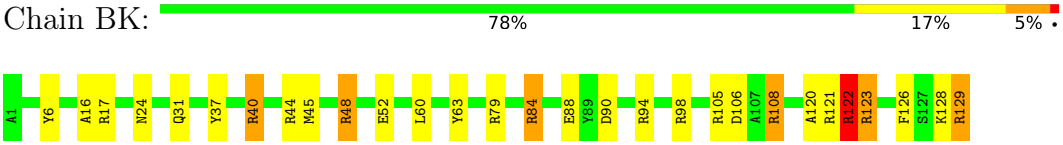
• Molecule 44: 30S ribosomal protein S8

Chain BJ:



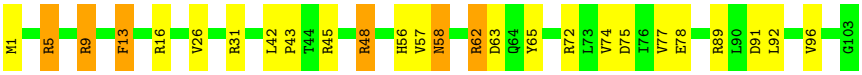
• Molecule 45: 30S ribosomal protein S9

Chain BK:

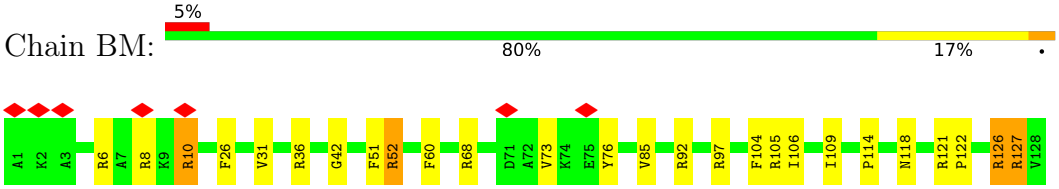


• Molecule 46: 30S ribosomal protein S10

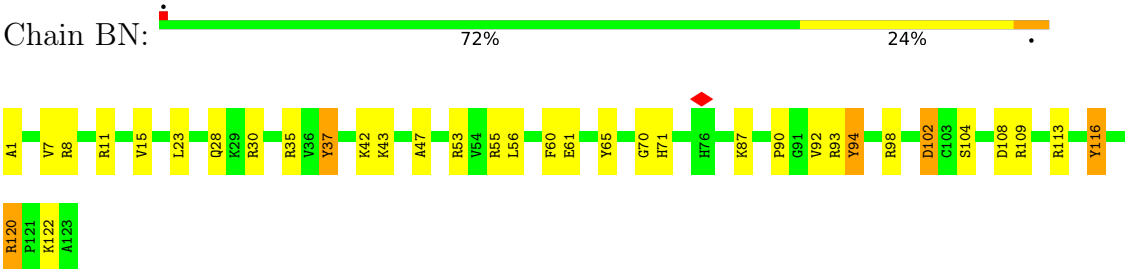
Chain BL:



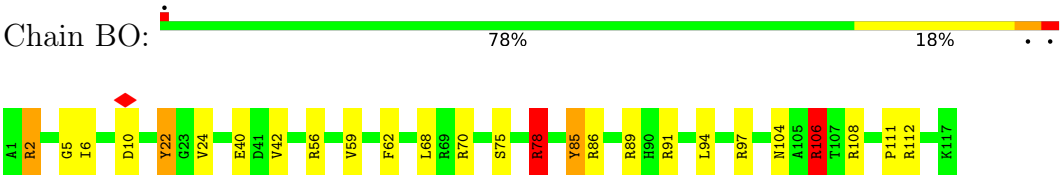
• Molecule 47: 30S ribosomal protein S11



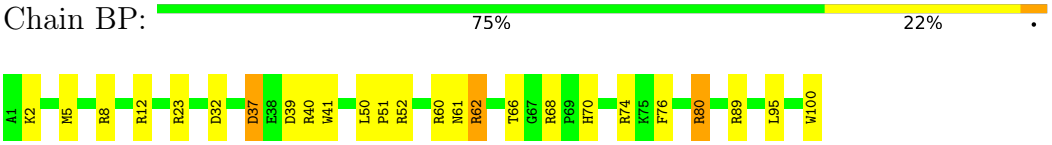
• Molecule 48: 30S ribosomal protein S12



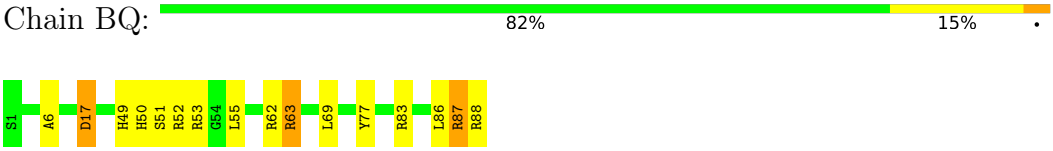
• Molecule 49: 30S ribosomal protein S13



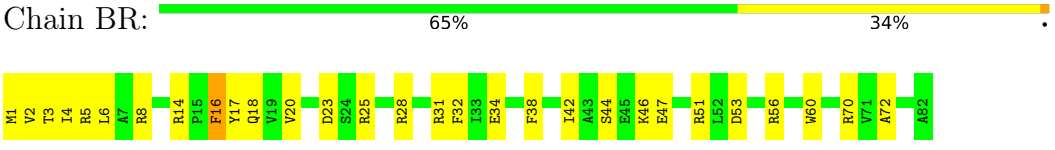
• Molecule 50: 30S ribosomal protein S14



• Molecule 51: 30S ribosomal protein S15

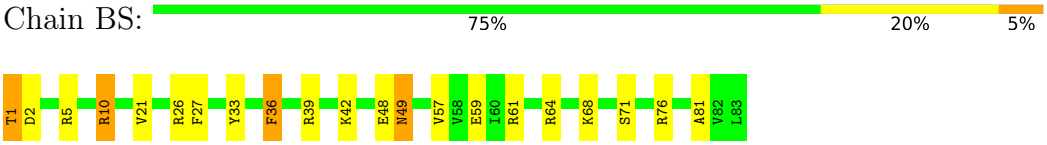


• Molecule 52: 30S ribosomal protein S16



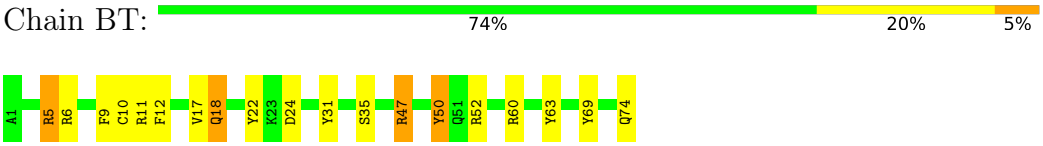
• Molecule 53: 30S ribosomal protein S17

Chain BS:



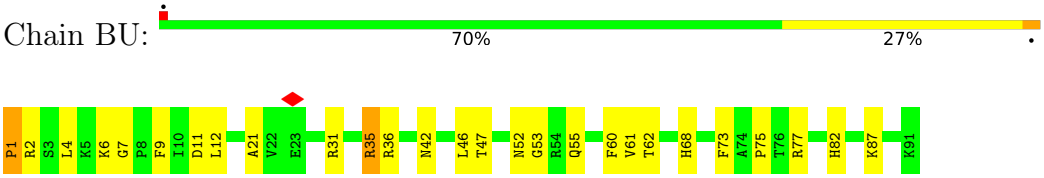
• Molecule 54: 30S ribosomal protein S18

Chain BT:



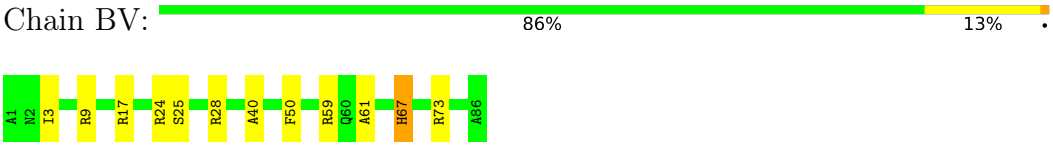
• Molecule 55: 30S ribosomal protein S19

Chain BU:



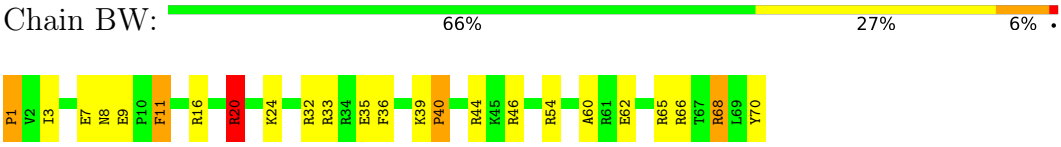
• Molecule 56: 30S ribosomal protein S20

Chain BV:



• Molecule 57: 30S ribosomal protein S21

Chain BW:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	58269	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	1.443	Depositor
Minimum map value	-0.456	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.182	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	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: 5MC, 2MA, H2U, OMU, 4OC, UR3, 5MU, OMG, MA6, OMC, PSU, 7MG, 2MG, 3TD, 4SU, 6MZ, CH, 1MG

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	3.07	298/2869 (10.4%)	3.56	669/4474 (15.0%)
2	AB	3.08	7422/69257 (10.7%)	3.52	15483/108040 (14.3%)
3	AC	1.42	3/1748 (0.2%)	1.86	30/2355 (1.3%)
4	AD	1.56	11/2131 (0.5%)	2.03	60/2863 (2.1%)
5	AE	1.49	5/1586 (0.3%)	1.92	39/2134 (1.8%)
6	AF	1.52	7/1571 (0.4%)	1.92	42/2113 (2.0%)
7	AG	1.53	3/1444 (0.2%)	2.02	45/1937 (2.3%)
8	AH	1.53	6/1343 (0.4%)	1.96	35/1816 (1.9%)
9	AI	1.45	3/1122 (0.3%)	1.94	25/1515 (1.7%)
10	AJ	1.52	5/1247 (0.4%)	1.94	27/1679 (1.6%)
11	AK	1.44	5/1046 (0.5%)	1.86	18/1410 (1.3%)
12	AL	1.50	6/1152 (0.5%)	2.08	30/1551 (1.9%)
13	AM	1.53	5/956 (0.5%)	1.95	25/1279 (2.0%)
14	AN	1.52	5/1062 (0.5%)	1.89	20/1413 (1.4%)
15	AO	1.49	3/1093 (0.3%)	2.07	38/1460 (2.6%)
16	AP	1.48	5/1021 (0.5%)	2.09	28/1364 (2.1%)
17	AQ	1.57	4/910 (0.4%)	1.90	27/1219 (2.2%)
18	AR	1.54	2/929 (0.2%)	1.95	26/1242 (2.1%)
19	AS	1.52	6/960 (0.6%)	2.20	39/1278 (3.1%)
20	AT	1.60	5/829 (0.6%)	1.89	18/1107 (1.6%)
21	AU	1.49	1/864 (0.1%)	1.96	21/1156 (1.8%)
22	AV	1.54	3/794 (0.4%)	1.90	17/1060 (1.6%)
23	AW	1.44	2/797 (0.3%)	1.90	13/1062 (1.2%)
24	AX	1.49	5/766 (0.7%)	1.79	15/1025 (1.5%)
25	AY	1.48	2/642 (0.3%)	1.92	14/848 (1.7%)
26	AZ	1.50	3/635 (0.5%)	2.21	25/848 (2.9%)
27	A0	1.37	1/510 (0.2%)	1.90	12/677 (1.8%)
28	A1	1.52	2/453 (0.4%)	2.11	13/605 (2.1%)
29	A2	1.55	3/559 (0.5%)	1.96	12/745 (1.6%)
30	A3	1.49	1/450 (0.2%)	2.05	15/599 (2.5%)
31	A4	1.46	1/448 (0.2%)	1.82	7/594 (1.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	A5	1.53	1/380 (0.3%)	2.15	14/498 (2.8%)
33	A6	1.55	4/513 (0.8%)	1.80	7/676 (1.0%)
34	A7	1.57	2/303 (0.7%)	1.98	6/397 (1.5%)
35	BA	3.07	3871/36769 (10.5%)	3.53	8462/57354 (14.8%)
36	BB	3.23	131/1108 (11.8%)	3.61	262/1724 (15.2%)
37	BC	3.09	176/1721 (10.2%)	3.61	392/2683 (14.6%)
38	BD	1.43	2/1904 (0.1%)	1.86	32/2565 (1.2%)
39	BE	1.55	11/1852 (0.6%)	1.94	38/2490 (1.5%)
40	BF	1.51	8/1665 (0.5%)	1.96	51/2227 (2.3%)
41	BG	1.54	5/1239 (0.4%)	2.01	27/1664 (1.6%)
42	BH	1.50	3/1121 (0.3%)	1.92	27/1509 (1.8%)
43	BI	1.54	5/1422 (0.4%)	2.05	48/1908 (2.5%)
44	BJ	1.49	3/989 (0.3%)	2.00	23/1326 (1.7%)
45	BK	1.55	5/1048 (0.5%)	2.08	34/1394 (2.4%)
46	BL	1.47	1/835 (0.1%)	2.19	25/1127 (2.2%)
47	BM	1.52	7/982 (0.7%)	2.02	28/1323 (2.1%)
48	BN	1.52	4/969 (0.4%)	2.10	39/1300 (3.0%)
49	BO	1.51	8/919 (0.9%)	1.98	30/1226 (2.4%)
50	BP	1.53	1/817 (0.1%)	2.02	23/1088 (2.1%)
51	BQ	1.43	1/724 (0.1%)	1.93	16/966 (1.7%)
52	BR	1.53	2/659 (0.3%)	2.14	25/884 (2.8%)
53	BS	1.55	6/681 (0.9%)	1.99	18/913 (2.0%)
54	BT	1.60	6/637 (0.9%)	2.07	18/851 (2.1%)
55	BU	1.53	3/744 (0.4%)	1.84	16/995 (1.6%)
56	BV	1.39	1/676 (0.1%)	1.86	14/895 (1.6%)
57	BW	1.46	5/598 (0.8%)	2.19	23/792 (2.9%)
All	All	2.69	12105/162469 (7.5%)	3.17	26586/242243 (11.0%)

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	69
2	AB	0	1654
3	AC	0	3
4	AD	0	11
5	AE	0	7
6	AF	0	2
7	AG	0	1
8	AH	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
9	AI	0	3
10	AJ	0	8
11	AK	0	1
12	AL	0	3
13	AM	0	3
14	AN	0	2
15	AO	0	3
16	AP	0	5
17	AQ	0	4
18	AR	0	6
19	AS	0	3
20	AT	0	5
21	AU	0	5
22	AV	0	1
24	AX	0	5
25	AY	0	4
26	AZ	0	2
27	A0	0	4
28	A1	0	4
29	A2	0	3
30	A3	0	1
31	A4	0	2
32	A5	0	2
33	A6	0	2
34	A7	0	2
35	BA	0	882
36	BB	0	30
37	BC	0	41
38	BD	0	4
39	BE	0	9
40	BF	0	3
41	BG	0	3
42	BH	0	9
43	BI	0	3
44	BJ	0	7
45	BK	0	5
46	BL	0	2
47	BM	0	1
48	BN	0	6
49	BO	0	4
50	BP	0	1
51	BQ	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	BR	0	2
53	BS	0	1
54	BT	0	2
55	BU	0	4
57	BW	0	4
All	All	0	2857

The worst 5 of 12105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	504	A	N3-C4	18.22	1.45	1.34
2	AB	2682	A	N3-C4	18.21	1.45	1.34
2	AB	744	U	C2-N3	17.97	1.50	1.37
35	BA	1484	C	N1-C6	16.21	1.46	1.37
2	AB	2829	A	P-O5'	15.96	1.75	1.59

The worst 5 of 26586 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
12	AL	120	ARG	NE-CZ-NH2	24.50	132.55	120.30
2	AB	1193	G	C8-N9-C4	-23.95	96.82	106.40
35	BA	581	G	N9-C4-C5	22.36	114.35	105.40
46	BL	45	ARG	NE-CZ-NH1	21.76	131.18	120.30
44	BJ	116	ARG	NE-CZ-NH2	-21.74	109.43	120.30

There are no chirality outliers.

5 of 2857 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	U	Sidechain
1	AA	2	G	Sidechain
1	AA	3	C	Sidechain
1	AA	4	C	Sidechain
1	AA	5	U	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	2566	0	1299	0	0
2	AB	62351	0	31248	0	0
3	AC	1733	0	1824	0	0
4	AD	2092	0	2170	0	0
5	AE	1565	0	1616	0	0
6	AF	1552	0	1619	0	0
7	AG	1420	0	1460	0	0
8	AH	1323	0	1374	0	0
9	AI	1111	0	1148	0	0
10	AJ	1233	0	1283	0	0
11	AK	1032	0	1088	0	0
12	AL	1129	0	1162	0	0
13	AM	947	0	1023	0	0
14	AN	1053	0	1129	0	0
15	AO	1074	0	1157	0	0
16	AP	1008	0	1045	0	0
17	AQ	900	0	935	0	0
18	AR	917	0	965	0	0
19	AS	947	0	1022	0	0
20	AT	816	0	839	0	0
21	AU	857	0	922	0	0
22	AV	787	0	846	0	0
23	AW	789	0	847	0	0
24	AX	753	0	780	0	0
25	AY	634	0	656	0	0
26	AZ	625	0	655	0	0
27	A0	509	0	543	0	0
28	A1	449	0	491	0	0
29	A2	549	0	552	0	0
30	A3	444	0	461	0	0
31	A4	441	0	485	0	0
32	A5	377	0	418	0	0
33	A6	504	0	574	0	0
34	A7	302	0	343	0	0
35	BA	33089	0	16599	0	0
36	BB	993	0	501	0	0
37	BC	1641	0	841	0	0
38	BD	1872	0	1885	0	0
39	BE	1822	0	1913	0	0
40	BF	1643	0	1710	0	0
41	BG	1225	0	1273	0	0
42	BH	1101	0	1050	0	0
43	BI	1400	0	1449	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	BJ	979	0	1034	0	0
45	BK	1036	0	1084	0	0
46	BL	825	0	865	0	0
47	BM	965	0	997	0	0
48	BN	955	0	1019	0	0
49	BO	910	0	981	0	0
50	BP	805	0	847	0	0
51	BQ	716	0	742	0	0
52	BR	649	0	666	0	0
53	BS	672	0	716	0	0
54	BT	626	0	651	0	0
55	BU	727	0	769	0	0
56	BV	670	0	722	0	0
57	BW	590	0	631	0	0
All	All	150700	0	102924	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

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
3	AC	232/234 (99%)	215 (93%)	12 (5%)	5 (2%)	6 35
4	AD	270/272 (99%)	237 (88%)	24 (9%)	9 (3%)	4 26
5	AE	207/209 (99%)	175 (84%)	24 (12%)	8 (4%)	3 23
6	AF	199/201 (99%)	173 (87%)	16 (8%)	10 (5%)	2 20
7	AG	176/178 (99%)	151 (86%)	15 (8%)	10 (6%)	1 18
8	AH	174/176 (99%)	159 (91%)	11 (6%)	4 (2%)	6 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	AI	147/149 (99%)	131 (89%)	12 (8%)	4 (3%)	5	31
10	AJ	162/164 (99%)	155 (96%)	6 (4%)	1 (1%)	25	66
11	AK	139/141 (99%)	134 (96%)	4 (3%)	1 (1%)	22	63
12	AL	140/142 (99%)	120 (86%)	15 (11%)	5 (4%)	3	25
13	AM	121/123 (98%)	105 (87%)	12 (10%)	4 (3%)	4	26
14	AN	142/144 (99%)	125 (88%)	14 (10%)	3 (2%)	7	36
15	AO	134/136 (98%)	124 (92%)	8 (6%)	2 (2%)	10	46
16	AP	125/127 (98%)	115 (92%)	9 (7%)	1 (1%)	19	60
17	AQ	115/117 (98%)	110 (96%)	5 (4%)	0	100	100
18	AR	112/114 (98%)	97 (87%)	13 (12%)	2 (2%)	8	40
19	AS	115/117 (98%)	108 (94%)	3 (3%)	4 (4%)	3	25
20	AT	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
21	AU	108/110 (98%)	99 (92%)	5 (5%)	4 (4%)	3	24
22	AV	98/100 (98%)	77 (79%)	18 (18%)	3 (3%)	4	27
23	AW	101/103 (98%)	89 (88%)	9 (9%)	3 (3%)	4	28
24	AX	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	14	52
25	AY	82/84 (98%)	64 (78%)	14 (17%)	4 (5%)	2	20
26	AZ	75/77 (97%)	68 (91%)	4 (5%)	3 (4%)	3	23
27	A0	61/63 (97%)	56 (92%)	4 (7%)	1 (2%)	9	44
28	A1	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
29	A2	68/70 (97%)	64 (94%)	3 (4%)	1 (2%)	10	46
30	A3	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	3	24
31	A4	52/54 (96%)	49 (94%)	1 (2%)	2 (4%)	3	24
32	A5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	22
33	A6	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	9	44
34	A7	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	1	12
38	BD	238/240 (99%)	218 (92%)	14 (6%)	6 (2%)	5	32
39	BE	230/232 (99%)	217 (94%)	9 (4%)	4 (2%)	9	42
40	BF	203/205 (99%)	186 (92%)	13 (6%)	4 (2%)	7	38
41	BG	164/166 (99%)	150 (92%)	12 (7%)	2 (1%)	13	50
42	BH	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
43	BI	176/178 (99%)	168 (96%)	5 (3%)	3 (2%)	9 42
44	BJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	19 60
45	BK	127/129 (98%)	114 (90%)	10 (8%)	3 (2%)	6 33
46	BL	101/103 (98%)	91 (90%)	4 (4%)	6 (6%)	1 17
47	BM	126/128 (98%)	109 (86%)	15 (12%)	2 (2%)	9 44
48	BN	121/123 (98%)	103 (85%)	16 (13%)	2 (2%)	9 42
49	BO	115/117 (98%)	109 (95%)	5 (4%)	1 (1%)	17 57
50	BP	98/100 (98%)	85 (87%)	6 (6%)	7 (7%)	1 14
51	BQ	86/88 (98%)	81 (94%)	4 (5%)	1 (1%)	13 50
52	BR	80/82 (98%)	76 (95%)	4 (5%)	0	100 100
53	BS	81/83 (98%)	73 (90%)	7 (9%)	1 (1%)	13 50
54	BT	72/74 (97%)	62 (86%)	7 (10%)	3 (4%)	3 22
55	BU	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	14 52
56	BV	84/86 (98%)	79 (94%)	4 (5%)	1 (1%)	13 50
57	BW	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2 22
All	All	6319/6423 (98%)	5708 (90%)	453 (7%)	158 (2%)	9 32

5 of 158 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AD	94	LEU
6	AF	62	GLN
6	AF	188	MET
7	AG	136	ILE
9	AI	3	VAL

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
3	AC	181/181 (100%)	176 (97%)	5 (3%)	43 65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	AD	217/217 (100%)	205 (94%)	12 (6%)	21 47
5	AE	164/164 (100%)	152 (93%)	12 (7%)	14 39
6	AF	165/165 (100%)	160 (97%)	5 (3%)	41 63
7	AG	149/149 (100%)	140 (94%)	9 (6%)	19 44
8	AH	137/137 (100%)	123 (90%)	14 (10%)	7 25
9	AI	114/114 (100%)	109 (96%)	5 (4%)	28 53
10	AJ	122/122 (100%)	115 (94%)	7 (6%)	20 45
11	AK	109/109 (100%)	104 (95%)	5 (5%)	27 52
12	AL	116/116 (100%)	107 (92%)	9 (8%)	12 36
13	AM	104/104 (100%)	98 (94%)	6 (6%)	20 45
14	AN	103/103 (100%)	102 (99%)	1 (1%)	76 86
15	AO	109/109 (100%)	101 (93%)	8 (7%)	14 39
16	AP	103/103 (100%)	99 (96%)	4 (4%)	32 56
17	AQ	87/87 (100%)	79 (91%)	8 (9%)	9 29
18	AR	99/99 (100%)	94 (95%)	5 (5%)	24 48
19	AS	89/89 (100%)	86 (97%)	3 (3%)	37 60
20	AT	84/84 (100%)	78 (93%)	6 (7%)	14 39
21	AU	93/93 (100%)	88 (95%)	5 (5%)	22 47
22	AV	84/84 (100%)	78 (93%)	6 (7%)	14 39
23	AW	84/84 (100%)	80 (95%)	4 (5%)	25 51
24	AX	78/78 (100%)	73 (94%)	5 (6%)	17 42
25	AY	62/62 (100%)	57 (92%)	5 (8%)	11 35
26	AZ	67/67 (100%)	60 (90%)	7 (10%)	7 24
27	A0	55/55 (100%)	52 (94%)	3 (6%)	21 47
28	A1	48/48 (100%)	42 (88%)	6 (12%)	4 19
29	A2	62/62 (100%)	61 (98%)	1 (2%)	62 79
30	A3	47/47 (100%)	45 (96%)	2 (4%)	29 53
31	A4	48/48 (100%)	44 (92%)	4 (8%)	11 34
32	A5	38/38 (100%)	35 (92%)	3 (8%)	12 35
33	A6	51/51 (100%)	50 (98%)	1 (2%)	55 74
34	A7	34/34 (100%)	33 (97%)	1 (3%)	42 64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
38	BD	198/198 (100%)	188 (95%)	10 (5%)	24 48
39	BE	189/189 (100%)	174 (92%)	15 (8%)	12 35
40	BF	172/172 (100%)	168 (98%)	4 (2%)	50 70
41	BG	125/125 (100%)	118 (94%)	7 (6%)	21 46
42	BH	116/116 (100%)	107 (92%)	9 (8%)	12 36
43	BI	146/146 (100%)	139 (95%)	7 (5%)	25 51
44	BJ	104/104 (100%)	99 (95%)	5 (5%)	25 51
45	BK	106/106 (100%)	100 (94%)	6 (6%)	20 45
46	BL	90/90 (100%)	83 (92%)	7 (8%)	12 36
47	BM	98/98 (100%)	96 (98%)	2 (2%)	55 74
48	BN	103/103 (100%)	99 (96%)	4 (4%)	32 56
49	BO	95/95 (100%)	89 (94%)	6 (6%)	18 43
50	BP	83/83 (100%)	79 (95%)	4 (5%)	25 51
51	BQ	76/76 (100%)	75 (99%)	1 (1%)	69 81
52	BR	65/65 (100%)	57 (88%)	8 (12%)	4 19
53	BS	77/77 (100%)	72 (94%)	5 (6%)	17 42
54	BT	64/64 (100%)	61 (95%)	3 (5%)	26 51
55	BU	78/78 (100%)	69 (88%)	9 (12%)	5 21
56	BV	65/65 (100%)	65 (100%)	0	100 100
57	BW	60/60 (100%)	55 (92%)	5 (8%)	11 34
All	All	5213/5213 (100%)	4919 (94%)	294 (6%)	25 46

5 of 294 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	BJ	68	LYS
55	BU	47	THR
45	BK	88	GLU
50	BP	66	THR
15	AO	136	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	119/120 (99%)	18 (15%)	13 (10%)
2	AB	2898/2904 (99%)	527 (18%)	180 (6%)
35	BA	1538/1542 (99%)	294 (19%)	112 (7%)
36	BB	46/47 (97%)	15 (32%)	6 (13%)
37	BC	76/77 (98%)	14 (18%)	1 (1%)
All	All	4677/4690 (99%)	868 (18%)	312 (6%)

5 of 868 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	9	G
1	AA	13	G
1	AA	14	U
1	AA	25	U
1	AA	26	C

5 of 312 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
35	BA	552	U
35	BA	1302	C
35	BA	681	A
35	BA	944	G
35	BA	1465	A

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

40 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	$\#\|Z\| > 2$
2	OMG	AB	2251	2	18,26,27	1.71	5 (27%)	19,38,41	1.37	1 (5%)
35	5MC	BA	967	35	18,22,23	1.05	1 (5%)	26,32,35	1.33	4 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	OMU	AB	2552	2	19,22,23	0.82	1 (5%)	26,31,34	1.36	3 (11%)
2	5MC	AB	1962	2	18,22,23	1.31	2 (11%)	26,32,35	1.51	6 (23%)
2	PSU	AB	2457	2	18,21,22	1.56	3 (16%)	22,30,33	2.33	5 (22%)
35	UR3	BA	1498	35	19,22,23	1.23	3 (15%)	26,32,35	1.91	7 (26%)
2	H2U	AB	2449	2	18,21,22	1.23	1 (5%)	21,30,33	2.82	9 (42%)
2	3TD	AB	1915	2	18,22,23	1.38	3 (16%)	22,32,35	2.17	7 (31%)
37	5MU	BC	55	37	19,22,23	1.01	1 (5%)	28,32,35	1.97	8 (28%)
2	CH	AB	2575	2	16,21,22	1.64	2 (12%)	20,30,33	1.55	4 (20%)
37	4SU	BC	8	37	18,21,22	1.95	6 (33%)	26,30,33	1.77	7 (26%)
2	2MG	AB	1835	2	18,26,27	1.79	4 (22%)	16,38,41	1.83	3 (18%)
2	PSU	AB	1917	2	18,21,22	1.39	4 (22%)	22,30,33	1.82	5 (22%)
2	7MG	AB	2069	2	22,26,27	4.67	4 (18%)	29,39,42	1.64	5 (17%)
35	5MC	BA	1407	35	18,22,23	1.58	3 (16%)	26,32,35	1.49	6 (23%)
37	PSU	BC	56	37	18,21,22	2.23	5 (27%)	22,30,33	1.22	1 (4%)
2	PSU	AB	746	2	18,21,22	2.04	5 (27%)	22,30,33	2.03	6 (27%)
2	PSU	AB	2580	2	18,21,22	1.85	5 (27%)	22,30,33	1.48	4 (18%)
35	2MG	BA	966	35	18,26,27	1.87	6 (33%)	16,38,41	1.50	4 (25%)
37	OMC	BC	33	37	19,22,23	1.24	3 (15%)	26,31,34	1.38	5 (19%)
35	4OC	BA	1402	35	20,23,24	1.24	4 (20%)	26,32,35	1.97	8 (30%)
2	5MU	AB	1939	2	19,22,23	1.35	2 (10%)	28,32,35	2.31	9 (32%)
35	2MG	BA	1516	35	18,26,27	1.64	4 (22%)	16,38,41	1.47	3 (18%)
2	PSU	AB	955	2	18,21,22	1.90	3 (16%)	22,30,33	1.56	4 (18%)
2	PSU	AB	2605	2	18,21,22	1.79	3 (16%)	22,30,33	1.92	7 (31%)
2	6MZ	AB	1618	2	18,25,26	1.81	6 (33%)	16,36,39	1.60	4 (25%)
35	7MG	BA	527	35	22,26,27	3.39	7 (31%)	29,39,42	1.61	2 (6%)
35	MA6	BA	1518	35	18,26,27	1.55	2 (11%)	19,38,41	1.30	3 (15%)
2	1MG	AB	745	2	18,26,27	2.01	9 (50%)	19,39,42	1.89	6 (31%)
2	PSU	AB	1911	2	18,21,22	2.38	8 (44%)	22,30,33	1.33	4 (18%)
35	MA6	BA	1519	35	18,26,27	1.50	4 (22%)	19,38,41	2.25	6 (31%)
35	2MG	BA	1207	35	18,26,27	1.59	4 (22%)	16,38,41	1.44	2 (12%)
2	2MA	AB	2503	2	17,25,26	1.22	2 (11%)	17,37,40	1.78	3 (17%)
2	OMC	AB	2498	2	19,22,23	1.30	5 (26%)	26,31,34	1.57	6 (23%)
2	6MZ	AB	2030	2	18,25,26	1.85	3 (16%)	16,36,39	1.95	3 (18%)
2	2MG	AB	2445	2	18,26,27	1.77	4 (22%)	16,38,41	1.76	4 (25%)
35	PSU	BA	516	35	18,21,22	1.67	4 (22%)	22,30,33	2.34	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
37	H2U	BC	21	37	18,21,22	1.65	6 (33%)	21,30,33	2.23	9 (42%)
2	5MU	AB	747	2	19,22,23	1.52	3 (15%)	28,32,35	2.79	17 (60%)
2	PSU	AB	2504	2	18,21,22	1.71	3 (16%)	22,30,33	2.17	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
2	OMG	AB	2251	2	-	0/5/27/28	0/3/3/3
35	5MC	BA	967	35	-	1/7/25/26	0/2/2/2
2	OMU	AB	2552	2	-	1/9/27/28	0/2/2/2
2	5MC	AB	1962	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2457	2	-	0/7/25/26	0/2/2/2
35	UR3	BA	1498	35	-	0/7/25/26	0/2/2/2
2	H2U	AB	2449	2	-	0/7/38/39	0/2/2/2
2	3TD	AB	1915	2	-	0/7/25/26	0/2/2/2
37	5MU	BC	55	37	-	0/7/25/26	0/2/2/2
2	CH	AB	2575	2	-	0/5/25/26	0/2/2/2
37	4SU	BC	8	37	-	0/7/25/26	0/2/2/2
2	2MG	AB	1835	2	-	0/5/27/28	0/3/3/3
2	PSU	AB	1917	2	-	3/7/25/26	0/2/2/2
2	7MG	AB	2069	2	-	0/7/37/38	0/3/3/3
35	5MC	BA	1407	35	-	0/7/25/26	0/2/2/2
37	PSU	BC	56	37	-	0/7/25/26	0/2/2/2
2	PSU	AB	746	2	-	1/7/25/26	0/2/2/2
2	PSU	AB	2580	2	-	3/7/25/26	0/2/2/2
35	2MG	BA	966	35	-	0/5/27/28	0/3/3/3
37	OMC	BC	33	37	-	0/9/27/28	0/2/2/2
35	4OC	BA	1402	35	-	0/9/29/30	0/2/2/2
2	5MU	AB	1939	2	-	0/7/25/26	0/2/2/2
35	2MG	BA	1516	35	-	0/5/27/28	0/3/3/3
2	PSU	AB	955	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2605	2	-	0/7/25/26	0/2/2/2
2	6MZ	AB	1618	2	-	1/5/27/28	0/3/3/3
35	7MG	BA	527	35	-	1/7/37/38	0/3/3/3
35	MA6	BA	1518	35	-	0/7/29/30	0/3/3/3
2	1MG	AB	745	2	-	0/3/25/26	0/3/3/3
2	PSU	AB	1911	2	-	2/7/25/26	0/2/2/2
35	MA6	BA	1519	35	-	0/7/29/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	2MG	BA	1207	35	-	0/5/27/28	0/3/3/3
2	2MA	AB	2503	2	-	0/3/25/26	0/3/3/3
2	OMC	AB	2498	2	-	0/9/27/28	0/2/2/2
2	6MZ	AB	2030	2	-	0/5/27/28	0/3/3/3
2	2MG	AB	2445	2	-	0/5/27/28	0/3/3/3
35	PSU	BA	516	35	-	1/7/25/26	0/2/2/2
37	H2U	BC	21	37	-	0/7/38/39	0/2/2/2
2	5MU	AB	747	2	-	0/7/25/26	0/2/2/2
2	PSU	AB	2504	2	-	2/7/25/26	0/2/2/2

The worst 5 of 153 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	2069	7MG	C8-N9	-20.69	1.34	1.46
35	BA	527	7MG	C8-N9	-14.00	1.38	1.46
2	AB	2030	6MZ	C6-N1	5.79	1.42	1.34
2	AB	1911	PSU	C2'-C1'	-5.36	1.46	1.53
2	AB	955	PSU	C2'-C1'	-5.26	1.46	1.53

The worst 5 of 209 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	AB	2457	PSU	C6-C5-C4	7.75	123.62	118.20
35	BA	516	PSU	C3'-C2'-C1'	7.65	110.55	101.64
2	AB	2449	H2U	O2-C2-N1	-7.16	114.12	123.11
2	AB	1939	5MU	C5M-C5-C4	6.70	126.14	118.77
2	AB	2504	PSU	C6-C5-C4	6.64	122.84	118.20

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AB	746	PSU	C2'-C1'-C5-C4
2	AB	2552	OMU	C1'-C2'-O2'-CM2
2	AB	1917	PSU	O4'-C4'-C5'-O5'
2	AB	1917	PSU	C3'-C4'-C5'-O5'
35	BA	527	7MG	C4'-C5'-O5'-P

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
2	AB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AB	2831:G	O3'	2832:U	P	1.76

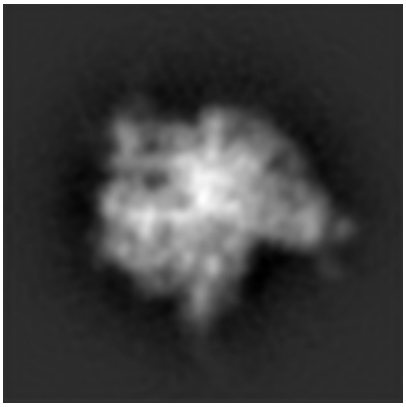
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-5360. These allow visual inspection of the internal detail of the map and identification of artifacts.

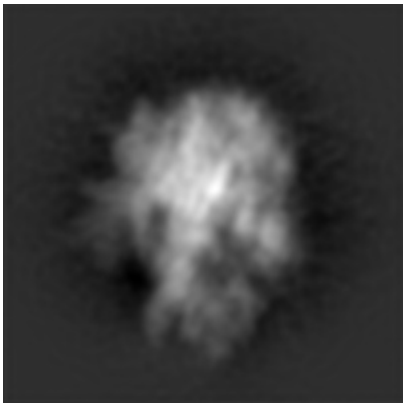
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

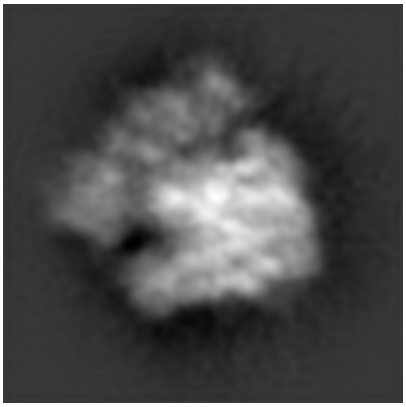
6.1.1 Primary map



X



Y

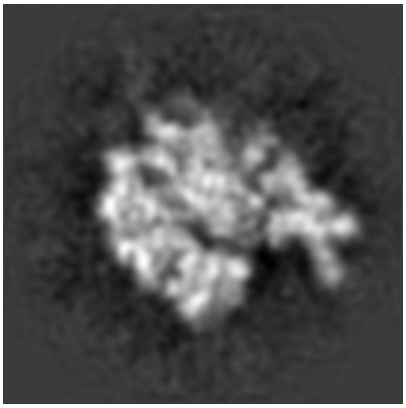


Z

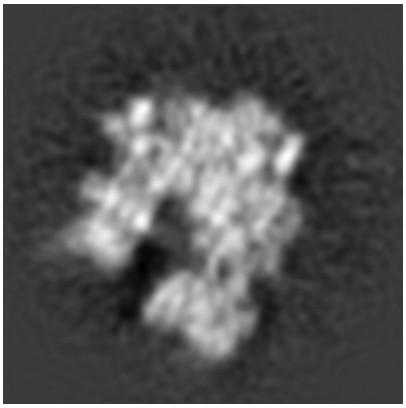
The images above show the map projected in three orthogonal directions.

6.2 Central slices

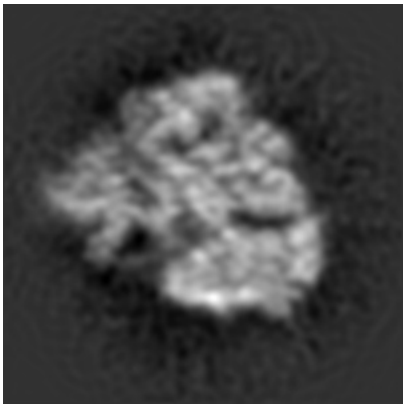
6.2.1 Primary map



X Index: 125



Y Index: 125

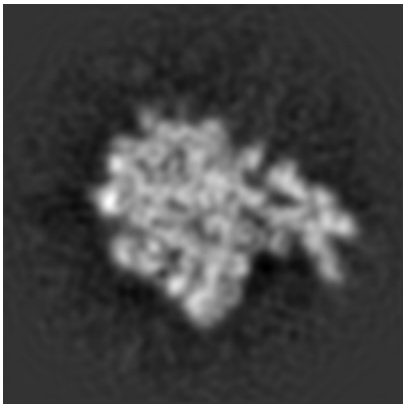


Z Index: 125

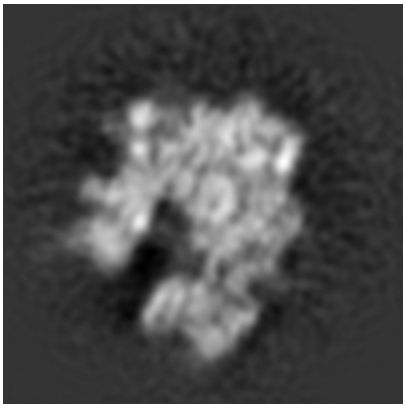
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

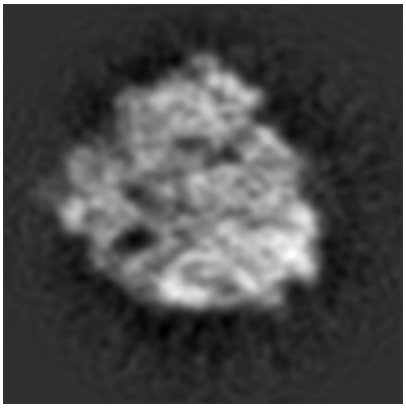
6.3.1 Primary map



X Index: 131



Y Index: 128

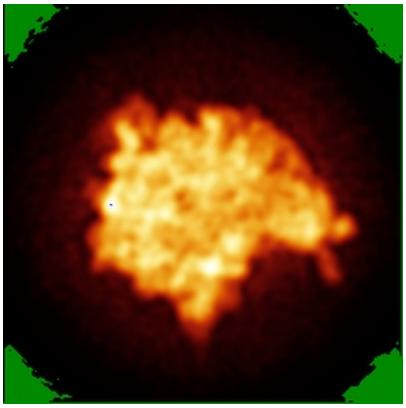


Z Index: 118

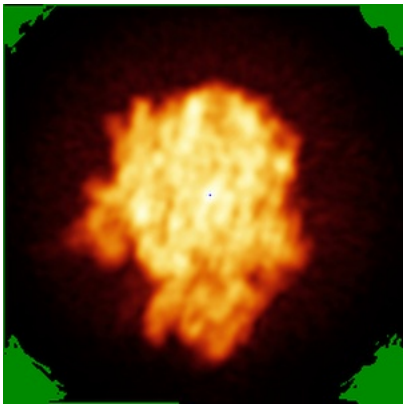
The images above show the largest variance slices of the map in three orthogonal directions.

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

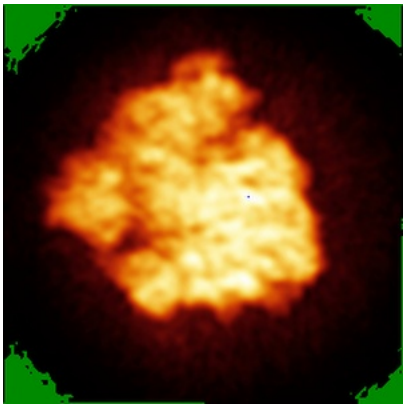
6.4.1 Primary map



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

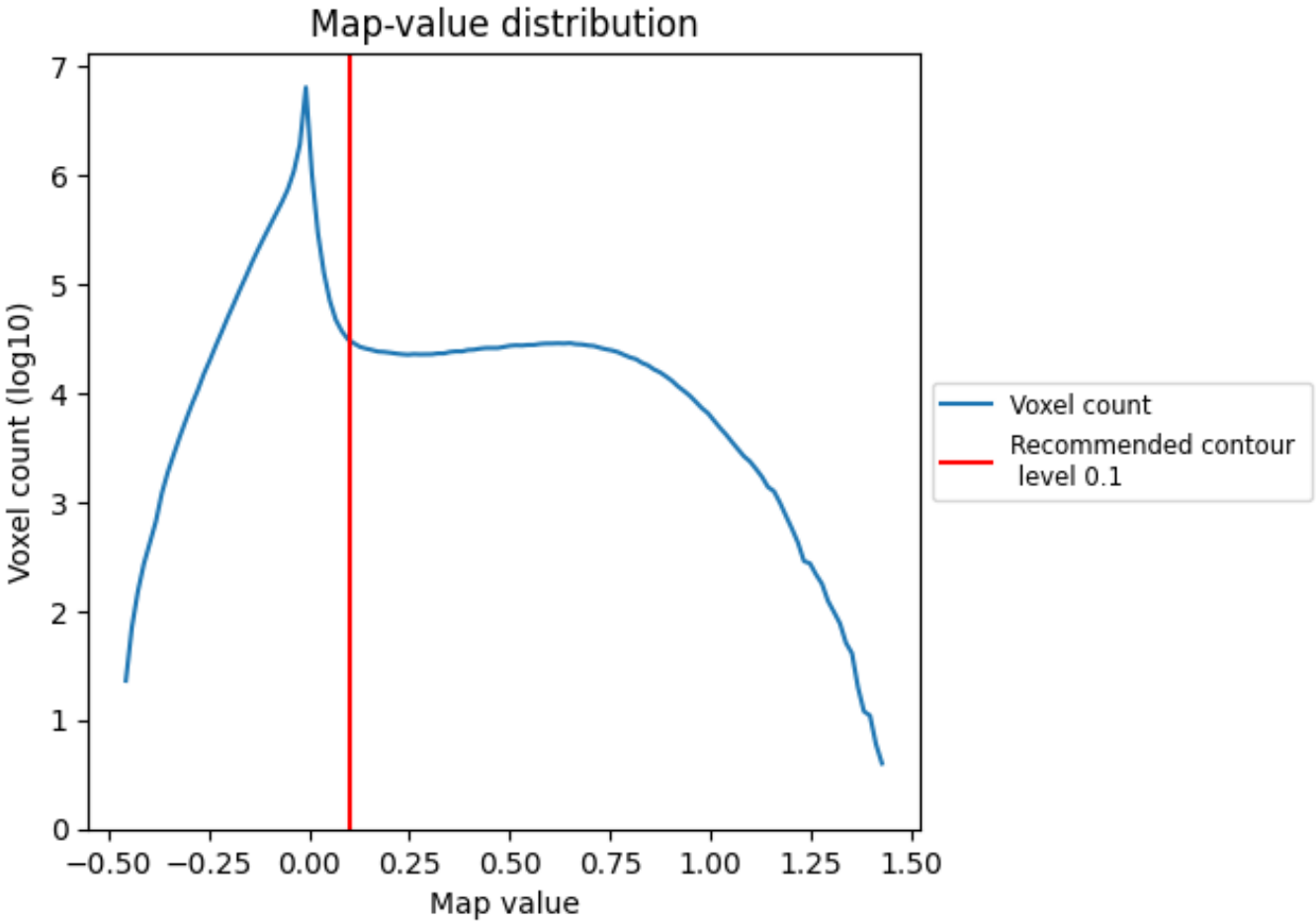
6.6 Mask visualisation (i)

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

7 Map analysis

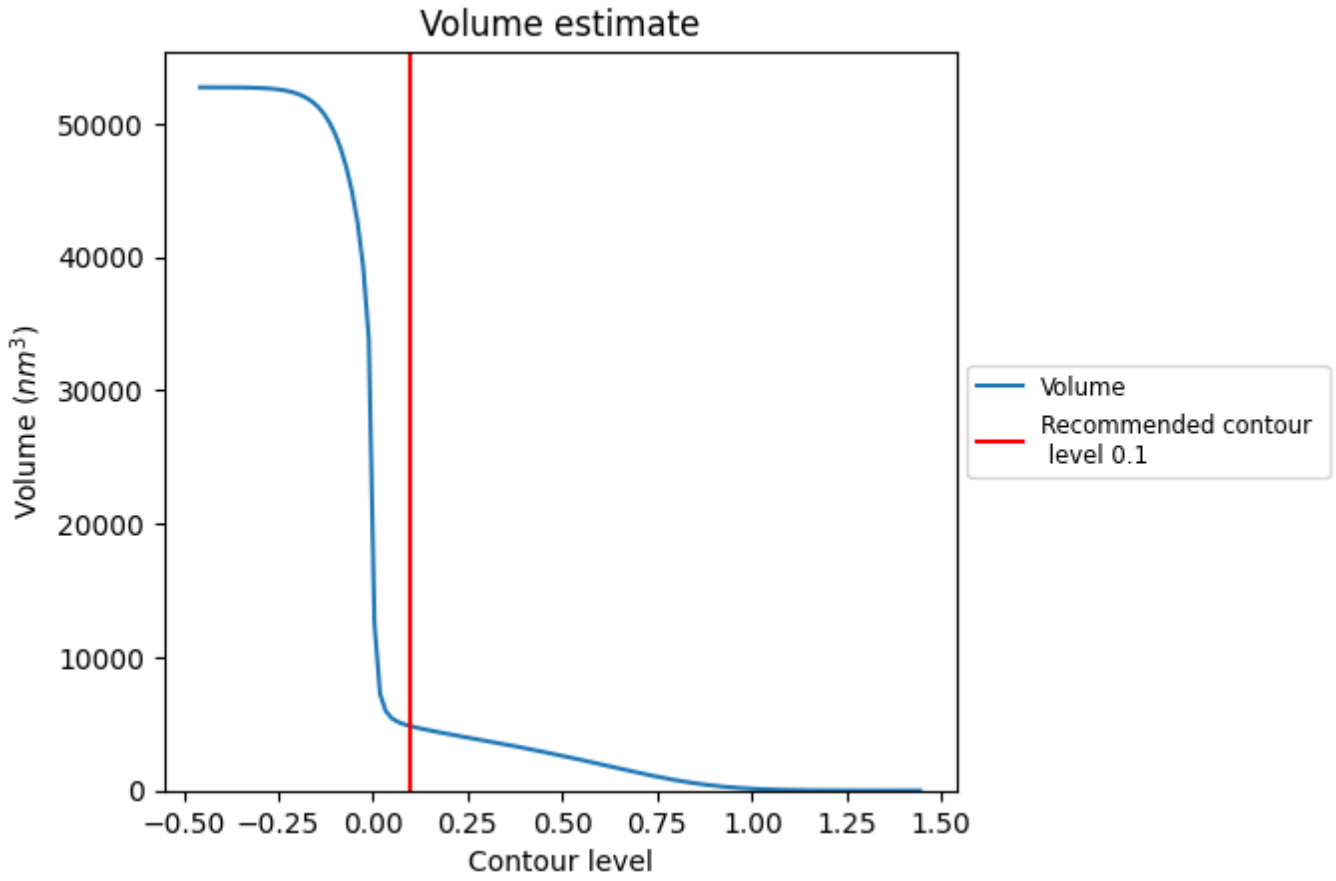
This section contains the results of statistical analysis of the map.

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.

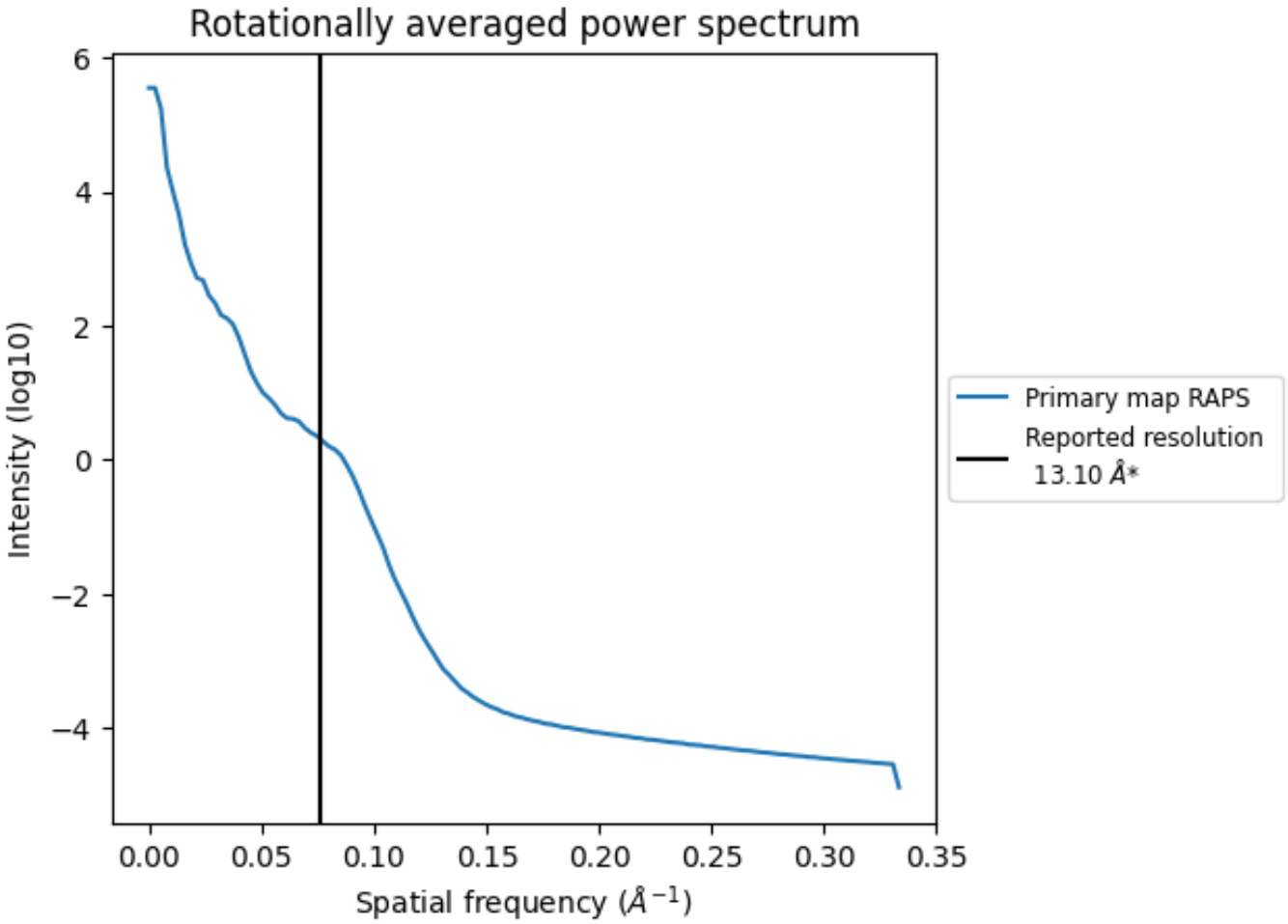
7.2 Volume estimate (i)



The volume at the recommended contour level is 4825 nm^3; this corresponds to an approximate mass of 4359 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 0.076 Å^{-1}

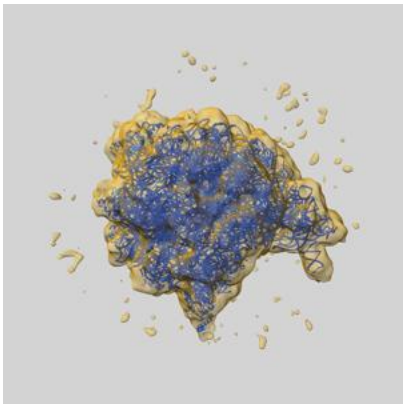
8 Fourier-Shell correlation (i)

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

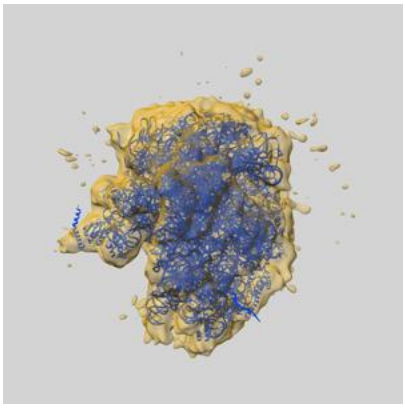
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-5360 and PDB model 4V6S. Per-residue inclusion information can be found in section 3 on page 14.

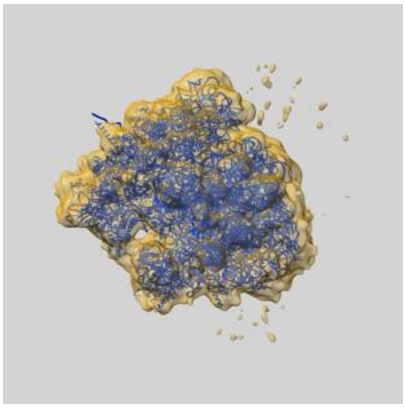
9.1 Map-model overlay



X



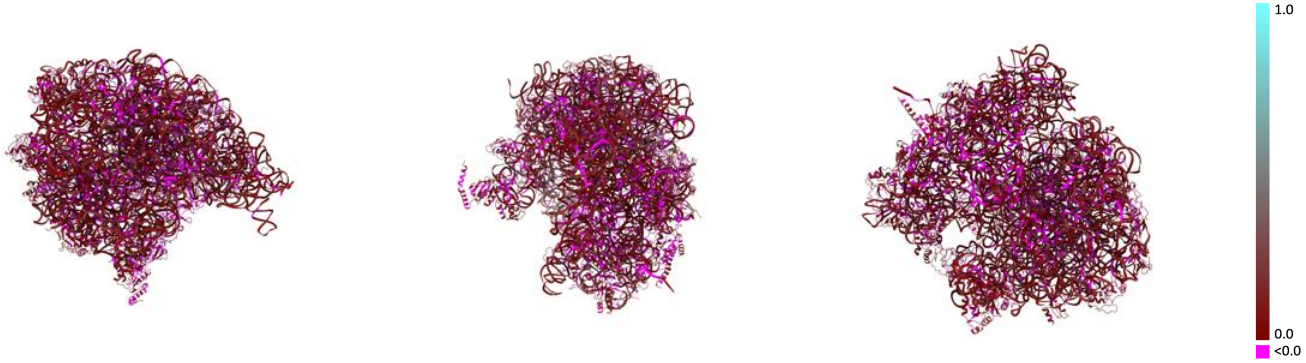
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

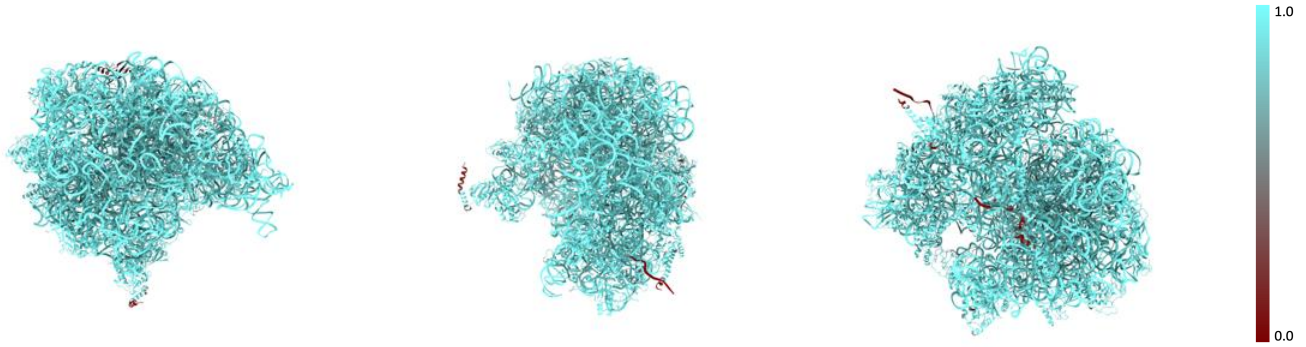
9.2 Q-score mapped to coordinate model



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.

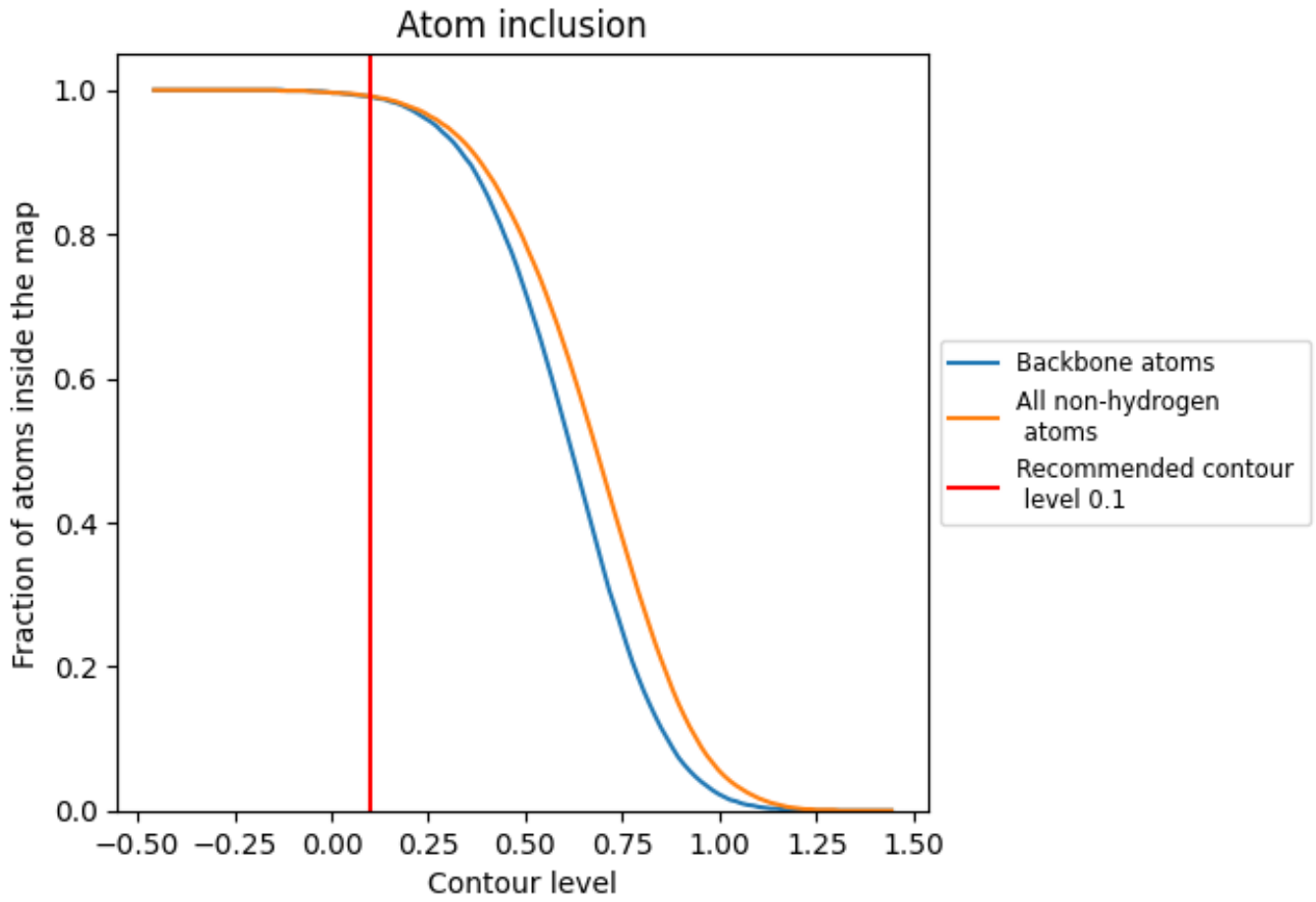
9.3 Atom inclusion mapped to coordinate model



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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9910	0.0680
A0	1.0000	0.0510
A1	0.9950	0.0290
A2	0.9110	0.0270
A3	1.0000	0.0260
A4	1.0000	0.0490
A5	1.0000	-0.0180
A6	1.0000	-0.0250
A7	1.0000	0.0160
AA	1.0000	0.0850
AB	0.9990	0.0850
AC	0.9610	0.0370
AD	1.0000	0.0210
AE	0.9960	0.0150
AF	0.9970	0.0470
AG	0.9980	0.0730
AH	0.9990	0.0210
AI	0.7900	0.0310
AJ	0.8700	0.0350
AK	0.9800	0.0440
AL	0.9990	0.0250
AM	0.9900	0.0340
AN	0.9940	0.0100
AO	1.0000	0.0310
AP	1.0000	0.0080
AQ	0.9930	0.0550
AR	0.9790	0.0230
AS	0.9980	0.0170
AT	1.0000	0.0470
AU	1.0000	0.0140
AV	1.0000	0.0310
AW	1.0000	0.0770
AX	1.0000	0.0740
AY	0.9980	0.0080
AZ	1.0000	0.0600

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Chain	Atom inclusion	Q-score
BA	0.9990	0.0840
BB	0.7340	-0.0130
BC	1.0000	0.0980
BD	0.9090	0.0220
BE	0.9980	0.0640
BF	1.0000	0.0460
BG	0.9970	0.0420
BH	0.9620	0.0290
BI	0.9930	0.0680
BJ	0.9730	0.0280
BK	0.9880	0.0480
BL	1.0000	0.0400
BM	0.9370	0.0550
BN	0.9770	0.0330
BO	0.9720	0.0480
BP	1.0000	0.0270
BQ	1.0000	0.0410
BR	1.0000	0.0480
BS	1.0000	0.0660
BT	1.0000	0.0540
BU	0.9820	0.0270
BV	1.0000	0.0460
BW	0.9960	0.0570