wwPDB EM Validation Summary Report ⓘ

Feb 22, 2024 – 10:36 PM EST

PDB ID	:	4V65
EMDB ID	:	EMD-1055
Title	:	Structure of the E. coli ribosome in the Pre-accommodation state
Authors	:	Devkota, B.; Caulfield, T.R.; Tan, R.-Z.; Harvey, S.C.
Deposited on	:	2008-08-03
Resolution	:	9.00 Å(reported)
Based on initial models	:	1EHZ, 2I2P

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

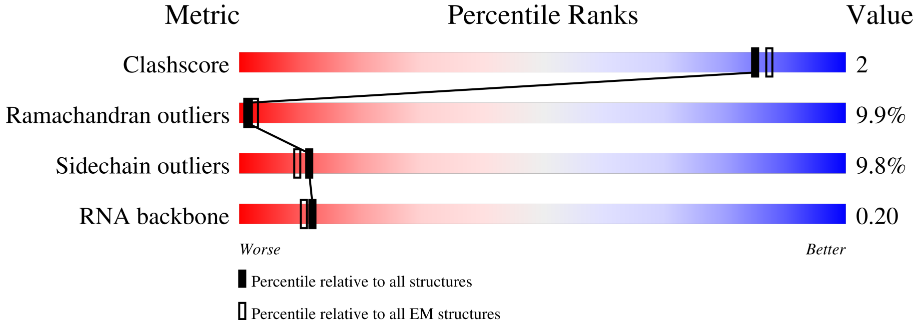
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

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

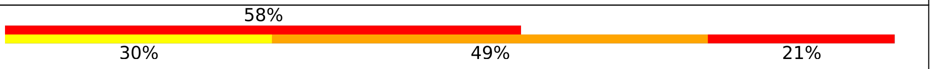
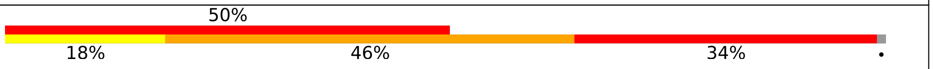
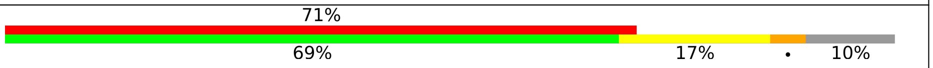
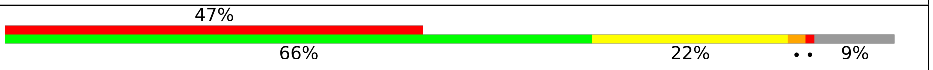
The reported resolution of this entry is 9.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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	76	 57% 11% 51% 37% •
1	AE	76	 58% 30% 49% 21%
1	AP	76	 50% 18% 46% 34% •
2	AM	20	 25% 15% 50% 35%
3	A1	1530	 65% 17% 45% 39%
4	AB	241	 71% 69% 17% • 10%
5	AC	129	 47% 66% 22% • • 9%

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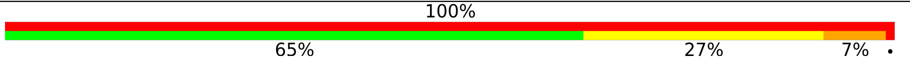
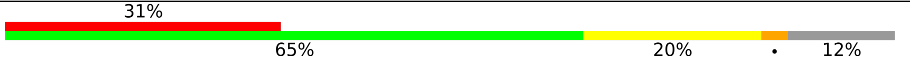
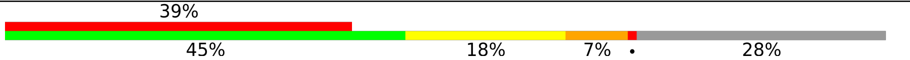
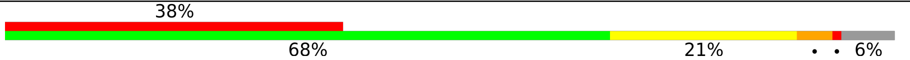
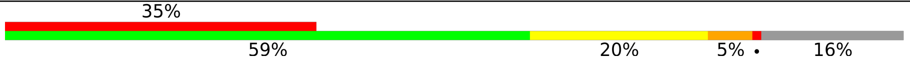
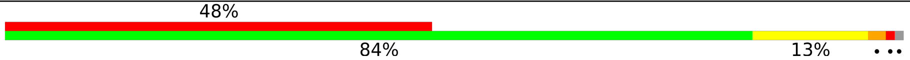
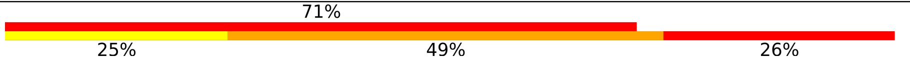
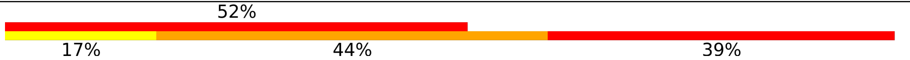
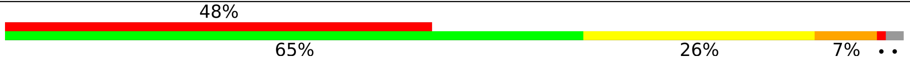
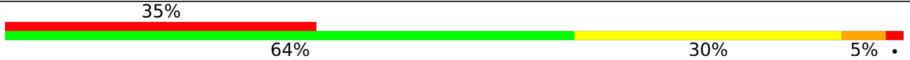
Mol	Chain	Length	Quality of chain
6	AD	124	
7	AF	118	
8	AG	101	
9	AH	89	
10	AI	82	
11	AJ	84	
12	AK	75	
13	AL	92	
14	AN	87	
15	AO	233	
16	AQ	71	
17	AR	206	
18	AS	159	
19	AT	135	
20	AU	179	
21	AV	130	
22	AW	130	
23	AX	103	
24	BA	117	
25	BB	2903	
26	BC	94	
27	BD	123	
28	BE	144	
29	BF	136	
30	BG	127	

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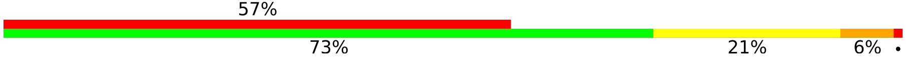
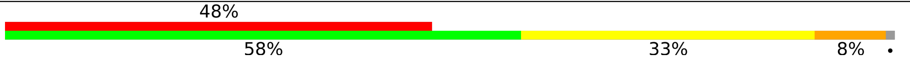
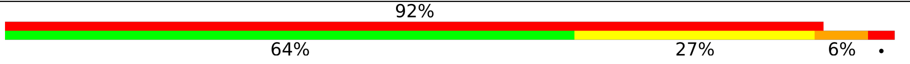
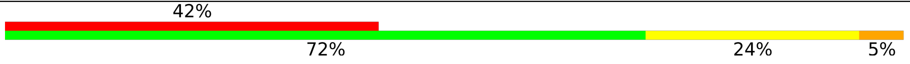
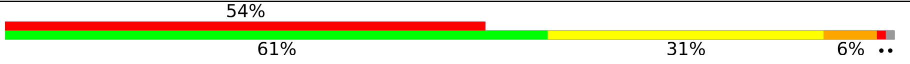
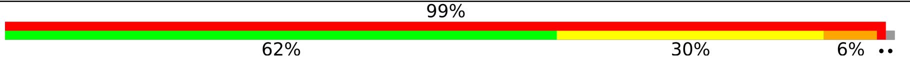
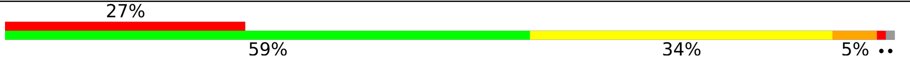
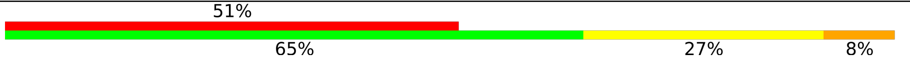
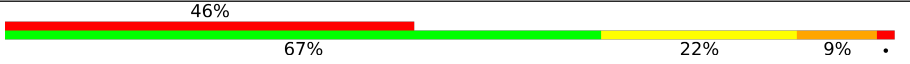
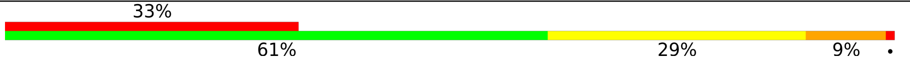
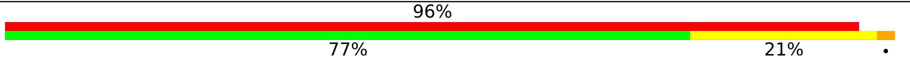
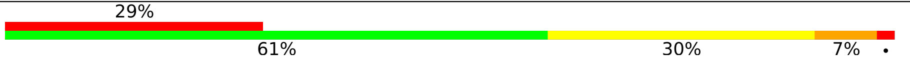
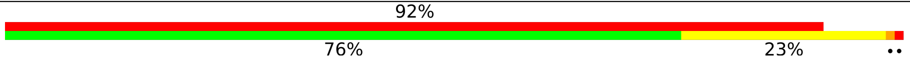
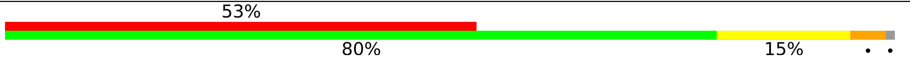
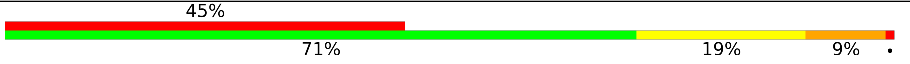
Mol	Chain	Length	Quality of chain
31	BH	117	 57% 73% 21% 6% •
32	BI	115	 48% 58% 33% 8% •
33	BJ	118	 84% 69% 19% 9% • •
34	BK	103	 92% 64% 27% 6% •
35	BL	110	 42% 72% 24% 5%
36	BM	99	 69% 69% 23% 7% •
37	BN	270	 54% 61% 31% 6% • •
38	BO	103	 99% 62% 30% 6% • •
39	BP	85	 27% 59% 34% 5% • •
40	BQ	63	 51% 65% 27% 8%
41	BR	59	 58% 71% 20% 5% • •
42	BS	70	 67% 71% 24% •
43	BT	57	 46% 49% 32% 16% • •
44	BU	54	 80% 65% 30% 6%
45	BV	46	 46% 67% 22% 9% •
46	BW	64	 73% 66% 19% 16%
47	BX	38	 68% 68% 18% 11% •
48	BY	209	 33% 61% 29% 9% •
49	BZ	213	 96% 77% 21% •
50	B1	201	 71% 65% 25% 8% •
51	B2	178	 29% 61% 30% 7% •
52	B3	177	 81% 76% 18% 6% •
53	B4	149	 92% 76% 23% • •
54	B5	142	 53% 80% 15% • •
55	B6	140	 45% 71% 19% 9% •

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 149248 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called A/T, P and E-site tRNAs.

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

- Molecule 2 is a RNA chain called mRNA model.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There are 7 discrepancies between the modelled and reference sequences:

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

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

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

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

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

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

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

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

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

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

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

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

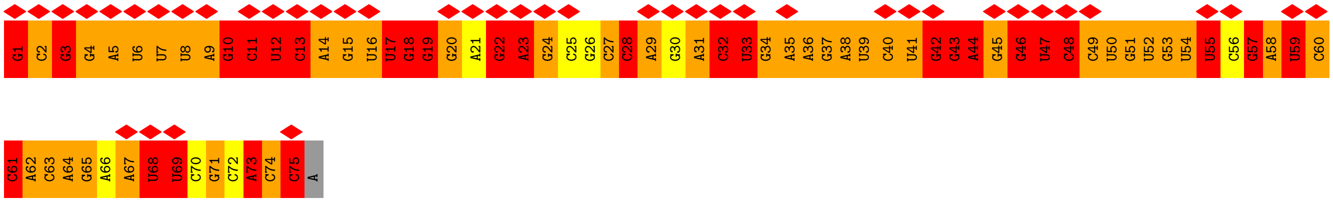
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	B6	140	1112	704	210	194	4	0	0

3 Residue-property plots ⓘ

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

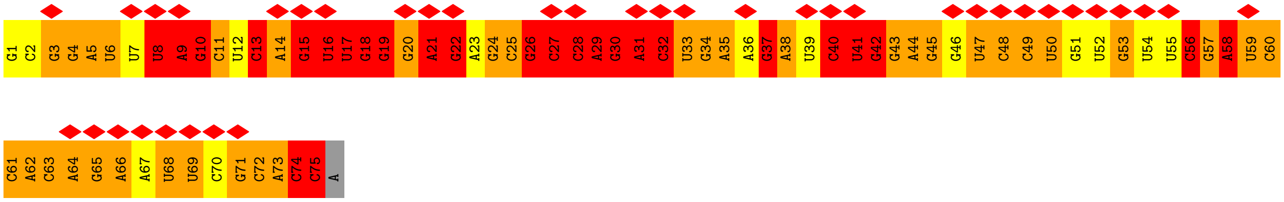
- Molecule 1: A/T, P and E-site tRNAs

Chain AA:



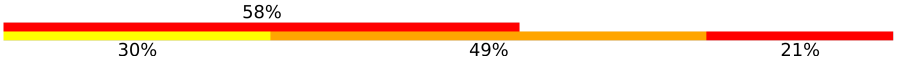
- Molecule 1: A/T, P and E-site tRNAs

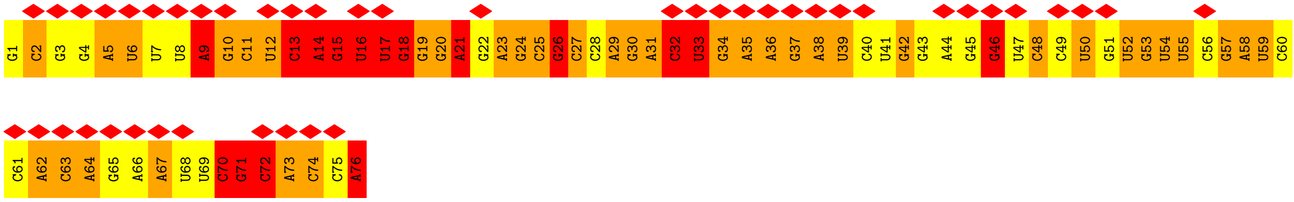
Chain AP:



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

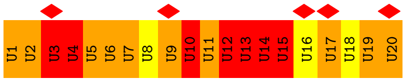
Chain AE:





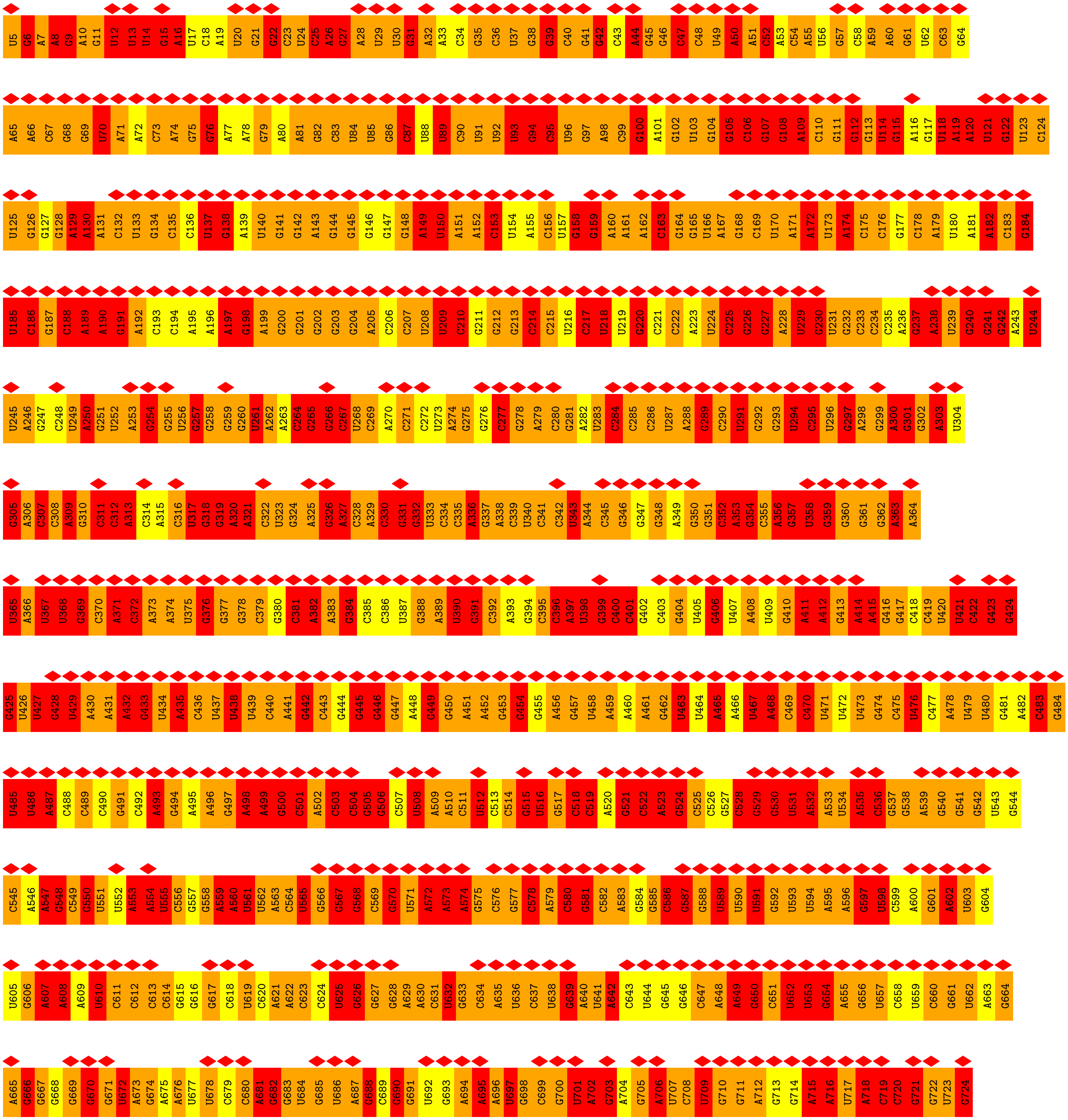
- Molecule 2: mRNA model

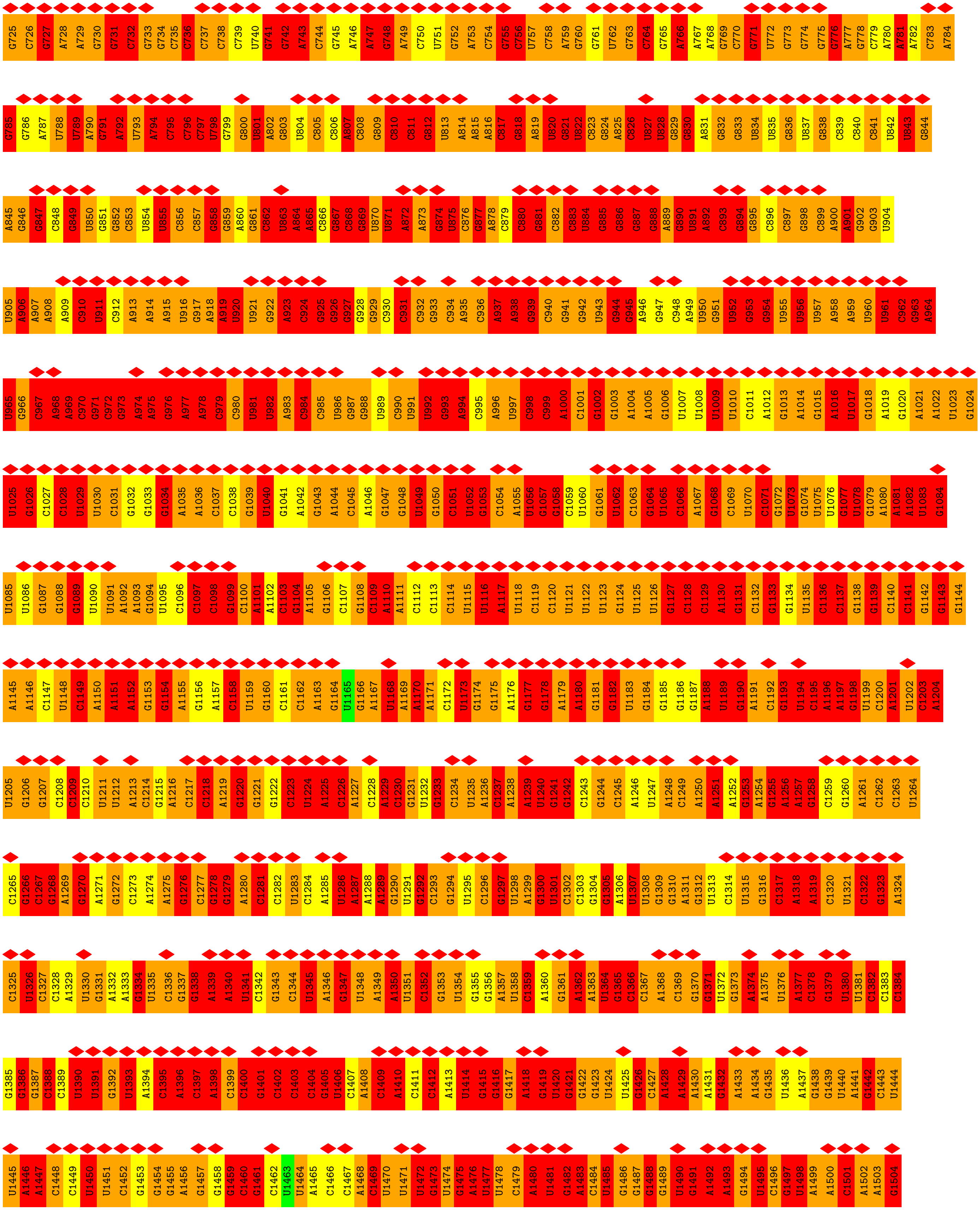
Chain AM:



- Molecule 3: 16S rRNA

Chain A1:

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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
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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 G1006 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
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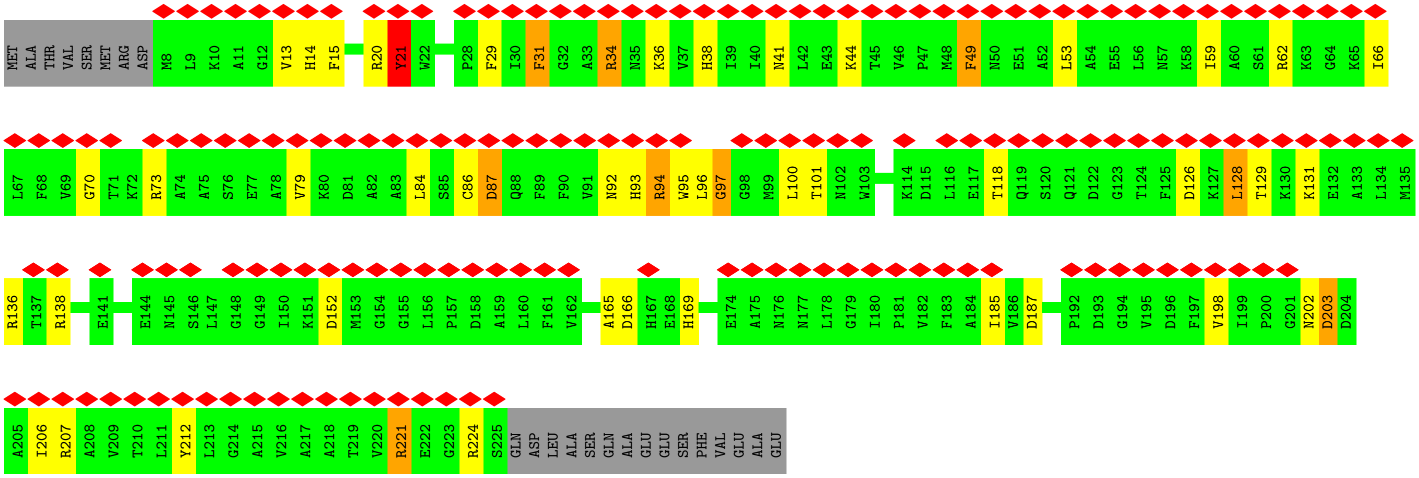
U1445 A1446 A1447 C1448 C1449 U1450 U1451 C1452 G1453 G1454 G1455 A1456 G1457 G1458 G1459 C1460 G1461 C1462 U1463 U1464 A1465 C1466 C1467 A1468 C1469 U1470 A1471 U1472 G1473 U1474 G1475 A1476 U1477 U1478 C1479 A1480 U1481 G1482 A1483 C1484 U1485 G1486 G1487 G1488 G1489 U1490 G1491 A1492 A1493 G1494 U1495 C1496 G1497 U1498 A1499 A1500 C1501 A1502 A1503 G1504

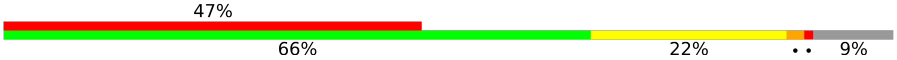
- Molecule 4: 30S ribosomal protein S2

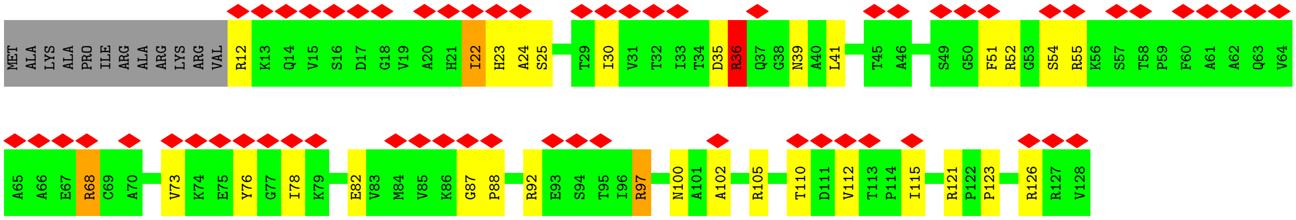
Chain AB:



- Molecule 5: 30S ribosomal protein S11

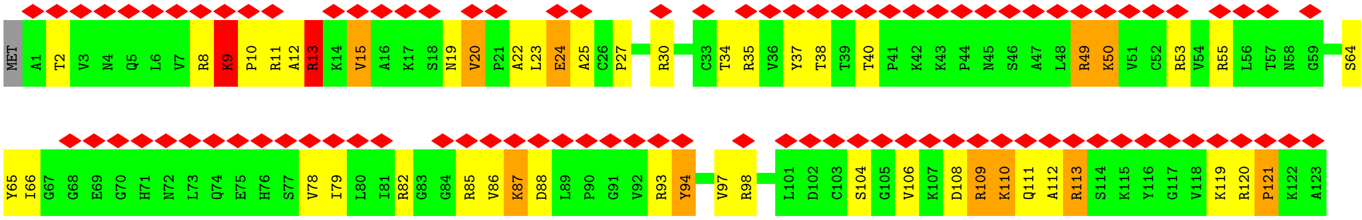
Chain AC:





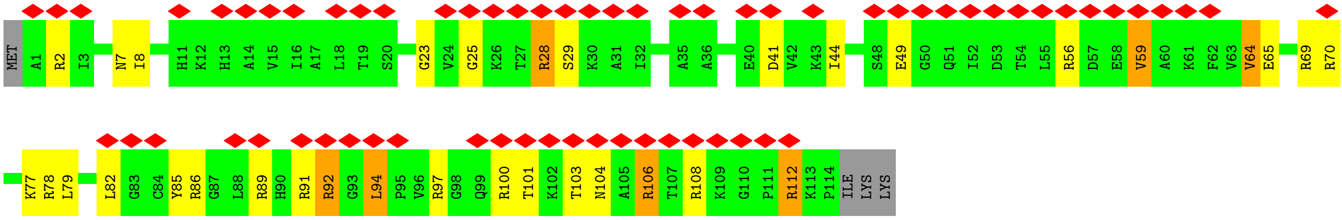
- Molecule 6: 30S ribosomal protein S12

Chain AD:



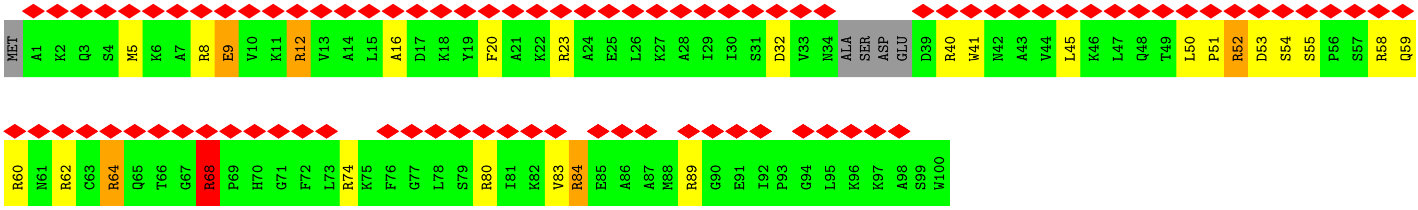
- Molecule 7: 30S ribosomal protein S13

Chain AF:



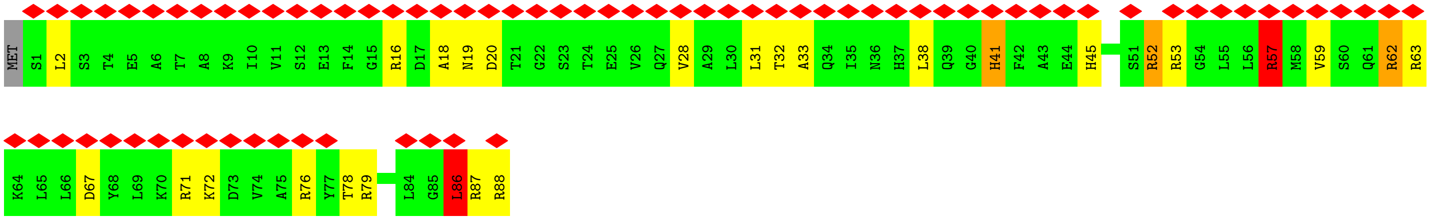
- Molecule 8: 30S ribosomal protein S14

Chain AG:



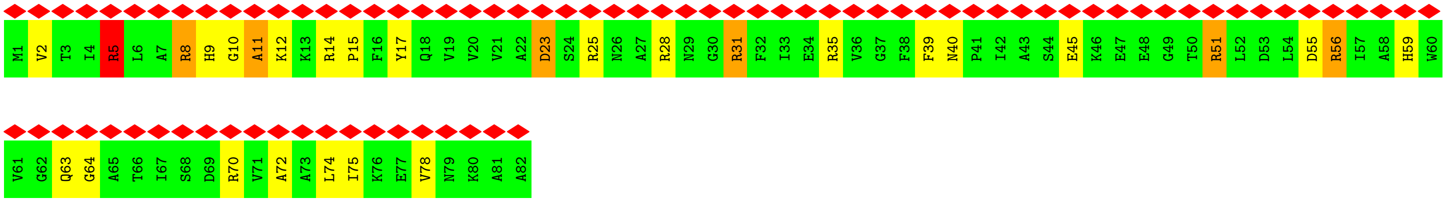
- Molecule 9: 30S ribosomal protein S15

Chain AH:



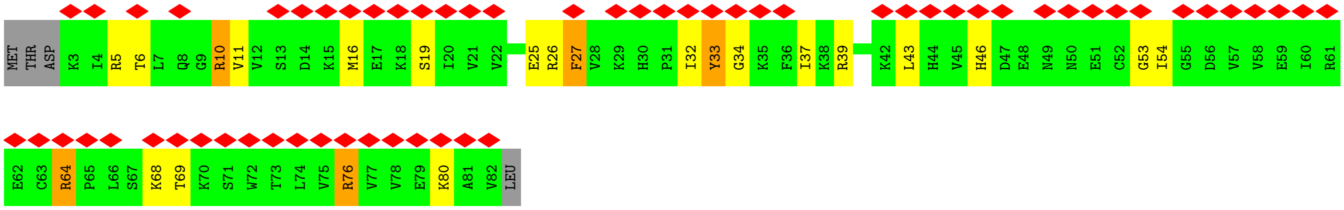
- Molecule 10: 30S ribosomal protein S16

Chain AI:

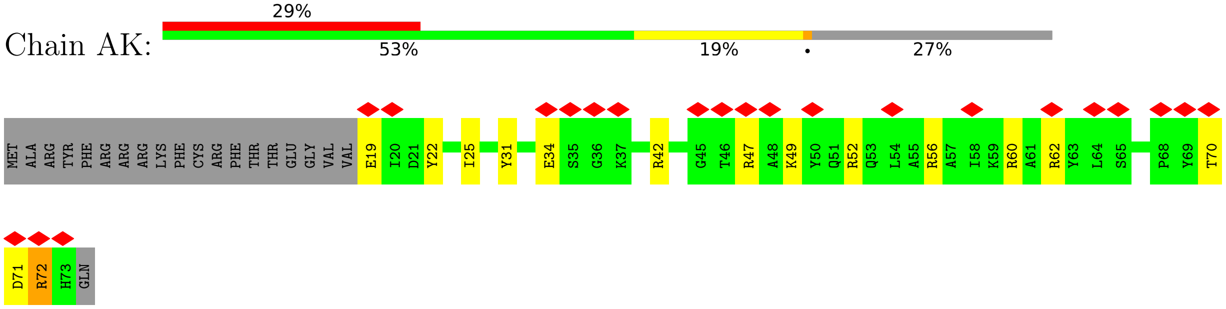


- Molecule 11: 30S ribosomal protein S17

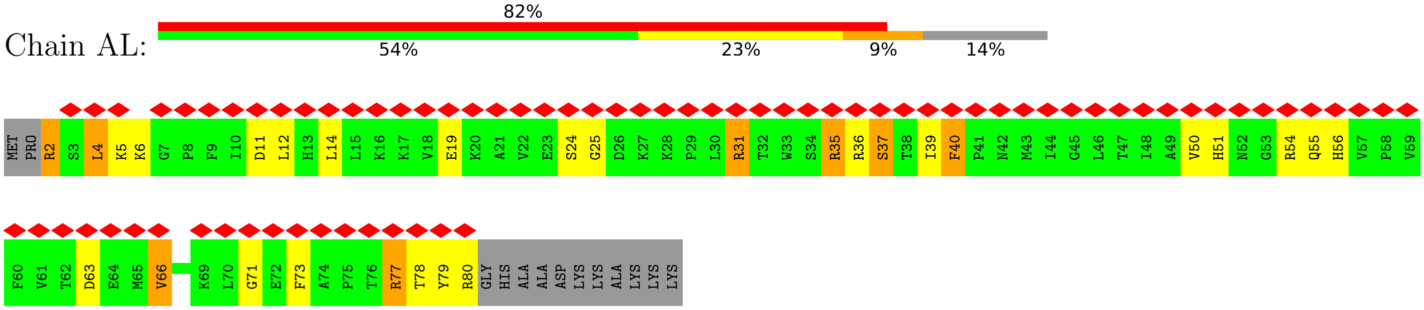
Chain AJ:



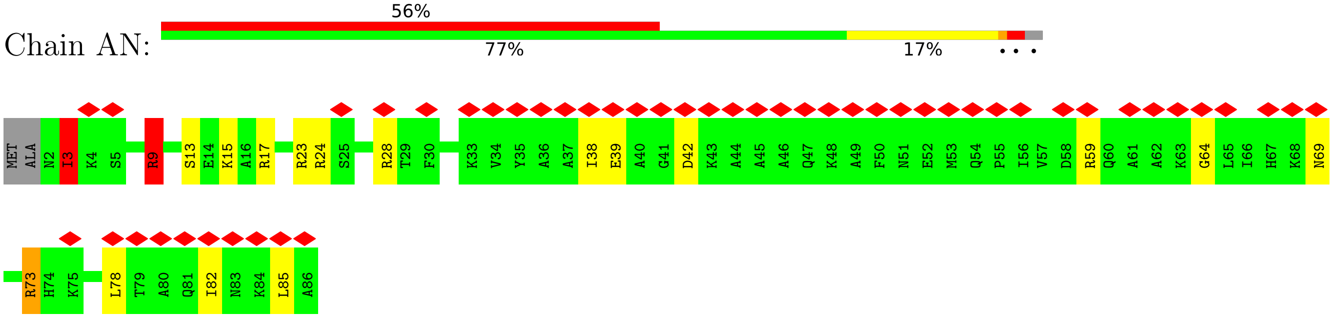
- Molecule 12: 30S ribosomal protein S18



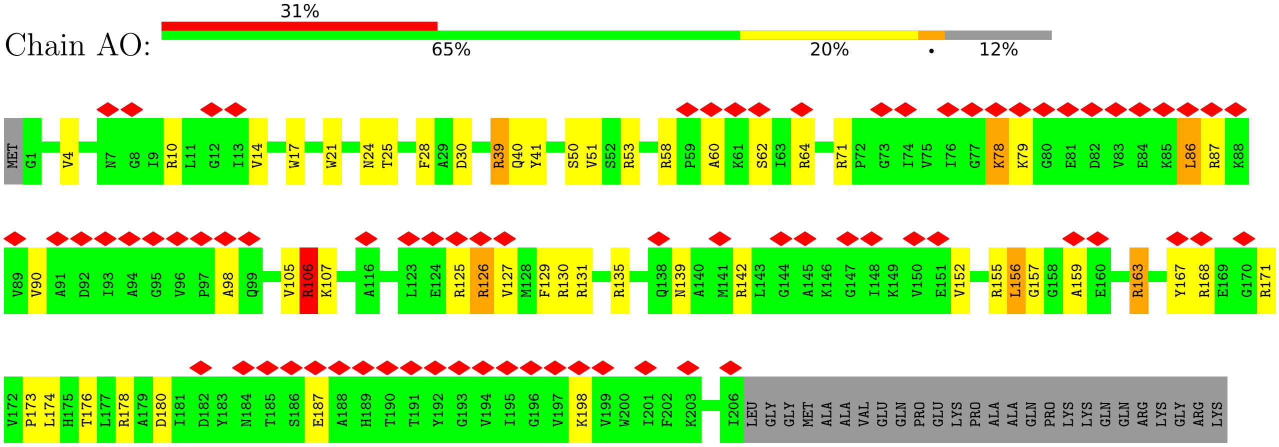
- Molecule 13: 30S ribosomal protein S19



- Molecule 14: 30S ribosomal protein S20

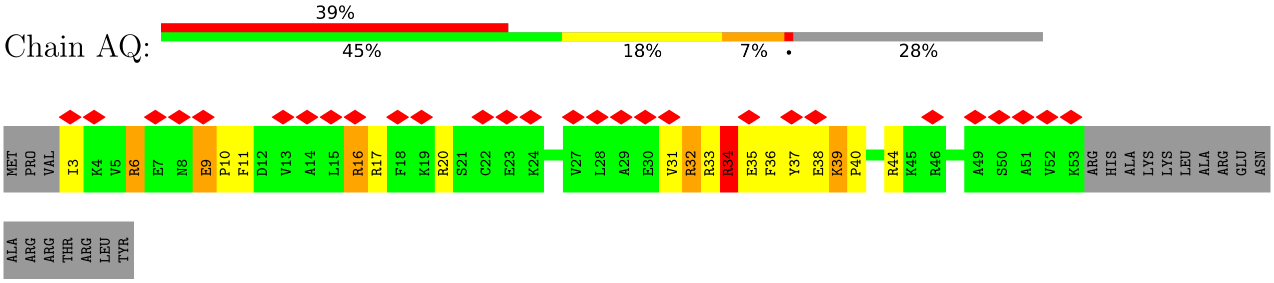


- Molecule 15: 30S ribosomal protein S3



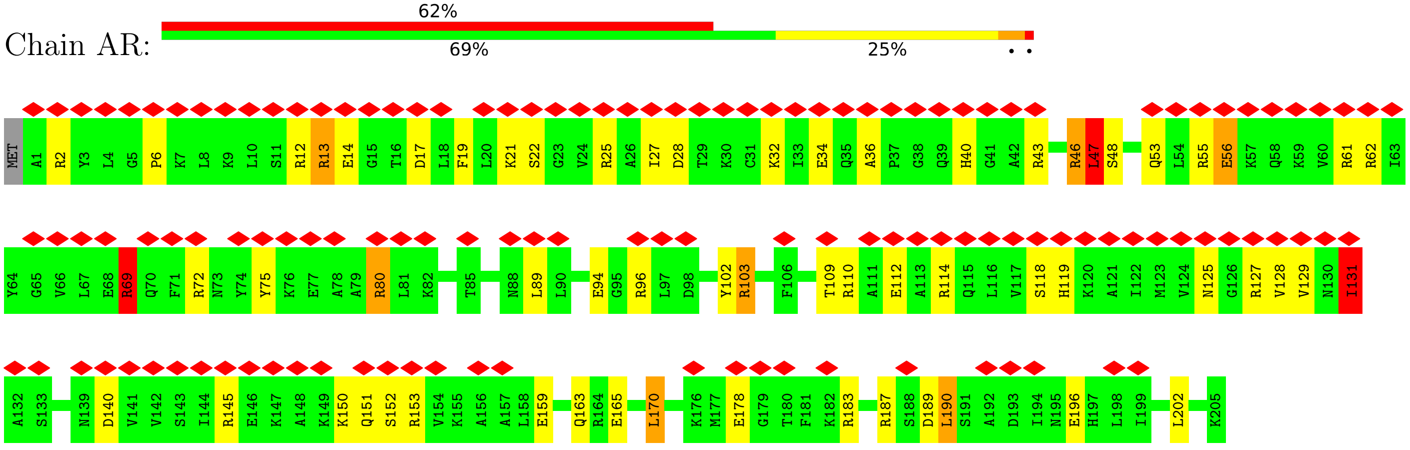
- Molecule 16: 30S ribosomal protein S21

Chain AQ:



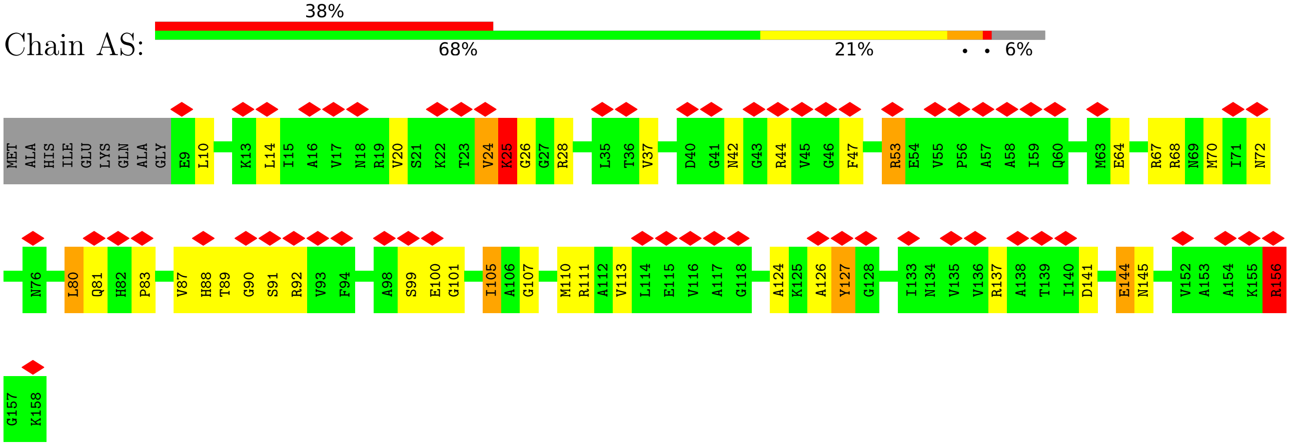
- Molecule 17: 30S ribosomal protein S4

Chain AR:



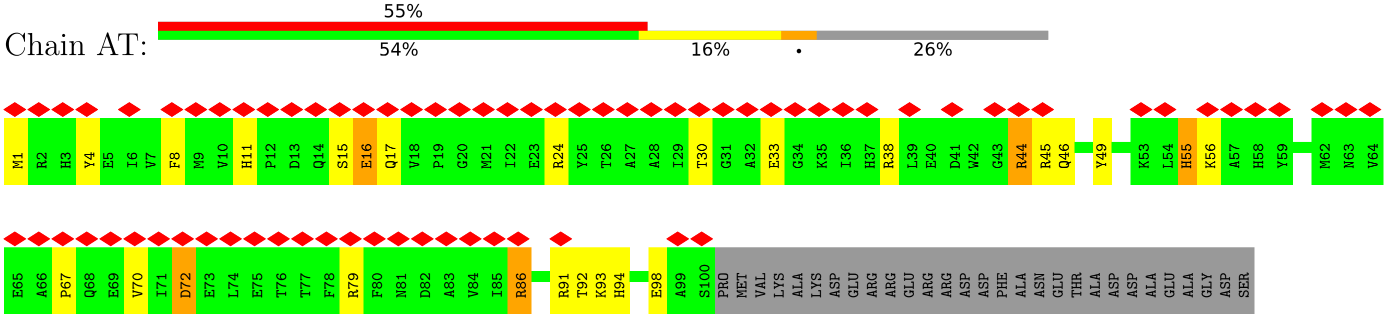
- Molecule 18: 30S ribosomal protein S5

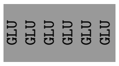
Chain AS:



- Molecule 19: 30S ribosomal protein S6

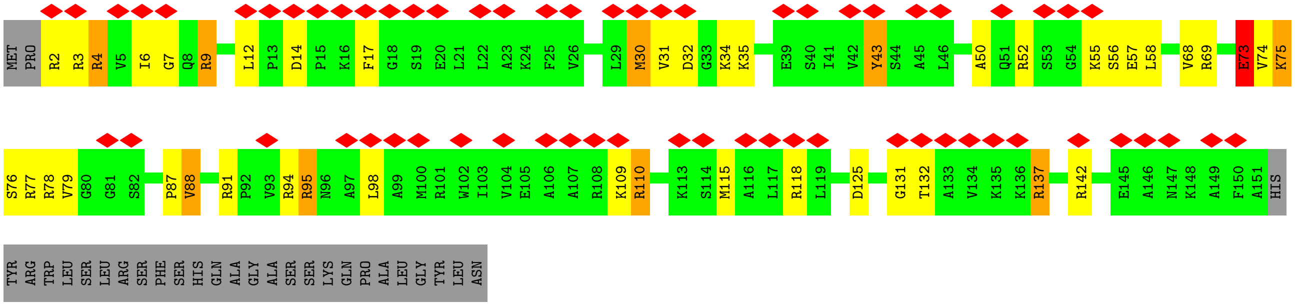
Chain AT:





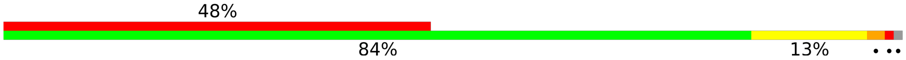
- Molecule 20: 30S ribosomal protein S7

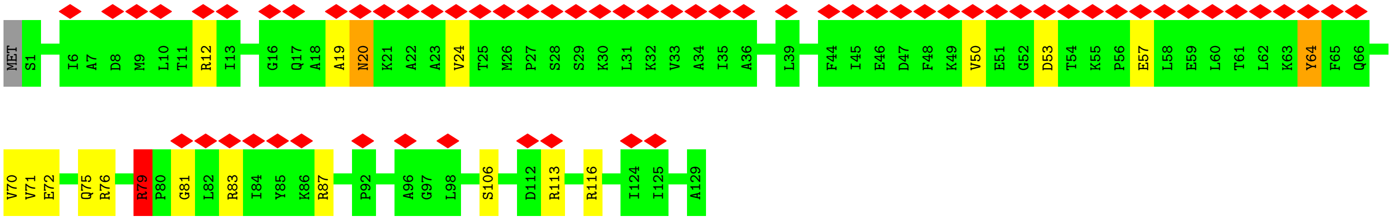
Chain AU:



- Molecule 21: 30S ribosomal protein S8

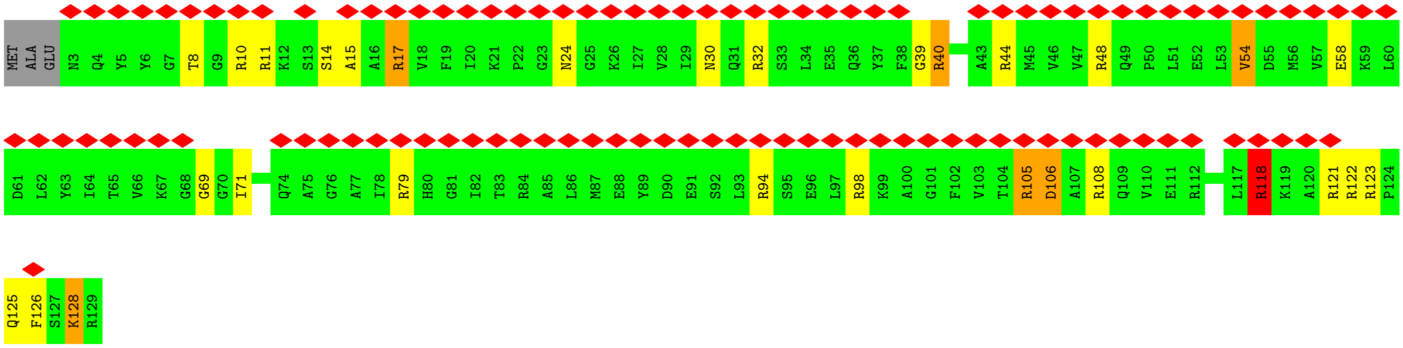
Chain AV:





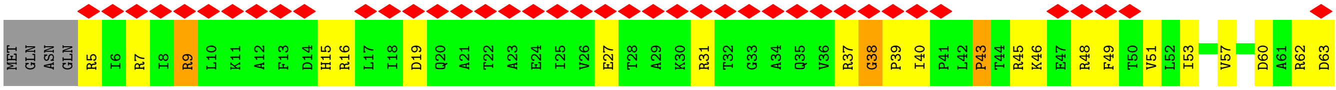
- Molecule 22: 30S ribosomal protein S9

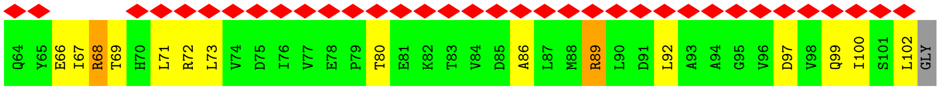
Chain AW:



- Molecule 23: 30S ribosomal protein S10

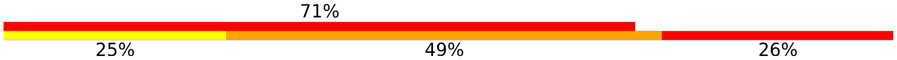
Chain AX:

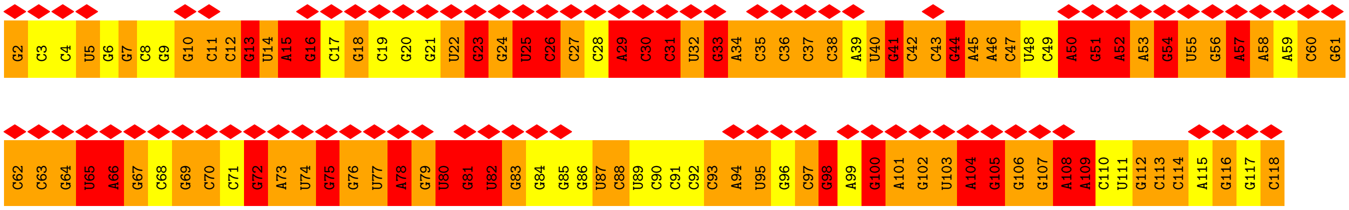




- Molecule 24: 5S rRNA

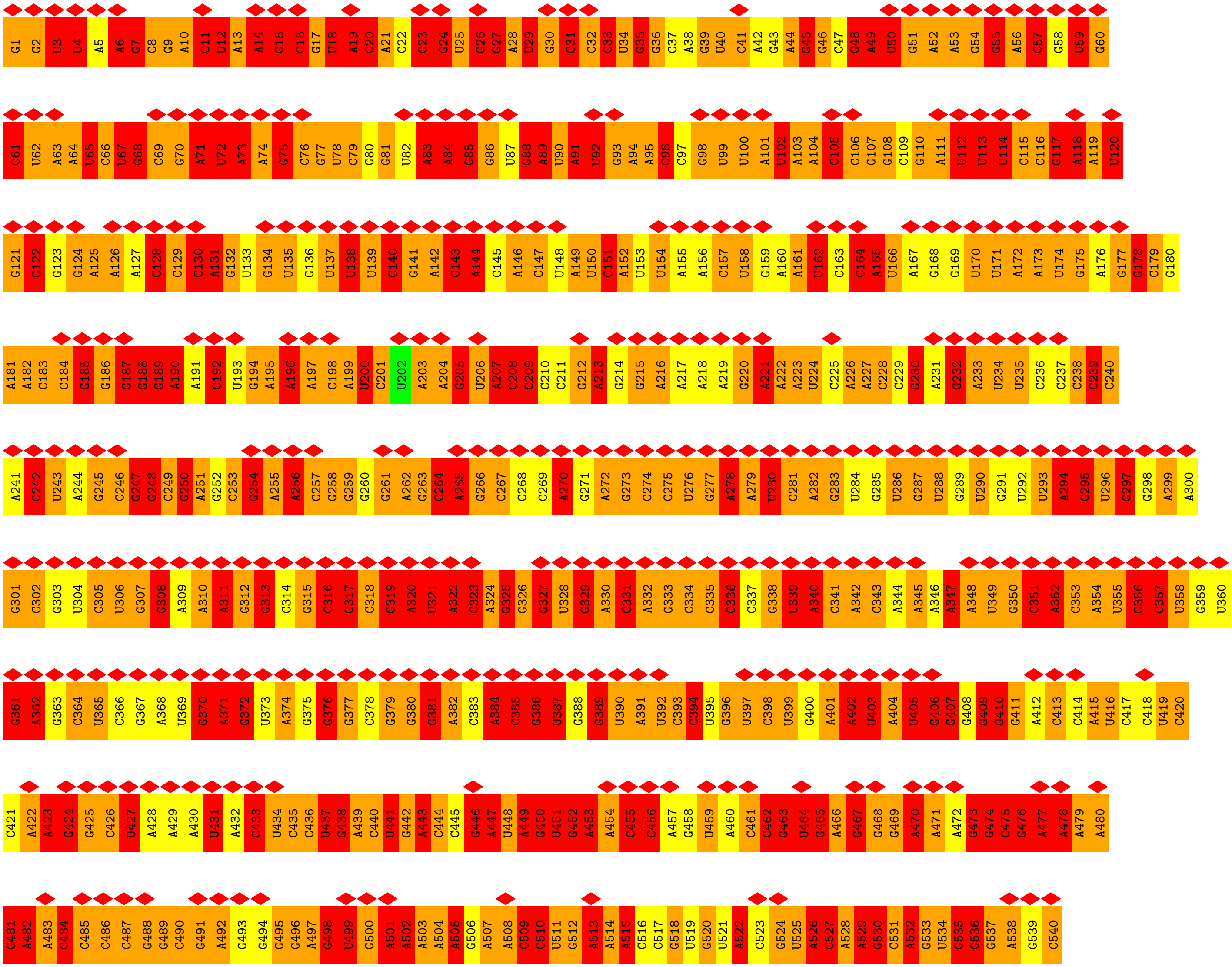
Chain BA:

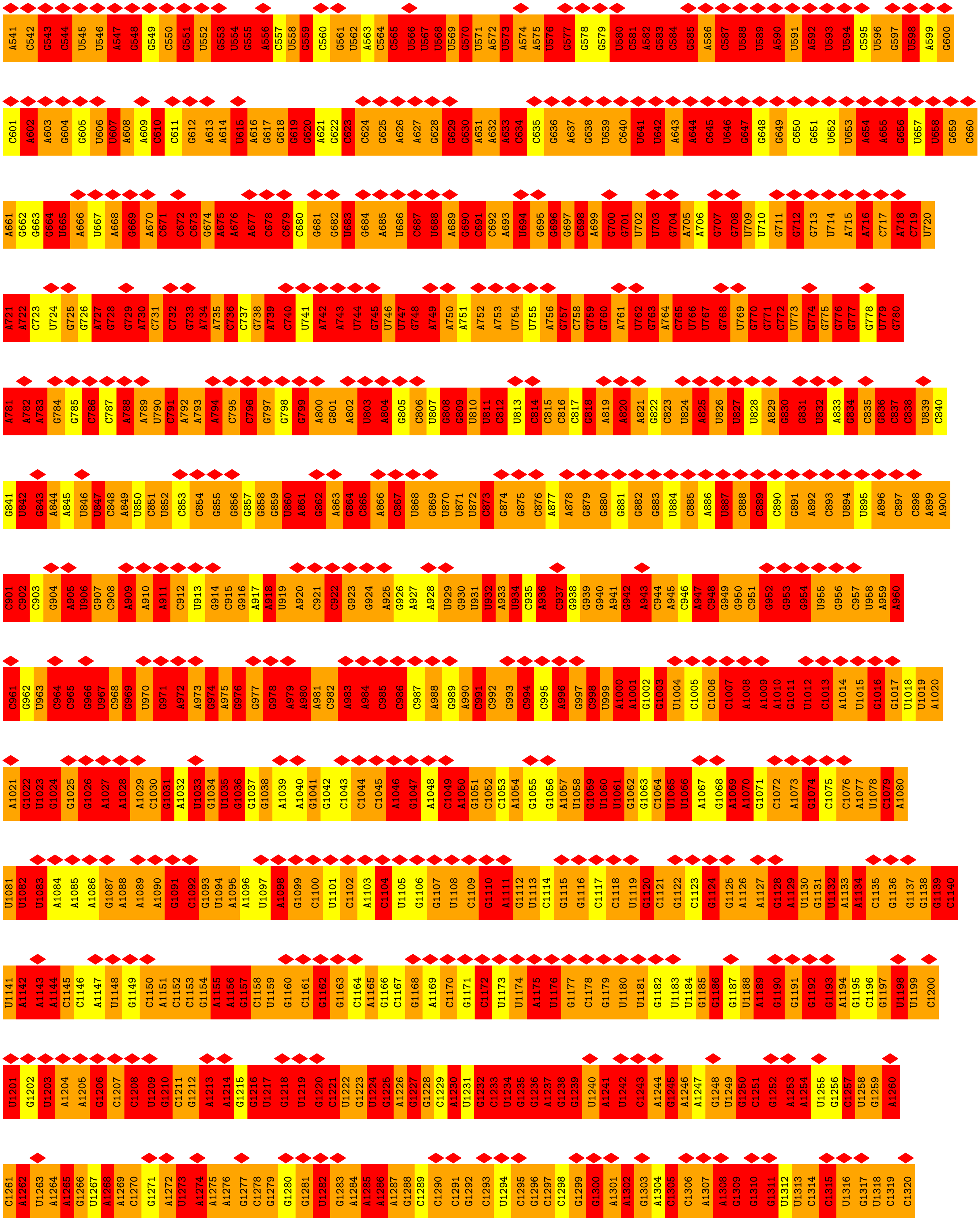




- Molecule 25: 23S rRNA

Chain BB:

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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 C635 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 C664 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 U713 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
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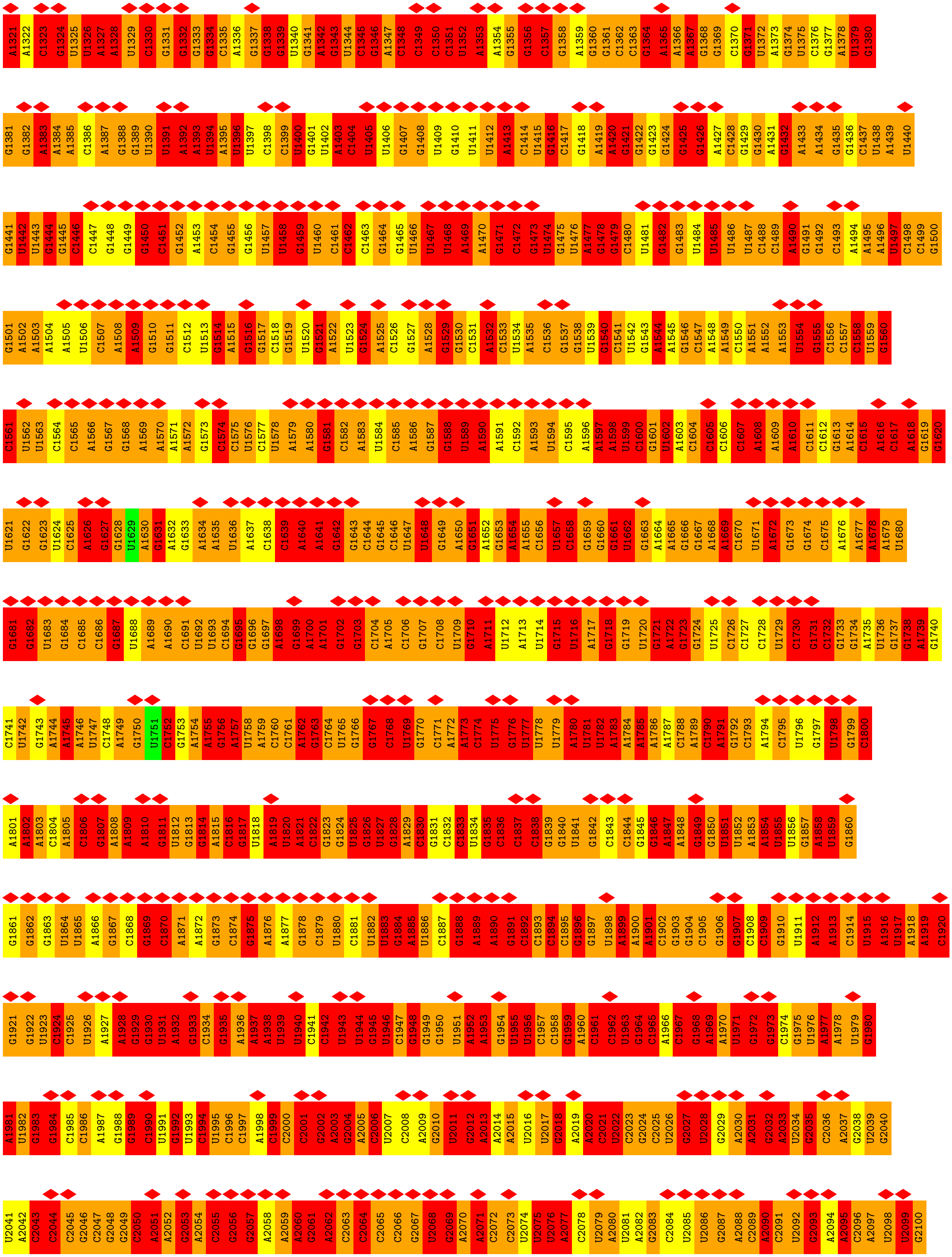
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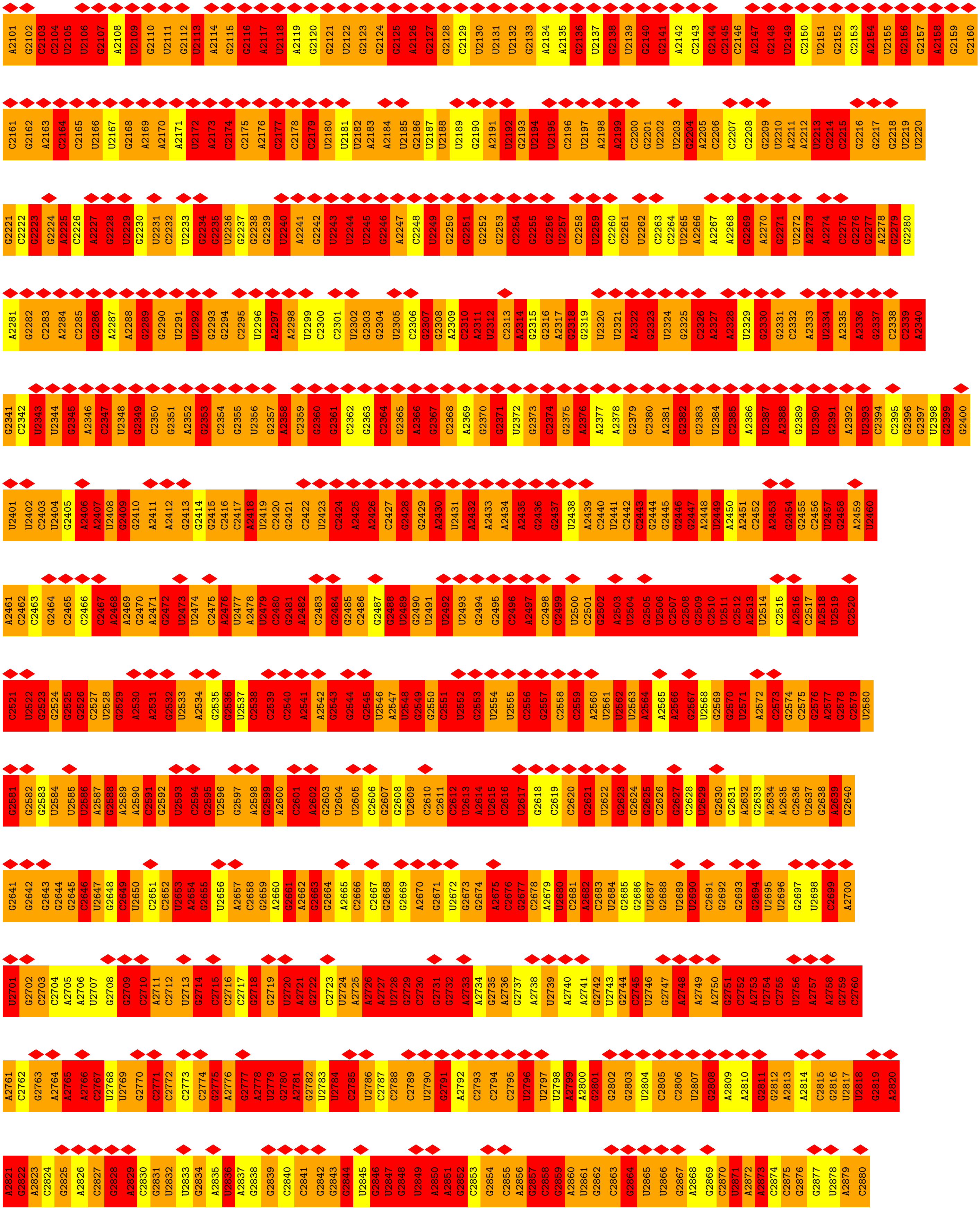
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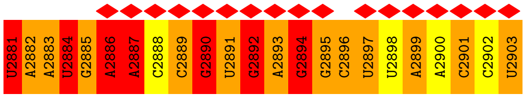

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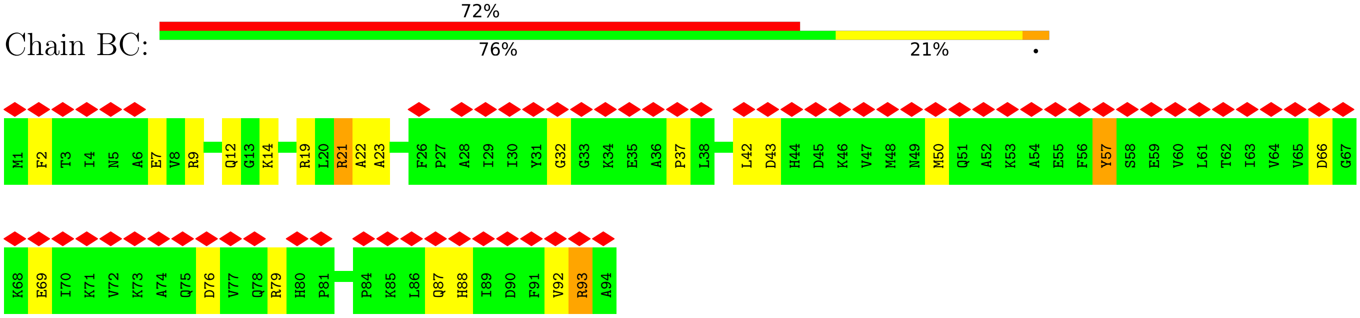

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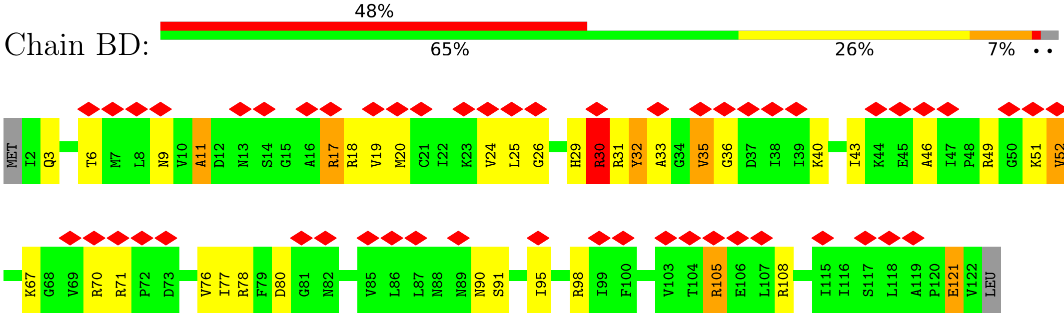
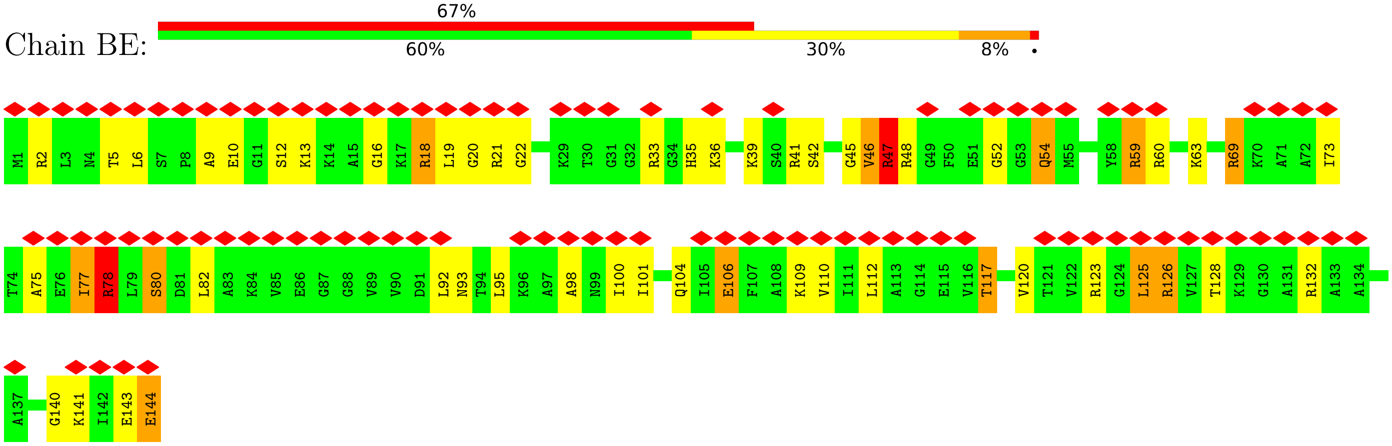
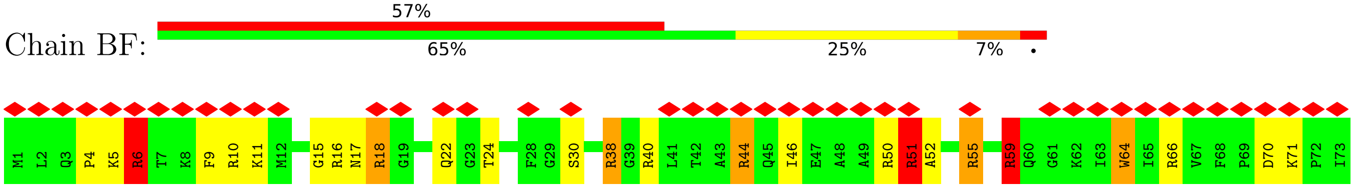
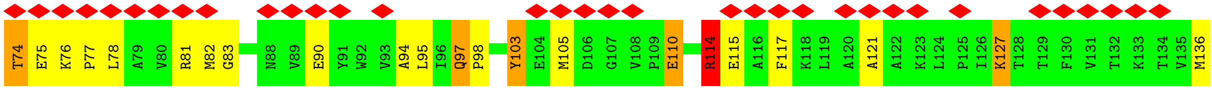


- Molecule 28: 50S ribosomal protein L15



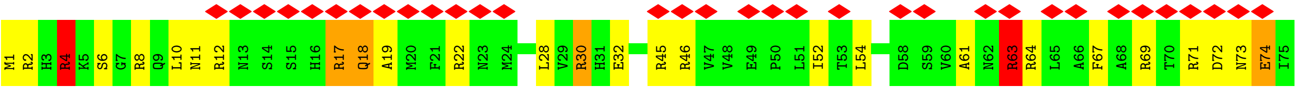
- Molecule 29: 50S ribosomal protein L16

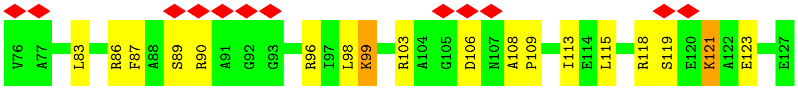




- Molecule 30: 50S ribosomal protein L17

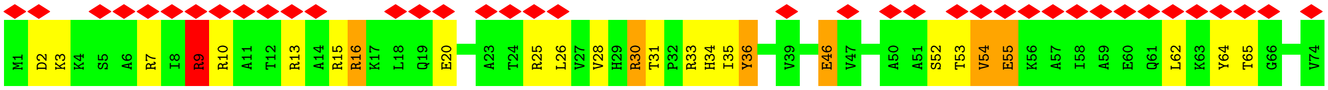
Chain BG:

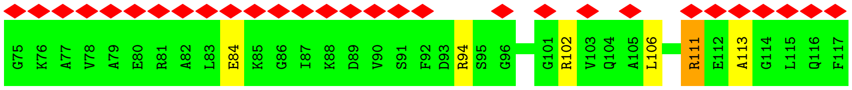




- Molecule 31: 50S ribosomal protein L18

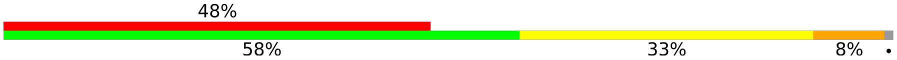
Chain BH:

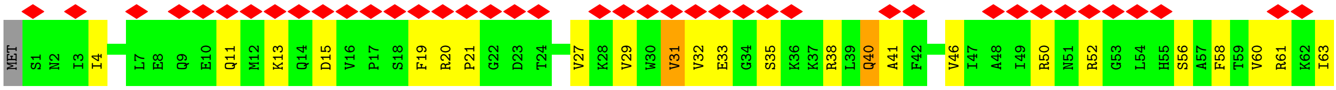


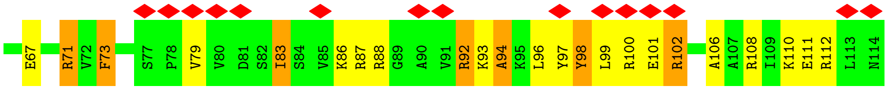


- Molecule 32: 50S ribosomal protein L19

Chain BI:

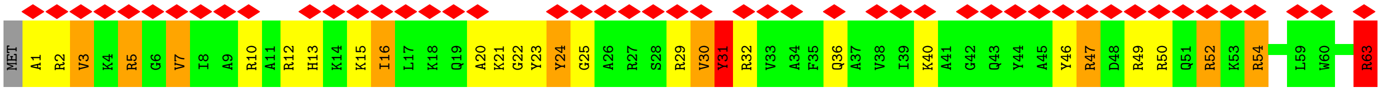


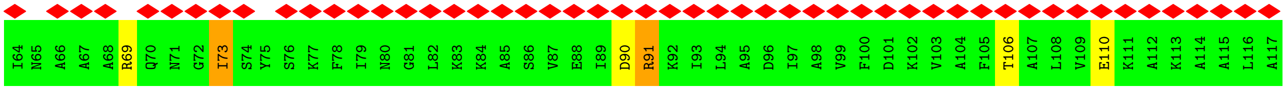




- Molecule 33: 50S ribosomal protein L20

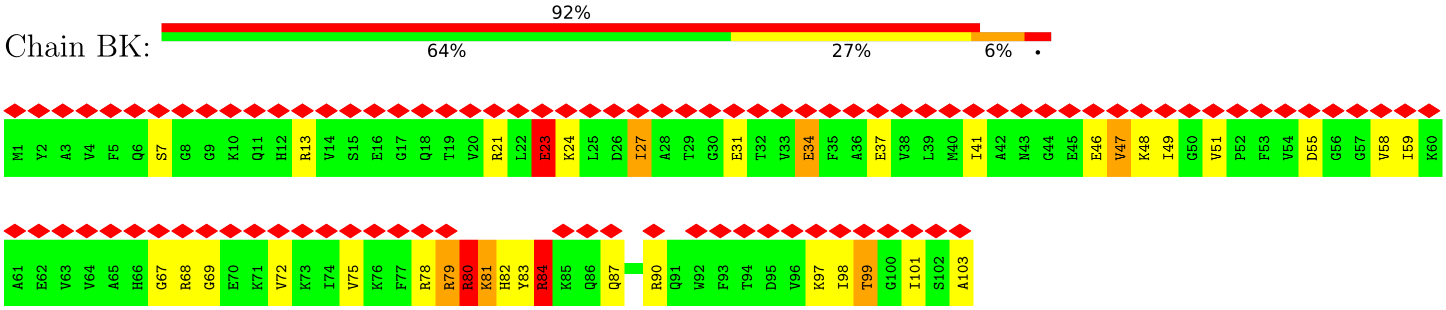
Chain BJ:





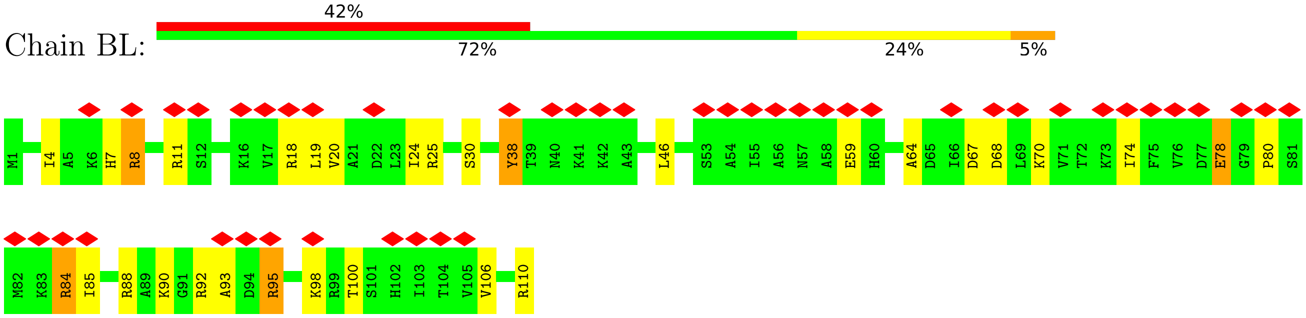
- Molecule 34: 50S ribosomal protein L21

Chain BK:



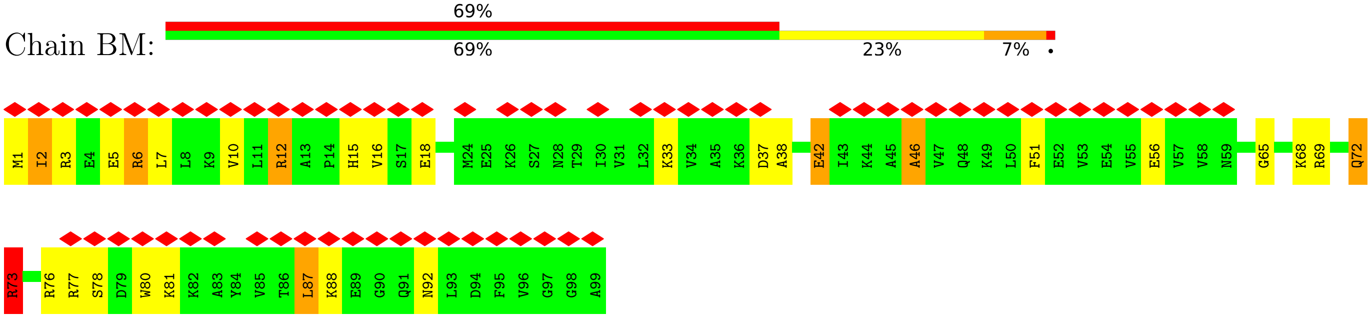
- Molecule 35: 50S ribosomal protein L22

Chain BL:



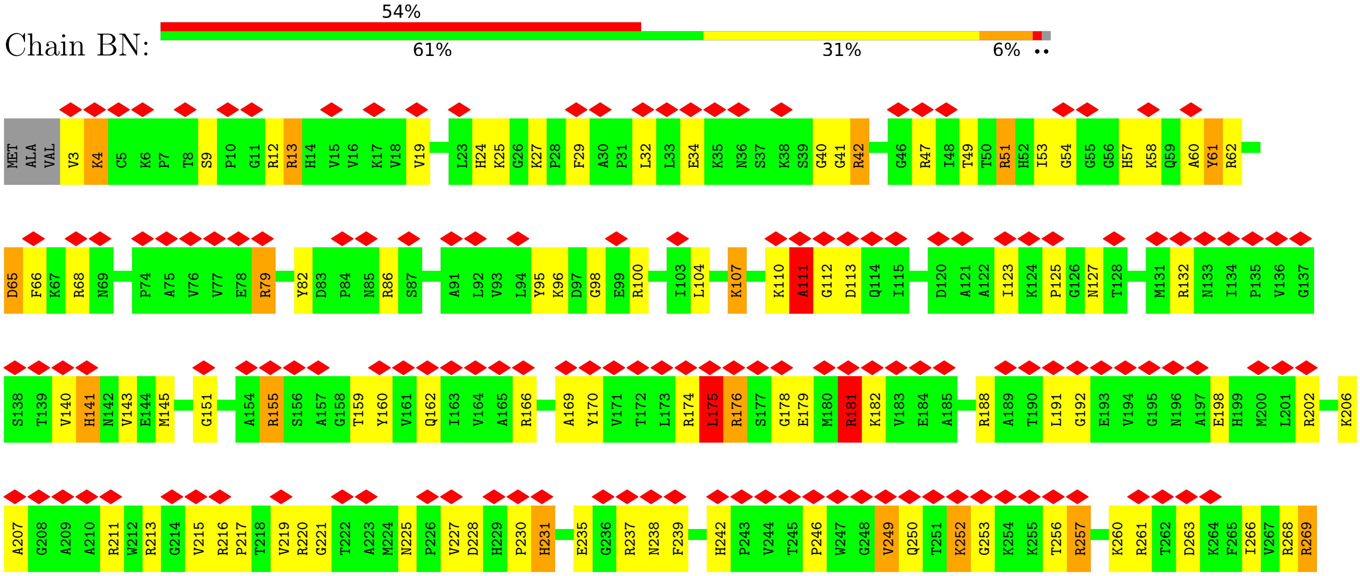
- Molecule 36: 50S ribosomal protein L23

Chain BM:

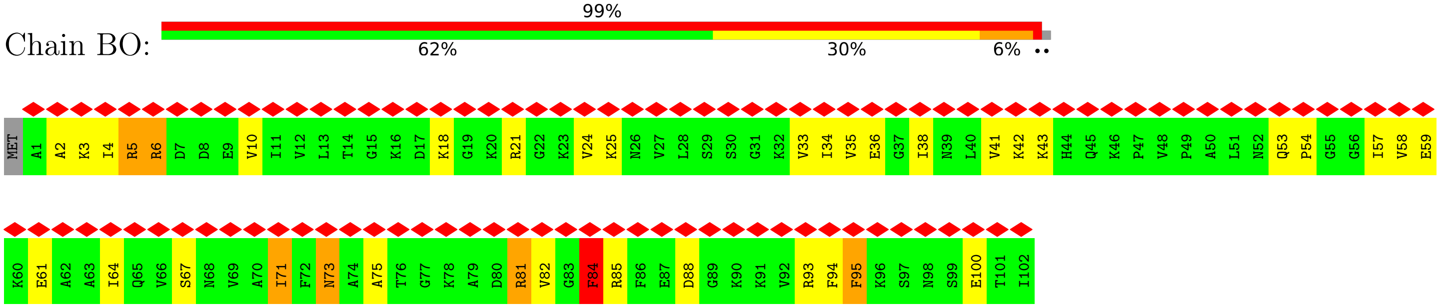


- Molecule 37: 50S ribosomal protein L2

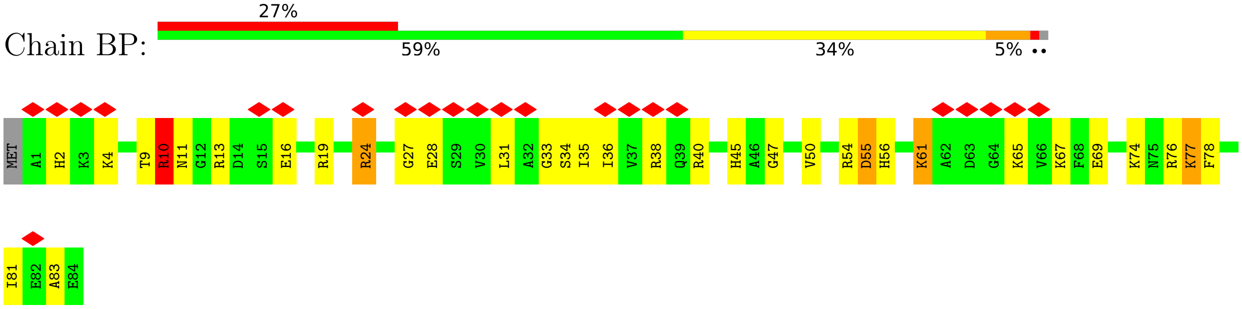
Chain BN:



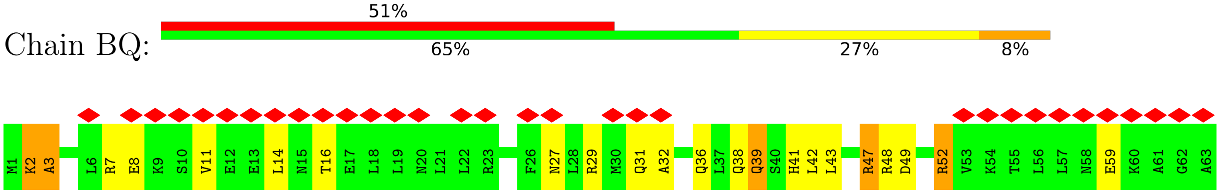
- Molecule 38: 50S ribosomal protein L24



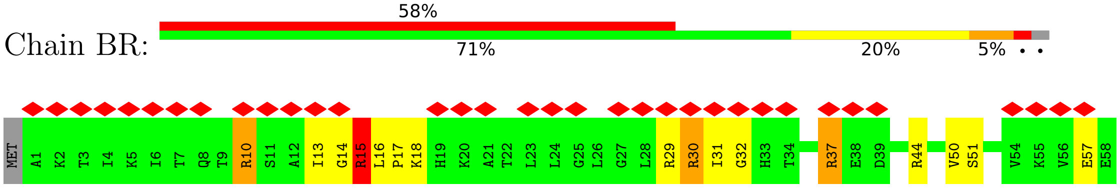
- Molecule 39: 50S ribosomal protein L27



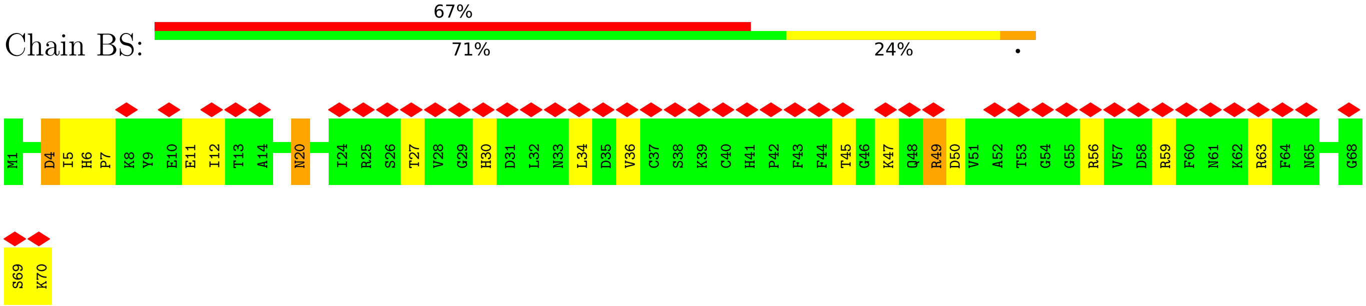
- Molecule 40: 50S ribosomal protein L29



- Molecule 41: 50S ribosomal protein L30

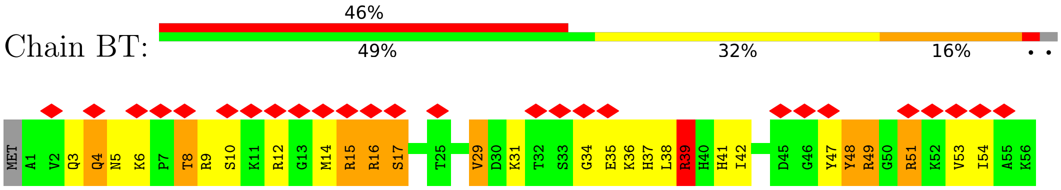


- Molecule 42: 50S ribosomal protein L31



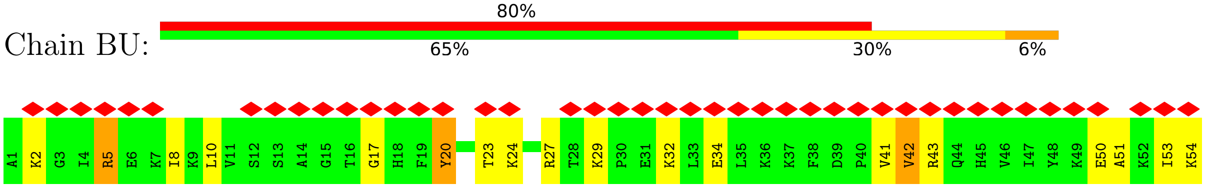
- Molecule 43: 50S ribosomal protein L32

Chain BT:



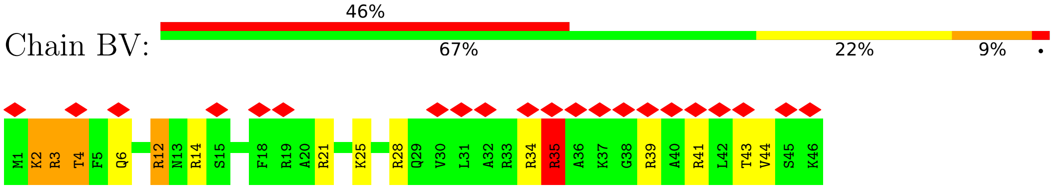
- Molecule 44: 50S ribosomal protein L33

Chain BU:



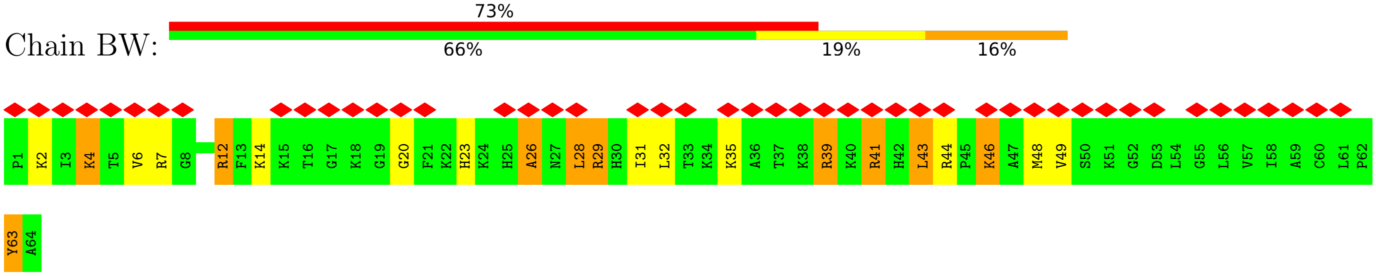
- Molecule 45: 50S ribosomal protein L34

Chain BV:



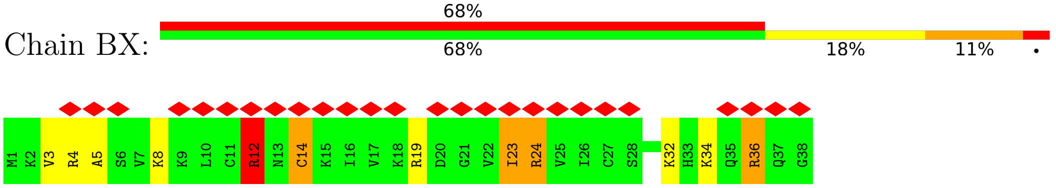
- Molecule 46: 50S ribosomal protein L35

Chain BW:



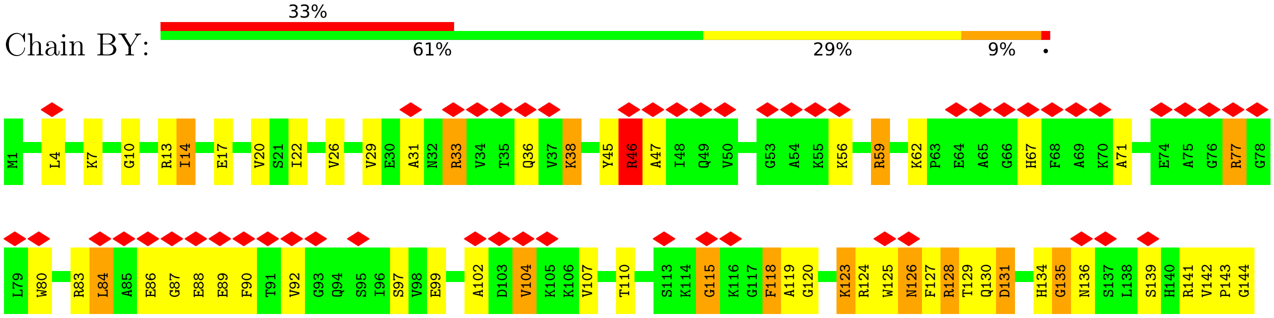
- Molecule 47: 50S ribosomal protein L36

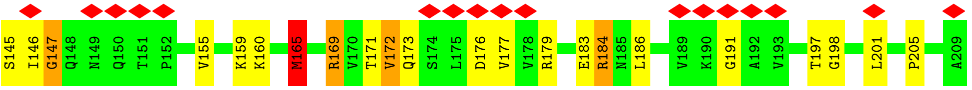
Chain BX:



- Molecule 48: 50S ribosomal protein L3

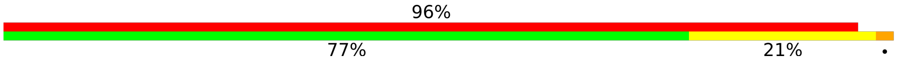
Chain BY:

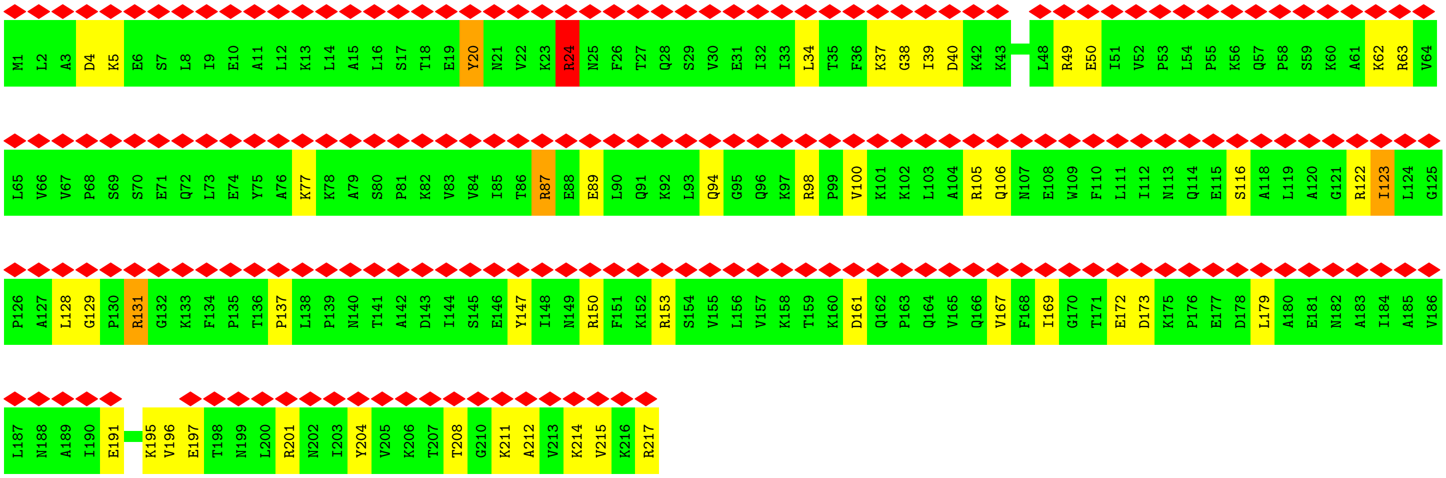




- Molecule 49: 50S ribosomal protein L1P

Chain BZ:



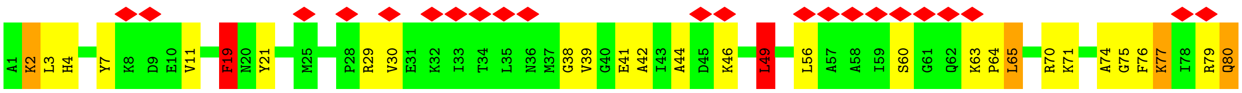


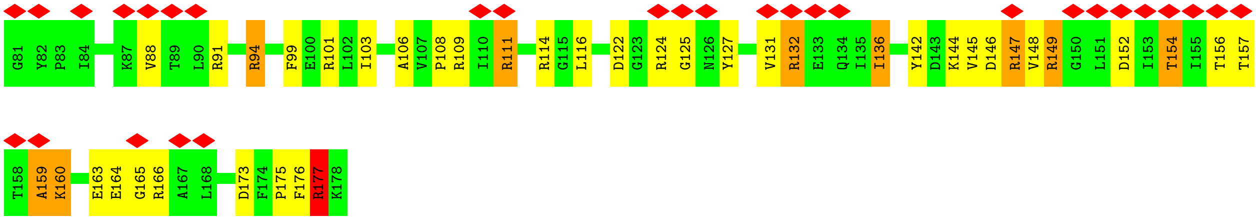
- Molecule 50: 50S ribosomal protein L4

Chain B1:

- Molecule 51: 50S ribosomal protein L5

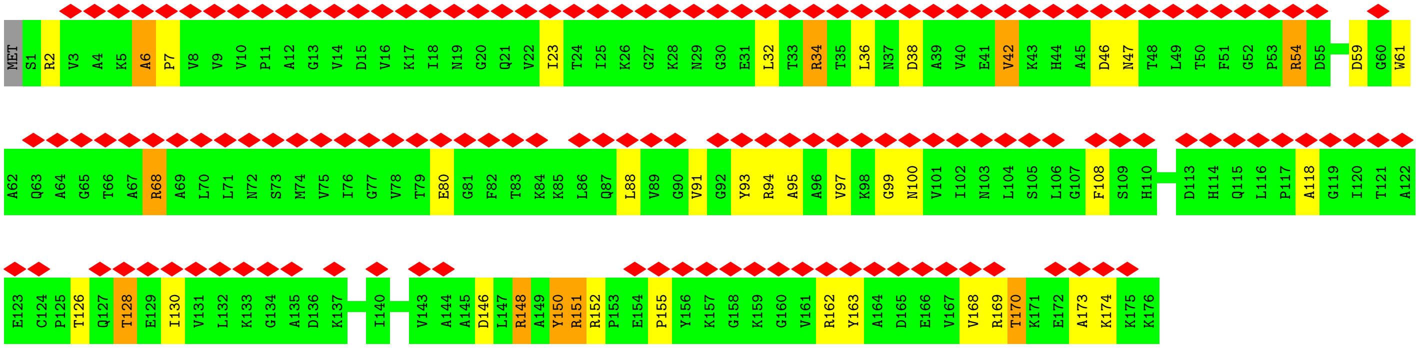
Chain B2:





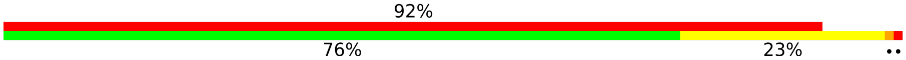
- Molecule 52: 50S ribosomal protein L6

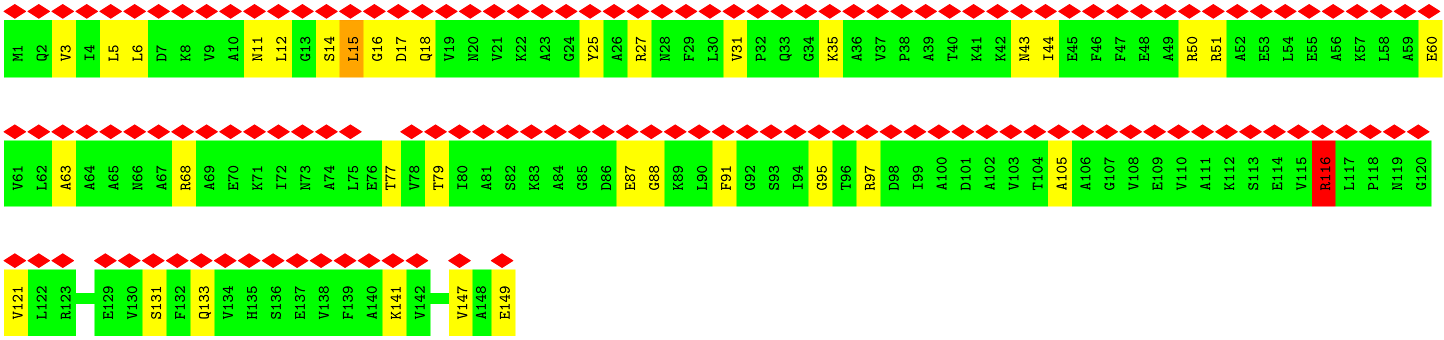
Chain B3:



- Molecule 53: 50S ribosomal protein L9

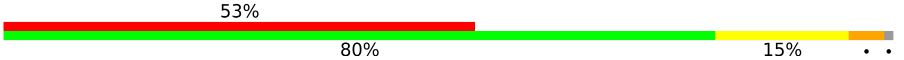
Chain B4:

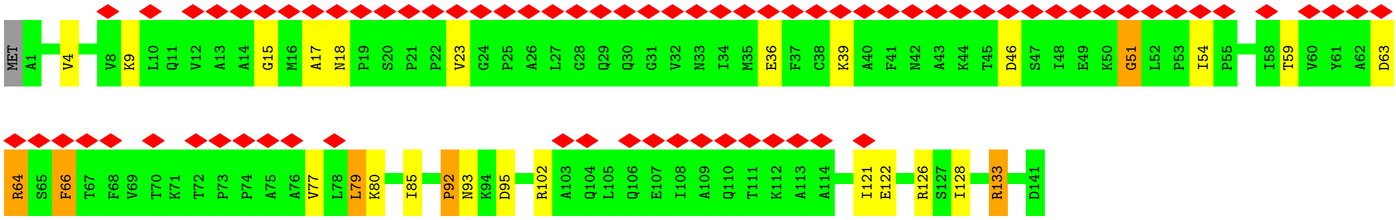




- Molecule 54: 50S ribosomal protein L11

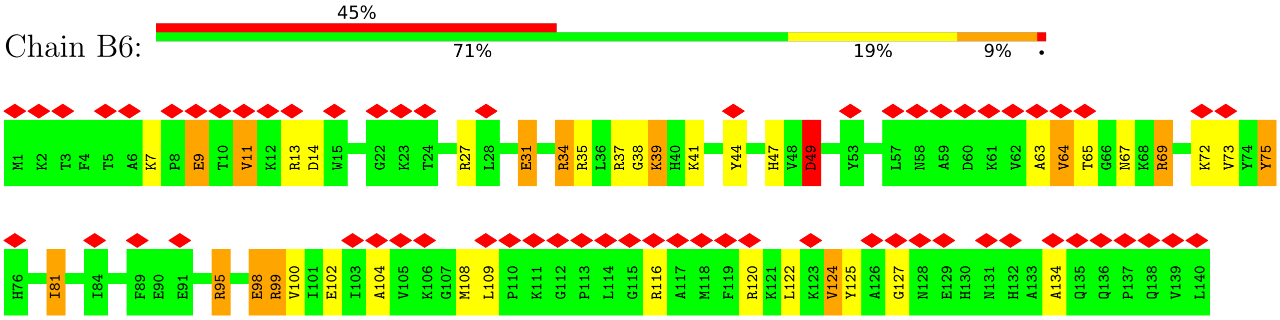
Chain B5:





- Molecule 55: 50S ribosomal protein L13

Chain B6:


45%
71%
19%
9%
•
M1
K2
T3
F4
T5
A6
K7
P8
E9
T10
V11
K12
R13
D14
W15
G22
K23
T24
R27
L28
E31
R34
R35
L36
R37
G38
K39
H40
K41
Y44
H47
V48
D49
Y53
L57
N58
A59
D60
K61
V62
A63
V64
T65
G66
N67
K68
R69
K72
V73
Y74
Y75
H76
I81
I84
F89
E90
E91
R95
E98
R99
V100
I101
E102
I103
A104
V105
K106
G107
M108
L109
P110
K111
G112
P113
L114
G115
R116
A117
M118
F119
R120
K121
L122
K123
V124
Y125
A126
G127
N128
E129
H130
N131
H132
A133
A134
Q135
Q136
P137
Q138
V139
L140

4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	75996	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose $(e^-/\text{Å}^2)$	15	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	250.984	Depositor
Minimum map value	-85.859	Depositor
Average map value	4.444	Depositor
Map value standard deviation	25.344	Depositor
Recommended contour level	57.2	Depositor
Map size (Å)	366.6, 366.6, 366.6	wwPDB
Map dimensions	130, 130, 130	wwPDB
Map angles (°)	90, 90, 90	wwPDB
Pixel spacing (Å)	2.82, 2.82, 2.82	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$ >5	RMSZ	#$|Z|$ >5
1	AA	2.55	109/1789 (6.1%)	3.85	439/2788 (15.7%)
1	AE	2.27	78/1814 (4.3%)	3.60	403/2827 (14.3%)
1	AP	3.55	99/1789 (5.5%)	3.96	389/2788 (14.0%)
2	AM	2.44	19/436 (4.4%)	3.59	99/672 (14.7%)
3	A1	2.55	1627/36759 (4.4%)	3.68	8418/57346 (14.7%)
4	AB	0.97	2/1735 (0.1%)	1.84	41/2338 (1.8%)
5	AC	1.10	5/892 (0.6%)	1.74	19/1205 (1.6%)
6	AD	1.14	2/968 (0.2%)	2.24	38/1300 (2.9%)
7	AF	1.16	7/892 (0.8%)	2.21	32/1193 (2.7%)
8	AG	1.13	3/785 (0.4%)	2.22	33/1046 (3.2%)
9	AH	1.13	5/723 (0.7%)	2.18	30/966 (3.1%)
10	AI	1.17	4/658 (0.6%)	2.16	20/884 (2.3%)
11	AJ	0.99	2/657 (0.3%)	1.87	11/881 (1.2%)
12	AK	1.19	5/462 (1.1%)	1.98	15/621 (2.4%)
13	AL	1.08	2/652 (0.3%)	1.96	14/877 (1.6%)
14	AN	1.03	4/670 (0.6%)	1.87	14/888 (1.6%)
15	AO	1.08	6/1651 (0.4%)	1.94	43/2225 (1.9%)
16	AQ	1.23	2/430 (0.5%)	2.26	19/570 (3.3%)
17	AR	1.08	2/1664 (0.1%)	1.94	46/2227 (2.1%)
18	AS	1.02	2/1118 (0.2%)	1.70	19/1504 (1.3%)
19	AT	1.03	1/835 (0.1%)	1.81	13/1128 (1.2%)
20	AU	1.12	4/1187 (0.3%)	1.97	33/1591 (2.1%)
21	AV	0.95	1/988 (0.1%)	1.65	14/1326 (1.1%)
22	AW	1.13	1/1033 (0.1%)	1.98	27/1375 (2.0%)
23	AX	1.03	2/796 (0.3%)	2.11	28/1077 (2.6%)
24	BA	2.22	97/2800 (3.5%)	3.50	592/4367 (13.6%)
25	BB	2.24	2712/69795 (3.9%)	3.62	15539/108884 (14.3%)
26	BC	1.01	1/765 (0.1%)	1.78	11/1025 (1.1%)
27	BD	1.11	4/939 (0.4%)	2.36	28/1258 (2.2%)
28	BE	1.13	2/1061 (0.2%)	1.97	25/1413 (1.8%)
29	BF	1.09	3/1092 (0.3%)	2.16	36/1460 (2.5%)
30	BG	1.16	6/1020 (0.6%)	2.13	43/1364 (3.2%)
31	BH	1.11	1/909 (0.1%)	2.12	33/1219 (2.7%)
32	BI	1.15	4/928 (0.4%)	2.04	30/1242 (2.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	BJ	1.18	4/959 (0.4%)	1.97	27/1278 (2.1%)
34	BK	1.05	1/828 (0.1%)	2.02	23/1107 (2.1%)
35	BL	0.98	0/863	1.86	17/1156 (1.5%)
36	BM	0.99	2/784 (0.3%)	1.93	18/1048 (1.7%)
37	BN	1.10	9/2092 (0.4%)	1.99	65/2813 (2.3%)
38	BO	1.03	1/787 (0.1%)	1.87	18/1051 (1.7%)
39	BP	1.05	1/641 (0.2%)	2.02	17/848 (2.0%)
40	BQ	1.02	0/509	2.09	13/677 (1.9%)
41	BR	0.99	2/452 (0.4%)	2.05	14/605 (2.3%)
42	BS	1.04	0/558	1.99	13/745 (1.7%)
43	BT	1.10	0/449	2.22	16/599 (2.7%)
44	BU	1.08	0/447	1.81	8/594 (1.3%)
45	BV	1.16	0/379	2.33	18/498 (3.6%)
46	BW	0.99	0/512	1.74	9/676 (1.3%)
47	BX	1.07	1/302 (0.3%)	2.23	8/397 (2.0%)
48	BY	0.99	3/1585 (0.2%)	1.98	42/2134 (2.0%)
49	BZ	0.98	3/1711 (0.2%)	1.64	26/2305 (1.1%)
50	B1	1.01	0/1570	1.86	35/2113 (1.7%)
51	B2	1.07	2/1443 (0.1%)	1.88	40/1937 (2.1%)
52	B3	1.01	0/1342	1.81	32/1816 (1.8%)
53	B4	0.97	1/1121 (0.1%)	1.74	16/1515 (1.1%)
54	B5	0.94	0/1045	1.71	11/1410 (0.8%)
55	B6	1.02	1/1135 (0.1%)	1.95	28/1529 (1.8%)
All	All	2.08	4855/162206 (3.0%)	3.29	27108/242726 (11.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	0	55
1	AE	0	49
1	AP	2	50
2	AM	0	9
3	A1	4	945
4	AB	0	3
5	AC	0	3
6	AD	0	7
7	AF	0	5
8	AG	0	4
9	AH	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	AI	0	3
11	AJ	0	4
13	AL	0	8
14	AN	1	1
15	AO	0	3
16	AQ	0	4
17	AR	0	7
18	AS	0	3
19	AT	0	4
20	AU	0	4
21	AV	0	2
22	AW	0	4
23	AX	0	4
24	BA	0	66
25	BB	3	1717
26	BC	0	3
27	BD	0	6
28	BE	0	6
29	BF	0	4
30	BG	0	4
31	BH	0	1
32	BI	0	4
33	BJ	0	4
34	BK	0	5
35	BL	0	5
36	BM	0	1
37	BN	0	12
38	BO	0	4
39	BP	0	3
40	BQ	0	3
41	BR	0	3
42	BS	0	3
43	BT	0	2
44	BU	0	5
45	BV	0	2
46	BW	0	4
47	BX	0	2
48	BY	0	9
49	BZ	0	2
50	B1	0	9
51	B2	0	6
52	B3	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
53	B4	0	4
54	B5	0	3
55	B6	0	8
All	All	10	3101

The worst 5 of 4855 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A1	1429	A	P-O5’	178.16	3.38	1.59
3	A1	1340	A	C3’-O3’	99.95	2.82	1.42
1	AP	31	A	C4’-C3’	53.26	2.11	1.53
1	AP	31	A	C2’-C1’	45.01	2.02	1.53
1	AP	31	A	C4’-O4’	44.63	2.03	1.45

The worst 5 of 27108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AP	74	C	P-O3’-C3’	-78.58	25.40	119.70
1	AP	74	C	O3’-P-O5’	-40.02	27.95	104.00
25	BB	2376	A	N1-C6-N6	-29.09	101.15	118.60
3	A1	1225	A	N1-C6-N6	-28.97	101.22	118.60
3	A1	1250	A	N1-C6-N6	-27.68	101.99	118.60

5 of 10 chirality outliers are listed below:

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

5 of 3101 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	G	Sidechain
1	AA	3	G	Sidechain
1	AA	4	G	Sidechain
1	AA	5	A	Sidechain
1	AA	6	U	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	1600	0	760	11	0
1	AE	1622	0	769	7	0
1	AP	1600	0	755	42	0
2	AM	397	0	202	6	0
3	A1	32828	0	15511	162	0
4	AB	1704	0	1732	9	0
5	AC	876	0	887	3	0
6	AD	954	0	1019	4	0
7	AF	883	0	944	1	0
8	AG	773	0	825	2	0
9	AH	715	0	742	2	0
10	AI	648	0	666	5	0
11	AJ	648	0	691	3	0
12	AK	455	0	478	0	0
13	AL	637	0	665	0	0
14	AN	664	0	714	4	0
15	AO	1624	0	1699	5	0
16	AQ	425	0	449	1	0
17	AR	1642	0	1710	9	0
18	AS	1105	0	1148	4	0
19	AT	817	0	808	2	0
20	AU	1174	0	1230	3	0
21	AV	978	0	1034	0	0
22	AW	1021	0	1070	1	0
23	AX	786	0	828	4	0
24	BA	2504	0	1208	11	0
25	BB	62317	0	29633	224	0
26	BC	752	0	780	4	0
27	BD	930	0	1000	5	0
28	BE	1052	0	1129	9	0
29	BF	1073	0	1157	8	0
30	BG	1007	0	1045	4	0
31	BH	899	0	935	2	0
32	BI	916	0	965	6	0
33	BJ	946	0	1022	8	0
34	BK	815	0	839	4	0
35	BL	856	0	922	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
36	BM	777	0	840	2	0
37	BN	2053	0	2122	9	0
38	BO	779	0	834	2	0
39	BP	633	0	656	1	0
40	BQ	508	0	543	3	0
41	BR	448	0	491	2	0
42	BS	548	0	552	2	0
43	BT	443	0	461	2	0
44	BU	440	0	485	2	0
45	BV	376	0	418	2	0
46	BW	503	0	574	7	0
47	BX	301	0	343	1	0
48	BY	1564	0	1616	7	0
49	BZ	1687	0	1814	3	0
50	B1	1551	0	1619	7	0
51	B2	1419	0	1460	8	0
52	B3	1322	0	1374	3	0
53	B4	1110	0	1148	2	0
54	B5	1031	0	1088	4	0
55	B6	1112	0	1147	2	0
All	All	149248	0	97556	534	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 534 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:BB:1687:G:C2’	25:BB:1687:G:C3’	1.91	1.47
25:BB:1687:G:C2’	25:BB:1687:G:C1’	1.93	1.45
1:AP:31:A:C2’	3:A1:1340:A:H3’	1.45	1.44
25:BB:1687:G:C3’	25:BB:1687:G:C4’	1.96	1.43
1:AP:31:A:C2’	1:AP:31:A:C3’	2.01	1.39

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	AB	216/241 (90%)	178 (82%)	33 (15%)	5 (2%)	6	34
5	AC	115/129 (89%)	91 (79%)	17 (15%)	7 (6%)	1	17
6	AD	121/124 (98%)	78 (64%)	28 (23%)	15 (12%)	0	5
7	AF	112/118 (95%)	80 (71%)	24 (21%)	8 (7%)	1	14
8	AG	94/101 (93%)	69 (73%)	20 (21%)	5 (5%)	2	19
9	AH	86/89 (97%)	73 (85%)	11 (13%)	2 (2%)	6	34
10	AI	80/82 (98%)	55 (69%)	15 (19%)	10 (12%)	0	5
11	AJ	78/84 (93%)	52 (67%)	18 (23%)	8 (10%)	0	8
12	AK	53/75 (71%)	44 (83%)	7 (13%)	2 (4%)	3	24
13	AL	77/92 (84%)	51 (66%)	19 (25%)	7 (9%)	1	11
14	AN	83/87 (95%)	66 (80%)	13 (16%)	4 (5%)	2	21
15	AO	204/233 (88%)	151 (74%)	38 (19%)	15 (7%)	1	14
16	AQ	49/71 (69%)	35 (71%)	8 (16%)	6 (12%)	0	6
17	AR	203/206 (98%)	161 (79%)	29 (14%)	13 (6%)	1	16
18	AS	148/159 (93%)	114 (77%)	20 (14%)	14 (10%)	0	10
19	AT	98/135 (73%)	80 (82%)	13 (13%)	5 (5%)	2	19
20	AU	148/179 (83%)	118 (80%)	19 (13%)	11 (7%)	1	14
21	AV	127/130 (98%)	103 (81%)	19 (15%)	5 (4%)	3	23
22	AW	125/130 (96%)	95 (76%)	23 (18%)	7 (6%)	2	19
23	AX	96/103 (93%)	78 (81%)	9 (9%)	9 (9%)	0	10
26	BC	92/94 (98%)	74 (80%)	14 (15%)	4 (4%)	2	22
27	BD	119/123 (97%)	90 (76%)	16 (13%)	13 (11%)	0	8
28	BE	142/144 (99%)	91 (64%)	30 (21%)	21 (15%)	0	3
29	BF	134/136 (98%)	73 (54%)	40 (30%)	21 (16%)	0	3
30	BG	125/127 (98%)	84 (67%)	32 (26%)	9 (7%)	1	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	BH	115/117 (98%)	72 (63%)	32 (28%)	11 (10%)	0	10
32	BI	112/115 (97%)	63 (56%)	32 (29%)	17 (15%)	0	4
33	BJ	115/118 (98%)	77 (67%)	27 (24%)	11 (10%)	0	10
34	BK	101/103 (98%)	59 (58%)	33 (33%)	9 (9%)	1	11
35	BL	108/110 (98%)	72 (67%)	27 (25%)	9 (8%)	1	12
36	BM	97/99 (98%)	69 (71%)	18 (19%)	10 (10%)	0	8
37	BN	265/270 (98%)	165 (62%)	61 (23%)	39 (15%)	0	4
38	BO	100/103 (97%)	60 (60%)	22 (22%)	18 (18%)	0	3
39	BP	82/85 (96%)	44 (54%)	21 (26%)	17 (21%)	0	2
40	BQ	61/63 (97%)	42 (69%)	14 (23%)	5 (8%)	1	12
41	BR	56/59 (95%)	38 (68%)	13 (23%)	5 (9%)	1	11
42	BS	68/70 (97%)	38 (56%)	22 (32%)	8 (12%)	0	6
43	BT	54/57 (95%)	32 (59%)	11 (20%)	11 (20%)	0	2
44	BU	52/54 (96%)	33 (64%)	14 (27%)	5 (10%)	0	10
45	BV	44/46 (96%)	33 (75%)	6 (14%)	5 (11%)	0	7
46	BW	62/64 (97%)	35 (56%)	20 (32%)	7 (11%)	0	7
47	BX	36/38 (95%)	23 (64%)	8 (22%)	5 (14%)	0	4
48	BY	207/209 (99%)	113 (55%)	54 (26%)	40 (19%)	0	2
49	BZ	211/213 (99%)	163 (77%)	33 (16%)	15 (7%)	1	14
50	B1	199/201 (99%)	111 (56%)	53 (27%)	35 (18%)	0	3
51	B2	176/178 (99%)	123 (70%)	26 (15%)	27 (15%)	0	3
52	B3	174/177 (98%)	149 (86%)	20 (12%)	5 (3%)	4	29
53	B4	147/149 (99%)	103 (70%)	33 (22%)	11 (8%)	1	13
54	B5	139/142 (98%)	113 (81%)	17 (12%)	9 (6%)	1	16
55	B6	138/140 (99%)	79 (57%)	41 (30%)	18 (13%)	0	5
All	All	5844/6172 (95%)	4093 (70%)	1173 (20%)	578 (10%)	1	9

5 of 578 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	AB	36	LYS
4	AB	97	GLY
4	AB	169	HIS

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Mol	Chain	Res	Type
6	AD	9	LYS
6	AD	15	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	AB	180/199 (90%)	164 (91%)	16 (9%)	9	30
5	AC	90/99 (91%)	81 (90%)	9 (10%)	7	26
6	AD	103/104 (99%)	87 (84%)	16 (16%)	2	14
7	AF	92/96 (96%)	84 (91%)	8 (9%)	10	31
8	AG	79/84 (94%)	75 (95%)	4 (5%)	24	48
9	AH	76/77 (99%)	73 (96%)	3 (4%)	32	56
10	AI	65/65 (100%)	61 (94%)	4 (6%)	18	43
11	AJ	74/78 (95%)	69 (93%)	5 (7%)	16	41
12	AK	48/66 (73%)	44 (92%)	4 (8%)	11	34
13	AL	70/79 (89%)	59 (84%)	11 (16%)	2	14
14	AN	65/66 (98%)	59 (91%)	6 (9%)	9	29
15	AO	170/190 (90%)	158 (93%)	12 (7%)	14	39
16	AQ	44/61 (72%)	40 (91%)	4 (9%)	9	29
17	AR	172/173 (99%)	156 (91%)	16 (9%)	9	28
18	AS	113/119 (95%)	98 (87%)	15 (13%)	4	18
19	AT	87/116 (75%)	77 (88%)	10 (12%)	5	21
20	AU	123/147 (84%)	108 (88%)	15 (12%)	5	20
21	AV	104/105 (99%)	98 (94%)	6 (6%)	20	45
22	AW	105/107 (98%)	98 (93%)	7 (7%)	16	41
23	AX	86/90 (96%)	78 (91%)	8 (9%)	9	28
26	BC	78/78 (100%)	74 (95%)	4 (5%)	24	48
27	BD	102/104 (98%)	98 (96%)	4 (4%)	32	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
28	BE	103/103 (100%)	84 (82%)	19 (18%)	1	9
29	BF	109/109 (100%)	95 (87%)	14 (13%)	4	18
30	BG	103/103 (100%)	90 (87%)	13 (13%)	4	19
31	BH	87/87 (100%)	81 (93%)	6 (7%)	15	40
32	BI	99/100 (99%)	96 (97%)	3 (3%)	41	63
33	BJ	89/90 (99%)	78 (88%)	11 (12%)	4	19
34	BK	84/84 (100%)	73 (87%)	11 (13%)	4	18
35	BL	93/93 (100%)	83 (89%)	10 (11%)	6	23
36	BM	83/83 (100%)	69 (83%)	14 (17%)	2	12
37	BN	213/215 (99%)	189 (89%)	24 (11%)	6	21
38	BO	83/84 (99%)	76 (92%)	7 (8%)	11	33
39	BP	62/63 (98%)	55 (89%)	7 (11%)	6	21
40	BQ	55/55 (100%)	47 (86%)	8 (14%)	3	15
41	BR	48/49 (98%)	46 (96%)	2 (4%)	30	54
42	BS	62/62 (100%)	58 (94%)	4 (6%)	17	42
43	BT	47/48 (98%)	35 (74%)	12 (26%)	0	3
44	BU	48/48 (100%)	45 (94%)	3 (6%)	18	43
45	BV	38/38 (100%)	34 (90%)	4 (10%)	7	24
46	BW	51/51 (100%)	43 (84%)	8 (16%)	2	14
47	BX	34/34 (100%)	30 (88%)	4 (12%)	5	20
48	BY	164/164 (100%)	145 (88%)	19 (12%)	5	21
49	BZ	187/187 (100%)	174 (93%)	13 (7%)	15	40
50	B1	165/165 (100%)	147 (89%)	18 (11%)	6	23
51	B2	149/149 (100%)	130 (87%)	19 (13%)	4	18
52	B3	137/138 (99%)	125 (91%)	12 (9%)	10	31
53	B4	114/114 (100%)	104 (91%)	10 (9%)	10	31
54	B5	109/110 (99%)	102 (94%)	7 (6%)	17	42
55	B6	114/114 (100%)	107 (94%)	7 (6%)	18	44
All	All	4856/5043 (96%)	4380 (90%)	476 (10%)	11	26

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

Mol	Chain	Res	Type
30	BG	115	LEU
52	B3	42	VAL
36	BM	80	TRP
51	B2	160	LYS
55	B6	81	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
34	BK	91	GLN
43	BT	4	GLN
40	BQ	41	HIS
44	BU	45	HIS
10	AI	26	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	75/76 (98%)	20 (26%)	8 (10%)
1	AE	75/76 (98%)	11 (14%)	1 (1%)
1	AP	74/76 (97%)	15 (20%)	6 (8%)
2	AM	20/20 (100%)	9 (45%)	7 (35%)
24	BA	116/117 (99%)	37 (31%)	11 (9%)
25	BB	2901/2903 (99%)	1516 (52%)	511 (17%)
3	A1	1529/1530 (99%)	753 (49%)	280 (18%)
All	All	4790/4798 (99%)	2361 (49%)	824 (17%)

5 of 2361 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	2	C
1	AA	3	G
1	AA	10	G
1	AA	13	C
1	AA	17	U

5 of 824 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
25	BB	914	G
25	BB	1567	G

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Mol	Chain	Res	Type
25	BB	2711	A
25	BB	974	G
25	BB	908	C

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
25	BB	1
1	AP	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	1959:G	O3'	1960:A	P	3.50
1	AP	74:C	O3'	75:C	P	1.08

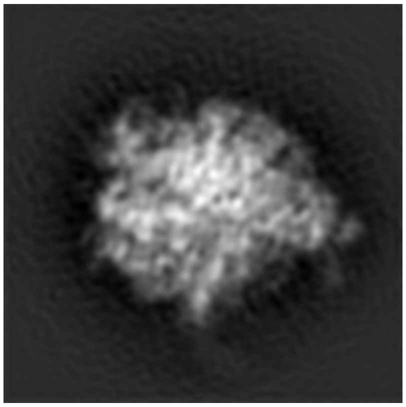
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-1055. These allow visual inspection of the internal detail of the map and identification of artifacts.

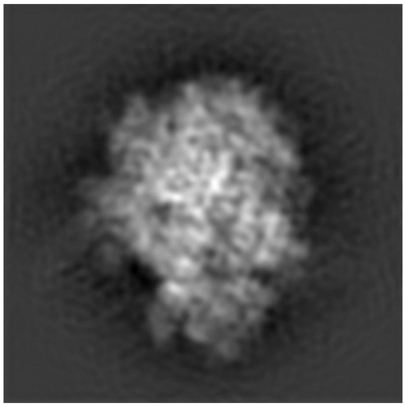
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections ⓘ

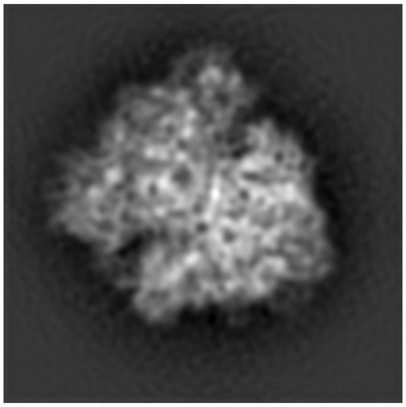
6.1.1 Primary map



X



Y

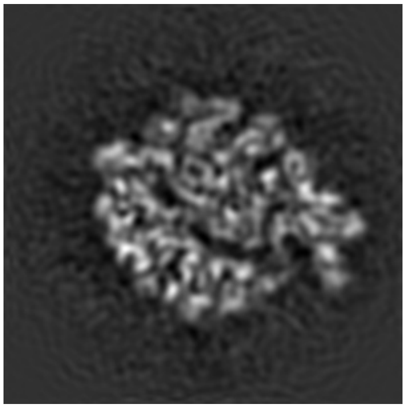


Z

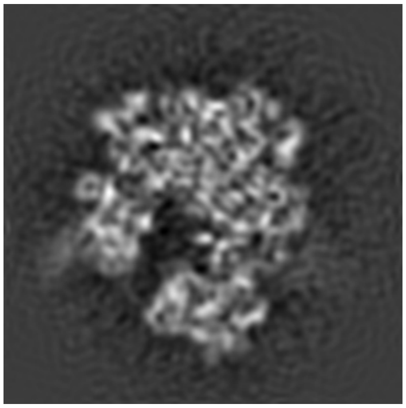
The images above show the map projected in three orthogonal directions.

6.2 Central slices ⓘ

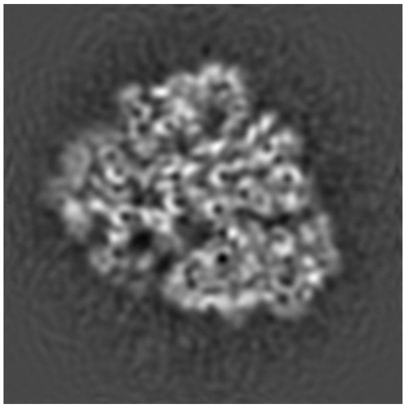
6.2.1 Primary map



X Index: 65



Y Index: 65

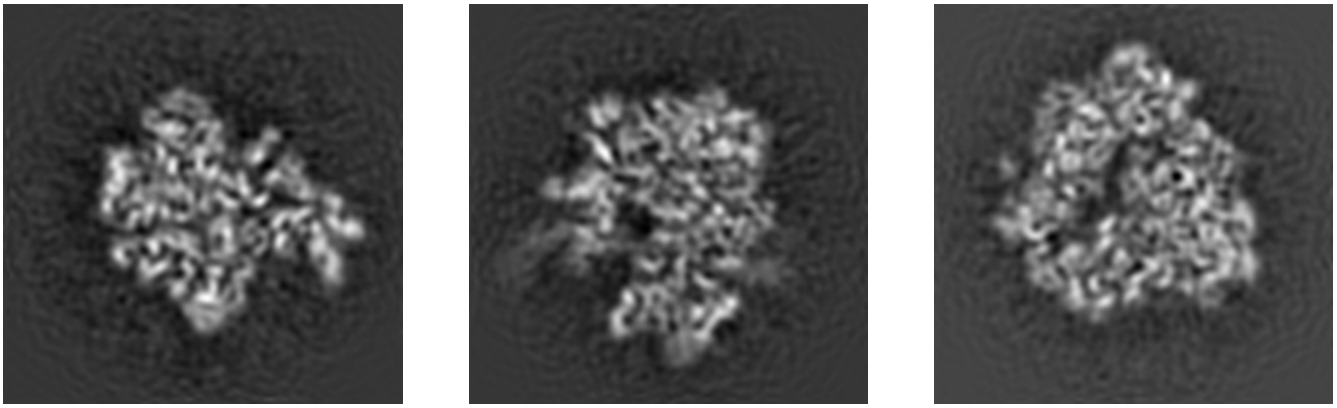


Z Index: 65

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

6.3 Largest variance slices ⓘ

6.3.1 Primary map

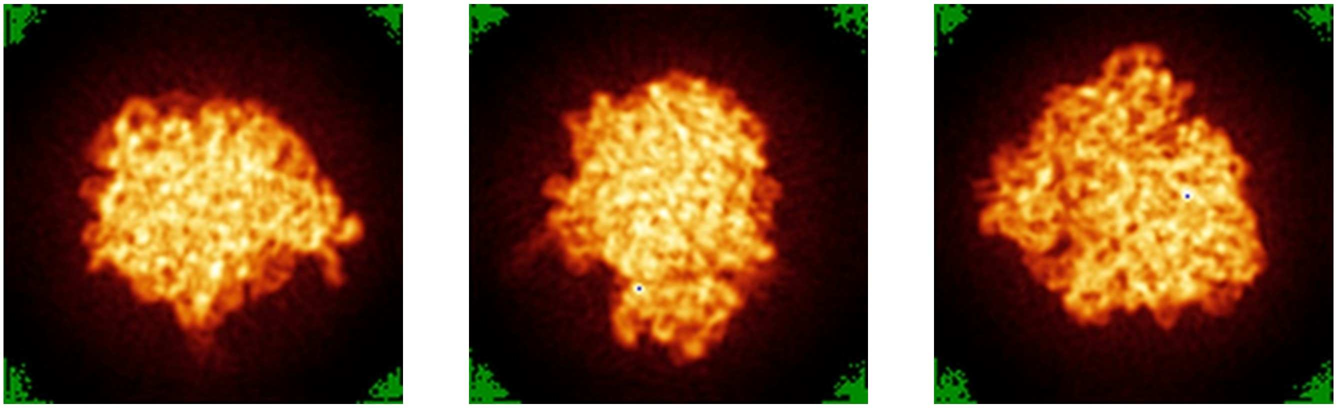


X Index: 68 Y Index: 68 Z Index: 59

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

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

6.4.1 Primary map

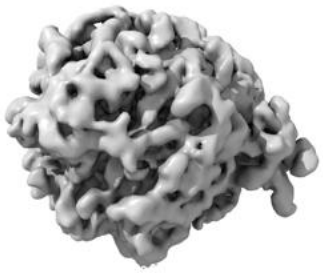


X Y Z

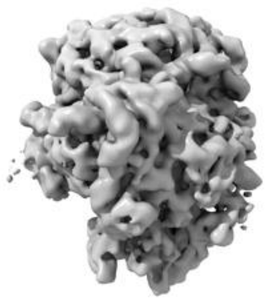
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

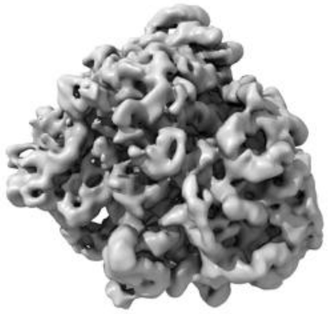
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 57.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

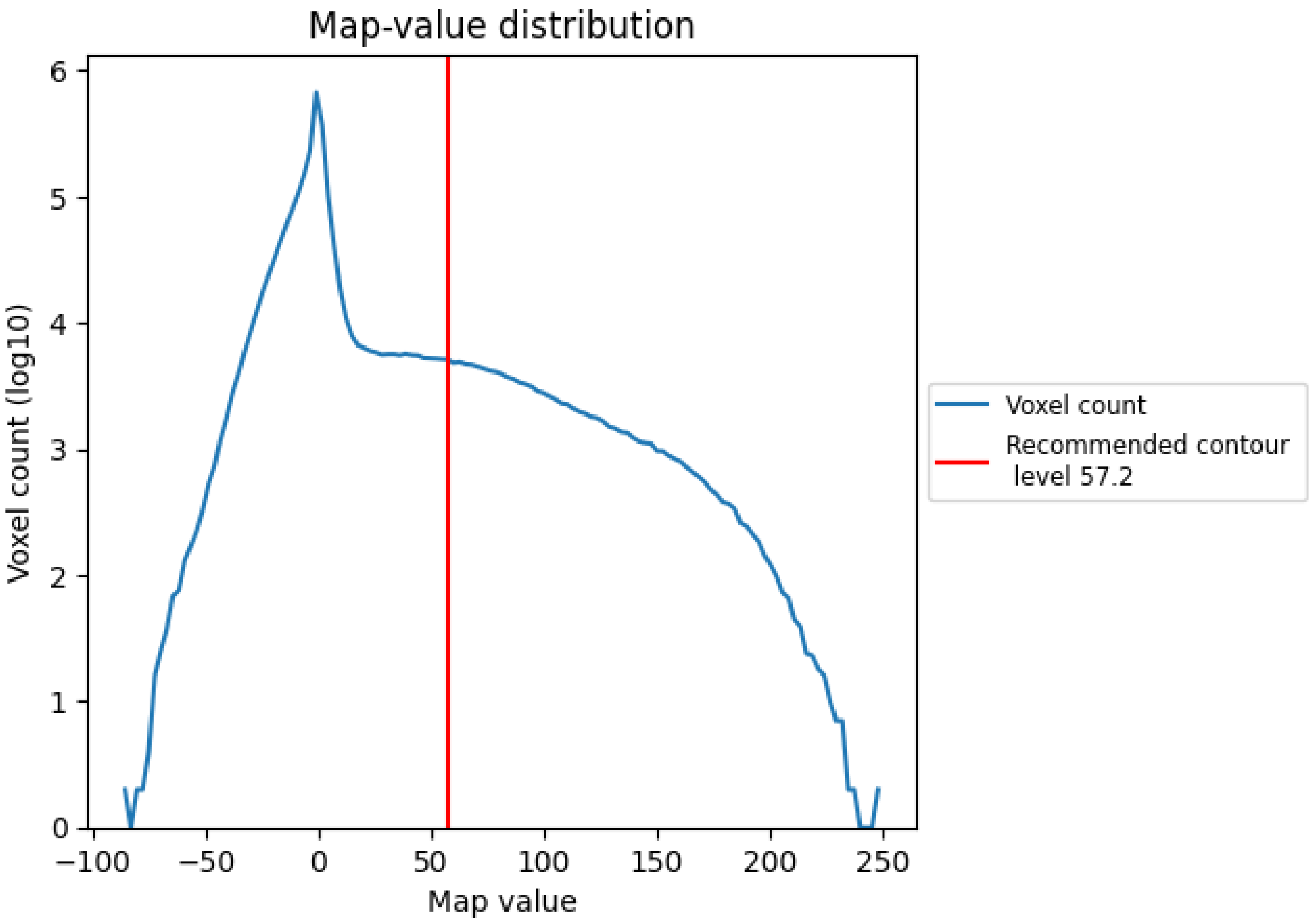
6.6 Mask visualisation ⓘ

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

7 Map analysis ⓘ

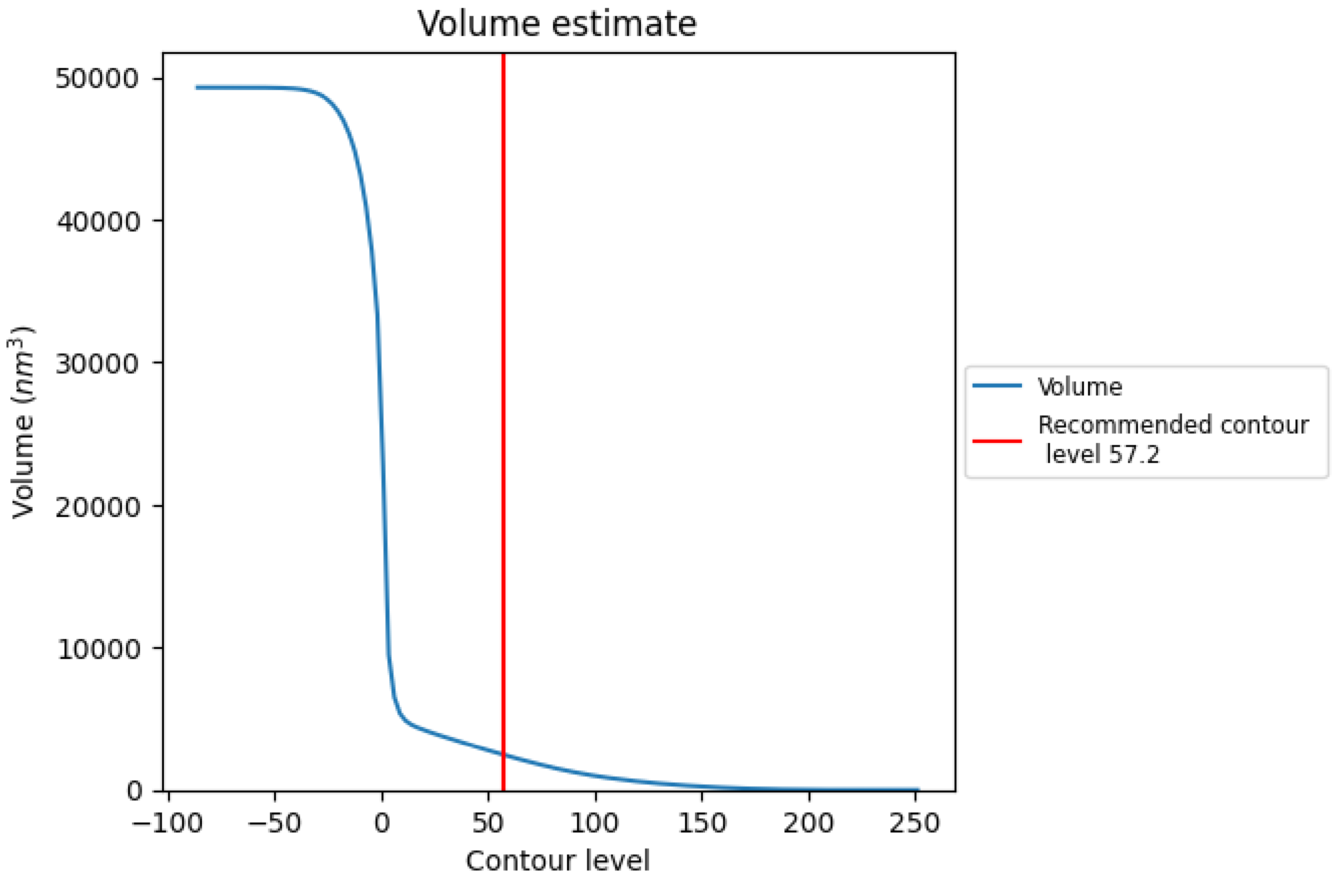
This section contains the results of statistical analysis of the map.

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.

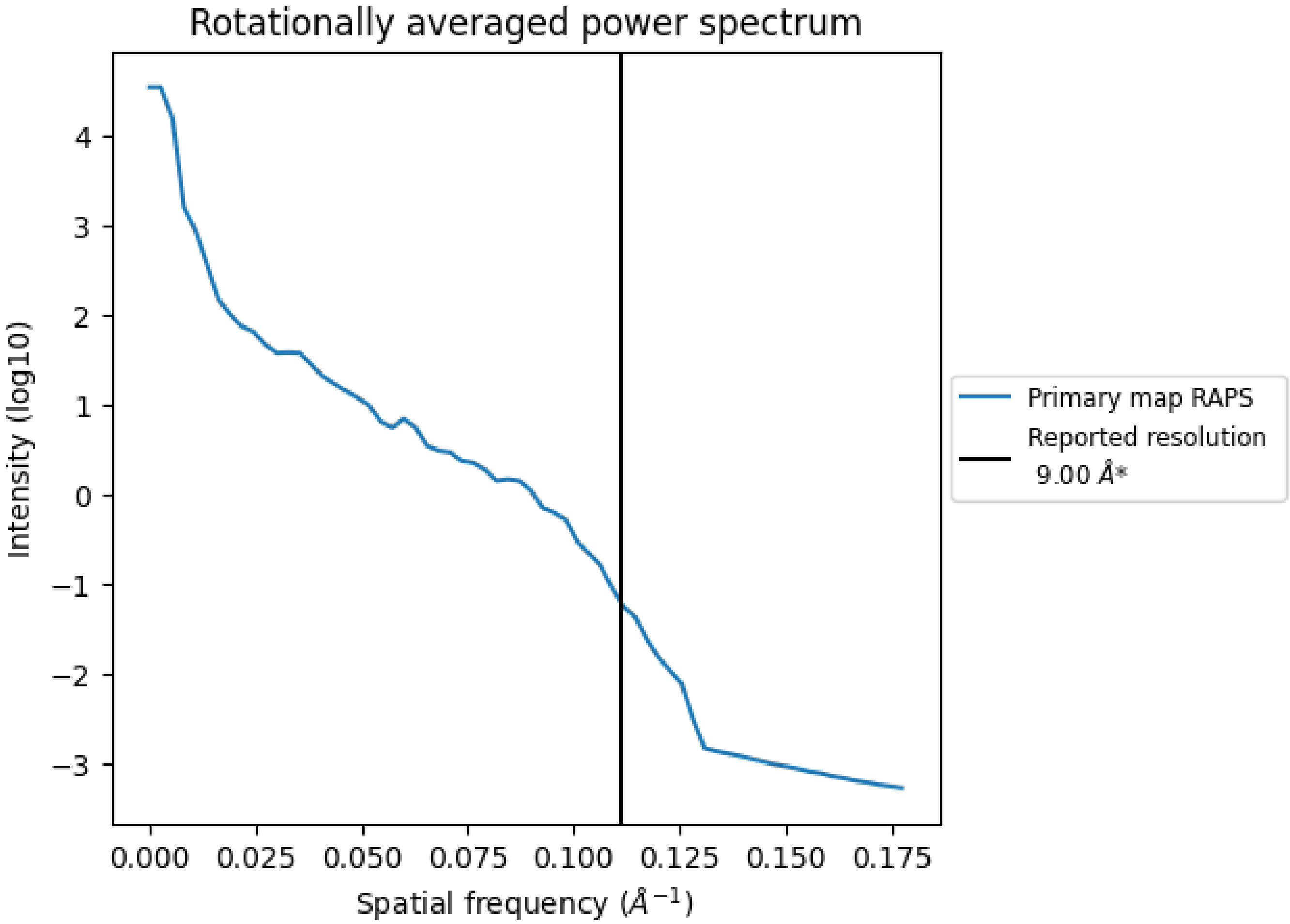
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 2467 nm^3; this corresponds to an approximate mass of 2228 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.111 $Å^{-1}$

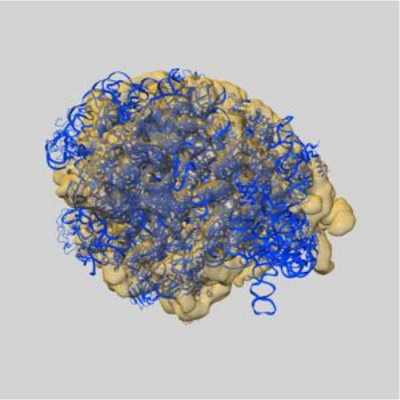
8 Fourier-Shell correlation ⓘ

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

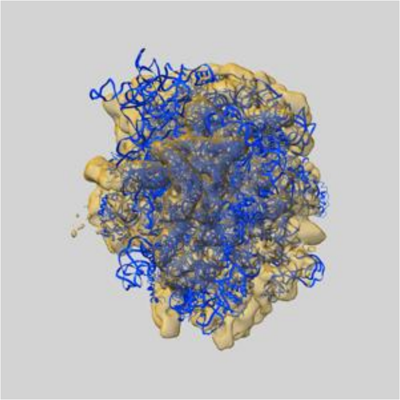
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-1055 and PDB model 4V65. Per-residue inclusion information can be found in section 3 on page 14.

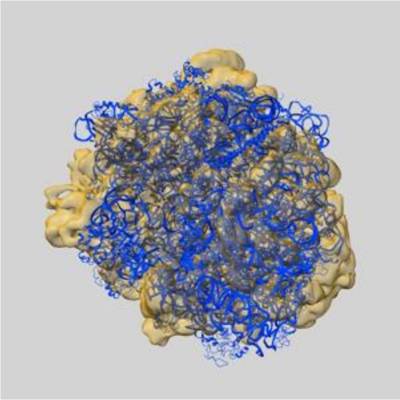
9.1 Map-model overlay



X



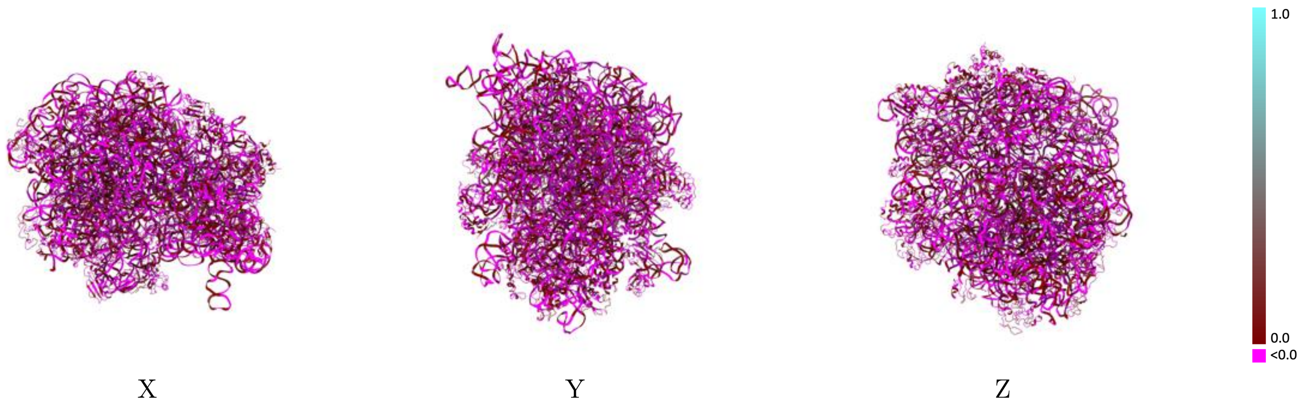
Y



Z

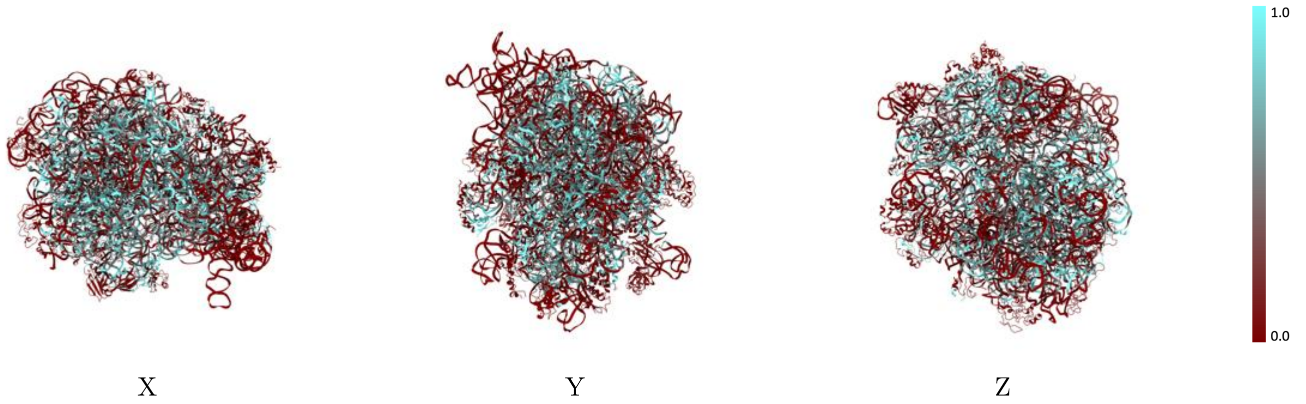
The images above show the 3D surface view of the map at the recommended contour level 57.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model



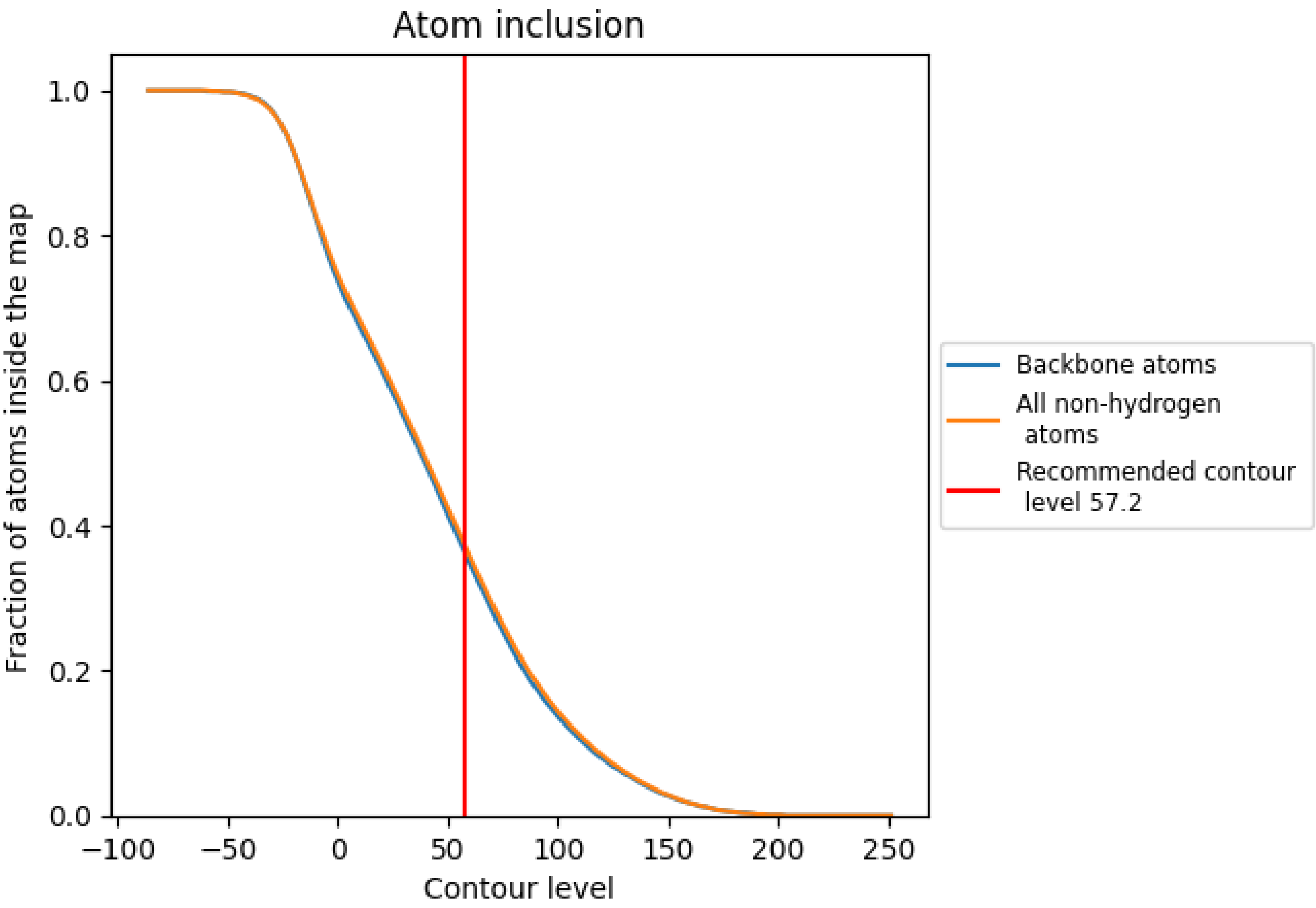
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (57.2).

9.4 Atom inclusion ⓘ



At the recommended contour level, 37% of all backbone atoms, 38% 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 (57.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	■ 0.3760	■ -0.0070
A1	■ 0.3220	■ -0.0130
AA	■ 0.3780	■ -0.0130
AB	■ 0.2190	■ -0.0010
AC	■ 0.4260	■ -0.0050
AD	■ 0.2170	■ -0.0200
AE	■ 0.4110	■ -0.0070
AF	■ 0.4210	■ -0.0010
AG	■ 0.0860	■ -0.0290
AH	■ 0.1550	■ -0.0100
AI	■ 0.0000	■ -0.0440
AJ	■ 0.2480	■ -0.0170
AK	■ 0.5960	■ 0.0120
AL	■ 0.0340	■ -0.0240
AM	■ 0.6420	■ 0.0200
AN	■ 0.4280	■ 0.0120
AO	■ 0.6140	■ 0.0210
AP	■ 0.4060	■ -0.0080
AQ	■ 0.3970	■ -0.0520
AR	■ 0.3640	■ -0.0030
AS	■ 0.5510	■ -0.0110
AT	■ 0.2370	■ -0.0150
AU	■ 0.5410	■ 0.0030
AV	■ 0.4380	■ 0.0190
AW	■ 0.1440	■ 0.0260
AX	■ 0.2300	■ 0.0050
B1	■ 0.2650	■ 0.0020
B2	■ 0.6520	■ 0.0280
B3	■ 0.1800	■ -0.0280
B4	■ 0.0720	■ -0.0250
B5	■ 0.4570	■ -0.0390
B6	■ 0.5180	■ 0.0080
BA	■ 0.2920	■ -0.0240
BB	■ 0.4270	■ -0.0050
BC	■ 0.2500	■ -0.0150

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Chain	Atom inclusion	Q-score
BD	■ 0.4830	■ 0.0040
BE	■ 0.3080	■ -0.0030
BF	■ 0.3510	■ -0.0060
BG	■ 0.5990	■ -0.0100
BH	■ 0.3760	■ -0.0030
BI	■ 0.4390	■ -0.0430
BJ	■ 0.1550	■ -0.0360
BK	■ 0.0730	■ -0.0250
BL	■ 0.5110	■ 0.0130
BM	■ 0.2860	■ -0.0330
BN	■ 0.4240	■ -0.0100
BO	■ 0.0000	■ -0.0070
BP	■ 0.6370	■ 0.0410
BQ	■ 0.4540	■ 0.0330
BR	■ 0.4200	■ -0.0110
BS	■ 0.3110	■ -0.0130
BT	■ 0.4940	■ -0.0230
BU	■ 0.1760	■ -0.0250
BV	■ 0.5110	■ 0.0300
BW	■ 0.2590	■ -0.0140
BX	■ 0.3060	■ -0.0010
BY	■ 0.5940	■ 0.0050
BZ	■ 0.0400	■ 0.0080