wwPDB EM Validation Summary Report ⓘ

Apr 16, 2024 – 01:39 am BST

PDB ID	:	6Q97
EMDB ID	:	EMD-4476
Title	:	Structure of tmRNA SmpB bound in A site of E. coli 70S ribosome
Authors	:	Rae, C.D.
Deposited on	:	2018-12-17
Resolution	:	3.90 Å(reported)

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

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

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

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

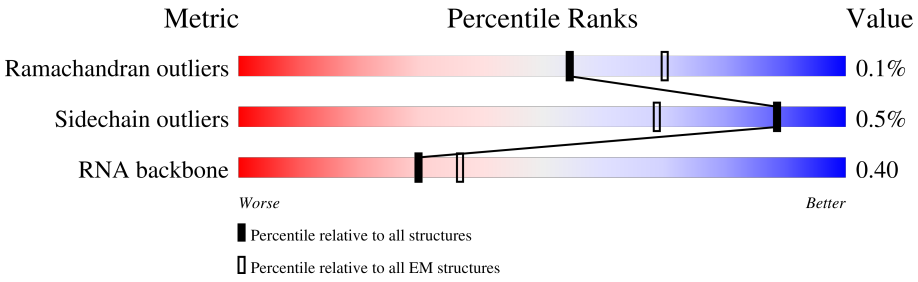
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.90 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	1	2903	87% 61% 35% ·
2	2	1534	83% 60% 34% 5%
3	3	120	94% 63% 33% ·
4	5	145	98% 95% 5%
5	6	28	86% 100%
6	8	77	92% 43% 52% 5%
7	9	6	83% 17% 33% 50%
8	B	270	81% 100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	C	209	94% 100%
10	D	201	86% 100%
11	E	177	95% 98%
12	F	175	100% 99%
13	G	149	81% 99%
14	H	130	100% 98%
15	I	135	100% 99%
16	J	141	96% 100%
17	K	123	93% 99%
18	L	144	69% 99%
19	M	136	93% 100%
20	N	119	89% 99%
21	O	115	79% 100%
22	P	114	85% 99%
23	Q	117	87% 99%
24	R	103	88% 100%
25	S	108	76% 98%
26	T	94	80% 100%
27	U	103	79% 100%
28	V	94	98% 99%
29	W	76	91% 100%
30	X	77	78% 99%
31	Y	58	88% 100%
32	Z	56	88% 100%
33	a	66	97% 100%

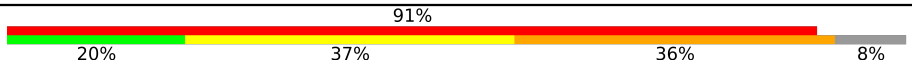
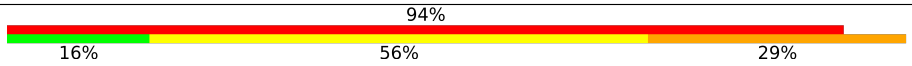
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	b	54	87% 100%
35	c	52	88% 100%
36	d	46	65% 100%
37	e	64	72% 95% 5%
38	f	37	100% 100%
39	g	225	100% 99%
40	h	208	98% 98%
41	i	205	99% 100%
42	j	156	99% 100%
43	k	104	76% 100%
44	l	151	66% 99%
45	m	129	99% 100%
46	n	126	80% 99%
47	o	99	97% 100%
48	p	117	85% 99%
49	q	123	76% 99%
50	r	115	70% 98%
51	s	100	90% 100%
52	t	87	60% 98%
53	u	81	98% 98%
54	v	80	88% 100%
55	w	65	85% 98%
56	x	82	85% 100%
57	y	85	76% 99%
58	z	70	81% 99%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	4	363	
60	7	77	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	6MZ	1	1618	X	-	-	-
1	PSU	1	1911	X	-	-	-
1	3TD	1	1915	X	-	-	-
1	PSU	1	1917	X	-	-	-
1	5MU	1	1939	X	-	-	-
1	6MZ	1	2030	X	-	-	-
1	G7M	1	2069	X	-	-	-
1	OMG	1	2251	X	-	-	-
1	PSU	1	2457	X	-	-	-
1	OMC	1	2498	X	-	-	-
1	2MA	1	2503	X	-	-	-
1	PSU	1	2504	X	-	-	-
1	OMU	1	2552	X	-	-	-
1	PSU	1	2580	X	-	-	-
1	PSU	1	2605	X	-	-	-
1	1MG	1	745	X	-	-	-
1	PSU	1	746	X	-	-	-
1	5MU	1	747	X	-	-	-
1	PSU	1	955	X	-	-	-
2	4OC	2	1402	X	-	-	-
2	PSU	2	516	X	-	-	-
2	7MG	2	527	X	-	-	-

2 Entry composition (i)

There are 63 unique types of molecules in this entry. The entry contains 156609 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 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	2903	62336	27816	11470	20147	2903	0	0

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1534	32929	14693	6041	10661	1534	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	120	2569	1144	468	837	120	0	0

- Molecule 4 is a protein called SsrA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	5	145	1170	741	216	209	4	0	0

- Molecule 5 is a protein called Nascent peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	6	28	140	84	28	28	0	0

- Molecule 6 is a RNA chain called tRNA-Met.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	8	77	1638	732	291	538	77	0	0

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	9	6	Total	C	N	O	P	0	0
			128	57	22	43	6		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	270	Total	C	N	O	S	0	0
			2078	1285	422	364	7		

- Molecule 9 is a protein called 50S ribosomal protein L3.

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

- Molecule 10 is a protein called 50S ribosomal protein L4.

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

- Molecule 11 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 12 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 13 is a protein called 50S ribosomal protein L9.

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

- Molecule 14 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	130	Total	C	N	O	S	0	0
			980	620	174	182	4		

- Molecule 15 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	135	Total	C	N	O	S	0	0
			984	622	171	185	6		

- Molecule 16 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 17 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 18 is a protein called 50S ribosomal protein L15.

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

- Molecule 19 is a protein called 50S ribosomal protein L16.

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

- Molecule 20 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 21 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	O	115	Total 884	C 548	N 177	O 159	0	0

- Molecule 22 is a protein called 50S ribosomal protein L19.

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

- Molecule 23 is a protein called 50S ribosomal protein L20.

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

- Molecule 24 is a protein called 50S ribosomal protein L21.

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

- Molecule 25 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	108	Total 840	C 522	N 164	O 152	S 2	0	0

- Molecule 26 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	94	Total 746	C 470	N 140	O 134	S 2	0	0

- Molecule 27 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	U	103	Total 788	C 498	N 148	O 142	0	0

- Molecule 28 is a protein called 50S ribosomal protein L25.

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

- Molecule 29 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 30 is a protein called 50S ribosomal protein L28.

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

- Molecule 31 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	58	Total	C	N	O	S	0	0
			477	294	93	89	1		

- Molecule 32 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	56	Total	C	N	O	S	0	0
			434	272	84	76	2		

- Molecule 33 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 34 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 35 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 36 is a protein called 50S ribosomal protein L34.

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

- Molecule 37 is a protein called 50S ribosomal protein L35.

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

- Molecule 38 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	37	Total	C	N	O	S	0	0
			297	183	64	46	4		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 44 is a protein called 30S ribosomal protein S7.

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

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	126	Total	C	N	O	S	0	0
			1010	628	202	177	3		

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

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

- Molecule 49 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	r	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

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

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	87	Total	C	N	O	S	0	0
			708	436	143	128	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	u	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	v	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	w	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	x	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

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

- Molecule 58 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 59 is a RNA chain called transfer-messenger RNA (tmRNA).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	4	334	Total	C	N	O	P	0	0
			7134	3184	1286	2330	334		

- Molecule 60 is a RNA chain called tRNA-Val.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	7	77	Total	C	N	O	P	0	0
			1644	732	292	543	77		

- Molecule 61 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
61	1	294	Total	Mg	0
			294	294	
61	2	128	Total	Mg	0
			128	128	
61	3	8	Total	Mg	0
			8	8	
61	8	2	Total	Mg	0
			2	2	
61	M	1	Total	Mg	0
			1	1	
61	Q	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	AltConf
61	X	1	Total Mg 1 1	0
61	y	1	Total Mg 1 1	0
61	7	3	Total Mg 3 3	0

- Molecule 62 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	AltConf
62	a	1	Total Zn 1 1	0
62	f	1	Total Zn 1 1	0

- Molecule 63 is water.

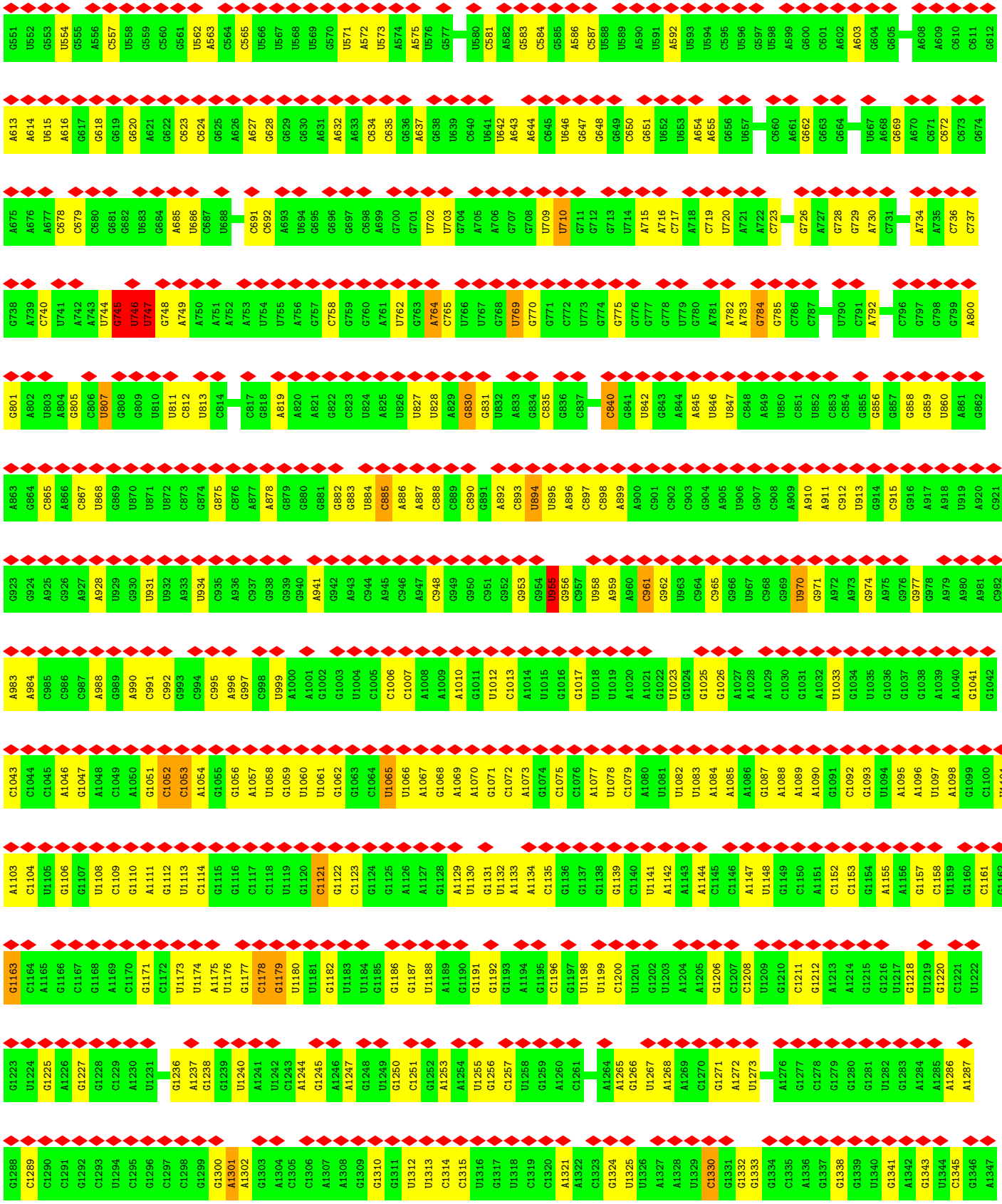
Mol	Chain	Residues	Atoms	AltConf
63	B	2	Total O 2 2	0

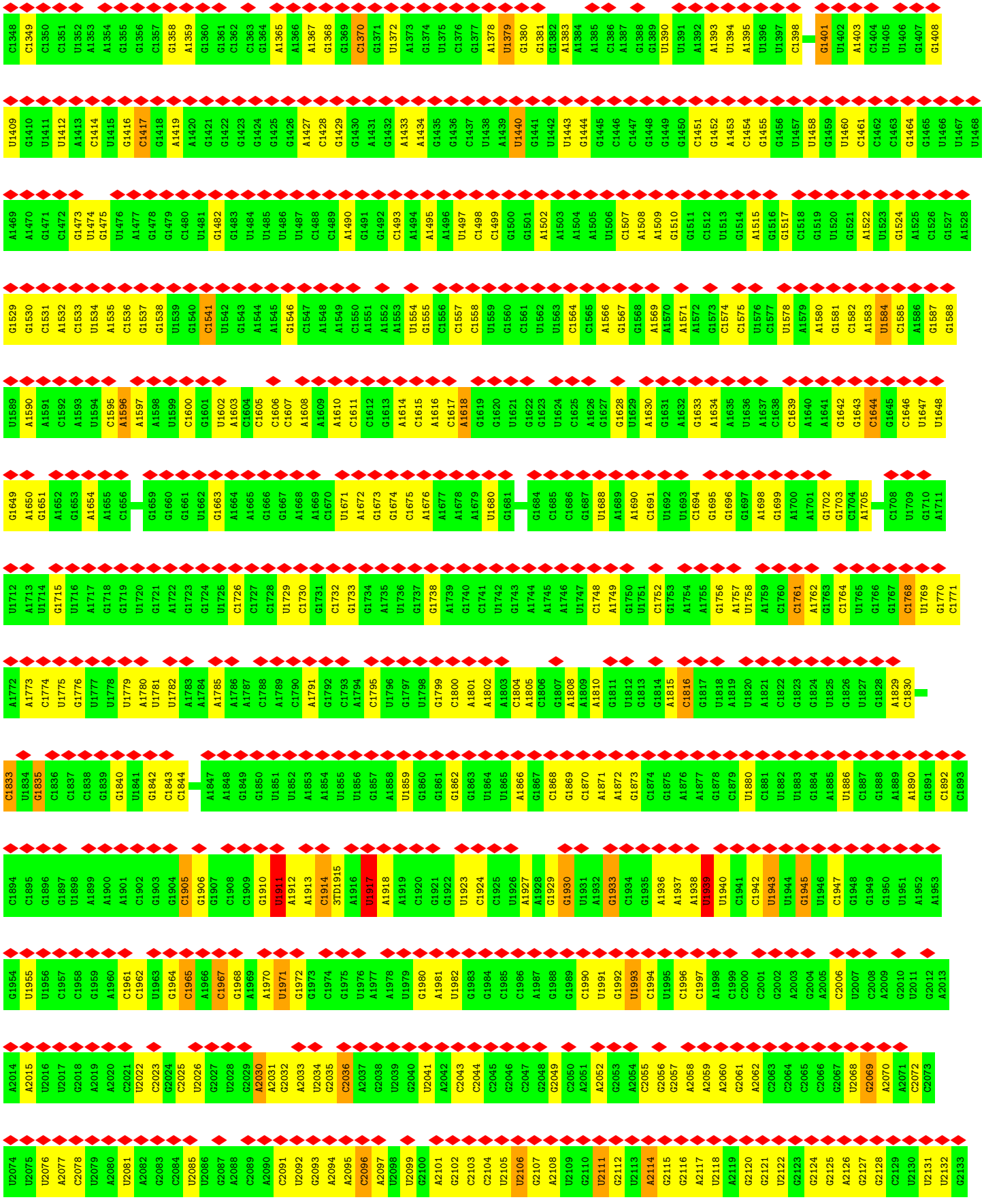
3 Residue-property plots (i)

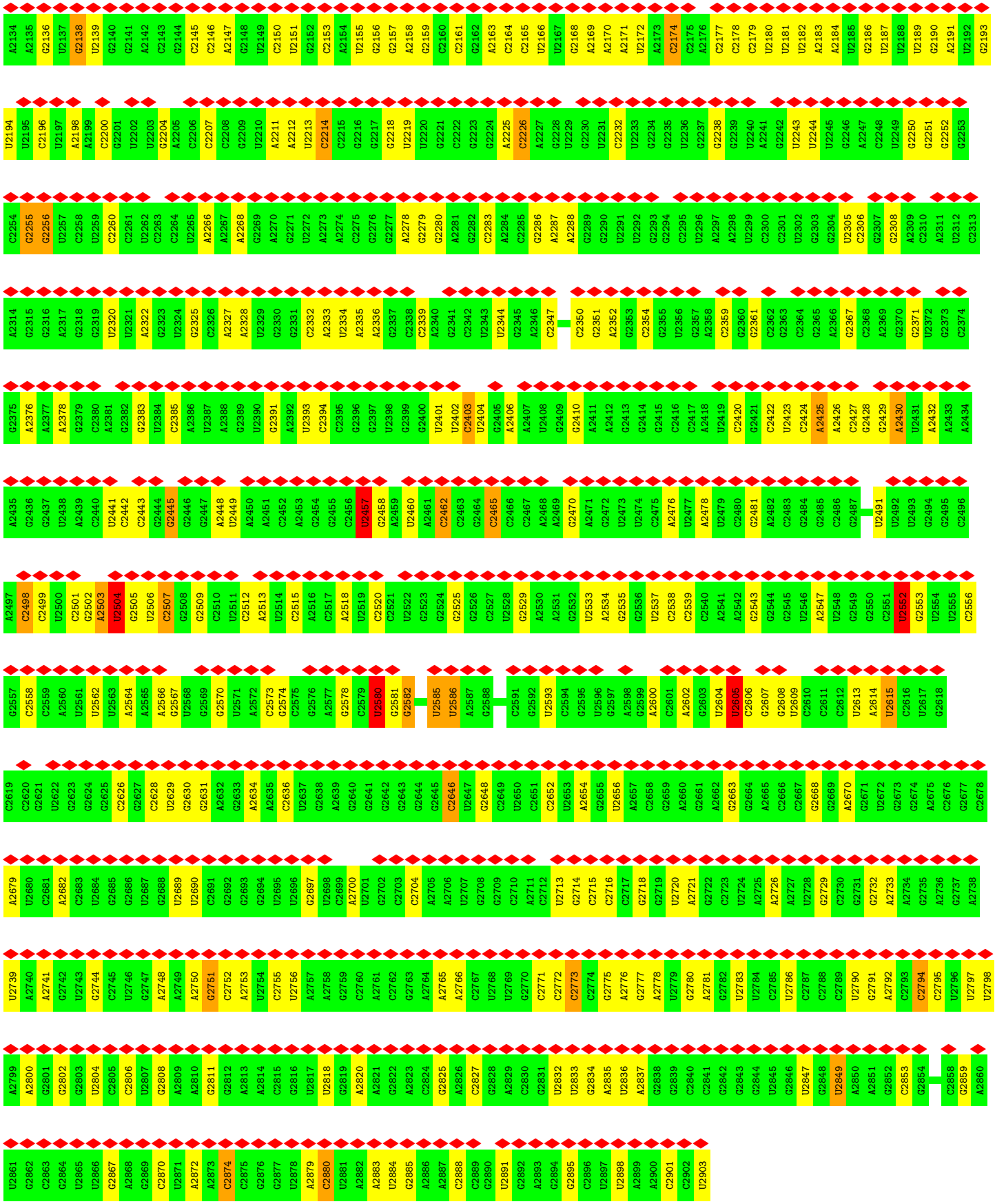
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 23S ribosomal RNA

Chain 1:

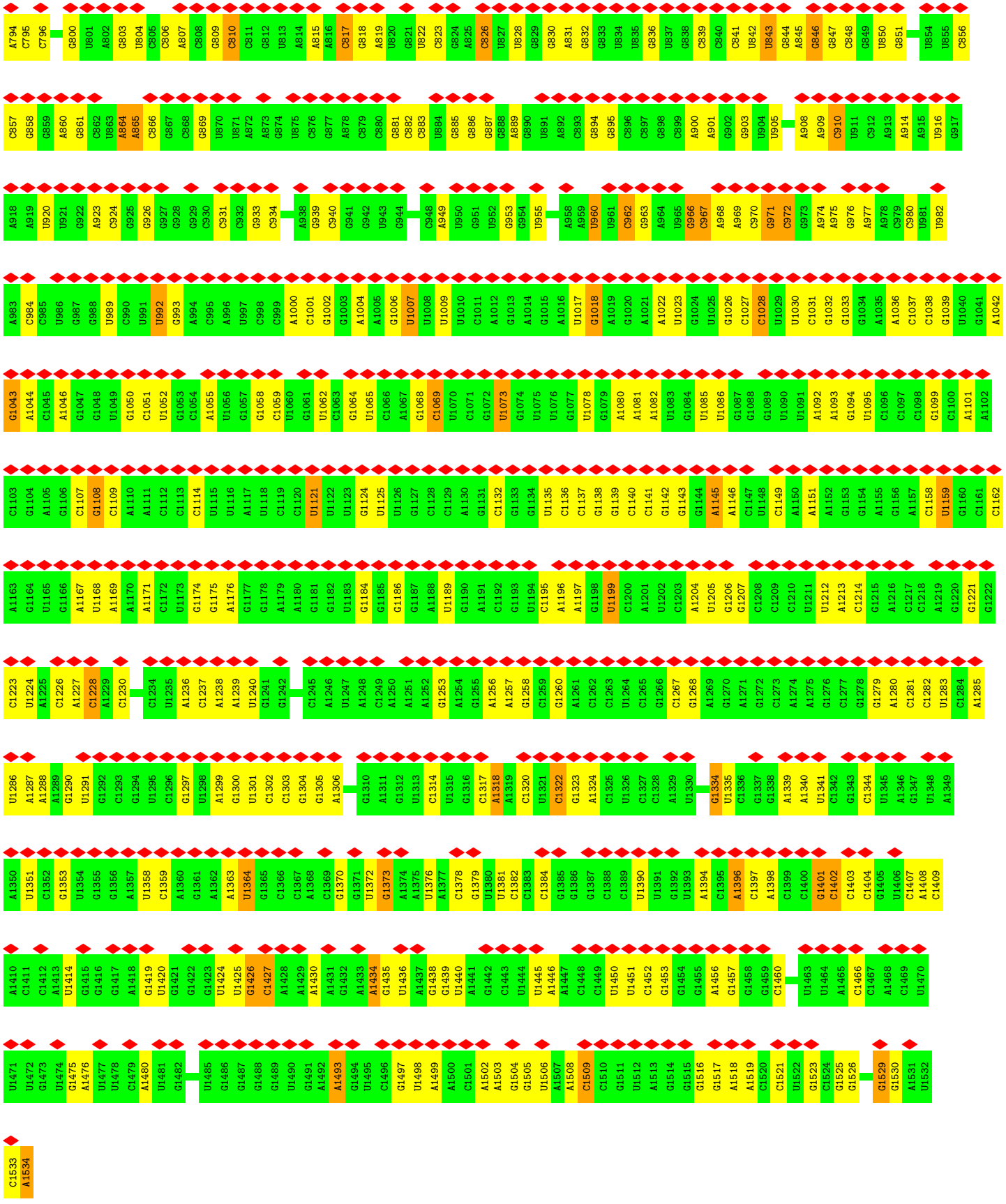

G551 U552 G553 U554 G555 A556 C557 U558 G559 C560 G561 U562 A563 C564 C565 U566 U567 U568 U569 G570 U571 A572 U573 A574 A575 U576 G577 U580 C581 A582 G583 C584 G585 A586 C587 U588 U589 A590 U591 A592 U593 U594 C595 U596 G597 U598 A599 G600 C601 A602 A603 G604 G605 A608 A609 C610 C611 G612
A613 A614 U615 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 C660 A661 G662 G663 G664 U667 A668 G669 A670 C671 C672 C673 G674
A675 A676 A677 C678 C679 C680 G681 G682 U683 G684 A685 U686 C687 U688 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 G726 A727 G728 G729 A730 C731 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 U790 C791 A792 C796 G797 G798 G799 A800
G801 A802 U803 A804 G805 C806 U807 G808 G809 U810 U811 C812 U813 C814 C817 G818 A819 A820 A821 G822 C823 U824 A825 U826 U827 U828 A829 G830 G831 U832 A833 G834 C835 G836 C837 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 A887 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 C948 G949 G950 C951 G952 C953 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 U1141 A1142 A1143 A1144 C1145 C1146 A1147 U1148 G1149 C1150 A1151 C1152 C1153 G1154 A1155 A1156 G1157 C1158 U1159 G1160 C1161 G1162
G1163 C1164 A1165 G1166 C1167 G1168 A1169 C1170 G1171 C1172 U1173 U1174 A1175 U1176 G1177 C1178 G1179 U1180 U1181 G1182 U1183 U1184 G1185 G1186 G1187 U1188 A1189 G1190 G1191 G1192 G1193 A1194 G1195 C1196 G1197 U1198 U1199 C1200 U1201 G1202 U1203 A1204 A1205 G1206 C1207 C1208 U1209 G1210 C1211 G1212 A1213 A1214 G1215 G1216 U1217 G1218 U1219 G1220 C1221 U1222
G1223 U1224 G1225 A1226 G1227 G1228 C1229 A1230 U1231 G1236 A1237 G1238 G1239 U1240 A1241 U1242 C1243 A1244 G1245 A1246 A1247 G1248 U1249 G1250 C1251 G1252 A1253 A1254 U1255 G1256 C1257 U1258 G1259 A1260 C1261 A1264 A1265 G1266 U1267 A1268 A1269 C1270 G1271 A1272 U1273 A1276 G1277 C1278 G1279 G1280 G1281 U1282 G1283 A1284 A1285 A1286 A1287
G1288 C1289 C1290 C1291 G1292 C1293 U1294 C1295 G1296 C1297 C1298 G1299 G1300 A1301 A1302 G1303 A1304 C1305 C1306 A1307 A1308 G1309 G1310 G1311 U1312 U1313 C1314 C1315 U1316 G1317 U1318 C1319 C1320 A1321 A1322 C1323 G1324 U1325 U1326 A1327 A1328 U1329 C1330 G1331 G1332 G1333 G1334 C1335 A1336 G1337 G1338 G1339 U1340 G1341 A1342 G1343 U1344 C1345 G1346 A1347


C1348 C1349 C1350 C1351 U1352 A1353 A1354 G1355 G1356 C1357 G1358 A1359 G1360 G1361 C1362 C1363 G1364 A1365 A1366 A1367 G1368 G1369 C1370 G1371 U1372 A1373 G1374 U1375 C1376 G1377 A1378 U1379 G1380 G1381 G1382 A1383 A1384 A1385 C1386 A1387 G1388 G1389 U1390 U1391 A1392 A1393 U1394 A1395 U1396 U1397 C1398 G1401 U1402 A1403 C1404 U1405 U1406 G1407 G1408
U1409 G1410 U1411 U1412 A1413 C1414 U1415 G1416 C1417 G1418 A1419 A1420 G1421 G1422 G1423 G1424 G1425 G1426 A1427 C1428 G1429 G1430 A1431 G1432 A1433 A1434 G1435 G1436 C1437 U1438 A1439 U1440 G1441 U1442 U1443 G1444 G1445 C1446 C1447 G1448 G1449 G1450 C1451 G1452 A1453 C1454 G1455 G1456 U1457 U1458 G1459 U1460 C1461 C1462 C1463 G1464 G1465 U1466 U1467 U1468
A1469 A1470 G1471 C1472 G1473 U1474 G1475 U1476 A1477 G1478 G1479 C1480 U1481 G1482 G1483 U1484 U1485 U1486 U1487 C1488 C1489 A1490 G1491 G1492 C1493 A1494 A1495 A1496 U1497 C1498 C1499 G1500 G1501 A1502 A1503 A1504 A1505 U1506 C1507 A1508 A1509 G1510 C1511 C1512 U1513 G1514 A1515 G1516 G1517 C1518 G1519 U1520 G1521 A1522 U1523 G1524 A1525 C1526 G1527 A1528
G1529 G1530 C1531 A1532 C1533 U1534 A1535 C1536 G1537 G1538 U1539 G1540 C1541 U1542 G1543 A1544 A1545 G1546 C1547 A1548 A1549 C1550 A1551 A1552 A1553 U1554 G1555 C1556 C1557 C1558 U1559 G1560 C1561 U1562 U1563 C1564 C1565 A1566 G1567 G1568 A1569 A1570 A1571 A1572 G1573 C1574 C1575 U1576 C1577 U1578 A1579 A1580 G1581 C1582 A1583 U1584 C1585 A1586 G1587 G1588
U1589 A1590 A1591 C1592 A1593 U1594 C1595 A1596 A1597 A1598 U1599 C1600 G1601 U1602 A1603 C1604 C1605 C1606 C1607 A1608 A1609 A1610 C1611 C1612 G1613 A1614 C1615 A1616 C1617 A1618 G1619 G1620 U1621 G1622 G1623 U1624 C1625 A1626 G1627 G1628 U1629 A1630 G1631 A1632 G1633 A1634 A1635 U1636 A1637 C1638 C1639 A1640 A1641 G1642 G1643 C1644 G1645 C1646 U1647 U1648
G1649 A1650 G1651 A1652 G1653 A1654 A1655 C1656 G1659 G1660 G1661 U1662 G1663 A1664 A1665 G1666 G1667 A1668 A1669 C1670 U1671 A1672 G1673 G1674 C1675 A1676 A1677 A1678 A1679 U1680 G1681 G1684 C1685 C1686 G1687 U1688 A1689 A1690 C1691 U1692 U1693 C1694 G1695 G1696 G1697 A1698 G1699 A1700 A1701 G1702 G1703 C1704 A1705 C1708 U1709 G1710 A1711
U1712 A1713 U1714 G1715 U1716 A1717 G1718 G1719 U1720 G1721 A1722 G1723 G1724 U1725 C1726 C1727 C1728 U1729 C1730 G1731 C1732 G1733 G1734 A1735 U1736 G1737 G1738 A1739 G1740 C1741 U1742 G1743 A1744 A1745 A1746 U1747 C1748 A1749 G1750 U1751 C1752 G1753 A1754 A1755 G1756 A1757 U1758 A1759 C1760 C1761 A1762 G1763 C1764 U1765 G1766 G1767 C1768 U1769 G1770 C1771
A1772 A1773 C1774 U1775 G1776 U1777 U1778 U1779 A1780 U1781 U1782 A1783 A1784 A1785 A1786 A1787 C1788 A1789 C1790 A1791 C1792 C1793 A1794 C1795 U1796 G1797 U1798 G1799 C1800 A1801 A1802 A1803 C1804 A1805 C1806 G1807 A1808 A1809 A1810 G1811 U1812 G1813 G1814 A1815 C1816 G1817 U1818 A1819 U1820 A1821 C1822 G1823 G1824 U1825 G1826 U1827 G1828 A1829 C1830
C1833 U1834 G1835 C1836 C1837 C1838 G1839 G1840 U1841 G1842 C1843 C1844 A1847 A1848 G1849 G1850 U1851 U1852 A1853 A1854 U1855 U1856 G1857 A1858 U1859 G1860 G1861 G1862 G1863 U1864 U1865 A1866 C1867 C1868 G1869 C1870 A1871 A1872 G1873 C1874 G1875 A1876 A1877 G1878 C1879 U1880 C1881 U1882 U1883 G1884 A1885 U1886 C1887 G1888 A1889 A1890 G1891 C1892 C1893
C1894 C1895 G1896 G1897 U1898 A1899 A1900 A1901 C1902 G1903 G1904 C1905 G1906 G1907 C1908 C1909 G1910 U1911 A1912 A1913 C1914 3TD1915 A1916 U1917 A1918 A1919 C1920 G1921 G1922 U1923 C1924 C1925 U1926 A1927 A1928 G1929 G1930 U1931 A1932 G1933 C1934 G1935 A1936 A1937 A1938 U1939 U1940 C1941 C1942 U1943 U1944 G1945 U1946 C1947 G1948 G1949 G1950 U1951 A1952 A1953
G1954 U1955 U1956 C1957 C1958 G1959 A1960 C1961 C1962 U1963 G1964 C1965 A1966 C1967 G1968 A1969 A1970 U1971 G1972 G1973 C1974 G1975 U1976 A1977 A1978 U1979 G1980 A1981 U1982 G1983 G1984 C1985 C1986 A1987 G1988 G1989 C1990 U1991 G1992 U1993 C1994 U1995 C1996 C1997 A1998 C1999 C2000 C2001 G2002 A2003 G2004 A2005 C2006 U2007 C2008 A2009 G2010 U2011 G2012 A2013
A2014 A2015 U2016 U2017 G2018 A2019 A2020 C2021 U2022 C2023 G2024 C2025 U2026 G2027 U2028 G2029 A2030 A2031 G2032 A2033 U2034 G2035 C2036 A2037 G2038 U2039 G2040 U2041 A2042 C2043 C2044 C2045 G2046 C2047 G2048 G2049 C2050 A2051 A2052 G2053 A2054 C2055 G2056 G2057 A2058 A2059 A2060 G2061 A2062 C2063 C2064 C2065 C2066 G2067 U2068 G2069 A2070 A2071 C2072 C2073
U2074 U2075 U2076 A2077 C2078 U2079 A2080 U2081 A2082 G2083 C2084 U2085 U2086 G2087 A2088 C2089 A2090 C2091 U2092 G2093 A2094 A2095 C2096 A2097 U2098 U2099 G2100 A2101 G2102 C2103 C2104 U2105 U2106 G2107 A2108 U2109 G2110 U2111 G2112 U2113 A2114 G2115 G2116 A2117 U2118 A2119 G2120 G2121 U2122 G2123 G2124 G2125 A2126 G2127 G2128 C2129 U2130 U2131 U2132 G2133


A2134 A2135 G2136 U2137 G2138 U2139 G2140 G2141 A2142 C2143 G2144 C2145 C2146 A2147 G2148 U2149 C2150 U2151 G2152 C2153 A2154 U2155 G2156 G2157 A2158 G2159 C2160 C2161 G2162 A2163 C2164 C2165 U2166 U2167 G2168 A2169 A2170 A2171 U2172 A2173 C2174 C2175 A2176 C2177 C2178 C2179 U2180 U2181 U2182 A2183 A2184 U2185 G2186 U2187 U2188 U2189 G2190 A2191 U2192 G2193
U2194 U2195 C2196 U2197 A2198 A2199 C2200 G2201 U2202 U2203 G2204 A2205 C2206 C2207 C2208 G2209 U2210 A2211 A2212 U2213 C2214 C2215 G2216 G2217 G2218 U2219 U2220 G2221 C2222 G2223 G2224 A2225 C2226 A2227 G2228 U2229 G2230 U2231 C2232 U2233 G2234 G2235 U2236 G2237 G2238 G2239 U2240 A2241 G2242 U2243 U2244 U2245 G2246 A2247 C2248 U2249 G2250 G2251 G2252 G2253
C2254 G2255 G2256 U2257 C2258 U2259 C2260 C2261 U2262 C2263 C2264 U2265 A2266 A2267 A2268 G2269 A2270 G2271 U2272 A2273 A2274 C2275 G2276 G2277 A2278 G2279 C2280 A2281 G2282 C2283 A2284 C2285 G2286 A2287 A2288 G2289 G2290 U2291 U2292 G2293 G2294 C2295 U2296 A2297 A2298 U2299 C2300 C2301 U2302 C2303 G2304 U2305 C2306 G2307 G2308 A2309 C2310 A2311 U2312 C2313
A2314 G2315 G2316 A2317 G2318 G2319 U2320 U2321 A2322 G2323 U2324 G2325 C2326 A2327 A2328 U2329 G2330 G2331 C2332 A2333 U2334 A2335 A2336 G2337 C2338 C2339 A2340 G2341 C2342 U2343 U2344 G2345 A2346 C2347 C2350 G2351 A2352 G2353 C2354 G2355 U2356 G2357 A2358 C2359 G2360 G2361 C2362 G2363 C2364 G2365 A2366 G2367 C2368 A2369 G2370 G2371 U2372 G2373 C2374
G2375 A2376 A2377 A2378 G2379 C2380 A2381 G2382 G2383 U2384 C2385 A2386 U2387 A2388 G2389 U2390 G2391 A2392 U2393 C2394 C2395 G2396 G2397 U2398 G2399 G2400 U2401 U2402 C2403 U2404 G2405 A2406 A2407 U2408 G2409 G2410 A2411 A2412 G2413 G2414 G2415 C2416 C2417 A2418 U2419 C2420 G2421 C2422 U2423 C2424 A2425 A2426 C2427 G2428 G2429 A2430 U2431 A2432 A2433 A2434
A2435 G2436 G2437 U2438 A2439 C2440 U2441 C2442 C2443 G2444 G2445 G2446 G2447 A2448 U2449 A2450 A2451 C2452 A2453 G2454 G2455 C2456 U2457 G2458 A2459 U2460 A2461 C2462 C2463 G2464 C2465 C2466 C2467 A2468 A2469 G2470 A2471 G2472 U2473 U2474 C2475 A2476 U2477 A2478 U2479 C2480 G2481 A2482 C2483 G2484 C2485 C2486 G2487 U2491 U2492 U2493 G2494 G2495 C2496
A2497 C2498 C2499 U2500 C2501 G2502 A2503 U2504 G2505 U2506 C2507 G2508 G2509 C2510 U2511 C2512 A2513 U2514 C2515 A2516 C2517 A2518 U2519 C2520 C2521 U2522 G2523 G2524 G2525 G2526 C2527 U2528 G2529 A2530 A2531 G2532 U2533 A2534 G2535 G2536 U2537 C2538 C2539 C2540 A2541 A2542 G2543 G2544 G2545 U2546 A2547 U2548 G2549 G2550 C2551 U2552 G2553 U2554 U2555 C2556
G2557 C2558 C2559 A2560 U2561 U2562 U2563 A2564 A2565 A2566 G2567 U2568 G2569 G2570 U2571 A2572 C2573 G2574 C2575 G2576 A2577 G2578 C2579 U2580 G2581 G2582 U2585 U2586 A2587 G2588 C2591 G2592 U2593 C2594 G2595 U2596 G2597 A2598 G2599 A2600 C2601 A2602 G2603 U2604 U2605 C2606 G2607 G2608 U2609 C2610 C2611 C2612 U2613 A2614 U2615 C2616 U2617 G2618
C2619 C2620 G2621 U2622 G2623 G2624 G2625 C2626 G2627 C2628 U2629 G2630 G2631 A2632 G2633 A2634 A2635 C2636 U2637 G2638 A2639 G2640 G2641 G2642 G2643 G2644 G2645 C2646 U2647 G2648 C2649 U2650 C2651 C2652 U2653 A2654 G2655 U2656 A2657 C2658 G2659 A2660 G2661 A2662 G2663 G2664 A2665 C2666 C2667 U2668 G2669 A2670 G2671 U2672 G2673 G2674 A2675 C2676 G2677 C2678
A2679 U2680 C2681 A2682 C2683 U2684 G2685 G2686 U2687 G2688 U2689 U2690 C2691 G2692 G2693 G2694 U2695 U2696 G2697 U2698 C2699 A2700 U2701 G2702 C2703 C2704 A2705 A2706 U2707 G2708 G2709 C2710 A2711 C2712 U2713 G2714 C2715 C2716 C2717 G2718 G2719 U2720 A2721 G2722 C2723 U2724 A2725 A2726 A2727 U2728 G2729 C2730 G2731 G2732 A2733 A2734 G2735 A2736 G2737 A2738
U2739 A2740 A2741 G2742 U2743 G2744 C2745 U2746 G2747 A2748 G2749 A2750 G2751 C2752 A2753 U2754 C2755 U2756 A2757 A2758 G2759 C2760 A2761 C2762 G2763 A2764 A2765 A2766 C2767 U2768 U2769 G2770 C2771 C2772 C2773 C2774 G2775 A2776 G2777 A2778 U2779 G2780 A2781 G2782 U2783 U2784 C2785 U2786 C2787 C2788 C2789 U2790 G2791 A2792 C2793 C2794 C2795 U2796 U2797 U2798
A2799 A2800 G2801 G2802 G2803 U2804 C2805 C2806 U2807 G2808 A2809 A2810 G2811 G2812 A2813 A2814 C2815 G2816 U2817 U2818 G2819 A2820 A2821 G2822 A2823 C2824 G2825 A2826 C2827 G2828 A2829 C2830 G2831 U2832 U2833 G2834 A2835 U2836 A2837 G2838 G2839 C2840 C2841 G2842 G2843 G2844 U2845 G2846 U2847 G2848 U2849 A2850 A2851 G2852 C2853 G2854 C2858 G2859 A2860
U2861 G2862 C2863 G2864 U2865 U2866 C2867 A2868 G2869 C2870 U2871 A2872 A2873 C2874 C2875 G2876 G2877 U2878 A2879 C2880 U2881 A2882 A2883 U2884 G2885 A2886 A2887 C2888 C2889 G2890 U2891 G2892 A2893 G2894 G2895 C2896 U2897 U2898 A2899 A2900 C2901 C2902 U2903

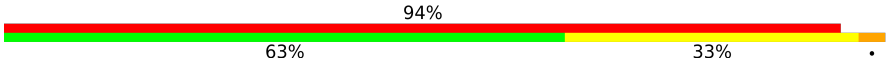
• Molecule 2: 16S ribosomal RNA

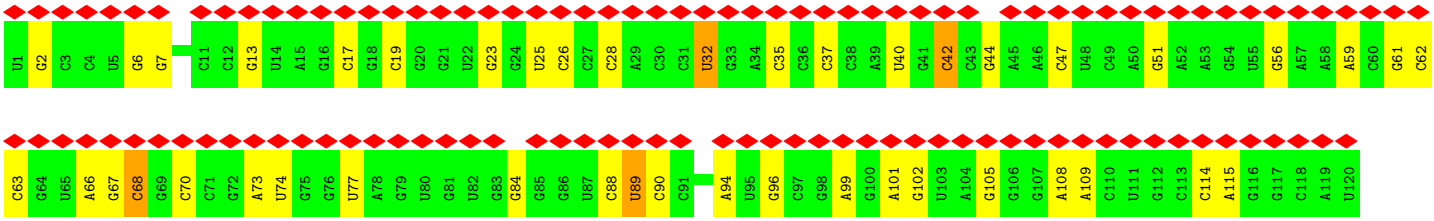
Chain 2:



- Molecule 3: 5S ribosomal RNA

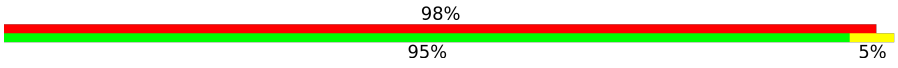
Chain 3:

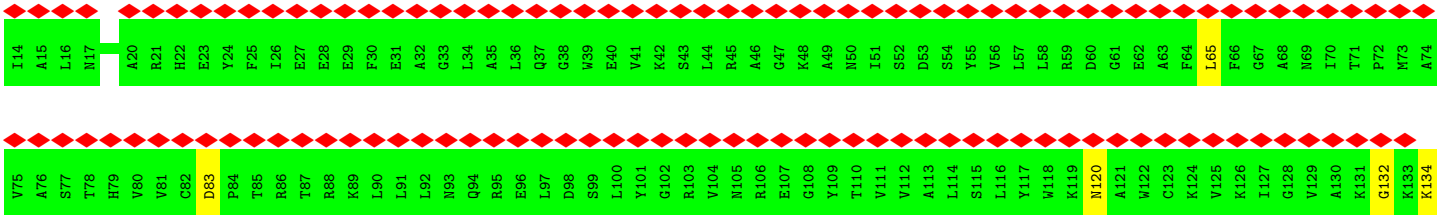




• Molecule 4: SsrA-binding protein

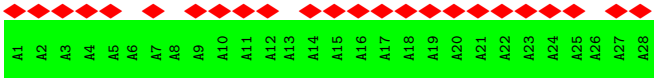
Chain 5:





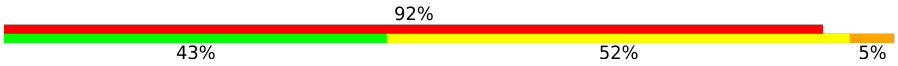
• Molecule 5: Nascent peptide

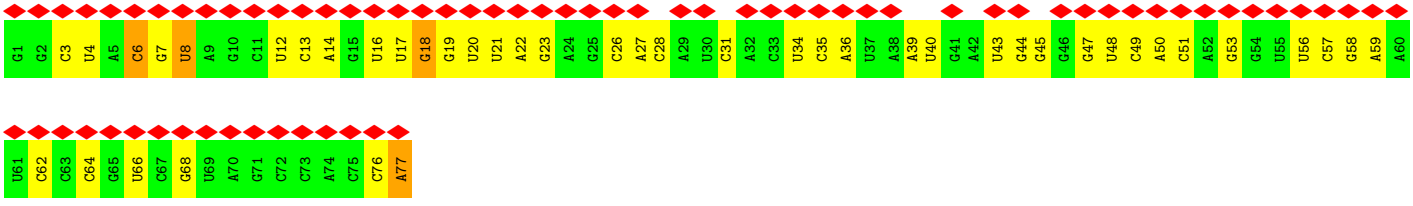
Chain 6:



• Molecule 6: tRNA-Met

Chain 8:



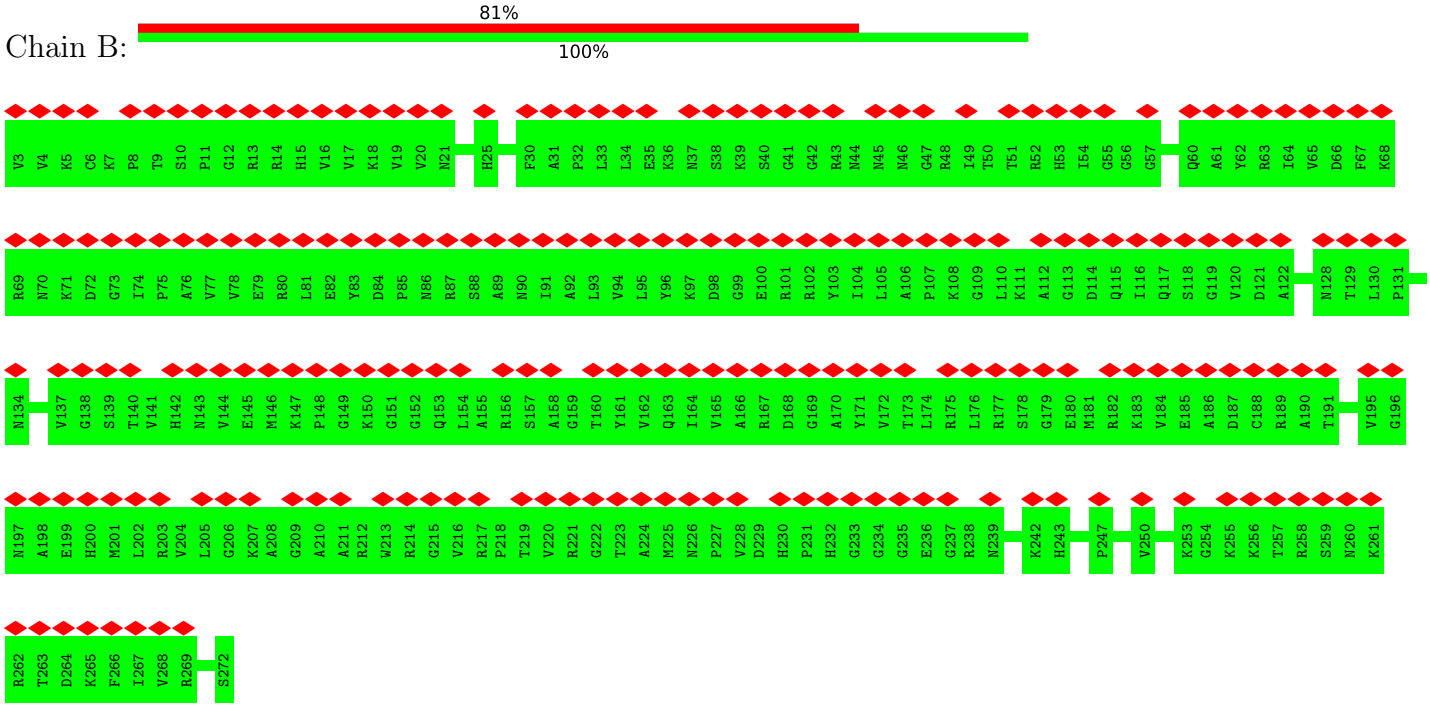


• Molecule 7: mRNA

Chain 9:

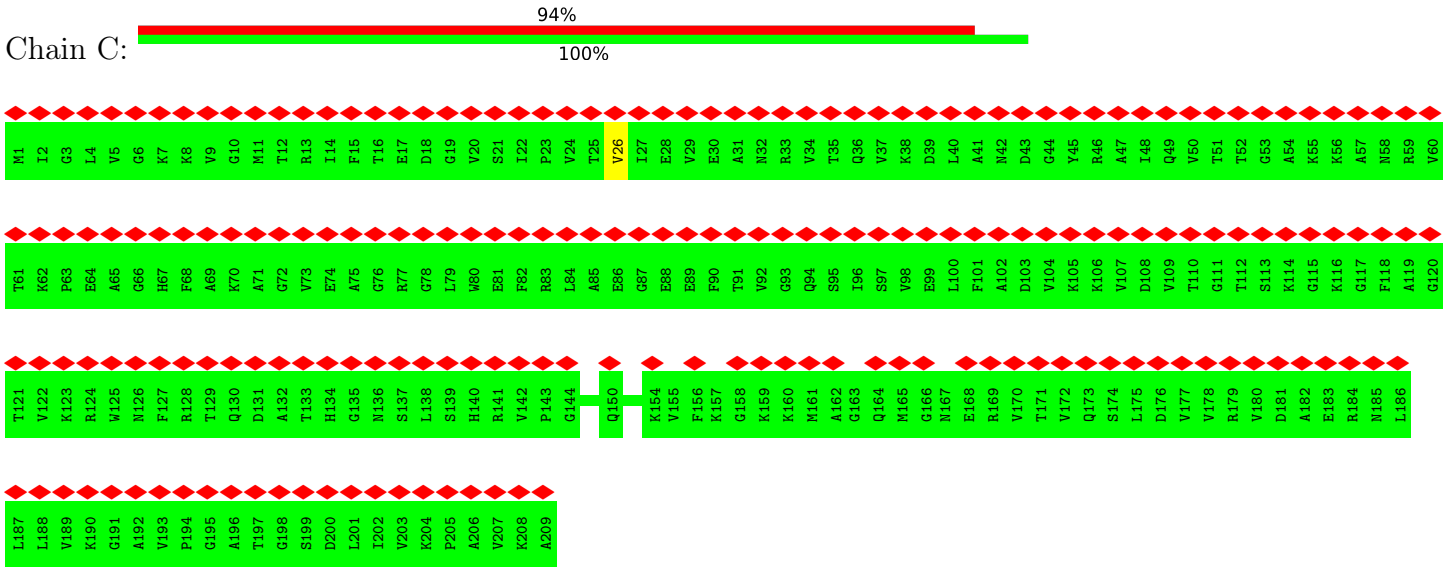
• Molecule 8: 50S ribosomal protein L2

Chain B:



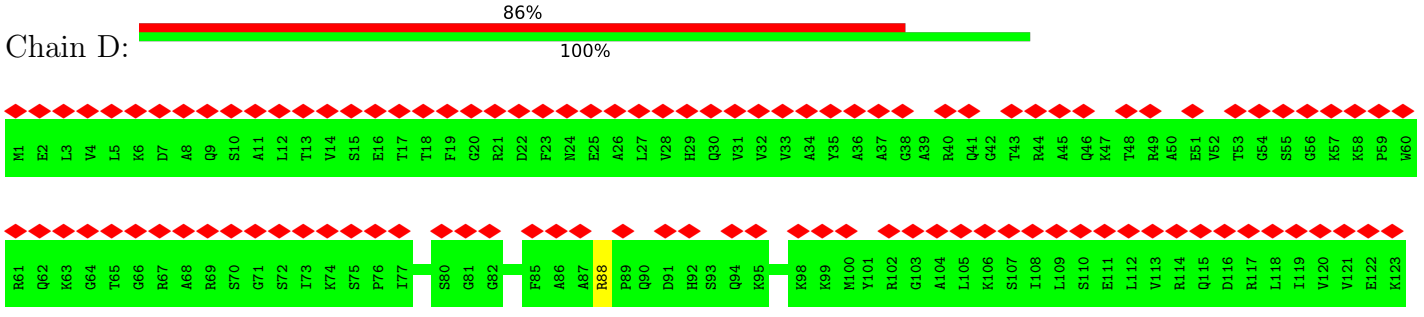
• Molecule 9: 50S ribosomal protein L3

Chain C:



• Molecule 10: 50S ribosomal protein L4

Chain D:



F124 S125 V126 E127 A128 P129 K130 T131 K132 L133 L134 A135 Q136 K137 L138 K139 D140 M141 A142 L143 E144 I148 I149 T150 G151 E152 L153 D154 E155 N156 L157 F158 L159 A160 A161 R162 N163 L164 H165 K166 V167 D168 V169 R170 D171 A172 T173 G174 I175 D176 P177 V178 S179 L180 I181 A182 F183 D184 K185

V186 V187 M188 T189 A190 D191 A192 V193 K194 E197 E198 M199 L200 A201

• Molecule 11: 50S ribosomal protein L5

Chain E: 95% 98%

A2 K3 L4 H5 D6 Y7 Y8 K9 D10 E11 V12 V13 K14 K15 L16 M17 T18 E19 F20 N21 Y22 N23 S24 V25 M26 Q27 V28 P29 R30 V31 E32 K33 I34 T35 L36 N37 M38 G39 V40 G41 E42 A43 I44 A45 D46 K47 K48 L49 L50 D51 N52 A53 A54 A55 D56 L57 A58 A59 I60 S61

G62 Q63 K64 P65 L66 I67 T68 K69 A70 R71 K72 S73 V74 A75 G76 F77 K78 I79 R80 Q81 G82 Y83 P84 I85 G86 C87 K88 V89 T90 L91 R92 G93 E94 R95 M96 W97 E98 F99 F100 E101 R102 L103 I104 T105 I106 A107 V108 P109 R110 I111 R112 D113 F114 R115 G116 L117 S118 A119 K120 S121

F122 D123 G124 R125 G126 N127 Y128 S129 M130 G131 V132 R133 E134 Q135 I136 I137 F138 P139 E140 I141 D142 Y143 V146 D147 R148 V149 R150 G151 L152 D153 I154 T155 I156 T157 T158 T159 A160 K161 S162 D163 E164 E165 G166 R167 A168 L169 L170 A171 A172 F173 D174 F175 P176 F177 R178

• Molecule 12: 50S ribosomal protein L6

Chain F: 100% 99%

S2 R3 V4 A5 K6 A7 P8 V9 V10 V11 P12 A13 G14 V15 D16 V17 K18 I19 N20 G21 Q22 V23 I24 T25 I26 K27 G28 K29 N30 G31 E32 L33 T34 R35 T36 L37 N38 D39 A40 V41 E42 V43 K44 H45 A46 D47 N48 T49 L50 T51 F52 G53 P54 R55 D56 G57 Y58 A59 D60 G61

W62 A63 Q64 A65 G66 T67 A68 R69 A70 L71 L72 N73 S74 M75 V76 I77 G78 V79 T80 E81 G82 F83 T84 K85 K86 L87 Q88 L89 V90 G91 V92 G93 Y94 R95 A96 A97 V98 K99 G100 N101 V102 I103 N104 L105 S106 L107 G108 F109 S110 H111 P112 V113 D114 H115 Q116 L117 P118 A119 G120 I121

T122 A123 E124 C125 P126 T127 Q128 T129 E130 I131 V132 L133 K134 G135 A136 D137 K138 Q139 V140 I141 G142 Q143 V144 A145 A146 D147 L148 R149 A150 Y151 R152 R153 P154 E155 P156 Y157 K158 G159 K160 G161 V162 R163 Y164 A165 D166 E167 V168 V169 R170 T171 K172 E173 A174 K175 K176

• Molecule 13: 50S ribosomal protein L9

Chain G: 81% 99%

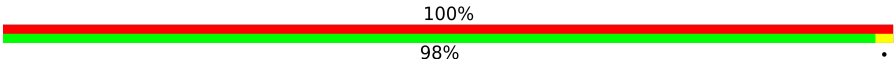
M1 Q2 V3 I4 L5 L6 D7 K8 V9 A10 N11 L12 G13 S14 L15 G16 D17 V21 K22 A23 G24 Y25 A26 R27 N28 F29 L30 V31 P32 Q33 G34 K35 A36 A39 T40 K41 K42 N43 I44 E45 F46 F47 E48 A49 R50 R51 A52 E53 L54 E55 A56 K57 L58 A59 E60 V61 L62 A63

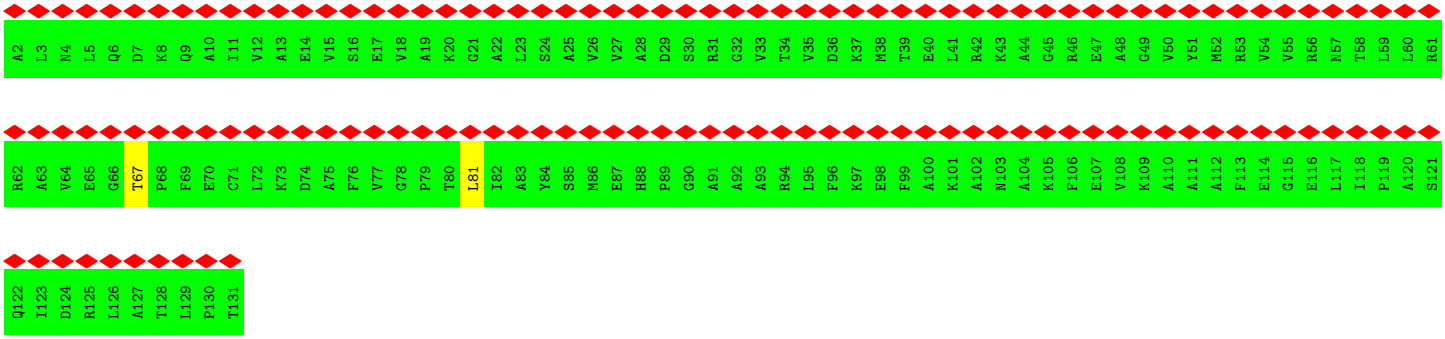
A64 A65 N66 A67 R68 A69 E70 K71 I72 N73 A74 L75 E76 I80 A81 S82 K83 L90 F91 T96 R97 D98 I99 A100 D101 A102 V103 T104 A105 A106 G107 V108 E109 V110 A111 K112 S113 E114 V115 R116 L117 P118 N119 G120 V121 L122 R123 T124 T125 G126 E127 S131 F132 Q133 V134 H135

S136 E137 V138 F139 A140 K141 V142 I143 V144 N145 V146 V147 A148 E149

• Molecule 14: 50S ribosomal protein L10

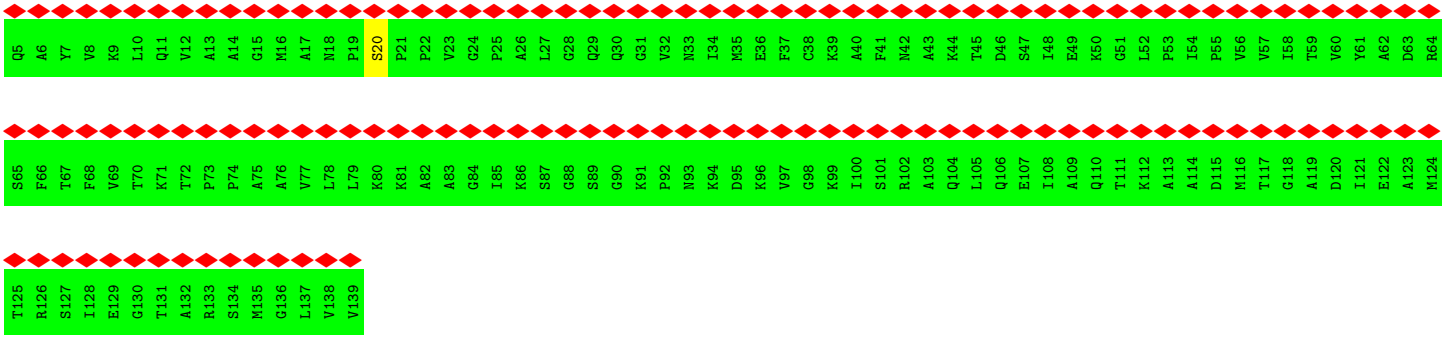
Chain H:





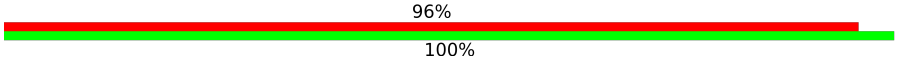
• Molecule 15: 50S ribosomal protein L11

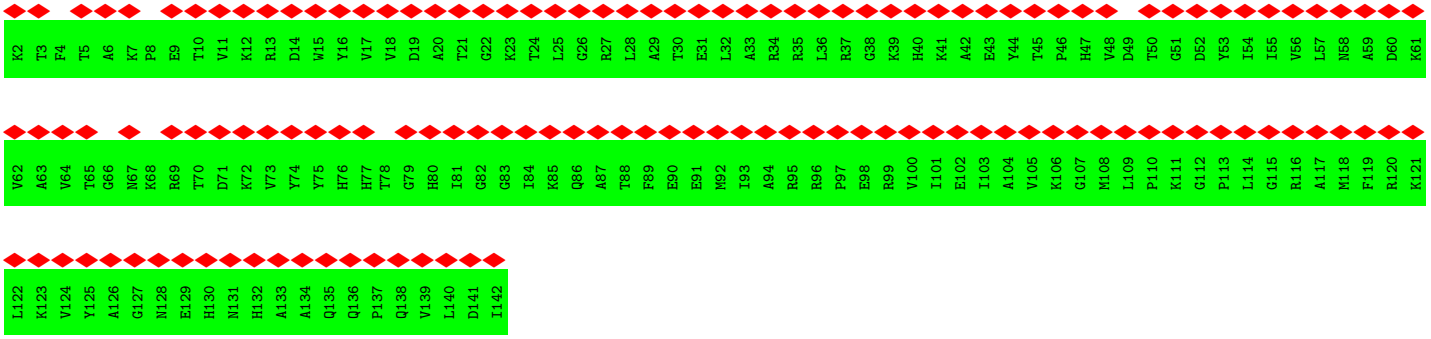
Chain I:



• Molecule 16: 50S ribosomal protein L13

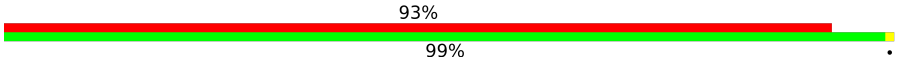
Chain J:

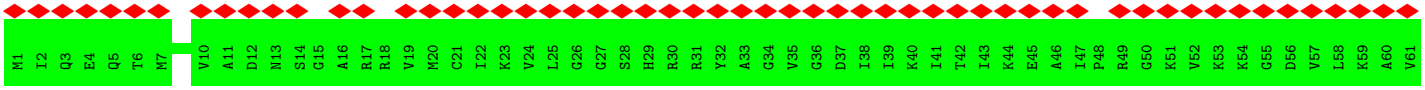


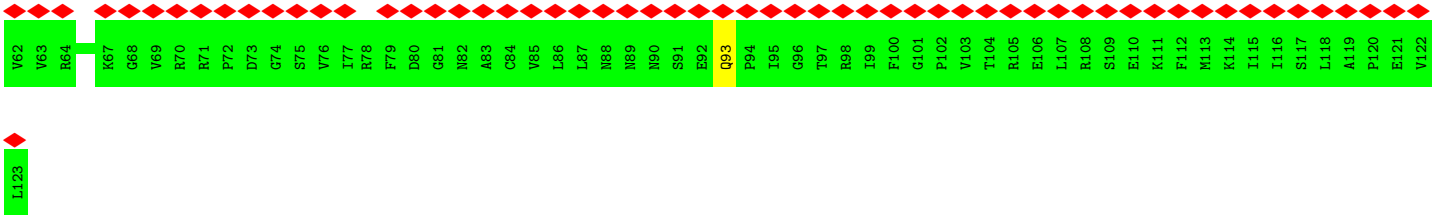


• Molecule 17: 50S ribosomal protein L14

Chain K:

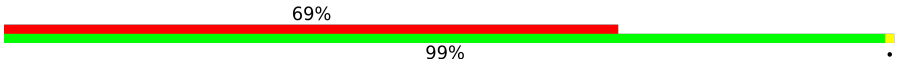


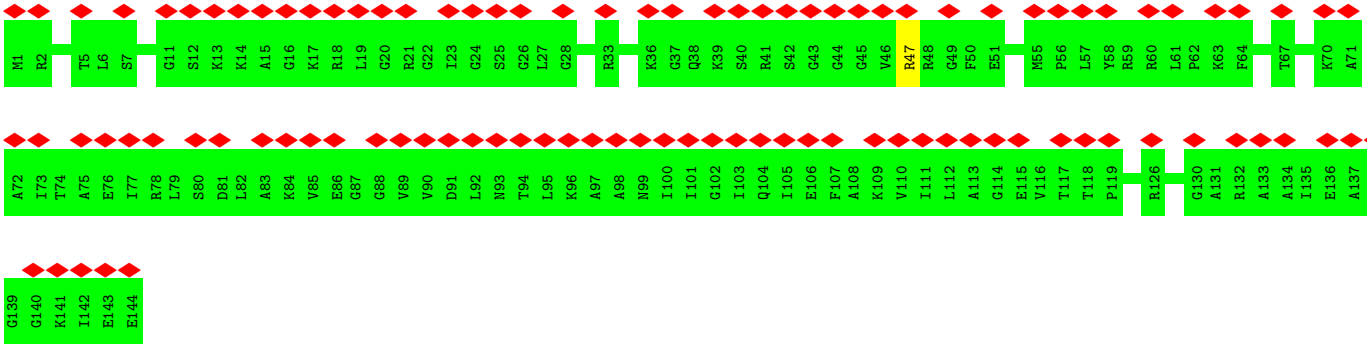




• Molecule 18: 50S ribosomal protein L15

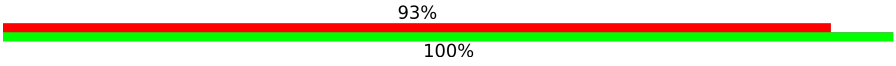
Chain L:

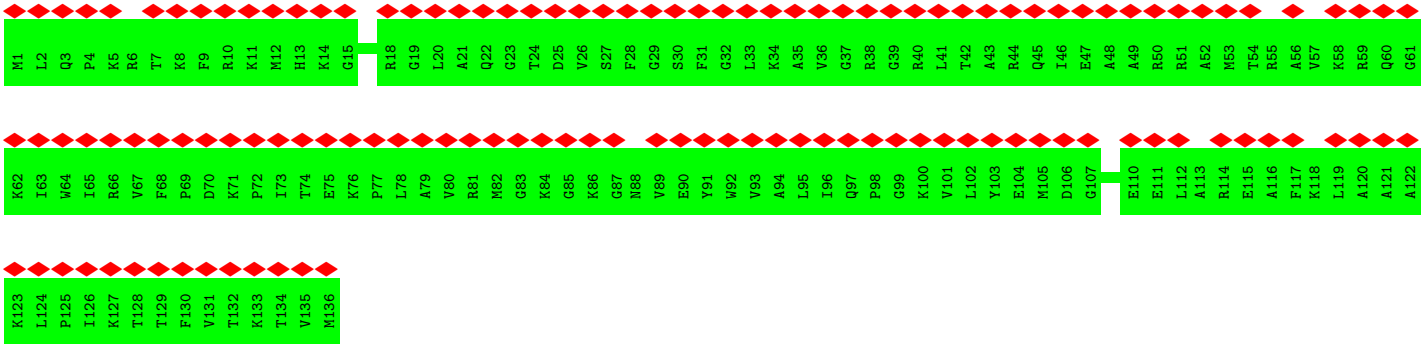




• Molecule 19: 50S ribosomal protein L16

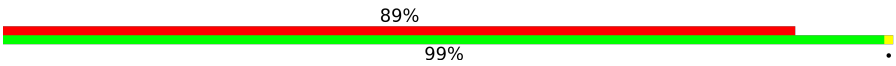
Chain M:

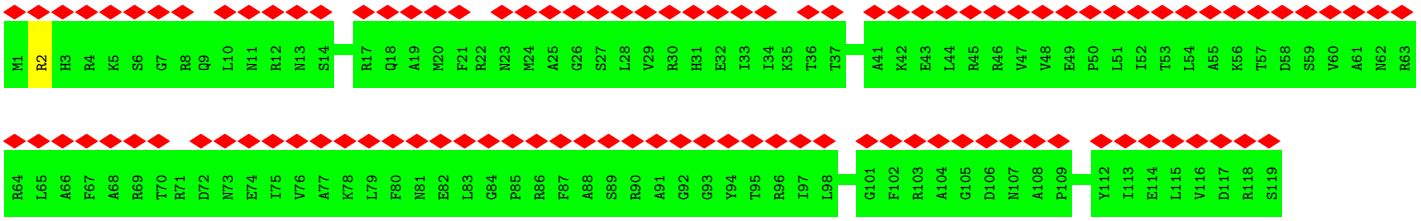




• Molecule 20: 50S ribosomal protein L17

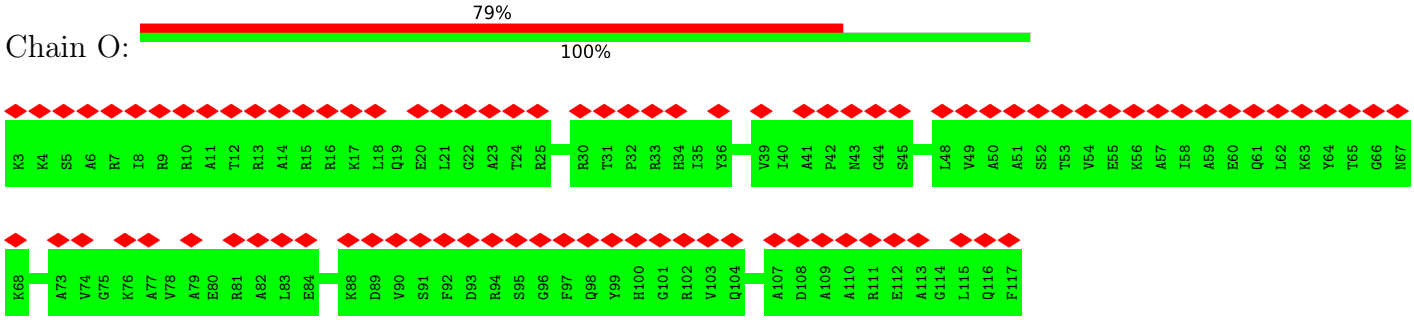
Chain N:





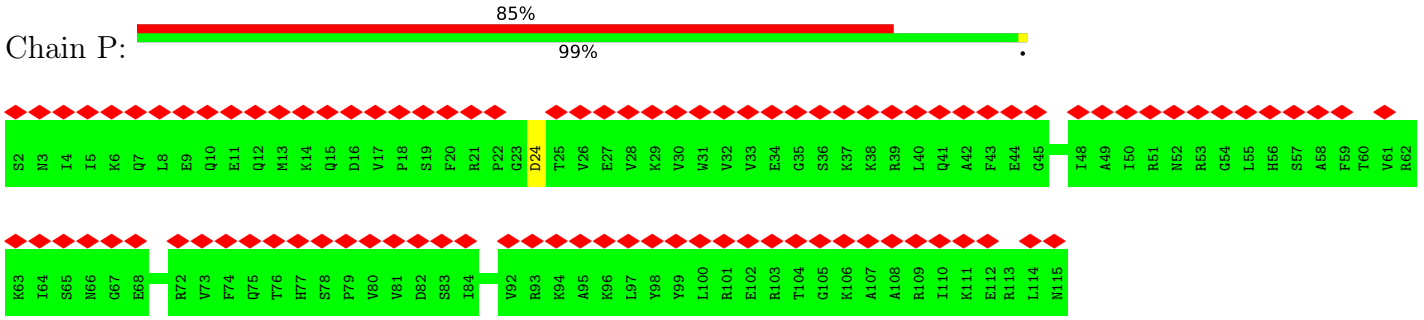
• Molecule 21: 50S ribosomal protein L18

Chain O:



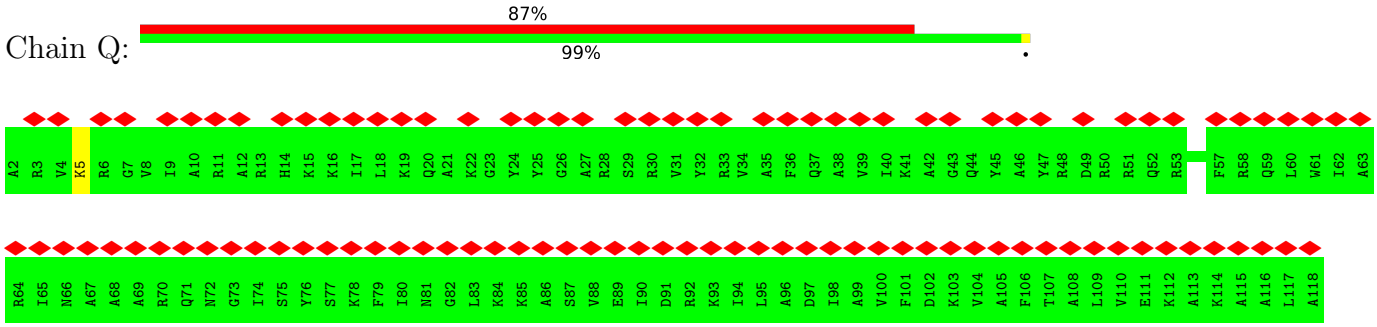
• Molecule 22: 50S ribosomal protein L19

Chain P:



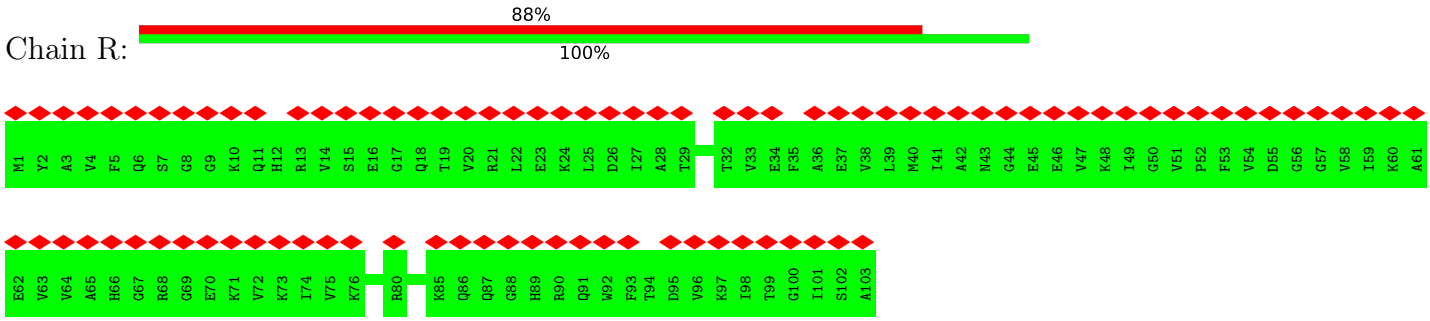
• Molecule 23: 50S ribosomal protein L20

Chain Q:



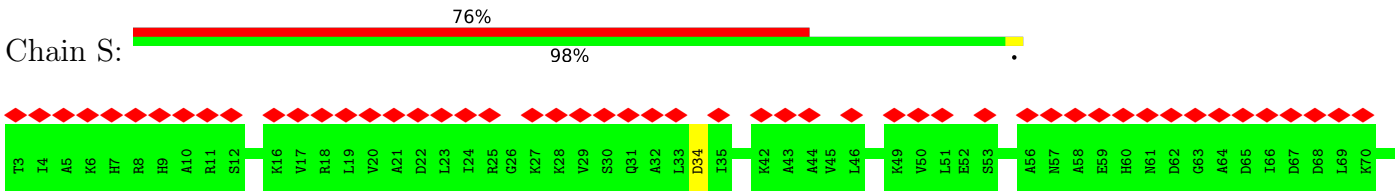
• Molecule 24: 50S ribosomal protein L21

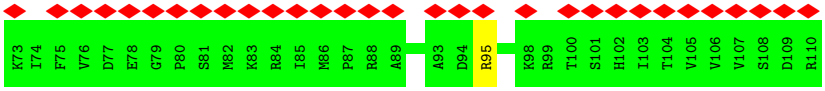
Chain R:



• Molecule 25: 50S ribosomal protein L22

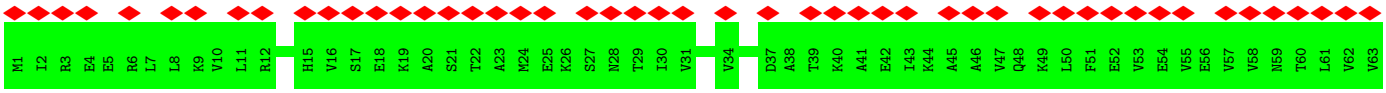
Chain S:

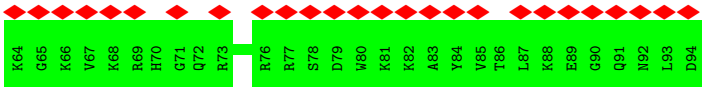




• Molecule 26: 50S ribosomal protein L23

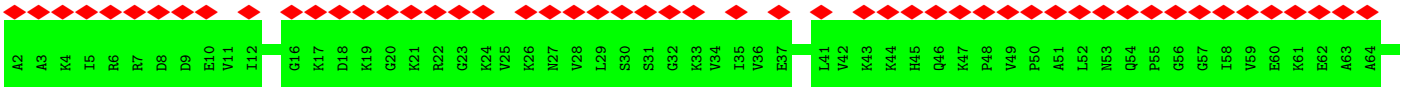
Chain T:

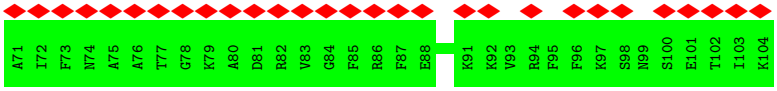




• Molecule 27: 50S ribosomal protein L24

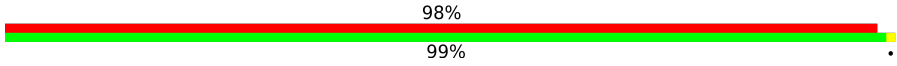
Chain U:

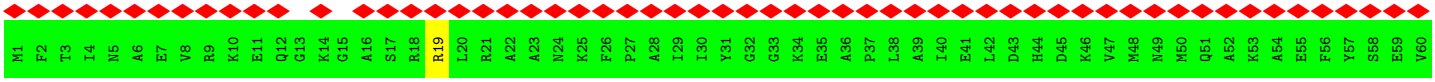


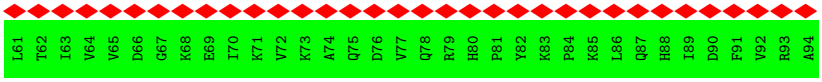


• Molecule 28: 50S ribosomal protein L25

Chain V:

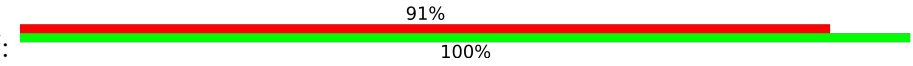


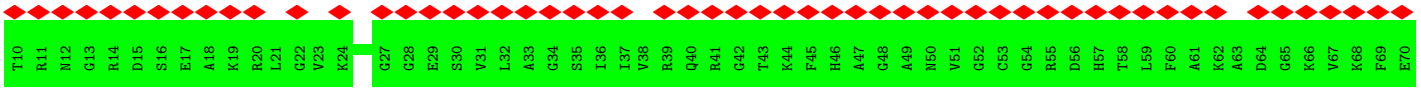


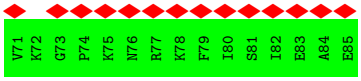


• Molecule 29: 50S ribosomal protein L27

Chain W:

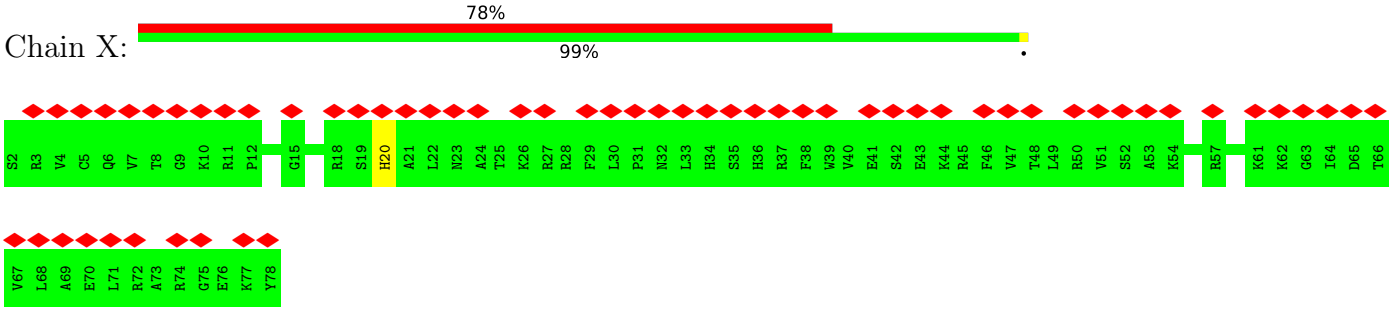






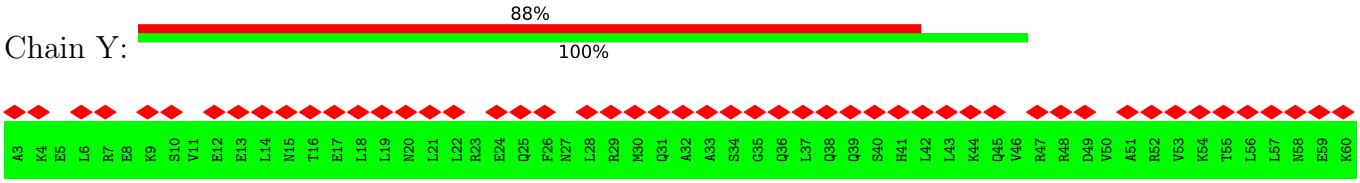
• Molecule 30: 50S ribosomal protein L28

Chain X:



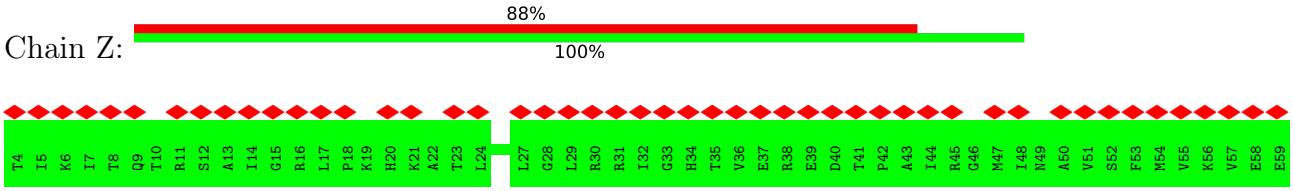
• Molecule 31: 50S ribosomal protein L29

Chain Y:



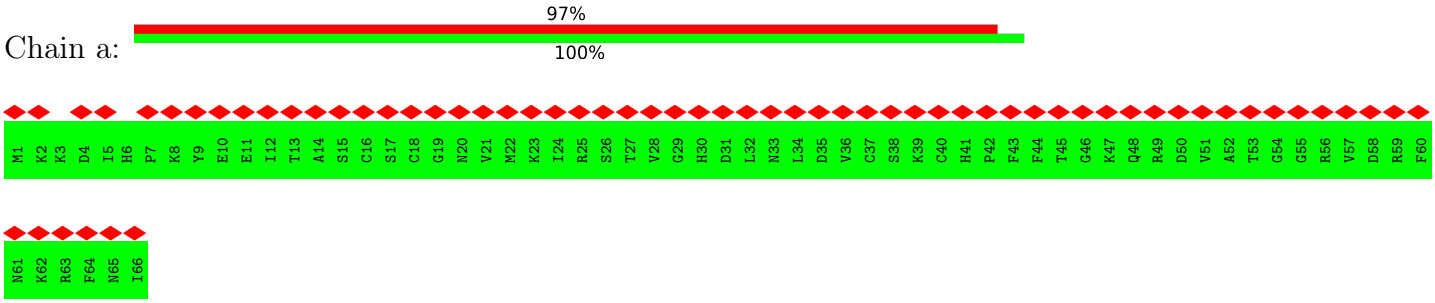
• Molecule 32: 50S ribosomal protein L30

Chain Z:



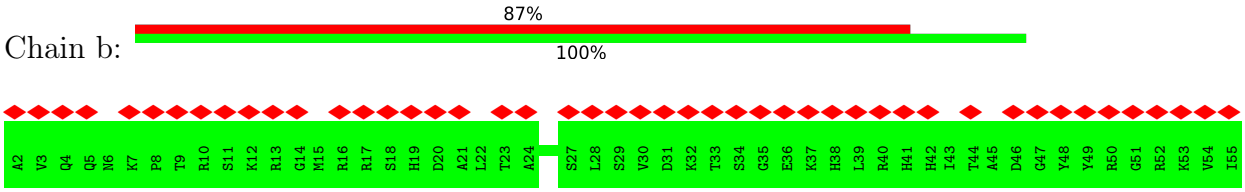
• Molecule 33: 50S ribosomal protein L31

Chain a:



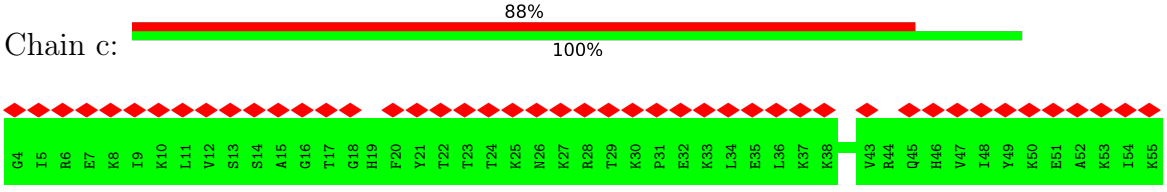
• Molecule 34: 50S ribosomal protein L32

Chain b:



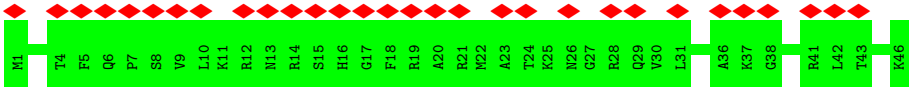
• Molecule 35: 50S ribosomal protein L33

Chain c:



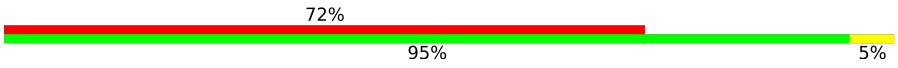
• Molecule 36: 50S ribosomal protein L34

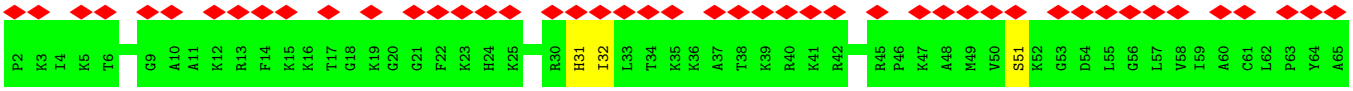
Chain d:



• Molecule 37: 50S ribosomal protein L35

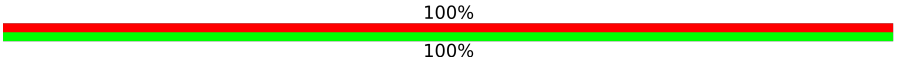
Chain e:

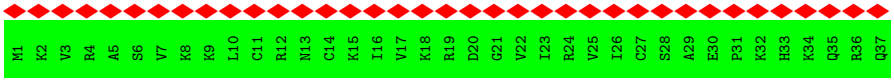




• Molecule 38: 50S ribosomal protein L36

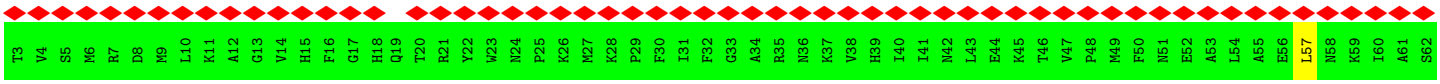
Chain f:

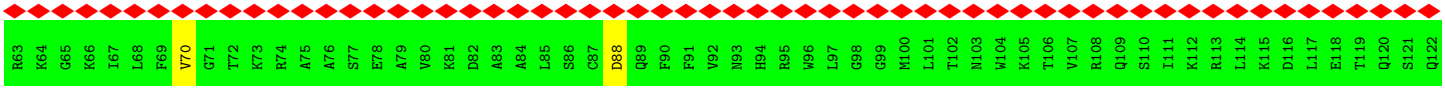


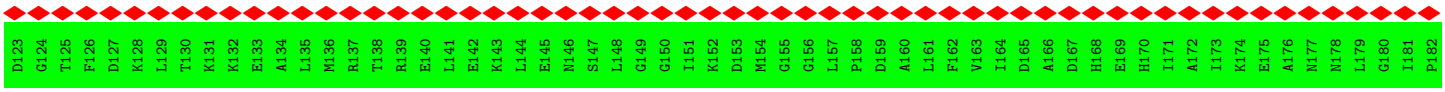


• Molecule 39: 30S ribosomal protein S2

Chain g:

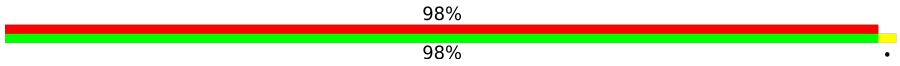


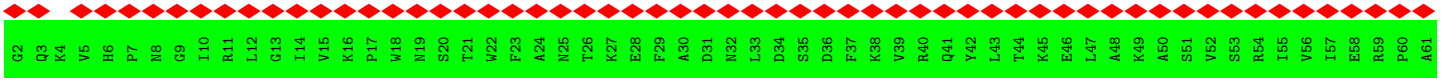




• Molecule 40: 30S ribosomal protein S3

Chain h:





K62 S63 I64 R65 V66 T67 I68 H69 T70 A71 R72 P73 G74 I75 V76 I77 G78 K79 K80 G81 E82 D83 V84 E85 K86 L87 R88 K89 V90 V91 A92 D93 I94 A95 G96 V97 P98 A99 Q100 I101 N102 I103 A104 E105 V106 R107 K108 P109 E110 L111 D112 A113 K114 L115 V116 A117 D118 S119 I120 T121

S122 Q123 L124 E125 R126 R127 V128 M129 F130 R131 R132 A133 M134 K135 R136 A137 V138 Q139 N140 A141 M142 R143 L144 G145 A146 K147 G148 I149 K150 V151 E152 V153 S154 G155 R156 L157 G158 G159 A160 E161 I162 A163 R164 T165 E166 W167 Y168 R169 E170 G171 R172 V173 P174 L175 H176 T177 L178 R179 A180 D181

I182 D183 Y184 N185 T186 S187 E188 A189 H190 T191 T192 Y193 G194 V195 I196 G197 V198 K199 V200 W201 I202 F203 K204 G205 E206 I207 L208 G209

• Molecule 41: 30S ribosomal protein S4

Chain i: 99% 100%

A2 R3 Y4 L5 G6 P7 K8 L9 K10 L11 S12 R13 R14 E15 G16 T17 D18 L19 F20 L21 K22 S23 G24 V25 R26 A27 I28 D29 T30 K31 C32 K33 I34 E35 Q36 A37 P38 G39 Q40 H41 G42 A43 R44 K45 P46 R47 L48 S49 D50 Y51 G52 V53 Q54 L55 R56 E57 K58 Q59 K60 V61

R62 R63 I64 Y65 G66 V67 L68 E69 R70 Q71 F72 R73 N74 Y75 Y76 K77 E78 A79 A80 R81 L82 K83 G84 N85 T86 G87 E88 N89 L90 L91 A92 L93 L94 E95 G96 R97 L98 D99 N100 V101 V102 Y103 R104 M105 G106 F107 G108 A109 T110 R111 A112 E113 A114 R115 Q116 L117 V118 S119 H120 K121

A122 I123 M124 V125 N126 G127 R128 V129 V130 N131 I132 A133 S134 Y135 Q136 V137 S138 P139 N140 D141 V142 V143 S144 I145 R146 E147 K148 A149 K150 K151 Q152 S153 R154 V155 K156 A157 A158 L159 E160 L161 A162 E163 Q164 R165 E166 K167 P168 T169 W170 L171 E172 V173 D174 A175 G176 K177 M178 E179 G180 T181

F182 K183 R184 K185 P186 E187 R188 S189 D190 L191 S192 A193 D194 I195 N196 E197 H198 L199 I200 V201 E202 L203 Y204 S205 K206

• Molecule 42: 30S ribosomal protein S5

Chain j: 99% 100%

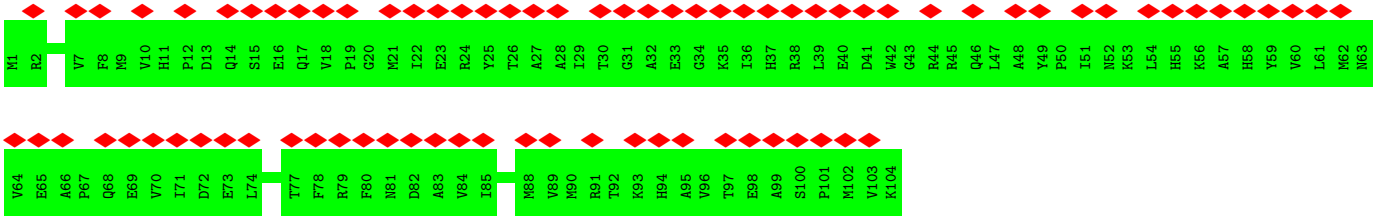
E10 L11 Q12 E13 K14 L15 I16 A17 V18 N19 R20 V21 S22 K23 T24 V25 K26 G27 G28 R29 I30 F31 S32 F33 T34 A35 L36 T37 V38 V39 G40 D41 G42 N43 G44 R45 V46 G47 F48 G49 Y50 G51 K52 A53 R54 E55 V56 P57 A58 A59 I60 Q61 K62 A63 M64 E65 K66 A67 R68 R69

N70 M71 I72 N73 V74 A75 L76 N77 N78 G79 T80 L81 Q82 H83 P84 V85 K86 G87 V88 H89 T90 G91 S92 R93 V94 F95 M96 Q97 P98 A99 S100 E101 G102 T103 G104 I105 I106 A107 G108 G109 A110 M111 R112 A113 V114 L115 E116 V117 A118 G119 V120 H121 N122 V123 L124 A125 K126 A127 Y128 G129

S130 T131 N132 P133 I134 N135 V136 V137 R138 A139 T140 I141 D142 G143 L144 E145 N146 M147 N148 S149 P150 E151 M152 V153 A154 A155 K156 R157 G158 K159 S160 V161 E162 E163 I164 L165

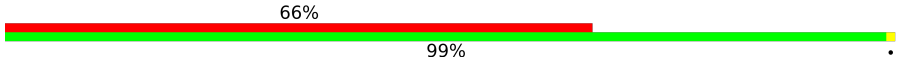
• Molecule 43: 30S ribosomal protein S6

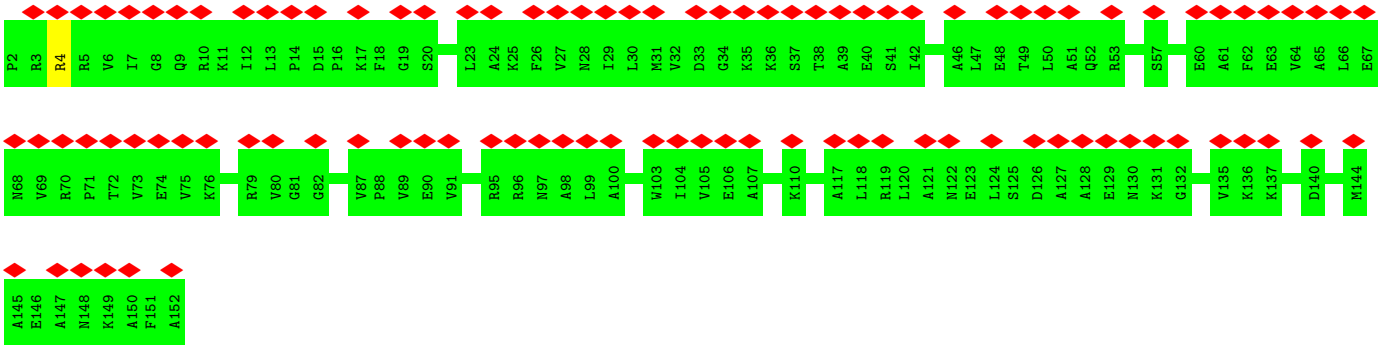
Chain k: 76% 100%



• Molecule 44: 30S ribosomal protein S7

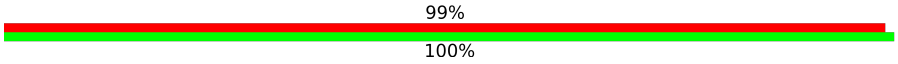
Chain l:

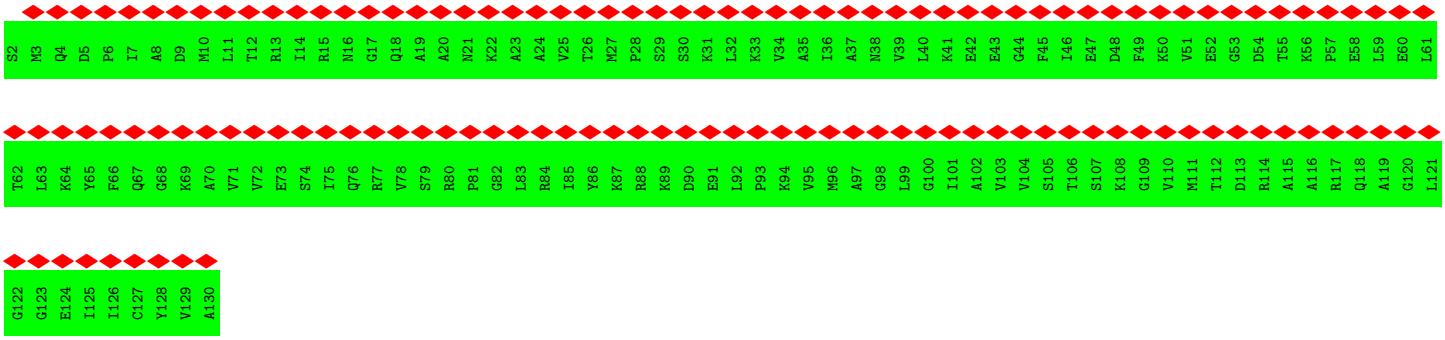




• Molecule 45: 30S ribosomal protein S8

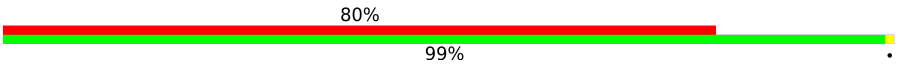
Chain m:

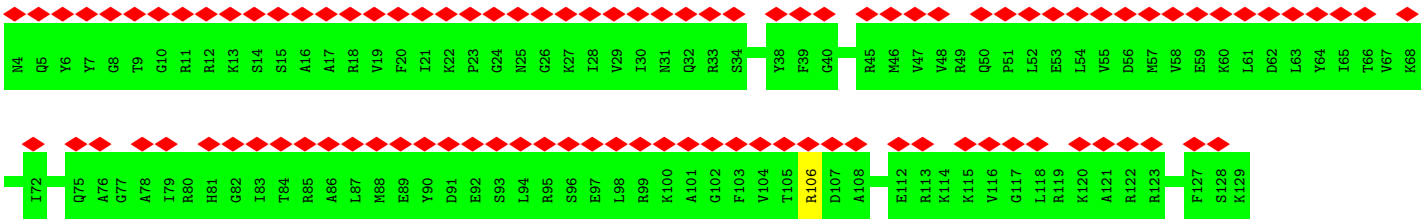




• Molecule 46: 30S ribosomal protein S9

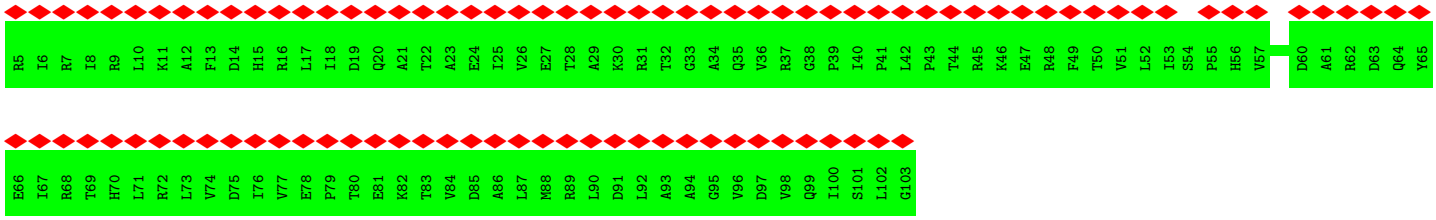
Chain n:





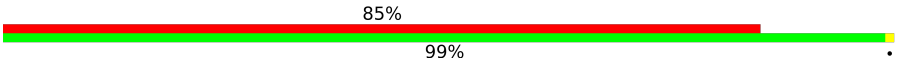
• Molecule 47: 30S ribosomal protein S10

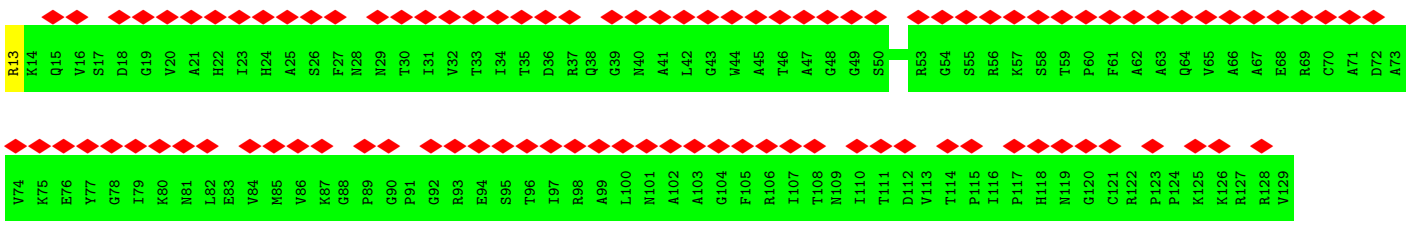
Chain o:



• Molecule 48: 30S ribosomal protein S11

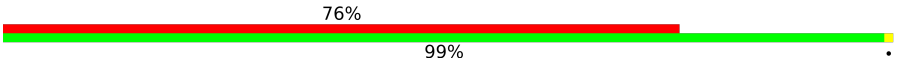
Chain p:

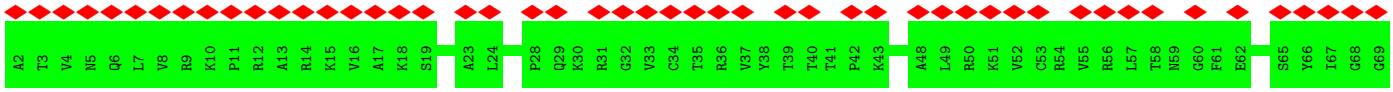


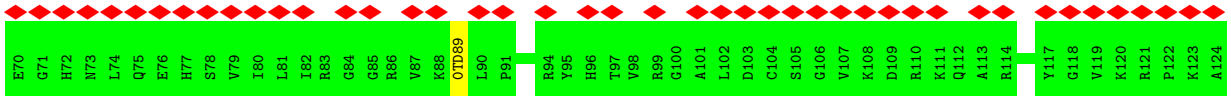


• Molecule 49: 30S ribosomal protein S12

Chain q:

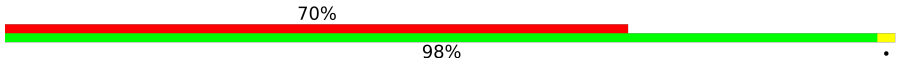


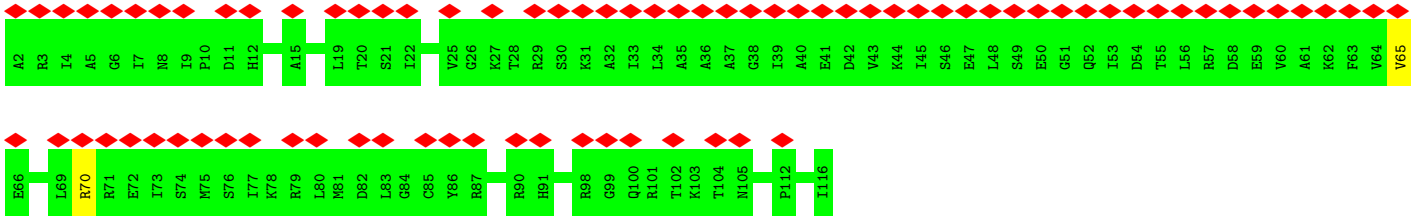




• Molecule 50: 30S ribosomal protein S13

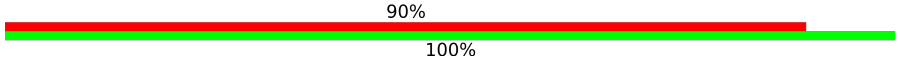
Chain r:

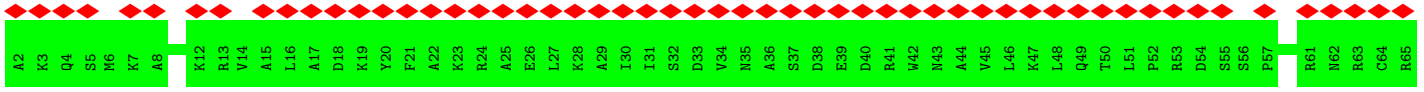


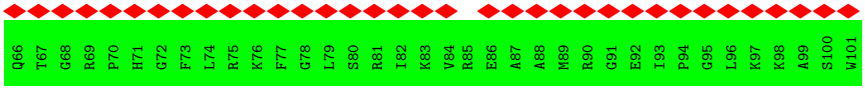


• Molecule 51: 30S ribosomal protein S14

Chain s:

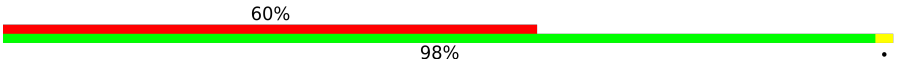


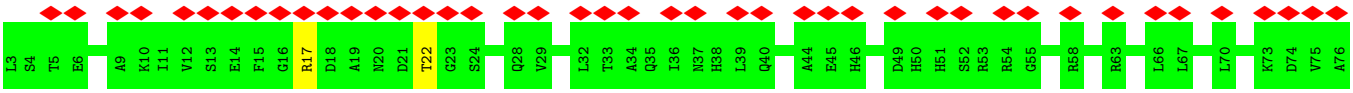


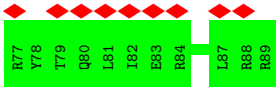


• Molecule 52: 30S ribosomal protein S15

Chain t:

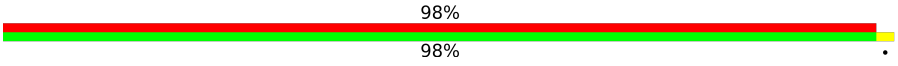


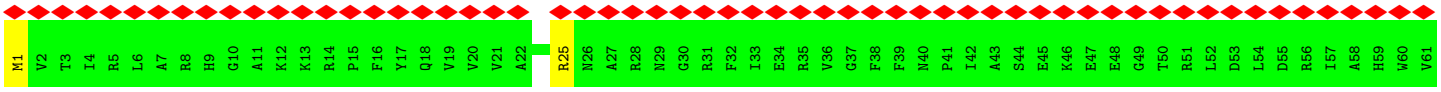


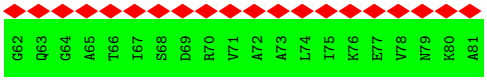


• Molecule 53: 30S ribosomal protein S16

Chain u:

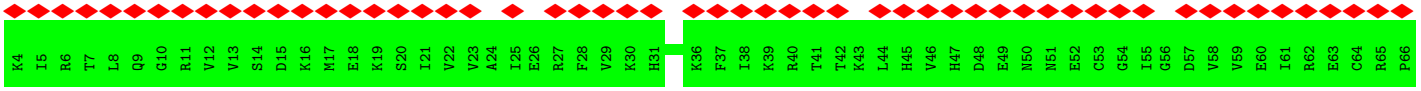


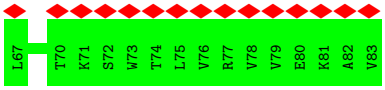




• Molecule 54: 30S ribosomal protein S17

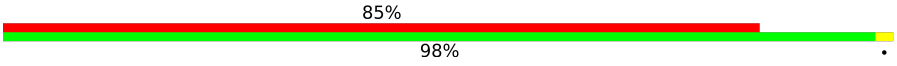
Chain v:

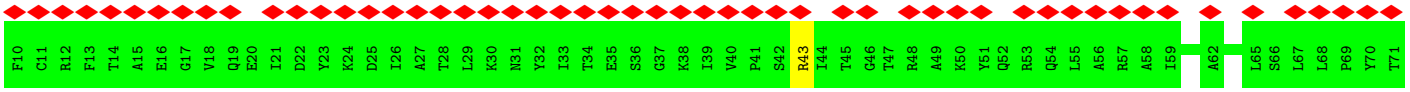




• Molecule 55: 30S ribosomal protein S18

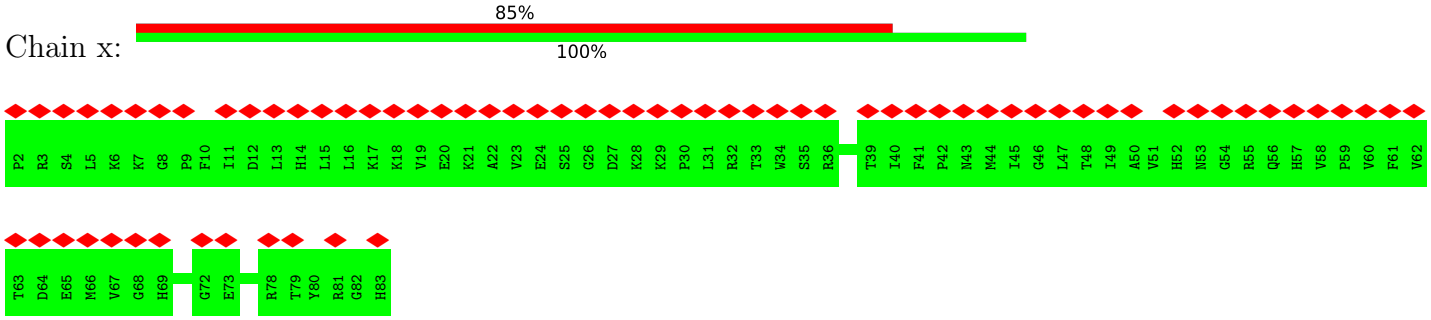
Chain w:





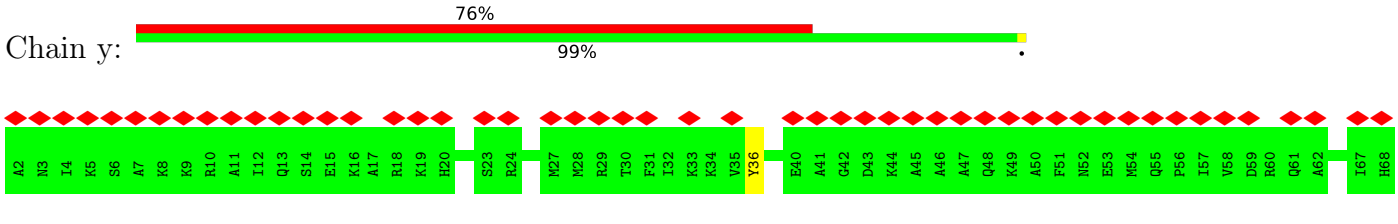
• Molecule 56: 30S ribosomal protein S19

Chain x:



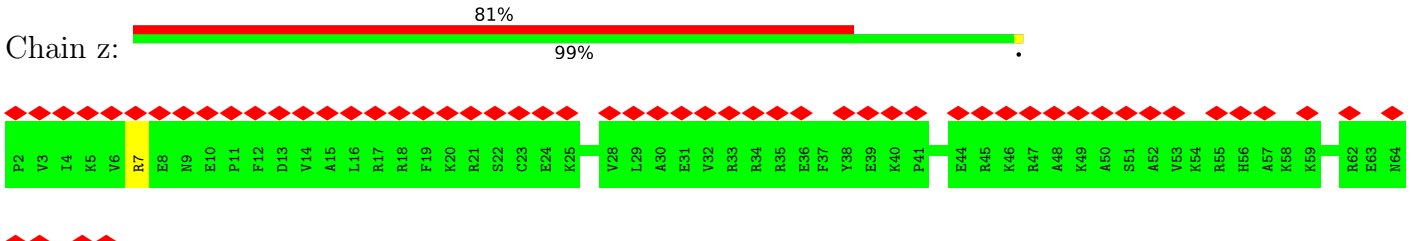
• Molecule 57: 30S ribosomal protein S20

Chain y:



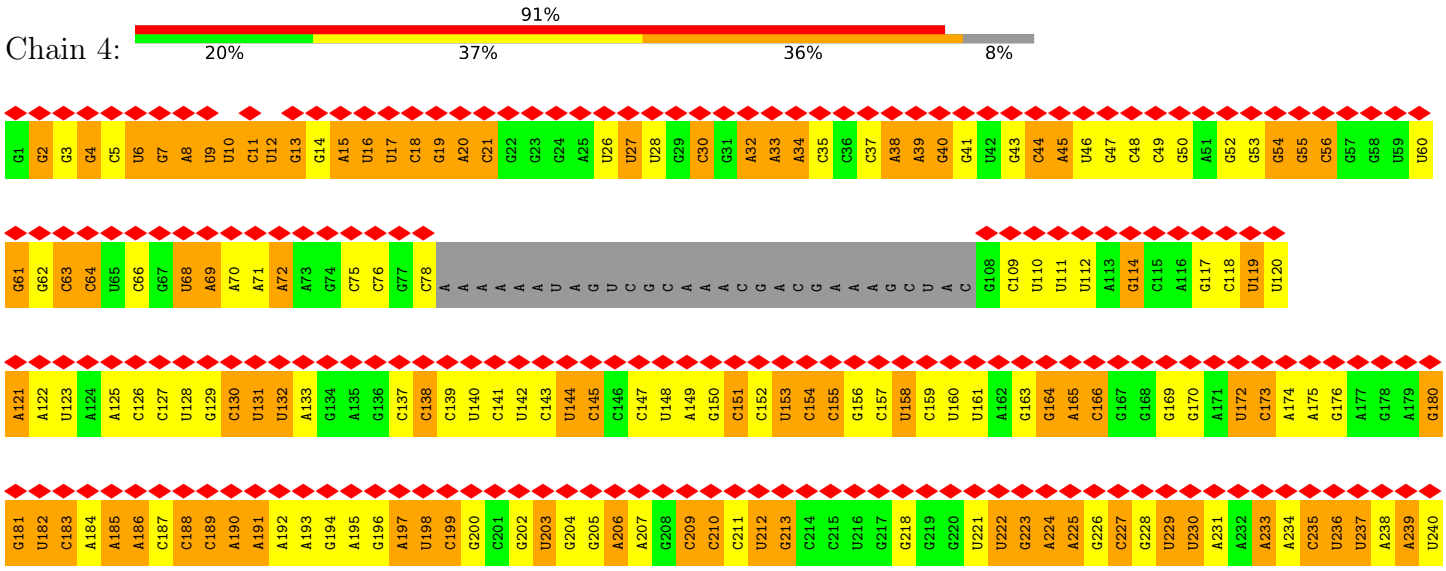
• Molecule 58: 30S ribosomal protein S21

Chain z:



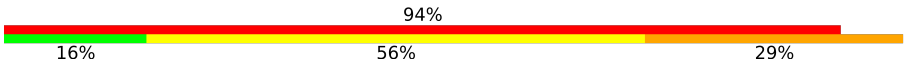
• Molecule 59: transfer-messenger RNA (tmRNA)

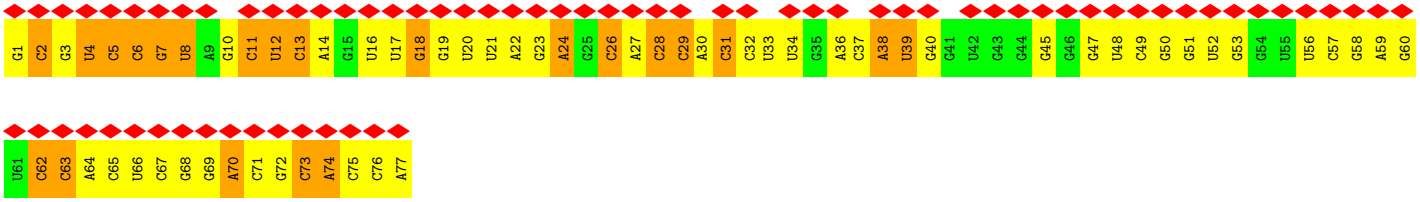
Chain 4:



- Molecule 60: tRNA-Val

Chain 7:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47776	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.508	Depositor
Minimum map value	-0.282	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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: OMG, 0TD, 2MA, PSU, MG, 5MU, 3TD, ZN, OMU, MA6, UR3, 6MZ, 1MG, 5MC, 4OC, 7MG, G7M, OMC, 2MG

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	1	1.04	5/69285 (0.0%)	1.22	519/108083 (0.5%)
2	2	1.31	47/36588 (0.1%)	1.40	436/57066 (0.8%)
3	3	0.50	0/2872	1.17	18/4478 (0.4%)
4	5	0.41	0/1191	0.71	1/1601 (0.1%)
5	6	0.33	0/139	0.91	0/193
6	8	5.08	5/1830 (0.3%)	1.48	17/2849 (0.6%)
7	9	0.93	1/142 (0.7%)	2.01	7/219 (3.2%)
8	B	0.46	0/2117	0.64	0/2845
9	C	0.34	0/1586	0.60	0/2134
10	D	0.31	0/1571	0.59	0/2113
11	E	0.35	0/1435	0.65	1/1926 (0.1%)
12	F	0.30	0/1333	0.57	0/1805
13	G	0.31	0/1122	0.64	1/1515 (0.1%)
14	H	0.32	0/993	0.69	1/1340 (0.1%)
15	I	0.31	0/998	0.66	0/1348
16	J	0.30	0/1144	0.56	0/1541
17	K	0.42	0/955	0.62	0/1279
18	L	0.30	0/1062	0.57	0/1413
19	M	0.33	0/1093	0.59	0/1460
20	N	0.33	0/964	0.64	0/1289
21	O	0.30	0/894	0.54	0/1198
22	P	0.40	0/929	0.59	1/1242 (0.1%)
23	Q	0.33	0/960	0.50	0/1278
24	R	0.31	0/829	0.56	0/1107
25	S	0.31	0/847	0.61	1/1134 (0.1%)
26	T	0.32	0/752	0.59	0/1005
27	U	0.30	0/796	0.53	0/1062
28	V	0.29	0/766	0.55	0/1025
29	W	0.35	0/589	0.55	0/779
30	X	0.37	0/635	0.62	0/848
31	Y	0.28	0/478	0.57	0/637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	Z	0.27	0/438	0.60	0/587
33	a	0.34	0/531	0.55	0/709
34	b	0.31	0/435	0.58	0/581
35	c	0.33	0/433	0.55	0/576
36	d	0.33	0/380	0.53	0/498
37	e	0.34	0/513	0.66	0/676
38	f	0.29	0/298	0.56	0/392
39	g	0.46	0/1791	0.70	1/2413 (0.0%)
40	h	0.51	0/1663	0.65	0/2241
41	i	0.58	0/1665	0.64	0/2227
42	j	0.61	0/1165	0.70	0/1568
43	k	0.58	0/867	0.66	0/1171
44	l	0.47	0/1195	0.60	0/1602
45	m	0.60	0/989	0.67	0/1326
46	n	0.49	0/1022	0.65	0/1361
47	o	0.51	0/800	0.63	0/1082
48	p	0.51	0/893	0.60	0/1205
49	q	0.61	0/960	0.67	0/1286
50	r	0.40	0/900	0.68	1/1204 (0.1%)
51	s	0.50	0/817	0.58	0/1088
52	t	0.58	0/716	0.65	0/956
53	u	0.63	0/653	0.71	0/877
54	v	0.58	0/658	0.68	0/881
55	w	0.63	0/544	0.66	0/731
56	x	0.48	0/675	0.63	0/908
57	y	0.48	0/670	0.61	0/888
58	z	0.44	0/597	0.55	0/792
59	4	0.74	1/7978 (0.0%)	2.10	509/12434 (4.1%)
60	7	0.74	1/1836 (0.1%)	2.21	114/2861 (4.0%)
All	All	1.09	60/168977 (0.0%)	1.22	1628/252933 (0.6%)

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	1	34	0
2	2	5	0
14	H	0	1
15	I	0	1
17	K	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
23	Q	0	1
30	X	0	1
37	e	0	2
39	g	0	1
40	h	0	2
53	u	0	1
All	All	39	11

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	388	G	P-O5'	205.16	3.65	1.59
6	8	77	A	N9-C4	114.08	2.06	1.37
6	8	77	A	N7-C5	106.12	2.02	1.39
6	8	77	A	C8-N7	92.91	1.96	1.31
6	8	77	A	N9-C8	85.15	2.05	1.37

The worst 5 of 1628 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	8	77	A	N7-C8-N9	-24.47	101.56	113.80
1	1	388	G	P-O5'-C5'	22.44	156.80	120.90
6	8	77	A	C5-N7-C8	20.39	114.09	103.90
60	7	72	G	OP1-P-O3'	-19.57	62.15	105.20
60	7	73	C	OP1-P-OP2	19.16	148.35	119.60

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	745	1MG	C1',C2'
1	1	746	PSU	C4',C3'
1	1	747	5MU	C4',C2'
1	1	955	PSU	C4',C3'
1	1	1618	6MZ	C2',C3'

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	H	67	THR	Peptide
15	I	20	SER	Peptide
17	K	93	GLN	Peptide
23	Q	5	LYS	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
30	X	20	HIS	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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
4	5	143/145 (99%)	112 (78%)	27 (19%)	4 (3%)	5 34
5	6	26/28 (93%)	17 (65%)	9 (35%)	0	100 100
8	B	268/270 (99%)	243 (91%)	25 (9%)	0	100 100
9	C	207/209 (99%)	194 (94%)	13 (6%)	0	100 100
10	D	199/201 (99%)	176 (88%)	23 (12%)	0	100 100
11	E	175/177 (99%)	157 (90%)	18 (10%)	0	100 100
12	F	173/175 (99%)	151 (87%)	22 (13%)	0	100 100
13	G	147/149 (99%)	133 (90%)	14 (10%)	0	100 100
14	H	128/130 (98%)	103 (80%)	25 (20%)	0	100 100
15	I	133/135 (98%)	108 (81%)	25 (19%)	0	100 100
16	J	139/141 (99%)	129 (93%)	10 (7%)	0	100 100
17	K	121/123 (98%)	105 (87%)	16 (13%)	0	100 100
18	L	142/144 (99%)	124 (87%)	18 (13%)	0	100 100
19	M	134/136 (98%)	128 (96%)	6 (4%)	0	100 100
20	N	117/119 (98%)	102 (87%)	15 (13%)	0	100 100
21	O	113/115 (98%)	103 (91%)	10 (9%)	0	100 100
22	P	112/114 (98%)	102 (91%)	10 (9%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	Q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
24	R	101/103 (98%)	90 (89%)	11 (11%)	0	100	100
25	S	106/108 (98%)	97 (92%)	9 (8%)	0	100	100
26	T	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
27	U	101/103 (98%)	91 (90%)	10 (10%)	0	100	100
28	V	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
29	W	74/76 (97%)	65 (88%)	9 (12%)	0	100	100
30	X	75/77 (97%)	66 (88%)	9 (12%)	0	100	100
31	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
32	Z	54/56 (96%)	51 (94%)	3 (6%)	0	100	100
33	a	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
34	b	52/54 (96%)	44 (85%)	8 (15%)	0	100	100
35	c	50/52 (96%)	45 (90%)	5 (10%)	0	100	100
36	d	44/46 (96%)	40 (91%)	4 (9%)	0	100	100
37	e	62/64 (97%)	53 (86%)	8 (13%)	1 (2%)	9	44
38	f	35/37 (95%)	35 (100%)	0	0	100	100
39	g	223/225 (99%)	198 (89%)	25 (11%)	0	100	100
40	h	206/208 (99%)	188 (91%)	17 (8%)	1 (0%)	29	67
41	i	203/205 (99%)	190 (94%)	13 (6%)	0	100	100
42	j	154/156 (99%)	135 (88%)	19 (12%)	0	100	100
43	k	102/104 (98%)	96 (94%)	6 (6%)	0	100	100
44	l	149/151 (99%)	140 (94%)	9 (6%)	0	100	100
45	m	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
46	n	124/126 (98%)	113 (91%)	11 (9%)	0	100	100
47	o	97/99 (98%)	87 (90%)	10 (10%)	0	100	100
48	p	115/117 (98%)	103 (90%)	12 (10%)	0	100	100
49	q	120/123 (98%)	105 (88%)	15 (12%)	0	100	100
50	r	113/115 (98%)	100 (88%)	13 (12%)	0	100	100
51	s	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
52	t	85/87 (98%)	79 (93%)	5 (6%)	1 (1%)	13	49
53	u	79/81 (98%)	71 (90%)	8 (10%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	v	78/80 (98%)	69 (88%)	9 (12%)	0	100	100
55	w	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
56	x	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
57	y	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
58	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
All	All	6017/6124 (98%)	5403 (90%)	607 (10%)	7 (0%)	54	84

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	5	137	ASP
52	t	22	THR
4	5	135	GLN
4	5	132	GLY
4	5	120	ASN

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	
4	5	121/121 (100%)	119 (98%)	2 (2%)	60	78
8	B	216/216 (100%)	216 (100%)	0	100	100
9	C	164/164 (100%)	163 (99%)	1 (1%)	86	91
10	D	165/165 (100%)	164 (99%)	1 (1%)	86	91
11	E	148/148 (100%)	146 (99%)	2 (1%)	67	81
12	F	136/136 (100%)	134 (98%)	2 (2%)	65	80
13	G	114/114 (100%)	113 (99%)	1 (1%)	78	87
14	H	99/99 (100%)	99 (100%)	0	100	100
15	I	104/104 (100%)	104 (100%)	0	100	100
16	J	115/115 (100%)	115 (100%)	0	100	100
17	K	104/104 (100%)	104 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
18	L	103/103 (100%)	102 (99%)	1 (1%)	76 86
19	M	109/109 (100%)	109 (100%)	0	100 100
20	N	99/99 (100%)	98 (99%)	1 (1%)	76 86
21	O	85/85 (100%)	85 (100%)	0	100 100
22	P	99/99 (100%)	99 (100%)	0	100 100
23	Q	89/89 (100%)	89 (100%)	0	100 100
24	R	84/84 (100%)	84 (100%)	0	100 100
25	S	91/91 (100%)	90 (99%)	1 (1%)	73 84
26	T	81/81 (100%)	81 (100%)	0	100 100
27	U	84/84 (100%)	84 (100%)	0	100 100
28	V	78/78 (100%)	77 (99%)	1 (1%)	69 82
29	W	58/58 (100%)	58 (100%)	0	100 100
30	X	67/67 (100%)	67 (100%)	0	100 100
31	Y	53/53 (100%)	53 (100%)	0	100 100
32	Z	47/47 (100%)	47 (100%)	0	100 100
33	a	59/59 (100%)	59 (100%)	0	100 100
34	b	46/46 (100%)	46 (100%)	0	100 100
35	c	47/47 (100%)	47 (100%)	0	100 100
36	d	38/38 (100%)	38 (100%)	0	100 100
37	e	51/51 (100%)	51 (100%)	0	100 100
38	f	34/34 (100%)	34 (100%)	0	100 100
39	g	187/187 (100%)	186 (100%)	1 (0%)	88 93
40	h	171/171 (100%)	170 (99%)	1 (1%)	86 91
41	i	172/172 (100%)	172 (100%)	0	100 100
42	j	119/119 (100%)	119 (100%)	0	100 100
43	k	91/91 (100%)	91 (100%)	0	100 100
44	l	124/124 (100%)	123 (99%)	1 (1%)	81 89
45	m	104/104 (100%)	104 (100%)	0	100 100
46	n	104/104 (100%)	103 (99%)	1 (1%)	76 86
47	o	86/86 (100%)	86 (100%)	0	100 100
48	p	90/90 (100%)	89 (99%)	1 (1%)	73 84

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	q	102/102 (100%)	102 (100%)	0	100 100
50	r	93/93 (100%)	92 (99%)	1 (1%)	73 84
51	s	83/83 (100%)	83 (100%)	0	100 100
52	t	75/75 (100%)	74 (99%)	1 (1%)	69 82
53	u	65/65 (100%)	64 (98%)	1 (2%)	65 80
54	v	74/74 (100%)	74 (100%)	0	100 100
55	w	56/56 (100%)	55 (98%)	1 (2%)	59 77
56	x	72/72 (100%)	72 (100%)	0	100 100
57	y	65/65 (100%)	64 (98%)	1 (2%)	65 80
58	z	60/60 (100%)	59 (98%)	1 (2%)	60 78
All	All	4981/4981 (100%)	4957 (100%)	24 (0%)	89 93

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	h	164	ARG
48	p	13	ARG
46	n	106	ARG
50	r	65	VAL
12	F	44	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
27	U	99	ASN
50	r	105	ASN
33	a	20	ASN
49	q	46	ASN
57	y	3	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2897/2903 (99%)	951 (32%)	24 (0%)
2	2	1526/1534 (99%)	428 (28%)	7 (0%)
3	3	119/120 (99%)	38 (31%)	0

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
59	4	332/363 (91%)	198 (59%)	33 (9%)
6	8	76/77 (98%)	43 (56%)	1 (1%)
60	7	76/77 (98%)	49 (64%)	2 (2%)
7	9	5/6 (83%)	4 (80%)	0
All	All	5031/5080 (99%)	1711 (34%)	67 (1%)

5 of 1711 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	2	G
1	1	10	A
1	1	11	C
1	1	12	U
1	1	18	U

5 of 67 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
59	4	261	G
59	4	299	C
60	7	13	C
2	2	120	A
1	1	2605	PSU

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

34 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	$\#\|Z\| > 2$
1	OMU	1	2552	61,1	19,22,23	2.76	7 (36%)	26,31,34	2.07	8 (30%)
2	2MG	2	966	2	18,26,27	2.95	6 (33%)	16,38,41	1.41	3 (18%)
49	0TD	q	89	49	7,9,10	1.39	0	6,11,13	1.90	2 (33%)
2	MA6	2	1518	2	18,26,27	1.00	1 (5%)	19,38,41	1.48	2 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	5MC	1	1962	1	18,22,23	2.15	3 (16%)	26,32,35	1.47	5 (19%)
1	2MG	1	1835	1	18,26,27	2.96	6 (33%)	16,38,41	1.78	4 (25%)
1	PSU	1	1917	1	18,21,22	2.09	5 (27%)	22,30,33	2.15	5 (22%)
1	PSU	1	2580	1	18,21,22	1.94	5 (27%)	22,30,33	2.16	6 (27%)
2	4OC	2	1402	2	20,23,24	2.57	5 (25%)	26,32,35	2.03	8 (30%)
2	PSU	2	516	2	18,21,22	2.29	6 (33%)	22,30,33	2.50	6 (27%)
1	G7M	1	2069	1	20,26,27	2.82	5 (25%)	17,39,42	0.83	0
1	OMC	1	2498	61,1	19,22,23	1.70	4 (21%)	26,31,34	2.22	6 (23%)
2	2MG	2	1516	2	18,26,27	2.94	6 (33%)	16,38,41	1.43	3 (18%)
2	5MC	2	1407	2	18,22,23	2.05	3 (16%)	26,32,35	1.49	4 (15%)
1	2MG	1	2445	1	18,26,27	2.90	5 (27%)	16,38,41	1.32	3 (18%)
1	PSU	1	955	1	18,21,22	1.98	4 (22%)	22,30,33	2.17	5 (22%)
1	6MZ	1	2030	1	18,25,26	1.91	1 (5%)	16,36,39	3.25	5 (31%)
1	3TD	1	1915	61,1,4	18,22,23	2.77	7 (38%)	22,32,35	1.87	4 (18%)
1	PSU	1	2605	1	18,21,22	2.07	6 (33%)	22,30,33	1.92	4 (18%)
1	PSU	1	2504	1	18,21,22	2.02	5 (27%)	22,30,33	2.24	6 (27%)
2	7MG	2	527	2	22,26,27	6.62	6 (27%)	29,39,42	2.60	9 (31%)
1	PSU	1	746	1	18,21,22	1.85	5 (27%)	22,30,33	2.00	4 (18%)
1	PSU	1	2457	1	18,21,22	1.99	5 (27%)	22,30,33	2.10	7 (31%)
2	MA6	2	1519	2	18,26,27	1.11	1 (5%)	19,38,41	1.39	2 (10%)
2	5MC	2	967	2	18,22,23	2.11	3 (16%)	26,32,35	1.52	4 (15%)
1	6MZ	1	1618	1	18,25,26	1.90	1 (5%)	16,36,39	2.53	5 (31%)
2	2MG	2	1207	2	18,26,27	3.02	6 (33%)	16,38,41	1.35	4 (25%)
1	5MU	1	747	1	19,22,23	2.10	7 (36%)	28,32,35	4.58	10 (35%)
1	1MG	1	745	1	18,26,27	2.97	7 (38%)	19,39,42	2.29	9 (47%)
1	2MA	1	2503	61,1	17,25,26	1.52	3 (17%)	17,37,40	1.30	2 (11%)
1	OMG	1	2251	1	18,26,27	2.98	7 (38%)	19,38,41	1.55	4 (21%)
1	5MU	1	1939	61,1	19,22,23	2.49	7 (36%)	28,32,35	3.58	10 (35%)
2	UR3	2	1498	2	19,22,23	2.99	7 (36%)	26,32,35	1.55	5 (19%)
1	PSU	1	1911	1	18,21,22	1.95	4 (22%)	22,30,33	2.22	4 (18%)

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
1	OMU	1	2552	61,1	2/2/5/5	3/9/27/28	0/2/2/2
2	2MG	2	966	2	-	2/5/27/28	0/3/3/3
49	0TD	q	89	49	-	2/7/12/14	-
2	MA6	2	1518	2	-	4/7/29/30	0/3/3/3
1	5MC	1	1962	1	-	4/7/25/26	0/2/2/2
1	PSU	1	1917	1	2/2/5/5	2/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
1	PSU	1	2580	1	2/2/5/5	4/7/25/26	0/2/2/2
2	4OC	2	1402	2	2/2/5/6	5/9/29/30	0/2/2/2
2	PSU	2	516	2	2/2/5/5	7/7/25/26	0/2/2/2
1	G7M	1	2069	1	1/1/5/5	1/3/25/26	0/3/3/3
1	OMC	1	2498	61,1	1/1/5/5	5/9/27/28	0/2/2/2
2	2MG	2	1516	2	-	2/5/27/28	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	4/5/27/28	0/3/3/3
1	PSU	1	955	1	2/2/5/5	4/7/25/26	0/2/2/2
1	6MZ	1	2030	1	2/2/5/6	3/5/27/28	0/3/3/3
1	3TD	1	1915	61,1,4	1/1/5/5	4/7/25/26	0/2/2/2
1	PSU	1	2605	1	2/2/5/5	3/7/25/26	0/2/2/2
1	PSU	1	2504	1	2/2/5/5	4/7/25/26	0/2/2/2
2	7MG	2	527	2	1/1/7/7	3/7/37/38	0/3/3/3
1	PSU	1	746	1	2/2/5/5	5/7/25/26	0/2/2/2
1	PSU	1	2457	1	2/2/5/5	2/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	6/7/29/30	0/3/3/3
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	6MZ	1	1618	1	2/2/5/6	3/5/27/28	0/3/3/3
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
1	5MU	1	747	1	2/2/5/5	5/7/25/26	0/2/2/2
1	1MG	1	745	1	2/2/5/5	1/3/25/26	0/3/3/3
1	2MA	1	2503	61,1	2/2/5/5	2/3/25/26	0/3/3/3
1	OMG	1	2251	1	1/1/5/5	1/5/27/28	0/3/3/3
1	5MU	1	1939	61,1	2/2/5/5	1/7/25/26	0/2/2/2
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	2/2/5/5	1/7/25/26	0/2/2/2

The worst 5 of 159 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	527	7MG	C8-N9	-28.63	1.30	1.46
1	1	2069	G7M	O6-C6	10.17	1.44	1.23
1	1	2251	OMG	O6-C6	9.17	1.41	1.23
2	2	1516	2MG	O6-C6	8.90	1.41	1.23
1	1	2445	2MG	O6-C6	8.76	1.41	1.23

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	1	747	5MU	C1'-N1-C2	10.73	136.99	117.57
1	1	747	5MU	C1'-N1-C6	-10.52	103.61	121.12
1	1	2030	6MZ	C9-N6-C6	-9.43	114.75	122.87
1	1	747	5MU	C5M-C5-C4	9.35	129.06	118.77
1	1	1939	5MU	N3-C2-N1	8.73	126.48	114.89

5 of 39 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	1	745	1MG	C1'
1	1	745	1MG	C2'
1	1	746	PSU	C4'
1	1	746	PSU	C3'
1	1	747	5MU	C4'

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	746	PSU	C2'-C1'-C5-C6
1	1	746	PSU	O4'-C1'-C5-C6
1	1	746	PSU	C3'-C4'-C5'-O5'
1	1	746	PSU	O4'-C4'-C5'-O5'
1	1	747	5MU	C3'-C4'-C5'-O5'

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)

Of 441 ligands modelled in this entry, 441 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	2	2
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	2314:A	O3'	2315:G	P	3.20
1	2	1276:G	O3'	1277:C	P	3.19
1	2	1383:C	O3'	1384:C	P	3.17

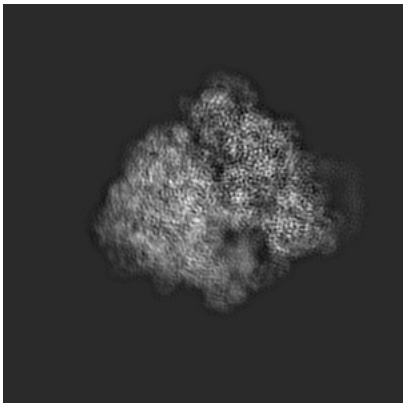
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4476. These allow visual inspection of the internal detail of the map and identification of artifacts.

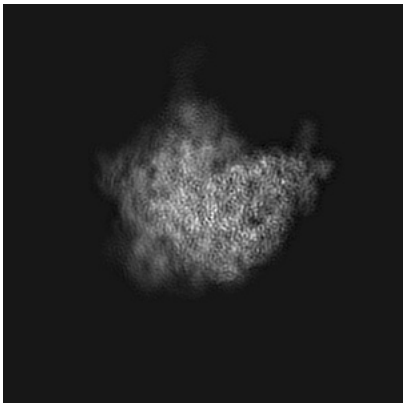
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

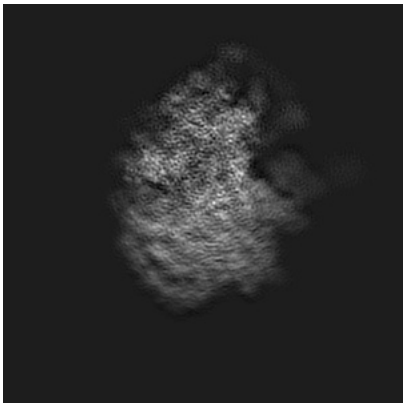
6.1.1 Primary map



X



Y

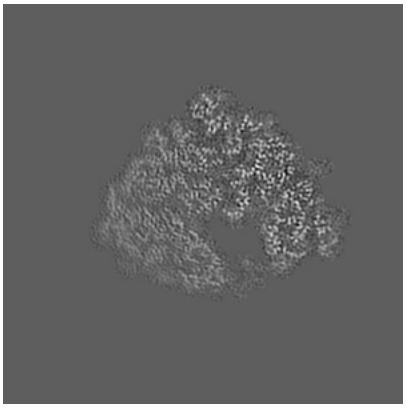


Z

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

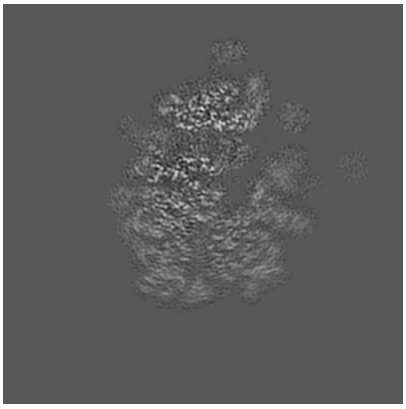
6.2 Central slices

6.2.1 Primary map



X Index: 190

Y Index: 190

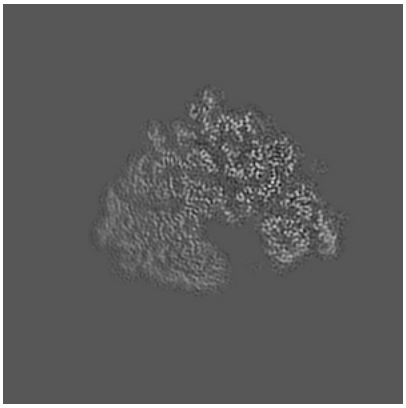


Z Index: 190

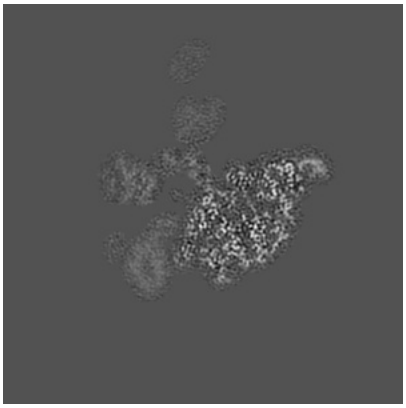
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

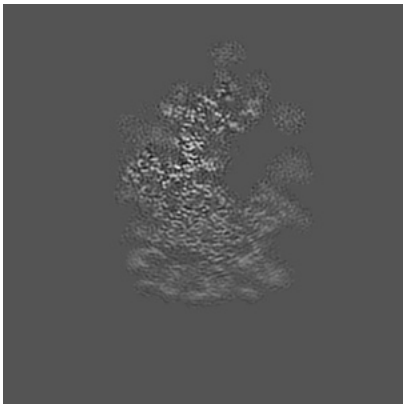
6.3.1 Primary map



X Index: 186



Y Index: 231

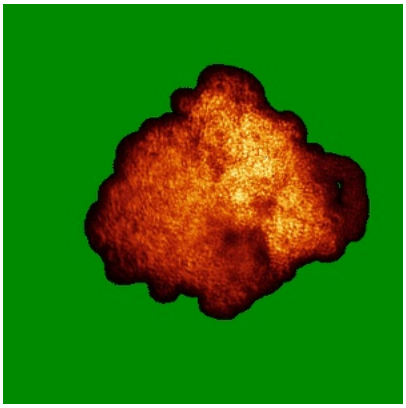


Z Index: 199

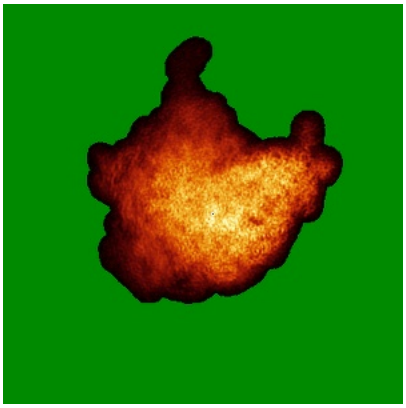
The images above show the largest variance slices of the map in three orthogonal directions.

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

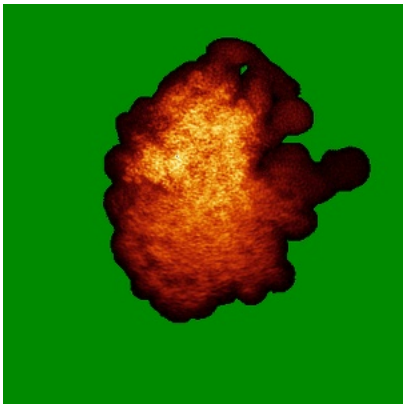
6.4.1 Primary map



X



Y

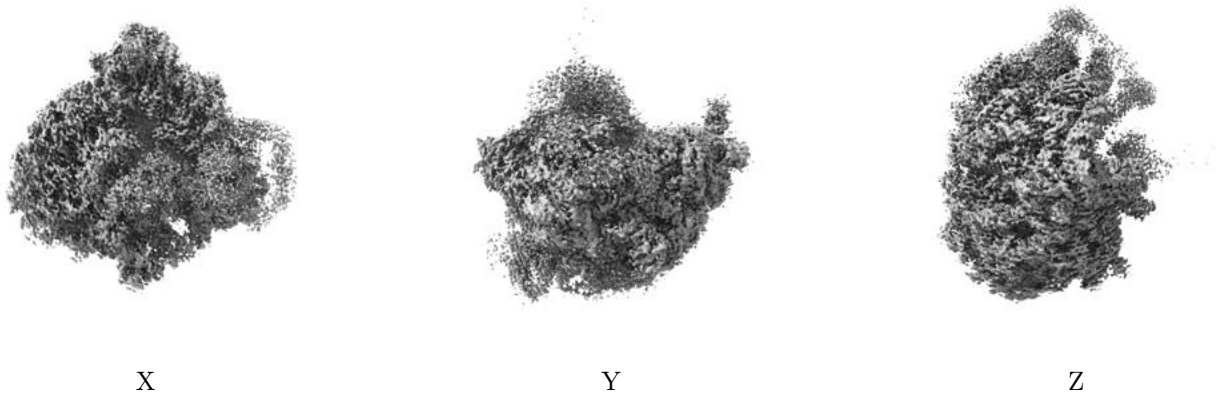


Z

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

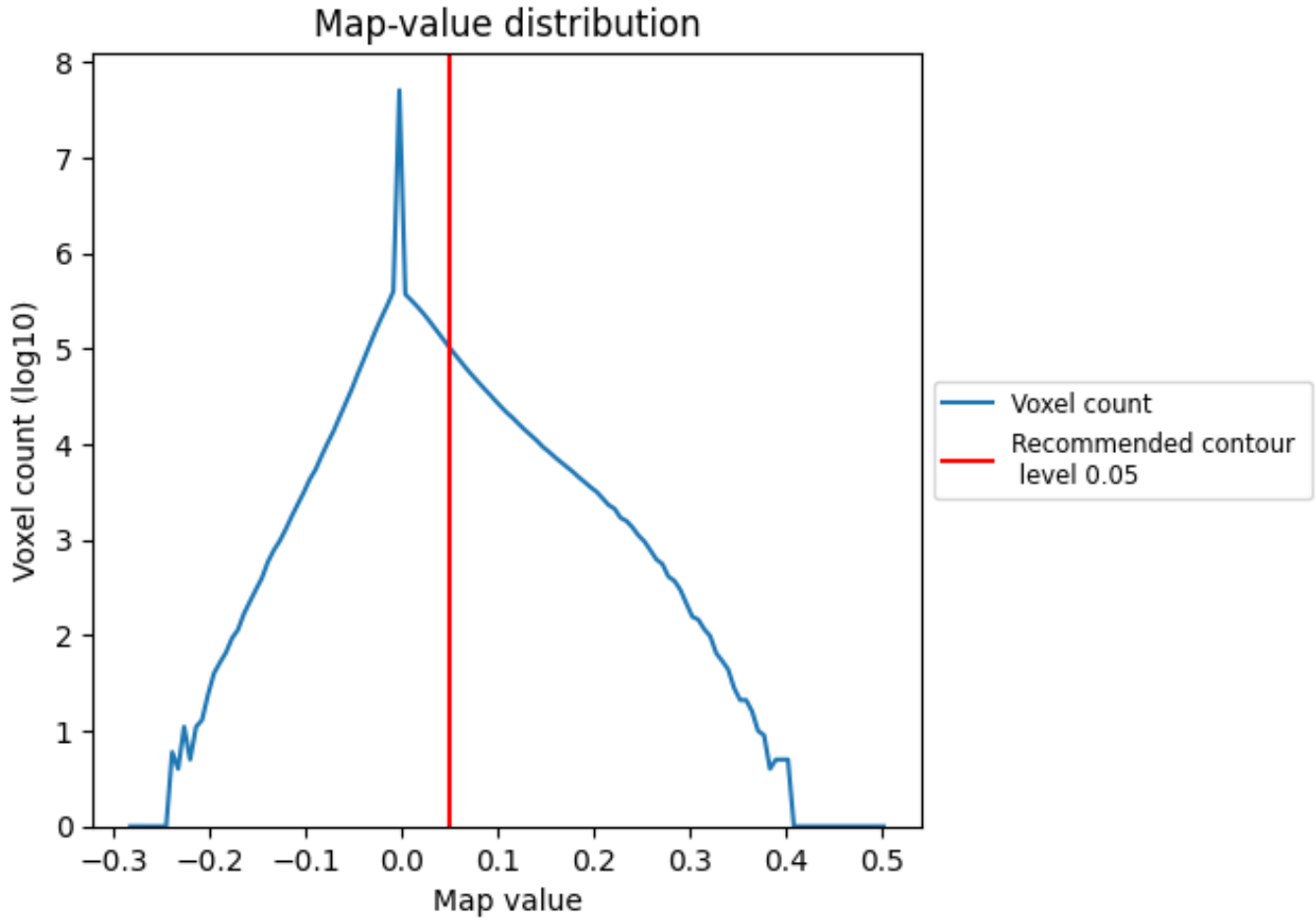
6.6 Mask visualisation (i)

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

7 Map analysis

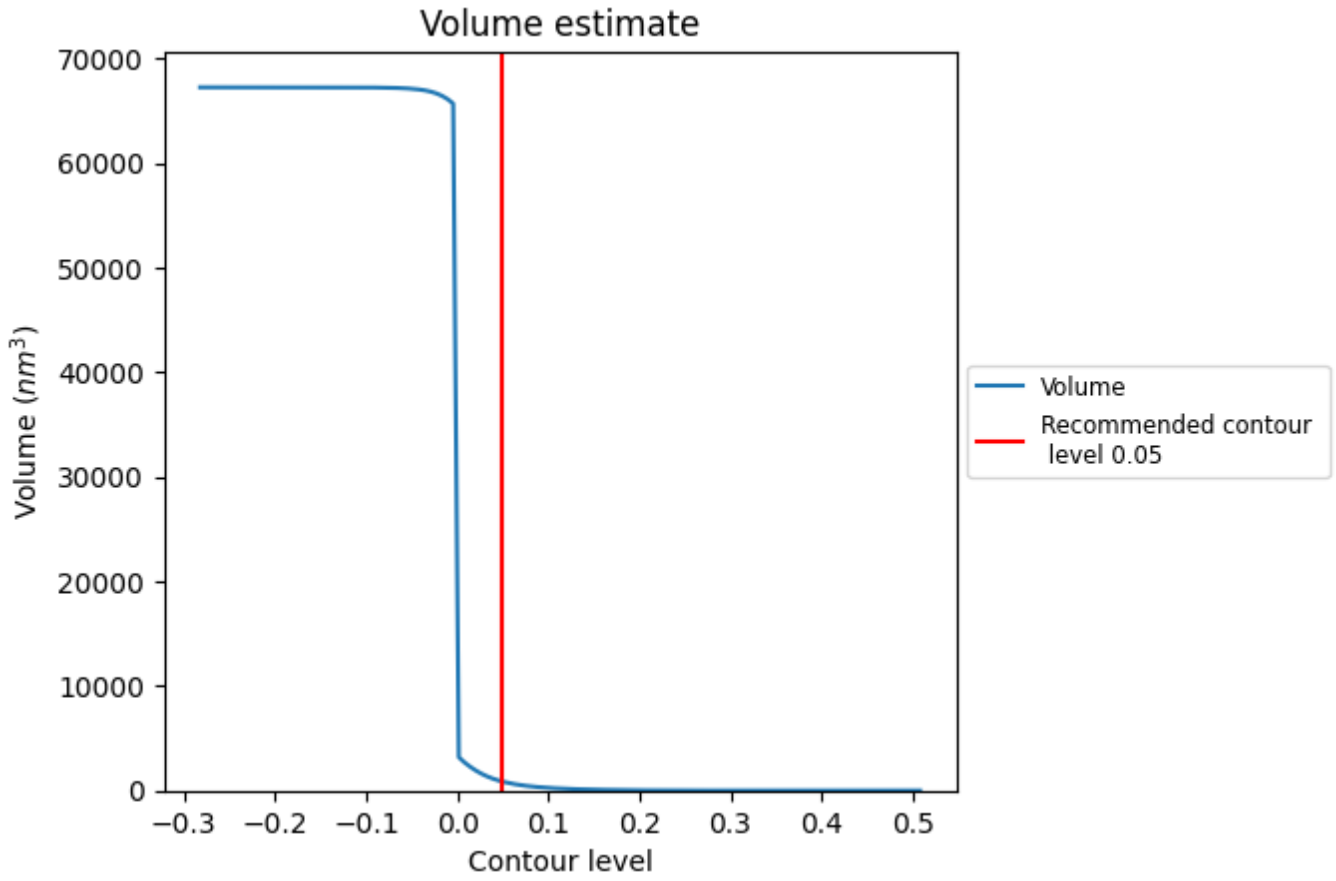
This section contains the results of statistical analysis of the map.

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.

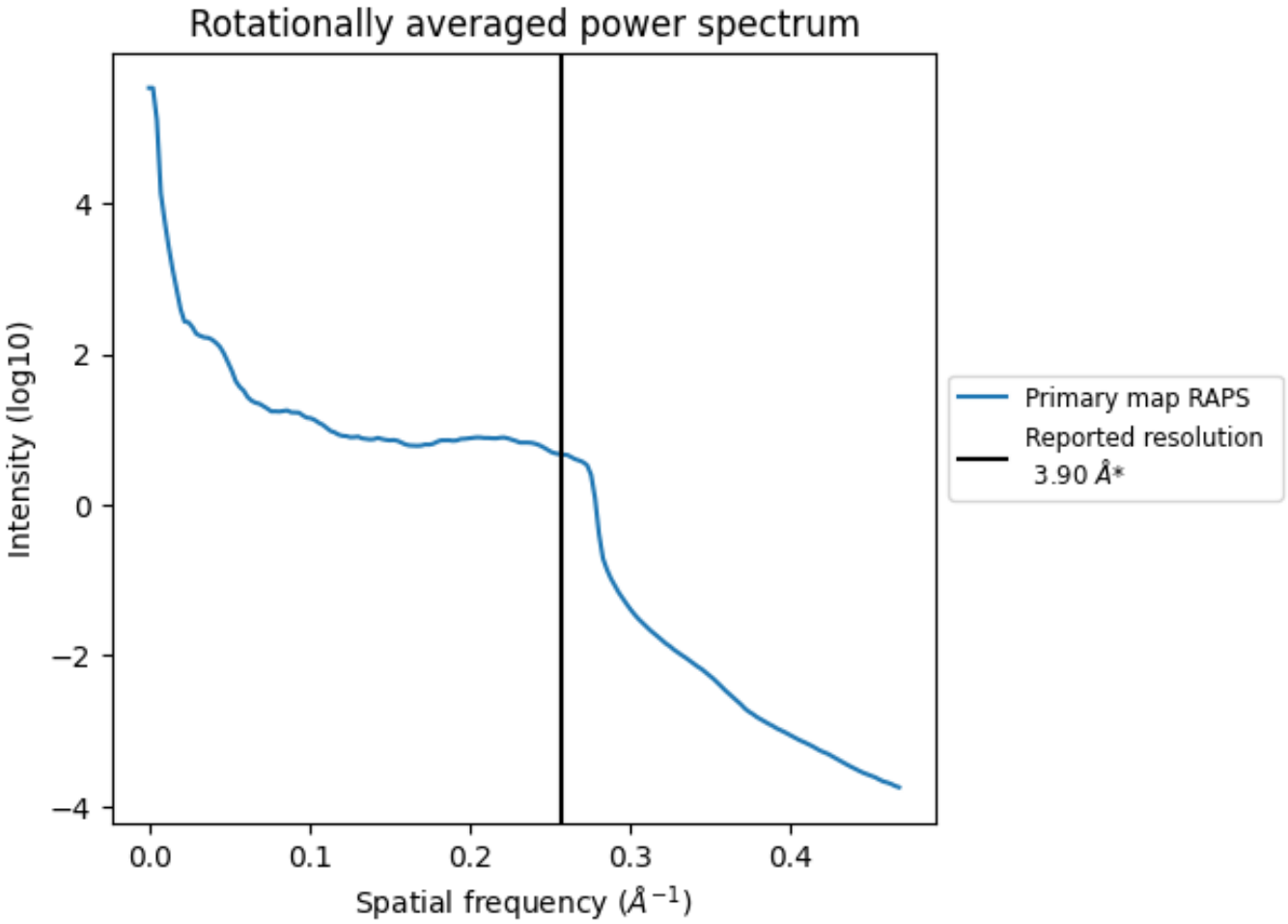
7.2 Volume estimate (i)



The volume at the recommended contour level is 855 nm^3; this corresponds to an approximate mass of 773 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 0.256 Å^{-1}

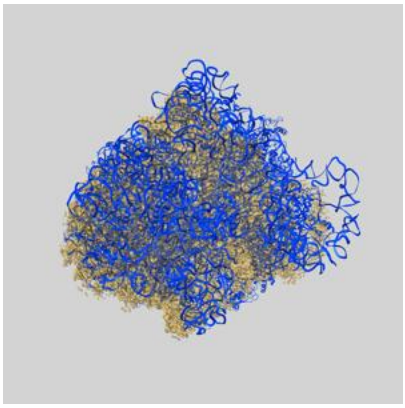
8 Fourier-Shell correlation

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

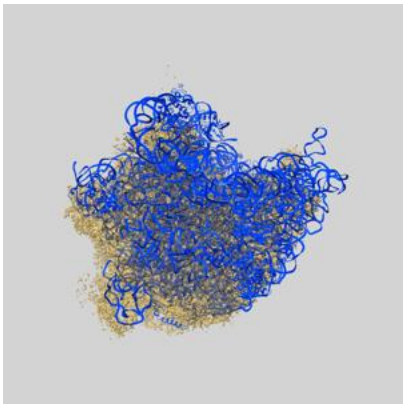
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4476 and PDB model 6Q97. Per-residue inclusion information can be found in section 3 on page 16.

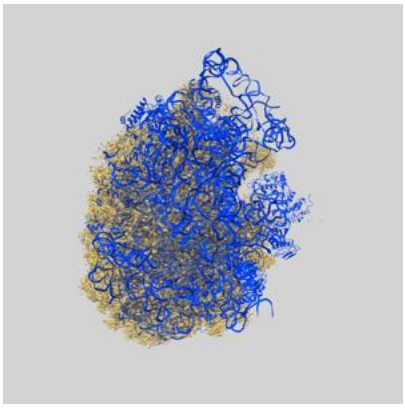
9.1 Map-model overlay



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05 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.

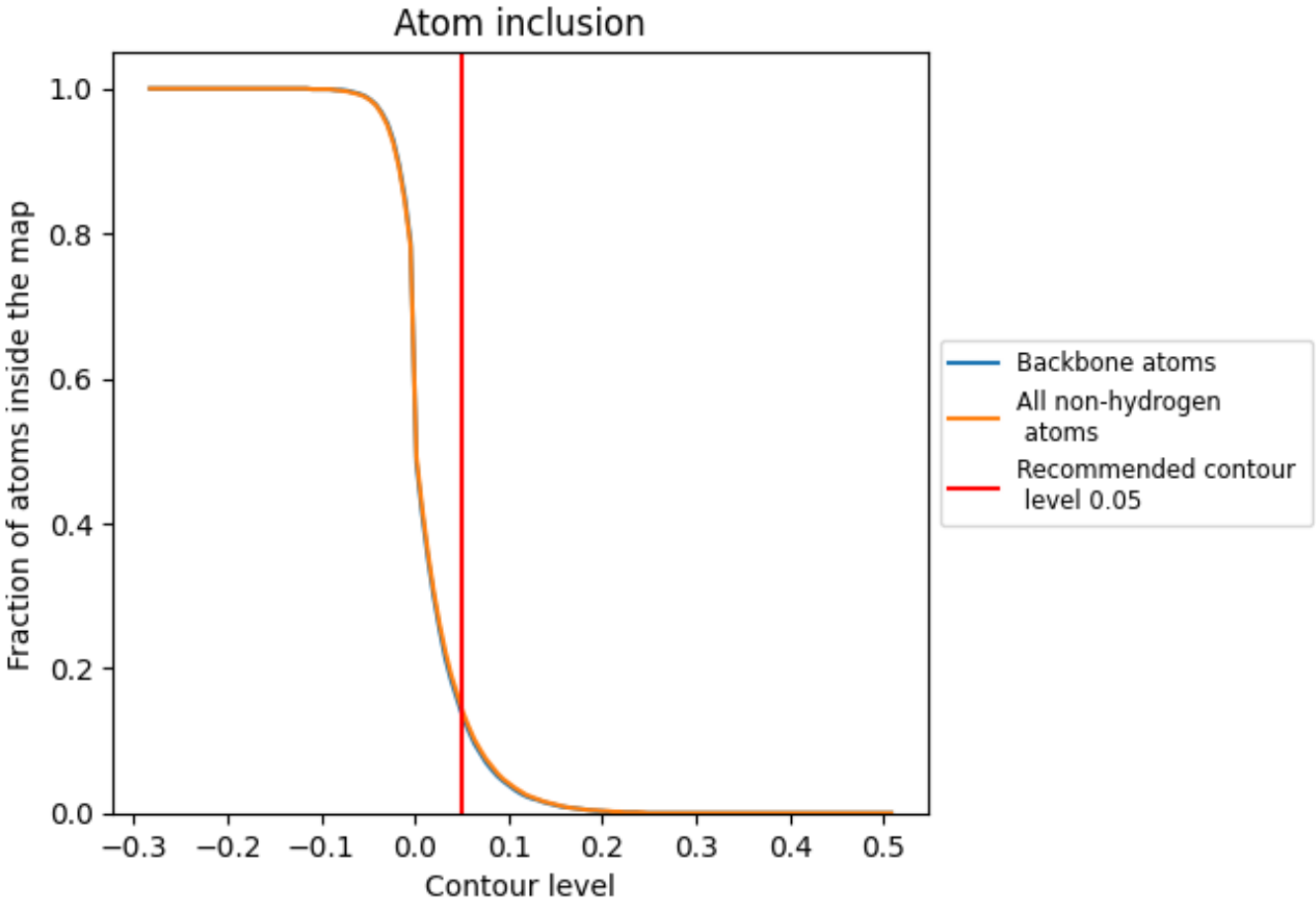
9.2 Q-score mapped to coordinate model

This section was not generated.

9.3 Atom inclusion mapped to coordinate model

This section was not generated.

9.4 Atom inclusion



At the recommended contour level, 14% of all backbone atoms, 14% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	0.1440
1	0.1690
2	0.1670
3	0.0810
4	0.0140
5	0.0260
6	0.1860
7	0.1050
8	0.1050
9	0.2340
B	0.1980
C	0.0560
D	0.1420
E	0.0460
F	0.0000
G	0.1630
H	0.0000
I	0.0000
J	0.0650
K	0.0710
L	0.2730
M	0.1040
N	0.1370
O	0.1820
P	0.1140
Q	0.1330
R	0.1360
S	0.2230
T	0.1900
U	0.1970
V	0.0240
W	0.1240
X	0.2190
Y	0.1330
Z	0.0900

Continued on next page...

Continued from previous page...

Chain	Atom inclusion
a	0.0350
b	0.1310
c	0.0860
d	0.2650
e	0.2750
f	0.0210
g	0.0090
h	0.0380
i	0.0230
j	0.0260
k	0.2410
l	0.3350
m	0.0070
n	0.1730
o	0.0580
p	0.1480
q	0.2100
r	0.2560
s	0.1080
t	0.3320
u	0.0180
v	0.0920
w	0.1950
x	0.1480
y	0.2090
z	0.1430