wwPDB EM Validation Summary Report (i)

Nov 7, 2026 – 01:26 pm GMT

PDB ID	:	9T8U / pdb_00009t8u
EMDB ID	:	EMD-55712
Title	:	Structural characterization of hibernating ribosomes in the Gram-negative pathogen Pseudomonas aeruginosa with bS21
Authors	:	Vasanthakrishnan, R.K.B.S.; Olivier, D.; Sophie, C.; Yann, L.C.; Sylvie, G.D.; Sassi, M.; Emmanuel, G.; Reynald, G.
Deposited on	:	2025-11-13
Resolution	:	2.79 Å(reported)
Based on initial model	:	7UNW

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

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

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

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

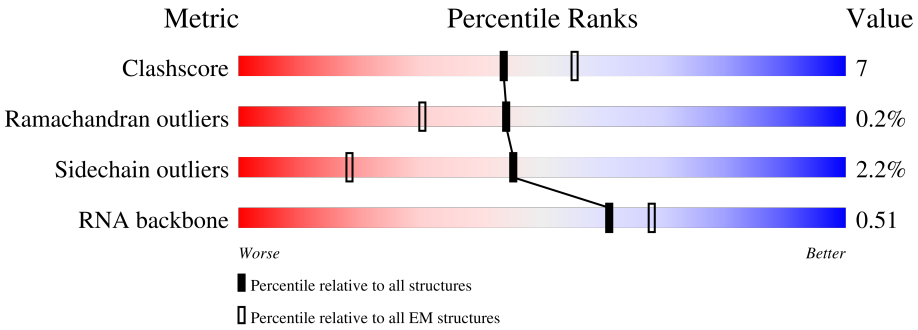
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

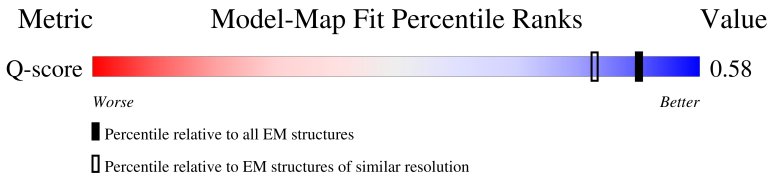
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.79 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.





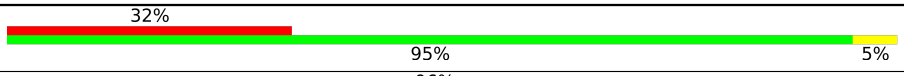
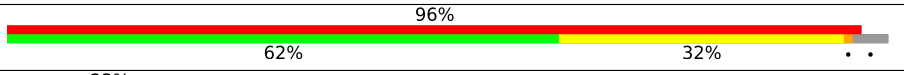
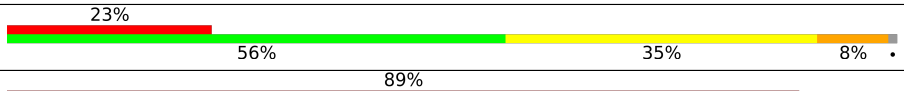
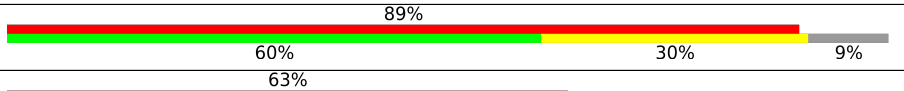
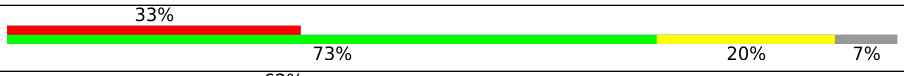
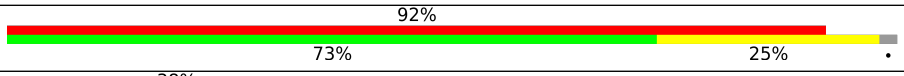
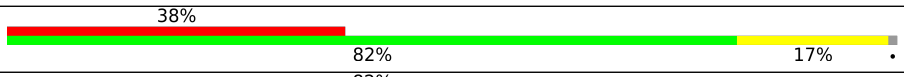
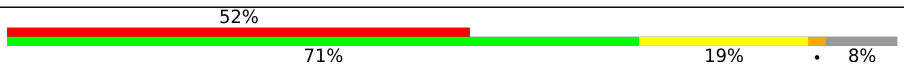
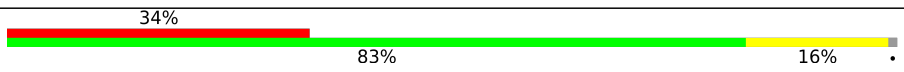
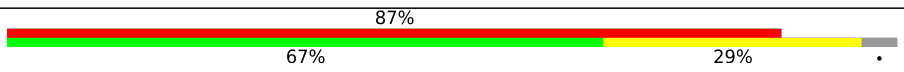
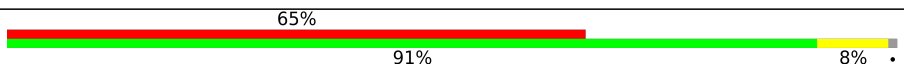
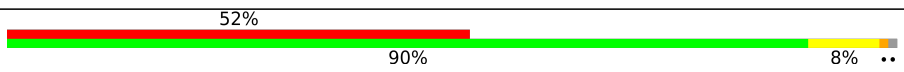
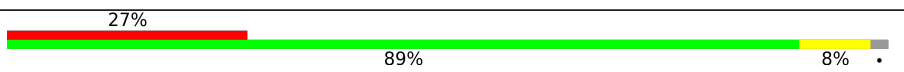
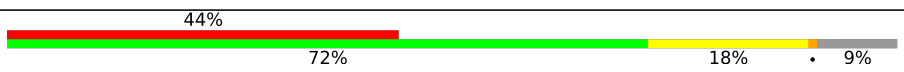
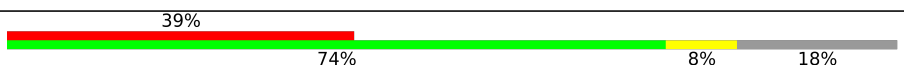
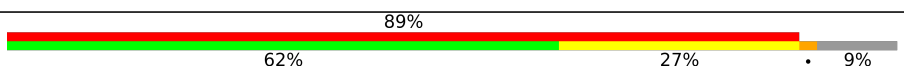
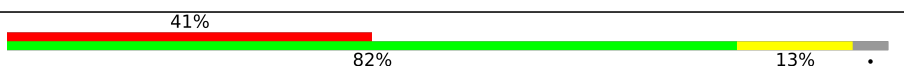
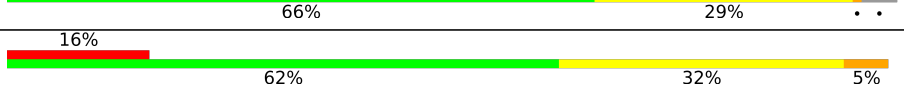
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10811 (2.29 - 3.29)

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	0	51	63% 78% 20% •
2	1	44	9% 86% 14%
3	2	64	14% 88% 11% •

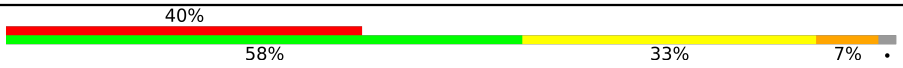
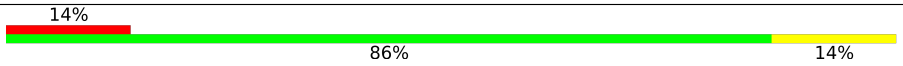
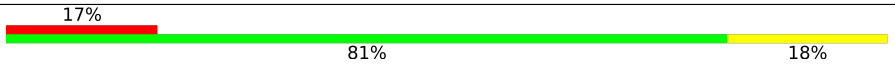
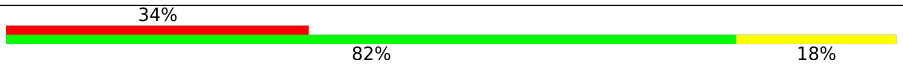
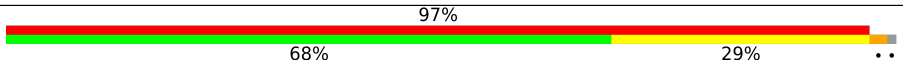
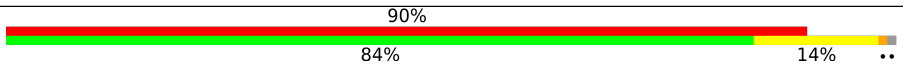
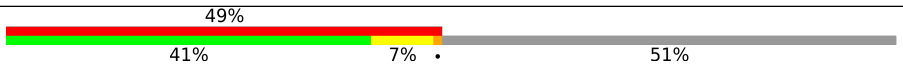
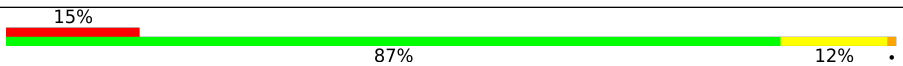
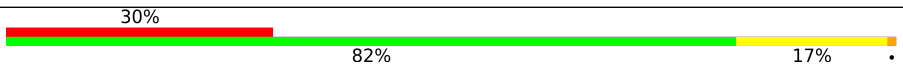
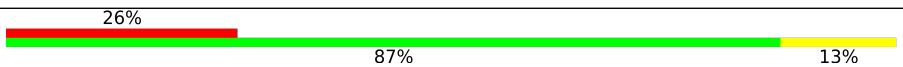
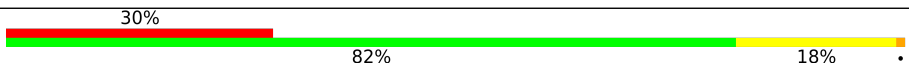
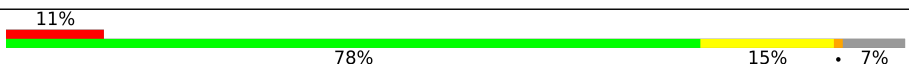
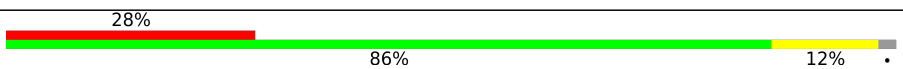
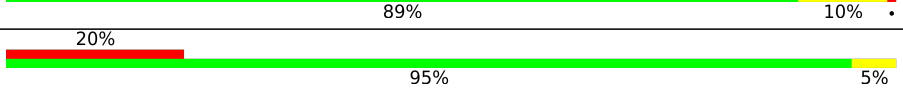
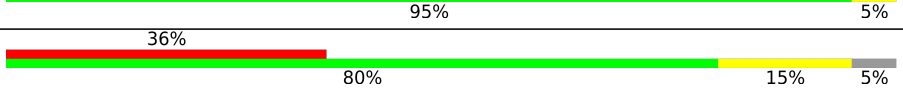
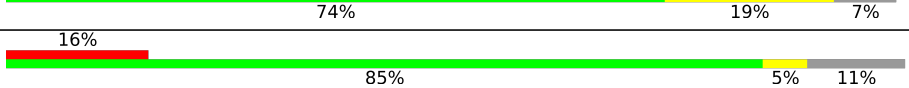
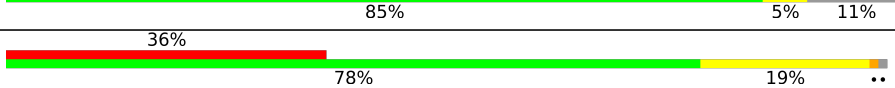
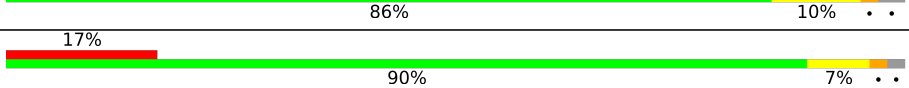
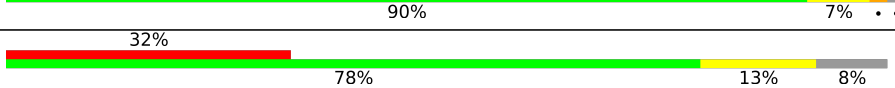
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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	71	
6	A	1536	
7	B	246	
8	C	228	
9	D	206	
10	E	166	
11	F	139	
12	G	156	
13	H	130	
14	I	130	
15	J	103	
16	K	129	
17	L	123	
18	M	118	
19	N	101	
20	O	89	
21	P	83	
22	Q	88	
23	R	76	
24	S	91	
25	T	91	
26	U	71	
27	X	102	
28	a	2891	

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Mol	Chain	Length	Quality of chain
29	b	120	
30	c	273	
31	d	211	
32	e	200	
33	f	179	
34	g	177	
35	h	148	
36	i	142	
37	j	122	
38	k	144	
39	l	137	
40	m	129	
41	n	116	
42	o	116	
43	p	118	
44	q	103	
45	r	110	
46	s	99	
47	t	104	
48	u	204	
49	v	85	
50	w	78	
51	x	63	
52	y	58	
53	z	60	

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 143222 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 protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	51	Total	C	N	O	S	0	0
			426	272	78	75	1		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			307	186	69	48	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	68	Total	C	N	O	S	0	0
			531	334	95	96	6		

- Molecule 6 is a RNA chain called 16S rRNA (1527-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	1527	Total	C	N	O	P	0	0
			32783	14628	6016	10612	1527		

- Molecule 7 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	224	Total	C	N	O	S	0	0
			1763	1112	322	319	10		

- Molecule 8 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	C	208	Total	C	N	O	S	0	0
			1664	1052	315	292	5		

- Molecule 9 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	D	205	Total	C	N	O	S	0	0
			1627	1003	316	303	5		

- Molecule 10 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E	154	Total	C	N	O	S	0	0
			1134	711	210	207	6		

- Molecule 11 is a protein called Small ribosomal subunit protein bS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	106	Total	C	N	O	S	0	0
			868	539	159	164	6		

- Molecule 12 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	153	Total	C	N	O	S	0	0
			1199	752	232	210	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	129	Total	C	N	O	S	0	0
			982	618	173	185	6		

- Molecule 14 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	127	Total	C	N	O	S	0	0
			1010	625	203	181	1		

- Molecule 15 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	J	99	Total	C	N	O	S	0	0
			793	496	150	146	1		

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	119	Total	C	N	O	S	0	0
			882	546	171	163	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	conflict	UNP E2RXU4

- Molecule 17 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	122	Total	C	N	O	S	0	0
			961	589	198	169	5		

- Molecule 18 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	113	Total	C	N	O	S	0	0
			883	541	178	160	4		

- Molecule 19 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	100	Total	C	N	O	S	0	0
			804	496	167	138	3		

- Molecule 20 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	88	Total	C	N	O	S	0	0
			703	434	139	129	1		

- Molecule 21 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	81	Total	C	N	O	S	0	0
			637	398	125	113	1		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	80	Total	C	N	O	S	0	0
			645	404	124	115	2		

- Molecule 23 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	R	62	Total	C	N	O	0	0
			494	316	86	92		

- Molecule 24 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	S	83	Total	C	N	O	S	0	0
			663	422	129	109	3		

- Molecule 25 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	87	Total	C	N	O	S	0	0
			671	414	138	117	2		

- Molecule 26 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	U	62	Total	C	N	O	S	0	0
			506	316	103	86	1		

- Molecule 27 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	98	Total	C	N	O	S	0	0
			796	498	143	152	3		

- Molecule 28 is a RNA chain called 23S rRNA (2890-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	2890	Total	C	N	O	P	0	0
			62019	27677	11363	20089	2890		

- Molecule 29 is a RNA chain called 5S rRNA (117-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	117	Total	C	N	O	P	0	0
			2495	1114	448	816	117		

- Molecule 30 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	272	Total	C	N	O	S	0	0
			2072	1276	426	364	6		

- Molecule 31 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	211	Total	C	N	O	S	0	0
			1589	982	304	297	6		

- Molecule 32 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	200	Total	C	N	O	S	0	0
			1524	956	283	282	3		

- Molecule 33 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	177	Total	C	N	O	S	0	0
			1418	905	253	256	4		

- Molecule 34 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	175	Total	C	N	O	S	0	0
			1326	835	244	245	2		

- Molecule 35 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	72	Total	C	N	O	S	0	0
			533	334	98	100	1		

- Molecule 36 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	142	Total	C	N	O	S	0	0
			1130	718	206	202	4		

- Molecule 37 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 39 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	137	Total	C	N	O	S	0	0
			1086	689	211	181	5		

- Molecule 40 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	120	Total	C	N	O	S	0	0
			959	600	192	162	5		

- Molecule 41 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	115	Total 881	C 544	N 174	O 161	S 2	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	114	Total 902	C 568	N 171	O 162	S 1	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	p	117	Total 936	C 592	N 196	O 148	0	0

- Molecule 44 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	103	Total 822	C 521	N 156	O 143	S 2	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	110	Total 833	C 515	N 161	O 153	S 4	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	94	Total 739	C 472	N 134	O 132	S 1	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	103	Total 800	C 503	N 152	O 143	S 2	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	190	Total	C	N	O	S	0	0
			1446	915	262	266	3		

- Molecule 49 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	v	76	Total	C	N	O	0	0
			575	364	111	100		

- Molecule 50 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 51 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	61	Total	C	N	O	S	0	0
			490	301	96	91	2		

- Molecule 52 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	57	Total	C	N	O	S	0	0
			445	277	87	79	2		

- Molecule 53 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	55	Total	C	N	O	S	0	0
			440	264	93	82	1		

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
54	3	1	Total	Zn	0
			1	1	
54	4	1	Total	Zn	0
			1	1	

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
55	A	93	Total Mg 93 93	0
55	M	1	Total Mg 1 1	0
55	X	1	Total Mg 1 1	0
55	a	251	Total Mg 251 251	0
55	b	5	Total Mg 5 5	0
55	c	1	Total Mg 1 1	0
55	p	1	Total Mg 1 1	0
55	z	1	Total Mg 1 1	0

- Molecule 56 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	AltConf
56	A	49	Total K 49 49	0
56	a	114	Total K 114 114	0
56	b	1	Total K 1 1	0
56	c	3	Total K 3 3	0
56	e	1	Total K 1 1	0
56	f	1	Total K 1 1	0

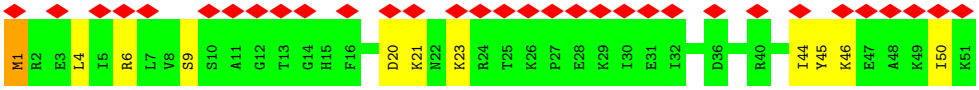
3 Residue-property plots (i)

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: Large ribosomal subunit protein bL33

Chain 0:

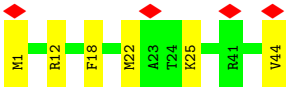




• Molecule 2: Large ribosomal subunit protein bL34

Chain 1:

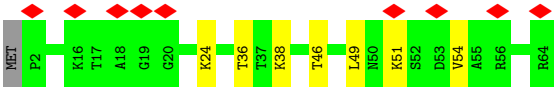




• Molecule 3: Large ribosomal subunit protein bL35

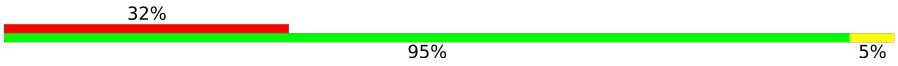
Chain 2:

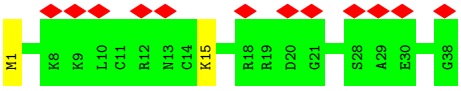




• Molecule 4: Large ribosomal subunit protein bL36

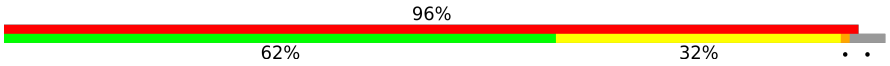
Chain 3:

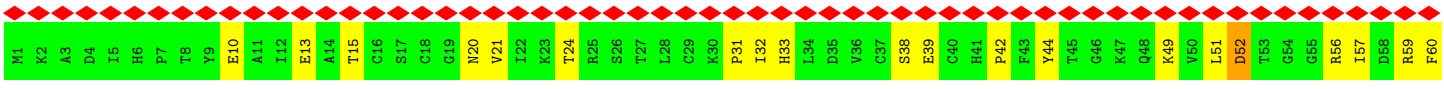


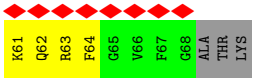


• Molecule 5: Large ribosomal subunit protein bL31

Chain 4:



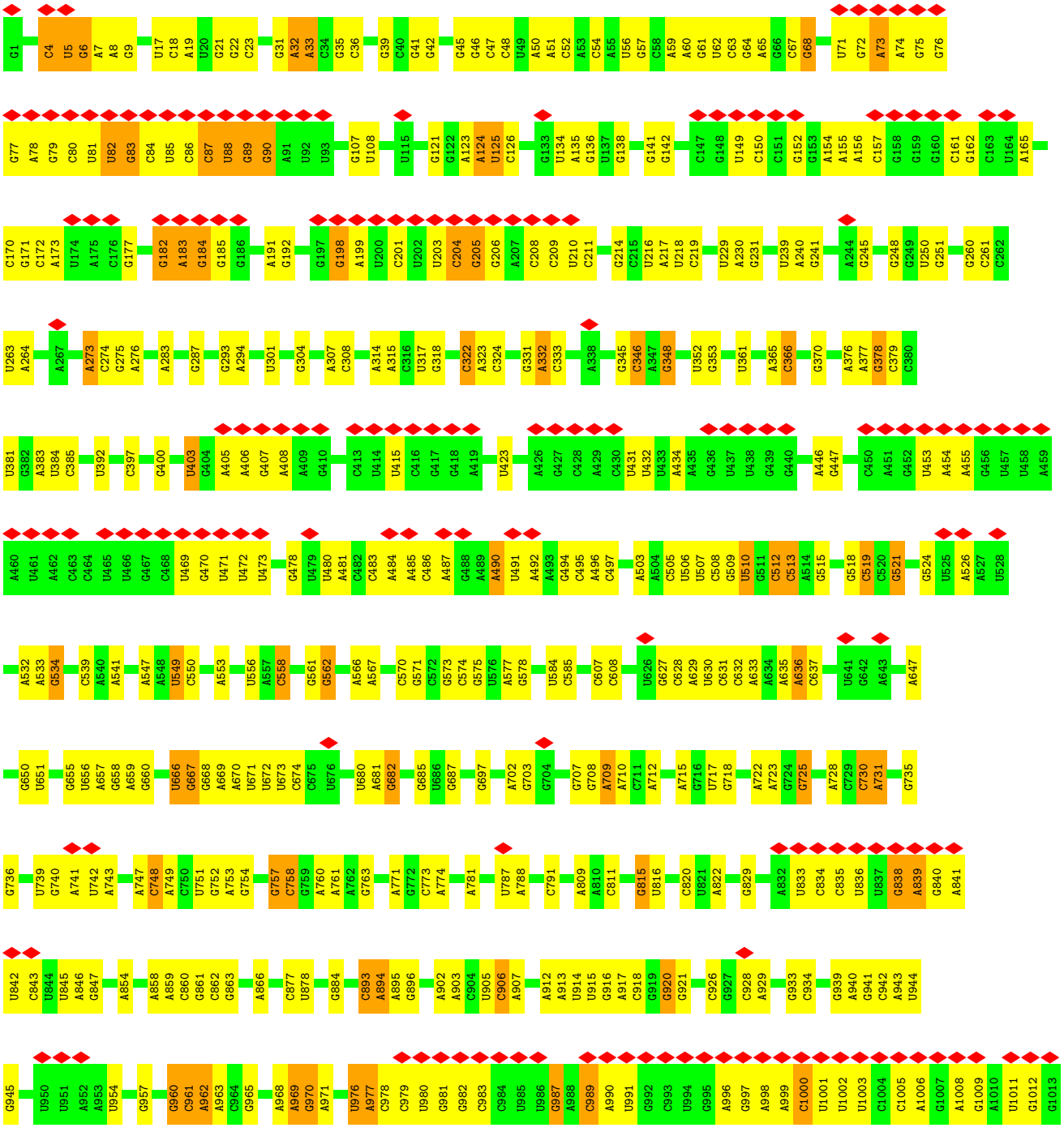


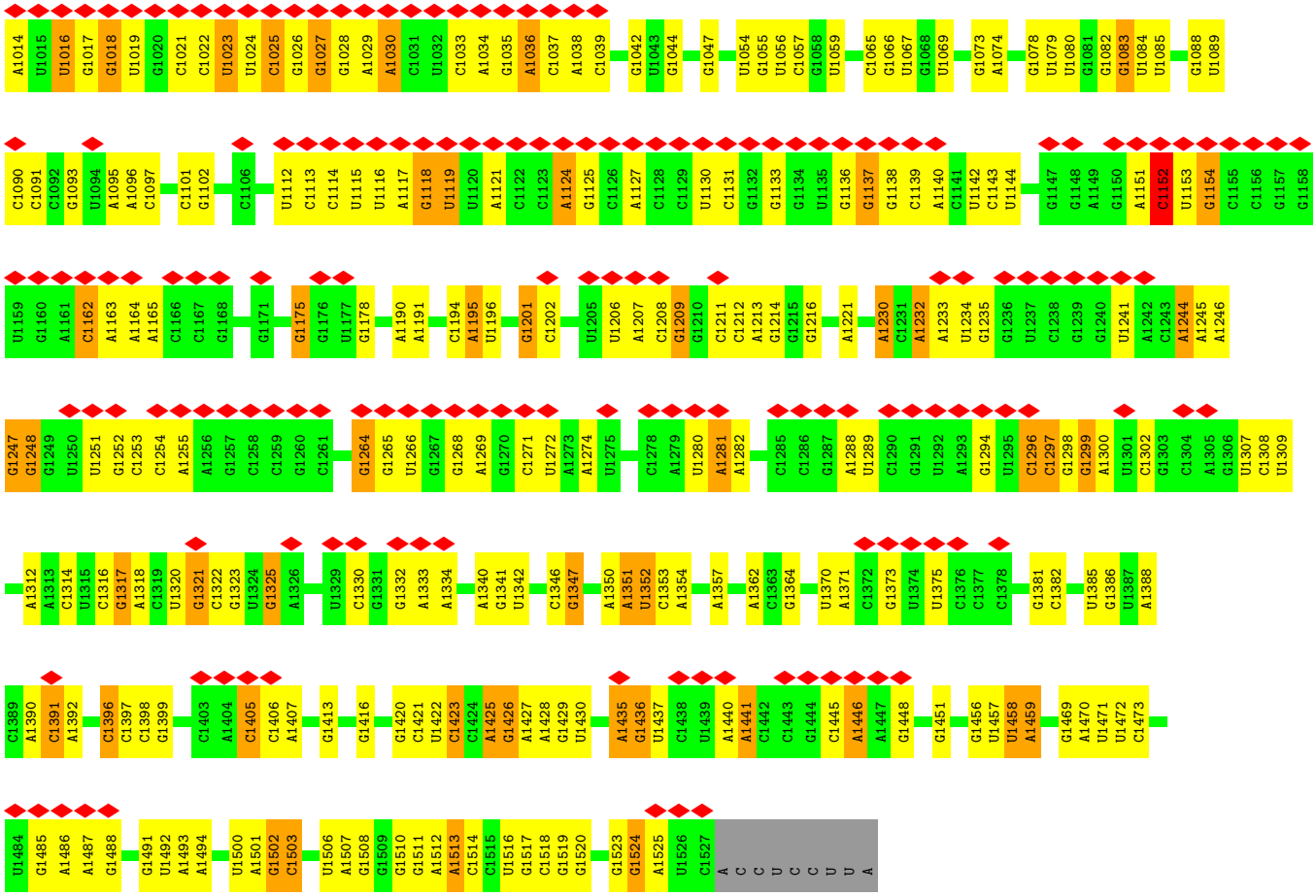


• Molecule 6: 16S rRNA (1527-MER)

Chain A:

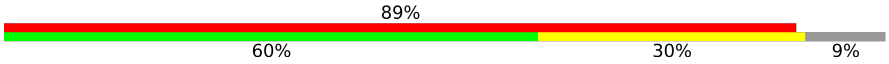






• Molecule 7: Small ribosomal subunit protein uS2

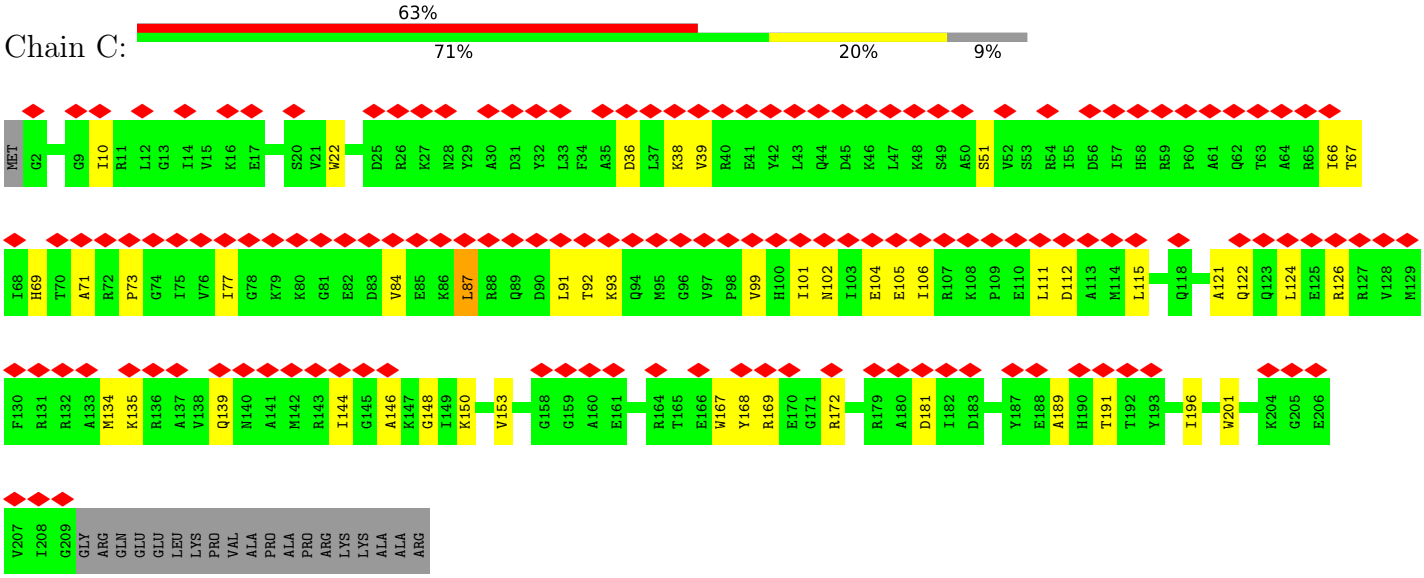
Chain B:





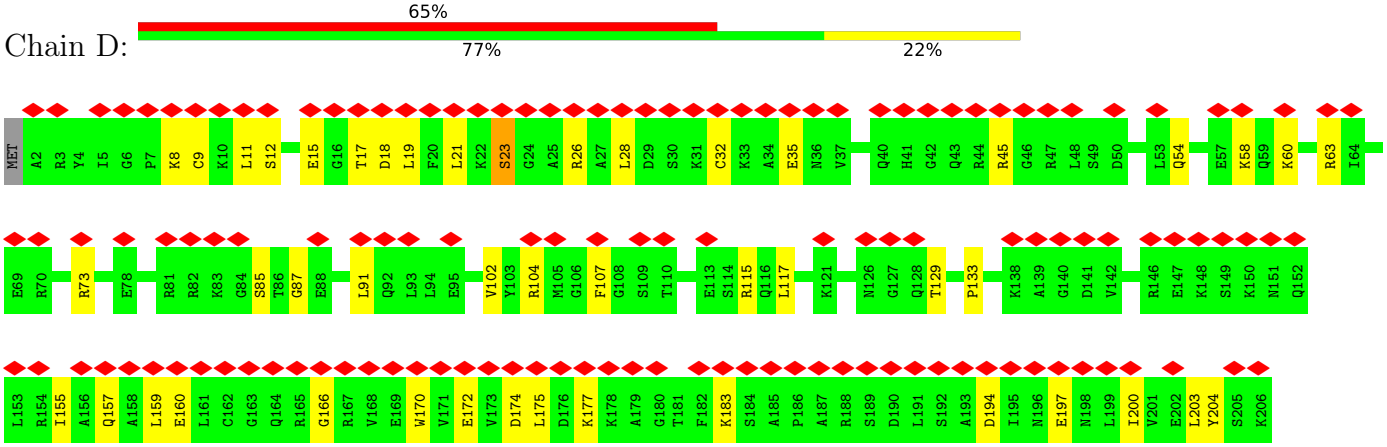
• Molecule 8: Small ribosomal subunit protein uS3

Chain C:



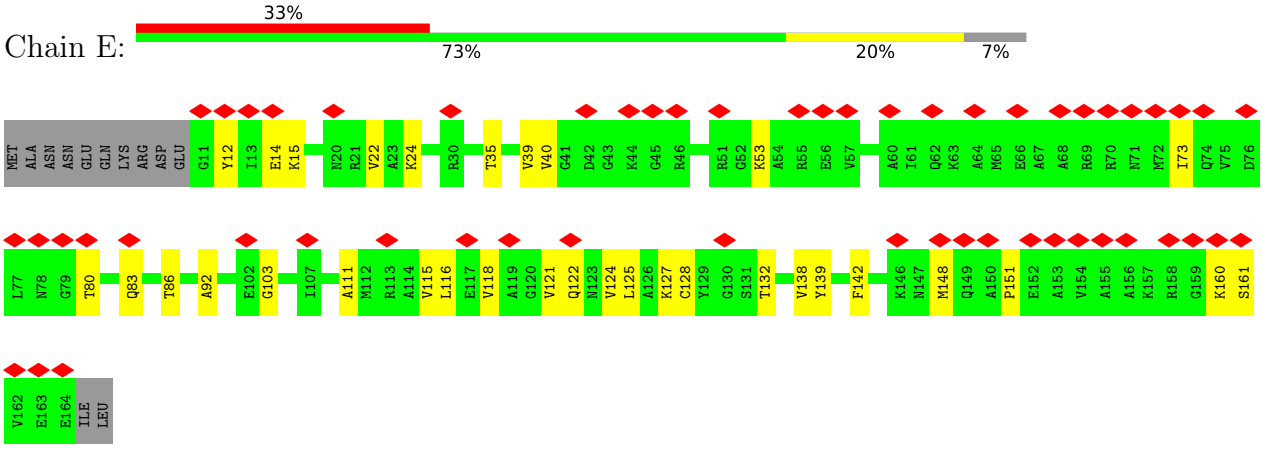
• Molecule 9: Small ribosomal subunit protein uS4

Chain D:



• Molecule 10: Small ribosomal subunit protein uS5

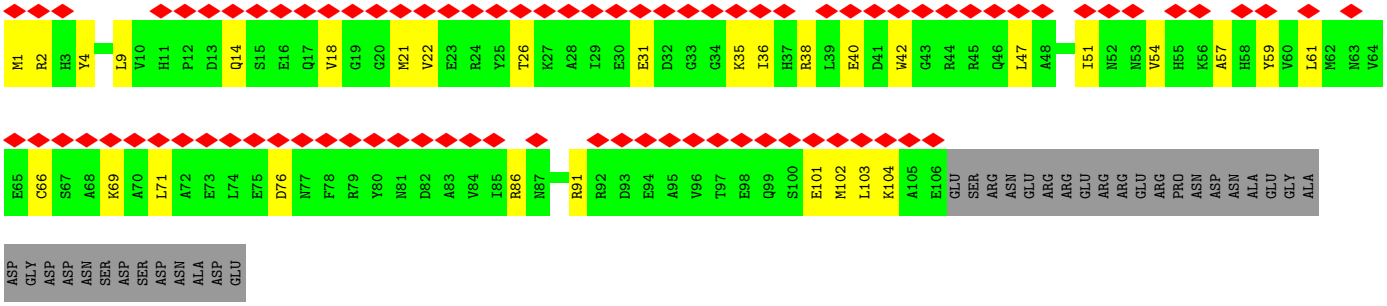
Chain E:



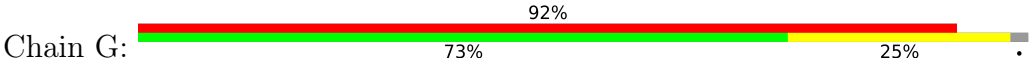
• Molecule 11: Small ribosomal subunit protein bS6

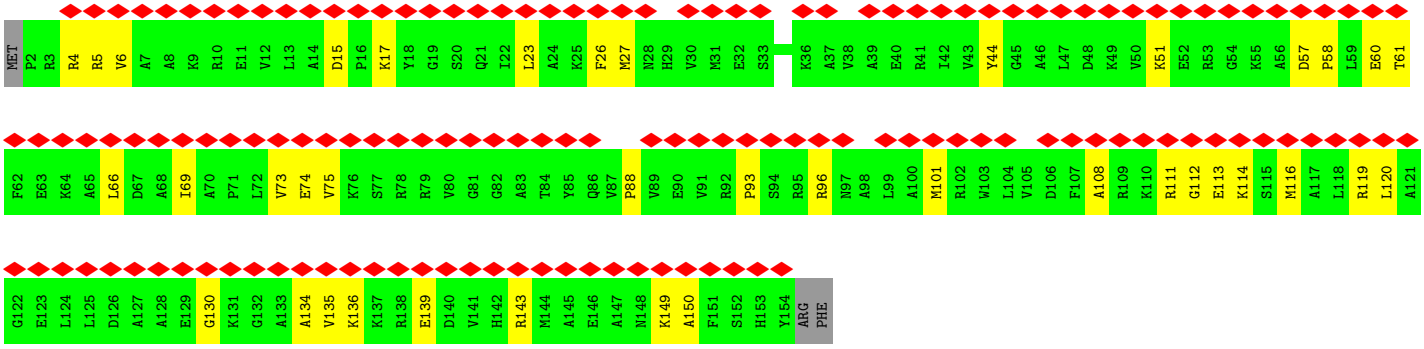
Chain F:



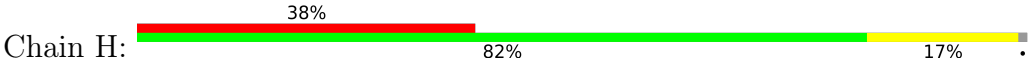


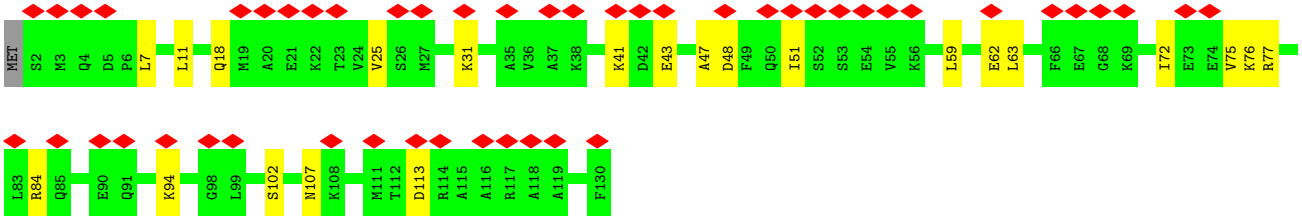
• Molecule 12: Small ribosomal subunit protein uS7



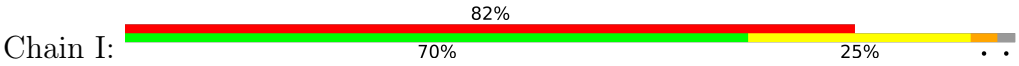


• Molecule 13: Small ribosomal subunit protein uS8





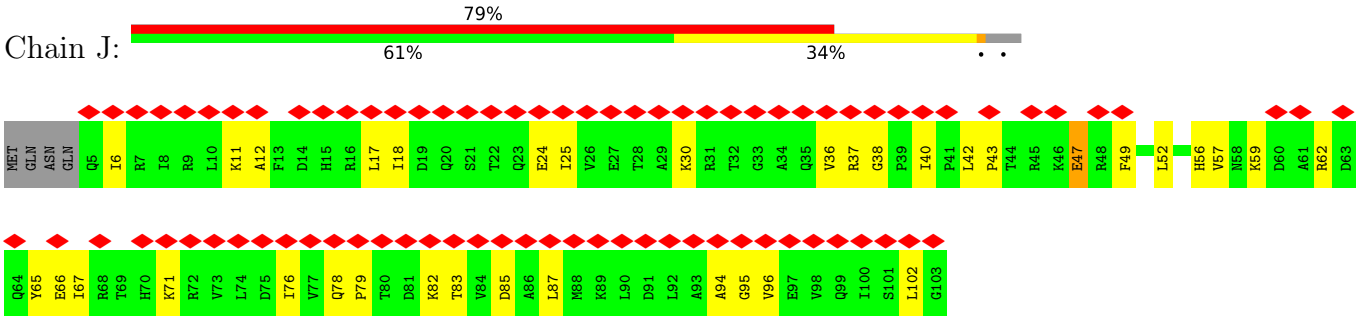
• Molecule 14: Small ribosomal subunit protein uS9





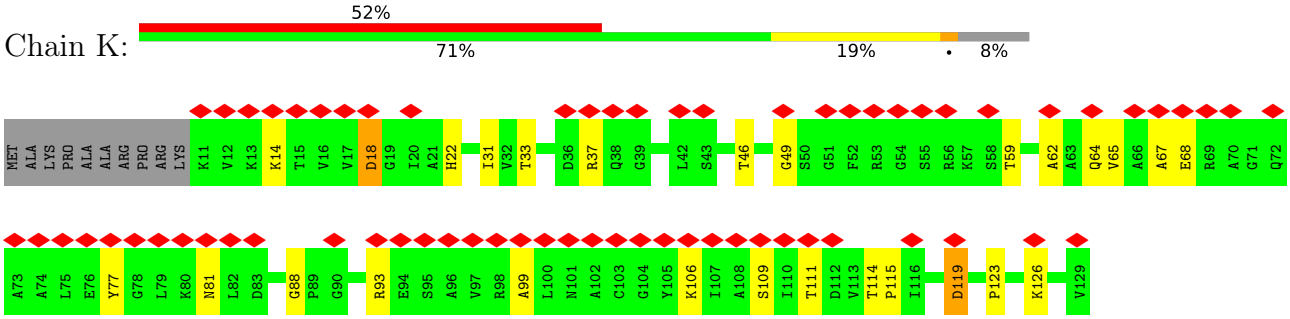
• Molecule 15: Small ribosomal subunit protein uS10

Chain J:



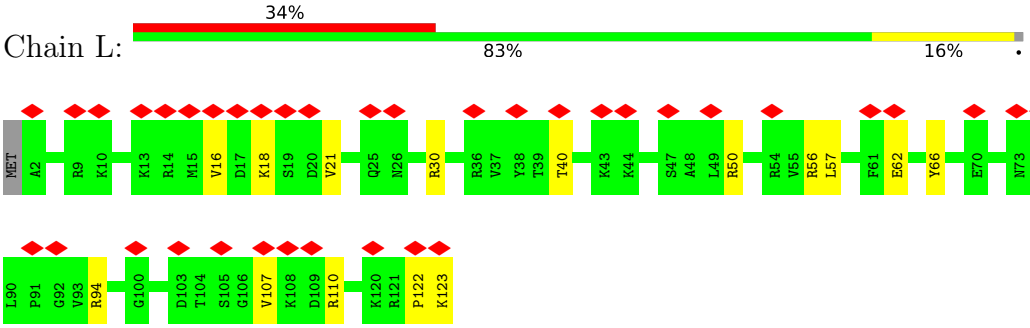
• Molecule 16: Small ribosomal subunit protein uS11

Chain K:



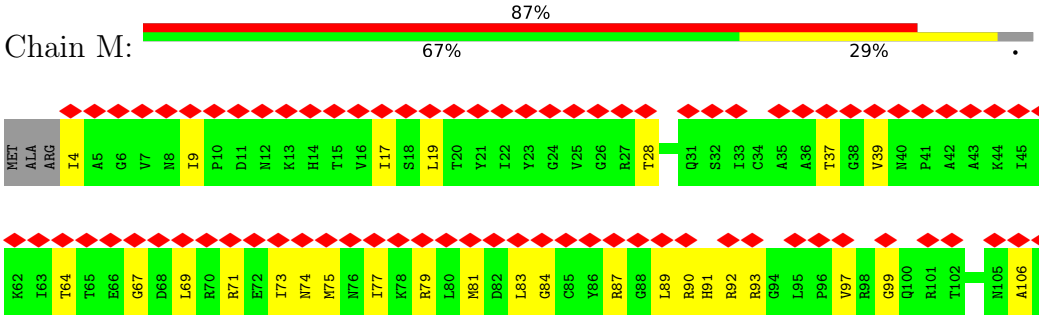
• Molecule 17: Small ribosomal subunit protein uS12

Chain L:



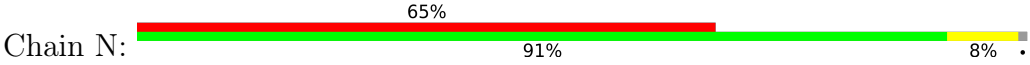
• Molecule 18: Small ribosomal subunit protein uS13

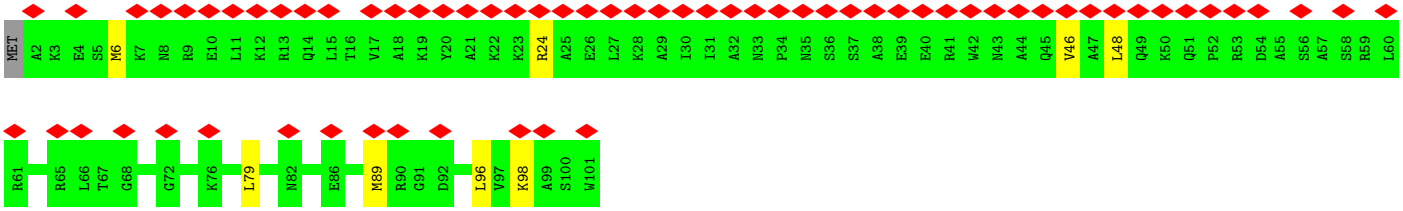
Chain M:



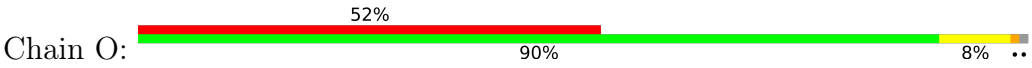
• Molecule 19: Small ribosomal subunit protein uS14

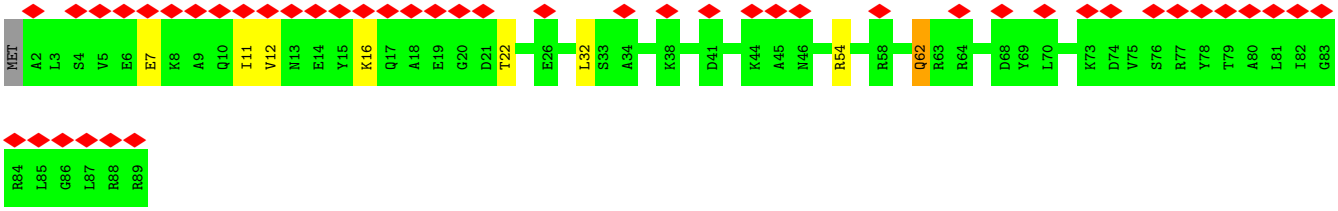
Chain N:



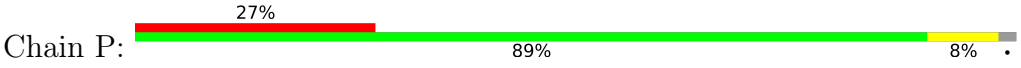


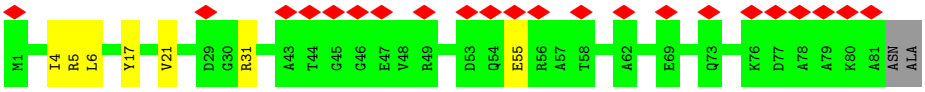
• Molecule 20: Small ribosomal subunit protein uS15





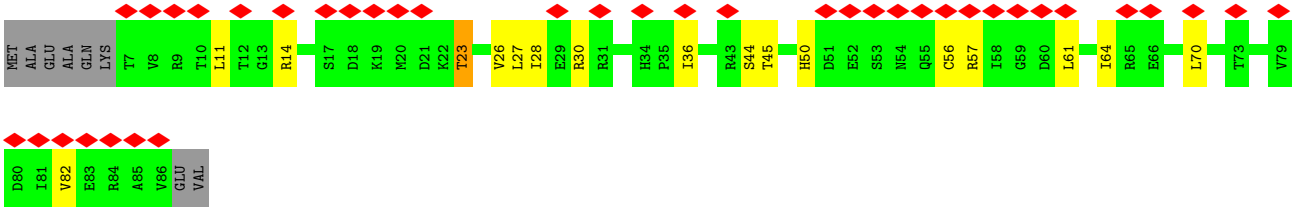
• Molecule 21: Small ribosomal subunit protein bS16





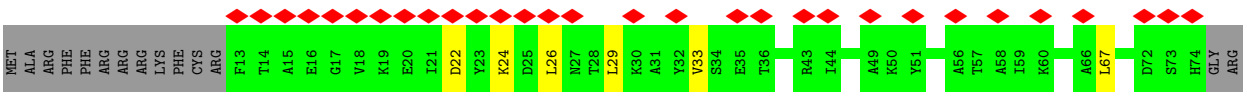
• Molecule 22: Small ribosomal subunit protein uS17



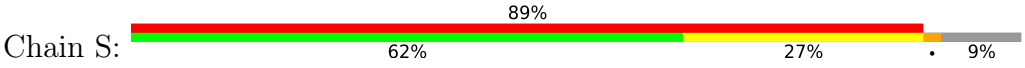


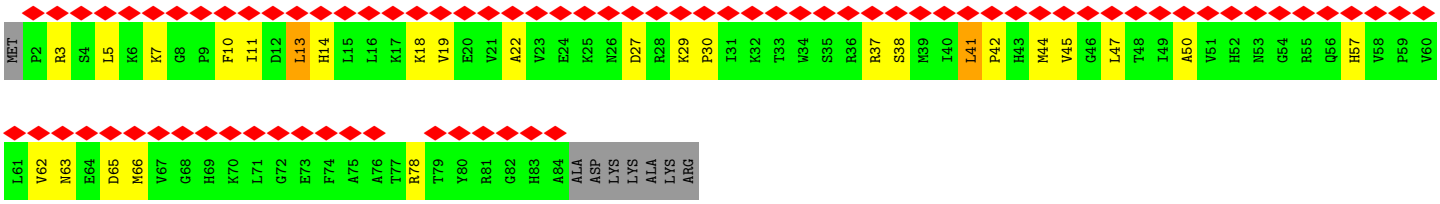
• Molecule 23: Small ribosomal subunit protein bS18





• Molecule 24: Small ribosomal subunit protein uS19

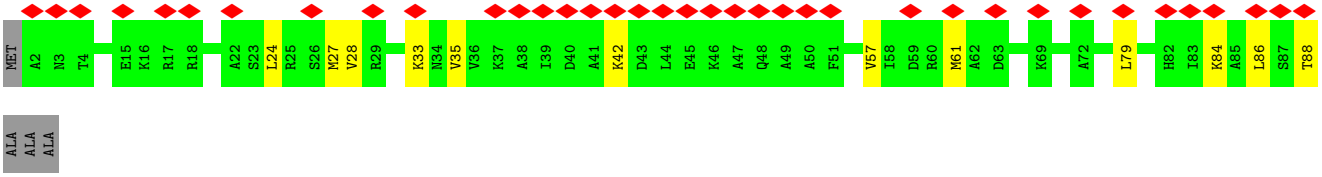




• Molecule 25: Small ribosomal subunit protein bS20

Chain T:

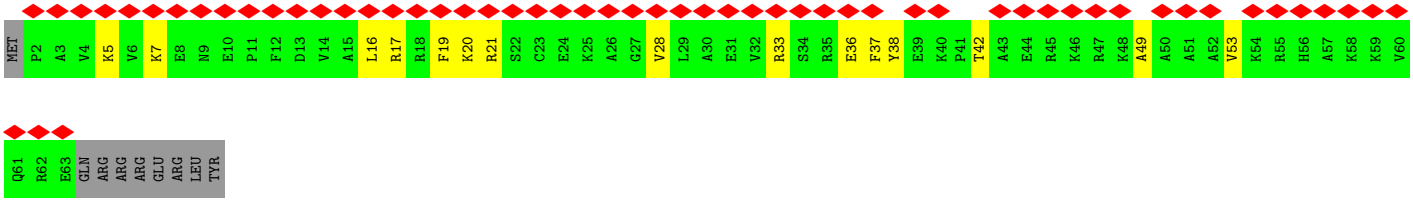




• Molecule 26: Small ribosomal subunit protein bS21

Chain U:

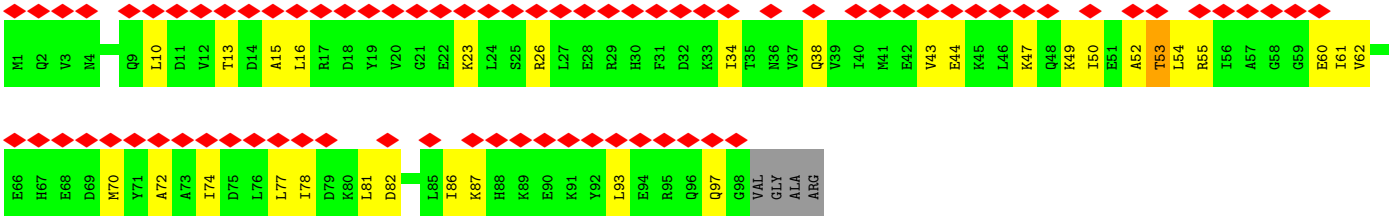




• Molecule 27: Ribosome hibernation promoting factor

Chain X:

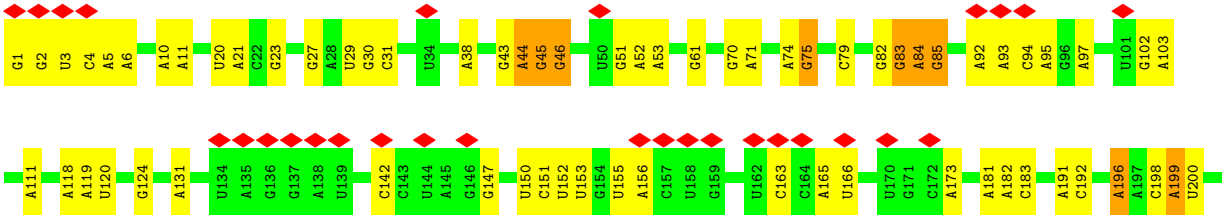


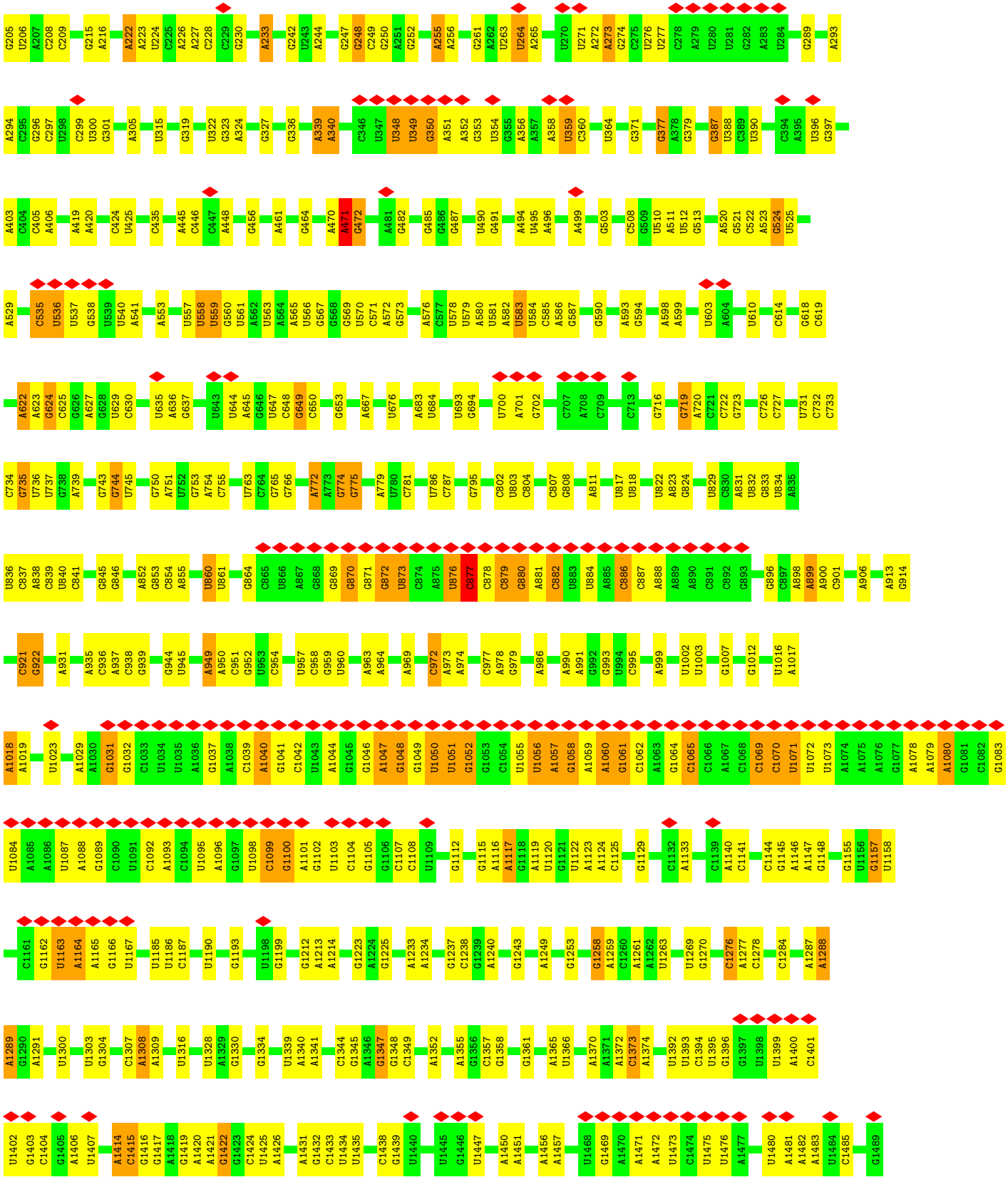


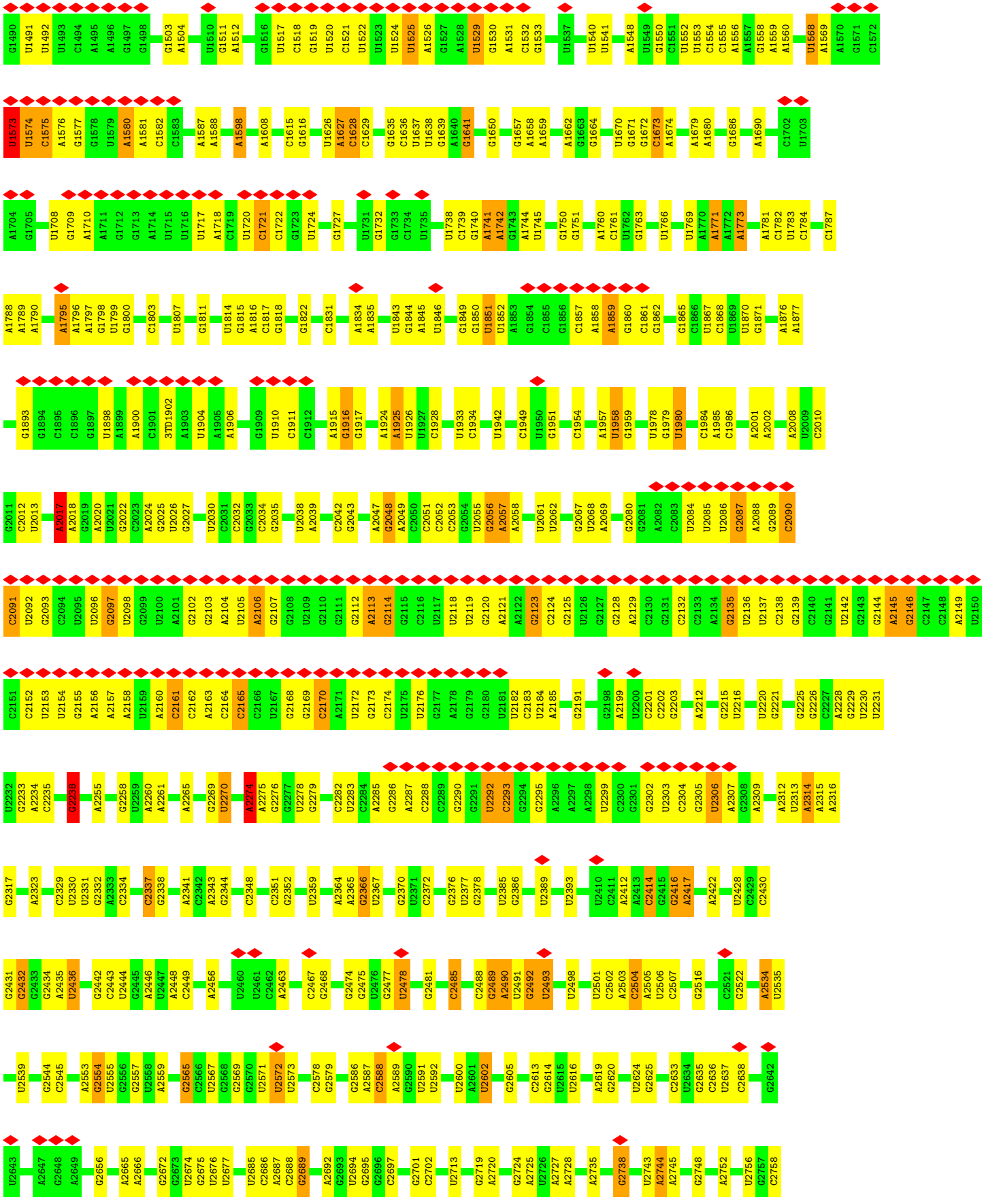
• Molecule 28: 23S rRNA (2890-MER)

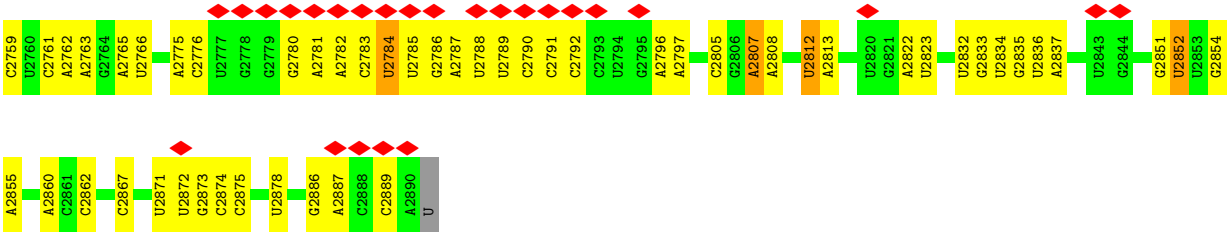
Chain a:






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A294 C295 G296 C297 U298 C299 U300 G301 A305 U315 G319 U322 G323 A324 G327 G336 A339 A340 C346 U347 U348 U349 G350 A351 A352 G353 U354 G355 A356 A357 A358 U359 C360 U364 G371 G377 A378 G379 G387 U388 C389 U390 C394 A395 U396 G397
A403 C404 C405 A406 A419 A420 C424 U425 C435 A445 C446 C447 A448 G456 A461 G464 A470 A471 G472 A481 G482 G485 G486 G487 U490 G491 A494 U495 A496 A499 G503 C508 G509 U510 A511 U512 G513 A520 G521 C522 A523 G524 U525
A529 C535 U536 U537 G538 U539 U540 A541 A553 U557 U558 U559 G560 U561 A562 U563 A564 A565 U566 G567 G568 G569 U570 C571 A572 G573 A576 C577 U578 U579 A580 U581 A582 U583 U584 C585 A586 G587 G590 A593 G594 A598 A599 U603 A604 U610 C614 G618 C619
A622 A623 G624 C625 G626 A627 G628 U629 C630 U635 A636 G637 U643 U644 A645 G646 U647 C648 G649 C650 G653 A667 U676 A683 U684 U693 G694 U700 A701 G702 C707 A708 C709 C713 G716 G719 A720 C721 C722 G723 C726 C727 U731 C732 C733
C734 G735 U736 U737 G738 A739 G743 G744 U745 G750 A751 U752 G753 A754 C755 U763 C764 G765 G766 A772 A773 G774 G775 A779 U780 C781 U786 C787 G795 C802 U803 C804 C807 G808 A811 U817 U818 U822 A823 G824 U829 C830 A831 U832 G833 U834 A835
U836 C837 A838 C839 U840 C841 G845 G846 A852 G853 C854 A855 U860 U861 G864 C865 U866 A867 G868 G869 G870 G871 G872 U873 C874 A875 U876 C877 C878 C879 G880 A881 C882 U883 U884 A885 C886 C887 A888 A889 A890 C891 C892 G893 G896 C897 A898 A899 A900 C901 A906 A913 G914
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A1018 A1019 U1023 A1029 A1030 G1031 G1032 C1033 U1034 U1035 A1036 G1037 A1038 C1039 A1040 G1041 C1042 U1043 A1044 G1045 G1046 A1047 G1048 G1049 U1050 U1051 G1052 G1053 C1054 U1055 U1056 A1057 G1058 A1059 A1060 G1061 C1062 A1063 G1064 C1065 C1066 A1067 C1068 C1069 C1070 U1071 U1072 U1073 A1074 A1075 A1076 G1077 A1078 A1079 A1080 G1081 C1082 G1083
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C1161 G1162 U1163 A1164 A1165 G1166 U1167 U1185 U1186 C1187 U1190 G1193 U1198 G1199 G1212 A1213 A1214 G1223 A1224 G1225 A1233 A1234 G1237 C1238 G1239 A1240 G1243 A1249 G1253 G1258 A1259 C1260 A1261 A1262 U1263 U1269 G1270 C1276 A1277 C1278 C1284 A1287 A1288
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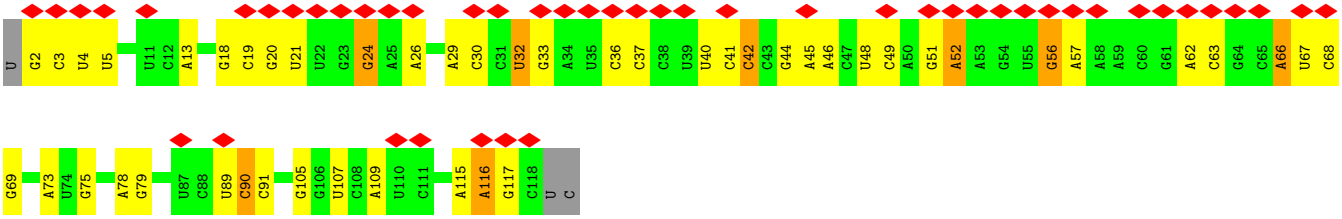

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U1573 U1574 C1575 A1576 G1577 G1578 U1579 A1580 A1581 C1582 C1583 A1587 A1588 A1598 A1608 C1615 G1616 U1626 A1627 C1628 C1629 G1635 C1636 U1637 U1638 G1639 A1640 G1641 G1650 G1657 A1658 A1659 A1662 G1663 G1664 U1670 G1671 G1672 C1673 A1674 A1679 A1680 G1686 A1690 C1702 U1703
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A1788 A1789 A1790 A1795 A1796 A1797 G1798 U1799 G1800 C1803 U1807 G1811 U1814 G1815 A1816 C1817 G1818 G1822 C1831 A1834 A1835 U1843 G1844 A1845 U1846 G1849 G1850 U1851 U1852 A1853 G1854 C1855 G1856 C1857 A1858 A1859 G1860 C1861 G1862 G1865 C1866 U1867 C1868 U1869 U1870 G1871 A1876 A1877
G1893 G1894 C1895 C1896 G1897 U1898 A1899 A1900 C1901 3TD1902 A1903 U1904 A1905 A1906 G1909 U1910 C1911 C1912 A1915 G1916 G1917 A1924 A1925 U1926 U1927 C1928 U1933 C1934 U1942 C1949 U1950 G1951 C1954 A1957 U1958 G1959 U1978 G1979 U1980 C1984 A1985 C1986 A2001 A2002 A2008 U2009 C2010
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C2091 U2092 G2093 C2094 U2095 U2096 G2097 U2098 G2099 U2100 A2101 G2102 G2103 A2104 U2105 A2106 G2107 G2108 U2109 G2110 G2111 G2112 A2113 G2114 G2115 C2116 U2117 U2118 U2119 G2120 A2121 A2122 G2123 C2124 G2125 U2126 G2127 G2128 A2129 C2130 G2131 C2132 C2133 A2134 G2135 U2136 U2137 C2138 G2139 C2140 G2141 U2142 G2143 G2144 A2145 G2146 C2147 C2148 A2149 U2150
C2151 C2152 U2153 U2154 G2155 A2156 A2157 A2158 U2159 A2160 C2161 C2162 A2163 C2164 C2165 C2166 U2167 G2168 G2169 C2170 A2171 U2172 G2173 C2174 U2175 U2176 G2177 A2178 G2179 G2180 U2181 U2182 C2183 U2184 A2185 G2191 G2198 A2199 U2200 C2201 C2202 G2203 A2212 G2215 U2216 U2220 G2221 G2225 G2226 C2227 A2228 G2229 U2230 U2231
U2232 G2233 A2234 C2235 G2238 A2255 G2258 U2259 A2260 A2261 A2265 G2269 U2270 A2274 A2275 G2276 G2277 U2278 G2279 C2282 U2283 C2284 A2285 G2286 A2287 C2288 C2289 G2290 G2291 U2292 C2293 G2294 G2295 A2296 A2297 A2298 U2299 C2300 G2301 G2302 U2303 C2304 G2305 U2306 A2307 G2308 A2309 A2312 U2313 A2314 A2315 A2316
G2317 A2323 C2329 U2330 U2331 G2332 A2333 C2334 C2337 G2338 A2341 C2342 A2343 G2344 C2348 C2351 G2352 U2359 A2364 A2365 G2366 U2367 G2370 U2371 C2372 G2376 U2377 G2378 U2385 G2386 U2389 U2393 U2410 C2411 A2412 A2413 C2414 G2415 G2416 A2417 A2422 U2428 C2429 C2430
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U2643 A2647 G2648 A2649 G2656 A2665 A2666 G2672 G2673 U2674 G2675 U2676 U2677 U2685 C2686 A2687 C2688 G2689 A2692 G2693 U2694 G2695 G2696 C2697 G2701 C2702 U2713 G2719 A2720 G2724 A2725 U2726 A2727 A2728 A2735 G2738 U2743 A2744 A2745 G2748 A2752 U2756 G2757 C2758



• Molecule 29: 5S rRNA (117-MER)

Chain b:

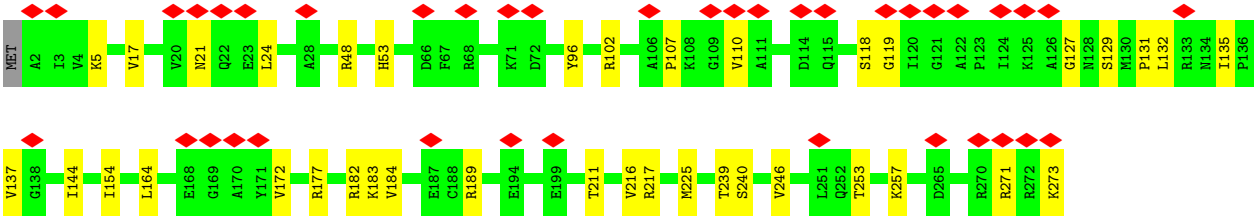




• Molecule 30: Large ribosomal subunit protein uL2

Chain c:

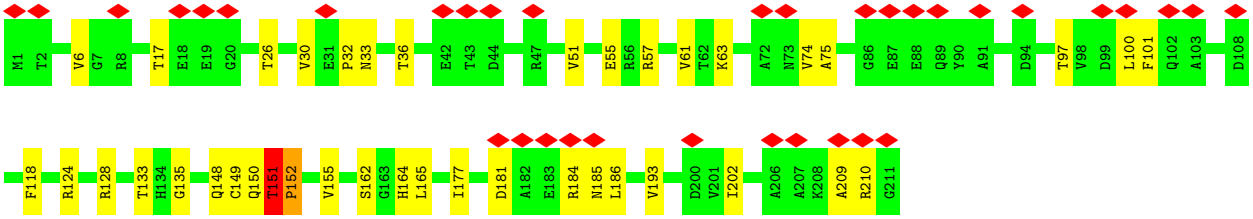




• Molecule 31: Large ribosomal subunit protein uL3

Chain d:

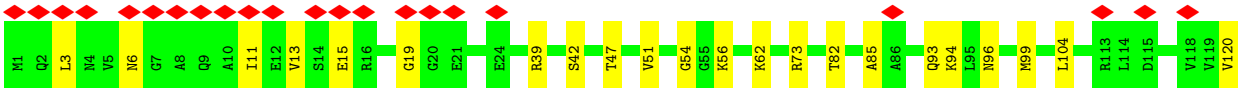




• Molecule 32: Large ribosomal subunit protein uL4

Chain e:

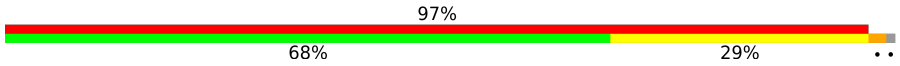


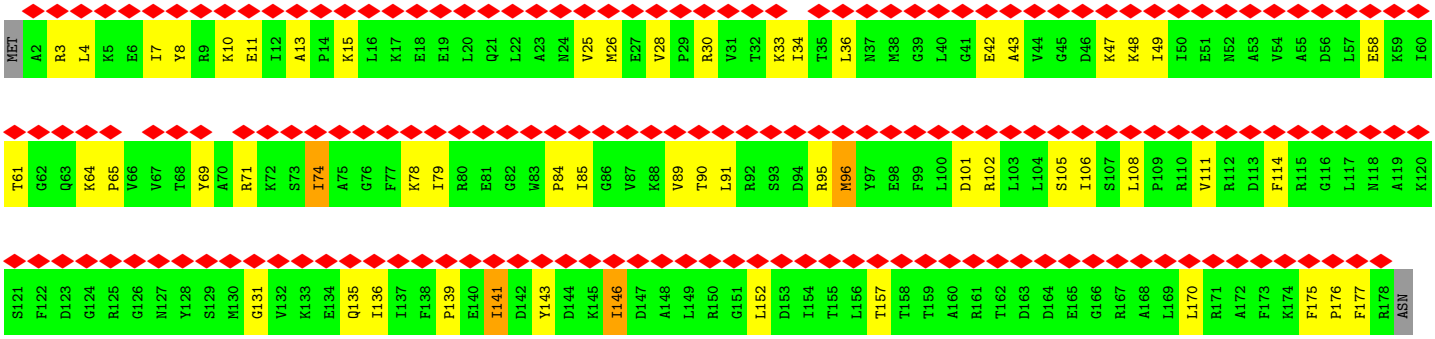




• Molecule 33: Large ribosomal subunit protein uL5

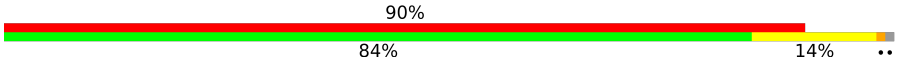
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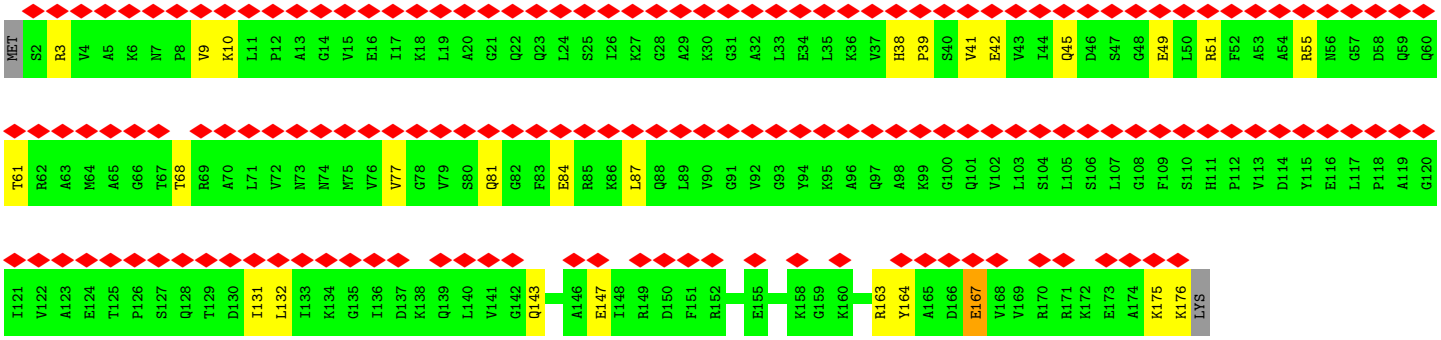




• Molecule 34: Large ribosomal subunit protein uL6

Chain g:

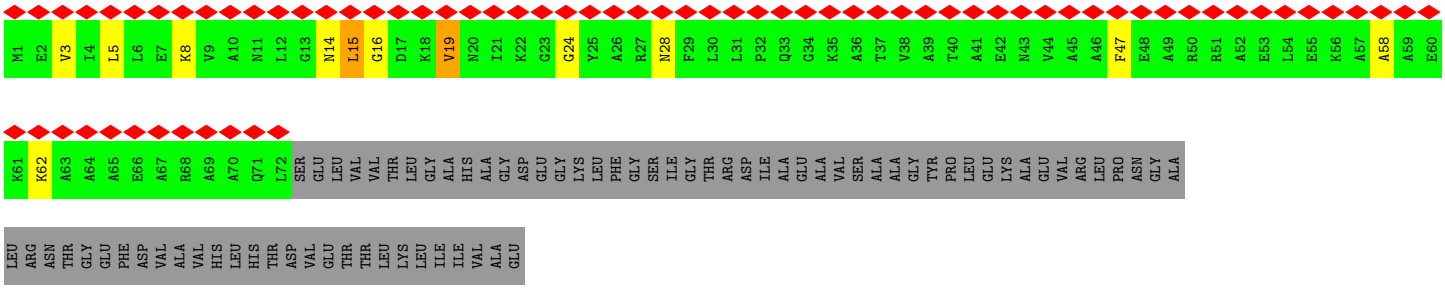




• Molecule 35: Large ribosomal subunit protein bL9

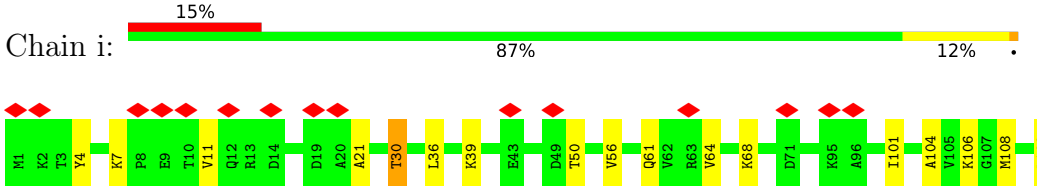
Chain h:





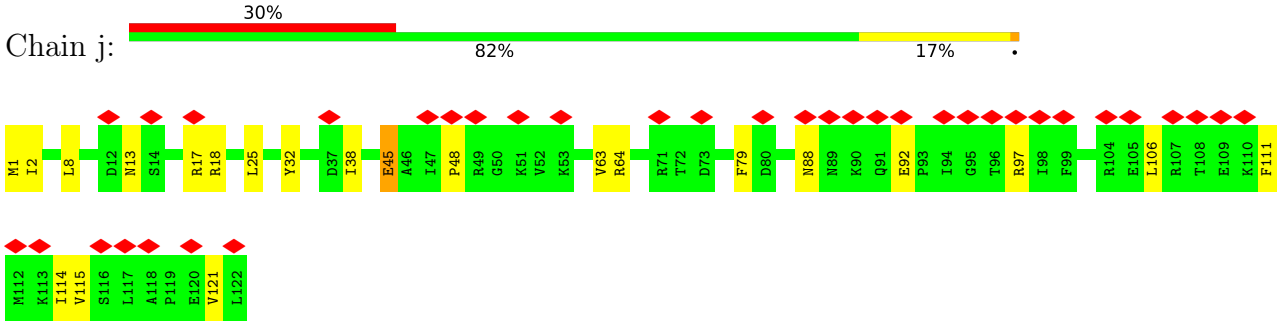
• Molecule 36: Large ribosomal subunit protein uL13

Chain i:



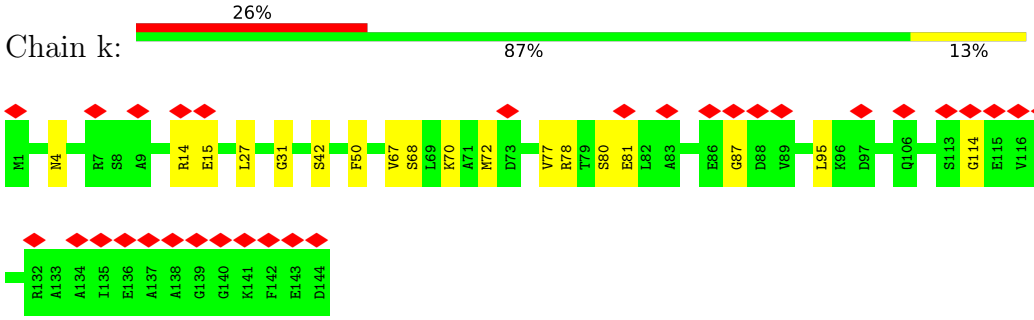
• Molecule 37: Large ribosomal subunit protein uL14

Chain j:



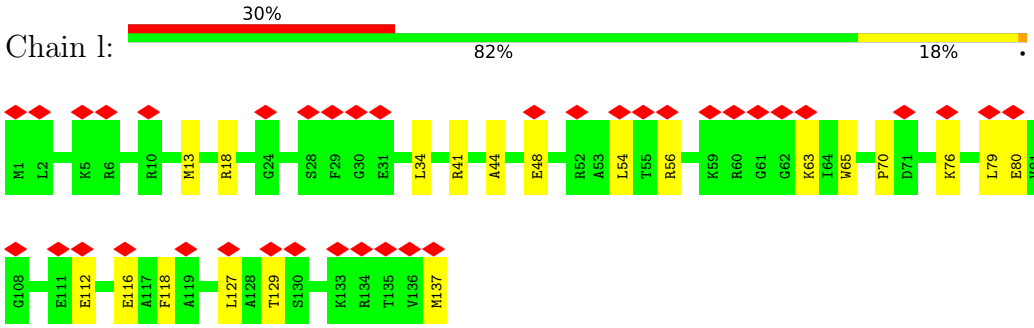
• Molecule 38: Large ribosomal subunit protein uL15

Chain k:



• Molecule 39: Large ribosomal subunit protein uL16

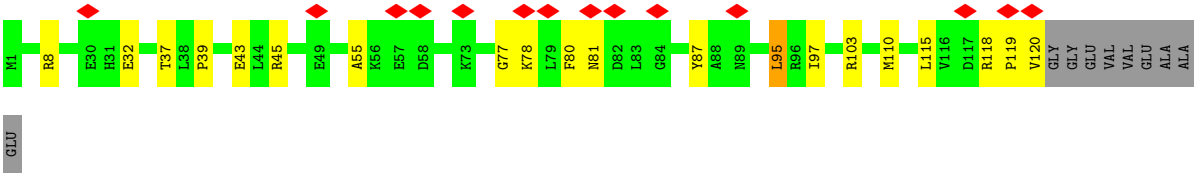
Chain l:



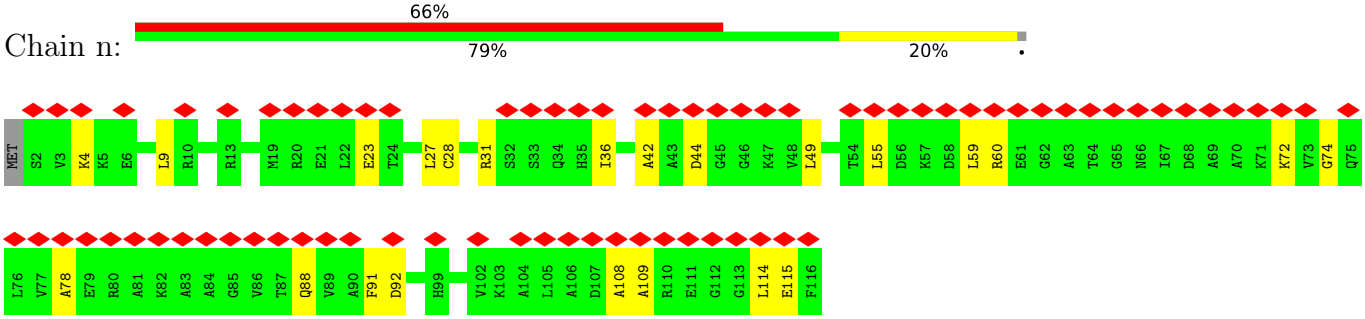
• Molecule 40: Large ribosomal subunit protein bL17

Chain m:

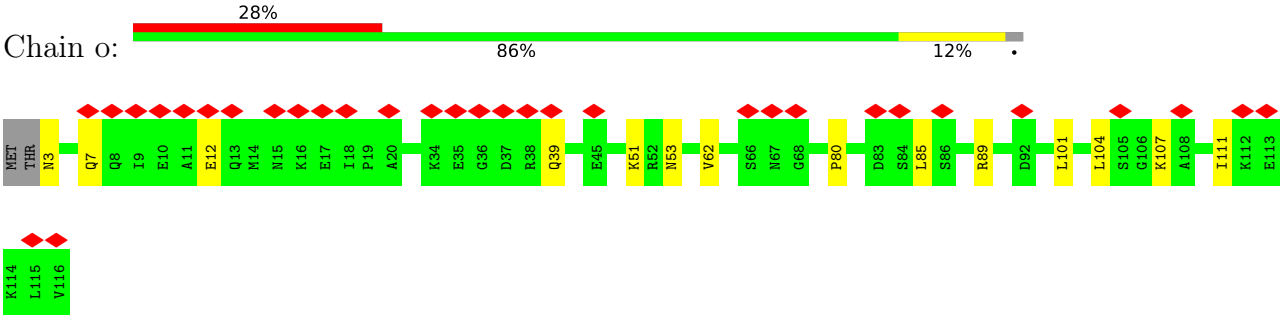




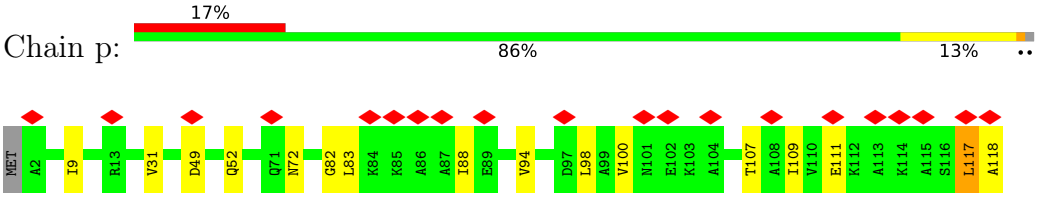
• Molecule 41: Large ribosomal subunit protein uL18



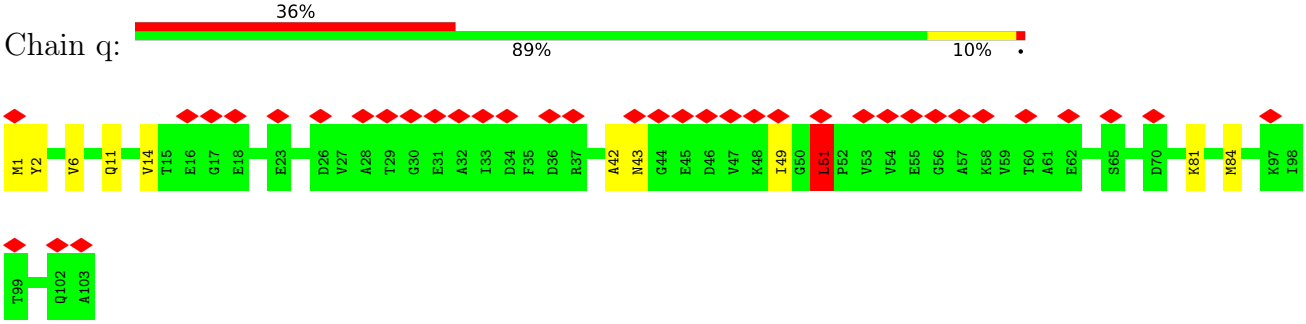
• Molecule 42: Large ribosomal subunit protein bL19



• Molecule 43: Large ribosomal subunit protein bL20

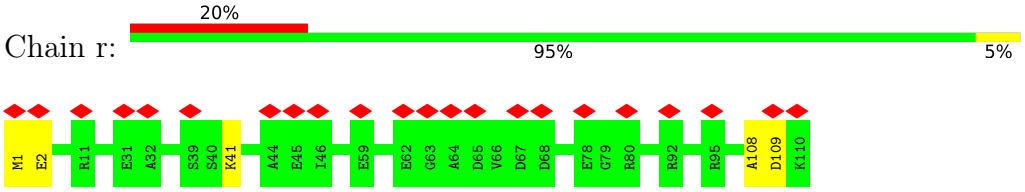


• Molecule 44: Large ribosomal subunit protein bL21



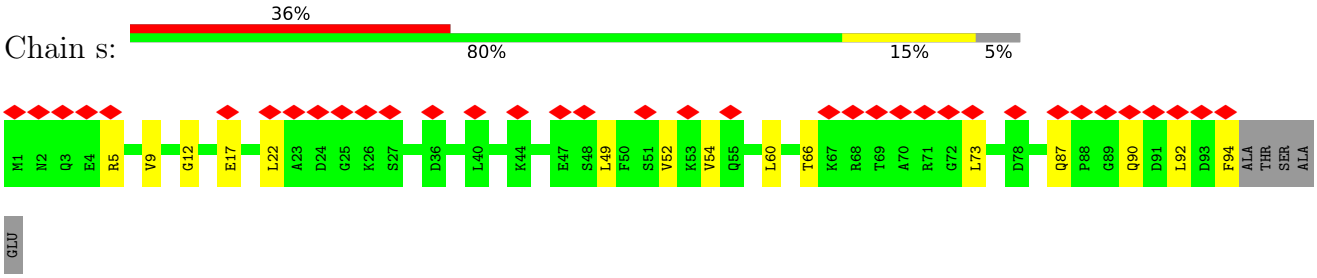
• Molecule 45: Large ribosomal subunit protein uL22

Chain r:



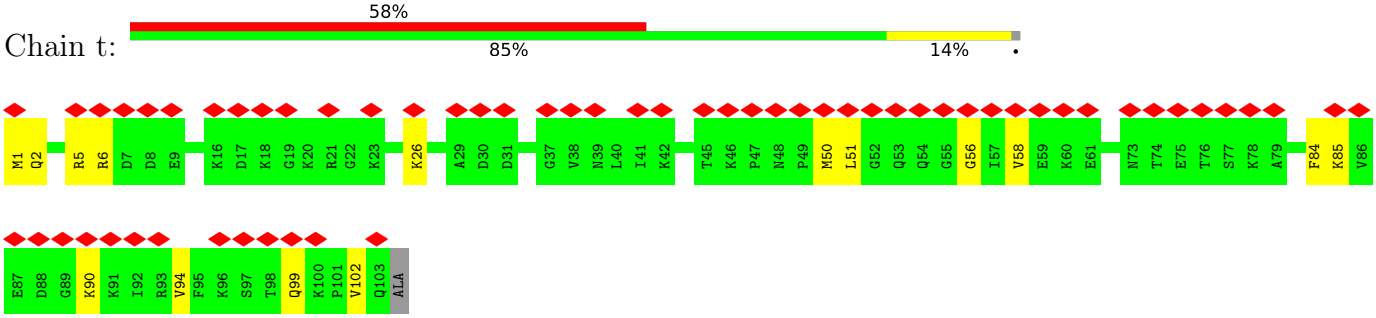
• Molecule 46: Large ribosomal subunit protein uL23

Chain s:



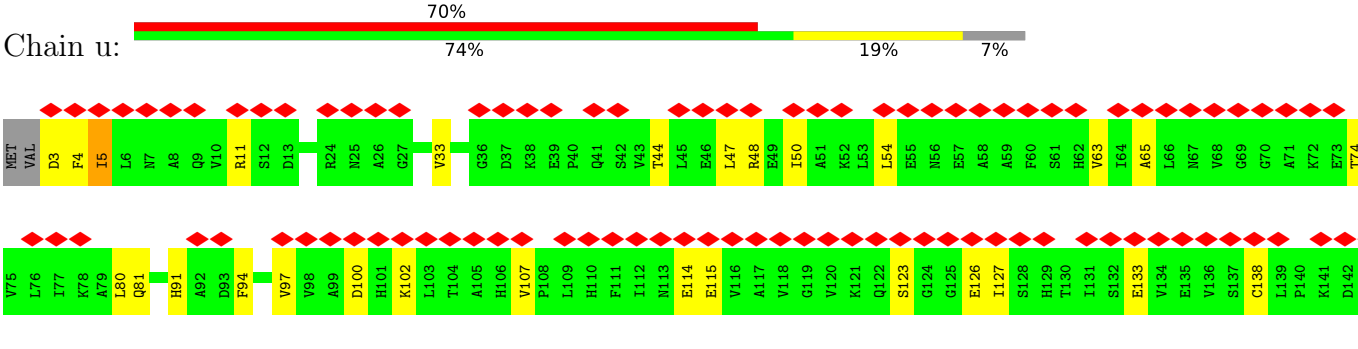
• Molecule 47: Large ribosomal subunit protein uL24

Chain t:



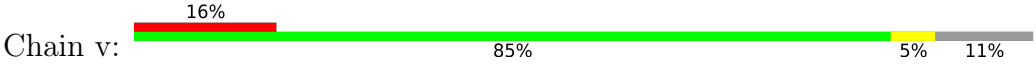
• Molecule 48: Large ribosomal subunit protein bL25

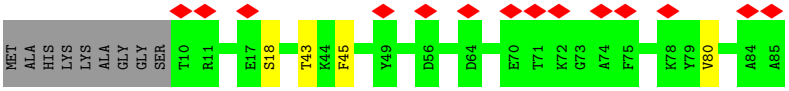
Chain u:



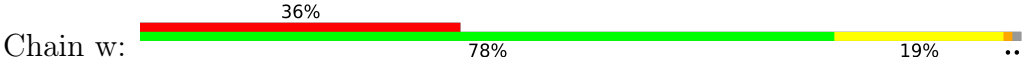
• Molecule 49: Large ribosomal subunit protein bL27

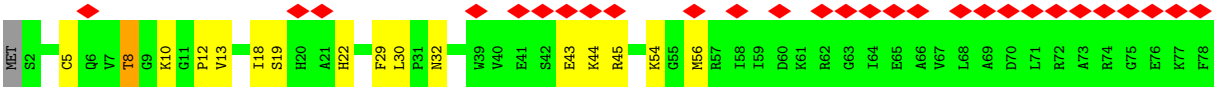
Chain v:



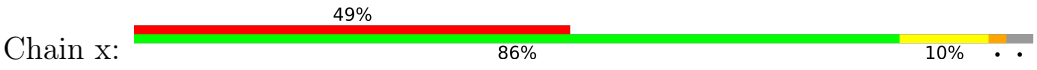


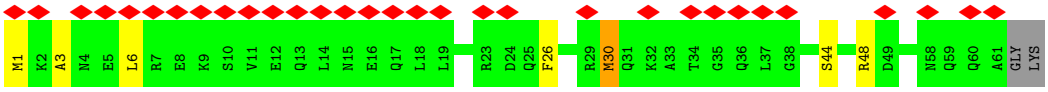
• Molecule 50: Large ribosomal subunit protein bL28



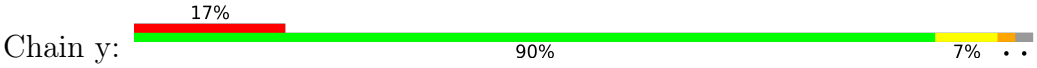


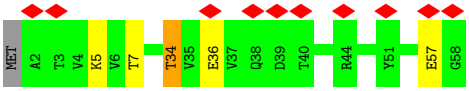
• Molecule 51: Large ribosomal subunit protein uL29



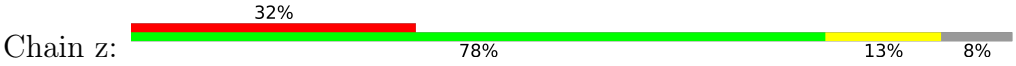


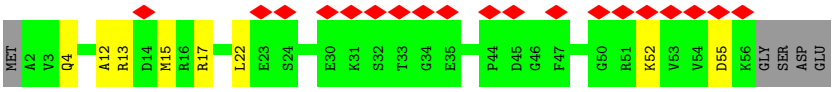
• Molecule 52: Large ribosomal subunit protein uL30





• Molecule 53: Large ribosomal subunit protein bL32





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	50773	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	35	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.311	Depositor
Minimum map value	-0.980	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: IAS, 4OC, MG, MS6, 5MU, 2MG, 7MG, G7M, ZN, OMC, 2MA, H2U, K, OMG, PSU, 5MC, 1MG, UR3, 3TD, 4D4, MEQ, 6MZ, OMU, MA6, D2T

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	0	0.18	0/433	0.34	0/576
2	1	0.22	0/368	0.32	0/482
3	2	0.19	0/511	0.29	0/668
4	3	0.19	0/308	0.30	0/404
5	4	0.16	0/542	0.48	0/728
6	A	0.43	0/36453	0.74	10/56863 (0.0%)
7	B	0.16	0/1791	0.38	0/2405
8	C	0.17	0/1693	0.33	0/2279
9	D	0.16	0/1646	0.35	1/2201 (0.0%)
10	E	0.19	0/1148	0.38	0/1544
11	F	0.16	0/882	0.38	0/1186
12	G	0.15	0/1217	0.31	0/1627
13	H	0.18	0/993	0.32	0/1332
14	I	0.16	0/1022	0.35	0/1365
15	J	0.20	0/803	0.42	0/1083
16	K	0.18	0/889	0.36	0/1199
17	L	0.18	0/964	0.33	0/1289
18	M	0.16	0/892	0.35	0/1199
19	N	0.17	0/816	0.34	0/1087
20	O	0.17	0/710	0.27	0/947
21	P	0.18	0/648	0.30	0/872
22	Q	0.16	0/653	0.31	0/881
23	R	0.17	0/502	0.31	0/677
24	S	0.14	0/678	0.30	0/912
25	T	0.21	0/678	0.30	0/904
26	U	0.16	0/513	0.41	0/680
27	X	0.19	0/803	0.39	0/1075
28	a	0.49	0/68901	0.74	16/107478 (0.0%)
29	b	0.38	0/2789	0.71	1/4345 (0.0%)
30	c	0.21	0/2108	0.31	0/2831
31	d	0.22	0/1601	0.41	1/2152 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	e	0.21	0/1544	0.36	0/2079
33	f	0.16	0/1439	0.39	0/1932
34	g	0.15	0/1344	0.36	0/1809
35	h	0.10	0/536	0.28	0/719
36	i	0.20	0/1156	0.31	0/1559
37	j	0.20	0/947	0.30	0/1268
38	k	0.18	0/1078	0.29	0/1436
39	l	0.20	0/1085	0.34	0/1449
40	m	0.21	0/975	0.33	0/1304
41	n	0.18	0/888	0.35	0/1183
42	o	0.20	0/911	0.29	0/1218
43	p	0.22	0/946	0.30	0/1257
44	q	0.20	0/835	0.36	0/1117
45	r	0.19	0/837	0.33	0/1114
46	s	0.18	0/749	0.36	0/1002
47	t	0.17	0/808	0.39	0/1079
48	u	0.18	0/1469	0.34	0/1988
49	v	0.22	0/583	0.34	0/774
50	w	0.21	0/641	0.32	0/854
51	x	0.17	0/491	0.33	0/654
52	y	0.19	0/449	0.34	0/602
53	z	0.21	0/446	0.35	0/594
All	All	0.40	0/154112	0.66	29/230262 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
31	d	0	1
39	l	0	1
44	q	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	2087	G	OP1-P-O3'	-11.03	74.91	108.00
28	a	2087	G	OP2-P-O3'	-10.27	77.19	108.00
6	A	1000	C	N3-C2-O2	-7.73	116.49	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	359	U	C2-N1-C1'	7.54	126.75	117.70
28	a	1300	U	C2-N1-C1'	7.15	126.28	117.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
31	d	151	THR	Peptide
39	l	82	4D4	Mainchain
44	q	51	LEU	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	426	0	457	8	0
2	1	365	0	409	4	0
3	2	506	0	569	4	0
4	3	307	0	342	2	0
5	4	531	0	529	20	0
6	A	32783	0	16501	372	0
7	B	1763	0	1811	44	0
8	C	1664	0	1723	27	0
9	D	1627	0	1665	27	0
10	E	1134	0	1181	24	0
11	F	868	0	846	21	0
12	G	1199	0	1253	24	0
13	H	982	0	1036	14	0
14	I	1010	0	1052	25	0
15	J	793	0	833	28	0
16	K	882	0	897	19	0
17	L	961	0	1010	9	0
18	M	883	0	929	25	0
19	N	804	0	841	5	0
20	O	703	0	727	4	0
21	P	637	0	648	4	0
22	Q	645	0	689	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	R	494	0	514	4	0
24	S	663	0	697	25	0
25	T	671	0	722	7	0
26	U	506	0	535	13	0
27	X	796	0	818	26	0
28	a	62019	0	31187	556	0
29	b	2495	0	1263	28	0
30	c	2072	0	2152	25	0
31	d	1589	0	1605	21	0
32	e	1524	0	1582	27	0
33	f	1418	0	1486	41	0
34	g	1326	0	1388	15	0
35	h	533	0	560	7	0
36	i	1130	0	1160	11	0
37	j	938	0	1012	12	0
38	k	1066	0	1112	10	0
39	l	1086	0	1145	15	0
40	m	959	0	1005	12	0
41	n	881	0	920	12	0
42	o	902	0	960	10	0
43	p	936	0	1025	10	0
44	q	822	0	858	7	0
45	r	833	0	897	4	0
46	s	739	0	788	9	0
47	t	800	0	863	7	0
48	u	1446	0	1486	22	0
49	v	575	0	598	2	0
50	w	630	0	653	12	0
51	x	490	0	520	5	0
52	y	445	0	472	3	0
53	z	440	0	437	6	0
54	3	1	0	0	0	0
54	4	1	0	0	0	0
55	A	93	0	0	0	0
55	M	1	0	0	0	0
55	X	1	0	0	0	0
55	a	251	0	0	0	0
55	b	5	0	0	0	0
55	c	1	0	0	0	0
55	p	1	0	0	0	0
55	z	1	0	0	0	0
56	A	49	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
56	a	114	0	0	0	0
56	b	1	0	0	0	0
56	c	3	0	0	0	0
56	e	1	0	0	0	0
56	f	1	0	0	0	0
All	All	143222	0	96368	1564	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 7.

The worst 5 of 1564 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)
6:A:74:A:H62	6:A:89:G:N2	1.53	1.06
6:A:74:A:N6	6:A:89:G:H21	1.60	0.98
6:A:75:G:H1	6:A:88:U:H3	1.14	0.94
28:a:1834:A:HO2'	28:a:1835:A:H8	1.06	0.92
6:A:74:A:H62	6:A:89:G:H21	0.92	0.92

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/51 (96%)	49 (100%)	0	0	100	100
2	1	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
3	2	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
4	3	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
5	4	66/71 (93%)	56 (85%)	9 (14%)	1 (2%)	8	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	B	222/246 (90%)	201 (90%)	20 (9%)	1 (0%)	24 55
8	C	206/228 (90%)	192 (93%)	14 (7%)	0	100 100
9	D	203/206 (98%)	191 (94%)	12 (6%)	0	100 100
10	E	152/166 (92%)	144 (95%)	8 (5%)	0	100 100
11	F	104/139 (75%)	102 (98%)	2 (2%)	0	100 100
12	G	151/156 (97%)	144 (95%)	7 (5%)	0	100 100
13	H	127/130 (98%)	117 (92%)	9 (7%)	1 (1%)	16 44
14	I	125/130 (96%)	117 (94%)	7 (6%)	1 (1%)	16 44
15	J	97/103 (94%)	92 (95%)	5 (5%)	0	100 100
16	K	115/129 (89%)	107 (93%)	7 (6%)	1 (1%)	14 41
17	L	119/123 (97%)	111 (93%)	8 (7%)	0	100 100
18	M	111/118 (94%)	102 (92%)	9 (8%)	0	100 100
19	N	98/101 (97%)	92 (94%)	6 (6%)	0	100 100
20	O	86/89 (97%)	84 (98%)	2 (2%)	0	100 100
21	P	79/83 (95%)	79 (100%)	0	0	100 100
22	Q	78/88 (89%)	77 (99%)	1 (1%)	0	100 100
23	R	60/76 (79%)	54 (90%)	6 (10%)	0	100 100
24	S	81/91 (89%)	78 (96%)	3 (4%)	0	100 100
25	T	85/91 (93%)	85 (100%)	0	0	100 100
26	U	60/71 (84%)	56 (93%)	3 (5%)	1 (2%)	7 25
27	X	96/102 (94%)	91 (95%)	5 (5%)	0	100 100
30	c	270/273 (99%)	262 (97%)	8 (3%)	0	100 100
31	d	208/211 (99%)	194 (93%)	11 (5%)	3 (1%)	9 30
32	e	198/200 (99%)	188 (95%)	10 (5%)	0	100 100
33	f	175/179 (98%)	160 (91%)	14 (8%)	1 (1%)	21 51
34	g	173/177 (98%)	160 (92%)	13 (8%)	0	100 100
35	h	70/148 (47%)	63 (90%)	7 (10%)	0	100 100
36	i	140/142 (99%)	135 (96%)	5 (4%)	0	100 100
37	j	120/122 (98%)	119 (99%)	1 (1%)	0	100 100
38	k	142/144 (99%)	135 (95%)	7 (5%)	0	100 100
39	l	133/137 (97%)	128 (96%)	5 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	m	118/129 (92%)	115 (98%)	3 (2%)	0	100	100
41	n	113/116 (97%)	103 (91%)	10 (9%)	0	100	100
42	o	112/116 (97%)	105 (94%)	7 (6%)	0	100	100
43	p	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
44	q	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
45	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
46	s	92/99 (93%)	86 (94%)	6 (6%)	0	100	100
47	t	101/104 (97%)	90 (89%)	11 (11%)	0	100	100
48	u	188/204 (92%)	182 (97%)	6 (3%)	0	100	100
49	v	74/85 (87%)	72 (97%)	2 (3%)	0	100	100
50	w	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
51	x	59/63 (94%)	59 (100%)	0	0	100	100
52	y	55/58 (95%)	54 (98%)	1 (2%)	0	100	100
53	z	53/60 (88%)	52 (98%)	1 (2%)	0	100	100
All	All	5702/6110 (93%)	5407 (95%)	285 (5%)	10 (0%)	44	72

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	d	149	CYS
31	d	152	PRO
7	B	126	PHE
26	U	28	VAL
13	H	84	ARG

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	
1	0	47/47 (100%)	46 (98%)	1 (2%)	47	79
2	1	37/37 (100%)	36 (97%)	1 (3%)	39	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	2	54/55 (98%)	54 (100%)	0	100	100
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	59/61 (97%)	56 (95%)	3 (5%)	21	54
7	B	187/202 (93%)	182 (97%)	5 (3%)	39	74
8	C	172/187 (92%)	169 (98%)	3 (2%)	53	83
9	D	173/174 (99%)	168 (97%)	5 (3%)	37	73
10	E	113/124 (91%)	109 (96%)	4 (4%)	32	67
11	F	91/119 (76%)	89 (98%)	2 (2%)	45	78
12	G	119/122 (98%)	114 (96%)	5 (4%)	26	61
13	H	108/109 (99%)	106 (98%)	2 (2%)	50	81
14	I	104/106 (98%)	99 (95%)	5 (5%)	23	56
15	J	88/92 (96%)	87 (99%)	1 (1%)	65	87
16	K	90/97 (93%)	89 (99%)	1 (1%)	65	87
17	L	105/106 (99%)	102 (97%)	3 (3%)	37	73
18	M	95/99 (96%)	95 (100%)	0	100	100
19	N	81/82 (99%)	80 (99%)	1 (1%)	63	87
20	O	74/75 (99%)	72 (97%)	2 (3%)	39	74
21	P	64/65 (98%)	63 (98%)	1 (2%)	55	83
22	Q	73/79 (92%)	71 (97%)	2 (3%)	39	74
23	R	52/64 (81%)	52 (100%)	0	100	100
24	S	72/78 (92%)	69 (96%)	3 (4%)	26	61
25	T	69/70 (99%)	69 (100%)	0	100	100
26	U	51/60 (85%)	50 (98%)	1 (2%)	48	80
27	X	86/88 (98%)	85 (99%)	1 (1%)	63	87
30	c	212/213 (100%)	210 (99%)	2 (1%)	70	89
31	d	161/161 (100%)	157 (98%)	4 (2%)	42	76
32	e	158/158 (100%)	158 (100%)	0	100	100
33	f	151/153 (99%)	148 (98%)	3 (2%)	48	80
34	g	139/141 (99%)	137 (99%)	2 (1%)	59	85
35	h	49/107 (46%)	47 (96%)	2 (4%)	27	62
36	i	119/119 (100%)	117 (98%)	2 (2%)	53	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	j	102/102 (100%)	101 (99%)	1 (1%)	68	88
38	k	106/106 (100%)	102 (96%)	4 (4%)	29	64
39	l	108/108 (100%)	104 (96%)	4 (4%)	30	65
40	m	99/104 (95%)	96 (97%)	3 (3%)	36	72
41	n	86/87 (99%)	84 (98%)	2 (2%)	44	78
42	o	96/98 (98%)	93 (97%)	3 (3%)	35	70
43	p	87/88 (99%)	84 (97%)	3 (3%)	32	68
44	q	86/86 (100%)	84 (98%)	2 (2%)	44	78
45	r	87/87 (100%)	87 (100%)	0	100	100
46	s	79/82 (96%)	76 (96%)	3 (4%)	29	64
47	t	88/88 (100%)	85 (97%)	3 (3%)	32	68
48	u	155/165 (94%)	150 (97%)	5 (3%)	34	70
49	v	56/61 (92%)	55 (98%)	1 (2%)	51	82
50	w	66/67 (98%)	65 (98%)	1 (2%)	57	84
51	x	54/55 (98%)	53 (98%)	1 (2%)	50	81
52	y	48/49 (98%)	47 (98%)	1 (2%)	47	79
53	z	48/52 (92%)	48 (100%)	0	100	100
All	All	4738/4969 (95%)	4634 (98%)	104 (2%)	45	78

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	d	181	ASP
38	k	72	MET
48	u	192	VAL
33	f	141	ILE
36	i	30	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 59 such sidechains are listed below:

Mol	Chain	Res	Type
30	c	261	ASN
49	v	57	HIS
34	g	59	GLN
48	u	180	ASN

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Mol	Chain	Res	Type
48	u	67	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
28	a	2889/2891 (99%)	521 (18%)	0
29	b	116/120 (96%)	19 (16%)	0
6	A	1526/1536 (99%)	291 (19%)	22 (1%)
All	All	4531/4547 (99%)	831 (18%)	22 (0%)

5 of 831 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	A	4	C
6	A	5	U
6	A	6	G
6	A	7	A
6	A	9	G

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
6	A	893	C
6	A	1162	C
6	A	1039	C
6	A	1164	A
6	A	314	A

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

38 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	$\#\|Z\|>2$
28	PSU	a	945	28	18,21,22	2.08	7 (38%)	22,30,33	1.87	4 (18%)
28	6MZ	a	2017	28	22,25,26	2.38	3 (13%)	30,36,39	2.39	9 (30%)
6	2MG	A	960	6	23,26,27	2.58	4 (17%)	32,38,41	2.08	9 (28%)
28	PSU	a	1898	28	18,21,22	1.97	7 (38%)	22,30,33	1.86	3 (13%)
28	2MG	a	2432	28	23,26,27	2.57	6 (26%)	32,38,41	2.08	11 (34%)
31	MEQ	d	150	31	8,9,10	0.84	0	5,10,12	0.42	0
28	PSU	a	2444	28	18,21,22	2.09	7 (38%)	22,30,33	1.83	5 (22%)
28	7MG	a	2056	28	22,26,27	1.20	1 (4%)	29,39,42	0.93	1 (3%)
28	OMC	a	2485	55,28	19,22,23	1.76	4 (21%)	26,31,34	0.97	2 (7%)
28	6MZ	a	1608	28	22,25,26	2.40	3 (13%)	30,36,39	2.21	10 (33%)
28	1MG	a	735	28	22,26,27	2.51	5 (22%)	33,39,42	2.01	6 (18%)
28	PSU	a	1904	28	18,21,22	1.98	7 (38%)	22,30,33	1.79	4 (18%)
17	D2T	L	89	17	7,9,10	1.24	1 (14%)	6,11,13	1.54	1 (16%)
28	2MG	a	1822	28	23,26,27	2.57	5 (21%)	32,38,41	2.06	10 (31%)
6	PSU	A	510	55,6,56	18,21,22	2.02	7 (38%)	22,30,33	1.82	5 (22%)
6	MA6	A	1513	6	23,26,27	1.21	3 (13%)	34,38,41	2.24	9 (26%)
6	4OC	A	1396	6	20,23,24	2.22	3 (15%)	26,32,35	0.95	2 (7%)
28	OMU	a	2539	56,28	19,22,23	2.61	7 (36%)	26,31,34	1.76	5 (19%)
28	PSU	a	2491	56,28	18,21,22	2.07	7 (38%)	22,30,33	1.84	4 (18%)
6	MA6	A	1512	6	23,26,27	1.20	3 (13%)	34,38,41	2.26	9 (26%)
28	3TD	a	1902	28	18,22,23	2.68	7 (38%)	22,32,35	1.70	2 (9%)
28	5MU	a	1926	56,28	19,22,23	2.50	7 (36%)	28,32,35	3.87	10 (35%)
28	5MC	a	1949	56,28	18,22,23	1.89	5 (27%)	26,32,35	1.29	2 (7%)
28	2MA	a	2490	55,56,28	22,25,26	1.33	2 (9%)	33,37,40	2.00	8 (24%)
28	PSU	a	2591	28	18,21,22	2.05	7 (38%)	22,30,33	1.80	3 (13%)
28	PSU	a	2592	28	18,21,22	2.05	7 (38%)	22,30,33	1.84	3 (13%)
39	MS6	l	83	39	5,7,8	0.56	0	2,7,9	1.66	1 (50%)
6	5MC	A	961	6	18,22,23	1.90	6 (33%)	26,32,35	1.30	2 (7%)
28	PSU	a	2567	28	18,21,22	2.11	8 (44%)	22,30,33	1.90	5 (22%)
28	H2U	a	2436	28	18,21,22	4.20	5 (27%)	21,30,33	4.70	6 (28%)
39	4D4	l	82	39	9,11,12	0.78	0	8,13,15	1.64	2 (25%)
6	2MG	A	1201	6,56	23,26,27	2.57	4 (17%)	32,38,41	2.12	12 (37%)
28	OMG	a	2238	56,28	23,26,27	2.34	6 (26%)	33,38,41	1.81	10 (30%)
6	UR3	A	1492	6	19,22,23	2.56	6 (31%)	26,32,35	1.29	2 (7%)
6	2MG	A	1510	6,56	23,26,27	2.58	5 (21%)	32,38,41	2.11	10 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
16	IAS	K	119	16,26	6,7,8	1.73	1 (16%)	6,8,10	2.58	1 (16%)
6	G7M	A	521	6,56	23,26,27	2.16	5 (21%)	35,39,42	1.88	7 (20%)
28	PSU	a	736	55,28	18,21,22	2.03	7 (38%)	22,30,33	1.79	3 (13%)

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
28	PSU	a	945	28	-	0/7/25/26	0/2/2/2
28	6MZ	a	2017	28	-	2/9/27/28	0/3/3/3
6	2MG	A	960	6	-	0/9/27/28	0/3/3/3
28	PSU	a	1898	28	-	0/7/25/26	0/2/2/2
28	2MG	a	2432	28	-	2/9/27/28	0/3/3/3
31	MEQ	d	150	31	-	3/8/9/11	-
28	PSU	a	2444	28	-	0/7/25/26	0/2/2/2
28	7MG	a	2056	28	-	2/7/37/38	0/3/3/3
28	OMC	a	2485	55,28	-	1/9/27/28	0/2/2/2
28	6MZ	a	1608	28	-	0/9/27/28	0/3/3/3
28	1MG	a	735	28	-	0/7/25/26	0/3/3/3
28	PSU	a	1904	28	-	0/7/25/26	0/2/2/2
17	D2T	L	89	17	-	4/7/12/14	-
28	2MG	a	1822	28	-	0/9/27/28	0/3/3/3
6	PSU	A	510	55,6,56	-	0/7/25/26	0/2/2/2
6	MA6	A	1513	6	-	2/11/29/30	0/3/3/3
6	4OC	A	1396	6	-	1/9/29/30	0/2/2/2
28	OMU	a	2539	56,28	-	0/9/27/28	0/2/2/2
28	PSU	a	2491	56,28	-	0/7/25/26	0/2/2/2
6	MA6	A	1512	6	-	0/11/29/30	0/3/3/3
28	3TD	a	1902	28	-	3/7/25/26	0/2/2/2
28	5MU	a	1926	56,28	-	0/7/25/26	0/2/2/2
28	5MC	a	1949	56,28	-	0/7/25/26	0/2/2/2
28	2MA	a	2490	55,56,28	-	2/7/25/26	0/3/3/3
28	PSU	a	2591	28	-	0/7/25/26	0/2/2/2
28	PSU	a	2592	28	-	0/7/25/26	0/2/2/2
39	MS6	l	83	39	-	2/4/6/8	-
6	5MC	A	961	6	-	0/7/25/26	0/2/2/2
28	PSU	a	2567	28	-	1/7/25/26	0/2/2/2
28	H2U	a	2436	28	-	1/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
39	4D4	l	82	39	-	4/11/12/14	-
6	2MG	A	1201	6,56	-	0/9/27/28	0/3/3/3
28	OMG	a	2238	56,28	-	3/9/27/28	0/3/3/3
6	UR3	A	1492	6	-	0/7/25/26	0/2/2/2
6	2MG	A	1510	6,56	-	0/9/27/28	0/3/3/3
16	IAS	K	119	16,26	-	4/7/7/8	-
6	G7M	A	521	6,56	-	3/7/25/26	0/3/3/3
28	PSU	a	736	55,28	-	1/7/25/26	0/2/2/2

The worst 5 of 178 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	a	1608	6MZ	C6-N6	10.12	1.45	1.34
28	a	2436	H2U	O4-C4	10.01	1.43	1.23
28	a	2017	6MZ	C6-N6	9.91	1.44	1.34
6	A	1201	2MG	O6-C6	9.15	1.41	1.23
6	A	960	2MG	O6-C6	9.10	1.40	1.23

The worst 5 of 198 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
28	a	2436	H2U	C4-N3-C2	-12.79	115.18	125.79
28	a	2436	H2U	O2-C2-N1	-11.13	109.14	123.11
28	a	1926	5MU	C4-N3-C2	-8.75	116.03	127.35
28	a	1926	5MU	C5M-C5-C4	8.47	128.09	118.77
28	a	1926	5MU	N3-C2-N1	8.38	126.01	114.89

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
17	L	89	D2T	CA-CB-CG-OD1
17	L	89	D2T	CA-CB-CG-OD2
39	l	82	4D4	O-C-CA-CB
39	l	82	4D4	CA-CB-CG-CD
16	K	119	IAS	N-CA-CB-CG

There are no ring outliers.

11 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
28	a	2017	6MZ	1	0
6	A	960	2MG	2	0
31	d	150	MEQ	1	0
28	a	735	1MG	1	0
6	A	510	PSU	1	0
6	A	1396	4OC	2	0
28	a	2490	2MA	1	0
6	A	961	5MC	1	0
6	A	1201	2MG	2	0
28	a	2238	OMG	1	0
16	K	119	IAS	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 525 ligands modelled in this entry, 525 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)

There are no chain breaks in this entry.

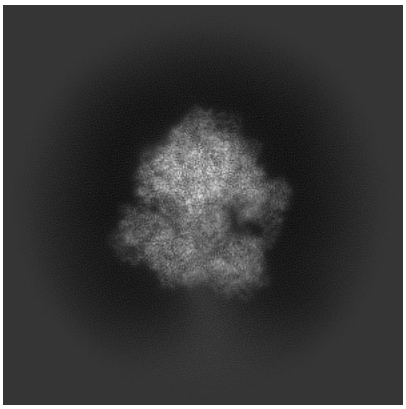
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55712. These allow visual inspection of the internal detail of the map and identification of artifacts.

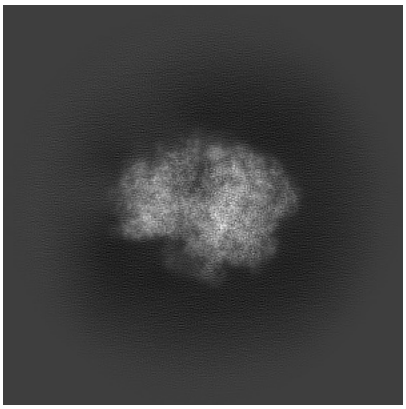
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

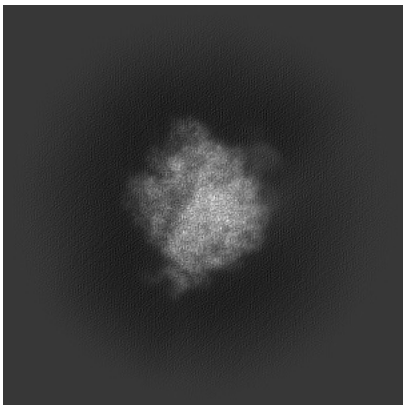
6.1.1 Primary map



X

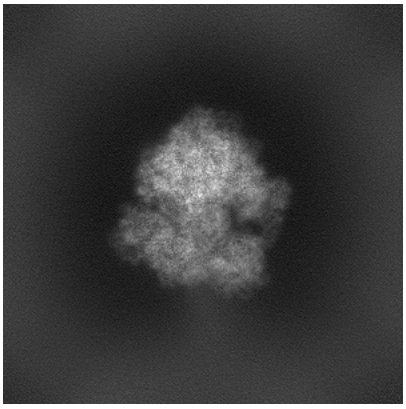


Y

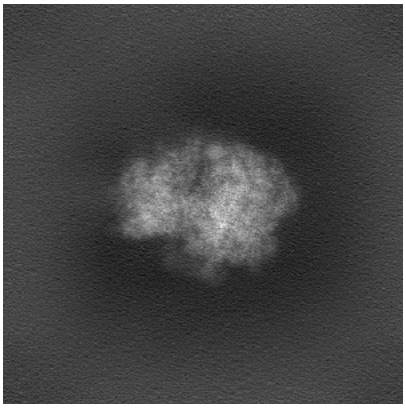


Z

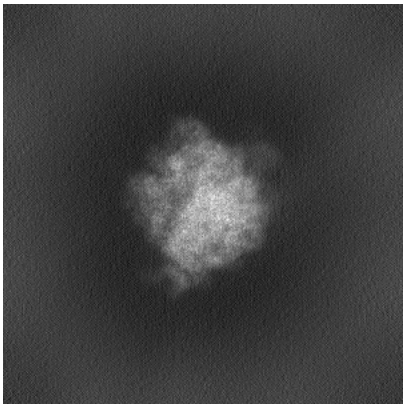
6.1.2 Raw map



X



Y

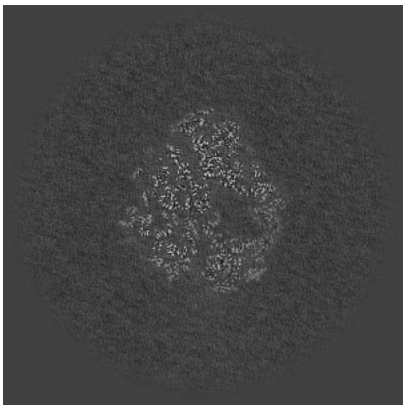


Z

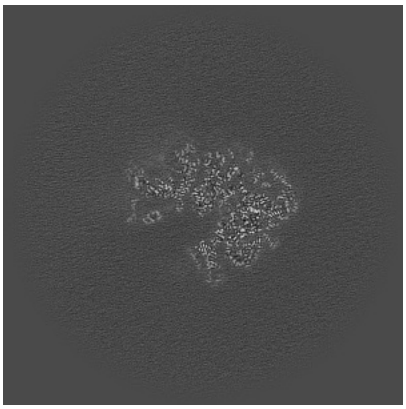
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

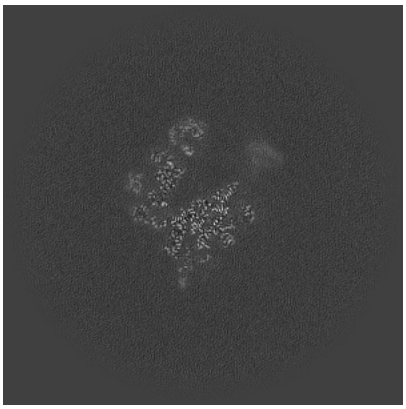
6.2.1 Primary map



X Index: 256

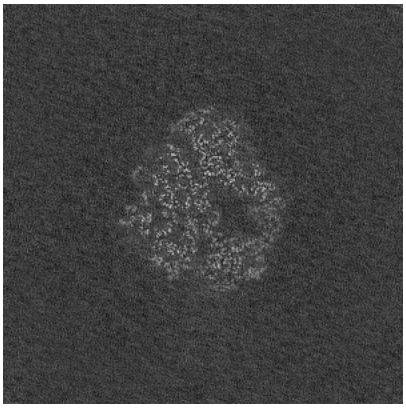


Y Index: 256

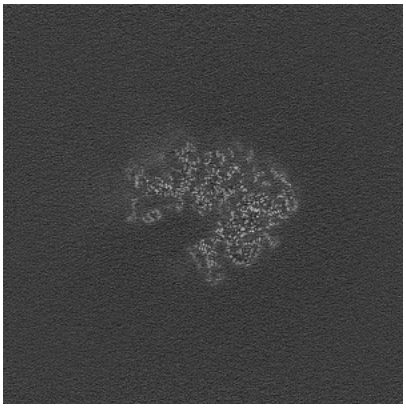


Z Index: 256

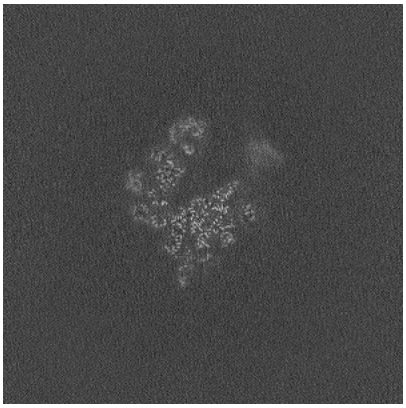
6.2.2 Raw map



X Index: 256



Y Index: 256

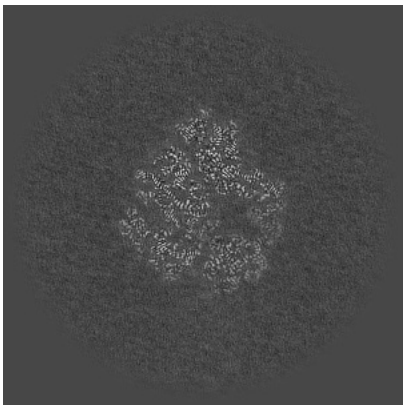


Z Index: 256

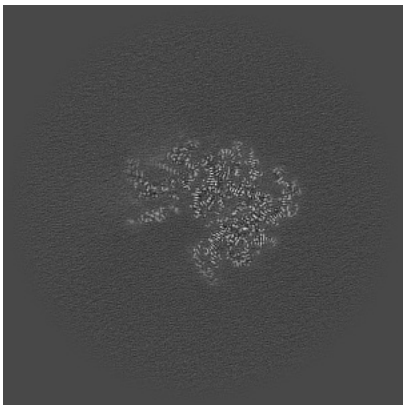
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

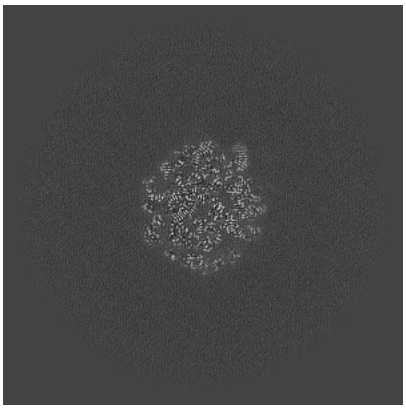
6.3.1 Primary map



X Index: 252

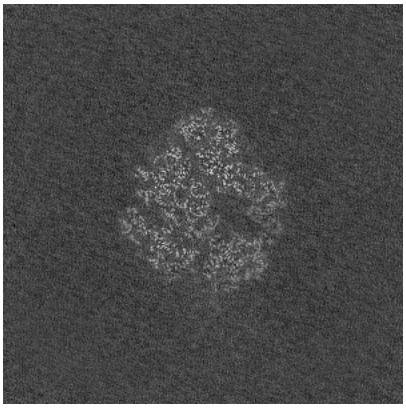


Y Index: 252

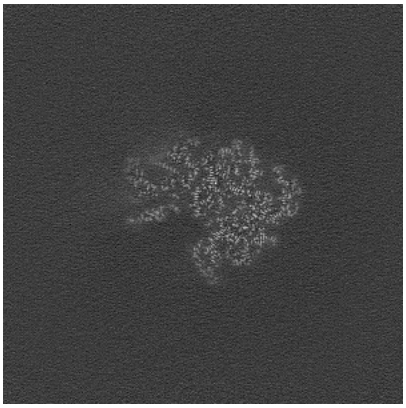


Z Index: 295

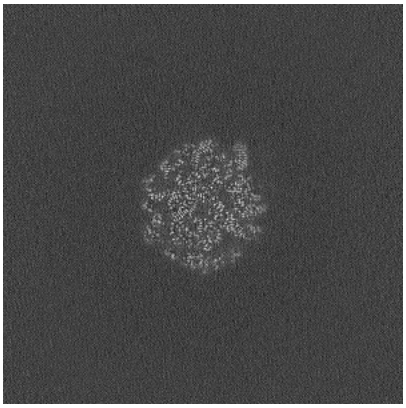
6.3.2 Raw map



X Index: 253



Y Index: 252

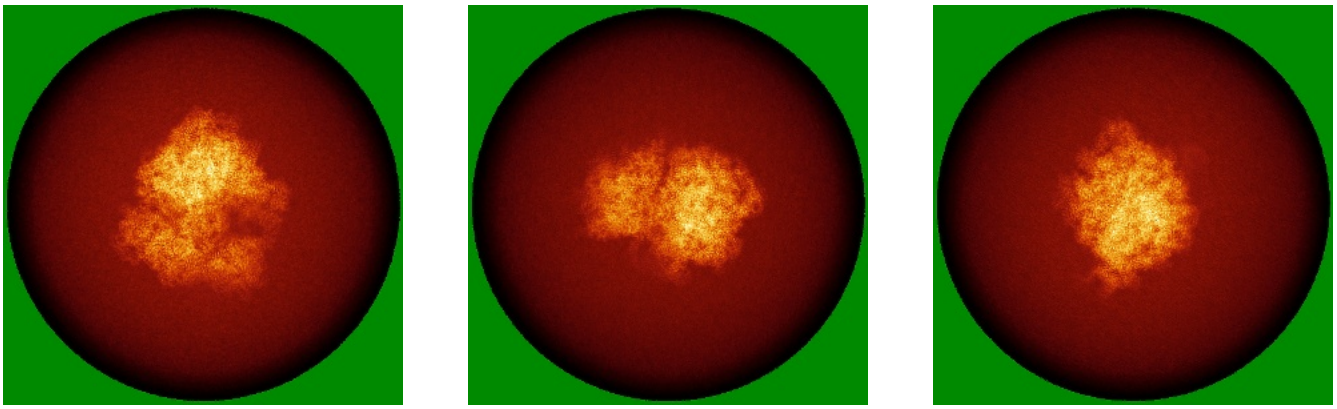


Z Index: 295

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

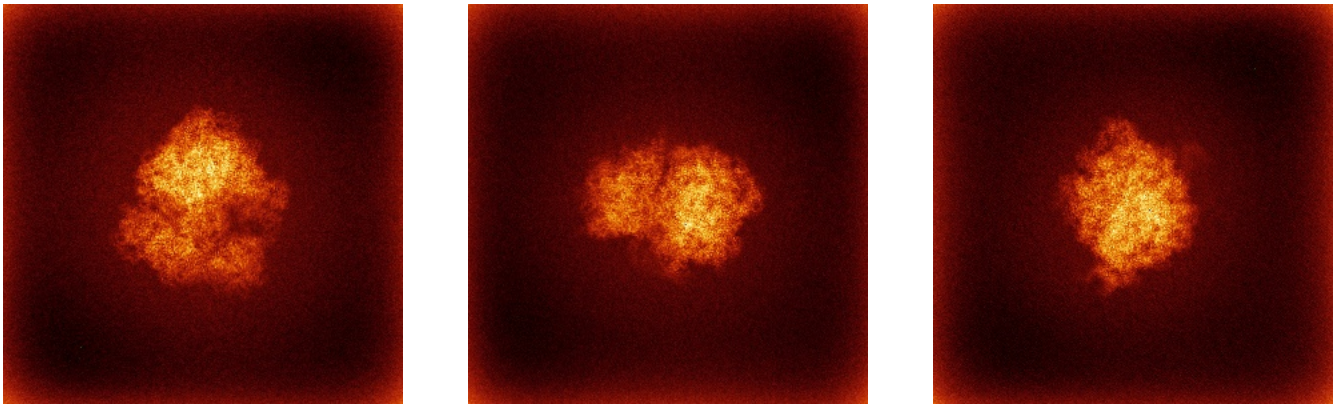
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



X Y Z

6.4.2 Raw 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 0.55. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

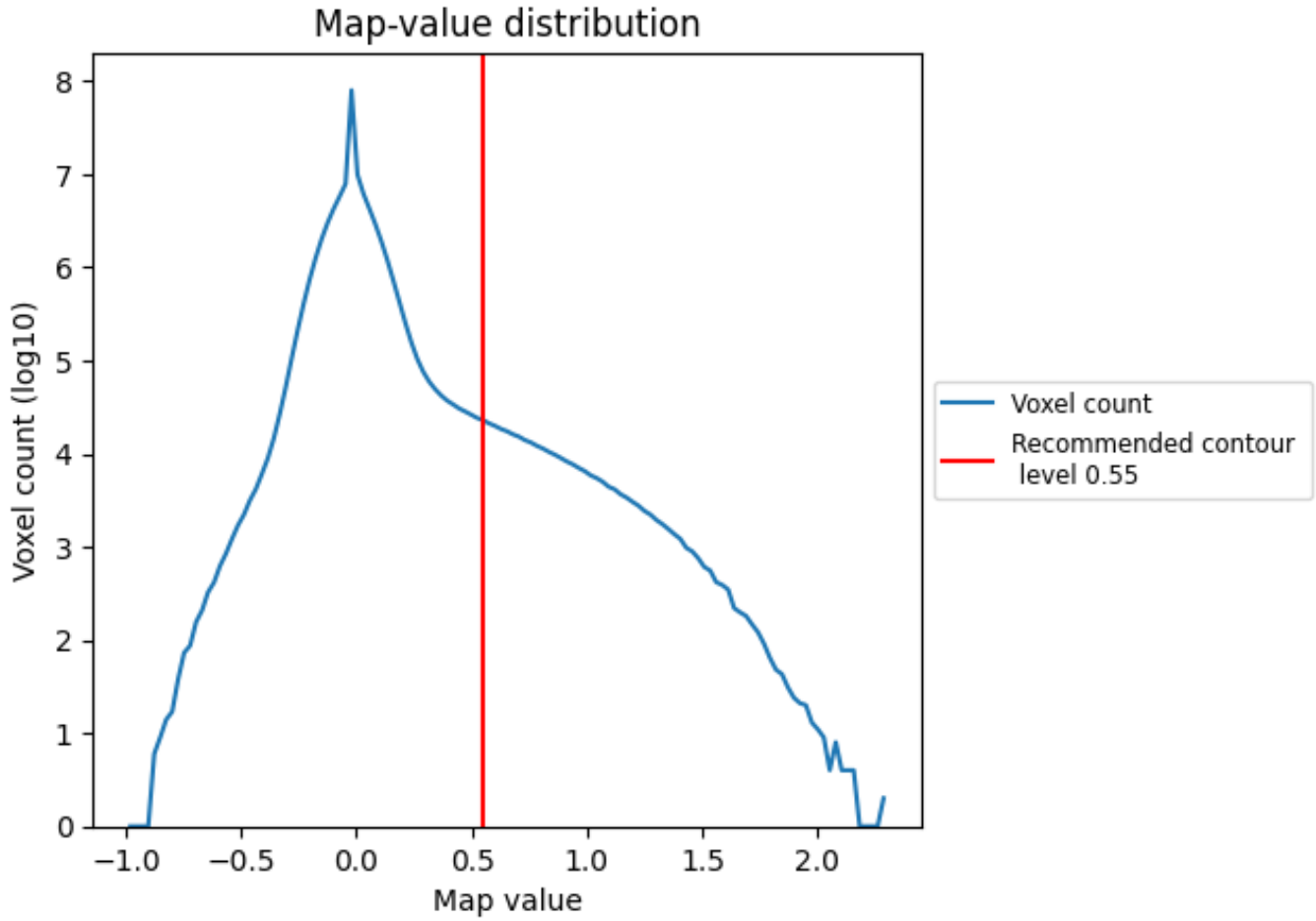
6.6 Mask visualisation (i)

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

7 Map analysis

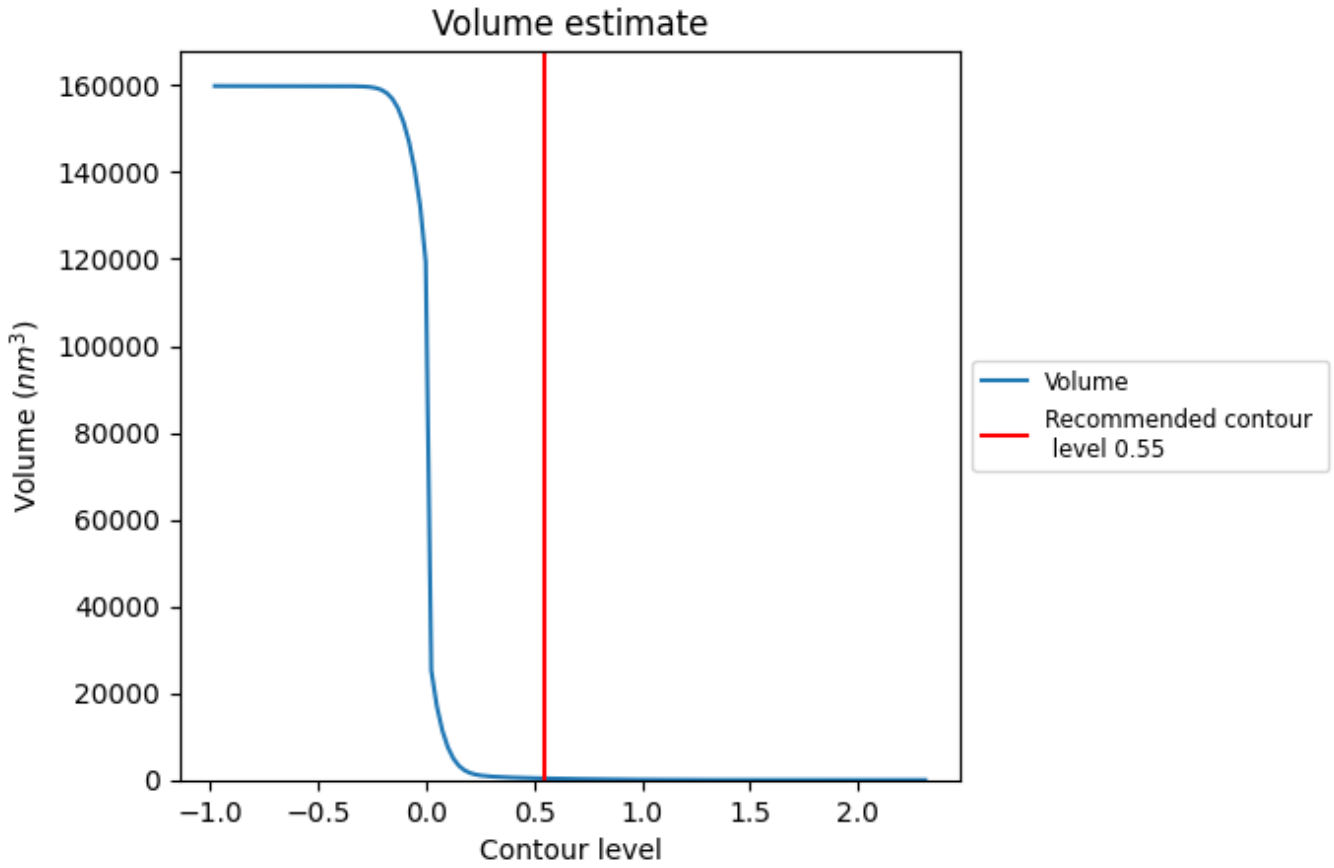
This section contains the results of statistical analysis of the map.

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.

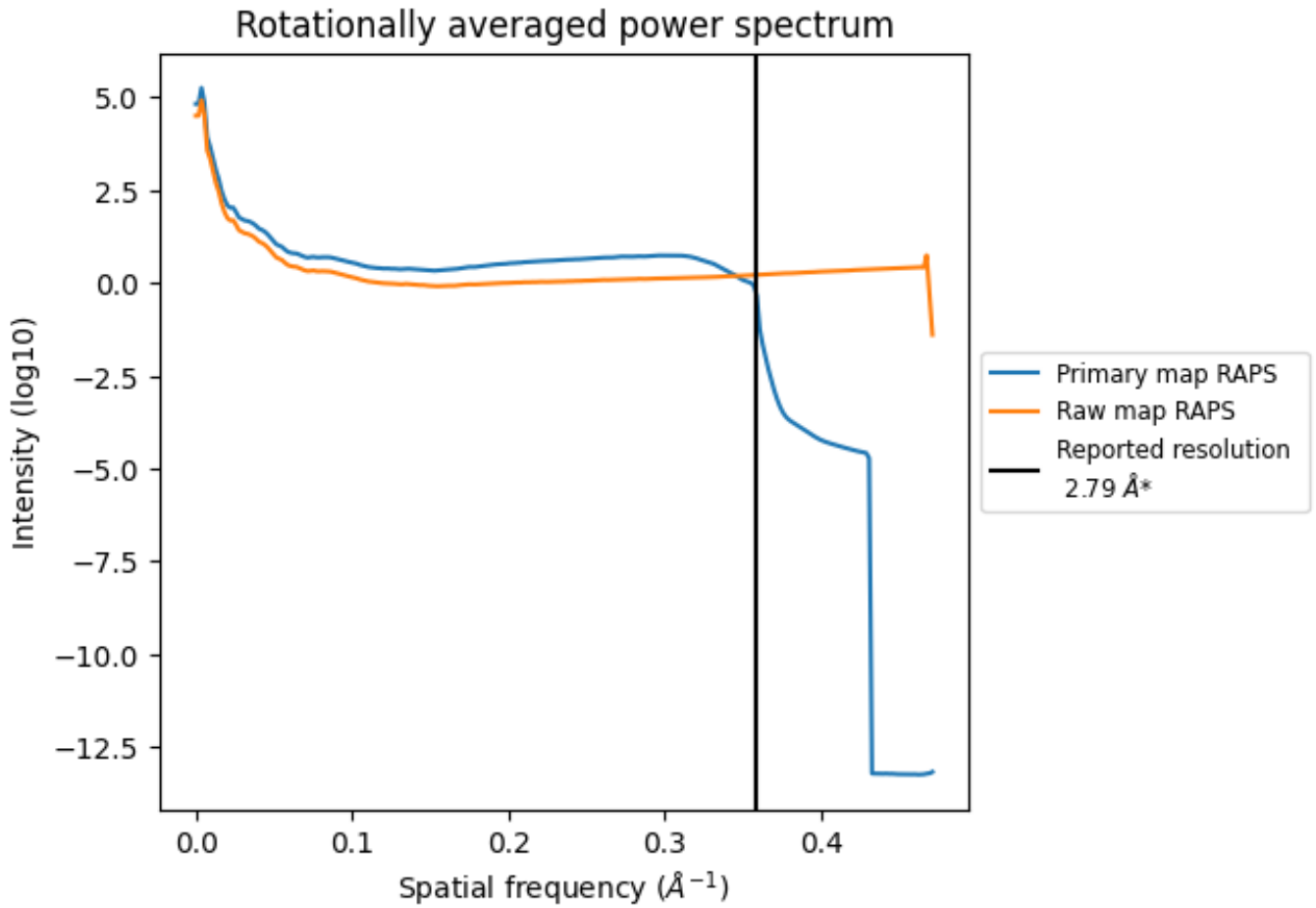
7.2 Volume estimate (i)



The volume at the recommended contour level is 353 nm^3; this corresponds to an approximate mass of 319 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)

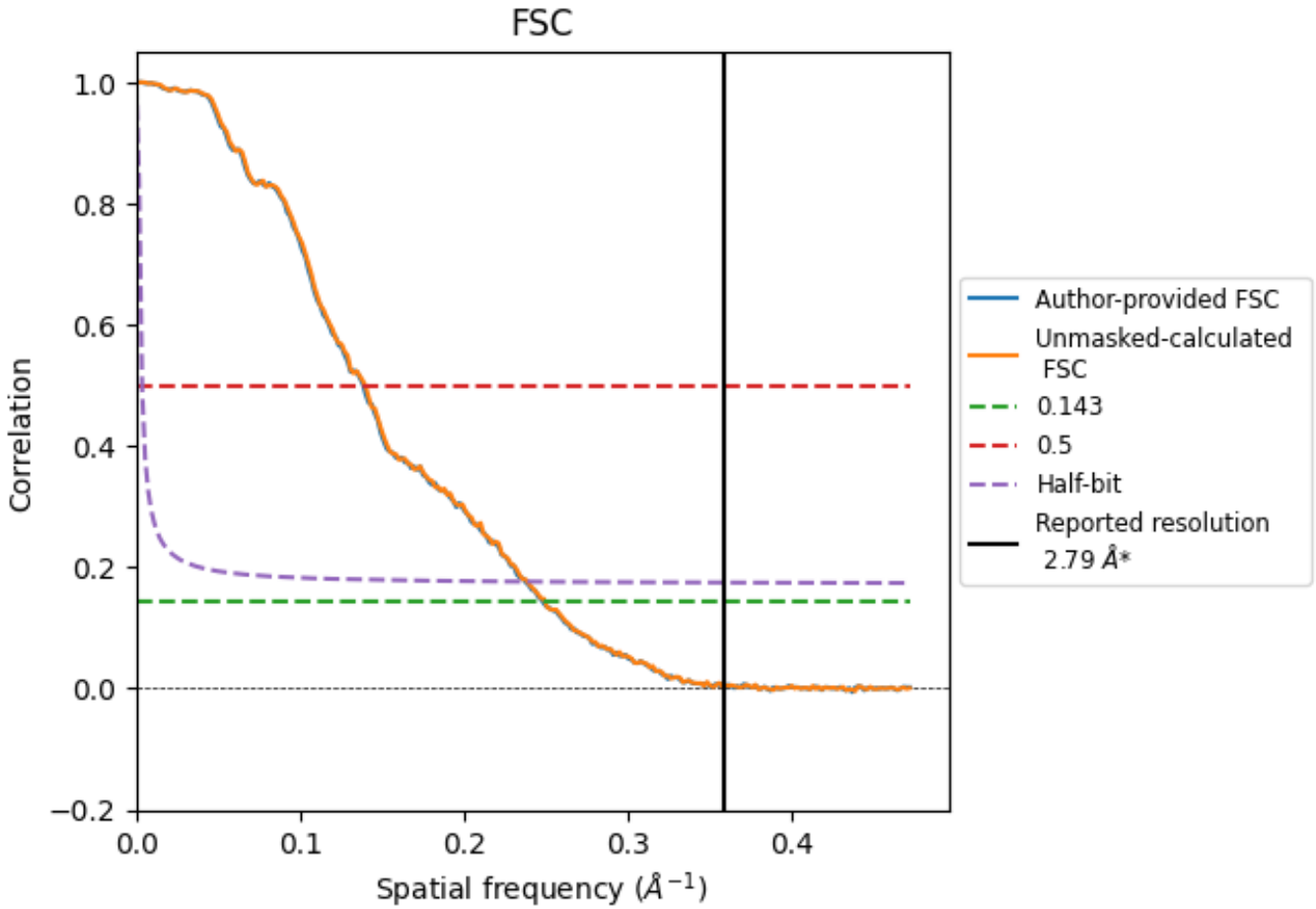


*Reported resolution corresponds to spatial frequency of 0.358 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.358 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.79	-	-
Author-provided FSC curve	4.03	7.22	4.21
Unmasked-calculated*	4.01	7.16	4.19

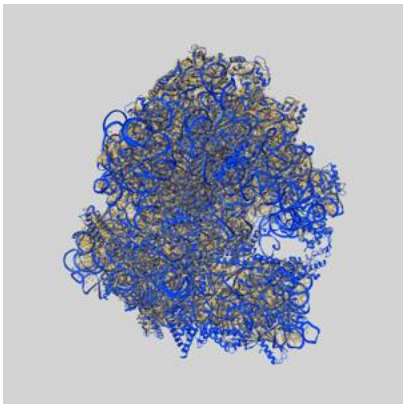
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 2.79 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.01 differs from the reported value 2.79 by more than 10 %

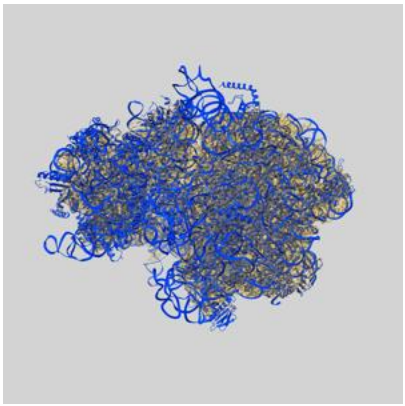
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55712 and PDB model 9T8U. Per-residue inclusion information can be found in section 3 on page 14.

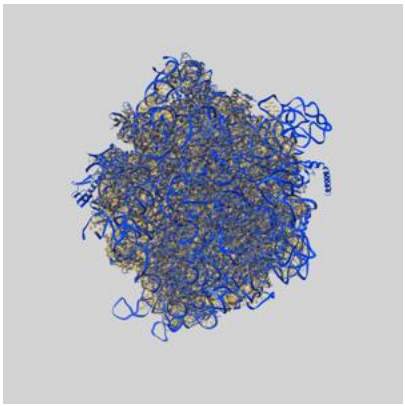
9.1 Map-model overlay



X



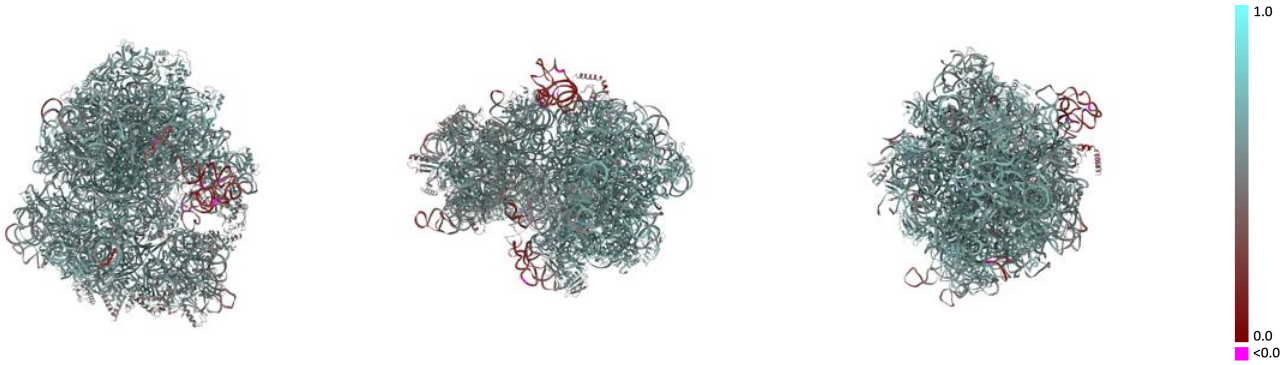
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

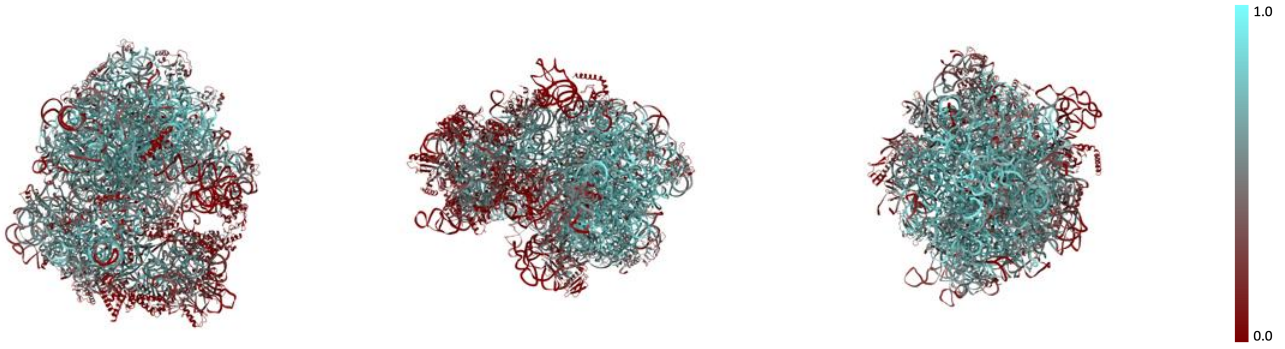
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

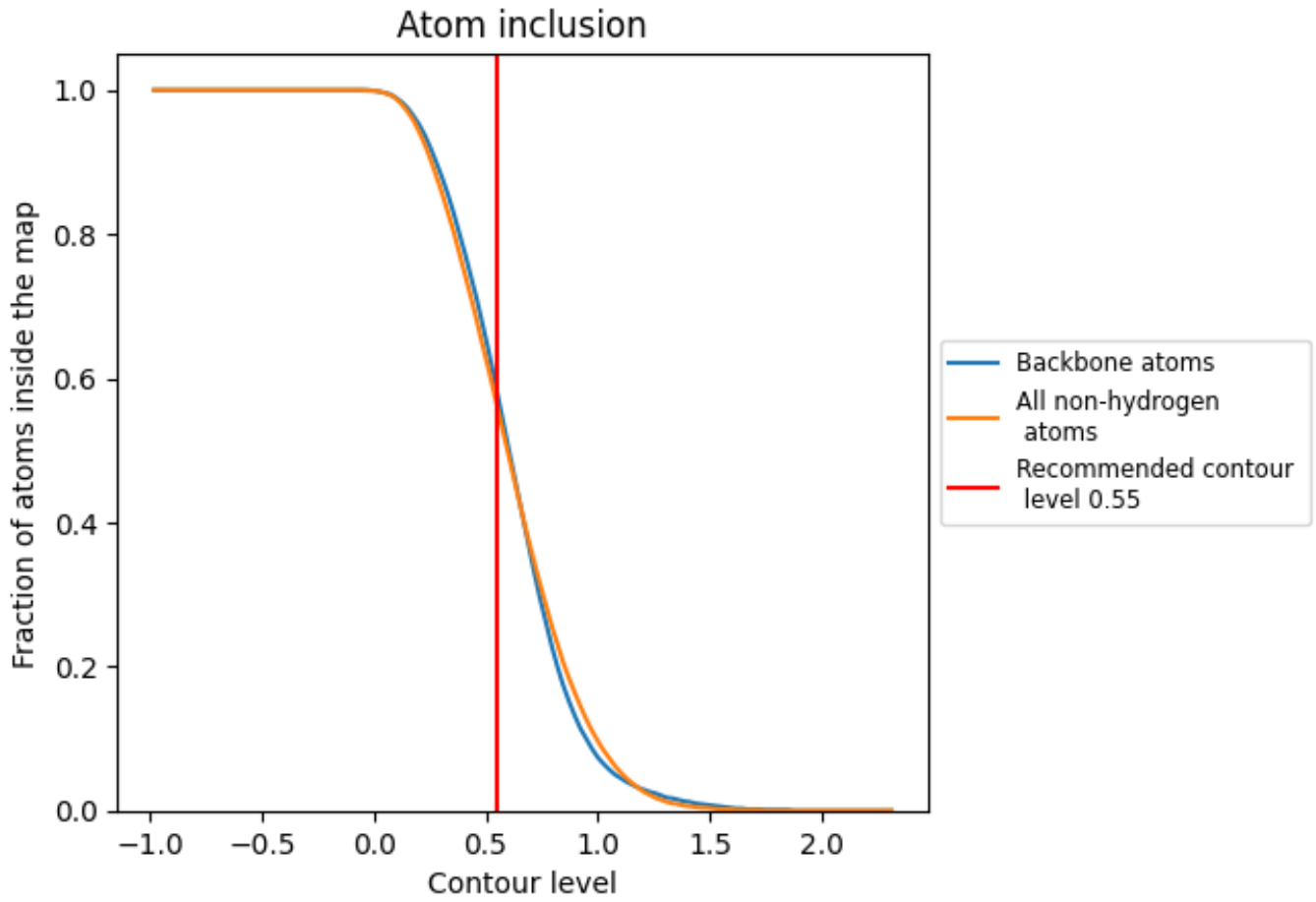
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.55).

9.4 Atom inclusion (i)



At the recommended contour level, 58% of all backbone atoms, 56% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5620	0.5800
0	0.3470	0.5950
1	0.7230	0.6320
2	0.6350	0.6330
3	0.5310	0.6130
4	0.0170	0.4300
A	0.5750	0.5760
B	0.0580	0.4920
C	0.3120	0.5660
D	0.3050	0.5650
E	0.4670	0.5900
F	0.2430	0.5590
G	0.1120	0.5130
H	0.4750	0.6020
I	0.1930	0.5430
J	0.1970	0.5040
K	0.3500	0.5710
L	0.4640	0.6020
M	0.1280	0.5250
N	0.3040	0.5560
O	0.4080	0.5840
P	0.5390	0.6060
Q	0.4050	0.5840
R	0.3910	0.5560
S	0.1350	0.5190
T	0.4500	0.5950
U	0.1460	0.5210
X	0.2520	0.5680
a	0.6790	0.5860
b	0.4850	0.5740
c	0.6350	0.6290
d	0.6320	0.6200
e	0.5320	0.6050
f	0.0730	0.5050
g	0.1620	0.5450



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Chain	Atom inclusion	Q-score
h	0.0000	0.3550
i	0.6140	0.6160
j	0.5280	0.6160
k	0.5720	0.6170
l	0.5320	0.6130
m	0.6600	0.6210
n	0.3310	0.5710
o	0.5280	0.6200
p	0.6570	0.6260
q	0.5110	0.6130
r	0.5850	0.6190
s	0.4610	0.5920
t	0.3500	0.5530
u	0.2500	0.5710
v	0.6100	0.6210
w	0.5270	0.6150
x	0.4060	0.5890
y	0.5590	0.6150
z	0.5730	0.6120