wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 02:40 PM EST

PDB ID	:	3JCS
EMDB ID	:	EMD-6583
Title	:	2.8 Angstrom cryo-EM structure of the large ribosomal subunit from the eukaryotic parasite Leishmania
Authors	:	Shalev-Benami, M.; Zhang, Y.; Matzov, D.; Halfon, Y.; Zackay, A.; Rozenberg, H.; Zimmerman, E.; Bashan, A.; Jaffe, C.L.; Yonath, A.; Skiniotis, G.
Deposited on	:	2016-01-21
Resolution	:	2.80 Å(reported)

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

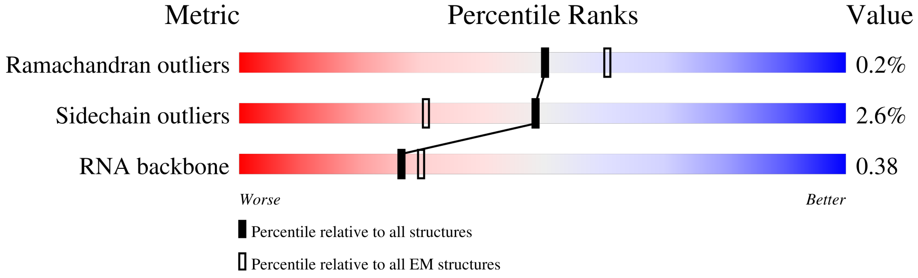
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance ⓘ

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

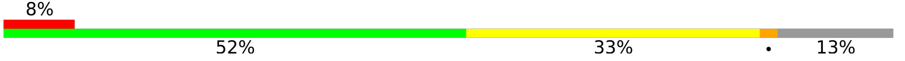
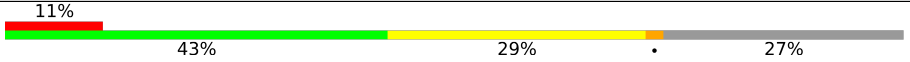
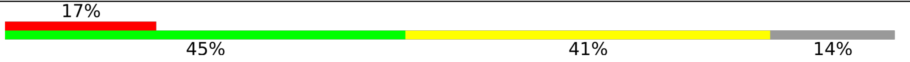
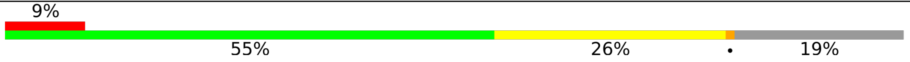
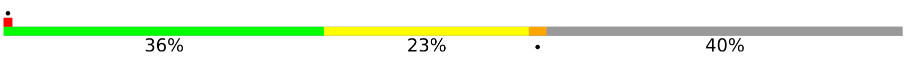
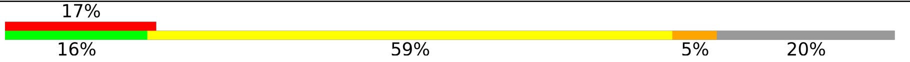
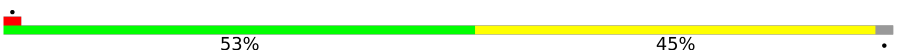
The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	1782	
2	2	1527	
3	3	213	
4	4	183	
5	5	133	
6	6	76	
7	7	171	
8	8	121	

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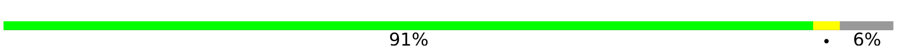
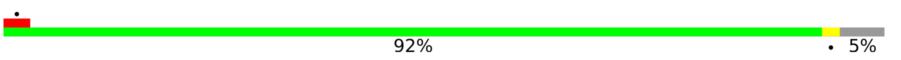
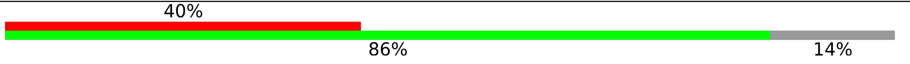
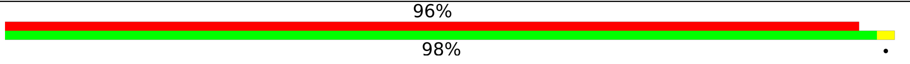
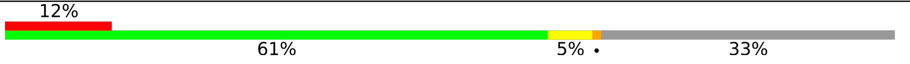
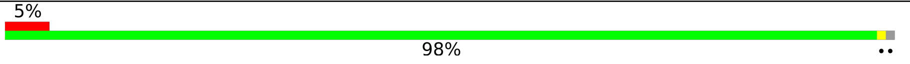
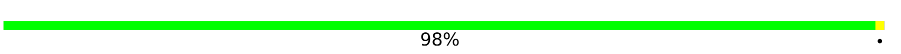
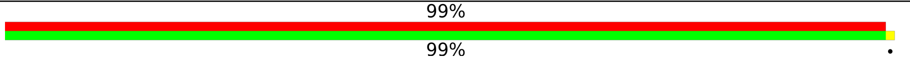
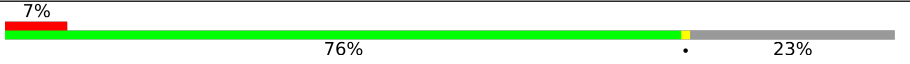
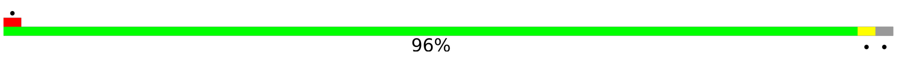
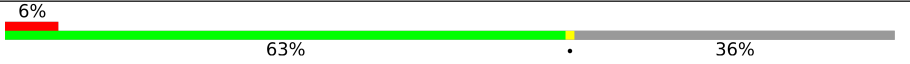
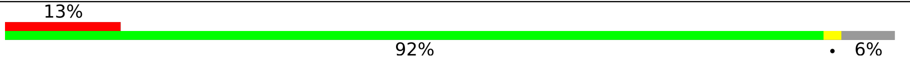
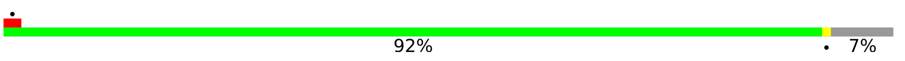
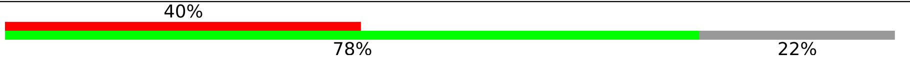
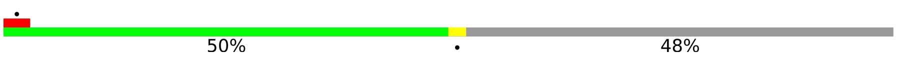
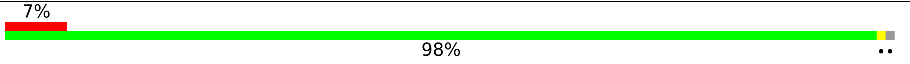
Mol	Chain	Length	Quality of chain
9	A	260	 91% • 6%
10	B	419	 • 92% • 5%
11	C	373	 • 80% 19%
12	D	188	 40% 86% 14%
13	E	190	 96% 98% •
14	F	195	 • 70% • 30%
15	G	348	 • 62% • 35%
16	H	222	 • 89% • 9%
17	I	220	 58% • 40%
18	J	139	 90% •• 8%
19	K	233	 12% 61% 5% • 33%
20	L	145	 5% 98% ••
21	M	204	 98% •
22	N	213	 99% 99% •
23	O	305	 7% 76% • 23%
24	P	198	 • 96% • •
25	Q	245	 6% 63% • 36%
26	R	179	 • 71% • • 27%
27	S	159	 13% 92% • 6%
28	T	166	 • 92% • 7%
29	U	129	 40% 78% 22%
30	V	145	 • 80% • 19%
31	W	143	 • 82% 18%
32	X	124	 • 50% • 48%
33	Y	134	 7% 98% ••

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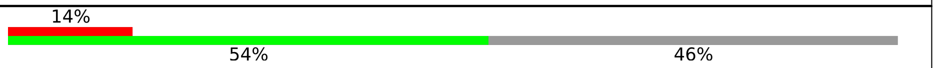
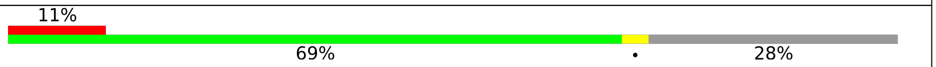
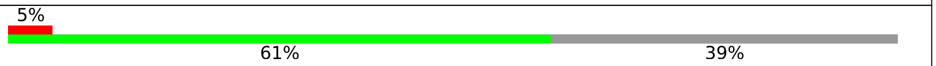
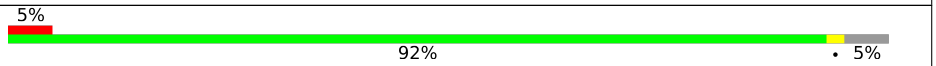
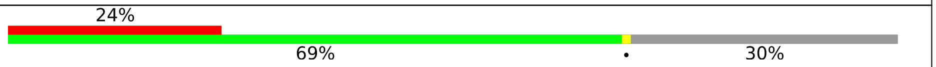
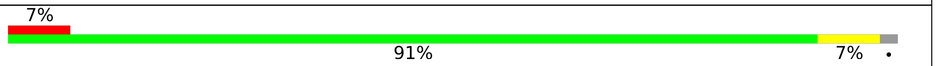
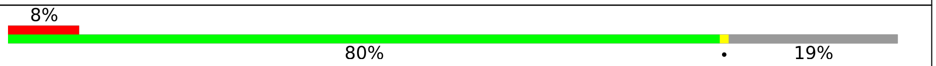
Mol	Chain	Length	Quality of chain
34	Z	147	 14% 54% 46%
35	a	127	 • 92% 6% •
36	b	70	 • 87% 6% 7%
37	c	252	 • 87% • 12%
38	d	104	 11% 69% • 28%
39	e	183	 5% 61% 39%
40	f	133	 5% 92% • 5%
41	g	144	 • 85% • 13%
42	h	168	 • 64% • 35%
43	i	105	 57% • 40%
44	j	83	 90% • 6%
45	k	83	 24% 69% • 30%
46	l	51	 92% 6% •
47	m	92	 7% 91% 7% •
48	n	106	 8% 80% • 19%

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 117257 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 26S alpha ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1554	33313	14886	6081	10792	1554	0	0

- Molecule 2 is a RNA chain called 26S delta ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	1119	23926	10702	4308	7797	1119	0	0

- Molecule 3 is a RNA chain called 26S gamma ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	3	184	3893	1740	662	1307	184	0	0

- Molecule 4 is a RNA chain called 26S delta ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	4	149	3177	1418	570	1040	149	0	0

- Molecule 5 is a RNA chain called 26S epsilon ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	5	80	1708	763	310	555	80	0	0

- Molecule 6 is a RNA chain called 26S zeta ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	61	1288	577	225	425	61	0	0

- Molecule 7 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	7	154	3280	1469	584	1074	153	0	0

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	8	119	2531	1132	450	830	119	0	0

- Molecule 9 is a protein called ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	A	245	1859	1158	384	307	10	2	0

- Molecule 10 is a protein called ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	B	396	3020	1908	592	508	12	2	0

- Molecule 11 is a protein called ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	301	2237	1413	428	384	12	1	0

- Molecule 12 is a protein called ribosomal protein L5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	D	161	799	476	161	162	0	0

- Molecule 13 is a protein called ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	E	190	1509	953	276	272	8	0	0

- Molecule 14 is a protein called ribosomal protein L6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	F	137	1002	641	192	167	2	1	0

- Molecule 15 is a protein called ribosomal protein L8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	G	226	1772	1113	353	299	7	1	0

- Molecule 16 is a protein called ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	H	202	1596	1019	307	263	7	0	0

- Molecule 17 is a protein called ribosomal protein L13e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	I	132	1061	666	221	169	5	0	0

- Molecule 18 is a protein called ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	128	924	588	171	160	5	0	0

- Molecule 19 is a protein called ribosomal protein L14e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	156	1061	661	212	184	4	0	0

- Molecule 20 is a protein called ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	144	1096	691	223	177	5	0	0

- Molecule 21 is a protein called ribosomal protein L15e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	M	203	1714	1080	362	264	8	0	0

- Molecule 22 is a protein called ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	N	213	1714	1077	340	281	16	0	0

- Molecule 23 is a protein called ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	O	235	1557	986	300	268	3	0	0

- Molecule 24 is a protein called ribosomal protein L18e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	P	195	1494	942	299	247	6	1	0

- Molecule 25 is a protein called ribosomal protein L19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Q	156	1162	730	243	186	3	0	0

- Molecule 26 is a protein called ribosomal protein L20e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	R	131	1019	651	197	167	4	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	158	ILE	LEU	VARIANT	UNP E9BRT7

- Molecule 27 is a protein called ribosomal protein L21e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	S	149	1112	704	218	187	3	2	0

- Molecule 28 is a protein called ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	T	154	1221	763	241	206	11	2	0

- Molecule 29 is a protein called ribosomal protein L22e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	U	100	541	331	101	109	0	0

- Molecule 30 is a protein called ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	V	118	892	566	171	153	2	0	0

- Molecule 31 is a protein called ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	W	117	896	562	187	144	3	1	0

- Molecule 32 is a protein called ribosomal protein L24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	X	64	508	333	96	76	3	0	0

- Molecule 33 is a protein called ribosomal protein L27e.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	Y	132	914	589	174	151	0	0

- Molecule 34 is a protein called ribosomal protein L28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	79	Total 538	C 329	N 111	O 95	S 3	0	0

- Molecule 35 is a protein called ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	124	Total 982	C 613	N 203	O 163	S 3	0	0

- Molecule 36 is a protein called ribosomal protein L29e.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	65	Total 503	C 309	N 113	O 80	S 1	0	0

- Molecule 37 is a protein called ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	222	Total 1732	C 1105	N 327	O 289	S 11	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
c	49	ALA	GLY	VARIANT	UNP E9BI29

- Molecule 38 is a protein called ribosomal protein L30e.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	75	Total 518	C 325	N 93	O 97	S 3	0	0

- Molecule 39 is a protein called ribosomal protein L31e.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	112	Total 824	C 531	N 155	O 136	S 2	1	0

- Molecule 40 is a protein called ribosomal protein L32e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	f	126	982	616	195	167	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	105	LYS	THR	VARIANT	UNP E9BFJ5

- Molecule 41 is a protein called ribosomal protein L33e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	g	125	983	612	205	161	5	0	0

- Molecule 42 is a protein called ribosomal protein L34e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	h	109	856	529	182	140	5	0	0

- Molecule 43 is a protein called ribosomal protein L36e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	i	63	494	316	100	76	2	1	0

- Molecule 44 is a protein called ribosomal protein L37e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	j	78	639	385	149	99	6	0	0

- Molecule 45 is a protein called ribosomal protein L38e.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	k	58	373	234	71	66	2	0	0

- Molecule 46 is a protein called ribosomal protein L39e.

Mol	Chain	Residues	Atoms	AltConf	Trace
46	l	50	Total C N O S 457 294 98 64 1	1	0

- Molecule 47 is a protein called ribosomal protein L43e.

Mol	Chain	Residues	Atoms	AltConf	Trace
47	m	90	Total C N O S 668 414 135 113 6	0	0

- Molecule 48 is a protein called ribosomal protein L44e.

Mol	Chain	Residues	Atoms	AltConf	Trace
48	n	86	Total C N O S 659 418 129 110 2	0	0

- Molecule 49 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
49	1	51	Total Mg 51 51	0
49	2	25	Total Mg 25 25	0
49	3	3	Total Mg 3 3	0
49	4	2	Total Mg 2 2	0
49	5	4	Total Mg 4 4	0
49	7	9	Total Mg 9 9	0
49	C	1	Total Mg 1 1	0
49	K	1	Total Mg 1 1	0
49	M	3	Total Mg 3 3	0
49	V	1	Total Mg 1 1	0
49	a	1	Total Mg 1 1	0
49	f	2	Total Mg 2 2	0

Continued on next page...

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Mol	Chain	Residues	Atoms	AltConf
49	g	1	Total Mg 1 1	0
49	h	1	Total Mg 1 1	0
49	j	4	Total Mg 4 4	0

- Molecule 50 is water.

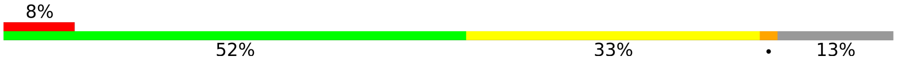
Mol	Chain	Residues	Atoms	AltConf
50	1	72	Total O 72 72	0
50	2	40	Total O 40 40	0
50	4	4	Total O 4 4	0
50	5	4	Total O 4 4	0
50	7	16	Total O 16 16	0
50	8	1	Total O 1 1	0
50	A	2	Total O 2 2	0
50	G	1	Total O 1 1	0
50	M	2	Total O 2 2	0
50	i	1	Total O 1 1	0
50	j	1	Total O 1 1	0

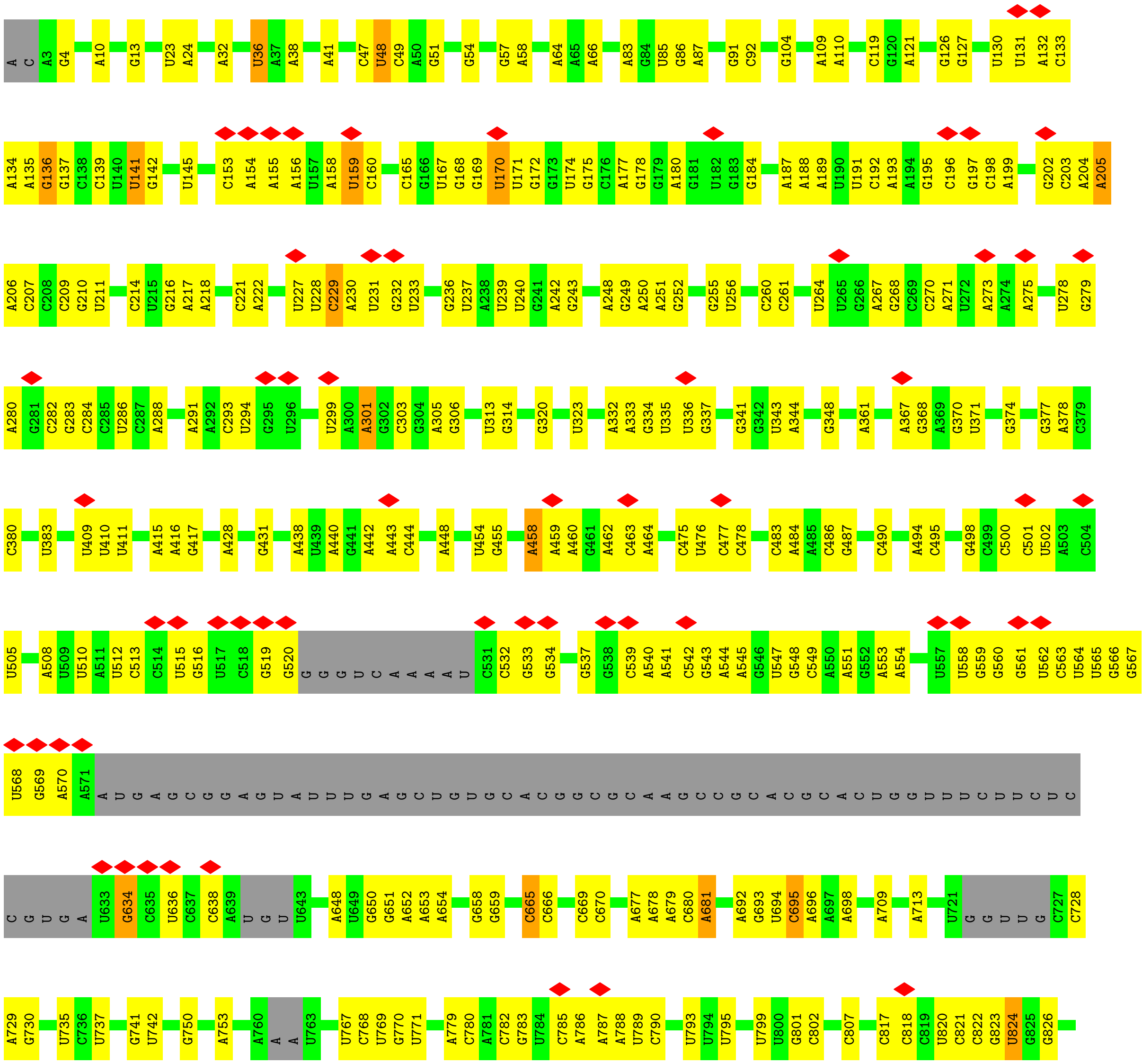
3 Residue-property plots ⓘ

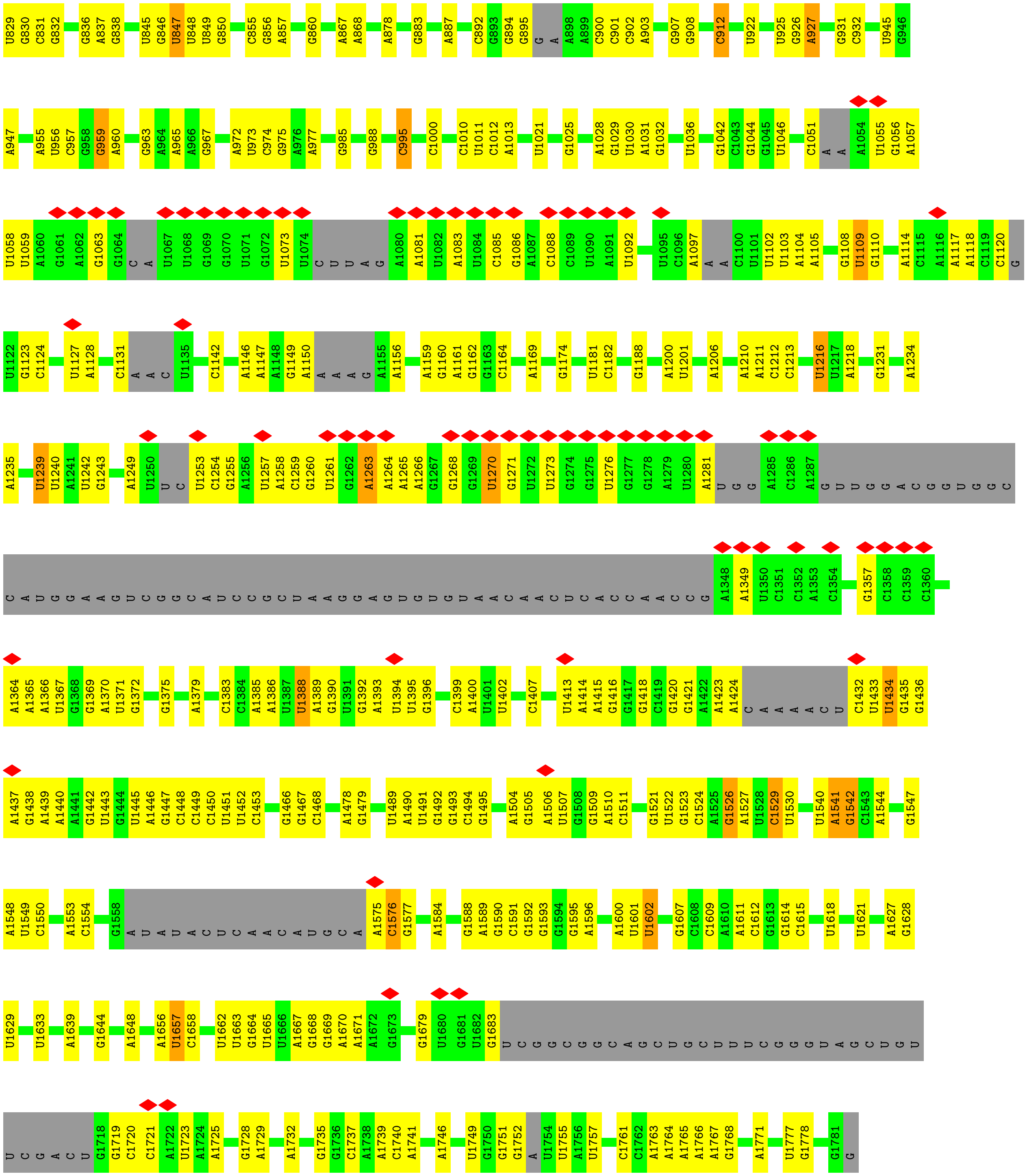
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 26S alpha ribosomal RNA

Chain 1:

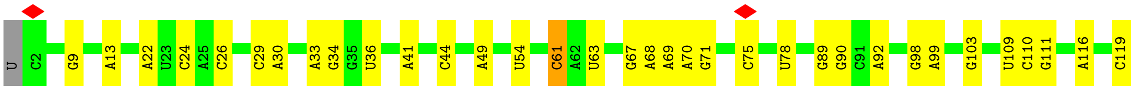


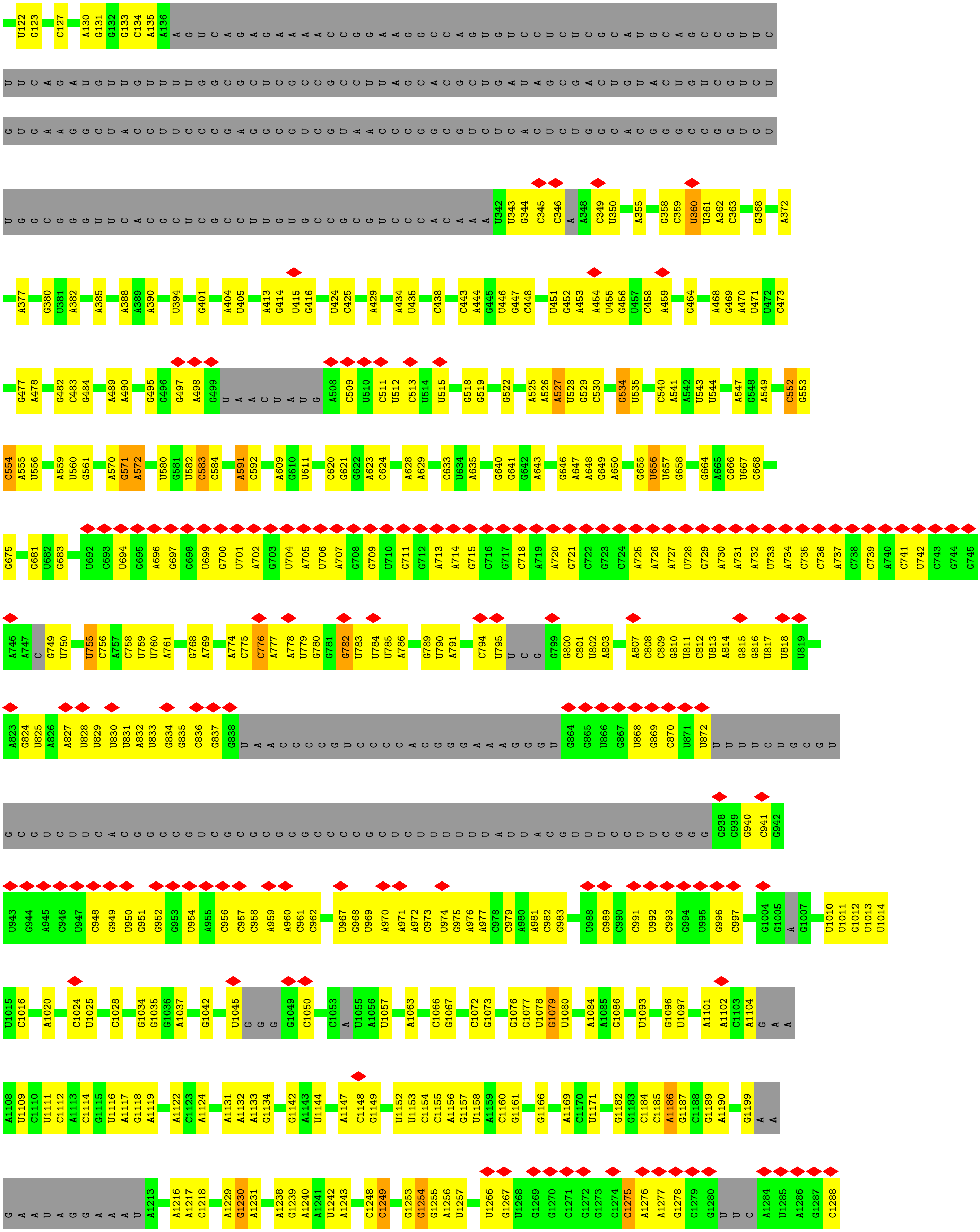


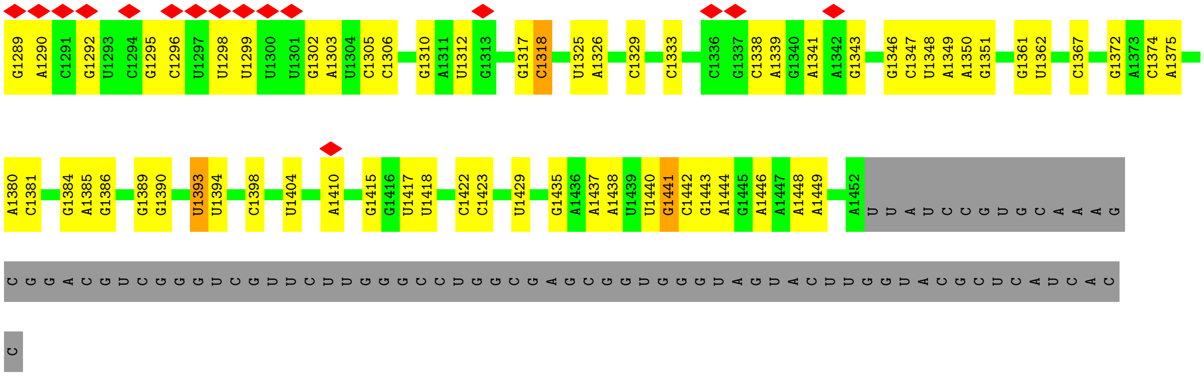


- Molecule 2: 26S delta ribosomal RNA

Chain 2:

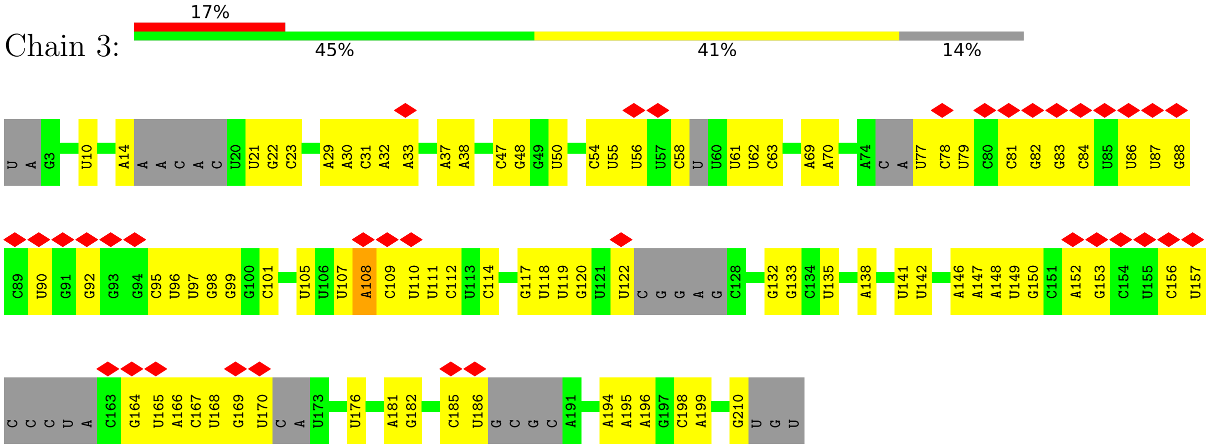




U122 G123 C127 A130 G131 G132 G133 C134 A135 A136 A G U C A G A G A A A A C C G G A A G G C C A G U G U C C U C U C G C A U G C A G C C G U U C
U U C A G A U G U U G U U U U G G C G C U C G C C G C C U U A G C A C G C U G A U A G C G A C U G U A C U G U C G U C U
G U G A A G G C U A C C U U C C C G A G G C G U C G U A A C C C G G C G U C U C A C U C U G G C A C G G G C C G G U C U
U G G C G G G U U C A C G C U C G C C U U G U G C C G C G U C C C A C A A A U342 U343 G344 C345 C346 A A348 C349 U350 A355 G358 C359 U360 U361 A362 C363 G368 A372
A377 G380 U381 A382 A385 A388 A389 A390 U394 G401 A404 U405 A413 G414 U415 G416 U424 C425 A429 A434 U435 C438 C443 A444 G445 U446 G447 C448 U451 G452 A453 A454 U455 G456 U457 C458 A459 G464 A468 G469 A470 U471 U472 C473
G477 A478 G482 C483 G484 A489 A490 G495 G496 G497 A498 G499 U A A C U A U G A508 C509 U510 C511 U512 C513 U514 U515 G518 G519 G522 A525 A526 A527 U528 G529 C530 G534 U535 C540 A541 A542 U543 U544 A547 G548 A549 C552 G553
C554 A555 U556 A559 U560 G561 A570 G571 A572 U580 G581 U582 C583 C584 A591 C592 A609 G610 U611 C620 G621 G622 A623 C624 A628 A629 C633 U634 A635 G640 G641 G642 A643 G646 A647 A648 G649 A650 G655 U656 U657 G658 G664 A665 C666 U667 C668
G675 G681 U682 G683 U692 C693 U694 G695 A696 G697 G698 U699 G700 U701 A702 G703 U704 A705 U706 A707 G708 G709 U710 G711 G712 A713 A714 G715 C716 G717 C718 A719 A720 G721 C722 G723 C724 A725 A726 A727 U728 G729 A730 A731 A732 U733 A734 C735 C736 A737 C738 C739 A740 C741 U742 C743 G744 G745
A746 A747 C G749 U750 U755 C756 A757 C758 U759 U760 A761 G768 A769 A774 C775 C776 A777 A778 U779 G780 G781 G782 U783 U784 U785 A786 G789 U790 A791 C794 U795 U C G G799 G800 C801 U802 A803 A807 C808 C809 G810 U811 C812 U813 A814 G815 G816 U817 U818 U819
A823 G824 U825 A826 A827 U828 U829 U830 U831 A832 U833 G834 G835 C836 G837 G838 U A A C C C C G U C C C C A C G G G A A A G G G U G864 G865 U866 G867 U868 G869 C870 U871 U872 U U U U C U G C G U
G C G U C U U C A C G G G C G U C G C G C G G G C C C C G C U C U U U U U U A U U A C G U U U C C U U C G G G G938 G939 G940 C941 G942
U943 G944 A945 C946 U947 C948 G949 U950 G951 G952 G953 U954 A955 C956 C957 C958 A959 A960 C961 C962 U967 G968 U969 A970 A971 A972 C973 U974 G975 A976 A977 C978 C979 A980 A981 C982 G983 U988 G989 C990 C991 U992 C993 G994 U995 G996 C997 G1004 G1005 A G1007 U1010 U1011 G1012 U1013 U1014
U1015 C1016 A1020 C1024 U1025 C1028 G1034 G1035 G1036 A1037 G1042 U1045 G G G G1049 C1050 C1053 A U1055 A1056 U1057 A1063 C1066 G1067 C1072 G1073 G1076 G1077 U1078 G1079 U1080 A1084 A1085 G1086 U1093 G1096 U1097 A1101 A1102 C1103 A1104 G A A
A1108 U1109 C1110 U1111 C1112 A1113 C1114 G1115 U1116 A1117 G1118 A1119 A1122 C1123 A1124 A1131 A1132 A1133 G1134 G1142 A1143 U1144 A1147 C1148 G1149 U1152 U1153 C1154 C1155 A1156 G1157 U1158 A1159 C1160 G1161 G1166 A1169 C1170 U1171 G1182 G1183 C1184 C1185 A1186 G1187 C1188 G1189 A1190 G1199 A A
G A A U A G G A A A U A1213 A1216 A1217 C1218 A1229 G1230 A1231 A1238 G1239 A1240 A1241 U1242 A1243 C1248 C1249 G1253 G1254 G1255 A1256 U1257 U1266 G1267 U1268 G1269 G1270 C1271 G1272 G1273 C1274 C1275 A1276 A1277 G1278 C1279 G1280 U U C A1284 U1285 A1286 G1287 C1288



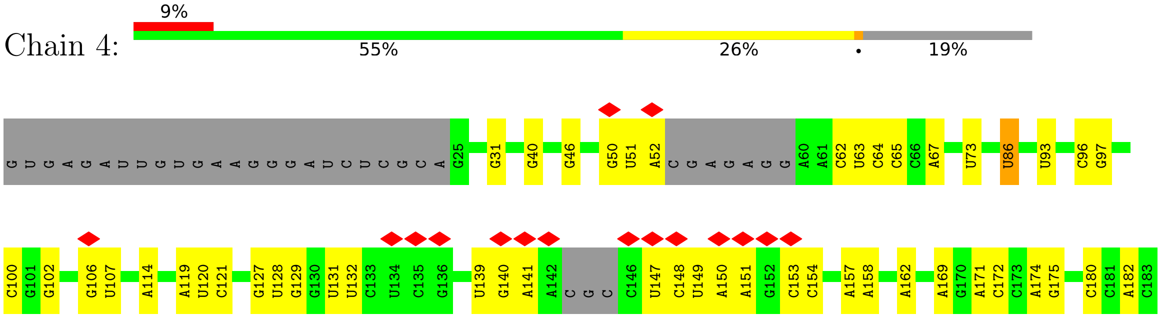
- Molecule 3: 26S gamma ribosomal RNA

Chain 3:



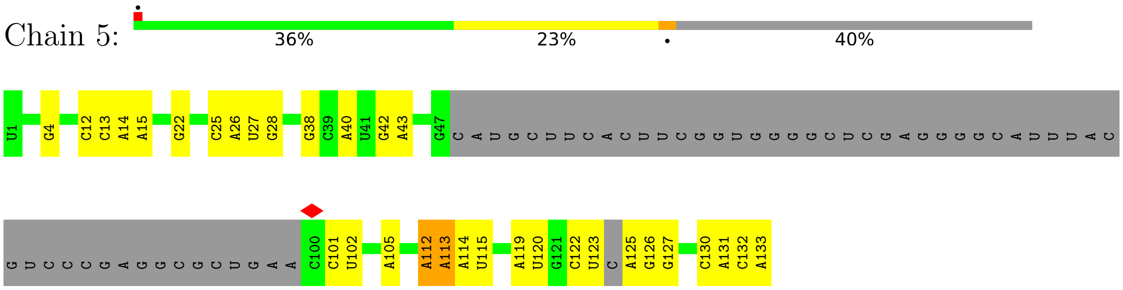
- Molecule 4: 26S delta ribosomal RNA

Chain 4:



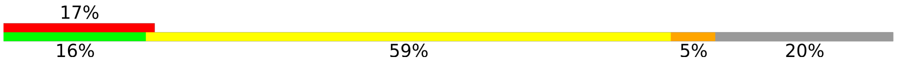
- Molecule 5: 26S epsilon ribosomal RNA

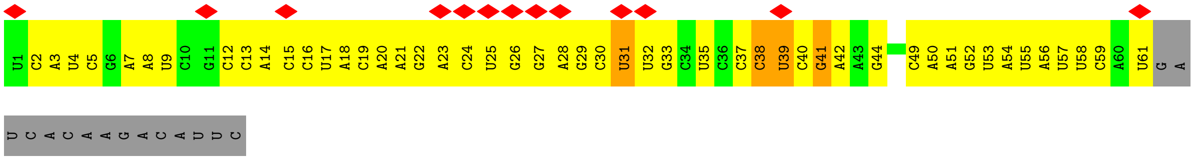
Chain 5:



- Molecule 6: 26S zeta ribosomal RNA

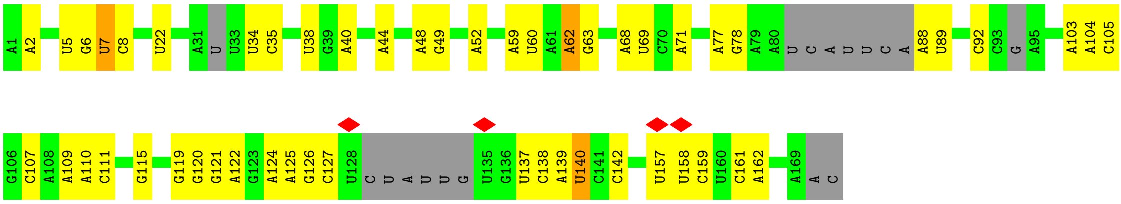
Chain 6:





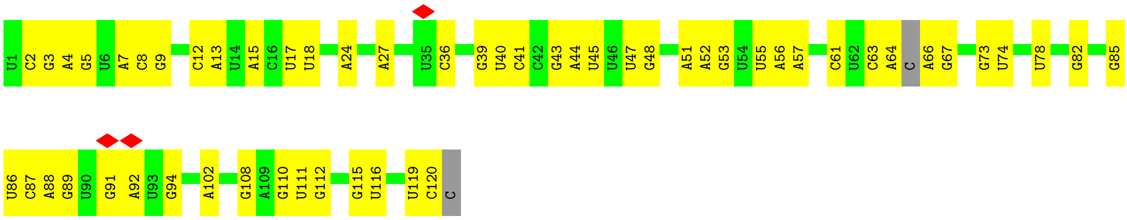
- Molecule 7: 5.8S ribosomal RNA

Chain 7:



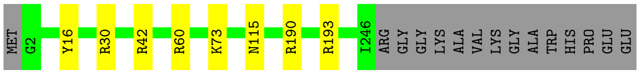
- Molecule 8: 5S ribosomal RNA

Chain 8:



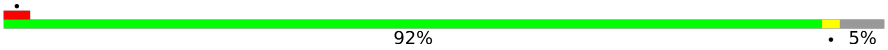
- Molecule 9: ribosomal protein L2

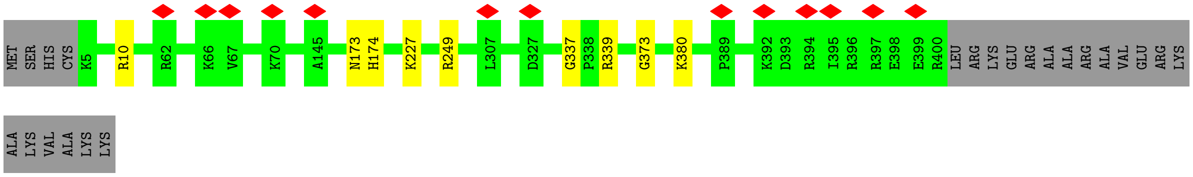
Chain A:



- Molecule 10: ribosomal protein L3

Chain B:



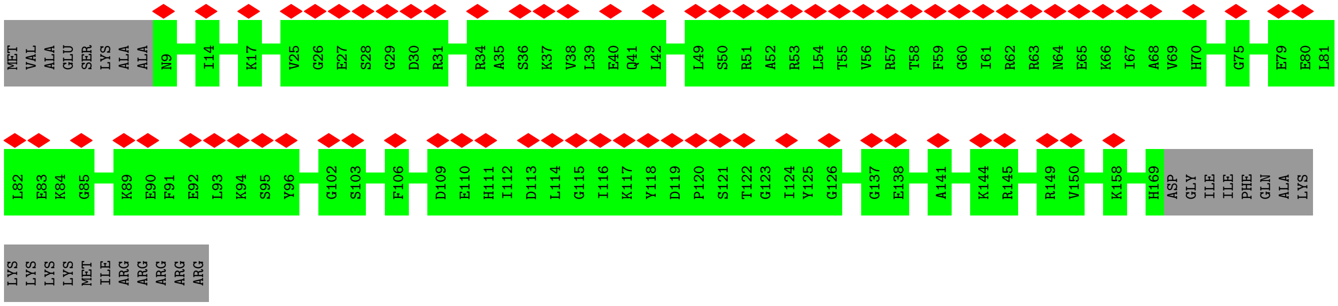


- Molecule 11: ribosomal protein L4

Chain C:

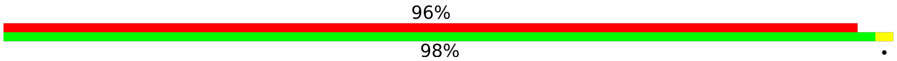
- Molecule 12: ribosomal protein L5

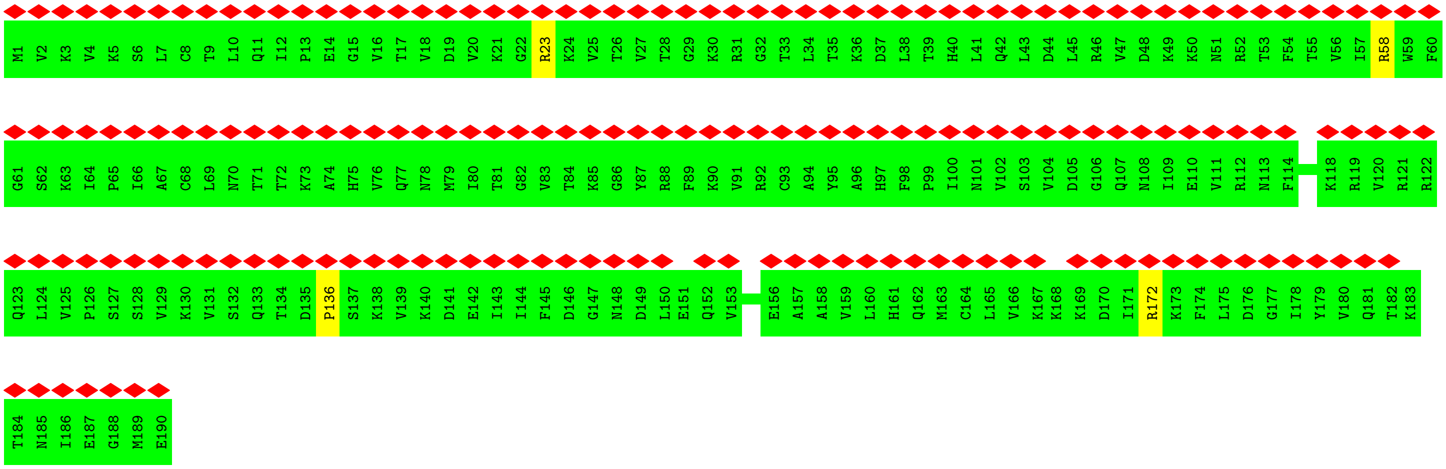
Chain D:



- Molecule 13: ribosomal protein L6

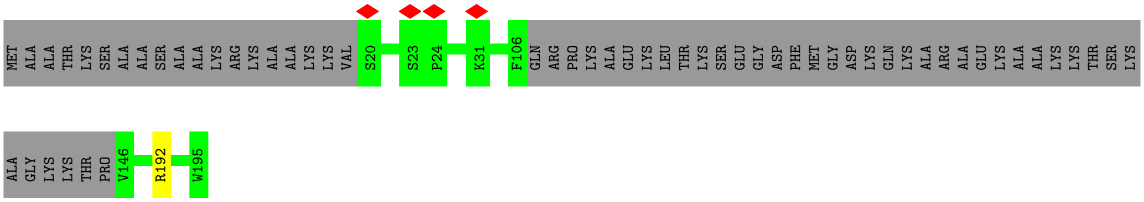
Chain E:



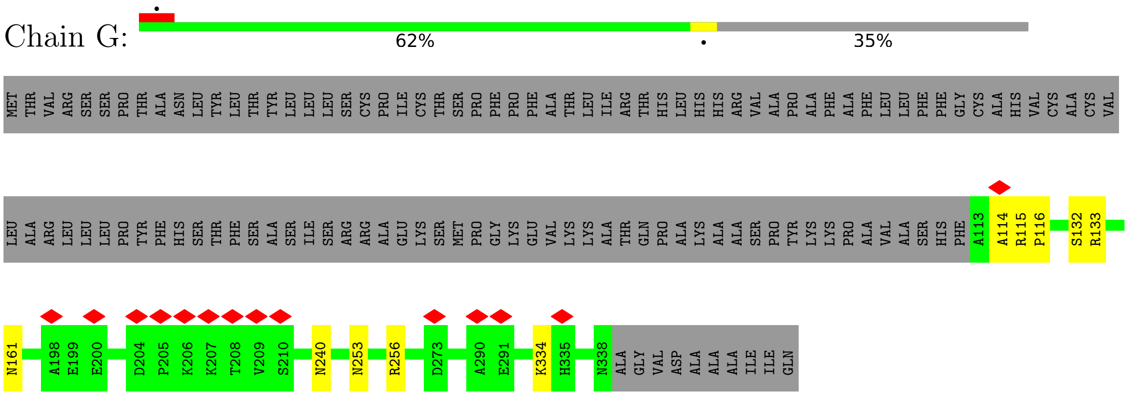


- Molecule 14: ribosomal protein L6e

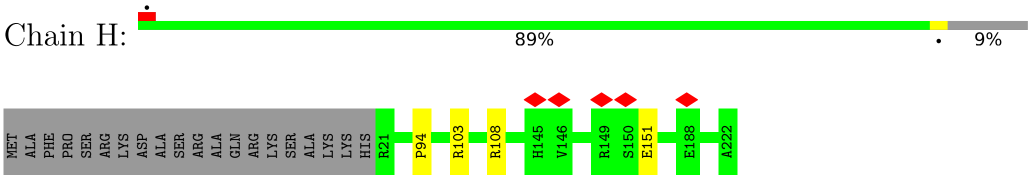
Chain F:



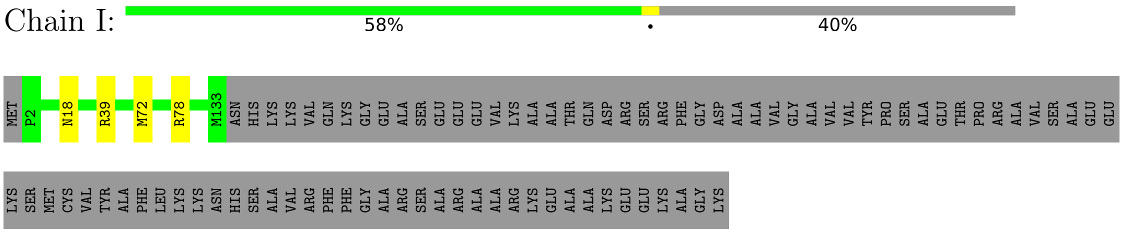
- Molecule 15: ribosomal protein L8e



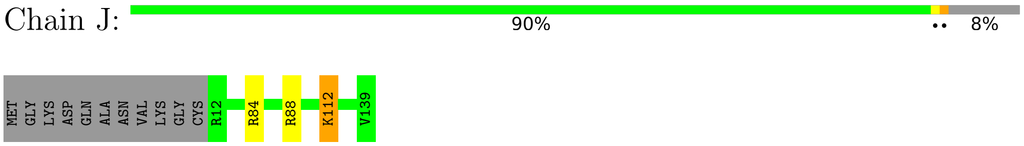
- Molecule 16: ribosomal protein L13



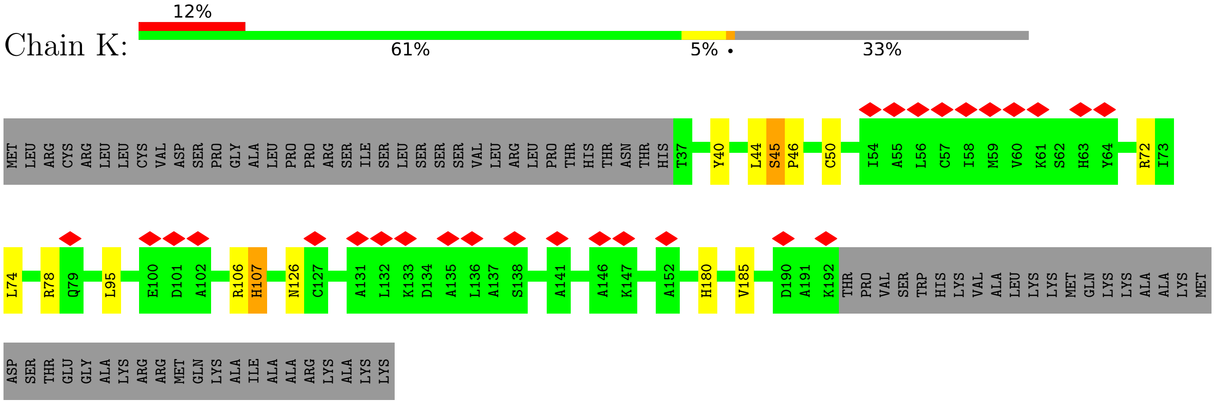
- Molecule 17: ribosomal protein L13e



- Molecule 18: ribosomal protein L14

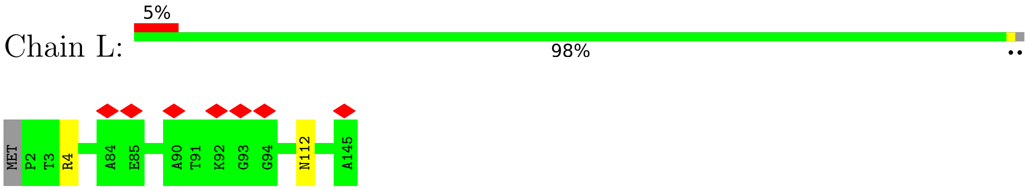


- Molecule 19: ribosomal protein L14e



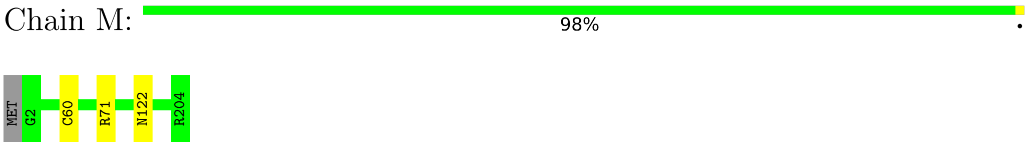
- Molecule 20: ribosomal protein L15

Chain L:



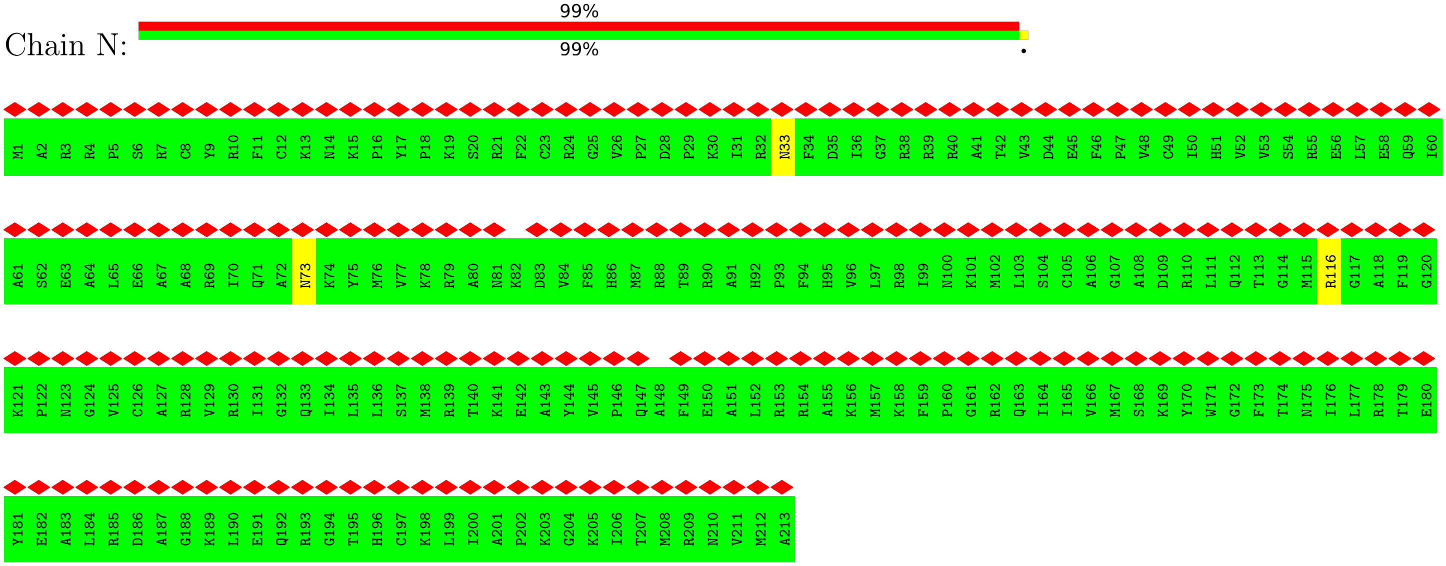
- Molecule 21: ribosomal protein L15e

Chain M:



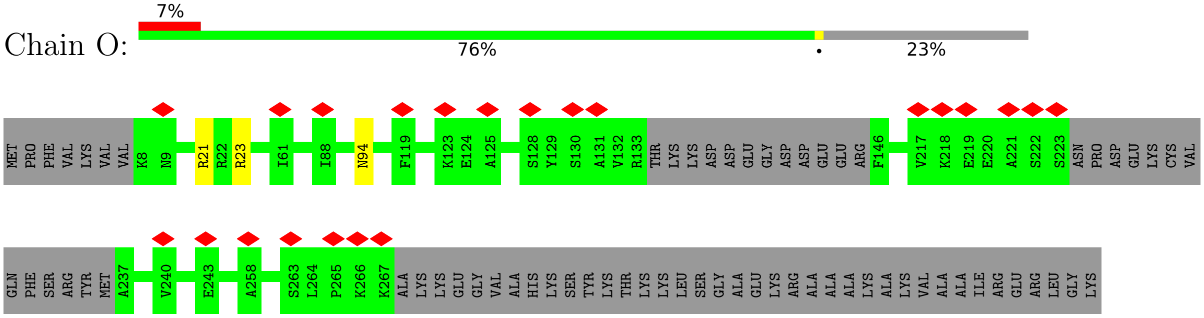
- Molecule 22: ribosomal protein L16

Chain N:



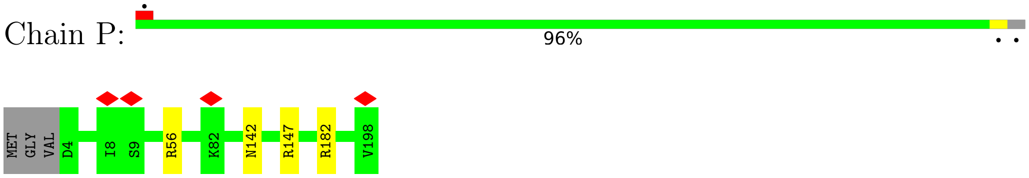
- Molecule 23: ribosomal protein L18

Chain O:

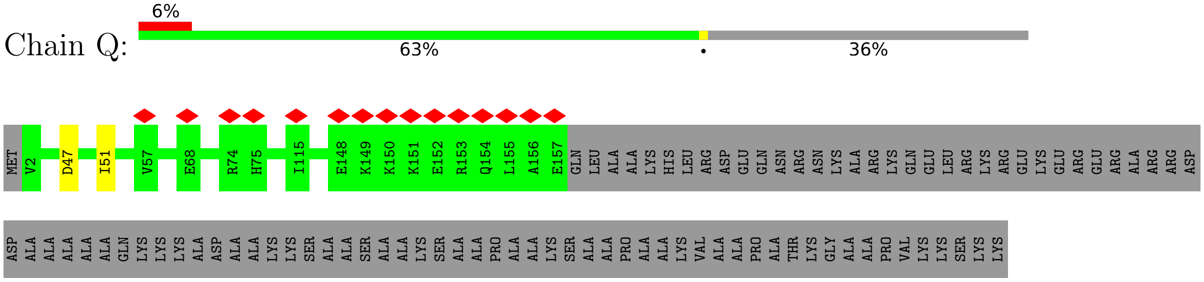


- Molecule 24: ribosomal protein L18e

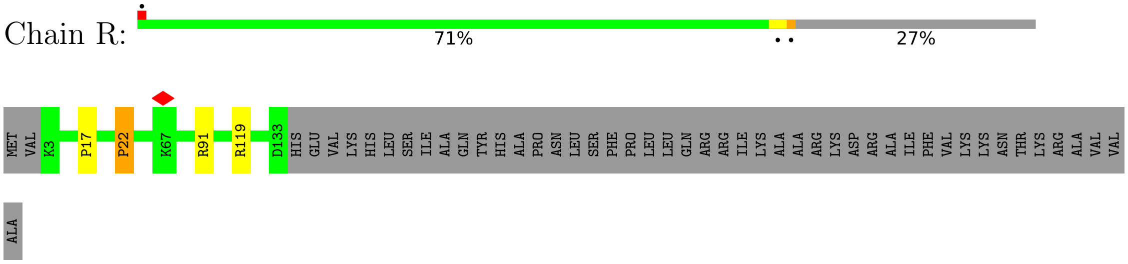
Chain P:



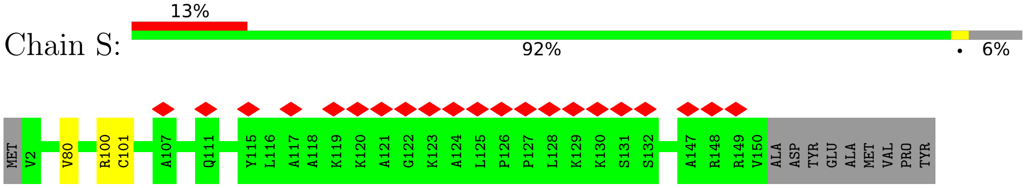
- Molecule 25: ribosomal protein L19e



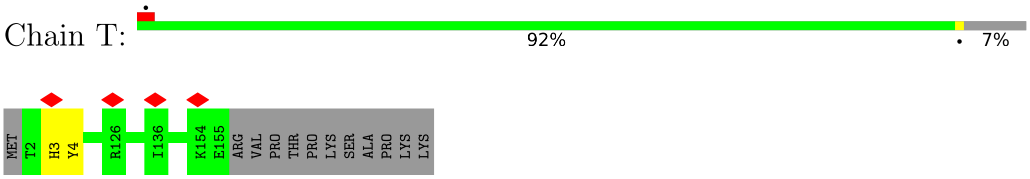
- Molecule 26: ribosomal protein L20e



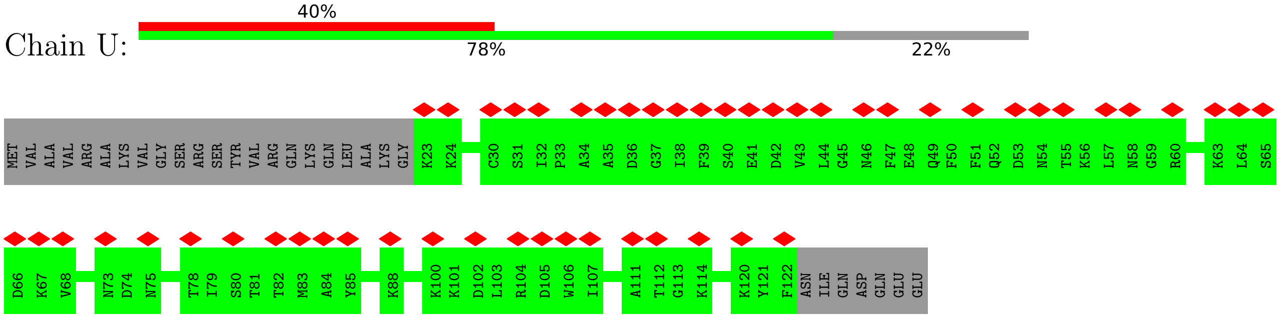
- Molecule 27: ribosomal protein L21e



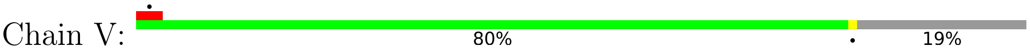
- Molecule 28: ribosomal protein L22

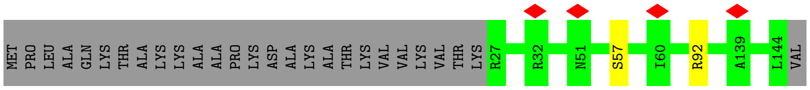


- Molecule 29: ribosomal protein L22e



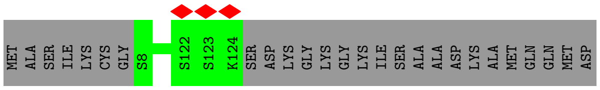
- Molecule 30: ribosomal protein L23





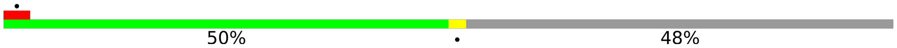
- Molecule 31: ribosomal protein L24

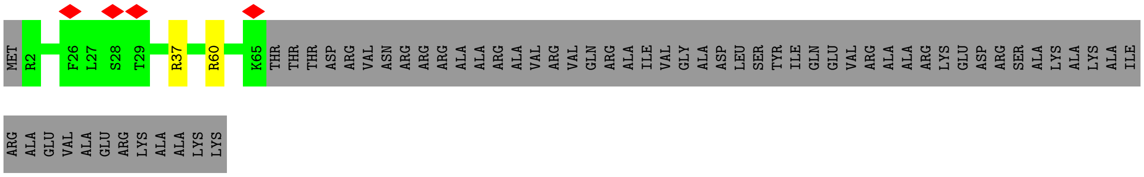
Chain W:



- Molecule 32: ribosomal protein L24e

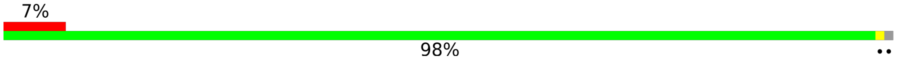
Chain X:

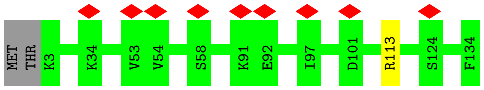




- Molecule 33: ribosomal protein L27e

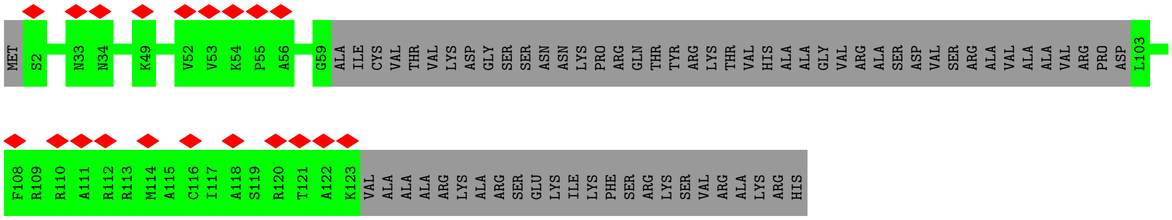
Chain Y:





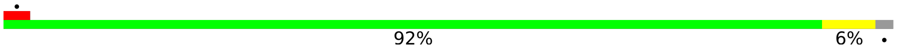
- Molecule 34: ribosomal protein L28e

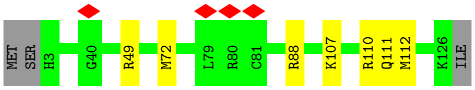
Chain Z:



- Molecule 35: ribosomal protein L29

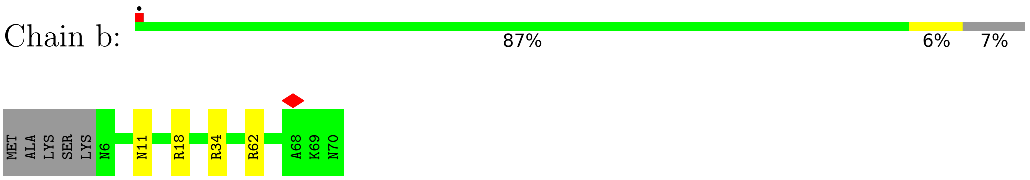
Chain a:





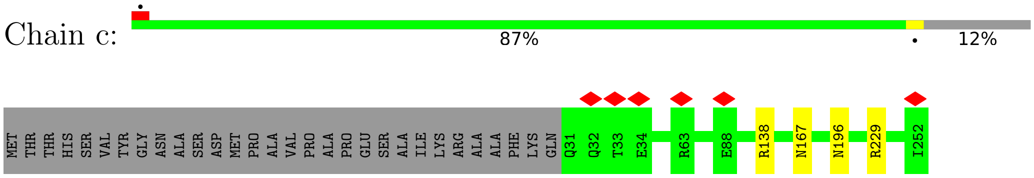
- Molecule 36: ribosomal protein L29e

Chain b:



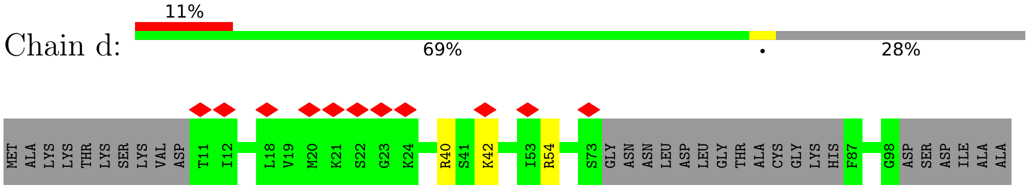
- Molecule 37: ribosomal protein L30

Chain c:



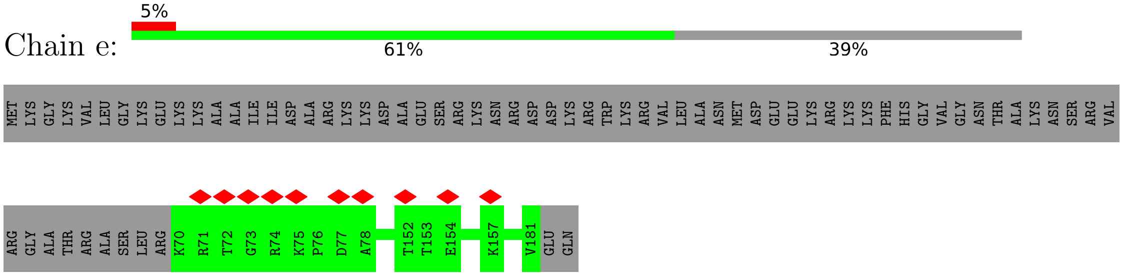
- Molecule 38: ribosomal protein L30e

Chain d:



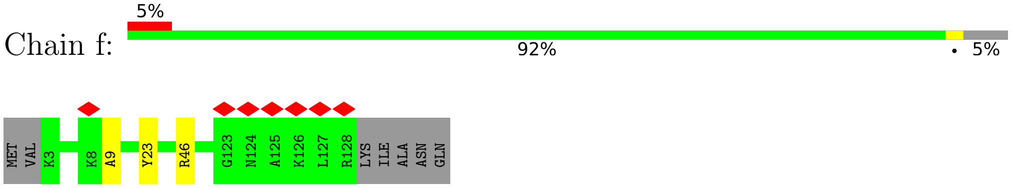
- Molecule 39: ribosomal protein L31e

Chain e:



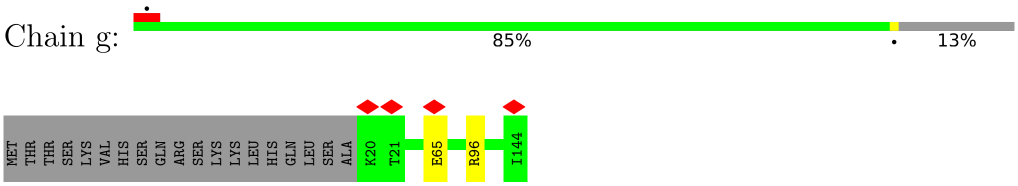
- Molecule 40: ribosomal protein L32e

Chain f:



- Molecule 41: ribosomal protein L33e

Chain g:



- Molecule 42: ribosomal protein L34e

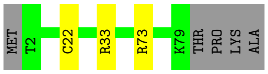
Chain h:

- Molecule 43: ribosomal protein L36e

Chain i:

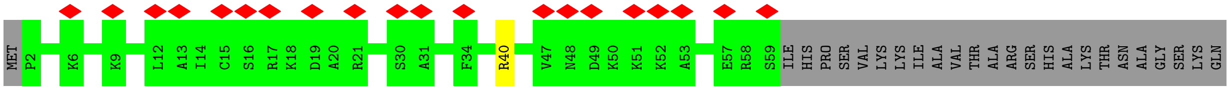
- Molecule 44: ribosomal protein L37e

Chain j:



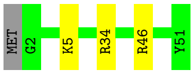
- Molecule 45: ribosomal protein L38e

Chain k:



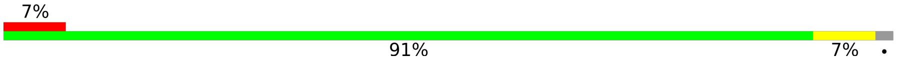
- Molecule 46: ribosomal protein L39e

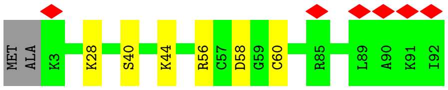
Chain l:



- Molecule 47: ribosomal protein L43e

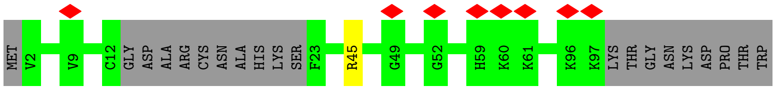
Chain m:





- Molecule 48: ribosomal protein L44e

Chain n:



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	107134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	30	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	25000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.231	Depositor
Minimum map value	-0.118	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	384.0, 384.0, 384.0	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, H2U, OMU, OMG, MG, A2M

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	0.75	8/36881 (0.0%)	0.90	48/57466 (0.1%)
2	2	0.60	0/26109	0.86	28/40668 (0.1%)
3	3	0.48	0/4337	0.84	1/6734 (0.0%)
4	4	0.69	0/3549	0.88	3/5525 (0.1%)
5	5	0.69	0/1908	0.91	3/2967 (0.1%)
6	6	0.39	2/1437 (0.1%)	0.79	4/2234 (0.2%)
7	7	0.76	0/3615	0.87	2/5622 (0.0%)
8	8	0.47	0/2828	0.82	0/4401
9	A	0.47	0/1903	0.56	0/2559
10	B	0.44	0/3086	0.55	0/4176
11	C	0.45	0/2284	0.60	0/3092
12	D	0.25	0/800	0.49	0/1111
13	E	0.29	0/1529	0.56	0/2056
14	F	0.40	0/1023	0.56	0/1390
15	G	0.38	0/1798	0.59	1/2423 (0.0%)
16	H	0.42	0/1628	0.60	0/2194
17	I	0.40	0/1084	0.57	0/1454
18	J	0.39	0/941	0.61	2/1277 (0.2%)
19	K	0.27	0/1077	0.59	1/1475 (0.1%)
20	L	0.43	0/1123	0.56	0/1505
21	M	0.49	0/1754	0.57	0/2342
22	N	0.27	0/1747	0.54	0/2338
23	O	0.32	0/1583	0.50	0/2157
24	P	0.42	0/1519	0.57	0/2040
25	Q	0.35	0/1179	0.53	0/1588
26	R	0.42	0/1044	0.59	1/1415 (0.1%)
27	S	0.43	0/1142	0.60	0/1547
28	T	0.45	0/1249	0.65	1/1679 (0.1%)
29	U	0.26	0/545	0.49	0/754
30	V	0.42	0/907	0.51	0/1227
31	W	0.37	0/910	0.56	0/1224
32	X	0.40	0/527	0.53	0/716

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Y	0.37	0/934	0.51	0/1274
34	Z	0.28	0/545	0.52	0/739
35	a	0.32	0/992	0.53	0/1326
36	b	0.34	0/514	0.50	0/690
37	c	0.42	0/1763	0.52	0/2374
38	d	0.31	0/525	0.50	0/719
39	e	0.37	0/838	0.57	0/1131
40	f	0.46	0/1002	0.55	0/1346
41	g	0.49	0/1003	0.53	0/1352
42	h	0.38	0/868	0.55	0/1160
43	i	0.38	0/499	0.56	0/662
44	j	0.50	0/651	0.61	0/869
45	k	0.30	0/378	0.57	0/518
46	l	0.43	0/470	0.51	0/627
47	m	0.43	0/680	0.53	0/913
48	n	0.34	0/667	0.56	0/889
All	All	0.59	10/125375 (0.0%)	0.79	95/185945 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	A	0	1
10	B	0	2
13	E	0	1
15	G	0	1
16	H	0	1
19	K	0	3
26	R	0	1
27	S	0	1
28	T	0	1
40	f	0	1
All	All	0	13

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	634	G	C1'-N9	-6.69	1.37	1.46
1	1	159	U	C1'-N1	6.17	1.58	1.48
1	1	568	U	C1'-N1	6.06	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	564	U	C1'-N1	5.95	1.57	1.48
1	1	565	U	C1'-N1	5.91	1.57	1.48

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
19	K	45	SER	C-N-CD	-11.87	94.48	120.60
1	1	1575	A	OP1-P-O3'	-11.81	79.22	105.20
1	1	1757	U	C2-N1-C1'	8.96	128.45	117.70
2	2	776	C	N1-C2-O2	8.91	124.25	118.90
2	2	776	C	C2-N1-C1'	8.72	128.39	118.80

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	A	60[B]	ARG	Mainchain
10	B	337	GLY	Peptide
10	B	373	GLY	Peptide
13	E	136	PRO	Peptide
15	G	114	ALA	Peptide

5.2 Too-close contacts ⓘ

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	A	245/260 (94%)	220 (90%)	25 (10%)	0	100	100
10	B	396/419 (94%)	352 (89%)	43 (11%)	1 (0%)	41	72

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	C	300/373 (80%)	269 (90%)	31 (10%)	0	100	100
12	D	159/188 (85%)	136 (86%)	23 (14%)	0	100	100
13	E	188/190 (99%)	160 (85%)	28 (15%)	0	100	100
14	F	134/195 (69%)	112 (84%)	22 (16%)	0	100	100
15	G	225/348 (65%)	205 (91%)	18 (8%)	2 (1%)	17	46
16	H	200/222 (90%)	175 (88%)	24 (12%)	1 (0%)	29	61
17	I	130/220 (59%)	120 (92%)	10 (8%)	0	100	100
18	J	126/139 (91%)	115 (91%)	11 (9%)	0	100	100
19	K	154/233 (66%)	136 (88%)	17 (11%)	1 (1%)	25	56
20	L	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
21	M	201/204 (98%)	187 (93%)	14 (7%)	0	100	100
22	N	211/213 (99%)	186 (88%)	25 (12%)	0	100	100
23	O	229/305 (75%)	205 (90%)	24 (10%)	0	100	100
24	P	194/198 (98%)	179 (92%)	15 (8%)	0	100	100
25	Q	154/245 (63%)	141 (92%)	13 (8%)	0	100	100
26	R	130/179 (73%)	104 (80%)	25 (19%)	1 (1%)	19	49
27	S	149/159 (94%)	125 (84%)	22 (15%)	2 (1%)	12	36
28	T	154/166 (93%)	127 (82%)	27 (18%)	0	100	100
29	U	98/129 (76%)	81 (83%)	17 (17%)	0	100	100
30	V	116/145 (80%)	99 (85%)	17 (15%)	0	100	100
31	W	116/143 (81%)	106 (91%)	10 (9%)	0	100	100
32	X	62/124 (50%)	59 (95%)	3 (5%)	0	100	100
33	Y	130/134 (97%)	111 (85%)	19 (15%)	0	100	100
34	Z	75/147 (51%)	65 (87%)	10 (13%)	0	100	100
35	a	122/127 (96%)	105 (86%)	17 (14%)	0	100	100
36	b	63/70 (90%)	53 (84%)	10 (16%)	0	100	100
37	c	220/252 (87%)	190 (86%)	30 (14%)	0	100	100
38	d	71/104 (68%)	63 (89%)	8 (11%)	0	100	100
39	e	111/183 (61%)	92 (83%)	19 (17%)	0	100	100
40	f	124/133 (93%)	110 (89%)	14 (11%)	0	100	100
41	g	123/144 (85%)	112 (91%)	11 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	h	106/168 (63%)	91 (86%)	15 (14%)	0	100	100
43	i	62/105 (59%)	57 (92%)	5 (8%)	0	100	100
44	j	76/83 (92%)	68 (90%)	8 (10%)	0	100	100
45	k	56/83 (68%)	52 (93%)	4 (7%)	0	100	100
46	l	49/51 (96%)	46 (94%)	2 (4%)	1 (2%)	7	24
47	m	88/92 (96%)	71 (81%)	16 (18%)	1 (1%)	14	41
48	n	82/106 (77%)	66 (80%)	16 (20%)	0	100	100
All	All	5771/7124 (81%)	5078 (88%)	683 (12%)	10 (0%)	50	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	G	132	SER
26	R	22	PRO
27	S	101	CYS
47	m	40	SER
10	B	380	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	A	188/204 (92%)	181 (96%)	7 (4%)	34	68
10	B	296/352 (84%)	288 (97%)	8 (3%)	44	78
11	C	222/302 (74%)	221 (100%)	1 (0%)	88	96
12	D	4/163 (2%)	4 (100%)	0	100	100
13	E	172/172 (100%)	169 (98%)	3 (2%)	60	87
14	F	92/154 (60%)	91 (99%)	1 (1%)	73	92
15	G	179/292 (61%)	173 (97%)	6 (3%)	37	71
16	H	166/188 (88%)	164 (99%)	2 (1%)	71	92
17	I	114/181 (63%)	110 (96%)	4 (4%)	36	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	J	91/111 (82%)	88 (97%)	3 (3%)	38	72
19	K	79/195 (40%)	68 (86%)	11 (14%)	3	11
20	L	105/115 (91%)	103 (98%)	2 (2%)	57	85
21	M	179/180 (99%)	176 (98%)	3 (2%)	60	87
22	N	178/179 (99%)	175 (98%)	3 (2%)	60	87
23	O	103/242 (43%)	100 (97%)	3 (3%)	42	76
24	P	149/164 (91%)	145 (97%)	4 (3%)	44	78
25	Q	100/196 (51%)	98 (98%)	2 (2%)	55	84
26	R	98/158 (62%)	96 (98%)	2 (2%)	55	84
27	S	100/133 (75%)	100 (100%)	0	100	100
28	T	125/144 (87%)	125 (100%)	0	100	100
29	U	13/114 (11%)	13 (100%)	0	100	100
30	V	86/124 (69%)	84 (98%)	2 (2%)	50	82
31	W	87/122 (71%)	87 (100%)	0	100	100
32	X	48/104 (46%)	46 (96%)	2 (4%)	30	63
33	Y	70/115 (61%)	69 (99%)	1 (1%)	67	90
34	Z	44/119 (37%)	44 (100%)	0	100	100
35	a	99/117 (85%)	92 (93%)	7 (7%)	14	39
36	b	48/58 (83%)	44 (92%)	4 (8%)	11	32
37	c	168/209 (80%)	164 (98%)	4 (2%)	49	81
38	d	47/90 (52%)	44 (94%)	3 (6%)	17	45
39	e	79/156 (51%)	79 (100%)	0	100	100
40	f	97/114 (85%)	95 (98%)	2 (2%)	53	84
41	g	98/121 (81%)	96 (98%)	2 (2%)	55	84
42	h	85/145 (59%)	84 (99%)	1 (1%)	71	92
43	i	47/89 (53%)	44 (94%)	3 (6%)	17	45
44	j	63/70 (90%)	60 (95%)	3 (5%)	25	58
45	k	26/74 (35%)	25 (96%)	1 (4%)	33	67
46	l	46/47 (98%)	44 (96%)	2 (4%)	29	62
47	m	63/74 (85%)	58 (92%)	5 (8%)	12	34
48	n	64/92 (70%)	63 (98%)	1 (2%)	62	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	4118/5979 (69%)	4010 (97%)	108 (3%)	49	79

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	P	56	ARG
35	a	72	MET
45	k	40	ARG
24	P	147	ARG
30	V	57	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 117 such sidechains are listed below:

Mol	Chain	Res	Type
23	O	31	HIS
44	j	16	HIS
27	S	58	HIS
44	j	12	HIS
37	c	196	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1535/1782 (86%)	588 (38%)	57 (3%)
2	2	1106/1527 (72%)	445 (40%)	28 (2%)
3	3	177/213 (83%)	83 (46%)	10 (5%)
4	4	146/183 (79%)	48 (32%)	5 (3%)
5	5	78/133 (58%)	30 (38%)	4 (5%)
6	6	60/76 (78%)	48 (80%)	15 (25%)
7	7	150/171 (87%)	50 (33%)	2 (1%)
8	8	118/121 (97%)	54 (45%)	5 (4%)
All	All	3370/4206 (80%)	1346 (39%)	126 (3%)

5 of 1346 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	G
1	1	10	A
1	1	13	G
1	1	23	U

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Mol	Chain	Res	Type
1	1	24	A

5 of 126 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	29	C
6	6	29	G
2	2	815	G
6	6	24	C
6	6	58	U

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

44 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	OMG	2	1079	2	18,26,27	0.99	1 (5%)	19,38,41	1.13	2 (10%)
2	H2U	2	1404	2	18,21,22	1.10	2 (11%)	21,30,33	1.65	2 (9%)
2	OMC	2	583	2	19,22,23	0.87	0	26,31,34	1.02	1 (3%)
2	A2M	2	591	2	18,25,26	0.98	1 (5%)	18,36,39	1.33	2 (11%)
1	A2M	1	1541	2,1	18,25,26	0.96	1 (5%)	18,36,39	1.21	2 (11%)
2	OMG	2	1254	2	18,26,27	1.04	1 (5%)	19,38,41	1.05	2 (10%)
1	OMC	1	1529	1	19,22,23	0.88	0	26,31,34	0.99	1 (3%)
1	OMG	1	1628	1	18,26,27	1.01	1 (5%)	19,38,41	1.18	2 (10%)
7	OMU	7	7	7,1	19,22,23	1.25	2 (10%)	26,31,34	2.12	6 (23%)
7	A2M	7	162	7,1	18,25,26	1.02	1 (5%)	18,36,39	1.22	2 (11%)
2	OMG	2	71	2	18,26,27	1.03	1 (5%)	19,38,41	1.05	2 (10%)
2	A2M	2	572	2	18,25,26	0.98	1 (5%)	18,36,39	1.19	2 (11%)
1	OMG	1	959	1	18,26,27	1.07	1 (5%)	19,38,41	1.25	2 (10%)
2	OMU	2	667	2	19,22,23	1.26	3 (15%)	26,31,34	1.83	6 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	A2M	2	382	2	18,25,26	0.93	1 (5%)	18,36,39	1.20	2 (11%)
2	OMG	2	1230	2	18,26,27	1.03	1 (5%)	19,38,41	1.05	2 (10%)
2	A2M	2	628	2	18,25,26	0.93	1 (5%)	18,36,39	1.24	2 (11%)
1	OMU	1	847	1	19,22,23	1.25	3 (15%)	26,31,34	1.81	6 (23%)
2	OMG	2	534	2	18,26,27	1.01	1 (5%)	19,38,41	1.04	2 (10%)
2	OMC	2	554	2	19,22,23	0.85	0	26,31,34	1.01	1 (3%)
2	OMG	2	641	2	18,26,27	1.04	1 (5%)	19,38,41	1.03	2 (10%)
2	OMG	2	655	2	18,26,27	1.02	1 (5%)	19,38,41	1.13	2 (10%)
2	OMU	2	656	2	19,22,23	1.23	3 (15%)	26,31,34	1.97	6 (23%)
2	OMU	2	1153	2	19,22,23	1.30	3 (15%)	26,31,34	1.99	6 (23%)
2	OMC	2	1318	2	19,22,23	0.86	0	26,31,34	0.99	2 (7%)
2	OMG	2	571	2	18,26,27	0.98	1 (5%)	19,38,41	1.10	2 (10%)
1	A2M	1	955	1	18,25,26	0.96	1 (5%)	18,36,39	1.33	2 (11%)
1	A2M	1	681	1	18,25,26	0.93	1 (5%)	18,36,39	1.24	2 (11%)
1	A2M	1	927	1	18,25,26	1.02	1 (5%)	18,36,39	1.29	2 (11%)
2	OMC	2	443	2	19,22,23	0.85	0	26,31,34	0.87	0
1	OMU	1	48	1	19,22,23	1.36	3 (15%)	26,31,34	1.84	6 (23%)
1	OMG	1	1526	1	18,26,27	1.00	1 (5%)	19,38,41	1.21	2 (10%)
1	OMU	1	36	1	19,22,23	1.31	3 (15%)	26,31,34	1.85	6 (23%)
1	OMG	1	1542	2,1	18,26,27	1.00	1 (5%)	19,38,41	1.17	2 (10%)
2	OMC	2	1398	2	19,22,23	0.86	0	26,31,34	1.06	1 (3%)
1	OMC	1	695	1	19,22,23	0.92	1 (5%)	26,31,34	1.19	2 (7%)
1	OMU	1	845	1	19,22,23	1.32	4 (21%)	26,31,34	1.97	6 (23%)
2	OMC	2	1249	2	19,22,23	0.85	0	26,31,34	1.00	1 (3%)
2	A2M	2	1186	2	18,25,26	0.95	1 (5%)	18,36,39	1.27	2 (11%)
1	A2M	1	678	2,1	18,25,26	0.97	1 (5%)	18,36,39	1.29	2 (11%)
1	OMG	1	856	1	18,26,27	1.01	1 (5%)	19,38,41	1.05	2 (10%)
2	A2M	2	527	2	18,25,26	0.95	1 (5%)	18,36,39	1.38	2 (11%)
2	OMU	2	1078	2	19,22,23	1.27	2 (10%)	26,31,34	1.81	6 (23%)
2	OMC	2	1160	2	19,22,23	0.86	0	26,31,34	0.97	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	2	1079	2	-	2/5/27/28	0/3/3/3
2	H2U	2	1404	2	-	3/7/38/39	0/2/2/2
2	OMC	2	583	2	-	2/9/27/28	0/2/2/2
2	A2M	2	591	2	-	3/5/27/28	0/3/3/3
1	A2M	1	1541	2,1	-	3/5/27/28	0/3/3/3
2	OMG	2	1254	2	-	4/5/27/28	0/3/3/3
1	OMC	1	1529	1	-	2/9/27/28	0/2/2/2
1	OMG	1	1628	1	-	0/5/27/28	0/3/3/3
7	OMU	7	7	7,1	-	4/9/27/28	0/2/2/2
7	A2M	7	162	7,1	-	1/5/27/28	0/3/3/3
2	OMG	2	71	2	-	2/5/27/28	0/3/3/3
2	A2M	2	572	2	-	2/5/27/28	0/3/3/3
1	OMG	1	959	1	-	0/5/27/28	0/3/3/3
2	OMU	2	667	2	-	3/9/27/28	0/2/2/2
2	A2M	2	382	2	-	1/5/27/28	0/3/3/3
2	OMG	2	1230	2	-	3/5/27/28	0/3/3/3
2	A2M	2	628	2	-	0/5/27/28	0/3/3/3
1	OMU	1	847	1	-	3/9/27/28	0/2/2/2
2	OMG	2	534	2	-	0/5/27/28	0/3/3/3
2	OMC	2	554	2	-	2/9/27/28	0/2/2/2
2	OMG	2	641	2	-	2/5/27/28	0/3/3/3
2	OMG	2	655	2	-	0/5/27/28	0/3/3/3
2	OMU	2	656	2	-	4/9/27/28	0/2/2/2
2	OMU	2	1153	2	-	2/9/27/28	0/2/2/2
2	OMC	2	1318	2	-	2/9/27/28	0/2/2/2
2	OMG	2	571	2	-	2/5/27/28	0/3/3/3
1	A2M	1	955	1	-	3/5/27/28	0/3/3/3
1	A2M	1	681	1	-	3/5/27/28	0/3/3/3
1	A2M	1	927	1	-	1/5/27/28	0/3/3/3
2	OMC	2	443	2	-	5/9/27/28	0/2/2/2
1	OMU	1	48	1	-	3/9/27/28	0/2/2/2
1	OMG	1	1526	1	-	1/5/27/28	0/3/3/3
1	OMU	1	36	1	-	2/9/27/28	0/2/2/2
1	OMG	1	1542	2,1	-	2/5/27/28	0/3/3/3
2	OMC	2	1398	2	-	0/9/27/28	0/2/2/2
1	OMC	1	695	1	-	0/9/27/28	0/2/2/2
1	OMU	1	845	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	2	1249	2	-	3/9/27/28	0/2/2/2
2	A2M	2	1186	2	-	3/5/27/28	0/3/3/3
1	A2M	1	678	2,1	-	4/5/27/28	0/3/3/3
1	OMG	1	856	1	-	0/5/27/28	0/3/3/3
2	A2M	2	527	2	-	1/5/27/28	0/3/3/3
2	OMU	2	1078	2	-	0/9/27/28	0/2/2/2
2	OMC	2	1160	2	-	0/9/27/28	0/2/2/2

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	36	OMU	C4-N3	-2.96	1.33	1.38
1	1	48	OMU	C4-N3	-2.95	1.33	1.38
1	1	845	OMU	C4-N3	-2.94	1.33	1.38
1	1	856	OMG	C6-N1	-2.89	1.33	1.37
2	2	1153	OMU	C4-N3	-2.83	1.33	1.38

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	1404	H2U	C4-N3-C2	-6.13	120.71	125.79
7	7	7	OMU	C2'-C1'-N1	-5.47	103.60	114.22
7	7	7	OMU	C4-N3-C2	-4.79	120.26	126.58
2	2	656	OMU	C4-N3-C2	-4.76	120.31	126.58
1	1	845	OMU	C4-N3-C2	-4.75	120.31	126.58

There are no chirality outliers.

5 of 83 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	48	OMU	C3'-C4'-C5'-O5'
1	1	48	OMU	O4'-C4'-C5'-O5'
1	1	681	A2M	O4'-C4'-C5'-O5'
1	1	681	A2M	C3'-C4'-C5'-O5'
1	1	1529	OMC	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 109 ligands modelled in this entry, 109 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

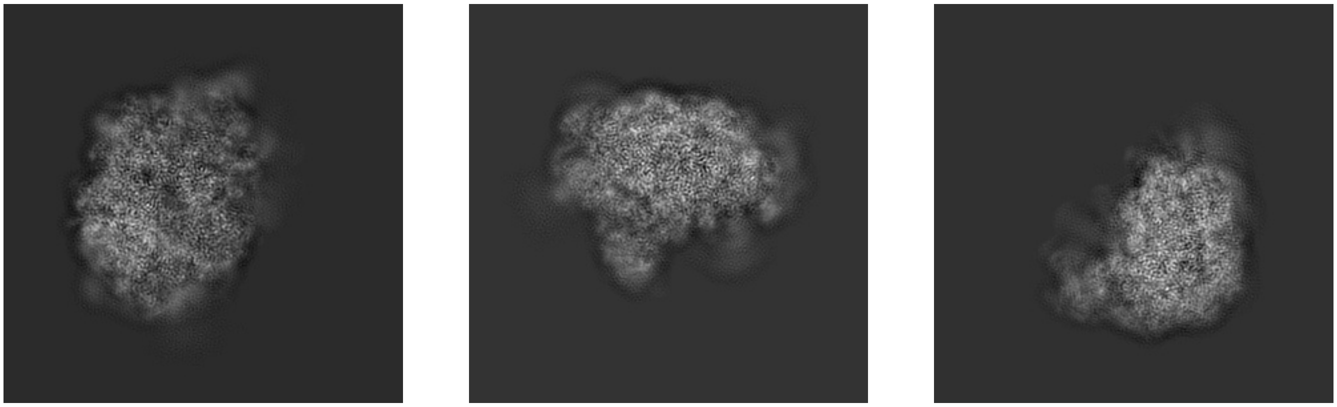
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-6583. 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

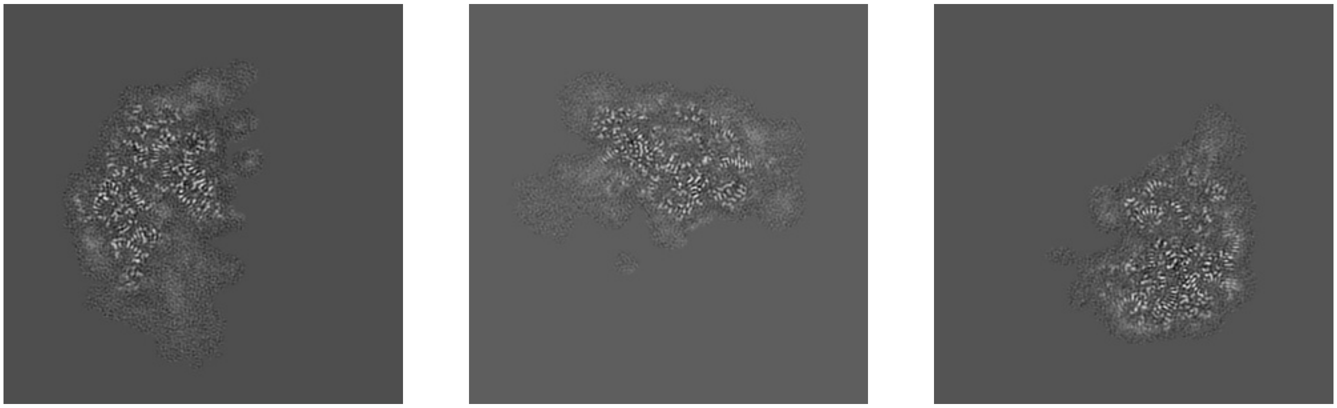


X Y Z

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

6.2 Central slices ⓘ

6.2.1 Primary map

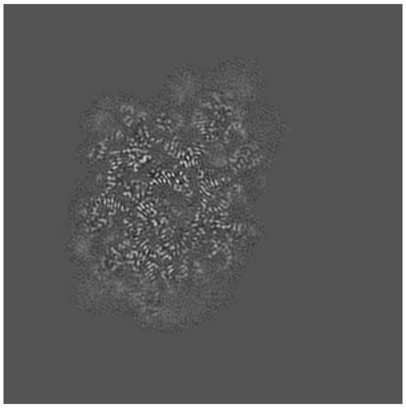


X Index: 192 Y Index: 192 Z Index: 192

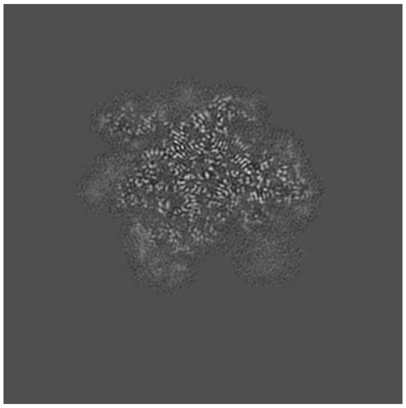
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

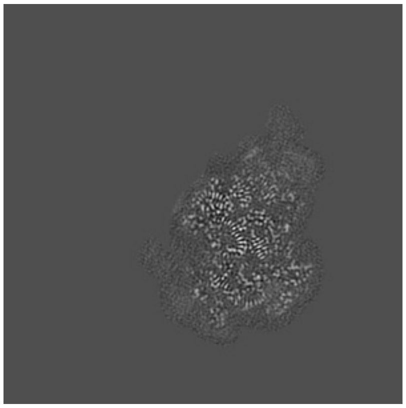
6.3.1 Primary map



X Index: 228



Y Index: 123



Z Index: 213

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

6.4 Orthogonal surface views

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

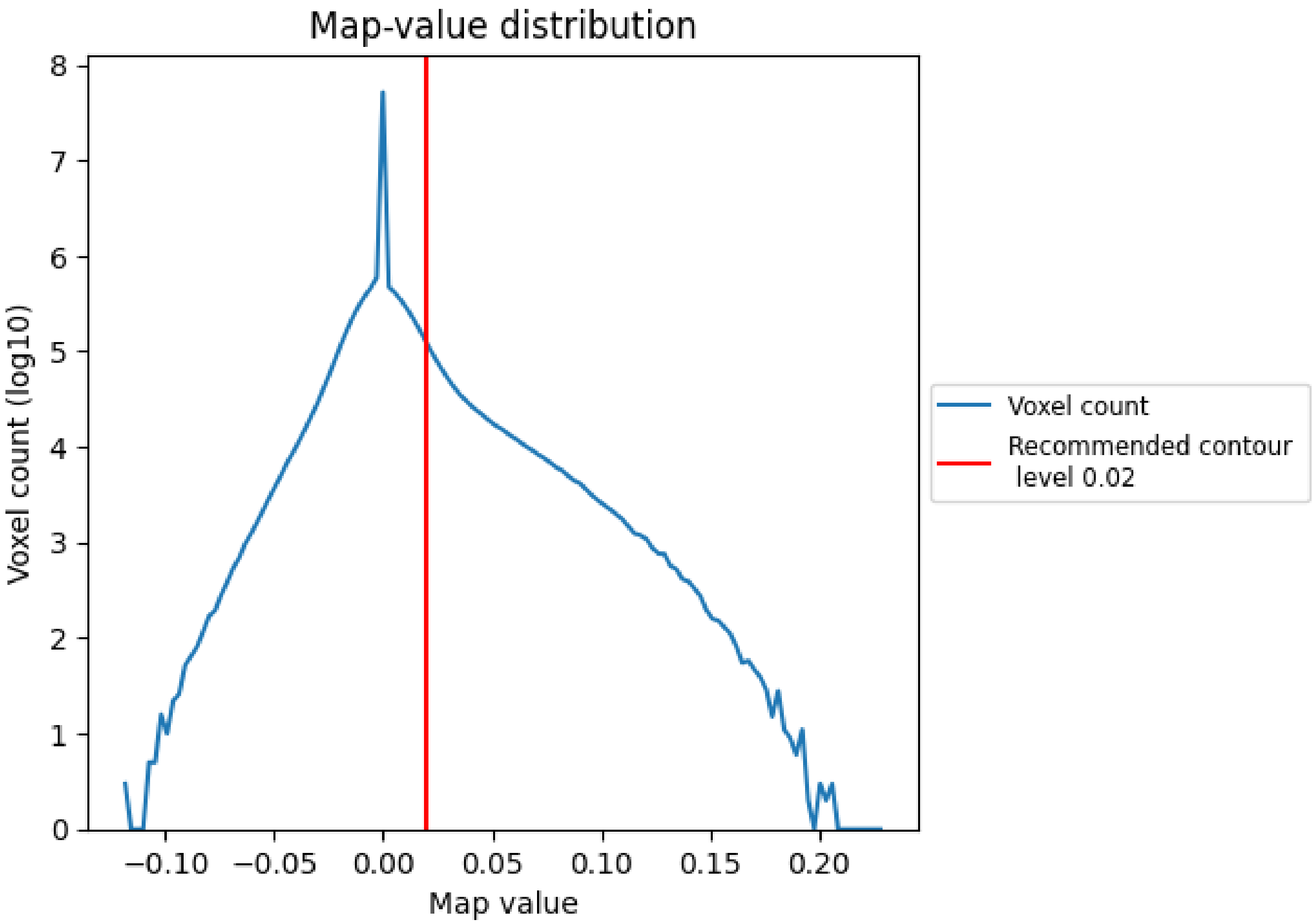
6.5 Mask visualisation (i)

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

7 Map analysis ⓘ

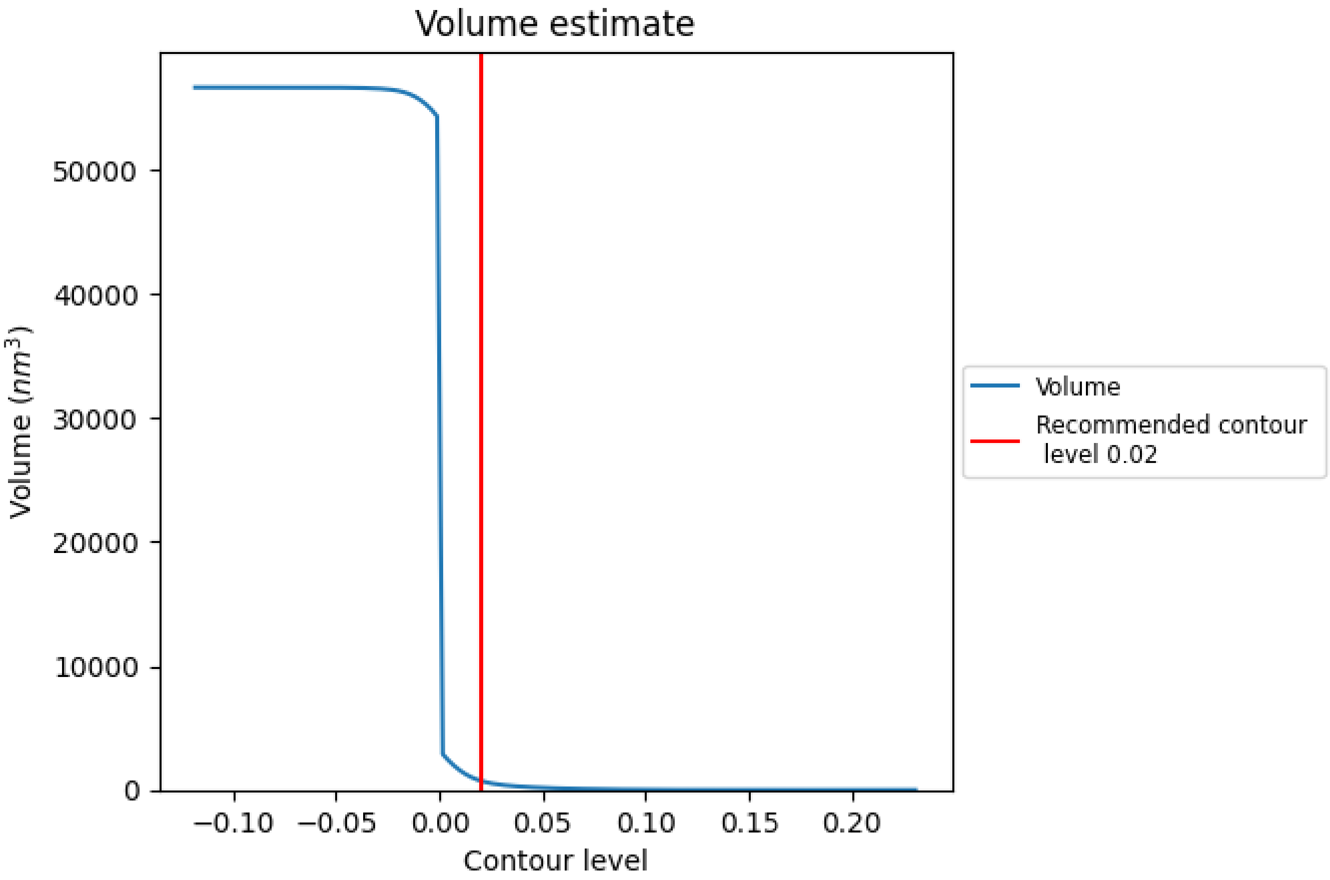
This section contains the results of statistical analysis of the map.

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.

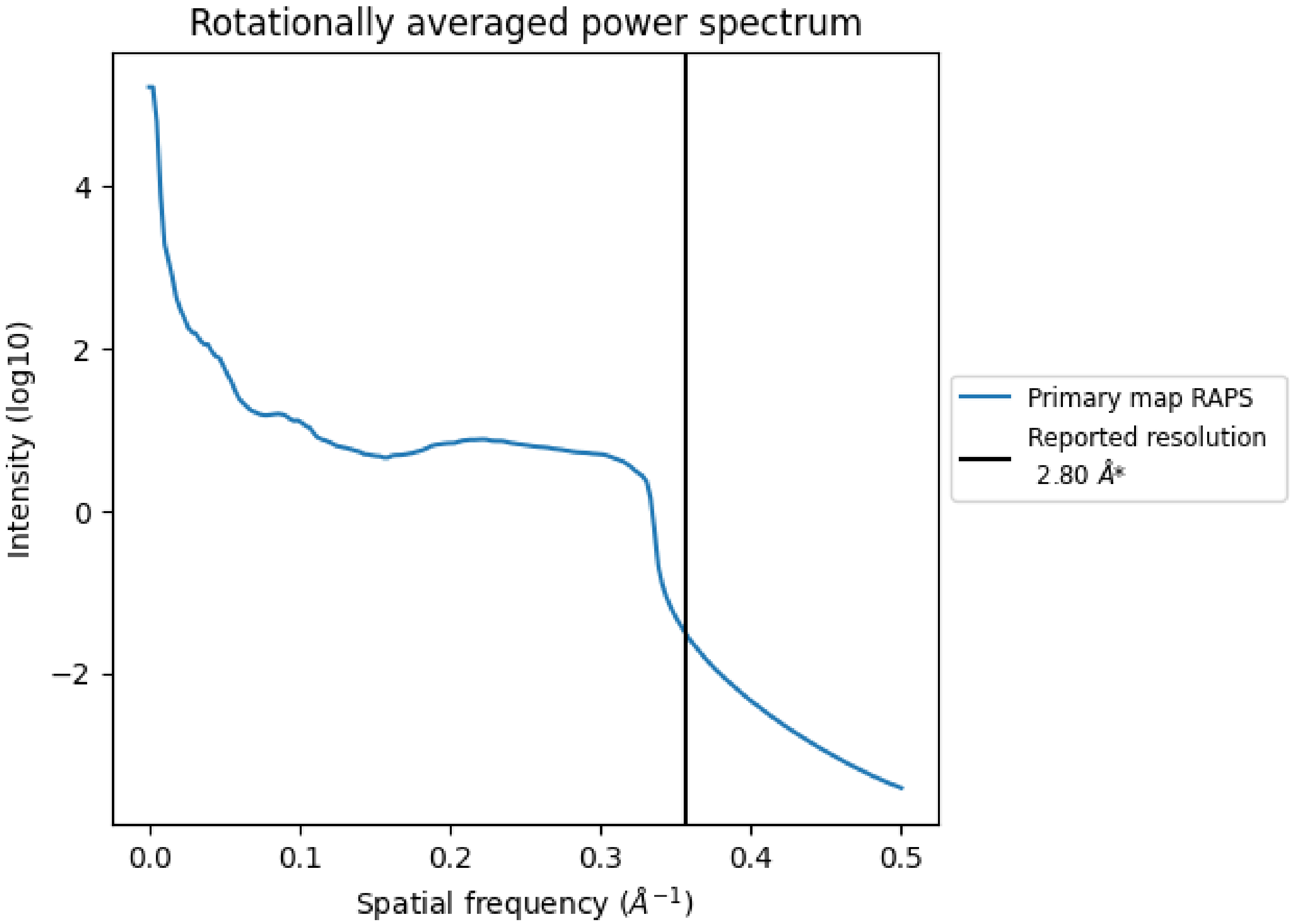
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 742 nm^3; this corresponds to an approximate mass of 670 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.357 $Å^{-1}$

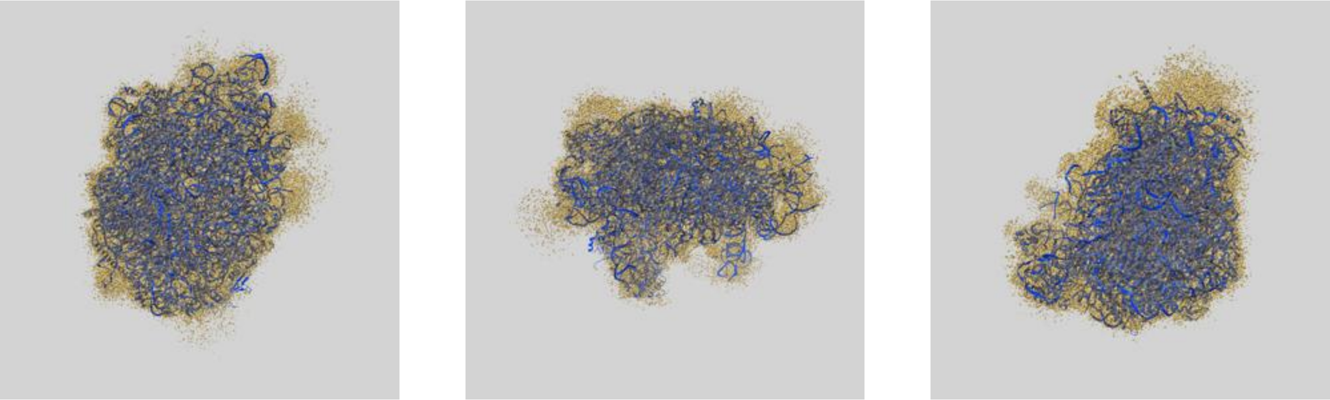
8 Fourier-Shell correlation ⓘ

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-6583 and PDB model 3JCS. Per-residue inclusion information can be found in section 3 on page 14.

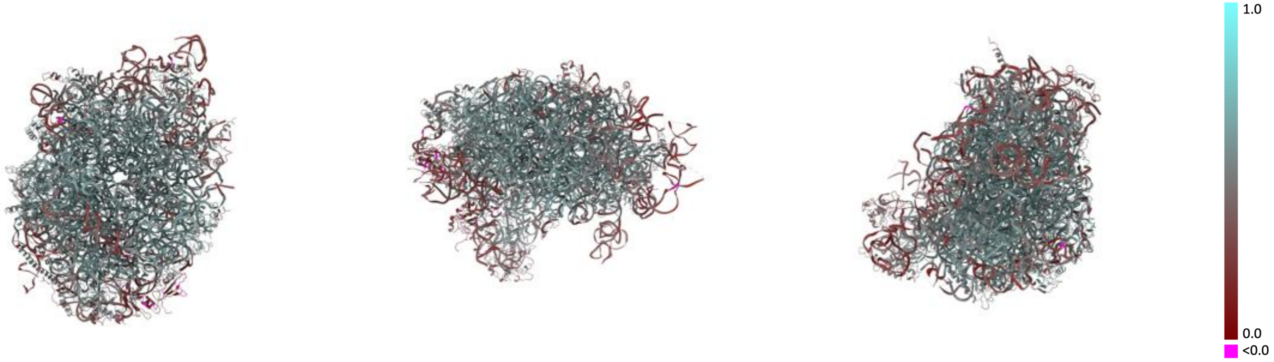
9.1 Map-model overlay ⓘ



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

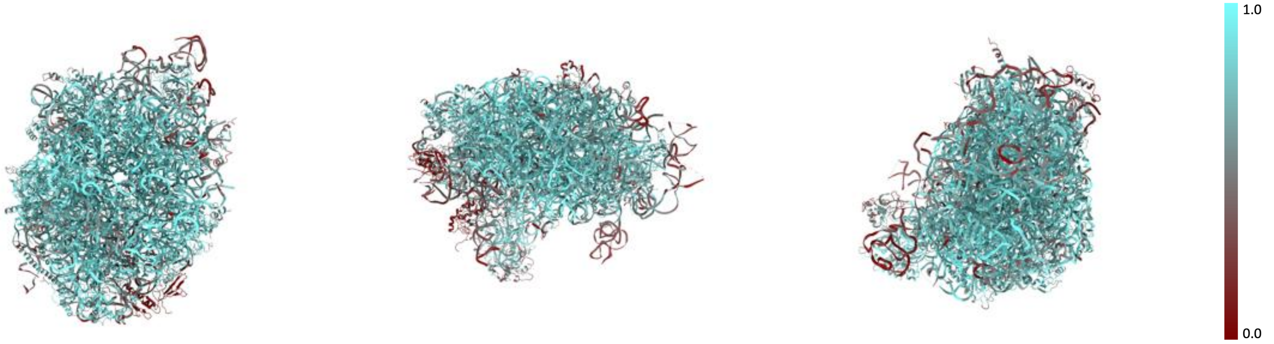
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

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

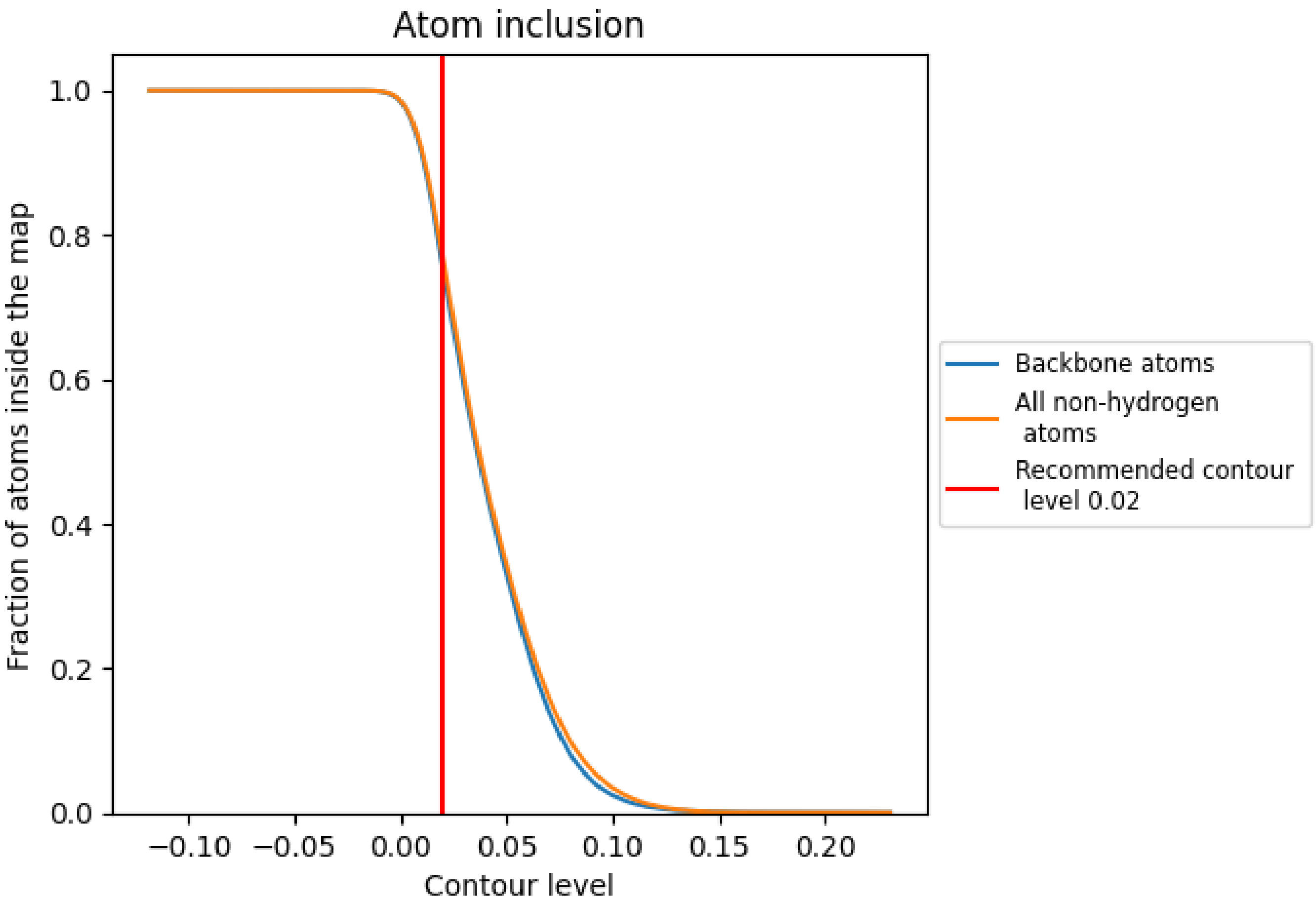
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion ⓘ



At the recommended contour level, 75% of all backbone atoms, 77% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7677	0.4990
1	0.8182	0.5060
2	0.7556	0.4850
3	0.6910	0.4460
4	0.7952	0.4970
5	0.8879	0.5440
6	0.6724	0.3910
7	0.8930	0.5550
8	0.8056	0.4420
A	0.8575	0.5770
B	0.8237	0.5530
C	0.8482	0.5580
D	0.4593	0.3530
E	0.1210	0.2290
F	0.8041	0.5200
G	0.7575	0.5140
H	0.7841	0.5300
I	0.8463	0.5620
J	0.8232	0.5510
K	0.7090	0.4450
L	0.8397	0.5570
M	0.8664	0.5820
N	0.0709	0.2100
O	0.7577	0.4740
P	0.8268	0.5570
Q	0.7303	0.5080
R	0.8151	0.5220
S	0.7307	0.5060
T	0.8349	0.5590
U	0.4480	0.3960
V	0.8283	0.5500
W	0.8306	0.5460
X	0.7286	0.5210
Y	0.7685	0.4950
Z	0.6279	0.4930

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Chain	Atom inclusion	Q-score
a	0.8038	0.5310
b	0.8320	0.5530
c	0.8069	0.5410
d	0.6437	0.4540
e	0.7910	0.5220
f	0.8237	0.5580
g	0.8669	0.5780
h	0.7497	0.5290
i	0.7340	0.5140
j	0.8740	0.5930
k	0.5531	0.4250
l	0.8278	0.5680
m	0.7578	0.5320
n	0.6646	0.4980