wwPDB EM Validation Summary Report (i)

Nov 29, 2022 – 10:58 PM EST

PDB ID	:	5T2A
EMDB ID	:	EMD-8343
Title	:	CryoEM structure of the Leishmania donovani 80S ribosome at 2.9 Angstrom resolution
Authors	:	Zhang, X.; Lai, M.; Zhou, Z.H.
Deposited on	:	2016-08-23
Resolution	:	2.90 Å(reported)

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

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

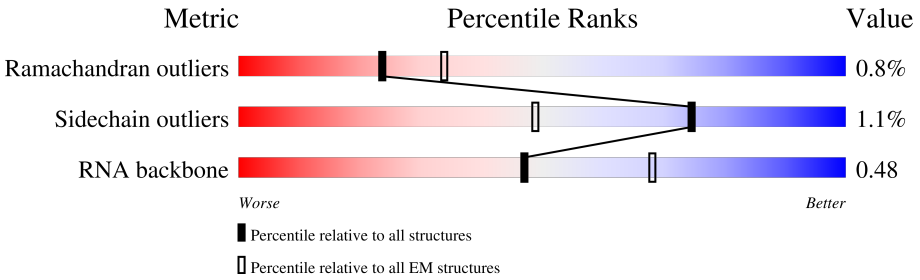
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1781	5% 74% 16% 10%
2	B	1465	7% 61% 11% 27%
3	C	262	• 52% 9% • 38%
4	D	120	91% 8% •
5	E	213	5% 69% 10% 21%
6	F	73	15% 75% 21% • •
7	G	183	• 89% 11% •
8	H	127	• 62% 11% 27%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	I	198	20% 94% 5%
10	J	213	29% 97%
11	K	188	52% 88% 11%
12	L	220	17% 80% 19%
13	M	222	17% 96%
14	N	175	36% 93%
15	O	204	7% 97%
16	P	166	7% 92% 7%
17	Q	179	13% 98%
18	R	245	24% 79% 20%
19	S	159	21% 97%
20	T	129	32% 94% 5%
21	U	139	9% 99%
22	V	145	17% 82% 17%
23	W	124	9% 51% 48%
24	X	143	15% 82% 16%
25	Y	134	26% 98%
26	Z	145	17% 97%
27	a	147	29% 97%
28	b	70	26% 96%
29	c	260	7% 94%
30	d	419	10% 94% 5%
31	e	104	15% 84% 5% 10%
32	f	183	8% 60% 40%
33	g	133	19% 95%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	h	168	15% 73% 26%
35	i	127	30% 98%
36	j	144	13% 90% 8%
37	k	105	44% 93% 6%
38	l	83	6% 93%
39	m	92	14% 98%
40	n	83	29% 89% 10%
41	o	51	10% 98%
42	p	373	23% 96%
43	q	128	5% 40% 59%
44	r	106	19% 86% 9%
45	s	305	28% 87% 13%
46	t	195	17% 67% 30%
47	u	252	17% 88% 10%
48	v	348	21% 66% 34%
49	w	190	13% 97%
50	0	264	30% 80% 16%
51	1	273	21% 92% 5%
52	2	2205	26% 47% 29% 6% 18%
53	3	249	53% 98%
54	4	200	32% 96%
55	5	220	11% 79% 17%
56	6	190	17% 84% 14%
57	7	312	99% 95%
58	8	57	63% 58% 9% 33%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	AC	246	36% 81% 17%
60	AD	153	61% 58% 39%
61	AE	173	8% 78% 19%
62	AG	151	14% 91% 7%
63	AH	144	24% 94% 6%
64	AI	152	80% 74% 20%
65	AJ	130	10% 93% 5%
66	AK	149	92% 88% 6%
67	AL	143	78% 83% 15%
68	AM	153	95% 89% 7%
69	AN	190	99% 96%
70	AO	179	79% 75% 6% 19%
71	AP	265	19% 85% 15%
72	AQ	116	81% 86% 12%
73	AR	164	14% 51% 49%
74	AS	143	21% 93% 5%
75	AT	137	42% 90% 8%
76	AV	112	33% 88% 7%
77	AW	86	34% 91% 5% 5%
78	AX	219	86% 86% 5% 7%
79	AY	66	61% 85% 15%
80	AZ	87	76% 72% 5% 22%

2 Entry composition (i)

There are 80 unique types of molecules in this entry. The entry contains 200172 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 LSU-alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1603	34365	15347	6297	11118	1603	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	761	U	A	conflict	GB 322500086
A	1393	G	A	conflict	GB 322500086
A	?	-	A	deletion	GB 322500086

- Molecule 2 is a RNA chain called LSU-beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	1064	22723	10152	4100	7407	1064	0	0

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	162	3449	1542	615	1130	162	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	141	C	U	conflict	GB 79677111
C	182	G	A	conflict	GB 79677111
C	185	C	G	conflict	GB 79677111
C	226	A	U	conflict	GB 79677111
C	228	C	U	conflict	GB 79677111
C	246	C	U	conflict	GB 79677111

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	D	119	2531	1132	452	828	119	0	0

- Molecule 5 is a RNA chain called srRNA1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	E	169	3589	1604	626	1190	169	0	0

- Molecule 6 is a RNA chain called srRNA3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	F	71	1508	676	273	488	71	0	0

- Molecule 7 is a RNA chain called srRNA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	G	183	3911	1744	704	1280	183	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	169	U	A	conflict	GB 5019758
G	171	U	A	conflict	GB 5019758

- Molecule 8 is a RNA chain called srRNA4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	H	93	1996	889	369	645	93	0	0

- Molecule 9 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	197	1539	968	307	258	6	0	0

- Molecule 10 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	211	1704	1071	338	279	16	0	0

- Molecule 11 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	K	167	1339	844	249	238	8	0	0

- Molecule 12 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	L	179	1435	901	296	230	8	0	0

- Molecule 13 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	M	221	1780	1126	354	293	7	0	0

- Molecule 14 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	N	168	1336	832	265	231	8	0	0

- Molecule 15 is a protein called eL15.

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

- Molecule 16 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	P	155	1245	776	246	212	11	0	1

- Molecule 17 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	Q	178	1456	927	280	244	5	0	0

- Molecule 18 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	R	196	1646	1010	360	271	5	0	0

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	S	158	1261	803	245	208	5	0	0

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	T	123	997	642	179	173	3	0	1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	U	137	1035	653	195	181	6	0	0

- Molecule 22 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	V	120	963	611	182	169	1	0	0

- Molecule 23 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	W	65	563	368	110	81	4	0	0

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	X	120	965	601	201	159	4	0	0

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Y	133	1079	688	215	173	3	0	0

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Z	144	1126	708	226	186	6	0	0

- Molecule 27 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	a	146	1140	698	243	194	5	0	0

- Molecule 28 is a protein called eL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	b	69	554	339	127	88	0	0

- Molecule 29 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	c	253	1921	1193	392	326	10	0	1

- Molecule 30 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	d	399	3183	2003	629	538	13	0	0

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	e	94	720	448	131	136	5	0	0

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	f	110	878	561	166	149	2	0	0

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	g	129	1050	664	209	174	3	0	0

- Molecule 34 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	h	124	1014	624	221	163	6	0	0

- Molecule 35 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	i	126	1056	658	218	176	4	0	0

- Molecule 36 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	j	132	1060	663	221	171	5	0	0

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	k	99	787	497	160	128	2	0	0

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	l	81	674	410	154	104	6	0	0

- Molecule 39 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	m	91	712	443	146	117	6	0	0

- Molecule 40 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	n	75	605	383	118	101	3	0	0

- Molecule 41 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	o	50	450	291	95	63	1	0	0

- Molecule 42 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	p	365	2825	1761	563	486	15	0	1

- Molecule 43 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	q	52	425	266	88	64	7	0	0

- Molecule 44 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	r	96	779	493	157	124	5	0	0

- Molecule 45 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	s	266	2094	1334	397	357	6	0	0

- Molecule 46 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	t	137	1054	668	197	187	2	0	0

- Molecule 47 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	u	228	1857	1180	358	308	11	0	0

- Molecule 48 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	v	230	1850	1160	368	315	7	0	0

- Molecule 49 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	w	187	1484	938	273	267	6	0	0

- Molecule 50 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	0	221	1786	1121	338	316	11	0	0

- Molecule 51 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	1	258	2037	1291	387	350	9	0	0

- Molecule 52 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
52	2	1814	38724	17307	6969	12635	1813	0	0

- Molecule 53 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
53	3	249	1994	1243	409	339	3	0	0

- Molecule 54 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	4	200	1667	1059	324	276	8	0	0

- Molecule 55 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	5	183	1473	921	308	242	2	0	1

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
5	220	ARG	LYS	conflict	UNP E9BH78

- Molecule 56 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	6	164	1362	862	265	227	8	0	0

- Molecule 57 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	7	308	2394	1500	426	456	12	0	0

- Molecule 58 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	8	38	314	194	63	52	5	0	0

- Molecule 59 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	AC	203	1622	1033	294	283	12	0	0

- Molecule 60 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AD	93	767	491	136	133	7	0	0

- Molecule 61 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	AE	140	1148	725	229	189	5	0	0

- Molecule 62 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	AG	141	1157	730	229	190	8	0	0

- Molecule 63 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	AH	136	1023	631	200	184	8	0	0

- Molecule 64 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	AI	121	984	626	188	166	4	0	0

- Molecule 65 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	AJ	129	1020	646	188	178	8	0	0

- Molecule 66 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	AK	140	1108	710	206	189	3	0	0

- Molecule 67 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	AL	121	983	613	192	173	5	0	0

- Molecule 68 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	AM	148	1186	743	237	202	4	0	0

- Molecule 69 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	AN	190	1493	927	287	271	8	0	0

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
70	AO	145	1150	729	224	193	4	0	0

- Molecule 71 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
71	AP	224	1722	1096	304	312	10	0	1

- Molecule 72 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
72	AQ	102	807	504	148	153	2	0	0

- Molecule 73 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
73	AR	83	630	388	116	122	4	0	0

- Molecule 74 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	AS	142	1114	703	222	187	2	0	0

- Molecule 75 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
75	AT	126	1033	661	198	172	2	0	0

- Molecule 76 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
76	AV	104	828	515	175	130	8	0	0

- Molecule 77 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
77	AW	82	646	396	128	114	8	0	0

- Molecule 78 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
78	AX	203	1595	1003	295	284	13	0	0

- Molecule 79 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
79	AY	56	452	285	94	72	1	0	0

- Molecule 80 is a protein called eS28.

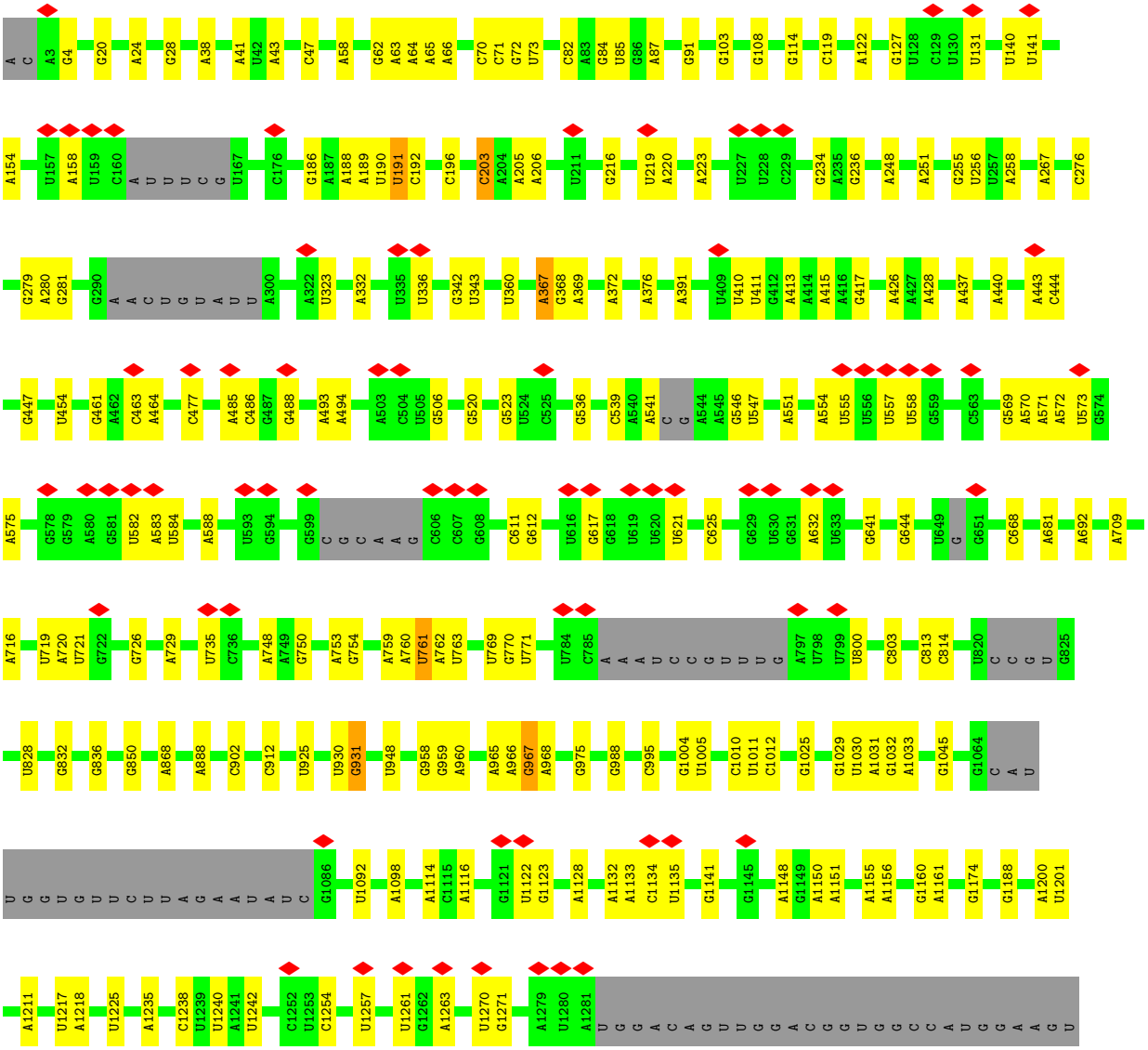
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
80	AZ	68	526	319	106	97	4	0	0

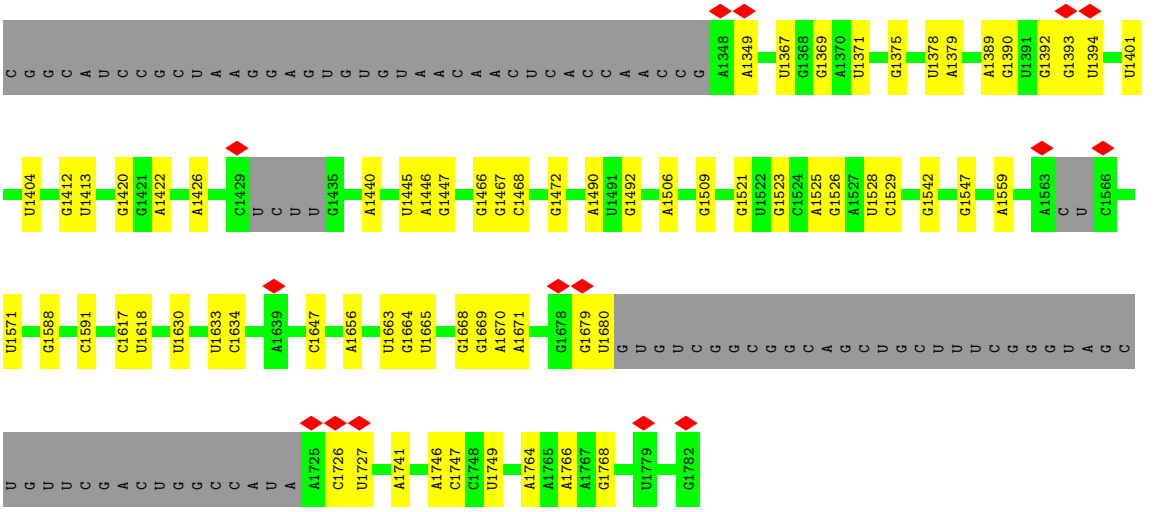
3 Residue-property plots (i)

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: LSU-alpha

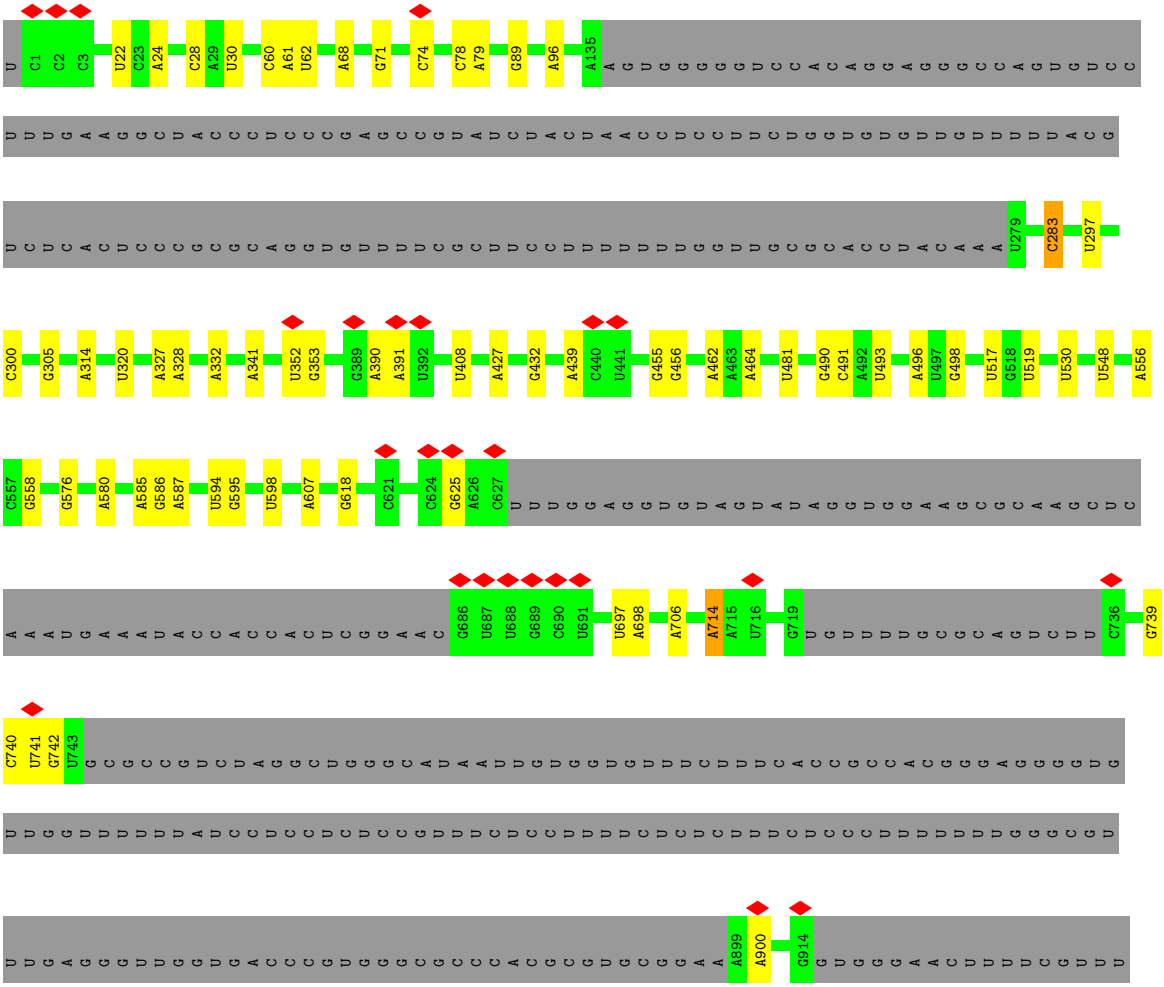
Chain A: 5% 74% 16% 10%

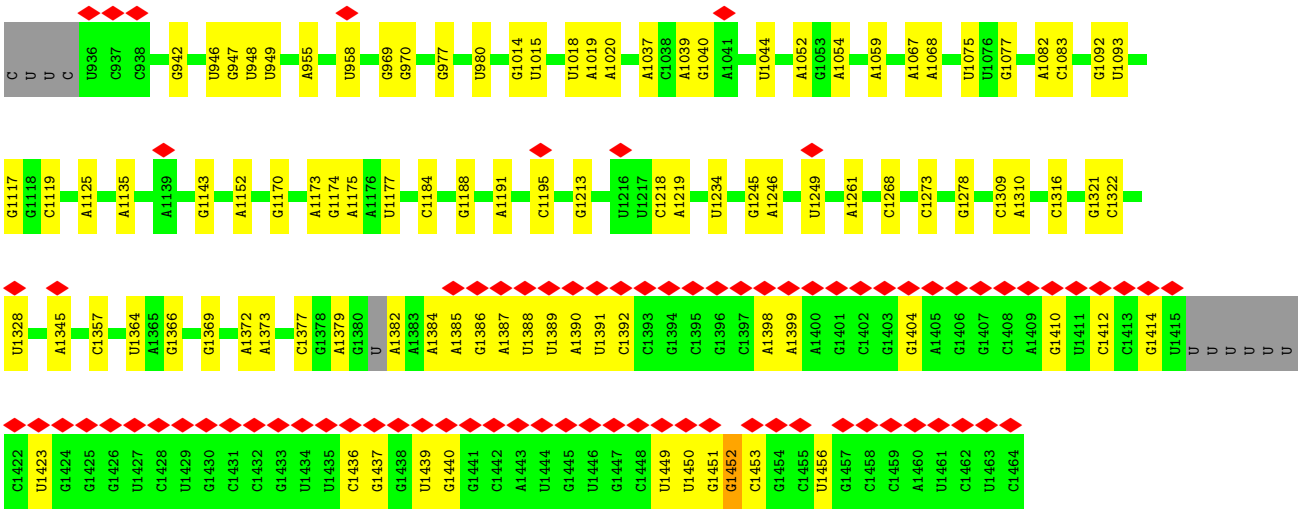




- Molecule 2: LSU-beta

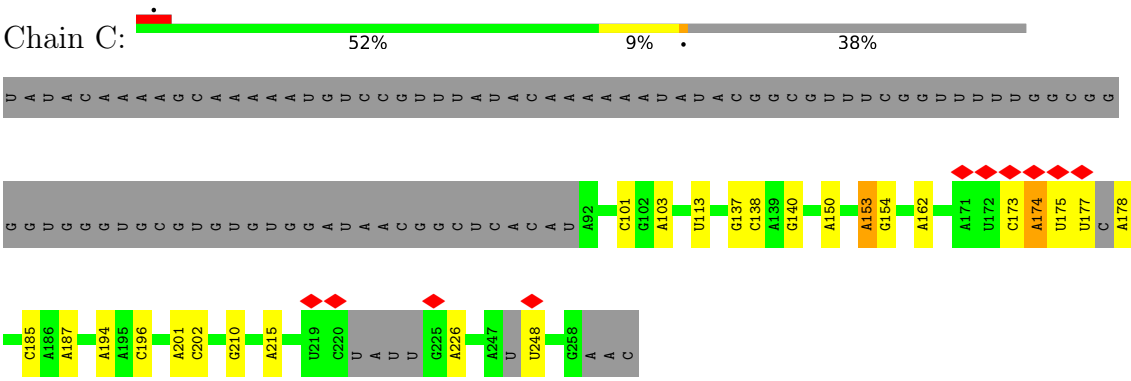
Chain B:





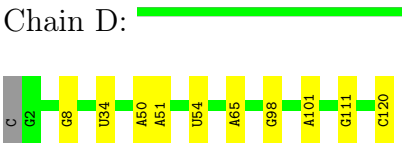
- Molecule 3: 5.8S rRNA

Chain C:



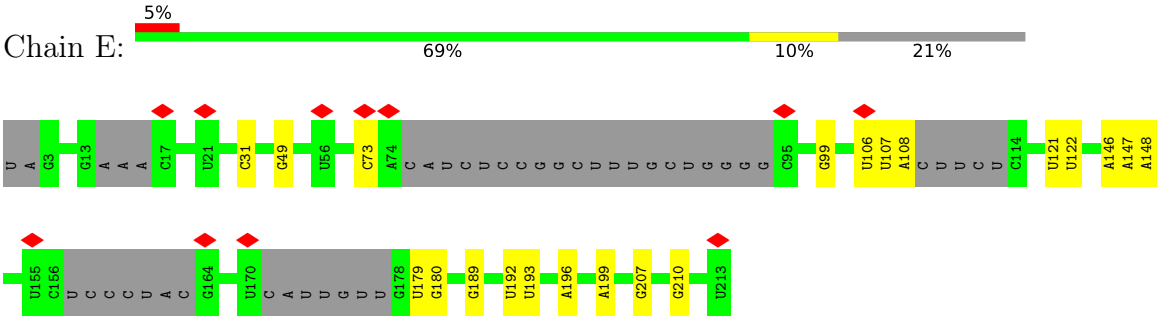
- Molecule 4: 5S rRNA

Chain D:



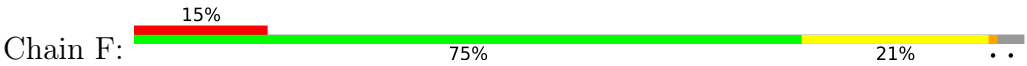
- Molecule 5: srRNA1

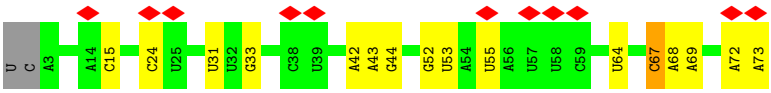
Chain E:



- Molecule 6: srRNA3

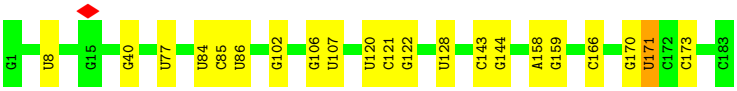
Chain F:





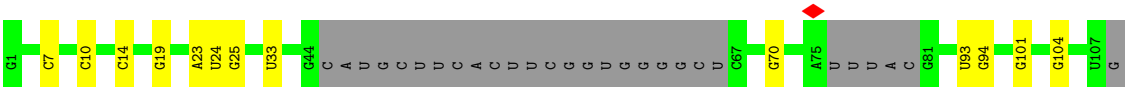
- Molecule 7: srRNA2

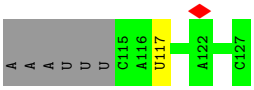
Chain G:



- Molecule 8: srRNA4

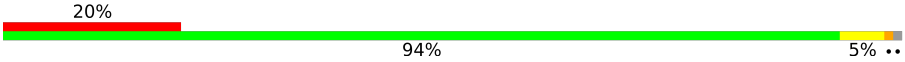
Chain H:

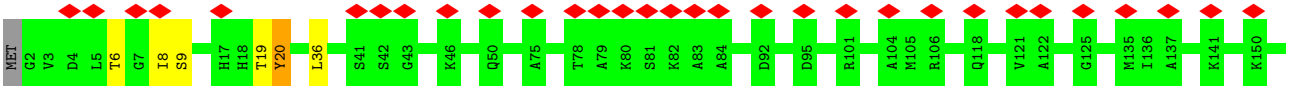


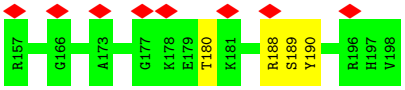


- Molecule 9: eL18

Chain I:

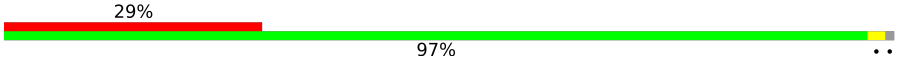


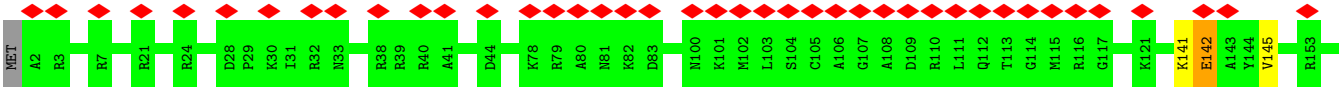


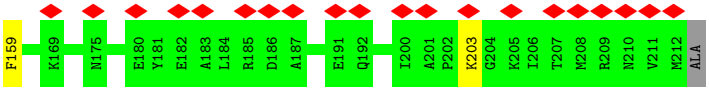


- Molecule 10: uL16

Chain J:

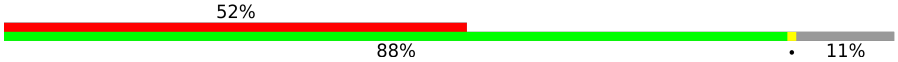


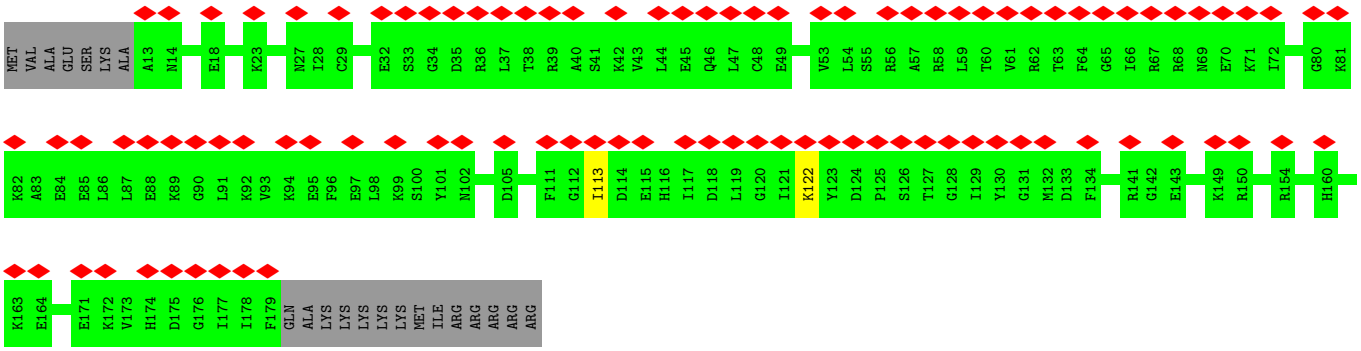




- Molecule 11: uL5

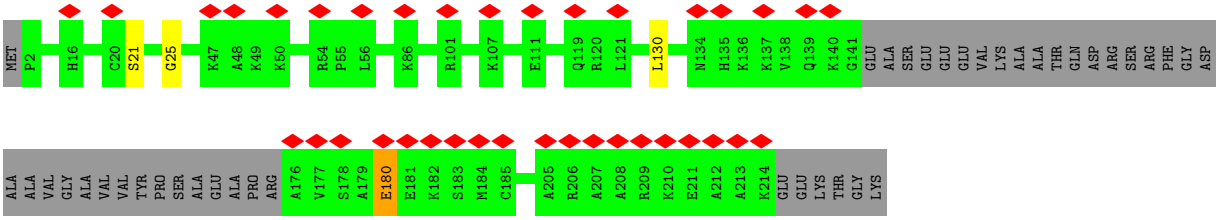
Chain K:





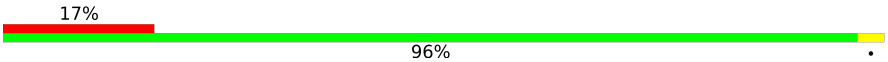
- Molecule 12: eL13

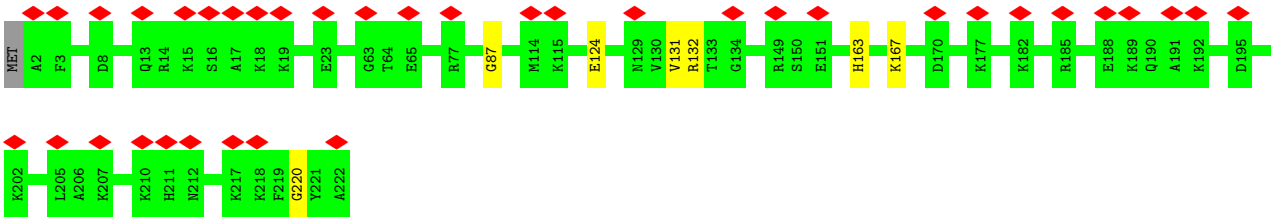
Chain L:



- Molecule 13: uL13

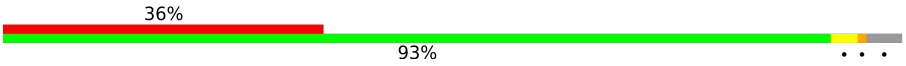
Chain M:

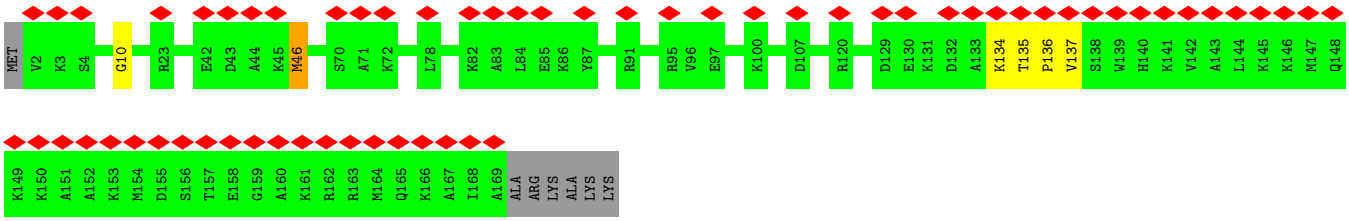




- Molecule 14: eL14

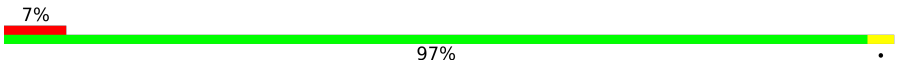
Chain N:

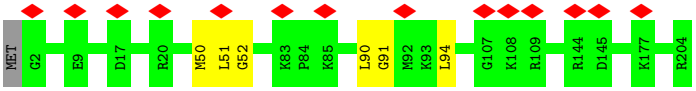




- Molecule 15: eL15

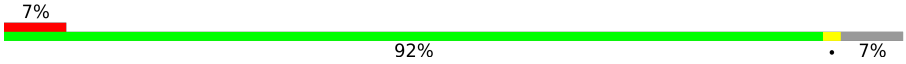
Chain O:

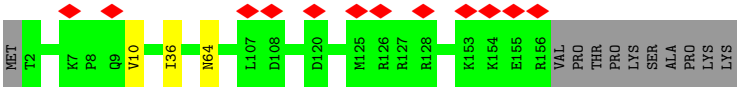




- Molecule 16: uL22

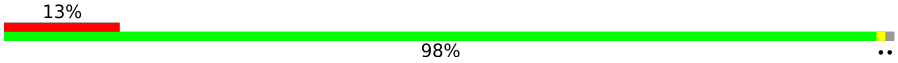
Chain P:

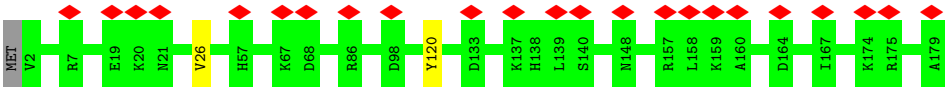




- Molecule 17: eL20

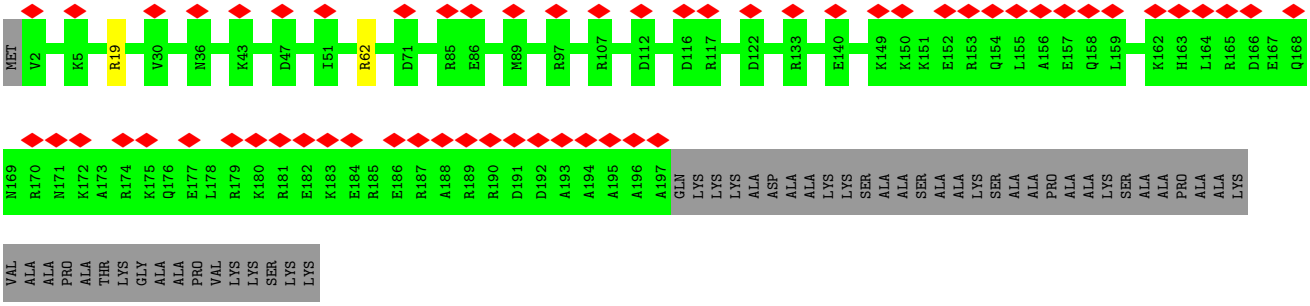
Chain Q:





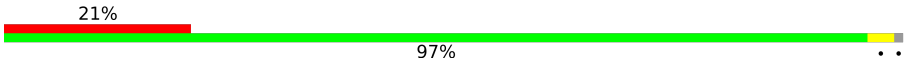
- Molecule 18: eL19

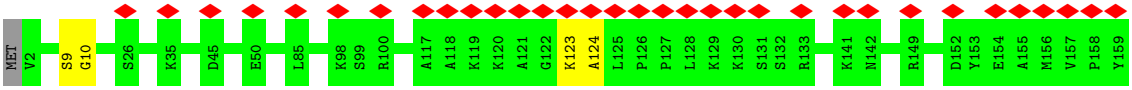
Chain R:



- Molecule 19: eL21

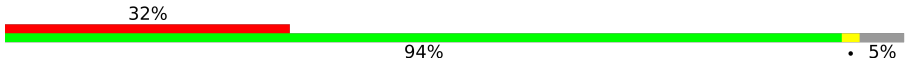
Chain S:

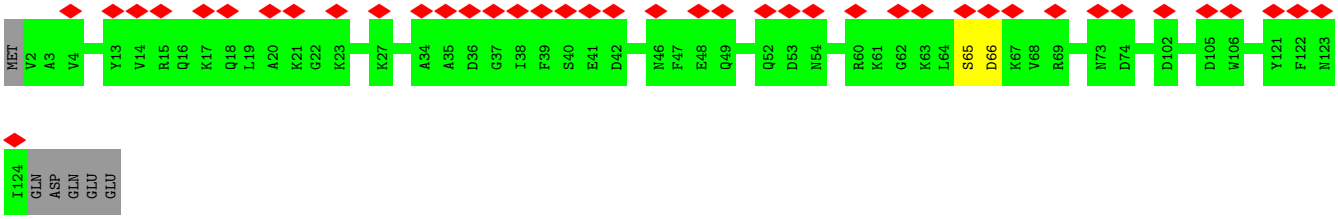




- Molecule 20: eL22

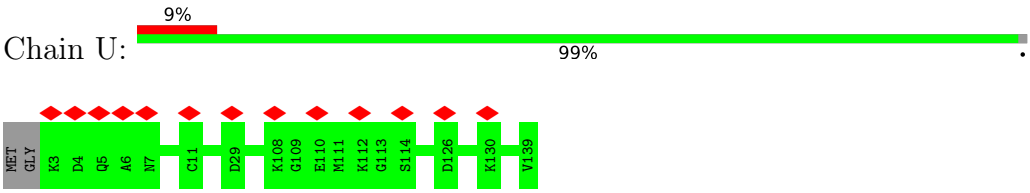
Chain T:





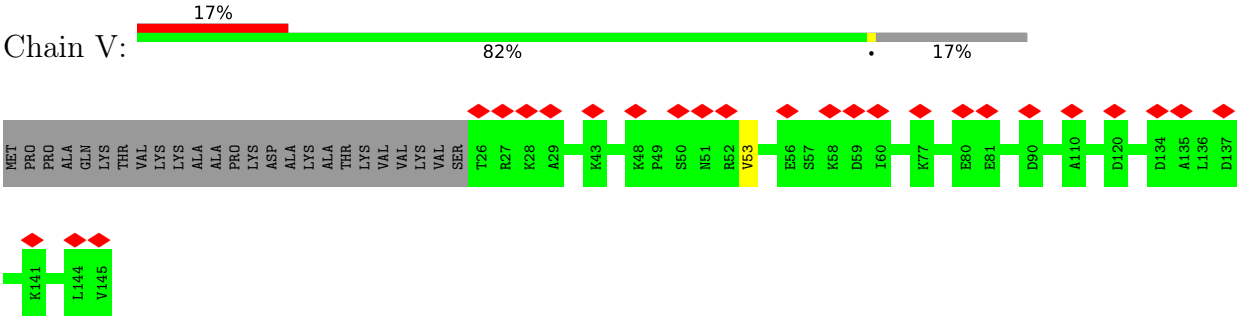
- Molecule 21: uL14

Chain U:



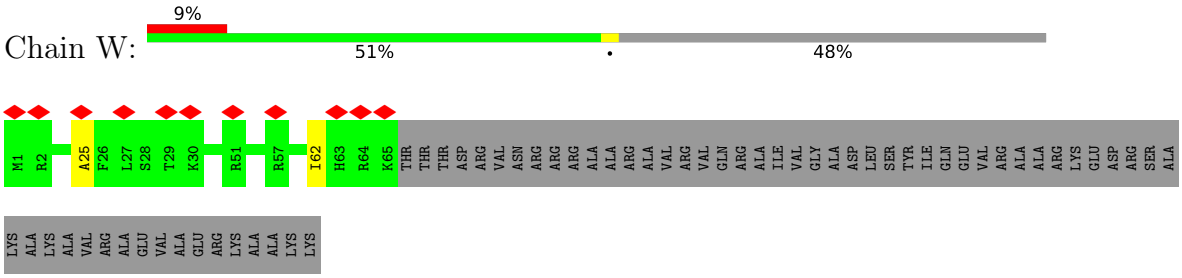
- Molecule 22: uL23

Chain V:



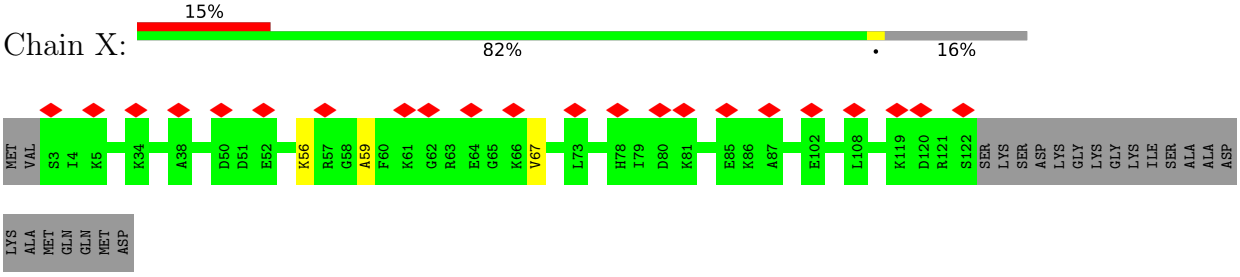
- Molecule 23: eL24

Chain W:



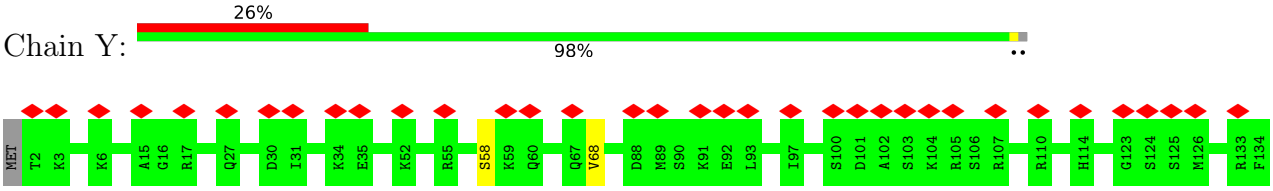
- Molecule 24: uL24

Chain X:



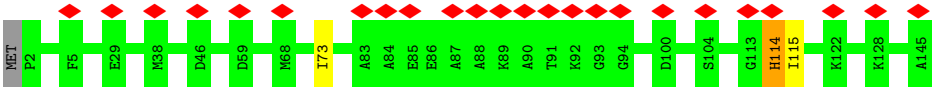
- Molecule 25: eL27

Chain Y:



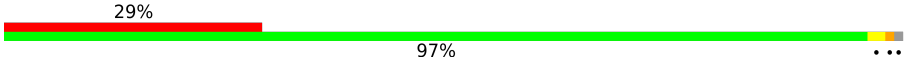
- Molecule 26: uL15

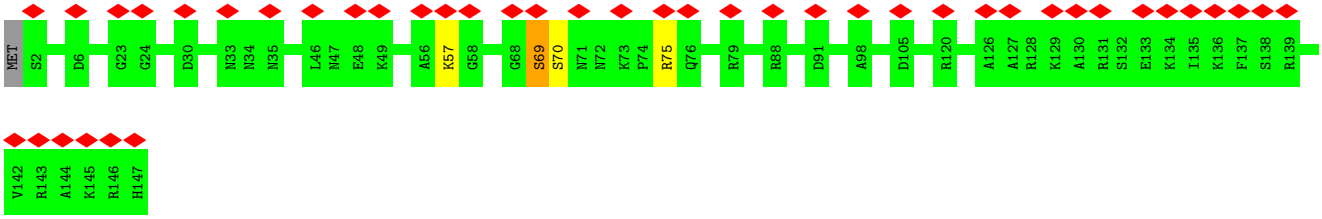
Chain Z:



- Molecule 27: eL28

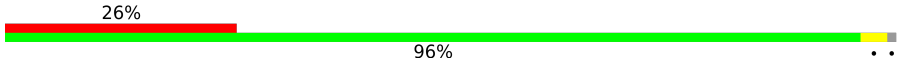
Chain a:

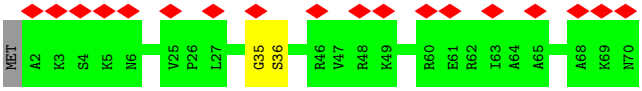




- Molecule 28: eL29

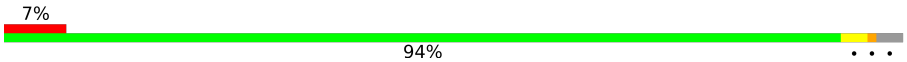
Chain b:

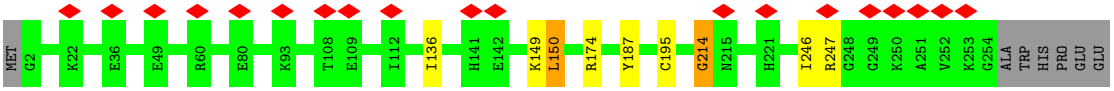




- Molecule 29: uL2

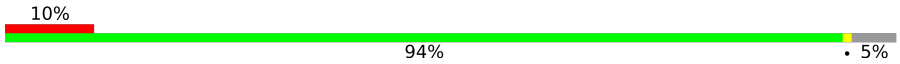
Chain c:

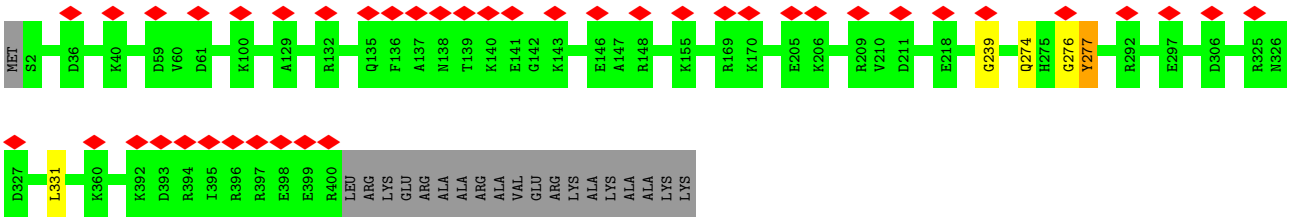




- Molecule 30: uL3

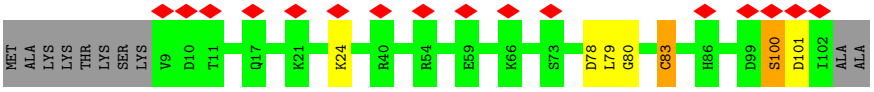
Chain d:





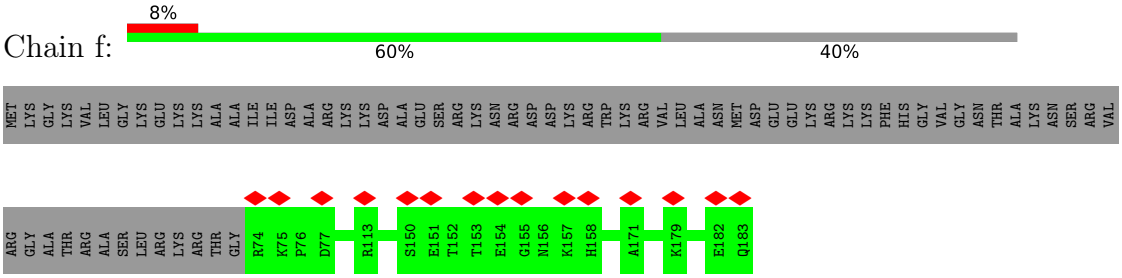
- Molecule 31: eL30

Chain e:



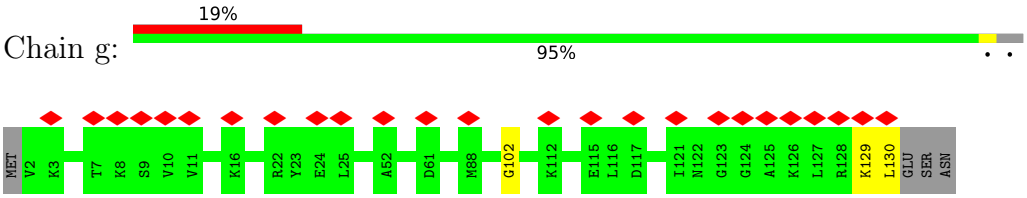
- Molecule 32: eL31

Chain f:



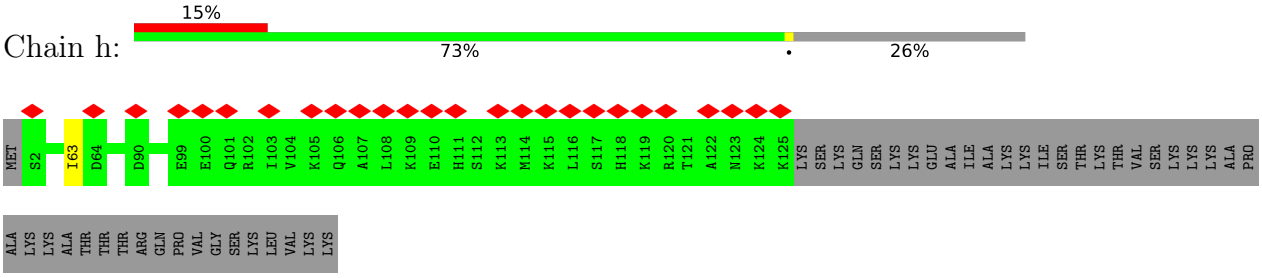
- Molecule 33: eL32

Chain g:



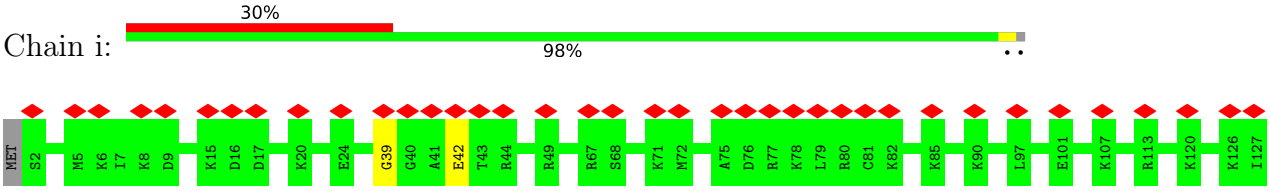
- Molecule 34: eL34

Chain h:



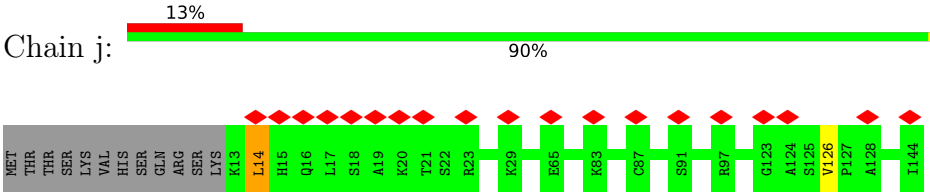
- Molecule 35: uL29

Chain i:



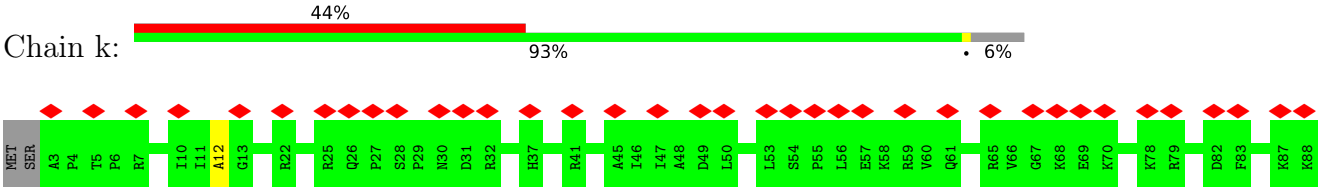
- Molecule 36: eL33

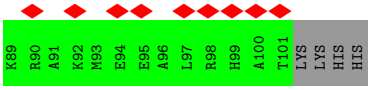
Chain j:



- Molecule 37: eL36

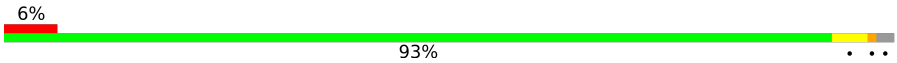
Chain k:

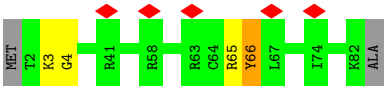




- Molecule 38: eL37

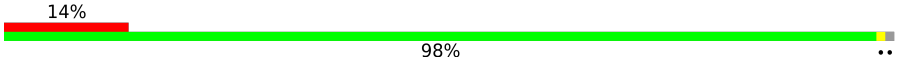
Chain l:

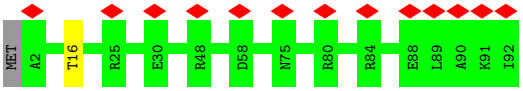




- Molecule 39: eL43

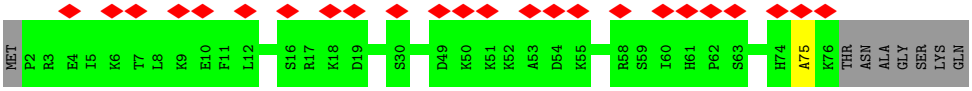
Chain m:





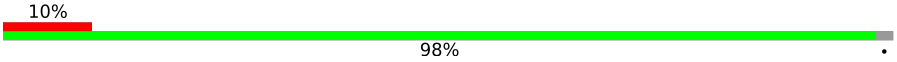
- Molecule 40: eL38

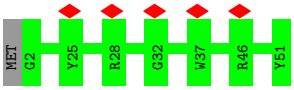
Chain n:



- Molecule 41: eL39

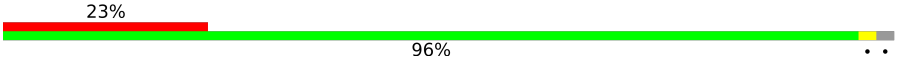
Chain o:

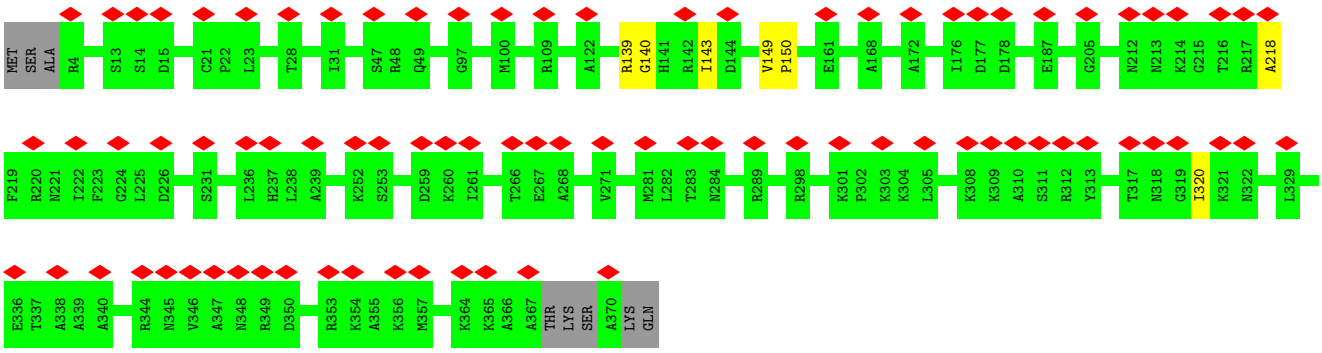




- Molecule 42: uL4

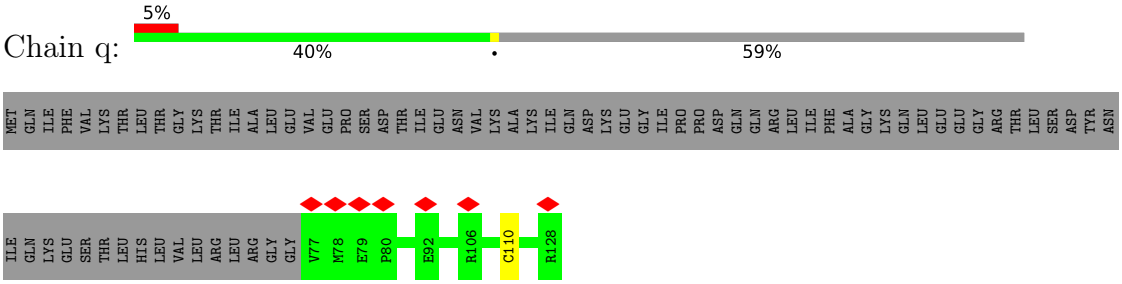
Chain p:





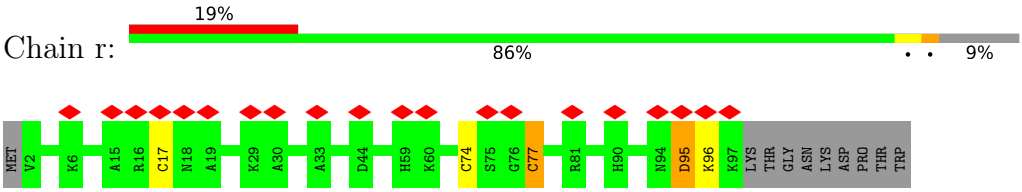
- Molecule 43: eL40

Chain q:



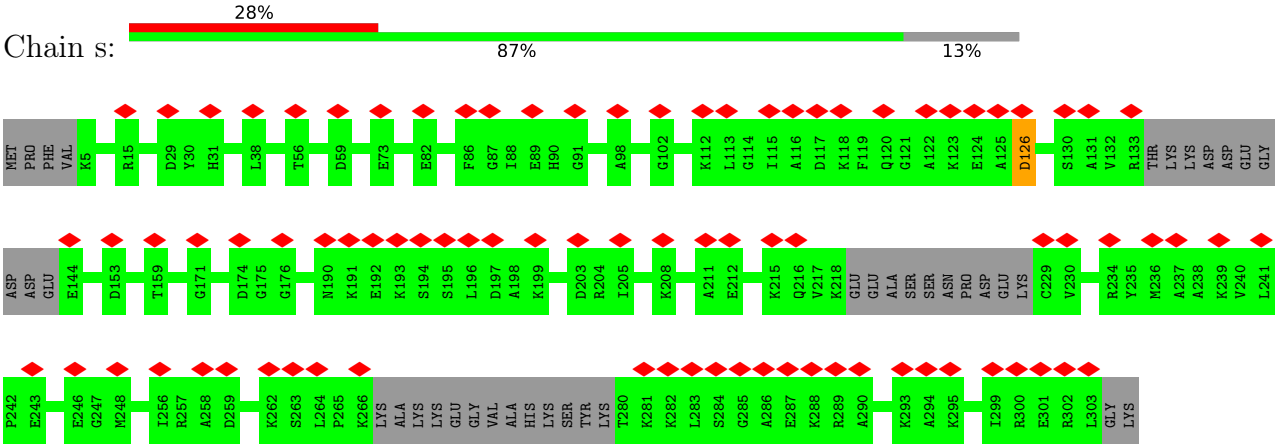
- Molecule 44: eL42

Chain r:



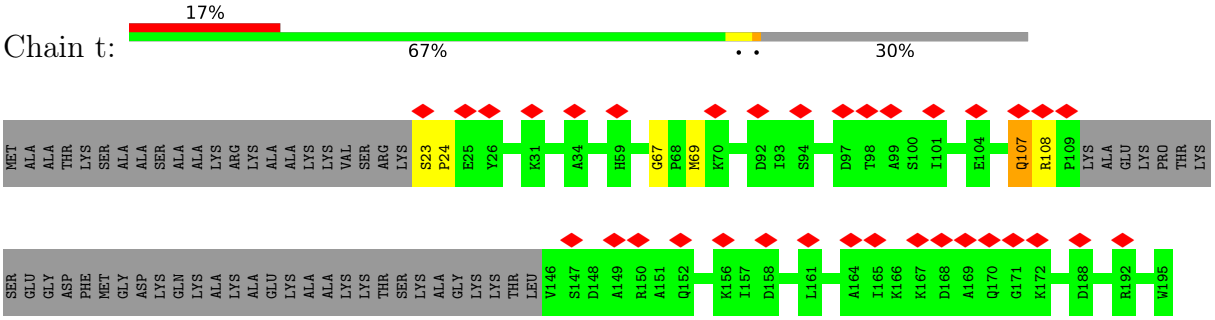
- Molecule 45: uL18

Chain s:



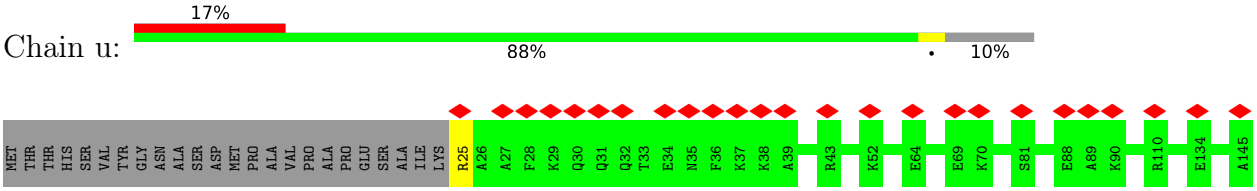
- Molecule 46: eL6

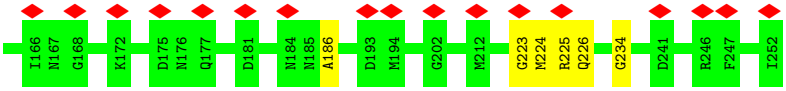
Chain t:



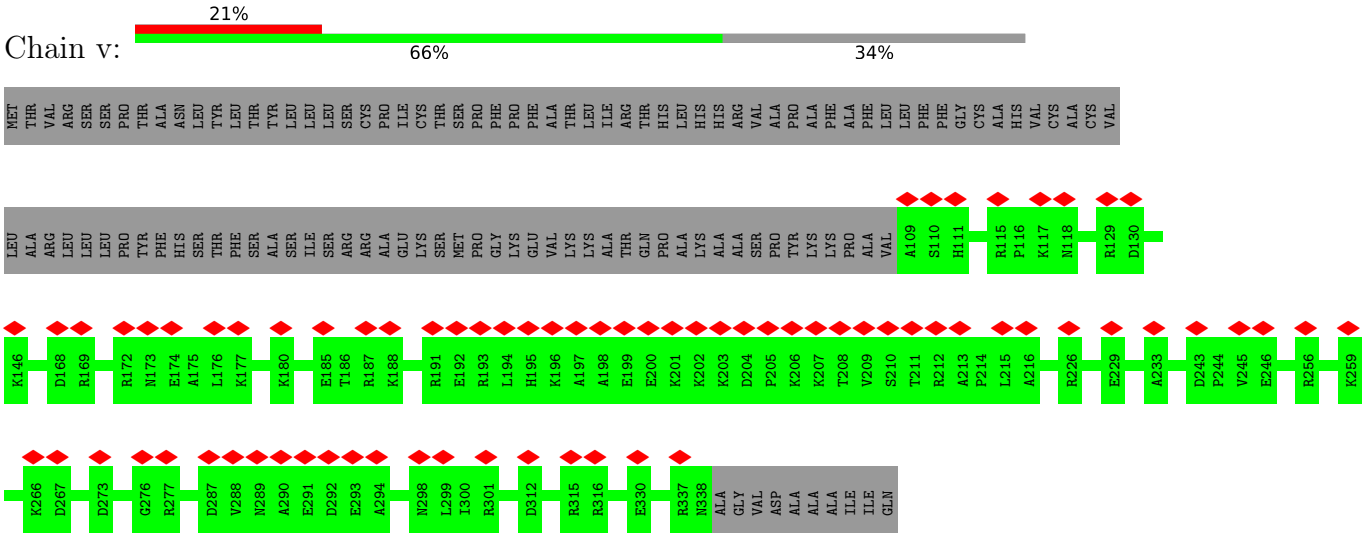
- Molecule 47: uL30

Chain u:

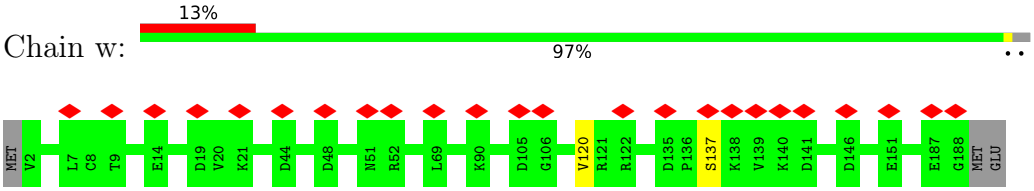




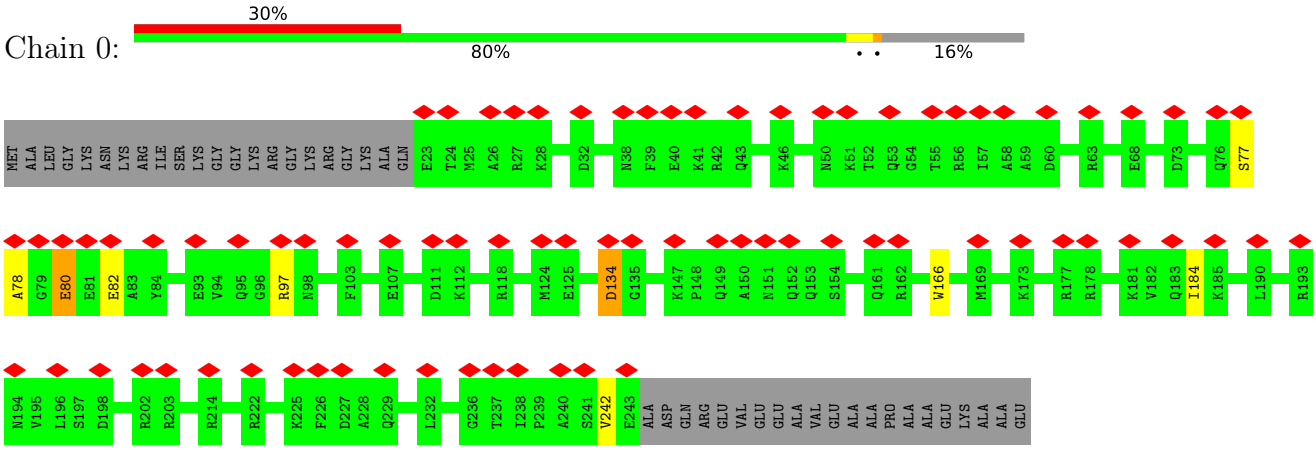
- Molecule 48: eL8



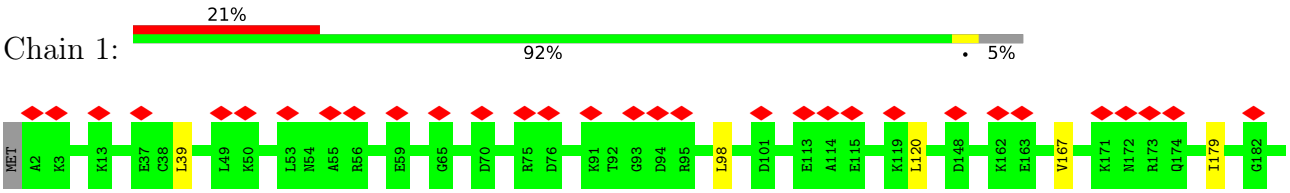
- Molecule 49: uL6

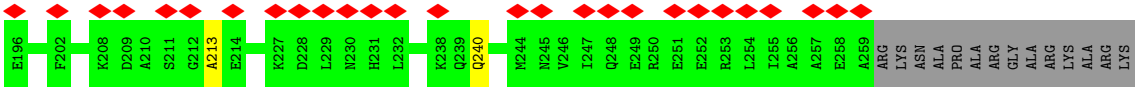


- Molecule 50: eS1



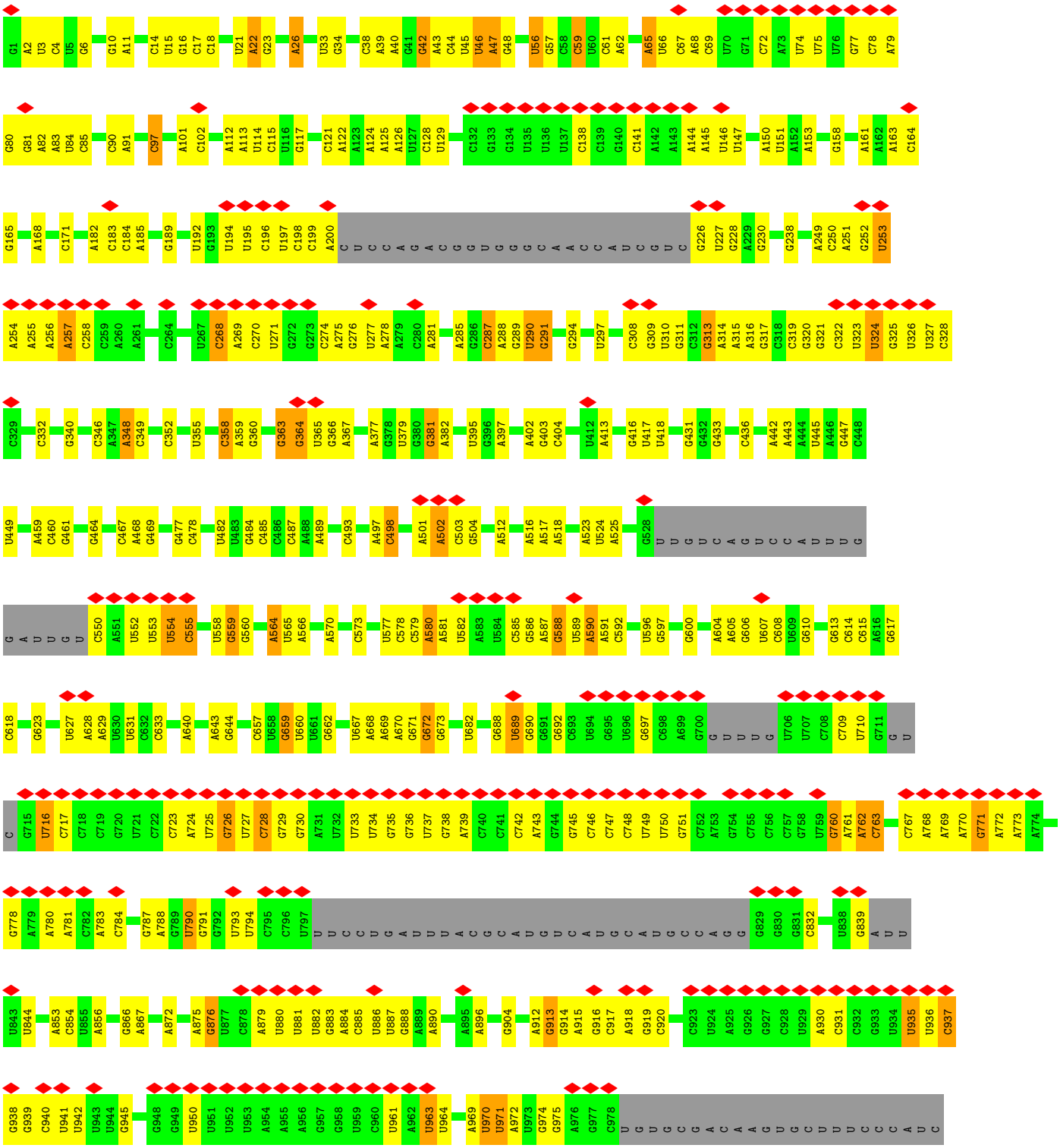
- Molecule 51: eS4



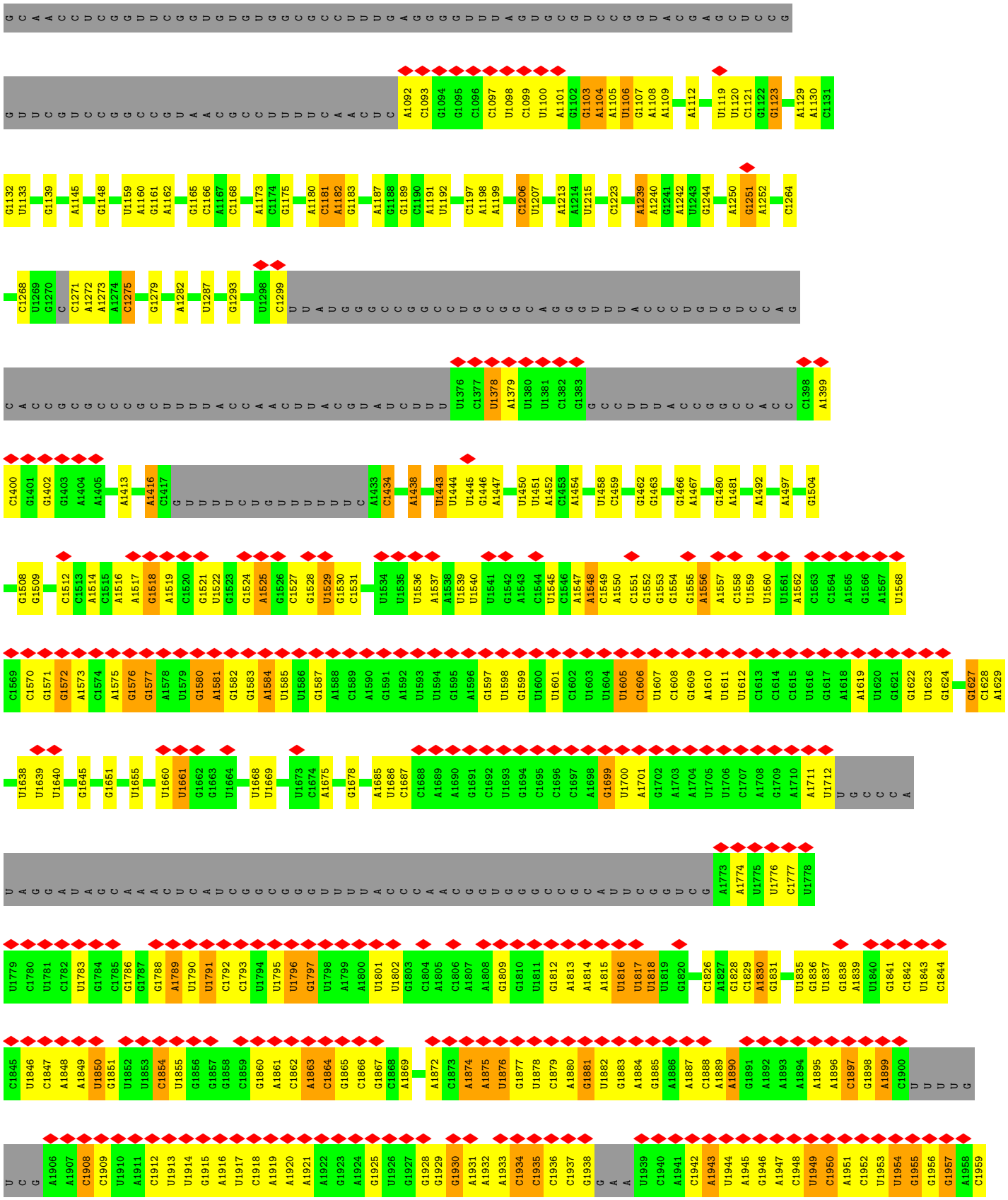


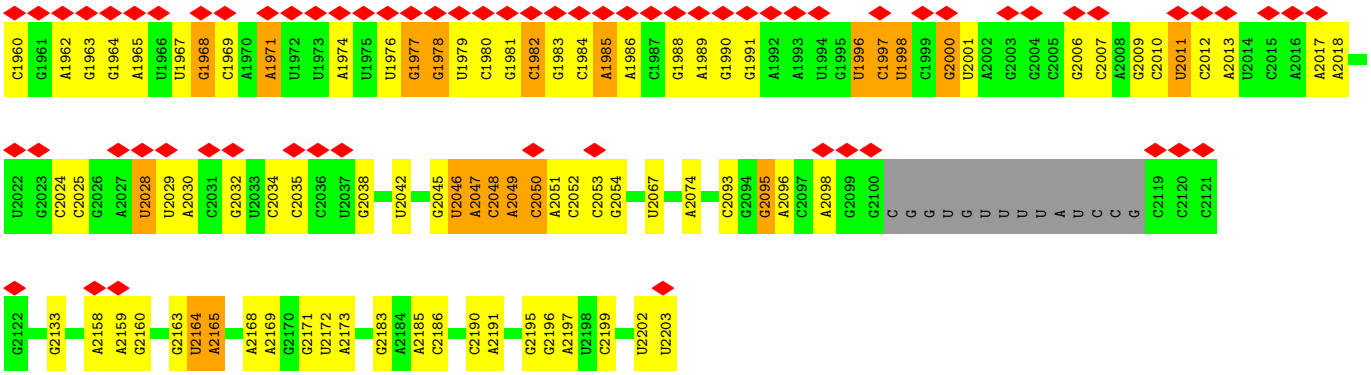
- Molecule 52: 18S rRNA

Chain 2:



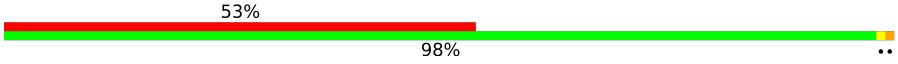
WORLDWIDE PDB PROTEIN DATA BANK

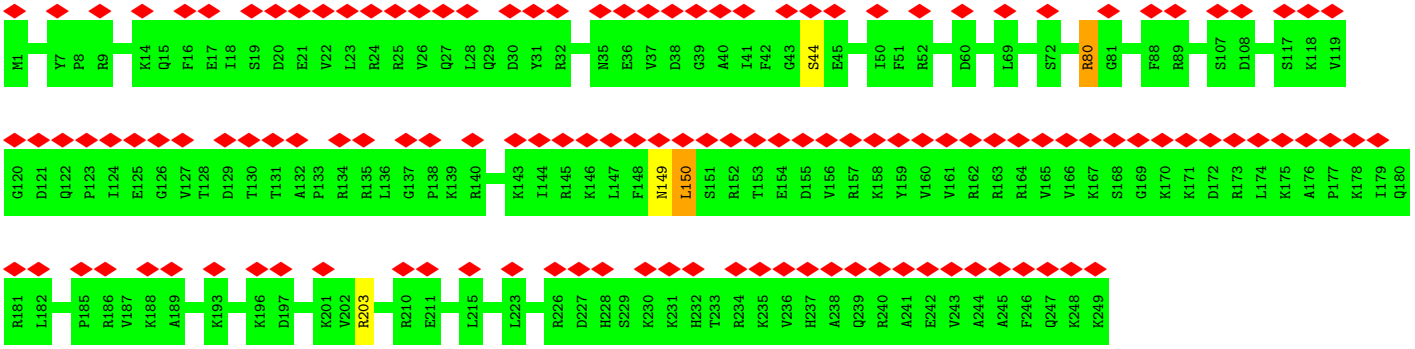

G C A A C C U C C G G U U C G G U G U G U G U G G C C U U U G A G G G G G U U U A G U G C G U C G G U A C G A G C U C C G
G U U C G U C C C G G C C G U A A C G C C U U U U C A A C U U C
A1092 C1093 G1094 G1095 C1096 C1097 U1098 C1099 U1100 A1101 G1102 G1103 A1104 A1105 U1106 G1107 A1108 A1109 A1112 U1119 U1120 C1121 G1122 G1123 A1129 A1130 C1131
G1132 U1133 G1139 A1145 G1148 U1159 A1160 G1161 A1162 G1165 C1166 A1167 C1168 A1173 C1174 G1175 A1180 C1181 A1182 G1183 A1187 G1188 G1189 C1190 A1191 U1192 C1197 A1198 A1199 C1206 U1207 A1213 A1214 U1215 C1223 A1239 A1240 G1241 A1242 U1243 G1244 A1250 G1251 A1252 C1264
C1268 U1269 G1270 C C1271 A1272 A1273 A1274 C1275 G1279 A1282 U1287 G1293 U1298 C1299 U U A U C G G G C C U G G C G G C A G G G U U U A C C U G U G G C C A G
C A C C G C G C C C G C U U U U A C A A C U U U A C C G U A U C U U U U U U U C A C C G G G C C A C C C 1398 A1399
C1400 G1401 G1402 G1403 A1404 A1405 A1413 A1416 C1417 G U U U U U C U G U U U U U U U C A1433 C1434 A1438 U1443 U1444 U1445 G1446 A1447 U1450 U1451 A1452 C1453 A1454 U1458 C1459 G1462 G1463 G1466 A1467 G1480 A1481 A1492 A1497 G1504
G1508 G1509 C1512 C1513 A1514 C1515 A1516 A1517 G1518 A1519 C1520 G1521 U1522 G1523 G1524 A1525 G1526 G1527 G1528 U1529 G1530 C1531 U1534 U1535 U1536 A1537 A1538 U1539 U1540 U1541 G1542 A1543 C1544 U1545 C1546 A1547 A1548 C1549 A1550 C1551 G1552 G1553 G1554 G1555 A1556 A1557 C1558 U1559 U1560 U1561 A1562 C1563 C1564 A1565 G1566 A1567 U1568
C1569 C1570 G1571 G1572 A1573 C1574 A1575 G1576 G1577 A1578 U1579 G1580 A1581 G1582 G1583 A1584 U1585 U1586 G1587 A1588 C1589 A1590 G1591 A1592 U1593 U1594 G1595 A1596 G1597 U1598 G1599 U1600 U1601 C1602 U1603 U1604 U1605 C1606 U1607 C1608 G1609 A1610 U1611 U1612 C1613 C1614 C1615 U1616 G1617 A1618 A1619 U1620 G1621 G1622 U1623 G1624 G1627 C1628 A1629
U1638 U1639 U1640 G1645 G1651 U1655 U1660 U1661 G1662 G1663 U1664 U1668 U1669 U1673 C1674 A1675 G1678 A1685 U1686 C1687 C1688 A1689 A1690 G1691 C1692 U1693 G1694 C1695 C1696 C1697 A1698 G1699 U1700 A1701 G1702 A1703 A1704 U1705 U1706 C1707 A1708 G1709 A1710 A1711 U1712 U G C C A
U A G G A U A G C A A A C U C A U C G G G C G G U U U G C A A C C A A C G G U G G C C G C A U U C G A1773 A1774 U1775 U1776 C1777 U1778
U1779 C1780 U1781 C1782 U1783 G1784 C1785 G1786 G1787 G1788 A1789 U1790 U1791 C1792 C1793 U1794 U1795 U1796 G1797 U1798 A1799 A1800 U1801 U1802 G1803 C1804 A1805 C1806 A1807 A1808 G1809 G1810 U1811 G1812 A1813 A1814 A1815 U1816 U1817 U1818 U1819 G1820 C1826 A1827 G1828 C1829 A1830 G1831 U1835 G1836 U1837 G1838 A1839 U1840 G1841 C1842 U1843 C1844
C1845 U1846 C1847 A1848 A1849 U1850 G1851 U1852 U1853 C1854 U1855 G1856 G1857 G1858 C1859 G1860 A1861 C1862 A1863 C1864 G1865 C1866 G1867 C1868 A1869 A1872 C1873 A1874 A1875 U1876 G1877 U1878 C1879 A1880 G1881 U1882 G1883 A1884 G1885 A1886 A1887 C1888 A1889 A1890 G1891 A1892 A1893 A1894 A1895 A1896 C1897 G1898 A1899 C1900 U U U U G
U C G A1906 A1907 C1908 C1909 U1910 A1911 C1912 U1913 U1914 G1915 A1916 U1917 C1918 A1919 A1920 A1921 A1922 G1923 A1924 G1925 U1926 G1927 G1928 G1929 G1930 A1931 A1932 A1933 C1934 C1935 C1936 C1937 G1938 G A A U1939 C1940 A1941 C1942 A1943 U1944 A1945 G1946 A1947 C1948 U1949 C1950 A1951 C1952 U1953 U1954 G1955 G1956 G1957 A1958 C1959



- Molecule 53: eS6

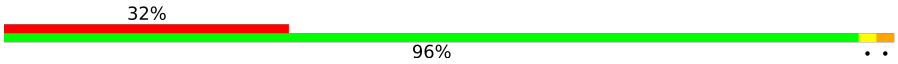
Chain 3:

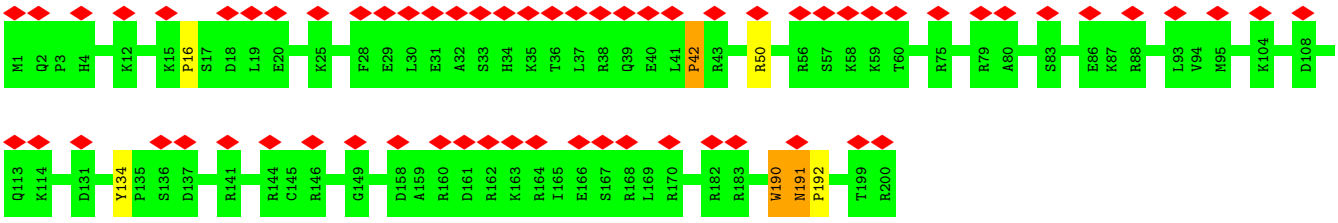




- Molecule 54: eS7

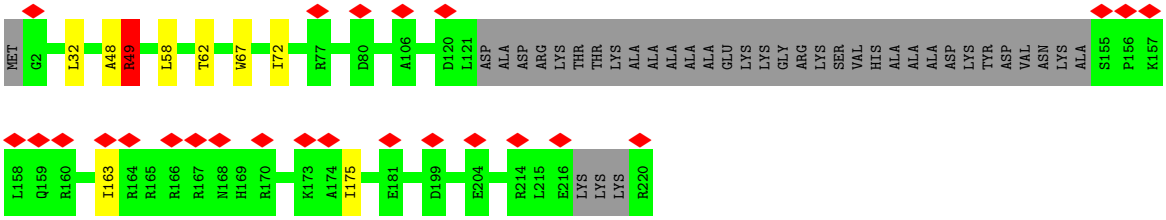
Chain 4:





- Molecule 55: eS8

Chain 5:



- Molecule 56: uS4

Chain 6: 17% 84% • • 14%

M1 R15 R16 P17 F18 E19 K20 E21 D24 R25 E26 M27 K28 R36 C37 R43 K50 R53 L61 F62 E63 N64 R67 E71 R78 D86 E87 E88 K89 D90 K91 D102 K114 A115 K119 S120 Q129 K137 E152 I155 D159

G164 ASN GLY ARG PRO GLY ARG VAL LYS ARG VAL ARG ALA LYS ALA ALA LYS ARG HIS ALA GLY GLY GLY ASP ASP ASP GLU

- Molecule 57: RACK1

Chain 7: 99% 95% • • •

M1 N2 Y3 E4 G5 H6 L7 R8 G9 H10 R11 G12 W13 V14 T15 S16 L17 A18 C19 P20 E21 Q22 A23 E24 S25 Y26 I27 K28 V29 V30 S31 T32 S33 R34 D35 G36 T37 A38 I39 A40 W41 K42 A43 N44 A45 D46 R47 H48 S49 V50 D51 S52 D53 Y54 G55 L56 P57 S58 H59 R60

L61 E62 G63 H64 T65 G66 F67 V68 S69 C70 V71 S72 L73 A74 H75 A76 T77 D78 Y79 A80 L81 T82 A83 S84 W85 D86 R87 S88 I89 R90 M91 W92 D93 L94 R95 N96 G97 Q98 S99 Q100 R101 K102 F103 L104 K105 H106 T107 K108 D109 V110 L111 A112 V113 A114 F115 S116 P117 D118 D119 R120

L121 I122 V123 S124 A125 G126 R127 D128 N129 V130 V131 R132 V133 W134 N135 V136 A137 G138 D139 C140 M141 H142 E143 F144 L145 R146 D147 G148 H149 K150 D151 W152 V153 S154 S155 I156 C157 F158 S159 P160 S161 L162 E163 H164 P165 I166 V167 V168 S169 G170 S171 W172 D173 N174 T175 I176 K177 V178 W179 N180

V181 N182 G183 G184 K185 C186 E187 R188 T189 L190 K191 G192 H193 S194 N195 Y196 V197 S198 T199 V200 T201 V202 S203 P204 D205 G206 S207 L208 C209 A210 S211 G212 G213 K214 D215 G216 V217 A218 L219 L220 W221 D222 L223 S224 T225 G226 E227 Q228 L229 F230 K231 I232 N233 V234 E235 S236 P237 I238 N239 Q240

I241 A242 F243 S244 P245 N246 R247 F248 W249 M250 C251 V252 A253 T254 E255 K256 S257 L258 S259 V260 Y261 D262 L263 E264 S265 K266 T267 V268 I269 A270 E271 L272 T273 P274 D275 G276 A277 K278 P279 S280 E281 C282 I283 S284 I285 A286 W287 S288 A289 D290 G291 N292 T293 L294 Y295 S296 G297 H298 K299 D300

N301 L302 I303 R304 V305 W306 S307 I308 SER ASP ALA GLU

- Molecule 58: uS14

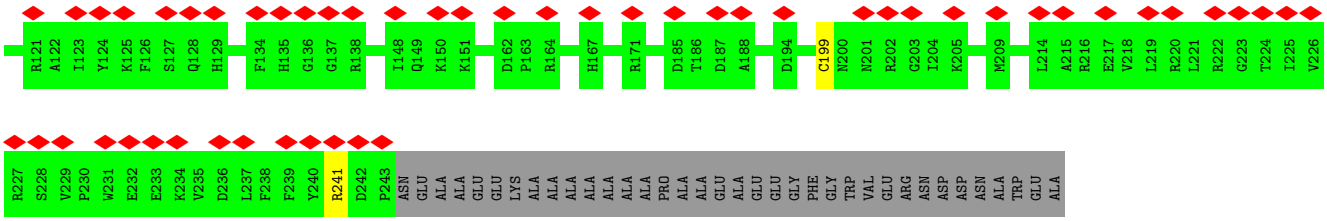
Chain 8: 63% 58% 9% 33%

MET GLY HIS LEU ASP GLN TRP ARG SER ARG GLN LYS ILE GLY MET GLY LYS GLY ALA R20 C21 C22 V23 I24 C25 S26 N27 Q28 K29 A30 L31 I32 R33 K34 Y35 E36 L37 N38 V39 C40 R41 Q42 R45 E46 N47 A48 E49 H50 I51 G52 F53 T54 K55 L56 R57

- Molecule 59: uS2

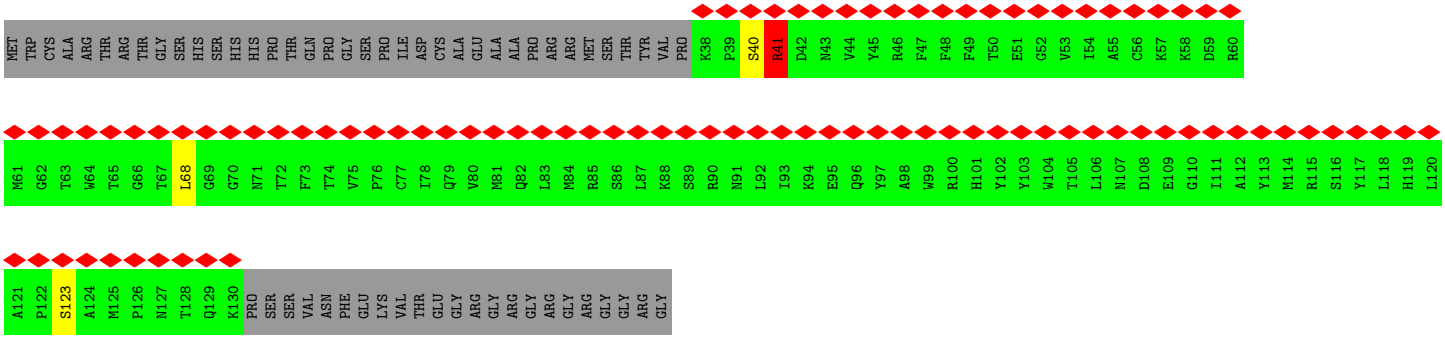
Chain AC: 36% 81% • 17%

MET SER ALA VAL GLU SER GLY S41 K42 V43 L44 R45 M46 K47 E48 S49 D50 A51 Q52 K53 L54 L55 A56 M57 R58 G62 T63 R64 N65 Q66 K71 Y75 G76 R77 T78 A79 E80 G81 S82 H83 D86 V87 M90 K93 A102 E105 N106 P107 K108 D109 S115



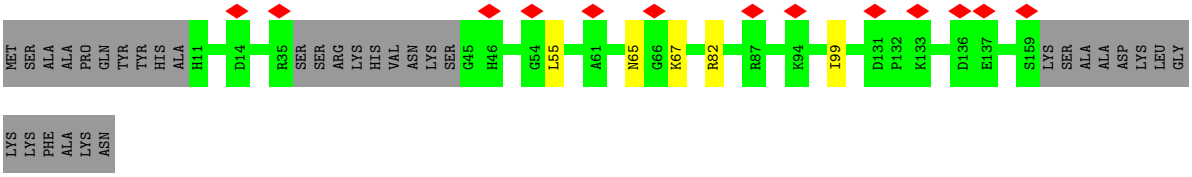
• Molecule 60: eS10

Chain AD:



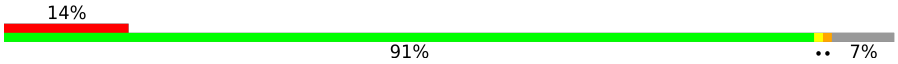
• Molecule 61: uS17

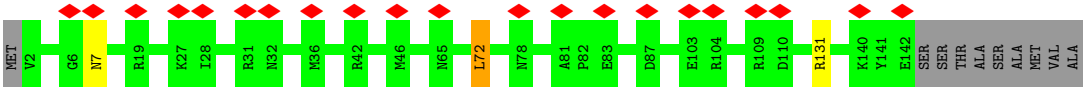
Chain AE:



• Molecule 62: uS15

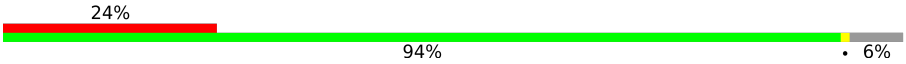
Chain AG:

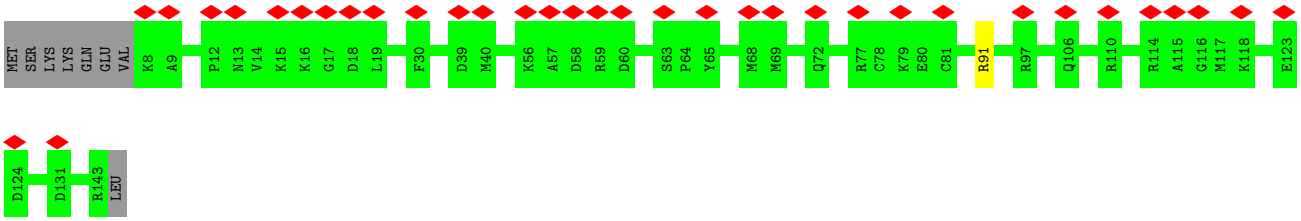




• Molecule 63: uS11

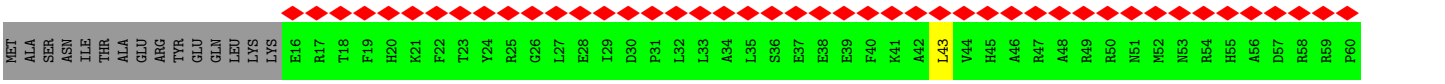
Chain AH:

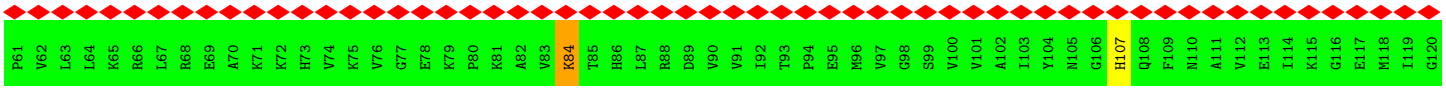




- Molecule 64: uS19

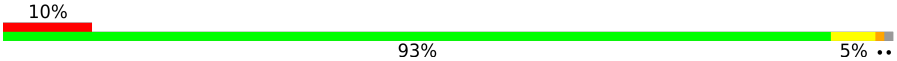
Chain AI:

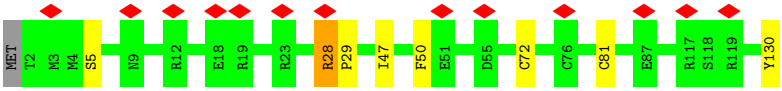




- Molecule 65: uS8

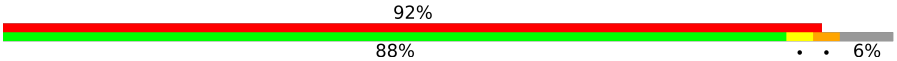
Chain AJ:

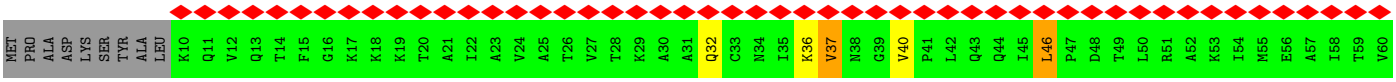


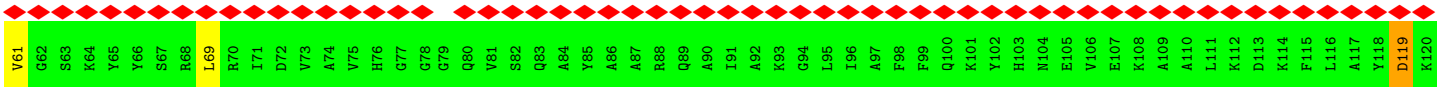


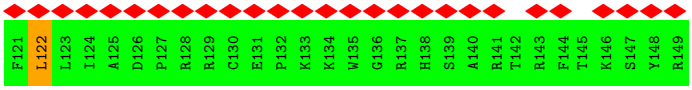
- Molecule 66: uS9

Chain AK:



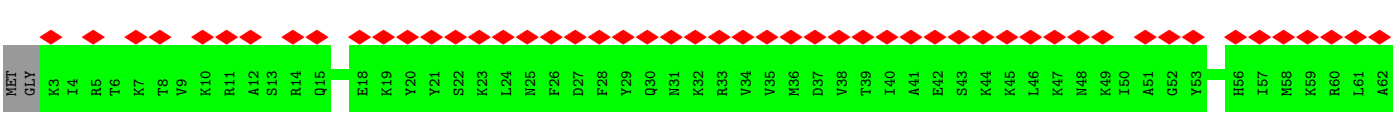


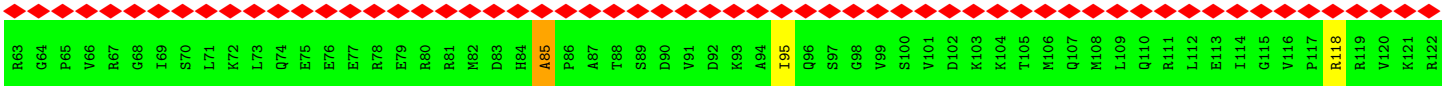


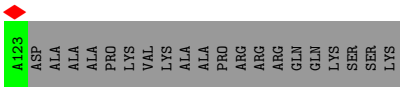


- Molecule 67: eS17

Chain AL:

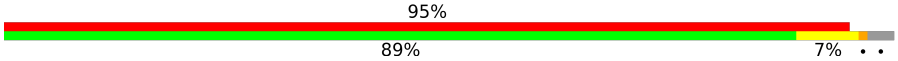


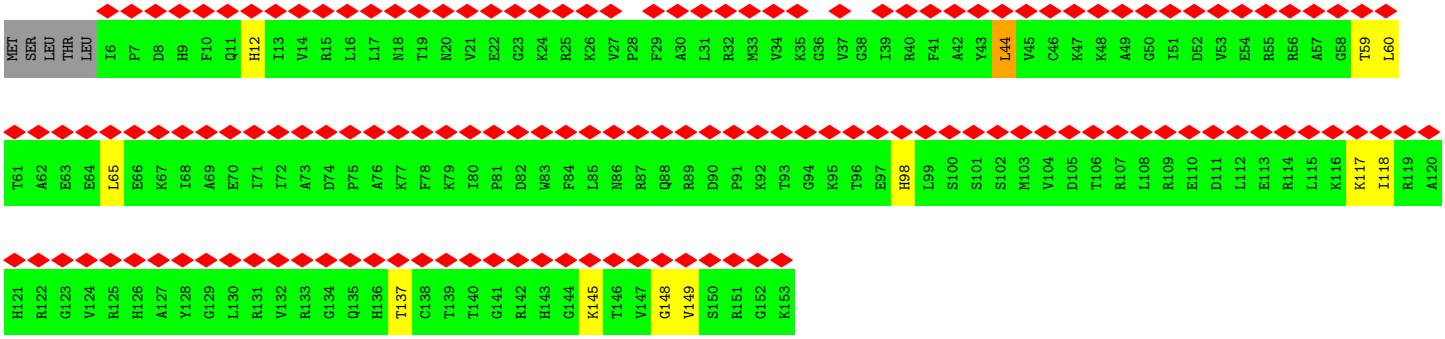




- Molecule 68: uS13

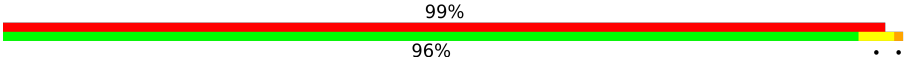
Chain AM:

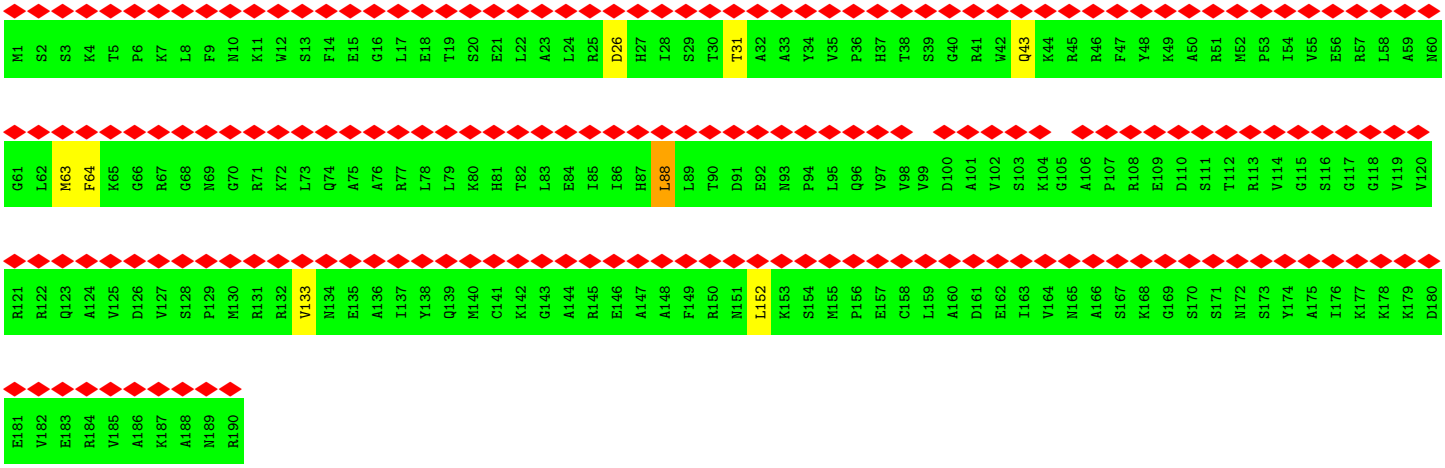




- Molecule 69: uS7

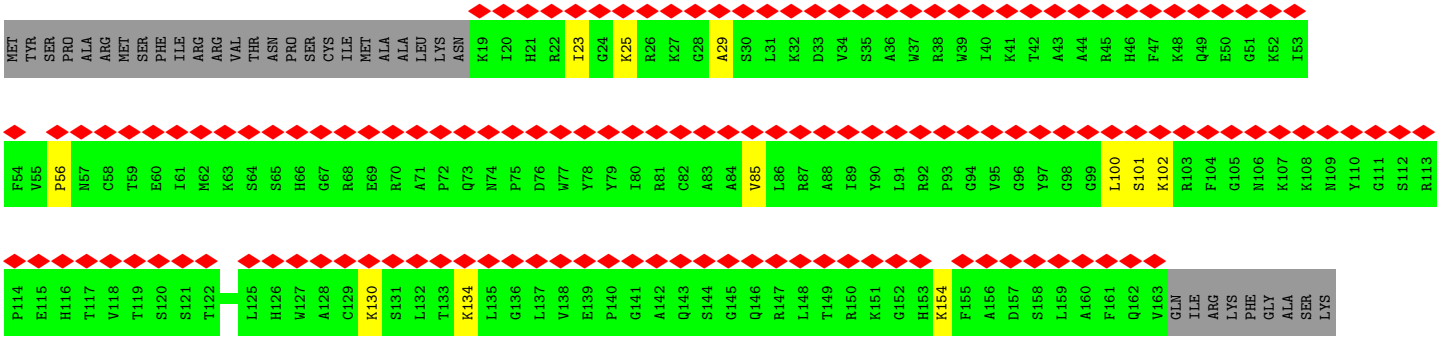
Chain AN:





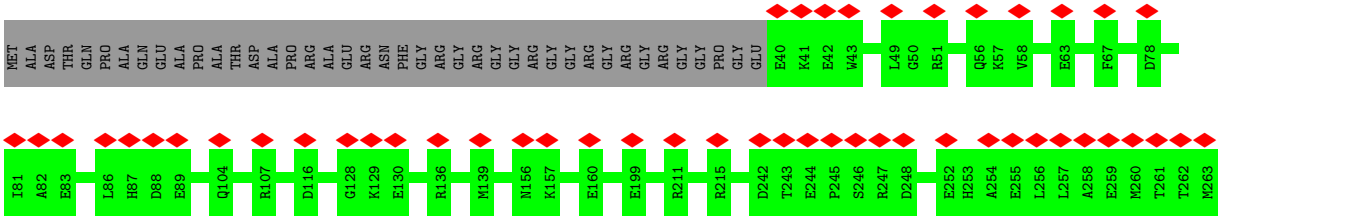
- Molecule 70: eS19

Chain AO:



- Molecule 71: uS5

Chain AP:

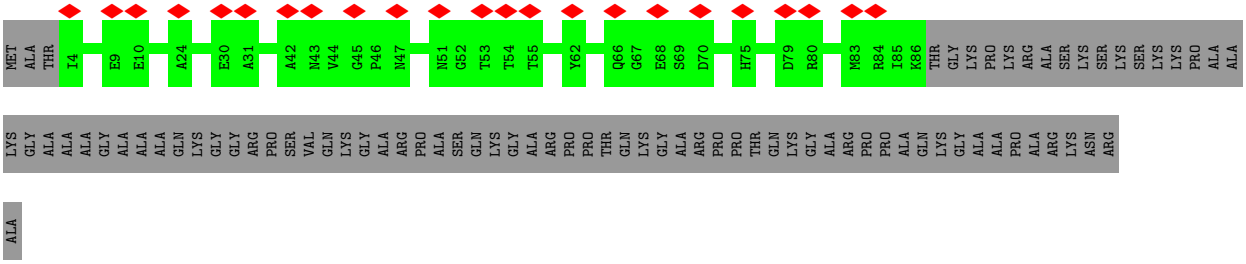


- Molecule 72: uS10

Chain AQ:

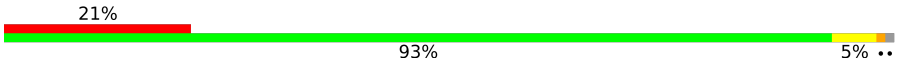
- Molecule 73: eS21

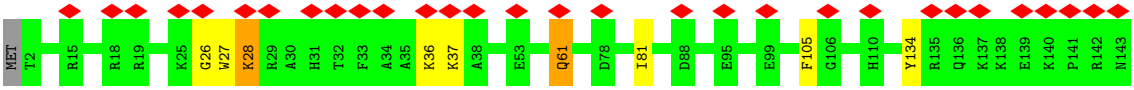
Chain AR:



- Molecule 74: uS12

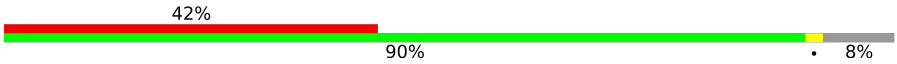
Chain AS:

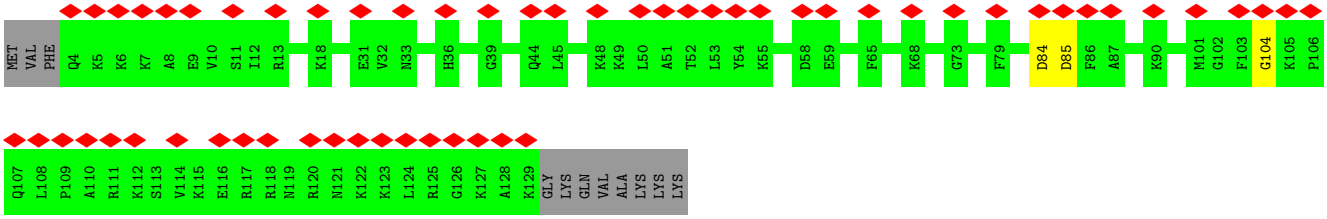




- Molecule 75: eS24

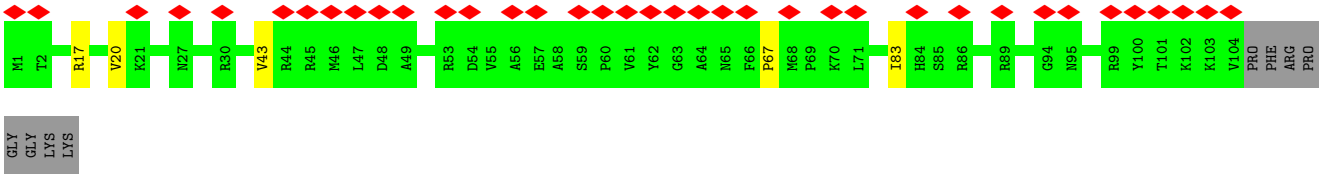
Chain AT:





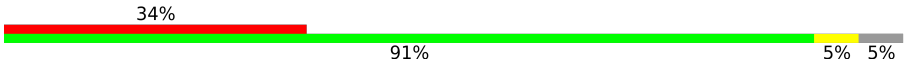
- Molecule 76: eS26

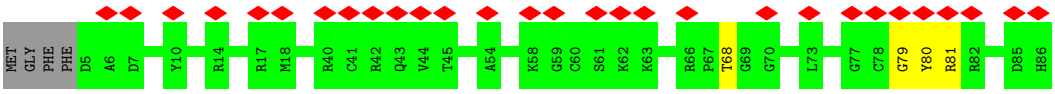
Chain AV:



- Molecule 77: eS27

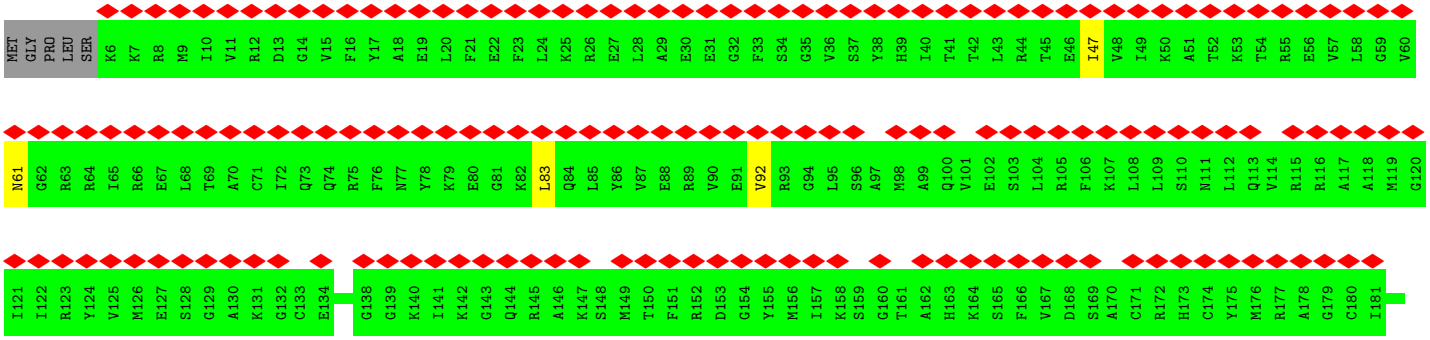
Chain AW:





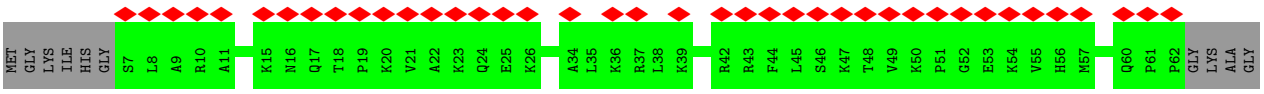
- Molecule 78: uS3

Chain AX:



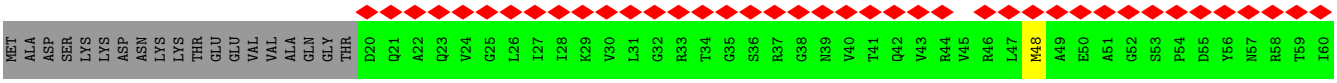
- Molecule 79: eS30

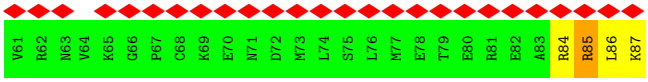
Chain AY:



- Molecule 80: eS28

Chain AZ:




V61
R62
M63
V64
K65
G66
P67
C68
K69
E70
N71
D72
M73
L74
S75
L76
M77
E78
T79
E80
R81
E82
A83
R84
R85
L86
K87

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	213108	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	317.31998, 317.31998, 317.31998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7932999, 0.7932999, 0.7932999	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	A	1.03	0/38479	0.88	24/59984 (0.0%)
2	B	1.05	0/25421	0.84	8/39614 (0.0%)
3	C	0.98	1/3855 (0.0%)	0.89	2/6002 (0.0%)
4	D	0.93	0/2829	0.79	0/4405
5	E	1.01	0/4004	0.83	1/6223 (0.0%)
6	F	0.84	0/1686	0.86	1/2623 (0.0%)
7	G	1.11	0/4373	0.88	8/6817 (0.1%)
8	H	1.15	0/2230	0.88	2/3470 (0.1%)
9	I	0.60	1/1564 (0.1%)	0.75	2/2092 (0.1%)
10	J	0.53	0/1737	0.62	0/2324
11	K	0.42	0/1362	0.56	0/1821
12	L	0.52	0/1463	0.60	2/1952 (0.1%)
13	M	0.59	0/1815	0.67	3/2436 (0.1%)
14	N	0.51	0/1355	0.66	3/1814 (0.2%)
15	O	0.65	2/1754 (0.1%)	0.71	5/2342 (0.2%)
16	P	0.61	0/1269	0.62	0/1700
17	Q	0.61	0/1490	0.60	0/2007
18	R	0.50	0/1665	0.54	0/2206
19	S	0.58	0/1290	0.71	2/1734 (0.1%)
20	T	0.52	0/1013	0.61	1/1350 (0.1%)
21	U	0.64	0/1052	0.64	0/1417
22	V	0.50	0/978	0.58	0/1318
23	W	0.65	0/584	0.53	0/785
24	X	0.54	0/980	0.67	0/1308
25	Y	0.56	0/1100	0.57	0/1470
26	Z	0.57	0/1153	0.72	2/1541 (0.1%)
27	a	0.47	0/1157	0.65	2/1548 (0.1%)
28	b	0.41	0/565	0.62	1/754 (0.1%)
29	c	0.69	2/1961 (0.1%)	0.72	1/2630 (0.0%)
30	d	0.64	0/3250	0.69	4/4368 (0.1%)
31	e	0.57	0/730	0.77	3/988 (0.3%)
32	f	0.55	0/893	0.61	0/1196
33	g	0.57	0/1071	0.71	1/1432 (0.1%)
34	h	0.57	0/1030	0.62	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	i	0.45	0/1067	0.59	1/1416 (0.1%)
36	j	0.63	0/1082	0.68	1/1454 (0.1%)
37	k	0.42	0/802	0.50	0/1073
38	l	0.64	1/688 (0.1%)	0.87	2/918 (0.2%)
39	m	0.63	0/724	0.66	0/964
40	n	0.54	0/614	0.58	1/818 (0.1%)
41	o	0.58	0/463	0.65	0/617
42	p	0.53	0/2874	0.67	3/3865 (0.1%)
43	q	0.61	0/431	0.66	1/572 (0.2%)
44	r	0.59	1/792 (0.1%)	0.69	2/1046 (0.2%)
45	s	0.49	0/2129	0.58	1/2846 (0.0%)
46	t	0.57	0/1074	0.78	5/1454 (0.3%)
47	u	0.57	0/1891	0.61	2/2531 (0.1%)
48	v	0.48	0/1878	0.57	0/2524
49	w	0.56	0/1504	0.64	0/2024
50	0	0.70	0/1811	0.76	4/2438 (0.2%)
51	1	0.80	0/2076	0.78	1/2799 (0.0%)
52	2	1.66	86/43318 (0.2%)	1.27	315/67487 (0.5%)
53	3	0.66	1/2019 (0.0%)	0.77	3/2694 (0.1%)
54	4	0.76	0/1697	0.88	4/2276 (0.2%)
55	5	0.89	2/1494 (0.1%)	1.01	7/2000 (0.3%)
56	6	0.75	1/1389 (0.1%)	0.73	1/1866 (0.1%)
57	7	0.46	1/2454 (0.0%)	0.75	6/3337 (0.2%)
58	8	0.73	0/317	1.00	3/421 (0.7%)
59	AC	0.68	0/1656	0.69	0/2238
60	AD	0.47	0/788	0.91	3/1064 (0.3%)
61	AE	0.98	0/1171	0.75	1/1570 (0.1%)
62	AG	0.83	0/1180	0.80	1/1581 (0.1%)
63	AH	0.78	0/1038	0.80	1/1392 (0.1%)
64	AI	1.11	1/1006 (0.1%)	0.94	8/1351 (0.6%)
65	AJ	0.94	2/1037 (0.2%)	0.89	1/1391 (0.1%)
66	AK	0.54	0/1128	0.82	3/1515 (0.2%)
67	AL	0.52	0/993	0.69	0/1322
68	AM	0.50	0/1206	0.88	2/1615 (0.1%)
69	AN	0.48	0/1516	0.75	2/2034 (0.1%)
70	AO	0.51	0/1180	0.78	1/1585 (0.1%)
71	AP	0.80	0/1758	0.76	0/2380
72	AQ	0.51	0/817	0.75	0/1107
73	AR	0.67	0/639	0.72	0/866
74	AS	0.81	0/1134	0.89	3/1517 (0.2%)
75	AT	0.68	0/1054	0.70	0/1405
76	AV	0.69	0/845	0.76	0/1130
77	AW	1.25	2/658 (0.3%)	0.80	1/883 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	AX	0.56	0/1616	0.83	6/2159 (0.3%)
79	AY	0.54	0/460	0.73	0/611
80	AZ	0.60	1/528 (0.2%)	0.83	1/705 (0.1%)
All	All	1.06	105/215154 (0.0%)	0.92	475/315901 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
9	I	0	1
13	M	0	2
16	P	0	2
20	T	0	1
23	W	0	1
24	X	0	1
28	b	0	1
29	c	0	1
31	e	0	1
37	k	0	1
38	l	0	3
39	m	0	1
47	u	0	1
50	0	0	1
53	3	0	1
54	4	0	1
55	5	0	2
57	7	0	1
58	8	0	1
59	AC	0	3
61	AE	0	1
62	AG	0	3
64	AI	0	3
66	AK	0	1
67	AL	0	1
68	AM	0	7
69	AN	0	4
70	AO	0	6
72	AQ	0	1
75	AT	0	2
77	AW	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
78	AX	0	1
All	All	0	58

The worst 5 of 105 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	2	1864	C	N3-C4	80.83	1.90	1.33
52	2	1864	C	C2-N3	72.70	1.94	1.35
52	2	1864	C	N1-C6	69.47	1.78	1.37
52	2	1864	C	N1-C2	48.39	1.88	1.40
52	2	1864	C	C4-C5	48.22	1.81	1.43

The worst 5 of 475 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
52	2	971	U	O5'-P-OP2	-31.09	73.39	110.70
52	2	1954	U	P-O3'-C3'	28.04	153.35	119.70
52	2	1818	U	O5'-P-OP2	-26.60	78.78	110.70
52	2	1818	U	O5'-P-OP1	-22.31	83.92	110.70
52	2	971	U	O5'-P-OP1	-21.05	85.44	110.70

There are no chirality outliers.

5 of 58 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	I	180	THR	Peptide
13	M	132	ARG	Peptide
13	M	163	HIS	Peptide
16	P	36	ILE	Peptide
16	P	64	ASN	Peptide

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	195/198 (98%)	180 (92%)	12 (6%)	3 (2%)	10	34
10	J	209/213 (98%)	193 (92%)	13 (6%)	3 (1%)	11	36
11	K	165/188 (88%)	152 (92%)	12 (7%)	1 (1%)	25	58
12	L	175/220 (80%)	159 (91%)	14 (8%)	2 (1%)	14	42
13	M	219/222 (99%)	212 (97%)	6 (3%)	1 (0%)	29	61
14	N	166/175 (95%)	153 (92%)	12 (7%)	1 (1%)	25	58
15	O	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
16	P	153/166 (92%)	145 (95%)	7 (5%)	1 (1%)	22	54
17	Q	176/179 (98%)	163 (93%)	11 (6%)	2 (1%)	14	42
18	R	194/245 (79%)	193 (100%)	1 (0%)	0	100	100
19	S	156/159 (98%)	144 (92%)	11 (7%)	1 (1%)	25	58
20	T	121/129 (94%)	116 (96%)	5 (4%)	0	100	100
21	U	135/139 (97%)	126 (93%)	9 (7%)	0	100	100
22	V	118/145 (81%)	106 (90%)	11 (9%)	1 (1%)	19	51
23	W	63/124 (51%)	61 (97%)	2 (3%)	0	100	100
24	X	118/143 (82%)	111 (94%)	5 (4%)	2 (2%)	9	31
25	Y	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	19	51
26	Z	142/145 (98%)	125 (88%)	14 (10%)	3 (2%)	7	26
27	a	144/147 (98%)	134 (93%)	9 (6%)	1 (1%)	22	54
28	b	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
29	c	251/260 (96%)	229 (91%)	20 (8%)	2 (1%)	19	51
30	d	397/419 (95%)	376 (95%)	20 (5%)	1 (0%)	41	71
31	e	92/104 (88%)	88 (96%)	4 (4%)	0	100	100
32	f	108/183 (59%)	102 (94%)	6 (6%)	0	100	100
33	g	127/133 (96%)	119 (94%)	8 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	h	122/168 (73%)	117 (96%)	4 (3%)	1 (1%)	19	51
35	i	124/127 (98%)	117 (94%)	6 (5%)	1 (1%)	19	51
36	j	130/144 (90%)	119 (92%)	11 (8%)	0	100	100
37	k	97/105 (92%)	94 (97%)	3 (3%)	0	100	100
38	l	79/83 (95%)	72 (91%)	7 (9%)	0	100	100
39	m	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
40	n	73/83 (88%)	70 (96%)	3 (4%)	0	100	100
41	o	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
42	p	362/373 (97%)	340 (94%)	20 (6%)	2 (1%)	25	58
43	q	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
44	r	94/106 (89%)	85 (90%)	8 (8%)	1 (1%)	14	42
45	s	258/305 (85%)	246 (95%)	12 (5%)	0	100	100
46	t	133/195 (68%)	123 (92%)	8 (6%)	2 (2%)	10	34
47	u	226/252 (90%)	209 (92%)	16 (7%)	1 (0%)	34	66
48	v	228/348 (66%)	218 (96%)	10 (4%)	0	100	100
49	w	185/190 (97%)	173 (94%)	11 (6%)	1 (0%)	29	61
50	0	219/264 (83%)	208 (95%)	10 (5%)	1 (0%)	29	61
51	1	256/273 (94%)	231 (90%)	22 (9%)	3 (1%)	13	40
53	3	247/249 (99%)	236 (96%)	10 (4%)	1 (0%)	34	66
54	4	198/200 (99%)	183 (92%)	11 (6%)	4 (2%)	7	27
55	5	178/220 (81%)	160 (90%)	16 (9%)	2 (1%)	14	42
56	6	162/190 (85%)	151 (93%)	9 (6%)	2 (1%)	13	40
57	7	306/312 (98%)	275 (90%)	28 (9%)	3 (1%)	15	45
58	8	36/57 (63%)	30 (83%)	5 (14%)	1 (3%)	5	19
59	AC	201/246 (82%)	193 (96%)	8 (4%)	0	100	100
60	AD	91/153 (60%)	78 (86%)	11 (12%)	2 (2%)	6	24
61	AE	136/173 (79%)	131 (96%)	4 (3%)	1 (1%)	22	54
62	AG	139/151 (92%)	133 (96%)	6 (4%)	0	100	100
63	AH	134/144 (93%)	126 (94%)	8 (6%)	0	100	100
64	AI	119/152 (78%)	102 (86%)	17 (14%)	0	100	100
65	AJ	127/130 (98%)	120 (94%)	6 (5%)	1 (1%)	19	51

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
66	AK	138/149 (93%)	118 (86%)	16 (12%)	4 (3%)	4	18
67	AL	119/143 (83%)	108 (91%)	8 (7%)	3 (2%)	5	21
68	AM	146/153 (95%)	125 (86%)	21 (14%)	0	100	100
69	AN	188/190 (99%)	165 (88%)	21 (11%)	2 (1%)	14	42
70	AO	143/179 (80%)	114 (80%)	25 (18%)	4 (3%)	5	19
71	AP	222/265 (84%)	216 (97%)	6 (3%)	0	100	100
72	AQ	100/116 (86%)	86 (86%)	13 (13%)	1 (1%)	15	45
73	AR	81/164 (49%)	78 (96%)	3 (4%)	0	100	100
74	AS	140/143 (98%)	132 (94%)	5 (4%)	3 (2%)	7	26
75	AT	124/137 (90%)	117 (94%)	6 (5%)	1 (1%)	19	51
76	AV	102/112 (91%)	90 (88%)	8 (8%)	4 (4%)	3	12
77	AW	80/86 (93%)	76 (95%)	4 (5%)	0	100	100
78	AX	201/219 (92%)	179 (89%)	17 (8%)	5 (2%)	5	21
79	AY	54/66 (82%)	48 (89%)	6 (11%)	0	100	100
80	AZ	66/87 (76%)	60 (91%)	4 (6%)	2 (3%)	4	17
All	All	10774/12317 (88%)	9993 (93%)	696 (6%)	85 (1%)	24	51

5 of 85 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	142	GLU
10	J	145	VAL
12	L	21	SER
24	X	59	ALA
26	Z	114	HIS

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	
9	I	163/164 (99%)	158 (97%)	5 (3%)	40	74

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	178/179 (99%)	175 (98%)	3 (2%)	60	86
11	K	145/163 (89%)	144 (99%)	1 (1%)	84	95
12	L	152/182 (84%)	151 (99%)	1 (1%)	84	95
13	M	188/189 (100%)	187 (100%)	1 (0%)	88	96
14	N	139/144 (96%)	136 (98%)	3 (2%)	52	81
15	O	179/180 (99%)	178 (99%)	1 (1%)	86	96
16	P	133/144 (92%)	133 (100%)	0	100	100
17	Q	156/158 (99%)	156 (100%)	0	100	100
18	R	168/196 (86%)	166 (99%)	2 (1%)	71	91
19	S	132/133 (99%)	131 (99%)	1 (1%)	81	94
20	T	107/114 (94%)	107 (100%)	0	100	100
21	U	110/111 (99%)	110 (100%)	0	100	100
22	V	103/123 (84%)	103 (100%)	0	100	100
23	W	60/104 (58%)	59 (98%)	1 (2%)	60	86
24	X	103/121 (85%)	103 (100%)	0	100	100
25	Y	114/115 (99%)	113 (99%)	1 (1%)	78	93
26	Z	114/115 (99%)	114 (100%)	0	100	100
27	a	118/119 (99%)	116 (98%)	2 (2%)	60	86
28	b	57/58 (98%)	57 (100%)	0	100	100
29	c	198/204 (97%)	193 (98%)	5 (2%)	47	78
30	d	337/351 (96%)	336 (100%)	1 (0%)	92	98
31	e	82/90 (91%)	77 (94%)	5 (6%)	18	48
32	f	97/156 (62%)	97 (100%)	0	100	100
33	g	113/117 (97%)	111 (98%)	2 (2%)	59	85
34	h	107/145 (74%)	107 (100%)	0	100	100
35	i	116/117 (99%)	116 (100%)	0	100	100
36	j	109/121 (90%)	107 (98%)	2 (2%)	59	85
37	k	81/87 (93%)	81 (100%)	0	100	100
38	l	69/70 (99%)	69 (100%)	0	100	100
39	m	73/74 (99%)	73 (100%)	0	100	100
40	n	68/74 (92%)	68 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	o	46/47 (98%)	46 (100%)	0	100	100
42	p	295/302 (98%)	293 (99%)	2 (1%)	84	95
43	q	46/113 (41%)	46 (100%)	0	100	100
44	r	83/92 (90%)	80 (96%)	3 (4%)	35	69
45	s	209/242 (86%)	208 (100%)	1 (0%)	88	96
46	t	111/152 (73%)	110 (99%)	1 (1%)	78	93
47	u	190/209 (91%)	187 (98%)	3 (2%)	62	86
48	v	196/292 (67%)	196 (100%)	0	100	100
49	w	169/172 (98%)	168 (99%)	1 (1%)	86	96
50	0	194/222 (87%)	189 (97%)	5 (3%)	46	77
51	1	215/225 (96%)	212 (99%)	3 (1%)	67	89
53	3	208/208 (100%)	206 (99%)	2 (1%)	76	92
54	4	186/186 (100%)	185 (100%)	1 (0%)	88	96
55	5	149/176 (85%)	147 (99%)	2 (1%)	69	90
56	6	147/164 (90%)	145 (99%)	2 (1%)	67	89
57	7	263/266 (99%)	259 (98%)	4 (2%)	65	87
58	8	35/49 (71%)	35 (100%)	0	100	100
59	AC	177/202 (88%)	177 (100%)	0	100	100
60	AD	82/129 (64%)	81 (99%)	1 (1%)	71	91
61	AE	124/150 (83%)	122 (98%)	2 (2%)	62	86
62	AG	125/132 (95%)	125 (100%)	0	100	100
63	AH	105/113 (93%)	105 (100%)	0	100	100
64	AI	104/130 (80%)	102 (98%)	2 (2%)	57	84
65	AJ	110/111 (99%)	105 (96%)	5 (4%)	27	61
66	AK	113/120 (94%)	108 (96%)	5 (4%)	28	61
67	AL	107/123 (87%)	107 (100%)	0	100	100
68	AM	125/130 (96%)	121 (97%)	4 (3%)	39	73
69	AN	159/159 (100%)	158 (99%)	1 (1%)	86	96
70	AO	118/147 (80%)	118 (100%)	0	100	100
71	AP	184/209 (88%)	184 (100%)	0	100	100
72	AQ	94/104 (90%)	94 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	AR	68/119 (57%)	68 (100%)	0	100	100
74	AS	115/116 (99%)	110 (96%)	5 (4%)	29	62
75	AT	111/120 (92%)	111 (100%)	0	100	100
76	AV	87/93 (94%)	86 (99%)	1 (1%)	73	92
77	AW	72/75 (96%)	71 (99%)	1 (1%)	67	89
78	AX	171/185 (92%)	167 (98%)	4 (2%)	50	80
79	AY	49/54 (91%)	49 (100%)	0	100	100
80	AZ	57/74 (77%)	54 (95%)	3 (5%)	22	54
All	All	9268/10330 (90%)	9167 (99%)	101 (1%)	74	92

5 of 101 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	3	150	LEU
64	AI	134	LEU
80	AZ	84	ARG
55	5	49	ARG
57	7	27	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 137 such sidechains are listed below:

Mol	Chain	Res	Type
68	AM	86	ASN
70	AO	46	HIS
75	AT	95	ASN
43	q	109	ASN
43	q	90	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1591/1781 (89%)	282 (17%)	1 (0%)
2	B	1058/1465 (72%)	162 (15%)	7 (0%)
3	C	160/262 (61%)	24 (15%)	1 (0%)
4	D	118/120 (98%)	10 (8%)	0
5	E	163/213 (76%)	20 (12%)	0
52	2	1801/2205 (81%)	656 (36%)	162 (8%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	F	70/73 (95%)	16 (22%)	1 (1%)
7	G	182/183 (99%)	18 (9%)	1 (0%)
8	H	89/127 (70%)	13 (14%)	0
All	All	5232/6429 (81%)	1201 (22%)	173 (3%)

5 of 1201 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	G
1	A	20	G
1	A	24	A
1	A	28	G
1	A	38	A

5 of 173 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	2	1575	A
52	2	1882	U
52	2	1581	A
52	2	1792	C
52	2	1930	G

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
52	2	2
77	AW	2
38	l	1
15	O	1
29	c	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1972:U	O3'	1973:U	P	6.52
1	2	1954:U	O3'	1955:G	P	2.07
1	AW	79:GLY	C	80:TYR	N	1.68
1	l	66:TYR	C	67:LEU	N	1.18
1	O	50:MET	C	51:LEU	N	1.15

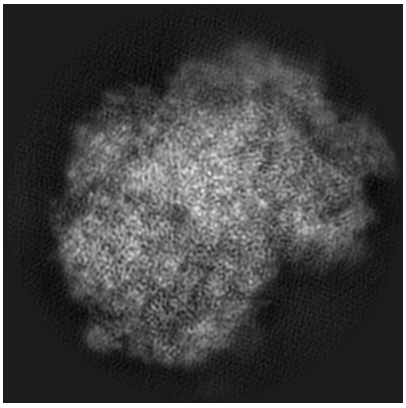
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-8343. These allow visual inspection of the internal detail of the map and identification of artifacts.

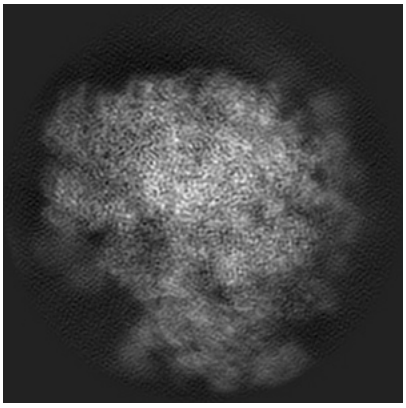
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

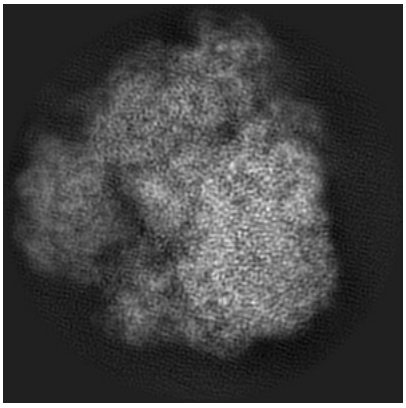
6.1.1 Primary map



X



Y

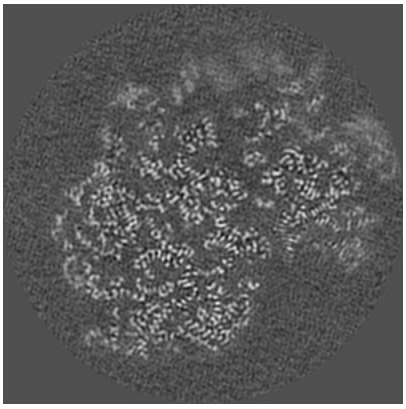


Z

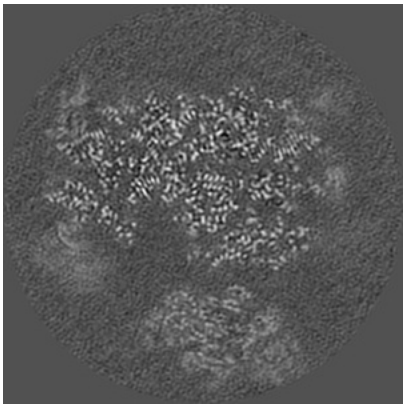
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

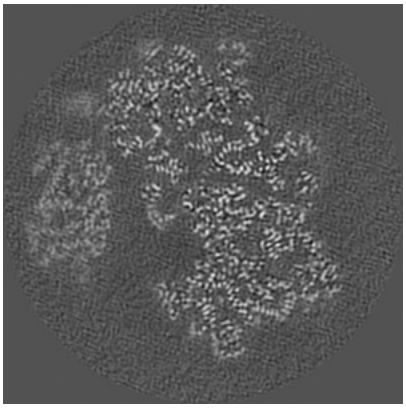
6.2.1 Primary map



X Index: 200



Y Index: 200

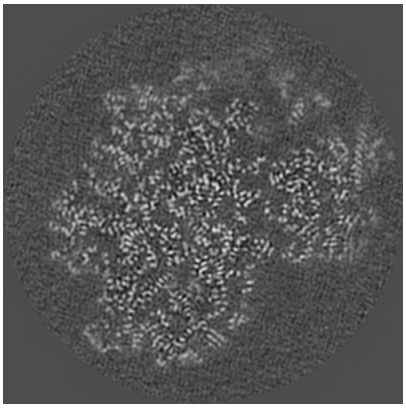


Z Index: 200

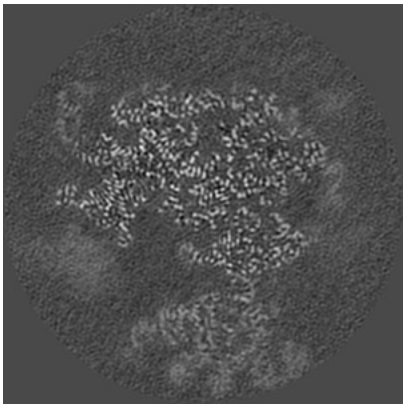
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

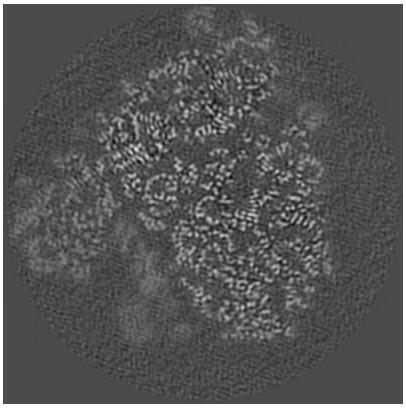
6.3.1 Primary map



X Index: 214



Y Index: 211

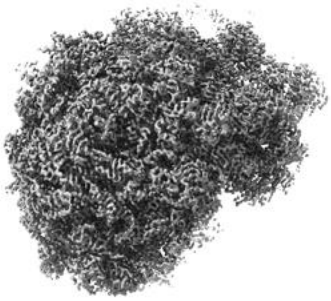


Z Index: 231

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

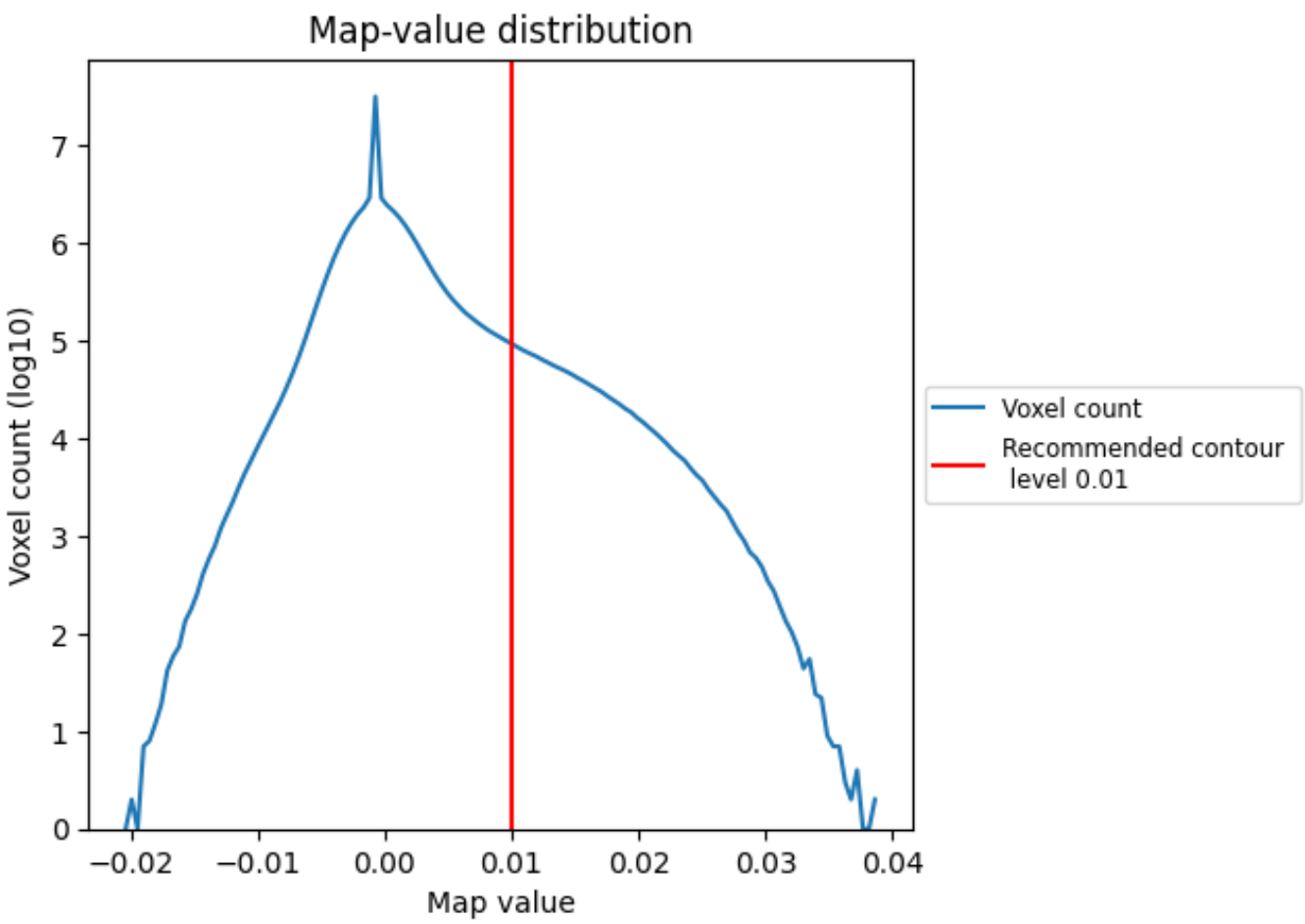
6.5 Mask visualisation (i)

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

7 Map analysis (i)

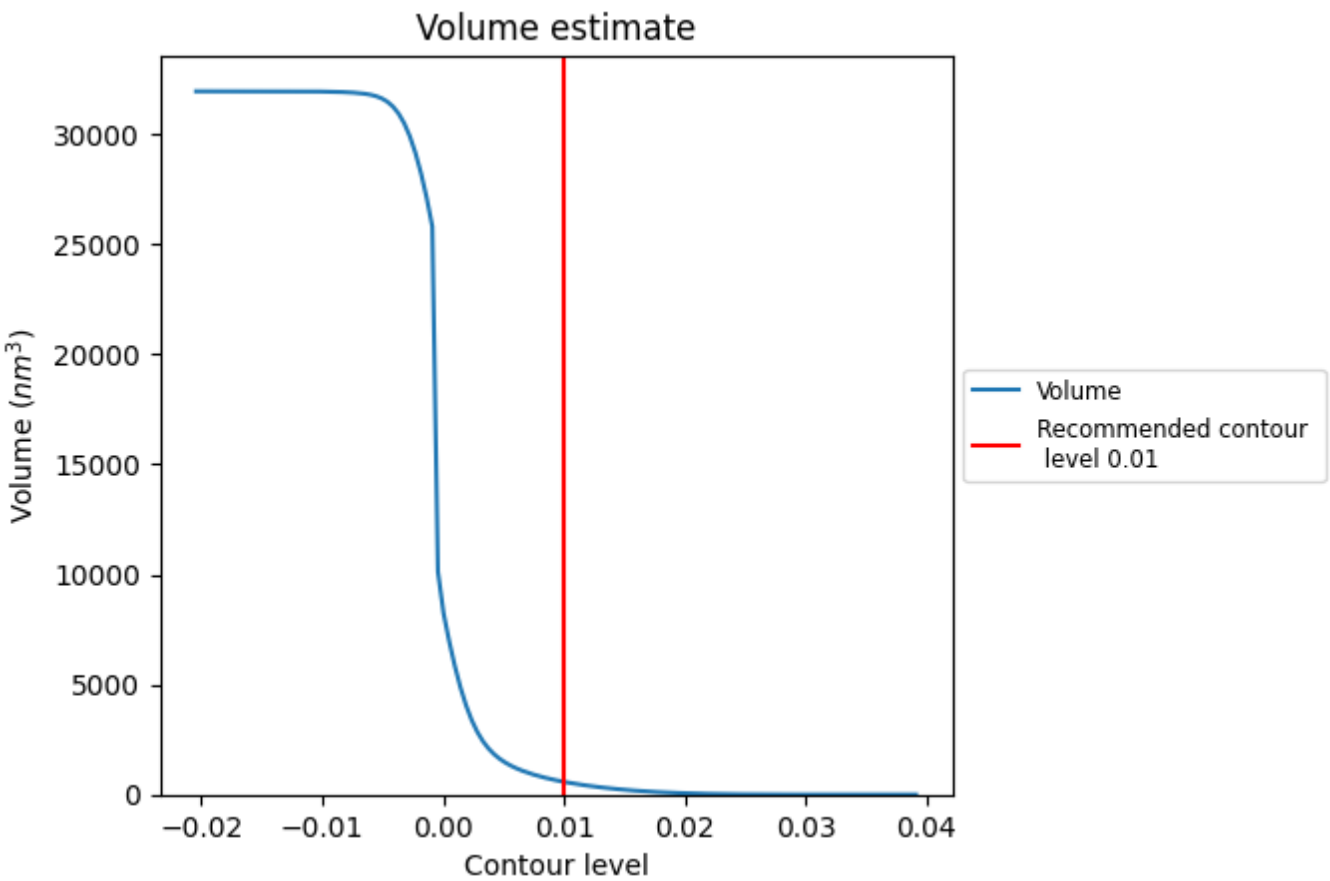
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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.

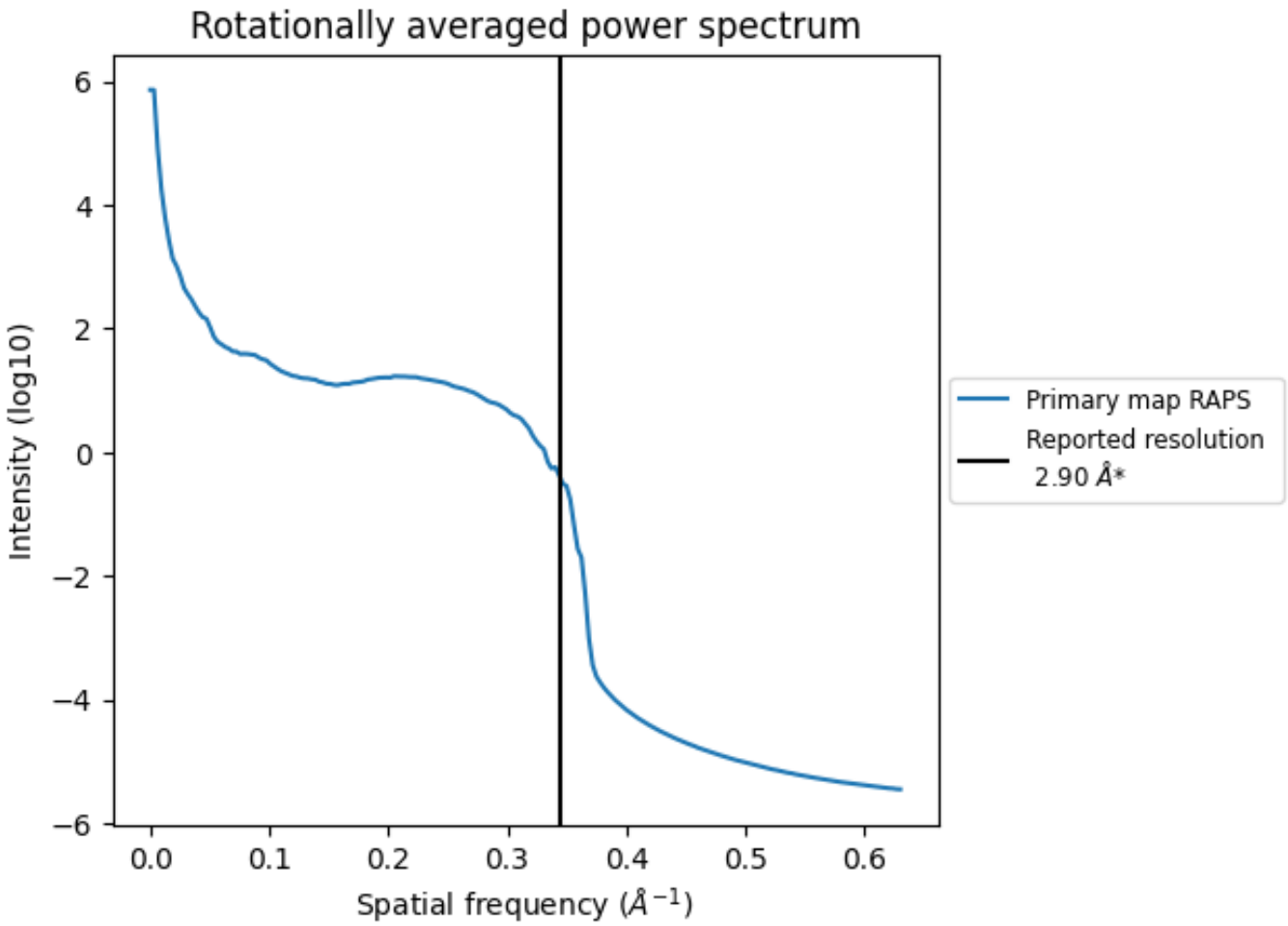
7.2 Volume estimate (i)



The volume at the recommended contour level is 580 nm^3; this corresponds to an approximate mass of 524 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 0.345 Å^{-1}

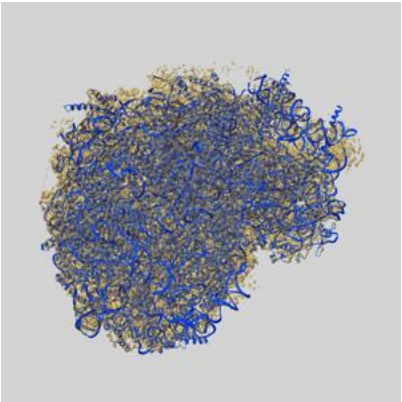
8 Fourier-Shell correlation (i)

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

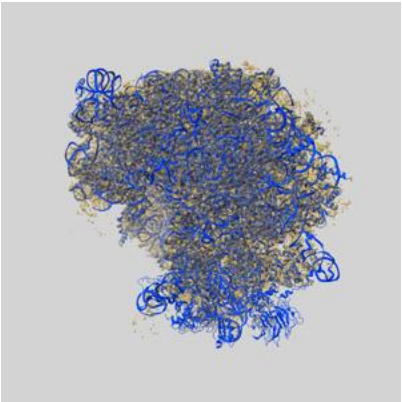
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8343 and PDB model 5T2A. Per-residue inclusion information can be found in section 3 on page 19.

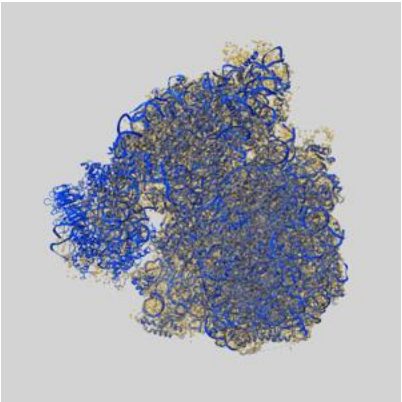
9.1 Map-model overlay (i)



X



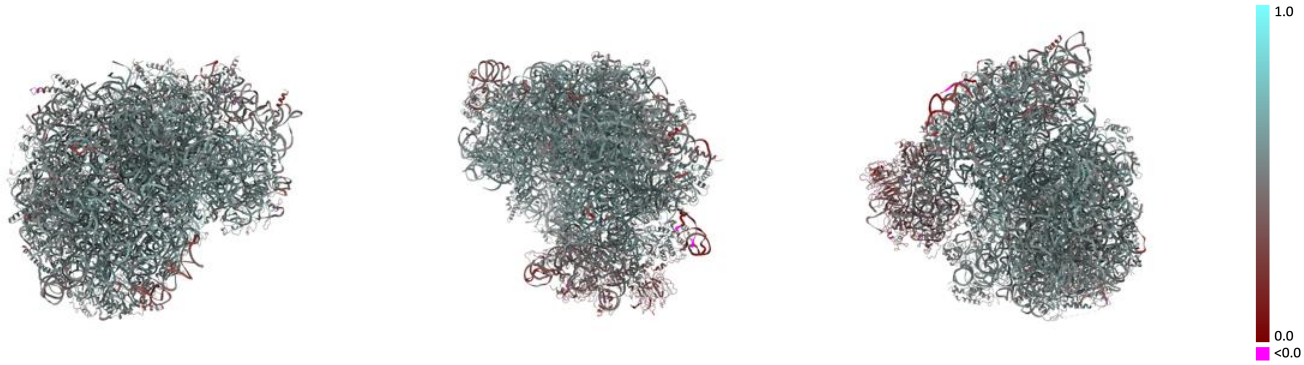
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 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.

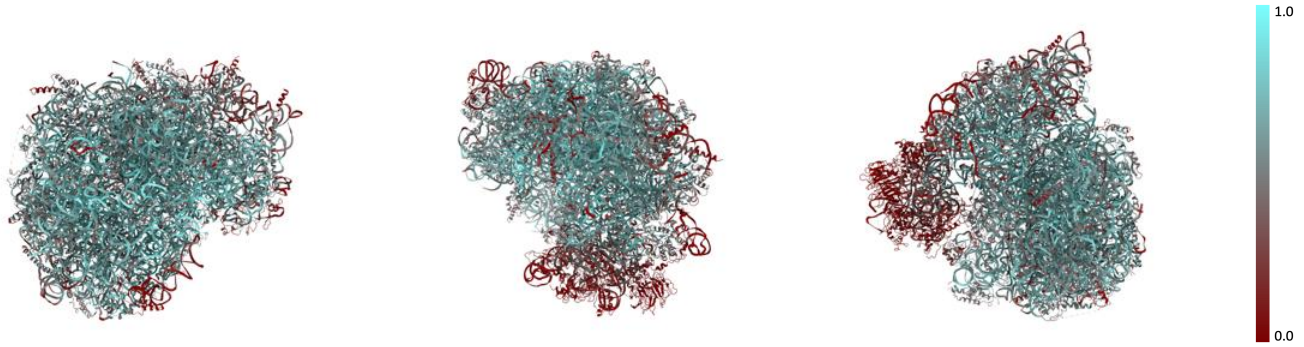
9.2 Q-score mapped to coordinate model (i)



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.

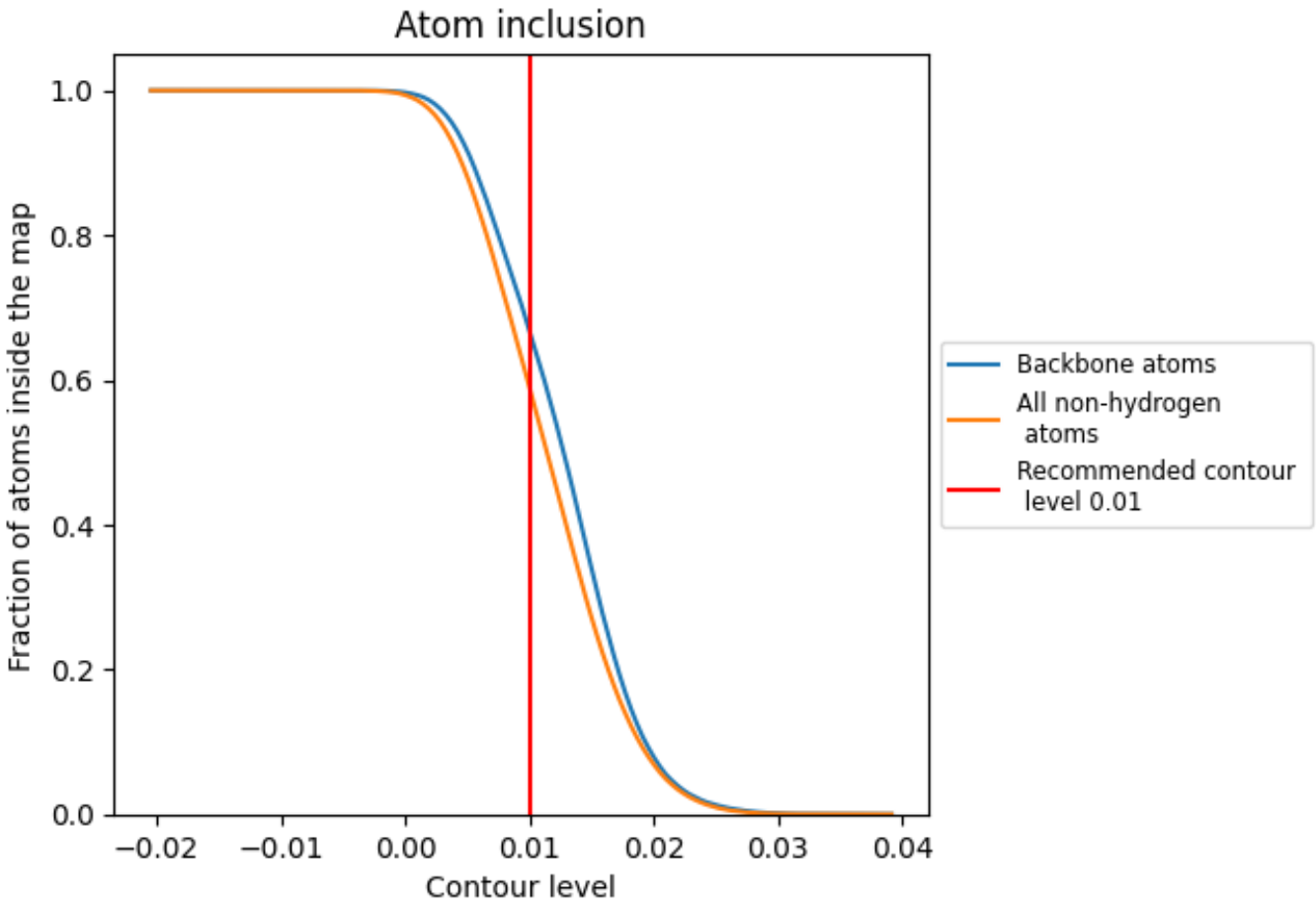
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 67% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5906	0.5270
0	0.4870	0.5380
1	0.5749	0.5500
2	0.5652	0.5170
3	0.3751	0.4970
4	0.4882	0.5230
5	0.6080	0.5580
6	0.5709	0.5410
7	0.0120	0.3000
8	0.1848	0.4210
A	0.7310	0.5530
AC	0.4354	0.5100
AD	0.0417	0.3510
AE	0.6514	0.5800
AG	0.6002	0.5550
AH	0.5066	0.5350
AI	0.0251	0.3360
AJ	0.6247	0.5560
AK	0.0971	0.3800
AL	0.1209	0.4060
AM	0.0602	0.2810
AN	0.0663	0.4100
AO	0.0933	0.3020
AP	0.5462	0.5370
AQ	0.0953	0.3610
AR	0.5048	0.5220
AS	0.5747	0.5450
AT	0.3946	0.5170
AV	0.4817	0.5210
AW	0.5064	0.5350
AX	0.1402	0.4060
AY	0.2779	0.4900
AZ	0.0828	0.3970
B	0.7220	0.5550
C	0.6959	0.5260

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
D	0.7294	0.5450
E	0.7225	0.5630
F	0.6247	0.5290
G	0.8077	0.5870
H	0.8136	0.5920
I	0.5681	0.5280
J	0.5369	0.5240
K	0.3566	0.4740
L	0.5427	0.5060
M	0.5964	0.5520
N	0.4571	0.4860
O	0.6253	0.5490
P	0.6678	0.5560
Q	0.6303	0.5640
R	0.5434	0.5340
S	0.5566	0.5280
T	0.4897	0.5240
U	0.6660	0.5740
V	0.5545	0.5270
W	0.6660	0.5680
X	0.5785	0.5310
Y	0.5476	0.5340
Z	0.6171	0.5510
a	0.5314	0.5130
b	0.5605	0.5210
c	0.6439	0.5610
d	0.6572	0.5620
e	0.5467	0.5370
f	0.6414	0.5550
g	0.5905	0.5430
h	0.5864	0.5450
i	0.5084	0.5100
j	0.6245	0.5510
k	0.4423	0.4950
l	0.6751	0.5540
m	0.6111	0.5560
n	0.5212	0.5150
o	0.6098	0.5530
p	0.5512	0.5170
q	0.6348	0.5550
r	0.5507	0.5370
s	0.4956	0.5110

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
t	0.5391	0.5230
u	0.5777	0.5330
v	0.4810	0.5010
w	0.6073	0.5500