



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 02:42 AM UTC

PDB ID : 5T2A / pdb_00005t2a
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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

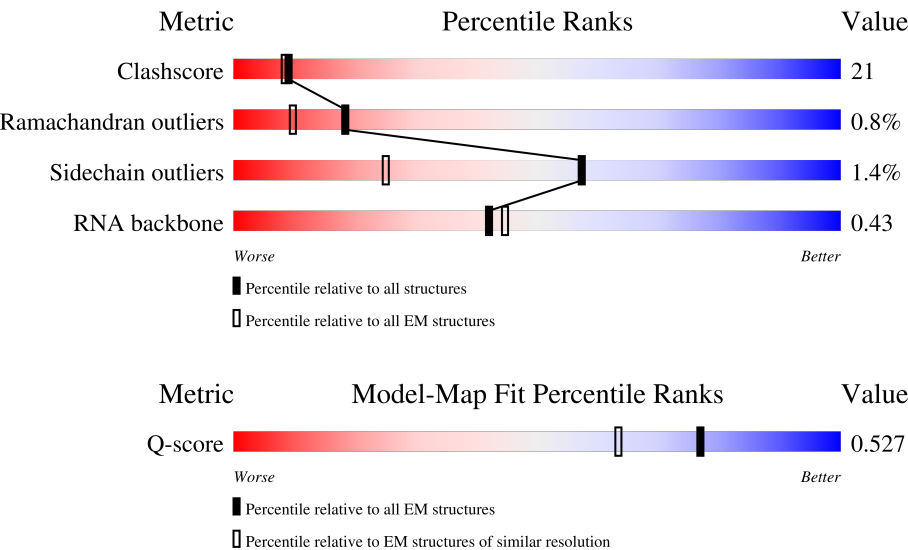
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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 $\leq 5\%$. 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% 49%34%7%10%
2	B	1465	7% 46%22%27%
3	C	262	. 30%25%7%38%

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Mol	Chain	Length	Quality of chain
4	D	120	
5	E	213	
6	F	73	
7	G	183	
8	H	127	
9	I	198	
10	J	213	
11	K	188	
12	L	220	
13	M	222	
14	N	175	
15	O	204	
16	P	166	
17	Q	179	
18	R	245	
19	S	159	
20	T	129	
21	U	139	
22	V	145	
23	W	124	
24	X	143	
25	Y	134	
26	Z	145	
27	a	147	
28	b	70	

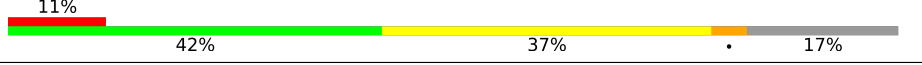
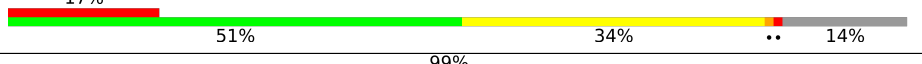
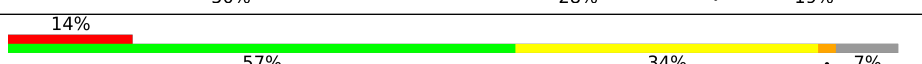
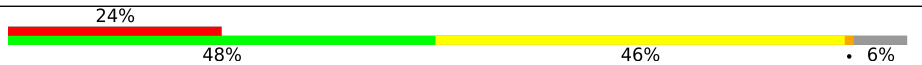
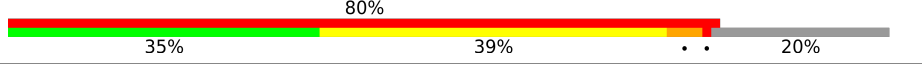
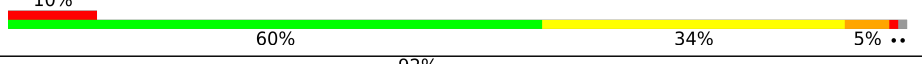
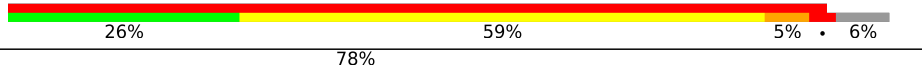
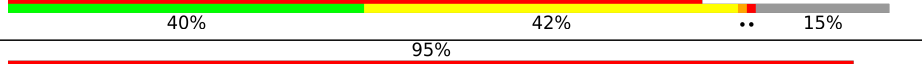
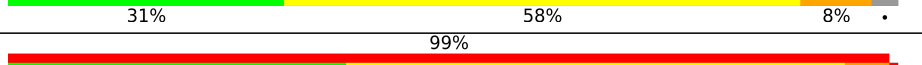
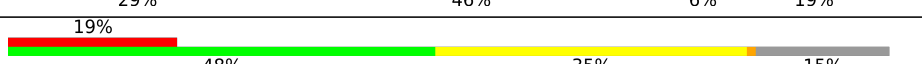
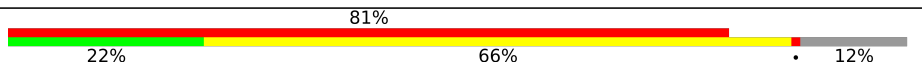
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Mol	Chain	Length	Quality of chain
29	c	260	
30	d	419	
31	e	104	
32	f	183	
33	g	133	
34	h	168	
35	i	127	
36	j	144	
37	k	105	
38	l	83	
39	m	92	
40	n	83	
41	o	51	
42	p	373	
43	q	128	
44	r	106	
45	s	305	
46	t	195	
47	u	252	
48	v	348	
49	w	190	
50	0	264	
51	1	273	
52	2	2205	
53	3	249	

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Mol	Chain	Length	Quality of chain
54	4	200	
55	5	220	
56	6	190	
57	7	312	
58	8	57	
59	AC	246	
60	AD	153	
61	AE	173	
62	AG	151	
63	AH	144	
64	AI	152	
65	AJ	130	
66	AK	149	
67	AL	143	
68	AM	153	
69	AN	190	
70	AO	179	
71	AP	265	
72	AQ	116	
73	AR	164	
74	AS	143	
75	AT	137	
76	AV	112	
77	AW	86	
78	AX	219	

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Mol	Chain	Length	Quality of chain
79	AY	66	61% 55% 29% 15%
80	AZ	87	76% 28% 45% 5% 22%

2 Entry composition

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
1	A	1603	Total	C	N	O	P	0	0
			34365	15347	6297	11118	1603		

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
2	B	1064	Total	C	N	O	P	0	0
			22723	10152	4100	7407	1064		

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

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

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
4	D	119	Total	C	N	O	P	0	0
			2531	1132	452	828	119		

- Molecule 5 is a RNA chain called srRNA1.

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

- Molecule 6 is a RNA chain called srRNA3.

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

- Molecule 7 is a RNA chain called srRNA2.

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

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
8	H	93	Total	C	N	O	P	0	0
			1996	889	369	645	93		

- Molecule 9 is a protein called eL18.

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

- Molecule 10 is a protein called uL16.

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

- Molecule 11 is a protein called uL5.

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

- Molecule 12 is a protein called eL13.

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

- Molecule 13 is a protein called uL13.

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

- Molecule 14 is a protein called eL14.

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

- Molecule 15 is a protein called eL15.

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

- Molecule 16 is a protein called uL22.

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

- Molecule 17 is a protein called eL20.

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

- Molecule 18 is a protein called eL19.

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

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.

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

- Molecule 21 is a protein called uL14.

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

- Molecule 22 is a protein called uL23.

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

- Molecule 23 is a protein called eL24.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called eL28.

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

- Molecule 28 is a protein called eL29.

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

- Molecule 29 is a protein called uL2.

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

- Molecule 30 is a protein called uL3.

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

- Molecule 31 is a protein called eL30.

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

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- Molecule 34 is a protein called eL34.

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

- Molecule 35 is a protein called uL29.

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

- Molecule 36 is a protein called eL33.

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

- Molecule 37 is a protein called eL36.

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

- Molecule 38 is a protein called eL37.

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

- Molecule 39 is a protein called eL43.

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

- Molecule 40 is a protein called eL38.

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

- Molecule 41 is a protein called eL39.

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

- Molecule 42 is a protein called uL4.

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

- Molecule 43 is a protein called eL40.

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

- Molecule 44 is a protein called eL42.

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

- Molecule 45 is a protein called uL18.

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

- Molecule 46 is a protein called eL6.

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

- Molecule 47 is a protein called uL30.

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

- Molecule 48 is a protein called eL8.

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

- Molecule 49 is a protein called uL6.

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

- Molecule 50 is a protein called eS1.

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

- Molecule 51 is a protein called eS4.

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

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

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

- Molecule 53 is a protein called eS6.

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

- Molecule 54 is a protein called eS7.

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

- Molecule 55 is a protein called eS8.

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

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
56	6	164	Total	C	N	O	S	0	0
			1362	862	265	227	8		

- Molecule 57 is a protein called RACK1.

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

- Molecule 58 is a protein called uS14.

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

- Molecule 59 is a protein called uS2.

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

- Molecule 60 is a protein called eS10.

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

- Molecule 61 is a protein called uS17.

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

- Molecule 62 is a protein called uS15.

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

- Molecule 63 is a protein called uS11.

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

- Molecule 64 is a protein called uS19.

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

- Molecule 65 is a protein called uS8.

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

- Molecule 66 is a protein called uS9.

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

- Molecule 67 is a protein called eS17.

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

- Molecule 68 is a protein called uS13.

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

- Molecule 69 is a protein called uS7.

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

- Molecule 70 is a protein called eS19.

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

- Molecule 71 is a protein called uS5.

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

- Molecule 72 is a protein called uS10.

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

- Molecule 73 is a protein called eS21.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called eS26.

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

- Molecule 77 is a protein called eS27.

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

- Molecule 78 is a protein called uS3.

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

- Molecule 79 is a protein called eS30.

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

- Molecule 80 is a protein called eS28.

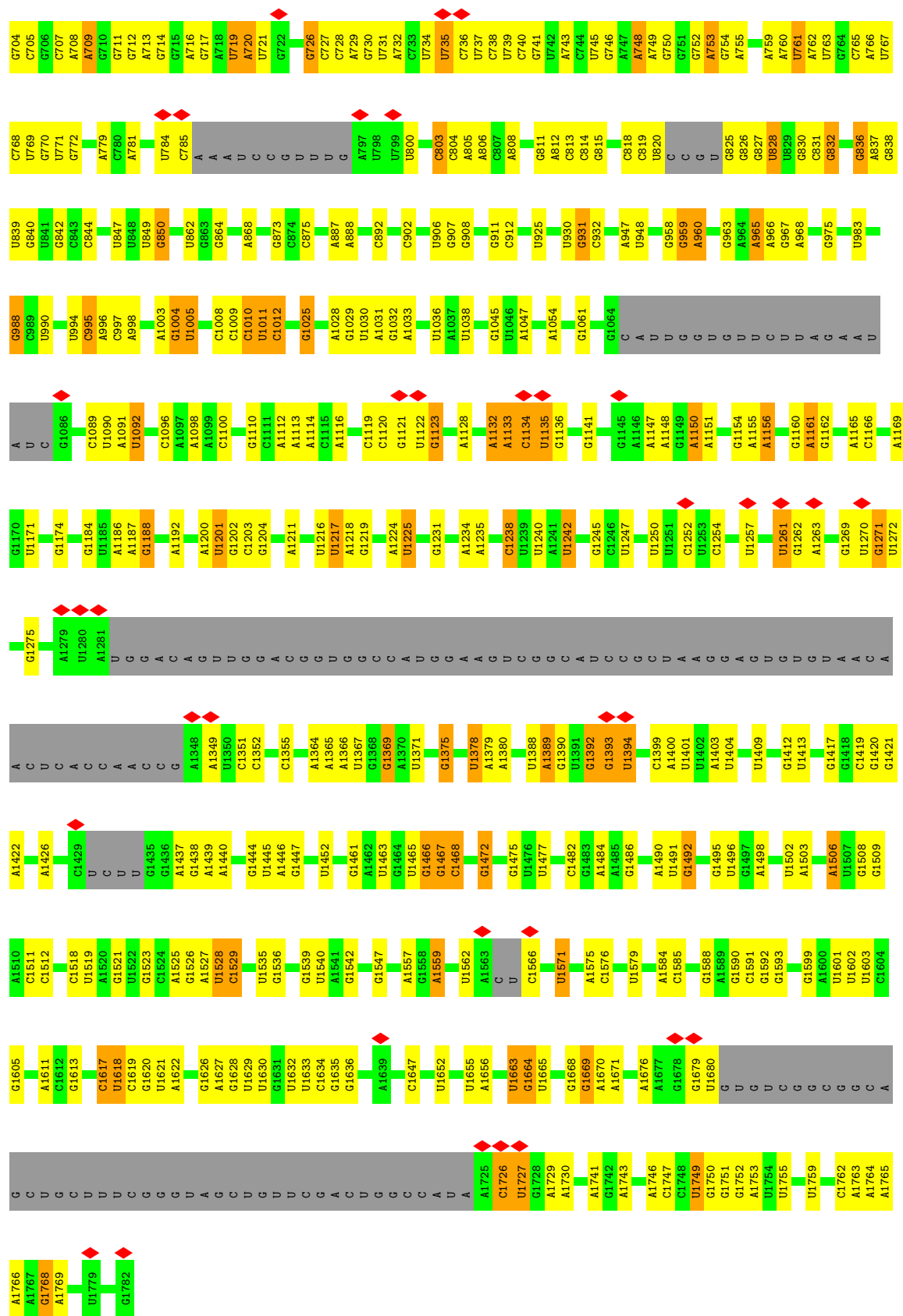
Mol	Chain	Residues	Atoms					AltConf	Trace
80	AZ	68	Total	C	N	O	S	0	0
			526	319	106	97	4		

3 Residue-property plots

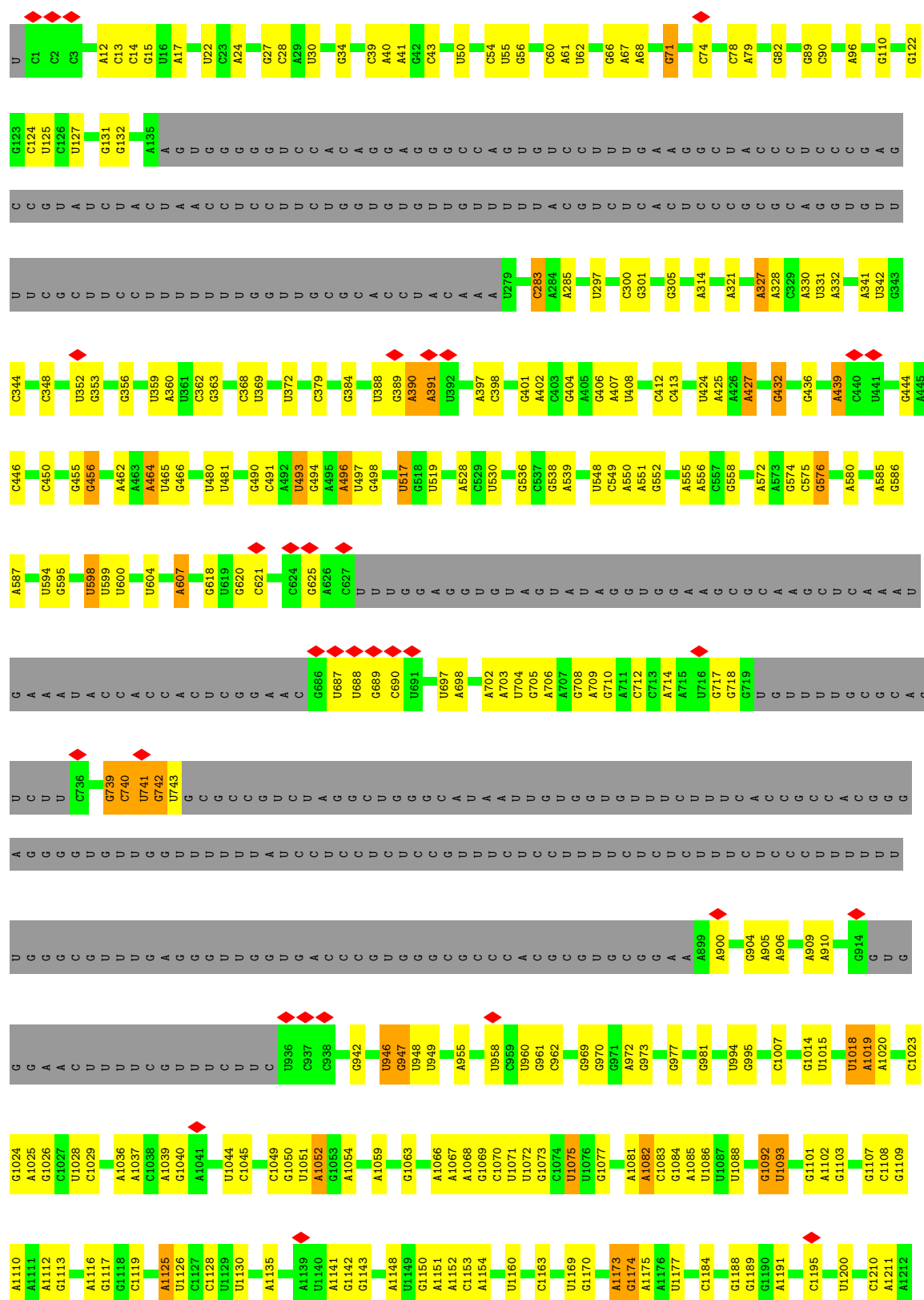
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

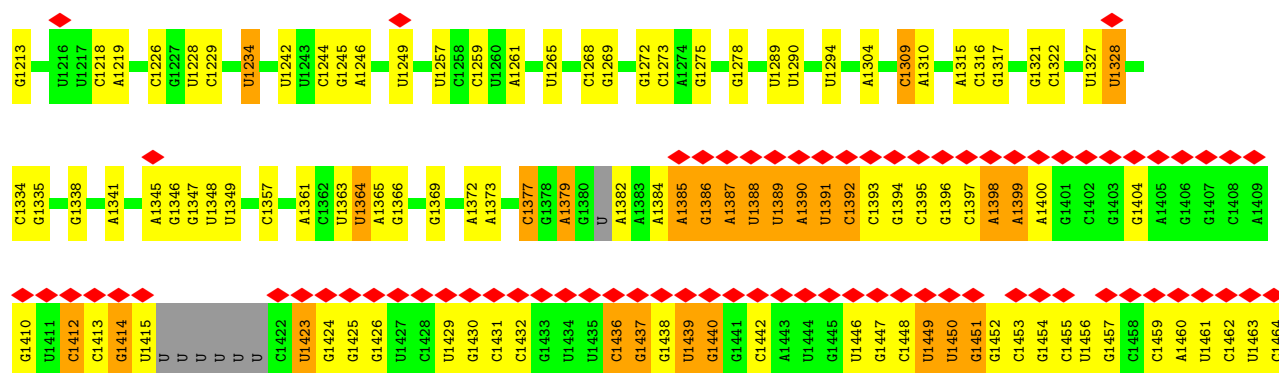
• Molecule 1: LSU-alpha



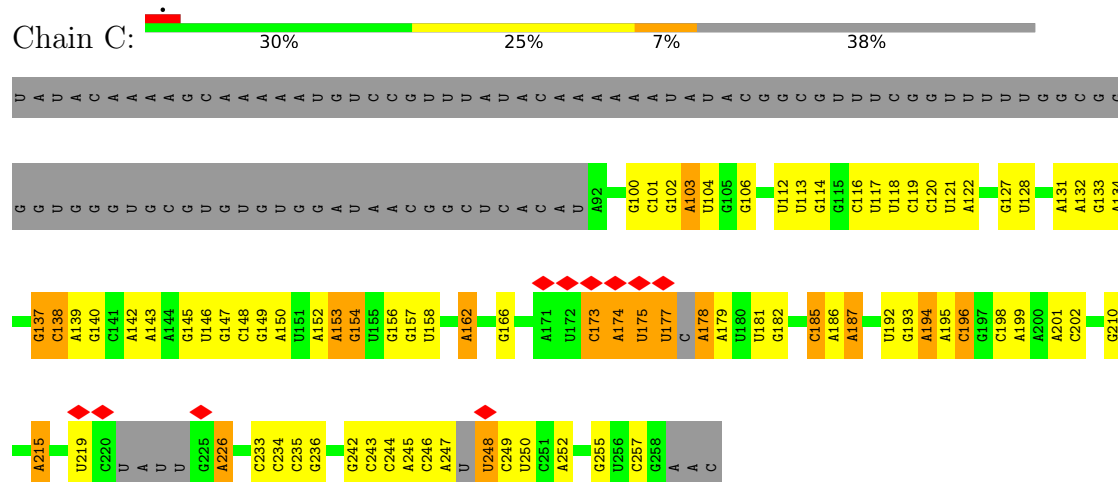


- Molecule 2: LSU-beta

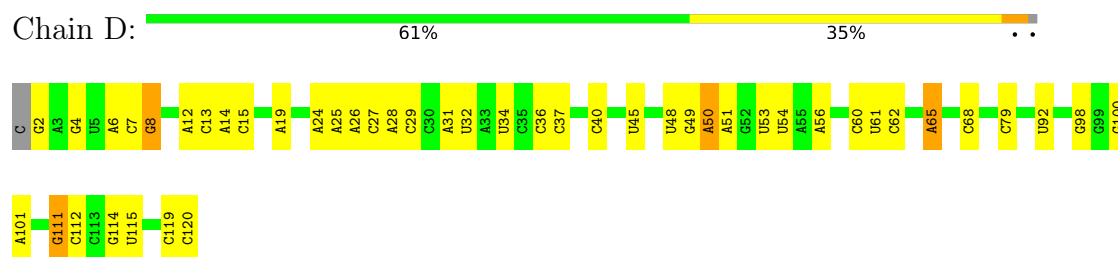




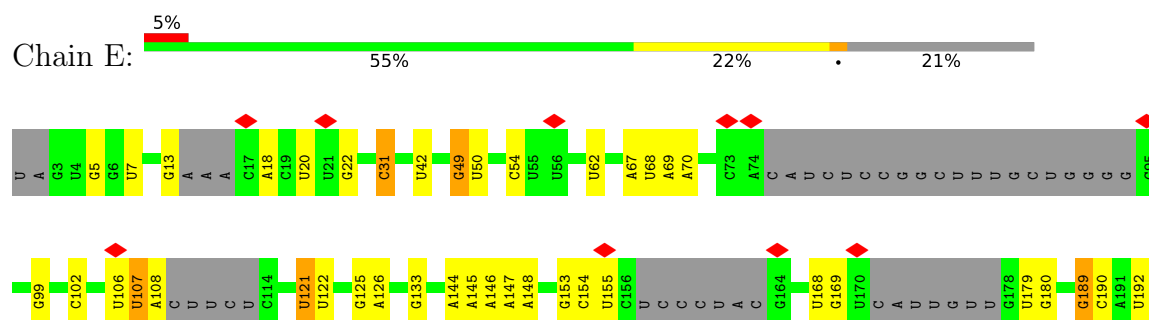
• Molecule 3: 5.8S rRNA



• Molecule 4: 5S rRNA



• Molecule 5: srRNA1

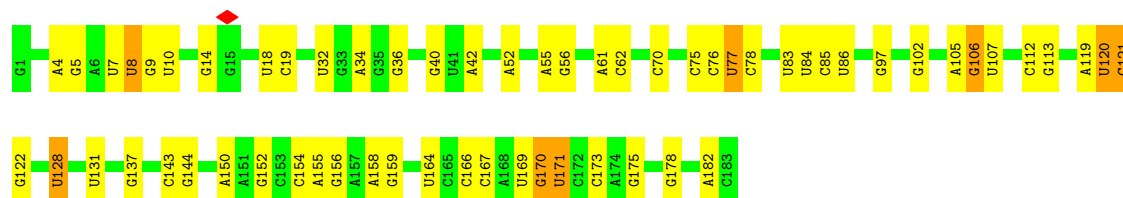




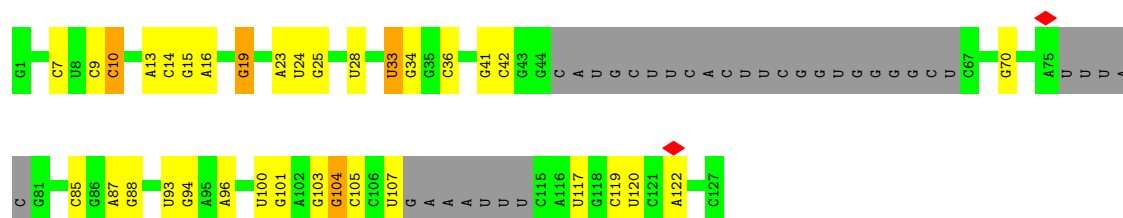
• Molecule 6: srRNA3



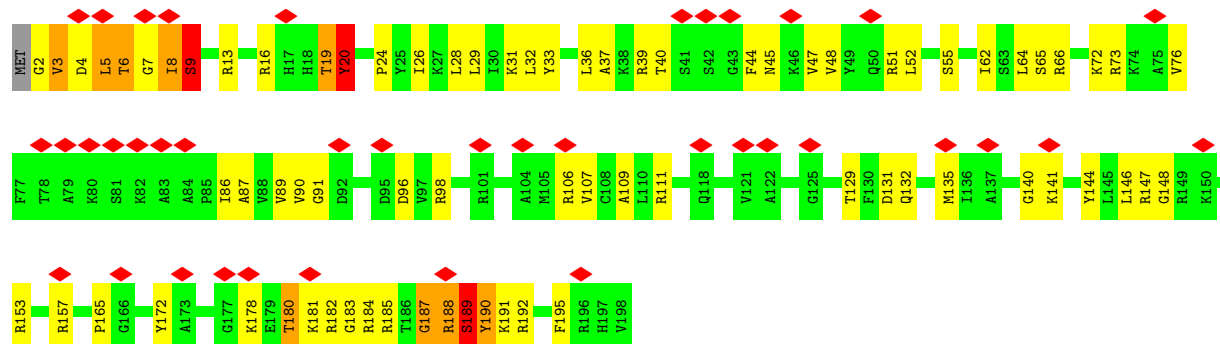
• Molecule 7: srRNA2



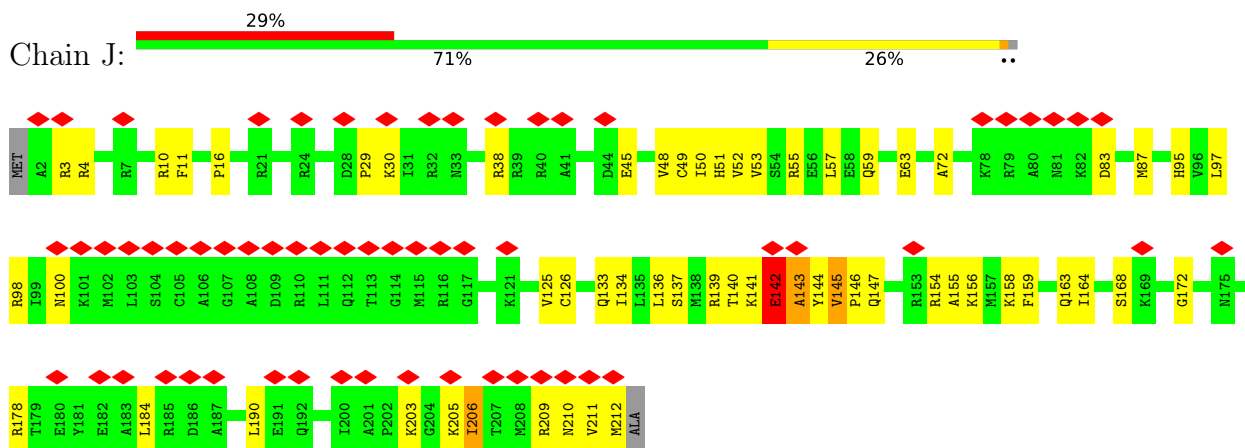
• Molecule 8: srRNA4



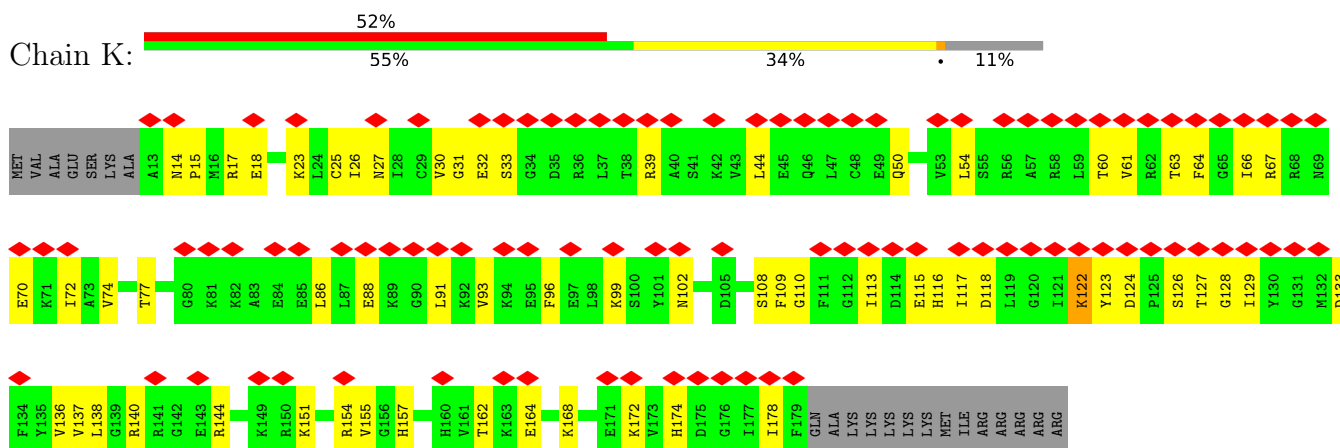
• Molecule 9: eL18



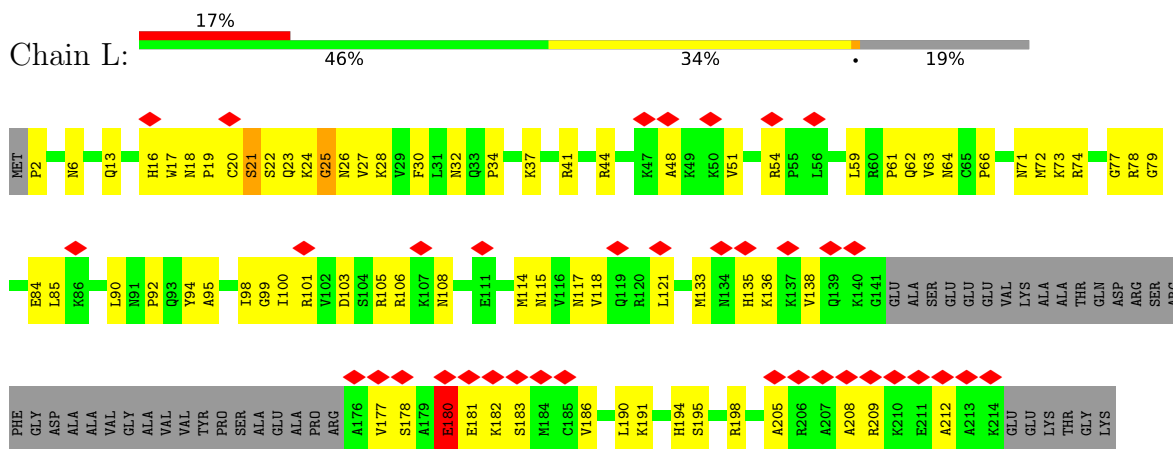
- Molecule 10: uL16



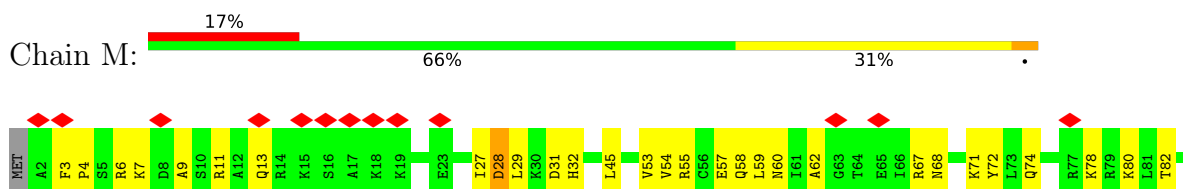
- Molecule 11: uL5

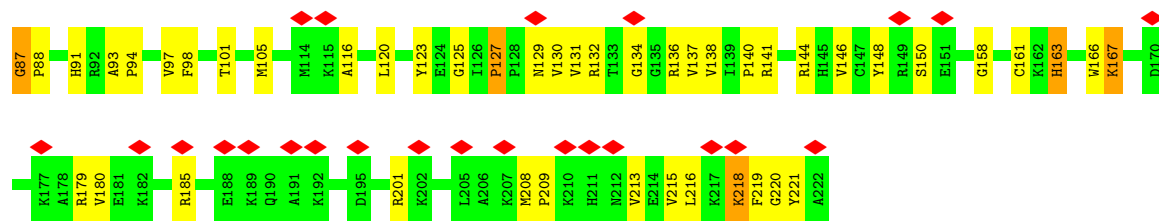


- Molecule 12: eL13

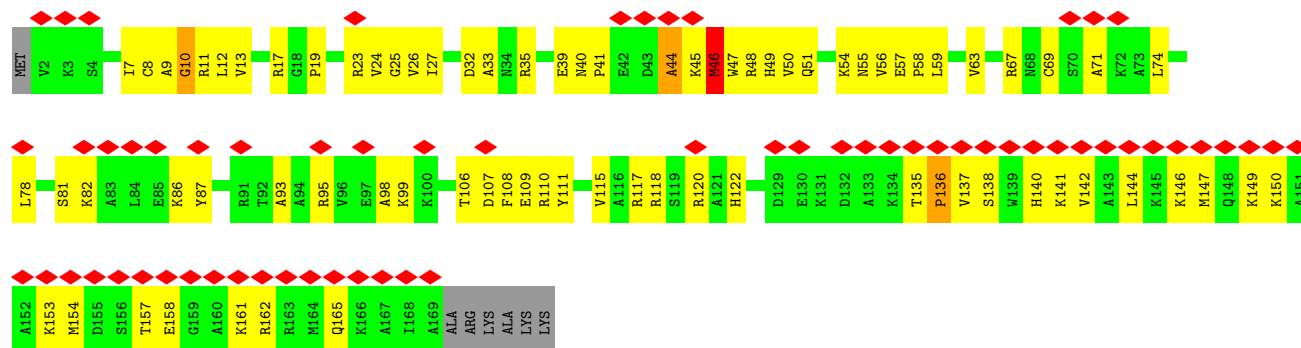


- Molecule 13: uL13

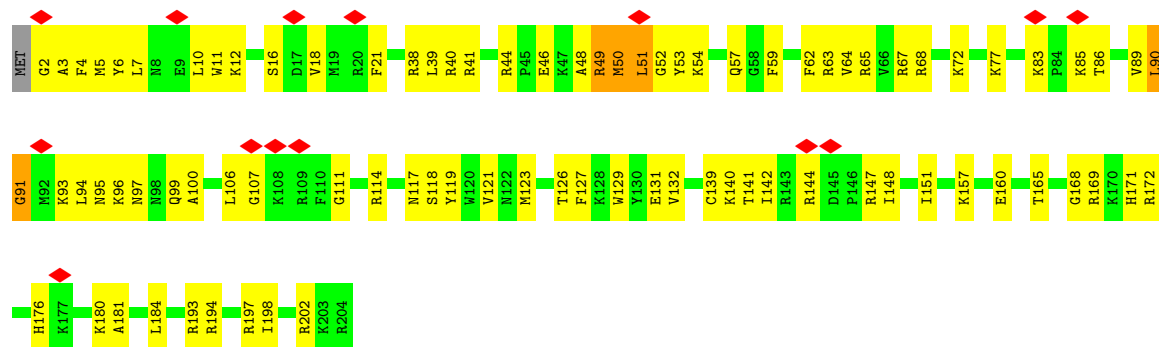




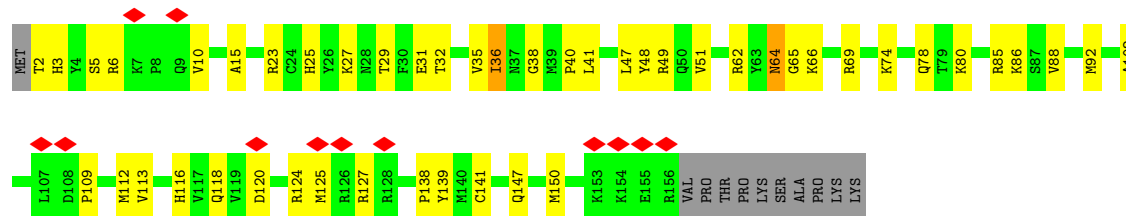
• Molecule 14: eL14



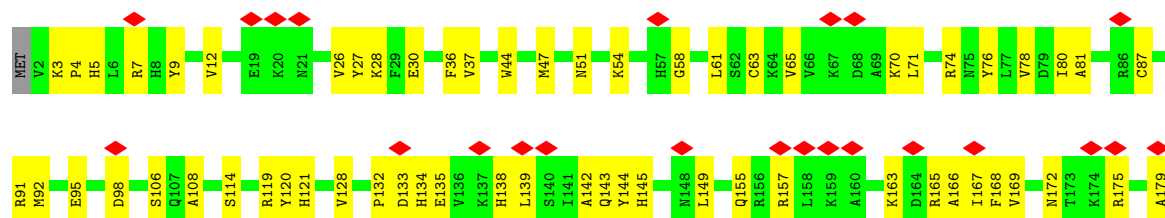
• Molecule 15: eL15



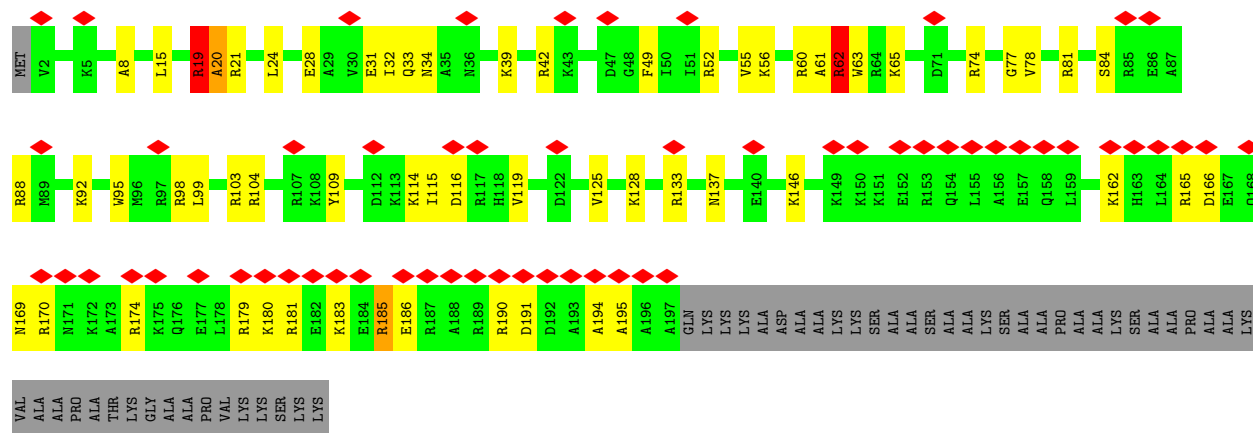
• Molecule 16: uL22



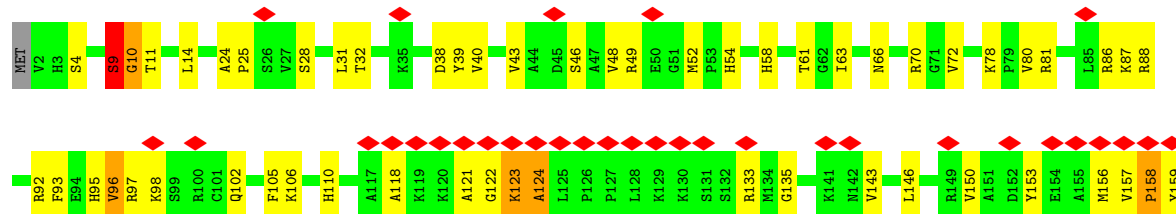
• Molecule 17: eL20



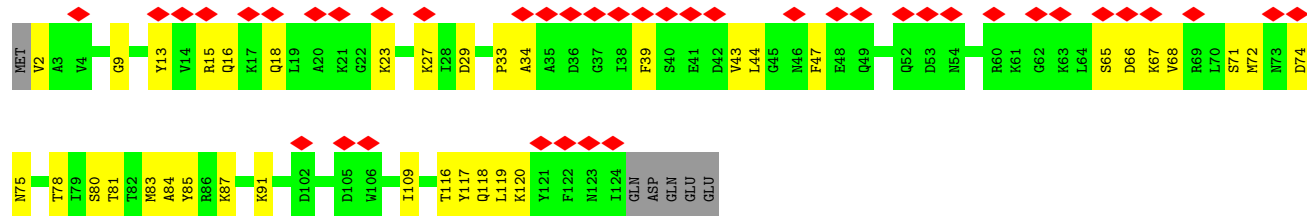
• Molecule 18: eL19



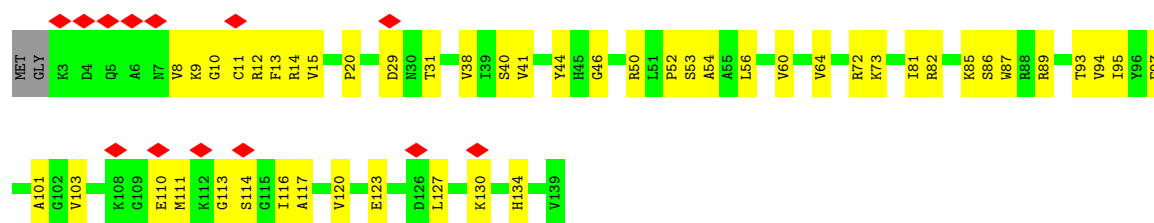
• Molecule 19: eL21



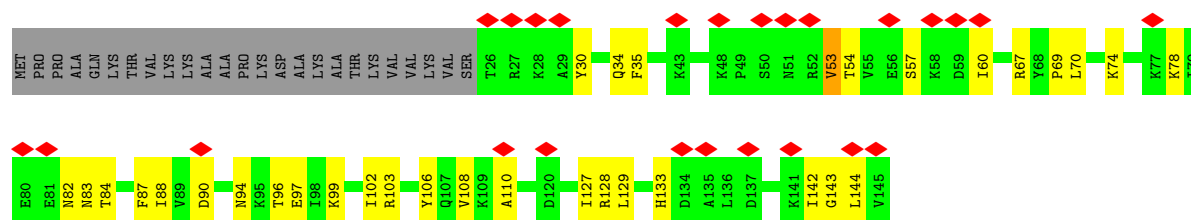
• Molecule 20: eL22



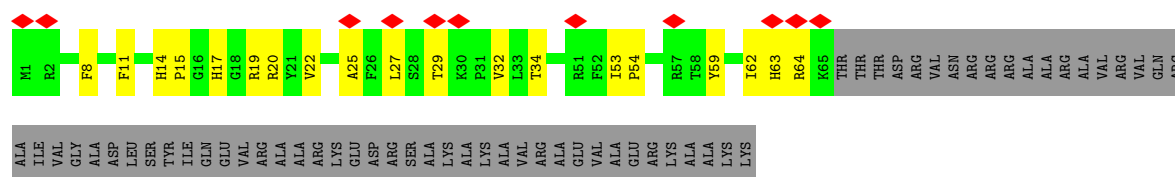
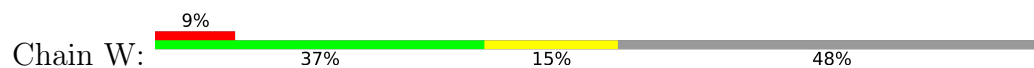
• Molecule 21: uL14



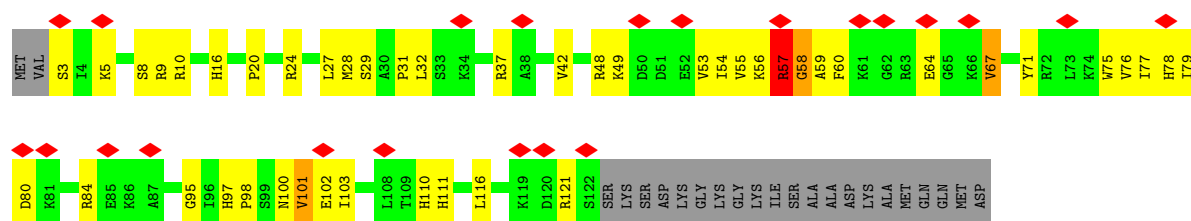
• Molecule 22: uL23



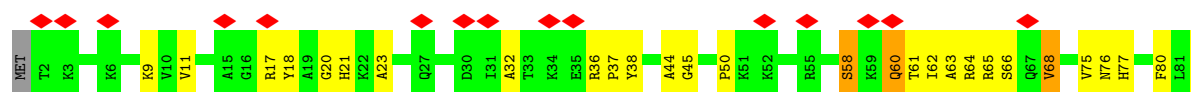
• Molecule 23: eL24

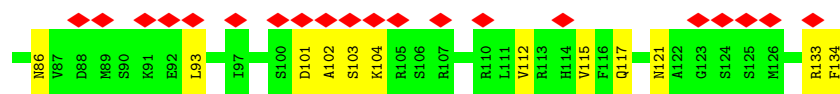


• Molecule 24: uL24

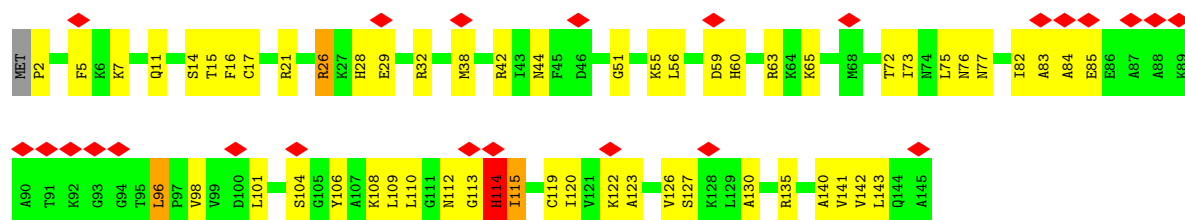


• Molecule 25: eL27

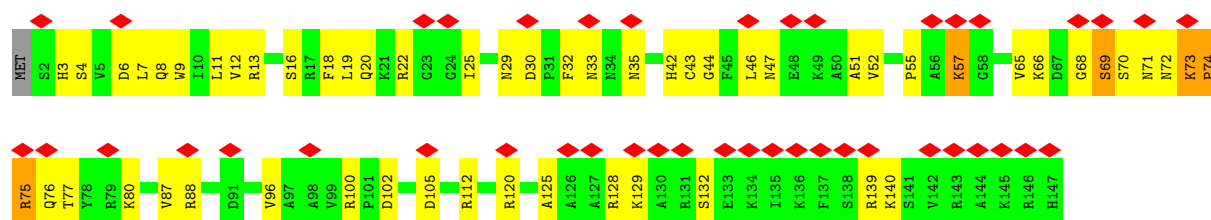




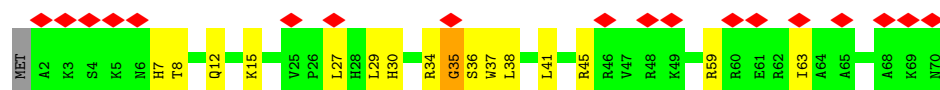
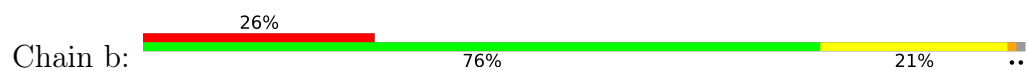
• Molecule 26: uL15



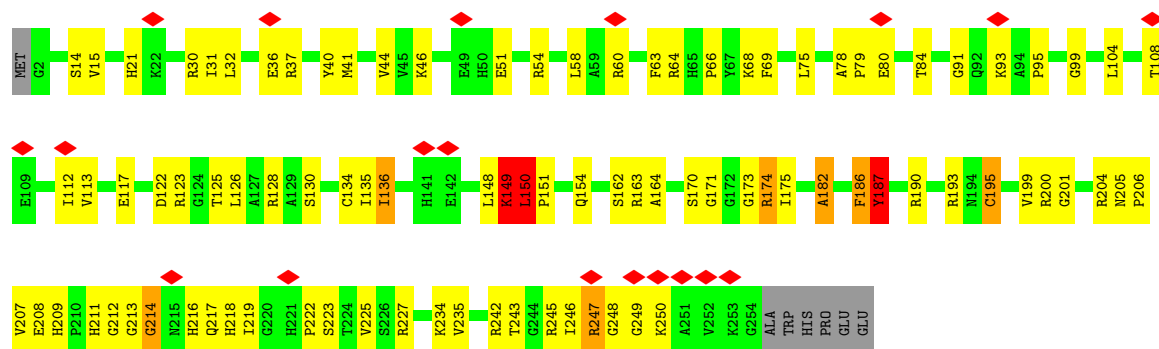
• Molecule 27: eL28



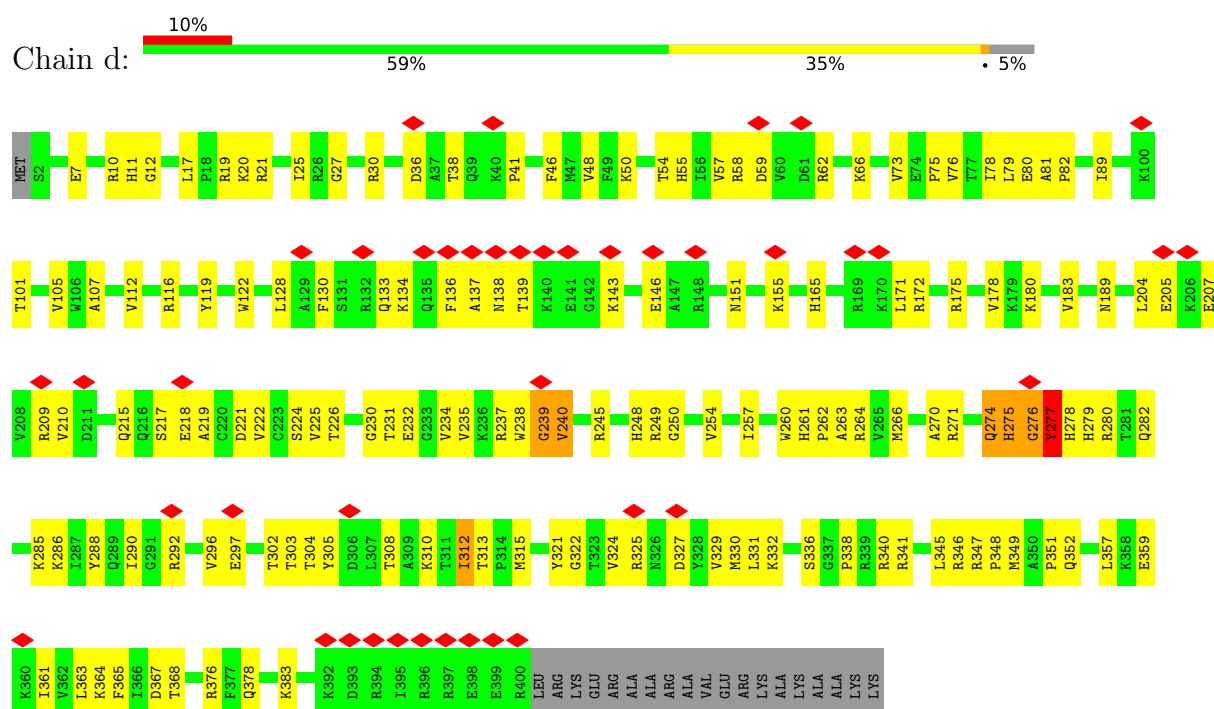
• Molecule 28: eL29



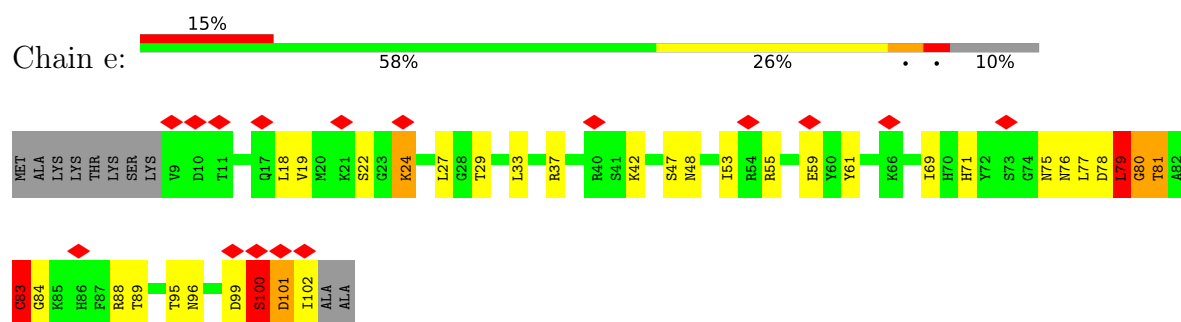
• Molecule 29: uL2



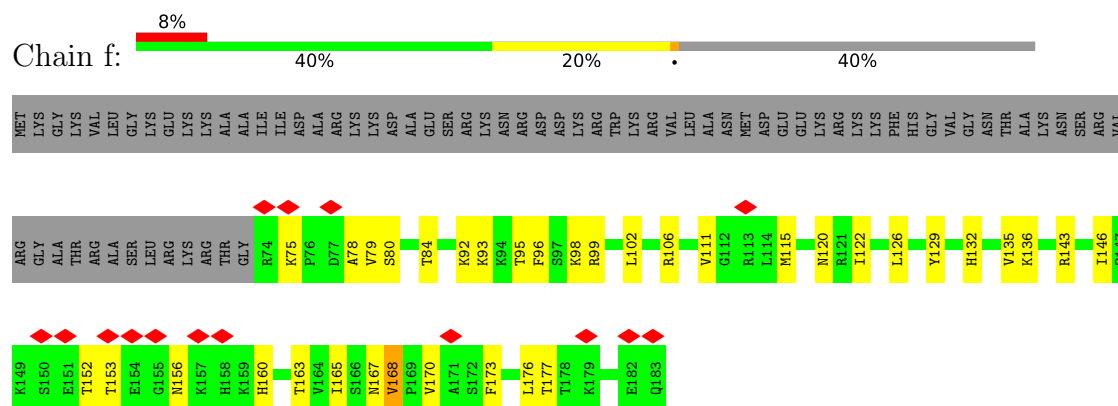
• Molecule 30: uL3



- Molecule 31: eL30

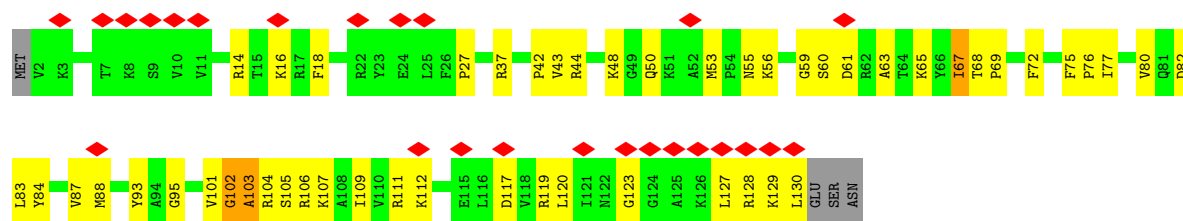


- Molecule 32: eL31

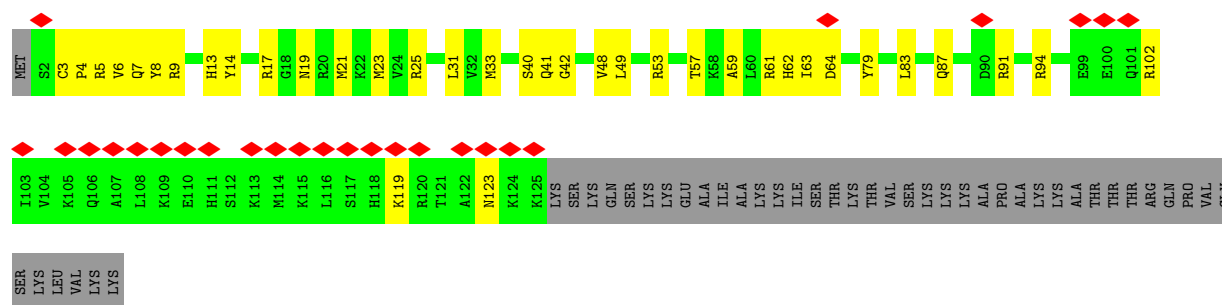


- Molecule 33: eL32

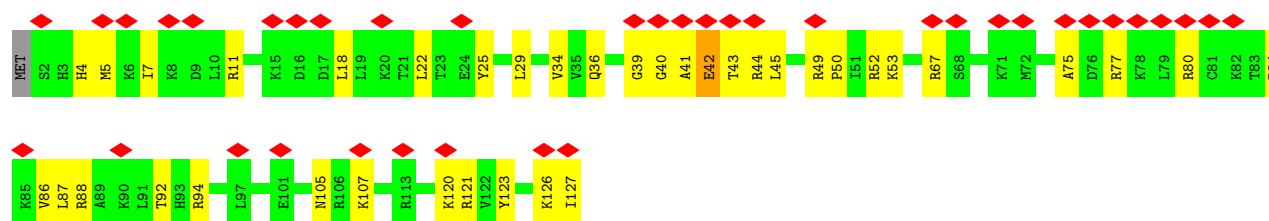




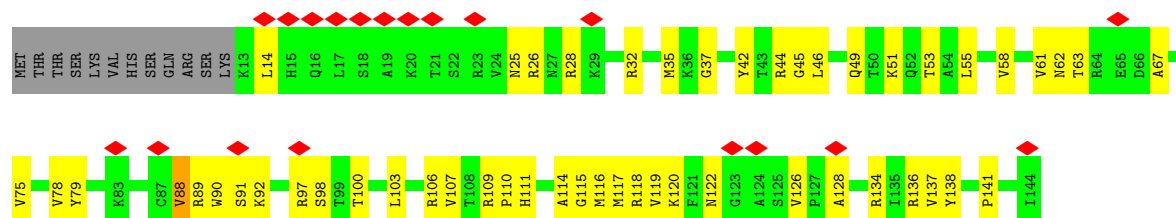
• Molecule 34: eL34



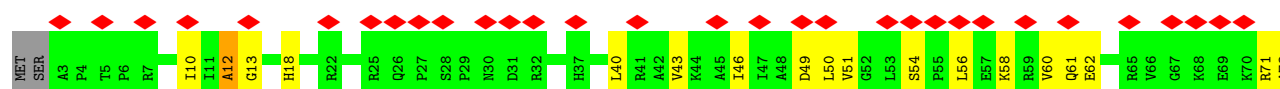
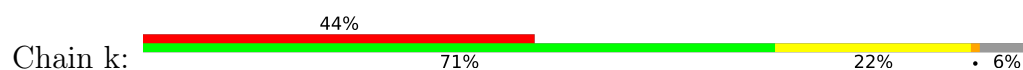
• Molecule 35: uL29

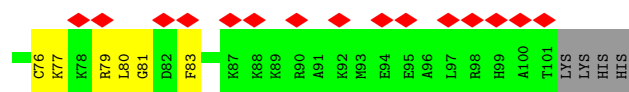


• Molecule 36: eL33

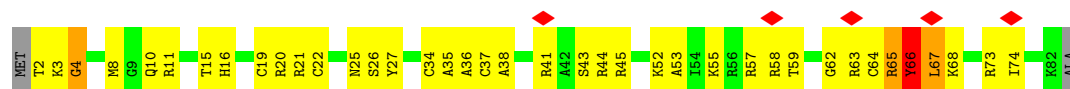


• Molecule 37: eL36

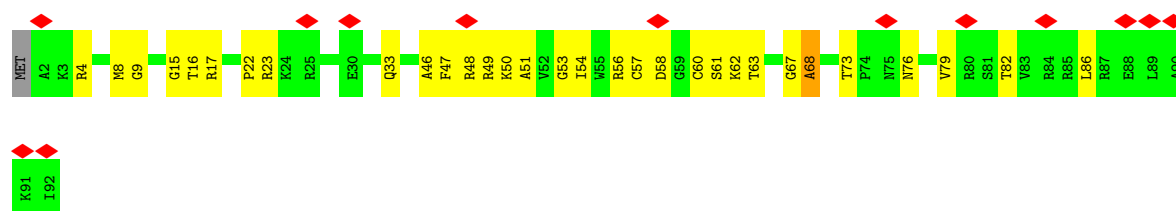




- Molecule 38: eL37



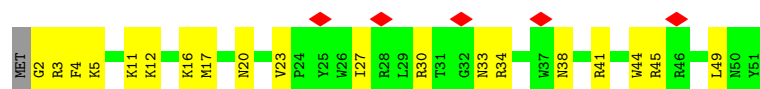
- Molecule 39: eL43



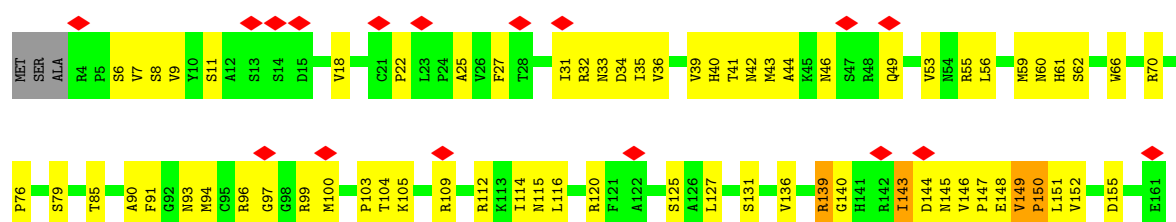
- Molecule 40: eL38

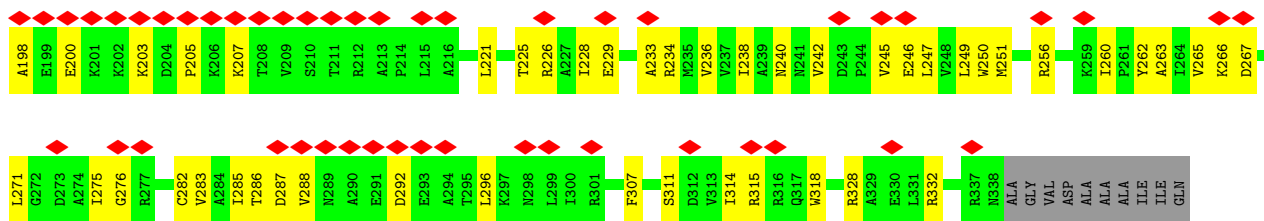


- Molecule 41: eL39

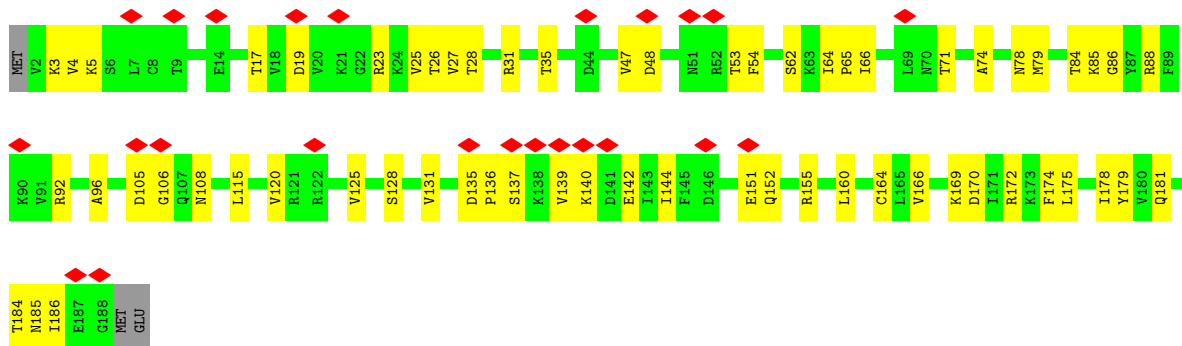


- Molecule 42: uL4

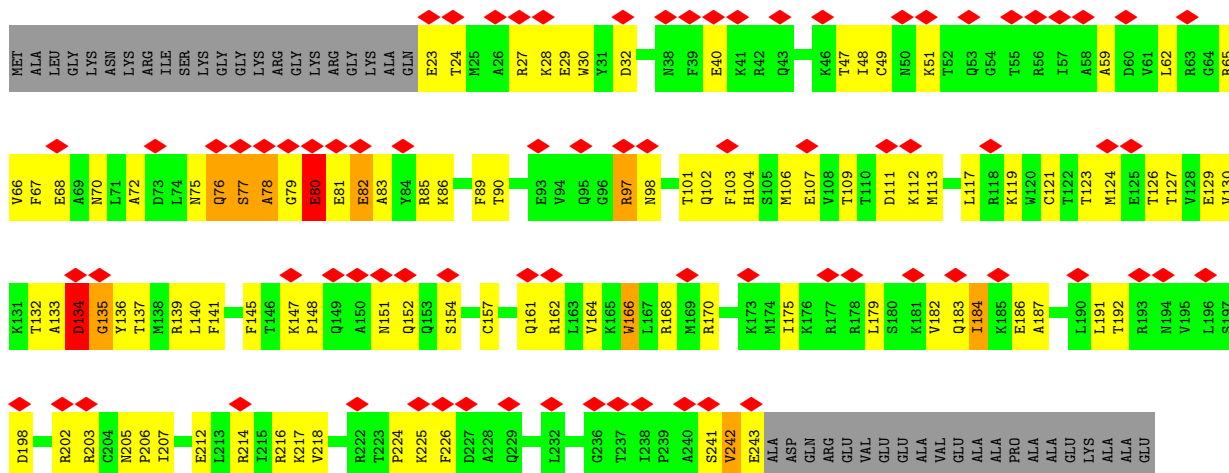




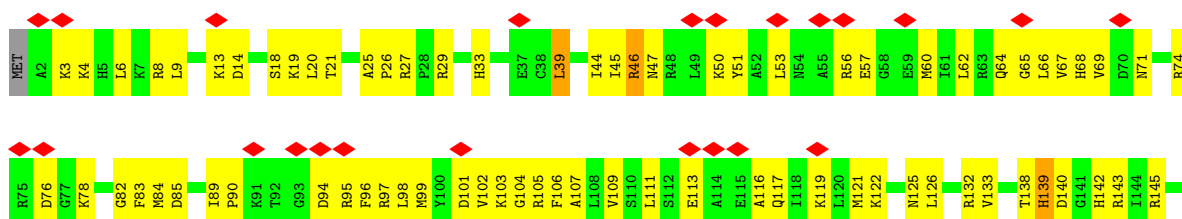
• Molecule 49: uL6

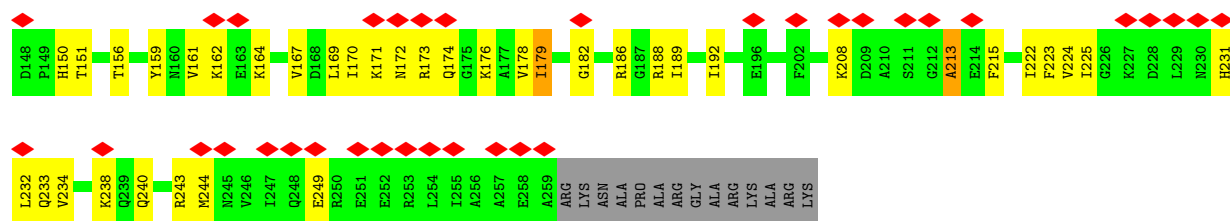


• Molecule 50: eS1

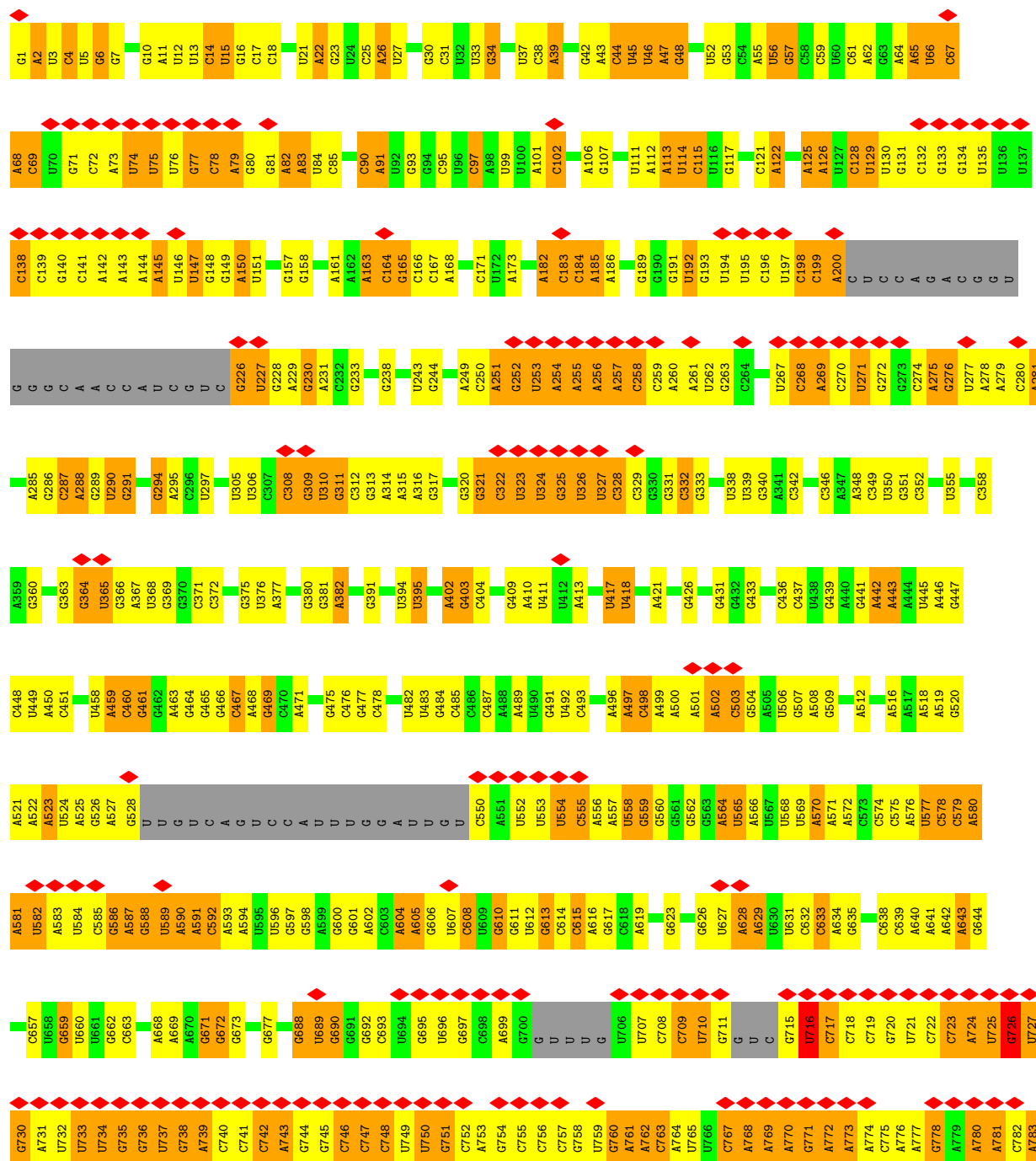
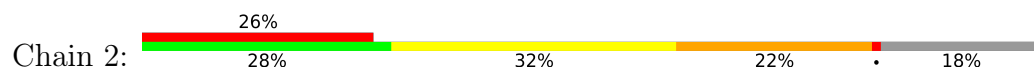


• Molecule 51: eS4

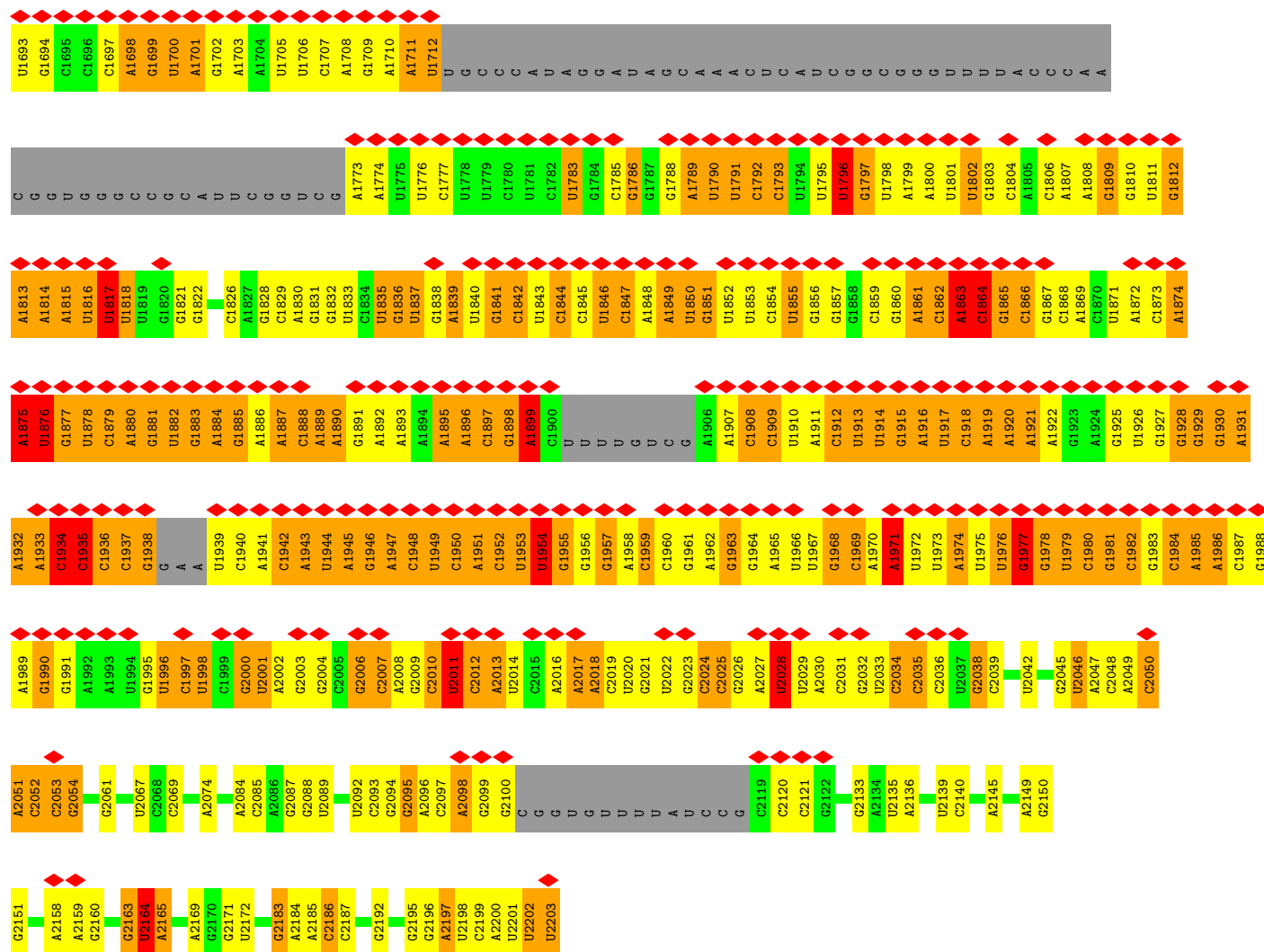




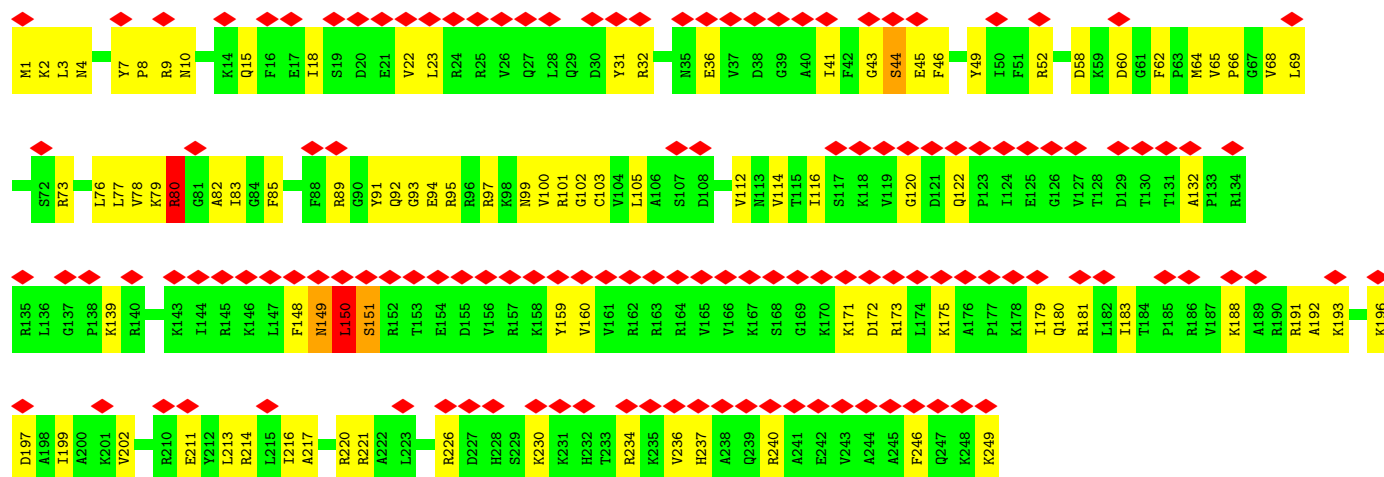
• Molecule 52: 18S rRNA



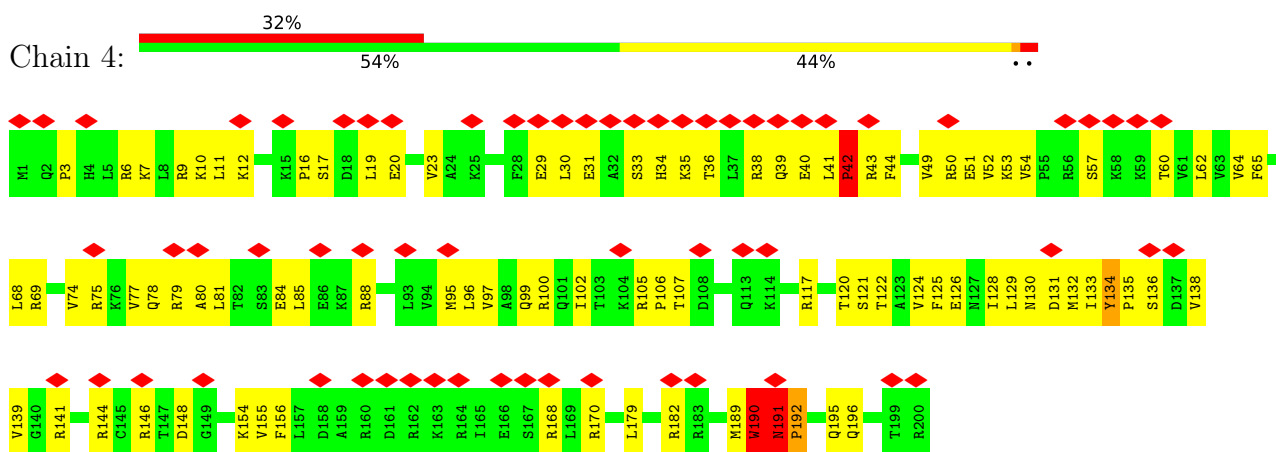




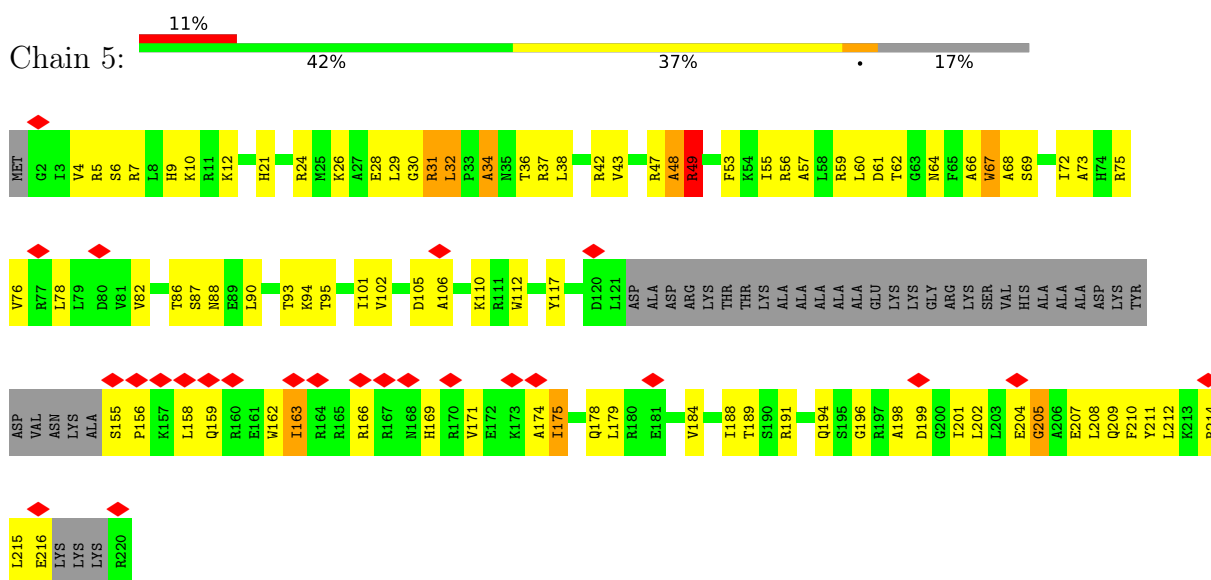
• Molecule 53: eS6



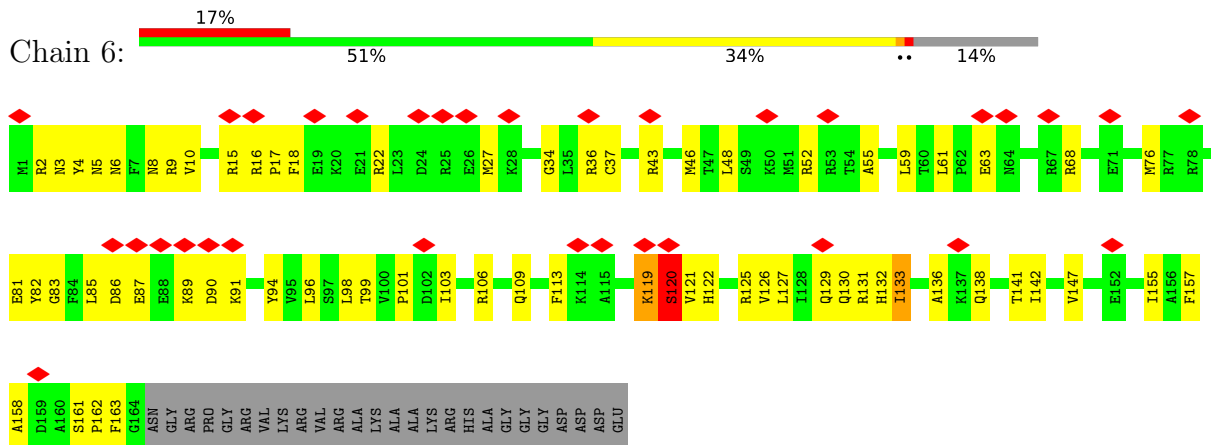
• Molecule 54: eS7



• Molecule 55: eS8

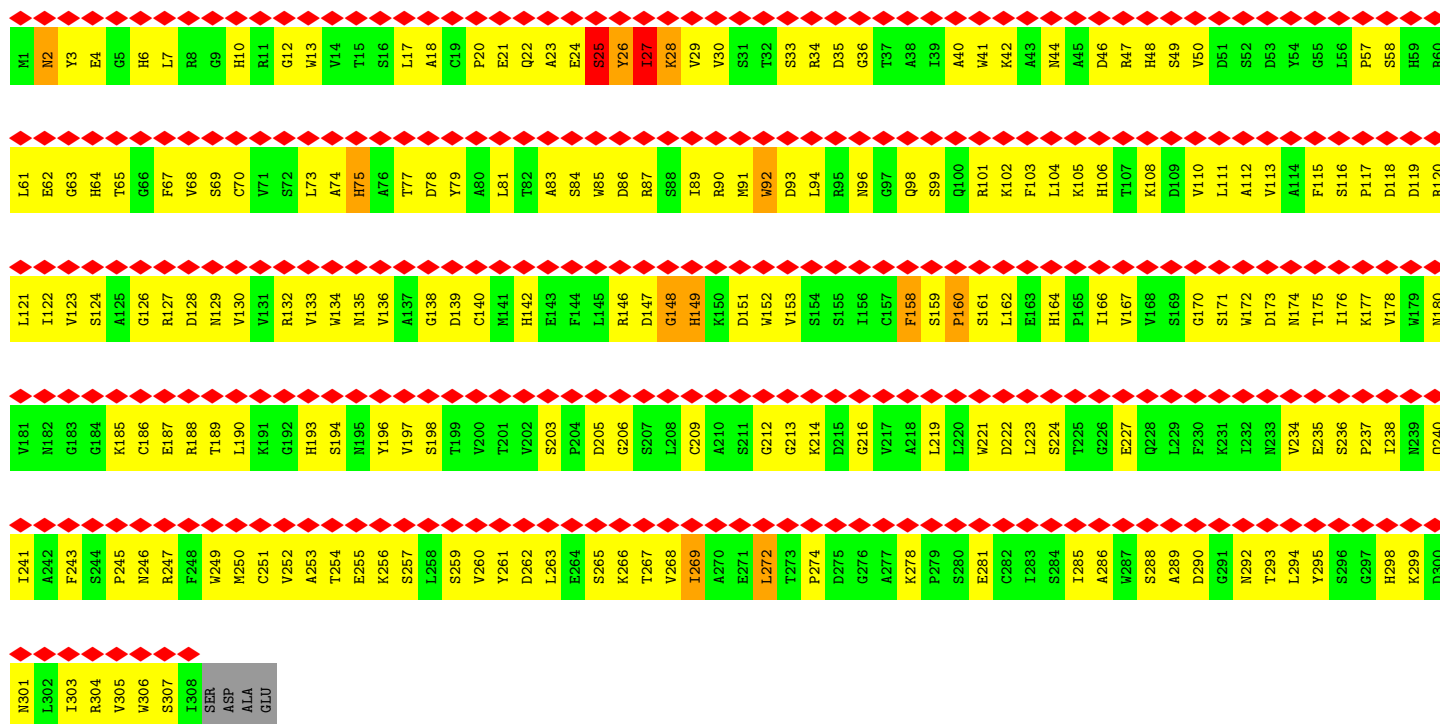


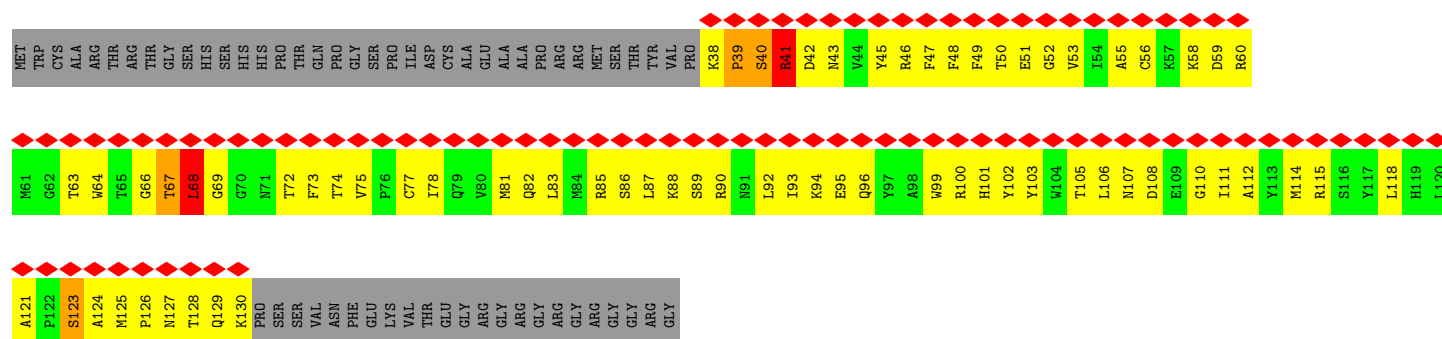
• Molecule 56: uS4



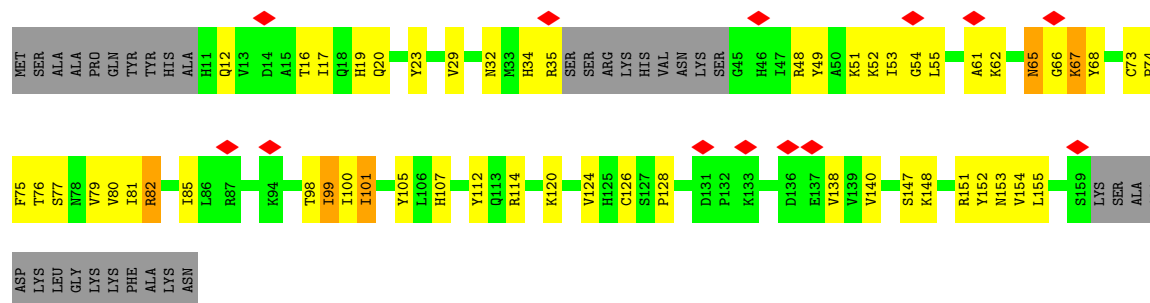
• Molecule 57: RACK1



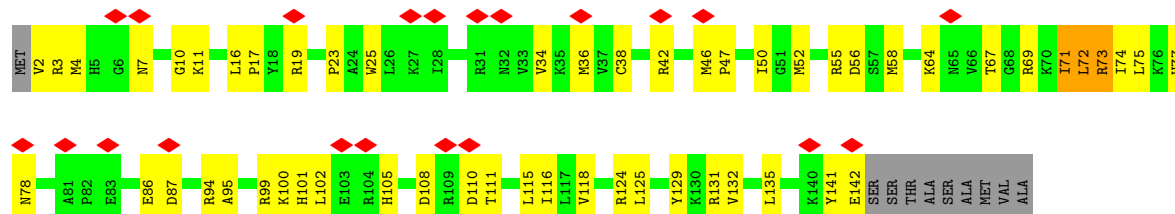




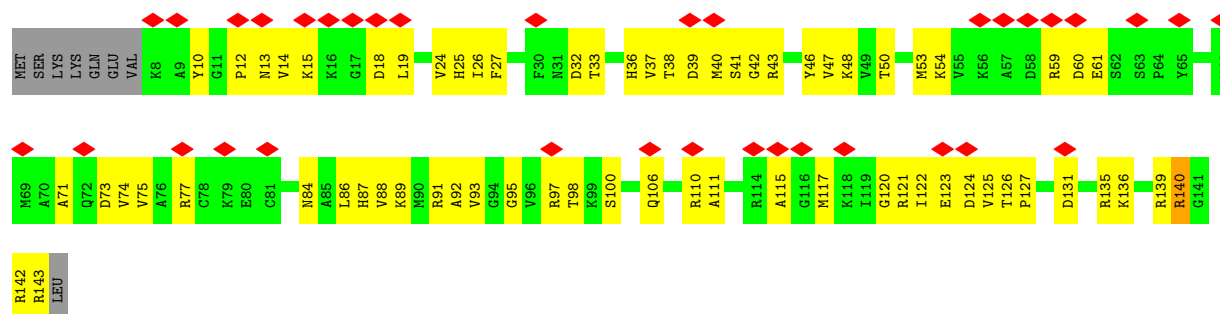
• Molecule 61: uS17



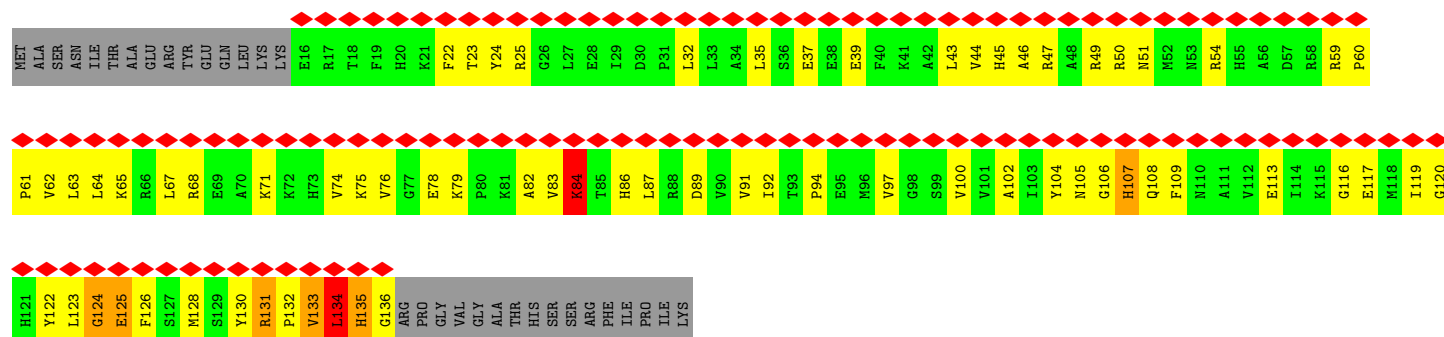
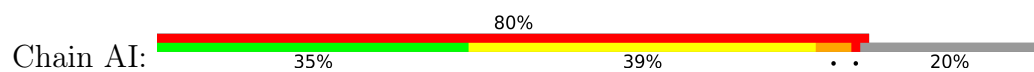
• Molecule 62: uS15



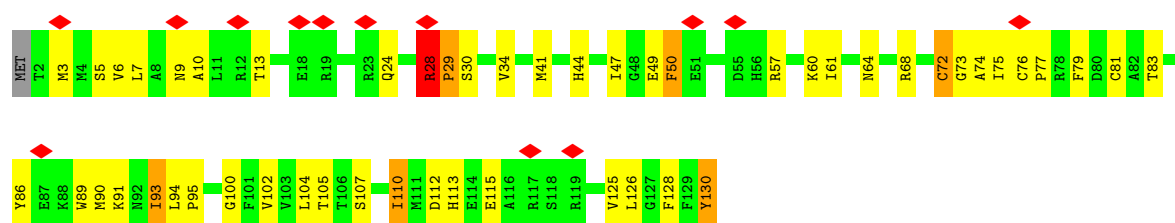
• Molecule 63: uS11



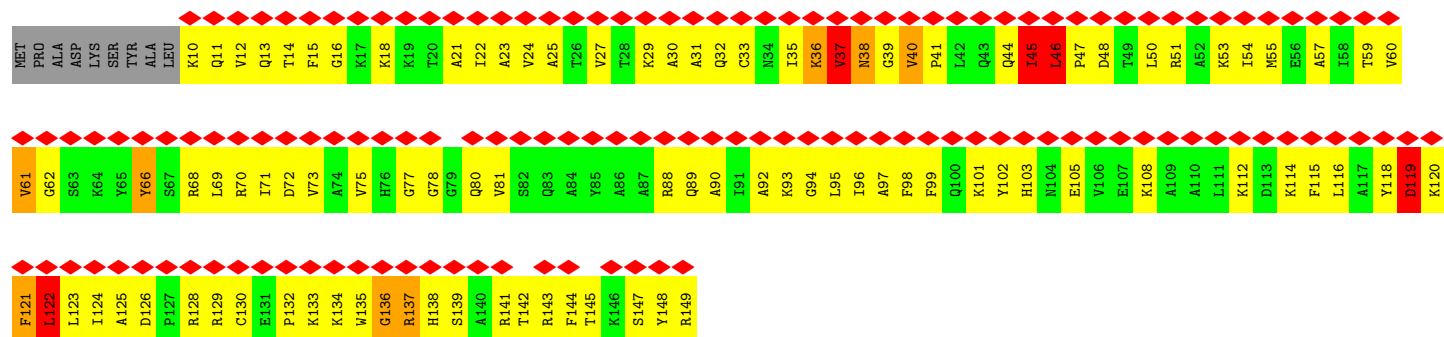
• Molecule 64: uS19



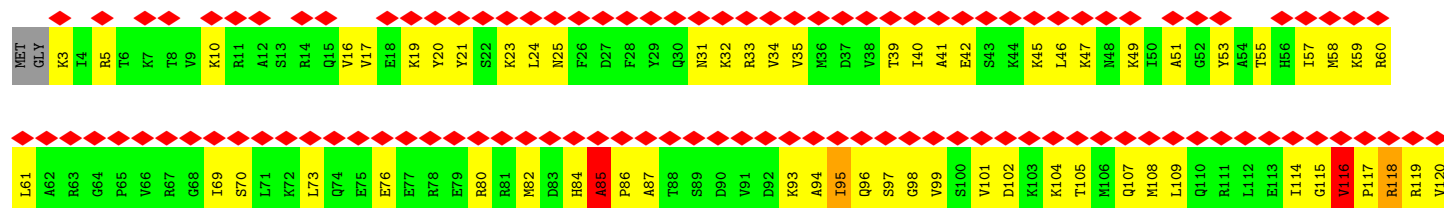
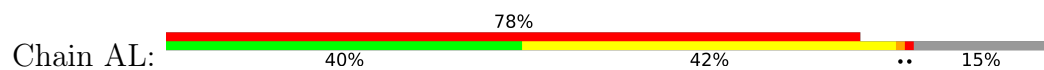
• Molecule 65: uS8

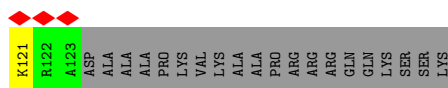


• Molecule 66: uS9

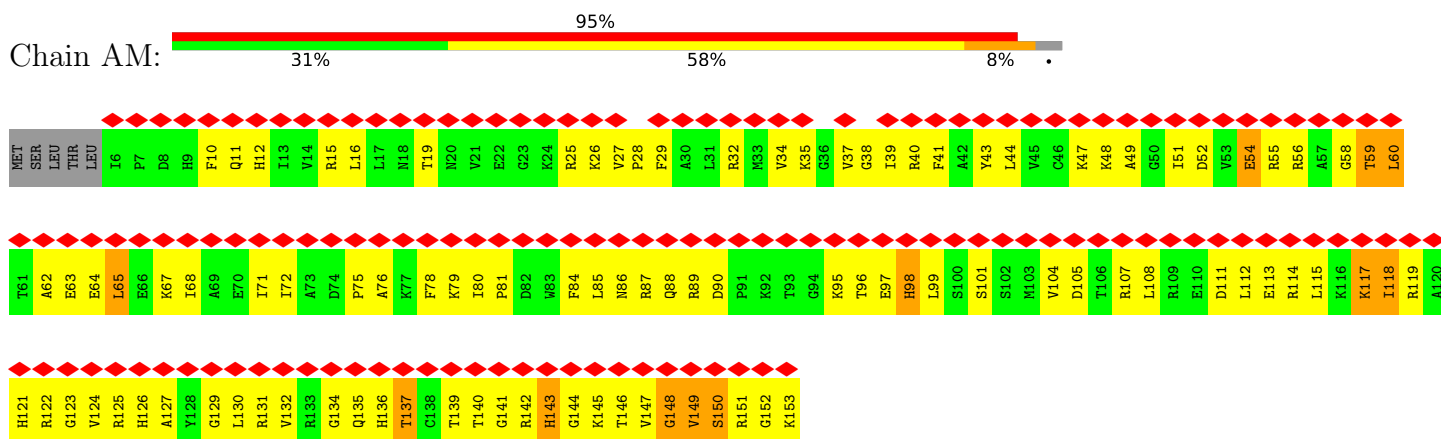


• Molecule 67: eS17

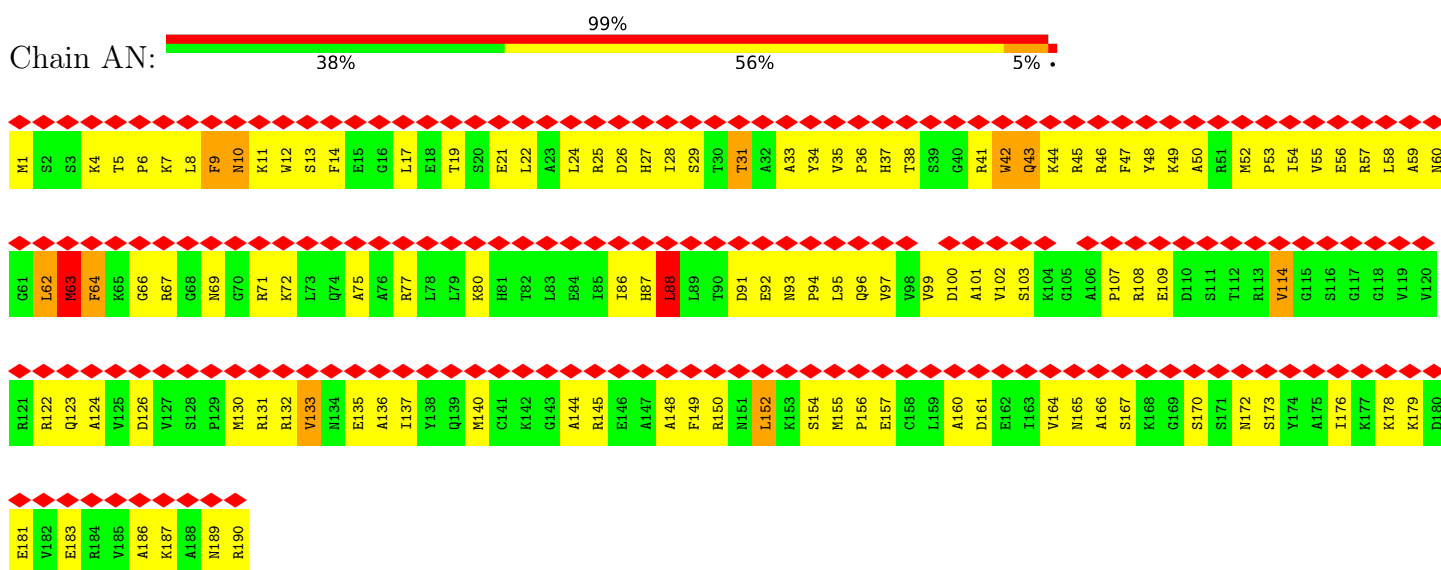




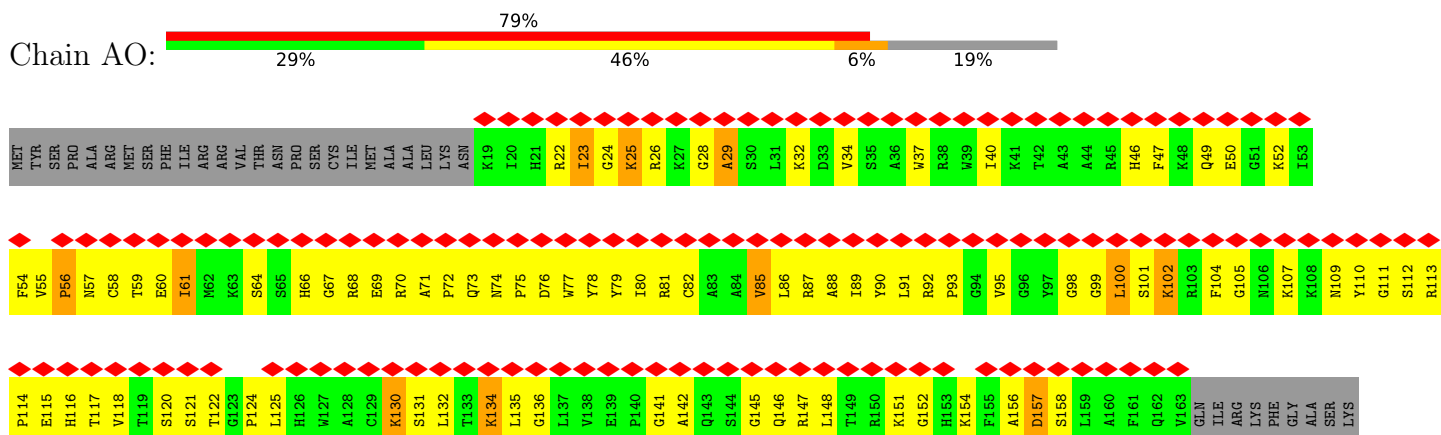
• Molecule 68: uS13



• Molecule 69: uS7

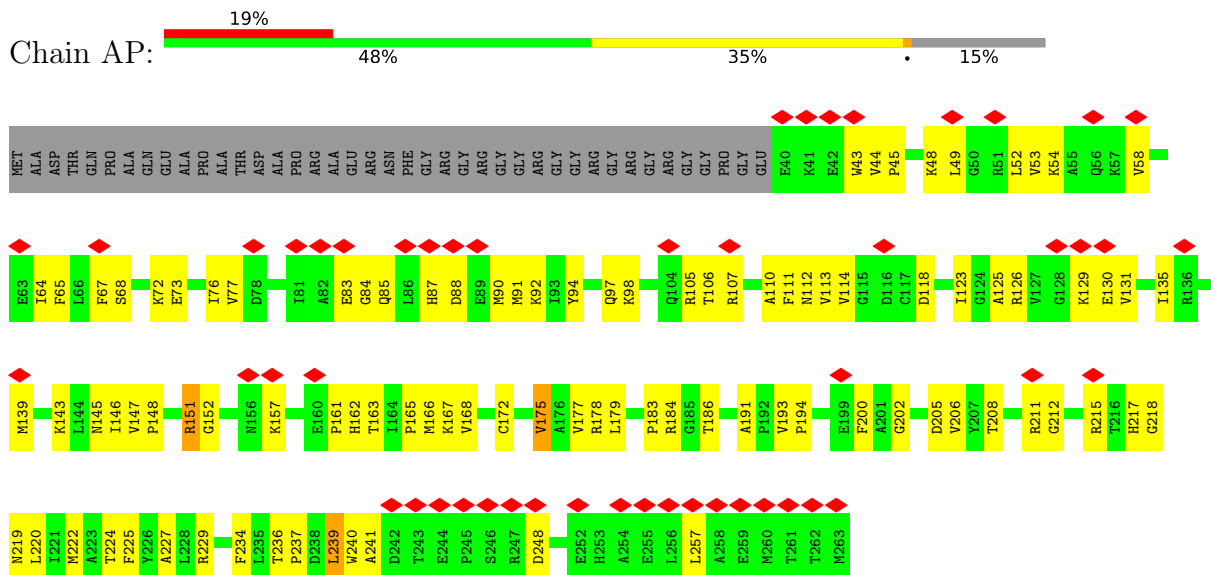


• Molecule 70: eS19



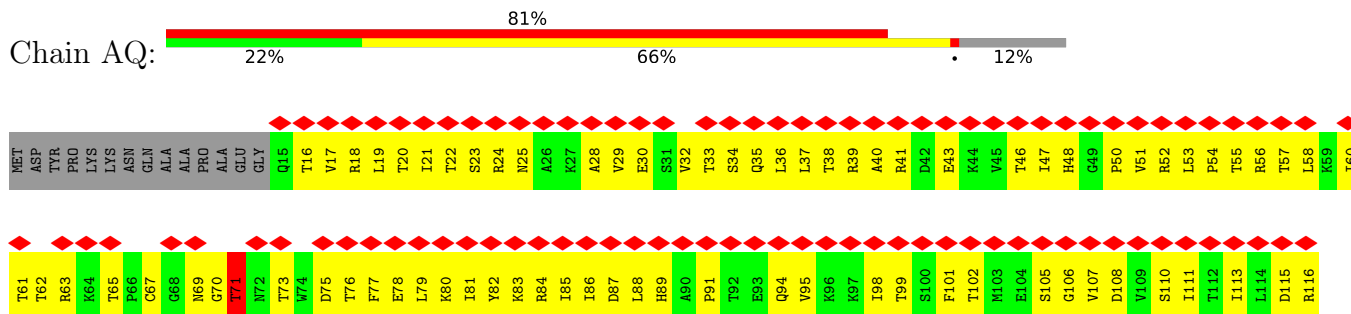
- Molecule 71: uS5

Chain AP:



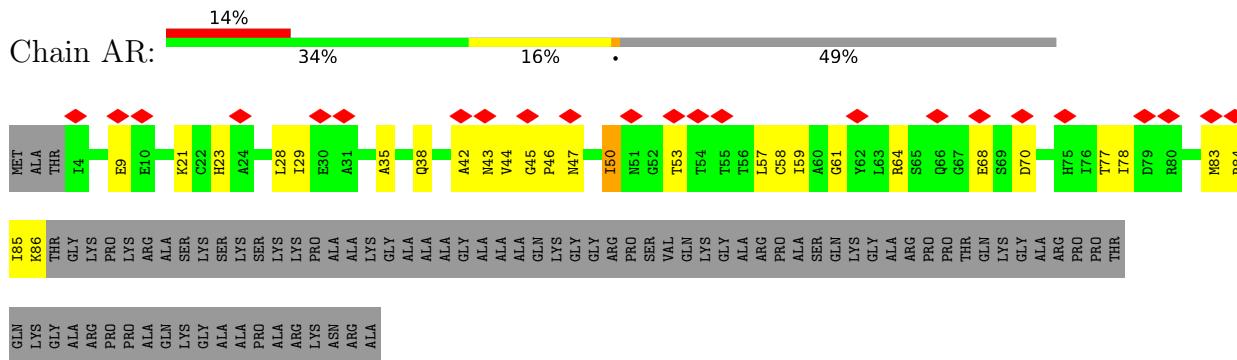
- Molecule 72: uS10

Chain AQ:



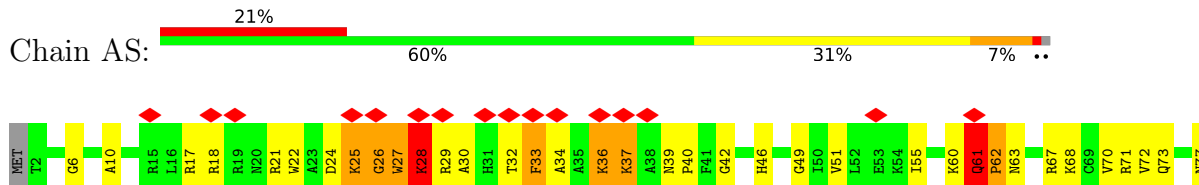
- Molecule 73: eS21

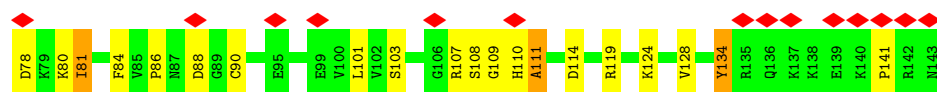
Chain AR:



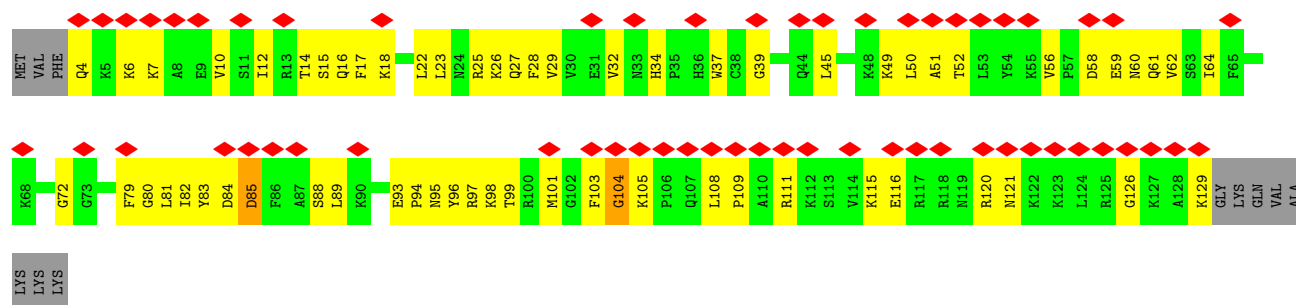
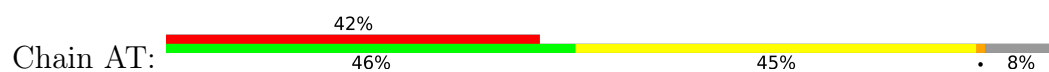
- Molecule 74: uS12

Chain AS:

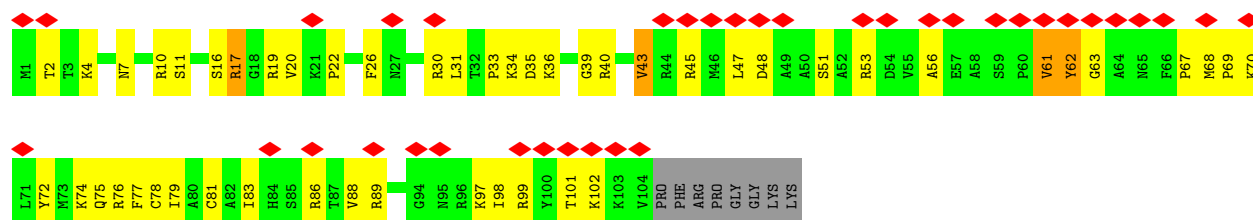




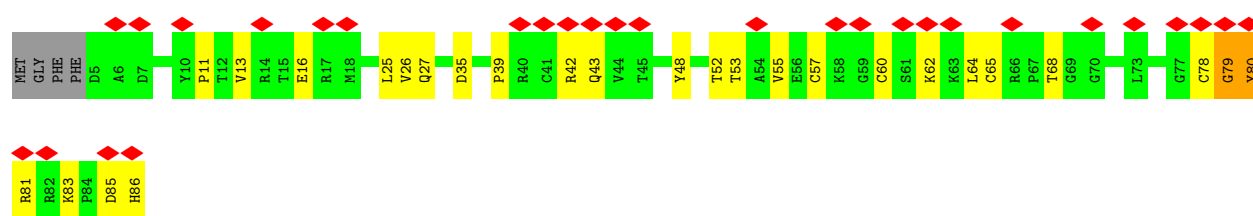
• Molecule 75: eS24



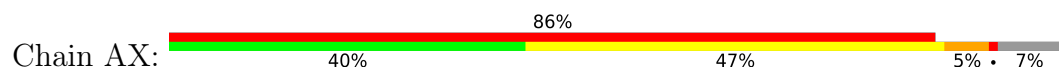
• Molecule 76: eS26

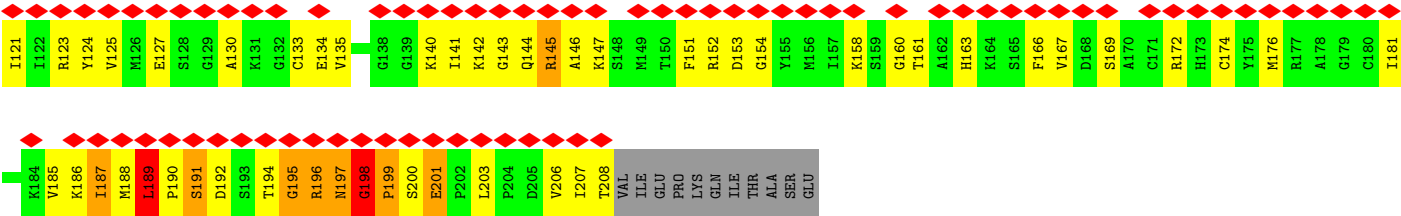


• Molecule 77: eS27



• Molecule 78: uS3

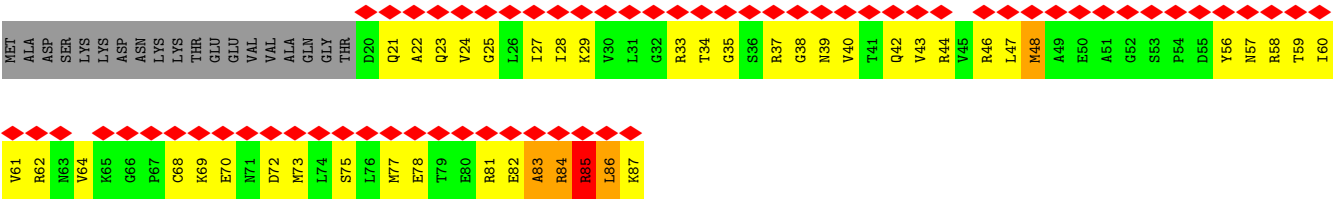
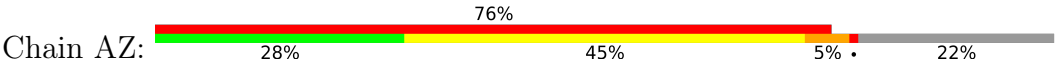




• Molecule 79: eS30



• Molecule 80: eS28



4 Experimental information

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 ($e^-/\text{\AA}^2$)	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 ($\text{\AA}$)	317.31998, 317.31998, 317.31998	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.7932999, 0.7932999, 0.7932999	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.50	0/38479	0.38	0/59984
2	B	0.51	0/25421	0.36	0/39614
3	C	0.47	0/3855	0.37	0/6002
4	D	0.45	0/2829	0.32	0/4405
5	E	0.49	0/4004	0.35	0/6223
6	F	0.42	0/1686	0.41	0/2623
7	G	0.54	0/4373	0.37	0/6817
8	H	0.55	0/2230	0.38	0/3470
9	I	0.66	2/1564 (0.1%)	0.96	10/2092 (0.5%)
10	J	0.47	0/1737	0.78	2/2324 (0.1%)
11	K	0.37	0/1362	0.63	0/1821
12	L	0.49	0/1463	0.74	1/1952 (0.1%)
13	M	0.55	0/1815	0.89	8/2436 (0.3%)
14	N	0.46	0/1355	0.83	5/1814 (0.3%)
15	O	0.67	2/1754 (0.1%)	0.97	9/2342 (0.4%)
16	P	0.57	0/1269	0.71	0/1700
17	Q	0.53	0/1490	0.72	0/2007
18	R	0.48	0/1665	0.72	3/2206 (0.1%)
19	S	0.51	0/1290	0.95	8/1734 (0.5%)
20	T	0.47	0/1013	0.75	2/1350 (0.1%)
21	U	0.58	0/1052	0.78	1/1417 (0.1%)
22	V	0.46	0/978	0.65	0/1318
23	W	0.58	0/584	0.65	0/785
24	X	0.52	0/980	0.81	2/1308 (0.2%)
25	Y	0.50	0/1100	0.68	0/1470
26	Z	0.57	1/1153 (0.1%)	0.87	5/1541 (0.3%)
27	a	0.47	0/1157	0.92	7/1548 (0.5%)
28	b	0.44	0/565	0.71	0/754
29	c	0.80	2/1961 (0.1%)	0.92	9/2630 (0.3%)
30	d	0.60	0/3250	0.87	8/4368 (0.2%)
31	e	0.54	0/730	1.08	9/988 (0.9%)
32	f	0.54	0/893	0.66	0/1196
33	g	0.53	0/1071	0.90	5/1432 (0.3%)
34	h	0.54	0/1030	0.73	0/1369

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	i	0.45	0/1067	0.71	1/1416 (0.1%)
36	j	0.55	0/1082	0.81	1/1454 (0.1%)
37	k	0.40	0/802	0.59	0/1073
38	l	0.71	1/688 (0.1%)	1.14	4/918 (0.4%)
39	m	0.55	0/724	0.80	1/964 (0.1%)
40	n	0.47	0/614	0.69	1/818 (0.1%)
41	o	0.56	0/463	0.73	0/617
42	p	0.51	0/2874	0.84	11/3865 (0.3%)
43	q	0.52	0/431	0.72	0/572
44	r	0.51	0/792	0.80	1/1046 (0.1%)
45	s	0.44	0/2129	0.68	1/2846 (0.0%)
46	t	0.55	0/1074	1.00	6/1454 (0.4%)
47	u	0.53	0/1891	0.79	6/2531 (0.2%)
48	v	0.46	0/1878	0.65	0/2524
49	w	0.52	0/1504	0.86	4/2024 (0.2%)
50	0	0.69	0/1811	1.00	9/2438 (0.4%)
51	1	0.79	0/2076	0.87	3/2799 (0.1%)
52	2	0.78	15/43318 (0.0%)	0.64	37/67487 (0.1%)
53	3	0.66	0/2019	0.98	5/2694 (0.2%)
54	4	0.73	0/1697	1.02	5/2276 (0.2%)
55	5	0.91	3/1494 (0.2%)	1.11	6/2000 (0.3%)
56	6	0.72	0/1389	0.82	1/1866 (0.1%)
57	7	0.43	0/2454	0.97	13/3337 (0.4%)
58	8	0.71	0/317	1.19	2/421 (0.5%)
59	AC	0.67	0/1656	0.81	0/2238
60	AD	0.45	0/788	1.37	8/1064 (0.8%)
61	AE	0.90	0/1171	0.83	0/1570
62	AG	0.82	0/1180	0.95	3/1581 (0.2%)
63	AH	0.76	0/1038	0.92	2/1392 (0.1%)
64	AI	1.40	4/1006 (0.4%)	1.45	14/1351 (1.0%)
65	AJ	0.87	0/1037	1.01	5/1391 (0.4%)
66	AK	0.53	0/1128	1.14	13/1515 (0.9%)
67	AL	0.51	0/993	0.87	4/1322 (0.3%)
68	AM	0.53	0/1206	1.10	6/1615 (0.4%)
69	AN	0.48	0/1516	0.98	8/2034 (0.4%)
70	AO	0.49	0/1180	0.97	2/1585 (0.1%)
71	AP	0.78	0/1758	0.88	3/2380 (0.1%)
72	AQ	0.53	0/817	0.89	1/1107 (0.1%)
73	AR	0.68	0/639	0.82	0/866
74	AS	0.79	0/1134	1.22	16/1517 (1.1%)
75	AT	0.66	0/1054	0.83	0/1405
76	AV	0.71	1/845 (0.1%)	1.01	3/1130 (0.3%)
77	AW	1.82	2/658 (0.3%)	1.06	4/883 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	AX	0.53	0/1616	1.13	8/2159 (0.4%)
79	AY	0.52	0/460	1.04	3/611 (0.5%)
80	AZ	0.77	1/528 (0.2%)	1.19	4/705 (0.6%)
All	All	0.62	34/215154 (0.0%)	0.67	319/315901 (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	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

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

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	AI	135	HIS	CB-CG	38.96	2.04	1.50
77	AW	80	TYR	C-N	-34.82	0.87	1.33
52	2	1954	U	O3'-P	31.14	2.07	1.61
52	2	1864	C	C2-N3	29.08	1.94	1.35
52	2	1864	C	N3-C4	28.34	1.90	1.33

The worst 5 of 319 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	2	1954	U	P-O3'-C3'	22.10	153.35	120.20
64	AI	131	ARG	N-CA-C	-21.01	76.87	109.64
64	AI	133	VAL	N-CA-C	20.95	130.53	110.42
60	AD	40	SER	N-CA-C	-20.35	80.16	110.28
53	3	150	LEU	N-CA-C	19.70	132.15	111.07

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34365	0	17292	604	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	22723	0	11462	311	0
3	C	3449	0	1745	94	0
4	D	2531	0	1283	41	0
5	E	3589	0	1818	34	0
6	F	1508	0	768	61	0
7	G	3911	0	1975	43	0
8	H	1996	0	1013	24	0
9	I	1539	0	1648	124	0
10	J	1704	0	1776	51	0
11	K	1339	0	1369	70	0
12	L	1435	0	1525	98	0
13	M	1780	0	1894	85	0
14	N	1336	0	1409	84	0
15	O	1714	0	1792	113	0
16	P	1245	0	1289	38	0
17	Q	1456	0	1498	64	0
18	R	1646	0	1749	84	0
19	S	1261	0	1317	61	0
20	T	997	0	1051	30	0
21	U	1035	0	1092	51	0
22	V	963	0	1032	34	0
23	W	563	0	577	13	0
24	X	965	0	1033	70	0
25	Y	1079	0	1148	33	0
26	Z	1126	0	1153	84	0
27	a	1140	0	1186	57	0
28	b	554	0	581	16	0
29	c	1921	0	1978	104	0
30	d	3183	0	3308	156	0
31	e	720	0	734	32	0
32	f	878	0	951	27	0
33	g	1050	0	1115	46	0
34	h	1014	0	1078	38	0
35	i	1056	0	1156	33	0
36	j	1060	0	1108	63	0
37	k	787	0	846	24	0
38	l	674	0	690	43	0
39	m	712	0	746	27	0
40	n	605	0	663	28	0
41	o	450	0	483	17	0
42	p	2825	0	2941	184	0
43	q	425	0	463	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	r	779	0	839	32	0
45	s	2094	0	2198	82	0
46	t	1054	0	1098	56	0
47	u	1857	0	1952	103	0
48	v	1850	0	1972	73	0
49	w	1484	0	1568	50	0
50	0	1786	0	1868	131	0
51	1	2037	0	2124	104	0
52	2	38724	0	19533	1773	0
53	3	1994	0	2134	107	0
54	4	1667	0	1782	117	0
55	5	1473	0	1561	132	0
56	6	1362	0	1416	75	0
57	7	2394	0	2312	234	0
58	8	314	0	323	78	0
59	AC	1622	0	1663	113	0
60	AD	767	0	758	111	0
61	AE	1148	0	1194	60	0
62	AG	1157	0	1230	52	0
63	AH	1023	0	1054	66	0
64	AI	984	0	1011	195	0
65	AJ	1020	0	1050	47	0
66	AK	1108	0	1167	179	0
67	AL	983	0	1054	91	0
68	AM	1186	0	1241	252	0
69	AN	1493	0	1538	162	0
70	AO	1150	0	1173	145	0
71	AP	1722	0	1768	83	0
72	AQ	807	0	851	109	0
73	AR	630	0	620	30	0
74	AS	1114	0	1170	79	0
75	AT	1033	0	1095	54	0
76	AV	828	0	874	50	0
77	AW	646	0	656	26	0
78	AX	1595	0	1662	176	0
79	AY	452	0	505	24	0
80	AZ	526	0	548	63	0
All	All	200172	0	148297	7022	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

The worst 5 of 7022 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:2:1864:C:C4	52:2:1864:C:C5	1.81	1.66
74:AS:27:TRP:CE3	74:AS:30:ALA:HB3	1.21	1.65
52:2:1863:A:H4'	64:AI:134:LEU:CD2	1.20	1.61
24:X:57:ARG:HD3	24:X:100:ASN:CG	1.24	1.60
69:AN:62:LEU:HD22	69:AN:75:ALA:CB	1.23	1.60

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	195/198 (98%)	180 (92%)	12 (6%)	3 (2%)	8	28
10	J	209/213 (98%)	193 (92%)	13 (6%)	3 (1%)	9	30
11	K	165/188 (88%)	152 (92%)	12 (7%)	1 (1%)	21	51
12	L	175/220 (80%)	159 (91%)	14 (8%)	2 (1%)	11	36
13	M	219/222 (99%)	212 (97%)	6 (3%)	1 (0%)	24	54
14	N	166/175 (95%)	153 (92%)	12 (7%)	1 (1%)	21	51
15	O	201/204 (98%)	192 (96%)	9 (4%)	0	100	100
16	P	153/166 (92%)	145 (95%)	7 (5%)	1 (1%)	18	48
17	Q	176/179 (98%)	163 (93%)	11 (6%)	2 (1%)	11	36
18	R	194/245 (79%)	193 (100%)	1 (0%)	0	100	100
19	S	156/159 (98%)	144 (92%)	11 (7%)	1 (1%)	21	51
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%)	16	44
23	W	63/124 (51%)	61 (97%)	2 (3%)	0	100	100
24	X	118/143 (82%)	111 (94%)	5 (4%)	2 (2%)	7	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	Y	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	16	44
26	Z	142/145 (98%)	125 (88%)	14 (10%)	3 (2%)	5	21
27	a	144/147 (98%)	134 (93%)	9 (6%)	1 (1%)	18	48
28	b	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
29	c	251/260 (96%)	229 (91%)	20 (8%)	2 (1%)	16	44
30	d	397/419 (95%)	376 (95%)	20 (5%)	1 (0%)	36	65
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
34	h	122/168 (73%)	117 (96%)	4 (3%)	1 (1%)	16	44
35	i	124/127 (98%)	117 (94%)	6 (5%)	1 (1%)	16	44
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%)	21	51
43	q	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
44	r	94/106 (89%)	85 (90%)	8 (8%)	1 (1%)	11	36
45	s	258/305 (85%)	246 (95%)	12 (5%)	0	100	100
46	t	133/195 (68%)	123 (92%)	8 (6%)	2 (2%)	8	28
47	u	226/252 (90%)	209 (92%)	16 (7%)	1 (0%)	30	59
48	v	228/348 (66%)	218 (96%)	10 (4%)	0	100	100
49	w	185/190 (97%)	173 (94%)	11 (6%)	1 (0%)	24	54
50	0	219/264 (83%)	208 (95%)	10 (5%)	1 (0%)	24	54
51	1	256/273 (94%)	231 (90%)	22 (9%)	3 (1%)	10	34
53	3	247/249 (99%)	236 (96%)	10 (4%)	1 (0%)	30	59
54	4	198/200 (99%)	183 (92%)	11 (6%)	4 (2%)	6	22
55	5	178/220 (81%)	160 (90%)	16 (9%)	2 (1%)	11	36
56	6	162/190 (85%)	151 (93%)	9 (6%)	2 (1%)	10	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	7	306/312 (98%)	275 (90%)	28 (9%)	3 (1%)	12	39
58	8	36/57 (63%)	30 (83%)	5 (14%)	1 (3%)	4	15
59	AC	201/246 (82%)	193 (96%)	8 (4%)	0	100	100
60	AD	91/153 (60%)	78 (86%)	11 (12%)	2 (2%)	5	20
61	AE	136/173 (79%)	131 (96%)	4 (3%)	1 (1%)	18	48
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%)	16	44
66	AK	138/149 (93%)	118 (86%)	16 (12%)	4 (3%)	3	15
67	AL	119/143 (83%)	108 (91%)	8 (7%)	3 (2%)	4	17
68	AM	146/153 (95%)	125 (86%)	21 (14%)	0	100	100
69	AN	188/190 (99%)	165 (88%)	21 (11%)	2 (1%)	11	36
70	AO	143/179 (80%)	114 (80%)	25 (18%)	4 (3%)	4	15
71	AP	222/265 (84%)	216 (97%)	6 (3%)	0	100	100
72	AQ	100/116 (86%)	86 (86%)	13 (13%)	1 (1%)	12	39
73	AR	81/164 (49%)	78 (96%)	3 (4%)	0	100	100
74	AS	140/143 (98%)	132 (94%)	5 (4%)	3 (2%)	5	21
75	AT	124/137 (90%)	117 (94%)	6 (5%)	1 (1%)	16	44
76	AV	102/112 (91%)	90 (88%)	8 (8%)	4 (4%)	2	10
77	AW	80/86 (93%)	76 (95%)	4 (5%)	0	100	100
78	AX	201/219 (92%)	179 (89%)	17 (8%)	5 (2%)	4	17
79	AY	54/66 (82%)	48 (89%)	6 (11%)	0	100	100
80	AZ	66/87 (76%)	60 (91%)	4 (6%)	2 (3%)	3	14
All	All	10774/12317 (88%)	9993 (93%)	696 (6%)	85 (1%)	18	44

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 ⓘ

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%)	157 (96%)	6 (4%)	30	64
10	J	178/179 (99%)	175 (98%)	3 (2%)	53	82
11	K	145/163 (89%)	144 (99%)	1 (1%)	76	92
12	L	152/182 (84%)	151 (99%)	1 (1%)	76	92
13	M	188/189 (100%)	187 (100%)	1 (0%)	81	93
14	N	139/144 (96%)	137 (99%)	2 (1%)	59	85
15	O	179/180 (99%)	177 (99%)	2 (1%)	65	88
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%)	165 (98%)	3 (2%)	51	80
19	S	132/133 (99%)	130 (98%)	2 (2%)	57	84
20	T	107/114 (94%)	106 (99%)	1 (1%)	70	90
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%)	53	82
24	X	103/121 (85%)	101 (98%)	2 (2%)	50	79
25	Y	114/115 (99%)	112 (98%)	2 (2%)	51	80
26	Z	114/115 (99%)	113 (99%)	1 (1%)	70	90
27	a	118/119 (99%)	116 (98%)	2 (2%)	53	82
28	b	57/58 (98%)	57 (100%)	0	100	100
29	c	198/204 (97%)	193 (98%)	5 (2%)	42	74
30	d	337/351 (96%)	335 (99%)	2 (1%)	78	93
31	e	82/90 (91%)	77 (94%)	5 (6%)	17	46
32	f	97/156 (62%)	95 (98%)	2 (2%)	47	77
33	g	113/117 (97%)	111 (98%)	2 (2%)	51	80
34	h	107/145 (74%)	107 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	i	116/117 (99%)	116 (100%)	0	100	100
36	j	109/121 (90%)	107 (98%)	2 (2%)	51	80
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
41	o	46/47 (98%)	46 (100%)	0	100	100
42	p	295/302 (98%)	294 (100%)	1 (0%)	86	96
43	q	46/113 (41%)	46 (100%)	0	100	100
44	r	83/92 (90%)	81 (98%)	2 (2%)	43	75
45	s	209/242 (86%)	208 (100%)	1 (0%)	81	93
46	t	111/152 (73%)	109 (98%)	2 (2%)	51	80
47	u	190/209 (91%)	185 (97%)	5 (3%)	40	73
48	v	196/292 (67%)	196 (100%)	0	100	100
49	w	169/172 (98%)	168 (99%)	1 (1%)	78	93
50	0	194/222 (87%)	189 (97%)	5 (3%)	40	73
51	1	215/225 (96%)	212 (99%)	3 (1%)	59	85
53	3	208/208 (100%)	205 (99%)	3 (1%)	59	85
54	4	186/186 (100%)	185 (100%)	1 (0%)	81	93
55	5	149/176 (85%)	145 (97%)	4 (3%)	39	73
56	6	147/164 (90%)	143 (97%)	4 (3%)	39	73
57	7	263/266 (99%)	259 (98%)	4 (2%)	57	84
58	8	35/49 (71%)	34 (97%)	1 (3%)	37	71
59	AC	177/202 (88%)	177 (100%)	0	100	100
60	AD	82/129 (64%)	80 (98%)	2 (2%)	43	75
61	AE	124/150 (83%)	121 (98%)	3 (2%)	43	75
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%)	50	79
65	AJ	110/111 (99%)	103 (94%)	7 (6%)	16	44
66	AK	113/120 (94%)	107 (95%)	6 (5%)	20	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	AL	107/123 (87%)	105 (98%)	2 (2%)	50	79
68	AM	125/130 (96%)	121 (97%)	4 (3%)	34	68
69	AN	159/159 (100%)	157 (99%)	2 (1%)	61	86
70	AO	118/147 (80%)	116 (98%)	2 (2%)	53	82
71	AP	184/209 (88%)	183 (100%)	1 (0%)	81	93
72	AQ	94/104 (90%)	93 (99%)	1 (1%)	65	88
73	AR	68/119 (57%)	66 (97%)	2 (3%)	37	71
74	AS	115/116 (99%)	111 (96%)	4 (4%)	32	66
75	AT	111/120 (92%)	111 (100%)	0	100	100
76	AV	87/93 (94%)	86 (99%)	1 (1%)	65	88
77	AW	72/75 (96%)	72 (100%)	0	100	100
78	AX	171/185 (92%)	167 (98%)	4 (2%)	44	76
79	AY	49/54 (91%)	49 (100%)	0	100	100
80	AZ	57/74 (77%)	54 (95%)	3 (5%)	20	52
All	All	9268/10330 (90%)	9137 (99%)	131 (1%)	57	85

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
71	AP	175	VAL
74	AS	28	LYS
80	AZ	87	LYS
42	p	320	ILE
36	j	126	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 174 such sidechains are listed below:

Mol	Chain	Res	Type
57	7	149	HIS
65	AJ	56	HIS
57	7	298	HIS
61	AE	20	GLN
68	AM	12	HIS

5.3.3 RNA ⓘ

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%)
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 oligosaccharides 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

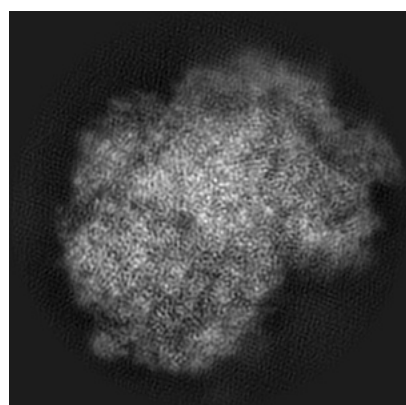
6 Map visualisation [i](#)

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.

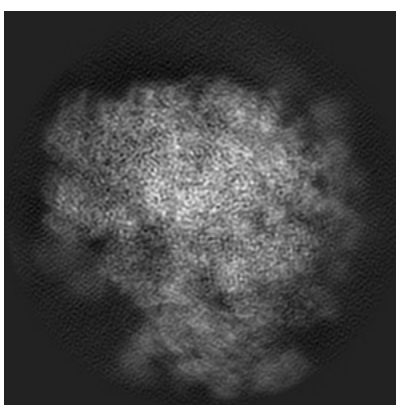
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

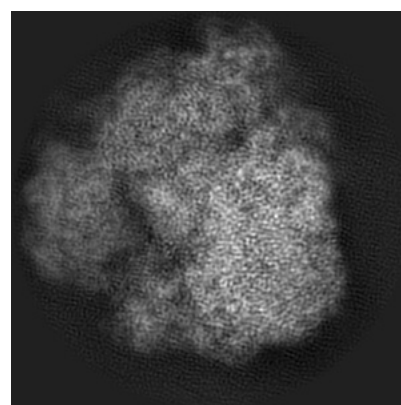
6.1.1 Primary map



X



Y

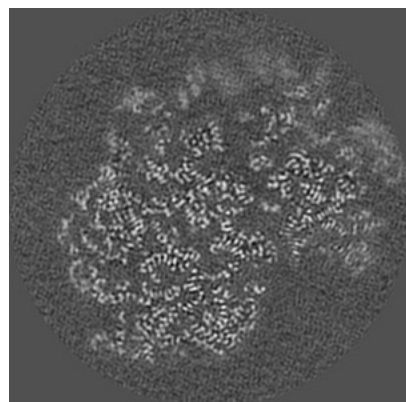


Z

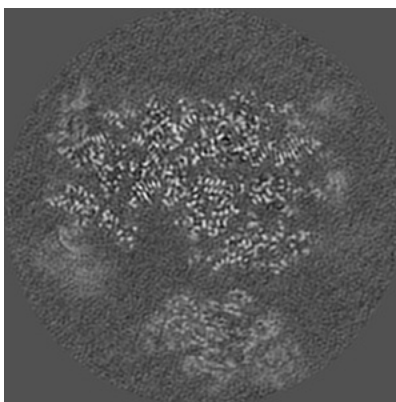
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

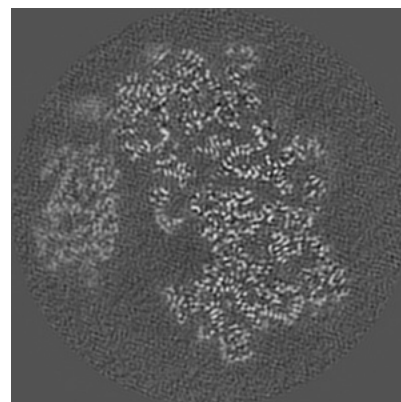
6.2.1 Primary map



X Index: 200



Y Index: 200

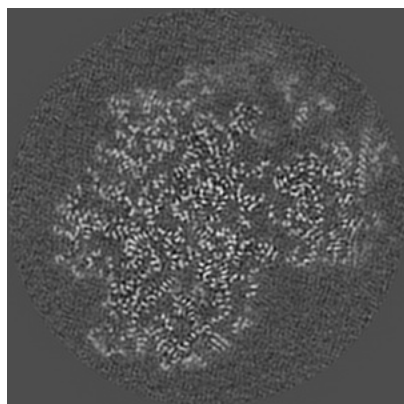


Z Index: 200

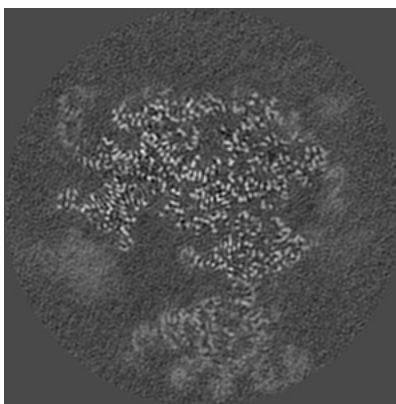
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

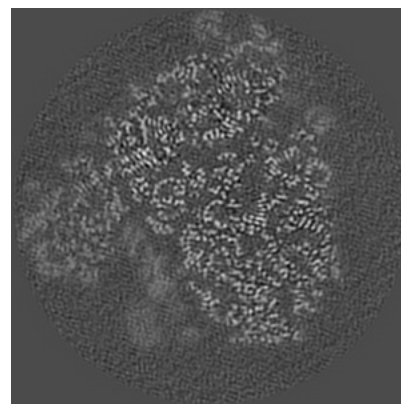
6.3.1 Primary map



X Index: 214



Y Index: 211

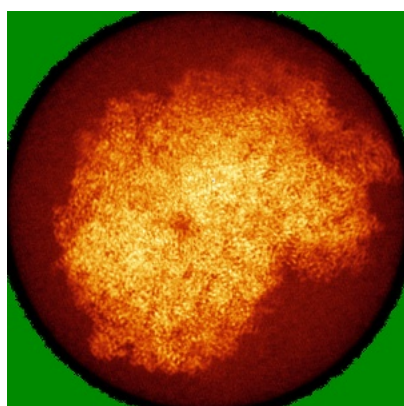


Z Index: 231

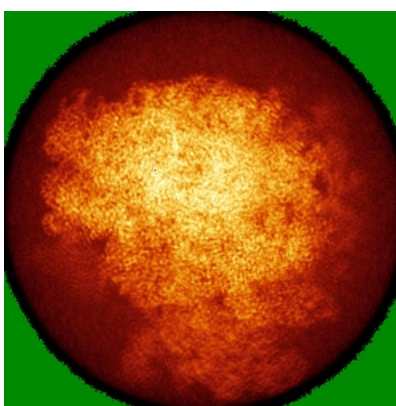
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

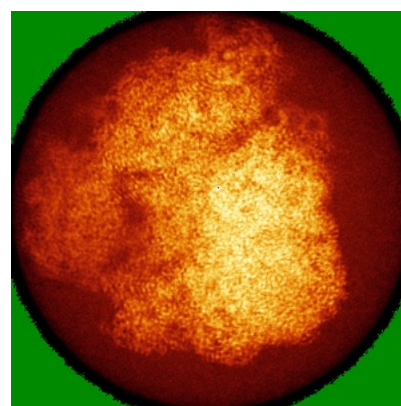
6.4.1 Primary map



X



Y

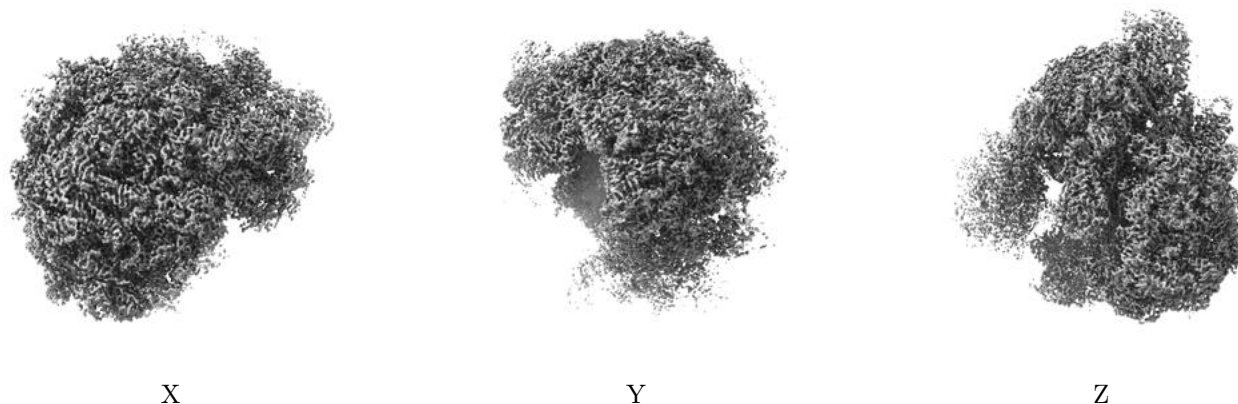


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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.

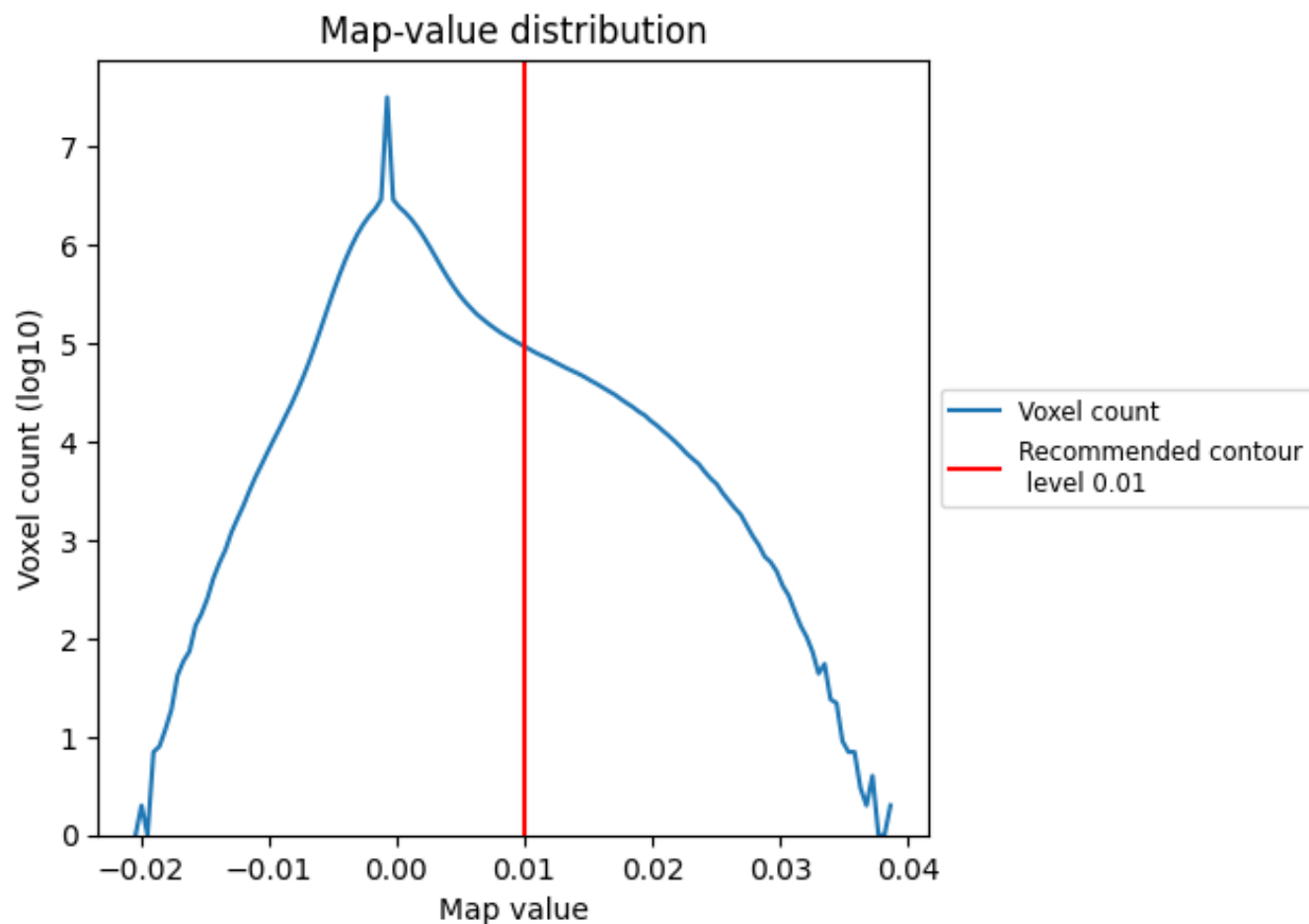
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

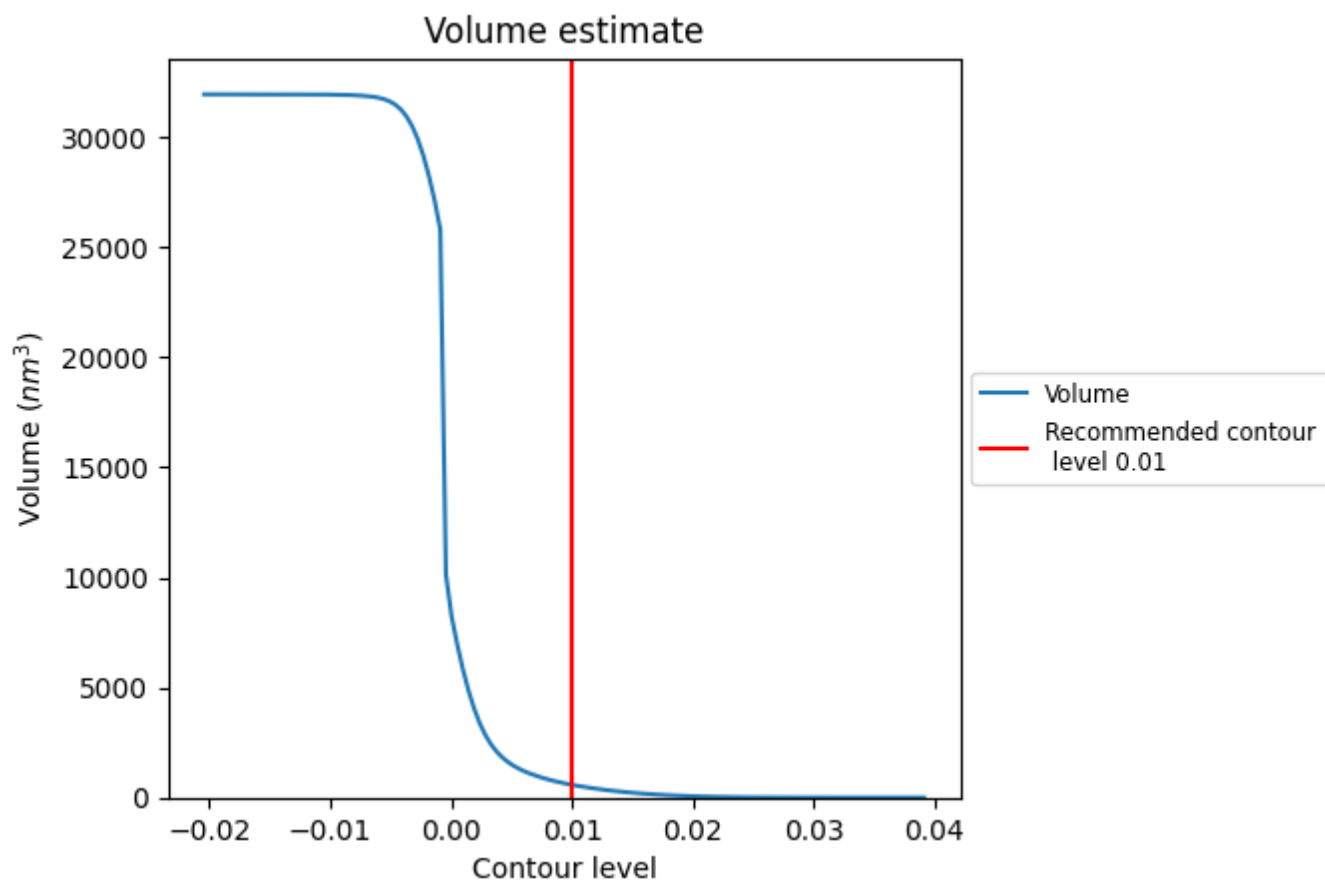
This section contains the results of statistical analysis of the map.

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.

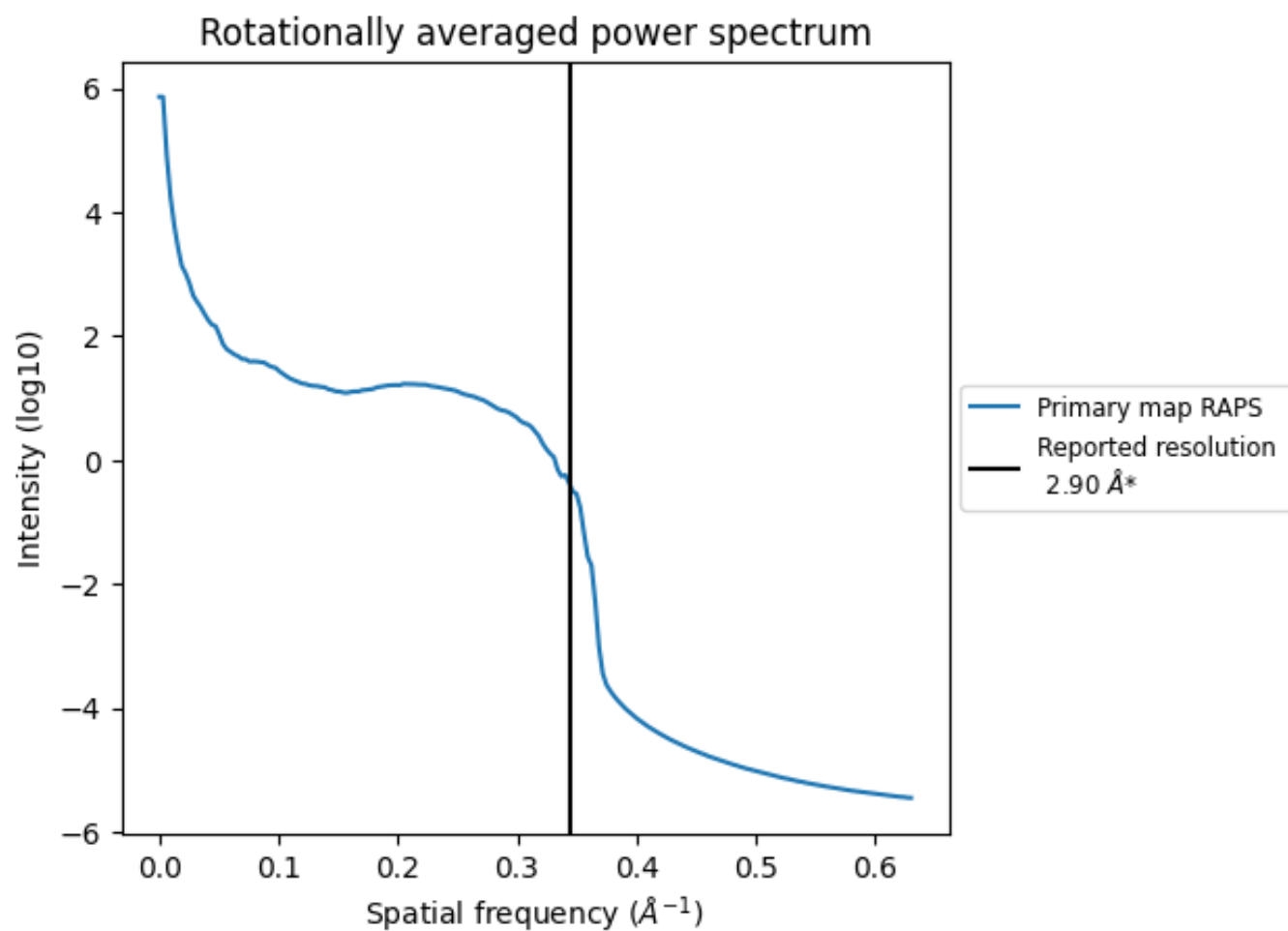
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 580 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

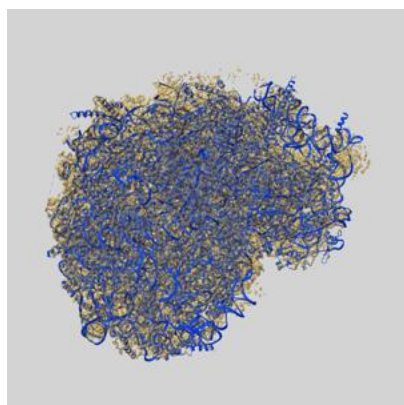
8 Fourier-Shell correlation

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

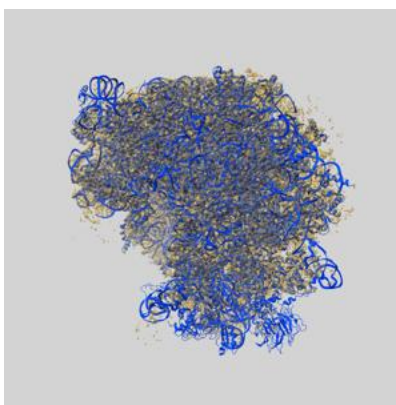
9 Map-model fit [i](#)

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 [20](#).

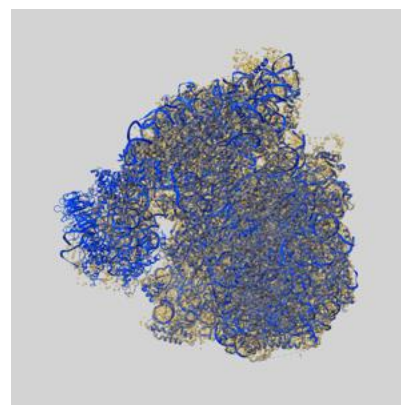
9.1 Map-model overlay [i](#)



X



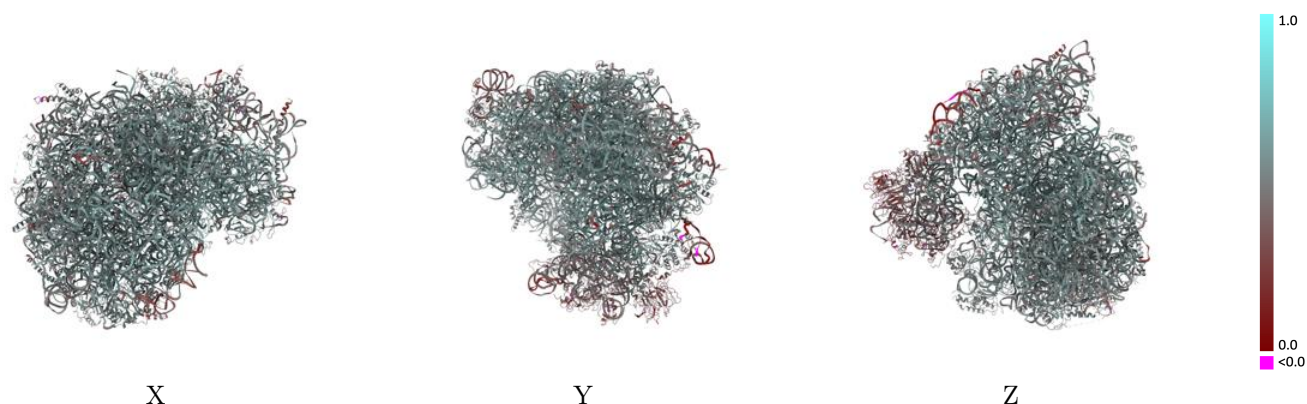
Y



Z

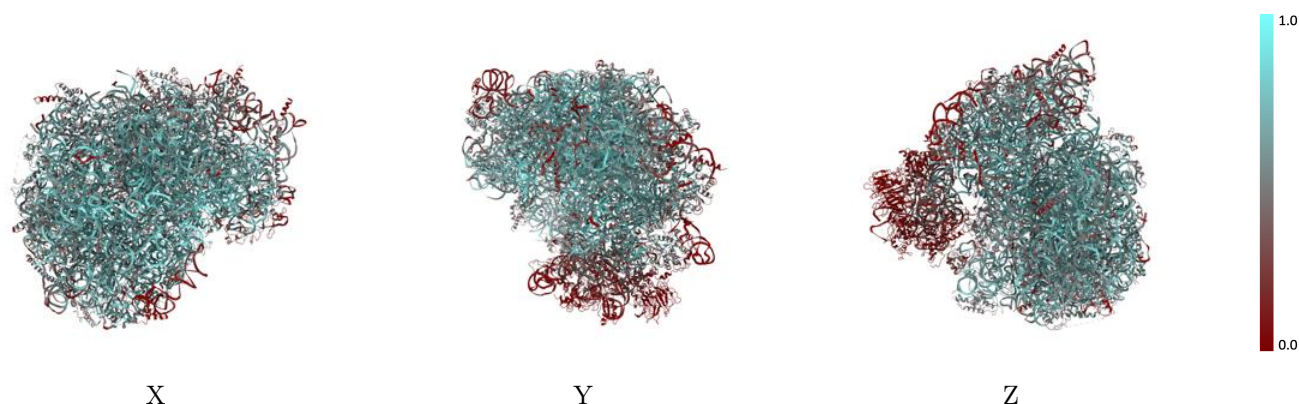
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



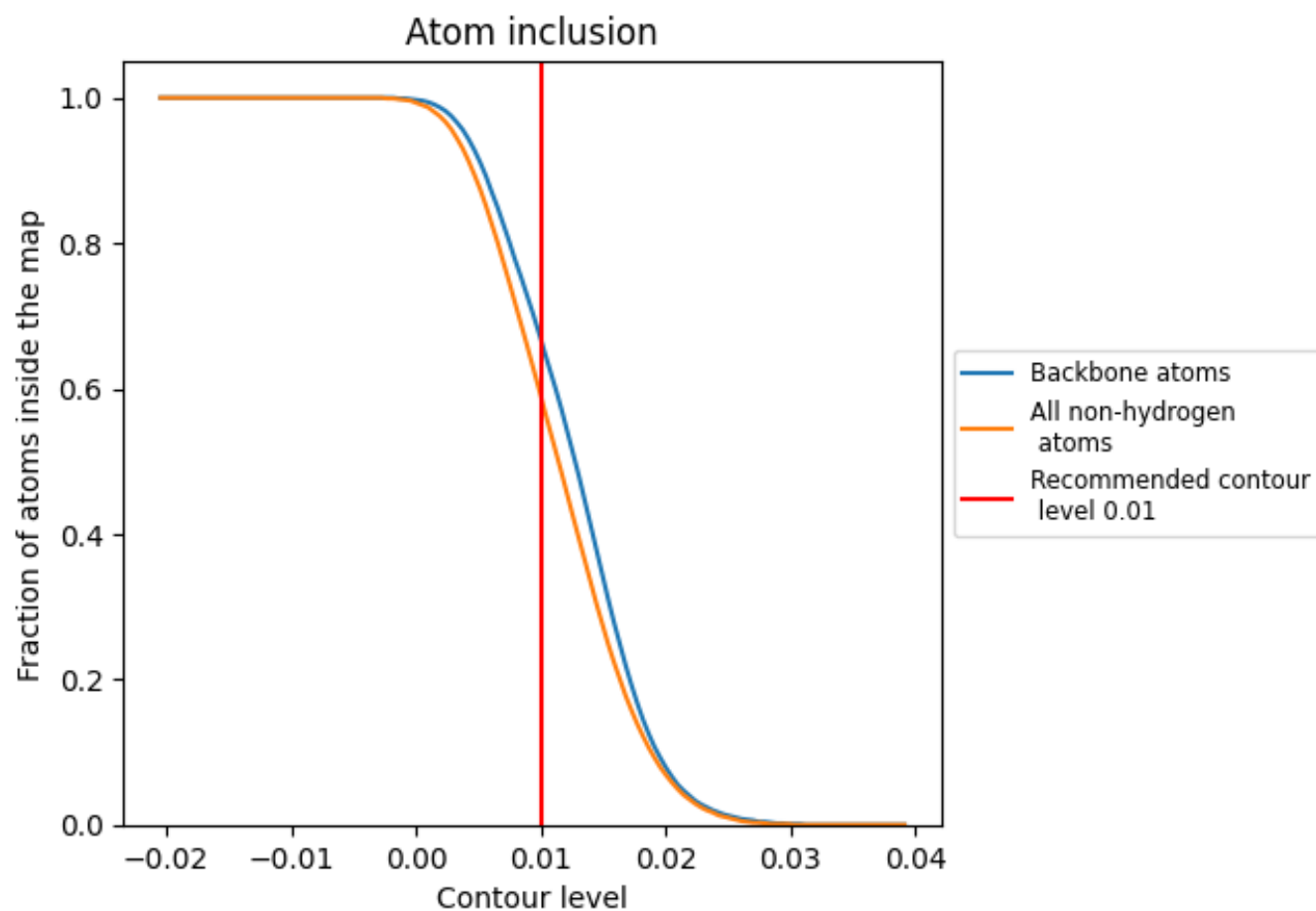
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 ⓘ

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	 0.5910	 0.5270
0	 0.4870	 0.5380
1	 0.5750	 0.5500
2	 0.5650	 0.5170
3	 0.3750	 0.4970
4	 0.4880	 0.5230
5	 0.6080	 0.5580
6	 0.5710	 0.5410
7	 0.0120	 0.3000
8	 0.1850	 0.4210
A	 0.7310	 0.5530
AC	 0.4350	 0.5100
AD	 0.0420	 0.3510
AE	 0.6510	 0.5800
AG	 0.6000	 0.5550
AH	 0.5070	 0.5350
AI	 0.0250	 0.3360
AJ	 0.6250	 0.5560
AK	 0.0970	 0.3800
AL	 0.1210	 0.4060
AM	 0.0600	 0.2810
AN	 0.0660	 0.4100
AO	 0.0930	 0.3020
AP	 0.5460	 0.5370
AQ	 0.0950	 0.3610
AR	 0.5050	 0.5220
AS	 0.5750	 0.5450
AT	 0.3950	 0.5170
AV	 0.4820	 0.5210
AW	 0.5060	 0.5350
AX	 0.1400	 0.4060
AY	 0.2780	 0.4900
AZ	 0.0830	 0.3970
B	 0.7220	 0.5550
C	 0.6960	 0.5260



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Chain	Atom inclusion	Q-score
D	 0.7290	 0.5450
E	 0.7230	 0.5630
F	 0.6250	 0.5290
G	 0.8080	 0.5870
H	 0.8140	 0.5920
I	 0.5680	 0.5280
J	 0.5370	 0.5240
K	 0.3570	 0.4740
L	 0.5430	 0.5060
M	 0.5960	 0.5520
N	 0.4570	 0.4860
O	 0.6250	 0.5490
P	 0.6680	 0.5560
Q	 0.6300	 0.5640
R	 0.5430	 0.5340
S	 0.5570	 0.5280
T	 0.4900	 0.5240
U	 0.6660	 0.5740
V	 0.5540	 0.5270
W	 0.6660	 0.5680
X	 0.5790	 0.5310
Y	 0.5480	 0.5340
Z	 0.6170	 0.5510
a	 0.5310	 0.5130
b	 0.5600	 0.5210
c	 0.6440	 0.5610
d	 0.6570	 0.5620
e	 0.5470	 0.5370
f	 0.6410	 0.5550
g	 0.5910	 0.5430
h	 0.5860	 0.5450
i	 0.5080	 0.5100
j	 0.6250	 0.5510
k	 0.4420	 0.4950
l	 0.6750	 0.5540
m	 0.6110	 0.5560
n	 0.5210	 0.5150
o	 0.6100	 0.5530
p	 0.5510	 0.5170
q	 0.6350	 0.5550
r	 0.5510	 0.5370
s	 0.4960	 0.5110

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Chain	Atom inclusion	Q-score
t	 0.5390	 0.5230
u	 0.5780	 0.5330
v	 0.4810	 0.5010
w	 0.6070	 0.5500