



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 06:51 PM UTC

PDB ID : 8VVU / pdb_00008vvu
EMDB ID : EMD-43569
Title : Anisomycin-bound mammalian ribosome with partially accommodated A-site tRNA
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.
Deposited on : 2024-01-31
Resolution : 3.80 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:

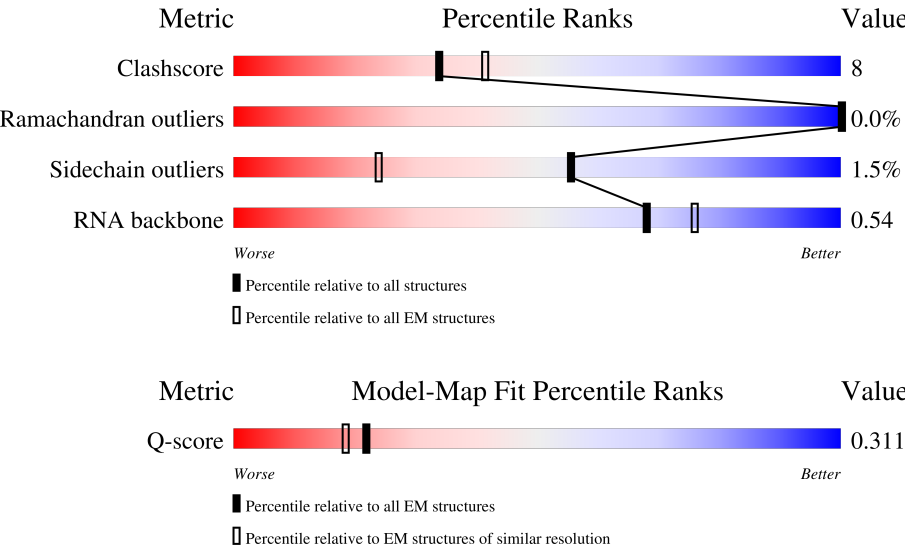
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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

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

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	10198 (3.30 - 4.30)

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	257	63% 75% 22% .
2	B	403	59% 75% 23% .
3	C	413	49% 70% 17% 12%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	D	297	
5	E	291	
6	F	249	
7	G	319	
8	H	192	
9	I	214	
10	J	178	
11	K	211	
12	L	218	
13	M	204	
14	N	203	
15	O	213	
16	P	188	
17	Q	212	
18	R	224	
19	S	160	
20	T	128	
21	U	140	
22	V	157	
23	W	156	
24	X	145	
25	Y	136	
26	Z	148	
27	AA	245	
28	BA	115	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	CA	125	
30	DA	135	
31	EA	110	
32	FA	129	
33	GA	123	
34	HA	105	
35	IA	97	
36	JA	70	
37	KA	51	
38	LA	128	
39	MA	25	
40	NA	106	
41	OA	92	
42	PA	137	
43	RA	165	
44	SA	76	
45	TA	76	
46	VA	12	
47	WA	3584	
48	XA	120	
49	YA	156	
50	ZA	1869	
51	AB	295	
52	BB	264	
53	CB	293	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	DB	281	
55	EB	263	
56	FB	204	
57	GB	249	
58	HB	432	
59	IB	208	
60	JB	194	
61	KB	165	
62	LB	158	
63	MB	132	
64	NB	151	
65	OB	151	
66	PB	145	
67	QB	172	
68	RB	135	
69	SB	152	
70	TB	145	
71	UB	119	
72	VB	83	
73	WB	130	
74	XB	143	
75	YB	131	
76	ZB	124	
77	AC	115	
78	BC	84	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	CC	69	
80	DC	56	
81	EC	133	
82	FC	188	
83	GC	317	
84	IC	4	
85	b	318	
86	At	74	

2 Entry composition

There are 91 unique types of molecules in this entry. The entry contains 218724 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	250	Total	C	N	O	S	0	0
			1914	1199	392	317	6		

- Molecule 2 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	397	Total	C	N	O	S	0	0
			3196	2035	603	545	13		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	362	Total	C	N	O	S	0	0
			2883	1812	577	480	14		

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2395	1514	439	428	14		

- Molecule 5 is a protein called L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	228	Total	C	N	O	S	0	0
			1823	1173	349	298	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	227	Total	C	N	O	S	0	0
			1897	1217	366	305	9		

- Molecule 7 is a protein called L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	229	Total	C	N	O	S	0	0
			1850	1181	356	309	4		

- Molecule 8 is a protein called L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 9 is a protein called L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	171	Total	C	N	O	S	0	0
			1372	867	256	243	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	46	ILE	-	insertion	UNP G1TPV0
K	47	ALA	-	insertion	UNP G1TPV0
K	48	PRO	-	insertion	UNP G1TPV0
K	49	ARG	-	insertion	UNP G1TPV0
K	50	PRO	-	insertion	UNP G1TPV0
K	51	ALA	-	insertion	UNP G1TPV0
K	52	ALA	-	insertion	UNP G1TPV0
K	53	GLY	-	insertion	UNP G1TPV0
K	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 13 is a protein called L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	156	Total	C	N	O	S	0	0
			1266	793	245	219	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	43	SER	ALA	conflict	UNP G1TVT6

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	ASP	ASN	conflict	UNP G1TFE0
P	14	ARG	TRP	conflict	UNP G1TFE0
P	53	MET	LEU	conflict	UNP G1TFE0
P	58	ARG	TRP	conflict	UNP G1TFE0
P	75	ARG	GLN	conflict	UNP G1TFE0
P	80	ALA	PRO	conflict	UNP G1TFE0
P	86	VAL	ILE	conflict	UNP G1TFE0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
P	104	ARG	HIS	conflict	UNP G1TFE0
P	110	ARG	CYS	conflict	UNP G1TFE0
P	137	VAL	GLY	conflict	UNP G1TFE0
P	157	GLY	ARG	conflict	UNP G1TFE0
P	181	ARG	TRP	conflict	UNP G1TFE0

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 18 is a protein called L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	101	Total	C	N	O	S	0	0
			826	530	144	150	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	18	LEU	VAL	conflict	UNP G1TSG1
T	32	GLY	ARG	conflict	UNP G1TSG1
T	36	ALA	GLU	conflict	UNP G1TSG1
T	39	PHE	SER	conflict	UNP G1TSG1
T	54	GLY	ARG	conflict	UNP G1TSG1
T	60	VAL	ALA	conflict	UNP G1TSG1
T	62	SER	THR	conflict	UNP G1TSG1
T	63	LEU	ILE	conflict	UNP G1TSG1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
T	97	ARG	HIS	conflict	UNP G1TSG1
T	106	THR	SER	conflict	UNP G1TSG1
T	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	135	Total	C	N	O	S	0	0
			1004	631	191	177	5		

- Molecule 22 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	110	Total	C	N	O	S	0	0
			887	555	179	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	78	SER	PHE	conflict	UNP G1SE28

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 24 is a protein called L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 25 is a protein called L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 26 is a protein called L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 27 is a protein called L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AA	107	Total	C	N	O	S	0	0
			873	542	195	133	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BA	99	Total	C	N	O	S	0	0
			769	486	135	141	7		

- Molecule 29 is a protein called L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	CA	108	Total	C	N	O	S	0	0
			893	563	172	156	2		

- Molecule 30 is a protein called L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DA	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	EA	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FA	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 33 is a protein called L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	GA	121	Total	C	N	O	S	0	0
			1008	637	203	167	1		

- Molecule 34 is a protein called L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	HA	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 35 is a protein called L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	IA	87	Total	C	N	O	S	0	0
			716	440	159	112	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	JA	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
JA	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	KA	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LA	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	MA	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	NA	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	OA	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 42 is a protein called L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	PA	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 43 is a protein called L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	RA	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 44 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	SA	76	Total	C	N	O	P	0	0
			1622	726	300	521	75		

- Molecule 45 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	TA	76	Total	C	N	O	P	0	0
			1615	722	286	532	75		

- Molecule 46 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	VA	12	Total	C	N	O	P	0	0
			249	112	39	86	12		

- Molecule 47 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	WA	3578	Total	C	N	O	P	0	0
			76735	34173	14061	24923	3578		

- Molecule 48 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	XA	119	Total	C	N	O	P	0	0
			2538	1132	454	834	118		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
XA	2	U	N	conflict	GB X06789.1
XA	36	C	N	conflict	GB X06789.1
XA	102	U	N	conflict	GB X06789.1
XA	112	U	N	conflict	GB X06789.1
XA	114	U	N	conflict	GB X06789.1
XA	119	U	C	conflict	GB X06789.1
XA	120	U	N	conflict	GB X06789.1

- Molecule 49 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	YA	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 50 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ZA	1716	Total	C	N	O	P	0	0
			36623	16347	6572	11989	1715		

- Molecule 51 is a protein called RPSA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AB	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 52 is a protein called S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called S2-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CB	220	Total	C	N	O	S	0	0
			1707	1105	293	300	9		

- Molecule 54 is a protein called S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DB	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EB	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	25	GLY	SER	conflict	UNP G1TK17
EB	51	ARG	LYS	conflict	UNP G1TK17
EB	78	THR	ALA	conflict	UNP G1TK17
EB	156	VAL	MET	conflict	UNP G1TK17

- Molecule 56 is a protein called S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FB	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GB	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	HB	185	Total	C	N	O	S	0	0
			1489	952	271	265	1		

- Molecule 59 is a protein called S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	IB	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 60 is a protein called S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	JB	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	KB	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LB	144	Total	C	N	O	S	0	0
			1180	752	223	199	6		

- Molecule 63 is a protein called S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	MB	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 64 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	NB	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	OB	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PB	129	Total	C	N	O	S	0	0
			1058	670	201	180	7		

- Molecule 67 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	QB	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RB	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 69 is a protein called S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SB	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	TB	142	Total	C	N	O	S	0	0
			1104	693	212	196	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
TB	119	GLY	TRP	conflict	UNP G1TN62

- Molecule 71 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	UB	102	Total	C	N	O	S	0	0
			808	507	154	143	4		

- Molecule 72 is a protein called S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	VB	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
VB	3	ASN	SER	conflict	UNP G1TM82
VB	4	ASP	ASN	conflict	UNP G1TM82
VB	33	GLN	PRO	conflict	UNP G1TM82
VB	50	PHE	SER	conflict	UNP G1TM82
VB	75	ALA	SER	conflict	UNP G1TM82
VB	76	ASP	HIS	conflict	UNP G1TM82
VB	81	LYS	GLN	conflict	UNP G1TM82

- Molecule 73 is a protein called S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	WB	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	XB	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	YB	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ZB	85	Total	C	N	O	S	0	0
			683	439	128	115	1		

- Molecule 77 is a protein called S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AC	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AC	28	ARG	CYS	conflict	UNP G1TFE8
AC	56	ALA	VAL	conflict	UNP G1TFE8
AC	109	ARG	PRO	conflict	UNP G1TFE8

- Molecule 78 is a protein called S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BC	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CC	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DC	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	EC	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	FC	69	Total	C	N	O	S	0	0
			564	357	105	95	7		

- Molecule 83 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	GC	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 84 is a protein called nascent chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
84	IC	4	Total	C	N	O	0	0
			20	12	4	4		

- Molecule 85 is a protein called RPLP0.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	b	167	Total	C	N	O	S	0	0
			1279	813	228	229	9		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	82	LEU	ILE	conflict	UNP G1SPK4

- Molecule 86 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
86	At	74	Total	C	N	O	P	S	0	0
			1582	705	282	520	74	1		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	I	1	Total	Mg	0
			1	1	
87	FA	1	Total	Mg	0
			1	1	
87	WA	80	Total	Mg	0
			80	80	

Continued on next page...

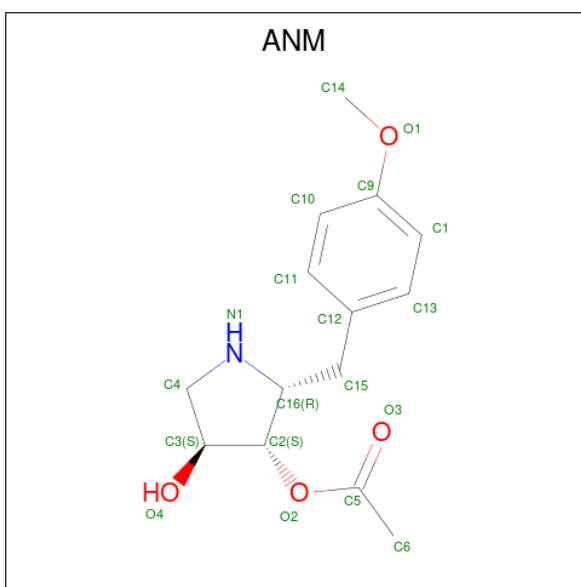
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
87	XA	1	Total 1	Mg 1	0
87	ZA	18	Total 18	Mg 18	0
87	AC	1	Total 1	Mg 1	0

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

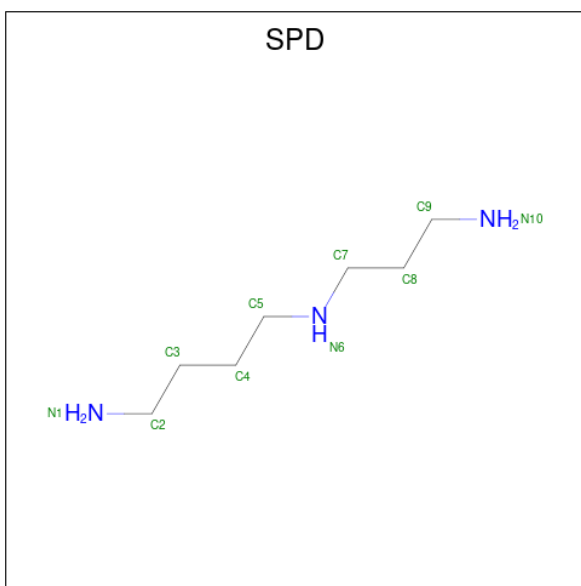
Mol	Chain	Residues	Atoms		AltConf
88	FA	1	Total 1	Zn 1	0
88	IA	1	Total 1	Zn 1	0
88	LA	1	Total 1	Zn 1	0
88	NA	1	Total 1	Zn 1	0
88	OA	1	Total 1	Zn 1	0
88	AC	1	Total 1	Zn 1	0
88	DC	1	Total 1	Zn 1	0
88	FC	1	Total 1	Zn 1	0

- Molecule 89 is ANISOMYCIN (CCD ID: ANM) (formula: C₁₄H₁₉NO₄).



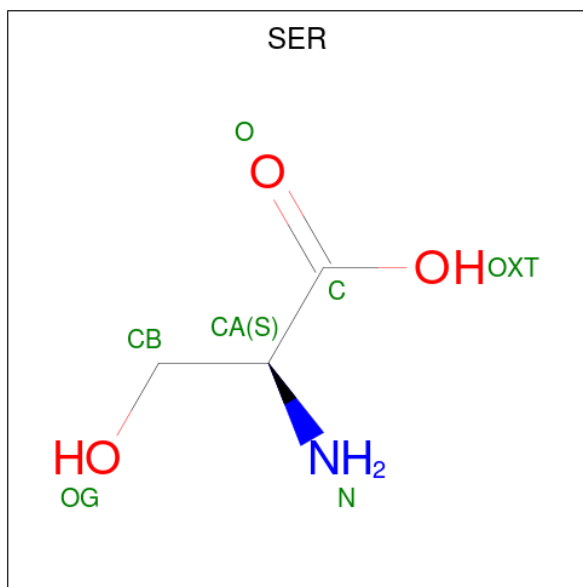
Mol	Chain	Residues	Atoms				AltConf
89	WA	1	Total	C	N	O	0
			19	14	1	4	

- Molecule 90 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			AltConf
90	WA	1	Total	C	N	0
			10	7	3	

- Molecule 91 is SERINE (CCD ID: SER) (formula: $C_3H_7NO_3$).

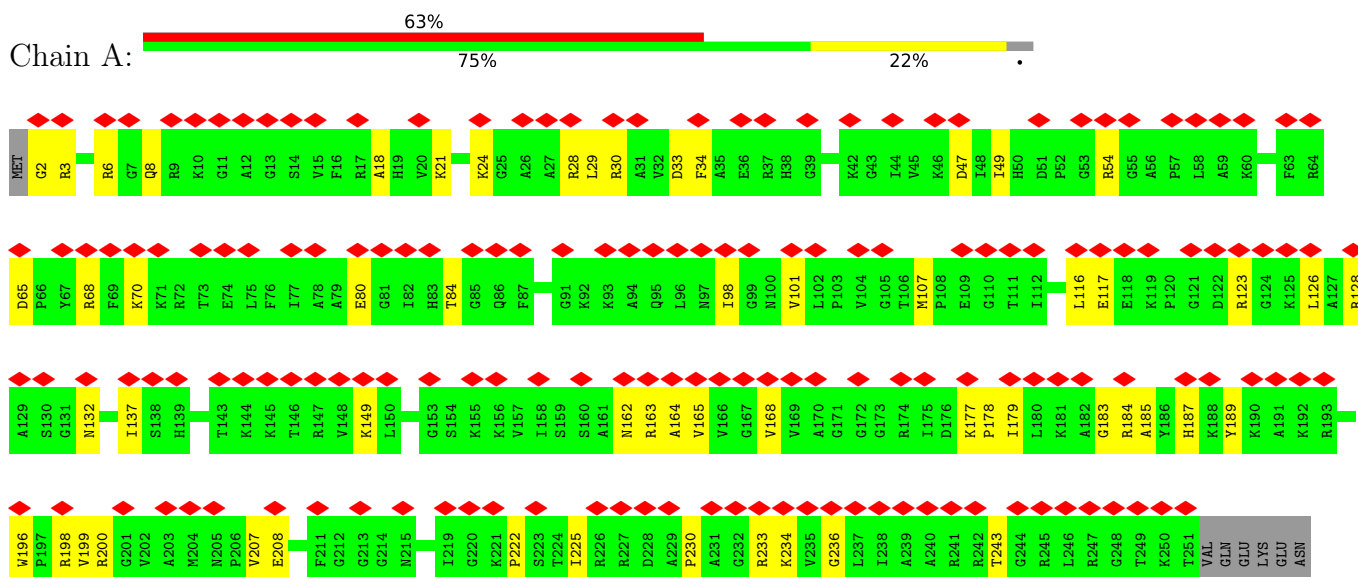


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
91	ZA	1	6	3	1	2	0

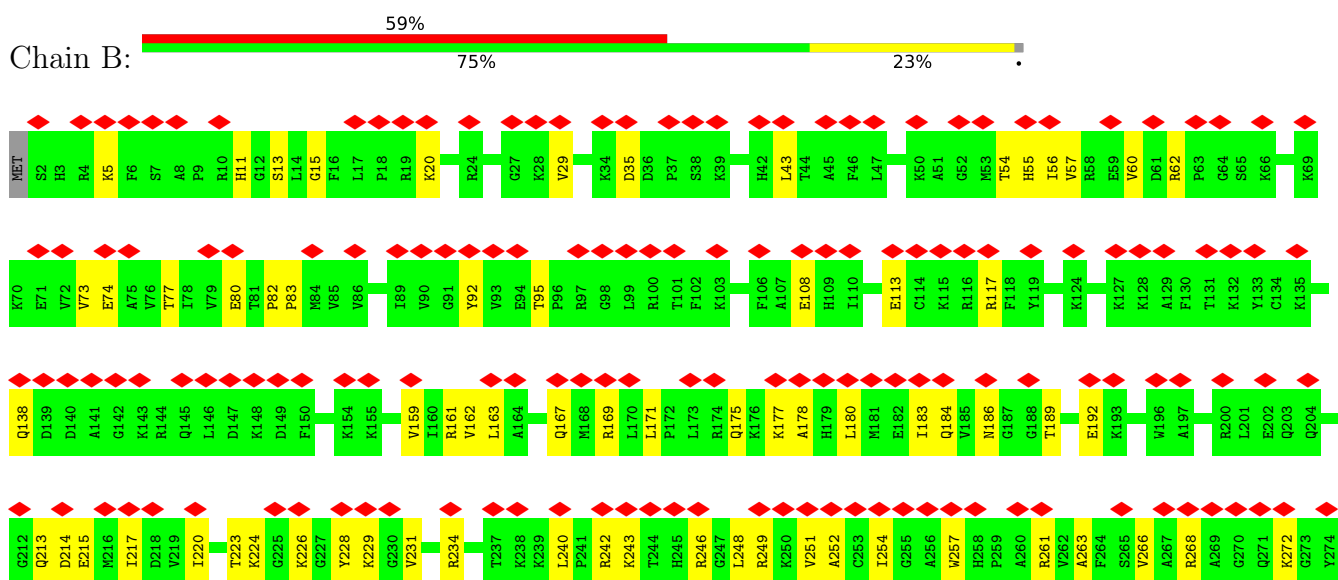
3 Residue-property plots

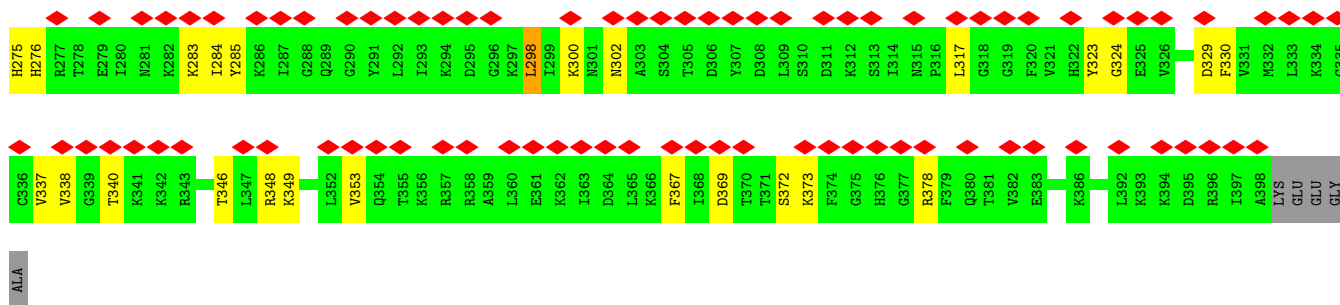
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: uL2

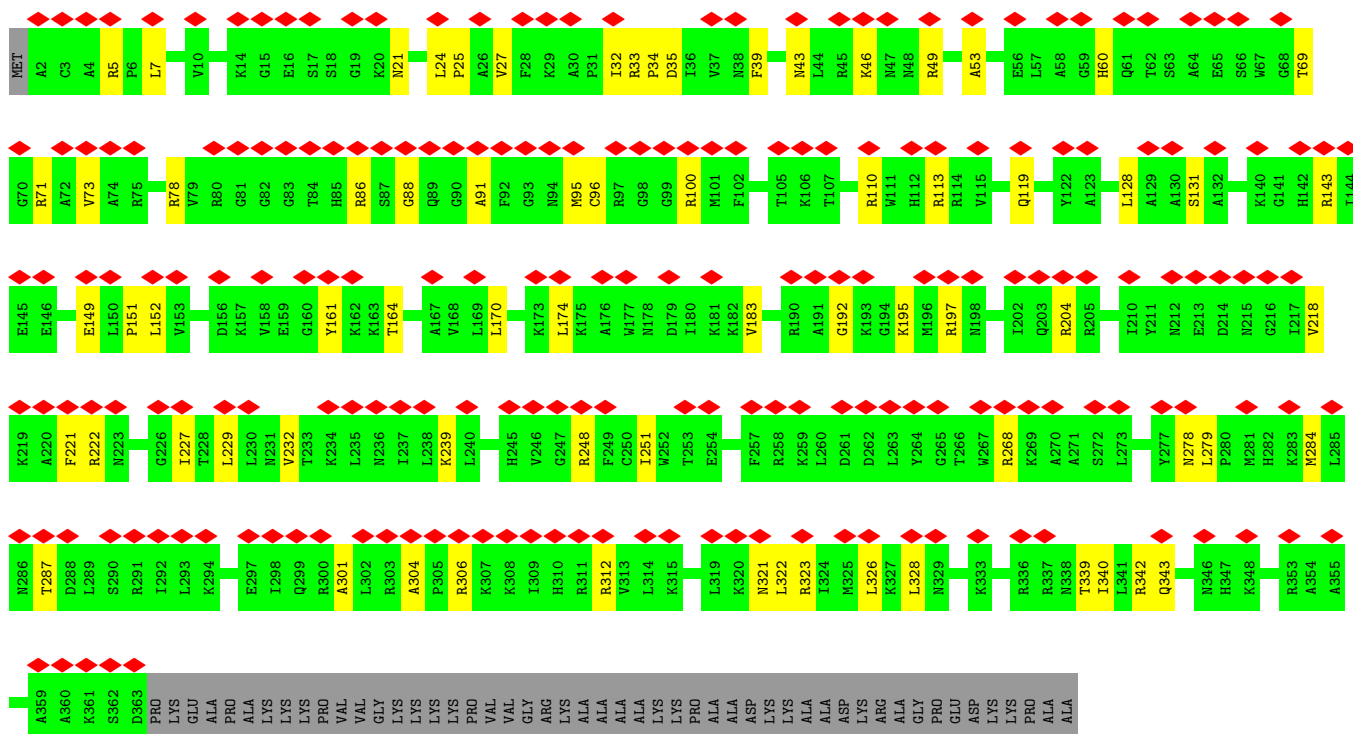


• Molecule 2: uL3

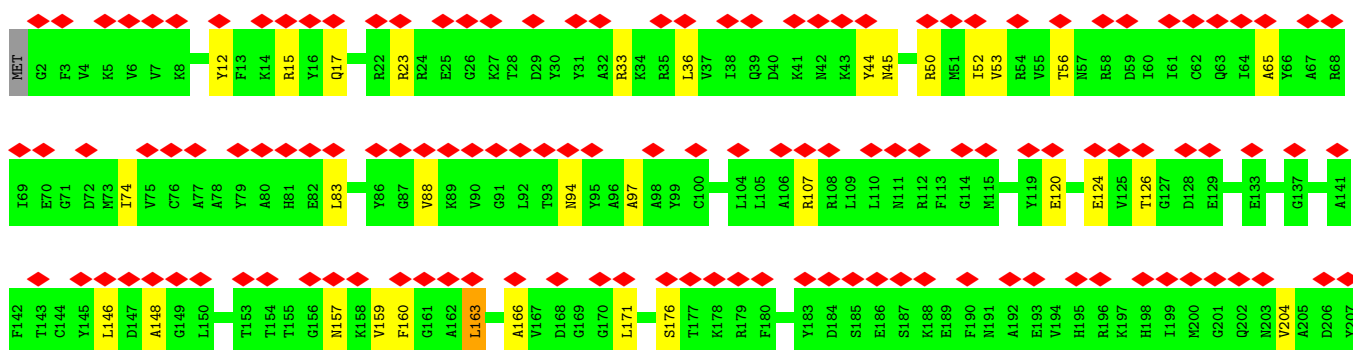
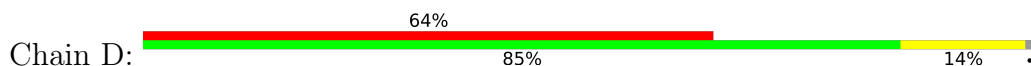




• Molecule 3: uL4

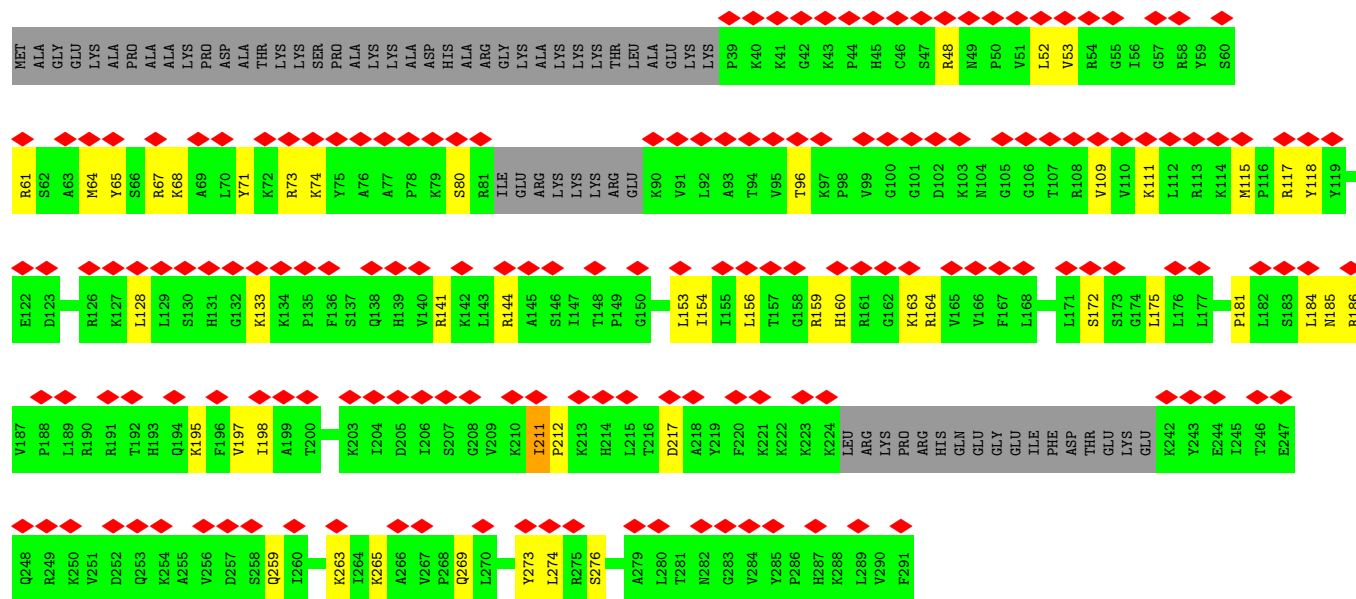


• Molecule 4: uL18

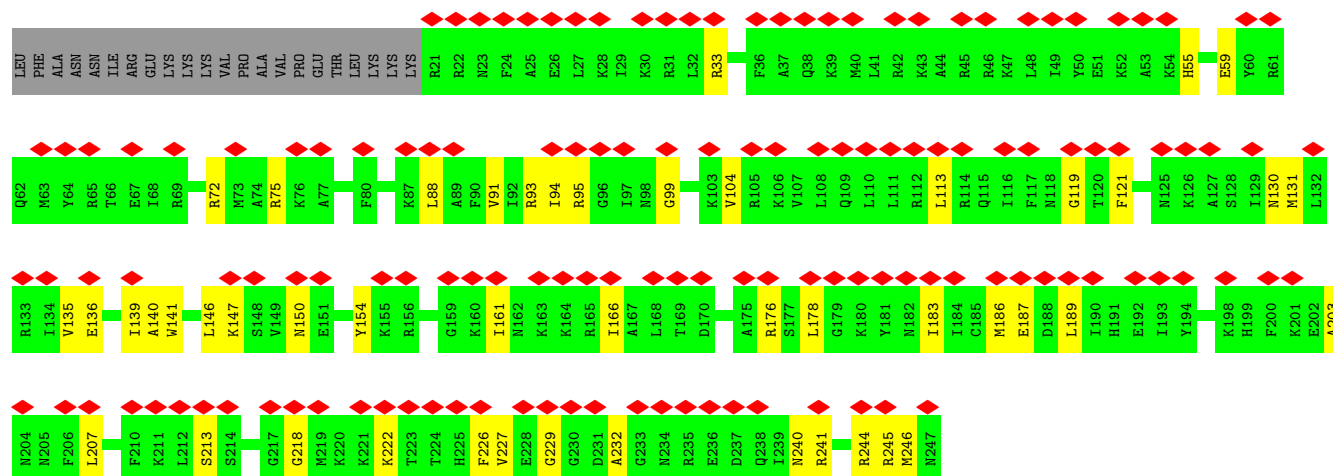
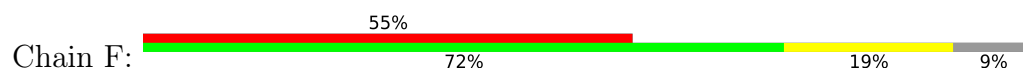




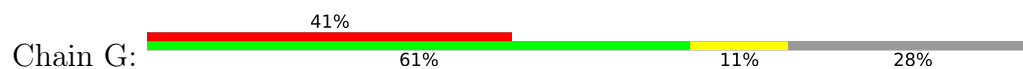
• Molecule 5: L6

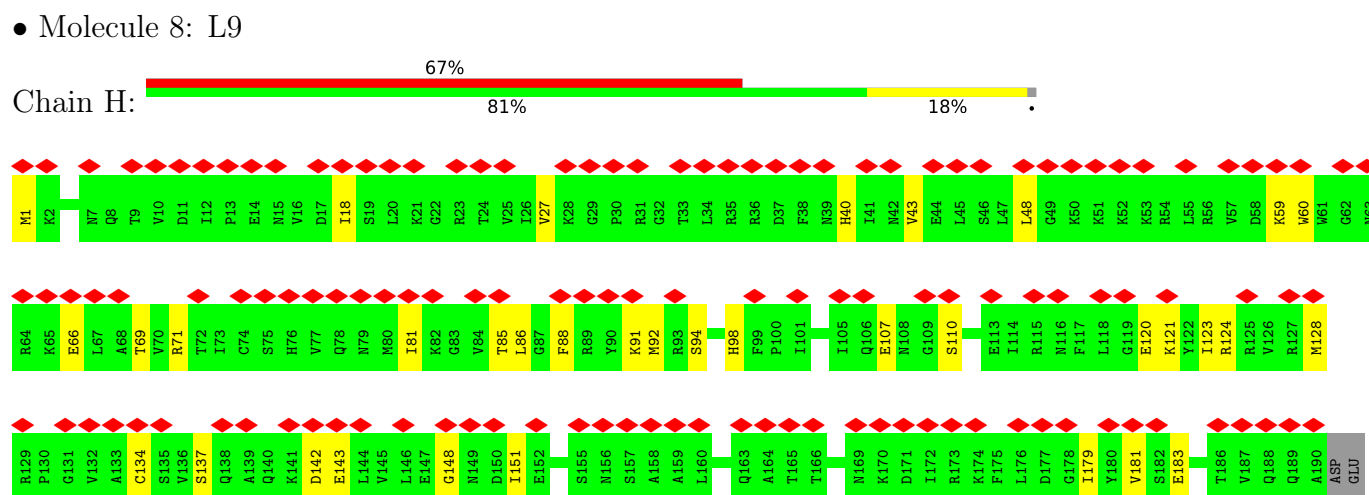


• Molecule 6: uL30



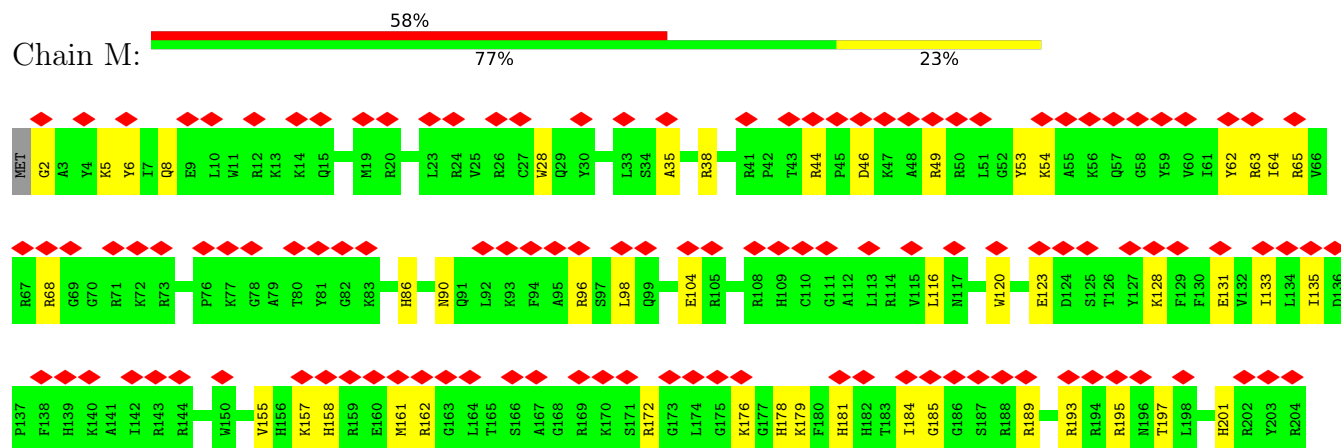
• Molecule 7: L7A



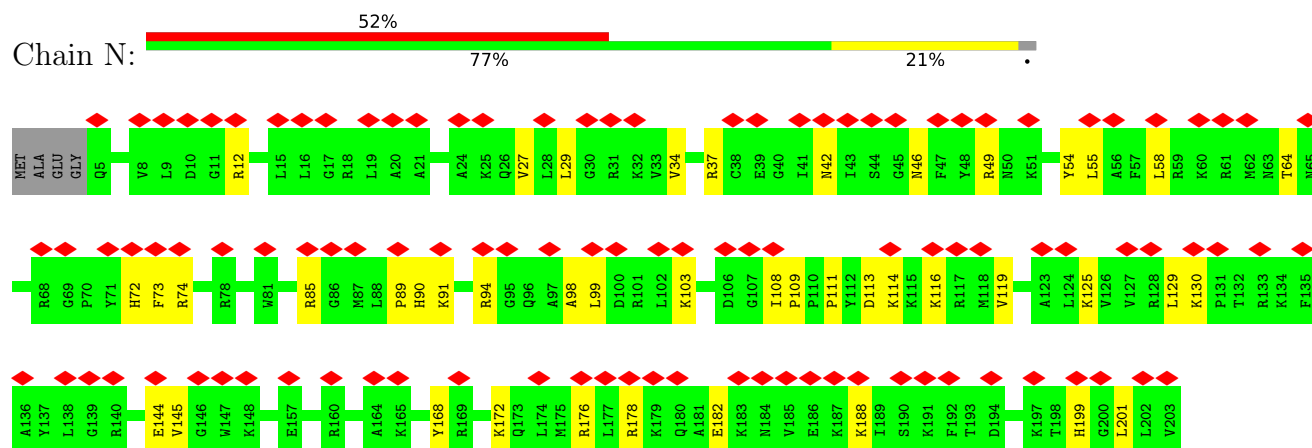


Chain I:

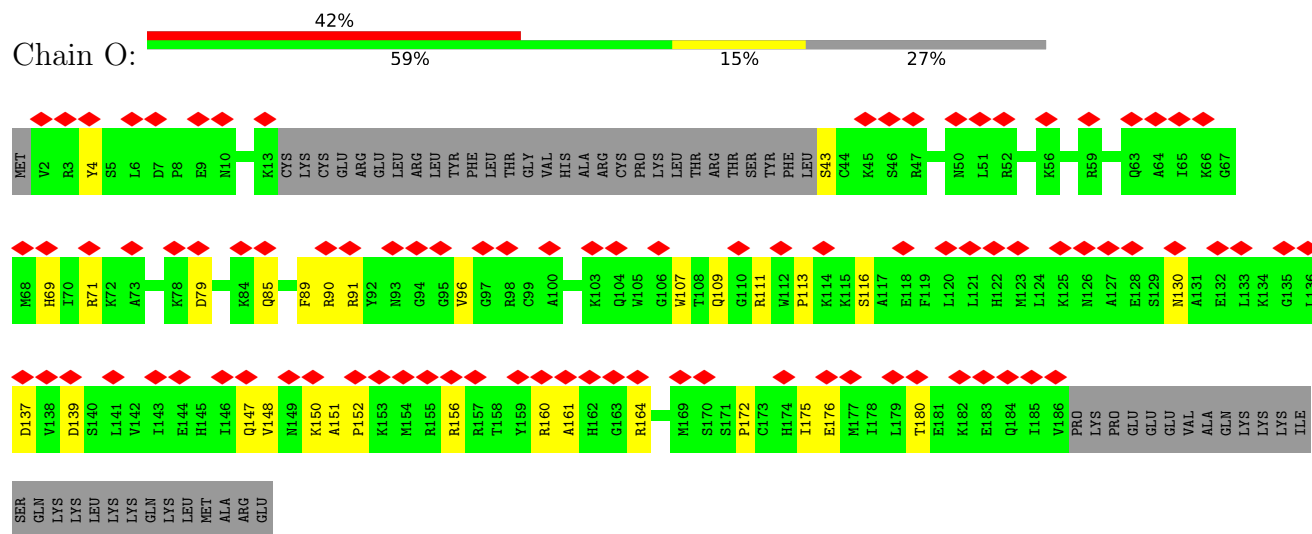
- Molecule 13: L15



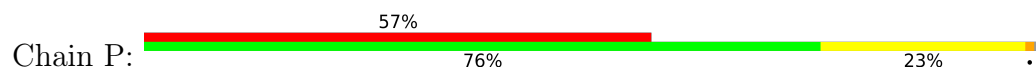
- Molecule 14: uL13

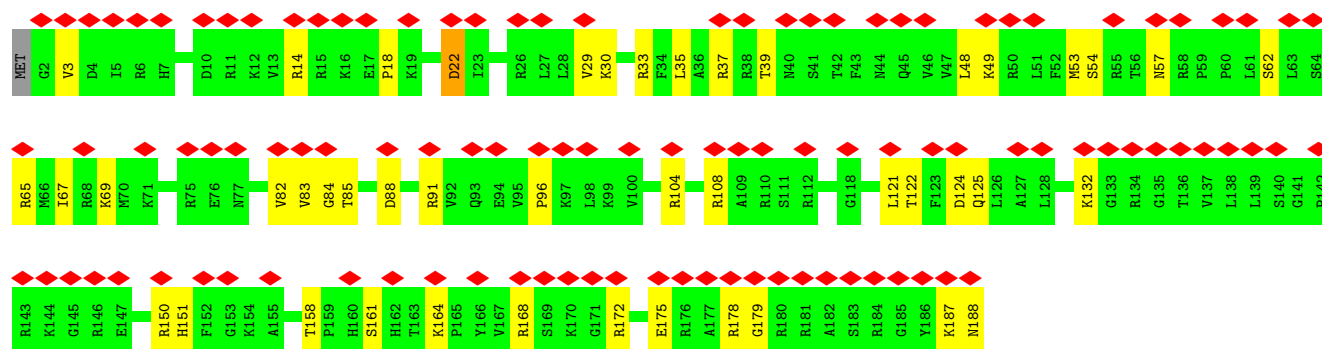


- Molecule 15: uL22

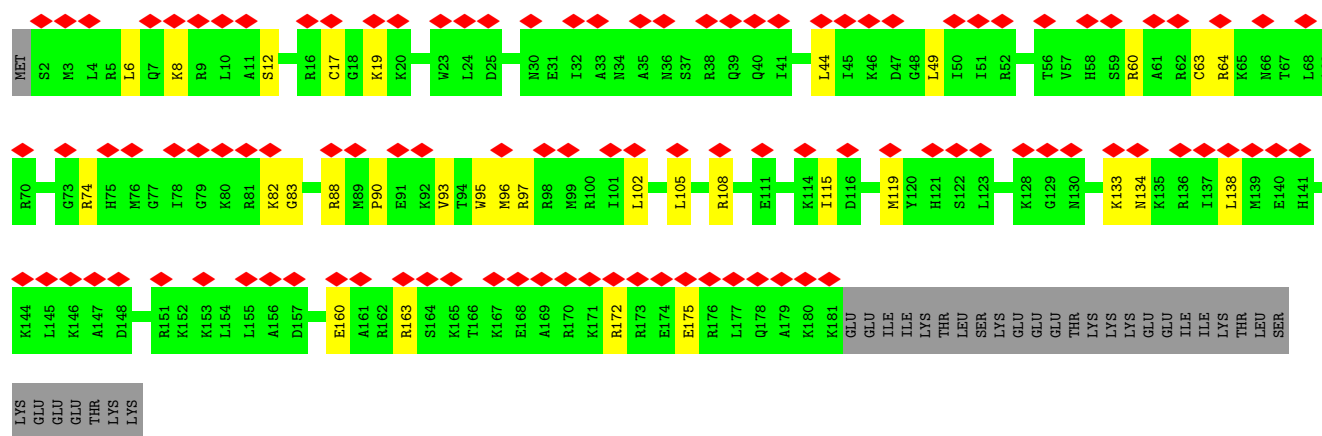


- Molecule 16: eL18

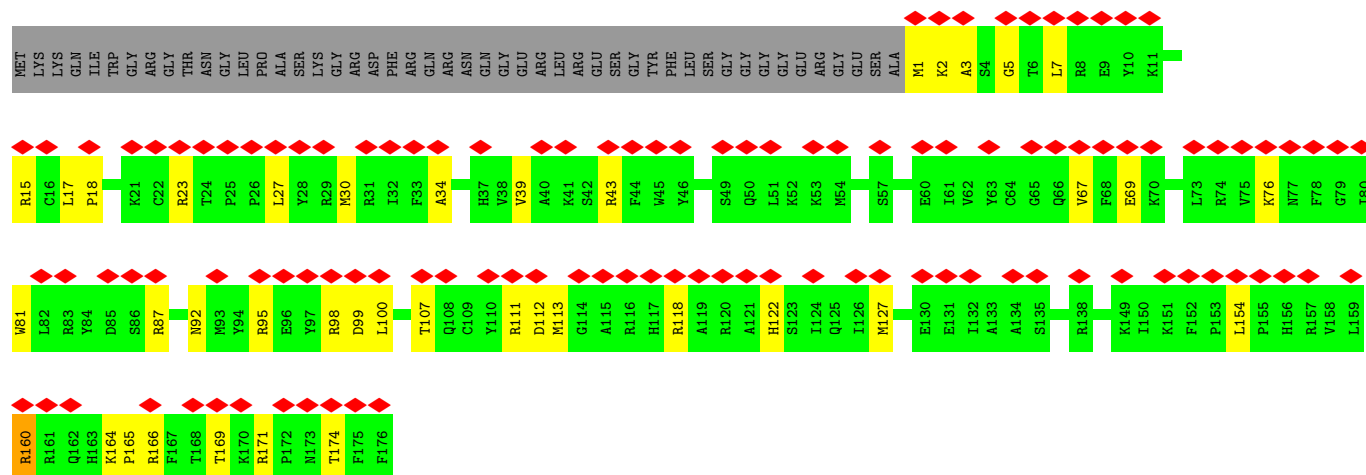




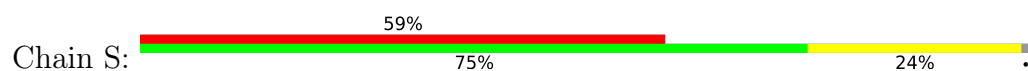
• Molecule 17: eL19

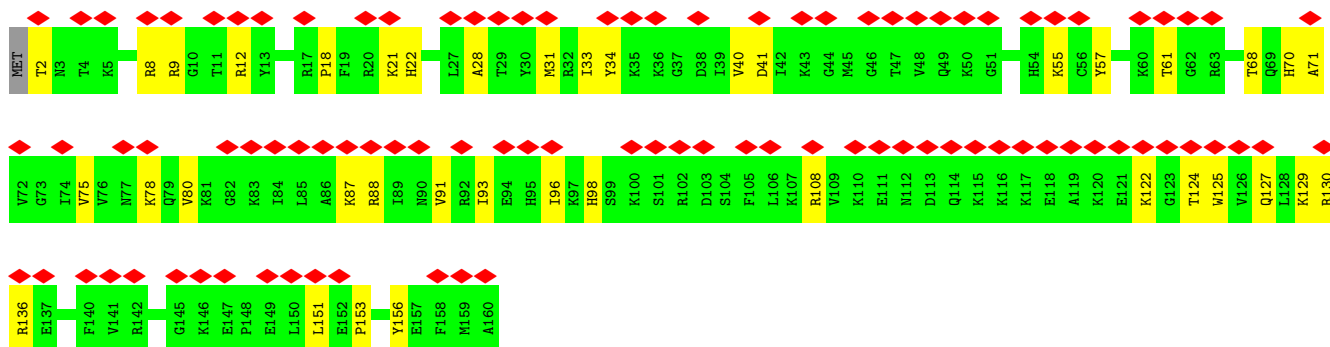


• Molecule 18: L18A

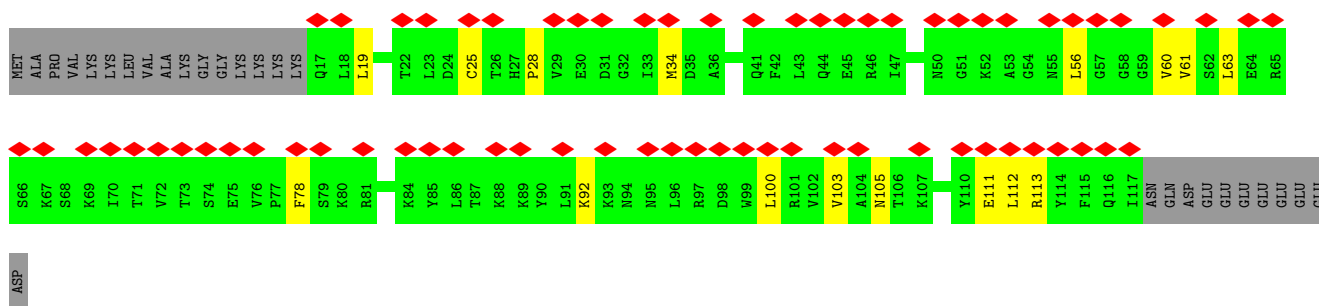


• Molecule 19: eL21

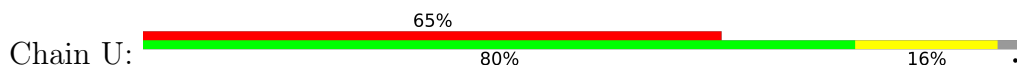




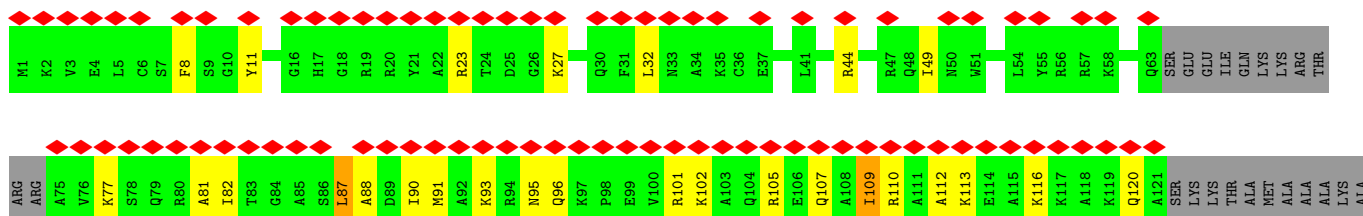
• Molecule 20: eL22



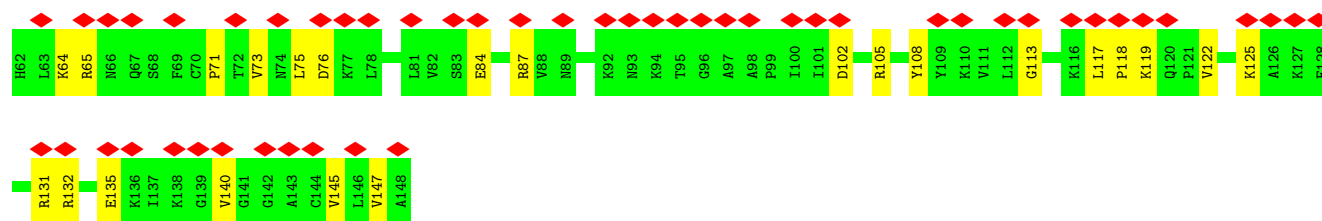
• Molecule 21: L23



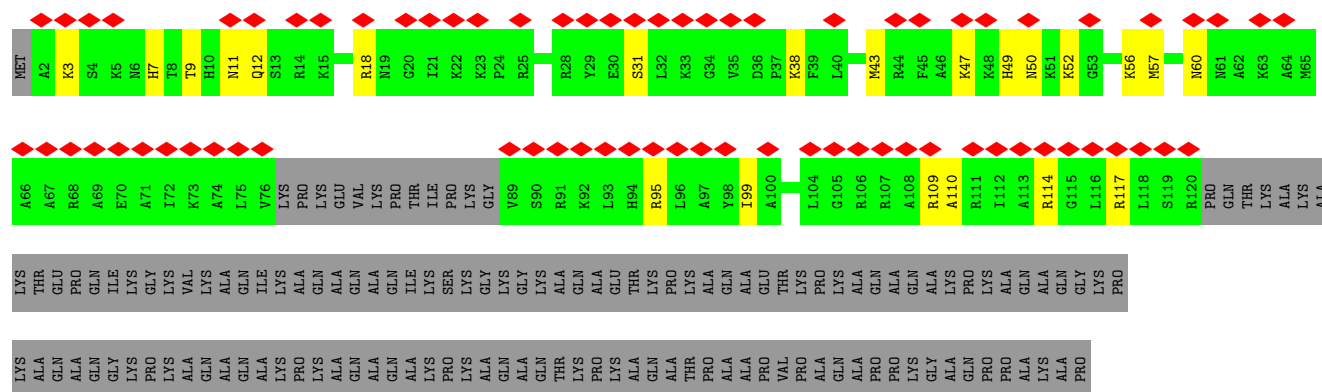
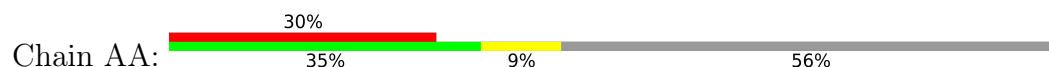
• Molecule 22: uL24



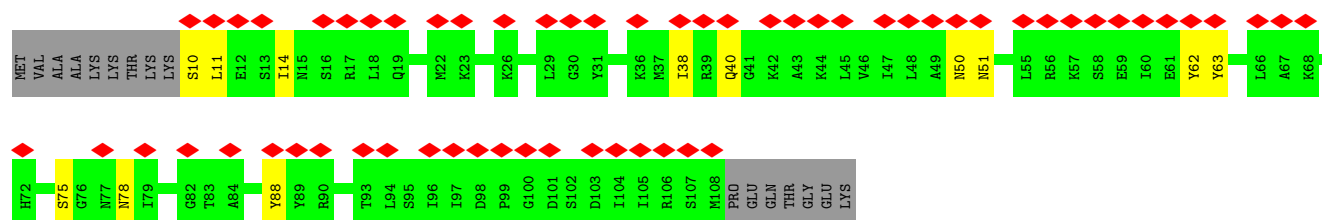
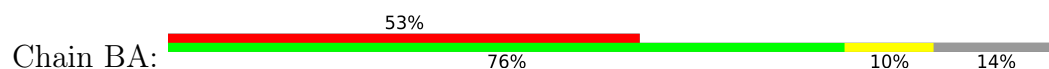
NET	P2	S3	R4	L5	R6	K7	T8	R9	R10	K10	L11	R12	G13	H14	V15	S16	H17	G18	H19	G20	R21	L22	G23	K24	H25	R26	K27	H28	P29	G30	R32	G33	N34	A35	G36	G37	N38	H39	H40	H41	R42	R43	L43	N44	F45	D46	K47	D48	F49	F50	G51	F52	F53	G54	K55	V56	G57	M58	R59	H60	V61	G62	R63	G64	R65	G66	R67	G68	R69	G70	R71	G72	R73	G74	R75	G76	R77	G78	R79	G80	R81	G82	R83	G84	R85	G86	R87	G88	R89	G90	R91	G92	R93	G94	R95	G96	R97	G98	R99	G100	R101	G102	R103	G104	R105	G106	R107	G108	R109	G110	R111	G112	R113	G114	R115	G116	R117	G118	R119	G120	R121	G122	R123	G124	R125	G126	R127	G128	R129	G130	R131	G132	R133	G134	R135	G136	R137	G138	R139	G140	R141	G142	R143	G144	R145	G146	R147	G148	R149	G150	R151	G152	R153	G154	R155	G156	R157	G158	R159	G160	R161	G162	R163	G164	R165	G166	R167	G168	R169	G170	R171	G172	R173	G174	R175	G176	R177	G178	R179	G180	R181	G182	R183	G184	R185	G186	R187	G188	R189	G190	R191	G192	R193	G194	R195	G196	R197	G198	R199	G200	R201	G202	R203	G204	R205	G206	R207	G208	R209	G210	R211	G212	R213	G214	R215	G216	R217	G218	R219	G220	R221	G222	R223	G224	R225	G226	R227	G228	R229	G230	R231	G232	R233	G234	R235	G236	R237	G238	R239	G240	R241	G242	R243	G244	R245	G246	R247	G248	R249	G250	R251	G252	R253	G254	R255	G256	R257	G258	R259	G260	R261	G262	R263	G264	R265	G266	R267	G268	R269	G270	R271	G272	R273	G274	R275	G276	R277	G278	R279	G280	R281	G282	R283	G284	R285	G286	R287	G288	R289	G290	R291	G292	R293	G294	R295	G296	R297	G298	R299	G300	R301	G302	R303	G304	R305	G306	R307	G308	R309	G310	R311	G312	R313	G314	R315	G316	R317	G318	R319	G320	R321	G322	R323	G324	R325	G326	R327	G328	R329	G330	R331	G332	R333	G334	R335	G336	R337	G338	R339	G340	R341	G342	R343	G344	R345	G346	R347	G348	R349	G350	R351	G352	R353	G354	R355	G356	R357	G358	R359	G360	R361	G362	R363	G364	R365	G366	R367	G368	R369	G370	R371	G372	R373	G374	R375	G376	R377	G378	R379	G380	R381	G382	R383	G384	R385	G386	R387	G388	R389	G390	R391	G392	R393	G394	R395	G396	R397	G398	R399	G400	R401	G402	R403	G404	R405	G406	R407	G408	R409	G410	R411	G412	R413	G414	R415	G416	R417	G418	R419	G420	R421	G422	R423	G424	R425	G426	R427	G428	R429	G430	R431	G432	R433	G434	R435	G436	R437	G438	R439	G440	R441	G442	R443	G444	R445	G446	R447	G448	R449	G450	R451	G452	R453	G454	R455	G456	R457	G458	R459	G460	R461	G462	R463	G464	R465	G466	R467	G468	R469	G470	R471	G472	R473	G474	R475	G476	R477	G478	R479	G480	R481	G482	R483	G484	R485	G486	R487	G488	R489	G490	R491	G492	R493	G494	R495	G496	R497	G498	R499	G500	R501	G502	R503	G504	R505	G506	R507	G508	R509	G510	R511	G512	R513	G514	R515	G516	R517	G518	R519	G520	R521	G522	R523	G52
-----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----



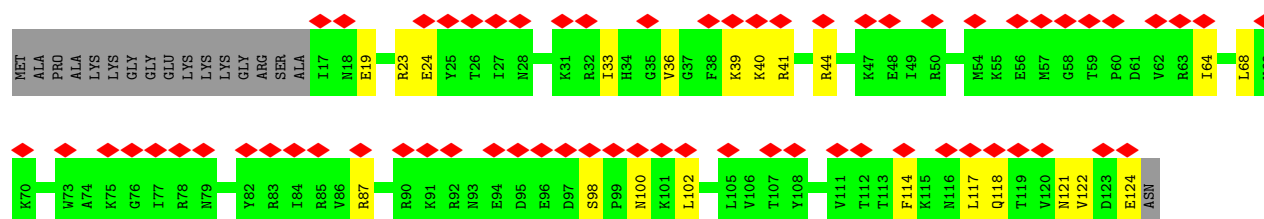
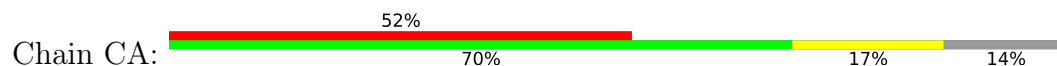
• Molecule 27: L29



• Molecule 28: eL30

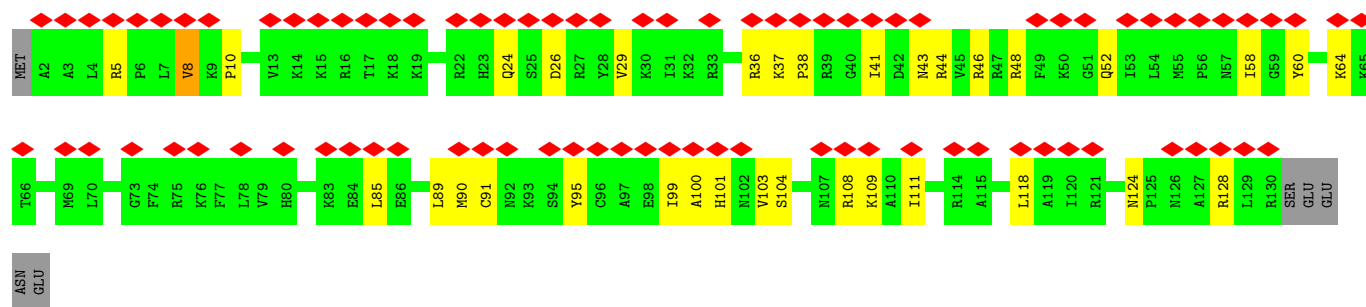


• Molecule 29: L31

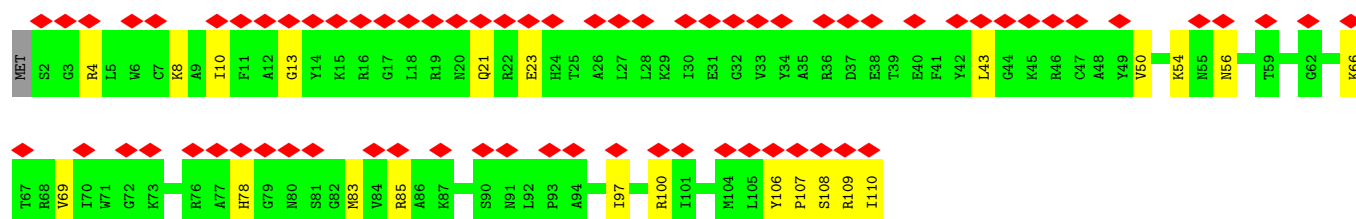
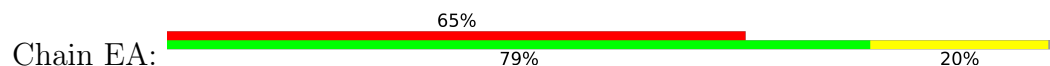


• Molecule 30: L32

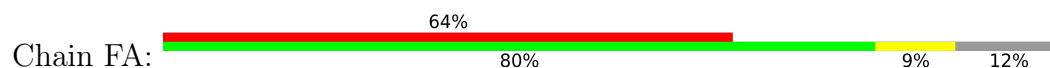




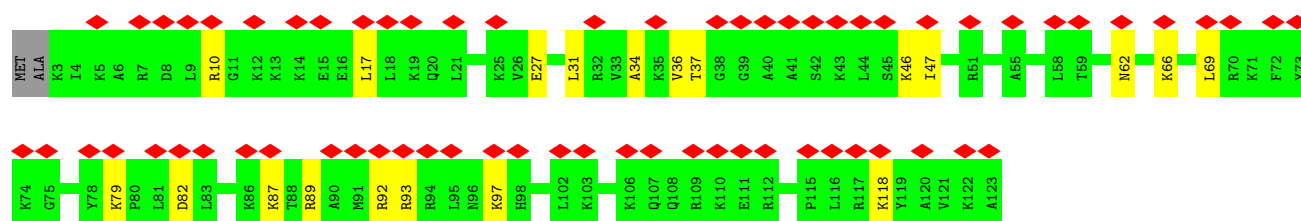
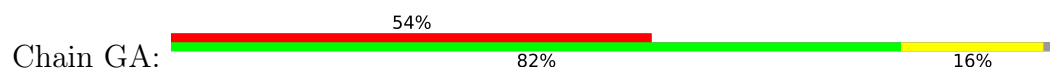
• Molecule 31: eL33



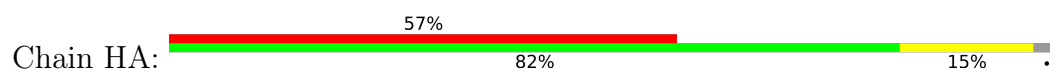
• Molecule 32: L34

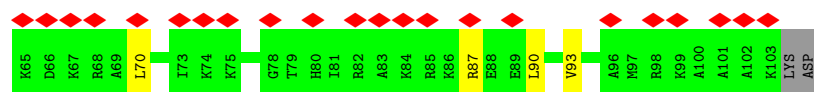


• Molecule 33: L35

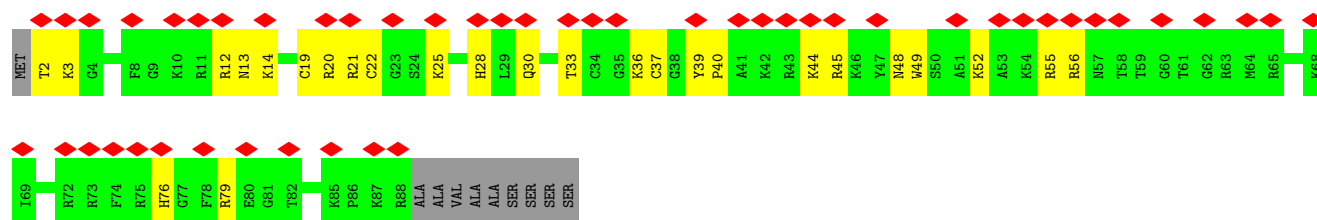


• Molecule 34: L36

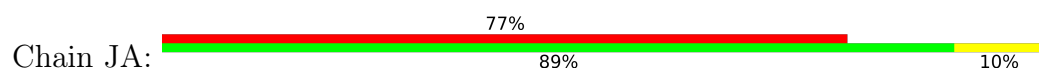




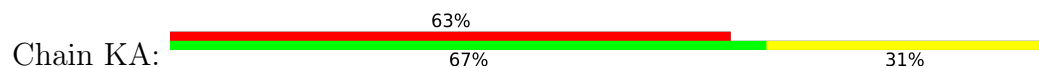
• Molecule 35: L37



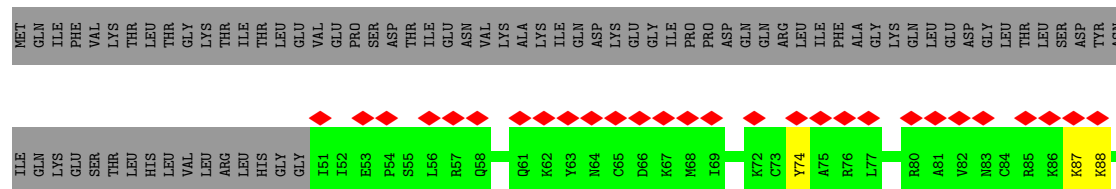
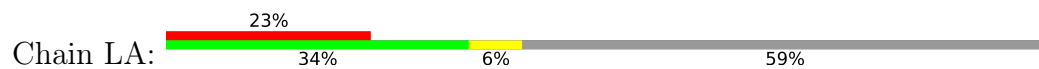
• Molecule 36: eL38



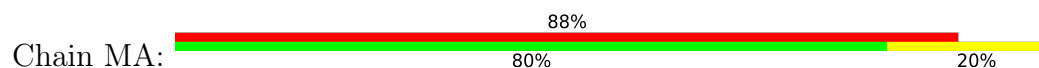
• Molecule 37: eL39



• Molecule 38: eL40

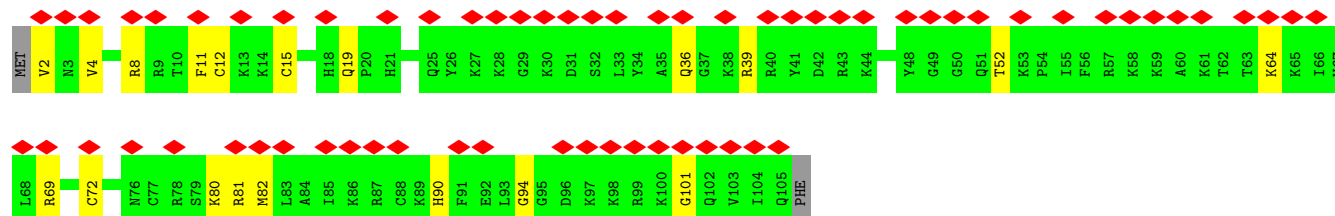
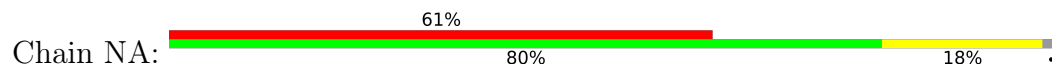


• Molecule 39: eL41

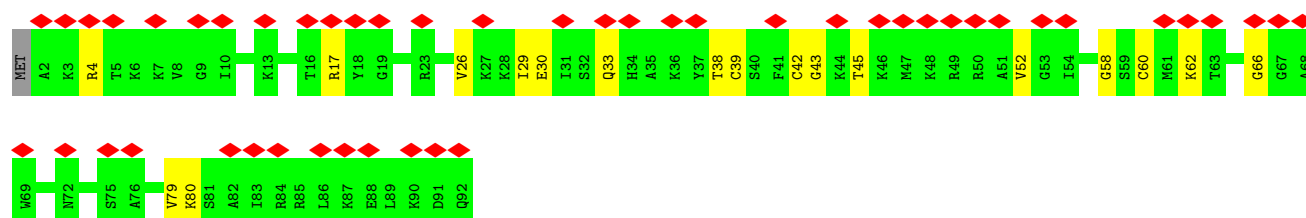
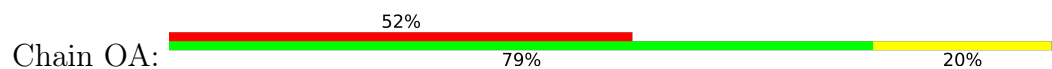




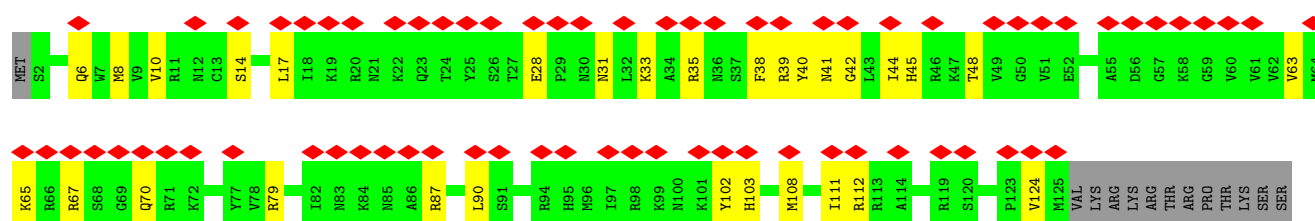
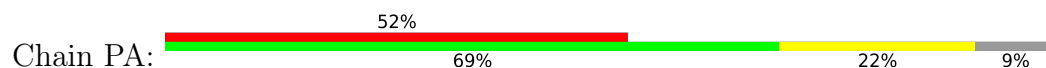
• Molecule 40: eL42



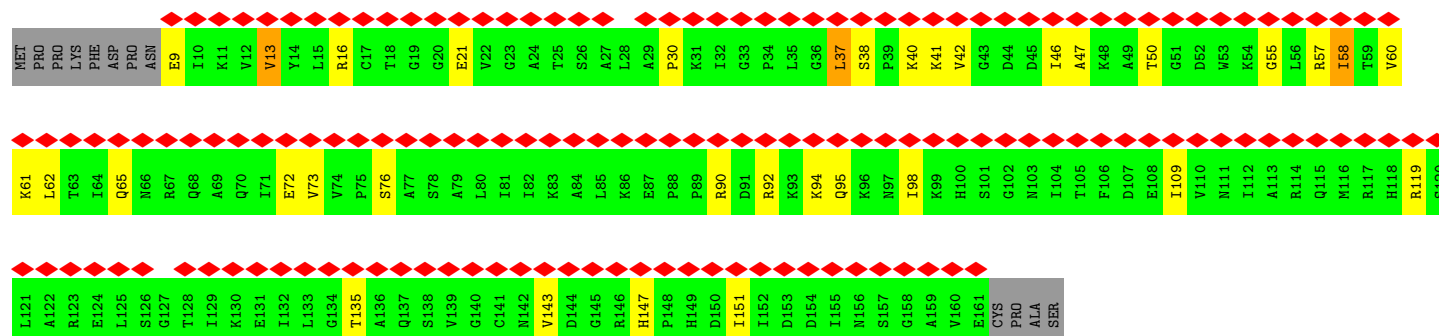
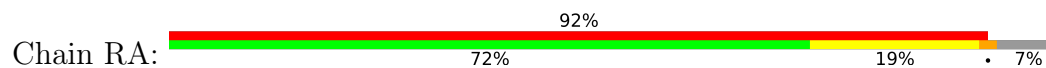
• Molecule 41: eL43



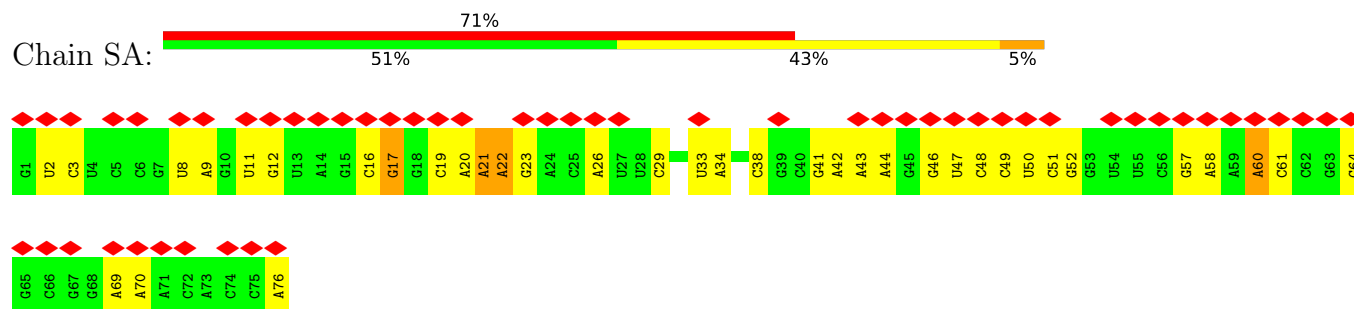
• Molecule 42: L28



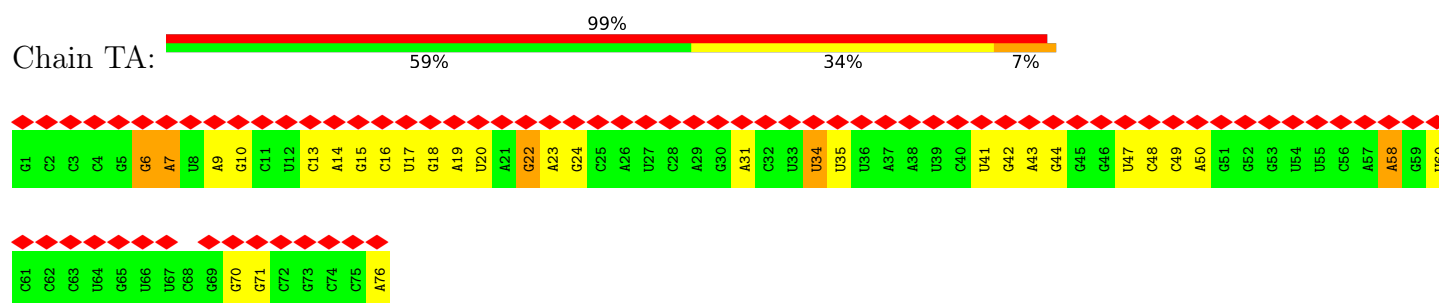
• Molecule 43: L12



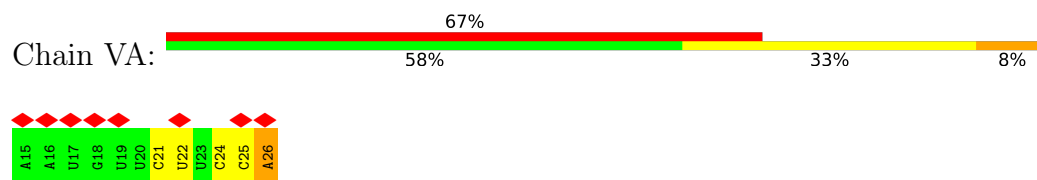
• Molecule 44: P-site tRNA



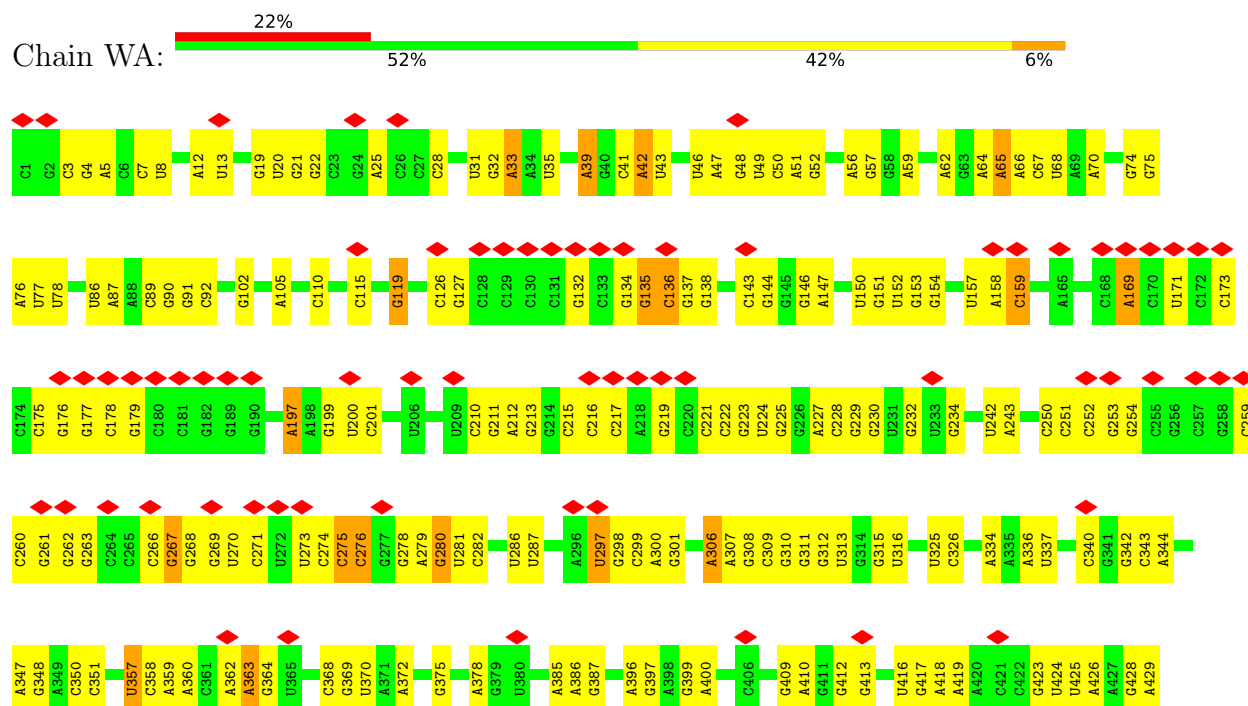
• Molecule 45: E-site tRNA

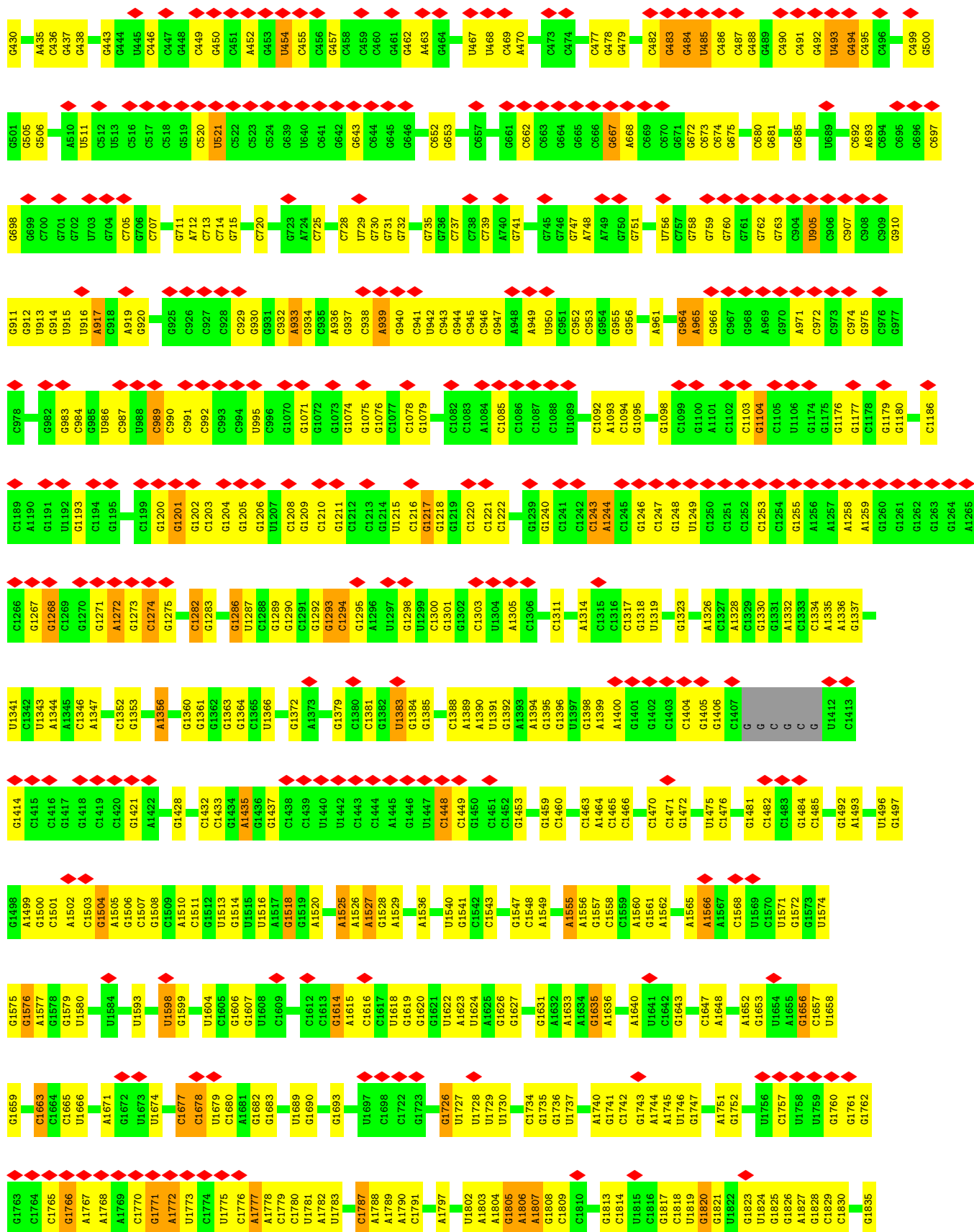


• Molecule 46: mRNA

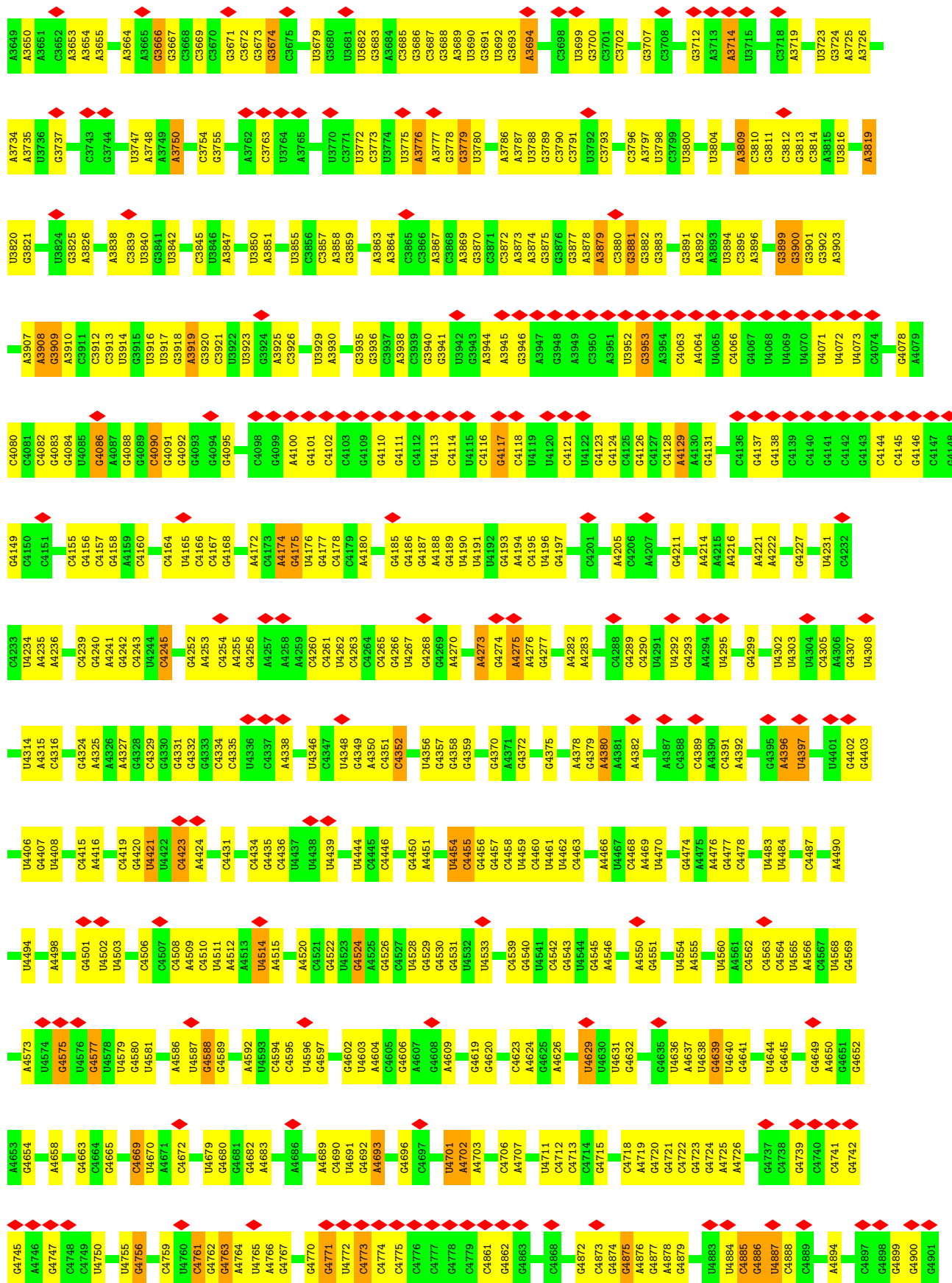


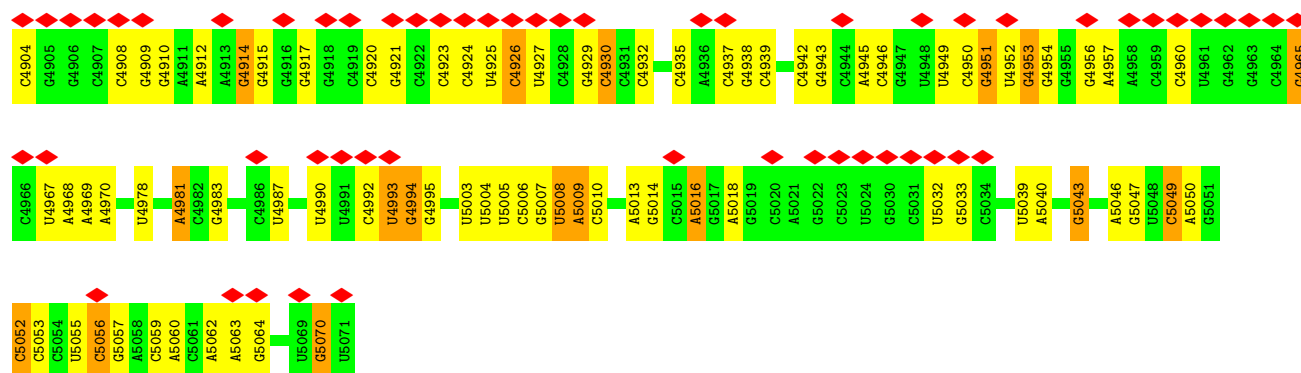
• Molecule 47: 28S rRNA



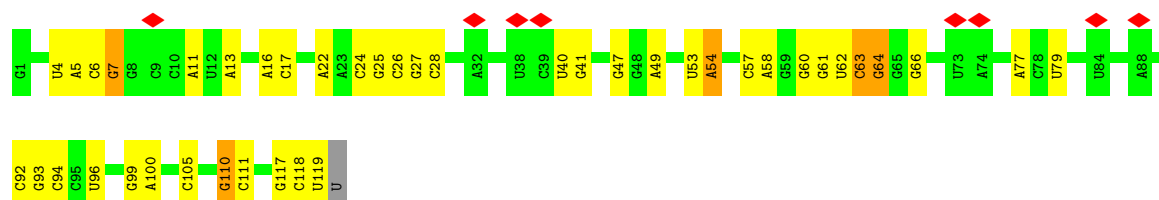


G2865	G2869	G2870	U2871	U2876	G2879	G2880	A2881	U2882	A2883	G2886	U2889	U2893	G2899	G2900	G2901	U2902	G2903	G2904	A3598	G3599	G3600	A3601	G3602	G3605	A3606	G3607	U3608	U3609	A3610	G3611	A3612	A3613	G3617	U3618	G3619	G3625	A3626	G3627	G3628	G3635	G3636	A3637	U3643	A3644	U3647	A3648											
G2778	G2779	G2780	G2786	G2787	G2788	A2789	U2790	A2791	U2792	G2793	G2796	A2797	G2798	G2799	A2800	G2807	A2808	G2813	A2814	A2815	G2816	G2819	A2827	U2828	G2829	U2830	G2831	G2832	G2833	A2834	A2835	U2836	A2837	U2838	U2839	G2840	G2844	U2845	A2846	A2847	G2850	A2851	G2857	G2858	A2859	A2860	G2861	G2862	G2863	G2864							
G2704	G2705	G2708	G2709	U2710	G2711	G2712	G2713	G2714	G2715	G2716	G2721	G2722	G2723	G2724	U2725	G2726	A2727	G2728	U2729	U2730	G2731	U2732	G2733	G2734	G2737	G2738	G2739	G2740	U2741	U2742	U2743	G2744	A2745	A2746	G2751	G2752	G2753	G2754	G2755	G2756	A2759	G2760	G2761	G2762	U2763	G2764	U2765	A2766	A2767	A2768	U2771	G2777					
U2633	U2634	U2635	G2636	G2640	U2641	G2642	A2643	A2644	G2645	A2649	G2650	G2651	G2654	G2655	G2656	G2657	U2658	G2659	A2660	A2661	A2662	U2663	G2664	G2669	G2670	G2671	G2673	G2674	G2677	A2678	G2679	G2682	G2683	G2684	G2685	G2686	G2687	G2688	U2689	G2690	G2691	U2692	U2693	U2694	G2695	G2696	A2697	A2698	A2699	G2700	G2701	U2627	U2702	G2703			
A2555	U2556	G2557	G2558	G2559	G2560	G2561	G2562	G2563	G2564	G2565	G2566	A2567	G2568	G2569	G2570	G2571	U2572	A2575	G2576	U2577	G2580	G2581	U2582	A2583	A2584	G2585	G2588	A2589	G2590	G2591	G2592	G2599	A2600	G2601	A2602	A2603	G2607	G2608	G2611	G2612	G2617	G2618	G2619	G2622	A2625	G2626	U2627	U2628	G2629								
G2483	G2484	G2485	A2486	U2487	G2488	G2489	A2490	G2491	U2492	G2493	G2494	G2495	U2496	U2497	G2498	A2499	G2500	G2501	U2502	G2503	A2504	G2505	G2506	G2507	G2508	A2509	A2514	A2515	G2516	G2517	G2518	A2519	G2520	U2521	G2522	G2523	G2524	U2527	G2528	A2529	G2530	A2531	U2532	A2539	U2540	G2541	G2542	G2543	G2544	A2545	G2546	U2547	G2548	G2549	G2554		
G2407	G2408	G2409	U2410	U2411	G2412	G2413	A2414	U2415	G2416	U2417	G2418	A2419	G2420	G2421	A2422	G2423	A2430	A2431	G2432	G2435	G2436	G2443	G2444	G2445	U2449	G2450	A2451	G2452	A2453	G2454	G2459	G2460	G2461	G2464	G2467	G2468	U2469	U2470	G2471	G2472	G2476	G2477	G2478	A2479	G2480	G2481	G2482										
C2327	G2328	G2329	G2330	U2331	G2332	G2333	A2334	G2335	C2336	C2337	G2338	C2342	A2343	U2346	G2347	G2348	A2349	G2350	A2351	U2352	G2353	U2354	A2362	G2363	U2364	A2365	U2371	A2372	U2373	U2374	C2375	A2376	A2377	A2378	C2379	G2380	A2383	A2384	G2385	U2386	U2387	U2388	G2389	A2390	A2391	G2392	G2396	A2397	U2398	G2399	G2402						
A2109	G2110	A2111	G2112	U2113	G2114	G2115	A2116	G2117	G2118	G2260	G2261	G2262	A2265	G2266	G2267	G2268	U2269	A2270	G2277	A2278	G2279	G2280	A2281	G2285	G2286	A2287	G2288	G2291	G2297	G2298	A2302	G2303	G2304	G2305	G2308	A2309	A2310	G2311	G2312	G2313	U2314	A2315	G2316	G2317	G2318	G2319	G2320	G2321	G2322	G2323	G2324						
U2040	G2041	A2042	A2043	G2048	A2049	U2050	G2053	G2054	C2055	U2056	G2057	G2058	A2059	G2060	G2061	G2062	U2063	C2064	G2067	G2068	G2069	G2070	A2071	U2072	A2073	G2077	G2078	C2079	G2080	G2081	U2082	G2083	G2084	G2085	U2086	C2089	U2092	G2093	G2094	G2095	G2096	A2097	G2098	A2099	G2100	G2101	G2102	A2103	G2104	A2105	A2106	A2107	G2108				
G1978	G1979	G1980	A1981	U1982	G1983	G1984	A1985	A1986	G1987	U1988	G1989	G1990	G1991	A1992	A1993	U1994	G1995	G1996	G1997	G1998	U1999	A2000	A2001	G2002	G2003	A2004	G2005	U2006	G2007	U2008	G2009	U2010	A2011	A2012	G2013	A2014	A2015	G2016	U2017	G2018	A2019	G2020	G2021	U2022	G2023	G2026	A2027	A2028	U2029	A2030	A2031	A2032	G2033	U2034	A2035	G2036	G2039
C1915	C1916	C1917	C1918	A1919	U1920	G1921	G1922	G1923	G1924	A1925	C1926	G1927	C1928	U1929	G1930	A1931	U1932	C1933	G1935	A1936	C1937	G1938	C1939	C1940	A1941	G1942	A1943	A1944	A1945	U1949	G1950	U1951	C1952	G1953	U1956	G1957	A1958	U1959	A1960	U1961	A1962	G1963	A1964	C1965	A1966	G1967	C1968	A1969	G1970	G1971	A1972	U1973	G1974	G1975	U1976	G1977	
U1836	G1837	A1838	A1839	G1843	G1844	G1848	G1849	C1850	U1851	A1852	G1853	U1854	G1855	G1856	G1857	U1864	U1865	G1866	G1870	U1871	A1872	A1873	G1874	U1878	G1879	G1880	C1881	G1882	G1883	U1884	G1885	C1886	G1887	A1890	A1893	G1897	A1898	A1899	C1900	G1901	C1902	C1903	G1904	U1908	A1909	G1912	G1913	G1914									

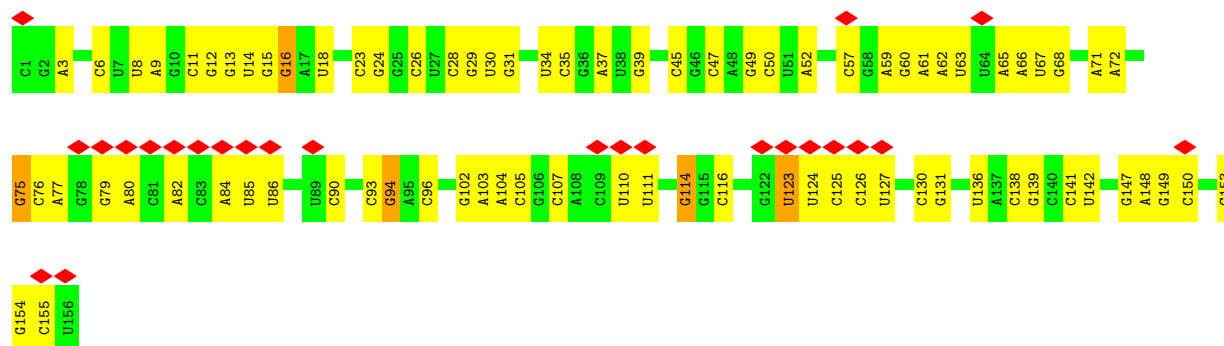




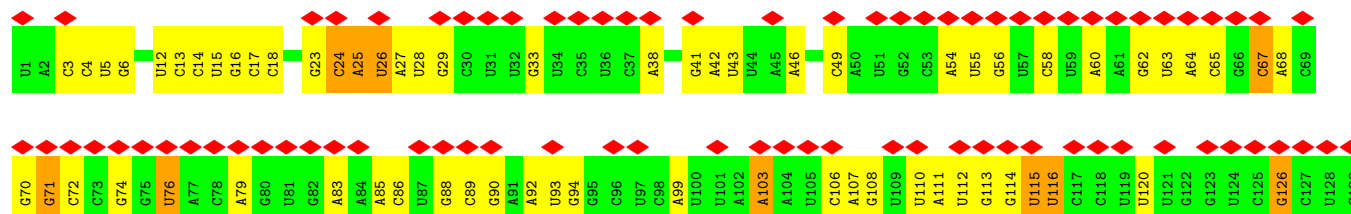
• Molecule 48: 5S rRNA

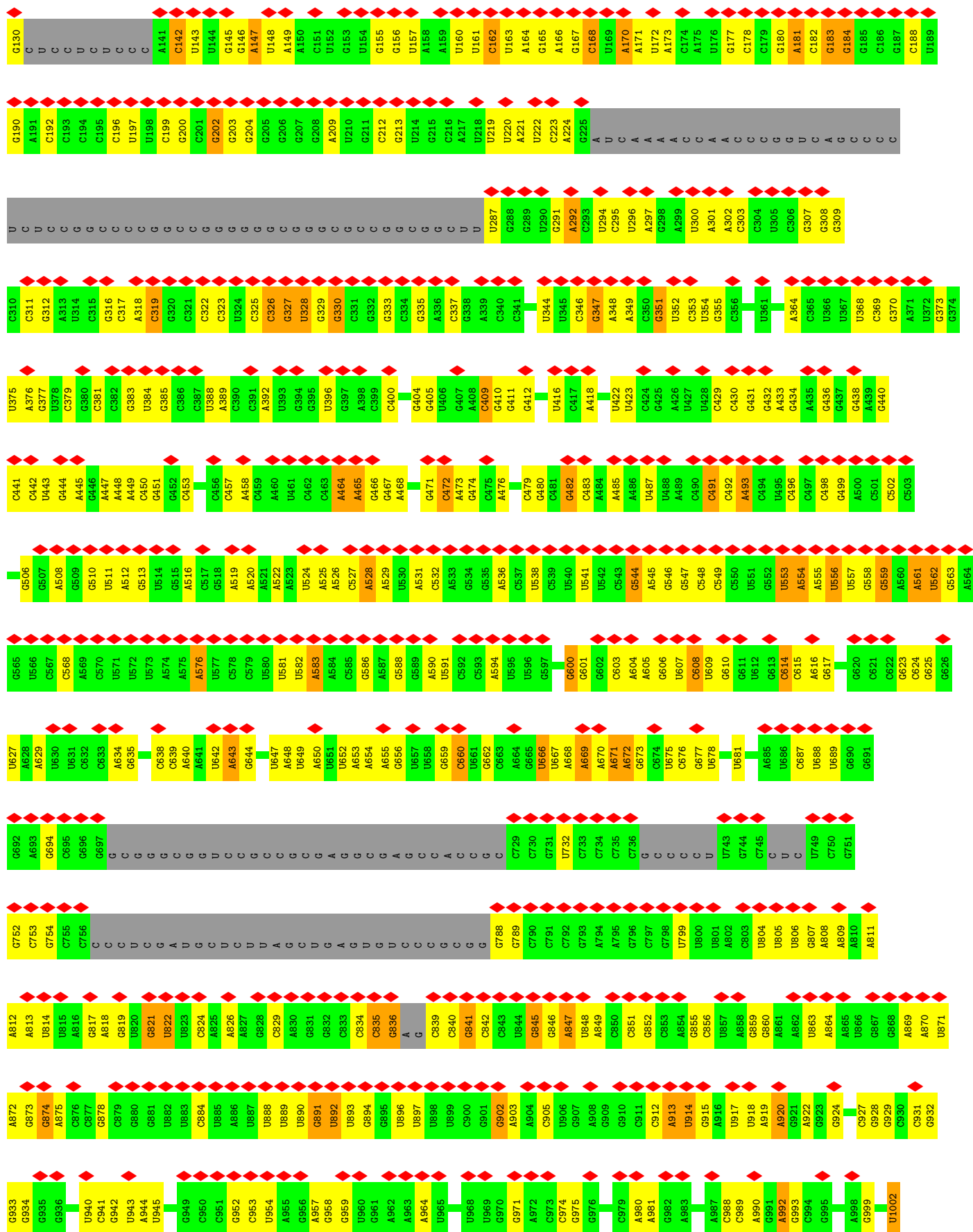


• Molecule 49: 5.8S rRNA

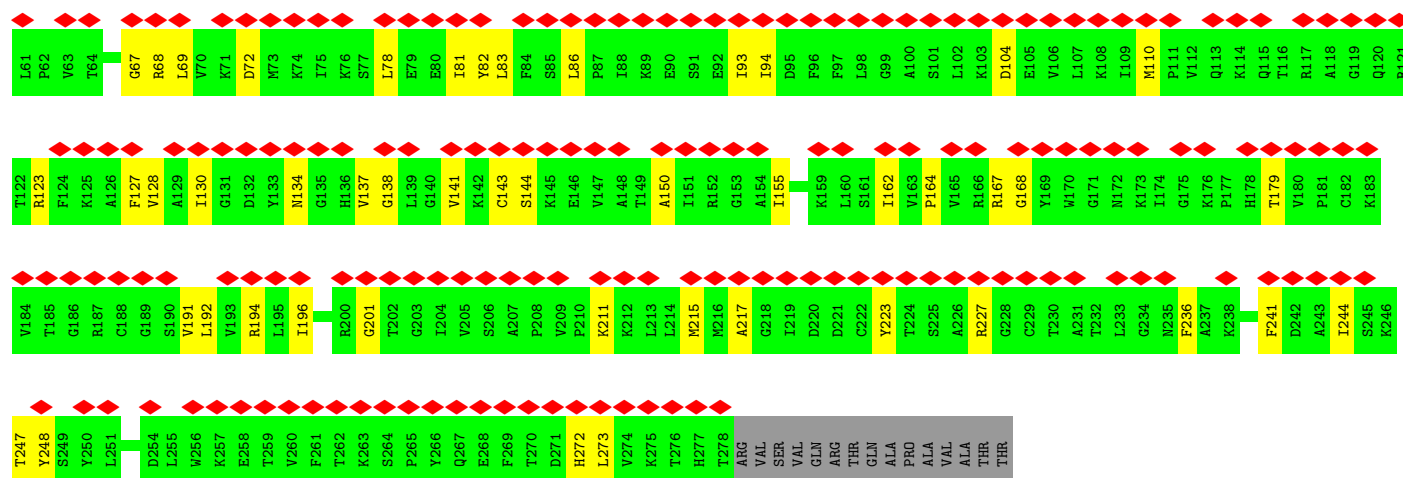


• Molecule 50: 18S rRNA

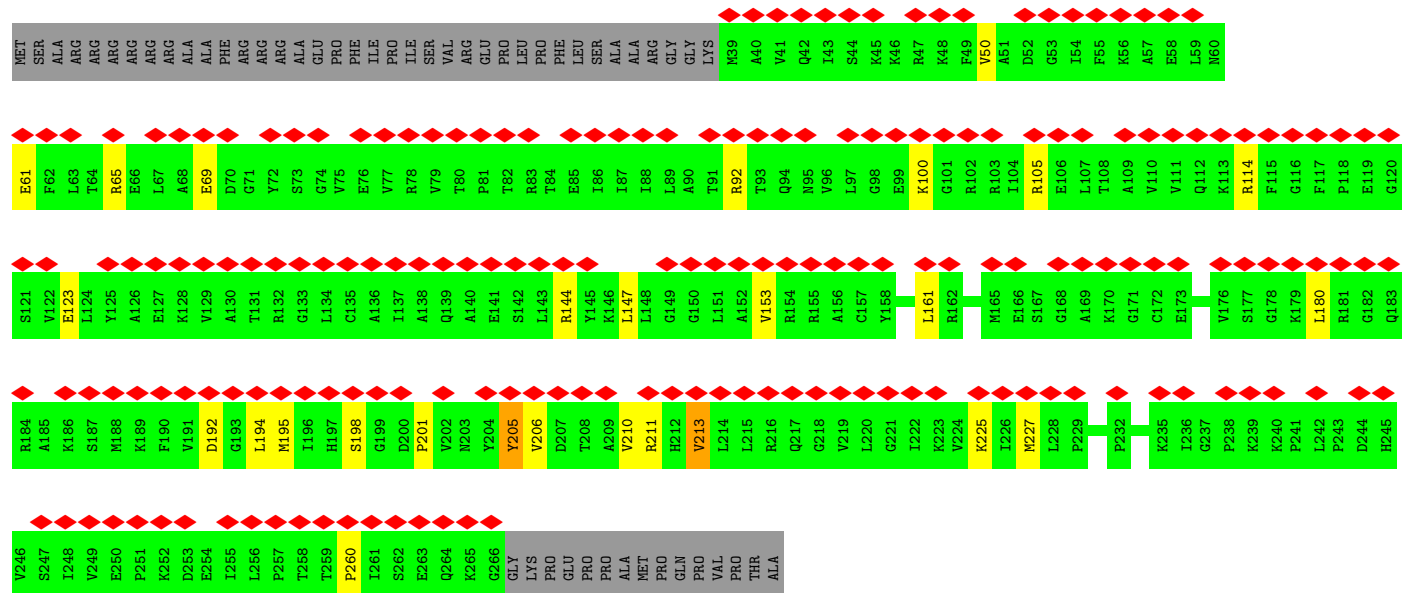
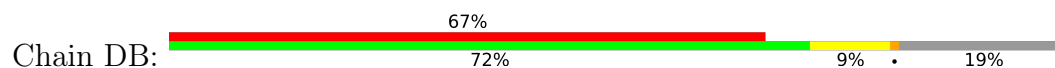




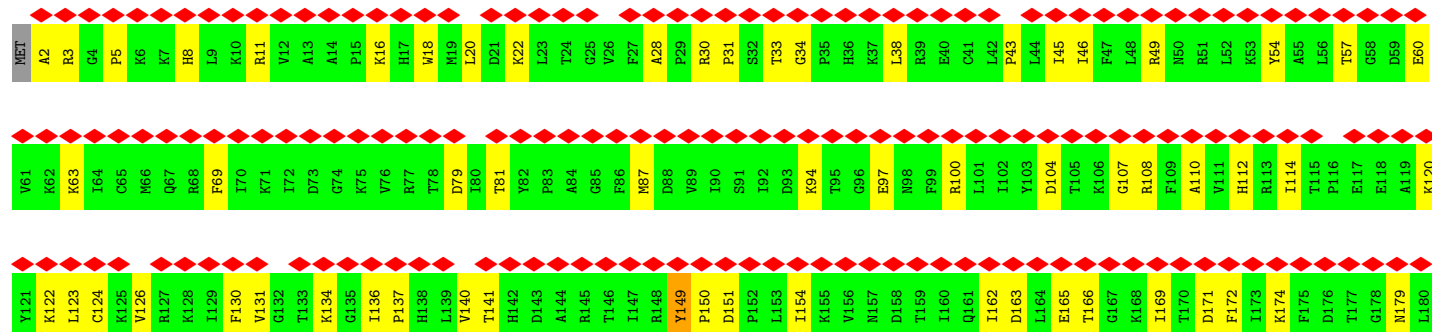
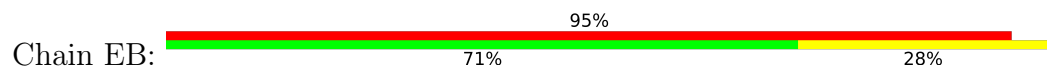
C1828	U1691	C1626	U1560	U1494	U1426	U1360	C1291	C1146	U1003
G1829	U1692	C1627	A1561	G1495	C1427	G1361	C1292	C1147	U1004
U1830	G1693	C1628	C1562	U1496	G1428	U1362	A1293	A1080	G1005
A1831	C1698	A1630	C1563	U1497	C1429	U1363	G1294	A1148	C1006
A1834	C1699	U1631	C1564	A1498	C1430	U1364	A1295	A1150	C1007
A1835	C1700	U1632	C1565	U1499	G1431	G1365	A1296	G1151	A1008
G1836	C1705	A1633	G1566	C1500	U1432	G1366	U1297	U1152	A1011
G1837	C1706	A1634	G1567	C1501	C1433	U1367	G1298	C1086	A1012
U1838	C1707	C1635	C1568	C1502	C1434	U1368	A1299	U1155	U1013
U1839	U1708	G1636	A1569	U1503	C1435	U1371	U1300	U1156	G1014
U1840	C1709	G1637	G1570	U1504	C1436	U1372	A1301	U1160	U1015
U1841	C1710	G1638	G1571	U1505	C1437	C1373	G1302	C1090	U1016
C1842	C1711	G1639	C1572	G1507	A1438	C1374	C1303	C1091	U1017
U1843	U1711	C1644	G1576	G1510	A1439	G1375	U1304	G1166	U1018
U1844	A1712	C1645	G1577	U1511	U1441	U1376	C1305	G1167	A1020
A1845	C1713	C1646	U1578	U1512	U1442	A1378	U1306	G1168	U1021
G1846	U1714	A1647	U1579	C1512	C1443	A1379	U1307	G1169	U1022
G1847	A1715	A1648	A1580	C1513	U1444	C1380	U1308	A1170	A1023
U1848	C1716	U1649	U1581	G1514	U1445	G1381	U1309	U1177	C1026
U1849	C1717	U1650	C1582	U1519	A1446	A1382	C1310	C1098	A1027
A1850	U1720	A1651	G1583	G1520	G1447	A1383	C1311	A1100	A1028
A1851	U1721	C1652	G1584	U1521	A1448	A1386	G1312	U1101	G1029
U1854	G1722	U1653	U1585	C1522	G1449	A1387	A1313	C1103	A1030
G1855	U1723	C1654	U1586	A1523	G1450	G1388	U1314	G1104	A1031
G1856	A1724	C1655	G1587	C1524	G1451	C1389	U1315	G1105	C1032
G1857	U1725	G1656	U1588	U1524	A1452	U1390	U1316	C1106	A1033
A1858	G1726	U1657	A1589	G1524	A1453	C1393	C1317	G1110	A1034
U1860	U1727	U1658	C1590	G1528	A1454	G1394	A1259	U1111	A1035
G1861	C1728	C1660	C1591	U1529	U1457	C1395	A1260	U1112	A1036
G1862	U1729	A1661	C1592	U1530	G1458	A1396	C1261	A1113	G1037
A1863	U1730	U1662	U1593	A1531	G1459	U1397	C1262	U1114	
U1864	A1731	C1663	U1594	C1532	G1460	G1398	U1263	U1115	G1043
A1866	G1732	A1664	U1596	A1533	G1461	U1401	C1264	C1116	G1044
U1867	U1733	C1665	U1599	U1534	U1462	A1402	A1265	C1117	U1045
U1868	G1734	U1666	G1600	U1535	U1463	C1403	C1266	C1118	U1046
A1869	A1735	U1667	U1601	U1536	U1464	U1404	C1267	U1119	C1047
U1870	G1736	G1668	A1602	A1537	A1465	A1405	C1268	U1120	G1048
A1801	U1737	U1669	G1603	C1538	G1466	G1406	G1270	G1203	
C1802	C1737	U1670	U1604	U1541	C1470	U1407	C1271	A1204	G1054
U1803	U1741	U1671	G1605	C1542	C1471	C1410	C1272	G1207	A1055
U1804	G1742	U1672	G1606	U1543	C1472	C1411	C1273	A1208	U1056
G1805	U1743	A1673	U1607	C1544	C1473	G1412	G1274	G1126	C1057
C1806	G1744	U1674	U1608	A1545	A1474	G1413	G1275	C1127	A1058
C1807	A1745	U1675	U1609	U1546	G1475	A1414	A1217	G1128	G1059
U1808	U1746	U1676	G1613	C1547	A1476	C1415	C1218	G1129	A1060
U1809	G1747	U1677	A1614	U1548	U1477	C1416	C1219	G1130	U1061
U1810	U1748	U1678	U1615	U1549	U1478	C1417	C1277	G1131	A1062
U1811	G1749	U1679	G1616	G1550	U1479	C1418	A1278	A1133	C1063
U1812	U1750	U1680	U1617	U1551	U1480	C1419	G1280	G1134	C1064
A1813	C1751	U1681	C1618	U1552	A1481	G1420	G1281	U1135	G1065
G1816	U1752	U1682	U1619	C1553	A1483	C1421	A1282	U1137	A1070
U1817	C1753	U1683	A1620	C1554	C1488	G1422	C1283	C1138	G1071
A1818	U1754	C1684	U1621	U1555	A1489	A1421	A1284	C1139	U1072
A1822	G1755	U1685	U1622	U1556	G1490	G1423	G1285	G1227	C1075
A1823	U1756	U1686	A1623	A1557	G1491	G1424	G1286	A1228	G1076
A1824	G1757	U1687	U1624	C1558	U1492	G1425	U1287	G1229	
A1825	U1758	U1688	U1625	C1559	C1493		U1288		
G1826		U1689							
U1827		U1690							



• Molecule 54: S3

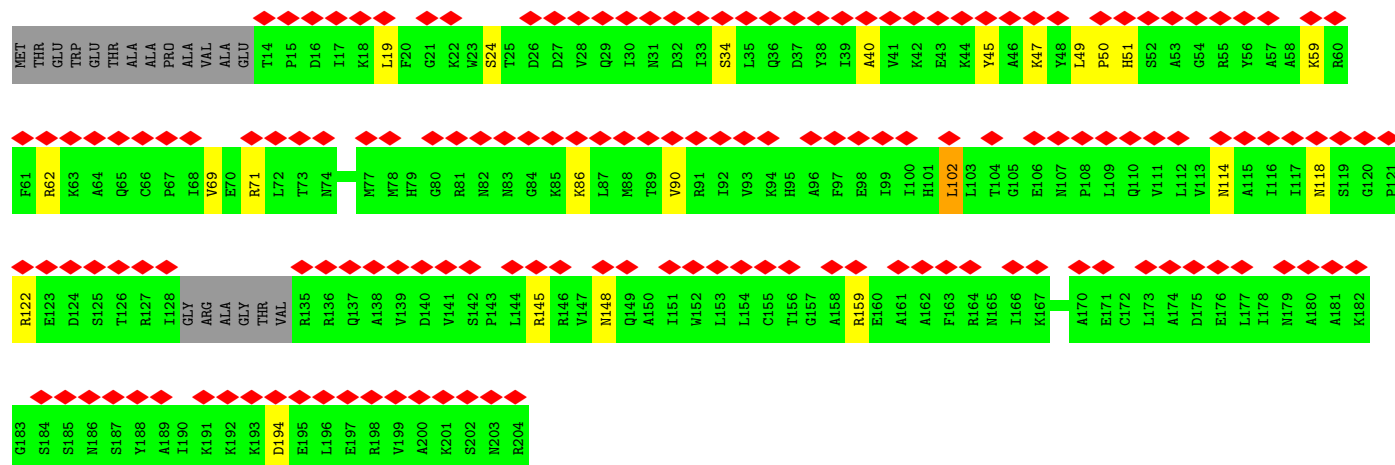
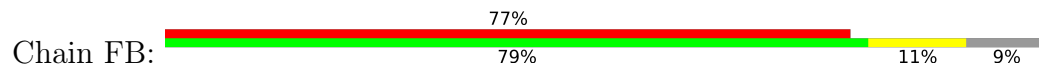


• Molecule 55: S4

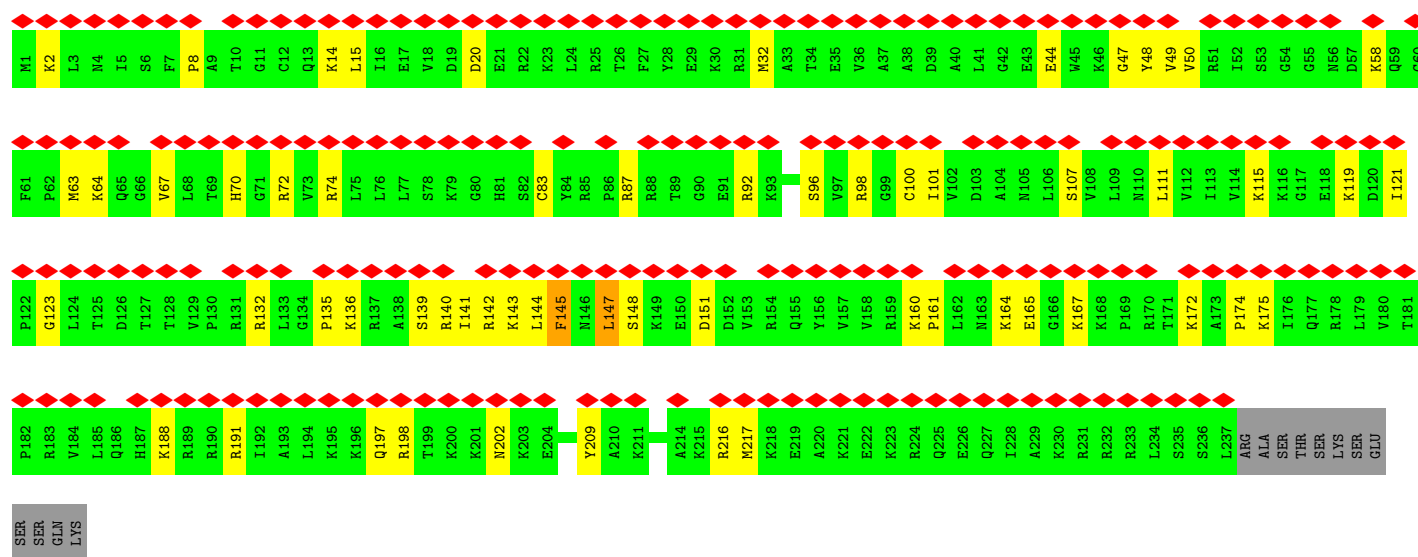
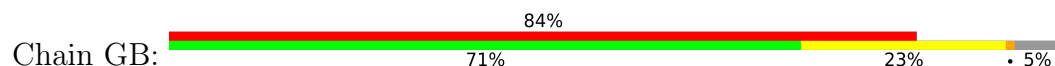




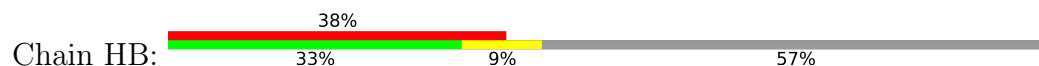
• Molecule 56: S5



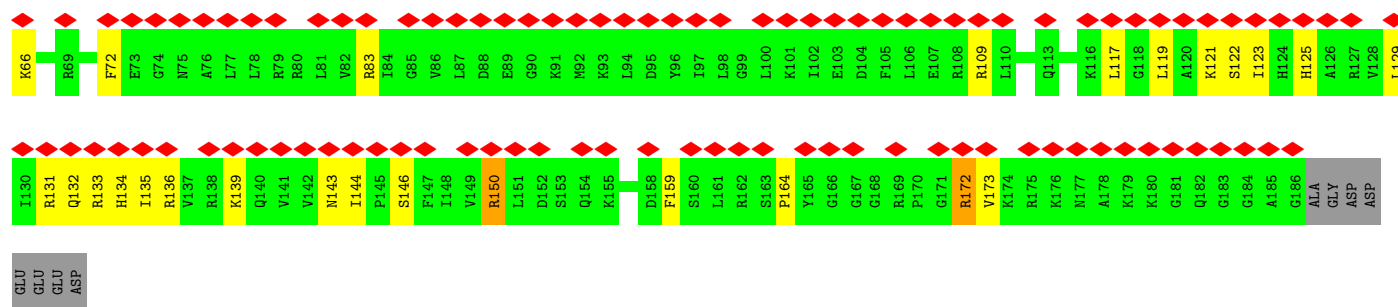
• Molecule 57: eS6



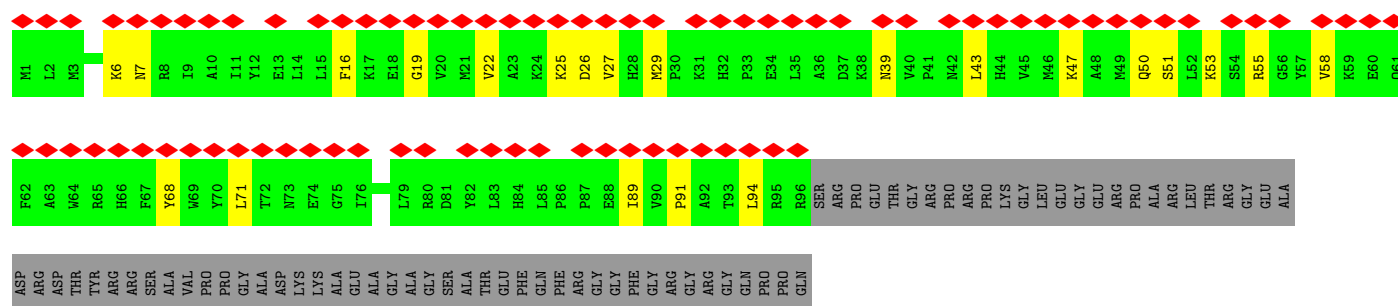
• Molecule 58: eS7



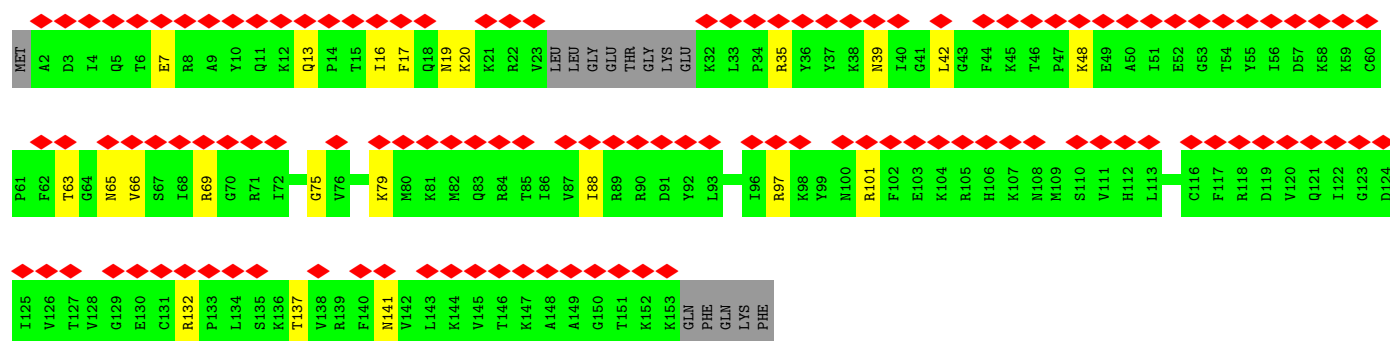
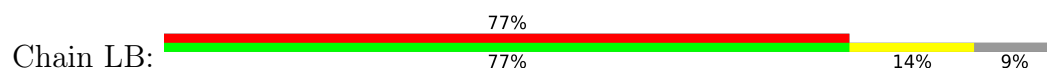




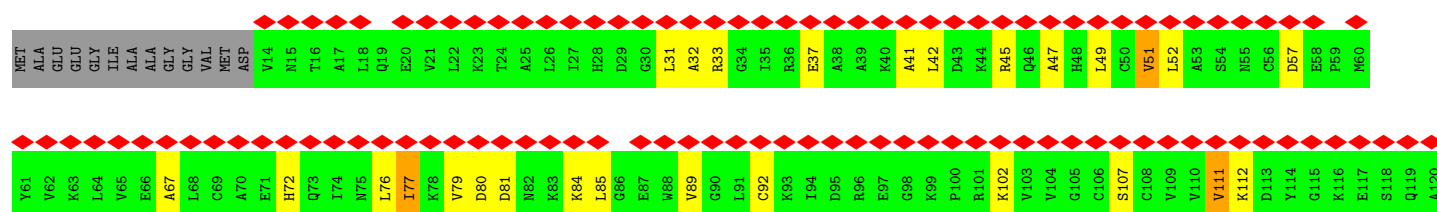
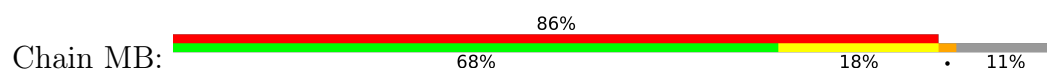
• Molecule 61: S10



• Molecule 62: S11

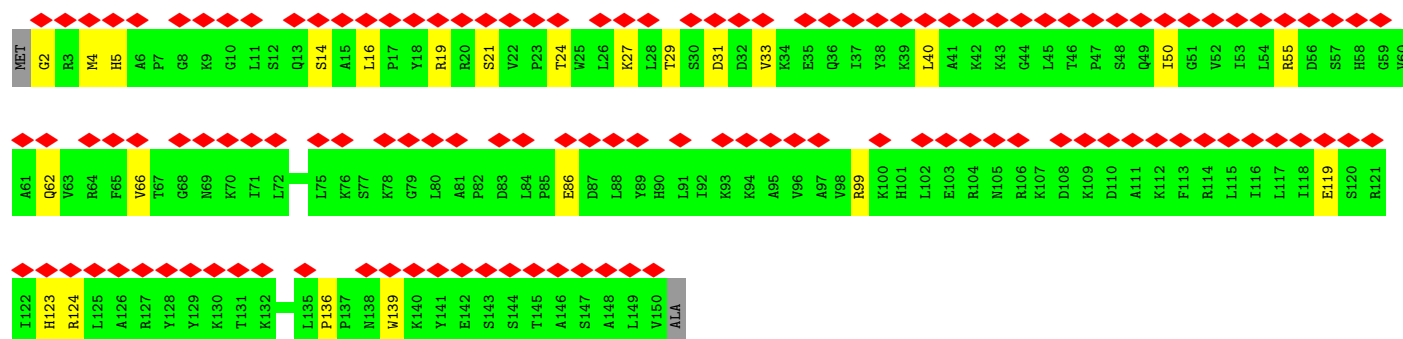
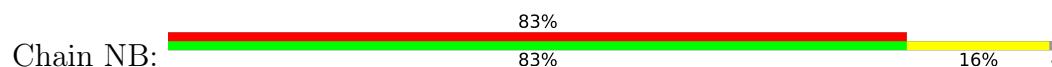


• Molecule 63: S12

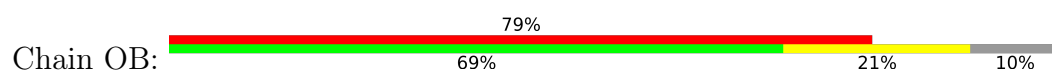




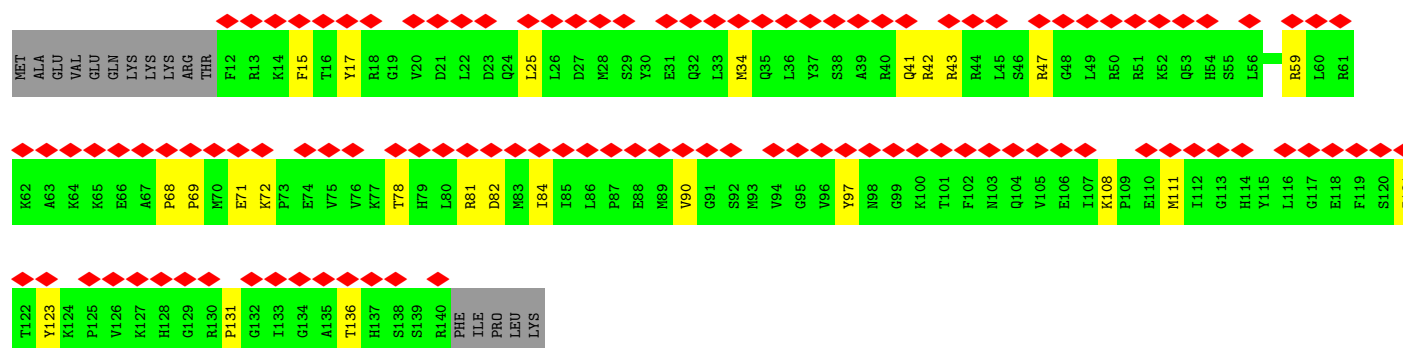
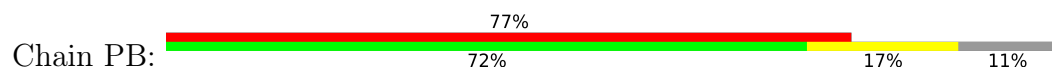
• Molecule 64: uS15



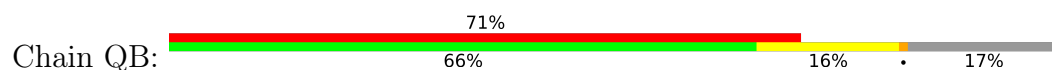
• Molecule 65: S14

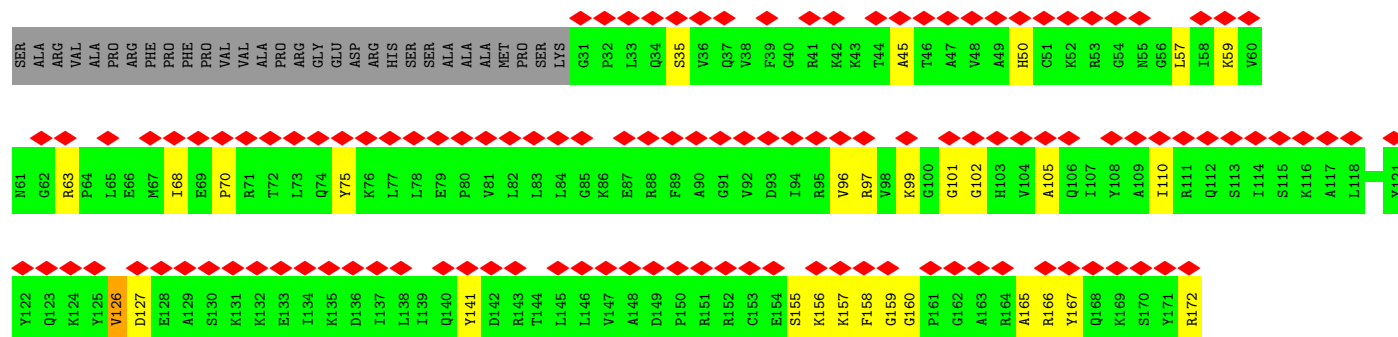


• Molecule 66: S15

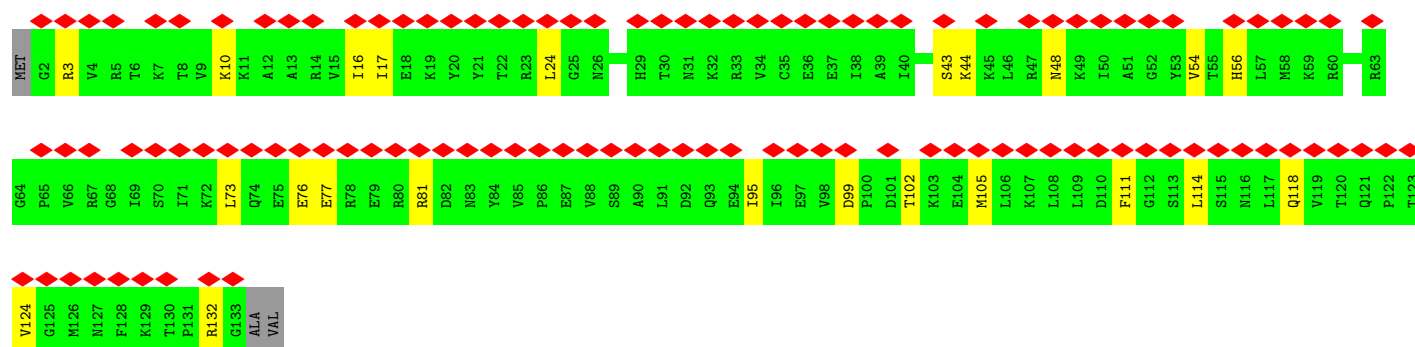
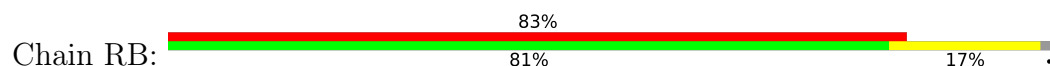


• Molecule 67: uS9

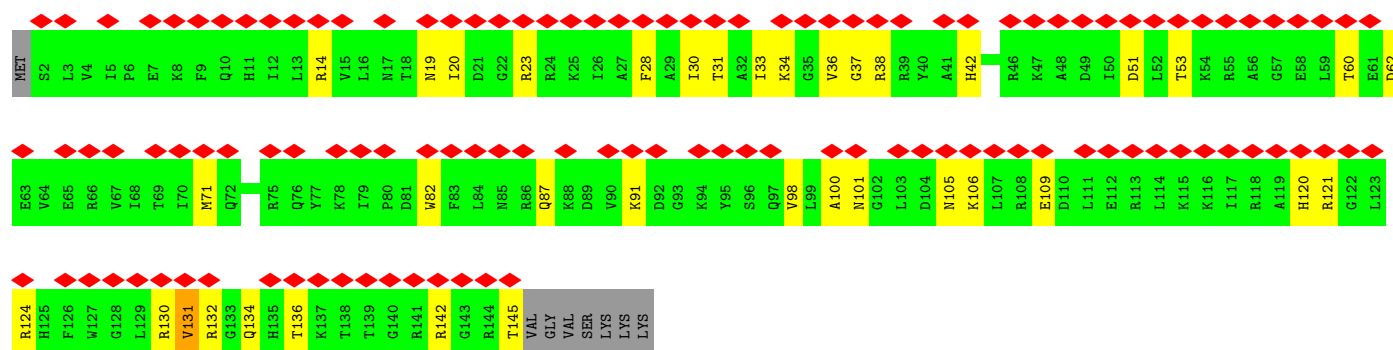
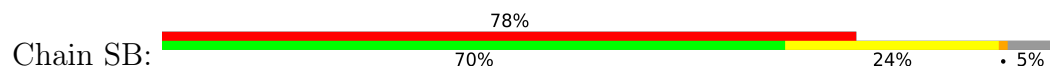




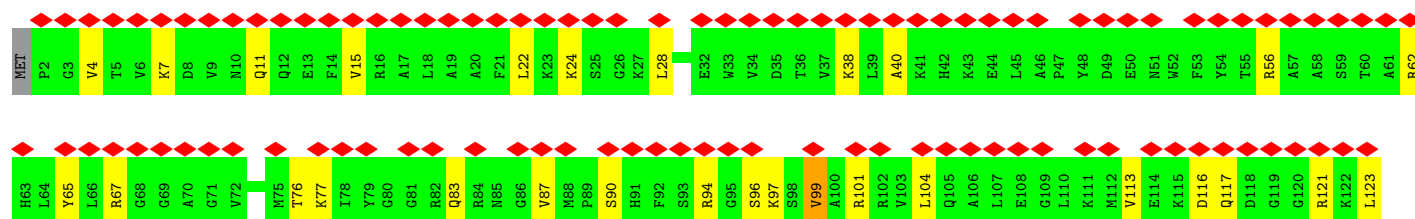
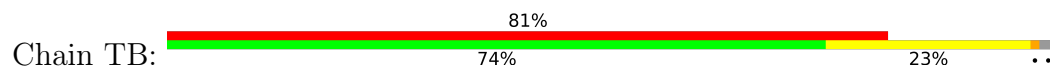
• Molecule 68: eS17



• Molecule 69: S18

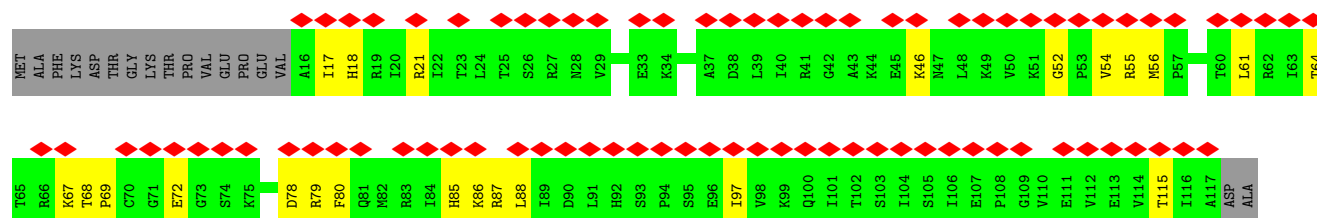
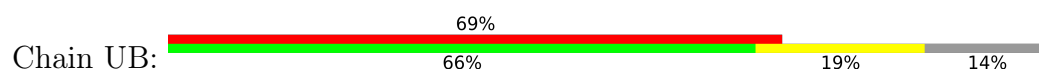


• Molecule 70: S19

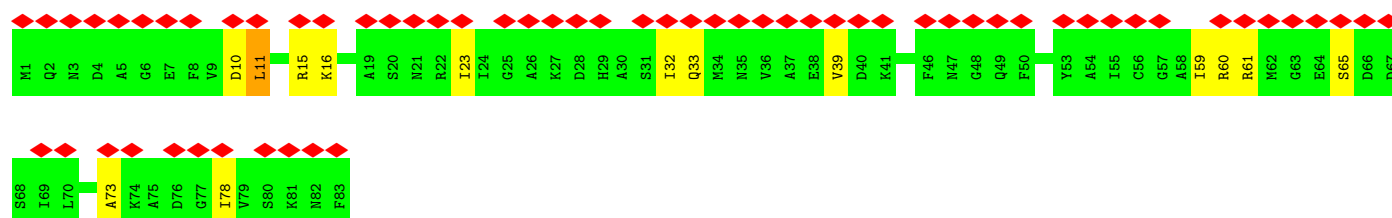
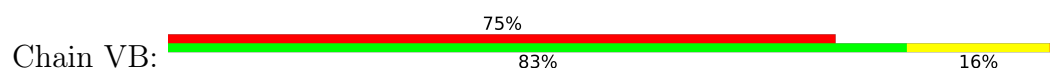




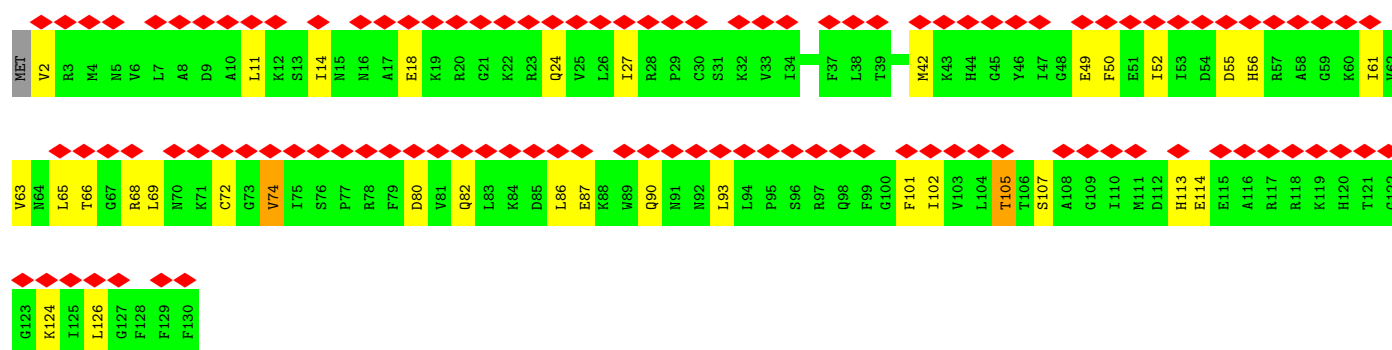
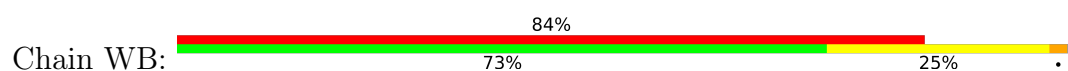
• Molecule 71: uS10



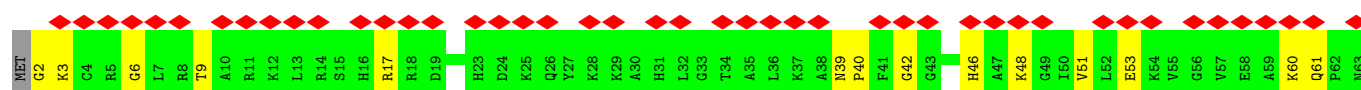
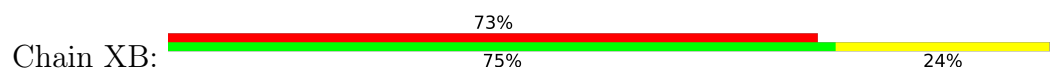
• Molecule 72: S21

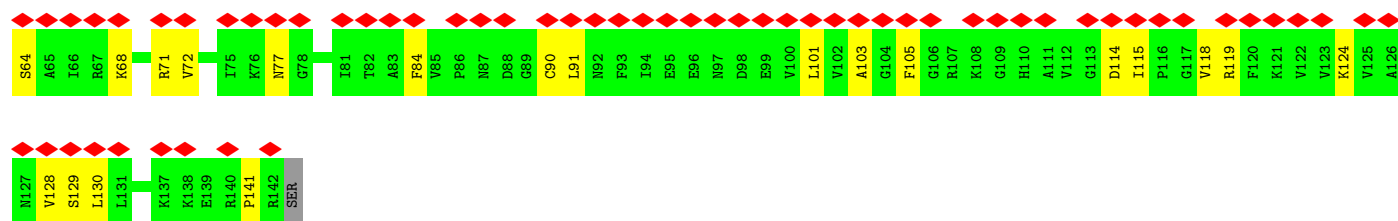


• Molecule 73: S15A

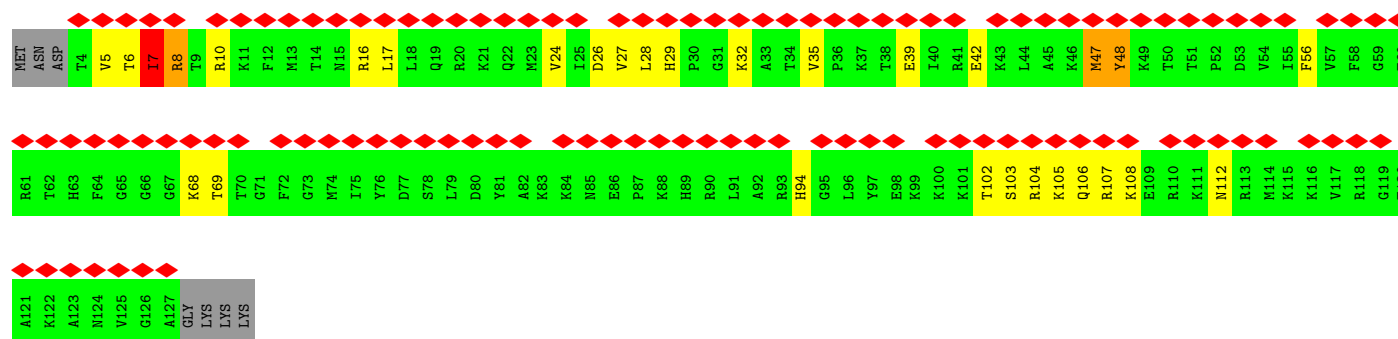
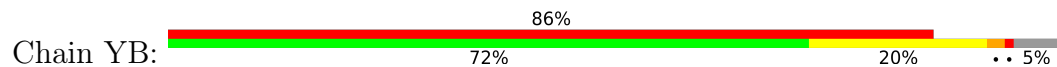


• Molecule 74: S23

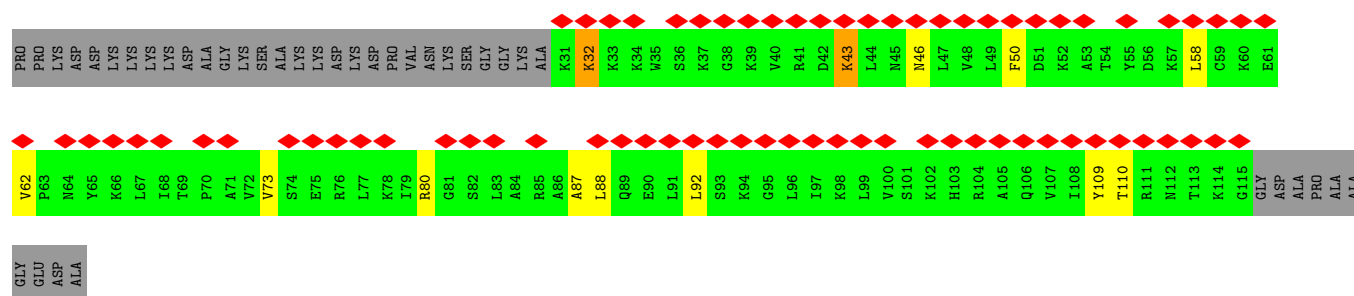




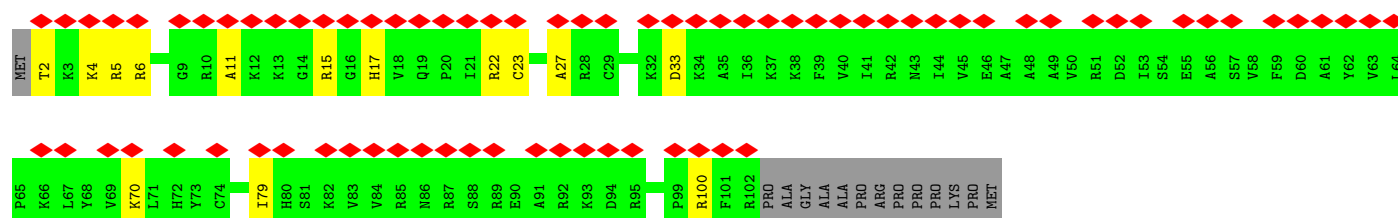
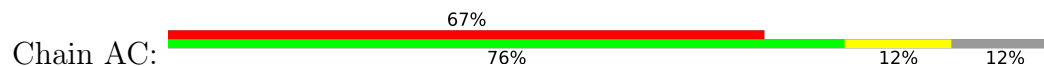
• Molecule 75: S24



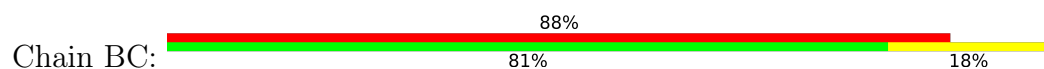
• Molecule 76: eS25



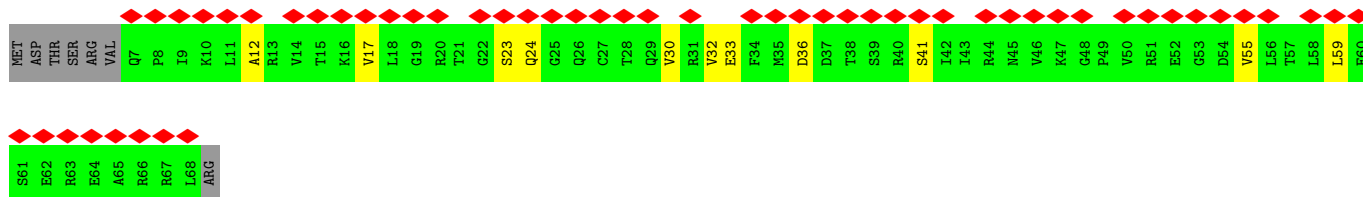
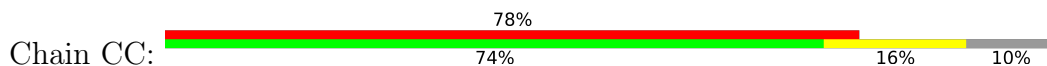
• Molecule 77: S26



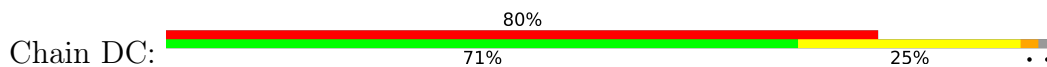
• Molecule 78: S27



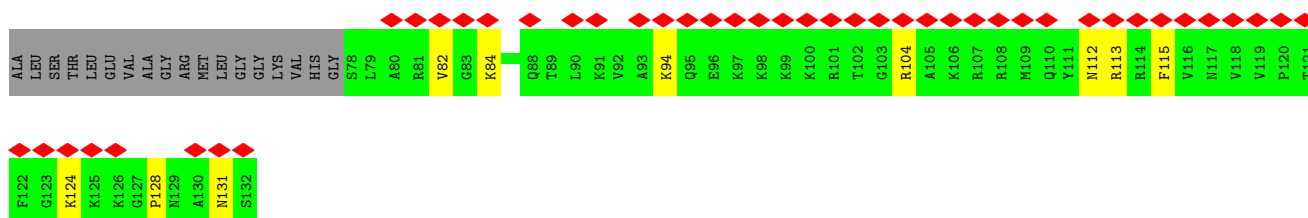
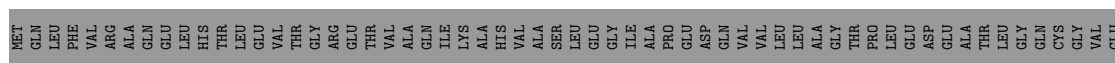
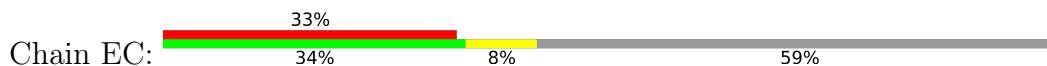
- Molecule 79: S28



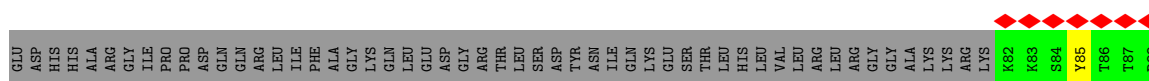
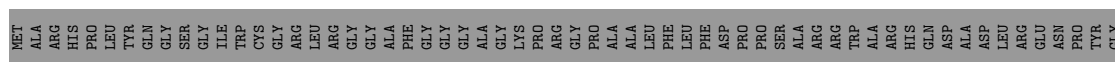
- Molecule 80: uS14

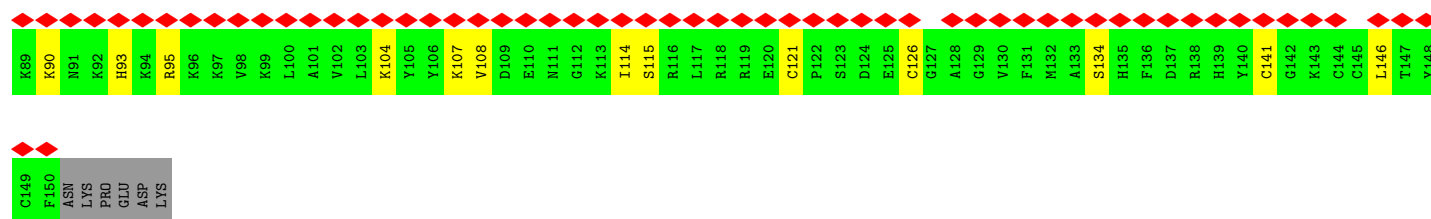


- Molecule 81: S30

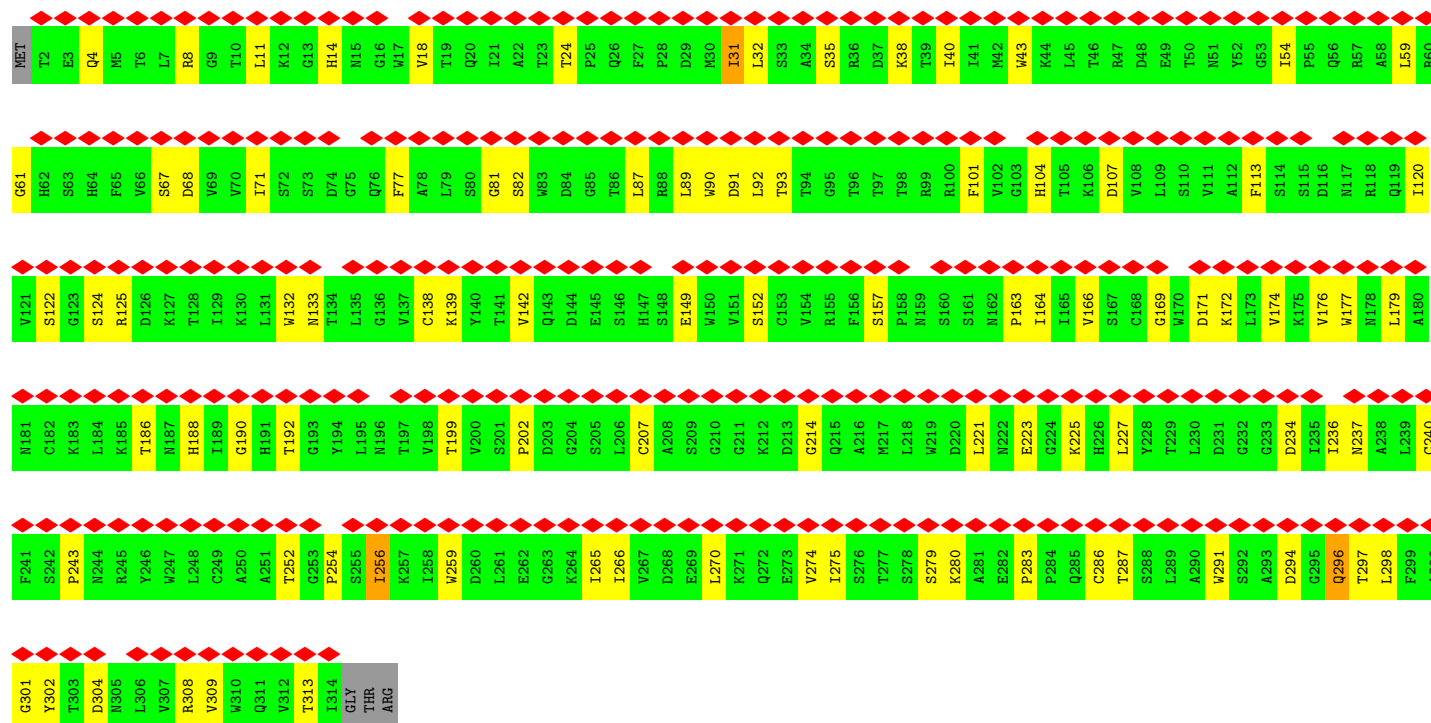
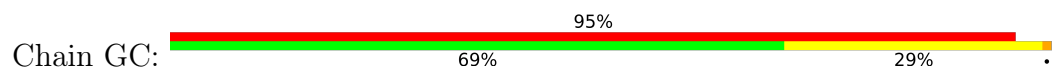


- Molecule 82: S27A

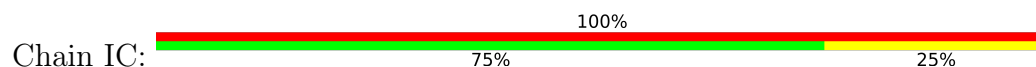




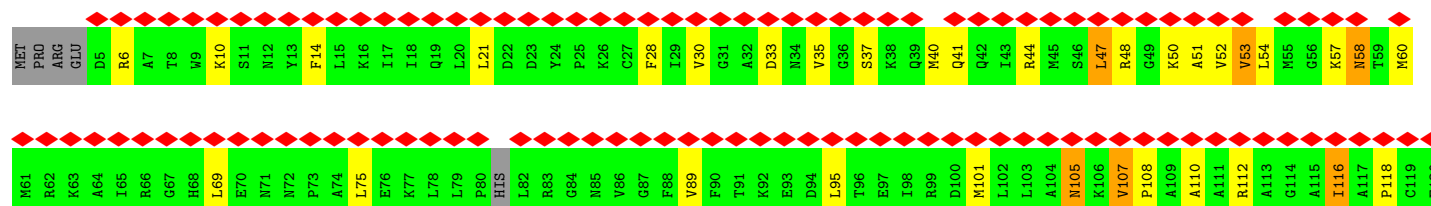
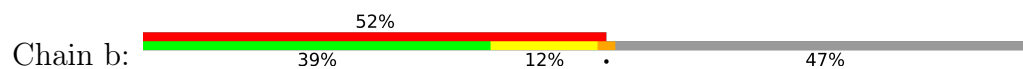
• Molecule 83: RACK1

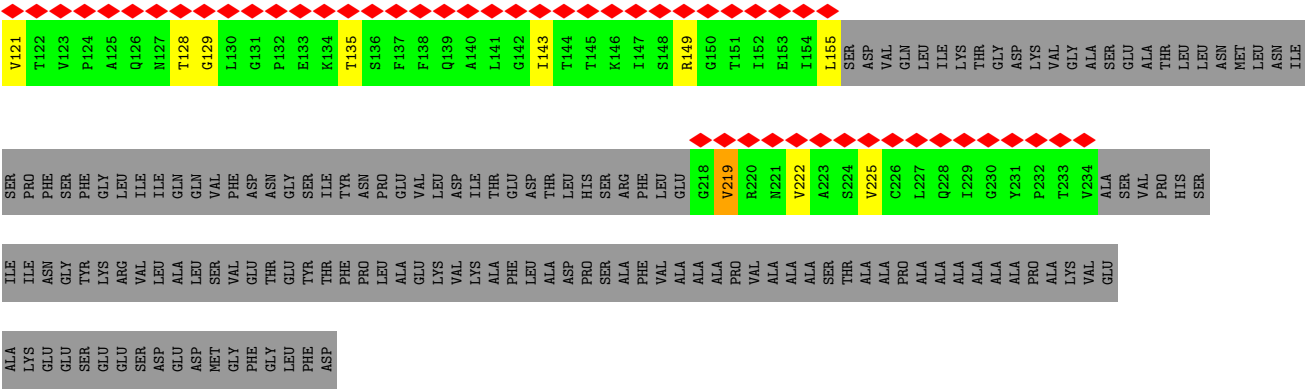


• Molecule 84: nascent chain

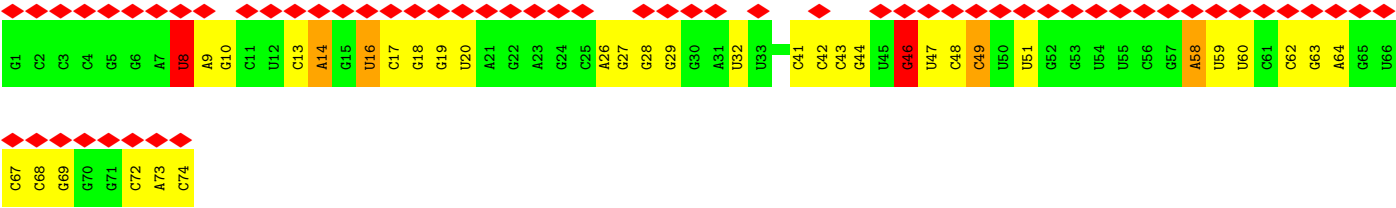
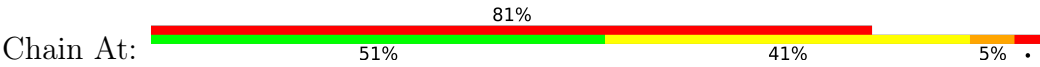


• Molecule 85: RPLP0





● Molecule 86: A-site tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1508	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	24.363	Depositor
Minimum map value	-18.068	Depositor
Average map value	0.008	Depositor
Map value standard deviation	1.504	Depositor
Recommended contour level	7	Depositor
Map size ($\text{\AA}$)	686.87994, 686.87994, 686.87994	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, ZN, H2U, MG, 7MG, SPD, ANM, 4SU

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	0.07	0/1952	0.21	0/2617
2	B	0.08	0/3264	0.22	0/4371
3	C	0.07	0/2937	0.20	0/3946
4	D	0.08	0/2441	0.21	0/3269
5	E	0.08	0/1859	0.22	0/2491
6	F	0.08	0/1933	0.22	0/2577
7	G	0.08	0/1881	0.20	0/2532
8	H	0.07	0/1535	0.24	0/2063
9	I	0.07	0/1702	0.19	0/2272
10	J	0.07	0/1395	0.23	0/1863
11	K	0.08	0/1733	0.21	0/2316
12	L	0.08	0/1158	0.20	0/1547
13	M	0.08	0/1746	0.22	0/2338
14	N	0.09	0/1662	0.22	0/2222
15	O	0.07	0/1292	0.22	0/1733
16	P	0.07	0/1539	0.23	0/2054
17	Q	0.08	0/1524	0.19	0/2013
18	R	0.08	0/1501	0.23	0/2012
19	S	0.07	0/1326	0.20	0/1770
20	T	0.08	0/840	0.25	0/1127
21	U	0.08	0/1018	0.23	0/1364
22	V	0.11	0/900	0.29	0/1194
23	W	0.07	0/984	0.20	0/1323
24	X	0.06	0/1132	0.19	0/1504
25	Y	0.07	0/1130	0.20	0/1507
26	Z	0.08	0/1191	0.21	0/1590
27	AA	0.06	0/886	0.16	0/1171
28	BA	0.07	0/779	0.18	0/1044
29	CA	0.08	0/908	0.20	0/1223
30	DA	0.07	0/1082	0.20	0/1443
31	EA	0.08	0/895	0.21	0/1198
32	FA	0.07	0/916	0.22	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	GA	0.07	0/1016	0.19	0/1341
34	HA	0.07	0/841	0.20	0/1112
35	IA	0.08	0/731	0.21	0/966
36	JA	0.07	0/575	0.20	0/761
37	KA	0.07	0/459	0.19	0/608
38	LA	0.08	0/435	0.24	0/575
39	MA	0.07	0/240	0.16	0/305
40	NA	0.07	0/864	0.20	0/1140
41	OA	0.08	0/718	0.20	0/953
42	PA	0.07	0/1010	0.22	0/1354
43	RA	0.10	0/1174	0.27	0/1582
44	SA	0.08	0/1815	0.21	0/2828
45	TA	0.09	0/1804	0.21	0/2810
46	VA	0.06	0/276	0.18	0/426
47	WA	0.09	0/85840	0.21	0/133885
48	XA	0.08	0/2836	0.18	0/4421
49	YA	0.09	0/3701	0.22	0/5766
50	ZA	0.40	6/40949 (0.0%)	0.22	0/63819
51	AB	0.09	0/1747	0.21	0/2374
52	BB	0.07	0/1756	0.22	0/2350
53	CB	0.07	0/1744	0.23	0/2358
54	DB	0.08	0/1796	0.21	0/2417
55	EB	0.09	0/2118	0.26	0/2849
56	FB	0.08	0/1492	0.23	0/2005
57	GB	0.10	0/1946	0.26	0/2590
58	HB	0.09	0/1511	0.24	0/2022
59	IB	0.08	0/1715	0.21	0/2287
60	JB	0.09	0/1550	0.23	0/2069
61	KB	0.08	0/834	0.23	0/1125
62	LB	0.07	0/1200	0.24	0/1604
63	MB	0.08	0/918	0.23	0/1233
64	NB	0.07	0/1226	0.20	0/1649
65	OB	0.07	0/1029	0.23	0/1380
66	PB	0.08	0/1079	0.21	0/1441
67	QB	0.09	0/1146	0.25	0/1534
68	RB	0.09	0/1082	0.24	0/1452
69	SB	0.08	0/1208	0.23	0/1618
70	TB	0.07	0/1123	0.20	0/1504
71	UB	0.08	0/818	0.23	0/1099
72	VB	0.06	0/643	0.20	0/860
73	WB	0.08	0/1051	0.25	0/1406
74	XB	0.07	0/1116	0.21	0/1490
75	YB	1.33	3/1028 (0.3%)	0.96	6/1366 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	ZB	0.07	0/691	0.21	0/922
77	AC	0.08	0/828	0.23	0/1109
78	BC	0.06	0/665	0.19	0/891
79	CC	0.09	0/490	0.25	0/656
80	DC	0.06	0/470	0.19	0/623
81	EC	0.07	0/447	0.20	0/587
82	FC	0.06	0/576	0.20	0/764
83	GC	0.09	0/2493	0.28	0/3394
84	IC	0.05	0/19	0.14	0/25
85	b	0.12	0/1298	0.28	0/1752
86	At	0.14	0/1652	0.19	0/2573
All	All	0.21	9/234830 (0.0%)	0.22	6/344944 (0.0%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
75	YB	7	ILE	CA-CB	38.96	1.99	1.54
50	ZA	836	G	N1-C2	34.92	2.07	1.37
50	ZA	836	G	C6-N1	34.13	2.07	1.39
50	ZA	836	G	C2-N3	33.58	2.00	1.32
50	ZA	836	G	C5-C6	32.20	2.06	1.42

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
75	YB	7	ILE	CA-CB-CG1	19.95	144.31	110.40
75	YB	7	ILE	CA-CB-CG2	14.62	135.35	110.50
75	YB	7	ILE	CG1-CB-CG2	-12.87	72.10	110.70
75	YB	7	ILE	N-CA-C	-11.20	91.64	107.99
75	YB	7	ILE	CB-CA-C	10.78	125.75	110.98

There are no chirality outliers.

There are no planarity outliers.

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	1914	0	2013	48	0
2	B	3196	0	3339	70	0
3	C	2883	0	3053	50	0
4	D	2395	0	2427	32	0
5	E	1823	0	1995	38	0
6	F	1897	0	2021	37	0
7	G	1850	0	1991	22	0
8	H	1516	0	1597	20	0
9	I	1664	0	1712	26	0
10	J	1372	0	1412	20	0
11	K	1702	0	1820	25	0
12	L	1137	0	1211	21	0
13	M	1701	0	1749	35	0
14	N	1630	0	1778	35	0
15	O	1266	0	1302	23	0
16	P	1515	0	1634	32	0
17	Q	1508	0	1664	22	0
18	R	1462	0	1508	31	0
19	S	1298	0	1366	31	0
20	T	826	0	852	12	0
21	U	1004	0	1063	16	0
22	V	887	0	935	27	0
23	W	967	0	1040	13	0
24	X	1115	0	1205	19	0
25	Y	1107	0	1182	27	0
26	Z	1162	0	1209	30	0
27	AA	873	0	949	18	0
28	BA	769	0	803	8	0
29	CA	893	0	932	12	0
30	DA	1064	0	1160	27	0
31	EA	876	0	912	18	0
32	FA	906	0	998	9	0
33	GA	1008	0	1142	17	0
34	HA	830	0	916	11	0
35	IA	716	0	750	24	0
36	JA	569	0	637	5	0
37	KA	447	0	480	14	0
38	LA	429	0	465	5	0
39	MA	239	0	289	5	0
40	NA	851	0	920	13	0
41	OA	708	0	757	16	0
42	PA	994	0	1051	21	0
43	RA	1160	0	1218	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	SA	1622	0	825	21	0
45	TA	1615	0	820	15	0
46	VA	249	0	128	3	0
47	WA	76735	0	38764	1133	0
48	XA	2538	0	1286	31	0
49	YA	3314	0	1683	48	0
50	ZA	36623	0	18504	679	0
51	AB	1710	0	1711	26	0
52	BB	1729	0	1803	24	0
53	CB	1707	0	1793	26	0
54	DB	1768	0	1863	18	0
55	EB	2076	0	2177	55	0
56	FB	1471	0	1522	18	0
57	GB	1923	0	2089	48	0
58	HB	1489	0	1582	25	0
59	IB	1686	0	1772	27	0
60	JB	1525	0	1640	37	0
61	KB	810	0	836	15	0
62	LB	1180	0	1254	18	0
63	MB	908	0	939	17	0
64	NB	1202	0	1289	16	0
65	OB	1016	0	1039	22	0
66	PB	1058	0	1104	17	0
67	QB	1128	0	1195	24	0
68	RB	1068	0	1121	16	0
69	SB	1190	0	1249	25	0
70	TB	1104	0	1140	24	0
71	UB	808	0	878	17	0
72	VB	636	0	637	12	0
73	WB	1034	0	1080	21	0
74	XB	1098	0	1167	22	0
75	YB	1011	0	1083	72	0
76	ZB	683	0	761	10	0
77	AC	814	0	864	13	0
78	BC	651	0	672	9	0
79	CC	488	0	514	8	0
80	DC	459	0	449	13	0
81	EC	443	0	492	11	0
82	FC	564	0	577	11	0
83	GC	2436	0	2393	51	0
84	IC	20	0	10	1	0
85	b	1279	0	1344	27	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	At	1582	0	807	18	0
87	AC	1	0	0	0	0
87	FA	1	0	0	0	0
87	I	1	0	0	0	0
87	WA	80	0	0	0	0
87	XA	1	0	0	0	0
87	ZA	18	0	0	0	0
88	AC	1	0	0	0	0
88	DC	1	0	0	0	0
88	FA	1	0	0	0	0
88	FC	1	0	0	0	0
88	IA	1	0	0	0	0
88	LA	1	0	0	0	0
88	NA	1	0	0	0	0
88	OA	1	0	0	0	0
89	WA	19	0	19	1	0
90	WA	10	0	19	1	0
91	ZA	6	0	4	0	0
All	All	218724	0	162355	3038	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 8.

The worst 5 of 3038 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)
75:YB:7:ILE:CB	75:YB:7:ILE:CG2	1.94	1.45
50:ZA:836:G:C4	50:ZA:836:G:C5	1.96	1.44
50:ZA:836:G:N1	75:YB:7:ILE:HA	1.22	1.43
50:ZA:836:G:C5	50:ZA:836:G:C6	2.06	1.42
75:YB:7:ILE:CA	75:YB:7:ILE:HB	1.49	1.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	248/257 (96%)	243 (98%)	5 (2%)	0	100	100
2	B	395/403 (98%)	386 (98%)	9 (2%)	0	100	100
3	C	360/413 (87%)	353 (98%)	7 (2%)	0	100	100
4	D	292/297 (98%)	286 (98%)	6 (2%)	0	100	100
5	E	222/291 (76%)	220 (99%)	2 (1%)	0	100	100
6	F	225/249 (90%)	219 (97%)	6 (3%)	0	100	100
7	G	225/319 (70%)	222 (99%)	3 (1%)	0	100	100
8	H	188/192 (98%)	183 (97%)	5 (3%)	0	100	100
9	I	201/214 (94%)	196 (98%)	5 (2%)	0	100	100
10	J	169/178 (95%)	168 (99%)	1 (1%)	0	100	100
11	K	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
12	L	136/218 (62%)	131 (96%)	5 (4%)	0	100	100
13	M	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
14	N	197/203 (97%)	195 (99%)	2 (1%)	0	100	100
15	O	154/213 (72%)	151 (98%)	3 (2%)	0	100	100
16	P	185/188 (98%)	182 (98%)	3 (2%)	0	100	100
17	Q	178/212 (84%)	174 (98%)	4 (2%)	0	100	100
18	R	174/224 (78%)	171 (98%)	3 (2%)	0	100	100
19	S	157/160 (98%)	154 (98%)	3 (2%)	0	100	100
20	T	99/128 (77%)	95 (96%)	4 (4%)	0	100	100
21	U	133/140 (95%)	130 (98%)	3 (2%)	0	100	100
22	V	106/157 (68%)	106 (100%)	0	0	100	100
23	W	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
24	X	132/145 (91%)	130 (98%)	2 (2%)	0	100	100
25	Y	133/136 (98%)	133 (100%)	0	0	100	100
26	Z	145/148 (98%)	142 (98%)	3 (2%)	0	100	100
27	AA	103/245 (42%)	100 (97%)	3 (3%)	0	100	100
28	BA	97/115 (84%)	96 (99%)	1 (1%)	0	100	100
29	CA	106/125 (85%)	105 (99%)	1 (1%)	0	100	100
30	DA	127/135 (94%)	125 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	EA	107/110 (97%)	107 (100%)	0	0	100	100
32	FA	112/129 (87%)	110 (98%)	2 (2%)	0	100	100
33	GA	119/123 (97%)	117 (98%)	2 (2%)	0	100	100
34	HA	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
35	IA	85/97 (88%)	83 (98%)	2 (2%)	0	100	100
36	JA	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
37	KA	48/51 (94%)	48 (100%)	0	0	100	100
38	LA	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
39	MA	23/25 (92%)	23 (100%)	0	0	100	100
40	NA	102/106 (96%)	100 (98%)	2 (2%)	0	100	100
41	OA	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
42	PA	122/137 (89%)	118 (97%)	4 (3%)	0	100	100
43	RA	151/165 (92%)	140 (93%)	11 (7%)	0	100	100
51	AB	215/295 (73%)	211 (98%)	4 (2%)	0	100	100
52	BB	211/264 (80%)	207 (98%)	4 (2%)	0	100	100
53	CB	218/293 (74%)	215 (99%)	3 (1%)	0	100	100
54	DB	226/281 (80%)	225 (100%)	1 (0%)	0	100	100
55	EB	260/263 (99%)	252 (97%)	8 (3%)	0	100	100
56	FB	181/204 (89%)	176 (97%)	5 (3%)	0	100	100
57	GB	235/249 (94%)	231 (98%)	4 (2%)	0	100	100
58	HB	181/432 (42%)	177 (98%)	4 (2%)	0	100	100
59	IB	204/208 (98%)	199 (98%)	5 (2%)	0	100	100
60	JB	183/194 (94%)	182 (100%)	1 (0%)	0	100	100
61	KB	94/165 (57%)	92 (98%)	2 (2%)	0	100	100
62	LB	140/158 (89%)	139 (99%)	1 (1%)	0	100	100
63	MB	115/132 (87%)	109 (95%)	6 (5%)	0	100	100
64	NB	147/151 (97%)	146 (99%)	1 (1%)	0	100	100
65	OB	134/151 (89%)	130 (97%)	4 (3%)	0	100	100
66	PB	127/145 (88%)	125 (98%)	2 (2%)	0	100	100
67	QB	140/172 (81%)	136 (97%)	4 (3%)	0	100	100
68	RB	130/135 (96%)	129 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	SB	142/152 (93%)	140 (99%)	2 (1%)	0	100	100
70	TB	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
71	UB	100/119 (84%)	97 (97%)	3 (3%)	0	100	100
72	VB	81/83 (98%)	81 (100%)	0	0	100	100
73	WB	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
74	XB	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
75	YB	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
76	ZB	83/124 (67%)	82 (99%)	1 (1%)	0	100	100
77	AC	99/115 (86%)	97 (98%)	2 (2%)	0	100	100
78	BC	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
79	CC	60/69 (87%)	60 (100%)	0	0	100	100
80	DC	53/56 (95%)	53 (100%)	0	0	100	100
81	EC	53/133 (40%)	50 (94%)	3 (6%)	0	100	100
82	FC	67/188 (36%)	66 (98%)	1 (2%)	0	100	100
83	GC	311/317 (98%)	299 (96%)	12 (4%)	0	100	100
84	IC	2/4 (50%)	2 (100%)	0	0	100	100
85	b	165/318 (52%)	154 (93%)	10 (6%)	1 (1%)	21	54
All	All	11553/13817 (84%)	11306 (98%)	246 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
85	b	225	VAL

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	
1	A	192/199 (96%)	192 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	344/348 (99%)	340 (99%)	4 (1%)	63	72
3	C	302/337 (90%)	301 (100%)	1 (0%)	86	84
4	D	247/250 (99%)	246 (100%)	1 (0%)	84	83
5	E	201/251 (80%)	200 (100%)	1 (0%)	81	81
6	F	198/218 (91%)	198 (100%)	0	100	100
7	G	197/273 (72%)	196 (100%)	1 (0%)	81	81
8	H	169/171 (99%)	165 (98%)	4 (2%)	43	62
9	I	175/181 (97%)	173 (99%)	2 (1%)	65	73
10	J	144/149 (97%)	140 (97%)	4 (3%)	38	58
11	K	175/176 (99%)	174 (99%)	1 (1%)	78	79
12	L	117/161 (73%)	117 (100%)	0	100	100
13	M	171/172 (99%)	169 (99%)	2 (1%)	63	72
14	N	171/173 (99%)	171 (100%)	0	100	100
15	O	137/190 (72%)	137 (100%)	0	100	100
16	P	164/165 (99%)	162 (99%)	2 (1%)	63	72
17	Q	159/191 (83%)	159 (100%)	0	100	100
18	R	157/192 (82%)	156 (99%)	1 (1%)	78	79
19	S	139/140 (99%)	138 (99%)	1 (1%)	76	77
20	T	91/114 (80%)	91 (100%)	0	100	100
21	U	103/107 (96%)	103 (100%)	0	100	100
22	V	89/126 (71%)	87 (98%)	2 (2%)	45	63
23	W	106/134 (79%)	106 (100%)	0	100	100
24	X	124/135 (92%)	121 (98%)	3 (2%)	43	62
25	Y	117/118 (99%)	116 (99%)	1 (1%)	70	74
26	Z	119/120 (99%)	118 (99%)	1 (1%)	73	76
27	AA	87/184 (47%)	87 (100%)	0	100	100
28	BA	85/98 (87%)	84 (99%)	1 (1%)	63	72
29	CA	98/110 (89%)	98 (100%)	0	100	100
30	DA	115/121 (95%)	114 (99%)	1 (1%)	70	74
31	EA	88/89 (99%)	88 (100%)	0	100	100
32	FA	98/109 (90%)	98 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	GA	109/110 (99%)	108 (99%)	1 (1%)	70	74
34	HA	86/89 (97%)	85 (99%)	1 (1%)	63	72
35	IA	74/80 (92%)	74 (100%)	0	100	100
36	JA	64/65 (98%)	64 (100%)	0	100	100
37	KA	47/48 (98%)	47 (100%)	0	100	100
38	LA	48/116 (41%)	46 (96%)	2 (4%)	26	50
39	MA	24/24 (100%)	24 (100%)	0	100	100
40	NA	92/94 (98%)	92 (100%)	0	100	100
41	OA	74/75 (99%)	73 (99%)	1 (1%)	59	70
42	PA	108/121 (89%)	106 (98%)	2 (2%)	50	66
43	RA	126/137 (92%)	119 (94%)	7 (6%)	19	45
51	AB	180/244 (74%)	177 (98%)	3 (2%)	53	67
52	BB	194/231 (84%)	192 (99%)	2 (1%)	68	74
53	CB	186/225 (83%)	185 (100%)	1 (0%)	81	81
54	DB	190/232 (82%)	187 (98%)	3 (2%)	55	68
55	EB	224/225 (100%)	219 (98%)	5 (2%)	45	63
56	FB	158/170 (93%)	156 (99%)	2 (1%)	61	71
57	GB	207/218 (95%)	204 (99%)	3 (1%)	59	70
58	HB	165/360 (46%)	162 (98%)	3 (2%)	51	67
59	IB	178/180 (99%)	177 (99%)	1 (1%)	78	79
60	JB	161/168 (96%)	154 (96%)	7 (4%)	26	50
61	KB	87/136 (64%)	86 (99%)	1 (1%)	65	73
62	LB	130/142 (92%)	129 (99%)	1 (1%)	73	76
63	MB	99/108 (92%)	95 (96%)	4 (4%)	28	52
64	NB	130/131 (99%)	130 (100%)	0	100	100
65	OB	106/119 (89%)	105 (99%)	1 (1%)	70	74
66	PB	115/130 (88%)	113 (98%)	2 (2%)	53	67
67	QB	117/140 (84%)	116 (99%)	1 (1%)	70	74
68	RB	119/121 (98%)	118 (99%)	1 (1%)	73	76
69	SB	125/132 (95%)	123 (98%)	2 (2%)	55	68
70	TB	112/115 (97%)	109 (97%)	3 (3%)	39	59

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	UB	93/107 (87%)	90 (97%)	3 (3%)	34	56
72	VB	67/67 (100%)	66 (98%)	1 (2%)	57	69
73	WB	112/113 (99%)	109 (97%)	3 (3%)	39	59
74	XB	113/115 (98%)	109 (96%)	4 (4%)	32	54
75	YB	107/113 (95%)	102 (95%)	5 (5%)	23	48
76	ZB	75/102 (74%)	73 (97%)	2 (3%)	39	59
77	AC	88/98 (90%)	87 (99%)	1 (1%)	65	73
78	BC	75/76 (99%)	74 (99%)	1 (1%)	61	71
79	CC	55/62 (89%)	55 (100%)	0	100	100
80	DC	48/49 (98%)	47 (98%)	1 (2%)	47	64
81	EC	46/106 (43%)	45 (98%)	1 (2%)	45	63
82	FC	62/154 (40%)	60 (97%)	2 (3%)	34	56
83	GC	272/275 (99%)	255 (94%)	17 (6%)	16	42
85	b	138/258 (54%)	119 (86%)	19 (14%)	3	18
All	All	10065/11683 (86%)	9911 (98%)	154 (2%)	55	69

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
81	EC	124	LYS
85	b	69	LEU
83	GC	14	HIS
83	GC	274	VAL
85	b	149	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
68	RB	29	HIS
85	b	71	ASN
70	TB	51	ASN
77	AC	43	ASN
28	BA	15	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	SA	75/76 (98%)	17 (22%)	3 (4%)
45	TA	75/76 (98%)	15 (20%)	0
46	VA	11/12 (91%)	3 (27%)	0
47	WA	3558/3584 (99%)	607 (17%)	22 (0%)
48	XA	118/120 (98%)	9 (7%)	0
49	YA	155/156 (99%)	35 (22%)	0
50	ZA	1707/1869 (91%)	311 (18%)	10 (0%)
86	At	73/74 (98%)	15 (20%)	0
All	All	5772/5967 (96%)	1012 (17%)	35 (0%)

5 of 1012 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	SA	9	A
44	SA	16	C
44	SA	17	G
44	SA	19	C
44	SA	20	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
50	ZA	561	A
50	ZA	752	G
50	ZA	890	U
47	WA	1820	G
47	WA	1806	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	H2U	At	20	86	18,21,22	0.44	0	19,30,33	1.05	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	PSU	At	32	86	18,21,22	4.57	6 (33%)	21,30,33	2.95	5 (23%)
86	4SU	At	8	86	18,21,22	3.87	8 (44%)	25,30,33	2.32	4 (16%)
86	H2U	At	16	86	18,21,22	0.47	0	19,30,33	1.02	1 (5%)
86	7MG	At	46	86	23,26,27	3.44	10 (43%)	27,39,42	2.22	9 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	H2U	At	20	86	-	1/7/38/39	0/2/2/2
86	PSU	At	32	86	-	0/7/25/26	0/2/2/2
86	4SU	At	8	86	-	0/7/25/26	0/2/2/2
86	H2U	At	16	86	-	1/7/38/39	0/2/2/2
86	7MG	At	46	86	-	3/7/37/38	0/3/3/3

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	At	32	PSU	C6-C5	12.62	1.49	1.35
86	At	32	PSU	C2-N1	10.00	1.49	1.36
86	At	46	7MG	C8-N9	8.71	1.51	1.45
86	At	8	4SU	C4-N3	8.22	1.46	1.37
86	At	32	PSU	C2-N3	7.55	1.49	1.37

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	At	8	4SU	C4-N3-C2	-7.97	119.68	127.31
86	At	32	PSU	N1-C2-N3	7.70	123.29	115.17
86	At	32	PSU	C4-N3-C2	-6.30	117.69	126.37
86	At	46	7MG	C2-N3-C4	5.68	122.08	112.30
86	At	8	4SU	C5-C4-N3	5.59	119.95	114.75

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	At	46	7MG	O4'-C4'-C5'-O5'

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
86	At	46	7MG	C3'-C4'-C5'-O5'
86	At	16	H2U	C4'-C5'-O5'-P
86	At	46	7MG	C4'-C5'-O5'-P
86	At	20	H2U	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	At	8	4SU	1	0
86	At	46	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 113 ligands modelled in this entry, 110 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
90	SPD	WA	5179	-	9,9,9	0.27	0	8,8,8	0.26	0
89	ANM	WA	5178	-	20,20,20	4.07	7 (35%)	24,27,27	1.47	2 (8%)
91	SER	ZA	1919	-	4,5,6	0.58	0	1,5,7	0.56	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
90	SPD	WA	5179	-	-	0/7/7/7	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
89	ANM	WA	5178	-	-	4/10/23/23	0/2/2/2
91	SER	ZA	1919	-	-	0/2/4/6	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	WA	5178	ANM	C3-C2	-11.63	1.32	1.53
89	WA	5178	ANM	C16-N1	-8.78	1.30	1.47
89	WA	5178	ANM	C2-C16	7.55	1.68	1.53
89	WA	5178	ANM	C4-C3	4.06	1.58	1.53
89	WA	5178	ANM	C4-N1	3.88	1.60	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	WA	5178	ANM	O2-C5-C6	5.41	120.73	111.09
89	WA	5178	ANM	C12-C15-C16	-2.05	109.93	113.40

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
89	WA	5178	ANM	C6-C5-O2-C2
89	WA	5178	ANM	O3-C5-O2-C2
89	WA	5178	ANM	C1-C9-O1-C14
89	WA	5178	ANM	C10-C9-O1-C14

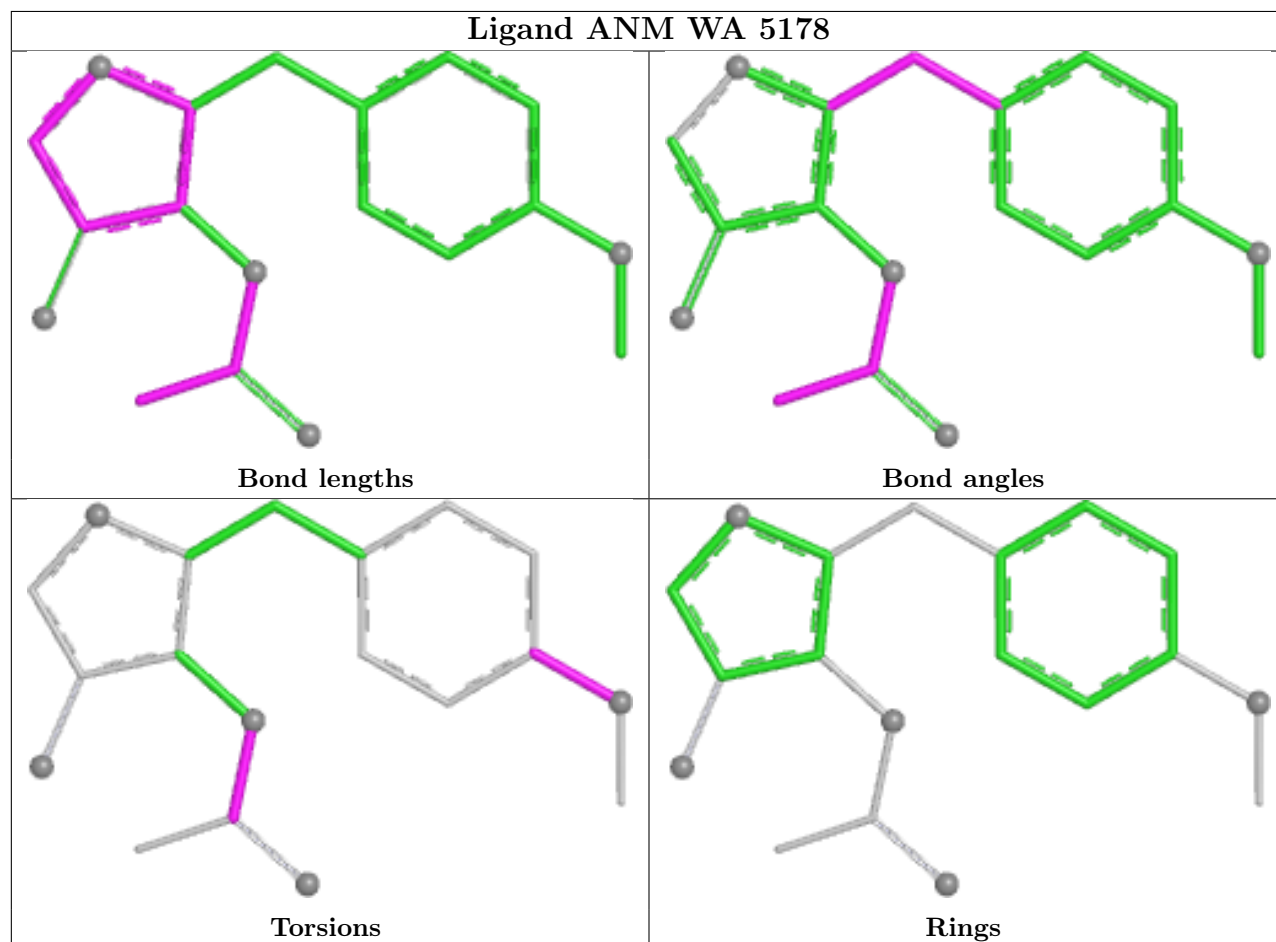
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
90	WA	5179	SPD	1	0
89	WA	5178	ANM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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
47	WA	20

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	WA	2118:C	O3'	2260:C	P	37.44
1	WA	1225:G	O3'	1239:G	P	19.90
1	WA	763:G	O3'	904:C	P	18.09
1	WA	996:C	O3'	1070:G	P	17.05
1	WA	524:C	O3'	639:G	P	16.87

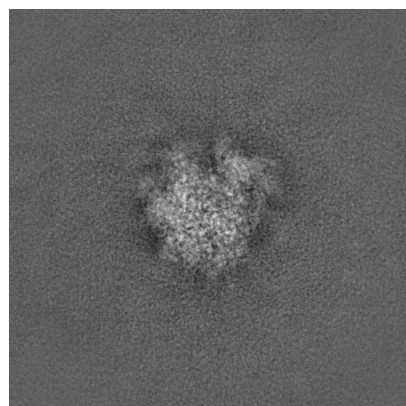
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43569. These allow visual inspection of the internal detail of the map and identification of artifacts.

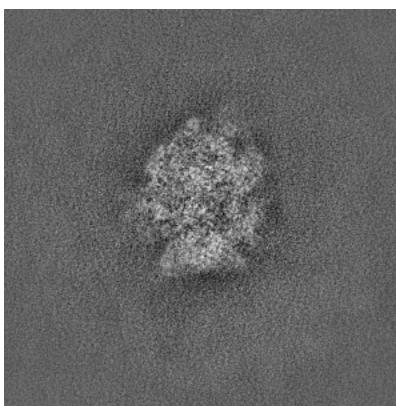
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

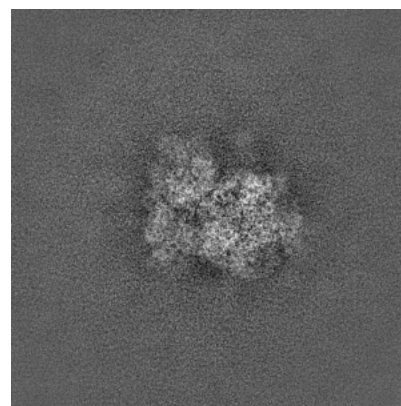
6.1.1 Primary map



X

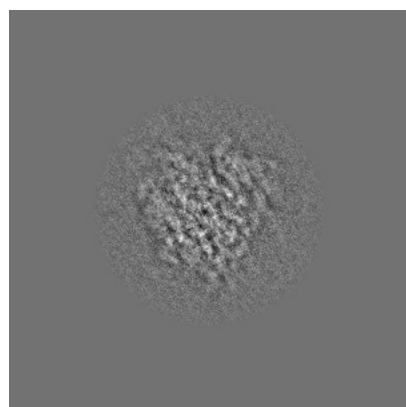


Y

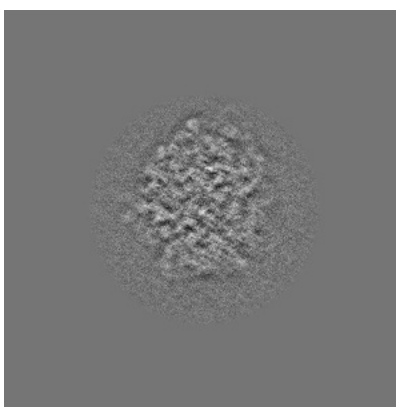


Z

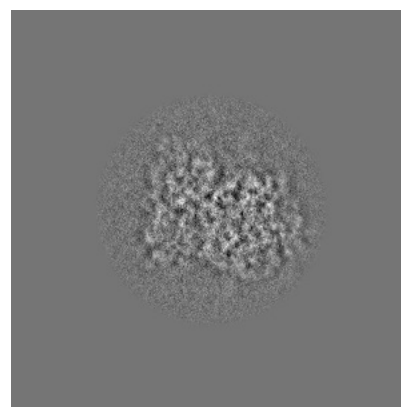
6.1.2 Raw map



X



Y

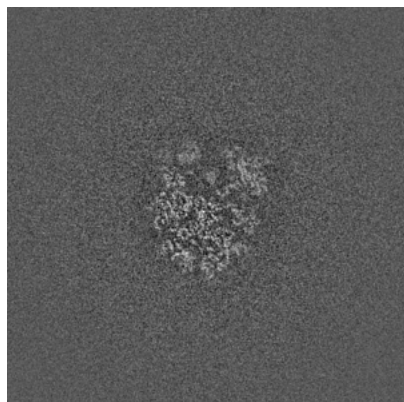


Z

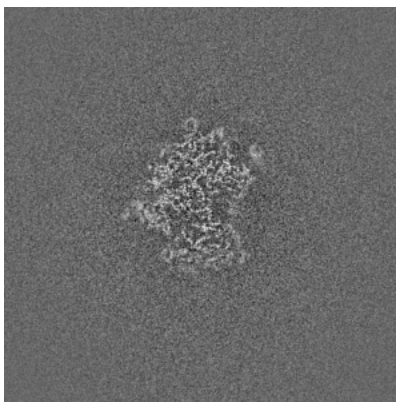
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

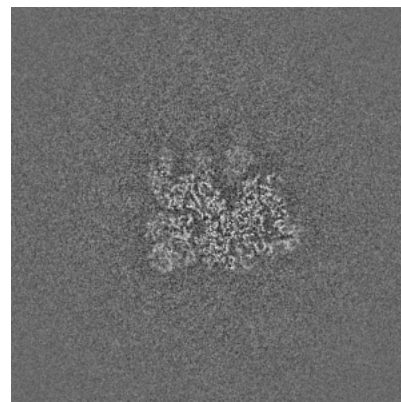
6.2.1 Primary map



X Index: 324

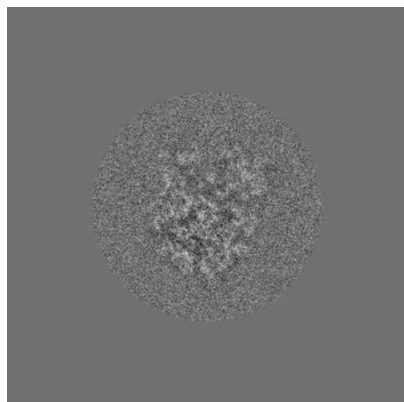


Y Index: 324

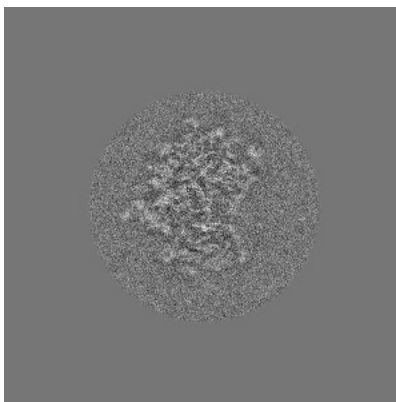


Z Index: 324

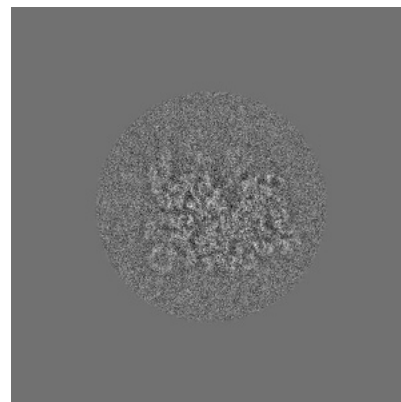
6.2.2 Raw map



X Index: 324



Y Index: 324

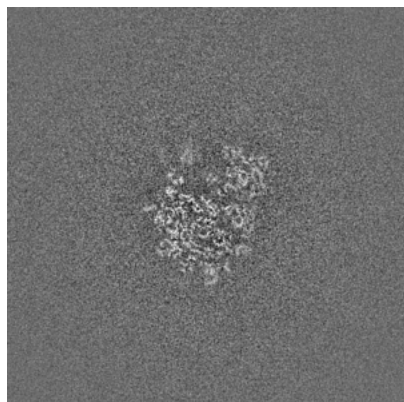


Z Index: 324

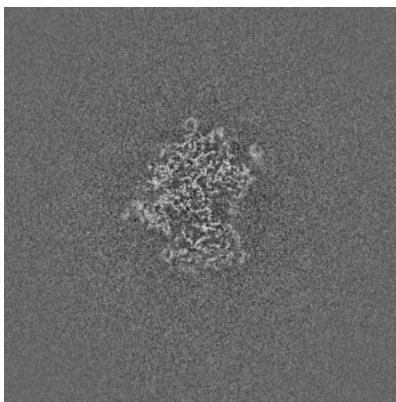
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

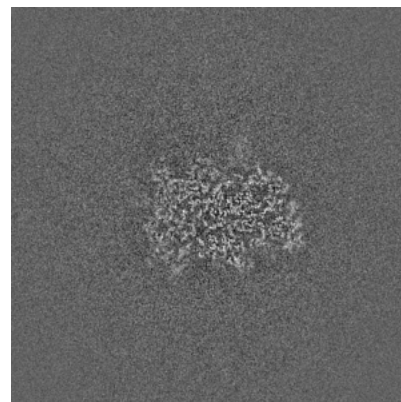
6.3.1 Primary map



X Index: 320

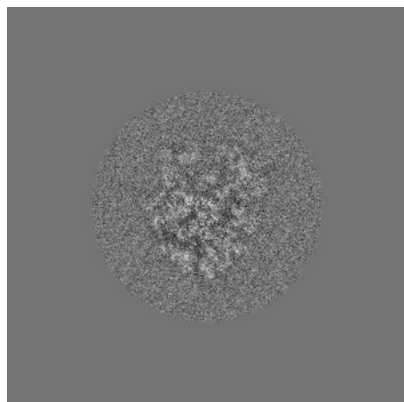


Y Index: 324

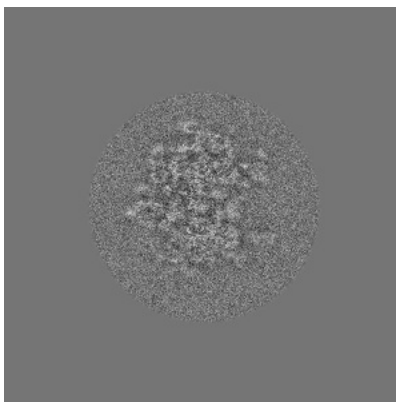


Z Index: 311

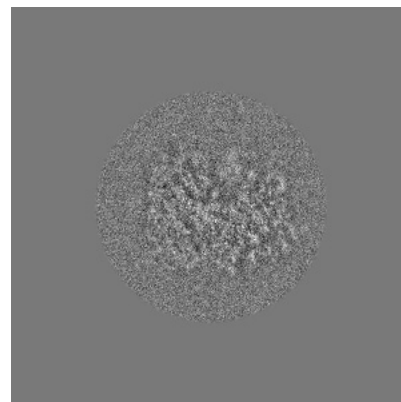
6.3.2 Raw map



X Index: 325



Y Index: 333

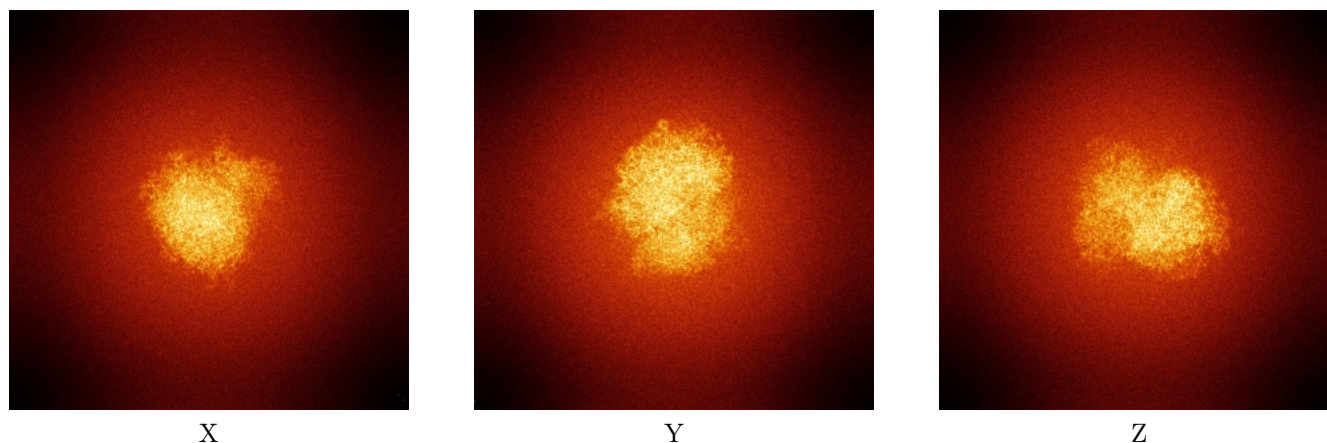


Z Index: 331

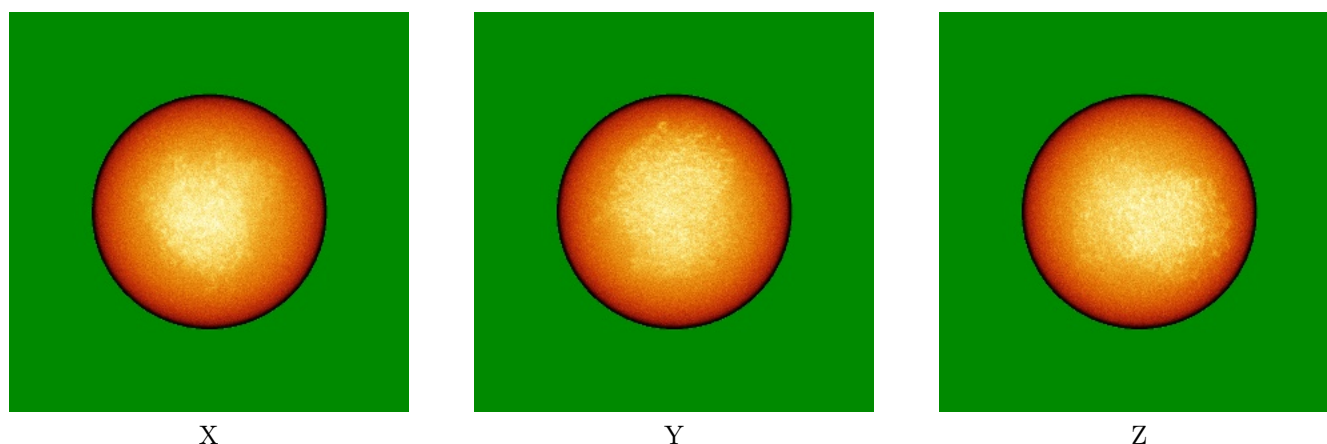
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

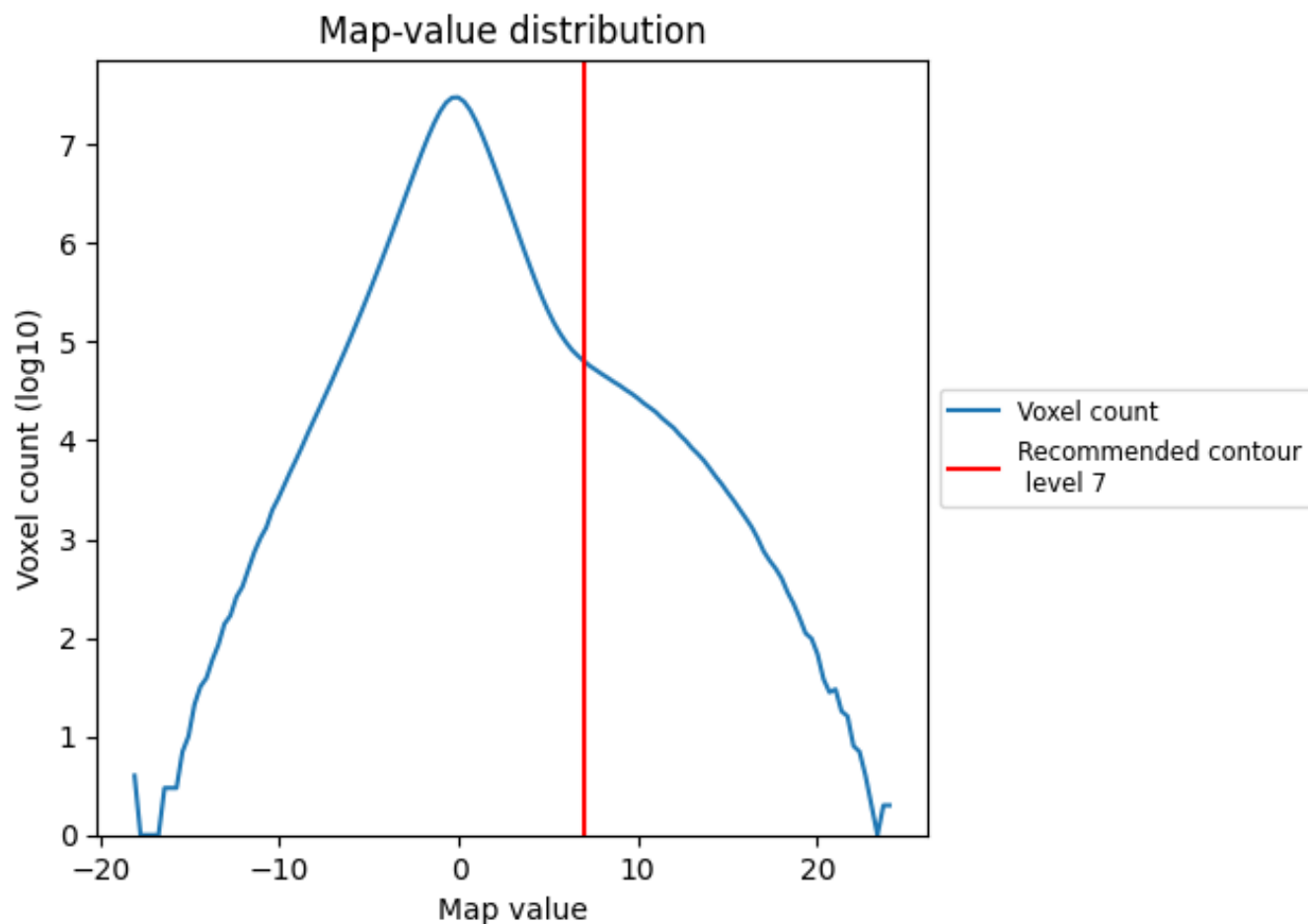
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

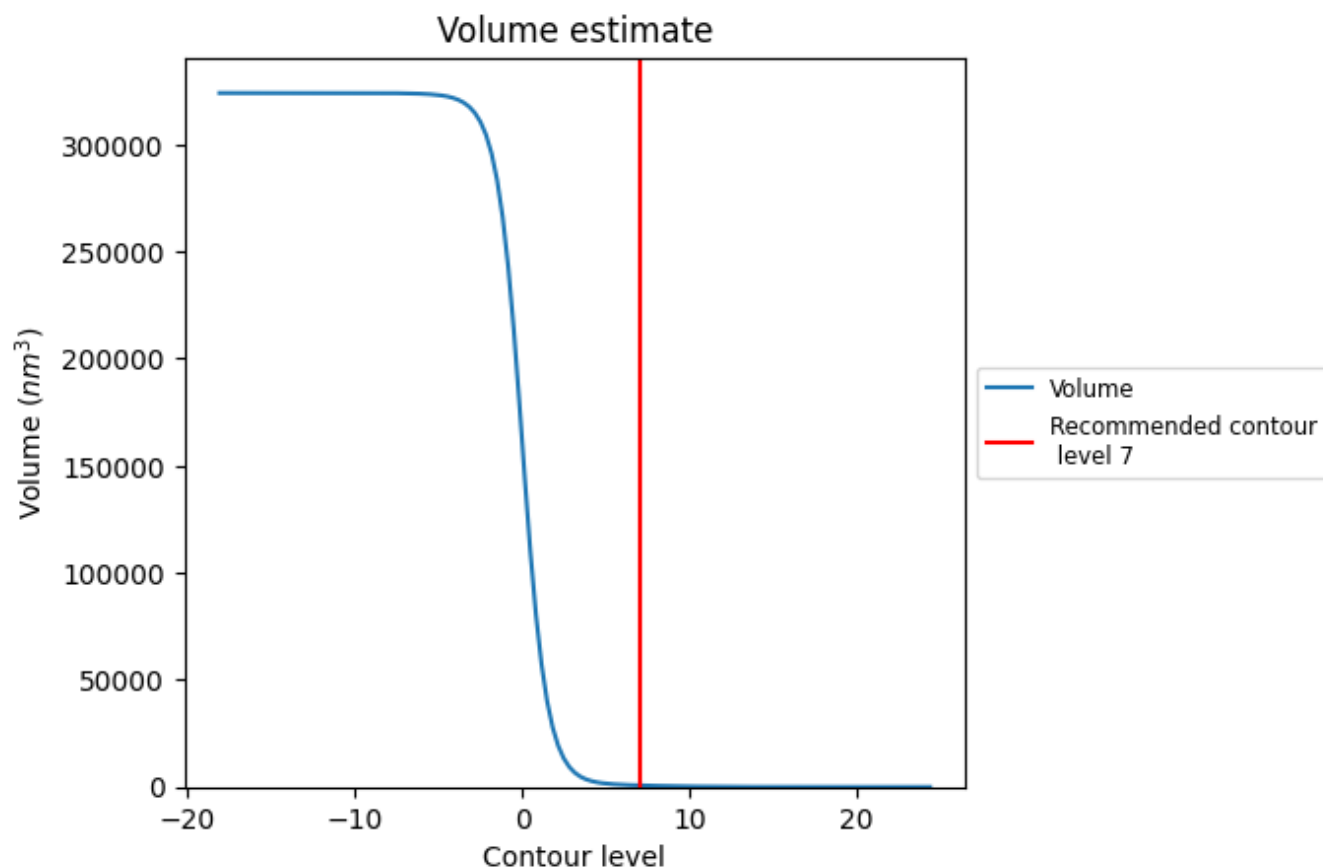
This section contains the results of statistical analysis of the map.

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.

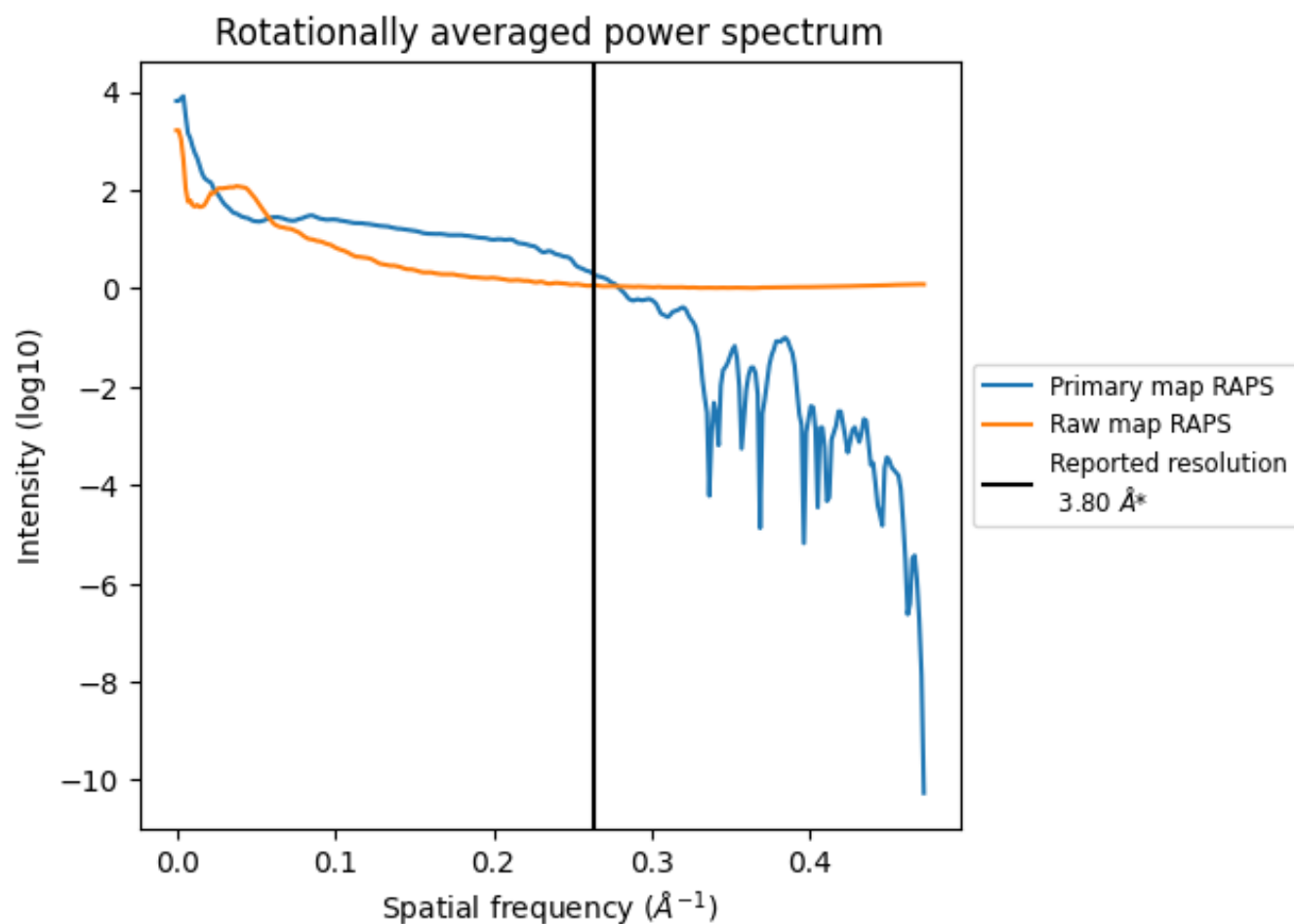
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 724 nm^3 ; this corresponds to an approximate mass of 654 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 ⓘ

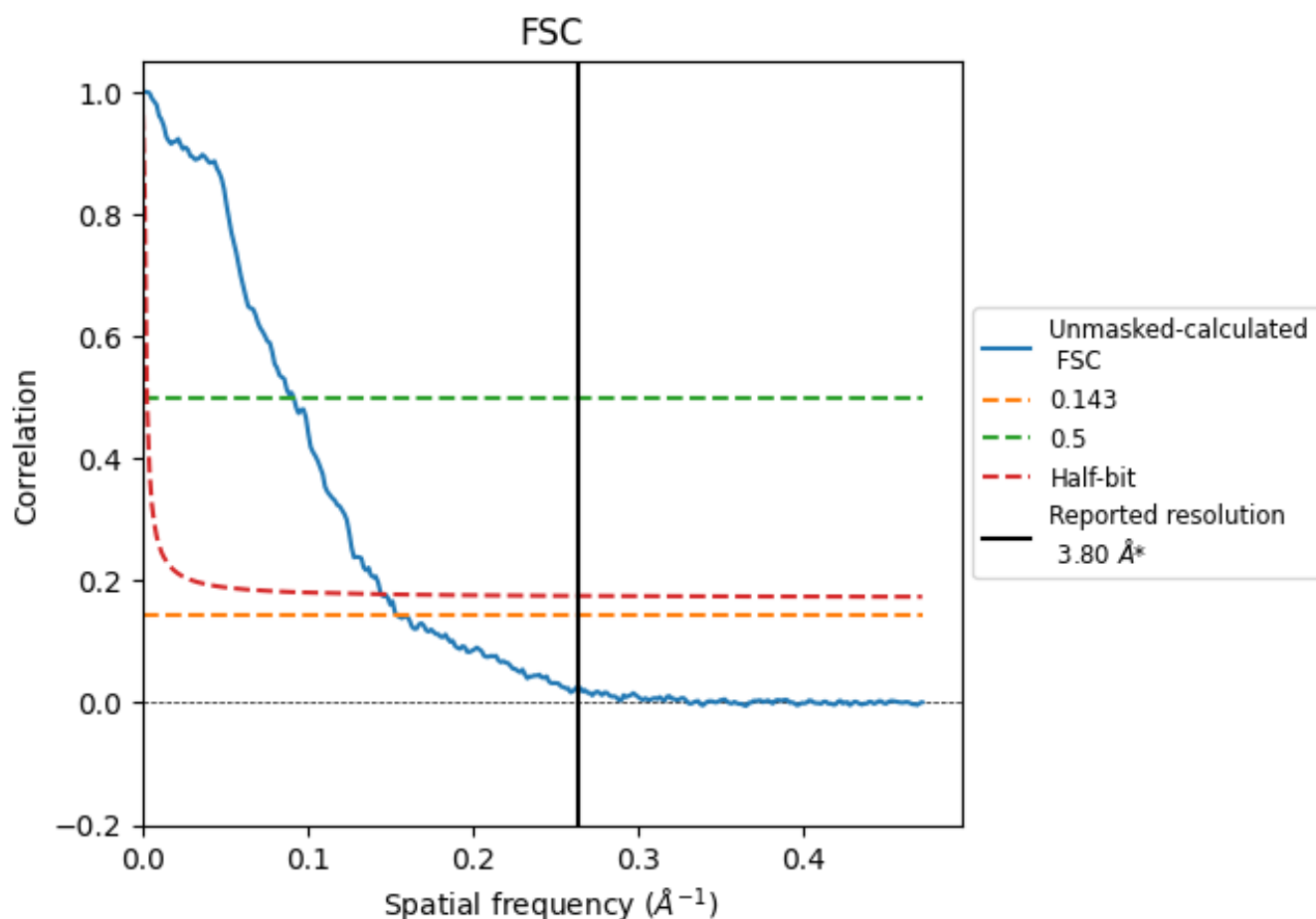


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

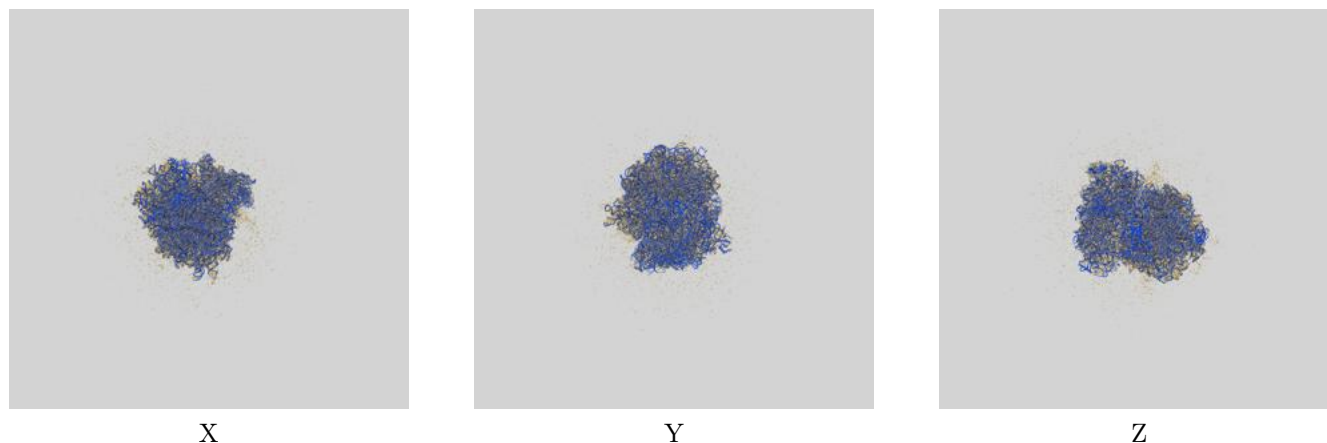
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.49	10.93	6.91

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.49 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

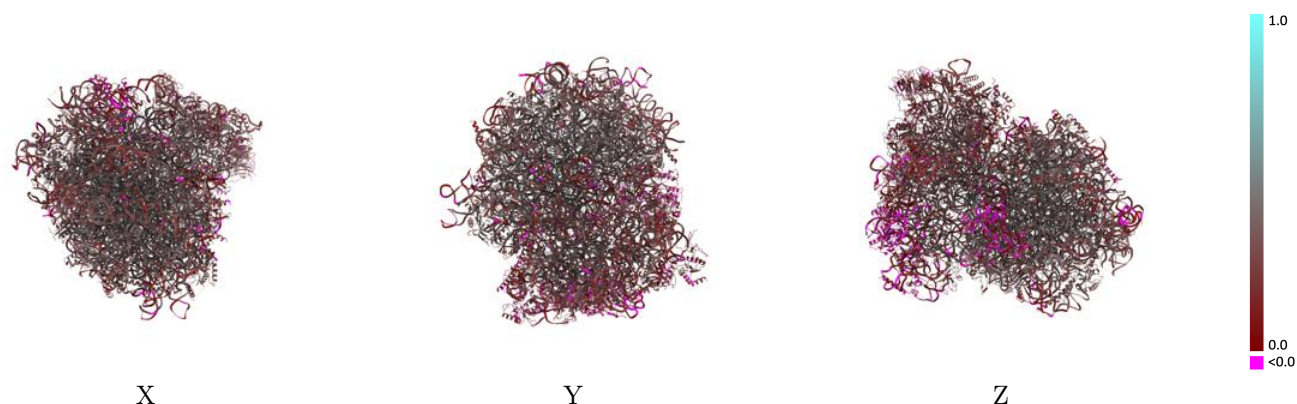
This section contains information regarding the fit between EMDB map EMD-43569 and PDB model 8VVU. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



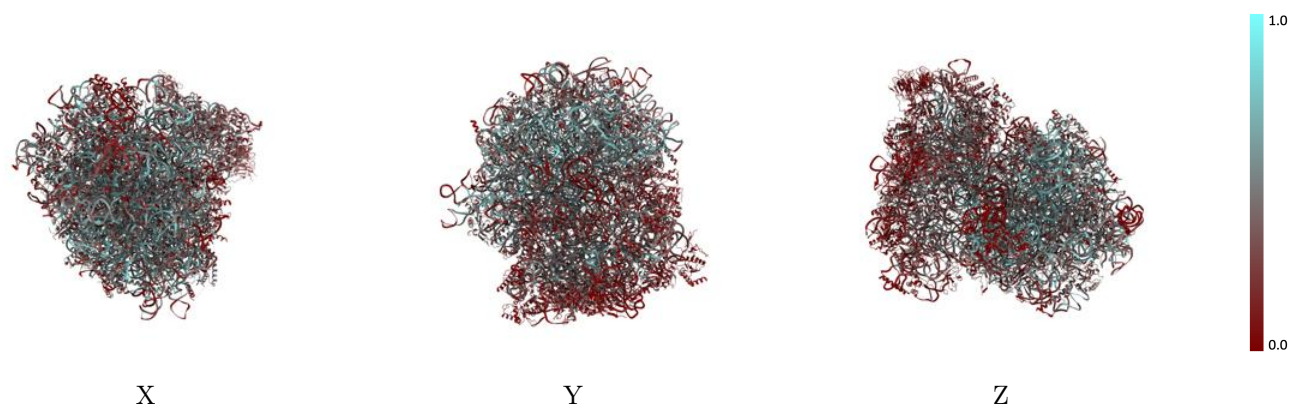
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



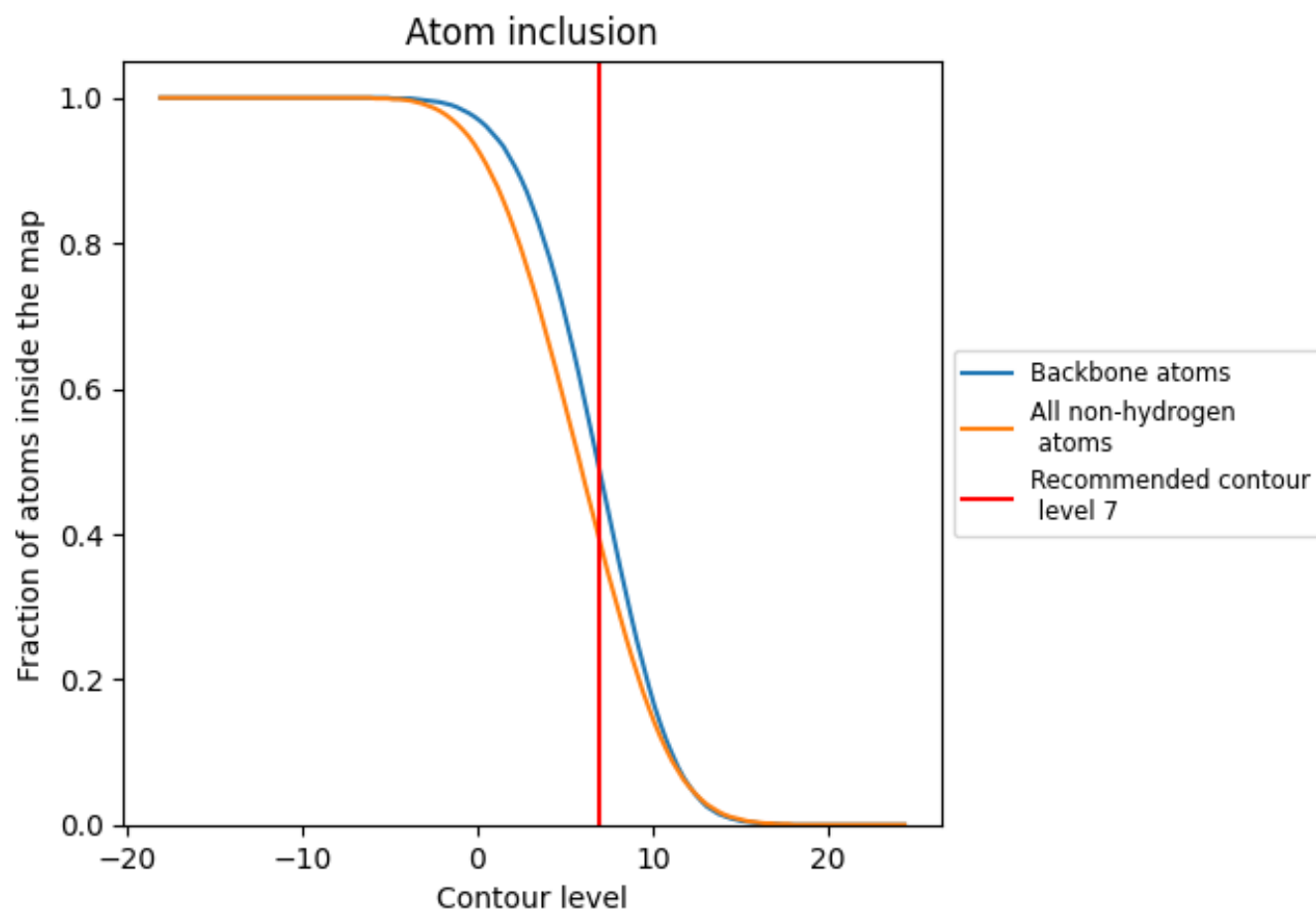
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7).

9.4 Atom inclusion [i](#)



At the recommended contour level, 48% of all backbone atoms, 39% 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 (7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3890	0.3110
A	0.3430	0.3890
AA	0.3150	0.2980
AB	0.2230	0.2650
AC	0.2340	0.3270
At	0.2220	0.2100
B	0.3600	0.3730
BA	0.3320	0.3210
BB	0.1800	0.2300
BC	0.1630	0.2540
C	0.3800	0.3740
CA	0.3550	0.3570
CB	0.2250	0.3050
CC	0.1790	0.2500
D	0.3380	0.3140
DA	0.3380	0.3840
DB	0.2270	0.2860
DC	0.2530	0.3310
E	0.2860	0.3230
EA	0.3490	0.3990
EB	0.0810	0.0240
EC	0.2230	0.2220
F	0.3760	0.3640
FA	0.3160	0.3660
FB	0.2190	0.2640
FC	0.0960	0.2040
G	0.3590	0.3140
GA	0.3970	0.3440
GB	0.1510	0.1960
GC	0.1170	0.2140
H	0.3320	0.3310
HA	0.3730	0.3390
HB	0.1480	0.2150
I	0.3490	0.3780
IA	0.3900	0.3970



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
IB	 0.2110	 0.2780
IC	 0.1000	 0.3680
J	 0.2820	 0.2820
JA	 0.2710	 0.3010
JB	 0.2530	 0.2520
K	 0.3810	 0.3560
KA	 0.3610	 0.3550
KB	 0.2220	 0.2430
L	 0.3720	 0.3480
LA	 0.3800	 0.3530
LB	 0.2170	 0.3180
M	 0.3680	 0.3950
MA	 0.2940	 0.3540
MB	 0.0780	 0.1740
N	 0.3890	 0.3610
NA	 0.3320	 0.3760
NB	 0.2250	 0.2840
O	 0.3880	 0.3750
OA	 0.3880	 0.3580
OB	 0.1800	 0.2650
P	 0.3920	 0.3870
PA	 0.3750	 0.3780
PB	 0.2040	 0.2490
Q	 0.3680	 0.3140
QB	 0.2110	 0.2720
R	 0.3500	 0.3790
RA	 0.0250	 0.0600
RB	 0.2000	 0.2580
S	 0.3380	 0.3630
SA	 0.3190	 0.2880
SB	 0.2400	 0.2660
T	 0.3070	 0.2930
TA	 0.0660	 0.1450
TB	 0.2060	 0.2670
U	 0.3190	 0.3800
UB	 0.2150	 0.2810
V	 0.2310	 0.2420
VA	 0.3330	 0.3430
VB	 0.2150	 0.2990
W	 0.3630	 0.3520
WA	 0.5260	 0.3490
WB	 0.1980	 0.3130

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
X	 0.3530	 0.3570
XA	 0.6260	 0.3690
XB	 0.2690	 0.3310
Y	 0.3700	 0.3410
YA	 0.5590	 0.3550
YB	 0.0960	 0.0590
Z	 0.3600	 0.3980
ZA	 0.3750	 0.2630
ZB	 0.1990	 0.2260
b	 0.0220	 0.0650