



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:06 PM UTC

PDB ID : 6SGB / pdb_00006sgb
EMDB ID : EMD-10180
Title : mt-SSU assemblosome of Trypanosoma brucei
Authors : Saurer, M.; Ramrath, D.J.F.; Niemann, M.; Calderaro, S.; Prange, C.; Mattei, S.; Scaiola, A.; Leitner, A.; Bieri, P.; Horn, E.K.; Leibundgut, M.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2019-08-03
Resolution : 3.30 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:

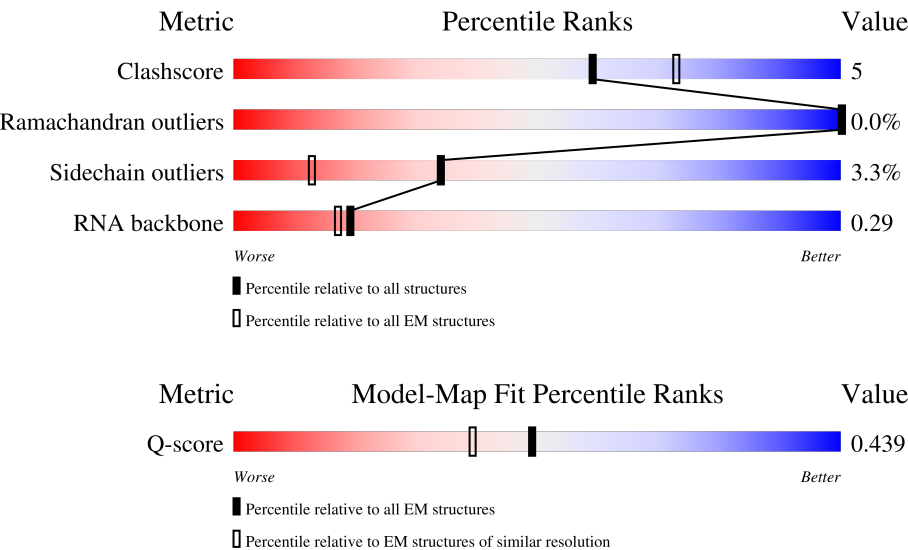
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	CE	435	15% 79% 11% 10%
2	CF	160	84% 15%
3	CH	282	7% 67% 11% 21%

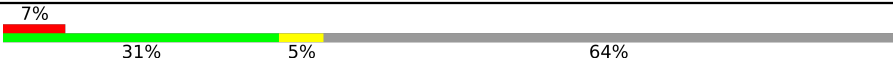
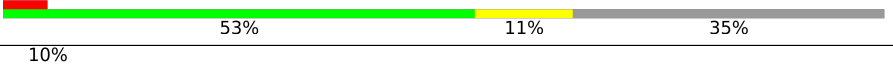
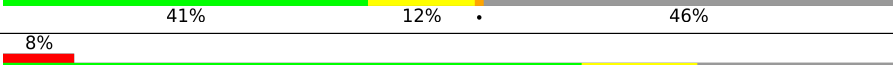
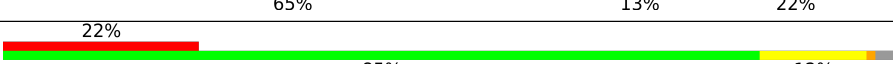
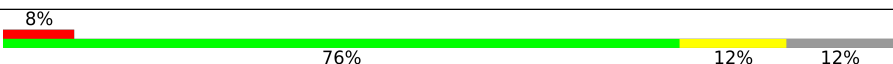
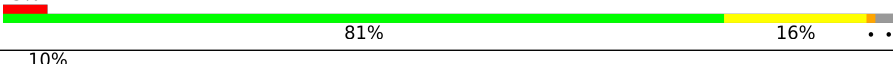
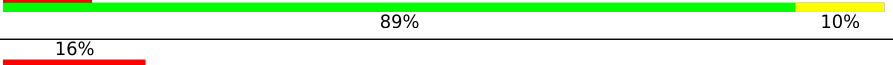
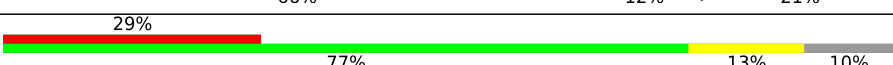
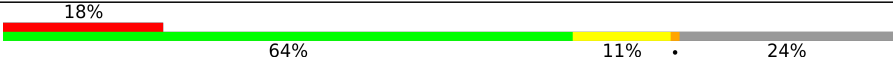
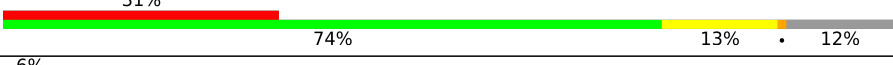
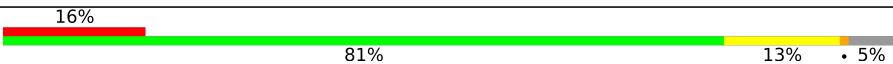
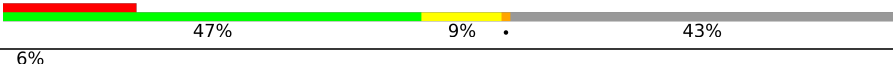
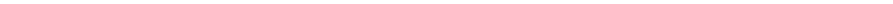
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Mol	Chain	Length	Quality of chain
4	CK	326	
5	CO	429	
6	CP	188	
7	CQ	336	
8	CR	320	
9	Ca	602	
10	Cb	311	
11	Cd	440	
12	Cj	257	
13	Cn	250	
14	Cp	187	
15	DD	812	
16	DI	407	
17	DL	307	
18	DO	282	
19	DP	274	
20	DR	270	
21	DU	228	
22	DZ	94	
23	F2	1024	
24	F3	966	
25	F5	754	
26	F6	676	
27	F7	679	
28	F8	726	

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Mol	Chain	Length	Quality of chain
29	F9	608	
30	FA	642	
31	FB	579	
31	FC	579	
32	FE	553	
33	FJ	362	
34	FM	370	
34	FN	370	
35	FO	334	
36	FP	349	
37	FQ	307	
37	FR	307	
37	FS	307	
37	FT	307	
37	FU	307	
38	FW	263	
39	FX	239	
40	FY	188	
41	FZ	178	
42	Fa	171	
43	Fb	151	
44	Fc	148	
45	Fd	143	
46	UA	21	
47	UB	27	

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Mol	Chain	Length	Quality of chain
47	Uk	27	44% 85% 15%
48	UC	10	10% 90% 10%
49	UD	9	56% 44%
49	UM	9	22% 78% 22%
49	UQ	9	56% 67% 33%
49	Uf	9	33% 56% 44%
50	UE	45	62% 91% 9%
50	UP	45	71% 78% 22%
51	UF	11	27% 82% 18%
51	Um	11	45% 91% 9%
52	UG	17	12% 65% 35%
53	UH	5	40% 80% 20%
54	UI	8	25% 62% 38%
54	UN	8	25% 88% 12%
55	UJ	16	56% 88% 12%
56	UK	24	79% 96% .
57	UL	22	32% 91% 9%
58	UO	30	37% 67% 33%
59	UY	468	100% 65% 35%
60	CA	620	41% 49% 42% 7% .
61	CC	74	45% 81% 19%
62	CI	443	15% 82% 13% 5%
63	CJ	817	24% 74% 11% . 14%
64	CN	166	70% 73% 17% . 8%
65	CS	244	34% 30% 5% 65%

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Mol	Chain	Length	Quality of chain
66	Cg	498	
67	Ci	181	
68	Ck	874	
69	DB	1181	
70	DC	1165	
71	DE	747	
72	DF	666	
73	DG	631	
74	DH	581	
75	DJ	396	
76	DK	324	
77	DT	247	
78	DV	183	
79	DW	179	
80	DX	169	
81	DY	163	
82	F1	1041	
83	F4	811	
84	FD	579	
85	FF	474	
86	FG	463	
87	FH	457	
88	FI	445	
89	FK	372	
90	FL	353	

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Mol	Chain	Length	Quality of chain
91	FV	264	
92	Fe	123	
93	Ua	47	
94	Ub	42	
95	Uc	12	
96	Ud	59	
97	Ue	29	
98	Ug	167	
99	Uh	255	
100	Ui	32	
101	Uj	19	
102	Ul	14	
103	Ux	110	

2 Entry composition

There are 110 unique types of molecules in this entry. The entry contains 240624 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 uS5m.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CE	392	Total	C	N	O	S	0	0
			3147	1992	579	561	15		

- Molecule 2 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CF	159	Total	C	N	O	S	0	0
			1317	835	234	242	6		

- Molecule 3 is a protein called uS8m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CH	222	Total	C	N	O	S	0	0
			1824	1144	349	321	10		

- Molecule 4 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CK	211	Total	C	N	O	S	0	0
			1721	1084	316	311	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	conflict	UNP Q389T7

- Molecule 5 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CO	358	Total	C	N	O	S	0	0
			2979	1891	557	514	17		

- Molecule 6 is a protein called bS16m.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CP	180	Total	C	N	O	S	0	0
			1489	956	274	250	9		

- Molecule 7 is a protein called uS17m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CQ	219	Total	C	N	O	S	0	0
			1805	1151	340	306	8		

- Molecule 8 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CR	153	Total	C	N	O	S	0	0
			1274	821	233	218	2		

- Molecule 9 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ca	512	Total	C	N	O	S	0	0
			4340	2778	770	771	21		

- Molecule 10 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Cb	153	Total	C	N	O	S	0	0
			1274	819	232	217	6		

- Molecule 11 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Cd	185	Total	C	N	O	S	0	0
			1616	1032	297	279	8		

- Molecule 12 is a protein called mS34.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Cj	226	Total	C	N	O	S	0	0
			1792	1138	310	340	4		

- Molecule 13 is a protein called mS38.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	Cn	27	Total	C	N	O	0	0
			234	155	44	35		

- Molecule 14 is a protein called mS41.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Cp	178	Total	C	N	O	S	0	0
			1506	952	272	277	5		

- Molecule 15 is a protein called mS51 (KRIPP1).

Mol	Chain	Residues	Atoms					AltConf	Trace
15	DD	786	Total	C	N	O	S	0	0
			6488	4110	1168	1169	41		

- Molecule 16 is a protein called mS56.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	DI	390	Total	C	N	O	S	0	0
			3182	2020	554	594	14		

- Molecule 17 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	DL	203	Total	C	N	O	S	0	0
			1656	1059	296	291	10		

- Molecule 18 is a protein called mS62 (KRIPP14).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	DO	204	Total	C	N	O	S	0	0
			1648	1031	300	307	10		

- Molecule 19 is a protein called mS63 (KRIPP16).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	DP	212	Total	C	N	O	S	0	0
			1800	1156	321	314	9		

- Molecule 20 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	DR	254	Total	C	N	O	S	0	0
			2042	1313	373	346	10		

- Molecule 21 is a protein called mS68.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	DU	219	Total	C	N	O	S	0	0
			1738	1095	308	331	4		

- Molecule 22 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	DZ	30	Total	C	N	O	S	0	0
			254	167	41	45	1		

- Molecule 23 is a protein called mt-SAF2 (KRIPP2).

Mol	Chain	Residues	Atoms					AltConf	Trace
23	F2	915	Total	C	N	O	S	0	0
			7274	4570	1281	1384	39		

- Molecule 24 is a protein called mt-SAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	F3	888	Total	C	N	O	S	0	0
			6879	4302	1222	1303	52		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F3	44	THR	ALA	conflict	UNP Q38E61
F3	190	VAL	ILE	conflict	UNP Q38E61
F3	303	ALA	SER	conflict	UNP Q38E61
F3	418	ASP	ASN	conflict	UNP Q38E61

- Molecule 25 is a protein called mt-SAF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	F5	480	Total	C	N	O	S	0	0
			3474	2167	646	647	14		

- Molecule 26 is a protein called mt-SAF6.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	F6	456	Total	C	N	O	S	0	0
			3646	2311	635	686	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F6	285	ARG	HIS	conflict	UNP Q38FQ8
F6	291	ILE	THR	conflict	UNP Q38FQ8
F6	602	ALA	VAL	conflict	UNP Q38FQ8
F6	676	CYS	PHE	conflict	UNP Q38FQ8

- Molecule 27 is a protein called mt-SAF7 (KRIPP10).

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F7	662	Total	C	N	O	S	0	0
			5225	3322	918	950	35		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F7	36	ILE	THR	conflict	UNP Q57UW6
F7	470	GLU	LYS	conflict	UNP Q57UW6
F7	474	VAL	ALA	conflict	UNP Q57UW6

- Molecule 28 is a protein called mt-SAF8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F8	513	Total	C	N	O	S	0	0
			3934	2493	721	701	19		

- Molecule 29 is a protein called mt-SAF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F9	216	Total	C	N	O	S	0	0
			1755	1088	325	337	5		

- Molecule 30 is a protein called mt-SAF10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	FA	579	Total	C	N	O	S	0	0
			4421	2801	785	813	22		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FA	173	ALA	THR	conflict	UNP Q386U1
FA	352	TYR	HIS	conflict	UNP Q386U1

- Molecule 31 is a protein called mt-SAF11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	FB	377	Total	C	N	O	S	0	0
			3055	1928	574	543	10		
31	FC	311	Total	C	N	O	S	0	0
			2572	1629	488	447	8		

- Molecule 32 is a protein called mt-SAF13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	FE	434	Total	C	N	O	S	0	0
			3523	2268	611	626	18		

- Molecule 33 is a protein called mt-SAF18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	FJ	353	Total	C	N	O	S	0	0
			2917	1843	550	516	8		

- Molecule 34 is a protein called mt-SAF21.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	FM	326	Total	C	N	O	S	0	0
			2449	1515	449	465	20		
34	FN	319	Total	C	N	O	S	0	0
			2392	1478	436	458	20		

- Molecule 35 is a protein called mt-SAF22 (KRIPP17).

Mol	Chain	Residues	Atoms					AltConf	Trace
35	FO	324	Total	C	N	O	S	0	0
			2671	1674	509	474	14		

- Molecule 36 is a protein called mt-SAF23.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	FP	348	Total	C	N	O	S	0	0
			2643	1682	464	487	10		

- Molecule 37 is a protein called mt-SAF24.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	FQ	257	Total	C	N	O	S	0	0
			2003	1265	358	373	7		
37	FR	243	Total	C	N	O	S	0	0
			1923	1217	344	355	7		
37	FS	277	Total	C	N	O	S	0	0
			2198	1389	397	404	8		
37	FT	233	Total	C	N	O	S	0	0
			1854	1177	331	339	7		
37	FU	270	Total	C	N	O	S	0	0
			2105	1331	380	386	8		

- Molecule 38 is a protein called mt-SAF26.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	FW	247	Total	C	N	O	S	0	0
			2034	1272	384	371	7		

- Molecule 39 is a protein called mt-SAF27 (KRIPP11).

Mol	Chain	Residues	Atoms					AltConf	Trace
39	FX	220	Total	C	N	O	S	0	0
			1741	1093	318	316	14		

- Molecule 40 is a protein called mt-SAF28.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	FY	160	Total	C	N	O	S	0	0
			1289	819	229	235	6		

- Molecule 41 is a protein called mt-SAF29.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	FZ	133	Total	C	N	O	S	0	0
			973	605	181	185	2		

- Molecule 42 is a protein called mt-SAF30.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Fa	163	Total	C	N	O	S	0	0
			1323	860	236	223	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Fa	73	ALA	VAL	conflict	UNP Q57VU7

- Molecule 43 is a protein called mt-SAF31.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Fb	129	Total	C	N	O	S	0	0
			1091	701	198	184	8		

- Molecule 44 is a protein called mt-SAF32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Fc	84	Total	C	N	O	S	0	0
			669	427	106	135	1		

- Molecule 45 is a protein called mt-SAF33.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Fd	96	Total	C	N	O	S	0	0
			758	481	147	122	8		

- Molecule 46 is a protein called UNK-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	UA	21	Total	C	N	O	0	0
			126	84	21	21		

- Molecule 47 is a protein called UNK-B, UNK-k.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	UB	27	Total	C	N	O	0	0
			162	108	27	27		
47	Uk	27	Total	C	N	O	0	0
			162	108	27	27		

- Molecule 48 is a protein called UNK-C.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	UC	10	Total	C	N	O	0	0
			60	40	10	10		

- Molecule 49 is a protein called UNK-D, UNK-M, UNK-Q, UNK-f.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	UD	9	Total	C	N	O	0	0
			54	36	9	9		
49	UM	9	Total	C	N	O	0	0
			54	36	9	9		
49	UQ	9	Total	C	N	O	0	0
			54	36	9	9		
49	Uf	9	Total	C	N	O	0	0
			54	36	9	9		

- Molecule 50 is a protein called UNK-E, UNK-P.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	UE	45	Total	C	N	O	0	0
			270	180	45	45		
50	UP	45	Total	C	N	O	0	0
			270	180	45	45		

- Molecule 51 is a protein called UNK-F, UNK-m.

Mol	Chain	Residues	Atoms				AltConf	Trace
51	UF	11	Total	C	N	O	0	0
			66	44	11	11		
51	Um	11	Total	C	N	O	0	0
			66	44	11	11		

- Molecule 52 is a protein called UNK-G.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	UG	17	Total	C	N	O	0	0
			102	68	17	17		

- Molecule 53 is a protein called UNK-H.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	UH	5	Total	C	N	O	0	0
			30	20	5	5		

- Molecule 54 is a protein called UNK-I, UNK-N.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	UI	8	Total	C	N	O	0	0
			48	32	8	8		
54	UN	8	Total	C	N	O	0	0
			48	32	8	8		

- Molecule 55 is a protein called UNK-J.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	UJ	16	Total	C	N	O	0	0
			96	64	16	16		

- Molecule 56 is a protein called UNK-K.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	UK	24	Total	C	N	O	0	0
			144	96	24	24		

- Molecule 57 is a protein called UNK-L.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	UL	22	Total	C	N	O	0	0
			132	88	22	22		

- Molecule 58 is a protein called UNK-O.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	UO	30	Total	C	N	O	0	0
			180	120	30	30		

- Molecule 59 is a protein called UNK-Y.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	UY	468	Total	C	N	O	0	0
			2808	1872	468	468		

- Molecule 60 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	CA	609	Total	C	N	O	P	0	0
			11352	5038	1602	4102	610		

- Molecule 61 is a protein called mS3m.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	CC	74	Total	C	N	O	S	0	0
			646	451	96	98	1		

- Molecule 62 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	CI	423	Total	C	N	O	S	0	0
			3357	2108	601	631	17		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CI	370	ALA	VAL	conflict	UNP Q57W62

- Molecule 63 is a protein called uS10m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CJ	701	Total	C	N	O	S	0	0
			5709	3605	1017	1064	23		

- Molecule 64 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CN	153	Total	C	N	O	S	0	0
			1285	820	242	216	7		

- Molecule 65 is a protein called uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	CS	85	Total	C	N	O	S	0	0
			708	463	121	121	3		

- Molecule 66 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cg	484	Total	C	N	O	S	0	0
			3922	2511	688	703	20		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cg	181	VAL	ALA	conflict	UNP Q585C2
Cg	498	ARG	MET	conflict	UNP Q585C2

- Molecule 67 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ci	147	Total	C	N	O	S	0	0
			1222	770	226	218	8		

- Molecule 68 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ck	638	Total	C	N	O	S	0	0
			5123	3220	927	953	23		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ck	107	SER	LEU	conflict	UNP Q387C7
Ck	144	PHE	LEU	conflict	UNP Q387C7
Ck	253	TYR	PHE	conflict	UNP Q387C7
Ck	339	GLU	VAL	conflict	UNP Q387C7
Ck	871	GLY	GLU	conflict	UNP Q387C7

- Molecule 69 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	DB	679	Total	C	N	O	S	0	0
			5688	3558	1062	1047	21		

- Molecule 70 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	DC	1028	Total	C	N	O	S	0	0
			8223	5194	1453	1546	30		

- Molecule 71 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	DE	590	Total	C	N	O	S	0	0
			4639	2957	832	834	16		

- Molecule 72 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	DF	491	Total	C	N	O	S	0	0
			3967	2496	745	703	23		

- Molecule 73 is a protein called mS54.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	DG	566	Total	C	N	O	S	0	0
			4575	2875	835	834	31		

- Molecule 74 is a protein called mS55 (KRIPP8).

Mol	Chain	Residues	Atoms					AltConf	Trace
74	DH	472	Total	C	N	O	S	0	0
			3849	2417	720	693	19		

- Molecule 75 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	DJ	308	Total	C	N	O	S	0	0
			2521	1612	446	450	13		

- Molecule 76 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	DK	245	Total	C	N	O	S	0	0
			1929	1213	349	362	5		

- Molecule 77 is a protein called mS67.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	DT	221	Total	C	N	O	S	0	0
			1912	1231	334	337	10		

- Molecule 78 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	DV	157	Total	C	N	O	S	0	0
			1323	840	248	231	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DV	163	ALA	THR	conflict	UNP Q57UZ6

- Molecule 79 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	DW	133	Total	C	N	O	S	0	0
			1140	730	216	190	4		

- Molecule 80 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	DX	115	Total	C	N	O	S	0	0
			967	612	182	166	7		

- Molecule 81 is a protein called mS72.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	DY	154	Total	C	N	O	S	0	0
			1295	829	247	214	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DY	34	HIS	ASP	conflict	UNP Q57YD4

- Molecule 82 is a protein called mt-SAF1 (RSM22).

Mol	Chain	Residues	Atoms					AltConf	Trace
82	F1	889	Total	C	N	O	S	0	0
			7194	4493	1372	1289	40		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F1	707	SER	GLY	conflict	UNP Q385R2
F1	973	THR	MET	conflict	UNP Q385R2

- Molecule 83 is a protein called mt-SAF4.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	F4	541	Total	C	N	O	S	0	0
			4382	2783	775	802	22		

- Molecule 84 is a protein called mt-SAF12 (KRIPP18).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	FD	394	Total	C	N	O	S	0	0
			3135	2004	546	566	19		

- Molecule 85 is a protein called mt-SAF14.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	FF	408	Total	C	N	O	S	0	0
			3265	2052	586	603	24		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FF	70	ALA	PRO	conflict	UNP Q57W60
FF	179	PHE	LEU	conflict	UNP Q57W60

- Molecule 86 is a protein called mt-SAF15.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	FG	169	Total	C	N	O	S	0	0
			1359	852	260	240	7		

- Molecule 87 is a protein called mt-SAF16.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	FH	317	Total	C	N	O	S	0	0
			2486	1555	440	471	20		

- Molecule 88 is a protein called mt-SAF17.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	FI	348	Total	C	N	O	S	0	0
			2786	1726	510	537	13		

- Molecule 89 is a protein called mt-SAF19.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	FK	208	Total	C	N	O	S	0	0
			1699	1084	284	325	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FK	38	HIS	ARG	conflict	UNP Q57XS8

- Molecule 90 is a protein called mt-SAF20.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	FL	320	Total	C	N	O	S	0	0
			2555	1609	470	459	17		

- Molecule 91 is a protein called mt-SAF25.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	FV	210	Total	C	N	O	S	0	0
			1636	1039	283	303	11		

- Molecule 92 is a protein called mt-SAF34.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Fe	122	Total	C	N	O	S	0	0
			1033	642	200	184	7		

- Molecule 93 is a protein called UNK-a.

Mol	Chain	Residues	Atoms				AltConf	Trace
93	Ua	47	Total	C	N	O	0	0
			282	188	47	47		

- Molecule 94 is a protein called UNK-b.

Mol	Chain	Residues	Atoms				AltConf	Trace
94	Ub	42	Total	C	N	O	0	0
			252	168	42	42		

- Molecule 95 is a protein called UNK-c.

Mol	Chain	Residues	Atoms				AltConf	Trace
95	Uc	12	Total	C	N	O	0	0
			72	48	12	12		

- Molecule 96 is a protein called UNK-d.

Mol	Chain	Residues	Atoms				AltConf	Trace
96	Ud	59	Total	C	N	O	0	0
			354	236	59	59		

- Molecule 97 is a protein called UNK-e.

Mol	Chain	Residues	Atoms				AltConf	Trace
97	Ue	29	Total	C	N	O	0	0
			174	116	29	29		

- Molecule 98 is a protein called UNK-g.

Mol	Chain	Residues	Atoms				AltConf	Trace
98	Ug	167	Total	C	N	O	0	0
			1002	668	167	167		

- Molecule 99 is a protein called UNK-h.

Mol	Chain	Residues	Atoms				AltConf	Trace
99	Uh	255	Total	C	N	O	0	0
			1530	1020	255	255		

- Molecule 100 is a protein called UNK-i.

Mol	Chain	Residues	Atoms				AltConf	Trace
100	Ui	32	Total	C	N	O	0	0
			192	128	32	32		

- Molecule 101 is a protein called UNK-j.

Mol	Chain	Residues	Atoms				AltConf	Trace
101	Uj	19	Total	C	N	O	0	0
			114	76	19	19		

- Molecule 102 is a protein called UNK-l.

Mol	Chain	Residues	Atoms				AltConf	Trace
102	Ul	14	Total	C	N	O	0	0
			84	56	14	14		

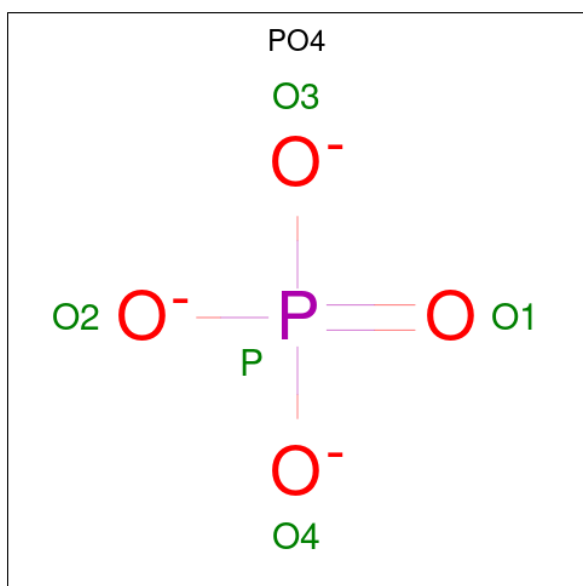
- Molecule 103 is a protein called UNK-x.

Mol	Chain	Residues	Atoms				AltConf	Trace
103	Ux	108	Total	C	N	O	0	0
			648	432	108	108		

- Molecule 104 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

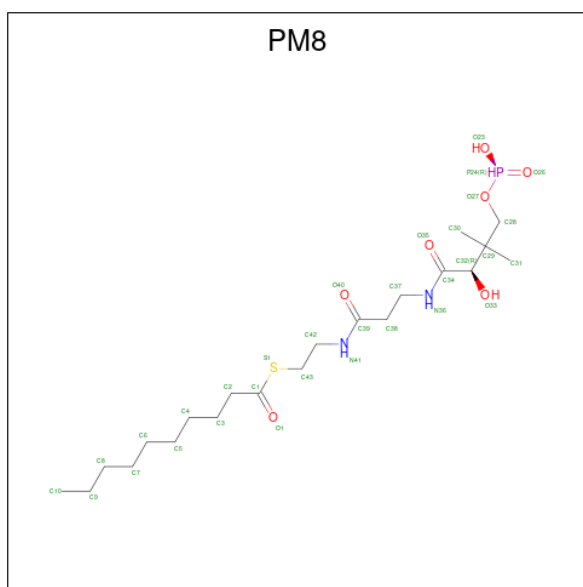
Mol	Chain	Residues	Atoms		AltConf
104	FP	1	Total	Mg	0
			1	1	
104	FW	1	Total	Mg	0
			1	1	
104	CA	2	Total	Mg	0
			2	2	
104	Cg	1	Total	Mg	0
			1	1	

- Molecule 105 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			AltConf
105	FW	1	Total	O	P	0
			5	4	1	

- Molecule 106 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: C₂₁H₄₁N₂O₇PS).

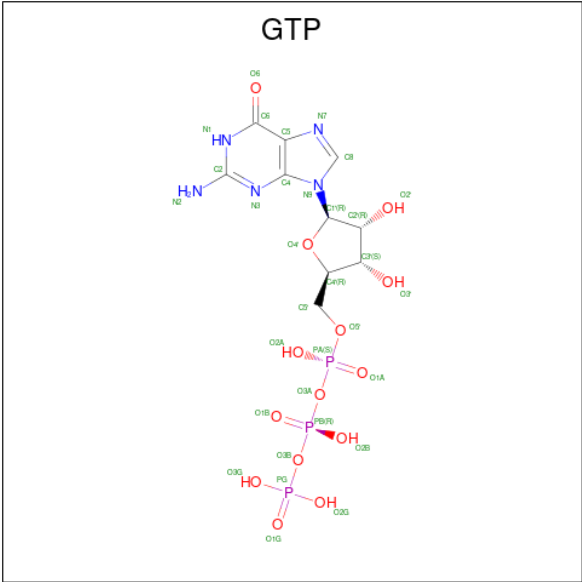


Mol	Chain	Residues	Atoms						AltConf
106	Fc	1	Total	C	N	O	P	S	0
			32	21	2	7	1	1	

- Molecule 107 is ZINC ION (CCD ID: ZN) (formula: Zn).

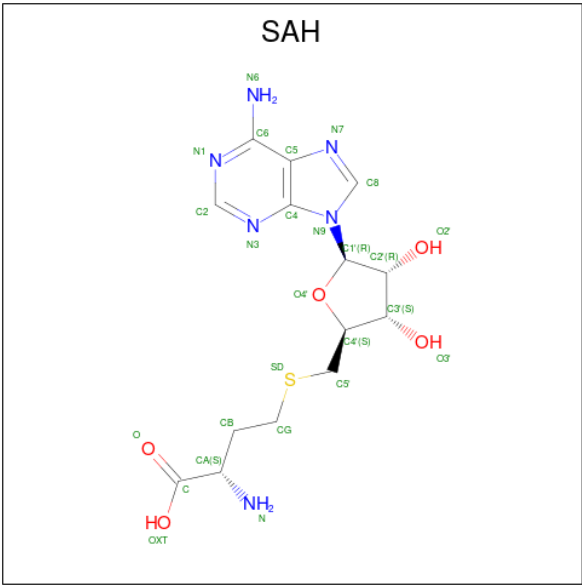
Mol	Chain	Residues	Atoms		AltConf
107	Fd	1	Total	Zn	0
			1	1	
107	F1	1	Total	Zn	0
			1	1	
107	FG	1	Total	Zn	0
			1	1	
107	FL	2	Total	Zn	0
			2	2	
107	Fe	1	Total	Zn	0
			1	1	

- Molecule 108 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
108	Cg	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 109 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					AltConf
109	F1	1	Total	C	N	O	S	0
			26	14	6	5	1	
109	FF	1	Total	C	N	O	S	0
			26	14	6	5	1	

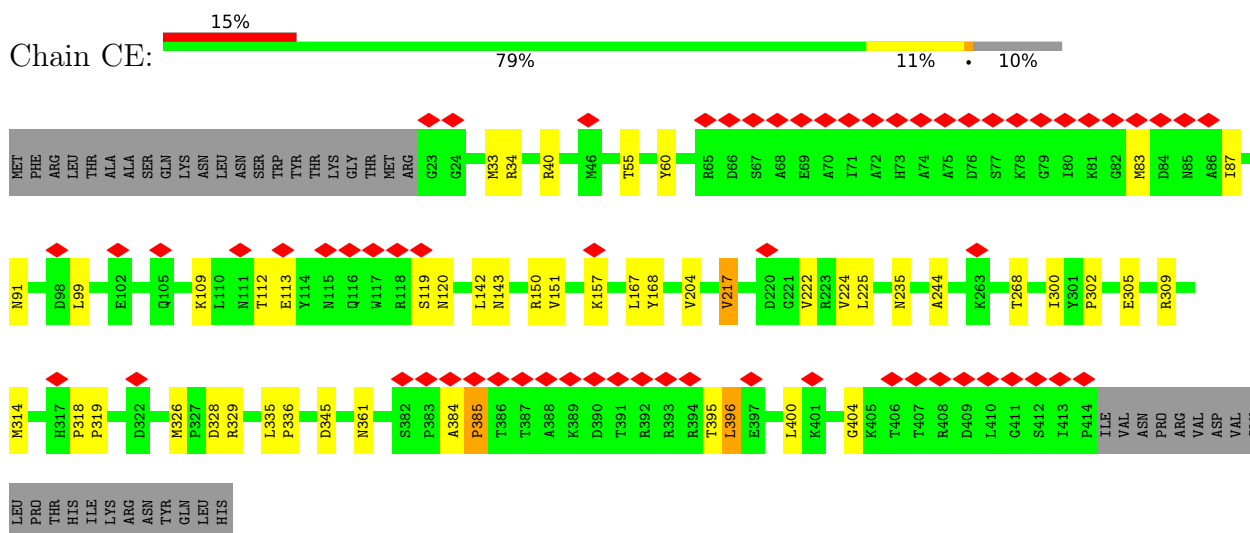
- Molecule 110 is water.

Mol	Chain	Residues	Atoms		AltConf
110	Cg	3	Total 3	O 3	0

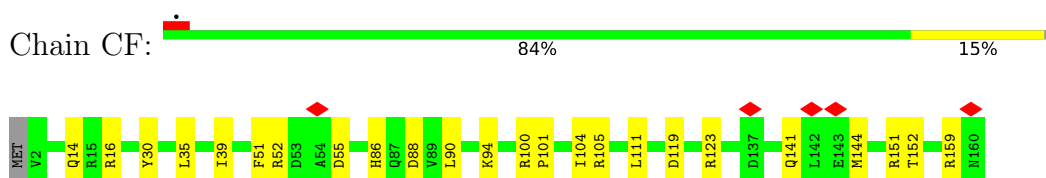
3 Residue-property plots

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.

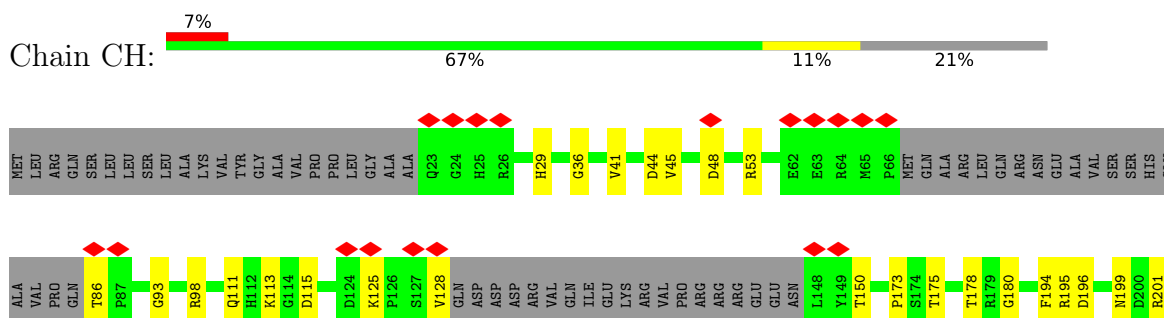
• Molecule 1: uS5m

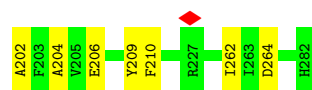


• Molecule 2: bS6m

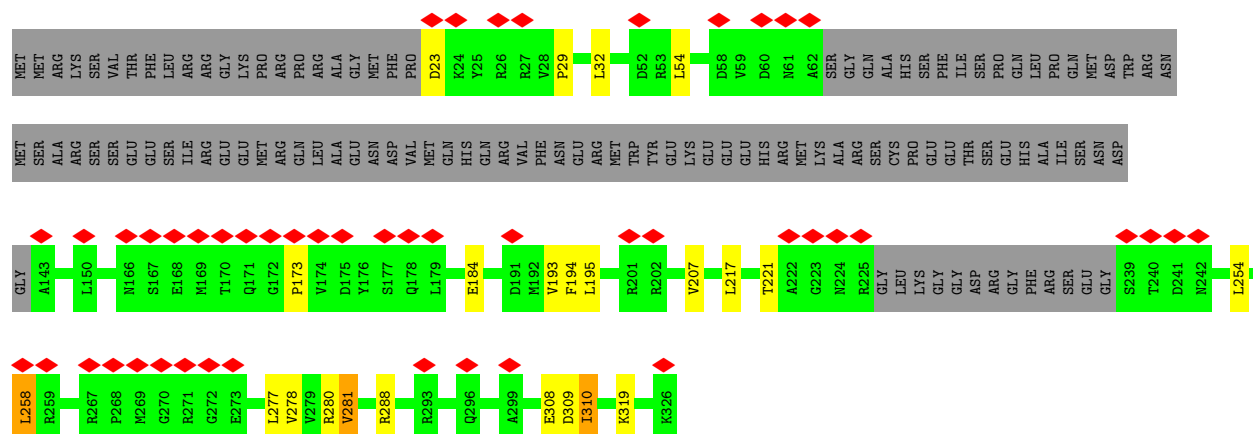


• Molecule 3: uS8m

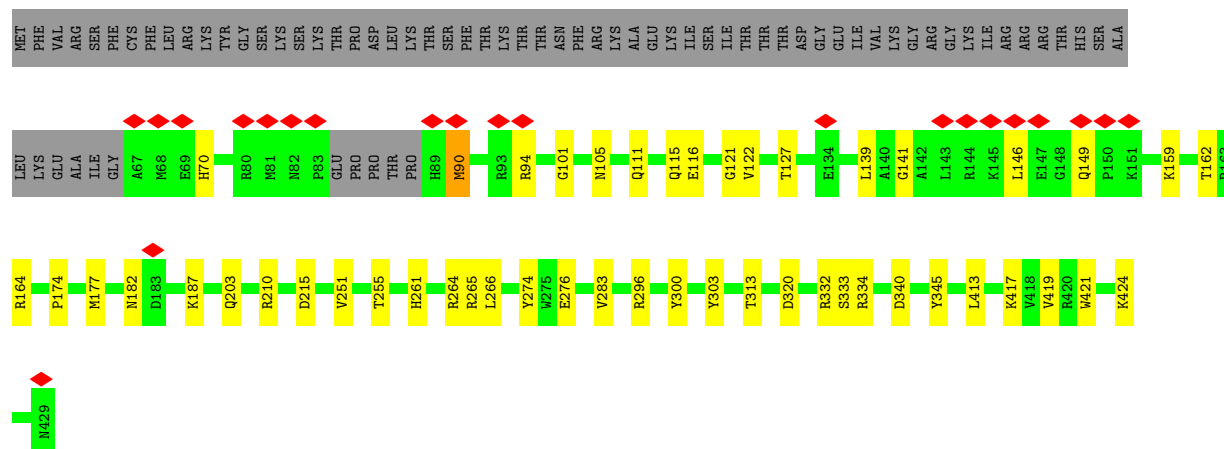
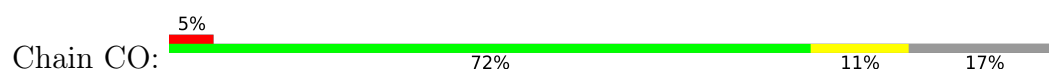




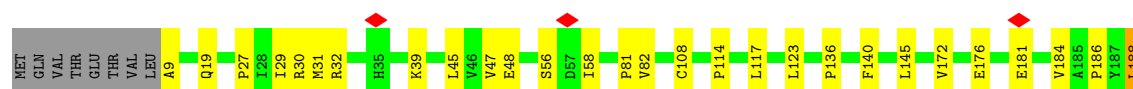
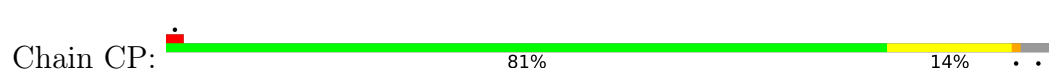
• Molecule 4: uS11m



• Molecule 5: uS15m



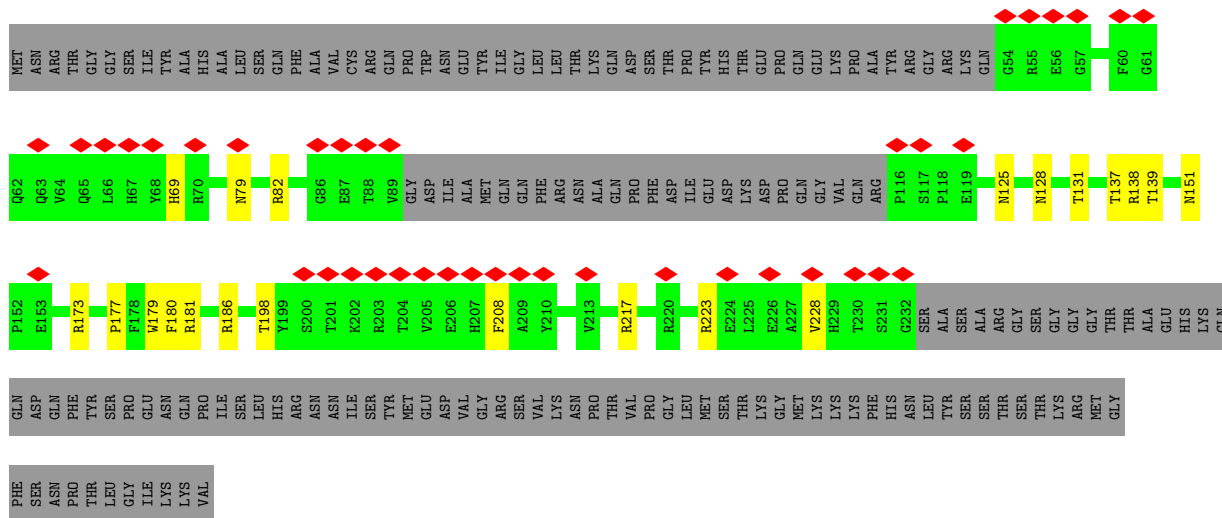
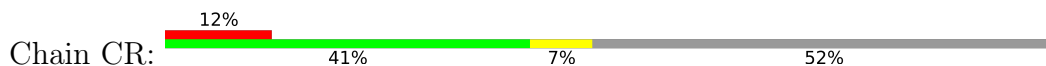
• Molecule 6: bS16m



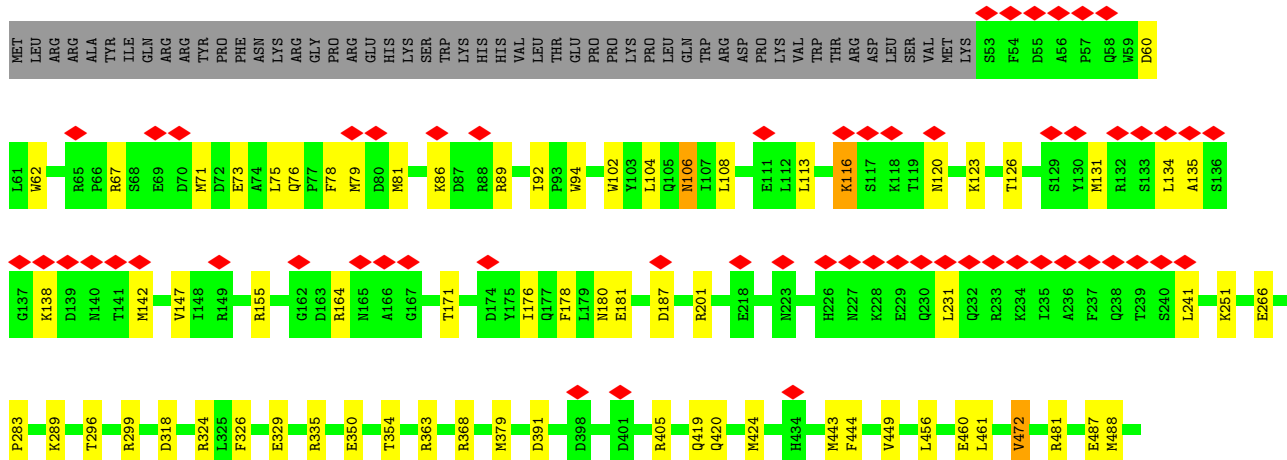
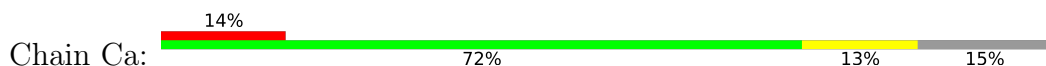
• Molecule 7: uS17m



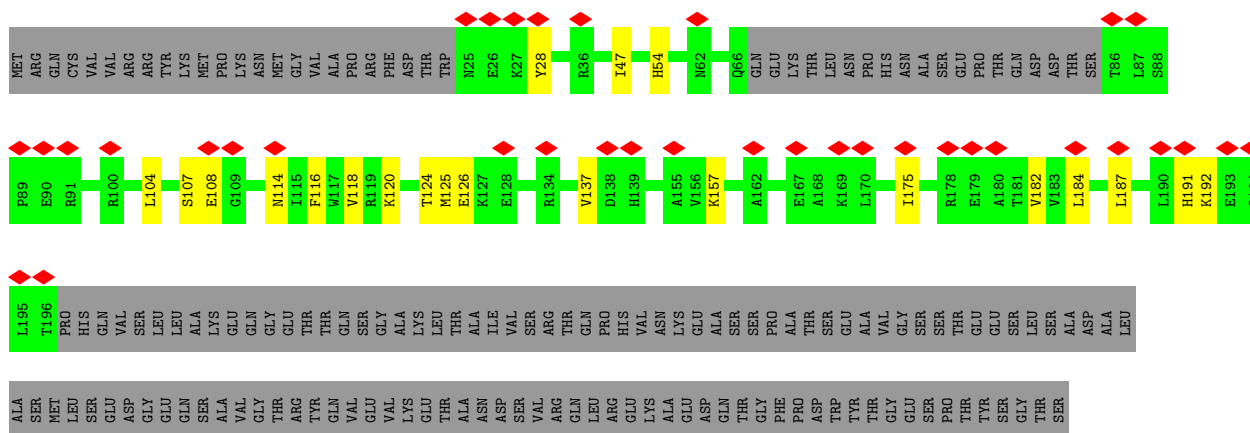
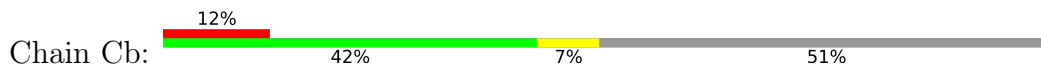
- Molecule 8: bS18m



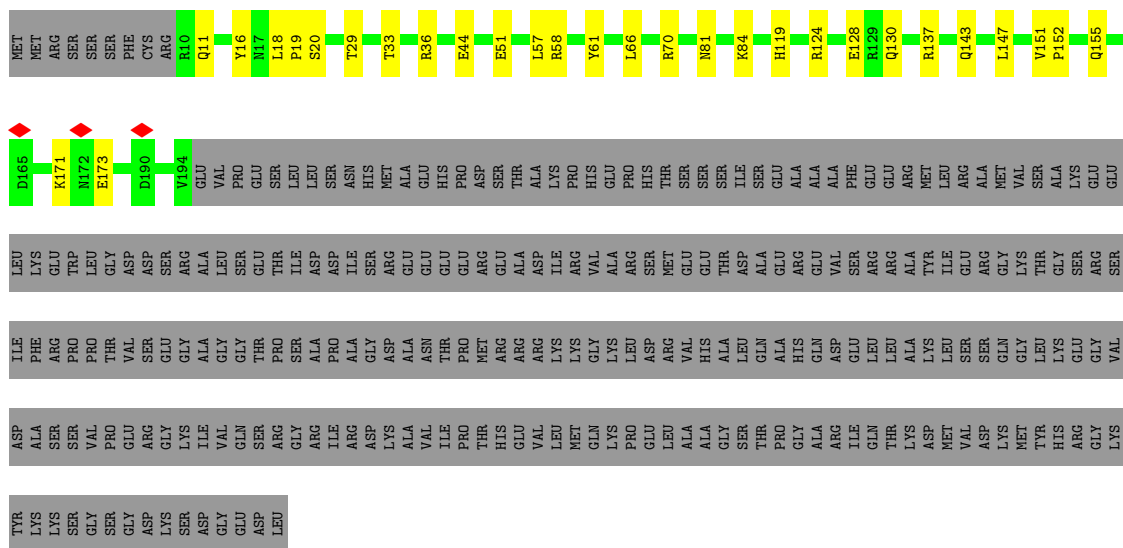
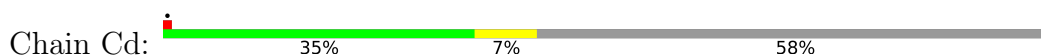
- Molecule 9: mS22



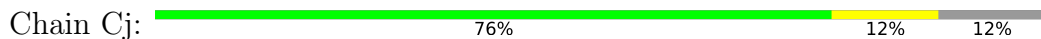
- Molecule 10: mS23



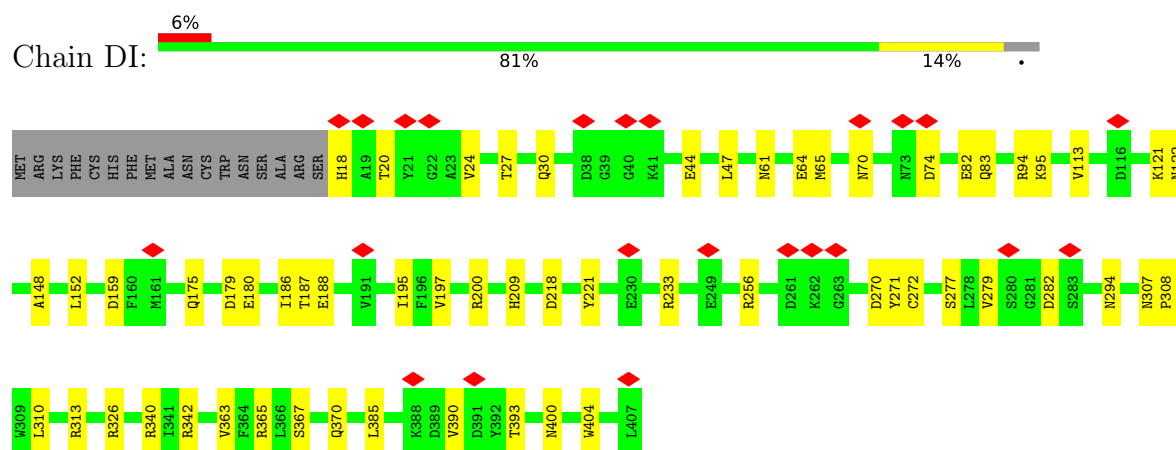
- Molecule 11: mS26



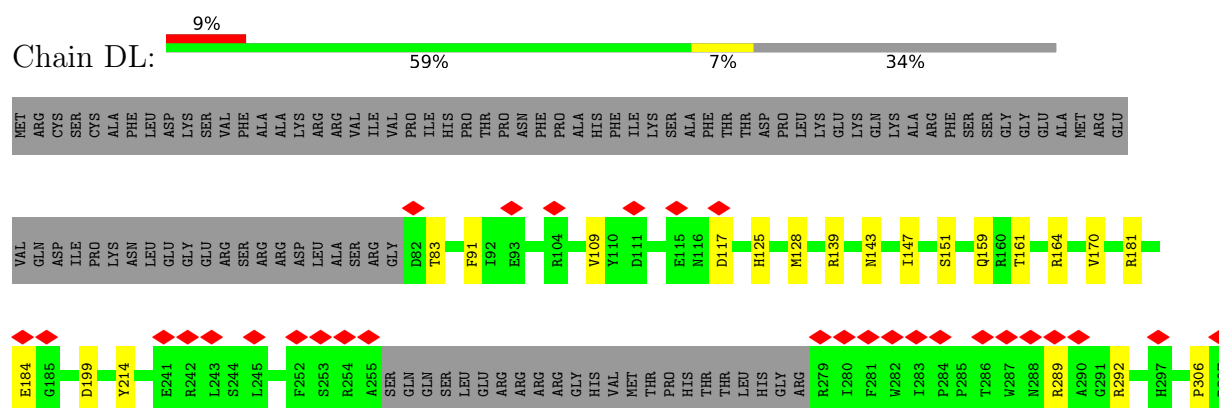
- Molecule 12: mS34



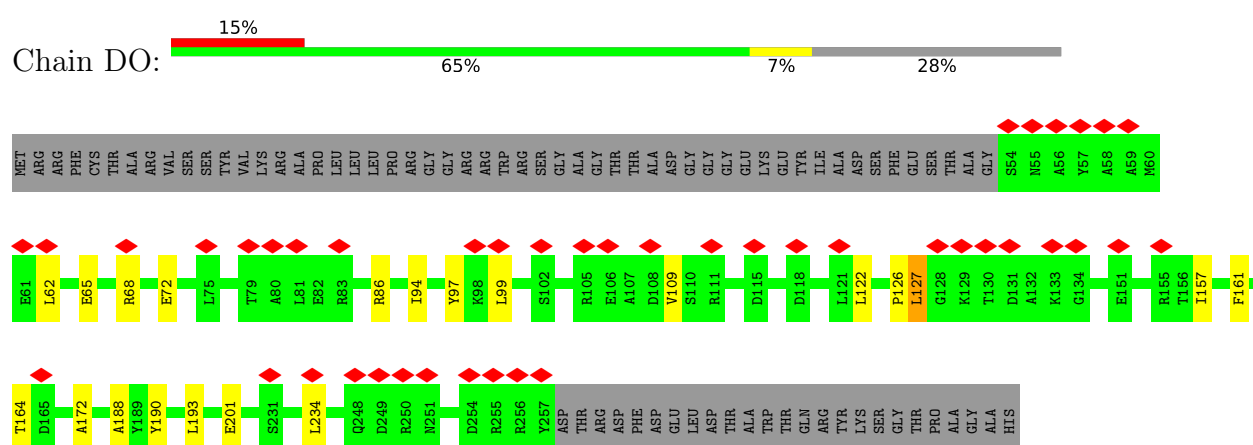
- Molecule 16: mS56



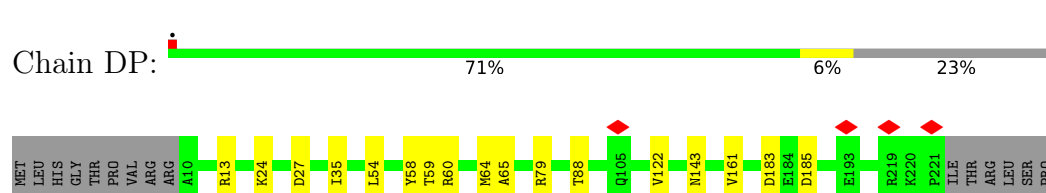
- Molecule 17: mS59



- Molecule 18: mS62 (KRIPP14)



- Molecule 19: mS63 (KRIPP16)



GLY SER GLY THR ILE SER ASP GLY GLU PRO SER THR ASP VAL GLY THR THR VAL ASP ASP GLU ILE ALA GLN LEU GLU ALA GLU LEU LEU ALA LEU ARG GLU GLY GLY LYS

• Molecule 20: mS65

Chain DR:  82% 12% 6%

MET PHE SER GLU SER LEU CYS ILE LEU S10 F13 M16 T17 K18 V33 V44 V60 I63 I64 E74 D88 I117 V118 L126 D129 D130 C135 L154 R158 S161 Q162 G163 GLY THR THR GLY SER GLU THR G171 K188 E189 L190

R221 R227 T232 P240 R250 A252 V254 P255 G260 R262 S263 H288 W270 F270

• Molecule 21: mS68

Chain DU:  19% 83% 12%

MET ARG ARG GLY ALA LEU SER LEU L9 K10 G15 Q18 E30 S31 T32 T33 Y34 P35 G36 P37 I38 R39 A40 L53 D71 T86 Q99 P106 K107 D108 S109 I111 V120 N122 Q123 P143 T146 N164 D165 L168 H169 R170 D171 D172

P175 R176 D177 W178 T179 V180 D181 E182 E186 D187 V188 K189 R190 S191 M196 E197 M198 Q199 P200 L201 Q202 N203 L204 A205 P206 E209 A210 R211 P212 K213 G214 Y221 M224 K225 Q226 S227 SER

• Molecule 22: mS73

Chain DZ:  10% 26% 5% 68%

MET LEU ARG ARG SER ILE LEU PHE ARG MET LYS TYR ALA ASP LEU LEU THR ARG GLY PHE PRO HIS GLY MET LYS LEU GLN ASN ILE PRO TRP TYR PHE SER THR TYR ARG SER MET THR HIS TRP PRO ILE THR GLY ASP ASN TRP

SER ASP L63 N64 E65 A66 E67 K68 H69 L72 W80 E85 G86 I87 F88 E92 ASP SER

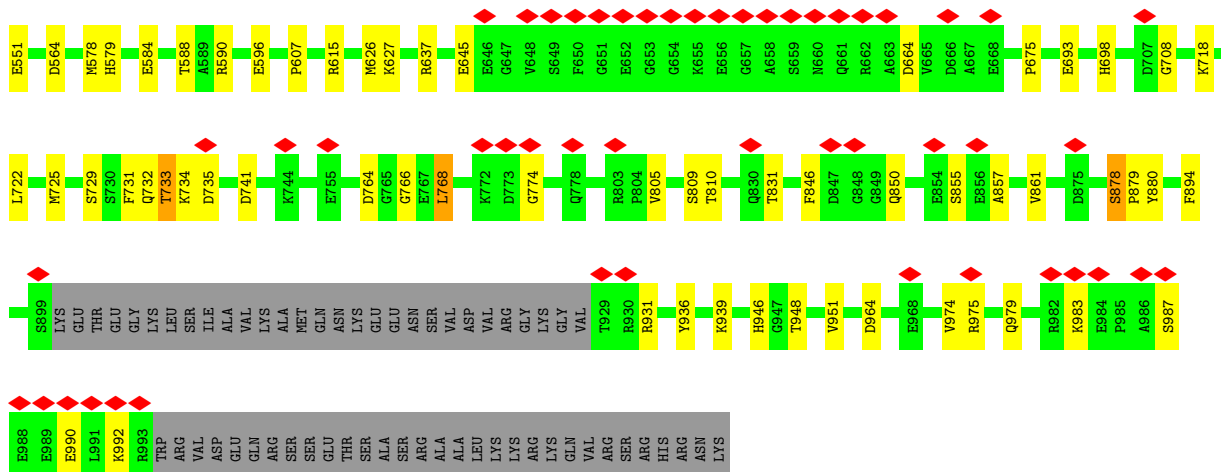
• Molecule 23: mt-SAF2 (KRIPP2)

Chain F2:  7% 78% 11% 11%

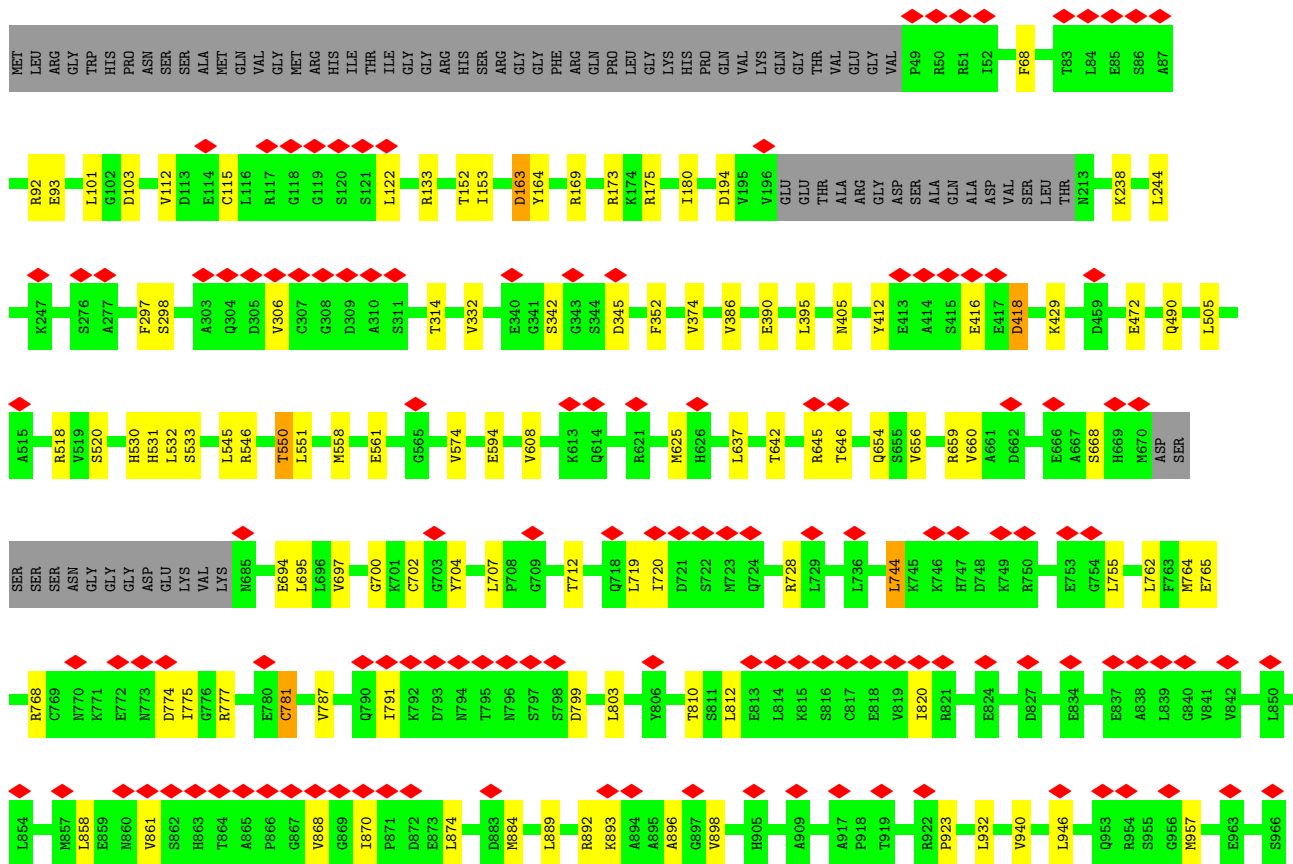
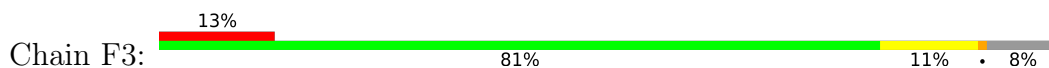
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G124 ASP MET SER GLY THR ALA LEU PRO PRO ASN PRO THR TYR ASP VAL GLU GLN ASP VAL R165 A166 E167 E168 L169 K172 Y173 N174 A178 T205 E206 I224 G225 R226

D230 M235 R245 S252 E266 T273 E281 Y284 D291 Q297 N301 M304 N307 V313 Q337 S351 R352 L377 V387 R417 D445 K448 E449 K450 D451 E470 R475 V478 W499 D504 D532 Q546

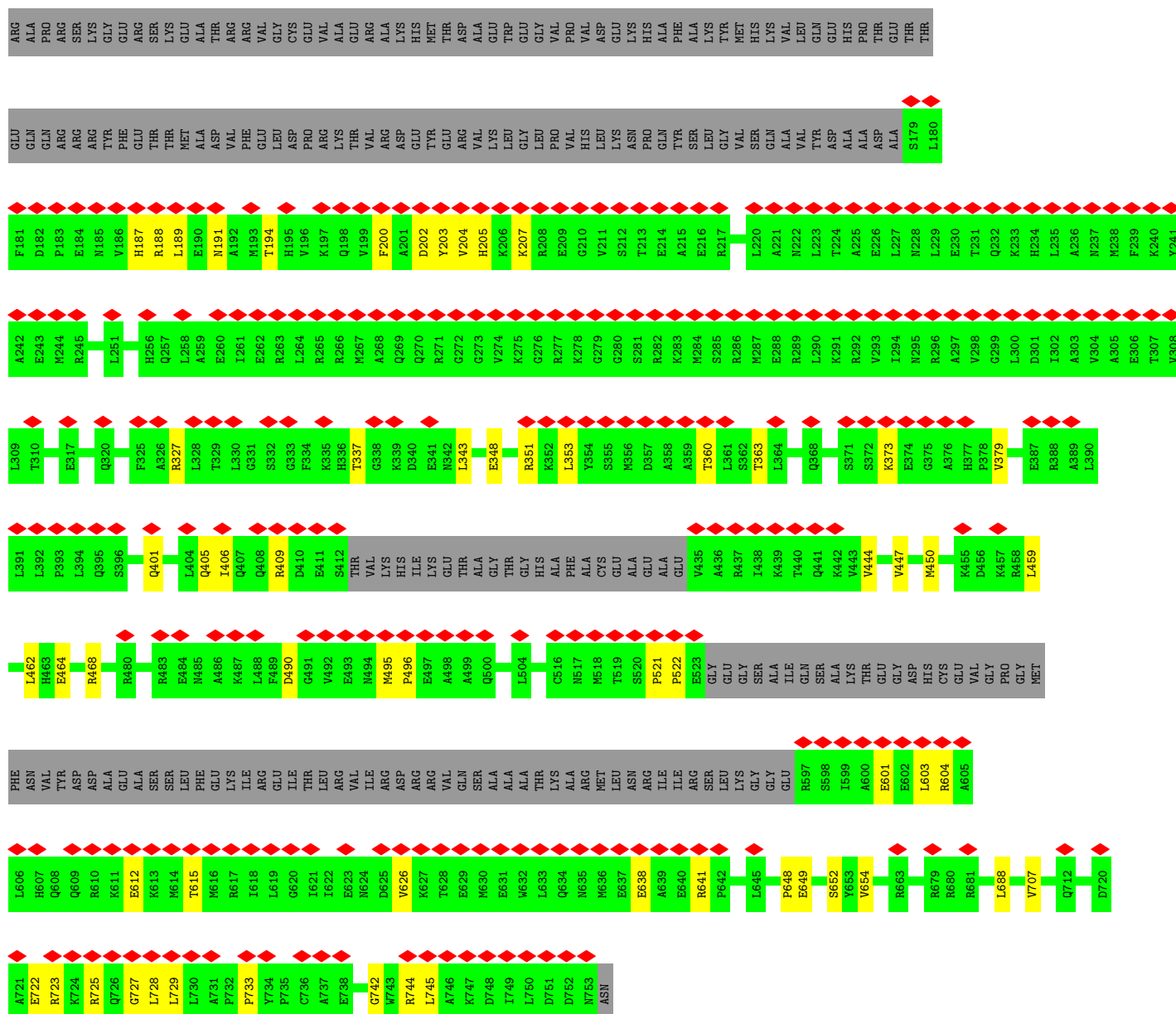


- Molecule 24: mt-SAF3

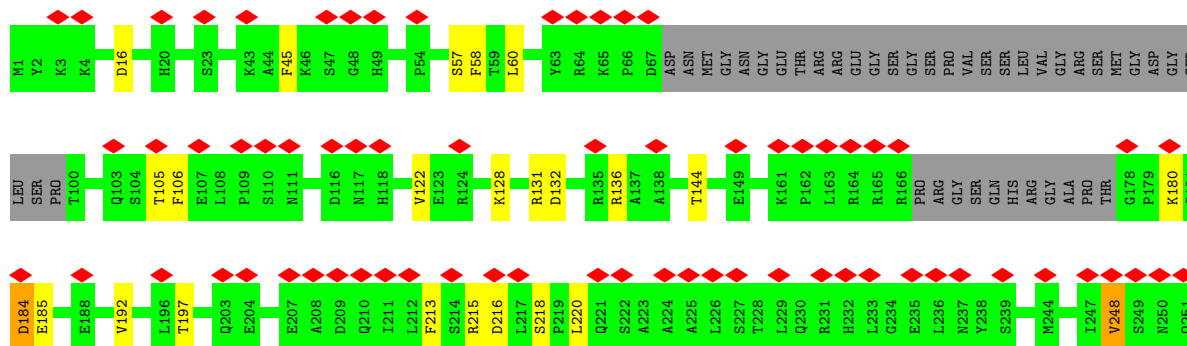


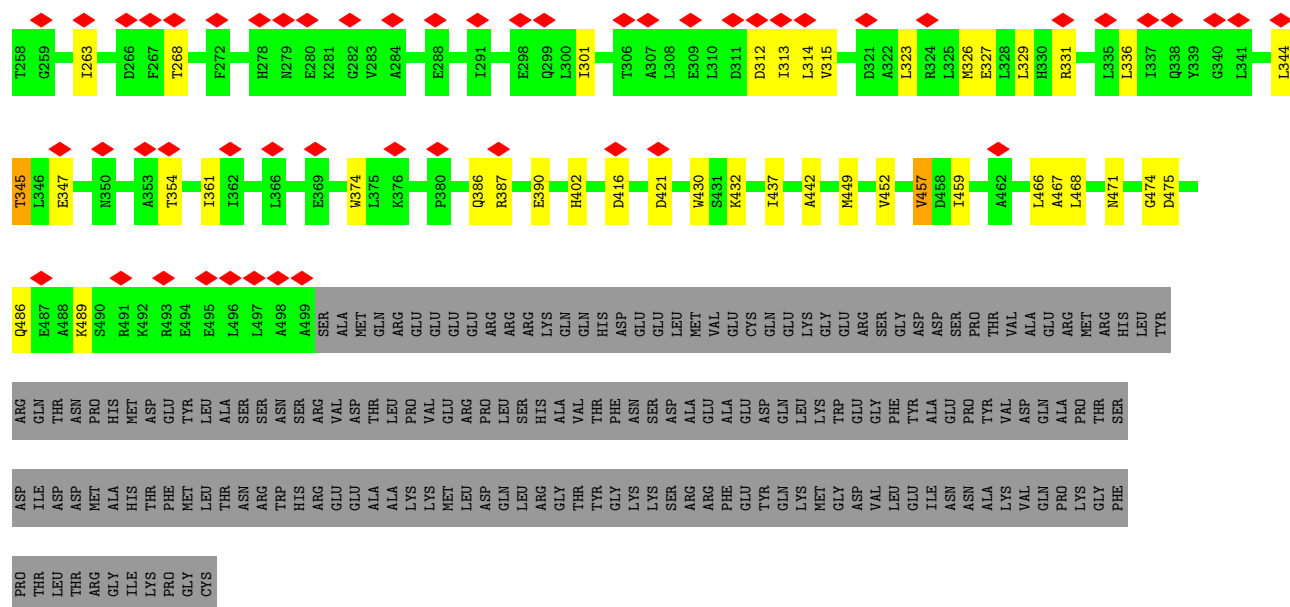
- Molecule 25: mt-SAF5



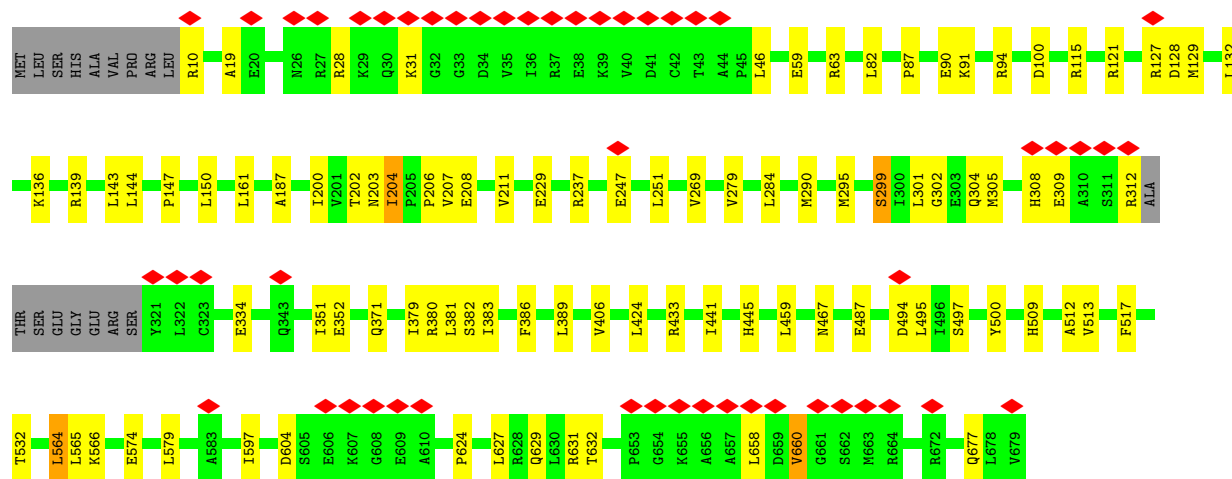
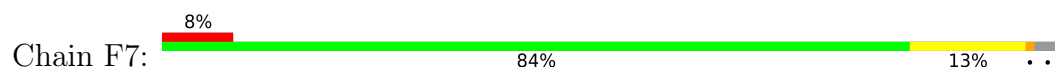


• Molecule 26: mt-SAF6

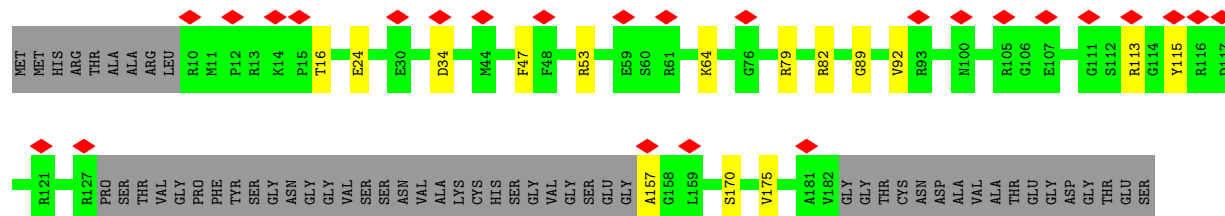


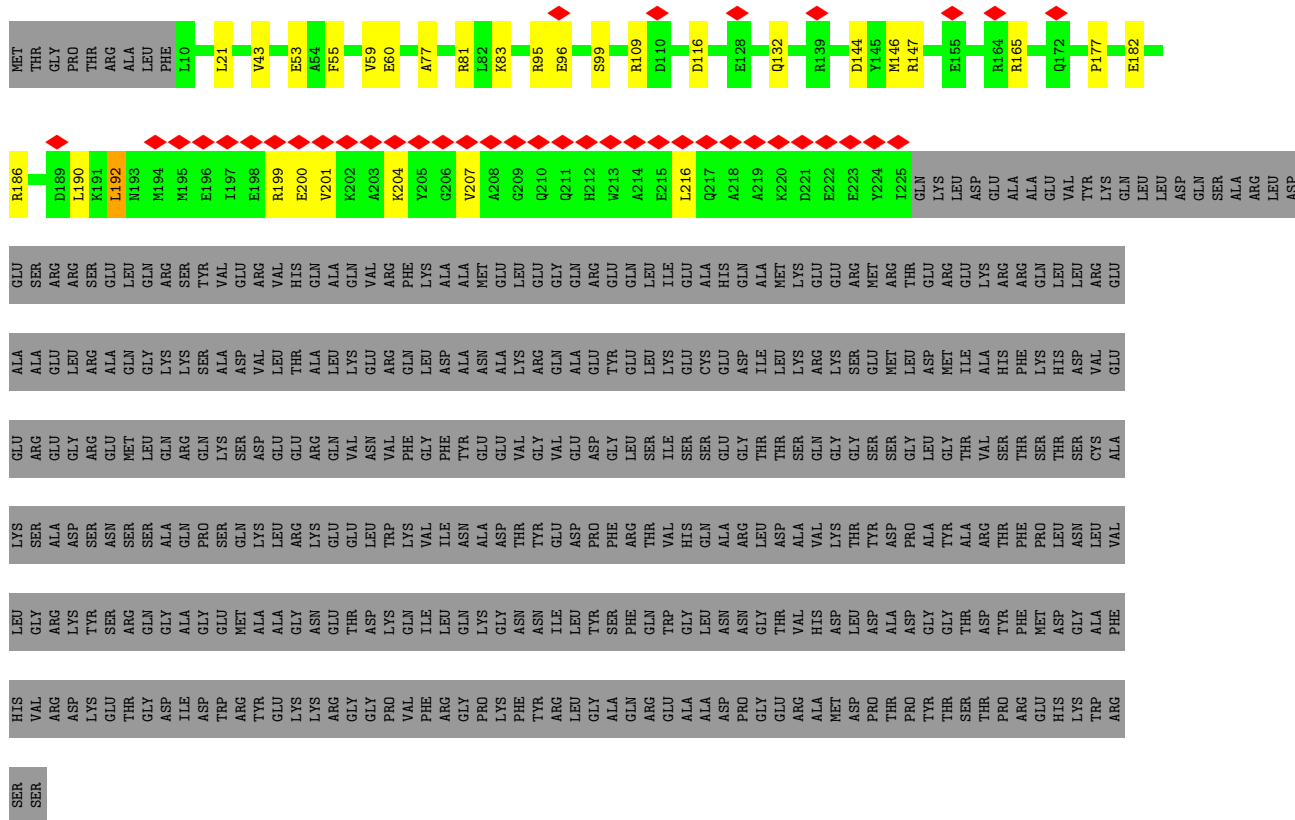


• Molecule 27: mt-SAF7 (KRIPP10)



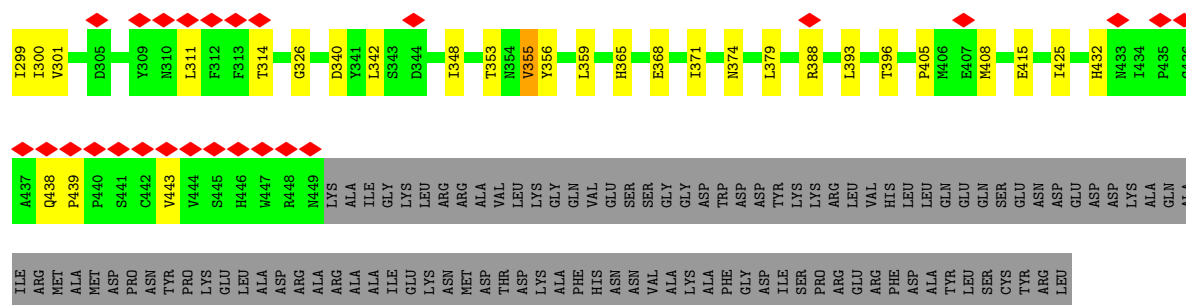
• Molecule 28: mt-SAF8



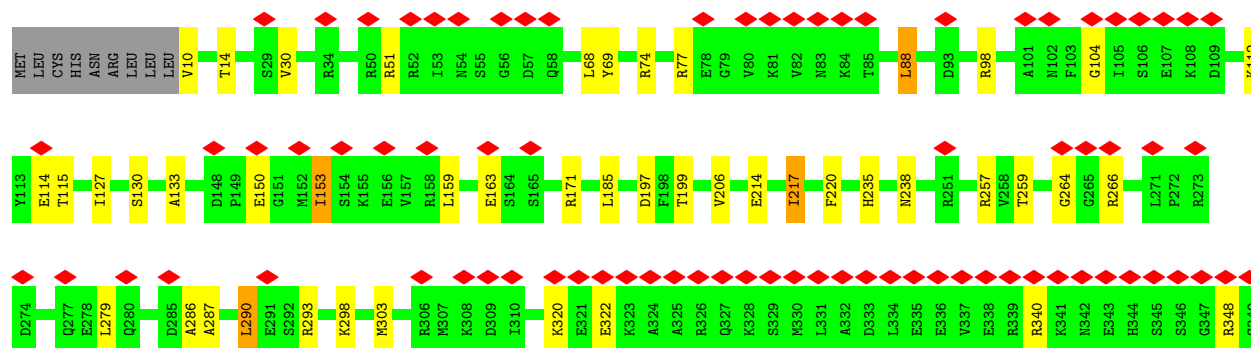
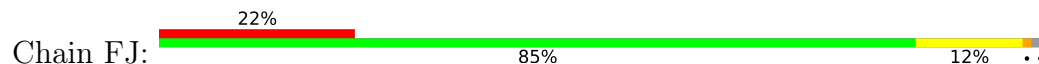


Chain FA:

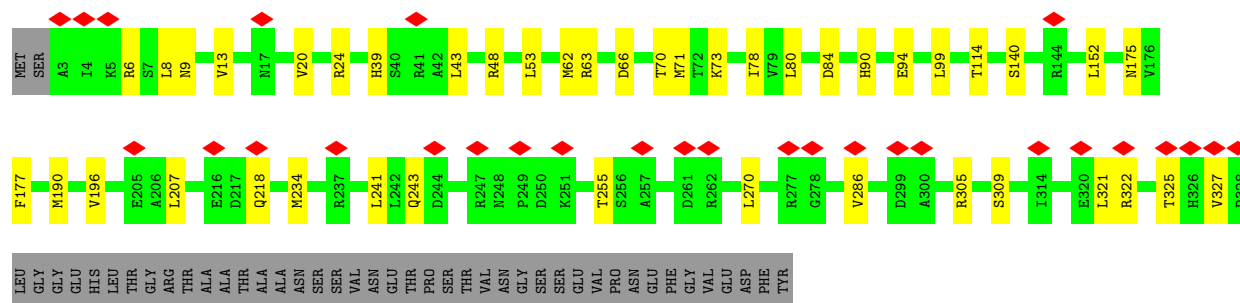
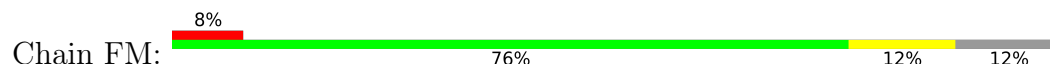




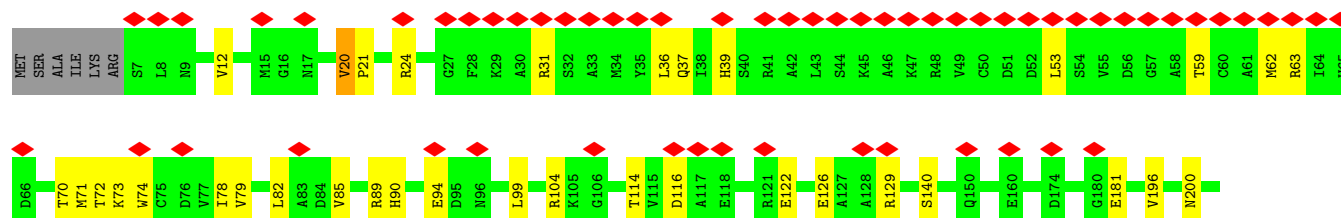
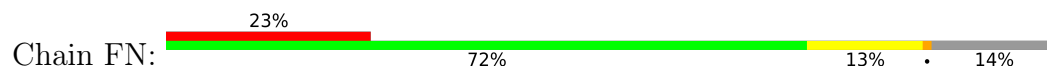
• Molecule 33: mt-SAF18

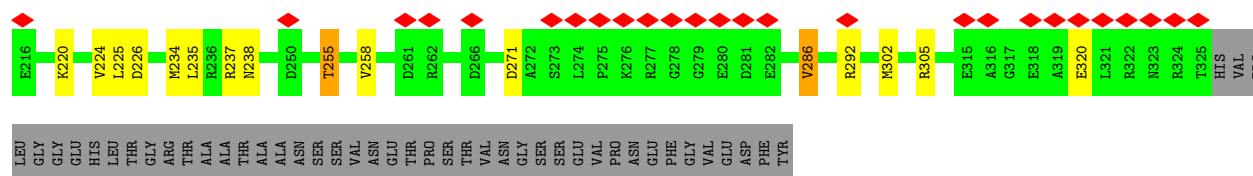


• Molecule 34: mt-SAF21

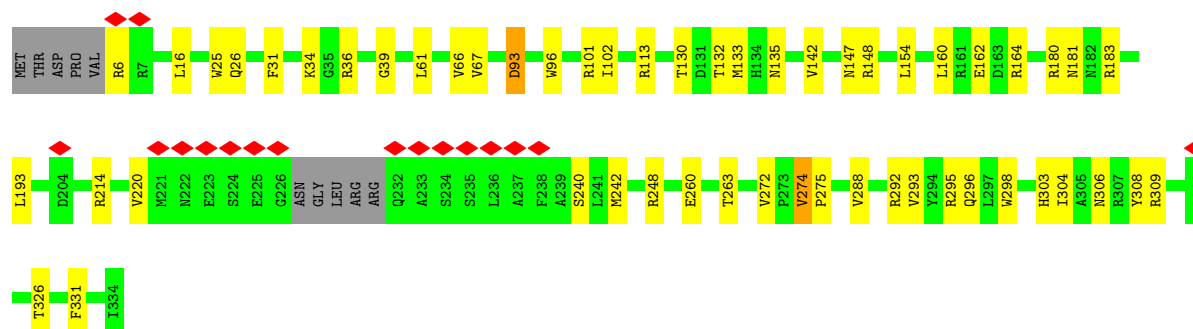
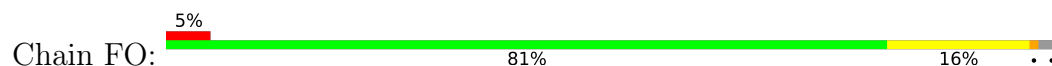


• Molecule 34: mt-SAF21

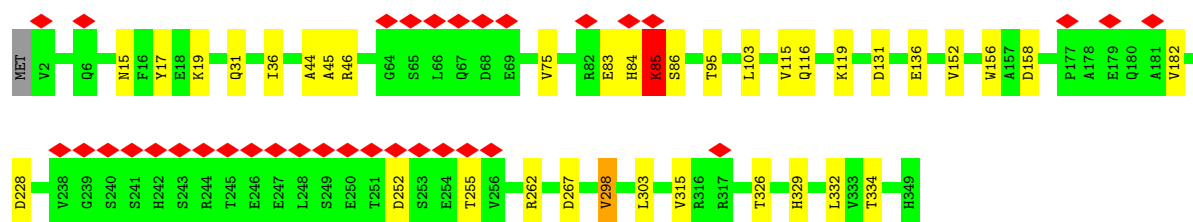
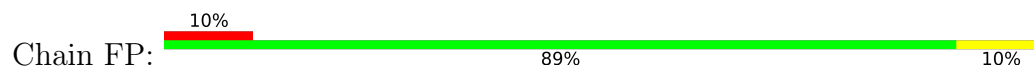




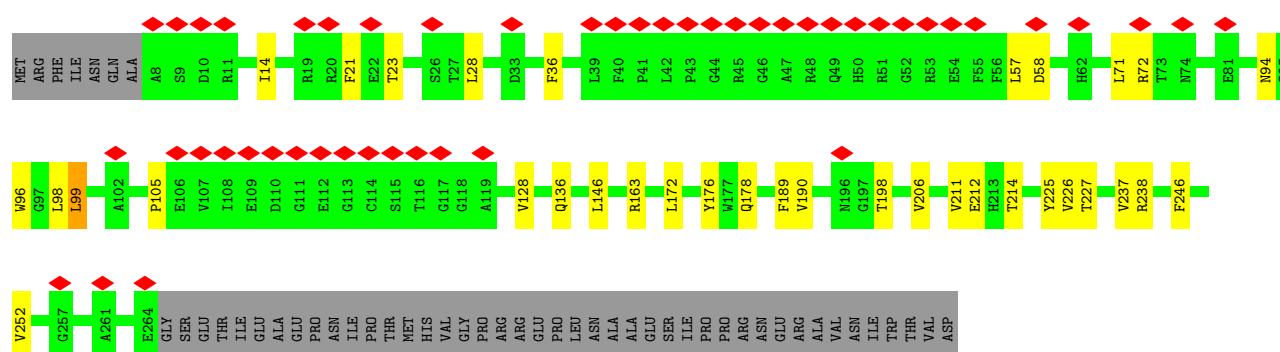
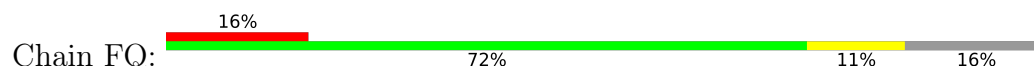
• Molecule 35: mt-SAF22 (KRIPP17)



• Molecule 36: mt-SAF23

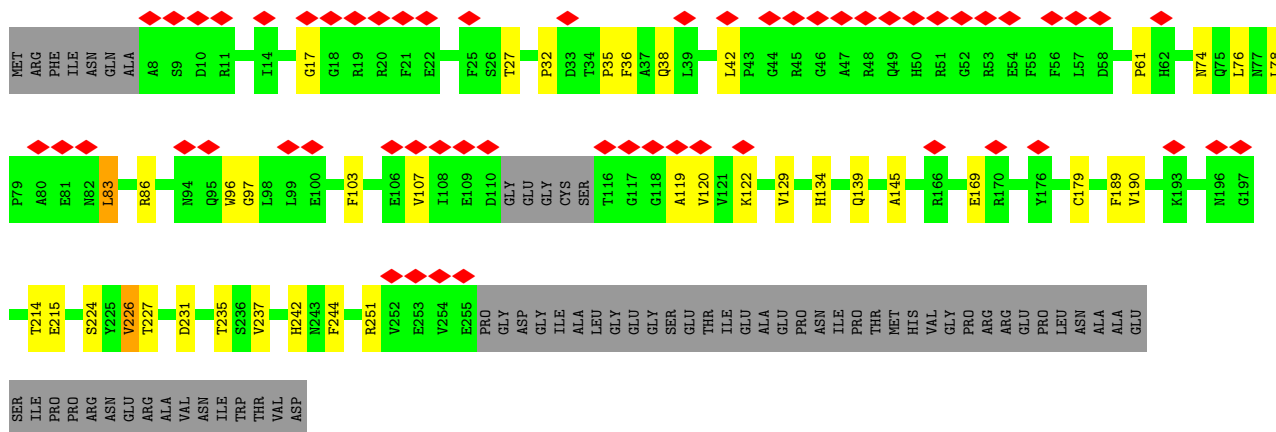


• Molecule 37: mt-SAF24

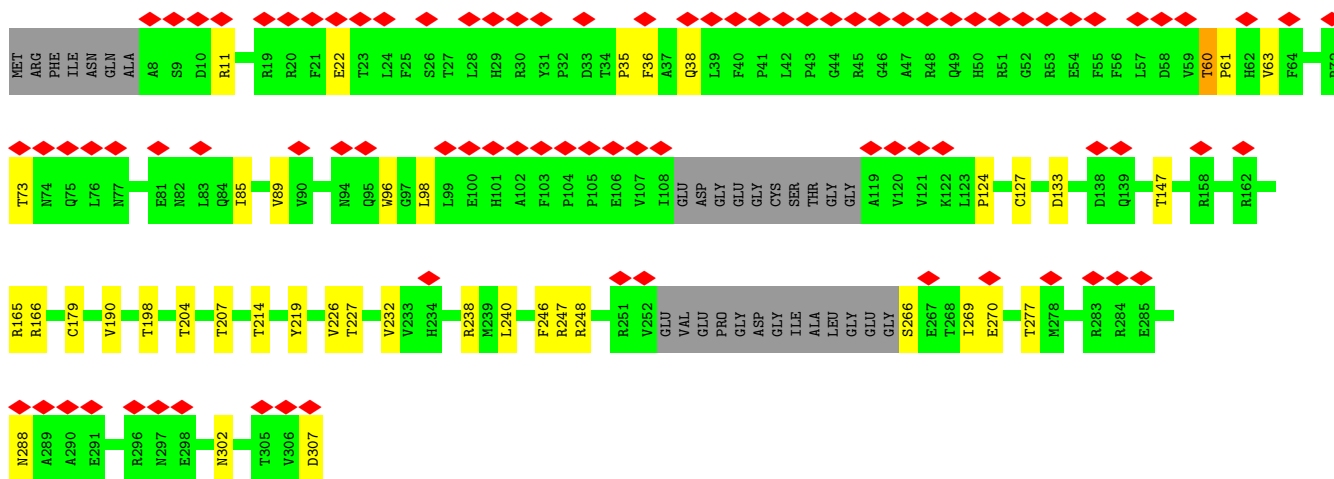
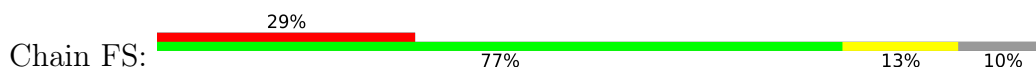


• Molecule 37: mt-SAF24

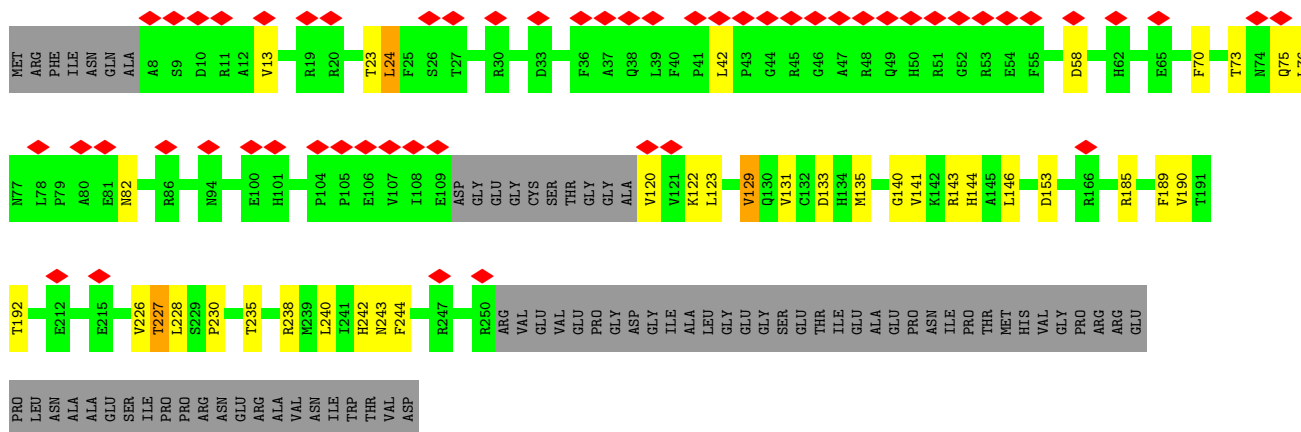




• Molecule 37: mt-SAF24

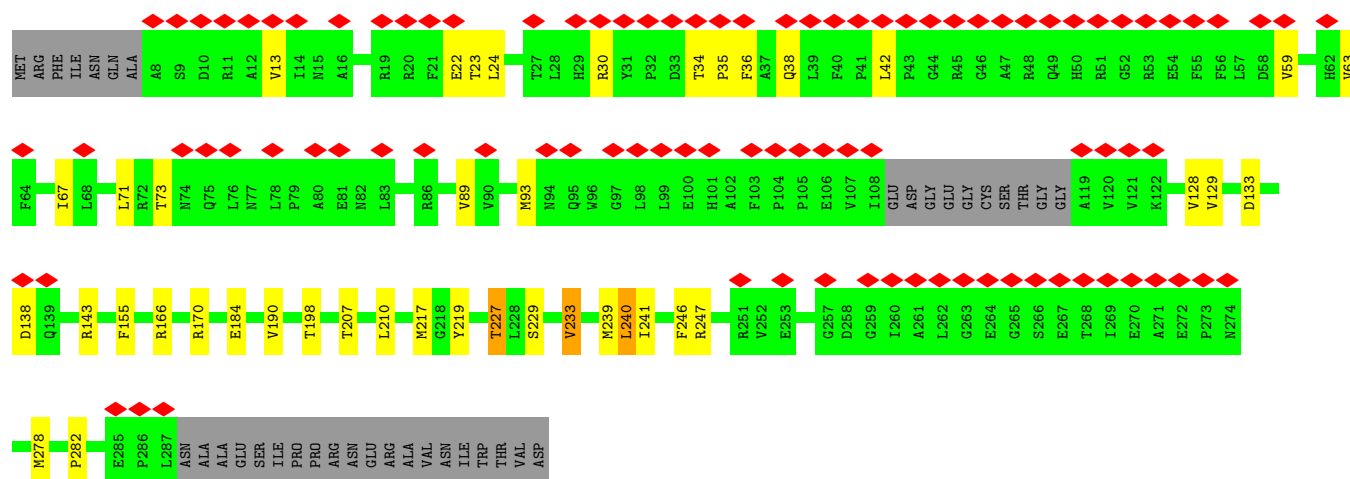


• Molecule 37: mt-SAF24



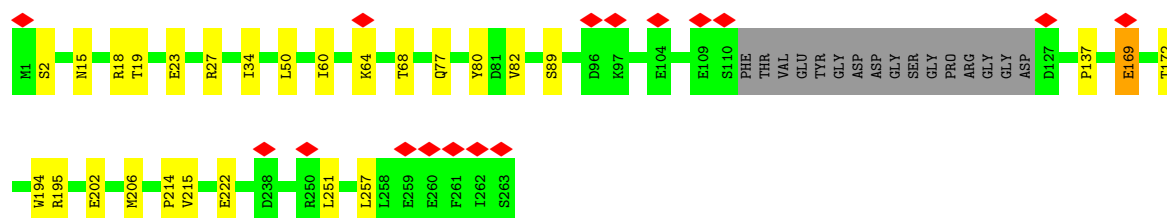
• Molecule 37: mt-SAF24

Chain FU: 



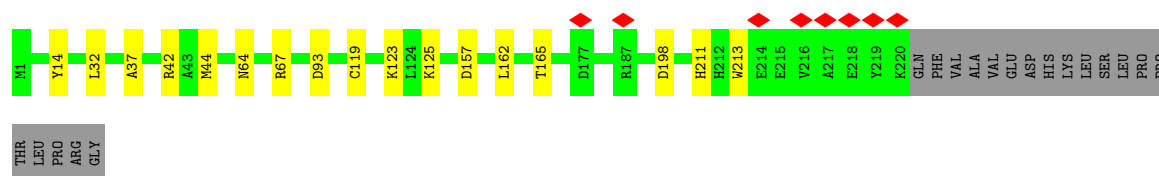
• Molecule 38: mt-SAF26

Chain FW: 



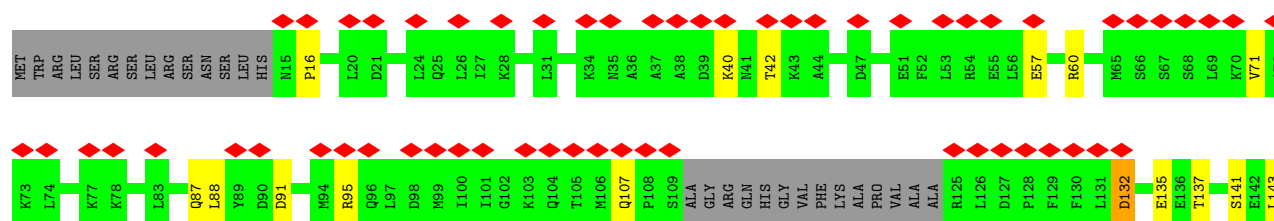
• Molecule 39: mt-SAF27 (KRIPP11)

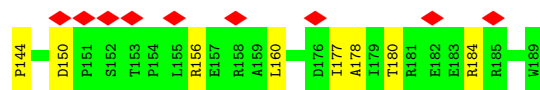
Chain FX: 



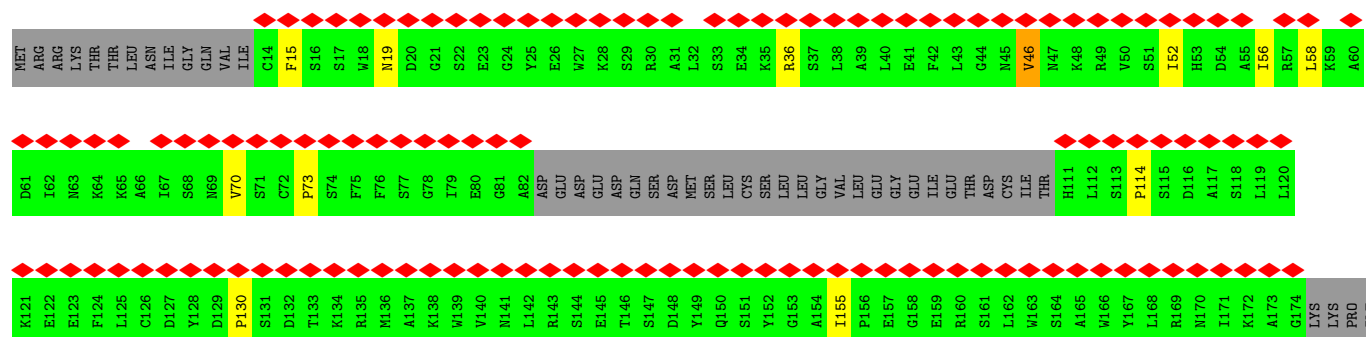
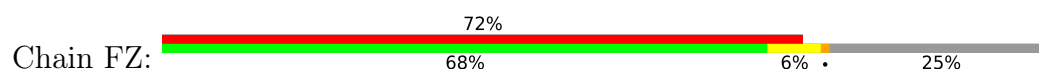
• Molecule 40: mt-SAF28

Chain FY: 

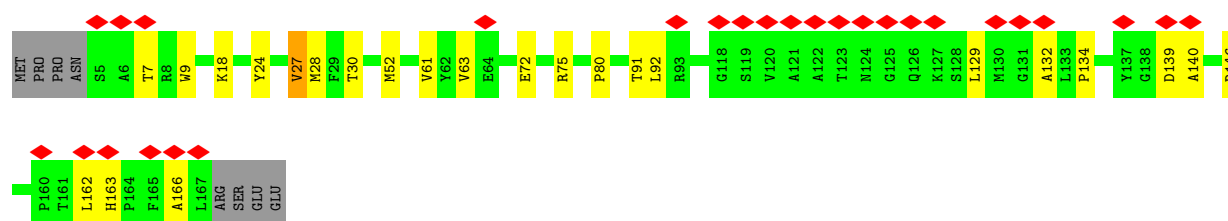
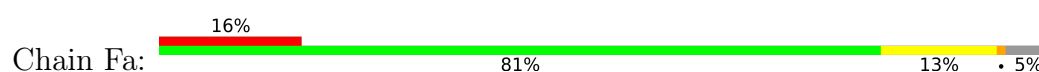




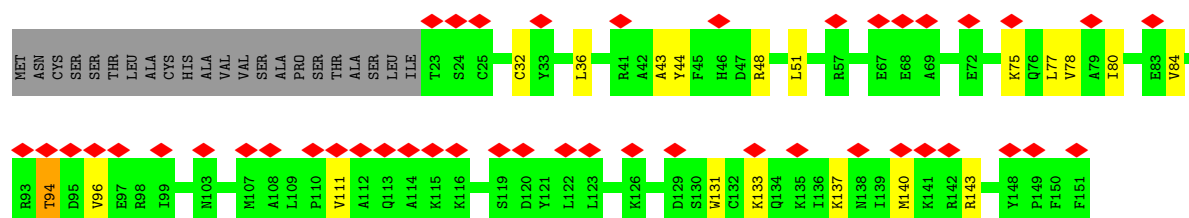
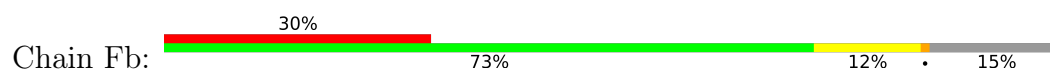
• Molecule 41: mt-SAF29



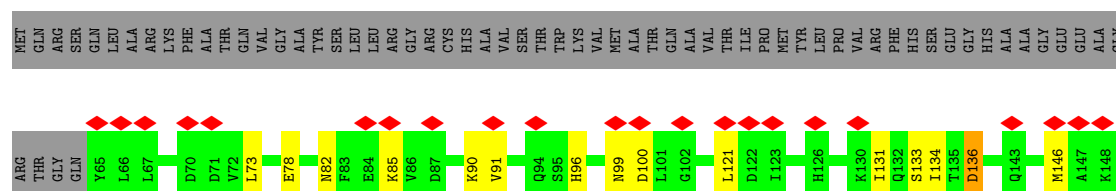
• Molecule 42: mt-SAF30



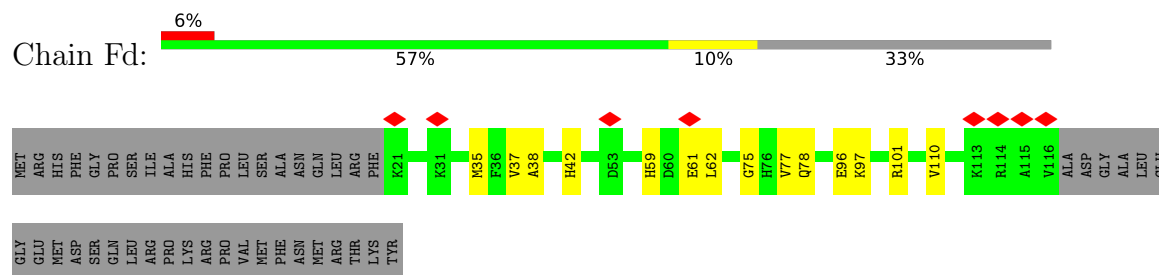
• Molecule 43: mt-SAF31



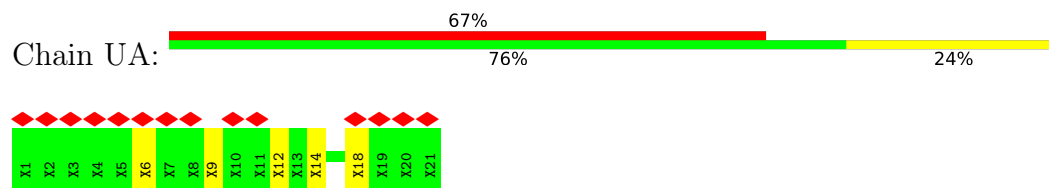
• Molecule 44: mt-SAF32



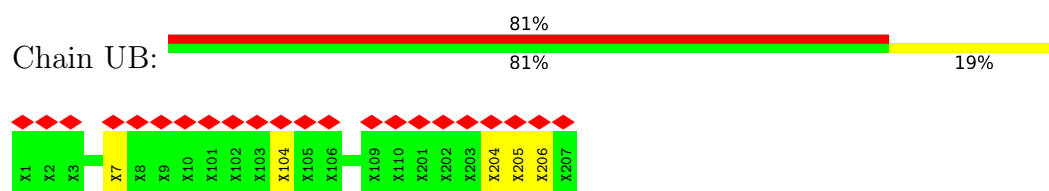
- Molecule 45: mt-SAF33



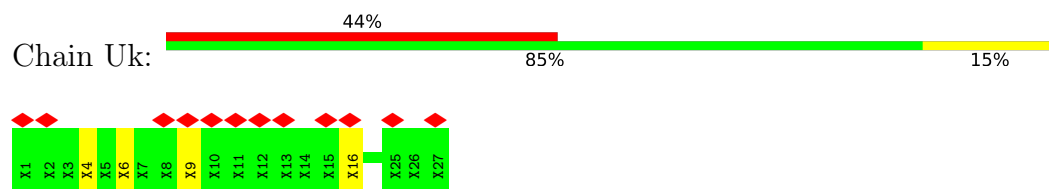
- Molecule 46: UNK-A



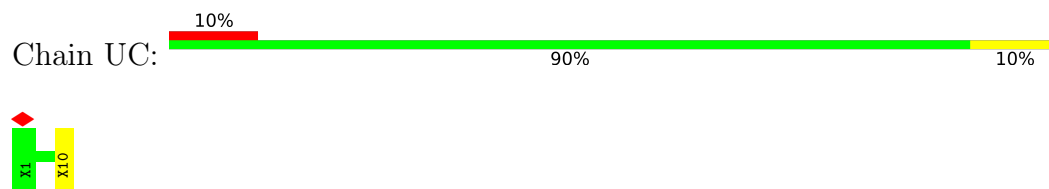
- Molecule 47: UNK-B, UNK-k



- Molecule 47: UNK-B, UNK-k



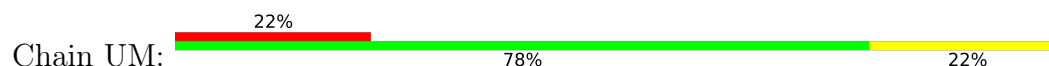
- Molecule 48: UNK-C

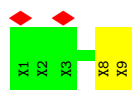


- Molecule 49: UNK-D, UNK-M, UNK-Q, UNK-f

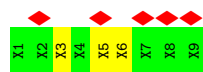


- Molecule 49: UNK-D, UNK-M, UNK-Q, UNK-f





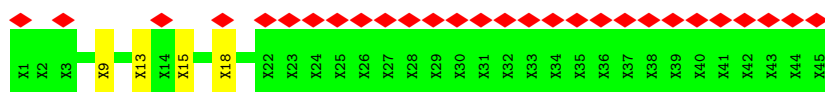
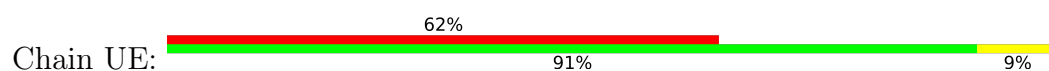
- Molecule 49: UNK-D, UNK-M, UNK-Q, UNK-f



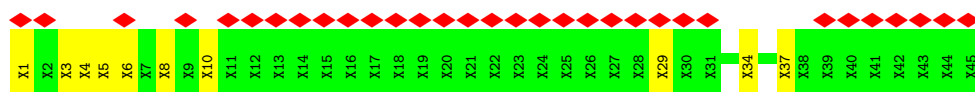
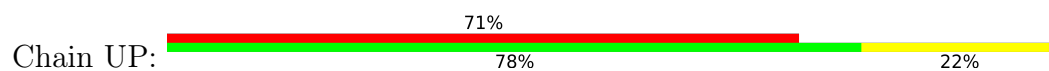
- Molecule 49: UNK-D, UNK-M, UNK-Q, UNK-f



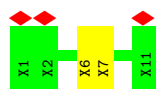
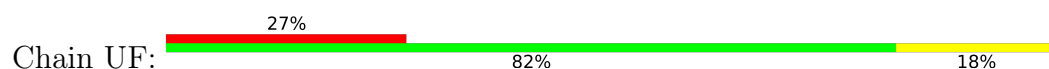
- Molecule 50: UNK-E, UNK-P



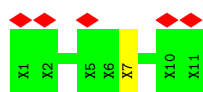
- Molecule 50: UNK-E, UNK-P



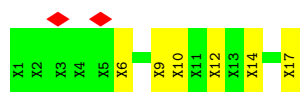
- Molecule 51: UNK-F, UNK-m



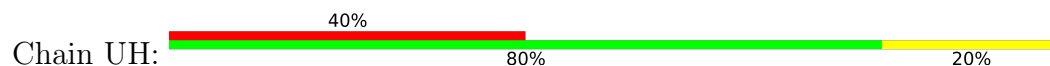
- Molecule 51: UNK-F, UNK-m



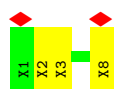
- Molecule 52: UNK-G



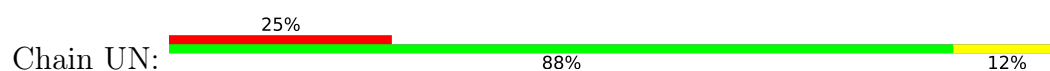
- Molecule 53: UNK-H



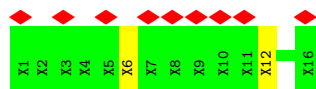
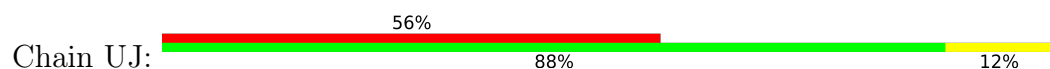
- Molecule 54: UNK-I, UNK-N



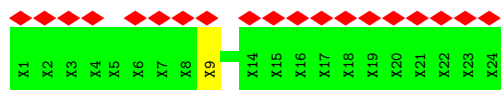
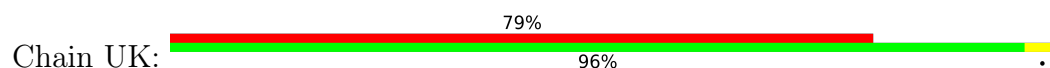
- Molecule 54: UNK-I, UNK-N



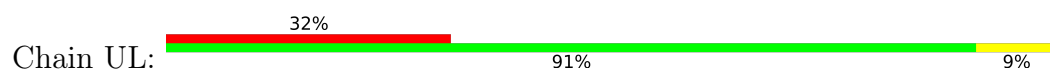
- Molecule 55: UNK-J



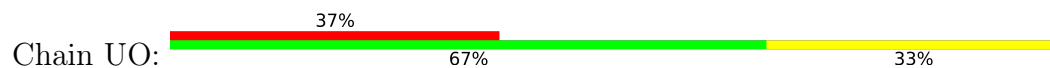
- Molecule 56: UNK-K



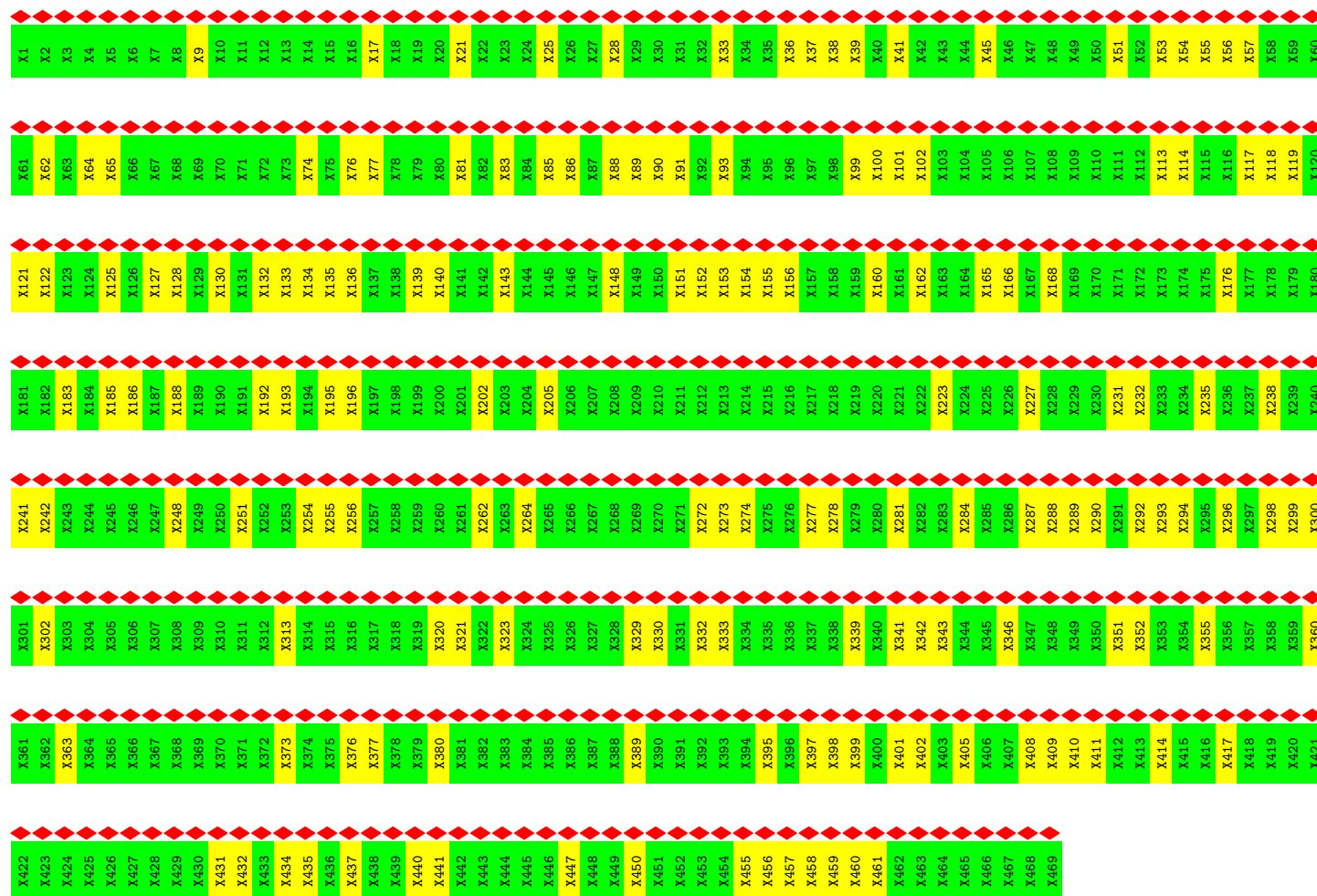
- Molecule 57: UNK-L



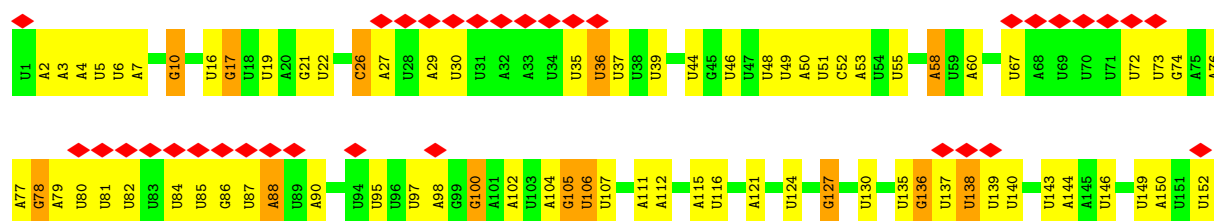
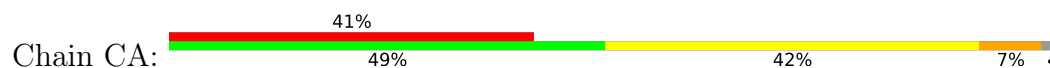
- Molecule 58: UNK-O

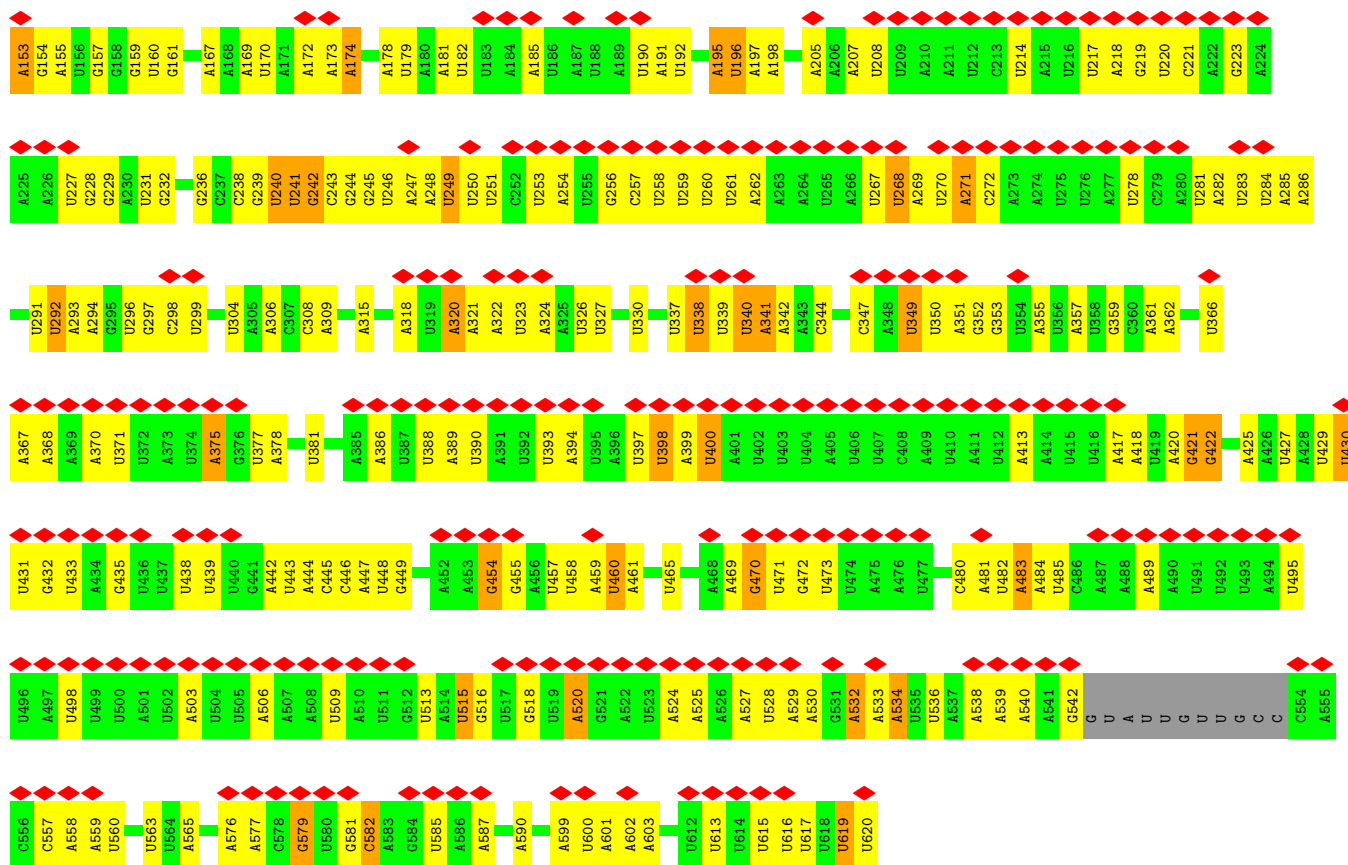


- Molecule 59: UNK-Y

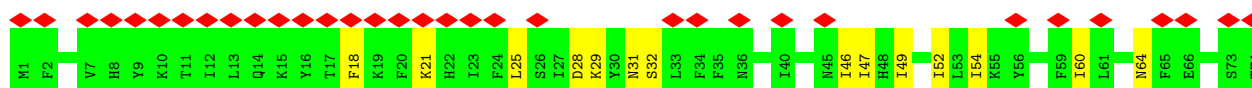
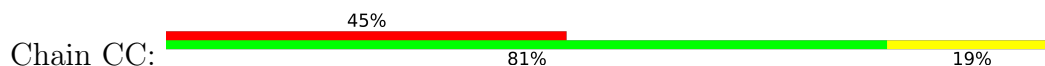


- Molecule 60: 9S rRNA

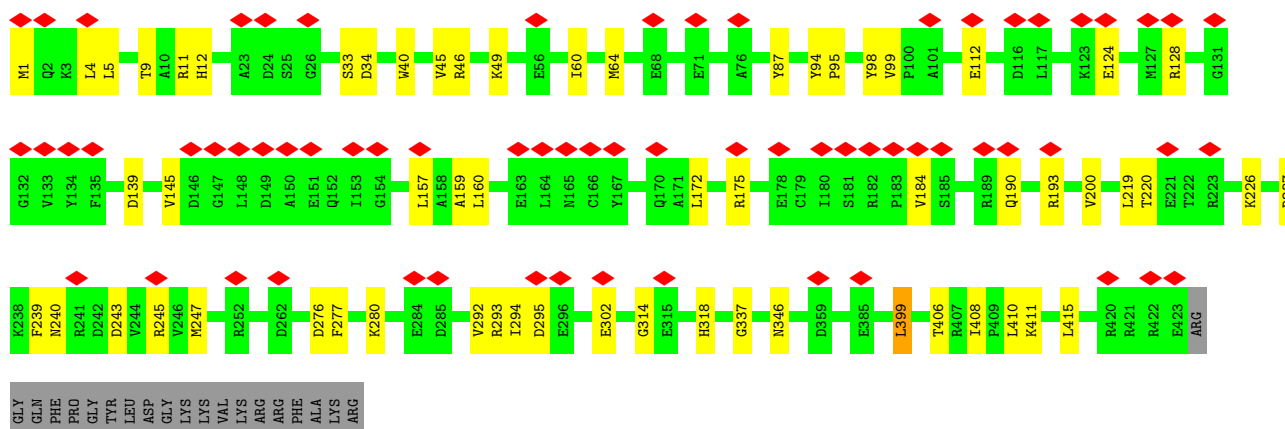
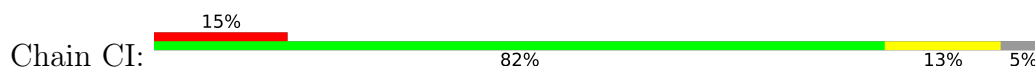


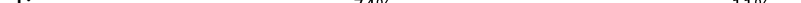


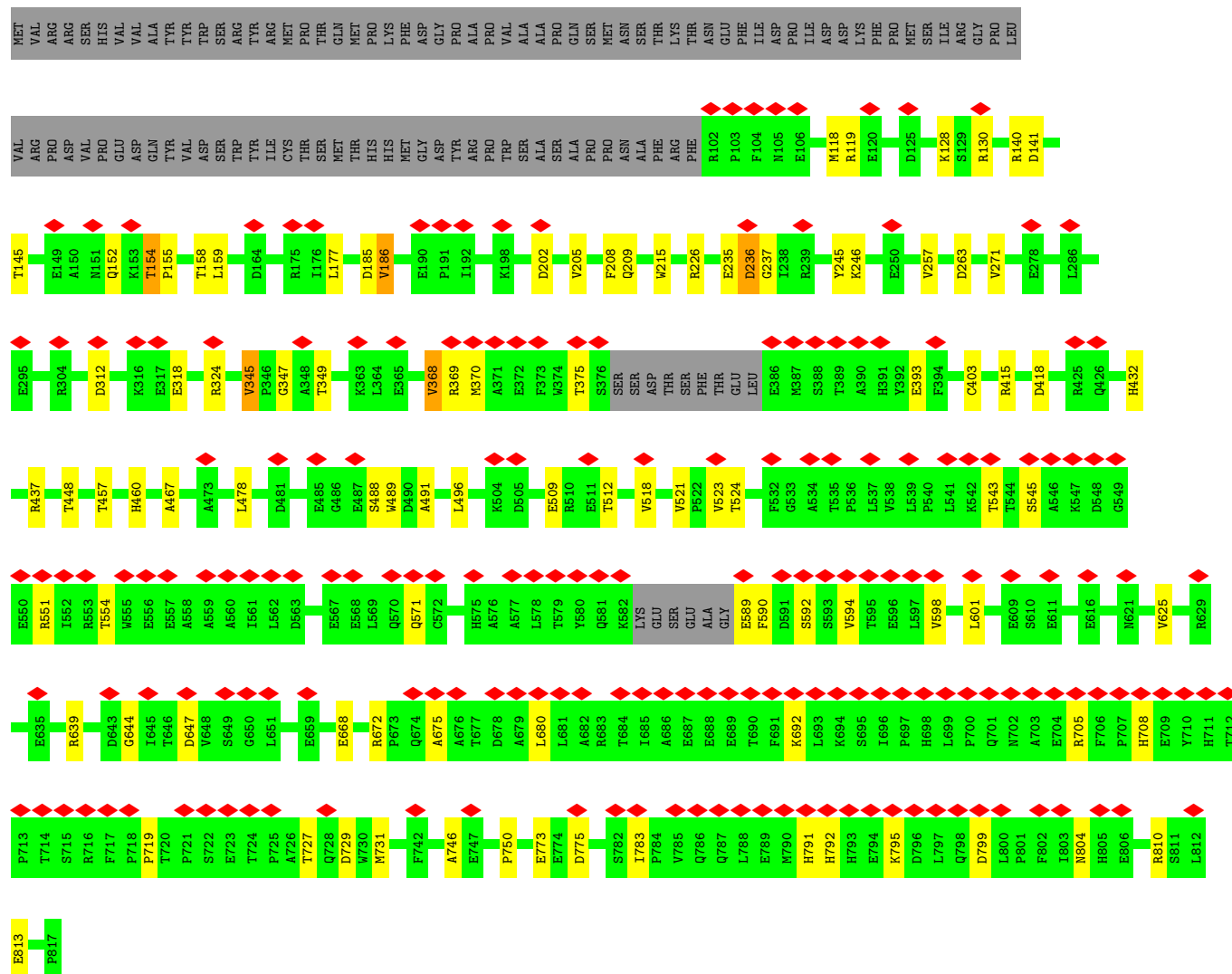
• Molecule 61: mS3m

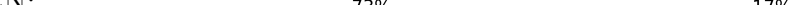


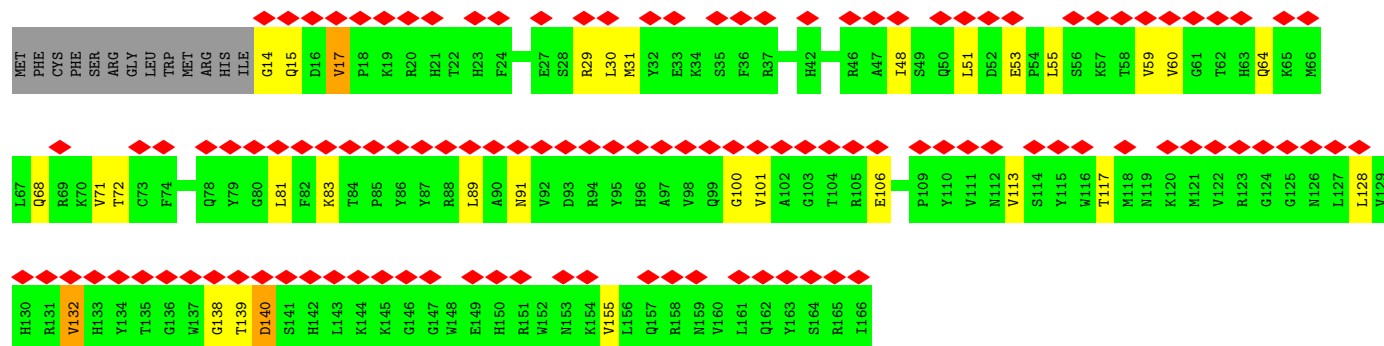
• Molecule 62: uS9m



Chain CJ: 



Chain CN: 



- Molecule 65: uS19m



MET ALA PHE ARG ASN THR PHE THR PRO GLY LYS PHE SER THR VAL SER LYS ASN ILE VAL LEU LEU ILE TRP ARG VAL LYS VAL PHE LEU ARG ALA GLY PHE LEU ALA HIS SER LEU VAL MET LEU PRO VAL SER LEU TYR SER LYS ILE LEU LEU CYS ASP VAL LYS LYS

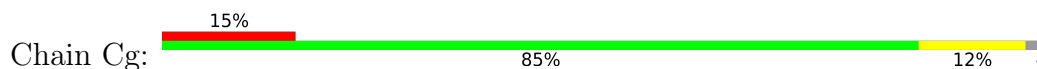
ILE VAL TYR PHE HIS CYS THR ARG LYS LYS SER MET LEU ARG CYS PRO CYS VAL TRP PRO ASP GLY PRO THR LYS SER SER VAL ILE THR GLY THR PHE LEU GLN LYS ARG PHE LEU LYS ILE ALA SER LEU TYR PHE GLY PHE TYR LEU LEU CYS ASP VAL LYS LYS ARG ARG GLN ARG

LYS Y50 P51 F52 L53 R54 R55 P56 H57 F58 LYS ASN THR HIS SER MET N65 P66 S67 A68 P69 Y70 F71 W72 S73 F74 W75 T76 A77 K78 S79 Q80 M81 A82 F83 L84 P85 E86 E87 N88 Y89 I90 T91 Q92 D93 Y94 T95 G96 F98 F99 V100 S101 K102 R103 Q104 V105 Y106 T107 I108

Q109 H110 A111 T112 S113 G114 A115 K116 F117 R118 V119 SER PHE PRO SER I125 F126 E127 N129 S130 S132 R133 W134 N135 I136 G137 E139 M140 N141 T142 L143 L144 PRO LYS ASP MET ASP ILE ASP GLN MET THR LYS GLN ARG LEU TYR VAL ARG GLY

LEU LEU PRO LYS

• Molecule 66: mS29



MET ARG SER LYS THR LEU K7 K8 S9 A12 M13 Y14 M15 V19 W33 D34 L39 K40 E41 T42 R43 K44 L45 K46 N47 G48 V49 P50 V51 R52 R56 T65 S70 F71 I74 V80 L85 I86 Q87 F88 F89 L93 G94 R96 Q99 P102

P103 G104 H105 P106 R107 G108 F109 L110 D123 T143 D148 G149 P150 K155 V163 R167 N170 I171 V172 T173 L174 Y175 D178 E186 S191 D202 R205 A217 D230 L231 P232 T233 E234 Q235 Q236 E237 F238 Q239 E248 A253 V254 A255 P256 A257

S258 L259 M270 L279 V284 E294 T295 H296 F304 L305 R306 G307 L308 A309 S310 F311 N312 E313 S314 S315 T316 D317 I318 D319 L320 Y321 E324 L325 P329 A330 S331 R332 V336 D347 D348 P349 N350 K351 D360 D365 G366 I367 V373 E374 T375 N380

D383 E384 P390 S394 E408 H458 Q461 R473 E484 C485 M486 S487 R488 C489 A490 SER SER GLY ALA VAL VAL ARG

• Molecule 67: mS33

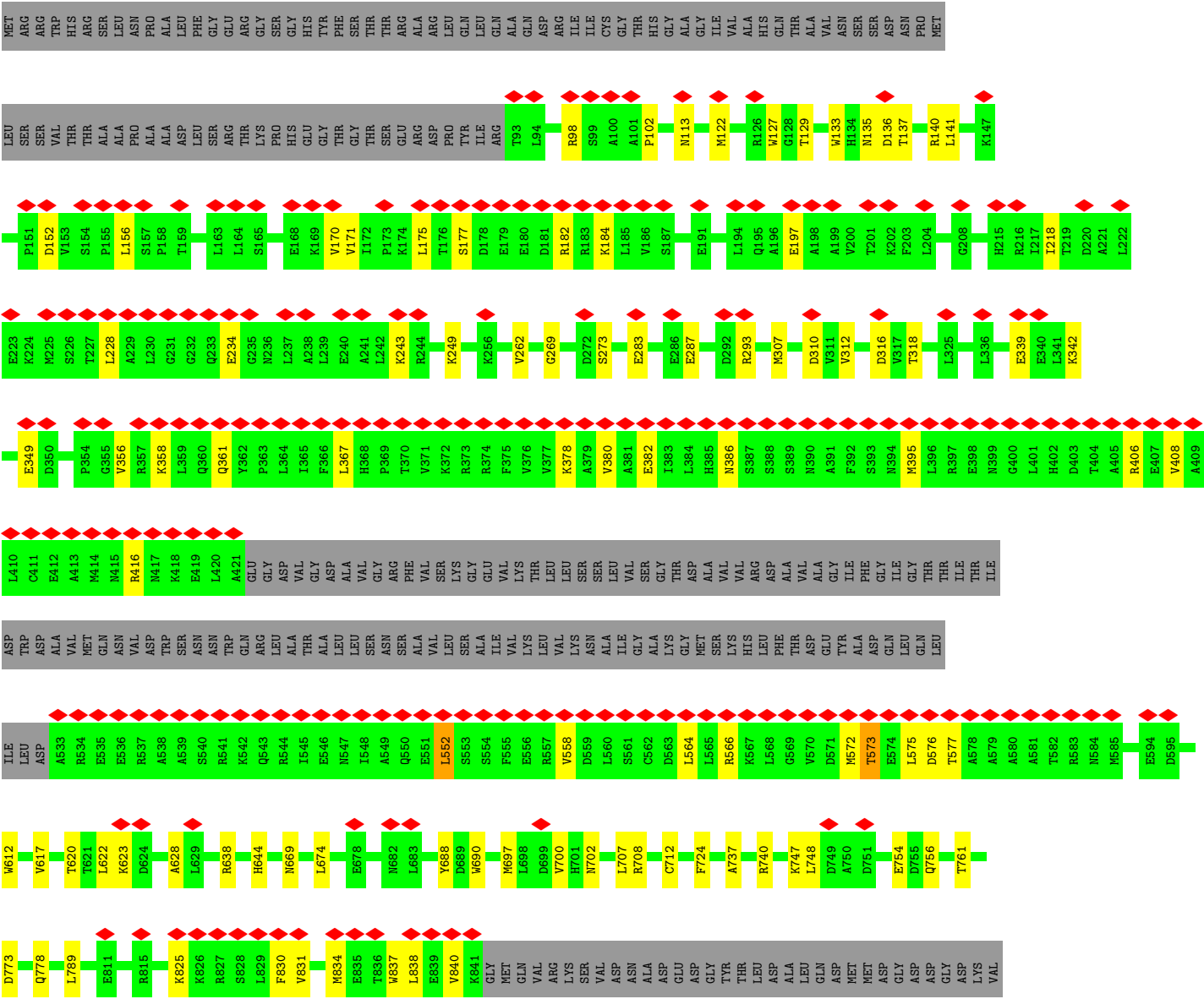


MET VAL LEU ARG TRP PHE PRO G11 R14 T22 D32 L33 R34 R39 Q42 E43 K48 G51 A52 Q53 Q54 L55 E56 R74 F78 G79 Y80 Q81 Q82 N83 L84 P85 D86 Y87 I88 M89 K90 K91 R92 N95 R96 E100 L101 F102 A103 R104

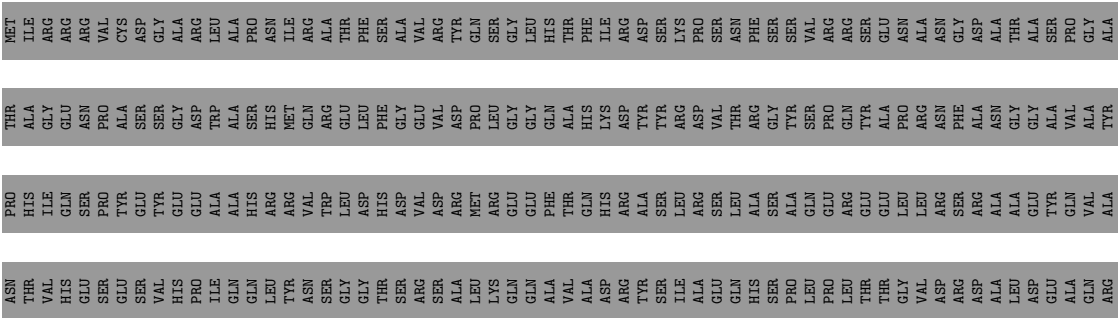
R105 D106 I107 P108 N109 E110 D111 A112 A113 M114 T127 S128 L129 Y133 R134 M135 K137 D138 T139 M140 K141 A142 Q143 R144 L145 N146 D146 R147 K148 L149 S150 G151 N152 R153 F154 K155 V156 L157 CYS SER SER GLY ALA LYS ASN PRO PRO SER GLY TRP GLU PRO ILE PRO ASP ALA THR GLU

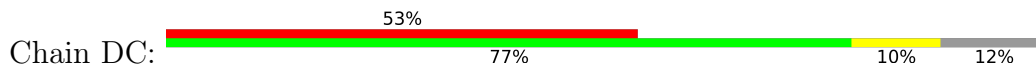
GLU GLU ASP

• Molecule 68: mS35

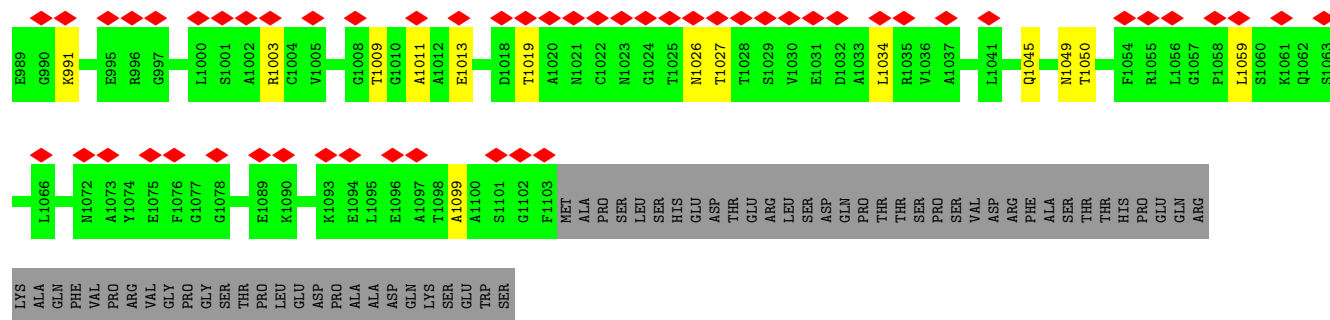


• Molecule 69: mS49

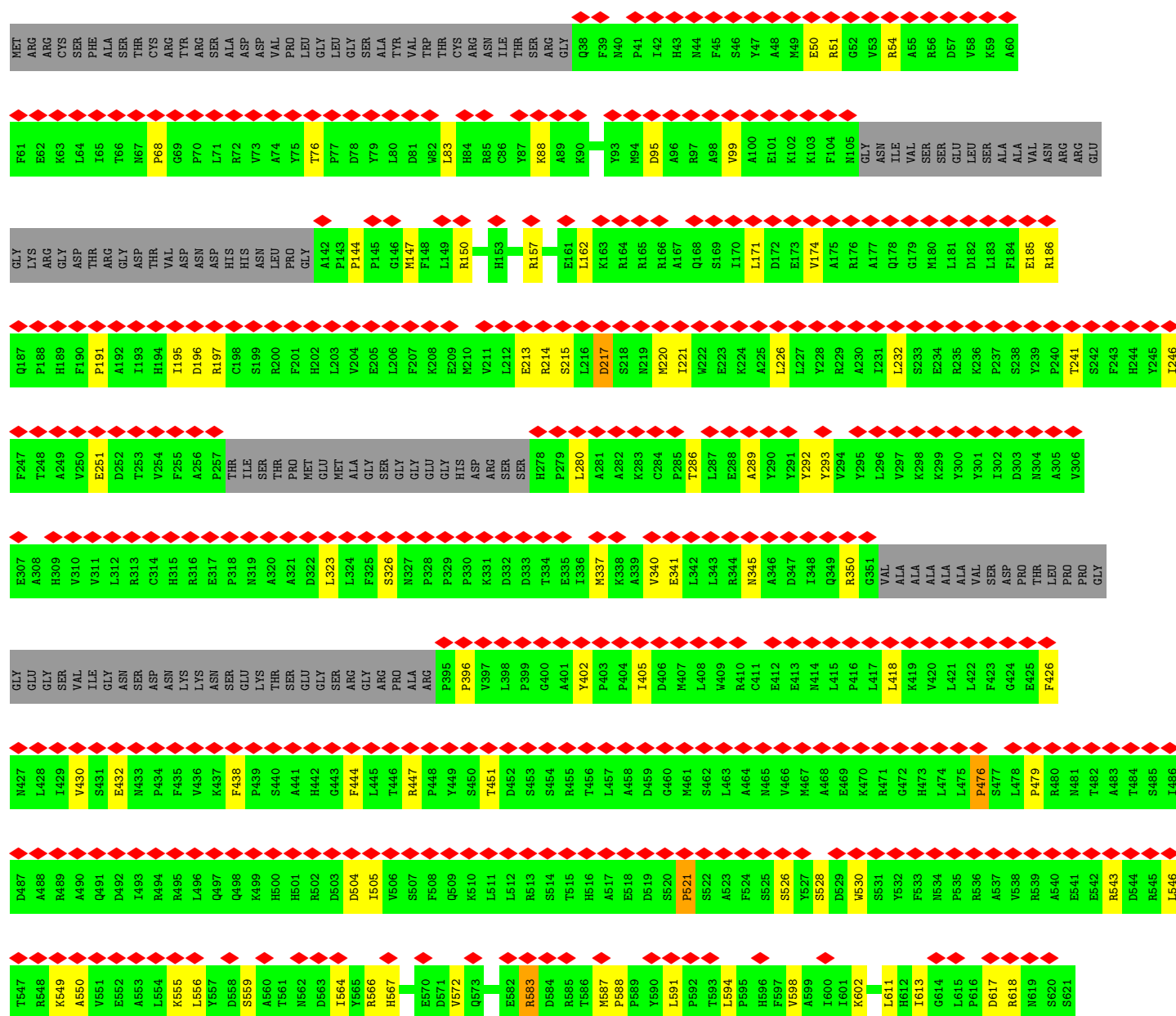


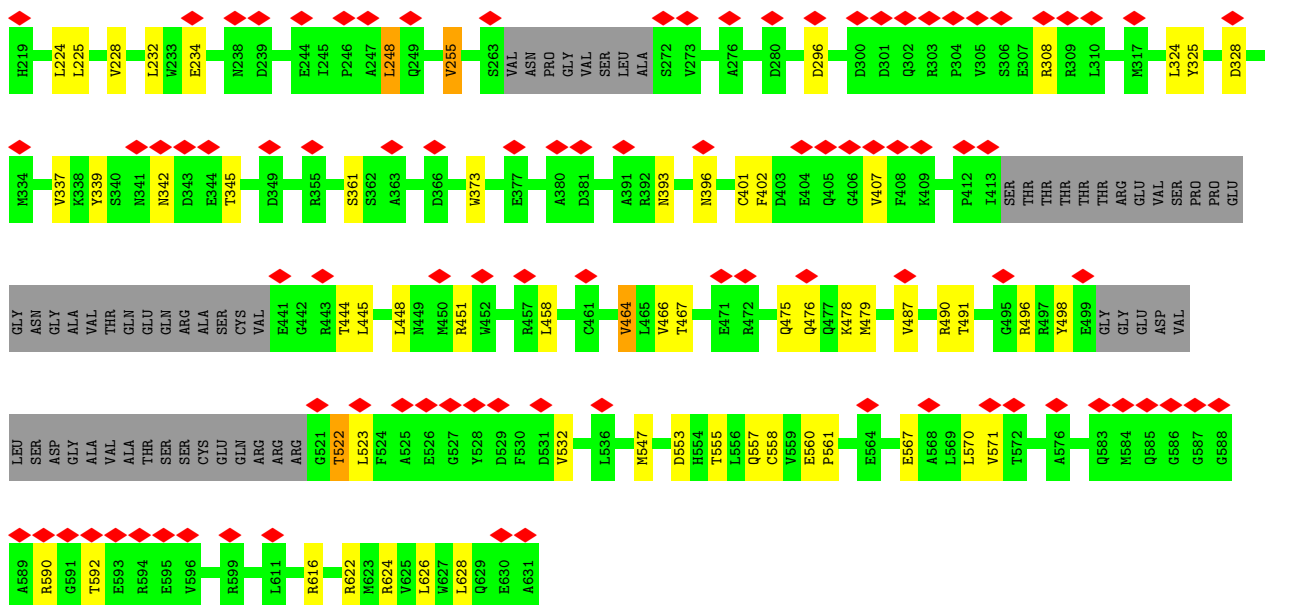




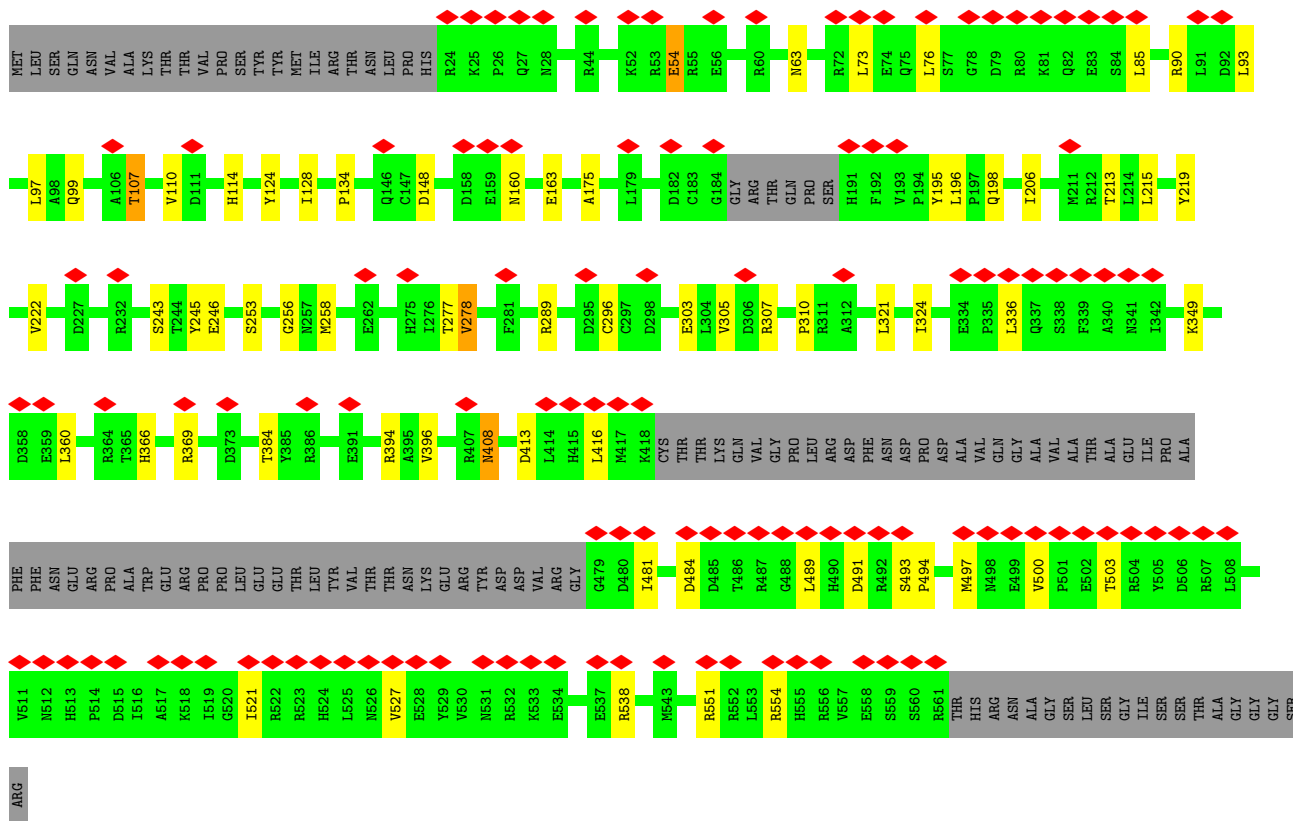


• Molecule 71: mS52



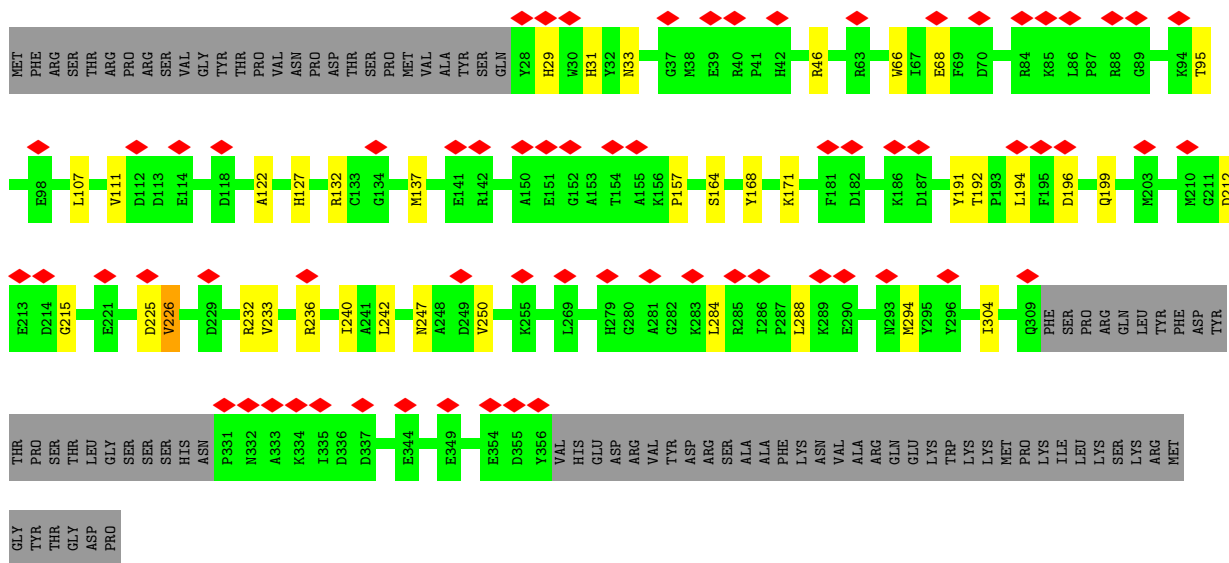


• Molecule 74: mS55 (KRIPP8)

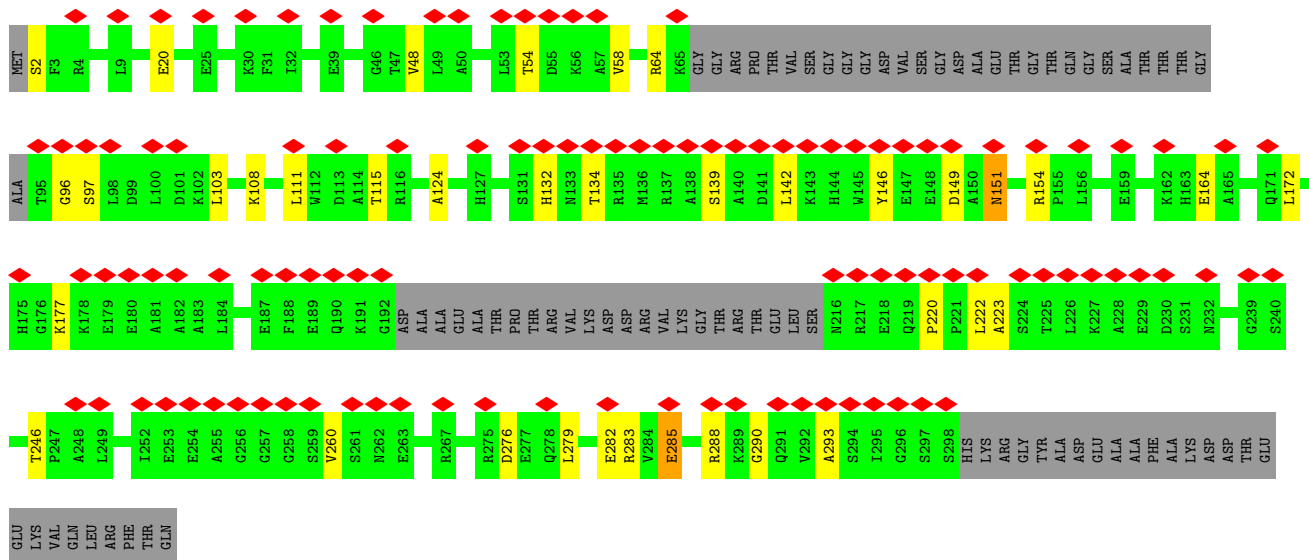


• Molecule 75: mS57

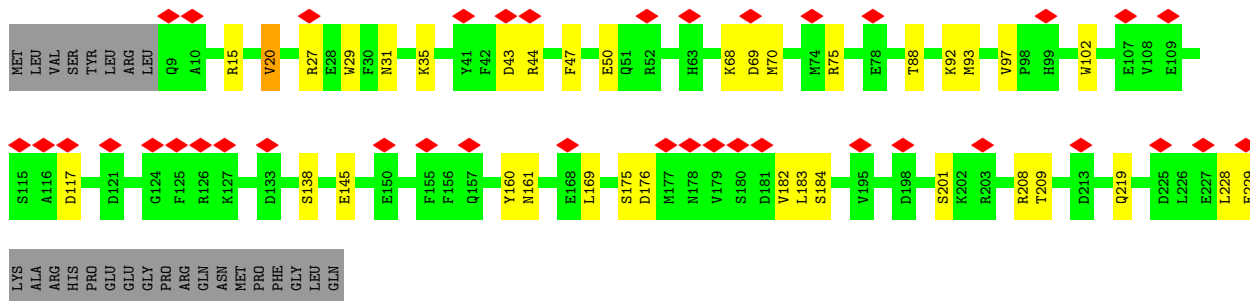
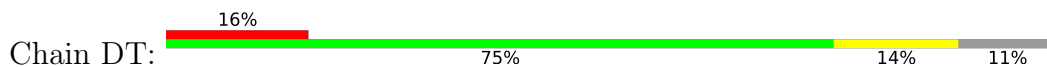




- Molecule 76: mS58

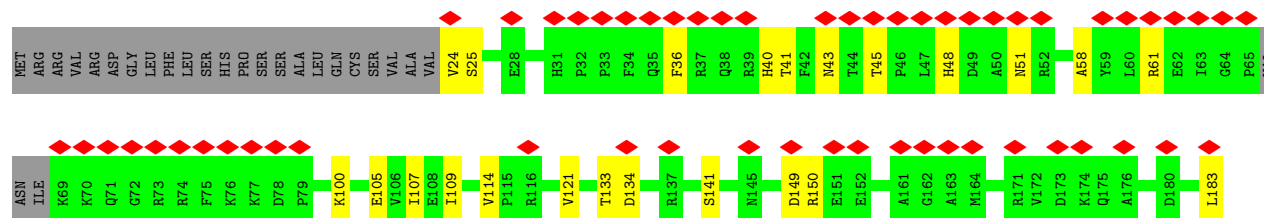


- Molecule 77: mS67



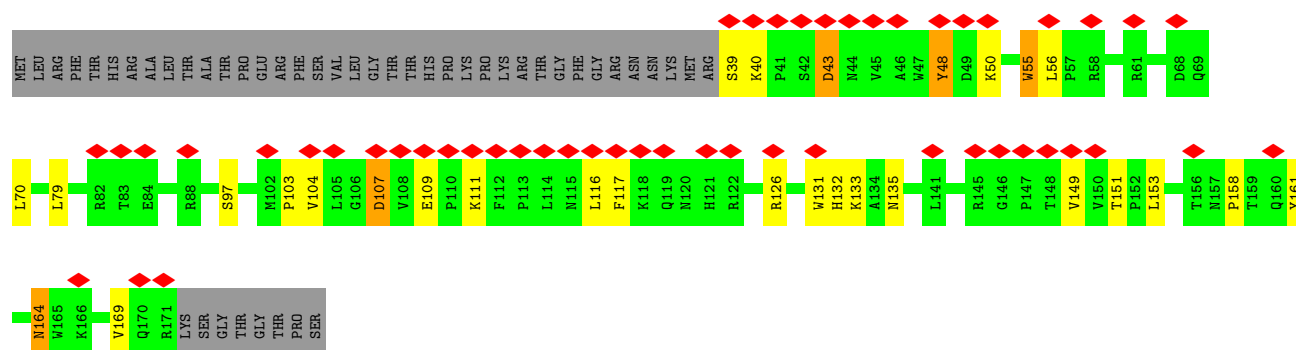
- Molecule 78: mS69

Chain DV: 



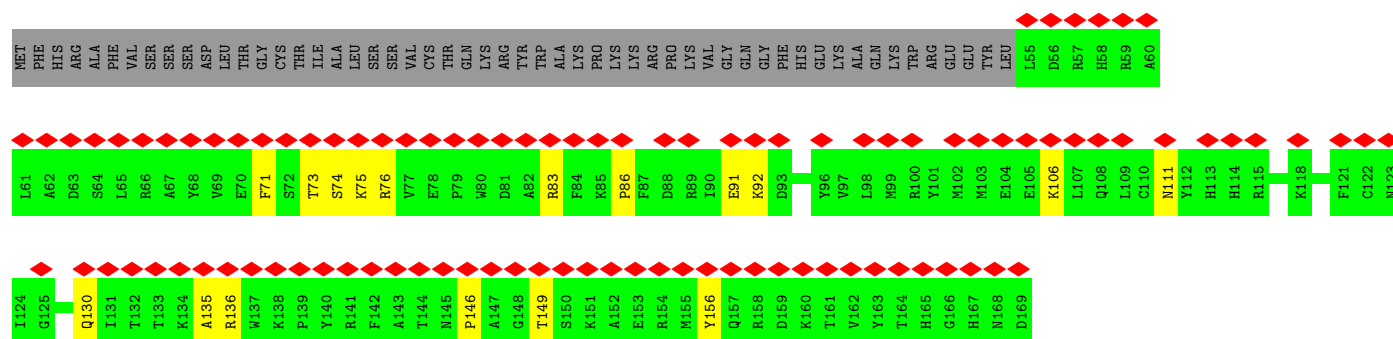
- Molecule 79: mS70

Chain DW: 



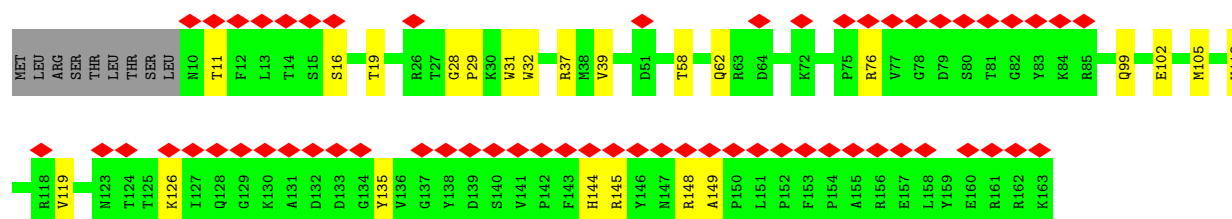
- Molecule 80: mS71

Chain DX: 



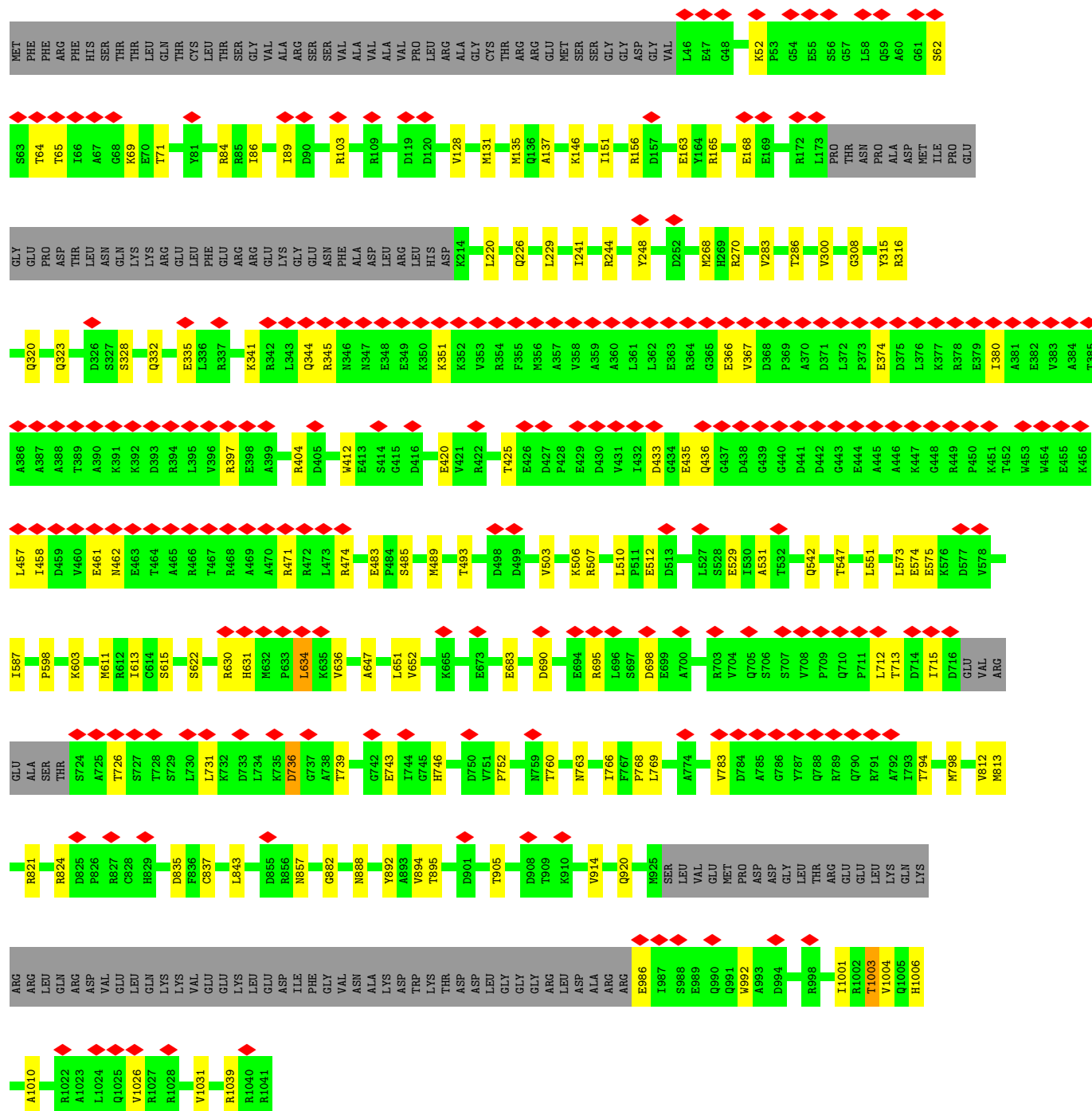
- Molecule 81: mS72

Chain DY: 



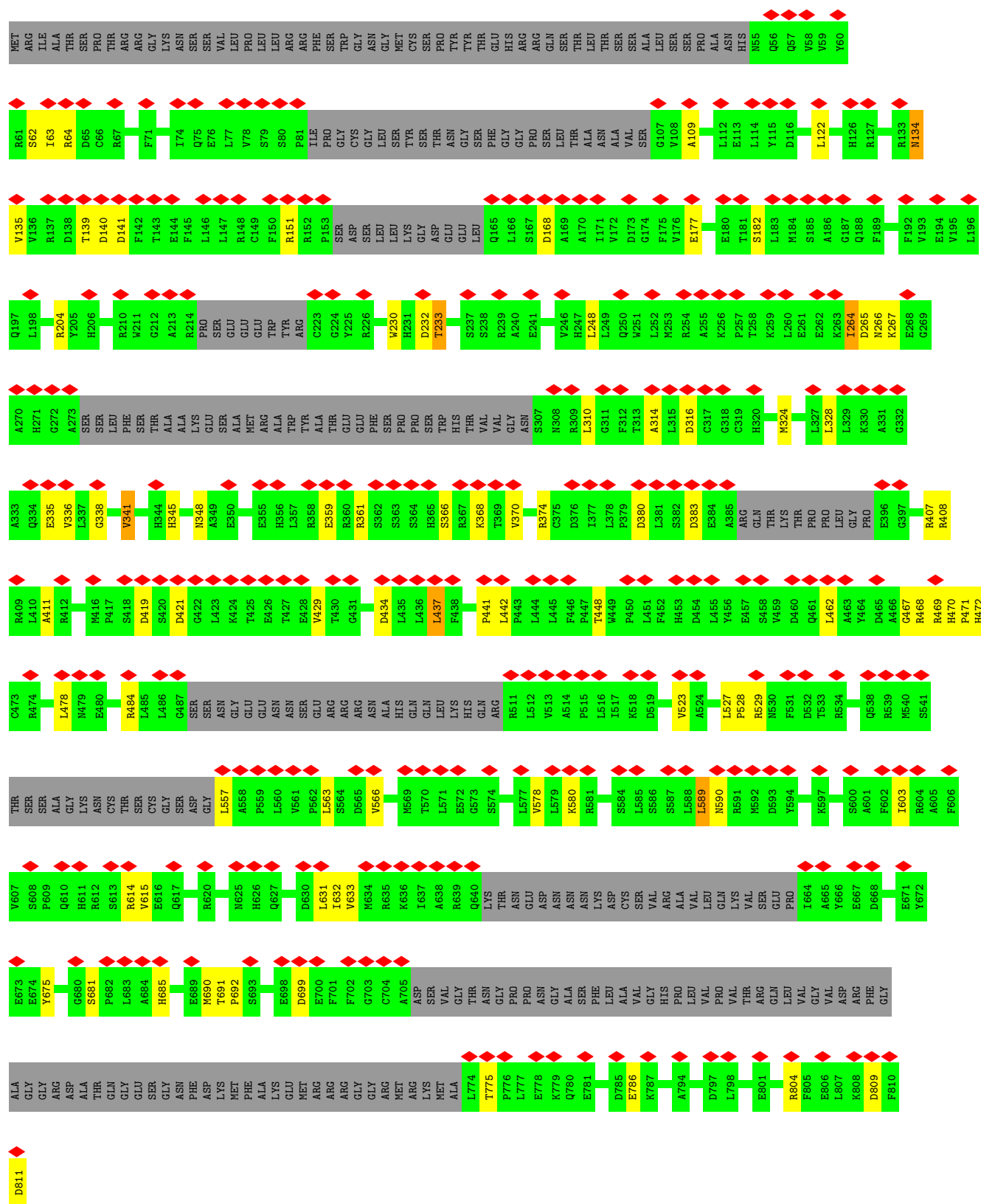
• Molecule 82: mt-SAF1 (RSM22)

Chain F1: 



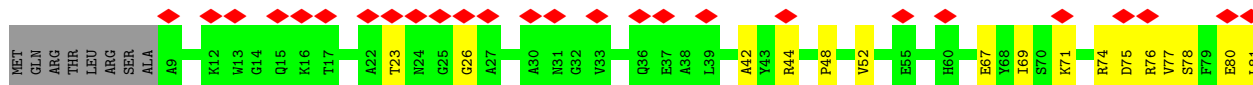
• Molecule 83: mt-SAF4

Chain F4: 



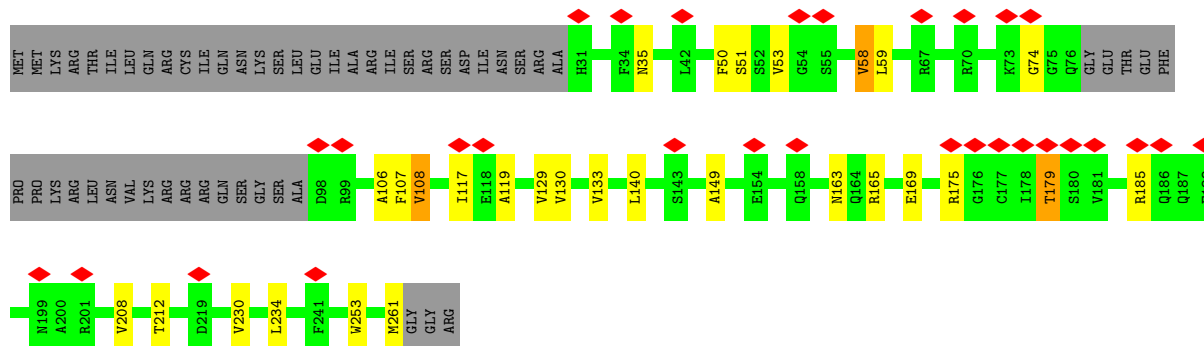
• Molecule 84: mt-SAF12 (KRIPP18)



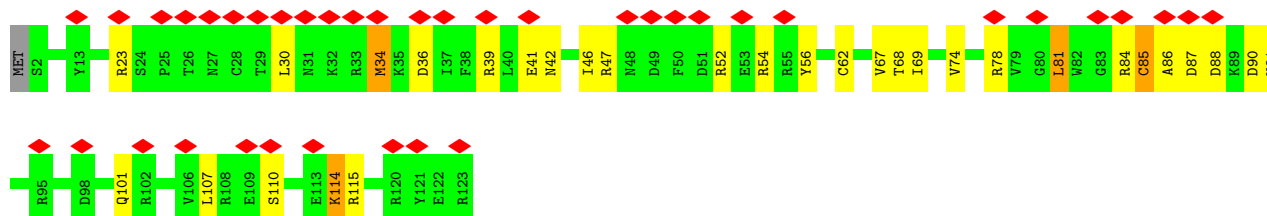
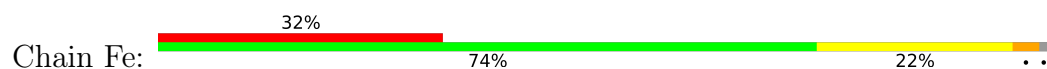




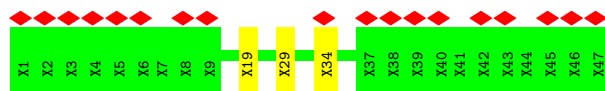
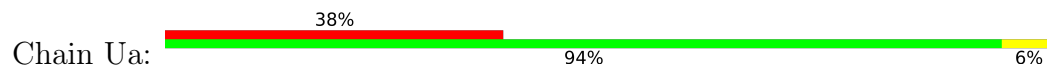
- Molecule 91: mt-SAF25



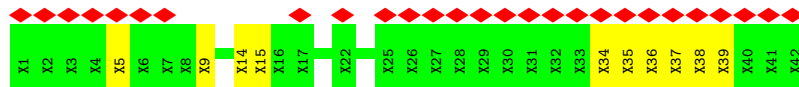
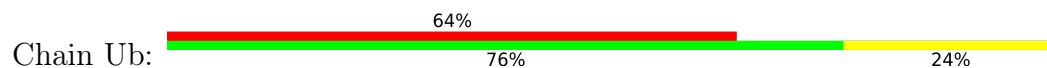
- Molecule 92: mt-SAF34



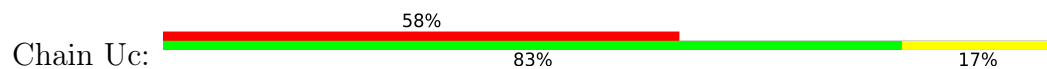
- Molecule 93: UNK-a

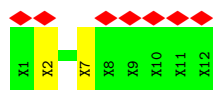


- Molecule 94: UNK-b

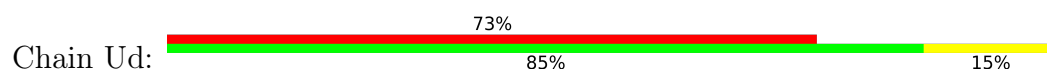


- Molecule 95: UNK-c

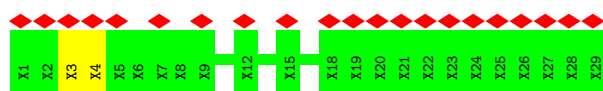
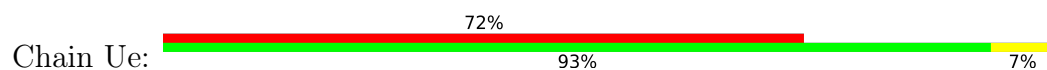




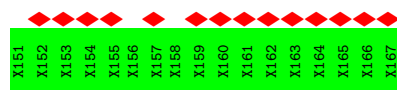
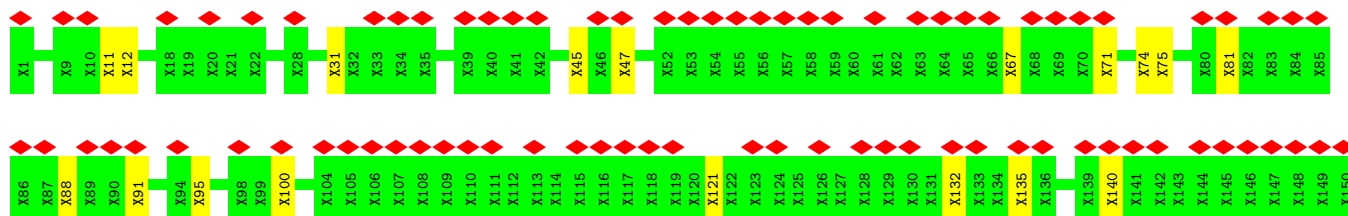
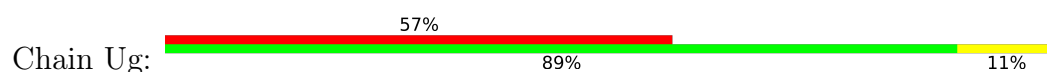
- Molecule 96: UNK-d



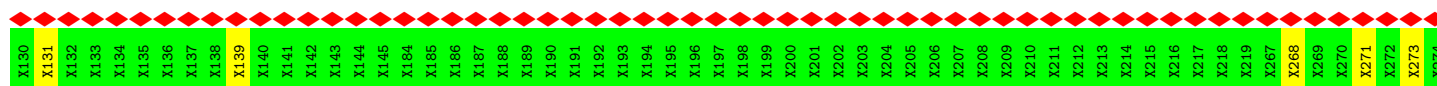
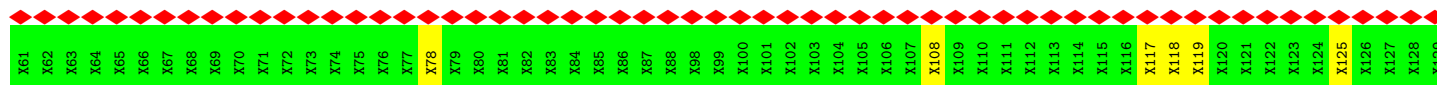
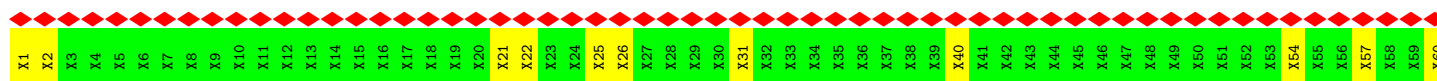
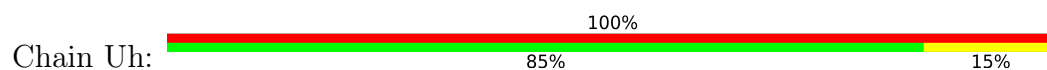
- Molecule 97: UNK-e

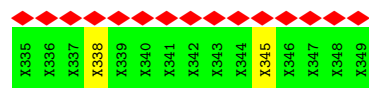
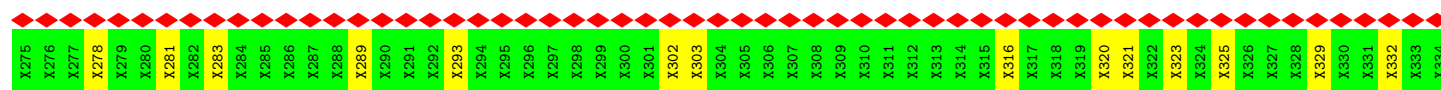


- Molecule 98: UNK-g

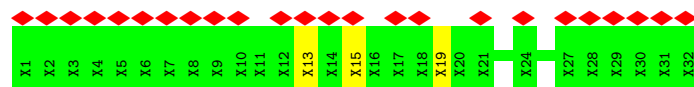
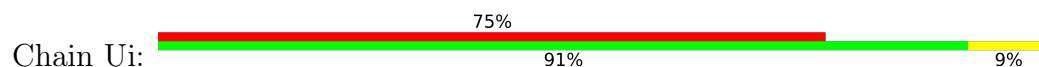


- Molecule 99: UNK-h

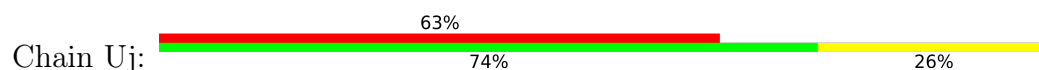




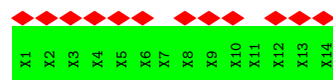
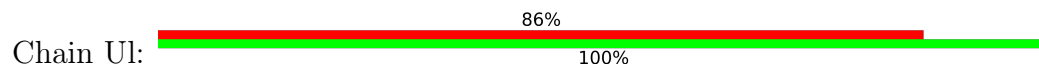
• Molecule 100: UNK-i



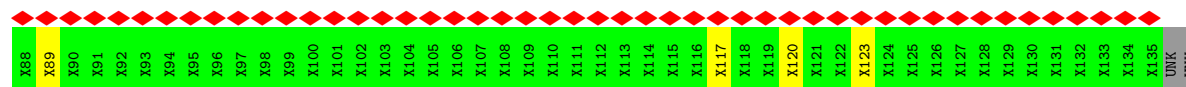
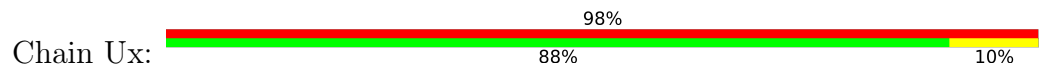
• Molecule 101: UNK-j



• Molecule 102: UNK-l



• Molecule 103: UNK-x



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	104838	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; On the fly in RELION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	100719	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.613	Depositor
Minimum map value	-0.285	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.09	Depositor
Map size (Å)	444.8, 444.8, 444.8	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PM8, PO4, UBD, GTP, SAH, MG, ZN

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	CE	0.16	0/3226	0.42	1/4364 (0.0%)
2	CF	0.14	0/1344	0.35	0/1813
3	CH	0.17	0/1864	0.41	0/2511
4	CK	0.17	0/1760	0.43	0/2372
5	CO	0.16	0/3057	0.39	0/4121
6	CP	0.18	0/1533	0.44	0/2074
7	CQ	0.17	0/1856	0.40	0/2509
8	CR	0.15	0/1315	0.43	0/1785
9	Ca	0.17	0/4474	0.42	1/6052 (0.0%)
10	Cb	0.17	0/1304	0.41	0/1751
11	Cd	0.23	0/1662	0.36	0/2234
12	Cj	0.15	0/1842	0.38	0/2511
13	Cn	0.20	0/245	0.51	0/333
14	Cp	0.14	0/1551	0.35	0/2103
15	DD	0.16	0/6678	0.38	0/9051
16	DI	0.14	0/3248	0.35	0/4401
17	DL	0.16	0/1699	0.40	0/2293
18	DO	0.12	0/1680	0.33	0/2265
19	DP	0.14	0/1854	0.36	0/2511
20	DR	0.16	0/2107	0.42	0/2871
21	DU	0.17	0/1780	0.51	2/2416 (0.1%)
22	DZ	0.14	0/263	0.33	0/355
23	F2	0.17	0/7432	0.40	2/10042 (0.0%)
24	F3	0.16	0/6999	0.41	4/9472 (0.0%)
25	F5	0.18	0/3533	0.45	3/4798 (0.1%)
26	F6	0.17	0/3728	0.45	0/5060
27	F7	0.18	0/5342	0.45	0/7236
28	F8	0.15	0/4025	0.37	0/5450
29	F9	0.15	0/1785	0.36	0/2399
30	FA	0.19	0/4507	0.46	0/6139
31	FB	0.16	0/3132	0.39	0/4248
31	FC	0.16	0/2635	0.41	0/3572

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	FE	0.15	0/3629	0.37	0/4935
33	FJ	0.22	0/2986	0.47	0/4030
34	FM	0.17	0/2489	0.39	0/3365
34	FN	0.14	0/2430	0.37	0/3285
35	FO	0.17	0/2733	0.42	0/3692
36	FP	0.16	0/2710	0.42	2/3709 (0.1%)
37	FQ	0.16	0/2048	0.36	0/2786
37	FR	0.14	0/1966	0.34	0/2673
37	FS	0.14	0/2249	0.35	0/3063
37	FT	0.15	0/1897	0.34	0/2580
37	FU	0.15	0/2154	0.37	0/2933
38	FW	0.14	0/2077	0.36	0/2805
39	FX	0.15	0/1783	0.39	0/2410
40	FY	0.19	0/1321	0.45	0/1788
41	FZ	0.14	0/989	0.49	3/1336 (0.2%)
42	Fa	0.15	0/1363	0.40	0/1853
43	Fb	0.14	0/1123	0.40	0/1513
44	Fc	0.11	0/679	0.29	0/923
45	Fd	0.16	0/779	0.38	0/1054
60	CA	0.16	0/12605	0.36	1/19567 (0.0%)
61	CC	0.15	0/666	0.37	0/900
62	CI	0.13	0/3424	0.36	0/4626
63	CJ	0.15	0/5865	0.40	0/7974
64	CN	0.12	0/1323	0.33	0/1790
65	CS	0.12	0/731	0.35	0/987
66	Cg	0.14	0/4043	0.35	0/5489
67	Ci	0.12	0/1256	0.36	0/1695
68	Ck	0.14	0/5215	0.37	0/7050
69	DB	0.14	0/5830	0.40	2/7889 (0.0%)
70	DC	0.14	0/8409	0.36	0/11399
71	DE	0.13	0/4756	0.39	3/6462 (0.0%)
72	DF	0.15	0/4056	0.41	0/5493
73	DG	0.13	0/4674	0.35	0/6333
74	DH	0.15	0/3935	0.41	2/5321 (0.0%)
75	DJ	0.13	0/2591	0.38	0/3508
76	DK	0.13	0/1965	0.37	0/2652
77	DT	0.13	0/1982	0.38	0/2686
78	DV	0.15	0/1358	0.39	0/1836
79	DW	0.24	0/1182	0.47	0/1613
80	DX	0.15	0/993	0.41	0/1336
81	DY	0.15	0/1337	0.39	0/1814
82	F1	0.16	0/7334	0.40	1/9883 (0.0%)
83	F4	0.14	0/4483	0.40	0/6061

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
84	FD	0.13	0/3216	0.36	0/4380
85	FF	0.15	0/3335	0.41	0/4498
86	FG	0.14	0/1386	0.40	0/1869
87	FH	0.14	0/2537	0.35	0/3442
88	FI	0.13	0/2834	0.36	0/3821
89	FK	0.13	0/1748	0.33	0/2378
90	FL	0.15	0/2613	0.38	0/3538
91	FV	0.13	0/1680	0.36	0/2281
92	Fe	0.16	0/1057	0.46	0/1421
All	All	0.15	0/237284	0.39	27/323837 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	DD	0	1
24	F3	0	1
27	F7	0	1
28	F8	0	1
36	FP	0	1
38	FW	0	1
74	DH	0	1
79	DW	0	1
85	FF	0	1
92	Fe	0	1
All	All	0	10

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	Ca	525	PRO	N-CA-CB	10.94	110.56	103.23
1	CE	385	PRO	N-CA-CB	8.12	111.78	103.25
21	DU	206	PRO	N-CA-CB	7.99	110.39	103.36
21	DU	200	PRO	N-CA-CB	7.55	110.36	103.19
25	F5	521	PRO	N-CA-CB	7.35	110.21	103.08

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	DD	414	ARG	Peptide
24	F3	490	GLN	Peptide
27	F7	381	LEU	Peptide
28	F8	644	ASP	Peptide
36	FP	84	HIS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CE	3147	0	3091	31	0
2	CF	1317	0	1309	18	0
3	CH	1824	0	1800	21	0
4	CK	1721	0	1689	15	0
5	CO	2979	0	2974	31	0
6	CP	1489	0	1510	19	0
7	CQ	1805	0	1811	32	0
8	CR	1274	0	1223	11	0
9	Ca	4340	0	4127	52	0
10	Cb	1274	0	1287	10	0
11	Cd	1616	0	1568	23	0
12	Cj	1792	0	1744	21	0
13	Cn	234	0	222	2	0
14	Cp	1506	0	1467	14	0
15	DD	6488	0	6251	67	0
16	DI	3182	0	3153	38	0
17	DL	1656	0	1632	13	0
18	DO	1648	0	1615	11	0
19	DP	1800	0	1765	12	0
20	DR	2042	0	2043	22	0
21	DU	1738	0	1640	18	0
22	DZ	254	0	230	4	0
23	F2	7274	0	7113	66	0
24	F3	6879	0	6854	54	0
25	F5	3474	0	3070	30	0
26	F6	3646	0	3608	40	0
27	F7	5225	0	5177	61	0
28	F8	3934	0	3908	32	0
29	F9	1755	0	1709	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	FA	4421	0	4534	43	0
31	FB	3055	0	3011	39	0
31	FC	2572	0	2544	42	0
32	FE	3523	0	3460	44	0
33	FJ	2917	0	2966	31	0
34	FM	2449	0	2440	24	0
34	FN	2392	0	2375	26	0
35	FO	2671	0	2636	44	0
36	FP	2643	0	2554	20	0
37	FQ	2003	0	1928	20	0
37	FR	1923	0	1862	21	0
37	FS	2198	0	2142	21	0
37	FT	1854	0	1802	23	0
37	FU	2105	0	2031	20	0
38	FW	2034	0	2035	17	0
39	FX	1741	0	1693	12	0
40	FY	1289	0	1291	19	0
41	FZ	973	0	869	8	0
42	Fa	1323	0	1336	12	0
43	Fb	1091	0	1085	11	0
44	Fc	669	0	663	8	0
45	Fd	758	0	764	8	0
46	UA	126	0	128	5	0
47	UB	162	0	169	5	0
47	Uk	162	0	164	3	0
48	UC	60	0	63	1	0
49	UD	54	0	57	5	0
49	UM	54	0	58	4	0
49	UQ	54	0	56	2	0
49	Uf	54	0	56	4	0
50	UE	270	0	272	2	0
50	UP	270	0	272	10	0
51	UF	66	0	70	3	0
51	Um	66	0	68	1	0
52	UG	102	0	104	5	0
53	UH	30	0	32	1	0
54	UI	48	0	50	4	0
54	UN	48	0	50	1	0
55	UJ	96	0	99	3	0
56	UK	144	0	146	1	0
57	UL	132	0	135	2	0
58	UO	180	0	183	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	UY	2808	0	2852	113	0
60	CA	11352	0	5672	102	0
61	CC	646	0	682	9	0
62	CI	3357	0	3310	42	0
63	CJ	5709	0	5508	63	0
64	CN	1285	0	1264	17	0
65	CS	708	0	688	9	0
66	Cg	3922	0	3811	40	0
67	Ci	1222	0	1192	16	0
68	Ck	5123	0	5154	55	0
69	DB	5688	0	5497	67	0
70	DC	8223	0	8043	65	0
71	DE	4639	0	4417	47	0
72	DF	3967	0	3957	39	0
73	DG	4575	0	4490	63	0
74	DH	3849	0	3811	39	0
75	DJ	2521	0	2464	20	0
76	DK	1929	0	1928	25	0
77	DT	1912	0	1787	22	0
78	DV	1323	0	1308	16	0
79	DW	1140	0	1117	17	0
80	DX	967	0	956	12	0
81	DY	1295	0	1290	20	0
82	F1	7194	0	7263	71	0
83	F4	4382	0	4291	54	0
84	FD	3135	0	3117	29	0
85	FF	3265	0	3204	46	0
86	FG	1359	0	1375	19	0
87	FH	2486	0	2430	32	0
88	FI	2786	0	2712	35	0
89	FK	1699	0	1589	17	0
90	FL	2555	0	2530	33	0
91	FV	1636	0	1567	18	0
92	Fe	1033	0	1004	17	0
93	Ua	282	0	285	3	0
94	Ub	252	0	255	9	0
95	Uc	72	0	75	3	0
96	Ud	354	0	356	8	0
97	Ue	174	0	176	4	0
98	Ug	1002	0	1025	11	0
99	Uh	1530	0	1558	30	0
100	Ui	192	0	194	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
101	Uj	114	0	117	5	0
102	Ul	84	0	86	0	0
103	Ux	648	0	656	6	0
104	CA	2	0	0	0	0
104	Cg	1	0	0	0	0
104	FP	1	0	0	0	0
104	FW	1	0	0	0	0
105	FW	5	0	0	1	0
106	Fc	32	0	39	1	0
107	F1	1	0	0	0	0
107	FG	1	0	0	0	0
107	FL	2	0	0	0	0
107	Fd	1	0	0	0	0
107	Fe	1	0	0	0	0
108	Cg	32	0	12	3	0
109	F1	26	0	19	2	0
109	FF	26	0	19	2	0
110	Cg	3	0	0	0	0
All	All	240624	0	230995	2162	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 5.

The worst 5 of 2162 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)
40:FY:87:GLN:HG2	97:Ue:4:UNK:HA	1.55	0.89
59:UY:355:UNK:HG1	60:CA:579:G:H5'	1.56	0.88
27:F7:206:PRO:HB3	59:UY:193:UNK:HB1	1.56	0.87
35:FO:148:ARG:HH21	54:UI:2:UNK:HB1	1.42	0.84
59:UY:9:UNK:HG1	59:UY:461:UNK:HB2	1.59	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CE	390/435 (90%)	375 (96%)	13 (3%)	2 (0%)	24	55
2	CF	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
3	CH	216/282 (77%)	211 (98%)	5 (2%)	0	100	100
4	CK	205/326 (63%)	190 (93%)	15 (7%)	0	100	100
5	CO	354/429 (82%)	345 (98%)	9 (2%)	0	100	100
6	CP	178/188 (95%)	170 (96%)	8 (4%)	0	100	100
7	CQ	217/336 (65%)	209 (96%)	8 (4%)	0	100	100
8	CR	149/320 (47%)	141 (95%)	8 (5%)	0	100	100
9	Ca	508/602 (84%)	490 (96%)	18 (4%)	0	100	100
10	Cb	149/311 (48%)	145 (97%)	4 (3%)	0	100	100
11	Cd	183/440 (42%)	182 (100%)	1 (0%)	0	100	100
12	Cj	224/257 (87%)	219 (98%)	5 (2%)	0	100	100
13	Cn	25/250 (10%)	23 (92%)	2 (8%)	0	100	100
14	Cp	176/187 (94%)	171 (97%)	5 (3%)	0	100	100
15	DD	782/812 (96%)	756 (97%)	26 (3%)	0	100	100
16	DI	388/407 (95%)	378 (97%)	10 (3%)	0	100	100
17	DL	199/307 (65%)	192 (96%)	7 (4%)	0	100	100
18	DO	202/282 (72%)	200 (99%)	2 (1%)	0	100	100
19	DP	210/274 (77%)	206 (98%)	4 (2%)	0	100	100
20	DR	250/270 (93%)	241 (96%)	9 (4%)	0	100	100
21	DU	217/228 (95%)	203 (94%)	14 (6%)	0	100	100
22	DZ	28/94 (30%)	27 (96%)	1 (4%)	0	100	100
23	F2	909/1024 (89%)	886 (98%)	23 (2%)	0	100	100
24	F3	882/966 (91%)	857 (97%)	25 (3%)	0	100	100
25	F5	474/754 (63%)	461 (97%)	12 (2%)	1 (0%)	43	71
26	F6	450/676 (67%)	436 (97%)	14 (3%)	0	100	100
27	F7	658/679 (97%)	615 (94%)	41 (6%)	2 (0%)	36	65
28	F8	493/726 (68%)	475 (96%)	18 (4%)	0	100	100
29	F9	214/608 (35%)	213 (100%)	1 (0%)	0	100	100
30	FA	573/642 (89%)	553 (96%)	20 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	FB	373/579 (64%)	363 (97%)	10 (3%)	0	100	100
31	FC	305/579 (53%)	294 (96%)	11 (4%)	0	100	100
32	FE	432/553 (78%)	416 (96%)	16 (4%)	0	100	100
33	FJ	351/362 (97%)	333 (95%)	18 (5%)	0	100	100
34	FM	324/370 (88%)	320 (99%)	4 (1%)	0	100	100
34	FN	317/370 (86%)	311 (98%)	6 (2%)	0	100	100
35	FO	320/334 (96%)	306 (96%)	14 (4%)	0	100	100
36	FP	346/349 (99%)	332 (96%)	13 (4%)	1 (0%)	36	65
37	FQ	255/307 (83%)	250 (98%)	5 (2%)	0	100	100
37	FR	239/307 (78%)	234 (98%)	5 (2%)	0	100	100
37	FS	271/307 (88%)	261 (96%)	10 (4%)	0	100	100
37	FT	229/307 (75%)	224 (98%)	5 (2%)	0	100	100
37	FU	266/307 (87%)	258 (97%)	8 (3%)	0	100	100
38	FW	243/263 (92%)	237 (98%)	6 (2%)	0	100	100
39	FX	218/239 (91%)	211 (97%)	7 (3%)	0	100	100
40	FY	156/188 (83%)	145 (93%)	11 (7%)	0	100	100
41	FZ	129/178 (72%)	125 (97%)	4 (3%)	0	100	100
42	Fa	161/171 (94%)	158 (98%)	3 (2%)	0	100	100
43	Fb	127/151 (84%)	124 (98%)	3 (2%)	0	100	100
44	Fc	82/148 (55%)	82 (100%)	0	0	100	100
45	Fd	94/143 (66%)	93 (99%)	1 (1%)	0	100	100
61	CC	72/74 (97%)	70 (97%)	2 (3%)	0	100	100
62	CI	421/443 (95%)	409 (97%)	12 (3%)	0	100	100
63	CJ	695/817 (85%)	659 (95%)	33 (5%)	3 (0%)	30	60
64	CN	151/166 (91%)	149 (99%)	2 (1%)	0	100	100
65	CS	79/244 (32%)	77 (98%)	2 (2%)	0	100	100
66	Cg	482/498 (97%)	461 (96%)	21 (4%)	0	100	100
67	Ci	145/181 (80%)	143 (99%)	2 (1%)	0	100	100
68	Ck	634/874 (72%)	606 (96%)	28 (4%)	0	100	100
69	DB	671/1181 (57%)	651 (97%)	20 (3%)	0	100	100
70	DC	1020/1165 (88%)	997 (98%)	23 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	DE	582/747 (78%)	566 (97%)	14 (2%)	2 (0%)	36	65
72	DF	485/666 (73%)	466 (96%)	19 (4%)	0	100	100
73	DG	558/631 (88%)	546 (98%)	12 (2%)	0	100	100
74	DH	466/581 (80%)	447 (96%)	19 (4%)	0	100	100
75	DJ	304/396 (77%)	298 (98%)	6 (2%)	0	100	100
76	DK	239/324 (74%)	229 (96%)	10 (4%)	0	100	100
77	DT	219/247 (89%)	211 (96%)	8 (4%)	0	100	100
78	DV	153/183 (84%)	147 (96%)	6 (4%)	0	100	100
79	DW	131/179 (73%)	120 (92%)	11 (8%)	0	100	100
80	DX	113/169 (67%)	106 (94%)	7 (6%)	0	100	100
81	DY	152/163 (93%)	149 (98%)	3 (2%)	0	100	100
82	F1	881/1041 (85%)	849 (96%)	32 (4%)	0	100	100
83	F4	521/811 (64%)	497 (95%)	24 (5%)	0	100	100
84	FD	392/579 (68%)	384 (98%)	8 (2%)	0	100	100
85	FF	404/474 (85%)	388 (96%)	15 (4%)	1 (0%)	43	71
86	FG	167/463 (36%)	162 (97%)	5 (3%)	0	100	100
87	FH	313/457 (68%)	303 (97%)	10 (3%)	0	100	100
88	FI	342/445 (77%)	333 (97%)	9 (3%)	0	100	100
89	FK	202/372 (54%)	202 (100%)	0	0	100	100
90	FL	314/353 (89%)	299 (95%)	15 (5%)	0	100	100
91	FV	206/264 (78%)	198 (96%)	8 (4%)	0	100	100
92	Fe	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
All	All	26932/35095 (77%)	26033 (97%)	887 (3%)	12 (0%)	100	100

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	CE	385	PRO
36	FP	85	LYS
63	CJ	592	SER
71	DE	521	PRO
1	CE	384	ALA

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	CE	325/372 (87%)	315 (97%)	10 (3%)	35	60
2	CF	143/144 (99%)	141 (99%)	2 (1%)	59	73
3	CH	195/246 (79%)	191 (98%)	4 (2%)	47	67
4	CK	184/284 (65%)	177 (96%)	7 (4%)	29	57
5	CO	314/377 (83%)	306 (98%)	8 (2%)	42	64
6	CP	160/168 (95%)	156 (98%)	4 (2%)	42	64
7	CQ	194/297 (65%)	187 (96%)	7 (4%)	31	58
8	CR	130/279 (47%)	124 (95%)	6 (5%)	24	53
9	Ca	449/543 (83%)	438 (98%)	11 (2%)	43	65
10	Cb	132/267 (49%)	123 (93%)	9 (7%)	14	42
11	Cd	168/381 (44%)	167 (99%)	1 (1%)	78	81
12	Cj	193/219 (88%)	187 (97%)	6 (3%)	35	60
13	Cn	22/210 (10%)	22 (100%)	0	100	100
14	Cp	166/175 (95%)	161 (97%)	5 (3%)	36	61
15	DD	691/711 (97%)	686 (99%)	5 (1%)	76	80
16	DI	350/365 (96%)	343 (98%)	7 (2%)	48	68
17	DL	173/263 (66%)	171 (99%)	2 (1%)	63	75
18	DO	170/229 (74%)	166 (98%)	4 (2%)	43	65
19	DP	191/239 (80%)	188 (98%)	3 (2%)	55	72
20	DR	221/235 (94%)	213 (96%)	8 (4%)	31	58
21	DU	179/201 (89%)	176 (98%)	3 (2%)	53	71
22	DZ	25/84 (30%)	23 (92%)	2 (8%)	11	36
23	F2	763/867 (88%)	740 (97%)	23 (3%)	36	61
24	F3	748/809 (92%)	719 (96%)	29 (4%)	28	56
25	F5	293/642 (46%)	278 (95%)	15 (5%)	21	50
26	F6	401/590 (68%)	387 (96%)	14 (4%)	32	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	F7	554/577 (96%)	540 (98%)	14 (2%)	42	64
28	F8	410/561 (73%)	399 (97%)	11 (3%)	39	63
29	F9	175/504 (35%)	171 (98%)	4 (2%)	44	66
30	FA	477/526 (91%)	453 (95%)	24 (5%)	22	50
31	FB	322/483 (67%)	309 (96%)	13 (4%)	28	56
31	FC	272/483 (56%)	260 (96%)	12 (4%)	25	54
32	FE	386/486 (79%)	378 (98%)	8 (2%)	47	67
33	FJ	314/323 (97%)	303 (96%)	11 (4%)	32	58
34	FM	257/292 (88%)	249 (97%)	8 (3%)	35	60
34	FN	251/292 (86%)	238 (95%)	13 (5%)	21	49
35	FO	281/290 (97%)	273 (97%)	8 (3%)	38	62
36	FP	270/286 (94%)	266 (98%)	4 (2%)	57	72
37	FQ	211/264 (80%)	203 (96%)	8 (4%)	29	57
37	FR	206/264 (78%)	198 (96%)	8 (4%)	28	56
37	FS	238/264 (90%)	227 (95%)	11 (5%)	24	53
37	FT	200/264 (76%)	190 (95%)	10 (5%)	22	50
37	FU	222/264 (84%)	210 (95%)	12 (5%)	20	49
38	FW	223/234 (95%)	219 (98%)	4 (2%)	51	70
39	FX	178/195 (91%)	178 (100%)	0	100	100
40	FY	141/163 (86%)	136 (96%)	5 (4%)	32	58
41	FZ	86/156 (55%)	84 (98%)	2 (2%)	44	66
42	Fa	141/149 (95%)	136 (96%)	5 (4%)	32	58
43	Fb	117/135 (87%)	114 (97%)	3 (3%)	40	64
44	Fc	78/127 (61%)	74 (95%)	4 (5%)	21	50
45	Fd	79/119 (66%)	77 (98%)	2 (2%)	42	64
61	CC	73/73 (100%)	69 (94%)	4 (6%)	19	48
62	CI	355/371 (96%)	349 (98%)	6 (2%)	53	71
63	CJ	619/723 (86%)	601 (97%)	18 (3%)	37	62
64	CN	138/150 (92%)	129 (94%)	9 (6%)	15	43
65	CS	76/220 (34%)	74 (97%)	2 (3%)	40	64
66	Cg	426/437 (98%)	414 (97%)	12 (3%)	38	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	Ci	130/160 (81%)	128 (98%)	2 (2%)	57	72
68	Ck	557/747 (75%)	537 (96%)	20 (4%)	31	58
69	DB	613/1030 (60%)	588 (96%)	25 (4%)	27	55
70	DC	867/985 (88%)	836 (96%)	31 (4%)	31	58
71	DE	464/644 (72%)	443 (96%)	21 (4%)	24	53
72	DF	417/560 (74%)	403 (97%)	14 (3%)	32	59
73	DG	490/543 (90%)	472 (96%)	18 (4%)	30	58
74	DH	413/504 (82%)	401 (97%)	12 (3%)	37	62
75	DJ	267/347 (77%)	261 (98%)	6 (2%)	45	66
76	DK	203/261 (78%)	194 (96%)	9 (4%)	25	54
77	DT	205/228 (90%)	199 (97%)	6 (3%)	37	62
78	DV	142/165 (86%)	137 (96%)	5 (4%)	32	58
79	DW	124/163 (76%)	113 (91%)	11 (9%)	9	32
80	DX	102/149 (68%)	102 (100%)	0	100	100
81	DY	137/146 (94%)	135 (98%)	2 (2%)	57	72
82	F1	764/895 (85%)	724 (95%)	40 (5%)	21	49
83	F4	479/703 (68%)	459 (96%)	20 (4%)	26	55
84	FD	338/494 (68%)	331 (98%)	7 (2%)	47	67
85	FF	348/400 (87%)	338 (97%)	10 (3%)	37	62
86	FG	147/414 (36%)	143 (97%)	4 (3%)	39	63
87	FH	270/390 (69%)	261 (97%)	9 (3%)	33	59
88	FI	297/380 (78%)	287 (97%)	10 (3%)	32	59
89	FK	181/308 (59%)	175 (97%)	6 (3%)	33	59
90	FL	279/309 (90%)	271 (97%)	8 (3%)	37	62
91	FV	184/231 (80%)	175 (95%)	9 (5%)	22	51
92	Fe	114/115 (99%)	104 (91%)	10 (9%)	9	32
All	All	23288/30143 (77%)	22523 (97%)	765 (3%)	34	59

5 of 765 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	Ck	367	LEU
73	DG	464	VAL

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Mol	Chain	Res	Type
69	DB	587	VAL
68	Ck	356	VAL
70	DC	839	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 475 such sidechains are listed below:

Mol	Chain	Res	Type
37	FS	213	HIS
87	FH	352	GLN
64	CN	99	GLN
85	FF	370	HIS
92	Fe	42	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
60	CA	606/620 (97%)	241 (39%)	7 (1%)

5 of 241 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
60	CA	3	A
60	CA	4	A
60	CA	5	U
60	CA	6	U
60	CA	7	A

5 of 7 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
60	CA	285	A
60	CA	296	U
60	CA	483	A
60	CA	349	U
60	CA	173	A

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

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
60	UBD	CA	620	-	22,25,26	0.64	0	32,37,40	0.66	1 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	UBD	CA	620	-	-	1/12/30/31	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	CA	620	UBD	O4P-P2-O5P	2.32	119.86	110.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	CA	620	UBD	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 11 are monoatomic - leaving 5 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
105	PO4	FW	301	-	4,4,4	1.04	0	6,6,6	0.48	0
109	SAH	FF	501	-	27,28,28	1.10	5 (18%)	36,40,40	2.08	9 (25%)
106	PM8	Fc	201	44	26,31,31	0.74	1 (3%)	30,38,38	0.91	1 (3%)
108	GTP	Cg	501	104	33,34,34	0.92	1 (3%)	50,54,54	1.66	9 (18%)
109	SAH	F1	1102	-	27,28,28	1.10	5 (18%)	36,40,40	2.09	10 (27%)

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
108	GTP	Cg	501	104	-	5/22/38/38	0/3/3/3
109	SAH	F1	1102	-	-	3/15/31/31	0/3/3/3
109	SAH	FF	501	-	-	1/15/31/31	0/3/3/3
106	PM8	Fc	201	44	-	2/36/38/38	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
106	Fc	201	PM8	C2-C1	2.60	1.53	1.50
109	F1	1102	SAH	C2-N1	2.53	1.38	1.33
109	F1	1102	SAH	C2-N3	2.51	1.38	1.33
109	FF	501	SAH	C2-N3	2.51	1.38	1.33
109	FF	501	SAH	C2-N1	2.49	1.38	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
109	F1	1102	SAH	N3-C2-N1	-5.60	120.11	128.58
109	FF	501	SAH	N3-C2-N1	-5.59	120.13	128.58
108	Cg	501	GTP	C5-C4-N3	-5.52	119.61	128.39
108	Cg	501	GTP	C2-N3-C4	4.99	120.90	112.30
109	F1	1102	SAH	C5-C4-N3	-4.67	120.29	126.72

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

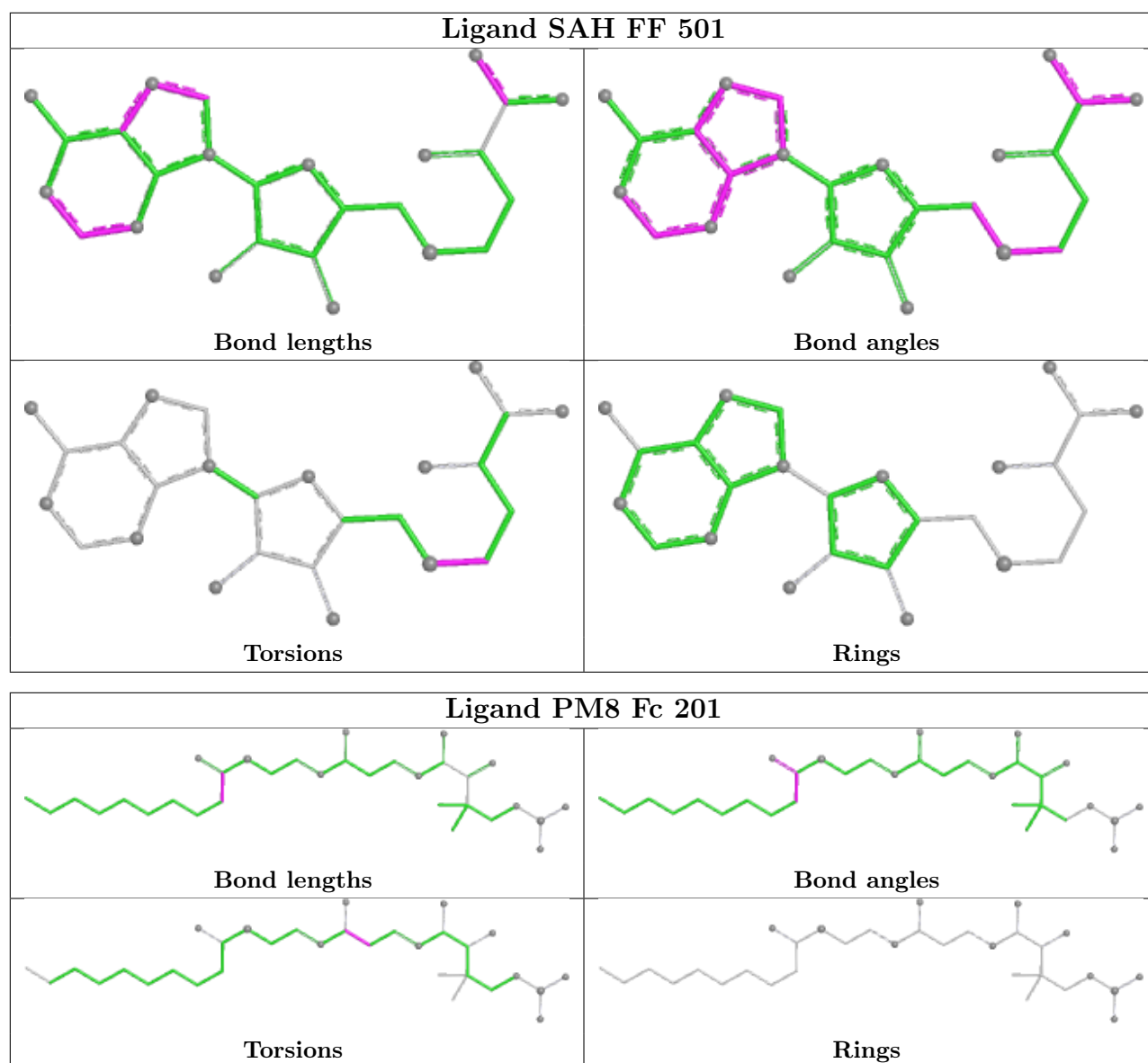
Mol	Chain	Res	Type	Atoms
108	Cg	501	GTP	C5'-O5'-PA-O3A
108	Cg	501	GTP	C5'-O5'-PA-O1A
108	Cg	501	GTP	C5'-O5'-PA-O2A
108	Cg	501	GTP	C3'-C4'-C5'-O5'
108	Cg	501	GTP	O4'-C4'-C5'-O5'

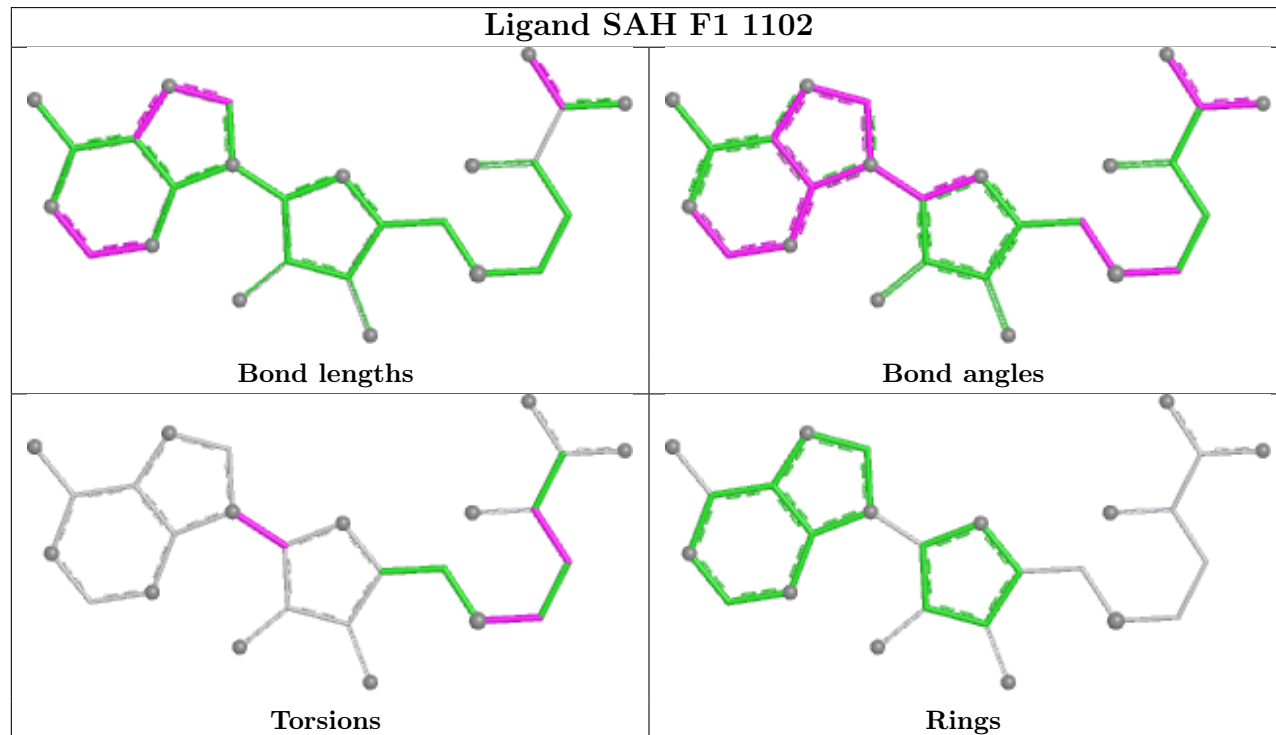
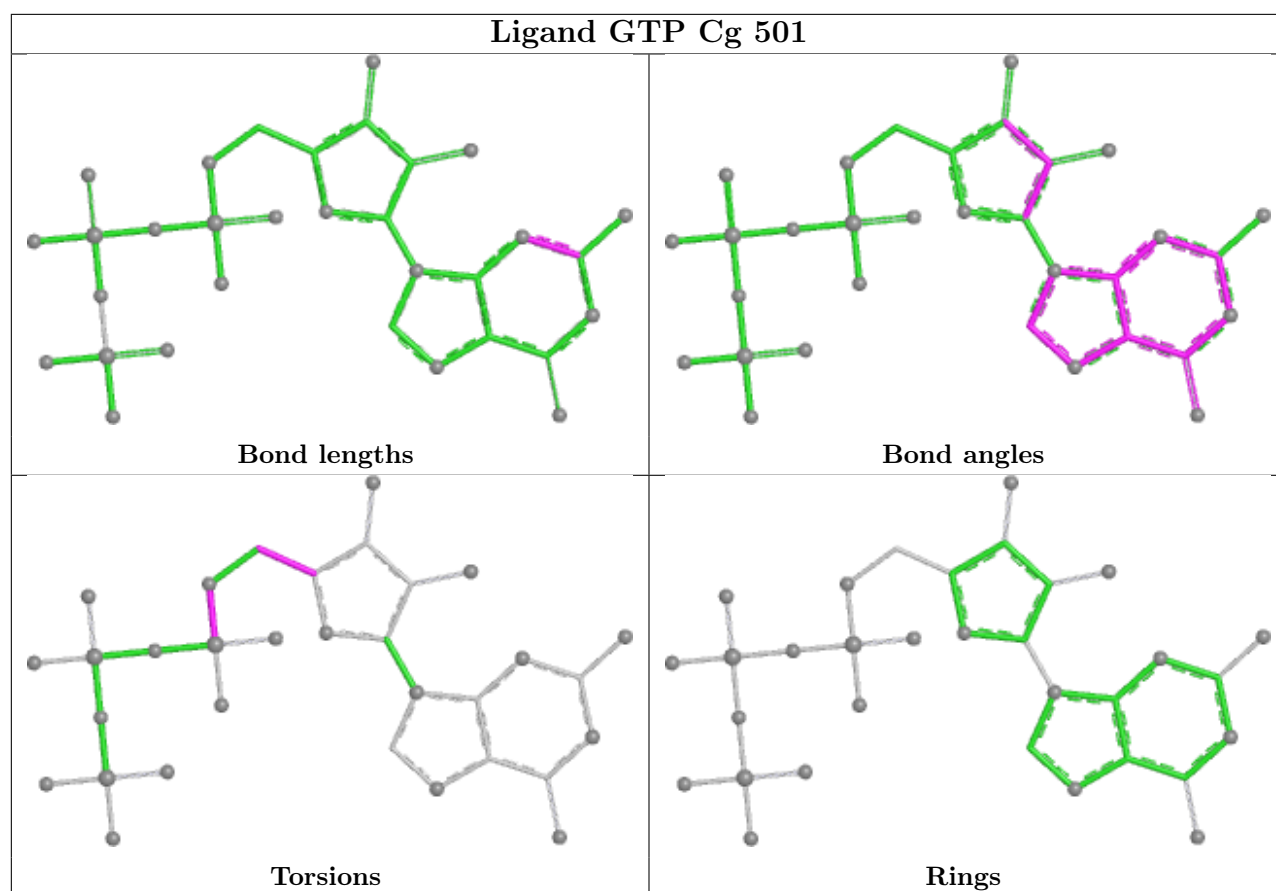
There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
105	FW	301	PO4	1	0
109	FF	501	SAH	2	0
106	Fc	201	PM8	1	0
108	Cg	501	GTP	3	0
109	F1	1102	SAH	2	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
59	UY	13
99	Uh	11
98	Ug	10
103	Ux	3
47	UB	2
60	CA	1

The worst 5 of 40 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	UY	347:UNK	C	348:UNK	N	76.88
1	UY	439:UNK	C	440:UNK	N	65.92
1	Uh	219:UNK	C	267:UNK	N	52.49
1	Uh	13:UNK	C	14:UNK	N	49.20
1	UB	10:UNK	C	101:UNK	N	45.40

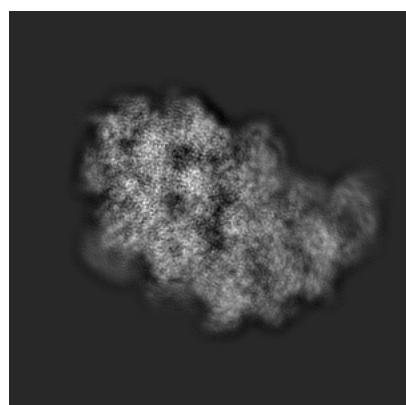
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10180. These allow visual inspection of the internal detail of the map and identification of artifacts.

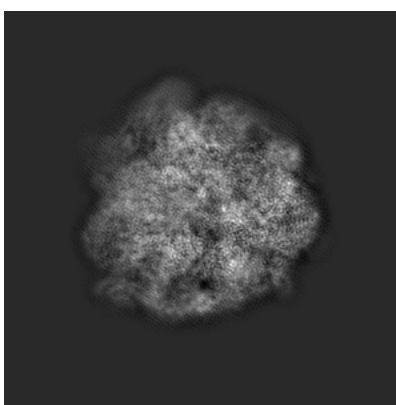
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

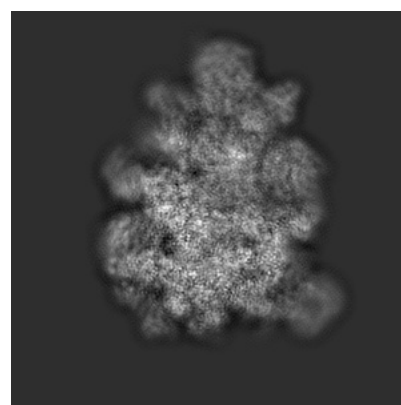
6.1.1 Primary map



X



Y

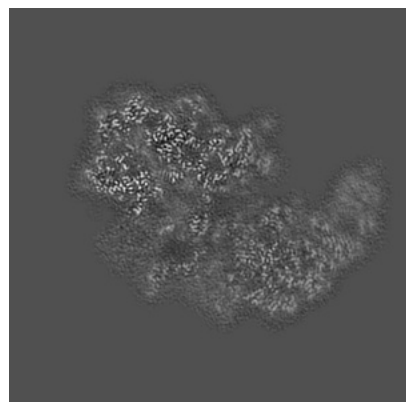


Z

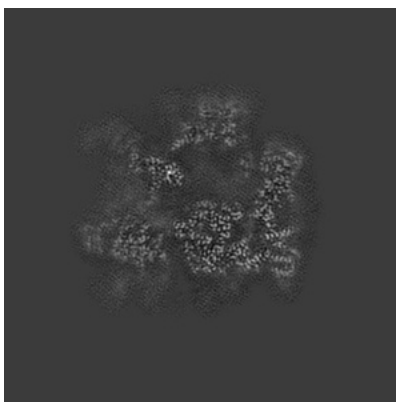
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

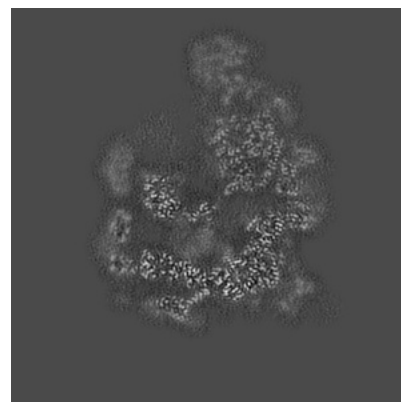
6.2.1 Primary map



X Index: 160



Y Index: 160

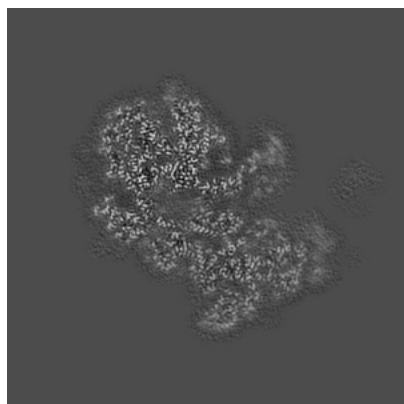


Z Index: 160

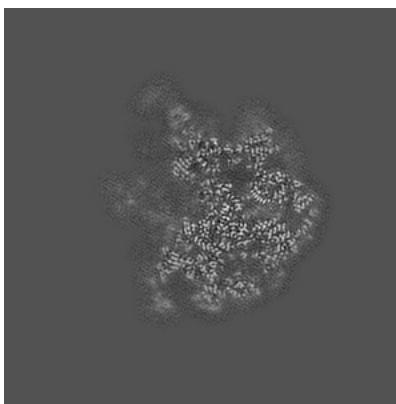
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

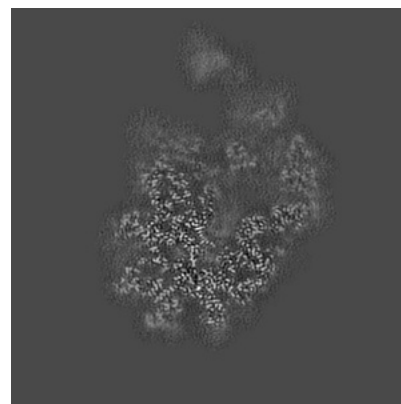
6.3.1 Primary map



X Index: 137



Y Index: 109

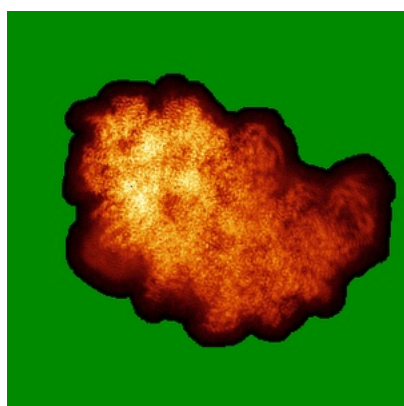


Z Index: 181

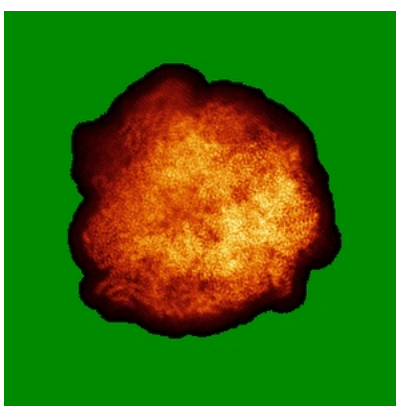
The images above show the largest variance slices of the map in three orthogonal directions.

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

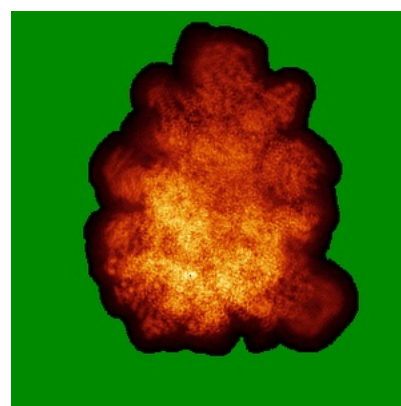
6.4.1 Primary map



X



Y

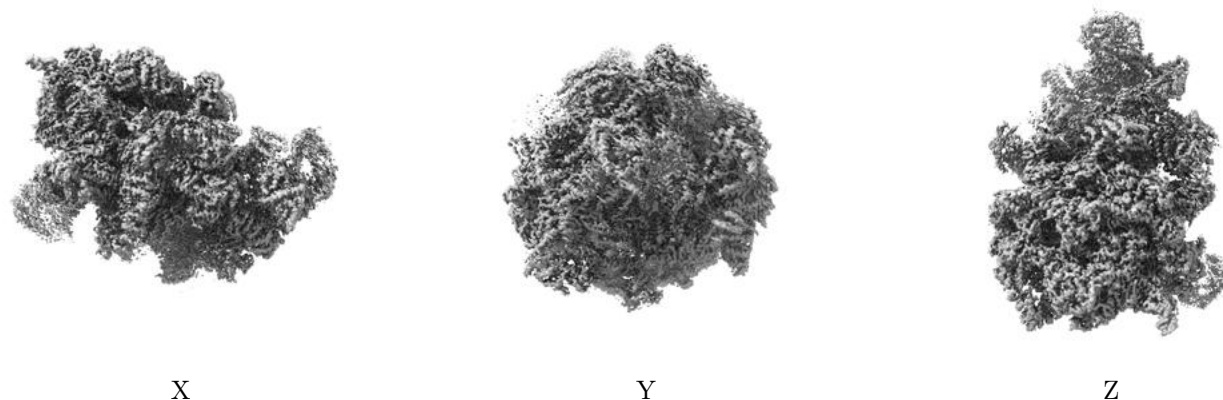


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.09. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

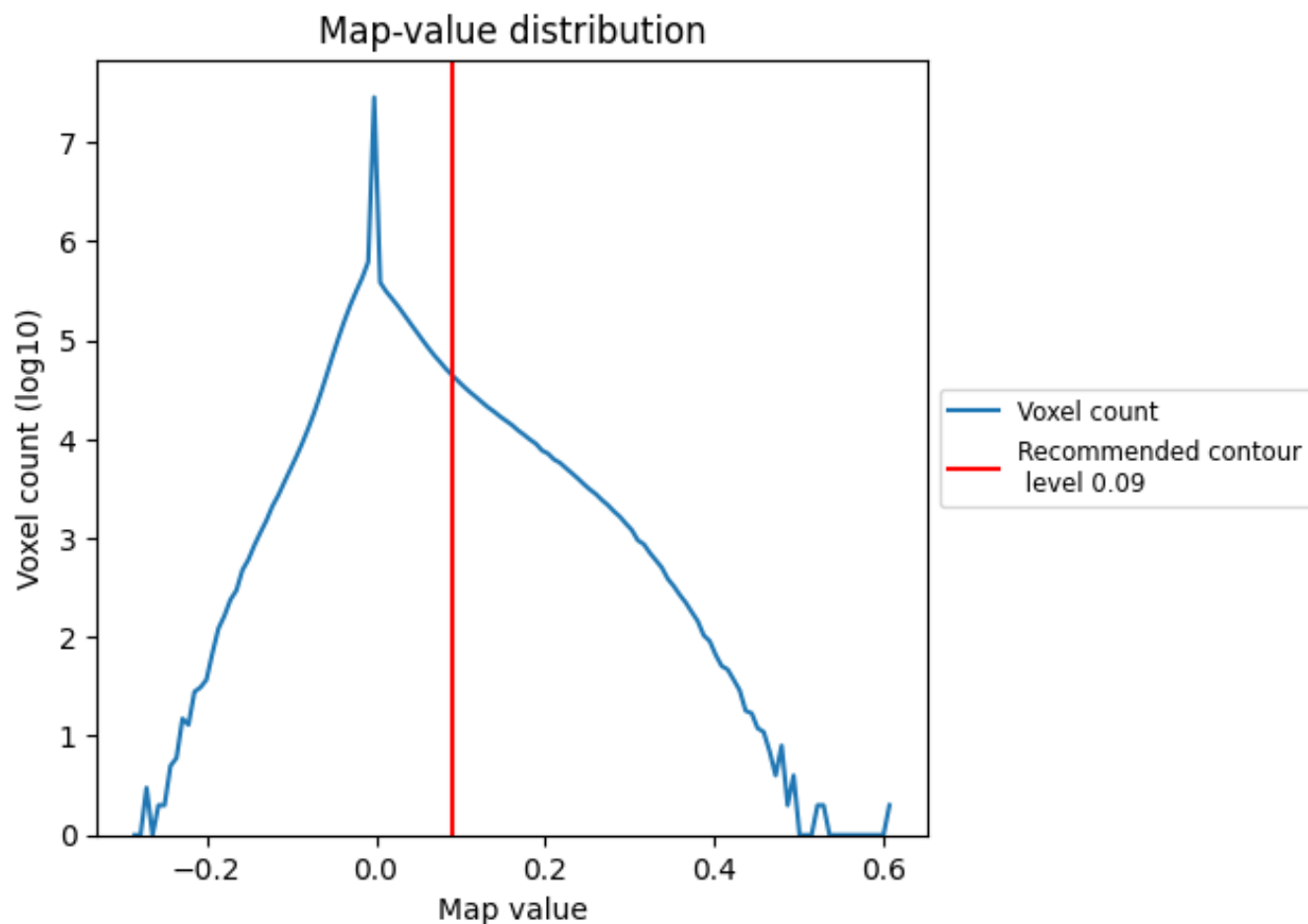
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

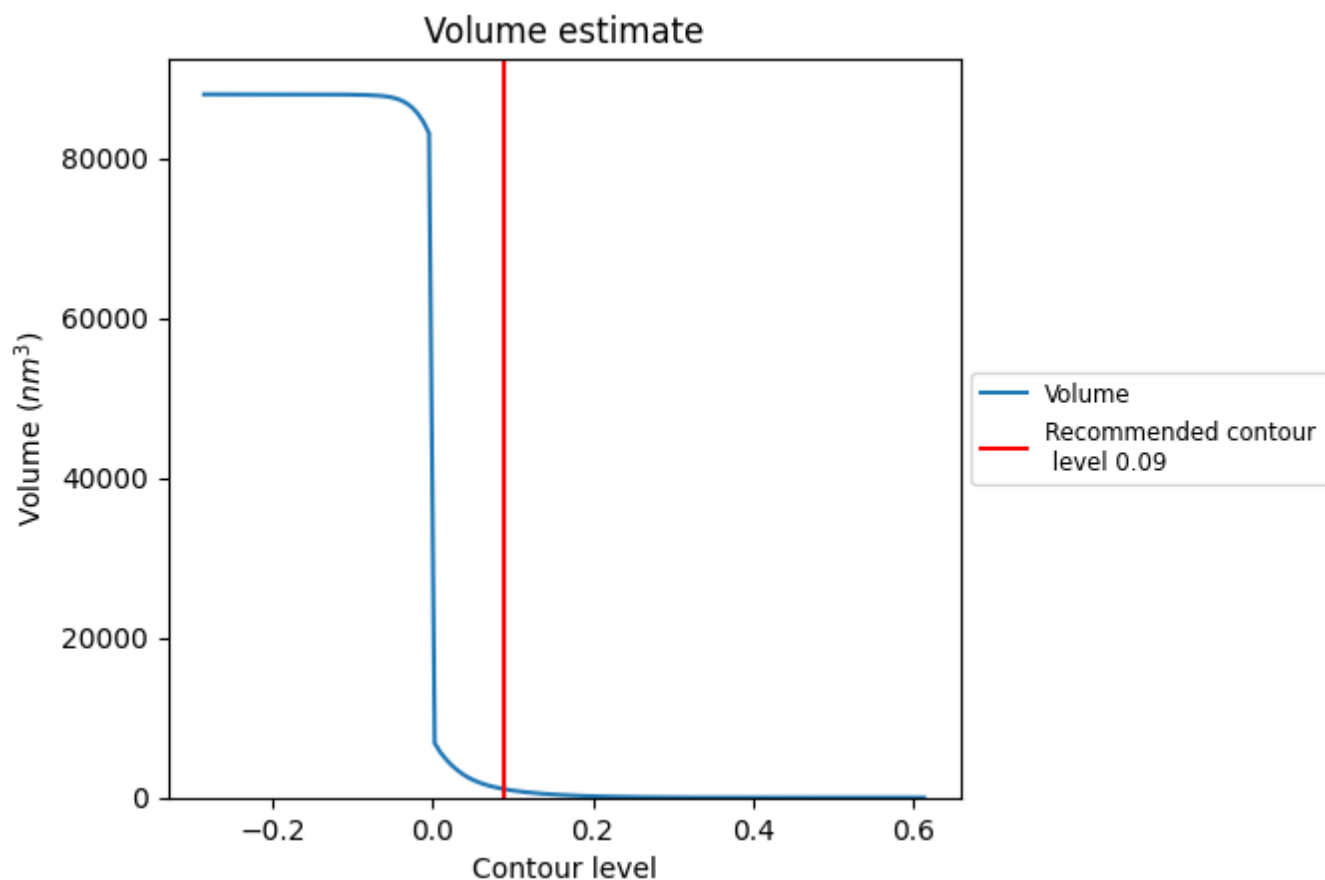
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

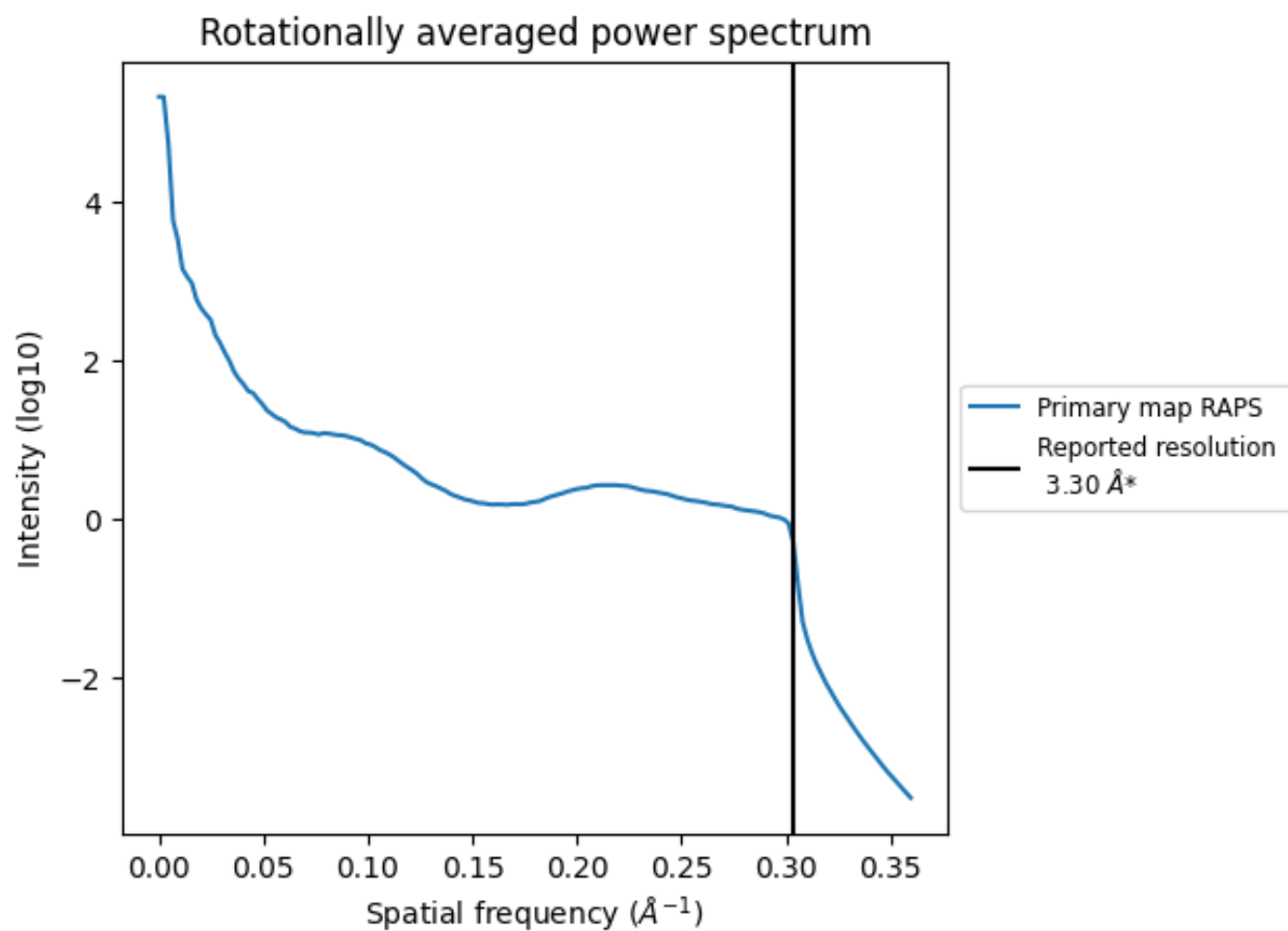
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1051 nm³; this corresponds to an approximate mass of 949 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 0.303 Å⁻¹

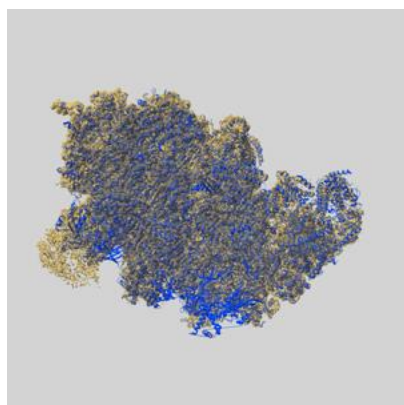
8 Fourier-Shell correlation

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

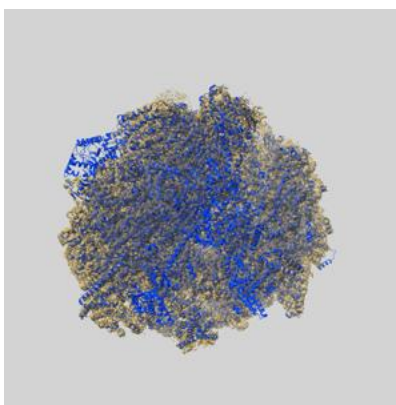
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10180 and PDB model 6SGB. Per-residue inclusion information can be found in section [3](#) on page [29](#).

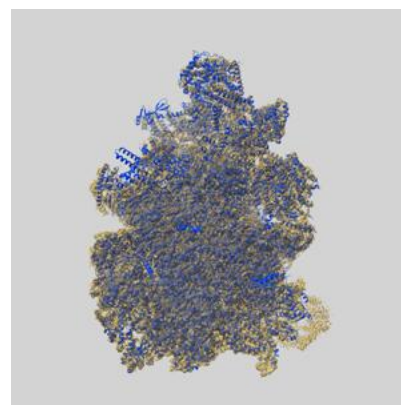
9.1 Map-model overlay [i](#)



X



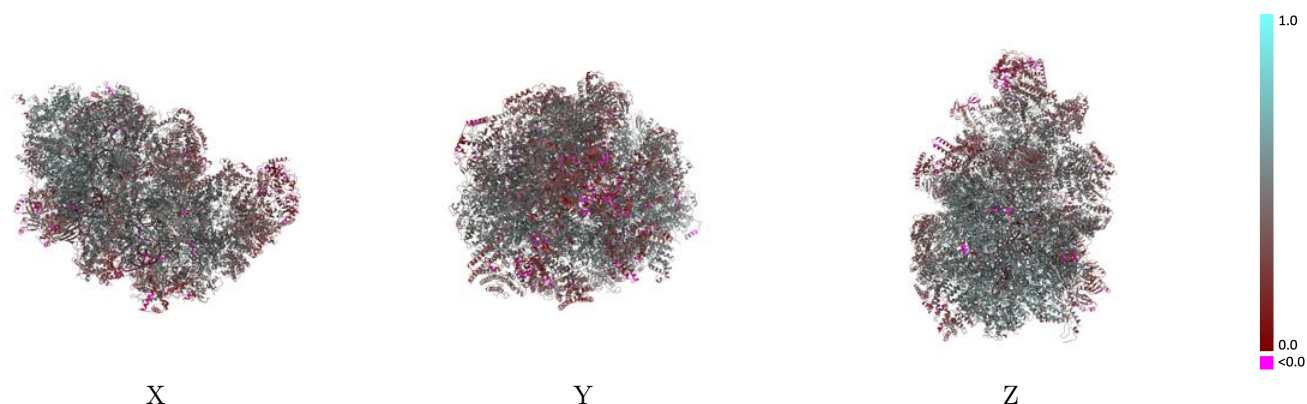
Y



Z

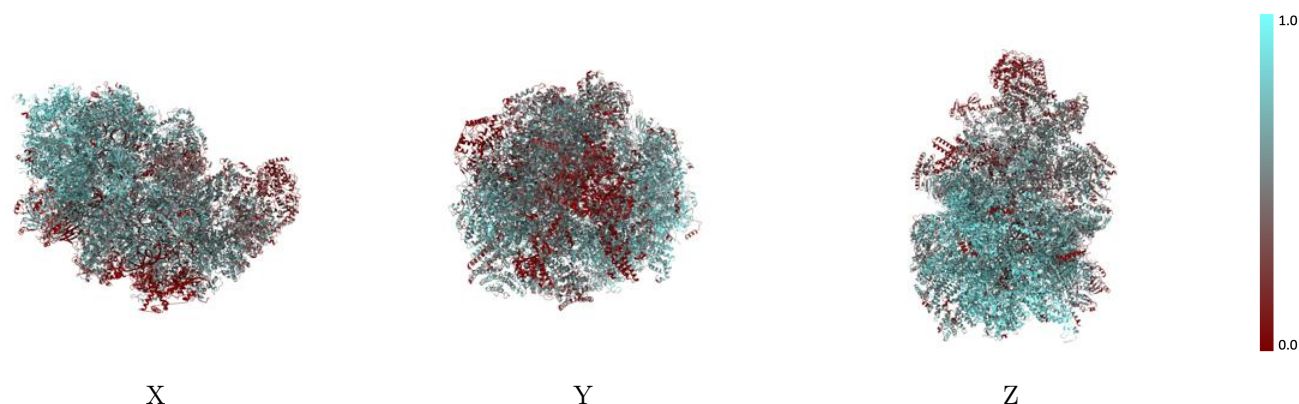
The images above show the 3D surface view of the map at the recommended contour level 0.09 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



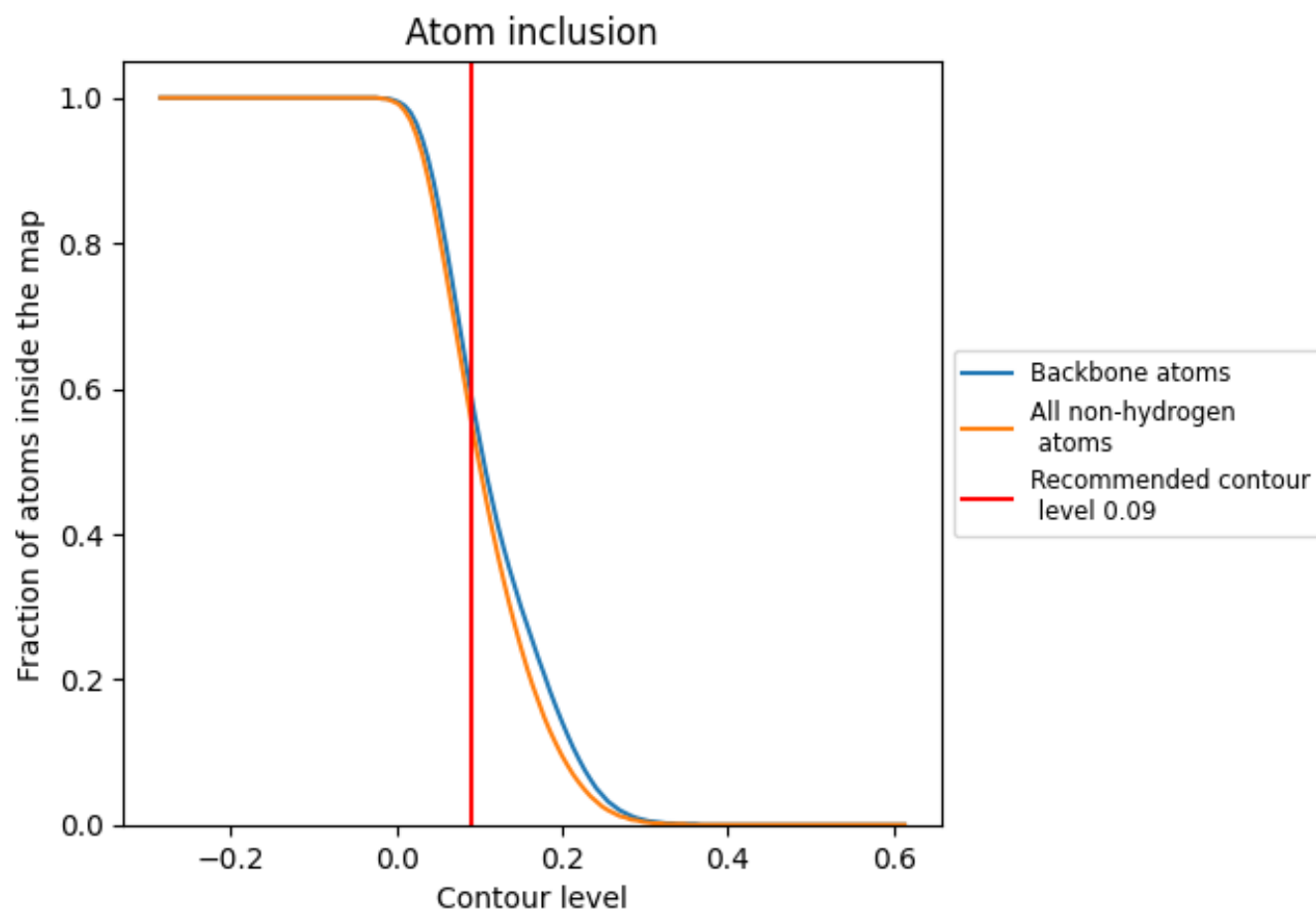
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.09).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.09) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5570	 0.4390
CA	 0.5680	 0.3950
CC	 0.4030	 0.4580
CE	 0.6660	 0.5010
CF	 0.7270	 0.5020
CH	 0.7430	 0.5320
CI	 0.6270	 0.4750
CJ	 0.5470	 0.4650
CK	 0.5810	 0.4280
CN	 0.2610	 0.4540
CO	 0.7470	 0.5240
CP	 0.7950	 0.5350
CQ	 0.7050	 0.5330
CR	 0.5780	 0.4330
CS	 0.0090	 0.3310
Ca	 0.6690	 0.4820
Cb	 0.5570	 0.4100
Cd	 0.7920	 0.5140
Cg	 0.6230	 0.4630
Ci	 0.5060	 0.4880
Cj	 0.8280	 0.5330
Ck	 0.4810	 0.3990
Cn	 0.3710	 0.4230
Cp	 0.7320	 0.5110
DB	 0.3630	 0.3750
DC	 0.3520	 0.3270
DD	 0.7860	 0.5270
DE	 0.2110	 0.2450
DF	 0.5020	 0.4460
DG	 0.5740	 0.4040
DH	 0.5160	 0.4690
DI	 0.7380	 0.4930
DJ	 0.5580	 0.4450
DK	 0.4150	 0.4110
DL	 0.6590	 0.5020



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Chain	Atom inclusion	Q-score
DO	 0.6010	 0.4040
DP	 0.8120	 0.4880
DR	 0.8120	 0.5200
DT	 0.5780	 0.4970
DU	 0.6660	 0.4940
DV	 0.5120	 0.4570
DW	 0.5020	 0.4300
DX	 0.1750	 0.3900
DY	 0.4940	 0.4530
DZ	 0.5020	 0.4430
F1	 0.5610	 0.4700
F2	 0.7170	 0.4830
F3	 0.6660	 0.4390
F4	 0.4000	 0.3780
F5	 0.3750	 0.3270
F6	 0.5400	 0.3490
F7	 0.7250	 0.4830
F8	 0.6430	 0.4750
F9	 0.6180	 0.4850
FA	 0.4950	 0.4040
FB	 0.7010	 0.5080
FC	 0.6290	 0.4310
FD	 0.5060	 0.4300
FE	 0.6910	 0.5100
FF	 0.5670	 0.4750
FG	 0.6250	 0.4950
FH	 0.5390	 0.4560
FI	 0.5050	 0.4660
FJ	 0.5850	 0.4700
FK	 0.5560	 0.4710
FL	 0.6010	 0.5180
FM	 0.6810	 0.4770
FN	 0.5260	 0.3790
FO	 0.7810	 0.5300
FP	 0.7500	 0.4830
FQ	 0.6330	 0.4440
FR	 0.5860	 0.4360
FS	 0.5320	 0.4180
FT	 0.6010	 0.4180
FU	 0.5180	 0.3810
FV	 0.5880	 0.4660
FW	 0.7340	 0.5020

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Chain	Atom inclusion	Q-score
FX	 0.7800	 0.4820
FY	 0.4670	 0.3860
FZ	 0.1280	 0.3860
Fa	 0.6370	 0.5130
Fb	 0.5360	 0.3440
Fc	 0.5160	 0.3280
Fd	 0.7300	 0.4900
Fe	 0.4810	 0.4460
UA	 0.3180	 0.2380
UB	 0.2040	 0.3200
UC	 0.7330	 0.4270
UD	 0.8520	 0.5070
UE	 0.2930	 0.2610
UF	 0.5610	 0.4540
UG	 0.7260	 0.4700
UH	 0.4000	 0.4990
UI	 0.6250	 0.4210
UJ	 0.3540	 0.3170
UK	 0.2430	 0.3550
UL	 0.5230	 0.3640
UM	 0.5740	 0.4650
UN	 0.5210	 0.3820
UO	 0.4440	 0.2880
UP	 0.2890	 0.2850
UQ	 0.4440	 0.3130
UY	 0.0030	 0.2760
Ua	 0.4430	 0.4270
Ub	 0.2540	 0.4040
Uc	 0.2780	 0.4630
Ud	 0.2820	 0.3520
Ue	 0.2760	 0.3380
Uf	 0.4810	 0.5010
Ug	 0.3720	 0.2800
Uh	 0.0200	 0.2690
Ui	 0.2290	 0.2920
Uj	 0.2980	 0.3120
Uk	 0.4010	 0.4570
Ul	 0.1790	 0.2220
Um	 0.3940	 0.4370
Ux	 0.0110	 0.2830