



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:49 AM UTC

PDB ID : 6YXX / pdb_00006yxx
EMDB ID : EMD-10999
Title : State A of the Trypanosoma brucei mitoribosomal large subunit assembly intermediate
Authors : Jaskolowski, M.; Ramrath, D.J.F.; Bieri, P.; Niemann, M.; Mattei, S.; Calderaro, S.; Leibundgut, M.A.; Horn, E.K.; Boehringer, D.; Schneider, A.; Ban, N.
Deposited on : 2020-05-04
Resolution : 3.90 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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 : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

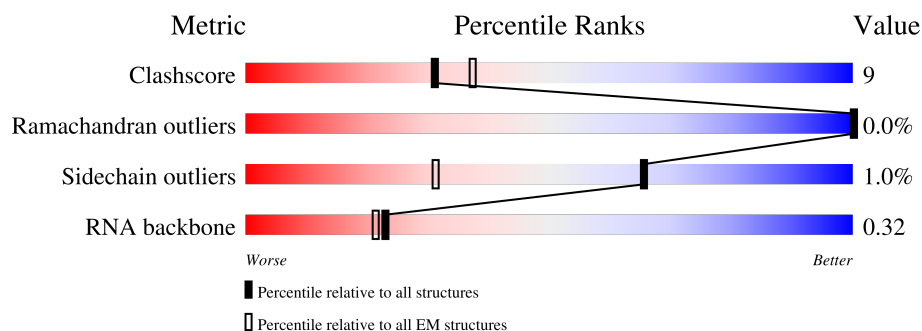
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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



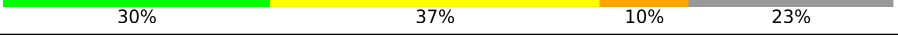
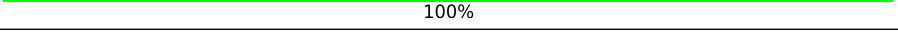
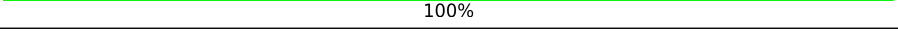
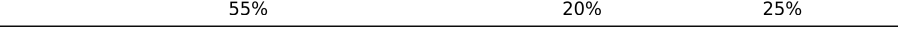
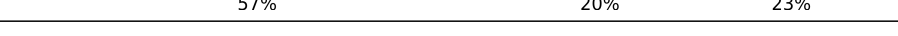
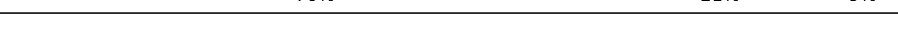
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102
RNA backbone	8273	3508

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A1	241	71% 18% 10%
2	E1	482	76% 22% .
3	A2	471	80% 18% .
4	E2	568	50% 15% 35%
5	A3	218	48% 21% 31%
6	E3	557	56% 16% 28%

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Mol	Chain	Length	Quality of chain
7	E4	439	
8	A5	80	
9	E5	376	
10	E6	531	
11	A8	181	
12	AA	1176	
13	BA	831	
14	EA	576	
15	UA	10	
15	Uf	10	
16	BB	541	
17	EB	754	
18	EC	406	
19	BD	547	
20	ED	616	
21	AE	473	
22	BE	449	
23	EE	586	
24	AF	459	
25	BF	426	
26	EF	373	
27	EG	156	
28	BH	349	
29	EH	634	
30	AI	263	

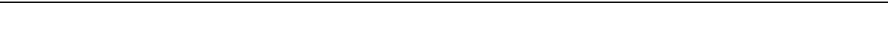
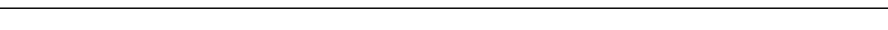
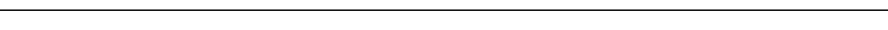
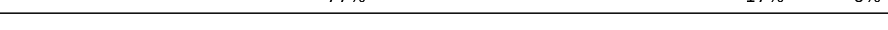
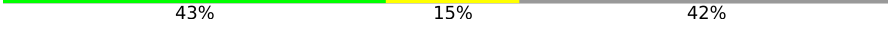
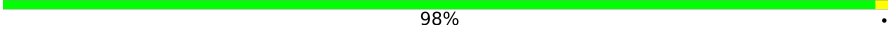
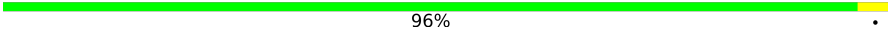
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Mol	Chain	Length	Quality of chain
31	BI	342	
32	UI	21	
32	Ur	21	
33	BJ	333	
34	AK	342	
35	BK	386	
36	UK	25	
37	BL	312	
38	EL	691	
39	EM	451	
40	UM	8	
41	AN	202	
42	BN	302	
43	EN	731	
44	BO	262	
45	EO	319	
45	EP	319	
46	AP	374	
47	BQ	231	
48	AR	301	
49	BR	205	
50	ER	148	
51	BS	198	
52	ES	524	
53	AT	144	

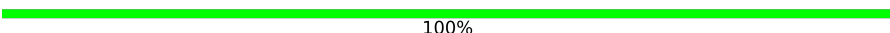
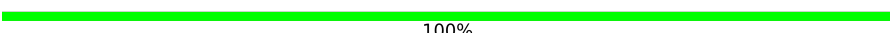
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Mol	Chain	Length	Quality of chain
54	BT	191	
55	ET	102	
56	AU	213	
57	BU	185	
58	AV	188	
59	BV	190	
60	AW	278	
61	BW	188	
62	AX	246	
63	AY	378	
64	BZ	190	
65	Ba	153	
66	Bb	162	
67	Bc	146	
68	Ae	197	
69	Af	189	
70	Bf	113	
71	Ag	260	
72	E7	97	
73	E8	786	
74	E9	343	
75	Al	218	
76	Ul	238	
77	Um	27	
78	Un	28	

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Mol	Chain	Length	Quality of chain
79	Ao	1520	 10% 88%
80	Ap	309	 68% 17% 15%
81	Up	87	 100%
82	Us	79	 100%
83	At	154	 75% 14% 10%
84	Av	242	 62% 17% 21%

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 183043 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 bL28m.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	217	Total	C	N	O	S	0	0
			1788	1138	324	317	9		

- Molecule 2 is a protein called mt-LAF21.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E1	473	Total	C	N	O	S	0	0
			3836	2376	745	703	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E1	379	SER	ALA	conflict	UNP Q57WG6

- Molecule 3 is a protein called uL29m.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A2	463	Total	C	N	O	S	0	0
			3739	2381	651	694	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A2	238	GLY	ALA	conflict	UNP Q38EM7

- Molecule 4 is a protein called DUF4379 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E2	369	Total	C	N	O	S	0	0
			2933	1839	550	517	27		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E2	167	THR	LYS	conflict	UNP C9ZTN9

- Molecule 5 is a protein called uL30m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A3	150	Total	C	N	O	S	0	0
			1226	781	236	203	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A3	198	UNK	ALA	conflict	UNP C9ZY77

- Molecule 6 is a protein called mt-LAF23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E3	403	Total	C	N	O	S	0	0
			3266	2062	590	591	23		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E3	1	MET	-	initiating methionine	UNP D0A795

- Molecule 7 is a protein called mt-LAF24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E4	434	Total	C	N	O	S	0	0
			3418	2159	623	622	14		

- Molecule 8 is a protein called bL32m.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A5	55	Total	C	N	O	S	0	0
			483	311	90	76	6		

- Molecule 9 is a protein called mt-LAF25.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E5	327	Total	C	N	O		0	0
			1635	981	327	327			

- Molecule 10 is a protein called KRIPP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	E6	434	Total	C	N	O	S	0	0
			3405	2143	608	635	19		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E6	360	SER	ALA	conflict	UNP Q4GZA2

- Molecule 11 is a protein called bL35m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A8	133	Total	C	N	O	S	0	0
			1136	712	233	184	7		

- Molecule 12 is a RNA chain called 12S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AA	904	Total	C	N	O	P	0	0
			18187	8161	2902	6220	904		

- Molecule 13 is a protein called mL67.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	BA	769	Total	C	N	O	S	0	0
			6059	3847	1074	1104	34		

- Molecule 14 is a protein called mt-EngA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	EA	532	Total	C	N	O	S	0	0
			4263	2672	785	785	21		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EA	12	UNK	ARG	conflict	UNP Q57TZ4

- Molecule 15 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	UA	10	Total	C	N	O	0	0
			50	30	10	10		
15	Uf	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 16 is a protein called mL68.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	BB	407	Total	C	N	O	S	0	0
			3322	2114	589	599	20		

- Molecule 17 is a protein called DEAD-box helicase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	EB	627	Total	C	N	O	S	0	0
			5039	3181	957	875	26		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EB	301	ALA	THR	conflict	UNP D0A9G9

- Molecule 18 is a protein called Pseudouridylate synthase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	EC	373	Total	C	N	O	S	0	0
			3005	1923	540	524	18		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EC	25	UNK	HIS	conflict	UNP Q38FJ3

- Molecule 19 is a protein called mL70.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	BD	419	Total	C	N	O	S	0	0
			3349	2134	586	609	20		

- Molecule 20 is a protein called mt-LAF4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	ED	598	Total	C	N	O	S	0	0
			4764	3026	850	865	23		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
ED	252	ARG	LYS	conflict	UNP Q385G9

- Molecule 21 is a protein called Ribosomal protein L3 mitochondrial, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AE	344	Total	C	N	O	S	0	0
			2802	1804	474	509	15		

- Molecule 22 is a protein called mL71.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BE	357	Total	C	N	O	S	0	0
			2822	1801	477	535	9		

- Molecule 23 is a protein called SpoU_methylase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	EE	431	Total	C	N	O	S	0	0
			3423	2132	646	632	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	337	ASP	GLY	conflict	UNP C9ZZ65

- Molecule 24 is a protein called Ribosomal protein L4/L1 family, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AF	419	Total	C	N	O	S	0	0
			3414	2181	584	626	23		

- Molecule 25 is a protein called Tetratricopeptide repeat.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BF	346	Total	C	N	O	S	0	0
			2847	1803	519	512	13		

- Molecule 26 is a protein called SpoU_methylase domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	EF	297	Total	C	N	O	S	0	0
			2268	1439	401	420	8		

- Molecule 27 is a protein called mt-LAF7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	EG	154	Total	C	N	O	S	0	0
			1295	812	256	218	9		

- Molecule 28 is a protein called mL74.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BH	236	Total	C	N	O	S	0	0
			1948	1250	346	349	3		

- Molecule 29 is a protein called mt-LAF8.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	EH	443	Total	C	N	O	S	0	0
			3508	2214	635	640	19		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EH	166	UNK	GLY	conflict	UNP A0A1G4IEQ9
EH	495	ARG	LYS	conflict	UNP A0A1G4IEQ9

- Molecule 30 is a protein called RIBOSOMAL_L9 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AI	240	Total	C	N	O	S	0	0
			1967	1260	345	353	9		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	249	UNK	LYS	conflict	UNP Q57UC5
AI	250	UNK	GLY	conflict	UNP Q57UC5
AI	251	UNK	PRO	conflict	UNP Q57UC5
AI	252	UNK	VAL	conflict	UNP Q57UC5

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Chain	Residue	Modelled	Actual	Comment	Reference
AI	253	UNK	LYS	conflict	UNP Q57UC5
AI	254	UNK	GLN	conflict	UNP Q57UC5
AI	255	UNK	ARG	conflict	UNP Q57UC5
AI	256	UNK	LYS	conflict	UNP Q57UC5
AI	257	UNK	ALA	conflict	UNP Q57UC5
AI	258	UNK	ARG	conflict	UNP Q57UC5

- Molecule 31 is a protein called mL75.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BI	303	Total	C	N	O	S	0	0
			2475	1580	447	433	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	227	ASN	ASP	conflict	UNP D0A108

- Molecule 32 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	UI	21	Total	C	N	O	0	0
			105	63	21	21		
32	Ur	21	Total	C	N	O	0	0
			105	63	21	21		

- Molecule 33 is a protein called mL76.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BJ	234	Total	C	N	O	S	0	0
			1944	1215	365	356	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BJ	329	GLU	ALA	conflict	UNP Q383M2

- Molecule 34 is a protein called Ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AK	248	Total	C	N	O	S	0	0
			2088	1335	385	356	12		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AK	327	UNK	ALA	conflict	UNP Q586R9

- Molecule 35 is a protein called Chaperone protein DNAj, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BK	228	Total	C	N	O	S	0	0
			1855	1153	353	341	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BK	33	UNK	HIS	conflict	UNP C9ZQR6
BK	60	UNK	PRO	conflict	UNP C9ZQR6
BK	348	VAL	LEU	conflict	UNP C9ZQR6

- Molecule 36 is a protein called UNK.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	UK	25	Total	C	N	O		0	0
			125	75	25	25			

- Molecule 37 is a protein called mL78.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BL	258	Total	C	N	O	S	0	0
			2014	1236	395	373	10		

- Molecule 38 is a protein called mt-LAF12.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	EL	532	Total	C	N	O	S	0	0
			4259	2732	744	754	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EL	104	UNK	ILE	conflict	UNP C9ZVC0
EL	108	GLU	GLY	conflict	UNP C9ZVC0
EL	126	VAL	LEU	conflict	UNP C9ZVC0
EL	188	SER	PHE	conflict	UNP C9ZVC0

- Molecule 39 is a protein called GTP-binding protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	EM	308	Total	C	N	O	S	0	0
			2432	1542	438	437	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EM	407	UNK	PRO	conflict	UNP Q38E75

- Molecule 40 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	UM	8	Total	C	N	O	0	0
			40	24	8	8		

- Molecule 41 is a protein called 50S ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AN	193	Total	C	N	O	S	0	0
			1639	1059	301	269	10		

- Molecule 42 is a protein called mL80.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BN	154	Total	C	N	O	S	0	0
			1320	839	239	237	5		

- Molecule 43 is a protein called mt-LAF14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	EN	638	Total	C	N	O	S	0	0
			5025	3152	909	936	28		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EN	18	GLU	GLY	conflict	UNP C9ZPS0
EN	310	LYS	ASN	conflict	UNP C9ZPS0
EN	676	CYS	TYR	conflict	UNP C9ZPS0

- Molecule 44 is a protein called mL81.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BO	192	Total	C	N	O	S	0	0
			1498	936	268	281	13		

- Molecule 45 is a protein called mt-LAF15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	EO	272	Total	C	N	O	S	0	0
			2126	1340	393	383	10		
45	EP	243	Total	C	N	O	S	0	0
			1911	1208	347	347	9		

- Molecule 46 is a protein called Ribosomal_L18e/L15P domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	AP	320	Total	C	N	O	S	0	0
			2615	1667	478	457	13		

- Molecule 47 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BQ	218	Total	C	N	O	S	0	0
			1651	1049	288	306	8		

- Molecule 48 is a protein called 50S ribosomal protein L17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	AR	267	Total	C	N	O	S	0	0
			2214	1399	403	399	13		

- Molecule 49 is a protein called mL84.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BR	196	Total	C	N	O	S	0	0
			1659	1064	299	287	9		

- Molecule 50 is a protein called Acyl carrier protein.

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

- Molecule 51 is a protein called mL85.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BS	161	Total	C	N	O	S	0	0
			1120	694	206	214	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BS	45	ILE	VAL	conflict	UNP Q38FG8
BS	173	UNK	LEU	conflict	UNP Q38FG8

- Molecule 52 is a protein called Lipase (Class 3).

Mol	Chain	Residues	Atoms					AltConf	Trace
52	ES	152	Total	C	N	O	S	0	0
			1259	779	246	230	4		

- Molecule 53 is a protein called bL19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	AT	143	Total	C	N	O	S	0	0
			1180	743	224	206	7		

- Molecule 54 is a protein called mL86.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BT	173	Total	C	N	O	S	0	0
			1435	884	278	267	6		

- Molecule 55 is a protein called mt-LAF19.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	ET	101	Total	C	N	O	S	0	0
			839	529	166	140	4		

- Molecule 56 is a protein called bL20m.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	AU	175	Total	C	N	O	S	0	0
			1423	895	280	243	5		

- Molecule 57 is a protein called mL87.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BU	150	Total	C	N	O	S	0	0
			1275	806	248	215	6		

- Molecule 58 is a protein called bL21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	AV	181	Total	C	N	O	S	0	0
			1424	909	257	252	6		

- Molecule 59 is a protein called mL88.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BV	90	Total	C	N	O	S	0	0
			763	492	133	136	2		

- Molecule 60 is a protein called uL22m.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	AW	278	Total	C	N	O	S	0	0
			2251	1427	417	393	14		

- Molecule 61 is a protein called mL89.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BW	188	Total	C	N	O	S	0	0
			1565	992	299	265	9		

- Molecule 62 is a protein called uL23m.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	AX	164	Total	C	N	O	S	0	0
			1387	896	244	242	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AX	126	TYR	HIS	conflict	UNP Q387G3

- Molecule 63 is a protein called uL24m.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	AY	340	Total	C	N	O	S	0	0
			2790	1741	497	537	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AY	345	GLU	VAL	conflict	UNP C9ZK52

- Molecule 64 is a protein called Peptidyl-prolyl cis-trans isomerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BZ	188	Total	C	N	O	S	0	0
			1396	883	241	266	6		

- Molecule 65 is a protein called mL93.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ba	153	Total	C	N	O	S	0	0
			1287	820	237	223	7		

- Molecule 66 is a protein called mL94.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bb	133	Total	C	N	O	S	0	0
			1048	661	196	188	3		

- Molecule 67 is a protein called mL95.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Bc	137	Total	C	N	O	S	0	0
			1194	776	216	201	1		

- Molecule 68 is a protein called mL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Ae	127	Total	C	N	O	S	0	0
			1031	667	190	169	5		

- Molecule 69 is a protein called mL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Af	139	Total	C	N	O	S	0	0
			1107	692	210	200	5		

- Molecule 70 is a protein called mL98.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Bf	87	Total	C	N	O	S	0	0
			725	462	131	132			

- Molecule 71 is a protein called L51_S25_CI-B8 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ag	186	Total	C	N	O	S	0	0
			1564	979	295	283	7		

- Molecule 72 is a protein called mt-LAF27.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	E7	97	Total	C	N	O	S	0	0
			815	501	175	135	4		

- Molecule 73 is a protein called KRIPP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	E8	154	Total	C	N	O	S	0	0
			1181	735	228	218			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E8	208	LYS	GLU	conflict	UNP Q57YZ6
E8	250	GLN	ARG	conflict	UNP Q57YZ6
E8	345	ILE	MET	conflict	UNP Q57YZ6
E8	630	UNK	LEU	conflict	UNP Q57YZ6

- Molecule 74 is a protein called mt-LAF29.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	E9	200	Total	C	N	O	S	0	0
			1642	1022	326	285	9		

- Molecule 75 is a protein called mL49.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Al	181	Total	C	N	O	S	0	0
			1440	936	250	247	7		

- Molecule 76 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	U1	238	Total	C	N	O	0	0
			1190	714	238	238		

- Molecule 77 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	Um	27	Total	C	N	O	0	0
			135	81	27	27		

- Molecule 78 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
78	Un	28	Total	C	N	O	0	0
			140	84	28	28		

- Molecule 79 is a protein called mL52.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ao	184	Total	C	N	O	S	0	0
			1443	903	263	270	7		

- Molecule 80 is a protein called mL53.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Ap	263	Total	C	N	O	S	0	0
			2161	1402	374	373	12		

- Molecule 81 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Up	87	Total	C	N	O	0	0
			435	261	87	87		

- Molecule 82 is a protein called UNK.

Mol	Chain	Residues	Atoms				AltConf	Trace
82	Us	79	Total	C	N	O	0	0
			395	237	79	79		

- Molecule 83 is a protein called mL63.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	At	138	Total	C	N	O	S	0	0
			1149	722	223	200	4		

- Molecule 84 is a protein called mL64.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Av	192	Total	C	N	O	S	0	0
			1633	1038	304	279	12		

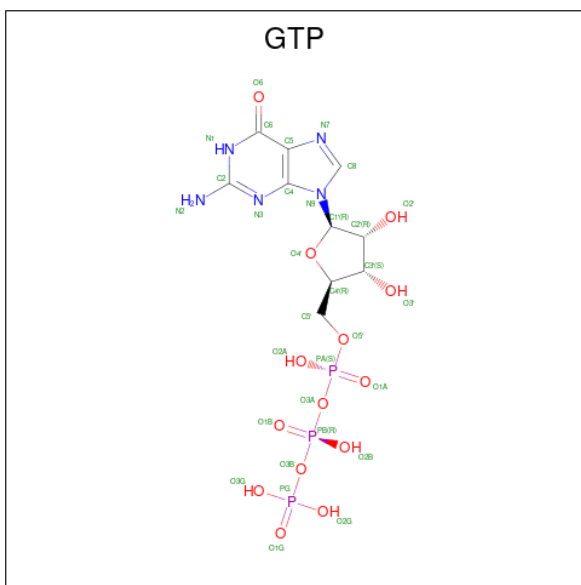
- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	E2	4	Total	Zn	0
			4	4	
85	A5	1	Total	Zn	0
			1	1	
85	EG	1	Total	Zn	0
			1	1	
85	E9	1	Total	Zn	0
			1	1	

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	A8	2	Total	Mg	0
			2	2	
86	AA	12	Total	Mg	0
			12	12	
86	EA	2	Total	Mg	0
			2	2	
86	EB	1	Total	Mg	0
			1	1	

- Molecule 87 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

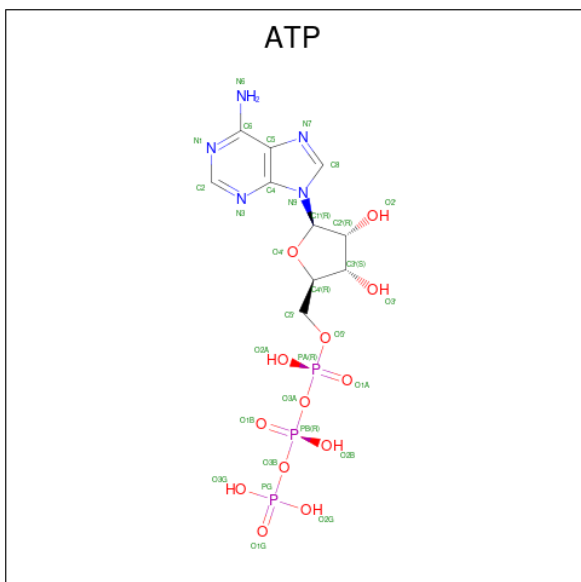


Mol	Chain	Residues	Atoms					AltConf
87	EA	1	Total 32	C 10	N 5	O 14	P 3	0
87	EA	1	Total 32	C 10	N 5	O 14	P 3	0

- Molecule 88 is SODIUM ION (CCD ID: NA) (formula: Na).

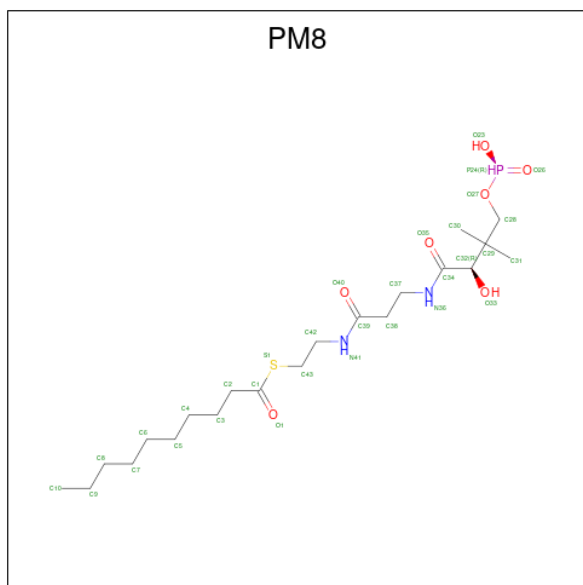
Mol	Chain	Residues	Atoms		AltConf
88	EA	2	Total 2	Na 2	0

- Molecule 89 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



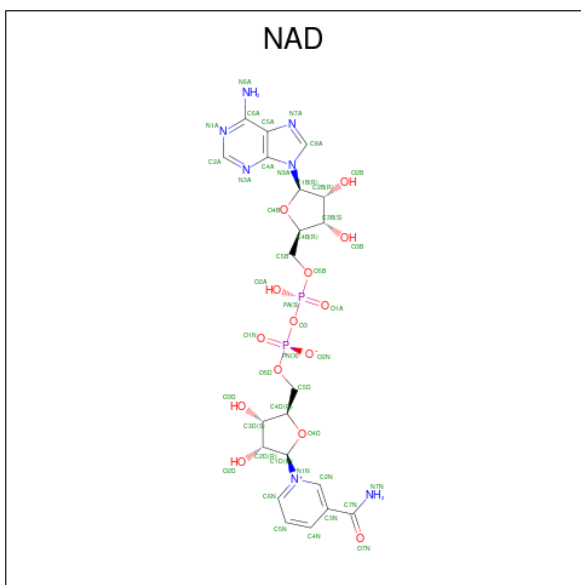
Mol	Chain	Residues	Atoms					AltConf
89	EB	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 90 is S-(2-{[N-(2-HYDROXY-4-{[HYDROXY(OXIDO)PHOSPHINO]OXY}-3,3-DIMETHYLBUTANOYL)-BETA-ALANYL]AMINO}ETHYL) DECANETHIOATE (CCD ID: PM8) (formula: $C_{21}H_{41}N_2O_7PS$).



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

- Molecule 91 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					AltConf
91	Av	1	Total 44	C 21	N 7	O 14	P 2	0

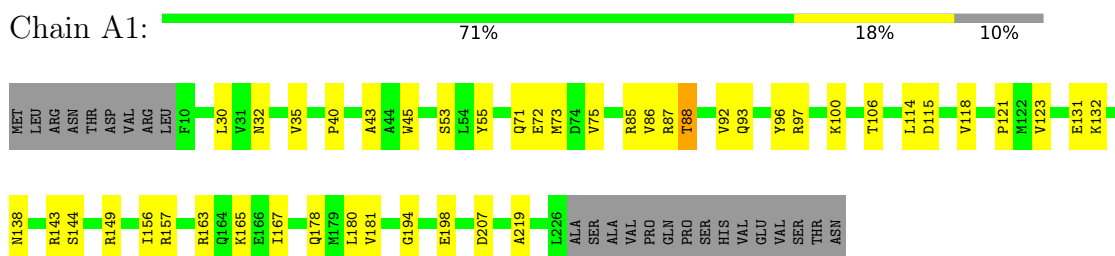
- Molecule 92 is water.

Mol	Chain	Residues	Atoms	AltConf
92	EA	4	Total O 4 4	0
92	EB	4	Total O 4 4	0

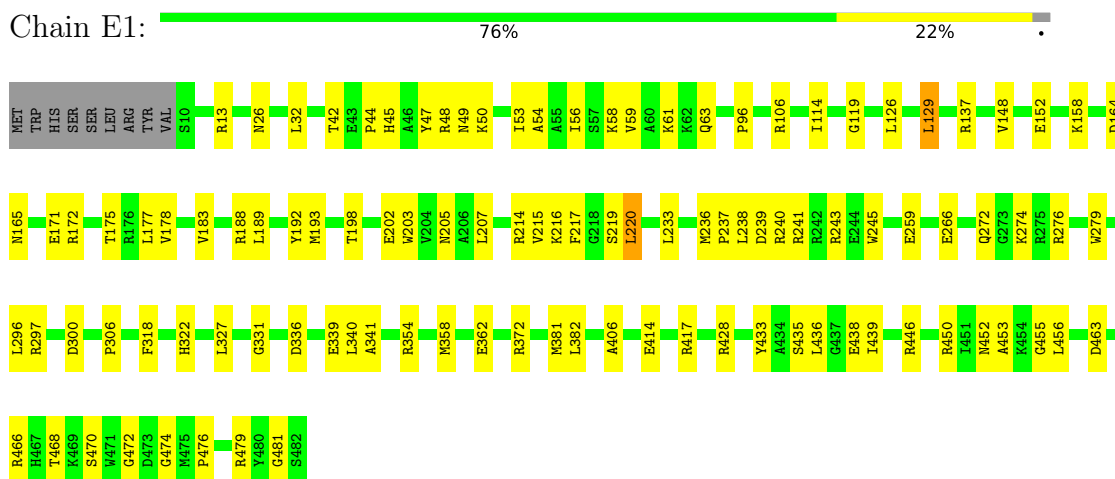
3 Residue-property plots

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. 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. 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.

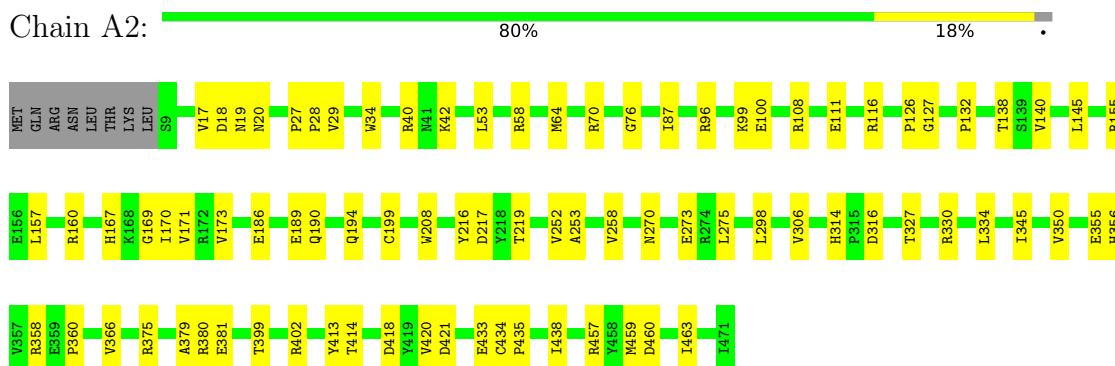
- Molecule 1: bL28m



- Molecule 2: mt-LAF21



- Molecule 3: uL29m



[illegible]

Chain A3: 48% 21% 31%

The sequence logo for Chain A3 displays the conservation of amino acids across 200 positions. The y-axis represents the information content in bits, ranging from 0.00 to 1.50. The x-axis shows positions 1 to 200. A color scale at the top indicates conservation levels: 48% (green), 21% (yellow), and 31% (grey). The logo shows that positions 1-100 are highly conserved (green/yellow), while positions 101-200 are less conserved (grey). Specific amino acids like MET, THR, SER, and GLN are highly conserved in the first 100 positions, while positions 101-200 show more variability with many positions having low information content.

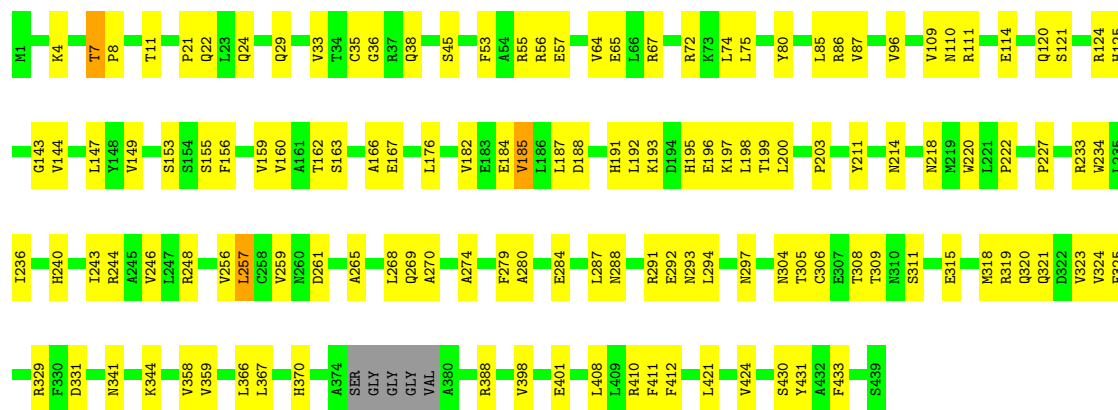
Position	Amino Acid	Information Content (bits)
1	MET	1.45
2	MET	1.45
3	ARG	1.45
4	ARG	1.45
5	MET	1.45
6	ARG	1.45
7	THR	1.45
8	THR	1.45
9	VAL	1.45
10	VAL	1.45
11	THR	1.45
12	THR	1.45
13	SER	1.45
14	SER	1.45
15	THR	1.45
16	THR	1.45
17	THR	1.45
18	THR	1.45
19	THR	1.45
20	THR	1.45
21	THR	1.45
22	THR	1.45
23	THR	1.45
24	THR	1.45
25	THR	1.45
26	THR	1.45
27	THR	1.45
28	THR	1.45
29	THR	1.45
30	THR	1.45
31	THR	1.45
32	THR	1.45
33	THR	1.45
34	THR	1.45
35	THR	1.45
36	THR	1.45
37	THR	1.45
38	THR	1.45
39	THR	1.45
40	THR	1.45
41	THR	1.45
42	THR	1.45
43	THR	1.45
44	THR	1.45
45	THR	1.45
46	THR	1.45
47	THR	1.45
48	THR	1.45
49	THR	1.45
50	THR	1.45
51	THR	1.45
52	THR	1.45
53	THR	1.45
54	THR	1.45
55	THR	1.45
56	THR	1.45
57	THR	1.45
58	THR	1.45
59	THR	1.45
60	THR	1.45
61	THR	1.45
62	THR	1.45
63	THR	1.45
64	THR	1.45
65	THR	1.45
66	THR	1.45
67	THR	1.45
68	THR	1.45
69	THR	1.45
70	THR	1.45
71	THR	1.45
72	THR	1.45
73	THR	1.45
74	THR	1.45
75	THR	1.45
76	THR	1.45
77	THR	1.45
78	THR	1.45
79	THR	1.45
80	THR	1.45
81	THR	1.45
82	THR	1.45
83	THR	1.45
84	THR	1.45
85	THR	1.45
86	THR	1.45
87	THR	1.45
88	THR	1.45
89	THR	1.45
90	THR	1.45
91	THR	1.45
92	THR	1.45
93	THR	1.45
94	THR	1.45
95	THR	1.45
96	THR	1.45
97	THR	1.45
98	THR	1.45
99	THR	1.45
100	THR	1.45
101	THR	1.45
102	THR	1.45
103	THR	1.45
104	THR	1.45
105	THR	1.45
106	THR	1.45
107	THR	1.45
108	THR	1.45
109	THR	1.45
110	THR	1.45
111	THR	1.45
112	THR	1.45
113	THR	1.45
114	THR	1.45
115	THR	1.45
116	THR	1.45
117	THR	1.45
118	THR	1.45
119	THR	1.45
120	THR	1.45
121	THR	1.45
122	THR	1.45
123	THR	1.45
124	THR	1.45
125	THR	1.45
126	THR	1.45
127	THR	1.45
128	THR	1.45
129	THR	1.45
130	THR	1.45
131	THR	1.45
132	THR	1.45
133	THR	1.45
134	THR	1.45
135	THR	1.45
136	THR	1.45
137	THR	1.45
138	THR	1.45
139	THR	1.45
140	THR	1.45

[illegible]



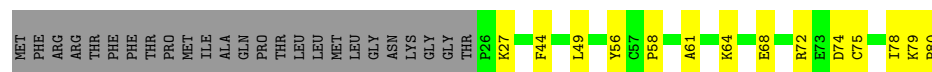
• Molecule 7: mt-LAF24

Chain E4: 69% 30% ..



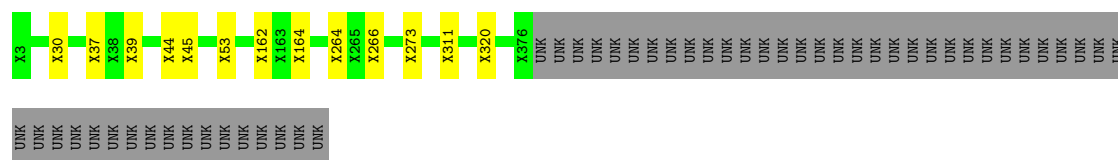
• Molecule 8: bL32m

Chain A5: 51% 18% 31%



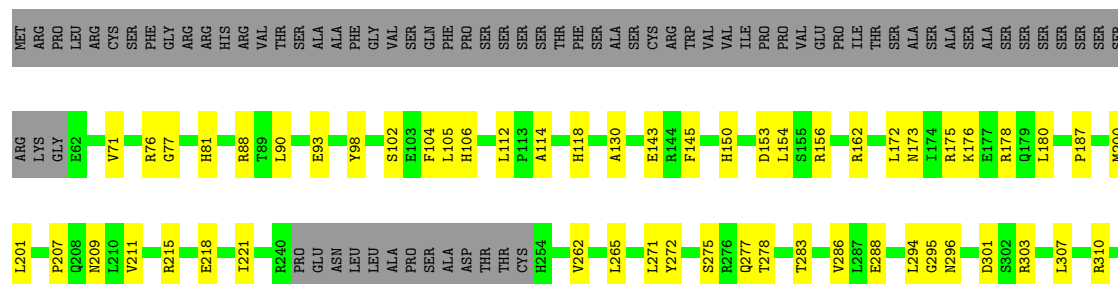
• Molecule 9: mt-LAF25

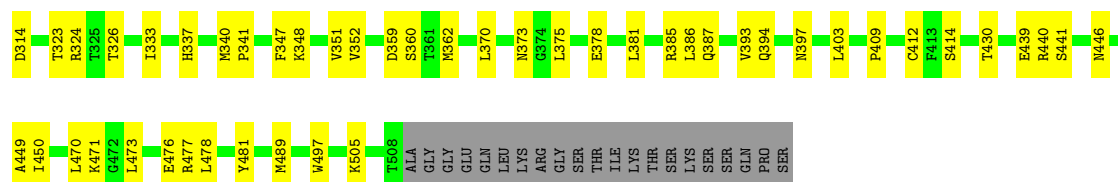
Chain E5: 84% 13%



• Molecule 10: KRIPP3

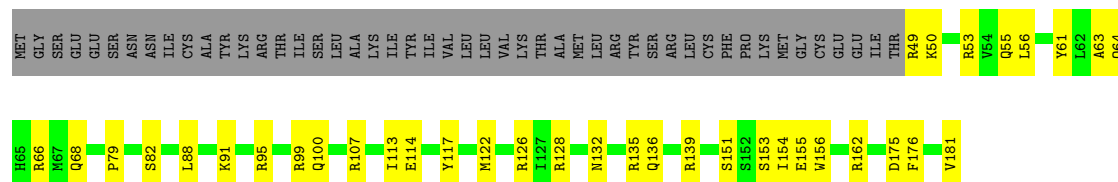
Chain E6: 63% 19% 18%





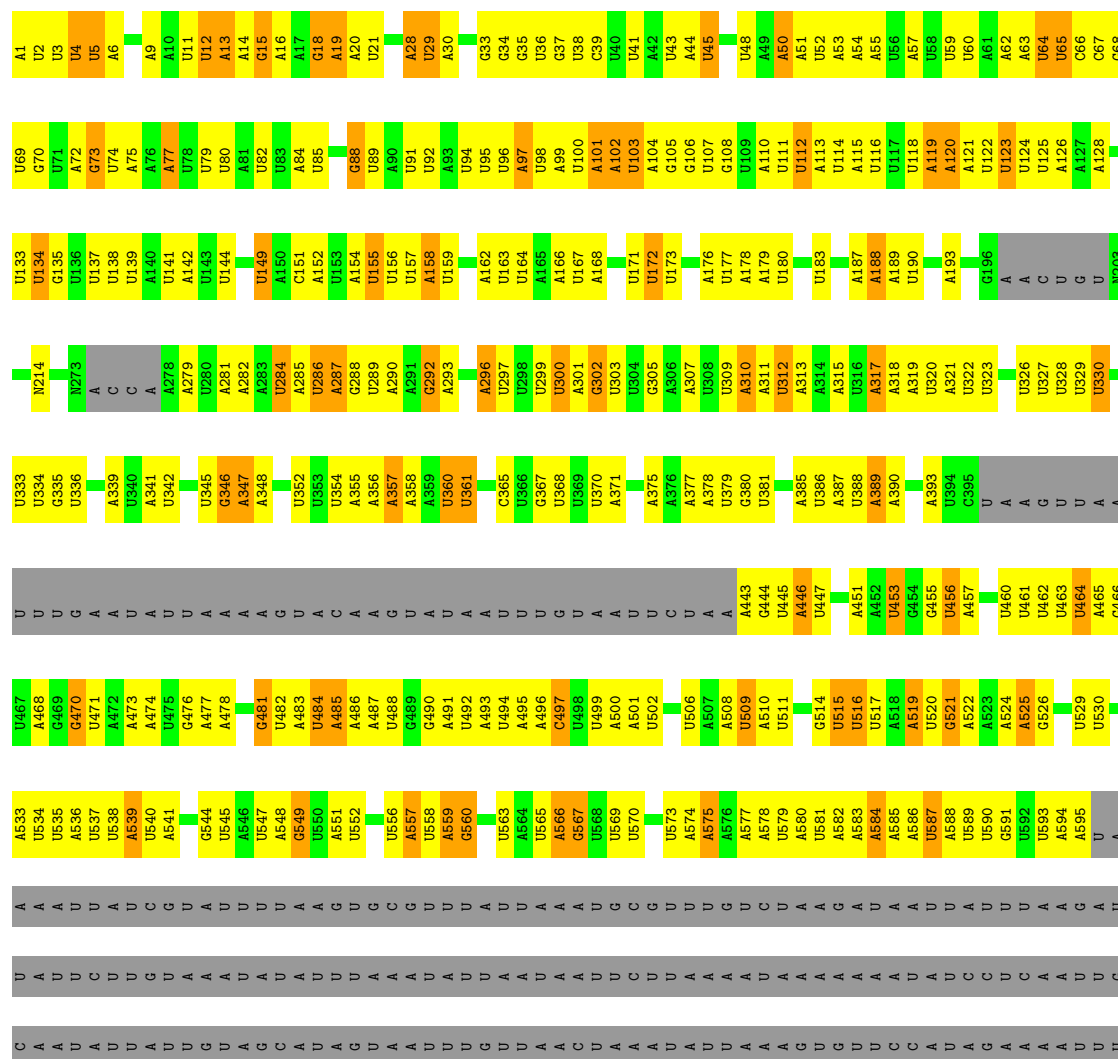
• Molecule 11: bL35m

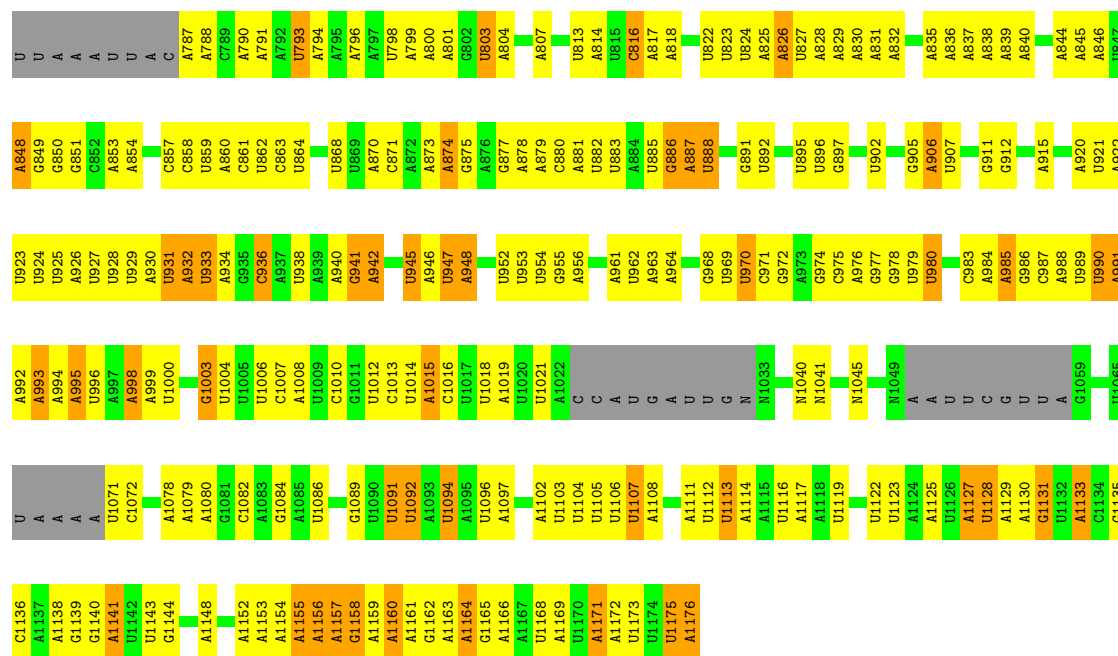
Chain A8:



• Molecule 12: 12S ribosomal RNA

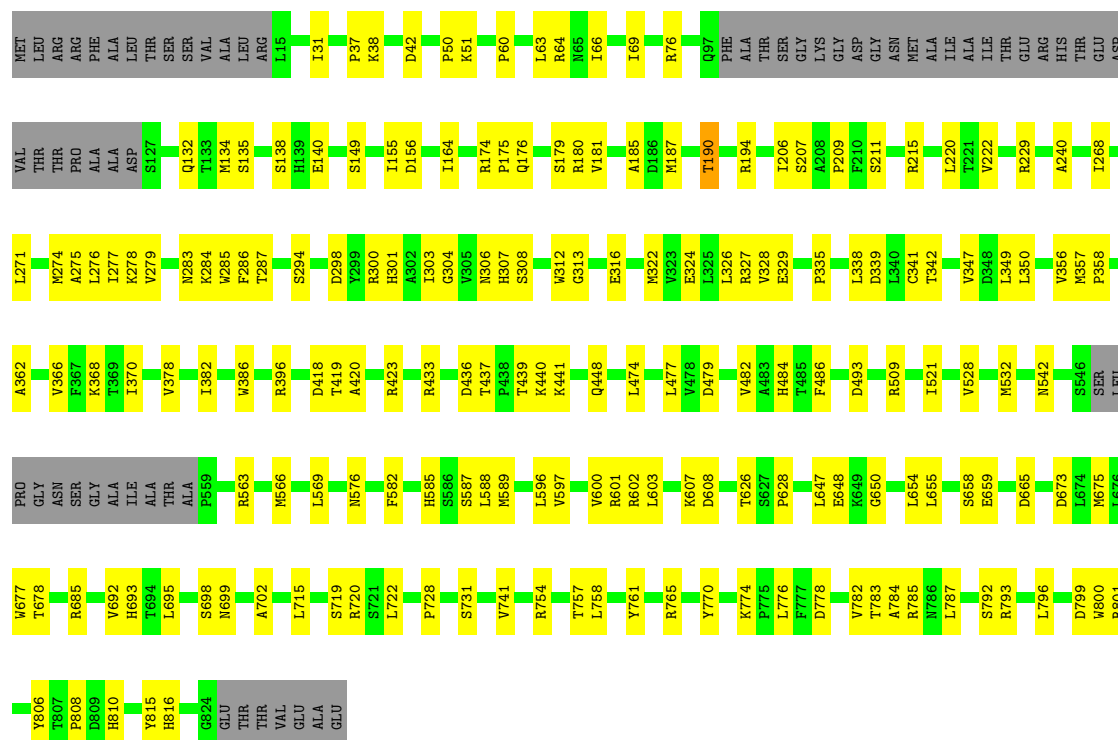
Chain AA:





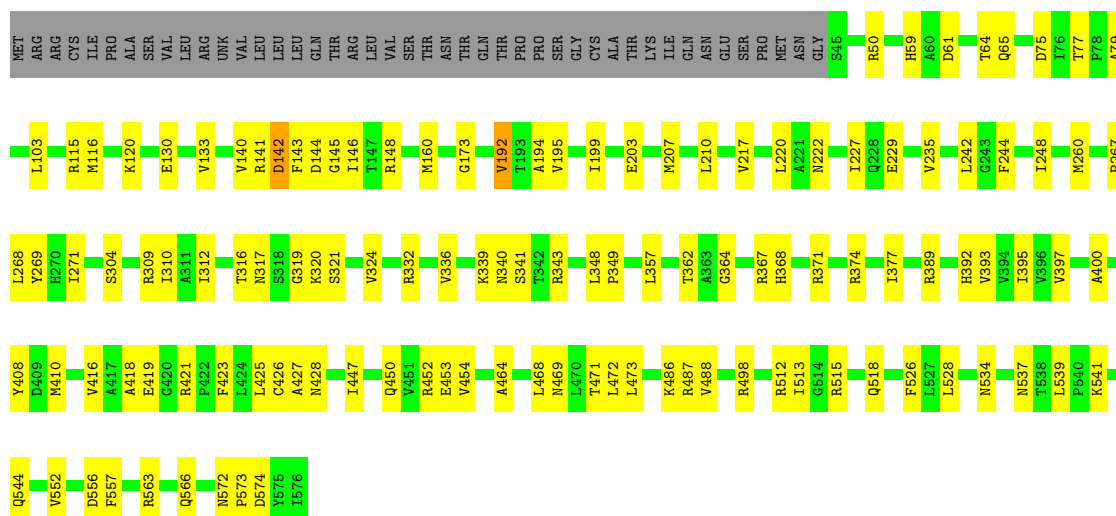
• Molecule 13: mL67

Chain BA: 71% 22% 7%



• Molecule 14: mt-EngA

Chain EA: 71% 21% 8%

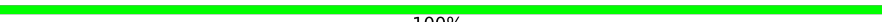


- Molecule 15: UNK

Chain UA:  100%

There are no outlier residues recorded for this chain.

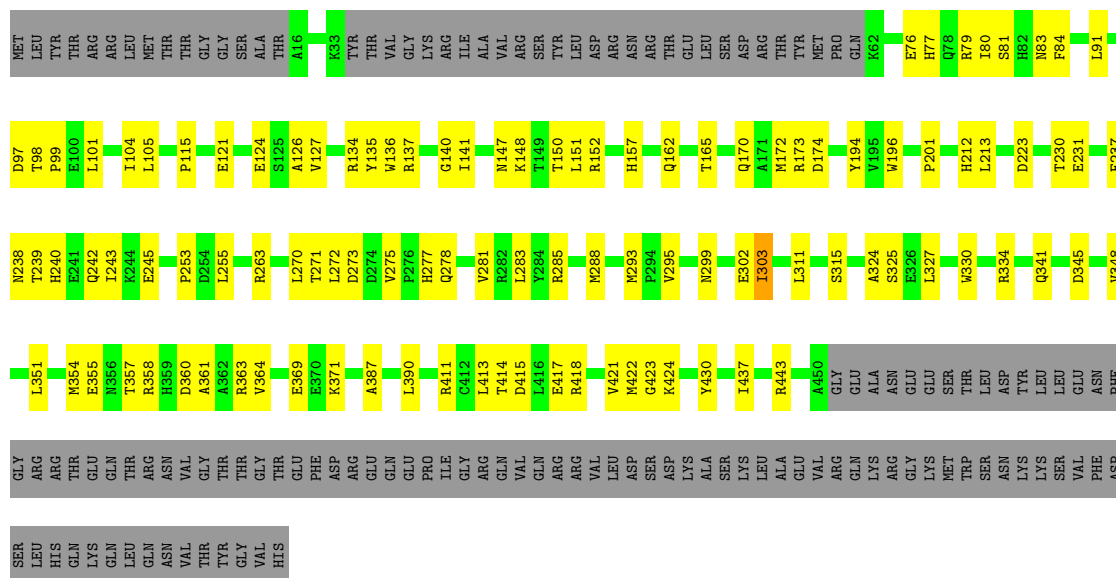
- Molecule 15: UNK

Chain Uf:  100%

There are no outlier residues recorded for this chain.

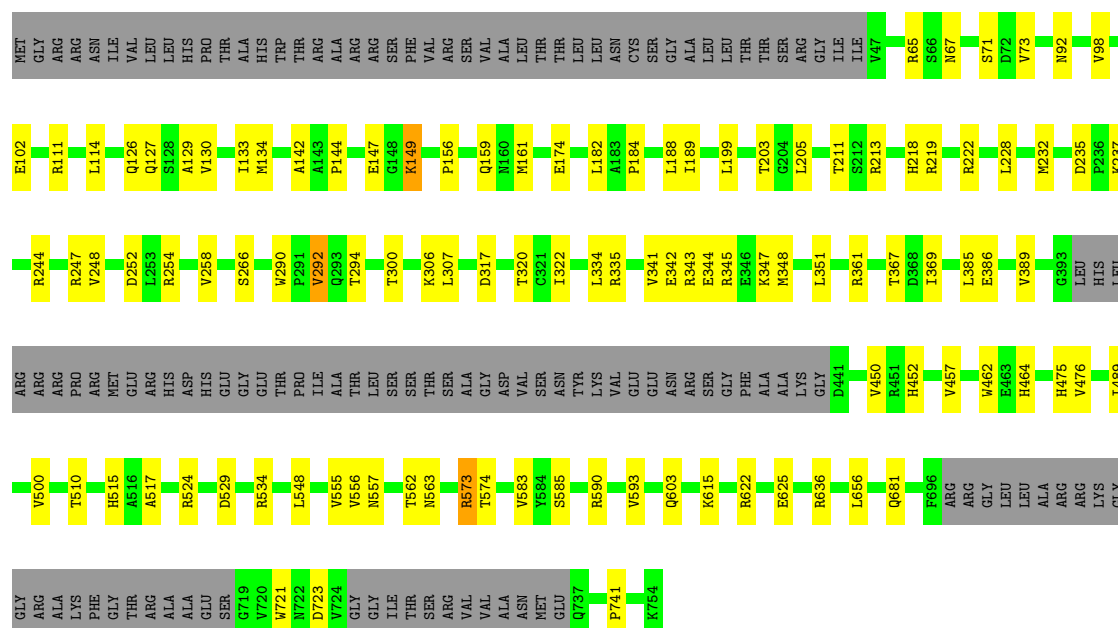
- Molecule 16: mL68

Chain BB:  55% 20% 25%



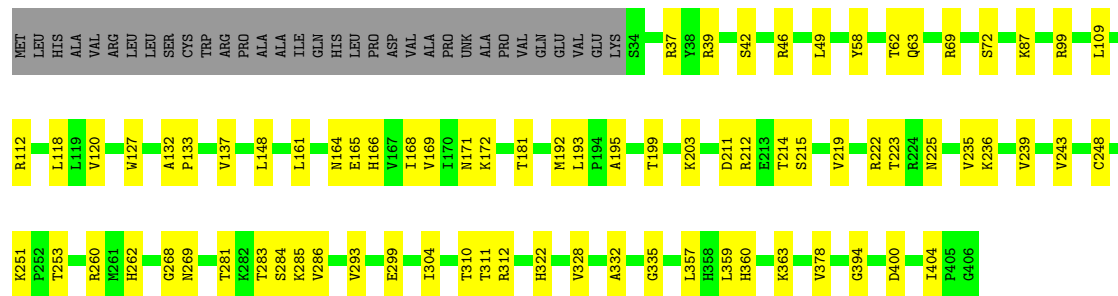
- Molecule 17: DEAD-box helicase, putative

Chain EB:  69% 14% 17%



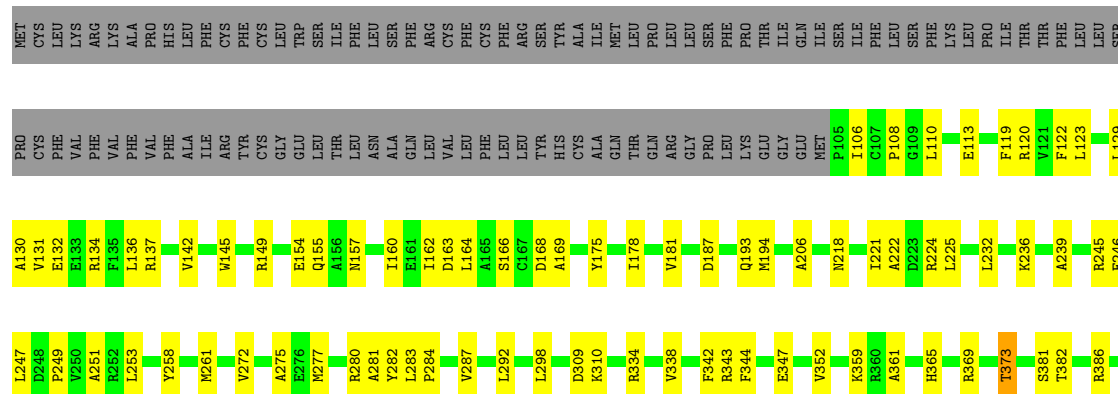
- Molecule 18: Pseudouridylate synthase, putative

Chain EC:  73% 19% 8%

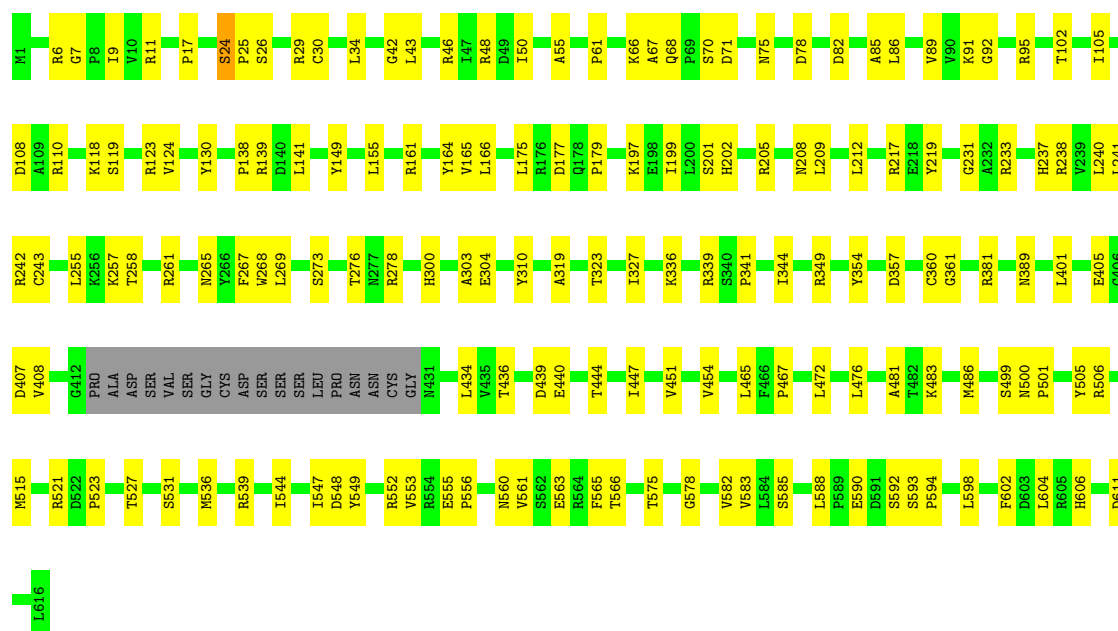


- Molecule 19: mL70

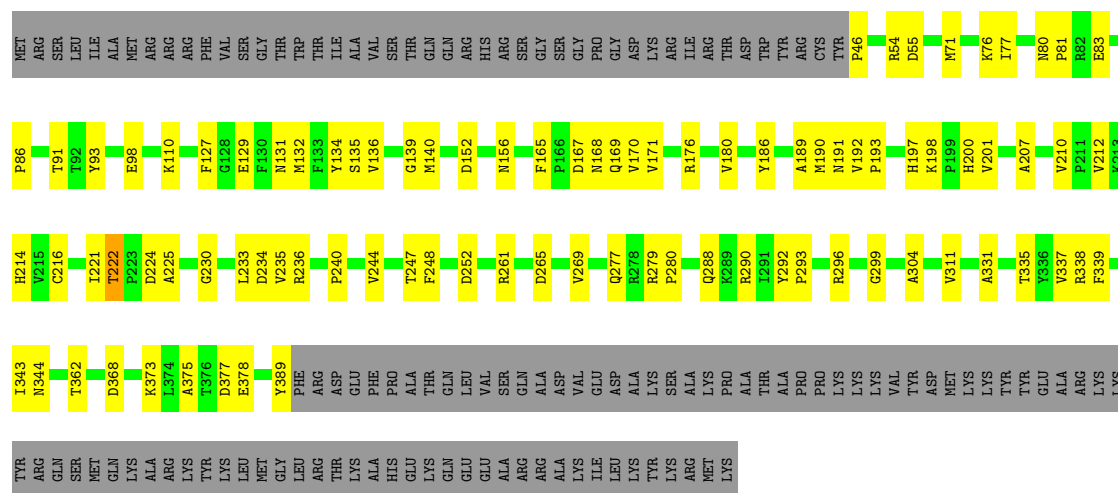
Chain BD:  57% 20% 23%



- Molecule 20: mt-LAF4



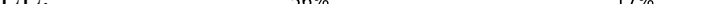
- Molecule 21: Ribosomal protein L3 mitochondrial, putative

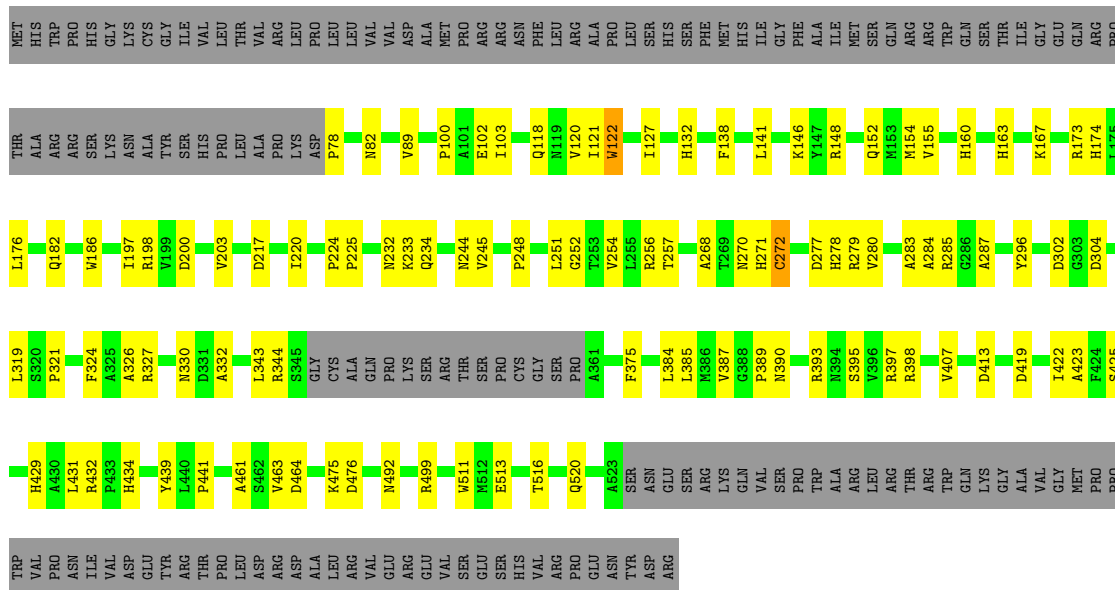


- Molecule 22: mL71

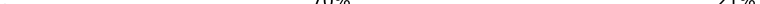


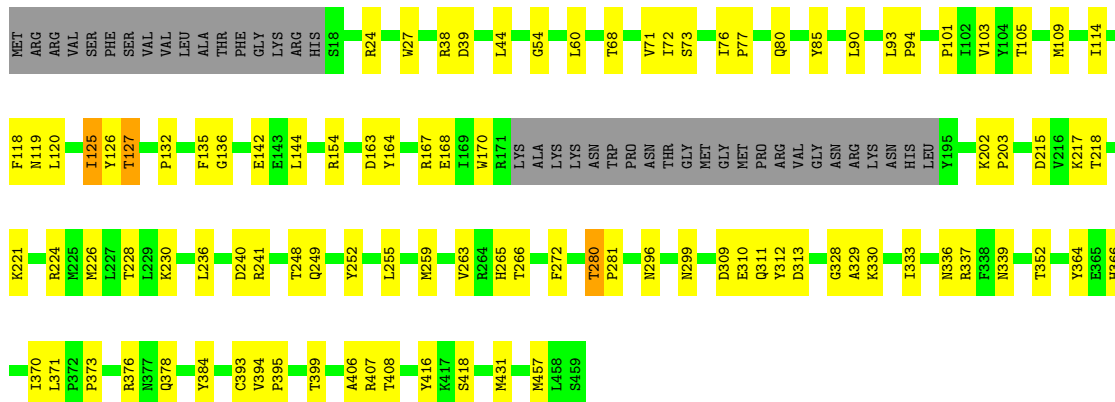
- Molecule 23: SpoU methylase domain-containing protein

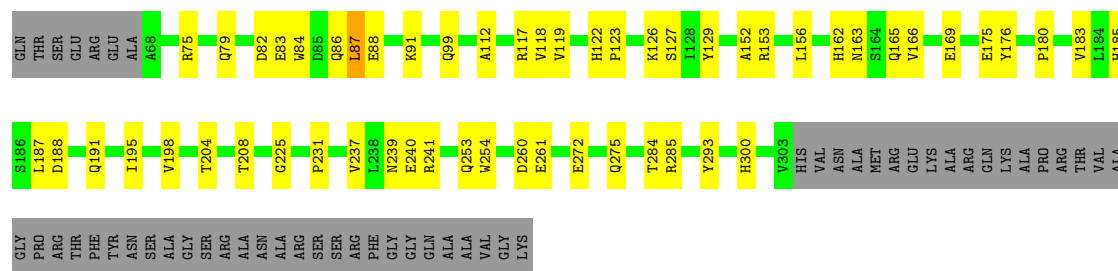
Chain EE:  56% 17% 26%



- Molecule 24: Ribosomal protein L4/L1 family, putative

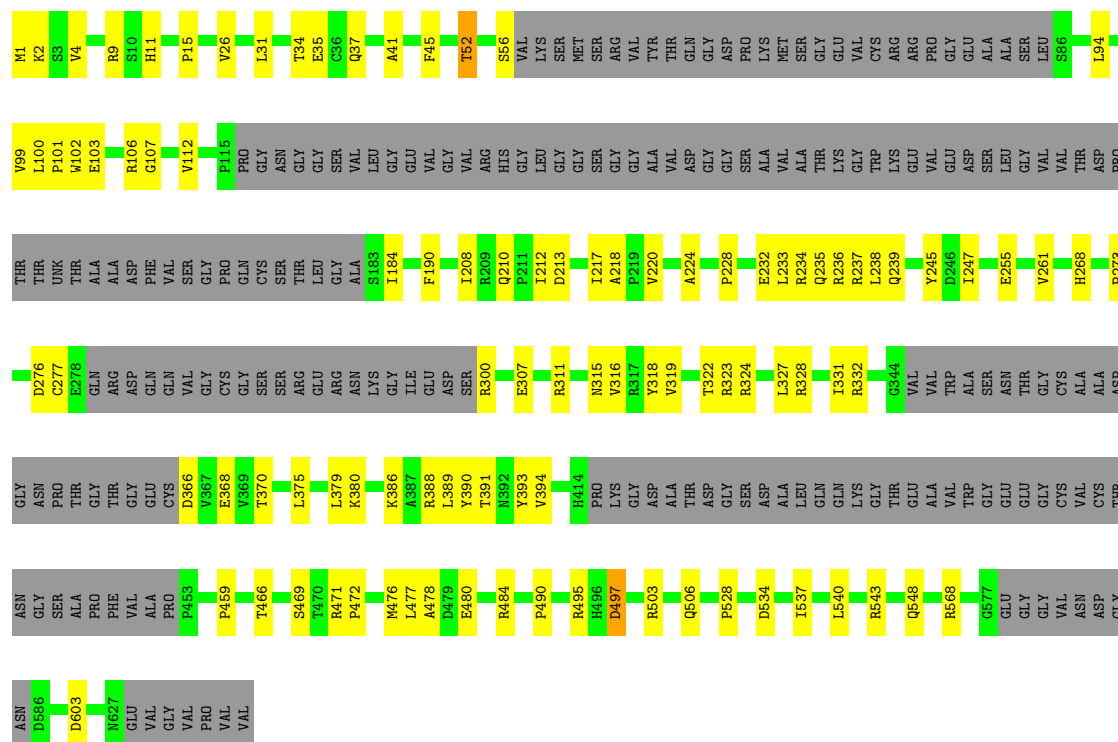
Chain AF:  70% 21% 9%





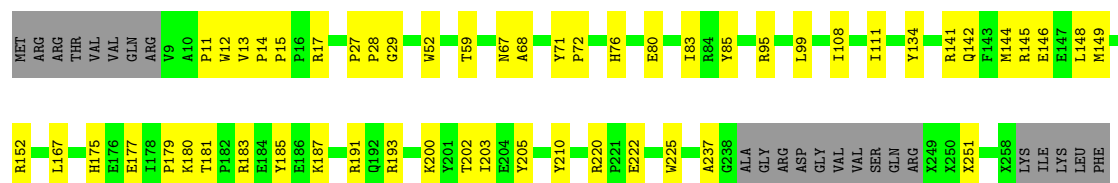
• Molecule 29: mt-LAF8

Chain EH: 54% 16% 30%



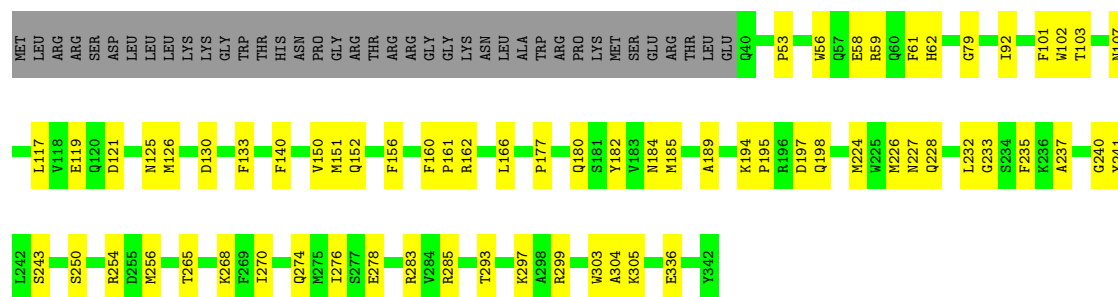
• Molecule 30: RIBOSOMAL_L9 domain-containing protein

Chain AI: 71% 20% 9%



• Molecule 31: mL75

Chain BI: 69% 20% 11%



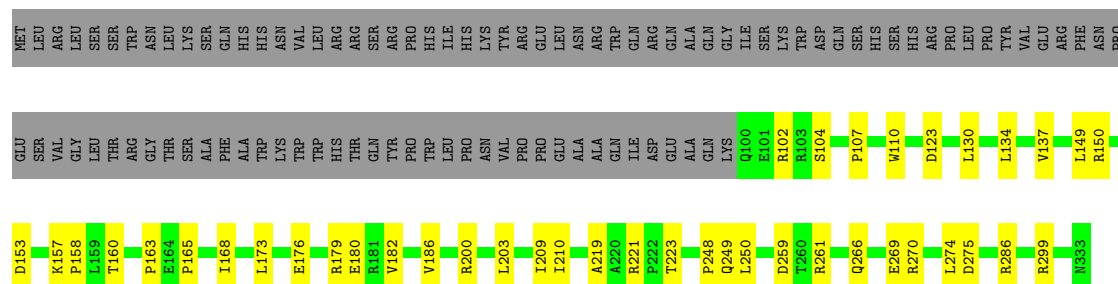
- Molecule 32: UNK



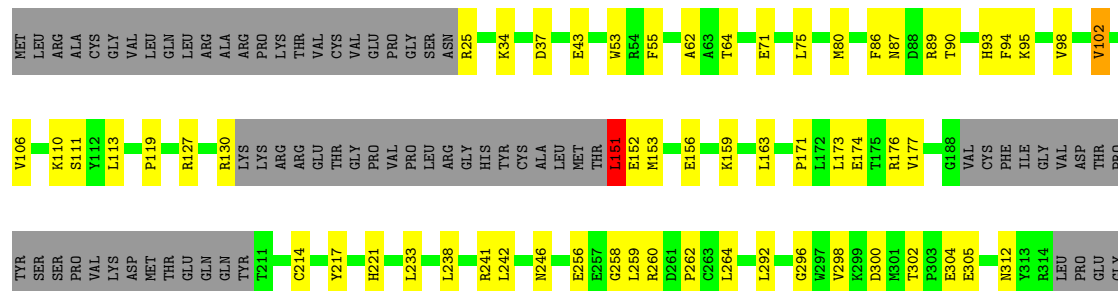
- Molecule 32: UNK



- Molecule 33: mL76



- Molecule 34: Ribosomal protein L11, putative



GLU
LYS
ARG
LYS
GLN
MET
ASP
GLU
UNK
GLN
MET
SER
GLY
GLU
VAL
TYR
TRP
THR
ASP
GLY
GLN
LEU

• Molecule 35: Chaperone protein DNAj, putative

Chain BK:  47% 11% 41%

MET TYR PHE PHE HIS ILE SER PHE HIS PHE VAL VAL ASN PHE THR THR ASP GLY VAL GLY GLU PRO SER ARG LEU UNK HIS LEU THR THR HIS PRO SER TYR MET ARG ARG VAL THR SER THR VAL HIS ARG THR VAL SER UNK

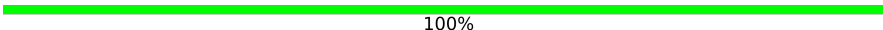
ALA LEU PRO SER PHE ASN GLY THR LEU LEU SER VAL CYS VAL CYS ALA SER CYS SER PRO ALA ALA PRO V84 L87 R90 L91 G92 L93 A97 R109 H14 V17 Y137 D138 Y139 L140 I141 L155 E156 ARG THR VAL PRO PRO VAL LYS GLN GLU GLY

GLU GLY VAL CYS ASP SER LYS LYS PHE LEU ASN ARG GLY VAL THR THR ARG PRO ARG H188 R189 K190 V193 R194 G195 E203 M208 Q212 V213 R216 K233 GLU ASP ASP GLY SER PRO ALA ARG GLU SER ILE ARG VAL VAL ALA ALA ALA GLU

ARG PHE ALA GLU LYS VAL ARG GLN TYR GLY PRO GLY MET ARG HIS ALA VAL VAL TYR T278 P284 Y291 R295 T301 V302 P303 V306 R307 E311 L328 R340 K344 V348 V349 D353 S356 L357 L358 R359 I363 P373 K376

L379 Y380 S381 R384 P385 Y386

• Molecule 36: UNK

Chain UK:  100%

There are no outlier residues recorded for this chain.

• Molecule 37: mL78

Chain BL:  66% 17% 17%

MET GLY ALA SER GLY LEU ILE ARG ARG GLY GLY VAL PHE PRO ASP VAL SER LEU THR LEU THR PRO SER ARG ARG V31 G36 L41 Y42 E43 D46 S51 G52 R53 A54 L55 A67 T68 M69 E71 S72 G73 Q74 R78 K79 N103 Y104 S105

E116 I119 V140 T143 Q144 R147 R158 L165 E169 L177 L180 L181 R189 P195 T196 S197 VAL LEU THR SER ARG ALA GLY VAL VAL ALA GLY S216 M219 S220 C221 R226 A227 D228 S229 R230 N237 Q238 Y239

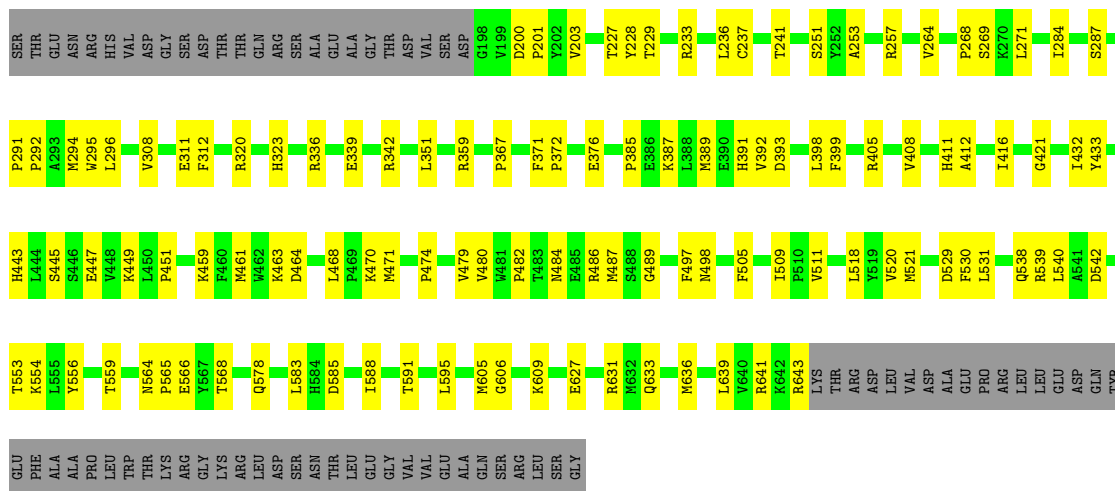
F240 D241 E244 R245 T250 T253 V254 L264 L285 A286 R287 D288 E289 V295 V304 A305 L306 GLN HIS ARG ILE PRO VAL PRO LYS

• Molecule 38: mt-LAF12

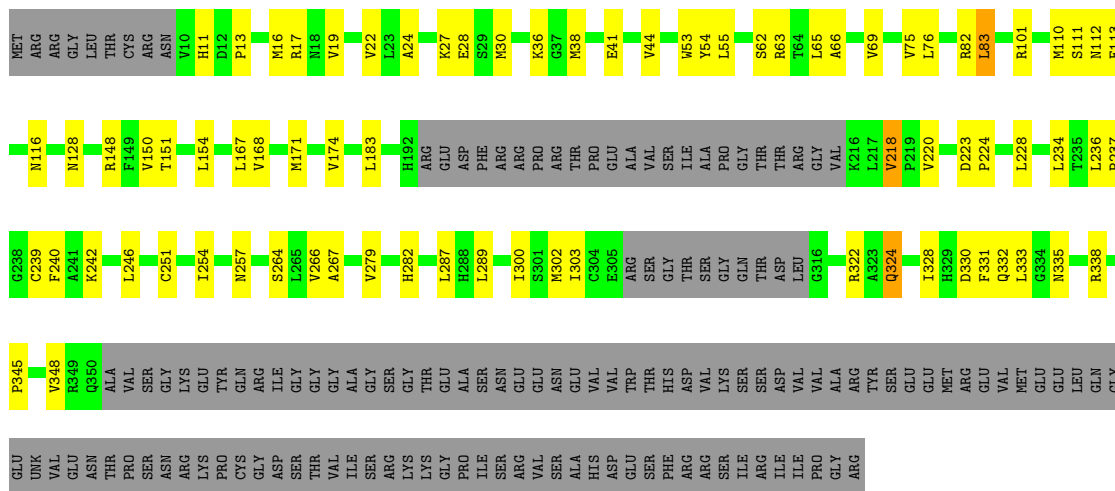
Chain EL:  58% 19% 23%

MET ARG ARG LEU PHE ILE THR THR ALA THR THR CYS HIS SER LEU HIS SER CYS THR ASP THR THR GLY ALA GLY LYS GLU SER THR PRO THR D49 E61 T62 R70 T71 Y72 S73 T74 M75

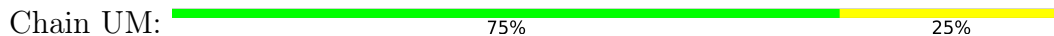
V78 R83 E92 PRO SER SER SER SER GLY HIS MET GLU GLN UNK LEU GLU ASN GLU ALA E110 H118 L123 W124 G125 S130 E131 D132 N133 K134 P135 P136 N151 SER GLU ASP ASP ASN MET ASP ASP ALA ALA LEU VAL SER ASP ILE PRO SER HIS TYR ILE SER



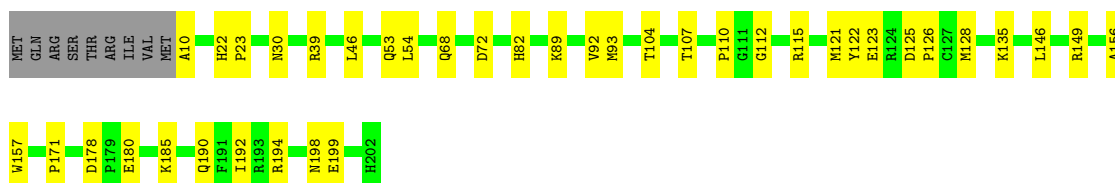
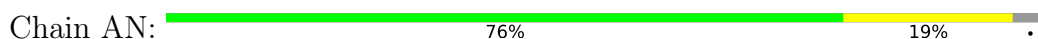
- Molecule 39: GTP-binding protein, putative



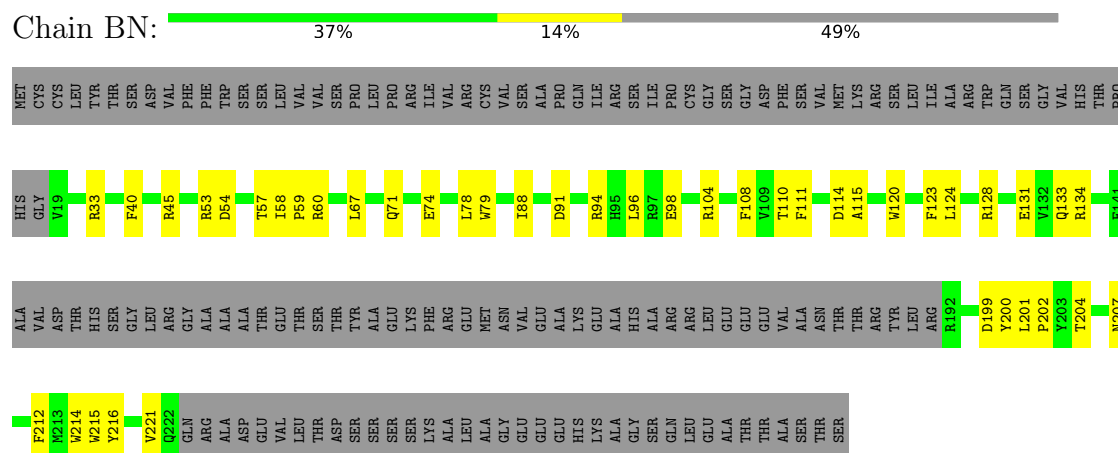
- Molecule 40: UNK



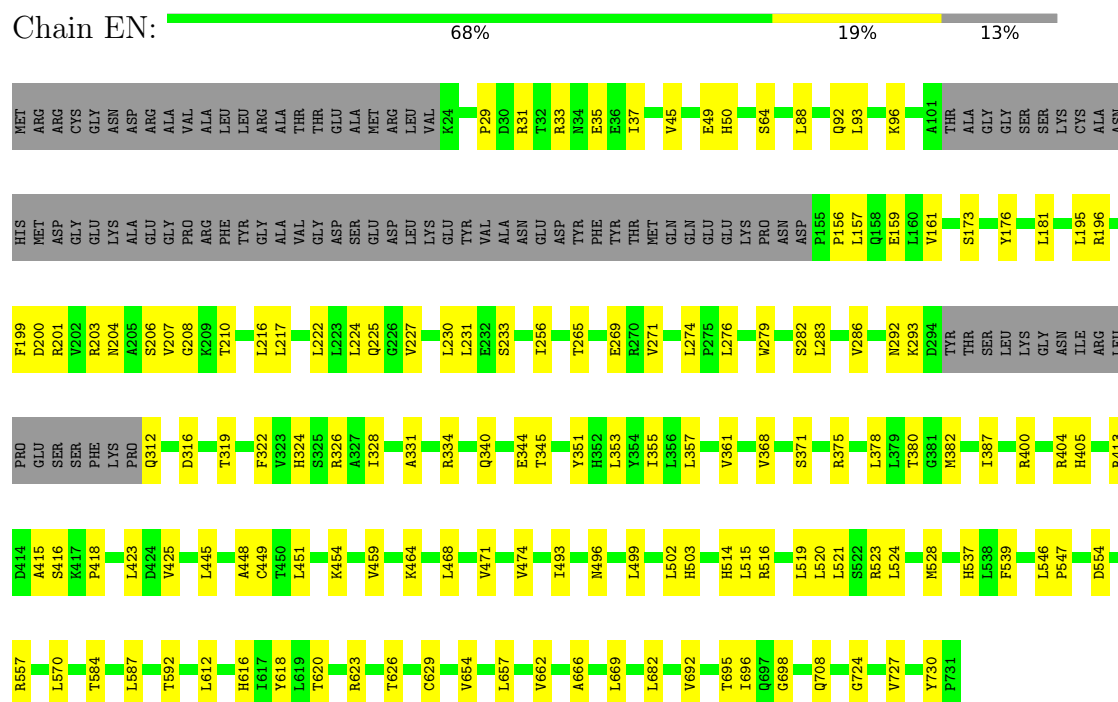
- Molecule 41: 50S ribosomal protein L13, putative



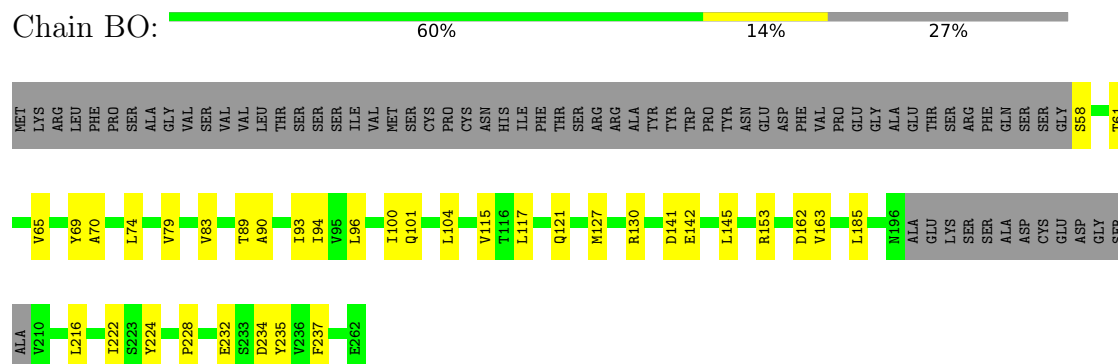
- Molecule 42: mL80



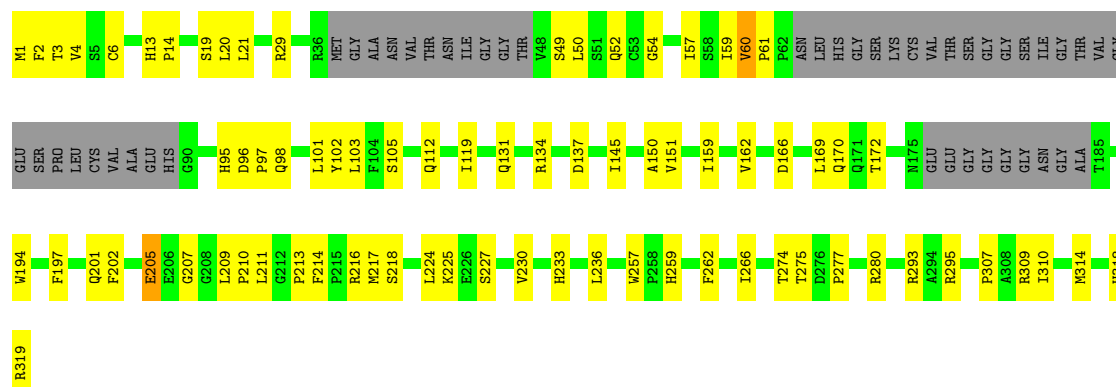
- Molecule 43: mt-LAF14



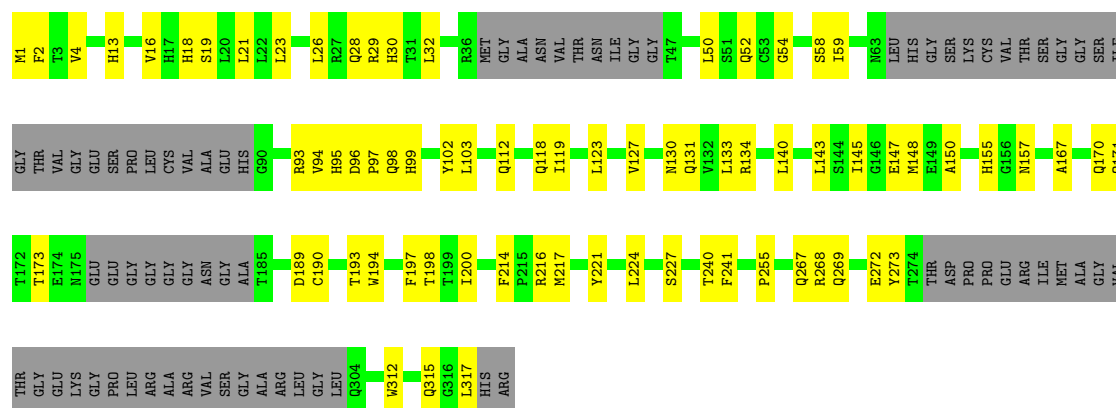
- Molecule 44: mL81



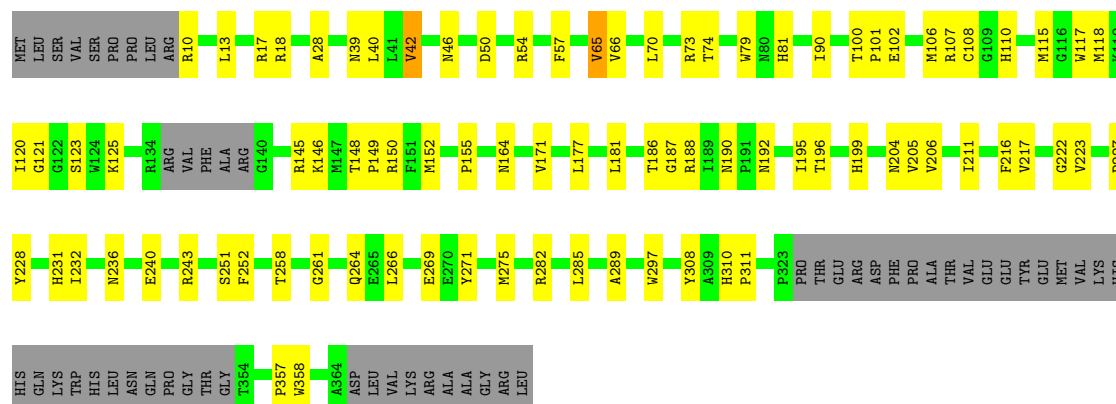
- Molecule 45: mt-LAF15a

Chain EO:  61% 24% 15%

- Molecule 45: mt-LAF15a

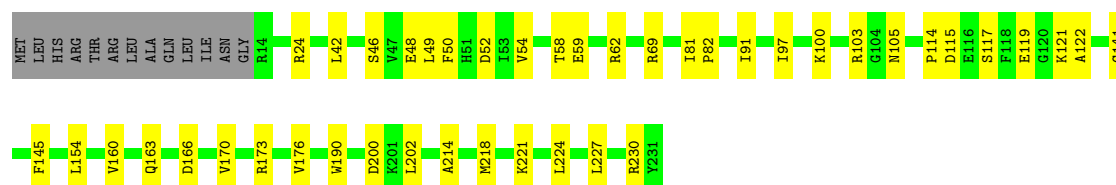
Chain EP:  53% 23% 24%

- Molecule 46: Ribosomal_L18e/L15P domain-containing protein

Chain AP:  63% 22% 14%

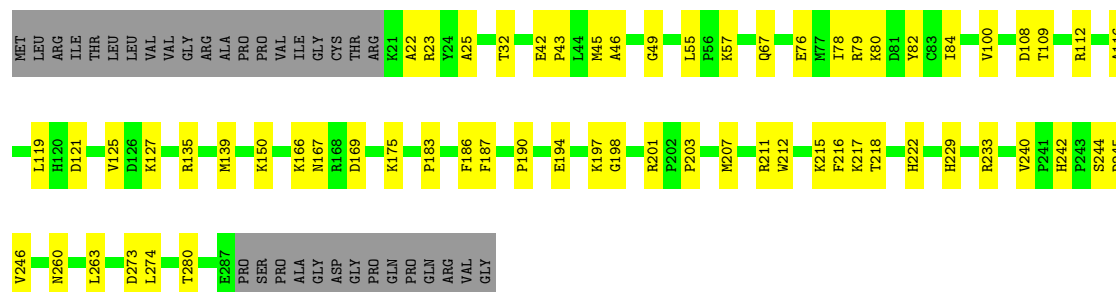
- Molecule 47: Peptidyl-prolyl cis-trans isomerase

Chain BQ:  76% 19% 6%



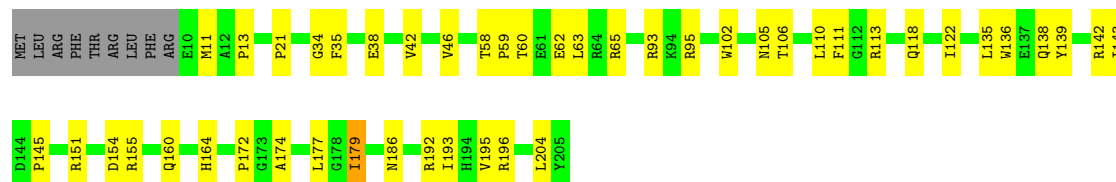
- Molecule 48: 50S ribosomal protein L17, putative

Chain AR:  68% 21% 11%

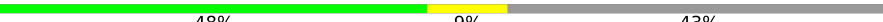


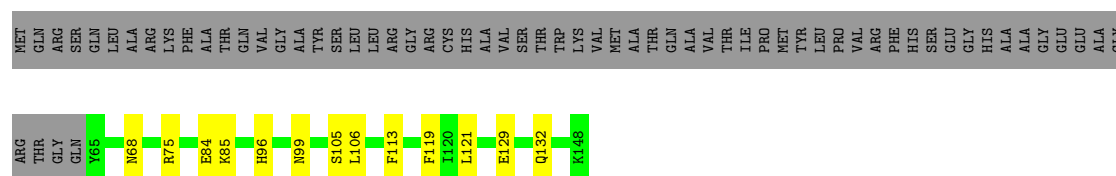
- Molecule 49: mL84

Chain BR:  73% 22% 5%



- Molecule 50: Acyl carrier protein

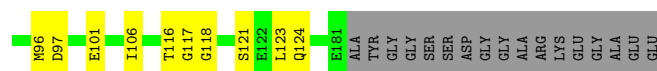
Chain ER:  48% 9% 43%



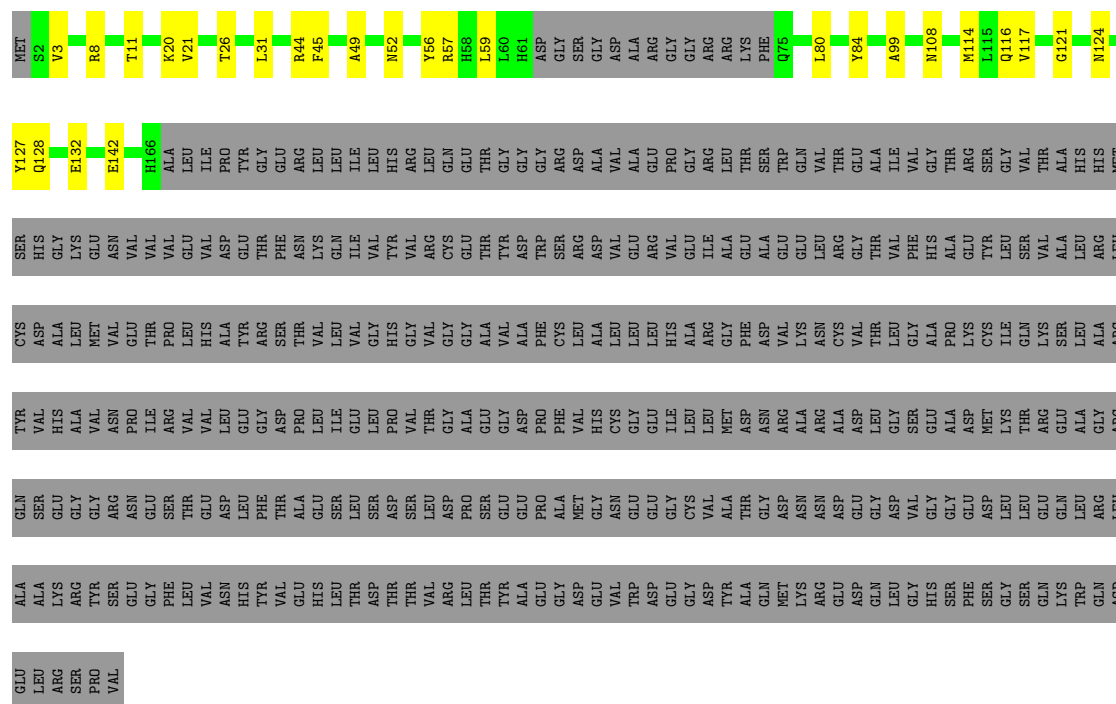
- Molecule 51: mL85

Chain BS:  63% 18% 19%

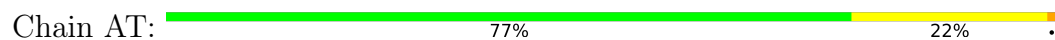




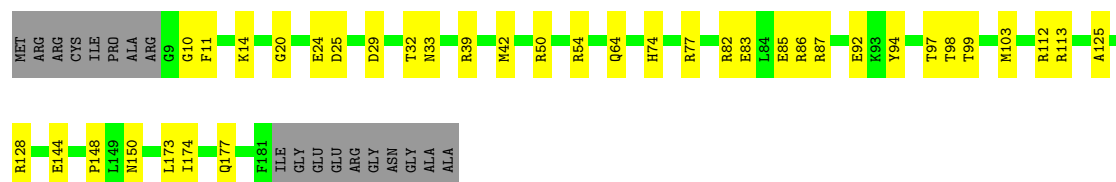
• Molecule 52: Lipase (Class 3)



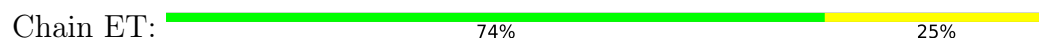
• Molecule 53: bL19m



• Molecule 54: mL86



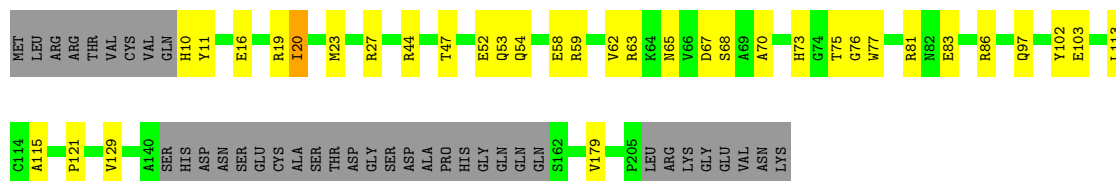
• Molecule 55: mt-LAF19





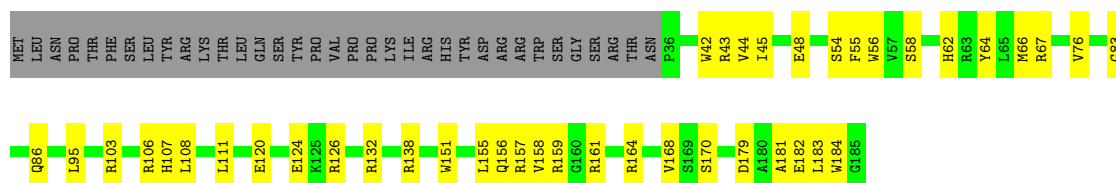
- Molecule 56: bL20m

Chain AU: 66% 16% 18%



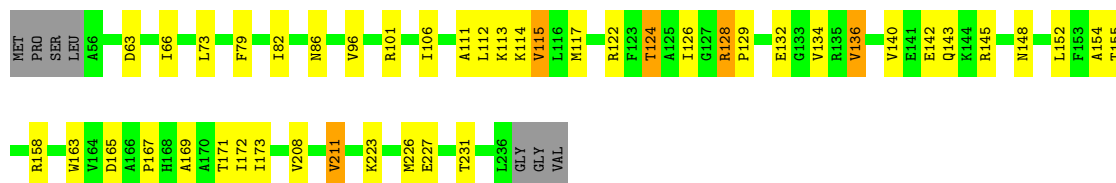
- Molecule 57: mL87

Chain BU: 58% 23% 19%



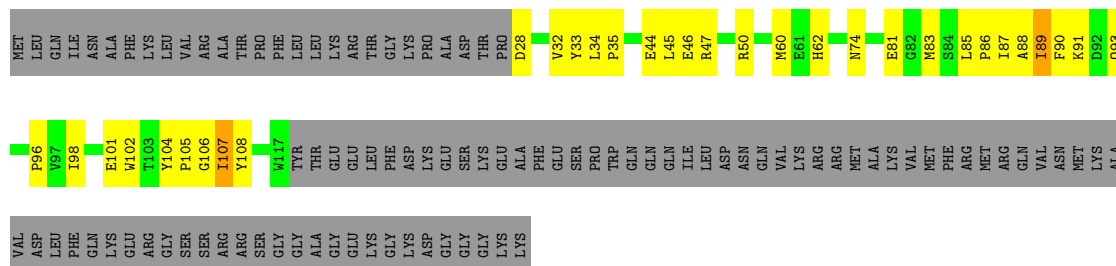
- Molecule 58: bL21m

Chain AV: 72% 21% 7%



- Molecule 59: mL88

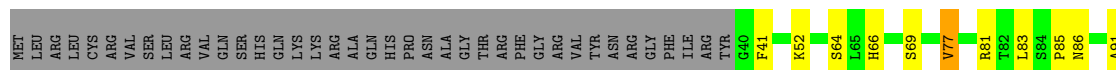
Chain BV: 31% 16% 53%



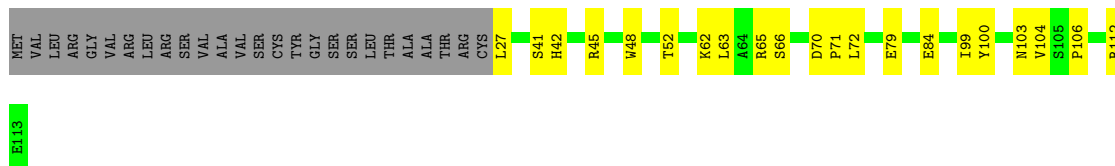
- Molecule 60: uL22m

Chain AW: 76% 24%

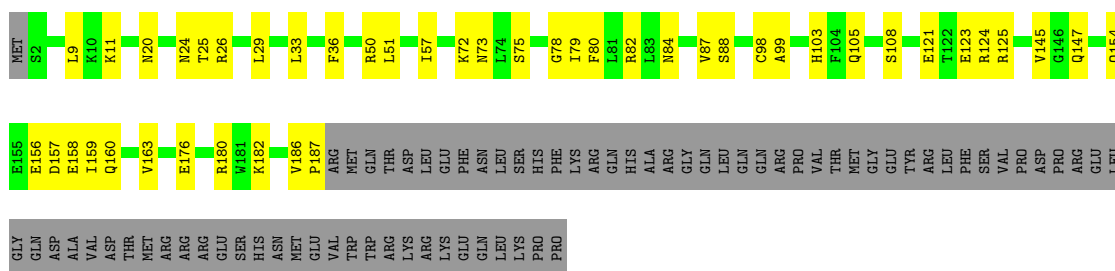




- Molecule 70: mL98



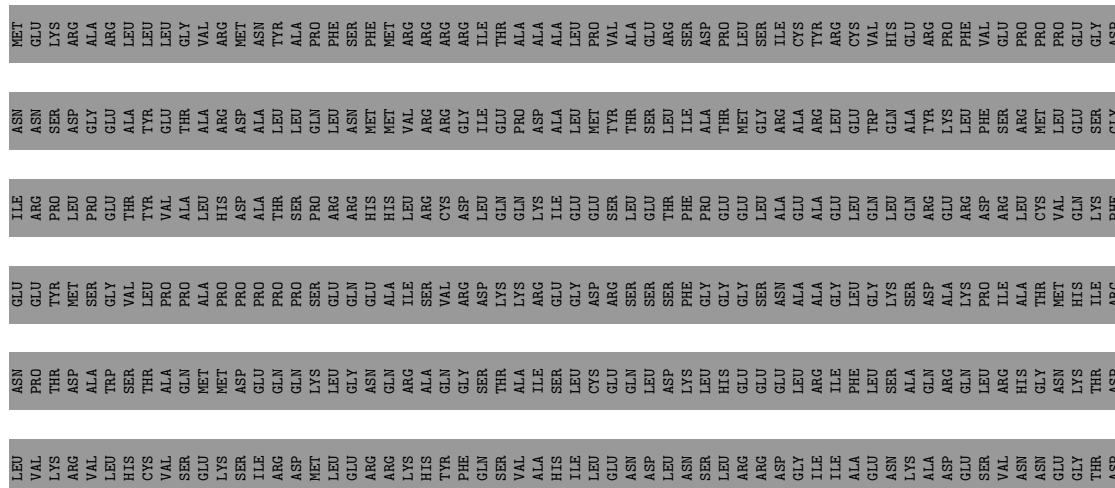
- Molecule 71: L51 S25 CI-B8 domain-containing protein

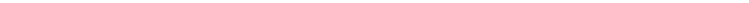


- Molecule 72: mt-LAF27



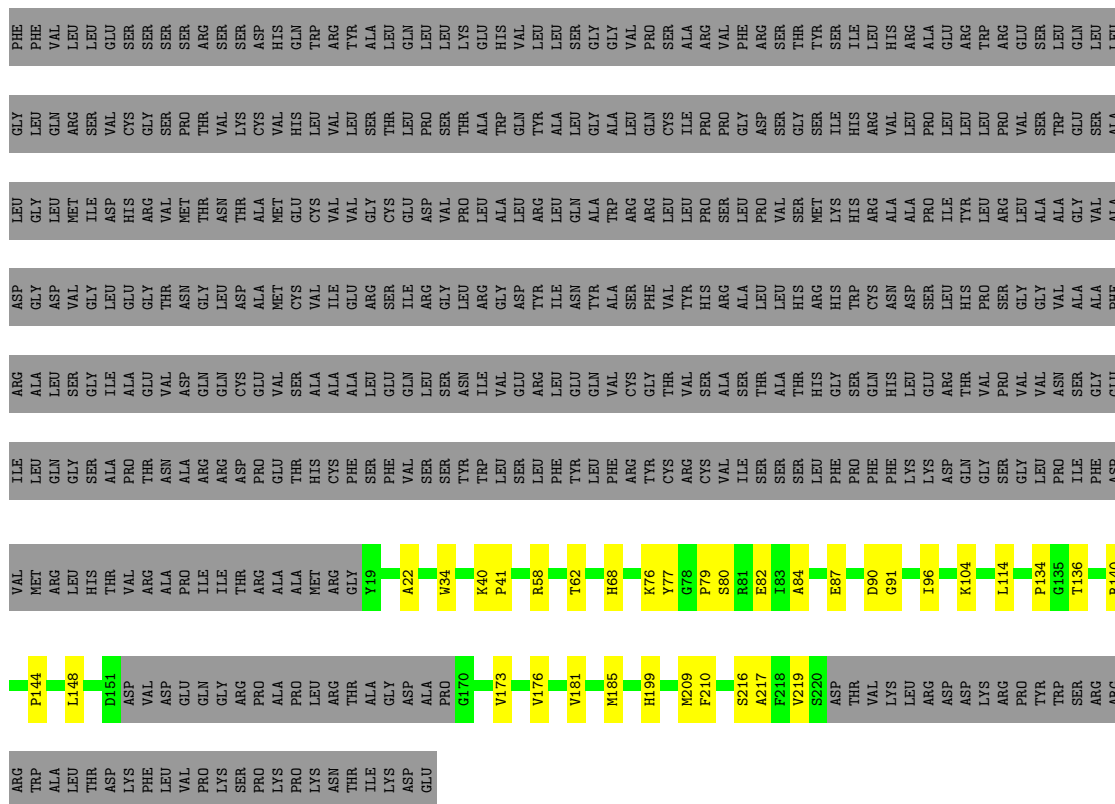
- Molecule 73: KRIPP9



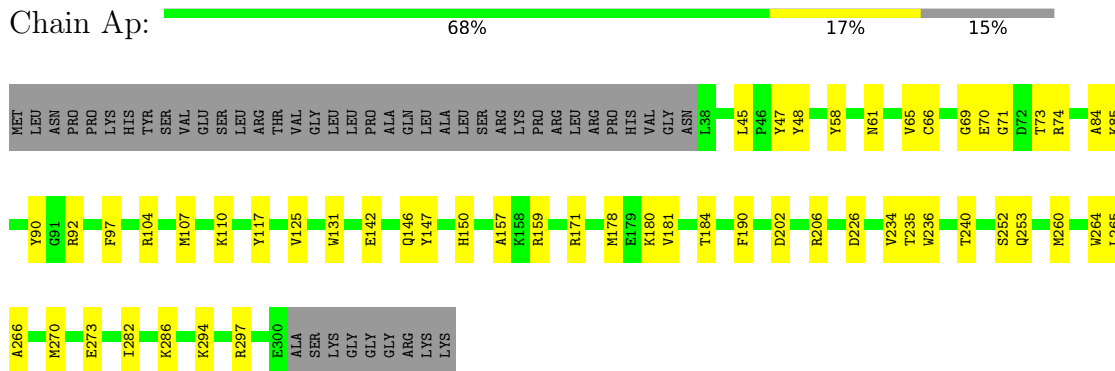
- Chain Un:  100%

- Molecule 79: mL52

[illegible]



- Molecule 80: mL53



- Molecule 81: UNK



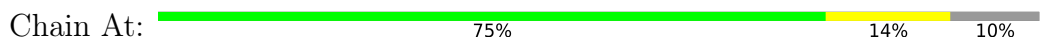
There are no outlier residues recorded for this chain.

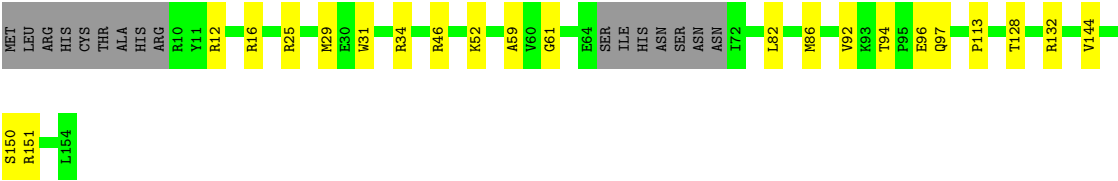
- Molecule 82: UNK



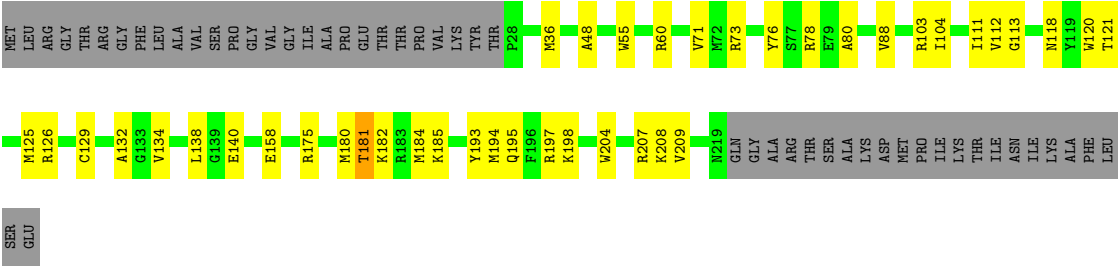
There are no outlier residues recorded for this chain.

- Molecule 83: mL63





• Molecule 84: mL64



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	16215	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	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, ZN, NA, ATP, MG, NAD, GTP

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	A1	0.10	0/1828	0.29	0/2466
2	E1	0.11	0/3906	0.32	1/5236 (0.0%)
3	A2	0.11	0/3844	0.27	0/5234
4	E2	0.09	0/3000	0.27	0/4067
5	A3	0.12	0/1246	0.29	0/1678
6	E3	0.09	0/3331	0.26	0/4491
7	E4	0.11	0/3491	0.33	1/4740 (0.0%)
8	A5	0.10	0/498	0.28	0/663
10	E6	0.10	0/3471	0.27	0/4710
11	A8	0.11	0/1163	0.31	0/1558
12	AA	0.09	0/19045	0.22	0/29609
13	BA	0.10	0/6192	0.27	0/8401
14	EA	0.09	0/4337	0.27	0/5856
16	BB	0.10	0/3411	0.28	0/4622
17	EB	0.09	0/5154	0.27	0/6977
18	EC	0.10	0/3090	0.26	0/4190
19	BD	0.11	0/3418	0.29	0/4629
20	ED	0.10	0/4877	0.28	0/6607
21	AE	0.10	0/2897	0.28	0/3938
22	BE	0.10	0/2896	0.26	0/3929
23	EE	0.10	0/3489	0.33	1/4722 (0.0%)
24	AF	0.10	0/3517	0.26	0/4775
25	BF	0.11	0/2909	0.31	0/3920
26	EF	0.10	0/2316	0.29	0/3148
27	EG	0.11	0/1331	0.28	0/1784
28	BH	0.09	0/2005	0.28	0/2734
29	EH	0.10	0/3586	0.28	0/4864
30	AI	0.09	0/1980	0.27	0/2693
31	BI	0.10	0/2548	0.25	0/3449
33	BJ	0.10	0/1985	0.28	0/2681
34	AK	0.23	0/2141	0.38	1/2886 (0.0%)
35	BK	0.10	0/1897	0.27	0/2556

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	BL	0.11	0/2055	0.29	0/2782
38	EL	0.09	0/4384	0.26	0/5967
39	EM	0.09	0/2480	0.26	0/3352
41	AN	0.10	0/1698	0.28	0/2308
42	BN	0.10	0/1353	0.29	0/1827
43	EN	0.10	0/5115	0.27	0/6936
44	BO	0.09	0/1518	0.27	0/2051
45	EO	0.11	0/2173	0.30	0/2956
45	EP	0.10	0/1953	0.27	0/2659
46	AP	0.10	0/2695	0.26	0/3657
47	BQ	0.09	0/1691	0.25	0/2293
48	AR	0.11	0/2279	0.30	0/3079
49	BR	0.10	0/1702	0.29	0/2296
50	ER	0.07	0/679	0.23	0/923
51	BS	0.12	0/1131	0.26	0/1547
52	ES	0.10	0/1276	0.27	0/1715
53	AT	0.10	0/1210	0.29	0/1632
54	BT	0.11	0/1465	0.28	0/1970
55	ET	0.10	0/858	0.29	0/1148
56	AU	0.11	0/1456	0.30	0/1971
57	BU	0.11	0/1315	0.30	0/1776
58	AV	0.10	0/1454	0.30	0/1973
59	BV	0.30	0/786	0.49	1/1063 (0.1%)
60	AW	0.11	0/2307	0.28	0/3119
61	BW	0.11	0/1612	0.28	0/2177
62	AX	0.11	0/1432	0.29	0/1947
63	AY	0.10	0/2846	0.27	0/3847
64	BZ	0.09	0/1422	0.25	0/1925
65	Ba	0.11	0/1329	0.37	1/1798 (0.1%)
66	Bb	0.09	0/1073	0.28	0/1454
67	Bc	0.09	0/1238	0.28	0/1685
68	Ae	0.10	0/1068	0.29	0/1447
69	Af	0.09	0/1134	0.25	0/1536
70	Bf	0.10	0/749	0.35	0/1012
71	Ag	0.11	0/1608	0.31	0/2180
72	E7	0.10	0/834	0.31	0/1118
73	E8	0.13	0/1202	0.31	0/1631
74	E9	0.09	0/1678	0.27	0/2257
75	Al	0.10	0/1484	0.26	0/2019
79	Ao	0.10	0/1486	0.26	0/2022
80	Ap	0.09	0/2231	0.25	0/3030
83	At	0.11	0/1179	0.32	0/1596
84	Av	0.10	0/1678	0.27	0/2261

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.10	0/183115	0.28	6/251755 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	BV	89	ILE	N-CA-C	-7.32	106.36	113.53
65	Ba	12	PRO	N-CA-CB	7.19	110.15	103.46
23	EE	441	PRO	N-CA-CB	7.13	110.73	103.25
2	E1	96	PRO	N-CA-CB	6.48	110.56	103.23
7	E4	203	PRO	N-CA-CB	6.26	110.15	103.52

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A1	1788	0	1814	39	0
2	E1	3836	0	3800	88	0
3	A2	3739	0	3689	66	0
4	E2	2933	0	2932	53	0
5	A3	1226	0	1282	38	0
6	E3	3266	0	3290	58	0
7	E4	3418	0	3384	84	0
8	A5	483	0	493	12	0
9	E5	1635	0	352	8	0
10	E6	3405	0	3405	76	0
11	A8	1136	0	1158	32	0
12	AA	18187	0	9203	387	0
13	BA	6059	0	6053	136	0
14	EA	4263	0	4306	91	0
15	UA	50	0	14	0	0
15	Uf	50	0	14	0	0
16	BB	3322	0	3244	80	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	EB	5039	0	5133	77	0
18	EC	3005	0	3010	52	0
19	BD	3349	0	3368	74	0
20	ED	4764	0	4771	98	0
21	AE	2802	0	2661	69	0
22	BE	2822	0	2754	48	0
23	EE	3423	0	3367	81	0
24	AF	3414	0	3316	76	0
25	BF	2847	0	2832	74	0
26	EF	2268	0	2299	50	0
27	EG	1295	0	1250	37	0
28	BH	1948	0	1910	36	0
29	EH	3508	0	3531	71	0
30	AI	1967	0	1887	44	0
31	BI	2475	0	2403	47	0
32	UI	105	0	23	1	0
32	Ur	105	0	23	1	0
33	BJ	1944	0	1922	26	0
34	AK	2088	0	2105	75	0
35	BK	1855	0	1827	29	0
36	UK	125	0	27	0	0
37	BL	2014	0	1903	38	0
38	EL	4259	0	4207	91	0
39	EM	2432	0	2465	55	0
40	UM	40	0	10	1	0
41	AN	1639	0	1612	30	0
42	BN	1320	0	1281	35	0
43	EN	5025	0	5101	92	0
44	BO	1498	0	1512	26	0
45	EO	2126	0	2134	57	0
45	EP	1911	0	1904	50	0
46	AP	2615	0	2546	74	0
47	BQ	1651	0	1571	28	0
48	AR	2214	0	2110	54	0
49	BR	1659	0	1638	33	0
50	ER	669	0	663	10	0
51	BS	1120	0	959	26	0
52	ES	1259	0	1265	22	0
53	AT	1180	0	1170	27	0
54	BT	1435	0	1397	39	0
55	ET	839	0	858	23	0
56	AU	1423	0	1447	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	BU	1275	0	1246	39	0
58	AV	1424	0	1457	40	0
59	BV	763	0	747	55	0
60	AW	2251	0	2292	61	0
61	BW	1565	0	1529	28	0
62	AX	1387	0	1364	44	0
63	AY	2790	0	2726	66	0
64	BZ	1396	0	1369	28	0
65	Ba	1287	0	1193	42	0
66	Bb	1048	0	1045	17	0
67	Bc	1194	0	1169	18	0
68	Ae	1031	0	1024	22	0
69	Af	1107	0	1087	25	0
70	Bf	725	0	687	17	0
71	Ag	1564	0	1507	41	0
72	E7	815	0	821	27	0
73	E8	1181	0	1122	26	0
74	E9	1642	0	1660	41	0
75	Al	1440	0	1448	32	0
76	Ul	1190	0	266	2	0
77	Um	135	0	32	1	0
78	Un	140	0	34	0	0
79	Ao	1443	0	1376	33	0
80	Ap	2161	0	2141	44	0
81	Up	435	0	95	0	0
82	Us	395	0	89	0	0
83	At	1149	0	1164	17	0
84	Av	1633	0	1611	32	0
85	A5	1	0	0	0	0
85	E2	4	0	0	0	0
85	E9	1	0	0	0	0
85	EG	1	0	0	0	0
86	A8	2	0	0	0	0
86	AA	12	0	0	0	0
86	EA	2	0	0	0	0
86	EB	1	0	0	0	0
87	EA	64	0	24	5	0
88	EA	2	0	0	0	0
89	EB	31	0	12	3	0
90	ER	32	0	39	5	0
91	Av	44	0	26	0	0
92	EA	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
92	EB	4	0	0	0	0
All	All	183043	0	169007	3098	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 9.

The worst 5 of 3098 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)
34:AK:127:ARG:HH21	59:BV:86:PRO:HB2	1.34	0.91
34:AK:217:TYR:CE1	59:BV:102:TRP:HB2	2.06	0.90
34:AK:221:HIS:ND1	59:BV:105:PRO:HA	1.89	0.88
12:AA:586:A:H61	48:AR:22:ALA:H	1.24	0.84
34:AK:174:GLU:OE2	59:BV:105:PRO:HB2	1.77	0.84

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	A1	215/241 (89%)	207 (96%)	8 (4%)	0	100	100
2	E1	471/482 (98%)	459 (98%)	12 (2%)	0	100	100
3	A2	461/471 (98%)	449 (97%)	12 (3%)	0	100	100
4	E2	359/568 (63%)	341 (95%)	18 (5%)	0	100	100
5	A3	147/218 (67%)	142 (97%)	5 (3%)	0	100	100
6	E3	401/557 (72%)	393 (98%)	8 (2%)	0	100	100
7	E4	430/439 (98%)	417 (97%)	13 (3%)	0	100	100
8	A5	53/80 (66%)	53 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	E6	430/531 (81%)	417 (97%)	13 (3%)	0	100	100
11	A8	131/181 (72%)	129 (98%)	2 (2%)	0	100	100
13	BA	763/831 (92%)	741 (97%)	22 (3%)	0	100	100
14	EA	530/576 (92%)	520 (98%)	10 (2%)	0	100	100
16	BB	403/541 (74%)	385 (96%)	18 (4%)	0	100	100
17	EB	619/754 (82%)	603 (97%)	16 (3%)	0	100	100
18	EC	371/406 (91%)	359 (97%)	12 (3%)	0	100	100
19	BD	417/547 (76%)	402 (96%)	15 (4%)	0	100	100
20	ED	594/616 (96%)	577 (97%)	17 (3%)	0	100	100
21	AE	342/473 (72%)	328 (96%)	14 (4%)	0	100	100
22	BE	353/449 (79%)	345 (98%)	8 (2%)	0	100	100
23	EE	427/586 (73%)	413 (97%)	13 (3%)	1 (0%)	43	74
24	AF	415/459 (90%)	405 (98%)	10 (2%)	0	100	100
25	BF	342/426 (80%)	328 (96%)	14 (4%)	0	100	100
26	EF	293/373 (79%)	283 (97%)	10 (3%)	0	100	100
27	EG	152/156 (97%)	150 (99%)	2 (1%)	0	100	100
28	BH	234/349 (67%)	228 (97%)	6 (3%)	0	100	100
29	EH	429/634 (68%)	425 (99%)	4 (1%)	0	100	100
30	AI	228/263 (87%)	224 (98%)	4 (2%)	0	100	100
31	BI	301/342 (88%)	295 (98%)	6 (2%)	0	100	100
33	BJ	232/333 (70%)	227 (98%)	5 (2%)	0	100	100
34	AK	242/342 (71%)	237 (98%)	5 (2%)	0	100	100
35	BK	222/386 (58%)	220 (99%)	2 (1%)	0	100	100
37	BL	254/312 (81%)	245 (96%)	9 (4%)	0	100	100
38	EL	526/691 (76%)	513 (98%)	13 (2%)	0	100	100
39	EM	302/451 (67%)	296 (98%)	6 (2%)	0	100	100
41	AN	191/202 (95%)	185 (97%)	6 (3%)	0	100	100
42	BN	150/302 (50%)	145 (97%)	5 (3%)	0	100	100
43	EN	632/731 (86%)	612 (97%)	20 (3%)	0	100	100
44	BO	188/262 (72%)	185 (98%)	3 (2%)	0	100	100
45	EO	264/319 (83%)	256 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	EP	233/319 (73%)	226 (97%)	7 (3%)	0	100	100
46	AP	314/374 (84%)	308 (98%)	6 (2%)	0	100	100
47	BQ	216/231 (94%)	206 (95%)	10 (5%)	0	100	100
48	AR	265/301 (88%)	252 (95%)	13 (5%)	0	100	100
49	BR	194/205 (95%)	190 (98%)	4 (2%)	0	100	100
50	ER	82/148 (55%)	79 (96%)	3 (4%)	0	100	100
51	BS	158/198 (80%)	152 (96%)	6 (4%)	0	100	100
52	ES	148/524 (28%)	146 (99%)	2 (1%)	0	100	100
53	AT	141/144 (98%)	137 (97%)	4 (3%)	0	100	100
54	BT	171/191 (90%)	165 (96%)	6 (4%)	0	100	100
55	ET	99/102 (97%)	96 (97%)	3 (3%)	0	100	100
56	AU	171/213 (80%)	167 (98%)	4 (2%)	0	100	100
57	BU	148/185 (80%)	141 (95%)	7 (5%)	0	100	100
58	AV	179/188 (95%)	172 (96%)	7 (4%)	0	100	100
59	BV	88/190 (46%)	86 (98%)	2 (2%)	0	100	100
60	AW	276/278 (99%)	270 (98%)	6 (2%)	0	100	100
61	BW	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
62	AX	162/246 (66%)	161 (99%)	1 (1%)	0	100	100
63	AY	338/378 (89%)	336 (99%)	2 (1%)	0	100	100
64	BZ	186/190 (98%)	178 (96%)	8 (4%)	0	100	100
65	Ba	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
66	Bb	129/162 (80%)	123 (95%)	6 (5%)	0	100	100
67	Bc	135/146 (92%)	131 (97%)	4 (3%)	0	100	100
68	Ae	123/197 (62%)	118 (96%)	5 (4%)	0	100	100
69	Af	137/189 (72%)	137 (100%)	0	0	100	100
70	Bf	85/113 (75%)	80 (94%)	5 (6%)	0	100	100
71	Ag	184/260 (71%)	175 (95%)	9 (5%)	0	100	100
72	E7	95/97 (98%)	87 (92%)	8 (8%)	0	100	100
73	E8	152/786 (19%)	146 (96%)	6 (4%)	0	100	100
74	E9	198/343 (58%)	193 (98%)	5 (2%)	0	100	100
75	Al	179/218 (82%)	177 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
79	Ao	180/1520 (12%)	175 (97%)	5 (3%)	0	100	100
80	Ap	261/309 (84%)	258 (99%)	3 (1%)	0	100	100
83	At	134/154 (87%)	128 (96%)	6 (4%)	0	100	100
84	Av	190/242 (78%)	185 (97%)	5 (3%)	0	100	100
All	All	19602/26562 (74%)	19044 (97%)	557 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	EE	121	ILE

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	A1	195/217 (90%)	192 (98%)	3 (2%)	57	70
2	E1	393/419 (94%)	390 (99%)	3 (1%)	73	77
3	A2	405/413 (98%)	401 (99%)	4 (1%)	68	75
4	E2	328/505 (65%)	323 (98%)	5 (2%)	57	70
5	A3	134/193 (69%)	132 (98%)	2 (2%)	57	70
6	E3	361/493 (73%)	361 (100%)	0	100	100
7	E4	367/378 (97%)	357 (97%)	10 (3%)	39	60
8	A5	52/73 (71%)	51 (98%)	1 (2%)	50	66
10	E6	372/454 (82%)	368 (99%)	4 (1%)	65	74
11	A8	118/161 (73%)	118 (100%)	0	100	100
13	BA	662/727 (91%)	657 (99%)	5 (1%)	73	77
14	EA	463/502 (92%)	460 (99%)	3 (1%)	78	80
16	BB	351/470 (75%)	347 (99%)	4 (1%)	65	74
17	EB	548/649 (84%)	543 (99%)	5 (1%)	70	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	EC	327/354 (92%)	322 (98%)	5 (2%)	57	70
19	BD	356/472 (75%)	355 (100%)	1 (0%)	86	85
20	ED	529/544 (97%)	525 (99%)	4 (1%)	73	77
21	AE	295/406 (73%)	292 (99%)	3 (1%)	68	75
22	BE	304/386 (79%)	302 (99%)	2 (1%)	76	78
23	EE	364/514 (71%)	361 (99%)	3 (1%)	73	77
24	AF	375/409 (92%)	369 (98%)	6 (2%)	55	69
25	BF	300/368 (82%)	295 (98%)	5 (2%)	53	68
26	EF	250/307 (81%)	250 (100%)	0	100	100
27	EG	134/136 (98%)	134 (100%)	0	100	100
28	BH	206/297 (69%)	202 (98%)	4 (2%)	50	66
29	EH	389/527 (74%)	387 (100%)	2 (0%)	81	82
30	AI	205/225 (91%)	203 (99%)	2 (1%)	68	75
31	BI	254/288 (88%)	253 (100%)	1 (0%)	84	83
33	BJ	208/298 (70%)	208 (100%)	0	100	100
34	AK	221/301 (73%)	218 (99%)	3 (1%)	59	71
35	BK	200/329 (61%)	196 (98%)	4 (2%)	48	65
37	BL	202/262 (77%)	201 (100%)	1 (0%)	81	82
38	EL	461/598 (77%)	455 (99%)	6 (1%)	61	71
39	EM	266/386 (69%)	262 (98%)	4 (2%)	57	70
41	AN	173/182 (95%)	173 (100%)	0	100	100
42	BN	142/265 (54%)	139 (98%)	3 (2%)	47	65
43	EN	564/640 (88%)	558 (99%)	6 (1%)	65	74
44	BO	162/225 (72%)	161 (99%)	1 (1%)	78	80
45	EO	232/263 (88%)	230 (99%)	2 (1%)	70	75
45	EP	211/263 (80%)	210 (100%)	1 (0%)	81	82
46	AP	277/330 (84%)	272 (98%)	5 (2%)	51	67
47	BQ	172/195 (88%)	171 (99%)	1 (1%)	78	80
48	AR	225/256 (88%)	224 (100%)	1 (0%)	84	83
49	BR	172/181 (95%)	169 (98%)	3 (2%)	53	68
50	ER	78/127 (61%)	77 (99%)	1 (1%)	61	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
51	BS	91/164 (56%)	89 (98%)	2 (2%)	45	64
52	ES	134/437 (31%)	134 (100%)	0	100	100
53	AT	123/124 (99%)	120 (98%)	3 (2%)	43	63
54	BT	151/163 (93%)	151 (100%)	0	100	100
55	ET	87/88 (99%)	87 (100%)	0	100	100
56	AU	151/184 (82%)	149 (99%)	2 (1%)	61	71
57	BU	134/168 (80%)	132 (98%)	2 (2%)	57	70
58	AV	153/158 (97%)	148 (97%)	5 (3%)	33	56
59	BV	79/163 (48%)	77 (98%)	2 (2%)	42	62
60	AW	246/246 (100%)	245 (100%)	1 (0%)	84	83
61	BW	164/164 (100%)	162 (99%)	2 (1%)	63	72
62	AX	153/221 (69%)	152 (99%)	1 (1%)	76	78
63	AY	305/337 (90%)	305 (100%)	0	100	100
64	BZ	148/160 (92%)	147 (99%)	1 (1%)	76	78
65	Ba	130/144 (90%)	129 (99%)	1 (1%)	73	77
66	Bb	113/135 (84%)	110 (97%)	3 (3%)	39	60
67	Bc	127/134 (95%)	125 (98%)	2 (2%)	55	69
68	Ae	110/172 (64%)	110 (100%)	0	100	100
69	Af	120/162 (74%)	118 (98%)	2 (2%)	53	68
70	Bf	77/98 (79%)	77 (100%)	0	100	100
71	Ag	170/239 (71%)	170 (100%)	0	100	100
72	E7	87/87 (100%)	87 (100%)	0	100	100
73	E8	112/678 (16%)	111 (99%)	1 (1%)	70	75
74	E9	177/292 (61%)	177 (100%)	0	100	100
75	Al	155/186 (83%)	154 (99%)	1 (1%)	78	80
79	Ao	151/1258 (12%)	150 (99%)	1 (1%)	76	78
80	Ap	229/267 (86%)	228 (100%)	1 (0%)	84	83
83	At	125/140 (89%)	124 (99%)	1 (1%)	73	77
84	Av	170/210 (81%)	169 (99%)	1 (1%)	78	80
All	All	17175/22967 (75%)	17011 (99%)	164 (1%)	65	75

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
45	EO	60	VAL
59	BV	32	VAL
46	AP	148	THR
51	BS	79	LEU
65	Ba	80	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 333 such sidechains are listed below:

Mol	Chain	Res	Type
47	BQ	143	GLN
64	BZ	147	ASN
48	AR	242	HIS
58	AV	143	GLN
68	Ae	115	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
12	AA	810/1176 (68%)	310 (38%)	3 (0%)

5 of 310 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
12	AA	2	U
12	AA	3	U
12	AA	4	U
12	AA	5	U
12	AA	11	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
12	AA	102	A
12	AA	484	U
12	AA	895	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 26 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
87	GTP	EA	1001	88,86	33,34,34	0.98	1 (3%)	50,54,54	1.56	9 (18%)
87	GTP	EA	1004	88,86	33,34,34	0.94	1 (3%)	50,54,54	1.57	8 (16%)
90	PM8	ER	200	50	26,31,31	0.52	0	30,38,38	1.35	2 (6%)
89	ATP	EB	1001	86	32,33,33	1.42	5 (15%)	48,52,52	1.75	9 (18%)
91	NAD	Av	301	-	46,48,48	0.57	1 (2%)	64,73,73	0.59	1 (1%)

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
87	GTP	EA	1001	88,86	-	0/22/38/38	0/3/3/3
87	GTP	EA	1004	88,86	-	1/22/38/38	0/3/3/3
90	PM8	ER	200	50	-	10/36/38/38	-
89	ATP	EB	1001	86	-	1/22/38/38	0/3/3/3
91	NAD	Av	301	-	-	4/30/62/62	0/5/5/5

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	EB	1001	ATP	C5-C4	4.65	1.47	1.39
89	EB	1001	ATP	C5-C6	2.73	1.48	1.41
89	EB	1001	ATP	C8-N7	2.35	1.36	1.31
91	Av	301	NAD	C2N-N1N	2.35	1.37	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
89	EB	1001	ATP	C5-N7	-2.31	1.34	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
89	EB	1001	ATP	C5-C4-N3	-5.91	118.58	126.72
87	EA	1004	GTP	C5-C4-N3	-5.01	120.42	128.39
87	EA	1004	GTP	C2-N3-C4	4.67	120.34	112.30
89	EB	1001	ATP	N3-C4-N9	4.62	135.02	127.17
87	EA	1001	GTP	C2-N3-C4	4.51	120.06	112.30

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
90	ER	200	PM8	O27-C28-C29-C30
90	ER	200	PM8	O27-C28-C29-C31
90	ER	200	PM8	O27-C28-C29-C32
90	ER	200	PM8	O33-C32-C34-N36
90	ER	200	PM8	N41-C42-C43-S1

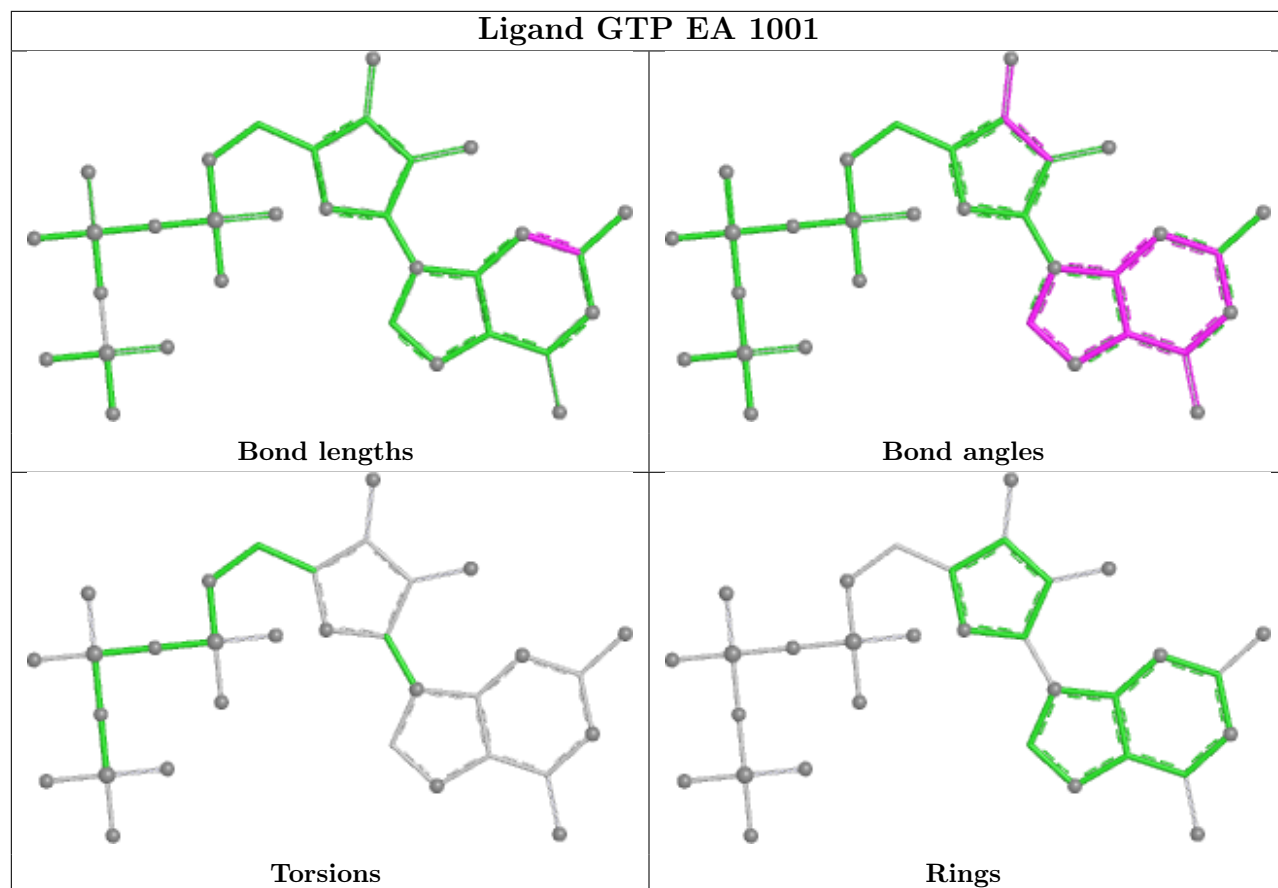
There are no ring outliers.

4 monomers are involved in 13 short contacts:

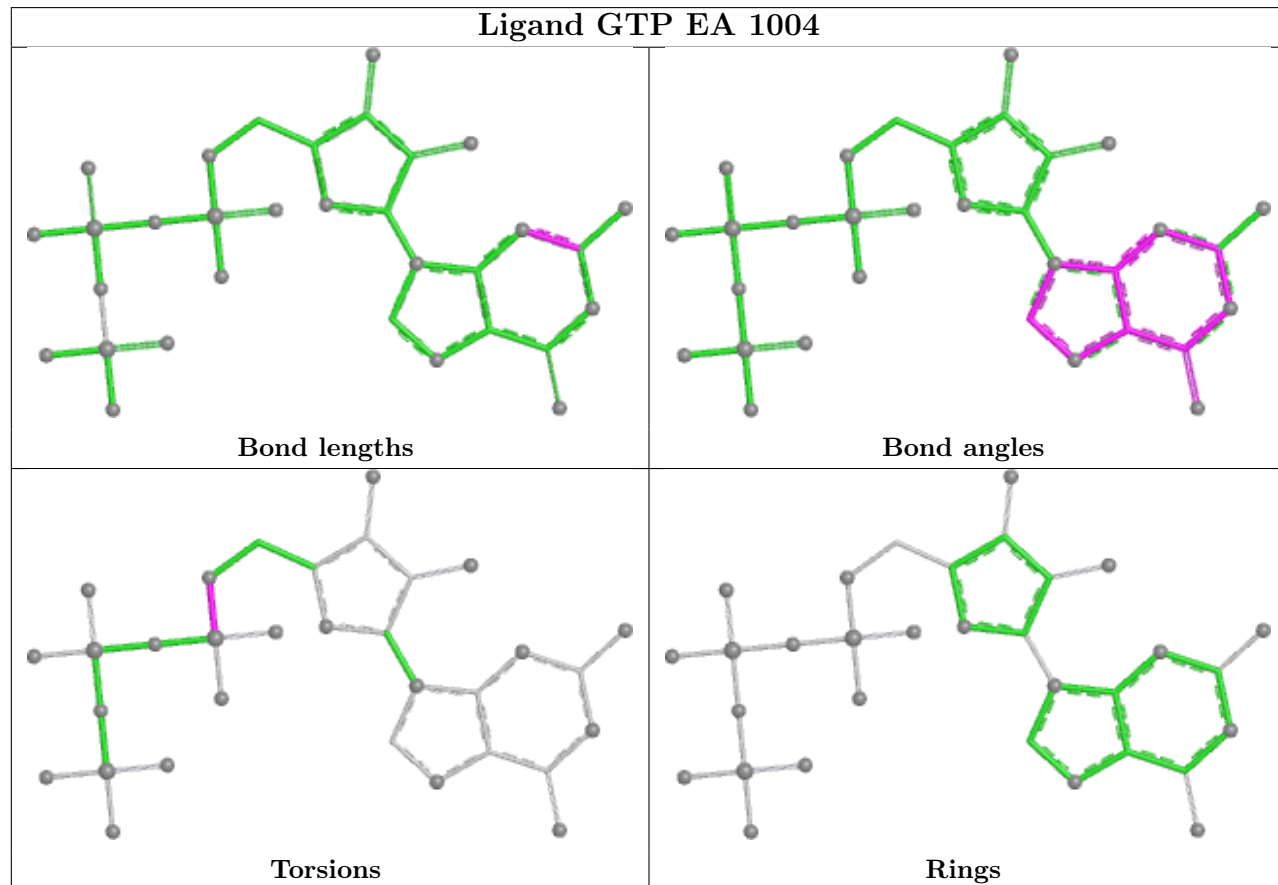
Mol	Chain	Res	Type	Clashes	Symm-Clashes
87	EA	1001	GTP	2	0
87	EA	1004	GTP	3	0
90	ER	200	PM8	5	0
89	EB	1001	ATP	3	0

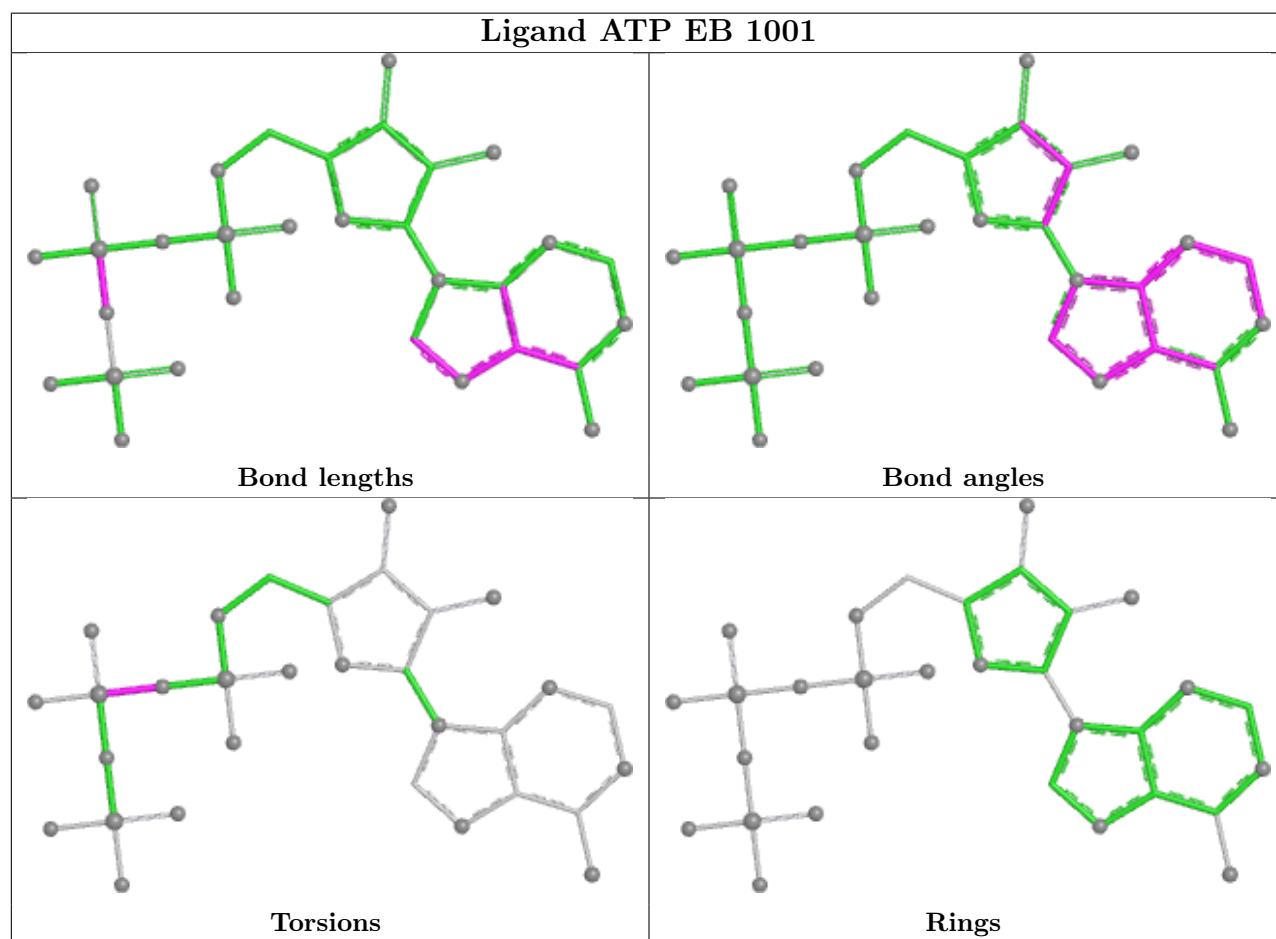
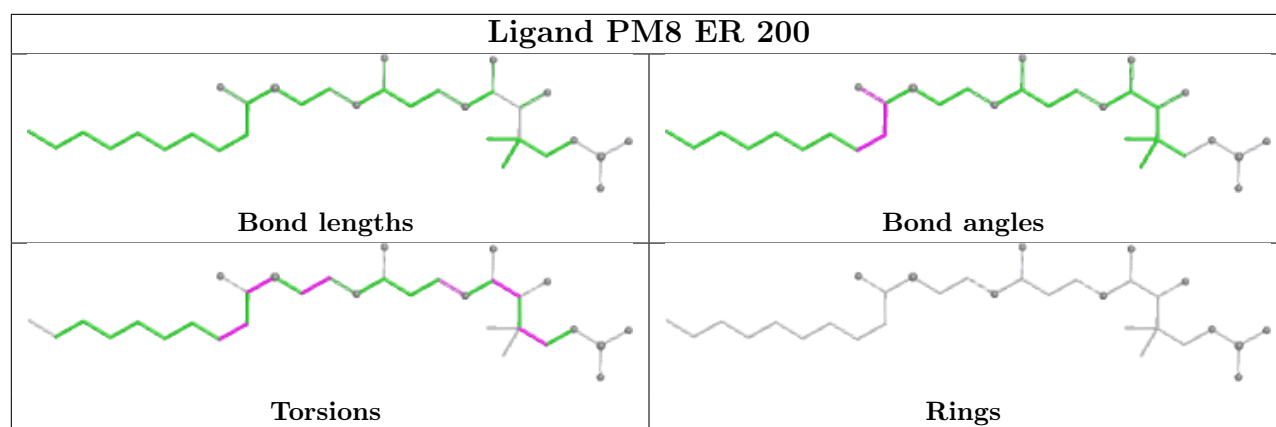
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

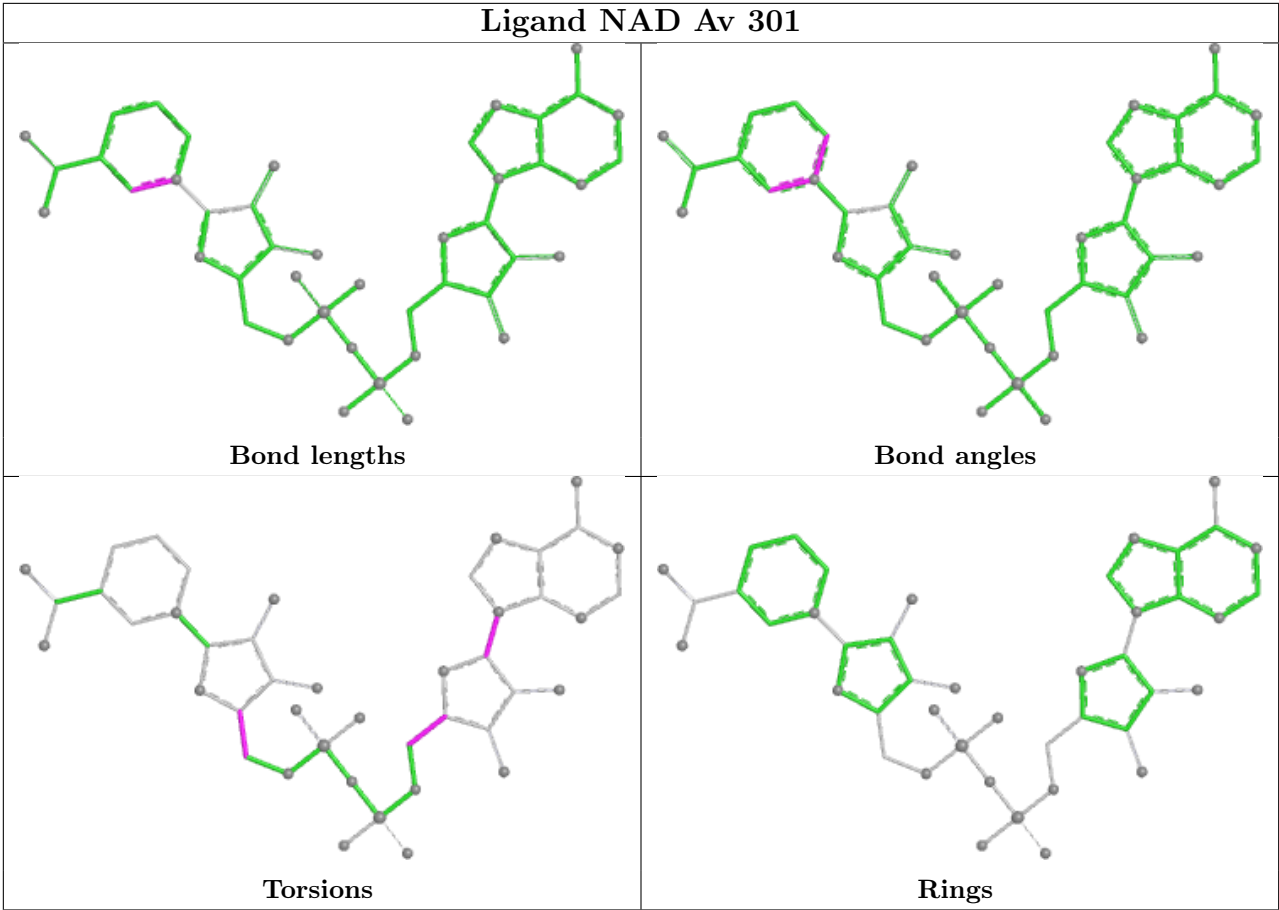
Ligand GTP EA 1001



Ligand GTP EA 1004







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
76	U1	7
9	E5	5
82	Us	4
81	Up	3
77	Um	1

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U1	249:UNK	C	280:UNK	N	50.91
1	U1	115:UNK	C	146:UNK	N	43.56

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U1	158:UNK	C	179:UNK	N	35.52
1	Us	63:UNK	C	82:UNK	N	32.92
1	U1	295:UNK	C	311:UNK	N	29.90

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10999. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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

7 Map analysis ⓘ

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

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

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

9 Map-model fit

This section was not generated.