



wwPDB EM Validation Summary Report ⓘ

Oct 12, 2024 – 10:51 pm BST

PDB ID : 6YXX
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:

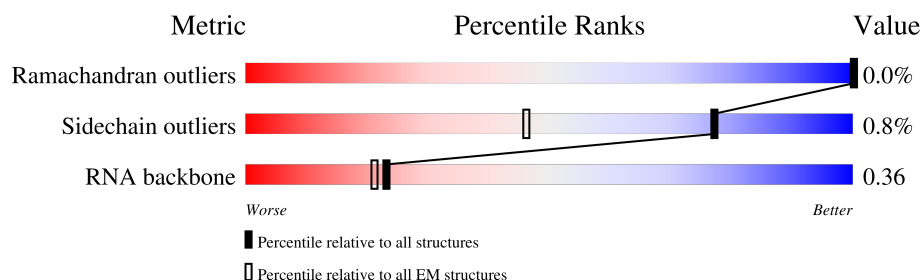
EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A1	241	<div> <div>6%</div> <div>89%</div> <div>10%</div> </div>
2	E1	482	<div> <div>14%</div> <div>97%</div> <div>..</div> </div>
3	A2	471	<div> <div>98%</div> <div>.</div> </div>
4	E2	568	<div> <div>8%</div> <div>65%</div> <div>35%</div> </div>
5	A3	218	<div> <div>69%</div> <div>31%</div> </div>
6	E3	557	<div> <div>6%</div> <div>72%</div> <div>28%</div> </div>
7	E4	439	<div> <div>5%</div> <div>96%</div> <div>..</div> </div>
8	A5	80	<div> <div>68%</div> <div>31%</div> </div>

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Mol	Chain	Length	Quality of chain
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	
31	BI	342	
32	UI	21	



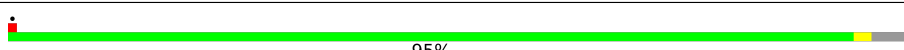
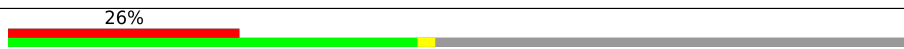
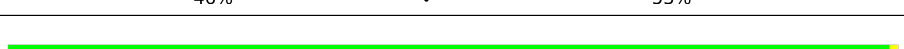
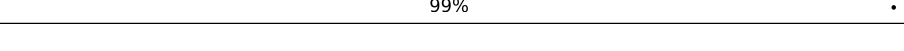
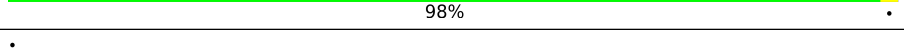

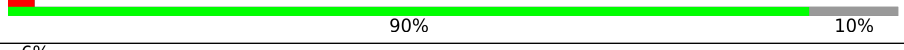
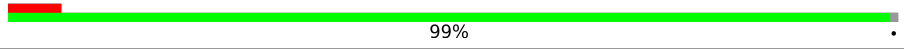
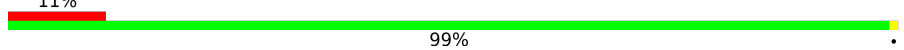

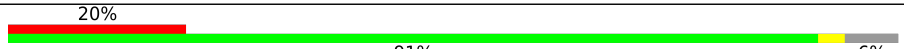


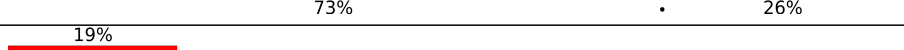


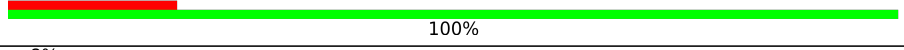




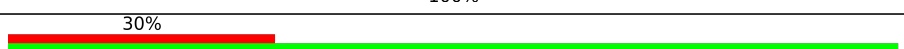
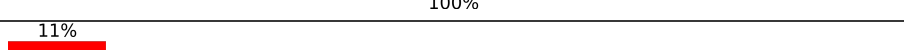
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Mol	Chain	Length	Quality of chain
32	Ur	21	100%
33	BJ	333	70%
34	AK	342	71%
35	BK	386	59%
36	UK	25	100%
37	BL	312	82%
38	EL	691	76%
39	EM	451	68%
40	UM	8	100%
41	AN	202	96%
42	BN	302	51%
43	EN	731	86%
44	BO	262	73%
45	EO	319	85%
45	EP	319	76%
46	AP	374	84%
47	BQ	231	94%
48	AR	301	88%
49	BR	205	94%
50	ER	148	56%
51	BS	198	79%
52	ES	524	29%
53	AT	144	98%
54	BT	191	91%
55	ET	102	99%

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Mol	Chain	Length	Quality of chain
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	
79	Ao	1520	
80	Ap	309	

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Mol	Chain	Length	Quality of chain
81	Up	87	<div> <div></div> <div>99%</div> <div>100%</div> </div>
82	Us	79	<div> <div></div> <div>97%</div> <div>100%</div> </div>
83	At	154	<div> <div></div> <div>89%</div> <div>10%</div> </div>
84	Av	242	<div> <div></div> <div>79%</div> <div>21%</div> </div>

2 Entry composition [i](#)

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		

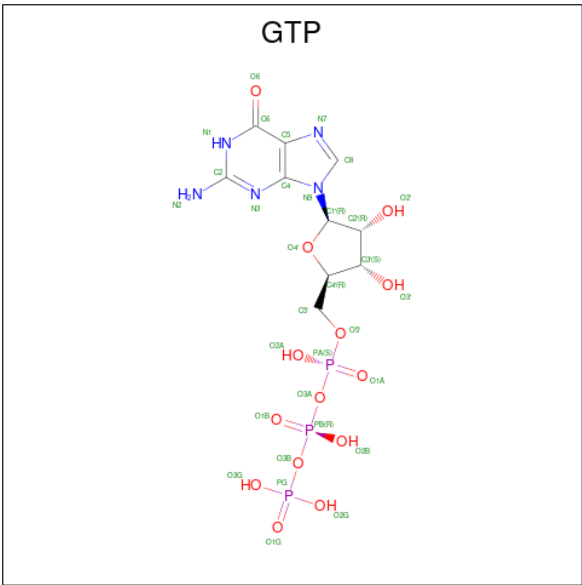
- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

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 (three-letter code: 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 (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

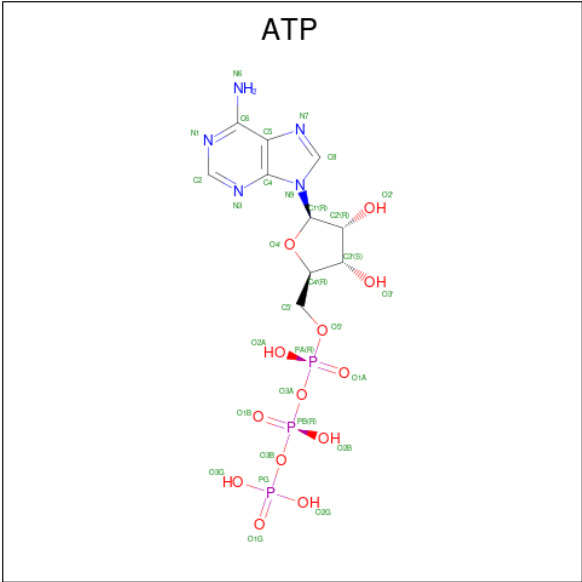


Mol	Chain	Residues	Atoms					AltConf
87	EA	1	Total	C	N	O	P	0
			32	10	5	14	3	
87	EA	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 88 is SODIUM ION (three-letter code: NA) (formula: Na).

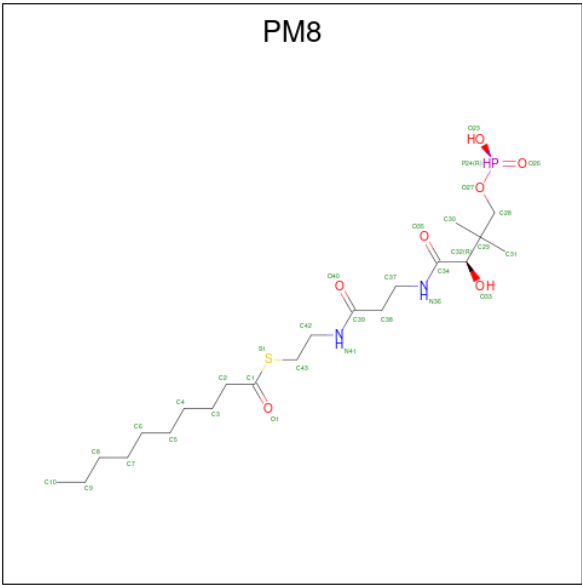
Mol	Chain	Residues	Atoms		AltConf
88	EA	2	Total	Na	0
			2	2	

- Molecule 89 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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 (three-letter code: PM8) (formula: C₂₁H₄₁N₂O₇PS).



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 (three-letter code: NAD)

NAD

The image displays the chemical structure of Nicotinamide Adenine Dinucleotide (NAD), a crucial coenzyme. The molecule is composed of two nucleotides linked by a pyrophosphate bridge. The top nucleotide consists of a nicotinamide ring (labeled with N1A, N2A, C3A, C4A, C5A, C6A) attached to a ribose sugar (labeled with C12R, C2R, C3R, C4R, C5R, C6R). The bottom nucleotide consists of an adenine ring (labeled with N1N, N2N, C3N, C4N, C5N, C6N) attached to a ribose sugar (labeled with C12R, C2R, C3R, C4R, C5R, C6R). The two ribose sugars are linked by a pyrophosphate bridge (labeled with C12R, C2R, C3R, C4R, C5R, C6R). The structure is shown in a 3D representation with various atoms and bonds labeled.

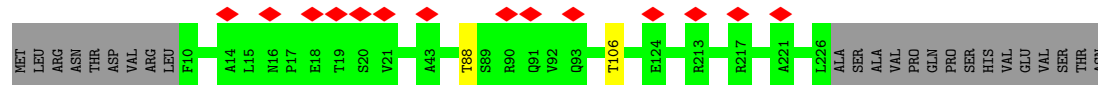
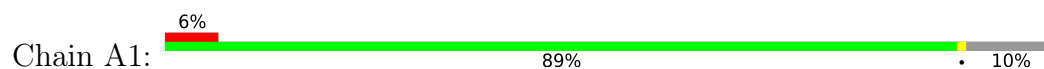
- Molecule 92 is water.



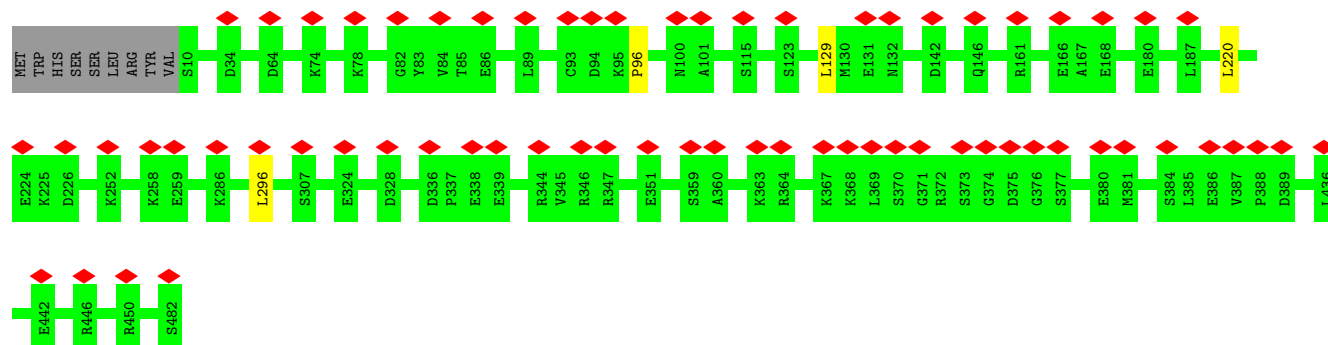
3 Residue-property plots [i](#)

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

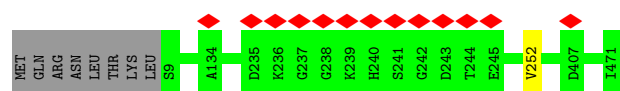
• Molecule 1: bL28m



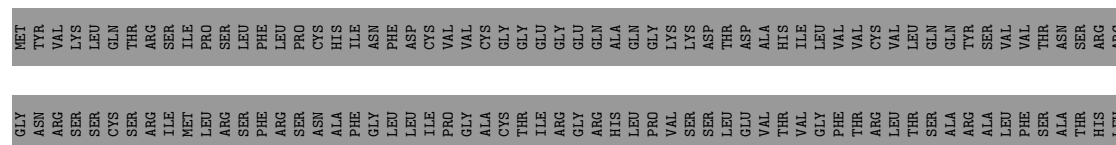
• Molecule 2: mt-LAF21

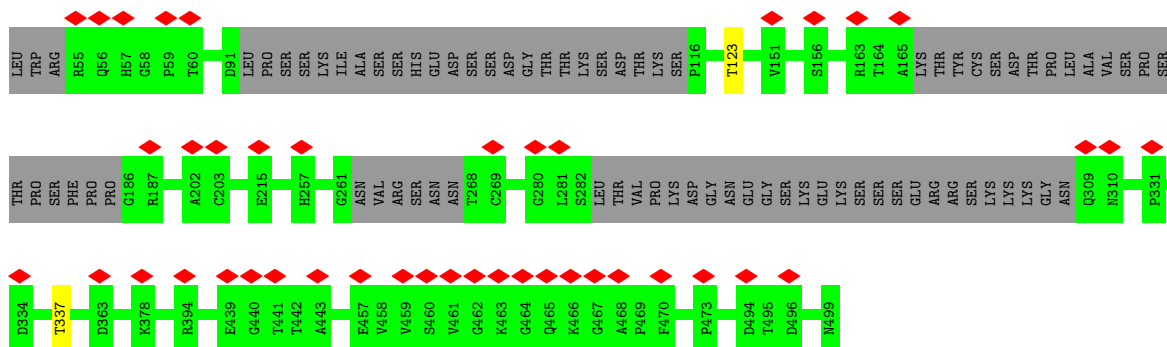


• Molecule 3: uL29m

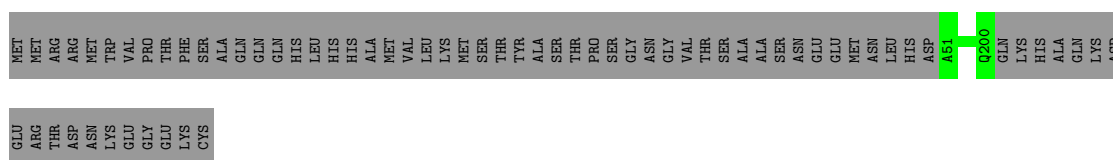


• Molecule 4: DUF4379 domain-containing protein

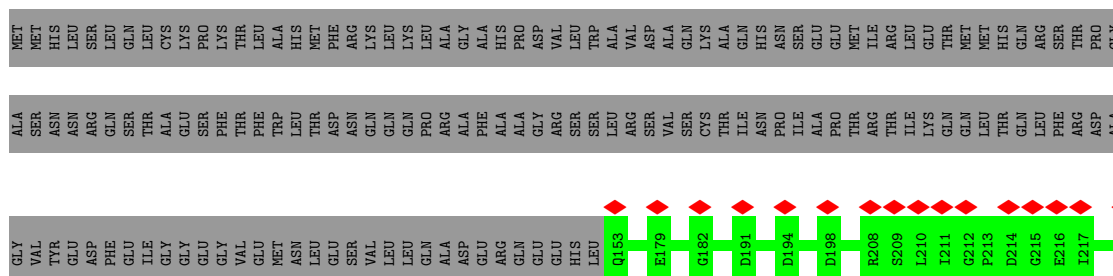
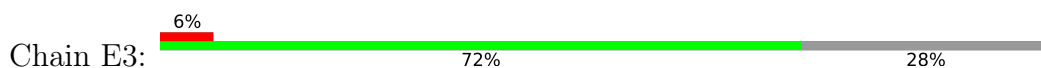




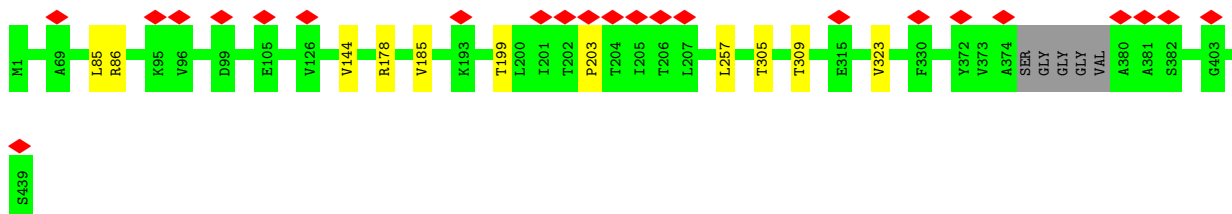
- Molecule 5: uL30m



- Molecule 6: mt-LAF23

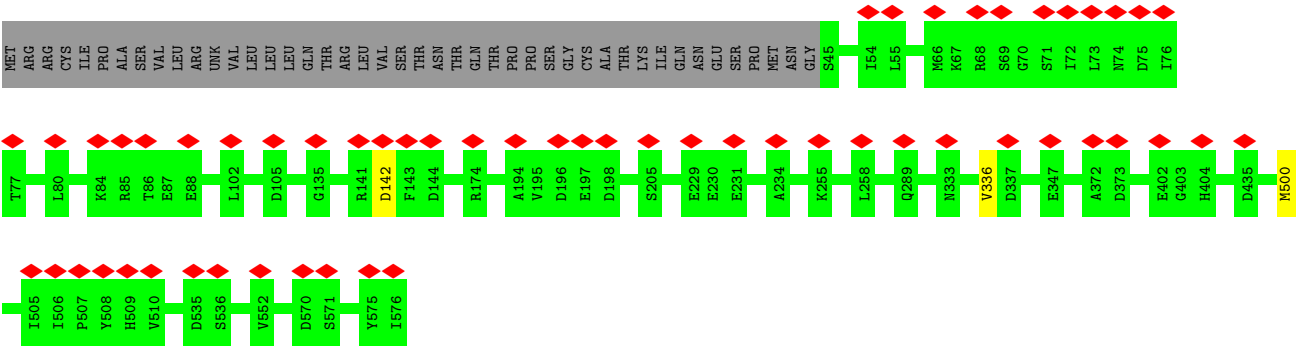
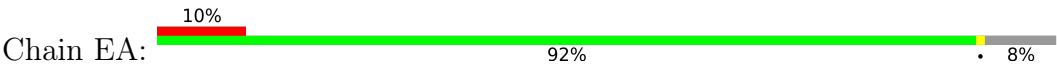


- Molecule 7: mt-LAF24



- Molecule 8: bL32m

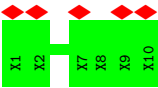




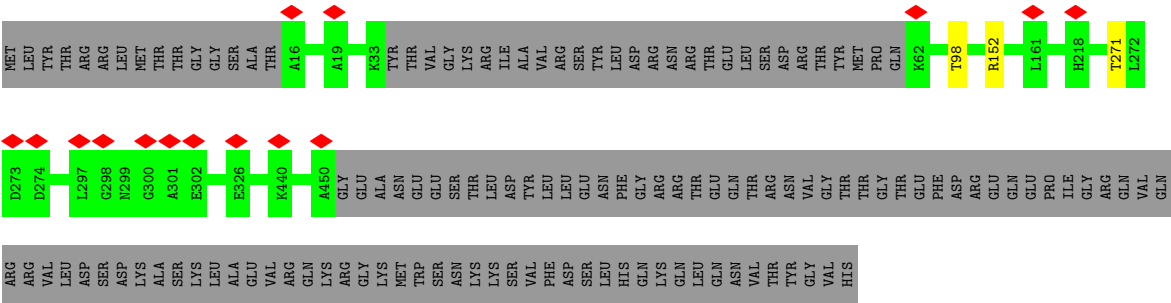
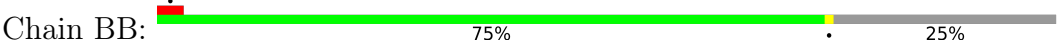
• Molecule 15: UNK



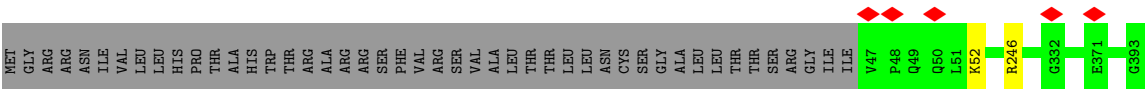
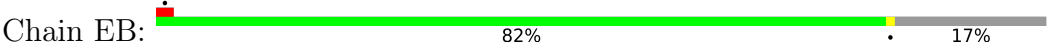
• Molecule 15: UNK



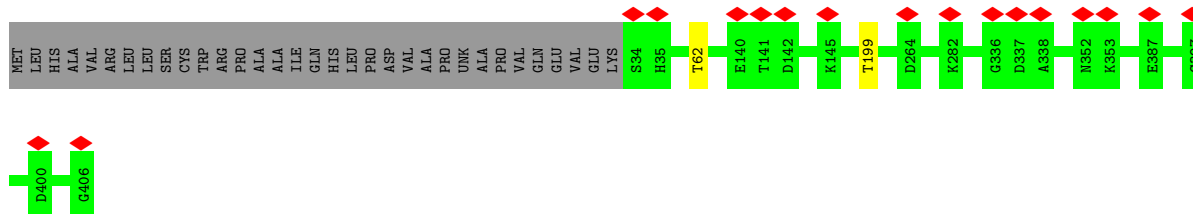
• Molecule 16: mL68



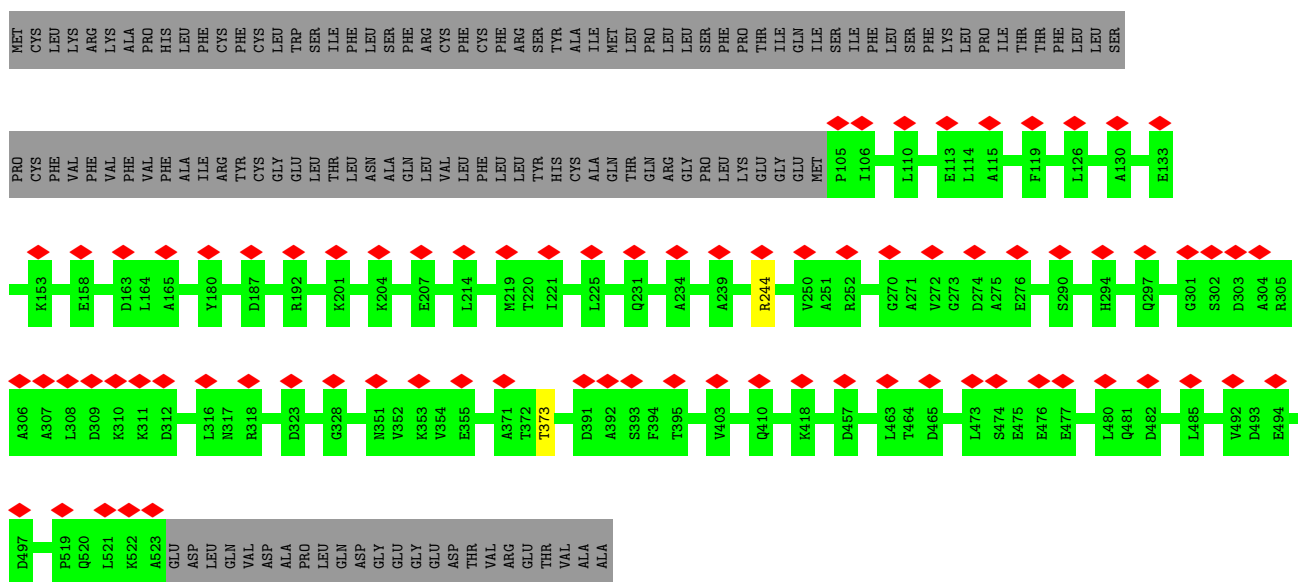
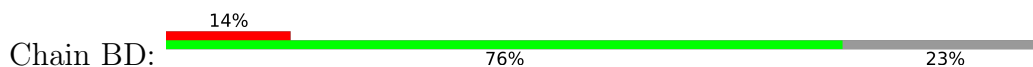
• Molecule 17: DEAD-box helicase, putative



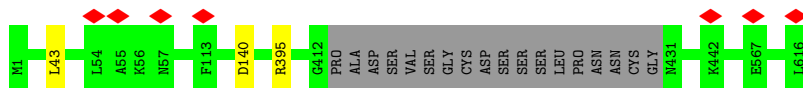
- Molecule 18: Pseudouridylate synthase, putative



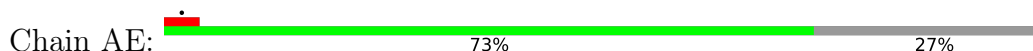
- Molecule 19: mL70

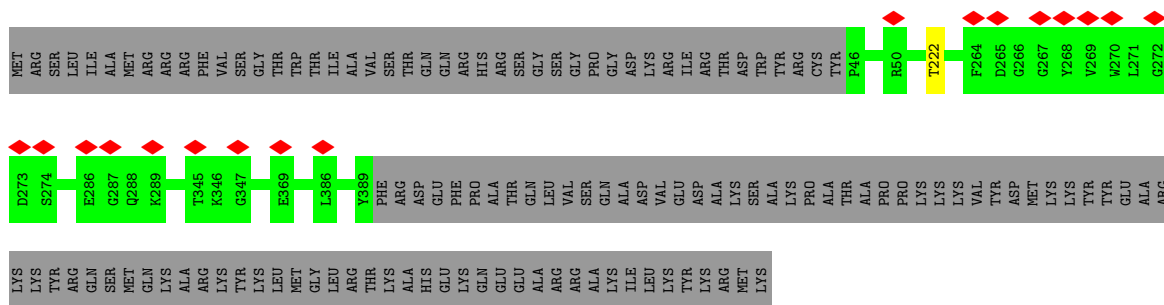


- Molecule 20: mt-LAF4

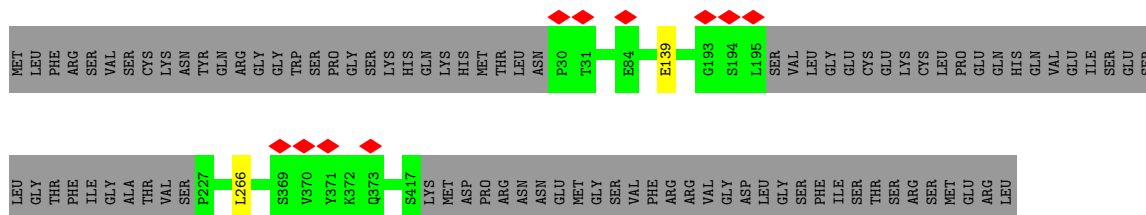
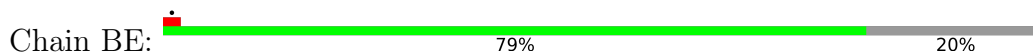


- Molecule 21: Ribosomal protein L3 mitochondrial, putative

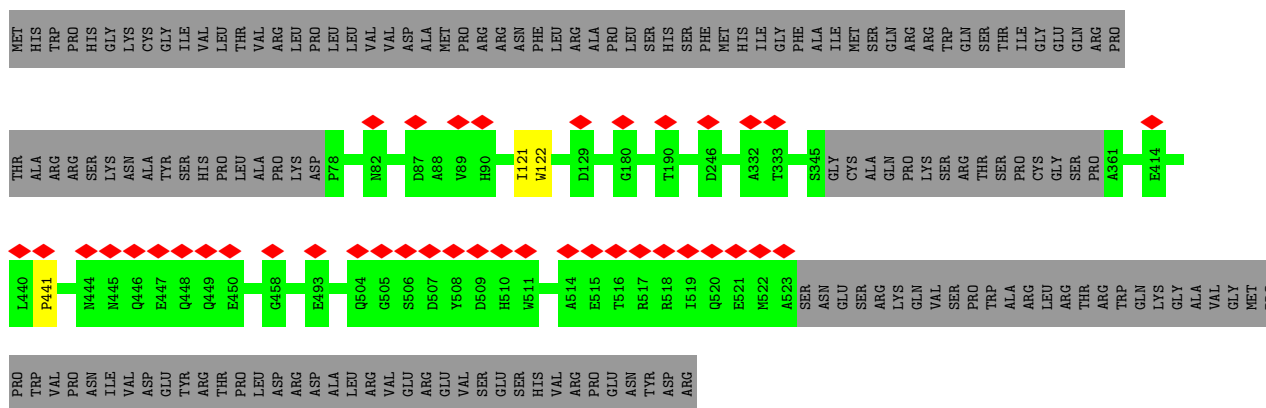
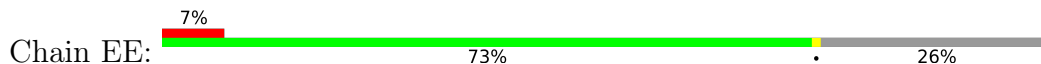




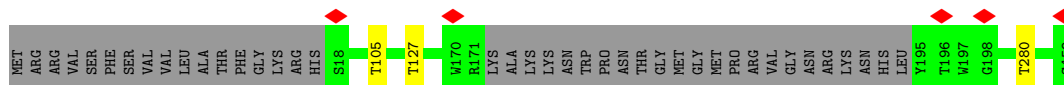
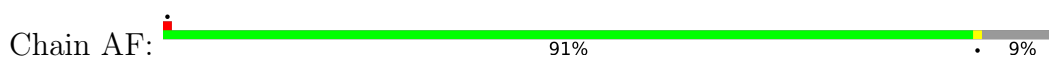
- Molecule 22: mL71



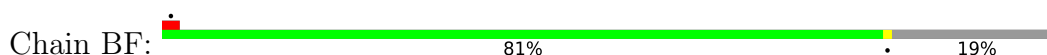
- Molecule 23: SpoU_methylase domain-containing protein

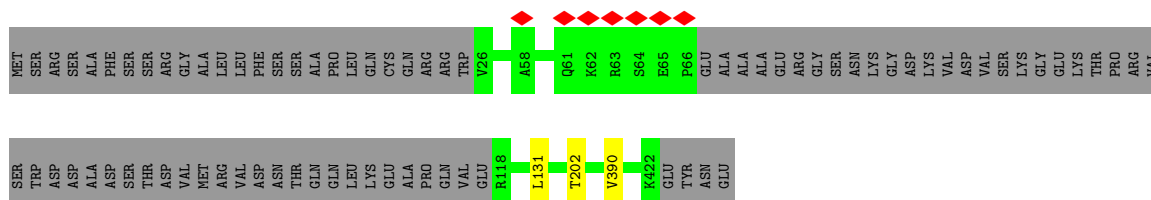


- Molecule 24: Ribosomal protein L4/L1 family, putative

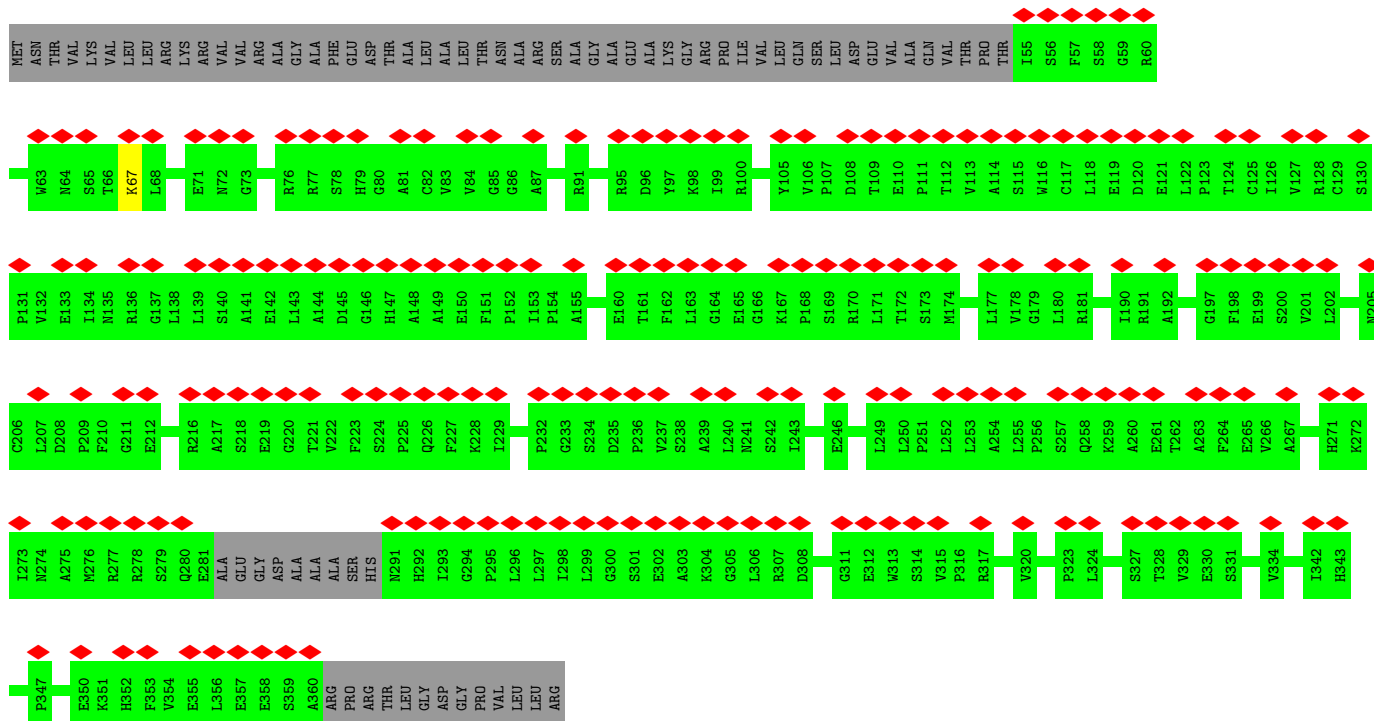
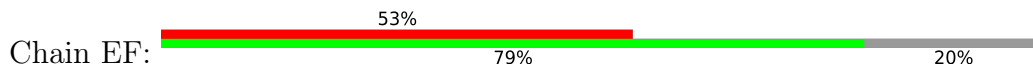


- Molecule 25: Tetratricopeptide repeat

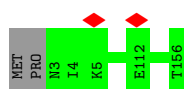




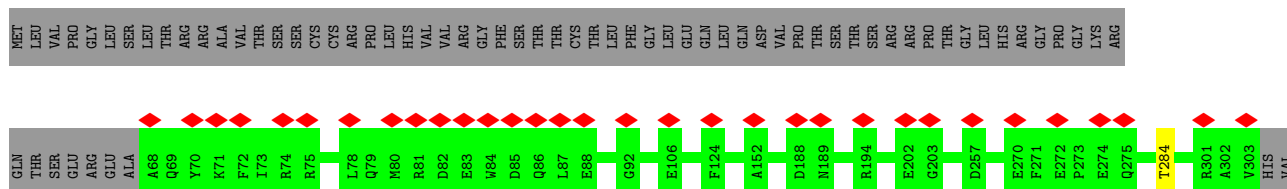
• Molecule 26: SpoU_methylase domain-containing protein

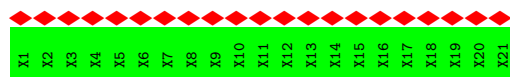


• Molecule 27: mt-LAF7

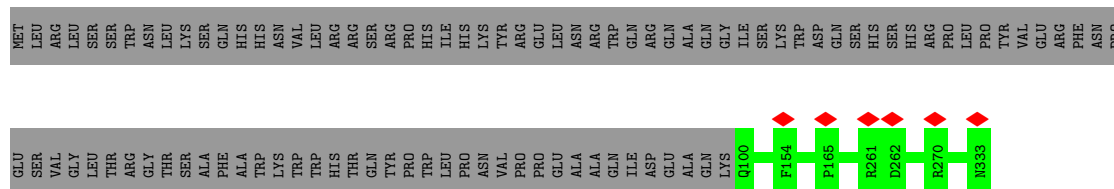


• Molecule 28: mL74

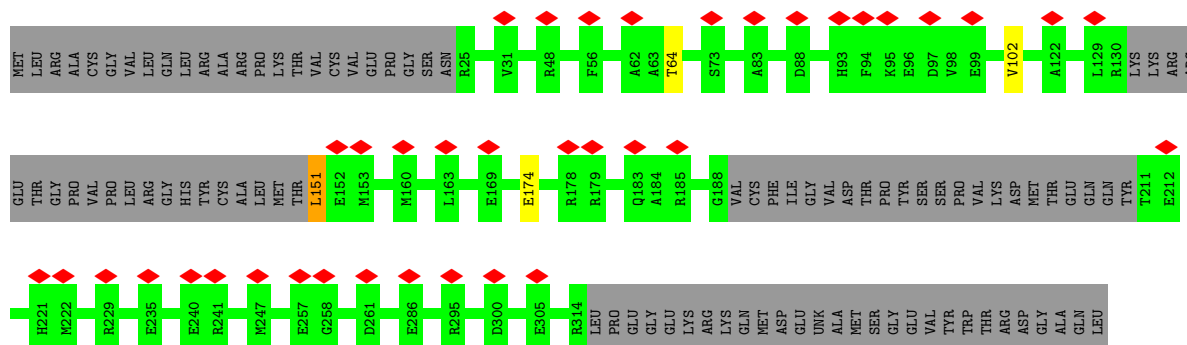
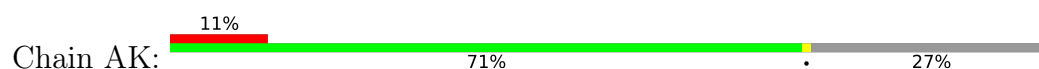




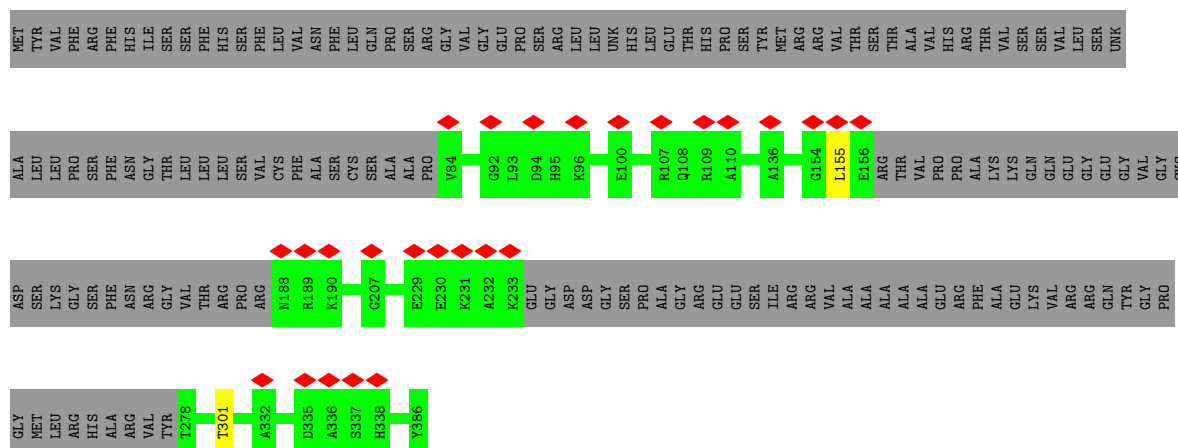
• Molecule 33: mL76



• Molecule 34: Ribosomal protein L11, putative



• Molecule 35: Chaperone protein DNAj, putative



• Molecule 36: UNK

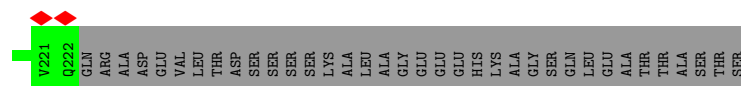
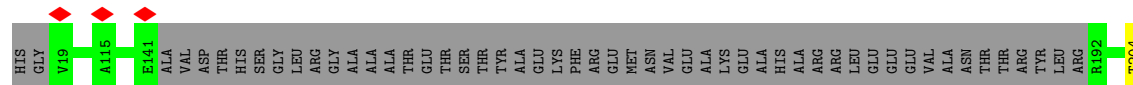


-

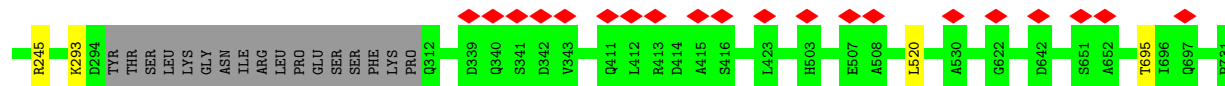
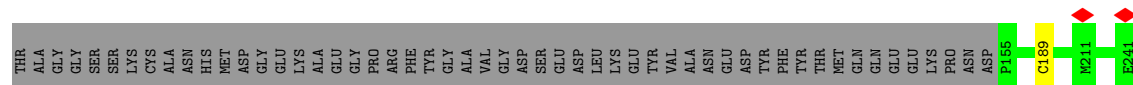
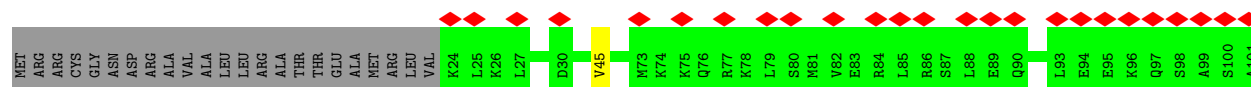
- Chain AN:  96%

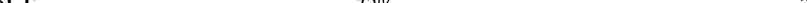


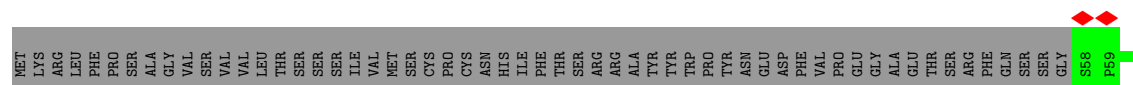
- Chain BN:  51% 49%



- Chain EN:  6% 86% 13%

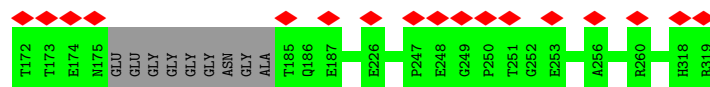
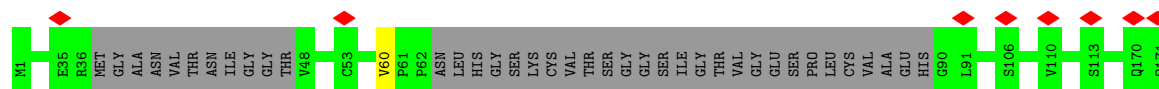
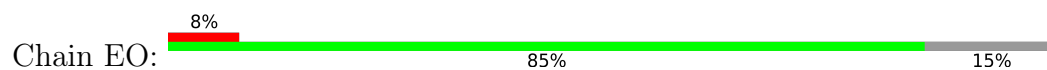


- Chain BO:  73% 27%

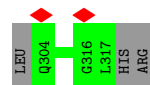
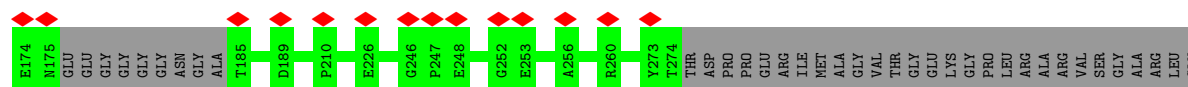
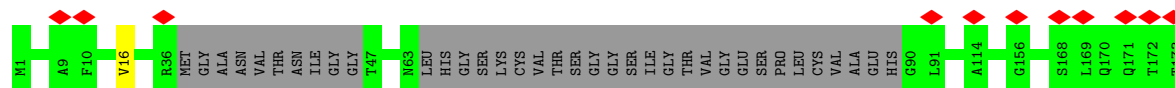
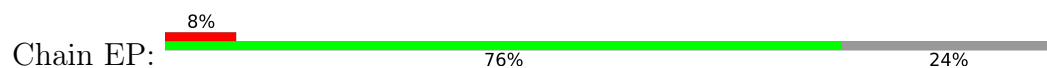




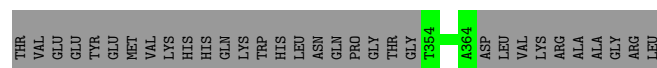
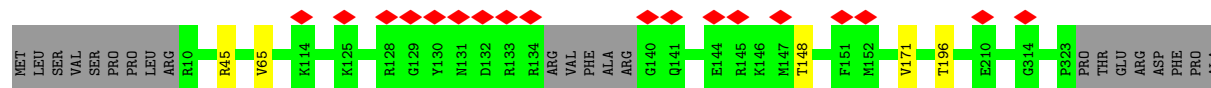
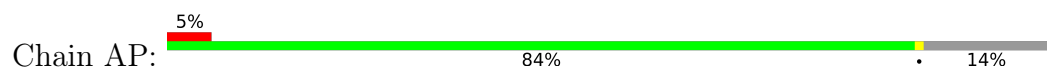
- Molecule 45: mt-LAF15a



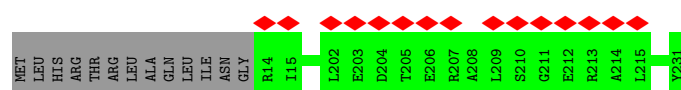
- Molecule 45: mt-LAF15a



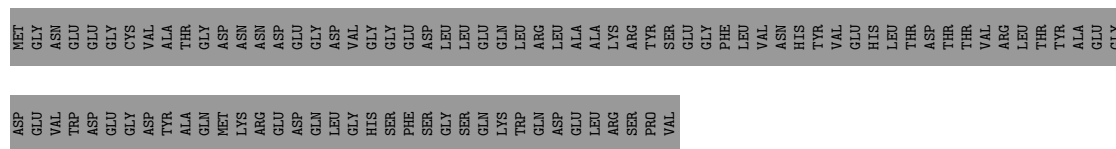
- Molecule 46: Ribosomal_L18e/L15P domain-containing protein



- Molecule 47: Peptidyl-prolyl cis-trans isomerase

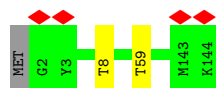


- Molecule 48: 50S ribosomal protein L17, putative



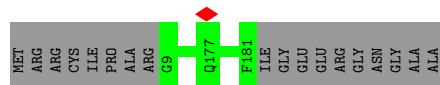
- Molecule 53: bL19m

Chain AT:



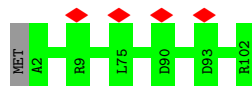
- Molecule 54: mL86

Chain BT:  91% 9%



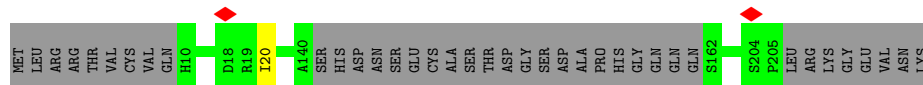
- Molecule 55: mt-LAF19

Chain ET:  99%

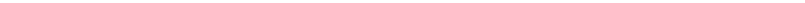


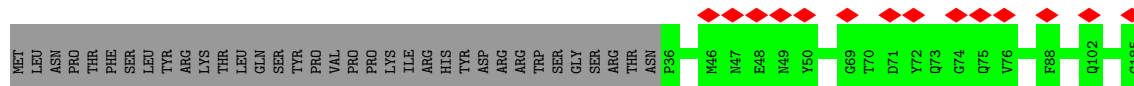
- Molecule 56: bL20m

Chain AU:



- Molecule 57: mL87

Chain BU: 

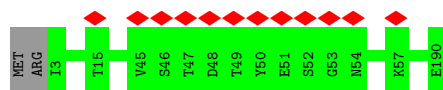


- Molecule 58: bL21m

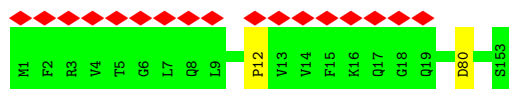
Chain AV:



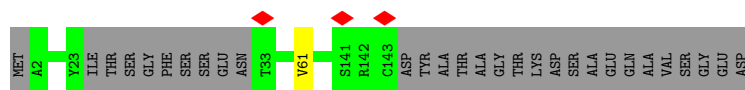
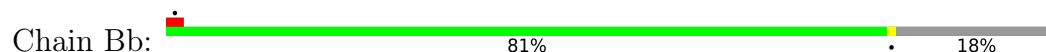
- Molecule 59: mL88



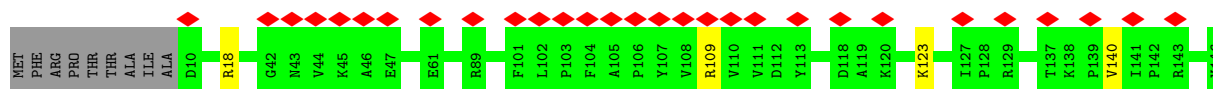
• Molecule 65: mL93



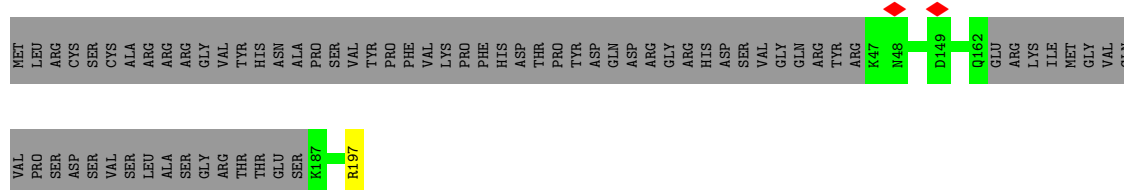
• Molecule 66: mL94



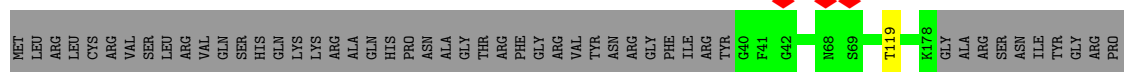
• Molecule 67: mL95



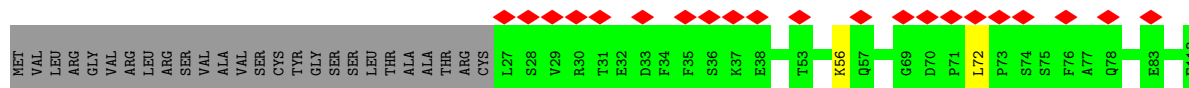
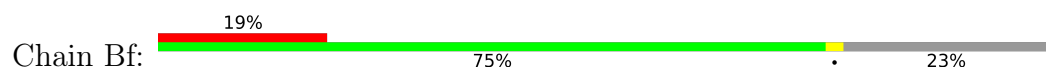
• Molecule 68: mL41



• Molecule 69: mL42



• Molecule 70: mL98



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

• Molecule 74: mt-LAF29



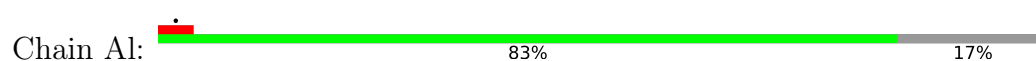
MET
PRO
HIS
GLN
SER
SER
SER
SER
LEU
GLN
GLN
SER
LYS
THR
SER
ASP
LYS
GLY
GLY
ALA
ALA
ARG
LEU
LEU
SER
PRO
GLN
SER
ASN
GLY
THR
SER
LEU
ILE
PRO
GLN
ASP
ARG
PRO
TYR
LEU
ALA
PRO
GLY
SER
MET
THR
TTR
ARG
GLY
PRO
LEU
LEU
LEU
ALA
ALA
LEU
MET
LEU
ASP
ASP
VAL
ARG
ARG
THR
LYS
PRO
THR
CYS
THR
PHE
VAL
LEU
PRO
ASN
SER

SER
GLY
VAL
VAL
GLU
GLU
MET
MET
VAL
SER
ASN
ALA
GLY
PHE
ASP
ASP
VAL
VAL
ARG
GLY
PRO
ALA
ALA
SER
GLY
SER
THR
SER
SER
VAL
ASP
GLY
TYR
LEU
VAL
PRO
THR
PRO
ARG
ARG
THR
LYS
LYS
LYS
ALA
ALA
MET
LEU
LEU
ALA
ALA
SER
SER
ARG
THR
PRO
THR
PHE
VAL
LEU
PRO
ASN
SER

ARG
SER
THR
ASP
GLY
GLU
GLY
GLY
ALA
ARG
GLN
GLN
ASN
ASP
ASP
ARG
ASP
GLY
THR
ASN
SER
SER
P144
Q145
L146
F147
S148
I149
E150
E153
T154
Q155
Q156
R157
A158
N161
E165
H169
D176
E182
E183
R184
R185
A186
Q189
S190
H191
Q192
R193
A194
P195
T196

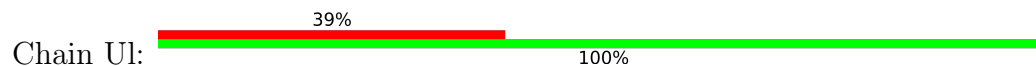
T197
K198
E199
V200
S201
D205
V206
A207
E231
R272
G273
E274
V275
A284
E285
A286
E287
K288
E289
R297
R298
R302
A316
N317
D318
L324
G343

• Molecule 75: mL49



MET
LEU
ASN
ARG
SER
ARG
LEU
ARG
ARG
VAL
TRP
GLY
GLY
THR
ALA
ALA
ASN
THR
SER
LEU
GLY
ARG
ASP
VAL
MET
PRO
SER
THR
GLY
LYS
TTR
ILE
ILE
ASN
ILE
VAL
SER
P38
Q101
R102
C103
Q104
E105
E106
P107
E108
A109
V113
F218

• Molecule 76: UNK



X1
X2
X3
X4
X5
X6
X7
X11
X21
X34
X35
X36
X37
X38
X39
X40
X41
X42
X43
X44
X45
X56
X57
X58
X59
X60
X66
X71
X77
X78
X79
X82
X85
X86
X89
X107
X111
X146
X147
X150
X151
X152
X153
X154
X155
X156
X157

X158
X179
X180
X186
X192
X193
X194
X197
X198
X199
X200
X201
X211
X214
X217
X218
X219
X220
X221
X232
X233
X234
X235
X236
X237
X249
X280
X281
X282
X283
X284
X285
X286
X287
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X295
X311
X312
X313
X314
X317
X318
X319
X326
X327
X332
X335

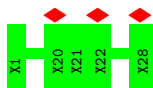
X336
X337
X348
X349
X350
X355
X356
X357
X358
X359
X360
X361
X362
X363

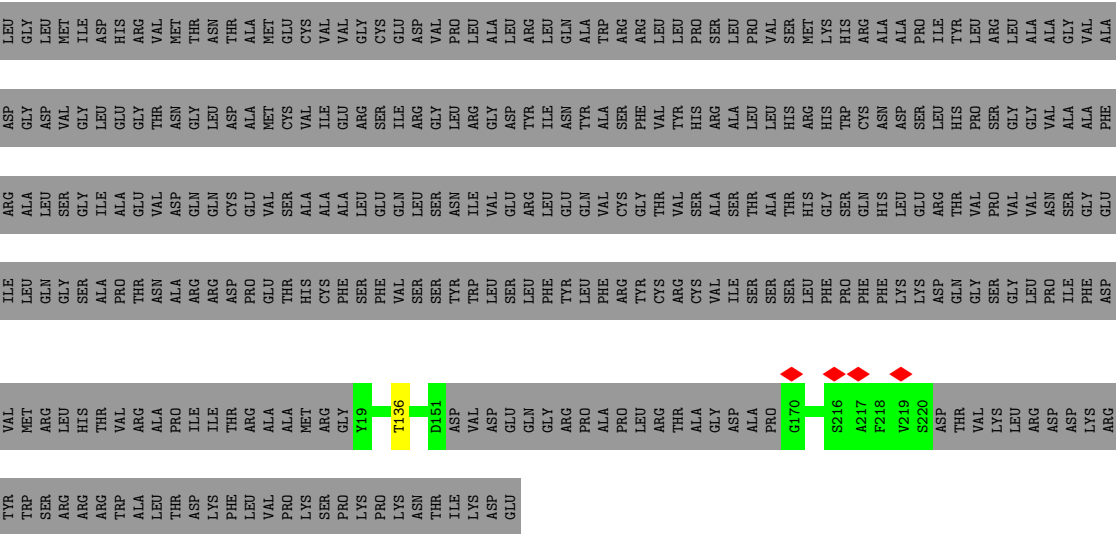
• Molecule 77: UNK



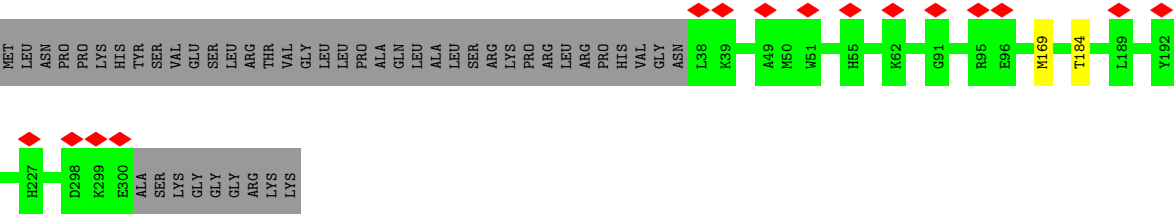
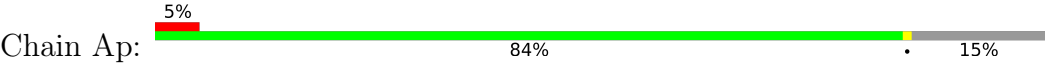
X1
X2
X10
X11
X12
X13
X14
X15
X104
X105

• Molecule 78: UNK

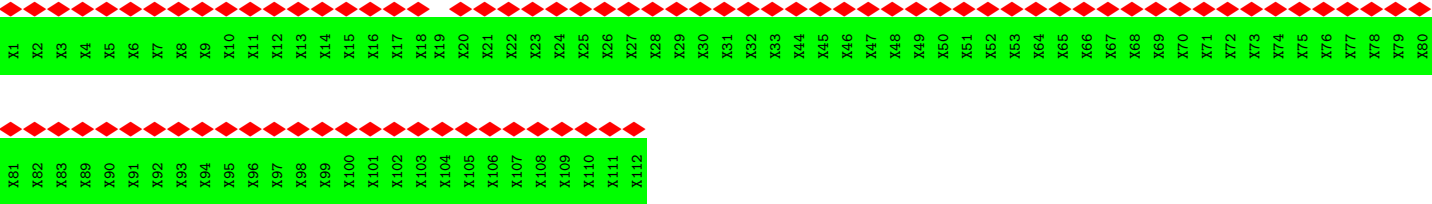
[illegible]



• Molecule 80: mL53



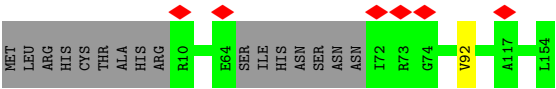
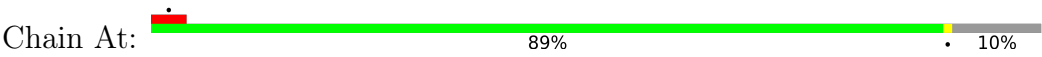
• Molecule 81: UNK



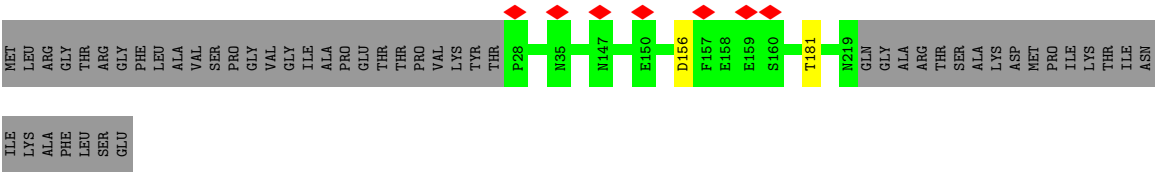
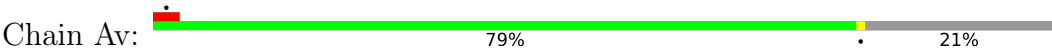
• Molecule 82: UNK



• 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
Maximum map value	0.197	Depositor
Minimum map value	-0.109	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	434.001, 434.001, 434.001	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.44667, 1.44667, 1.44667	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, GTP, ZN, NA, NAD, PM8, MG

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	0.24	0/1828	0.39	0/2466
2	E1	0.23	0/3906	0.39	1/5236 (0.0%)
3	A2	0.25	0/3844	0.39	0/5234
4	E2	0.23	0/3000	0.39	0/4067
5	A3	0.24	0/1246	0.39	0/1678
6	E3	0.24	0/3331	0.38	0/4491
7	E4	0.24	0/3491	0.43	1/4740 (0.0%)
8	A5	0.23	0/498	0.37	0/663
10	E6	0.23	0/3471	0.39	0/4710
11	A8	0.23	0/1163	0.38	0/1558
12	AA	0.18	0/19045	0.75	7/29609 (0.0%)
13	BA	0.24	0/6192	0.39	0/8401
14	EA	0.23	0/4337	0.39	0/5856
16	BB	0.24	0/3411	0.39	0/4622
17	EB	0.23	0/5154	0.39	0/6977
18	EC	0.25	0/3090	0.41	0/4190
19	BD	0.24	0/3418	0.40	0/4629
20	ED	0.24	0/4877	0.40	0/6607
21	AE	0.26	0/2897	0.41	0/3938
22	BE	0.24	0/2896	0.39	0/3929
23	EE	0.23	0/3489	0.40	1/4722 (0.0%)
24	AF	0.25	0/3517	0.39	0/4775
25	BF	0.25	0/2909	0.41	0/3920
26	EF	0.24	0/2316	0.42	0/3148
27	EG	0.25	0/1331	0.40	0/1784
28	BH	0.24	0/2005	0.40	0/2734
29	EH	0.24	0/3586	0.39	0/4864
30	AI	0.24	0/1980	0.38	0/2693
31	BI	0.24	0/2548	0.37	0/3449
33	BJ	0.23	0/1985	0.37	0/2681
34	AK	0.34	1/2141 (0.0%)	0.46	1/2886 (0.0%)
35	BK	0.24	0/1897	0.37	0/2556

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
37	BL	0.23	0/2055	0.38	0/2782
38	EL	0.24	0/4384	0.38	0/5967
39	EM	0.24	0/2480	0.39	0/3352
41	AN	0.24	0/1698	0.39	0/2308
42	BN	0.24	0/1353	0.40	0/1827
43	EN	0.23	0/5115	0.38	0/6936
44	BO	0.24	0/1518	0.38	0/2051
45	EO	0.24	0/2173	0.40	0/2956
45	EP	0.23	0/1953	0.39	0/2659
46	AP	0.23	0/2695	0.40	0/3657
47	BQ	0.25	0/1691	0.41	0/2293
48	AR	0.24	0/2279	0.39	0/3079
49	BR	0.25	0/1702	0.40	0/2296
50	ER	0.24	0/679	0.38	0/923
51	BS	0.24	0/1131	0.37	0/1547
52	ES	0.23	0/1276	0.37	0/1715
53	AT	0.24	0/1210	0.40	0/1632
54	BT	0.24	0/1465	0.39	0/1970
55	ET	0.25	0/858	0.38	0/1148
56	AU	0.24	0/1456	0.37	0/1971
57	BU	0.24	0/1315	0.39	0/1776
58	AV	0.25	0/1454	0.45	0/1973
59	BV	0.40	0/786	0.51	1/1063 (0.1%)
60	AW	0.24	0/2307	0.40	0/3119
61	BW	0.25	0/1612	0.37	0/2177
62	AX	0.25	0/1432	0.40	0/1947
63	AY	0.24	0/2846	0.39	0/3847
64	BZ	0.25	0/1422	0.42	0/1925
65	Ba	0.24	0/1329	0.41	1/1798 (0.1%)
66	Bb	0.24	0/1073	0.42	0/1454
67	Bc	0.24	0/1238	0.38	0/1685
68	Ae	0.24	0/1068	0.39	0/1447
69	Af	0.24	0/1134	0.40	0/1536
70	Bf	0.25	0/749	0.43	0/1012
71	Ag	0.24	0/1608	0.39	0/2180
72	E7	0.23	0/834	0.38	0/1118
73	E8	0.23	0/1202	0.40	0/1631
74	E9	0.23	0/1678	0.37	0/2257
75	Al	0.25	0/1484	0.39	0/2019
79	Ao	0.24	0/1486	0.39	0/2022
80	Ap	0.24	0/2231	0.39	0/3030
83	At	0.23	0/1179	0.39	0/1596
84	Av	0.24	0/1678	0.37	0/2261

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.24	1/183115 (0.0%)	0.45	13/251755 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	AK	174	GLU	CB-CG	-5.46	1.41	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	AK	151	LEU	CA-CB-CG	-7.51	98.02	115.30
12	AA	159	U	C2-N1-C1'	6.69	125.73	117.70
23	EE	441	PRO	N-CA-CB	6.20	110.73	103.30
2	E1	96	PRO	N-CA-CB	6.05	110.56	103.30
12	AA	159	U	N1-C2-O2	6.01	127.00	122.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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%)	44	75
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	A1	179/218 (82%)	177 (99%)	2 (1%)	0	100	100
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%)	193 (99%)	2 (1%)	73	81
2	E1	393/419 (94%)	390 (99%)	3 (1%)	79	84
3	A2	405/413 (98%)	404 (100%)	1 (0%)	92	94
4	E2	328/505 (65%)	326 (99%)	2 (1%)	84	88
5	A3	134/193 (69%)	134 (100%)	0	100	100
6	E3	361/493 (73%)	361 (100%)	0	100	100
7	E4	367/378 (97%)	357 (97%)	10 (3%)	40	60
8	A5	52/73 (71%)	51 (98%)	1 (2%)	52	70
10	E6	372/454 (82%)	369 (99%)	3 (1%)	79	84
11	A8	118/161 (73%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	BA	662/727 (91%)	659 (100%)	3 (0%)	86	90
14	EA	463/502 (92%)	460 (99%)	3 (1%)	84	88
16	BB	351/470 (75%)	348 (99%)	3 (1%)	75	83
17	EB	548/649 (84%)	543 (99%)	5 (1%)	75	83
18	EC	327/354 (92%)	325 (99%)	2 (1%)	84	88
19	BD	356/472 (75%)	354 (99%)	2 (1%)	84	88
20	ED	529/544 (97%)	526 (99%)	3 (1%)	84	88
21	AE	295/406 (73%)	294 (100%)	1 (0%)	91	92
22	BE	304/386 (79%)	302 (99%)	2 (1%)	81	86
23	EE	364/514 (71%)	363 (100%)	1 (0%)	91	92
24	AF	375/409 (92%)	372 (99%)	3 (1%)	79	84
25	BF	300/368 (82%)	297 (99%)	3 (1%)	73	81
26	EF	250/307 (81%)	249 (100%)	1 (0%)	89	91
27	EG	134/136 (98%)	134 (100%)	0	100	100
28	BH	206/297 (69%)	205 (100%)	1 (0%)	86	90
29	EH	389/527 (74%)	386 (99%)	3 (1%)	79	84
30	AI	205/225 (91%)	204 (100%)	1 (0%)	86	90
31	BI	254/288 (88%)	253 (100%)	1 (0%)	89	91
33	BJ	208/298 (70%)	208 (100%)	0	100	100
34	AK	221/301 (73%)	218 (99%)	3 (1%)	62	75
35	BK	200/329 (61%)	198 (99%)	2 (1%)	73	81
37	BL	202/262 (77%)	201 (100%)	1 (0%)	86	90
38	EL	461/598 (77%)	457 (99%)	4 (1%)	75	83
39	EM	266/386 (69%)	263 (99%)	3 (1%)	70	79
41	AN	173/182 (95%)	173 (100%)	0	100	100
42	BN	142/265 (54%)	141 (99%)	1 (1%)	81	86
43	EN	564/640 (88%)	558 (99%)	6 (1%)	70	79
44	BO	162/225 (72%)	161 (99%)	1 (1%)	84	88
45	EO	232/263 (88%)	231 (100%)	1 (0%)	89	91
45	EP	211/263 (80%)	210 (100%)	1 (0%)	86	90
46	AP	277/330 (84%)	272 (98%)	5 (2%)	54	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	BQ	172/195 (88%)	172 (100%)	0	100	100
48	AR	225/256 (88%)	224 (100%)	1 (0%)	89	91
49	BR	172/181 (95%)	169 (98%)	3 (2%)	56	72
50	ER	78/127 (61%)	77 (99%)	1 (1%)	65	76
51	BS	91/164 (56%)	87 (96%)	4 (4%)	24	48
52	ES	134/437 (31%)	134 (100%)	0	100	100
53	AT	123/124 (99%)	121 (98%)	2 (2%)	58	73
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%)	150 (99%)	1 (1%)	81	86
57	BU	134/168 (80%)	134 (100%)	0	100	100
58	AV	153/158 (97%)	150 (98%)	3 (2%)	50	68
59	BV	79/163 (48%)	77 (98%)	2 (2%)	42	62
60	AW	246/246 (100%)	244 (99%)	2 (1%)	79	84
61	BW	164/164 (100%)	161 (98%)	3 (2%)	54	71
62	AX	153/221 (69%)	153 (100%)	0	100	100
63	AY	305/337 (90%)	305 (100%)	0	100	100
64	BZ	148/160 (92%)	148 (100%)	0	100	100
65	Ba	130/144 (90%)	129 (99%)	1 (1%)	79	84
66	Bb	113/135 (84%)	112 (99%)	1 (1%)	75	83
67	Bc	127/134 (95%)	123 (97%)	4 (3%)	35	56
68	Ae	110/172 (64%)	109 (99%)	1 (1%)	75	83
69	Af	120/162 (74%)	119 (99%)	1 (1%)	79	84
70	Bf	77/98 (79%)	75 (97%)	2 (3%)	41	61
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%)	75	83
74	E9	177/292 (61%)	175 (99%)	2 (1%)	70	79
75	Al	155/186 (83%)	155 (100%)	0	100	100
79	Ao	151/1258 (12%)	150 (99%)	1 (1%)	81	86
80	Ap	229/267 (86%)	227 (99%)	2 (1%)	75	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	At	125/140 (89%)	124 (99%)	1 (1%)	79	84
84	Av	170/210 (81%)	168 (99%)	2 (1%)	67	78
All	All	17175/22967 (75%)	17046 (99%)	129 (1%)	77	84

5 of 129 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
67	Bc	140	VAL
70	Bf	72	LEU
24	AF	127	THR
24	AF	105	THR
74	E9	298	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 267 such sidechains are listed below:

Mol	Chain	Res	Type
67	Bc	66	HIS
71	Ag	73	ASN
80	Ap	150	HIS
23	EE	429	HIS
23	EE	160	HIS

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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
90	PM8	ER	200	50	25,31,31	0.54	0	30,38,38	1.34	2 (6%)
87	GTP	EA	1001	86,88	26,34,34	1.18	2 (7%)	32,54,54	1.54	7 (21%)
87	GTP	EA	1004	86,88	26,34,34	1.14	2 (7%)	32,54,54	1.46	7 (21%)
89	ATP	EB	1001	86	26,33,33	0.94	1 (3%)	31,52,52	1.50	5 (16%)
91	NAD	Av	301	-	42,48,48	0.64	1 (2%)	50,73,73	0.91	3 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
90	PM8	ER	200	50	-	11/36/38/38	-
87	GTP	EA	1001	86,88	-	0/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
87	GTP	EA	1004	86,88	-	2/18/38/38	0/3/3/3
89	ATP	EB	1001	86	-	1/18/38/38	0/3/3/3
91	NAD	Av	301	-	-	3/26/62/62	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	EA	1001	GTP	C5-C6	-4.04	1.39	1.47
87	EA	1004	GTP	C5-C6	-3.96	1.39	1.47
89	EB	1001	ATP	C5-C4	2.44	1.47	1.40
87	EA	1004	GTP	C2-N3	2.16	1.38	1.33
91	Av	301	NAD	C2N-N1N	2.14	1.37	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
91	Av	301	NAD	O4D-C1D-C2D	-3.72	101.48	106.93
89	EB	1001	ATP	PA-O3A-PB	-3.71	120.09	132.83
87	EA	1004	GTP	PB-O3B-PG	-3.57	120.56	132.83
87	EA	1001	GTP	PB-O3B-PG	-3.52	120.74	132.83
87	EA	1001	GTP	PA-O3A-PB	-3.27	121.61	132.83

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

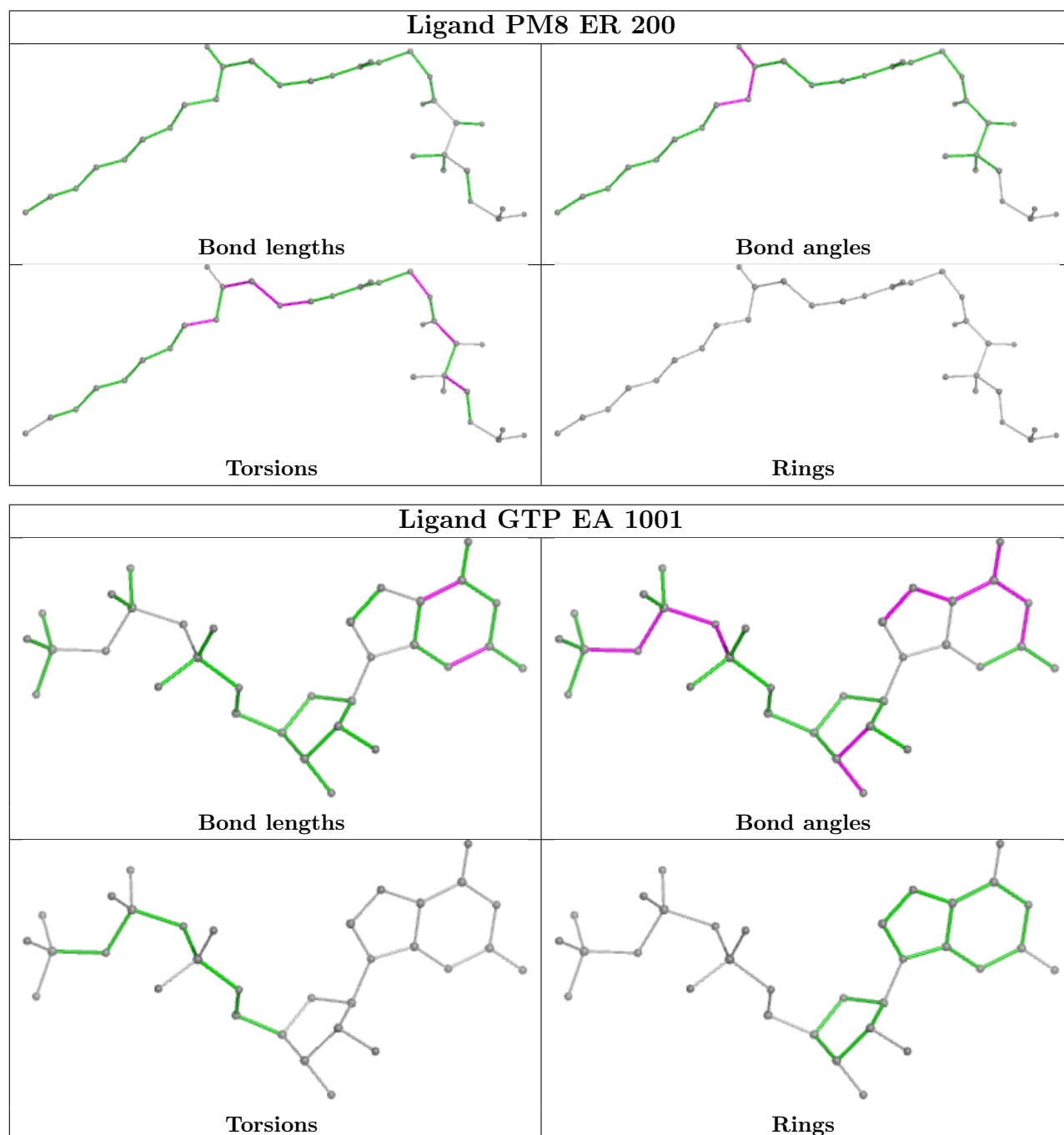
Mol	Chain	Res	Type	Atoms
90	ER	200	PM8	O27-C28-C29-C32
90	ER	200	PM8	O33-C32-C34-N36
90	ER	200	PM8	N41-C42-C43-S1
90	ER	200	PM8	O1-C1-S1-C43
90	ER	200	PM8	C2-C1-S1-C43

There are no ring outliers.

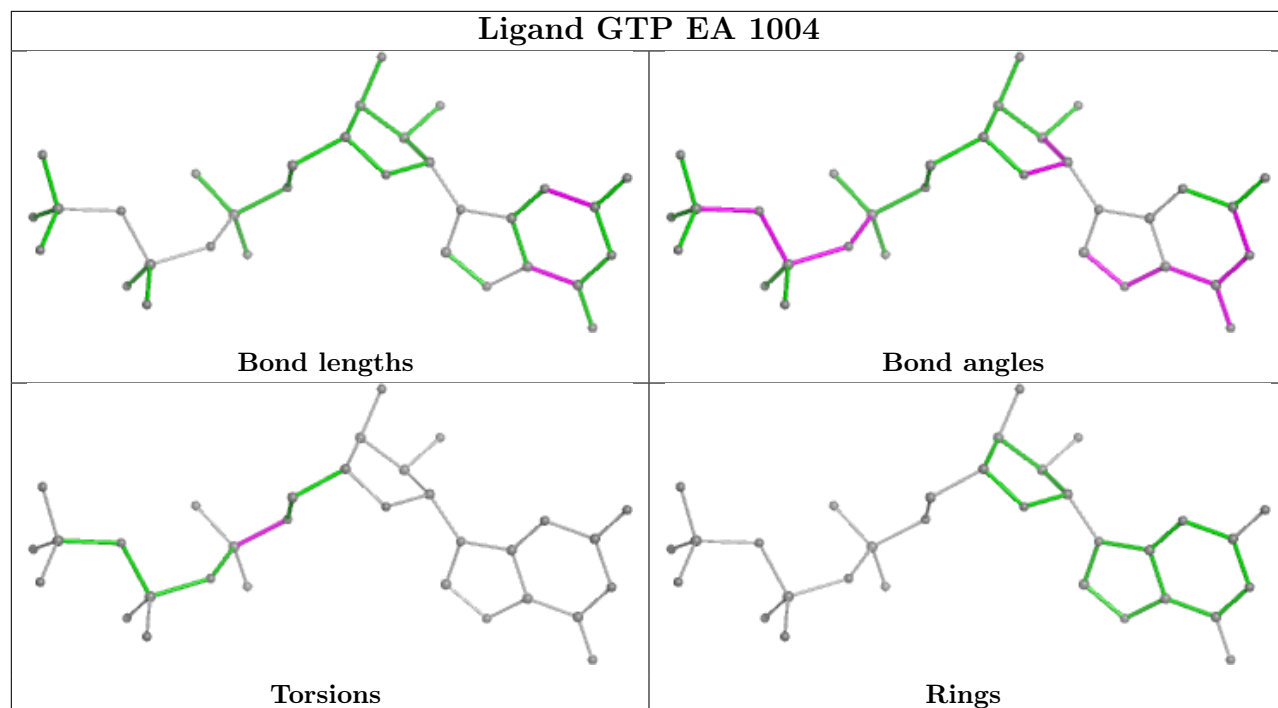
No monomer is involved in short contacts.

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

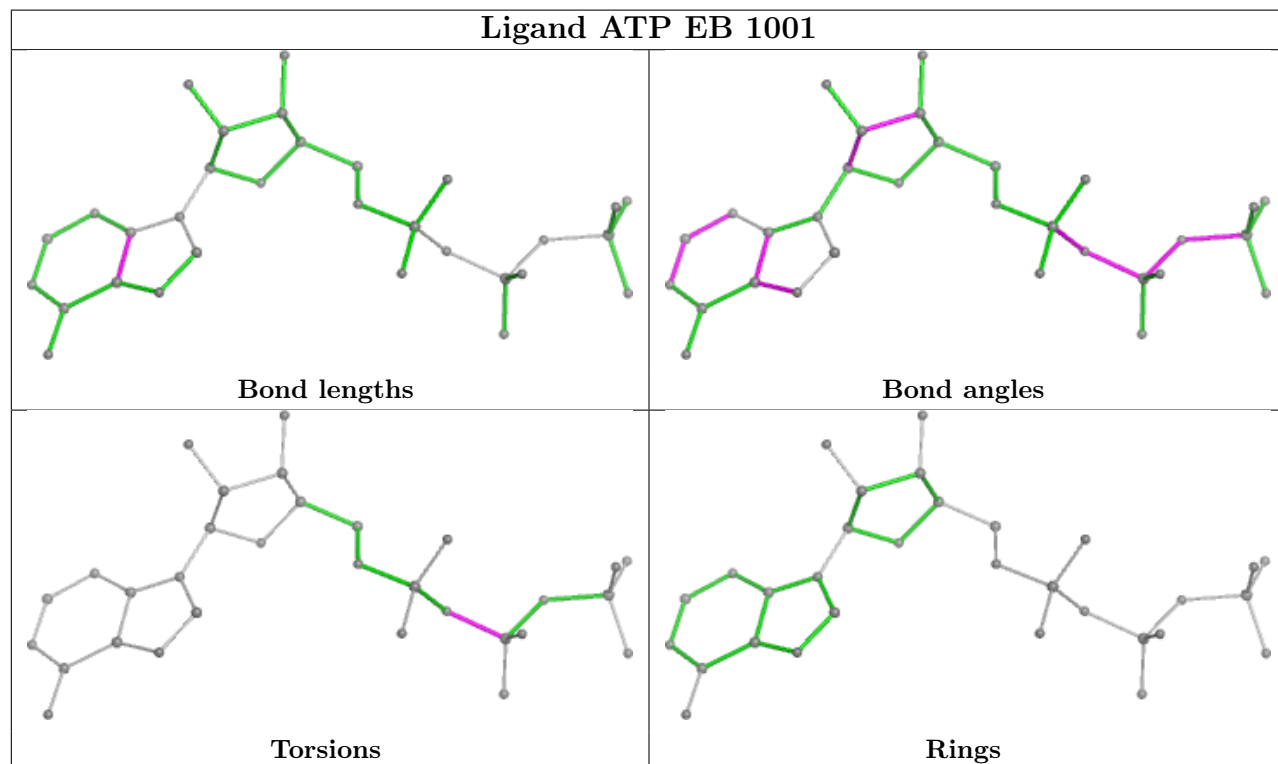
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

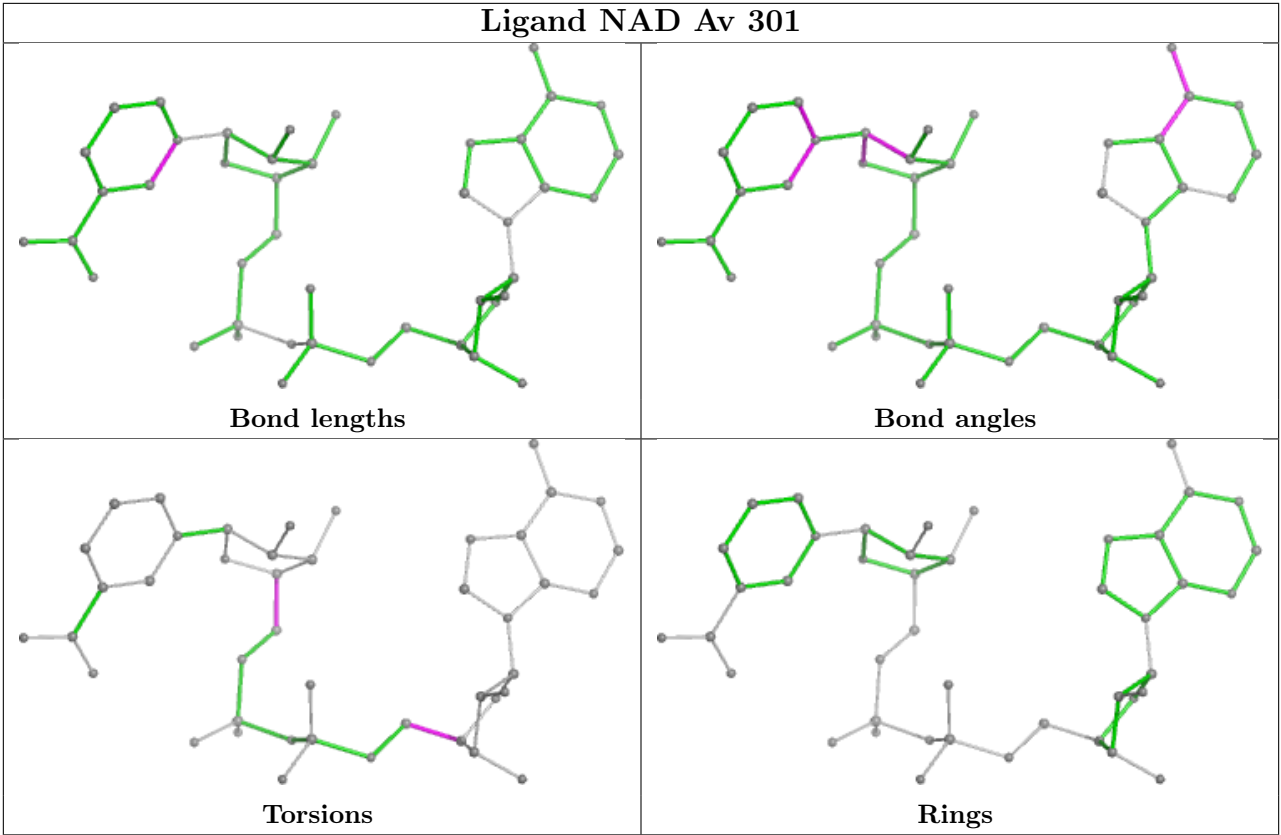


Ligand GTP EA 1004



Ligand ATP EB 1001





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
1	U1	158:UNK	C	179:UNK	N	35.52

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

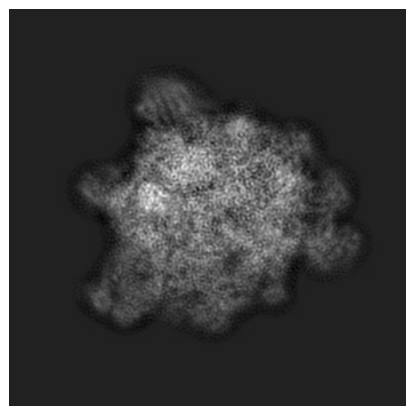
6 Map visualisation [i](#)

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.

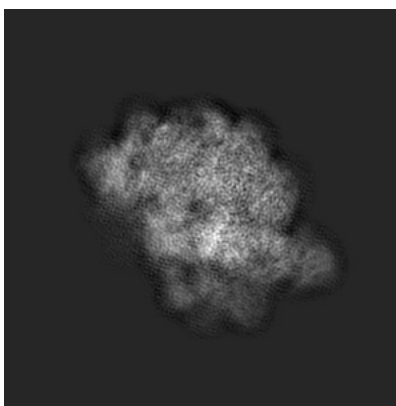
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

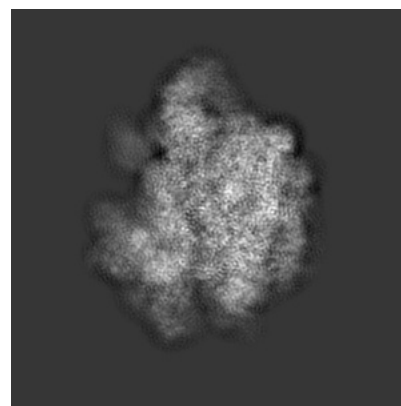
6.1.1 Primary map



X

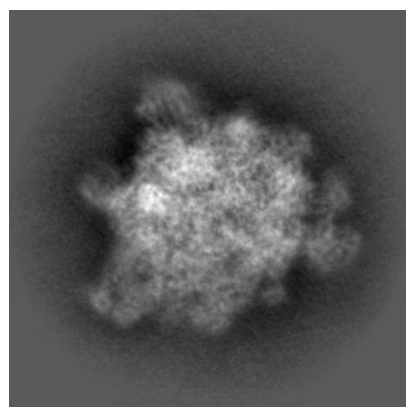


Y

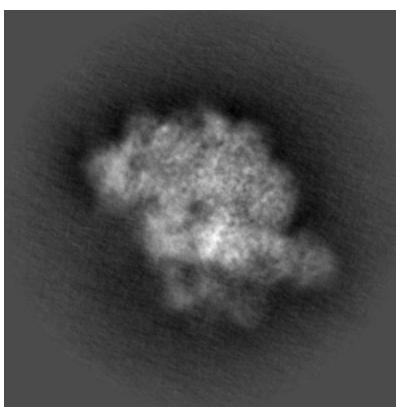


Z

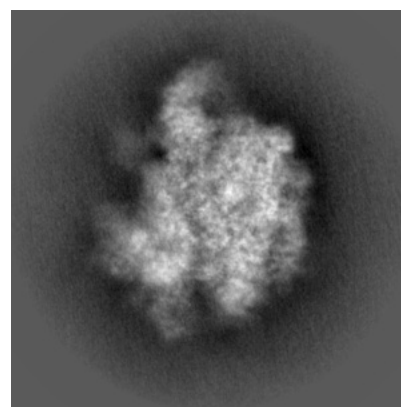
6.1.2 Raw map



X



Y

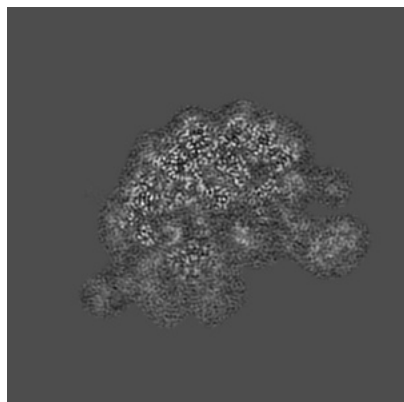


Z

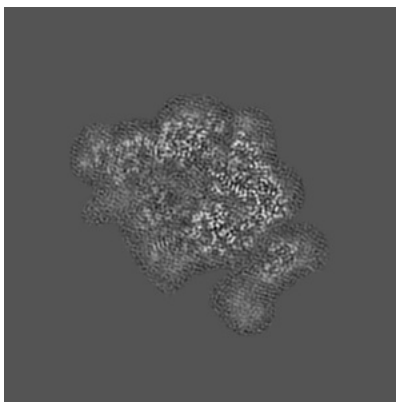
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

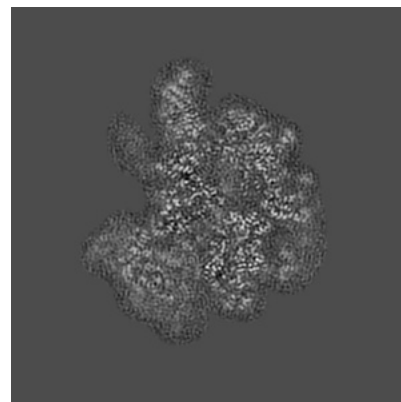
6.2.1 Primary map



X Index: 150

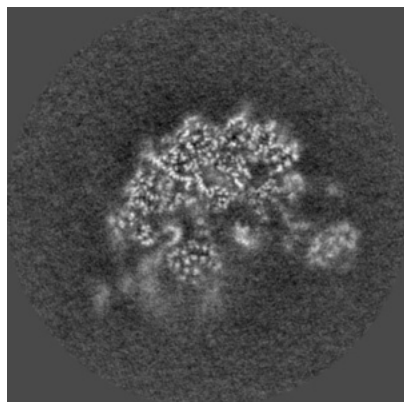


Y Index: 150

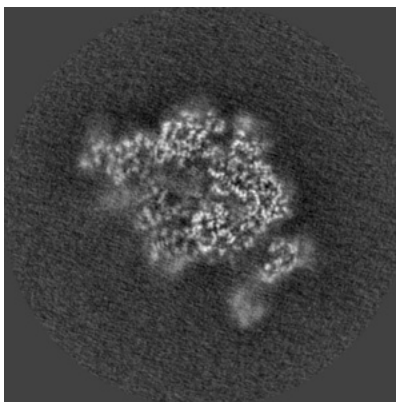


Z Index: 150

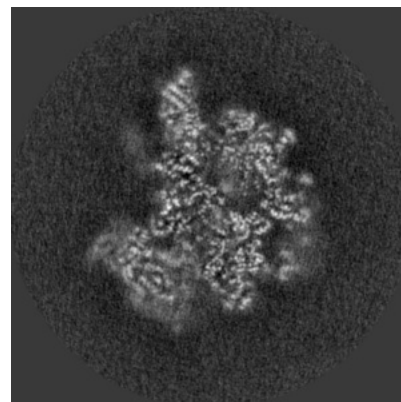
6.2.2 Raw map



X Index: 150



Y Index: 150

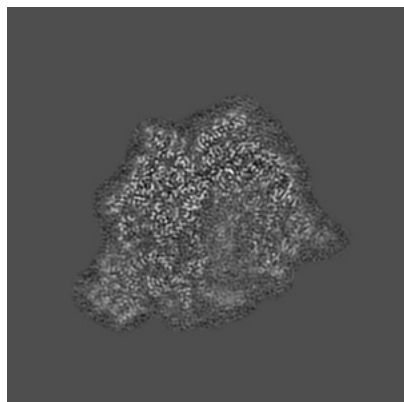


Z Index: 150

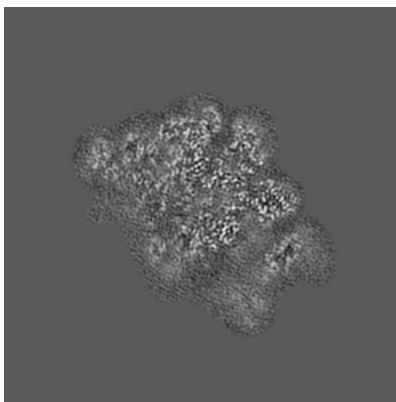
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

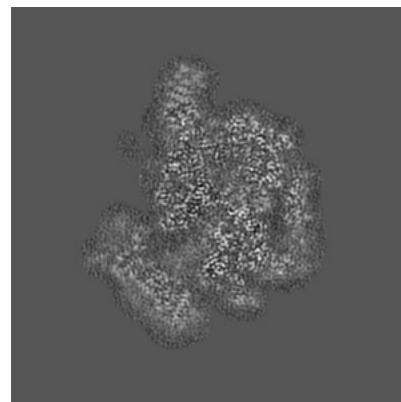
6.3.1 Primary map



X Index: 168

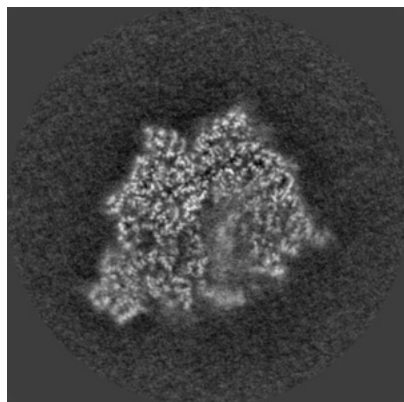


Y Index: 143

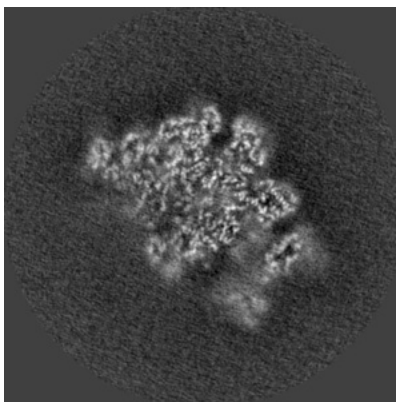


Z Index: 157

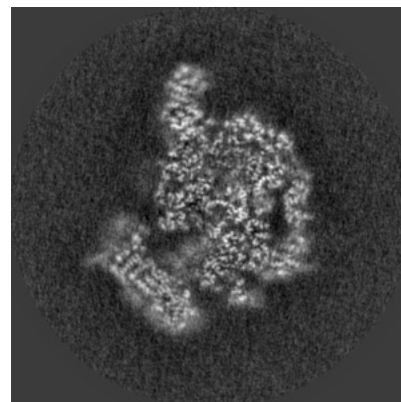
6.3.2 Raw map



X Index: 168



Y Index: 143

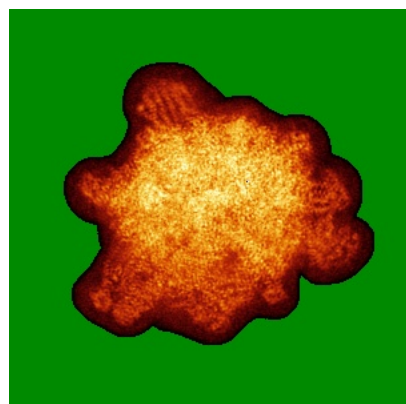


Z Index: 158

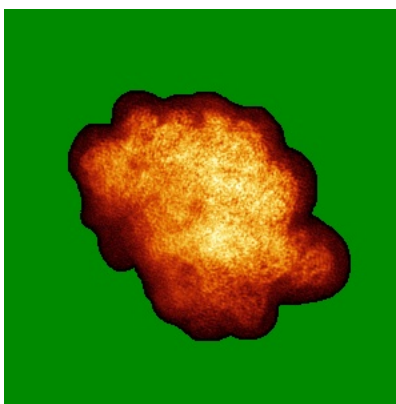
The images above show the largest variance slices of the map in three orthogonal directions.

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

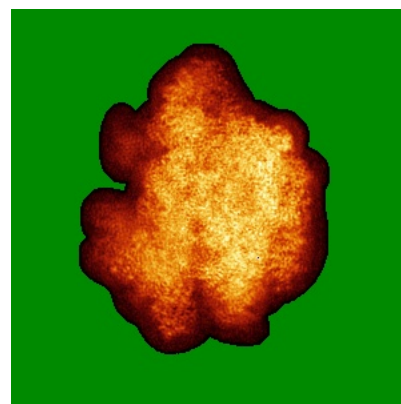
6.4.1 Primary map



X

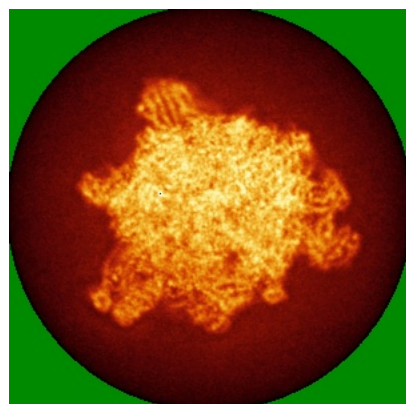


Y

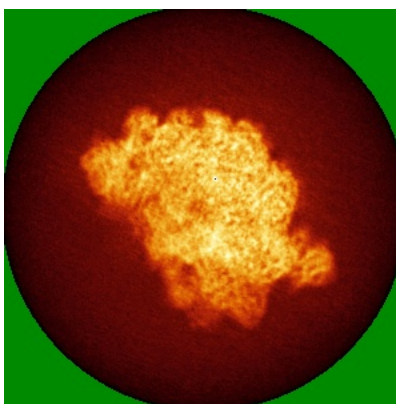


Z

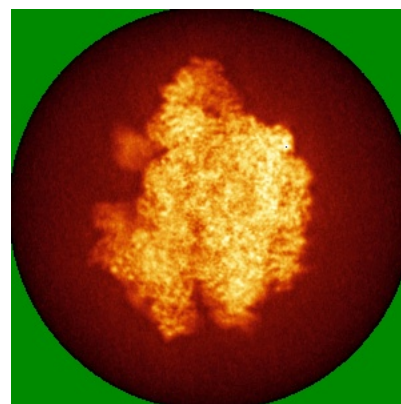
6.4.2 Raw map



X



Y

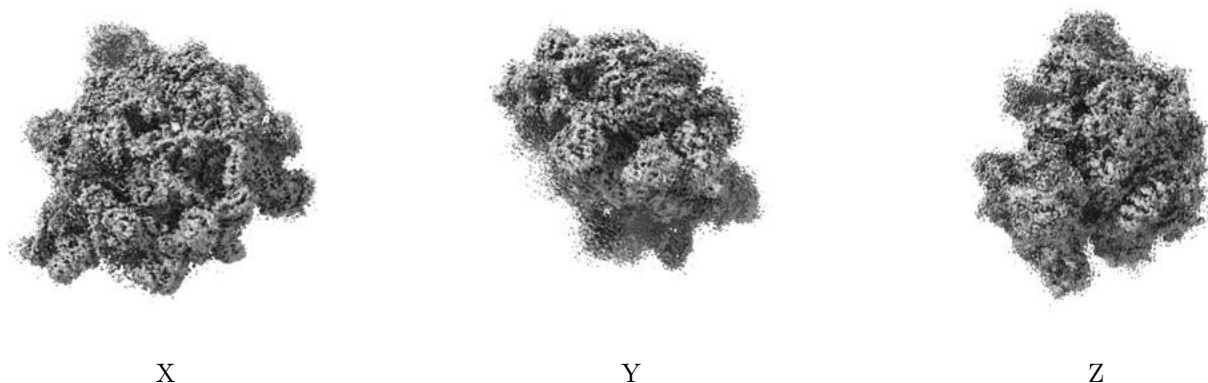


Z

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.

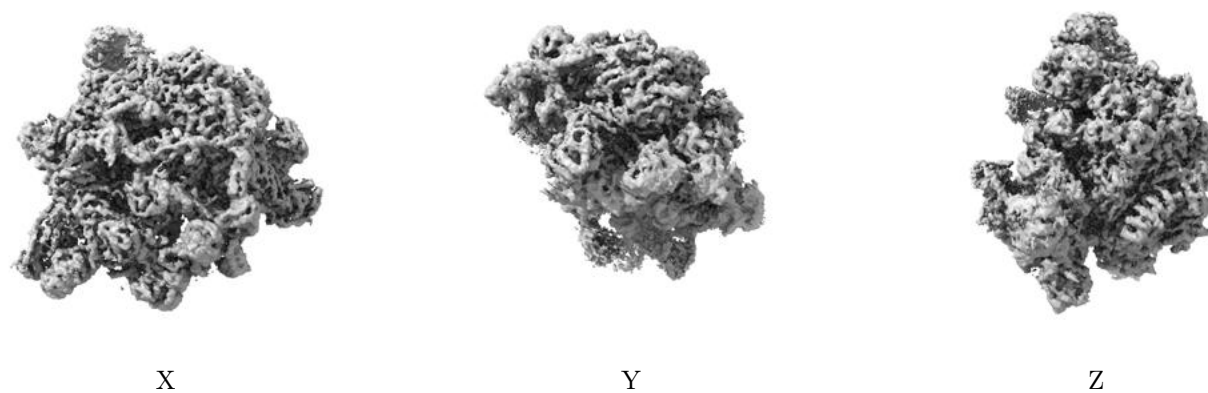
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

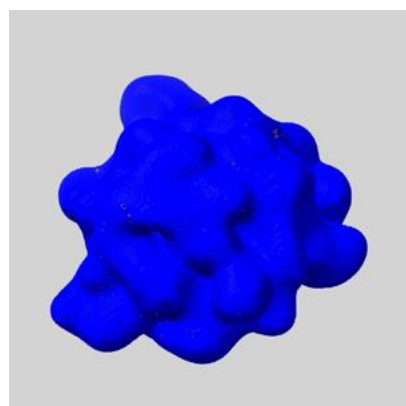
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

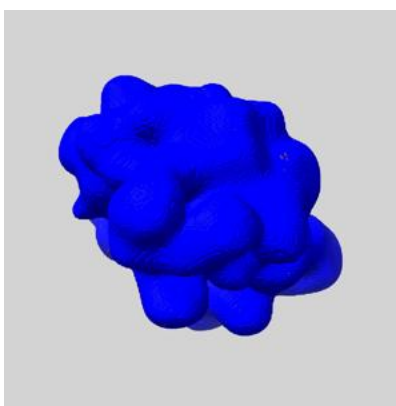
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

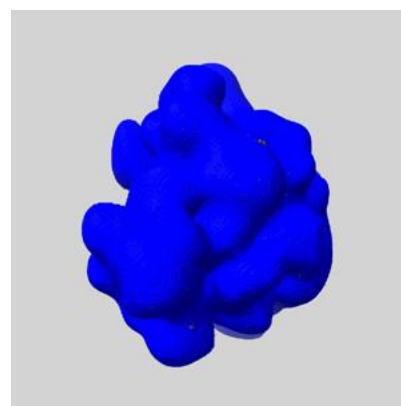
6.6.1 emd_10999_msk_1.map [i](#)



X



Y

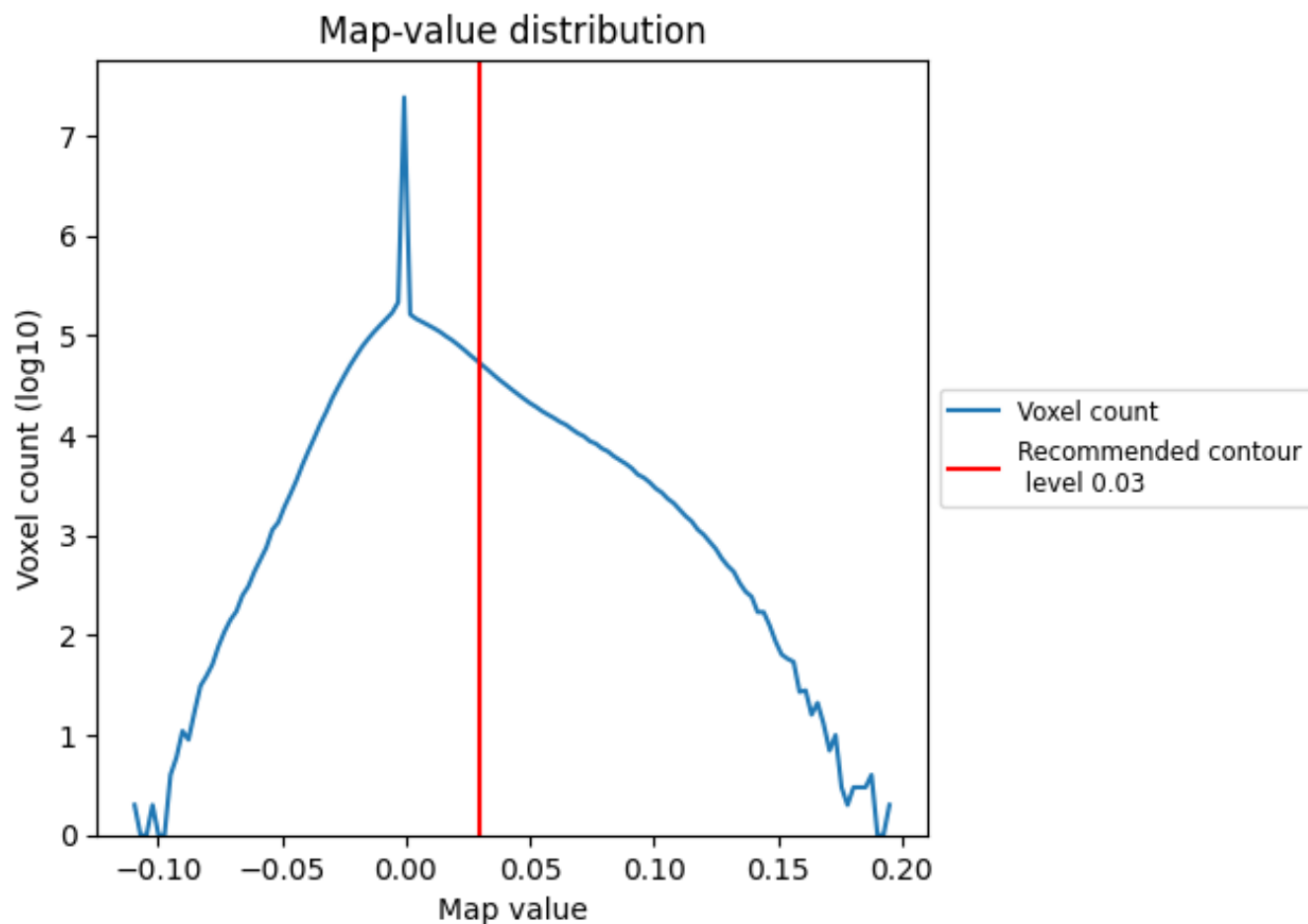


Z

7 Map analysis [i](#)

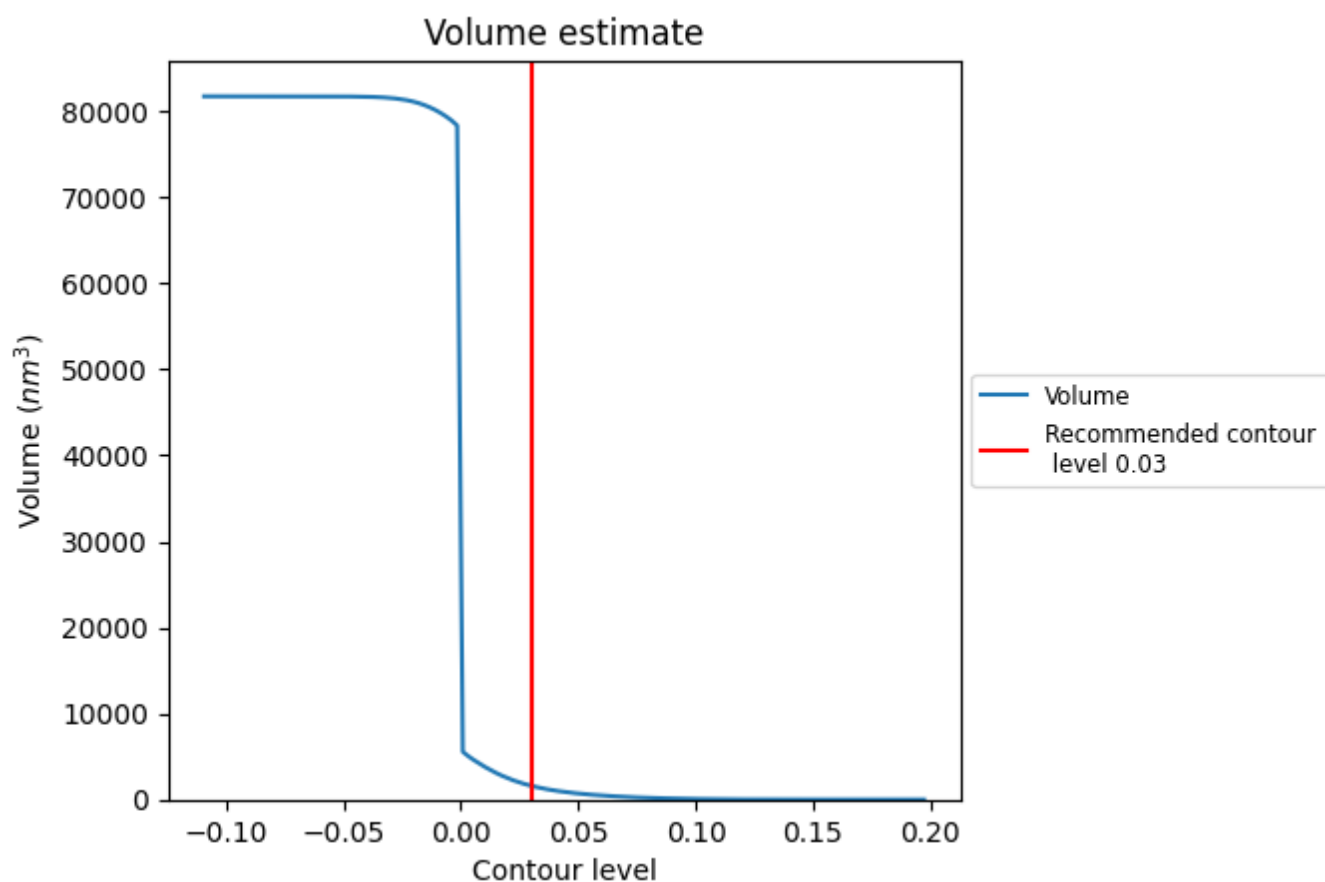
This section contains the results of statistical analysis of the map.

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.

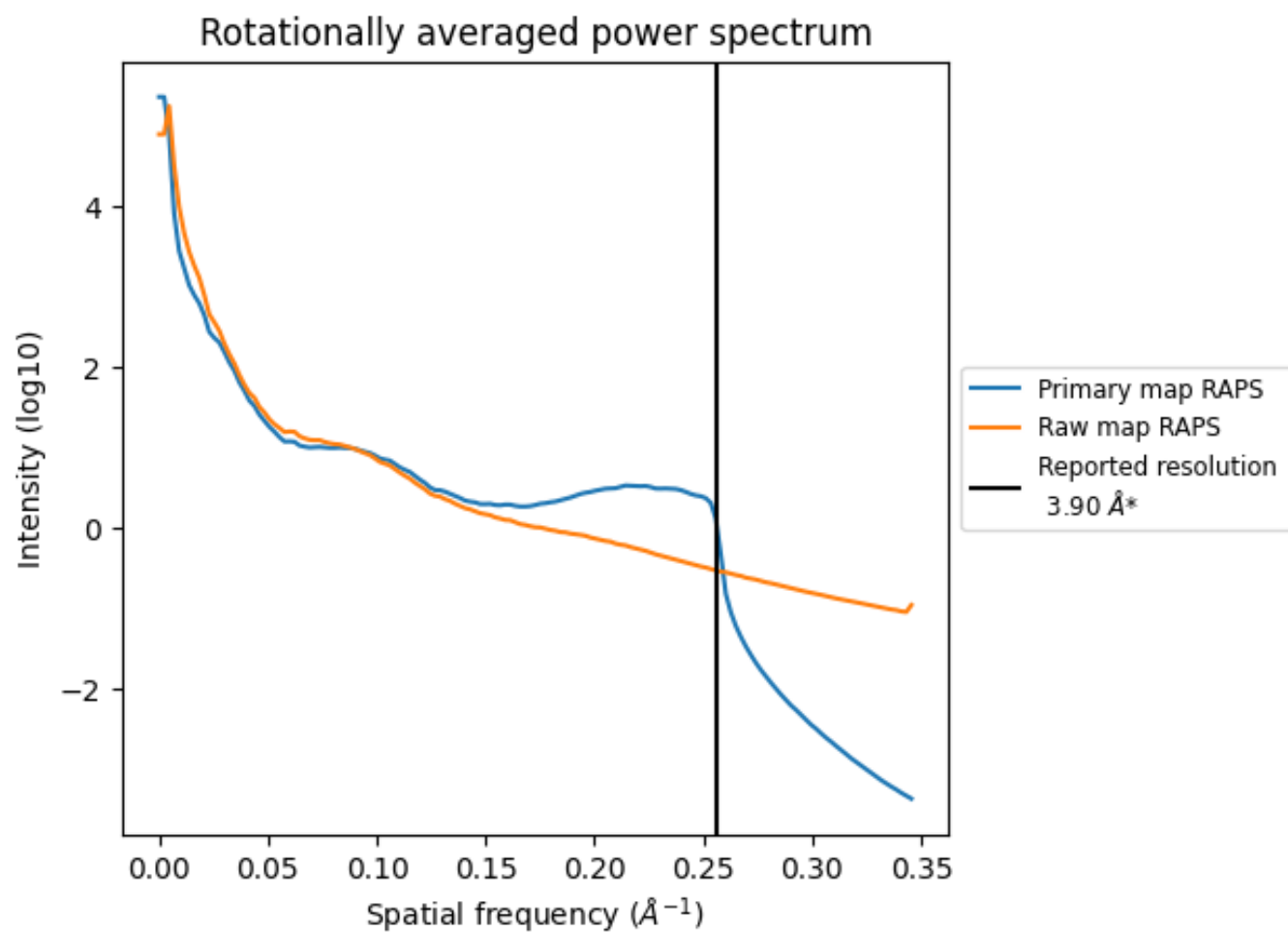
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1601 nm³; this corresponds to an approximate mass of 1446 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 ⓘ

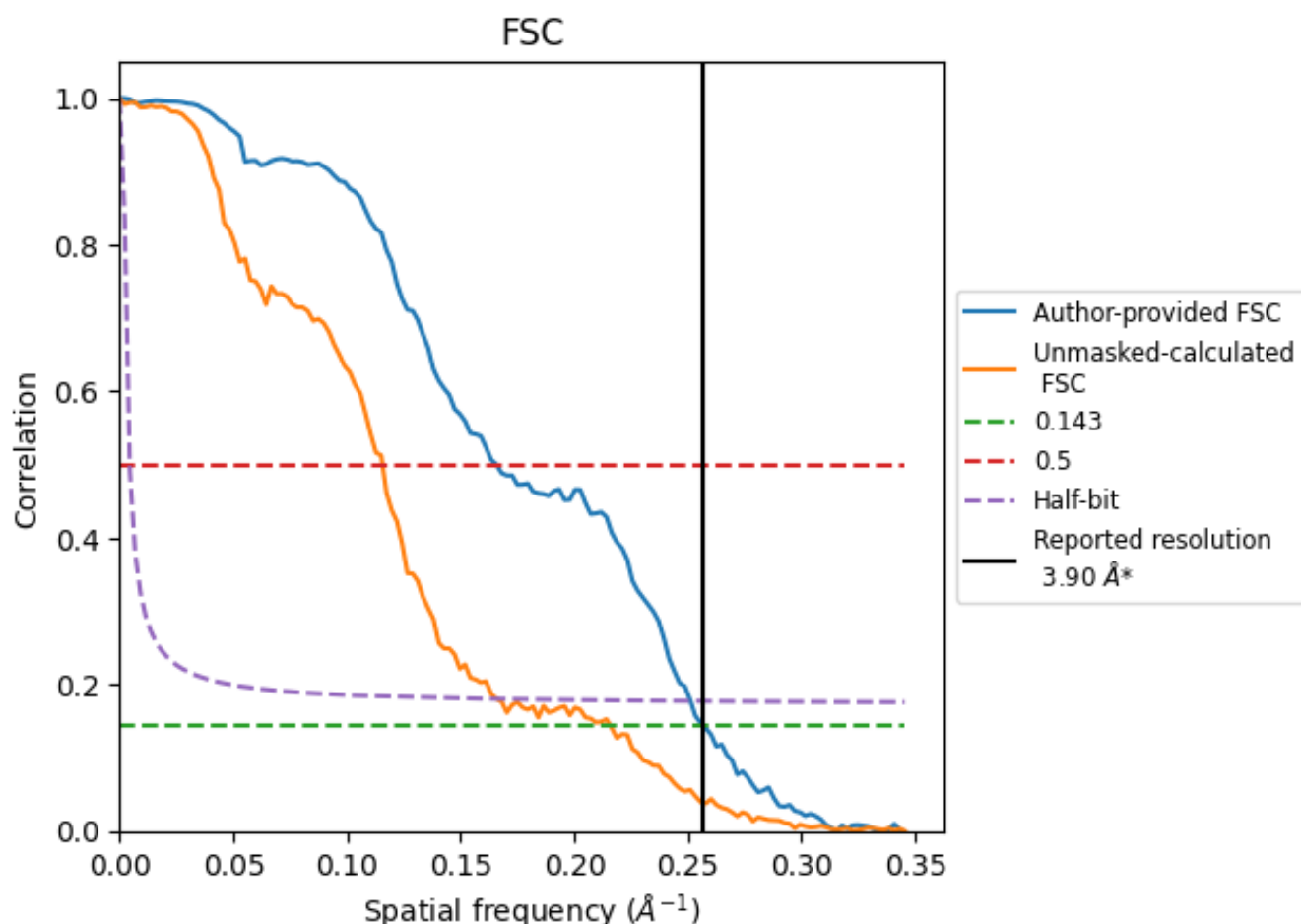


*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

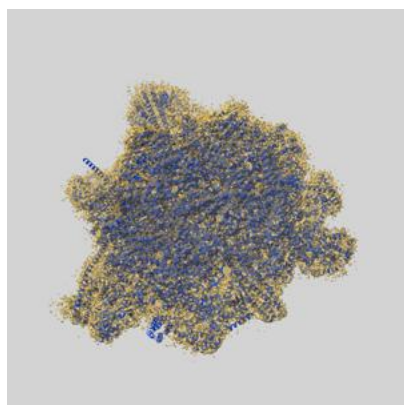
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.89	6.03	3.98
Unmasked-calculated*	4.63	8.64	6.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.63 differs from the reported value 3.9 by more than 10 %

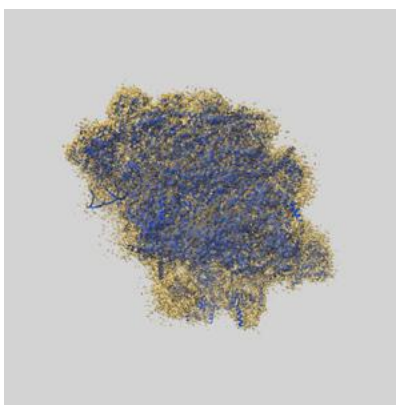
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10999 and PDB model 6YXX. Per-residue inclusion information can be found in section [3](#) on page [26](#).

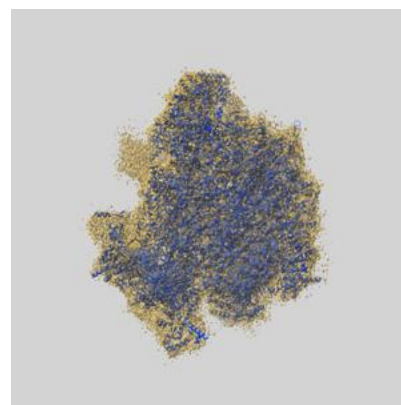
9.1 Map-model overlay [i](#)



X



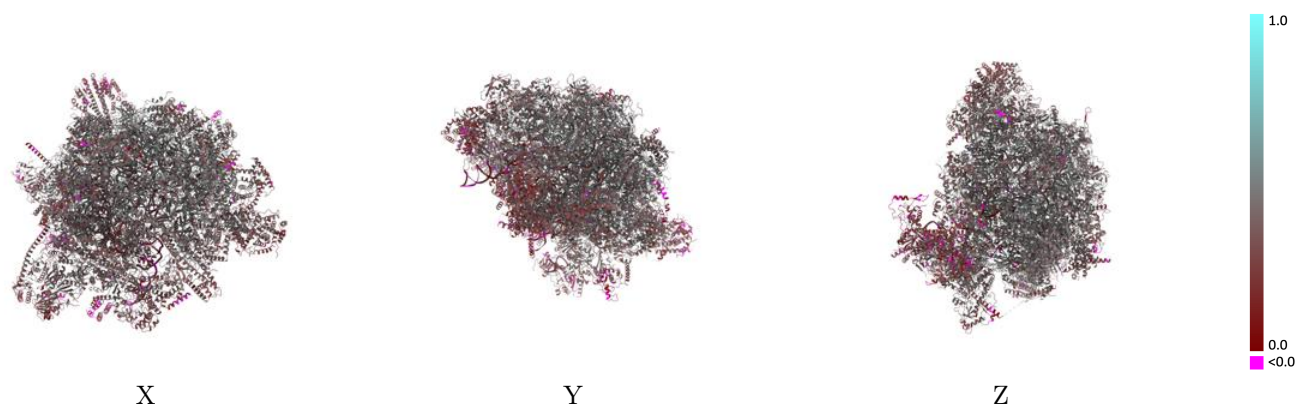
Y



Z

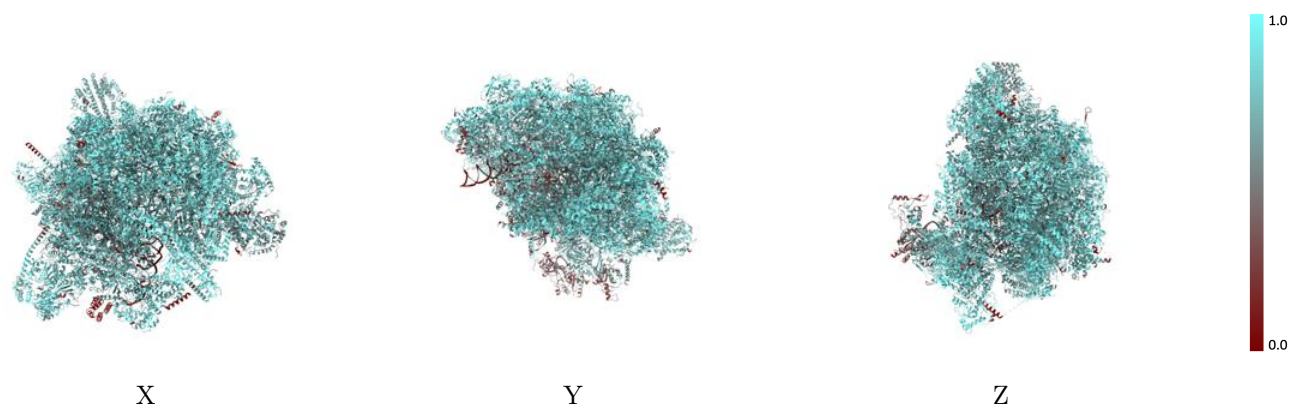
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



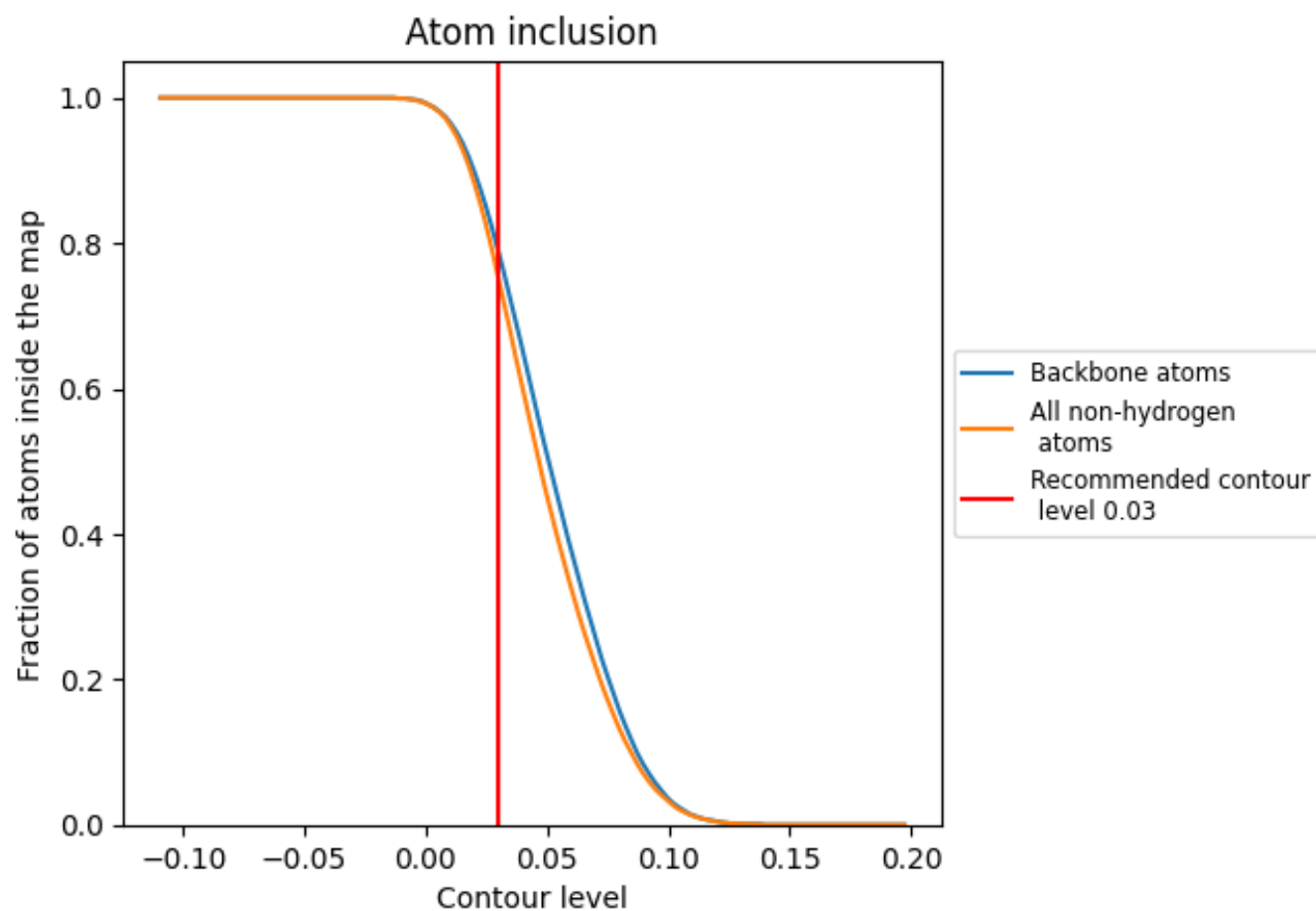
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 75% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7510	 0.3890
A1	 0.7500	 0.3900
A2	 0.8500	 0.4290
A3	 0.8040	 0.4430
A5	 0.8580	 0.4800
A8	 0.6970	 0.4360
AA	 0.7510	 0.3430
AE	 0.8060	 0.4560
AF	 0.8400	 0.4530
AI	 0.7460	 0.3920
AK	 0.6670	 0.3000
AN	 0.7850	 0.4520
AP	 0.7930	 0.4350
AR	 0.7970	 0.4380
AT	 0.7860	 0.4370
AU	 0.8330	 0.4590
AV	 0.8540	 0.4670
AW	 0.8070	 0.4480
AX	 0.8260	 0.4500
AY	 0.7970	 0.4080
Ae	 0.8240	 0.4290
Af	 0.8210	 0.4340
Ag	 0.8130	 0.4310
Al	 0.8040	 0.4410
Ao	 0.8180	 0.4570
Ap	 0.7960	 0.4250
At	 0.7940	 0.4280
Av	 0.7860	 0.4260
BA	 0.8300	 0.4230
BB	 0.7900	 0.3550
BD	 0.6260	 0.3090
BE	 0.8360	 0.4090
BF	 0.8480	 0.4380
BH	 0.6560	 0.3800
BI	 0.8390	 0.4280

























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Chain	Atom inclusion	Q-score
BJ	 0.7850	 0.3360
BK	 0.7280	 0.3670
BL	 0.8180	 0.4040
BN	 0.7800	 0.3940
BO	 0.8110	 0.4000
BQ	 0.8230	 0.4210
BR	 0.8070	 0.4380
BS	 0.7900	 0.3800
BT	 0.8550	 0.4260
BU	 0.7230	 0.3950
BV	 0.4030	 0.0930
BW	 0.8770	 0.4480
BZ	 0.8300	 0.3780
Ba	 0.8070	 0.4310
Bb	 0.8280	 0.3960
Bc	 0.6580	 0.3960
Bf	 0.6500	 0.3730
E1	 0.6730	 0.4160
E2	 0.6850	 0.3830
E3	 0.6990	 0.3940
E4	 0.7620	 0.3490
E5	 0.8340	 0.3500
E6	 0.6930	 0.3920
E7	 0.7010	 0.4230
E8	 0.5010	 0.3100
E9	 0.5810	 0.3770
EA	 0.7050	 0.3890
EB	 0.7850	 0.4530
EC	 0.7650	 0.4450
ED	 0.8470	 0.4290
EE	 0.7240	 0.3530
EF	 0.3230	 0.2350
EG	 0.8030	 0.4750
EH	 0.8060	 0.4040
EL	 0.8360	 0.4000
EM	 0.6170	 0.3150
EN	 0.7690	 0.3530
EO	 0.7500	 0.2990
EP	 0.7050	 0.2070
ER	 0.7680	 0.3110
ES	 0.7640	 0.2940
ET	 0.7450	 0.4380

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Chain	Atom inclusion	Q-score
UA	 0.8400	 0.4510
UI	 0.1050	 0.1140
UK	 0.5360	 0.2010
UM	 0.7000	 0.4390
Uf	 0.5400	 0.2210
Ul	 0.5530	 0.2870
Um	 0.6670	 0.2980
Un	 0.7570	 0.3850
Up	 0.0620	 0.1140
Ur	 0.1140	 0.1340
Us	 0.0860	 0.0630