



wwPDB EM Validation Summary Report ⓘ

Nov 4, 2024 – 01:38 am GMT

PDB ID : 7PUA
EMDB ID : EMD-13660
Title : Middle assembly intermediate of the Trypanosoma brucei mitoribosomal small subunit
Authors : Lenarcic, T.; Leibundgut, M.; Saurer, M.; Ramrath, D.J.F.; Fluegel, T.; Boehringer, D.; Ban, N.
Deposited on : 2021-09-29
Resolution : 3.60 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

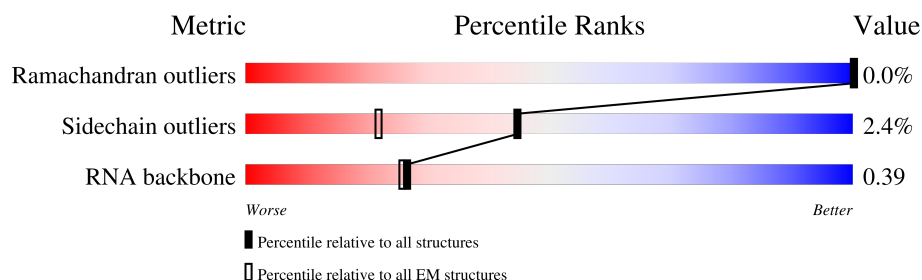
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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	CA	621	<div> <div>22%</div> <div>49%</div> <div>31%</div> <div>19%</div> </div>
2	CB	3	<div> <div>33%</div> <div>67%</div> </div>
3	CC	74	<div> <div>22%</div> <div>100%</div> </div>
4	CE	435	<div> <div>9%</div> <div>84%</div> <div>14%</div> </div>
5	CF	160	<div> <div>13%</div> <div>92%</div> <div>5%</div> </div>
6	CH	282	<div> <div>77%</div> <div>22%</div> </div>
7	CI	443	<div> <div>7%</div> <div>94%</div> <div>5%</div> </div>
8	CJ	817	<div> <div>6%</div> <div>93%</div> </div>

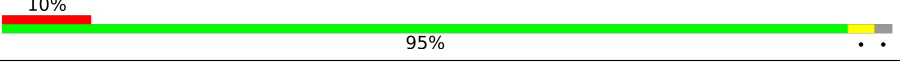
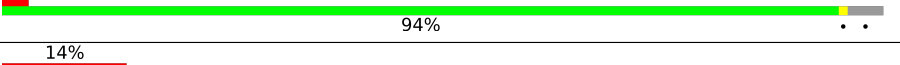
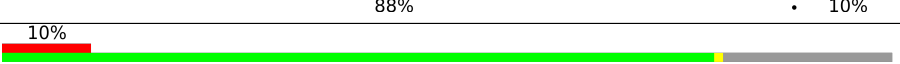
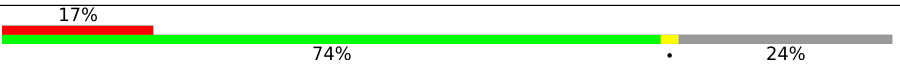


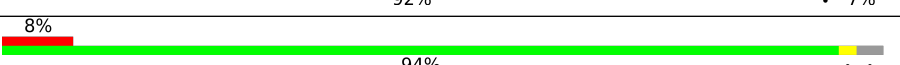
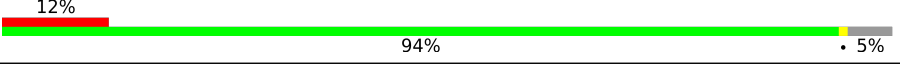
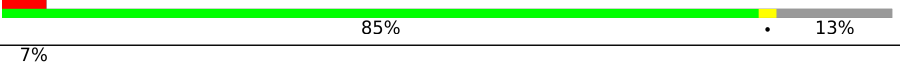

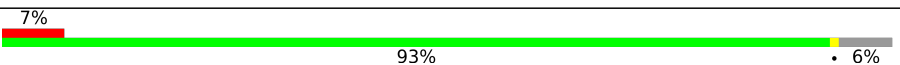
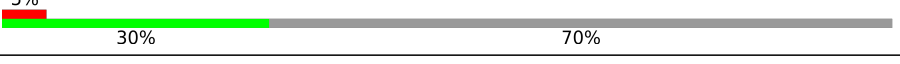

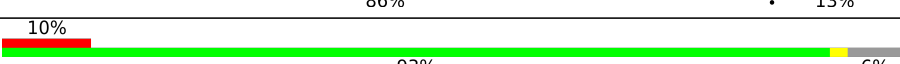

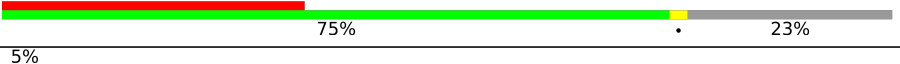
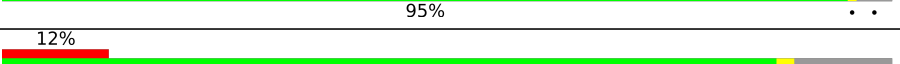
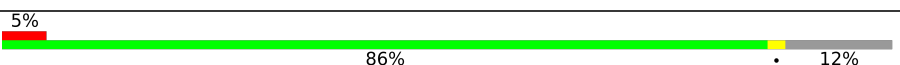

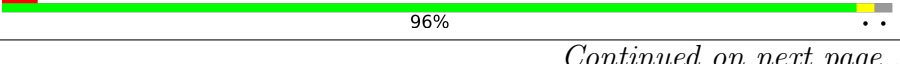



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Mol	Chain	Length	Quality of chain
9	CK	326	
10	CL	87	
11	CN	166	
12	CO	429	
13	CP	188	
14	CQ	307	
15	CR	320	
16	CS	244	
17	CU	193	
18	Ca	602	
19	Cb	325	
20	Cd	440	
21	Cg	498	
22	Ci	181	
23	Cj	257	
24	Ck	874	
25	Cm	215	
26	Cn	250	
27	Cp	187	
28	DB	1181	
29	DC	1165	
30	DD	812	
31	DE	747	
32	DF	666	
33	DG	631	

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Mol	Chain	Length	Quality of chain
34	DH	581	
35	DI	407	
36	DJ	396	
37	DK	324	
38	DL	307	
39	DO	282	
40	DP	274	
41	DR	270	
42	DT	247	
43	DU	228	
44	DV	183	
45	DW	179	
46	DX	169	
47	DY	163	
48	DZ	94	
49	Da	64	
50	F2	1024	
51	F3	966	
52	F5	754	
53	F6	676	
54	F7	679	
55	F9	607	
56	FM	370	
56	FN	370	
57	FO	334	

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Mol	Chain	Length	Quality of chain
58	FP	349	
59	FW	263	
60	FX	239	
61	FZ	178	
62	Fb	151	
63	Fc	148	
64	Fd	143	
65	Ff	848	
66	Fg	550	
67	Fh	318	
68	Fi	629	
69	IA	787	
70	IB	803	
71	U8	30	
72	UC	9	
73	UD	13	
74	UF	36	
75	UG	15	
76	UI	6	
77	UK	24	
78	UM	8	
78	UN	8	
78	UQ	8	
79	UP	32	
80	Ua	10	

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Mol	Chain	Length	Quality of chain
81	Ug	271	<div><div></div><div></div><div></div></div>

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 205280 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CA	501	Total	C	N	O	P	0	0
			9866	4403	1529	3433	501		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CA	614	U	-	expression tag	GB 13740
CA	615	U	-	expression tag	GB 13740
CA	616	U	-	expression tag	GB 13740
CA	617	U	-	expression tag	GB 13740
CA	618	U	-	expression tag	GB 13740
CA	619	U	-	expression tag	GB 13740
CA	620	U	-	expression tag	GB 13740
CA	621	U	-	expression tag	GB 13740

- Molecule 2 is a RNA chain called 9S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	3	Total	C	N	O	P	0	0
			64	29	12	20	3		

- Molecule 3 is a protein called uS3m.

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

- Molecule 4 is a protein called Ribosomal_S5_C domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CE	373	Total	C	N	O	S	0	0
			3024	1915	556	538	15		

- Molecule 5 is a protein called bS6m.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	CF	155	Total	C	N	O	S	0	0
			1279	810	226	237	6		

- Molecule 6 is a protein called 30S ribosomal protein S8, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	CH	219	Total	C	N	O	S	0	0
			1799	1130	343	317	9		

- Molecule 7 is a protein called uS9m.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CI	421	Total	C	N	O	S	0	0
			3352	2111	598	627	16		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 8 is a protein called LysM domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	CJ	782	Total	C	N	O	S	0	0
			6376	4034	1122	1191	29		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CJ	488	SER	ASN	conflict	UNP C9ZPU0

- Molecule 9 is a protein called uS11m.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	CK	177	Total	C	N	O	S	0	0
			1440	895	273	264	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CK	3	ARG	GLN	conflict	UNP Q389T7
CK	138	UNK	ILE	conflict	UNP Q389T7

- Molecule 10 is a protein called uS12m.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	CL	83	Total	C	N	O	S	0	0
			701	480	109	102	10		

- Molecule 11 is a protein called uS14m.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	CN	157	Total	C	N	O	S	0	0
			1322	843	251	220	8		

- Molecule 12 is a protein called uS15m.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CO	360	Total	C	N	O	S	0	0
			2989	1899	557	517	16		

- Molecule 13 is a protein called bS16m.

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

- Molecule 14 is a protein called 30S Ribosomal protein S17, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	CQ	247	Total	C	N	O	S	0	0
			2015	1279	379	348	9		

- Molecule 15 is a protein called bS18m.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	CR	124	Total	C	N	O	S	0	0
			1051	680	196	173	2		

- Molecule 16 is a protein called uS19m.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	CS	99	Total	C	N	O	S	0	0
			822	534	144	140	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
CS	-11	ILE	ASN	conflict	UNP A0A3L6L621
CS	-10	VAL	CYS	conflict	UNP A0A3L6L621
CS	-9	TYR	LEU	conflict	UNP A0A3L6L621
CS	-8	PHE	LEU	conflict	UNP A0A3L6L621
CS	-7	HIS	PRO	conflict	UNP A0A3L6L621
CS	-6	CYS	LEU	conflict	UNP A0A3L6L621
CS	-5	CYS	LEU	conflict	UNP A0A3L6L621
CS	-4	THR	TYR	conflict	UNP A0A3L6L621
CS	-3	ARG	GLU	conflict	UNP A0A3L6L621
CS	-2	LYS	GLU	conflict	UNP A0A3L6L621
CS	?	-	VAL	deletion	UNP A0A3L6L621
CS	?	-	ARG	deletion	UNP A0A3L6L621

- Molecule 17 is a protein called bS21m.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	CU	35	Total	C	N	O	S	0	0
			288	182	57	47	2		

- Molecule 18 is a protein called mS22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Ca	501	Total	C	N	O	S	0	0
			4247	2720	753	753	21		

- Molecule 19 is a protein called mS23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Cb	149	Total	C	N	O	S	0	0
			1242	801	226	209	6		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cb	302	GLY	ARG	conflict	UNP C9ZNU0
Cb	312	UNK	-	expression tag	UNP C9ZNU0

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Chain	Residue	Modelled	Actual	Comment	Reference
Cb	313	CYS	-	expression tag	UNP C9ZNU0
Cb	314	SER	-	expression tag	UNP C9ZNU0
Cb	315	ARG	-	expression tag	UNP C9ZNU0
Cb	316	ASP	-	expression tag	UNP C9ZNU0
Cb	317	GLY	-	expression tag	UNP C9ZNU0
Cb	318	PHE	-	expression tag	UNP C9ZNU0
Cb	319	ALA	-	expression tag	UNP C9ZNU0
Cb	320	LEU	-	expression tag	UNP C9ZNU0
Cb	321	MET	-	expression tag	UNP C9ZNU0
Cb	322	LYS	-	expression tag	UNP C9ZNU0
Cb	323	ALA	-	expression tag	UNP C9ZNU0
Cb	324	ASN	-	expression tag	UNP C9ZNU0
Cb	325	LYS	-	expression tag	UNP C9ZNU0

- Molecule 20 is a protein called mS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Cd	205	Total	C	N	O	S	0	0
			1768	1124	323	312	9		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cd	299	UNK	GLY	conflict	UNP Q38DK6
Cd	364	UNK	GLY	conflict	UNP Q38DK6

- Molecule 21 is a protein called mS29.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Cg	487	Total	C	N	O	S	0	0
			3943	2524	691	708	20		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cg	181	VAL	ALA	conflict	UNP Q585C2
Cg	498	ARG	-	expression tag	UNP Q585C2

- Molecule 22 is a protein called mS33.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ci	165	Total	C	N	O	S	0	0
			1348	848	247	244	9		

- Molecule 23 is a protein called mS34.

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

- Molecule 24 is a protein called mS35.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Ck	673	Total	C	N	O	S	0	0
			5371	3371	974	1002	24		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ck	107	SER	LEU	conflict	UNP Q387C7
Ck	144	PHE	LEU	conflict	UNP Q387C7
Ck	253	TYR	PHE	conflict	UNP Q387C7
Ck	339	GLU	VAL	conflict	UNP Q387C7
Ck	815	GLY	ARG	conflict	UNP Q387C7
Ck	871	GLY	GLU	conflict	UNP Q387C7

- Molecule 25 is a protein called mS37.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Cm	31	Total	C	N	O	S	0	0
			232	136	43	47	6		

- Molecule 26 is a protein called mS38.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Cn	49	Total	C	N	O	S	0	0
			425	278	88	56	3		

- Molecule 27 is a protein called Protein FYV4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Cp	168	Total	C	N	O	S	0	0
			1428	904	259	260	5		

- Molecule 28 is a protein called mS49.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	DB	1106	Total	C	N	O	S	0	0
			9112	5669	1712	1703	28		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DB	359	ILE	THR	conflict	UNP C9ZJE4

- Molecule 29 is a protein called mS50.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	DC	1099	Total	C	N	O	S	0	0
			8766	5528	1548	1659	31		

- Molecule 30 is a protein called mS51.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	DD	764	Total	C	N	O	S	0	0
			6308	3998	1131	1143	36		

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DD	1	UNK	-	expression tag	UNP D0A752
DD	2	UNK	-	expression tag	UNP D0A752
DD	3	UNK	-	expression tag	UNP D0A752
DD	4	UNK	-	expression tag	UNP D0A752
DD	5	UNK	-	expression tag	UNP D0A752
DD	6	UNK	-	expression tag	UNP D0A752
DD	7	UNK	-	expression tag	UNP D0A752
DD	8	UNK	-	expression tag	UNP D0A752
DD	9	UNK	-	expression tag	UNP D0A752
DD	10	UNK	-	expression tag	UNP D0A752
DD	11	UNK	-	expression tag	UNP D0A752
DD	12	UNK	-	expression tag	UNP D0A752
DD	13	UNK	-	expression tag	UNP D0A752
DD	14	UNK	-	expression tag	UNP D0A752
DD	15	UNK	-	expression tag	UNP D0A752
DD	16	UNK	-	expression tag	UNP D0A752
DD	17	UNK	-	expression tag	UNP D0A752
DD	26	UNK	ARG	conflict	UNP D0A752

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Chain	Residue	Modelled	Actual	Comment	Reference
DD	27	UNK	MET	conflict	UNP D0A752
DD	28	UNK	MET	conflict	UNP D0A752
DD	29	UNK	ARG	conflict	UNP D0A752
DD	30	UNK	ALA	conflict	UNP D0A752
DD	31	UNK	GLY	conflict	UNP D0A752
DD	32	UNK	SER	conflict	UNP D0A752
DD	33	UNK	GLY	conflict	UNP D0A752
DD	34	UNK	TYR	conflict	UNP D0A752
DD	35	UNK	GLN	conflict	UNP D0A752
DD	36	UNK	GLN	conflict	UNP D0A752
DD	37	UNK	LEU	conflict	UNP D0A752
DD	38	UNK	ARG	conflict	UNP D0A752
DD	39	UNK	ARG	conflict	UNP D0A752
DD	40	UNK	MET	conflict	UNP D0A752
DD	41	UNK	GLY	conflict	UNP D0A752
DD	42	UNK	MET	conflict	UNP D0A752
DD	43	UNK	PRO	conflict	UNP D0A752
DD	44	UNK	MET	conflict	UNP D0A752
DD	45	UNK	GLN	conflict	UNP D0A752
DD	46	UNK	VAL	conflict	UNP D0A752
DD	47	UNK	GLY	conflict	UNP D0A752
DD	48	UNK	MET	conflict	UNP D0A752
DD	49	UNK	GLY	conflict	UNP D0A752
DD	50	UNK	TRP	conflict	UNP D0A752
DD	51	UNK	ARG	conflict	UNP D0A752
DD	52	UNK	LYS	conflict	UNP D0A752
DD	53	UNK	VAL	conflict	UNP D0A752
DD	54	UNK	ASP	conflict	UNP D0A752
DD	55	UNK	SER	conflict	UNP D0A752
DD	56	UNK	PHE	conflict	UNP D0A752

- Molecule 31 is a protein called mS52.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	DE	628	Total	C	N	O	S	0	0
			5114	3243	926	924	21		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DE	378	UNK	LYS	conflict	UNP Q386Q7
DE	384	UNK	THR	conflict	UNP Q386Q7

- Molecule 32 is a protein called mS53.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	DF	594	Total	C	N	O	S	0	0
			4785	3001	904	855	25		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DF	18	THR	ALA	conflict	UNP C9ZXX4
DF	372	ASN	ASP	conflict	UNP C9ZXX4
DF	406	ASN	SER	conflict	UNP C9ZXX4
DF	636	UNK	GLY	conflict	UNP C9ZXX4
DF	638	LYS	ARG	conflict	UNP C9ZXX4

- Molecule 33 is a protein called mS54.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	DG	557	Total	C	N	O	S	0	0
			4511	2835	826	819	31		

- Molecule 34 is a protein called mS55.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	DH	568	Total	C	N	O	S	0	0
			4608	2888	858	840	22		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DH	75	GLN	LYS	conflict	UNP A0A3L6LGC8

- Molecule 35 is a protein called mS56.

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

- Molecule 36 is a protein called mS57.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	DJ	356	Total	C	N	O	S	0	0
			2908	1855	511	528	14		

- Molecule 37 is a protein called mS58.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	DK	264	Total	C	N	O	S	0	0
			2092	1317	375	395	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DK	97	ASP	SER	conflict	UNP A0A3L6L3U6

- Molecule 38 is a protein called mS59.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	DL	234	Total	C	N	O	S	0	0
			1904	1216	342	335	11		

- Molecule 39 is a protein called mS62.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	DO	194	Total	C	N	O	S	0	0
			1567	981	286	291	9		

- Molecule 40 is a protein called mS63.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	DP	210	Total	C	N	O	S	0	0
			1784	1145	318	312	9		

- Molecule 41 is a protein called mS65.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	DR	252	Total	C	N	O	S	0	0
			2034	1309	371	344	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
DR	128	PRO	SER	conflict	UNP C9ZPP1

- Molecule 42 is a protein called Rhodanese domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	DT	239	Total	C	N	O	S	0	0
			2058	1321	364	362	11		

- Molecule 43 is a protein called Ubiquitin-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	DU	217	Total	C	N	O	S	0	0
			1730	1091	305	329	5		

- Molecule 44 is a protein called mS69.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	DV	160	Total	C	N	O	S	0	0
			1346	855	252	235	4		

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 45 is a protein called mS70.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	DW	136	Total	C	N	O	S	0	0
			1160	741	220	194	5		

- Molecule 46 is a protein called mS71.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	DX	129	Total	C	N	O	S	0	0
			1097	697	206	187	7		

- Molecule 47 is a protein called mS72.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 48 is a protein called mS73.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	DZ	28	Total	C	N	O	S	0	0
			237	156	39	41	1		

- Molecule 49 is a protein called mS74.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Da	36	Total	C	N	O	S	0	0
			320	202	70	46	2		

- Molecule 50 is a protein called PPR_long domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	F2	890	Total	C	N	O	S	0	0
			7125	4483	1254	1349	39		

- Molecule 51 is a protein called mt-SAF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	F3	911	Total	C	N	O	S	0	0
			7039	4391	1250	1346	52		

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 52 is a protein called mt-SAF5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	F5	620	Total	C	N	O	S	0	0
			5056	3154	938	933	31		

- Molecule 53 is a protein called DUF4460 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	F6	522	Total	C	N	O	S	0	0
			4195	2655	729	794	17		

There are 4 discrepancies between the modelled and reference sequences:

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

- Molecule 54 is a protein called mt-SAF7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	F7	652	Total	C	N	O	S	0	0
			5166	3284	908	938	36		

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 55 is a protein called mt-SAF9.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	F9	540	Total	C	N	O	S	0	0
			4422	2732	830	845	15		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F9	?	-	GLU	deletion	UNP C9ZSL5

- Molecule 56 is a protein called mt-SAF21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FM	327	Total	C	N	O	S	0	0
			2457	1521	450	466	20		
56	FN	320	Total	C	N	O	S	0	0
			2403	1484	440	459	20		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FM	326	HIS	ARG	conflict	UNP C9ZJW2
FM	330	UNK	GLY	conflict	UNP C9ZJW2
FN	326	HIS	ARG	conflict	UNP C9ZJW2
FN	330	UNK	GLY	conflict	UNP C9ZJW2

- Molecule 57 is a protein called mt-SAF22.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	FO	328	Total	C	N	O	S	0	0
			2700	1692	513	481	14		

- Molecule 58 is a protein called mt-SAF23.

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

- Molecule 59 is a protein called LMWPc domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	FW	238	Total	C	N	O	S	0	0
			1960	1227	375	352	6		

- Molecule 60 is a protein called mt-SAF27.

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

- Molecule 61 is a protein called mt-SAF29.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	FZ	160	Total	C	N	O	S	0	0
			1262	786	212	257	7		

- Molecule 62 is a protein called mt-SAF31.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Fb	125	Total	C	N	O	S	0	0
			1061	682	194	178	7		

- Molecule 63 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Fc	83	Total	C	N	O	S	0	0
			660	421	104	134	1		

- Molecule 64 is a protein called DUF4379 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Fd	93	Total	C	N	O	S	0	0
			738	469	143	118	8		

- Molecule 65 is a protein called DNA photolyase, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Ff	623	Total	C	N	O	S	0	0
			5006	3176	896	911	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ff	109	ALA	VAL	conflict	UNP D0A9A9
Ff	127	UNK	TYR	conflict	UNP D0A9A9
Ff	138	GLN	ARG	conflict	UNP D0A9A9

- Molecule 66 is a protein called Acyl transferase-like protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Fg	520	Total	C	N	O	S	0	0
			4048	2545	710	763	30		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Fg	159	ILE	VAL	conflict	UNP C9ZYZ4
Fg	271	ILE	VAL	conflict	UNP C9ZYZ4
Fg	363	MET	ARG	conflict	UNP C9ZYZ4
Fg	399	UNK	GLU	conflict	UNP C9ZYZ4
Fg	436	ASP	GLU	conflict	UNP C9ZYZ4

- Molecule 67 is a protein called mt-SAF37.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Fh	239	Total	C	N	O	S	0	0
			1867	1159	346	348	14		

- Molecule 68 is a protein called mt-SAF38.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Fi	475	Total	C	N	O	S	0	0
			3797	2410	693	670	24		

- Molecule 69 is a protein called Translation initiation factor IF-2, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	IA	704	Total	C	N	O	S	0	0
			5478	3433	986	1032	27		

- Molecule 70 is a protein called mt-SAF39.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	IB	491	Total	C	N	O	S	0	0
			3867	2415	723	712	17		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
IB	98	LYS	GLU	conflict	UNP D0A0V4
IB	206	ILE	MET	conflict	UNP D0A0V4
IB	572	HIS	ARG	conflict	UNP D0A0V4
IB	798	PRO	ALA	conflict	UNP D0A0V4

- Molecule 71 is a protein called Unk8.

Mol	Chain	Residues	Atoms				AltConf	Trace
71	U8	30	Total	C	N	O	0	0
			150	90	30	30		

- Molecule 72 is a protein called UnkC.

Mol	Chain	Residues	Atoms				AltConf	Trace
72	UC	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 73 is a protein called UnkD.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	UD	13	Total	C	N	O	0	0
			65	39	13	13		

- Molecule 74 is a protein called UnkF.

Mol	Chain	Residues	Atoms				AltConf	Trace
74	UF	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 75 is a protein called UnkG.

Mol	Chain	Residues	Atoms				AltConf	Trace
75	UG	15	Total	C	N	O	0	0
			75	45	15	15		

- Molecule 76 is a protein called UnkI.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	UI	6	Total	C	N	O	0	0
			30	18	6	6		

- Molecule 77 is a protein called UnkK.

Mol	Chain	Residues	Atoms				AltConf	Trace
77	UK	24	Total	C	N	O	0	0
			120	72	24	24		

- Molecule 78 is a protein called Unk.

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

- Molecule 79 is a protein called UnkP.

Mol	Chain	Residues	Atoms				AltConf	Trace
79	UP	32	Total	C	N	O	0	0
			160	96	32	32		

- Molecule 80 is a protein called Unka.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	Ua	10	Total	C	N	O	0	0
			50	30	10	10		

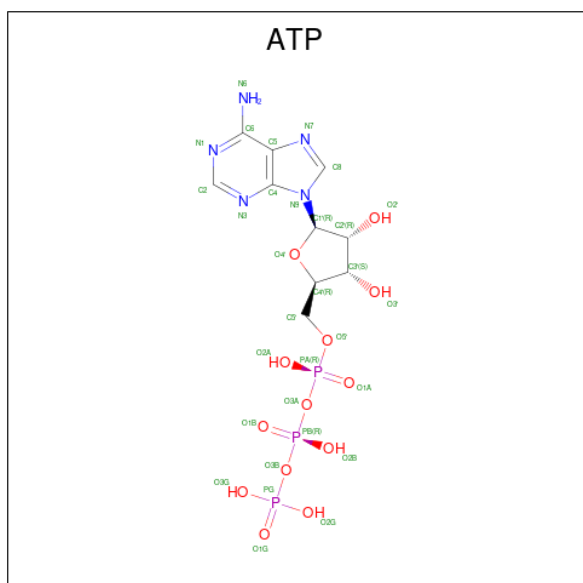
- Molecule 81 is a protein called Unkg.

Mol	Chain	Residues	Atoms				AltConf	Trace
81	Ug	238	Total	C	N	O	0	0
			1190	714	238	238		

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

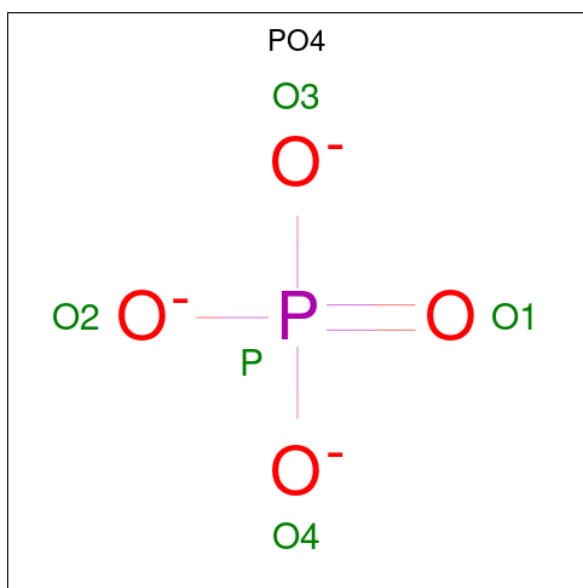
Mol	Chain	Residues	Atoms		AltConf
82	CA	4	Total	Mg	0
			4	4	
82	CQ	1	Total	Mg	0
			1	1	
82	Cg	1	Total	Mg	0
			1	1	
82	IA	1	Total	Mg	0
			1	1	

- Molecule 83 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



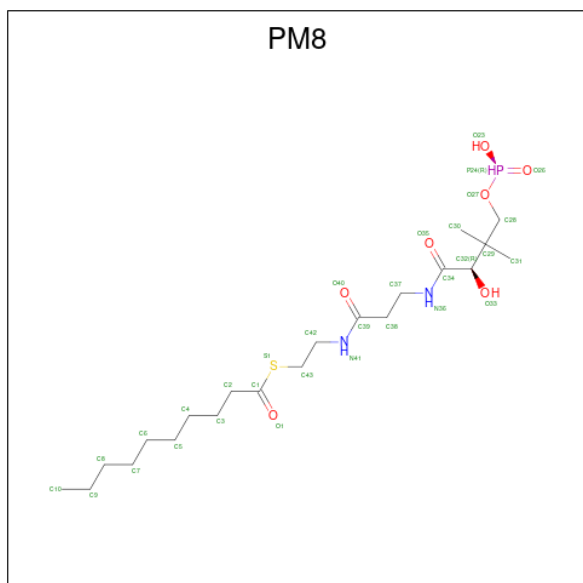
Mol	Chain	Residues	Atoms					AltConf
83	Cg	1	Total	C	N	O	P	0
			31	10	5	13	3	

- Molecule 84 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



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

- Molecule 85 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).

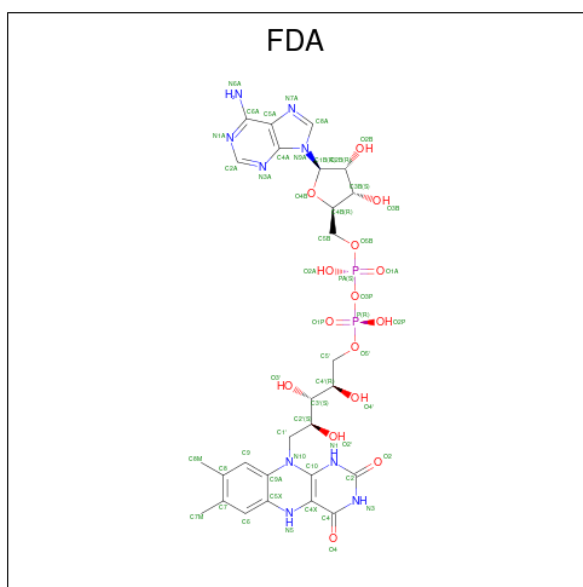


Mol	Chain	Residues	Atoms					AltConf
85	Fc	1	Total	C	N	O	P	S
			32	21	2	7	1	1
								0

- Molecule 86 is ZINC ION (three-letter code: ZN) (formula: Zn).

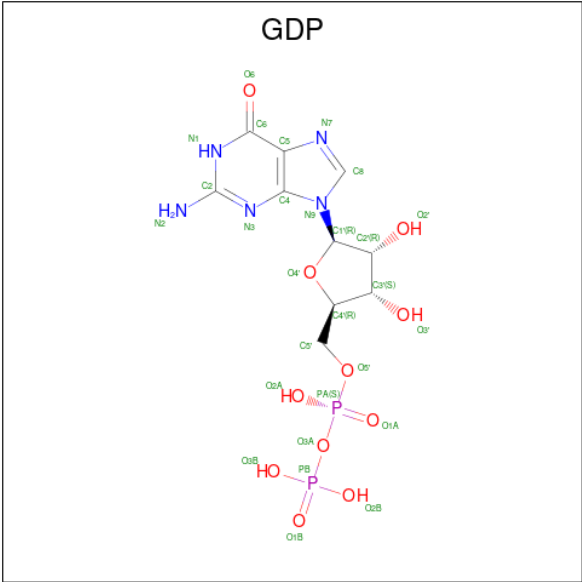
Mol	Chain	Residues	Atoms		AltConf
86	Fd	1	Total	Zn	0
			1	1	

- Molecule 87 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula: C₂₇H₃₅N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					AltConf
87	Ff	1	Total	C	N	O	P	
			53	27	9	15	2	0

- Molecule 88 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
88	IA	1	Total	C	N	O	P	0
			28	10	5	11	2	

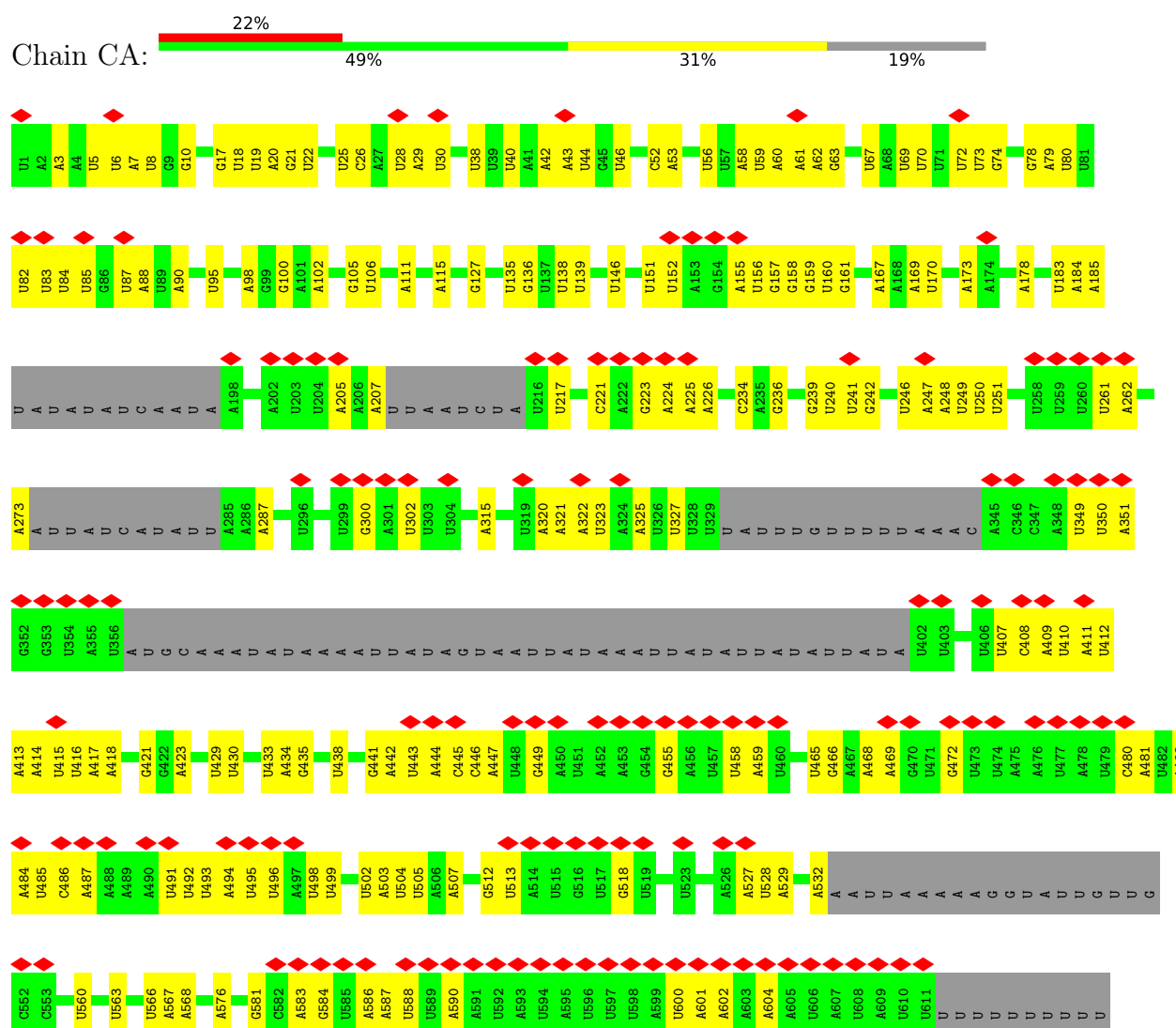
- Molecule 89 is water.

Mol	Chain	Residues	Atoms		AltConf
89	Cg	3	Total	O	0
			3	3	
89	IA	2	Total	O	0
			2	2	

3 Residue-property plots

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

• Molecule 1: 9S rRNA



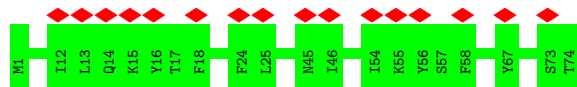
• Molecule 2: 9S rRNA




A1
A2
U3

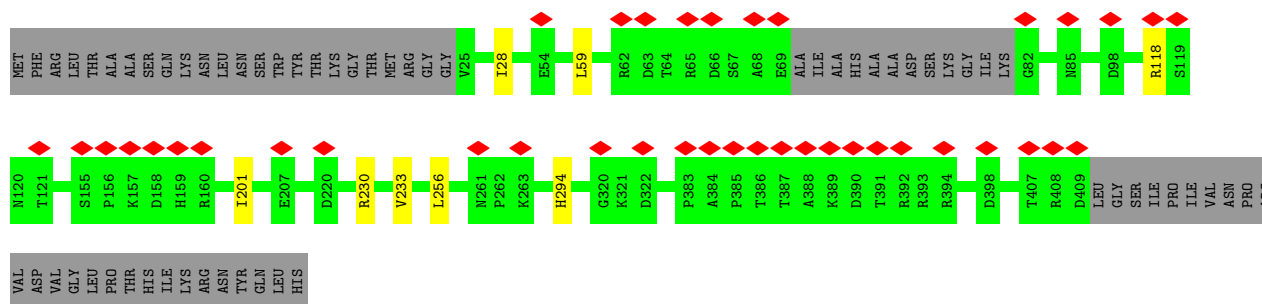
- Molecule 3: uS3m

Chain CC:  22% 100%



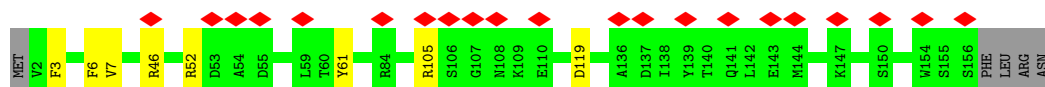
- Molecule 4: Ribosomal_S5_C domain-containing protein

Chain CE:  9% 84% 14%




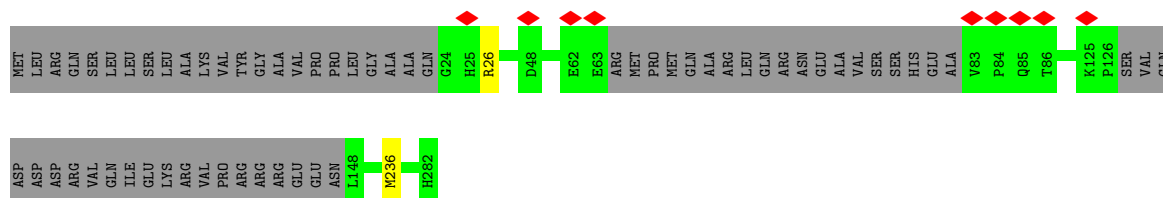
- Molecule 5: bS6m

Chain CF:  13% 92% 5%



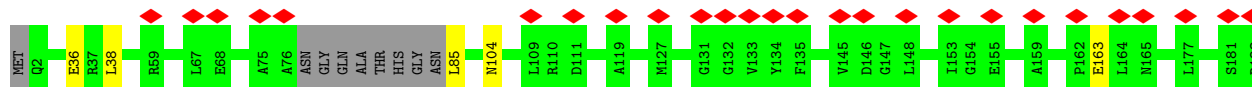
- Molecule 6: 30S ribosomal protein S8, putative


Chain CH:  77% 22%

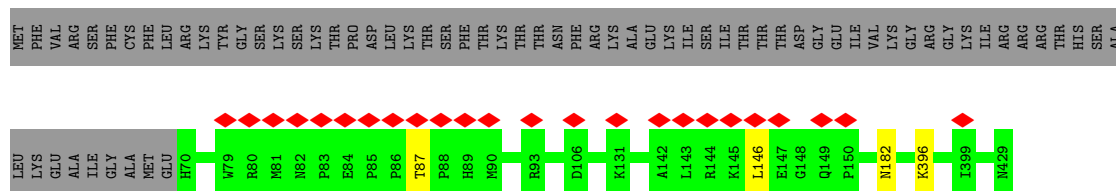


- Molecule 7: uS9m

Chain CI:  7% 94% 5%

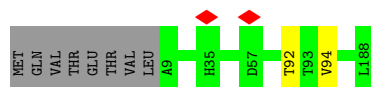


Chain CO:  6% 83% 16%

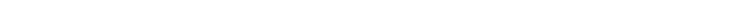


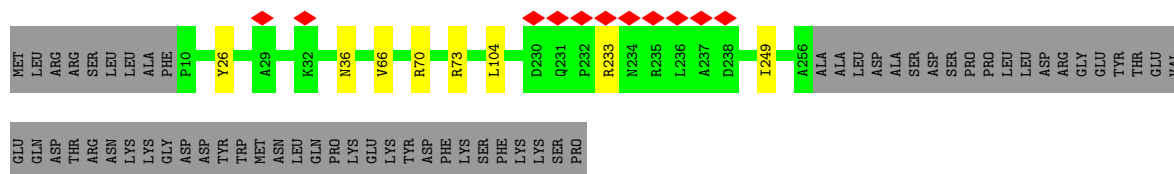
- Molecule 13: bS16m

Chain CP:  95% ..



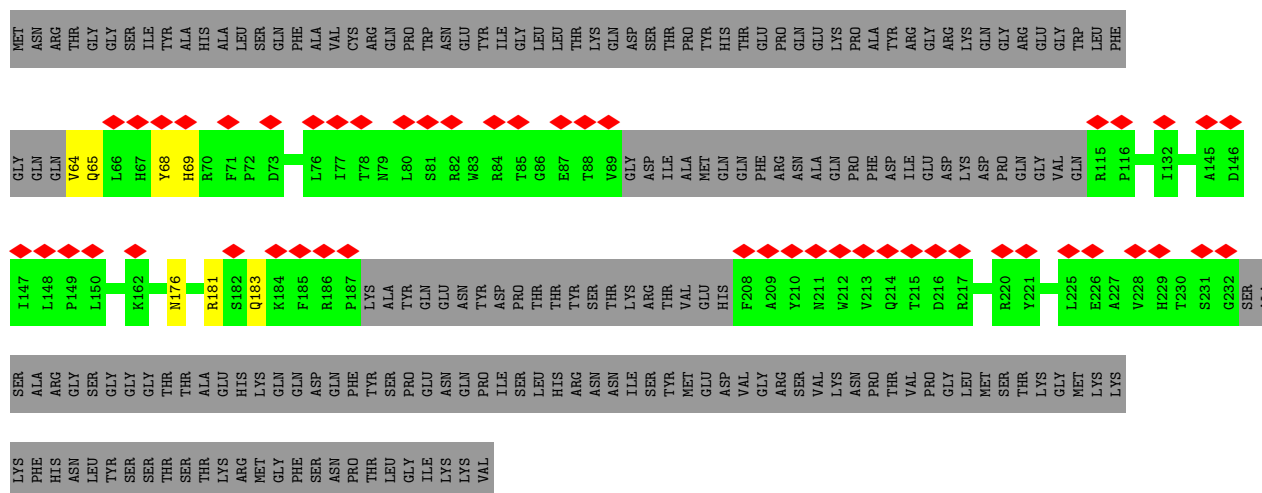
- Molecule 14: 30S Ribosomal protein S17, putative

Chain CQ:  78% 20%



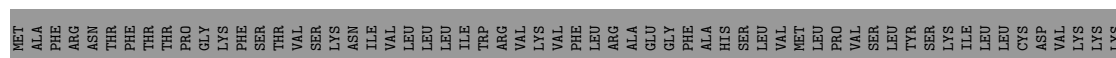
- Molecule 15: bS18m

Chain CR: 



- Molecule 16: uS19m

Chain CS: 



GLY	GLY	GLN	ARG	SER	ALA	VAL	GLY	THR	ARG	GLY	THR	GLN	VAL	GLY	VAL	LYS	GLY	THR	ALA	ASN	ASP	SER	VAL	ARG	GLN	LEU	ARG	GLY	LYS	ALA	ASP	GLN	THR	THR	GLY	GLY	THR	GLY	THR	UNK	CYS	SER	ARG	ASP	GLY	PHE	ALA	ALA	MET
LYS	ALA	ASN	LYS																																														

• Molecule 20: mS26



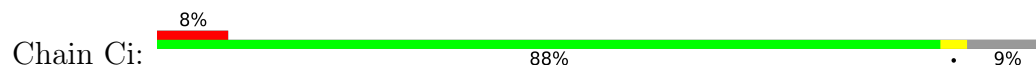
LYS	ASP	MET	VAL	LYS	ASP	LYS	THR	HIS	ARG	GLY	LYS	TYR	LYS	SER	SER	SER	GLY	ASP	SER	SER	ASP	GLY	LYS	ILE	VAL	GLN	GLY	VAL	THR	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
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• Molecule 21: mS29



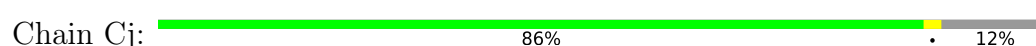
MET	ARG	LYS	T5	L6	K7	K8	S9	R43	K44	L45	K46	M47	G48	R52	R107	E114	T139	G236	Q262	L269	H296	D347	D468	S487	R488	C489	A490	S491	SER	GLY	ALA	VAL	GLY	VAL	VAL	ARG
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• Molecule 22: mS33



MET	VAL	LEU	ARG	TRP	PHE	PRO	LEU	GLY	G11	V15	R34	D75	G79	L84	D106	D111	H136	Q143	D146	R147	K148	L149	S150	G151	K155	K163	E170	D174	A175	THR	GLU	GLU	GLY	ASP
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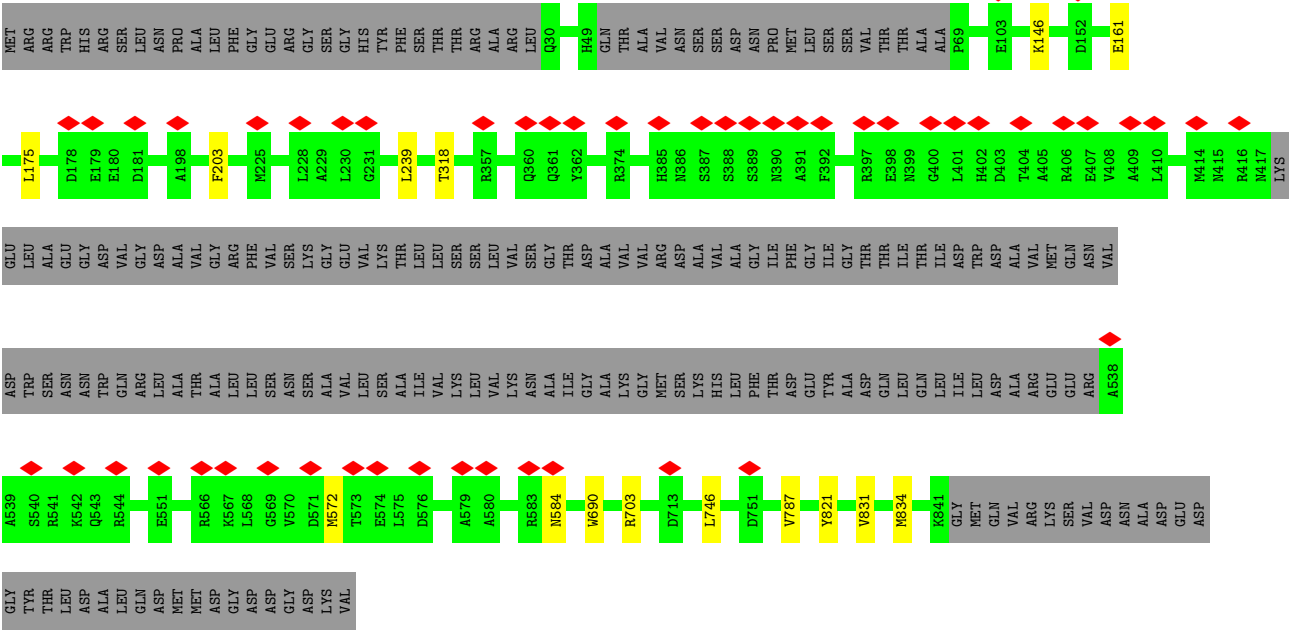
• Molecule 23: mS34



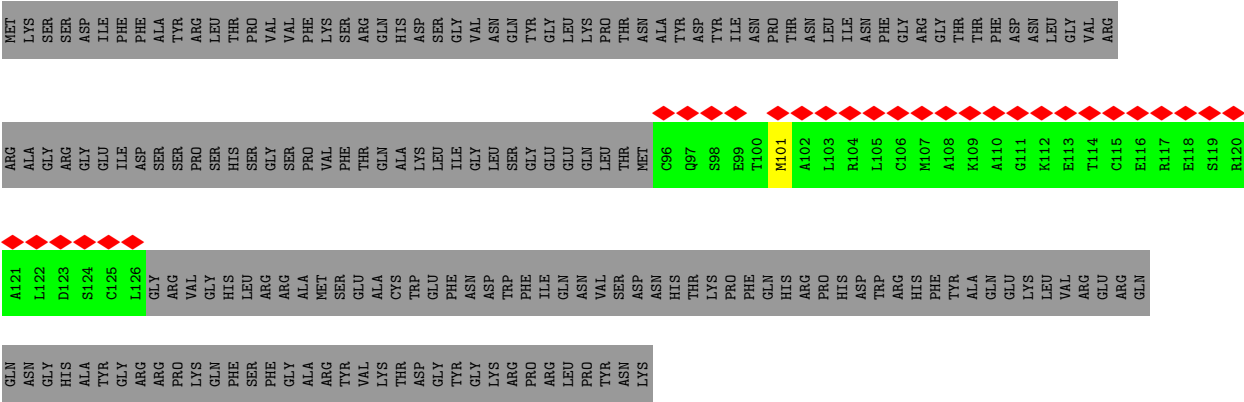
MET	LEU	ARG	CYS	ALA	ARG	VAL	ALA	LEU	R10	S30	R118	Y126	D167	Y209	P235	THR	GLY	THR	ALA	ASP	VAL	ASP	LYS	ASP	PRO	THR	THR	SER	ASP	GLY	SER	VAL	HIS	TYR	ASP	GLY	LYS
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• Molecule 24: mS35

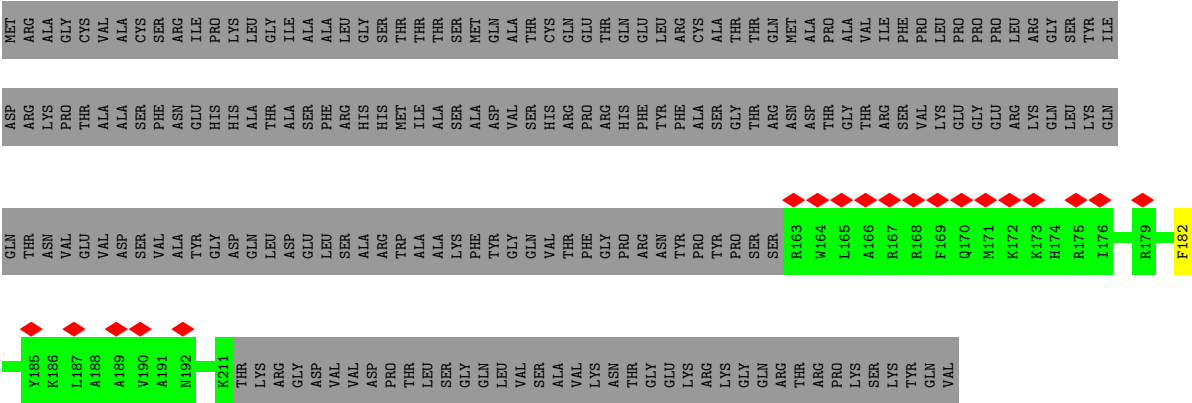





• Molecule 25: mS37

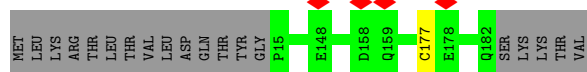


• Molecule 26: mS38



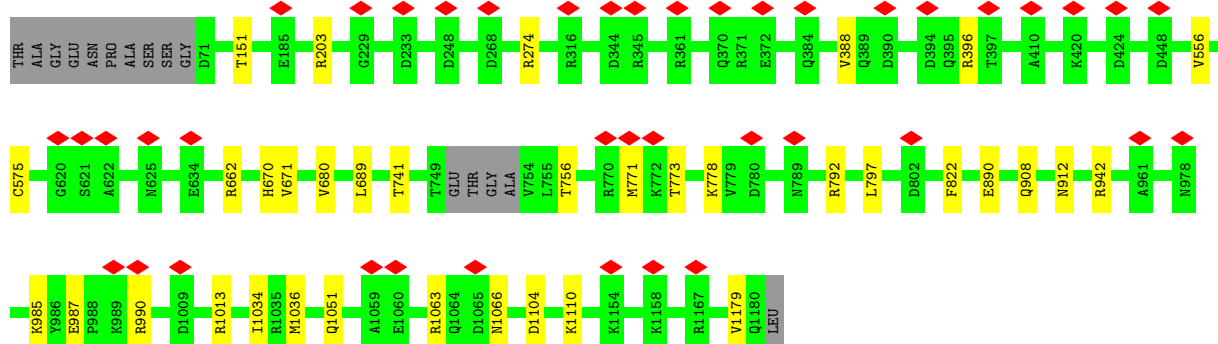
- Molecule 27: Protein FYV4, mitochondrial

Chain Cp:  89% 10%



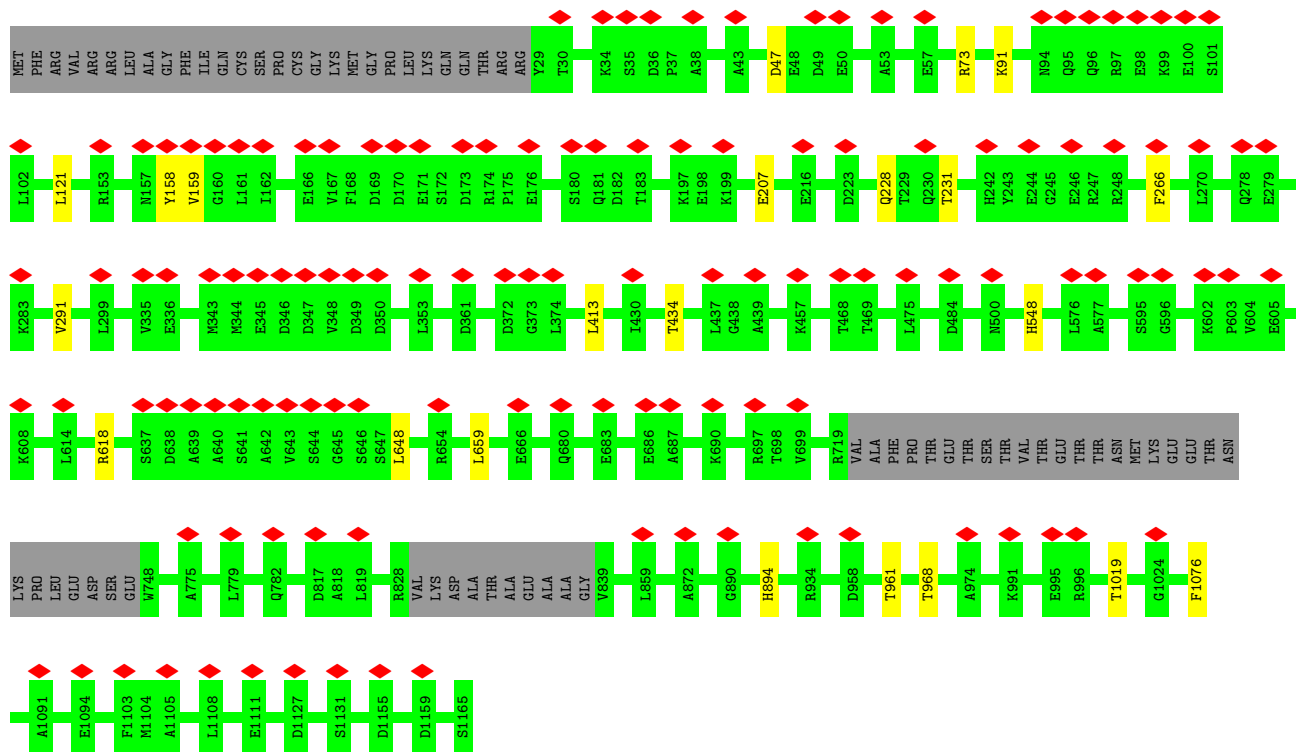
- Molecule 28: mS49

Chain DB:  91% 6%

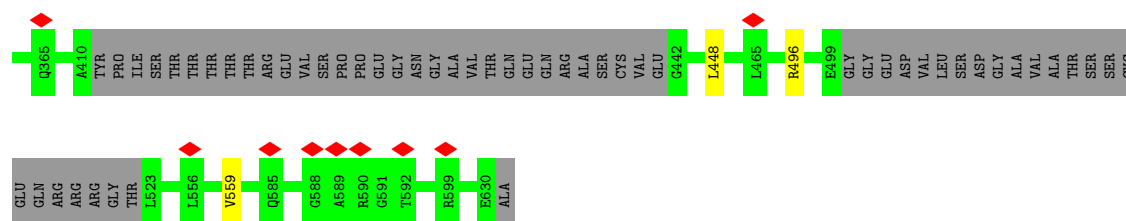


- Molecule 29: mS50

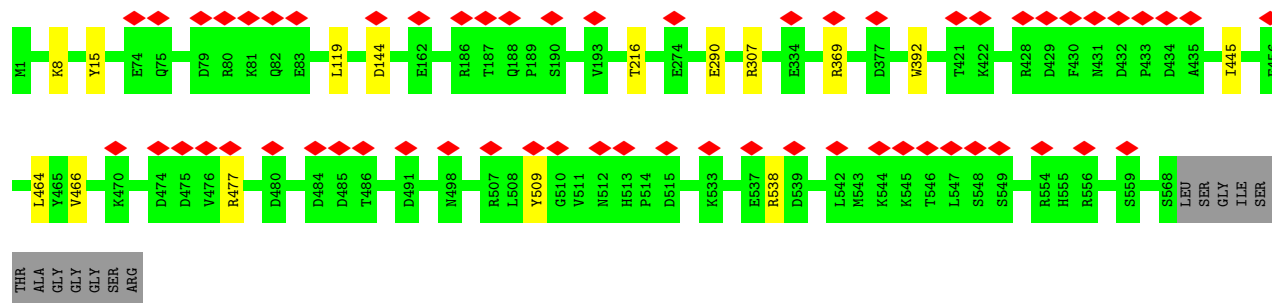
Chain DC:  11% 92% 6%



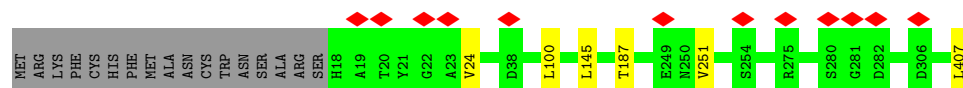
Amino Acid	Count
MET	1
PHE	2
ARG	2
ARG	2
ALA	2
ILE	2
PRO	2
LEU	2
LEU	2
SER	2
A11	3
N12	3
H63	4
H78	4
D98	4
A110	4
D118	4
D119	4
L127	4
D135	4
H143	4
E175	4
R186	4
Y211	4
T220	4
H229	4
L250	4
R261	4
P262	4
SER	4
VAL	4
ASN	4
PRO	4
GLY	4
VAL	4
SER	4
SER	4
LEU	4
ALA	4
S272	4
D300	4
E307	4
D349	4



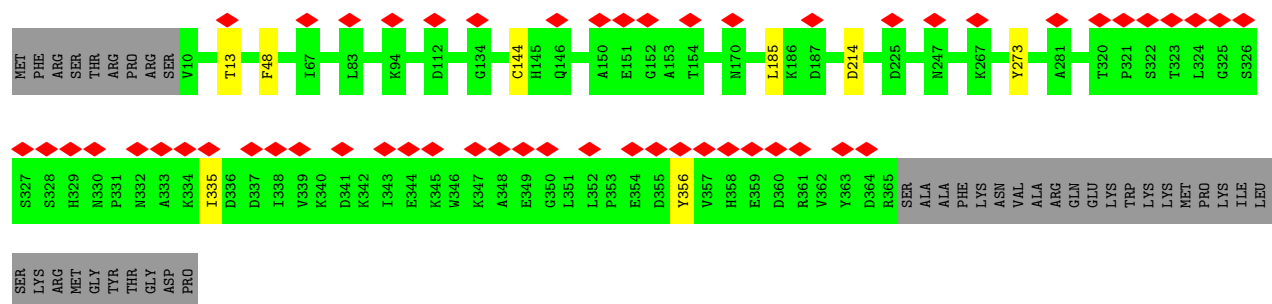
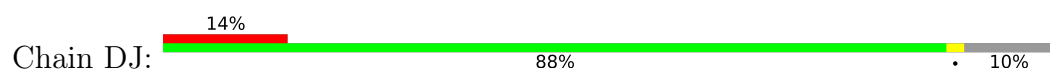
• Molecule 34: mS55



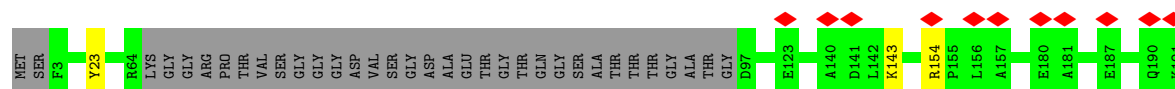
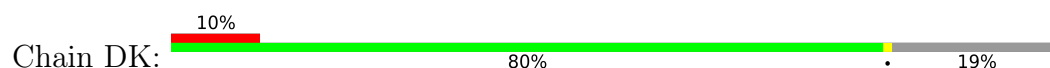
• Molecule 35: mS56

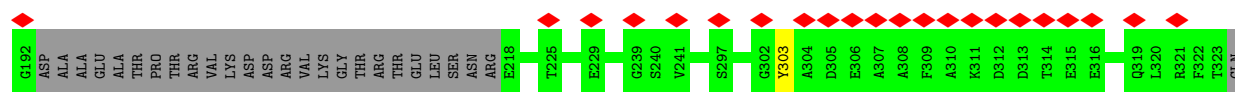


• Molecule 36: mS57

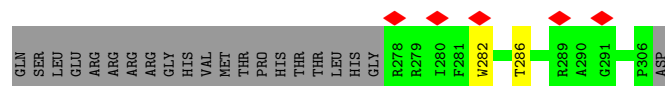
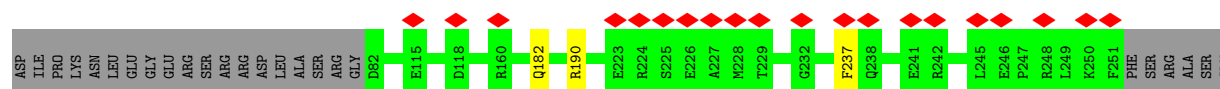
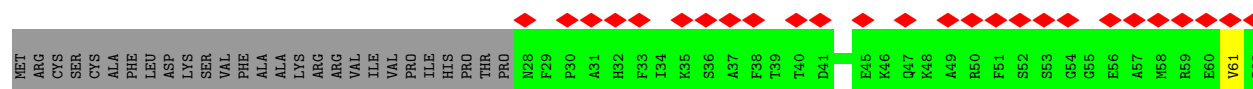
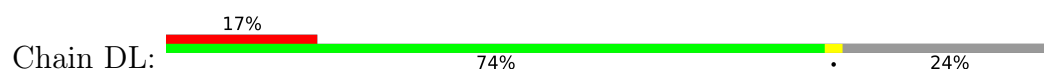


• Molecule 37: mS58

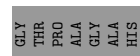
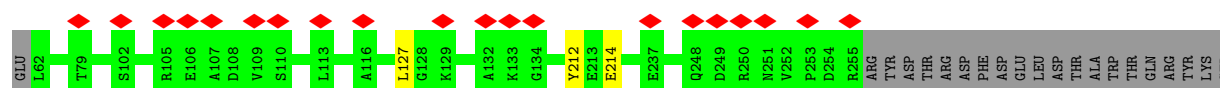
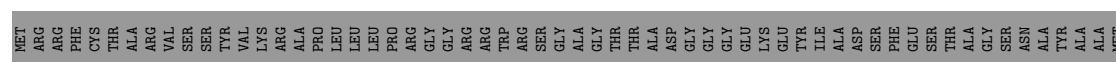




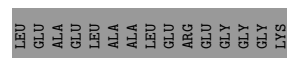
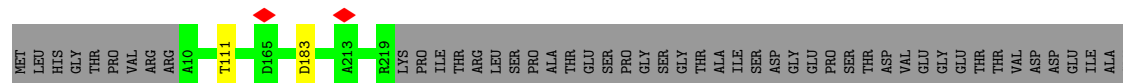
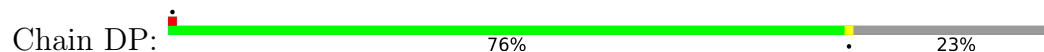
• Molecule 38: mS59



• Molecule 39: mS62



• Molecule 40: mS63

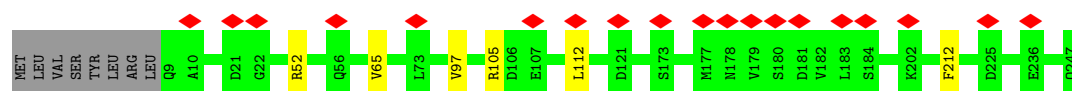


• Molecule 41: mS65



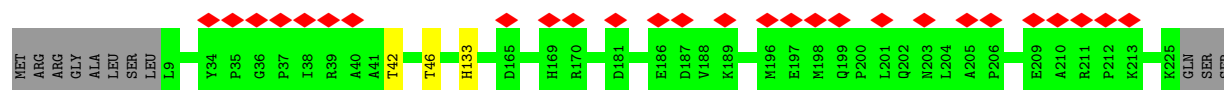
• Molecule 42: Rhodanese domain-containing protein

Chain DT: 




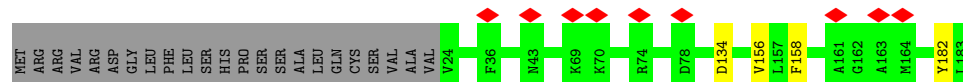
- Molecule 43: Ubiquitin-like domain-containing protein

Chain DU: 




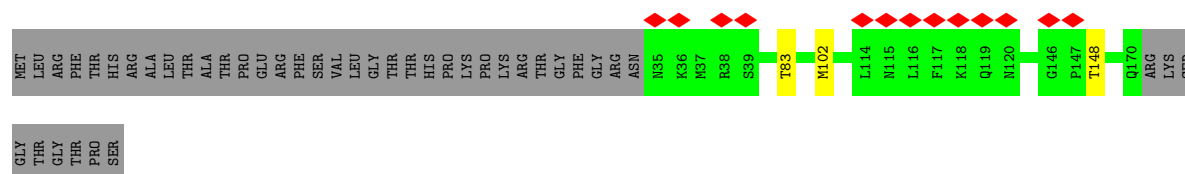
- Molecule 44: mS69

Chain DV: 




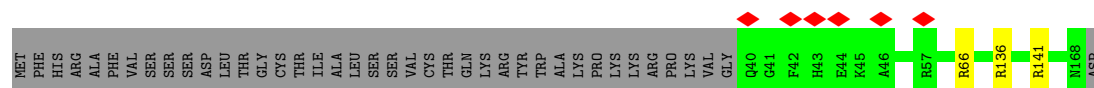
- Molecule 45: mS70

Chain DW: 



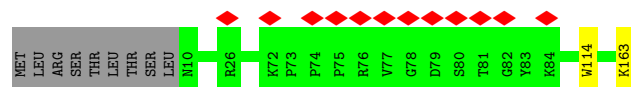
- Molecule 46: mS71

Chain DX: 



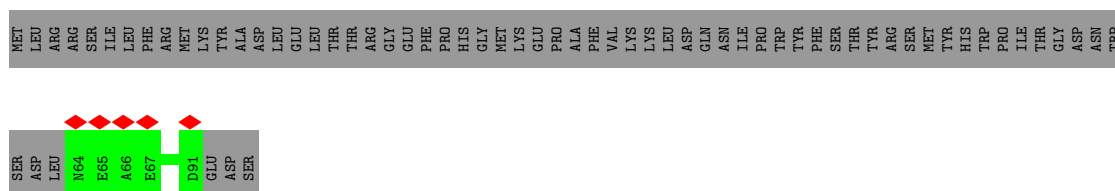
- Molecule 47: mS72

Chain DY: 

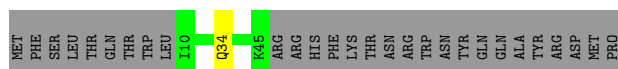


- Molecule 48: mS73

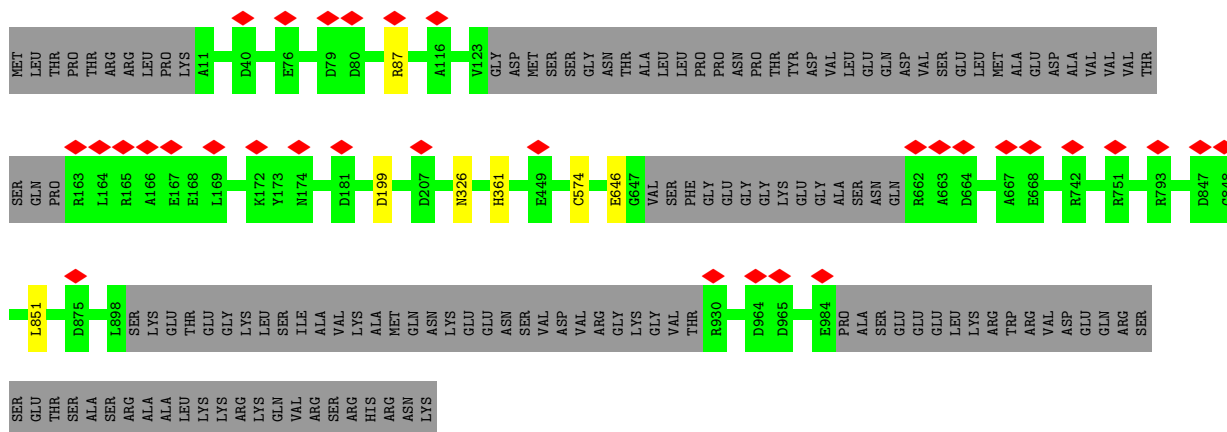
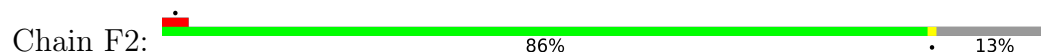
Chain DZ: 



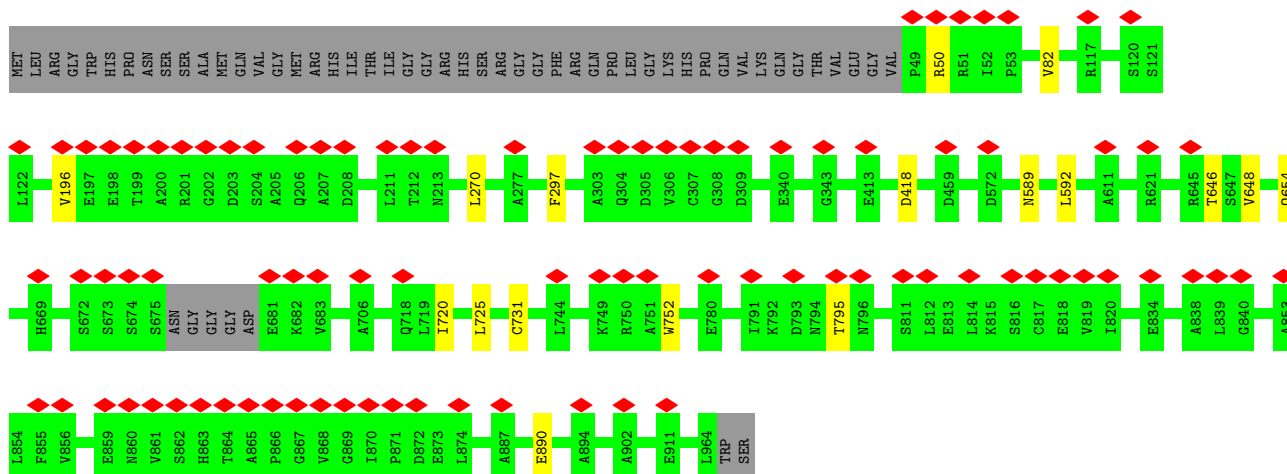
• Molecule 49: mS74




• Molecule 50: PPR_long domain-containing protein

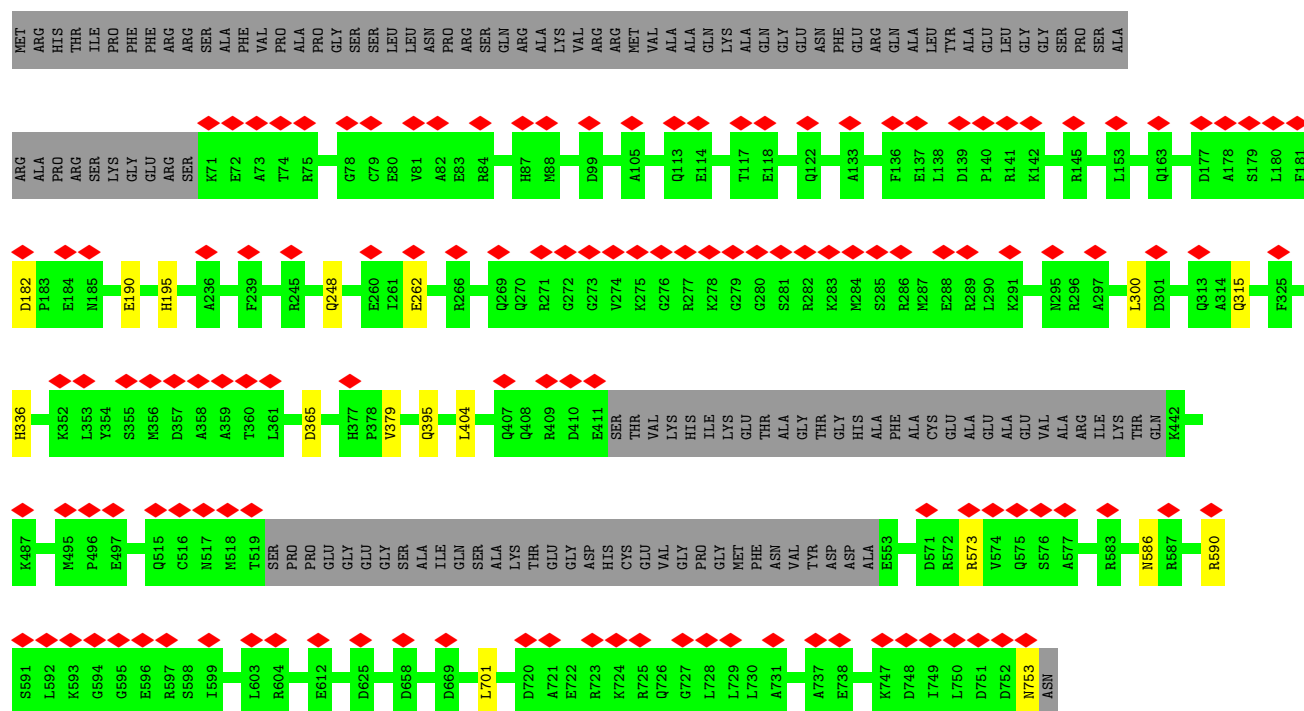


• Molecule 51: mt-SAF3




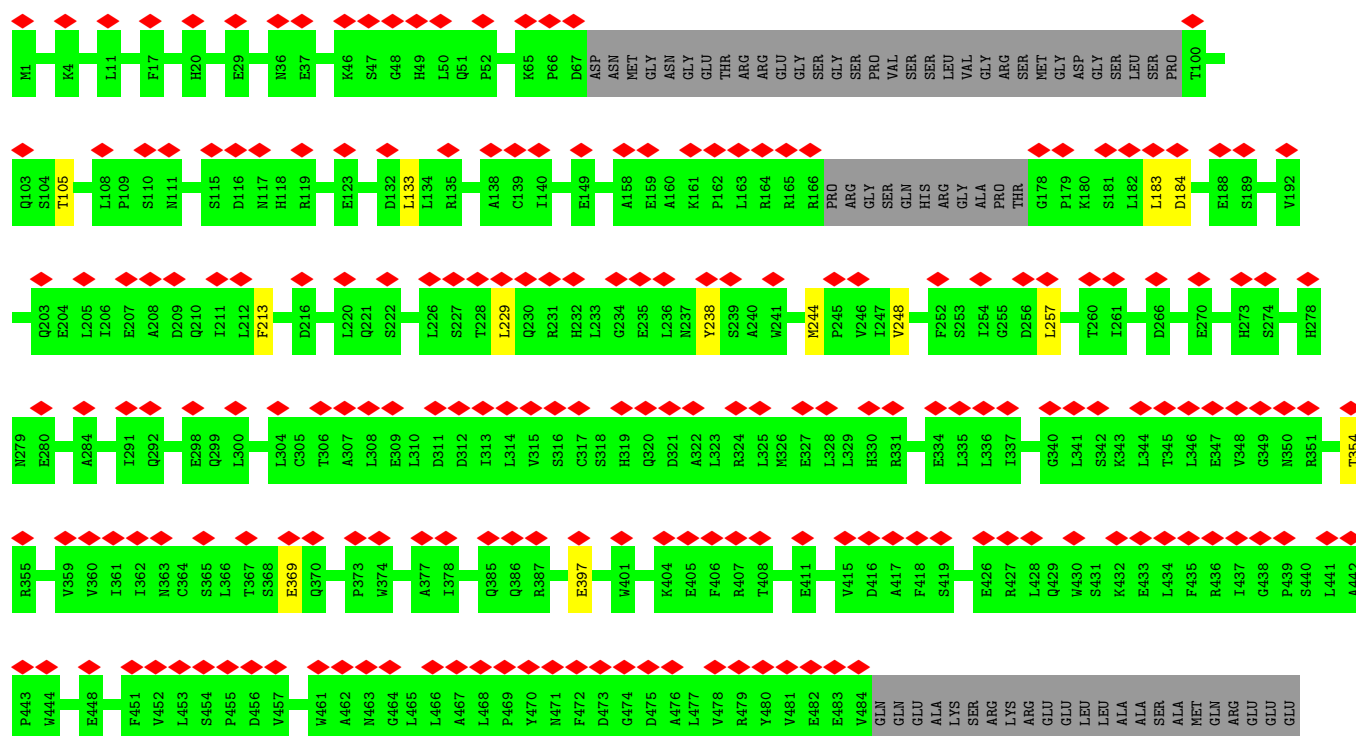
• Molecule 52: mt-SAF5

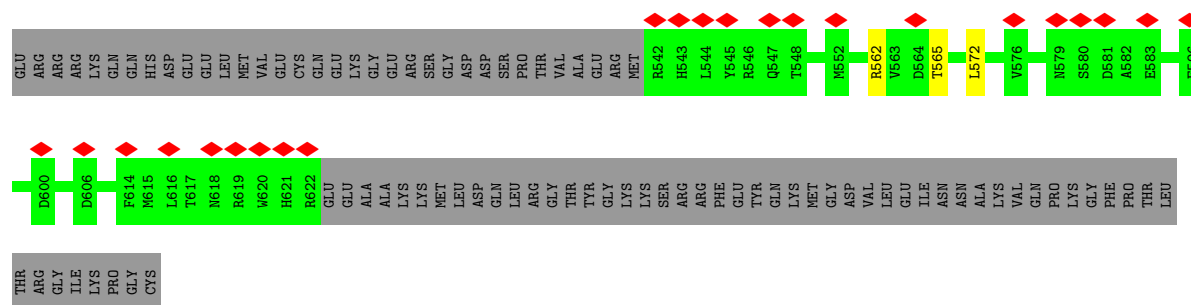
Chain F5: 



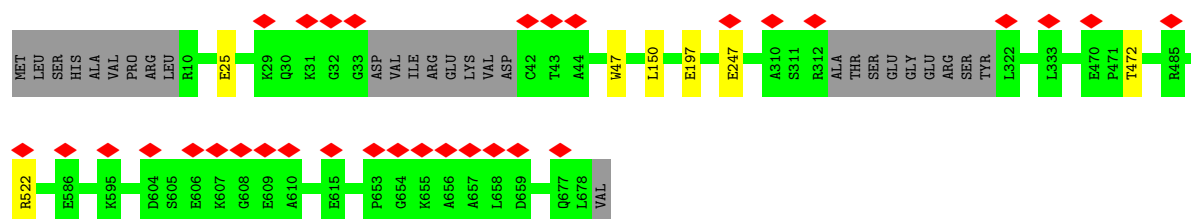
• Molecule 53: DUF4460 domain-containing protein

Chain F6: 

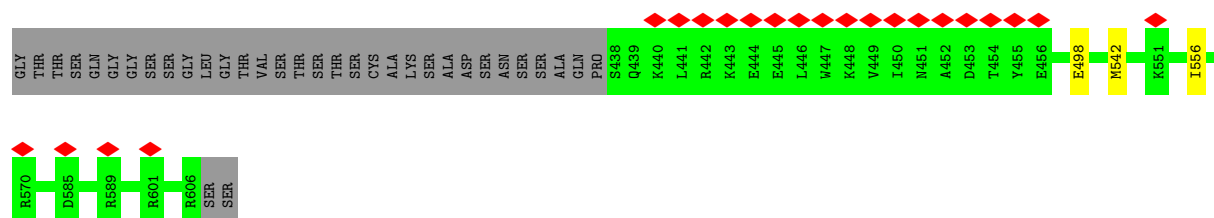
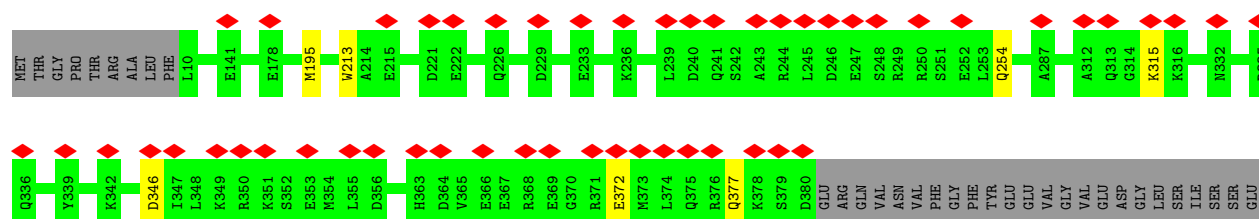




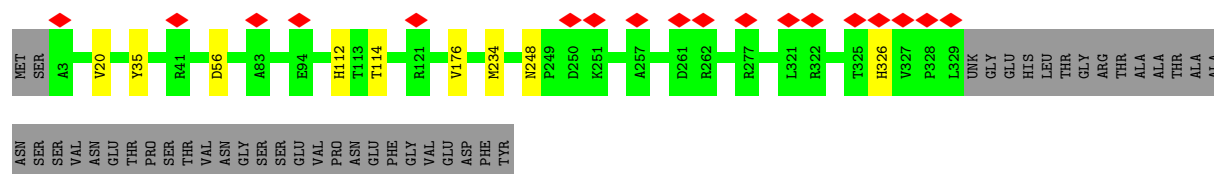
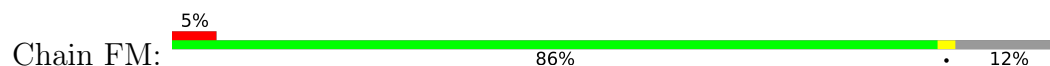
• Molecule 54: mt-SAF7



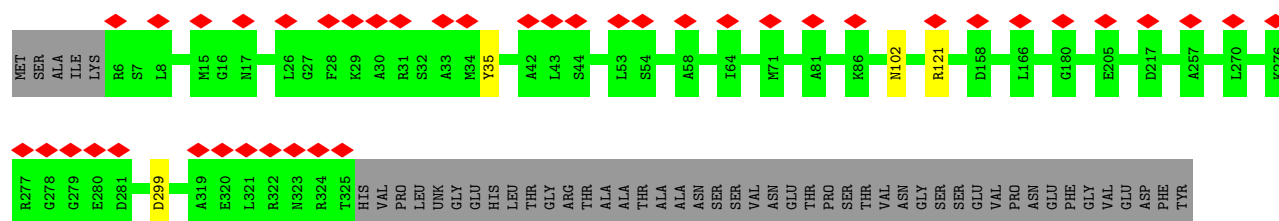
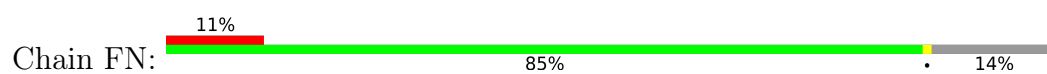
• Molecule 55: mt-SAF9



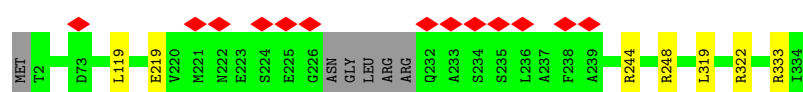
• Molecule 56: mt-SAF21



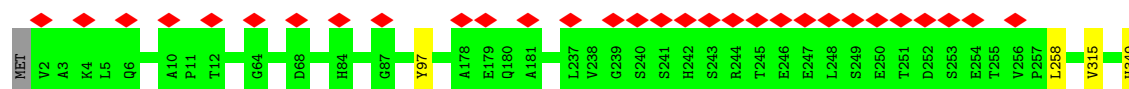
• Molecule 56: mt-SAF21



• Molecule 57: mt-SAF22



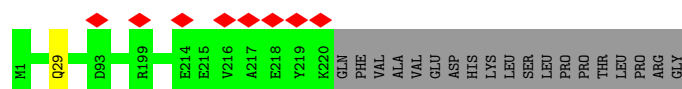
• Molecule 58: mt-SAF23



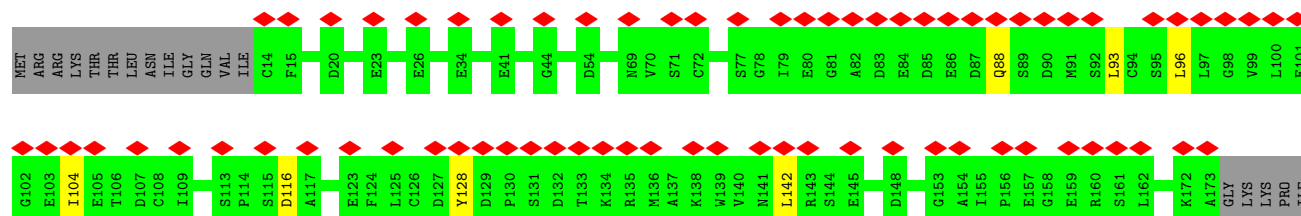
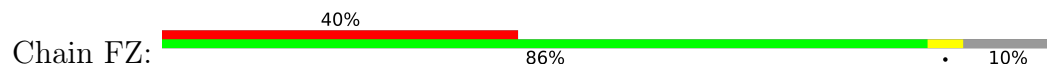
• Molecule 59: LMWPc domain-containing protein



• Molecule 60: mt-SAF27



• Molecule 61: mt-SAF29



MET ASN CYS SER SER THR LEU ALA CYS HIS ALA VAL VAL SER SER PRO SER THR SER LEU ILE THR SER CYS CYS R26 T27 R93 T94 K101 L122 D129 F150 PHE

ARG	THR	GLY	GLN	Y65	L66	L67	E84	G102	E110	I120	L121	D122	D125	H126	D136	A147	LYS
ARG	THR	GLY	GLN	Y65	L66	L67	E84	G102	E110	I120	L121	D122	D125	H126	D136	A147	LYS

Chain Fd:

59%

64%

35%

Met

Arg

His

Phe

Gly

Pro

Ser

Ile

Ala

His

Phe

Pro

Leu

Ser

Ala

Asn

Gln

Leu

Arg

Phe

Lys

Ala

Ser

H24

I25

R26

I27

A28

N29

R30

K31

R32

V33

E34

M35

F36

V37

A38

K39

R40

F41

H42

L43

L47

A48

T49

A50

A51

P52

D53

I54

A55

A56

E57

W58

H59

D60

E61

L62

M63

P64

M65

H66

Y68

P69

A70

I71

I72

G73

I74

G75

H76

V77

Q78

P79

V80

W81

W82

K83

C84

A85

I86

C87

S88

H89

S90

Y91

Q92

M93

S94

V95

E96

K97

R98

V99

V100

R101

G102

G103

G104

C105

P106

Q107

C108

V109

V110

M111

G112

K113

R114

A115

V116

ALA

ASP

GLY

ALA

LEU

C

GLY

GLU

MET

ASP

SER

GLN

LEU

ARG

PRO

ARG

PRO

VAL

MET

PHE

ASN

MET

ARG

THR

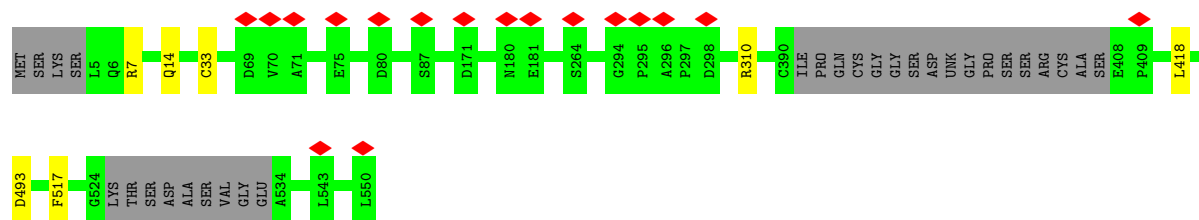
LYS

TYR

[illegible]

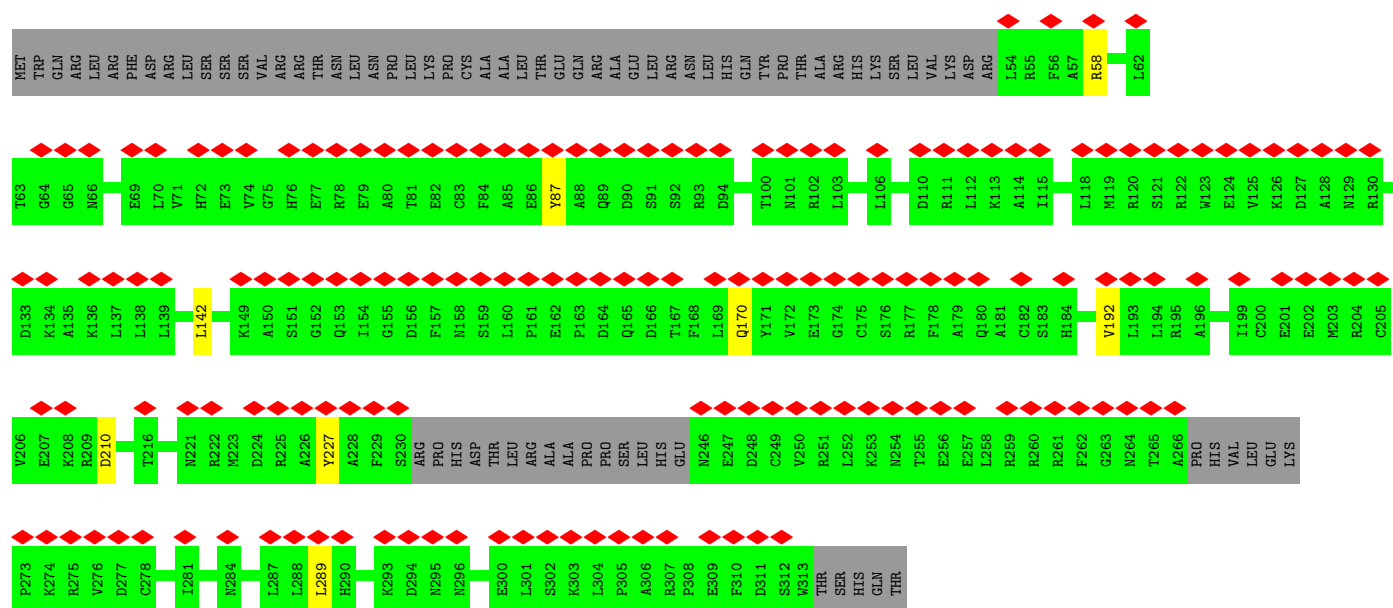
- Molecule 66: Acyl transferase-like protein, putative

Chain Fg:  93% 5%




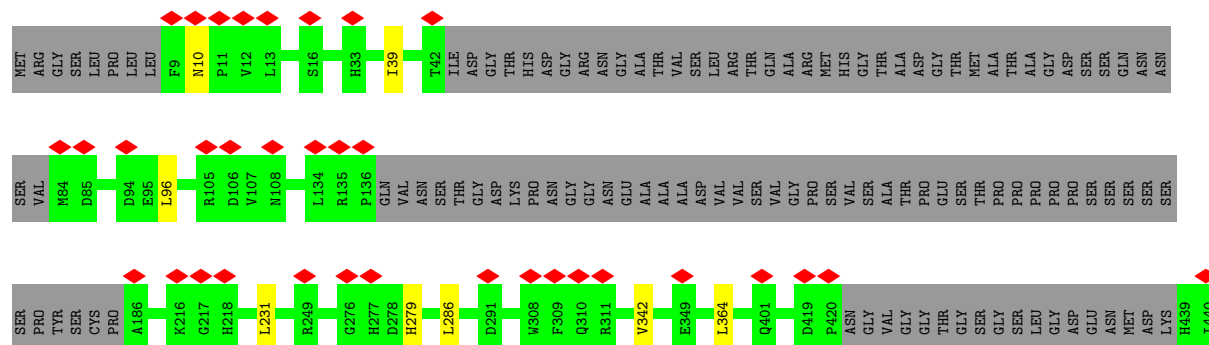
- Molecule 67: mt-SAF37

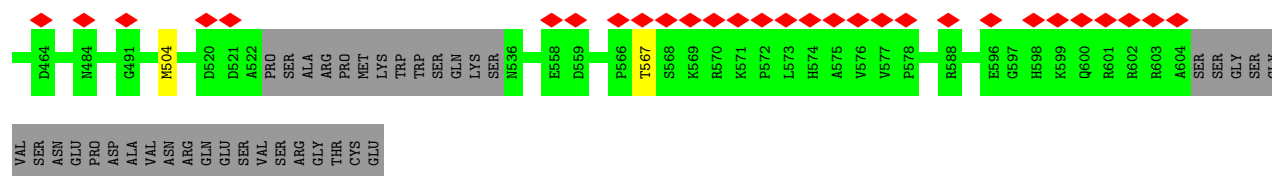
Chain Fh:  52% 73% 25%



- Molecule 68: mt-SAF38

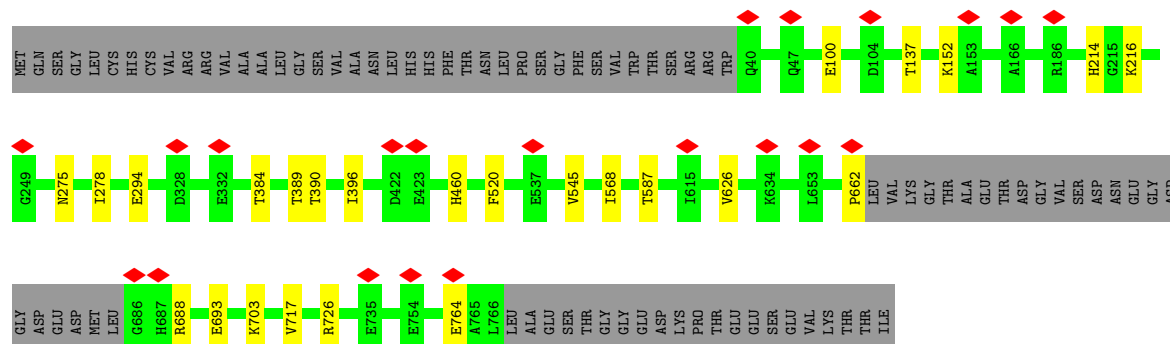
Chain Fi:  10% 74% 24%





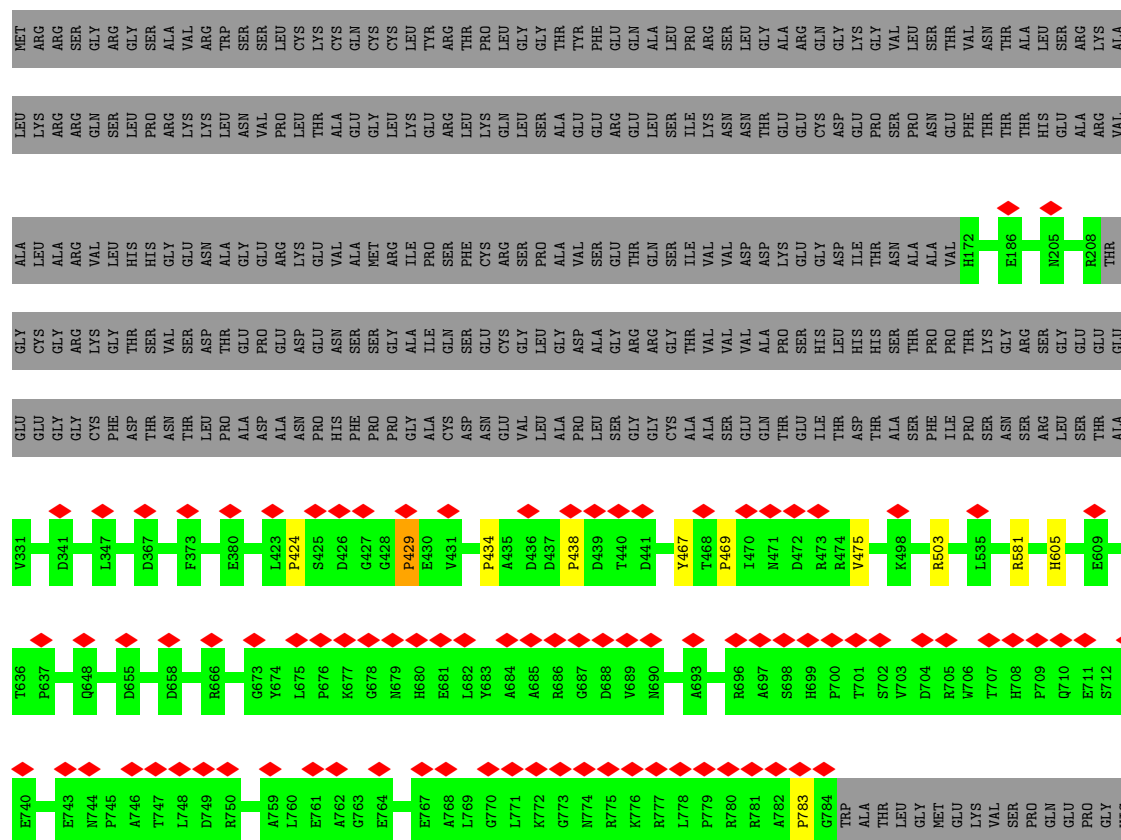
- Molecule 69: Translation initiation factor IF-2, putative

Chain IA: 86% 11%

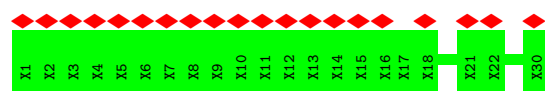


- Molecule 70: mt-SAF39

Chain IB: 13% 60% 39%



- Molecule 71: Unk8



- Molecule 72: UnkC

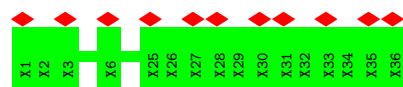


There are no outlier residues recorded for this chain.

- Molecule 73: UnkD



- Molecule 74: UnkF



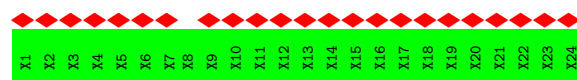
- Molecule 75: UnkG



- Molecule 76: UnkI



- Molecule 77: UnkK



- Molecule 78: Unk

Chain UM:  100%

There are no outlier residues recorded for this chain.

- Molecule 78: Unk

Chain UN:  25%  100%

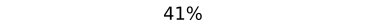



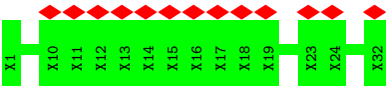
- Molecule 78: Unk

Chain UQ:  25%  100%



- Molecule 79: UnkP

Chain UP:  41%  100%

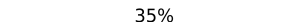




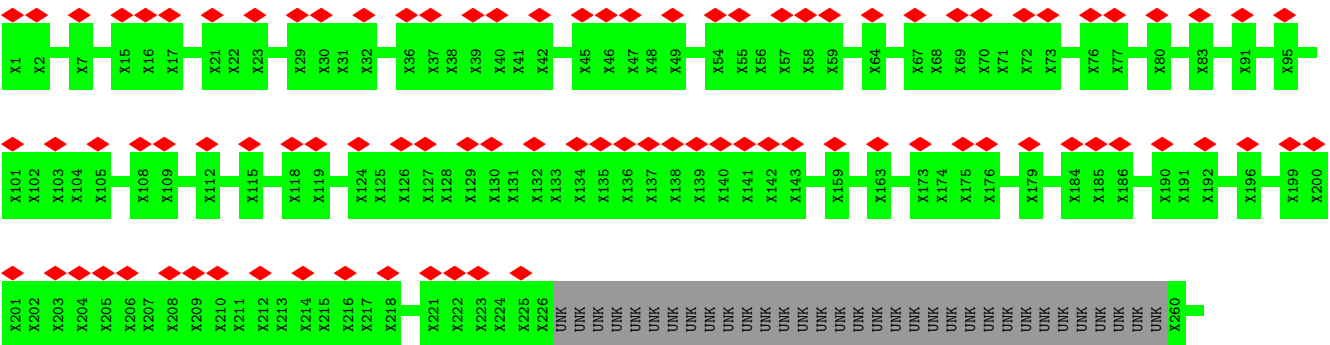
- Molecule 80: Unka

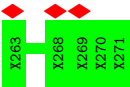
Chain Ua:  10%  100%



- Molecule 81: Unkg

Chain Ug:  35%  88%  12%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	38531	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 ($e^-/\text{\AA}^2$)	40	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	0.264	Depositor
Minimum map value	-0.127	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	500.4, 500.4, 500.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.39, 1.39, 1.39	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, ZN, MG, PM8, ATP, FDA, GDP

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	CA	0.19	1/11001 (0.0%)	0.71	2/17084 (0.0%)
2	CB	0.17	0/71	0.61	0/108
3	CC	0.26	0/666	0.43	0/900
4	CE	0.25	0/3100	0.51	0/4193
5	CF	0.25	0/1305	0.50	0/1761
6	CH	0.24	0/1839	0.51	0/2479
7	CI	0.24	0/3420	0.48	0/4619
8	CJ	0.25	0/6561	0.48	1/8927 (0.0%)
9	CK	0.25	0/1468	0.53	0/1971
10	CL	0.30	0/726	0.51	0/981
11	CN	0.24	0/1361	0.48	0/1840
12	CO	0.25	0/3070	0.49	0/4145
13	CP	0.25	0/1533	0.49	0/2074
14	CQ	0.26	0/2072	0.50	0/2808
15	CR	0.25	0/1083	0.49	0/1467
16	CS	0.25	0/851	0.47	0/1150
17	CU	0.22	0/296	0.48	0/397
18	Ca	0.25	0/4378	0.47	0/5921
19	Cb	0.25	0/1273	0.48	0/1711
20	Cd	0.26	0/1818	0.45	0/2447
21	Cg	0.25	0/4064	0.45	0/5518
22	Ci	0.25	0/1388	0.48	0/1878
23	Cj	0.25	0/1842	0.48	0/2511
24	Ck	0.23	0/5469	0.48	0/7396
25	Cm	0.23	0/231	0.49	0/305
26	Cn	0.24	0/434	0.52	0/573
27	Cp	0.25	0/1472	0.49	0/1996
28	DB	0.24	0/9332	0.50	0/12641
29	DC	0.24	0/8971	0.47	0/12172
30	DD	0.26	0/6494	0.48	0/8808
31	DE	0.24	0/5246	0.48	0/7111
32	DF	0.24	0/4895	0.51	0/6635

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	DG	0.25	0/4608	0.49	0/6242
34	DH	0.24	0/4716	0.49	0/6392
35	DI	0.25	0/3248	0.47	0/4401
36	DJ	0.25	0/2993	0.46	0/4063
37	DK	0.24	0/2132	0.46	0/2877
38	DL	0.25	0/1952	0.49	0/2629
39	DO	0.24	0/1597	0.50	0/2153
40	DP	0.24	0/1837	0.46	0/2488
41	DR	0.26	0/2099	0.50	0/2861
42	DT	0.25	0/2133	0.46	0/2889
43	DU	0.25	0/1772	0.49	0/2404
44	DV	0.25	0/1382	0.51	0/1871
45	DW	0.24	0/1202	0.47	0/1639
46	DX	0.24	0/1128	0.49	0/1516
47	DY	0.25	0/1337	0.51	0/1814
48	DZ	0.24	0/246	0.39	0/332
49	Da	0.24	0/332	0.52	0/441
50	F2	0.25	0/7281	0.46	0/9837
51	F3	0.24	0/7158	0.47	0/9686
52	F5	0.24	0/5144	0.48	1/6918 (0.0%)
53	F6	0.24	0/4297	0.46	0/5841
54	F7	0.25	0/5281	0.46	0/7149
55	F9	0.25	0/4497	0.49	0/6031
56	FM	0.24	0/2497	0.47	0/3376
56	FN	0.24	0/2441	0.47	0/3299
57	FO	0.24	0/2763	0.52	0/3735
58	FP	0.25	0/2710	0.46	0/3709
59	FW	0.24	0/2002	0.52	0/2704
60	FX	0.25	0/1783	0.46	0/2410
61	FZ	0.23	0/1287	0.43	0/1737
62	Fb	0.25	0/1092	0.45	0/1471
63	Fc	0.24	0/670	0.44	0/912
64	Fd	0.23	0/759	0.48	0/1028
65	Ff	0.25	0/5149	0.48	0/7008
66	Fg	0.24	0/4129	0.47	0/5595
67	Fh	0.24	0/1902	0.48	0/2566
68	Fi	0.25	0/3899	0.50	0/5296
69	IA	0.26	0/5577	0.49	1/7550 (0.0%)
70	IB	0.24	0/3944	0.55	5/5333 (0.1%)
73	UD	0.25	0/64	0.42	0/88
75	UG	0.24	0/74	0.39	0/102
All	All	0.24	1/208844 (0.0%)	0.50	10/284920 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CA	302	U	C1'-N1	6.06	1.57	1.48

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	IB	429	PRO	N-CA-CB	6.89	111.57	103.30
70	IB	424	PRO	N-CA-CB	6.48	111.08	103.30
8	CJ	540	PRO	N-CA-CB	6.41	110.99	103.30
1	CA	70	U	C2-N1-C1'	6.38	125.35	117.70
69	IA	662	PRO	N-CA-CB	5.96	110.45	103.30

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	
3	CC	72/74 (97%)	68 (94%)	4 (6%)	0	100	100
4	CE	369/435 (85%)	357 (97%)	12 (3%)	0	100	100
5	CF	153/160 (96%)	150 (98%)	3 (2%)	0	100	100
6	CH	213/282 (76%)	208 (98%)	5 (2%)	0	100	100
7	CI	417/443 (94%)	406 (97%)	11 (3%)	0	100	100
8	CJ	776/817 (95%)	748 (96%)	27 (4%)	1 (0%)	48	79
9	CK	173/326 (53%)	170 (98%)	3 (2%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	CL	81/87 (93%)	78 (96%)	3 (4%)	0	100	100
11	CN	155/166 (93%)	147 (95%)	8 (5%)	0	100	100
12	CO	358/429 (83%)	341 (95%)	17 (5%)	0	100	100
13	CP	178/188 (95%)	168 (94%)	10 (6%)	0	100	100
14	CQ	245/307 (80%)	239 (98%)	6 (2%)	0	100	100
15	CR	118/320 (37%)	110 (93%)	8 (7%)	0	100	100
16	CS	97/244 (40%)	88 (91%)	9 (9%)	0	100	100
17	CU	31/193 (16%)	30 (97%)	1 (3%)	0	100	100
18	Ca	497/602 (83%)	486 (98%)	11 (2%)	0	100	100
19	Cb	145/325 (45%)	141 (97%)	4 (3%)	0	100	100
20	Cd	203/440 (46%)	199 (98%)	4 (2%)	0	100	100
21	Cg	485/498 (97%)	472 (97%)	13 (3%)	0	100	100
22	Ci	163/181 (90%)	157 (96%)	6 (4%)	0	100	100
23	Cj	224/257 (87%)	220 (98%)	4 (2%)	0	100	100
24	Ck	667/874 (76%)	650 (98%)	17 (2%)	0	100	100
25	Cm	29/215 (14%)	29 (100%)	0	0	100	100
26	Cn	47/250 (19%)	47 (100%)	0	0	100	100
27	Cp	166/187 (89%)	163 (98%)	3 (2%)	0	100	100
28	DB	1102/1181 (93%)	1061 (96%)	41 (4%)	0	100	100
29	DC	1093/1165 (94%)	1049 (96%)	44 (4%)	0	100	100
30	DD	760/812 (94%)	733 (96%)	27 (4%)	0	100	100
31	DE	620/747 (83%)	600 (97%)	20 (3%)	0	100	100
32	DF	592/666 (89%)	567 (96%)	25 (4%)	0	100	100
33	DG	549/631 (87%)	533 (97%)	16 (3%)	0	100	100
34	DH	566/581 (97%)	549 (97%)	17 (3%)	0	100	100
35	DI	388/407 (95%)	378 (97%)	10 (3%)	0	100	100
36	DJ	354/396 (89%)	341 (96%)	13 (4%)	0	100	100
37	DK	258/324 (80%)	247 (96%)	11 (4%)	0	100	100
38	DL	228/307 (74%)	226 (99%)	2 (1%)	0	100	100
39	DO	192/282 (68%)	188 (98%)	4 (2%)	0	100	100
40	DP	208/274 (76%)	201 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	DR	248/270 (92%)	239 (96%)	9 (4%)	0	100	100
42	DT	237/247 (96%)	232 (98%)	5 (2%)	0	100	100
43	DU	215/228 (94%)	209 (97%)	6 (3%)	0	100	100
44	DV	158/183 (86%)	149 (94%)	9 (6%)	0	100	100
45	DW	134/179 (75%)	132 (98%)	2 (2%)	0	100	100
46	DX	127/169 (75%)	117 (92%)	10 (8%)	0	100	100
47	DY	152/163 (93%)	144 (95%)	8 (5%)	0	100	100
48	DZ	26/94 (28%)	24 (92%)	2 (8%)	0	100	100
49	Da	34/64 (53%)	33 (97%)	1 (3%)	0	100	100
50	F2	882/1024 (86%)	866 (98%)	16 (2%)	0	100	100
51	F3	907/966 (94%)	877 (97%)	30 (3%)	0	100	100
52	F5	614/754 (81%)	600 (98%)	14 (2%)	0	100	100
53	F6	514/676 (76%)	507 (99%)	7 (1%)	0	100	100
54	F7	646/679 (95%)	614 (95%)	32 (5%)	0	100	100
55	F9	536/607 (88%)	523 (98%)	13 (2%)	0	100	100
56	FM	325/370 (88%)	316 (97%)	9 (3%)	0	100	100
56	FN	318/370 (86%)	309 (97%)	9 (3%)	0	100	100
57	FO	324/334 (97%)	312 (96%)	12 (4%)	0	100	100
58	FP	346/349 (99%)	335 (97%)	11 (3%)	0	100	100
59	FW	234/263 (89%)	229 (98%)	5 (2%)	0	100	100
60	FX	218/239 (91%)	212 (97%)	6 (3%)	0	100	100
61	FZ	158/178 (89%)	153 (97%)	5 (3%)	0	100	100
62	Fb	123/151 (82%)	117 (95%)	6 (5%)	0	100	100
63	Fc	81/148 (55%)	79 (98%)	2 (2%)	0	100	100
64	Fd	91/143 (64%)	89 (98%)	2 (2%)	0	100	100
65	Ff	619/848 (73%)	587 (95%)	32 (5%)	0	100	100
66	Fg	514/550 (94%)	493 (96%)	21 (4%)	0	100	100
67	Fh	233/318 (73%)	226 (97%)	7 (3%)	0	100	100
68	Fi	465/629 (74%)	447 (96%)	18 (4%)	0	100	100
69	IA	700/787 (89%)	678 (97%)	22 (3%)	0	100	100
70	IB	487/803 (61%)	466 (96%)	19 (4%)	2 (0%)	30	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
73	UD	11/13 (85%)	11 (100%)	0	0	100	100
75	UG	13/15 (87%)	10 (77%)	3 (23%)	0	100	100
All	All	23662/28884 (82%)	22880 (97%)	779 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
70	IB	429	PRO
70	IB	783	PRO
8	CJ	540	PRO

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	
3	CC	73/73 (100%)	73 (100%)	0	100	100
4	CE	314/372 (84%)	306 (98%)	8 (2%)	42	66
5	CF	139/144 (96%)	131 (94%)	8 (6%)	17	46
6	CH	192/246 (78%)	190 (99%)	2 (1%)	73	85
7	CI	354/371 (95%)	348 (98%)	6 (2%)	56	75
8	CJ	691/723 (96%)	671 (97%)	20 (3%)	37	63
9	CK	150/283 (53%)	146 (97%)	4 (3%)	40	65
10	CL	75/79 (95%)	70 (93%)	5 (7%)	13	41
11	CN	142/150 (95%)	142 (100%)	0	100	100
12	CO	316/377 (84%)	312 (99%)	4 (1%)	65	81
13	CP	160/168 (95%)	158 (99%)	2 (1%)	65	81
14	CQ	216/270 (80%)	208 (96%)	8 (4%)	29	58
15	CR	111/279 (40%)	104 (94%)	7 (6%)	15	44
16	CS	90/220 (41%)	89 (99%)	1 (1%)	70	83
17	CU	31/169 (18%)	29 (94%)	2 (6%)	14	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	Ca	440/543 (81%)	433 (98%)	7 (2%)	58	76
19	Cb	128/277 (46%)	123 (96%)	5 (4%)	27	57
20	Cd	186/381 (49%)	181 (97%)	5 (3%)	40	65
21	Cg	429/437 (98%)	420 (98%)	9 (2%)	48	71
22	Ci	144/160 (90%)	139 (96%)	5 (4%)	31	60
23	Cj	193/219 (88%)	187 (97%)	6 (3%)	35	62
24	Ck	583/746 (78%)	568 (97%)	15 (3%)	41	65
25	Cm	26/184 (14%)	25 (96%)	1 (4%)	28	57
26	Cn	43/210 (20%)	42 (98%)	1 (2%)	45	68
27	Cp	157/175 (90%)	156 (99%)	1 (1%)	84	92
28	DB	972/1030 (94%)	936 (96%)	36 (4%)	29	58
29	DC	929/985 (94%)	907 (98%)	22 (2%)	44	67
30	DD	673/673 (100%)	661 (98%)	12 (2%)	54	74
31	DE	552/642 (86%)	536 (97%)	16 (3%)	37	63
32	DF	504/560 (90%)	496 (98%)	8 (2%)	58	76
33	DG	483/543 (89%)	470 (97%)	13 (3%)	40	65
34	DH	496/504 (98%)	481 (97%)	15 (3%)	36	63
35	DI	350/365 (96%)	344 (98%)	6 (2%)	56	75
36	DJ	312/347 (90%)	304 (97%)	8 (3%)	41	65
37	DK	218/261 (84%)	214 (98%)	4 (2%)	54	74
38	DL	199/263 (76%)	193 (97%)	6 (3%)	36	63
39	DO	163/229 (71%)	160 (98%)	3 (2%)	54	74
40	DP	189/239 (79%)	187 (99%)	2 (1%)	70	83
41	DR	221/235 (94%)	218 (99%)	3 (1%)	62	79
42	DT	220/228 (96%)	214 (97%)	6 (3%)	40	65
43	DU	179/201 (89%)	176 (98%)	3 (2%)	56	75
44	DV	145/165 (88%)	141 (97%)	4 (3%)	38	64
45	DW	126/163 (77%)	123 (98%)	3 (2%)	44	67
46	DX	114/149 (76%)	111 (97%)	3 (3%)	41	65
47	DY	137/146 (94%)	135 (98%)	2 (2%)	60	78
48	DZ	23/84 (27%)	23 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
49	Da	32/59 (54%)	31 (97%)	1 (3%)	35	62
50	F2	752/867 (87%)	745 (99%)	7 (1%)	75	87
51	F3	767/809 (95%)	750 (98%)	17 (2%)	47	69
52	F5	533/642 (83%)	517 (97%)	16 (3%)	36	63
53	F6	462/590 (78%)	446 (96%)	16 (4%)	31	60
54	F7	553/577 (96%)	546 (99%)	7 (1%)	65	81
55	F9	449/503 (89%)	439 (98%)	10 (2%)	47	69
56	FM	258/292 (88%)	249 (96%)	9 (4%)	31	60
56	FN	252/292 (86%)	248 (98%)	4 (2%)	58	76
57	FO	285/290 (98%)	278 (98%)	7 (2%)	42	66
58	FP	270/286 (94%)	266 (98%)	4 (2%)	60	78
59	FW	214/234 (92%)	213 (100%)	1 (0%)	86	93
60	FX	178/195 (91%)	177 (99%)	1 (1%)	84	92
61	FZ	140/156 (90%)	133 (95%)	7 (5%)	20	49
62	Fb	113/135 (84%)	111 (98%)	2 (2%)	54	74
63	Fc	77/127 (61%)	74 (96%)	3 (4%)	27	57
64	Fd	77/119 (65%)	75 (97%)	2 (3%)	41	65
65	Ff	524/715 (73%)	509 (97%)	15 (3%)	37	63
66	Fg	446/469 (95%)	439 (98%)	7 (2%)	58	76
67	Fh	189/281 (67%)	181 (96%)	8 (4%)	25	54
68	Fi	413/536 (77%)	403 (98%)	10 (2%)	44	67
69	IA	590/661 (89%)	566 (96%)	24 (4%)	26	55
70	IB	393/675 (58%)	386 (98%)	7 (2%)	54	74
All	All	20555/24778 (83%)	20063 (98%)	492 (2%)	45	67

5 of 492 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	DG	186	ARG
67	Fh	58	ARG
42	DT	52	ARG
66	Fg	33	CYS
69	IA	460	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 421 such sidechains are listed below:

Mol	Chain	Res	Type
40	DP	116	HIS
51	F3	432	GLN
69	IA	40	GLN
41	DR	62	HIS
46	DX	130	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CA	494/621 (79%)	188 (38%)	5 (1%)
2	CB	2/3 (66%)	2 (100%)	0
All	All	496/624 (79%)	190 (38%)	5 (1%)

5 of 190 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CA	3	A
1	CA	5	U
1	CA	6	U
1	CA	7	A
1	CA	8	U

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	CA	151	U
1	CA	169	A
1	CA	349	U
1	CA	465	U
1	CA	566	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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
85	PM8	Fc	201	63	25,31,31	0.20	0	30,38,38	0.46	0
84	PO4	IA	1001	82	4,4,4	0.94	0	6,6,6	0.46	0
88	GDP	IA	1000	82	24,30,30	0.95	1 (4%)	30,47,47	1.35	4 (13%)
87	FDA	Ff	901	-	52,58,58	0.74	2 (3%)	60,89,89	0.75	3 (5%)
83	ATP	Cg	1000	82	26,33,33	0.60	0	31,52,52	0.76	1 (3%)
84	PO4	FW	301	-	4,4,4	0.97	0	6,6,6	0.41	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
83	ATP	Cg	1000	82	-	2/18/38/38	0/3/3/3
85	PM8	Fc	201	63	-	7/36/38/38	-
88	GDP	IA	1000	82	-	0/12/32/32	0/3/3/3
87	FDA	Ff	901	-	-	12/30/50/50	0/6/6/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
87	Ff	901	FDA	C10-N1	-2.70	1.32	1.37
87	Ff	901	FDA	C4X-N5	-2.68	1.30	1.35
88	IA	1000	GDP	C6-N1	-2.41	1.34	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
88	IA	1000	GDP	PA-O3A-PB	-3.78	119.86	132.83
88	IA	1000	GDP	C3'-C2'-C1'	3.32	105.97	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	Ff	901	FDA	P-O3P-PA	-2.83	123.12	132.83
87	Ff	901	FDA	N3-C2-N1	2.35	119.57	115.80
83	Cg	1000	ATP	C5-C6-N6	2.31	123.86	120.35

There are no chirality outliers.

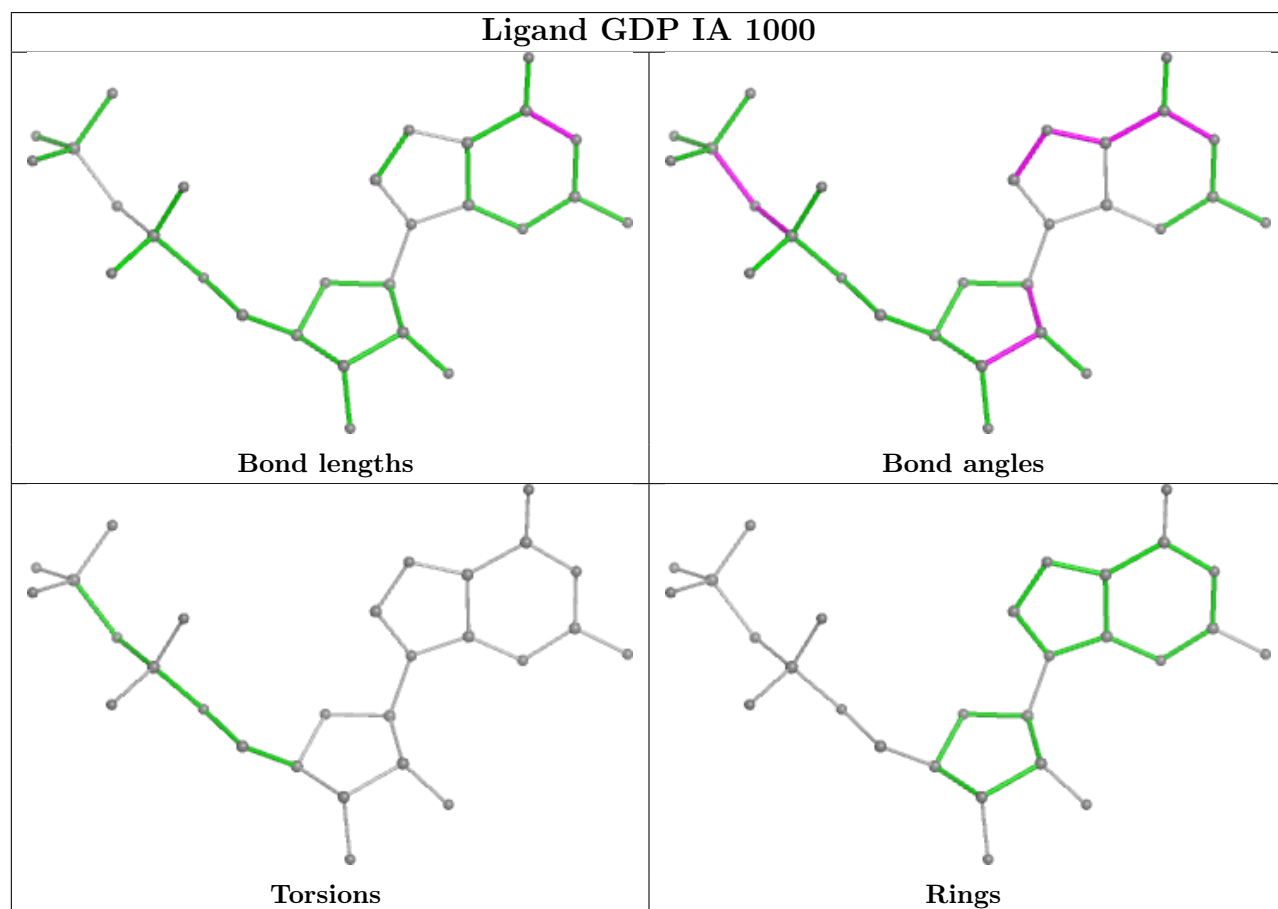
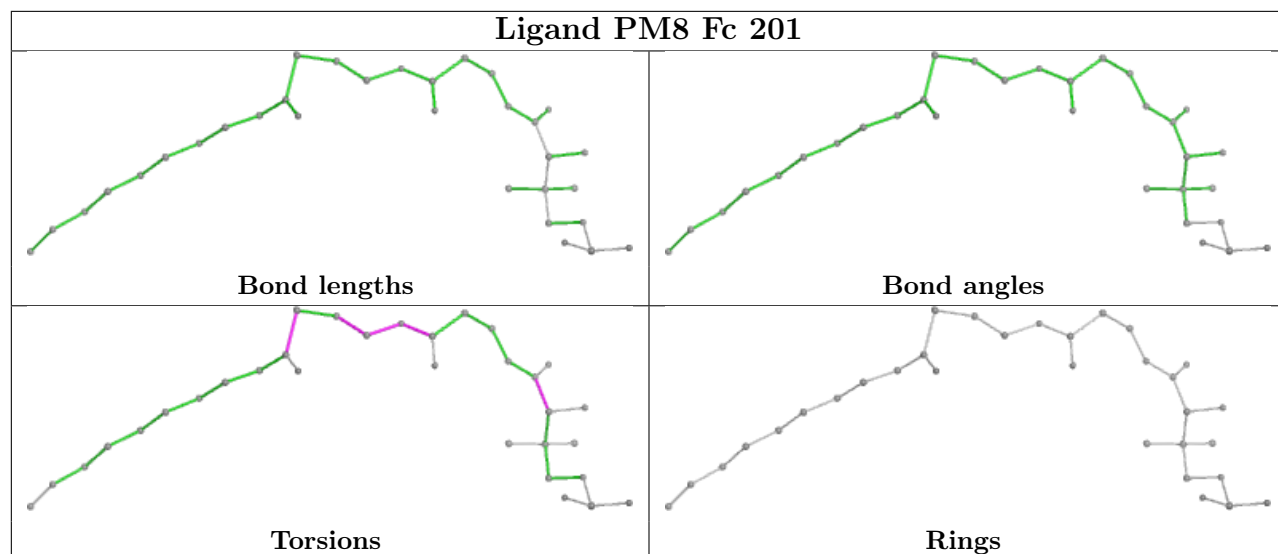
5 of 21 torsion outliers are listed below:

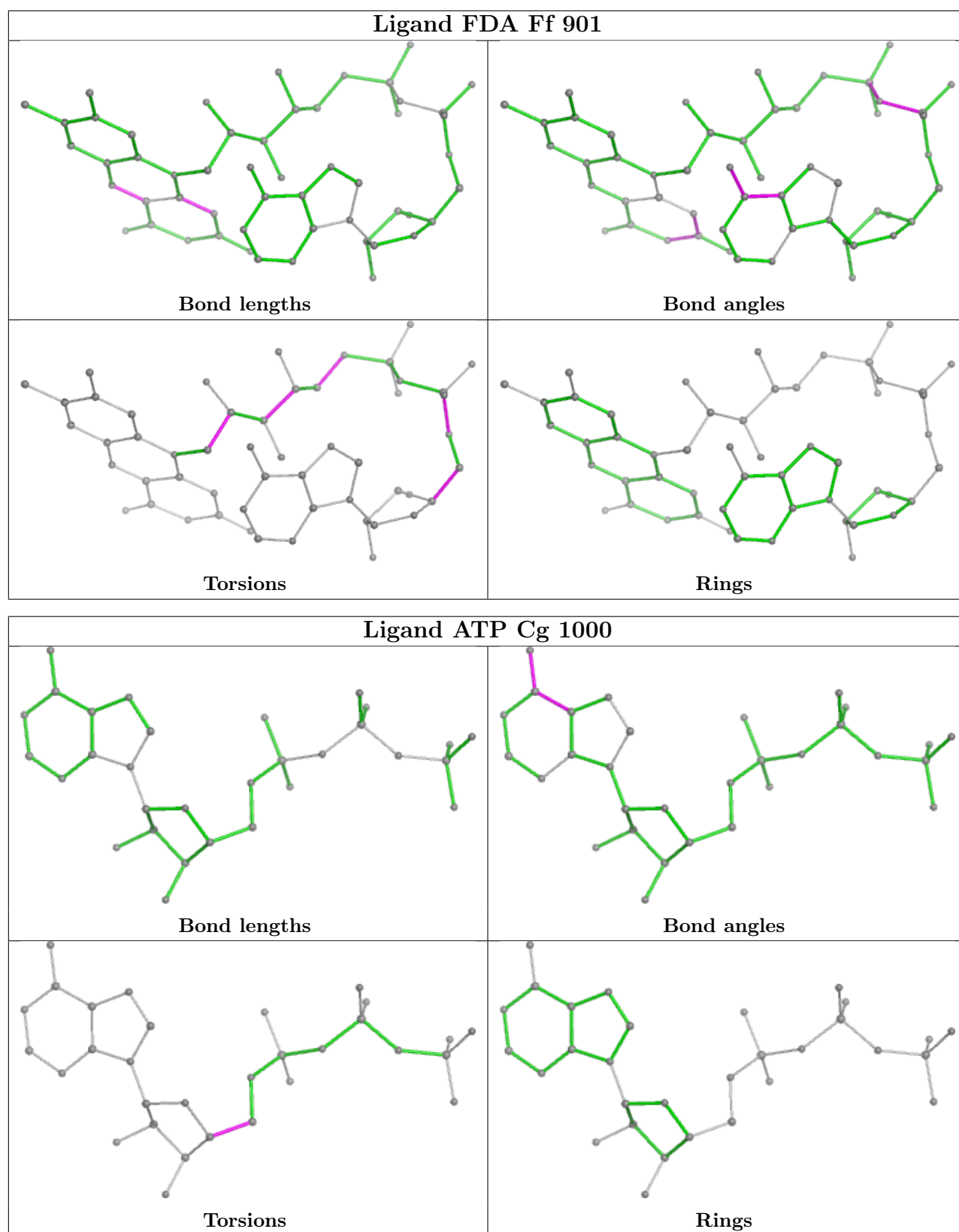
Mol	Chain	Res	Type	Atoms
83	Cg	1000	ATP	O4'-C4'-C5'-O5'
85	Fc	201	PM8	O1-C1-S1-C43
85	Fc	201	PM8	C2-C1-S1-C43
87	Ff	901	FDA	C5B-O5B-PA-O1A
87	Ff	901	FDA	C5B-O5B-PA-O2A

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.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

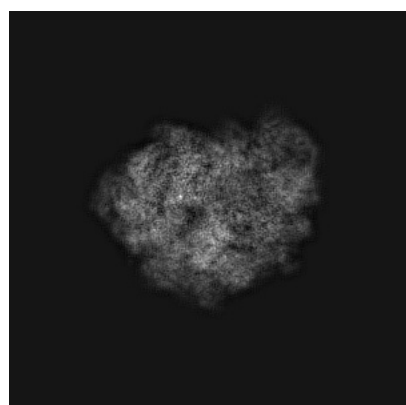
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13660. These allow visual inspection of the internal detail of the map and identification of artifacts.

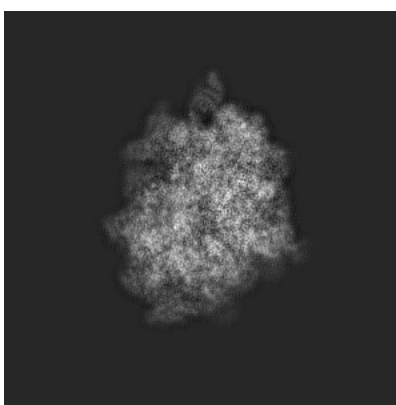
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

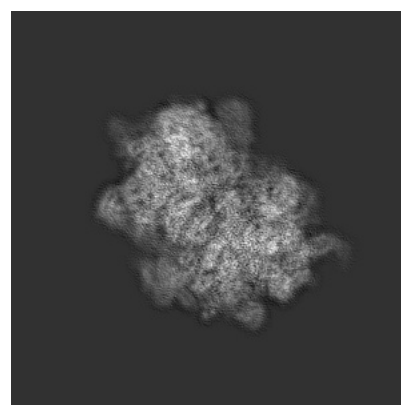
6.1.1 Primary map



X



Y

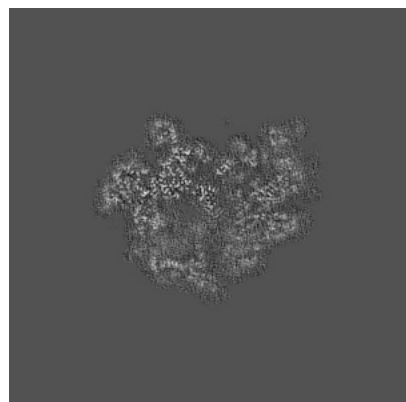


Z

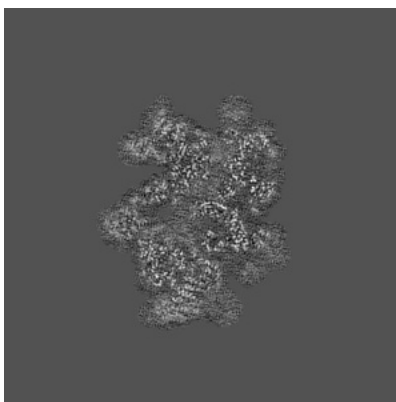
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

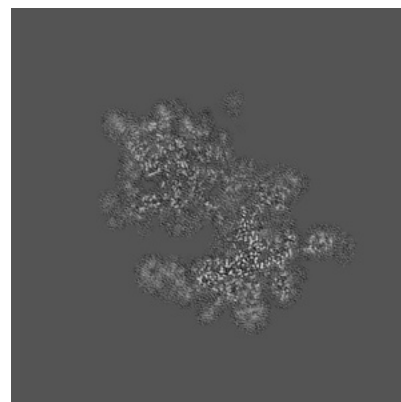
6.2.1 Primary map



X Index: 180



Y Index: 180

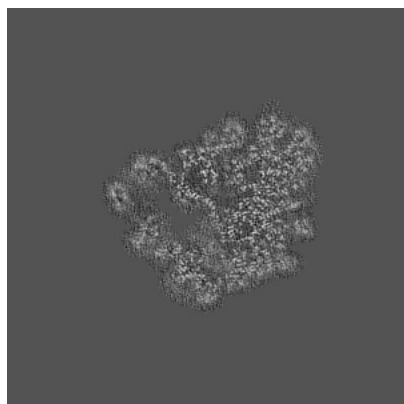


Z Index: 180

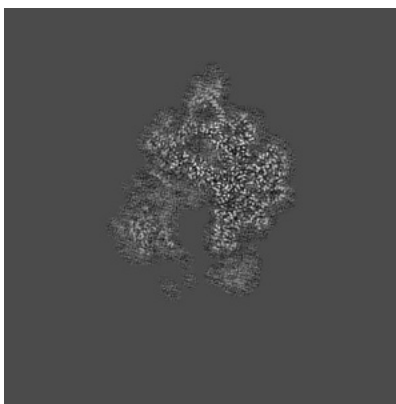
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

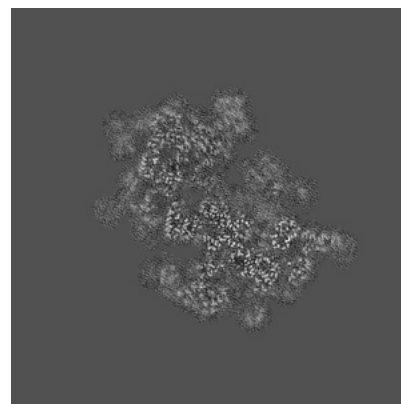
6.3.1 Primary map



X Index: 157



Y Index: 154

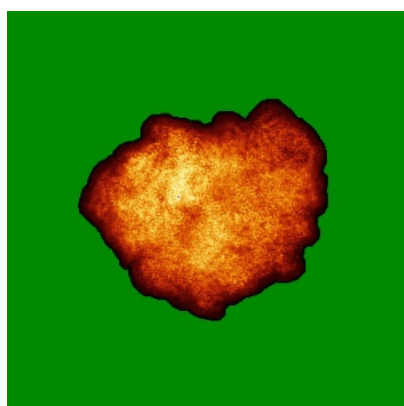


Z Index: 192

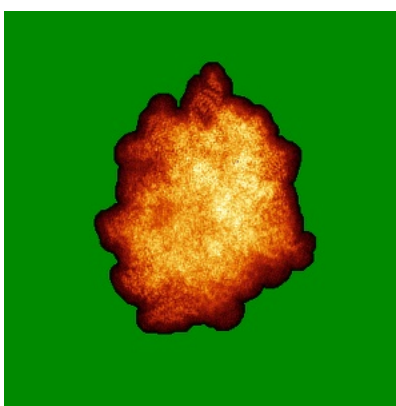
The images above show the largest variance slices of the map in three orthogonal directions.

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

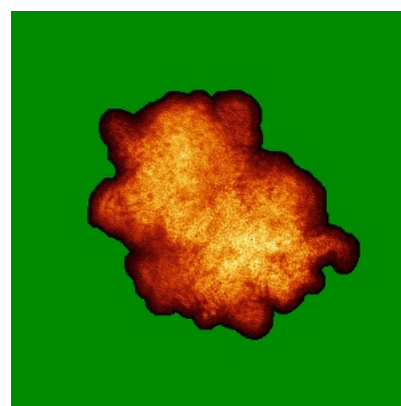
6.4.1 Primary map



X



Y

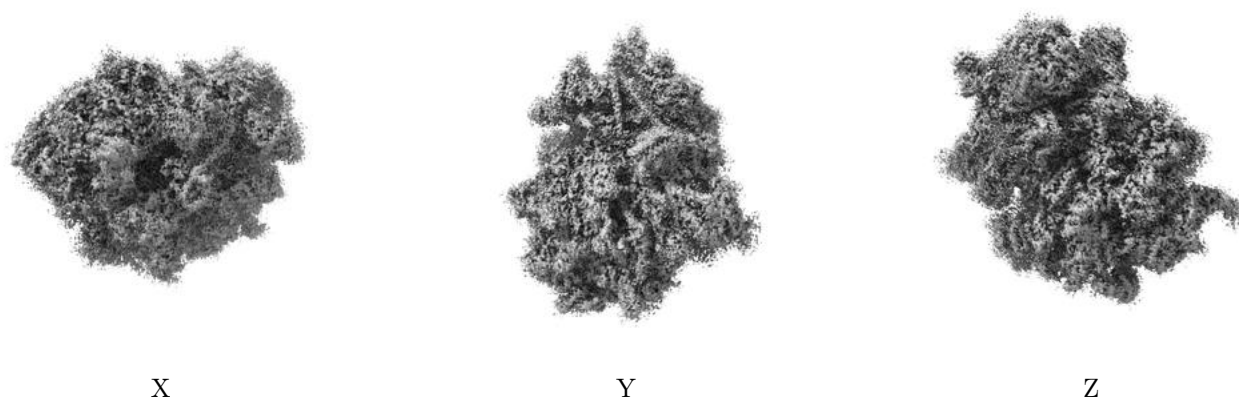


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

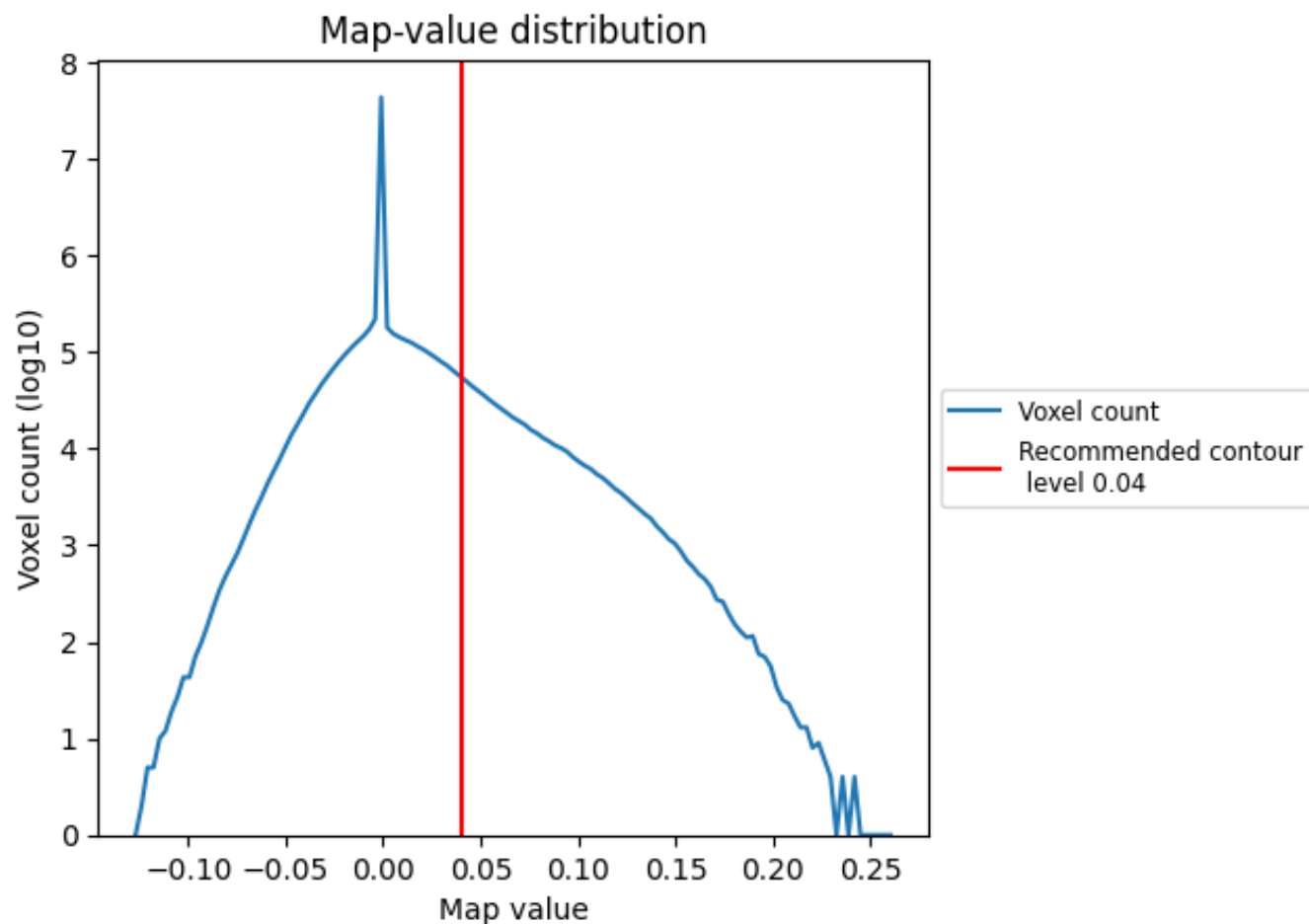
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

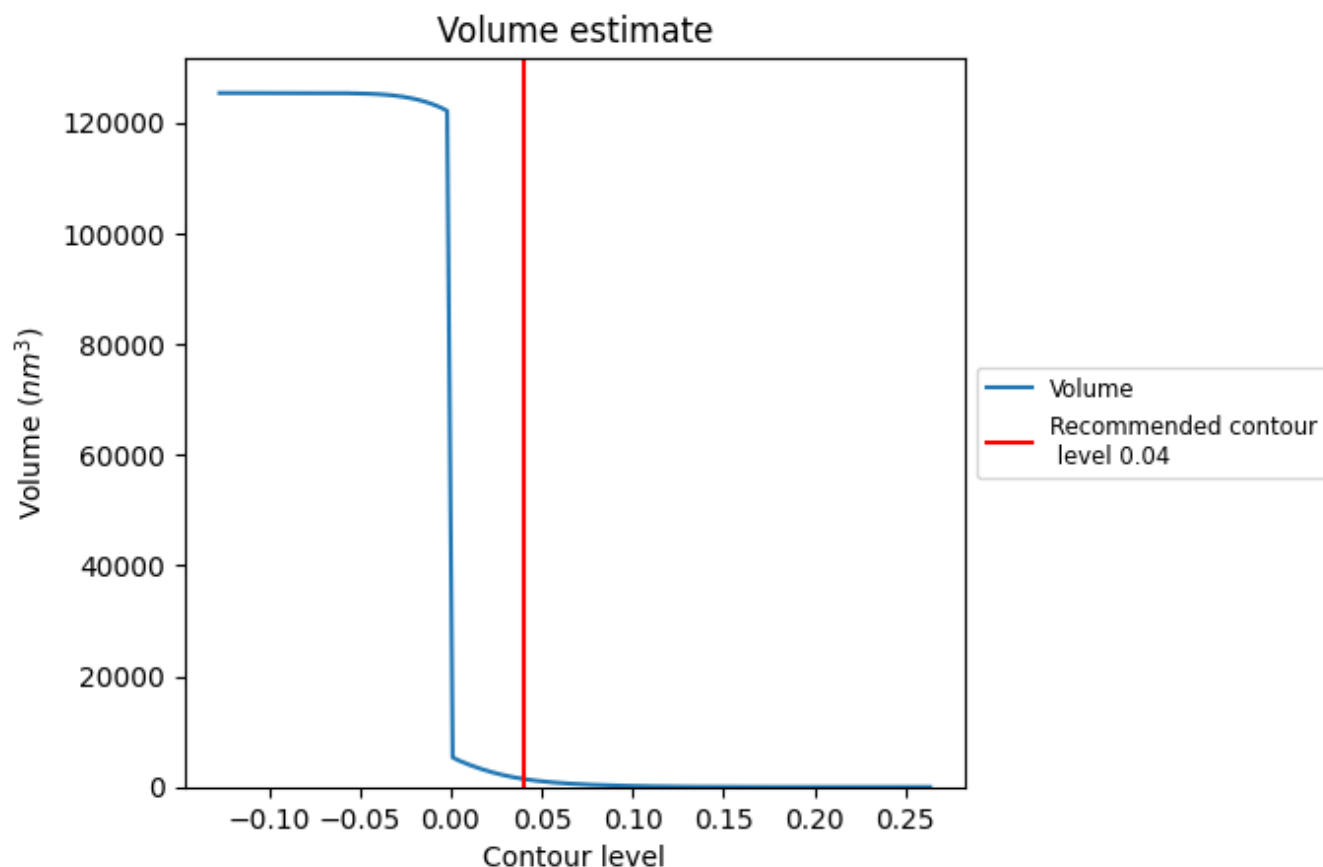
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

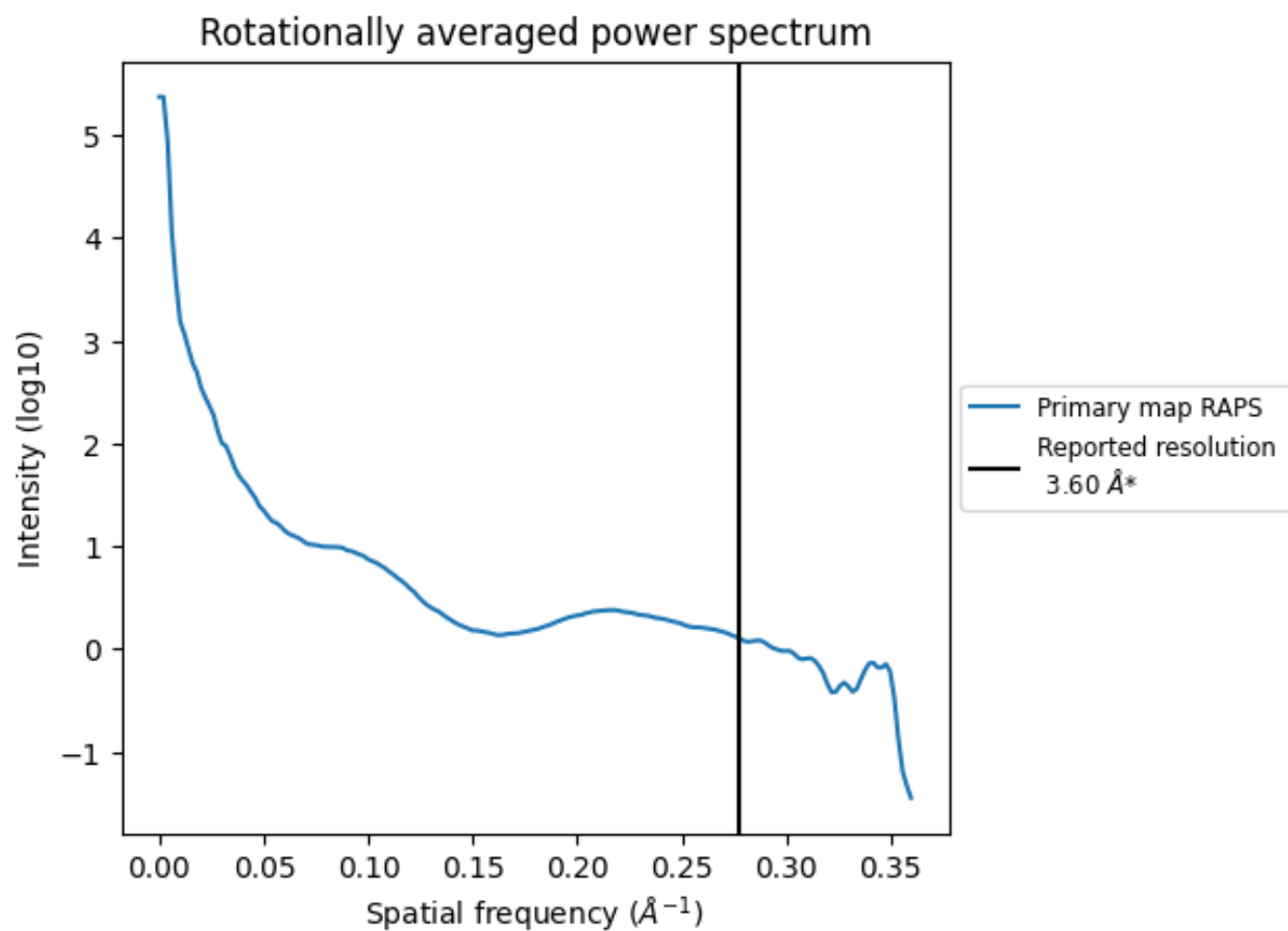
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1447 nm^3 ; this corresponds to an approximate mass of 1307 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 0.278 Å⁻¹

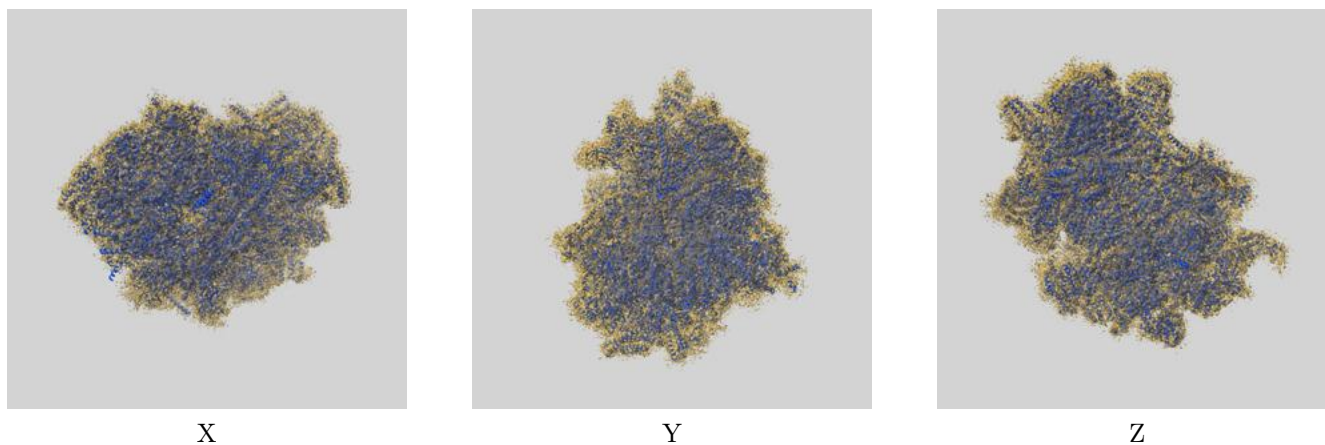
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

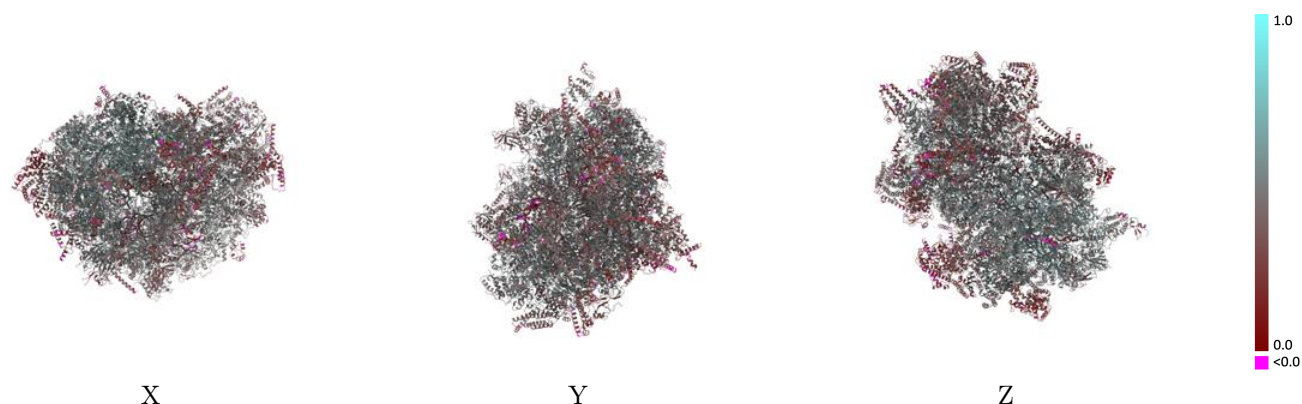
This section contains information regarding the fit between EMDB map EMD-13660 and PDB model 7PUA. Per-residue inclusion information can be found in section [3](#) on page [28](#).

9.1 Map-model overlay [i](#)



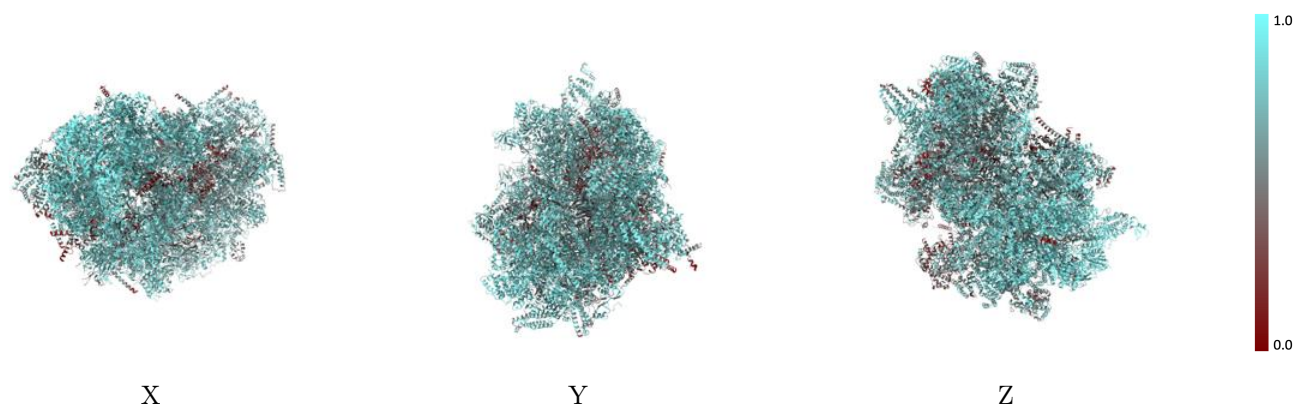
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



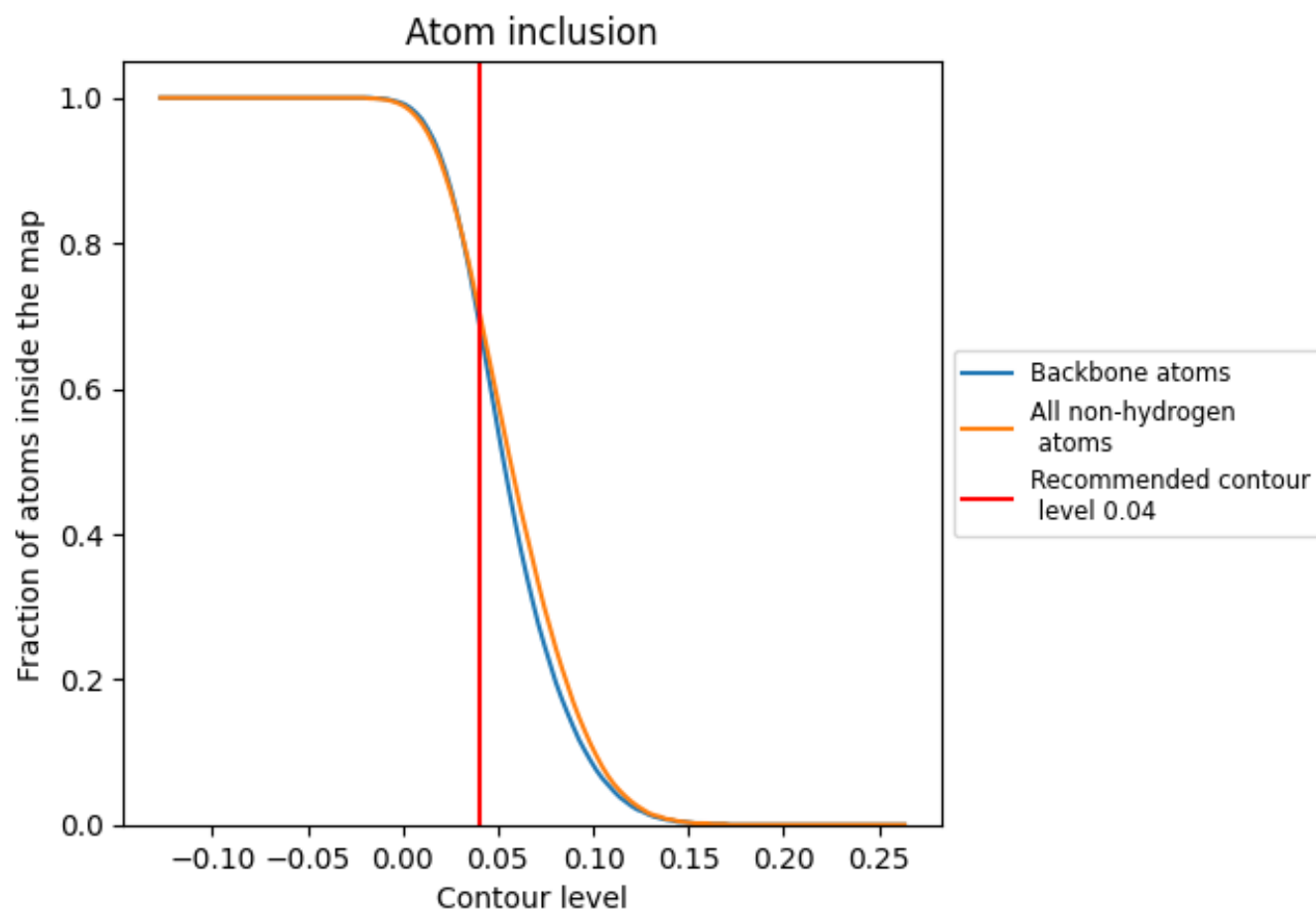
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 71% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7100	 0.4360
CA	 0.6750	 0.3930
CB	 0.7660	 0.5060
CC	 0.5800	 0.4770
CE	 0.7400	 0.4900
CF	 0.6810	 0.3790
CH	 0.7930	 0.5280
CI	 0.7290	 0.4640
CJ	 0.7620	 0.4680
CK	 0.7270	 0.4190
CL	 0.6900	 0.4860
CN	 0.7470	 0.4770
CO	 0.7800	 0.4940
CP	 0.8410	 0.5340
CQ	 0.8140	 0.5310
CR	 0.4710	 0.2810
CS	 0.6920	 0.4050
CU	 0.1400	 0.2270
Ca	 0.7750	 0.4990
Cb	 0.5580	 0.3210
Cd	 0.7460	 0.4670
Cg	 0.8240	 0.4850
Ci	 0.7470	 0.4780
Cj	 0.8650	 0.5050
Ck	 0.7320	 0.4280
Cm	 0.0530	 0.2130
Cn	 0.4860	 0.3440
Cp	 0.8160	 0.4790
DB	 0.7600	 0.4710
DC	 0.6870	 0.3600
DD	 0.8490	 0.5190
DE	 0.7060	 0.4070
DF	 0.7510	 0.4320
DG	 0.7460	 0.4180
DH	 0.6910	 0.4450



















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Chain	Atom inclusion	Q-score
DI	 0.8250	 0.4890
DJ	 0.6850	 0.4120
DK	 0.6660	 0.4120
DL	 0.6510	 0.4720
DO	 0.7120	 0.3850
DP	 0.8560	 0.4490
DR	 0.8660	 0.5010
DT	 0.6990	 0.4590
DU	 0.7470	 0.4740
DV	 0.7800	 0.4910
DW	 0.7600	 0.4650
DX	 0.7890	 0.4570
DY	 0.7750	 0.4850
DZ	 0.6840	 0.4660
Da	 0.7880	 0.5410
F2	 0.8020	 0.4910
F3	 0.7150	 0.4020
F5	 0.5900	 0.3510
F6	 0.4590	 0.2390
F7	 0.7810	 0.4650
F9	 0.6810	 0.4310
FM	 0.7480	 0.4610
FN	 0.6640	 0.3450
FO	 0.8140	 0.4930
FP	 0.8140	 0.4800
FW	 0.8240	 0.4960
FX	 0.8310	 0.4700
FZ	 0.4680	 0.3690
Fb	 0.7530	 0.4010
Fc	 0.7080	 0.3510
Fd	 0.1810	 0.3420
Ff	 0.7490	 0.4420
Fg	 0.7710	 0.4280
Fh	 0.3060	 0.3430
Fi	 0.6850	 0.4200
IA	 0.7420	 0.4340
IB	 0.6230	 0.4120
U8	 0.3930	 0.4110
UC	 0.8440	 0.4780
UD	 0.7080	 0.3490
UF	 0.6110	 0.2410
UG	 0.8530	 0.3110

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Chain	Atom inclusion	Q-score
UI	 0.8000	 0.4160
UK	 0.0750	 0.0870
UM	 0.8000	 0.4530
UN	 0.7000	 0.3720
UP	 0.6000	 0.4030
UQ	 0.7000	 0.3670
Ua	 0.7400	 0.2550
Ug	 0.5460	 0.2760